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Shade-Inducible Gene Expression Change in *Arabidopsis thaliana* at Different Temperatures

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Abstract

We tested whether the plant response to an environmental factor could be affected by the context of another factor by using shade avoidance response at different temperatures. Depleting the red light (R; λ_{max} = 660 nm) and/or enriching the far-red light (FR; λ_{max} = 730 nm) results in a low R:FR ratio in the environment, which induces shade avoidance response such as elongation of petioles and reduction of plant pigments. On the other hand, warmer environmental temperature is known to mimic shade avoidance response under normal light condition, suggesting a potential crosstalk between the temperature and the light quality signals. Therefore, we investigated the patterns of gene expression responses to low R:FR ratio in different temperature contexts (22˚C and 26˚C) through microarray analyses. Similar, yet distinct patterns between the two responses were implicated by the levels of correlation in the commonly affected MapMan bins. However, the induction levels of typical shade genes such as *ATHB*2, *IAA*29, *IAA*19, *HFR*1, *YUC*8, and *FT* were very similar at both temperatures. Moreover, petiole length, chlorophylls, carotenoids, and anthocyanins contents did not support any statistically significant interaction between the light quality and the high temperature responses despite the obvious independent effect of each signal, which suggests cumulative effects of two independent responses. Nevertheless, other types of low R: FR-responsive genes with differential expression patterns at different temperatures were identified. They are overrepresented in secondary metabolism, lipid transport, oxidative stress, jasmonic acid, ethylene, light, pathogen defense responses, and extracellular region.

Keywords

Shade Avoidance, Temperature, Microarray, Crosstalk, Gene Expression

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1. Introduction

Plant development is greatly affected by environmental factors such as light, temperature, and water. Those factors are not only important physiological components to support normal growth of a plant, but are also important signals for making decisions to turn on/off certain pathways and responses. Therefore, many studies so far have produced significant amount of information on the regulatory roles of those factors during plant development. Among those factors, light is an important factor that affects not only photosynthesis but also various stages of plant development from seed germination to morphogenesis and to flowering. All those aspects of plant development are regulated by light intensity, quality, and directionality. Light quality that can be measured by the ratio of red (R; λ_{max} = 660 nm) to far-red (FR; λ_{max} = 730 nm) light irradiances is an indirect measure of plant population density in surrounding area [1]. Low R:FR ratio in the environment indicates that there is less red light available for photosynthesis due to its consumption through the photosynthesis of neighboring plants and to the reflection of far-red light which is not absorbed by those plants nearby. Under this condition plants exhibit a set of reactions called shade avoidance response including elongational growth, reduction of pigments levels, and accelerated flowering [2].

The change in R:FR ratio is sensed by the photoreceptor phytochromes. Particularly, phytochrome B (PHYB) is known to play a major role in shade avoidance response in Arabidopsis [3]. Phytochrome-interacting basic Helix-Loop-Helix (bHLH) transcription factors, PIF4, PIF5, and PIF7 (PHYTOCHROME INTERACTING FACTOR), which are normally repressed through the interaction with the light-activated PHYB, accumulate in the nucleus under low R:FR condition and activate a set of gene expression that lead to shade avoidance response [4] [5]. On the other hand, shade promotes the expression of negative regulators, PAR1, PAR2 (PHYTOCHROME RAPIDLY REGULATED), and HFR1 (LONG HYPOCOTYL IN FAR-RED LIGHT), which bind to PIF4 and PIF5 to inhibit their DNA binding. This in turn suppresses the shade avoidance response [6]-[10]. HFR1 is degraded through COP1 (CONSTITUTIVELY PHOTOMORPHOGENIC1) and SPA (SUPPRESSOR OF PHYA-105) mediated ubiquitination in response to low R:FR light [11] [12]. Furthermore, shade avoidance response involves phytohormone signals such as auxin, brassinosteroids and gibberellins [13] [14], forming a complicated signaling network.

On the other hand, it is known that warmer environmental temperature mimics shade avoidance response such as elongational growth under non-shade condition [15] [16], suggesting a potential crosstalk between the temperature and the light quality signals. Although it is not clear how the non-stressful ambient temperature is perceived by plants, several cellular components are known to mediate the signal. SPATULA, a transcription factor involved in floral organogenesis, and DELLA, a repressor of the gibberellin signaling, mediate temperature dependent growth regulation [17] [18]. PIF4 and some miRNAs regulate temperature dependent induction of flowering [19] [20]. H2A.Z-nucleosome appears to be the gate keeper of the temperature dependent expression of many genes [21].

The phenotypic similarity between the shade avoidance and warm temperature responses led to a notion of signal integration between the two. So far, one of the integration mechanisms seems to occur through the phytohormone auxin, which is required for the elongational growth during shade avoidance response as well as high temperature-induced cell elongation [15] [22]. Furthermore, the control of auxin biosynthesis and signaling by shade and high temperature is regulated by the transcription factor PIF4 and PIF7 [4] [23]-[25]. However, it is not clear how light and temperature signals interact to control the mechanism leading to this response. In order to better understand the integration process of the two signals, we compared the global gene expression patterns during the shade avoidance responses under two different temperature conditions.

2. Materials and Methods

2.1. Plant Material and Growth Conditions

Arabidopsis thaliana ecotype Columbia was used for all experiments. Surface sterilized seeds were sown on 0.8% agar plates containing full strength Murashige and Skoog salts (pH 5.7) supplemented with 1% sucrose and kept at 4˚C for 3 days for stratification. Seeds were germinated at 22˚C under cool white fluorescent light (80 μmol/m^{2}sec) and grown for 10 days under the same condition. Then plants were treated with either one of the following four conditions for 24 hours before the harvest for total RNA extraction. The four conditions were created by combining a light condition and a temperature condition: either with (W + FR) or without (WL) supplemental far-red light (740 nm LED, 6 μmol/m^{2}sec) at either 22˚C or 26˚C. Those conditions were named as

W+FR22˚C, WL22˚C, W+FR26˚C and WL26˚C. The R:FR ratio was ca. 0.6 with the far-red light supplementation and ca. 4 without the supplementation. For the phenotypic study, seven-day-old seedlings grown under the above mentioned standard condition were treated with either one of the six conditions indicated in the result for additional 7 days before the analysis.

2.2. RNA Isolation and Microarray Experiment

The whole seedlings were instantly frozen by pouring liquid nitrogen directly on the plate containing agar medium, and the areal part of the seedlings (approximately 100 mg) were collected by scraping with a pre-chilled spatula. The total RNA samples were prepared using TRI Reagent ^{TM} (SIGMA, St Louis, MO, USA) by following the manufacturer's guide. The total RNAs were treated with DNase I and purified using RNeasy Mini Spin Columns (QIAGEN, Hilden, Germany). Three independent experiments were done for three replicates. The microarray experiments were carried out using Affymetrix ATH1 gene expression array by the Heflin Center for Genomic Sciences (University of Alabama, Birmingham, AL). The raw data is available at GEO in NCBI (GSE64197).

2.3. Microarray Data Analyses

The raw data were RMA-normalized by Bioconductor *Affy* package and *MAS*5 *detection calls* (***P****resent/****M****arginal/****A****bsent*) were determined independently to select the genes with significant signal intensity. After eliminating all genes that had more than three ***A*** (Absent) calls for inconsistent signal intensity among the 12 chip data, 15,128 genes were recovered. These genes were used in MapMan analysis to identify significantly responded functional gene clusters [26]. On the other hand, these 15,128 genes were further filtered by Bioconductor LIMMA package (multiple testing adjustments, FDR < 0.05) for the statistically significant difference in gene expression levels [27] [28]. An additional *ad hoc* filtration procedure was applied for the genes that could not pass LIMMA but consistently up- or down-regulated (1.5 fold or $\log_2$ ratio = ±0.585) in all three replicates in any of the five comparisons mentioned in the results. Genes that passed any of those two filtration methods were pooled and used for hierarchical clustering (*Cluster*, v. 3.0, centered Pearson correlation, average linkage method) [29] [30]. The clusters were visualized by using TreeView (v. 1.60) [30], and the enriched GO (Gene Ontology) terms were found by using a web-based program, Functional Annotation Tool with *medium* classification stringency (DAVID Bioinformatics Resources 6.7, NIAID/NIH) [31].

2.4. Pigment Extraction and Petiole Length Analysis

Chlorophylls and carotenoids were extracted by grinding 100 mg of the areal part of plants in cold 80% acetone with a mortar and a pestle. After 1 hour of incubation on ice in a dark place, the debris was pelleted by centrifugation. The absorbance (wavelength at 663.2 nm, 646.8 nm and 470 nm) of the supernatant was measured by using a spectrophotometer, and the data was analyzed as described previously [32]: Chlorophyll $\boldsymbol{a} = (12.25 \times A_{663.2}) - (2.79 \times A_{646.8})$; Chlorophyll $\boldsymbol{b} = (21.5 \times A_{646.8}) - (5.1 \times A_{663.2})$; Carotenoids $= \{(1000 \times A_{470}) - (1.82 \times \mathrm{Chl.}\boldsymbol{a}) - (85.02 \times \mathrm{Chl.}\boldsymbol{b})\}/198$. The resulting concentrations were shown as μg/10 mg plant fresh weight. The relative amount of pigment level was shown as the percentage (%) of the amount of Chlorophyll ***a*** from the samples grown at 22˚C under white light (WL) condition.

Anthocyanin was extracted by grinding 100 mg of the areal part of plants in 1% HCl in methanol. After 1 hour of incubation on ice in a dark place, the debris was pelleted by centrifugation. The absorbance (wavelength at 530 nm and 657 nm) of the supernatant was measured by using a spectrophotometer, and the data was analyzed as described previously [33]: Anthocyanin $= A_{530} - (0.25 \times A_{657})$. The resulting concentrations were shown with arbitrary unit per 100 mg plant fresh weight. The relative amount of anthocyanin level was shown as the percentage (%) of the amount of anthocyanin from the samples grown at 22˚C under white light condition.

For the petiole length analysis, the longest petiole of each plant was collected and photographed. The lengths of petioles in the digital images were determined by using NIH Image J program [34].

3. Results

3.1. The Microarray Experiments

To compare shade avoidance responses under different temperature contexts, we carried out a microarray gene expression study. Treatment conditions were generated by combining a temperature (22˚C or 26˚C) and a light condition (high or low R:FR ratio). The light environment with low R:FR ratio was produced by supplemental far-red LED lights (W+FR) in addition to regular white lights (WL). The combinations of them resulted in four different conditions (WL22˚C, W+FR22˚C, WL26˚C, and W+FR26˚C; **Figure 1**). In addition to the standard temperature (22˚C) for Arabidopsis, a higher but relatively mild temperature of 26˚C was used in order to minimize any heat-related stress responses. After eliminating all genes that had more than three *Absent* calls (MAS5 detection calls) among the 12 chips data (three replicates per condition), 15,128 genes were recovered. Unlike traditional microarray analyses in which only two different conditions are compared (control vs. treatment) several different comparisons of expression data are possible with four different experimental conditions (**Figure 1**). Each comparison was named as treatment "***effect***", and a specific number is given such as "**W+FR effect at 22˚C**", (comparison <1>; W+FR22˚C vs. WL22˚C). Likewise, other four "***effects***" were named as "**W+FR effect at 26˚C**" (comparison <2>; W+FR26˚C vs. WL26˚C), "**high temperature (26˚C) effect under WL**" (comparison <3>; WL26˚C vs. WL22˚C), "**high temperature (26˚C) effect under W+FR**" (comparison <4>; W+FR26˚C vs. W+FR22˚C), and "**combined effect of both W+FR and high temperature (26˚C)**" (comparison <5>; W+FR26˚C vs. WL22˚C). The scatter plots of average signal intensity of three replicates support the general assumption in microarray experiments that most genes do not show any significant difference in their expression levels in response to any treatments (**Supplement Figure S1**).

In all five treatment effects, there are not many genes that exhibited two fold (average log$_2$Ratio = ±1) or higher expression change. Even when the cut-off value was set to 1.414 fold (average log$_2$Ratio = ±0.5) or higher, the percentages of differentially expressed genes were as low as 0.72% (109 genes for <2> W+FR effect at 26˚C) and at most 2.01% (304 genes for <5> W+FR+26˚C effect) of 15,128 genes (**Supplement Figure S2**). This result suggests that our conditions were mild enough and did not overload the plants with dramatic or saturated levels of stimuli that lead to a ceiling effect which can be a problem when expecting potential additive effects. Although the RT-PCR results for several selected genes across different treatment effects confirmed the microarray data, the absolute values of the average log$_2$Ratio from the microarray experiments were slightly lower than those of the RT-PCR results in general (microarray:RT-PCR = 0.85:1; **Supplement Figure S3**). Therefore, we do not rule out the possibility of reduced technical sensitivity of detection for the gene expression change, while it is not likely to affect the result of our study that tested overall tendency of the responses.

3.2. Overview of Gene Expression Patterns in Different Environmental Contexts

In order to obtain a bird's eye view on the five different treatment "***effects***" mentioned above (**Figure 1**; <1> ~ <5>), we carried out pair wise comparisons among those "***effects***" using scatter plots (**Figure 2**). In general, the W+FR (low R:FR) effects at 22˚C and at 26˚C (<2> vs. <1>) exhibited limited levels of correlation with somewhat less prominent gene expression change at 26˚C than the one at 22˚C (**Figure 2(a)**). On the other hand, the high temperature (26˚C) ***effects*** under the two different light conditions (<4> vs. <3>) are relatively similar to each other (**Figure 2(b)**). These data suggest that the overall pattern of gene expression change in response to low R:FR is dependent on the ambient temperature, whereas response to high temperature (26˚C) treatment is relatively less affected by the ambient R:FR light ratio. Note that the levels of correlation in these comparisons

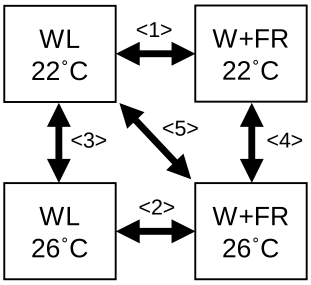
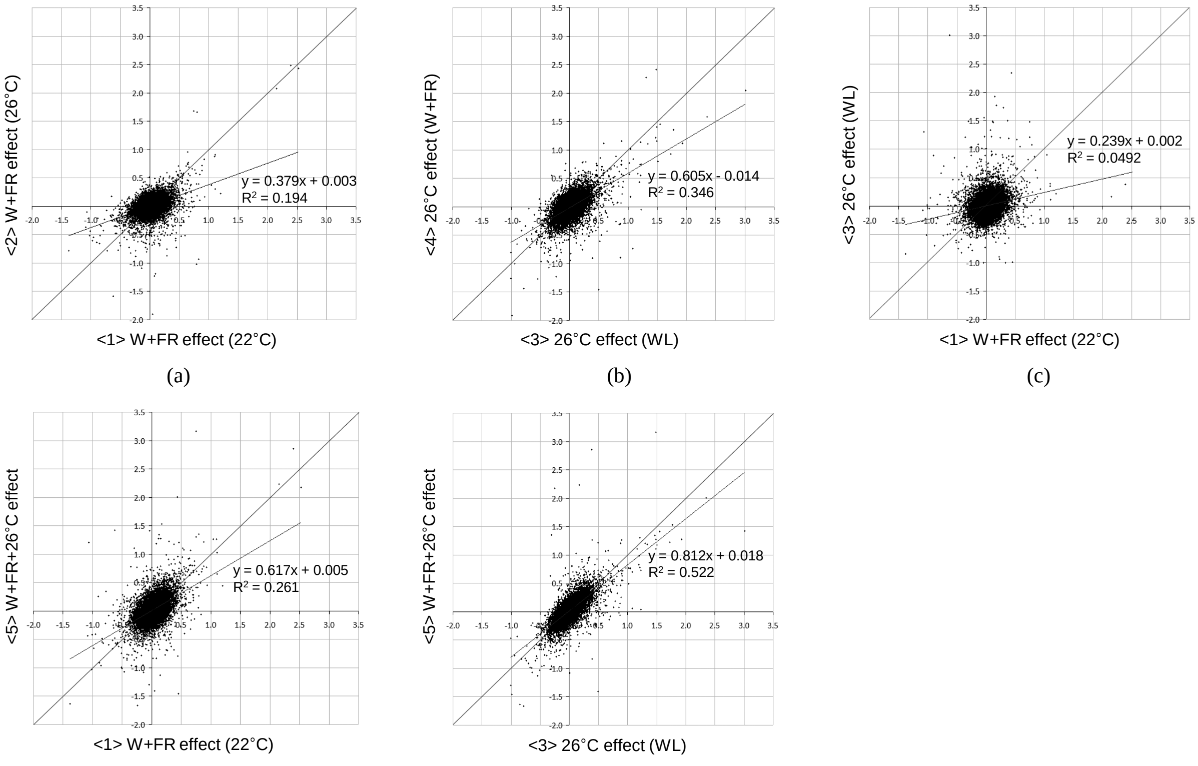


Figure 1. Microarray experimental design. The comparisons of data from different conditions were shown by arrows between the boxes. WL, white light only (high R:FR). W+FR, white light with supplemental far-red light (low R:FR). Numbers next to the arrows are the serial numbers of treatment effects used in this study (see text).



(a) (b) (c)

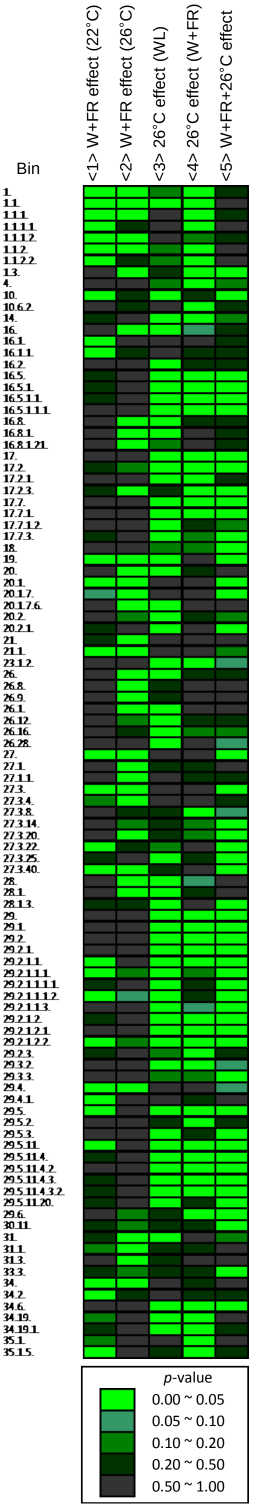
(d) (e)

Figure 2. Comparisons among different treatment effects. The measure of treatment effect (any one of <1>. through <5> in **Figure 1**) on each individual gene was determine6d by the average of $\log_2$ (treated/untreated). In each scatter plot two different effects were compared. (a) Between the two W+FR effects (26˚C vs. 22˚C); (b) between the two 26˚C effects (W+FR vs. WL); (c) between the W+FR effect at 22˚C and 26˚C effect under WL; (d) between the combined effect of W+FR+26˚C and W+FR effect at 22˚C; (e) between the combined effect of W+FR+26˚C and 26˚C effect under WL. The trend line is shown in each panel in addition to a diagonal line for the hypothetical perfect correlation.

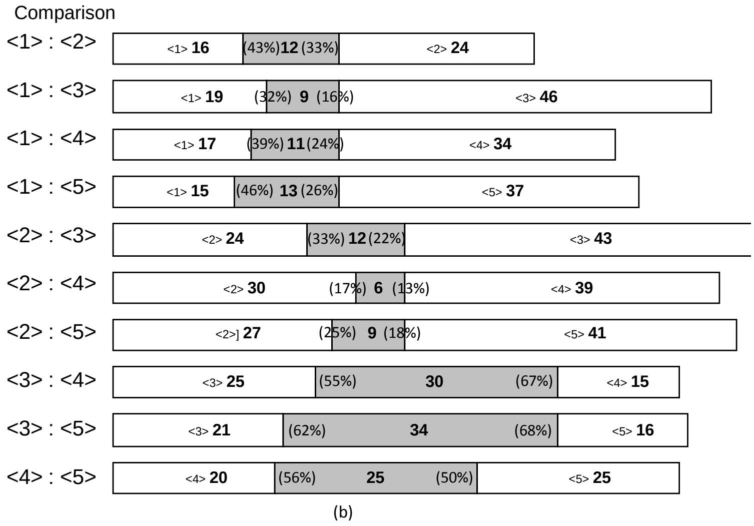
contrast with the absence of correlation between the high temperature only effect and the W+FR only effect (<3> vs. <1>; **Figure 2(c)**). When the combined effect of low R:FR and high temperature (<5> W+FR+26˚C effect) is compared with either of any single treatment effect such as low R:FR only (<1> W+FR effect at 22˚C) or high temperature only (<3> 26˚C effect under WL), a higher level of correlation was found with high temperature only treatment (<5> vs. <3>) and a less pronounced correlation with low R:FR only treatment (<5> vs. <1>) (**Figure 2(d)** and **Figure 2(e)**), suggesting that the high temperature has more influence than the light quality on the combined effect under this condition.

3.3. The Most Affected Gene Ontology Terms in Each Treatment Effect

To identify significantly affected functional gene clusters, we conducted MapMan analysis [26] using the 15,128 genes. First, significantly affected MapMan bins in at least one of the five different treatment effects were determined (**Figure 3(a)**; **Supplement Table S1**). Again, there is a general tendency that similar treatments affect similar functional groups with less pronounced resemblance between the W+FR effects at different temperatures (<1> and <2>) than the temperature effects under different light conditions (<3> and <4>), confirming the pattern of individual gene expression as shown in the scatter plots above (**Figure 2**). Overall, more bins are affected by 26˚C treatments than by low R:FR light (W+FR) treatment. Next, the numbers of common MapMan bins significantly affected in two different treatment effects were identified, and the percentage of the overlapped bins to the total significant bins in each treatment effect was determined and shown with modified Venn diagrams (**Figure 3(b)**). Relatively higher level of overlap was observed between the two high temperature effects (<3>:<4>, 54.5% of 26˚C effect under WL and 66.7% of 26˚C effect under W+FR), whereas the number of bins responded to both W+FR effects is relatively low (<1>:<2>, 42.9% of W+FR at 22˚C and 33.3% of W+FR at



(a)



(b)

Bin	Name	BH corrected p-value				
		<1> W+FR effect (22° C)	<2> W+FR effect (26° C)	<3> 26° C effect (WL)	<4> 26° C effect (WFR)	<5> W+FR+ 26° C effect
1.1.	PS.lightreaction	0.000	0.001	0.006	0.000	0.813
1.3.	PS.calvin cyle	0.729	0.006	0.412	0.027	0.005
10.	cell wall	0.017	0.225	0.009	0.474	0.012
14.	S-assimilation	0.301	0.628	0.029	0.009	0.137
16.1.	secondary metabolism.isoprenoids	0.017	0.525	0.653	0.772	0.309
16.5.	secondary metabolism.sulfur-containing	0.406	0.779	0.000	0.000	0.000
16.8.	secondary metabolism.flavonoids	0.885	0.002	0.020	0.452	0.484
17.2.	hormone metabolism.auxin	0.472	0.159	0.017	0.003	0.001
17.7.	hormone metabolism.jasmonate	0.660	0.532	0.000	0.000	0.000
19.	tetrapyrrole synthesis	0.000	0.015	0.015	0.949	0.000
20.1.7.	stress.biotic.PR-proteins	0.081	0.000	0.880	0.883	0.022
20.2.1.	stress.abiotic.heat	0.343	0.637	0.004	0.544	0.047
21.1.	redox.thioredoxin	0.026	0.014	0.920	0.800	0.124
27.1.1.	RNA.processing.splicing	0.948	0.023	0.934	0.347	0.329
27.3.	RNA.regulation of transcription	0.000	0.000	0.735	0.666	0.000
27.3.4.	RNA.regulation of transcription.ARF, Auxin Response	0.100	0.010	0.714	0.970	0.464
27.3.22.	RNA.regulation of transcription.HB,Homeobox	0.017	0.335	0.148	0.758	0.022
27.3.40.	RNA.regulation of transcription.Aux/IAA family	0.002	0.045	0.261	0.766	0.022
28.1.	DNA.synthesis/chromatin structure	0.990	0.003	0.000	0.386	0.538
29.1.	protein.aa activation	0.895	0.975	0.009	0.018	0.043
29.2.1.1.	protein.synthesis.ribosomal protein.prokaryotic	0.021	0.690	0.000	0.004	0.000
29.2.1.2.	protein.synthesis.ribosomal protein.eukaryotic	0.450	0.525	0.000	0.000	0.000
29.2.3.	protein.synthesis.initiation	0.202	0.789	0.189	0.002	0.484
29.4.	protein.postranslational modification	0.005	0.007	0.991	0.970	0.097
29.5.11.	protein.degradation.ubiquitin	0.030	0.982	0.007	0.000	0.022
29.6.	protein.folding	0.826	0.133	0.229	0.029	0.007
30.11.	signalling.light	0.285	0.122	0.216	0.439	0.006
34.	transport	0.002	0.014	0.596	0.347	0.510

(c)

Figure 3. Significantly affected MapMan bins. (a) A heat map visualizing the significantly responded MapMan bins. The brightness of color reflects *p*-values (Benjamini-Hochberg corrected); (b) venn diagrams showing the numbers of the overlapped (grey) and the non-overlapped (white) significant bins (*p*-value < 0.05); rectangular shape was used to save space. The percentages indicate the proportions of the overlapped bins to the total number of significant bins in each treatment effect; (c) the *p*-values of some notable bins in (a) are shown. The full list is provided in **Supplement Table S1**.

26˚C), confirming the limited similarity between the two W+FR treatment effects compared with the one between the two high temperature effects (**Figure 2**). The combined effect of W+FR and high temperature (<5> W+FR+26˚C) is similar to any of the two high temperature effects (<3> or <4>), which contrasts with lower levels of overlap with any of the W+FR effects (<1> or <2>), suggesting a stronger influence of high temperature than the low R:FR effect in the combined response. Together with the scatter plot data (**Figure 2**) these results suggest that there are higher levels of overlap between the similar treatment effects in terms of individual gene expression (**Figure 2**) as well as functional gene clusters (**Figure 3(a)** and **Figure 3(b)**).

Figure 3(c) lists some of the notable MapMan bins shown in **Figure 3(a)**, (the full list of significant bins is provided in **Supplement Table S1**). It is intriguing that the supplemental far-red light treatment (W+FR) led to a slightly different pattern of response at 26˚C compared with the response at 22˚C as shown in the scatter plot and MapMan analysis (**Figure 2(a)** and **Figure 3**). For example, *protein degradation* family responded significantly at 22˚C whereas genes for *DNA synthesis/chromatin structure* are affected more at 26˚C. Also, different classes of *secondary metabolism* responded at different temperatures. While *isoprenoids-related* genes are more affected at 22˚C, more *flavonoids-related* genes are affected at 26˚C. Therefore, there is some level of distinction in the pattern of gene expression responses to low R:FR light treatment depending on the temperature context. In the same way, there is also some distinction in the high temperature responses under different light conditions, although the degree of similarity is higher than in the two W+FR responses.

3.4. Low R:FR Light and High Temperature Conditions Affect Different Sets of Auxin-Related Genes

The common MapMan bins responded to W+FR under both temperature conditions are *photosystems*, *tetrapyrrole synthesis*, *thioredoxin*, *AUX/IAA family*, *post-translational modification*, and *transport* (**Figure 3(c)**; **Supplement Table S1**) while genes related to *photosystems*, *auxin and jasmonate metabolism* as well as *protein synthesis/degradation* are affected by 26˚C treatments regardless of the light condition. Notable common themes between the W+FR responsive groups and the high temperature responsive groups are "*photosystems*" and "*auxin*". Particularly, identifying "*auxin*" as a common response confirms the previous notion that both low R:FR ratio and high temperature can independently trigger cell elongation via auxin synthesis and signaling [4] [23]-[25].

However, low R:FR condition affected more of *regulation of transcription* (bin #27.3) including *AUX/IAA genes* whereas high temperature condition affected more of *auxin metabolism* (bin #17.2). Therefore, we dissected the expression pattern within those notable bins by interrogating and visualizing individual gene expression in those clusters (**Figure 4**). In general, many *AUX/IAA genes*, *homeobox transcription factors*, and *indole*-3-*acetic acid amido synthetases* (*GH*3*s*) that convert active IAA to inactive IAA compounds are mostly up-regulated by low R:FR (W+FR) but not by high temperature (bin #17.2.3, #27.3.22, #27.3.40), while *IAA-amino acid conjugate hydrolases* that convert inactive IAA compounds to active IAA are up-regulated mostly by high temperature but not by low R:FR (bin #17.2.1). This suggests that the mode of regulation for auxin signaling can be different between the light quality and the temperature responses under our experimental conditions.

3.5. Classification of Responsive Genes According to Gene Expression Patterns

To have a closer look at the responsive genes, we identified 484 genes that exhibited statistically significant response to any of the above mentioned five treatment effects. In addition, 27 additional, non-overlapping genes were selected that could not pass the stringent statistical test but were consistently up- or down-regulated by at least 1.5-fold in all three replicates in any of the above five treatment effects (*Materials and Methods*). Those 511 responsive genes were clustered based on their expression patterns by hierarchical clustering (**Figure 5**). Then 11 arbitrary clusters were formed by grouping the nodes with genes that exhibited similar expression patterns (**Figure 5**; the full list of genes for each cluster is provided in **Supplement Table S2**). To correlate the gene expression pattern and the function of those genes, highly enriched Gene Ontology (GO) terms in each cluster were identified by a web-based program, Functional Annotation Tool (DAVID Bioinformatics Resources 6.7, NIAID/NIH; [31]). The genes in cluster [*a*] generally exhibit up-regulation upon low R:FR (W+FR) treatment at both temperatures (<1> and <2>) but are not responsive to high temperature (26˚C) under any light conditions applied (**Figure 5**). Again, strong enrichment of *auxin response* related genes were found in this cluster (**Table 1**). On the other hand, genes up-regulated only upon high temperature treatment regardless of the light

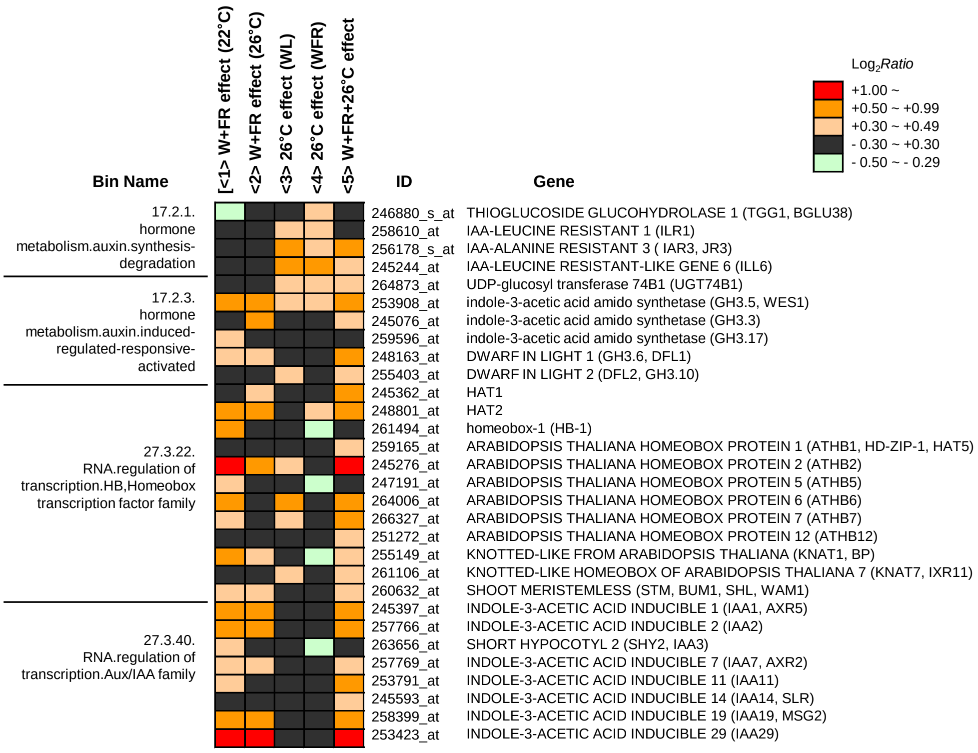
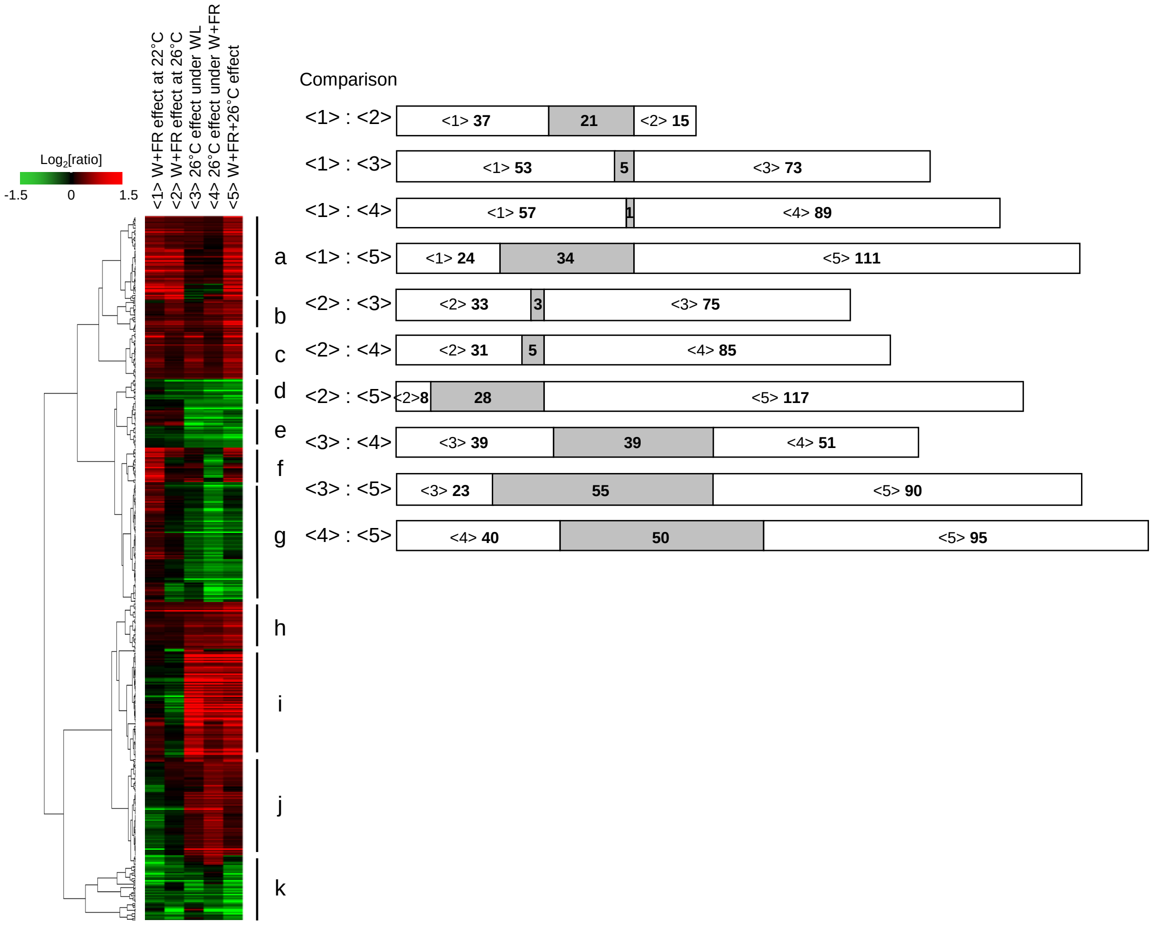


Figure 4. Individual gene expression patterns in auxin related MapMan bins. The expression levels of genes that belong to auxin related MapMan bins were shown in a heat map. Only those with the $\log_2$ Ratio of greater than ±0.3 in any of the five treatment effects are shown.

Table 1. Gene ontology analyses of 11 clusters. Enriched GO terms in each cluster were identified through the web-based program, Functional Annotation Tool (DAVID [31]). BP: Biological Process, MP: Molecular Function.

Cluster	Category	GO#	Term	*p*-value	Adj. *p*-value (Benjamini)
a	BP	GO:0009733	response to auxin stimulus	6.27E−09	1.37E−06
	BP	GO:0009734	auxin mediated signaling pathway	1.18E−05	1.28E−03
	BP	GO:0009725	response to hormone stimulus	7.46E−05	5.40E−03
	BP	GO:0009719	response to endogenous stimulus	1.33E−04	7.24E−03
	BP	GO:0010033	response to organic substance	6.24E−04	2.69E−02
	MF	GO:0003700	transcription factor activity	1.26E−04	9.67E−03
	MF	GO:0046983	protein dimerization activity	2.08E−04	7.98E−03
	MF	GO:0030528	transcription regulator activity	4.27E−04	1.09E−02
c	BP	GO:0042546	cell wall biogenesis	1.95E−04	3.62E−02
	BP	GO:0009834	secondary cell wall biogenesis	3.55E−04	3.30E−02
i	BP	GO:0009408	response to heat	2.37E−06	6.86E−04
	BP	GO:0010035	response to inorganic substance	7.29E−06	1.06E−03
	BP	GO:0006979	response to oxidative stress	9.91E−06	9.57E−04
	BP	GO:0000302	response to reactive oxygen species	6.20E−05	4.48E−03
	BP	GO:0009644	response to high light intensity	6.94E−05	4.02E−03
	BP	GO:0042542	response to hydrogen peroxide	2.66E−04	1.10E−02
	BP	GO:0009642	response to light intensity	5.17E−04	1.86E−02
k	BP	GO:0009753	response to jasmonic acid stimulus	1.12E−04	5.41E−03
	BP	GO:0009628	response to abiotic stimulus	3.99E−05	6.56E−03
	BP	GO:0006970	response to osmotic stress	8.83E−04	4.74E−02



(a) (b)

Figure 5. Expression patterns of the responsive genes. (a) Statistically significant responsive genes in at least one of the five comparisons were clustered using hierarchical clustering. Eleven clusters (a - k) are labeled next to the thumbnail image; (b) The numbers of the commonly responded (grey) and of the uniquely responded genes (white) (1.5 fold or higher) are shown in modified Venn diagrams for pair wise comparisons between different treatment effects. Rectangular shape was used to save space. The size of the boxes roughly corresponds to the number of responded genes in each category.

condition (<3> and <4>) are related to *heat stress*, *oxidative stress*, *high light intensity*, and *jasmonic acid* (**Table 1**, cluster [*i*]). Genes that show a down-regulation trend in all treatments (cluster [*k*]) are *abiotic stress* related, such as *low temperature*/*osmotic stress* induced genes. In clusters [*b*] and [*c*], the W+FR responsive gene expressions were dependent on the temperature and the high temperature responsive gene expressions were dependent on the light quality. Highly enriched in cluster [*c*] are the *cell wall biogenesis* related genes, but no significant GO terms were identified in cluster [*b*] (**Figure 5**; **Table 1**). This may be due to the small number of genes in this group (23 genes).

3.6. Shade Avoidance Response under Different Temperature Conditions

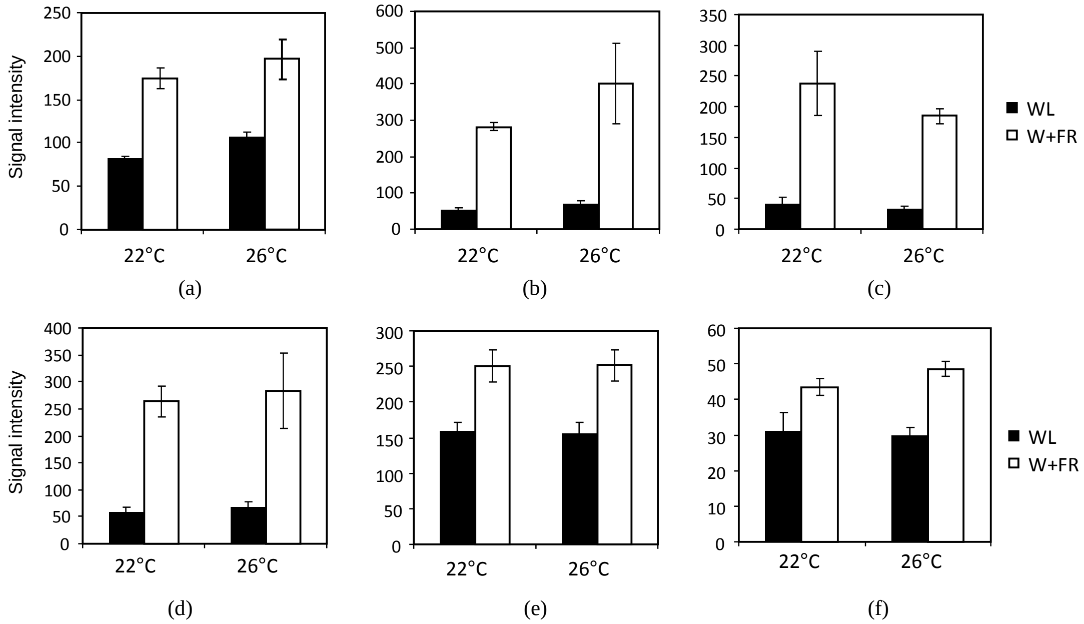
In a number of previous reports important signature genes for shade avoidance response have been revealed. We looked specifically into some of those genes in our microarray data (**Table 2**). Despite the overall distinct patterns of gene expression responses among the different treatments shown above, most of those genes did not show differential expression patterns in response to W+FR at two different temperatures we tested (<1> vs. <2>). Of those genes *ATHB*2, *HFR*1, *IAA*29 and *FT* are highly induced by low R:FR treatment (W+FR) as shown in many previous studies. In a different temperature context, however, the induction levels of those genes were strikingly similar. Not only the ratio of the signal intensities (**Table 2**) but also the actual normalized signal intensities of the microarray chips support the observation that those genes did not respond differentially at 22°C

Table 2. Expression responses of shade induced genes. Average log$_2$Ratio (±SD) in five different treatment effects are listed.

ID	Locus	Gene	<1> W+FR effect at 22˚C	<2> W+FR effect at 26˚C	<3> 26˚C effect under WL	<4> 26˚C effect under W+FR	<5> W+FR+26˚C effect	Shade induced expression (References)
263739_at	AT2G21320	*BBX*18	0.15 ± 0.19	0.19 ± 0.14	0.13 ± 0.06	0.17 ± 0.12	0.32 ± 0.08	[35]
252917_at	AT4G38960	*BBX*19	−0.09 ± 0.09	−0.08 ± 0.07	−0.09 ± 0.17	−0.09 ± 0.12	−0.18 ± 0.21	[35]
262975_at	AT1G75540	*BBX*21	0.02 ± 0.13	0.00 ± 0.08	−0.04 ± 0.09	−0.06 ± 0.10	−0.04 ± 0.06	[35]
263128_at	AT1G78600	*BBX*22	−0.54 ± 0.29	−0.16 ± 0.18	−0.20 ± 0.10	0.18 ± 0.38	−0.36 ± 0.22	[35]
260956_at	AT1G06040	BBX24	−0.04 ± 0.10	0.05 ± 0.12	0.23 ± 0.22	0.31 ± 0.02	0.28 ± 0.11	[35]
250569_at	AT5G08130	*BIM*1	0.20 ± 0.19	0.03 ± 0.09	0.16 ± 0.22	−0.01 ± 0.09	0.19 ± 0.20	[10]
259417_at	AT1G02340	*HFR*1	2.39 ± 0.19	2.48 ± 0.39	0.38 ± 0.21	0.47 ± 0.48	2.86 ± 0.29	[10]
252890_at	AT4G39400	*BRI*1	0.39 ± 0.17	0.22 ± 0.10	0.12 ± 0.09	−0.05 ± 0.09	0.34 ± 0.13	[36]
264508_at	AT1G09570	*PHYA*	0.10 ± 0.13	−0.08 ± 0.11	0.23 ± 0.17	0.05 ± 0.08	0.15 ± 0.12	[36]
248801_at	AT5G47370	*HAT*2	0.61 ± 0.02	0.71 ± 0.20	0.22 ± 0.20	0.31 ± 0.39	0.92 ± 0.39	[36] [37]
263981_at	AT2G42870	*PAR*1	0.07 ± 0.48	0.04 ± 0.16	−0.05 ± 0.10	−0.08 ± 0.58	−0.01 ± 0.25	[37]
245276_at	AT4G16780	*ATHB*2/HAT4	1.10 ± 0.05	0.87 ± 0.12	0.39 ± 0.14	0.16 ± 0.26	1.26 ± 0.22	[36]-[38]
262850_at	AT1G14920	*GAI*	0.09 ± 0.05	0.11 ± 0.13	−0.02 ± 0.12	0.00 ± 0.06	0.09 ± 0.05	[36]
258399_at	AT3G15540	*IAA*19	0.66 ± 0.20	0.69 ± 0.14	−0.02 ± 0.16	0.01 ± 0.18	0.67 ± 0.03	[36]
253423_at	AT4G32280	*IAA*29	2.15 ± 0.13	2.07 ± 0.60	0.17 ± 0.43	0.09 ± 0.27	2.24 ± 0.17	[36]
260364_at	AT1G70560	*TAA1/ SAV*3	−0.06 ± 0.12	0.04 ± 0.29	−0.32 ± 0.20	−0.21 ± 0.21	−0.27 ± 0.10	[22]
253794_at	AT4G28720	*YUC8*	0.48 ± 0.27	0.71 ± 0.14	−0.07 ± 0.26	0.16 ± 0.10	0.65 ± 0.28	[24]
261109_at	AT1G75450	*CKX5*	0.20 ± 0.13	0.26 ± 0.11	0.24 ± 0.20	0.30 ± 0.21	0.51 ± 0.24	[24]
264638_at	AT1G65480	*FT*	2.52 ± 0.69	2.43 ± 0.17	−0.25 ± 0.44	−0.34 ± 0.42	2.18 ± 0.27	[10] [39] [40]
246525_at	AT5G15840	*CO*	0.65 ± 0.07	0.58 ± 0.36	−0.19 ± 0.28	−0.26 ± 0.19	0.39 ± 0.18	[41]
245325_at	AT4G14130	*XTH*15	0.49 ± 0.08	0.31 ± 0.10	−0.01 ± 0.10	−0.19 ± 0.04	0.30 ± 0.11	[42]
264157_at	AT1G65310	*XTH*17	0.38 ± 0.50	0.29 ± 0.06	0.42 ± 0.06	0.33 ± 0.39	0.71 ± 0.12	[42]
250214_at	AT5G13870	*XTH*5	0.17 ± 0.10	−0.02 ± 0.12	0.16 ± 0.17	−0.03 ± 0.12	0.14 ± 0.11	[42]

and at 26˚C (**Figure 6**). This suggests that at least the major responders in the shade avoidance response are not among the differentially expressed genes in different temperature contexts. Although many of the genes in **Table 2** did not exhibit significant levels of expression changes after 24 hours of supplemental far-red light treatment under our conditions, it is not uncommon that the expression levels of typical shade inducible genes decrease after an extended period of treatment (References in **Table 2**).

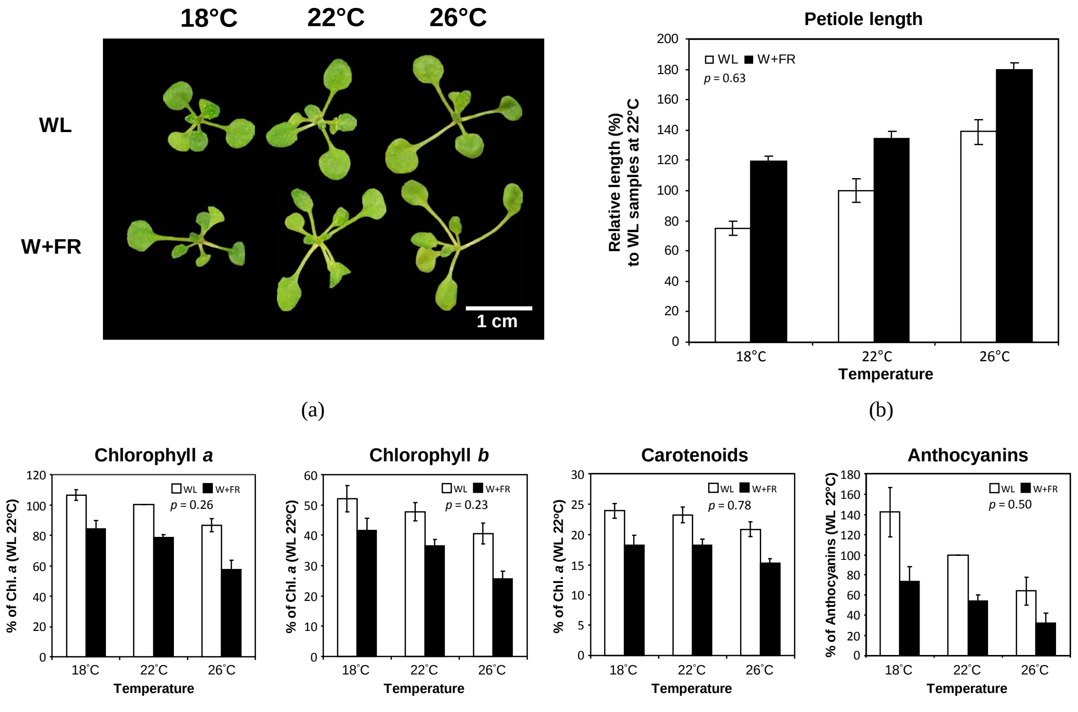
To investigate the consequence of the above mentioned gene expression response at the phenotypic level, we analyzed typical phenotypes under the conditions we used for this experiment (**Figure 7**). An additional temperature (18˚C) was used to show the trend outside the range used in this study. As expected, the supplementation of far-red light (W+FR) induced petiole elongation and reduction of pigments content at all temperatures tested. In general, those phenotypic changes were enhanced when higher ambient temperature was used. However, two-way ANOVA analyses failed to support the idea of statistically significant interaction between the two factors, low R:FR ratio and high temperature. This suggests that the phenotypic responses to low R:FR ratio are not differentially regulated at different temperature conditions, and that the enhanced responses at a higher temperature are due to additive effects of the two responses.



(a) (b) (c)

(d) (e) (f)

Figure 6. Microarray signal intensities of shade responsive genes. Normalized average signal intensities of shade inducible genes under indicated conditions. Error bars indicate standard deviations of three replicates. (a) *ATHB*2; (b) *HFR*1; (c) *FT*; (d) *IAA*29; (e) *IAA*19; (f) *YUC*8.



(a) (b)

(c) (d) (e) (f)

Figure 7. Phenotypic study did not support any statistically significant interaction between the two factors. (a) Representative plants grown under indicated conditions; (b) the lengths of petioles are shown as relative values (%) to the average length of WL-treated plants at 22˚C. (c)-(e) the levels of chlorophyll *a*, chlorophyll *b* and carotenoids are shown as relative values (%) to the amount of chlorophyll *a* in WL22˚C; (f) the levels of anthocyanins are shown as relative values (%) to the anthocyanin level in WL22˚C. All error bars indicate SE (for petiole length $n = 19$ plants, otherwise $n = 5 - 7$ independent experiments). The *p*-values shown are for the interaction tests between the two factors determined by two-way ANOVA using the data from 22˚C and 26˚C conditions.

3.7. Differentially Expressed Genes under Different Environmental Contexts

Although the typical shade responsive genes did not behave differently upon supplemental far-red light (W+FR) treatments at two different temperatures (**Table 2**; **Figure 6**), our cluster analysis (**Figure 5**) as well as the scatter plots (**Figure 2(a)**) indicates that there are genes differentially responded to the supplemental far-red light under different temperature conditions (<2> vs. <1>). Therefore, we searched such genes by generating $\log_2$Ratios of W+FR effects at 26˚C and at 22˚C ([W+FR effect at 26˚C]/[W+FR effect at 22˚C]) among the 15,128 genes mentioned earlier. A positive value indicates a higher level of induction at 26˚C than at 22˚C, and a negative value indicates a lower level induction at 26˚C than at 22˚C. The $\log_2$Ratios for the vast majority of the genes (14,410 or 95.3%) fell into a range between −0.3 and +0.3, meaning very similar levels of gene expression change between the two treatment effects. The genes outside of this range (718% or 4.7%) were further subdivided into four ranges: less than or equal to −0.5 [α], −0.5 - −0.3 [β], +0.3 - +0.5 [γ], and higher than +0.5 [δ] (**Figure 8**). Only 1% of 15,128 genes belong to the group [α] (124 genes) and the group [δ] (25 genes). Again, the statistically significant groups of genes in each range were identified through Functional Annotation Tool (DAVID Bioinformatics Resources 6.7, NIAID/NIH [31]; **Tables 3-6**). Many genes that exhibited reduced levels of expression in response to low R:FR ratio at 26˚C (<2> W+FR effect at 26˚C) are involved in various processes such as *secondary metabolism*, *lipid transport*, *oxidative stress*, and *jasmonic acid response*. Many of those gene products are targeted to the *extracellular region* or *cell wall*. It is intriguing that quite a few of those genes are also involved in pathogen defense mechanisms (Group [α] and [β] in **Table 3** and **Table 4**; **Supplement Table S3**). On the other hand, there are not many genes with enhanced response to low R:FR ratio at 26˚C (<2> W+FR effect at 26˚C). Pathogenesis-related thaumatin superfamily proteins in group [γ] are the only statistically significant group in this category when multiple test corrections were applied to the *p*-value (**Table 5**). Therefore, in order to find at least a tendency of this differential response, additional GO terms were identified by less stringent statistical approach without multiple test corrections (p-value < 0.02; **Table 5** and **Table 6**). In this analysis many *transcription factors* that are related to pathogen defense process, *light response*, and *ethylene signaling* were found in group [γ]. At the extreme end of up regulated genes at 26˚C (group [δ]) were genes whose products are targeted to the extracellular region or cell wall, which are also related to defense mechanisms against pathogens (**Table 6**; **Supplement Table S3**).

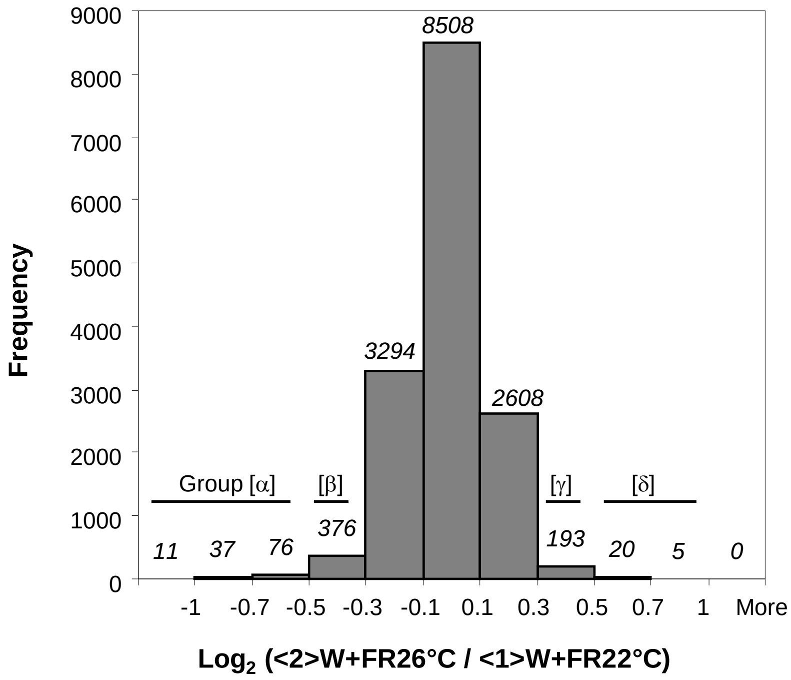


Figure 8. Histogram showing the numbers of genes differentially responded. The frequencies of Log_2 [(W+FR effect at 26˚C)/(W+FR effect at 22˚C)] among the 15,128 genes are shown.

Table 3. Functional classification of the genes in group [α]. Genes with the log transformed ratio ([<2>W+FR effect at 26˚C]/[<1>W+FR effect at 22˚C]) of less than or equal to −0.5 were analyzed by the Functional Annotation Tool (DAVID Bioinformatics Resources 6.7, NIAID/NIH [31]). Shown are clusters with multiple test corrected *p*-values of 0.05 or less (Benjamini).

Cluster	Classification Type	Category	Term	Count	*p*-value	Benjamini
1	Gene Ontology	GOTERM_CC_FAT	GO:0005618~cell wall	12	0.001	0.028
			GO:0030312~external encapsulating structure	12	0.001	0.016
	Functional Categories	SP_PIR_KEYWORDS	disulfide bond	17	0.000	0.000
			signal	20	0.000	0.001
			secreted	11	0.003	0.040
		UP_SEQ_FEATURE	signal peptide	20	0.000	0.031
2	Gene Ontology	GOTERM_MF_FAT	GO:0008289~lipid binding	8	0.000	0.018
		GOTERM_BP_FAT	GO:0006869~lipid transport	6	0.001	0.041
			GO:0010876~lipid localization	6	0.003	0.046
	Functional Categories	SP_PIR_KEYWORDS	Lipid-binding	5	0.000	0.003
	Protein Domains	SMART	SM00499:AAI	6	0.000	0.000
		INTERPRO	IPR003612:Plant lipid transfer protein/seed storage/trypsin-α amylase inhibito	6	0.000	0.017
			IPR000528:Plant lipid transfer protein/Par allergen	4	0.000	0.022
			IPR013770:Plant lipid transfer protein and hydrophobic protein, helical	5	0.000	0.018
3	Gene Ontology	GOTERM_BP_FAT	GO:0019748~secondary metabolic process	11	0.001	0.028
			GO:0009698~phenylpropanoid metabolic process	7	0.001	0.031
			GO:0009699~phenylpropanoid biosynthetic process	6	0.002	0.041
			GO:0009718~anthocyanin biosynthetic process	3	0.002	0.038
4	Gene Ontology	GOTERM_BP_FAT	GO:0006979~response to oxidative stress	10	0.000	0.020
			GO:0000302~response to reactive oxygen species	7	0.000	0.036
			GO:0034614~cellular response to reactive oxygen species	6	0.000	0.029
			GO:0034599~cellular response to oxidative stress	6	0.000	0.025
			GO:0006800~oxygen and reactive oxygen species metabolic process	6	0.001	0.033
			GO:0042542~response to hydrogen peroxide	6	0.001	0.037
			GO:0033554~cellular response to stress	10	0.002	0.039
			GO:0042744~hydrogen peroxide catabolic process	5	0.003	0.049
			GO:0070301~cellular response to hydrogen peroxide	5	0.003	0.049
			GO:0042743~hydrogen peroxide metabolic process	5	0.003	0.049
			GO:0010035~response to inorganic substance	11	0.003	0.048

Continued

	Functional Categories	SP_PIR_KEYWORDS	hydrogen peroxide	5	0.001	0.023
			Pyrrolidone carboxylic acid	4	0.002	0.043
			peroxidase	5	0.004	0.050
			Secreted	11	0.003	0.040
		UP_SEQ_FEATURE	disulfide bond	14	0.000	0.004
	Protein Domains	INTERPRO	IPR000823:Plant peroxidase	5	0.001	0.028
			IPR002016:Haem peroxidase, plant/fungal/bacterial	5	0.001	0.036
			IPR019794:Peroxidase, active site	5	0.001	0.034
			IPR019793:Peroxidases heam-ligand binding site	5	0.002	0.036
5	Functional Categories	SP_PIR_KEYWORDS	glycosidase	10	0.000	0.002
			polysaccharide degradation	4	0.002	0.043
7	Functional Categories	SP_PIR_KEYWORDS	glycosidase	10	0.000	0.002
9	Gene Ontology	GOTERM_BP_FAT	GO:0010035~response to inorganic substance	11	0.003	0.048

Table 4. Functional classification of the genes in group [*β*]. Genes with the log transformed ratio ([<2>W+FR effect at 26˚C]/[<1>W+FR effect at 22˚C]) of −0.5 - −0.3 were analyzed by the Functional Annotation Tool. Shown are clusters with multiple test corrected *p*-values of 0.05 or less (Benjamini).

Cluster	Classification Type	Category	Term	Count	*p*-value	Benjamini
1	Gene Ontology	GOTERM_BP_FAT	GO:0019748~secondary metabolic process	30	0.000	0.000
			GO:0006575~cellular amino acid derivative metabolic process	21	0.000	0.000
			GO:0009698~phenylpropanoid metabolic process	16	0.000	0.000
			GO:0009699~phenylpropanoid biosynthetic process	12	0.000	0.003
			GO:0009813~flavonoid biosynthetic process	8	0.000	0.005
			GO:0009812~flavonoid metabolic process	8	0.000	0.007
			GO:0019438~aromatic compound biosynthetic process	14	0.000	0.013
			GO:0042398~cellular amino acid derivative biosynthetic process	13	0.000	0.013
2	Functional Categories	UP_SEQ_FEATURE	signal peptide	45	0.000	0.000
		SP_PIR_KEYWORDS	signal	45	0.000	0.000
			glycoprotein	36	0.000	0.007
			Secreted	24	0.000	0.029
			disulfide bond	21	0.001	0.029
4	Functional Categories	SP_PIR_KEYWORDS	oxidoreductase	29	0.001	0.035
20	Gene Ontology	GOTERM_BP_FAT	GO:0009753~response to jasmonic acid stimulus	12	0.000	0.013

Table 5. Functional classification of the genes in group [*γ*]. Genes with the log transformed ratio ([<2>W+FR effect at 26˚C]/[<1>W+FR effect at 22˚C]) of 0.3 - 0.5 were analyzed by the Functional Annotation Tool. Shown are clusters *p*-values of 0.02 or less.

Cluster	Classification Type	Category	Term	Count	*p*-value	Benjamini
1	Protein Domains	INTERPRO	IPR017949:Thaumatin, conserved site	4	0.000	**0.041**
			IPR001938:Thaumatin, pathogenesis-related	4	0.001	0.112
		SMART	SM00205:THN	4	0.001	**0.044**
		PIR_SUPERFAMILY	PIRSF002703:Thaumatin	4	0.001	0.094
			PIRSF002703:pathogenesis-related group 5 protein, thaumatin type	3	0.010	0.334
2	Gene Ontology	GOTERM_MF_FAT	GO:0030528~transcription regulator activity	29	0.001	0.138
			GO:0003700~transcription factor activity	25	0.003	0.241
			GO:0003677~DNA binding	32	0.004	0.238
		GOTERM_BP_FAT	GO:0045449~regulation of transcription	29	0.004	0.519
			GO:0006355~regulation of transcription, DNA-dependent	18	0.010	0.664
			GO:0051252~regulation of RNA metabolic process	18	0.010	0.620
	Functional Categories	SP_PIR_KEYWORDS	nucleus	30	0.001	0.104
			DNA-binding	21	0.004	0.225
			transcription regulation	18	0.007	0.256
			Transcription	18	0.008	0.232
3	Functional Categories	UP_SEQ_FEATURE	zinc finger region:B box-type 1; atypical	3	0.013	0.789
			zinc finger region:B box-type 2; atypical	3	0.012	0.937
4	Gene Ontology	GOTERM_BP_FAT	GO:0009627~systemic acquired resistance	5	0.000	0.141
			GO:0009814~defense response, incompatible interaction	5	0.014	0.625
5	Gene Ontology	GOTERM_BP_FAT	GO:0009314~response to radiation	12	0.004	0.469
			GO:0009639~response to red or far red light	6	0.020	0.608
6	Gene Ontology	GOTERM_MF_FAT	GO:0015294~solute:cation symporter activity	6	0.005	0.218
			GO:0015293~symporter activity	6	0.009	0.318
7	Gene Ontology	GOTERM_BP_FAT	GO:0009723~response to ethylene stimulus	9	0.002	0.487
			GO:0000160~two-component signal transduction system	7	0.013	0.657
			GO:0009725~response to hormone stimulus	16	0.016	0.639
			GO:0009755~hormone-mediated signaling	10	0.017	0.612
			GO:0032870~cellular response to hormone stimulus	10	0.017	0.612
			GO:0009873~ethylene mediated signaling pathway	6	0.017	0.593
9	Protein Domains	INTERPRO	IPR013770:Plant lipid transfer protein and hydrophobic protein, helical	4	0.014	0.630
10	Protein Domains	INTERPRO	IPR011616:bZIP transcription factor, Bzip-1	4	0.008	0.559
11	Gene Ontology	GOTERM_CC_FAT	GO:0048046~apoplast	9	0.011	0.693
	Functional Categories	SP_PIR_KEYWORDS	disulfide bond	11	0.012	0.268

Table 6. Functional classification of the genes in group [*δ*]. Genes with the log transformed ratio ([<2>W+FR effect at 26˚C]/[<1>W+FR effect at 22˚C]) of higher than 0.5 were analyzed by the Functional Annotation Tool. Shown are clusters *p*-values of 0.02 or less.

Cluster	Classification Type	Category	Term	Count	*p*-value	Benjamini
1	Gene Ontology	GOTERM_CC_FAT	GO:0005576~extracellular region	5	0.007	0.072
			GO:0005618~cell wall	4	0.016	0.085
			GO:0030312~external encapsulating structure	4	0.017	0.060

4. Discussion

Light and temperature are important environmental factors for plant development and survival. Both light and temperature can regulate various aspects of physiological process such as seed germination, flowering, plant architecture and cold tolerance. Many studies so far suggest integration of light quality and temperature signals in plants [43]. In the present study the gene expression patterns of shade avoidance response at different temperatures were investigated in order to better understand the integration process between the light quality and the temperature signals, which revealed similarities and differences in the responses in different temperature contexts. Despite the distinctions in global gene expression patterns, the most representative shade induced genes did not show any differential responses at different temperatures. On the other hand, we identified some other shade responsive genes that are differentially regulated under different temperature conditions.

4.1. Experimental Condition

Global gene expression change in response to low R:FR light under the standard temperature condition has been studied before [10] [24] [36] [44] [45]. Comparing our results with the previous reports from other labs did not result in any strong correlation beside several marker genes for shade avoidance response such as *ATHB*2, *HFR*1, *FT* and other auxin related genes (Data not shown; **Table 2**). This may be attributed to the difference in experimental conditions used in other studies. None of the previous studies were carried out under the same condition as we used (*Materials and Methods*; *Results*), suggesting that the developmental and environmental contexts also affect the overall response pattern of the whole transcriptome. In addition, we used 24 hr of treatment to avoid very early response that may potentially be variable due to the change of two different environmental factors at the same time. But this may have contributed to low responsiveness of some shade responsive genes in our study (**Table 2**), as shown by previous reports that the induction levels of many shade responsive genes were reduced after 24 hours of treatment [22] [36] (References in **Table 2**).

4.2. The Shade Avoidance Response and the High Temperature Response

Comparing the overall gene expression responses to low R:FR light condition (W+FR) at 22˚C and to high temperature (26˚C) condition under WL confirmed the different nature of the two stimuli by showing no correlation between the two responses (**Figure 2(c)**). Likewise, only a small portion of the significantly responded MapMan bins exhibited an overlap between the two treatment effects (**Figure 3**). On the other hand, it was reported that warmer environmental temperature under non-shade condition induces phenotypic responses similar to shade avoidance response such as elongational growth through auxin biosynthesis as in shade avoidance response [15] [22]. Our phenotypic analyses also indicate that the high temperature effect is similar to the low R:FR light (W+FR) effect in terms of petiole length and pigment contents (**Figure 7**). Indeed, the auxin related genes were overrepresented both in W+FR effect at both temperatures and in 26˚C effect regardless of the light condition (**Figure 3**).

However, the auxin related MapMan bins that responded to light quality and the ones that responded to high temperature were not identical. The genes responded to supplemental far-red light were *AUX/IAA genes*, *homeobox transcription factors*, and *indole*-3-*acetic acid amido synthetases* (*GH3s*), whereas the high temperature mostly induced *IAA-amino acid conjugate hydrolases* (**Figure 4**). This suggests that the mode of regulation for the auxin content and the response is at least to some degree different in those responses. In addition to biosynthesis and degradation, active auxin levels are regulated by forming inactive conjugates with other compounds and by reversing the conjugation reactions through hydrolysis of some conjugates [46]. Indole-3-acetic acid amido synthetases (GH3s) conjugate auxins to amino acids to reduce the levels of active auxin [47], whereas IAA-amino acid conjugate hydrolases increase the levels of active auxin by reversing the auxin conjugation reaction and drives cell expansion [48] [49]. Interestingly, no significant induction of well-known auxin-inducible genes such as *Aux/IAA*, *GH3s* (**Figure 4**) was detected under our high temperature condition, while induction of those genes normally occurred by low R:FR light treatment. Thus we think that our high temperature condition (26˚C) did not induce a significant level of auxin biosynthesis after 24 hr of treatment. The normalized signal intensities of microarray data also indicated that the typical shade induced genes known to be regulated by PIF4/PIF5 are not induced by our high temperature condition (**Figure 6**). This result seems to speak against the previous notion that high temperature increases auxin biosynthesis through a common pathway (PIF4) shared by the light quality response pathway [23] [25]. However, it may be due to potentially different kinetics of auxin biosynthesis in response to different stimuli and/or due to a relatively small temperature difference between the test and control samples (26˚C − 22˚C = 4˚C) compared with the previous PIF4 studies (28˚C − 20˚C = 8˚C [23]; 29˚C − 22˚C = 7˚C [25]). Nevertheless, plant phenotypes measured after a week long treatment exhibited high temperature induced petiole elongation and reduction of pigments levels as well as enhanced responses when both treatments were applied together. This may indicate a slower kinetics of PIF4 activation and auxin induction by 26˚C treatment compared with low R:FR treatment, which may eventually have led to the exhibited phenotypes. Alternatively, this may be due to the results of an accumulation of small differences over time, or even be due to a PIF4-independent process. In fact, 26˚C treatment alone could induce cell wall related genes in our study (Cluster [c] in **Figure 5**; **Table 1**). Further comparative investigation on the dynamics of shade avoidance response and of temperature response will be needed to answer this question.

4.3. The Shade Responsive Genes in the Context of Different Temperatures

The expression levels of the majority of genes (**Figure 2** and **Figure 8**) and the comparisons of the most affected gene ontology terms (**Figure 3**) indicate that the gene expression changes in response to low R:FR at 22˚C and at 26˚C share similar yet distinct characteristics. On the one hand, many of the responsive genes to each stimulus are involved in the same biological processes. The overrepresented gene families at both temperatures are *photosystems*, *tetrapyrrole synthesis*, *thioredoxin*, *AUX/IAA family*, *post-translational modification*, and *transport* (**Figure 3** and **Figure 4**). In the same way, the high temperature responses under different light conditions (WL vs. W+FR) resulted in similar gene expression changes in several common groups (**Figure 2** and **Figure 8**), including the genes for *photosystems*, *auxin metabolism*, *jasmonate metabolism* as well as *protein synthesis/degradation*. Furthermore, we found that the induction levels of traditional shade responsive genes such as *ATHB*2, *HFR*1, *FT*, *IAA*29, *IAA*19, and *YUC*8 are not differentially affected in different temperature context (**Table 2**; **Figure 6**), suggesting that the high temperature did not affect the response patterns of those shade induced genes under our experimental condition. On the other hand, the global gene expression patterns and the MapMan analyses implied limited overlap and distinctions between the two responses (**Figure 2** and **Figure 3**). The ratios between the two W+FR responses at different temperatures (26˚C/22˚C) indicated that there are differentially responded genes (**Figure 8**). The top 4.7% of genes showing differential expression are enriched in *secondary metabolism*, *lipid transport*, *oxidative stress*, and *jasmonic acid response* as well as to *pathogen/defense response*. The most affected compartment is *cell wall* or *extracellular space*, which is also implied by the hierarchical clustering and classification of responsive genes (cluster [*c*]; **Figure 5**; **Table 1**). In addition, although statistically not significant, we also found *transcription factors for pathogen defense process*, *light response* and *ethylene signaling*. Again, the auxin response related genes are not enriched among the differentially responded ones in the different temperature contexts. It is not known how such differential regulation of cohorts of genes under different temperature contexts is regulated.

The significant representation of *defense* related genes among the differentially regulated genes is intriguing. Since our experimental plants were grown under a sterile condition, it is not likely that the plants were consistently infected by pathogens in multiple independent replicates. Given the previously reported connections among temperature, light, and pathogen defense mechanisms, it is not surprising that the genes for defense responses were found differentially regulated under our experimental condition. Jasmonic acid and salicylic acid are not only related to defense mechanisms against various pathogens but also to the regulation of hyponastic growth which is induced by low light intensities [50]. On the other hand, low R:FR ratio compromises both salicylic acid- and jasmonic acid-mediated pathogen defense [51] [52]. Furthermore, high temperature also compromises defense responses [53] [54]. Therefore, our finding corroborates the notion of crosstalk or pathway sharing among light, temperature, and defense responses. To better understand the mechanisms of plant response to environmental factors in the field where multiple factors fluctuate independently, further dissection of the signaling network that integrates different pathways will be required.

5. Conclusion

Our results suggest that there are clear differences in the gene expression patterns in response to low R:FR condition at different temperatures. However, we did not detect any significantly different expression behaviors among the representative shade induced genes under the conditions we tested. Our data also indicate that there is a possibility of differential regulation in auxin content/response in warm temperature response and in shade response. Further investigation is needed to address this in more detail. Despite the similar expression patterns of shade inducible genes, we identified subsets of genes that are differentially regulated under different temperature conditions, which are overrepresented in secondary metabolism, lipid transport, oxidative stress, jasmonic acid, ethylene, light, pathogen defense responses, and extracellular region.

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Supplement

Table S1. Significantly responded MapMan bins in at least one treatment effect.

Bin	Name	BH corrected *p*-value				
		<1> W+FR effect (22˚C)	<2> W+FR effect (26˚C)	<3> 26˚C effect (WL)	<4> 26˚C effect (W+FR)	<5> W+FR+ 26˚C effect
1.	PS	0.000	0.000	0.155	0.025	0.267
1.1.	PS.lightreaction	0.000	0.001	0.006	0.000	0.813
1.1.1.	PS.lightreaction.photosystem II	0.000	0.004	0.880	0.007	0.354
1.1.1.1.	PS.lightreaction.photosystem II.LHC-II	0.035	0.395	0.703	0.035	0.738
1.1.1.2.	PS.lightreaction.photosystem II.PSII polypeptide subunits	0.000	0.024	0.991	0.191	0.397
1.1.2.	PS.lightreaction.photosystem I	0.000	0.047	0.164	0.006	0.853
1.1.2.2.	PS.lightreaction.photosystem I.PSI polypeptide subunits	0.017	0.374	0.199	0.007	0.891
1.3.	PS.calvin cyle	0.729	0.006	0.412	0.027	0.005
4.	glycolysis	0.826	0.906	0.189	0.045	0.190
10.	cell wall	0.017	0.225	0.009	0.474	0.012
10.6.2.	cell wall.degradation.mannan-xylose-arabinose-fucose	0.878	0.428	0.541	0.035	0.298
14.	S-assimilation	0.301	0.628	0.029	0.009	0.137
16.	secondary metabolism	0.994	0.008	0.000	0.080	0.369
16.1.	secondary metabolism.isoprenoids	0.017	0.525	0.653	0.772	0.309
16.1.1.	secondary metabolism.isoprenoids.non-mevalonate pathway	0.005	0.428	0.935	0.461	0.451
16.2.	secondary metabolism.phenylpropanoids	0.712	0.789	0.010	0.446	0.426
16.5.	secondary metabolism.sulfur-containing	0.406	0.779	0.000	0.000	0.000
16.5.1.	secondary metabolism.sulfur-containing.glucosinolates	0.241	0.852	0.000	0.000	0.000
16.5.1.1.	secondary metabolism.sulfur-containing.glucosinolates.synthesis	0.288	0.984	0.000	0.001	0.000
16.5.1.1.1.	secondary metabolism.sulfur-containing.glucosinolates.synthesis.aliphatic	0.519	0.928	0.000	0.002	0.000
16.8.	secondary metabolism.flavonoids	0.885	0.002	0.020	0.452	0.484
16.8.1.	secondary metabolism.flavonoids.anthocyanins	0.660	0.003	0.017	0.913	0.497
16.8.1.21.	secondary metabolism.flavonoids.anthocyanins.anthocyanin 5-aromatic acyltransferase	0.660	0.047	0.181	0.970	0.279
17.	hormone metabolism	0.885	0.843	0.000	0.000	0.000
17.2.	hormone metabolism.auxin	0.472	0.159	0.017	0.003	0.001
17.2.1.	hormone metabolism.auxin.synthesis-degradation	0.793	0.525	0.011	0.032	0.267
17.2.3.	hormone metabolism.auxin.induced-regulated-responsive-activated	0.262	0.028	0.229	0.041	0.009
17.7.	hormone metabolism.jasmonate	0.660	0.532	0.000	0.000	0.000
17.7.1.	hormone metabolism.jasmonate.synthesis-degradation	0.879	0.757	0.002	0.002	0.017
17.7.1.2.	hormone metabolism.jasmonate.synthesis-degradation.lipoxygenase	0.660	0.976	0.025	0.403	0.160
17.7.3.	hormone metabolism.jasmonate.induced-regulated-responsive-activated	0.375	0.555	0.000	0.144	0.003

Continued

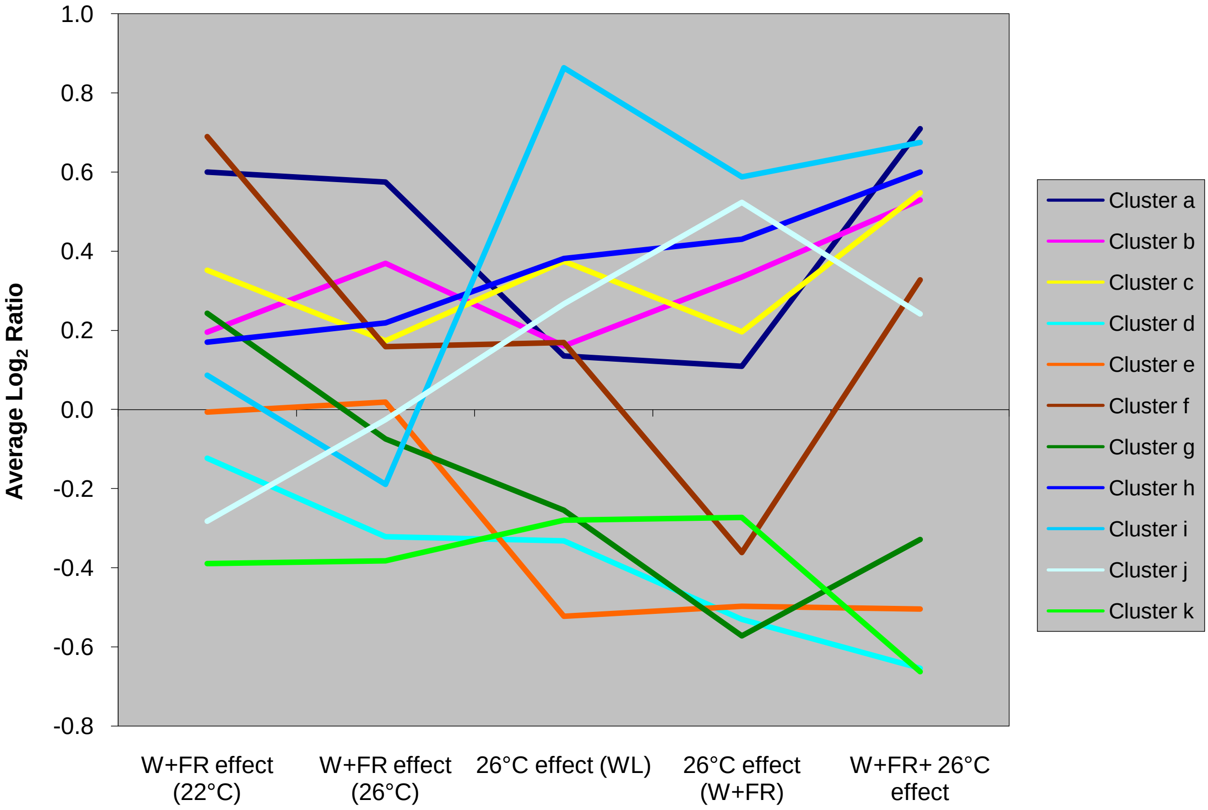
18.	Co-factor and vitamine metabolism	0.729	0.628	0.164	0.128	0.043
19.	tetrapyrrole synthesis	0.000	0.015	0.015	0.949	0.000
20.	stress	0.543	0.000	0.035	0.463	0.791
20.1.	stress.biotic	0.008	0.000	0.799	0.656	0.017
20.1.7.	stress.biotic.PR-proteins	0.081	0.000	0.880	0.883	0.022
20.1.7.6.	stress.biotic.PR-proteins.proteinase inhibitors	0.660	0.030	0.028	0.699	0.612
20.2.	stress.abiotic	0.810	0.165	0.006	0.495	0.192
20.2.1.	stress.abiotic.heat	0.343	0.637	0.004	0.544	0.047
21.	redox	0.214	0.008	0.835	0.531	0.560
21.1.	redox.thioredoxin	0.026	0.014	0.920	0.800	0.124
23.1.2.	nucleotide metabolism.synthesis.purine	0.769	0.756	0.081	0.037	0.097
26.	misc	0.983	0.000	0.000	0.303	0.344
26.1.	misc.cytochrome P450	0.971	0.015	0.002	0.970	0.528
26.8.	misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases	0.660	0.004	0.347	0.841	0.751
26.9.	misc.glutathione S transferases	0.672	0.002	0.323	0.911	0.517
26.12.	misc.peroxidases	0.825	0.196	0.003	0.499	0.484
26.16.	misc.myrosinases-lectin-jacalin	0.948	0.202	0.024	0.144	0.117
26.28.	misc.GDSL-motif lipase	0.660	0.604	0.010	0.600	0.097
27.	RNA	0.000	0.000	0.809	0.835	0.000
27.1.	RNA.processing	0.660	0.041	0.216	0.383	0.970
27.1.1.	RNA.processing.splicing	0.948	0.023	0.934	0.347	0.329
27.3.	RNA.regulation of transcription	0.000	0.000	0.735	0.666	0.000
27.3.4.	RNA.regulation of transcription.ARF, Auxin Response Factor family	0.100	0.010	0.714	0.970	0.464
27.3.8.	RNA.regulation of transcription.C2C2(Zn) DOF zinc finger family	0.885	0.392	0.483	0.041	0.097
27.3.14.	RNA.regulation of transcription.CCAAT box binding factor family, HAP2	0.879	0.191	0.323	0.107	0.022
27.3.20.	RNA.regulation of transcription.G2-like transcription factor family, GARP	0.689	0.023	0.265	0.149	0.011
27.3.22.	RNA.regulation of transcription.HB,Homeobox transcription factor family	0.017	0.335	0.148	0.758	0.022
27.3.25.	RNA.regulation of transcription.MYB domain transcription factor family	0.285	0.757	0.074	0.397	0.009
27.3.40.	RNA.regulation of transcription.Aux/IAA family	0.002	0.045	0.261	0.766	0.022
28.	DNA	0.628	0.000	0.000	0.088	0.685
28.1.	DNA.synthesis/chromatin structure	0.990	0.003	0.000	0.386	0.538
28.1.3.	DNA.synthesis/chromatin structure.histone	0.231	0.467	0.000	0.544	0.022
29.	protein	0.826	0.577	0.000	0.001	0.000
29.1.	protein.aa activation	0.895	0.975	0.009	0.018	0.043
29.2.	protein.synthesis	0.898	0.789	0.000	0.000	0.000
29.2.1.	protein.synthesis.ribosomal protein	0.885	0.852	0.000	0.000	0.000

Continued

29.2.1.1.	protein.synthesis.ribosomal protein.prokaryotic	0.021	0.690	0.000	0.004	0.000
29.2.1.1.1.	protein.synthesis.ribosomal protein.prokaryotic.chloroplast	0.000	0.191	0.000	0.128	0.000
29.2.1.1.1.1.	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.30S subunit	0.225	0.966	0.013	0.497	0.006
29.2.1.1.1.2.	protein.synthesis.ribosomal protein.prokaryotic.chloroplast.50S subunit	0.002	0.059	0.003	0.242	0.000
29.2.1.1.3.	protein.synthesis.ribosomal protein.prokaryotic.unknown organellar	0.955	0.894	0.029	0.058	0.023
29.2.1.2.	protein.synthesis.ribosomal protein.eukaryotic	0.450	0.525	0.000	0.000	0.000
29.2.1.2.1.	protein.synthesis.ribosomal protein.eukaryotic.40S subunit	0.689	0.852	0.000	0.000	0.000
29.2.1.2.2.	protein.synthesis.ribosomal protein.eukaryotic.60S subunit	0.013	0.106	0.000	0.000	0.000
29.2.3.	protein.synthesis.initiation	0.202	0.789	0.189	0.002	0.484
29.3.2.	protein.targeting.mitochondria	0.979	0.928	0.011	0.035	0.083
29.3.3.	protein.targeting.chloroplast	0.885	0.756	0.104	0.172	0.023
29.4.	protein.postranslational modification	0.005	0.007	0.991	0.970	0.097
29.4.1.	protein.postranslational modification.kinase	0.021	0.593	0.950	0.308	0.612
29.5.	protein.degradation	0.019	0.966	0.009	0.000	0.032
29.5.2.	protein.degradation.autophagy	0.571	0.963	0.233	0.008	0.344
29.5.3.	protein.degradation.cysteine protease	0.771	0.779	0.003	0.386	0.015
29.5.11.	protein.degradation.ubiquitin	0.030	0.982	0.007	0.000	0.022
29.5.11.4.	protein.degradation.ubiquitin.E3	0.276	0.894	0.000	0.000	0.000
29.5.11.4.2.	protein.degradation.ubiquitin.E3.RING	0.879	0.894	0.006	0.000	0.005
29.5.11.4.3.	protein.degradation.ubiquitin.E3.SCF	0.254	0.779	0.006	0.000	0.007
29.5.11.4.3.2.	protein.degradation.ubiquitin.E3.SCF.FBOX	0.344	0.678	0.009	0.000	0.004
29.5.11.20.	protein.degradation.ubiquitin.proteasom	0.225	0.966	0.002	0.446	0.005
29.6.	protein.folding	0.826	0.133	0.229	0.029	0.007
30.11.	signalling.light	0.285	0.122	0.216	0.439	0.006
31.	cell	0.454	0.000	0.096	0.906	0.174
31.1.	cell.organisation	0.112	0.009	0.216	0.449	0.584
31.3.	cell.cycle	0.729	0.015	0.309	0.970	0.612
33.3.	development.squamosa promoter binding like (SPL)	0.225	0.125	0.398	0.464	0.012
34.	transport	0.002	0.014	0.596	0.347	0.510
34.2.	transporter.sugars	0.000	0.351	0.631	0.392	0.272
34.6.	transport.sulphate	0.729	0.852	0.010	0.008	0.043
34.19.	transport.Major Intrinsic Proteins	0.109	0.529	0.017	0.010	0.544
34.19.1.	transport.Major Intrinsic Proteins.PIP	0.214	0.815	0.010	0.000	0.242
35.1.	not assigned.no ontology	0.100	0.809	0.657	0.001	0.528
35.1.5.	not assigned.no ontology.pentatricopeptide (PPR) repeat-containing protein	0.017	0.996	0.238	0.000	0.287

Table S2. The expression levels of genes in each cluster. Statistically significant genes were grouped by hierarchical clustering. Eleven arbitrary clusters were formed by grouping the nodes with genes that exhibited similar expression patterns (**Figure 5**). Individual gene expression data for each cluster is included in separate spreadsheets.

	Average Gene Expression ($\log_2$ ratio)				
	W+FR effect (22˚C)	W+FR effect (26˚C)	26˚C effect (WL)	26˚C effect (W+FR)	W+FR+ 26˚C effect
Cluster a	0.60	0.57	0.14	0.11	0.71
Cluster b	0.19	0.37	0.16	0.33	0.53
Cluster c	0.35	0.17	0.37	0.20	0.55
Cluster d	−0.12	−0.32	−0.33	−0.53	−0.65
Cluster e	−0.01	0.02	−0.52	−0.50	−0.50
Cluster f	0.69	0.16	0.17	−0.36	0.33
Cluster g	0.24	−0.07	−0.25	−0.57	−0.33
Cluster h	0.17	0.22	0.38	0.43	0.60
Cluster i	0.09	−0.19	0.86	0.59	0.67
Cluster j	−0.28	−0.03	0.27	0.52	0.24
Cluster k	−0.39	−0.38	−0.28	−0.27	−0.66



(a)

ID	Locus	Description	W+FR effect (22˚C)	W+FR effect (26˚C)	26˚C effect (WL)	26˚C effect (W+FR)	W+FR+ 26˚C effect
244933_at	ATCG01070	NADH-ubiquinone/plastoquinone oxidoreductase chain 4L	0.45	0.25	0.25	0.05	0.50
244937_at	ATCG01110	NAD(P)H dehydrogenase subunit H	0.45	0.45	0.04	0.04	0.49
244959_s_at	AT2G07708	[AT2G07708, unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:ATMG00500.1); Has 9 Blast hits to 9 proteins in 2 species: Archae-0; Bacteria-0; Metazoa-0; Fungi-0; Plants-9; Viruses-0; Other Eukaryotes-0 (source: NCBI BLink).];[ATMG00500, hypothetical protein]; [ATMG00490, Mitovirus RNA-dependent RNA polymerase]	0.33	0.28	0.24	0.19	0.52
244977_at	ATCG00730	photosynthetic electron transfer D	0.72	0.66	0.22	0.16	0.88
245000_at	ATCG00210	electron transporter, transferring electrons within cytochrome b6/f complex of photosystem IIs	0.64	0.46	0.47	0.29	0.93
245076_at	AT2G23170	Auxin-responsive GH3 family protein	0.23	0.51	−0.12	0.16	0.39
245276_at	AT4G16780	homeobox protein 2	1.10	0.87	0.39	0.16	1.26
245336_at	AT4G16515	Encodes a root meristem growth factor (RGF). Belongs to a family of functionally redundant homologous peptides that are secreted, tyrosine-sulfated, and expressed mainly in the stem cell area and the innermost layer of central columella cells. RGFs are required for maintenance of the root stem cell niche and transit amplifying cell proliferation. Members of this family include: At5g60810 (RGF1), At1g13620 (RGF2), At2g04025 (RGF3), At3g30350 (RGF4), At5g51451 (RGF5), At4g16515 (RGF6), At3g02240 (RGF7), At2g03830 (RGF8) and At5g64770 (RGF9).	0.76	0.64	0.06	−0.06	0.70
245397_at	AT4G14560	indole-3-acetic acid inducible	0.57	0.59	0.11	0.13	0.70
245645_at	AT1G24764	microtubule-associated proteins 70-2	0.37	0.35	0.12	0.10	0.47
246225_at	AT4G36910	Cystathionine beta-synthase (CBS) family protein	0.27	0.16	0.19	0.08	0.35
247474_at	AT5G62280	Protein of unknown function (DUF1442)	0.80	1.66	−0.30	0.55	1.35
247854_at	AT5G58200	Calcineurin-like metallo-phosphoesterase superfamily protein	0.21	0.20	0.16	0.15	0.36
247880_at	AT5G57780	EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 12 growth stages; BEST *Arabidopsis thaliana* protein match is: sequence-specific DNA binding transcription factors (TAIR:AT4G30410.1); Has 123 Blast hits to 123 proteins in 11 species: Archae-0; Bacteria-0; Metazoa-0; Fungi-0; Plants-123; Viruses-0; Other Eukaryotes-0 (source: NCBI BLink).	0.36	0.25	0.24	0.12	0.48
248801_at	AT5G47370	Homeobox-leucine zipper protein 4 (HB-4)/HD-ZIP protein	0.61	0.71	0.22	0.31	0.92
249894_at	AT5G22580	Stress responsive A/B Barrel Domain	0.46	0.49	0.05	0.08	0.53
249917_at	AT5G22460	alpha/beta-Hydrolases superfamily protein	0.78	0.59	−0.17	−0.37	0.42
250012_x_at	AT5G18060	SAUR-like auxin-responsive protein family	0.88	0.72	0.49	0.33	1.21
250120_at	AT5G16490	ROP-interactive CRIB motif-containing protein 4	0.32	0.27	0.29	0.24	0.56
250327_at	AT5G12050	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT3G13980.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae-0; Bacteria-0; Metazoa-736; Fungi-347; Plants-385; Viruses-0; Other Eukaryotes-339 (source: NCBI BLink).	0.64	0.76	0.04	0.16	0.80
250872_at	AT5G03960	IQ-domain 12	0.57	0.55	0.07	0.05	0.63

Continued

251010_at	AT5G02550	unknown protein; Has 3 Blast hits to 3 proteins in 1 species: Archae-0; Bacteria-0; Metazoa-0; Fungi-0; Plants-3; Viruses-0; Other Eukaryotes-0 (source: NCBI BLink).	0.44	0.41	0.14	0.11	0.55
251017_at	AT5G02760	Protein phosphatase 2C family protein	0.65	0.77	0.04	0.16	0.81
251072_at	AT5G01740	Nuclear transport factor 2 (NTF2) family protein	0.55	0.49	0.26	0.19	0.74
251144_at	AT5G01210	HXXXD-type acyl-transferase family protein	0.36	0.34	0.24	0.22	0.58
251271_at	AT3G62050	Putative endonuclease or glycosyl hydrolase	0.37	0.27	0.16	0.06	0.43
252204_at	AT3G50340	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT5G67020.1); Has 128 Blast hits to 128 proteins in 39 species: Archae-0; Bacteria-46; Metazoa-0; Fungi-3; Plants-76; Viruses-0; Other Eukaryotes-3 (source: NCBI BLink).	0.33	0.39	0.12	0.18	0.50
252296_at	AT3G48970	Heavy metal transport/detoxification superfamily protein	0.43	0.46	0.08	0.11	0.54
252983_at	AT4G37980	elicitor-activated gene 3-1	0.32	0.35	0.09	0.12	0.44
253191_at	AT4G35350	xylem cysteine peptidase 1	0.44	0.39	0.16	0.11	0.55
253423_at	AT4G32280	indole-3-acetic acid inducible 29	2.15	2.07	0.17	0.09	2.24
253791_at	AT4G28640	indole-3-acetic acid inducible 11	0.33	0.29	0.21	0.17	0.50
253794_at	AT4G28720	Flavin-binding monooxygenase family protein	0.48	0.71	−0.07	0.16	0.65
254319_at	AT4G22560	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT4G12450.1); Has 380 Blast hits to 380 proteins in 21 species: Archae-0; Bacteria-0; Metazoa-0; Fungi-6; Plants-374; Viruses-0; Other Eukaryotes-0 (source: NCBI BLink).	0.37	0.30	0.18	0.11	0.48
254328_at	AT4G22570	adenine phosphoribosyl transferase 3	0.34	0.28	0.25	0.19	0.53
255538_at	AT4G01680	myb domain protein 55	0.41	0.21	0.26	0.07	0.48
255694_at	AT4G00050	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	0.36	0.28	0.26	0.19	0.54
256384_at	AT1G66660	Protein with RING/U-box and TRAF-like domains	0.27	0.23	0.23	0.19	0.46
257650_at	AT3G16800	Protein phosphatase 2C family protein	0.68	0.54	0.25	0.11	0.80
257766_at	AT3G23030	indole-3-acetic acid inducible 2	0.52	0.51	0.17	0.16	0.68
258399_at	AT3G15540	indole-3-acetic acid inducible 19	0.66	0.69	−0.02	0.01	0.67
258807_at	AT3G04030	Homeodomain-like superfamily protein	0.48	0.48	0.02	0.01	0.50
259417_at	AT1G02340	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	2.39	2.48	0.38	0.47	2.86
259773_at	AT1G29500	SAUR-like auxin-responsive protein family	0.55	0.55	0.23	0.24	0.78
259784_at	AT1G29450	SAUR-like auxin-responsive protein family	0.39	0.45	0.16	0.22	0.61
260753_at	AT1G49230	RING/U-box superfamily protein	0.55	0.52	−0.05	−0.08	0.47
261023_at	AT1G12200	Flavin-binding monooxygenase family protein	0.42	0.32	0.24	0.15	0.56
261292_at	AT1G36940	unknown protein; Has 21 Blast hits to 21 proteins in 8 species: Archae-0; Bacteria-0; Metazoa-0; Fungi-0; Plants-21; Viruses-0; Other Eukaryotes-0 (source: NCBI BLink).	0.44	0.27	0.18	0.00	0.44
262050_at	AT1G80130	Tetratricopeptide repeat (TPR)-like superfamily protein	1.11	0.91	0.11	−0.09	1.02

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263002_at	AT1G54200	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT3G13980.1); Has 1084 Blast hits to 581 proteins in 136 species: Archae-0; Bacteria-72; Metazoa-212; Fungi-78; Plants-102; Viruses-0; Other Eukaryotes-620 (source: NCBI BLink).	0.60	0.39	0.29	0.09	0.69
263971_at	AT2G42800	receptor like protein 29	0.53	0.58	−0.19	−0.14	0.39
264100_at	AT1G78970	lupeol synthase 1	0.93	0.83	−0.06	−0.16	0.77
264594_at	AT2G17640	Trimeric LpxA-like enzymes superfamily protein	0.32	0.27	0.08	0.04	0.36
264638_at	AT1G65480	PEBP (phosphatidylethanolamine-binding protein) family protein	2.52	2.43	−0.25	−0.34	2.18
264947_at	AT1G77020	DNAJ heat shock N-terminal domain-containing protein	0.40	0.26	0.18	0.04	0.45
265194_at	AT1G05010	ethylene-forming enzyme	0.33	0.22	0.14	0.03	0.36
265494_at	AT2G15680	Calcium-binding EF-hand family protein	0.46	0.37	0.29	0.19	0.66
266415_at	AT2G38530	lipid transfer protein 2	0.70	0.38	0.33	0.00	0.71
266516_at	AT2G47880	Glutaredoxin family protein	0.64	0.96	−0.33	−0.01	0.63
267141_at	AT2G38090	Duplicated homeodomain-like superfamily protein	0.52	0.44	0.19	0.11	0.63
267460_at	AT2G33810	squamosa promoter binding protein-like 3	0.33	0.50	0.09	0.26	0.58

(b)

ID	Locus	Description	W+FR effect (22˚C)	W+FR effect (26˚C)	26˚C effect (WL)	26˚C effect (W+FR)	W+FR+ 26˚C effect
247648_at	AT5G60020	laccase 17	0.16	0.33	0.17	0.34	0.50
248121_at	AT5G54690	galacturonosyltransferase 12	0.13	0.27	0.13	0.26	0.39
248282_at	AT5G52900	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae-12; Bacteria-1396; Metazoa-17338; Fungi-3422; Plants-5037; Viruses-0; Other Eukaryotes-2996 (source: NCBI BLink).	0.13	0.34	0.10	0.31	0.44
249614_at	AT5G37300	O-acyltransferase (WSD1-like) family protein	0.47	0.56	0.30	0.39	0.86
251056_at	AT5G01770	HEAT repeat ;WD domain, G-beta repeat protein protein	0.17	0.18	0.16	0.17	0.35
252200_at	AT3G50280	HXXXD-type acyl-transferase family protein	0.25	0.30	0.24	0.29	0.54
253182_at	AT4G35190	Putative lysine decarboxylase family protein	0.16	0.49	0.08	0.41	0.57
253660_at	AT4G30140	GDSL-like Lipase/Acylhydrolase superfamily protein	−0.13	0.36	−0.13	0.36	0.23
253908_at	AT4G27260	Auxin-responsive GH3 family protein	0.52	0.63	0.32	0.43	0.95
254758_at	AT4G13260	Flavin-binding monooxygenase family protein	0.10	0.37	0.13	0.39	0.50
255957_at	AT1G22160	Protein of unknown function (DUF581)	0.17	0.52	0.13	0.48	0.66
258338_at	AT3G16150	N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein	−0.11	0.42	0.02	0.55	0.44
259180_at	AT3G01680	CONTAINS InterPro DOMAIN/s: Mediator complex subunit Med28 (InterPro:IPR021640); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G01670.1); Has 122 Blast hits to 112 proteins in 13 species: Archae-0; Bacteria-0; Metazoa-0; Fungi-0; Plants-122; Viruses-0; Other Eukaryotes-0 (source: NCBI BLink).	0.14	0.20	0.15	0.21	0.35

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259783_at	AT1G29510	SAUR-like auxin-responsive protein family	0.22	0.33	0.19	0.30	0.52
259787_at	AT1G29460	SAUR-like auxin-responsive protein family	0.30	0.41	0.18	0.29	0.59
259839_at	AT1G52190	Major facilitator superfamily protein	0.14	0.32	0.15	0.32	0.47
259971_at	AT1G76580	Squamosa promoter-binding protein-like (SBP domain) transcription factor family protein	0.17	0.25	0.10	0.17	0.34
261077_at	AT1G07430	highly ABA-induced PP2C gene 2	0.44	0.61	0.35	0.52	0.96
262872_at	AT1G64690	branchless trichome	0.20	0.23	0.10	0.14	0.33
264021_at	AT2G21200	SAUR-like auxin-responsive protein family	0.38	0.40	0.26	0.28	0.66
264795_at	AT1G08680	ARF GAP-like zinc finger-containing protein ZIGA4	0.31	0.35	0.20	0.25	0.55
267077_at	AT2G40970	Homeodomain-like superfamily protein	0.11	0.39	0.26	0.53	0.64
267515_at	AT2G45680	TCP family transcription factor	0.03	0.24	0.11	0.32	0.35

(c)

ID	Locus	Description	W+FR effect (22˚C)	W+FR effect (26˚C)	26˚C effect (WL)	26˚C effect (W+FR)	W+FR+ 26˚C effect
244903_at	ATMG00660	hypothetical protein	0.62	0.23	0.49	0.11	0.73
249070_at	AT5G44030	cellulose synthase A4	0.20	0.14	0.29	0.24	0.43
249383_at	AT5G39860	basic helix-loop-helix (bHLH) DNA-binding family protein	1.04	0.37	0.90	0.23	1.27
251505_at	AT3G59052	[AT3G59052, conserved peptide upstream open reading frame 18]; [AT3G59050, polyamine oxidase 3]	0.19	0.17	0.21	0.19	0.38
251791_at	AT3G55500	expansin A16	0.49	0.24	0.42	0.17	0.66
251925_at	AT3G54000	CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP022260 (InterPro: IPR016802); Has 94 Blast hits to 94 proteins in 14 species: Archae-0; Bacteria-0; Metazoa-0; Fungi-0; Plants-94; Viruses-0; Other Eukaryotes-0 (source: NCBI BLink).	0.33	0.16	0.40	0.23	0.56
252025_at	AT3G52900	Family of unknown function (DUF662)	0.28	0.18	0.34	0.23	0.52
252938_at	AT4G39190	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT2G21560.1); Has 5536 Blast hits to 3562 proteins in 401 species: Archae-12; Bacteria-497; Metazoa-1363; Fungi-374; Plants-149; Viruses-22; Other Eukaryotes-3119 (source: NCBI BLink).	0.30	0.13	0.27	0.09	0.39
253620_at	AT4G30520	Leucine-rich repeat protein kinase family protein	0.22	0.12	0.26	0.15	0.38
253919_at	AT4G27350	Protein of unknown function (DUF1223)	0.29	0.17	0.37	0.24	0.53
254258_at	AT4G23410	tetraspanin5	0.26	0.13	0.29	0.16	0.42
254305_at	AT4G22200	potassium transport 2/3	0.27	0.15	0.34	0.22	0.49
254609_at	AT4G18970	GDSL-like Lipase/Acylhydrolase superfamily protein	0.27	0.16	0.22	0.11	0.38
255760_at	AT1G16780	Inorganic H pyrophosphatase family protein	0.28	0.15	0.32	0.19	0.47
256389_at	AT3G06220	AP2/B3-like transcriptional factor family protein	0.30	0.07	0.35	0.12	0.42
258876_at	AT3G03120	ADP-ribosylation factor B1C	0.22	0.17	0.26	0.21	0.43
259165_at	AT3G01470	[AT3G01470, homeobox 1]; [AT3G01472, conserved peptide upstream open reading frame 33]	0.22	0.18	0.29	0.24	0.46

Continued

259166_at	AT3G01670	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT3G01680.1); Has 121 Blast hits to 111 proteins in 12 species: Archae-0; Bacteria-0; Metazoa-0; Fungi-0; Plants-121; Viruses-0; Other Eukaryotes-0 (source: NCBI BLink).	0.25	0.12	0.35	0.21	0.47
259381_s_at	AT3G16410	[AT3G16410, nitrile specifier protein 4];[AT3G16390, nitrile specifier protein 3]; [AT3G16400, nitrile specifier protein 1]	0.50	0.16	0.54	0.20	0.70
259937_s_at	AT3G13080	[AT3G13080, multidrug resistance-associated protein 3];[AT1G71330, non-intrinsic ABC protein 5]	0.22	0.18	0.24	0.20	0.42
260112_at	AT1G63310	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT2G20362.1); Has 78 Blast hits to 77 proteins in 11 species: Archae-0; Bacteria-0; Metazoa-0; Fungi-0; Plants-78; Viruses-0; Other Eukaryotes-0 (source: NCBI BLink).	0.25	0.20	0.32	0.27	0.52
260666_at	AT1G19300	Nucleotide-diphospho-sugar transferases superfamily protein	0.31	0.17	0.29	0.15	0.46
262204_at	AT2G01100	unknown protein; Has 19420 Blast hits to 10641 proteins in 779 species: Archae-0; Bacteria-1003; Metazoa-10257; Fungi-1826; Plants-1570; Viruses-56; Other Eukaryotes-4708 (source: NCBI BLink).	0.35	0.14	0.37	0.16	0.52
262615_at	AT1G13950	eukaryotic elongation factor 5A-1	0.51	0.05	0.67	0.21	0.72
262733_s_at	AT1G28660	[AT1G28660, GDSL-like Lipase/Acylhydrolase superfamily protein]; [AT1G28670, GDSL-like Lipase/Acylhydrolase superfamily protein]	0.36	0.12	0.30	0.06	0.41
263545_at	AT2G21560	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT4G39190.1); Has 3685 Blast hits to 2305 proteins in 270 species: Archae-0; Bacteria-156; Metazoa-1145; Fungi-322; Plants-177; Viruses-6; Other Eukaryotes-1879 (source: NCBI BLink).	0.36	0.21	0.30	0.15	0.51
264156_at	AT1G65280	DNAJ heat shock N-terminal domain-containing protein	0.30	0.11	0.31	0.12	0.42
264157_at	AT1G65310	xyloglucan endotransglucosylase/hydrolase 17	0.38	0.29	0.42	0.33	0.71
265228_s_at	ATMG01190	[ATMG01190, ATP synthase subunit 1]; [AT2G07698, ATPase, F1 complex, alpha subunit protein]	0.42	0.14	0.42	0.14	0.56
265230_s_at	ATMG00480	[ATMG00480, Plant mitochondrial ATPase, F0 complex, subunit 8 protein]; [AT2G07707, Plant mitochondrial ATPase, F0 complex, subunit 8 protein]	0.30	0.23	0.40	0.32	0.63
265463_at	AT2G37090	Nucleotide-diphospho-sugar transferases superfamily protein	0.39	0.18	0.42	0.21	0.60
265576_at	AT2G20190	CLIP-associated protein	0.22	0.13	0.23	0.13	0.35
266613_at	AT2G14900	Gibberellin-regulated family protein	0.66	0.45	0.62	0.41	1.07
267094_at	AT2G38080	Laccase/Diphenol oxidase family protein	0.42	0.14	0.51	0.23	0.65

(d)

ID	Locus	description	W+FR effect (22˚C)	W+FR effect (26˚C)	26˚C effect (WL)	26˚C effect (W+FR)	W+FR+ 26˚C effect
245319_at	AT4G16146	cAMP-regulated phosphoprotein 19-related protein	−0.06	−0.21	−0.30	−0.46	−0.52
246270_at	AT4G36500	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT2G18210.1); Has 50 Blast hits to 50 proteins in 7 species: Archae-0; Bacteria-0; Metazoa-0; Fungi-0; Plants-50; Viruses-0; Other Eukaryotes-0 (source: NCBI BLink).	−0.13	−0.21	−0.28	−0.36	−0.49
247444_at	AT5G62630	hipl2 protein precursor	−0.11	−0.20	−0.25	−0.34	−0.44

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247766_at	AT5G58870	FTSH protease 9	−0.21	−0.27	−0.25	−0.31	−0.52
249061_at	AT5G44550	Uncharacterised protein family (UPF0497)	−0.17	−0.33	−0.29	−0.46	−0.62
249918_at	AT5G19240	Glycoprotein membrane precursor GPI-anchored	−0.15	−0.26	−0.34	−0.45	−0.60
250942_at	AT5G03350	Legume lectin family protein	−0.24	−0.88	−0.79	−1.43	−1.67
252102_at	AT3G50970	dehydrin family protein	0.14	−0.58	−0.55	−1.27	−1.13
252853_at	AT4G39710	FK506-binding protein 16-2	−0.04	−0.19	−0.25	−0.40	−0.44
253859_at	AT4G27657	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G54145.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae-12; Bacteria-1396; Metazoa-17338; Fungi-3422; Plants-5037; Viruses-0; Other Eukaryotes-2996 (source: NCBI BLink).	−0.14	−0.21	−0.20	−0.27	−0.41
256060_at	AT1G07050	CCT motif family protein	−0.35	−0.49	−0.47	−0.61	−0.96
261166_s_at	AT3G15750	[AT3G15750, Essential protein Yae1, N-terminal]; [AT1G34570, Essential protein Yae1, N-terminal]	−0.16	−0.25	−0.28	−0.37	−0.52
262450_at	AT1G11320	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, plastid; EXPRESSED IN: 7 plant structures; EXPRESSED DURING: C globular stage, F mature embryo stage, petal differentiation and expansion stage, E expanded cotyledon stage, D bilateral stage; Has 46 Blast hits to 46 proteins in 14 species: Archae-0; Bacteria-2; Metazoa-0; Fungi-0; Plants-44; Viruses-0; Other Eukaryotes-0 (source: NCBI BLink).	0.01	−0.15	−0.19	−0.34	−0.34
262693_at	AT1G62780	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, chloroplast stroma; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 14 growth stages; Has 94 Blast hits to 94 proteins in 35 species: Archae-6; Bacteria-10; Metazoa-21; Fungi-2; Plants-48; Viruses-0; Other Eukaryotes-7 (source: NCBI BLink).	0.05	−0.21	−0.24	−0.50	−0.45
265075_at	AT1G55450	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	−0.30	−0.39	−0.31	−0.41	−0.71

(e)

ID	Locus	Description	W+FR effect (22˚C)	W+FR effect (26˚C)	26˚C effect (WL)	26˚C effect (W+FR)	W+FR+ 26˚C effect
245306_at	AT4G14690	Chlorophyll A-B binding family protein	−0.12	0.16	−1.29	−1.02	−1.14
245937_at	AT5G19750	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	0.00	−0.04	−0.47	−0.52	−0.52
246293_at	AT3G56710	sigma factor binding protein 1	−0.10	−0.22	−0.45	−0.56	−0.66
247347_at	AT5G63780	RING/FYVE/PHD zinc finger superfamily protein	−0.07	−0.11	−0.32	−0.36	−0.43
247362_at	AT5G63140	purple acid phosphatase 29	0.25	0.22	−0.49	−0.52	−0.27
248062_at	AT5G55450	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	0.23	0.17	−0.94	−1.00	−0.77
248614_at	AT5G49560	Putative methyltransferase family protein	0.39	0.30	−0.57	−0.66	−0.27
248744_at	AT5G48250	B-box type zinc finger protein with CCT domain	−0.03	−0.02	−0.49	−0.48	−0.51
249174_at	AT5G42900	cold regulated gene 27	−0.26	−0.27	−0.56	−0.56	−0.83
249477_s_at	AT5G38940	[AT5G38940, RmlC-like cupins superfamily protein]; [AT5G38930, RmlC-like cupins superfamily protein]	0.17	0.43	−0.63	−0.37	−0.20

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250837_at	AT5G04620	biotin F	−0.03	−0.05	−0.51	−0.54	−0.56
251701_at	AT3G56650	Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein	−0.14	−0.07	−0.36	−0.29	−0.43
252468_at	AT3G46970	Alpha-glucan phosphorylase 2	−0.15	−0.11	−0.29	−0.25	−0.40
252659_at	AT3G44430	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT5G41660.1); Has 6 Blast hits to 6 proteins in 1 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−6; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.18	−0.12	−0.38	−0.32	−0.50
253215_at	AT4G34950	Major facilitator superfamily protein	−0.17	−0.22	−0.56	−0.61	−0.79
254080_at	AT4G25630	fibrillarin 2	0.11	0.15	−0.54	−0.49	−0.38
254563_at	AT4G19120	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	−0.16	−0.01	−0.56	−0.42	−0.58
254572_at	AT4G19380	Long-chain fatty alcohol dehydrogenase family protein	0.22	0.15	−0.56	−0.63	−0.41
255300_at	AT4G04870	cardiolipin synthase	0.00	0.01	−0.36	−0.35	−0.35
256036_at	AT1G07110	fructose-2,6-bisphosphatase	−0.02	−0.01	−0.39	−0.38	−0.40
256741_at	AT3G29375	XH domain-containing protein	0.20	0.21	−0.40	−0.39	−0.19
257315_at	AT3G30775	Methylenetetrahydrofolate reductase family protein	−0.30	−0.13	−0.74	−0.56	−0.86
257516_at	AT1G69040	ACT domain repeat 4	−0.09	−0.06	−0.54	−0.51	−0.59
258232_at	AT3G27750	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 12 growth stages; BEST *Arabidopsis thaliana* protein match is: Vacuolar sorting protein 9 (VPS9) domain (TAIR: AT5G09320.1); Has 106 Blast hits to 106 proteins in 16 species: Archae-0; Bacteria-0; Metazoa-0; Fungi-4; Plants-102; Viruses-0; Other Eukaryotes-0 (source: NCBI BLink).	−0.08	−0.09	−0.35	−0.37	−0.45
258321_at	AT3G22840	Chlorophyll A-B binding family protein	0.33	0.54	−1.01	−0.80	−0.47
258834_at	AT3G07270	GTP cyclohydrolase I	−0.07	−0.12	−0.27	−0.32	−0.39
259258_at	AT3G07670	Rubisco methyltransferase family protein	0.08	0.06	−0.33	−0.35	−0.26
261483_at	AT1G14270	CAAX amino terminal protease family protein	−0.13	−0.11	−0.28	−0.26	−0.39
262703_at	AT1G16510	SAUR-like auxin-responsive protein family	−0.09	−0.17	−0.31	−0.39	−0.47
262892_at	AT1G79440	aldehyde dehydrogenase 5F1	−0.03	−0.08	−0.36	−0.41	−0.44
263497_at	AT2G42540	cold-regulated 15a	−0.26	−0.30	−0.68	−0.72	−0.98
264668_at	AT1G09780	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	0.10	0.08	−0.49	−0.51	−0.41
264824_at	AT1G03420	transposable element gene	−0.01	0.11	−0.57	−0.45	−0.46
266778_at	AT2G29090	cytochrome P450, family 707, subfamily A, polypeptide 2	0.23	0.46	−0.90	−0.66	−0.43
267578_at	AT2G30695	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: protein folding, protein transport; LOCATED IN: chloroplast stroma, chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Trigger factor, ribosome-binding, bacterial (InterPro:IPR008881); Has 253 Blast hits to 253 proteins in 72 species: Archae-0; Bacteria-138; Metazoa-0; Fungi-0; Plants-40; Viruses-0; Other Eukaryotes-75 (source: NCBI BLink).	−0.05	−0.10	−0.33	−0.38	−0.43

(f)

ID	Locus	Description	W+FR effect (22˚C)	W+FR effect (26˚C)	26˚C effect (WL)	26˚C effect (W+FR)	W+FR+ 26˚C effect
245216_at	AT4G16143	importin alpha isoform 2	0.32	−0.12	0.03	−0.42	−0.09
245904_at	AT5G11110	sucrose phosphate synthase 2F	0.61	0.12	0.29	−0.20	0.41
248268_at	AT5G53480	ARM repeat superfamily protein	0.71	0.09	0.10	−0.52	0.19
249953_at	AT5G18960	FAR1-related sequence 12	0.62	−0.07	0.22	−0.47	0.15
249986_at	AT5G18460	Protein of Unknown Function (DUF239)	0.58	−0.10	0.11	−0.56	0.02
250155_at	AT5G15160	BANQUO 2	0.88	0.63	0.16	−0.09	0.79
250657_at	AT5G07000	sulfotransferase 2B	0.85	0.56	0.13	−0.16	0.69
251012_at	AT5G02580	Plant protein 1589 of unknown function	0.77	0.43	0.18	−0.17	0.61
251887_at	AT3G54170	FKBP12 interacting protein 37	0.37	0.01	0.04	−0.33	0.04
252549_at	AT3G45860	cysteine-rich RLK (RECEPTOR-like protein kinase) 4	0.70	0.25	0.43	−0.02	0.68
254341_at	AT4G22130	STRUBBELIG-receptor family 8	0.50	0.03	0.05	−0.42	0.08
254390_at	AT4G21940	calcium-dependent protein kinase 15	0.49	0.28	0.12	−0.09	0.40
254737_at	AT4G13840	HXXXD-type acyl-transferase family protein	0.58	0.02	0.09	−0.47	0.11
256781_at	AT3G13650	Disease resistance-responsive (dirigent-like protein) family protein	0.71	0.16	0.13	−0.42	0.29
257876_at	AT3G17130	Plant invertase/pectin methylesterase inhibitor superfamily protein	0.53	0.13	0.31	−0.08	0.45
258125_s_at	AT3G23530	[AT3G23530, Cyclopropane-fatty-acyl-phospholipid synthase];[AT3G23510, Cyclopropane-fatty-acyl-phospholipid synthase]	0.70	0.27	−0.03	−0.46	0.24
258270_at	AT3G15650	alpha/beta-Hydrolases superfamily protein	0.66	−0.17	0.02	−0.82	−0.16
261917_at	AT1G65920	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain	0.79	0.39	0.25	−0.15	0.64
264006_at	AT2G22430	homeobox protein 6	0.85	0.11	0.63	−0.11	0.74
264342_at	AT1G12080	Vacuolar calcium-binding protein-related	0.83	0.39	0.10	−0.33	0.50
264400_at	AT1G61800	glucose-6-phosphate/phosphate translocator 2	1.10	0.30	0.35	−0.45	0.65
265393_at	AT2G20830	transferases; folic acid binding	0.39	−0.15	−0.05	−0.59	−0.20
265665_at	AT2G27420	Cysteine proteinases superfamily protein	1.20	0.22	0.22	−0.76	0.44
266606_at	AT2G46310	cytokinin response factor 5	0.68	−0.01	0.29	−0.40	0.27
267595_at	AT2G32990	glycosyl hydrolase 9B8	0.80	0.19	0.07	−0.54	0.26

(g)

ID	Locus	description	W+FR effect (22˚C)	W+FR effect (26˚C)	26˚C effect (WL)	26˚C effect (W+FR)	W+FR+ 26˚C effect
245197_at	AT1G67800	Copine (Calcium-dependent phospholipid-binding protein) family	0.19	0.02	−0.35	−0.52	−0.34
245265_at	AT4G14400	ankyrin repeat family protein	0.26	−0.47	−0.22	−0.96	−0.70
245346_at	AT4G17090	chloroplast beta-amylase	0.33	0.02	−0.26	−0.57	−0.24
245367_at	AT4G16265	RNA polymerases M/15 Kd subunit	0.26	0.15	−0.25	−0.36	−0.10

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246464_at	AT5G16980	Zinc-binding dehydrogenase family protein	0.26	−0.13	−0.24	−0.63	−0.37
246603_at	AT1G31690	Copper amine oxidase family protein	0.16	−0.01	−0.24	−0.40	−0.24
247191_at	AT5G65310	homeobox protein 5	0.36	0.02	−0.12	−0.46	−0.10
247348_at	AT5G63810	beta-galactosidase 10	0.17	0.03	−0.34	−0.48	−0.31
247541_at	AT5G61660	glycine-rich protein	0.30	0.13	−0.48	−0.66	−0.36
247739_at	AT5G59240	Ribosomal protein S8e family protein	0.22	−0.03	−0.21	−0.46	−0.24
247814_at	AT5G58310	methyl esterase 18	0.66	0.05	−0.36	−0.97	−0.31
248075_at	AT5G55740	Tetratricopeptide repeat (TPR)-like superfamily protein	0.15	−0.11	−0.13	−0.39	−0.24
248169_at	AT5G54610	ankyrin	0.20	−0.25	−0.18	−0.63	−0.43
249266_at	AT5G41670	6-phosphogluconate dehydrogenase family protein	0.27	−0.06	−0.11	−0.44	−0.17
249718_at	AT5G35740	Carbohydrate-binding X8 domain superfamily protein	0.14	−0.02	−0.48	−0.63	−0.50
250445_at	AT5G10760	Eukaryotic aspartyl protease family protein	0.11	−0.11	−0.49	−0.71	−0.60
250503_at	AT5G09820	Plastid-lipid associated protein PAP/fibrillin family protein	0.14	−0.02	−0.21	−0.37	−0.23
251155_at	AT3G63160	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast outer membrane, thylakoid, chloroplast thylakoid membrane, chloroplast, chloroplast envelope; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST *Arabidopsis thaliana* protein match is: outer envelope membrane protein 7 (TAIR:AT3G52420.1); Has 26 Blast hits to 26 proteins in 8 species: Archae-0; Bacteria-0; Metazoa-0; Fungi-0; Plants-26; Viruses-0; Other Eukaryotes-0 (source: NCBI BLink).	0.11	−0.02	−0.42	−0.55	−0.44
251319_at	AT3G61610	Galactose mutarotase-like superfamily protein	0.24	0.12	−0.35	−0.48	−0.23
251705_at	AT3G56400	WRKY DNA-binding protein 70	0.13	−0.53	−0.15	−0.80	−0.67
251789_at	AT3G55450	PBS1-like 1	0.18	0.07	−0.26	−0.37	−0.20
252387_at	AT3G47800	Galactose mutarotase-like superfamily protein	0.25	−0.30	−0.02	−0.58	−0.32
252607_at	AT3G44990	xyloglucan endo-transglycosylase-related 8	0.56	−0.02	−0.38	−0.95	−0.40
252828_at	AT4G39960	Molecular chaperone Hsp40/DnaJ family protein	0.29	0.08	−0.33	−0.54	−0.25
253005_at	AT4G38100	unknown protein; LOCATED IN: chloroplast thylakoid membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT4G01150.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae-12; Bacteria-1396; Metazoa-17338; Fungi-3422; Plants-5037; Viruses-0; Other Eukaryotes-2996 (source: NCBI BLink).	0.10	0.02	−0.36	−0.45	−0.35
253209_at	AT4G34830	Pentatricopeptide repeat (PPR) superfamily protein	0.40	0.09	−0.12	−0.43	−0.03
253396_at	AT4G32720	La protein 1	0.43	0.04	−0.08	−0.47	−0.04
253518_at	AT4G31400	damaged DNA binding; DNA-directed DNA polymerases	0.07	−0.07	−0.22	−0.36	−0.29
254016_at	AT4G26150	cytokinin-responsive gata factor 1	0.13	−0.08	−0.35	−0.56	−0.43
254641_at	AT4G18800	RAB GTPase homolog A1D	0.31	0.09	−0.19	−0.41	−0.10
254723_at	AT4G13510	ammonium transporter 1;1	0.10	−0.12	−0.18	−0.40	−0.30
254870_at	AT4G11900	S-locus lectin protein kinase family protein	0.30	0.00	−0.13	−0.43	−0.13
255278_at	AT4G04940	transducin family protein/WD-40 repeat family protein	0.23	−0.11	−0.12	−0.46	−0.23

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256052_at	AT1G06960	RNA-binding (RRM/RBD/RNP motifs) family protein	0.17	0.05	−0.31	−0.43	−0.26
256091_at	AT1G20693	high mobility group B2	0.04	−0.09	−0.33	−0.46	−0.42
256617_at	AT3G22240	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT3G22235.2); Has 177 Blast hits to 177 proteins in 14 species: Archae-0; Bacteria-0; Metazoa-0; Fungi-0; Plants-177; Viruses-0; Other Eukaryotes-0 (source: NCBI BLink).	0.31	−0.20	−0.22	−0.73	−0.42
256766_at	AT3G22231	pathogen and circadian controlled 1	0.38	−0.33	−0.36	−1.07	−0.69
257180_at	AT3G13180	NOL1/NOP2/sun family protein/antitermination NusB domain-containing protein	0.01	−0.09	−0.32	−0.42	−0.41
257382_at	AT2G40750	WRKY DNA-binding protein 54	0.44	−0.56	−0.23	−1.23	−0.79
257763_s_at	AT3G23120	[AT3G23120, receptor like protein 38]; [AT3G23110, receptor like protein 37]	0.46	−0.05	−0.08	−0.59	−0.13
257926_at	AT3G23280	XB3 ortholog 5 in *Arabidopsis thaliana*	0.06	0.00	−0.26	−0.32	−0.26
258293_at	AT3G23430	phosphate 1	0.24	−0.27	0.09	−0.43	−0.19
258447_at	AT3G22450	Ribosomal L18p/L5e family protein	0.11	−0.27	−0.05	−0.43	−0.32
258554_at	AT3G06980	DEA(D/H)-box RNA helicase family protein	0.33	−0.04	−0.03	−0.40	−0.07
258633_at	AT3G07990	serine carboxypeptidase-like 27	0.29	0.04	−0.19	−0.44	−0.15
258742_at	AT3G05800	AtBS1(activation-tagged BRI1 suppressor 1)-interacting factor 1	0.38	0.07	−0.15	−0.46	−0.07
258956_at	AT3G01440	PsbQ-like 1	0.04	−0.13	−0.34	−0.52	−0.48
259466_at	AT1G19050	response regulator 7	0.18	−0.05	−0.31	−0.54	−0.36
259561_at	AT1G21250	cell wall-associated kinase	0.31	−0.34	−0.22	−0.87	−0.57
259891_at	AT1G72730	DEA(D/H)-box RNA helicase family protein	0.20	0.07	−0.27	−0.40	−0.20
260211_at	AT1G74440	Protein of unknown function (DUF962)	0.02	−0.29	−0.17	−0.49	−0.46
260522_x_at	AT2G41730	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT5G24640.1); Has 25 Blast hits to 25 proteins in 5 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−25; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.02	−0.50	−0.34	−0.85	−0.84
260560_at	AT2G43590	Chitinase family protein	−0.04	−0.29	−1.01	−1.26	−1.30
260837_at	AT1G43670	Inositol monophosphatase family protein	0.18	0.05	−0.29	−0.42	−0.24
261046_at	AT1G01390	UDP-Glycosyltransferase superfamily protein	0.67	0.31	−0.37	−0.73	−0.06
261226_at	AT1G20190	expansin 11	0.34	0.08	−0.44	−0.70	−0.36
261339_at	AT1G35710	Protein kinase family protein with leucine-rich repeat domain	0.29	−0.14	−0.36	−0.80	−0.50
261651_at	AT1G27760	Interferon-related developmental regulator family protein/IFRD protein family	0.14	0.02	−0.25	−0.38	−0.24
262212_at	AT1G74890	response regulator 15	0.10	−0.09	−0.18	−0.37	−0.26
262374_s_at	AT1G72910	[AT1G72910, Toll-Interleukin-Resistance (TIR) domain-containing protein];[AT1G72930, toll/interleukin-1 receptor-like]	0.10	−0.13	−0.42	−0.64	−0.55
262518_at	AT1G17170	glutathione S-transferase TAU 24	0.33	−0.14	−0.49	−0.96	−0.63
262634_at	AT1G06690	NAD(P)-linked oxidoreductase superfamily protein	0.02	−0.06	−0.31	−0.39	−0.37
262766_at	AT1G13160	ARM repeat superfamily protein	0.19	−0.06	−0.07	−0.33	−0.13

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262797_at	AT1G20840	tonoplast monosaccharide transporter1	0.08	−0.01	−0.27	−0.36	−0.28
263133_at	AT1G78450	SOUL heme-binding family protein	0.72	0.07	−0.21	−0.86	−0.14
263221_at	AT1G30620	NAD(P)-binding Rossmann-fold superfamily protein	0.23	−0.06	−0.11	−0.41	−0.17
263493_at	AT2G42520	P-loop containing nucleoside triphosphate hydrolases superfamily protein	0.47	0.11	−0.05	−0.42	0.06
263705_at	AT1G31190	Myo-inositol monophosphatase like 1	0.13	−0.06	−0.23	−0.42	−0.29
263776_s_at	AT2G46440	[AT2G46440, cyclic nucleotide-gated channels]; [AT2G46430, cyclic nucleotide gated channel 3]	0.23	−0.06	−0.32	−0.60	−0.37
263842_at	AT2G36835	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast envelope; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 26 Blast hits to 26 proteins in 11 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−26; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.04	−0.05	−0.37	−0.47	−0.42
263951_at	AT2G35960	NDR1/HIN1-like 12	0.09	0.02	−0.36	−0.43	−0.34
264071_at	AT2G27920	serine carboxypeptidase-like 51	0.57	0.30	−0.20	−0.47	0.09
264577_at	AT1G05260	Peroxidase superfamily protein	0.53	−0.34	0.19	−0.67	−0.14
264748_at	AT1G70070	DEAD/DEAH box helicase, putative	0.22	0.04	−0.22	−0.40	−0.18
264771_at	AT1G22940	thiamin biosynthesis protein, putative	0.31	0.00	−0.07	−0.38	−0.07
265560_at	AT2G05520	glycine-rich protein 3	0.06	−0.15	−0.21	−0.42	−0.36
265611_at	AT2G25510	unknown protein; Has 2 Blast hits to 2 proteins in 1 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−2; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.14	−0.11	−0.27	−0.52	−0.37
265837_at	AT2G14560	Protein of unknown function (DUF567)	0.45	−0.47	−0.99	−1.91	−1.46
265886_at	AT2G25620	DNA-binding protein phosphatase 1	0.41	0.19	−0.21	−0.43	−0.02
266078_at	AT2G40670	response regulator 16	0.60	0.22	−0.33	−0.72	−0.11
266464_at	AT2G47800	multidrug resistance-associated protein 4	0.30	0.07	−0.16	−0.39	−0.09
266479_at	AT2G31160	Protein of unknown function (DUF640)	0.35	−0.01	−0.09	−0.44	−0.10
266578_at	AT2G23910	NAD(P)-binding Rossmann-fold superfamily protein	0.25	−0.52	−0.17	−0.93	−0.69
266951_at	AT2G18940	Tetratricopeptide repeat (TPR)-like superfamily protein	0.22	−0.05	−0.24	−0.52	−0.30
267076_at	AT2G41090	Calcium-binding EF-hand family protein	0.28	−0.32	−0.15	−0.76	−0.47
267138_s_at	AT2G38230	[AT2G38230, pyridoxine biosynthesis 1.1]; [AT2G38210, putative PDX1-like protein 4]	0.07	−0.12	−0.34	−0.54	−0.47
267592_at	AT2G39710	Eukaryotic aspartyl protease family protein	0.10	−0.16	−0.13	−0.40	−0.29

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ID	Locus	description	W+FR effect (22˚C)	W+FR effect (26˚C)	26˚C effect (WL)	26˚C effect (W+FR)	W+FR+ 26˚C effect
244951_s_at	AT2G07723	[AT2G07723, pseudogene, similar to orf454~homology with two ORFs from Marchantia polymorpha mtDNA (orf169 and orf322), high similarity to 3'-terminal part of ccl1 of Rhodobacter, blastp match of 76% identity and 3.4e−193 P-value to GP|459537|emb|CAA54966.1||X78036 orf454~homology with two ORFs from Marchantia polymorpha mtDNA (orf169 and orf322), high similarity to 3'-terminal part of ccl1 of Rhodobacter {Oenothera berteriana}]; [ATMG00180, cytochrome C biogenesis 452]	0.16	0.19	0.30	0.33	0.49

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245627_at	AT1G56600	galactinol synthase 2	0.38	0.24	0.67	0.53	0.91
245792_at	AT1G32100	pinoresinol reductase 1	0.09	0.14	0.27	0.31	0.40
245903_at	AT5G11100	Calcium-dependent lipid-binding (CaLB domain) family protein	0.21	0.24	0.31	0.34	0.55
246425_at	AT5G17420	Cellulose synthase family protein	0.24	0.29	0.30	0.36	0.60
246540_at	AT5G15600	SPIRAL1-like4	0.13	0.13	0.25	0.25	0.39
247035_at	AT5G67110	basic helix-loop-helix (bHLH) DNA-binding superfamily protein	0.03	0.11	0.47	0.55	0.57
247295_at	AT5G64180	unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae−0; Bacteria−0; Metazoa−736; Fungi−347; Plants−385; Viruses−0; Other Eukaryotes−339 (source: NCBI BLink).	0.26	0.17	0.42	0.34	0.59
249035_at	AT5G44190	GOLDEN2-like 2	0.11	0.15	0.32	0.36	0.47
249408_at	AT5G40330	myb domain protein 23	0.16	0.13	0.45	0.41	0.57
250926_at	AT5G03555	permease, cytosine/purines, uracil, thiamine, allantoin family protein	0.16	0.18	0.24	0.26	0.42
251069_at	AT5G01930	Glycosyl hydrolase superfamily protein	0.19	0.26	0.26	0.33	0.52
252429_at	AT3G47500	cycling DOF factor 3	0.12	0.22	0.20	0.29	0.42
253277_at	AT4G34230	cinnamyl alcohol dehydrogenase 5	0.18	0.16	0.34	0.32	0.50
254153_at	AT4G24450	phosphoglucan, water dikinase	0.13	0.29	0.37	0.53	0.66
254574_at	AT4G19430	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae−12; Bacteria−1396; Metazoa−17338; Fungi−3422; Plants−5037; Viruses−0; Other Eukaryotes−2996 (source: NCBI BLink).	0.75	1.68	1.48	2.42	3.16
254633_at	AT4G18640	Leucine-rich repeat protein kinase family protein	0.09	0.22	0.30	0.43	0.52
257017_at	AT3G19620	Glycosyl hydrolase family protein	0.33	0.40	0.43	0.51	0.83
257896_at	AT3G16920	Chitinase-like protein 2	0.15	0.13	0.40	0.39	0.53
258038_at	AT3G21260	Glycolipid transfer protein (GLTP) family protein	0.07	0.09	0.36	0.38	0.45
258647_at	AT3G07870	F-box and associated interaction domains-containing protein	0.15	0.08	0.30	0.23	0.38
258935_at	AT3G10120	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT5G03890.1); Has 57 Blast hits to 57 proteins in 10 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−57; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.21	0.16	0.49	0.44	0.65
259142_at	AT3G10200	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	0.08	0.16	0.24	0.32	0.40
259564_at	AT1G20540	Transducin/WD40 repeat-like superfamily protein	0.09	0.16	0.17	0.24	0.33
259934_at	AT1G71340	PLC-like phosphodiesterases superfamily protein	−0.01	0.09	0.23	0.32	0.32
260902_at	AT1G21440	Phosphoenolpyruvate carboxylase family protein	0.16	0.11	0.27	0.23	0.39
261109_at	AT1G75450	cytokinin oxidase 5	0.20	0.26	0.24	0.30	0.51
261272_at	AT1G26665	Mediator complex, subunit Med10	0.16	0.11	0.29	0.25	0.40
262357_at	AT1G73040	Mannose-binding lectin superfamily protein	0.16	0.21	0.58	0.64	0.79
262796_at	AT1G20850	xylem cysteine peptidase 2	0.20	0.20	0.41	0.41	0.60
264255_at	AT1G09140	SERINE-ARGININE PROTEIN 30	0.05	0.15	0.36	0.46	0.51
264873_at	AT1G24100	UDP-glucosyl transferase 74B1	0.08	0.08	0.38	0.38	0.45
265510_at	AT2G05630	Ubiquitin-like superfamily protein	0.20	0.13	0.35	0.28	0.48
265902_at	AT2G25590	Plant Tudor-like protein	0.12	0.10	0.52	0.50	0.63

(i)

ID	Locus	description	W+FR effect (22˚C)	W+FR effect (26˚C)	26˚C effect (WL)	26˚C effect (W+FR)	W+FR+ 26˚C effect
245275_at	AT4G15210	beta-amylase 5	0.15	−0.66	1.93	1.12	1.27
245422_at	AT4G17470	alpha/beta-Hydrolases superfamily protein	0.38	−0.33	1.51	0.80	1.17
245465_at	AT4G16590	cellulose synthase-like A01	−0.02	−0.48	1.58	1.12	1.10
245928_s_at	AT5G24770	[AT5G24770, vegetative storage protein 2]; [AT5G24780, vegetative storage protein 1]	−0.30	−0.39	1.49	1.40	1.10
246884_at	AT5G26220	ChaC-like family protein	−0.26	−0.34	0.89	0.81	0.55
246944_at	AT5G25450	Cytochrome bd ubiquinol oxidase, 14kDa subunit	−0.11	−0.33	0.70	0.48	0.37
247293_at	AT5G64510	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 10 growth stages; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae−798; Bacteria−22429; Metazoa−974; Fungi−991; Plants−531; Viruses−0; Other Eukaryotes−9610 (source: NCBI BLink).	−0.08	−0.10	0.71	0.68	0.60
247657_at	AT5G59845	Gibberellin-regulated family protein	0.11	0.05	0.42	0.35	0.47
248091_at	AT5G55120	galactose-1-phosphate guanylyltransferase (GDP)s; GDP-D-glucose phosphorylases; quercetin 4'-O-glucosyltransferases	0.16	−0.03	0.42	0.23	0.39
248332_at	AT5G52640	heat shock protein 90.1	0.17	−0.24	1.77	1.36	1.53
248434_at	AT5G51440	HSP20-like chaperones superfamily protein	−0.07	−0.53	1.02	0.57	0.49
248657_at	AT5G48570	FKBP-type peptidyl-prolyl cis-trans isomerase family protein	0.13	−0.13	1.47	1.22	1.34
248676_at	AT5G48850	Tetratricopeptide repeat (TPR)-like superfamily protein	−0.13	−0.38	1.08	0.84	0.70
248802_at	AT5G47435	formyltetrahydrofolate deformylase, putative	−0.03	0.00	0.42	0.44	0.42
249774_at	AT5G24150	FAD/NAD(P)-binding oxidoreductase family protein	0.05	−0.03	0.57	0.49	0.54
249775_at	AT5G24160	squalene monoxygenase 6	−0.08	−0.25	0.63	0.46	0.38
249866_at	AT5G23010	methylthioalkylmalate synthase 1	0.14	0.02	0.33	0.21	0.35
250304_at	AT5G12110	Glutathione S-transferase, C-terminal-like; Translation elongation factor EF1B/ribosomal protein S6	0.07	−0.15	1.34	1.11	1.18
250793_at	AT5G05600	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	−0.35	−0.43	1.21	1.13	0.78
251028_at	AT5G02230	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	0.23	−0.04	0.71	0.44	0.67
251770_at	AT3G55970	jasmonate-regulated gene 21	0.00	−0.65	1.31	0.66	0.66
252114_at	AT3G51450	Calcium-dependent phosphotriesterase superfamily protein	0.21	−0.18	0.75	0.36	0.57
252265_at	AT3G49620	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	0.14	−0.40	1.42	0.88	1.02
252363_at	AT3G48460	GDSL-like Lipase/Acylhydrolase superfamily protein	0.19	−0.10	0.50	0.21	0.40
252677_at	AT3G44320	nitrilase 3	0.21	−0.20	0.64	0.23	0.44
253332_at	AT4G33420	Peroxidase superfamily protein	−0.02	−0.17	0.89	0.74	0.72
253519_at	AT4G31240	protein kinase C-like zinc finger protein	0.20	−0.13	0.59	0.26	0.46

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253640_at	AT4G30630	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT5G57910.1); Has 33 Blast hits to 33 proteins in 10 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−33; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.21	0.09	0.33	0.21	0.42
253697_at	AT4G29700	Alkaline-phosphatase-like family protein	0.47	−0.11	0.72	0.15	0.61
253842_at	AT4G27860	vacuolar iron transporter (VIT) family protein	0.00	−0.30	0.66	0.36	0.36
254234_at	AT4G23680	Polyketide cyclase/dehydrase and lipid transport superfamily protein	0.53	−0.06	1.17	0.58	1.11
254385_s_at	AT4G21830	[AT4G21830, methionine sulfoxide reductase B7]; [AT4G21840, methionine sulfoxide reductase B8]	−0.14	−0.53	0.87	0.48	0.34
254839_at	AT4G12400	stress-inducible protein, putative	−0.09	0.00	0.79	0.89	0.79
254848_at	AT4G11960	PGR5-like B	−0.06	−0.06	0.58	0.58	0.52
255283_at	AT4G04620	Ubiquitin-like superfamily protein	−0.01	−0.08	0.43	0.36	0.35
255786_at	AT1G19670	chlorophyllase 1	0.09	−0.22	0.89	0.58	0.67
255793_at	AT2G33250	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT3G04310.1); Has 41 Blast hits to 41 proteins in 12 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−41; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.03	−0.03	0.35	0.36	0.33
256178_s_at	AT1G51760	[AT1G51760, peptidase M20/M25/M40 family protein];[AT1G51780, IAA-leucine resistant (ILR)-like gene 5]	0.21	−0.02	0.59	0.36	0.57
256245_at	AT3G12580	heat shock protein 70	0.43	−0.34	2.35	1.58	2.01
256433_at	AT3G10985	senescence associated gene 20	0.03	0.01	0.58	0.55	0.58
256603_at	AT3G28270	Protein of unknown function (DUF677)	0.58	−0.28	1.05	0.18	0.76
257239_at	no_match	no_match	−0.06	−0.09	0.65	0.63	0.57
257339_s_at	ATMG00040	[ATMG00040, ATP synthase subunit C family protein];[AT2G07671, ATP synthase subunit C family protein];[ATMG01080, mitochondrial F0-ATPase subunit 9]	0.23	−0.08	0.72	0.40	0.64
257421_at	AT1G12030	Protein of unknown function (DUF506)	0.09	−0.20	0.97	0.67	0.77
257830_at	AT3G26690	nudix hydrolase homolog 13	0.25	0.02	0.55	0.31	0.57
257890_s_at	AT3G42570	[AT3G42570, peroxidase family protein]; [AT3G17070, Peroxidase family protein]	0.30	−0.06	0.61	0.25	0.55
258133_at	AT3G24500	multiprotein bridging factor 1C	0.11	−0.22	1.49	1.16	1.27
258263_at	AT3G15780	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT1G52550.1); Has 20 Blast hits to 20 proteins in 5 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−20; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.06	−0.02	0.43	0.34	0.41
258815_at	AT3G04000	NAD(P)-binding Rossmann-fold superfamily protein	0.10	0.03	0.41	0.34	0.44
258990_at	AT3G08840	D-alanine—D-alanine ligase family	0.11	−0.21	0.55	0.23	0.34
259042_at	AT3G03450	RGA-like 2	0.21	0.04	0.52	0.35	0.56
259802_at	AT1G72260	thionin 2.1	−0.25	−0.27	1.04	1.02	0.77

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260004_at	AT1G67860	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT1G67865.1); Has 13 Blast hits to 13 proteins in 2 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−13; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.01	−0.09	0.48	0.40	0.39
260248_at	AT1G74310	heat shock protein 101	0.21	0.01	0.60	0.39	0.60
261081_at	AT1G07350	RNA-binding (RRM/RBD/RNP motifs) family protein	0.03	0.03	0.68	0.68	0.71
261713_at	AT1G32640	Basic helix-loop-helix (bHLH) DNA-binding family protein	0.26	−0.19	0.72	0.28	0.53
262354_at	AT1G64200	vacuolar H+-ATPase subunit E isoform 3	0.03	−0.20	0.74	0.51	0.54
262608_at	AT1G14120	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	0.25	−0.21	1.20	0.74	0.99
262637_at	AT1G06640	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	0.13	−0.15	0.70	0.41	0.55
262884_at	AT1G64720	Polyketide cyclase/dehydrase and lipid transport superfamily protein	0.03	−0.26	0.75	0.45	0.49
263150_at	AT1G54050	HSP20-like chaperones superfamily protein	0.21	−0.10	0.55	0.24	0.45
263161_at	AT1G54020	GDSL-like Lipase/Acylhydrolase superfamily protein	0.30	−0.50	1.73	0.93	1.23
263374_at	AT2G20560	DNAJ heat shock family protein	0.24	−0.38	1.19	0.57	0.81
263539_at	AT2G24850	tyrosine aminotransferase 3	−0.08	−0.20	0.82	0.70	0.62
263866_at	AT2G36950	Heavy metal transport/detoxification superfamily protein	−0.07	−0.10	0.38	0.36	0.29
263972_at	AT2G42760	unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1685 (InterPro:IPR012881); Has 170 Blast hits to 164 proteins in 34 species: Archae−0; Bacteria−1; Metazoa−26; Fungi−10; Plants−107; Viruses−0; Other Eukaryotes−26 (source: NCBI BLink).	−0.09	−0.16	0.50	0.43	0.34
264514_at	AT1G09500	NAD(P)-binding Rossmann-fold superfamily protein	0.30	0.10	0.54	0.34	0.65
265122_at	AT1G62540	flavin-monooxygenase glucosinolate S-oxygenase 2	0.49	0.09	0.74	0.35	0.83
265233_s_at	ATMG00590	[ATMG00590, Cytochrome b/b6 protein]; [AT2G07718, Cytochrome b/b6 protein]	0.04	−0.15	0.61	0.42	0.46
265572_at	no_match	no_match	−0.20	−0.29	0.45	0.37	0.17
266005_at	AT2G37340	arginine/serine-rich zinc knuckle-containing protein 33	0.06	0.01	0.34	0.29	0.35
266142_at	AT2G39030	Acyl-CoA N-acyltransferases (NAT) superfamily protein	−0.63	−1.59	3.01	2.05	1.42
266368_at	AT2G41380	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	0.35	−0.13	0.84	0.37	0.72
266555_at	AT2G46270	G-box binding factor 3	0.29	0.05	0.76	0.52	0.81
266589_at	AT2G46250	myosin heavy chain-related	0.00	−0.24	0.77	0.54	0.54
266614_at	AT2G14910	unknown protein; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT5G14970.1); Has 605 Blast hits to 425 proteins in 102 species: Archae−0; Bacteria−300; Metazoa−25; Fungi−0; Plants−89; Viruses−0; Other Eukaryotes−191 (source: NCBI BLink).	0.05	−0.08	0.56	0.43	0.48
266988_at	AT2G39310	jacalin-related lectin 22	0.21	0.02	0.52	0.33	0.54
266989_at	AT2G39330	jacalin-related lectin 23	−0.04	−0.13	1.55	1.45	1.42
267336_at	AT2G19310	HSP20-like chaperones superfamily protein	0.09	−0.16	0.52	0.27	0.36
267425_at	AT2G34810	FAD-binding Berberine family protein	−0.02	−0.50	1.23	0.75	0.73

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ID	Locus	description	W+FR effect (22˚C)	W+FR effect (26˚C)	26˚C effect (WL)	26˚C effect (W+FR)	W+FR+ 26˚C effect
245001_at	ATCG00220	photosystem II reaction center protein M	−0.43	0.05	−0.05	0.42	0.00
245449_at	AT4G16870	transposable element gene	−0.08	0.01	0.31	0.40	0.33
245602_at	AT4G14270	Protein containing PAM2 motif which mediates interaction with the PABC domain of polyadenyl binding proteins.	−0.23	−0.05	0.22	0.41	0.18
245734_at	AT1G73480	alpha/beta-Hydrolases superfamily protein	−0.47	−0.05	0.23	0.65	0.18
245864_at	AT1G58070	unknown protein; Has 286 Blast hits to 266 proteins in 81 species: Archae−2; Bacteria−25; Metazoa−90; Fungi−19; Plants−78; Viruses−4; Other Eukaryotes−68 (source: NCBI BLink).	−0.08	0.20	0.19	0.46	0.38
247356_at	AT5G63800	Glycosyl hydrolase family 35 protein	−0.37	−0.05	0.14	0.46	0.09
247452_at	AT5G62430	cycling DOF factor 1	0.03	0.19	0.24	0.40	0.42
247509_at	AT5G62020	heat shock transcription factor B2A	−0.20	0.07	0.13	0.40	0.20
247638_at	AT5G60490	FASCICLIN-like arabinogalactan-protein 12	−0.04	0.21	0.19	0.44	0.40
247899_at	AT5G57345	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae-12; Bacteria-1396; Metazoa-17338; Fungi-3422; Plants-5037; Viruses-0; Other Eukaryotes-2996 (source: NCBI BLink).	−0.30	−0.13	0.28	0.45	0.15
248382_at	AT5G51890	Peroxidase superfamily protein	−0.13	0.06	0.45	0.64	0.51
248793_at	AT5G47240	nudix hydrolase homolog 8	−0.52	−0.25	0.18	0.45	−0.07
249265_at	AT5G41700	ubiquitin conjugating enzyme 8	−0.12	0.05	0.22	0.39	0.27
249439_at	AT5G40020	Pathogenesis-related thaumatin superfamily protein	−0.09	0.06	0.55	0.71	0.61
250183_at	AT5G14510	ARM repeat superfamily protein	−0.17	0.11	0.19	0.47	0.30
250478_at	AT5G10250	Phototropic-responsive NPH3 family protein	−0.15	0.18	0.11	0.44	0.29
251257_at	AT3G62290	ADP-ribosylation factor A1E	−0.21	−0.17	0.34	0.38	0.17
251324_at	AT3G61430	plasma membrane intrinsic protein 1A	−0.45	−0.18	0.10	0.37	−0.08
251962_at	AT3G53420	plasma membrane intrinsic protein 2A	−0.23	−0.10	0.22	0.35	0.12
253263_at	AT4G34000	abscisic acid responsive elements-binding factor 3	−0.12	0.14	0.29	0.55	0.43
253270_at	AT4G34160	CYCLIN D3;1	−0.06	0.11	0.20	0.37	0.31
254239_at	AT4G23400	plasma membrane intrinsic protein 1;5	−0.23	0.07	0.31	0.61	0.38
254327_at	AT4G22490	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	−0.09	0.24	0.28	0.60	0.51
254564_at	AT4G19170	nine-cis-epoxycarotenoid dioxygenase 4	−0.25	−0.09	0.33	0.48	0.24
254688_at	AT4G13830	DNAJ-like 20	−0.28	−0.01	0.31	0.58	0.30
254691_at	AT4G17840	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Abortive infection protein (InterPro:IPR003675); BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT2G35260.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae−12; Bacteria−1396; Metazoa−17338; Fungi−3422; Plants−5037; Viruses−0; Other Eukaryotes−2996 (source: NCBI BLink).	−0.30	−0.01	0.24	0.53	0.23

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255469_at	AT4G03030	Galactose oxidase/kelch repeat superfamily protein	−0.15	0.08	0.16	0.38	0.23
255602_at	AT4G01026	PYR1-like 7	−0.42	−0.11	0.16	0.47	0.05
255626_at	AT4G00780	TRAF-like family protein	−0.04	0.15	0.23	0.42	0.38
256096_at	AT1G13650	BEST *Arabidopsis thaliana* protein match is: 18S pre−ribosomal assembly protein gar2−related (TAIR:AT2G03810.4); Has 3688 Blast hits to 1629 proteins in 255 species: Archae−22; Bacteria−222; Metazoa−684; Fungi−292; Plants−62; Viruses−14; Other Eukaryotes−2392 (source: NCBI BLink).	−0.42	−0.31	0.54	0.65	0.23
256454_at	AT1G75280	NmrA-like negative transcriptional regulator family protein	−0.22	−0.02	0.27	0.47	0.25
256527_at	AT1G66100	Plant thionin	−0.95	−0.55	0.14	0.55	−0.41
256789_at	AT3G13672	TRAF-like superfamily protein	−0.37	−0.01	0.08	0.44	0.07
257021_at	AT3G19710	branched-chain aminotransferase4	−0.12	−0.04	0.36	0.43	0.31
257422_at	AT1G11940	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	−0.14	0.10	0.12	0.36	0.22
257615_at	AT3G26510	Octicosapeptide/Phox/Bem1p family protein	−0.13	−0.06	0.38	0.45	0.32
257628_at	AT3G26290	cytochrome P450, family 71, subfamily B, polypeptide 26	−0.36	−0.05	0.25	0.56	0.20
258124_at	AT3G18215	Protein of unknown function, DUF599	−0.22	−0.12	0.37	0.47	0.25
258188_at	AT3G17800	Protein of unknown function (DUF760)	−0.09	0.12	0.21	0.42	0.32
258890_at	AT3G05690	nuclear factor Y, subunit A2	0.01	0.23	0.21	0.44	0.44
259015_at	AT3G07350	Protein of unknown function (DUF506)	−0.35	−0.12	0.35	0.58	0.23
259022_at	AT3G07420	asparaginyl-tRNA synthetase 2	−0.13	0.19	0.03	0.35	0.23
259441_at	AT1G02300	Cysteine proteinases superfamily protein	−0.05	0.13	0.28	0.46	0.41
259544_at	AT1G20620	catalase 3	−0.41	−0.10	0.28	0.58	0.18
259666_at	AT1G55310	SC35-like splicing factor 33	−0.14	0.01	0.30	0.45	0.31
259766_at	AT1G64360	unknown protein; Has 6 Blast hits to 6 proteins in 2 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−6; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.13	0.02	0.55	0.71	0.58
260169_at	AT1G71990	fucosyltransferase 13	−0.11	−0.05	0.30	0.36	0.26
260431_at	AT1G68190	B-box zinc finger family protein	−0.35	−0.03	0.22	0.55	0.19
261026_at	AT1G01240	unknown protein; INVOLVED IN: N-terminal protein myristoylation; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 11 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G46550.1); Has 95 Blast hits to 78 proteins in 16 species: Archae−0; Bacteria−2; Metazoa−11; Fungi−0; Plants−80; Viruses−0; Other Eukaryotes−2 (source: NCBI BLink).	−0.46	0.00	0.03	0.49	0.03
261276_at	AT1G26670	Vesicle transport v-SNARE family protein	−0.05	0.05	0.31	0.42	0.36
261315_at	AT1G53170	ethylene response factor 8	−0.21	−0.07	0.21	0.35	0.14
261845_at	AT1G15960	NRAMP metal ion transporter 6	−0.42	0.06	0.10	0.59	0.16

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261887_at	AT1G80780	Polynucleotidyl transferase, ribonuclease H-like superfamily protein	−0.19	−0.12	0.29	0.36	0.17
262113_at	AT1G02820	Late embryogenesis abundant 3 (LEA3) family protein	−1.09	−0.37	−0.08	0.65	−0.44
262399_at	AT1G49500	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 10 growth stages; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT3G19030.1); Has 24 Blast hits to 24 proteins in 2 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−24; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.65	−0.25	0.00	0.41	−0.24
262607_at	AT1G13990	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3110 (InterPro:IPR021503); Has 25 Blast hits to 25 proteins in 8 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−25; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.28	0.02	0.46	0.76	0.48
262826_at	AT1G13080	cytochrome P450, family 71, subfamily B, polypeptide 2	−0.27	−0.15	0.44	0.56	0.29
262844_at	AT1G14890	Plant invertase/pectin methylesterase inhibitor superfamily protein	−0.15	−0.01	0.30	0.44	0.29
263114_at	AT1G03130	photosystem I subunit D-2	−0.18	0.01	0.18	0.38	0.20
263296_at	AT2G38800	Plant calmodulin-binding protein-related	−0.18	0.04	0.26	0.49	0.31
263433_at	AT2G22240	myo-inositol-1-phosphate synthase 2	−0.35	−0.08	0.21	0.47	0.13
264338_at	AT1G70300	K+ uptake permease 6	−0.22	0.03	0.47	0.73	0.50
264339_at	AT1G70290	trehalose-6-phosphatase synthase S8	−0.50	0.06	0.22	0.78	0.28
265111_at	AT1G62510	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	−1.07	−0.10	1.31	2.28	1.21
265481_at	AT2G15960	unknown protein; Has 14 Blast hits to 14 proteins in 5 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−14; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.59	−0.03	0.23	0.78	0.20
265760_at	AT2G01220	Nucleotidylyl transferase superfamily protein	−0.08	0.01	0.31	0.40	0.32
266106_at	AT2G45170	AUTOPHAGY 8E	−0.35	−0.05	0.16	0.47	0.12
266363_at	AT2G41250	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	−0.63	−0.26	0.09	0.46	−0.17
266899_at	AT2G34620	Mitochondrial transcription termination factor family protein	−0.26	−0.08	0.26	0.44	0.18
266910_at	AT2G45920	U-box domain-containing protein	−0.11	−0.02	0.45	0.54	0.43
267262_at	AT2G22990	sinapoylglucose 1	−0.54	−0.20	0.15	0.50	−0.04
267265_at	AT2G22980	serine carboxypeptidase-like 13	−0.19	0.06	0.21	0.46	0.27
267389_at	AT2G44460	beta glucosidase 28	−0.90	−0.63	0.89	1.16	0.25
267532_at	AT2G42040	CONTAINS InterPro DOMAIN/s: WRC (InterPro: IPR014977); Has 219 Blast hits to 219 proteins in 19 species: Archae−0; Bacteria−0; Metazoa−3; Fungi−0; Plants−215; Viruses−0; Other Eukaryotes−1 (source: NCBI BLink).	−0.06	0.11	0.22	0.39	0.33
267644_s_at	AT2G32880	[AT2G32880, TRAF-like family protein]; [AT2G32870, TRAF-like family protein]	−0.36	−0.13	0.31	0.54	0.18

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ID	Locus	description	W+FR effect (22˚C)	W+FR effect (26˚C)	26˚C effect (WL)	26˚C effect (W+FR)	W+FR+ 26˚C effect
246228_at	AT4G36430	Peroxidase superfamily protein	−0.05	−0.80	0.11	−0.64	−0.69
247478_at	AT5G62360	Plant invertase/pectin methylesterase inhibitor superfamily protein	−1.02	−0.52	−0.51	−0.01	−1.03
247793_at	AT5G58650	plant peptide containing sulfated tyrosine 1	−0.37	−0.30	−0.20	−0.13	−0.50
248050_at	AT5G56100	glycine-rich protein/oleosin	−0.33	−0.28	−0.14	−0.09	−0.42
248197_at	AT5G54190	protochlorophyllide oxidoreductase A	−0.28	−0.19	−0.20	−0.12	−0.39
248337_at	AT5G52310	low-temperature-responsive protein 78 (LTI78)/desiccation-responsive protein 29A (RD29A)	−0.48	−0.06	−0.76	−0.34	−0.82
249741_at	AT5G24470	pseudo-response regulator 5	−0.23	−0.03	−0.45	−0.25	−0.48
249850_at	AT5G23240	DNAJ heat shock N-terminal domain-containing protein	−0.39	−0.59	−0.18	−0.38	−0.77
251036_at	AT5G02160	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 121 Blast hits to 121 proteins in 17 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−121; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.63	−0.16	−0.31	0.15	−0.47
251744_at	AT3G56010	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 25 Blast hits to 25 proteins in 12 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−25; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.49	−0.26	−0.18	0.05	−0.44
252374_at	AT3G48100	response regulator 5	−0.11	−0.34	−0.11	−0.33	−0.44
252562_s_at	AT3G46320	[AT3G46320, Histone superfamily protein]; [AT3G45930, Histone superfamily protein]	−0.17	0.00	−0.37	−0.20	−0.37
252629_at	AT3G44970	Cytochrome P450 superfamily protein	−0.50	−0.70	−0.31	−0.51	−1.01
253004_at	AT4G38280	[AT4G38280, BEST *Arabidopsis thaliana* protein match is: Integral membrane protein hemolysin−III homolog (TAIR:AT2G45250.1); Has 65 Blast hits to 65 proteins in 13 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−2; Plants−63; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).]; [AT4G38330, Integral membrane protein hemolysin−III homolog]; [AT2G45250, Integral membrane protein hemolysin−III homolog]	−0.58	−0.47	−0.10	0.01	−0.58
253496_at	AT4G31870	glutathione peroxidase 7	−0.46	−0.47	−0.09	−0.09	−0.55
253627_at	AT4G30650	Low temperature and salt responsive protein family	−0.46	−0.43	−0.64	−0.60	−1.07
254543_at	AT4G19810	Glycosyl hydrolase family protein with chitinase insertion domain	−0.28	−0.46	−0.25	−0.43	−0.71
254889_at	AT4G11650	osmotin 34	0.05	−1.90	0.49	−1.46	−1.41
255331_at	AT4G04330	Chaperonin-like RbcX protein	−0.42	−0.34	−0.43	−0.34	−0.77

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256796_at	AT3G22210	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; Has 26 Blast hits to 26 proteins in 13 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−26; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.20	−0.21	−0.19	−0.20	−0.40
257939_at	AT3G19930	sugar transporter 4	−0.24	−0.27	−0.14	−0.16	−0.40
257985_at	AT3G20810	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	−0.22	−0.47	−0.12	−0.37	−0.59
258419_at	AT3G16670	Pollen Ole e 1 allergen and extensin family protein	−0.42	−0.01	−0.83	−0.41	−0.83
259207_at	AT3G09050	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; Has 120 Blast hits to 120 proteins in 47 species: Archae−4; Bacteria−10; Metazoa−33; Fungi−2; Plants−44; Viruses−0; Other Eukaryotes−27 (source: NCBI BLink).	−0.25	−0.19	−0.30	−0.24	−0.49
260064_at	AT1G73730	ETHYLENE-INSENSITIVE3-like 3	−0.11	−0.25	−0.11	−0.24	−0.36
261068_at	AT1G07450	NAD(P)-binding Rossmann-fold superfamily protein	−0.37	−0.44	−0.15	−0.22	−0.59
261569_at	AT1G01060	Homeodomain-like superfamily protein	−0.60	−0.35	−0.25	0.00	−0.60
261638_at	AT1G49975	INVOLVED IN: photosynthesis; LOCATED IN: photosystem I, chloroplast, thylakoid membrane; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Photosystem I reaction centre subunit N (InterPro:IPR008796); Has 34 Blast hits to 34 proteins in 14 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−34; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.31	−0.15	−0.21	−0.06	−0.36
262119_s_at	AT1G02930	[AT1G02930, glutathione S-transferase 6]; [AT1G02920, glutathione S-transferase 7]	−0.35	−0.73	0.17	−0.21	−0.56
262899_at	AT1G59870	ABC-2 and Plant PDR ABC-type transporter family protein	−0.36	−0.19	−0.42	−0.24	−0.60
263495_at	AT2G42530	cold regulated 15b	−0.42	−0.28	−0.58	−0.44	−0.86
263922_s_at	AT2G36580	[AT2G36580, Pyruvate kinase family protein]; [AT3G52990, Pyruvate kinase family protein]	−0.20	−0.20	−0.25	−0.25	−0.45
264511_at	AT1G09350	galactinol synthase 3	−0.73	−0.02	−0.58	0.13	−0.60
265478_at	AT2G15890	maternal effect embryo arrest 14	−0.56	−0.21	−0.42	−0.06	−0.63
265962_at	AT2G37460	nodulin MtN21 /EamA-like transporter family protein	−0.26	−0.10	−0.47	−0.31	−0.57
265999_at	AT2G24100	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT4G30780.1); Has 101 Blast hits to 101 proteins in 16 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−95; Viruses−0; Other Eukaryotes−6 (source: NCBI BLink).	−0.46	−0.33	−0.17	−0.05	−0.51
266746_s_at	AT2G02930	[AT2G02930, glutathione S-transferase F3]; [AT4G02520, glutathione S-transferase PHI 2]	−0.52	−0.34	−0.65	−0.48	−0.99
267053_s_at	AT2G38380	[AT2G38380, Peroxidase superfamily protein]; [AT2G38390, Peroxidase superfamily protein]	−0.14	−1.09	0.01	−0.94	−1.08
267344_at	AT2G44230	Plant protein of unknown function (DUF946)	−0.23	−0.40	−0.04	−0.20	−0.44
267461_at	AT2G33830	Dormancy/auxin associated family protein	−1.38	−0.79	−0.85	−0.25	−1.64

Table S3. The treatment effects and their ratios in group [α] [β]; [γ]; [δ] Values are the $\log_2$ transformed averages of three replicates.

(a)

ID	Locus	Description	Treatment Effects				**FR effect ratio 26˚C/22˚C**
			<1> W+FR effect (22˚C)	<2> W+FR effect (26˚C)	<3> 26˚C effect (WL)	<4> 26˚C effect (W+FR)	
254889_at	AT4G11650	osmotin 34	0.05	−1.90	0.49	−1.46	**−1.95**
262260_at	AT1G70850	MLP-like protein 34	0.79	−1.02	1.08	−0.73	**−1.81**
260130_s_at	AT1G66280	[AT1G66280, Glycosyl hydrolase superfamily protein]; [AT1G66270, Glycosyl hydrolase superfamily protein]	0.83	−0.93	0.87	−0.89	**−1.76**
250500_at	AT5G09530	hydroxyproline-rich glycoprotein family protein	0.07	−1.22	0.39	−0.91	**−1.30**
266353_at	AT2G01520	MLP-like protein 328	0.09	−1.18	1.23	−0.05	**−1.28**
256601_s_at	AT3G28290	[AT3G28290, Protein of unknown function (DUF677)]; [AT3G28300, Protein of unknown function (DUF677)]	0.45	−0.72	0.87	−0.30	**−1.17**
262832_s_at	AT1G14870	[AT1G14870, PLANT CADMIUM RESISTANCE 2]; [AT1G14880, PLANT CADMIUM RESISTANCE 1]	0.29	−0.87	0.85	−0.31	**−1.17**
254044_at	AT4G25820	xyloglucan endotransglucosylase/hydrolase 14	0.60	−0.51	0.51	−0.60	**−1.11**
260408_at	AT1G69880	thioredoxin H-type 8	0.53	−0.53	0.64	−0.42	**−1.06**
249375_at	AT5G40730	arabinogalactan protein 24	0.29	−0.76	0.55	−0.50	**−1.05**
246825_at	AT5G26260	TRAF-like family protein	0.44	−0.61	0.79	−0.25	**−1.05**
257382_at	AT2G40750	WRKY DNA-binding protein 54	0.44	−0.56	−0.23	−1.23	**−1.00**
265665_at	AT2G27420	Cysteine proteinases superfamily protein	1.20	0.22	0.22	−0.76	**−0.98**
266142_at	AT2G39030	Acyl-CoA N-acyltransferases (NAT) superfamily protein	−0.63	−1.59	3.01	2.05	**−0.96**
267053_s_at	AT2G38380	[AT2G38380, Peroxidase superfamily protein]; [AT2G38390, Peroxidase superfamily protein]	−0.14	−1.09	0.01	−0.94	**−0.95**
265837_at	AT2G14560	Protein of unknown function (DUF567)	0.45	−0.47	−0.99	−1.91	**−0.92**
264577_at	AT1G05260	Peroxidase superfamily protein	0.53	−0.34	0.19	−0.67	**−0.87**
265334_at	AT2G18370	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	0.17	−0.70	0.44	−0.42	**−0.87**
256603_at	AT3G28270	Protein of unknown function (DUF677)	0.58	−0.28	1.05	0.18	**−0.86**
262517_at	AT1G17180	glutathione S-transferase TAU 25	0.34	−0.51	0.33	−0.52	**−0.85**
257217_at	AT3G14940	phosphoenolpyruvate carboxylase 3	0.52	−0.34	0.25	−0.60	**−0.85**
246855_at	AT5G26280	TRAF-like family protein	0.37	−0.47	0.48	−0.36	**−0.85**
258270_at	AT3G15650	alpha/beta-Hydrolases superfamily protein	0.66	−0.17	0.02	−0.82	**−0.84**
262373_at	AT1G73120	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; EXPRESSED IN: root, cultured cell; Has 36 Blast hits to 36 proteins in 8 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−36; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.66	−0.18	0.32	−0.51	**−0.84**
256994_s_at	AT3G25830	[AT3G25830, terpene synthase-like sequence-1,8-cineole]; [AT3G25820, terpene synthase-like sequence-1,8-cineole]	0.17	−0.66	0.65	−0.18	**−0.83**
247874_at	AT5G57710	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein	0.57	−0.26	0.39	−0.44	**−0.83**
253073_at	AT4G37410	cytochrome P450, family 81, subfamily F, polypeptide 4	0.39	−0.42	0.88	0.07	**−0.81**
245275_at	AT4G15210	beta-amylase 5	0.15	−0.66	1.93	1.12	**−0.81**

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264400_at	AT1G61800	glucose-6-phosphate/phosphate translocator 2	1.10	0.30	0.35	−0.45	**−0.80**
263161_at	AT1G54020	GDSL-like Lipase/Acylhydrolase superfamily protein	0.30	−0.50	1.73	0.93	**−0.80**
266229_at	AT2G28840	XB3 ortholog 1 in *Arabidopsis thaliana*	0.69	−0.09	0.37	−0.41	**−0.78**
256245_at	AT3G12580	heat shock protein 70	0.43	−0.34	2.35	1.58	**−0.77**
256243_at	AT3G12500	basic chitinase	0.18	−0.59	0.37	−0.41	**−0.77**
262128_at	AT1G52690	Late embryogenesis abundant protein (LEA) family protein	0.93	0.16	0.29	−0.47	**−0.77**
266578_at	AT2G23910	NAD(P)-binding Rossmann-fold superfamily protein	0.25	−0.52	−0.17	−0.93	**−0.77**
249599_at	AT5G37990	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	0.39	−0.36	1.19	0.44	**−0.76**
264613_at	AT1G04640	lipoyltransferase 2	0.75	0.00	0.42	−0.33	**−0.75**
246228_at	AT4G36430	Peroxidase superfamily protein	−0.05	−0.80	0.11	−0.64	**−0.75**
265058_s_at	AT1G52040	[AT1G52040, myrosinase-binding protein 1]; [AT1G52030, myrosinase-binding protein 2]	0.39	−0.35	0.81	0.07	**−0.75**
247718_at	AT5G59310	lipid transfer protein 4	0.72	−0.02	0.82	0.08	**−0.74**
264006_at	AT2G22430	homeobox protein 6	0.85	0.11	0.63	−0.11	**−0.74**
256933_at	AT3G22600	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	0.08	−0.66	0.44	−0.30	**−0.73**
245265_at	AT4G14400	ankyrin repeat family protein	0.26	−0.47	−0.22	−0.96	**−0.73**
262133_at	AT1G78000	sulfate transporter 1;2	0.04	−0.68	0.76	0.03	**−0.72**
252102_at	AT3G50970	dehydrin family protein	0.14	−0.58	−0.55	−1.27	**−0.72**
256766_at	AT3G22231	pathogen and circadian controlled 1	0.38	−0.33	−0.36	−1.07	**−0.71**
245422_at	AT4G17470	alpha/beta-Hydrolases superfamily protein	0.38	−0.33	1.51	0.80	**−0.71**
250558_at	AT5G07990	Cytochrome P450 superfamily protein	−0.05	−0.75	0.36	−0.34	**−0.70**
256787_at	AT3G13790	Glycosyl hydrolases family 32 protein	0.06	−0.63	0.61	−0.09	**−0.70**
249953_at	AT5G18960	FAR1-related sequence 12	0.62	−0.07	0.22	−0.47	**−0.69**
255516_at	AT4G02270	root hair specific 13	0.20	−0.49	0.30	−0.39	**−0.69**
266330_at	AT2G01530	MLP-like protein 329	0.19	−0.50	0.61	−0.07	**−0.69**
267545_at	AT2G32690	glycine-rich protein 23	0.66	−0.02	0.44	−0.24	**−0.68**
250090_at	AT5G17330	glutamate decarboxylase	0.29	−0.39	0.54	−0.14	**−0.68**
251531_at	AT3G58550	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	0.08	−0.59	0.33	−0.35	**−0.68**
266941_at	AT2G18980	Peroxidase superfamily protein	0.08	−0.59	0.52	−0.16	**−0.67**
249986_at	AT5G18460	Protein of Unknown Function (DUF239)	0.58	−0.10	0.11	−0.56	**−0.67**
249383_at	AT5G39860	basic helix-loop-helix (bHLH) DNA-binding family protein	1.04	0.37	0.90	0.23	**−0.67**
247717_at	AT5G59320	lipid transfer protein 3	0.75	0.09	1.21	0.55	**−0.66**
256924_at	AT3G29590	HXXXD-type acyl-transferase family protein	0.22	−0.44	0.29	−0.37	**−0.66**
265118_at	AT1G62660	Glycosyl hydrolases family 32 protein	0.43	−0.23	0.74	0.08	**−0.66**
251705_at	AT3G56400	WRKY DNA-binding protein 70	0.13	−0.53	−0.15	−0.80	**−0.66**
248185_at	AT5G54060	UDP-glucose: flavonoid 3-o-glucosyltransferase	−0.01	−0.66	0.45	−0.21	**−0.66**

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259561_at	AT1G21250	cell wall-associated kinase	0.31	−0.34	−0.22	−0.87	**−0.65**
256577_at	AT3G28220	TRAF-like family protein	0.32	−0.33	0.42	−0.23	**−0.65**
250942_at	AT5G03350	Legume lectin family protein	−0.24	−0.88	−0.79	−1.43	**−0.65**
249215_at	AT5G42800	dihydroflavonol 4-reductase	−0.07	−0.72	0.33	−0.31	**−0.65**
263133_at	AT1G78450	SOUL heme-binding family protein	0.72	0.07	−0.21	−0.86	**−0.64**
253582_at	AT4G30670	Putative membrane lipoprotein	0.30	−0.33	0.45	−0.18	**−0.63**
248268_at	AT5G53480	ARM repeat superfamily protein	0.71	0.09	0.10	−0.52	**−0.62**
250083_at	AT5G17220	glutathione S-transferase phi 12	0.24	−0.37	0.22	−0.39	**−0.61**
259040_at	AT3G09270	glutathione S-transferase TAU 8	0.16	−0.45	0.52	−0.10	**−0.61**
247814_at	AT5G58310	methyl esterase 18	0.66	0.05	−0.36	−0.97	**−0.61**
267595_at	AT2G32990	glycosyl hydrolase 9B8	0.80	0.19	0.07	−0.54	**−0.61**
267076_at	AT2G41090	Calcium-binding EF-hand family protein	0.28	−0.32	−0.15	−0.76	**−0.60**
245816_at	AT1G26210	SOB five-like 1	0.57	−0.03	0.14	−0.46	**−0.60**
256937_at	AT3G22620	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	−0.06	−0.66	0.30	−0.29	**−0.59**
253608_at	AT4G30290	xyloglucan endotransglucosylase/hydrolase 19	0.08	−0.51	0.30	−0.29	**−0.59**
255604_at	AT4G01080	TRICHOME BIREFRINGENCE-LIKE 26	0.37	−0.22	0.34	−0.24	**−0.59**
254234_at	AT4G23680	Polyketide cyclase/dehydrase and lipid transport superfamily protein	0.53	−0.06	1.17	0.58	**−0.58**
254833_s_at	AT4G12280	[AT4G12280, copper amine oxidase family protein]; [AT4G12290, Copper amine oxidase family protein]	0.42	−0.16	0.33	−0.25	**−0.58**
251292_at	AT3G61920	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: shoot, hypocotyl, root, egg cell; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT1G64700.1); Has 77 Blast hits to 77 proteins in 8 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−77; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.42	−0.16	0.24	−0.34	**−0.58**
253697_at	AT4G29700	Alkaline-phosphatase-like family protein	0.47	−0.11	0.72	0.15	**−0.58**
252607_at	AT3G44990	xyloglucan endo-transglycosylase-related 8	0.56	−0.02	−0.38	−0.95	**−0.57**
245624_at	AT4G14090	UDP-Glycosyltransferase superfamily protein	0.19	−0.37	0.23	−0.34	**−0.57**
253510_at	AT4G31730	glutamine dumper 1	0.30	−0.27	0.14	−0.43	**−0.57**
258546_at	AT3G07060	NHL domain-containing protein	0.55	−0.01	0.09	−0.47	**−0.56**
259327_at	AT3G16460	Mannose-binding lectin superfamily protein	0.31	−0.26	0.55	−0.01	**−0.56**
245317_at	AT4G15610	Uncharacterised protein family (UPF0497)	−0.09	−0.65	0.58	0.02	**−0.56**
254737_at	AT4G13840	HXXXD-type acyl-transferase family protein	0.58	0.02	0.09	−0.47	**−0.56**
259878_at	AT1G76790	O-methyltransferase family protein	0.27	−0.29	0.31	−0.25	**−0.56**
260332_at	AT1G70470	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT1G23530.1); Has 64 Blast hits to 64 proteins in 22 species: Archae−0; Bacteria−2; Metazoa−7; Fungi−10; Plants−43; Viruses−0; Other Eukaryotes−2 (source: NCBI BLink).	0.51	−0.05	0.34	−0.22	**−0.56**

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264287_at	AT1G61930	Protein of unknown function, DUF584	0.48	−0.08	0.24	−0.32	**−0.56**
261033_at	AT1G17380	jasmonate-zim-domain protein 5	0.28	−0.28	0.91	0.35	**−0.56**
248867_at	AT5G46830	NACL-inducible gene 1	0.24	−0.31	0.71	0.15	**−0.56**
252387_at	AT3G47800	Galactose mutarotase-like superfamily protein	0.25	−0.30	−0.02	−0.58	**−0.56**
254283_s_at	AT4G22870	[AT4G22870, 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein]; [AT4G22880, leucoanthocyanidin dioxygenase]	0.03	−0.52	0.31	−0.25	**−0.55**
256781_at	AT3G13650	Disease resistance-responsive (dirigent-like protein) family protein	0.71	0.16	0.13	−0.42	**−0.55**
249790_at	AT5G24290	Vacuolar iron transporter (VIT) family protein	0.25	−0.30	0.26	−0.28	**−0.55**
250483_at	AT5G10300	methyl esterase 5	0.16	−0.39	0.67	0.12	**−0.55**
264998_at	AT1G67330	Protein of unknown function (DUF579)	0.20	−0.34	0.22	−0.32	**−0.54**
246273_at	AT4G36700	RmlC-like cupins superfamily protein	−0.24	−0.78	0.16	−0.38	**−0.54**
265393_at	AT2G20830	transferases;folic acid binding	0.39	−0.15	−0.05	−0.59	**−0.54**
249567_at	AT5G38020	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	0.39	−0.14	0.34	−0.20	**−0.54**
255595_at	AT4G01700	Chitinase family protein	0.39	−0.14	0.09	−0.44	**−0.53**
245628_at	AT1G56650	production of anthocyanin pigment 1	−0.06	−0.58	0.58	0.05	**−0.53**
256981_at	AT3G13380	BRI1-like 3	0.36	−0.17	0.02	−0.50	**−0.52**
259548_at	AT1G35260	MLP-like protein 165	0.56	0.04	0.08	−0.45	**−0.52**
265091_s_at	AT1G03940	[AT1G03940, HXXXD-type acyl-transferase family protein];[AT1G03495, HXXXD-type acyl-transferase family protein]	−0.11	−0.63	0.38	−0.15	**−0.52**
250927_at	AT5G03270	lysine decarboxylase family protein	0.19	−0.33	0.34	−0.18	**−0.52**
256418_at	AT3G06160	AP2/B3-like transcriptional factor family protein	0.58	0.06	0.16	−0.36	**−0.52**
248315_at	AT5G52630	mitochondrial RNAediting factor 1	0.37	−0.15	0.28	−0.24	**−0.52**
260522_x_at	AT2G41730	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT5G24640.1); Has 25 Blast hits to 25 proteins in 5 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−25; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.02	−0.50	−0.34	−0.85	**−0.52**
260943_at	AT1G45145	thioredoxin H-type 5	0.27	−0.25	0.27	−0.25	**−0.52**
258293_at	AT3G23430	phosphate 1	0.24	−0.27	0.09	−0.43	**−0.52**
264223_s_at	AT3G16030	lectin protein kinase family protein	0.25	−0.26	0.18	−0.34	**−0.51**
257952_at	AT3G21770	Peroxidase superfamily protein	0.16	−0.35	0.10	−0.41	**−0.51**
260146_at	AT1G52770	Phototropic-responsive NPH3 family protein	0.21	−0.30	−0.12	−0.63	**−0.51**
256617_at	AT3G22240	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT3G22235.2); Has 177 Blast hits to 177 proteins in 14 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−177; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.31	−0.20	−0.22	−0.73	**−0.51**
257798_at	AT3G15950	DNA topoisomerase-related	0.42	−0.09	0.53	0.02	**−0.51**
256017_at	AT1G19180	Jasmonate-zim-domain protein 1	−0.01	−0.52	0.62	0.11	**−0.51**
266209_at	AT2G27550	centroradialis	0.58	0.08	0.13	−0.38	**−0.50**
265067_at	AT1G03850	Glutaredoxin family protein	0.07	−0.44	0.37	−0.13	**−0.50**
257763_s_at	AT3G23120	[AT3G23120, receptor like protein 38]; [AT3G23110, receptor like protein 37]	0.46	−0.05	−0.08	−0.59	**−0.50**

(b)

ID	Locus	Description	Treatment Effects <1> W+FR effect (22˚C)	<2> W+FR effect (26˚C)	<3> 26˚C effect (WL)	<4> 26˚C effect (W+FR)	**FR effect ratio 26˚C/22˚C**
259169_at	AT3G03520	non-specific phospholipase C3	0.35	−0.15	0.20	−0.30	**−0.50**
262661_s_at	AT1G14230	[AT1G14230, GDA1/CD39 nucleoside phosphatase family protein];[AT1G14250, GDA1/CD39 nucleoside phosphatase family protein]	−0.33	−0.83	0.69	0.19	**−0.50**
258184_at	AT3G21510	histidine-containing phosphotransmitter 1	0.28	−0.22	0.19	−0.30	**−0.50**
258751_at	AT3G05890	Low temperature and salt responsive protein family	0.04	−0.46	0.29	−0.20	**−0.50**
246390_at	AT1G77330	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	0.32	−0.18	0.22	−0.28	**−0.50**
266884_at	AT2G44790	uclacyanin 2	0.02	−0.47	0.21	−0.28	**−0.49**
245904_at	AT5G11110	sucrose phosphate synthase 2F	0.61	0.12	0.29	−0.20	**−0.49**
261806_at	AT1G30510	root FNR 2	0.33	−0.15	0.06	−0.43	**−0.49**
245054_at	AT2G26460	RED family protein	0.57	0.09	0.21	−0.27	**−0.48**
253046_at	AT4G37370	cytochrome P450, family 81, subfamily D, polypeptide 8	−0.08	−0.56	0.45	−0.03	**−0.48**
257644_at	AT3G25780	allene oxide cyclase 3	0.22	−0.26	0.60	0.12	**−0.48**
251254_at	AT3G62270	HCO3-transporter family	0.26	−0.22	0.04	−0.44	**−0.48**
262317_at	AT2G48140	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	−0.14	−0.62	0.23	−0.25	**−0.48**
267425_at	AT2G34810	FAD-binding Berberine family protein	−0.02	−0.50	1.23	0.75	**−0.48**
257765_at	AT3G23020	Tetratricopeptide repeat (TPR)-like superfamily protein	0.21	−0.26	0.35	−0.13	**−0.48**
266368_at	AT2G41380	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	0.35	−0.13	0.84	0.37	**−0.48**
254341_at	AT4G22130	STRUBBELIG-receptor family 8	0.50	0.03	0.05	−0.42	**−0.48**
263098_at	AT2G16005	MD-2-related lipid recognition domain-containing protein	−0.01	−0.49	0.32	−0.15	**−0.47**
256090_at	no_match	no_match	0.23	−0.24	0.42	−0.05	**−0.47**
262518_at	AT1G17170	glutathione S-transferase TAU 24	0.33	−0.14	−0.49	−0.96	**−0.47**
265389_at	AT2G20690	lumazine-binding family protein	0.36	−0.11	0.08	−0.39	**−0.47**
259609_at	AT1G52410	TSK-associating protein 1	0.37	−0.10	0.62	0.15	**−0.47**
247704_at	AT5G59510	ROTUNDIFOLIA like 5	0.33	−0.14	0.42	−0.04	**−0.47**
258983_at	AT3G08860	PYRIMIDINE 4	0.11	−0.36	0.91	0.45	**−0.47**
262615_at	AT1G13950	eukaryotic elongation factor 5A-1	0.51	0.05	0.67	0.21	**−0.46**
262608_at	AT1G14120	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	0.25	−0.21	1.20	0.74	**−0.46**
263369_at	AT2G20480	unknown protein; Has 19 Blast hits to 19 proteins in 10 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−19; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.43	−0.02	0.19	−0.27	**−0.46**
248169_at	AT5G54610	ankyrin	0.20	−0.25	−0.18	−0.63	**−0.46**
257375_at	AT2G38640	Protein of unknown function (DUF567)	−0.01	−0.46	0.18	−0.27	**−0.45**
259835_at	AT1G52160	tRNAse Z3	0.28	−0.17	0.05	−0.40	**−0.45**

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248434_at	AT5G51440	HSP20-like chaperones superfamily protein	−0.07	−0.53	1.02	0.57	**−0.45**
252549_at	AT3G45860	cysteine-rich RLK (RECEPTOR-like protein kinase) 4	0.70	0.25	0.43	−0.02	**−0.45**
258537_at	AT3G04210	Disease resistance protein (TIR-NBS class)	0.01	−0.44	−0.23	−0.68	**−0.45**
266503_at	AT2G47780	Rubber elongation factor protein (REF)	0.07	−0.38	0.59	0.14	**−0.45**
252698_at	AT3G43670	Copper amine oxidase family protein	0.31	−0.14	0.16	−0.29	**−0.45**
253456_at	AT4G32050	neurochondrin family protein	0.30	−0.15	0.33	−0.12	**−0.45**
264005_at	AT2G22470	arabinogalactan protein 2	0.46	0.01	0.41	−0.04	**−0.45**
261221_at	AT1G19960	BEST *Arabidopsis thaliana* protein match is: transmembrane receptors (TAIR:AT2G32140.1); Has 41 Blast hits to 41 proteins in 17 species: Archae−0; Bacteria−2; Metazoa−23; Fungi−0; Plants−11; Viruses−0; Other Eukaryotes−5 (source: NCBI BLink).	0.31	−0.14	−0.03	−0.48	**−0.45**
253532_at	AT4G31570	CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro: IPR009053); BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT1G24460.1); Has 194354 Blast hits to 66887 proteins in 3244 species: Archae−3688; Bacteria−38556; Metazoa−84828; Fungi−17265; Plants−10589; Viruses−805; Other Eukaryotes−38623 (source: NCBI BLink).	0.49	0.04	0.25	−0.20	**−0.45**
249754_at	AT5G24530	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	0.06	−0.39	0.12	−0.33	**−0.45**
259694_at	AT1G63180	UDP-D-glucose/UDP-D-galactose 4-epimerase 3	0.40	−0.05	0.32	−0.13	**−0.45**
245216_at	AT4G16143	importin alpha isoform 2	0.32	−0.12	0.03	−0.42	**−0.45**
250292_at	AT5G13220	jasmonate-zim-domain protein 10	0.23	−0.22	0.47	0.03	**−0.45**
252234_at	AT3G49780	phytosulfokine 4 precursor	0.20	−0.25	0.22	−0.22	**−0.45**
259677_at	AT1G77740	phosphatidylinositol-4-phosphate 5-kinase 2	0.17	−0.28	0.09	−0.35	**−0.44**
263829_at	AT2G40435	BEST *Arabidopsis thaliana* protein match is: transcription regulators (TAIR:AT3G56220.1); Has 289 Blast hits to 289 proteins in 30 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−289; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.22	−0.22	0.34	−0.11	**−0.44**
256321_at	AT1G55020	lipoxygenase 1	−0.06	−0.50	0.50	0.06	**−0.44**
261713_at	AT1G32640	Basic helix-loop-helix (bHLH) DNA-binding family protein	0.26	−0.19	0.72	0.28	**−0.44**
248118_at	AT5G55050	GDSL-like Lipase/Acylhydrolase superfamily protein	0.22	−0.22	0.31	−0.13	**−0.44**
253145_at	AT4G35560	Transducin/WD40 repeat-like superfamily protein	0.47	0.03	0.15	−0.29	**−0.44**
250438_at	AT5G10580	Protein of unknown function, DUF599	0.02	−0.42	0.15	−0.29	**−0.44**
251634_at	AT3G57480	zinc finger (C2H2 type, AN1-like) family protein	0.28	−0.16	0.30	−0.14	**−0.44**
247684_at	AT5G59670	Leucine-rich repeat protein kinase family protein	0.49	0.05	−0.32	−0.76	**−0.44**
251304_at	AT3G61990	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	0.53	0.09	0.03	−0.41	**−0.44**
249289_at	AT5G41040	HXXXD-type acyl-transferase family protein	0.00	−0.43	0.19	−0.24	**−0.44**
248559_at	AT5G50012	[AT5G50012, conserved peptide upstream open reading frame 36];[AT5G50011, conserved peptide upstream open reading frame 37];[AT5G50010, sequence-specific DNA binding transcription factors;transcription regulators]	0.24	−0.20	0.16	−0.27	**−0.44**
264142_at	AT1G78930	Mitochondrial transcription termination factor family protein	0.21	−0.22	0.22	−0.22	**−0.44**

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250194_at	AT5G14550	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	0.37	−0.07	0.15	−0.29	**−0.43**
261402_at	AT1G79670	Wall-associated kinase family protein	0.13	−0.30	0.35	−0.08	**−0.43**
250968_at	AT5G02890	HXXXD-type acyl-transferase family protein	0.49	0.06	0.17	−0.26	**−0.43**
258125_s_at	AT3G23530	[AT3G23530, Cyclopropane-fatty-acyl-phospholipid synthase];[AT3G23510, Cyclopropane-fatty-acyl-phospholipid synthase]	0.70	0.27	−0.03	−0.46	**−0.43**
264342_at	AT1G12080	Vacuolar calcium-binding protein-related	0.83	0.39	0.10	−0.33	**−0.43**
261339_at	AT1G35710	Protein kinase family protein with leucine-rich repeat domain	0.29	−0.14	−0.36	−0.80	**−0.43**
261431_at	AT1G18710	myb domain protein 47	0.41	−0.03	0.17	−0.26	**−0.43**
264782_at	AT1G08810	myb domain protein 60	0.25	−0.18	0.13	−0.30	**−0.43**
260693_at	AT1G32450	nitrate transporter 1.5	−0.06	−0.49	0.14	−0.29	**−0.43**
257517_at	AT3G16330	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT1G52140.1); Has 109 Blast hits to 109 proteins in 16 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−109; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.51	0.09	0.28	−0.15	**−0.43**
264960_at	AT1G76930	extensin 4	−0.20	−0.63	0.03	−0.40	**−0.43**
261494_at	AT1G28420	homeobox-1	0.56	0.14	0.08	−0.35	**−0.42**
252108_at	AT3G51530	F-box/RNI-like/FBD-like domains-containing protein	0.23	−0.20	0.34	−0.08	**−0.42**
266316_at	AT2G27080	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family	0.00	−0.42	0.38	−0.04	**−0.42**
254432_at	AT4G20830	FAD-binding Berberine family protein	0.05	−0.37	0.29	−0.13	**−0.42**
249979_s_at	AT5G18860	[AT5G18860, inosine-uridine preferring nucleoside hydrolase family protein];[AT5G18890, Inosine-uridine preferring nucleoside hydrolase family protein]	0.23	−0.19	0.07	−0.35	**−0.42**
252073_at	AT3G51750	unknown protein; Has 15 Blast hits to 14 proteins in 5 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−15; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.37	−0.05	0.06	−0.36	**−0.42**
247808_at	AT5G58190	evolutionarily conserved C-terminal region 10	0.51	0.09	0.14	−0.28	**−0.42**
245055_at	AT2G26470	unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF159 (InterPro:IPR003738); Has 3646 Blast hits to 3636 proteins in 1001 species: Archae−41; Bacteria−1922; Metazoa−142; Fungi−125; Plants−44; Viruses−14; Other Eukaryotes−1358 (source: NCBI BLink).	0.21	−0.21	0.10	−0.32	**−0.42**
248332_at	AT5G52640	heat shock protein 90.1	0.17	−0.24	1.77	1.36	**−0.42**
251400_at	AT3G60420	Phosphoglycerate mutase family protein	0.25	−0.17	−0.35	−0.76	**−0.42**
262644_at	AT1G62710	beta vacuolar processing enzyme	0.50	0.09	0.03	−0.39	**−0.41**
253246_at	AT4G34600	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: pollen tube growth; LOCATED IN: endomembrane system; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: M germinated pollen stage, LP.04 four leaves visible, 4 anthesis, petal differentiation and expansion stage; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT2G16385.1); Has 17 Blast hits to 17 proteins in 4 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−17; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.03	−0.38	0.26	−0.15	**−0.41**

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245252_at	AT4G17500	ethylene responsive element binding factor 1	0.02	−0.39	0.46	0.04	**−0.41**
262801_at	AT1G21010	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT1G76600.1); Has 206 Blast hits to 206 proteins in 13 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−206; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.16	−0.25	0.22	−0.19	**−0.41**
252123_at	AT3G51240	flavanone 3-hydroxylase	0.05	−0.37	0.00	−0.41	**−0.41**
248145_at	AT5G54880	DTW domain-containing protein	0.22	−0.19	0.11	−0.30	**−0.41**
254371_at	AT4G21760	beta-glucosidase 47	0.06	−0.35	−0.06	−0.47	**−0.41**
261768_at	AT1G15550	gibberellin 3-oxidase 1	0.03	−0.38	0.11	−0.29	**−0.41**
264580_at	AT1G05340	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 7 growth stages; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT2G32210.1); Has 189 Blast hits to 189 proteins in 27 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−21; Plants−168; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.35	−0.06	0.39	−0.02	**−0.41**
249600_s_at	AT5G37940	[AT5G37940, Zinc-binding dehydrogenase family protein]; [AT5G38000, Zinc-binding dehydrogenase family protein]	0.42	0.01	0.22	−0.19	**−0.41**
258079_at	AT3G25940	TFIIB zinc-binding protein	0.33	−0.08	0.14	−0.27	**−0.41**
252677_at	AT3G44320	nitrilase 3	0.21	−0.20	0.64	0.23	**−0.41**
266352_at	AT2G01610	Plant invertase/pectin methylesterase inhibitor superfamily protein	0.30	−0.10	0.10	−0.30	**−0.40**
260549_at	AT2G43535	Scorpion toxin-like knottin superfamily protein	0.09	−0.32	0.30	−0.10	**−0.40**
259009_at	AT3G09260	Glycosyl hydrolase superfamily protein	0.28	−0.12	0.47	0.07	**−0.40**
245253_at	AT4G15440	hydroperoxide lyase 1	0.33	−0.08	0.46	0.06	**−0.40**
262131_at	AT1G02900	rapid alkalinization factor 1	−0.05	−0.45	0.16	−0.24	**−0.40**
249361_at	AT5G40540	Protein kinase superfamily protein	0.31	−0.09	0.10	−0.30	**−0.40**
261917_at	AT1G65920	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain	0.79	0.39	0.25	−0.15	**−0.40**
254783_at	AT4G12830	alpha/beta-Hydrolases superfamily protein	0.16	−0.24	−0.08	−0.48	**−0.40**
263544_at	AT2G21590	Glucose-1-phosphate adenylyltransferase family protein	0.49	0.10	0.12	−0.28	**−0.40**
265214_at	AT1G05000	Phosphotyrosine protein phosphatases superfamily protein	0.22	−0.17	−0.07	−0.47	**−0.40**
249545_at	AT5G38030	MATE efflux family protein	0.12	−0.28	0.24	−0.16	**−0.40**
248353_at	AT5G52320	cytochrome P450, family 96, subfamily A, polypeptide 4	0.41	0.01	0.12	−0.28	**−0.40**
267307_at	AT2G30210	laccase 3	0.24	−0.16	0.00	−0.40	**−0.40**
261428_at	AT1G18870	isochorismate synthase 2	0.13	−0.27	0.34	−0.05	**−0.40**
250045_at	AT5G17700	MATE efflux family protein	0.09	−0.30	0.34	−0.05	**−0.39**
246464_at	AT5G16980	Zinc-binding dehydrogenase family protein	0.26	−0.13	−0.24	−0.63	**−0.39**
254909_at	AT4G11210	Disease resistance-responsive (dirigent-like protein) family protein	0.50	0.11	0.30	−0.09	**−0.39**

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265122_at	AT1G62540	flavin-monooxygenase glucosinolate S-oxygenase 2	0.49	0.09	0.74	0.35	**−0.39**
257876_at	AT3G17130	Plant invertase/pectin methylesterase inhibitor superfamily protein	0.53	0.13	0.31	−0.08	**−0.39**
253396_at	AT4G32720	La protein 1	0.43	0.04	−0.08	−0.47	**−0.39**
252511_at	AT3G46280	protein kinase-related	0.18	−0.21	0.67	0.28	**−0.39**
260551_at	AT2G43510	trypsin inhibitor protein 1	−0.11	−0.50	0.83	0.44	**−0.39**
256875_at	AT3G26330	cytochrome P450, family 71, subfamily B, polypeptide 37	0.31	−0.09	0.32	−0.07	**−0.39**
262553_at	AT1G31360	RECQ helicase L2	0.35	−0.04	0.15	−0.24	**−0.39**
252114_at	AT3G51450	Calcium-dependent phosphotriesterase superfamily protein	0.21	−0.18	0.75	0.36	**−0.39**
256352_at	AT1G54970	proline-rich protein 1	0.30	−0.09	0.14	−0.25	**−0.39**
252131_at	AT3G50930	cytochrome BC1 synthesis	0.14	−0.25	0.25	−0.14	**−0.39**
255535_at	AT4G01790	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	0.36	−0.03	0.17	−0.22	**−0.39**
260416_at	AT1G69670	cullin 3B	0.22	−0.17	0.16	−0.23	**−0.39**
259672_at	AT1G68990	male gametophyte defective 3	0.29	−0.10	0.24	−0.15	**−0.39**
266078_at	AT2G40670	response regulator 16	0.60	0.22	−0.33	−0.72	**−0.39**
259982_at	AT1G76410	RING/U-box superfamily protein	0.35	−0.03	0.11	−0.27	**−0.39**
264859_at	AT1G24280	glucose-6-phosphate dehydrogenase 3	0.28	−0.10	0.05	−0.34	**−0.39**
244903_at	ATMG00660	hypothetical protein	0.62	0.23	0.49	0.11	**−0.39**
250960_at	AT5G02940	Protein of unknown function (DUF1012)	0.18	−0.21	0.37	−0.01	**−0.38**
258257_at	AT3G26770	NAD(P)-binding Rossmann-fold superfamily protein	0.16	−0.23	0.23	−0.16	**−0.38**
254042_at	AT4G25810	xyloglucan endotransglycosylase 6	0.00	−0.38	0.73	0.34	**−0.38**
257673_at	AT3G20370	TRAF-like family protein	0.05	−0.33	0.35	−0.04	**−0.38**
258447_at	AT3G22450	Ribosomal L18p/L5e family protein	0.11	−0.27	−0.05	−0.43	**−0.38**
266081_at	AT2G37840	Protein kinase superfamily protein	0.30	−0.08	0.13	−0.25	**−0.38**
251111_at	AT5G01310	APRATAXIN-like	0.36	−0.02	0.21	−0.17	**−0.38**
252014_at	AT3G52870	IQ calmodulin-binding motif family protein	0.36	−0.02	0.29	−0.09	**−0.38**
251980_at	AT3G53270	Small nuclear RNA activating complex (SNAPc), subunit SNAP43 protein	0.19	−0.19	0.30	−0.08	**−0.38**
263478_at	AT2G31880	Leucine-rich repeat protein kinase family protein	0.21	−0.17	0.03	−0.35	**−0.38**
253917_at	AT4G27380	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae−12; Bacteria−1396; Metazoa−17338; Fungi−3422; Plants−5037; Viruses−0; Other Eukaryotes−2996 (source: NCBI BLink).	0.38	0.00	0.00	−0.38	**−0.38**
247198_at	AT5G65290	LMBR1-like membrane protein	0.32	−0.06	0.31	−0.06	**−0.38**
246255_at	AT4G36650	plant-specific TFIIB-related protein	0.25	−0.12	0.11	−0.27	**−0.38**
252367_at	AT3G48360	BTB and TAZ domain protein 2	−0.14	−0.52	−0.43	−0.81	**−0.38**
261958_at	AT1G64500	Glutaredoxin family protein	0.32	−0.06	0.31	−0.07	**−0.38**
262811_at	AT1G11700	Protein of unknown function, DUF584	0.54	0.16	0.25	−0.13	**−0.38**
262831_at	AT1G14730	Cytochrome b561/ferric reductase transmembrane protein family	0.32	−0.05	0.11	−0.27	**−0.38**

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251668_at	AT3G57010	Calcium-dependent phosphotriesterase superfamily protein	0.36	−0.01	0.15	−0.23	**−0.38**
259899_at	AT1G71210	Pentatricopeptide repeat (PPR) superfamily protein	0.29	−0.08	0.04	−0.33	**−0.38**
251556_at	AT3G58840	Tropomyosin-related	0.24	−0.14	0.34	−0.04	**−0.38**
250879_at	AT5G04060	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	0.26	−0.12	0.33	−0.05	**−0.38**
252478_at	AT3G46540	ENTH/VHS family protein	0.24	−0.13	0.22	−0.16	**−0.38**
262119_s_at	AT1G02930	[AT1G02930, glutathione S-transferase 6]; [AT1G02920, glutathione S-transferase 7]	−0.35	−0.73	0.17	−0.21	**−0.38**
259394_at	AT1G06420	unknown protein; Has 1017 Blast hits to 654 proteins in 124 species: Archae−0; Bacteria−39; Metazoa−232; Fungi−69; Plants−40; Viruses−0; Other Eukaryotes−637 (source: NCBI BLink).	0.37	0.00	0.34	−0.03	**−0.38**
257580_at	AT3G06210	ARM repeat superfamily protein	0.41	0.03	0.28	−0.09	**−0.37**
259384_at	AT3G16450	Mannose-binding lectin superfamily protein	−0.05	−0.42	0.62	0.25	**−0.37**
250930_at	AT5G03160	homolog of mamallian P58IPK	0.24	−0.14	0.05	−0.32	**−0.37**
263073_at	AT2G17500	Auxin efflux carrier family protein	0.22	−0.16	0.47	0.09	**−0.37**
262711_at	AT1G16500	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT1G79160.1); Has 136 Blast hits to 134 proteins in 17 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−4; Plants−131; Viruses−1; Other Eukaryotes−0 (source: NCBI BLink).	0.16	−0.21	0.11	−0.26	**−0.37**
260087_at	AT1G73200	Putative integral membrane protein conserved region (DUF2404)	0.18	−0.20	0.22	−0.16	**−0.37**
256188_at	AT1G30160	Protein of unknown function (DUF295)	0.15	−0.22	0.28	−0.09	**−0.37**
253326_at	AT4G33440	Pectin lyase-like superfamily protein	0.36	−0.01	0.20	−0.17	**−0.37**
259786_at	AT1G29660	GDSL-like Lipase/Acylhydrolase superfamily protein	0.33	−0.04	0.36	−0.01	**−0.37**
258139_at	AT3G24520	heat shock transcription factor C1	0.60	0.23	0.19	−0.18	**−0.37**
254053_s_at	AT4G25310	[AT4G25310, 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein];[AT4G25300, 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein]	0.05	−0.32	0.21	−0.16	**−0.37**
250167_at	AT5G15310	myb domain protein 16	0.25	−0.12	0.28	−0.08	**−0.37**
258724_at	AT3G09600	Homeodomain-like superfamily protein	0.10	−0.27	0.19	−0.18	**−0.37**
258554_at	AT3G06980	DEA(D/H)-box RNA helicase family protein	0.33	−0.04	−0.03	−0.40	**−0.37**
255858_at	AT1G67030	zinc finger protein 6	0.07	−0.29	0.12	−0.25	**−0.37**
259640_at	AT1G52400	beta glucosidase 18	0.21	−0.16	0.51	0.14	**−0.36**
263493_at	AT2G42520	P-loop containing nucleoside triphosphate hydrolases superfamily protein	0.47	0.11	−0.05	−0.42	**−0.36**
246235_at	AT4G36830	GNS1/SUR4 membrane protein family	0.14	−0.22	0.08	−0.29	**−0.36**
261046_at	AT1G01390	UDP-Glycosyltransferase superfamily protein	0.67	0.31	−0.37	−0.73	**−0.36**
261382_at	AT1G05470	DNAse I-like superfamily protein	0.18	−0.18	−0.01	−0.37	**−0.36**
252994_at	AT4G38480	Transducin/WD40 repeat-like superfamily protein	0.42	0.06	0.12	−0.24	**−0.36**
251887_at	AT3G54170	FKBP12 interacting protein 37	0.37	0.01	0.04	−0.33	**−0.36**
266743_at	AT2G02990	ribonuclease 1	0.17	−0.20	0.91	0.55	**−0.36**

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247124_at	AT5G66060	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	0.31	−0.05	0.04	−0.32	**−0.36**
247486_at	AT5G62140	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 13 growth stages; Has 60 Blast hits to 60 proteins in 24 species: Archae−0; Bacteria−14; Metazoa−0; Fungi−0; Plants−45; Viruses−0; Other Eukaryotes−1 (source: NCBI BLink).	0.19	−0.18	0.05	−0.32	**−0.36**
264898_at	AT1G23205	Plant invertase/pectin methylesterase inhibitor superfamily protein	0.29	−0.07	0.04	−0.32	**−0.36**
246468_at	AT5G17050	UDP-glucosyl transferase 78D2	0.08	−0.29	0.15	−0.21	**−0.36**
263788_at	AT2G24580	FAD-dependent oxidoreductase family protein	0.30	−0.06	0.16	−0.20	**−0.36**
257735_at	AT3G27400	Pectin lyase-like superfamily protein	0.22	−0.14	0.02	−0.34	**−0.36**
259680_at	AT1G77690	like AUX1 3	0.42	0.06	0.21	−0.15	**−0.36**
263954_at	AT2G35840	Sucrose-6F-phosphate phosphohydrolase family protein	0.33	−0.02	0.02	−0.33	**−0.36**
248092_at	AT5G55170	small ubiquitin-like modifier 3	0.23	−0.13	−0.09	−0.45	**−0.36**
252937_at	AT4G39180	Sec14p-like phosphatidylinositol transfer family protein	0.32	−0.04	0.23	−0.13	**−0.36**
256379_at	AT1G66840	Plant protein of unknown function (DUF827)	0.35	−0.01	0.11	−0.25	**−0.36**
247965_at	AT5G56540	arabinogalactan protein 14	0.21	−0.15	0.39	0.03	**−0.36**
257890_s_at	AT3G42570	[AT3G42570, peroxidase family protein]; [AT3G17070, Peroxidase family protein]	0.30	−0.06	0.61	0.25	**−0.36**
250682_x_at	AT5G06630	proline-rich extensin-like family protein	0.11	−0.24	0.21	−0.15	**−0.36**
266479_at	AT2G31160	Protein of unknown function (DUF640)	0.35	−0.01	−0.09	−0.44	**−0.36**
267166_at	AT2G37720	TRICHOME BIREFRINGENCE-LIKE 15	0.04	−0.32	0.02	−0.34	**−0.36**
262773_at	AT1G13220	nuclear matrix constituent protein-related	0.42	0.07	0.22	−0.14	**−0.35**
265341_at	AT2G18360	alpha/beta-Hydrolases superfamily protein	0.18	−0.18	−0.07	−0.42	**−0.35**
267048_at	AT2G34200	RING/FYVE/PHD zinc finger superfamily protein	0.41	0.05	0.13	−0.23	**−0.35**
251647_at	AT3G57770	Protein kinase superfamily protein	0.45	0.10	0.13	−0.22	**−0.35**
246898_at	AT5G25580	BEST *Arabidopsis thaliana* protein match is: DDT domain superfamily (TAIR:AT1G18950.1); Has 178 Blast hits to 178 proteins in 75 species: Archae−0; Bacteria−4; Metazoa−51; Fungi−33; Plants−60; Viruses−1; Other Eukaryotes−29 (source: NCBI BLink).	0.27	−0.08	0.00	−0.35	**−0.35**
250446_at	AT5G10770	Eukaryotic aspartyl protease family protein	0.33	−0.02	0.17	−0.18	**−0.35**
266000_at	AT2G24180	cytochrome p450 71b6	0.20	−0.15	0.20	−0.15	**−0.35**
253879_s_at	AT4G27560	[AT4G27560, UDP-Glycosyltransferase superfamily protein];[AT4G27570, UDP-Glycosyltransferase superfamily protein]	0.34	−0.02	0.07	−0.28	**−0.35**
258726_at	AT3G11745	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 5 Blast hits to 5 proteins in 2 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−5; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.38	0.03	0.28	−0.07	**−0.35**
258201_at	AT3G13910	Protein of unknown function (DUF3511)	0.42	0.07	0.18	−0.17	**−0.35**

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254350_at	AT4G22280	F-box/RNI-like superfamily protein	0.15	−0.20	0.28	−0.07	**−0.35**
262137_at	AT1G77920	bZIP transcription factor family protein	0.35	0.00	0.06	−0.29	**−0.35**
254190_at	AT4G23885	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT5G24165.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae−12; Bacteria−1396; Metazoa−17338; Fungi−3422; Plants−5037; Viruses−0; Other Eukaryotes−2996 (source: NCBI BLink).	0.30	−0.05	0.23	−0.12	**−0.35**
248136_at	AT5G54910	DEA(D/H)-box RNA helicase family protein	0.10	−0.25	0.15	−0.20	**−0.35**
257793_at	AT3G26960	Pollen Ole e 1 allergen and extensin family protein	0.06	−0.29	0.43	0.08	**−0.35**
262482_at	AT1G17020	Senescence-related gene 1	0.15	−0.19	0.56	0.22	**−0.35**
259794_at	AT1G64330	myosin heavy chain-related	0.36	0.01	0.07	−0.28	**−0.35**
259278_at	AT3G01160	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cytosol, nucleus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: NUC153 (InterPro: IPR012580); Has 36638 Blast hits to 21323 proteins in 1057 species: Archae−109; Bacteria−2369; Metazoa−13796; Fungi−4858; Plants−1657; Viruses−489; Other Eukaryotes−13360 (source: NCBI BLink).	0.35	0.00	0.10	−0.25	**−0.35**
260074_at	AT1G73640	RAB GTPase homolog A6A	0.20	−0.15	0.14	−0.20	**−0.35**
256008_s_at	AT1G34040	[AT1G34040, Pyridoxal phosphate (PLP)-dependent transferases superfamily protein];[AT1G34060, Pyridoxal phosphate (PLP)-dependent transferases superfamily protein]	0.15	−0.20	0.33	−0.02	**−0.35**
249626_at	AT5G37540	Eukaryotic aspartyl protease family protein	0.32	−0.02	0.38	0.03	**−0.35**
258211_at	AT3G17890	unknown protein; Has 31 Blast hits to 31 proteins in 12 species: Archae−0; Bacteria−4; Metazoa−5; Fungi−10; Plants−12; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.15	−0.20	0.19	−0.16	**−0.35**
247189_at	AT5G65390	arabinogalactan protein 7	0.15	−0.19	0.31	−0.04	**−0.35**
250149_at	AT5G14700	NAD(P)-binding Rossmann-fold superfamily protein	0.35	0.01	0.21	−0.14	**−0.35**
263250_at	AT2G31390	pfkB-like carbohydrate kinase family protein	0.28	−0.07	−0.02	−0.36	**−0.35**
247678_at	AT5G59520	ZRT/IRT-like protein 2	0.11	−0.24	0.28	−0.07	**−0.34**
255278_at	AT4G04940	transducin family protein/WD-40 repeat family protein	0.23	−0.11	−0.12	−0.46	**−0.34**
261609_at	AT1G49740	PLC-like phosphodiesterases superfamily protein	0.34	0.00	0.12	−0.22	**−0.34**
250533_at	AT5G08640	flavonol synthase 1	0.20	−0.14	−0.01	−0.36	**−0.34**
265483_at	AT2G15790	peptidyl-prolyl cis-trans isomerase/cyclophilin-40 (CYP40)/rotamase	0.32	−0.03	0.06	−0.28	**−0.34**
253732_at	AT4G29140	MATE efflux family protein	0.29	−0.05	0.08	−0.26	**−0.34**
259381_s_at	AT3G16410	[AT3G16410, nitrile specifier protein 4]; [AT3G16390, nitrile specifier protein 3]; [AT3G16400, nitrile specifier protein 1]	0.50	0.16	0.54	0.20	**−0.34**
255587_at	AT4G01480	pyrophosphorylase 5	0.00	−0.34	0.17	−0.17	**−0.34**
252888_at	AT4G39210	Glucose-1-phosphate adenylyltransferase family protein	0.49	0.15	−0.05	−0.39	**−0.34**
248596_at	AT5G49330	myb domain protein 111	0.39	0.05	0.07	−0.27	**−0.34**
254907_at	AT4G11190	Disease resistance-responsive (dirigent-like protein) family protein	0.07	−0.26	0.07	−0.27	**−0.34**

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266219_at	AT2G28880	para-aminobenzoate (PABA) synthase family protein	0.25	−0.09	0.26	−0.08	**−0.34**
248553_at	AT5G50170	C2 calcium/lipid-binding and GRAM domain containing protein	0.07	−0.27	0.25	−0.09	**−0.34**
250043_at	AT5G18430	GDSL-like Lipase/Acylhydrolase superfamily protein	0.27	−0.07	0.06	−0.28	**−0.34**
250528_at	AT5G08600	U3 ribonucleoprotein (Utp) family protein	0.32	−0.01	0.10	−0.24	**−0.34**
266321_at	AT2G46660	cytochrome P450, family 78, subfamily A, polypeptide 6	0.19	−0.14	0.13	−0.21	**−0.34**
251298_at	AT3G62040	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	−0.06	−0.40	0.33	−0.01	**−0.34**
248153_at	AT5G54250	cyclic nucleotide-gated cation channel 4	0.23	−0.10	0.22	−0.11	**−0.34**
247191_at	AT5G65310	homeobox protein 5	0.36	0.02	−0.12	−0.46	**−0.34**
259568_at	AT1G20490	AMP-dependent synthetase and ligase family protein	0.26	−0.08	0.30	−0.04	**−0.34**
249266_at	AT5G41670	6-phosphogluconate dehydrogenase family protein	0.27	−0.06	−0.11	−0.44	**−0.34**
250670_at	AT5G06860	polygalacturonase inhibiting protein 1	−0.07	−0.40	0.29	−0.05	**−0.33**
250722_at	AT5G06190	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT3G58540.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae−12; Bacteria−1396; Metazoa−17338; Fungi−3422; Plants−5037; Viruses−0; Other Eukaryotes−2996 (source: NCBI BLink).	0.39	0.05	0.11	−0.22	**−0.33**
258397_at	AT3G15357	unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: shoot apex, hypocotyl, root, leaf; Has 6931 Blast hits to 2036 proteins in 230 species: Archae−7; Bacteria−933; Metazoa−1824; Fungi−836; Plants−482; Viruses−218; Other Eukaryotes−2631 (source: NCBI BLink).	0.16	−0.18	0.19	−0.14	**−0.33**
258133_at	AT3G24500	multiprotein bridging factor 1C	0.11	−0.22	1.49	1.16	**−0.33**
253519_at	AT4G31240	protein kinase C-like zinc finger protein	0.20	−0.13	0.59	0.26	**−0.33**
258472_at	AT3G06080	Plant protein of unknown function (DUF828)	0.43	0.09	0.24	−0.10	**−0.33**
257902_at	AT3G28450	Leucine-rich repeat protein kinase family protein	0.23	−0.10	0.25	−0.08	**−0.33**
261032_at	AT1G17430	alpha/beta-Hydrolases superfamily protein	0.23	−0.10	−0.05	−0.38	**−0.33**
263085_at	AT2G16090	RING/U-box superfamily protein	0.11	−0.23	0.35	0.01	**−0.33**
255081_at	AT4G09140	MUTL-homologue 1	0.08	−0.25	0.12	−0.22	**−0.33**
256021_at	AT1G58270	TRAF-like family protein	0.30	−0.03	0.21	−0.12	**−0.33**
264479_at	AT1G77280	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	0.13	−0.20	0.30	−0.03	**−0.33**
256910_at	AT3G24080	KRR1 family protein	0.38	0.05	0.01	−0.32	**−0.33**
264884_at	AT1G61170	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 12 growth stages; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT1G11125.1); Has 54 Blast hits to 54 proteins in 15 species: Archae−0; Bacteria−0; Metazoa−17; Fungi−0; Plants−34; Viruses−1; Other Eukaryotes−2 (source: NCBI BLink).	0.32	−0.01	0.06	−0.27	**−0.33**
259507_at	AT1G43910	P-loop containing nucleoside triphosphate hydrolases superfamily protein	0.51	0.18	−0.08	−0.41	**−0.33**

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267302_at	AT2G30105	CONTAINS InterPro DOMAIN/s: Leucine-rich repeat, typical subtype (InterPro:IPR003591), Leucine-rich repeat (InterPro:IPR001611), Ubiquitin (InterPro:IPR000626), Ubiquitin supergroup (InterPro:IPR019955); BEST *Arabidopsis thaliana* protein match is: Leucine-rich repeat (LRR) family protein (TAIR:AT5G07910.1).	0.26	−0.07	0.07	−0.26	**−0.33**
246340_s_at	AT3G44860	[AT3G44860, farnesoic acid carboxyl-O-methyltransferase]; [AT3G44870, S-adenosyl-L-methionine-dependent methyltransferases superfamily protein]	0.13	−0.20	0.64	0.31	**−0.33**
252997_at	AT4G38400	expansin-like A2	0.40	0.07	0.11	−0.22	**−0.33**
251637_at	AT3G57570	ARM repeat superfamily protein	0.20	−0.13	0.18	−0.15	**−0.33**
260547_at	AT2G43550	Scorpion toxin-like knottin superfamily protein	0.05	−0.28	0.04	−0.29	**−0.33**
264851_at	AT2G17290	Calcium-dependent protein kinase family protein	0.01	−0.32	−0.03	−0.36	**−0.33**
250541_at	AT5G09520	hydroxyproline-rich glycoprotein family protein	−0.02	−0.35	0.20	−0.13	**−0.33**
261957_at	AT1G64660	methionine gamma-lyase	0.62	0.29	0.43	0.10	**−0.33**
249092_at	AT5G43710	Glycosyl hydrolase family 47 protein	0.33	0.00	0.12	−0.21	**−0.33**
258252_at	AT3G15720	Pectin lyase-like superfamily protein	0.09	−0.24	0.17	−0.16	**−0.33**
264475_s_at	AT1G77150	[AT1G77150, Pentatricopeptide repeat (PPR) superfamily protein];[AT1G77170, Tetratricopeptide repeat (TPR)-like superfamily protein]	0.39	0.07	0.10	−0.22	**−0.33**
250985_at	AT5G02830	Tetratricopeptide repeat (TPR)-like superfamily protein	0.30	−0.03	0.07	−0.26	**−0.33**
249459_at	AT5G39580	Peroxidase superfamily protein	0.07	−0.26	0.54	0.22	**−0.33**
266781_at	AT2G28940	Protein kinase superfamily protein	0.15	−0.18	0.15	−0.17	**−0.33**
255881_at	AT1G67070	Mannose-6-phosphate isomerase, type I	0.00	−0.33	0.35	0.02	**−0.33**
255065_s_at	AT4G08870	[AT4G08870, Arginase/deacetylase superfamily protein]; [AT4G08900, arginase]	0.03	−0.30	0.61	0.28	**−0.33**
260701_at	AT1G32330	heat shock transcription factor A1D	0.15	−0.17	0.23	−0.10	**−0.33**
266532_at	AT2G16890	UDP-Glycosyltransferase superfamily protein	0.69	0.36	0.00	−0.33	**−0.33**
261106_at	AT1G62990	KNOTTED-like homeobox of *Arabidopsis thaliana* 7	0.29	−0.04	0.37	0.04	**−0.33**
258990_at	AT3G08840	D-alanine--D-alanine ligase family	0.11	−0.21	0.55	0.23	**−0.33**
255926_at	AT1G22190	Integrase-type DNA-binding superfamily protein	−0.01	−0.34	0.14	−0.18	**−0.33**
254812_at	AT4G12250	UDP-D-glucuronate 4-epimerase 5	0.18	−0.15	0.18	−0.15	**−0.33**
257112_at	AT3G20120	cytochrome P450, family 705, subfamily A, polypeptide 21	0.23	−0.10	0.06	−0.27	**−0.33**
254389_s_at	AT4G21903	[AT4G21903, MATE efflux family protein]; [AT4G21910, MATE efflux family protein]	0.28	−0.05	0.40	0.08	**−0.33**
259379_at	AT3G16350	Homeodomain-like superfamily protein	0.26	−0.06	0.20	−0.12	**−0.32**
254447_at	AT4G20860	FAD-binding Berberine family protein	0.00	−0.32	0.49	0.16	**−0.32**
261922_at	AT1G65890	acyl activating enzyme 12	0.35	0.02	0.26	−0.07	**−0.32**
256623_at	AT3G19960	myosin 1	0.34	0.01	0.17	−0.15	**−0.32**
264567_s_at	AT1G05250	[AT1G05250, Peroxidase superfamily protein]; [AT1G05240, Peroxidase superfamily protein]	0.21	−0.12	0.39	0.06	**−0.32**
259977_at	AT1G76590	PLATZ transcription factor family protein	0.15	−0.18	0.04	−0.28	**−0.32**
260718_at	AT1G48110	evolutionarily conserved C-terminal region 7	0.10	−0.22	0.02	−0.31	**−0.32**

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246420_at	AT5G16870	Peptidyl-tRNA hydrolase II (PTH2) family protein	0.37	0.05	−0.03	−0.35	**−0.32**
251086_at	AT5G01450	RING/U-box superfamily protein	0.16	−0.17	0.21	−0.11	**−0.32**
262643_at	AT1G62770	Plant invertase/pectin methylesterase inhibitor superfamily protein	0.34	0.02	0.17	−0.15	**−0.32**
253344_at	AT4G33550	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	0.46	0.14	0.55	0.23	**−0.32**
254413_at	AT4G21440	MYB-like 102	0.08	−0.24	0.22	−0.10	**−0.32**
246099_at	AT5G20230	blue-copper-binding protein	−0.27	−0.59	0.56	0.24	**−0.32**
255004_at	AT4G09970	unknown protein; LOCATED IN: chloroplast; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 13 growth stages; Has 15 Blast hits to 15 proteins in 6 species: Archae−0; Bacteria−2; Metazoa−0; Fungi−0; Plants−13; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.24	−0.08	0.07	−0.25	**−0.32**
260090_at	AT1G73310	serine carboxypeptidase−like 4	0.23	−0.09	0.14	−0.18	**−0.32**
266415_at	AT2G38530	lipid transfer protein 2	0.70	0.38	0.33	0.00	**−0.32**
264183_at	AT1G65380	Leucine-rich repeat (LRR) family protein	0.21	−0.11	0.11	−0.22	**−0.32**
255777_at	AT1G18630	glycine-rich RNA-binding protein 6	0.29	−0.03	0.04	−0.28	**−0.32**
249410_at	AT5G40380	cysteine-rich RLK (RECEPTOR-like protein kinase) 42	0.02	−0.30	0.20	−0.12	**−0.32**
262618_at	AT1G06560	NOL1/NOP2/sun family protein	0.25	−0.07	0.18	−0.15	**−0.32**
248472_at	AT5G50860	Protein kinase superfamily protein	0.23	−0.10	0.20	−0.12	**−0.32**
253913_at	AT4G27370	P-loop containing nucleoside triphosphate hydrolases superfamily protein	0.27	−0.05	0.25	−0.07	**−0.32**
262671_at	AT1G76040	calcium-dependent protein kinase 29	0.29	−0.03	0.21	−0.11	**−0.32**
248693_at	AT5G48330	Regulator of chromosome condensation (RCC1) family protein	0.33	0.01	0.19	−0.14	**−0.32**
246494_at	AT5G16190	cellulose synthase like A11	0.10	−0.22	0.51	0.19	**−0.32**
251910_at	AT3G53810	Concanavalin A-like lectin protein kinase family protein	0.09	−0.23	0.17	−0.15	**−0.32**
261907_at	AT1G65060	4-coumarate:CoA ligase 3	0.27	−0.05	0.03	−0.29	**−0.32**
245123_at	AT2G47450	chloroplast signal recognition particle component (CAO)	0.35	0.03	0.16	−0.16	**−0.32**
247464_at	AT5G62070	IQ-domain 23	0.05	−0.27	0.15	−0.17	**−0.32**
264908_at	AT2G17440	plant intracellular ras group-related LRR 5	0.24	−0.08	0.33	0.01	**−0.32**
256205_at	AT1G50890	ARM repeat superfamily protein	0.17	−0.15	0.19	−0.13	**−0.32**
258923_at	AT3G10450	serine carboxypeptidase-like 7	0.28	−0.04	0.38	0.06	**−0.32**
253639_at	AT4G30550	Class I glutamine amidotransferase-like superfamily protein	0.12	−0.20	0.43	0.12	**−0.32**
247878_at	AT5G57760	unknown protein; Has 5 Blast hits to 5 proteins in 2 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−5; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.32	0.00	−0.41	−0.73	**−0.32**
266290_at	AT2G29490	glutathione S-transferase TAU 1	−0.01	−0.33	0.17	−0.15	**−0.32**
251509_at	AT3G59010	pectin methylesterase 61	0.21	−0.10	0.32	0.00	**−0.32**
263174_at	AT1G54040	epithiospecifier protein	0.19	−0.12	0.22	−0.10	**−0.32**
255786_at	AT1G19670	chlorophyllase 1	0.09	−0.22	0.89	0.58	**−0.32**
260211_at	AT1G74440	Protein of unknown function (DUF962)	0.02	−0.29	−0.17	−0.49	**−0.32**
245074_at	AT2G23200	Protein kinase superfamily protein	0.08	−0.23	0.00	−0.31	**−0.32**

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264289_at	AT1G61890	MATE efflux family protein	0.24	−0.08	0.39	0.08	**−0.32**
262745_at	AT1G28600	GDSL-like Lipase/Acylhydrolase superfamily protein	0.00	−0.31	0.09	−0.22	**−0.32**
251140_at	AT5G01090	Concanavalin A-like lectin family protein	0.35	0.03	0.16	−0.16	**−0.32**
254238_at	AT4G23540	ARM repeat superfamily protein	0.33	0.02	0.00	−0.32	**−0.31**
260262_at	AT1G68470	Exostosin family protein	0.33	0.02	0.22	−0.10	**−0.31**
260585_at	AT2G43650	Sas10/U3 ribonucleoprotein (Utp) family protein	0.30	−0.01	0.04	−0.27	**−0.31**
259705_at	AT1G77450	NAC domain containing protein 32	0.29	−0.02	0.47	0.15	**−0.31**
266356_at	AT2G32300	uclacyanin 1	0.18	−0.13	0.18	−0.14	**−0.31**
263150_at	AT1G54050	HSP20-like chaperones superfamily protein	0.21	−0.10	0.55	0.24	**−0.31**
253209_at	AT4G34830	Pentatricopeptide repeat (PPR) superfamily protein	0.40	0.09	−0.12	−0.43	**−0.31**
261526_at	AT1G14370	protein kinase 2A	0.25	−0.07	0.09	−0.22	**−0.31**
245297_at	AT4G16510	YbaK/aminoacyl-tRNA synthetase-associated domain	0.26	−0.05	0.10	−0.21	**−0.31**
256571_at	AT3G30730	unknown protein; Has 59 Blast hits to 59 proteins in 7 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−59; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.06	−0.25	0.38	0.07	**−0.31**
248294_at	AT5G53060	RNA-binding KH domain-containing protein	0.27	−0.04	0.16	−0.16	**−0.31**
263706_s_at	AT1G31180	[AT1G31180, isopropylmalate dehydrogenase 3]; [AT5G14200, isopropylmalate dehydrogenase 1]	0.22	−0.10	0.31	0.00	**−0.31**
262340_at	AT1G64100	[AT1G64100, pentatricopeptide (PPR) repeat-containing protein]; [AT1G64105, NAC domain containing protein 27]	0.23	−0.08	0.23	−0.08	**−0.31**
259143_at	AT3G10190	Calcium-binding EF-hand family protein	0.15	−0.16	0.13	−0.18	**−0.31**
253029_at	AT4G38170	FAR1-related sequence 9	0.28	−0.03	0.13	−0.18	**−0.31**
257339_s_at	ATMG00040	[ATMG00040, ATP synthase subunit C family protein]; [AT2G07671, ATP synthase subunit C family protein]; [ATMG01080, mitochondrial F0-ATPase subunit 9]	0.23	−0.08	0.72	0.40	**−0.31**
259746_at	AT1G71060	Tetratricopeptide repeat (TPR)-like superfamily protein	0.23	−0.08	0.04	−0.27	**−0.31**
256050_at	AT1G07000	exocyst subunit exo70 family protein B2	0.19	−0.12	0.10	−0.21	**−0.31**
249286_at	AT5G41580	RING/U-box superfamily protein	0.19	−0.12	0.24	−0.07	**−0.31**
258742_at	AT3G05800	AtBS1(activation-tagged BRI1 suppressor 1)-interacting factor 1	0.38	0.07	−0.15	−0.46	**−0.31**
246968_at	AT5G24870	RING/U-box superfamily protein	0.34	0.03	0.34	0.03	**−0.31**
263684_at	AT1G26900	Pentatricopeptide repeat (PPR) superfamily protein	0.09	−0.22	0.23	−0.08	**−0.31**
247305_at	AT5G63905	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 12 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae−12; Bacteria−1396; Metazoa−17338; Fungi−3422; Plants−5037; Viruses−0; Other Eukaryotes−2996 (source: NCBI BLink).	0.06	−0.25	0.20	−0.11	**−0.31**
262659_at	AT1G14240	GDA1/CD39 nucleoside phosphatase family protein	0.13	−0.18	0.21	−0.10	**−0.31**
245346_at	AT4G17090	chloroplast beta-amylase	0.33	0.02	−0.26	−0.57	**−0.31**
250762_at	AT5G05990	Mitochondrial glycoprotein family protein	0.08	−0.23	0.09	−0.22	**−0.31**

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265672_at	AT2G31980	PHYTOCYSTATIN 2	0.40	0.09	0.28	−0.03	**−0.31**
264771_at	AT1G22940	thiamin biosynthesis protein, putative	0.31	0.00	−0.07	−0.38	**−0.31**
264902_at	AT1G23060	BEST *Arabidopsis thaliana* protein match is: TPX2 (targeting protein for Xklp2) protein family (TAIR: AT1G70950.1); Has 449 Blast hits to 419 proteins in 98 species: Archae−0; Bacteria−40; Metazoa−139; Fungi−21; Plants−158; Viruses−3; Other Eukaryotes−88 (source: NCBI BLink).	0.30	−0.01	0.21	−0.10	**−0.31**
250494_at	AT5G09740	histone acetyltransferase of the MYST family 2	0.17	−0.14	0.21	−0.10	**−0.31**
245747_at	AT1G51100	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, chloroplast stroma; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 26 Blast hits to 26 proteins in 9 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−26; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.19	−0.11	0.14	−0.16	**−0.31**
251752_at	AT3G55740	proline transporter 2	0.41	0.10	0.00	−0.30	**−0.31**
253485_at	AT4G31800	WRKY DNA-binding protein 18	−0.03	−0.34	0.16	−0.15	**−0.31**
255121_at	AT4G08480	mitogen-activated protein kinase kinase kinase 9	0.17	−0.14	0.04	−0.27	**−0.31**
263156_at	AT1G54030	GDSL-like Lipase/Acylhydrolase superfamily protein	0.34	0.04	0.24	−0.06	**−0.31**
252194_at	AT3G50110	PTEN 3	0.14	−0.16	0.20	−0.11	**−0.31**
249983_at	AT5G18470	Curculin-like (mannose-binding) lectin family protein	0.01	−0.29	0.01	−0.30	**−0.31**
248952_at	AT5G45410	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT4G25030.2); Has 124 Blast hits to 124 proteins in 34 species: Archae−2; Bacteria−31; Metazoa−0; Fungi−0; Plants−91; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	0.14	−0.16	0.33	0.03	**−0.31**
258214_at	AT3G17970	translocon at the outer membrane of chloroplasts 64−III	0.28	−0.02	0.01	−0.29	**−0.31**
249991_at	AT5G18550	Zinc finger C-x8-C-x5-C-x3-H type family protein	0.36	0.06	0.11	−0.20	**−0.30**
263274_at	AT2G11520	calmodulin-binding receptor-like cytoplasmic kinase 3	0.17	−0.13	0.05	−0.25	**−0.30**
254161_at	AT4G24370	unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae−12; Bacteria−1396; Metazoa−17338; Fungi−3422; Plants−5037; Viruses−0; Other Eukaryotes−2996 (source: NCBI BLink).	0.08	−0.23	0.28	−0.02	**−0.30**
259574_at	AT1G35310	MLP-like protein 168	0.23	−0.08	0.10	−0.21	**−0.30**
256751_at	AT3G27170	chloride channel B	0.05	−0.26	0.17	−0.13	**−0.30**
250955_at	AT5G03190	conserved peptide upstream open reading frame 47	0.38	0.07	0.23	−0.07	**−0.30**
257207_at	AT3G14900	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: embryo development; LOCATED IN: chloroplast; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 13 growth stages; Has 17135 Blast hits to 10204 proteins in 644 species: Archae−47; Bacteria−1684; Metazoa−5536; Fungi−2506; Plants−1043; Viruses−361; Other Eukaryotes−5958 (source: NCBI BLink).	0.14	−0.16	−0.12	−0.42	**−0.30**
259985_at	AT1G76620	Protein of unknown function, DUF547	0.27	−0.03	0.07	−0.24	**−0.30**
258003_at	AT3G29030	expansin A5	0.33	0.03	0.14	−0.16	**−0.30**
265200_s_at	AT2G36800	[AT2G36800, don-glucosyltransferase 1]; [AT2G36790, UDP-glucosyl transferase 73C6]	0.24	−0.07	0.13	−0.18	**−0.30**

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260367_at	AT1G69760	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT1G26920.1); Has 51 Blast hits to 51 proteins in 15 species: Archae−0; Bacteria−2; Metazoa−2; Fungi−7; Plants−29; Viruses−0; Other Eukaryotes−11 (source: NCBI BLink).	0.29	−0.02	0.23	−0.07	**−0.30**
255900_at	AT1G17830	Protein of unknown function (DUF789)	0.07	−0.24	0.23	−0.08	**−0.30**
246133_at	AT5G20960	aldehyde oxidase 1	0.45	0.15	−0.13	−0.43	**−0.30**
247210_at	AT5G65020	annexin 2	0.31	0.01	0.16	−0.14	**−0.30**
256291_at	AT3G12200	NIMA-related kinase 7	0.19	−0.11	0.04	−0.27	**−0.30**
264271_at	AT1G60270	beta glucosidase 6	0.22	−0.08	0.42	0.12	**−0.30**
263734_at	AT1G60030	nucleobase-ascorbate transporter 7	0.25	−0.05	0.13	−0.17	**−0.30**
261335_at	AT1G44800	nodulin MtN21 /EamA-like transporter family protein	0.11	−0.19	−0.08	−0.38	**−0.30**
262220_at	AT1G74740	calcium-dependent protein kinase 30	0.15	−0.15	0.29	−0.02	**−0.30**
255032_at	AT4G09500	UDP-Glycosyltransferase superfamily protein	0.30	0.00	0.25	−0.05	**−0.30**
247248_at	AT5G64560	magnesium transporter 9	0.22	−0.08	0.11	−0.19	**−0.30**
263586_at	AT2G25350	Phox (PX) domain-containing protein	0.20	−0.10	0.23	−0.07	**−0.30**

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ID	Locus	Description	Treatment Effects				**FR effect ratio 26˚C/22˚C**
			<1> W+FR effect (22˚C)	<2> W+FR effect (26˚C)	<3> 26˚C effect (WL)	<4> 26˚C effect (W+FR)	
260371_at	AT1G69690	TCP family transcription factor	−0.20	0.10	−0.17	0.13	**0.30**
262607_at	AT1G13990	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF3110 (InterPro:IPR021503); Has 25 Blast hits to 25 proteins in 8 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−25; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.28	0.02	0.46	0.76	**0.30**
246211_at	AT4G36730	G-box binding factor 1	−0.27	0.04	−0.02	0.28	**0.30**
245845_at	AT1G26150	proline-rich extensin-like receptor kinase 10	−0.25	0.06	0.03	0.33	**0.30**
251497_at	AT3G59060	phytochrome interacting factor 3-like 6 (PIF5)	−0.12	0.18	0.09	0.39	**0.30**
262635_at	AT1G06570	phytoene desaturation 1	−0.30	0.00	0.13	0.43	**0.30**
244990_s_at	ATCG00870	[ATCG00870, Protein precursor Ycf15, putative, chloroplast];[ATCG01270, Protein precursor Ycf15, putative, chloroplast]	0.29	0.59	0.32	0.62	**0.30**
245049_at	ATCG00050	ribosomal protein S16	−0.19	0.12	−0.36	−0.06	**0.30**
261165_at	AT1G34430	2-oxoacid dehydrogenases acyltransferase family protein	−0.21	0.10	−0.22	0.08	**0.30**
254683_at	AT4G13800	Protein of unknown function (DUF803)	−0.16	0.14	−0.08	0.23	**0.30**
259544_at	AT1G20620	catalase 3	−0.41	−0.10	0.28	0.58	**0.30**
248014_at	AT5G56340	RING/U-box superfamily protein	−0.10	0.20	−0.20	0.10	**0.30**

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264899_at	AT1G23130	Polyketide cyclase/dehydrase and lipid transport superfamily protein	−0.14	0.16	−0.04	0.26	**0.30**
253597_at	AT4G30690	Translation initiation factor 3 protein	−0.34	−0.03	0.01	0.32	**0.30**
249378_at	AT5G40450	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, plasma membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae−12; Bacteria−1396; Metazoa−17338; Fungi−3422; Plants−5037; Viruses−0; Other Eukaryotes−2996 (source: NCBI BLink).	−0.27	0.03	−0.15	0.15	**0.30**
247958_at	AT5G57070	Hydroxyproline-rich glycoprotein family protein	−0.14	0.17	−0.18	0.13	**0.30**
251154_at	AT3G63110	isopentenyltransferase 3	−0.31	0.00	−0.38	−0.08	**0.31**
255460_at	AT4G02800	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 9 growth stages; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT5G01970.1); Has 3209 Blast hits to 2720 proteins in 308 species: Archae−13; Bacteria−213; Metazoa−1207; Fungi−247; Plants−183; Viruses−21; Other Eukaryotes−1325 (source: NCBI BLink).	−0.11	0.20	−0.25	0.05	**0.31**
248342_at	AT5G52230	methyl-CPG-binding domain protein 13	−0.12	0.18	−0.09	0.21	**0.31**
253003_s_at	AT4G38300	[AT4G38300, glycosyl hydrolase family 10 protein]; [AT4G38650, Glycosyl hydrolase family 10 protein]	−0.14	0.16	−0.08	0.22	**0.31**
247066_at	AT5G66940	Dof-type zinc finger DNA-binding family protein	−0.28	0.03	−0.15	0.16	**0.31**
267428_at	AT2G34840	Coatomer epsilon subunit	−0.06	0.24	−0.06	0.24	**0.31**
253875_at	AT4G27520	early nodulin-like protein 2	−0.27	0.04	−0.16	0.15	**0.31**
254826_at	AT4G12640	RNA recognition motif (RRM)-containing protein	−0.07	0.24	−0.14	0.17	**0.31**
253881_at	AT4G27640	ARM repeat superfamily protein	0.11	0.42	−0.11	0.20	**0.31**
266106_at	AT2G45170	AUTOPHAGY 8E	−0.35	−0.05	0.16	0.47	**0.31**
255602_at	AT4G01026	PYR1-like 7	−0.42	−0.11	0.16	0.47	**0.31**
266072_at	AT2G18700	trehalose phosphatase/synthase 11	−0.29	0.02	−0.07	0.24	**0.31**
251365_at	AT3G61310	AT hook motif DNA-binding family protein	−0.14	0.17	−0.28	0.03	**0.31**
253051_at	AT4G37490	CYCLIN B1;1	−0.11	0.20	−0.40	−0.09	**0.31**
256812_at	AT3G21350	RNA polymerase transcriptional regulation mediator-related	−0.17	0.14	−0.08	0.23	**0.31**
257628_at	AT3G26290	cytochrome P450, family 71, subfamily B, polypeptide 26	−0.36	−0.05	0.25	0.56	**0.31**
267232_at	AT2G44190	Family of unknown function (DUF566)	−0.20	0.11	−0.24	0.07	**0.31**
260192_at	AT1G67630	DNA polymerase alpha 2	−0.14	0.17	−0.19	0.12	**0.31**
248352_at	AT5G52300	CAP160 protein	−0.03	0.29	−0.01	0.31	**0.31**
250470_at	AT5G10160	Thioesterase superfamily protein	−0.19	0.13	0.02	0.33	**0.31**
255094_at	AT4G08590	ORTHRUS-like	−0.07	0.24	−0.16	0.15	**0.31**
266516_at	AT2G47880	Glutaredoxin family protein	0.64	0.96	−0.33	−0.01	**0.31**
267171_at	AT2G37590	DNA binding with one finger 2.4	−0.20	0.12	−0.08	0.24	**0.31**
245330_at	AT4G14930	Survival protein SurE-like phosphatase/nucleotidase	−0.14	0.17	−0.09	0.23	**0.32**

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267354_at	AT2G39880	myb domain protein 25	−0.12	0.19	−0.17	0.15	**0.32**
264529_at	AT1G30820	CTP synthase family protein	−0.06	0.26	−0.53	−0.21	**0.32**
245719_at	AT5G04110	DNA GYRASE B3	−0.02	0.30	−0.07	0.25	**0.32**
247356_at	AT5G63800	Glycosyl hydrolase family 35 protein	−0.37	−0.05	0.14	0.46	**0.32**
261700_at	AT1G32690	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 11 growth stages; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT2G35200.1); Has 45 Blast hits to 45 proteins in 8 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−45; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.17	0.15	−0.28	0.04	**0.32**
259022_at	AT3G07420	asparaginyl-tRNA synthetase 2	−0.13	0.19	0.03	0.35	**0.32**
256152_at	AT1G55150	DEA(D/H)-box RNA helicase family protein	−0.27	0.06	−0.11	0.21	**0.32**
260431_at	AT1G68190	B-box zinc finger family protein	−0.35	−0.03	0.22	0.55	**0.32**
247332_at	AT5G63440	Protein of unknown function (DUF167)	0.02	0.34	−0.28	0.04	**0.32**
253182_at	AT4G35190	Putative lysine decarboxylase family protein	0.16	0.49	0.08	0.41	**0.32**
258828_at	AT3G07130	purple acid phosphatase 15	−0.15	0.17	−0.11	0.22	**0.33**
254327_at	AT4G22490	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	−0.09	0.24	0.28	0.60	**0.33**
266719_at	AT2G46830	circadian clock associated 1	−0.31	0.01	0.07	0.39	**0.33**
251024_at	AT5G02180	Transmembrane amino acid transporter family protein	−0.37	−0.04	−0.14	0.19	**0.33**
263391_at	AT2G11810	monogalactosyldiacylglycerol synthase type C	−0.49	−0.16	−0.22	0.10	**0.33**
251588_at	AT3G58090	Disease resistance-responsive (dirigent-like protein) family protein	−0.07	0.25	−0.20	0.13	**0.33**
260011_at	AT1G68110	ENTH/ANTH/VHS superfamily protein	−0.25	0.07	0.02	0.35	**0.33**
254998_at	AT4G09760	Protein kinase superfamily protein	−0.22	0.11	−0.15	0.18	**0.33**
253666_at	AT4G30270	xyloglucan endotransglucosylase/hydrolase 24	−0.41	−0.08	0.53	0.86	**0.33**
259792_at	AT1G29690	MAC/Perforin domain-containing protein	−0.31	0.02	−0.23	0.09	**0.33**
254818_at	AT4G12470	azelaic acid induced 1	−0.84	−0.51	0.02	0.35	**0.33**
250478_at	AT5G10250	Phototropic-responsive NPH3 family protein	−0.15	0.18	0.11	0.44	**0.33**
256125_at	AT1G18250	Pathogenesis-related thaumatin superfamily protein	−0.15	0.18	−0.27	0.06	**0.33**
266944_at	no_match	no_match	−0.24	0.09	−0.13	0.20	**0.33**
252332_at	AT3G48810	Pentatricopeptide repeat (PPR) superfamily protein	−0.20	0.13	−0.18	0.15	**0.33**
254051_at	AT4G25270	Tetratricopeptide repeat (TPR)-like superfamily protein	−0.13	0.20	−0.30	0.03	**0.33**
266101_at	AT2G37940	Arabidopsis Inositol phosphorylceramide synthase 2	−0.18	0.15	−0.36	−0.03	**0.33**
258497_at	AT3G02380	CONSTANS-like 2	−0.57	−0.23	−0.03	0.30	**0.33**
260603_at	AT1G55960	Polyketide cyclase/dehydrase and lipid transport superfamily protein	−0.29	0.04	−0.01	0.33	**0.33**
255061_at	AT4G08930	APR-like 6	−0.39	−0.06	−0.16	0.17	**0.34**
260276_at	AT1G80450	VQ motif-containing protein	−0.17	0.17	−0.32	0.01	**0.34**

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249505_at	AT5G38870	transposable element gene	−0.11	0.23	−0.27	0.07	**0.34**
261613_at	AT1G49720	abscisic acid responsive element-binding factor 1	0.02	0.36	−0.42	−0.08	**0.34**
252414_at	AT3G47420	phosphate starvation-induced gene 3	−0.48	−0.14	0.21	0.54	**0.34**
256532_at	AT1G33350	Pentatricopeptide repeat (PPR) superfamily protein	−0.13	0.21	−0.15	0.19	**0.34**
260799_at	AT1G78270	UDP-glucosyl transferase 85A4	−0.28	0.06	−0.39	−0.06	**0.34**
260393_at	AT1G73920	alpha/beta-Hydrolases superfamily protein	−0.28	0.06	−0.19	0.14	**0.34**
262396_at	AT1G49470	Family of unknown function (DUF716)	−0.16	0.18	−0.15	0.18	**0.34**
253701_at	AT4G29890	choline monooxygenase, putative (CMO-like)	−0.24	0.10	0.05	0.39	**0.34**
256873_at	AT3G26310	cytochrome P450, family 71, subfamily B, polypeptide 35	−0.17	0.16	−0.18	0.16	**0.34**
246782_at	AT5G27320	alpha/beta-Hydrolases superfamily protein	0.03	0.37	−0.17	0.17	**0.34**
255036_at	AT4G09560	Protease-associated (PA) RING/U-box zinc finger family protein	−0.31	0.03	−0.15	0.19	**0.34**
267525_at	AT2G30560	glycine-rich protein	−0.14	0.20	−0.15	0.19	**0.34**
251172_at	AT3G63190	ribosome recycling factor, chloroplast precursor	−0.24	0.11	−0.27	0.07	**0.34**
267262_at	AT2G22990	sinapoylglucose 1	−0.54	−0.20	0.15	0.50	**0.34**
246935_at	AT5G25350	EIN3-binding F box protein 2	−0.06	0.28	−0.38	−0.04	**0.34**
256320_at	AT3G12170	Chaperone DnaJ-domain superfamily protein	−0.12	0.22	−0.37	−0.02	**0.34**
258434_at	AT3G16770	ethylene-responsive element binding protein	−0.11	0.23	0.08	0.43	**0.34**
245828_at	AT1G57820	Zinc finger (C3HC4-type RING finger) family protein	−0.09	0.25	−0.08	0.26	**0.34**
263036_at	AT1G23890	NHL domain-containing protein	−0.26	0.08	−0.19	0.15	**0.34**
266917_at	AT2G45830	downstream target of AGL15 2	−0.10	0.24	−0.13	0.21	**0.35**
261972_at	AT1G64600	methyltransferases;copper ion binding	−0.25	0.10	−0.30	0.05	**0.35**
246880_s_at	AT5G26000	[AT5G26000, thioglucoside glucohydrolase 1]; [AT5G25980, glucoside glucohydrolase 2]	−0.34	0.01	0.06	0.41	**0.35**
247243_at	AT5G64700	nodulin MtN21 /EamA-like transporter family protein	−0.07	0.28	−0.19	0.16	**0.35**
255957_at	AT1G22160	Protein of unknown function (DUF581)	0.17	0.52	0.13	0.48	**0.35**
254625_at	AT4G18470	negative regulator of systemic acquired resistance (SNI1)	−0.13	0.23	−0.17	0.19	**0.35**
262479_at	AT1G11130	Leucine-rich repeat protein kinase family protein	−0.07	0.28	−0.30	0.05	**0.35**
258239_at	AT3G27690	photosystem II light harvesting complex gene 2.3	−0.57	−0.22	−0.06	0.29	**0.35**
247696_at	AT5G59780	myb domain protein 59	−0.47	−0.12	0.26	0.61	**0.35**
260417_at	AT1G69770	chromomethylase 3	−0.36	−0.01	0.02	0.37	**0.35**
253953_at	AT4G26750	hydroxyproline-rich glycoprotein family protein	−0.08	0.28	−0.21	0.14	**0.35**
259980_at	AT1G76520	Auxin efflux carrier family protein	−0.24	0.12	−0.26	0.09	**0.35**
245925_at	AT5G28770	bZIP transcription factor family protein	−0.31	0.04	−0.13	0.23	**0.35**
250810_at	AT5G05090	Homeodomain-like superfamily protein	−0.25	0.10	−0.24	0.12	**0.36**
247266_at	AT5G64570	beta-D-xylosidase 4	−0.36	−0.01	−0.27	0.08	**0.36**
246260_at	AT1G31820	Amino acid permease family protein	−0.28	0.07	0.09	0.44	**0.36**
247327_at	AT5G64120	Peroxidase superfamily protein	−0.79	−0.43	0.21	0.56	**0.36**

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265478_at	AT2G15890	maternal effect embryo arrest 14	−0.56	−0.21	−0.42	−0.06	**0.36**
253514_at	AT4G31805	WRKY family transcription factor	−0.01	0.34	−0.41	−0.06	**0.36**
245935_at	AT5G19840	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	−0.09	0.27	−0.18	0.18	**0.36**
255217_s_at	AT3G30465	[AT3G30465, transposable element gene]; [AT4G07680, transposable element gene]; [AT2G07395, transposable element gene]	−0.18	0.18	−0.24	0.12	**0.36**
260970_at	AT1G53640	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 11 growth stages; Has 1186 Blast hits to 678 proteins in 89 species: Archae−0; Bacteria−50; Metazoa−731; Fungi−92; Plants−226; Viruses−4; Other Eukaryotes−83 (source: NCBI BLink).	−0.39	−0.03	−0.19	0.17	**0.36**
250911_at	AT5G03730	Protein kinase superfamily protein	−0.28	0.08	−0.12	0.25	**0.36**
251084_at	AT5G01520	RING/U-box superfamily protein	−0.31	0.05	0.20	0.56	**0.36**
249862_at	AT5G22920	CHY-type/CTCHY-type/RING-type Zinc finger protein	−0.21	0.15	−0.37	−0.01	**0.36**
256789_at	AT3G13672	TRAF-like superfamily protein	−0.37	−0.01	0.08	0.44	**0.36**
266672_at	AT2G29650	phosphate transporter 4;1	−0.52	−0.15	0.00	0.37	**0.36**
257271_at	AT3G28007	Nodulin MtN3 family protein	−0.30	0.07	−0.20	0.16	**0.36**
259364_at	AT1G13260	related to ABI3/VP1 1	−0.02	0.35	−0.30	0.07	**0.37**
250665_at	AT5G06980	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT3G12320.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae−12; Bacteria−1396; Metazoa−17338; Fungi−3422; Plants−5037; Viruses−0; Other Eukaryotes−2996 (source: NCBI BLink).	−0.61	−0.24	0.01	0.37	**0.37**
262121_at	AT1G02800	cellulase 2	−0.15	0.22	0.06	0.42	**0.37**
266363_at	AT2G41250	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein	−0.63	−0.26	0.09	0.46	**0.37**
259414_at	AT1G02420	Pentatricopeptide repeat (PPR) superfamily protein	−0.16	0.21	−0.30	0.07	**0.37**
259490_at	no_match	no_match	−0.30	0.07	−0.11	0.26	**0.37**
255895_at	AT1G18020	[AT1G18020, FMN-linked oxidoreductases superfamily protein];[AT1G17990, FMN-linked oxidoreductases superfamily protein]	−0.21	0.17	−0.23	0.14	**0.37**
254805_at	AT4G12480	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	−0.98	−0.61	−0.05	0.32	**0.37**
263128_at	AT1G78600	light-regulated zinc finger protein 1	−0.54	−0.16	−0.20	0.18	**0.37**
253125_at	AT4G36040	Chaperone DnaJ-domain superfamily protein	−0.13	0.24	−0.01	0.36	**0.37**
258488_at	AT3G02420	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0121 (InterPro:IPR005344); Has 72 Blast hits to 71 proteins in 25 species: Archae−0; Bacteria−0; Metazoa−2; Fungi−2; Plants−60; Viruses−0; Other Eukaryotes−8 (source: NCBI BLink).	−0.23	0.15	−0.20	0.18	**0.37**
247713_at	AT5G59330	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	−0.03	0.34	−0.36	0.01	**0.37**

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261753_at	AT1G76340	golgi nucleotide sugar transporter 3	−0.35	0.02	−0.22	0.15	**0.37**
263560_s_at	AT2G15350	[AT2G15350, fucosyltransferase 10]; [AT2G15370, fucosyltransferase 5]	−0.12	0.26	−0.30	0.07	**0.37**
260640_at	AT1G53350	Disease resistance protein (CC-NBS-LRR class) family	−0.13	0.24	−0.36	0.01	**0.37**
259686_at	AT1G63100	GRAS family transcription factor	−0.12	0.25	−0.39	−0.02	**0.38**
246932_at	AT5G25190	Integrase-type DNA-binding superfamily protein	−0.36	0.02	−0.34	0.04	**0.38**
264261_at	AT1G09240	nicotianamine synthase 3	−0.18	0.19	−0.22	0.16	**0.38**
249748_at	AT5G24620	Pathogenesis-related thaumatin superfamily protein	−0.06	0.32	−0.19	0.19	**0.38**
254169_at	AT4G24290	MAC/Perforin domain-containing protein	−0.22	0.16	−0.27	0.11	**0.38**
247887_at	AT5G57880	multipolar spindle 1	−0.23	0.15	0.00	0.38	**0.38**
267364_at	AT2G40080	Protein of unknown function (DUF1313)	−0.01	0.37	−0.26	0.12	**0.38**
255627_at	AT4G00955	FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 9 growth stages; CONTAINS InterPro DOMAIN/s: EGF-like (InterPro:IPR006210); BEST *Arabidopsis thaliana* protein match is: Protein kinase superfamily protein (TAIR:AT2G23450.1); Has 94 Blast hits to 88 proteins in 13 species: Archae−0; Bacteria−0; Metazoa−10; Fungi−0; Plants−84; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.25	0.13	−0.44	−0.06	**0.38**
261492_at	AT1G14290	sphingoid base hydroxylase 2	−0.33	0.05	−0.06	0.32	**0.38**
252072_at	AT3G51710	D-mannose binding lectin protein with Apple-like carbohydrate-binding domain	−0.07	0.31	−0.06	0.32	**0.38**
257199_at	AT3G23710	Tic22-like family protein	−0.27	0.11	−0.17	0.21	**0.38**
259661_at	AT1G55265	Protein of unknown function, DUF538	−0.29	0.09	−0.50	−0.12	**0.38**
256025_at	AT1G58370	glycosyl hydrolase family 10 protein/carbohydrate-binding domain-containing protein	−0.30	0.08	0.10	0.49	**0.38**
257191_at	AT3G13175	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 12 growth stages; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT4G16400.1); Has 29 Blast hits to 29 proteins in 8 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−29; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.13	0.26	−0.32	0.06	**0.38**
266867_at	AT2G45770	signal recognition particle receptor protein, chloroplast (FTSY)	−0.28	0.10	−0.32	0.07	**0.38**
249769_at	AT5G24120	sigma factor E	−0.50	−0.12	0.14	0.53	**0.39**
252100_at	AT3G51110	Tetratricopeptide repeat (TPR)-like superfamily protein	−0.09	0.30	−0.18	0.21	**0.39**
252663_at	AT3G44070	Glycosyl hydrolase family 35 protein	−0.19	0.20	−0.21	0.18	**0.39**
251869_at	AT3G54500	BEST *Arabidopsis thaliana* protein match is: dentin sialophosphoprotein-related (TAIR:AT5G64170.1); Has 183 Blast hits to 175 proteins in 44 species: Archae−0; Bacteria−4; Metazoa−38; Fungi−11; Plants−120; Viruses−0; Other Eukaryotes−10 (source: NCBI BLink).	−0.38	0.01	0.16	0.55	**0.39**
266385_at	AT2G14610	Pathogenesis-related gene 1	−0.36	0.03	−0.25	0.14	**0.39**
260037_at	AT1G68840	related to ABI3/VP1 2	−0.50	−0.11	−0.30	0.10	**0.39**
245337_at	AT4G16566	histidine triad nucleotide-binding 4	−0.36	0.03	−0.24	0.16	**0.39**

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261248_at	AT1G20030	Pathogenesis-related thaumatin superfamily protein	−0.37	0.03	−0.10	0.29	**0.40**
264377_at	AT2G25060	early nodulin-like protein 14	−0.25	0.15	−0.08	0.32	**0.40**
248482_at	no_match	no_match	−0.11	0.29	−0.18	0.22	**0.40**
262399_at	AT1G49500	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 10 growth stages; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT3G19030.1); Has 24 Blast hits to 24 proteins in 2 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−24; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.65	−0.25	0.00	0.41	**0.41**
256527_at	AT1G66100	Plant thionin	−0.95	−0.55	0.14	0.55	**0.41**
257330_at	ATMG01290	hypothetical protein	0.09	0.49	−0.01	0.39	**0.41**
247939_at	AT5G57160	DNA ligase IV	−0.03	0.37	−0.37	0.04	**0.41**
258419_at	AT3G16670	Pollen Ole e 1 allergen and extensin family protein	−0.42	−0.01	−0.83	−0.41	**0.41**
256266_at	AT3G12320	unknown protein; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT5G06980.4); Has 102 Blast hits to 102 proteins in 16 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−98; Viruses−0; Other Eukaryotes−4 (source: NCBI BLink).	−0.52	−0.10	0.23	0.65	**0.41**
248337_at	AT5G52310	low-temperature-responsive protein 78 (LTI78)/desiccation-responsive protein 29A (RD29A)	−0.48	−0.06	−0.76	−0.34	**0.41**
245734_at	AT1G73480	alpha/beta-Hydrolases superfamily protein	−0.47	−0.05	0.23	0.65	**0.41**
245749_at	AT1G51090	Heavy metal transport/detoxification superfamily protein	−0.23	0.19	−0.48	−0.07	**0.42**
267568_at	AT2G30780	Tetratricopeptide repeat (TPR)-like superfamily protein	−0.39	0.03	−0.20	0.21	**0.42**
250971_at	AT5G02810	pseudo-response regulator 7	−0.24	0.18	−0.08	0.34	**0.42**
259925_at	AT1G75040	pathogenesis-related gene 5	−0.39	0.03	−0.48	−0.06	**0.42**
245769_at	AT1G30220	inositol transporter 2	−0.20	0.22	−0.08	0.35	**0.42**
266572_at	AT2G23840	HNH endonuclease	−0.41	0.02	0.07	0.50	**0.43**
256269_at	AT3G12250	TGACG motif-binding factor 6	−0.11	0.31	−0.15	0.27	**0.43**
248756_at	AT5G47560	tonoplast dicarboxylate transporter	−0.30	0.13	−0.14	0.29	**0.43**
261423_at	AT1G18750	AGAMOUS-like 65	−0.15	0.29	−0.07	0.38	**0.44**
254770_at	AT4G13340	Leucine-rich repeat (LRR) family protein	−0.25	0.20	−0.36	0.10	**0.45**
248620_at	AT5G49320	Protein of unknown function (DUF1218)	−0.25	0.21	−0.14	0.31	**0.46**
246043_at	AT5G19380	CRT (chloroquine-resistance transporter)-like transporter 1	−0.07	0.39	−0.13	0.32	**0.46**
261026_at	AT1G01240	unknown protein; INVOLVED IN: N-terminal protein myristoylation; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 11 growth stages; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT2G46550.1); Has 95 Blast hits to 78 proteins in 16 species: Archae−0; Bacteria−2; Metazoa−11; Fungi−0; Plants−80; Viruses−0; Other Eukaryotes−2 (source: NCBI BLink).	−0.46	0.00	0.03	0.49	**0.46**
253061_at	AT4G37610	BTB and TAZ domain protein 5	−0.51	−0.05	−0.60	−0.14	**0.46**
248910_at	AT5G45820	CBL-interacting protein kinase 20	−0.65	−0.19	0.15	0.62	**0.46**

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258225_at	AT3G15630	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST *Arabidopsis thaliana* protein match is: unknown protein (TAIR:AT1G52720.1); Has 61 Blast hits to 61 proteins in 13 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−61; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.52	−0.06	−0.41	0.05	**0.46**
251036_at	AT5G02160	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 121 Blast hits to 121 proteins in 17 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−121; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.63	−0.16	−0.31	0.15	**0.47**
247524_at	AT5G61440	atypical CYS HIS rich thioredoxin 5	−0.16	0.31	−0.53	−0.06	**0.47**
263836_at	AT2G40330	PYR1-like 6	−0.39	0.08	−0.33	0.14	**0.47**
266656_at	AT2G25900	Zinc finger C-x8-C-x5-C-x3-H type family protein	−0.66	−0.18	−0.33	0.15	**0.47**
262224_at	AT1G74900	Pentatricopeptide repeat (PPR) superfamily protein	−0.23	0.24	−0.26	0.21	**0.48**
263443_at	AT2G28630	3-ketoacyl-CoA synthase 12	−0.34	0.13	−0.28	0.20	**0.48**
245001_at	ATCG00220	photosystem II reaction center protein M	−0.43	0.05	−0.05	0.42	**0.48**
258402_at	AT3G15450	Aluminium induced protein with YGL and LRDR motifs	−0.83	−0.34	−0.22	0.26	**0.48**
253660_at	AT4G30140	GDSL-like Lipase/Acylhydrolase superfamily protein	−0.13	0.36	−0.13	0.36	**0.48**
261845_at	AT1G15960	NRAMP metal ion transporter 6	−0.42	0.06	0.10	0.59	**0.49**
259751_at	AT1G71030	MYB-like 2	−0.64	−0.15	−0.15	0.34	**0.49**

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ID	Locus	Description	Treatment Effects				**FR effect ratio 26˚C/22˚C**
			<1> W+FR effect (22˚C)	<2> W+FR effect (26˚C)	<3> 26˚C effect (WL)	<4> 26˚C effect (W+FR)	
262986_at	AT1G23390	Kelch repeat-containing F-box family protein	−0.84	−0.34	−0.21	0.29	**0.50**
247478_at	AT5G62360	Plant invertase/pectin methylesterase inhibitor superfamily protein	−1.02	−0.52	−0.51	−0.01	**0.50**
257365_x_at	AT2G26020	plant defensin 1.2b	−0.66	−0.16	−0.51	0.00	**0.51**
265117_at	AT1G62500	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	−0.36	0.15	−0.41	0.10	**0.51**
246815_at	AT5G27220	Frigida-like protein	−0.38	0.13	−0.27	0.25	**0.51**
255822_at	AT2G40610	expansin A8	−0.01	0.51	−0.13	0.39	**0.51**
245264_at	AT4G17245	RING/U-box superfamily protein	−0.44	0.08	−0.29	0.23	**0.51**
259058_at	AT3G03470	cytochrome P450, family 87, subfamily A, polypeptide 9	−0.09	0.43	0.27	0.79	**0.52**
258901_at	AT3G05640	Protein phosphatase 2C family protein	−0.36	0.17	−0.06	0.47	**0.53**
258338_at	AT3G16150	N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein	−0.11	0.42	0.02	0.55	**0.53**
253161_at	AT4G35770	Rhodanese/Cell cycle control phosphatase superfamily protein	−0.77	−0.23	0.58	1.12	**0.54**

Continued

262259_s_at	AT1G53890	[AT1G53890, Protein of unknown function (DUF567)]; [AT1G53870, Protein of unknown function (DUF567)]	−0.62	−0.07	−0.50	0.06	**0.55**
265481_at	AT2G15960	unknown protein; Has 14 Blast hits to 14 proteins in 5 species: Archae−0; Bacteria−0; Metazoa−0; Fungi−0; Plants−14; Viruses−0; Other Eukaryotes−0 (source: NCBI BLink).	−0.59	−0.03	0.23	0.78	**0.55**
264339_at	AT1G70290	trehalose-6-phosphatase synthase S8	−0.50	0.06	0.22	0.78	**0.56**
260287_at	AT1G80440	Galactose oxidase/kelch repeat superfamily protein	−0.54	0.02	0.00	0.56	**0.56**
260556_at	AT2G43620	Chitinase family protein	−1.01	−0.44	0.02	0.59	**0.58**
265511_at	AT2G05540	Glycine-rich protein family	−0.48	0.11	0.10	0.68	**0.58**
267461_at	AT2G33830	Dormancy/auxin associated family protein	−1.38	−0.79	−0.85	−0.25	**0.59**
261937_at	AT1G22570	Major facilitator superfamily protein	−0.73	−0.07	−0.52	0.14	**0.66**
257206_at	AT3G16530	Legume lectin family protein	−0.88	−0.21	−0.70	−0.03	**0.67**
262113_at	AT1G02820	Late embryogenesis abundant 3 (LEA3) family protein	−1.09	−0.37	−0.08	0.65	**0.72**
248622_at	AT5G49360	beta-xylosidase 1 (BXL1)	−0.65	0.17	−0.06	0.76	**0.83**
247474_at	AT5G62280	Protein of unknown function (DUF1442)	0.80	1.66	−0.30	0.55	**0.86**
254574_at	AT4G19430	unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 13 growth stages; Has 30201 Blast hits to 17322 proteins in 780 species: Archae−12; Bacteria−1396; Metazoa−17338; Fungi−3422; Plants−5037; Viruses−0; Other Eukaryotes−2996 (source: NCBI BLink).	0.75	1.68	1.48	2.42	**0.93**
265111_at	AT1G62510	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein	−1.07	−0.10	1.31	2.28	**0.97**

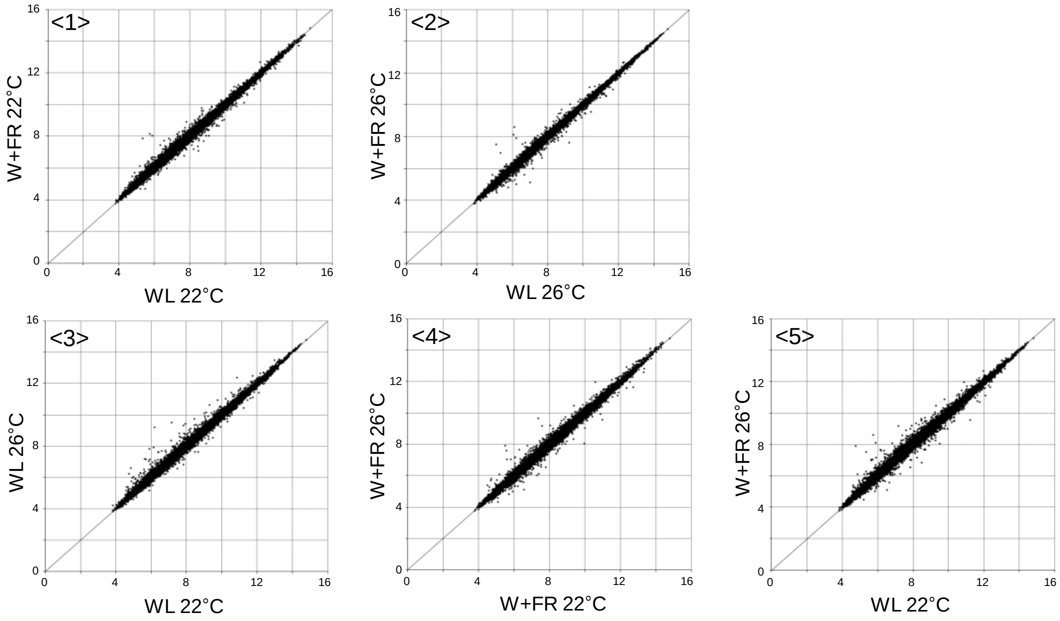
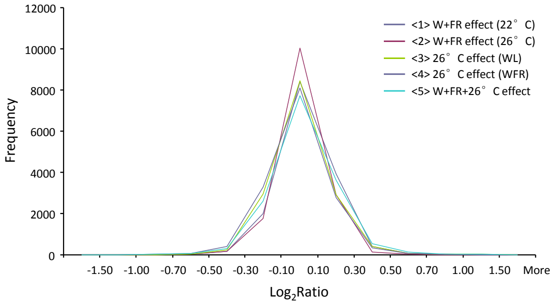
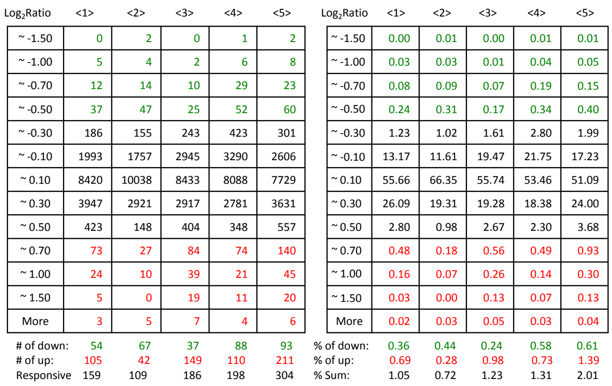


Figure S1. Microarray scatter plots. The scatter plots compare the log transformed average signal intensities between the indicated conditions. <1> W+FR effect at 22˚C (W+FR22˚C vs. WL22˚C), <2> W+FR effect at 26˚C (W+FR26˚C vs. WL26˚C), <3> high temperature (26˚C) effect under WL condition (WL26˚C vs. WL22˚C), <4> high temperature effect under W+FR condition (W+FR26˚C vs. W+FR22˚C), and <5> combined effect of both W+FR and high temperature (W+FR26˚C vs. WL22˚C).



(a)



Log_2Ratio	<1>	<2>	<3>	<4>	<5>
~ -1.50	0	2	0	1	2
~ -1.00	5	4	2	6	8
~ -0.70	12	14	10	29	23
~ -0.50	37	47	25	52	60
~ -0.30	186	155	243	423	301
~ -0.10	1993	1757	2945	3290	2606
~ 0.10	8420	10038	8433	8088	7729
~ 0.30	3947	2921	2917	2781	3631
~ 0.50	423	148	404	348	557
~ 0.70	73	27	84	74	140
~ 1.00	24	10	39	21	45
~ 1.50	5	0	19	11	20
More	3	5	7	4	6
# of down:	54	67	37	88	93
# of up:	105	42	149	110	211
Responsive	159	109	186	198	304

Log_2Ratio	<1>	<2>	<3>	<4>	<5>
~ -1.50	0.00	0.01	0.00	0.01	0.01
~ -1.00	0.03	0.03	0.01	0.04	0.05
~ -0.70	0.08	0.09	0.07	0.19	0.15
~ -0.50	0.24	0.31	0.17	0.34	0.40
~ -0.30	1.23	1.02	1.61	2.80	1.99
~ -0.10	13.17	11.61	19.47	21.75	17.23
~ 0.10	55.66	66.35	55.74	53.46	51.09
~ 0.30	26.09	19.31	19.28	18.38	24.00
~ 0.50	2.80	0.98	2.67	2.30	3.68
~ 0.70	0.48	0.18	0.56	0.49	0.93
~ 1.00	0.16	0.07	0.26	0.14	0.30
~ 1.50	0.03	0.00	0.13	0.07	0.13
More	0.02	0.03	0.05	0.03	0.04
% of down:	0.36	0.44	0.24	0.58	0.61
% of up:	0.69	0.28	0.98	0.73	1.39
% Sum:	1.05	0.72	1.23	1.31	2.01

(b) (c)

Figure S2. Number of genes showing different ranges of average $\log_2$Ratio. (a) Histogram. Five different treatment effects were shown with different colors; (b) Same data shown in a table format; (c) Same data shown as the percentage of 15,128 genes.

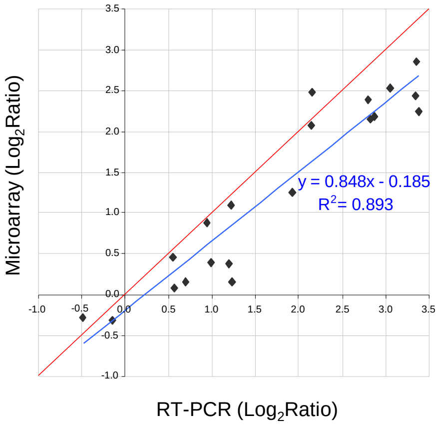


Figure S3. Real-times PCR results. The microarray results for *ATHB2*, *HFR1*, *FT* and *IAA*29 in different treatment effects were compared with the real-time PCR results. The blue line indicates the trend line. Real-time PCR: For reverse transcription reactions, 1 mg of total RNA and 0.5 mg of oligo (dT) primer were incubated at 70˚C for 10 min and chilled on ice. To this mixture, 4 ml of 5× reaction buffer, 40 units of RNasin (Promega, Madison, WI, USA), 20 mM of each dNTPs and 200 units of M-MLV reverse transcriptase (Promega) were added in a total volume of 20 ml. The reaction was incubated at 42˚C for 50 min, and then inactivated at 70˚C for 15 min. The first strand cDNAs were diluted to 100 ml, and 1 ml (1/100 of the initial amount) was used for a 40 ml real-time PCR reaction using SYBR Premix Ex Taq II (TaKaRa, Shiga, Japan) according to manufacturer's instruction. As a housekeeping control gene *EF1a* was used. Following PCR primers were used: EF1a-forward, GATGAGACTTTCGTTATGATCGAC; EF1a-reverse, ATTGAAAACCATAATAAAAAGTCTCAGA; ATHB2-forward, 5'-CACAGTACTCTCAATCCGAAGCA-3'; ATHB2-reverse, 5'-AGCATCTCCGTAAGAACTCGC-3'; FT-forward, 5'-TGTTCCAAGTCCTAGCAACCC-3'; FT-reverse, 5'-ACACAATCTCATTGCCAAAGGT-3'; HFR1-forward, 5'-AAGTAGTGATGATGAATCGGAGGA-3'; HFR1-reverse, 5'-ATGGTCTTGTCGAGAACCGA-3'; IAA29-forward, 5'-ACCGAATATGAAGATTGCGACAG-3'; IAA29-reverse, 5'-CGAAGTAGCCAGTCACCCTC-3'.