Examination of the functions of Clade III Cytokinin Response Factors in relation to Cytokinin and the Oxidative Stress Response

by

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Abstract

Cytokinin response factors (CRFs) are a family of transcription factors belonging to the AP2/ERF transcription factor family. A subset of these CRFs have been shown to play a role in both the cytokinin (CK) signal cascade and the response to oxidative stress across several species of angiosperms. In order to investigate the roles Clade III CRFs play in responses to CK and oxidative stress, members of this group of CRFs were examined in both *Arabidopsis thaliana* and *Solanum lycopersicum* (tomato).

AtCRF6 of Arabidopsis has already been shown to be involved in the oxidative stress response in Zwack et al 2016, but its function in the CK signal cascade remained mostly unstudied. By analyzing the transcriptome of CK-treated *Atcrf6* mutant plant, several genes involved in potassium (K+) transport were found to be AtCRF6-dependandly CK-regulated. To further explore the possible connection by AtCRF6 between CK and K+ uptake and transport, mutants of the AtCRF6-depentanly CK-regulated K+ transporters, *hak5, skor* and *nrt1.5*, alongside mutant *Atrf6*, were grown in the presence of CK and reduced K+ levels, and their shoot and root growth, FV/FM levels, and the ionomic content of their roots and shoots were analyzed and compared.

After investigating the role of AtCRF6 in CK signaling, the roles of Clade III CRFs in oxidative stress was explored in both Arabidopsis and tomato. While Arabidopsis has two Clade III CRFs, AtCRF5 and AtCRF6, tomato only has one: SlCRF5. Both AtCRF6 and SlCRF5 have been linked to the oxidative stress response, but remaining homolog, AtCRF5 in Arabidopsis, had not been linked. To better understand how these Clade III CRFs are connected to oxidative stress, the transcriptome of oxidative stress-treated *Atcrf5* was analyzed and compared to those of oxidative stress-treated *Atcrf6* and SlCRF5AS. Genes that were differentially regulated in the presence of oxidative stress were identified in each line, and those that diverged from the regulation observes in wildtype were deemed Clade III CRF-dependently oxidative stress-regulated genes (CDRGs). The functions of the CDRGs of each line were investigated and then compared using GO enrichment analysis. From these genes, several tomato CDRGs were found to be involved in the regulation of CK biosynthesis. To investigate the potential link formed by Clade III CRFs between oxidative stress and CK biosynthesis, CK measurements were taken from the oxidative stress-treated and untreated *Atcrf5*, *Atcrf6,* and SlCRF5AS lines, and altered CK levels analyzed.

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List of Abbreviations

-7G	-7-*N*-glucoside
-9G	-9-*N*-glucoside
-O	-O-glucoside
-OG	-R-O-glucoside
AP2/ERF	APETELA 2/ Ethylene Responsive Factor
CDRGs	Clade III CRF-dependent Oxidative Stress-Regulated Genes
CK	Cytokinin
Col	Columbia-0
CRF(s)	Cytokinin Response Factor(s)
cZ	*cis*-Zeatin
DEG	Differentially Expressed Gene
DHZ	Dihydrozeatin
FC	Fold Change
GUS	ß-glucuronidase
H_2O_2	Hydrogen peroxide
iP	Isopentenyl adenine
K+	Potassium
MAP K	MAP Kinase
MES	2-(*N*-morpholino)ethanesulfonic acid
MS	Murashige and Skoog basal salt mixture
ROS	Reactive Oxygen Species
SlCRF5AS	SlCRF5-Antisense line
tZ	*trans*-Zeatin
WT	Wildtype

Chapter 1: Introduction and Background

Arabidopsis

Arabidopsis thaliana is the classic plant model organism. It is a eudicot belonging to the brassica (mustard/crucifer) family "Brassicaceae". It is a small, herbaceous plant with simple lyrate leaves that grow in a basal rosette which can measure around 7-10cm in diameter at maturity. Flowers are small (about 3-4mm across), 4 petalled, and white and are arranged in a cymose corymb which can measure 20cm tall. Blooming occurs about 2 weeks after germination and produces mature seeds after about 6 weeks. The fruit of A. thaliana are siliques which contain many round brown seeds each of which measuring less than a millimeter across. One plant can produce around 10,000 seeds.

A. *thaliana* is diploid with a fully sequenced genome consisting of 5 chromosomes (Berardini *et al.*, 2015). The sequence of the genome is known and has been well annotated. Many distinct ecotypes are available to use as wildtype and for transforming backgrounds. Our research was conducted using Columbia-0 ecotype of Arabidopsis.

Tomato

Solanum lycopersicum (tomato) is an emerging model organism in plant genetics since the fully sequenced "Heinz 1706" tomato genome (diploid, consisting of 12 chromosomes) was published in in 2012 (Sato *et al.*, 2012).

Tomato is a eudicot belonging to the deadly nightshade/potato family, Solanaceae. It is a pubescent herbaceous vining plant with alternately arranged oddly pinnate leaves. Leaflets have serrate margins. Flowers are 5 petalled, and typically yellow with a superior ovary containing two carpels. Fruit are berries that become red with maturity.

Human beings have breeding tomatoes for hundreds of years, which has resulted in the creation of many different cultivars. These cultivars have a great range in the variation of their sizes, life spans, growth habits and flowering time. This research utilized “MicroTom” (MT), a small cultivar bred in the University of Florida and only grows to be about 20cm tall with yellow flowers about 2cm across and produce round red berries approximately 1.5cm in diameter.

Oxidative stress

The means by which oxidative stress occurs is through reactive oxygen species (ROS). When ROS are created in a plant cell, they cause damage at the tissue and cellular levels, destroying photosynthetic machinery, rupturing membranes and can ultimately cause cellular death (Zwack and Rashotte, 2015). ROS are common byproducts of most abiotic and several biotic stresses, and contribute significantly to the damage those stresses create within a plant (Dunque *et al.*, 2013; Dumont and Rivoal, 2019).

Hydrogen peroxide was used in this research to apply oxidative stress to plants.

Cytokinin

Cytokinin (CK) is a plant hormone crucial to plant growth and development. CKs are adenine derivatives which are synthesized in the root and are involved in cellular division, root growth inhibition, shoot growth and initiation, delaying senescence, apical dominance, and responses in biotic and abiotic stresses (Mok and Mok, 2001).

CKs function through two component signaling, which involves a receptor kinase phosphorylating a response regulating transcription factor (Mok and Mok, 2001; Kieber and Schaller, 2014). Cytokinins are perceived by receptors called histidine kinases (HKs, or AHKs in Arabidopsis) which are receptors localized to the membrane of the endoplasmic reticulum (ER) (Mok and Mok, 2001; Nishimura *et al.*, 2004; Keshishian and Rashotte, 2015). These receptors pass the cytokinin signal when the conformational change caused by CK binding causes the HK to phosphorylate a histidine phosphotransfer protein (HPs, or AHPs in Arabidopsis) (Mok and Mok, 2001; Keshishian and Rashotte, 2015). HPs are not membrane-bound, and are therefore free to carry the signal beyond the ER. HPs then phosphorylate response regulators (RRs, or ARRs in Arabidopsis) of which there are two types: Type-A RRs and Type-B RRs (Keshishian and Rashotte, 2015). Type-B RRs are positive response regulators which, once phosphorylated by HPs, move from the cytosol into the nucleus, where they can affect the CK-triggered transcriptional changes (Keshishian and Rashotte, 2015). Type-A RRs are negative response regulators which competitively bind to HPs, and prevent the CK-triggered transcriptional changes (Keshishian and Rashotte, 2015).

CK Biosynthesis and Degradation

The CK biosynthetic pathway is largely understood, though not all genes involved have been identified. There are four active forms of cytokinins: Isopentenyl adenine (iP), Dihydrozeatin (DHZ), *cis*-Zeatin (cZ), and *trans*-Zeatin (tZ) (Sakakibara, 2006). The transported forms of these cytokinins (iPR, DHZR, cZR and tR) have a Riboside group. These forms are interchangeable by an adenosine nucleosidase which cleaves the riboside to create active forms and a purine nucleoside phosphorylase which can attach the riboside. In both the transported and active forms, tZ and cZ are interconvertible (tZ to cZ and visaversa and tZR to cZR and vice versa) by a zeatin *cis-trans* isomerase (Sakakibara, 2006). Both the active and transported form of tZ can be converted to DHZ of the same form by a zeatin reductase, but DHZ cannot be converted back. The conjugate forms of CK fall into two types: N-glucosides and O-glucosides, depending when a glucoside is added. N-glucosides can be 7G or 9G depending where the glucoside is added by CK N-glucosyltransferase (CK-N-GT) (Sakakibara, 2006). Unlike the N-glucosides, when a glucoside is added to an oxygen molecule by zeatin O-glucosyltransferase (ZOG), the conjugate can be converted back into the active form. Interestingly, in Arabidopsis, O-glucoside conjugation of DHZ produces a molecule identical to that created when tZ is converted to its O-glusoside conjugate (tZOG or tZROG). For decades the conjugate CKs were thought to be inactive, but were recently shown to have limited and specific CK activity (Tucker Hallmark *et al*., 2020).

CK levels are regulated not just through their synthesis and glycosylation, but also through degradation. CK degradation is conducted by cytokinin oxidases/dehydrogenases (CKXs), and is irreversible (Mok and Mok, 2001). CKXs cleave the side chains from CKs, converting them into an adenine and an aldehyde (Mok and Mok, 2001).

CRFs

Cytokinin Response Factors (CRFs) are a group of the APETELA2/Ethylene Responsive Factor (AP2/ERF) transcription factors (TFs). They were first discovered as a group of related unknown genes in a list of the genes most highly upregulated by CK (Rashotte *et al.*, 2006). They contain an AP2/ERF domain, which have a DNA binding site, a CRF domain, which delineates the CRFs, and a clade specific domain, which identifies to which of 5 clades within CRFs a single representative belongs. CRFs are common to all land plants, and most angiosperms contain a gene from each of the 5 clades (Rashotte and Goertzen, 2010).

Though not all CRF Clades are induced in the presence of CK, Clade III has been shown to be CK-upregulated via Type-B RRs across several species (Zwack *et al.*, 2013, 2016; Gupta and Rashotte, 2014; Melton *et al.*, 2019).

Clade III CRFs

Arabidopsis thaliana (Arabidopsis) contains two members of Clade III: *AtCRF5* and *AtCRF6* (Rashotte *et al.*, 2006). The presence of two representatives of Clade III in Arabidopsis is thought to be due to the alpha duplication event in plants. Since the duplication event, *AtCRF5* and *AtCRF6* have diverged and now share only about 50% identity with one another, with the majority of sequence conservation occurring in the AP2/ERF, CRK, putative MAP K, and clade specific domains.

Both Clade III AtCRFs are expressed specifically in the vasculature, and are upregulated in plants treated with CK (Rashotte *et al.*, 2006; Zwack *et al.*, 2012, 2013). Previous work has shown that AtCRF6 is induced not only by CK, but also by oxidative stress, and may play a role in the mitigation of the damage it causes (Zwack and Rashotte, 2015; Zwack *et al.*, 2016). While its role in oxidative stress has been investigated, the role of AtCRF6 in the cytokinin signaling cascade has been relatively unexplored.

AtCRF5 has not been as well investigated as its paralog, and its potential involvement in the oxidative stress response had not been explored. It had been found that while a single homozygous mutant *Atcrf5* or *Atcrf6* mutant plant can survive, a homozygous double knockout of the Clade III CRFs in Arabidopsis is embryo lethal. This indicates that there is some shared crucial function between the genes, but other studies have shown that AtCRF5 and AtCRF6 do not carry out entirely identical functions.

Solanum lycopersicum, tomato, has only one Clade III CRF: SlCRF5. The *SlCRF5* sequence shares about 30% identity with those of the Clade III AtCRFs, however, the conservation of sequence is almost exclusively located in the functional domains, which share closer to 50% identity with the AtCRF orthologs. As with the orthologs in Arabidopsis, SlCRF5 is expressed in the vasculature and has been shown to be upregulated when treated with exogenous cytokinin, and, like AtCRF6, is upregulated in oxidative stress conditions (Gupta and Rashotte, 2014; Keshishian *et al.*, 2018).

Potassium and Potassium Deficiency

Potassium (K+) is a cation crucial for a range of processes; it is the means by which a plant can open and close its stomata, it neutralizes charged molecules, helps maintain neutral cellular pH, serves as an activator for enzymes, allows for the charge imbalance that drives ATP synthase, and is important for nutrient and metabolite transport through the vasculature (Beringer and Troldenier 1980, Demidchik, 2014, Prajapati et al 2012). Because of the wide range of critical functions K+ fulfills, plants that grow in soil containing insufficient levels of the cation cannot thrive. K+ deficiency in plants causes reduced rate of photosynthesis, slowed nutrient transport, and diminished growth (Prajapati et al 2012).

HAK5, SKOR, NRT1.5

High- Affinity Potassium transporter 5 (HAK5), Stelar Potassium Outward Rectifier (SKOR) and Nitrate transporter 1.5 are all transporters involved in the uptake/transportation of K+. HAK5 is a powerful K+ absorbing transporter that pulls K+ from the environment into the root (Nam *et al.*, 2012). NRT1.5 and SKOR are both expressed in the pericycle of the root and allow for the shootward transportation of K+. They release K+ from inside the cells into the apoplasm, which makes the cation available to be loaded into the vasculature (Gaymard *et al.*, 1998; Li *et al.*, 2017).

HAK5 is expressed in the epidermal layer of the roots, particularly in the root hairs (Nieves-Cordones *et al*, 2010). It is a highly affective K+ and sodium symporting channel located in the cellular membrane when it is expressed. Though the *HAK5* gene is constantly transcribed, it is only translated when a plant is in soil with low levels of K+ (Nieves-Cordones *et al.*, 2010; Nam *et al.*, 2012).

SKOR is a voltage-gated K+ rectifying channel, which opens or closes in response to differences in voltage across the cellular membrane (Gaymard *et al.*, 1998). The expression of SKOR is regulated by both high and low K+ conditions (Gaymard *et al.*, 1998).

NRT1.5 is a low-affinity NO_3- transporter that is crucial to the long distance transportation of nitrate, but also functions as a H+/K+ antiporter which functions in maintaining K+ concentration homeostasis in the root (Lin *et al.*, 2008; Li *et al.*, 2017).

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Chapter 2: Cytokinin regulated targets of Cytokinin Response Factor 6 are involved in potassium transport

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Running title: CRF6 cytokinin regulated targets

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Abstract

Cytokinin (CK) is a plant hormone crucial to plant development and growth. Cytokinin Response Factor 6 (CRF6) is a CK induced transcription factor that is part of the CK signaling cascade. While the role of CRF6 has been examined in oxidative stress response, there has been surprisingly little investigation of CRF6 in the context of CK signaling, including identifying CK-regulated targets of CRF6. Here we conduct a transcriptomic study of Arabidopsis examining the CRF6 mutant (*crf6*) in the presence and absence of CK, revealing 163 downstream CRF6-dependent CK-regulated differentially expressed genes (DEGs). 15.3% of these DEGS were found as overlapping with larger number of standardly identified CK-regulated

DEGs, suggesting that CRF6 is involved in regulating a subset of downstream CK responses through these gene targets. The general transcriptional regulation of CRF6-dependent CK-regulated DEGs, indicates that CRF6 may function as a negative regulator of CK-response. We investigated one subset of CRF6 CK-dependent targets (*SKOR*, *HAK5* and *NRT1. 5*) involved in an underexamined functional role of CK-response: the uptake and transportation of potassium. To determine how CK and CRF6 are involved in potassium acquisition and distribution, ionomic and physiological experiments were conducted on plants grown in media with sufficient and deficient potassium concentrations and in the presence and absence of CK. In order to investigate how CK alone affects potassium transport, similar experiments were performed on *skor, hak5,* and *nrt1.5* mutant lines of these CRF6-dependent CK regulated targets. These findings indicate novel connections between CK and potassium transport, which appear to be regulated in a CRF6-dependent manner.

Keywords: Cytokinin, Cytokinin Response Factor, CRF6, Potassium, Transport

1 Introduction

Cytokinin (CK) is an important plant hormone involved in growth, development and response to environmental stimuli (Mok and Mok, 2001; Werner and Schmulling, 2009). It is involved in the regulation of leaf senescence, root cell division, shoot cell elongation, formation of lateral roots, protection from pathogens, and plays a role in response to nutrient deprivation (Zwack et al, 2013; Kieber and Schaller, 2014; Argueso, Ferreira, Kieber, 2009; Böttger, 1974). Initial regulation of these varied roles is carried out through the two-component CK signaling pathway (TCS). One branch of the TCS leads to a set of transcription factors called Cytokinin Response

Factors (CRFs). CRFs were first identified from an examination of genes induced in *Arabidopsis thaliana* treated with exogenous CK (Rashotte et al., 2003;2016). CRFs belong the *AP2/ERF* super-family of transcription factors and are present and highly conserved among all land plants (Zwack et al., 2012, Rashotte and Geortzen, 2010). Within the CRFs there are five evolutionarily distinct clades, each with unique functional regulation (Hallmark and Rashotte, 2019). Cytokinin Response Factor 6 (CRF6) is one of two members of CRF clade III in Arabidopsis and may be the CRF gene best examined for stress-response function. CRF6 is known to be CK-induced, expressed in the vasculature, and has been shown to be involved in mitigation of oxidative stress, yet its role in the CK signal cascade is underexplored, particularly in relation CK-regulated downstream targets of this transcription factor (Rashotte et al., 2006; Zwack et al., 2012; Zwack et al., 2016; Hallmark and Rashotte, 2019).

In order to determine downstream targets of CRF6 and potential roles that CRF6 plays in regulating CK response, the transcriptome of a knockout CRF6 mutant line (*crf6*-2) responding to CK treatment was analyzed and compared to that of wildtype (WT) for mis-regulated genes. This analysis revealed numerous CK-regulated differentially expressed genes (DEGs) with altered regulation in a *crf6* mutant background. These DEGs were considered to be CK regulated in a CRF6 dependent manner or CRF6 CK-regulated targets. Among these CRF6 targets were genes involved in CK signaling, plant growth and development and biosynthetic processes as well a subset identified as having potassium uptake and transport functions.

Although CK has been previously linked to physiological changes in plant growth resulting from potassium deficiency (Nam *et al.*, 2012), the mechanisms and genes by connecting these processes have yet to be identified. Potassium (K+) is crucial for processes from plant-wide growth to cellular functions where it has many critical roles, including ionic balance, neutralizing negative charges on proteins, maintaining cellular pH, and enzymatic activation (Beringer and Troldenier 1980, Demidchik, 2014, Prajapati et al 2012). In order to investigate the means by which CRF6 and CK are connected to potassium uptake, transportation and deficiency, the CRF6-dependent CK-induced regulation of high-affinity potassium transporter 5 (*HAK5*), stellar potassium outward rectifying transporter (*SKOR*), and nitrate transporter 1.5 (*NRT1.5*) were explored.

2 Results

2.1 CK transcriptional response in WT and crf6 A. thaliana seedlings

To determine the transcriptional effects of CK on *A. thaliana,* 10-day old seedlings were exogenously treated with CK (2µM 6-benzyl adenine or BA) or a control (0.2% DMSO) for 6 hours and changes in transcriptomic responses were analyzed using Affymetrix Arabidopsis ST 1.0 microarrays. Statistically significant DEGs were identified and fold change (FC) of transcription levels was calculated in response to CK. CK treatment of wildtype (WT), Col-0, plants resulted in 580 DEGs that were transcriptionally altered in response to the hormone. Significant (padj >0.05) DEGs were found to be induced to 150% and repressed to 50% of their original (control) expression levels were selected and further analyzed for Gene Ontology (GO) terms using GO Enrichment Analysis (Table 1).

There were 429 CK induced DEGs of which the most highly upregulated genes included several type-A Arabidopsis Response Regulators (*ARRs*): *ARR3, ARR5, ARR6, ARR7, ARR15, and ARR16* (Table S1). Type-A ARRs are well known as highly CK inducible and serve as negative regulators of CK response in plants. GO-enrichment analysis of CK induced genes in the WT background treated samples included the enrichment terms “cytokinin signaling” and “hormone response” as expected (Table 1). There were 151 CK-repressed genes, including the most highly repressed genes: *HAK5*, *NRT2.1*, connected to ion transport and reduction and in growth regulation (Table 1, S1). Overall, these findings are consistent with previous transcriptome analysis of CK treated Arabidopsis and show a standard transcriptional response to CK occurred in this study (Table S1; Bhargava et al., 2013).

2.2 CRF6-*dependently CK regulated genes*

In order to determine genes that are regulated in a CK-dependent manner by the transcription factor CRF6 a genome-wide transcriptome analysis of *crf6-2*, a knockout line confirmed in Zwack et al 2012, and WT seedlings treated for 6 hours with CK (2 µM BA) or with 0.2% DMSO. Transcriptomes were analyzed using Affymetrix Arabidopsis ST 1.0 microarrays. Differences in gene expression between the WT and *crf6-2* mutant with and without exogenous CK treatment are depicted in heat maps of fold change (FC) differences (Figure 1; Table S2). As noted above, CK treatment of WT revealed a total of 579 significant DEGs in CK treated vs control plants: 429 induced and 151 repressed. CK treatment of *crf6* resulted in 163 significantly differentially regulated genes vs control treatment: 98 induced and 65 repressed (Fig. 1). Genes that are induced or repressed after CK treatment to a greater or lesser degree (a difference in regulation of at least 50%) in the mutant background, as compared to the regulation observed in WT were determined to be CRF6-dependantly regulated genes (CDRGs). Of the 98 genes exhibiting at least a 50% difference in CK induction in *crf6* vs WT, 64 CDRGs were found to be part of 428 CK induced DEGs of WT (Fig. 1). Whereas, of the 65 genes that were at least 50% differentially repressed in *crf6* background, 55 CDRGs were found to be part of the 151 CK-repressed DEGs of WT (Fig. 1). These findings indicate that CRF6 is required for a subset of WT-CK gene regulation (~15% of the induced WT DEGs, 64 of 429, and ~36% of the repressed

WT DEGs, 55 of 151). Additionally, this indicates that CRF6 is required for hindering the irregular CK regulation of a subset of genes in WT plants (34 induced CDRGs and 10 repressed). Since CRF6 appears to be responsible for a larger regulation of CK-repressed CDRGs, we focused additional examinations on this gene set. An examination of CRF6 dependent CK-repressed CDRGs for GO term enrichment analysis (Table 2) revealed several terms related to ion transport. A more detailed examination of these "Metal and Ion Transport(?)" related genes as seen in Table 3 revealed that three of the top four CDRGs in this group were involved as having functions related to potassium (K+) uptake or transport; high-affinity potassium transporter 5 (*HAK5*), stellar potassium outward rectifying transporter (*SKOR*), and nitrate transporter 1.5 (*NRT1.5*). To investigate the potential relationships between potassium, CK, and CRF6, these genes were selected for further investigation.

In order to ensure that transcriptome findings and this CRF6-CK-postassium connection was valid before further examination, qRT-PCR expression analysis was conducted. RNA of *crf6* and WT seedlings was extracted in new biological replicates treated as they had been for the microarray analysis (Table 4). qRT-PCR expression analysis indicates a significant reduction in FC between the WT, and *crf6* in expression of the three K+ related genes, confirming general microarray expression findings and that their CK repression is CRF6-dependent.

2.3 Physiological examinations of CRF6*-dependent CK-potassium interactions*

In order to determine if CRF6 is involved in CK regulated potassium interactions, several mutant lines were examined, to observe the response of K+ mutants to altered CK treatment and CRF6 to altered K+ content. The three potential CRF6-dependent CK regulated target genes function in different aspects of potassium movement: both SKOR and NRT1.5 are transporters involved in loading K+ into the root xylem, allowing for movement of K+ to aerial tissues, and

HAK5 is a K+ transporter involved in facilitating K+ into the root in K+ deficient environments (Geirth et al, 2005, Rubio et al, 2008 Ahn et al, 2004; Park et al., 2008). Along with mutants of these three K+ related lines, two *CRF6* altered lines (the mutant knockout *crf6-2* and overexpressor *CRF6OE,* previously described in Zwack et al 2012; 2016) were examined.

Seedlings four days after germination (DAG) were transferred to one of four types of media to grow for 10 days. These Murashige and Skoog(MS)-based media types contained the standard K+ levels of MS media (Standard K), or reduced K+ levels (Low K), and each K+ media either did not contain or contained (+ CK) CK as detailed in Material and Methods. Measurements were taken of maximum quantum yield of photosystem II, or Fv/Fm, as well as growth of root and shoot tissues separately in order to examine changes related to K+ and CK. Under standard growth conditions mutant and altered lines showed only minor physiological or growth differences from WT plants, but significant differences were found within treatment groups.

2.4 Fv/Fm response to cytokinin and low K^+

In order to determine if there were connections between CRF6, CK response and potassium, with photosynthetic efficiency (as an indicator of plant fitness), measurements of maximum quantum yield of photosystem II or Fv/Fm was conducted in distinct mutant lines and under altered growing conditions (Figure 2). Specifically, Fv/Fm was measured in seedlings that were grown for ten days on MS media with normal or low K+ levels +/- CK under standard growth conditions. The highest Fv/Fm levels for all genotypes were found when grown on standard media without CK (Fig. 2). While only small changes in Fv/Fm levels found from these examinations, even minor differences in photosystem II maximum quantum yield are well-known to be of great importance to photosynthetic performance.

Interestingly, although *crf6* shows significantly, albeit slightly higher Fv/Fm levels compared to WT on standard media to WT, the converse was found when grown on CK supplemented media (Fig. 2). *crf6* showed a stronger reduction in Fv/Fm (7% compared to 3.2% in WT) when compared to non-CK supplemented media. These changes in response to CK are consistent with CRF6 playing a role in CK-regulated processes such as photosynthesis. Moreover, an examination of *crf6* under low vs standard K^+ conditions revealed a much larger reduction in Fv/Fm levels than WT (9.2% in *crf6* and 5.6% in WT: Fig. 2). However, unlike WT where Fv/Fm levels were reduced by 3.2%, *crf6* demonstrated a slight but significant recovery of about 2.5% when CK was present in the low K^+ media (Fig. 2).

The *CRF6OE* line reacted very differently to the growing conditions than either the WT or *crf6* line. On standard K^+ media, in the presence CK the *CRF6OE* line exhibited a greater reduction in Fv/Fm levels (5.6% compared to 3.2% in WT: Fig. 2). Unlike the *crf6* line, when CK was added to the low K^+ media, there was no recovery in photosynthetic response.

When CK was added to the standard media each of the three potassium-related transporter mutant lines showed small but significant reductions in Fv/Fm levels as compared to those of the WT (*hak5* 1.9%, *skor* 1.6%, *nrt1.5* 1.6%: Fig. 2).

The *skor* mutant exhibited a different pattern of Fv/Fm levels across growing conditions. This includes the minor reduction (1.6%) in when CK was added to standard media, yet distinctly when CK was added to the low potassium media, there was a 4.7% reduction compared to that of the WT (Fig. 2).

The *nrt1.5* mutant line had Fv/Fm levels similar to WT when grown on standard media. On all other media there was a significantly greater reduction in Fv/Fm levels than observed in WT. *nrt1.5* plants grown on standard media with CK were reduced in Fv/Fm by 1.6%, those grown on low potassium by 1.2%, and those on low potassium with CK by 2.7% (Fig. 2). Overall, these findings suggest that there are connections between CK and potassium that appear to be CRF6 related, as measured by examination of photosynthetic response.

2.5 Root growth in response to CK and low K^+

Root growth as a measure of overall plant health was assessed in seedlings grown on media with different CK and K^+ levels, as conducted for Fv/Fm analyses. Once germinated on standard media, 4 day old seedlings were transferred to different treatment media and after 10 days primary root growth was measured (Figure 3). On standard MS media without CK, *nrt1.5* and WT root growth were similar, while *crf6, skor,* and *hak5* mutant lines as well as the *CRF6OE* line had significantly longer roots (Fig. 3). Roots were 33.2%, 26.8%, 38.4%, and 11.9% longer for *crf6, CRF6OE*, *hak5*, and *skor*, respectively than those of WT. CK treatment generally resulted in a strong reduction of root growth for all genotypes. Despite the greater growth on standard media of some lines, there was no increase in root length vs. WT for any lines when CK was present in the media. Root growth of both *crf6* and *CRF6OE* lines was more strongly reduced when grown on the standard media plus CK than was that of the WT line. *crf6* root growth was slightly, though significantly more affected (85.9% of the growth than observed in WT), whereas roots of the *CRF6OE* line grew only 41.2% of the length of WT (Fig. 3). As observed in *crf6*, root growth in the *nrt1.5* line was slightly more strongly affected (growing 9.8% less) than that of the WT line.

When all lines were grown on low K+ media, only the root growth of *CRF6OE* and *skor* plants differed significantly from that of WT. *CRF6OE* showed 22.2% longer root growth than observed in WT, while that of *skor* was 6.9% shorter (Fig. 3).

Roots of WT*,* *crf6* and *skor* lines grown on low K+ media in the presence of CK did not grow significantly shorter than they had on the same media without CK (Fig. 3), but *CRF6OE*, *hak5*, and *nrt1.5* plants did show diminished root growth when CK was added to the low potassium media (75.1% and 74.0% of their growth without CK, respectively). When CK was present in the low K+ media, the increased root growth observed in *CRF6OE* on standard media without CK was negated. Roots of the *CRF6OE* line grew only 60.1% and 44.1% of the total length of the WT growing on low potassium media with and without CK, respectively. Root growth of *CRF6OE* plants was not significantly different from WT when grown on either media containing CK.

2.6 Rosette diameter in response to CK and low K^+

Above ground plant size as measured by rosette diameter (shoot growth) was conducted when seedlings were 14 days old. The shoot growth of WT, *CRF6OE*, *crf6, hak5, skor,* and *nrt1.5* exposed to the same set of CK and K+ media treatments showed a different pattern than observed in roots (Fig. 3, 4). On standard media, *crf6* and *CRF6OE* had larger shoots than those of WT (by 15.3% and 24.0% respectively) while the *hak5* and *nrt1.5* seedlings had smaller shoots (by 5.2% and 23.4% of that of WT) (Fig. 4).

With the addition of CK to the standard media, *crf6* seedlings grew to have 19.1% larger rosettes than WT, while both *hak5* and *skor* had smaller rosettes (by 14.7% and 6.9% respectively). The *CRF6OE* and *nrt1.5* lines, which had been significantly different in size from the WT on standard media, exhibited growth similar to that of WT when CK was added (Fig. 4).

When the plants were grown on low K+ media, both altered CRF6 lines exhibited growth similar to that of WT, while all K+ related lines all grew smaller shoots. *hak5, skor,* and *nrt1.5* grew to be 10.3%, 15.5%, and 12.5% of the size of the rosettes of WT, respectively.

When CK was added to the low K+ media, the lines exhibited different levels of growth. The *crf6*, *CRF6OE*, *hak5* and *nrt1.5* lines all grew significantly smaller shoots than did WT, by 13.9%, 19.0%, 21.1%, and 25.2%. The *skor* line did not differ from WT; though the low K+ media without CK did grow smaller than did WT, the addition of CK resulted in larger rosettes in the *skor* line and phenotypic rescue (Fig. 4).

Most genotypes grew smaller shoots on low K+ media with CK compared to standard K+ media with CK (Fig. 4). However, the shoots of both the WT and *skor* seedlings grew larger rosettes on the low K+ media with CK than they had on the standard K+ media with CK. WT and *skor* exhibited an increase in growth by 10.8% and 12.5% on low K+ media with CK, while *crf6, CRF6OE*, and *nrt1.5* grew rosettes that were 19.9%, 10.1%, and 15.1% smaller than they had been when they were grown on standard K+ media with CK.

2.7 Measurements of plant potassium levels in response to CK and low K+ conditions

To further investigate the potential relationship between CK, CRF6 and potassium movement, the K+ content of the roots and shoots of WT, *crf6*, *CRF6OE*, *hak5, skor,* and *nrt1.5* were analyzed after plants were grown on media containing normal and reduced K+ levels in the presence and absence of cytokinin as done in other analyses (Figure 5).

2.7.1 K+ concentration in aerial tissue (shoots)

In order to better understand if K+ levels were altered in response to CK, seedling tissue (split into shoots and roots) of CRF6 altered lines and the K+ transporting mutants was examined using ICP-OES analysis to measure free ion levels (Figure 5; Table 5). When seedlings were grown on standard media, the K+ concentration of the aerial or shoot tissue varied from that of the WT in both the *crf6* and *hak5* (both were reduced, to 88.5% and 82.4%, respectively, of wildtype) (Fig. 5). The K+ content of the *CRF6OE*, *skor*, and *nrt1.5* shoots did not differ significantly from that of WT.

When CK was added to the standard media, the shoot tissue of *crf6, hak5* and *nrt1.5* had higher concentrations of K+ compared to WT (112.6%, 102.1%, and 113.9% of WT, respectively). Only *skor* shoot tissue did not show significant differences vs. WT in K+ concentration. The *CRF6OE* shoots were greatly reduced in K+ concentration, containing only 57.7% of the K+ present in WT.

The K+ concentration of WT shoots with CK added to standard media increased to 107.1% of that measured without the hormone. The *crf6, hak5* and *nrt1.5* lines, which had shown higher K+ levels vs. WT on standard media with CK, increased in shoot K+ concentration to 136.4%, 132.7% and 125.4%, respectively, compared to K+ concentrations without CK (Fig. 5). On standard media with CK, *CRF6OE* shoots were reduced to 57.4% of the K+ concentration of that measured without CK.

The levels of K+ present in the shoots differed when seedlings were grown on reduced K+ media (Fig. 5). Shoot tissue of the *crf6*, *CRF6OE*, *hak5* and *skor* lines contained lower K+ concentration than was observed in WT (68.9%, 42.2%, 82.7%, and 89.4% of the WT K+ concentration, respectively). When grown on low K+ media, only the K+ concentration of *nrt1.5* seedlings did not differ significantly from that of WT.

The K+ concentration in WT shoots increased to 159.7% of that observed on standard media when the seedlings were grown on low K+ media (Fig. 5). Shoots of *nrt1.5* increased in K+ concentration by 161.3% when grown on low K+ media compared to that measured on standard media. The *crf6*, *hak5,* and *skor* shoots had increased in K+ concentration when grown on low K+ media, but not to the degree observed in WT (measuring 124.5%, 160.4% and

146.7%, respectively, of their K+ concentration when grown on standard media). The *CRF6OE* line alone showed a reduction in shoot K+ concentration when grown on reduced K+ media (57.4% of that measured when the plants grew on standard media).

The concentration of K+ in shoot tissues shifted when CK was added to the low K+ media. Compared to that of WT, *skor* and *nrt1.5* showed greater concentrations of K+ (118.1% and 122.0%, respectively) of that in WT shoots, while the shoots of *CRF6OE* contained 48.6% of the K+ concentration measured in the WT. Neither the *crf6* nor the *hak5* shoot tissues differed significantly in K+ concentrations from that of WT when the seedlings were grown on reduced K+ media with CK.

The addition of CK to the reduced K+ media caused significant changes in K+ levels in shoot tissues of both WT and *CRF6OE* seedlings. The presence of CK in low K+ media yielded reduced K+ concentrations in shoots of WT and *CRF6OE* (to 74.1% and 85.4% of the concentrations observed on low K+ media without CK).

K+ concentrations of shoot tissues were affected differently when the plants were grown in the presence of CK on standard vs. low K+ media (Fig. 5). The WT, *skor* and *nrt1.5* lines all showed a greater concentration of K+ in the shoot when grown on low K+ media with CK, 110.6%, 134.0%, and 118.7%, respectively, as compared to concentrations of those grown on standard media with CK. The K+ concentrations of *crf6*, *CRF6OE*, and *hak5* seedlings were not significantly affected.

2.7.2 K+ concentration in root tissue

The K+ concentrations measured by ICP-OES of roots collected with the shoot samples varied when grown on standard media (Fig. 5; Table 5). Roots of *CRF6OE* and *nrt1.5* contained

K+ at 84.2%, and 140.6% of the concentration observed in WT, respectively. K+ concentrations in the roots of the other lines were not significantly affected.

The *CRF6OE* and *nrt1.5* roots, alone, showed significant differences in K+ levels vs. WT when CK was added to the standard media, as they had when grown on standard media without CK (Fig. 5). The *CRF6OE* roots contained 73.8% of the K+ concentration measured in the WT roots, while that of *nrt1.5* measured 137.4% of WT.

Only in *CRF6OE* did the addition of CK to the standard media result in a significant change of root K+ concentration. The addition of CK to the standard media caused the K+ level in *CRF6OE* roots to decrease to 86.4% of that measured when grown on media without the hormone (Fig. 5).

The K+ concentration in the roots of *crf6* and *CRF6OE* differed significantly from that of WT when grown on reduced K+ media. Roots of *crf6* and *CRF6OE* contained 61.7% and 70.1%, respectively, of the K+ in WT roots (Fig. 5).

When the plants were grown on low K+ media the K+ concentration of the roots, compared to that measured on standard media, was reduced in all lines except WT and *skor* seedlings, which did not show a significant change in root K+ concentration. In the roots of *crf6, CRF6OE*, *hak5,* and *nrt1.5*, K+ root concentrations were 54.2%, 74.2%, 84.3%, and 63.5%, respectively, of those observed when the seedlings grew on standard media (Fig. 5).

K+ concentration of the roots of WT seedlings grown on low K+ media did not differ significantly from that of WT seedlings grown on low K+ media with added CK. The K+ concentration in the roots of *CRF6OE* and *nrt1.5* diverged from that of WT; K+ concentration in *CRF6OE* roots was 82.7%, and in *nrt1.5* roots was 129.4% of that measured in WT.

The addition of CK caused a significant change in the K+ concentration of *crf6* roots. The K+ concentration of *crf6* roots grown on reduced K+ media with CK was 141.5% of the concentration of seedlings grown on low K+ media without the CK. As observed in the shoots, the addition of CK to the low K+ media resulted in a return to WT equivalent K+ concentrations.

Root K+ concentrations of seedlings grown on either media containing CK differed in all lines. In all lines grown on low K+ media with CK the K+ concentration was reduced, compared to that of those grown on standard media with CK. The concentration of K+ in the roots of plants grown on low K+ media with CK was 74.3% in WT, 79.7% in *crf6*, 83.3% in *CRF6OE*, 73.3% in *hak5*, 75.7% in *skor*, and 70.1% in *nrt1.5* of the concentration measured in roots of the same lines grown on standard media with CK.

3 Discussion

Cytokinin Response Factors (CRFs) are known to be important AP2/ERF transcription factors connected to CK signaling and involved in the regulation of different abiotic stress responses (Rashotte et al., 2006; Hallmark and Rashotte, 2019). CRF6 has been previously examined for roles in senescence and oxidative stress response (Zwack et al., 2013; 2016), yet surprisingly there has been less examination of the role of CRF6 in CK response. Here we used a subtractive transcriptomic approach to identify potential CK regulated targets of CRF6 in Arabidopsis. CK treatment (2µM BA for 6h) of seedlings (10d) with and without CRF6 (WT and *crf6*) followed by genome-wide transcript analysis revealed numerous CK-regulated genes. Analysis of CK treatment in WT revealed 580 significantly Differentially Expressed Genes (DEGs) with least a 50% change in the transcription levels (Fig. 1; Table S1). Importantly, and as expected, many (n=108) of those DEGs are well-known CK-regulated genes, appearing on the CK “golden list” of genes, defined by Bhargava et al., 2013 including some of the most typical genes; several type-A Response Regulators (ARRs, negative regulators of CK response) and cytokinin oxidases (CKXs), which can also be noted from several cytokinin-related terms identified in the GO enrichment analysis (Table 1). A similar examination for CK-altered DEGs in the *crf6* background compared to those observed in WT revealed genes that require CRF6 for CK regulated activity.

Roughly a 35% (55 of the 151) of WT CK-repressed genes and 15% (64 of the 428) WT CK-induced genes were found to be altered in transcription by at least 50% when CRF6 was absent (Fig. 1). This indicates that CRF6 is responsible for about 20% of the standard transcriptional response to CK (36.4% of repressed genes and 15.0% of induced genes) under the conditions examined. The bias towards affecting the CK-repressed genes, suggests that CRF6 primarily functions as a negative regulator of cytokinin response, at least at this point in development.

The up regulated DEGs are involved in metabolic processes, and the repressed DEGs function primarily in ion transport and immune responses to both biotic and abiotic stimuli, including responses to oxygen species (Table 1). In Zwack et al., 2013 and 2016 it was found that CRF6 may also be involved in regulation of a small subset of oxidative stress responses (~15%). While there is only minor overlap between the lists of the CRF6 dependent DEGs relating to oxidative stress and CK treatment, there were specific CK-related DEGs found as regulated by oxidative stress (Table 1, 2). These same genes do not appear to be connected to non-oxidative stress CRF6-CK signaling roles of CRF6, as they were not found to be similarly regulated with CK treatment. This could suggest that there are different functional roles for CRF6 even in a CK-based manner under stress conditions.

As a major theme from GO-enrichment terms of CRF6-CK-regulated DEGs was ion transport (Table 2, 5), we examined several of the specific DEGs that function with distinct roles in potassium transport: *HAK5*, *SKOR*, and *NRT1.5* (Table 2). *HAK5* is a cell membrane localized potassium channel that acquires K+ from the external environment in K+ limited conditions (Geirth et al, 2005, Rubio et al, 2008 Ahn et al, 2004). *SKOR* and *NRT1.5*, are K+ efflux transporters that release potassium into the apoplasm of the stele, allowing for the ion to be transported to the aerial tissues (Park et al 2008). *SKOR* is the primary driver of K+ loading into the xylem when a plant is in an environment with low K+ content (Gaymard et al, 1998, Drechsler et at, 2015). *NRT1.5* (also known as AtNPF7.3) is a K+/H+ coupled antiporter and, like *SKOR*, is expressed in the root pericycle and localized to the cell membrane (Li et al, 2017, Drechsler et al, 2015). As there has been little examination of CK and potassium transport we decided to further investigate this connection and how CRF6 was involved in any potential regulation. This was conducted in by examining knockout mutants of *HAK5*, *SKOR*, and *NRT1.5*, which lack their respective gene expression and should roughly mimic the effects of cytokinin treatment in a WT background as seen from transcriptomic results

We found that growth was affected for potassium mutants by exogenous addition of CK; the rosettes of the mutants grew smaller than those of the WT in the presence of CK in both types of media (Fig. 4). This establishes a potassium-CK link. Similar effects in CRF6 altered backgrounds indicate that CRF6 is involved in this potassium-CK growth connection. Similar examination for photosynthetic response supports this connection further. All of the examined potassium mutants exhibited a greater sensitivity to CK when grown on standard media. *skor* and *ntr1.5* both experienced a larger reduction in Fv/Fm when CK was present in the low K+ condition (Fig. 2). The *crf6* mutants exhibited the opposite response; when CK was present in the low K+ media, the plants had an increase in Fv/Fm levels. CRF6 represses the three K+ transporter; it could be that without a functional CRF6 gene, these transporters are no longer repressed, making the low potassium media less stressful to the plants.

The altered *CRF6* lines themselves exhibited interesting patterns across the phenotypic analyses as compared to WT. Results from Fv/Fm analysis suggest that the *crf6* plants, when grown with sufficient potassium quantities, are more photosynthetically efficient than WT, in contrast, the addition of CK, which significantly reduces the *crf6* Fv/Fm levels below that of WT grown in the same condition (Fig. 2). This exaggerated reduction of Fv/Fm readings with exogenous CK on standard media is a pattern mirrored in *crf6* growth data for roots (Fig. 3) and shoots (Fig. 4).

When *crf6* mutants were grown on reduced K+ media, the Fv/Fm pattern was reversed from that measured on that with standard K+. On low K+ media without CK treatment, the mutant Fv/Fm measurements were lower than those of WT, but with the addition of CK the mutant Fv/Fm readings increased to nearly that of WT grown on reduced K+ without CK (Fig. 2). When the mutant plants were grown on low K+ media, CK nearly rescued the mutant phenotype, restoring the measurements to levels similar to those observed in WT grown on the same media without the addition of CK.

Both trends, the larger changes in response to CK on standard media and the near phenotypic rescue on reduced potassium media in response to CK, were observed in the K+ ionomics analysis of the shoots and roots of *crf6* plants (Fig. 5). The connections between Fv/Fm, growth and ionic content suggests a notable link between K+, *CRF6*, and overall plant function.

Although our testing conditions are designed to further investigate the microarray data, the conditions are not perfectly parallel; our transcriptomes were analyzed after a 6 hour 2µM CK treatment, whereas plants were grown on plates with 0.1µM, and were left to grow on the media for 10 days. This is, in part, due to the difficulty of tracking CK-based short-term growth responses that would be similar to initial transcriptomic treatments. Long-term exposure to exogenous CK, albeit at lower concentration, may have introduced additional unforeseen factors to these analyses. This could have obfuscated the effects of the K+ poor environment, the transcriptional problems experienced in the mutant lines, and the effect of CK itself, as a long-term continuing signal could cause enough stress to overwhelm other phenotypic responses. The *CRF6OE* line adds confounding factors itself; because the gene is constitutively expressed throughout the entire plant, rather than only in the xylem, as CRF6 is naturally, this creates additional complications in analyzing the data of the line. Furthermore, the K+ mutants are a proxy for K-transport. To that end, K+ levels were directly examined in plants and specifically in roots vs shoots. Because the transporters are responsible not just for K+ uptake, but also for making any K+ present available to the rest of the plant, the K+ levels of the root and aerial tissues were measured separately. The genes we examined are only part of a larger system. While *HAK5*, *NRT1.5* and *SKOR* are very important to the transport and uptake of K+, they are not the only genes responsible for K+ acquisition and movement. Similarly, CRF6 is not the whole of CK-response and other CK-regulated genes may be involved, (ARR3 – as a CRF6-CK DEG suggests that there is feedback to the TCS as an example). Despite these potential problems, the connections between CRF6, K+ and CK were still observed, which lends greater support to our hypothesis as we have been able to provide evidence for novel regulation of potassium transport mediated by CK through modulation of three important K-transporters and CRF6, a key CK-regulator of CK response.

4 Material and Methods

4.1 Plant Materials and Growth Conditions

CRF6 mutant and altered transgenic lines were (*crf6-2*) and CRF6-overexpressor (19.3) were previously described in Zwack et al., 2016, while *hak5* (SALK_074868C)*, nrt1.5* (sail.72.FC.11)*,* and *skor* (SALK.030047C) mutant lines were obtained from ABRC Stock Center. All lines are in the Col-0 WT Arabidopsis background. All seeds that were grown on sterile media were surface sterilized in a solution of 70% ethanol for 10 minutes then a solution of 20% bleach and 0.5% tween solution, followed by 5 washes with sterile water. After the final wash, seeds were placed individually in rows onto media plates made with 0.8% agar and buffered to pH5.7 with MES contained full strength Murashige and Skoog (MS) medium, and 1% sucrose. Experimental growth media contained either MS or MS that was without potassium phosphate ("Murashige and Skoog (MS) Modified Medium w/o Potassium Phosphate" from Plantmedia, which contained monosodium phosphate rather than monopotassium phosphate) referred to as "low K+", at the recommended concentration, both with and without 0.1µM BA. After at least 24 hours at 4°C, the plated seeds were moved into a controlled environmental chamber and grown under standard conditions of 16 h of 100µE light at 22°C and 8 h of darkness at 18°C.

4.2 Transcript Expression Analysis

Plants for this analysis were grown for ten days under standard growth and media conditions. Seedlings were then lifted from the plates, transferred to 3mM MES buffer pH 5.7 and allowed to gently shake for 1 hr. After which, 2µM of CK (Benzyl Adenine or BA) was added or 0.2% DMSO vehicle control. Following 6 hours of treatment plants were harvested and immediately frozen in liquid nitrogen. At least ten individual seedlings were pooled from each line in each treatment group of 2 biological replicates.

RNA was isolated from the seedlings using the Qiagen RNAEasy Plant Mini-kit according to the procedure specified by the manufacturer. Utilization of the Affymetrix Arabidopsis Gene 1.0 ST arrays, and preprocessing of the data were performed by the Heflin Center for Genomic Science at the University of Alabama at Birmingham as a service. Normalization and differential expression analyses were performed using the FlexArray 1.6 software from McGill University and Genome Quebec. Fold change in expression was calculated by Cyber-T analysis, and adjusted P values (padj) were determined using the Benjamini Hochberg method of False Discovery Rate (FDR). Sequence data from this article can be found in the GenBank/EMBL data libraries under accession numbers GSE84770.

4.3 Realtime qRT-PCR verification of microarray DEGs

Plants for verification were sterilized and grown on 1xMS, 1% Sucrose, pH5.7 agar plates until day 10, then treated in a similar manner as for RNAseq analysis. qRT-PCR verification was carried out using Sybr-Green and sequence specific (listed below)

primers. Reactions were carried out as previously described (Zwack et al., 2013). The following primers were used:

SKOR F, CCACGGATGTTCCTACCGAG, SKOR R, ACGCGGTTAATATGCGGGAA,

HAK5 F, CAGCTCAGAAGAGCCCATATG, HAK5 R, CCTAGATCAGCAAACATTGCC,

NRT1.5 F, GGGTTTTCTTTTTGGTTTGATG, NRT1.5 R, TATCTCGGTGTTCCAACAAGG

and the positive control, *tubulin 4*,

TUB F, ACCAATGAAAGTAGACGCCA, TUB R, AGAGGTTGACGAGCAAGATGA.

4.4 Physiological Analyses (Shoot and Root Growth, F_v/F_m assays)

Each of the 3 biological replicates conducted for the physiological analyses (except rosette measurements) contained at least 10 seedlings per line per treatment and was conducted when the plants were 14 days old, after 10 days of growing on the various media. Rosette diameter data was acquired from 2 biological reps with more than 10 seedlings per treatment per line. Seeds of WT, *crf6-2, CRF6OE, hak5, skor, and nrt1.5* lines were sterilized and sewn on standard media plates, then placed in 4°C conditions for 24 hrs. Four days after the seeds were moved from 4°C conditions to the growth chamber under standard growing conditions, a minimum of 10 seedlings from each line were transferred to four types of experimental plates (Standard media, media +CK (0.1µM BA), low K+ media, and low potassium media +CK (0.1µM BA) and their root lengths were noted. The seedlings were then allowed to grow on these vertically aligned plates for 10 days, after which root growth was measured and the Fv/Fm assay was performed.

Root growth was measured from the noted initial root length to the end of the primary root and rosette diameter were both measured using ImageJ software (NIH).

Fv/Fm measurements were taken with a Handy FluorCam from Photon System Industries in a darkroom using FluorCam 7 software and following the standard procedures to measure Fv/Fm as in Zwack et al., 2016. Plants to be examined were dark adapted for 30m and Fv/Fm measurements performed as in Zwack et al., 2016. There were three biological replicates analyzed using Student’s t-Test.

4.5 Ionomics

For ionomic ICP-OES measurements the aerial tissue, “shoots” (including leaves, petioles, and the stem) and roots from 10d old plants as treated in the text were digested in 200uL of concentrated nitric acid (Optima) in semi-sealed acid washed microcentrifuge tubes heated to 98^{o}C for 1h. Digests were diluted to 1mL with ultra-pure metal free water, then analyzed by Inductively Coupled Plasma with Optical Emission Spectroscopy (ICP-OES, Perkin Elmer 7100 DV, Waltham, MA) with simultaneous measurement of C, Ca, Co, Cu, Fe, K, Mg, Mn, Mo, Na, P, S, Zn. Metal concentrations were determined by comparing emission intensities to a standard curve created from certified metal standards (SPEX, Metuchen, NJ). Individual readings are the average of two intensity measurements that varied by less than 5%. Repeated analysis of individual samples showed less than 5% variability. Each replicate was normalized to the phosphorus measurements.

4.6 Statistical Analyses

Statistical data are presented as the means of two to three biological replicates ± SD. 1 factor ANOVA, followed by posthoc, tests were used in combination with two-tailed Student’s t-tests to determine significance between treatment groups, tissue types and lines. ANOVA was used when comparing data of 5 or more groups and was followed by posthoc tests for specific comparisons. When comparing two sets of data within a data set of 4 or fewer means, e.g. comparisons made within a line between the two treatments without exogenous cytokinin, a two-tailed Student’s t-test was used to determine the statistical significance of observed differences.

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7 Conflict of Interest

The authors declare no conflict of interest.

8 Author contributions

AMH and AMR wrote the paper. AMH, PJZ, and AMR designed the experiments and analyzed the data. AMH and PJZ conducted the experimentation and collected the data. PAC provided instrumentation and instructed and assisted in all ICP-OES ionomic analysis.

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10 Figures and legends

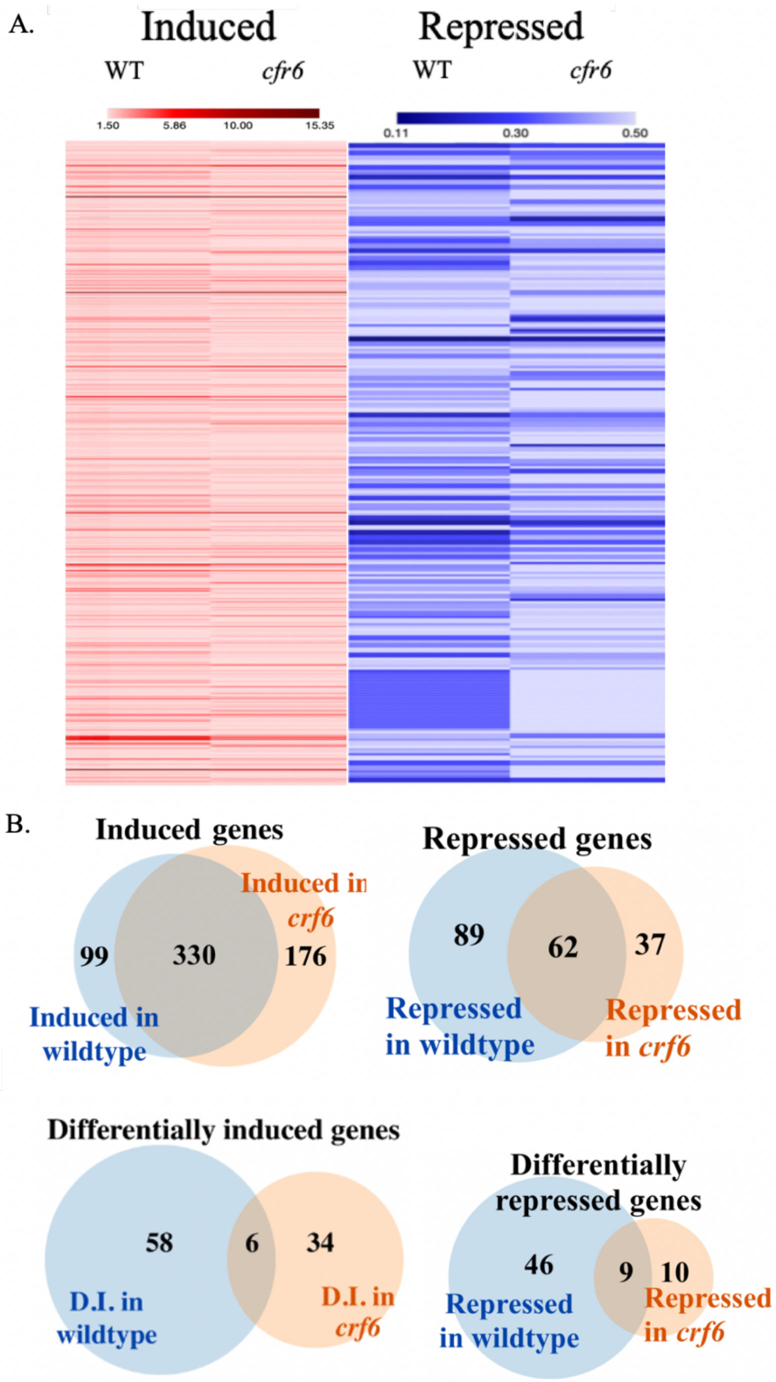

Figure 1. A. Heat map depicting the fold change in expression of genes in WT and crf6 mutant plants when treated and untreated with CK and separated into induced and repressed categories. B. Venn diagrams illustrating the cross over between the genes between genes that were induced (addition of CK caused 1.5 times greater transcription of the gene) and were repressed (addition of CK caused transcription of the gene to be reduced to half or lower) and the genes that were differentially altered in transcription in the crf6 mutant plants.

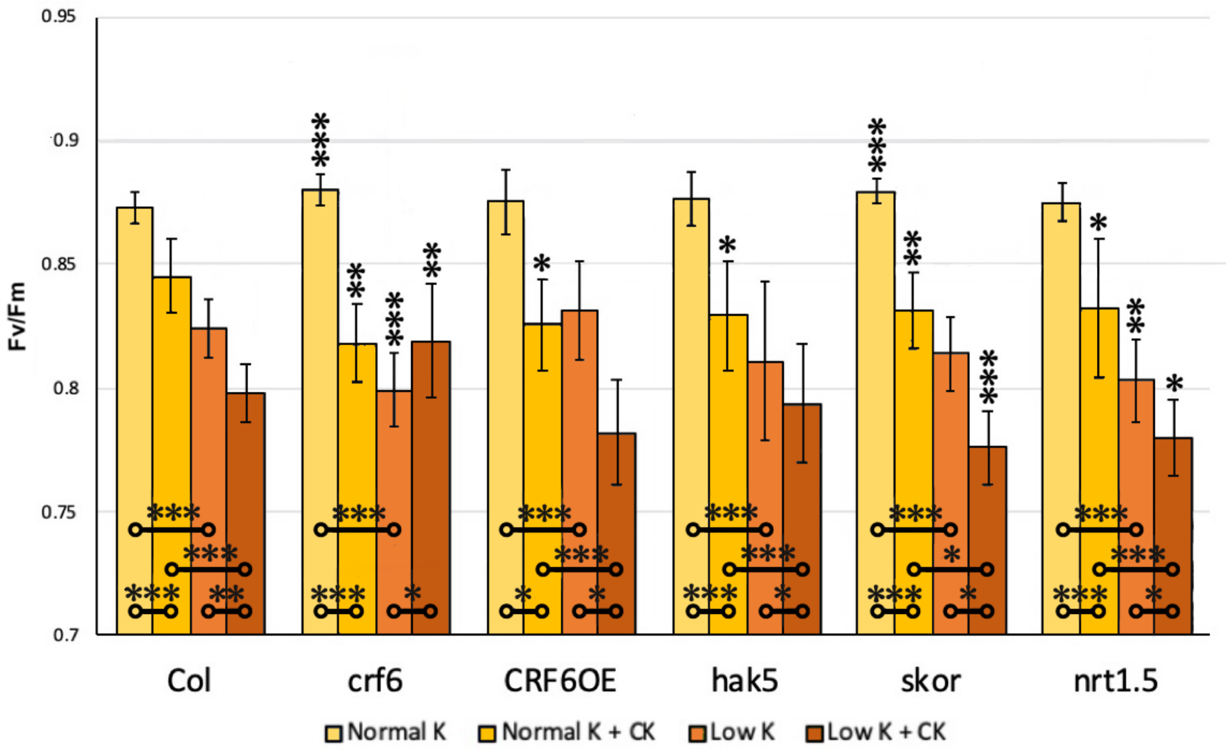

Figure 2. FV/FM measurements of altered lines ± CK. FV/FM measurements were taken to gauge the overall health of the plants after 10 days. Asterisks on comparison bars indicate significance level; *= p≤ 0.05, ** = p≤ 0.005, *** = p≤ 0.0005. Comparison bars between treatments within a line are indicated closer to the x axis with each end indicating the compared data. The asterisks above the bars indicate the significance level of the data as compared to the same treatment in WT.

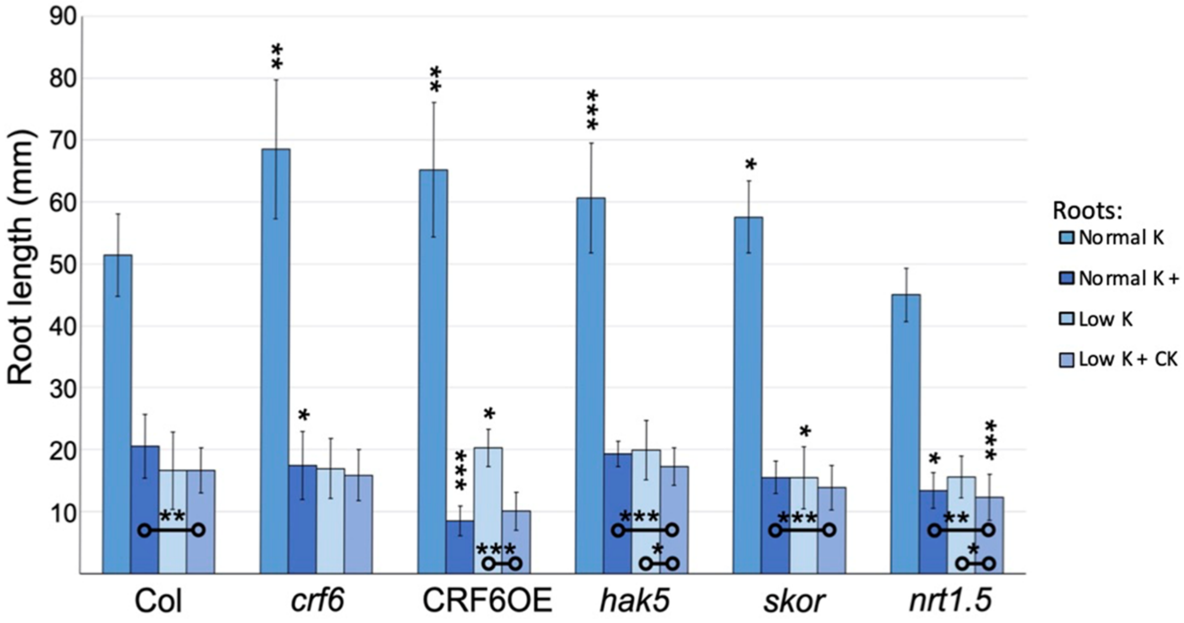

Figure 3. Root growth of altered lines ± CK. Root growth, in millimeters, 10 days after transfer to treatment and control plates. Asterisks indicate significance level; *= $p \leq 0.05$, ** = $p \leq 0.005$, *** = $p \leq 0.0005$ when an ANOVA AdHoc test was used. Asterisks above the error bars indicate significance of the length of the roots of that line as compared to that of the wildtype grown in the same treatment. The asterisks on comparison bars closer to the x axis indicate significance of differences within lines between different treatments. All plant roots grown on standard potassium media were significantly different from those grown on treatment plates ($p<.0005$).

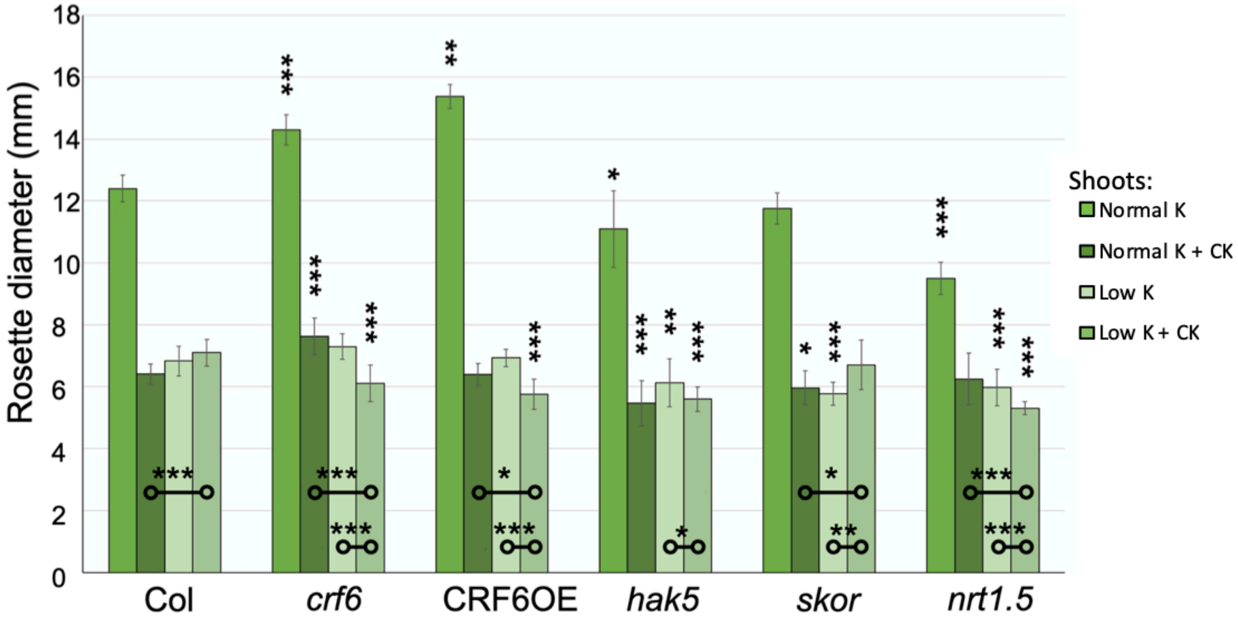

Figure 4. Rosette diameter of altered lines ± CK. Rosete diameter, in millimeters, 10 days after transfer to treatment and control plates. Asterisks indicate significance level; *= p≤ 0.05, ** = p≤ 0.005, *** = p≤ 0.0005 when an ANOVA AdHoc test was used. Asterisks above the error bars indicate significance of the length of the roots of that line as compared to that of the wildtype grown in the same treatment. The asterisks on comparison bars closer to the x axis indicate significance of differences within lines between different treatments. All plant rosettes grown on standard potassium media were significantly wider than those grown on treatment plates (p<.0005).

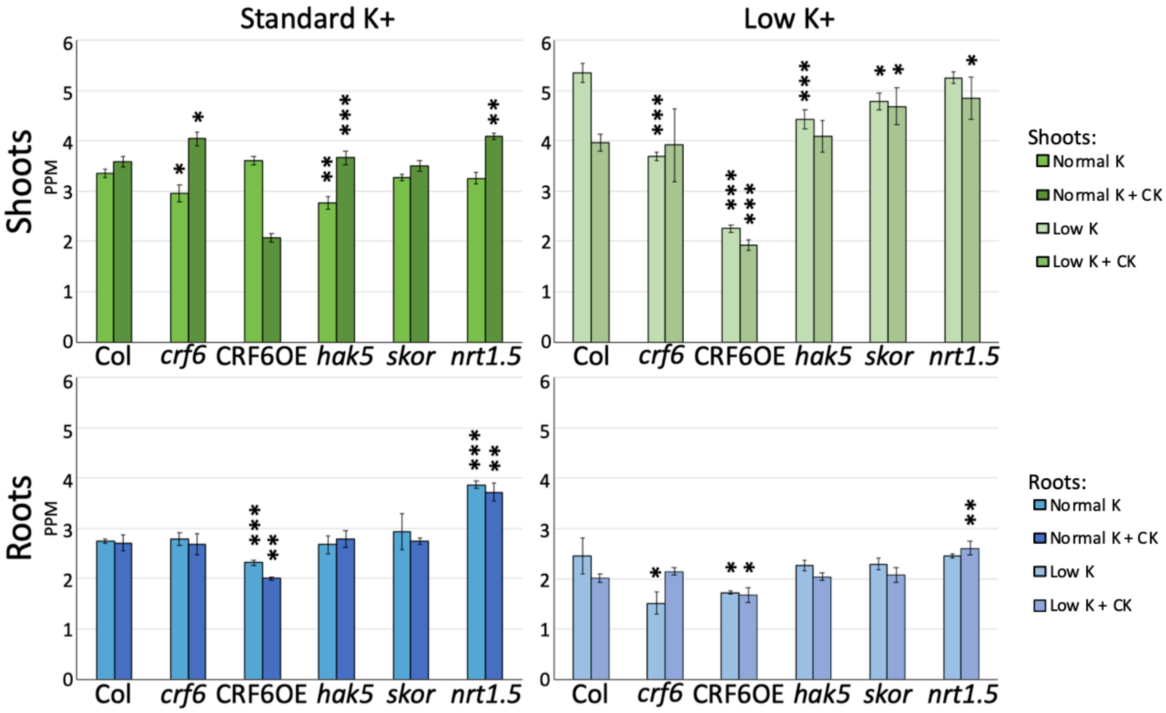

Figure 5. Potassium levels in roots and shoot of altered lines ± CK. Potassium levels as measured by ICP-OES collected from A. shoots and B. roots. Asterisks indicate significance level; *= p≤ 0.05, ** = p≤ 0.005, *** = p≤ 0.0005 when an AdHoc test was used to compare that line, treatment and tissue type to the WT of the same treatment and tissue type.

11 Supplementary data

Supplemental data is found either in Supplemental Tables S1 and S2 (appendix i) or for sequence data in the GenBank/EMBL data libraries under accession numbers GSE84770.

12 Tables

Table 1. GO term enrichment analysis of DEGs (the Genes that were induced to at least 150% and repressed by at least half of their transcription in WT with the addition of CK). Fold enrichment (FE) of the terms and false discovery rate (FDR) are indicated.

GO biological process complete	FE	FDR
de novo' IMP biosynthetic process	35.15	2.70E-03
IMP biosynthetic process	26.36	4.91E-03
cytokinin catabolic process	26.36	3.09E-02
IMP metabolic process	23.43	6.47E-03
purine ribonucleoside monophosphate biosynthetic process	23.07	3.48E-05
purine ribonucleoside monophosphate metabolic process	23.07	3.34E-05
purine nucleoside monophosphate biosynthetic process	23.07	3.21E-05
purine nucleoside monophosphate metabolic process	23.07	3.09E-05
rRNA pseudouridine synthesis	22.6	3.98E-02
syncytium formation	19.77	3.56E-04
ribonucleoside monophosphate biosynthetic process	12.73	5.62E-04
cleavage involved in rRNA processing	12.65	2.42E-03
nucleoside monophosphate biosynthetic process	12.41	1.57E-04
ribonucleoside monophosphate metabolic process	12.3	6.51E-04
nucleoside monophosphate metabolic process	12.05	1.84E-04
maturation of LSU-rRNA from tricistronic rRNA transcript	11.72	3.87E-02
snRNA metabolic process	11.46	1.23E-02
RNA phosphodiester bond hydrolysis, endonucleolytic	10.54	4.92E-02
maturation of SSU-rRNA from tricistronic rRNA transcript	10.54	1.50E-03
maturation of SSU-rRNA	10.14	4.23E-05
cytokinin-activated signaling pathway	9.95	4.63E-05
cellular response to cytokinin stimulus	9.41	7.04E-05
ribosomal large subunit biogenesis	8.87	1.01E-08
cytokinin metabolic process	8.79	1.02E-02
purine ribonucleoside metabolic process	8.79	2.89E-02
rRNA processing	8.71	1.12E-19
plant-type cell wall loosening	8.55	1.13E-02
rRNA metabolic process	8.5	1.88E-19
response to cytokinin	8.41	6.14E-07
RNA phosphodiester bond hydrolysis	8.2	4.76E-03
ribosome biogenesis	8.11	2.66E-26
purine nucleoside metabolic process	7.99	3.89E-02
ribosomal small subunit biogenesis	7.97	1.18E-05
ribosomal large subunit assembly	7.36	2.05E-02
translational elongation	7.32	4.91E-02
cellular hormone metabolic process	7.24	8.46E-03
ribonucleoprotein complex biogenesis	7	9.36E-25
maturation of LSU-rRNA	6.88	2.65E-02
ribosome assembly	6.82	2.84E-04
ncRNA processing	6.28	2.70E-16
inorganic anion transport	5.98	7.65E-04
glycosyl compound biosynthetic process	5.86	2.26E-02
ncRNA metabolic process	5.57	1.77E-15
nucleic acid phosphodiester bond hydrolysis	5.27	1.81E-02
cytoplasmic translation	5.2	3.76E-02
ribonucleotide biosynthetic process	5.17	4.78E-03
purine ribonucleotide biosynthetic process	5.02	2.28E-02
ribose phosphate biosynthetic process	4.93	6.10E-03

amine metabolic process	4.61	1.85E-02
purine-containing compound biosynthetic process	4.56	1.95E-02
purine nucleotide biosynthetic process	4.54	3.68E-02
ribonucleoprotein complex assembly	4.45	2.07E-03
ribonucleoprotein complex subunit organization	4.37	2.39E-03
nucleotide biosynthetic process	4.33	4.64E-03
nucleoside phosphate biosynthetic process	4.27	4.65E-03
embryo sac development	4.03	1.29E-02
plant-type cell wall organization	3.8	4.95E-02
RNA processing	3.35	9.17E-10
organelle assembly	3.31	4.19E-02
plant-type cell wall organization or biogenesis	3.15	1.86E-02
hormone metabolic process	3.05	2.36E-02
cellular component biogenesis	2.89	8.54E-11
gene expression	2.82	2.34E-12
translation	2.69	4.72E-03
peptide biosynthetic process	2.66	5.12E-03
RNA metabolic process	2.62	1.15E-08
peptide metabolic process	2.55	3.76E-03
regulation of hormone levels	2.54	2.88E-02
nucleobase-containing compound biosynthetic process	2.5	2.49E-02
cellular nitrogen compound biosynthetic process	2.37	3.55E-05
amide biosynthetic process	2.31	2.80E-02
cellular response to hormone stimulus	2.28	1.30E-02
response to osmotic stress	2.23	4.01E-02
cellular amide metabolic process	2.22	1.60E-02
cellular response to endogenous stimulus	2.21	1.61E-02
response to hormone	2.21	1.37E-05
heterocycle biosynthetic process	2.2	2.65E-02
response to endogenous stimulus	2.18	2.48E-05
nucleic acid metabolic process	2.17	2.31E-06
cellular nitrogen compound metabolic process	2.15	3.19E-11
heterocycle metabolic process	2.15	4.05E-09
nucleobase-containing compound metabolic process	2.15	9.17E-08
cellular aromatic compound metabolic process	2.06	3.10E-08
aromatic compound biosynthetic process	2.03	4.93E-02
organic cyclic compound metabolic process	2.03	3.63E-08
cellular response to organic substance	2.03	3.79E-02
response to lipid	2.02	4.17E-02
organic cyclic compound biosynthetic process	2.01	3.89E-02
organonitrogen compound biosynthetic process	2.01	2.86E-03
response to organic substance	1.97	7.44E-05
response to acid chemical	1.97	4.94E-03
response to chemical	1.92	2.46E-07
response to inorganic substance	1.89	4.16E-02
response to oxygen-containing compound	1.82	4.62E-03
cellular response to chemical stimulus	1.78	4.45E-02
cellular component organization or biogenesis	1.74	4.20E-05
cellular biosynthetic process	1.68	3.04E-03
organic substance biosynthetic process	1.65	4.57E-03
biosynthetic process	1.64	2.99E-03
system development	1.6	3.98E-02
anatomical structure development	1.55	4.93E-03
developmental process	1.55	4.58E-03
multicellular organism development	1.54	1.79E-02
multicellular organismal process	1.5	2.24E-02

nitrogen compound metabolic process	**1.43**	**5.54E-04**
response to stimulus	**1.41**	**2.05E-03**
organic substance metabolic process	**1.4**	**1.06E-04**
metabolic process	**1.4**	**1.54E-05**
cellular metabolic process	**1.38**	**2.87E-04**
primary metabolic process	**1.33**	**1.05E-02**
cellular process	**1.28**	**4.93E-04**
protein modification process	**0.47**	**3.53E-02**
cellular protein modification process	**0.47**	**3.49E-02**
vesicle-mediated transport	**< 0.01**	**3.02E-02**

Table 2. The GO analysis of term enrichment in genes that were differentially regulated in the crf6 plants when treated with CK as compared to wildtype.

Up regulated		
GO biological process complete	**FE**	**FDR**
thalianol metabolic process (GO:0080003)	**> 100**	**3.01E-03**
tricyclic triterpenoid metabolic process (GO:0010683)	**> 100**	**2.63E-03**
Down regulated		
GO biological process complete	**FE**	**FDR**
inorganic cation transmembrane transport (GO:0098662)	**13.2**	**3.19E-02**
cation transmembrane transport (GO:0098655)	**12.38**	**3.13E-02**
inorganic ion transmembrane transport (GO:0098660)	**12.03**	**3.27E-02**
innate immune response (GO:0045087)	**10.35**	**3.19E-02**
immune response (GO:0006955)	**10.21**	**2.86E-02**
ion transmembrane transport (GO:0034220)	**9.35**	**3.09E-02**
immune system process (GO:0002376)	**8.34**	**3.68E-02**
response to bacterium (GO:0009617)	**7.59**	**3.27E-02**
response to external biotic stimulus (GO:0043207)	**5.57**	**2.12E-02**
response to other organism (GO:0051707)	**5.57**	**1.06E-02**
response to biotic stimulus (GO:0009607)	**5.57**	**7.13E-03**
transmembrane transport (GO:0055085)	**5.55**	**3.62E-02**
defense response to other organism (GO:0098542)	**5.42**	**4.03E-02**
response to acid chemical (GO:0001101)	**4.59**	**3.21E-02**
multi-organism process (GO:0051704)	**4.15**	**3.45E-02**
response to external stimulus (GO:0009605)	**4**	**3.48E-02**
response to oxygen-containing compound (GO:1901700)	**3.78**	**4.31E-02**
GO cellular component complete		
extracellular region (GO:0005576)	**2.85**	**1.24E-02**
cell periphery (GO:0071944)	**2.62**	**7.57E-03**

Table 3. Metal and ion related DEGs in WT and crf6 in response to CK. Fold change in expression of the DEGs identified as “Metal and ion transport related” from GO enrichment analysis are noted as fully described in Supplemental Table1 and 2. Delta values for each gene is the FC crf6 vs crf6+CK value divided by the FC WT vs WT+CK values. Genes labeled as “increased” and “reduced” are alternatively regulated.

At#	Gene Description	Symbol	Predicted Gene Function	FC Col vs Col+CK	padj	FC crf6 vs crf6+CK	padj	Delta crf6 to Col CK Treatment Regulation	
AT5G09690	Magnesium Transporter 7	MGT7	Magnesium transport	**0.4487**	0.006995	**0.9287**	0.90282	**2.0700**	Increased
AT4G13420	Affinity K+ Transporter 5	HAK5	K+ uptake	**0.1670**	1.67E-05	**0.3398**	0.01742	**2.0353**	Increased
AT3G02850	Stelar K+ Outward Rectifier	SKOR	K+ transport/homeostasis	**0.3872**	0.032512	**0.6207**	0.13213	**1.6029**	Increased
AT1G32450	Nitrate Transporter 1.5	NRT1.5	K+ transport/homeostasis, Nitrate transport	**0.4822**	0.004754	**0.7577**	0.08566	**1.5713**	Increased
AT1G01580	Ferric Reduction Oxidase 2	FRO2	Iron uptake	**0.2160**	0.000411	**0.2742**	0.00166	**1.2691**	Similar
AT2G30766	Fe-Uptake-Inducing Peptide1	FEP1	Iron uptake regulator	**1.6023**	0.76095	**2.0110**	0.00545	**1.2551**	Similar
AT4G19690	Iron-Regulated Transporter 1	IRT1	Iron homeostasis	**0.3255**	0.004095	**0.4083**	0.01516	**1.2545**	Similar
AT3G12750	Zinc Transporter 1 Precursor	ZIP1	Zinc transport	**0.4139**	0.002764	**0.5082**	0.01088	**1.2277**	Similar
AT4G27860	Membrane of ER Body 1	MEB1	Manganese homeostasis, Intracellular iron sequestering	**1.3726**	0.22509	**1.5344**	0.00323	**1.1178**	Similar
AT4G34600	Casparian Strip Integrity Factor 2	CIF2	Iron homeostasis	**0.4165**	0.009451	**0.4599**	0.00212	**1.1043**	Similar
AT5G24580	Heavy Metal Associated Protein 47	HMP47	Metal ion transport	**1.7219**	0.16163	**1.8898**	0.01047	**1.0975**	Similar
AT2G28160	Arabidopsis Fe-Deficiency Induced Transcription Factor 1	FIT1	Iron uptake regulator	**0.3868**	0.00663	**0.4121**	0.00043	**1.0653**	Similar
AT3G59820	Leucine Zipper-EF-Hand-Containing Transmembrane Protein 1	LETM1	Metal ion homeostasis	**1.6059**	0.05732	**1.5005**	0.01275	**0.9344**	Similar
AT1G58340	Arabidopsis Abnormal Shoot4	ABS4	Iron homeostasis	**3.4829**	0.00052	**2.4905**	0.00244	**0.7151**	Similar
AT3G63380	Auto-Inhibited Ca2+ Atpase 12	ACA12	Calcium transport	**0.6466**	0.42115	**0.4436**	0.01875	**0.6862**	Reduced
AT2G24720	Glutamate Receptor 2.2	GLR2.2	Calcium homeostasis	**1.0045**	0.99762	**0.4180**	0.00393	**0.4161**	Reduced

Table 4. Verification of CRF6 CK regulated targets. The fold change difference in expression of HAK5, NRT1.5 and SKOR in WT and crf6 in the presence of CK (+) 2µM BA or absence of CK (Control) as conducted for transcriptome analysis, as determined via qRT-PCR. Presented as an Average ± Standard Deviation. All data from microarray has an adjusted $p < 0.05$

Genotype	**qRT-PCR**		**Microarray**	
	WT control vs WT+CK	crf6 control vs crf6+CK	WT control vs WT+CK	crf6 control vs crf6+CK
HAK5	-4.64±1.26	-0.23±1.24	-5.99	-2.94
NRT1.5	-5.08±1.87	-0.83±1.69	-2.07	-1.32
SKOR	-3.19±2.10	-0.54±1.51	-2.58	-1.61

Table 5. Additional comparisons made of the ionomics data shown in Figure 5 using ANOVA PostHoc tests. The compared treatments are labeled along the top, and the line and tissue types are listed in the first two columns. Asterisks indicate significance level; *= $p \leq 0.05$, ** = $p \leq 0.005$, *** = $p \leq 0.0005$.

		Standard K+ vs Standard K+ + CK	Standard K+ vs Low K+	Low K+ vs Low K+ + CK	Standard K+ + CK Low K+ +CK
Shoots	WT	*	***	***	*
	crf6	**	**		
	CRF6OE	***	***	*	
	hak5	**	***		
	skor	*	***		*
	nrt1.5	***	***		*
Roots	WT				**
	crf6		**	*	*
	CRF6OE	**	***		*
	hak5		*		**
	skor				**
	nrt1.5		***		**

Chapter 3: The Clade III CRFs from Arabidopsis and tomato share a common role in oxidative stress response

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Abstract

Cytokinin response factors (CRFs) are transcription factors involved in cytokinin (CK) signaling, however, CRFs appear to have functional roles beyond CK response. Several CRFs have stress-based connections, including oxidative stress in CRF Clade III members, such as AtCRF6. Here we expand initial findings for Clade III CRFs by analyzing two other members AtCRF5 of Arabidopsis and SlCRF5 of tomato for functional roles in oxidative stress response. Oxidative stress-induced differences were examined from transcriptomic responses of AtCRF5 and SlCRF5 altered lines and compare to previous AtCRF6 findings. Transcriptomic data indicates AtCRF5 is necessary for proper regulation of over 240 genes, and SlCRF5 for nearly 420 genes involved in oxidative stress response. Although it is difficult to directly compare Arabidopsis and tomato orthologs, we found similarities in functions of genes regulated by Clade III members as indicated by GO term enrichment. Examination of CK measurements conducted in a parallel manner to transcriptome analysis also indicates that changes in CK levels in response to oxidative stress are also regulated by each Clade III CRF member. Overall, these findings suggest that, in addition to their role in CK signaling. a role in the oxidative stress response is shared among Clade III CRFs .

Abbreviations:

CRF: CK Response Factor; CK: CK; ROS: Reactive Oxygen Species; MAP K: MAP Kinase; SlCRF5AS: SlCRF5-Antisense line; WT: Wildtype; DEG: Differentially Expressed Gene; FC: Fold Change; CDRGs: Clade III CRF-dependent Oxidative Stress-Regulated Genes; iP: Isopentenyl adenine; DHZ: Dihydrozeatin; cZ: *cis*-Zeatin; tZ: *trans*-Zeatin

Introduction

Cytokinin (CK) is a hormone critical to plant growth and development and is involved in regulation of senescence, root and shoot development and stress responses (Mok and Mok, 2001; Werner and Schmülling, 2009; Zwack and Rashotte, 2015). One downstream target of the CK signaling pathway is a group of transcription factors called CK Response Factors or CRFs (Rashotte et al., 2006). CRFs are a subgroup of APETALA2/Ethelene Responsive Factors (AP2/ERF) transcription factors, common to all land plants that were identified as being regulated by CK (Rashotte *et al.*, 2006; Rashotte and Goertzen, 2010). CRF proteins have been determined to have several conserved domains including: a CRF-group specific CRF domain, which distinguishes CRFs from other ERFs and is involved in protein-protein interactions, an AP2/ERF DNA-binding transcription factor domain, a putative MAP Kinase motif, and a C-terminal CRF clade specific region that delineates CRFs into clades (Rashotte and Goertzen, 2010; Zwack *et al.*, 2012).

The clade specific region defines five separate clades in angiosperms (Zwack *et al.*, 2012; Hallmark and Rashotte, 2019). In most angiosperm species, at least one member of each clade is present. The conservation of these five clades and the retention of a gene from each in nearly all angiosperms suggests that members of each clade serves a distinct function (Zwack *et al.*, 2012). This is supported by previous findings, for example, Clade I CRFs have been linked to salt stress, Clade II CRFs to cold/freezing responses, as well as Clade III CRFs and oxidative stress (Keshishian et al., 2018; Zwack et al., 2016b; Hallmark and Rashotte, 2019).

Initially, Clade III CRFs were studied in Arabidopsis in the context of their response CKs, but AtCRF6 has also been studied in its role in senescence and abiotic stress responses, particularly oxidative stress (Rashotte *et al.*, 2006; Zwack *et al.*, 2013, 2016*a*). Interestingly AtCRF5, the other Clade III CRF in Arabidopsis, has not been heavily investigated. Although

AtCRF5 is known to be rapidly and strongly induced by CK, it has not been examined for connections to oxidative stress response (Rashotte et al., 2006; Bhargava et al., 2013). In two other species where only a single Clade III CRF member is present, *Solanum lycopersicum* (tomato) and in Marshallia (an asterid) there is evidence of the regulation of these genes in response to oxidative stress (Gupta and Rashotte, 2014; Keshishian *et al.*, 2018; Melton *et al.*, 2019).

In order to better investigate connections between Clade III CRFs and oxidative stress, we have built on earlier studies of AtCRF6 oxidative stress treatment transcriptomic data (Zwack et. al. 2016a), and initial findings in tomato and the Clade III CRF, SlCRF5 (Gupta et al. 2014; Keshishian et al. 2018). Here we investigate the previously unexplored role of the homologous AtCRF5 in oxidative stress and expand upon those initially conducted on SlCRF5 in tomato with an attempt to connect these findings to those from previous Clade III oxidative stress studies. Specifically, we conducted and examined expression analyses of AtCRF5 and SlCRF5 altered lines in response to oxidative stress in comparison to each other and to existing parallel *Atcrf6* data. Then we more deeply investigated links between Clade III CRF roles in oxidative stress and CK by measuring CK levels of in lines with reduced or lacking expression of these three homologous Clade III CRFs after the plants had been exposed to oxidative stress (H_2O_2).

Results

Similarities between Clade III CRF sequences and domains

To investigate the possibility of Clade III CRFs sharing functional roles, the protein sequences of AtCRF5, AtCRF6 and SlCRF5 were aligned using BLAST and their conserved domains were examined (Fig. 1B). The previously identified structure, locations and sequences of the CRF, AP2/ERF domain, putative MAP Kinase (MAP K) binding motif and the C-terminal

Clade III-specific domain are all retained in AtCRF5, AtCRF6 and SlCRF5 (Fig. 1) (Nakano *et al.*, 2006; Rashotte and Goertzen, 2010; Zwack et al., 2012). The highest density of conserved amino acids is within the three domains but is entirely conserved within the putative MAP K binding motif. The AP2/ERF domain, which contains the amino acids used for binding to DNA and functioning as a transcription factor is the next most highly conserved sequence region, followed by the CRF domain and then the Clade III specific sequence (Fig. 1). Though sequence conservation has previously been examined, direct comparison of these three genes with domains clearly defined had not yet been conducted. A full protein amino acid sequence comparison of these Clade III proteins revealed that the two Arabidopsis CRFs were more closely related to each other, with 54.4% identity, than they were to the tomato CRF, SlCRF5, which shared 36.5% with AtCRF5 and 37.4% identity with AtCRF6, with the majority of the similarities within the conserved domains (Fig. 1). This pattern of similarity suggests that a single Arabidopsis Clade III gene was duplicated after the species had diverged (Fig. 1A). To investigate how this duplication affected the oxidative stress-related function the Clade III CRFs, the SlCRF5-Antisense lines (SlCRF5AS), its wildtype (WT) tomato background “MicroTom” or MT, the Arabidopsis mutants *Atcrf5* and *Atcrf6* and their WT background Columbia-0 were analyzed transcriptionally.

While the sole member of Clade III in tomato, SlCRF5, has been shown to be induced by oxidative stress, there are two members of Clade III in Arabidopsis, and only AtCRF6 has been shown to be similarly induced by oxidative stress(Zwack *et al.*, 2012, 2016*c*; Keshishian *et al.*, 2018). The examination of the other Arabidopsis Clade III member, AtCRF5, for a similar oxidative stress response may either solidify the general role of CRF Clade III genes in this abiotic stress response or potentially reveal divergence in gene function after duplication.

Promoter reporter line GUS expression analysis

In order to investigate if induction in response to oxidative stress is a common response shared by all three of these Clade III CRFs, reporter GUS staining was conducted on SlCRF5::GUS, and AtCRF5::GUS, (Fig. 2; Zwack et al., 2013; 2016; Keshishian et al., 2018). Whole plants were floated in 3mM MES were treated with 20mM H_2O_2 for 6hrs and then stained with GUS solution. As seen in previous studies, SlCRF5 is strongly induced in the vasculature as well as other tissues throughout the plant when exposed to exogenous hydrogen peroxide (Fig. 2). Interestingly, a strong induction of AtCRF5 GUS expression in vascular tissue, especially in leaves, was observed but less so in other tissues. This pattern is similar to what has been previously noted for AtCRF6, that there is oxidative stress regulation that is largely limited to vascular tissues (Zwack et al., 2013). Despite some differences between Arabidopsis and tomato Clade III CRF patterns, there is a common increase in expression for each of these CRFs in response to oxidative stress.(Fig. 2). After confirming that AtCRF5 is induced by oxidative stress, a more detailed examination of differences in transcriptional response to oxidative stress was investigated in backgrounds with reduced expression of both AtCRF5 (the *crf5-6* mutant) and SlCRF5 (SlCRF5AS).

Transcriptomic response to oxidative stress treatment

Whole 10 day old *Atcrf5,* SLCRF5AS plants and their WT counterparts (Columbia-0 and MicroTom, respectively) were floated in 3mM MES solutions with and without 20mM H_2O_2 for 6 hours, after which RNA was extracted. Three biological replicates of each line in both the H_2O_2 treated and untreated conditions were sequenced using illumine sequencing. Alignment to the *Arabidopsis thaliana* and *Solanum lycopersicum* reference genomes yielded approximately 20M reads per sample. From this alignment, transcriptomic analysis was performed to identify differentially expressed genes (DEGs). Statistically significant DEG) were identified as those genes with expression levels that were induced or repressed to levels greater than 150% or less than 50%, respectively, of those measured under control conditions (Table S1-3). Heatmaps show the down regulated DEGs in blue and up regulated DEGs in red, and the Venn diagrams below the heatmaps indicating the number of genes that were differentially up or down regulated in the mutant and WT backgrounds (Fig. 3). The two Arabidopsis Clade III CRF mutants differed significantly both in their response to hydrogen peroxide, and in their divergence from WT in the specific set of regulated genes.

While a standard way to compare transcriptomes is through the examination of changes in DEGs within samples, in analysis of the AtCRF5 stress transcriptomic data that there were several DEGs that were uniquely regulated by oxidative stress in the *Atcrf5* background and not in WT. Because of this we determined the numbers of unique Clade III regulated oxidative stress DEGs in each sample set (Fig 3). The transcriptomic response of *Atcrf5* to oxidative stress showed the greatest divergence from that of WT; of the 166 genes induced, 3 were exclusively induced in WT and 7 were so in the mutant, and of the 131 genes that were in the repressed, 13 were exclusively repressed in WT and 19 were also repressed in the mutant (Fig. 3). The *Atcrf6* transcriptome response showed minor deviation in contrast to WT; of the 464 repressed genes, only 3 were repressed only in the mutant, and did not diverge from 278 H_2O_2 up regulated genes observed in WT.

Much like in *Atcrf6*, an examination of the SlCRF5AS transcriptome showed only minor differences in regulation from WT in response to oxidative stress. Of the 288 DEGs that were H_2O_2 induced in the SlCRF5AS background, only three genes were exclusive to SlCRF5AS, and of the 131 H_2O_2 repressed DEGs 22 were exclusive to SlCRF5AS (Fig. 3).

Genes that were H_2O_2 regulated in the mutant/altered backgrounds differentially as compared to transcriptional changes measured in WT were identified for further investigation into the roles of these CRFs. To identify these alternatively oxidative stress-regulated genes (CDRGs), the foldchange (FC) of each gene in the mutant/AS was divided by the FC in WT and those with significant FC/FC quotients greater than 1.5 and less than 0.5 were selected for further investigation (Table S4-6). These CDRGs were then sorted into groups; those that were more strongly regulated in WT, those that were more strongly regulated in the mutants/AS, and those that were regulated in the opposite direction in the mutant/AS from that in WT (Fig. 4).

137 CDRGs were found in the *Atcrf5* data; 84 had been induced in WT, and 53 had been repressed (Fig 4). Of the *AtCRF5* CDRGs from the induced list, 72.6% (61) were more strongly induced in the *Atcrf5*, only 2.4% (2) were more strongly induced in WT, and the remaining 27.4% (23) were repressed in the *Atcrf5*, rather than induced as they had been in WT. Of the repressed *AtCRF5* CDRGs identified repressed WT DEGs, 84.9% (45) were more strongly repressed in the mutant, zero were more strongly repressed in WT, and the remaining 15.1% (8) were induced in the mutant contrary to the induction observed in WT. These significant deviations of *Atcrf5* from the oxidative stress-induced WT regulation of genes was not present in the two other Clade III CRFs, as shown in the DEG Venn diagrams of Figure 3, and highlighted in Figure 4.

Only 54 CDRGs were found in the *Atcrf6* data. Of the 38 genes that were induced in WT, 47.4% (18) were more induced in the mutant and 52.6% (20) were more induced in WT (Fig. 4). The last 29.6% (16) CDRGs were found in the repressed list and were, like those on the induced list, split fairly evenly; 43.8% (7) were more strongly repressed in the *Atcrf6* and 56.3% (9) were more strongly repressed in WT (Fig. 4).

The SlCRF5AS transcriptome results revealed 418 CDRGs (Fig. 4). Of these CDRGs, 68.7% (287) were induced; 17.1% (49) of these genes were more strongly induced in WT, and 82.9% (238) were more strongly induced in SlCRF5AS. Of the 131 repressed CDRGs, only 3.1% were more strongly repressed in WT, while the remaining 96.9% were more strongly repressed in SlCRF5AS. The greater repression or induction in SlCRF5AS in response to oxidative stress than observed in WT may indicate that the tomato Clade III CRF plays a role in mitigating transcriptional responses to $H_2O_{2.}$.

Since the orthologs of most Arabidopsis genes are not currently known in tomato, there is a difficulty in making direct comparisons between CDRGs from our transcriptome findings presented here. Instead of making direct comparisons, we looked to compare similar Gene Ontology (GO) enrichment terms for specific functions that are well defined in each species. GO term lists were assembled and shared terms were identified (Fig. 5, Table S7).

The shared terms between all three sets of CDRGs relate to the response to oxidative stress, including response to: chemicals, stress, abiotic stimulus, oxygen-containing compounds, and oxidative stress (Fig. 5). The terms shared solely between the two sets of Arabidopsis CDRGs were very similar to that of the terms common to all three but with the inclusion of response to hypoxia, decreased oxygen levels and nitrogen compounds (Fig. 5). The only two terms shared between solely the CDRGs of *Atcrf6* and SlCRF5AS were those relating to the response to hydrogen peroxide, but those shared between the CDRGs of *Atcrf5* and SlCRF5AS were response to heat and temperature stimulus. Terms that were identified as unique to each set of CDRGs included more terms relating to oxidative stress but included responses to biotic stresses as well. The terms unique to the *Atcrf5* CDRGs included responses to the following: high light (and red/far red light), salt, abscisic acid, alcohol, lipids, hormones, organic substances, endogenous stimulus, organonitrogen compound, and to organic cyclic compound. Terms unique to the *Atcrf6* CDRGs included toxin metabolic and catabolic process and detoxification as well as many relating to defense responses to fungi and bacteria. SlCRF5AS CDRG unique terms include regulation of: jasmonic acid signaling, response to wounding, defense responses, sterol and steroid metabolism, signaling, osmotic stress, salt stress, and protein complex oligomerization.

A closer investigation of the tomato CDRGs revealed several genes that are involved in CK signaling and biosynthesis (Table 2). In the *Atcrf5* background, UGT76C2, a gene known to be responsible for conversion of CKs into *N*-conjugated forms was 2.7 fold induced (padj 0.018), but was not significantly altered in expression in WT (Sakakibara, 2006).

Previous work has shown that AtCRF6, AtCRF5 and SlCRF5 are all induced by CK, but to determine if these CRF Clade III genes might also be involved in regulating CK biosynthetic process, the levels of different CKs in *Atcrf5*, *Atcrf6*, and SlCRF5AS were investigated (Rashotte et al., 2003; Zwack et al., 2013; Gupta and Rashotte, 2014).

CK levels in response to oxidative stress

The Clade III altered lines were treated with or without H_2O_2 in MES buffer as they had been in the transcriptomic analysis, then their CK levels were measured by LC-MS/MS and examined in context of CK biosynthetic pathway metabolites (Fig. 6). Measured CKs are displayed in a table form similar to the CK biosynthesis pathway with CK type in columns (iP, tZ, DHZ, and cZ) and specific form in rows with the precursor CK names are followed by the abbreviation -RMP (riboside-monophosphate), -R (riboside), - (active form), 7N and 9N (*N*-glucosides), and OG and ROG (*O*-glucoside and riboside- *O*-glucoside, respectively) (Sakakibara, 2006).

In the mutant/AS lines, even before treatment, the levels of CK conjugates significantly deviate from that measured in WT (Fig, 6). Both the Clade III Arabidopsis mutants had only about half of iPRMP and iPR levels measured in WT (44.1% in *Atcrf5,* and 63.0% in *Atcrf6*). iP7G levels in *Atcrf5* were also reduced, measuring 80.6% of those in WT, which contributed to a significantly lower level total iP-types in *Atcrf5* (76.3% of that in WT) (Fig. 6). In *Atcrf6* levels of the active tZ, the precursor tZR and the reversible metabolite tZROG were about 70% of that measured in the WT. Both *Atcrf6* and *Atcrf5* had lower concentrations of the tZ7G and tZ9G conjugates; *Atcrf6* contained about 70%, and *Atcrf5* contained about 75% of both the tZ7G and tZ9G conjugates, respectively (Fig. 6). Ultimately the two Arabidopsis Clade III mutants contained only 75.7% (*Atcrf5*) and 69.1% (*Atcrf6*) of the total tZ-types measured in WT. For DHZ compounds, *Atcrf5* contained 71.4% of the DHZ9G, and *Atcrf6* contained 68.8% of the DHZ7G in WT. *Atcrf6* contained 72.5% of the total DHZ-types measured in WT (Fig. 6). In the cZ-types, *Atcrf5* contained 64.3% of the cZROG measured in WT, and *Atcrf6* contained 60.7% of the active cZ measured in WT, but both *Atcrf5* and *Atcrf6* contained 58.1% and 51.9%, respectively of the cZRMP, and overall, about 60% of the total cZs found in WT.

As found in the untreated *Atcrf5* and *Atcrf6* lines, SlCRF5AS contained disparate levels of CKs as compared to WT (Fig. 6). In tomato, the conjugates forms were the only CK levels to deviate from those measured in WT; in both tZ and DHZ, the 7G levels were 59.5% and 36.5% of WT, respectively (Fig. 6). In the DHZ conjugates, the 9G and OG were also significantly reduced in concentration (28.7% and 44.5% of those observed in WT). These reduced levels resulted in an overall reduction of all tZ levels to 61.4% of WT and of all DHZs to 35.3% of the total in WT (Fig. 6). The only increase in levels in the SlCRF5AS lines was found in the cZROG, which contained 250% of the level measured in WT.

H_2O_2 treatment resulted in different changes to CK levels in each line. H_2O_2 treated WT tomato CK levels, as compared to untreated were reduced in iPR (51.2% of that in WT untreated), tZR (40.7%), tZ (75.0%), tZROG (56.3%), DHZ7G (9.3%), DHZ9G (81.0%), and DHZOG (58.5%) (Fig. 6). In contrast, WT tomato had increased levels of cZ (144.4%). When SlCRF5AS was treated with H_2O_2, the only CK level that was shifted similar to WT was the total cZ measurement (153.0% of that measured in SlCRF5AS untreated) (Fig. 6). The H_2O_2 treated SlCRF5AS line had increased levels of iP7G (138.7%), tZ7G (139.7%), DHZ9G (174.4%), DHZOG (193.4%), cZRMP (180.0%), and cZR (176.5%), as compared to SlCRF5AS untreated.

When the Arabidopsis WT was treated with H_2O_2, significant changes were measured in the concentrations of iPRMP (28.6% of untreated), iP9G (82.2%), tZRMP (38.3%), tZ9G (84.5%), and cZROG (72.0%), with only two CKs increased; DHZR (589.0%) and cZR (307.0%)(Fig. 6). When *Atcrf5* was treated with H_2O_2, as compared to the untreated line, significant increases (between 125% and 175% of untreated) in the levels of iP7G, iP9G, tZR, tZ7G, tZ9G, tZOG, tZROG, DHZR (392.3%), DHZ7G, DHZ9G, and cZOG, with even greater increases in cZRMP (251.1%), cZR (334.4%), cZ (185.0%), and cZROG (187.0%)(Fig. 6). *Atcrf6* CK measurements were not as widely affected by the H_2O_2 treatment as were those of *Atcrf5*. In the treated *Atcrf6* plants, the levels were decreased in iPRMP (64.3%) and DHZ9G (53.3%) and increased in iPR (151.2%), tZR (147.1%), DHZR (700%), cZR (372.3%) and in cZ (152.9%), as compared to *Atcrf6* untreated plants (Fig. 6).

In order to compare general changes in the levels of each CK between different lines treated with oxidative stress were calculated and presented as a percentage of the untreated; %=(untreated level-treated level)/(untreated level). These values were then compared between each wildtype background and the altered lines (excluding values for DHZOG, which was not detected in Arabidopsis). Types of CKs that are differentially regulated between altered lines and WT by at least 20% are shown in Figure 6.

The three altered Clade III CRF lines shared 10 differentially regulated levels of CKs; iPRMP, iP9G, tZRMP, tZ7G, tZ9G, tZOG, tZROG, DHZ7G, cZRMP, and cZOG, all of which were up regulated (or less down regulated) in the mutant/AS lines (Fig. 6). Interestingly, CKs common to two of the three altered lines were also more upregulated (or less down regulated) than they were in the WT; in *Atcrf5* and SlCRF5AS, iP, iP7G and DHZ9G, in *Atcrf5* and *Atcrf6*, cZ, cZ9G and cZROG, and in *Atcrf6* and SlCRF5AS, tZR. Uniquely altered in concentration in *Atcrf5* was a less upregulated iPR. In only *Atcrf6* iP, iP7G, tZ and DHZ9G were more down regulated than in the WT. Only in SlCRF5AS were iPR, tZ, and cZR more upregulated (or less down regulated), and were cZ, cZ9G and cZROG more down regulated (or less up regulated). The differentially regulated levels of these various kinds of CKs in the altered line suggest that, in response to oxidative stress the Clade III CRFs affect the CK biosynthetic pathway.

Discussion

In order to examine connections between Clade III CRFs in Arabidopsis and tomato we conducted a general inspection between the amino acid sequences of these CRFs revealing several highly conserved domains; the CRF domain, the AP2/ERF domain, the putative MAP K binding site and the Clade III specific region (Fig. 1). The protein sequence BLAST alignments showed that the Arabidopsis Clade III CRFs were more closely related to one another than they were to the tomato CRF (Fig. 1). This indicates that though AtCRF5 and AtCRF6 are distinct from one another, they are still more similar to each other than they are to SlCRF5 and could potentially mean that their functions are also more similar to one another than to that of SlCRF5.

Despite the differences in the sequences, previous work has indicated that these Clade III CRFs are all induced by CK, and this common response indicated that they may have common functionality (Rashotte et al., 2006; Shi, Gupta, and Rashotte, 2011; Gupta and Rashotte, 2014). While this induction by cytokinin of Clade III member transcripts has been examined in several species and appears to be a common feature of this group among CRFs, as reviewed in Hallmark and Rashotte, 2019, we wanted to further investigate if there were other functional common transcriptional roles that belong to this clade. Recent work has indicated that each CRF clade contains as set of strongly conserved promoter cis-elements, including the Clade III CRFs that appear to have some connections to stress responses (Powell et al., 2019). The primary work has been with the oxidative stress response with AtCRF6 in Arabidopsis, where there have been clear connections established (Zwack *et al.*, 2013, 2016*a*). Additionally, there has been some limited examination of oxidative stress response in Clade III CRFs outside of Arabidopsis, including in tomato, an asterid genus, Marshallia, and a few Brassicas which suggests that CRFs in this clade could be generally responsive to oxidative stress (Gupta and Rashotte, 2014; Melton et al., 2019; Kong et al., 2018). These reports lead us to conduct a more careful examination of oxidative stress response by H_2O_2 treatment of AtCRF5, an Arabidopsis paralog of AtCRF6 previously unexamined for oxidative stress and its paralog tomato gene, SlCRF5 that is known to be induced by H_2O_2 (Gupta and Rashotte, 2014).

To conduct these examinations, we used H_2O_2 in this study because it is a general oxidative stressor, exposing every organelle and tissue to the reactive oxygen species that create oxidative stress, and because it was the primary oxidative stressor used in previous studies (Zwack et al., 2016; Keshishian et al., 2018). Initial examinations made use of promoter GUS lines for both AtCRF5 and SlCRF5 that had been previous examined, but not for response to oxidative stress. Results from this, shown in Figure 2, revealing that both AtCRF5 and SlCRF5 can be induced by oxidative stress treatment. Specifically, AtCRF5 oxidative stress GUS expression seems to be primarily induced following vascular tissue as seen in leaves and cotyledons, which is similar to that previously found for AtCRF6 (Fig. 2A; Zwack et al., 2013). SlCRF5 oxidative stress expression appears to be more broadly induced throughout the plant than either of the Arabidopsis Clade III CRFs (Fig. 2B). While it is unknown why this difference might be, the general induction of SlCRF5 is consistent with previous qPCR examinations (Gupta and Rashotte, 2014). Together this provides good evidence for oxidative stress induction of this Clade, although possible differences between Arabidopsis and tomato tissue specificity.

After finding that AtCRF5 and SlCRF5 are both linked to oxidative stress response from reporter line analyses, RNAseq transcriptome analyses were performed on H_2O_2 treated and untreated *Atcrf5* and SlCRF5AS lines and their respective WTs then compared to the previously examined *Atcrf6* transcriptome (Fig. 3; Zwack et al., 2016). Selected DEGs were confirmed by qPCR after oxidative stress-treatment to validate RNAseq results (Table 1) then DEGs were generally compared to each other (Fig 3-5).

A comparison of the total number of genes that were similarly regulated after loss or reduction of a Clade III CRF compared to WT revealed some small, but interesting differences. Transcriptome analysis revealed that in the *Atcrf5* background nearly 10% (26 of the 281) of DEGs after exposed to oxidative stress were not also differentially expressed in WT, and nearly 6% (16 of 271) of the DEGs found in WT were not differentially expressed in the mutant background. This was not similarly observed in *Atcrf6* (only 99.6% of DEGs in the *Atcrf6* background were also differentially expressed in WT). However, in the SlCRF5AS background there was about 6% (25 of 419) of DEGs that were not differentially expressed in WT. Although these are small differences, it appears to suggest that AtCRF5 may have a slightly distinct or different influence on the transcriptional oxidative stress response than do its homologs. In contrast, changes in AtCRF6 are almost solely within the standard WT oxidative stress responsive DEGs, with SlCRF5 intriguingly in between AtCRF5 and AtCRF6 numbers.

Our analysis of the DEGs showed that in each line many genes were altered in expression when exposed to oxidative stress. Though the majority of the genes were altered in the mutant/AS background in a manner similar to that in WT, a number were differentially regulated without the fully functional Clade III CRF (Fig. 3, 4).

Clade III CRF-dependently oxidative stress-regulated genes (CDRGs) were identified from each of the altered lines (Table 1). CDRGs were identified as those with at least a 50% difference between the WT and modified lines in the FC in regulation between the treated and untreated plants, and therefor were should rely on each CRFs for proper regulation in oxidative stress.

In both the *Atcrf5* and SlCRF5AS transcriptomic data, at least 80% of the DEGs found were also differentially regulated (i.e., were CDRGs), while only about 7% of the DEGs found in *Atcrf6* were found to be CDRGs (Fig. 4). Interestingly, most of the *Atcrf5* CDRGs were found to be regulated in the opposite direction from that observed in WT; 56.3% of genes induced in WT were repressed in the mutant background, and 67.8% of genes repressed in WT were induced in the mutant background. Not a single CDRG in either *Atcrf6* or SlCRF5AS showed a similar pattern of opposing regulation (Fig. 4). This indicates that AtCRF5 plays a pivotal role in the transcriptional response to oxidative stress and suggests that AtCRF5 is required for either the transcriptional regulation of those genes, or that it is key to the induction or repression of transcription factors that control their regulation (such as one of the WRKYs, ERFs, RAPs and/or ZATs that are all among the *Atcrf5* CDRGs) (Table S5).

While no SlCRF5AS CDRGs were expressed in opposition to what was observed in WT, nearly every gene from the DEG list was differentially regulated between the WT and mutant background(418 of 419), suggesting that the proper transcriptional response of tomato to oxidative stress relies on SlCRF5. Most (87.3%) of the SlCRF5AS CDRGs were exaggerated in their transcriptional regulation as compared to WT, which suggests that SlCRF5 normal functions as a major negative regulator of the oxidative stress response.

The CDRGs of each of the three modified lines were themselves investigated by searching for similarities in their known functions (via GO term enrichment analysis) to find what Clade III CRFs may share (Fig. 4, 5). The only common GO terms found between the three CRFs were those involved in stress responses (Fig. 5), further supporting that these Clade III CRFs are all involved in regulating the oxidative stress response. The GO terms involving more specific or unique functions seemed to be specific to only one of the three Clade III CRFs. Interestingly, all *Atcrf5* specific GO terms were related to abiotic stresses (salt, light, drought, and abscisic acid), those unique to *Atcrf6* were terms related to biotic stresses (infectious bacteria and fungi), while the terms unique to SlCRF5AS included responses to both biotic (e.g., response to the jasmonic acid pathway and wounding) and abiotic (e.g., osmotic stress, salt stress stimuli) (Fig. 5). These findings could be the result of the paralogous Arabidopsis genes undergoing subfunctionalization after the Clade III CRF duplication event that gave rise to AtCRF5 and AtCRF6, where in the functions of the original Clade III CRF in biotic and abiotic stressed were divided such that AtCRF5 took on more of the roles in abiotic and AtCRF6 took on the biotic stress responses.

Despite the lack of GO enrichment term list inclusion of CK terms, and because Clade III CRFs are induced by CK and involved in the CK signal cascade, the CDRG lists were manually examined for CK regulating genes (Zwack *et al.*, 2016*a*; Keshishian *et al.*, 2018). Since CK metabolism can only be moderately predicted by changes studied at the transcript levels, we took an independent approach and directly measured CK levels by LC-MS/MS after OX stress treatment (Fig. 6). As CK levels have been shown to be influenced by various stresses (Nishiyama *et al.*, 2011; Keshishian *et al.*, 2018), and Clade III CRFs have been linked to oxidative stress and CK (reviewed in Hallmark and Rashotte, 2019), we investigated the possibility of the involvement of Clade III CRFs in the regulation of CK levels in oxidative stress. It was found that even without oxidative stress treatment CK levels differed between the WT and altered lines (Fig. 6). The forms of CK found in significantly different quantities in Clade III mutants/AS were all (except cZROG in SlCRF5AS) in lower concentrations than had been found in the WTs. The tomato AS line had reduced levels of the CK *N*- and *O*-conjugates but levels of the active base forms and precursor RMP forms similar to those in WT (Fig. 6). The Arabidopsis plants, however, had lower levels in both the RMP precursors and the conjugates, and *Atcrf6* even contained less of the active tZ and cZ base forms (Fig. 6). These differences in CK levels indicate that these Clade III CRFs have a significant effect on the CK biosynthetic pathway even under standard conditions. This is potentially not too surprising, since each of these Clade III genes are induced by CK and are known to be connected to other CK signaling pathway genes that can influence CK biosynthesis (Rashotte *et al.*, 2006; Sakakibara, 2006; Cutcliffe *et al.*, 2011; Zwack *et al.*, 2012).

CK levels measured in this study after exposing plants to oxidative stress indicate that they also have an effect on the regulation of CK creation and conjugation under oxidative stress similar to previous findings (Fig. 6; Nishiyama *et al.*, 2011; Keshishian *et al.*, 2018). When exposed to oxidative stress, the WT tomato had reduced levels in all of the DHZ conjugates, while levels of both DHZ9G and DHZOG were increased in the altered line. Three genes within the list of SlCRF5AS CDRGs are thought to be part of CK biosynthesis and are predicted to function in *O*- and *N*-conjugation of CK, which could be part of the difference seen in levels of these conjugate forms compared to WT (Table 2).These CK-related CDRGs may be contributing to the divergence from WT CK regulation, and this potential link warrants further investigation. The reduction observed in DHZ conjugates in WT plus oxidative stress resulted in levels comparable to those measured in the AS line without oxidative treatment (Fig. 6). This could mean that under standard conditions SlCRF5 is involved in suppressing the reduction of DHZ conjugates which occurs during oxidative stress. SlCRF5 may also play a role in the regulation of tZR (transported form of tZ) concentrations, as the tZR levels in WT were reduced to less than half of those measured when the plant was not exposed to H_2O_2, but the tZR levels remained unchanged in SlCRF5AS plus H_2O_2.

The CK measurements in Arabidopsis suggest that both Clade III CRFs influence the changes in CK levels that occur as a response to oxidative stress. The *Atcrf5* data indicate that this gene could play an important role in preventing an increase in the levels of nearly every CK conjugate with oxidative stress, as all but cZ9G were increased, including iP9G and tZ9G which were both reduced in WT + H_2O_2. Interestingly, UGT76C2 was strongly induced (2.7 FC) in the *Atcrf5* mutant background in the presence of H_2O_2, but not in WT. UGT76C2 is a major CK biosynthesis enzyme involved the *N*-conjugation of active CKs forms (Hou et al., 2004; Wang et al., 2011). An increase in UGT76C2 expression should result in higher levels of both iP9G and tZ9G levels as seen (Fig. 6). While additional study is needed to further examine if specific

CRFs affect UGT76C2 regulation, is it interesting to note that there is no corresponding increase in either UGT76C2 expression or CK *N*-conjugate form levels in the AtCRF6 mutants background with H_2O_2, in fact, there is a significant decrease of *N*-conjugates in *Atcrf6*when treated with oxidative stress (Zwack *et al.*, 2016*b*), again potentially suggesting a divergence of gene function between this pair. AtCRF5 may also influence the levels of CK precursors and transported forms, as the reductions in iPRMP and tZRMP were not present as they had been in WT after oxidative stress treatment. Also, cZRMP and cZ were highly increased in the mutant, which did not occur in WT. In the mutant background, the increases of many CKs that are decreased in WT with oxidative stress is very similar to that observed in the SlCRF5AS background, which suggests that, like SlCRF5, AtCRF5 could be involved in suppressing some of the pathways that increase different parts of CK biosynthesis.

AtCRF6, like the other two Clade III CRFs, was also found to influence the CK biosynthetic pathway (Fig 6). The reduction in the precursors of iP and tZ observed in WT in response to oxidative stress does not occur to the same degree in *Atcrf6,* in fact, the transported forms of all CKs are upregulated in the mutant, as they had been for DHZR and cZR levels in tomato. A previous examination for oxidative stress regulated CK-related genes in AtCRF6 from Zwack et. al 2016, found both the CK transporter ABCG14 and the CK biosynthesis enzyme LOG7 involved in converting CK RMP precursor forms into the active form. Each of these could be related to changes seen in CK levels, from increases in active CKs with LOG7 to regulation of riboside transported forms with ABCG14 in the mutant line. AtCRF6 may function as a negative regulator in the formation of iP9G and tZ9G in oxidative stress, as the oxidative stress-induced reduction of these CKs was not observed in *Atcrf6* as they were in WT. This is similar to trends observed in the other Clade III mutant CK measurements.

Unlike the patterns observed in the transcriptomic data, the overall examination of CK concentrations suggest that, in this role, SlCRF5 may function more like AtCRF5 than like AtCRF6, which showed less differential CK regulation from WT than had the other CRFs. Moreover, these data further connect oxidative stress and CK and suggest that CRFs are involved in contributing to that connection.

Though the mechanisms remain unclear, the results here show that Clade III CRFs in tomato and Arabidopsis are regulating factors in both oxidative stress response and in CK biosynthesis. The functions of Arabidopsis Clade III CRFs are not fully overlapping and to differ from each other and from that of tomato. The patterns of transcriptional regulation by AtCRF6 and SlCRF5 and of the CK biosynthetic regulation by AtCRF5 and SlCRF5 suggest that the AtCRFs may have begun to subfunctionalize after genetic duplication, yet that the ancestral single Clade III gene of these group may have played a role very similar to that of SlCRF5.

The CRF Clade III CRFs have been connected to the oxidative response by work done in Marshallia, an asterid, and several Brassicas (Melton et al., 2019; Kong et al., 2018). Linking a species from each Solanales, Asterales and Brassicales plant groups suggests that the role in oxidative stress could be common to most if not all Clade III CRFs. The involvement of Clade III CRFs in the oxidative stress response, in combination with the presence of a member in every angiosperm species examined, suggests that Clade III CRFs could provide a starting place to begin to examine and understand the oxidative stress response pathway in angiosperms as a whole (Zwack et al., 2012; Powell *et al.*, 2019).

Methods

Growth conditions and plant materials

Arabidopsis seeds were hydrated for 30min, placed on pre-soaked soil, Sunshine mix #8 or Promix BX, and put into a growth chamber set to 22˚C/18˚C on a long day cycle (16hrs light in 24 hour cycle). Tomato seeds were treated the same but put into a chamber at 26˚C/22˚C on the same 16:8 hour light:dark cycle. Arabidopsis mutants *crf5-6* and *crf6-2* were used for analysis along with their wildtype background, Columbia-0, as previously described in Rashotte et al., 2006 and Zwack et al., 2016a. Arabidopsis transgenic promoter::GUS lines of CRF5 and CRF6 were used as previously described in Zwack et al 2012. Tomato transgenic lines the SlCRF5-Antisense knockdown (SlCRF5AS) and promoterSlCRF5::GUS line were previously described in Gupta and Rashotte, 2014. Growth of *crf6-2* mutants and comparable WT samples used for transcriptome analysis previously described in Zwack et al., 2016 were grown on plates containing full-strength Murashige and Skoog (MS) medium and 1% Sucrose buffered with MES at pH 5.7, but treated in a manner similar to described here with age of plants as well as timing, amount and method of treatment with hydrogen peroxide treatment.

Oxidative stress treatments

Ten days after germination, plants were removed from the growth chamber, and soil was gently washed from their roots. The plants were then pat-dried, placed into beakers containing 3mM MES buffer pH5.7 and put on a slowly revolving shaker for 1hr. After 1hr, the tomato and Arabidopsis plants were divided into two roughly equal groups, and one group was put into a fresh beaker of MES buffer pH5.7 and the other into a fresh beaker of MES pH5.7 plus 20mM H_2O_2. These beakers were then placed again onto the slow shaker for 6hrs.

GUS Staining

After the GUS expressing plants were treated as detailed above for in the oxidative stress treatment of plant section. PromoterAtCRF6::GUS, promoterAtCRF5::GUS and promoterSlCRF5::GUS were dried and placed into GUS staining solution in a manner similar to Zwack et al., 2012 and Gupta and Rashotte 2014. More specifically, plants were vacuum treated for 20 minutes to increase GUS solution penetration into tissue, and then placed at 35˚C for12 hours, after which, they were removed from the GUS staining solution and placed in 70% ethanol until the plant tissue had cleared. They were then placed in dH_2O for microscopy. Cleared samples were examined under Nikon SMZ1500 with a 0.5x lens and photographed.

Transcriptomic data

To evaluate the role of CRF5 during stress response, wild-type Arabidopsis and *crf5* loss of function mutants were treated with or without 20mM H_2O_2 in 3mM MES buffer for 6 hours. Three biological replicates of each treatment were performed. RNA was extracted using a Qiagen RNeasy Mini Kit and sent to HudsonAlpha (Huntsville, AL) for library preparation and sequencing on an Illumina HiSeq 2500. Single end 50 base pair reads were generated; there are approximately 25 million reads per sample. Quality was checked with FastQC (Andrews, 2010). Trimming was performed using Trimmomatic with the settings -headcrop 10, -leading 30, -trailing 30, -minlength 32 (Bolger et al., 2014). Reads were mapped to the genome using HISAT2 using default parameters (Pertea et al., 2016). The reference genome and gene annotation file used were the TAIR10 version of the *Arabidopsis thaliana* genome (Berardini *et al.*, 2015). The .sam files output from HISAT2 were converted to the binary .bam files and indexed with Samtools (Li *et al.*, 2009). After mapping, transcripts were assembled and abundances were estimated using StringTie using default parameters. Counts table from StringTie were read into the R package Ballgown, where differential gene expression analysis was performed (Pertea et al., 2016). Lowly expressed transcripts were filtered out. Transcripts with a q-value (an adjusted p-value) of less than 0.05 were called significantly differentially expressed. Raw sequence data is available for download at NCBI Sequence Read Archive under the BioProject ID PRJNA554020.

The tomato transcriptomic data of SlCRF5AS was collected as detailed below in the same manner as its wildtype MT background which was previously detailed in Keshishian et. al. 2018. Specifically, three independent biological replicates were used to isolate total RNA using the Qiagen RNeasy Plant Mini-kit according to the manufacturer's instructions. Total RNA then used for messenger RNA isolation with polyA selection and subsequent library construction with the TruSeq RNA sample preparation protocol from Illumina (San Diego, CA). Three biological replicates for SlCRF5AS both ± 20mM H_2O_2 in 3mM MES buffer for 6 hours were sequenced, analyzed, and compared to MT wildtype under the same treatment conditions as detailed in Keshishian et al., 2018. Single-end (1x54bp) sequencing was performed on the 6 SlCRF5AS samples by the Illumina GAIIX platform, and were directly compared to wildtype MT samples as detailed in Keshishian et al., 2018. Raw sequence data is available for download at NCBI Sequence Read Archive under the BioProject ID: PRJNA476376, SRA accession: SRP150651 as referenced in Zwack et al 2016.

Transcriptomic data for *Atcrf6* ± H_20_2 and wildtype Col-0 was conducted with those lines grown under previously described growing conditions. They were then examined using Hybridization to Affymetrix Arabidopsis Gene 1.0 ST arrays as detailed in Zwack et. al. 2016. Raw sequence data can be found in the GenBank/EMBL data libraries under accession numbers GSE84770.

RNA extraction, cDNA synthesis and qPCR

After the mutant and wildtype lines of both Arabidopsis and tomato were treated as detailed above in the "oxidative stress treatment" section, plants were pat-dried and frozen in liquid nitrogen. Plants, still frozen, were ground to a fine powder and then RNA was extracted using the RNeasy Kit from Qiagen, following the recommended procedure. RNA was then converted to cDNA using qScript Supermix from Quantabio, using the recommended procedure. qPCR was conducted on the cDNA using Fast SYBR green from Applied biosystems master mix from and following the recommended procedures. Primers are provided in Supplementary Table S3.

Quantification of CKs

CK extraction and measurement were conducted as described in Svačinová *et al.*, 2012. In this study, plants were treated in an identical manner as done for oxidative stress treatment in RNAsequencing experiments detailed above as part of a split experimental design. Samples were analyzed using Acquity UPLC® I-class system (Waters, Milford, MA, USA) coupled to a triple quadrupole mass spectrometer (Xevo™ TQ-S MS; Waters, Manchester, UK) equipped with an electrospray interface. Data were processed by MassLynx™ software using a standard isotope dilution method. Values are means of five biological replicates in pmol/g (fresh weight) ± standard deviation. The change in CK levels was calculated and presented as a percentage of the untreated; %=(untreated level-treated level)/(untreated level). Statistical analyses were conducted using the Student's T-Test with $p < 0.05$.

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Figures and Tables

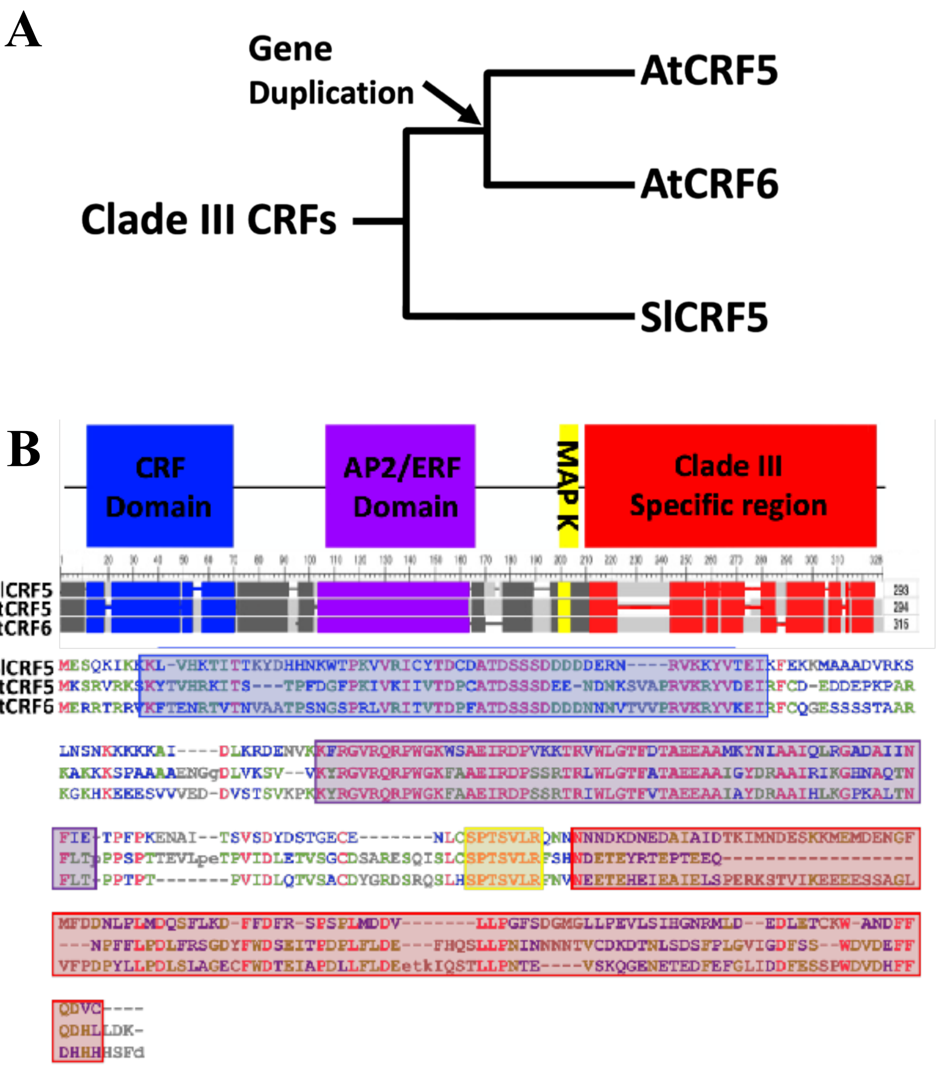


Figure 1. Sequence comparison of Clade III CRFs in Arabidopsis and tomato. A. Cladogram illustrating the inferred evolutionary relationship of these genes of interest, based on the amino acid alignment. B. Structure of the Clade III CRFs, followed by an amino acid alignment of the AtCRF5, AtCRF6 and SlCRF5 proteins. The CRF domain is indicated in blue, AP2/ERF domain in purple, the putative MAP K binding site in yellow and the Clade III specific region in all three visualizations. Lines in the first representations indicate areas without strong conservation. In the second visualization, the areas of low conservation are indicated by a light grey bar, while a line indicates where a sequence has a gap. Amino acids shown in red in the full sequence are those conserved across all three proteins, green indicates that the amino acid is common to two of the sequences and blue are amino acids that are unique to all 3. Grey letters are those located at the same point in the alignment as a gap in another sequence, and the lower-case letters are those that are "low complexity" and were therefore discounted by BLAST in determining the alignment.

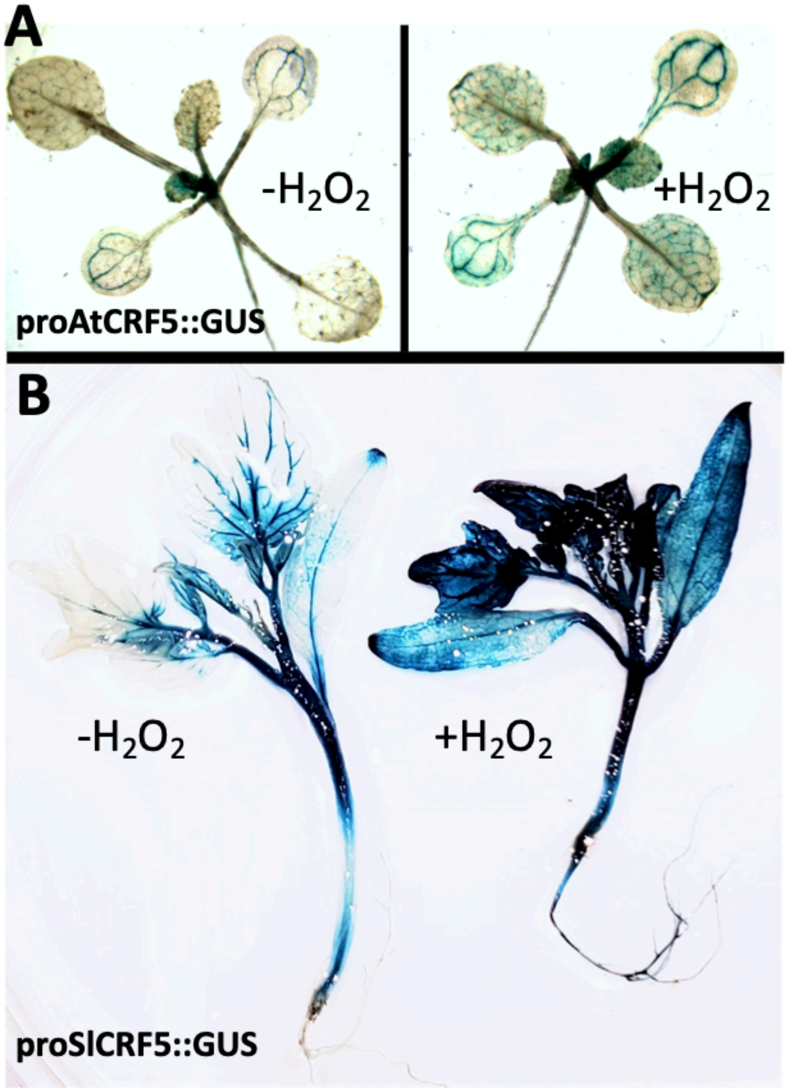


Figure 2. Promoter expression analysis to AtCRF5 and SlCRF5 in response to H_2O_2 treatment. GUS staining was conducted on 10d old promoterSlCRF5::GUS, and promoterAtCRF5::GUS lines after 6 hours treatment in either 3mM MES or 3mM MES+H_2O_2 in three independent biological replicates. Images shown are of representative plants.

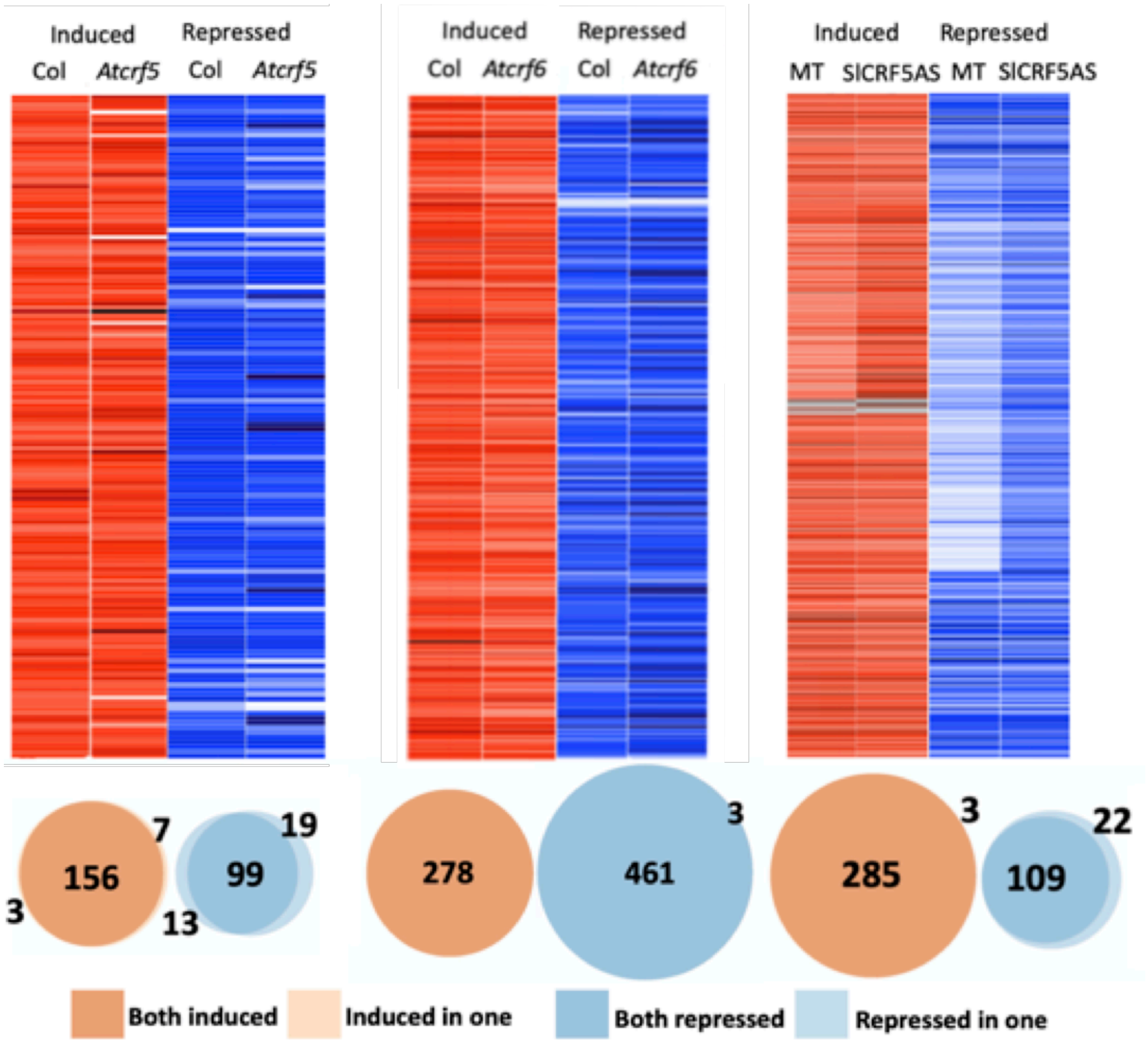


Figure 3. Visualization of transcriptomic response to H_2O_2 in *AtCRF5*, *AtCRF6*, and SlCRF5AS lines. Heat maps and Venn diagrams depicting the differences and similarities in the transcriptomic responses in 10d old plants of *AtCRF5*, *AtCRF6*, and SlCRF5AS lines and their respective WT backgrounds in the presence or absence of 6h treatment with 20mM H_2O_2. The red half of the heatmap shows upregulated genes, and the blue shows those that were down regulated. Deeper coloration of a band indicated a stronger induction or repression when the plant is treated with H_2O_2. Orange Venn diagrams indicate the number of genes that were induced at least 1.5 times after treatment with hydrogen peroxide. The blue Venn diagrams indicate the number of genes that were repressed by at least 50% of their original levels. Numbers to the top right above the circles indicate the number of genes affected only in the mutant/AS plants, those to the bottom left, the number affected only in the WT, and the number in the middle indicated the number of genes that were affected in both.

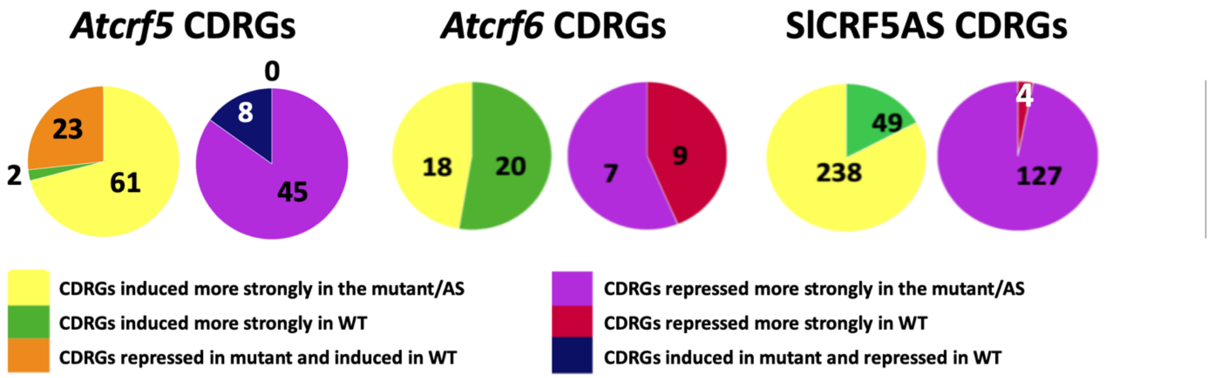


Figure 4. Differentially Regulated Genes or CDRGs of the transcriptomic response to H_2O_2 in *AtCRF5*, *AtCRF6*, and SlCRF5AS lines. Pie charts for each set of transcriptomes indicating the number of CDRGs that are more strongly induced or repressed in WT than in the mutant/AS with colors indicating level of change of induction or repression as indicated.

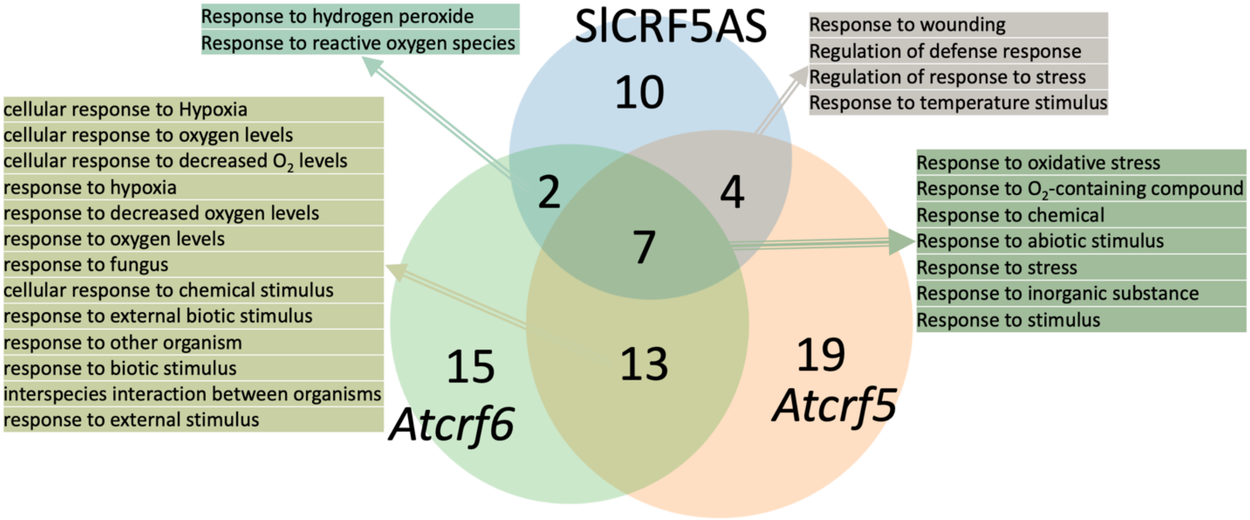
A

			qRT-PCR		RNAseq
Gene	**Solyc Number**	**Description**	**MT vs. MT+H_2O_2**	**Slcrf5 vs. Slcrf5+H_2O_2**	**MT vs. MT+H_2**
-	Solyc02g084790	Peroxidase	1.92 ± 0.10	-101.04 ± 8.43	1.60421516
K+ uptake permease 7	Solyc01g105150	K+ transporter family protein	1.85 ± 0.08	1.63 ± 0.02	0.78646129
-	Solyc02g084800	Peroxidase	-1.40 ± 0.02	-1.12 ± 0.02	2.00109846
HSP70	Solyc01g099660	Heat shock protein	-8.40 ± 0.13	-3.20 ± 0.08	4.44471952
ERF4	Solyc12g009240	Pathogenesis-related ethylene response factor	-7.36 ± 0.18	-2.68 ± 0.03	2.73780506
ERF13	Solyc10g076370	Pathogenesis-related ethylene response factor	-1.85 ± 0.04	-3.65 ± 0.06	2.63524145
WRKY53	Solyc08g008280	WRKY involved in response to microbial infection	-2.85 ± 0.06	-3.06 ± 0.06	1.40148626

B

			qRT-PCR		RNAseq	
Gene	**At Number**	**Description**	**WT vs. WT+ H_2O_2**	***Atcrf5* vs. *Atcrf5*+H_2O_2**	**WT vs. WT+ H_2O_2**	***Atcrf5* vs. *Atcrf5*+H_2O_2**
HSP15.4	At4g21870	Heat shock protein	2.77 ± 0.12	-6.93 ± 0.01	2.15	-10.50
CSY3	At2g42790	Citrate synthase	-2.82 ± 0.07	5.58 ± 0.21	-1.69	1.76
PER49	At4g36430	Peroxidase	-1.57 ± 0.07	-4.02 ± 0.08	-2.95	-22.69
WRKY6	At1g62300	WRKY transcription factor	2.14 ± 0.11	6.59 ± 0.52	2.51	3.31
WRKY40	At1g80840	WRKY transcription factor	3.14 ± 0.19	4.42 ± 0.18	5.05	9.21

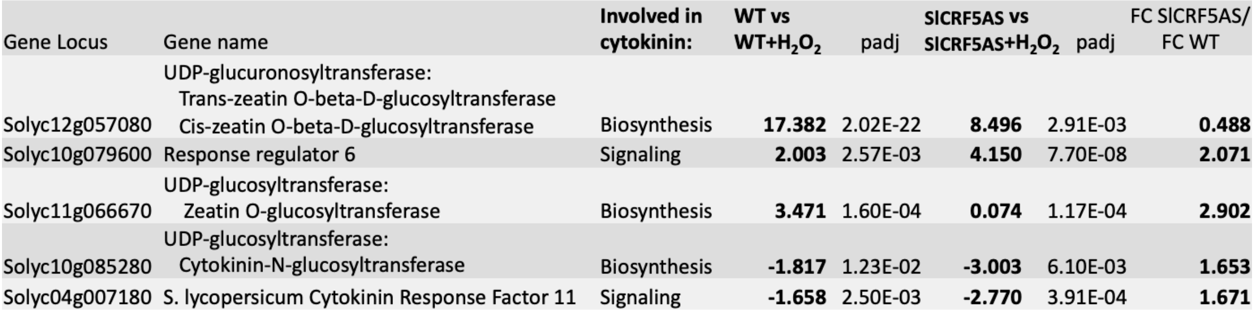
Table 1. Validation of transcriptome analysis to H_2O_2 in *AtCRF5* and SlCRF5AS lines. A. Results from qRT-PCR confirmation of the tomato transcriptome data. B. Results from qPCR confirmation of the *Atcrf5* transcriptome data. Data is expressed in fold change ± standard error. Data is expressed as the average in fold change ± standard error of 3 biological replicates.



GO Terms unique to the CRDG set in:

Atcrf6	SlCRF5AS	*Atcrf5*
Toxin catabolic process	Protein complex oligomerization	Response to salt
Toxin metabolic process	Regulation of jasmonic acid mediated signaling pathway	Response to desiccation
Detoxification	Response to salt stress	Response to salicylic acid
Glutathione metabolic process	Response to osmotic stress	Regulation of immune system process
Defense response to bacterium, incompatible interaction	Response to heat	Regulation of response to biotic stimulus
Response to toxic substance	Regulation of signal transduction	Regulation of response to external stimulus
Response to chitin	Steroid metabolic process	Response to organic cyclic compound
Secondary metabolic process	Regulation of cell communication	Response to water
Defense response, incompatible interaction	Regulation of signaling	Response to acid chemical
Response to nitrogen compound	Sterol metabolic process	Response to water deprivation
Defense response to fungus		Response to abscisic acid
Defense response to bacterium		Response to alcohol
Response to bacterium		Response to lipid
Defense response to other organism		Regulation of response to stimulus
Defense response		Response to hormone
		Response to organic substance
		Response to endogenous stimulus
		Cellular response to stress
		cellular response to stimulus

Figure 5. Illuminated Venn diagram of GO terms from the transcriptomic response to H_2O_2 in *AtCRF5*, *AtCRF6*, and SlCRF5AS lines. The Clade III CRF Differentially Regulated Genes or CDRGs found by comparing FCs of expression in transcriptomic response to H_2O_2 in AtCRF5, AtCRF6, and SlCRF5AS lines were examined in Panther Database using GO term enrichment analysis. Terms found relating to biological function from the three sets of CDRGs were compared to investigate commonalities and unique functions. The GO terms that are unique to the set of CDRGs from SlCRF5AS, *Atcrf5*, and *Atcrf6* are shown in light blue, pink, and light green, respectively.



Gene Locus	Gene name	**Involved in cytokinin:**	**WT vs WT+H_2O_2**	padj	**SlCRF5AS vs SlCRF5AS+H_2O_2**	padj	FC SlCRF5AS/ FC WT
Solyc12g057080	UDP-glucuronosyltransferase: Trans-zeatin O-beta-D-glucosyltransferase Cis-zeatin O-beta-D-glucosyltransferase	Biosynthesis	**17.382**	2.02E-22	**8.496**	2.91E-03	**0.488**
Solyc10g079600	Response regulator 6	Signaling	**2.003**	2.57E-03	**4.150**	7.70E-08	**2.071**
Solyc11g066670	UDP-glucosyltransferase: Zeatin O-glucosyltransferase	Biosynthesis	**3.471**	1.60E-04	**0.074**	1.17E-04	**2.902**
Solyc10g085280	UDP-glucosyltransferase: Cytokinin-N-glucosyltransferase	Biosynthesis	**-1.817**	1.23E-02	**-3.003**	6.10E-03	**1.653**
Solyc04g007180	S. lycopersicum Cytokinin Response Factor 11	Signaling	**-1.658**	2.50E-03	**-2.770**	3.91E-04	**1.671**

Table 2. Tomato Differentially Regulated Genes or CDRGs involved in CK Biosynthesis. SlCRF5AS CDRGs that are involved in CK biosynthesis and signaling are presented. Values are displayed in fold change (FC) from RNA-sequencing transcriptome results.

WT	iP	tZ	DHZ	cZ	WT+H2O2	iP	tZ	DHZ	cZ
RMP	3.95±0.45	0.81±0.05	ND	10.00±2.15	RMP	1.13	0.31±0.08	ND	9.92±2.57
R	0.63±0.17	0.14±0.03	0.009±0.002	0.57±0.09	R	1.11±0.37	0.18±0.03	0.053±0.015	1.75±0.50
-	0.85±0.19	0.16±0.02	ND	0.28±0.06	-	0.79±0.19	0.16±0.03	ND	0.25±0.07
7G	15.75±0.54	21.33±1.53	1.38±0.12		7G	15.85±4.49	17.90±2.52	1.09±0.22	
9G	2.14±0.04	11.94±0.98	0.14±0.02	0.32±0.05	9G	1.76±0.25	10.09±0.89	0.14±0.03	0.23±0.07
OG		2.83±0.54	ND	0.73±0.13	OG		2.34±0.26	ND	0.61±0.11
ROG		0.58±0.03	ND	1.43±0.25	ROG		0.47±0.13	ND	1.03±0.14
Total	23.30±1.03	37.80±2.86	1.53±0.11	13.34±1.89	Total	20.65±4.25	31.56±3.45	1.28±0.23	13.80±2.71
crf5	iP	tZ	DHZ	cZ	*crf5* +H2O2	iP	tZ	DHZ	cZ
RMP	1.74±0.13	0.72±0.09	ND	5.81±0.70	RMP	1.59±0.32	0.75±0.06	ND	14.59±1.83
R	0.70±0.15	0.17±0.02	0.013±0.004	0.61±0.13	R	0.89±0.23	0.24±0.04	0.051±0.015	2.04±0.56
-	0.68±0.15	0.16±0.02	ND	0.20±0.04	-	0.87±0.26	0.18±0.04	ND	0.37±0.08
7G	12.69±0.49	16.01±2.24	1.03±0.23		7G	17.70±1.43	22.85±2.62	1.65±0.24	
9G	1.97±0.15	8.82±0.94	0.10±0.01	0.31±0.05	9G	2.54±0.26	11.97±2.02	0.16±0.03	0.39±0.07
OG		2.22±0.33	ND	0.56±0.04	OG		3.38±0.73	ND	0.97±0.17
ROG		0.54±0.08	ND	0.92±0.19	ROG		0.75±0.09	ND	1.72±0.24
Total	17.78±0.76	28.63±3.47	1.15±0.24	8.40±0.85	Total	23.59±1.61	40.11±5.03	1.86±0.26	20.08±2.48
crf6	iP	tZ	DHZ	cZ	*crf6* +H2O2	iP	tZ	DHZ	cZ
RMP	2.49±0.71	0.58±0.12	ND	5.19±1.41	RMP	1.60±0.45	0.44±0.10	ND	8.73±2.11
R	0.84±0.17	0.17±0.03	0.009±0.002	0.65±0.07	R	1.27±0.32	0.25±0.06	0.063±0.015	2.42±0.64
-	0.99±0.21	0.11±0.02	ND	0.17±0.03	-	0.72±0.20	0.08±0.02	ND	0.26±0.05
7G	13.10±1.89	15.07±2.02	0.95±0.19		7G	13.06±1.38	15.28±3.69	1.18±0.25	
9G	1.89±0.26	7.91±0.86	0.15±0.05	0.27±0.06	9G	1.87±0.31	7.99±2.09	0.08±0.02	0.34±0.06
OG		1.87±0.58	ND	0.61±0.12	OG		2.28±0.51	ND	0.74±0.11
ROG		0.42±0.06	ND	1.01±0.25	ROG		0.49±0.12	ND	0.91±0.13
Total	19.31±2.98	26.11±3.41	1.11±0.22	7.91±1.76	Total	18.53±1.66	26.81±6.47	1.32±0.25	13.40±2.26
MT	iP	tZ	DHZ	cZ	MT+H2O2	iP	tZ	DHZ	cZ
RMP	0.69±0.21	0.32±0.08	ND	0.98±0.17	RMP	0.52±0.14	0.22±0.07	ND	1.44±0.37
R	1.27±0.42	0.27±0.08	0.033±0.008	0.31±0.07	R	0.65±0.19	0.11±0.03	0.046±0.010	0.44±0.12
-	0.50±0.08	0.16±0.02	ND	0.09±0.01	-	0.49±0.13	0.12±0.02	ND	0.13±0.01
7G	26.82±5.27	15.69±3.38	4.03±1.13		7G	23.47±4.85	12.54±3.37	1.46±0.42	
9G	0.15±0.04	0.42±0.10	1.36±0.48	0.12±0.04	9G	0.14±0.03	0.33±0.07	0.34±0.07	0.32±0.05
OG		0.13±0.03	0.137±0.031	0.21±0.02	OG		0.12±0.02	0.076±0.019	0.20±0.04
ROG		0.32±0.09	ND	0.04±0.01	ROG		0.18±0.06	ND	0.04±0.01
Total	29.43±5.69	17.32±3.60	5.53±1.56	1.75±0.25	Total	25.14±4.90	13.64±3.53	1.92±0.43	2.33±0.27
SlCRF5AS	iP	tZ	DHZ	cZ	*Sl5AS* +H2O2	iP	tZ	DHZ	cZ
RMP	0.56±0.15	0.27±0.09	ND	0.75±0.21	RMP	0.58±0.19	0.28±0.07	ND	1.35±0.36
R	1.16±0.32	0.21±0.05	0.025±0.007	0.34±0.10	R	0.89±0.29	0.21±0.07	0.054±0.016	0.60±0.12
-	0.45±0.09	0.12±0.04	ND	0.10±0.02	-	0.46±0.03	0.14±0.03	ND	0.11±0.02
7G	17.97±3.03	9.33±1.40	1.47±0.49		7G	24.93±2.94	13.03±1.50	1.36±0.39	
9G	0.15±0.02	0.38±0.03	0.39±0.11	0.14±0.04	9G	0.18±0.04	0.38±0.10	0.68±0.19	0.13±0.04
OG		0.10±0.02	0.061±0.014	0.25±0.04	OG		0.10±0.03	0.179±0.027	0.30±0.08
ROG		0.22±0.07	ND	0.10±0.03	ROG		0.21±0.07	ND	0.08±0.02
Total	20.28±3.44	10.63±1.50	1.95±0.48	1.68±0.22	Total	27.03±3.01	14.36±1.55	2.23±0.41	2.57±0.27

Figure 6. SlCRF5AS, *Atcrf5*, and *Atcrf6* have altered CK levels with and without oxidative stress treatment. Specific amounts of CK compounds measured by LC-MS/MS in pmol/g FW from 10d WT/MT, *Atcrf5*, *Atcrf6,* and SlCRF5AS seedlings either MES-Buffer treated (Control) or Oxidative stress (20mM H_2O_2) treatment for 6h (n=5). Measured CKs are displayed as an average±SD in table format similar to the CK biosynthesis pathway with CK type in columns (iP, tZ, DHZ, and cZ) and specific form in rows with the precursor CK names are followed by the abbreviation -RMP (riboside-monophosphate), -R (riboside), - (active form), 7N and 9N (N-glucosides), and OG and ROG (O-glucosides). In the left column of tables, comparisons were made between the CK levels of altered lines and WT that were not treated with oxidative stress, which can be viewed in a vertical manner. The types of CKs that were significantly ($p<0.05$) lower than WT are shown in blue, and those that were significantly higher are shown in yellow. In the right column of tables, comparisons between the CK levels of the oxidative stress- treated altered lines and were compared to their levels when the plants were untreated, that can be viewed in a horizonal manner. CKs that were statistically significantly increased ($p<0.05$) are shown in green, and those that were significantly decreased are shown in red.

Appendix i

Table S1. Differentially Expressed Genes (DEGs) of WT and *Atcrf6* when treated with CK. **A:** Genes up regulated or **B:** down regulated in WT (Col-0) + CK (2µM BA) for 6 hours vs WT control (DMSO) treated.

A: Genes upregulated in WT+CK

Locus	Gene Name	FC Col vs Col+CK	
AT1G01580	FRO2 Ferric reduction oxidase 2	**0.2160317**	0.00041111
AT1G02850	BGLU11 Beta-glucosidase 11	**0.445186**	0.03701988
AT1G05240	Peroxidase 1;PER1	**0.3155674**	0.00150599
AT1G05250	Peroxidase 2;PER2	**0.4484239**	0.07876532
AT1G05280	ERV-F (C)1 provirus ancestral Env polyprotein, putative (DUF604);YUP8H12	**0.4942268**	0.09177532
AT1G05700	Probable LRR receptor-like serine/threonine-protein kinase At1g05700;At1g05700	**0.3041005**	0.00800003
AT1G06160	Ethylene-responsive transcription factor ERF094;ERF094	**0.4086025**	0.0460856
AT1G07560	Probable LRR receptor-like serine/threonine-protein kinase At1g07560;At1g07560	**0.374009**	0.01931315
AT1G08090	High-affinity nitrate transporter 2	**0.2004786**	4.16E-05
AT1G09090	Respiratory burst oxidase homolog protein B;RBOHB	**0.4293914**	0.02738988
AT1G11450	WAT1-related protein At1g11450;At1g11450	**0.3109932**	0.00756822
AT1G12040	Leucine-rich repeat extensin-like protein 1;LRX1	**0.4139433**	0.00945624
AT1G12200	Flavin-containing monooxygenase FMO GS-OX-like 2;At1g12200	**0.4497702**	0.00314421
AT1G15125	F9L1	**0.4576241**	0.00593898
AT1G15210	ABC transporter G family member 35;ABCG35	**0.4669921**	0.00406729
AT1G16400	Hexahomomethionine N-hydroxylase;CYP79F2	**0.4604671**	0.03157225
AT1G17745	D-3-phosphoglycerate dehydrogenase 2, chloroplastic;PGDH2	**0.4362313**	0.00945624
AT1G18570	Transcription factor MYB51;MYB51	**0.4762942**	0.1017379
AT1G22065	Uncharacterized protein;At1g22065	**0.4590044**	0.04192173
AT1G29020	Calcium-binding EF-hand family protein;At1g29020	**0.3377178**	0.00333505
AT1G29025	Calcium-binding EF-hand family protein;At1g29025	**0.3258421**	0.02546473

AT1G32450	Protein NRT1/ PTR FAMILY 7	**0.4821955**	0.00475434
AT1G43910	AAA-ATPase At1g43910;At1g43910	**0.4230368**	0.00362479
AT1G48930	Endoglucanase 5;At1g48930	**0.3732709**	0.02601139
AT1G49470	At1g49470;At1g49470	**0.3052409**	0.00677131
AT1G49570	Peroxidase 10;PER10	**0.3983394**	0.00269459
AT1G49860	Glutathione S-transferase F14;GSTF14	**0.2316277**	1.67E-05
AT1G51470	Myrosinase 5;TGG5	**0.4569031**	0.01370738
AT1G52070	Jacalin-related lectin 10;JAL10	**0.3603311**	0.05501631
AT1G54890	Late embryogenesis abundant (LEA) protein-like protein;T24C10	**0.2809655**	0.00138095
AT1G61840	Cysteine/Histidine-rich C1 domain family protein;At1g61840	**0.3473339**	0.00409503
AT1G62620	Flavin-containing monooxygenase FMO GS-OX-like 3;At1g62620	**0.4593752**	0.02665674
AT1G66783		**0.4689285**	0.0104615
AT1G67710	Two-component response regulator ARR11;ARR11	**0.4747106**	0.01478609
AT1G71960	ABC transporter G family member 25;ABCG25	**0.4411634**	0.00797514
AT1G75388		**0.4444737**	0.01358592
AT1G75750	Gibberellin-regulated protein 1;GASA1	**0.486776**	0.00843617
AT1G77330	1-aminocyclopropane-1-carboxylate oxidase 5;At1g77330	**0.4558307**	0.03487898
AT1G78000	Sulfate transporter 1	**0.4994527**	0.00556499
AT1G78090	Trehalose-phosphate phosphatase B;TPPB	**0.444038**	0.00699505
AT2G02820	Transcription factor MYB88;MYB88	**0.4751797**	0.02058503
AT2G14610	Pathogenesis-related protein 1;At2g14610	**0.4865079**	0.1170302
AT2G20030	Putative RING-H2 finger protein ATL12;ATL12	**0.3582342**	0.00158426
AT2G26820	Immune-associated nucleotide-binding protein 10;IAN10	**0.4713122**	0.00431779
AT2G27550	Protein CENTRORADIALIS-like;CEN	**0.1051558**	3.46E-06
AT2G28160	Transcription factor FER-LIKE IRON DEFICIENCY-INDUCED TRANSCRIPTION FACTOR;FIT	**0.3868162**	0.00663484
AT2G30840	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein;At2g30840	**0.4313751**	0.02767822
AT2G32620	Cellulose synthase-like protein B2;CSLB2	**0.4716358**	0.03588106
AT2G38600	HAD superfamily, subfamily IIIB acid phosphatase;At2g38600	**0.3706823**	0.0119781
AT2G40970	Transcription factor MYBC1;MYBC1	**0.4927815**	0.03358984
AT2G41180	Sigma factor binding protein 2, chloroplastic;SIB2	**0.4888148**	0.04031834

AT2G43120	Pirin-like protein 2;PRN2	**0.460499**	0.01835485
AT2G44340	VQ motif-containing protein 18;VQ18	**0.4649186**	0.04022465
AT3G01190	Peroxidase 27;PER27	**0.3972007**	0.02099124
AT3G02020	Aspartokinase 3, chloroplastic;AK3	**0.4561816**	0.00960114
AT3G02850	Potassium channel SKOR;SKOR	**0.3872199**	0.03251222
AT3G03470	Cytochrome P450 89A9;CYP89A9	**0.4067615**	0.00300811
AT3G09925	Pollen Ole e 1 allergen and extensin family protein;At3g09925	**0.4245363**	0.01426181
AT3G10320	F14P13	**0.4248616**	0.00699505
AT3G12580	Probable mediator of RNA polymerase II transcription subunit 37c;MED37C	**0.4657653**	0.00663484
AT3G12750	Zinc transporter 1;ZIP1	**0.4139375**	0.00276349
AT3G13100	ABC transporter C family member 7;ABCC7	**0.4920988**	0.03434855
AT3G13760	Cysteine/Histidine-rich C1 domain family protein;At3g13760	**0.4454036**	0.02861287
AT3G14680	Cytochrome P450 72A14;CYP72A14	**0.4553176**	0.03072796
AT3G20380	TRAF-like family protein;At3g20380	**0.2069236**	5.17E-06
AT3G20590	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family;At3g20590	**0.4139863**	0.05269799
AT3G23175	HR-like lesion-inducing protein-like protein;At3g23175	**0.363206**	0.00774154
AT3G23190	At3g23190;At3g23190	**0.4341408**	0.0121343
AT3G23430	Phosphate transporter PHO1;PHO1	**0.3710537**	0.0003242
AT3G23550	Protein DETOXIFICATION 18;DTX18	**0.3981627**	0.02170681
AT3G23800	Selenium-binding protein 3;SBP3	**0.4826302**	0.02682966
AT3G25930	Adenine nucleotide alpha hydrolases-like superfamily protein;At3g25930	**0.452908**	0.07083233
AT3G26610	Pectin lyase-like superfamily protein;PGX1	**0.4373469**	0.105539
AT3G46330	Probable LRR receptor-like serine/threonine-protein kinase MEE39;MEE39	**0.3573253**	0.03588106
AT3G47480	Probable calcium-binding protein CML47;CML47	**0.3834858**	0.02546473
AT3G49960	Peroxidase 35;PER35	**0.2966472**	0.00797514
AT3G50770	Probable calcium-binding protein CML41;CML41	**0.3722916**	0.01125173
AT3G54590	Extensin-2;EXT2	**0.3875099**	0.00528005
AT3G60330	ATPase 7, plasma membrane-type;AHA7	**0.4079106**	0.00797514
AT3G62040	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein;At3g62040	**0.4363326**	0.00747382
AT3G62270	Probable boron transporter 2;BOR2	**0.3139485**	0.00018707
AT3G63110	Adenylate isopentenyltransferase 3, chloroplastic;IPT3	**0.4566814**	0.01075015

AT4G00670	At4g00670;At4g00670	**0.4558892**	0.05390174
AT4G00910		**0.268936**	0.00051999
AT4G01440	WAT1-related protein At4g01440;At4g01440	**0.4090347**	0.0024237
AT4G02270	At4g02270;RHS13	**0.3980372**	0.01020888
AT4G08290	WAT1-related protein At4g08290;At4g08290	**0.4642761**	0.06603646
AT4G08770	Peroxidase 37;PER37	**0.2311234**	6.53E-05
AT4G08780	Peroxidase 38;PER38	**0.1580135**	2.06E-05
AT4G12480	Lipid transfer protein EARLI 1;EARLI1	**0.4871372**	0.03512343
AT4G13420	Potassium transporter 5;POT5	**0.166967**	1.67E-05
AT4G14020	At4g14020;dl3050c	**0.2932098**	0.00439834
AT4G14130	Xyloglucan endotransglucosylase/hydrolase protein 15;XTH15	**0.2374919**	2.41E-05
AT4G14400	Protein ACCELERATED CELL DEATH 6;ACD6	**0.4043776**	0.02565311
AT4G15390	HSR201-like protein;dl3740c	**0.3329275**	0.00203918
AT4G19370	Protein MODIFYING WALL LIGNIN-2;MWL2	**0.4220278**	0.04607134
AT4G19690	Fe(2+) transport protein 1;IRT1	**0.3254708**	0.00409503
AT4G19700	E3 ubiquitin-protein ligase BOI;BOI	**0.4603267**	0.01536603
AT4G21680	Protein NRT1/ PTR FAMILY 7	**0.3885656**	0.02145855
AT4G21830	Peptide methionine sulfoxide reductase B7;MSRB7	**0.3925763**	0.00994393
AT4G22940	Protein kinase superfamily protein;At4g22940	**0.4123768**	0.02652598
AT4G23700	Cation/H(+) antiporter 17;CHX17	**0.3805031**	0.0061116
AT4G26010	Peroxidase 44;PER44	**0.3842015**	0.00872417
AT4G27830	Beta-glucosidase 10;BGLU10	**0.4789825**	0.01460666
AT4G28410	Tyrosine transaminase family protein;Root System Architecture 1	**0.4336656**	0.02546473
AT4G31910	Brassinosteroid-related acyltransferase 1;BAT1	**0.4122096**	0.02663028
AT4G33420	Peroxidase 47;PER47	**0.3947688**	0.00122227
AT4G34600	Protein CASPARIAN STRIP INTEGRITY FACTOR 2;CIF2	**0.4165004**	0.00945144
AT4G36430	Peroxidase 49;PER49	**0.4427088**	0.00246184
AT4G37160	Pectinesterase like protein;C7A10	**0.3675481**	0.05035474
AT4G37990	Cinnamyl alcohol dehydrogenase 8;CAD8	**0.3332138**	0.01033603
AT5G02350	Cysteine/Histidine-rich C1 domain family protein;At5g02350	**0.4867102**	0.05590459
AT5G04950	Nicotianamine synthase 1;NAS1	**0.4120639**	0.07056488
AT5G05500	At5g05500;MOP10	**0.4757778**	0.040305
AT5G06640	Proline-rich extensin-like family protein;EXT10	**0.4939134**	0.02147749

AT5G07690	Transcription factor MYB29;MYB29	**0.4844535**	0.04397743
AT5G09440	Protein EXORDIUM-like 4;EXL4	**0.3202022**	0.00311326
AT5G09690	Magnesium transporter MRS2-7;MRS2-7	**0.4486617**	0.00699505
AT5G11920	Beta-fructofuranosidase, insoluble isoenzyme CWINV6;CWINV6	**0.3809491**	0.00202142
AT5G15130	Probable WRKY transcription factor 72;WRKY72	**0.4919437**	0.00888449
AT5G17820	Peroxidase 57;PER57	**0.487622**	0.02176296
AT5G19890	Peroxidase 59;PER59	**0.2823497**	2.91E-05
AT5G24210	Alpha/beta-Hydrolases superfamily protein;MOP9	**0.4817027**	0.1372141
AT5G24880	Chromo domain cec-like protein;At5g24880	**0.4621923**	0.01775185
AT5G27060	Receptor-like protein 53;RLP53	**0.2857459**	0.01010253
AT5G35190	Proline-rich extensin-like family protein;EXT13	**0.3249343**	0.0060992
AT5G36350	ECA1 gametogenesis related family protein;At5g36350	**0.3368983**	0.0024237
AT5G44420	Defensin-like protein 16;PDF1	**0.4220775**	0.03153818
AT5G45380	Urea-proton symporter DUR3	**0.4537895**	0.02145855
AT5G47450	Aquaporin TIP2-3	**0.4136192**	0.01370738
AT5G49770	Probable leucine-rich repeat receptor-like protein kinase At5g49770;At5g49770	**0.4828008**	0.01577858
AT5G52640	Heat shock protein 90-1;HSP90-1	**0.4397117**	0.04833907
AT5G53550	Metal-nicotianamine transporter YSL3;YSL3	**0.4644693**	0.05421218
AT5G54020	Cysteine/Histidine-rich C1 domain family protein;At5g54020	**0.3500918**	0.0024237
AT5G57090	Auxin efflux carrier component 2;PIN2	**0.4974057**	0.04752789
AT5G57625	At5g57625;At5g57625	**0.3029801**	0.0024237
AT5G57685	Protein GLUTAMINE DUMPER 3;GDU3	**0.4093013**	0.00122227
AT5G61160	Agmatine coumaroyltransferase;ACT	**0.3569812**	0.00998652
AT5G63660	Defensin-like protein 6;PDF2	**0.394996**	0.04191931
AT5G63850	Amino acid permease 4;AAP4	**0.3571792**	9.08E-05
AT5G67400	Peroxidase 73;PER73	**0.2324367**	2.41E-05

B. Genes downregulated in WT+CK

Locus	Gene Name	**FC Col vs Col+CK**	`
AT1G03110	tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit;TRM82	**1.609319**	0.1337594
AT1G03360	Exosome complex component RRP4 homolog;RRP4	**1.599499**	0.1134706
AT1G03530	F21B7	**1.679574**	0.04870566

AT1G03850	Monothiol glutaredoxin-S13;GRXS13	**1.805145**	0.0121343
AT1G03930	Casein kinase 1-like protein 9;CKL9	**1.639022**	0.06761884
AT1G04240	Auxin-responsive protein IAA3;IAA3	**2.522851**	0.02264461
AT1G04250	Auxin-responsive protein IAA17;IAA17	**2.158674**	0.01329574
AT1G04360	RING-H2 finger protein ATL1;ATL1	**2.288473**	0.01818643
AT1G04870	Protein arginine N-methyltransferase PRMT10;PRMT10	**1.553643**	0.08456481
AT1G06720	p-loop containing nucleoside triphosphate hydrolases superfamily protein;At1g06720	**2.10177**	0.00587363
AT1G07070	60S ribosomal protein L35a-1;RPL35AA	**1.715846**	0.08131951
AT1G08610	Pentatricopeptide repeat-containing protein At1g08610;At1g08610	**2.482881**	0.03301833
AT1G09390	GDSL esterase/lipase At1g09390;At1g09390	**1.64265**	0.07876532
AT1G09460	Carbohydrate-binding X8 domain superfamily protein;At1g09460	**1.620883**	0.08131951
AT1G10460	Germin-like protein subfamily 1 member 1;GLP7	**2.632758**	0.03039011
AT1G10470	Two-component response regulator ARR4;ARR4	**6.904682**	3.46E-06
AT1G10490	RNA cytidine acetyltransferase 1;At1g10490	**2.068264**	0.07471388
AT1G12420	ACT domain-containing protein ACR8;ACR8	**2.266247**	0.0034776
AT1G12740	Cytochrome P450, family 87, subfamily A, polypeptide 2;CYP87A2	**1.576079**	0.1938137
AT1G13420	Cytosolic sulfotransferase 8;SOT8	**2.330218**	0.012503
AT1G13740	Ninja-family protein AFP2;AFP2	**1.700254**	0.1774408
AT1G14620	At1g14620/T5E21_15;DECOY	**1.5838**	0.1027776
AT1G14630		**2.043214**	0.00610844
AT1G14710	Hydroxyproline-rich glycoprotein family protein;At1g14710	**1.505534**	0.1107365
AT1G14960	Major latex protein, putative;MLP4	**2.331284**	0.02546473
AT1G14980	10 kDa chaperonin, mitochondrial;CPN10	**1.666909**	0.04758653
AT1G15510	Pentatricopeptide repeat-containing protein At1g15510, chloroplastic;PCMP-H73	**1.786901**	0.08590664
AT1G16445	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein;At1g16445	**1.529235**	0.2026991
AT1G16530	LOB domain-containing protein 3;LBD3	**4.025589**	6.53E-05
AT1G17190	Glutathione S-transferase U26;GSTU26	**2.309707**	0.03690256
AT1G17880	Basic transcription factor 3;BTF3	**1.541292**	0.1133822
AT1G18080	Receptor for activated C kinase 1A;RACK1A	**1.539626**	0.143179
AT1G18330	Protein REVEILLE 7;RVE7	**1.72693**	0.04900061
AT1G18400	Transcription factor BEE 1;BEE1	**2.506293**	0.06603646
AT1G18800	NAP1-related protein 2;NRP2	**1.986949**	0.0263177

AT1G18850	F6A14	**1.520673**	0.184384
AT1G19050	Two-component response regulator ARR7;ARR7	**12.64522**	1.24E-06
AT1G19450	Sugar transporter ERD6-like 4;At1g19450	**1.608906**	0.136987
AT1G21830	At1g21820;At1g21820	**1.60836**	0.1246796
AT1G23280	Protein MAK16 homolog;At1g23280	**1.936048**	0.00998652
AT1G25260	Ribosome assembly factor mrt4;RDP1	**1.564813**	0.08467864
AT1G26770	Expansin-A10;EXPA10	**2.551755**	0.01336631
AT1G26880	60S ribosomal protein L34-1;RPL34A	**1.715109**	0.02971688
AT1G26945	Transcription factor PRE6;PRE6	**2.020518**	0.0170821
AT1G27400	60S ribosomal protein L17-1;RPL17A	**1.568423**	0.1963832
AT1G27470	Transducin family protein / WD-40 repeat family protein;At1g27470	**1.850295**	0.02613401
AT1G28100	Protein NEOXANTHIN-DEFICIENT 1;NDX1	**3.36474**	1.67E-05
AT1G29250	Alba DNA/RNA-binding protein;At1g29250	**1.778178**	0.0323764
AT1G29440	Auxin-responsive protein SAUR63;SAUR63	**2.225223**	0.02582617
AT1G29450	Auxin-responsive protein SAUR64;SAUR64	**2.313432**	0.0024237
AT1G29940	DNA-directed RNA polymerase I subunit 2;NRPA2	**1.651446**	0.05196404
AT1G30240	Proline-, glutamic acid/leucine-rich protein;At1g30240	**1.718828**	0.07894262
AT1G30820	CTP synthase;At1g30820	**1.960518**	0.00854327
AT1G30960	GTP-binding protein ERG;ERG	**1.672771**	0.184495
AT1G31180	3-isopropylmalate dehydrogenase 3, chloroplastic;IMDH3	**1.890562**	0.00737875
AT1G31320	LOB domain-containing protein 4;LBD4	**2.162005**	0.00797514
AT1G31660	Bystin-like protein;atENP1	**1.712448**	0.04701149
AT1G31710	Amine oxidase;At1g31710	**1.592601**	0.08795864
AT1G31860	Histidine biosynthesis bifunctional protein hisIE, chloroplastic;HISN2	**2.035757**	0.01207643
AT1G31970	DEAD-box ATP-dependent RNA helicase 5;RH5	**1.790385**	0.0267373
AT1G34065	Probable S-adenosylmethionine carrier 2, chloroplastic;SAMC2	**1.943369**	0.04639221
AT1G34520	Probable long-chain-alcohol O-fatty-acyltransferase 8;At1g34520	**2.212956**	0.04724351
AT1G35625	Receptor homology region, transmembrane domain- and RING domain-containing protein 6;RMR6	**1.787985**	0.4737058
AT1G45015	At1g45015;At1g45015	**1.837635**	0.3897125
AT1G47395		**3.128823**	0.2242512
AT1G48570	T1N15	**1.831423**	0.07637351

AT1G48920	Nucleolin 1;NUCL1	**1.778246**	0.03858467
AT1G53542	At1g53545;At1g53542	**1.580789**	0.3670031
AT1G56110	At1g56110/T6H22_9;NOP56	**1.727014**	0.07522284
AT1G56430	Probable nicotianamine synthase 4;NAS4	**1.977894**	0.1028168
AT1G58170	Dirigent protein 19;DIR19	**1.642872**	0.1662641
AT1G58320	Protein PLANT CADMIUM RESISTANCE 9;PCR9	**1.858714**	0.1217066
AT1G58340	Protein DETOXIFICATION 48;DTX48	**3.482902**	0.00051999
AT1G59940	Two-component response regulator ARR3;ARR3	**3.419286**	0.00593898
AT1G59990	DEAD-box ATP-dependent RNA helicase 22;RH22	**1.864954**	0.0684125
AT1G60640	Stress response protein;At1g60640	**1.997195**	0.0317466
AT1G61275		**1.547662**	0.08811447
AT1G63660	At1g63660;At1g63660	**1.710722**	0.09695979
AT1G63810	Nucleolar protein;At1g63810	**1.800659**	0.05209653
AT1G64390	Endoglucanase 6;At1g64390	**1.994421**	0.0730842
AT1G64590	At1g64590/F1N19_15;At1g64590	**3.326327**	0.0024237
AT1G64600	At1g64600;At1g64600	**1.568945**	0.1366396
AT1G67110	CK hydroxylase;CYP735A2	**2.040022**	0.06752574
AT1G67120	Midasin;MDN1	**1.839859**	0.05407404
AT1G67195		**1.744278**	0.07809581
AT1G68290	Endonuclease 2;ENDO2	**2.038291**	0.01973099
AT1G68480	Zinc finger protein JAGGED;JAG	**1.97058**	0.03098868
AT1G68990	DNA-directed RNA polymerase 1, mitochondrial;RPOT1	**1.909249**	0.02652598
AT1G69040	ACT domain-containing protein ACR4;ACR4	**3.333621**	6.53E-05
AT1G69070	Nucleolar-like protein;At1g69070	**1.538133**	0.09251168
AT1G69200	Fructokinase-like 2, chloroplastic;FLN2	**1.931324**	0.05994079
AT1G69530	Expansin-A1;EXPA1	**4.052634**	9.29E-05
AT1G70310	Spermidine synthase 2;SPDSYN2	**1.719245**	0.04271341
AT1G70850	MLP-like protein 34;MLP34	**1.885706**	0.03218536
AT1G72040	At1g72040;dNK	**2.176078**	0.00593898
AT1G72140	Protein NRT1/ PTR FAMILY 5	**1.650943**	0.08824208
AT1G72370	40S ribosomal protein Sa-1;RPSaA	**1.600719**	0.06696358
AT1G72440	CCAAT-binding factor;EDA25	**1.819144**	0.04328867
AT1G73300	Serine carboxypeptidase-like 2;SCPL2	**1.922608**	0.08578942
AT1G74458	Transmembrane protein;At1g74458	**1.862261**	0.03588106
AT1G74560	NAP1-related protein 1;NRP1	**2.091235**	0.0060992
AT1G74670	Gibberellin-regulated protein 6;GASA6	**2.586444**	0.00314421

AT1G74890	Two-component response regulator ARR15;ARR15	**13.27505**	2.06E-05
AT1G75450	CK dehydrogenase 5;CKX5	**3.144956**	0.00931949
AT1G75670	DNA-directed RNA polymerase;At1g75670	**1.528541**	0.1277123
AT1G76300	Small nuclear ribonucleoprotein SmD3a;SMD3A	**1.688141**	0.04933487
AT1G76410	RING-H2 finger protein ATL8;ATL8	**1.532955**	0.4599539
AT1G77030	Putative DEAD-box ATP-dependent RNA helicase 29;RH29	**1.931879**	0.01397838
AT1G77110	Auxin efflux carrier component 6;PIN6	**1.92101**	0.1138644
AT1G77940	60S ribosomal protein L30-2;RPL30B	**1.688667**	0.1009996
AT1G78120	Tetratricopeptide repeat (TPR)-like superfamily protein;TPR12	**2.892877**	0.0007283
AT1G78290	Serine/threonine-protein kinase SRK2C;SRK2C	**1.501365**	0.1893246
AT1G78580	Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 1;TPS1	**2.265619**	0.00528005
AT1G78930	Mitochondrial transcription termination factor family protein;YUP8H12R	**1.538607**	0.3573925
AT1G79150	Binding protein;YUP8H12R	**1.584409**	0.1651273
AT1G79520	Metal tolerance protein 9;MTP9	**1.732812**	0.04271341
AT1G80050	Adenine phosphoribosyltransferase 2;APT2	**1.885608**	0.01414177
AT1G80270	Pentatricopeptide repeat-containing protein At1g80270, mitochondrial;At1g80270	**1.987645**	0.08398219
AT1G80710	DROUGHT SENSITIVE 1;DROUGHT SENSITIVE 1	**1.801471**	0.09025822
AT1G80720	Mitochondrial glycoprotein family protein;At1g80720	**1.883864**	0.02861287
AT1G80750	60S ribosomal protein L7-1;RPL7A	**1.517988**	0.1149133
AT2G01530	MLP-like protein 329;MLP329	**1.763779**	0.02665674
AT2G01830	Histidine kinase 4;AHK4	**2.700244**	0.00338833
AT2G01880	Purple acid phosphatase 7;PAP7	**1.546825**	0.3621549
AT2G03090	Expansin-A15;EXPA15	**2.465295**	0.04833907
AT2G05220	40S ribosomal protein S17-2;RPS17B	**1.776004**	0.01294938
AT2G14247	Expressed protein;At2g14247	**2.061651**	0.4238566
AT2G15220	At2g15220/F15A23	**2.004858**	0.02156521
AT2G16005	MD-2-related lipid-recognition protein ROSY1;ROSY1	**2.063338**	0.1257192
AT2G17820	Histidine kinase 1;AHK1	**2.276236**	0.00409503
AT2G18020	60S ribosomal protein L8-1;RPL8A	**1.735564**	0.04607134
AT2G18220	Nucleolar complex protein 2 homolog;At2g18220	**1.667498**	0.109629
AT2G18300	Transcription factor HBI1;HBI1	**1.604179**	0.09189603

AT2G18470	Proline-rich receptor-like protein kinase PERK4;PERK4	**1.887982**	0.1384876
AT2G18900	Transducin/WD40 repeat-like superfamily protein;At2g18900	**1.800366**	0.03938199
AT2G19050	GDSL esterase/lipase At2g19050;At2g19050	**1.58486**	0.369397
AT2G19500	CK dehydrogenase 2;CKX2	**1.780096**	0.2414698
AT2G19540	Putative WD-40 repeat protein;heat stress tolerant DWD 1	**1.620445**	0.06709675
AT2G19670	Probable protein arginine N-methyltransferase 1	**1.82453**	0.06492835
AT2G20490	H/ACA ribonucleoprotein complex subunit 3-like protein;At2g20490	**1.577779**	0.09076886
AT2G21580	40S ribosomal protein S25-2;RPS25B	**1.548225**	0.1348298
AT2G21770	Probable cellulose synthase A catalytic subunit 9 [UDP-forming];CESA9	**2.113289**	0.04123227
AT2G21790	Ribonucleoside-diphosphate reductase large subunit;RNR1	**1.537573**	0.2382508
AT2G22770	Transcription factor NAI1;NAI1	**2.187564**	0.01224024
AT2G23930	Probable small nuclear ribonucleoprotein G;At2g23930	**1.505142**	0.1286439
AT2G24120	DNA-directed RNA polymerase 3, chloroplastic;RPOT3	**1.931223**	0.04284261
AT2G25160	At2g25160;CYP82F1	**1.94892**	0.0769961
AT2G27720	60S acidic ribosomal protein P2-1;RPP2A	**1.547023**	0.1532057
AT2G27840	Histone deacetylase HDT4;HDT4	**1.960002**	0.01797868
AT2G28450	Zinc finger CCCH domain-containing protein 24;At2g28450	**1.649479**	0.05498861
AT2G28950	Expansin-A6;EXPA6	**1.519388**	0.2275225
AT2G30540	Monothiol glutaredoxin-S9;GRXS9	**7.56854**	3.91E-06
AT2G30766	Uncharacterized protein;At2g30766	**1.602317**	0.7609543
AT2G31840	Thioredoxin-like fold domain-containing protein MRL7L, chloroplastic;MRL7L	**1.828227**	0.0460856
AT2G32510	Mitogen-activated protein kinase kinase kinase 17;MAPKKK17	**2.14319**	0.03321527
AT2G32550	Cell differentiation, Rcd1-like protein;At2g32550	**3.50872**	0.0006853
AT2G34260	WD repeat-containing protein 55;WDR55	**1.729182**	0.08665627
AT2G34357	ARM repeat superfamily protein;At2g34357	**1.754403**	0.040305
AT2G34510	Uncharacterized protein At2g34510;At2g34510	**1.97384**	0.01490982
AT2G34570	PIN domain-like family protein;MEE21	**1.511992**	0.1932211
AT2G34610	Cotton fiber protein;At2g34610	**1.535172**	0.3897125
AT2G34900	Transcription factor GTE1;GTE1	**1.536183**	0.09011099

AT2G35040	AICARFT/IMPCHase bienzyme family protein;At2g35040	**1.587322**	0.08710881
AT2G35980	NDR1/HIN1-like protein 10;NHL10	**2.948876**	0.01579078
AT2G37270	40S ribosomal protein S5-1;RPS5A	**1.797056**	0.02782588
AT2G37690	Phosphoribosylaminoimidazole carboxylase like protein;At2g37690	**2.209791**	0.00333505
AT2G37990	Ribosome biogenesis regulatory protein homolog;At2g37990	**1.528212**	0.1107365
AT2G38760	Annexin D3;ANN3	**1.550695**	0.3550552
AT2G39700	Expansin-A4;EXPA4	**1.733521**	0.03102705
AT2G40200	Transcription factor bHLH51;BHLH51	**1.518009**	0.3795503
AT2G40230	HXXXD-type acyl-transferase family protein;T07M07	**1.769486**	0.09169842
AT2G40360	Ribosome biogenesis protein BOP1 homolog;BOP1	**1.634699**	0.06726571
AT2G40610	Expansin-A8;EXPA8	**1.66677**	0.1651373
AT2G40670	Two-component response regulator ARR16;ARR16	**4.556402**	6.53E-05
AT2G40700	DEAD-box ATP-dependent RNA helicase 17;RH17	**1.660543**	0.08685086
AT2G41310	Two-component response regulator ARR8;ARR8	**4.080865**	0.00019825
AT2G41990	At2g41990;At2g41990	**1.519309**	0.236109
AT2G43110	At2g43110;At2g43110	**1.833875**	0.08120963
AT2G43200	Probable methyltransferase PMT19;At2g43200	**2.32458**	0.02349394
AT2G43550	Defensin-like protein 197;ATTI6	**2.224629**	0.01756647
AT2G43650	Sas10/U3 ribonucleoprotein (Utp) family protein;EMB2777	**1.759621**	0.04833907
AT2G44860	Probable ribosome biogenesis protein RLP24;At2g44860	**1.601873**	0.04595334
AT2G45860	At2g45860;At2g45860	**1.708742**	0.08398219
AT2G46310	Ethylene-responsive transcription factor CRF5;CRF5	**2.638147**	0.00077259
AT2G47180	Galactinol synthase 1;GOLS1	**1.977949**	0.04989076
AT2G47260	WRKY transcription factor 23;WRKY23	**1.950285**	0.04496275
AT3G01160	Pre-rRNA-processing ESF1-like protein;At3g01160	**1.511452**	0.1147029
AT3G01260	Galactose mutarotase-like superfamily protein;At3g01260	**1.960681**	0.09572745
AT3G02790	Protein METHYLENE BLUE SENSITIVITY 1;MBS1	**1.843254**	0.04863318
AT3G02885	Gibberellin-regulated protein 5;GASA5	**3.02348**	0.0022791

AT3G03630	S-sulfo-L-cysteine synthase (O-acetyl-L-serine-dependent), chloroplastic;CS26	**1.871266**	0.06718762
AT3G03820	Putative auxin-induced protein;SAUR29	**3.545404**	0.00052413
AT3G03920	Putative H/ACA ribonucleoprotein complex subunit 1-like protein 1;At3g03920	**2.135924**	0.00410596
AT3G04920	40S ribosomal protein S24-1;RPS24A	**1.527582**	0.09295034
AT3G05060	Probable nucleolar protein 5-2;NOP5-2	**1.735625**	0.03591786
AT3G05640	Probable protein phosphatase 2C 34;At3g05640	**1.920571**	0.04758653
AT3G05770	F10A16	**2.071047**	0.1059362
AT3G06020	Protein FANTASTIC FOUR 4;FAF4	**2.442333**	0.03652287
AT3G06070	At3g06070;At3g06070	**1.756441**	0.06491593
AT3G06530	Uncharacterized protein At3g06530;At3g06530	**2.031387**	0.03225492
AT3G07050	Guanine nucleotide-binding protein-like NSN1;NSN1	**1.741874**	0.02328438
AT3G07230	At3g07230;T1B9	**1.504527**	0.1085437
AT3G07860	U11/U12 small nuclear ribonucleoprotein 25 kDa protein;SNRNP25	**1.635283**	0.0557518
AT3G08030	F17A17	**1.529007**	0.1024134
AT3G08520		**1.911599**	0.01198817
AT3G10690	DNA gyrase subunit A, chloroplastic/mitochondrial;GYRA	**1.502219**	0.2663701
AT3G11964	rRNA biogenesis protein RRP5;RRP5	**1.62695**	0.04480164
AT3G12270	Probable protein arginine N-methyltransferase 3;PRMT3	**1.889271**	0.03225492
AT3G13860	Chaperonin CPN60-like 2, mitochondrial;At3g13860	**1.570262**	0.1683146
AT3G14540	Terpenoid synthase 19;TPS19	**2.182112**	0.0323764
AT3G15720	Probable polygalacturonase At3g15720;At3g15720	**3.020547**	0.01929576
AT3G15950		**1.645704**	0.02145855
AT3G16080	60S ribosomal protein L37-3;RPL37C	**1.611959**	0.1024134
AT3G16310	Nuclear pore complex protein NUP35;NUP35	**1.63926**	0.06603646
AT3G16430	PYK10-binding protein 2;PBP2	**1.654597**	0.1978031
AT3G16450	Jacalin-related lectin 33;JAL33	**1.733929**	0.1413011
AT3G16460	Jacalin-related lectin 34;JAL34	**1.682341**	0.07456891
AT3G16810	Pumilio homolog 24;APUM24	**2.007236**	0.00990354
AT3G17170	AT3g17170/K14A17_29;RFC3	**1.953722**	0.05309439
AT3G18130	Receptor for activated C kinase 1C;RACK1C	**1.85152**	0.04666066
AT3G18400	NAC domain containing protein 58;NAC058	**1.951272**	0.02350499
AT3G18600	DEAD-box ATP-dependent RNA helicase 51;RH51	**1.947624**	0.01370738

AT3G19270	Abscisic acid 8'-hydroxylase 4;CYP707A4	**1.698693**	0.3027884
AT3G20440	1,4-alpha-glucan-branching enzyme 3, chloroplastic/amyloplastic;SBE3	**2.039358**	0.01879332
AT3G21300	RNA methyltransferase family protein;At3g21300	**1.531144**	0.2282919
AT3G21540	Transducin family protein / WD-40 repeat family protein;At3g21540	**1.675132**	0.0563826
AT3G21950	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein;At3g21950	**2.20764**	0.2050454
AT3G22310	DEAD-box ATP-dependent RNA helicase 9, mitochondrial;RH9	**1.656915**	0.0832644
AT3G22800	Leucine-rich repeat extensin-like protein 6;LRX6	**1.551501**	0.2068662
AT3G23830	Glycine-rich RNA-binding protein 4, mitochondrial;RBG4	**1.970122**	0.03000901
AT3G26490	BTB/POZ domain-containing protein At3g26490;At3g26490	**1.785546**	0.0233806
AT3G27550	RNA-binding CRS1 / YhbY (CRM) domain protein;At3g27550	**1.771185**	0.07554355
AT3G29250	Short-chain dehydrogenase reductase 4;SDR4	**2.829761**	0.00817073
AT3G29575	Ninja-family protein AFP3;AFP3	**1.680179**	0.1173622
AT3G29670	Phenolic glucoside malonyltransferase 2;PMAT2	**2.032725**	0.02156781
AT3G44550	Probable fatty acyl-CoA reductase 5;FAR5	**1.658403**	0.09961662
AT3G44750	Histone deacetylase HDT1;HDT1	**1.937559**	0.02613401
AT3G44990	Xyloglucan endotransglucosylase/hydrolase protein 31;XTH31	**1.949812**	0.2157494
AT3G45700	Protein NRT1/ PTR FAMILY 2	**2.54875**	0.03127348
AT3G46210	Exosome complex exonuclease RRP46 homolog;RRP46	**1.893874**	0.04626588
AT3G46370	Leucine-rich repeat protein kinase family protein;F18L15	**2.021561**	0.00977719
AT3G46700	UDP-glycosyltransferase 76E3;UGT76E3	**1.863384**	0.07085542
AT3G47750	ABC transporter A family member 4;ABCA4	**1.769283**	0.1495056
AT3G48100	Two-component response regulator ARR5;ARR5	**8.690385**	3.46E-06
AT3G49660	COMPASS-like H3K4 histone methylase component WDR5A;WDR5A	**1.619176**	0.08955052
AT3G50300	HXXXD-type acyl-transferase family protein;At3g50300	**1.81881**	0.271773
AT3G50700	Zinc finger protein GAI-ASSOCIATED FACTOR 1;GAF1	**1.788438**	0.04141424
AT3G53870	40S ribosomal protein S3-2;RPS3B	**1.773968**	0.0460856

AT3G54720	Probable glutamate carboxypeptidase AMP1;AMP1	**2.407565**	0.00094079
AT3G55010	Phosphoribosylformylglycinamidine cyclo-ligase, chloroplastic;PUR5	**1.655773**	0.1030011
AT3G55400	Methionine--tRNA ligase, chloroplastic/mitochondrial;OVA1	**1.528557**	0.185016
AT3G55515	DVL8;DVL8	**2.82586**	0.0026948
AT3G56990	AT3g56990/F24I3_70;F24I3	**1.509138**	0.2740389
AT3G57010	Protein STRICTOSIDINE SYNTHASE-LIKE 8;SSL8	**1.798551**	0.09961662
AT3G57040	Two-component response regulator ARR9;ARR9	**2.722807**	0.00146923
AT3G57150	H/ACA ribonucleoprotein complex subunit 4;CBF5	**1.7605**	0.02705577
AT3G57660	DNA-directed RNA polymerase I subunit 1;NRPA1	**1.847834**	0.04104207
AT3G59670	Elongation factor;At3g59670	**2.049632**	0.02170681
AT3G59820	LETM1-like protein;LETM1	**1.60592**	0.05732435
AT3G60245	60S ribosomal protein L37a-2;RPL37AC	**1.617628**	0.08398219
AT3G61630	Ethylene-responsive transcription factor CRF6;CRF6	**1.599859**	0.2171922
AT3G61640	Arabinogalactan protein 20;AGP20	**2.108797**	0.00319755
AT3G62050	At3g62050;At3g62050	**1.783591**	0.2489289
AT3G62530	ARM repeat superfamily protein;At3g62530	**1.753126**	0.01931315
AT3G62740	Beta-glucosidase 7;BGLU7	**2.723874**	0.04439262
AT3G62870	60S ribosomal protein L7a-2;RPL7AB	**1.580395**	0.04648841
AT3G62930	Monothiol glutaredoxin-S6;GRXS6	**2.790541**	0.03510008
AT3G63440	CK dehydrogenase 6;CKX6	**3.072536**	3.91E-05
AT4G00100	40S ribosomal protein S13-2;RPS13B	**1.560491**	0.07178079
AT4G00620	Bifunctional protein FolD 4, chloroplastic;FOLD4	**1.858231**	0.08015399
AT4G02850	At4g02850;At4g02850	**2.548733**	0.00122227
AT4G03270	Putative cyclin-D6-1;CYCD6-1	**2.093127**	0.00663484
AT4G03420	AT4g03420/F9H3_4;At4g03420	**1.669273**	0.1608276
AT4G03610	Metallo-hydrolase/oxidoreductase superfamily protein;At4g03610	**3.859998**	2.90E-05
AT4G04940	Putative WD-repeat membrane protein;At4g04940	**2.053628**	0.0121343
AT4G07825	At4g07825;At4g07825	**1.5002**	0.1161083
AT4G09320	Nucleoside diphosphate kinase 1;NDK1	**1.687948**	0.04031834
AT4G09730	DEAD-box ATP-dependent RNA helicase 39;RH39	**1.580329**	0.1226391
AT4G11190	Dirigent protein 13;DIR13	**6.459466**	1.24E-06

AT4G11210	Dirigent protein 14;DIR14	**2.065742**	0.1797162
AT4G12545	Putative lipid-binding protein AIR1B;AIR1B	**2.755444**	0.02156521
AT4G13575	Uncharacterized protein;At4g13575	**1.656072**	0.04141424
AT4G13750	Protein NO VEIN;NOV	**1.678212**	0.08148013
AT4G13850	Glycine-rich RNA-binding protein 2, mitochondrial;RBG2	**1.542606**	0.102679
AT4G15230	ABC transporter G family member 30;ABCG30	**4.424809**	5.50E-05
AT4G15640	Adenylyl cyclase;At4g15640	**1.626195**	0.1214165
AT4G15680	Monothiol glutaredoxin-S4;GRXS4	**2.157567**	0.08473578
AT4G15770	60S ribosome subunit biogenesis protein NIP7 homolog;At4g15770	**1.796912**	0.1651373
AT4G16000	Uncharacterized protein At4g16000;At4g16000	**1.755863**	0.1885728
AT4G16008	Uncharacterized protein;At4g16008	**1.564764**	0.08955052
AT4G16630	DEAD-box ATP-dependent RNA helicase 28;RH28	**1.798881**	0.02483081
AT4G17560	50S ribosomal protein L19-1, chloroplastic;At4g17560	**1.694107**	0.03800414
AT4G18440	Adenylosuccinate lyase;At4g18440	**1.750813**	0.03588106
AT4G19030	Aquaporin NIP1-1;NIP1-1	**4.129609**	0.00068787
AT4G19380	Long-chain-alcohol oxidase FAO4A;FAO4A	**1.829146**	0.02352201
AT4G20020	Multiple organellar RNA editing factor 1, mitochondrial;MORF1	**1.830687**	0.04741865
AT4G21140	Copper ion-binding protein;At4g21140	**1.540304**	0.3043555
AT4G21760	Beta-glucosidase 47;BGLU47	**2.564024**	0.04246434
AT4G22230	Defensin-like protein 96;At4g22230	**1.765278**	0.2193707
AT4G22570	Adenine phosphoribosyltransferase 3;APT3	**1.844743**	0.02479369
AT4G22760	Pentatricopeptide repeat-containing protein At4g22760;PCMP-E6	**2.119884**	0.04666066
AT4G23540	ARM repeat superfamily protein;At4g23540	**1.519735**	0.113638
AT4G23750	Ethylene-responsive transcription factor CRF2;CRF2	**2.746758**	0.00064562
AT4G24015	Probable E3 ubiquitin-protein ligase RHA4A;RHA4A	**1.571372**	0.1239137
AT4G24780	Probable pectate lyase 18;At4g24780	**1.841128**	0.05828388
AT4G24890	Probable inactive purple acid phosphatase 24;PAP24	**3.1302**	0.0024237
AT4G25340	Peptidyl-prolyl cis-trans isomerase FKBP53;FKBP53	**1.665921**	0.08084642
AT4G25410	Transcription factor bHLH126;BHLH126	**1.895259**	0.1502001
AT4G25730	Putative rRNA methyltransferase;At4g25730	**1.662973**	0.04757972
AT4G25890	60S acidic ribosomal protein P3-1;RPP3A	**2.481126**	0.0376892

AT4G26110	Nucleosome assembly protein 1;1;NAP1;1	**1.578889**	0.08824208
AT4G26150	Putative GATA transcription factor 22;GATA22	**2.285104**	0.03701988
AT4G26190	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein;At4g26190	**1.623812**	0.04576277
AT4G26260	Inositol oxygenase 4;MIOX4	**1.646805**	0.5585479
AT4G26600	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein;At4g26600	**1.641324**	0.09136122
AT4G27970	S-type anion channel SLAH2;SLAH2	**1.891702**	0.09138294
AT4G28250	Expansin-B3;EXPB3	**3.732378**	0.00044308
AT4G28450	AT4g28450/F20O9_130;At4g28450	**1.531431**	0.2101443
AT4G29310	DUF1005 family protein (DUF1005);At4g29310	**2.042739**	0.0167684
AT4G29410	60S ribosomal protein L28-2;RPL28C	**1.76878**	0.03456338
AT4G29610	Cytidine deaminase 6;CDA6	**1.804295**	0.04607134
AT4G29720	Probable polyamine oxidase 5;PAO5	**1.717958**	0.06761884
AT4G29740	CK dehydrogenase 4;CKX4	**3.078228**	0.00085649
AT4G30990	ARM repeat superfamily protein;At4g30990	**1.626014**	0.0607667
AT4G31120	Protein arginine N-methyltransferase 1	**1.656215**	0.07181998
AT4G31210	DNA topoisomerase, type IA, core;At4g31210	**1.822211**	0.04883703
AT4G31700	40S ribosomal protein S6-1;RPS6A	**1.606477**	0.06482993
AT4G34290	SWIB/MDM2 domain superfamily protein;At4g34290	**1.804833**	0.0460856
AT4G34588		**1.671705**	0.0978812
AT4G34610	BEL1-like homeodomain protein 6;BLH6	**2.124856**	0.02145855
AT4G35160	Acetylserotonin O-methyltransferase;ASMT	**1.922329**	0.02578319
AT4G36540	Transcription factor BEE 2;BEE2	**1.534065**	0.1117273
AT4G36570		**2.793783**	0.00333505
AT4G37070	Patatin-like protein 1;PLP1	**1.793248**	0.2283984
AT4G37409	Uncharacterized protein;At4g37409	**1.533746**	0.355067
AT4G37410	Cytochrome P450 81F4;CYP81F4	**1.775863**	0.04607134
AT4G37750	AP2-like ethylene-responsive transcription factor ANT;ANT	**1.522672**	0.1850873
AT4G38840	At4g38840;SAUR14	**1.684103**	0.03157831
AT4G39250	Protein RADIALIS-like 1;RL1	**2.218401**	0.029248
AT4G39300	At4g39300;T22F8	**1.648941**	0.09788006
AT4G39410	Probable WRKY transcription factor 13;WRKY13	**1.732422**	0.1550352
AT4G39770	Probable trehalose-phosphate phosphatase H;TPPH	**1.717637**	0.1309255

AT5G04130	DNA gyrase subunit B, mitochondrial;GYRBM	**1.506348**	0.1974773
AT5G05860	UDP-glycosyltransferase 76C2;UGT76C2	**2.83293**	0.0003242
AT5G05965	Cell wall RBR3-like protein;At5g05965	**3.426558**	0.01495157
AT5G08610	DEAD-box ATP-dependent RNA helicase 26;RH26	**2.426001**	0.0024237
AT5G08620	DEAD-box ATP-dependent RNA helicase 25;RH25	**1.589513**	0.1038256
AT5G09520	Protein PELPK2;PELPK2	**1.591967**	0.2050454
AT5G09840	Emb;CAB71880	**2.156214**	0.02349247
AT5G11240	At5g11240;At5g11240	**1.636859**	0.07105914
AT5G11420	Uncharacterized protein At5g11420;At5g11420	**1.651446**	0.02816873
AT5G11630	Uncharacterized protein T22P22_20;NOXY2	**1.534161**	0.08228556
AT5G13180	NAC domain-containing protein 83;NAC083	**1.51992**	0.07328616
AT5G13330	Ethylene-responsive transcription factor ERF113;ERF113	**1.574065**	0.2623998
AT5G14050	U3 small nucleolar RNA-associated protein 18 homolog;At5g14050	**1.867082**	0.01441836
AT5G14070	Glutaredoxin-C8;GRXC8	**1.641677**	0.1581535
AT5G14520	Pescadillo homolog;PES	**1.505414**	0.04666066
AT5G14580	Polyribonucleotide nucleotidyltransferase 2, mitochondrial;PNP2	**1.852887**	0.06261995
AT5G14650	Pectin lyase-like superfamily protein;At5g14650	**3.737931**	0.00047184
AT5G15550	Ribosome biogenesis protein WDR12 homolog;WDR12	**1.717**	0.03223325
AT5G16750	Transducin family protein / WD-40 repeat family protein;TORMOZEMBRYO DEFECTIVE	**1.674616**	0.03652287
AT5G16930	AAA-type ATPase family protein;At5g16930	**1.723045**	0.08746755
AT5G18020	Auxin-responsive protein SAUR20;SAUR20	**2.870068**	0.0121343
AT5G19110	Eukaryotic aspartyl protease family protein;At5g19110	**2.244875**	0.04529116
AT5G19257		**2.522152**	0.04233433
AT5G19260	Protein FANTASTIC FOUR 3;FAF3	**2.963845**	0.00026127
AT5G19300	At5g19300;At5g19300	**1.762246**	0.04228324
AT5G20160	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein;At5g20160	**2.277759**	0.00677131
AT5G21482	CK dehydrogenase 7;CKX7	**1.656462**	0.0323764
AT5G22650	Histone deacetylase HDT2;HDT2	**1.758926**	0.01982637
AT5G22930	Enabled-like protein (DUF1635);MRN17	**1.900818**	0.09138294
AT5G23300	Dihydroorotate dehydrogenase (quinone), mitochondrial;PYRD	**1.950339**	0.0332582

AT5G23360	GEM-like protein 7;At5g23360	**2.255012**	0.0323764
AT5G24580	Heavy metal-associated isoprenylated plant protein 9;HIPP09	**1.721892**	0.1616317
AT5G24920	Protein GLUTAMINE DUMPER 5;GDU5	**2.890963**	0.00383839
AT5G25190	Ethylene-responsive transcription factor ERF003;ERF003	**2.261085**	0.00568866
AT5G26180	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein;At5g26180	**1.758951**	0.01532765
AT5G26220	Gamma-glutamylcyclotransferase 2-1;GGCT2;1	**2.580606**	0.00281301
AT5G26260	F9D12	**3.918727**	6.54E-05
AT5G26290	TRAF-like family protein;At5g26290	**2.101887**	0.03514296
AT5G27120	Probable nucleolar protein 5-1;NOP5-1	**2.318867**	0.0031413
AT5G28919	Uncharacterized protein;At5g28919	**1.5124**	0.1121387
AT5G36150	Tirucalladienol synthase;PEN3	**1.703693**	0.1651373
AT5G36180	Serine carboxypeptidase-like 1;SCPL1	**1.648558**	0.2604626
AT5G38020	At5g38020;At5g38020	**1.719471**	0.09334951
AT5G40480	Nuclear pore complex protein GP210;GB210	**1.785533**	0.1051183
AT5G40770	Prohibitin-3, mitochondrial;PHB3	**1.584442**	0.1030011
AT5G41520	40S ribosomal protein S10-2;RPS10B	**1.564211**	0.1392596
AT5G43590	Patatin-like protein 4;PLP4	**2.080874**	0.1406769
AT5G45670	GDSL esterase/lipase At5g45670;At5g45670	**1.673032**	0.04639221
AT5G47950	Acetyl-CoA:benzylalcohol acetyltranferase-like protein;At5g47950	**2.937757**	0.00414292
AT5G47980	BAHD acyltransferase At5g47980;BAHD1	**2.865178**	0.0114611
AT5G47990	Cytochrome P450 705A5;CYP705A5	**4.415709**	0.00117014
AT5G48000	Cytochrome P450 708A2;CYP708A2	**3.293086**	0.00649898
AT5G48010	Thalianol synthase;THAS1	**4.393574**	0.00102398
AT5G48110	Inactive terpenoid synthase 20, chloroplastic;TPS20	**1.619283**	0.09169842
AT5G48900	Probable pectate lyase 20;At5g48900	**1.626905**	0.04888036
AT5G50600	11-beta-hydroxysteroid dehydrogenase 1A;HSD1	**1.783443**	0.3935866
AT5G50700		**1.817651**	0.2996219
AT5G50717		**2.953468**	0.00078637
AT5G50915	Transcription factor bHLH137;BHLH137	**3.549215**	8.62E-05
AT5G51540	Mitochondrial intermediate peptidase, mitochondrial;OCT1	**2.156385**	0.04833907
AT5G51780	Transcription factor bHLH36;BHLH36	**1.672238**	0.419074
AT5G52470	Probable mediator of RNA polymerase II transcription subunit 36b;MED36B	**1.96147**	0.01106303
AT5G52650	40S ribosomal protein S10-3;RPS10C	**1.629546**	0.03153818

AT5G55280	Cell division protein FtsZ homolog 1, chloroplastic;FTSZ1	**1.724771**	0.07952109
AT5G55920	Nucleolar protein-like;OLI2	**1.588362**	0.1133822
AT5G56710	60S ribosomal protein L31-3;RPL31C	**1.6508**	0.05963742
AT5G56970	CK dehydrogenase 3;CKX3	**2.623122**	0.01325929
AT5G57400	Transmembrane protein;MSF19	**1.967216**	0.08993461
AT5G58370	AT5G58370 protein;MCK7	**2.01253**	0.0131706
AT5G59010	Serine/threonine-protein kinase BSK5;BSK5	**1.593352**	0.08214582
AT5G60760	P-loop NTPase domain-containing protein LPA1 homolog 1;At5g60760	**2.502188**	0.0607667
AT5G60890	Transcription factor MYB34;MYB34	**1.760866**	0.06558514
AT5G61440	Thioredoxin-like 1-2, chloroplastic;At5g61440	**1.699329**	0.03214488
AT5G62170	LOW protein: M-phase inducer phosphatase-like protein;TRM25	**1.508704**	0.1635589
AT5G62270	Gb;AAC32909	**1.739744**	0.04031834
AT5G62920	Two-component response regulator ARR6;ARR6	**8.498334**	1.15E-05
AT5G62960	At5g62960;MJH22	**2.254043**	0.00865473
AT5G64080	Non-specific lipid-transfer protein-like protein At5g64080;At5g64080	**1.86903**	0.09138294
AT5G64850	At5g64850;MXK3	**1.633187**	0.09138294
AT5G65140	Probable trehalose-phosphate phosphatase J;TPPJ	**2.41399**	0.00122227
AT5G65445		**2.079526**	0.04833907
AT5G65510	AP2-like ethylene-responsive transcription factor AIL7;AIL7	**2.441707**	0.02957487
AT5G66170	Thiosulfate sulfurtransferase 18;STR18	**1.641916**	0.09317483
AT5G66590	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein;At5g66590	**1.954568**	0.03358984
AT5G67240	Small RNA degrading nuclease 3;SDN3	**1.564379**	0.07876532
AT5G67620	At5g67620;At5g67620	**1.515816**	0.4117399

Table S2. AtCRF6-dependently cytokinin-regulated genes. Genes **A:** up regulated or **B:** down regulated in *crf6* + CK (2µM BA) for 6 hours vs *crf6* control (DMSO) treated.

A: Up regulated +CK

Locus	Gene Name	Description	FC Col ± CK	FC *crf6* ± CK
AT1G07100	-	pre-tRNA tRNA-Ile	0.9255257	1.746994
AT1G11670	DTX36	Protein Detoxification 36	1.171153	1.855805
AT1G12740	CYP87A2	Cytochrome P450, Family 87, Subfamily A, Polypeptide 2	1.576079	2.410254
AT1G13609	-	Defensin-like protein 287	1.359438	2.331955
AT1G30730	-	Berberine Bridge Enzyme-Like 11	1.207393	2.056983
AT1G34520	-	Long-Chain-Alcohol O-Fatty-Acyltransferase 10-Related	2.212956	4.091713
AT1G34670	MYB93	Transcription Factor MYB93	1.096731	1.659933
AT1G35625	RMR6	Receptor Homology Region, Transmembrane Domain- And Ring Domain-Containing Protein 2-Related	1.787985	2.682847
AT1G47510	IP5P11	Type IV inositol polyphosphate 5-phosphatase 11	1.154962	2.301573
AT1G53220	-	PRE-tRNA tRNA-Ile	0.9255257	1.746994
AT1G53543	-	Hypothetical Protein	1.089295	1.957198
AT1G59940	ARR3	Type A Response Regulator 3	3.419286	1.185598
AT1G66280	BGLU22	Beta-Glucosidase 22	0.9760791	1.836393
AT1G66725	MIR163	MicroRNA163	1.108632	1.975455
AT1G66800	-	Nad(P)-Binding Rossmann-Fold Superfamily Protein	2.040022	3.097233
AT1G67110	CYP735A2	Cytochrome P450, Family 735, Subfamily A, Polypeptide 2	1.650943	3.386465
AT1G72140	TOB1	Transporter Of IBA1	1.922608	3.399741
AT1G73300	SCPL2	Serine Carboxypeptidase-Like 1	1.532955	2.500558
AT1G76410	ATL8	Ring-H2 Finger Protein ATL8	1.401192	2.335255
AT1G77520	-	O-Methyltransferase Family Protein	1.024905	1.915067
AT2G01520	MLP328	MLP-like Protein 328	1.546825	3.236916
AT2G01880	PAP7	Purple Acid Phosphatase 7	1.149328	2.606114
AT2G19060	-	SGNH Hydrolase-Type Esterase Superfamily Protein	1.289691	2.16223
AT2G20080	TIE2	TCP Interactor Containing Ear Motif Protein 2	1.217887	2.135139
AT2G20722	-	snoRNA	1.259377	2.110164
AT2G22860	ATPSK2	Phytosulfokine 2 Precursor	1.94892	3.22498
AT2G25160	CYP82F1	Cytochrome P450, Family 82, Subfamily F, Polypeptide 1	1.201765	1.986295

AT2G32990	GH9B8	Glycosyl Hydrolase 9B8	1.056377	1.675504
AT2G34500	CYP710A1	Cytochrome P450, Family 710, Subfamily A, Polypeptide 1	0.9457626	1.542649
AT2G35770	SCPL28	Serine Carboxypeptidase-Like 28	1.550695	2.606701
AT2G38760	ANN3	Annexin 3	1.165824	2.593122
AT2G41260	M17	Late Embryogenesis Abundant Protein M10-Related	0.781049	1.749315
AT2G44080	ARL	Argos-Like Protein	1.367111	2.099048
AT3G05835	-	pre-tRNA tRNA-Ile	1.026369	1.604729
AT3G06680	RPL29B	Ribosomal L29E Protein Family	0.838327	1.674964
AT3G09270	GSTU8	Glutathione S-Transferase TAU8	0.9255257	1.746994
AT3G12502	-	Natural Antisense Transcript Overlaps With At3G12500	1.381365	2.643895
AT3G15055	-	pre-tRNA tRNA-Ile	0.51679	2.432956
AT3G21510	AHP1	Histidine-Containing Phosphotransfer Protein 1	3.549215	1.301919
AT3G22640	PAP85	Cupin Family Protien	1.018199	1.652987
AT3G25830	TPS27	Terpene Synthase-Like Sequence-1,8-Cineole	2.870068	1.17349
AT3G32400	FH17	Formin-J, Actin-Binding Fh2/Drf Autoregulatory Protein	1.242659	1.922142
AT3G44300	NIT2	Nitrilase 2	2.442333	0.9543266
AT3G45070	SOT5	Sulfotransferase 202B1	1.225733	2.425555
AT3G45710	NPF2.5	Protein NRT1/ PTR Family 2.5	1.364342	2.165267
AT3G49330	-	Plant Invertase/Pectin Methylesterase Inhibitor Superfamily Protein	1.10213	1.848526
AT3G52900	-	RAB6-Interacting Golgin	1.798551	2.845101
AT3G57010	SSL8	Protein Strictosidine Synthase-Like 8	1.156175	2.557094
AT3G59900	ARGOS	Protein Auxin-Regulated Gene Involved In Organ Size	1.07358	1.709518
AT3G60660	-	Spindle And Kinetochore-Associated Protein 1	0.8237166	1.81118
AT3G61400	-	1-Aminocyclopropane-1-Carboxylate Oxidase Homolog 8	0.7866125	2.015517
AT4G08360	-	KOW Domain-Containing Protein-Related	4.129609	2.021512
AT4G11210	DIR14	Disease Resistance-Responsive (Dirigent-Like Protein) Family Protein	1.202657	2.294572
AT4G15990	-	Hypothetical Protein	1.755863	3.2554
AT4G16000	-	Hypothetical Protein	1.049498	1.875181
AT4G18630	-	Hypothetical Protein	2.564024	4.406307
AT4G21760	BGLU47	Beta-Glucosidase 47	1.170784	1.76403

AT4G21870	HSP15.4	15.4 Kda Class V Heat Shock Protein	1.765278	4.47735
AT4G22230.1	-	Defensin-Like Protein 96	2.522152	1.245802
AT4G22230.2			0.8367131	2.112967
AT4G23420	-	Nad(P)-Binding Rossmann-Fold Superfamily Protein-Related	2.113289	1.052106
AT4G28530	KIR1	NAC Transcription Factor	1.433866	2.284542
AT4G28840	TIE1	TCP Interactor Containing Ear Motif Protein 1	1.081883	1.933681
AT4G34790	SAUR3	Small Auxin Upregulated Rna 3	1.273514	2.014309
AT4G36635	-	pre-tRNA tRNA-Ile	0.9255257	1.746994
AT4G37070	PLP1	Patatin-Like Protein 1	1.793248	2.949888
AT4G37409	-	Hypothetical Protein	1.533746	2.443806
AT4G39070	BBX20	B-Box Zinc Finger Protein 20	1.480413	2.308091
AT5G04770	CAT6	Cationic Amino Acid Transporter 6	1.433319	2.192505
AT5G08350	-	Gem-Like Protein 4	1.152207	1.932154
AT5G13330	ERF113	Ethylene-Responsive Transcription Factor 113	1.574065	2.851676
AT5G14070	GRXC3	Glutaredoxin-C8	1.641677	3.270078
AT5G19260	FAF3	Protein Fantastic Four 3	2.963845	4.525007
AT5G19600	SULTR3	Sulfate Transporter 3.5-Related	1.07767	1.710698
AT5G23830	MRO11.13	MD-2-Related Lipid Recognition Domain-Containing Protein	1.26297	2.290679
AT5G36180	SCPL1	Serine Carboxypeptidase-Like 1	1.648558	2.588901
AT5G38020	-	S-Adenosyl-L-Methionine-Dependent Methyltransferases Superfamily Protein	1.719471	3.096138
AT5G38200	MXA21.22	Class I Glutamine Amidotransferase-Like Superfamily Protein	0.9976323	1.574567
AT5G38910	Putative germin-like protein subfamily 1 member 9;At5g38910;ortholog	Germin-Like Protein Subfamily 1 Member 10-Related	0.7394426	1.733485
AT5G47980	BAHD1	BAHD Acyltransferase Bia1	2.865178	4.889612
AT5G47990	Cytochrome P450 705A5;CYP705A5;ortholog	Cytochrome P450 705A5	4.415709	6.93353

AT5G48000	Cytochrome P450 708A2;CYP708A2;ortholog	Cytochrome P450 708A2	3.293086	6.137346
AT5G48010	THAS1	Arabidiol Synthase-Related	4.393574	8.475862
AT5G48110	TPS20	Alpha-Barbatene Synthase-Related	1.619283	2.530312
AT5G50600	HSD1	11-Beta-Hydroxysteroid Dehydrogenase 1A	1.783443	3.817624
AT5G50700	HSD7	Hydroxysteroid Dehydrogenase 1	1.817651	3.840356
AT5G51780	BHLH36	Transcription Factor BHLH36	1.672238	2.741718
AT5G62920	ARR6	Two-Component Response Regulator ARR6	8.498334	13.77614
AT5G64100	PER69	Peroxidase 69	0.9085829	1.538117
AT5G64120	PER71	Peroxidase 71	1.072323	2.022311
AT5G65030	MXK3.28	OSJNBA0006M15.15 Protein	1.466549	2.35215
AT5G66170	STR18	Thiosulfate Sulfurtransferase 18	1.641916	3.004698
AT5G67620	-	Expressed Protein	1.515816	2.331155

B: Genes Down regulated +CK

Locus	Gene Name		FC Col ±	FC *crf6* ± CK
AT1G02850	BGLU11	Beta-Blucosidase 11	0.445186	0.7228033
AT1G06160	ERF094	Ethylene-Responsive Transcription Factor	0.4086025	0.7701279
AT1G07560	-	Leucine-Rich Repeat Protein Kinase Family Protein	0.374009	0.6433162
AT1G15125	-	S-Adenosyl-L-Methionine-Dependent Methyltransferases Superfamily Protein	0.4576241	0.7043576
AT1G17570.1	-	Pre-tRNA tRNA-Ser	1.14922	0.4540947
AT1G29020	-	Calcium-Binding EF-Hand Family Protein	0.3377178	0.1644197
AT1G32450	NRT1.5	Nitrate Transporter 1.5	0.4821955	0.7576876
AT1G51470	TGG5	Myrosinase 5	0.4569031	1.045367
AT1G54890	T24C10.2	Late Embryogenesis Abundant (LEA) Protein-like Protein	0.2809655	0.497385
AT1G62620	-	Flavin-Containing Monooxygenase	0.4593752	1.257981
AT2G02820	MYB88`	Transcription Factor MYB88	0.4751797	0.7403119
AT2G13810	ALD1	Aminotransferase ALD1	0.9862429	0.3297569
AT2G14610	ATPR1	Pathogenesis-Related Protein 1	0.4865079	0.2081867
AT2G20030	ATL12	Ring-H2 Finger Protein ATL12	0.3582342	0.6480176
AT2G24720	GLR2.2	Glutamate Receptor 2.2	1.004519	0.4180203
AT2G24850	TAT3	Aminotransferase TAT3	1.07083	0.2032518

AT2G32620	CSLB2	Cellulose Synthase-Like Protein B2	0.4716358	0.7917984
AT2G43120	PRN2	Pirin-Like Protein 2	0.460499	0.7752508
AT3G02850	SKOR	Stellar Potassium Outward Rectifying Transporter	0.3872199	0.6206815
AT3G05950	-	Germin-Like Protein Subfamily 1 Member 6	0.9286005	0.3163251
AT3G10320	MUCI21	Mucilage-Related 21	0.4248616	0.6487502
AT3G12580	HSP70	Heat Shock Protein 70	0.4657653	0.7290906
AT3G13100	ABCC7	ABC Transporter C Family Member 7	0.4920988	0.9315628
AT3G13760	-	Cysteine/Histidine-Rich C1 Domain Family Protein	0.4454036	0.7036598
AT3G20380	-	TRAF-LIKE FAMILY PROTEIN	0.2069236	0.3426316
AT3G23800	SBP3	Selenium-Binding Protein 3	0.4826302	0.8336392
AT3G25010	RLP41	Receptor-like protein 41	0.6986395	0.1985343
AT3G46330	MEE39	Probable LRR Receptor-Like Serine/Threonine-Protein Kinase	0.3573253	0.7001058
AT3G49960	PER35	Peroxidase 35-Related	0.2966472	0.7075676
AT3G54590	EXT2	Extensin-2	0.3875099	0.8573077
AT3G60330	AHA7	Atpase 7	0.4079106	0.7820106
AT4G02270	RHS13	Pollen Ole E I Family Allergen	0.3980372	0.6185812
AT4G08770	PER37	Peroxidase 37	0.2311234	0.3594069
AT4G10860.1	-	Hypothetical Protein	0.7359145	0.3293618
AT4G12480	EARLI1	Lipid Transfer Protein Earli 1	0.4871372	0.9126034
AT4G13420	HAK5	High Affinity K+ Transporter 5	0.166967	0.3398311
AT4G14020	RALF	`Rapid Alkalinization Factor	0.2932098	0.4443536
AT4G21680	NRT1.8	Nitrate Transporter 1.8	0.3885656	0.694006
AT4G22940	-	Protein Kinase Superfamily Protein	0.4123768	0.9223716
AT4G23150	CRK7	Cysteine-Rich Receptor-Like Protein Kinase 7	1.058033	0.4465195
AT4G27830	BGLU10	Beta-Glucosidase 10	0.4789825	0.9854879
AT4G32950	-	Protein Phosphatase 2C Family Protein;	0.6743993	0.2242928
AT4G36430	PER49	Peroxidase 49	0.4427088	0.7527277
AT4G37990	CAD8	Cinnamyl Alcohol Dehydrogenase 8	0.3332138	1.08942
AT5G05500	MOP10		0.4757778	0.9069783
AT5G07690	MYB29	Transcription Factor MYB29	0.4844535	0.8528625
AT5G09690	MRS2-7	Magnesium transporter MRS2-7	0.4486617	0.9287325
AT5G26300	-	TRAF-like Family Protein	1.348986	0.42143
AT5G27060	RLP53	Receptor-Like Protein 19-Related	0.2857459	0.7147249
AT5G35190	EXT13	Extensin-2-Related	0.3249343	0.5240204
AT5G36350	-	Encodes A ECA1 Gametogenesis Related Family Protein	0.3368983	0.8850495

AT5G36380	-	Encodes A ECA1 Gametogenesis Related Family Protein	0.3368983	0.8850495
AT5G36390	-	Encodes A ECA1 Gametogenesis Related Family Protein	0.3368983	0.8850495
AT5G36400	-	Encodes A ECA1 Gametogenesis Related Family Protein	0.3368983	0.8850495
AT5G36410	-	Encodes A ECA1 Gametogenesis Related Family Protein	0.3368983	0.8850495
AT5G36420	-	Encodes A ECA1 Gametogenesis Related Family Protein	0.3368983	0.8850495
AT5G36430	-	Encodes A ECA1 Gametogenesis Related Family Protein	0.3368983	0.8850495
AT5G36440	-	Encodes A ECA1 Gametogenesis Related Family Protein	0.3368983	0.8850495
AT5G36450	-	Encodes A ECA1 Gametogenesis Related Family Protein	0.3368983	0.8850495
AT5G36460	-	Encodes A ECA1 Gametogenesis Related Family Protein	0.3368983	0.8850495
AT5G36470	-	Encodes A ECA1 Gametogenesis Related Family Protein	0.3368983	0.8850495
AT5G49850	JAL46	Jacalin-related lectin 46	1.079853	0.4167979
AT5G54020	-	Cysteine/Histidine-rich C1 domain family protein	0.3500918	0.5367901
AT5G61160	ACT	Agmatine coumaroyltransferase	0.3569812	0.889234
AT5G63850	AAP4	Amino Acid Permease 4	0.3571792	0.5767908

Appendix ii: Chapter 3 Supplemental Tables

Table S1. Differentially Expressed Genes (DEGs) of WT and SlCRF5AS when treated with oxidative stress

Solyc#	FC MT vs MT+ H_2O_2	padj	**FC SlCRF5AS vs SlCRF5AS+H_2O_2**	padj
Solyc11g071750	Inf	2.07E-16	139.893734	1.53E-15
Solyc01g090310	Inf	5.11E-12	Inf	1.68E-10
Solyc06g054630	Inf	4.90E-09	Inf	9.56E-09
Solyc04g025750	Inf	1.69E-05	218.09178	2.06E-07
Solyc06g070910	Inf	0.01980631	Inf	5.45E-06
Solyc05g055080	Inf	4.41E-06	114.660614	7.67E-06
Solyc11g069280	Inf	0.00587458	190.95717	1.36E-05
Solyc05g014300	Inf	0.00024205	Inf	5.35E-05
Solyc01g090300	Inf	0.00028336	Inf	0.00014773
Solyc04g010270	Inf	0.00010209	136.943018	0.00018535
Solyc02g094040	Inf	1.60E-07	30.6828599	0.00018707
Solyc02g091810	Inf	0.0002749	93.8106553	0.00071529
Solyc01g098060	Inf	0.00731027	Inf	0.00279106
Solyc03g117260	Inf	0.00012936	Inf	0.00291158
Solyc09g075700	Inf	0.00047195	Inf	0.00525326
Solyc10g081550	Inf	0.00187811	Inf	0.00791027
Solyc12g005920	Inf	0.00230785	Inf	0.00933476
Solyc01g110890	Inf	0.0122242	Inf	0.00981567
Solyc02g091820	Inf	0.01016388	Inf	0.01942166
Solyc08g036660	Inf	4.29E-30	15.8279995	0.01957629
Solyc01g106270	Inf	0.02073757	Inf	0.02018657
Solyc12g099130	Inf	0.00243922	17.6801124	0.03715459
Solyc01g102960	612.920381	2.87E-12	75.1217672	1.50E-05
Solyc08g007830	368.034121	3.43E-46	46.0316518	1.32E-06
Solyc08g036620	238.591767	1.04E-14	62.1419869	0.00933476
Solyc03g111280	215.739844	1.04E-06	19.6590659	2.87E-05
Solyc05g014280	210.406645	8.15E-09	Inf	8.41E-07
Solyc02g093180	182.821721	2.39E-10	17.8742716	0.01015324
Solyc08g036640	177.802669	9.40E-84	40.6898663	8.60E-07
Solyc07g056510	124.81848	2.28E-11	24.9140916	2.08E-17
Solyc03g111300	112.050849	2.16E-11	40.6564633	7.03E-11
Solyc01g103630	101.681246	2.24E-05	Inf	0.0034887
Solyc03g098300	100.179562	0.00023571	Inf	1.09E-10
Solyc10g085850	97.8989033	1.50E-17	40.3028034	1.66E-22

Solyc09g005830	90.0263972	1.07E-06	13.7294593	4.64E-09
Solyc04g079730	86.4712999	1.32E-99	33.3048426	1.02E-50
Solyc11g073060	85.9968809	8.42E-12	15.5640448	0.00108861
Solyc04g080840	83.2496983	4.14E-17	Inf	3.74E-13
Solyc10g083990	76.9096754	0.00099332	13.6518005	0.00015876
Solyc09g092480	76.8861045	1.39E-48	37.6113828	1.14E-31
Solyc08g068630	76.7125193	9.19E-08	175.25081	7.13E-08
Solyc01g108240	76.688418	3.58E-24	138.984821	2.44E-13
Solyc10g008360	73.688302	0.00086395	17.3013466	0.04935102
Solyc03g123540	61.7195557	3.37E-10	109.569857	0.00612494
Solyc07g053230	58.0174121	4.61E-10	12.0703184	0.01156009
Solyc02g067750	47.2152468	4.83E-20	126.636352	1.87E-09
Solyc10g050960	45.7255325	0.01526324	16.9131562	0.01590303
Solyc08g078090	45.534717	1.46E-05	19.4697974	7.57E-11
Solyc01g087590	45.4423194	4.74E-52	79.3844419	1.51E-54
Solyc08g081550	45.4402261	4.71E-05	21.0521207	0.0132541
Solyc08g062340	43.8632202	3.09E-33	119.243345	8.83E-32
Solyc08g068450	40.83782	0.00082191	16.1300627	0.0015671
Solyc01g090800	39.7866055	3.71E-07	180.281966	6.50E-08
Solyc03g026270	34.6715842	5.92E-05	11.9326595	0.01209749
Solyc07g048060	34.3980014	8.52E-17	16.4845598	8.82E-10
Solyc03g093110	34.2338574	1.31E-06	104.551669	2.45E-21
Solyc09g008970	33.5260704	7.59E-05	63.7836191	2.69E-05
Solyc02g070040	33.2685724	0.00540161	15.2330966	1.38E-09
Solyc11g007500	32.9070896	1.35E-26	49.7756175	7.02E-24
Solyc03g083690	31.0824474	0.03021462	103.323468	0.00011085
Solyc02g073580	27.711054	5.07E-48	46.9414489	8.72E-23
Solyc01g091250	26.9543708	0.02966276	Inf	0.00367541
Solyc09g092490	25.43907	0.00063804	39.531641	3.02E-12
Solyc10g012090	23.2216546	0.00041138	9.50972358	0.00222132
Solyc02g079180	22.4264	0.00320537	42.7255053	1.62E-06
Solyc01g099660	21.7767917	0.00090679	360.338491	5.37E-24
Solyc08g080430	21.1675866	0.00012156	134.805517	4.25E-06
Solyc06g083900	20.1837161	3.48E-09	9.05574376	0.02500439
Solyc01g095140	19.9590173	3.05E-59	5.13490574	1.14E-10
Solyc09g075950	18.5949811	0.00012553	5.41773531	0.01849396
Solyc12g057080	17.3821551	2.02E-22	8.49579828	0.00291375
Solyc01g095770	16.9993828	1.72E-07	52.1754937	7.91E-05
Solyc01g079200	16.6489618	2.17E-18	6.60877064	0.00041325
Solyc04g008470	16.4023838	0.01479856	261.702432	9.20E-08

Solyc08g076620	16.1275131	0.00239168	105.351456	0.02147803
Solyc01g111430	16.051951	2.72E-10	4.71331479	1.94E-05
Solyc06g076300	15.9247258	1.18E-13	39.7377489	1.96E-12
Solyc06g060870	15.7572692	0.03705046	Inf	0.01239775
Solyc02g078890	15.5408644	1.28E-07	27.0067787	3.26E-08
Solyc01g005160	15.3559865	0.00032143	38.2847497	1.46E-05
Solyc11g020330	15.1898456	0.01325939	41.4213012	0.00410806
Solyc05g013710	15.1132573	0.00080937	28.1886026	0.01047824
Solyc03g117130	14.9317753	0.00010833	29.400021	0.00022462
Solyc01g098690	14.8767623	0.00011905	31.8147645	4.04E-10
Solyc06g054150	14.525047	1.22E-09	4.83673625	0.0015792
Solyc02g063480	14.5249352	0.00075111	66.4181961	1.33E-07
Solyc05g054650	14.2219704	0.00425403	6.27686063	0.00311366
Solyc12g100240	14.0528407	0.00076802	23.1180752	0.01715038
Solyc03g117960	13.5309907	8.26E-08	26.0243933	7.52E-05
Solyc09g061890	13.1301101	2.57E-05	4.52057458	0.01953374
Solyc02g092450	13.0504722	0.00491842	20.9335085	0.00792907
Solyc09g018460	12.9298312	0.0017036	Inf	0.00119984
Solyc03g120100	12.6627903	1.33E-08	31.5558324	0.00092046
Solyc03g020050	12.327982	4.10E-05	27.7243549	0.00106566
Solyc02g090360	12.1498738	3.69E-62	18.9923559	7.53E-45
Solyc02g064980	11.9854021	1.86E-11	46.123412	9.47E-16
Solyc11g011030	11.8424213	2.58E-37	5.21384169	0.0002336
Solyc11g006300	11.7538339	0.00755127	21.1016985	0.00107592
Solyc03g093120	11.7377367	2.27E-18	21.5315492	5.86E-13
Solyc02g084130	11.7042704	0.02891651	51.7459195	0.00848453
Solyc02g077370	11.6932321	0.000352	5.50388549	0.01821539
Solyc09g011860	11.6866737	6.83E-35	4.91151592	1.39E-06
Solyc09g009220	11.5632979	6.89E-20	5.21084257	0.01706345
Solyc02g063520	11.3772513	7.25E-09	20.931446	0.00137723
Solyc12g011300	11.285312	0.00193237	91.2896712	8.01E-05
Solyc11g011330	11.1388599	6.27E-47	17.6033062	2.89E-11
Solyc08g076010	11.0699757	0.00928872	44.2375637	0.00097791
Solyc06g075630	10.909748	6.26E-05	124.187597	6.88E-06
Solyc06g069420	10.8482763	6.43E-13	19.3233956	6.23E-22
Solyc02g064680	10.4894739	1.53E-56	16.1875297	9.73E-17
Solyc09g011510	10.0148365	1.01E-12	20.4779765	2.87E-15
Solyc01g079670	9.94829647	0.00612456	27.4296903	0.00011649
Solyc07g065660	9.93063527	2.52E-19	16.0774932	1.15E-29
Solyc12g017240	9.73703904	4.16E-15	17.4741765	1.47E-08

Solyc02g087350	9.64488023	1.56E-24	15.2532453	7.68E-17
Solyc03g116060	9.64179439	1.59E-09	74.3423834	1.55E-26
Solyc02g068460	9.57389587	0.02073757	44.9652161	0.0108467
Solyc08g066320	9.48144173	9.88E-07	27.9175934	7.58E-10
Solyc01g087980	9.3773355	1.60E-22	14.9105449	1.08E-50
Solyc10g084110	9.32256478	6.60E-17	15.3475421	0.00028075
Solyc06g060110	9.30356486	3.73E-61	15.4833377	4.53E-39
Solyc03g120990	8.81581485	4.77E-20	22.2224839	0.00168776
Solyc06g011470	8.65006761	0.00031326	3.99210976	0.02322599
Solyc05g053010	8.36856938	1.03E-06	13.5810439	3.74E-08
Solyc02g069490	8.31407118	2.41E-37	13.1764433	3.91E-39
Solyc05g008220	8.2769837	1.16E-13	3.75401906	1.46E-05
Solyc03g096760	8.23417287	4.70E-05	15.6117606	2.68E-08
Solyc02g091180	8.12306078	6.03E-06	18.1064722	1.86E-09
Solyc07g062480	8.12072654	0.0023166	2.4743494	0.00101046
Solyc07g040960	7.96355994	2.39E-27	15.9751776	8.55E-08
Solyc12g088170	7.91490918	1.97E-06	14.0094729	0.00517532
Solyc07g052370	7.87610887	0.0009522	2.43440173	0.01922994
Solyc12g010980	7.80385253	3.61E-28	3.06620744	0.00084666
Solyc03g096770	7.68513275	2.08E-07	15.4589859	0.00017494
Solyc07g043460	7.5490347	1.49E-11	12.3145127	9.32E-16
Solyc09g011520	7.45946493	8.24E-11	16.4961446	2.79E-09
Solyc12g055710	7.40327198	0.00601265	225.602878	1.42E-08
Solyc06g076080	7.23451914	3.16E-07	2.91243589	0.04424697
Solyc09g091210	7.09506126	0.03423369	136.837403	0.01614934
Solyc06g073830	6.90189577	1.07E-24	3.19817187	0.01357345
Solyc08g062690	6.83737142	8.20E-41	3.27917603	0.0108467
Solyc12g006380	6.81350156	0.00094528	14.0833513	1.03E-19
Solyc04g008100	6.80175685	9.05E-16	13.5666965	0.01481865
Solyc12g096770	6.79109508	1.45E-11	3.1934648	0.00340095
Solyc12g005370	6.72908652	0.01722169	Inf	2.48E-13
Solyc12g006460	6.68999876	1.47E-12	10.681595	6.15E-12
Solyc12g009240	6.67054697	0.01821434	85.0325521	0.02675443
Solyc12g098590	6.638142	1.04E-06	16.0294044	5.13E-06
Solyc01g080030	6.62690837	0.0011135	15.5629471	1.61E-07
Solyc06g074140	6.45769411	0.00023564	32.0906214	0.00028609
Solyc02g091920	6.34602922	8.41E-21	10.5660926	1.02E-09
Solyc08g079090	6.31975677	2.09E-20	11.4640332	1.19E-08
Solyc07g052610	6.31884727	0.00558271	10.1699844	0.02720671
Solyc03g046380	6.2543982	8.69E-10	16.900636	1.37E-16

Solyc07g043490	6.24806976	7.80E-08	25.5526924	0.00501082
Solyc10g076370	6.2127907	0.00904353	29.829234	0.00616616
Solyc03g123620	6.20034777	1.92E-33	11.1541874	9.16E-35
Solyc01g087630	6.16937627	8.45E-05	16.3064536	1.29E-08
Solyc07g007260	6.14506396	0.00089056	12.6358901	1.98E-05
Solyc10g006690	6.11539753	3.80E-21	10.3745213	6.97E-25
Solyc03g025490	6.09135939	0.00059325	20.6815513	3.71E-06
Solyc03g007530	6.02584104	1.21E-18	9.20079371	6.10E-11
Solyc09g005410	5.92708247	0.00093885	12.0710732	0.00013243
Solyc01g005500	5.76620708	0.00889238	9.61618203	1.30E-05
Solyc08g080190	5.53778233	3.28E-05	8.41399993	2.54E-05
Solyc10g006700	5.33346294	2.97E-14	8.21891561	8.30E-14
Solyc04g071480	5.29627321	1.49E-17	9.59583487	5.78E-11
Solyc02g088240	5.24822989	0.00015263	10.4608556	3.24E-05
Solyc03g097370	5.20965608	5.22E-24	7.97639687	0.00036036
Solyc05g051480	5.07482185	0.01912406	8.76462771	0.00299595
Solyc01g107800	5.05781028	6.27E-06	8.83629689	1.74E-05
Solyc12g096430	5.02303402	0.0030461	8.91418753	0.00221073
Solyc07g042630	5.00982296	0.00243698	11.5253637	0.00773454
Solyc02g083870	5.00883488	0.03754308	22.9545686	0.0011145
Solyc07g007870	5.0087501	0.01556362	2.01744965	0.01104572
Solyc02g084780	4.84831175	3.28E-07	25.9272008	4.77E-10
Solyc05g054250	4.82844784	0.02408499	46.7474901	4.47E-06
Solyc01g086660	4.7950038	3.72E-12	14.2187158	1.77E-07
Solyc03g026280	4.77727702	1.31E-09	10.8544351	6.19E-10
Solyc02g080010	4.70019356	1.16E-08	8.41412225	6.54E-12
Solyc01g009160	4.69678926	1.70E-07	7.50727994	2.87E-14
Solyc04g007750	4.68259302	0.00030351	14.5248976	0.00102588
Solyc04g074740	4.65224306	0.00933873	8.3638693	0.00023617
Solyc06g005750	4.56926569	4.17E-11	11.2904915	7.47E-29
Solyc06g071070	4.51933104	1.20E-25	2.05286488	0.00383087
Solyc12g098540	4.50065791	0.00013342	9.72541746	1.96E-09
Solyc02g089640	4.49908088	2.83E-10	7.27081483	4.71E-09
Solyc04g015360	4.37756749	1.50E-09	12.3279132	2.30E-16
Solyc01g096510	4.37742509	0.01332751	10.9371083	0.01713334
Solyc08g079650	4.35745638	2.12E-05	7.27109166	9.15E-09
Solyc04g074450	4.2855177	5.12E-20	9.26709649	1.12E-31
Solyc06g062920	4.2774939	2.40E-11	6.52949989	9.82E-14
Solyc03g111100	4.25983849	0.01288102	20.087199	6.50E-05
Solyc11g072200	4.19478702	6.18E-06	8.87319467	0.01755972

Solyc01g106510	4.11392486	0.01511327	6.24944099	0.00533867
Solyc09g065610	4.11102869	4.69E-07	7.46589124	1.54E-08
Solyc02g080200	4.08075593	0.00047715	11.0687014	0.04698201
Solyc04g077280	4.07870293	0.0456041	7.02904595	0.00434132
Solyc06g075650	4.07057983	0.00016307	13.0384956	2.84E-08
Solyc11g066250	4.05044716	2.93E-06	8.87993892	2.68E-09
Solyc02g082650	4.04790063	0.00293533	16.7321751	0.04950701
Solyc03g118540	4.03180368	2.53E-07	6.90332826	0.01839653
Solyc09g011030	4.03004302	1.74E-15	1.99360282	0.01341513
Solyc05g055010	4.01981683	0.00705941	7.22361032	0.00063168
Solyc10g083870	4.01141206	2.55E-05	7.83129938	6.81E-10
Solyc01g090610	4.00582355	7.03E-05	10.3941505	0.00383487
Solyc02g084800	4.00304673	9.04E-05	21.7103253	7.20E-05
Solyc03g007080	3.9954494	0.0463154	6.35378742	0.03673845
Solyc12g089020	3.90863414	0.00047592	9.41721509	0.00237371
Solyc07g051820	3.90130603	0.01008168	13.4891703	1.47E-07
Solyc09g005400	3.89737519	4.57E-08	8.41439819	0.00674303
Solyc07g064820	3.86339905	1.10E-13	1.90548988	0.03194766
Solyc08g016150	3.83080248	0.00330533	6.377544	0.00013549
Solyc09g082270	3.76829417	0.03506048	20.4728731	5.76E-12
Solyc03g113080	3.7572938	2.91E-07	5.90220925	4.42E-08
Solyc01g098800	3.727238	0.0001732	5.85138666	1.29E-08
Solyc02g069910	3.71190787	0.0002749	12.2788547	1.26E-08
Solyc12g040790	3.6413725	2.60E-05	6.25048175	4.78E-20
Solyc07g062500	3.60464186	1.82E-16	7.76625117	7.58E-17
Solyc05g006750	3.571081	0.03821985	20.1338135	2.83E-08
Solyc02g084640	3.5430009	0.01538003	6.17638236	0.00014935
Solyc10g006670	3.50640627	0.0072246	7.44461766	0.02634726
Solyc11g066670	3.47144298	0.00016009	10.0736133	0.00011689
Solyc06g083130	3.43098248	0.04258022	6.40020195	0.01605466
Solyc01g097240	3.42889749	0.00605538	5.72809916	0.0013005
Solyc04g074420	3.4092956	2.91E-06	6.93999998	8.00E-09
Solyc04g074440	3.37119585	1.64E-08	7.65944336	7.59E-07
Solyc09g007760	3.34855723	6.55E-08	5.5650529	5.00E-10
Solyc03g119640	3.28690619	0.00636258	6.90249473	0.00050735
Solyc04g071030	3.2852815	6.91E-08	5.73131339	1.92E-07
Solyc02g088740	3.23832768	0.03562332	7.56580956	0.00148408
Solyc06g053640	3.22649976	0.00023738	5.17526502	0.04513737
Solyc09g091160	3.20903079	2.62E-05	6.34529836	1.02E-09
Solyc03g121420	3.1988807	0.01228497	10.2418294	0.00179338

Solyc10g009150	3.19495656	3.27E-07	7.15287917	0.00166614
Solyc08g078930	3.18479486	0.01252857	14.2268049	0.01032694
Solyc07g065320	3.14877016	9.77E-10	5.00409128	0.00016359
Solyc05g052980	3.12823848	1.01E-08	7.23531506	0.00545317
Solyc02g064970	3.11712083	0.00903707	5.89406375	0.03337279
Solyc11g020230	3.09203434	1.32E-05	8.44343192	1.50E-12
Solyc05g056550	3.08297288	0.00089566	6.67255003	2.58E-06
Solyc02g084790	3.04030311	0.00637058	28.3279174	8.01E-11
Solyc03g112060	3.03698704	4.25E-06	4.87362815	4.94E-05
Solyc02g081450	3.03447141	0.02270135	21.7550635	3.22E-09
Solyc11g010960	3.02268436	0.01747775	4.54575046	0.02280603
Solyc07g062520	3.0092509	0.00210592	4.57196017	0.00076605
Solyc06g082080	2.99866436	1.69E-05	4.95131787	2.05E-07
Solyc07g006230	2.96766787	0.00270292	5.55155418	0.00998814
Solyc02g085020	2.96593763	0.01160805	5.27043317	2.33E-06
Solyc04g078270	2.94433433	0.01601543	6.97964724	0.00053196
Solyc06g072710	2.92829129	0.00256634	7.46135538	3.55E-05
Solyc02g070980	2.89614003	4.73E-12	4.79159988	9.45E-06
Solyc09g007770	2.891383	7.10E-07	5.8961866	2.04E-11
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Solyc01g007010	2.81205057	0.00683189	4.98153118	0.00011386
Solyc04g082970	2.78977384	0.03695168	5.06654561	0.00274808
Solyc02g094030	2.73393351	3.13E-10	4.45690657	3.88E-12
Solyc05g052300	2.7180307	0.02966276	9.36197437	0.00460263
Solyc04g079230	2.70468698	0.04067795	4.26567201	0.01221763
Solyc04g007990	2.68919894	0.00077755	4.51907694	5.15E-05
Solyc09g082630	2.67394616	7.94E-07	4.62092605	2.55E-09
Solyc04g077470	2.64678206	7.19E-05	5.89578796	0.00291375
Solyc08g008280	2.64173592	2.09E-05	7.01354568	2.44E-13
Solyc03g116530	2.63983738	0.01245135	5.33075051	1.89E-05
Solyc10g079620	2.61617694	0.03358911	7.79501952	0.00021986
Solyc04g074430	2.6085768	1.10E-05	4.63066706	6.37E-09
Solyc03g096780	2.60234922	6.47E-05	7.33495102	0.00023735
Solyc02g070970	2.58215553	6.69E-10	4.8309998	0.00018234
Solyc10g005200	2.55668521	0.03228727	5.30700115	0.00153103
Solyc06g074090	2.53840082	8.32E-05	5.04980075	4.24E-08
Solyc08g005610	2.52743027	0.04244392	8.61365779	7.25E-19
Solyc06g074030	2.51881577	1.41E-09	4.86158837	1.74E-15
Solyc07g006020	2.50110995	0.00887818	3.99067057	0.00110949
Solyc01g097770	2.44461997	8.04E-07	3.68237359	0.00445807

Solyc03g118470	2.41566404	1.15E-07	5.01967798	4.95E-16
Solyc10g081710	2.37798444	0.00822713	4.86377352	0.00023291
Solyc08g081420	2.35804321	0.03227962	4.7354009	0.00081381
Solyc04g007390	2.31045466	0.04203483	4.82412255	2.46E-07
Solyc03g115900	2.29107501	3.73E-05	3.56584448	1.42E-05
Solyc01g058020	2.28713789	0.01427681	3.763624	0.0004164
Solyc09g011550	2.21462254	0.03884186	3.43661805	0.03015465
Solyc06g064550	2.17588017	0.00013741	4.34685429	7.61E-09
Solyc02g070950	2.17539348	3.18E-07	3.80258569	2.04E-05
Solyc11g012360	2.15398454	0.01568947	5.34664034	1.96E-10
Solyc07g009150	2.14967601	0.00243698	3.69039806	5.10E-05
Solyc06g005160	2.12733403	1.35E-05	3.21426397	1.45E-14
Solyc04g007760	2.1127602	0.00035496	4.3808529	0.03218715
Solyc02g088230	2.11097441	0.02728739	3.53710843	0.00206669
Solyc07g055810	2.08121197	0.00016903	3.45226965	3.93E-07
Solyc01g102390	2.05331117	0.00093566	4.04929956	3.81E-06
Solyc08g068390	2.05168281	0.00134995	3.26434405	9.22E-05
Solyc10g079600	2.0034247	0.00256634	4.14956656	7.70E-08
Solyc07g043400	1.98964711	6.42E-05	3.46509246	0.00109904
Solyc03g059260	1.97061165	0.0012827	3.32566384	0.04508445
Solyc03g013440	1.93484194	0.04885596	2.97077435	0.00712663
Solyc12g098910	1.92642077	0.00133585	2.92304004	0.00012375
Solyc05g010320	1.92579255	0.00139761	3.33498937	1.28E-06
Solyc10g084360	1.90645267	0.0473664	3.98515356	0.00258528
Solyc06g072350	1.82206531	0.03915198	2.7980833	0.01088747
Solyc08g081190	1.82023157	1.99E-07	3.69979863	4.64E-18
Solyc08g082090	1.80714594	0.00210592	3.42066275	7.92E-07
Solyc02g089080	1.76235663	0.02703783	3.42362439	0.00853472
Solyc03g117480	1.7483851	0.00296679	2.72580417	0.00302679
Solyc10g077040	1.73796241	0.00211037	2.63071049	0.00037435
Solyc01g105150	1.7248385	0.0141718	2.8314081	0.00458568
Solyc01g074030	1.72100225	0.02993372	3.6507987	0.0068869
Solyc04g015750	1.69540803	0.01604773	3.06012814	0.000375
Solyc07g063480	1.69522575	0.04319462	3.65895088	0.00208181
Solyc04g017620	1.69360283	0.00239168	2.71151343	2.15E-05
Solyc03g116340	1.6882044	0.00057485	2.69073761	5.45E-06
Solyc03g082620	1.68166604	0.02010359	2.56647265	0.00014677
Solyc10g009210	1.6190047	0.04225234	2.50324162	0.00350773
Solyc01g109500	1.599236	0.0117182	4.32099888	0.00564944
Solyc02g067860	1.59190909	0.04816324	2.61994906	0.00531688

Solyc03g005120	1.56121572	0.04360965	2.34824442	0.00261464
Solyc05g014470	1.47343908	0.00561747	2.41538595	1.42E-08
Solyc02g068900	1.47295679	0.03034074	2.32379037	4.60E-05
Solyc07g043390	1.37726684	0.03538552	2.39733384	0.02498136
Solyc11g006460	-1.3145774	0.04341116	-1.9933894	0.00058854
Solyc12g009960	-1.3390328	0.0306801	-2.0140674	0.00165922
Solyc01g108500	-1.3390702	0.01561389	-2.0387506	0.00100044
Solyc12g006550	-1.3552305	0.03930254	-2.1611182	0.00312395
Solyc12g035130	-1.3598058	0.01608954	-2.2111792	0.00010015
Solyc12g008370	-1.3885464	0.02600822	-2.1396078	0.00147219
Solyc08g007990	-1.3951862	0.02837238	-2.225371	0.00110241
Solyc05g012580	-1.4082252	0.00272393	-2.6208826	0.00035796
Solyc01g079350	-1.4097625	0.03463706	-2.1321751	0.00613544
Solyc10g079370	-1.4143875	0.03526489	-2.1707436	0.00071896
Solyc03g031720	-1.4196148	0.01032185	-2.1526268	0.00278756
Solyc11g069090	-1.4196978	0.0016232	-2.3009417	9.16E-05
Solyc08g067950	-1.4247058	0.02062893	-2.2397433	0.00962346
Solyc03g115940	-1.4258295	0.01511525	-2.207151	0.00306329
Solyc02g085580	-1.4275528	0.01573727	-2.2503236	0.00177882
Solyc12g007200	-1.4308272	0.03811341	-2.1565427	0.01995923
Solyc10g086540	-1.4379076	0.0052521	-2.330597	0.00026075
Solyc09g007540	-1.4380254	0.00649274	-2.1587328	0.00076376
Solyc07g007330	-1.4527976	0.04790788	-2.3592807	0.0007815
Solyc07g063050	-1.4783096	0.02621419	-2.5749901	0.00026213
Solyc01g096020	-1.481626	0.04888397	-2.507298	0.00106065
Solyc02g063270	-1.4921508	0.04830653	-2.3947499	0.00078692
Solyc03g110910	-1.5035659	0.01639708	-2.3074592	0.00116702
Solyc02g070800	-1.5055416	0.02568532	-2.3432687	0.00036456
Solyc06g035450	-1.5060668	0.00017676	-2.6588914	6.52E-06
Solyc11g017140	-1.5272526	0.04132926	-2.3901271	0.00024726
Solyc10g078920	-1.529706	0.00840526	-2.9483945	0.00011156
Solyc06g073740	-1.5317883	0.04650668	-2.369781	0.00279221
Solyc05g048750	-1.5335167	0.03105356	-2.5029946	0.00169949
Solyc02g092140	-1.5341985	0.01231042	-2.3885561	0.01618447
Solyc01g104720	-1.5391906	0.01109516	-2.8505952	0.02849715
Solyc03g031890	-1.5498463	0.00176745	-2.3992648	0.00033991
Solyc11g072810	-1.5503124	0.04286928	-2.4753065	0.00686254
Solyc11g005330	-1.5755884	2.12E-05	-2.4795701	4.71E-06
Solyc01g097270	-1.5786859	3.25E-05	-2.9312952	6.23E-07
Solyc02g071620	-1.5813666	0.00079755	-2.3872667	0.00104451

Solyc01g111600	-1.5861247	0.00012685	-2.4630707	2.53E-05
Solyc10g085460	-1.6007199	0.01807647	-2.4026501	0.00285635
Solyc12g010900	-1.6021432	0.01423322	-3.1149511	0.00315748
Solyc12g095960	-1.6266598	0.00015769	-2.5243277	0.00021269
Solyc06g082010	-1.6299925	0.00127708	-2.5629728	7.99E-06
Solyc07g061940	-1.636335	2.09E-05	-3.2852082	1.42E-07
Solyc02g083130	-1.6498267	0.00279712	-2.6553617	0.00071304
Solyc05g047420	-1.6510107	0.04325976	-3.8160343	0.00027377
Solyc03g113130	-1.6574044	0.02003106	-2.6634228	0.0020738
Solyc04g007180	-1.6580164	0.00250004	-2.7702846	0.00039067
Solyc03g044330	-1.6786165	6.03E-06	-2.6479199	2.92E-06
Solyc04g016190	-1.6832262	0.02873864	-4.022662	2.73E-06
Solyc04g071620	-1.7019281	1.40E-06	-3.0818116	0.01869779
Solyc09g074930	-1.7089897	0.02279032	-3.2013413	5.98E-06
Solyc08g065940	-1.7093636	1.89E-05	-2.7763243	1.21E-05
Solyc11g062130	-1.7119834	1.43E-07	-2.624125	2.41E-06
Solyc04g082420	-1.746573	8.35E-05	-3.9153105	3.02E-07
Solyc12g009880	-1.7544517	0.00814497	-3.0467714	0.00097607
Solyc01g103540	-1.7547962	2.80E-08	-2.8013584	1.78E-07
Solyc11g027840	-1.7553028	0.00013454	-2.6753908	0.00657796
Solyc10g084350	-1.7577298	0.02853689	-2.8720953	0.04813309
Solyc01g107100	-1.7729867	5.84E-07	-2.8472132	5.69E-07
Solyc02g084230	-1.786081	2.69E-05	-2.7428326	4.48E-05
Solyc01g096470	-1.8024431	0.02503987	-2.8301902	0.0041797
Solyc01g108910	-1.8124407	8.15E-08	-3.3355219	0.00156277
Solyc10g085280	-1.8171549	0.01230412	-3.0034999	0.00610138
Solyc06g073090	-1.8174295	0.00011886	-2.727985	2.45E-05
Solyc11g071620	-1.8236581	0.04328106	-2.7998761	0.00379218
Solyc12g021340	-1.8523555	0.00463563	-2.7880554	0.00434132
Solyc02g090430	-1.8538411	0.00271976	-3.1652038	0.00114707
Solyc01g109600	-1.8673798	0.02504283	-2.8984715	2.63E-06
Solyc03g083720	-1.8855478	1.23E-05	-3.1517401	3.80E-05
Solyc02g077590	-1.8916156	0.00986919	-3.9723391	2.87E-07
Solyc07g066330	-1.8945847	0.00207449	-2.8518266	0.01147822
Solyc02g080410	-1.9071476	7.82E-07	-2.8839423	1.72E-06
Solyc03g121250	-1.9141287	0.00225219	-2.9108419	0.00318118
Solyc08g061590	-1.9208892	8.26E-07	-3.1266815	1.23E-05
Solyc06g069410	-1.9345014	1.44E-06	-2.9798231	1.09E-05
Solyc10g080610	-1.9998472	9.46E-09	-3.4090188	3.25E-09
Solyc04g007000	-2.0046598	1.21E-08	-3.0915239	5.01E-07

Solyc11g072970	-2.0274359	0.00163244	-3.1948823	0.00606695
Solyc08g077440	-2.0275158	0.00116379	-3.4640539	5.47E-09
Solyc01g073800	-2.0365966	0.00318099	-3.2754034	0.00353435
Solyc04g007420	-2.0594998	0.00917332	-3.1486809	0.00319278
Solyc10g078440	-2.0601223	0.00206905	-3.1706244	0.0036354
Solyc07g005300	-2.0714505	0.00146001	-3.6566553	1.61E-07
Solyc03g026140	-2.0804293	0.03898152	-4.8366496	0.00184056
Solyc02g090680	-2.0883393	0.00087548	-4.6341482	0.00025175
Solyc03g095780	-2.1073492	1.18E-07	-3.5507272	1.14E-06
Solyc02g078230	-2.1547118	4.10E-06	-3.2635037	0.00015923
Solyc09g075460	-2.1589418	8.66E-05	-3.384602	5.43E-06
Solyc02g088470	-2.202813	0.00970327	-3.71356	0.03736325
Solyc02g078380	-2.2255923	8.30E-09	-3.5919312	3.67E-06
Solyc08g076970	-2.2281799	4.17E-06	-3.4908255	0.01151629
Solyc06g007430	-2.2870732	3.40E-07	-3.8872633	3.18E-06
Solyc06g073080	-2.2938643	0.00820262	-3.8615414	0.0331686
Solyc08g067320	-2.3055764	6.17E-08	-3.4709105	1.60E-06
Solyc04g078190	-2.3145845	4.65E-06	-4.2847279	2.28E-06
Solyc07g054780	-2.3667344	0.00033905	-5.4207182	1.13E-06
Solyc12g007070	-2.3673919	0.00156275	-4.0468242	0.00025445
Solyc11g011630	-2.3690307	0.0395528	-6.8164347	0.01775267
Solyc11g066400	-2.3892151	0.0189532	-4.434897	0.00063168
Solyc11g040040	-2.4047253	0.01224047	-3.8595398	0.01905333
Solyc04g071140	-2.4320165	3.35E-19	-5.0520114	5.38E-15
Solyc10g085160	-2.4493152	0.01369898	-5.1089563	0.00290992
Solyc04g071130	-2.5447625	4.23E-14	-4.5317516	4.38E-06
Solyc08g065950	-2.5547906	0.00016956	-5.7377362	3.80E-08
Solyc02g063230	-2.5569947	0.00074819	-5.3525626	0.00229758
Solyc03g083770	-2.5597623	5.57E-05	-4.6411967	2.10E-12
Solyc05g007510	-2.5698274	1.22E-08	-5.6018392	3.69E-08
Solyc01g096260	-2.5892607	7.76E-05	-3.9506285	1.57E-06
Solyc05g006900	-2.5914389	0.00012197	-4.6444316	1.02E-06
Solyc06g007580	-2.5964245	2.82E-05	-5.1809392	4.98E-05
Solyc12g011100	-2.7431251	0.02322911	-7.9095989	0.00291375
Solyc08g066120	-2.8856918	0.00047798	-5.5885789	0.00558984
Solyc01g105430	-2.8952329	0.00161374	-5.1156122	0.00131444
Solyc02g085910	-2.9374322	3.09E-06	-5.881849	0.00670567
Solyc09g061390	-3.0296272	0.02152613	-4.7907818	0.0456557
Solyc05g055540	-3.1595	0.00017844	-6.1768356	0.00033155
Solyc10g050980	-3.2474051	0.00511689	-43.902968	0.00207242

Solyc01g073840	-3.351545	2.95E-07	-7.2450085	0.00245427
Solyc11g010290	-3.5248981	1.53E-05	-5.6155105	0.01270998
Solyc03g113890	-3.5741536	0.03071994	-13.613106	0.00369399
Solyc07g039420	-3.7424218	6.70E-05	-9.8637477	0.00319929
Solyc02g088340	-4.1485614	5.05E-17	-6.226479	1.17E-15
Solyc08g067330	-4.1923206	6.18E-37	-6.5181117	3.95E-10
Solyc08g075920	-4.5519596	8.31E-16	-7.6321118	7.08E-15
Solyc01g073810	-4.5915903	3.97E-23	-7.556841	1.61E-10
Solyc10g047400	-4.8718536	0.00315226	-7.5510273	0.01772721
Solyc01g087770	-5.3537875	0.00021979	-12.487301	1.69E-05
Solyc05g047530	-6.6483108	3.39E-22	-3.317812	7.56E-05
Solyc01g090760	-10.244729	0.00012964	-4.2947949	0.04695771
Solyc10g050990	-11.556154	3.42E-09	-28.87426	7.87E-16
Solyc09g010860	-15.637046	3.49E-10	-4.9770932	0.01484891
Solyc07g026650	-98.417219	3.10E-49	-41.896416	1.98E-05

Table S2. Differentially Expressed Genes (DEGs) of WT and *Atcrf5* when treated with oxidative stress. All foldchange (FC) values are statistically significant.

Gene number	name	Col FC	*Atcrf5* FC
AT5G42092.1	.	-56.58597	-60.053914
AT4G31580.2	RSZ22	-22.534067	-38.628249
AT3G03670.1	PER28	-21.888547	-70.335666
AT1G49570.1	PER10	-19.79984	-54.134287
AT4G30170.1	PER45	-15.45716	-13.536152
AT2G30670.1	.	-14.24961	-29.263682
AT5G61250.3	AtGUS1	-13.503749	-15.600634
AT5G35620.2	EIF(ISO)4E	-12.720314	-14.24947
AT5G22555.1	.	-10.744485	-46.721056
AT1G12010.1	.	-10.682397	-7.1414978
AT1G26240.1	.	-10.146069	-43.050602
AT1G52120.1	JAL12	-9.4085453	-20.456931
AT4G11290.1	PER39	-9.0407042	-15.331307
AT4G13890.1	SHM5	-8.627148	-21.57666
AT2G21045.1	HAC1	-7.8778632	-15.567709
AT3G57470.3	Insulinase (Peptidase family M16) family protein;(source:Araport11)	-6.4188212	-5.1616266
AT5G41290.1	CRRSP58	-5.7345707	-18.912336
AT1G36060.1	ERF055	-5.1951263	-9.0300191
AT5G41300.1	CRRSP59	-5.1113137	-11.915701
AT2G40080.1	ELF4	-4.9191975	2.22737188
AT1G13670.1	hypothetical protein;(source:Araport11)	-4.7422701	-5.1984991
AT1G08090.1	NRT2.1	-4.6067521	-12.958706
AT4G16240.1	hypothetical protein;(source:Araport11)	-4.3495494	-9.1538583
AT5G55450.1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein;(source:Araport11)	-4.1737781	-8.0651247
AT1G13930.1	Involved in response to salt stress. Knockout mutants are hypersensitive to salt stress. The mRNA is cell-to-cell mobile.	-4.0593761	2.39873167
AT4G01610.1	CATHB3	-3.4968319	-2.1960713
AT1G62770.1	PMEI9	-3.3307742	-5.8995728

AT3G16770.1	RAP2-3	-3.3219661	-2.5870147
AT1G68560.1	XYL1	-3.3079045	-2.045082
AT3G43800.1	GSTU27	-3.2633604	-4.3546778
AT5G58570.1	.	-3.0579579	-6.9317022
AT5G39610.1	NAC92	-3.0521108	2.07233213
AT4G34810.1	.	-2.9799666	-17.420868
AT4G36430.1	PER49	-2.9538976	-22.687819
AT5G43060.1	RD21B	-2.9254496	-4.0023809
AT1G21520.1	hypothetical protein;(source:Araport11)	-2.8708879	3.65755658
AT3G47860.1	CHL	-2.7952938	-2.7985111
AT1G49660.1	CXE5	-2.7601405	-4.1632779
AT4G03510.3	RMA1	-2.7345263	-3.0370036
AT1G14210.1	Ribonuclease T2 family protein;(source:Araport11)	-2.7074903	-6.1611655
AT2G06925.1	PLA2-ALPHA	-2.6510659	-2.730395
AT5G57760.1	hypothetical protein;(source:Araport11)	-2.6194176	-23.205162
AT5G23575.1	Transmembrane CLPTM1 family protein;(source:Araport11)	-2.5037518	-2.6891163
AT5G64330.1	RPT3	-2.4540073	-3.018691
AT1G26920.1	zinc finger CCHC domain protein;(source:Araport11)	-2.4040274	1.8053323
AT3G05945.1	-	-2.3715005	-2.7997461
AT2G25490.1	EBF1	-2.2992387	-2.0192061
AT3G23150.1	ETR2	-2.2650411	-3.7596438
AT5G25460.1	.	-2.2517385	-4.1364477
AT1G15500.1	AATP2	-2.1481268	-2.6014556
AT1G20693.1	HMGB2	-2.1428151	-7.8610421
AT2G32650.1	RmlC-like cupins superfamily protein;(source:Araport11	-2.1239499	-2.1290115
AT5G58710.1	CYP20-1	-2.1178226	-1.5340558
AT3G23760.1	transferring glycosyl group transferase;(source:Araport11)	-2.1157173	-2.5423544
AT3G54920.1	PMR6	-2.0915395	-2.0686484
AT5G49440.1	hypothetical protein;(source:Araport11)	-2.0894211	-2.5451156
AT1G12050.1	FAH	-2.082582	-1.7481654
AT4G28270.1	RMA2	-2.0537552	-3.301408
AT2G32520.1	alpha/beta-Hydrolases superfamily protein;(source:Araport11)	-1.9989378	-1.9120786

AT1G70310.1	SPDSYN2	-1.9860323	-1.9260467
AT5G01020.1	PBL8	-1.9856834	-2.129376
AT1G24880.2	.	-1.9766551	-3.5981476
AT1G78080.1	RAP2-4	-1.959857	-1.2089064
AT5G43700.1	IAA4	-1.9583547	-2.6688292
AT1G20693.3	HMGB2	-1.9542857	-8.9807921
AT1G20900.1	AHL27	-1.9365083	-4.6016048
AT1G20693.2	HMGB2	-1.9336791	-7.9606639
AT5G08100.1	Encodes an asparaginase that catalyzes the degradation of L-asparagine to L-aspartic acid and ammonia.	-1.9296482	-2.7845162
AT4G32940.1	GAMMA-VPE	-1.9131189	-1.3622273
AT1G49600.1	ATRBP47A	-1.8997761	-4.1108429
AT2G20725.1	CAAX amino terminal protease family protein;(source:Araport11)	-1.8663863	-2.6711265
AT5G48810.1	CYTB5-D	-1.8573602	-2.1003563
AT4G26840.1	SUMO1	-1.8404426	-1.9112884
AT5G02502.1	OST4B	-1.8308276	-2.5172906
AT2G28720.1	.	-1.8249161	-3.4534161
AT4G19700.1	BOI	-1.8201274	2.08925238
AT4G38800.1	MTN1	-1.8180517	-2.3212264
AT1G59900.1	E1 ALPHA	-1.800394	-1.4905096
AT2G35795.1	TIM14-1	-1.799879	-2.0600912
AT4G26870.1	.	-1.7944866	-2.1085912
AT5G36230.1	.	-1.7921908	-1.8135614
AT3G26520.1	TIP1-2	-1.7913156	-1.887663
AT1G31812.1	ACBP6	-1.7800623	-1.8081246
AT3G06580.1	GAL1	-1.7784208	-1.7065374
AT3G48750.1	CDKA-1	-1.7695006	-2.0347031
AT4G08035.1	.	-1.7685669	-3.5635884
AT3G09860.1	.	-1.7622346	-1.7120408
AT2G30980.1	ASK6	-1.748039	-1.6427914
AT1G19600.1	.	-1.7414082	-1.4655864
AT3G11780.1	.	-1.7316293	-5.2052174
AT2G47690.1	.	-1.724839	-2.0830912
AT4G32240.1	.	-1.7161766	-1.4840233
AT5G26800.1	.	-1.697457	-1.8864836
AT4G38490.1	.	-1.6920495	-1.9791071
AT2G42790.1	CSY3	-1.689335	2.1365182

AT3G14430.1	.	-1.6700709	-1.8791386
AT1G02160.1	.	-1.642644	-1.9805478
AT4G14615.1	.	-1.6387964	-1.7666613
AT1G05720.1	.	-1.6039893	-2.4937964
AT3G61200.1	.	-1.5946938	-1.7222769
AT5G52920.1	PKP2	-1.5878767	-2.0627031
AT4G16450.1	.	-1.5831715	-2.8614928
AT3G10860.1	.	-1.5786947	-1.6356868
AT5G66240.3	.	-1.5682367	-2.3079543
AT5G21020.2	.	-1.563458	-1.7695254
AT5G55190.1	RAN3	-1.5632082	-1.2579729
AT3G54366.1	.	-1.5612081	-3.4725433
AT5G26360.1	CCT3	-1.5605292	-2.3260197
AT5G03730.1	CTR1	-1.5551377	-2.5750363
AT3G60210.1	CPN10-1	-1.549054	-1.8730023
AT5G65670.1	IAA9	-1.5476982	-2.3382455
AT1G54630.1	ACP3	-1.5007754	-2.0835995
AT3G48680.1	GAMMACAL2	-1.4855064	-1.563399
AT4G26080.1	ABI1	-1.479499	3.45684174
AT1G74230.1	RBG5	-1.4607256	-1.4688686
AT3G16640.1	TCTP1	-1.460661	-1.6536345
AT5G07580.1	ERF106	-1.4559748	-6.3831582
AT3G53670.1	.	-1.4554498	-2.1927965
AT1G47420.1	SDH5	-1.4542877	-1.5506682
AT1G09640.1	.	-1.4256569	-1.4629761
AT2G25310.1	.	-1.4179713	-2.7189212
AT5G10360.1	RPS6B	-1.4176654	-1.5470005
AT1G34430.1	EMB3003	-1.4106026	-1.6930205
AT2G35680.1	DSP8	-1.3921955	-1.3509717
AT4G32930.1	.	-1.3839182	-1.3915762
AT1G74560.1	NRP1	-1.3790578	-1.6450902
AT2G46490.1	.	-1.3718195	-2.2778207
AT3G48140.1	.	-1.3592036	-2.9642452
AT2G44610.1	RABH1B	-1.3564535	-1.7339566
AT3G01520.1	.	-1.3467654	-1.6755928
AT4G38920.1	VHA-c3	-1.3436264	-1.3490301
AT3G02220.1	.	-1.3413413	-1.395387
AT4G32150.1	VAMP711	-1.3380218	-1.7529122
AT5G13780.1	NAA10	-1.3304245	-1.5758352
AT3G28710.1	VHA-D1	-1.3299407	-1.5310796

AT5G21274.1	CAM6	-1.3052241	-1.6555515
AT1G30580.1	YchF1	-1.3049608	-1.426388
AT4G02080.1	SAR1A	-1.2537595	-1.5269219
AT3G49470.1	NACA2	-1.2480151	-1.6418156
AT5G46430.1	RPL32B	-1.1892196	-1.4315019
AT3G48760.1	PAT05	1.37808066	1.40276977
AT3G56940.1	CRD1	1.4251936	1.58339277
AT5G59420.1	ORP3C	1.43898579	1.49373327
AT4G17245.1	.	1.44924269	2.61288501
AT4G30600.1	.	1.45322378	2.05820015
AT5G37070.1	.	1.47927731	1.42656325
AT3G53120.1	VPS37-1	1.49665169	1.43910702
AT2G43820.1	UGT74F2	1.5067065	8.184118
AT5G20900.1	TIFY3B	1.52404306	2.98672761
AT2G31880.1	SOBIR1	1.55183679	1.85695358
AT1G42990.1	BZIP60	1.56998472	3.37574191
AT3G60690.1	.	1.59923438	3.43553044
AT5G50960.1	NBP35	1.61947104	2.06819531
AT3G06070.1	.	1.64672511	-3.8645254
AT4G25670.1	.	1.6798573	3.72765554
AT1G78570.1	RHM1	1.68086075	1.76116685
AT3G21690.1	DTX40	1.71667254	2.17362346
AT1G09970.1	LRR XI-23	1.72415898	2.14037002
AT1G08940.1	.	1.76747743	1.88599662
AT5G58430.1	EXO70B1	1.76998319	1.75639545
AT4G11600.1	GPX6	1.8566134	1.86510035
AT1G72450.1	TIFY11B	1.8637611	4.3147218
AT5G54940.2	.	1.89473814	3.84614665
AT5G47200.1	RABD2B	1.90887505	1.66371486
AT3G17390.1	METK4	1.91756472	-2.3168255
AT4G30390.1	.	1.93121539	1.68070225
AT1G04430.1	.	1.93354035	-1.915571
AT3G12740.1	ALIS1	1.94041103	2.28171717
AT1G28190.1	.	1.96124295	6.82238106
AT4G08950.1	EXO	1.96861496	-7.979055
AT2G38210.1	PDX1L4	1.98359563	4.30626297
AT5G42570.1	.	1.99027594	2.22497458
AT5G04760.1	.	1.99227452	4.65323927
AT2G37470.1	.	1.99568216	2.63668739
AT1G30320.1	.	2.0677013	4.0517827

AT2G33590.1	.	2.07530459	2.93250056
AT2G33700.1	PP2C27	2.08830257	2.35192265
AT3G17800.1	.	2.09795801	2.18681753
AT4G22690.1	CYP706A1	2.12701805	3.87679273
AT3G51890.1	.	2.12891929	1.99346431
AT2G40880.1	CYS3	2.13415979	1.764128
AT4G21870.1	HSP15.4	2.15257613	-10.496815
AT4G01070.1	UGT72B1	2.17671101	3.3591702
AT2G18700.1	TPS11	2.1914193	3.17474477
AT5G22060.1	ATJ2	2.23231599	1.75680543
AT2G37110.1	.	2.3176027	2.21658465
AT4G17530.1	RABD2C	2.32804894	1.55058946
AT4G01026.1	PYL7	2.34538221	6.85639799
AT5G39050.1	PMAT1	2.36291754	5.66578982
AT2G30250.1	WRKY25	2.41657762	1.85471934
AT2G10940.1	.	2.42112898	-6.0475683
AT3G55970.1	JRG21	2.45555166	13.4358915
AT1G69870.1	NPF2.13	2.48267673	4.52374257
AT4G17500.1	ERF1A	2.4924714	3.56486611
AT1G62300.1	WRKY6	2.51105992	3.31488793
AT5G54170.1	.	2.53077398	6.02621497
AT4G27520.1	ENODL2	2.54570385	4.98517074
AT4G13010.1	CEQORH	2.59764014	2.27553106
AT1G66580.1	RPL10C	2.63639218	2.72349701
AT1G37130.1	NIA2	2.66661016	2.1785458
AT1G09310.1	.	2.70158364	4.67769487
AT1G21010.1	.	2.71247435	4.82392793
AT1G72900.1	.	2.71767318	4.50440866
AT3G63380.1	ACA12	2.72888134	2.12782075
AT1G69890.1	.	2.73145691	3.30067225
AT4G30530.1	GGP1	2.81014495	2.38344607
AT3G56880.1	.	2.81081053	5.07523399
AT2G03760.1	SOT12	2.88688731	13.4686678
AT5G62070.1	IQD23	2.91752227	2.21855938
AT3G53650.1	.	2.94983457	4.34137686
AT2G15970.1	COR413PM1	2.98040883	2.13054419
AT3G50910.1	.	3.00052314	2.33845417
AT5G60800.1	.	3.03957735	9.23179704
AT1G55920.1	SAT1	3.05157693	2.01355615
AT4G21570.1	.	3.13721869	4.15741928

AT1G17050.1	SPS2	3.13748172	2.61998658
AT1G23710.1	.	3.21729324	7.31986051
AT5G62470.2	MYB96	3.21978273	3.28109299
AT1G61890.1	DTX37	3.25460553	9.58652077
AT4G39670.1	.	3.45002781	8.88921807
AT4G18170.1	WRKY28	3.51772419	5.26501876
AT5G03030.1	.	3.52135371	1.41009099
AT5G59550.2	.	3.57116068	-16.153066
AT2G26530.1	AR781	3.64525628	5.45691468
AT5G27760.1	.	3.65112028	3.33664839
AT2G40000.1	HSPRO2	3.66250778	5.51923254
AT1G15430.1	.	3.66778764	4.89732161
AT2G29460.1	GSTU4	3.73045269	16.9771337
AT4G20830.2	.	3.73535947	3.3370568
AT5G62020.1	HSFB2A	3.7356831	4.22437418
AT1G03220.1	.	3.78197939	3.45753156
AT2G38470.1	WRKY33	3.81321037	4.43618321
AT5G65300.1	.	3.82237999	10.6765903
AT5G57510.1	.	3.85771562	10.2200062
AT5G39660.1	CDF2	3.87537736	2.29065303
AT1G21790.1	.	3.89900662	3.00634968
AT4G34135.1	UGT73B2	3.89954254	3.38191856
AT5G13630.1	CHLH	3.90574014	2.89088927
AT2G43520.1	ATTI2	3.96863246	6.04121253
AT5G67030.1	ZEP	3.98976829	3.6125526
AT4G24110.1	.	4.02989546	6.121489
AT3G55980.1	SZF1	4.066676	5.92248824
AT5G02940.1	.	4.21692373	4.30055473
AT5G54300.1	.	4.26730703	6.98049604
AT1G05560.2	UGT1	4.30162955	25.5369155
AT1G05562.1	.	4.30162955	25.5371171
AT4G29780.1	.	4.35685791	12.1857536
AT1G05560.1	UGT1	4.36624177	26.1190035
AT5G04340.1	ZAT6	4.38389574	4.17105934
AT2G37970.1	SOUL-1	4.38693369	11.4168882
AT1G76070.1	.	4.4456638	3.85246304
AT4G15630.1	.	4.5173292	9.78014004
AT1G28480.1	GRXC9	4.60379064	7.97552733
AT1G77450.1	NAC032	4.62178268	8.15638464
AT2G29420.1	GSTU7	4.65974366	2.58741039

AT5G64310.1	AGP1	4.84825825	17.3388368
AT4G10040.1	CYTC-2	4.85405138	4.36592142
AT4G17490.1	ERF6	4.88270935	3.22455004
AT1G44350.1	ILL6	4.89351487	14.07725
AT3G25780.1	AOC3	5.03273813	10.0320085
AT1G80840.1	WRKY40	5.04984744	9.20749125
AT1G67920.1	.	5.09486858	12.4670524
AT1G57630.1	.	5.27683017	3.73843209
AT5G08790.1	NAC081	5.43528261	4.61627408
AT5G49480.1	ATCP1	5.5461904	3.36052106
AT5G52570.1	BETA-OHASE 2	5.58801245	7.02188756
AT3G19615.1	.	5.61204456	8.44291334
AT3G22370.1	AOX1A	5.685871	8.99865418
AT2G05070.1	LHCB2.2	5.73813602	2.75729304
AT4G36500.1	.	5.78472141	3.96573861
AT5G64230.1	.	5.9114601	9.93688038
AT3G07090.1	.	5.91347988	2.36111989
AT4G01950.2	ATGPAT3	5.95191979	8.27702038
AT3G57020.1	SSL9	6.06174216	6.89707863
AT5G58070.1	TIL	6.14892832	2.8961631
AT3G08590.2	.	6.16394266	2.91447807
AT2G31380.1	BBX25	6.20761839	4.66430666
AT4G17090.1	BAM3	6.35576783	12.2754701
AT3G26830.1	CYP71B15	6.45288359	29.4380012
AT1G26380.1	FOX1	6.8446253	13.8550953
AT1G14200.1	.	7.14957495	1.7521033
AT1G09070.1	SRC2	7.25672104	4.61055156
AT5G64750.1	ABR1	7.49960662	3.25113154
AT3G16530.1	.	7.52339498	2.89589211
AT3G04010.1	.	7.72691406	5.96557882
AT4G36010.1	.	7.7901095	8.26543087
AT2G34500.1	CYP710A1	8.03005454	6.43192931
AT3G25760.1	AOC1	8.06874097	10.6185897
AT4G21920.1	.	8.22623889	3.08267144
AT3G28220.1	.	8.68652835	17.232205
AT3G15356.1	LEC	8.74176817	3.12082492
AT2G29450.1	GSTU5	8.83964835	13.9601394
AT1G71520.1	ERF020	8.98141155	11.2483429
AT3G55840.1	HSPRO1	9.3237266	5.48061131
AT2G05100.1	LHCB2.1	9.44222814	3.36776198

AT4G34131.1	UGT73B3	9.51739686	2.77756451
AT5G05410.1	DREB2A	9.72291057	5.15433452
AT3G49620.1	DIN11	10.004486	89.4826348
AT4G01870.1	.	10.7992536	10.8276832
AT5G52310.1	RD29A	10.8478064	18.5000835
AT1G05675.1	UGT74E1	10.8958555	7.52309006
AT3G44860.1	FAMT	11.8591301	67.9085097
AT1G76600.1	.	12.1118695	9.6024283
AT1G15010.1	.	12.3357874	12.8032046
AT1G05680.1	UGT74E2	12.8562048	12.4335905
AT2G15480.1	UGT73B5	14.7128055	3.5022327
AT3G09350.1	Fes1A	23.9130573	4.62687662
AT2G20560.1	.	32.8638727	4.24380689
AT5G54165.1	.	44.2195182	9.03749719
AT5G05410.2	DREB2A	44.2709844	228.129622

Table S3. Differentially Expressed Genes (DEGs) of WT and *Atcrf6* when treated with oxidative stress

At Number	**FC Col vs Col+H2O2**	padj	**FC *crf6* vs *crf6*+H2O2**	padj
AT1G51830.1	**-14.711321**	9.07E-08	**-18.800251**	1.96E-09
AT1G51840.1	**-14.60206**	1.44E-07	**-14.19686**	4.29E-08
AT1G51850.1	**-12.493233**	2.81E-05	**-7.740681**	1.79E-06
AT3G20380.1	**-11.627789**	1.02E-07	**-5.9601966**	1.20E-05
AT1G08090.1	**-11.439563**	3.07E-06	**-5.411806**	5.51E-07
AT1G49860.1	**-10.780036**	3.34E-07	**-4.8989758**	0.00077849
AT1G51470.1	**-10.626356**	2.62E-07	**-10.805507**	4.44E-07
AT3G01420.1	**-10.24686**	3.61E-07	**-5.9269094**	1.79E-09
AT1G26250.1	**-9.7530622**	1.36E-07	**-4.5462605**	3.24E-06
AT3G28550.1	**-9.2661488**	0.00010929	**-6.1699754**	1.41E-07
AT5G67400.1	**-9.1894619**	1.57E-06	**-10.459123**	7.74E-08
AT3G54040.1	**-9.0480378**	2.20E-07	**-4.6571261**	6.82E-07
AT1G52060.1	**-8.3937191**	0.00018444	**-6.871596**	1.93E-06
AT4G30170.1	**-8.0038803**	2.77E-06	**-4.9553253**	4.37E-08
AT5G19890.1	**-7.7363094**	7.23E-06	**-2.5611913**	0.0010409
AT3G48340.1	**-7.6649673**	9.35E-05	**-6.4553487**	8.65E-07
AT5G43350.1	**-7.3920757**	1.06E-05	**-4.1893608**	2.50E-06
AT2G28960.1	**-6.841438**	2.31E-05	**-5.8138757**	2.01E-05
AT2G26820.1	**-6.7816196**	2.21E-05	**-5.6102681**	1.93E-06
AT4G11650.1	**-6.6379156**	2.04E-06	**-4.2694501**	3.57E-08
AT5G35190.1	**-6.4295161**	0.00026831	**-3.3396341**	0.00053648
AT2G21045.1	**-6.3644892**	0.000296	**-3.6503505**	2.27E-05
AT4G14630.1	**-6.3413511**	1.61E-05	**-3.8737213**	2.24E-06
AT2G20030.1	**-6.3120116**	1.53E-05	**-8.1292353**	3.51E-08
AT1G08320.1	**-6.2648516**	0.00010656	**-4.2051137**	9.20E-06
AT1G05700.1	**-6.2181475**	7.88E-05	**-5.4349244**	2.28E-05
AT3G14940.1	**-6.2079219**	2.08E-05	**-8.999191**	3.95E-08
AT3G01190.1	**-6.0663121**	5.50E-05	**-4.9615308**	2.27E-06
AT1G51860.1	**-5.9282445**	2.83E-05	**-3.9877226**	0.00055452
AT4G15230.1	**-5.8810764**	7.94E-05	**-5.1340421**	0.0001008
AT5G42180.1	**-5.8432069**	0.00017514	**-4.3066619**	3.66E-05
AT3G09220.1	**-5.8137541**	9.73E-05	**-6.4242126**	1.22E-07
AT1G07560.1	**-5.7962312**	1.23E-05	**-3.0932105**	0.00072214
AT2G01530.1	**-5.7924943**	0.00015857	**-8.0004736**	8.81E-09
AT3G62270.1	**-5.7283906**	0.00013941	**-5.2260475**	1.01E-05
AT2G46750.1	**-5.649743**	1.44E-05	**-2.6400584**	0.00091789

AT1G52070.1	**-5.6170214**	2.71E-05	**-5.9090863**	3.16E-06
AT5G44380.1	**-5.5640872**	1.58E-05	**-5.8421316**	6.13E-06
AT5G59090.1	**-5.511634**	1.44E-05	**-4.2274575**	2.78E-07
AT1G73260.1	**-5.4931352**	1.31E-05	**-5.1948781**	6.58E-06
AT3G46280.1	**-5.431686**	0.00117562	**-4.4192762**	8.60E-06
AT1G18860.1	**-5.4101166**	2.42E-05	**-3.3414051**	6.96E-05
AT3G62040.1	**-5.2921365**	7.81E-06	**-4.2129778**	1.32E-07
AT5G43580.1	**-5.1535792**	0.0002798	**-3.3324191**	0.00067108
AT1G73280.1	**-5.1467784**	0.00197883	**-4.6422044**	0.00117434
AT4G12500.1	**-4.9876829**	0.00618418	**-3.7604234**	0.00447416
AT5G43520.1	**-4.9415709**	6.55E-05	**-2.3254343**	0.02319035
AT3G60330.2	**-4.9223257**	1.96E-05	**-3.5690373**	0.00086541
AT5G63600.2	**-4.807861**	0.00017118	**-3.5314363**	1.72E-05
AT3G09925.1	**-4.7334589**	0.0005929	**-5.2071183**	5.70E-06
AT5G60530.1	**-4.7301475**	0.00067116	**-4.7908942**	5.91E-05
AT1G12040.1	**-4.7252637**	6.59E-05	**-2.0824544**	0.03706526
AT1G66270.1	**-4.6795185**	9.81E-05	**-3.1882499**	4.53E-06
AT1G05240.1	**-4.5278781**	0.0003204	**-4.7548517**	4.82E-05
AT4G30140.1	**-4.4613022**	9.60E-06	**-3.9936278**	1.63E-06
AT5G26280.1	**-4.4420793**	2.31E-05	**-3.8439909**	1.93E-06
AT1G47600.1	**-4.3567119**	0.00121996	**-10.367276**	5.34E-08
AT4G13420.1	**-4.3466525**	0.00474119	**-3.2326336**	0.00703826
AT2G01520.1	**-4.3394585**	0.00029286	**-3.7552141**	1.61E-05
AT2G18980.1	**-4.326109**	0.00030664	**-3.4213124**	0.0002053
AT2G35770.1	**-4.2842277**	0.00065208	**-2.5264998**	9.46E-05
AT4G32650.1	**-4.2757573**	0.00014553	**-3.4653361**	5.45E-06
AT3G21710.1	**-4.2686355**	0.00114966	**-3.6435753**	0.00054588
AT2G46740.1	**-4.2683986**	0.00051155	**-2.4084999**	0.00651662
AT4G32950.1	**-4.2254211**	0.00016835	**-10.266909**	4.91E-08
AT2G39530.1	**-4.2015306**	0.00139373	**-2.9399365**	0.00044044
AT3G06390.1	**-4.1942421**	7.81E-06	**-3.1402074**	2.27E-05
AT5G06090.1	**-4.17433**	0.00654187	**-2.6549876**	0.00316434
AT3G49960.1	**-4.1728547**	0.00030845	**-2.941944**	0.00027981
AT1G23720.1	**-4.1671615**	0.0006659	**-3.0808533**	7.97E-05
AT2G40370.1	**-4.1562863**	0.0002798	**-3.0720569**	2.94E-05
AT1G29280.1	**-4.1559685**	4.93E-05	**-2.7733697**	2.57E-06
AT4G15390.1	**-4.1470064**	8.82E-05	**-4.7623379**	2.65E-06
AT5G23830.1	**-4.1064456**	0.00132836	**-3.372621**	0.00021612
AT1G07610.1	**-4.0505985**	6.59E-05	**-3.6253991**	1.41E-07
AT4G26010.1	**-4.0139557**	0.00335927	**-2.8314575**	0.00227325

AT5G64100.1	**-4.0054233**	0.00020305	**-2.2246372**	6.69E-05
AT3G22240.1	**-3.9957597**	0.00015546	**-3.1612606**	1.83E-06
AT1G71380.1	**-3.9810106**	0.00031371	**-2.4900764**	0.00818873
AT3G23175.1	**-3.9611381**	0.00152324	**-3.0055311**	6.25E-05
AT1G66280.1	**-3.9210089**	8.40E-05	**-4.6386815**	2.63E-07
AT5G57625.1	**-3.8563078**	0.00081803	**-4.3687333**	0.00032001
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AT4G30210.1	**1.796178**	0.02280704	**1.530598**	0.02069442
AT1G33600.1	**1.807744**	0.04374305	**1.528965**	0.03881812
AT1G20510.1	**1.810471**	0.01473963	**1.609659**	0.00619489
AT1G49050.1	**1.813309**	0.04390077	**1.611668**	0.02324468
AT5G27600.1	**1.818709**	0.01757144	**2.016118**	0.00093265
AT4G30390.1	**1.842545**	0.03127664	**1.611434**	0.01860462
AT4G16760.1	**1.850609**	0.01506702	**1.835483**	0.02993966
AT3G22890.1	**1.854236**	0.03224102	**2.089098**	0.00021612
AT1G61275.1	**1.856828**	0.04889652	**2.449335**	0.00029616
AT1G07890.1	**1.85715**	0.01595188	**1.7148**	0.00255415
AT3G12145.1	**1.869082**	0.01851953	**1.780077**	0.00349042
AT5G67600.1	**1.882154**	0.03127664	**1.575184**	0.03754747
AT1G76520.1	**1.882911**	0.02512714	**2.377557**	5.90E-06
AT1G64710.1	**1.893703**	0.03147242	**2.357708**	6.50E-05
AT5G46470.1	**1.90587**	0.01761535	**1.51369**	0.02479476
AT4G08470.1	**1.909639**	0.03543589	**1.657691**	0.03656989
AT5G23850.1	**1.913495**	0.02200715	**1.878831**	0.0024429
AT4G28490.1	**1.914198**	0.03316454	**1.986901**	0.02115417
AT2G34355.1	**1.919067**	0.02139356	**1.756776**	0.04844092
AT3G05360.1	**1.928942**	0.03922153	**2.028425**	0.00170499
AT2G41380.1	**1.933661**	0.01789702	**2.235798**	0.00013222
AT4G08950.1	**1.93823**	0.04678292	**2.297102**	3.21E-05
AT3G56200.1	**1.941841**	0.03566818	**1.812536**	0.01080939
AT4G02520.1	**1.943255**	0.00408112	**3.023721**	5.97E-07
AT5G24760.1	**1.945573**	0.03035606	**1.816221**	0.0115457
AT2G37040.1	**1.946227**	0.01486261	**1.885765**	0.00612048
AT3G50910.1	**1.950839**	0.0184592	**1.814497**	0.00146234
AT5G20830.1	**1.951651**	0.01554374	**1.651824**	0.02165382
AT1G71140.1	**1.959126**	0.03201406	**2.217832**	0.02024936
AT5G42650.1	**1.963755**	0.01757144	**2.206172**	0.00010562

AT4G02940.1	**1.963912**	0.01385572	**1.857516**	0.00037491
AT5G37770.1	**1.966098**	0.01962234	**2.078863**	0.00365878
AT3G28180.1	**1.971529**	0.03135106	**1.624662**	0.01058715
AT5G02290.1	**1.976592**	0.02279122	**1.579875**	0.02021298
AT5G17990.1	**1.978422**	0.0167066	**1.883845**	0.00104134
AT4G31860.1	**1.981661**	0.01514118	**1.925009**	8.12E-05
AT1G74100.1	**1.990899**	0.0154499	**2.249594**	3.93E-05
AT2G04400.1	**1.993792**	0.0167066	**2.293467**	1.64E-05
AT1G11050.1	**2.000388**	0.0177042	**1.818545**	0.00271212
AT1G52400.1	**2.019055**	0.01480432	**1.703887**	0.00255788
AT2G31955.1	**2.024604**	0.03763202	**1.706429**	0.00351051
AT1G17290.1	**2.024906**	0.02739312	**1.765951**	0.00225629
AT2G06050.1	**2.025376**	0.04403716	**1.782349**	0.03100793
AT4G25810.1	**2.026416**	0.01132429	**2.614799**	1.89E-05
AT4G18010.1	**2.02896**	0.02937131	**1.758201**	0.01156832
AT4G32300.1	**2.03412**	0.00576549	**1.705081**	0.00723279
AT2G43820.1	**2.041713**	0.02258425	**1.837113**	0.02003359
AT1G74440.1	**2.041989**	0.03035606	**1.879391**	0.00172579
AT2G41410.1	**2.057675**	0.01439933	**2.651576**	4.54E-06
AT5G64250.1	**2.065971**	0.01060075	**1.978573**	0.0003478
AT4G02890.2	**2.070107**	0.02695098	**1.911884**	0.03016394
AT5G19440.1	**2.072605**	0.00539156	**2.216456**	2.01E-05
AT1G76970.1	**2.077488**	0.01889703	**1.791496**	0.0083352
AT5G61600.1	**2.082743**	0.01407965	**2.690296**	1.91E-05
AT5G47910.1	**2.083631**	0.01296124	**1.629196**	0.00892168
AT2G22500.1	**2.084462**	0.04273684	**1.717786**	0.02353674
AT3G46600.1	**2.091706**	0.0104823	**1.742109**	0.00356653
AT1G27770.1	**2.095573**	0.01744944	**1.740287**	0.00378852
AT1G12200.1	**2.106343**	0.01484196	**2.416602**	0.00098839
AT3G51890.1	**2.113758**	0.02863957	**2.000187**	0.00021563
AT4G12120.1	**2.115157**	0.01413002	**1.824631**	0.00044113
AT3G26980.1	**2.121111**	0.01441124	**1.840752**	0.00337445
AT1G27760.1	**2.128608**	0.01061097	**1.598008**	0.00929938
AT5G44070.1	**2.129995**	0.02412237	**1.593595**	0.03513307
AT4G39030.1	**2.134488**	0.01005963	**1.833506**	0.02613882
AT2G37760.1	**2.135457**	0.00954217	**2.094571**	0.0102523
AT1G55530.1	**2.13822**	0.01595233	**1.611791**	0.01087978
AT2G41100.4	**2.139013**	0.01132429	**3.132273**	4.32E-07
AT1G32940.1	**2.149044**	0.01228082	**2.030282**	0.00935938
AT3G13330.1	**2.153167**	0.00602172	**1.625428**	0.00274959

AT5G14760.1	**2.154032**	0.00603447	**1.650697**	0.00463844
AT3G21250.1	**2.155967**	0.01392092	**1.911911**	0.00200616
AT3G61825.1	**2.162455**	0.02007597	**2.05476**	0.01173354
AT4G18950.1	**2.163009**	0.03900803	**1.52709**	0.03887561
AT5G58070.1	**2.16508**	0.00939179	**1.533996**	0.03249506
AT5G47730.1	**2.165147**	0.00665502	**1.834498**	0.00109283
AT5G41740.1	**2.172671**	0.00786084	**1.976791**	0.00051932
AT4G28390.1	**2.175308**	0.02110888	**2.301246**	0.00109283
AT2G37940.1	**2.178266**	0.00889429	**1.650594**	0.00153934
AT1G25370.1	**2.179905**	0.01969363	**1.958542**	0.01650509
AT5G59550.1	**2.185359**	0.04374305	**1.957897**	0.00708319
AT5G35690.1	**2.185503**	0.00827979	**1.688556**	0.04352782
AT2G16900.1	**2.186934**	0.00294151	**1.898237**	0.00194875
AT4G23570.1	**2.210189**	0.01851953	**1.928521**	0.00837696
AT1G33110.1	**2.213608**	0.00187713	**2.232043**	0.00016284
AT4G14680.1	**2.214268**	0.00429178	**2.44257**	0.00074258
AT2G05380.1	**2.224622**	0.00232372	**2.049696**	4.77E-05
AT2G13790.1	**2.23137**	0.01301609	**2.125254**	0.00010173
AT2G43000.1	**2.23274**	0.03548053	**3.10832**	0.00017537
AT4G19880.1	**2.235194**	0.00510566	**2.119443**	7.32E-05
AT2G25140.1	**2.237108**	0.00535293	**1.490933**	0.0398636
AT5G17380.1	**2.243918**	0.01068266	**2.027863**	0.00035415
AT4G01010.1	**2.247966**	0.02260259	**2.270508**	0.00029737
AT4G28400.1	**2.248293**	0.00220194	**1.732427**	0.00807521
AT4G30490.1	**2.253777**	0.020257	**1.779578**	0.00321318
AT5G26920.2	**2.254957**	0.03381923	**1.889173**	0.00408372
AT3G04010.1	**2.258555**	0.00280388	**2.416041**	0.00036363
AT3G12510.1	**2.259299**	0.04999103	**2.256333**	0.01944194
AT2G47730.1	**2.268879**	0.00433876	**2.382003**	8.13E-05
AT1G52410.1	**2.285841**	0.00500093	**1.875662**	0.00484723
AT1G08050.1	**2.287307**	0.01653208	**1.662167**	0.023483
AT5G18470.1	**2.291179**	0.00481643	**2.548379**	0.00080249
AT3G10500.1	**2.294381**	0.01448107	**1.993136**	0.00273874
AT3G04210.1	**2.296935**	0.00448773	**2.01704**	0.00020087
AT3G51860.1	**2.303272**	0.02421266	**2.512903**	0.00035397
AT2G04040.1	**2.310132**	0.009801	**7.453174**	9.49E-07
AT1G36370.1	**2.316658**	0.04123699	**1.920704**	0.00809373
AT3G44720.1	**2.318859**	0.02268188	**2.105737**	0.00282203
AT4G04020.1	**2.35171**	0.00464532	**1.82886**	0.00188256
AT2G26530.1	**2.355225**	0.04678292	**2.373753**	7.55E-06

AT2G38290.1	**2.355903**	0.00843189	**2.461401**	8.13E-05
AT1G15415.1	**2.358648**	0.00995543	**3.813802**	0.00016953
AT3G19010.1	**2.362452**	0.01885214	**1.823898**	0.01179309
AT5G15870.1	**2.367017**	0.01332084	**1.442739**	0.02846672
AT4G09030.1	**2.376297**	0.00671782	**1.740033**	0.00860822
AT4G34150.1	**2.378208**	0.00489336	**2.191206**	5.62E-05
AT4G01895.1	**2.383613**	0.04553307	**1.703905**	0.03117113
AT4G11600.1	**2.397008**	0.01413002	**1.83004**	0.0014873
AT5G22060.1	**2.397831**	0.00176043	**1.954155**	5.45E-05
AT4G31800.1	**2.409744**	0.04967597	**2.569513**	0.00019289
AT3G17700.1	**2.412569**	0.00624347	**1.87115**	0.00724694
AT2G41010.1	**2.413413**	0.0167066	**2.219723**	0.00242329
AT5G45110.1	**2.417138**	0.00360546	**1.705961**	0.00242329
AT1G72680.1	**2.430015**	0.01595233	**2.147808**	0.00371496
AT3G26910.1	**2.431725**	0.00946128	**2.194786**	2.27E-05
AT5G10830.1	**2.44562**	0.00320272	**1.927512**	0.00358246
AT2G40140.1	**2.445637**	0.01229994	**1.827739**	0.00191108
AT5G03630.1	**2.4515**	0.00844788	**2.107701**	8.78E-05
AT4G26070.3	**2.460821**	0.00623544	**1.680004**	0.02672446
AT1G50740.1	**2.461222**	0.00824645	**1.54925**	0.01717334
AT1G17990.1	**2.466465**	0.00114109	**2.23476**	0.00061428
AT4G39230.1	**2.47526**	0.00120433	**2.397324**	3.65E-05
AT4G33050.3	**2.475972**	0.01095328	**2.862102**	6.71E-06
AT4G01950.1	**2.48018**	0.00211966	**1.525048**	0.03504174
AT5G20000.1	**2.481952**	0.00546832	**1.75419**	0.00413942
AT5G03380.1	**2.48524**	0.00211966	**1.582565**	0.00844867
AT5G13750.1	**2.48949**	0.00045918	**2.088888**	0.00035415
AT2G46400.1	**2.492226**	0.03901142	**2.143852**	0.02039014
AT1G01720.1	**2.504461**	0.00470532	**2.157581**	0.00037802
AT2G23420.1	**2.511118**	0.00062361	**1.691655**	0.00508308
AT1G18020.1	**2.512067**	0.00547819	**2.272248**	5.45E-05
AT2G38340.1	**2.513434**	0.0180535	**2.270461**	0.00676084
AT4G33930.1	**2.514985**	0.0040627	**5.22429**	5.59E-06
AT4G10040.1	**2.51802**	0.00277569	**1.682924**	0.00910892
AT1G70530.1	**2.525843**	0.01480432	**1.893611**	0.00029494
AT4G26270.1	**2.527411**	0.00283565	**1.945472**	0.00785195
AT4G15760.1	**2.529356**	0.00238554	**2.058838**	0.00135471
AT1G30755.1	**2.529908**	0.04736631	**2.453336**	0.00011347
AT4G05020.1	**2.536053**	0.00167213	**1.825435**	0.00513156
AT3G11840.1	**2.552224**	0.02279738	**1.71335**	0.01607879

AT2G20142.1	**2.556943**	0.00576549	**3.012268**	0.00111795
AT2G38470.1	**2.557484**	0.00038299	**3.127934**	5.77E-08
AT1G55450.1	**2.561369**	0.02170154	**2.177556**	4.25E-05
AT1G76070.1	**2.563731**	0.01130185	**2.476075**	0.00020996
AT3G09010.1	**2.566051**	0.01417907	**2.843731**	7.92E-06
AT4G15550.1	**2.576656**	0.00451857	**2.137879**	0.00073036
AT4G28140.1	**2.578068**	0.02114913	**2.045325**	0.02070983
AT5G14730.1	**2.584061**	0.00838714	**2.444298**	7.32E-05
AT3G25770.1	**2.586632**	0.00062562	**2.123001**	7.09E-06
AT1G17380.1	**2.588184**	0.04403716	**2.351196**	0.01772363
AT2G39650.1	**2.600294**	0.00462575	**2.492554**	4.92E-05
AT1G03905.1	**2.627007**	0.02477926	**1.912799**	0.04179269
AT2G41880.1	**2.635031**	0.00253181	**2.495796**	1.89E-05
AT5G13370.1	**2.63833**	0.00905375	**2.888559**	7.99E-05
AT1G53990.1	**2.63844**	0.02137139	**2.550977**	0.00262935
AT3G47540.1	**2.642008**	0.0267404	**2.606574**	0.00222556
AT2G15780.1	**2.645105**	0.03069222	**4.010327**	1.34E-05
AT1G26730.1	**2.650859**	0.03763202	**2.682578**	0.00383483
AT4G35190.1	**2.662857**	0.00330749	**3.525884**	0.00068317
AT1G02930.1	**2.665498**	0.00638122	**4.504385**	4.57E-07
AT2G22880.1	**2.67515**	0.02955624	**3.29618**	8.05E-05
AT2G26190.1	**2.675391**	0.00777216	**1.931745**	0.00353186
AT4G29780.1	**2.67554**	0.0211318	**2.737426**	0.00020134
AT4G12720.4	**2.677933**	0.00312188	**2.342648**	8.98E-05
AT5G65600.1	**2.680923**	0.02561875	**2.795313**	0.00109101
AT1G32920.1	**2.681007**	0.00435568	**1.880687**	0.00145301
AT4G17490.1	**2.688488**	0.04603722	**5.439975**	4.03E-05
AT2G24600.1	**2.695214**	0.02200715	**2.791905**	3.66E-05
AT5G35735.1	**2.701667**	0.00075715	**2.099346**	3.26E-05
AT4G21320.1	**2.701967**	0.01298558	**2.338008**	0.03133995
AT1G17745.1	**2.714243**	0.00012173	**3.19943**	1.28E-05
AT5G35320.1	**2.720374**	0.00259873	**1.923188**	0.00232149
AT4G15420.1	**2.728437**	0.0011001	**1.982987**	0.0022904
AT2G03760.1	**2.729516**	0.00776715	**2.656966**	6.98E-05
AT2G30140.1	**2.731389**	0.00467624	**3.355389**	5.03E-06
AT4G27970.1	**2.73902**	0.01134424	**3.211317**	0.00147752
AT1G55850.1	**2.744389**	0.00193944	**2.038927**	0.00066916
AT2G36790.1	**2.753898**	0.02139356	**2.056769**	0.02021298
AT4G33070.1	**2.755444**	0.00043051	**3.802571**	7.83E-06
AT5G20910.1	**2.77288**	0.00118804	**2.295471**	0.00015082

AT3G25610.1	**2.775408**	0.00691465	**1.848872**	0.00950053
AT1G72930.2	**2.81954**	0.00114127	**2.736876**	7.67E-05
AT2G40340.1	**2.823344**	0.0060277	**3.634709**	1.28E-05
AT1G62300.1	**2.823403**	0.00766995	**2.507448**	5.90E-06
AT4G17615.1	**2.826291**	0.00288084	**1.916834**	0.00441801
AT4G27280.1	**2.826771**	0.00061336	**2.962613**	2.38E-05
AT5G47070.1	**2.827173**	0.0012779	**1.673444**	0.04872024
AT3G15356.1	**2.829829**	0.00202489	**7.371509**	3.63E-08
AT1G66880.1	**2.83627**	0.00025108	**2.414375**	0.00029768
AT2G41090.1	**2.837322**	0.00018022	**2.077142**	0.00891644
AT2G34660.2	**2.85675**	0.00011749	**1.877555**	0.00134418
AT4G23190.1	**2.862161**	0.01994251	**3.567986**	3.27E-05
AT2G45570.1	**2.873472**	0.00891839	**3.182565**	0.00019401
AT3G09440.1	**2.88157**	0.00091017	**2.180101**	6.06E-05
AT5G02780.1	**2.887898**	0.04889652	**3.765301**	6.97E-05
AT5G10380.1	**2.890492**	0.00335927	**2.492641**	0.00035865
AT4G36500.1	**2.89403**	0.00221169	**2.232902**	0.00024535
AT3G26840.1	**2.905729**	0.00142965	**3.30406**	3.32E-05
AT5G50915.1	**2.916827**	0.00284528	**2.103009**	0.02502642
AT1G14642.1	**2.91706**	0.00106672	**3.042126**	5.03E-06
AT3G13080.1	**2.917485**	0.00024208	**2.828221**	1.83E-05
AT1G07410.1	**2.920125**	0.00929749	**2.499691**	0.00831545
AT1G14640.1	**2.942444**	0.00167213	**2.267614**	0.00143145
AT1G62180.1	**2.944056**	0.00047703	**1.970559**	0.00472903
AT4G39950.1	**2.947874**	0.00046382	**2.132107**	0.00384686
AT2G24500.1	**2.959021**	0.00050376	**2.411825**	9.00E-06
AT2G23680.1	**2.966332**	0.00624347	**2.888049**	0.00029596
AT1G21110.1	**2.968337**	0.01558217	**2.465833**	0.01048818
AT5G39670.1	**2.968594**	0.00046382	**2.627927**	0.00176223
AT1G09070.1	**2.970807**	0.00131518	**2.087932**	0.0004926
AT3G08970.1	**2.973743**	0.00352209	**2.313176**	0.00191324
AT4G16820.1	**2.974351**	0.01304198	**3.218459**	0.00054669
AT5G52050.1	**2.974722**	0.01407075	**4.57896**	2.25E-05
AT1G74360.1	**2.980377**	0.0067766	**3.03095**	3.49E-05
AT5G41750.1	**3.000889**	0.02298006	**2.324314**	0.01203174
AT1G76960.1	**3.002678**	0.00380918	**2.140718**	0.01570401
AT1G22400.1	**3.015736**	0.00614778	**2.883158**	0.00913326
AT3G44190.1	**3.024664**	0.00045918	**2.296274**	0.00015416
AT1G66600.1	**3.026038**	0.01198815	**2.298042**	0.01944135
AT5G22530.1	**3.028157**	0.00475839	**2.763708**	0.00163024

AT5G01100.1	**3.031086**	0.00118804	**2.32483**	0.00296458
AT4G24380.1	**3.036249**	0.00060026	**2.390512**	8.18E-06
AT3G45140.1	**3.038965**	1.49E-05	**1.724771**	1.30E-05
AT3G07090.1	**3.042411**	0.0001299	**2.082642**	0.00024535
AT4G22530.1	**3.067153**	0.000849	**3.118593**	5.03E-06
AT4G13395.1	**3.068099**	0.00482843	**2.414995**	0.0010665
AT5G42830.1	**3.070726**	0.01264926	**3.518426**	0.00031545
AT2G23321.1	**3.08377**	0.02328244	**2.846166**	0.0067448
AT1G15430.1	**3.090885**	0.00233896	**2.348981**	0.00496
AT2G22860.1	**3.090981**	0.00867433	**4.241266**	6.97E-06
AT5G51190.1	**3.115902**	0.00843189	**2.59492**	0.01055459
AT2G29720.1	**3.119284**	0.00407677	**2.397756**	5.67E-05
AT5G60900.1	**3.122334**	0.01352679	**2.506197**	0.02355304
AT1G76690.1	**3.125366**	0.00119346	**2.170338**	0.01045824
AT4G21390.1	**3.128357**	0.00932251	**2.434854**	0.00181691
AT1G72920.1	**3.132696**	0.00031371	**4.605092**	5.03E-06
AT5G57220.1	**3.137075**	0.01514118	**4.486032**	3.95E-08
AT4G04610.1	**3.138641**	0.00016835	**2.421221**	0.0001583
AT1G52560.1	**3.142102**	0.00297212	**2.339954**	0.01270923
AT4G24570.1	**3.143017**	0.00666944	**3.156061**	3.08E-06
AT1G76470.1	**3.143453**	0.02279122	**4.65419**	4.14E-05
AT1G59590.1	**3.146973**	0.0081638	**1.974942**	0.01542795
AT5G42530.1	**3.148108**	2.04E-06	**1.892581**	0.0083352
AT3G28580.1	**3.169181**	0.00152652	**3.84943**	0.00049222
AT2G35930.1	**3.173028**	0.00337311	**2.929958**	1.75E-06
AT5G64750.1	**3.17525**	0.0012018	**5.538288**	3.08E-06
AT5G04340.1	**3.19481**	0.01041582	**2.974887**	0.00073822
AT2G46830.1	**3.201737**	0.00036299	**2.646104**	0.03307794
AT3G55980.1	**3.206635**	0.00704335	**2.013283**	0.01620494
AT4G37030.1	**3.2139**	0.00121912	**2.156602**	0.01235623
AT5G64310.1	**3.22574**	6.26E-05	**1.903336**	0.00016538
AT2G40000.1	**3.226791**	0.00843189	**2.183004**	0.00024065
AT5G56030.1	**3.23961**	0.00277201	**1.916163**	0.02132433
AT1G26380.1	**3.279759**	0.00524644	**2.311333**	0.00258822
AT5G57010.1	**3.280817**	0.00204326	**2.279741**	0.01960686
AT3G22370.1	**3.284332**	0.00017865	**2.642155**	0.00036128
AT5G08760.1	**3.284947**	0.00038729	**2.729345**	6.93E-05
AT4G23030.1	**3.306615**	0.00097645	**2.545158**	0.00687877
AT1G21520.1	**3.309986**	0.00046917	**2.086883**	0.00888279
AT3G44830.1	**3.312189**	0.00223472	**4.657869**	0.0016745

AT1G02850.1	**3.325658**	0.00022707	**5.971983**	1.08E-06
AT1G69730.1	**3.32605**	0.00045091	**2.134399**	0.00111704
AT4G37290.1	**3.328345**	0.00906768	**3.598074**	0.0017366
AT5G52570.1	**3.331958**	0.00690084	**2.351099**	0.03399573
AT3G56400.1	**3.33688**	1.61E-05	**2.140934**	0.02353674
AT3G28930.1	**3.338847**	0.0015411	**3.154628**	0.00017039
AT4G18880.1	**3.344255**	0.00060026	**2.038489**	0.00695256
AT1G52040.1	**3.346864**	0.01582121	**2.029923**	0.01524219
AT4G23180.1	**3.348465**	0.00049006	**2.01646**	0.0001881
AT5G26220.1	**3.348674**	0.00046917	**2.709807**	0.00429221
AT1G02920.1	**3.352587**	0.00073252	**3.724056**	1.59E-06
AT3G09405.1	**3.361826**	0.00123931	**5.792897**	1.70E-07
AT3G55840.1	**3.376667**	0.00067478	**2.051615**	0.03586398
AT1G66580.1	**3.392903**	1.25E-05	**2.659601**	5.74E-06
AT3G02840.1	**3.394443**	0.01833004	**3.105219**	0.00010679
AT4G11370.1	**3.407196**	0.00050992	**2.112915**	0.00031034
AT3G14200.1	**3.409925**	0.00114235	**2.619325**	2.84E-06
AT4G33540.1	**3.433476**	9.84E-05	**3.001732**	6.65E-05
AT1G07135.1	**3.445767**	0.00205586	**3.415697**	5.54E-07
AT4G36010.1	**3.461195**	0.00012139	**2.727757**	8.76E-05
AT3G63380.1	**3.46231**	0.00259873	**2.971065**	0.00011175
AT1G79710.1	**3.474824**	0.00010768	**2.301501**	0.00038089
AT1G18570.1	**3.479825**	0.00056651	**3.691571**	1.91E-07
AT1G60730.1	**3.482009**	0.00023932	**3.76577**	2.06E-07
AT1G66700.1	**3.496787**	0.0014078	**2.435495**	0.00520262
AT2G32200.1	**3.504321**	0.00067803	**2.507683**	0.00694841
AT3G16530.1	**3.516171**	0.00010355	**6.994907**	2.91E-08
AT2G34500.1	**3.52006**	0.00036299	**3.940149**	3.21E-05
AT4G25200.1	**3.522171**	0.00176683	**3.605852**	6.48E-06
AT1G10370.1	**3.529429**	0.00125213	**3.631536**	4.87E-05
AT3G54150.1	**3.563043**	0.00210706	**4.151032**	5.79E-06
AT5G36970.1	**3.56811**	0.02555807	**4.624701**	0.00012222
AT3G23230.1	**3.579393**	0.01238867	**2.159317**	0.00711676
AT1G30070.1	**3.596715**	7.94E-05	**2.214798**	0.00027981
AT3G50770.1	**3.610491**	0.00016467	**4.104681**	2.47E-06
AT4G23220.1	**3.624784**	0.00422956	**2.44329**	0.00105424
AT5G06530.1	**3.628517**	0.00392115	**2.454314**	0.00271234
AT1G28190.1	**3.634949**	0.00099354	**3.337667**	3.72E-07
AT4G08870.1	**3.64523**	0.00046382	**2.638037**	0.00029171
AT3G25760.1	**3.667711**	5.36E-05	**3.758104**	3.21E-05

AT1G59865.1	**3.671997**	0.00653993	**2.839388**	0.00334036
AT3G28220.1	**3.678876**	0.00048832	**3.299506**	2.49E-05
AT5G19240.1	**3.686061**	0.00083567	**2.591729**	0.00028482
AT3G23120.1	**3.68739**	0.00068841	**2.464457**	0.04752154
AT2G29450.1	**3.729365**	5.36E-05	**2.058766**	0.00116185
AT2G36950.1	**3.732792**	0.00097148	**2.158299**	0.00015082
AT4G11000.1	**3.760254**	0.02301739	**2.718075**	0.00156625
AT1G14040.1	**3.791346**	0.00017177	**2.377096**	0.00726816
AT1G10585.1	**3.791779**	0.00103542	**2.897583**	0.0144026
AT5G39050.1	**3.79829**	0.00046382	**5.169107**	3.95E-08
AT1G61340.1	**3.813128**	0.00038203	**3.806407**	1.32E-05
AT1G19020.1	**3.815256**	0.00047703	**4.601343**	2.00E-06
AT5G61820.1	**3.817664**	0.0002798	**3.631889**	5.97E-07
AT1G67810.1	**3.829816**	0.00058262	**3.221427**	0.00213686
AT2G33710.1	**3.851259**	0.00824645	**1.985476**	0.0428424
AT2G37430.1	**3.883897**	0.00618418	**3.150957**	0.00015082
AT5G14700.1	**3.907267**	7.35E-05	**2.435419**	9.15E-05
AT4G21680.1	**3.913122**	0.00012278	**11.35067**	7.07E-09
AT1G78380.1	**3.919256**	4.98E-06	**2.48233**	7.14E-05
AT1G69920.1	**3.921403**	0.00073233	**6.536077**	1.41E-07
AT1G75270.1	**3.972301**	0.0020669	**2.731191**	0.00225629
AT5G05300.1	**3.973609**	0.00442954	**3.198832**	0.00018465
AT1G24145.1	**4.002593**	3.31E-05	**3.706673**	2.65E-05
AT4G13180.1	**4.018745**	1.44E-05	**4.673295**	3.95E-08
AT5G64905.1	**4.055233**	0.00193392	**3.152967**	0.00385115
AT5G10695.1	**4.11237**	0.00031563	**3.105047**	1.24E-05
AT5G27760.1	**4.148932**	0.00021188	**3.061386**	2.38E-05
AT3G04220.1	**4.159644**	0.00038203	**3.228077**	0.00029596
AT1G27730.1	**4.173868**	9.19E-05	**5.27209**	9.40E-09
AT2G29460.1	**4.208395**	0.00529549	**5.007741**	1.60E-05
AT5G25930.1	**4.234583**	0.007405	**2.900386**	0.00117384
AT5G22300.1	**4.251848**	0.0075735	**5.459315**	1.03E-06
AT2G46240.1	**4.258927**	6.59E-05	**2.952486**	4.53E-06
AT1G72520.1	**4.322632**	0.01539545	**3.375485**	4.10E-05
AT5G27420.1	**4.324745**	0.00625665	**2.495372**	0.01385623
AT1G72900.1	**4.335114**	0.00031709	**5.423071**	2.37E-06
AT3G23250.1	**4.33582**	6.26E-05	**4.713275**	3.39E-06
AT3G43250.1	**4.341218**	0.01025134	**3.677346**	0.0007717
AT5G54860.1	**4.368385**	8.51E-05	**2.897011**	3.81E-05
AT1G64940.1	**4.375719**	0.00016835	**3.828661**	6.39E-05

AT4G11480.1	**4.397382**	0.00463281	**3.673041**	5.67E-05
AT1G24147.1	**4.41877**	0.00047394	**3.211718**	0.03120665
AT2G33380.1	**4.46647**	0.00067116	**3.609377**	7.93E-05
AT5G54490.1	**4.510149**	3.64E-05	**5.35919**	2.14E-06
AT1G14200.1	**4.549033**	2.06E-05	**4.004453**	2.93E-05
AT4G14365.1	**4.553276**	0.00044561	**2.993721**	0.00302601
AT2G17040.1	**4.559798**	1.71E-06	**3.665754**	5.49E-07
AT1G70440.1	**4.568197**	0.00045918	**2.868815**	0.0032928
AT5G59820.1	**4.568293**	0.00082071	**3.640698**	0.00016463
AT5G22520.1	**4.571983**	0.00016962	**3.441661**	0.00081181
AT3G26830.1	**4.590766**	7.76E-05	**10.4667**	2.30E-07
AT3G53230.1	**4.608748**	5.47E-05	**3.167578**	1.51E-05
AT1G57630.1	**4.671238**	0.00012565	**5.569817**	1.19E-06
AT3G59140.1	**4.672258**	0.00016962	**2.645077**	0.00135042
AT5G24110.1	**4.708818**	0.00170942	**2.265257**	0.02994424
AT5G24780.1	**4.72325**	2.06E-06	**3.808796**	7.97E-05
AT3G14620.1	**4.75795**	7.88E-05	**4.060338**	2.60E-05
AT5G64510.1	**4.763988**	1.52E-05	**3.415662**	0.00012222
AT1G35710.1	**4.767028**	3.31E-05	**2.960365**	0.01659985
AT4G14400.1	**4.840698**	2.60E-06	**2.130615**	0.04611462
AT4G24160.1	**4.847699**	1.83E-05	**4.056906**	7.84E-07
AT5G48540.1	**4.886969**	6.57E-05	**3.009555**	0.00140705
AT3G02800.1	**4.931238**	0.0002798	**3.564019**	5.78E-07
AT1G17147.1	**5.022498**	0.00213059	**2.856335**	0.00031512
AT2G42540.1	**5.022724**	4.74E-06	**1.738225**	0.00074067
AT4G35180.1	**5.025005**	0.00041377	**6.037035**	5.62E-05
AT2G02010.1	**5.031924**	2.31E-05	**3.528732**	0.0003385
AT3G25250.1	**5.092874**	0.00068089	**3.846936**	0.00022579
AT3G29000.1	**5.113461**	0.00179347	**6.483353**	4.76E-07
AT4G11280.1	**5.115712**	1.32E-05	**6.326006**	5.31E-09
AT1G77450.1	**5.188545**	1.53E-05	**4.236315**	1.50E-07
AT3G46230.1	**5.192484**	0.00013474	**2.734164**	0.00231259
AT3G60120.1	**5.211487**	0.00036299	**6.656528**	4.53E-06
AT1G21250.1	**5.251047**	1.06E-05	**3.900813**	0.00019774
AT5G63790.1	**5.321637**	1.22E-05	**4.145525**	1.07E-07
AT3G46080.1	**5.347057**	0.00051112	**2.665867**	0.00068931
AT5G40000.1	**5.370197**	0.00024849	**7.750127**	0.00018772
AT1G76680.1	**5.524964**	1.26E-05	**5.317913**	6.12E-07
AT1G32350.1	**5.548451**	0.00340579	**3.54801**	0.00135471
AT5G08790.1	**5.582804**	4.20E-06	**4.148687**	3.40E-06

AT5G51830.1	**5.585398**	4.01E-06	**4.764088**	1.65E-07
AT1G59860.1	**5.622883**	7.64E-05	**2.707619**	0.00165626
AT1G69930.1	**5.675018**	0.00185595	**8.612398**	4.03E-06
AT1G80820.1	**5.877306**	7.42E-06	**4.419199**	6.84E-08
AT1G79410.1	**5.890439**	1.53E-05	**3.256371**	5.34E-05
AT4G23600.1	**5.999803**	4.08E-05	**3.359066**	9.99E-07
AT2G28210.1	**6.0871**	2.34E-06	**4.247694**	4.08E-07
AT1G67920.1	**6.162988**	0.00027103	**3.153054**	0.00027205
AT3G56710.1	**6.166492**	0.00320311	**2.651098**	0.00274776
AT3G48850.1	**6.262831**	1.82E-05	**6.89789**	2.72E-07
AT5G25450.1	**6.335506**	1.22E-05	**4.139367**	5.63E-05
AT4G34131.1	**6.368969**	9.35E-05	**2.706597**	0.00229318
AT5G49480.1	**6.479287**	1.71E-06	**4.150845**	2.10E-07
AT4G12735.1	**6.609793**	2.71E-07	**3.875346**	0.00038549
AT2G15490.1	**6.775959**	1.06E-05	**6.049748**	2.75E-07
AT3G24500.1	**6.81137**	1.32E-07	**3.436345**	2.84E-06
AT1G22810.1	**6.943052**	7.67E-06	**5.253741**	8.65E-07
AT5G48570.1	**7.020798**	5.00E-06	**4.114152**	1.41E-07
AT4G34135.1	**7.17702**	5.18E-06	**5.64436**	3.69E-07
AT4G21990.1	**7.222834**	2.88E-07	**4.197339**	5.52E-07
AT5G40990.1	**7.740437**	7.94E-07	**10.26431**	5.34E-08
AT2G30770.1	**7.82345**	1.44E-05	**6.648482**	0.00399121
AT2G29490.1	**8.132055**	0.00014079	**4.29709**	4.71E-06
AT1G76600.1	**8.184419**	2.77E-06	**4.02103**	5.62E-05
AT4G08555.1	**8.308828**	0.00010659	**2.763124**	0.00142484
AT1G54050.1	**8.376456**	2.40E-07	**3.16354**	0.00024535
AT1G05560.1	**8.501869**	1.54E-07	**4.932845**	1.28E-05
AT4G22710.1	**8.523081**	8.37E-08	**7.556771**	2.05E-08
AT2G41730.1	**8.538987**	2.42E-05	**5.068645**	1.60E-05
AT1G16030.1	**8.543221**	2.68E-07	**4.964523**	2.53E-06
AT1G21120.1	**8.548878**	1.92E-06	**6.002048**	2.30E-07
AT3G28210.1	**8.570326**	8.63E-07	**4.725199**	5.52E-05
AT2G26150.1	**8.690204**	2.68E-07	**4.836555**	3.21E-05
AT2G36800.1	**8.707026**	1.06E-05	**5.702265**	2.74E-07
AT1G05680.1	**8.846642**	2.00E-06	**3.199785**	0.00269403
AT2G44460.1	**8.917133**	1.25E-05	**15.26071**	3.21E-05
AT2G29420.1	**9.18653**	1.36E-07	**5.563026**	1.21E-07
AT1G80840.1	**9.386908**	3.64E-05	**6.509244**	9.83E-09
AT4G37370.1	**9.416755**	1.01E-05	**5.84029**	3.94E-06
AT4G01870.1	**9.600702**	1.23E-06	**9.651679**	7.23E-08

AT1G66570.1	**9.843525**	2.23E-05	**3.322939**	0.03674477
AT5G16980.1	**10.00733**	3.46E-05	**10.2454**	7.07E-09
AT4G12400.1	**10.05646**	1.17E-05	**4.944056**	2.96E-05
AT3G12580.1	**10.25667**	1.67E-09	**10.79065**	1.96E-09
AT2G15480.1	**10.28122**	2.20E-07	**6.889241**	2.22E-09
AT1G17180.1	**10.70713**	1.43E-05	**10.23639**	1.41E-06
AT5G12030.1	**10.75734**	1.22E-05	**6.173228**	1.41E-07
AT5G05410.1	**11.28813**	1.22E-06	**7.369798**	8.18E-06
AT1G71520.1	**11.6442**	2.68E-07	**4.371353**	1.10E-05
AT5G51440.1	**12.3364**	2.68E-07	**8.196966**	7.43E-07
AT1G05675.1	**13.07945**	1.48E-05	**6.071382**	1.17E-05
AT3G09350.1	**13.14384**	2.71E-07	**8.328403**	7.58E-08
AT1G07400.1	**13.30268**	1.02E-07	**8.105718**	7.72E-07
AT5G52640.1	**13.52381**	1.32E-07	**13.50072**	5.15E-09
AT3G28740.1	**13.85894**	1.04E-05	**11.92035**	5.34E-08
AT5G22140.1	**14.37659**	1.53E-07	**5.076714**	1.75E-06
AT1G15520.1	**14.41906**	9.99E-07	**15.52504**	6.27E-06
AT1G56240.1	**15.29062**	8.49E-07	**6.382515**	2.84E-06
AT1G56250.1	**16.13107**	5.76E-07	**9.564801**	1.44E-07
AT1G71000.1	**16.65075**	2.20E-07	**13.9477**	3.20E-08
AT1G74310.1	**19.18398**	1.03E-08	**12.75451**	2.32E-08
AT1G53540.1	**21.56254**	1.67E-09	**12.3797**	3.57E-07
AT5G54165.1	**25.09556**	3.84E-08	**7.747576**	4.31E-07
AT1G17170.1	**27.29519**	1.67E-09	**13.3998**	4.67E-08
AT2G29500.1	**36.26485**	1.67E-09	**20.00432**	5.31E-09
AT5G12020.1	**43.87919**	1.22E-08	**14.81298**	5.01E-09

Table S4. Clade III CRF-Dependently Oxidative Stress-Regulated Genes (CDRGs) of SlCRF5

Gene Locus	WT vs WT+H2O2 fc	padj	SlCRF5AS vs SlCRF5AS+H2O2 fc	padj
Solyc07g026650	**-98.417219**	3.10E-49	**-41.896416**	1.98E-05
Solyc09g010860	**-15.637046**	3.49E-10	**-4.9770932**	0.01484891
Solyc10g050990	**-11.556154**	3.42E-09	**-28.87426**	7.87E-16
Solyc01g090760	**-10.244729**	1.30E-04	**-4.2947949**	0.04695771
Solyc05g047530	**-6.6483108**	3.39E-22	**-3.317812**	7.56E-05
Solyc01g087770	**-5.3537875**	2.20E-04	**-12.487301**	1.69E-05
Solyc10g047400	**-4.8718536**	3.15E-03	**-7.5510273**	0.01772721
Solyc01g073810	**-4.5915903**	3.97E-23	**-7.556841**	1.61E-10
Solyc08g075920	**-4.5519596**	8.31E-16	**-7.6321118**	7.08E-15
Solyc08g067330	**-4.1923206**	6.18E-37	**-6.5181117**	3.95E-10
Solyc02g088340	**-4.1485614**	5.05E-17	**-6.226479**	1.17E-15
Solyc07g039420	**-3.7424218**	6.70E-05	**-9.8637477**	0.00319929
Solyc03g113890	**-3.5741536**	3.07E-02	**-13.613106**	0.00369399
Solyc11g010290	**-3.5248981**	1.53E-05	**-5.6155105**	0.01270998
Solyc01g073840	**-3.351545**	2.95E-07	**-7.2450085**	0.00245427
Solyc10g050980	**-3.2474051**	5.12E-03	**-43.902968**	0.00207242
Solyc05g055540	**-3.1595**	1.78E-04	**-6.1768356**	0.00033155
Solyc09g061390	**-3.0296272**	2.15E-02	**-4.7907818**	0.0456557
Solyc02g085910	**-2.9374322**	3.09E-06	**-5.881849**	0.00670567
Solyc01g105430	**-2.8952329**	1.61E-03	**-5.1156122**	0.00131444
Solyc08g066120	**-2.8856918**	4.78E-04	**-5.5885789**	0.00558984
Solyc12g011100	**-2.7431251**	2.32E-02	**-7.9095989**	0.00291375
Solyc06g007580	**-2.5964245**	2.82E-05	**-5.1809392**	4.98E-05
Solyc05g006900	**-2.5914389**	1.22E-04	**-4.6444316**	1.02E-06
Solyc01g096260	**-2.5892607**	7.76E-05	**-3.9506285**	1.57E-06
Solyc05g007510	**-2.5698274**	1.22E-08	**-5.6018392**	3.69E-08
Solyc03g083770	**-2.5597623**	5.57E-05	**-4.6411967**	2.10E-12
Solyc02g063230	**-2.5569947**	7.48E-04	**-5.3525626**	0.00229758
Solyc08g065950	**-2.5547906**	1.70E-04	**-5.7377362**	3.80E-08
Solyc04g071130	**-2.5447625**	4.23E-14	**-4.5317516**	4.38E-06
Solyc10g085160	**-2.4493152**	1.37E-02	**-5.1089563**	0.00290992
Solyc04g071140	**-2.4320165**	3.35E-19	**-5.0520114**	5.38E-15
Solyc11g040040	**-2.4047253**	1.22E-02	**-3.8595398**	0.01905333
Solyc11g066400	**-2.3892151**	1.90E-02	**-4.434897**	0.00063168
Solyc11g011630	**-2.3690307**	3.96E-02	**-6.8164347**	0.01775267
Solyc12g007070	**-2.3673919**	1.56E-03	**-4.0468242**	0.00025445

Solyc07g054780	**-2.3667344**	3.39E-04	**-5.4207182**	1.13E-06
Solyc04g078190	**-2.3145845**	4.65E-06	**-4.2847279**	2.28E-06
Solyc08g067320	**-2.3055764**	6.17E-08	**-3.4709105**	1.60E-06
Solyc06g073080	**-2.2938643**	8.20E-03	**-3.8615414**	0.0331686
Solyc06g007430	**-2.2870732**	3.40E-07	**-3.8872633**	3.18E-06
Solyc08g076970	**-2.2281799**	4.17E-06	**-3.4908255**	0.01151629
Solyc02g078380	**-2.2255923**	8.30E-09	**-3.5919312**	3.67E-06
Solyc02g088470	**-2.202813**	9.70E-03	**-3.71356**	0.03736325
Solyc09g075460	**-2.1589418**	8.66E-05	**-3.384602**	5.43E-06
Solyc02g078230	**-2.1547118**	4.10E-06	**-3.2635037**	0.00015923
Solyc03g095780	**-2.1073492**	1.18E-07	**-3.5507272**	1.14E-06
Solyc02g090680	**-2.0883393**	8.75E-04	**-4.6341482**	0.00025175
Solyc03g026140	**-2.0804293**	3.90E-02	**-4.8366496**	0.00184056
Solyc07g005300	**-2.0714505**	1.46E-03	**-3.6566553**	1.61E-07
Solyc10g078440	**-2.0601223**	2.07E-03	**-3.1706244**	0.0036354
Solyc04g007420	**-2.0594998**	9.17E-03	**-3.1486809**	0.00319278
Solyc01g073800	**-2.0365966**	3.18E-03	**-3.2754034**	0.00353435
Solyc08g077440	**-2.0275158**	1.16E-03	**-3.4640539**	5.47E-09
Solyc11g072970	**-2.0274359**	1.63E-03	**-3.1948823**	0.00606695
Solyc04g007000	**-2.0046598**	1.21E-08	**-3.0915239**	5.01E-07
Solyc10g080610	**-1.9998472**	9.46E-09	**-3.4090188**	3.25E-09
Solyc06g069410	**-1.9345014**	1.44E-06	**-2.9798231**	1.09E-05
Solyc08g061590	**-1.9208892**	8.26E-07	**-3.1266815**	1.23E-05
Solyc03g121250	**-1.9141287**	2.25E-03	**-2.9108419**	0.00318118
Solyc02g080410	**-1.9071476**	7.82E-07	**-2.8839423**	1.72E-06
Solyc07g066330	**-1.8945847**	2.07E-03	**-2.8518266**	0.01147822
Solyc02g077590	**-1.8916156**	9.87E-03	**-3.9723391**	2.87E-07
Solyc03g083720	**-1.8855478**	1.23E-05	**-3.1517401**	3.80E-05
Solyc01g109600	**-1.8673798**	2.50E-02	**-2.8984715**	2.63E-06
Solyc02g090430	**-1.8538411**	2.72E-03	**-3.1652038**	0.00114707
Solyc12g021340	**-1.8523555**	4.64E-03	**-2.7880554**	0.00434132
Solyc11g071620	**-1.8236581**	4.33E-02	**-2.7998761**	0.00379218
Solyc06g073090	**-1.8174295**	1.19E-04	**-2.727985**	2.45E-05
Solyc10g085280	**-1.8171549**	1.23E-02	**-3.0034999**	6.10E-03
Solyc01g108910	**-1.8124407**	8.15E-08	**-3.3355219**	0.00156277
Solyc01g096470	**-1.8024431**	2.50E-02	**-2.8301902**	0.0041797
Solyc02g084230	**-1.786081**	2.69E-05	**-2.7428326**	4.48E-05
Solyc01g107100	**-1.7729867**	5.84E-07	**-2.8472132**	5.69E-07
Solyc10g084350	**-1.7577298**	2.85E-02	**-2.8720953**	0.04813309
Solyc11g027840	**-1.7553028**	1.35E-04	**-2.6753908**	0.00657796

Solyc01g103540	**-1.7547962**	2.80E-08	**-2.8013584**	1.78E-07
Solyc12g009880	**-1.7544517**	8.14E-03	**-3.0467714**	0.00097607
Solyc04g082420	**-1.746573**	8.35E-05	**-3.9153105**	3.02E-07
Solyc11g062130	**-1.7119834**	1.43E-07	**-2.624125**	2.41E-06
Solyc08g065940	**-1.7093636**	1.89E-05	**-2.7763243**	1.21E-05
Solyc09g074930	**-1.7089897**	2.28E-02	**-3.2013413**	5.98E-06
Solyc04g071620	**-1.7019281**	1.40E-06	**-3.0818116**	0.01869779
Solyc04g016190	**-1.6832262**	2.87E-02	**-4.022662**	2.73E-06
Solyc03g044330	**-1.6786165**	6.03E-06	**-2.6479199**	2.92E-06
Solyc04g007180	**-1.6580164**	2.50E-03	**-2.7702846**	3.91E-04
Solyc03g113130	**-1.6574044**	2.00E-02	**-2.6634228**	0.0020738
Solyc05g047420	**-1.6510107**	4.33E-02	**-3.8160343**	0.00027377
Solyc02g083130	**-1.6498267**	2.80E-03	**-2.6553617**	0.00071304
Solyc07g061940	**-1.636335**	2.09E-05	**-3.2852082**	1.42E-07
Solyc06g082010	**-1.6299925**	1.28E-03	**-2.5629728**	7.99E-06
Solyc12g095960	**-1.6266598**	1.58E-04	**-2.5243277**	0.00021269
Solyc12g010900	**-1.6021432**	1.42E-02	**-3.1149511**	0.00315748
Solyc10g085460	**-1.6007199**	1.81E-02	**-2.4026501**	0.00285635
Solyc01g111600	**-1.5861247**	1.27E-04	**-2.4630707**	2.53E-05
Solyc02g071620	**-1.5813666**	7.98E-04	**-2.3872667**	0.00104451
Solyc01g097270	**-1.5786859**	3.25E-05	**-2.9312952**	6.23E-07
Solyc11g005330	**-1.5755884**	2.12E-05	**-2.4795701**	4.71E-06
Solyc11g072810	**-1.5503124**	4.29E-02	**-2.4753065**	0.00686254
Solyc03g031890	**-1.5498463**	1.77E-03	**-2.3992648**	0.00033991
Solyc01g104720	**-1.5391906**	1.11E-02	**-2.8505952**	0.02849715
Solyc02g092140	**-1.5341985**	1.23E-02	**-2.3885561**	0.01618447
Solyc05g048750	**-1.5335167**	3.11E-02	**-2.5029946**	0.00169949
Solyc06g073740	**-1.5317883**	4.65E-02	**-2.369781**	0.00279221
Solyc10g078920	**-1.529706**	8.41E-03	**-2.9483945**	0.00011156
Solyc11g017140	**-1.5272526**	4.13E-02	**-2.3901271**	0.00024726
Solyc06g035450	**-1.5060668**	1.77E-04	**-2.6588914**	6.52E-06
Solyc02g070800	**-1.5055416**	2.57E-02	**-2.3432687**	0.00036456
Solyc03g110910	**-1.5035659**	1.64E-02	**-2.3074592**	0.00116702
Solyc02g063270	**-1.4921508**	4.83E-02	**-2.3947499**	0.00078692
Solyc01g096020	**-1.481626**	4.89E-02	**-2.507298**	0.00106065
Solyc07g063050	**-1.4783096**	2.62E-02	**-2.5749901**	0.00026213
Solyc07g007330	**-1.4527976**	4.79E-02	**-2.3592807**	0.0007815
Solyc09g007540	**-1.4380254**	6.49E-03	**-2.1587328**	0.00076376
Solyc10g086540	**-1.4379076**	5.25E-03	**-2.330597**	0.00026075
Solyc12g007200	**-1.4308272**	3.81E-02	**-2.1565427**	0.01995923

Solyc02g085580	**-1.4275528**	1.57E-02	**-2.2503236**	0.00177882
Solyc03g115940	**-1.4258295**	1.51E-02	**-2.207151**	0.00306329
Solyc08g067950	**-1.4247058**	2.06E-02	**-2.2397433**	0.00962346
Solyc11g069090	**-1.4196978**	1.62E-03	**-2.3009417**	9.16E-05
Solyc03g031720	**-1.4196148**	1.03E-02	**-2.1526268**	0.00278756
Solyc10g079370	**-1.4143875**	3.53E-02	**-2.1707436**	0.00071896
Solyc01g079350	**-1.4097625**	3.46E-02	**-2.1321751**	0.00613544
Solyc05g012580	**-1.4082252**	2.72E-03	**-2.6208826**	0.00035796
Solyc08g007990	**-1.3951862**	2.84E-02	**-2.225371**	0.00110241
Solyc12g008370	**-1.3885464**	2.60E-02	**-2.1396078**	0.00147219
Solyc12g035130	**-1.3598058**	1.61E-02	**-2.2111792**	0.00010015
Solyc12g006550	**-1.3552305**	3.93E-02	**-2.1611182**	0.00312395
Solyc01g108500	**-1.33907**	1.56E-02	**-2.0387506**	0.00100044
Solyc12g009960	**-1.3390328**	3.07E-02	**-2.0140674**	0.00165922
Solyc11g006460	**-1.3145774**	4.34E-02	**-1.9933894**	0.00058854

Table S5. Clade III CRF-Dependently Oxidative Stress-Regulated Genes (CDRGs) of AtCRF5. All fold changes are statistically significant

At Number	name	FC Col vs. Col + H_2O_2	FC *Atcrf5* vs *Atcrf5* + H_2O_2
AT5G59550.2	.	3.57116068	-16.153066
AT4G21870.1	HSP15.4	2.15257613	-10.496815
AT4G08950.1	EXO	1.96861496	-7.979055
AT2G10940.1	.	2.42112898	-6.0475683
AT3G06070.1	.	1.64672511	-3.8645254
AT3G17390.1	METK4	1.91756472	-2.3168255
AT1G04430.1	.	1.93354035	-1.915571
AT5G03030.1	.	3.52135371	1.41009099
AT1G14200.1	.	7.14957495	1.7521033
AT1G26920.1	.	-2.4040274	1.8053323
AT5G39610.1	NAC92	-3.0521108	2.07233213
AT4G19700.1	BOI	-1.8201274	2.08925238
AT2G42790.1	CSY3	-1.689335	2.1365182
AT2G40080.1	ELF4	-4.9191975	2.22737188
AT3G07090.1	.	5.91347988	2.36111989
AT1G13930.1	.	-4.0593761	2.39873167
AT2G05070.1	LHCB2.2	5.73813602	2.75729304
AT4G34131.1	UGT73B3	9.51739686	2.77756451
AT3G16530.1	.	7.52339498	2.89589211
AT5G58070.1	TIL	6.14892832	2.8961631
AT3G08590.2	.	6.16394266	2.91447807
AT4G21920.1	.	8.22623889	3.08267144
AT3G15356.1	LEC	8.74176817	3.12082492
AT5G64750.1	ABR1	7.49960662	3.25113154
AT2G05100.1	LHCB2.1	9.44222814	3.36776198
AT4G26080.1	ABI1	-1.479499	3.45684174
AT2G15480.1	UGT73B5	14.7128055	3.5022327
AT1G21520.1	.	-2.8708879	3.65755658
AT2G20560.1	.	32.8638727	4.24380689
AT3G09350.1	Fes1A	23.9130573	4.62687662
AT5G54165.1	.	44.2195182	9.03749719
AT4G31580.2	RSZ22	-22.534067	-38.628249
AT3G03670.1	PER28	-21.888547	-70.335666
AT1G49570.1	PER10	-19.79984	-54.134287
AT2G30670.1	.	-14.24961	-29.263682

AT5G22555.1	.	-10.744485	-46.721056
AT1G26240.1	.	-10.146069	-43.050602
AT1G52120.1	JAL12	-9.4085453	-20.456931
AT4G11290.1	PER39	-9.0407042	-15.331307
AT4G13890.1	SHM5	-8.627148	-21.57666
AT2G21045.1	HAC1	-7.8778632	-15.567709
AT5G41290.1	CRRSP58	-5.7345707	-18.912336
AT1G36060.1	ERF055	-5.1951263	-9.0300191
AT5G41300.1	CRRSP59	-5.1113137	-11.915701
AT1G08090.1	NRT2.1	-4.6067521	-12.958706
AT4G16240.1	.	-4.3495494	-9.1538583
AT5G55450.1	.	-4.1737781	-8.0651247
AT1G62770.1	PMEI9	-3.3307742	-5.8995728
AT5G58570.1	.	-3.0579579	-6.9317022
AT4G34810.1	.	-2.9799666	-17.420868
AT4G36430.1	PER49	-2.9538976	-22.687819
AT1G49660.1	CXE5	-2.7601405	-4.1632779
AT1G14210.1	.	-2.7074903	-6.1611655
AT5G57760.1	.	-2.6194176	-23.205162
AT3G23150.1	ETR2	-2.2650411	-3.7596438
AT5G25460.1	.	-2.2517385	-4.1364477
AT1G20693.1	HMGB2	-2.1428151	-7.8610421
AT4G28270.1	RMA2	-2.0537552	-3.301408
AT1G24880.2	.	-1.9766551	-3.5981476
AT1G20693.3	HMGB2	-1.9542857	-8.9807921
AT1G20900.1	AHL27	-1.9365083	-4.6016048
AT1G20693.2	HMGB2	-1.9336791	-7.9606639
AT1G49600.1	ATRBP47A	-1.8997761	-4.1108429
AT2G28720.1	.	-1.8249161	-3.4534161
AT4G08035.1	.	-1.7685669	-3.5635884
AT3G11780.1	.	-1.7316293	-5.2052174
AT1G05720.1	.	-1.6039893	-2.4937964
AT4G16450.1	.	-1.5831715	-2.8614928
AT3G54366.1	.	-1.5612081	-3.4725433
AT5G03730.1	CTR1	-1.5551377	-2.5750363
AT5G65670.1	IAA9	-1.5476982	-2.3382455
AT5G07580.1	ERF106	-1.4559748	-6.3831582
AT3G53670.1	.	-1.4554498	-2.1927965
AT2G25310.1	.	-1.4179713	-2.7189212
AT2G46490.1	.	-1.3718195	-2.2778207

AT3G48140.1	.	-1.3592036	-2.9642452
AT4G17245.1	.	1.44924269	2.61288501
AT2G43820.1	UGT74F2	1.5067065	8.184118
AT5G20900.1	TIFY3B	1.52404306	2.98672761
AT1G42990.1	BZIP60	1.56998472	3.37574191
AT3G60690.1	.	1.59923438	3.43553044
AT4G25670.1	.	1.6798573	3.72765554
AT1G72450.1	TIFY11B	1.8637611	4.3147218
AT5G54940.2	.	1.89473814	3.84614665
AT1G28190.1	.	1.96124295	6.82238106
AT2G38210.1	PDX1L4	1.98359563	4.30626297
AT5G04760.1	.	1.99227452	4.65323927
AT1G30320.1	.	2.0677013	4.0517827
AT4G22690.1	CYP706A1	2.12701805	3.87679273
AT4G01070.1	UGT72B1	2.17671101	3.3591702
AT4G01026.1	PYL7	2.34538221	6.85639799
AT5G39050.1	PMAT1	2.36291754	5.66578982
AT3G55970.1	JRG21	2.45555166	13.4358915
AT1G69870.1	NPF2.13	2.48267673	4.52374257
AT5G54170.1	.	2.53077398	6.02621497
AT4G27520.1	ENODL2	2.54570385	4.98517074
AT1G09310.1	.	2.70158364	4.67769487
AT1G21010.1	.	2.71247435	4.82392793
AT1G72900.1	.	2.71767318	4.50440866
AT3G56880.1	.	2.81081053	5.07523399
AT2G03760.1	SOT12	2.88688731	13.4686678
AT5G60800.1	.	3.03957735	9.23179704
AT1G23710.1	.	3.21729324	7.31986051
AT1G61890.1	DTX37	3.25460553	9.58652077
AT4G39670.1	.	3.45002781	8.88921807
AT2G40000.1	HSPRO2	3.66250778	5.51923254
AT2G29460.1	GSTU4	3.73045269	16.9771337
AT5G65300.1	.	3.82237999	10.6765903
AT5G57510.1	.	3.85771562	10.2200062
AT2G43520.1	ATTI2	3.96863246	6.04121253
AT4G24110.1	.	4.02989546	6.121489
AT5G54300.1	.	4.26730703	6.98049604
AT1G05562.1	.	4.30162955	25.5371171
AT1G05560.2	UGT1	4.30162955	25.5369155
AT4G29780.1	.	4.35685791	12.1857536

AT1G05560.1	UGT1	4.36624177	26.1190035
AT2G37970.1	SOUL-1	4.38693369	11.4168882
AT4G15630.1	.	4.5173292	9.78014004
AT1G28480.1	GRXC9	4.60379064	7.97552733
AT1G77450.1	NAC032	4.62178268	8.15638464
AT5G64310.1	AGP1	4.84825825	17.3388368
AT1G44350.1	ILL6	4.89351487	14.07725
AT3G25780.1	AOC3	5.03273813	10.0320085
AT1G80840.1	WRKY40	5.04984744	9.20749125
AT1G67920.1	.	5.09486858	12.4670524
AT3G19615.1	.	5.61204456	8.44291334
AT3G22370.1	AOX1A	5.685871	8.99865418
AT5G64230.1	.	5.9114601	9.93688038
AT4G17090.1	BAM3	6.35576783	12.2754701
AT3G26830.1	CYP71B15	6.45288359	29.4380012
AT1G26380.1	FOX1	6.8446253	13.8550953
AT3G28220.1	.	8.68652835	17.232205
AT2G29450.1	GSTU5	8.83964835	13.9601394
AT3G49620.1	DIN11	10.004486	89.4826348
AT5G52310.1	RD29A	10.8478064	18.5000835
AT3G44860.1	FAMT	11.8591301	67.9085097
AT5G05410.2	DREB2A	44.2709844	228.129622

Table S6. Clade III CRF-Dependently Oxidative Stress-Regulated Genes (CDRGs) of AtCRF6

Gene locus and name	**Col vs Col+H2O2**		**crf6 vs crf6+H2O2**	
AT1G08090	**-11.439563**	3.07E-06	**-5.411806**	5.51E-07
AT1G49860	**-10.780036**	3.34E-07	**-4.8989758**	0.00077849
AT1G26250	**-9.7530622**	1.36E-07	**-4.5462605**	3.24E-06
AT5G19890	**-7.7363094**	7.23E-06	**-2.5611913**	0.0010409
AT2G46750	**-5.649743**	1.44E-05	**-2.6400584**	0.00091789
AT5G43520	**-4.9415709**	6.55E-05	**-2.3254343**	0.02319035
AT1G12040	**-4.7252637**	6.59E-05	**-2.0824544**	0.03706526
AT1G47600	**-4.3567119**	0.00121996	**-10.367276**	5.34E-08
AT4G32950	**-4.2254211**	0.00016835	**-10.266909**	4.91E-08
AT5G66690	**-3.7844928**	0.00705608	**-6.7106618**	4.66E-06
AT2G32660	**-3.2879422**	0.00716705	**-5.2002107**	3.89E-05
AT3G16440	**-2.7659304**	0.00934758	**-4.4632058**	3.68E-05
AT5G14650	**-2.713839**	0.03655819	**-6.1216482**	4.95E-08
AT5G48290	**-2.654316**	0.02338015	**-4.3738849**	0.00022543
AT1G29020	**-2.41471**	0.0352376	**-4.0644921**	5.47E-05
AT2G30210	**-2.3799313**	0.02279122	**-3.5933635**	4.90E-06
AT5G12020	**43.87919**	1.22E-08	**14.81298**	5.01E-09
AT1G17170	**27.29519**	1.67E-09	**13.3998**	4.67E-08
AT5G54165	**25.09556**	3.84E-08	**7.747576**	4.31E-07
AT1G56240	**15.29062**	8.49E-07	**6.382515**	2.84E-06
AT5G22140	**14.37659**	1.53E-07	**5.076714**	1.75E-06
AT1G05675	**13.07945**	1.48E-05	**6.071382**	1.17E-05
AT1G71520	**11.6442**	2.68E-07	**4.371353**	1.10E-05
AT4G12400	**10.05646**	1.17E-05	**4.944056**	2.96E-05
AT1G66570	**9.843525**	2.23E-05	**3.322939**	0.03674477
AT2G44460	**8.917133**	1.25E-05	**15.26071**	3.21E-05
AT1G05680	**8.846642**	2.00E-06	**3.199785**	0.00269403
AT1G54050	**8.376456**	2.40E-07	**3.16354**	0.00024535
AT4G08555	**8.308828**	0.00010659	**2.763124**	0.00142484
AT1G76600	**8.184419**	2.77E-06	**4.02103**	5.62E-05
AT4G34131	**6.368969**	9.35E-05	**2.706597**	0.00229318
AT3G56710	**6.166492**	0.00320311	**2.651098**	0.00274776
AT1G69930	**5.675018**	0.00185595	**8.612398**	4.03E-06
AT1G59860	**5.622883**	7.64E-05	**2.707619**	0.00165626
AT3G46080	**5.347057**	0.00051112	**2.665867**	0.00068931
AT2G42540	**5.022724**	4.74E-06	**1.738225**	0.00074067
AT4G14400	**4.840698**	2.60E-06	**2.130615**	0.04611462

AT5G24110	**4.708818**	0.00170942	**2.265257**	0.02994424
AT3G26830	**4.590766**	7.76E-05	**10.4667**	2.30E-07
AT1G69920	**3.921403**	0.00073233	**6.536077**	1.41E-07
AT4G21680	**3.913122**	0.00012278	**11.35067**	7.07E-09
AT3G16530	**3.516171**	0.00010355	**6.994907**	2.91E-08
AT3G09405	**3.361826**	0.00123931	**5.792897**	1.70E-07
AT1G02850	**3.325658**	0.00022707	**5.971983**	1.08E-06
AT5G64750	**3.17525**	0.0012018	**5.538288**	3.08E-06
AT5G52050	**2.974722**	0.01407075	**4.57896**	2.25E-05
AT3G15356	**2.829829**	0.00202489	**7.371509**	3.63E-08
AT4G17490	**2.688488**	0.04603722	**5.439975**	4.03E-05
AT1G02930	**2.665498**	0.00638122	**4.504385**	4.57E-07
AT2G15780	**2.645105**	0.03069222	**4.010327**	1.34E-05
AT4G33930	**2.514985**	0.0040627	**5.22429**	5.59E-06
AT1G15415	**2.358648**	0.00995543	**3.813802**	0.00016953
AT2G04040	**2.310132**	0.009801	**7.453174**	9.49E-07
AT4G02520	**1.943255**	0.00408112	**3.023721**	5.97E-07

Table S7. GO term enrichment analysis of SlCRF5 CDRGs

Analysis Type:	PANTHER Overrepresentation Test (Released 20200728)	
Annotation Version and Release Date:	GO Ontology database DOI: 10.5281	zenodo.3954044 Released 2020-07-16
Analyzed List:	Client Text Box Input (Solanum lycopersicum)	
Reference List:	Solanum lycopersicum (all genes in database)	
Test Type:	FISHER	
Correction:	FDR	

GO biological process complete	#in Ref. list	#in input (126)	Expe -cted	over/ under	Fold Enrich -ment	Pval (raw)	FDR
response to wounding (GO:0009611)	16	5	0.16	+	30.32	1.91E-06	3.43E-03
protein complex oligomerization (GO:0051259)	17	5	0.18	+	28.54	2.45E-06	2.94E-03
regulation of jasmonic acid mediated signaling pathway (GO:2000022)	19	5	0.2	+	25.53	3.89E-06	2.80E-03
response to hydrogen peroxide (GO:0042542)	21	5	0.22	+	23.1	5.93E-06	3.55E-03
response to salt stress (GO:0009651)	21	5	0.22	+	23.1	5.93E-06	3.04E-03
response to osmotic stress (GO:0006970)	22	5	0.23	+	22.05	7.21E-06	3.24E-03
regulation of defense response (GO:0031347)	23	5	0.24	+	21.09	8.71E-06	3.47E-03
response to reactive oxygen species (GO:0000302)	42	6	0.43	+	13.86	9.24E-06	3.32E-03
response to heat (GO:0009408)	45	6	0.46	+	12.94	1.32E-05	4.32E-03
regulation of response to stress (GO:0080134)	47	5	0.48	+	10.32	1.88E-04	3.38E-02
response to temperature stimulus (GO:0009266)	60	6	0.62	+	9.7	5.87E-05	1.40E-02
regulation of signal transduction (GO:0009966)	51	5	0.53	+	9.51	2.68E-04	4.58E-02
steroid metabolic process (GO:0008202)	72	7	0.74	+	9.43	1.67E-05	4.63E-03

regulation of cell communication (GO:0010646)	52	5	0.54	+	9.33	2.91E-04	4.75E-02
regulation of signaling (GO:0023051)	52	5	0.54	+	9.33	2.91E-04	4.55E-02
response to oxidative stress (GO:0006979)	65	6	0.67	+	8.96	8.86E-05	1.99E-02
sterol metabolic process (GO:0016125)	66	6	0.68	+	8.82	9.58E-05	2.02E-02
response to inorganic substance (GO:0010035)	83	7	0.86	+	8.18	3.92E-05	1.01E-02
response to abiotic stimulus (GO:0009628)	214	10	2.21	+	4.53	1.12E-04	2.24E-02
response to oxygen-containing compound (GO:1901700)	219	10	2.26	+	4.43	1.34E-04	2.54E-02
response to chemical (GO:0042221)	424	16	4.37	+	3.66	1.42E-05	4.26E-03
response to stress (GO:0006950)	665	22	6.85	+	3.21	2.87E-06	2.58E-03
response to stimulus (GO:0050896)	1270	34	13.09	+	2.6	6.71E-07	2.41E-03

Table S8. GO term enrichment analysis of AtCRF5 CDRGs

Analysis Type:	PANTHER Overrepresentation Test (Released 20200728)	
Annotation Version and Release Date:	GO Ontology database DOI: 10.5281	zenodo.4033054 Released 2020-09-10
Analyzed List:	Client Text Box Input (Arabidopsis thaliana)	There are duplicate IDs in the file. The unique set of IDs will be used.
Reference List:	Arabidopsis thaliana (all genes in database)	
Test Type:	FISHER	
Correction:	FDR	

GO biological process complete	#in Ref. list	#in input (126)	Expe -cted	over/ under -	Fold Enrich -ment	Pval (raw)	FDR
response to salt (GO:1902074)	24	4	0.11	+	36.26	7.85E-06	2.61E-03
response to desiccation (GO:0009269)	24	3	0.11	+	27.2	2.52E-04	3.77E-02
cellular response to hypoxia (GO:0071456)	235	15	1.08	+	13.89	6.45E-13	4.83E-10
cellular response to oxygen levels (GO:0071453)	237	15	1.09	+	13.77	7.24E-13	4.81E-10
cellular response to decreased oxygen levels (GO:0036294)	237	15	1.09	+	13.77	7.24E-13	4.33E-10
response to hypoxia (GO:0001666)	261	16	1.2	+	13.34	1.88E-13	2.82E-10
response to decreased oxygen levels (GO:0036293)	265	16	1.22	+	13.14	2.35E-13	2.34E-10
response to oxygen levels (GO:0070482)	266	16	1.22	+	13.09	2.48E-13	2.12E-10
response to salicylic acid (GO:0009751)	155	7	0.71	+	9.83	1.00E-05	3.01E-03
regulation of immune system process (GO:0002682)	122	5	0.56	+	8.92	3.01E-04	4.29E-02
regulation of response to biotic stimulus (GO:0002831)	175	6	0.8	+	7.46	1.90E-04	2.99E-02
regulation of response to external stimulus (GO:0032101)	180	6	0.83	+	7.25	2.20E-04	3.38E-02

response to wounding (GO:0009611)	216	7	0.99	+	7.05	7.75E-05	1.33E-02
regulation of defense response (GO:0031347)	255	8	1.17	+	6.83	2.96E-05	6.10E-03
response to organic cyclic compound (GO:0014070)	280	8	1.29	+	6.22	5.61E-05	1.02E-02
response to fungus (GO:0009620)	347	9	1.59	+	5.64	3.98E-05	7.67E-03
cellular response to chemical stimulus (GO:0070887)	1080	27	4.96	+	5.44	7.76E-13	4.22E-10
response to water (GO:0009415)	363	9	1.67	+	5.39	5.58E-05	1.04E-02
response to oxidative stress (GO:0006979)	455	11	2.09	+	5.26	1.02E-05	2.92E-03
regulation of response to stress (GO:0080134)	387	9	1.78	+	5.06	8.99E-05	1.49E-02
response to acid chemical (GO:0001101)	395	9	1.82	+	4.96	1.05E-04	1.69E-02
response to water deprivation (GO:0009414)	354	8	1.63	+	4.92	2.69E-04	3.93E-02
response to abscisic acid (GO:0009737)	496	11	2.28	+	4.83	2.23E-05	4.95E-03
response to alcohol (GO:0097305)	500	11	2.3	+	4.79	2.40E-05	5.13E-03
response to oxygen-containing compound (GO:1901700)	1504	30	6.91	+	4.34	8.91E-12	4.44E-09
response to temperature stimulus (GO:0009266)	615	12	2.83	+	4.25	3.21E-05	6.40E-03
response to lipid (GO:0033993)	670	13	3.08	+	4.22	1.57E-05	3.76E-03
response to chemical (GO:0042221)	2674	51	12.29	+	4.15	1.27E-19	3.81E-16
regulation of response to stimulus (GO:0048583)	736	14	3.38	+	4.14	9.04E-06	2.85E-03
response to hormone (GO:0009725)	1237	23	5.69	+	4.05	1.28E-08	5.48E-06
response to organic substance (GO:0010033)	1699	31	7.81	+	3.97	3.42E-11	1.58E-08
response to endogenous stimulus (GO:0009719)	1267	23	5.82	+	3.95	1.98E-08	7.89E-06
cellular response to stress (GO:0033554)	1118	20	5.14	+	3.89	2.36E-07	8.31E-05
response to abiotic stimulus (GO:0009628)	2126	38	9.77	+	3.89	1.94E-13	2.32E-10

response to external biotic stimulus (GO:0043207)	1092	17	5.02	+	3.39	1.26E-05	3.42E-03
response to other organism (GO:0051707)	1092	17	5.02	+	3.39	1.26E-05	3.27E-03
response to biotic stimulus (GO:0009607)	1093	17	5.02	+	3.38	1.27E-05	3.17E-03
response to stress (GO:0006950)	3089	47	14.2	+	3.31	3.41E-14	6.81E-11
interspecies interaction between organisms (GO:0044419)	1120	17	5.15	+	3.3	1.73E-05	3.99E-03
response to inorganic substance (GO:0010035)	908	13	4.17	+	3.12	3.15E-04	4.29E-02
response to stimulus (GO:0050896)	5562	73	25.56	+	2.86	3.17E-20	1.90E-16
cellular response to stimulus (GO:0051716)	2515	33	11.56	+	2.86	2.72E-08	1.02E-05
response to external stimulus (GO:0009605)	1509	19	6.94	+	2.74	6.70E-05	1.18E-02
macromolecule metabolic process (GO:0043170)	5483	10	25.2	-	0.4	3.05E-04	4.24E-02

Table S9. GO term enrichment analysis of AtCRF6 CDRGs

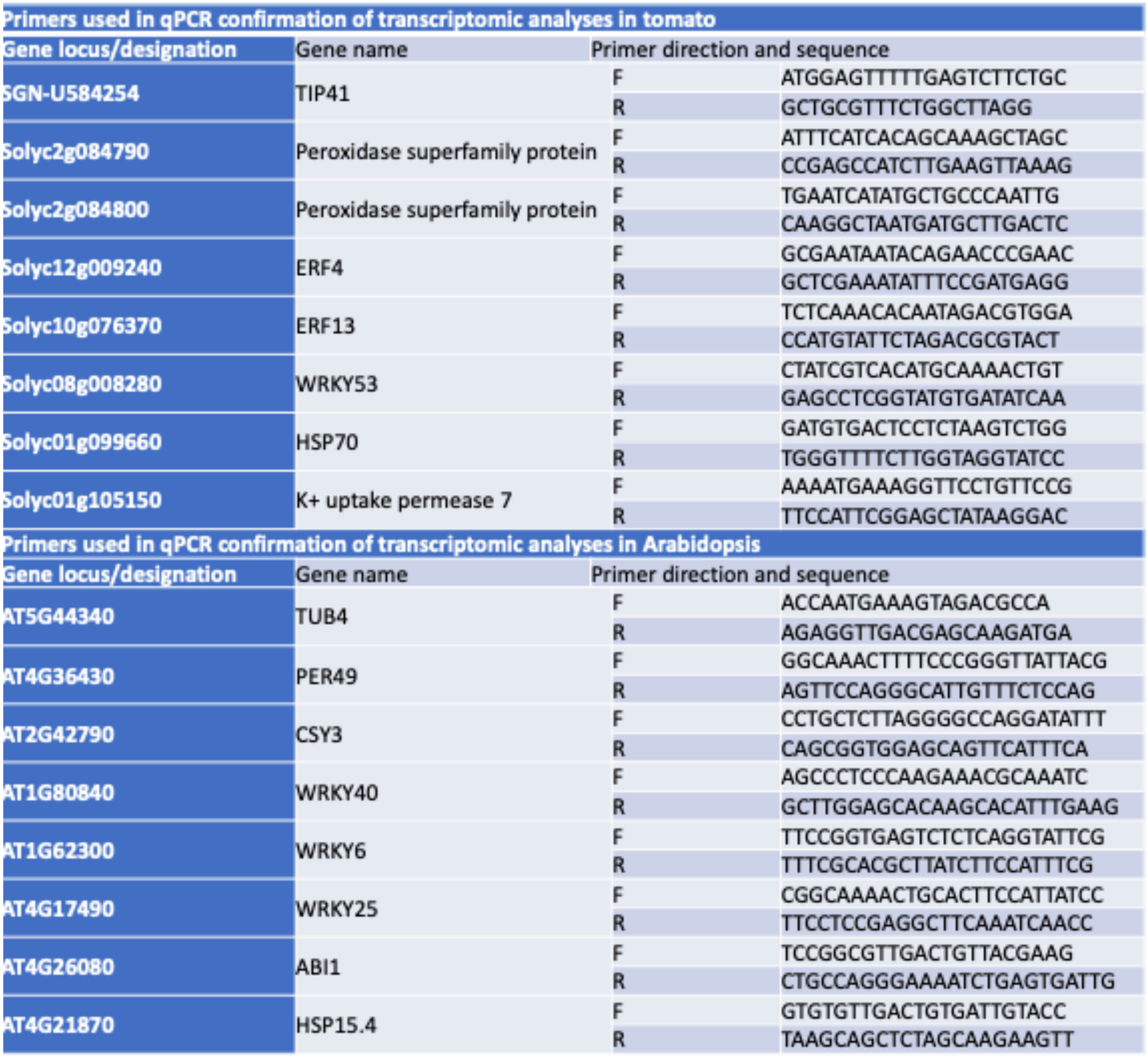
Analysis Type:	PANTHER Overrepresentation Test (Released 20200728)
Annotation Version and Release Date:	GO Ontology database DOI: 10.5281 zenodo.3954044 Released 2020-07-16
Analyzed List:	Client Text Box Input (Arabidopsis thaliana)
Reference List:	Arabidopsis thaliana (all genes in database)
Test Type:	FISHER
Correction:	FDR

GO biological process complete	#in Ref. list	#in input (75)	Expe -cted	over/ under	Fold Enrich -ment	Pval (raw)	FDR
toxin catabolic process (GO:0009407)	46	6	0.13	+	47.68	6.20E-09	9.27E-06
toxin metabolic process (GO:0009404)	59	7	0.16	+	43.37	5.78E-10	3.46E-06
response to hydrogen peroxide (GO:0042542)	70	6	0.19	+	31.33	6.32E-08	3.44E-05
detoxification (GO:0098754)	100	7	0.27	+	25.59	1.77E-08	1.77E-05
glutathione metabolic process (GO:0006749)	44	3	0.12	+	24.92	2.90E-04	4.82E-02
defense response to bacterium, incompatible interaction (GO:0009816)	44	3	0.12	+	24.92	2.90E-04	4.69E-02
response to toxic substance (GO:0009636)	120	7	0.33	+	21.32	5.81E-08	3.48E-05
response to reactive oxygen species (GO:0000302)	155	8	0.42	+	18.87	1.55E-08	1.85E-05
response to chitin (GO:0010200)	139	5	0.38	+	13.15	4.73E-05	1.29E-02
secondary metabolic process (GO:0019748)	302	9	0.83	+	10.89	1.76E-07	8.12E-05
defense response, incompatible interaction (GO:0009814)	181	5	0.5	+	10.1	1.58E-04	2.78E-02
response to oxidative stress (GO:0006979)	455	12	1.24	+	9.64	4.98E-09	9.93E-06
response to nitrogen compound (GO:1901698)	306	8	0.84	+	9.56	2.30E-06	7.65E-04
cellular response to hypoxia (GO:0071456)	235	6	0.64	+	9.33	5.18E-05	1.29E-02
cellular response to oxygen levels (GO:0071453)	237	6	0.65	+	9.25	5.42E-05	1.30E-02

cellular response to decreased oxygen levels (GO:0036294)	237	6	0.65	+	9.25	5.42E-05	1.25E-02
defense response to fungus (GO:0050832)	250	6	0.68	+	8.77	7.23E-05	1.55E-02
response to hypoxia (GO:0001666)	261	6	0.71	+	8.4	9.12E-05	1.82E-02
response to decreased oxygen levels (GO:0036293)	265	6	0.72	+	8.28	9.89E-05	1.91E-02
response to oxygen levels (GO:0070482)	266	6	0.73	+	8.25	1.01E-04	1.89E-02
response to fungus (GO:0009620)	347	7	0.95	+	7.37	5.18E-05	1.35E-02
defense response to bacterium (GO:0042742)	413	7	1.13	+	6.2	1.50E-04	2.72E-02
response to bacterium (GO:0009617)	506	8	1.38	+	5.78	7.96E-05	1.64E-02
response to external biotic stimulus (GO:0043207)	1092	15	2.99	+	5.02	2.55E-07	1.09E-04
response to other organism (GO:0051707)	1092	15	2.99	+	5.02	2.55E-07	1.02E-04
response to biotic stimulus (GO:0009607)	1093	15	2.99	+	5.02	2.58E-07	9.66E-05
defense response to other organism (GO:0098542)	805	11	2.2	+	5	1.28E-05	3.64E-03
interspecies interaction between organisms (GO:0044419)	1120	15	3.06	+	4.9	3.51E-07	1.24E-04
response to inorganic substance (GO:0010035)	908	12	2.48	+	4.83	6.90E-06	2.17E-03
response to oxygen-containing compound (GO:1901700)	1511	19	4.13	+	4.6	1.88E-08	1.61E-05
cellular response to chemical stimulus (GO:0070887)	1088	13	2.98	+	4.37	8.01E-06	2.40E-03
response to external stimulus (GO:0009605)	1508	18	4.13	+	4.36	1.05E-07	5.23E-05
defense response (GO:0006952)	952	11	2.6	+	4.22	5.81E-05	1.29E-02
response to chemical (GO:0042221)	2682	27	7.34	+	3.68	9.65E-10	2.89E-06
response to stress (GO:0006950)	3090	27	8.45	+	3.19	2.03E-08	1.52E-05

response to abiotic stimulus (GO:0009628)	2126	16	5.82	+	2.75	1.80E-04	3.07E-02
response to stimulus (GO:0050896)	5567	37	15.23	+	2.43	2.10E-08	1.40E-05

Table S10. Primers used in qRT-PCR confirmation of transcritomic data.



Primers used in qPCR confirmation of transcriptomic analyses in tomato			
Gene locus/designation	Gene name	Primer direction and sequence	
SGN-U584254	TIP41	F	ATGGAGTTTTTGAGTCTTCTGC
		R	GCTGCGTTTCTGGCTTAGG
Solyc2g084790	Peroxidase superfamily protein	F	ATTTCATCACAGCAAAGCTAGC
		R	CCGAGCCATCTTGAAGTTAAAG
Solyc2g084800	Peroxidase superfamily protein	F	TGAATCATATGCTGCCCAATTG
		R	CAAGGCTAATGATGCTTGACTC
Solyc12g009240	ERF4	F	GCGAATAATACAGAACCCGAAC
		R	GCTCGAAATATTTCCGATGAGG
Solyc10g076370	ERF13	F	TCTCAAACACAATAGACGTGGA
		R	CCATGTATTCTAGACGCGTACT
Solyc08g008280	WRKY53	F	CTATCGTCACATGCAAAACTGT
		R	GAGCCTCGGTATGTGATATCAA
Solyc01g099660	HSP70	F	GATGTGACTCCTCTAAGTCTGG
		R	TGGGTTTTCTTGGTAGGTATCC
Solyc01g105150	K+ uptake permease 7	F	AAAATGAAAGGTTCCTGTTCCG
		R	TTCCATTCGGAGCTATAAGGAC
Primers used in qPCR confirmation of transcriptomic analyses in Arabidopsis			
Gene locus/designation	Gene name	Primer direction and sequence	
AT5G44340	TUB4	F	ACCAATGAAAGTAGACGCCA
		R	AGAGGTTGACGAGCAAGATGA
AT4G36430	PER49	F	GGCAAACTTTTCCCGGGTTATTACG
		R	AGTTCCAGGGCATTGTTTCTCCAG
AT2G42790	CSY3	F	CCTGCTCTTAGGGGCCAGGATATTT
		R	CAGCGGTGGAGCAGTTCATTTCA
AT1G80840	WRKY40	F	AGCCCTCCCAAGAAACGCAAATC
		R	GCTTGGAGCACAAGCACATTTGAAG
AT1G62300	WRKY6	F	TTCCGGTGAGTCTCTCAGGTATTCG
		R	TTTCGCACGCTTATCTTCCATTTCG
AT4G17490	WRKY25	F	CGGCAAAACTGCACTTCCATTATCC
		R	TTCCTCCGAGGCTTCAAATCAACC
AT4G26080	ABI1	F	TCCGGCGTTGACTGTTACGAAG
		R	CTGCCAGGGAAAATCTGAGTGATTG
AT4G21870	HSP15.4	F	GTGTGTTGACTGTGATTGTACC
		R	TAAGCAGCTCTAGCAAGAAGTT