

## Strigolactones are involved in sugar signaling to modulate early seedling development in *Arabidopsis*

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**Abstract** Strigolactones are a novel class of plant hormones that interact with multiple signaling molecules, including auxin, abscisic acid, ethylene, and brassinosteroid, to regulate plant growth and development. Recently, researchers have shown that sugars are involved in bud outgrowth control, suggesting a potential interaction between sugars and strigolactone signaling. To better understand the relationship between strigolactones and sugar in plant development, the sugar sensitivity of strigolactone biosynthesis and signaling mutants (*max1* and *max2*) was evaluated in early seedling development with a low-glucose assay. Both *max1* and *max2* displayed obvious hyposensitivity to glucose repression, as do *gin* mutants, but they were hypersensitive like the wild type to the high-glucose conditions used for *gin* mutant screening. The strigolactones acted synergistically with glucose in repressing seedling establishment. A further comparative transcriptomic analysis indicated that the expression of stress-related genes in the *max2* mutant is impaired by glucose, and a carbohydrate analysis revealed a reduced hexose content in the *max* mutants. Our results suggest that the roles of strigolactones in the regulation of early seedling development are probably independent of the HXK1 signaling pathway. Taken together, these findings provide evidence that strigolactones are involved in sugar signaling, thus modulating early seedling development.

**Key words:** Early seedling development, glucose insensitive, stress response, strigolactone, sugar metabolism.

In plants, sugars are produced in the photosynthetic process and play important roles in plant growth and development as essential structural components and energy sources. In addition to these metabolic functions, sugars also act as central signaling molecules, modulating plant growth and development. Microarray experiments have shown that sugars regulate the gene expression involved in photosynthesis, carbohydrate and nitrogen metabolism, signal transduction, and stress responses (Price et al. 2004; Villadsen and Smith 2004). Sugar-regulated gene expression allows the plant to adjust its cellular activity to the nutrient availability. In this way, sugars control plant resource allocation and adaptive developmental changes, enhancing their survival and/or competitiveness (Koch 1996).

High exogenous sugars have been shown to be potent negative regulators, inhibiting early seedling establishment in *Arabidopsis thaliana*, including by blocking seedling cotyledon expansion, chlorophyll accumulation, and root development (Jang and Sheen 1994; Jang et al. 1997). Sugar-induced arrest of early seedling developmental is a typical phenotype and has

been used to genetically identify the components of sugar signaling in *Arabidopsis*. Mutants capable of proper development at high exogenous glucose (>330 mM) or high sucrose concentrations (>300 mM) in MS medium are referred to as *glucose-insensitive* (*gin*) or *sugar-insensitive* (*sis*) mutants, respectively (Laby et al. 2000; Zhou et al. 1998). This specific developmental suppression is not induced by an osmotic control treatment with sorbitol or mannitol. Several *gin* mutants have been isolated and their causal genes identified and characterized at the molecular level. As a consequence, most abscisic acid (ABA) biosynthesis and signaling mutants have also been identified as *gin* mutants (e.g., *gin1/aba2*, *gin5/aba3*, and *gin6/abi4*), which indicates that the two signaling molecules interact closely (Arenas-Huertero et al. 2000; Dekkers et al. 2008; Zhou et al. 1998). Ethylene is another hormone that interacts with sugar signals to control seedling development. The treatment of wild-type seedlings with the ethylene precursor 1-amino cyclopropane-1-carboxylic acid phenocopies the *gin* phenotype (Ghassemian et al. 2000), and consistent with this, ethylene-insensitive mutants,

*etr1-1* and ethylene insensitive 2 (*ein2*), display glucose hypersensitivity (Zhou et al. 1998). However, a recent study has demonstrated some ABA and ethylene mutants that had been identified as *gin* mutants showed normal responses to glucose in a low-sugar assay, in which 2% glucose without MS was used as the screening medium. This result suggests that sugar acts in another specific signaling pathway that is uncoupled from ABA and ethylene signaling in *Arabidopsis* (Cho et al. 2010).

Studies of sugar sensors have characterized at least three signaling pathways in plants. HEXOKINASE1 (HXK1) that was identified as causal gene of *gin2* was first characterized as a glucose sensor that mediates photosynthetic gene expression and growth control in early seedling development (Jang et al. 1997; Moore et al. 2003). HXK1 is a dual-function enzyme with a distinct regulatory function in plants. Its enzymatic function is to catalyze the first step in glycolysis, the transformation of glucose into glucose-6-phosphate. It also functions as a sugar sensor, controlling sugar inhibition in early seedling development through an HXK1-containing nuclear complex. This complex is thought to bind to the promoters of various genes and control their transcription in the presence of high levels of glucose (Cho et al. 2007; Moore et al. 2003). The plant Snf1-related kinase 1 (SnRK1), a homologue of the animal AMP-activated protein kinase (AMPK) and yeast sucrose non-fermenting 1 (SNF1) kinase, is another sugar or energy sensor, which is activated by the energy deprivation induced by dark or stress to restore the cellular energy balance (Baena-Gonzalez and Sheen 2008; Baena-Gonzalez et al. 2007). Sugars can repress SnRK1 kinase activity by an unknown mechanism and the SnRK1 mutants *Atkin10* and *Atkin11* also display *gin* phenotypes (Cho et al. 2012). Unlike the activation of SnRK1 by sugar starvation, the plant target of rapamycin (TOR) kinase senses high sugar status to promote cell proliferation and growth (Deprost et al. 2007; Xiong and Sheen 2014; Xiong et al. 2013). Thus, diverse sugar signaling pathways cross each other and interconnect with other hormone molecules to control plant growth and development.

Strigolactones (SLs) are a group of carotenoid-derived plant secondary metabolites found in both monocots and dicots. SLs were originally identified as germination stimulants of root parasitic plants and host recognition signals for arbuscular mycorrhizal fungi in plant root exudates (Xie et al. 2010). Recent research has discovered their key roles as plant hormones in controlling shoot branching (Gomez-Roldan et al. 2008; Umehara et al. 2008; Xie et al. 2010). This finding greatly stimulated SL studies and many new roles for SLs in plant growth and development were reported, including its regulation of stem secondary growth (Agusti et al. 2011), leaf senescence (Yamada et al. 2014) and

root development (Koltai, 2011; Koren et al. 2013). In addition to physiological research, important progress in SL biosynthesis and its perception molecular mechanism has been made in the past several years. DWARF 27 (D27), MORE AXILLARY GROWTH 3 (MAX3), MAX4, MAX1 are involved in the SL biosynthetic pathway (Abe et al. 2014; Arite et al. 2007; Booker et al. 2004; Waters et al. 2012), whereas an  $\alpha/\beta$ -fold hydrolase DWARF 14/DECREASED APICAL DOMINANCE2/HTD2 (D14/DAD2/HTD2) and MORE AXILLARY GROWTH 2 (MAX2) play central roles in SL signal perception and transduction (Arite et al. 2009; Nakamura et al. 2013; Nelson et al. 2011). Further studies identified the signal transduction downstream from the SL signal. D53, a heat shock protein, and BES1, a key brassinosteroid signaling protein, have been identified as D14- or MAX2-interacting proteins and can be ubiquitinated and degraded by proteasomes in an SL-dependent manner (Jiang et al. 2013; Wang et al. 2013; Zhou et al. 2013). DELLA, a key protein in gibberellin signaling, also interacts with D14 in an SL-dependent manner, but the function of this interaction is still unknown (Nakamura et al. 2013).

These studies demonstrate the important roles of SL in modulating plant growth and development, and more physiological functions of SL signaling remain to be identified. In the present study, we examined the responses of SL mutants to glucose during early seedling development and analyzed the possible mechanism relating SL and sugar signaling. We demonstrate that SL mutants are hyposensitive to sugar-induced arrest of seedling establishment and that the expression of glucose-induced stress response genes is impaired in the *max2* mutant treated with glucose. Further evidence suggests that SLs are also involved in the regulation of sugar metabolism.

## Materials and methods

### Chemicals

The GR24 used in the experiments was synthesized as described previously (Mangnus et al. 1992), and was separated into  $(\pm)$ -GR24 and  $(\pm)$ -2-epi-GR24 with silica gel column chromatography. We used one isomer with the same relative stereochemistry as (+)-strigol and dissolved in dimethyl sulfoxide (DMSO) as a stock solution.

### Plant material

*Arabidopsis thaliana* MORE AXILLARY SHOOT mutants *max1-1* and *max2-1*, and the WT Columbia-0 were used in this study (Mashiguchi et al. 2009). The HEXOKINASE1 mutant (*hxk1*, SAIL\_680\_D02) was obtained from the *Arabidopsis* Biological Resource Center of Ohio State University (<http://www.arabidopsis.org/abrc/>).

### **Sugar repression assays**

For the low-glucose assay experiments, *Arabidopsis* WT and *max* mutant seeds were surface-sterilized with 70% ethanol solution for 30 min, sown on medium containing 2% glucose or mannitol and 0.8% agar, and then placed in the dark for 3 days at 4°C. The seeds were grown at 23°C under fluorescent white light with a 16 h light/8 h dark photoperiod for 3–4 days. Radicle emergence, cotyledon expansion, and greening, and root emergence were then scored, and representative seedlings were photographed under a microscope (Olympus SZX12). For the high-glucose assay, sterilized seeds were sown on 0.8% agar medium, cold stratified in the dark for 3 days, and then transferred to Petri dishes containing 6% glucose or mannitol 1/2 MS medium (Murashige and Skoog 1962). The seeds were grown at 23°C under fluorescent white light with a 16 h light/8 h dark photoperiod for 1 week. Each experiment was conducted as two independent replicates and all replicates showed similar results.

### **Assays of SL and glucose effects on early seedling development**

To assay the synergistic effects of SL and glucose, *Arabidopsis* WT and *max* mutant seeds were sown on agar medium with 1% or 2% glucose or mannitol and various concentrations of GR24. After cold stratification for 3 days, the dishes were transferred to a growth chamber at 23°C under fluorescent white light with a 16 h light/8 h dark photoperiod. Radicle emergence and seedling cotyledon expansion were scored after growth for 3 days, and representative seedlings were photographed under a microscope (Olympus). Each experiment was conducted as two independent replicates and all replicates showed similar results.

### **RNA isolation and expression analyses with RT-PCR**

To determine the gene expression in seedlings in response to glucose, *A. thaliana* seeds of various genotypes were surface-sterilized and allowed to imbibe water in the dark at 4°C for 3 days. The seeds were then transferred to Petri dishes containing water with 2% glucose or mannitol. The cultures were shaken at 140 rpm at 23°C for 3 days under fluorescent white light with a 16 h light/8 h dark photoperiod. The seedlings were collected and rinsed three times with sterile distilled water, and excess water was removed by centrifugation. Total RNA was extracted from the seedlings with Plant RNA Reagent (Invitrogen, Carlsbad, CA, USA). The gene-specific primers are described in Supplemental Table 1.

### **Digital gene expression (DGE) profiling**

Seedling and RNA samples were prepared as described above. A total amount of 3 µg of RNA per sample was used as the input material for the preparation of the RNA library. Sequence libraries were generated with the NEBNext® Ultra™ RNA Library Prep Kit for Illumina® (NEB, USA), according to manufacturer's recommendations, and index codes were added to attribute the sequences to each sample.

Briefly, mRNA was purified from the total RNA with poly-T oligo-attached magnetic beads. Fragmentation was performed with divalent cations at elevated temperature in NEBNext First Strand Synthesis Reaction Buffer (5×). The first-strand cDNA was synthesized with a random hexamer primer and M-MuLV reverse transcriptase (RNase H<sup>-</sup>). The second-strand cDNA was synthesized with DNA polymerase I and RNase H. The remaining overhangs were converted to blunt ends with exonuclease/polymerase activities. After the adenylatation of the 3' ends of the DNA fragments, NEBNext Adaptor with a hairpin loop structure was ligated in preparation for hybridization. To preferentially select cDNA fragments of 150–200 bp, the library fragments were purified with the AMPure XP system (Beckman Coulter, Beverly, USA). The size-selected, adaptor-ligated cDNA was incubated with 3 µl of USER Enzyme (NEB) at 37°C for 15 min and then for 5 min at 95°C before PCR. PCR was performed with Phusion High-Fidelity DNA Polymerase, universal PCR primers, and Index (X) Primer. The PCR products were purified (AMPure XP system) and the library quality was assessed with the Agilent Bioanalyzer 2100 system. The index-coded samples were clustered on a cBot Cluster Generation System using the TruSeq PE Cluster Kit v3-cBot-HS (Illumina), according to the manufacturer's instructions. After cluster generation, the library was sequenced on an Illumina Hiseq 2000/2500 platform, generating 100 bp/50 bp single-end reads.

### **DGE data analysis**

Clean data were obtained by removing from the raw data any reads containing adapter sequences, reads containing poly-N, and low-quality reads. The Q20, Q30, and GC contents of the clean data were calculated. All the downstream analyses were based on high-quality clean data. The reference genome was built using Bowtie v2.0.6 and single-end clean reads were aligned with the reference genome with TopHat v2.0.9. HTSeq v0.6.1 was used to count the read numbers mapped to each gene. A differential expression analysis was performed with the DESeq R package (1.10.1). The resulting *p* values were adjusted with Benjamini and Hochberg's approach to control the false discovery rate (Benjamini and Hochberg, 1995). A Gene Ontology (GO) enrichment analysis of the differentially expressed genes was implemented in the GOseq R package, in which any gene length bias was corrected. GO terms with corrected *p* values <0.05 were considered to indicate significantly enriched differentially expressed genes. The DGE data have been deposited in the DNA databank of Japan (DDBJ) with accession number DRA004567.

### **Measurement of carbohydrate content**

The plants used for the carbohydrate analysis were grown under 16 h light/8 h dark cycles at 23°C in a growth chamber. The carbohydrate contents were determined with enzyme assays (Bergmeyer and Bernt, 1974). Sugars were extracted from the 2-week-old seedlings with 1 ml of 80% ethanol. The supernatant was used to measure the hexose and sucrose contents, and

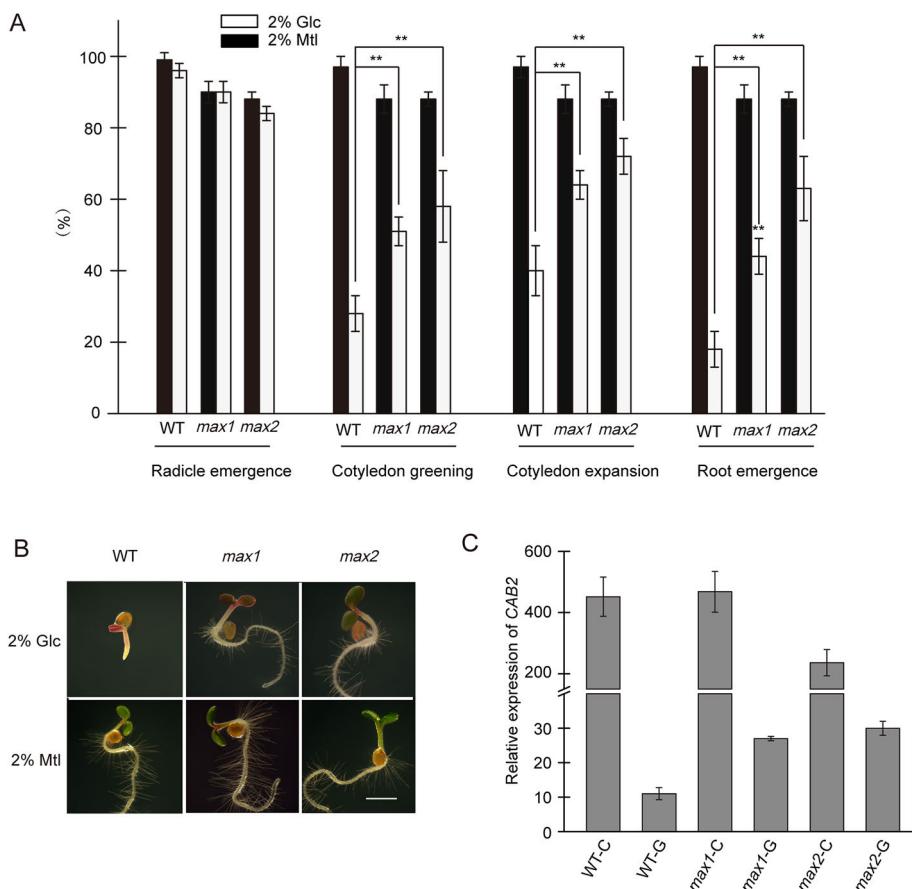


Figure 1. Response to glucose (Glc) of *max* mutants in the early seedling developmental stage. (A) Wild-type (WT), *max1*, and *max2* *Arabidopsis thaliana* seedlings were grown in agar medium with 2% glucose (Glc). The percentages of seed germination, cotyledon greening, cotyledon expansion and root emergence were scored 3 days after stratification. Error bars represent standard deviations (SD; *t* test: \*\**p*<0.01). (B) Representative images of WT and *max* seedlings after 4 days of growth. Wild-type (WT), *max1*, and *max2* *A. thaliana* seedlings were grown in agar medium with or without 2% glucose or mannitol (Mtl). Scale bar indicates 2 mm. (C) Relative transcript levels of *CAB2* in 3-d-old *Arabidopsis* seedlings treated with 2% glucose. Wild-type (WT), *max1*, and *max2* *A. thaliana* seedlings were grown in agar medium with (G) or without (C) 2% glucose. Values are means±SD (*N*=3).

the pellet to measure the starch content. Commercial kits (R-Biopharm; Roche, <http://www.roche.com>; F-kit #716260 and F-kit #207748) were used to determine the soluble sugar and starch contents, respectively. The results are the means of three replicate analyses for each plant.

## Results

### *SL* mutants are hyposensitive to glucose-induced seedling developmental arrest in low glucose

To determine the potential involvement of SL in sugar signaling during early seedling development in *Arabidopsis*, the SL-biosynthetic mutant *max1* and the signaling mutant *max2* were subjected to a glucose repression assay. Seeds were germinated on agar plates containing 2% glucose or 2% mannitol without MS salt and their growth was checked after 3–4 days. As shown in Figure 1A and B, 2% glucose significantly inhibited early seedling development, including cotyledon expansion, chlorophyll accumulation, and root development in the wild-type (WT) plants, whereas both the *max1* and *max2*

mutants were hyposensitive to repression by glucose, especially the SL-insensitive mutant *max2*, which showed stronger insensitivity to glucose repression than *max1*. Real-time reverse transcription (RT)-PCR was used to measure the expression of chlorophyll *a/b* binding protein 2 (*CAB2*), a marker gene for glucose signaling. *CAB2* expression was strongly suppressed by glucose treatments in all the seedlings, but the fold repression was lower in the *max* mutants than in the WT plants (41-fold reduction in the WT, 17.3-fold in *max1*, and 7.8-fold in *max2*) (Figure 1C). We also checked the sucrose sensitivity of the plants using medium that contained 4% sucrose without MS salt. The results were similar to those for glucose (Supplemental Figure 1), indicating that the *max* mutants are also *sugar insensitive mutants (sis)*. The classical sugar repression assay uses high concentrations of glucose (6–7%) or sucrose (10%), but the medium contains MS salts (Dekkers 2006). The high-sugar method has advantages for the long-term observation of seedling growth supported by full-nutrient medium. However, this method induces high osmotic stress and

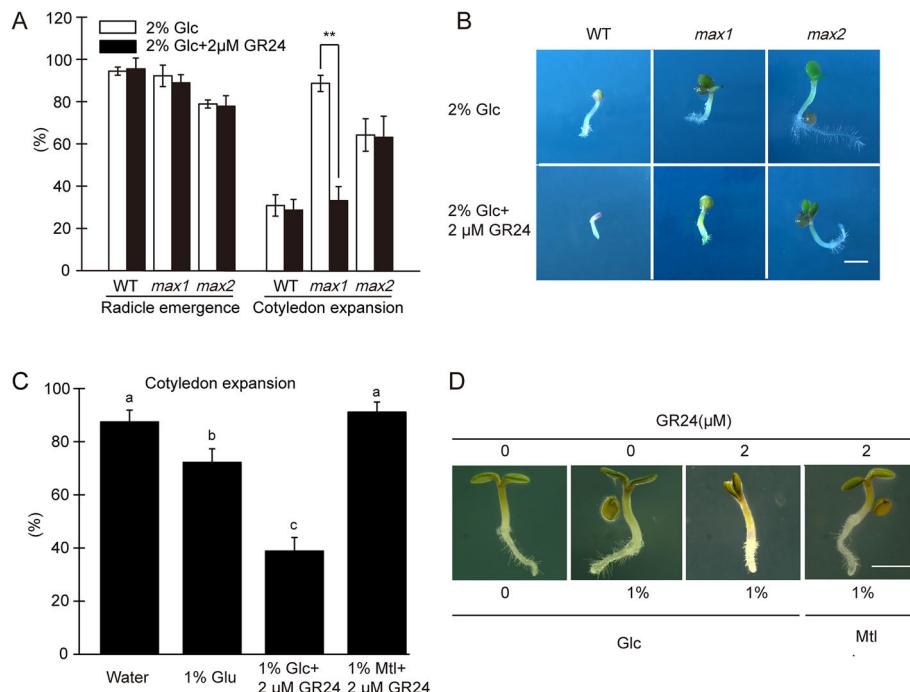


Figure 2. Synergistic effects of SL on glucose repression in early seedling development. (A) and (B) WT, *max1*, and *max2* seedlings were grown in agar medium containing 2% glucose with or without 2  $\mu$ M GR24. The percentages of seed germination and cotyledon expansion were scored 3 days after stratification. Error bars represent standard deviations (SD;  $t$  test: \*\* $p$ <0.01). Representative images of WT and *max* seedlings after 3 days of growth. Scale bar indicates 1 mm. (C) and (D) WT seedlings were grown in agar medium containing 1% glucose or 1% mannitol as the control, with or without 2  $\mu$ M GR24. The percentage cotyledon expansion was scored 3 days after stratification. Representative images of WT seedlings after 3 days of growth. Scale bar indicates 1 mm. Data are the means $\pm$ SD of three samples and Fisher's least-significant difference (LSD) test was applied to determine statistical significance.

introduces nitrogen resources, such as nitrate, etc., that are antagonistic to glucose and thus complicate the screening system (Moore et al. 2003). Some *gin* mutants screened with the high-sugar method, such as *ctr1-1* and *gin1-3*, displayed a normal response to a low glucose concentration without MS salt (Cho et al. 2010), suggesting the specificity of sugar signaling. Because *max* mutants show *gin* phenotypes in the low-glucose assay, we were interested to know whether they could be isolated with the high-glucose screening method used to isolate *gin* mutants. As shown in Supplemental Figure 2, 6% glucose significantly delayed the germination of the *max* mutants compared with that of the WT, and the germination of the *max2* mutant was retarded more severely than that of the *max1* mutant. Ultimately, there were no obvious differences in sugar sensitivity in phenotypes of the *max* mutants and the WT (data are not shown), which is consistent with Bu's report that *max2* mutants are hypersensitive to the osmotic stress induced by 4% glucose (Bu et al. 2014). Our results suggest that the *gin* phenotype of the *max* mutants is easily masked in the screening assay for *gin* mutants.

#### ***SL acts synergistically with glucose to suppress seedling establishment***

The observation that SL mutants show low sensitivity to repression by glucose suggests that SLs are involved in

sugar signaling to control early seedling development. The synthetic SL analogue, GR24, was added to the medium to determine the sugar response of the *max* mutants. As shown in Figure 2A and B, the addition of 2  $\mu$ M GR24 to agar medium was sufficient for the SL-deficient mutant *max1* to mimic the phenotype of the WT seedlings under low-glucose conditions, but not for the SL-insensitive mutant *max2* to do so, which indicates that SLs contribute to the developmental arrest induced by glucose. When GR24 was added to the medium containing glucose, WT seedling development was especially inhibited, even when the concentration of glucose was low (1%) and thus insufficient to repress development alone (Figure 2C and D). This result suggests that the SLs in plants amplify the sensitivity of plants to sugar repression during seedling establishment.

#### ***Comparative transcriptomic analysis reveals that *max2* and *hxk1* mutants are differentially regulated by sugar in early seedling development***

To better understand the roles of SL in sugar signaling, a comparative transcriptomic analysis of *max2*, *hxk1*, and WT seedlings grown with 2% glucose for 3 days after germination was conducted using the short-read sequencing technology (Illumina) combined with a tag-based digital gene expression (DGE) system. As the control, we performed the same analysis of

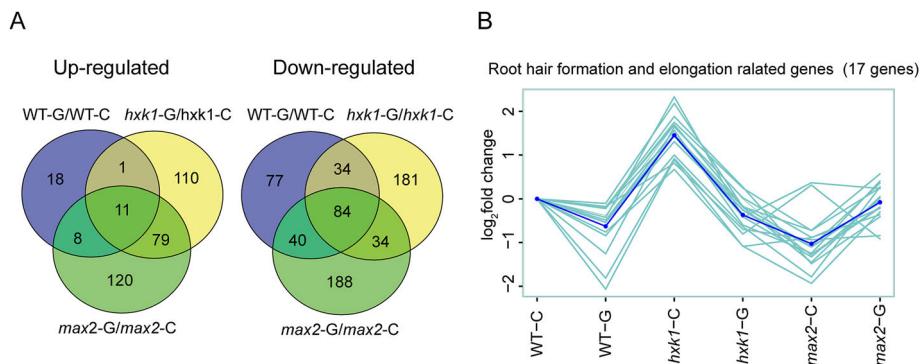


Figure 3. Differential gene expression analysis of WT, *hxk1* mutant, and *max2* mutant seedlings treated with 2% glucose. (A) Venn diagrams showing the differential gene expression in overlapping and nonoverlapping upregulated and downregulated gene sets (1.5 fold) induced by glucose. WT-G/WT-C, WT with 2% glucose treatment vs WT with 2% mannitol treatment; *hxk1*-G/*hxk1*-C, *hxk1* with 2% glucose treatment vs *hxk1* with 2% mannitol treatment; *max2*-G/ *max2*-C, *max2* with 2% glucose treatment vs *max2* with 2% mannitol treatment. (B) Cluster analysis of the differential expression patterns of genes associated with trichoblast differentiation, root hair formation, and elongation in WT, *hxk1* mutant, and *max2* mutant after treatment with glucose or mannitol.

identical seedlings but treated with 2% mannitol. We used 3-day-grown plants for this experiment because at this stage, the phenotypes of plants grown with and without glucose are very different. A comparison of the seedling transcriptomes after treatment with 2% glucose revealed 219, 202, and 39 upregulated genes and 334, 347, and 236 downregulated genes in *max2*, *hxk1*, and WT, respectively, using the criteria of a fold change of  $\geq 1.5$  and a false-discovery-rate-corrected *p* value (*q* value)  $< 0.05$  (*max2*-G vs *max2*-C; *hxk1*-G vs *hxk1*-C; WT-G vs WT-C; Supplemental Table 2). First, we analyzed the expression of SL biosynthesis, perception, and responsive genes in response to glucose treatment. The results showed that SL biosynthesis genes *D27*, *MAX1*, *MAX3*, and *MAX4* were expressed at low levels in the seedlings and their expression did not increase significantly in the plants treated with glucose. Nor did the expression levels of SL signaling marker genes, such as *STH7*, *KUF1*, and *IAA1*, obviously change in the plants treated with glucose (Supplemental Table 3). These results indicate that 2% glucose is insufficient to induce SL biosynthesis or SL-specific signal transduction at this developmental stage, which is consistent with the report by Price et al. that low concentration of glucose only induces the biosynthesis of a few hormones (Price et al. 2004).

A Venn diagram constructed from the three gene sets, which identified 18, 110, and 120 specifically upregulated genes and 77, 181, and 188 specifically downregulated genes in the WT, *hxk1*, and *max2* seedlings, respectively (Figure 3A). Because of the phenotypic similarity during early seedling development under the glucose treatment, a transcriptomic comparison of the *hxk1* and *max2* mutants could be helpful in investigating the relationship between SL and HXK1 signaling. About 1/2 the total significantly upregulated genes and 2/3 of the total significantly downregulated genes in *max2* differed

from the corresponding genes in the *hxk1* mutant. This implies that the glucose responses of the two mutants differ, suggesting that the mechanism of hyposensitivity to glucose in the *max2* seedlings differs from that in the *hxk1* mutant. We functionally classified these gene sets to gain insight into the crosstalk using a Gene Ontology enrichment analysis. A series of root-hair-specific genes, *RHS15*, *RHS17*, *RHS19* (Won et al. 2009), and *AtPRP3* (a gene encoding a proline-rich structural cell wall protein that regulates trichoblast differentiation, root hair formation, and elongation) (Bernhardt and Tierney 2000) were significantly enriched in the gene set specifically downregulated in the *hxk1* mutant treated with glucose. These genes showed the different pattern of regulation in the *max2* mutant (Figure 3B; Supplemental Table 4). Changes in the expression of these genes in the *max2* mutant after treatment with glucose did not differ greatly from those in the WT without glucose treatment. These results suggest that the negative regulation of root hair development by glucose is independent of HXK1 but related to SL signaling during early seedling development. The fluctuation in the expression levels of these root-hair-development genes in the *max2* mutant was relatively small compared with those in the WT and *hxk1* mutant during glucose treatment. This result suggests a positive role for SL signaling in root hair development, which is consistent with our phenotypic results for GR24 (Figure 2) and previous reports (Koltai and Kapulnik 2011) in which SL positively regulated root hair elongation and played an important role in modulating the root system architecture.

A close look at the expression levels of genes specifically induced and repressed in glucose-treated plants revealed an unexpected role of sugar in the stress responses of the *hxk1* and *max2* mutants. The expression of a number of genes responsible for stimulus and stress responses was induced in the *hxk1* mutant by glucose

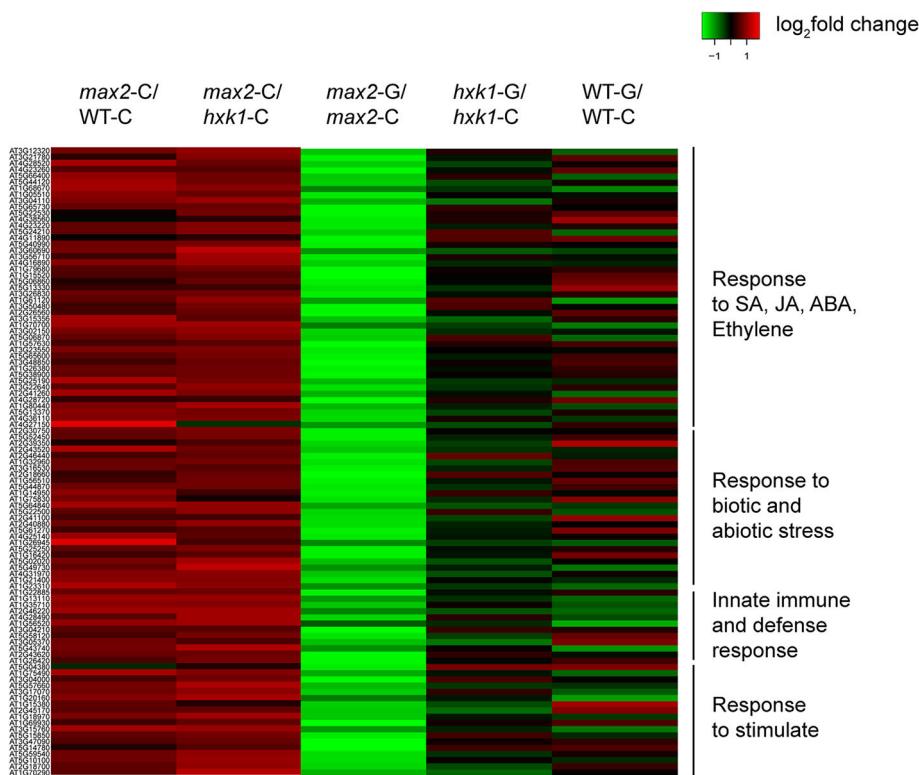


Figure 4. Differential regulation of stress- and defense-response genes by glucose in WT, *hxp1* mutant, and *max2* mutant. Color indicates the fold change in gene expression levels: red indicates upregulated and green indicates downregulated expression relative to the control treatment.

treatment, including the salicylic acid biosynthesis genes *SARD1* (*SAR DEFICIENT 1*), *DLO1* (*DMR6-LIKE OXYGENASE 1*), *ATLTP4.4* (*ARABIDOPSIS THALIANA LIPID TRANSFER PROTEIN 1*), and the salicylic acid response genes encoding the WRKY family transcription factors WRKY38, WRKY44, WRKY62, and WRKY70 (Supplemental Table 5). These results are consistent with the results of other experiments, indicating that sugar induces a stress-like response and activates the expression of defense-related genes in seedlings, independently of HXP1 signaling (Ehness et al. 1997; Xiao et al. 2000). However, the activation of the expression of stress-related genes was completely abolished in the *max2* mutant treated with glucose. On the contrary, the expression levels of the stress response genes were significantly repressed by glucose treatment and constituted more than half the genes with specifically downregulated expression in the *max2* mutant. In contrast to the genes for root hair development and flavonoid biosynthesis, these stress-related genes were more strongly expressed in *max2* than in WT or the *hxp1* mutant without glucose treatment. The repressed genes included *PAD3* (*PHYTOALEXIN DEFICIENT 3*) and *CRK14*, which are involved in salicylic acid biosynthesis. Many genes of the MAPK phosphorylation cascades were also repressed by glucose in the *max2* mutant, which have been shown to have important plant antifungal activities and are associated with the onset of systemic

acquired resistance (Figure 4; Supplemental Table 6). Furthermore, the expression of some ABA- and ethylene-response genes was also repressed by glucose, including one ABA transporter gene *ABCG40*, one UDP-glucosyl transferase gene *UGT71B6*, one ABA-regulated gene *ATD18*, and two ethylene-induced transcription factor genes, *ESE3* and *RAP2.6* (Figure 4; Supplemental Table 6). In addition to genes responsive to stress hormones, many genes involved in biotic and abiotic stresses and the innate immune response were also repressed by glucose (Figure 4; Supplemental Table 6). The reliability of our transcriptome data was confirmed by examining the expression of several genes with real-time quantitative RT-PCR (RT-qPCR; Supplemental Figure 3).

**Sugar metabolism is misregulated in *max* mutant**  
Sugars can also act as energy signals to modulate their own metabolism in response to environment changes (Baena-Gonzalez et al. 2007; Xiong et al. 2013). To examine the possible effects of SLs on sugar metabolism, seedlings of *max1*, *max2*, and WT were grown for 2 weeks and harvested to determine their sugar contents. As shown in Figure 5, the starch and sucrose contents of the seedlings did not differ greatly, but intriguingly, the hexose contents (including the glucose and fructose contents) were significantly lower in the *max* mutants than in the WT. Although the underlying mechanism is still unknown, these results provide evidence that SLs are

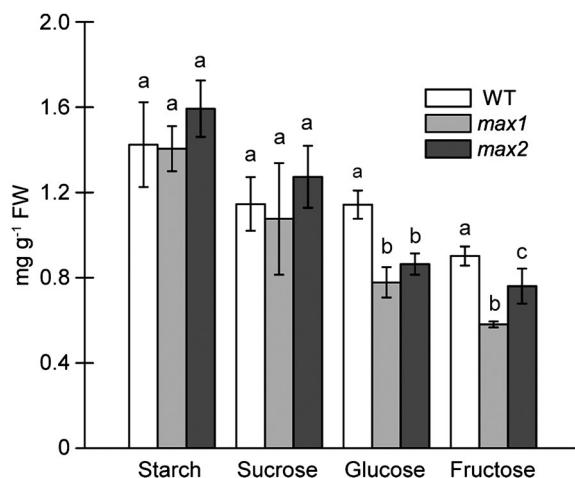


Figure 5. Carbohydrate contents of WT, *max1* mutant, and *max2* mutant plants. 10-d-old seedlings were harvested and their starch, sucrose, glucose, and fructose contents measured. Data are the means $\pm$ SD of three samples and Fisher's least-significant difference (LSD) test was applied to determine statistical significance.

also involved in modulating the plant's sugar metabolism. Hexoses are metabolically active sugars and also important signaling molecules. Therefore, this reduced hexose content may contribute to the hyposensitivity of the *max* mutants to repression by exogenous sugar.

## Discussion

As an easily detectable phenotype, the early developmental arrest in seedlings induced by exogenous sugar has been used extensively to isolate the *gin/sis* mutants of *Arabidopsis* (Dekkers and Smeekens 2007). This classic high-sugar strategy has been validated in various studies and many *gin* mutants have been isolated with this method. However, the use of high sugar concentrations, exceeding the physiological range, inevitably induces osmotic stress and therefore possibly disturbs sugar-specific signaling pathways (Cho et al. 2010). This defect has been ignored because the arrested phenotypes cannot be fully simulated by osmoregulatory treatments with mannitol or sorbitol. More importantly, osmotic stress often positively cooperates with the effects of sugar to inhibit early seedling development (Jossier et al. 2009; Leon and Sheen 2003). A recent study demonstrated that *gin* mutants identified with the high-sugar strategy, *gin1-3* and *ctr1-1*, displayed the normal sugar-arrested phenotype during seedling establishment in a low-sugar assay (2% glucose without inorganic salt). The discordant results for these mutants suggested that plants have specific sugar signaling pathways that are uncoupled from ABA and ethylene signaling (Cho et al. 2010). *Arabidopsis* seedlings can be successfully established under natural conditions, without any exogenous factors, and the nutrient and energy demands in this process are met by the endogenous catabolites

of lipids and the starch reserve in the endosperm of the seeds. Therefore, the low-sugar assay avoids high osmotic stress and can be used to observe the sugar-specific responses during seedling establishment in a short developmental time window (3–5 days after germination).

In this study, mutants of the plant hormone SL clearly displayed the *gin* phenotype during seedling establishment under low-glucose conditions (Figure 1A and B), which is often assumed to involve osmotic hypersensitivity, and have never been screened with the classic high-sugar method (Bu et al. 2014; Shen et al. 2012). Our results indicate that SL signaling interacts with a sugar-specific signaling pathway and also that osmotic stress does not always cooperate with sugar signaling in repressing seedling establishment. Therefore, SLs may play important roles in uncoupling the osmotic response from the sugar response in early seedling development.

A further comparative transcriptomic profile analysis provided new insights into the cross-talk between sugar and SL signaling. The rate of gene overlap between the *hxk1* and *max2* mutants was low and their gene expression patterns differed during root development and the stress response (Figures 3 and 4), supporting the idea that SL signaling regulates early seedling development in an HXK1-independent manner. The differential regulation by glucose of the stress-related genes in the *hxk1* and *max2* mutants, in particular, suggests a possible mechanistic interaction between sugar and SL signaling (Figure 4). It has been reported that elevated levels of intracellular glucose induce gene expression patterns consistent with the stress and defense responses (Ehness et al. 1997; Price et al. 2004; Xiao et al. 2000) and that the expression of these genes is independent of the HXK1 signaling pathway (Xiao et al. 2000). These results are consistent with our finding that glucose still activates a series of stress-related genes in the HXK1 signaling mutant *hxk1* (Supplementary Table 5). On the contrary, the expression of a large number of stress- and defense-related genes was strongly repressed by glucose in the *max2* mutant (Figure 4). The stress response induced by sugar possibly contributes to the developmental arrest of seedlings (Price et al. 2004). The differential regulation of the stress response in the *max2* mutant and the *hxk1* mutant under low-glucose conditions suggests that SL and sugar signaling interact in regulating early seedling development.

The change in the carbohydrate contents of the *max* mutant indicates that SLs are also involved in the regulation of sugar metabolism (Figure 5). Although the exact mechanism is still unknown, the regulation of sugar metabolism by SLs may account for the hyperstressed phenotype of the *max2* mutant. Metabolic sugars act as energy signals to repress various stress

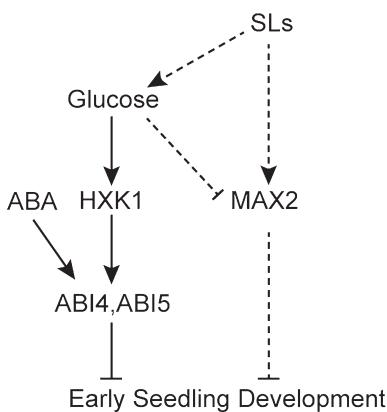


Figure 6. A proposed model of the interactions between SL and sugar signaling in modulating early seedling development.

responses and facilitate plant development (Baena-Gonzalez and Sheen 2008; Xiong et al. 2013). Compared with other carbohydrate species, hexoses are highly active metabolic sugars in plants and powerful signaling molecules that regulate gene expression. Therefore, a low hexose content is possibly an important indicator of stress or low energy levels. Consequently, the *max* mutants display a hyperstressed phenotype.

The transcriptional repression of stress-related genes by glucose and the misregulation of sugar metabolism in SL mutants suggest that SL signaling interacts with these signaling networks. SLs have also been shown to positively regulate the expression of light-harvesting genes (Mayzlish-Gati et al. 2010). Because light harvesting is directly related to sugar acquisition in seedlings, a low hexose content is likely to result from the low-efficiency photosynthesis of the mutants. The *max2* mutant also displays delayed leaf senescence (Woo et al. 2001) and reduced light responses (Shen et al. 2007), and these phenotypes correlate strongly with plant sugar homeostasis. Recent research into the roles of sugar as an initial regulator of bud outgrowth and an inhibitor of SL signal transduction provides compelling evidence of an interaction between SL and sugars (Barbier et al. 2015; Mason et al. 2014).

Based on these results, a hypothetical model is proposed to explain the hyposensitivity of SL mutants to repression by sugar (Figure 6). Sugar-induced HXK1-dependent signaling and the MAX2-dependent stress response together contribute to the repression of early seedling development. A deficiency in SL signaling results in the dysfunction of the plant stress-resistance system and thus manifests as the hyposensitive phenotype during treatment with low exogenous sugar. In conclusion, our study demonstrates that SLs are involved in sugar-controlled early seedling development, and possible roles of SL in regulating the stress response and sugar metabolism, which contribute to the sugar-hyposensitivity of the *max* mutants. Our findings extend

our knowledge of SL signaling and functions, but more research is required to clarify the cross-talk mechanism between SL and sugar signaling.

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## SUPPORTING INFORMATION

**Supplemental Figure 1.** Hyposensitivity to 4% sucrose of *max* mutants. Wild-type (WT), *max1*, and *max2* *Arabidopsis thaliana* seedlings were grown on agar medium with 4% sucrose (Suc) or 2% mannitol (Mtl). Representative images of WT and *max* seedlings were photographed after 3 days' growth.

**Supplemental Figure 2. *max* mutants are hypersensitive to high glucose**

**during germination.** Seed germination rates of WT and *max* mutants were evaluated during treatment with 6% glucose. Data are the means ± SD of three samples.

**Supplemental Figure 3. Real-time quantitative RT–PCR (RT–qPCR)**

**confirmation of transcriptome data.** Eight genes were selected and their expression was assessed with RT–qPCR in seedling samples obtained after treatment with 2% glucose (or mannitol as the control) in the WT, *hxk1* mutant, and *max2* mutant. Data are means ± SE (N = 3).

**Supplemental Table 1. Primers used for quantitative RT–PCR.**

**Supplemental Table 2.** Genes upregulated and downregulated by glucose in the comparisons WT-G vs WT-C (A), *max2*-G vs *max2*-C (B), and *hxk1*-G vs *hxk1*-C (C) using the criteria of fold change  $\geq 1.5$  and a false-discovery-rate-corrected *P* value (*q* value)  $< 0.05$ .

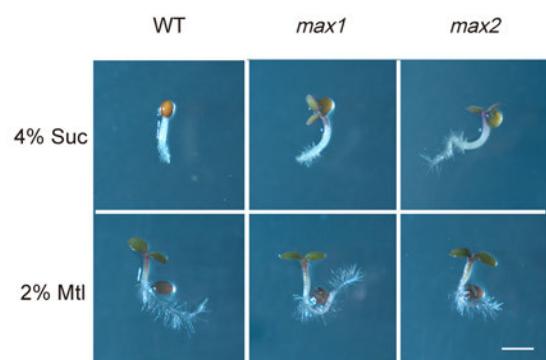
**Supplemental Table 3.** Changes in the expression of genes involved in SL biosynthesis, perception, and responsive in response to glucose in *max2*, *hxk1* and WT seedling.

**Supplemental Table 4.** Changes in the expression of genes involved in root hair formation and elongation in response to glucose in *max2*, *hxk1* and WT seedling.

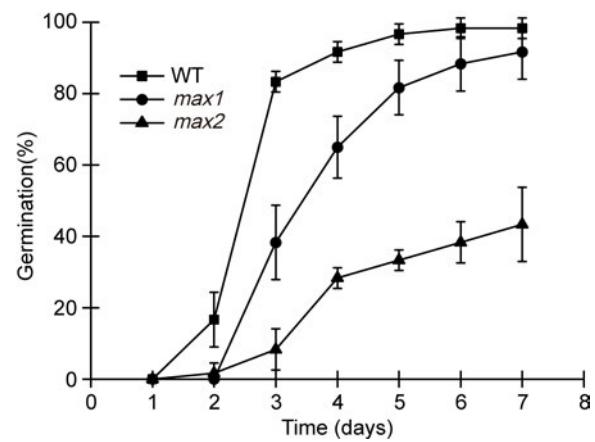
**Supplemental Table 5.** Stress-related genes whose expression was specifically induced by glucose in the *hxk1* mutant.

**Supplemental Table 6.** Stress-related genes whose expression was specifically repressed by glucose in the *max2* mutant.

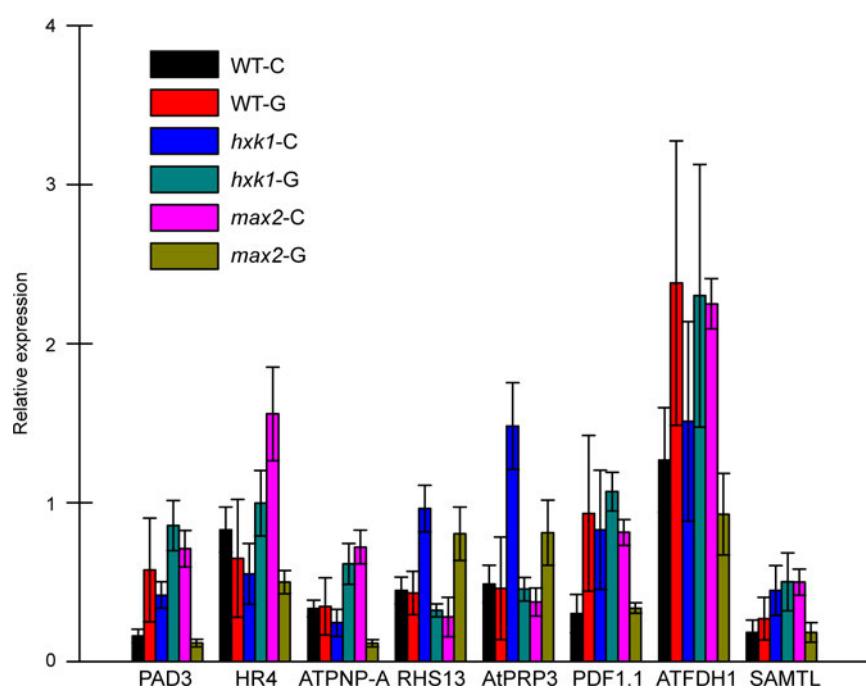
Supplementary Figure 1



Supplementary Figure 2



Supplementary Figure 3



Supplementary Table 1 List of primers used for quantitative RT-PCR

Gene	AGI	Forward	Reverse
CAB2	AT1G29920	CGTTGAAGGTTACAGAGTCG	CCTTACCACTGACGATGGC
PAD3	AT3G26830	GGCTGAAGCGGTCTAAAGAG	TCCAGGCTTAAGATGCTCGT
HR4	AT3G50480	CATCTCGAGAGACGAGAGCTAA	CTGAAGCCGTCGTAATGACTT
ATPNP-A	AT2G18660	TGTGGTAGTGATGATAAGTGT	TGTAGGGAGGGTCGTAATAG
RHS13	AT4G02270	GTGCAACGGCAAGAATTG	TGGCGATGAAGTAACCTTAG
AtPRP3	AT3G62680	CCCTATTCTAGGAGCAAAGATAC	CCCTTAGAGTCAGTTGGATTAC
PDF1.1	AT1G75830	GTGCGAGAGGCCAAGTG	TTGTGAGCTGGGAAGACATAG
ATFDH1	AT5G14780	CGAATACCGTACCAAGAAC	CCTCTTGCCTGTTCACTATC
SAMTL	AT5G04380	AGTGAGTATAAAAGTGGATGAAGAGAGAAGT	TTATTTCCGAACCAGTGAACACTATTAGAG
SAND	AT2G28390	CAGACAAG/GCGATGGCGATA	GCTTCTCTCAAGGGTTCTGGGT

Supplemental Table 2A Up-regulated genes in the WT-G/WT-C comparison

Gene_id	readcount(WT-G)	readcount(WT-C)	log <sub>2</sub> FoldChange	pval	padj
AT1G72570	71.45362903	2.640132404	4.7583	3.46E-11	7.04E-08
AT1G61800	4245.744401	346.7448321	3.6141	6.62E-11	1.16E-07
AT5G55410	90.72005041	7.737386263	3.5515	2.13E-08	1.27E-05
AT5G66780	151.2312563	17.68597257	3.0961	1.85E-07	8.37E-05
AT1G12130	174.7155749	21.88038992	2.9973	1.92E-07	8.52E-05
AT3G48700	3674.392078	601.240244	2.6115	3.68E-07	0.0001425
AT3G21720	138848.213	24579.75916	2.498	8.01E-07	0.00028784
AT1G65090	62.82188505	7.392909467	3.0871	1.49E-06	0.00047369
AT2G24560	48.78254219	2.656805704	4.1986	1.77E-06	0.00054785
AT1G67105	483.7628942	85.96272084	2.4925	2.17E-06	0.00064479
AT5G57390	1437.310409	275.0894971	2.3854	2.88E-06	0.00082789
AT5G20710	219.6105339	30.62898915	2.842	8.05E-06	0.0017558
AT2G27380	955.247433	192.2793064	2.3127	1.07E-05	0.0022166
AT1G67100	426.3634601	89.97303819	2.2445	1.13E-05	0.0023172
AT3G29970	285.970535	20.13992569	3.8277	1.39E-05	0.0027431
AT2G40220	100.6230606	7.493939488	3.7471	2.06E-05	0.0039075
AT4G36880	7912.642989	1797.643505	2.1381	3.34E-05	0.0057891
AT4G31020	241.996193	49.47257186	2.2903	3.80E-05	0.0064917
AT1G27461	53.91094416	7.527187249	2.8404	4.56E-05	0.0076194
AT3G61920	22.10396389	0.860261878	4.6834	4.82E-05	0.0080041
AT5G13170	81.63433667	13.11640414	2.6378	6.70E-05	0.010297
AT1G13270	137.569446	32.18070062	2.0959	0.00010231	0.014685
AT2G04530	83.29567894	17.26795034	2.2701	0.00011685	0.016031
AT4G39500	204.5299	52.15735817	1.9714	0.00012416	0.016855
AT3G22840	5325.628696	1436.982962	1.8899	0.000126	0.016907
AT4G15210	18.97757516	1.871376	3.3421	0.00012961	0.017109
AT3G08770	111.5388507	27.07857497	2.0423	0.00018196	0.021923
AT1G02205	553.2885741	128.096364	2.1108	0.00020341	0.024232
AT4G27570	23.10407518	0.768756404	4.9095	0.00021295	0.025123
AT3G12145	187.7829012	44.53807058	2.076	0.00022678	0.026498
AT3G42725	21.70319318	3.040589957	2.8355	0.00038378	0.038569
AT2G28900	4647.252326	1383.636132	1.7479	0.00043863	0.042507
AT3G54090	66.83033442	16.72606625	1.9984	0.00049098	0.046474
AT4G09020	920.4507962	264.3374997	1.8	0.00049598	0.046766
AT2G05710	15330.58171	4609.878043	1.7336	0.00052458	0.047801
AT3G21730	97.78483093	9.164542181	3.4155	0.00052373	0.047801
AT1G66060	19.65497754	2.731637877	2.8471	0.00053383	0.048233
AT3G50230	68.90451635	17.90242896	1.9444	0.00054848	0.049244

Supplemental Table 2B Down-regulated genes in the WT-G/WT-C comparison

Gene_id	readcount(WT-G)	readcount(WT-C)	log <sub>2</sub> FoldChange	pval	padj
AT1G74670	6.940787078	404.4124469	-5.8646	1.19E-18	2.90E-14
AT5G42530	13.3832801	400.8227021	-4.9045	3.90E-15	4.76E-11
AT2G34430	215.7647853	4924.713149	-4.5125	1.17E-14	9.51E-11
AT5G37990	19.85392603	469.29074	-4.563	4.42E-14	2.70E-10
AT1G32450	34.4166965	774.5215464	-4.4921	8.55E-14	4.17E-10
AT2G22990	35.16576378	616.9238025	-4.1328	2.71E-12	1.10E-08
AT5G14740	283.525031	4194.108186	-3.8868	3.43E-12	1.20E-08
AT3G15450	50.92651093	970.9107267	-4.2528	1.40E-11	4.28E-08
AT3G47340	1.809007553	211.8024829	-6.8714	2.52E-11	6.84E-08
AT4G26530	1.412717915	263.2616204	-7.5419	3.04E-11	7.04E-08
AT5G25980	5.96338971	117.3788236	-4.2989	3.27E-11	7.04E-08
AT1G66970	16.27141867	245.5946951	-3.9159	5.48E-11	1.03E-07
AT3G54890	560.9235369	6979.982122	-3.6373	7.40E-11	1.21E-07
AT5G04950	7.113498484	139.1022241	-4.2894	9.85E-11	1.50E-07
AT2G05540	0.351819729	43.56804668	-6.9523	2.41E-10	3.46E-07
AT3G01500	457.8096466	4755.851139	-3.3769	2.74E-10	3.71E-07
AT1G68520	19.09072835	280.2306569	-3.8757	3.21E-10	4.12E-07
AT3G62410	16.9350693	227.3904628	-3.7471	5.51E-10	6.72E-07
AT3G06070	28.59828166	334.1522025	-3.5465	9.37E-10	1.04E-06
AT3G55240	0	33.27587495	#NAME?	9.00E-10	1.04E-06
AT2G34420	2678.04436	26672.87007	-3.3161	1.07E-09	1.13E-06
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AT5G37970	0	31.50552897	#NAME?	1.79E-09	1.75E-06
AT2G05520	250.3006511	2486.943255	-3.3126	1.93E-09	1.81E-06
AT5G48490	32.74232736	387.791806	-3.5661	2.14E-09	1.94E-06
AT3G62550	1.412717915	50.56465945	-5.1616	3.28E-09	2.86E-06
AT2G29290	22.85969887	267.9650481	-3.5512	3.54E-09	2.98E-06
AT2G05070	216.8559853	2206.005556	-3.3466	6.06E-09	4.93E-06
AT1G73830	6.0417223	91.79855284	-3.9254	7.80E-09	6.14E-06
AT5G02160	28.70028608	291.0386912	-3.3421	8.09E-09	6.17E-06
AT1G29920	655.2161132	6208.690634	-3.2442	9.06E-09	6.71E-06
AT5G44440	134.9051564	1198.517749	-3.1512	1.14E-08	8.18E-06
AT1G21500	14.53434679	169.5850138	-3.5445	1.24E-08	8.65E-06
AT1G23840	2.166266281	48.27090268	-4.4779	1.70E-08	1.15E-05
AT5G54270	730.4304755	6432.734012	-3.1386	1.77E-08	1.17E-05
AT2G28630	40.00773917	390.9666328	-3.2887	1.87E-08	1.20E-05
AT3G05730	22.21140732	227.3684991	-3.3557	1.93E-08	1.21E-05
AT5G19190	19.53596898	208.5367607	-3.4161	2.09E-08	1.27E-05
AT2G05100	357.3383075	2959.413844	-3.0499	2.83E-08	1.65E-05
AT1G49130	1.613582233	57.52954518	-5.156	5.42E-08	3.03E-05
AT1G64370	77.83195759	562.9270044	-2.8545	5.59E-08	3.03E-05
AT4G28040	15.76672769	153.5914081	-3.2841	5.48E-08	3.03E-05
AT1G73870	6.013569388	81.0869733	-3.7532	7.50E-08	3.98E-05
AT2G22980	3.897212014	61.88622092	-3.9891	9.56E-08	4.91E-05
AT4G01390	6.610723343	79.53209349	-3.5887	9.64E-08	4.91E-05
AT1G10070	17.38766476	151.7032599	-3.1251	1.06E-07	5.27E-05
AT3G47470	1527.303061	11417.56923	-2.9022	1.10E-07	5.35E-05
AT1G66100	5.34352184	69.63164731	-3.7039	1.17E-07	5.50E-05
AT3G08940	852.3639424	6622.395511	-2.9578	1.17E-07	5.50E-05
AT5G42580	6.945268158	92.31156677	-3.7324	1.31E-07	6.03E-05
AT4G27300	45.4528695	296.4155114	-2.7052	2.03E-07	8.85E-05
AT4G12480	16.77840412	132.0778094	-2.9767	2.10E-07	9.01E-05
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AT1G29910	1280.981415	8424.316072	-2.7173	8.68E-07	0.00030736
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AT3G58550	33.08789578	209.2121086	-2.6606	1.07E-06	0.00036771
AT1G25230	94.2866367	647.8455396	-2.7805	1.12E-06	0.00037792
AT1G79040	1749.48772	10003.37572	-2.5155	1.13E-06	0.00037792
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AT4G37150	9.944373313	83.27999427	-3.066	3.89E-06	0.0010446
AT2G38390	51.09351257	277.8607194	-2.4431	4.04E-06	0.001069
AT3G44970	85.39365788	506.9750738	-2.5697	4.07E-06	0.001069
AT3G05160	35.86817455	220.3204832	-2.6188	4.16E-06	0.0010819
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AT3G16120	1.418156914	27.97069903	-4.3018	4.59E-06	0.0011442
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AT3G55970	5.516233246	52.81447095	-3.2592	6.03E-06	0.0014105
AT2G32880	0.351819729	19.22954508	-5.7723	6.16E-06	0.00142
AT1G78450	4.098076332	43.53361102	-3.4091	6.57E-06	0.0014989
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AT2G18300	47.04003131	253.1868916	-2.4282	3.14E-05	0.0054832
AT2G39470	33.30657655	174.1415928	-2.3864	3.43E-05	0.0058917
AT1G52230	233.0160587	1128.041776	-2.2753	4.34E-05	0.0073644
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AT4G31910	47.43344719	245.43071	-2.3713	5.21E-05	0.0084875
AT1G66130	37.46571056	192.7756489	-2.3633	5.30E-05	0.008517
AT5G46270	5.164413517	41.37829289	-3.0022	5.28E-05	0.008517
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AT4G05180	810.9490557	3548.982236	-2.1297	7.75E-05	0.011547
AT3G44260	529.8381902	2000.758049	-1.9169	7.88E-05	0.011661
AT2G15020	1.602704236	50.88899579	-4.9888	8.27E-05	0.012163
AT1G31580	229.9544115	1017.913201	-2.1462	8.71E-05	0.012658
AT4G24230	136.8613459	518.4762416	-1.9216	8.66E-05	0.012658
AT3G25690	180.4813495	820.9869321	-2.1855	0.00010015	0.014472
AT3G44870	0.351819729	13.97646834	-5.312	0.00010283	0.014685
AT4G19170	8.034319256	79.82098672	-3.3125	0.00010712	0.015209
AT1G19150	58.13930299	270.4400502	-2.2177	0.0001087	0.015344
AT1G31330	1076.2565759	4646.663474	-2.1102	0.0001134	0.015916
AT5G47000	9.352387585	51.17820507	-2.4521	0.00011474	0.016012
AT2G39980	106.3027723	453.6888518	-2.0935	0.00011607	0.016017
AT5G56100	36.25358619	163.3997148	-2.1722	0.00011609	0.016017
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AT5G39530	63.69169339	292.3545579	-2.1985	0.00012492	0.016855
AT1G75460	15.9416257	86.17589051	-2.4345	0.00012863	0.017109
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AT5G36910	50.50004468	224.4196123	-2.1518	0.00013105	0.017206
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AT4G15396	8.090625081	45.48021455	-2.4909	0.00013958	0.017847
AT5G48000	257.2305397	1131.734129	-2.1374	0.00013933	0.017847
AT5G45820	5.801556302	37.60815515	-2.6965	0.00014565	0.018525
AT4G23170	16.9255656	78.89472351	-2.2207	0.00014642	0.018527
AT3G55630	29.03103696	122.5087322	-2.0772	0.00015037	0.018831
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AT1G35250	4.796276792	34.78023884	-2.8583	0.00017444	0.021515
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AT3G50560	4.304379649	34.60536686	-3.0071	0.00018211	0.021923
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AT4G14540	29.70935952	136.9054979	-2.2042	0.0001953	0.02338
AT1G78230	26.22666998	117.0748422	-2.1583	0.00020668	0.024501
AT2G30424	5.304490931	37.56805515	-2.8242	0.00022329	0.026217
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AT1G53940	10.28979612	58.22226014	-2.5004	0.00025592	0.029069
AT1G77530	11.02063058	61.95936917	-2.4911	0.00026249	0.029665
AT4G21445	4.232714747	32.08790841	-2.9224	0.00026359	0.029665
AT1G15040	5.387991749	47.34038391	-3.1353	0.00027938	0.031223
AT1G50732	6.030844303	37.57946129	-2.6395	0.00028128	0.031223
AT5G10180	111.25915	403.6223822	-1.8591	0.00028025	0.031223
AT5G63560	47.45565731	174.2952937	-1.8769	0.00028821	0.031847
AT3G26180	61.05570234	242.9605022	-1.9925	0.00028989	0.031889
AT4G27654	42.35732408	178.1720465	-2.0726	0.00029878	0.03272
AT2G29310	32.13402463	140.9072809	-2.1326	0.00031148	0.033958
AT4G16990	165.7791715	623.4753967	-1.9111	0.00031764	0.034475
AT5G06690	21.40224027	94.63500348	-2.1446	0.00032941	0.035595
AT1G11260	630.5483279	2439.974924	-1.9522	0.00034366	0.036073
AT1G15980	100.3383168	400.9876542	-1.9987	0.00034641	0.036073
AT1G23130	66.13798933	244.2006863	-1.8845	0.00034698	0.036073
AT1G29930	8512.680092	32729.22752	-1.9429	0.00034318	0.036073
AT1G70260	0.709078457	13.95284396	-4.2985	0.00034595	0.036073
AT2G25150	5.288173934	35.88058148	-2.7624	0.00034001	0.036073
AT4G32280	1.608143235	17.96892448	-3.482	0.00034434	0.036073
AT5G02760	76.52256021	319.4257633	-2.0615	0.00034713	0.036073
AT5G04140	1182.154082	4203.178802	-1.8301	0.00033936	0.036073
AT2G39010	164.3212965	620.8065723	-1.9176	0.00035517	0.036615
AT4G22200	1.954523965	19.39924874	-3.3111	0.00035534	0.036615
AT4G04630	0.351819729	12.07909217	-5.1015	0.00035795	0.036729
AT4G27710	19.5868358	89.2071536	-2.1873	0.0003635	0.036987
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AT1G15820	1512.701551	5644.844588	-1.8998	0.00037956	0.038303
AT2G25900	38.78404966	167.4091408	-2.1098	0.00038964	0.038998
AT5G59520	42.145311	165.0837236	-1.9698	0.00039406	0.039279
AT2G39250	13.83614633	68.6459385	-2.3107	0.00040824	0.0402
AT5G42600	5.738853559	305.1755846	-5.7327	0.00040816	0.0402
AT5G62280	181.4051724	651.7696766	-1.8451	0.00040597	0.0402
AT1G30380	1435.64763	5157.941148	-1.8451	0.00041776	0.040972
AT1G03400	15.61768812	65.79182434	-2.0747	0.00042297	0.041317
AT2G34350	4.963549199	37.34912413	-2.9116	0.00043456	0.04228
AT1G42430	117.7980251	450.2317125	-1.9344	0.00045273	0.0437
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AT5G38980	61.60253101	248.5045496	-2.0122	0.00047099	0.045106
AT5G44190	148.7395121	593.0540161	-1.9954	0.00048363	0.045956
AT5G66570	2561.924787	9286.823799	-1.858	0.00048271	0.045956
AT3G21055	302.7820911	1128.639449	-1.8982	0.00049909	0.046828
AT4G35190	83.65174673	275.0278734	-1.7171	0.00050048	0.046828
AT1G72910	21.33505645	131.5950335	-2.6248	0.00050566	0.047032
AT3G01260	2.311782693	20.26804494	-3.1321	0.00050651	0.047032
AT4G27520	208.980125	709.2430495	-1.7629	0.00050885	0.047071
AT4G04330	4.243592745	30.03958116	-2.8235	0.00051513	0.047276
AT3G26460	38.0914338	137.2020536	-1.8488	0.00052061	0.047797
AT2G24850	0.899064778	13.05913664	-3.8605	0.0005303	0.048143
AT4G11470	21.09082575	73.16914957	-1.7946	0.00053524	0.048233
AT1G73330	1190.803632	4072.436878	-1.774	0.00055133	0.049319

Supplemental Table 2C Up-regulated genes in the *hxk1* -G/*hxk1* -C comparison

Gene_id	readcount( <i>hxk1</i> -G)	readcount( <i>hxk1</i> -C)	log <sub>2</sub> FoldChange	pval	padj
AT2G28900	6937.31967	1215.851292	2.5124	9.16E-116	4.52E-112
AT4G09020	1911.794623	272.4337619	2.811	1.22E-115	5.03E-112
AT5G07990	2365.308575	357.9744752	2.7241	1.93E-115	6.79E-112
AT3G52180	1318.745478	176.1357895	2.9044	9.45E-110	2.59E-106
AT1G32900	6056.151421	1129.674711	2.4225	2.01E-106	4.95E-103
AT2G29670	1798.962976	244.8541353	2.8772	7.90E-97	1.50E-93
AT1G80130	2415.026514	302.5334654	2.9969	2.24E-90	3.45E-87
AT3G48700	2888.947555	661.6377572	2.1264	5.07E-79	6.95E-76
AT4G39210	1021.271444	185.9927356	2.457	5.71E-78	7.41E-75
AT3G22840	7738.975718	1565.896629	2.3052	2.71E-76	3.18E-73
AT5G42800	5179.443601	1399.257467	1.8881	2.13E-68	2.19E-65
AT4G22880	3647.842161	972.7715532	1.9069	2.81E-67	2.78E-64
AT1G61800	5156.262122	211.7280722	4.606	1.56E-62	1.28E-59
AT1G24020	2440.667225	664.5057762	1.8769	7.31E-62	5.63E-59
AT1G45191	377.6660257	51.94918461	2.8619	2.90E-61	2.17E-58
AT5G13930	14197.89673	4315.488919	1.7181	6.44E-61	4.67E-58
AT4G14090	1063.112262	284.1303624	1.9037	2.39E-52	1.31E-49
AT2G40840	3199.26338	1016.716122	1.6538	1.89E-51	9.52E-49
AT5G17220	1236.17747	368.9296921	1.7445	2.52E-47	1.09E-44
AT5G20190	3041.423796	1024.856807	1.5693	1.10E-46	4.62E-44
AT1G62540	265.4563482	40.44963257	2.7143	1.02E-45	4.07E-43
AT3G21560	3209.432621	1096.266893	1.5497	1.02E-45	4.07E-43
AT4G03210	2063.893372	701.9420057	1.5559	1.83E-43	6.75E-41
AT3G29590	749.7845108	211.8632503	1.8233	2.29E-43	8.19E-41
AT2G21590	236.8156328	35.48311977	2.7386	4.42E-43	1.56E-40
AT1G48660	647.3875443	178.707491	1.857	2.85E-42	9.62E-40
AT5G54060	1278.299601	414.5543048	1.6246	3.99E-42	1.33E-39
AT5G47500	1427.352752	473.2087749	1.5928	5.16E-42	1.70E-39
AT4G17770	1087.021395	344.1385823	1.6593	6.90E-42	2.21E-39
AT3G55120	1224.196906	401.7650267	1.6074	6.09E-41	1.86E-38
AT1G62710	891.8149317	282.823308	1.6568	2.35E-39	6.67E-37
AT1G11600	824.7553224	264.5556286	1.6404	9.52E-38	2.50E-35
AT4G15620	458.4559501	121.9875811	1.91	9.76E-38	2.53E-35
AT2G23910	452.4415222	121.3730362	1.8983	4.65E-37	1.14E-34
AT5G03210	562.5162052	174.2840836	1.6905	3.74E-34	8.55E-32
AT1G30530	888.6099934	310.4010807	1.5174	7.45E-34	1.65E-31
AT1G56650	444.125958	128.6560835	1.7874	9.98E-34	2.20E-31
AT3G62610	135.7795455	15.46305156	3.1344	1.64E-33	3.52E-31
AT1G65060	823.1907277	227.9695897	1.8524	1.43E-31	2.85E-29
AT5G16990	495.9610806	159.2991733	1.6385	5.35E-31	1.02E-28
AT1G12130	153.7942764	23.86015605	2.6883	7.10E-31	1.33E-28
AT3G12145	258.8091261	62.14077301	2.0583	1.02E-30	1.90E-28
AT5G48880	1226.956788	262.2384699	2.2261	1.09E-30	2.01E-28
AT4G08870	950.8260263	303.6700922	1.6467	1.19E-29	2.09E-27
AT5G42600	228.4395173	52.76322063	2.1142	1.20E-29	2.09E-27
AT1G60090	388.8825062	121.754659	1.6754	1.71E-28	2.81E-26
AT2G23000	291.1490824	81.1915356	1.8424	3.89E-28	6.27E-26
AT5G62210	131.9938184	20.34297103	2.6979	2.66E-27	4.11E-25
AT5G23940	338.8156323	106.64649532	1.6674	4.69E-26	6.73E-24
AT5G50360	160.1498679	31.60467593	2.3412	1.18E-25	1.67E-23
AT3G08770	208.5220605	52.82756485	1.9808	2.53E-25	3.49E-23
AT3G21730	74.59439677	5.163525802	3.8526	3.44E-25	4.68E-23
AT1G03940	380.7237808	132.8466	1.519	4.98E-24	6.18E-22
AT4G09820	273.4544174	83.92996531	1.704	5.49E-24	6.77E-22
AT3G61250	105.6279192	16.09307077	2.7145	2.67E-23	3.17E-21
AT4G29030	343.751053	118.2792528	1.5392	3.85E-23	4.50E-21
AT2G37260	308.5552286	104.3570515	1.564	1.45E-22	1.67E-20
AT5G50800	127.8316339	17.64073131	2.8573	2.23E-21	2.40E-19
AT1G65340	174.2447708	46.86173825	1.8946	4.03E-21	4.26E-19
AT3G29320	1789.146229	574.4167104	1.6391	9.72E-20	9.63E-18
AT1G12064	269.8174769	94.88053803	1.5078	1.15E-19	1.13E-17
AT3G25795	66.13829639	7.144192544	3.2106	5.24E-19	4.77E-17
AT5G20710	168.6897323	49.91346617	1.7569	1.33E-18	1.15E-16
AT4G17470	362.9071946	78.65850215	2.2059	3.04E-18	2.51E-16
AT4G12870	112.5591283	11.95575203	3.2349	4.51E-18	3.68E-16
AT3G02410	126.8576719	34.98639773	1.8583	1.59E-16	1.15E-14
AT2G11810	161.1711064	51.88609716	1.6352	5.26E-16	3.68E-14
AT4G28680	121.4619637	27.74757612	2.1301	1.26E-15	8.43E-14
AT1G17260	99.8687328	24.24244263	2.0425	1.77E-15	1.18E-13
AT5G41460	125.2812311	36.65160024	1.7732	3.36E-15	2.18E-13

AT3G05190	454.5549443	153.9108319	1.5624	8.06E-15	4.99E-13
AT5G37970	83.9413155	18.2197146	2.2039	1.20E-14	7.29E-13
AT5G57550	104.0844645	28.19078411	1.8845	1.96E-14	1.17E-12
AT1G76620	54.19987052	7.935034784	2.772	6.99E-14	3.93E-12
AT5G45850	91.95174357	23.81995029	1.9487	8.53E-14	4.74E-12
AT1G19630	142.7028805	5.734161255	4.6373	6.47E-13	3.32E-11
AT4G24260	53.61497326	9.228780872	2.5384	2.23E-12	1.08E-10
AT3G55110	95.17467199	28.61729222	1.7337	6.42E-12	2.96E-10
AT4G33905	58.06477848	11.98977598	2.2759	1.19E-11	5.36E-10
AT3G50610	37.79412406	2.311605308	4.0312	1.38E-11	6.10E-10
AT4G11310	54.64164604	10.80396725	2.3384	1.38E-11	6.11E-10
AT2G25625	183.7099626	61.70406311	1.574	2.48E-11	1.06E-09
AT4G28950	54.15819284	11.06500818	2.2912	3.35E-11	1.43E-09
AT1G28610	102.6619669	34.48691669	1.5738	4.31E-11	1.81E-09
AT4G02160	56.75713188	12.31205041	2.2047	5.33E-11	2.21E-09
AT1G22380	83.25433483	25.15606817	1.7266	5.92E-11	2.43E-09
AT1G74810	322.5975384	13.32557757	4.5975	9.23E-11	3.69E-09
AT5G48100	107.1039639	21.59804902	2.31	1.23E-10	4.85E-09
AT3G49580	94.09613951	31.25054358	1.5903	1.24E-10	4.89E-09
AT1G14520	254.2867209	49.08458421	2.3731	1.34E-10	5.26E-09
AT1G04570	52.17469715	10.52036093	2.3102	1.83E-10	7.02E-09
AT3G58060	63.97047607	17.01287812	1.9108	3.05E-10	1.14E-08
AT1G01520	206.6053072	37.11398624	2.4768	4.00E-10	1.46E-08
AT5G01760	457.2047509	91.81766785	2.316	4.54E-10	1.65E-08
AT2G24645	65.62429711	18.4102295	1.8337	5.55E-10	1.99E-08
AT2G41090	1821.182889	424.8207159	2.0999	1.03E-09	3.57E-08
AT3G08860	94.45771856	15.80017193	2.5797	1.26E-09	4.28E-08
AT2G02540	87.19927468	30.01897567	1.5384	1.47E-09	4.98E-08
AT3G13784	26.15788708	1.005179312	4.7017	1.50E-09	5.06E-08
AT5G24770	88.45173811	30.96508751	1.5142	2.01E-09	6.65E-08
AT2G43480	59.93126092	16.55080841	1.8564	2.30E-09	7.50E-08
AT3G21950	63.62012716	19.97553039	1.6712	2.22E-08	6.45E-07
AT5G23010	141.7263329	11.47482061	3.6266	2.72E-08	7.74E-07
AT5G09470	25.71563678	3.030383877	3.0851	3.64E-08	1.01E-06
AT2G27402	79.99933743	19.08880232	2.0673	4.45E-08	1.23E-06
AT1G65890	18.24832974	1.03270516	4.1433	7.45E-08	1.98E-06
AT1G60450	92.16650119	28.45800685	1.6954	9.92E-08	2.56E-06
AT2G14520	61.24175621	20.6414233	1.569	1.17E-07	2.99E-06
AT1G72570	50.70451432	15.03067373	1.7542	1.39E-07	3.50E-06
AT5G55340	41.88282501	9.422090196	2.1522	2.51E-07	6.07E-06
AT2G37770	309.0259332	78.93592667	1.969	2.71E-07	6.50E-06
AT4G36830	44.83954485	12.66185069	1.8243	2.78E-07	6.66E-06
AT1G62580	356.3434454	29.4167986	3.5986	3.44E-07	8.12E-06
AT5G06250	41.98474384	11.71172308	1.8419	4.79E-07	1.10E-05
AT4G13770	138.6086467	18.19652082	2.9293	5.15E-07	1.17E-05
AT3G27970	39.48266565	10.54788678	1.9043	6.82E-07	1.51E-05
AT1G25425	69.65285545	24.32068811	1.518	7.36E-07	1.62E-05
AT4G26790	50.97245743	16.72493973	1.6077	7.85E-07	1.73E-05
AT1G35290	103.1065911	29.18792768	1.8207	1.68E-06	3.44E-05
AT4G15210	18.28219929	2.118295984	3.1095	2.39E-06	4.71E-05
AT4G36950	31.75807231	7.894829028	2.0081	2.96E-06	5.68E-05
AT1G54040	33.05363776	8.539694185	1.9526	3.23E-06	6.17E-05
AT1G62560	58.80884145	8.221435527	2.8386	3.56E-06	6.74E-05
AT3G02020	49.63901255	2.078090228	4.5781	3.92E-06	7.35E-05
AT2G15490	520.2403895	166.5729593	1.643	4.25E-06	7.94E-05
AT4G12030	45.55116261	12.78680003	1.8328	4.84E-06	8.92E-05
AT4G28640	350.2195022	122.621304	1.514	4.95E-06	9.10E-05
AT2G36750	141.805105	35.83725212	1.9844	5.28E-06	9.61E-05
AT1G70810	244.0587896	71.9862648	1.7614	7.94E-06	0.00013933
AT1G07900	258.2904305	37.95988017	2.7664	7.99E-06	0.00014005
AT5G11930	85.95070803	19.67211768	2.1274	8.16E-06	0.00014289
AT2G22190	347.9325579	106.431719	1.7089	1.00E-05	0.00017259
AT3G12520	41.3863411	14.03600829	1.56	1.16E-05	0.00019786
AT5G66816	39.84566904	3.070589633	3.6978	1.20E-05	0.00020281
AT5G11920	53.84123871	15.5456291	1.7922	1.40E-05	0.00023337
AT3G10570	28.76235889	7.487811017	1.9416	1.44E-05	0.0002385
AT4G21930	20.83803631	4.103294793	2.3444	2.57E-05	0.00039944
AT4G37295	62.08173045	19.75686126	1.6518	2.81E-05	0.00043186
AT5G14200	340.9426629	83.61356059	2.0277	5.20E-05	0.0007449
AT4G26950	257.084294	71.90616538	1.8381	5.32E-05	0.00075991
AT5G24640	29.4919668	8.851454743	1.7363	5.54E-05	0.00078912
AT3G58990	80.12663126	19.77233558	2.0188	5.89E-05	0.00083053

AT5G23020	651.0502405	179.2107112	1.8611	9.40E-05	0.001254
AT5G45860	15.95948628	2.663571622	2.583	0.00010611	0.0013982
AT2G14560	122.5878566	0.706098661	7.4397	0.00014153	0.0018089
AT1G45616	40.82513136	9.63363285	2.0833	0.0001524	0.0019268
AT4G04760	28.94637332	9.769096059	1.5671	0.00017714	0.002209
AT5G22570	360.2455274	124.0548453	1.538	0.00017787	0.0022159
AT5G64060	12.82466101	1.726123914	2.8933	0.00018637	0.0023067
AT2G01580	25.32076151	7.879983087	1.6841	0.0002424	0.0028941
AT4G29150	18.94264377	4.497632896	2.0744	0.00024806	0.0029475
AT3G07150	30.10978405	10.52252696	1.5168	0.00025078	0.0029769
AT5G07530	55.55536694	14.85870845	1.9026	0.00028151	0.0032973
AT3G19710	133.8563424	12.3544222	3.4376	0.00029594	0.0034369
AT1G13230	24.33386729	7.648634041	1.6697	0.0002993	0.0034694
AT1G54020	20.8491679	5.8167388	1.8417	0.00037983	0.0042569
AT1G16400	78.69252729	13.67970991	2.5242	0.00042811	0.0047018
AT4G30830	19.95180117	5.407554756	1.8835	0.00047244	0.0051203
AT3G22231	31.71143519	0.326606499	6.6013	0.00051527	0.0055046
AT5G55450	34.6941179	10.93572678	1.6656	0.0005259	0.0055964
AT4G01895	23.90559726	7.962560632	1.586	0.00055579	0.0058739
AT1G15790	20.85982471	6.278808508	1.7322	0.00058399	0.0061195
AT1G19640	8.686850485	0.653212998	3.7332	0.00068132	0.0069447
AT5G26790	21.7664239	6.902329624	1.6569	0.0007187	0.0072776
AT1G26540	18.6131337	5.243937314	1.8276	0.00072769	0.0073565
AT5G05340	172.9087919	5.490132301	4.977	0.00075817	0.0076245
AT5G03350	297.4264985	24.77224394	3.5857	0.00076596	0.007693
AT3G03190	15.0088355	1.060231009	3.8234	0.00084992	0.0083961
AT1G24070	20.21642082	6.130665391	1.7214	0.0009184	0.0089401
AT5G42610	13.24417335	2.743983134	2.271	0.001189	0.011093
AT1G15630	8.023557325	0.665892905	3.5909	0.0013549	0.012383
AT2G17470	16.42210064	4.377015629	1.9076	0.0014567	0.013205
AT1G73805	26.86058256	9.29867851	1.5304	0.0014818	0.013365
AT1G21270	70.36858164	19.14046662	1.8783	0.0015497	0.013844
AT3G44910	10.93496583	0	Inf	0.0015835	0.014072
AT5G44360	9.725604412	1.371991567	2.8255	0.0018874	0.016443
AT5G01900	15.96043584	2.718623319	2.5536	0.0019822	0.017132
AT2G30770	766.2253282	17.92496601	5.4177	0.0020955	0.017849
AT5G39520	14.16570238	1.726123914	3.0368	0.0022048	0.018638
AT5G02210	5.080178391	0	Inf	0.002431	0.020197
AT2G26400	269.0923436	24.54459858	3.4546	0.0024463	0.02029
AT2G41280	164.734728	46.42719439	1.8271	0.0024881	0.02054
AT4G14390	18.58163805	6.143345299	1.5968	0.0026501	0.021588
AT3G49700	12.11969017	2.758829075	2.1352	0.0026851	0.021809
AT4G35180	48.69026089	2.839240586	4.1001	0.0027426	0.022166
AT1G19960	1144.167171	214.7358906	2.4137	0.0031122	0.024582
AT4G10500	18.64842759	2.444902483	2.9312	0.0031328	0.024721
AT3G25882	146.2007752	46.1423313	1.6638	0.0040142	0.030281
AT1G71000	28.90042263	9.332386166	1.6308	0.0041754	0.031315
AT2G41730	391.2877605	130.8739732	1.5801	0.0043066	0.032152
AT1G50090	11.20148461	0.326606499	5.1	0.004442	0.033023
AT1G05550	169.5543951	48.43539119	1.8076	0.0051609	0.037409
AT4G30250	16.36549313	5.477452393	1.5791	0.0052356	0.037862
AT4G12890	10.59005115	2.389850786	2.1477	0.0055482	0.0396
AT5G50790	11.17732231	2.716457285	2.0408	0.0058082	0.041052
AT3G22235	51.77550181	3.409876039	3.9245	0.0058219	0.041137
AT3G56400	329.5108559	74.87314972	2.1378	0.0060928	0.042689
AT1G33960	13.5464608	0.339286406	5.3193	0.0061744	0.043121
AT2G43100	107.1926404	31.67457357	1.7588	0.0064845	0.044931
AT3G44830	12.57164773	2.459748424	2.3536	0.0071452	0.048715
AT2G32487	5.455639157	0.326606499	4.0621	0.0071979	0.048898

Supplemental Table 2D Down-regulated genes in the *hxk1* -G/*hxk1* -C comparison

Gene_id	readcount( <i>hxk1</i> -G)	readcount( <i>hxk1</i> -C)	log <sub>2</sub> FoldChange	pval	padj
AT5G19120	84.45821053	1120.52821	-3.7298	7.52E-149	1.86E-144
AT3G15450	135.2450321	1451.018892	-3.4234	5.49E-134	6.77E-130
AT2G20670	74.68729478	862.563695	-3.5297	1.08E-124	8.84E-121
AT2G34430	1142.48229	11262.20038	-3.3012	1.66E-117	1.02E-113
AT5G14740	1106.877383	6105.646105	-2.4636	4.35E-111	1.34E-107
AT3G01500	849.8245622	9101.295574	-3.4208	3.48E-101	7.80E-98
AT5G48485	240.7219083	1484.535848	-2.6246	5.50E-98	1.13E-94
AT3G47340	10.95438033	309.0931171	-4.8185	9.76E-97	1.72E-93
AT2G22990	98.48954886	757.8237682	-2.9438	3.53E-92	5.80E-89
AT5G38410	5302.255939	24444.65318	-2.2048	6.40E-89	9.29E-86
AT2G05520	818.2784402	3412.08326	-2.06	1.00E-76	1.24E-73
AT2G05100	1166.534755	4929.627722	-2.0792	5.64E-74	6.33E-71
AT3G47470	5370.309386	19446.1963	-1.8564	7.80E-71	8.37E-68
AT3G54890	2408.274838	11410.37109	-2.2443	1.77E-66	1.68E-63
AT2G13360	1774.402111	6201.651586	-1.8053	3.95E-64	3.61E-61
AT3G46780	1131.1535172	4047.152683	-1.8386	5.34E-64	4.70E-61
AT4G10340	4934.83829	16685.48074	-1.7575	8.12E-64	6.91E-61
AT1G80920	378.7122775	1503.740026	-1.9894	1.82E-62	1.45E-59
AT4G26530	12.53587906	387.8925962	-4.9515	1.57E-59	1.10E-56
AT3G08940	3362.911948	10885.31124	-1.6946	7.39E-59	5.06E-56
AT2G34420	13957.04969	43647.6863	-1.6449	2.14E-57	1.43E-54
AT5G64040	1890.245143	5996.04579	-1.6654	2.38E-55	1.55E-52
AT3G50820	853.556779	3482.42587	-2.0285	5.55E-55	3.51E-52
AT1G79040	5354.310937	16413.53683	-1.6161	9.94E-55	6.13E-52
AT5G02160	93.55961391	482.3296142	-2.3661	3.16E-54	1.90E-51
AT2G30570	2116.438416	6555.616426	-1.6311	1.33E-53	7.79E-51
AT1G11260	899.5243646	2909.027308	-1.6933	4.29E-53	2.46E-50
AT1G08380	3504.792242	10581.28032	-1.5941	1.36E-52	7.62E-50
AT5G38420	1650.582616	5483.042516	-1.732	2.90E-52	1.55E-49
AT3G61470	4430.693568	13231.25682	-1.5783	4.22E-52	2.21E-49
AT3G21055	671.7149058	2472.242448	-1.8799	1.18E-51	6.08E-49
AT4G28750	2500.356097	7506.968781	-1.5861	2.33E-51	1.15E-48
AT1G32060	1510.494667	4609.0309	-1.6094	5.29E-51	2.56E-48
AT3G26650	2568.268675	7585.610508	-1.5625	5.21E-50	2.47E-47
AT1G61520	3451.639686	10023.54492	-1.538	3.27E-49	1.52E-46
AT1G64720	4525.442969	12865.12588	-1.5073	7.05E-48	3.22E-45
AT4G02770	2653.852195	7628.64603	-1.5233	9.14E-48	4.10E-45
AT1G29670	529.1047822	1684.822851	-1.671	2.12E-47	9.36E-45
AT5G54270	3082.452269	11465.66932	-1.8952	1.09E-46	4.62E-44
AT5G20630	718.8744281	2542.220569	-1.8223	1.37E-46	5.61E-44
AT1G29920	2660.417878	10373.03009	-1.9631	1.33E-45	5.22E-43
AT4G23700	117.9718771	520.0275796	-2.1401	9.58E-45	3.64E-42
AT2G39730	5923.421176	24102.48595	-2.0247	1.89E-43	6.86E-41
AT5G51720	188.2607516	680.693191	-1.8543	9.31E-43	3.23E-40
AT4G24230	195.7124424	694.3555372	-1.8269	5.27E-42	1.71E-39
AT5G40890	339.103103	1066.116201	-1.6526	9.20E-42	2.91E-39
AT2G37130	1462.853765	4827.765563	-1.7226	3.08E-41	9.62E-39
AT2G28630	60.2060626	494.659617	-3.0385	3.42E-41	1.05E-38
AT4G02290	128.3693678	491.9434802	-1.9382	2.35E-40	6.89E-38
AT3G22142	37.33789348	229.6833542	-2.6209	4.31E-40	1.25E-37
AT1G20340	1878.311939	6201.885174	-1.7233	7.19E-38	1.93E-35
AT1G31330	2484.312637	8358.746646	-1.7504	7.26E-38	1.93E-35
AT2G39470	78.33021033	336.8545986	-2.1045	1.19E-37	3.05E-35
AT3G06070	115.7405907	528.2496435	-2.1903	2.50E-37	6.29E-35
AT5G28770	62.32629624	291.5980153	-2.2261	3.02E-37	7.53E-35
AT1G25230	248.0200322	857.997105	-1.7905	3.09E-37	7.62E-35
AT2G15020	6.416471959	107.7010457	-4.0691	5.23E-37	1.27E-34
AT5G48490	102.9090196	523.8935932	-2.3479	6.49E-35	1.51E-32
AT1G03600	437.3154953	1265.737145	-1.5332	7.25E-34	1.63E-31
AT4G21280	1849.333088	5414.692682	-1.5499	3.20E-33	6.80E-31
AT2G05070	827.7557893	3804.83843	-2.2006	9.97E-33	2.08E-30
AT1G15980	235.4592529	690.0347988	-1.5512	1.99E-32	4.13E-30
AT1G19150	131.1227247	432.3595628	-1.7213	1.73E-31	3.40E-29
AT1G21500	71.99023515	333.7527399	-2.2129	3.65E-31	7.03E-29
AT1G73870	25.53990525	159.2017498	-2.64	3.91E-31	7.48E-29
AT4G28040	24.43025335	194.5221968	-2.9932	2.03E-30	3.72E-28
AT4G39710	48.49902621	218.3984514	-2.1709	3.23E-30	5.82E-28
AT2G29290	63.79284542	336.1707449	-2.3977	4.21E-29	7.27E-27
AT4G16870	125.3627859	392.0114092	-1.6448	7.11E-28	1.13E-25
AT1G07180	100.651935	333.7218662	-1.7293	7.58E-28	1.20E-25
AT5G19190	59.96228179	232.7932404	-1.9569	4.32E-27	6.54E-25
AT1G05135	1256.383388	4291.275987	-1.7721	4.62E-27	6.94E-25
AT3G55630	60.74849721	232.9648539	-1.9392	1.15E-26	1.72E-24
AT1G68190	43.38861192	213.9437832	-2.3018	1.82E-26	2.68E-24
AT2G05440	0	124.7724025	#NAME?	5.37E-26	7.66E-24
AT4G01870	73.80369668	258.3445517	-1.8075	1.25E-25	1.75E-23
AT5G64570	122.1063642	366.2336342	-1.5846	2.44E-25	3.38E-23
AT1G74670	54.63526225	784.80494	-3.8444	3.55E-25	4.79E-23
AT5G21430	142.0550065	406.9396593	-1.5184	4.42E-25	5.89E-23

AT1G12900	827.2682601	2660.864024	-1.6855	4.80E-25	6.36E-23
AT4G04040	125.3544044	369.9759822	-1.5614	6.71E-25	8.85E-23
AT1G55810	323.6894734	965.8858922	-1.5772	1.79E-24	2.33E-22
AT1G15820	4160.554248	11855.3268	-1.5107	1.27E-23	1.54E-21
AT3G61060	157.520806	626.6139043	-1.992	2.13E-23	2.55E-21
AT2G05510	6.739123461	120.0496024	-4.1549	2.46E-23	2.93E-21
AT3G62410	33.5978069	345.1387969	-3.3607	3.74E-23	4.40E-21
AT5G64110	70.22614633	234.1119946	-1.7371	1.24E-22	1.43E-20
AT1G25440	149.9847633	553.681224	-1.8842	1.59E-22	1.82E-20
AT5G52250	115.4537079	329.487717	-1.5129	2.17E-22	2.46E-20
AT5G44190	299.7471579	967.8724995	-1.6911	2.28E-22	2.57E-20
AT4G16690	23.11479862	141.2752815	-2.6116	5.88E-22	6.54E-20
AT3G27690	285.338145	2660.480834	-3.2209	8.97E-22	9.92E-20
AT3G12910	12.19666174	87.78489908	-2.8475	1.15E-21	1.26E-19
AT3G62040	85.28019462	257.6694059	-1.5952	3.41E-21	3.64E-19
AT3G19850	6.075830301	66.8582964	-3.46	3.89E-21	4.14E-19
AT4G37925	167.9387122	491.4009594	-1.549	1.22E-20	1.26E-18
AT1G75460	24.99431177	158.8590718	-2.6681	1.72E-20	1.77E-18
ATCG00490	103.4831145	328.9554021	-1.6685	9.22E-20	9.17E-18
AT5G03545	207.0375357	591.0757413	-1.5135	1.35E-19	1.31E-17
AT5G38430	418.7069258	1695.628037	-2.0178	1.98E-19	1.89E-17
AT5G58260	88.24947039	252.2788589	-1.5154	2.65E-19	2.50E-17
AT3G07350	29.40148975	124.1541186	-2.0782	6.15E-19	5.54E-17
AT3G16250	87.75077717	303.7668789	-1.7915	7.24E-19	6.50E-17
AT1G70760	53.08177113	175.7726767	-1.7274	1.08E-18	9.42E-17
AT3G20470	111.2375014	531.1520195	-2.2555	1.07E-18	9.42E-17
AT2G22980	14.72833646	86.54742605	-2.5549	1.11E-18	9.64E-17
AT5G59750	34.28051456	132.0922598	-1.9461	2.72E-18	2.26E-16
AT1G32450	442.9776518	1590.968524	-1.8446	4.14E-18	3.39E-16
AT1G54740	80.89496962	251.328415	-1.6355	4.56E-18	3.72E-16
AT4G00970	15.7583327	98.06710077	-2.6377	7.51E-18	6.06E-16
AT5G47240	25.72249534	111.4158721	-2.1149	7.97E-18	6.40E-16
AT1G68520	54.33128733	493.9451519	-3.1845	1.68E-17	1.31E-15
AT3G17050	87.20195877	698.1515308	-3.0011	2.06E-17	1.60E-15
AT3G21670	59.29993819	180.8947754	-1.609	2.79E-17	2.16E-15
AT1G49130	9.561954035	67.48213381	-2.8191	4.14E-17	3.15E-15
AT1G66100	34.30420208	127.2185222	-1.8909	4.58E-17	3.46E-15
AT3G22060	134.6113724	531.3850995	-1.981	6.06E-17	4.53E-15
AT3G14770	22.41953503	126.8727377	-2.5006	7.26E-17	5.36E-15
AT4G11470	5.766684289	67.56502344	-3.5505	8.59E-17	6.31E-15
AT1G76080	329.5553264	964.0469161	-1.5486	9.71E-17	7.10E-15
AT3G54580	2585.833658	13475.24444	-2.3816	1.39E-16	1.00E-14
AT5G06690	37.42552186	131.589356	-1.8139	1.78E-16	1.28E-14
AT4G19170	11.55278308	101.84969	-3.1401	1.92E-16	1.37E-14
AT2G40610	291.0295497	1222.458456	-2.0705	3.53E-16	2.50E-14
AT1G15040	14.801035	115.2309164	-2.9608	6.36E-16	4.39E-14
AT4G34560	27.87564897	108.4532198	-1.96	7.78E-16	5.34E-14
AT3G55240	4.514695632	47.78434002	-3.4038	1.06E-15	7.09E-14
AT3G49940	64.79229557	252.3954208	-1.9618	2.32E-15	1.53E-13
AT2G37980	33.77116453	118.9305806	-1.8163	2.69E-15	1.76E-13
AT5G59080	43.70952889	139.3075756	-1.6723	2.83E-15	1.84E-13
AT1G03130	649.687562	3016.609224	-2.2151	4.49E-15	2.85E-13
AT3G22420	52.30922578	154.9769285	-1.5669	5.20E-15	3.29E-13
AT3G22540	26.93280632	101.3248137	-1.9116	1.09E-14	6.64E-13
AT3G15630	62.88370774	311.8540725	-2.3101	1.98E-14	1.18E-12
AT1G70880	18.54634416	81.4343432	-2.1345	2.43E-14	1.43E-12
AT4G27710	52.26137596	158.7406206	-1.6029	2.61E-14	1.53E-12
AT3G04530	49.13910663	148.0810615	-1.5914	3.83E-14	2.21E-12
AT2G16005	0.973863512	30.39783945	-4.9641	4.03E-14	2.32E-12
AT3G06750	65.38215228	233.5113863	-1.8365	4.55E-14	2.60E-12
AT3G21870	3.220079739	39.24775655	-3.6074	4.54E-14	2.60E-12
AT4G02270	120.1368017	384.7951091	-1.6794	5.99E-14	3.39E-12
AT1G78230	30.78610792	140.2505725	-2.1877	1.00E-13	5.52E-12
AT4G13500	44.56047014	141.8730911	-1.6708	1.45E-13	7.95E-12
AT2G25900	45.25905719	181.8965277	-2.0068	1.49E-13	8.16E-12
AT3G19800	54.53080493	172.9606457	-1.6653	1.64E-13	8.95E-12
AT5G24160	115.388131	335.3595429	-1.5392	2.05E-13	1.10E-11
AT5G18670	291.693957	993.3158086	-1.7678	2.27E-13	1.22E-11
AT1G78450	37.8208719	117.7395305	-1.6383	3.49E-13	1.84E-11
AT1G66760	73.37706264	304.2865264	-2.052	5.80E-13	3.00E-11
AT3G26165	7.701855384	50.23357457	-2.7054	7.47E-13	3.79E-11
AT1G14150	28.2013608	139.0889022	-2.3022	1.09E-12	5.49E-11
AT4G33880	37.12845699	113.6213898	-1.6136	1.47E-12	7.29E-11
AT5G15600	40.72257316	119.6094655	-1.5544	2.36E-12	1.14E-10
AT2G34620	94.11671521	269.4704771	-1.5176	4.75E-12	2.22E-10
AT5G65690	18.69601427	102.5795754	-2.4559	5.53E-12	2.57E-10
AT1G77145	10.30031964	54.07677311	-2.3923	5.81E-12	2.69E-10
AT2G44380	66.74783073	248.435937	-1.8961	7.65E-12	3.49E-10
AT1G22690	18.31416972	71.4075936	-1.9631	1.26E-11	5.65E-10
ATCG00350	36.35802241	108.76002	-1.5808	1.31E-11	5.87E-10
AT1G70820	30.70676245	96.95768358	-1.6588	1.33E-11	5.93E-10

AT1G52230	574.6726562	2304.399215	-2.0036	1.34E-11	5.93E-10
AT5G65800	12.2470971	57.10499096	-2.2212	1.81E-11	7.89E-10
AT2G33830	192.0678394	834.4220827	-2.1192	4.17E-11	1.75E-09
AT1G22630	48.40026624	162.8974294	-1.7509	4.50E-11	1.88E-09
AT3G49110	7.647621779	44.35839668	-2.5361	7.67E-11	3.10E-09
AT1G61080	21.55556307	74.98726889	-1.7986	7.86E-11	3.16E-09
AT5G44585	29.24581209	89.3947378	-1.612	1.20E-10	4.77E-09
AT3G51540	16.13141956	62.44264807	-1.9527	1.53E-10	5.94E-09
AT4G15740	6.151852304	39.35352787	-2.6774	1.69E-10	6.50E-09
ATCG00020	55.16898623	184.2736674	-1.7399	2.53E-10	9.51E-09
AT5G61440	78.04268813	307.4000682	-1.9778	3.52E-10	1.30E-08
AT2G32550	5.454214816	36.888819	-2.7577	3.97E-10	1.45E-08
AT4G20820	26.2579068	81.53700381	-1.6347	5.10E-10	1.84E-08
AT1G14960	623.1880881	1914.13497	-1.619	6.13E-10	2.19E-08
AT1G49500	5.797230376	37.11398624	-2.6785	6.32E-10	2.25E-08
AT1G74458	24.0266204	77.09596026	-1.682	6.53E-10	2.32E-08
AT4G08620	10.20488314	50.32512834	-2.302	7.35E-10	2.58E-08
AT3G50560	23.82214336	74.94860078	-1.6536	1.24E-09	4.23E-08
AT5G61160	4.139234866	31.83106452	-2.943	1.67E-09	5.60E-08
AT3G01440	29.07931303	95.22939363	-1.7114	2.29E-09	7.49E-08
AT1G15890	18.08885383	62.46304744	-1.7879	2.33E-09	7.58E-08
AT5G45820	6.440159478	36.9339852	-2.5198	2.65E-09	8.56E-08
ATCG00340	41.04237598	127.5896311	-1.6363	3.14E-09	1.00E-07
AT2G47560	28.49299143	82.0612517	-1.5261	3.36E-09	1.07E-07
AT3G59930	4.449330438	31.82704875	-2.8386	5.24E-09	1.62E-07
AT5G04960	131.9554642	474.5343663	-1.8465	9.90E-09	2.98E-07
AT4G12830	14.38437134	52.32930516	-1.8631	1.48E-08	4.38E-07
AT3G14260	49.80925835	144.1806807	-1.5334	1.91E-08	5.58E-07
AT4G20450	5.058864773	31.15528613	-2.6226	2.44E-08	7.01E-07
AT2G43920	5.432426418	31.91427045	-2.5545	2.65E-08	7.58E-07
AT3G62550	4.470644056	29.06451599	-2.7007	3.48E-08	9.74E-07
AT4G33666	9.937414802	50.51316512	-2.3457	7.04E-08	1.88E-06
AT4G21445	8.363249423	44.68405851	-2.4176	8.43E-08	2.21E-06
AT3G05730	71.11085858	268.5423177	-1.917	9.23E-08	2.40E-06
AT1G12010	13.81155523	48.27271422	-1.8053	9.25E-08	2.40E-06
AT2G18180	0.962731923	17.18917547	-4.1582	1.23E-07	3.15E-06
AT2G39510	6.415997179	106.7425745	-4.0563	1.34E-07	3.39E-06
AT4G25220	3.926949695	26.57724172	-2.7587	1.67E-07	4.16E-06
AT5G27290	19.07985649	66.41697776	-1.7995	1.71E-07	4.26E-06
AT3G28550	2410.772812	7943.735131	-1.7203	2.22E-07	5.44E-06
AT2G28990	18.30303813	54.93565905	-1.5857	2.61E-07	6.30E-06
AT5G06800	21.22225476	60.23063229	-1.5049	2.71E-07	6.51E-06
AT5G46270	21.16802116	60.16073465	-1.5069	2.73E-07	6.55E-06
AT1G50732	16.96389588	52.34198507	-1.6255	3.23E-07	7.68E-06
AT4G04330	5.444507568	28.90306458	-2.4083	3.51E-07	8.26E-06
AT2G26215	2.87706418	22.13899259	-2.9439	3.69E-07	8.66E-06
AT5G44417	12.80382217	44.14807539	-1.7858	3.94E-07	9.20E-06
AT2G47750	4.802053245	27.18962058	-2.5013	4.09E-07	9.52E-06
AT4G14250	1.294615893	17.20618745	-3.7323	4.45E-07	1.03E-05
AT4G36570	1.924989066	19.41540882	-3.3343	4.45E-07	1.03E-05
AT2G03310	5.112148817	27.66716461	-2.4362	4.55E-07	1.05E-05
AT5G24580	37.2539648	123.7449303	-1.7319	4.66E-07	1.07E-05
AT3G24310	11.26352634	40.64231351	-1.8513	5.78E-07	1.31E-05
AT1G23840	9.263464833	50.9730688	-2.4601	5.92E-07	1.34E-05
AT4G33730	21.52549177	66.2150043	-1.6211	6.17E-07	1.39E-05
ATCG00120	18.96300782	55.12833999	-1.5396	6.36E-07	1.43E-05
AT4G12330	13.7966254	45.42634715	-1.7192	6.51E-07	1.45E-05
AT5G49360	377.2084368	1454.352896	-1.9469	7.34E-07	1.62E-05
AT3G22150	44.69578375	149.103877	-1.7381	8.36E-07	1.83E-05
AT3G48320	17.94060807	52.14650971	-1.5393	1.08E-06	2.31E-05
AT4G24700	17.44877341	50.82956984	-1.5425	1.21E-06	2.55E-05
AT5G26320	4.503564043	25.14740404	-2.4813	1.22E-06	2.57E-05
AT2G28780	0.973388732	15.08355939	-3.9538	1.25E-06	2.64E-05
AT5G28145	3.87271609	32.50904436	-3.0694	1.29E-06	2.71E-05
AT1G61810	2.246691007	18.90045344	-3.0725	1.70E-06	3.47E-05
AT4G40090	174.3083354	513.5582123	-1.5589	1.76E-06	3.58E-05
AT1G32928	46.10667498	144.1027473	-1.6441	2.02E-06	4.03E-05
AT5G24420	0.641504762	17.16999746	-4.7423	2.29E-06	4.52E-05
AT1G01190	2.87753896	24.83442212	-3.1094	2.61E-06	5.08E-05
AT4G38390	13.72345208	42.68732447	-1.6372	2.98E-06	5.72E-05
AT5G52790	26.82291477	77.95890159	-1.5392	3.39E-06	6.45E-05
AT5G18840	1.925463846	17.06639217	-3.1479	3.83E-06	7.22E-05
AT5G66260	3.176502943	20.6414233	-2.7	3.88E-06	7.30E-05
AT5G05965	3.807825676	22.14671204	-2.5401	4.60E-06	8.52E-05
AT2G05540	5.432901198	72.0798041	-3.7298	5.09E-06	9.32E-05
AT4G23280	11.31090138	42.14976829	-1.8978	5.72E-06	0.00010342
AT3G46900	8.023082545	30.75815361	-1.9387	6.76E-06	0.00012022
AT3G54590	588.107688	2958.604845	-2.3308	7.15E-06	0.00012628
AT2G42870	14.09796329	41.79626432	-1.5679	7.76E-06	0.00013633
AT5G61550	14.41966523	42.0848311	-1.5453	8.92E-06	0.00015531
AT3G48940	7.369021853	29.06172157	-1.9796	9.15E-06	0.00015875

AT5G50915	5.830625143	26.75444833	-2.1981	1.18E-05	0.00019989
AT2G47050	10.235904	34.1535	-1.7384	1.52E-05	0.00024998
AT5G49740	15.4138928	53.82313535	-1.804	1.64E-05	0.00026718
AT5G44572	11.24316228	35.51682743	-1.6595	1.67E-05	0.00027277
AT3G22210	13.0800482	41.43779991	-1.6636	1.83E-05	0.00029489
AT5G67400	129.5249233	367.0832546	-1.5029	2.06E-05	0.00032786
AT5G38310	12.7945897	37.66327765	-1.5576	2.32E-05	0.00036577
AT5G06640	447.5908341	2300.82858	-2.3619	2.48E-05	0.0003886
AT5G62360	3.551014149	19.25458579	-2.4389	2.62E-05	0.0004063
AT2G38820	15.97937555	51.70763378	-1.6942	3.47E-05	0.00052115
AT1G76110	9.61571286	31.4113666	-1.7078	3.53E-05	0.00052785
AT3G12540	10.62249636	33.02738712	-1.6365	3.66E-05	0.00054648
AT4G13390	291.6064272	1085.861491	-1.8967	3.72E-05	0.00055439
AT2G36120	590.5301207	1868.423441	-1.6617	3.95E-05	0.00058377
AT5G59340	1.603761905	13.7220817	-3.097	4.69E-05	0.00067965
AT1G42560	0	7.987920447	#NAME?	5.01E-05	0.00072251
AT2G29090	9.018259675	29.35091673	-1.7025	5.11E-05	0.0007343
AT5G06630	133.3683531	550.5735099	-2.0455	5.17E-05	0.00074164
AT2G20570	57.64289224	163.2896099	-1.5022	5.57E-05	0.00079326
AT4G11521	9.051654443	29.18729929	-1.6891	6.30E-05	0.00088155
AT5G43230	8.642798909	29.10038968	-1.7515	7.09E-05	0.00097776
AT1G51880	11.20929274	32.46171212	-1.534	9.39E-05	0.0012537
AT4G19680	29.9211864	91.783956	-1.6171	0.00010817	0.00142
AT1G29720	0.641504762	22.26145959	-5.1169	0.00019447	0.0023961
AT1G53080	1.283959084	11.23697346	-3.1296	0.00021928	0.0026527
AT1G23720	1207.416791	3552.066006	-1.5567	0.00022684	0.0027335
AT5G42510	37.76758785	116.7485646	-1.6282	0.00024313	0.0029011
AT5G39000	6.728466652	22.9889023	-1.7726	0.00024546	0.0029236
AT3G05640	10.53439321	30.00350135	-1.51	0.00024654	0.0029334
AT1G61950	1.571791478	11.95791807	-2.9275	0.00026267	0.0031002
AT4G16240	1.283009524	11.00995648	-3.1012	0.00030291	0.0035018
AT4G29180	19.86417279	62.87470961	-1.6623	0.00031897	0.0036561
AT5G47450	75.24508251	285.7002804	-1.9248	0.00033717	0.0038434
AT4G13900	5.532135941	19.85058106	-1.8433	0.0003889	0.0043427
AT5G40860	8.654405278	25.8600008	-1.5792	0.00039654	0.004408
AT4G08410	90.44114281	360.280194	-1.9941	0.0004497	0.0049061
AT2G25470	3.20989771	15.10057137	-2.234	0.00047744	0.0051676
AT2G24980	221.3791667	1054.443373	-2.2519	0.00050576	0.0054254
AT4G13570	5.145543585	18.84756778	-1.873	0.00052775	0.0056113
AT5G10570	8.343360146	24.850448942	-1.5746	0.00053165	0.0056502
AT5G54790	4.161023264	16.99370011	-2.03	0.00058603	0.0061331
AT2G35890	3.551488929	15.04335364	-2.0826	0.00083302	0.0082617
AT1G26240	2.502078194	12.99495529	-2.3768	0.00085292	0.0084156
AT1G13700	7.990162558	23.34086861	-1.5466	0.0009005	0.0088006
AT4G28530	4.504513603	16.82019718	-1.9008	0.00096618	0.0093352
AT3G62680	244.6558151	889.428877	-1.8621	0.00097589	0.0094106
AT4G13493	5.732339961	19.1995341	-1.7439	0.00098236	0.0094582
ATCG00730	9.979567257	28.40634254	-1.5092	0.0010091	0.0096758
AT1G07450	1.925938626	11.478208	-2.5753	0.001026	0.0097904
AT1G12610	5.486660023	18.64157855	-1.7645	0.0010297	0.0098215
AT5G24313	10.06909475	32.79666646	-1.7036	0.001069	0.010134
AT5G65158	0.33188397	6.847277927	-4.3668	0.001093	0.010318
AT1G34047	2.235084638	11.93255825	-2.4165	0.0011205	0.010557
AT1G65484	7.050168593	21.25443054	-1.592	0.0011514	0.010791
AT3G23230	4.802053245	17.26742095	-1.8463	0.0011698	0.010942
AT3G60650	1.251039097	9.74157021	-2.961	0.0011856	0.011073
AT2G34180	5.057915212	22.86395296	-2.1765	0.0012849	0.011827
AT1G02570	3.231211328	15.13211299	-2.2275	0.0012944	0.011903
AT1G79700	42.36257851	127.2652218	-1.587	0.0013096	0.012027
AT2G37370	3.453678527	15.11943308	-2.1302	0.0013371	0.012252
AT4G33720	0.973388732	19.72531963	-4.3409	0.0013806	0.01259
AT4G08400	58.32939814	194.5484887	-1.7378	0.0014576	0.013209
AT3G05770	0.962731923	8.535362119	-3.1482	0.0014682	0.013266
AT2G05160	5.765734729	30.20917429	-2.3894	0.0014855	0.013383
AT1G58037	4.86789322	16.71225982	-1.7795	0.0015237	0.013662
AT2G29010	16.36739225	49.7733546	-1.6045	0.001566	0.013946
AT4G37540	0.320752381	6.469951798	-4.3342	0.0016638	0.014689
AT4G09530	3.219604959	13.4505269	-2.0627	0.0019256	0.016736
AT4G13440	3.817532924	14.41550046	-1.9169	0.0023376	0.019572
AT2G42140	0.652636351	7.146358577	-3.4529	0.0024185	0.020121
AT1G29110	4.813184835	16.34481918	-1.7638	0.0024278	0.020185
AT1G61300	6.041485973	18.79035005	-1.637	0.0024681	0.020399
AT1G74830	6.397057462	18.83272184	-1.5578	0.0026591	0.021648
AT5G12270	2.267529845	10.93789281	-2.2701	0.0027321	0.022111
AT4G30320	9.8396044	27.98727301	-1.5081	0.0027673	0.022315
AT1G68110	4.183286442	14.78447874	-1.8214	0.0028259	0.022669
AT5G54585	1.914807037	19.69901514	-3.3629	0.0030806	0.024395
AT3G28560	3.573277327	15.19645721	-2.0884	0.0034319	0.026588
AT3G28220	2.866407371	12.04049561	-2.0706	0.0034897	0.027001
AT4G12320	0.320752381	5.86745843	-4.1932	0.0036331	0.027962
AT5G45830	0.310095572	5.869624463	-4.2425	0.0036425	0.028025

AT5G07650	4.460936807	14.70406723	-1.7208	0.0043741	0.032587
AT4G21370	0	4.429901292	#NAME?	0.004625	0.034147
AT5G17590	3.839796103	13.4505269	-1.8086	0.0049958	0.036427
AT2G12460	4.847054383	15.11325128	-1.6406	0.0050682	0.036843
AT5G35190	142.2418035	637.4500434	-2.164	0.005198	0.037638
AT5G59260	0.310095572	5.557863905	-4.1637	0.0053889	0.038642
AT4G10510	3.231211328	12.14626694	-1.9104	0.0056156	0.039959
AT4G37610	43.3492096	268.3790039	-2.6302	0.0058314	0.04118
AT2G31540	3.87224131	13.16412616	-1.7654	0.0063646	0.044224
AT4G14280	4.813184835	14.75262083	-1.6159	0.0064381	0.044659
AT5G23160	1.283484304	7.865137146	-2.6154	0.006459	0.044767

Supplemental Table 2E Up-regulated genes in the *max2*-G/*max2*-C comparison

Gene_id	readcount( <i>max2</i> -G)	readcount( <i>max2</i> -C)	log <sub>2</sub> FoldChange	pval	padj
AT1G26240	0.2977447	1645.93975	-12.433	9.34E-05	0.0041436
AT1G26390	0.2977447	543.7070336	-10.835	0.00046837	0.014754
AT2G30750	5.819094672	8531.311242	-10.518	0.00010927	0.004678
AT3G60120	0.5954894	303.9426045	-8.9955	6.44E-05	0.0031561
AT4G31970	4.634745743	2134.399828	-8.8471	3.64E-05	0.0019794
AT1G79680	0.307657075	113.435155	-8.5263	4.87E-05	0.0025111
AT1G26380	8.634320154	3084.810664	-8.4809	1.07E-05	0.00071458
AT3G26830	7.651842244	1776.253384	-7.8588	0.00010457	0.0045485
AT3G19615	0.307657075	56.37767541	-7.5177	0.00077251	0.021806
AT1G57630	0.605401775	108.4104295	-7.4844	0.0014689	0.035308
AT1G67980	1.233943237	160.7282274	-7.0252	0.00087702	0.023884
AT1G33030	0.307657075	32.52736697	-6.7242	0.00093261	0.025025
AT3G47340	2.467886474	234.2215565	-6.5685	0.00014604	0.0058429
AT1G15520	7.750998429	689.3672575	-6.4747	0.00047356	0.014836
AT5G38900	7.691524177	665.5583016	-6.4352	0.00064292	0.018844
AT4G00970	1.257082923	108.2107895	-6.4276	0.00056836	0.017102
AT3G48850	2.798683235	240.7864081	-6.4269	0.001766	0.04035
AT1G18970	5.86868898	446.9925684	-6.2511	0.00084202	0.023153
AT5G65600	2.196596396	163.4136783	-6.2171	0.00062927	0.018489
AT5G48430	3.056746002	204.5978395	-6.0647	0.0021746	0.046752
AT4G26530	4.618203497	308.5499596	-6.062	5.15E-07	5.14E-05
AT4G18990	0.2977447	19.56793242	-6.0383	0.00081963	0.022588
AT5G61160	0.2977447	17.7157004	-5.8948	1.45E-07	1.74E-05
AT2G15020	1.21080355	69.75740774	-5.8483	1.25E-08	2.14E-06
AT5G25250	8.224191957	453.6381104	-5.7855	0.0015139	0.036024
AT3G49110	2.454659163	129.2801491	-5.7188	0.00046981	0.014762
AT2G18660	6.775117959	308.4286098	-5.5085	1.13E-05	0.00074494
AT1G69930	12.93826914	558.3509344	-5.4315	0.0014501	0.035027
AT2G26560	47.7697358	2054.413425	-5.4265	0.0022208	0.047509
AT1G24145	2.147002087	92.25109491	-5.4252	1.69E-06	0.00014953
AT1G29720	0.307657075	13.18061606	-5.421	0.00014493	0.0058143
AT2G36770	3.969837284	169.2386942	-5.4138	0.00047401	0.014836
AT3G04210	1.862484698	77.47769372	-5.3785	7.01E-21	1.90E-17
AT3G55240	1.247170548	48.3396373	-5.2765	2.03E-15	1.65E-12
AT1G32960	1.214118486	44.19258578	-5.1858	0.0017623	0.04035
AT1G26420	17.70543441	611.0564231	-5.109	0.0018071	0.041141
AT5G24160	21.4304038	722.1375501	-5.0745	0.00020169	0.0076087
AT3G23550	0.641768773	20.93606492	-5.0278	3.95E-08	5.82E-06
AT2G05540	1.554827623	50.6308009	-5.0252	0.0001221	0.0050676
AT3G16530	140.8255747	4555.515993	-5.0156	0.00032485	0.01098
AT3G14620	35.13580881	1032.13606	-4.8765	0.00025231	0.008991
AT3G26230	8.627690282	228.3105781	-4.7259	0.00031792	0.010824
AT2G43620	12.41903995	323.5491401	-4.7034	0.00033462	0.011255
AT4G11890	0.926286162	23.26539382	-4.6506	2.97E-07	3.26E-05
AT1G66100	1.842659948	44.59761637	-4.5971	0.0014581	0.035152
AT4G23220	5.150871277	122.6347875	-4.5734	5.08E-05	0.0026022
AT3G48650	7.608845375	179.7369311	-4.5621	0.00079806	0.022144
AT3G48310	0.939513472	21.83777892	-4.5388	1.43E-05	0.00091277
AT1G23840	2.18668402	47.61352765	-4.4446	0.0016629	0.038751
AT3G26165	1.521775561	30.33107308	-4.317	1.49E-09	3.18E-07
AT1G22890	9.805474203	186.307992	-4.248	0.00035621	0.011767
AT2G21910	0.605401775	11.36914795	-4.2311	0.00015559	0.0061645
AT3G56710	6.169716184	112.5362839	-4.189	0.0011904	0.029876
AT1G74670	29.77999529	525.3680109	-4.1409	0.0012878	0.031735
AT3G62550	2.183369085	36.95662376	-4.0812	4.98E-06	0.00038021
AT3G09160	0.641768773	10.80248313	-4.0732	0.00022259	0.0081062
AT2G22990	40.68057461	631.1701683	-3.9556	9.32E-15	5.84E-12
AT3G60650	0.605401775	9.320847143	-3.9445	0.0010126	0.02656
AT4G18250	13.89100992	210.3453565	-3.9205	0.00011978	0.005014
AT3G47090	0.8932341	13.4140173	-3.9086	9.37E-05	0.0041436
AT1G10070	7.648527308	111.3075608	-3.8632	1.33E-13	7.07E-11
AT4G19170	6.530282503	92.97600756	-3.8316	3.59E-17	4.87E-14
AT3G21870	3.073288249	42.52361423	-3.7904	1.44E-05	0.00091345
AT5G05965	0.628541462	8.441647258	-3.7474	0.0019699	0.043538
AT3G50480	18.84025389	252.6291951	-3.7451	0.00072463	0.020776
AT3G15450	67.814407078	880.8925481	-3.6993	1.09E-09	2.45E-07
AT4G21650	1.554827623	19.93010436	-3.6801	4.08E-06	0.00031493
AT1G49130	4.009486786	50.28687877	-3.6487	1.52E-11	5.32E-09
AT5G42530	52.73214222	659.2322521	-3.644	6.53E-05	0.003185
AT3G22060	65.11795126	810.6769791	-3.638	1.55E-05	0.0009787
AT4G14450	2.78217342	34.58916921	-3.636	0.00037276	0.012227
AT4G11521	2.778858485	34.405769	-3.6301	1.17E-05	0.00076761
AT4G36850	10.81768924	130.9517445	-3.5976	2.17E-08	3.49E-06
AT2G34430	719.2917449	8580.220382	-3.5764	0.0017991	0.04105
AT1G68520	24.81448521	285.0455184	-3.5219	2.48E-06	0.00020518
AT5G45820	1.80629295	20.21052404	-3.484	5.73E-05	0.0028904
AT3G26280	2.517480782	27.95093012	-3.4728	1.88E-07	2.17E-05
AT3G55970	4.644658119	50.6707518	-3.4475	1.19E-09	2.62E-07
AT1G73870	15.12823566	164.7477304	-3.4449	2.41E-19	4.33E-16

AT2G43920	2.768946109	28.85666418	-3.3815	2.18E-07	2.48E-05
AT3G48320	5.514752532	57.4045891	-3.3798	2.76E-11	8.89E-09
AT3G26220	15.617939	162.4837292	-3.379	6.04E-08	8.30E-06
AT4G23170	8.707021717	89.20026501	-3.3568	0.0016861	0.038957
AT2G05520	483.5283951	4938.870177	-3.3525	0.0014769	0.035394
AT5G24210	18.05608835	181.3743362	-3.3284	4.86E-09	9.08E-07
AT5G14740	492.0162903	4933.082246	-3.3257	1.38E-19	2.81E-16
AT3G14770	10.52985691	102.4595264	-3.2825	6.20E-15	4.21E-12
AT1G21400	30.79880776	298.4842591	-3.2767	1.37E-21	4.18E-18
AT4G33666	11.97561598	111.059581	-3.2132	6.45E-08	8.72E-06
AT1G69730	8.333260518	76.54506134	-3.1994	2.00E-12	8.60E-10
AT2G25510	8.654144904	79.3460258	-3.1967	1.03E-12	4.74E-10
AT5G43450	89.96560252	805.0971779	-3.1617	8.95E-06	0.00061653
AT5G22530	3.351208198	29.96203821	-3.1604	0.0014198	0.034431
AT2G20670	118.2510404	1029.120985	-3.1215	4.15E-16	4.41E-13
AT4G16690	17.96994819	155.1358249	-3.1099	1.63E-12	7.23E-10
AT4G36110	2.792085796	23.80954452	-3.0921	6.54E-06	0.0004773
AT1G75490	2.117264961	17.93202902	-3.0823	6.37E-05	0.0031365
AT2G47750	3.685319895	29.91806726	-3.0212	0.00033474	0.011255
AT3G06070	43.3274037	340.2540929	-2.9733	1.69E-16	1.97E-13
AT3G27690	290.4606746	2215.373135	-2.9311	0.0020582	0.044882
AT2G39855	2.160229398	16.44458737	-2.9284	0.00020808	0.0077304
AT1G15380	11.17494062	84.68068768	-2.9218	1.97E-05	0.0012043
AT3G16120	3.394172635	25.63167119	-2.9168	1.19E-05	0.00078139
AT1G65800	1.855887259	14.00579486	-2.9158	0.00061933	0.018306
AT5G49740	5.901741042	43.63016545	-2.8861	2.91E-08	4.48E-06
AT3G62410	34.62013827	254.7512938	-2.8794	0.00015215	0.0060476
AT1G68190	26.16433816	191.9840026	-2.8753	2.59E-08	4.05E-06
AT4G00750	23.65652604	167.8320971	-2.8267	5.51E-15	3.85E-12
AT2G18700	123.762592	849.0700828	-2.7783	1.07E-19	2.38E-16
AT1G79700	15.4325778	101.9634514	-2.724	0.00070531	0.020332
AT3G01500	1044.422657	6880.473526	-2.7198	1.44E-09	3.10E-07
AT1G16420	3.099742871	20.1920498	-2.7036	0.00011979	0.005014
AT1G08900	27.63983435	174.9502958	-2.6621	4.38E-07	4.55E-05
AT1G07180	38.63932615	241.6753434	-2.6449	4.31E-15	3.10E-12
AT1G05675	80.56682759	495.4852013	-2.6206	0.00032206	0.010934
AT4G13900	2.497656031	15.3092477	-2.6158	0.00078755	0.02205
AT5G02160	52.00779194	315.9584036	-2.6029	0.0014149	0.034347
AT1G66970	32.60841565	195.6151385	-2.5847	7.02E-14	4.08E-11
AT4G27300	55.21349972	326.3085727	-2.5631	3.93E-06	0.00030429
AT2G28630	40.16162156	237.1356351	-2.5618	4.25E-10	1.02E-07
AT3G54890	1590.670634	9341.941225	-2.5541	1.07E-07	1.36E-05
AT2G39350	94.64991014	555.3908639	-2.5528	9.23E-06	0.00063221
AT4G23260	45.80824134	268.175984	-2.5495	0.00098213	0.025927
AT5G61270	13.42772877	77.4441569	-2.5279	1.86E-09	3.79E-07
AT4G04330	2.729264176	15.73350067	-2.5273	0.0010239	0.026628
AT5G52570	42.52654949	243.416466	-2.517	1.90E-11	6.29E-09
AT4G37980	34.32877972	190.0185466	-2.4686	9.31E-13	4.38E-10
AT2G41260	73.60638086	406.5222277	-2.4654	3.12E-15	2.31E-12
AT5G46490	6.146608929	33.4512111	-2.4442	8.11E-06	0.00057274
AT2G33070	8.756648457	47.54336687	-2.4408	7.31E-05	0.003437
AT1G66760	85.14577172	458.2227062	-2.428	8.97E-15	5.77E-12
AT3G19800	30.51125158	163.8775432	-2.4252	6.71E-12	2.60E-09
AT1G16260	22.88914646	122.7355827	-2.4228	1.09E-10	2.98E-08
AT2G05100	762.0510732	4062.101075	-2.4143	3.13E-07	3.40E-05
AT1G80440	593.5219822	3151.292228	-2.4086	1.75E-05	0.0010918
AT5G49730	2.778858485	14.69779891	-2.403	0.0017274	0.039761
AT5G54710	31.01743231	163.6115975	-2.3991	6.07E-09	1.10E-06
AT3G47250	59.73847819	312.672377	-2.3879	9.47E-14	5.38E-11
AT5G59080	21.26489978	110.7730762	-2.3811	0.0018312	0.041488
AT2G03310	4.006204282	20.63075694	-2.3645	0.00036823	0.012115
AT2G29290	58.27000201	297.3020461	-2.3511	2.38E-05	0.0014007
AT3G62740	3.68200496	18.68067261	-2.343	0.00078838	0.02205
AT2G05380	2186.825079	11089.75168	-2.3423	0.0011387	0.02879
AT5G48490	71.35066791	361.2000881	-2.3398	4.52E-07	4.66E-05
AT3G04000	24.98658667	126.3827141	-2.3386	0.00056829	0.017102
AT2G05070	656.6031197	3272.07295	-2.3171	3.80E-05	0.0020569
AT5G22500	580.2099845	2888.575034	-2.3157	8.27E-16	7.78E-13
AT1G21500	56.12309721	278.5580152	-2.3113	6.39E-08	8.68E-06
AT3G16220	26.14779592	129.5367179	-2.3086	3.88E-10	9.48E-08
AT3G05730	57.39309887	282.0782462	-2.2971	3.63E-11	1.12E-08
AT1G61300	4.707447306	23.02192262	-2.29	0.0002241	0.00814
AT3G19850	5.236832583	25.50028204	-2.2837	0.00021578	0.0079559
AT5G25980	90.96712492	436.2063007	-2.2616	1.59E-11	5.41E-09
AT2G34420	6970.157608	33349.60644	-2.2584	4.36E-08	6.39E-06
AT5G02020	153.8468155	735.816318	-2.2579	4.26E-14	2.54E-11
AT1G64370	88.19193907	421.5541429	-2.257	2.56E-13	1.31E-10
AT3G22142	28.35077847	135.2801015	-2.2545	3.78E-06	0.00029627
AT1G14950	6.841254514	32.55471416	-2.2505	7.78E-05	0.0036134
AT5G47590	9.66635994	45.88959764	-2.2471	3.06E-06	0.00024814
AT5G25190	48.82208776	231.4884733	-2.2453	1.62E-11	5.43E-09

AT5G64770	11.68446872	54.99090913	-2.2346	9.25E-07	8.73E-05
AT4G37610	39.63202501	185.9140742	-2.2299	0.0019529	0.043274
AT1G61810	6.798290077	31.65017711	-2.219	0.00057992	0.017351
AT4G35190	38.75837194	180.2841248	-2.2177	1.16E-10	3.12E-08
AT3G22500	10.55962647	49.0513126	-2.2157	1.88E-06	0.00016419
AT5G06860	24.02393352	111.1456174	-2.2099	0.0010822	0.027758
AT4G28490	30.36557231	140.0704125	-2.2056	0.0011132	0.028345
AT5G66640	7.281363549	33.50500776	-2.2021	0.00073202	0.020904
AT2G13360	972.4687497	4474.453663	-2.202	8.62E-15	5.70E-12
AT5G19190	33.57790996	154.4004186	-2.2011	3.08E-10	7.60E-08
AT3G52748	34.68606354	159.4743717	-2.2009	0.0009453	0.025233
AT1G80180	125.2675001	572.3552913	-2.1919	1.40E-10	3.64E-08
AT5G58120	53.38427836	242.0877002	-2.181	0.0019536	0.043274
AT1G73830	19.09454673	86.18232387	-2.1742	0.0021687	0.046707
AT3G45730	72.469124	325.5032049	-2.1672	0.00027578	0.0096032
AT5G10100	49.063397	219.705018	-2.1628	8.02E-11	2.28E-08
AT3G02150	12.69671618	56.62218407	-2.1569	1.43E-06	0.00012716
AT4G28520	230.8454998	1022.085223	-2.1465	1.24E-13	6.75E-11
ATCG00630	6.457548509	28.38098874	-2.1359	0.00016174	0.0063874
AT2G23240	6.17303112	27.06829877	-2.1326	0.00025689	0.0091143
AT5G06690	20.24936981	88.72834555	-2.1315	4.96E-08	7.18E-06
AT1G35710	48.21653957	210.7769169	-2.1281	1.89E-10	4.76E-08
AT1G79040	2692.734851	11767.9332	-2.1277	3.81E-14	2.33E-11
AT4G27360	6.4079542	27.82760092	-2.1186	0.00026237	0.0092549
AT4G01390	14.00007848	60.45198735	-2.1104	1.36E-06	0.00012269
AT2G43520	6.484003131	27.91136321	-2.1059	0.00025997	0.0091994
AT5G54740	108.1332941	464.6159976	-2.1032	3.88E-12	1.61E-09
AT3G47470	3609.045986	15474.92018	-2.1002	5.50E-06	0.00041026
AT2G45170	124.2024082	529.3829758	-2.0916	5.27E-08	7.53E-06
AT1G17810	11.42309101	48.62125398	-2.0896	6.54E-06	0.0004773
AT1G20160	17.3314295	73.64634909	-2.0872	0.0023315	0.049604
AT1G75100	60.08599605	252.6243828	-2.0719	1.29E-10	3.43E-08
AT4G38560	5.895111171	24.77451673	-2.0713	0.00079029	0.022059
AT5G57240	187.0540354	782.115567	-2.0641	2.61E-12	1.10E-09
AT5G02760	104.7095632	436.9569697	-2.0611	5.44E-06	0.00040699
AT3G21370	17.39096861	71.26476488	-2.0349	1.29E-06	0.00011788
AT1G80920	339.3625007	1388.1193	-2.0322	1.47E-12	6.67E-10
AT3G15356	255.0043716	1042.964229	-2.0321	4.41E-12	1.77E-09
AT5G06870	51.8918498	211.7035192	-2.0285	1.30E-07	1.59E-05
AT2G39730	4134.456954	16552.58241	-2.0013	7.75E-13	3.71E-10
AT5G48485	216.2120543	865.3281243	-2.0008	5.89E-05	0.0029414
AT5G28770	28.13945007	112.5618058	-2.0001	0.00042799	0.013712
AT5G19120	158.0221473	631.0060355	-1.9975	0.00020322	0.0076385
AT5G62280	197.3539256	783.1421548	-1.9885	8.60E-12	3.23E-09
AT5G44572	8.545076344	33.83388712	-1.9853	0.00017348	0.0067853
AT1G21680	193.1278455	761.8116079	-1.9799	3.45E-05	0.0019017
AT1G03400	12.28987049	48.44307084	-1.9788	1.81E-05	0.0011227
AT3G29240	647.0657845	2538.030867	-1.9717	8.28E-08	1.08E-05
AT5G54270	2261.864202	8869.390325	-1.9713	0.00012818	0.0052485
AT1G05135	865.9877322	3391.146472	-1.9694	3.14E-05	0.0017788
AT2G40610	168.6110234	660.0725097	-1.9689	6.86E-05	0.003264
AT4G17245	155.9536973	608.7856059	-1.9648	4.64E-11	1.35E-08
AT3G05260	6.219310492	24.23580752	-1.9623	0.00075113	0.021301
AT1G29920	2193.134008	8444.476049	-1.945	3.91E-09	7.47E-07
AT5G04140	1530.427389	5886.899263	-1.9436	5.29E-12	2.09E-09
AT5G04190	14.55257101	55.84059224	-1.94	0.0012623	0.031231
AT2G23590	6.513772688	24.75484549	-1.9261	0.00087826	0.023884
AT2G25450	236.3755925	896.8342364	-1.9238	0.00073789	0.021023
AT4G10340	3305.966821	12501.14332	-1.9189	6.77E-09	1.20E-06
AT1G54870	32.42667796	122.267339	-1.9148	0.00012143	0.0050503
AT3G51895	172.6931145	648.2789648	-1.9084	6.97E-05	0.0033093
AT4G36040	520.3894447	1937.621814	-1.8966	4.01E-07	4.21E-05
AT1G31580	255.3916854	949.292755	-1.8941	1.10E-10	2.98E-08
AT3G60690	11.21793749	41.62404999	-1.8916	8.07E-05	0.003728
AT3G06750	42.986272	158.4060507	-1.8817	3.67E-08	5.46E-06
AT1G23130	69.0875124	253.5629408	-1.8758	3.83E-09	7.37E-07
AT5G14780	417.3037697	1531.44561	-1.8757	0.0010333	0.026832
AT1G75460	29.36326965	107.5348261	-1.8727	0.0013661	0.033362
AT1G61520	2034.028537	7448.123899	-1.8725	7.16E-08	9.51E-06
AT5G15850	7.711348928	28.23455683	-1.8724	0.00071297	0.020528
AT1G05510	7.790767987	28.44507979	-1.8702	0.00053217	0.016261
AT5G04380	40.43898922	147.7281939	-1.8691	5.85E-08	8.17E-06
AT3G09450	6.153206369	22.44602068	-1.867	0.0020461	0.044705
AT4G04040	62.79571162	227.3879165	-1.8564	2.29E-06	0.00019255
AT1G75830	106.694555	385.7022	-1.854	1.38E-09	3.02E-07
AT1G66725	44.15739361	158.6916027	-1.8455	6.02E-05	0.0029947
AT5G59750	28.39730156	101.9300543	-1.8438	5.49E-07	5.39E-05
AT4G16890	173.3552279	617.1588374	-1.8319	2.49E-09	4.90E-07
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AT1G03130	721.192693	2565.407785	-1.8307	0.0017313	0.039814
AT5G44120	386.2101254	1358.61299	-1.8147	1.56E-10	3.97E-08

AT5G47560	509.7446531	1789.965983	-1.8121	2.48E-05	0.0014337
AT2G39470	73.57378379	258.0375547	-1.8103	7.22E-05	0.0034145
AT2G33830	91.01135704	318.503268	-1.8072	0.00031657	0.010793
AT3G55500	9.735811431	33.96160054	-1.8025	0.00032472	0.01098
AT2G41100	1560.409111	5438.562147	-1.8013	0.00025006	0.0089236
AT1G23310	2237.248277	7762.017751	-1.7947	1.33E-10	3.50E-08
AT5G66400	99.08592095	340.6488688	-1.7815	5.66E-09	1.03E-06
AT1G76080	235.792388	808.9090306	-1.7785	8.32E-10	1.92E-07
AT2G39980	139.8593304	479.7611522	-1.7783	2.65E-09	5.18E-07
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AT2G30570	1406.834478	4788.77762	-1.7672	2.01E-10	5.02E-08
AT5G46270	9.600288248	32.62000222	-1.7646	0.00065408	0.019125
AT3G08940	2321.09819	7872.825295	-1.7621	5.42E-05	0.0027594
AT1G68250	60.45961083	204.1003926	-1.7552	5.59E-08	7.86E-06
AT3G54500	364.6692239	1227.704383	-1.7513	8.94E-10	2.04E-07
AT4G17840	242.3362879	814.955722	-1.7497	0.00018391	0.007135
AT3G15760	74.59615491	250.4858056	-1.7476	1.41E-07	1.71E-05
AT3G17070	19.19722913	64.33224053	-1.7446	1.83E-05	0.0011358
AT4G24230	145.3385935	485.2644158	-1.7394	7.26E-09	1.28E-06
AT4G39710	38.74867085	128.6661468	-1.7314	7.20E-07	6.91E-05
AT3G21670	48.53407659	160.7928322	-1.7281	2.97E-07	3.26E-05
AT3G05160	56.07678541	185.6571214	-1.7272	1.60E-05	0.0010035
AT2G35390	175.1641371	579.0196509	-1.7249	0.0016544	0.038627
AT1G03620	7.919817386	26.12037936	-1.7216	0.0020751	0.04521
AT4G24700	12.1640484	40.04442195	-1.719	0.00023713	0.008512
AT1G62630	13.00109075	42.78793385	-1.7186	0.00020342	0.0076385
AT4G27150	22.95200051	75.17595627	-1.7117	0.00020808	0.0077304
AT3G46780	944.4276422	3077.850627	-1.7044	8.83E-08	1.15E-05
AT3G04110	24.78164443	80.47153975	-1.6992	0.00024076	0.0086294
AT1G58561	10.71521812	34.78761218	-1.6989	0.00090523	0.024505
AT5G44585	19.87560861	64.32324767	-1.6943	8.42E-05	0.0038524
AT3G21780	48.0311135	154.7352632	-1.6878	7.70E-07	7.35E-05
AT3G12320	29.81985607	95.90009661	-1.6853	0.00016977	0.0066507
AT5G13330	81.8834172	262.0426488	-1.6782	0.00046057	0.014565
AT3G10740	172.3097495	550.7488486	-1.6764	1.77E-08	2.96E-06
AT1G70820	29.03907033	92.1710886	-1.6663	6.58E-06	0.00047894
AT4G28750	1688.791108	5357.556287	-1.6656	1.56E-09	3.28E-07
AT5G13370	203.783102	644.3168394	-1.6607	0.0001867	0.0071668
AT5G35660	101.5933105	321.1573715	-1.6605	5.48E-08	7.79E-06
AT1G08380	2289.149761	7231.591816	-1.6595	1.69E-09	3.53E-07
AT3G02380	144.0408863	454.845865	-1.6589	2.31E-08	3.66E-06
AT5G03490	38.4010557	120.8997104	-1.6546	0.0001956	0.0074316
AT1G65490	68.51527667	214.9125166	-1.6493	0.00021222	0.0078603
AT3G22640	75.4920701	236.4112912	-1.6469	3.98E-07	4.19E-05
AT3G07350	52.33855627	162.9327308	-1.6383	7.82E-05	0.0036278
AT5G64040	1304.73861	4043.584235	-1.6319	7.04E-06	0.00050942
AT1G13110	436.1827472	1347.768776	-1.6276	0.0011389	0.02879
AT1G56250	68.37699084	210.9487256	-1.6253	0.0015745	0.037294
AT2G40880	102.6824845	316.2576166	-1.6229	1.21E-07	1.51E-05
AT3G26650	1844.032739	5678.455962	-1.6226	4.53E-09	8.52E-07
AT3G49160	110.1557418	339.0744083	-1.6221	0.00019609	0.0074316
AT1G56520	14.7974389	45.41676507	-1.6179	0.00038125	0.01246
AT4G17810	32.63839649	99.9438345	-1.6145	9.06E-06	0.00062198
AT1G70700	50.09243043	153.0879729	-1.6117	1.91E-06	0.00016514
AT4G14540	42.45713043	129.5664195	-1.6096	0.0006441	0.018856
AT3G01060	74.50645611	227.0499398	-1.6076	4.60E-07	4.71E-05
AT3G22420	37.33931122	113.4213543	-1.6029	6.16E-06	0.00045484
AT1G11260	588.3033489	1785.81642	-1.602	1.32E-08	2.23E-06
AT1G65486	39.7377462	120.3189402	-1.5983	4.00E-05	0.0021417
AT1G52190	98.10354033	295.5971185	-1.5913	2.00E-07	2.30E-05
AT5G56100	39.07946761	117.7449431	-1.5912	0.00056104	0.016974
AT1G70290	242.943721	731.1260531	-1.5895	5.58E-08	7.86E-06
AT1G06430	385.5564304	1160.066531	-1.5892	5.91E-06	0.00043742
AT3G05370	16.02475226	48.09878454	-1.5857	0.00035729	0.011787
AT1G56510	145.7684492	436.7579173	-1.5832	0.00034552	0.011546
AT5G61660	11.37681164	34.0487943	-1.5815	0.0013063	0.032158
AT1G02610	17.51347576	52.40225323	-1.5812	0.00032521	0.01098
AT1G66910	14.14907269	42.22790753	-1.5775	0.00063273	0.018568
AT3G26740	496.9917452	1483.170771	-1.5774	1.97E-08	3.23E-06
AT5G38410	5013.130972	14955.63284	-1.5769	9.65E-09	1.68E-06
AT1G55960	114.4097388	341.2284266	-1.5765	1.77E-07	2.06E-05
AT2G28490	29.1580837	86.93998015	-1.5761	2.30E-05	0.001363
AT4G25140	41.98062197	124.8808832	-1.5728	0.00019361	0.0073721
AT5G59540	368.9390644	1096.219572	-1.5711	3.79E-08	5.61E-06
AT2G46220	154.6145527	459.1917435	-1.5704	1.30E-07	1.59E-05
AT5G56840	20.90083968	61.97899591	-1.5682	0.00011767	0.0049593
AT2G26690	195.1714822	577.8729947	-1.566	6.78E-08	9.08E-06
AT4G05180	1468.295352	4326.532005	-1.5591	1.47E-08	2.48E-06
AT3G55630	51.81279451	152.4421545	-1.5569	2.11E-05	0.0012773
AT1G22885	39.04310061	114.8262306	-1.5563	1.21E-05	0.00079043
AT1G31330	2045.573582	5994.122732	-1.551	8.71E-06	0.00060684

AT5G43740	24.52333795	71.69660909	-1.5477	7.51E-05	0.0035106
AT5G52450	76.16381972	222.6288628	-1.5475	0.00018655	0.0071668
AT1G55670	2149.883044	6270.962667	-1.5444	1.84E-08	3.03E-06
AT3G26180	89.86009261	260.6070631	-1.5361	9.74E-07	9.16E-05
AT3G50820	851.1252292	2467.888288	-1.5358	3.11E-08	4.75E-06
AT5G51720	126.5770048	366.9333214	-1.5355	2.90E-07	3.22E-05
AT3G22150	43.95904881	126.3376507	-1.5231	0.00012809	0.0052485
AT2G45850	44.38896933	127.3971637	-1.5211	8.86E-06	0.00061185
AT1G26945	62.78604296	180.0483296	-1.5199	3.46E-06	0.00027546
AT5G57660	143.8260965	411.5189128	-1.5166	4.24E-07	4.43E-05
AT5G44870	82.27420807	235.3798889	-1.5165	2.05E-06	0.00017517
AT4G28720	49.61905805	141.7223565	-1.5141	0.00027182	0.0094866
AT5G64840	735.2424965	2099.019551	-1.5134	7.51E-08	9.92E-06
AT2G16380	18.72759425	53.44280789	-1.5128	0.00045622	0.014478
AT1G69160	83.92463323	238.6054111	-1.5075	4.32E-05	0.0022906
AT5G49690	89.28114545	253.5312292	-1.5057	8.71E-05	0.003941
AT1G68670	129.3664095	366.8358927	-1.5037	9.20E-07	8.72E-05
AT3G47295	14.70156522	41.65259419	-1.5024	0.0010693	0.027457
AT4G23280	0	94.79652799	#NAME?	2.53E-06	0.00020867
AT5G40990	0	312.8616171	#NAME?	2.57E-05	0.0014836
AT2G46440	0	7.580697178	#NAME?	0.00034763	0.011566
AT1G61120	0	10.60203013	#NAME?	0.00035554	0.011767
AT5G24420	0	17.16170416	#NAME?	0.0016238	0.038196
AT5G65730	0	8.327555169	#NAME?	0.0016266	0.038196

Supplemental Table 2F Down-regulated genes in the *max2* -G/*max2* -C comparison

Gene_id	readcount( <i>max2</i> -G)	readcount( <i>max2</i> -C)	log <sub>2</sub> FoldChange	pval	padj
AT5G07990	2026.600877	143.4652647	3.8203	1.36E-34	3.33E-30
AT5G48880	1800.049218	141.3738257	3.6704	3.69E-32	4.50E-28
AT5G62210	220.2674303	9.452824875	4.5424	9.06E-29	7.38E-25
AT1G24020	3200.801436	386.8657802	3.0485	1.33E-24	8.15E-21
AT5G08640	1665.127968	205.5954056	3.0178	1.54E-23	7.52E-20
AT5G13930	11359.24485	1519.019159	2.9027	2.38E-23	9.71E-20
AT1G65060	886.8421306	105.4370281	3.0723	3.05E-23	1.07E-19
AT1G45191	358.5259299	40.70408619	3.1388	1.28E-20	3.13E-17
AT4G14090	1037.917415	159.5346473	2.7017	2.66E-19	4.33E-16
AT5G05270	1647.82621	258.157348	2.6742	2.49E-19	4.33E-16
AT3G48700	2337.016639	406.5684837	2.5231	4.15E-18	6.34E-15
AT4G12870	118.4819823	9.15474399	3.694	1.06E-17	1.52E-14
AT2G23910	559.9138794	95.12847022	2.5573	9.98E-17	1.28E-13
AT5G54060	1108.408584	202.0383461	2.4558	1.55E-16	1.90E-13
AT3G21730	96.48938488	7.742416114	3.6395	4.02E-16	4.41E-13
AT4G22880	3010.32299	599.1185978	2.329	4.58E-16	4.67E-13
AT3G55120	1097.413723	207.4367349	2.4034	6.60E-16	6.46E-13
AT3G29590	660.5380208	121.2326098	2.4459	9.06E-16	8.20E-13
AT4G40010	252.2471905	36.64029307	2.7833	1.05E-15	9.14E-13
AT4G39210	975.9630527	190.8670922	2.3543	1.31E-15	1.11E-12
AT1G30530	942.4980294	183.9956564	2.3568	2.92E-15	2.31E-12
AT4G15210	63.00044258	2.913046517	4.4348	3.02E-15	2.31E-12
AT5G42800	3370.983637	781.7044358	2.1085	1.11E-13	6.14E-11
AT2G28900	6126.726696	784.2376788	2.9658	1.66E-13	8.61E-11
AT4G27570	50.44308437	2.422916902	4.3798	5.64E-13	2.82E-10
AT3G58060	118.2173221	16.25396008	2.8626	6.37E-13	3.11E-10
AT5G47500	1432.619581	342.3221299	2.0652	1.99E-12	8.60E-10
AT5G20710	242.5614451	48.98141589	2.308	4.09E-12	1.66E-09
AT2G23000	282.0211898	60.57874802	2.2189	7.46E-12	2.85E-09
AT1G56650	321.7380872	71.76686996	2.1645	1.08E-11	3.99E-09
AT3G08860	282.4940905	61.71313494	2.1946	1.38E-11	4.96E-09
AT3G52180	796.9476053	181.1065608	2.1376	1.38E-11	4.96E-09
AT3G05190	397.5325338	93.23204282	2.0922	1.40E-11	4.96E-09
AT4G03210	1676.283654	438.0969378	1.9359	1.58E-11	5.41E-09
AT5G17220	875.7790694	224.7804376	1.9621	2.37E-11	7.73E-09
AT3G29320	1885.504353	503.9533683	1.9036	2.94E-11	9.33E-09
AT2G23010	501.1086906	122.1893824	2.036	3.16E-11	9.91E-09
AT4G28680	132.5018855	23.56026767	2.4916	3.72E-11	1.12E-08
AT2G41990	125.3795426	21.55153377	2.5404	3.82E-11	1.14E-08
AT1G06000	690.6472199	175.9094227	1.9731	4.13E-11	1.22E-08
AT3G62610	84.14943265	9.843316581	3.0957	5.26E-11	1.51E-08
AT5G23010	60.14239908	6.264800178	3.263	8.89E-11	2.50E-08
AT3G21560	2893.985474	821.3837165	1.8169	1.06E-10	2.96E-08
AT1G54010	9791.579162	2818.453209	1.7966	1.41E-10	3.64E-08
AT1G61800	2684.209551	187.1538706	3.8422	4.03E-10	9.74E-08
AT4G04750	356.2794306	91.22162784	1.9656	4.60E-10	1.09E-07
AT1G12064	227.5887519	55.94142716	2.0244	7.37E-10	1.73E-07
AT3G08770	229.4842238	56.65594532	2.0181	7.87E-10	1.83E-07
AT5G17050	1739.353319	523.401887	1.7326	1.05E-09	2.38E-07
AT1G15330	184.4302163	43.65267956	2.0789	1.12E-09	2.50E-07
AT4G01490	149.6980356	33.86279548	2.1443	1.44E-09	3.10E-07
AT1G03495	347.4000637	96.32589092	1.8506	1.75E-09	3.63E-07
AT1G03940	347.8864197	96.15314927	1.8552	1.84E-09	3.79E-07
AT1G35290	99.92010336	19.20799495	2.3791	2.26E-09	4.53E-07
AT1G48660	584.0859295	171.4855029	1.7681	2.24E-09	4.53E-07
AT3G22840	4983.07428	1231.859192	2.0162	2.47E-09	4.90E-07
AT1G60090	348.7414666	98.83458014	1.8191	2.89E-09	5.62E-07
AT3G21720	92109.89629	28950.31178	1.6698	5.56E-09	1.03E-06
AT1G62540	128.2738066	29.30923691	2.1298	5.66E-09	1.03E-06
AT4G09020	1164.190778	226.9604917	2.3588	6.72E-09	1.20E-06
AT5G16350	388.4027089	112.8335968	1.7834	6.70E-09	1.20E-06
AT1G26290	67.30812906	11.10921255	2.599	9.69E-09	1.68E-06
AT1G65340	165.6499723	41.83516155	1.9854	1.09E-08	1.88E-06
AT4G11460	52.29209805	7.314956116	2.8377	1.81E-08	3.01E-06
AT5G53210	134.1889863	32.37854105	2.0512	1.99E-08	3.25E-06
AT3G05600	138.2315575	33.85236136	2.0298	2.11E-08	3.42E-06
AT4G02850	89.01976775	18.5021253	2.2664	2.23E-08	3.56E-06
AT5G20740	269.2480188	78.72509563	1.774	2.49E-08	3.92E-06
AT2G41090	978.4367249	321.1033459	1.6074	2.66E-08	4.14E-06
AT5G45850	83.02836034	16.78365661	2.3065	2.74E-08	4.24E-06
AT5G57390	690.2805443	230.4211601	1.5829	3.36E-08	5.10E-06
AT3G14550	78.85005459	15.79416026	2.3197	3.57E-08	5.39E-06
AT1G62500	154.613285	40.61108877	1.9287	3.61E-08	5.41E-06
AT1G12805	377.6495472	49.3530692	2.9358	4.90E-08	7.13E-06
AT2G40840	2297.49074	795.4624644	1.5302	5.06E-08	7.28E-06
AT5G48100	50.63145194	7.712674911	2.7147	6.05E-08	8.30E-06
AT2G47880	94.56690607	21.5899235	2.131	6.25E-08	8.54E-06
AT5G06250	54.55500985	9.176425259	2.5717	8.24E-08	1.08E-05
AT4G34790	63.17616755	11.85406051	2.414	1.00E-07	1.30E-05
AT3G23730	535.5238218	178.1539122	1.5878	1.01E-07	1.30E-05
AT1G72570	92.11588711	21.77048083	2.0811	1.03E-07	1.31E-05
AT1G53070	292.2302272	91.45657043	1.6759	1.10E-07	1.39E-05
AT5G23940	329.8709881	105.2241111	1.6484	1.14E-07	1.43E-05
AT5G66816	28.12269654	2.12341458	3.7273	1.24E-07	1.54E-05

AT2G25530	309.0055573	100.1639786	1.6253	1.29E-07	1.59E-05
AT4G22230	97.11813762	23.09667222	2.0721	1.39E-07	1.69E-05
AT5G27410	800.7030584	281.0410428	1.5105	1.49E-07	1.78E-05
AT1G17260	93.77653322	22.94337738	2.0311	1.51E-07	1.80E-05
AT3G18200	126.2064121	33.9066267	1.8961	1.68E-07	1.96E-05
AT3G25795	48.21312734	7.98485936	2.5934	1.68E-07	1.96E-05
AT3G19710	64.92592775	10.9985192	2.5615	2.14E-07	2.44E-05
AT1G12130	116.7486022	32.15819237	1.8601	2.44E-07	2.77E-05
AT2G29670	1016.577736	237.0254937	2.1006	2.53E-07	2.85E-05
AT4G22770	172.0773778	52.25403573	1.7194	2.83E-07	3.16E-05
AT5G22020	526.5609153	184.0225548	1.5167	2.94E-07	3.25E-05
AT1G32900	3579.365071	848.1574274	2.0773	3.09E-07	3.37E-05
AT1G67100	396.1732716	137.6793316	1.5248	3.73E-07	3.96E-05
AT3G02410	140.7825454	41.00880557	1.7795	3.87E-07	4.10E-05
AT2G42610	61.61820385	13.28689247	2.2134	4.69E-07	4.75E-05
AT3G27400	160.9617974	48.76669651	1.7254	4.93E-07	4.94E-05
AT5G17040	65.86568493	14.39687515	2.1938	4.93E-07	4.94E-05
AT1G06475	47.62779403	8.327555169	2.5158	5.34E-07	5.29E-05
AT5G49330	135.135276	39.75309947	1.7653	5.41E-07	5.33E-05
AT3G19430	154.2959593	46.65860558	1.7255	5.56E-07	5.44E-05
AT4G17770	800.0999469	200.8962282	1.9937	7.16E-07	6.89E-05
AT5G42860	195.8437684	64.85316863	1.5945	1.42E-06	0.00012716
AT1G19540	240.6997239	84.41161968	1.5117	1.92E-06	0.00016605
AT1G60270	150.4394479	49.14455626	1.6141	2.00E-06	0.00017132
AT5G55340	50.22142104	9.506257375	2.4014	2.35E-06	0.00019576
AT1G31320	100.3005269	30.13642573	1.7347	2.73E-06	0.00022444
AT5G25090	66.702516	16.76920243	1.9919	3.39E-06	0.00027168
AT2G40220	70.98356901	18.92093677	1.9075	3.42E-06	0.00027312
AT4G38210	159.1159365	54.41358575	1.548	3.83E-06	0.0002988
AT1G01580	96.81373062	29.06517711	1.7359	3.89E-06	0.00030318
AT1G52240	178.8065574	61.87259959	1.531	3.91E-06	0.00030318
AT5G02180	99.61530622	30.25311644	1.7193	5.16E-06	0.00039023
AT2G32990	179.9347794	62.0943697	1.5349	5.27E-06	0.00039624
AT4G30650	183.4081538	64.51184511	1.5074	5.80E-06	0.0004306
AT2G27402	59.1599536	15.00594976	1.9791	7.97E-06	0.00056464
AT3G57780	151.1174049	52.85848186	1.5155	8.74E-06	0.00060691
AT3G29410	29.56842317	4.318147304	2.7756	9.90E-06	0.00067421
AT5G45860	17.24553305	1.019826143	4.0798	1.01E-05	0.00068404
AT3G28570	34.35544563	6.539189767	2.3934	1.10E-05	0.00073157
AT2G14060	70.18924739	19.75937274	1.8287	1.30E-05	0.00084173
AT4G31020	131.7681594	38.7427547	1.766	1.42E-05	0.00091259
AT4G13770	85.50588304	17.83202695	2.2616	1.87E-05	0.0011502
AT2G14210	56.03734719	14.92017744	1.9091	2.16E-05	0.0013033
AT1G60630	207.0290931	57.51285553	1.8479	2.27E-05	0.0013536
AT5G41460	79.49203465	25.3287374	1.65	2.34E-05	0.0013772
AT5G23020	355.2434912	90.03009751	1.9803	2.81E-05	0.0016073
AT3G61250	46.1190345	11.66865028	1.9827	3.25E-05	0.0018244
AT4G17920	15.67744569	1.042928848	3.91	3.26E-05	0.0018259
AT2G25220	80.81215047	26.4126546	1.6133	3.60E-05	0.001972
AT1G67481	16.86179462	1.433420554	3.5562	3.61E-05	0.0019745
AT2G33400	78.82381125	25.68368225	1.6178	4.03E-05	0.0021528
AT5G11440	16.80539159	1.349658259	3.6383	4.33E-05	0.0022906
AT2G46410	86.58803699	29.14372235	1.571	4.40E-05	0.002325
AT1G25425	56.19597763	16.4769272	1.77	5.49E-05	0.0027858
AT5G39220	23.1538391	3.46584575	2.74	5.83E-05	0.0029258
AT5G19100	76.38244426	25.40870407	1.5879	5.90E-05	0.0029414
AT1G80340	73.11102249	15.42476123	2.2448	6.50E-05	0.0031756
AT4G15480	93.25998512	26.81416902	1.7983	6.60E-05	0.0031995
AT5G45780	74.34113094	24.90068881	1.578	6.63E-05	0.0032098
AT5G63087	11.72411822	0.360161911	5.0247	6.72E-05	0.0032331
AT3G55110	63.34121658	18.68990972	1.7609	6.82E-05	0.0032515
AT1G28610	79.92499395	27.47525469	1.5405	7.03E-05	0.0033285
AT5G66800	79.26726765	27.29327592	1.5382	7.25E-05	0.003422
AT2G34490	256.7789453	80.50751565	1.6733	8.58E-05	0.0039078
AT2G21590	194.3268352	26.98311504	2.8484	8.80E-05	0.0039631
AT3G14190	77.08362243	26.4891898	1.541	8.79E-05	0.0039631
AT1G76620	33.73995263	7.971178883	2.0816	8.89E-05	0.0039864
AT1G34245	32.76400729	7.4059455	2.1454	9.27E-05	0.0041197
AT1G16400	46.28429481	9.946383855	2.2183	0.00010228	0.0044567
AT5G24990	72.42217835	24.90933734	1.5397	0.00010927	0.004678
AT5G63090	21.00680458	3.219775928	2.7058	0.00010993	0.0046857
AT1G65900	55.19684348	16.99074811	1.6998	0.0001271	0.0052307
AT1G63100	77.5863418	27.38046968	1.5027	0.00013764	0.0055799
AT4G28950	50.1450311	15.39443144	1.7037	0.00013979	0.0056389
AT1G80130	1096.296714	344.3119308	1.6709	0.00016432	0.0064682
AT5G19040	69.8716455	24.08415854	1.5366	0.0001667	0.006541
AT3G57510	23.11087467	4.171715393	2.4699	0.00017849	0.0069587
AT5G38100	50.56863032	13.11473941	1.9471	0.0001803	0.0070183
AT1G06830	49.14604337	15.13307459	1.6994	0.00019025	0.0072666
AT1G57560	70.55005742	17.80169715	1.9866	0.00022284	0.0081062
AT2G11810	43.97203241	12.99662727	1.7584	0.00022243	0.0081062
AT5G38020	588.8945645	170.453018	1.7886	0.00023214	0.008382
AT5G02190	60.2879968	20.62411845	1.5475	0.00027048	0.0094726
AT5G49870	44.01195806	13.02174	1.757	0.00027165	0.0094866
AT4G28430	32.94608599	8.824911874	1.9005	0.00034593	0.011546
AT3G46940	87.85135966	29.32712255	1.5828	0.00035038	0.011637

AT4G24260	29.68743654	7.512810499	1.9824	0.00035314	0.011713
AT1G14750	55.83219367	19.44198478	1.5219	0.00035621	0.011767
AT2G38160	40.56460003	12.10013033	1.7452	0.00041891	0.013492
AT4G26960	38.01409962	11.39225066	1.7385	0.00043161	0.01381
AT1G19830	16.7426024	2.483576491	2.753	0.0004428	0.014113
AT1G43800	3778.028141	504.2676439	2.9054	0.00045664	0.014478
AT2G24645	46.63875111	15.57842023	1.582	0.00047463	0.014837
AT2G19590	1481.688323	420.1601044	1.8182	0.00055175	0.016748
AT1G51870	40.98181309	9.799954044	2.0641	0.00068867	0.019923
AT2G43480	28.6652767	7.797858642	1.8782	0.00075589	0.021411
AT4G12890	8.95520454	0.383264616	4.5463	0.00077658	0.021845
AT5G66815	33.44220793	9.646883634	1.7935	0.00077615	0.021845
AT4G29150	24.66877351	3.182219044	2.9546	0.00078613	0.02205
AT5G50790	12.75950537	1.410317848	3.1775	0.00079391	0.022079
AT1G22260	31.43753774	9.122992759	1.7849	0.00087501	0.023872
AT1G23790	35.38402406	11.05519145	1.6784	0.00087837	0.023884
AT3G42725	19.9747648	4.330591455	2.2055	0.0009218	0.024817
AT2G18450	24.98330417	6.181037884	2.015	0.00096494	0.02568
AT1G35310	37.94796306	12.18389262	1.639	0.00097474	0.025815
AT2G17890	31.30177085	9.033424812	1.7929	0.00098028	0.025906
AT5G51850	42.16926568	14.5744697	1.5327	0.00098499	0.025943
AT4G04760	24.01398871	5.949422241	2.0131	0.0010112	0.026551
AT5G11930	50.69402984	15.73291208	1.688	0.0010207	0.026599
AT4G14819	33.13476213	10.26555952	1.6905	0.0010341	0.026832
AT4G08040	69.1642276	22.76483008	1.6032	0.0010483	0.02709
AT1G06420	30.15065283	8.801809169	1.7763	0.0010543	0.027186
AT1G27740	24.72852391	6.157935179	2.0057	0.0011072	0.028283
AT3G14540	32.41007085	9.639656544	1.7494	0.0011104	0.028304
AT1G73580	22.36970599	5.084676536	2.1373	0.0011189	0.028463
AT1G19630	66.52332968	10.86314272	2.6144	0.0011822	0.029701
AT2G34700	6.811484957	0	Inf	0.0012339	0.030747
AT3G51240	6.814799892	0	Inf	0.0012322	0.030747
AT2G26040	134.5340343	45.50491159	1.5639	0.0012526	0.031091
AT4G02160	25.75749247	7.214729614	1.836	0.0012695	0.031365
AT5G60880	35.50321628	11.31049839	1.6503	0.0013879	0.033793
AT4G12480	127.9362503	33.45403415	1.9352	0.0013946	0.033922
AT3G50230	30.96769158	9.454246312	1.7117	0.0014704	0.035308
AT2G44990	15.58157201	2.866841107	2.4423	0.0014726	0.035327
AT5G49270	91.19262305	25.16285868	1.8576	0.0015952	0.037675
AT1G76780	38.40133184	13.16616188	1.5443	0.0016486	0.038565
AT2G47540	80.21302087	23.15875325	1.7923	0.0016835	0.038941
AT3G03660	67.2554311	20.90715656	1.6857	0.0016838	0.038941
AT1G74420	26.43234574	7.666469501	1.7857	0.0019033	0.042646
AT5G61290	58.12420875	20.43231397	1.5083	0.0020344	0.044602
AT4G23560	401.8359617	131.5800063	1.6107	0.0020818	0.045275
AT5G26790	12.35269211	1.732922875	2.8335	0.002107	0.045742
AT1G04660	34.25932823	11.23396319	1.6086	0.002135	0.046145
AT4G34950	51.38536049	15.89901523	1.6924	0.0021815	0.046859

Supplemental Table 3 Changes in the level of expression of genes involved in SL-biosynthesis, -perception and -responsive that responding to glucose in the three plants

Function	Name	AGI	WT-G/WT-C		<i>hxk1</i> -G/ <i>hxk1</i> -C		<i>max2</i> -G/ <i>max2</i> -C	
			Fold change	Corrected p value	Fold change	Corrected p value	Fold change	Corrected p value
SLs biosynthesis	D27	AT1G03055	-1.7443	1.0000	-1.2028	0.2836	-2.4618	0.1195
	MAX1	AT2G26170	-0.2772	1.0000	0.2346	0.3217	0.2346	0.9059
	MAX3	AT2G44990	1.1704	1.0000	0.9318	0.0595	2.4423	0.0353
	MAX4	AT4G32810	0.4732	1.0000	-0.0785	0.9040	-0.0759	1.0000
SLs perception	D14	AT3G03990	-0.8256	1.0000	-0.5449	0.0010	-0.9184	0.0457
	MAX2	AT2G42620	-1.0328	1.0000	-1.1874	0.0000	-0.7258	0.2012
SLs responsive	STH7	At4G39070	-0.7826	1.0000	-0.6856	0.0034	0.0905	1.0000
	KUF1	At1G31350	-0.4385	1.0000	-0.3329	0.1373	-0.0496	1.0000
	IAA1	At4G14560	0.2534	1.0000	0.2923	0.2403	-0.6473	0.4073
	DLK2	At3G24420	-0.6350	1.0000	-0.4627	0.2395	-0.5799	0.6228

Supplemental Table 4 Changes in the level of expression of genes involved in root hair formation and elongation that responding to glucose in the three plants

AGI	Description	WT-G/WT-C		<i>hxk1</i> -G/ <i>hxk1</i> -C		<i>max2</i> -G/ <i>max2</i> -C	
		Fold change	Corrected p value	Fold change	Corrected p value	Fold change	Corrected p value
AT4G33880	RSL2	-0.20895	1	-1.6136	7.29E-11	1.0732	0.68361
AT4G02270	RHS13	-0.38028	1	-1.6794	3.39E-12	1.091	0.62662
AT4G25220	RHS15	-0.42579	1	-2.7587	4.16E-06	-0.13149	1
AT4G29180	RHS16	-0.53468	1	-1.6623	0.0036561	1.5061	0.15172
AT5G67400	RHS19	-0.22241	1	-1.5029	0.00032786	0.97917	0.62345
AT4G40090	AGP3	-0.53951	1	-1.5589	3.58E-05	1.0855	0.71975
AT3G62680	ATPRP3	-0.18535	1	-1.8621	0.0094106	1.4442	0.20796
AT5G06640	Proline-rich extensin-like family protein	-0.10477	1	-2.3619	0.0003886	1.2895	0.16544
AT5G35190	proline-rich extensin-like family protein	-0.48821	1	-2.164	0.037638	1.6505	0.050175
AT4G30320	CAP superfamily protein	-0.17471	1	-1.5081	0.022315	0.094209	1
AT4G33730	CAP superfamily protein	-1.2543	1	-1.6211	1.39E-05	0.51883	1
AT5G04960	Plant invertase/pectin methylesterase inhibitor superfamily	-0.48562	1	-1.8465	2.98E-07	1.3394	0.52725
AT3G48940	Remorin family protein	-2.0668	1	-1.9796	0.00015875	0.66926	0.9648
AT1G20340	DRT112	-1.8143	0.059836	-1.7233	1.93E-35	-1.2277	0.032666
AT3G12540	DUF547	-0.84194	1	-1.6365	0.00054648	2.0572	0.13568
AT5G24313	unknown protein	-0.17908	1	-1.7036	0.010134	1.0613	0.87133
AT5G43230	unknown protein	-0.75914	1	-1.7515	0.00097776	1.6348	0.26244

Supplemental Table 5 List of stress-related genes that specially activated by glucose in *hxk1* mutant.

Function	AGI	Description	<i>hxk1</i> -G/ <i>hxk1</i> -C		<i>max2</i> -G/ <i>max2</i> -C		WT-G/WT-C	
			Fold change	Corrected pvalue	Fold change	Corrected pvalue	Fold change	Corrected pvalue
Salicylic synthesis related	AT4G10500	DMR6-LIKE OXYGENASE 1	2.9312	0.024721	-4.7963	0.70107	-0.002	1
	AT5G55450	ATLTP4.4	1.6656	0.0055964	0.9988	0.54082	0.3957	1
	AT5G22570	WRKY38	1.538	0.0022159	1.1541	0.52938	-0.625	1
	AT1G33960	AIG1	5.3193	0.043121	-3.0305	0.7021	-10.5627	1
	AT2G14560	LURP1	7.4397	0.0018089	-10.1672	0.96574	-9.6772	1
	AT3G56400	WRKY70	2.1378	0.042689	-0.4243	0.9464	-0.3987	1
	AT2G30770	CYP71A13	5.4177	0.017849	-8.0126	0.30382	4.0701	1
Response to salicylic acid	AT1G73805	SAR DEFICIENT 1	1.5304	0.013365	-1.9282	0.36445	-1.8576	0.75223
	AT3G22231	PCC1	6.6013	0.0055046	0	NA	-9.9817	1
	AT5G11920	AtcwINV6	1.7922	0.00023337	-0.2762	0.99777	-0.8049	1
	AT1G19640	JMT	3.7332	0.0069447	1.3107	0.79252	1.0445	1
	AT5G01900	WRKY62	2.5536	0.017132	1.8789	0.91593	0.2519	1
	AT2G26400	ARD	3.4546	0.02029	1.9519	0.46531	0.3267	1
Response to jasmonic acid	AT5G03350	Legume lectin family protein	3.5857	0.007693	0.5231	0.92032	-0.4065	1
	AT1G54040	ESP	1.9526	6.17E-05	1.2008	0.27642	-0.6187	1
	AT4G12030	BAT5	1.8328	8.92E-05	0.9754	0.66318	-0.7921	1
	AT4G33905	Mpv17/PMP22 family protein	2.2759	5.36E-10	0.2167	1	1.616	1
Reponse to stress	AT5G24770	VSP2	1.5142	6.65E-08	0.0082	1	-1.1534	0.98533
	AT4G36950	MAPKKK21	2.0081	5.68E-05	0.437	0.9464	2.4207	1
	AT4G08870	Arginase/deacetylase superfamily protein	1.6467	2.09E-27	0.3568	0.83055	-0.0416	1
	AT3G03190	ATGSTF11	3.8234	0.0083961	2.5821	0.083289	0.0933	1
	AT1G71000	Chaperone DnaJ-domain superfamily protein	1.6308	0.031315	0.9373	0.7914	0.4358	1
	AT1G26540	Agenet domain-containing protein	1.8276	0.0073565	1.495	0.41376	1.0753	1
	AT5G03210	unknown protein	1.6905	8.55E-32	-0.0586	1	1.3116	1
	AT5G16990	Zinc-binding dehydrogenase family protein	1.6385	1.02E-28	1.3291	0.041918	0.5868	1
	AT4G35180	LHT7	4.1001	0.022166	-3.0117	0.74399	3.9329	1
	AT1G01520	ASG4	2.4768	1.46E-08	0.9712	0.15911	0.8666	1
	AT5G14200	ATIMD1	2.0277	0.0007449	1.2129	0.0051121	-0.1326	1
	AT1G45616	AtRLP6	2.0833	0.0019268	1.6508	0.56722	1.3088	1
	AT3G07150	unknown protein	1.5168	0.0029769	0.5217	0.82533	0.4233	1
	AT2G37770	AKR4C9	1.969	6.50E-06	-1.2386	0.65859	1.0494	1

Supplemental Table 6 List of stress-related genes that specially repressed by glucose in *max2* mutant

Biological function	AGI	Description	<i>max2</i> -C/WT-C		<i>max2</i> -C/ <i>hxk1</i> -C		<i>hxk1</i> -G/ <i>hxk1</i> -C		<i>max2</i> -G/ <i>max2</i> -C		WT-G/WT-C	
			Fold change	Corrected pvalue	Fold change	Corrected pvalue	Fold change	Corrected pvalue	Fold change	Corrected pvalue	Fold change	Corrected pvalue
Response to SA, JA, ABA, Ethylene stress hormones	AT3G12320	Unknown protein	0.77203	0.072014	1.0289	0.008561	-1.6853	0.00016977	0.15572	0.50045	-0.91517	0.077807
	AT3G21780	UGT71B6	0.3924	0.26304	1.069	0.00092382	-1.6878	7.70E-07	-0.056665	0.89472	0.73331	0.86944
	AT4G28520	CRU3	2.0487	1.58E-12	1.3589	9.74E-07	-2.1465	1.24E-13	-0.61051	0.063793	0.31454	0.96205
	AT4G23260	CRK18	0.70939	0.21234	0.66436	0.24247	-2.5495	0.00098213	-0.22487	0.61553	0.79712	0.83062
	AT5G66400	ATD18	1.1793	7.83E-05	0.88933	0.0018914	-1.7815	5.66E-09	0.31773	0.22024	-0.91309	0.041567
	AT5G44120	ATCRA1	2.2711	8.61E-15	1.7662	2.99E-10	-1.8147	1.56E-10	-0.38656	0.17554	0.70958	0.66189
	AT1G68670	Mby-like transcription factor family protein	0.86953	0.0038424	0.64086	0.030642	-1.5037	9.20E-07	-0.85291	2.24E-06	-1.5542	0.0010878
	AT1G05510	DUF1264	1.2362	0.013135	0.99705	0.02801	-1.8702	0.00053217	0.17664	0.64366	-0.20067	0.85448
	AT3G04110	ATGLR1.1	-0.15905	0.58699	-0.019568	0.90648	-1.6992	0.00024076	-1.3668	5.37E-10	-0.65609	0.21848
	AT5G65730	XTH6	-0.30088	0.79389	-0.23984	0.83598	#NAME?	0.0016266	-2.2316	0.0088383	-3.9448	0.0078662
Response to biotic and abiotic stress	AT5G22530	Unknown protein	0.73328	0.30424	2.2112	0.010591	-3.1604	0.0014198	0.9629	0.14311	1.8895	0.57256
	AT4G38560	PEARL14	0.55002	0.4041	1.1031	0.034112	-2.0713	0.00079029	1.0071	0.28074	2.423	0.48246
	AT4G23220	CRK14	0.61967	0.37233	1.1014	0.12505	-4.5734	5.08E-05	-0.3253	6.15E-05	-0.37584	0.49878
	AT5G24210	Alpha/beta-Hydrolases superfamily protein	0.61397	0.257	1.0707	0.010897	-3.3284	4.86E-09	0.49127	0.49625	-1.9792	0.0064783
	AT4G11890	Protein kinase superfamily protein	0.47404	0.3916	1.142	0.033558	-4.6506	2.97E-07	1.9584	0.087879	2.4587	0.52039
	AT5G40990	GLIP1	6.9071	0.0010588	7.3362	0.0006207	#NAME?	2.57E-05	0.49417	0.74931	-0.76555	0.53423
	AT3G60690	SAUR-like auxin-responsive protein family	-0.11068	0.79173	0.38443	0.36763	-1.8916	8.07E-05	-1.4992	8.31E-06	-1.3283	0.016279
	AT3G56710	SIB1	0.40142	0.19375	3.4355	0.0047452	-4.180	0.0011904	0.86152	0.10192	0.09429	0.81517
	AT4G16890	BAL	2.3187	0.066202	0.55232	0.057809	-1.8319	2.49E-09	-0.74305	4.66E-09	-0.68463	0.16977
	AT1G79680	ATWAKL10	5.3772	0.0022779	3.1945	0.02038	-8.5263	4.87E-05	0.12326	0.87503	1.1975	0.77873
Innate immune response	AT1G15520	ABC40	5.3772	0.0022779	5.5355	0.0017707	-6.4747	0.00047356	2.758	0.030708	5.7643	0.20997
	AT5G06860	ATPGIP1	0.48563	0.21187	1.493	0.015145	-2.2099	0.0010822	0.27611	0.45989	1.5545	0.60712
	AT5G13330	Rap2.6L	0.48563	0.21187	0.51781	0.17814	-1.6782	0.00046057	-0.30612	0.20885	1.2281	0.63164
	AT3G26830	PAD3	0.63119	0.41704	5.7294	0.0017833	-7.8588	0.00010457	1.0774	0.17949	3.0665	0.44265
	AT1G61120	TPS4	0.63119	0.41704	3.7989	0.003766	#NAME?	0.00035554	0.25153	1	#NAME?	0.0018775
	AT3G50480	HR4	0.71474	0.31952	1.477	0.074607	-3.7451	0.00072463	0.84025	0.29404	-0.26521	0.56102
	AT2G26560	PLA2A	1.8978	0.13598	2.6838	0.060031	-5.4265	0.0022208	-0.11366	0.81258	2.2529	0.5264
	AT3G15356	Legume lectin family protein	1.1536	6.86E-05	0.46731	0.09978	-2.0321	4.41E-12	-1.229	7.87E-25	0.20593	0.7707
	AT1G70700	JAZ9	0.07638	0.78242	0.080057	0.78864	-1.6117	1.91E-06	-1.2384	6.17E-09	-1.5869	0.0027787
	AT3G2150	PTF1	0.51982	0.18065	0.67134	0.082066	-2.1569	1.43E-06	-0.77376	0.0069737	-0.611	0.18266
Defense response	AT5G06870	ATPGIP2	0.32088	0.33559	0.57126	0.065943	-2.0285	1.30E-07	0.11427	0.45654	-1.2285	0.016353
	AT1G57630	Toll-Interleukin-Resistance (TIR) domain	3.7033	0.039983	4.3851	0.020495	-7.4844	0.0014689	5.2252	0.038987	3.7642	0.36875
	AT3G23550	MATE efflux family protein	0.92969	0.084532	0.94068	0.070861	-5.0278	3.95E-08	-1.0983	0.044389	-1.2592	0.079421
	AT5G65600	Concanavalin A-like lectin protein kinase E	2.1854	0.088878	2.7614	0.045488	-6.2171	0.00062927	-0.88626	0.014521	1.3941	0.71487
	AT3G48850	PTH3-2	3.7774	0.029961	5.1418	0.0073293	-6.4269	0.001766	2.1415	0.071598	4.3546	0.30826
	AT1G26380	FAD-binding Berberine family protein	2.8868	0.034702	3.2623	0.021424	-8.4809	1.07E-05	-0.9874	0.022995	1.1681	0.77287
	AT5G38900	Thioredoxin superfamily protein	4.4341	0.0807016	4.8393	0.0051945	-6.4352	0.00064292	1.5797	0.12174	2.3751	0.51035
	AT5G25190	Integrase-type DNA-binding superfamily protein	0.99556	0.0015938	0.44808	0.14134	-2.4253	1.62E-11	-1.0785	5.11E-11	-0.9337	0.14971
	AT3G22640	PAP85	1.2529	3.86E-05	1.7311	1.19E-07	-1.6469	3.98E-07	0.01768	0.97052	0.77861	0.60551
	AT2G14260	ATM17	1.8955	4.30E-10	1.4432	6.73E-07	-2.4654	3.12E-15	-0.31612	0.29399	-1.4659	0.0032841
Response to biotic and abiotic stress	AT4G28720	YUC8	0.080686	0.75411	0.12399	0.01061	-1.5141	0.0007182	0.028578	0.83621	0.42828	0.81989
	AT1G80440	Galactose oxidase/kelch repeat superfamily	0.49314	0.35559	0.90216	0.034884	-2.4086	1.75E-05	-0.88197	3.28E-16	-1.3424	0.015539
	AT5G13370	Auxin-responsive GH3 family protein	0.96743	0.0140369	0.80229	0.038179	-1.6607	0.0001867	-0.60726	2.56E-06	0.1384	0.92978
	AT4G36110	SAUR-like auxin-responsive protein family	1.1059	0.03746	0.98284	0.058143	-3.0921	6.54E-06	-0.25586	0.60845	-1.0843	0.17342
	AT4G27150	AT2S2	4.2322	4.54E-11	-0.04286	0.98165	-1.7117	0.00020808	-0.48371	0.30215	1.4123	0.15421
	AT2G30750	CYP71A12	6.2095	0.0069588	6.8919	0.0035958	-10.518	0.00010927	1.7536	0.14687	1.2764	0.72833
	AT5G52450	MATE efflux family protein	0.41841	0.19432	0.54844	0.10233	-1.5475	0.00018655	-0.32332	0.06043	0.24138	0.94732
	AT2G39350	ABC2-type transporter family protein	0.15797	0.73288	0.73576	0.081667	-2.5528	9.23E-06	-0.8606	6.90E-05	1.7734	0.56967
	AT2G43520	ATT12	0.53282	0.2905	0.087621	0.91335	-2.1059	0.00025997	-1.0512	0.0027331	-0.927	0.12064
	AT2G46440	ATCNG11	0.066947	1	1.2409	0.16083	#NAME?	0.00034763	1.7195	0.10952	-3.8198	0.0054076
Innate immune response	AT1G32960	ATSBT3.3	3.2739	0.019598	3.7056	0.010628	-5.1858	1.30E-07	0.11427	0.45654	-1.2285	0.016353
	AT3G16530	Legume lectin family protein	2.6482	0.020977	2.1564	0.043277	-5.0156	0.00032485	-0.39133	0.42526	2.1242	0.57493
	AT2G18660	PNP-A	1.6413	0.055694	2.7224	0.0062244	-5.5085	1.13E-05	2.6205	0.064037	0.73718	0.91495
	AT1G56510	DR2	0.048346	0.95662	0.28662	0.4151	-1.5832	0.00034552	-0.39265	0.0088894	0.21153	0.90641
	AT5G44870	Disease resistance protein (TIR-NBS-LRR)	0.26876	0.41685	0.27231	0.39112	-1.5165	2.05E-06	-0.54736	0.00027505	0.044664	0.8017
	AT1G14950	OLE1	1.8694	5.87E-05	1.3139	0.011775	-1.5728	0.00019361	0.3388	0.32757	0.66013	0.3426
	AT1G26945	KDR	0.65038	0.032982	-0.25655	0.39845	-1.5199	3.46E-06	-1.0485	4.98E-12	-1.2444	0.04428
	AT5G25250	SPFH/Band 7/PHB domain-containing mer	2.6396	0.065219	3.4089	0.026936	-5.7855	0.0015139	-0.14182	0.7756	1.0797	0.76644
	AT1G62020	Sal Induced Serine rich protein	0.174	0.11943	1.1072	0.040607	-2.7036	0.00011979	-0.14444	0.84481	1.4337	0.63552
	AT5G02020	Thiamin diphosphate-binding fold (THDP)	0.174	0.11943	1.06432	0.54526	-1.7947	1.33E-10	-1.1741	6.38E-30	-1.5202	0.0015911
Response to stimulate	AT1G22885	unknown protein	-0.075947	0.81689	-0.032165	0.91229	-1.5563	1.21E-05	-0.56407	0.0012559	-0.34612	0.36948
	AT1G13110	CYP71B7	0.33232	0.42584	0.32345	0.42433	-1.6276	0.00011389	-0.99149	1.55E-18	-1.34	0.010861
	AT1G35710	Protein kinase family protein with leucine-rich repeats	0.97489	0.0022367	0.86862	0.0048251	-2.1281	1.89E-10	-0.16365	0.65359	-1.0476	0.03486
	AT2G46220	DUF2358	0.28565	0.30005	0.30492	0.26014	-1.5704	1.30E-07	-1.265	1.19E-20	-1.4043	0.0026541
	AT4G28490	RLK5	0.17009	0.76383	0.75818	0.15187	-2.0506	0.00011132	-0.21868	0.29693	-1.1131	0.012865
	AT1G56520	Disease resistance protein (TIR-NBS-LRR)	0.34689	0.42423	0.46539	0.25121	-1.6179	0.000				