# CIRCADIAN REGULATION AND NATURAL VARIATION OF LOW TEMPERATURE SIGNALING IN *ARABIDOPSIS*

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## ABSTRACT

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Many plants increase in freezing tolerance in response to low non-freezing temperature through a process known as cold-acclimation. In *Arabidopsis*, cold acclimation is associated with the induction or repression of over a thousand genes. The *CBF* cold response pathway has a central role in these changes. Within minutes of transfer to low temperature, genes encoding three closely related transcription factors, *CBF1-3*, are induced and alter expression of more than one hundred target genes, which go on to impart freezing tolerance. An abiotic stress such as freezing can limit the productivity and relative fitness of a plant. Consequently, there is considerable interest in finding upstream regulators of the *CBF* pathway in hopes of expanding the geographical range and yield of important food and biofuel crops. Previous studies have shown that *CBF1-3* are subject to circadian regulation and that cold induction of *CBF1-3* is gated by the circadian clock. We identify specific clock components involved in the circadian oscillations, and thus, upstream regulation of *CBF* genes. We also demonstrate the involvement of these identified clock components in gating cold-regulated expression of *CBF1-3* and CBF-target-genes. Furthermore, we show that these clock components affect plant freezing tolerance.

Investigating natural variation of cold response pathways in ecotypes of *Arabidopsis* provides another means of distinguishing genes important for freezing

tolerance. In previous studies, two *Arabidopsis* populations collected from Sweden (SW) and Italy (IT) were tested for fitness (survival and seed set) in reciprocal transplant experiments. Reciprocal transplant experiments revealed that home accessions at both sites had a strong advantage in terms of seed-set and survival. SW and IT recombinant inbred lines (RILs) were used to define fitness QTL in both locations. Since there is substantial variation in temperature across latitudes, genes associated with freezing tolerance may potentially underlie identified fitness QTL. This study shows that there are differences in the cold-acclimated freezing tolerance of SW and IT ecotypes under laboratory conditions. Through RNA-seq experiments, a set of genes that may contribute to differences in freezing tolerance between SW and IT is defined. RILs are used to map expression QTL (eQTL) for a subset of these low-temperature associated genes. Some of the eQTL mapped for these low-temperature associated genes overlap with previously identified fitness QTL and this study offers hypotheses as to the genes underlying these eQTL.

This dissertation is dedicated to all of my family, but particularly to my parents, Jim and Gail, and my new parents John and Sara for their encouragement, to my undergraduate advisor J. Gary Tallman for his role in sparking my enthusiasm for scientific research, and especially to my husband Jackson Gehan for his support and the tent-cot.

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## PREFACE

In Chapter Two, *cca1-1*, and the restored *cca1-1 CCA1p:CCA1-GFP* lines were procured by Eva Farre and generously donated by Jose Pruneda-Paz of the Kay Lab (San Diego, California). Other T-DNA mutant lines, used in Chapters Two and Four, were obtained from the Arabidopsis Biological Resource Center unless otherwise specified. In Chapter Three, the Schemske and Agren labs conducted reciprocal transplant experiments with the Swedish (SW) and Italian (IT) ecotypes and provided data for fitness QTL. Recombinant inbred lines (RILs) were generated and genotyped by members of the Schemske Lab. Avery Mendelsen and Nicolas Batora aided in sterilization, planting and transplanting of RILs used in eQTL analysis. SW and IT versions of *CBF2* were sequenced by Chin-Mei Lee. Alignment and assembly of SW and IT RNA-seq data to the Columbia-0 (COL-0) genome was performed by Pingsha Hu.

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## KEY TO ABBREVIATIONS

| | |
|---|---|
| ABA | ABSCISIC ACID |
| ACT | ACTIN |
| AP2 | APETALA2 |
| BOA | BROTHER OF LUX ARRHYTHMO |
| BP | BASE PAIR |
| CAMTA | CALMODULIN-BINDING TRANSCRIPTIONAL ACTIVATOR |
| CBF | C-REPEAT BINDING FACTOR |
| CBS | CCA1 BINDING SITE |
| CCA1 | CIRCADIAN CLOCK ASSOCIATED 1 |
| CHE | CCA1 HIKING EXPEDITION |
| CHIP | CHROMATIN IMMUNOPRECIPATION |
| COR | COLD-RESPONSIVE GENE |
| COS | COLD-STANDARD GENE |
| CRT | C-REPEAT |
| CVI | CAPE VERDE ISLANDS |
| DAVID | DATABASE FOR ANNOTATION VISUALIZATION AND INTEGRATED DISCOVERY |
| DGDG | DI-GALACTOSYLDIACYLGLYCEROL |
| DRE | DROUGHT RESPONSE ELEMENT |
| DREB | DEHYDRATION RESPONSIVE ELEMENT BINDING FACTOR |
| DUF | DOMAIN OF UNKNOWN FUNCTION |
| EE | EVENING ELEMENT |
| ELF | EARLY FLOWERING |
| EQTL | EXPRESSION QUANTITATIVE TRAIT LOCI |
| FDR | FALSE DISCOVERY RATE |
| FTD | FREEZING TOLERANCE DIFFERENCE |
| GI | GIGANTEA |
| GO | GENE ONTOLOGY |
| ICE1 | INDUCER OF CBF EXPRESSION1 |
| ICER | INDUCER OF CBF EXPRESSION REGION |
| IT | ITALIAN ECOTYPE |
| LEA | LATE EMBRYOGENESIS ABUNDANT |
| LER | LANSBERG ERRECTA |
| LHCB | LIGH HARVESTING COMPLEX |
| LHY | LATE ELONGATED HYPOCOTYL |
| LOD | LOGARITHM OF ODDS |
| LUX | LUX ARRHYTHMO |
| MGDG | MONO-GALACTOSYLDIACYLGLYCEROL |
| NLS | NUCLEAR LOCALIZATION SIGNAL |

| | |
|---|---|
| P5CS | Δ-PYRROLINE-5-CARBOXYLATE SYNTHASE |
| PAG | PHOTOSYNTHESIS ASSOCIATED GENE |
| PBS | PUTATIVE BOA BINDING SITE |
| PR | PATHOGENESIS-RELATED |
| PRR | PSEUDO-RESPONSE REGULATOR |
| QTL | QUANTITATIVE TRAIT LOCI |
| RILS | RECOMBINANT INBRED LINES |
| RVE | REVEILLE |
| SFR2 | SENSITIVE TO FREEZING 2 |
| SUMO | SMALL UBIQUITIN-RELATED MODIFIER |
| SW | SWEDISH ECOTYPE |
| T1ME | TOC1 MORNING ELEMENT |
| TBS | TCP BINDING SITE |
| TF | TRANSCRIPTION FACTOR |
| TOC1 | TIMING OF CAB 1 |
| UBQ | UBIQUITIN |
| ZT | ZEITGEBER TIME |

# CHAPTER ONE

LITERATURE REVIEW

## CHAPTER ONE

LITERATURE REVIEW

***Cold-acclimation and freezing tolerance.*** The geographic range of plants is limited by a number of abiotic factors, including low temperature (1-3). Plants can vary greatly in their tolerance to temperature changes. In fact, in the deserts of Southern California plants thrive in an environment that goes from freezing to scorching in a single day, with temperature swings of approximately 50°C (4, 5). For plants growing in temperate and tropical climates the average difference between day and night temperatures is much narrower than these extreme desert conditions. However, temperate and tropical plants are still exposed to temperature fluctuations of approximately 10-15°C in a single day (5).

In addition to constraining the geographical locations that a plant can grow, low temperatures can also decrease plant productivity and cause crop loss (6). Most temperate plants, such as winter wheat, barley and *Arabidopsis*, can increase their tolerance to freezing temperature by prior exposure to low non-freezing temperatures, a process known as cold-acclimation (6-8). Many economically important crops such as commercial citrus trees (9), maize (10), tomato (11) and soybean (12) are chilling-sensitive and cannot cold-acclimate. In fact, in 2007, after 4 days of freezing temperatures, the California citrus industry suffered $480 million dollars of damage (13). Chilling-sensitive crops cannot cold acclimate but can reduce damage by cold through prior exposure to low temperatures (8). Consequently, a better understanding of the mechanisms of cold-acclimation may also lead to enhancements in chilling tolerance (8,

14, 15).

Freezing tolerance is an agronomically important trait and considerable effort has gone into breeding plants with greater freezing tolerance (6, 16-19). Closely related species of plants can differ significantly in their ability to cold-acclimate (15). For example, the common cultivated potato, *Solanum tuberosum*, and the wild potato *Solanum commersonii*, are closely related evolutionarily (15). Both species are chilling tolerant and have similar basal freezing tolerance, but *Solanum commersonii* can cold-acclimate while *Solanum tuberosum* cannot (15). Even ecotypes within a species can vary greatly in their basal and cold-acclimated freezing tolerance (2, 3, 20-24). Traditional breeding methods, thus far, have only achieved limited success in increasing plant freezing tolerance (19). In comparison to traditional breeding methods, transgenic plants have been much more successful in increasing freezing tolerance of important crop species (25-30). Therefore there is considerable interest in continuing to elucidate the molecular mechanisms underlying the process of cold-acclimation.

***Molecular changes associated with plant cold-acclimation.*** At freezing temperatures ice forms on the outside of leaf surfaces and subsequently propagates to the intercellular space of plant tissue (31-33). This intercellular ice can cause physical damage to plant cells and tissue (31-33). However, the dehydration that accompanies freezing is the primary source of damage (31-33). The severe cellular dehydration that accompanies freezing, is the result of the chemical potential of the cell moving unfrozen water from the intracellular (cytoplasm) space to the intercellular space where the water

is frozen (31-33).

Under non-acclimated conditions (no prior exposure to low temperatures), dehydration as a result of freezing can also instigate two forms of membrane damage. First, is endocytotic vesiculation, which alone is not damaging (31-33). However, the surface area reduction is not reversible, and cell lysis occurs when cells regain their volume during thawing (31-33). Secondly, during severe dehydration hexagonal II phase regions can form between the plasma membrane and endomembranes, such as the chloroplast envelope (31-33). These hexagonal II phase regions can result in a loss of osmotic responsiveness (31-33). Therefore, the plant cell can never recover from freeze-induced dehydration.

Cold-acclimated (prior exposure to low, non-freezing temperatures) plant cells respond differently to cellular dehydration as a result of freezing (31-33). Rather than endocytotic vesiculation, exocytotic vesicles continuous with the plasma membrane are formed (31-33). Therefore cells are not disrupted when they regain their volume during thawing. Hexagonal II phase regions in the plasma membrane also do not form with cold-acclimation (31-33). Consequently, assessment of membrane damage after freeze/thaw is a means of quantitatively measuring plant freezing tolerance (electrolyte leakage assay) and distinguishing plants that can and cannot cold-acclimate.

It has long been observed that there are significant changes in membrane lipid composition during cold-acclimation (31, 32, 34, 35). These changes include an increase in fatty acid unsaturation and phospholipid content as well as a drastic decrease in chloroplast-specific mono-galactosyldiacylglycerol (MGDG; (35)). A recent

study by Moellering et al. 2010 found that the gene SENSITIVE TO FREEZING 2 (SFR2) encodes a galactolipid remodeling enzyme vital to this chloroplast-specific decrease in MGDG (35). MGDG is prone to the formation of hexagonal II phase lipid structures (35). As previously mentioned, these hexagonal II phase regions can result in a loss of osmotic responsiveness during freezing (31-33). SFR2 is thus hypothesized to increase plant freezing tolerance by decreasing the formation of hexagonal II phase lipids by converting MGDG to di-galactosyldiacylglycerol (DGDG) and oligogalactolipids, which are not prone to hexagonal II phase formation *in vitro* (35).

Along with changes in lipid composition, Guy et al. 1985, showed through *in vitro* translation of mRNA in non-acclimated and cold-acclimated samples, that there are many gene expression changes during the process of cold-acclimation (36). Since then, many studies have detailed the changes in gene expression that occur during the process of cold acclimation (37-45). These studies found that many of the cold-responsive genes encode hydrophilic proteins. These hydrophilic COLD-RESPONSIVE (COR) polypeptides have simple, repetitive, amino-acid composition (37-45).

COR6.6, also known as KIN2, is almost identical to KIN1, a small hydrophilic protein that is hypothesized to act as an antifreeze protein due to sequence similarity with arctic fish antifreeze proteins (37, 39, 46-48). COR6.6 is targeted to the cytoplasm and has been shown to have cryoprotective properties by reducing the amount of freeze-induced membrane fusions *in vitro* (46-48). *COR15A* is a cold-regulated gene specifically localized to the stroma of chloroplasts (38). Current data support the hypothesis that COR15A increases freezing tolerance by preventing the formation of

hexagonal II phase regions, which normally form between the plasma membrane and chloroplasts (41, 46). Fittingly, overexpression of *COR15A* leads to an increase in non-acclimated freezing tolerance of chloroplasts *in vitro* and an increase in the acclimated and non-acclimated freezing tolerance of protoplasts (41). COR47 has sequence homology with LATE EMBRYOGENESIS ABUNDANT (LEA) proteins, which respond to ABSCISIC ACID (ABA), water stress, and drought (39). Like COR47, COR78 is another hydrophilic protein that resembles LEA proteins, which responds to cold, ABA and drought (49, 50). Mutation or overexpression of *COR78* has little impact on plant freezing tolerance (51). Accordingly, the function of COR78 and many of these COR proteins in freezing tolerance have yet to be entirely elucidated (51).

Transcriptional changes at low temperature are also accompanied by extensive changes in metabolic profile, which include the accumulation of certain amino acids and sugars, such as proline and sucrose (44, 52, 53). Free proline has been shown to have cryoprotective properties in plants (52) and the low-temperature induced increase in free proline has been linked to the increase in transcripts for $\Delta^1$*-pyrroline-5-carboxylate synthase* (*P5CS*), a key enzyme in the proline biosynthetic pathway (54). Fructose, glucose, and sucrose are sugars up-regulated by low-temperature and the synthesis of these sugars is associated with the raffinose pathway (44, 52, 53). These solutes accumulate in the cytoplasm, decreasing the chemical potential driving dehydration (31, 34, 53). The increase in these solutes with cold-acclimation also possibly reduces hexagonal II phase formation by increasing the distance between membranes (34). The up-regulation of the raffinose pathway by cold has been specifically linked to the gene

*GALACTINOL SYNTHASE3 (GOLS3)*, a key enzyme in the raffinose biosynthetic pathway (55). *GOLS1* and *GOLS2* are regulated by other stresses (55). While these are two examples of genes driving metabolic changes during cold-acclimation, the genes responsible for many of the other metabolic changes remain unidentified (44).

PATHOGENESIS-RELATED (PR) proteins accumulate in the intercellular fluid (apoplasts) of plants at low-temperature and have been shown to have antifreeze activity (56-58). High concentrations of these PR antifreeze proteins in the apoplast can decrease the freezing temperature of the intercellular fluid, thus preventing ice formation (56). At lower concentrations, the growth of ice in the intercellular space is also limited by PR antifreeze proteins, which adhere onto ice and prevent large ice crystals from forming (56). This decrease in intercellular ice formation by PR proteins thus, decreases the amount of membrane damage by intercellular ice and suggests an interesting relationship between cold and biotic stresses (56).

***CBF pathway of cold-acclimation.*** Promoter analysis of the *COR* genes identified the C-REPEAT/DEHYDRATION RESPONSE ELEMENT (CRT/DRE) as a novel and significantly overrepresented cis-element (40, 50). This element was found to be responsive to cold and drought but not ABA (40, 50). A transcriptional activator, C-REPEAT BINDING FACTOR1 (CBF1), was identified as binding to the CRT/DRE through a yeast-1-hybrid screen (59). Two closely related genes *CBF2* and *CBF3*, located in tandem to *CBF1* on chromosome 4, were subsequently identified and shown to bind to the CRT/DRE (42). *CBF1-3* all contain a NUCLEAR LOCALIZATION SIGNAL

(NLS), an APETALA2 (AP2) DNA binding domain, followed by an acidic activation domain (59).

Within minutes of exposure to cold, *CBF1-3* gene expression is rapidly induced in *Arabidopsis* (42). CBF transcription factors bind to the CRT/DRE element in the promoters of *COR* genes, which leads to activation of COR gene expression (42). Constitutive over-expression of *CBFs* in *Arabidopsis* results in expression of *COR* genes under warm temperatures and constitutive freezing tolerance without prior cold acclimation (45, 54, 60-62). Phenotypically, *CBF* over-expressing plants are dwarf compared to wild-type plants. CBF1-3 also regulate many of the metabolic changes associated with cold acclimation (44, 62). In fact, both *P5CS* and *GOLS3* are CBF target genes (44, 54, 55).

Genomic analysis also revealed the existence of a closely related AP2 transcription factor on chromosome 5 named *CBF4* (63). Although closely related in terms of transcript sequence, the regulation of *CBF4* seems to have diverged significantly from *CBF1-3*, since *CBF4* appears to be specifically up-regulated by drought but not low-temperature (63). Overexpression of *CBF4* leads to the activation of genes containing CRT/DRE elements (63). Consequently, both drought and freezing tolerance are increased in *CBF4* overexpressing plants (63).

***CBF pathway in important plant species.*** Although the CBF pathway was identified in the model plant, *Arabidopsis*, it appears to be conserved in many economically important plant species that can cold-acclimate, such as wheat, rye,

poplar and barley (64-66). Overexpression of the *CBF* genes in these plants also leads to an increase in freezing tolerance (64-66). The *CBF* genes are also present in plants that do not cold-acclimate such as rice, and tomato (67, 68). Interestingly, overexpression of *CBF* genes in rice and tomato does not lead to an increase in freezing tolerance, but the CBF regulons of these two species are significantly smaller than other species that do cold-acclimate (67, 68). *Solanum commersonii* and *Solanum tuberosum*, two evolutionarily close potato species, differ in their ability to cold acclimate and also have significant differences in the genes that comprise their CBF regulons, although the number of CBF regulated genes is similar (15). Chapter Three of this study will detail variations in the low-temperature response of two *Arabidopsis* ectoypes with differing freezing tolerance.

***Natural variation of CBF genes in Arabidopsis*.** Previous studies on the natural variation of freezing tolerance in *Arabidopsis* have implicated the *CBFs* as a source of significant variation. Alonso-Blanco et al. 2005 mapped differences in freezing tolerance using recombinant inbred lines (RILs) from *Arabidopsis* accessions LANDSBERG ERECTA (LER) and CAPE VERDE ISLANDS (CVI) (20). Seven different quantitative trait loci (QTL) on chromosomes 1,4, and 5 were found, but the single QTL on chromosome 4 explained the most variance and also contained the *CBF* locus (20). CVI freezing tolerance was significantly reduced in comparison to LER, as was *CBF2* expression. Introduction of the Ler-*CBF2* transgene into CVI significantly reduced differences in freezing tolerance between LER and CVI (20).

*CBF* expression in the Versailles collection of *Arabidopsis* was also found to vary significantly (24). Although freezing tolerance did not simply correlate with *CBF* expression in the 8 accessions tested, the most freezing-sensitive Versailles accessions were also the accessions with the lowest cold-induced *CBF* expression levels (24). The most freezing tolerant Versailles accessions varied significantly in their *CBF* expression, suggesting the importance of CBF-independent pathways of freezing tolerance for some accessions (24). Freezing tolerance QTL mapped for two Versailles RIL populations were not completely overlapping (24). However, both populations had a common QTL on chromosome 4 that overlapped with the *CBF* locus and explained the most variance (24). Further analysis of *CBF* gene sequence in the 48 Versailles accessions showed a number of polymorphisms in both the promoter and coding sequences of *CBF1-3* (22).

A study by Zhen et al. 2008 further analyzed *CBF* sequence in 24 accession of *Arabidopsis* and found a large bias toward nonsynonymous changes in the activation domain compared to the DNA binding domain of *CBF* genes (23). Zhen et al. 2008 also showed that the *CBF* genes undergo relaxed purifying selection in *Arabidopsis* accession native to southern latitudes in comparison to accessions native to northern latitudes (23). The 10 southern latitude accessions tested had 1.5 to 4.6-fold more polymorphisms in the individual *CBF* genes in comparison to the 14 northern latitude accessions tested (23). The four accessions (CO-1, CVI-0, CVI-1, and ITA-0) with the lowest CBF expression originated from southern latitudes and had the lowest survival rates in freezing tolerance assays (23). CO-1, CVI-1, ITA-0 and two additional

southern accessions, Can-0 and L1-0, also had reduced expression of three CBF target genes (COR6.6, COR15A, COR78) in comparison to northern accessions (23).

***CBF-independent pathways of cold-acclimation in Arabidopsis.*** Microarray analysis of *CBF* overexpressing plants revealed that only 12% of the cold-responsive transcriptome is part of the CBF regulon (69). Furthermore, 28% of cold-responsive genes are not affected by expression of the *CBF* genes (69). This indicates that there are CBF-independent pathways regulating expression of cold-induced genes.

Through an EMS mutant screen, ESKIMO1 (ESK1) was identified as a plant with constitutive freezing tolerance without prior cold acclimation (70). The *esk1* mutant has constitutively high levels of proline (70), similar to *CBF* overexpressing plants (62). However, ESK1-regulated genes do not overlap significantly with CBF regulated genes, suggesting that ESK1 is part of a CBF-independent pathway (70, 71). ESK1 encodes DOMAIN OF UNKNOWN FUNCTION 231 (DUF231) protein and it was recently shown that ESK1 is important for production of functional xylem and consequently water transport (71, 72).

*Hos9* and *hos10* mutant plants were identified in a mutant screen using plants expressing the *COR78* promoter driving the expression of a luciferase reporter gene (73-75). The *hos9* and *hos10* mutants both have reduced freezing tolerance compared to wild-type plants in whole plant freeze tests (73, 74). Though the gene underlying the *hos10* mutation has yet to be found (75), the gene underlying the *hos9* mutation is a constitutively active homeodomain transcription factor (73). Microarray analysis of the

*hos9* mutant reveals that genes regulated by HOS9 are significantly different from those regulated by the CBFs (73).

***Upstream regulation of CBF pathway in Arabidopsis.*** *CBF* genes significantly impact freezing tolerance in economically important species, and appear to be under substantial selective pressure (22-24). Consequently, there is considerable interest in finding upstream regulators of the *CBF* genes. In 2004, Novillo et al. isolated a *cbf2* mutant that had increased freezing tolerance and higher expression of *CBF1* and *CBF3* (76). This therefore suggests that CBF2 negatively regulates *CBF1* and *CBF3*. However, this hypothesis was not substantiated by microarray studies (45, 61). Plants overexpressing *CBF2* did not have significantly reduced *CBF1* or *CBF3* expression (45, 61).

In 2003, Zarka et al. used 5' and 3' deletions of the *CBF2* promoter to identify a ~155 base pair (bp) fragment required for cold induction (77). Interestingly, the Arabidopsis accession, CVI, which was found to have reduced *CBF2* expression in comparison to LER, has a 1630 bp deletion in the *CBF2* promoter that intrudes on this important ~155 bp region (20). Zarka et al. 2003 also identified two short elements, INDUCTION OF CBF EXPRESSION REGION 1 (ICER1) and ICER2, within this ~155 bp region important for cold-regulated expression (77). Subsequent mutations performed within this ~155 bp region further identified sequences important for cold-induced *CBF* expression (78). One element found through this mutational analysis was identified as a binding site for the CALMODULIN BINDING TRANSCRIPTION

ACTIVATOR (CAMTA) family of calmodulin binding transcription factors (78). CAMTA3 was found to positively regulate *CBF1* and *CBF2*, but not *CBF3*, which does not contain a CAMTA binding site *(78)*. Interestingly, exposure to cold temperature results in a rapid spike of cytosolic calcium (79). Although the connection between calcium and cold is still not well understood, these cold-induced increases in cytosolic calcium are also required for normal activation of CBF regulated genes (79). In plants, calcium can be perceived by calmodulin (78). Therefore, as a calmodulin binding transcription factor, CAMTA3, is a putative connection between calcium, cold and the *CBF* genes (80).

In 2003, INDUCER OF CBF EXPRESSION1 (ICE1) was identified through a mutant screen using plants expressing a luciferase reporter gene under the control of the *CBF3* promoter (81). *ICE1*, is a constitutively expressed, nuclear localized, MYC family transcription factor that positively regulates *CBF3*, but has little effect on *CBF1* or *CBF2* (81). Upon exposure to cold, *ICE1* transcripts are only slightly up-regulated (81), but ICE1 is post-transcriptionally regulated through sumoylation by SIZ1, a SMALL UBIQUITIN-RELATED MODIFIER (SUMO) E3 ligase (82). Sumoylation is a reversible post-transcriptional modification that is most notably known to affect subnuclear targeting, transcriptional regulation and ubiquitin mediated-protein degradation (82). Miura et al. 2007 demonstrated that cold-induced sumoylation of ICE1 leads to enhanced protein stability by reducing polyubiquitination, which normally leads to degradation (82).

*MYB15* was identified through microarray experiments as a cold-regulated gene with higher expression in *ice1* mutants (83). This suggests that ICE1 normally represses expression of *MYB15*. Consistent with this idea, ICE1 sumoylation by SIZ1 also represses expression of *MYB15* (82). Subsequent yeast-2-hybrid and pull-down assays also suggested interaction of MYB15 with ICE1 (83). Overexpression of *MYB15* reduces expression of *CBF*s and MYB15 RNAi lines have been shown to increase *CBF* expression (83). *CBF1-3* promoters contain the known binding site for MYB15 and *in vitro* binding assays suggest that MYB15 negatively regulates *CBF* genes directly (83). But CBF target genes are not affected by overexpression or reduction of *MYB15* expression (83). Agarwal et al. 2006 explain this confounding result by suggesting that MYB15 negatively regulates *CBF* genes, but induces expression of other cold-regulated transcription factors, which up-regulate *COR* genes (83). This is a reasonable hypothesis, however, *in vivo* binding assays are needed to confirm the MYB15-CBF interaction.

ZAT12 is a transcription factor that was found to have a similar cold induction pattern to the *CBF* genes (45, 69). *ZAT12* overexpressing plants had significantly reduced *CBF* expression but only slightly reduced CBF target gene expression (45). ZAT12 is thus another potential negative regulator of the *CBF* genes. *ZAT12* overexpressing plants are dwarf as are *CBF* overexpressing plants, but are only slightly more freezing tolerant than wild-type plants (45). Microarray analysis of *ZAT12* overexpressing plants further supports the role of ZAT12 in cold signaling (45).

However, further evidence is needed to show that ZAT12 is directly involved in the negative regulation of *CBF* genes.

***Upstream CBF regulation by the circadian clock.*** Circadian clocks give an internal estimate of time, allowing organisms to predict daily changes in their environment such as the onset of day or night, or changes between day and night temperature (84, 85). Not surprisingly, the ability to anticipate and respond to environmental changes provides an adaptive advantage for plants (84, 86, 87).

The *Arabidopsis* circadian clock is composed of several interlocking feedback loops and additional components of the *Arabidopsis* clock continue to be found each year (88, 89). Morning-expressed MYB transcription factors CIRCADIAN CLOCK ASSOCIATED 1 (CCA1) and LATE ELONGATED HYPOCOTYL (LHY) directly repress the expression of *TIMING OF CAB1* (*TOC1*) by binding to an EVENING ELEMENT (EE; AAAATATCT) in the *TOC1* promoter (90). EARLY FLOWERING 3 (ELF3), ELF4, LUX ARRHYTHMO (LUX), and GIGANTEA (GI) promote expression of *CCA1* and *LHY*, but there is no evidence that these transcription factors directly regulate *CCA1* or *LHY* (90-92). Recently, BROTHER OF LUX ARRHYTHMO (BOA) was identified as a clock component that positively regulates *CCA1* expression by binding to PUTATIVE BOA BINDING SITE 3 (PBS3) and PBS4 elements in the *CCA1* promoter (89).

TOC1, up until very recently (93), was also widely hypothesized to promote expression of *CCA1* and *LHY* since *toc1* mutants have reduced expression of *CCA1* and *LHY* (90). However, this hypothesis was confounded for many years by the result

that *TOC1* overexpressing plants also have low expression of *CCA1* and *LHY* (94). In 2012, Gendron et al. showed that TOC1 generally acts as a repressor, which can bind to a new cis-element TOC1 MORNING ELEMENT (T1ME) through its CCT domain (93). Although, Gendron et al. 2012 also demonstrated that TOC1 represses expression of *CCA1* and *LHY,* they do not negate genetic data (90) that suggests that TOC1 is somehow necessary for activation of *CCA1* and *LHY* (93). Although the role of TOC1 in the circadian clock still seems unsettled there is evidence that suggests that the increase in *CCA1* and *LHY* could be partially explained by the repression of CCA1 HIKING EXPEDITION (CHE) by TOC1 (93, 95).

Pruneda-Paz et al. 2009 demonstrated that CHE represses *CCA1* through the TCP-BINDING SITE (TBS; GGTCCCAC) in the *CCA1* promoter (95). CCA1 and LHY also repress *CHE* through the CCA1-BINDING SITE (CBS; AAAAATCT) in the *CHE* promoter (95). The TOC1 protein binds directly to the N-terminal domain of CHE, which binds directly to TBS, and chromatin immunoprecipitation (ChIP) experiments have shown enrichment of TOC1 at TBS elements in the *CCA1* promoter (95). TOC1 is thus hypothesized to promote expression of *CCA1* by antagonizing the CCA1 inhibitor, CHE (95). PRR1 was found to be identical to TOC1 (96) and PRR7 and 9, were subsequently identified as components of the circadian clock that form a 'morning expressed' feedback loop with CCA1 and LHY (97-102). CCA1 and LHY positively regulate *PRR7*, and *9*, which then directly repress *CCA1* and *LHY* expression (97-102).

In 2000, Harmer et al. demonstrated that components of key transcriptional pathways such as photosynthesis, phenylpropanoid biosynthesis, cell elongation, and

starch mobilization, are all under concerted regulation by the circadian clock (84). Harmer et al. 2000 also showed that *CBF3* expression is rhythmic under warm conditions (84). This result led Fowler et al. 2005 to examine the expression of *CBF* genes under circadian conditions (103). In 2005, Fowler et al. used northern blot analysis to demonstrate that the amplitude of *CBF1-3* cold-induction is dependent on the time of day that the plants are exposed to cold (103). This gating of cold-induced gene expression was observed under both diurnal and light-entrained circadian conditions (103). Peak *CBF* expression was at ZEITGEBER TIME 4 (4 hours after dawn; ZT4) and ZT28, and troughs of expression were at ZT16 and ZT40 (103).

Fowler et al. 2005 used *CCA1* overexpressing plants to show that gated cold-induced expression of *CBF* genes is dependent on the circadian clock (103), since overexpression of central clock component *CCA1* disrupts normal clock function (90, 104). However, the specific clock components regulating *CBF* expression are still unclear. A study by Nakamichi et al. 2009 showed that the *prr9/prr7/prr5* triple mutant disrupted gated cold-induced expression of *CBF* genes. The triple mutant had constitutively high *CBF* expression (105). Therefore, PRR9, PRR7 and PRR5, potentially act as negative regulators of *CBF* expression, though no evidence of in vivo interaction with the *CBF* genes was provided (105). In Chapter Two of this study an alternate mechanism is suggested for both the circadian regulation and gated cold-induction of *CBF* genes.

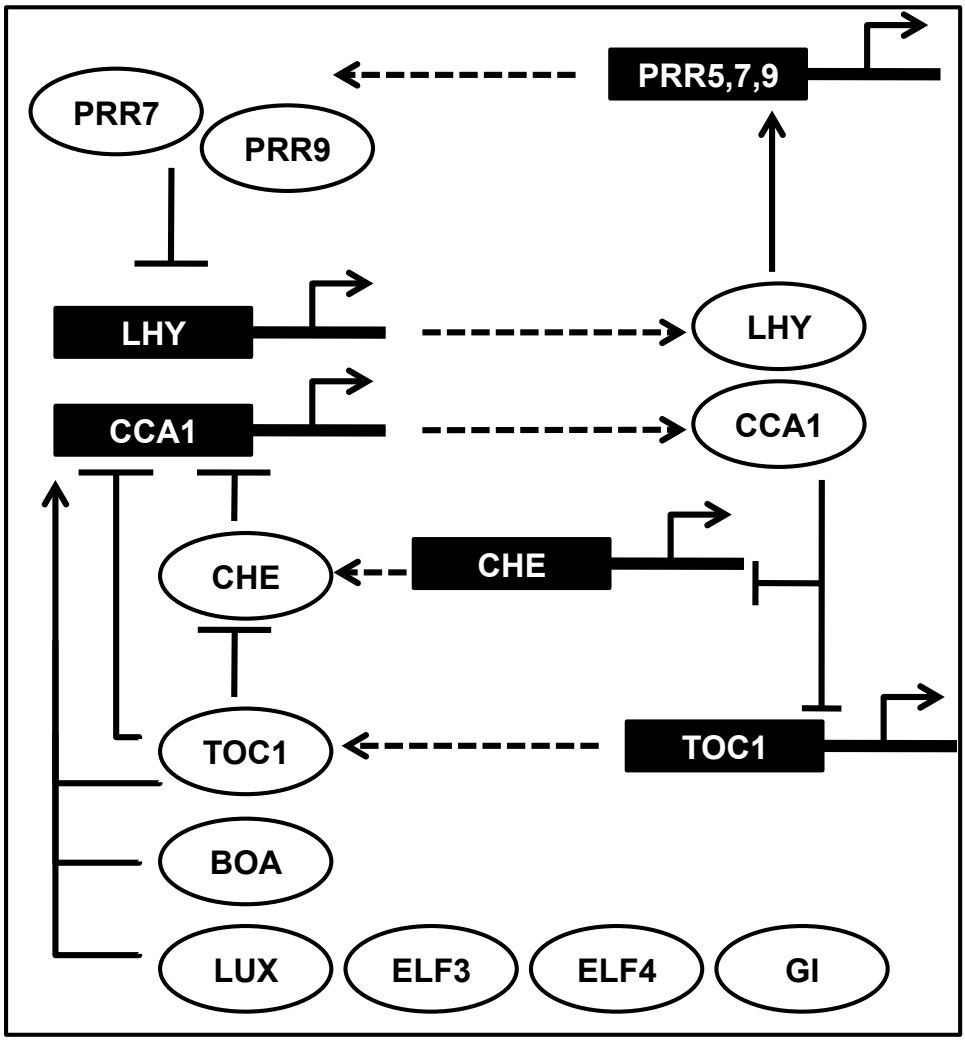


**Figure 1.1.** Regulation of central components of the *Arabidopsis* circadian clock based on previous literature. Ovals represent proteins, and rectangles represent a gene and promoter region. Solid lines ending in arrows (that are not attached to genes) represent positive regulation, while solid lines ending in a perpendicular line represent negative regulation. Dotted lines represent transcription and translation of a gene to a protein. For details on the regulation of central clock components please refer 'upstream CBF regulation by the circadian clock' section of Chapter One, which begins on page 15.

## LITERATURE CITED

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1. Zhen Y & Ungerer MC (2008) Clinal Variation In Freezing Tolerance Among Natural Accessions Of Arabidopsis Thaliana. *New Phytologist* 177(2):419-427.

2. Lefebvre V, Kiani SP, & Durand-Tardif M (2009) A Focus On Natural Variation For Abiotic Constraints Response In The Model Species Arabidopsis Thaliana. *International Journal of Molecular Sciences* 10(8):3547-3582.

3. Fournier-Level A, Korte A, Cooper MD, Nordborg M, Schmitt J, & Wilczek AM (2011) A Map Of Local Adaptation In Arabidopsis Thaliana. *Science* 334(6052):86-89.

4. Koehler PA, Anderson RS, & Spaulding WG (2005) Development Of Vegetation In The Central Mojave Desert Of California During The Late Quaternary. *Palaeogeography, Palaeoclimatology, Palaeoecology* 215(3–4):297-311.

5. Walbot V (2011) How Plants Cope With Temperature Stress. *Bmc Biology* 9.

6. Thomashow MF (1998) Role of Cold-Responsive Genes in Plant Freezing Tolerance. *Plant Physiology* 118(1):1-8.

7. Thomashow MF (2001) So What's New in the Field of Plant Cold Acclimation? Lots! *Plant Physiology* 125(1):89-93.

8. Chinnusamy V, Zhu J, & Zhu JK (2007) Cold Stress Regulation Of Gene Expression In Plants. *Trends in Plant Science* 12(10):444-451.

9. Zhang C-k, Lang P, Dane F, Ebel RC, Singh NK, Locy RD, & Dozier WA (2005) Cold Acclimation Induced Genes Of Trifoliate Orange (Poncirus trifoliata ). *Plant Cell Reports* 23(10):764-769.

10. Baczek-Kwinta R, Niewiadomska E, & Miszalski Z (2005) Physiological Role Of Reactive Oxygen Species In Chill-Sensitive Plants. *Phyton-Annales Rei Botanicae* 45(3):25-37.

11. Venema JH, Linger P, van Heusden AW, van Hasselt PR, & Bruggemann W (2005) The Inheritance Of Chilling Tolerance In Tomato (Lycopersicon Spp.). *Plant Biology* 7(2):118-130.

12. Strauss AJ, Kruger GHJ, Strasser RJ, & Van Heerden PDR (2006) Ranking Of Dark Chilling Tolerance In Soybean Genotypes Probed By The Chlorophyll A Fluorescence Transient O-J-I-P. *Environmental and Experimental Botany* 56(2):147-157.

13. Byron K (2007) Freeze Kills $480 Million Worth Of Citrus *CNNMoney.*

14. Jaglo KR, Kleff S, Amundsen KL, Zhang X, Haake V, Zhang JZ, Deits T, & Thomashow MF (2001) Components Of The Arabidopsis C-Repeat/Dehydration-Responsive Element Binding Factor Cold-Response Pathway Are Conserved In Brassica Napus And Other Plant Species. *Plant Physiology* 127(3):910-917.

15. Carvallo MA, Pino M-T, Jeknić Z, Zou C, Doherty CJ, Shiu S-H, Chen THH, & Thomashow MF (2011) A Comparison Of The Low Temperature Transcriptomes And CBF Regulons Of Three Plant Species That Differ In Freezing Tolerance: Solanum Commersonii, Solanum Tuberosum, And Arabidopsis Thaliana. *Journal of Experimental Botany* 62(11):3807-3819.

16. Larsen A (1994) Breeding Winter Hardy Grasses. *Euphytica* 77(3):231-237.

17. Trognitz BR (2003) Prospects Of Breeding Quinoa For Tolerance To Abiotic Stress. *Food Reviews International* 19(1-2):129-137.

18. Owens CL (2005) Breeding Temperate Fruit Crops For Improved Freezing Tolerance. *Hortscience* 40(7):1950-1953.

19. Sanghera GS, Wani SH, Hussain W, & Singh NB (2011) Engineering Cold Stress Tolerance In Crop Plants. *Current Genomics* 12(1):30-43.

20. Alonso-Blanco C, Gomez-Mena C, Llorente F, Koornneef M, Salinas J, & Martínez-Zapater JM (2005) Genetic And Molecular Analyses Of Natural Variation Indicate CBF2 As A Candidate Gene For Underlying A Freezing Tolerance Quantitative Trait Locus In Arabidopsis. *Plant Physiology* 139(3):1304-1312.

21. Le MQ, Engelsberger WR, & Hincha DK (2008) Natural Genetic Variation In Acclimation Capacity At Sub-Zero Temperatures After Cold Acclimation At 4°C In Different Arabidopsis Thaliana Accessions. *Cryobiology* 57(2):104-112.

22. McKhann HI, Gery C, Berard A, Leveque S, Zuther E, Hincha DK, De Mita S, Brunel D, & Teoule E (2008) Natural Variation In CBF Gene Sequence, Gene Expression And Freezing Tolerance In The Versailles Core Collection Of Arabidopsis Thaliana. *Bmc Plant Biology* 8.

23. Zhen Y & Ungerer MC (2008) Relaxed Selection On The CBF/DREB1 Regulatory Genes And Reduced Freezing Tolerance In The Southern Range Of Arabidopsis Thaliana. *Molecular Biology and Evolution* 25(12):2547-2555.

24. Gery C, Zuther E, Schulz E, Legoupi J, Chauveau A, McKhann H, Hincha DK, & Téoulé E (2011) Natural Variation In The Freezing Tolerance Of Arabidopsis Thaliana: Effects Of Rnai-Induced CBF Depletion And QTL Localisation Vary Among Accessions. *Plant Science* 180(1):12-23.

25. Zhao X, Zhan LP, & Zou XZ (2011) Improvement Of Cold Tolerance Of The Half-High Bush Northland Blueberry By Transformation With The LEA Gene From Tamarix Androssowii. *Plant Growth Regulation* 63(1):13-22.

26. Li HW, Zang BS, Deng XW, & Wang XP (2011) Overexpression Of The Trehalose-6-Phosphate Synthase Gene Ostps1 Enhances Abiotic Stress Tolerance In Rice. *Planta* 234(5):1007-1018.

27. Xu MY, Li LH, Fan YL, Wan JM, & Wang L (2011) Zmcbf3 Overexpression Improves Tolerance To Abiotic Stress In Transgenic Rice (Oryza Sativa) Without Yield Penalty. *Plant Cell Reports* 30(10):1949-1957.

28. Morran S, Eini O, Pyvovarenko T, Parent B, Singh R, Ismagul A, Eliby S, Shirley N, Langridge P, & Lopato S (2011) Improvement Of Stress Tolerance Of Wheat And Barley By Modulation Of Expression Of DREB/CBF Factors. *Plant Biotechnology Journal* 9(2):230-249.

29. Kim YH, Kim MD, Park SC, Yang KS, Jeong JC, Lee HS, & Kwak SS (2011) SCOF-1-Expressing Transgenic Sweetpotato Plants Show Enhanced Tolerance To Low-Temperature Stress. *Plant Physiology and Biochemistry* 49(12):1436-1441.

30. Navarro M, Ayax C, Martinez Y, Laur J, El Kayal W, Marque C, & Teulieres C (2011) Two Egucbf1 Genes Overexpressed In Eucalyptus Display A Different Impact On Stress Tolerance And Plant Development. *Plant Biotechnology Journal* 9(1):50-63.

31. Steponkus PL (1984) Role Of The Plasma Membrane In Freezing Injury And Cold Acclimation. *Annual Review of Plant Physiology* 35(1):543-584.

32. Uemura M & Steponkus PL (1999) Cold Acclimation In Plants: Relationship Between The Lipid Composition And The Cryostability Of The Plasma Membrane. *Journal of Plant Research* 112(1106):245-254.

33. Verslues PE, Agarwal M, Katiyar-Agarwal S, Zhu J, & Zhu J-K (2006) Methods And Concepts In Quantifying Resistance To Drought, Salt And Freezing, Abiotic Stresses That Affect Plant Water Status. *The Plant Journal* 45(4):523-539.

34. Uemura M, Warren G, & Steponkus PL (2003) Freezing Sensitivity In The Sfr4 Mutant Of Arabidopsis Is Due To Low Sugar Content And Is Manifested By Loss Of Osmotic Responsiveness. *Plant Physiology* 131(4):1800-1807.

35. Moellering ER, Muthan B, & Benning C (2010) Freezing Tolerance In Plants Requires Lipid Remodeling At The Outer Chloroplast Membrane. *Science* 330(6001):226-228.

36. Guy CL, Niemi KJ, & Brambl R (1985) Altered Gene-Expression During Cold-Acclimation Of Spinach. *Proceedings of the National Academy of Sciences of the United States of America* 82(11):3673-3677.

37. Kurkela S & Franck M (1990) Cloning And Characterization Of A Cold-Inducible And ABA-Inducible Arabidopsis Gene. *Plant Molecular Biology* 15(1):137-144.

38. Lin CT & Thomashow MF (1992) Dna-Sequence Analysis Of A Complementary-Dna For Cold-Regulated Arabidopsis Gene COR15 And Characterization Of The Cor-15 Polypeptide. *Plant Physiology* 99(2):519-525.

39. Gilmour SJ, Artus NN, & Thomashow MF (1992) Cdna Sequence-Analysis And Expression Of 2 Cold-Regulated Genes Of Arabidopsis-Thaliana. *Plant Molecular Biology* 18(1):13-21.

40. Baker SS, Wilhelm KS, & Thomashow MF (1994) The 5′ -Region Of Arabidopsis Thaliana COR15a Has Cis-Acting Elements That Confer Cold-, Drought- And ABA-Regulated Gene Expression. *Plant Molecular Biology* 24(5):701-713.

41. Artus NN, Uemura M, Steponkus PL, Gilmour SJ, Lin C, & Thomashow MF (1996) Constitutive Expression Of The Cold-Regulated Arabidopsis Thaliana COR15a Gene Affects Both Chloroplast And Protoplast Freezing Tolerance. *Proceedings of the National Academy of Sciences of the United States of America* 93(23):13404-13409.

42. Gilmour SJ, Zarka DG, Stockinger EJ, Salazar MP, Houghton JM, & Thomashow MF (1998) Low Temperature Regulation Of The Arabidopsis CBF Family Of AP2 Transcriptional Activators As An Early Step In Cold-Induced COR gene Expression. *The Plant Journal* 16(4):433-442.

43. Thomashow MF (1999) Plant Cold Acclimation: Freezing Tolerance Genes And Regulatory Mechanisms. *Annual Review of Plant Physiology and Plant Molecular Biology* 50(1):571-599.

44. Cook D, Fowler S, Fiehn O, & Thomashow MF (2004) A Prominent Role For The CBF Cold Response Pathway In Configuring The Low-Temperature Metabolome Of Arabidopsis. *Proceedings of the National Academy of Sciences of the United States of America* 101(42):15243-15248.

45. Vogel JT, Zarka DG, Van Buskirk HA, Fowler SG, & Thomashow MF (2005) Roles Of The CBF2 And ZAT12 Transcription Factors In Configuring The Low Temperature Transcriptome Of Arabidopsis. *Plant Journal* 41(2):195-211.

46. Webb MS, Gilmour SJ, Thomashow MF, & Steponkus PL (1996) Effects Of COR6.6 And COR15am Polypeptides Encoded By COR (Cold-Regulated) Genes Of Arabidopsis Thaliana On Dehydration-Induced Phase Transitions Of Phospholipid Membranes. *Plant Physiology* 111(1):301-312.

47. Glimour SJ, Lin C, & Thomashow MF (1996) Purification And Properties Of Arabidopsis Thaliana COR (Cold-Regulated) Gene Polypeptides COR15am And COR6.6 Expressed In Escherichia Coli. *Plant Physiology* 111(1):293-299.

48. Uemura M, Gilmour SJ, Thomashow MF, & Steponkus PL (1996) Effects Of COR6.6 And COR15am Polypeptides Encoded By COR (Cold-Regulated) Genes Of Arabidopsis Thaliana On The Freeze-Induced Fusion And Leakage Of Liposomes. *Plant Physiology* 111(1):313-327.

49. Horvath DP, McLarney BK, & Thomashow MF (1993) Regulation Of Arabidopsis-Thaliana L (Heyn) COR78 In Response To Low-Temperature. *Plant Physiology* 103(4):1047-1053.

50. Yamaguchishinozaki K & Shinozaki K (1994) A Novel Cis-Acting Element In An Arabidopsis Gene Is Involved In Responsiveness To Drought, Low-Temperature, Or High-Salt Stress. *Plant Cell* 6(2):251-264.

51. Msanne J, Lin JS, Stone JM, & Awada T (2011) Characterization Of Abiotic Stress-Responsive Arabidopsis Thaliana RD29A And RD29B Genes And Evaluation Of Transgenes. *Planta* 234(1):97-107.

52. Koster KL & Lynch DV (1992) Solute Accumulation And Compartmentation During The Cold-Acclimation Of Puma Rye. *Plant Physiology* 98(1):108-113.

53. Wanner LA & Junttila O (1999) Cold-induced freezing tolerance in Arabidopsis. *Plant Physiology* 120(2):391-399.

54. Gilmour SJ, Sebolt AM, Salazar MP, Everard JD, & Thomashow MF (2000) Overexpression Of The Arabidopsis CBF3 Transcriptional Activator Mimics Multiple Biochemical Changes Associated With Cold Acclimation. *Plant Physiology* 124(4):1854-1865.

55. Taji T, Ohsumi C, Iuchi S, Seki M, Kasuga M, Kobayashi M, Yamaguchi-Shinozaki K, & Shinozaki K (2002) Important Roles Of Drought- And Cold-Inducible Genes For Galactinol Synthase In Stress Tolerance In Arabidopsis Thaliana. *Plant Journal* 29(4):417-426.

56. Griffith M, Ala P, Yang DSC, Hon WC, & Moffatt BA (1992) Antifreeze Protein Produced Endogenously In Winter Rye Leaves. *Plant Physiology* 100(2):593-596.

57. Marentes E, Griffith M, Mlynarz A, & Brush RA (1993) Proteins Accumulate In The Apoplast Of Winter Rye Leaves During Cold Acclimation. *Physiologia Plantarum* 87(4):499-507.

58. Hon WC, Griffith M, Mlynarz A, Kwok YC, & Yang D (1995) Antifreeze Proteins In Winter Rye Are Similar To Pathogenesis-Related Proteins. *Plant Physiology* 109(3):879-889.

59. Stockinger EJ, Gilmour SJ, & Thomashow MF (1997) Arabidopsis Thaliana CBF1 Encodes An AP2 Domain-Containing Transcriptional Activator That Binds To The C-Repeat/DRE, A Cis-Acting DNA Regulatory Element That Stimulates Transcription In Response To Low Temperature And Water Deficit. *Proceedings of the National Academy of Sciences of the United States of America* 94(3):1035-1040.

60. Jaglo-Ottosen KR, Gilmour SJ, Zarka DG, Schabenberger O, & Thomashow MF (1998) Arabidopsis CBF1 Overexpression Induces COR Genes And Enhances Freezing Tolerance. *Science* 280(5360):104-106.

61. Liu Q, Kasuga M, Sakuma Y, Abe H, Miura S, Yamaguchi-Shinozaki K, & Shinozaki K (1998) Two Transcription Factors, DREB1 And DREB2, With An EREBP/AP2 DNA Binding Domain Separate Two Cellular Signal Transduction Pathways In Drought- And Low-Temperature-Responsive Gene Expression, Respectively, In Arabidopsis. *Plant Cell* 10(8):1391-1406.

62. Gilmour SJ, Fowler SG, & Thomashow MF (2004) Arabidopsis Transcriptional Activators CBF1, CBF2, And CBF3 Have Matching Functional Activities. *Plant Molecular Biology* 54(5):767-781.

63. Haake V, Cook D, Riechmann J, Pineda O, Thomashow MF, & Zhang JZ (2002) Transcription Factor CBF4 Is A Regulator Of Drought Adaptation In Arabidopsis. *Plant Physiology* 130(2):639-648.

64. Jaglo KR, Kleff S, Amundsen KL, Zhang X, Haake V, Zhang JZ, Deits T, & Thomashow MF (2001) Components Of The Arabidopsis C-Repeat/Dehydration-Responsive Element Binding Factor Cold-Response Pathway Are Conserved Inbrassica Napus And Other Plant Species. *Plant Physiology* 127(3):910-917.

65. Choi DW, Rodriguez EM, & Close TJ (2002) Barley CBF3 Gene Identification, Expression Pattern, And Map Location. *Plant Physiology* 129(4):1781-1787.

66. Benedict C, Skinner JS, Meng R, Chang YJ, Bhalerao R, Huner NPA, Finn CE, Chen THH, & Hurry V (2006) The CBF1-Dependent Low Temperature Signalling Pathway, Regulon And Increase In Freeze Tolerance Are Conserved In Populus Spp. *Plant Cell and Environment* 29(7):1259-1272.

67. Dubouzet JG, Sakuma Y, Ito Y, Kasuga M, Dubouzet EG, Miura S, Seki M, Shinozaki K, & Yamaguchi-Shinozaki K (2003) OsDREB Genes In Rice, Oryza Sativa L., Encode Transcription Activators That Function In Drought-, High-Salt-And Cold-Responsive Gene Expression. *Plant Journal* 33(4):751-763.

68. Zhang X, Fowler SG, Cheng HM, Lou YG, Rhee SY, Stockinger EJ, & Thomashow MF (2004) Freezing-Sensitive Tomato Has A Functional CBF Cold Response Pathway, But A CBF Regulon That Differs From That Of Freezing-Tolerant Arabidopsis. *Plant Journal* 39(6):905-919.

69. Fowler S & Thomashow MF (2002) Arabidopsis Transcriptome Profiling Indicates That Multiple Regulatory Pathways Are Activated during Cold Acclimation in Addition to the CBF Cold Response Pathway. *The Plant Cell* 14(8):1675-1690.

70. Xin Z & Browse J (1998) Eskimo1 Mutants Of Arabidopsis Are Constitutively Freezing-Tolerant. *Proceedings of the National Academy of Sciences of the United States of America* 95(13):7799-7804.

71. Xin ZG, Mandaokar A, Chen JP, Last RL, & Browse J (2007) Arabidopsis ESK1 Encodes A Novel Regulator Of Freezing Tolerance. *Plant Journal* 49(5):786-799.

72. Lefebvre V, Fortabat MN, Ducamp A, North HM, Maia-Grondard A, Trouverie J, Boursiac Y, Mouille G, & Durand-Tardif M (2011) ESKIMO1 Disruption In Arabidopsis Alters Vascular Tissue And Impairs Water Transport. *Plos One* 6(2).

73. Zhu JH, Shi HZ, Lee BH, Damsz B, Cheng S, Stirm V, Zhu JK, Hasegawa PM, & Bressan RA (2004) An Arabidopsis Homeodomain Transcription Factor Gene, HOS9, Mediates Cold Tolerance Through A CBF-Independent Pathway. *Proceedings of the National Academy of Sciences of the United States of America* 101(26):9873-9878.

74. Zhu JH, Verslues PE, Zheng XW, Lee B, Zhan XQ, Manabe Y, Sokolchik I, Zhu YM, Dong CH, Zhu JK, Hasegawa PM, & Bressan RA (2005) HOS10 Encodes An R2R3-Type MYB Transcription Factor Essential For Cold Acclimation In Plants (Retracted Article. See Vol. 107, Pg. 13972, 2010). *Proceedings of the National Academy of Sciences of the United States of America* 102(28):9966-9971.

75. Zhu JH, Verslues PE, Zheng XW, Lee BH, Zhan XQ, Manabe Y, Sokolchik I, Zhu YM, Dong CH, Zhu JK, Hasegawa PM, & Bressan RA (2010) HOS10 Encodes An R2R3-Type MYB Transcription Factor Essential For Cold Acclimation In Plants (Retraction Of Vol 102, 9966, 2005). *Proceedings of the National Academy of Sciences of the United States of America* 107(31):13972-13972.

76. Novillo F, Alonso JM, Ecker JR, & Salinas J (2004) CBF2/DREB1C Is A Negative Regulator Of CBF1/DREB1B And CBF3/DREB1A Expression And Plays A Central Role In, Stress Tolerance In Arabidopsis. *Proceedings of the National Academy of Sciences of the United States of America* 101(11):3985-3990.

77. Zarka DG, Vogel JT, Cook D, & Thomashow MF (2003) Cold Induction Of Arabidopsis CBF Genes Involves Multiple ICE (Inducer Of CBF Expression) Promoter Elements And A Cold-Regulatory Circuit That Is Desensitized By Low Temperature. *Plant Physiology* 133(2):910-918.

78. Doherty CJ, Van Buskirk HA, Myers SJ, & Thomashow MF (2009) Roles For Arabidopsis CAMTA Transcription Factors In Cold-Regulated Gene Expression And Freezing Tolerance. *Plant Cell* 21(3):972-984.

79. Knight H, Trewavas AJ, & Knight MR (1996) Cold Calcium Signaling In Arabidopsis Involves Two Cellular Pools And A Change In Calcium Signature After Acclimation. *Plant Cell* 8(3):489-503.

80. Dodd AN, Jakobsen MK, Baker AJ, Telzerow A, Hou SW, Laplaze L, Barrot L, Poethig RS, Haseloff J, & Webb AAR (2006) Time Of Day Modulates Low-Temperature CA2+ Signals In Arabidopsis. *Plant Journal* 48(6):962-973.

81. Chinnusamy V, Ohta M, Kanrar S, Lee B-h, Hong X, Agarwal M, & Zhu J-K (2003) ICE1: A Regulator Of Cold-Induced Transcriptome And Freezing Tolerance In Arabidopsis. *Genes & Development* 17(8):1043-1054.

82. Miura K, Jin JB, Lee J, Yoo CY, Stirm V, Miura T, Ashworth EN, Bressan RA, Yun DJ, & Hasegawa PM (2007) SIZ1-Mediated Sumoylation Of ICE1 Controls CBF3/DREB1A Expression And Freezing Tolerance In Arabidopsis. *Plant Cell* 19(4):1403-1414.

83. Agarwal M, Hao YJ, Kapoor A, Dong CH, Fujii H, Zheng XW, & Zhu JK (2006) A R2R3 Type MYB Transcription Factor Is Involved In The Cold Regulation Of CBF Genes And In Acquired Freezing Tolerance. *Journal of Biological Chemistry* 281(49):37636-37645.

84. Harmer SL, Hogenesch LB, Straume M, Chang HS, Han B, Zhu T, Wang X, Kreps JA, & Kay SA (2000) Orchestrated Transcription Of Key Pathways In Arabidopsis By The Circadian Clock. *Science* 290(5499):2110-2113.

85. Pruneda-Paz JL & Kay SA (2010) An Expanding Universe Of Circadian Networks In Higher Plants. *Trends in Plant Science* 15(5):259-265.

86. Dodd AN, Salathia N, Hall A, Kévei E, Tóth R, Nagy F, Hibberd JM, Millar AJ, & Webb AAR (2005) Plant Circadian Clocks Increase Photosynthesis, Growth, Survival, And Competitive Advantage. *Science* 309(5734):630-633.

87. Michael TP, Salomé PA, Yu HJ, Spencer TR, Sharp EL, McPeek MA, Alonso JM, Ecker JR, & McClung CR (2003) Enhanced Fitness Conferred By Naturally Occurring Variation In The Circadian Clock. *Science* 302(5647):1049-1053.

88. Rawat R, Takahashi N, Hsu PY, Jones MA, Schwartz J, Salemi MR, Phinney BS, & Harmer SL (2011) REVEILLE8 And PSEUDO-REPONSE REGULATOR5 Form A Negative Feedback Loop Within The Arabidopsis Circadian Clock. *Plos Genetics* 7(3).

89. Dai SH, Wei XP, Pei LP, Thompson RL, Liu Y, Heard JE, Ruff TG, & Beachy RN (2011) BROTHER OF LUX ARRHYTHMO Is A Component Of The Arabidopsis Circadian Clock. *Plant Cell* 23(3):961-972.

90. Alabadi D, Oyama T, Yanovsky MJ, Harmon FG, Mas P, & Kay SA (2001) Reciprocal Regulation Between TOC1 And LHY/CCA1 Within The Arabidopsis Circadian Clock. *Science* 293(5531):880-883.

91. McClung CR (2006) Plant Circadian Rhythms. *Plant Cell* 18(4):792-803.

92. Yakir E, Hilman D, Hassidim M, & Green RM (2007) CIRCADIAN CLOCK ASSOCIATED1 Transcript Stability And The Entrainment Of The Circadian Clock In Arabidopsis. *Plant Physiology* 145(3):925-932.

93. Gendron JM, Pruneda-Paz JL, Doherty CJ, Gross AM, Kang SE, & Kay SA (2012) Arabidopsis Circadian Clock Protein, TOC1, Is A DNA-Binding Transcription Factor. *Proceedings of the National Academy of Sciences of the United States of America* 109(8):3167-3172.

94. Mas P, Alabadi D, Yanovsky MJ, Oyama T, & Kay SA (2003) Dual Role Of TOC1 In The Control Of Circadian And Photomorphogenic Responses In Arabidopsis. *Plant Cell* 15(1):223-236.

95. Pruneda-Paz JL, Breton G, Para A, & Kay SA (2009) A Functional Genomics Approach Reveals CHE As A Component Of The Arabidopsis Circadian Clock. *Science* 323(5920):1481-1485.

96. Mizuno T (2004) Plant Response Regulators Implicated In Signal Transduction And Circadian Rhythm. *Current Opinion in Plant Biology* 7(5):499-505.

97. Salome PA & McClung CR (2005) PSEUDO-RESPONSE REGULATOR 7 And 9 Are Partially Redundant Genes Essential For The Temperature Responsiveness Of The Arabidopsis Circadian Clock. *Plant Cell* 17(3):791-803.

98. Nakamichi N, Kita M, Ito S, Sato E, Yamashino T, & Mizuno T (2005) The Arabidopsis Pseudo-Response Regulators, PRR5 And PRR7, Coordinately Play Essential Roles For Circadian Clock Function. *Plant and Cell Physiology* 46(4):609-619.

99. Fujimori T, Sato E, Yamashino T, & Mizuno T (2005) PRR5 (PSEUDO-RESPONSE REGULATOR 5) Plays Antagonistic Roles To CCA1 (CIRCADIAN CLOCK-ASSOCIATED-1) In Arabidopsis Thaliana. *Bioscience Biotechnology and Biochemistry* 69(2):426-430.

100. Farre EM, Harmer SL, Harmon FG, Yanovsky MJ, & Kay SA (2005) Overlapping And Distinct Roles Of PRR7 And PRR9 In The Arabidopsis Circadian Clock. *Current Biology* 15(1):47-54.

101. Farre EM & Kay SA (2007) PRR7 Protein Levels Are Regulated By Light And The Circadian Clock In Arabidopsis. *Plant Journal* 52(3):548-560.

102. Nakamichi N, Kiba T, Henriques R, Mizuno T, Chua NH, & Sakakibara H (2010) PSEUDO-RESPONSE REGULATORS 9, 7, And 5 Are Transcriptional Repressors In The Arabidopsis Circadian Clock. *Plant Cell* 22(3):594-605.

103. Fowler SG, Cook D, & Thomashow MF (2005) Low Temperature Induction Of Arabidopsis CBF1, 2, And 3 Is Gated By The Circadian Clock. *Plant Physiology* 137:961-968.

104. Wang ZY & Tobin EM (1998) Constitutive Expression Of The CIRCADIAN CLOCK ASSOCIATED 1 (CCA1) Gene Disrupts Circadian Rhythms And Suppresses Its Own Expression. *Cell* 93(7):1207-1217.

105. Nakamichi N, Kusano M, Fukushima A, Kita M, Ito S, Yamashino T, Saito K, Sakakibara H, & Mizuno T (2009) Transcript Profiling Of An Arabidopsis PSEUDO RESPONSE REGULATOR Arrhythmic Triple Mutant Reveals A Role For The Circadian Clock In Cold Stress Response. *Plant and Cell Physiology* 50(3):447-462.

## CHAPTER TWO

## CIRCADIAN CLOCK-ASSOCIATED 1 and LATE ELONGATED HYPOCOTYL regulate expression of the CBF cold response pathway and freezing tolerance in *Arabidopsis*

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## CHAPTER TWO

## CIRCADIAN CLOCK-ASSOCIATED 1 and LATE ELONGATED HYPOCOTYL regulate expression of the CBF cold response pathway and freezing tolerance in *Arabidopsis*


### SUMMARY

The C-REPEAT BINDING FACTOR (CBF) cold response pathway has a prominent role in cold acclimation, the process whereby certain plants increase in freezing tolerance in response to low non-freezing temperatures. In *Arabidopsis*, the CBF pathway is characterized by rapid induction of the *C-REPEAT BINDING FACTOR 1* (*CBF1*), *CBF2* and *CBF3* genes, which encode transcriptional activators, followed by induction of the CBF-targeted genes known as the CBF regulon. Expression of the CBF regulon results in an increase in freezing tolerance. Previous studies established that *CBF1, CBF2* and *CBF3* are subject to circadian regulation and that their cold induction is gated by the circadian clock.

Here we present the results of genetic analysis and chromatin-immunoprecipitation experiments indicating that both of these forms of regulation involve direct positive action of two transcription factors that are core components of the clock, i.e., CIRCADIAN CLOCK ASSOCIATED 1 (CCA1) and LATE ELONGATED HYPOCOTYL (LHY). In plants carrying the *cca1*-11/*lhy*-21 double mutation, cold induction of *CBF1*, *CBF2* and *CBF3* was greatly impaired and circadian regulation of *CBF1* and *CBF3* was essentially eliminated; circadian regulation of *CBF2* continued, though with significantly reduced amplitude. Circadian regulation and cold induction of the CBF regulon genes *COLD-REGULATED GENE15A* (*COR15A*), *COR47* and

*COR78* were also greatly diminished in plants carrying the *cca1*-11/*lhy*-21 double mutation. Furthermore, the *cca1*-11/*lhy*-21 double mutation resulted in impaired freezing tolerance in both non-acclimated and cold-acclimated plants. These results indicate that CCA1/LHY-mediated output from the circadian clock contributes to plant cold tolerance through regulation of the CBF cold response pathway.

## INTRODUCTION

A general feature of plants from temperate environments is that they increase in freezing tolerance in response to low non-freezing temperatures, a process called cold acclimation (1, 2). It is now well established that cold acclimation involves extensive changes in gene expression (3-6). The best understood cold regulatory pathway is the CBF pathway. This pathway, which is widely conserved in plants (7), is best characterized in *Arabidopsis* (8, 9). When *Arabidopsis* plants are transferred from warm to cold temperature, *C-REPEAT BINDING FACTOR 1* (*CBF1*), *CBF2* and *CBF3*–also known as *DROUGHT REPONSE ELEMENT BINDING FACTOR1B* (*DREB1B*), *DREB1C* and *DREB1A*, respectively—are rapidly induced. These genes, which are physically linked in tandem array, encode transcription factors that are members of the AP2/ERF family of DNA binding proteins (10). The CBF proteins bind to the CRT/DRE regulatory element present in the promoters of about 100 cold-regulated (COR) genes, known as the CBF regulon, and induce their expression (4, 6, 11). Constitutive overexpression of *CBF1, CBF2* and *CBF3* at warm temperature results in constitutive expression of the CBF regulon and an increase in freezing tolerance (12-14). The mechanisms whereby expression of the CBF regulon promotes freezing tolerance are not completely understood, but involve the synthesis of low molecular weight cryoprotectants such as sucrose and raffinose and proteins that have cryoprotective properties (1, 2).

Given their importance in cold acclimation, efforts have been directed at understanding the mechanisms involved in cold-induction of *CBF1, CBF2* and *CBF3*. To date, two positive regulators have been identified: INDUCER OF CBF EXPRESSION

1 (ICE1), a MYC family transcription factor that positively regulates *CBF3* (15), and CALMODULIN BINDING TRANSCRIPTION ACTIVATOR 3 (CAMTA3), a CAMTA family transcription factor that positively regulates *CBF1* and *CBF2* (16). The *ICE1* and *CAMTA3* genes are transcribed at warm temperature, indicating that their activities involve posttranscriptional regulatory mechanisms that are responsive to low temperature (16-18).

Another factor that affects the expression of *CBF1, CBF2* and *CBF3* is the circadian clock (19-22). At warm temperature, the transcript levels for *CBF1, CBF2* and *CBF3* oscillate with a peak at about 8 h after dawn (ZEITGEBER TIME 8; ZT8), and a trough at about ZT20. Moreover, cold-induction of *CBF1, CBF2* and *CBF3* is "gated" by the clock (22); if plants are exposed to low temperature at ZT4, the increase in *CBF1, CBF2* and *CBF3* transcript levels is much greater than if plants are exposed to low temperature at ZT16. These results indicate that cold induction of *CBF1, CBF2* and *CBF3* involves the integration of low temperature and clock regulatory pathways.

The circadian clock of *Arabidopsis* consists of multiple interlocking regulatory feedback loops (23, 24). Key components of the core feedback loop are CIRCADIAN CLOCK ASSOCIATED 1 (CCA1) and LATE ELONGATED HYPOCOTYL (LHY), MYB transcription factors that have partially overlapping functions (25-28), and TIMING OF CAB 1 (TOC1), a PSEUDO RESPONSE REGULATOR (PRR) protein (29). Expression of *CCA1* and *LHY* peaks just after dawn, while the expression of *TOC1* peaks in the early evening. CCA1 and LHY bind to the Evening Element (EE) (19) present in the promoter of *TOC1* and repress its transcription (30). TOC1 is necessary for the

induction of both *CCA1* and *LHY* (28). TOC1 is known to inhibit the repression of *CCA1* by the TCP transcription factor CCA1 HIKING EXPEDITION 1 (CHE1) (31), but the means by which *LHY* expression is activated by TOC1 remains unknown. CCA1 and LHY also regulate expression of PSEUDO RESPONSE REGULATOR 7 (PRR7) and PRR9 (32, 33), two components of the morning regulatory loop. CCA1 and LHY bind to the promoters of these two genes to induce their expression and the PRR7 and PRR9 proteins then negatively regulate *CCA1* and *LHY* (32, 33).

It was recently reported that *Arabidopsis* plants carrying the *prr5/prr7/prr9* triple mutation constitutively express *CBF1*, *CBF2* and *CBF3* at high levels and display constitutively high levels of freezing tolerance (34). Thus, it was proposed that PRR5, PRR7 and PRR9 might act as direct negative regulators of *CBF1*, *CBF2* and *CBF3* (34). Here we present results indicating that the clock also provides positive regulation of the CBF cold response pathway and enhances freezing tolerance through action of the core clock components CCA1 and LHY.

## RESULTS

***CCA1 and LHY have a direct role in circadian regulation of CBF1, CBF2 and CBF3.*** Consistent with previous reports (19-21), we found that *CBF1, CBF2* and *CBF3* are subject to circadian regulation (Fig. 2.1). Transcript levels for *CBF1, CBF2* and *CBF3* oscillated with a peak occurring at about ZT8 followed by a second peak about 24 h later. The oscillation patterns for the three *CBF* genes were similar, though we observed one consistent difference; whereas the ZT8 peak for *CBF1* was lower than the second peak, the ZT8 peaks for *CBF2* and *CBF3* were greater than the second peak. Thus, the transition from dark to light may have a specific effect on the regulation of *CBF1*.

Three lines of evidence led us to think that CCA1 and LHY might drive circadian regulation of *CBF1, CBF2* and *CBF3*. First, the protein levels for *CCA1* and *LHY* peak in the early morning (ZT1-3) (26, 35, 36), just prior to when the transcript levels of *CBF1, CBF2,* and *CBF3* begin to increase. Second, the transcript levels for *PRR7* (32, 36) and *LIGHT HARVESTING COMPLEX B* (*LHCB*) (24, 35, 37)**,** both of which are induced by CCA1 and LHY, peak similarly to the *CBF* genes. Lastly, the promoter regions of *CBF1, CBF2* and *CBF3* have several EE (AAAATATCT) (19) and CCA1-Binding Sites (CBS; AATCT) (35) (Fig. 2.2), which mediate binding of CCA1 and LHY (30, 35, 38) to target promoters. To determine whether CCA1 and LHY were involved in circadian regulation of *CBF1*, *CBF2* and *CBF3*, we asked whether their expression was affected in plants carrying either the single *cca1*-11 or *lhy*-21 null mutations or the *cca1*-11/*lhy*-21 double mutation. We found that the single mutations had differing effects on

the three *CBF* genes; whereas cycling of *CBF1* was severely disrupted, *CBF2* and *CBF3* transcript levels cycled with approximately the same amplitudes as in the wild-type plants, though the peaks were about 2 h earlier than in the wild-type plants (Fig. A2.1). Period shortening of output genes such as *LHCB* has been previously observed in *cca1* and *lhy* mutant plants (39, 40), which we also observed in our experiments (Fig. A2.2). The *cca1*-11/*lhy*-21 double mutations also had differing effects on the circadian regulation of the three *CBF* genes (Fig. 2.1); whereas circadian regulation of *CBF1* and *CBF3* was essentially eliminated in the double mutant plants, *CBF2* transcript levels clearly continued to cycle, though the amplitude was diminished and the period was greatly shortened. Period shortening of output genes such as *LHCB* has also been previously observed in *cca1-11/lhy-21* double mutant plants (40, 41) and in our experiments (Fig. A2.3). From these results we concluded that circadian regulation of *CBF1* and *CBF3* is dependent on the action of either CCA1 or LHY and that circadian regulation of *CBF2* involves action of CCA1 and LHY, but can be driven to a considerable degree by other unknown factors.

CCA1 and LHY may impart circadian regulation of *CBF1, CBF2* and *CBF3* by binding to the EE and CBS motifs present in the *CBF* promoters and act as positive regulators stimulating transcription. To test this hypothesis, we conducted chromatin immunoprecipitation (ChIP) experiments to determine whether CCA1 binds directly to the promoter regions of *CBF1, CBF2* and *CBF3*. This was assessed by comparing ChIP results obtained with plants carrying the *cca1*-1 mutation and *cca1*-1 plants that had been restored with a construct encoding the CCA1 protein tagged with green

fluorescent protein (GFP) under the endogenous CCA1 promoter (31). Chromatin was isolated from plants harvested at ZT4, the point when *CBF* transcript levels begin to rise. In mock experiments where rabbit immunoglobulin was used for precipitation, no specific binding was detected for any of the sub-regions (A to O) of the *CBF1-3* locus tested or for *TOC1*, *ACTIN7* or *UBIQUITIN10* (Fig. A2.4). In contrast, test experiments indicated that specific binding of the CCA1-GFP protein occurred throughout most of the *CBF1-3* locus and as well as within the promoter region of *TOC1*, a positive control, but not in the promoters of *ACTIN7* or *UBIQUITIN10*, two negative controls (31) (Fig. 2.2). Significant CCA1-GFP binding occurred in the promoter regions of *CBF1* (C), *CBF2* (L), and *CBF3* (G and I). We also observed CCA1 associated with the coding region of *CBF1* (E). This could be due to the tandem connection of the CBF genes and consequently, close proximity to several CCA1 binding sites located in the adjacent *CBF3* promoter (Fig. 2.2). Thus, although it is possible that there is CCA1 binding within the *CBF1* transcript region, the actual binding site could be downstream in the *CBF3* promoter. In sum, the results of our genetic and ChIP experiments supported the model that circadian regulation of *CBF1, CBF2* and *CBF3* involves action of CCA1 and LHY binding to the promoters of these genes and up-regulating their transcription during the morning hours.

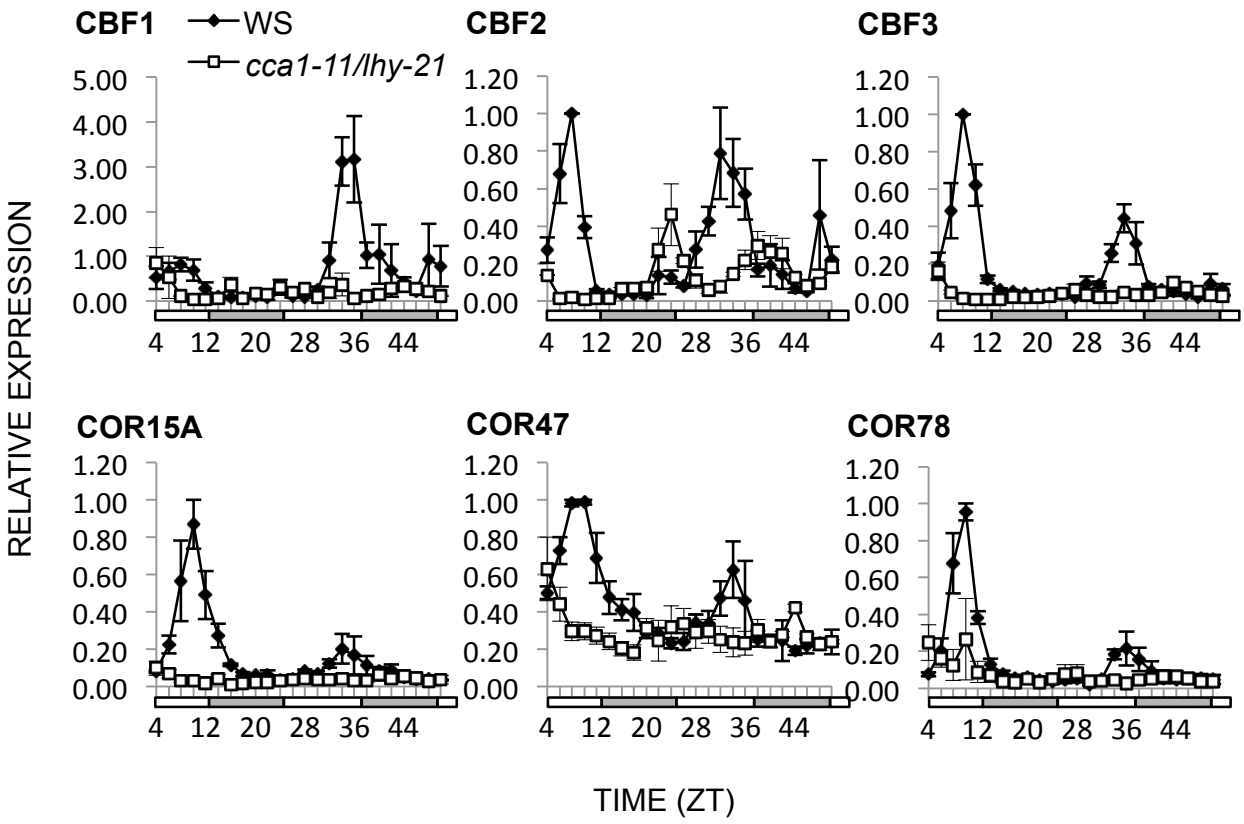


**Figure 2.1.** Effects of the *cca1-11/lhy-21* double mutation on circadian regulation of *CBF1*, *CBF2*, *CBF3* and CBF-targeted genes *COR15A*, *COR47* and *COR78*. Wild-type Ws-2 (WS) and *cca111/lhy-21* double mutant plants were grown at 22$^0$C under a 12 h photoperiod to the four leaf stage and transferred to constant light at ZT0 (subjective day and night are indicated by white and gray bars, respectively). Plants were harvested every 2 h and the transcript levels for the indicated genes were determined by qRT-PCR. Gene expression was normalized to IPP2 for each sample. Gene expression is relative to one wild-type sample set to a value of 1 for each biological replicate. Values are averages from three independent biological experiments (n=3). Error bars indicate ±SEM.

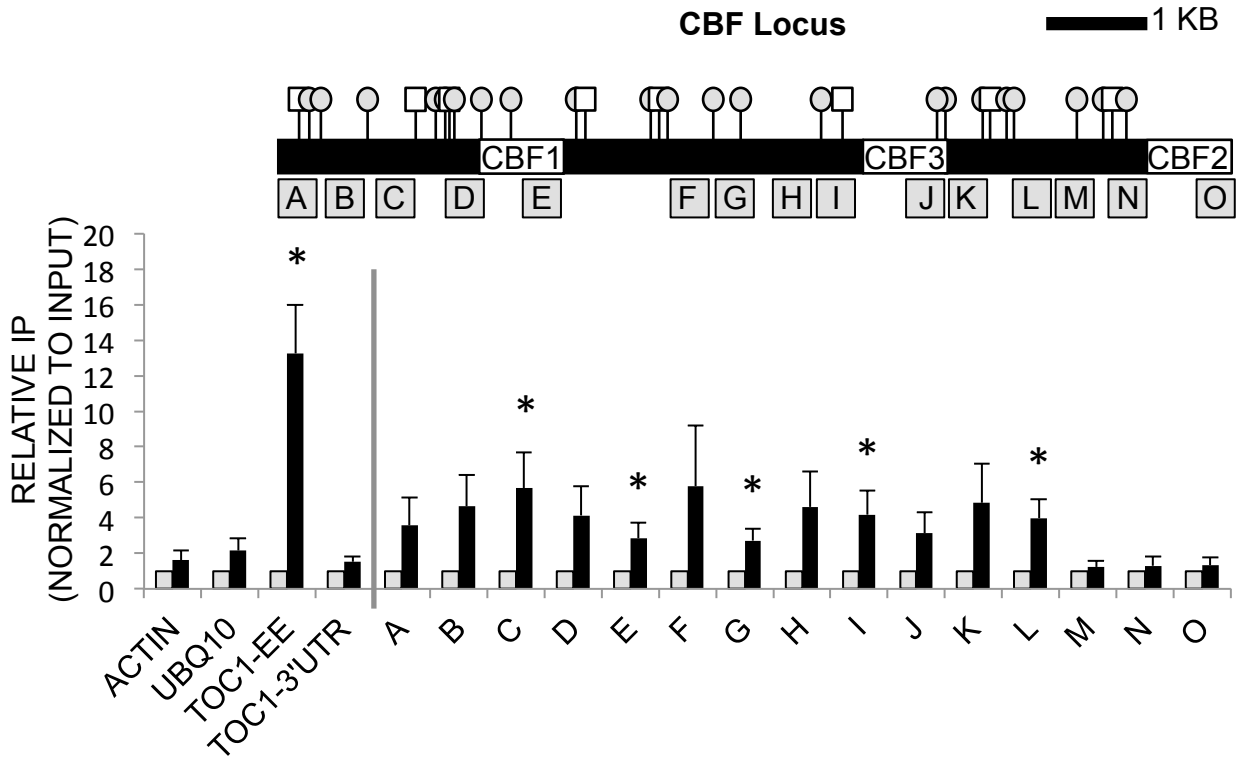


**Figure 2.2.** Binding of CCA1 at the *CBF1-3* locus. *cca1-1* and *cca1-1 CCA1p:CCA1-GFP* plants were grown at 22$^0$C under a 12 h photoperiod to the four leaf stage. Tissue was fixed at ZT4 and ChIP was performed using anti-GFP antibody. Immunoprecipitated DNA was quantified by qRT-PCR using primers specific to regions within the *CBF1-3* locus (boxes A through O). The levels of immunoprecipitated DNA were normalized to the respective input DNA. Immunoprecipitation in *cca1-1 CCA1p:CCA1-GFP* plants (black bars) is relative to *cca1-1* plants (gray bars) set to a value of 1. Primer pairs directed to the 3'-untranslated region of *TOC1* (TOC1-3'UTR), *ACTIN7* (ACTIN) and *UBIQUITIN10* (UBQ10) were used as negative controls (31). Primers near the EE element in the *TOC1* promoter (TOC1-EE) were used as a positive control. Values represent the average of five independent biological experiments (n=5). Error bars indicate ± SEM. *=p<0.05 using a paired, one-tailed t-test. In the *CBF* locus diagram, the transcribed regions are indicted with white boxes and the approximate positions of CBS (AATCT), and EE (AAAATATCT) motifs are indicated by gray circles, and white squares respectively.

***Rhythmic expression of CBF regulon COR genes and freezing tolerance is impaired in plants carrying the cca1-11/lhy-21 double mutation.*** Harmer *et al.* (19) suggested that the circadian regulation of *CBF1*, *CBF2* and *CBF3* could potentially result in rhythmic expression of CBF regulon *COR* genes. To test this, we examined the transcript levels for three CBF-inducible genes—*COR15A*, *COR47* and *COR78*—in wild-type plants and in plants carrying the *cca1*-11/*lhy*-21 double mutation. The results indicated that the transcript levels for all three *COR* genes oscillated with a period of about 24 h in wild-type plants, though the amplitude of the second peak was much less than that of the first for *COR15A* and *COR78* (Fig. 2.1). For all three genes, the first peak was at about ZT10, which was consistent with the transcript levels of *CBF1*, *CBF2* and *CBF3* peaking just before this at about ZT8 (19, 20) (Fig. 2.1). Moreover, the oscillation in *COR* transcript levels was largely reduced in the *cca1*-11/*lhy*-21 double mutant plants (Fig. 2.1). These results were consistent with the model that circadian-regulated expression of *CBF1*, *CBF2* and *CBF3* imparts rhythmic expression of CBF-targeted *COR* genes at "basal" non-acclimating temperatures.

The decrease in expression of the CBF-targeted *COR* genes in the *cca1*-11/*lhy*-21 double mutant plants could potentially result in a decrease in basal freezing tolerance. We tested this using the electrolyte leakage assay to compare the freezing tolerance of wild-type and *cca1*-11/*lhy*-21 plants. The results indicated that the *cca1*-11/*lhy*-21 double mutation reduced freezing tolerance by about 50%; whereas the $EL_{50}$ (temperature at which cell damage results in release of 50% of total electrolytes) of wild-

type plants was about -4°C, it was about -2°C in the *cca1*-11/*lhy*-21 mutant plants (Fig. 2.3). Thus, the circadian clock is required for maximum basal freezing tolerance.

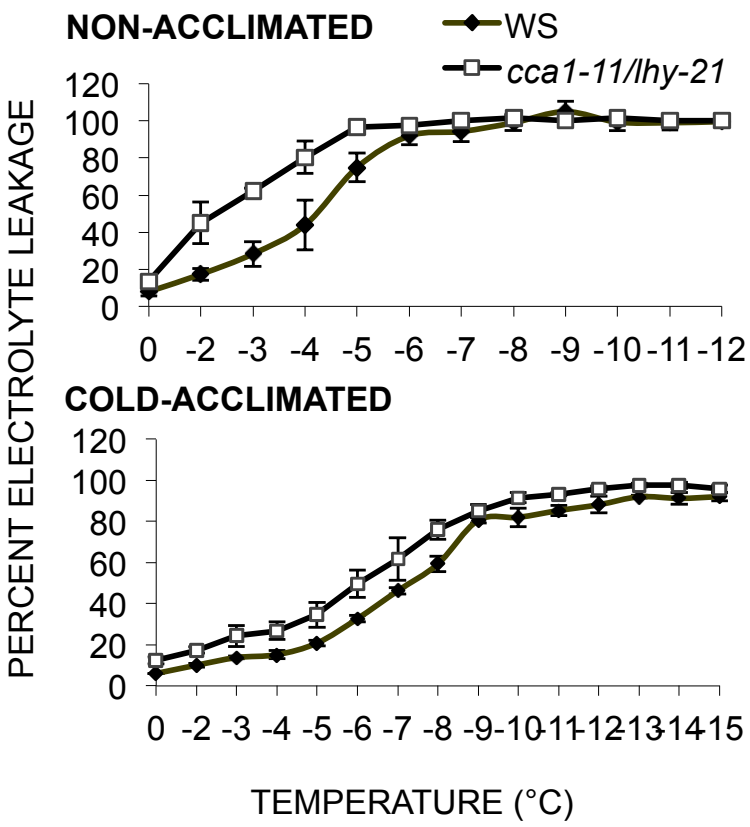


**Figure 2.3.** Effect of the *cca1-11/lhy-21* double mutation on plant freezing tolerance. *cca1*-11/*lhy*-21 double mutant and wild-type Ws-2 (WS) plants were grown at $22^0$C under a 12 h photoperiod for approximately 18 days and either tested directly for freezing tolerance (non-acclimated plants; top graph) or were transferred at ZT4 to $4^0$C for 7 days under a 12 h photoperiod and then tested for freezing tolerance (cold-acclimated plants; bottom graph). Freezing tolerance was tested using the electrolyte leakage test. The results presented are average values from three independent experiments (n=3). Error bars indicate ±SEM.

***CCA1 and LHY regulate cold induction of CBF1, CBF2 and CBF3.*** Fowler *et al.* (22) reported that cold induction of *CBF1*, *CBF2*, and *CBF3* is gated by the circadian clock. Given our results indicating a role for CCA1 and LHY in the circadian regulation of *CBF1, CBF2* and *CBF3*, we asked whether these transcription factors also had a role in the gating phenomenon. As previously reported (22, 34), cold-induction of *CBF1*, *CBF2*, and *CBF3* was much greater in the subjective day than in the subjective evening (Fig. 2.4). This cold induction was little affected by the single *cca1*-11 and *lhy*-21 mutations (Fig. A2.1), but was greatly reduced in the *cca1*-11/*lhy*-21 double mutants and the period of cycling was shortened (Fig. 2.4) as was the period of cycling for *LHCB* (Fig. A2.3). Thus, CCA1 and LHY have a major role in the induction of *CBF1*, *CBF2* and *CBF3* expression in response to low temperature.

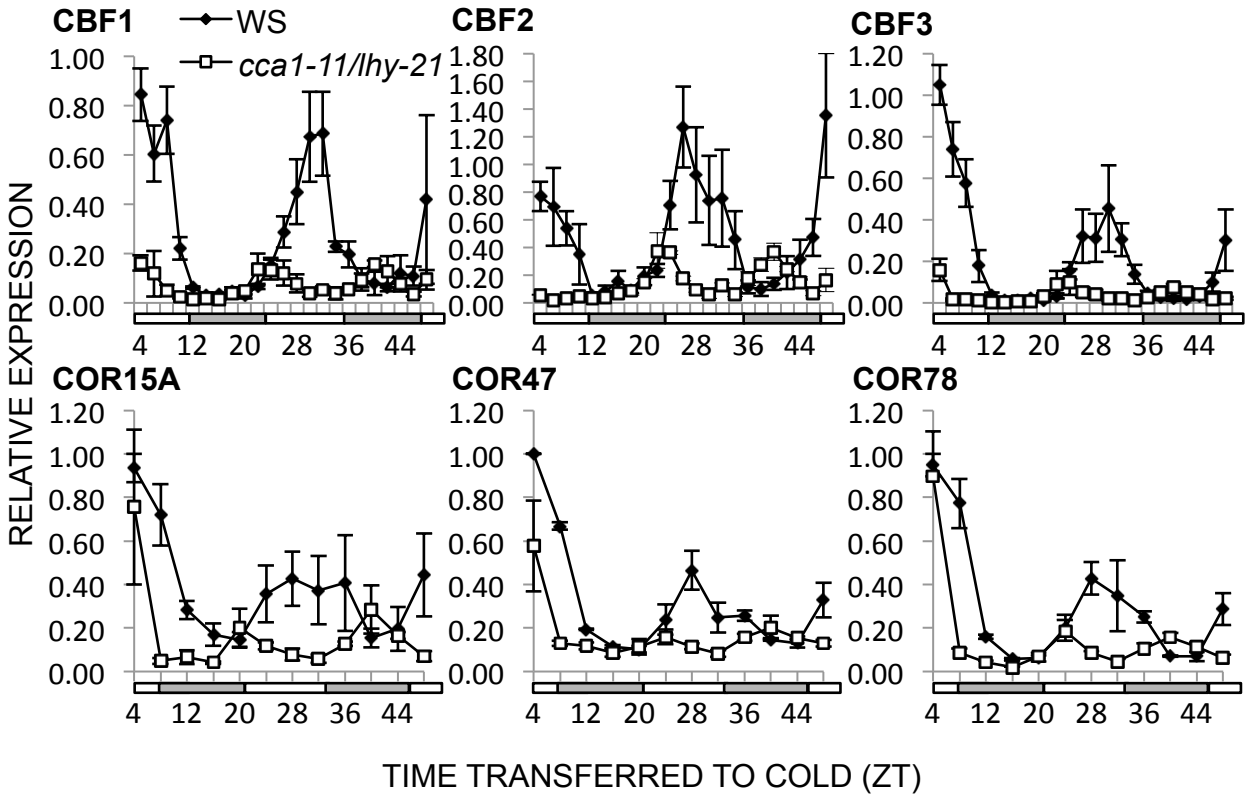


**Figure 2.4.** Effects of the *cca1-11/lhy*-21double mutation on cold induction of *CBF1*, *CBF2*, *CBF3* and CBF-targeted genes *COR15A*, *COR47* and *COR78*. Wild-type Ws-2 (WS) and *cca1*-11*/lhy*-21 double mutant plants were grown at 22$^0$C under a 12 h photoperiod to the four leaf stage and transferred to constant light at ZT0 (subjective day and night are indicated by white and gray bars, respectively). Plants were transferred to cold temperature (4$^0$C) for 2 h, every 2 h (*CBF* genes) or for 4 h, every 4 h (*COR* genes) at the start of constant light conditions. Transcript levels for the indicated genes were determined by qRT-PCR. Horizontal axis represents time (ZT) when plants were transferred to cold temperature. Gene expression was normalized to UBQ10 for each sample. Gene expression is relative to one wild-type sample set to a value of 1 for each biological replicate. Values are averages from three independent biological experiments (n=3). Error bars indicate ±SEM. See Table A2.1 for primer pair sequences.

***Cold induction of CBF-targeted COR genes and freezing tolerance is impaired in plants carrying the cca1-11/lhy-21 double mutation.*** The finding that cold induction of *CBF1*, *CBF2* and *CBF3* was impaired in plants carrying the *cca1*-11/*lhy*-21 double mutation prompted us to determine whether the double mutation also impaired cold induction of CBF-targeted *COR* genes and the freezing tolerance of cold-acclimated plants. In wild-type plants, the degree to which *COR15A*, *COR47* and *COR78* were induced by low temperature cycled with peaks in the late day and troughs in the late subjective evening (Fig. 2.4), times that were consistent with the cycling of *CBF1*, *CBF2* and *CBF3* cold induction (Fig. 2.4). In plants carrying the *cca1*-11/*lhy*-21 double mutation, the peak following the night to day transition was little affected, but the subsequent peaks were greatly diminished and the period of cycling was shortened (Fig. 2.4). In addition, the freezing tolerance of cold-acclimated plants carrying the *cca1*-11/*lhy*-21 double mutation was about 1°C less than that of cold-acclimated wild-type plants (Fig. 2.3). These results indicate that CCA1 and LHY are required for *Arabidopsis* plants to attain maximum levels of *COR* gene induction and freezing tolerance in response to low temperature.

## DISCUSSION

The CBF cold response pathway is highly conserved among plants and has a major role in plant freezing tolerance (1-3, 9). Accordingly, there is considerable interest in understanding the mechanisms that control expression of this stress response pathway. Here we establish that the CBF pathway is subject to positive regulation by the circadian clock components CCA1 and LHY. We show that these factors have roles in both circadian regulation and cold induction of the pathway and that they are required for plants to attain maximum freezing tolerance at both basal and cold acclimating temperatures.

At basal growth temperature, the transcript levels for *CBF1, CBF2*, and *CBF3* oscillate with peaks and troughs occurring at about ZT8 and ZT20, respectively (19-21) (Fig. 2.1). Our genetic and ChIP analyses indicate that this circadian regulation is due to direct action of CCA1 and LHY binding at the *CBF1-3* locus—presumably at the EE, CBS, and related motifs—and inducing transcription of the *CBF* genes. In the morning hours when CCA1 and LHY protein levels peak (25, 35, 36), the transcript levels of *CBF1, CBF2*, and *CBF3* peak; and in the evening hours, when CCA1 and LHY protein levels are low, the transcript levels for *CBF1, CBF2*, and *CBF3* are low (Fig. 2.5). The finding that circadian regulation of *CBF1* and *CBF3* is nearly eliminated in plants carrying the *cca1*-11/*lhy*-21 double mutation indicates that no other regulatory proteins are sufficient to impart positive circadian regulation of these genes. In contrast, circadian regulation of *CBF2* continues in plants carrying the *cca1*-11/*lhy*-21 double mutation, albeit with reduced amplitude and shortened periodicity. Thus, at least one

additional regulatory protein appears to drive positive circadian regulation of *CBF2*. Prime candidates for this residual regulation are the four REVEILLE (RVE) proteins RVE1, RVE3, RVE4 and RVE8 (42). These MYB-like transcription factors fall into the CCA1 subfamily, bind to the EE motif, are circadian-regulated, and like CCA1 and LHY, have peak transcript levels at dawn (42).

Kidokoro *et al.* (21) reported that circadian regulation of *CBF1*, *CBF2*, and *CBF3* also involves negative regulation. These investigators found that PIF7 binds to a G-box element in the promoter of *CBF2* and that this element was required for down-regulation of the *CBF2* promoter during the subjective evening. In addition, it was found that PIF7 physically interacts with TOC1 (21). Thus, circadian-controlled down-regulation of the *CBF* genes appears to involve action of a PIF7-TOC1 protein complex binding to G-box elements in their promoters (Fig. 2.5).

In addition to establishing a role for CCA1 and LHY in circadian regulation of *CBF1*, *CBF2* and *CBF3,* our results indicate that CCA1 and LHY also act as positive regulators of *CBF* cold induction. This is evidenced by the finding that cold induction of *CBF1*, *CBF2* and *CBF3* is greatly impaired in plants carrying the *cca1*-11/*lhy*-21 double mutation (Fig. 2.4). We propose that the gating of *CBF1*, *CBF2* and *CBF3* cold induction results, in part, from positive synergistic interaction between cold-signaling and clock output pathways, the former mediated by ICE1 and CAMTA3, and the latter by CCA1 and LHY (Fig. 2.5). If the temperature drops in the morning, CCA1 and LHY are present at the *CBF* locus and can act with ICE1 and CAMTA3 to induce high level expression of C*BF1*, *CBF2* and *CBF3*. In contrast, if the temperature drops in the

evening, CCA1 and LHY are at low levels and consequently, there is little synergy between the low temperature and clock pathways and the induction of *CBF1*, *CBF2* and *CBF3* is low, approximating the peak levels obtained with circadian regulation (Fig. 2.5).

Cold induction of *CBF1*, *CBF2* and *CBF3* during the evening hours may also involve negative regulation. Such regulation would not appear to involve PIF7, as Kidokoro *et al.* (21) showed that the gating of *CBF1*, *CBF2*, and *CBF3* expression is not impaired in plants carrying the *pif7*-2 mutation (21). However, Nakamichi *et al.* (34) found that circadian regulation of *CBF1*, *CBF2* and *CBF3*, and the gating of their cold induction, does not occur in plants carrying the *prr9*-11*/prr7*-10*/prr5*-10 triple mutation. When plants were grown at basal temperature, the transcript levels for *CBF1*, *CBF2* and *CBF3* remained high throughout the day in the triple mutant plants (34). Similarly, the cold induction of *CBF1*, *CBF2* and *CBF3* in the triple mutant plants remained at about the peak levels observed in wild-type plants regardless of the time of day at which the mutant plants were exposed to low temperature (34). Nakamichi et al. (34) concluded that PRR9, PRR7 and PRR5 are negative regulators of *CBF1*, *CBF2* and *CBF3* and proposed two possible mechanisms. One was that PRR9, PRR7 and PRR5 directly repress expression of the *CBF* genes. Alternatively, they suggested that aberrant expression of the *CBF* genes might result from the "circadian disorder" caused by the *prr9*-11*/prr7*-10*/prr5*-10 triple mutation. Our results provide no direct evidence in favor of, or against, the first model. However, the consistently high *CBF* expression may be partially explained by the constitutively elevated expression of *CCA1* and *LHY* in the triple mutant plants (34, 43).

A final point regards the role of the clock in freezing tolerance. Our results indicate that CCA1 and LHY are required for *Arabidopsis* to attain maximum levels of freezing tolerance at both non-acclimating and cold-acclimating temperatures (Fig. 2.3). Recently, Espinoza et al. (44) independently reached the same conclusion as they also found that the *cca1*-11/*lhy*-21 double mutation resulted in impaired freezing tolerance. Our results also indicate a mechanism whereby cold-signaling and clock regulatory pathways are integrated to condition freezing tolerance; the positive regulation of the CBF cold response pathway mediated through CCA1 and LHY binding at the *CBF1-3* locus and inducing expression of *CBF1*, *CBF2* and *CBF3* (Fig. 2.5). Taken together, our results suggest that the integration of cold signaling pathways with the circadian clock may have been an important evolutionary event that has contributed to plant adaptation to cold environments.

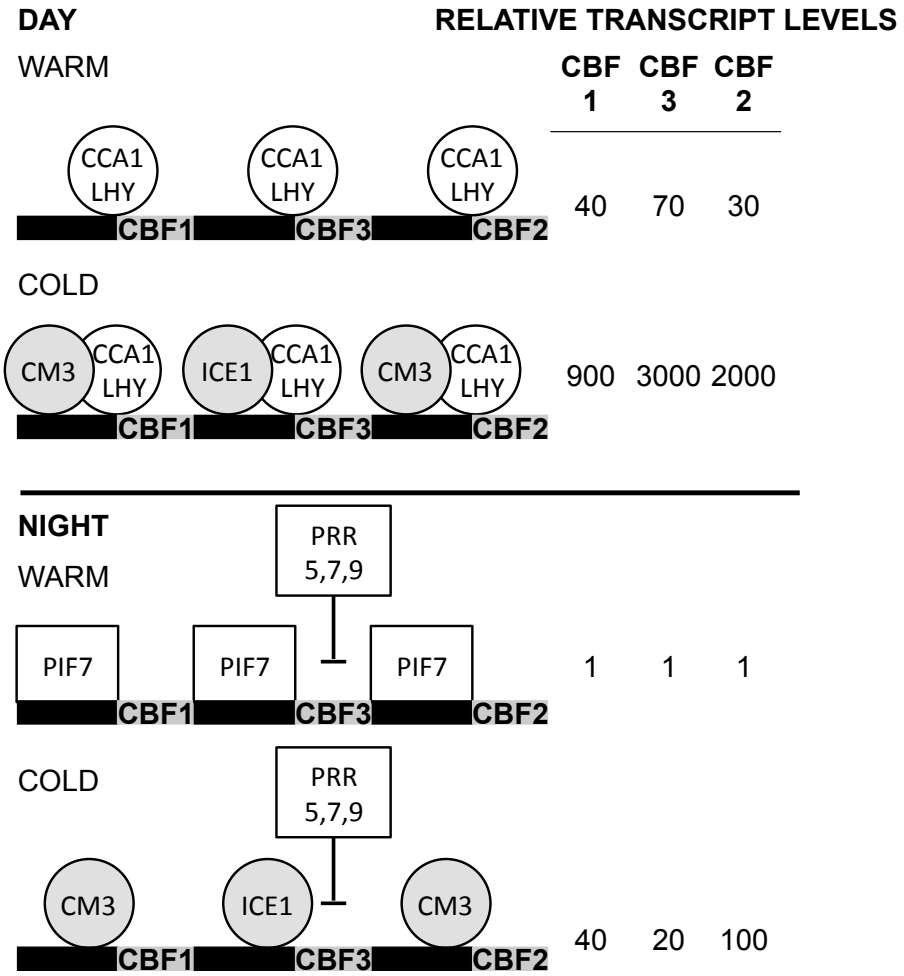


**Figure 2.5.** Model for circadian regulation and gated cold-induction of *CBF1*, *CBF2* and *CBF3.* During the day, CCA1 and LHY bind throughout the *CBF* locus and promote *CBF* transcription. In the evening, CCA1 and LHY are at low levels and have little effect on *CBF* expression. Oscillations in CCA1 and LHY binding at the *CBF* locus largely account for the circadian regulation of the *CBF* genes. Circadian regulation also involves repression in the evening hours mediated by PIF7 (21) and PRR5, PRR7 and PR9 (34). Transfer of plants to low temperature in the day or evening results in activation of ICE1 (15) and CAMTA3 (CM3) (16), and possibly other transcription factors, that stimulate transcription of the *CBF* genes. If the temperature drops during the day, the clock and cold-signaling pathways act synergistically to induce *CBF* expression to high levels. If plants are exposed to cold temperatures in the evening, there is no positive synergy between the two pathways and there is repression by PRR5, PRR7 and PR9 (34) leading to *CBF* induction at moderate levels. Relative transcript levels were calculated using peak and trough values obtained for the *CBF* genes in the experiments presented in Fig. 2.2.1 and Fig. 4 (the values obtained for plants grown at warm temperature and harvested in the evening were set to 1). See Discussion for details.

## MATERIALS AND METHODS

**Plant Material and Growth Conditions.** *Arabidopsis thaliana* ecotype WS-2 and mutants in this background were grown as described previously (16). Homozygous T-DNA mutant lines were obtained from the *Arabidopsis* Biological Resource Center (45). Null mutations were checked by qRT-PCR. These lines were *cca1-11*(CS9378), *lhy-21* (CS9379) and *cca1-11/lhy-21*(CS9380). Restored *cca1-1* line, CCA1p:CCA1-GFP under the CCA1 endogenous promoter and *cca1-1* (31), used in ChIP experiments, were generously donated by the Kay Lab (University of California, San Diego).

All seeds were stratified for 3 to 5 days in the dark at $4^0$C. Except for freezing tolerance tests, plants were grown at $22^0$C under sterile conditions on Gamborg's B5 medium (Caisson Laboratories) without sucrose at ~100 $\mu$mol $m^{-2}s^{-1}$ in a 12 h photoperiod. For circadian experiments, plants were sampled at $22^0$C in 100 $\mu$mol $m^{-2}s^{-1}$ constant light or at $4^0$C in 35 $\mu$mol $m^{-2}s^{-1}$ constant light. For electrolyte leakage experiments plants were grown as described (16) at ~100 $\mu$mol $m^{-2}s^{-1}$ under a 12 h photoperiod. Cold temperature treatment for plants grown on soil was at $4^0$C in light at 35 $\mu$mol $m^{-2}s^{-1}$ under a 12 h photoperiod.

**RNA Analysis.** RNA extraction was performed as described (16). For qRT-PCR (Applied Biosystems 7500 FAST Real-Time PCR System in FAST mode), cDNA was made as described in (16) except that total RNA of either 0.2 or 0.025 $\mu$g was used for a

40 μL reverse-transcription reaction. In the 10 μL PCR reactions, 2 μL of diluted cDNA was used. UBQ10 or IPP2 were used as reference genes. All primer sets can be found in Table A2.1.

**Chromatin Immunoprecipatation.** ChIP experiments were carried out as described by Pruneda-Paz et al. (31) with a few modifications. CCA1p:CCA1-GFP and *cca1-1* lines were sampled at ZT4 instead of ZT3. DNA was also purified by PCR Clean-Up Kit (Qiagen) instead of phenol-chloroform extraction. Immunoprecipitated DNA was analyzed with Applied Biosystems FAST real-time PCR in FAST mode (using presets). For each biological replicate immunoprecipitated DNA was normalized to the input DNA as in (31) and each of these values were expressed relative to the *cca1-1* line set to a value of 1. A one-tailed paired t-test was performed to assess the statistical significance of enrichment in the CCA1p:CCA1-GFP line compared to *cca1-1* plants for each primer pair used across biological replicates. Primers pairs used in ChIP experiments can be found in Table A2.1.

**Freezing Tolerance Tests.** Electrolyte leakage assays were performed as described in (16). For cold acclimation, plants were transferred to $4^0$C at ZT4 for 7 days under a 12 h photoperiod. Assays for acclimated and non-acclimated plants started at ~ZT2 in all biological replicates.

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We thank Steve Kay for providing us with the Arabidopsis lines carrying the *cca1-1* mutation and the restored line expressing the CCA1-GFP fusion and are grateful to Sarah Gilmour for her help in preparing the manuscript. This research was funded by grants from the NSF Plant Genome Project (DBI 0701709); the Division of Chemical Sciences, Geosciences, and Biosciences, Office of Basic Energy Sciences of the U.S. Department of Energy (DE-FG02-91ER20021); and the Michigan Agricultural Experiment Station.

# APPENDIX

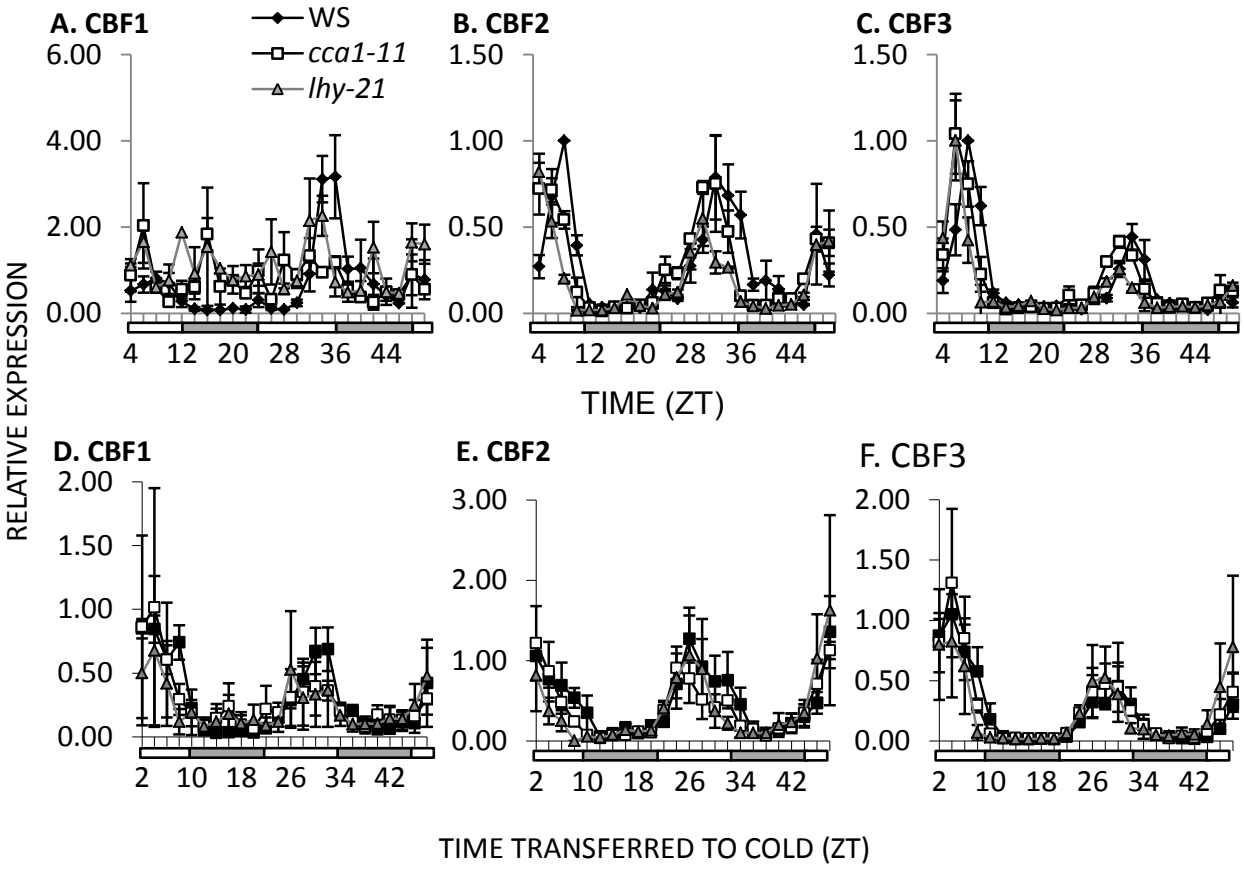


**Figure A2.1.** Circadian rhythms and gated expression of CBF genes in *cca1-11* and *lhy-21.* qRT-PCR analysis for *CBF1, CBF2* and *CBF3* in *cca1-11*(white boxes), *lhy-*21(grey triangles) and wild-type (WS) (black diamonds). Expression for each gene was relative to one wild-type sample (WS) set to a value of 1 in each biological replicate. Values are averages of three independent experiments (n=3) for WS, error bars indicate ± SEM. Values are average of two independent experiments (n=2) for *cca1-11* and *lhy-21*, error bars indicate ± range. (A-C) Plants were grown with a 12 h photoperiod at $22^0$C to the four leaf stage and transferred to constant light at ZT0 (subjective day and night are indicated by white and gray bars, respectively). Plants were harvested every 2 h and the transcript levels for the indicated genes were determined by qRT-PCR. Gene expression was normalized to IPP2 for each sample. (D-F) Plants were grown with a 12 h-photoperiod at $22^0$C to the four leaf stage and transferred to constant light at ZT0 (subjective day and night are indicated by white and gray bars, respectively). Plants were dropped to cold temperature ($4^0$C) for 2 h, every 2 h, for 48 h at the start of constant light conditions and the transcript levels for the indicated genes were determined by qRT-PCR. Gene expression was normalized to UBQ10 for each sample. See Table A2.1 for primer pair sequences.

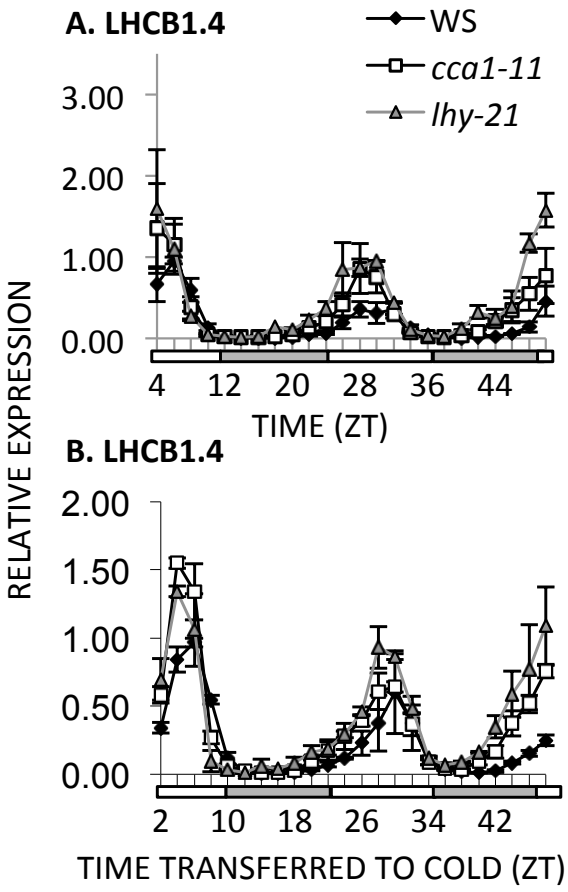


**Figure A2.2.** Robust circadian rhythms and gated expression of *LHCB1.4* in *cca1-11* and *lhy-21* plants. qRT-PCR analysis of *LHCB1.4* in *cca1-11* (white boxes) *, lhy-21* (grey triangles) and wild-type (WS) (black diamonds). Expression for *LHCB1.4* was relative to one wild-type sample (WS) set to a value of 1 in each biological replicate. Values are averages from three independent experiments (n=3) for WS, error bars indicate ± SEM. Values are averages from two independent experiments (n=2) for *cca1-11* and *lhy-21*, error bars indicate ± range. (A) Plants were grown with a 12 h photoperiod at $22^0$C to the four leaf stage and transferred to constant light at ZT0 (subjective day and night are indicated by white and gray bars, respectively). Plants were harvested every 2 h and the transcript levels for *LHCB1.4* were determined by qRT-PCR. Gene expression was normalized to IPP2 for each sample. (B) Plants were grown with a 12 h photoperiod at $22^0$C to the four leaf stage and transferred to constant light at ZT0 (subjective day and night are indicated by white and gray bars, respectively). Plants were dropped to cold temperature ($4^0$C) for 2 h, every 2 h, for 48 h at the start of constant light conditions and the transcript levels for *LHCB1.4* were determined by qRT-PCR. Horizontal axis represents time (ZT) when plants were dropped to cold temperature. Gene expression was normalized to UBQ10 for each sample. See Table A2.1 for primer pair sequences

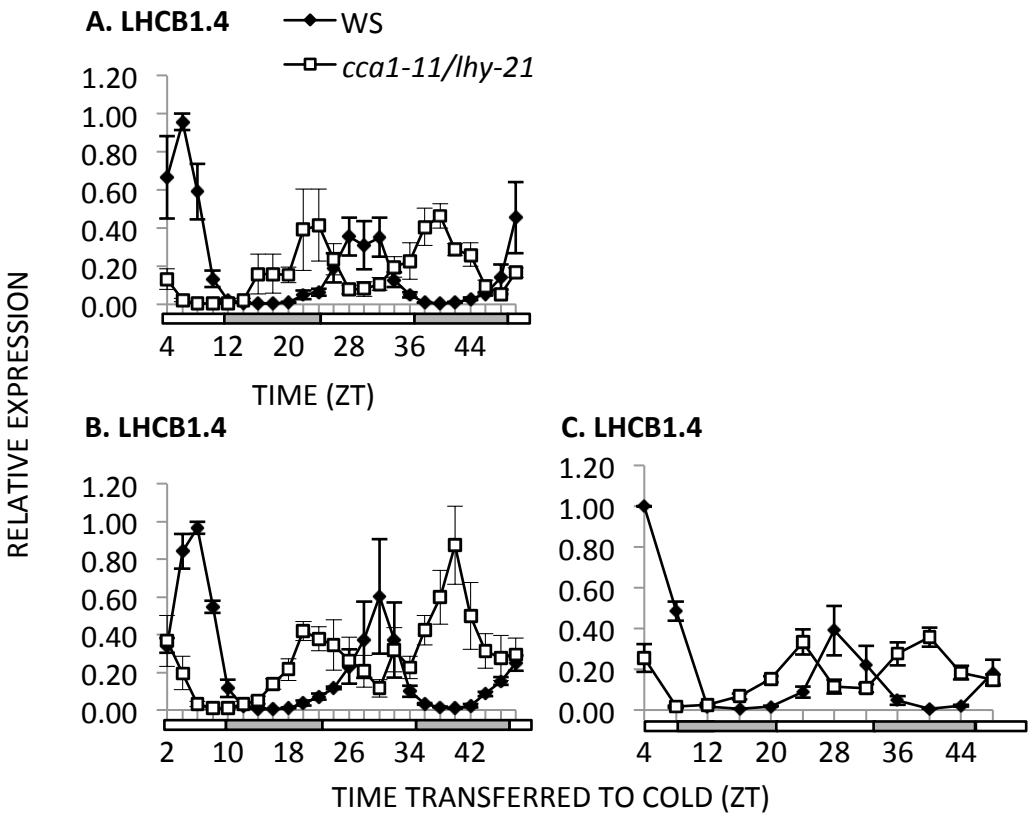


**Figure A2.3.** Robust circadian rhythms and gated expression of *LHCB1.4* in *cca1-11/lhy-21* plants. qRT-PCR analysis *LHCB1.4* in *cca1-11/lhy-21* (white boxes), and wild-type (WS) (black diamonds). Expression for *LHCB1.4* was relative to one wild-type sample (WS) set to a value of 1 in each biological replicate. Values are averages of three independent experiments (n=3). Error bars indicate ± SEM. (A) Plants were grown with a 12 h photoperiod at 22$^0$C to the four leaf stage and transferred to constant light at ZT0 (subjective day and night are indicated by white and gray bars, respectively). Plants were harvested every 2 h and the transcript levels for *LHCB1.4* were determined by qRT-PCR. Gene expression was normalized to IPP2 for each sample. (B) Plants were grown with a 12 h photoperiod at 22$^0$C to the four leaf stage and transferred to constant light at ZT0 (subjective day and night are indicated by white and gray bars, respectively). Plants were dropped to cold temperature (4$^0$C) for 2 h, every 2 h, for 48 h at the start of constant light conditions and the transcript levels for the indicated genes were determined by qRT-PCR. Horizontal axis represents time (ZT) when plants were dropped to cold temperature. Gene expression was normalized to UBQ10 for each sample. (C) Plants were grown with a 12 h photoperiod at 22$^0$C to the four leaf stage and transferred to constant light at ZT0 (subjective day and night are indicated by white and gray bars, respectively). Plants were dropped to cold temperature for 4 h, every 4 h, for 48 h at the start of constant light conditions and the transcript levels for *LHCB1.4* were determined by qRT-PCR. Horizontal axis represents time (ZT) when plants were dropped to cold temperature. Gene expression was normalized to UBQ10 for each sample. See Table A2.1 for primer pair sequences.

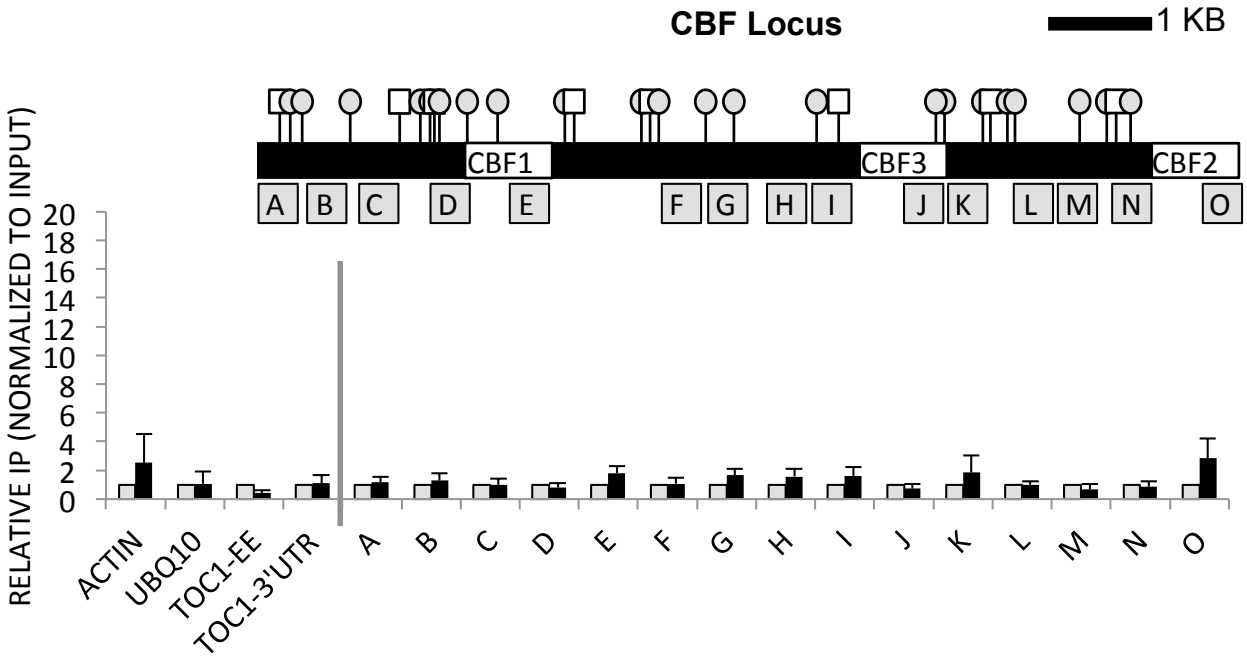


**Figure A2.4.** Mock experiments testing CCA1 binding at the *CBF1-3* locus. *cca1-1* and *cca1-1 CCA1p:CCA1-GFP* plants were grown at $22^0$C under a 12 h photoperiod to the four leaf stage. Tissue was fixed at ZT4 and ChIP was performed using rabbit-IgG (Jackson ImmunoResearch) antibody. Immunoprecipitated DNA was quantified by qRT-PCR using primers specific to regions within the *CBF1-3* locus (boxes A through O). The levels of immunoprecipitated DNA were normalized to the respective input DNA. Immunoprecipitation in *cca1-1 CCA1p:CCA1-GFP* plants (black bars) is relative to *cca1-1* plants (gray bars) set to a value of 1. Primer pairs directed to the 3'-untranslated region of *TOC1* (TOC1-3'UTR), *ACTIN7* (ACT) and *UBBIQUITIN10* (UBQ10) were used as negative controls (32). Primers near the EE element in the *TOC1* promoter (TOC1-EE) were used as a positive control. Values represent the average of five independent biological experiments (n=5). Error bars indicate ± SEM. *=p<0.05 using a paired, one-tailed t-test. See Table A2.1 for primer pair sequences. In the *CBF* locus diagram, the transcribed regions are indicted with white boxes and the approximate positions of CBS (AATCT), and EE (AAAATATCT) motifs are indicated by gray circles, and white squares.

**Table A2.1.** Primer pairs used for qRT-PCR and ChIP experiments. Primers used in this study were designed with Primer Express 3.0, using presets optimized for qRT-PCR. For locations of primer pairs on *CBF1-3* please see Fig. 2.2 or Fig. A2.4**.**

**qRT-PCR Primers**

| Name | Forward (FW) | FW | Reverse (RV) | RV | ATG |
|---|---|---|---|---|---|
| CBF1 | GGAGACAATGTTTGGGATGC | +671 | CGACTATCGAATATTAGTAACTCC | +793 | AT4G25490 |
| CBF2 | CGACGGATGCTCATGGTCTT | +560 | TCTTCATCCATATAAAACGCATCTTG | +628 | AT4G25470 |
| CBF3 | TTCCGTCCGTACAGTGGAAT | +694 | AACTCCATAACGATACGTCGTC | +741 | AT4G25480 |
| COR15A | GAAAAAAACAGTGAAACCGCAGAT | +704 | CCACATACGCCGCAGCTT | +750 | AT2G42540 |
| COR47 | CGGTACCAGTGTCGGAGAGT | +748 | ACAGCTGGTGAATCCTCTGC | +855 | AT1G20440 |
| COR78 | GAAAGGAGGAGGAGGAATGG | +2251 | AACCAGCCAGATGATTTTGG | +2351 | AT5G52310 |
| IPP2 | ATTTGCCCATCGTCCTCTGT | +115 | GAGAAAGCACGAAAATTCGGTAA | +155 | AT3G02780 |
| UBQ10 | GGCCTTGTATAATCCCTGATGAATAAG | +1833 | AAAGAGATAACAGGAACGGAAACATAGT | +1866 | AT4G05320 |
| LHCB1.4 | GCCTTCGCTACCAACTTCGTC | +829 | AACCGGATACACACAACTCGATC | +873 | AT2G34430 |

**ChIP Primers**

| Name | Forward (FW) | FW | Reverse (RV) | RV | ATG |
|---|---|---|---|---|---|
| ACTIN | CGTTTCGCTTTCCTTAGTGTTA | +54 | AGCGAACGGATCTAGAGACTC | +167 | AT5G09810 |
| UBQ10 | TCCAGGACAAGGAGGTATTCCTCCG | +1616 | CCACCAAAGTTTTACATGAAACGAA | +1796 | AT4G05320 |
| TOC1 | TTTTATGGCCTGCACTTTTTATTG | -186 | GGTGGGACTTGGGATATTTTAGG | -144 | AT5G61380 |
| TOC1 3'UTR | GCTACAGCCAAAAAAACATCGA | +3212 | GAGCCGCAAGAGCCAACAT | +3256 | AT5G61380 |
| CBF1-A | AGAACCACGACGATATAGAGAGTGAA | -1997 | CGCCTGCCAAAATCATTCTAC | -1951 | AT4G25490 |
| CBF1-B | TGCTTTCAAGGCCGAATGAT | -1312 | CGTTCTCATTCCACGTGTGATG | -1274 | AT4G25490 |

**Table A2.1. (cont'd)**

| | | | | | |
|---|---|---|---|---|---|
| CBF1-C | TTACCACTCTTTTTTTCCCTCTTTG | -845 | CTCGCTCTCACGTTATTGACATTT | -801 | AT4G25490 |
| CBF1-D | TCTTTACAAGGGTCAAAGGACACA | -186 | GCGAAGCAATCCCACGAT | -142 | AT4G25490 |
| CBF1-E | GGAGACAATGTTTGGGATGC | +671 | CGACTATCGAATATTAGTAACTCC | +793 | AT4G25490 |
| CBF3-F | AGTTCTATCGGACTAATTCTTGGCTTA | -1859 | GATGATCAAGCGTAATTGCTTTGT | -1752 | AT4G25480 |
| CBF3-G | TGACTAAGGACGTGGTGGTTGA | -1235 | AGCGCACTTCCTTCTCACTCA | -1178 | AT4G25480 |
| CBF3-H | TGTTACATTTGATCATTCACCCAAA | -604 | CGTATATAAGCACGTAAGTCACCAAGT | -550 | AT4G25480 |
| CBF3-I | CGTGGCATTACCAGAGACACA | -124 | GCGGAAGATATTTTAGAGGCAAAA | -83 | AT4G25480 |
| CBF3-J | TTCCGTCCGTACAGTGGAAT | +694 | AACTCCATAACGATACGTCGTC | +741 | AT4G25480 |
| CBF2-K | CAAGAGAGCACTGTCCGTAGCTT | -1851 | TGGTTACAAGAGGAGCCACGTA | -1811 | AT4G25470 |
| CBF2-L | TTTGCCGGAAAACTCAACTCA | -1147 | CCTTCTTTTTGGTCTGAAA | -1108 | AT4G25470 |
| CBF2-M | GAGAGATGCTGGAAATTGTGATCA | -943 | AAATATGGTAAGTGGTTAGGCGAAA | -897 | AT4G25470 |
| CBF2-N | GGGATCGCTTAGCTGTTTCTTA | -142 | TCGAACGCGGAGTTTCTGT | -100 | AT4G25470 |
| CBF2-O | CGACGGATGCTCATGGTCTT | +560 | TCTTCATCCATATAAAACGCATCTTG | +628 | AT4G25470 |

## LITERATURE CITED

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1. Thomashow MF (1999) Plant Cold Acclimation: Freezing Tolerance Genes And Regulatory Mechanisms. *Annu Rev Plant Physiol Plant Mol Biol* 50:571-599.

2. Ruelland EVM, Zachowski A, Vaughn H (2009) Cold Signaling And Cold Acclimation In Plants. *Adv Bot Res* 49:36-54.

3. Chinnusamy V, Zhu J, Zhu JK (2007) Cold Stress Regulation Of Gene Expression In Plants. *Trends Plant Sci* 12:444-451.

4. Maruyama K, Sakuma Y, Kasuga M, Ito Y, Seki M, Goda H, Shimada Y, Yoshida S, Shinozaki K, & Yamaguchi-Shinozaki K (2004) Identification Of Cold-Inducible Downstream Genes Of The Arabidopsis DREB1A/CBF3 Transcriptional Factor Using Two Microarray Systems. *Plant J* 38:982-993.

5. Hannah MA, Heyer AG, Hincha DK (2005) A Global Survey Of Gene Regulation During Cold Acclimation In Arabidopsis Thaliana. *PLoS Genet* 1:e26.

6. Fowler S, Thomashow MF (2002) Arabidopsis Transcriptome Profiling Indicates That Multiple Regulatory Pathways Are Activated During Cold Acclimation In Addition To The CBF Cold Response Pathway. *Plant Cell* 14:1675-1690.

7. Chew YH, Halliday KJ (2010) A Stress-Free Walk From Arabidopsis To Crops. *Curr Opin Biotechnol* 22:1-6.

8. Hua J (2009) From Freezing To Scorching, Transcriptional Responses To Temperature Variations In Plants. *Curr Opin Plant Biol* 12:568-573.

9. Thomashow MF (2010) Molecular Basis Of Plant Cold Acclimation: Insights Gained From Studying The CBF Cold Response Pathway. *Plant Physiol* 154:571-577.

10. Riechmann JL, Meyerowitz EM (1998) The AP2/EREBP Family Of Plant Transcription Factors. *Biol Chem* 379:633-646.

11. Vogel JT, Zarka DG, Van Buskirk HA, Fowler SG, Thomashow MF (2005) Roles Of The CBF2 And ZAT12 Transcription Factors In Configuring The Low Temperature Transcriptome Of Arabidopsis. *Plant J* 41:195-211.

12. Liu Q, Kasuga M, Sakuma Y, Abe H, Miura S, Yamaguchi-Shinozaki K, & Shinozaki K (1998) Two Transcription Factors, DREB1 And DREB2, With An EREBP/AP2 DNA Binding Domain Separate Two Cellular Signal Transduction Pathways In Drought- And Low-Temperature-Responsive Gene Expression, Respectively, In Arabidopsis. *Plant Cell* 10:1391-1406.

13. Jaglo-Ottosen KR, Gilmour SJ, Zarka DG, Schabenberger O, Thomashow MF (1998) Arabidopsis CBF1 Overexpression Induces COR Genes And Enhances Freezing Tolerance. *Science* 280:104-106.

14. Gilmour SJ, Fowler SG, Thomashow MF (2004) Arabidopsis Transcriptional Activators CBF1, CBF2, And CBF3 Have Matching Functional Activities. *Plant Mol.Biol.* 54:767-781.

15. Chinnusamy V, Ohta M, Kanrar S, Lee B-h, Hong X, Agarwal M, & Zhu J-K (2003) ICE1: A Regulator Of Cold-Induced Transcriptome And Freezing Tolerance In Arabidopsis. *Genes Dev.* 17:1043-1054.

16. Doherty CJ, Van Buskirk HA, Myers SJ, Thomashow MF (2009) Roles For Arabidopsis CAMTA Transcription Factors In Cold-Regulated Gene Expression And Freezing Tolerance. *Plant Cell* 21:972-984.

17. Miura K, Jin JB, Lee J, Yoo CY, Stirm V, Miura T, Ashworth EN, Bressan RA, Yun DJ, & Hasegawa PM (2007) SIZ1-Mediated Sumoylation Of ICE1 Controls CBF3/DREB1A Expression And Freezing Tolerance In Arabidopsis. *Plant Cell* 19:1403-1414.

18. Knight H, Trewavas AJ, & Knight MR (1996) Cold Calcium Signaling In Arabidopsis Involves Two Cellular Pools And A Change In Calcium Signature After Acclimation. *Plant Cell* 8:489-503.

19. Harmer SL, Hogenesch LB, Straume M, Chang HS, Han B, Zhu T, Wang X, Kreps JA, & Kay SA (2000) Orchestrated Transcription Of Key Pathways In Arabidopsis By The Circadian Clock. *Science* 290:2110-2113.

20. Bieniawska Z, Espinoza C, Schlereth A, Sulpice R, Hincha DK, & Hannah MA (2008) Disruption Of The Arabidopsis Circadian Clock Is Responsible For Extensive Variation In The Cold-Responsive Transcriptome. *Plant Physiol.* 147:263-279.

21. Kidokoro S, Maruyama K, Nakashima K, Imura Y, Narusaka Y, Shinwari ZK, Osakabe Y, Fujita Y, Mizoi J, Shinozaki K, & Yamaguchi-Shinozaki K (2009) The Phytochrome-Interacting Factor PIF7 Negatively Regulates DREB1 Expression Under Circadian Control In Arabidopsis. *Plant Physiol.* 151:2046-2057.

22. Fowler SG, Cook D, Thomashow MF (2005) Low Temperature Induction Of Arabidopsis CBF1, 2, And 3 Is Gated By The Circadian Clock. *Plant Physiol.* 137:961-968.

23. Pruneda-Paz JL, Kay SA (2010) An Expanding Universe Of Circadian Networks In Higher Plants. *Trends Plant Sci* 15:259-265.

24. Harmer SL (2009) The Circadian System In Higher Plants. *Annu Rev Plant Biol.* 60:357-377.

25. Wang ZY, Tobin EM (1998) Constitutive Expression Of The Circadian Clock Associated 1 (CCA1) Gene Disrupts Circadian Rhythms And Suppresses Its Own Expression. *Cell* 93:1207-1217.

26. Schaffer R, Ramsay N, Samach A, Corden S, Putterill J, Carre IA, & Coupland G (1998) The Late Elongated Hypocotyl Mutation Of Arabidopsis Disrupts Circadian Rhythms And The Photoperiodic Control Of Flowering. *Cell*. 93:1219-1229.

27. Mizoguchi T, Wheatley K, Hanzawa Y, Wright L, Mizoguchi M, Song H-R, CarrÈ IA, & Coupland G (2002) LHY And CCA1 Are Partially Redundant Genes Required To Maintain Circadian Rhythms In Arabidopsis. *Dev Cell* 2:629-641.

28. Alabadi D, Yanovsky MJ, Más P, Harmer SL, Kay SA (2002) Critical Role For CCA1 And LHY In Maintaining Circadian Rhythmicity In Arabidopsis. *Curr Biol* 12:757-761.

29. Matsushika A, Makino S, Kojima M, Mizuno T (2000) Circadian Waves Of Expression Of The APRR1/TOC1 Family Of Pseudo-Response Regulators In Arabidopsis Thaliana: Insight Into The Plant Circadian Clock. *Plant Cell Physiol.* 41:1002-1012.

30. Alabadi D, Oyama T, Yanovsky MJ, Harmon FG, Mas P, & Kay SA (2001) Reciprocal Regulation Between TOC1 And LHY/CCA1 Within The Arabidopsis Circadian Clock. *Science* 293:880-883.

31. Pruneda-Paz JL, Breton G, Para A, Kay SA (2009) A Functional Genomics Approach Reveals CHE As A Component Of The Arabidopsis Circadian Clock. *Science* 323:1481-1485.

32. Farre EM, Harmer SL, Harmon FG, Yanovsky MJ, & Kay SA (2005) Overlapping And Distinct Roles Of PRR7 And PRR9 In The Arabidopsis Circadian Clock. *Curr Biol* 15:47-54.

33. Nakamichi N, Kiba T, Henriques R, Mizuno T, Chua NH, & Sakakibara H (2010) Pseudo-Response Regulators 9, 7, And 5 Are Transcriptional Repressors In The Arabidopsis Circadian Clock. *Plant Cell* 22:594-605.

34. Nakamichi N, Kusano M, Fukushima A, Kita M, Ito S, Yamashino T, Saito K, Sakakibara H, & Mizuno T (2009) Transcript Profiling Of An Arabidopsis Pseudo Response Regulator Arrhythmic Triple Mutant Reveals A Role For The Circadian Clock In Cold Stress Response. *Plant Cell Physiol.* 50:447-462.

35. Wang ZY & Tobin EM (1997) A Myb-Related Transcription Factor Is Involved In The Phytochrome Regulation Of An Arabidopsis LHCB Gene. *Plant Cell* 9:491-507.

36. Hamilton EE, Kay SA (2008) SnapShot: Circadian Clock Proteins. *Cell* 135:368-368e1.

37. Mockler TC, Priest HD, Shen R, Sullivan CM, Givan SA, McEntee C, Kay SA Chory, J. (2007) The Diurnal Project: Diurnal And Circadian Expression Profiling, Model-Based Pattern Matching And Promoter Analysis. *Cold Spring Harb Symp Quant Biol* 72:353-363.

38. Green RM, Tobin EM (1999) Loss Of The Circadian Clock-Associated Protein I In Arabidopsis Results In Altered Clock-Regulated Gene Expression. *Proc Natl Acad Sci USA* 96:4176-4179.

39. Hall A, Bastow RM, Davis SJ, Hanano S, McWatters HG, Hibberd V, Doyle MR, Sung SB, Halliday KJ, Amasino RM, & Millar AJ (2003) The Time For Coffee Gene Maintains The Amplitude And Timing Of Arabidopsis Circadian Clocks. *Plant Cell* 15:2719-2729.

40. Gould PD, Locke JCW, Larue C, Southern MM, Davis SJ, Hanano S, Moyle R, Milich R, Putterill J, Millar AJ, & Hall A (2006) The Molecular Basis Of Temperature Compensation In The Arabidopsis Circadian Clock. *Plant Cell* 18:1177-1187.

41. Locke JCW, Southern MM, Kozma-Bognar L, Hibberd V, Brown PE, Turner MS, & Millar AJ (2005) Extension Of A Genetic Network Model By Iterative Experimentation And Mathematical Analysis. *Mol Syst Biol* 1:1-9.

42. Gong W, He K, Covington M, Dinesh-Kumar SP, Snyder M, Harmer SL, Zhu YX, & Deng XW (2008) The Development Of Protein Microarrays And Their Applications In DNA-Protein And Protein-Protein Interaction Analyses Of Arabidopsis Transcription Factors. *Mol Plant* 1:27-41.

43. Fukushima A, Kusano M, Nakamichi N, Kobayashi M, Hayashi N, Sakakibara H, Mizuno T, & Saito K (2009) Impact Of Clock-Associated Arabidopsis Pseudo-Response Regulators In Metabolic Coordination. *Proc Natl Acad Sci USA* 106:7251-7256.

44. Espinoza C, Degenkolbe T, Caldana C, Zuther E, Leisse A, Willmitzer L, Hincha DK, & Hannah MA (2010) Interaction With Diurnal And Circadian Regulation Results In Dynamic Metabolic And Transcriptional Changes During Cold Acclimation In Arabidopsis. *PLoS One* 5:e14101.

45. Alonso JM, et al. (2003) Genome-Wide Insertional Mutagenesis Of Arabidopsis Thaliana. *Science* 301:653-657.

# CHAPTER THREE

## Natural variation in the low temperature response of *Arabidopsis* ecotypes from Sweden and Italy

## CHAPTER THREE

## Natural variation in the low temperature response of *Arabidopsis* ecotypes from Sweden and Italy

### SUMMARY

In previous studies, three accessions from two *Arabidopsis* ecotypes collected from Sweden (SW) and Italy (IT) were tested for fitness (survival and fruit-number) in reciprocal transplant experiments. There is substantial variation in temperature across latitudes and minimum winter soil temperature was found to correlated with fitness in these experiments. Consequently, genes associated with freezing tolerance may underlie identified fitness QTLs. This project assessed differences in freezing tolerance between SW and IT accessions using electrolyte leakage assays under laboratory conditions. The SW accession was able to maintain greater freezing tolerance, compared to IT, after 2 weeks of cold-acclimation.

RNA-seq experiments on non-acclimated, 1 week cold-acclimated, and 2 week cold-acclimated SW and IT accessions were analyzed to find genes that may contribute to differences in freezing tolerance. This transcriptomic data was also used to determine general differences between SW and IT and assess if SW and IT reach similar levels of freezing tolerance with similar transcriptional changes.

SW and IT recombinant inbred lines (RILs) were used in expression QTL (eQTL) analysis on genes potentially contributing to differences in freezing tolerance. CBF regulon genes were overrepresented in the list of genes that may potentially contribute to differences in freezing tolerance. Variation in CBF regulon genes, which were

selected for eQTL analysis, indeed mapped to the CBF locus. Interestingly, the location of the CBF locus also overlaps with a fitness QTL.

Based on gene expression levels, CBF2 regulatory sequences may have diverged between SW and IT. However, there is also a 13 base pair deletion in the coding region of IT-CBF2 that results in a predicted protein with a DNA binding domain but without an activation domain. This truncated protein could potentially act as a dominant negative version of CBF2 in IT, able to bind to downstream target genes but incapable of activating transcription. Consistent with this hypothesis, expression of up-regulated CBF target genes is generally lower in IT compared to SW. This would potentially be the first example of a naturally occurring dominant negative version of a CBF. Further work is necessary to confirm this hypothesis. Altogether, results from this study suggest that CBF2 is an excellent candidate gene for differences in freezing tolerance and possibly differences in fitness between SW and IT.

## INTRODUCTION

Adaptation of plants and other organisms to their local environment has been frequently observed and is driven by random mutation and natural selection (1-5). With rapid change in global environmental conditions, understanding the molecular mechanisms underlying local adaptation are of particular interest (1-5). *Arabidopsis* is a model plant native to a wide geographical range (Europe to Central Asia) and thus wide range of climatic conditions (6, 7). Two naturally occurring populations of *Arabidopsis* from Rodasen, Sweden (SW) and Castelnuovo di Porto, Italy (IT) were recently collected (8). In reciprocal transplant experiments with three accessions from each SW and IT population, accessions originating from the experimental sites had a strong advantage in terms of fruit-number and survival throughout five years of experimentation (8). Barrett et al. 2011 defined an adaptive allele as one that functionally affects a phenotypic trait to increase fitness (5). Consequently, it can be very difficult to demonstrate that specific alleles are adaptive (1-5). Reciprocal transplant experiments with recombinant inbred lines (RILs) allow fitness to be measured then mapped to specific genetic regions (quantitative trait loci; QTL) and for segregating traits to be identified (5, 9). This method thus connects specific genetic regions to a phenotypic trait that impacts fitness, though these regions can still often span several hundred genes (5).

The Schemske lab sequenced SW and IT accessions and 141,437 single nucleotide polymorphisms (SNPs) were found (Schemske, unpublished). A population of RILs was created by crossing a randomly selected individual from the SW ecotype

(male parent) to a randomly selected individual from the IT ecotype (female parent), seeds from the F1 generation were used to establish a large number of lines that were selfed by single-seed descent for nine generations (Schemske and Agren, unpublished). SW and IT RILs used in this study were from the F10 generation. 384 of the 141,437 SNPs with an average spacing of ~1.1 cm across the *Arabidopsis* genome were selected to genotype the RIL population (Schemske, unpublished). 400 genotyped RILs were then grown at both the Swedish and Italian sites and QTL for fitness were mapped by measuring both fruit-number and survival over these 384 markers (Table 3.1; Schemske and Agren, unpublished).

Both minimum winter soil temperature and flowering-time were found to correlate with fitness of the parent lines during previous reciprocal transplant experiments (8). Other recent studies on local adaptation in various *Arabidopsis* ecotypes have also shown temperature variation to be particularly linked to identified 'local alleles' (1, 2). Sweden has significantly lower average air and soil temperatures in comparison to Italy, especially during winter months (8). Therefore, freezing tolerance is a potential trait underlying fitness QTL mapped in the RILs. Ideally, the SW and IT RILs would be quantitatively (or even semi-quantitatively) tested for differences in freezing tolerance (10) in order to map freezing tolerance QTL and determine if they overlap with fitness QTL. The Schemske lab is currently optimizing freezing tolerance protocols for mass screening of RILs. Keeping this in mind, a reductionist approach has been taken to determine if freezing tolerance related genes underlie previously identified fitness QTL (Table 3.1; Schemske and Agren, unpublished).

Results and analyses are broken into three sections. First, significant differences in SW and IT freezing tolerance are shown under controlled laboratory conditions. Second, RNA-seq experiments are used to define a set of genes possibly contributing to differences in freezing tolerance. This is the first look at the transcriptomes of these two *Arabidopsis* accessions. Therefore in this second section, basal differences between SW and IT transcriptomes are observed. Further analysis of RNA-seq data in this section also suggests that the cold-response of the SW and IT accessions is significantly different. Third, a subset of the genes that possibly contribute to differences in freezing tolerance are used to map QTL for differences in gene expression (expression QTL; eQTL; (11-14)). Some of the eQTL were found to overlap with previously defined fitness QTL (Table 3.1). Consequently, the genes underlying eQTL mapped for genes possibly contributing to differences in freezing tolerance might also underlie fitness QTL. This study therefore provides evidence in support of freezing tolerance as a trait underlying SW and IT fitness QTL (Table 3.1) and suggests candidate genes contributing to these QTL.

**Table 3.1.** Locations of fitness QTL. 400 RILs were grown at both Swedish and Italian field sites in 2009. Fruit-number and survival-until-fruit-set were fitness traits measured (Data courtesy of the Schemske Lab, unpublished). RQTL (15) was used to perform interval mapping using the multiple imputation method as described by the reference manual (http://www.rqtl.org/) for each fitness trait at each location. To detect QTL, estimated genome-wide significance thresholds ($\alpha$=0.01) for the logarithm of odds (LOD) values were calculated for each trait using 1000 permutations in RQTL. To estimate the location of each QTL a Bayes credible interval (99%) was calculated in RQTL. No QTL are reported for survival-until-fruit-set at the Italian field site because no QTL were detected above the calculated significance threshold of 3.42 ($\alpha$=0.01) or even a less stringent LOD threshold of 2.54 ($\alpha$=0.05). For locations of markers based on the Col-0 genome please see Table A3.1. 'MB' indicates the megabases contained within the QTL. '# GENES' indicates the number of genes contained within the QTL based on the Col-0 genome. %VAR indicates the estimated proportion of phenotypic variance explained by the QTL.

| **FRUIT-NUMBER ITALY 2009 (LOD THRESHOLD 3.17)** | | | | | | | |
|---|---|---|---|---|---|---|---|
| CHR | LEFT (CM) | PEAK (CM) | RIGHT (CM) | MB | # GENES | LOD | %VAR |
| 1 | 57.35 | 58.00 | 62.48 | 2.00 | 584 | 18.35 | 11.66 |
| 2 | 22.00 | 26.84 | 46.00 | 6.59 | 1803 | 8.04 | 4.81 |
| 4 | 44.31 | 57.69 | 60.00 | 6.91 | 2065 | 14.37 | 8.91 |
| 5 | 0.00 | 1.40 | 4.59 | 1.16 | 365 | 9.18 | 5.52 |
| 5 | 68.69 | 75.80 | 77.42 | 3.19 | 988 | 18.14 | 11.52 |
| **FRUIT-NUMBER SWEDEN 2009 (LOD THRESHOLD 3.08)** | | | | | | | |
| CHR | LEFT (CM) | PEAK (CM) | RIGHT (CM) | MB | # GENES | LOD | %VAR |
| 2 | 50.00 | 55.27 | 58.59 | 4.32 | 1427 | 12.26 | 11.68 |
| **SURVIVAL SWEDEN 2009 (LOD THRESHOLD 2.99)** | | | | | | | |
| CHR | LEFT (CM) | PEAK (CM) | RIGHT (CM) | MB | # GENES | LOD | %VAR |
| 1 | 76.9 | 78.6 | 83 | 2.31 | 695 | 6.26 | 7.27 |
| 5 | 64 | 71.3 | 78.2 | 4.89 | 1505 | 4.63 | 4.8 |

## RESULTS AND DISCUSSION: FREEZING TOLERANCE OF SW AND IT

***Summary: Freezing tolerance of SW and IT.*** Minimum winter soil temperature was correlated with the relative fitness of the parent lines during previous reciprocal transplant experiments (8). If freezing tolerance is a trait underlying fitness QTL mapped for the RILS, then SW and IT accessions should differ in freezing tolerance. SW and IT have similar freezing tolerance without cold-acclimation and with 1 week of cold-acclimation (Fig 3.1). But SW was significantly more freezing tolerant than IT with both 2 and 3 weeks of cold-acclimation (Fig. 3.2). Consequently, genes contributing to differences in freezing tolerance between SW and IT may also be candidates for genes underlying fitness QTL.

***Freezing tolerance of SW and IT.*** If freezing tolerance is a trait underlying fitness QTL found using the SW and IT RILs, then a significant difference in the freezing tolerance of the SW and IT accessions might be expected. Electrolyte leakage assays were used to assess the freezing tolerance of both SW and IT accessions (16). The $EL_{50}$ (temperature at which cell damage results in release of 50% of total electrolytes) of SW and IT accessions was the same under non-acclimated conditions ($EL_{50}$=-2.5; Fig. 3.1). Hannah et al. 2006 found that nine accessions of *Arabidopsis* generally had similar non-acclimated freezing tolerance despite differing levels of freezing tolerance at 2 weeks of cold-acclimation (6). Accordingly, differences in the cold-acclimated freezing tolerance of the SW and IT accessions were determined.

After 1 week of cold-acclimation at 4°C, both SW and IT can increase their freezing tolerance to a similar degree ($EL_{50}$=-5.5; Fig. 3.1). However after 2 weeks of

cold-acclimation at 4°C, IT is unable to maintain freezing tolerance similar to 1 week of cold-acclimation (Fig 3.1) and decreases in freezing tolerance ($EL_{50}$=-4.5; Fig. 3.2). On the other hand, the SW accession increases in freezing tolerance after 2 weeks of cold-acclimation ($EL_{50}$=-6.5; Fig. 3.2) in comparison to 1 week of cold-acclimation (Fig 3.1). After 3 weeks of cold-acclimation at 4°C there is still a substantial difference in freezing tolerance between SW ($EL_{50}$=-5.5) and IT ($EL_{50}$=-4.5) though the SW line has decreased its freezing tolerance in comparison to 2 weeks of cold-acclimation (Fig 3.2).

The study by Hannah et al. 2006 also found that the cold-acclimated freezing tolerance of nine accessions of *Arabidopsis* correlated considerably with the accession's average home temperature in the coldest month of the growing season (6). A separate study using 71 accessions of Arabidopsis found a similar correlation with the latitude of origin (17). Data from this study corroborates both of these previous studies. SW, the accession with the colder home winter temperature and higher latitude (8), has greater freezing tolerance than IT after 2 weeks of cold-acclimation (Fig. 3.2).

The SW accession was significantly more freezing tolerant than the IT accession at both 2 ($p \leq 0.026$ at $EL_{50}$ calculated by Student's t test) and 3 ($p \leq 0.015$ at $EL_{50}$ calculated by Student's t test) weeks of cold-acclimation (Fig 3.2). Therefore, freezing tolerance is a potential trait contributing to local adaptation (1-5). Consequently, genes contributing to differences in freezing tolerance between SW and IT may also be candidates for genes underlying fitness QTL.

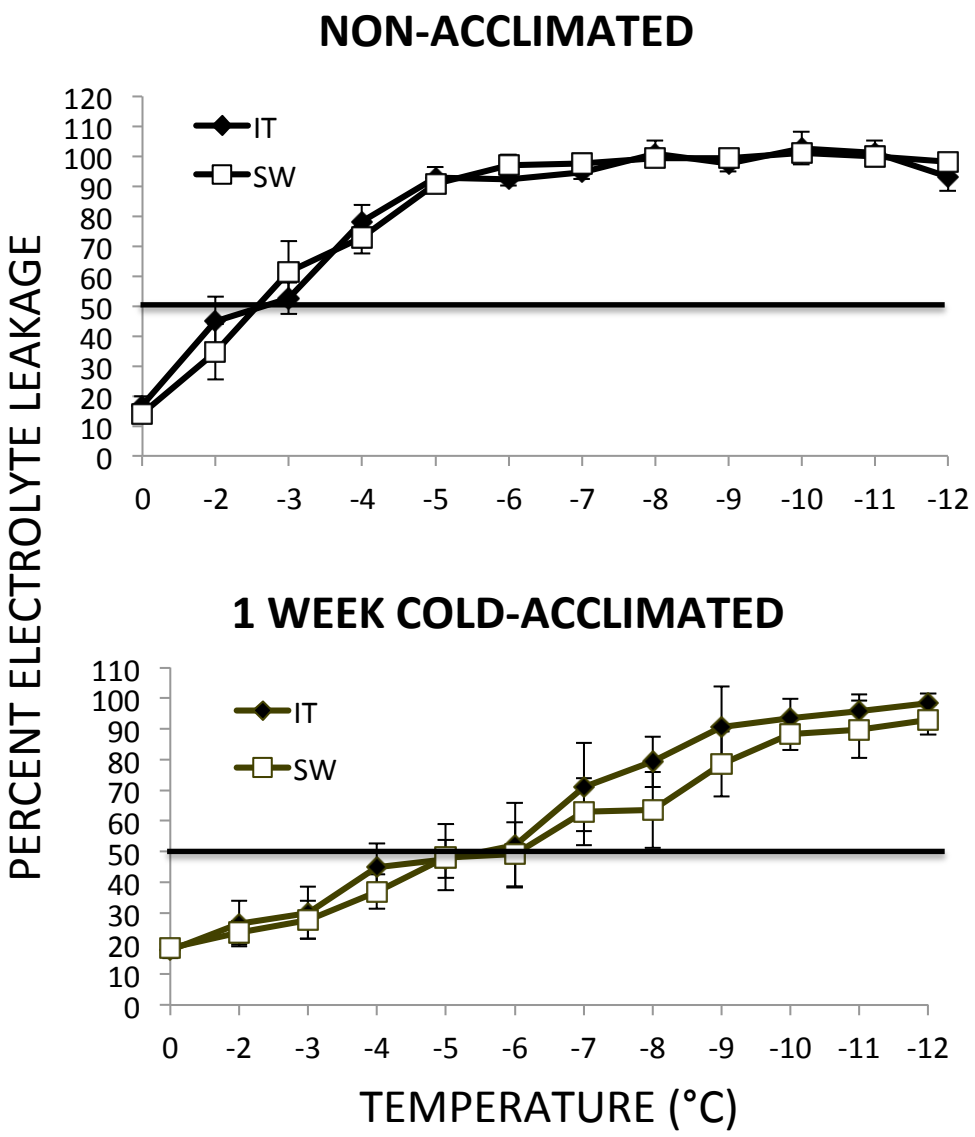


**Figure 3.1.** Freezing tolerance of SW and IT accessions without cold-acclimation or with 1 week of cold-acclimation. Plants were grown at 22$^0$C under a 12 h photoperiod for approximately 18 days and either tested directly for freezing tolerance (non-acclimated plants; top graph) or were transferred at ZT4 to 4$^0$C for 7 days under a 12 h photoperiod and then tested for freezing tolerance (cold-acclimated plants; bottom graph). Freezing tolerance was tested using the electrolyte leakage test. For non-acclimated samples the results presented are average values from six independent experiments (n=6). For 1 week cold-acclimated samples the results presented are average values from four independent experiments (n=4). Error bars indicate ±SEM.

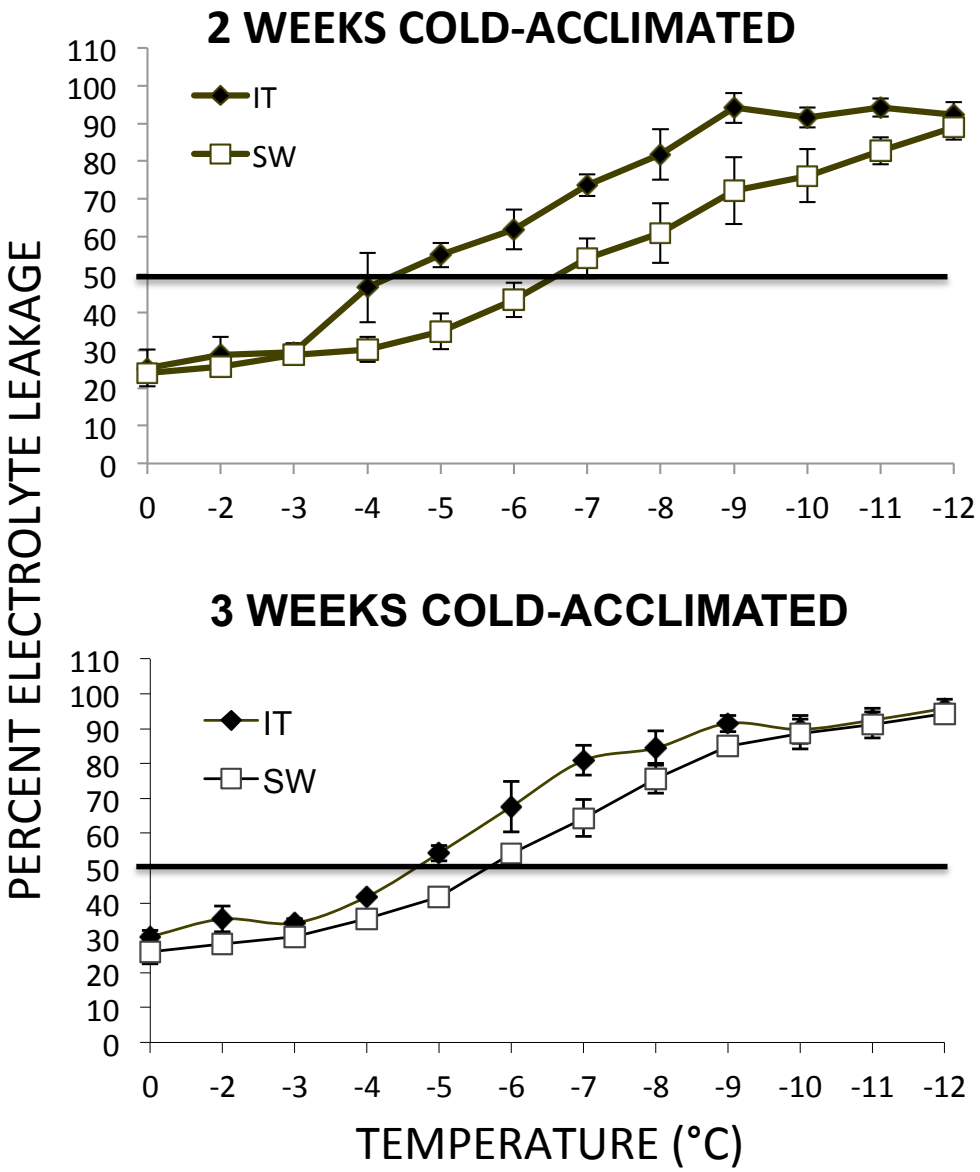


**Figure 3.2.** Freezing tolerance of SW and IT accessions with 2 or 3 weeks of cold-acclimation. Plants were grown at 22$^{0}$C under a 12 h photoperiod for approximately 18 days then transferred at ZT4 to 4$^{0}$C for 2 weeks (2 week cold-acclimated plants; top graph) or 3 weeks (3 week cold-acclimated plants; bottom graph) under a 12 h photoperiod and then tested for freezing tolerance. Freezing tolerance was tested using the electrolyte leakage test. For 2 week cold –acclimated samples the results presented are average values from five independent experiments (n=5). For 3 week cold-acclimated samples the results presented are average values from four independent experiments (n=4). Error bars indicate ±SEM.

## RESULTS AND DISCUSSION: SW AND IT RNA-SEQ EXPERIMENTS

This second section of experiments analyzes RNA-seq data from non-acclimated, 1 week cold-acclimated and 2 week cold-acclimated SW and IT samples. The ultimate goal of these experiments is to determine the genes that potentially contribute to differences in freezing tolerance seen after 2 weeks of cold-acclimation in SW and IT. However, the transcriptomes of these accessions have never been examined and transcriptional changes prior to 2 weeks of cold-acclimation may contribute to differences in freezing tolerance. Furthermore, the freezing tolerance of SW and IT are the same at 1 week of cold-acclimation, which allows the opportunity to determine if SW and IT attain similar levels of freezing tolerance with similar transcriptional changes. Therefore analysis of RNA-seq data is partitioned into four subsections. First, basal differences between SW and IT transcriptomes are examined. Second, sets of cold-regulated genes for SW and IT are defined. Third, SW and IT cold-regulated transcripts at 1 week of cold-acclimation are compared. Fourth, two sets of genes that may contribute to differences in freezing tolerance are defined.

## ANALYSIS OF SW AND IT BASAL TRANSCRIPTOMES

***Summary: Analysis of SW and IT basal (non-acclimated) transcriptomes.*** In the first section of results it is demonstrated that SW has significantly ($p \leq 0.026$) higher freezing tolerance in comparison to IT after 2 weeks of cold-acclimation (Fig 3.2). Although SW and IT have similar levels of freezing tolerance under non-acclimated conditions, basal (non-acclimated) transcriptome differences were first evaluated to examine general variance and to determine if genes previously associated with cold-

acclimation are enriched in differentially expressed genes. There are a total of 1259 genes differentially expressed between SW and IT under non-acclimated conditions. Analysis of these differentially expressed genes does not overtly suggest that there will be greater freezing tolerance in SW after 2 weeks of cold-acclimation but does indicate that there might be differences in known pathways of cold-acclimation between SW and IT.

***Analysis of SW and IT basal transcriptomes.*** SW has significantly ($p \leq 0.026$) higher freezing tolerance in comparison to IT after 2 weeks of cold-acclimation (Fig 3.2). RNA-seq experiments were conducted on rosette tissue collected before the start of electrolyte leakage assays (Fig 3.1 and 3.2). For RNA-seq experiments average correlation between biological replicates was $R^2=0.90$, suggesting that RNA-seq data in this study is repeatable (Table A3.9). Altogether, SW and IT transcriptomes under non-acclimated, 1 week cold-acclimated, and 2 week cold-acclimated conditions, represent a total of 25,678 genes (76.4%) from the *Arabidopsis* Col-0 genome. On average, there were 23,264 genes (69.2%) represented in each sample (Table A3.9). Pairwise comparisons between non-acclimated and cold-acclimated samples or between SW and IT samples were calculated using a two-tailed Student's t test in the cuffdiff program within Cufflinks (18). Genes were considered differentially expressed between non-acclimated and cold-acclimated samples or between SW and IT samples if the Benjamini-Hochberg (false discovery rate; FDR) corrected p-value was ≤0.050. While analyzing differentially expressed genes a ≥3 fragments per kilobase of exon per million

fragments mapped (FPKM) threshold (i.e. one sample in the pairwise comparison had to be ≥3FPKM) was used (19, 20).

Genes differentially expressed between SW and IT without treatment (non-acclimated conditions) were first evaluated to examine general variance and to determine if genes previously associated with cold-acclimation are enriched in differentially expressed genes. Altogether, 1259 genes were differentially expressed between SW and IT under non-acclimated conditions that met the ≥3FPKM criteria (19, 20) in either SW or IT (Fig. 3.3). Of these differentially expressed genes, 887 genes have higher expression in IT and 372 are higher in SW (Fig. 3.3).

Although these basal differences in gene expression do not manifest into differences in non-acclimated freezing tolerance, it is of interest to determine if the 1259 genes differentially expressed between SW and IT have previously been correlated with increases in freezing tolerance. In 2006, Hannah et al. analyzed the freezing tolerance and transcriptomes of nine accessions of *Arabidopsis* after two weeks of cold acclimation to define a set of genes (henceforth referred to as Hannah genes) positively and negatively correlated with increases in freezing tolerance associated with cold-acclimation (6). The Hannah gene set is significantly enriched in genes from the CBF regulon (6). The CBFs are a fundamental component of the most well described pathway of cold-acclimation. Overexpression of *CBF* genes leads to constitutive activation of CBF target genes and a plant with much higher freezing tolerance (21-25). The Hannah gene set is also enriched in genes from the ZAT12 regulon, and overexpression of ZAT12 leads to a slight increase in plant freezing tolerance (25).

There significant overlap (40 genes; p=1.5E-08; calculated using a hypergeometric distribution in R) between the 887 genes with higher expression in IT and Hannah genes positively correlated with freezing tolerance (Fig. 3.3). A significant number of these (36 of the 40) overlapping genes have greater than 2-fold higher expression in IT compared to SW (Fig 3.4). Since the CBF regulon is enriched in the Hannah gene set, it was determined if the genes with higher basal expression in IT are also enriched in CBF regulated genes (25). Indeed, the genes with higher basal expression in IT are enriched (26 genes; p=0.00056) in genes up-regulated by CBFs (25). The CBF pathway of cold-acclimation appears to be differentially regulated between SW and IT. Since there is no difference in freezing tolerance between SW and IT under non-acclimated conditions (Fig 3.1) significant overlap between genes with higher in expression in SW, Hannah genes positively correlated with freezing tolerance, and CBF regulon genes, might also be expected. This was not the case. There is not significant overlap between Hannah genes positively or negatively correlated with freezing tolerance and the 372 genes with higher expression in SW (Fig 3.3). These 372 genes also are not enriched in CBF regulon genes. Consequently, it was of interest to determine what types of genes are enriched.

Gene ontology (GO) enrichment analysis showed that no cold related GO categories were specifically enriched in the 372 genes with higher expression in SW (Table 3.2). 'Response to abiotic stimulus' and 'response to water deprivation' were enriched GO categories in the 887 genes with higher expression in IT (Table 3.3). Defense response related GO categories were significantly enriched in both sets of

genes (Table 3.2 and 3.3). Cold-related GO categories were not specifically enriched in SW or IT, but previous research by Hon et al. 1995 showed that defense response related genes, PR2, PR3 and PR5 encode proteins with antifreeze properties (26). Interestingly, PR3 expression is significantly higher (17.5 fold; $p \leq 0.05$) in SW compared to IT at non-acclimated conditions.

In summary, SW has higher basal expression of 372 genes, which includes a pathogenesis related gene with antifreeze properties. IT has higher basal expression of 887 genes, which are significantly enriched in genes previously positively correlated with cold-acclimation. Given this enrichment of genes positively correlated with freezing tolerance, is it interesting that IT is not more freezing tolerant than SW under non-acclimated conditions. Ultimately, comparison of SW and IT basal transcriptomes does not reveal any obvious suggestion for the higher level of freezing tolerance in SW seen later at 2 weeks of cold-acclimation, but does suggest that genes associated with cold-acclimation may be differentially regulated between SW and IT.

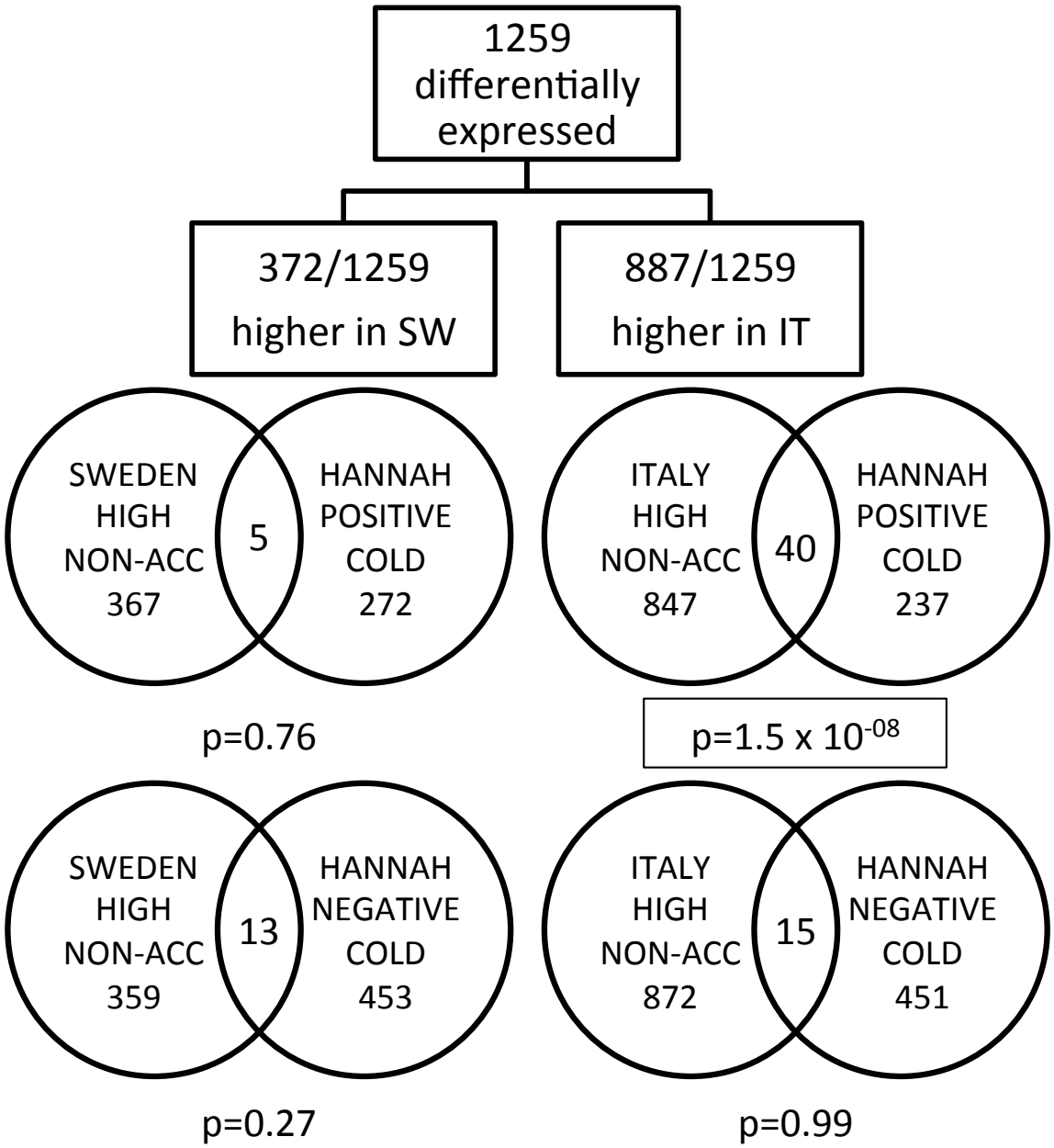


**Figure 3.3** 1259 genes differentially expressed between SW and IT under non-acclimated conditions. (Plants were grown at 22$^0$C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Genes were considered differentially expressed if the FDR corrected p-value was ≤0.05. ≥3FPKM was used as the cut-off for differential expression. P-values (calculated using a hypergeometric distribution in R) represent overlap between differentially expressed genes and Hannah genes; 277 Hannah genes positively correlated with freezing tolerance and 466 Hannah genes negatively correlated with freezing tolerance; (6)).

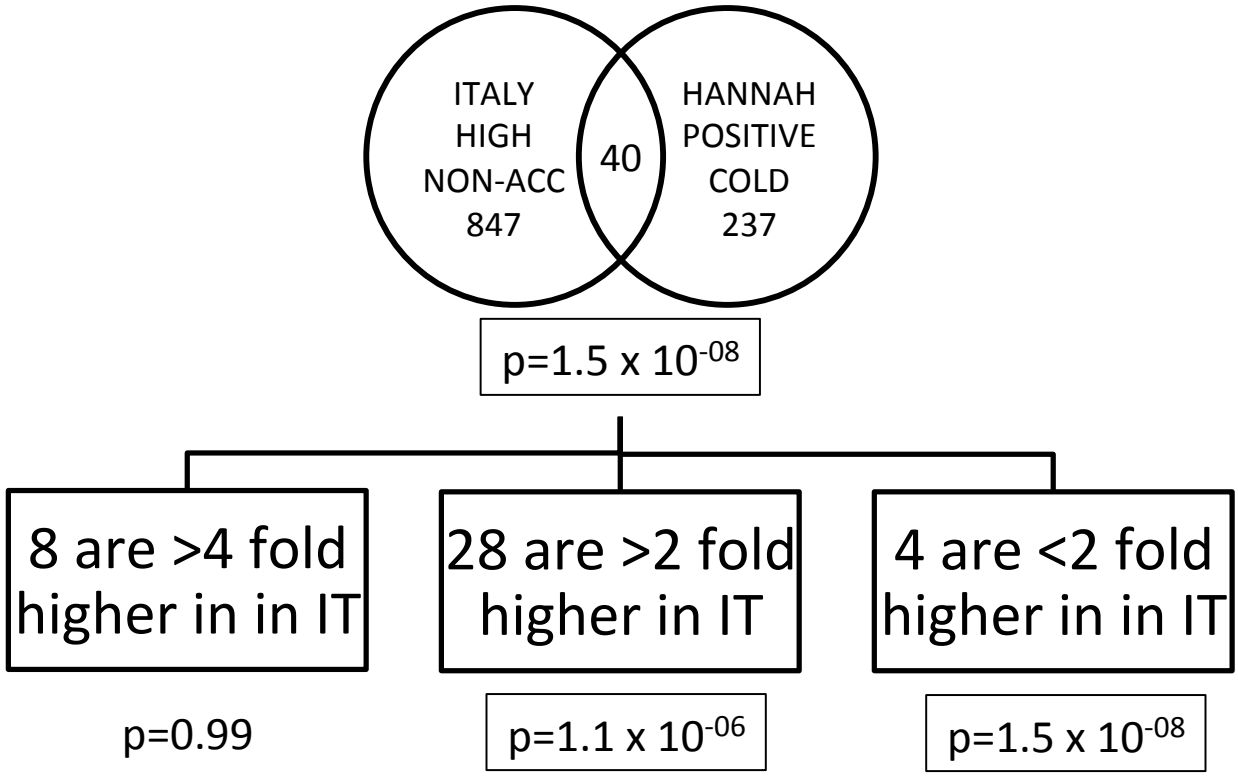


**Figure 3.4.** Fold change of 40 Hannah genes positively correlated with freezing tolerance that have higher expression in IT. P-values represent the significance of overlap between 'IT High' and Hannah genes if 4- fold, 2-fold, or no fold change cut-offs were applied (from left to right).

**Table 3.2** GO categories significantly enriched in 372 genes with higher expression in SW under non-acclimated conditions. GO enrichment was determined using the database for annotation visualization and integrated discovery (DAVID; **david**.abcc.ncifcrf.gov; (27)). 'GO TERM CATEGORY' denotes if the GO term was categorized as a biological process (BP), cellular component (CC), or molecular function (MF) in the DAVID database. '# HITS' denotes the number of genes with that GO category in the 372 genes with higher expression in SW. '# GENES IN GO' denotes the total number of genes in that GO category included in the DAVID database. GO category was considered significantly enriched if the FDR corrected hypergeometric p-value was ≤0.050.

| GO TERM CATEGORY | HIGH IN SW (372 GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| BP | Apoptosis | 15 | 172 | 3.45E-05 |
| BP | Programmed Cell Death | 16 | 223 | 4.76E-05 |
| BP | Defense Response | 36 | 1030 | 5.30E-05 |
| BP | Cell Death | 16 | 254 | 1.87E-04 |
| MF | Amine Biosynthetic Process | 13 | 204 | 1.79E-03 |
| BP | Carbohydrate Binding | 14 | 215 | 2.62E-03 |
| BP | Nitrogen Biosynthetic Process | 19 | 506 | 1.16E-02 |
| CC | Oxidation Reduction | 32 | 1186 | 1.23E-02 |
| BP | Biogenic Amine Biosynthetic Process | 6 | 40 | 1.25E-02 |
| CC | External Encapsulating Structure | 22 | 620 | 1.26E-02 |
| BP | Cell Wall | 22 | 611 | 2.05E-02 |
| MF | Immune Response | 13 | 293 | 3.00E-02 |
| BP | Amino Acid Biosynthetic Process | 10 | 184 | 3.86E-02 |
| MF | Amino Acid Derivative Biosynthetic Process | 10 | 194 | 4.31E-02 |
| BP | Innate Immune Response | 12 | 275 | 4.59E-02 |
| MF | Sugar Binding | 9 | 124 | 4.74E-02 |
| BP | Biogenic Amine Metabolic Process | 6 | 59 | 4.85E-02 |

**Table 3.3.** GO categories significantly enriched in 887 genes with higher expression in IT under non-acclimated conditions. GO enrichment was determined using DAVID (**david**.abcc.ncifcrf.gov; (27)). 'GO TERM CATEGORY' denotes if the GO term was categorized as a biological process (BP), cellular component (CC), or molecular function (MF) in the DAVID database. '# HITS' denotes the number of genes with that GO category in the 887 genes with higher expression in IT. '# GENES IN GO' denotes the total number of genes in that GO category included in the DAVID database. GO category was considered significantly enriched if the FDR corrected hypergeometric p-value was ≤0.050.

| GO TERM CATEGORY | HIGH IN IT (887 GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| BP | Secondary Metabolic Process | 37 | 423 | 1.24E-04 |
| BP | Defense Response | 65 | 1030 | 1.62E-04 |
| BP | Apoptosis | 21 | 172 | 2.49E-04 |
| BP | Phenylpropanoid Metabolic Process | 20 | 166 | 4.47E-04 |
| BP | Programmed Cell Death | 23 | 223 | 6.89E-04 |
| BP | Flavonoid Biosynthetic Process | 11 | 53 | 1.03E-03 |
| BP | Cell Death | 24 | 254 | 1.25E-03 |
| BP | Flavonoid Metabolic Process | 11 | 57 | 1.53E-03 |
| BP | Phenylpropanoid Biosynthetic Process | 16 | 128 | 1.80E-03 |
| BP | Immune Response | 25 | 293 | 2.99E-03 |
| BP | Amino Acid Derivative Metabolic Process | 24 | 280 | 3.77E-03 |
| BP | Response To Water Deprivation | 18 | 176 | 4.74E-03 |
| BP | Response To Abiotic Stimulus | 64 | 1197 | 6.22E-03 |
| BP | Oxidation Reduction | 63 | 1186 | 7.34E-03 |
| BP | Response To Water | 18 | 185 | 7.55E-03 |
| BP | Amino Acid Derivative Biosynthetic Process | 18 | 194 | 1.17E-02 |
| BP | Innate Immune Response | 22 | 275 | 1.43E-02 |
| BP | Response To Salicylic Acid Stimulus | 15 | 150 | 1.97E-02 |
| BP | Aromatic Compound Biosynthetic Process | 18 | 215 | 3.23E-02 |
| BP | Response To Organic Substance | 59 | 1176 | 4.06E-02 |

## SW AND IT COLD-INDUCED GENES

***Summary: SW and IT cold-induced genes.*** In this second subsection of RNA-seq analysis cold-regulated genes for SW and IT are defined. SW and IT cold-regulated genes are also compared in greater detail in the third and fourth RNA-seq experiment subsections. However general analysis reveals that SW cold-regulated genes are more enriched in genes previously associated with increases in freezing tolerance than IT cold-regulated genes. The quantity of cold-regulated genes in SW and IT also suggests that there could be differences their capacity to cold-acclimate.

***SW and IT cold-induced genes.*** To find genes contributing to differences in freezing tolerance seen after 2 weeks of cold-acclimation (Fig 3.2) sets of cold-responsive genes were first defined for both SW and IT. RNA-seq data generated from SW and IT rosette tissue under non-acclimated, 1week cold-acclimated and 2 week cold acclimated conditions, was collected before electrolyte leakage experiments.

Fold change cut-offs were not used while defining sets of cold-responsive genes. A fold change threshold is an arbitrary value and not necessarily biologically significant especially since transcription factors can have compounding downstream effects (28). Furthermore, if fold change cut-offs were applied when defining cold-induced genes important similarities between SW and IT cold-responsive genes might later have been missed. For example, a gene up-regulated 2-fold by cold in SW and 1.9-fold in IT would have been removed from the list of IT cold-responsive genes if a 2-fold threshold had been applied. Instead, genes were considered differentially expressed in response to cold if the FDR corrected p-value comparing non-acclimated to cold samples was

≤0.050 (as determined by cuffdiff program within Cufflinks). Although a fold-change threshold was not used, a ≥3FPKM cut-off for differential expression was used while defining cold-responsive genes (19, 20). This means that the sample with higher expression (FPKM) was greater or equal to ≥3FPKM, otherwise interesting genes may have been removed. For example, a gene down-regulated from 15,000FPKM to 1FPKM, after 1 week of cold-acclimation, would have been filtered out if both non-acclimated and cold samples were required to have ≥3FPKM. While a threshold of ≥3FPKM (19, 20) for differentially expressed genes is still an arbitrary cut-off, it allows small but significant (≤0.050) fold-change differences to be included in analysis.

Based on the methods above, there are a total of 2307 genes up-regulated by cold in SW and 2310 genes up-regulated by cold in IT (Fig. 3.5 and 3.6). There are also a total of 3252 genes down-regulated by cold in SW and 2658 genes down-regulated by cold in IT (Fig. 3.5 and 3.6). Both SW and IT increase their freezing tolerance after 1 and 2 weeks of cold-acclimation in comparison to basal freezing tolerance (Fig. 3.1 and 3.2). The defined cold-regulated genes are presumed to instigate these increases in freezing tolerance associated with cold-acclimation. A previous study by Hannah et al. 2006 defined a set of genes positively and negatively correlated with increases in freezing tolerance associated with cold acclimation (this set of genes is detailed in earlier analysis of basal transcriptomes; (6)). Therefore it was determined if SW and IT cold-regulated genes are enriched in genes previously associated with cold-acclimation. Fittingly, genes up-regulated by cold in SW and IT are enriched for Hannah genes positively correlated but not negatively correlated with increases in freezing tolerance

(Fig 3.7 and 3.8). Interestingly, the number of Hannah genes positively correlated with freezing tolerance, which overlap with SW genes up-regulated by cold, is more significant than with the genes up-regulated by cold in IT (Fig. 3.7 and 3.8). In SW, genes down-regulated by cold are significantly enriched in Hannah genes negatively correlated with freezing tolerance (Fig. 3.6). However, this is not also the case for the 2658 IT genes down-regulated by cold (Fig. 3.8). This suggests that there may be significant differences in the genes that comprise SW and IT cold-regulated transcriptomes, which will be further analyzed in the following subsections.

SW and IT have similar freezing tolerance at 1 week of cold-acclimation and differing freezing tolerance at 2 weeks of cold-acclimation. Therefore it was also of interest to determine if there is significant overlap between cold-regulated genes at 1 and 2 weeks of cold-acclimation, or if discrete sets of genes are cold-regulated with 1 and 2 weeks of cold-acclimation (Fig 3.5 and 3.6). There is significant overlap in genes up-regulated by cold at 1 week and 2 weeks of cold-acclimation in both SW (1013 genes; Fig 3.5) and IT (1007; Fig. 3.6). There is also significant overlap in genes down-regulated by cold at 1 and 2 weeks of cold acclimation in both SW (1275 genes; Fig 3.5) and IT (1376 genes; Fig 3.6).

Hannah et al. 2006 found that the cold-acclimation capacity of nine accessions of *Arabidopsis* was positively correlated with the number of genes that significantly change in expression in response to cold (6). Consequently, it was of interest to determine if this correlation was also corroborated with sets of SW and IT cold-regulated genes. At 2 weeks of cold-acclimation there are more cold-regulated genes in SW (1978 genes

up-regulated by cold; 3205 genes down-regulated by cold; Fig 3.5) than in IT (1552 genes up-regulated by cold; 1796 genes down-regulated by cold; Fig 3.6). Based on this result Hannah et al. 2006 would hypothesize that SW has a greater capacity to cold acclimate than IT. This hypothesis is substantiated in electrolyte leakage assays performed in this study. SW has greater freezing tolerance than IT with 2 weeks of cold-acclimation (Fig. 3.2).

The number of gene expression changes from 1 to 2 weeks of cold-acclimation are also consistent with the 'gene number to cold-acclimation correlation' hypothesis by Hannah et al. 2006. Electrolyte leakage assays show that SW increases in freezing tolerance from 1 to 2 weeks of cold-acclimation (Fig 3.1 and 3.2), and the number of gene expression changes in SW also increases from 2664 cold-regulated genes at 1 week of cold-acclimation to 5183 cold-regulated genes at 2 weeks of cold-acclimation (Fig 3.5). Furthermore, IT decreases in freezing tolerance from 1 to 2 weeks of cold-acclimation and the number of gene expression changes also decreases from 4011 cold-regulated genes at 1 week of cold-acclimation to 3348 cold-regulated genes at 2 weeks of cold-acclimation.

Unfortunately, the 'gene number to cold-acclimation correlation' hypothesis by Hannah et al. 2006 is not infallible and is inconsistent with gene expression changes at 1 week of cold-acclimation. At 1 week of cold-acclimation there are 2664 cold-regulated genes in SW (1342 genes up-regulated by cold; 1322 genes down-regulated by cold; Fig 3.5), and 4011 cold-regulated genes in IT (1746 genes up-regulated by cold; 2265 genes down-regulated by cold; Fig 3.6). According to Hannah et al. 2006, this would

suggest that IT has a greater capacity to cold-acclimate than SW. But electrolyte leakage assays determined that SW and IT have similar freezing tolerance with 1 week of cold-acclimation (Fig 3.1).

Altogether, SW cold-regulated genes appear to be more enriched in genes previously associated with increases in freezing tolerance than IT cold-regulated genes. The quantity of cold-regulated genes in SW and IT, also suggests that there could be differences their capacity to cold-acclimate. Therefore in the next subsections of this study SW and IT cold-regulated genes will be compared in more detail. Since both SW and IT have similar freezing tolerance after 1 week of cold-acclimation, a more detailed comparison of transcriptomes at this time-point may reveal if SW and IT achieve this level of freezing tolerance by similar or divergent mechanisms.

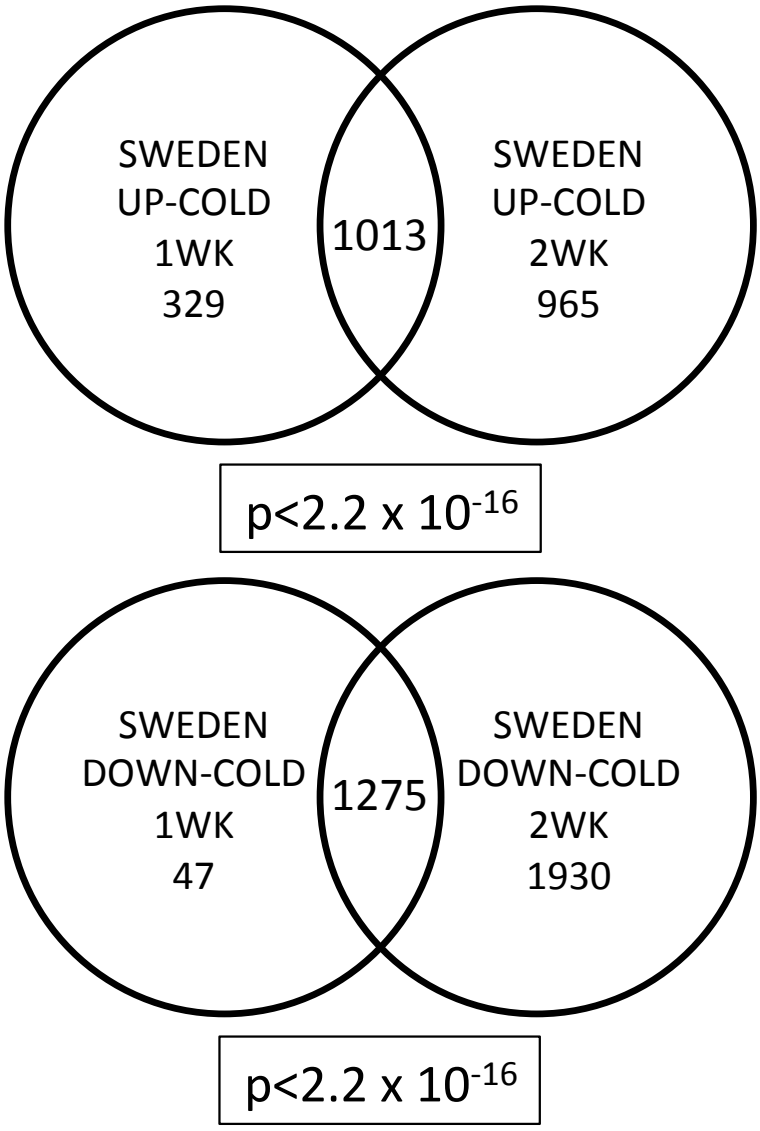


**Figure 3.5** Cold-responsive genes in SW. Plants were grown at 22$^0$C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled directly or transferred to 4$^0$C for 1 or 2 weeks under a 12 h photoperiod then sampled. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Genes were considered differentially expressed from non-acclimated conditions if the FDR corrected p-value was ≤0.05. ≥3FPKM was used as the cut-off for differential expression (19, 20). P-values represent overlap between differentially expressed cold-responsive genes at 1 and 2 weeks of cold-acclimation (calculated using a hypergeometric distribution in R).

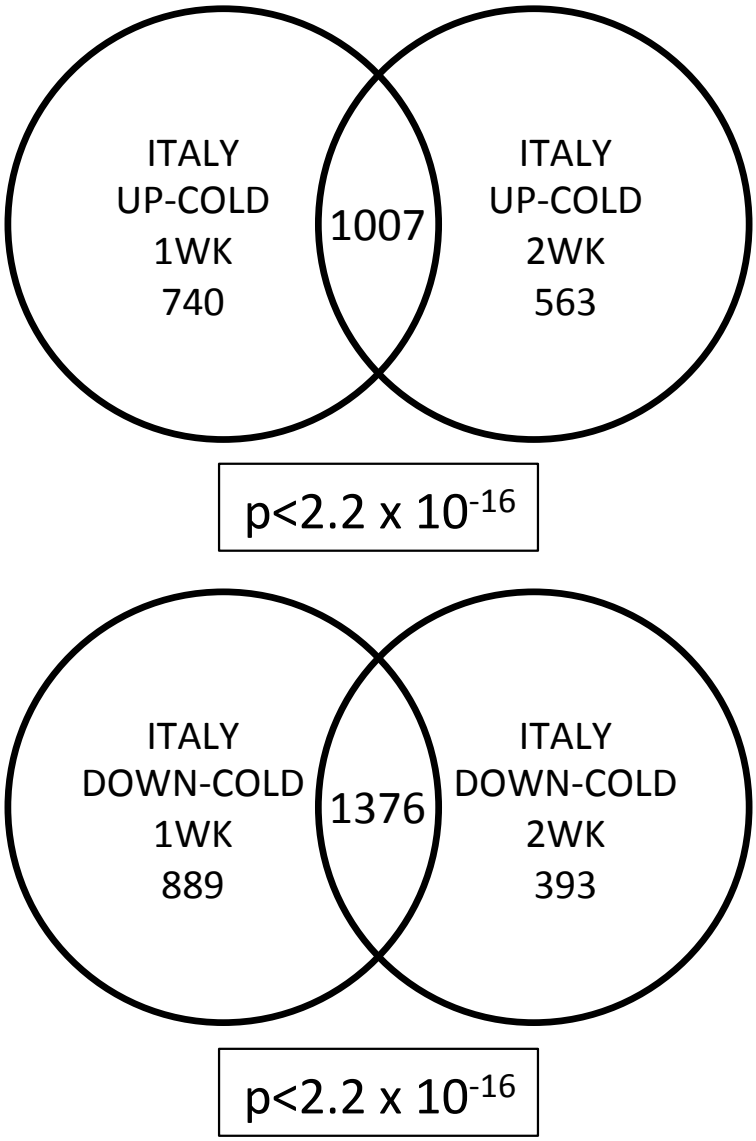


**Figure 3.6.** Cold-responsive genes in IT. Plants were grown at 22$^{0}$C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled directly or transferred to 4$^{0}$C for 1 or 2 weeks under a 12 h photoperiod then sampled. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Genes were considered differentially expressed from non-acclimated conditions if the FDR corrected p-value was ≤0.05. ≥3FPKM was used as the cut-off for differential expression (19, 20). P-values represent overlap between differentially expressed cold-responsive genes at 1 and 2 weeks of cold-acclimation (calculated using a hypergeometric distribution in R).

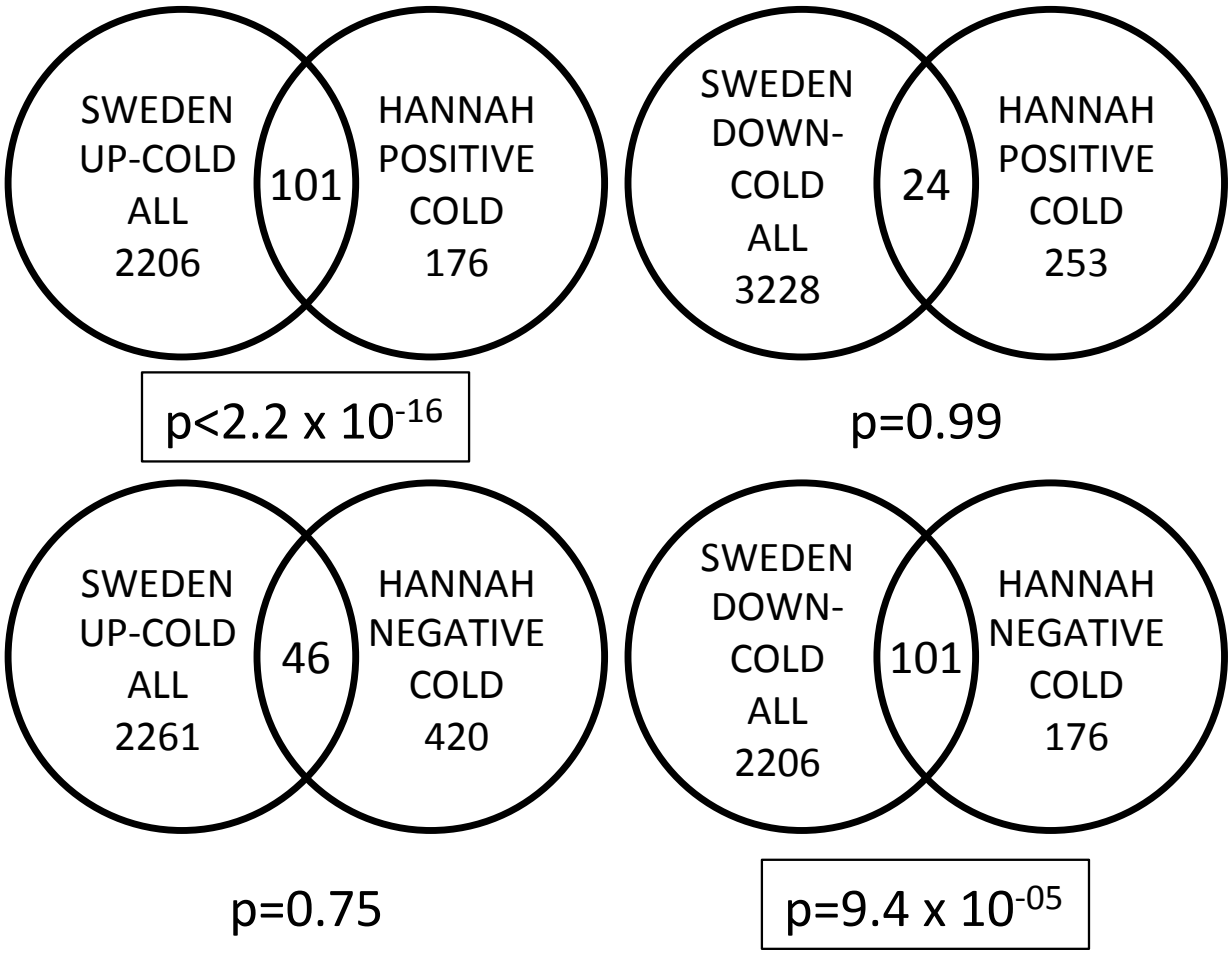


**Figure 3.7.** Overlap between the SW cold-responsive genes set and the Hannah genes set (6). Plants were grown at 22°C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Genes were considered differentially expressed if the FDR corrected p-value was ≤0.05. ≥3FPKM was used as the cut-off for differential expression (19, 20). P-values (calculated using a hypergeometric distribution in R) represent overlap between differentially expressed genes and Hannah genes (277 Hannah genes positively correlated with freezing tolerance and 466 Hannah genes negatively correlated with freezing tolerance; (6)).

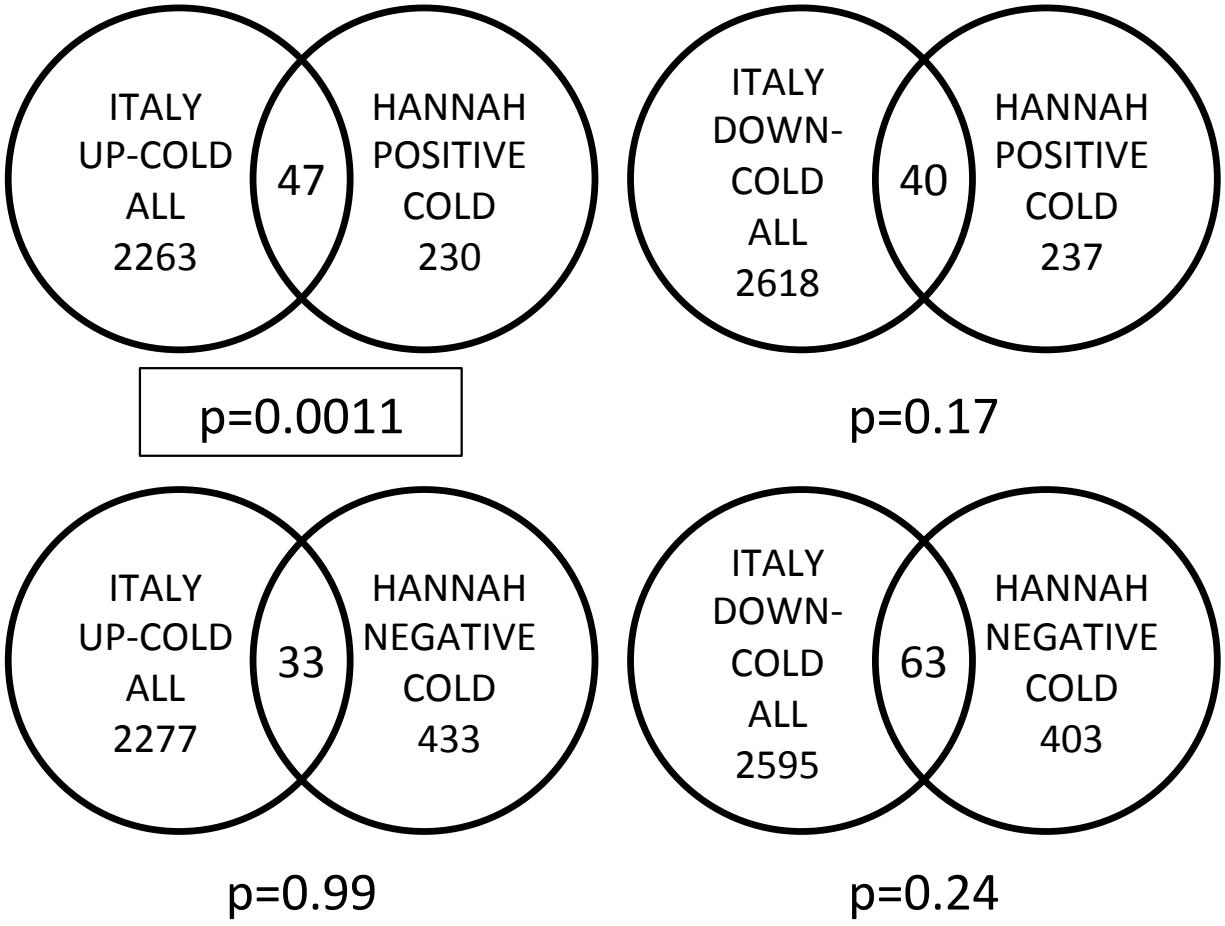


**Figure 3.8.** Overlap between the IT cold-responsive genes set and the Hannah genes set (6). Plants were grown at 22°C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Genes were considered differentially expressed if the FDR corrected p-value was ≤0.05. ≥3FPKM was used as the cut-off for differential expression (19, 20). P-values (calculated using a hypergeometric distribution in R) represent overlap between differentially expressed genes and Hannah genes (277 Hannah genes positively correlated with freezing tolerance and 466 Hannah genes negatively correlated with freezing tolerance; (6)).

## SW AND IT TRANSCRIPTOMES AT 1 WEEK OF COLD-ACCLIMATION.

***Summary: SW and IT transcriptomes at 1 week of cold-acclimation.*** SW and IT have similar freezing tolerance after 1 week of cold-acclimation. Therefore, the SW and IT cold-response at 1 week of cold-acclimation was examined to determine if this level of freezing tolerance is attained by similar transcriptional changes. Although there are a significant number of genes that respond similarly to cold in SW and IT, the majority of cold-responsive genes are differentially regulated, either in terms of induction pattern (up-regulated by cold / down-regulated by cold / not regulated by cold) or in terms of expression level (FPKM). Furthermore, these differentially expressed cold-regulated genes are enriched in genes that have previously been correlated with cold-acclimation. Analysis of RNA-seq data also suggests that there may be differences in the regulation of the CBF pathway of cold-acclimation between SW and IT. Overall, data suggests that SW and IT may reach similar levels of freezing tolerance through significantly different transcriptional changes at 1 week of cold-acclimation.

***SW and IT transcriptomes at 1 week of cold-acclimation: Analysis of non-overlapping cold-regulated genes.*** SW and IT have similar freezing tolerance after 1 week of cold-acclimation. Therefore, the SW and IT cold-response at 1 week of cold-acclimation was examined to determine if this level of freezing tolerance is attained by similar transcriptional mechanisms. First, for a gene to 'respond similarly' to cold it must have a similar induction pattern (increase in response to cold or decrease in response to cold). Even if a gene ultimately has a similar level of expression at 1 week of cold-

acclimation despite dissimilar induction patterns (i.e. the gene is constitutively on in one ecotype) the change in induction would indicate altered regulation of that gene.

There are a significant number of genes commonly up-regulated (734 genes) and down-regulated (946 genes) by cold between SW and IT with 1 week of cold-acclimation (Fig. 3.9). But there are also 608 genes only up-regulated by cold in SW and 1012 genes only up-regulated by cold in IT at 1 week of cold-acclimation (Fig. 3.9). There are also 376 genes only down-regulated by cold in SW and 1319 genes only down-regulated by cold in IT at 1 week of cold-acclimation (Fig. 3.9). To determine if SW and IT use similar transcriptional mechanisms to attain similar levels of freezing tolerance, the cold-genes, which are uniquely expressed in SW or IT, were first examined. The genes with overlapping induction patterns in SW and IT were next examined to determine the genes that have significantly different levels of expression. Lastly, genes that do appear to respond similarly to cold in SW and IT, in terms of induction pattern and expression level, were further analyzed.

It is possible that cold-responsive genes that are differentially regulated between SW and IT do not play a role in increases in freezing tolerance associated with cold-acclimation. To appraise if non-overlapping cold-responsive genes have been previously associated with cold-acclimation enrichment of Hannah genes (6), which have been previously positively and negatively correlated with increases in freezing tolerance associate with cold-acclimation, was tested (Fig. 3.10). The 608 genes uniquely up-regulated by cold in SW at 1 week of cold-acclimation are enriched (55 genes overlapping) in Hannah genes that are positively correlated with freezing

tolerance (Fig. 3.10). Of the 55 overlapping Hannah genes, 20 are greater than 4-fold induced by cold in SW, 33 are greater than 2-fold induced and only 2 are less than 2-fold induced (Fig. 3.11). This suggests that genes uniquely up-regulated by cold in SW may contribute to cold-acclimation in some way. The 608 genes only up-regulated in SW are also enriched (56 genes; $p< 2.2E-16$) in genes up-regulated by the CBFs (CBF regulon; (25)). The CBFs are central components of the most well described pathway of cold-acclimation. Since these CBF regulon genes are only expressed in SW it suggests that there might be some difference in the CBF pathway of cold-acclimation between SW and IT. 'Response to cold' and other related abiotic stress GO categories are also enriched in the 608 genes only up-regulated in SW (Table 3.4). Interestingly, the 1012 genes that are exclusively up-regulated by cold in IT at 1 week of cold-acclimation are not enriched in Hannah genes (Fig. 3.10) or in CBF regulon genes. 'Response to cold' or other related abiotic stress categories are also markedly absent from the GO terms enriched in the 1012 genes only up-regulated by cold in IT (Table 3.5).

The 376 genes that are uniquely down-regulated by cold in SW are enriched (40 genes) in Hannah genes that negatively correlate with freezing tolerance (Fig 3.12). Of the 40 overlapping Hannah genes, 5 are greater than 4-fold reduced by cold, 30 of these genes are greater than 2-fold reduced and 5 are less than 2-fold reduced (Fig 3.13). For these 376 genes there are no biological process GO categories significantly enriched above the threshold (FDR p-value ≤0.050) but molecular function GO categories enriched include 'water transport' (Table 3.6). The 1319 genes only down-regulated by cold in IT are not significantly enriched (5 genes) in Hannah genes

negatively correlated with freezing tolerance (Fig. 3.12). Remarkably, the 1319 genes only down-regulated in IT are enriched (32 genes) in Hannah genes that are positively correlated with increases in freezing tolerance (Fig. 3.12). Of the 32 overlapping Hannah genes, 6 are greater than 4-fold reduced by cold, 20 are greater than 2-fold reduced 6 are less than 2-fold reduced (Fig. 3.14). Furthermore, these 1319 gene that are only down-regulated by cold in IT are enriched (23 genes; p=0.021) in genes up-regulated by the CBFs (25). This indicates that CBF regulon genes may be uniquely repressed in IT and again suggests that the CBF pathway of cold-acclimation may be regulated differently between SW and IT. For the 1319 genes only down-regulated in IT, 'defense response' related GO categories such as 'innate immune response' and 'response to biotic stimulus' are significantly enriched (Table 3.7). This is interesting considering that 'defense response' was also enriched in genes with higher expression in IT under basal conditions (Table 3.3).

Altogether, analysis of RNA-seq data at 1 week of cold-acclimation indicates that genes uniquely cold-regulated in SW are enriched in genes previously associated with cold acclimation. This enrichment of genes correlated with cold-acclimation in cold-regulated genes uniquely expressed SW is curious considering that there is no significant difference in freezing tolerance between SW and IT at 1 week of cold acclimation (Fig. 3.1). Therefore cold-regulated genes uniquely expressed in IT at 1 week of cold-acclimation may potentially be part of pathways of cold-acclimation currently not well described allowing IT to achieve a similar level of freezing tolerance to SW at 1 week of cold-acclimation (Fig 3.1). Differences in gene expression at 1 week of

cold-acclimation may also take time to manifest into differences in freezing tolerance (Fig 3.2). Consequently genes differentially regulated between SW and IT at 1 week of cold-acclimation, which remain differentially regulated at 2 weeks of cold-acclimation, are included in the list of genes that potentially contribute to differences in freezing tolerance. Genes that potentially contribute to differences in freezing tolerance will be described in more detail in the next subsection of RNA-seq analysis but first genes with similar cold induction patterns but significantly different levels of expression will be examined.

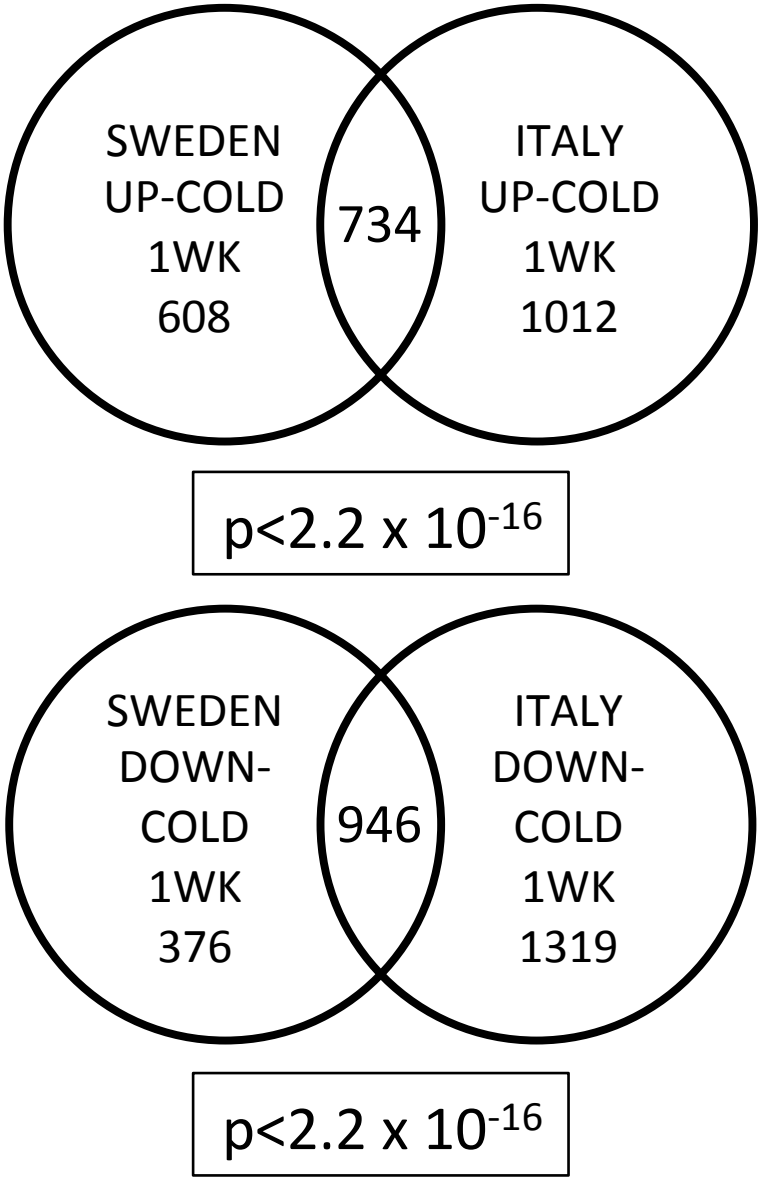


**Figure 3.9.** Overlap between SW and IT response at 1 week of cold-acclimation. Plants were grown at 22$^0$C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled directly or transferred to 4$^0$C for 1 week under a 12 h photoperiod then sampled. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Genes were considered differentially expressed from non-acclimated conditions if the FDR corrected p-value was ≤0.05.≥3FPKM was used as the cut-off for differential expression (19, 20). P-values represent overlap between SW and IT cold-responsive genes (calculated using a hypergeometric distribution in R).

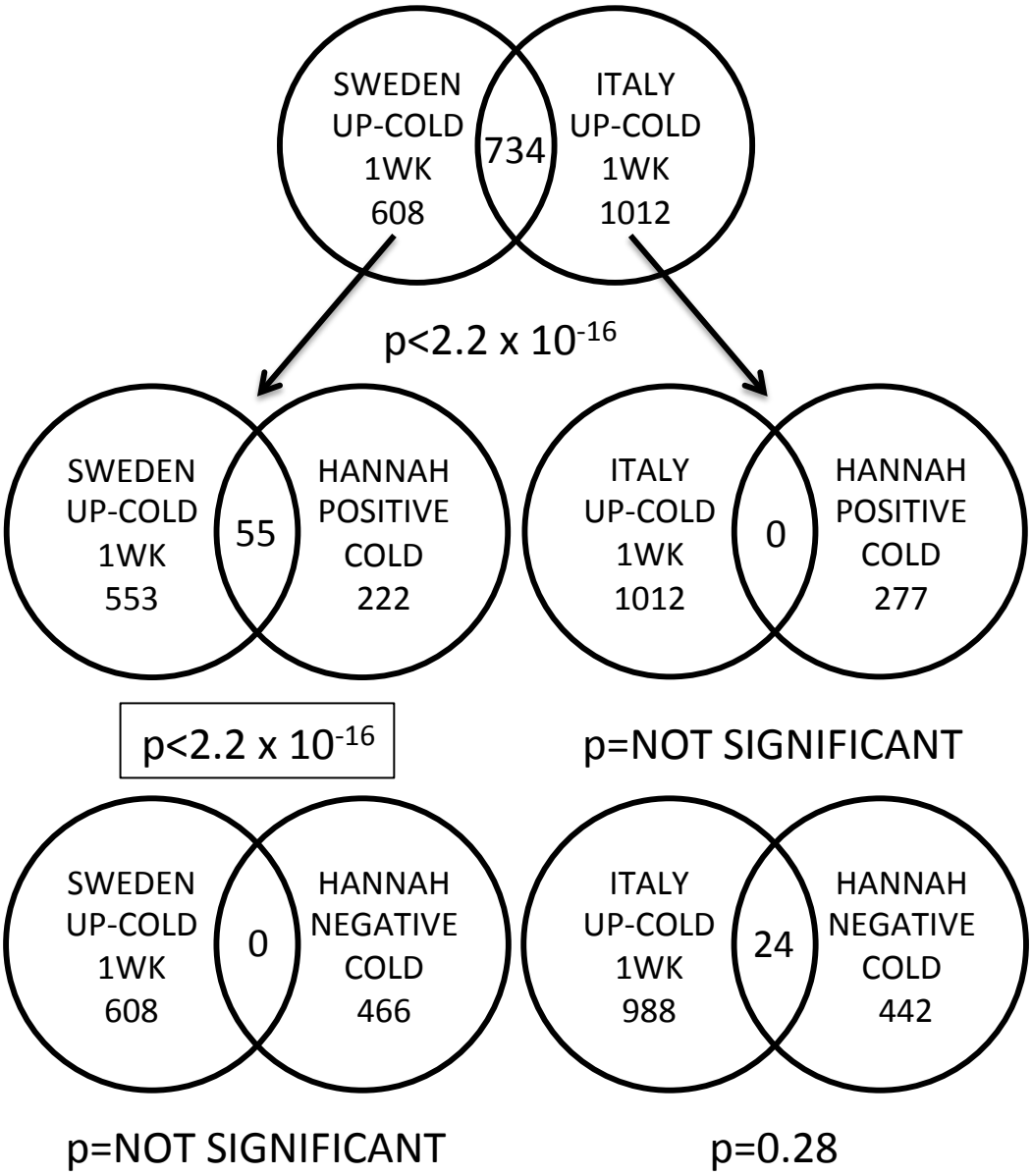


**Figure 3.10.** Overlap between genes uniquely up-regulated in SW or IT at 1 week of cold-acclimation and the Hannah genes set. Plants were grown at 22$^0$C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled directly or transferred to 4$^0$C for 1 week under a 12 h photoperiod then sampled. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Genes were considered differentially expressed from non-acclimated conditions if the FDR corrected p-value was ≤0.05. ≥3FPKM was used as the cut-off for differential expression (19, 20). P-values (calculated using a hypergeometric distribution in R) represent overlap between differentially expressed genes and Hannah genes (277 genes positively correlated with freezing tolerance and 466 genes negatively correlated with freezing tolerance; (6)).

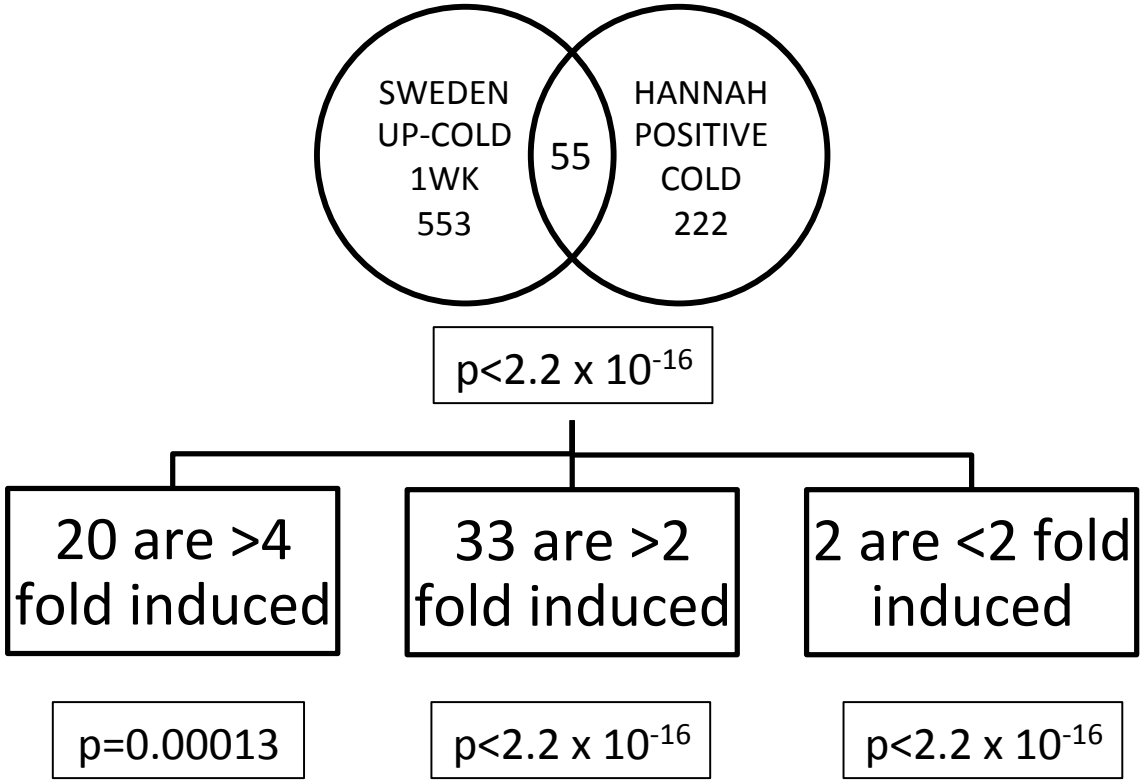


**Figure 3.11.** Fold change of 55 Hannah genes, which overlap with 608 genes only up-regulated in SW at 1 week of cold-acclimation. P-values represent the significance of overlap between gene only up-regulated in SW and Hannah genes if 4-fold, 2-fold, or no fold change cut-offs were applied (from left to right).

**Table 3.4.** GO categories significantly enriched in 608 genes only up-regulated in SW at 1 week of cold-acclimation. GO enrichment was determined using DAVID (**david**.abcc.ncifcrf.gov; (27)). 'GO TERM CATEGORY' denotes if the GO term was categorized as a biological process (BP), cellular component (CC), or molecular function (MF) in the DAVID database. '# HITS' denotes the number of genes with that GO category in the 608 genes only up-regulated in SW at 1 week of cold-acclimation. '# GENES IN GO' denotes the total number of genes in that GO category included in the DAVID database. GO category was considered significantly enriched if the FDR corrected hypergeometric p-value was ≤0.050.

| GO TERM CATEGORY | SW ONLY UP-COLD (608 GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| BP | Response To Organic Substance | 66 | 1176 | 1.70E-07 |
| BP | Response To Endogenous Stimulus | 59 | 975 | 2.24E-07 |
| BP | Response To Ethylene Stimulus | 22 | 256 | 2.96E-04 |
| BP | Secondary Metabolic Process | 29 | 423 | 3.36E-04 |
| BP | Phenylpropanoid Biosynthetic Process | 15 | 128 | 4.21E-04 |
| BP | Ethylene Mediated Signaling Pathway | 17 | 170 | 4.63E-04 |
| BP | Response To Abiotic Stimulus | 56 | 1197 | 5.27E-04 |
| BP | Response To Jasmonic Acid Stimulus | 16 | 156 | 6.27E-04 |
| BP | Response To Abscisic Acid Stimulus | 22 | 285 | 6.41E-04 |
| BP | Response To Water | 17 | 185 | 9.88E-04 |
| BP | Phenylpropanoid Metabolic Process | 16 | 166 | 9.97E-04 |
| BP | Response To Cold | 19 | 233 | 1.16E-03 |
| BP | Response To Temperature Stimulus | 24 | 354 | 1.33E-03 |
| BP | Response To Water Deprivation | 16 | 176 | 1.59E-03 |
| MF | UDP-Glucosyltransferase Activity | 13 | 119 | 3.36E-03 |
| MF | Glutathione Transferase Activity | 9 | 49 | 3.57E-03 |
| BP | Response To Oxidative Stress | 20 | 287 | 4.32E-03 |
| BP | Two-Component Signal Transduction | 17 | 218 | 4.42E-03 |
| BP | Amino Acid Derivative Biosynthetic Process | 16 | 194 | 4.55E-03 |
| BP | Toxin Metabolic Process | 8 | 46 | 4.92E-03 |
| MF | Quercetin 3-O-Glucosyltransferase Activity | 7 | 23 | 4.94E-03 |
| MF | Transcription Regulator Activity | 72 | 1913 | 5.96E-03 |
| BP | Hormone-Mediated Signaling | 25 | 432 | 7.29E-03 |
| BP | Cellular Response To Hormone Stimulus | 25 | 432 | 7.29E-03 |
| BP | Carbohydrate Transport | 10 | 83 | 7.33E-03 |
| MF | Glucosyltransferase Activity | 13 | 137 | 8.06E-03 |
| MF | Transcription Factor Activity | 64 | 1678 | 8.12E-03 |
| BP | Response To Wounding | 13 | 147 | 9.93E-03 |
| BP | Response To Chitin | 12 | 127 | 1.01E-02 |
| MF | Solute: Cation Symporter Activity | 12 | 126 | 1.15E-02 |
| BP | Response To Carbohydrate Stimulus | 15 | 199 | 1.31E-02 |

**Table 3.4 (cont'd)**

| | | | | |
|---|---|---|---|---|
| BP | Response To Inorganic Substance | 28 | 540 | 1.32E-02 |
| BP | Regulation Of Transcription | 73 | 2024 | 2.14E-02 |
| BP | Aromatic Compound Biosynthetic Process | 15 | 215 | 2.58E-02 |
| CC | Vacuole | 30 | 643 | 2.80E-02 |
| MF | Sugar: Hydrogen Symporter Activity | 10 | 99 | 2.81E-02 |
| BP | Negative Regulation Of ABA Signaling | 5 | 19 | 2.83E-02 |
| MF | Symporter Activity | 12 | 146 | 3.14E-02 |
| CC | Plasma Membrane | 76 | 2228 | 3.85E-02 |
| BP | Flavonoid Biosynthetic Process | 7 | 53 | 4.65E-02 |

**Table 3.5.** GO categories significantly enriched in 1012 genes only up-regulated in IT at 1 week of cold-acclimation. GO enrichment was determined using DAVID (**david**.abcc.ncifcrf.gov; (27)). 'GO TERM CATEGORY' denotes if the GO term was categorized as a biological process (BP), cellular component (CC), or molecular function (MF) in the DAVID database. '# HITS' denotes the number of genes with that GO category in the 1012 genes only up-regulated in IT at 1 week of cold-acclimation. '# GENES IN GO' denotes the total number of genes in that GO category included in the DAVID database. GO category was considered significantly enriched if the FDR corrected hypergeometric p-value was ≤0.050.

| GO TERM CATEGORY | IT ONLY UP-COLD (1012 GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| MF | Structural Constituent Of Ribosome | 147 | 394 | 1.30E-97 |
| CC | Non-Membrane-Bounded Organelle | 232 | 1144 | 6.95E-96 |
| CC | Cytosolic Part | 126 | 271 | 1.09E-95 |
| CC | Ribosomal Subunit | 128 | 294 | 1.94E-93 |
| CC | Nucleolus | 103 | 332 | 3.13E-57 |
| CC | Cytosol | 145 | 708 | 1.01E-56 |
| CC | Membrane-Enclosed Lumen | 134 | 667 | 4.44E-51 |
| BP | Ribosome Biogenesis | 84 | 242 | 1.21E-50 |
| CC | Nuclear Lumen | 113 | 472 | 1.54E-50 |
| CC | Intracellular Organelle Lumen | 132 | 659 | 3.72E-50 |
| BP | Translation | 173 | 1231 | 3.19E-46 |
| BP | RNA Processing | 72 | 436 | 4.78E-21 |
| MF | RNA Binding | 128 | 1351 | 5.49E-16 |
| CC | Mitochondrion | 114 | 1349 | 1.58E-10 |
| MF | Purine NTP-Dependent Helicase Activity | 26 | 113 | 8.97E-10 |
| MF | ATP-Dependent Helicase Activity | 26 | 113 | 8.97E-10 |
| MF | Translation Factor Activity | 27 | 149 | 7.50E-08 |
| CC | Plastid | 205 | 3259 | 1.76E-07 |
| CC | Chloroplast | 197 | 3192 | 1.67E-06 |
| CC | Cell Wall | 52 | 611 | 1.06E-04 |
| MF | ATPase Activity | 44 | 467 | 1.22E-04 |
| CC | External Encapsulating Structure | 52 | 620 | 1.51E-04 |
| BP | Embryonic Development, Seed Dormancy | 37 | 372 | 3.10E-04 |
| BP | RNA Modification | 20 | 133 | 3.47E-04 |
| MF | Macromolecule Transmembrane Transporter | 12 | 51 | 3.83E-04 |
| BP | Chromatin Assembly | 14 | 71 | 6.54E-04 |
| CC | Plasma Membrane | 135 | 2228 | 7.25E-04 |
| BP | Nucleosome Assembly | 13 | 69 | 1.94E-03 |
| BP | Seed Development | 38 | 432 | 2.29E-03 |
| BP | Mitochondrion Organization | 9 | 32 | 2.48E-03 |
| MF | RNA Methyltransferase Activity | 8 | 26 | 3.05E-03 |

**Table 3.5 (cont'd)**

| | | | | |
|---|---|---|---|---|
| CC | Small Nucleolar Ribonucleoprotein Complex | 14 | 100 | 3.83E-03 |
| BP | Cellular Macromolecular Complex Assembly | 23 | 208 | 3.93E-03 |
| BP | Nucleotide Biosynthetic Process | 20 | 170 | 4.66E-03 |
| MF | Pseudouridine Synthase Activity | 7 | 20 | 4.81E-03 |
| BP | Fruit Development | 38 | 452 | 4.87E-03 |
| BP | Nitrogen Compound Biosynthetic Process | 41 | 506 | 4.87E-03 |
| BP | Pseudouridine Synthesis | 7 | 21 | 6.82E-03 |
| BP | Response To Cadmium Ion | 29 | 327 | 1.01E-02 |
| MF | DNA-Directed RNA Polymerase Activity | 11 | 63 | 1.02E-02 |
| CC | Vacuole | 46 | 643 | 1.22E-02 |
| MF | Exonuclease Activity | 8 | 34 | 1.52E-02 |
| BP | Regulation Of Macromolecule Biosynthetic Process | 11 | 69 | 1.68E-02 |
| MF | RNA Polymerase Activity | 11 | 69 | 1.91E-02 |
| CC | CUL4 RING Ubiquitin Ligase Complex | 14 | 122 | 1.98E-02 |
| MF | Ribonuclease Activity | 12 | 84 | 2.26E-02 |
| BP | Purine Nucleotide Metabolic Process | 16 | 140 | 2.28E-02 |
| MF | GTPase Activity | 13 | 97 | 2.36E-02 |
| BP | Protein Folding | 23 | 251 | 2.52E-02 |
| BP | Translational Initiation | 11 | 74 | 2.60E-02 |
| MF | Nuclease Activity | 19 | 188 | 2.80E-02 |
| BP | Protein Localization In Organelle | 11 | 76 | 3.11E-02 |
| BP | Negative Regulation Of DNA Replication | 4 | 6 | 3.19E-02 |
| MF | 3'-5'-Exoribonuclease Activity | 7 | 30 | 3.29E-02 |
| MF | Intramolecular Transferase Activity | 9 | 53 | 3.70E-02 |
| BP | Response To Metal Ion | 30 | 384 | 4.14E-02 |
| CC | Nucleosome | 9 | 63 | 4.20E-02 |
| BP | Pyrimidine Nucleotide Metabolic Process | 6 | 22 | 4.23E-02 |
| MF | GTP Binding | 23 | 263 | 4.29E-02 |
| BP | Regulation Of DNA Replication | 5 | 14 | 4.61E-02 |
| MF | Exoribonuclease Activity | 7 | 33 | 4.84E-02 |

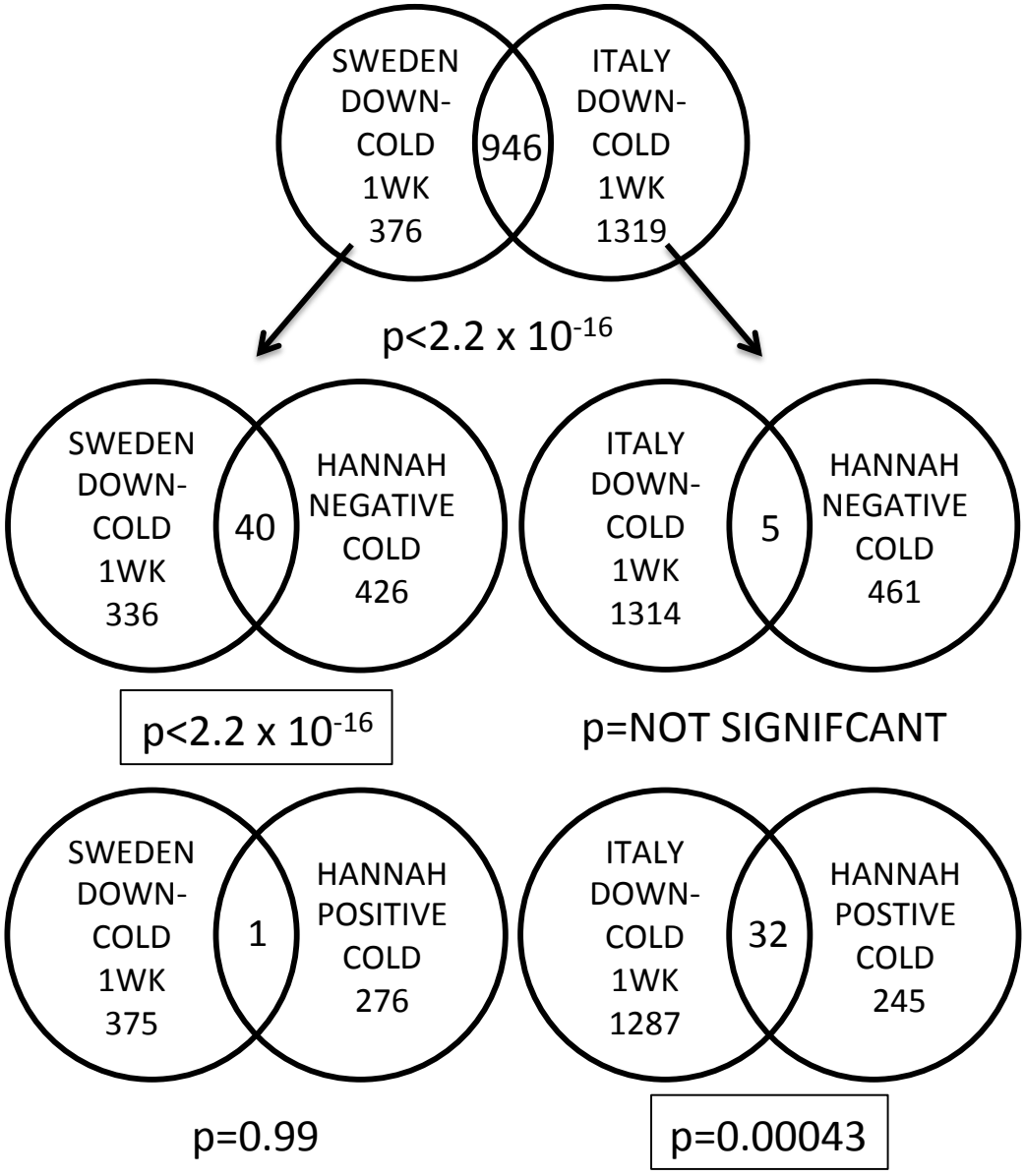


**Figure 3.12.** Overlap between genes uniquely down-regulated in SW or IT at 1 week of cold-acclimation and the Hannah genes set. Plants were grown at 22$^0$C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled directly or transferred to 4$^0$C for 1 week under a 12 h photoperiod then sampled. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Genes were considered differentially expressed from non-acclimated conditions if the FDR corrected p-value was ≤0.05. ≥3FPKM was used as the cut-off for differential expression (19, 20). P-values (calculated using a hypergeometric distribution in R) represent overlap between differentially expressed genes and Hannah genes (277 genes positively correlated with freezing tolerance and 466 genes negatively correlated with freezing tolerance; (6)).

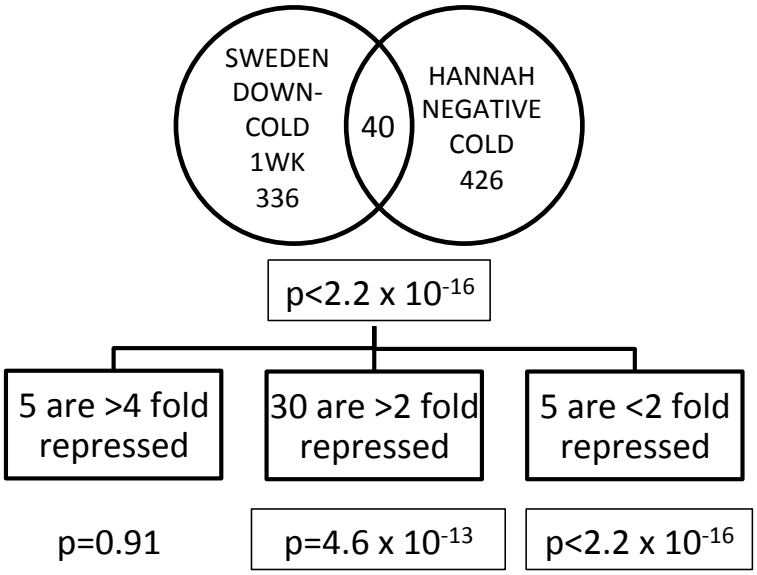


**Figure 3.13.** Fold change of 40 Hannah genes that overlap with 376 genes only down-regulated in SW at 1 week of cold-acclimation. P-values represent the significance of overlap between gene only up-regulated in SW and Hannah genes if 4-fold, 2-fold, or no fold change cut-offs were applied (from left to right).

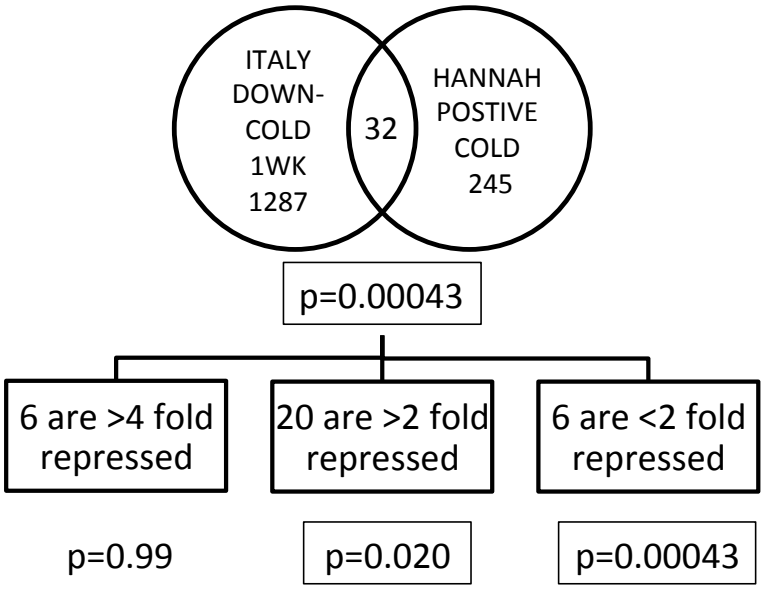


**Figure 3.14.** Fold change of 32 Hannah genes that overlap with 1319 genes only down-regulated in IT at 1 week of cold-acclimation. P-values represent the significance of overlap between gene only up-regulated in SW and Hannah genes if 4-fold, 2-fold, or no fold change cut-offs were applied (from left to right).

**Table 3.6.** GO categories significantly enriched in 376 genes only down-regulated in SW at 1 week of cold-acclimation. GO enrichment was determined using DAVID (**david**.abcc.ncifcrf.gov; (27)). 'GO TERM CATEGORY' denotes if the GO term was categorized as a biological process (BP), cellular component (CC), or molecular function (MF) in the DAVID database. '# HITS' denotes the number of genes with that GO category in the 376 genes only down-regulated in SW at 1 week of cold-acclimation. '# GENES IN GO' denotes the total number of genes in that GO category included in the DAVID database. GO category was considered significantly enriched if the FDR corrected hypergeometric p-value was ≤0.050.

| GO TERM CATEGORY | SW ONLY DOWN-COLD (376 GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| CC | Anchored To Plasma Membrane | 9 | 66 | 2.08E-03 |
| CC | Anchored To Membrane | 18 | 320 | 2.44E-03 |
| CC | External Encapsulating Structure | 26 | 620 | 2.70E-03 |
| CC | Cell Wall | 25 | 611 | 4.29E-03 |
| MF | Channel Activity | 11 | 126 | 4.76E-03 |
| MF | Passive Transmembrane Transporter Activity | 11 | 126 | 4.76E-03 |
| CC | Apoplast | 18 | 382 | 8.16E-03 |
| CC | Intrinsic To Plasma Membrane | 9 | 103 | 8.33E-03 |
| MF | Substrate Specific Channel Activity | 11 | 125 | 8.87E-03 |
| CC | Intrinsic To Membrane | 66 | 2658 | 2.21E-02 |
| MF | Water Transporter Activity | 6 | 37 | 2.89E-02 |
| MF | Water Channel Activity | 6 | 37 | 2.89E-02 |
| CC | Plasma Membrane | 56 | 2228 | 4.16E-02 |

**Table 3.7.** GO categories significantly enriched in 1319 genes only down-regulated in IT at 1 week of cold-acclimation. GO enrichment was determined using DAVID (**david**.abcc.ncifcrf.gov; (27)). 'GO TERM CATEGORY' denotes if the GO term was categorized as a biological process (BP), cellular component (CC), or molecular function (MF) in the DAVID database. '# HITS' denotes the number of genes with that GO category in 1319 genes only down-regulated in IT at 1 week of cold-acclimation. '# GENES IN GO' denotes the total number of genes in that GO category included in the DAVID database. GO category was considered significantly enriched if the FDR corrected hypergeometric p-value was ≤0.050.

| GO TERM CATEGORY | IT ONLY DOWN-COLD (1319 GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| BP | Immune Response | 50 | 293 | 1.06E-10 |
| BP | Cell Death | 38 | 254 | 2.26E-06 |
| BP | Response To Organic Substance | 102 | 1176 | 1.37E-05 |
| BP | Apoptosis | 28 | 172 | 2.85E-05 |
| BP | Response To Chitin | 21 | 127 | 9.75E-04 |
| BP | Defense Response | 84 | 1030 | 1.82E-03 |
| BP | Response To Carbohydrate Stimulus | 26 | 199 | 3.29E-03 |
| CC | Intrinsic To Membrane | 169 | 2658 | 1.79E-02 |
| BP | Response To Wounding | 20 | 147 | 1.89E-02 |
| CC | CCAAT-Binding Factor Complex | 6 | 13 | 2.50E-02 |
| BP | Plant-Type Hypersensitive Response | 10 | 45 | 3.97E-02 |
| BP | Amine Transport | 12 | 67 | 4.65E-02 |
| BP | Protein Ubiquitination | 17 | 125 | 4.83E-02 |

***SW and IT transcriptomes at 1 week of cold-acclimation: Analysis of cold-induced genes with overlapping induction patterns but different levels of expression.*** Though there are 1620 genes exclusively up-regulated by cold in either SW or IT there are also a significant number of genes commonly up-regulated by cold (734 genes) between SW and IT (Fig. 3.9). There are also a significant number of genes commonly down-regulated by cold (946 genes) in addition to the 1695 genes exclusively down-regulated in either SW or IT (Fig. 3.9). The 734 commonly up-regulated and 946 commonly down-regulated genes have similar cold-induction patterns and thus met the first requirement of 'responding similarly' (Fig. 3.9). The second measure for 'responding similarly' was that the gene must have a similar level of expression between SW and IT. Genes must have similar levels of expression in order to 'respond similarly' because statistically significant variances would again indicate that the gene has altered regulation between SW and IT. Statistically significant differences in expression level (FPKM) were measured by a FDR corrected p-value of ≤0.050.

A significant number of genes (105 genes out of 734) commonly up-regulated by cold in SW and IT have different induction levels (Fig. 3.15). There are 77 differentially expressed up-regulated genes with higher expression in SW and 28 with higher expression in IT (Fig 3.15). Again, these differentially expressed genes may not be associated with cold-acclimation. Therefore it was determined if these differentially expressed genes were enriched in Hannah genes that have been previously positively and negatively correlated with increases in freezing tolerance associated with cold-acclimation (6). The 77 genes with higher expression in SW are significantly enriched

(13 genes) in Hannah genes positively correlated with increases in freezing tolerance (Fig. 3.16). Of the 13 overlapping Hannah genes, 7 have greater than 4-fold higher expression in SW compared to IT, 5 are greater than 2-fold higher and 1 is less than 2-fold higher (Fig. 3.17). The 77 genes up-regulated by cold with higher expression in SW are enriched in cold-related GO terms such as 'response to cold', 'response to abiotic stimulus' and 'cold-acclimation' (Table 3.8). The 77 genes with higher expression in SW are also significantly enriched (14 genes; p=1.3E-13) in genes up-regulated by the CBFs (25). The 28 genes up-regulated by cold with higher expression in IT do not include any genes regulated by the CBFs. This suggests that SW and IT may differ in the CBF pathway of cold-acclimation, which is similar what was observed in genes that were uniquely cold regulated in either SW or IT. Furthermore, there is also no overlap between the 28 up-regulated genes with higher expression in IT and Hannah genes positively correlated with freezing tolerance (Fig. 3.16). These 28 genes are also not enriched in GO terms related to stress (Table 3.9).

A significant number of genes (105 out of 946 genes) commonly down-regulated by cold in SW and IT have significant differences in expression level (Fig. 3.18). There are 36 differentially expressed genes with higher expression in SW (more repressed in IT) and 69 with higher expression in IT (more repressed in SW; Fig 3.18). The 36 genes that are more repressed by cold in IT (higher expression in SW) do not significantly overlap with Hannah genes negatively correlated with increases in freezing tolerance or with CBF regulon genes (Fig. 3.19). These 36 genes do not have any statistically overrepresented GO terms. There is significant overlap (6 genes) between the 63

genes more repressed by cold in SW (higher in IT) and Hannah genes negatively correlated with freezing tolerance (Fig. 3.19). Of the 6 overlapping Hannah genes, 2 are greater than 4-fold repressed in SW compared to IT and 4 are greater than 2-fold repressed (Fig. 3.20). These 69 genes are not enriched in GO terms specifically related to cold but are enriched in GO terms such as 'response to endogenous stimulus' (Table 3.10). The 69 genes down-regulated by cold that are more repressed in SW (higher in IT) are also significantly enriched (4 genes; p=0.0072) in genes down-regulated by CBFs, again suggesting that SW and IT have differences in the CBF pathway of cold-acclimation.

Analysis of both non-overlapping cold genes and genes with common induction patterns but significantly different levels of expression suggests that the differentially expressed genes in SW are more enriched in genes previously correlated (Hannah genes) and associated (CBF regulon) with cold-acclimation. There is no difference in freezing tolerance between SW and IT at 1 week of cold-acclimation (Fig. 3.1). This suggests that IT may reach a similar level of freezing tolerance to SW through pathways of cold-acclimation not yet well defined. However, there are a significant number of genes with similar induction patterns and no significant difference in expression level (629 genes commonly up-regulated, and 841 genes commonly down-regulated). Next, these cold-regulated genes that respond similarly in SW and IT will be further analyzed to determine if they have been previously associated with cold-acclimation.

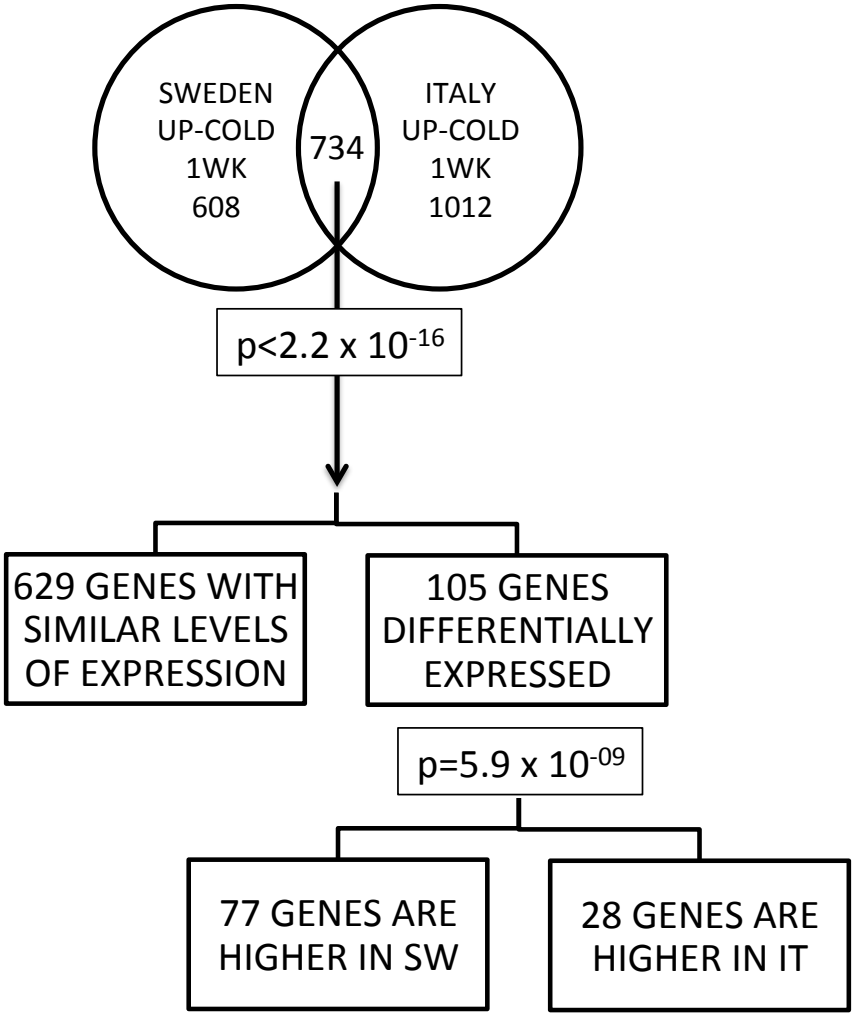


**Figure 3.15.** 105 genes commonly up-regulated by cold but significantly different in expression level. 77 genes are higher in expression in SW and 28 genes are higher in IT. Plants were grown at 22$^0$C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled directly or transferred to 4$^0$C for 1 week under a 12 h photoperiod then sampled. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Genes were considered differentially expressed from non-acclimated conditions if the FDR corrected p-value was ≤0.05. Genes were considered differentially expressed between SW and IT if the FDR corrected p-value was ≤0.05. ≥3FPKM was used as the cut-off for differential expression (19, 20). P-values represent overlap between SW and IT cold-responsive genes (calculated using a hypergeometric distribution in R).

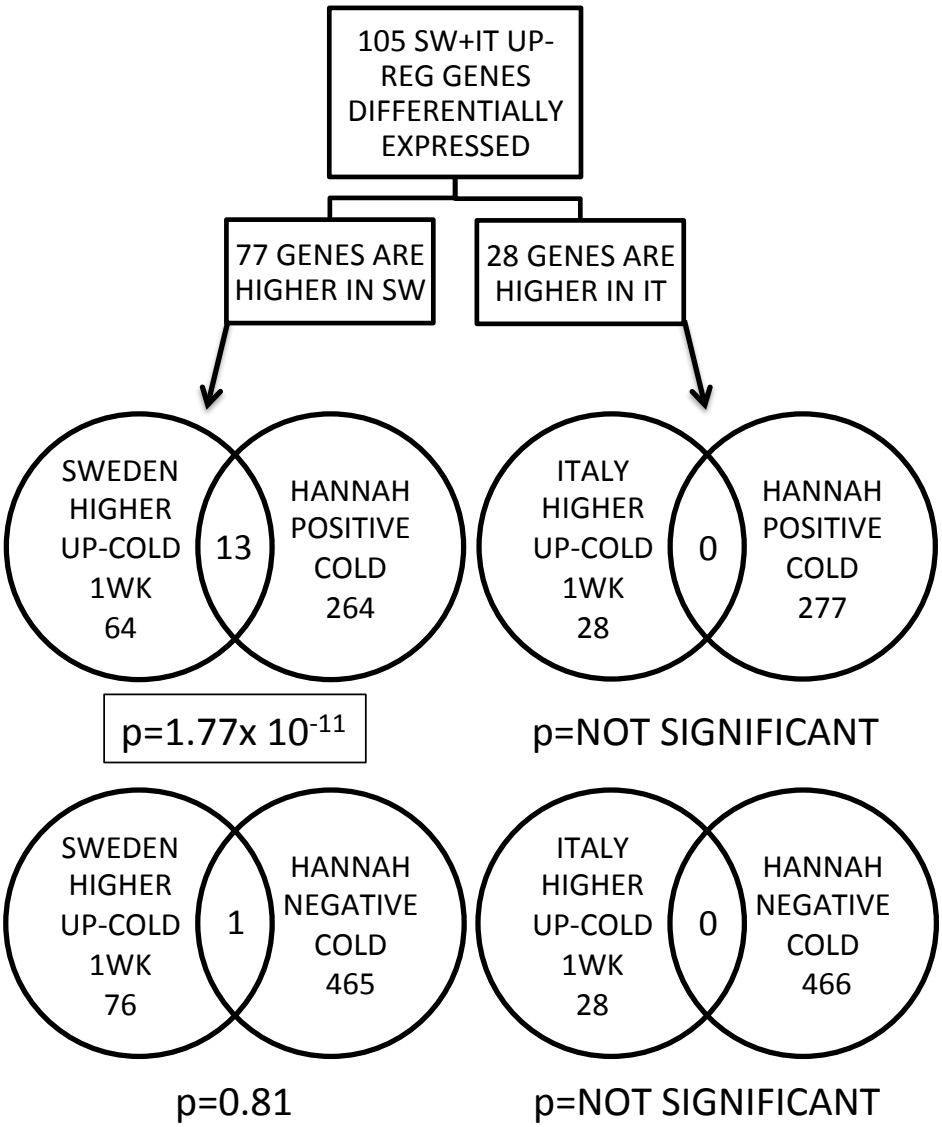


**Figure 3.16.** 105 genes commonly up-regulated by cold but significantly different in expression level and their overlap with the Hannah genes set. Plants were grown at 22$^0$C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled directly or transferred to 4$^0$C for 1 week under a 12 h photoperiod then sampled. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Genes were considered differentially expressed from non-acclimated conditions if the FDR corrected p-value was ≤0.05. Genes were considered differentially expressed between SW and IT if the FDR corrected p-value was ≤0.05. ≥3FPKM was used as the cut-off for differential expression (19, 20). P-values (calculated using a hypergeometric distribution in R) represent overlap between differentially expressed genes and Hannah genes (277 genes positively correlated with freezing tolerance and 466 genes negatively correlated with freezing tolerance; (6)).

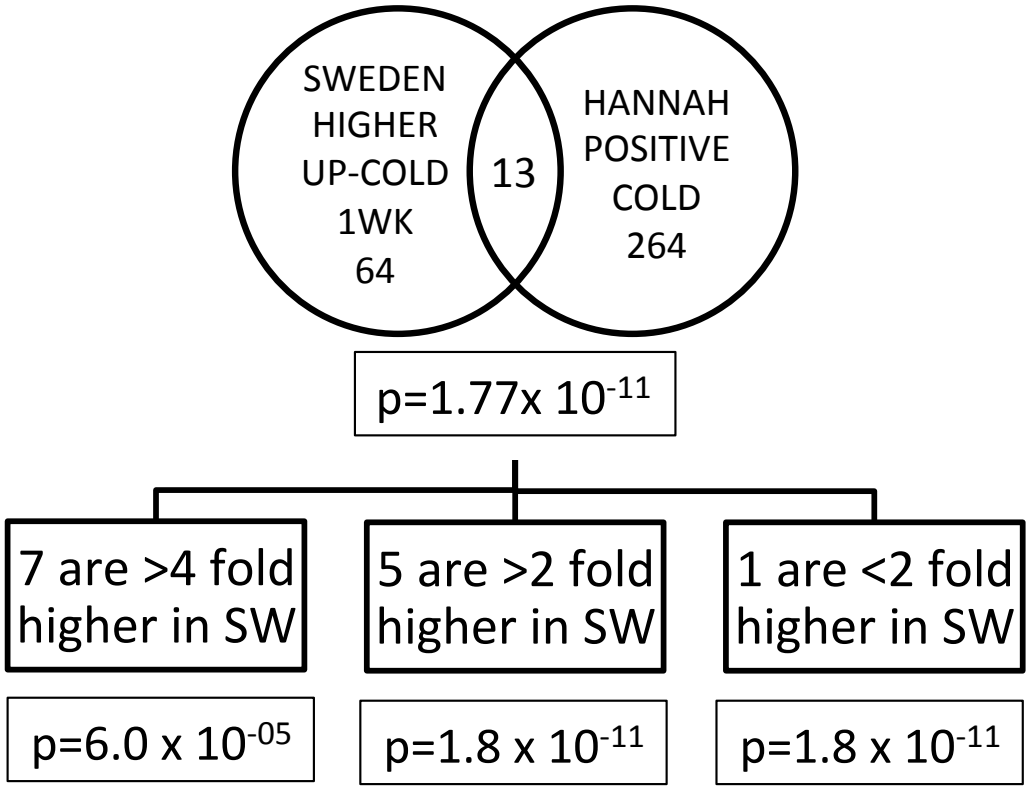


**Figure 3.17.** Fold change of 13 Hannah genes that overlap with 77 genes with up-regulated induction pattern, but higher expression level in SW. P-values represent the significance of overlap between gene only up-regulated in SW and Hannah genes if 4-fold, 2-fold, or no fold change cut-offs were applied (from left to right).

**Table 3.8.** GO categories significantly enriched in 77 genes with up-regulated induction pattern and higher expression level in SW at 1 week of cold-acclimation. GO enrichment was determined using DAVID (**david**.abcc.ncifcrf.gov; (27)). 'GO TERM CATEGORY' denotes if the GO term was categorized as a biological process (BP), cellular component (CC), or molecular function (MF) in the DAVID database. '# HITS' denotes the number of genes with that GO category in 77 genes with up-regulated induction pattern and higher expression level in SW at 1 week of cold-acclimation. '# GENES IN GO' denotes the total number of genes in that GO category included in the DAVID database. GO category was considered significantly enriched if the FDR corrected hypergeometric p-value was ≤0.050.

| GO TERM CATEGORY | SW HIGHER UP-COLD (77 GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| BP | Response To Temperature Stimulus | 11 | 354 | 1.92E-04 |
| BP | Response To Cold | 9 | 233 | 3.22E-04 |
| BP | Response To Abiotic Stimulus | 17 | 1197 | 3.93E-04 |
| BP | Response To Water | 8 | 185 | 5.03E-04 |
| BP | Response To Abscisic Acid Stimulus | 9 | 285 | 5.66E-04 |
| BP | Response To Water Deprivation | 7 | 176 | 2.17E-03 |
| BP | Oxidation Reduction | 14 | 1186 | 1.46E-02 |
| BP | Secondary Metabolic Process | 8 | 423 | 3.21E-02 |
| BP | Aromatic Compound Biosynthetic Process | 6 | 215 | 3.50E-02 |
| BP | Heat Acclimation | 3 | 16 | 3.81E-02 |
| BP | Response To Desiccation | 3 | 18 | 4.38E-02 |
| BP | Cold Acclimation | 3 | 20 | 4.95E-02 |

**Table 3.9.** GO categories significantly enriched in 28 genes with up-regulated induction pattern and higher expression level in IT at 1 week of cold-acclimation. GO enrichment was determined using DAVID (**david**.abcc.ncifcrf.gov; (27)). 'GO TERM CATEGORY' denotes if the GO term was categorized as a biological process (BP), cellular component (CC), or molecular function (MF) in the DAVID database. '# HITS' denotes the number of genes with that GO category in 28 genes with up-regulated induction pattern and higher expression level in IT at 1 week of cold-acclimation. '# GENES IN GO' denotes the total number of genes in that GO category included in the DAVID database. GO category was considered significantly enriched if the FDR corrected hypergeometric p-value was ≤0.050.

| GO TERM CATEGORY | IT HIGHER UP-COLD (28 GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| BP | Ribonucleoprotein Complex Biogenesis | 5 | 249 | 1.02E-02 |

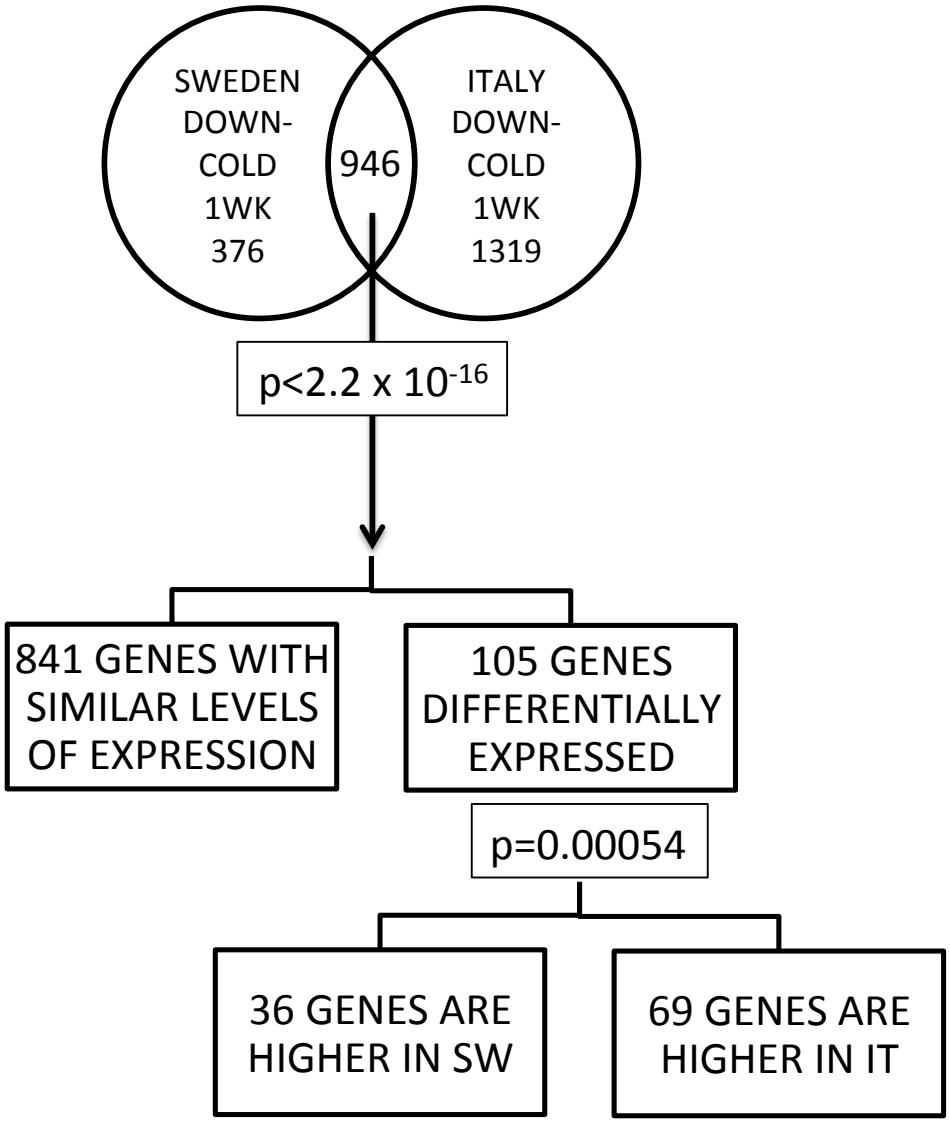


**Figure 3.18.** 105 genes commonly down-regulated by cold but significantly different in expression level. 36 genes more repressed in IT (higher in expression in SW) and 69 genes more repressed in SW (higher expression in IT). Plants were grown at 22$^0$C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled directly or transferred to 4$^0$C for 1 week under a 12 h photoperiod then sampled. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Genes were considered differentially expressed from non-acclimated conditions if the FDR corrected p-value was ≤0.05. Genes were considered differentially expressed between SW and IT if the FDR corrected p-value was ≤0.05. ≥3FPKM was used as the cut-off for differential expression (19, 20). P-values represent overlap between SW and IT cold-responsive genes (calculated using a hypergeometric distribution in R).

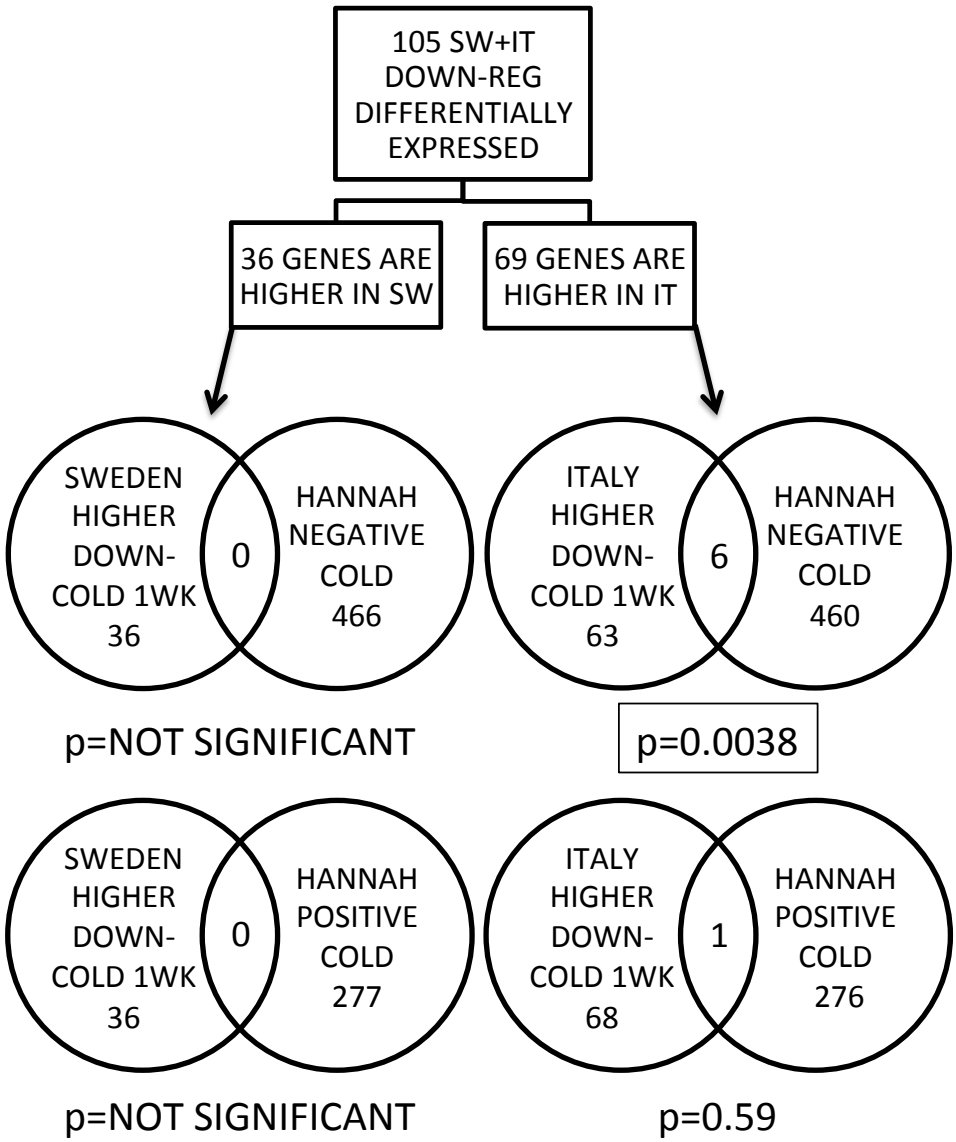


**Figure 3.19.** 105 genes commonly down-regulated by cold but significantly different in expression level and their overlap with the Hannah genes set. Plants were grown at 22$^0$C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled directly or transferred to 4$^0$C for 1 week under a 12 h photoperiod then sampled. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Genes were considered differentially expressed from non-acclimated conditions if the FDR corrected p-value was ≤0.05. Genes were considered differentially expressed between SW and IT if the FDR corrected p-value was ≤0.05. ≥3FPKM was used as the cut-off for differential expression (19, 20). P-values (calculated using a hypergeometric distribution in R) represent overlap between differentially expressed genes and Hannah genes (277 genes positively correlated with freezing tolerance and 466 genes negatively correlated with freezing tolerance; (6)).

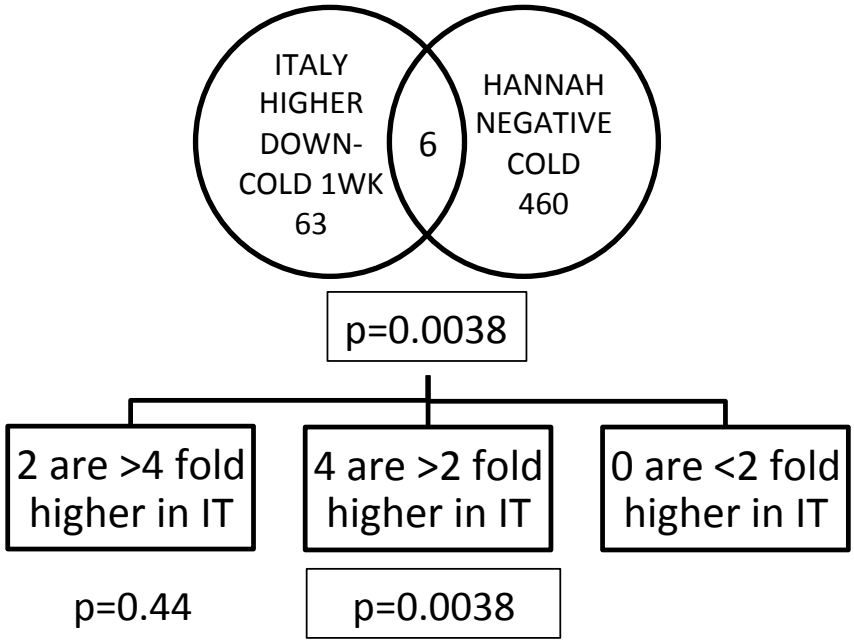


**Figure 3.20.** Fold change of 6 Hannah genes that overlap with 69 genes with down-regulated induction pattern, but higher expression level in IT. P-values represent the significance of overlap between gene only up-regulated in SW and Hannah genes if 4-fold, 2-fold, or no fold change cut-offs were applied (from left to right).

**Table 3.10.** GO categories significantly enriched in 69 genes with down-regulated induction pattern and higher expression level in IT at 1 week of cold-acclimation. GO enrichment was determined using DAVID (**david**.abcc.ncifcrf.gov; (27)). 'GO TERM CATEGORY' denotes if the GO term was categorized as a biological process (BP), cellular component (CC), or molecular function (MF) in the DAVID database. '# HITS' denotes the number of genes with that GO category in 69 genes with down-regulated induction pattern and higher expression level in IT at 1 week of cold-acclimation. '# GENES IN GO' denotes the total number of genes in that GO category included in the DAVID database. GO category was considered significantly enriched if the FDR corrected hypergeometric p-value was ≤0.050.

| GO TERM CATEGORY | IT HIGHER UP-COLD (69 GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| BP | Response To Organic Substance | 19 | 1176 | 1.81E-06 |
| BP | Response To Endogenous Stimulus | 13 | 975 | 5.03E-03 |
| BP | Response To Hormone Stimulus | 12 | 909 | 8.78E-03 |

***SW and IT transcriptomes at 1 week of cold-acclimation: Analysis of genes that respond similarly to cold in SW and IT.*** Analysis of cold-responsive genes, which are differentially regulated between SW and IT, suggests that SW and IT may differ in their transcriptional mechanisms of cold-acclimation. However, there are a significant number of genes that are regulated similarly between SW and IT. There are 629 genes up-regulated by cold in both SW and IT with similar expression level. However, these genes may not be associated with increasing freezing tolerance. Therefore it was subsequently determined if genes commonly up-regulated by cold are enriched in genes previously associated with cold-acclimation. Hannah genes have been positively and negatively correlated with increases in freezing tolerance associated with cold-acclimation (6). The 629 genes commonly up-regulated by cold in SW and IT are not significantly enriched in Hannah genes positively or negatively correlated with increases in freezing tolerance (Fig. 3.21). However, these 629 up-regulated genes are enriched (15 genes; p=0.0045) in genes up-regulated by the CBFs. Abiotic stress GO terms, such as 'response to cold', 'response to temperature stimulus', 'cold-acclimation', 'response to salt stress' and 'response to osmotic stress' are significantly enriched in these 629 genes (Table 3.11). Similar GO terms are also enriched in the 277 Hannah genes positively correlated with increases in freezing tolerance (Table A3.2).

The 841 genes commonly down-regulated by cold with similar expression levels in SW and IT are not significantly enriched in Hannah genes (Fig. 3.22) or in CBF regulon genes (11 genes; p=0.33). Noteworthy overrepresented GO terms for these 841 genes include biotic stress related categories such as 'immune response', 'defense

response to bacterium' and 'apoptosis' (Table 3.12). Photosynthesis and light related GO categories are also enriched (Table 3.12). Defense response and photosynthesis related GO terms are also overrepresented in the 466 Hannah genes negatively correlated with increases in freezing tolerance (Table A3.2).

In summary, 1725 out of 2354 genes up-regulated by 1 week of cold are exclusively expressed in either SW or IT (Fig. 3.9) or have significantly different levels of expression between SW and IT (Fig. 3.15). 1800 out of 2641 genes down-regulated by 1 week of cold are exclusively expressed in either SW or IT (Fig 3.9) or have significantly different levels of expression between SW and IT (Fig 3.18). Therefore, the majority of cold-responsive genes are not regulated similarly between SW and IT. Although all of these differentially regulated genes may not play a role in cold-acclimation, comparisons of differentially-regulated genes to the Hannah gene set (6) and to the CBF regulon (25) suggests enrichment of genes correlated with cold-acclimation. There are a significant number of genes regulated similarly by cold in SW and IT. Though genes commonly up-regulated by cold are enriched in CBF regulon genes, common cold-regulated genes between SW and IT are not as enriched in genes previously associated with cold-acclimation in comparison to differentially regulated genes (Fig 3.10, 3.12, 3.16, 3.19, 3.21, 3.22). Overall, analysis of RNA-seq data suggests that SW and IT reach similar levels of freezing tolerance at 1 week of cold-acclimation (Fig. 3.2) through different transcriptional changes. Furthermore, IT appears to be consistently less enriched in Hannah genes and CBF regulated genes than SW, suggesting that IT possibly reaches a similar level of freezing tolerance

through CBF-independent pathways, which are much less well described. These differences in cold-response will be taken into account while defining sets of candidate genes that may contribute to differences in freezing tolerance (FTD genes) in the next section of this study.

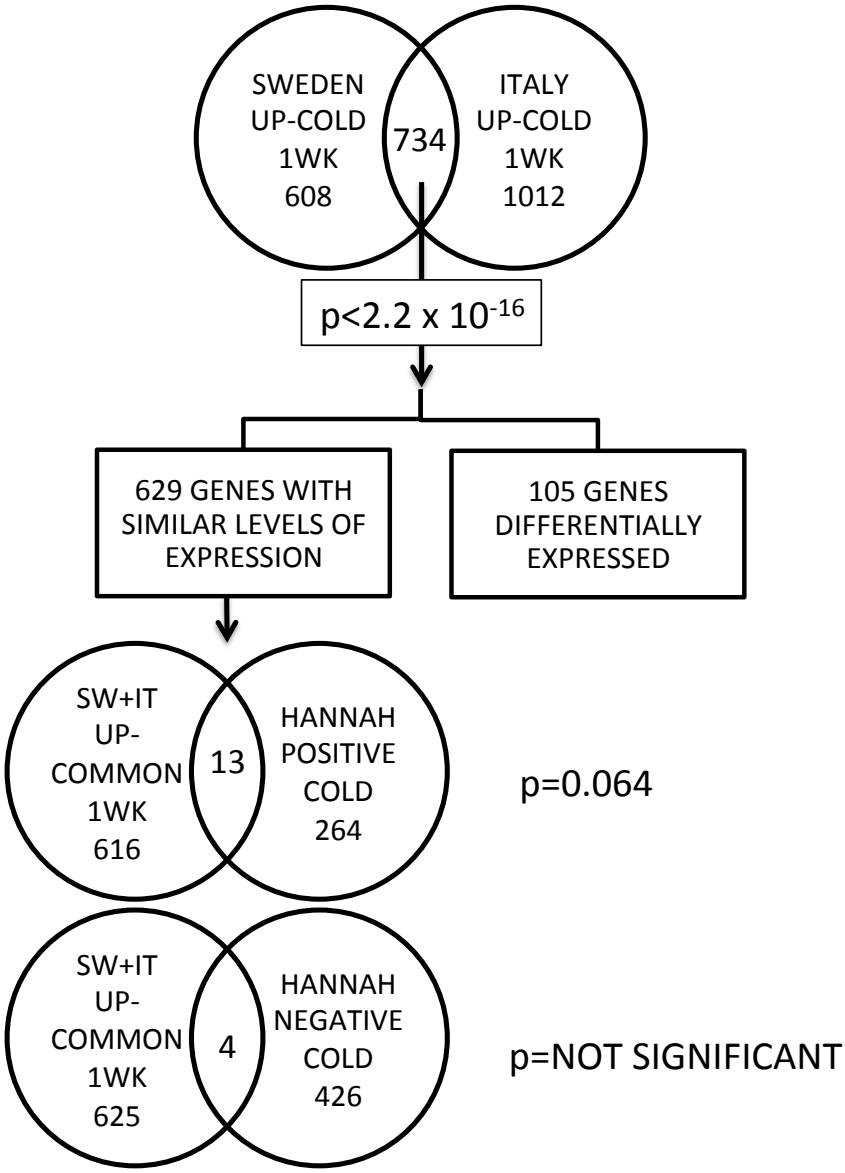


**Figure 3.21.** 629 genes with up-regulated induction patterns and similar expression levels and their overlap with the Hannah genes set. Plants were grown at 22$^0$C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled directly or transferred to 4$^0$C for 1 week under a 12 h photoperiod then sampled. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Genes were considered differentially expressed from non-acclimated conditions if the FDR corrected p-value was ≤0.05. Genes were not differentially expressed between SW and IT if the FDR corrected p-value was ≥0.05. ≥3FPKM was used as the cut-off for differential expression (19, 20). P-values (calculated using a hypergeometric distribution in R) represent overlap between differentially expressed genes and Hannah genes (277 genes positively correlated with freezing tolerance and 466 genes negatively correlated with freezing tolerance; (6)).

**Table 3.11** GO categories significantly enriched in 629 genes with up-regulated induction patterns and similar expression levels in SW and IT. GO enrichment was determined using DAVID (**david**.abcc.ncifcrf.gov; (27)). 'GO TERM CATEGORY' denotes if the GO term was categorized as a biological process (BP), cellular component (CC), or molecular function (MF) in the DAVID database. '# HITS' denotes the number of genes with that GO category in 629 genes with up-regulated induction patterns and similar expression levels in SW and IT. '# GENES IN GO' denotes the total number of genes in that GO category included in the DAVID database. GO category was considered significantly enriched if the FDR corrected hypergeometric p-value was ≤0.050.

| GO TERM CATEGORY | SW+IT COMMON UP-COLD (629 GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| CC | Cytosolic Ribosome | 62 | 317 | 2.73E-31 |
| CC | Ribosome | 73 | 470 | 9.99E-31 |
| MF | Structural Constituent Of Ribosome | 65 | 394 | 9.01E-29 |
| CC | Ribonucleoprotein Complex | 81 | 671 | 7.15E-27 |
| MF | Structural Molecule Activity | 71 | 538 | 7.25E-26 |
| CC | Non-Membrane-Bounded Organelle | 103 | 1144 | 1.55E-24 |
| CC | Cytosol | 75 | 708 | 1.99E-21 |
| CC | Membrane-Enclosed Lumen | 63 | 667 | 1.78E-15 |
| CC | Nucleolus | 44 | 332 | 1.89E-15 |
| CC | Nuclear Lumen | 51 | 472 | 1.92E-14 |
| CC | Organelle Lumen | 60 | 659 | 8.27E-14 |
| BP | Ribosome Biogenesis | 31 | 242 | 2.45E-09 |
| BP | Circadian Rhythm | 12 | 39 | 1.11E-06 |
| BP | Translation | 69 | 1231 | 1.77E-06 |
| BP | Response To Abiotic Stimulus | 65 | 1197 | 1.17E-05 |
| BP | Response To Osmotic Stress | 31 | 399 | 3.87E-05 |
| BP | Response To Temperature Stimulus | 29 | 354 | 3.89E-05 |
| BP | Response To Cold | 23 | 233 | 4.19E-05 |
| CC | Plastid | 128 | 3259 | 1.05E-03 |
| CC | External Encapsulating Structure | 36 | 620 | 1.27E-03 |
| CC | Chloroplast | 125 | 3192 | 1.37E-03 |
| BP | Response To Salt Stress | 26 | 369 | 1.96E-03 |
| CC | Plant-Type Cell Wall | 20 | 270 | 3.06E-03 |
| BP | Response To Cadmium Ion | 23 | 327 | 6.06E-03 |
| CC | Plasma Membrane | 89 | 2228 | 8.74E-03 |
| BP | Cold Acclimation | 6 | 20 | 1.03E-02 |
| CC | Mitochondrion | 58 | 1349 | 1.69E-02 |
| BP | Response To Metal Ion | 24 | 384 | 1.96E-02 |
| BP | Response To Inorganic Substance | 30 | 540 | 2.02E-02 |
| BP | Protein Folding | 18 | 251 | 2.57E-02 |

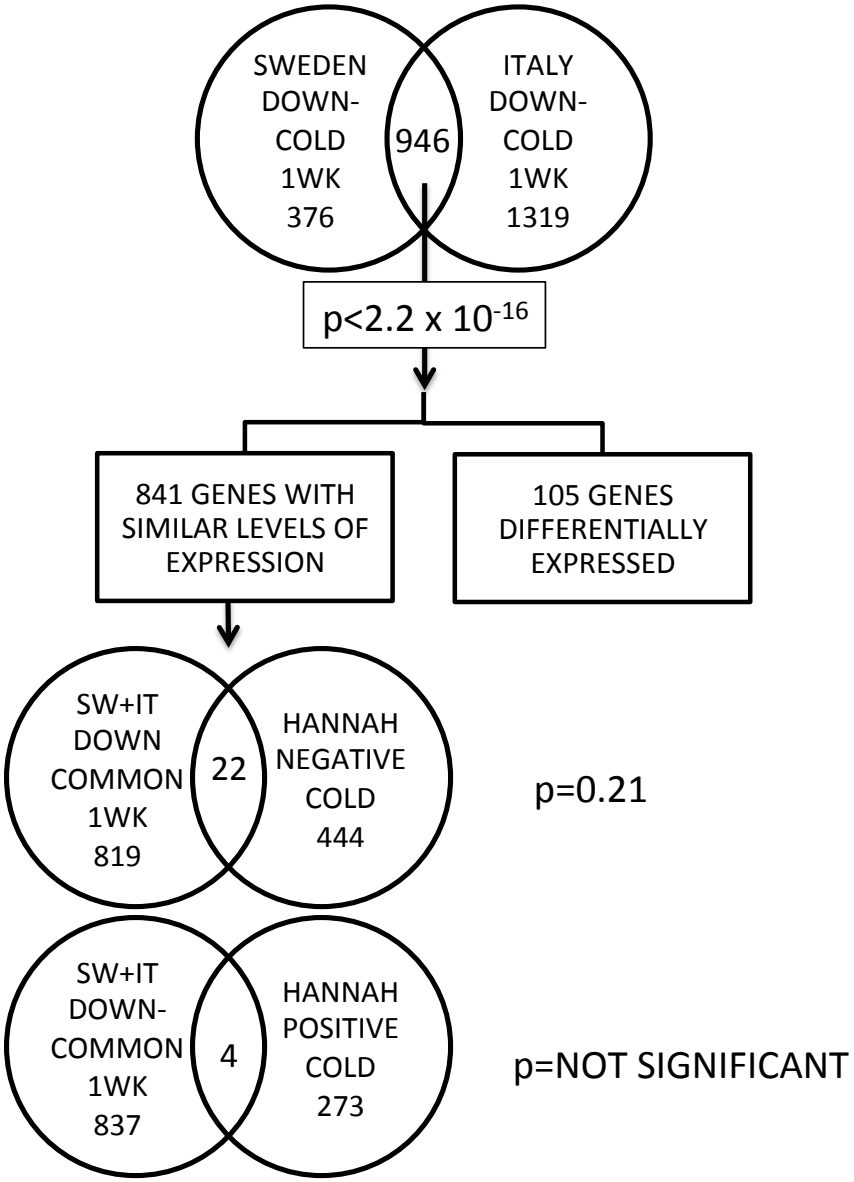


**Figure 3.22.** 841 genes with down-regulated induction patterns and similar expression levels and their overlap with the Hannah genes set. Plants were grown at 22$^0$C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled directly or transferred to 4$^0$C for 1 week under a 12 h photoperiod then sampled. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Genes were considered differentially expressed from non-acclimated conditions if the FDR corrected p-value was ≤0.05. Genes were not differentially expressed between SW and IT if the FDR corrected p-value was ≥0.05. ≥3FPKM was used as the cut-off for differential expression (19, 20). P-values (calculated using a hypergeometric distribution in R) represent overlap between differentially expressed genes and Hannah genes (277 genes positively correlated with freezing tolerance and 466 genes negatively correlated with freezing tolerance; (6)).

**Table 3.12.** GO categories significantly enriched in 841 genes with down-regulated induction patterns and similar expression levels in SW and IT. GO enrichment was determined using DAVID (**david**.abcc.ncifcrf.gov; (27)). 'GO TERM CATEGORY' denotes if the GO term was categorized as a biological process (BP), cellular component (CC), or molecular function (MF) in the DAVID database. '# HITS' denotes the number of genes with that GO category in 841 genes with down-regulated induction patterns and similar expression levels in SW and IT. '# GENES IN GO' denotes the total number of genes in that GO category included in the DAVID database. GO category was considered significantly enriched if the FDR corrected hypergeometric p-value was ≤0.050.

| GO TERM CATEGORY | SW+IT COMMON DOWN-COLD 841 GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| BP | Response To Abiotic Stimulus | 75 | 1197 | 5.31E-04 |
| CC | Organelle Subcompartment | 30 | 349 | 5.70E-04 |
| CC | Thylakoid Membrane | 27 | 305 | 6.39E-04 |
| BP | Response To Light Stimulus | 39 | 466 | 6.43E-04 |
| BP | Programmed Cell Death | 25 | 223 | 7.54E-04 |
| BP | Response To Radiation | 39 | 482 | 8.59E-04 |
| BP | Response To Bacterium | 25 | 244 | 1.21E-03 |
| CC | Photosynthetic Membrane | 27 | 330 | 1.37E-03 |
| BP | Cell Death | 27 | 254 | 1.45E-03 |
| CC | Chloroplast | 145 | 3192 | 1.71E-03 |
| BP | Response To Blue Light | 11 | 55 | 2.34E-03 |
| BP | Response To Far Red Light | 10 | 44 | 2.52E-03 |
| BP | Protein Amino Acid Phosphorylation | 65 | 1065 | 2.68E-03 |
| BP | Immune Response | 27 | 293 | 2.76E-03 |
| CC | Plastid | 146 | 3259 | 2.87E-03 |
| MF | Protein Serine/Threonine Kinase Activity | 58 | 975 | 9.41E-03 |
| BP | Response To Red Light | 10 | 56 | 1.05E-02 |
| MF | Protein Kinase Activity | 66 | 1110 | 1.10E-02 |
| BP | Apoptosis | 18 | 172 | 1.11E-02 |
| BP | Photosynthesis | 18 | 175 | 1.18E-02 |
| MF | Nucleoside Binding | 123 | 2536 | 1.20E-02 |
| MF | Adenyl Ribonucleotide Binding | 115 | 2368 | 1.29E-02 |
| MF | Adenyl Nucleotide Binding | 123 | 2528 | 1.54E-02 |
| BP | Phosphorylation | 66 | 1178 | 1.57E-02 |
| BP | Response To Organic Substance | 66 | 1176 | 1.60E-02 |
| CC | Vacuole | 38 | 643 | 2.02E-02 |
| MF | ATP Binding | 112 | 2340 | 2.38E-02 |
| BP | Phosphate Metabolic Process | 69 | 1273 | 2.68E-02 |
| CC | Cell Wall | 35 | 611 | 4.49E-02 |
| CC | Interchromatin Granule | 3 | 3 | 4.79E-02 |

## GENES CONTRIBUTING TO DIFFERENCES IN FREEZING TOLERANCE

***Summary: Genes contributing to differences in freezing tolerance.*** In the next section of RNA-seq analysis two sets of genes that may possibly contribute to differences in freezing tolerance between SW and IT at 2 weeks of cold-acclimation are defined (Fig. 3.2). Category 1 FREEZING TOLERANCE DIFFERENCE (FTD) candidate genes are cold-regulated genes, which are differentially expressed between SW and IT at only 2 weeks of cold-acclimation, the point at which freezing tolerance differs. Analysis of SW and IT transcriptomes with 1 week of cold- suggests that SW and IT may potentially differ in their transcriptional mechanisms of cold-acclimation. Therefore, Category 2 FTD candidate genes are differentially expressed between SW and IT at both 1 week and 2 weeks of cold-acclimation. Analysis of Category 1 and Category 2 FTD genes suggests that the CBF pathway of cold-acclimation may be differentially regulated between SW and IT.

***Genes contributing to differences in freezing tolerance: Category 1 FREEZING TOLERANCE DIFFERENCE (FTD) candidate genes.*** SW and IT have no difference in freezing tolerance with 1 week of cold-acclimation or under non-acclimated conditions (Fig. 3.1). But after 2 weeks of cold-acclimation there is a significant difference in freezing tolerance between SW and IT (Fig 3.2; $p \leq 0.026$). To determine if genes associated with differences in freezing tolerance possibly underlie fitness QTL, candidate genes contributing to differences in freezing tolerance were first defined. It is possible that differentially expressed cold genes between SW and IT are involved in differences between SW and IT not related to freezing tolerance. However, even if

these differentially expressed genes were not related to freezing tolerance, these genes would still represent differences between SW and IT that could potentially contribute to differences in fitness between SW and IT. Examination of SW and IT transcriptomes at 1 week of cold suggests that SW and IT may differ in their mechanisms of cold-acclimation, since the majority of cold-regulated genes are differentially regulated between SW and IT. Although is possible that genes expressed similarly between SW and IT are responsible for cold-acclimation (Fig. 3.21-3.22), it seems likely that at least a portion of differentially regulated cold genes between SW and IT contribute cold-acclimation in some way since differentially regulated cold genes at 1 week of cold-acclimation are significantly enriched in genes regulated by the CBFs, master regulators of the most well defined pathway of cold-acclimation (21, 24, 29). Consequently, differences in gene expression at 1 week of cold-acclimation may contribute to the differences in freezing tolerance seen later at 2 weeks of cold-acclimation. These genes were defined as Category 2 FTD genes and will be described later. However, genes that are differentially expressed only at 2 weeks of cold-acclimation also seem like good candidates for genes contributing to differences in freezing tolerance. Therefore, Category 1 FTD candidate genes are cold-regulated genes (in either SW or IT) that have no difference in expression level between SW and IT at 1 week of cold-acclimation and non-acclimated conditions, but different levels of expression at 2 weeks of cold-acclimation. Again, differential expression was determined by a FDR corrected p-value ≤0.050 (30) and a ≥3FPKM threshold for either sample in the pairwise comparison (19, 20).

There are 2130 Category 1 FTD candidate genes (Fig. 3.23; Table A3.3 and A3.4). Of these 2130 Category 1 FTD genes, 474 have higher expression in SW at 2 weeks of cold-acclimation (Fig. 3.23, Table A3.3). Again, all these differentially expressed genes may not necessarily contribute to cold-acclimation. Consequently, enrichment of genes that have been previously associated with cold-acclimation was tested. The CBFs are central components of the most well described pathway of cold-acclimation. The 474 Category 1 FTD candidate genes with higher expression in SW are significantly enriched (33 genes; p=3.2E-17; Table A3.3) in genes up-regulated by the CBFs. This suggests that the CBF pathway of cold-acclimation differs between SW and IT, which is similar to what was seen at 1 week of cold-acclimation. These 474 genes are also significantly enriched in Hannah genes positively and negatively correlated with freezing tolerance (Fig 3.23). There are 15 Hannah genes positively correlated with freezing tolerance that overlap with the Category 1 genes with higher expression in SW. This overlap is statistically significant however the majority of these genes have less than 2-fold higher expression in SW compared to IT (Fig 3.24). There are 20 Hannah genes negatively correlated with freezing tolerance that overlap with the Category 1 genes with higher expression in SW. This overlap is again statistically significant but all of these genes are less than 2-fold higher in SW compared to IT (Fig. 3.25). Interesting GO categories overrepresented in these 474 genes include 'response to temperature', 'response to cold' and 'photosynthesis' (Table 3.13).

Out of 2130 Category 1 FTD genes, 1656 Category 1 FTD candidate genes have higher expression in IT at 2 weeks of cold-acclimation (Fig 2.23; Table A.3.4). These

1656 genes are not significantly enriched in Hannah genes positively or negatively correlated with freezing tolerance (Fig. 3.23) and are also not enriched in genes up-regulated (6 genes; p=0.99) or down-regulated (21 genes; p=0.29) by the CBFs. However, this genes set is significantly enriched in a number of notable GO terms, most of which related to defense response and biotic stress (Table 3.14). Temperature-related GO terms are not enriched in these 1656 Category 1 genes, but other abiotic stress categories such as 'response to salt stress' and 'response to osmotic stress' are enriched. Altogether, Category 1 FTD candidate genes with higher expression in SW appear to be more enriched in genes that have been previously associated with cold-acclimation than IT. This difference is consistent with analysis of SW and IT transcriptomes at 1 week of cold-acclimation and again suggests that IT may cold-acclimate using pathways not yet well defined.

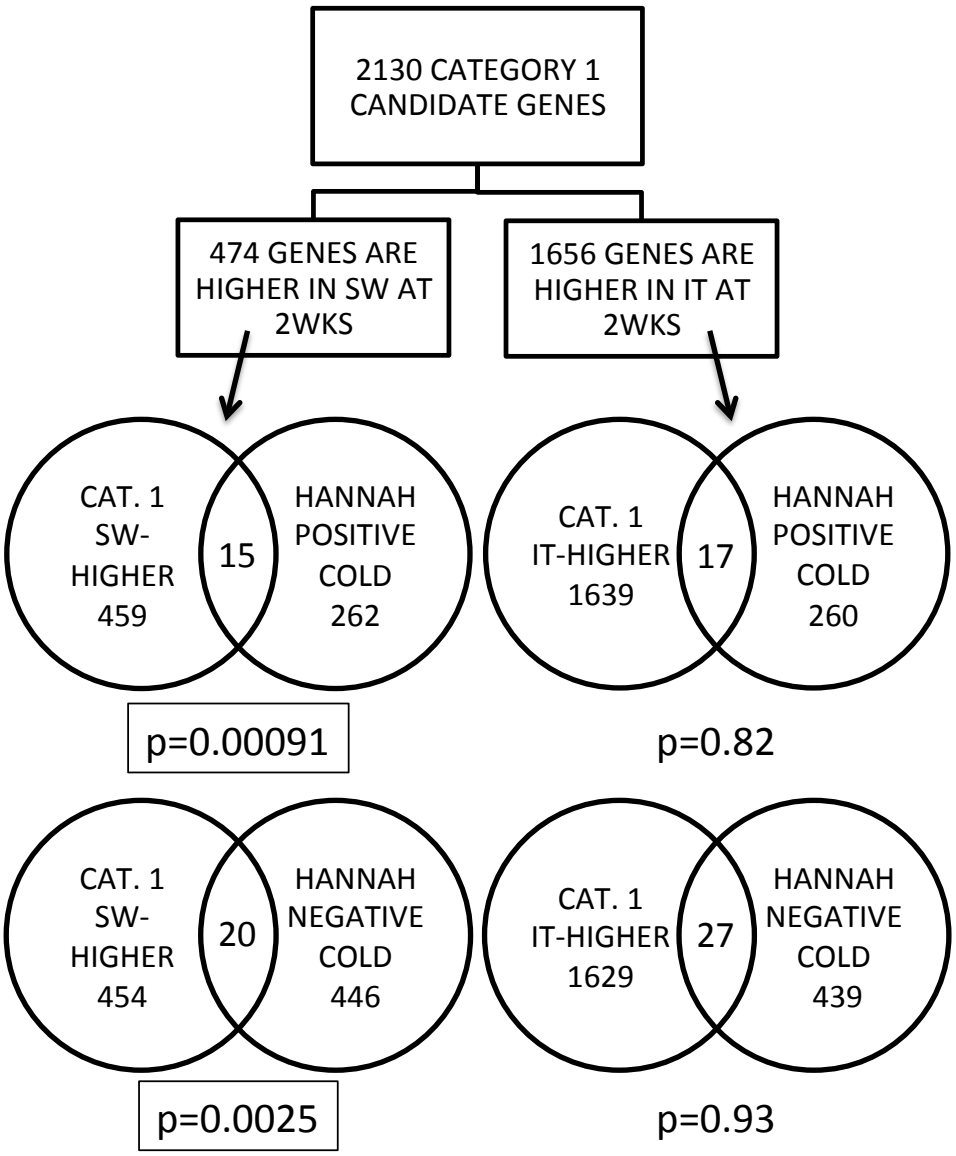


**Figure 3.23.** 2130 Category 1 FTD candidate genes and overlap with the Hannah gene set. Plants were grown at 22$^{0}$C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled directly or transferred to 4$^{0}$C for 1 week under a 12 h photoperiod then sampled. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Genes were considered differentially expressed from non-acclimated conditions if the FDR corrected p-value was ≤0.05. ≥3FPKM was used as the cut-off for differential expression (19, 20). P-values (calculated using a hypergeometric distribution in R) represent overlap between differentially expressed genes and Hannah genes (277 Hannah genes positively correlated with freezing tolerance and 466 Hannah genes negatively correlated with freezing tolerance; (6)).

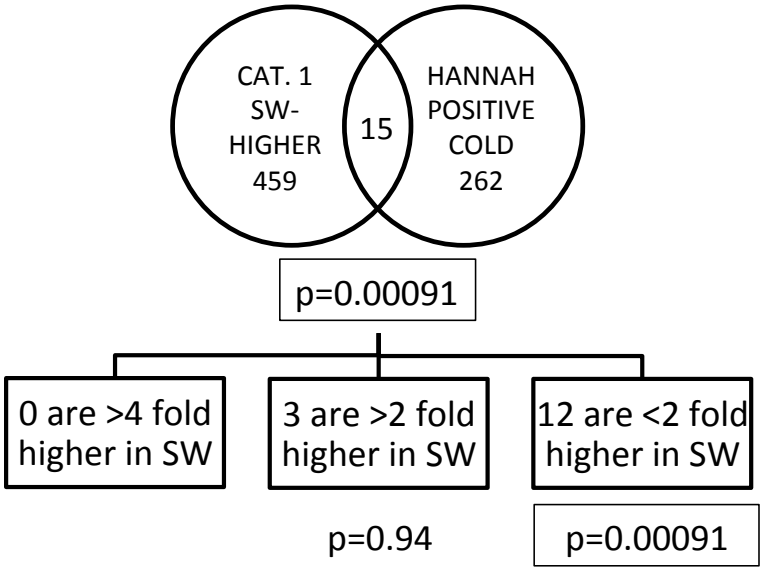


**Figure 3.24.** Fold change of 15 Hannah genes that overlap with 474 Category 1 FTD genes with higher expression in SW. P-values represent the significance of overlap between gene only up-regulated in SW and Hannah genes if 4-fold, 2-fold, or no fold change cut-offs were applied (from left to right).

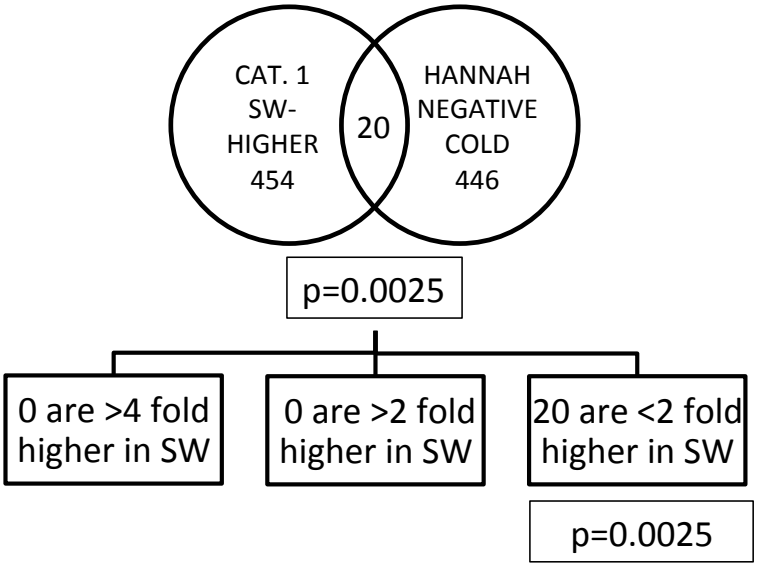


**Figure 3.25.** Fold change of 20 Hannah genes that overlap with 474 Category 1 FTD genes with higher expression in SW. P-values represent the significance of overlap between gene only up-regulated in SW and Hannah genes if 4-fold, 2-fold, or no fold change cut-offs were applied (from left to right).

**Table 3.13.** GO categories significantly enriched in 474 Category 1 genes with higher expression in SW at 2 weeks of cold-acclimation. 'GO enrichment was determined using DAVID (**david**.abcc.ncifcrf.gov; (27)). GO TERM CATEGORY' denotes if the GO term was categorized as a biological process (BP), cellular component (CC), or molecular function (MF) in the DAVID database. '# HITS' denotes the number of genes with that GO category in 474 Category 1 genes with higher expression in SW at 2 weeks of cold-acclimation. '# GENES IN GO' denotes the total number of genes in that GO category included in the DAVID database. GO category was considered significantly enriched if the FDR corrected hypergeometric p-value was ≤0.050.

| GO TERM CATEGORY | SW HIGH CATEGORY 1 (474 GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| CC | Chloroplast | 155 | 3192 | 3.54E-24 |
| CC | Plastid | 156 | 3259 | 5.20E-24 |
| CC | Organelle Subcompartment | 32 | 349 | 6.21E-10 |
| CC | Thylakoid Membrane | 29 | 305 | 2.44E-09 |
| CC | Photosynthetic Membrane | 29 | 330 | 1.24E-08 |
| CC | Organelle Membrane | 45 | 849 | 9.29E-07 |
| BP | Starch Metabolic Process | 10 | 34 | 3.53E-06 |
| BP | Photosynthesis | 19 | 175 | 4.41E-06 |
| CC | Plastid Envelope | 28 | 461 | 3.35E-05 |
| CC | Chloroplast Envelope | 26 | 440 | 1.23E-04 |
| CC | Photosystem | 9 | 72 | 1.43E-03 |
| BP | Response To Abiotic Stimulus | 45 | 1197 | 2.26E-03 |
| BP | Carbohydrate Biosynthetic Process | 15 | 189 | 2.75E-03 |
| BP | Cellular Glucan Metabolic Process | 12 | 124 | 2.89E-03 |
| BP | Response To Temperature Stimulus | 20 | 354 | 3.83E-03 |
| BP | Response To Cold | 16 | 233 | 4.10E-03 |
| BP | Oligosaccharide Metabolic Process | 8 | 51 | 4.22E-03 |
| BP | Starch Catabolic Process | 5 | 13 | 5.73E-03 |
| BP | Carbohydrate Biosynthetic Process | 16 | 254 | 6.92E-03 |
| BP | Cellular Polysaccharide Catabolic Process | 5 | 15 | 8.16E-03 |
| BP | Glucan Metabolic Process | 12 | 151 | 8.73E-03 |
| BP | Cellular Polysaccharide Metabolic Process | 12 | 154 | 8.90E-03 |
| BP | Photosynthesis, Light Reaction | 9 | 85 | 9.97E-03 |
| BP | Starch Biosynthetic Process | 5 | 17 | 1.12E-02 |
| BP | Generation Of Precursor Metabolites And Energy | 19 | 404 | 3.06E-02 |
| CC | Photosystem II | 6 | 52 | 3.53E-02 |
| CC | Plastid Outer Membrane | 5 | 34 | 3.86E-02 |
| CC | Chloroplast Photosystem II | 4 | 18 | 3.94E-02 |
| CC | Oxygen Evolving Complex | 4 | 18 | 3.94E-02 |
| BP | Glycoside Metabolic Process | 8 | 84 | 4.23E-02 |

**Table 3.14.** GO categories significantly enriched in 1656 Category 1 genes with higher expression in IT at 2 weeks of cold-acclimation. GO enrichment was determined using DAVID (**david**.abcc.ncifcrf.gov; (27)). 'GO TERM CATEGORY' denotes if the GO term was categorized as a biological process (BP), cellular component (CC), or molecular function (MF) in the DAVID database. '# HITS' denotes the number of genes with that GO category in 1656 Category 1 genes with higher expression in IT at 2 weeks of cold-acclimation. '# GENES IN GO' denotes the total number of genes in that GO category included in the DAVID database. GO category was considered significantly enriched if the FDR corrected hypergeometric p-value was ≤0.050.

| GO TERM CATEGORY | IT HIGH CATEGORY 1 GENES (1656 GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| CC | Plasma Membrane | 277 | 2228 | 9.35E-25 |
| BP | Response To Chitin | 43 | 127 | 1.38E-14 |
| MF | Nucleoside Binding | 288 | 2536 | 2.55E-13 |
| BP | Response To Carbohydrate Stimulus | 50 | 199 | 6.49E-12 |
| BP | Immune Response | 63 | 293 | 6.57E-12 |
| BP | Protein Amino Acid Phosphorylation | 146 | 1065 | 6.95E-12 |
| BP | Response To Organic Substance | 157 | 1176 | 7.34E-12 |
| MF | Protein Kinase Activity | 150 | 1110 | 2.27E-11 |
| MF | Purine Nucleotide Binding | 300 | 2785 | 2.77E-11 |
| MF | Adenyl Ribonucleotide Binding | 262 | 2368 | 6.58E-11 |
| BP | Innate Immune Response | 58 | 275 | 6.76E-11 |
| BP | Response To Wounding | 40 | 147 | 1.11E-10 |
| CC | Endoplasmic Reticulum | 74 | 446 | 1.12E-10 |
| MF | ATP Binding | 257 | 2340 | 2.42E-10 |
| BP | Phosphate Metabolic Process | 159 | 1273 | 6.15E-10 |
| BP | Response To Bacterium | 52 | 244 | 6.63E-10 |
| CC | Intrinsic To Membrane | 262 | 2658 | 9.77E-10 |
| BP | Phosphorylation | 148 | 1178 | 2.08E-09 |
| BP | Cell Death | 52 | 254 | 2.15E-09 |
| BP | Defense Response To Bacterium | 42 | 184 | 6.69E-09 |
| BP | Ribonucleotide Binding | 274 | 2621 | 8.30E-09 |
| BP | Nucleotide Binding | 332 | 3333 | 1.08E-08 |
| BP | Programmed Cell Death | 45 | 223 | 8.10E-08 |
| BP | Defense Response | 127 | 1030 | 1.94E-07 |
| BP | Callose Deposition During Defense Response | 12 | 18 | 4.77E-07 |
| BP | Plant-Type Hypersensitive Response | 17 | 45 | 3.31E-06 |
| BP | Polysaccharide Localization | 12 | 21 | 3.45E-06 |
| CC | External Encapsulating Structure | 78 | 620 | 6.92E-06 |
| CC | Integral To Membrane | 207 | 2193 | 7.12E-06 |
| CC | Cell Wall | 76 | 611 | 1.06E-05 |
| BP | Amino Acid Derivative Metabolic Process | 44 | 280 | 1.14E-04 |

**Table 3.14 (cont'd)**

| | | | | |
|---|---|---|---|---|
| CC | Endoplasmic Reticulum Part | 20 | 92 | 2.89E-04 |
| CC | Vacuole | 72 | 643 | 6.41E-04 |
| BP | Phospholipid Transport | 8 | 14 | 1.16E-03 |
| BP | Indole Derivative Metabolic Process | 13 | 42 | 1.42E-03 |
| BP | Aromatic Compound Biosynthetic Process | 34 | 215 | 1.50E-03 |
| BP | Response To Inorganic Substance | 66 | 540 | 1.52E-03 |
| BP | Secondary Metabolic Process | 55 | 423 | 1.52E-03 |
| BP | Apoptosis | 29 | 172 | 1.88E-03 |
| MF | Calcium Ion Binding | 54 | 405 | 1.95E-03 |
| BP | Response To Abiotic Stimulus | 123 | 1197 | 2.22E-03 |
| BP | Response To Endogenous Stimulus | 104 | 975 | 2.24E-03 |
| BP | Defense Response To Fungus | 10 | 26 | 2.28E-03 |
| BP | Cell Wall Modification | 24 | 135 | 3.87E-03 |
| BP | Response To Jasmonic Acid Stimulus | 26 | 156 | 5.30E-03 |
| MF | Phospholipid-Translocating ATPase Activity | 7 | 12 | 6.64E-03 |
| MF | Aminophospholipid Transporter Activity | 7 | 12 | 6.64E-03 |
| BP | Response To Salt Stress | 47 | 369 | 7.50E-03 |
| BP | Indole Derivative Biosynthetic Process | 11 | 37 | 7.62E-03 |
| BP | Sulfur Metabolic Process | 27 | 171 | 8.46E-03 |
| BP | Response To Endoplasmic Reticulum Stress | 7 | 14 | 8.55E-03 |
| MF | FAD Binding | 27 | 164 | 9.39E-03 |
| BP | Response To Osmotic Stress | 49 | 399 | 1.16E-02 |
| BP | Response To Oxidative Stress | 38 | 287 | 1.41E-02 |
| BP | Positive Regulation Of Response To Stimulus | 13 | 55 | 1.45E-02 |
| BP | Regulation Of Innate Immune Response | 10 | 35 | 2.02E-02 |
| BP | Response To Light Stimulus | 54 | 466 | 2.06E-02 |
| BP | Salicylic Acid Mediated Signaling Pathway | 9 | 29 | 2.27E-02 |
| MF | Calmodulin Binding | 27 | 175 | 2.46E-02 |
| BP | S-Glycoside Metabolic Process | 11 | 44 | 2.71E-02 |
| BP | Glucosinolate Metabolic Process | 11 | 44 | 2.71E-02 |
| BP | Positive Regulation Of Defense Response | 9 | 31 | 3.50E-02 |
| MF | Protein Tyrosine Kinase Activity | 40 | 312 | 3.85E-02 |
| BP | Response To Radiation | 54 | 482 | 4.00E-02 |
| BP | Response To Ozone | 8 | 25 | 4.01E-02 |
| MF | Acid-Amino Acid Ligase Activity | 38 | 294 | 4.27E-02 |
| BP | Amino Acid Derivative Biosynthetic Process | 27 | 194 | 4.35E-02 |
| MF | Ligase Activity | 43 | 349 | 4.62E-02 |
| MF | Cofactor Binding | 59 | 525 | 4.63E-02 |
| BP | Intracellular Signaling Cascade | 80 | 790 | 4.81E-02 |
| BP | Response To Hormone Stimulus | 90 | 909 | 4.87E-02 |

***Genes contributing to differences in freezing tolerance: Category 2 FTD candidate genes.*** Though there is no difference in freezing tolerance between SW and IT with 1 week of cold-acclimation, analysis of SW and IT transcriptomes suggests that they reach this similar level of freezing tolerance by different mechanisms (Fig 3.9). It is possible that transcriptional differences at 1 week of cold-acclimation do not result in differences in freezing tolerance until 2 weeks of cold-acclimation. It is also possible that differences in cold-regulated gene expression at 1 week and 2 weeks of cold-acclimation couple to result in differences in freezing tolerance at 2 weeks of cold-acclimation. Based on this, Category 2 FTD candidate genes are cold-induced genes (in either SW or IT) with significantly different levels of expression at both 1 and 2 weeks of cold-acclimation.

There are 798 Category 2 FTD candidate genes (Fig 3.26). Out of 798 Category 2 genes, 294 have higher expression in SW compared to IT at 2 weeks of cold-acclimation (Fig 3.26; Table A3.5). It was also determined if these genes have been previously associated with cold-acclimation. These 294 genes are significantly enriched (39 genes; $p<2.2E-16$) in genes up-regulated the CBFs (Table A3.5). These 294 genes are also significantly enriched in Hannah genes positively correlated with freezing tolerance (Fig 3.26). There are 32 Hannah genes positively correlated with freezing tolerance that overlap with the Category 2 genes with higher expression in SW. This overlap is statistically significant, and 8 genes have greater than 4-fold higher expression in SW compared to IT, 15 are greater than 2-fold higher and 9 are less than 2-fold higher (Fig 3.27). 'Response to cold' is the GO category most overrepresented in

these 294 genes, and other abiotic stress GO terms such as 'response to water deprivation' are also enriched (Table 3.15).

There are 504 out of 798 Category 2 FTD candidate genes with higher expression in IT compared to SW at 2 weeks of cold-acclimation (Fig. 3.26; Table A3.6). The 504 genes with higher expression in IT are not enriched in genes up-regulated (2 genes; p=0.97) or down-regulated (3 genes; p=0.92) by the CBFs (Table A3.6). However, these 504 genes are significantly enriched in Hannah genes both positively and negatively correlated with increases in freezing tolerance. There are 12 Hannah genes positively correlated with freezing tolerance that overlap with the Category 2 genes with higher expression in IT than SW. This overlap is statistically significant, but less significant than the overlap between Category 2 genes with higher expression in SW and Hannah genes positively correlated with freezing tolerance (Fig 3.27). Of the 12 genes high in IT that overlap with the Hannah gene set, 2 are greater than 4-fold higher in IT compared to SW, 7 are greater than 2 fold higher, and 3 are less than 2-fold higher (Fig. 3.28). There are 25 Hannah genes negatively correlated with freezing tolerance that overlap with the Category 2 genes with higher expression in IT compared to SW. These 25 genes negatively correlated with freezing tolerance thus, have lower expression in SW. Of these 25 genes, 4 have greater than 4-fold higher expression in IT, 10 are greater than 2-fold higher, and 11 are less than 2-fold higher (Fig 3.29). The 504 Category 2 FTD candidate genes are not enriched in temperature-related GO terms. But 'defense response' and 'biotic interaction' related GO terms are highly enriched (Table 3.16).

In Summary, Category 2 FTD candidate genes with higher expression in SW are more enriched in genes that have been previously associated with cold-acclimation than IT. This is consistent with analysis of Category 1 FTD genes and cold-regulated transcriptomes at 1 week of cold-acclimation. This again suggests that IT may cold-acclimate using pathways not yet well defined. Since IT decreases in freezing tolerance from 1 to 2 weeks of cold-acclimation it also suggests that IT pathways of cold-acclimation are not as efficient as pathways in SW.

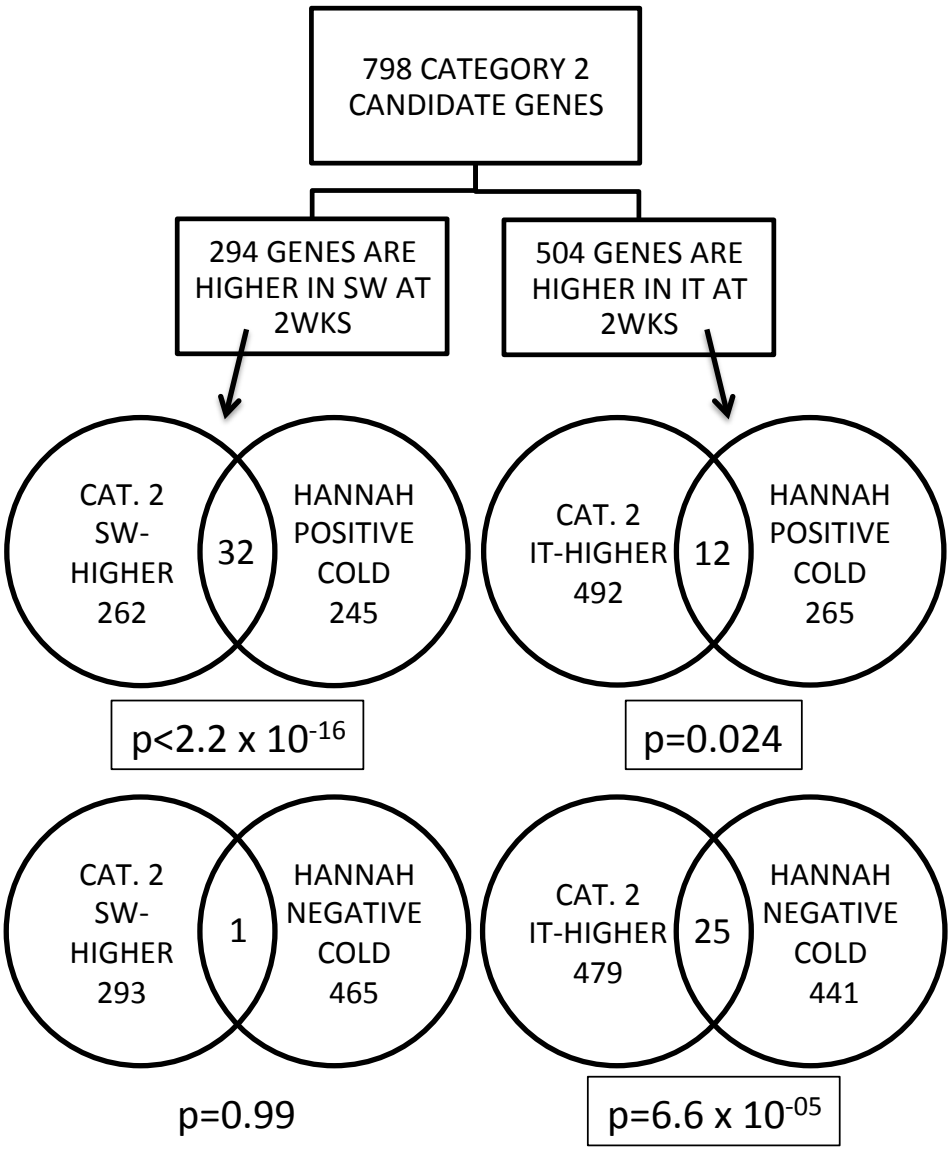


**Figure 3.26.** 798 Category 2 FTD candidate genes and their overlap with the Hannah gene set. Plants were grown at 22$^0$C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled directly or transferred to 4$^0$C for 1 week under a 12 h photoperiod then sampled. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Genes were considered differentially expressed from non-acclimated conditions if the FDR corrected p-value was ≤0.05. ≥3FPKM was used as the cut-off for differential expression (19, 20). Genes were considered differentially expressed between SW and IT if the FDR corrected p-value was ≤0.05. P-values (calculated using a hypergeometric distribution in R) represent overlap between differentially expressed genes and Hannah genes (277 genes positively correlated with freezing tolerance and 466 genes negatively correlated with freezing tolerance; (6)).

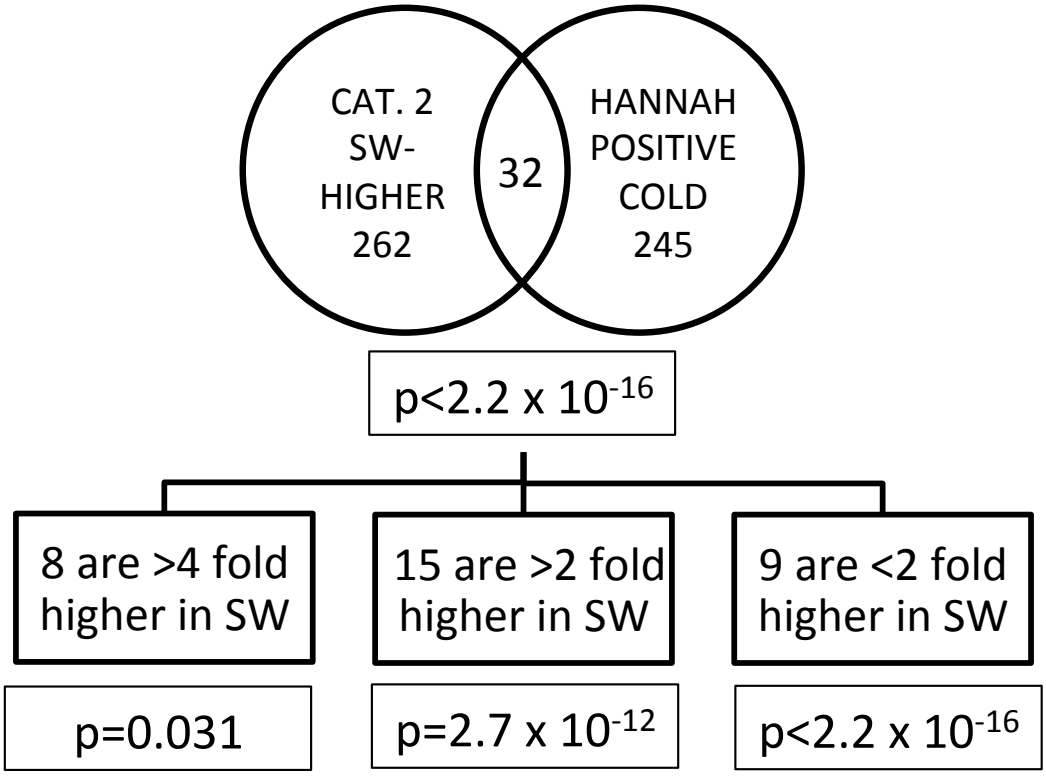


**Figure 3.27.** Fold change of 32 Hannah genes that overlap with 294 Category 2 FTD genes with higher expression in SW. P-values represent the significance of overlap between gene only up-regulated in SW and Hannah genes if 4-fold, 2-fold, or no fold change cut-off were applied (from left to right).

**Table 3.15.** GO categories significantly enriched in 294 Category 2 genes with higher expression in SW at 2 weeks of cold-acclimation. GO enrichment was determined using DAVID (**david**.abcc.ncifcrf.gov; (27)). 'GO TERM CATEGORY' denotes if the GO term was categorized as a biological process (BP), cellular component (CC), or molecular function (MF) in the DAVID database. '# HITS' denotes the number of genes with that GO category in 294 Category 2 genes with higher expression in SW at 2 weeks of cold-acclimation. '# GENES IN GO' denotes the total number of genes in that GO category included in the DAVID database. GO category was considered significantly enriched if the FDR corrected hypergeometric p-value was ≤0.050.

| GO TERM CATEGORY | SW HIGH CATEGORY 2 (294 GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| BP | Response To Cold | 22 | 233 | 1.81E-09 |
| BP | Response To Temperature Stimulus | 25 | 354 | 1.04E-08 |
| BP | Response To Water | 17 | 185 | 4.77E-07 |
| BP | Response To Water Deprivation | 16 | 176 | 1.41E-06 |
| BP | Response To Abiotic Stimulus | 40 | 1197 | 8.06E-06 |
| BP | Cold Acclimation | 6 | 20 | 4.48E-04 |
| BP | Response To Abscisic Acid Stimulus | 13 | 285 | 2.96E-02 |
| BP | Programmed Cell Death | 11 | 223 | 4.33E-02 |
| BP | Response To Organic Substance | 30 | 1176 | 4.46E-02 |

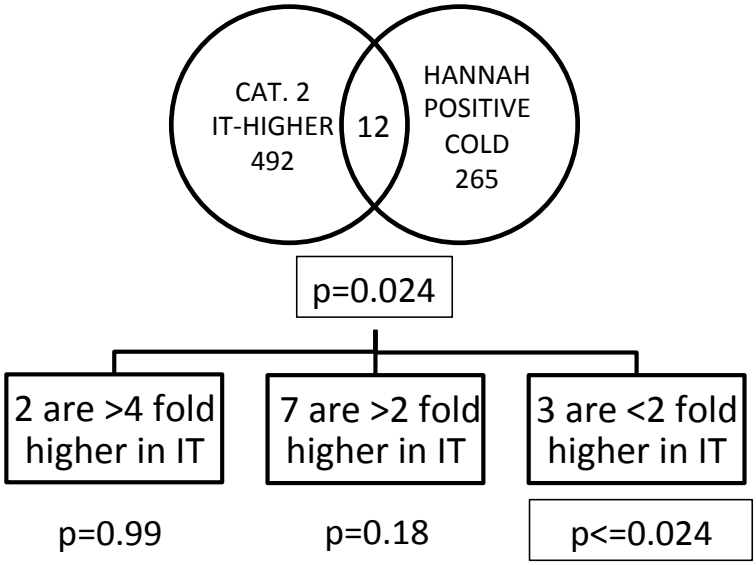


**Figure 3.28.** Fold change of 12 Hannah genes that overlap with 504 Category 2 FTD genes with higher expression in IT. P-values represent the significance of overlap between gene only up-regulated in SW and Hannah genes if 4-fold, 2-fold, or no fold change cut-off were applied (from left to right).

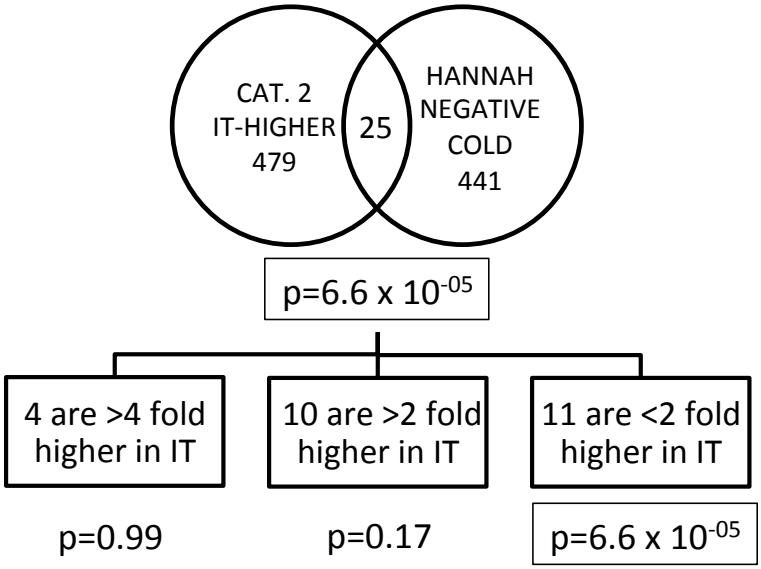


**Figure 3.29.** Fold change of 25 Hannah genes that overlap with 504 Category 2 FTD genes with higher expression in IT. P-values represent the significance of overlap between gene only up-regulated in SW and Hannah genes if 4-fold, 2-fold, or no fold change cut-off were applied (from left to right).

**Table 3.16.** GO categories significantly enriched in 504 Category 2 genes with higher expression in IT at 2 weeks of cold-acclimation. GO enrichment was determined using DAVID (**david**.abcc.ncifcrf.gov; (27)). 'GO TERM CATEGORY' denotes if the GO term was categorized as a biological process (BP), cellular component (CC), or molecular function (MF) in the DAVID database. '# HITS' denotes the number of genes with that GO category in 504 Category 2 genes with higher expression in IT at 2 weeks of cold-acclimation. '# GENES IN GO' denotes the total number of genes in that GO category included in the DAVID database. GO category was considered significantly enriched if the FDR corrected hypergeometric p-value was ≤0.050.

| GO TERM CATEGORY | IT HIGH CATEGORY 2 (504 GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| BP | Innate Immune Response | 26 | 275 | 1.55E-06 |
| BP | Defense Response | 56 | 1030 | 1.74E-06 |
| BP | Response To Bacterium | 21 | 244 | 1.51E-04 |
| BP | Response To Organic Substance | 54 | 1176 | 1.77E-04 |
| BP | Response To Endogenous Stimulus | 44 | 975 | 2.46E-03 |
| BP | Secondary Metabolic Process | 25 | 423 | 3.26E-03 |
| BP | Response To Salicylic Acid Stimulus | 14 | 150 | 3.59E-03 |
| CC | Vacuole | 31 | 643 | 4.25E-03 |
| BP | Response To Hormone Stimulus | 39 | 909 | 1.60E-02 |
| BP | Oxidation Reduction | 47 | 1186 | 1.70E-02 |
| CC | Extracellular Region | 44 | 1225 | 2.13E-02 |
| CC | Apoplast | 20 | 382 | 2.82E-02 |
| BP | Toxin Metabolic Process | 7 | 46 | 3.46E-02 |
| CC | Intrinsic To Plasma Membrane | 9 | 103 | 3.75E-02 |
| BP | Cell Death | 16 | 254 | 3.82E-02 |
| BP | Systemic Acquired Resistance | 6 | 32 | 3.96E-02 |
| CC | External Encapsulating Structure | 26 | 620 | 4.25E-02 |
| BP | Response To Jasmonic Acid Stimulus | 12 | 156 | 4.29E-02 |
| CC | Anchored To Plasma Membrane | 7 | 66 | 4.76E-02 |
| CC | Cell Wall | 25 | 611 | 4.91E-02 |

***Summary of SW and IT transcriptomes.*** Through analysis of basal, as well as 1 and 2 week cold-acclimated transcriptomes two sets of FTD candidate genes have been defined. Furthermore, several interesting trends regarding differences between SW and IT seem to have emerged through this investigation. Analysis of RNA-seq data suggests that SW and IT cold-acclimate through significantly different transcriptional changes. Comparisons of SW and IT cold-regulated transcriptomes to CBF regulon genes (25) and Hannah genes (6), which are enriched in CBF regulon genes, seem to indicate that SW is more enriched in genes that have been previously associated with cold-acclimation. This suggests that SW may use previously defined pathways of cold-acclimation, such as the CBF pathway, while IT may use pathways of cold-acclimation not yet well defined. However, differences between SW and IT were determined without fold-change thresholds. Therefore, the fold-change of expression data was visually examined using heatmaps to ensure that these trends are consistent.

Visual analysis of cold-regulated genes suggests that most genes have similar rather than opposite cold-induction patterns in SW and IT, however most cold-regulated genes differ between SW and IT in terms of expression level (Fig 3.9, 3.23, 3.26). This seems consistent with previous analysis using FDR corrected p-value thresholds. Under non-acclimated conditions, genes up-regulated by the CBFs (25) appear to have higher expression in IT, which is consistent with previous analysis of basal transcriptomes using FDR corrected p-value thresholds. The difference in basal expression of CBF regulon genes again suggests that the CBF pathway of cold-acclimation is regulated differently between SW and IT. The CBFs are cold-responsive

genes (29). With the addition of cold, genes up-regulated by the CBFs generally have higher expression in SW than IT, and genes down-regulated by the CBFs are more repressed in SW (Fig 3.31). There also appears to be more CBF regulon genes responsive to cold in SW in comparison to IT (Fig. 3.3.1). Altogether, analysis of RNA-seq data using fold-change values still indicates that the CBF pathway of cold-acclimation may be differentially regulated between SW and IT. Fold-change analysis of Hannah genes (6), shows that SW generally has higher expression of genes previously positively correlated with freezing tolerance, and has lower expression of genes previously negatively correlated with freezing tolerance in comparison to IT (Fig. 3.32). Altogether, analysis of RNA-seq data by fold-change still suggests that SW is more enriched in genes that have been previously associated with cold-acclimation than IT (Fig. 3.31 and 3.32).

GO enrichment analysis also revealed several trends in SW and IT transcriptomes. Under all conditions, IT seems to be enriched in genes related to biotic stress. Therefore, biotic stress related genes were pulled from TAIR (www.arabidopsis.org), to determine if this is generally the case. Differentially expressed biotic genes between SW and IT were defined by a FDR corrected p-value ≤0.050 (384 genes differentially expressed out of 925). A heatmap was generated for these biotic stress genes to visually compare fold-change differences between SW and IT expression. IT does appear to have higher expression of biotic stress related genes under both warm and cold conditions in comparison to SW (Fig 3.33), but this difference is most pronounced at 2 weeks of cold-acclimation. Also, more biotic stress related

genes appear to be up-regulated by cold in IT at 2 weeks of cold-acclimation in comparison to SW (Fig. 3.33). Examination of IT transcripts suggests that IT is less enriched in pathways of cold-acclimation that have been previously defined. Consequently, some of these biotic stress related genes may function in cold-acclimation, especially since pathogens related proteins have previously been shown to have antifreeze properties (26). Furthermore, resistance to biotic stress may be an interesting trait segregating between the SW and IT ecotypes and should be tested in the SW and IT RILs in the future.

Photosynthesis was another interesting reoccurring GO term for SW and IT. It is well known that many transcriptional as well a metabolic changes occur during cold-acclimation (23, 31-34). Photosynthesis provides the energy for these necessary changes to occur (35). Increased photosynthetic capacity is consequently corrleated with cold-acclimation (24, 36-39). Therefore, differentially expressed photosynthesis associated genes (list of genes provided by Hu and Thomashow, unpublished) between SW and IT were determined by a FDR corrected p-value ≤0.050 (52 genes differentially expressed out of 244). A heatmap was generated for these photosynthesis genes to visually compare the fold-change differences between SW and IT expression (Fig 3.34). Although most photosynthesis related genes appear to be down-regulated by cold in both SW and IT, SW appears to have higher expression of photosynthesis related genes under both warm and cold conditions in comparison to IT (Fig 3.34). This may indicate that there are differences in the photosynthetic capacity of SW and IT. Differences in photosynthetic capacity would correlate with differences in freezing

tolerance between SW and IT at 2 weeks of cold-acclimation. Nevertheless, differences in photosynthetic capacity would need to be measured experimentally. Variations in photosynthetic capacity would also be an interesting trait to screen and map in the SW and IT RILs.

In the next section of this study, expression of Category 1 and Category 2 FTD genes are examined in the SW and IT RILs, which were constructed by the Schemske Lab. This eQTL analysis allows expression differences to be mapped to specific genetic locations, and genes potentially important for differences in freezing tolerance as well as fitness QTL can also be determined (Table 3.1). FTD candidate genes that are also CBF regulon genes will be targeted for this study since CBF regulon genes appear to be enriched in differentially expressed genes. Furthermore, FTD candidate genes annotated as 'photosynthesis related' and 'biotic stress related' will be included in eQTL analysis since those GO terms appear to be overrepresented.

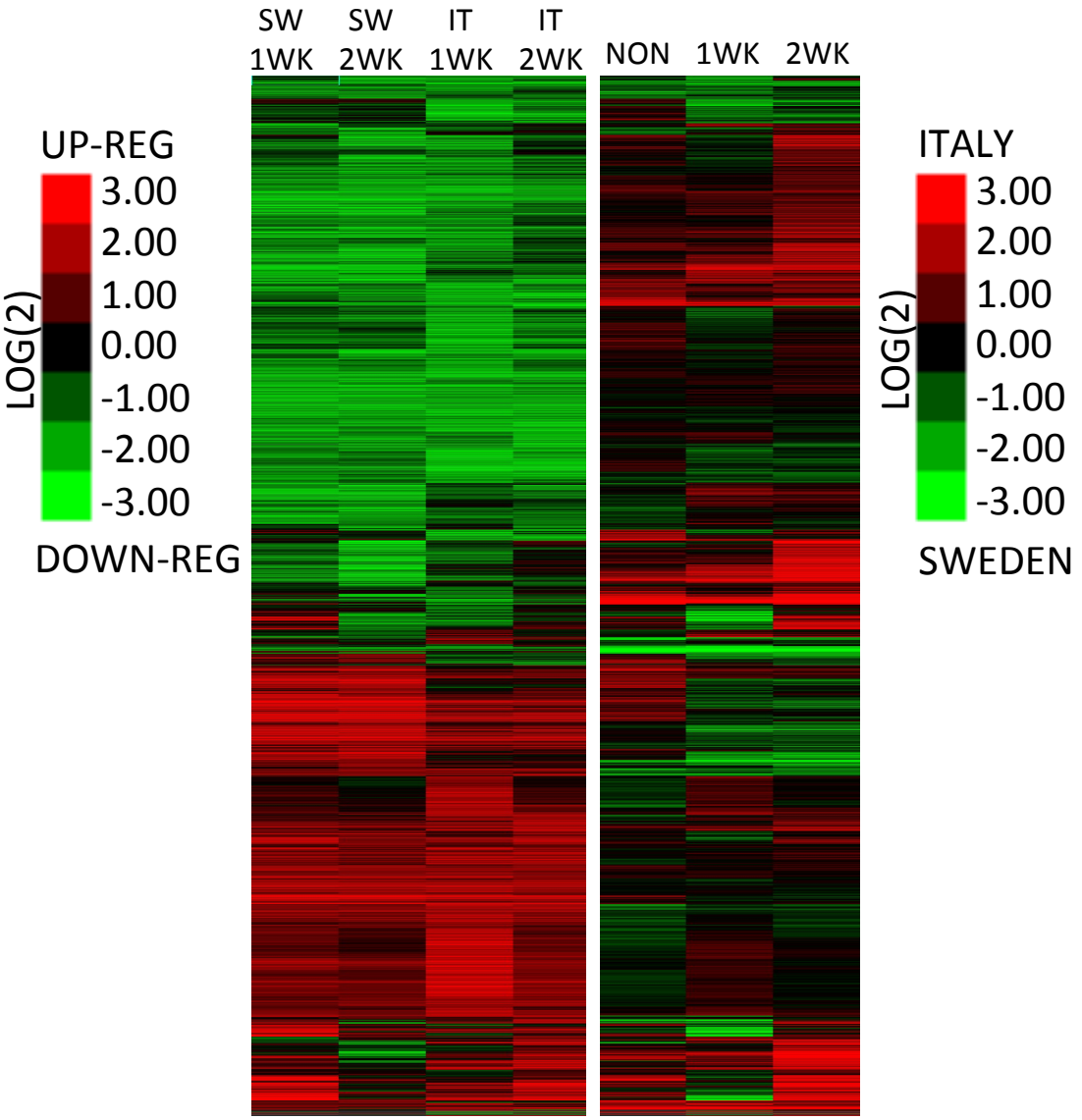


**Figure 3.30.** Fold change of cold regulated genes in SW and IT (7863 genes). Gene expression was measured by RNA-seq. The results are averages from three independent experiments (n=3). ≥3FPKM was used as the cut-off for differential expression (19, 20). Genes were considered differentially regulated between non-acclimated and cold conditions if the FDR corrected p-value was ≤0.050. Left panel values are the logarithm (base=2) of the fold-change between non-acclimated and cold conditions; negative values denote genes down-regulated by cold (green), positive values denote genes up-regulated by cold (red). Right panel values are the logarithm (base=2) of the fold-change between SW and IT; negative values denote higher fold expression in SW (green) and positive values denote higher fold expression IT (red). Hierarchical clustering of genes was performed with the program, Cluster (40), and heatmap was generated using MapleTree (40). For interpretation of the references to color in this and all other figures, the reader is referred to the electronic version of this dissertation.

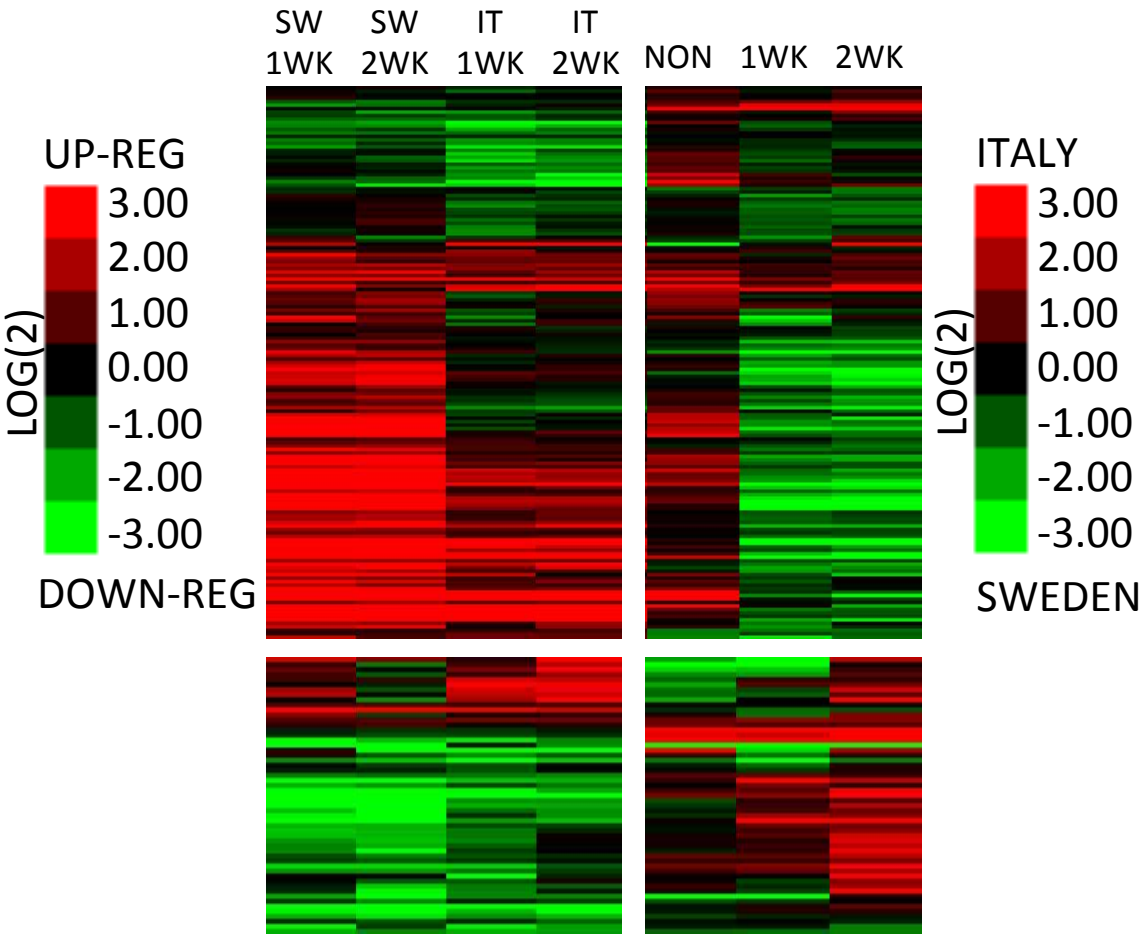


**Figure 3.31.** Fold change of CBF regulon genes in SW and IT. Top panels: 159 genes up-regulated by CBFs; Bottom panels: 55 genes down-regulated by CBFs (25). Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). ≥3FPKM was used as the cut-off for differential expression (19, 20). Left panels are the logarithm (base=2) of the fold-change between non-acclimated and cold conditions; negative values denote genes down-regulated by cold (green), positive values denote genes up-regulated by cold (red). Right panels are the logarithm (base=2) of the fold-change between SW and IT; negative values denote higher fold expression in SW (green) and positive values denote higher fold expression IT (red). Hierarchical clustering of genes was performed with the program, Cluster (40), and heatmap was generated using MapleTree (40).

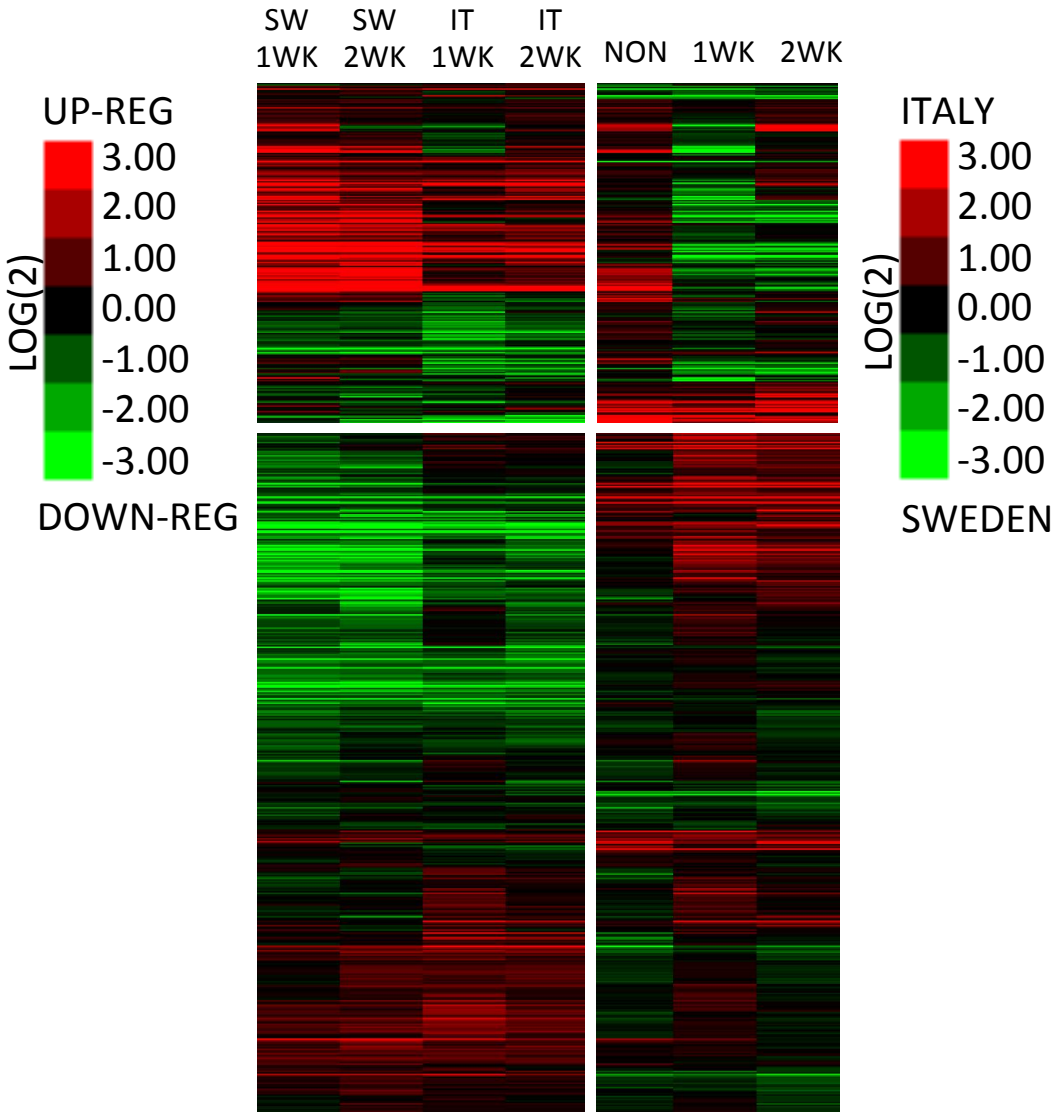


**Figure 3.32.** Fold change of Hannah genes in SW and IT. Top panels: 253 Hannah genes positively correlated with freezing tolerance; Bottom panels: 461 Hannah genes negatively correlated with freezing tolerance; (6). Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). ≥3FPKM was used as the cut-off for differential expression (19, 20). Left panels are the logarithm (base=2) of the fold-change between non-acclimated and cold conditions; negative values denote genes down-regulated by cold (green), positive values denote genes up-regulated by cold (red). Right panels are the logarithm (base=2) of the fold-change between SW and IT; negative values denote higher fold expression in SW (green) and positive values denote higher fold expression IT (red). Hierarchical clustering of genes was performed with the program, Cluster (40), and heatmap was generated using MapleTree (40).

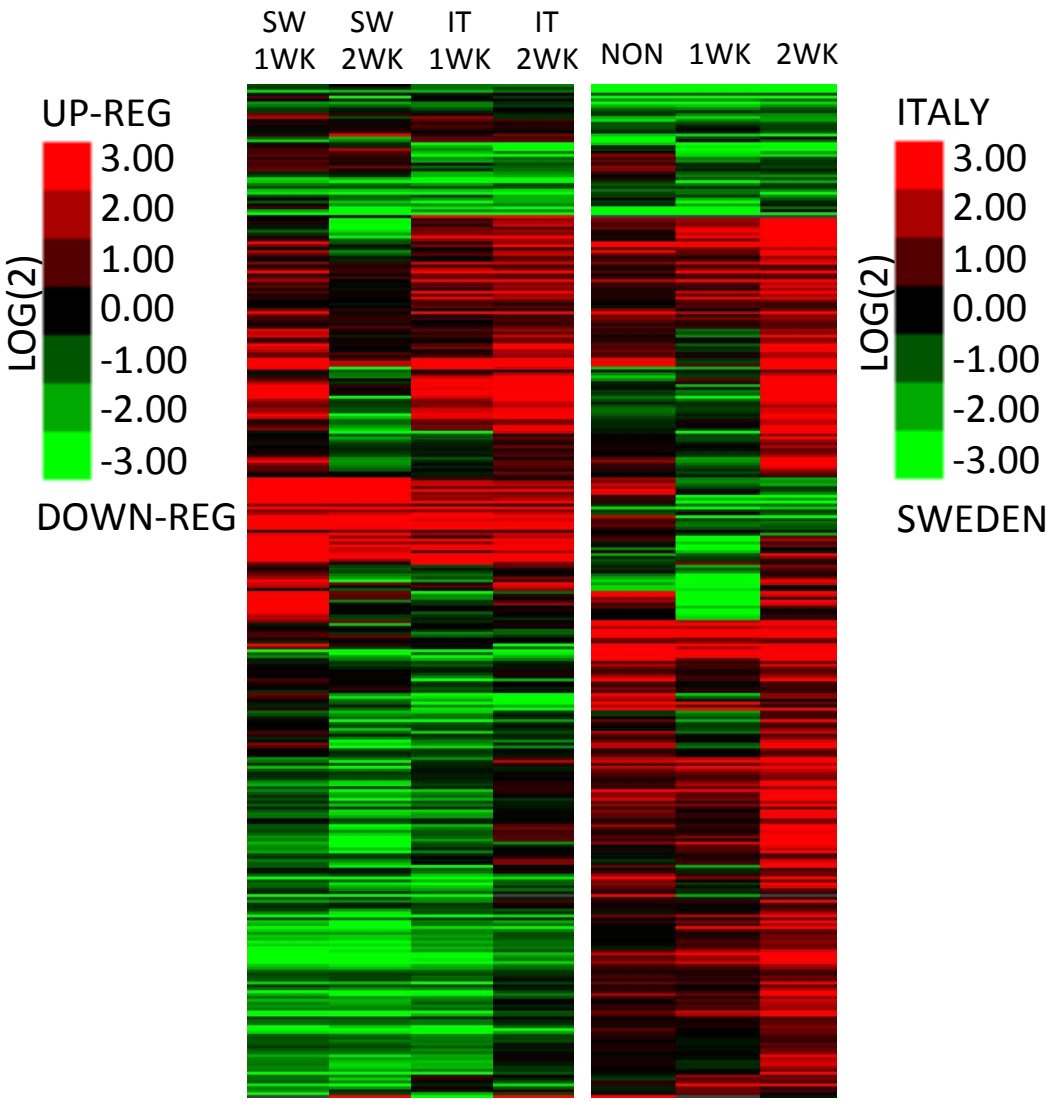


**Figure 3.33.** Fold change of differentially expressed biotic stress genes in SW and IT (348 genes). Gene expression was measured by RNA-seq. The results are averages from three independent experiments (n=3). ≥3FPKM was used as the cut-off for differential expression (19, 20). Genes were included if they were differentially expressed (FDR corrected p-value<0.05) between SW and IT in any sample (non-acclimated, 1 week of cold-acclimation, or 2 weeks of cold-acclimation). Left panels are the logarithm (base=2) of the fold-change between non-acclimated and cold conditions; negative values denote genes down-regulated by cold (green), positive values denote genes up-regulated by cold (red). Right panels are the logarithm (base=2) of the fold-change between SW and IT; negative values denote higher fold expression in SW (green) and positive values denote higher fold expression IT (red). Hierarchical clustering of genes was performed with the program, Cluster (40), and heatmap was generated using MapleTree (40).

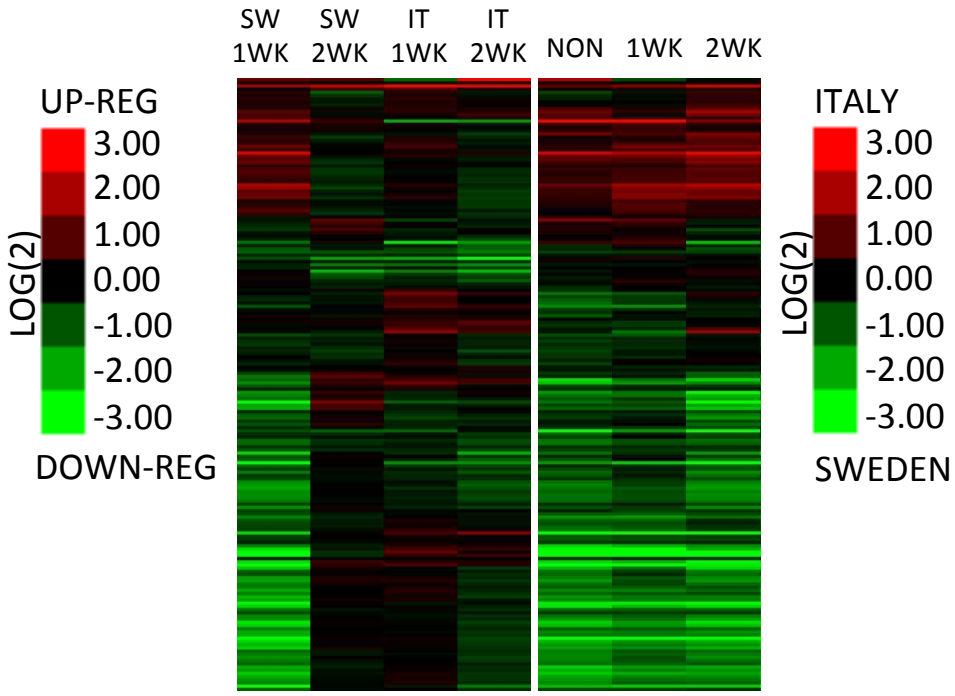


**Figure 3.34.** Fold change of differentially expressed photosynthesis associated genes in SW and IT (53 genes). Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). ≥3FPKM was used as the cut-off for differential expression (19, 20). Genes were included in the heatmap if they were differentially expressed (FDR corrected p-value<0.05) between SW and IT in any sample (non-acclimated, 1 week of cold-acclimation, or 2 weeks of cold-acclimation). Left panels are the logarithm (base=2) of the fold-change between non-acclimated and cold conditions; negative values denote genes down-regulated by cold (green), positive values denote genes up-regulated by cold (red). Right panels are the logarithm (base=2) of the fold-change between SW and IT; negative values denote higher fold expression in SW (green) and positive values denote higher fold expression IT (red). Hierarchical clustering of genes was performed with the program, Cluster (40), and heatmap was generated using MapleTree (40).

## RESULTS AND DISCUSSION: SW AND IT EQTL MAPPING

***Summary: SW and IT eQTL mapping:*** In the second section of this study Category 1 and Category 2 FTD genes, which possibly contribute to differences in freezing tolerance between SW and IT accessions at 2 weeks of cold-acclimation, were determined. FTD genes are enriched in CBF regulon genes and QTL mapped for differences in expression (eQTL) for several CBF-regulated FTD candidate genes mapped to the CBF locus on chromosome 4. This eQTL on chromosome 4 also overlaps with a fitness QTL mapped in the SW and IT RILs (Table 3.1). Consequently, the CBFs are candidates for regulating differences in FTD gene expression and fitness between SW and IT. Analysis of IT-CBF2 coding sequence reveals a deletion in the activation domain. Based on previous studies conducted in the Thomashow lab, it is hypothesized that IT-CBF2 functions as a dominant negative version of CBF2. RNA-seq data is generally consistent with this hypothesis.

***SW and IT eQTL mapping:*** The ultimate goal of this project is to determine the genes underlying the fitness QTL mapped using the SW and IT RILs (Table 3.1). In general, QTL peaks can span a large genomic region encompassing numerous genes (12, 13, 41). The fitness QTL found for the SW and IT RILs are certainly no exception (Table 3.1). For example, the fruit-set fitness QTL on chromosome 4 spans a region containing 2065 genes (Table 3.1). Many of these genes might contain polymorphisms, which may or may not contribute to fitness (12, 13). Moreover, 24% of genes in the *Arabidopsis* (Col-0) genome are included within SW and IT fitness QTL (Table 3.1).

Consequently, determining the specific genes responsible for a QTL can be extremely challenging (5, 12, 13, 41).

Minimum winter temperature was strongly correlated with fitness of the SW and IT parent lines in reciprocal transplant experiments (8), and freezing tolerance was found to be significantly different ($p \leq 0.026$ at 2 weeks of cold-acclimation) between SW and IT in laboratory experiments (Fig. 3.2). From analysis of RNA-seq data, genes that may contribute to differences in freezing tolerance between SW and IT have been defined (Table A3.3-A3.6). Similar to traditional QTL, an eQTL marks a position in the genome where a polymorphism is associated with differences in the relative abundance of a specific gene (12). Although correlative, eQTL mapped for FTD candidate genes, which also overlap with specific fitness QTL, can be determined. This will help to prioritize the tedious construction of near-isogenic lines (9) or complementation lines (41), which are needed to confirm if a gene affects freezing tolerance as well as plant fitness.

An eQTL is normally classified as being cis- or trans- to the gene used for mapping. Trans-eQTL are not physically linked to the gene of interest, and thus, are indicative of a polymorphism that alters the regulation of the gene of interest (12). Likely candidates for trans-eQTL are transcription factor polymorphisms. A cis-eQTL is located in or near the gene of interest. This can result when there is a deletion of an entire gene or a polymorphism in the promoter or coding region that affects regulation or function of that gene (12).

10 FTD candidate genes (Table 3.17; Fig. 3.35 and 3.36) were selected for eQTL analysis with the SW and IT RIL population generated by the Schemske Lab (Schemske and Agren, unpublished). From analysis of SW and IT transcriptomes in the second section of this study, CBF regulon genes are consistently differentially regulated between SW and IT. Therefore, 1-Category 1 and 3-Category 2 FTD genes that are also regulated by the CBFs, were selected for eQTL analysis (Table 3.17). Even if eQTL mapped for these CBF regulated genes do not overlap with fitness QTL, it will determine if differences in CBF regulated genes map cis- to the gene itself, or trans- to novel loci or the CBF locus. COR314, SZF1, and DI21 were chosen for eQTL analysis because they are FTD candidate genes not included in the CBF regulon, and thus represent genes that are potentially regulated by CBF-independent (42) pathways of cold-acclimation (Table 3.17). ZAT12, a Category 1 FTD gene was selected for eQTL analysis because ZAT12 regulon genes are enriched in the Hannah gene set (6), which was found to have differing enrichment in SW and IT in the second section of this study. Biotic stress was a GO category overrepresented in Category 2 FTD genes (Table 3.16) and a number of biotic stress genes appear to be differentially regulated by cold between SW and IT (Fig 3.33). Therefore, PR5, a Category 2 FTD gene that encodes a protein, which has been previously been shown to have antifreeze properties (26), was selected for eQTL analysis (Table 3.17). Photosynthesis was a GO category overrepresented in Category 1 FTD candidate genes (Table 3.13), and a number of photosynthesis related genes are differentially regulated between SW and IT (Fig. 3.34). Therefore ZAT10, a Category 1 FTD gene and a photosynthesis-related transcription

factor, was selected for eQTL analysis (Table 3.17). Altogether, 4 of these FTD genes have higher expression in IT and 6 have higher expression in SW at 2 weeks of cold-acclimation (Fig 3.35 and 3.36; Table A3.3-3.6).

SW and IT accessions, sampled at the same time as RNA-seq experiments, were also analyzed by qRT-PCR (Fig. 3.35 and 3.36). This ensured that expression differences measured by qRT-PCR were similar to RNA-seq experiments (Fig. 3.35 and 3.36). 544 genotyped RILs were grown similarly to plants used in electrolyte leakage experiments and sampled at 2 weeks of cold-acclimation, which is the acclimation period with the greatest difference in freezing tolerance (Fig. 3.2). For the RILs, expression of the 10 FTD genes was measured using qRT-PCR and differences were mapped using RQTL (15). RQTL was also used to calculate genome wide logarithm of odds (LOD) threshold values as well as the percent of phenotypic variance explained by each QTL (Table 3.18 and 3.19). Distinct eQTL above LOD thresholds were found for all genes except ZAT10 (Table 3.18 and 3.19).

Quantitative traits like differences in gene expression are defined by small and intermediate effect QTL (43). The average percent of variance explained by each eQTL in this study (Table 3.18 and 3.19) is lower (5.32%) than previous genome wide eQTL studies in *Arabidopsis,* which see percent variance explained by eQTL averaging from 10-30% (13, 44). However, the 'Beavis effect' indicates that percent variance of a QTL is greatly overestimated if only 100 lines are tested, and are only slightly overestimated with 500 lines tested (43). This study uses 544 RILs, more than double the number of RILs used in eQTL studies by West et al. 2007 (211 lines used) and Keurentjes et al.

2007 (160 lines used) (13, 44). Consequently, the lower percent variance explained by eQTL in this study may be due to the Beavis effect (43). When 160 SW and IT RILs are randomly selected for COR15A eQTL analysis, the same QTL on chromosome 4 is found (Table 3.18). However, the LOD score for the COR15A eQTL decreases from 10.09 to 6.19 with 160 samples, while the percent variance explained by the eQTL increases from 8.39% to 16.33% with 160 samples suggesting that the lower percent variance explained by eQTL with 544 RILs may be due to the Beavis effect (Table 3.18). The eQTL, which were found to overlap with fitness QTL (Table 3.1), will be analyzed next and candidates for the genes underlying them will be provided. Genes with eQTL that do not overlap with fitness QTL will be discussed in more detail in Chapter Four of this study.

Expression differences in CBF regulon gene, COR78, map to two eQTL (Fig 3.37; Table 3.1 and 3.18). The first eQTL maps to a region on chromosome 5, which overlaps with a previously identified fitness QTL (Fig 3.37; Table 3.1 and 3.18). This may be a cis-eQTL since the COR78 gene is located (between markers 60.60 and 61.28) within the eQTL peak on chromosome 5. COR78 is a Hannah gene positively correlated with increases in freezing tolerance and is regularly used as a marker gene for both cold and salt stress (6, 16, 45, 46). Although the coding sequence of COR78 is conserved between SW, IT and Col-0, it is known that the response of COR78 to cold and salt stress is driven through its promoter (47). In fact, the COR78 promoter is often employed as a stress-inducible promoter for other genes (48-52). Therefore, polymorphisms in this region are likely to influence expression. According to the effect

plot, the SW genotype at this eQTL is associated with higher expression of COR78 (Fig. 3.35). Currently, there is little evidence to indicate that COR78 alone can affect freezing tolerance (53). However, these results advocate sequencing of the COR78 promoter, construction of near-isogenic lines (9) for the region containing COR78 and suggest that complementation lines (41) should be made.

There is an alternate hypothesis for the COR78 eQTL on chromosome 5. COR78 is known to be regulated by cold-induced transcription factors CBF1-3 (24), which are located on chromosome 4. But CBF4, a closely related transcription factor, is located within the peak of the chromosome 5 eQTL (Fig 3.37; Table 3.19), and moreover between the same SW and IT RIL markers as COR78 (markers 60.60 and 61.28). CBF4 has also been shown to regulate COR78, and overexpression of CBF4 results in constitutive freezing and drought tolerance (54). CBF4 expression is not known to be cold-regulated but it is regulated by drought (54). The RNA-seq data is consistent with this result and CBF4 is not significantly ($p>0.050$) induced by cold (Fig. 3.43; Table 3.20). There are also no differences in CBF4 expression level between SW and IT (Fig. 3.43; Table 3.20). However, CBF4 may be regulated by cold post-transcriptionally and this regulation may differ between SW and IT. Therefore, CBF4 coding and promoter regions in SW and IT should be sequenced and complementation lines (41) for CBF4 should be made.

COR78, also has a trans-eQTL on chromosome 4, which explains more of the expression variance than the trans/cis-eQTL on chromosome 5 (Fig 3.37; Table 3.18). Interestingly, this trans-eQTL on chromosome 4 overlaps with a previously defined

fitness QTL (Table 3.1 and 3.20). 5 other FTD genes used for eQTL analysis, COR15A, COR47, COR314, EARLY RESPONSIVE TO DEHYDRATION10 (ERD10) and ZAT12, also have an eQTL that overlaps with this fitness QTL on chromosome 4 (Fig. 3.37-3.42; Table 3.1, 3.18 and 3.19). CBF1-3 are located in tandem array on chromosome 4 between SW and IT RIL markers 50.20 and 50.60. The CBF locus is thus contained within the chromosome 4 eQTL of all 6 FTD genes (Fig. 3.37-3.42; Table 3.1, 3.18 and 3.19). Expression of *COR15A*, *COR47*, *COR78*, and *ERD10* was mapped knowing that they were previously found to be regulated by the CBF genes (Table 3.17; (25)). Based on the CBF regulon defined by Vogel et al. 2005, expression differences mapping to the CBF locus for COR314 and ZAT12 were not expected (25). However, in a separate analysis of *CBF* overexpression lines by Maruyama et al. 2004, *COR314* was found to be regulated by CBF genes (55). Furthermore, though ZAT12 is not part of the CBF regulon, it does have a regulatory relationship with the transcription factors (25).

The 6 effect plots for the chromosome 4 eQTL also all indicate that the SW genotype is associated with higher expression (Fig. 3.37-3.42). This is interesting considering that ZAT12 has an opposite induction pattern compared to the other genes used for mapping (Fig. 3.35 and 3.36). However, the details of the CBF-ZAT12 relationship have yet to be elucidated. ZAT12 is a cold-regulated transcription factor known to induce and repress cold-responsive genes (25, 42). CBF and ZAT12 regulons overlap and both regulons are overrepresented in the Hannah gene set (6, 25). Overexpression of *ZAT12* down-regulates *CBF* expression and these plants are slightly more freezing tolerant than wild-type plants, but not nearly as freezing tolerant as *CBF*

overexpressing plants (25). *CBF* and *ZAT12* overexpressing plants both have a dwarf phenotype. However plants overexpressing *both ZAT12* and *CBF2* are similar in size to wild-type plants (Doherty, unpublished). Consequently, it may be possible that the CBFs regulate ZAT12 in some way, but further work is necessary to elucidate the relationship of the CBFs to ZAT12.

Previous natural variation studies on freezing tolerance have also implicated the CBFs as a source of variation. Alonso-Blanco et al. 2005 used RILs constructed from *Arabidopsis* accessions LER and CVI to map differences in freezing tolerance (10). Seven different QTL on chromosomes 1,4, and 5 were found, but the single QTL on chromosome 4, which contained the CBF locus, explained the most variance (10). CVI freezing tolerance was significantly reduced in comparison to LER, as was CBF2 expression. The CVI-CBF2 promoter was found to have a 1630 bp deletion (starting at -160), reducing the promoter region to 378 bp (10). Introduction of the Ler-CBF2 transgene into CVI significantly reduced differences in freezing tolerance between LER and CVI (10).

*CBF* expression in the Versailles core collection of Arabidopsis (48 accessions tested) was also found to vary significantly (56). However, freezing tolerance did not correlate simply with *CBF* expression level in the 8 accessions tested (56). The most freezing-sensitive Versailles accessions were also the accessions with the lowest maximal cold-induced *CBF* expression levels. But the most freezing tolerant Versailles accessions varied significantly in their *CBF* expression, suggesting the importance of CBF-independent pathways of freezing tolerance for some accessions (56). It should

be pointed out, however, that in this Versailles study, *CBF* expression measured after hours in cold was correlated with freezing tolerance assays conducted after 2 weeks of cold-acclimation (56). Therefore in the Versailles study, *CBF* expression and freezing tolerance assays were conducted at very different time-points. In future studies, *CBF* expression should be measured at several time-points, but especially at time-points just as to 2 week cold-acclimated freezing tolerance assays are conducted to determine if *CBF* expression and CBF regulon gene expression correlates with differences in freezing tolerance between accessions.

Freezing tolerance QTL differed between two Versailles RIL populations (56). However, in both populations a common QTL on chromosome 4 explained the most variance in freezing tolerance and overlapped with the CBF locus (56). Further analysis of CBF gene sequence in the 48 Versailles accessions showed a number of polymorphisms in both the promoter and coding sequences of CBF genes (57). The most notable of these accessions were Bl-1 with a 10 amino acid deletion at the end of the activation domain in CBF1, Condara with a premature stop codon in the activation domain of CBF3, and Gre-0 with a glycine to arginine change in the activation domain of CBF2 (57). Unfortunately, these 3 particular accessions were not chosen for freezing tolerance assays or tested for CBF target gene expression (57).

A recent study by Zhen et al. 2008 further showed that CBF genes undergo relaxed selection in *Arabidopsis* accessions native to southern latitudes(58). Analysis of CBF sequence in 24 accession of *Arabidopsis* (9 accessions overlap with 48 Versailles accessions previously mentioned (56, 57)) found a large bias toward nonsynonymous

changes in the activation domain compared to DNA binding domain of CBF genes (58). Southern latitude accession had 1.3 to 4.6-fold more polymorphisms in the individual CBF genes and also had reduced expression of CBF target genes (58).

CBF1 and CBF3 coding sequences were found to be conserved between SW and IT. Transcripts for CBF1 and CBF3 are also not significantly ($p>0.050$) differentially regulated between SW and IT at 2 weeks of cold-acclimation in RNA-seq experiments (Fig. 3.43; Table 3.20). This suggests that any polymorphisms in CBF1 and CBF3 promoters have little effect on gene expression. On the other hand, CBF2 transcripts are differentially regulated between SW and IT at 2 weeks of cold-acclimation (Fig. 3.43; Table 3.20). CBF2 expression is 1.5-fold higher in SW compared to IT at 2 weeks of cold-acclimation (Table 3.20). CBF1, 2 and 3 are known to regulate over a hundred target genes (25, 59, 60). Therefore, polymorphisms in the CBF2 promoter could contribute to differences in *CBF2* expression and have compounding effects on target gene regulation. The coding sequence of CBF2 is conserved between SW and Col-0 (Fig. 3.44). However, there is a 13 basepair (bp) deletion (+384 to +397) in the activation domain (61) of IT-CBF2, though surrounding coding sequences are conserved between SW, IT, and Col-0 (Fig 3.44). This leads to a predicted protein (Fig. 3.42) with a nuclear localization signal (NLS) and DNA binding domain, but missing activation domain (61). This predicted protein would be similar to the Versailles accession, Condara, which has a premature stop codon in the activation domain of CBF3 (57). Freezing tolerance and CBF target gene expression was not tested in

Condara (56, 57). However, Condara freezing tolerance and CBF target gene expression may be predicted to be diminished in comparison to SW, similar to IT.

A similar truncated version of CBF2 (CBF2ΔC), predicted to have a missing activation domain, was previously identified through an EMS screen of *CBF2* overexpressing plants (Gilmour and Thomashow, unpublished). At 2 weeks of cold-acclimation, the combined expression level of IT-CBF1 (3.02 FPKM) and IT-CBF3 (35.85 FPKM) is similar to IT-CBF2 (33.23 FPKM). Interestingly, CBF2ΔC was shown to function as a dominant negative protein in plants with equal expression of *CBF2* and *CBF2ΔC* (Doherty, unpublished). CBF2ΔC overexpressing plants are also significantly impaired in cold-acclimation (Doherty, unpublished) and IT is less freezing tolerant than SW at 2 weeks of cold-acclimation. Transcriptional analysis of *CBF2ΔC* overexpressing plants revealed that 40% of cold-induced genes were affected (Doherty, unpublished). CBF regulon genes are overrepresented in genes differentially expressed between SW and IT; Category 1 FTD genes include 61 CBF regulon genes (p=4.3E-13; Table A3.3-3.4) and Category 2 FTD genes include 51 gene CBF regulon genes (p<2.2E-16; Table A3.5-A3.6). In general, cold-regulated gene expression is consistent with IT-CBF2 acting as a dominant negative version of CBF2; genes up-regulated by CBFs have lower expression in IT than SW and gene down-regulated by CBFs have higher expression in in IT than SW (Fig 3.31). Furthermore, there are fewer CBF regulon genes up-regulated by cold in IT in comparison to SW (Fig 3.31). Based on these results, I postulate that IT-CBF2 may function as a natural version of CBF2ΔC, in addition to effects of possible promoter polymorphisms. More experiments are necessary to test

this hypothesis, which would include determining CBF1-3 protein levels in IT and SW, as well as transforming the IT-CBF2 and SW-CBF2 into SW and IT, respectively.

It is interesting that differences in freezing tolerance are not seen at both 1 and 2 weeks of cold-acclimation since IT-CBF2 would presumably act as a dominant negative protein at both times. Category 2 FTD candidate genes are enriched in CBF regulon genes and were defined as cold-regulated genes that are differentially expressed between SW and IT at both 1 and 2 weeks of cold acclimation. Therefore, IT-CBF2 does appear to be acting as a dominant negative version of CBF2 at both 1 and 2 weeks of cold-acclimation. However, there are also known to be CBF-independent pathways of cold acclimation (42), which are of varying importance to *Arabidopsis* accessions (56). Therefore, there may be CBF-independent pathways of cold-acclimation, which compensate for the dominant negative IT-CBF2 at 1 week of cold but not 2 weeks. The analysis of IT transcriptomes at 1 and 2 weeks of cold-acclimation did reveal numerous genes, which are exclusively cold-regulated at either 1 or 2 weeks of cold-acclimation (Fig. 3.6).

It is also of note that at 2 weeks of cold-acclimation SW freezing tolerance increases in addition to IT freezing tolerance decreasing. SW-*CBF2* expression is significantly higher in comparison to IT-*CBF2* at only 2 weeks of cold-acclimation. Therefore, in addition to IT-CBF2 possibly acting as a dominant negative protein, reducing freezing tolerance through interruption of the CBF pathway of cold-acclimation, polymorphisms in the SW-CBF2 promoter could be contributing to higher *CBF2* expression and subsequent increase in freezing tolerance at 2 weeks of cold-

acclimation. Overall, CBF2 appears to be an excellent candidate gene to explain differences in cold-regulated gene expression and differences in freezing tolerance and fitness between SW and IT. Sequencing the CBF2 promoter in SW and IT, near-isogenic lines (9) for the region containing CBF2, and complementation lines (41) should be made a top priority in order to test how great a role CBF2 plays in differential expression of FTD candidate genes, freezing tolerance, and fitness.

**Table 3.17.** 10 FTD candidate genes for eQTL analysis. Genes are ordered by their AGI numbers. Genes were considered significantly different between SW and IT under non-acclimated conditions if they had a Benjamini-Hochberg corrected p-value (FDR P-VALUE) of <0.05 and a minimum of ≥3FPKM in either SW or IT. The differential expression of each gene is also represented by the logarithm (base=2) of the fold change (LOG2.FC). This table also denotes if a gene was previously described as positively or negatively correlating with freezing tolerance (HANNAH;(6)), a transcription factor (TF), a gene previously described as up- or down-regulated by 1 week of cold (COS, (25)), identified as an up- or down-regulated component of the CBF regulon (CBF REGULON; (25)) or identified as a photosynthesis associated genes (PAG; Hu and Thomashow, unpublished). Shaded genes have higher expression in SW and non-shaded genes have higher expression in IT.

CATEGORY 1 FTD CANDIDATES FOR eQTL ANALYSIS

| AGI | NAME | SHORT DESCRIPTION | SW.IT.2WK LOG2FC | SW.IT.2WK FDR P-VALUE | HANNAH? | TF? | COS? | CBF REG? | PAG? |
|---|---|---|---|---|---|---|---|---|---|
| AT1G27730 | ZAT10 | Salt Tolerance Zinc Finger | 2.11 | 0.00E+00 | NO | YES | UP | NO | YES |
| AT1G29390 | COR314 | Cold Regulated 314 | -0.97 | 1.74E-08 | NO | NO | NO | NO | NO |
| AT2G42540 | COR15A | Cold-Regulated 15a | -1.88 | 2.90E-08 | NO | NO | UP | UP | NO |
| AT3G55980 | SZF1 | Salt-Inducible Zinc Finger 1 | 1.63 | 0.00E+00 | NO | YES | DOWN | NO | NO |
| AT5G59820 | ZAT12 | C2H2-Type Zinc Finger Family | 1.75 | 1.85E-14 | NO | YES | NO | NO | NO |

CATEGORY 2 FTD CANDIDATES FOR eQTL ANALYSIS

| AGI | NAME | SHORT DESCRIPTION | SW.IT.2WK LOG2FC | SW.IT.2WK. FDR P-VALUE | HANNAH? | TF? | COS? | CBF REG? | PAGs |
|---|---|---|---|---|---|---|---|---|---|
| AT1G20440 | COR47 | Cold-Regulated 47 | -2.51 | 0.00E+00 | NO | NO | UP | UP | NO |
| AT1G20450 | ERD10 | Dehydrin Family Protein | -1.96 | 0.00E+00 | NO | NO | UP | UP | NO |
| AT1G75040 | PR5 | Pathogenesis-Related 5 | 4.50 | 0.00E+00 | NO | NO | UP | NO | NO |
| AT4G15910 | DI21 | Drought-Induced 21 | -2.58 | 0.00E+00 | NO | NO | NO | NO | NO |
| AT5G52310 | COR78 | Cold-Regulated 78 | -2.83 | 0.00E+00 | POSITIVE | NO | UP | UP | NO |

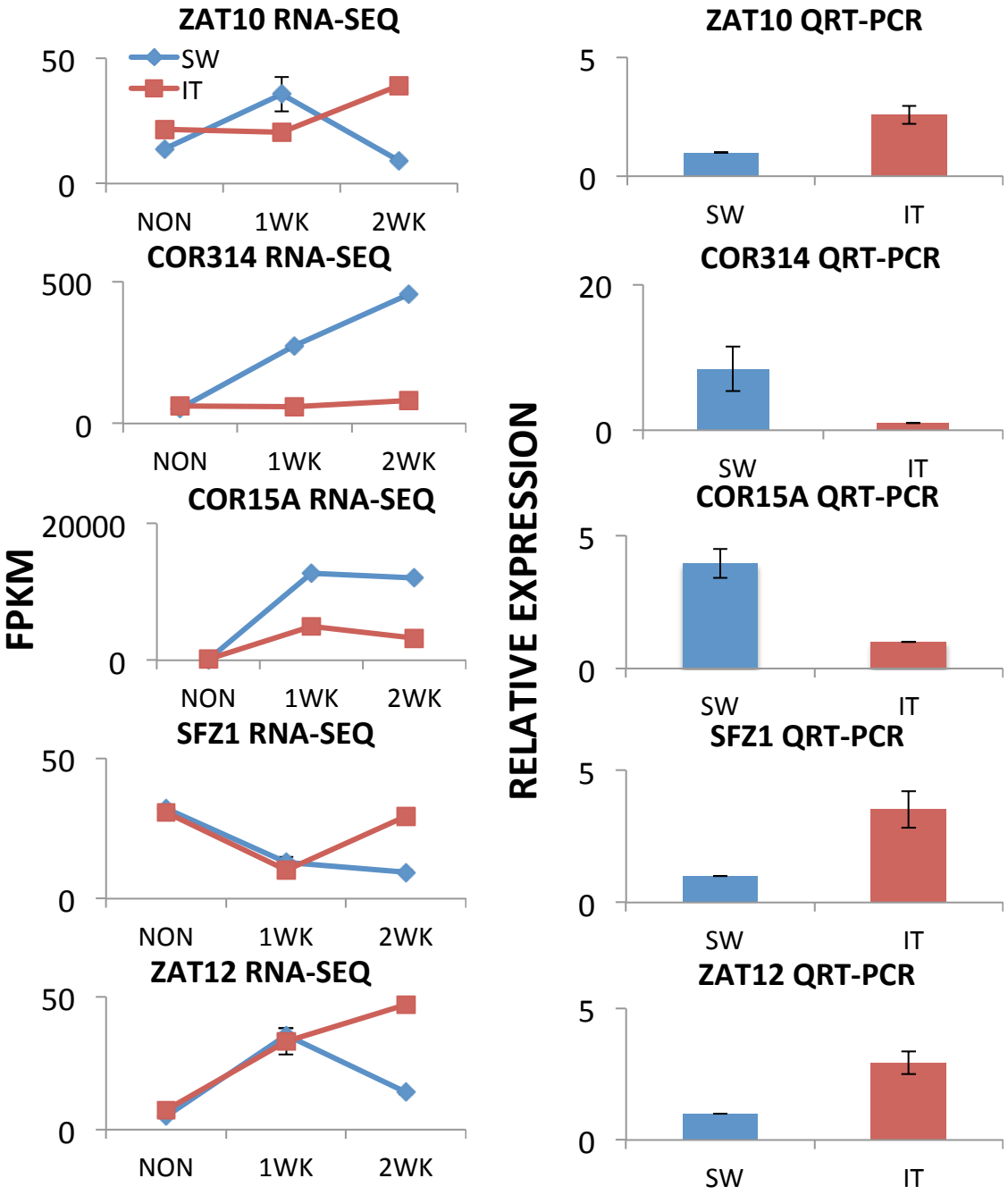


**Figure 3.35.** Category 1 FTD candidate genes for eQTL analysis. IT samples are shown in red, and SW in blue. The results presented are average values from three independent experiments (n=3). Error bars indicate ±SEM. For RNA-seq experiments, plants were grown at 22$^0$C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled directly or transferred to 4$^0$C for 1 or 2 weeks under a 12 h photoperiod then sampled. For qRT-PCR experiments, plants were grown at 22$^0$C under a 12 h photoperiod for approximately 18 days before rosette tissue was transferred to 4$^0$C for 2 weeks under a 12 h photoperiod then sampled. IPP2 was used as a housekeeping gene. Primer sequences can be found in Table A3.6.

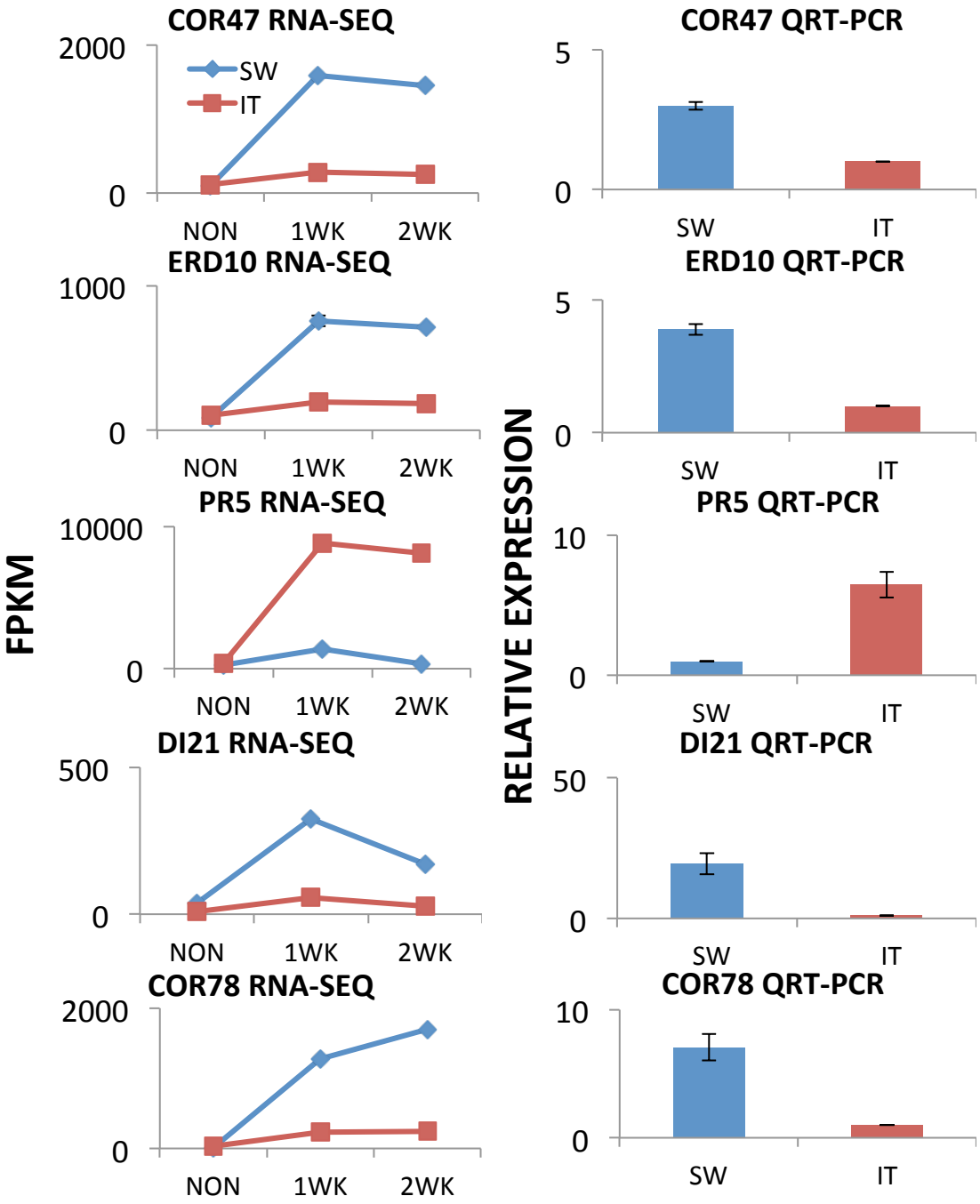


**Figure 3.36.** Category 2 FTD candidate genes for eQTL analysis. IT samples are shown in red, and SW in blue. The results presented are average values from three independent experiments (n=3). Error bars indicate ±SEM. For RNA-seq experiments, plants were grown at 22°C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled directly or transferred to 4°C for 1 or 2 weeks under a 12 h photoperiod then sampled. For qRT-PCR experiments, plants were grown at 22°C under a 12 h photoperiod for approximately 18 days before rosette tissue was transferred to 4°C for 2 weeks under a 12 h photoperiod then sampled. IPP2 was used as a housekeeping gene. Primer sequences can be found in Table A3.6.

**Table 3.18.** Locations of eQTL for Category 1 FTD candidate genes. 544 RILs were used for eQTL mapping. RQTL (15) was used to perform interval mapping using the multiple imputation method as described by the reference manual (http://www.rqtl.org/). To detect eQTL, estimated genome-wide significance thresholds (**α**=0.01) for the logarithm of odds (LOD) values were calculated for each trait using 1000 permutations in RQTL. To estimate the location of each eQTL a Bayes credible interval (99%) was calculated in RQTL. For locations of markers based on the Col-0 genome please see Table A3.1. QTL are categorized as cis- or trans- (CIS/TRANS?). Shaded QTL overlap with previously identified fitness QTL (Schemske and Agren, unpublished). 'MB' indicates the number of megabases contained within the eQTL. '# GENES' indicates the number of genes contained within the eQTL based on the Col-0 genome. %VAR indicates the estimated proportion of phenotypic variance explained by the QTL.

**AT1G27730-ZAT10 (LOD THRESHOLD=3.04)**

| CHR | LEFT (CM) | PEAK (CM) | RIGHT (CM) | MB | # GENES | CIS/ TRAN? | LOD | %VAR |
|---|---|---|---|---|---|---|---|---|
| | | NO QTL | | | | | | |

**AT1G29390-COR314 (LOD THRESHOLD=3.33)**

| CHR | LEFT (CM) | PEAK (CM) | RIGHT (CM) | MB | # GENES | CIS/ TRAN? | LOD | %VAR |
|---|---|---|---|---|---|---|---|---|
| 4 | 50.00 | 55.52 | 58.00 | 4.94 | 1575 | TRANS | 6.35 | 5.35 |

**AT2G42540-COR15A (LOD THRESHOLD=3.13)**

| CHR | LEFT (CM) | PEAK (CM) | RIGHT (CM) | MB | # GENES | CIS/ TRAN? | LOD | %VAR |
|---|---|---|---|---|---|---|---|---|
| 4 | 50.000 | 50.004 | 55.520 | 3.790 | 1153 | TRANS | 10.09 | 8.390 |

**AT3G55980-STZ1 (LOD THRESHOLD=2.81)**

| CHR | LEFT (CM) | PEAK (CM) | RIGHT (CM) | MB | # GENES | CIS/ TRAN? | LOD | %VAR |
|---|---|---|---|---|---|---|---|---|
| 4 | 32.00 | 33.42 | 36.00 | 1.73 | 477 | TRANS | 5.46 | 3.85 |
| 5 | 20.00 | 22.00 | 36.74 | 3.50 | 805 | TRANS | 3.87 | 2.40 |

**AT5G59820-ZAT12 (LOD THRESHOLD=3.15)**

| CHR | LEFT (CM) | PEAK (CM) | RIGHT (CM) | MB | # GENES | CIS/ TRAN? | LOD | %VAR |
|---|---|---|---|---|---|---|---|---|
| 3 | 9.64 | 11.18 | 22.00 | 3.20 | 951 | TRANS | 5.25 | 4.10 |
| 4 | 50.00 | 50.60 | 56.60 | 4.66 | 1410 | TRANS | 4.46 | 4.37 |
| 5 | 10.00 | 48.00 | 56.60 | 15.66 | 4071 | TRANS | 6.54 | 4.91 |

**Table 3.19.** Locations of eQTL for Category 2 FTD candidate genes. 544 RILs were used for eQTL mapping. RQTL (15) was used to perform interval mapping using the multiple imputation method as described by the reference manual (http://www.rqtl.org/). To detect eQTL, estimated genome-wide significance thresholds (**α**=0.01) for the logarithm of odds (LOD) values were calculated for each trait using 1000 permutations in RQTL. To estimate the location of each eQTL a Bayes credible interval (99%) was calculated in RQTL. For locations of markers based on the Col-0 genome please see Table A3.1. QTL are categorized as cis- or trans- (CIS/TRANS?). Shaded QTL overlap with previously identified fitness QTL (Schemske and Agren, unpublished). 'MB' indicates the number of megabases contained within the eQTL. '# GENES' indicates the number of genes contained within the eQTL based on the Col-0 genome. %VAR indicates the estimated proportion of phenotypic variance explained by the QTL.

**AT1G20440-COR47 (LOD THRESHOLD=2.83)**

| CHR | LEFT (CM) | PEAK (CM) | RIGHT (CM) | MB | # GENES | CIS/ TRAN? | LOD | %VAR |
|---|---|---|---|---|---|---|---|---|
| 1 | 10 | 14.05 | 18.12 | 3.19 | 967 | CIS | 7.59 | 6.89 |
| 4 | 46.00 | 50.20 | 58.00 | 5.77 | 1977 | TRANS | 6.76 | 6.35 |

**AT1G20450-ERD10 (LOD THRESHOLD=3.25)**

| CHR | LEFT (CM) | PEAK (CM) | RIGHT (CM) | MB | # GENES | CIS/ TRAN? | LOD | %VAR |
|---|---|---|---|---|---|---|---|---|
| 4 | 50.00 | 55.52 | 56.30 | 4.36 | 1322 | TRANS | 12.79 | 10.50 |

**AT1G75040-PR5 (LOD THRESHOLD=3.05)**

| CHR | LEFT (CM) | PEAK (CM) | RIGHT (CM) | MB | # GENES | CIS/ TRAN? | LOD | %VAR |
|---|---|---|---|---|---|---|---|---|
| 2 | 40.25 | 46.95 | 48.04 | 1.73 | 450 | TRANS | 6.07 | 3.87 |
| 3 | 9.64 | 11.18 | 12.64 | 1.16 | 356 | TRANS | 7.63 | 4.25 |
| 5 | 42.00 | 54.27 | 56.60 | 4.68 | 1697 | TRANS | 5.87 | 4.63 |

**AT4G15910-DI21 (LOD THRESHOLD=2.85)**

| CHR | LEFT (CM) | PEAK (CM) | RIGHT (CM) | MB | # GENES | CIS/ TRAN? | LOD | %VAR |
|---|---|---|---|---|---|---|---|---|
| 4 | 34.00 | 34.49 | 35.77 | 0.64 | 179 | CIS | 28.96 | 11.92 |

**AT5G52310-COR78 (LOD THRESHOLD=3.00)**

| CHR | LEFT (CM) | PEAK (CM) | RIGHT (CM) | MB | # GENES | CIS/ TRAN? | LOD | %VAR |
|---|---|---|---|---|---|---|---|---|
| 4 | 48.00 | 55.52 | 60.44 | 6.35 | 1910 | TRANS | 6.39 | 5.18 |
| 5 | 54.83 | 64.62 | 78.17 | 7.83 | 2342 | CIS | 4.20 | 3.50 |

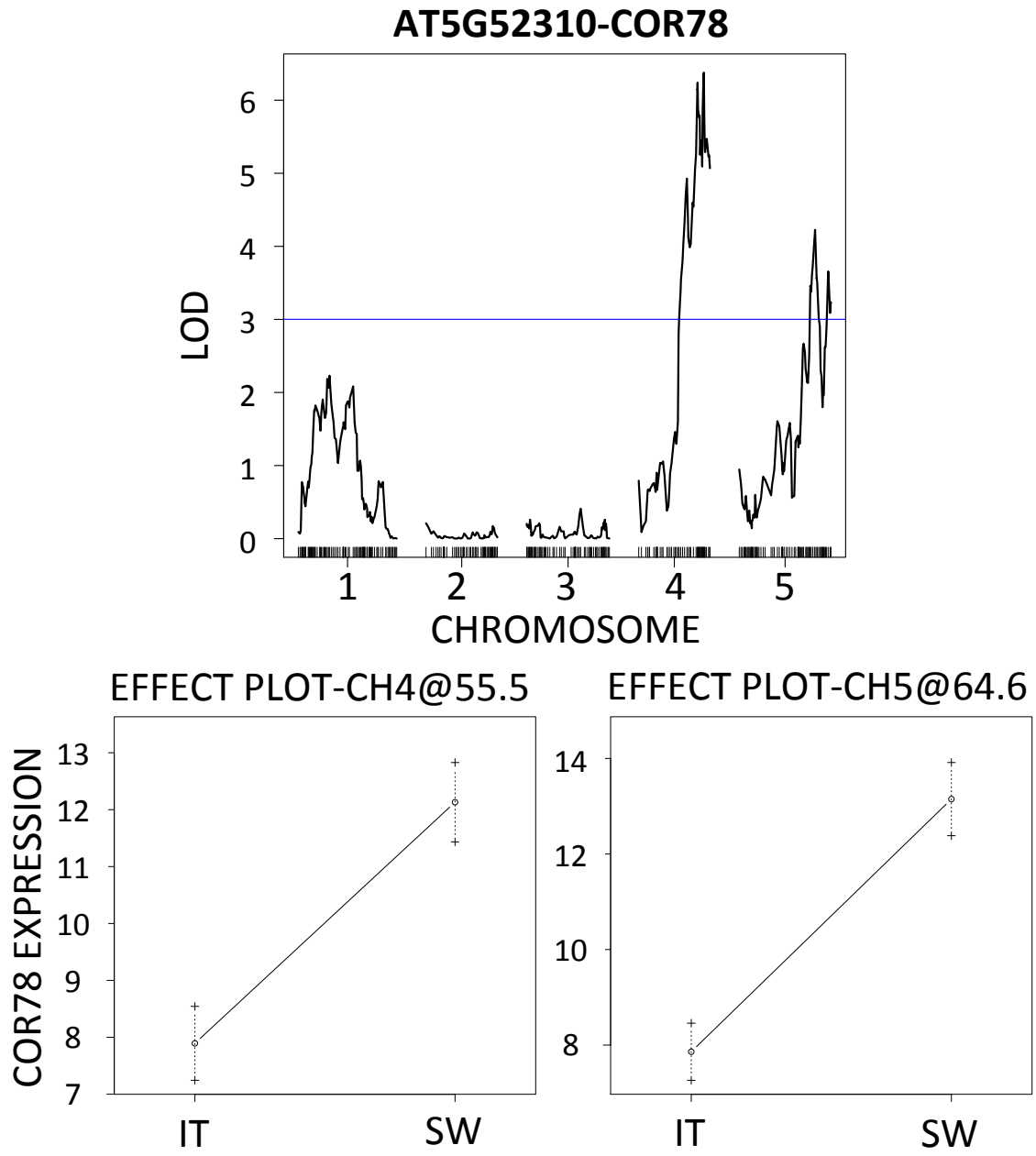


**Figure 3.37.** eQTL for Category 2 FTD gene COR78. 544 RILs were used for eQTL mapping by qRT-PCR. RQTL (15) was used to perform interval mapping using the multiple imputation method as described by the reference manual (http://www.rqtl.org/) for each fitness trait at each location. To detect QTL, estimated genome-wide significance thresholds (**α**=0.01) for the logarithm of odds (LODs) values were calculated for each trait using 1000 permutations in RQTL (shown in blue). Effects plots represent expression averages for the genotype groups (IT or SW) at eQTL on chromosome 4 and 5. Effect plots were constructed using 'effectplot' function in R/QTL(15).

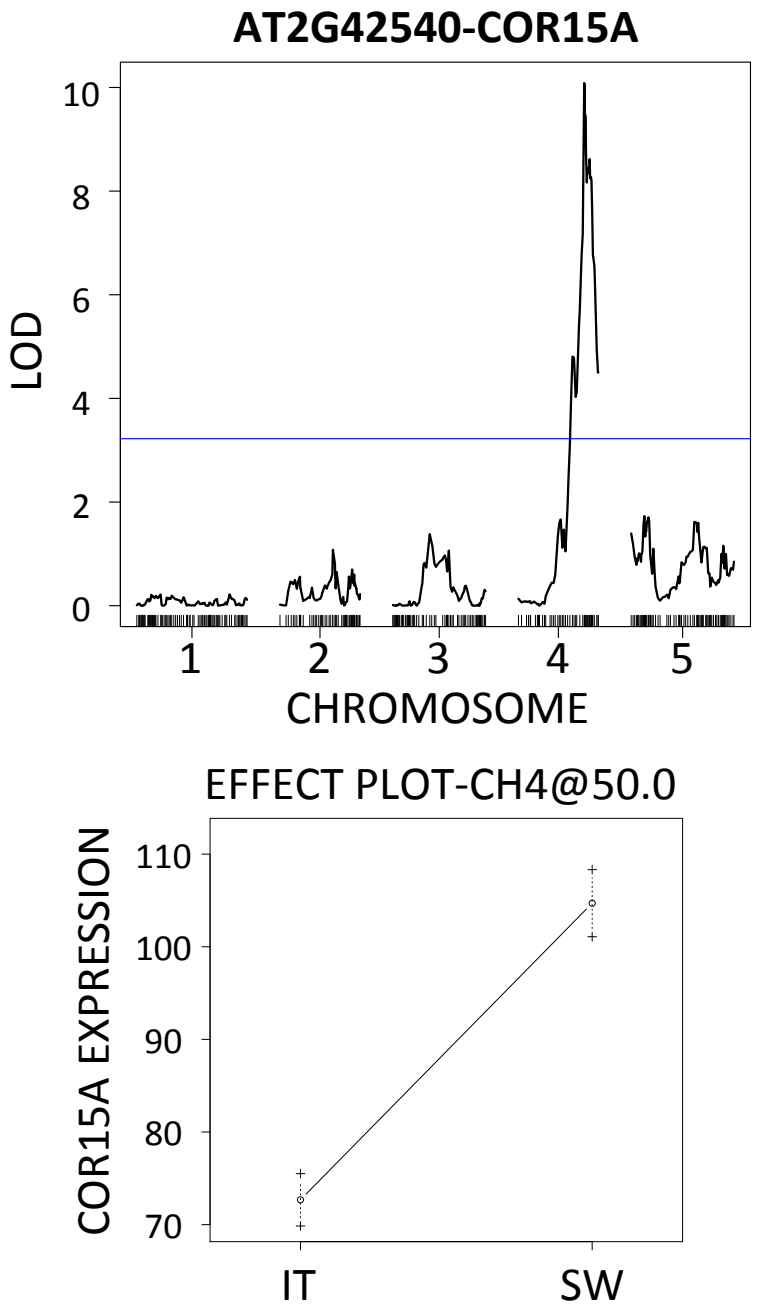


**Figure 3.38.** eQTL for Category 1 FTD gene COR15A. 544 RILs were used for eQTL mapping by qRT-PCR. RQTL (15) was used to perform interval mapping using the multiple imputation method as described by the reference manual (http://www.rqtl.org/) for each fitness trait at each location. To detect QTL, estimated genome-wide significance thresholds (**α**=0.01) for the logarithm of odds (LODs) values were calculated for each trait using 1000 permutations in RQTL (shown in blue). Effect plot represents expression averages for the genotype groups (IT or SW) at eQTL on chromosome 4. Effect plots were constructed using 'effectplot' function in R/QTL(15).

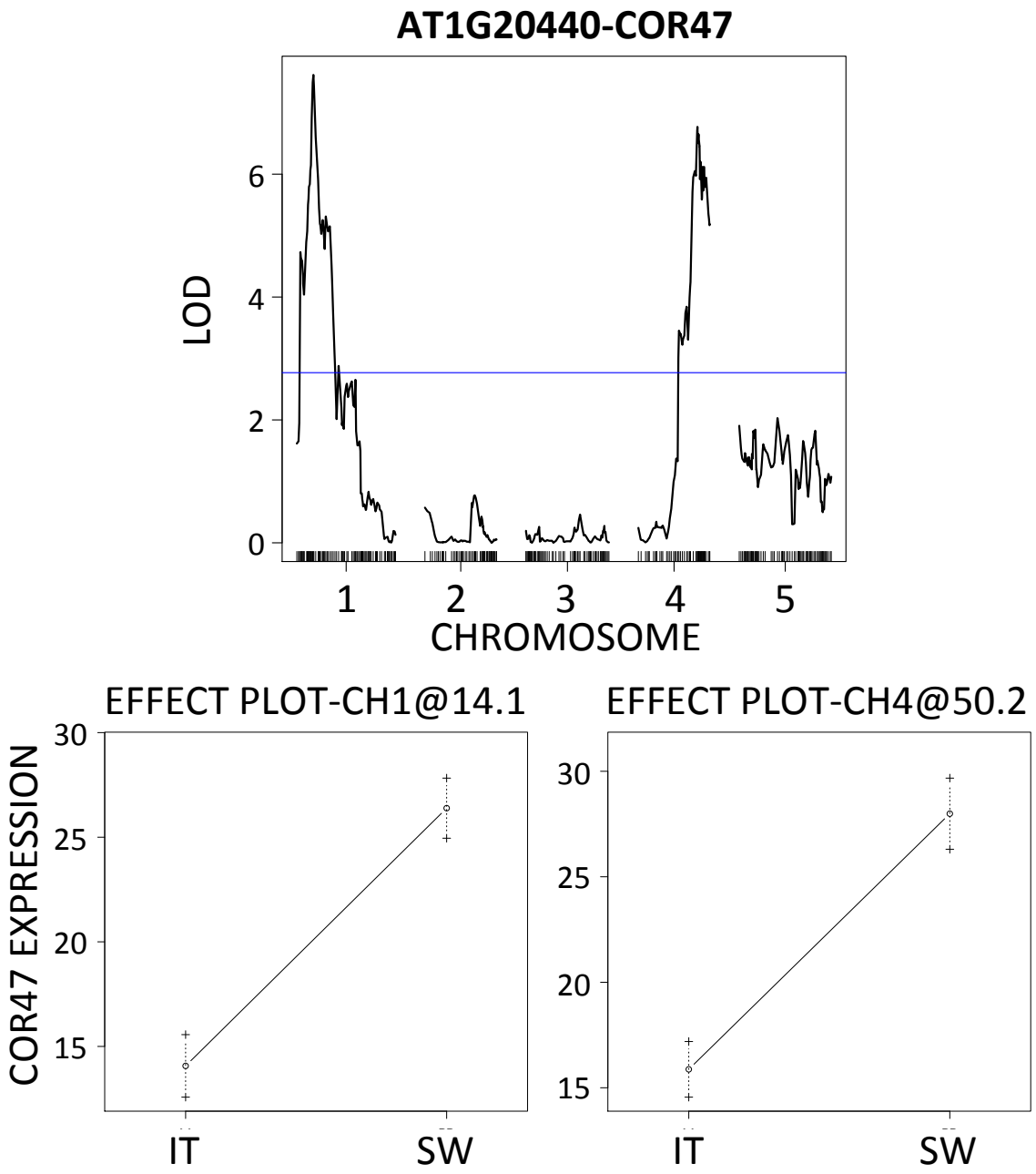


**Figure 3.39.** eQTL for Category 2 FTD gene COR47. 544 RILs were used for eQTL mapping by qRT-PCR. RQTL (15) was used to perform interval mapping using the multiple imputation method as described by the reference manual (http://www.rqtl.org/) for each fitness trait at each location. To detect QTL, estimated genome-wide significance thresholds (**α**=0.01) for the logarithm of odds (LODs) values were calculated for each trait using 1000 permutations in RQTL (shown in blue). Effect plots represent expression averages for the genotype groups (IT or SW) at eQTL on chromosome 1 and 4. Effect plots were constructed using 'effectplot' function in R/QTL(15).

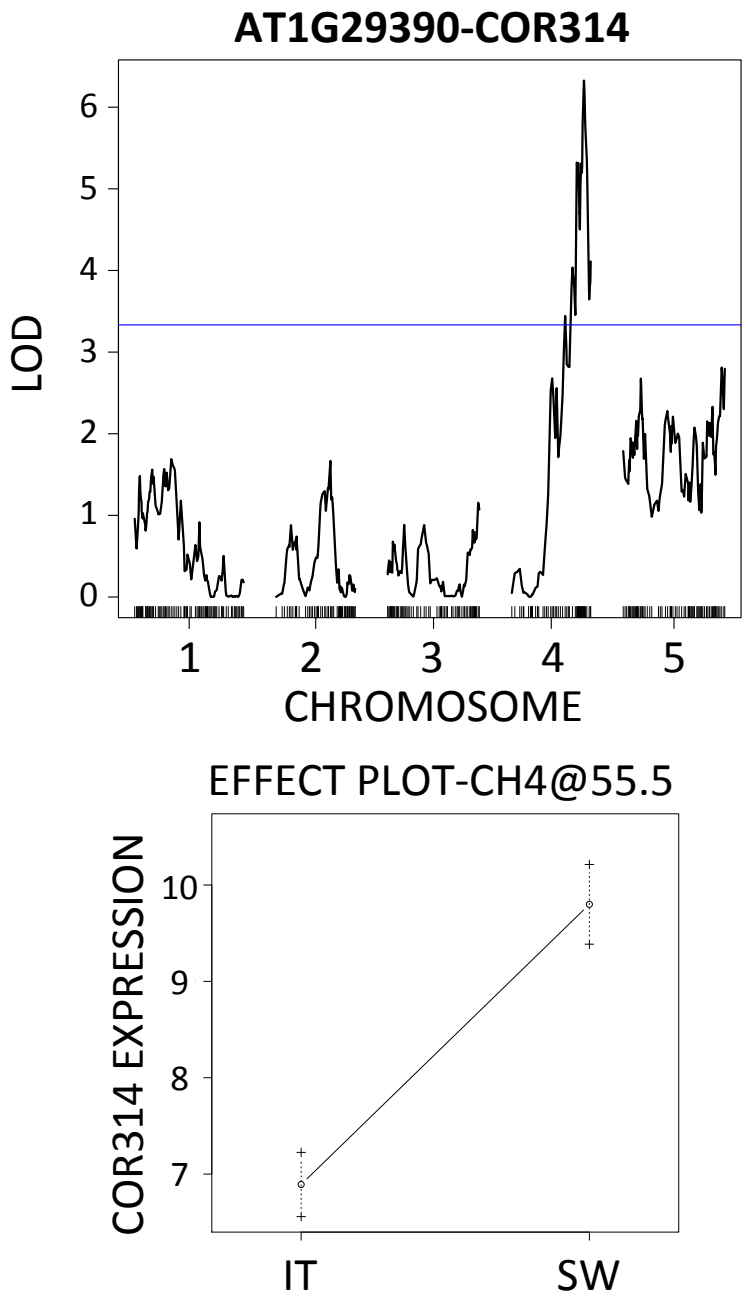


**Figure 3.40.** eQTL for Category 1 FTD gene COR314. 544 RILs were used for eQTL mapping by qRT-PCR. RQTL (15) was used to perform interval mapping using the multiple imputation method as described by the reference manual (http://www.rqtl.org/) for each fitness trait at each location. To detect QTL, estimated genome-wide significance thresholds ($\alpha$=0.01) for the logarithm of odds (LODs) values were calculated for each trait using 1000 permutations in RQTL (shown in blue). Effect plot represents expression averages for the genotype groups (IT or SW) at eQTL on chromosome 4. Effect plots were constructed using 'effectplot' function in R/QTL(15).

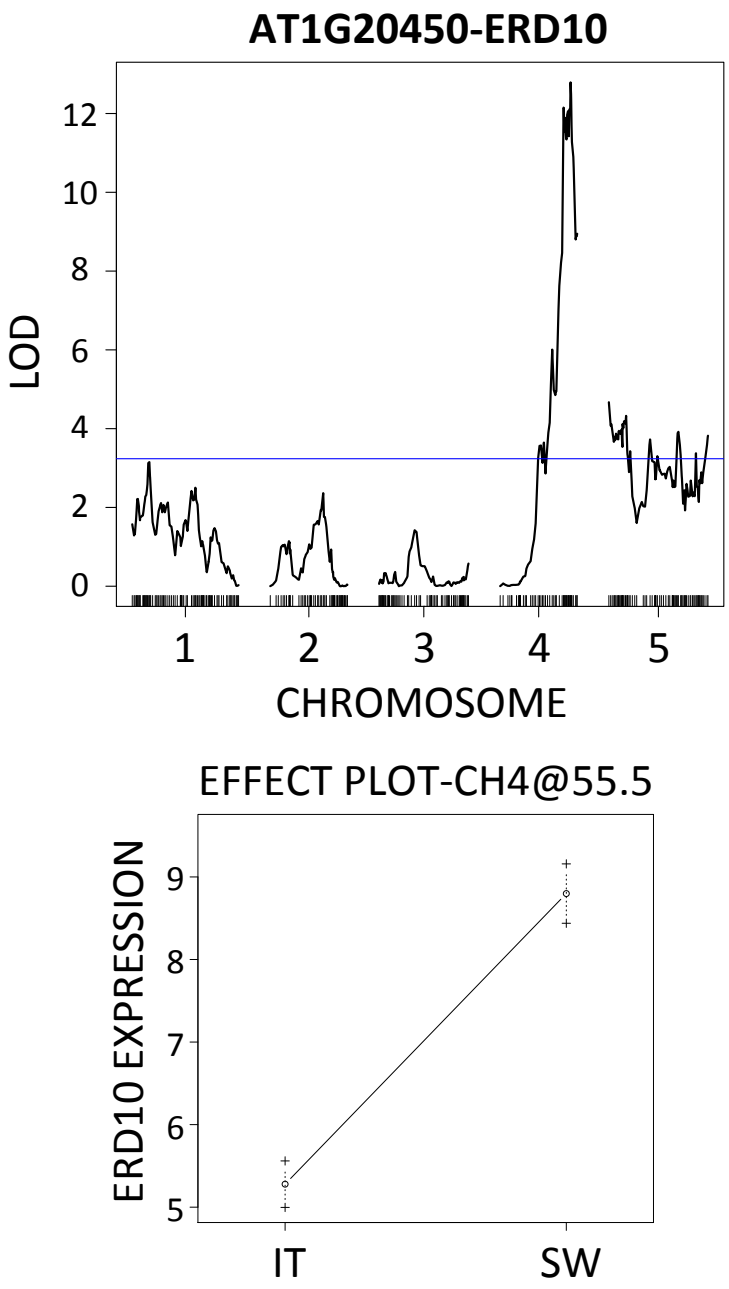


**Figure 3.41.** eQTL for Category 2 FTD gene ERD10. 544 RILs were used for eQTL mapping by qRT-PCR. RQTL (15) was used to perform interval mapping using the multiple imputation method as described by the reference manual (http://www.rqtl.org/) for each fitness trait at each location. To detect QTL, estimated genome-wide significance thresholds (**α**=0.01) for the logarithm of odds (LODs) values were calculated for each trait using 1000 permutations in RQTL (shown in blue). Effect plot represents expression averages for the genotype groups (IT or SW) at eQTL on chromosome 4. Effect plots were constructed using 'effectplot' function in R/QTL(15).

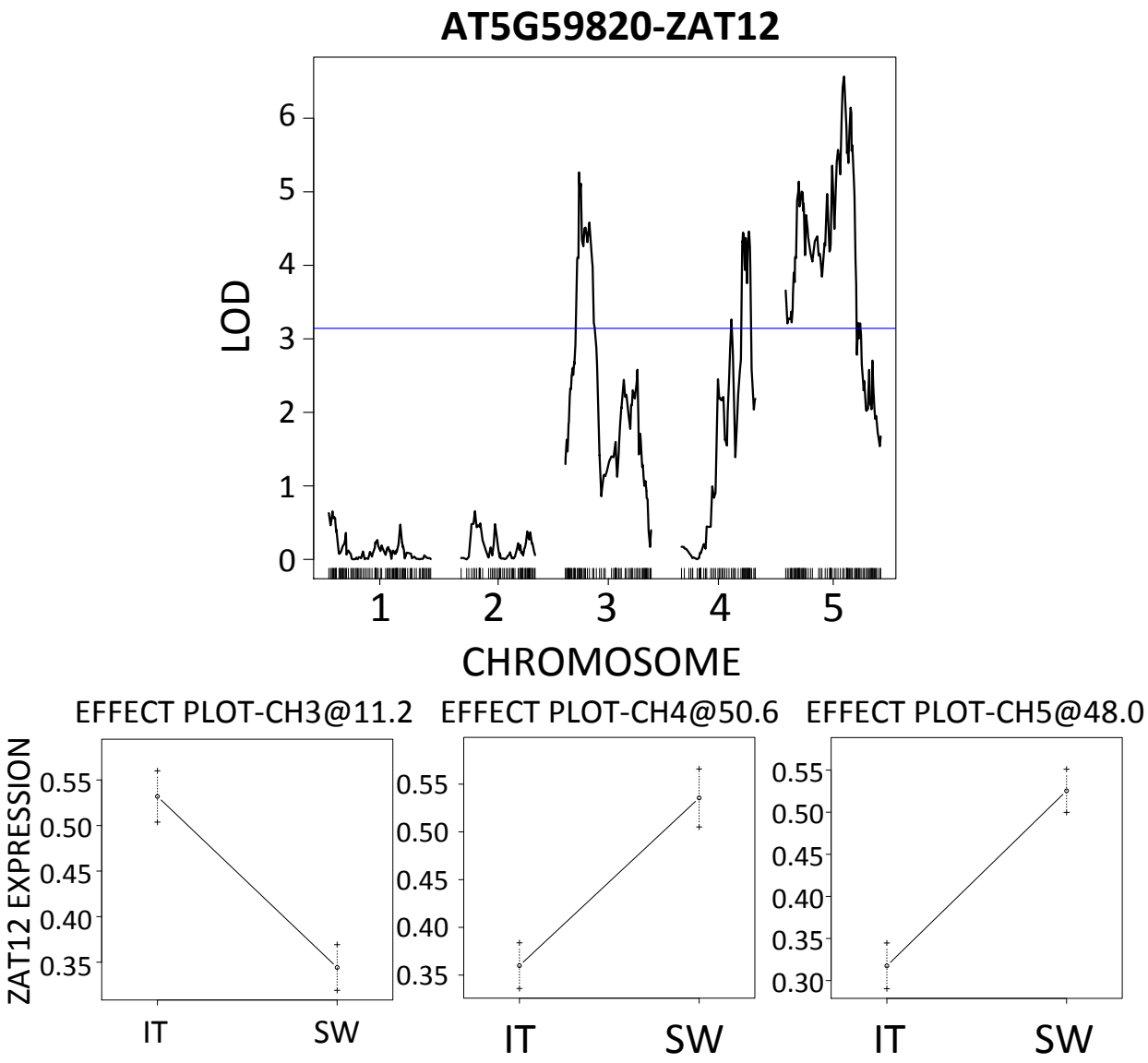


**Figure 3.42.** eQTL for Category 1 FTD gene ZAT12. 544 RILs were used for eQTL mapping by qRT-PCR. RQTL (15) was used to perform interval mapping using the multiple imputation method as described by the reference manual (http://www.rqtl.org/) for each fitness trait at each location. To detect QTL, estimated genome-wide significance thresholds (**α**=0.01) for the logarithm of odds (LODs) values were calculated for each trait using 1000 permutations in RQTL (shown in blue). Effect plots represent expression averages for the genotype groups (IT or SW) at eQTL on chromosomes 1, 4 and 5. Effect plots were constructed using 'effectplot' function in R/QTL(15).

**Table 3.20.** Expression of CBF genes. Gene expression was measured by RNA-seq. The results presented are average values from three independent experiments (n=3). Comparisons of SW and IT under non-acclimated conditions, 1 week of cold-acclimation, and 2 weeks of cold-acclimation and the corrected p-value (FDR P-VALUE) for that comparison. The comparison of each gene is also represented by the logarithm (base=2) of the fold change (LOG2FC). This table also denotes if a gene was previously described as positively or negatively correlating with freezing tolerance (HANNAH;(6)), a transcription factor (TF), a gene previously described as up- or down-regulated by 1 week of cold (COS, (24)), identified as an up- or down-regulated component of the CBF regulon (CBF REGULON; (24)). Shaded genes have significantly different expression between SW and IT at 2 weeks of cold-acclimation.

| AGI | NAME | SW.IT. NON | NON.FDR. P-VALUE | SW.IT. 1WK | 1WK.FDR. P-VALUE | SW.IT. 2WK | 2WK.FDR. P-VALUE | HANNAH? | TF? | COS? | CBF REG? |
|---|---|---|---|---|---|---|---|---|---|---|---|
| AT4G25490 | CBF1 | 1.66 | 5.32E-01 | -0.33 | 8.52E-01 | -0.73 | 2.03E-01 | POSITIVE | YES | NO | NO |
| AT4G25470 | CBF2 | 0.55 | 7.41E-01 | -0.40 | 5.24E-01 | -0.58 | 8.06E-03 | NO | YES | UP | UP |
| AT4G25480 | CBF3 | 1.76 | 2.01E-02 | -0.44 | 4.65E-01 | -0.40 | 6.84E-02 | NO | YES | UP | NO |
| AT5G51990 | CBF4 | 0.00 | 1.00E+00 | -1.96 | 3.85E-01 | 0.89 | 6.76E-01 | NO | YES | NO | NO |

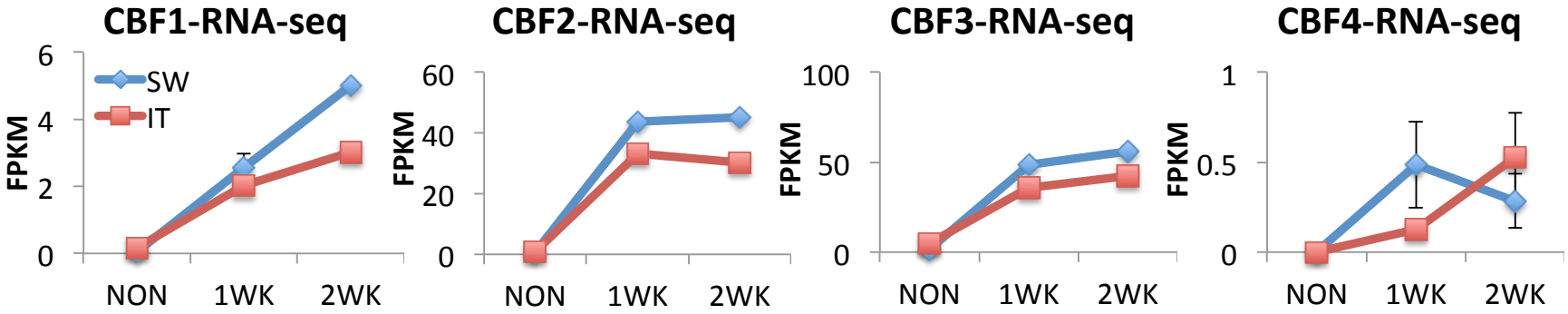


**Figure 3.43.** CBF gene expression. IT samples are shown in red, and SW in blue. Gene expression was measured by RNA-seq (FPKM). The results presented are average values from three independent experiments (n=3). Error bars indicate ±SEM. Plants were grown at 22°C under a 12 h photoperiod for approximately 18 days before rosette tissue was sampled directly or transferred to 4°C for 1 or 2 weeks under a 12 h photoperiod then sampled.

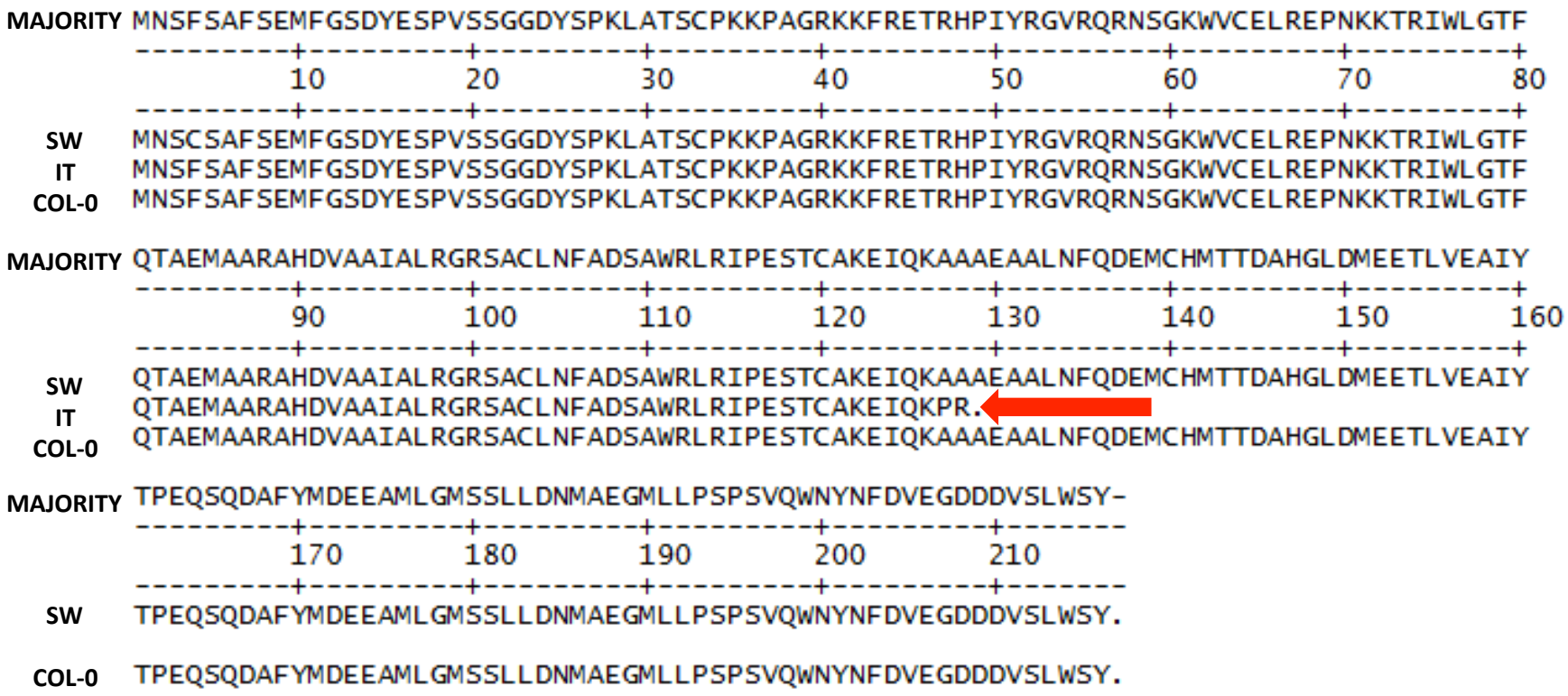


**Figure 3.44.** Protein prediction for CBF2 in SW, IT and COL-0.

## CONCLUSIONS

SW and IT ecotypes are adapted to their respective environments and both minimum winter temperature and flowering time were correlated with relative fitness of the SW and IT accessions in reciprocal transplant experiments (8). Temperature has previously been shown to be a strong selective pressure and freezing tolerance correlates with both latitude and minimum average temperature (6, 8, 17, 62). This study shows that SW and IT have significant differences in freezing tolerance at 2 weeks of cold acclimation, but not at 1 week of cold-acclimation or under non-acclimated conditions. This difference in freezing tolerance at 2 weeks of cold acclimation is due to both an increase in SW freezing tolerance as well as a reduction in IT freezing tolerance.

eQTL mapping revealed CBF2 as an excellent candidate gene to explain differences in cold-regulated gene expression and consequently freezing tolerance. Analysis of SW and IT CBF2 coding sequence exposed a 13 bp deletion in IT-CBF2 resulting in a predicted premature stop in the activation domain. Based on transcriptome and freezing tolerance analysis of a similar truncated version of CBF2, IT-CBF2 is predicted to function as a dominant negative version of CBF2. Transcriptional analyses are generally consistent with IT-CBF2 acting as a dominant negative version of CBF2, though additional experiments are needed to confirm. This is by no means the first example of CBF genes significantly contributing to differences in freezing tolerance between different accessions of *Arabidopsis* (10, 56-58). A similar premature stop in the activation domain of CBF3 was previously identified in the Condara accession, but

the effect of this truncation was not tested on CBF target genes or freezing tolerance (57). Therefore, this could possibly be the first natural example of a dominant negative version of CBF2.

The higher level of freezing tolerance in SW at 2 weeks of cold-acclimation could also be explained through *CBF2* expression, which is significantly higher than in IT at only this time-point. Therefore, the CBF2 promoter should be sequenced in SW and IT in the near future. SW photosynthetic capacity may also be greater than that of IT based on analysis of differentially regulated photosynthesis associate genes. However, photosynthetic capacity would need to be measured experimentally. Increased photosynthetic capacity is associated with higher levels of freezing tolerance, so differences in photosynthesis may also be a segregating trait between SW and IT.

Transcriptional analysis suggests that SW and IT reach similar levels of freezing tolerance at 1 week of cold-acclimation through significantly divergent transcriptional mechanisms. Both transcriptomic analysis and CBF2 sequence analysis suggest that IT may use CBF-independent mechanisms to cold-acclimate. These CBF-independent mechanisms might include genes annotated as biotic stress genes, since cold-regulated genes only found in IT were enriched in biotic stress GO terms. Biotic stress genes were also more highly expressed in IT compared to SW, regardless of cold-regulation. The mechanisms by which IT cold-acclimates do not seem to be as efficient as SW since there is a decrease in freezing tolerance at 2 weeks of cold-acclimation. I speculate that lower photosynthetic capacity in IT could be associated with the reduced number of cold-regulated genes from 1 to 2 weeks of cold-acclimation in IT, which may

synergistically combine with the dominant negative effect of IT-CBF2 to result in reduced freezing tolerance at 2 weeks of cold-acclimation.

Altogether, progress has been made towards discerning genetic differences between SW and IT that potentially contribute to differences in freezing tolerance and fitness. Other potentially segregating traits such as pathogen resistance, and photosynthetic capacity, that may contribute to fitness have also been identified. Genomic sequence of SW and IT parent lines should soon be available. This will make the RNA-seq data generated in this study more powerful, since locations of sequence differences across the SW and IT genomes will allow FTD candidate genes to be further prioritized for eQTL screening. In the near future, the Schemske lab plans to map differences in freezing tolerance in the SW and IT RILs. Based on results from this study overlap between freezing tolerance QTL and fitness QTL is expected (Table 3.1). A freezing tolerance QTL overlapping with the CBF locus is also expected. It will be interesting to see how much overlap there is between fitness and freezing tolerance QTL.

## MATERIALS AND METHODS

**Plant Material and Growth Conditions.** Swedish (SW) and Italian (IT) accessions used in this study were collected from their native habitats by members of Schemske and Agren labs (Schemske and Agren, unpublished). Recombinant inbred lines (RILs) used in this study were constructed by the Schemske lab by crossing a randomly selected individual from the SW ecotype (male parent) to a randomly selected individual from the IT ecotype (female parent), seeds from the F1 generation were used to establish a large number of lines that were selfed by single-seed descent for nine generations (Schemske and Agren, unpublished). SW and IT RILs used in this study were from the F10 generation.

All seeds were stratified for 5 days in the dark at $4^0$C. For electrolyte leakage experiments, plants were grown as described by Dong et al. 2011(16), with slight modification. Plant were germinated on plates at $22^0$C under sterile conditions on Gamborg's B5 medium (Caisson Laboratories) with 1% sucrose at ~100 $\mu$mol $m^{-2}s^{-1}$ in a 12 h photoperiod for 7 days before transfer to soil for an additional 11 days, plants were then assayed for freezing tolerance directly (non-acclimated conditions) or transferred cold-acclimated conditions for 1, 2 or 3 weeks at ~35 $\mu$mol $m^{-2}s^{-1}$ in a 12 h photoperiod. For eQTL experiments RILs were grown as described by Dong et al. 2011(16), with slight modification. RILs were germinated on plates at $22^0$C under sterile conditions on Gamborg's B5 medium (Caisson Laboratories) with 1% sucrose at ~100

$\mu$mol $m^{-2}s^{-1}$ in a 12 h photoperiod for 7 days then transfer to soil for an additional 11 days before 2 week cold treatment at ~35 $\mu$mol $m^{-2}s^{-1}$ in a 12 h photoperiod.

**Freezing Tolerance Tests.** Electrolyte leakage assays were performed as described in Dong et al. 2011(16). For cold acclimation, plants were transferred to 4$^0$C at ZT4 for 1 week, 2 weeks, or 3 weeks at ~35 $\mu$mol $m^{-2}s^{-1}$ under a 12 h photoperiod. Electrolyte leakage assays for acclimated and non-acclimated plants were started at ~ZT4 in for all biological replicates. Tissue for RNA-seq experiments described below was collected before the start of each electrolyte leakage assay.

**RNA-seq Experiments.** Randomly selected rosette tissue (three technical replicates for each biological replication) from each electrolyte leakage experiment (non-acclimated, 1 week acclimated, 2 week acclimated, 3 week acclimated) was collected for RNA-seq analysis. RNA from 3 out of the 6 biological replication sets (SW, IT, at non-acclimated, 1 week acclimated, and 2 week acclimated) was chosen at random for further analysis. RNA was isolated as described in Dong et al. 2011 (16) from 2 technical replicates from selected biological replications; one technical replication was used for qRT-PCR analysis experiments and the other was submitted for RNA-seq analysis at MSU's Research Technology Support Facility (RTSF).

For qRT-PCR analysis, cDNA was made as described in Dong et al. 2011 (16). Expression of known cold-induced genes (CBF1, CBF2, CBF3, COR15A, COR47,

COR78) was tested using qRT-PCR (Applied Biosystems 7500 FAST Real-Time PCR System in FAST mode) as a means of ensuring that submitted RNA-seq samples were responding to cold. IPP2 (AT3G02780) was used as a reference gene.

For RNA-seq samples RNA quality was determined by an Agilent 2100 Bioanalyzer using manufacturer protocols ((Agilent RNA 6000 Nano Kit, Cat. 5067-1511, Agilent Technologies, Santa Clara, CA, USA). Sequencing was performed on an Illumina Genome Analyzer II (GA II). Like-treated samples (i.e. 3 biological replicates of SW and IT non-acclimated samples) were multiplexed in two lanes resulting in single-end reads ~75 bp in length with an average of 45,257,092 reads passing the Illumina purity filters for each sample (please see Table A3.8 for details). Sample preparation, including mRNA purification, cDNA preparation, end repair of cDNA, adaptor ligation, and cDNA amplification, was performed by MSU RTSF and conducted according to the manufacturer protocols (mRNA-Seq Sample Preparation Kit, Cat. RS-930-1001, Illumina Inc., San Diego, CA, USA).

**RNA-seq Analysis.** SW and IT RNA-seq data was aligned to TAIR10 sequence using Tophat (18). For Tophat, minimum intron length was set to 7 bp and maximum intron length was set to 12000 bp, all other parameters were set to defaults (18). Cufflinks was used to estimate transcript abundance based on unique reads in order to address the challenges associated with 'multi-mapping reads' (63), rRNA was also masked to improve robustness of transcript abundance estimates, all other parameters were set to default values (18). When comparing treatments for differential expression,

the cuffdiff program within Cufflinks was used for pairwise comparisons with default settings (18). Cuffdiff assigns p-values based a two-tailed Student's t-test; this value is then adjusted using a Benjamini-Hochberg correction for 'multiple-testing'(18).

While analyzing differentially expressed genes in RNA-seq data, a cut-off of ≥3FPKM was used for differentially expressed genes (19, 20). This means that, when treatments were compared, one value in the comparison had to be ≥3FPKM. When testing for significant overlap between two sets of genes, a hypergeometric probability was calculated using the 'stats' package in R (64). Gene ontology (GO) enrichment was determined using the database for annotation visualization and integrated discovery tool (DAVID; **david**.abcc.ncifcrf.gov; (27)). The default DAVID gene ontology settings 'GOTERM_BP_FAT', 'GOTERM_MF_FAT', and 'GOTERM_CC_FAT' were used for analysis (27). GO category was considered significantly enriched if its Benjamini-Hochberg corrected (FDR corrected) hypergeometric p-value was <0.050.

**eQTL Experiments.** RIL seed stratification, germination, and movement to low temperature conditions was staggered to allow all RILs to be grown then cold acclimated in the same set of growth chambers and to ensure that a manageable number of RILs, at the same age, could be samples within an hour. Plant tissue was collected and quickly frozen in liquid nitrogen between ZT4-ZT5 after 2 weeks of cold acclimation. RNA extraction and cDNA synthesis for RILs was performed as described by Dong et al. 2011(16). These samples were tested for expression of 10 Freezing Tolerance Difference (FTD) candidate genes (see Table 3.17) by qRT-PCR (Applied

Biosystems 7500 FAST Real-Time PCR System in FAST mode) with IPP2 (AT3G02780) as a housekeeping gene. All primer sets can be found in Table A3.7.

**eQTL Mapping and Analysis.** SW and IT parent lines were sequenced by the Schemske lab using the Illumina GAII platform. Paired end reads were mapped to the COL-0 reference sequence (TAIRv9) and approximately 141,437 single nucleotide polymorphisms (SNPs) were found (Schemske, unpublished). 384 of these SNPs with an average spacing of ~1.1 cm across the *Arabidopsis* genome were selected to genotype the RIL population (Schemske, unpublished). Expression data for the10 FTD candidate genes generated during the eQTL experiments described above was used to map eQTL over these 384 markers. RQTL (15) was used to perform interval mapping using the multiple imputation method as described by the reference manual (http://www.rqtl.org/). To detect QTL, estimated genome-wide significance thresholds ($\alpha$=0.01 and $\alpha$=0.05) for the logarithm of odds (LOD) values were calculated for each FTD gene of interest using 1000 permutations in RQTL. To estimate the location of each QTL both a Bayes credible interval (99%) and LOD support interval were calculated in RQTL. The SeqViewer tool on TAIR (www.arabidopsis.org) was used to identify all genes within the QTL interval and this list was compared to SW and IT RNA-seq data described above to find candidate transcription factors.

**CBF sequencing.** Genomic DNA was extracted from SW, IT and COL-0 using a QIAGEN DNeasy Plant Mini Kit using manufacturer protocols (Cat. 69104, Qiagen,

Valencia, CA). CBF1-3, COR78, COR15A and COR47 coding sequences were amplified by PCR using TaKaRa LA Taq Hot-Start DNA Polymerase (Cat. RR042A, Mountain View, CA). Primers used to amplify CBF1, 2 and 3 coding sequence in SW, IT and Col-0, can be found in Table A3.8. PCR products were cloned into PCR2.1-TOPO, transformed into *E. coli* competent cells, and screened using manufacturer protocols (Cat. K4500-02, Invitrogen, Carlsbad, CA). Selected clones were sequenced by MSU RTSF. Sequence alignment was performed using the Lasergene Suite of tools (www.dnastar.com).

**ACKNOWLEDGEMENTS**

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# APPENDIX

**Table A3.1.** SW and IT markers used for mapping both fitness QTL and eQTL. Marker locations in centimorgans (CM), and marker locations in megabases (MB) based on the Col-0 genome.

| CHROMOSOME | MARKER (CM) | MARKER LOCATIONS (MB) |
|---|---|---|
| 1 | 0 | 0.371484 |
| 1 | 1.422 | 0.658928 |
| 1 | 2.075 | 0.95079 |
| 1 | 3.013 | 1.247666 |
| 1 | 3.384 | 1.545309 |
| 1 | 3.943 | 1.831853 |
| 1 | 4.408 | 2.112359 |
| 1 | 5.25 | 2.402241 |
| 1 | 5.343 | 2.689578 |
| 1 | 6.112 | 2.97831 |
| 1 | 6.206 | 3.270056 |
| 1 | 8.36 | 4.139064 |
| 1 | 8.842 | 4.434414 |
| 1 | 9.507 | 4.716592 |
| 1 | 9.916 | 5.008647 |
| 1 | 10.312 | 5.305697 |
| 1 | 11.03 | 5.588245 |
| 1 | 11.501 | 5.876257 |
| 1 | 11.97 | 6.486531 |
| 1 | 12.636 | 6.750734 |
| 1 | 13.483 | 7.043318 |
| 1 | 14.053 | 7.332032 |
| 1 | 14.525 | 7.621705 |
| 1 | 16.069 | 7.906548 |
| 1 | 18.117 | 8.199225 |
| 1 | 18.877 | 8.511642 |
| 1 | 19.638 | 8.846085 |
| 1 | 20.792 | 9.081675 |
| 1 | 21.941 | 9.389545 |
| 1 | 22.704 | 9.64586 |
| 1 | 23.652 | 9.948571 |
| 1 | 24.623 | 10.232305 |
| 1 | 25.681 | 10.517662 |
| 1 | 26.545 | 10.817536 |
| 1 | 28.103 | 11.101365 |
| 1 | 29.502 | 11.402119 |
| 1 | 30.882 | 11.697338 |
| 1 | 32.413 | 11.966262 |
| 1 | 33.796 | 12.344267 |
| 1 | 35.512 | 12.843656 |
| 1 | 37.885 | 13.156629 |
| 1 | 38.268 | 13.451072 |
| 1 | 38.363 | 13.753592 |
| 1 | 38.459 | 14.004113 |
| 1 | 38.459 | 15.522314 |
| 1 | 38.554 | 15.889605 |
| 1 | 39.911 | 16.136207 |
| 1 | 40.59 | 16.445556 |

**Table A3.1 (cont'd)**

| | | |
|---|---|---|
| 1 | 42.502 | 16.923537 |
| 1 | 43.493 | 17.203021 |
| 1 | 46.721 | 17.775164 |
| 1 | 47.977 | 18.059668 |
| 1 | 48.931 | 18.352147 |
| 1 | 49.788 | 18.65907 |
| 1 | 50.352 | 18.926903 |
| 1 | 51.496 | 19.240146 |
| 1 | 52.543 | 19.529287 |
| 1 | 53.291 | 19.800653 |
| 1 | 54.325 | 20.108938 |
| 1 | 54.603 | 20.38011 |
| 1 | 55.197 | 20.668556 |
| 1 | 55.601 | 20.964571 |
| 1 | 55.904 | 21.251788 |
| 1 | 56.275 | 21.551115 |
| 1 | 57.347 | 22.152521 |
| 1 | 58.632 | 22.412767 |
| 1 | 58.823 | 22.723886 |
| 1 | 60.236 | 22.988965 |
| 1 | 60.984 | 23.292064 |
| 1 | 61.076 | 23.580047 |
| 1 | 61.824 | 23.857523 |
| 1 | 62.477 | 24.155803 |
| 1 | 63.146 | 24.435268 |
| 1 | 64.88 | 24.765127 |
| 1 | 66.846 | 25.032697 |
| 1 | 67.637 | 25.324254 |
| 1 | 68.419 | 25.609182 |
| 1 | 70.447 | 25.889912 |
| 1 | 71.997 | 26.181454 |
| 1 | 74.435 | 26.760155 |
| 1 | 75.399 | 27.057077 |
| 1 | 76.971 | 27.352821 |
| 1 | 77.163 | 27.626189 |
| 1 | 77.86 | 27.917735 |
| 1 | 78.551 | 28.220678 |
| 1 | 79.56 | 28.509198 |
| 1 | 80.38 | 28.806377 |
| 1 | 80.886 | 29.077284 |
| 1 | 82.142 | 29.384089 |
| 1 | 83.088 | 29.659444 |
| 1 | 83.845 | 30.245282 |
| 2 | 0 | 0.365473 |
| 2 | 4.606 | 0.661681 |
| 2 | 6.33 | 0.954162 |
| 2 | 8.55 | 1.258538 |
| 2 | 10.17 | 1.532339 |
| 2 | 11.4 | 1.871886 |
| 2 | 12.822 | 2.135186 |
| 2 | 14.736 | 2.433194 |
| 2 | 15.107 | 4.621443 |

**Table A3.1 (cont'd)**

| | | |
|---|---|---|
| 2 | 15.2 | 5.049931 |
| 2 | 15.48 | 5.295348 |
| 2 | 15.761 | 5.587569 |
| 2 | 17.687 | 5.95692 |
| 2 | 22.613 | 6.764214 |
| 2 | 24.312 | 7.047117 |
| 2 | 25.601 | 7.340228 |
| 2 | 26.841 | 7.626054 |
| 2 | 27.893 | 7.920385 |
| 2 | 29.449 | 8.197294 |
| 2 | 30.714 | 8.502011 |
| 2 | 31.706 | 8.779839 |
| 2 | 31.992 | 9.065286 |
| 2 | 32.589 | 9.36707 |
| 2 | 34.308 | 9.647248 |
| 2 | 35.592 | 9.940989 |
| 2 | 37.365 | 10.225771 |
| 2 | 38.247 | 10.536215 |
| 2 | 39.837 | 10.837886 |
| 2 | 40.254 | 11.106932 |
| 2 | 41.761 | 11.38934 |
| 2 | 42.345 | 11.679435 |
| 2 | 43.114 | 11.966391 |
| 2 | 44.28 | 12.267422 |
| 2 | 46.948 | 12.547427 |
| 2 | 48.042 | 12.838094 |
| 2 | 48.734 | 13.135793 |
| 2 | 49.409 | 13.420085 |
| 2 | 49.516 | 13.716369 |
| 2 | 49.704 | 13.995766 |
| 2 | 50.366 | 14.319012 |
| 2 | 50.646 | 14.575482 |
| 2 | 51.02 | 14.868193 |
| 2 | 52.453 | 15.16817 |
| 2 | 53.036 | 15.447154 |
| 2 | 53.415 | 15.747054 |
| 2 | 54.399 | 16.06694 |
| 2 | 54.885 | 16.319037 |
| 2 | 55.269 | 16.60741 |
| 2 | 56.022 | 16.898396 |
| 2 | 56.402 | 17.18517 |
| 2 | 56.779 | 17.476046 |
| 2 | 56.874 | 17.779 |
| 2 | 58.025 | 18.063832 |
| 2 | 58.313 | 18.358707 |
| 2 | 58.594 | 18.639532 |
| 2 | 59.444 | 18.932927 |
| 2 | 60.487 | 19.233555 |
| 2 | 60.86 | 19.529865 |
| 3 | 0 | 0.370926 |
| 3 | 0.094 | 0.656579 |
| 3 | 1.032 | 0.961179 |

**Table A3.1 (cont'd)**

| | | |
|---|---|---|
| 3 | 1.688 | 1.270326 |
| 3 | 2.155 | 1.525377 |
| 3 | 2.533 | 1.825965 |
| 3 | 2.82 | 2.112696 |
| 3 | 3.487 | 2.398036 |
| 3 | 3.96 | 2.692472 |
| 3 | 4.523 | 2.975352 |
| 3 | 5.092 | 3.269092 |
| 3 | 6.349 | 3.565378 |
| 3 | 7.208 | 4.141096 |
| 3 | 7.313 | 4.427835 |
| 3 | 8.176 | 4.718296 |
| 3 | 9.637 | 5.295658 |
| 3 | 10.681 | 5.619526 |
| 3 | 11.184 | 5.875889 |
| 3 | 11.853 | 6.175656 |
| 3 | 12.641 | 6.457498 |
| 3 | 13.533 | 6.74919 |
| 3 | 14.728 | 7.051377 |
| 3 | 15.618 | 7.329844 |
| 3 | 16.51 | 7.628106 |
| 3 | 18.033 | 7.914025 |
| 3 | 19.705 | 8.200995 |
| 3 | 22.343 | 8.497891 |
| 3 | 23.319 | 8.776721 |
| 3 | 25.381 | 9.13927 |
| 3 | 28.021 | 9.654017 |
| 3 | 29.512 | 9.940341 |
| 3 | 31.527 | 10.234401 |
| 3 | 32.697 | 10.587664 |
| 3 | 37.858 | 11.114247 |
| 3 | 39.55 | 11.399488 |
| 3 | 40.641 | 11.747164 |
| 3 | 41.121 | 12.041893 |
| 3 | 41.309 | 12.56772 |
| 3 | 41.402 | 15.210147 |
| 3 | 42.553 | 15.514979 |
| 3 | 43.813 | 15.759118 |
| 3 | 44.974 | 16.058567 |
| 3 | 45.949 | 16.36229 |
| 3 | 49.119 | 16.648133 |
| 3 | 50.183 | 16.899341 |
| 3 | 51.952 | 17.225206 |
| 3 | 53.323 | 17.486181 |
| 3 | 54.095 | 17.781386 |
| 3 | 54.672 | 18.077874 |
| 3 | 55.367 | 18.350962 |
| 3 | 57.064 | 18.651512 |
| 3 | 58.618 | 18.955604 |
| 3 | 59.188 | 19.220884 |
| 3 | 60.383 | 19.514107 |
| 3 | 61.53 | 19.799867 |

**Table A3.1 (cont'd)**

| | | |
|---|---|---|
| 3 | 63.124 | 20.092191 |
| 3 | 63.604 | 20.401811 |
| 3 | 64.18 | 20.665136 |
| 3 | 64.928 | 20.960795 |
| 3 | 65.487 | 21.25848 |
| 3 | 65.858 | 21.558962 |
| 3 | 66.606 | 21.840004 |
| 3 | 66.791 | 22.14465 |
| 3 | 67.54 | 22.441322 |
| 3 | 68.386 | 22.70487 |
| 3 | 69.618 | 22.986945 |
| 3 | 70.466 | 23.275556 |
| 4 | 0 | 0.384888 |
| 4 | 2.329 | 0.680041 |
| 4 | 6.129 | 0.982791 |
| 4 | 7.648 | 1.238231 |
| 4 | 8.975 | 1.535171 |
| 4 | 9.255 | 2.717267 |
| 4 | 12.891 | 2.396469 |
| 4 | 14.399 | 2.133635 |
| 4 | 15.265 | 1.828832 |
| 4 | 15.674 | 3.900172 |
| 4 | 15.767 | 5.080132 |
| 4 | 18.335 | 5.587712 |
| 4 | 19.776 | 5.924099 |
| 4 | 20.73 | 6.171429 |
| 4 | 24.028 | 6.498644 |
| 4 | 25.332 | 6.754691 |
| 4 | 26.733 | 7.042854 |
| 4 | 27.984 | 7.346579 |
| 4 | 29.948 | 7.616384 |
| 4 | 31.047 | 7.918274 |
| 4 | 32.149 | 8.211444 |
| 4 | 33.418 | 8.498174 |
| 4 | 34.491 | 8.815569 |
| 4 | 35.766 | 9.140013 |
| 4 | 37.38 | 9.650672 |
| 4 | 39.077 | 9.942702 |
| 4 | 41.05 | 10.236673 |
| 4 | 42.292 | 10.522219 |
| 4 | 43.507 | 10.831675 |
| 4 | 44.312 | 11.15739 |
| 4 | 46.649 | 11.714851 |
| 4 | 48.883 | 12.292822 |
| 4 | 50.004 | 12.5471 |
| 4 | 50.195 | 12.843072 |
| 4 | 50.574 | 13.151997 |
| 4 | 51.142 | 13.421012 |
| 4 | 51.331 | 13.720933 |
| 4 | 51.993 | 14.008832 |
| 4 | 52.369 | 14.292115 |
| 4 | 52.847 | 14.584632 |

**Table A3.1 (cont'd)**

| | | |
|---|---|---|
| 4 | 53.543 | 14.869919 |
| 4 | 53.935 | 15.162178 |
| 4 | 54.131 | 15.450267 |
| 4 | 54.523 | 15.735751 |
| 4 | 55.222 | 16.026122 |
| 4 | 55.523 | 16.337059 |
| 4 | 55.916 | 16.606958 |
| 4 | 56.299 | 16.90214 |
| 4 | 56.593 | 17.202249 |
| 4 | 57.696 | 17.486207 |
| 4 | 59.526 | 17.796648 |
| 4 | 60.435 | 18.063371 |
| 4 | 60.721 | 18.347312 |
| 5 | 0 | 0.367158 |
| 5 | 1.428 | 0.655985 |
| 5 | 2.63 | 0.949897 |
| 5 | 3.939 | 1.245151 |
| 5 | 4.594 | 1.528949 |
| 5 | 4.913 | 1.839919 |
| 5 | 5.695 | 2.111365 |
| 5 | 6.678 | 2.408921 |
| 5 | 7.459 | 2.685965 |
| 5 | 7.652 | 2.985496 |
| 5 | 8.525 | 3.270887 |
| 5 | 9.384 | 3.57043 |
| 5 | 10.048 | 3.852246 |
| 5 | 10.434 | 4.13647 |
| 5 | 10.717 | 4.426649 |
| 5 | 10.811 | 4.726262 |
| 5 | 11.39 | 5.013068 |
| 5 | 11.972 | 5.336868 |
| 5 | 13.126 | 5.656316 |
| 5 | 13.602 | 5.889105 |
| 5 | 14.471 | 6.473301 |
| 5 | 14.668 | 6.752582 |
| 5 | 14.963 | 7.071294 |
| 5 | 15.919 | 7.334179 |
| 5 | 16.811 | 7.618492 |
| 5 | 18.508 | 7.914975 |
| 5 | 20.419 | 8.232952 |
| 5 | 21.967 | 8.569949 |
| 5 | 27.139 | 9.0801 |
| 5 | 28.533 | 9.376062 |
| 5 | 29.833 | 9.6691 |
| 5 | 32.507 | 9.969215 |
| 5 | 34.144 | 10.233797 |
| 5 | 36.082 | 10.639041 |
| 5 | 36.645 | 10.929784 |
| 5 | 36.738 | 11.415254 |
| 5 | 37.016 | 13.106228 |
| 5 | 38.26 | 13.707451 |
| 5 | 40.107 | 14.015641 |

**Table A3.1 (cont'd)**

| | | |
|---|---|---|
| 5 | 41.4 | 14.545953 |
| 5 | 43.043 | 14.876427 |
| 5 | 44.949 | 15.185072 |
| 5 | 46.891 | 15.464485 |
| 5 | 48.063 | 15.768401 |
| 5 | 49.947 | 16.043932 |
| 5 | 50.244 | 16.326685 |
| 5 | 50.244 | 16.611838 |
| 5 | 50.244 | 16.897426 |
| 5 | 50.45 | 17.196046 |
| 5 | 50.962 | 17.503065 |
| 5 | 51.576 | 17.787766 |
| 5 | 52.441 | 18.072654 |
| 5 | 53.407 | 18.382907 |
| 5 | 54.267 | 18.640297 |
| 5 | 54.836 | 18.926019 |
| 5 | 56.611 | 19.227434 |
| 5 | 57.476 | 19.550188 |
| 5 | 57.664 | 19.797944 |
| 5 | 58.578 | 20.09524 |
| 5 | 59.597 | 20.390151 |
| 5 | 60.101 | 20.67101 |
| 5 | 60.596 | 20.961565 |
| 5 | 61.278 | 21.249178 |
| 5 | 62.603 | 21.548963 |
| 5 | 64.099 | 21.864028 |
| 5 | 64.62 | 22.116026 |
| 5 | 66.055 | 22.406706 |
| 5 | 66.456 | 22.711593 |
| 5 | 67.732 | 23.006666 |
| 5 | 68.693 | 23.277096 |
| 5 | 69.359 | 23.580206 |
| 5 | 70.123 | 23.87063 |
| 5 | 70.596 | 24.172305 |
| 5 | 70.983 | 24.444383 |
| 5 | 71.373 | 24.725353 |
| 5 | 72.063 | 25.017566 |
| 5 | 72.931 | 25.350635 |
| 5 | 73.61 | 25.599724 |
| 5 | 74.474 | 25.889576 |
| 5 | 75.802 | 26.180944 |
| 5 | 77.422 | 26.468215 |
| 5 | 78.174 | 26.757861 |

**Table A3.2.** GO categories of Hannah genes positively (277 genes) and negatively (466 genes) correlated with freezing tolerance (6). GO enrichment was determined using DAVID (**david**.abcc.ncifcrf.gov; (27)). 'GO TERM CATEGORY' denotes if the GO term was categorized as a biological process (BP), cellular component (CC), or molecular function (MF) in the DAVID database. '# HITS' denotes the number of genes with that GO category in Hannah genes positively (277 genes) and negatively (466 genes) correlated with freezing tolerance. '# GENES IN GO' denotes the total number of genes in that GO category included in the DAVID database. GO category was considered significantly enriched if the FDR corrected hypergeometric p-value was ≤0.050.

| GO TERM CATEGORY | HANNAH POSITIVE (277GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| BP | Response To Water Deprivation | 16 | 176 | 2.68E-07 |
| BP | Response To Abiotic Stimulus | 34 | 1197 | 1.22E-04 |
| BP | Response To Cold | 11 | 233 | 3.66E-02 |
| BP | Response To Oxidative Stress | 12 | 287 | 3.82E-02 |
| BP | Carbohydrate Biosynthetic Process | 11 | 254 | 4.13E-02 |
| BP | Response To Osmotic Stress | 14 | 399 | 4.43E-02 |

| GO TERM CATEGORY | HANNAH NEGATIVE (466 GENES) | # HITS | # GENES IN GO | FDR P-VALUE |
|---|---|---|---|---|
| CC | Chloroplast | 225 | 3192 | 3.34E-51 |
| CC | Thylakoid | 80 | 491 | 1.27E-37 |
| CC | Photosynthetic Membrane | 56 | 330 | 7.22E-27 |
| MF | rRNA Binding | 21 | 76 | 4.55E-15 |
| CC | Organelle Membrane | 65 | 849 | 8.10E-13 |
| MF | Structural Constituent Of Ribosome | 32 | 394 | 6.55E-09 |
| MF | Structural Molecule Activity | 37 | 538 | 1.04E-08 |
| CC | Ribosome | 38 | 470 | 5.16E-08 |
| BP | Photosynthesis | 18 | 175 | 7.19E-05 |
| BP | Chlorophyll Biosynthetic Process | 8 | 34 | 1.69E-03 |
| BP | Pigment Metabolic Process | 11 | 101 | 4.09E-03 |
| BP | Nitrogen Compound Biosynthetic Process | 26 | 506 | 4.52E-03 |
| BP | Tetrapyrrole Biosynthetic Process | 8 | 50 | 5.27E-03 |
| CC | Anchored To Plasma Membrane | 8 | 66 | 1.11E-02 |
| CC | NAD(P)H Dehydrogenase Complex | 4 | 10 | 1.14E-02 |
| BP | Porphyrin Metabolic Process | 8 | 61 | 1.71E-02 |
| BP | Response To Cold | 15 | 233 | 1.81E-02 |
| BP | Heterocycle Biosynthetic Process | 11 | 132 | 2.06E-02 |
| BP | Ribosome Biogenesis | 15 | 242 | 2.27E-02 |
| CC | Non-Membrane-Bounded Organelle | 46 | 1144 | 4.37E-02 |

**Table A3.3**. 474 Category 1 FTD Candidate Genes with higher expression in SW at 2 weeks of cold-acclimation. Genes are ordered by their AGI numbers. FPKM values are the average of three biological replicates (n=3). Standard error (SE) values are also given for each FPKM value. Genes were considered significantly different between SW and IT under non-acclimated conditions if they had a Benjamini-Hochberg corrected p-value (FDR P-VALUE) of <0.05 and a minimum of ≥3FPKM in IT. The differential expression of each gene is also represented by the logarithm (base=2) of the fold change (LOG2.FC). This table also denotes if a gene was previously described as positively or negatively correlating with freezing tolerance (HANNAH;(6)), a transcription factor (TF), a gene previously described as up- or down-regulated by 1 week of cold (COS, (25)), identified as an up- or down-regulated component of the CBF regulon (CBF REGULON; (25)).

| AGI | SW.2WK FPKM | SW.2WK SE | IT.2WK FPKM | IT.2WK SE | SW.IT.2WK LOG2FC | SW.IT.2WK FDR P-VALUE | HANNAH? | TF? | COS? | CBF REG? |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G01210 | 25.47 | 0.77 | 14.97 | 0.99 | -0.77 | 1.60E-02 | NO | NO | NO | NO |
| AT1G01640 | 10.27 | 0.35 | 6.01 | 0.37 | -0.77 | 4.09E-02 | NO | NO | NO | NO |
| AT1G02300 | 30.44 | 0.44 | 20.14 | 0.38 | -0.60 | 6.08E-03 | NO | NO | NO | NO |
| AT1G02460 | 17.43 | 0.27 | 10.21 | 0.22 | -0.77 | 3.71E-04 | NO | NO | UP | NO |
| AT1G03310 | 36.19 | 1.34 | 25.42 | 0.39 | -0.51 | 1.53E-03 | NO | NO | NO | NO |
| AT1G04240 | 61.42 | 1.64 | 35.21 | 0.91 | -0.80 | 2.00E-05 | NO | YES | NO | NO |
| AT1G04350 | 20.72 | 0.41 | 14.58 | 0.65 | -0.51 | 3.30E-02 | NO | NO | DOWN | NO |
| AT1G04570 | 132.07 | 1.41 | 40.21 | 0.74 | -1.72 | 0.00E+00 | NO | NO | NO | NO |
| AT1G04620 | 75.99 | 0.87 | 52.13 | 0.61 | -0.54 | 3.74E-03 | NO | NO | NO | NO |
| AT1G06360 | 67.20 | 1.07 | 44.29 | 2.60 | -0.60 | 1.52E-03 | NO | NO | NO | NO |
| AT1G06700 | 59.72 | 0.38 | 40.10 | 1.11 | -0.57 | 4.17E-04 | NO | NO | NO | NO |
| AT1G06980 | 16.78 | 0.31 | 6.63 | 0.48 | -1.34 | 6.39E-05 | NO | NO | NO | NO |
| AT1G07200 | 12.97 | 0.13 | 9.36 | 0.30 | -0.47 | 1.02E-02 | NO | NO | NO | NO |
| AT1G07280 | 131.04 | 0.92 | 96.96 | 0.44 | -0.43 | 5.00E-03 | NO | NO | NO | NO |
| AT1G08500 | 10.71 | 0.34 | 6.35 | 0.26 | -0.75 | 4.21E-02 | NO | NO | NO | NO |
| AT1G08570 | 53.28 | 0.33 | 39.07 | 0.74 | -0.45 | 1.10E-02 | NO | NO | NO | UP |
| AT1G09750 | 80.53 | 1.54 | 53.50 | 1.12 | -0.59 | 1.43E-03 | NO | NO | NO | NO |
| AT1G10522 | 64.52 | 1.31 | 47.36 | 0.80 | -0.45 | 2.86E-02 | NO | NO | NO | NO |

**Table A3.3 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G10760 | 109.27 | 1.78 | 75.43 | 0.21 | -0.53 | 1.53E-02 | NO | NO | NO | NO |
| AT1G11700 | 23.34 | 0.66 | 15.93 | 0.52 | -0.55 | 4.48E-02 | NO | NO | NO | NO |
| AT1G12090 | 1320.94 | 3.95 | 788.36 | 2.37 | -0.74 | 6.44E-04 | NO | NO | NO | NO |
| AT1G12250 | 70.97 | 0.66 | 52.09 | 0.62 | -0.45 | 1.99E-02 | NO | NO | NO | NO |
| AT1G12710 | 47.22 | 1.05 | 27.27 | 0.94 | -0.79 | 2.17E-05 | NO | NO | NO | NO |
| AT1G13560 | 56.05 | 1.41 | 44.22 | 0.22 | -0.34 | 3.15E-02 | NO | NO | NO | NO |
| AT1G14150 | 156.49 | 3.14 | 87.89 | 0.69 | -0.83 | 7.20E-10 | NEGATIVE | NO | NO | NO |
| AT1G14200 | 20.79 | 0.48 | 13.80 | 0.25 | -0.59 | 4.86E-02 | NO | NO | NO | NO |
| AT1G15405 | 155.32 | 3.67 | 75.96 | 1.76 | -1.03 | 2.04E-04 | NO | NO | NO | NO |
| AT1G15470 | 25.73 | 0.62 | 18.39 | 0.19 | -0.48 | 3.06E-02 | NO | NO | NO | NO |
| AT1G16410 | 152.60 | 2.38 | 114.96 | 3.13 | -0.41 | 6.93E-03 | NO | NO | NO | NO |
| AT1G18360 | 31.45 | 0.78 | 17.57 | 0.35 | -0.84 | 1.06E-05 | NO | NO | NO | NO |
| AT1G19570 | 236.89 | 2.40 | 180.50 | 2.14 | -0.39 | 1.65E-02 | NO | NO | NO | NO |
| AT1G19960 | 407.82 | 4.55 | 204.76 | 3.28 | -0.99 | 3.13E-08 | NO | NO | NO | NO |
| AT1G20010 | 306.54 | 1.71 | 203.60 | 3.80 | -0.59 | 3.35E-03 | NO | NO | NO | NO |
| AT1G20610 | 9.37 | 0.37 | 6.25 | 0.12 | -0.58 | 3.38E-02 | NO | NO | NO | NO |
| AT1G21500 | 93.57 | 1.25 | 66.71 | 1.82 | -0.49 | 2.30E-02 | NEGATIVE | NO | DOWN | NO |
| AT1G21790 | 21.97 | 0.81 | 13.68 | 0.45 | -0.68 | 2.96E-03 | NO | NO | UP | UP |
| AT1G22540 | 5.53 | 0.05 | 2.57 | 0.22 | -1.10 | 6.12E-04 | NO | NO | NO | NO |
| AT1G22700 | 210.12 | 1.87 | 155.66 | 1.31 | -0.43 | 1.49E-02 | NEGATIVE | NO | NO | NO |
| AT1G22740 | 21.91 | 0.48 | 15.01 | 0.47 | -0.55 | 4.26E-02 | NO | NO | NO | NO |
| AT1G22940 | 37.65 | 0.29 | 22.38 | 0.42 | -0.75 | 3.87E-05 | NO | NO | NO | NO |
| AT1G23080 | 30.07 | 0.51 | 23.66 | 1.11 | -0.35 | 4.99E-02 | NO | NO | NO | NO |
| AT1G25422 | 3.05 | 0.18 | 1.05 | 0.17 | -1.54 | 2.17E-02 | NO | NO | NO | NO |
| AT1G26230 | 25.78 | 0.28 | 16.38 | 0.28 | -0.65 | 3.47E-04 | NO | NO | NO | NO |
| AT1G26761 | 42.88 | 0.49 | 29.43 | 0.43 | -0.54 | 7.04E-03 | NO | NO | NO | NO |
| AT1G27050 | 18.95 | 0.27 | 11.42 | 0.75 | -0.73 | 1.56E-02 | NO | YES | NO | NO |
| AT1G27385 | 39.61 | 1.11 | 28.36 | 0.48 | -0.48 | 3.05E-02 | NO | NO | NO | NO |
| AT1G27910 | 10.36 | 0.36 | 7.23 | 0.19 | -0.52 | 2.46E-02 | NO | NO | NO | UP |

**Table A3.3 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G28070 | 23.20 | 1.28 | 10.83 | 0.12 | -1.10 | 1.48E-04 | NO | NO | NO | NO |
| AT1G28410 | 16.64 | 0.43 | 10.44 | 0.42 | -0.67 | 5.00E-03 | NO | NO | NO | NO |
| AT1G29390 | 119.79 | 1.15 | 61.03 | 0.97 | -0.97 | 1.74E-08 | NO | NO | NO | NO |
| AT1G30250 | 32.50 | 3.31 | 16.63 | 1.77 | -0.97 | 2.57E-03 | NO | NO | NO | NO |
| AT1G30500 | 6.98 | 0.10 | 2.87 | 0.13 | -1.28 | 5.45E-03 | POSITIVE | YES | NO | NO |
| AT1G30510 | 16.04 | 0.32 | 11.62 | 0.57 | -0.47 | 3.60E-02 | NO | NO | NO | NO |
| AT1G30910 | 21.79 | 0.33 | 14.17 | 0.25 | -0.62 | 1.12E-02 | NO | NO | NO | NO |
| AT1G31230 | 37.24 | 0.75 | 23.59 | 0.43 | -0.66 | 2.71E-04 | NO | NO | NO | NO |
| AT1G31460 | 6.20 | 0.22 | 3.68 | 0.23 | -0.75 | 1.98E-02 | NO | NO | NO | NO |
| AT1G31850 | 37.44 | 0.79 | 21.90 | 0.66 | -0.77 | 1.75E-07 | NO | NO | NO | NO |
| AT1G32070 | 67.46 | 0.29 | 41.51 | 0.68 | -0.70 | 3.57E-06 | NO | NO | NO | NO |
| AT1G32090 | 10.05 | 0.13 | 5.76 | 0.30 | -0.80 | 2.72E-04 | NO | NO | NO | NO |
| AT1G32860 | 47.13 | 0.47 | 20.18 | 0.94 | -1.22 | 7.28E-12 | POSITIVE | NO | UP | UP |
| AT1G33230 | 47.77 | 0.56 | 25.24 | 0.51 | -0.92 | 2.64E-07 | POSITIVE | NO | UP | UP |
| AT1G33265 | 96.99 | 2.21 | 60.14 | 0.97 | -0.69 | 1.94E-04 | NO | NO | NO | NO |
| AT1G35420 | 106.21 | 0.47 | 65.65 | 0.21 | -0.69 | 7.39E-05 | NO | NO | NO | NO |
| AT1G35720 | 1410.82 | 2.15 | 881.87 | 13.58 | -0.68 | 1.10E-02 | NO | NO | NO | NO |
| AT1G44800 | 32.53 | 1.45 | 24.01 | 0.58 | -0.44 | 4.12E-02 | NO | NO | NO | NO |
| AT1G45191 | 6.22 | 0.41 | 3.89 | 0.17 | -0.68 | 3.94E-02 | NO | NO | NO | NO |
| AT1G46480 | 9.94 | 0.05 | 5.86 | 0.26 | -0.76 | 3.02E-02 | NO | YES | NO | NO |
| AT1G47580 | 26.14 | 0.50 | 16.71 | 0.87 | -0.65 | 1.52E-02 | NO | NO | NO | NO |
| AT1G47710 | 97.26 | 1.00 | 62.81 | 1.00 | -0.63 | 6.18E-04 | POSITIVE | NO | UP | UP |
| AT1G48600 | 27.78 | 1.09 | 13.49 | 2.54 | -1.04 | 3.27E-11 | NO | NO | DOWN | NO |
| AT1G49160 | 10.37 | 0.47 | 5.44 | 0.16 | -0.93 | 2.19E-05 | NO | NO | NO | NO |
| AT1G49560 | 32.95 | 0.48 | 14.60 | 0.47 | -1.17 | 9.27E-10 | NO | YES | NO | NO |
| AT1G50840 | 16.86 | 0.55 | 12.58 | 0.17 | -0.42 | 4.15E-02 | NO | NO | NO | NO |
| AT1G51400 | 461.22 | 4.33 | 326.84 | 8.80 | -0.50 | 8.19E-03 | NO | NO | DOWN | NO |
| AT1G51610 | 78.50 | 0.56 | 52.66 | 0.20 | -0.58 | 2.07E-03 | NO | NO | UP | NO |
| AT1G51650 | 424.94 | 1.52 | 305.12 | 5.02 | -0.48 | 1.31E-02 | NO | NO | NO | NO |

**Table A3.3 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G52220 | 644.30 | 1.76 | 383.59 | 3.87 | -0.75 | 2.38E-05 | NO | NO | NO | NO |
| AT1G53035 | 118.69 | 0.58 | 81.77 | 0.85 | -0.54 | 4.63E-03 | NO | NO | UP | NO |
| AT1G53160 | 28.70 | 0.45 | 11.38 | 0.44 | -1.33 | 3.57E-08 | NO | YES | NO | NO |
| AT1G53520 | 30.41 | 0.64 | 17.49 | 1.51 | -0.80 | 3.78E-04 | NEGATIVE | NO | NO | NO |
| AT1G53590 | 25.97 | 0.66 | 19.04 | 0.24 | -0.45 | 2.64E-02 | NO | NO | NO | NO |
| AT1G54000 | 6.48 | 0.16 | 2.46 | 0.35 | -1.40 | 7.26E-05 | NO | NO | NO | NO |
| AT1G54410 | 5206.40 | 93.83 | 3059.92 | 56.05 | -0.77 | 1.53E-02 | NO | NO | NO | UP |
| AT1G55690 | 30.71 | 0.68 | 18.98 | 0.47 | -0.69 | 1.03E-07 | NO | NO | NO | UP |
| AT1G56300 | 139.89 | 1.20 | 57.61 | 0.35 | -1.28 | 1.91E-14 | NO | NO | NO | NO |
| AT1G58235 | 19.26 | 0.37 | 12.75 | 0.23 | -0.60 | 3.05E-02 | NO | NO | NO | NO |
| AT1G60590 | 10.21 | 0.50 | 6.22 | 0.31 | -0.71 | 4.05E-03 | NO | NO | NO | NO |
| AT1G60680 | 5.12 | 0.26 | 2.45 | 0.14 | -1.06 | 1.63E-02 | NO | NO | NO | NO |
| AT1G61520 | 3383.70 | 29.25 | 2573.50 | 20.66 | -0.39 | 4.52E-02 | NO | NO | NO | NO |
| AT1G61740 | 29.12 | 0.79 | 18.64 | 0.19 | -0.64 | 1.12E-03 | NO | NO | NO | NO |
| AT1G62290 | 4.52 | 0.25 | 1.02 | 0.40 | -2.15 | 1.62E-07 | NO | NO | NO | NO |
| AT1G62960 | 21.40 | 0.28 | 15.66 | 0.53 | -0.45 | 4.27E-02 | NO | NO | NO | NO |
| AT1G63240 | 13.97 | 0.17 | 6.57 | 0.19 | -1.09 | 7.02E-07 | NO | NO | NO | NO |
| AT1G64770 | 162.85 | 1.36 | 105.16 | 0.89 | -0.63 | 5.19E-06 | NEGATIVE | NO | NO | NO |
| AT1G65590 | 8.75 | 0.17 | 4.97 | 0.51 | -0.82 | 2.04E-03 | NO | NO | NO | NO |
| AT1G65960 | 428.15 | 4.52 | 315.59 | 1.53 | -0.44 | 1.43E-03 | NO | NO | NO | UP |
| AT1G66430 | 84.72 | 0.21 | 48.52 | 1.26 | -0.80 | 5.16E-06 | NO | NO | NO | NO |
| AT1G67080 | 26.70 | 0.67 | 18.08 | 1.23 | -0.56 | 1.87E-02 | NO | NO | DOWN | NO |
| AT1G67105 | 10.03 | 0.25 | 4.38 | 0.75 | -1.20 | 6.29E-03 | NO | NO | NO | NO |
| AT1G69523 | 18.79 | 0.25 | 12.89 | 0.25 | -0.54 | 2.88E-02 | NO | NO | NO | NO |
| AT1G69830 | 74.14 | 1.14 | 49.51 | 0.25 | -0.58 | 2.02E-03 | NO | NO | NO | NO |
| AT1G69910 | 7.96 | 0.14 | 4.99 | 0.11 | -0.67 | 1.21E-02 | NO | NO | NO | NO |
| AT1G70560 | 9.96 | 0.47 | 4.21 | 0.28 | -1.24 | 3.36E-05 | NO | NO | NO | NO |
| AT1G70640 | 130.29 | 1.29 | 29.31 | 1.21 | -2.15 | 0.00E+00 | NO | NO | NO | NO |
| AT1G71000 | 5.59 | 0.75 | 0.45 | 0.04 | -3.64 | 6.49E-04 | NO | NO | NO | NO |

**Table A3.3 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G71710 | 36.99 | 0.91 | 23.05 | 0.25 | -0.68 | 1.14E-04 | NO | NO | NO | UP |
| AT1G71720 | 61.67 | 1.19 | 42.54 | 0.72 | -0.54 | 6.14E-03 | NO | NO | NO | NO |
| AT1G73655 | 305.45 | 3.02 | 187.61 | 1.76 | -0.70 | 6.71E-05 | NEGATIVE | NO | NO | NO |
| AT1G74070 | 33.66 | 0.36 | 20.20 | 0.58 | -0.74 | 2.03E-04 | NEGATIVE | NO | DOWN | NO |
| AT1G74520 | 88.76 | 0.82 | 46.38 | 1.35 | -0.94 | 3.37E-07 | NO | NO | NO | UP |
| AT1G74560 | 103.91 | 1.15 | 63.58 | 0.98 | -0.71 | 1.62E-05 | NO | NO | NO | NO |
| AT1G74680 | 17.75 | 0.34 | 12.35 | 0.22 | -0.52 | 2.03E-02 | NO | NO | NO | NO |
| AT1G74840 | 79.97 | 0.42 | 48.23 | 0.36 | -0.73 | 4.45E-05 | NO | YES | NO | NO |
| AT1G75750 | 829.59 | 17.38 | 397.91 | 13.34 | -1.06 | 0.00E+00 | NO | NO | NO | NO |
| AT1G75780 | 8.56 | 0.28 | 5.13 | 0.16 | -0.74 | 1.31E-02 | NO | NO | NO | NO |
| AT1G76020 | 34.81 | 0.39 | 18.91 | 0.21 | -0.88 | 1.38E-04 | NO | NO | NO | NO |
| AT1G76790 | 39.90 | 0.40 | 22.05 | 0.50 | -0.86 | 9.83E-06 | NO | NO | NO | NO |
| AT1G77490 | 80.16 | 0.27 | 43.63 | 0.63 | -0.88 | 3.79E-07 | NO | NO | NO | NO |
| AT1G77540 | 80.90 | 0.53 | 55.05 | 1.53 | -0.56 | 1.86E-02 | NO | NO | NO | NO |
| AT1G77580 | 18.10 | 0.58 | 9.44 | 0.32 | -0.94 | 5.71E-08 | NO | NO | NO | NO |
| AT1G78610 | 21.05 | 0.41 | 13.62 | 0.52 | -0.63 | 9.33E-04 | NO | NO | NO | NO |
| AT1G78820 | 36.71 | 0.99 | 23.28 | 0.47 | -0.66 | 6.50E-04 | NO | NO | NO | NO |
| AT1G78995 | 92.65 | 1.12 | 63.84 | 0.17 | -0.54 | 5.56E-03 | NO | NO | NO | NO |
| AT1G79790 | 44.79 | 0.57 | 30.37 | 0.34 | -0.56 | 5.87E-03 | NO | NO | NO | NO |
| AT1G80940 | 28.45 | 0.61 | 15.51 | 0.42 | -0.88 | 2.64E-06 | NO | NO | NO | NO |
| AT2G01275 | 3.28 | 0.06 | 1.00 | 0.02 | -1.71 | 3.80E-03 | NO | NO | NO | NO |
| AT2G02080 | 48.63 | 7.69 | 33.63 | 6.37 | -0.53 | 2.69E-03 | NO | YES | NO | NO |
| AT2G02100 | 1972.26 | 17.76 | 1127.29 | 16.33 | -0.81 | 6.08E-05 | NO | NO | UP | NO |
| AT2G02510 | 218.11 | 1.02 | 144.88 | 2.60 | -0.59 | 2.54E-03 | NO | NO | NO | NO |
| AT2G02740 | 60.75 | 1.14 | 45.57 | 0.56 | -0.41 | 4.83E-02 | NO | YES | NO | NO |
| AT2G12400 | 6.92 | 0.26 | 2.77 | 0.06 | -1.32 | 7.71E-06 | NO | NO | NO | NO |
| AT2G13550 | 12.11 | 0.16 | 6.50 | 0.29 | -0.90 | 1.66E-03 | NO | NO | NO | NO |
| AT2G14045 | 36.12 | 0.61 | 25.84 | 0.58 | -0.48 | 3.52E-02 | NO | NO | NO | NO |
| AT2G14170 | 42.86 | 0.45 | 33.09 | 0.31 | -0.37 | 4.08E-02 | NO | NO | NO | NO |

**Table A3.3 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT2G16600 | 3296.96 | 32.69 | 2148.89 | 37.50 | -0.62 | 3.34E-02 | NO | NO | NO | NO |
| AT2G18328 | 279.10 | 1.40 | 156.19 | 0.16 | -0.84 | 1.94E-06 | NO | NO | NO | NO |
| AT2G18890 | 18.94 | 0.81 | 12.95 | 0.52 | -0.55 | 1.88E-02 | NO | NO | NO | NO |
| AT2G19170 | 8.96 | 0.40 | 6.41 | 0.32 | -0.48 | 4.55E-02 | NO | NO | NO | NO |
| AT2G19860 | 38.60 | 0.69 | 25.07 | 0.73 | -0.62 | 8.34E-04 | NO | NO | NO | NO |
| AT2G20270 | 116.11 | 2.13 | 90.45 | 1.59 | -0.36 | 3.40E-02 | NO | NO | NO | NO |
| AT2G21130 | 94.42 | 0.81 | 69.47 | 1.15 | -0.44 | 3.53E-02 | NO | NO | UP | NO |
| AT2G21250 | 186.46 | 1.25 | 124.95 | 2.36 | -0.58 | 1.36E-03 | NO | NO | NO | NO |
| AT2G21320 | 143.22 | 1.58 | 107.75 | 0.65 | -0.41 | 3.95E-02 | NO | NO | UP | NO |
| AT2G21340 | 26.91 | 0.52 | 14.72 | 0.19 | -0.87 | 2.93E-06 | NO | NO | NO | NO |
| AT2G21370 | 38.41 | 0.32 | 24.58 | 0.05 | -0.64 | 5.96E-05 | NO | NO | NO | NO |
| AT2G21380 | 19.13 | 0.26 | 11.92 | 0.29 | -0.68 | 1.98E-04 | NO | NO | NO | NO |
| AT2G21590 | 21.42 | 0.90 | 7.47 | 0.30 | -1.52 | 0.00E+00 | NO | NO | NO | NO |
| AT2G22080 | 166.15 | 1.73 | 118.32 | 1.75 | -0.49 | 9.38E-03 | NO | NO | UP | UP |
| AT2G22122 | 38.51 | 0.36 | 20.34 | 0.34 | -0.92 | 1.15E-03 | NO | NO | NO | NO |
| AT2G22190 | 50.97 | 1.12 | 24.29 | 0.55 | -1.07 | 7.57E-09 | NO | NO | UP | NO |
| AT2G22240 | 28.57 | 0.59 | 19.55 | 1.04 | -0.55 | 2.72E-03 | NO | NO | NO | NO |
| AT2G22260 | 3.76 | 0.09 | 0.97 | 0.17 | -1.96 | 1.19E-03 | NO | NO | NO | NO |
| AT2G22540 | 84.61 | 0.49 | 61.71 | 0.44 | -0.46 | 1.74E-02 | NO | YES | NO | NO |
| AT2G23340 | 20.71 | 0.63 | 11.81 | 0.61 | -0.81 | 3.15E-03 | NO | YES | NO | UP |
| AT2G23670 | 257.19 | 2.55 | 192.22 | 6.07 | -0.42 | 3.45E-02 | NEGATIVE | NO | NO | NO |
| AT2G23910 | 13.22 | 0.17 | 8.49 | 0.20 | -0.64 | 2.32E-02 | NO | NO | NO | NO |
| AT2G24120 | 35.58 | 1.32 | 26.22 | 0.27 | -0.44 | 2.04E-02 | NO | NO | NO | NO |
| AT2G24150 | 25.03 | 0.54 | 17.12 | 0.86 | -0.55 | 1.59E-02 | NO | NO | NO | NO |
| AT2G24270 | 308.66 | 1.27 | 221.62 | 3.10 | -0.48 | 3.31E-04 | NO | NO | NO | NO |
| AT2G27530 | 746.39 | 6.61 | 599.41 | 9.34 | -0.32 | 2.99E-02 | NO | NO | NO | NO |
| AT2G28840 | 243.86 | 5.26 | 150.48 | 0.45 | -0.70 | 7.13E-08 | NO | NO | NO | NO |
| AT2G29170 | 43.52 | 4.05 | 22.93 | 2.63 | -0.92 | 4.64E-02 | NO | NO | NO | NO |
| AT2G29320 | 43.57 | 0.77 | 25.32 | 0.77 | -0.78 | 6.28E-05 | NO | NO | NO | NO |

**Table A3.3 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT2G29630 | 895.67 | 12.20 | 601.79 | 3.34 | -0.57 | 2.82E-02 | NO | NO | NO | NO |
| AT2G30170 | 37.95 | 0.32 | 25.86 | 0.53 | -0.55 | 2.65E-03 | NO | NO | NO | NO |
| AT2G31230 | 35.16 | 0.60 | 22.22 | 0.41 | -0.66 | 4.59E-03 | NO | YES | NO | NO |
| AT2G31360 | 401.48 | 3.45 | 243.17 | 1.55 | -0.72 | 1.83E-04 | NO | NO | UP | NO |
| AT2G31840 | 70.59 | 1.42 | 50.54 | 0.54 | -0.48 | 1.61E-02 | NO | NO | NO | NO |
| AT2G33860 | 28.37 | 0.72 | 14.92 | 0.56 | -0.93 | 1.91E-07 | NO | YES | NO | NO |
| AT2G34650 | 9.26 | 0.46 | 5.41 | 0.14 | -0.78 | 4.67E-03 | NO | NO | NO | NO |
| AT2G34720 | 77.83 | 0.49 | 48.17 | 0.37 | -0.69 | 2.51E-04 | POSITIVE | YES | NO | NO |
| AT2G34850 | 5.32 | 0.17 | 1.80 | 0.11 | -1.56 | 1.63E-03 | NO | NO | NO | NO |
| AT2G35040 | 118.97 | 2.09 | 52.20 | 1.24 | -1.19 | 0.00E+00 | NO | NO | NO | NO |
| AT2G35700 | 21.89 | 0.61 | 6.63 | 0.41 | -1.72 | 8.95E-06 | NO | YES | NO | NO |
| AT2G35840 | 152.42 | 1.79 | 113.57 | 0.20 | -0.42 | 6.53E-03 | NO | NO | NO | NO |
| AT2G35960 | 85.68 | 1.59 | 60.07 | 1.26 | -0.51 | 9.64E-03 | NO | NO | UP | UP |
| AT2G36145 | 303.95 | 3.11 | 193.43 | 0.86 | -0.65 | 2.30E-04 | NEGATIVE | NO | NO | NO |
| AT2G36290 | 26.32 | 0.45 | 18.51 | 0.14 | -0.51 | 2.14E-02 | NO | NO | NO | NO |
| AT2G36390 | 100.24 | 1.80 | 50.23 | 0.53 | -1.00 | 9.34E-09 | NO | NO | NO | NO |
| AT2G36460 | 213.52 | 2.93 | 137.55 | 2.00 | -0.63 | 2.49E-04 | POSITIVE | NO | NO | NO |
| AT2G36470 | 24.80 | 0.29 | 14.94 | 0.34 | -0.73 | 3.06E-04 | NO | NO | NO | NO |
| AT2G37020 | 34.09 | 0.78 | 25.16 | 0.53 | -0.44 | 1.77E-02 | NO | NO | NO | NO |
| AT2G37600 | 127.87 | 1.66 | 82.01 | 1.93 | -0.64 | 2.04E-04 | NO | NO | NO | NO |
| AT2G37990 | 91.18 | 1.43 | 67.54 | 1.43 | -0.43 | 3.15E-02 | NO | NO | NO | NO |
| AT2G39470 | 170.35 | 0.85 | 112.01 | 0.33 | -0.60 | 1.10E-04 | NO | NO | NO | NO |
| AT2G40350 | 4.18 | 0.43 | 0.57 | 0.15 | -2.87 | 1.15E-02 | NO | YES | NO | NO |
| AT2G40840 | 109.73 | 1.47 | 49.12 | 0.61 | -1.16 | 3.96E-11 | NO | NO | NO | NO |
| AT2G41870 | 25.76 | 0.64 | 15.18 | 0.25 | -0.76 | 1.82E-04 | NO | NO | NO | UP |
| AT2G42130 | 144.72 | 1.35 | 87.94 | 1.79 | -0.72 | 2.64E-10 | NO | NO | NO | NO |
| AT2G42530 | 3092.92 | 21.48 | 1922.89 | 30.40 | -0.69 | 8.67E-03 | NO | NO | UP | UP |
| AT2G42540 | 12067.70 | 189.81 | 3281.28 | 31.62 | -1.88 | 2.90E-08 | NO | NO | UP | UP |
| AT2G43550 | 107.72 | 0.78 | 60.57 | 2.05 | -0.83 | 1.59E-05 | NEGATIVE | NO | NO | NO |

**Table A3.3 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT2G44040 | 37.40 | 0.68 | 26.32 | 0.42 | -0.51 | 1.42E-02 | NO | NO | NO | NO |
| AT2G45560 | 29.52 | 0.25 | 13.52 | 0.61 | -1.13 | 5.15E-11 | NO | NO | NO | NO |
| AT2G46660 | 8.99 | 0.69 | 4.76 | 0.04 | -0.92 | 4.05E-04 | NO | NO | NO | NO |
| AT2G46680 | 81.38 | 2.39 | 44.11 | 1.95 | -0.88 | 2.87E-07 | POSITIVE | YES | NO | NO |
| AT2G47260 | 5.95 | 0.44 | 3.32 | 0.12 | -0.84 | 9.12E-03 | NO | YES | NO | NO |
| AT2G47420 | 48.41 | 0.75 | 31.99 | 0.74 | -0.60 | 2.48E-03 | NO | NO | NO | NO |
| AT2G47840 | 75.32 | 1.30 | 54.88 | 1.18 | -0.46 | 2.99E-02 | NO | NO | NO | NO |
| AT3G02020 | 76.86 | 1.20 | 55.74 | 1.34 | -0.46 | 2.32E-02 | NO | NO | NO | NO |
| AT3G02630 | 38.21 | 0.17 | 27.17 | 0.54 | -0.49 | 1.53E-02 | NO | NO | NO | NO |
| AT3G02730 | 303.82 | 0.78 | 224.60 | 2.28 | -0.44 | 2.46E-02 | NO | NO | NO | NO |
| AT3G03770 | 30.27 | 1.04 | 21.27 | 0.56 | -0.51 | 3.92E-04 | NO | NO | NO | UP |
| AT3G04860 | 7.36 | 0.22 | 4.14 | 0.28 | -0.83 | 1.50E-02 | NO | NO | NO | NO |
| AT3G05640 | 5.18 | 0.34 | 2.96 | 0.21 | -0.81 | 3.24E-02 | NO | NO | NO | NO |
| AT3G05730 | 822.32 | 4.21 | 458.72 | 6.35 | -0.84 | 5.89E-06 | NEGATIVE | NO | NO | NO |
| AT3G06035 | 82.79 | 1.81 | 59.35 | 1.30 | -0.48 | 2.29E-02 | NO | NO | NO | NO |
| AT3G06040 | 120.35 | 2.40 | 94.29 | 2.11 | -0.35 | 3.35E-02 | NO | NO | NO | NO |
| AT3G06510 | 103.37 | 0.41 | 78.63 | 0.56 | -0.39 | 3.14E-03 | NO | NO | NO | NO |
| AT3G08940 | 829.78 | 18.07 | 577.56 | 7.35 | -0.52 | 2.85E-02 | NO | NO | NO | NO |
| AT3G09540 | 18.48 | 0.87 | 8.35 | 0.52 | -1.15 | 2.17E-07 | NO | NO | UP | UP |
| AT3G09910 | 9.47 | 0.14 | 5.33 | 0.34 | -0.83 | 2.26E-02 | NO | NO | NO | NO |
| AT3G10920 | 493.76 | 4.17 | 346.63 | 2.61 | -0.51 | 1.22E-02 | NO | NO | NO | NO |
| AT3G11260 | 4.94 | 0.67 | 1.95 | 0.18 | -1.34 | 3.93E-02 | NO | YES | NO | NO |
| AT3G11410 | 58.31 | 1.19 | 31.89 | 1.05 | -0.87 | 1.07E-06 | NO | NO | NO | NO |
| AT3G11670 | 44.57 | 0.27 | 27.41 | 0.42 | -0.70 | 6.02E-05 | NO | NO | NO | UP |
| AT3G11720 | 18.99 | 0.67 | 13.54 | 0.27 | -0.49 | 6.04E-03 | NO | NO | NO | NO |
| AT3G12120 | 314.36 | 0.78 | 248.61 | 2.27 | -0.34 | 2.71E-02 | NO | NO | NO | NO |
| AT3G12490 | 638.39 | 4.59 | 403.22 | 5.61 | -0.66 | 4.40E-05 | POSITIVE | NO | NO | NO |
| AT3G12670 | 52.00 | 0.38 | 35.81 | 0.78 | -0.54 | 4.39E-03 | NO | NO | UP | NO |
| AT3G12990 | 19.86 | 0.36 | 12.46 | 0.47 | -0.67 | 2.00E-03 | NO | NO | NO | NO |

**Table A3.3 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G13350 | 32.03 | 0.63 | 19.79 | 0.30 | -0.69 | 5.90E-04 | NO | YES | NO | NO |
| AT3G14200 | 50.43 | 0.68 | 37.16 | 0.72 | -0.44 | 3.15E-02 | NO | NO | NO | NO |
| AT3G14210 | 121.91 | 3.44 | 75.14 | 2.50 | -0.70 | 1.17E-04 | NO | NO | NO | NO |
| AT3G15140 | 13.31 | 0.97 | 7.44 | 0.21 | -0.84 | 2.06E-03 | NO | NO | NO | NO |
| AT3G15270 | 5.97 | 0.11 | 2.12 | 0.43 | -1.49 | 5.11E-03 | NO | YES | NO | NO |
| AT3G15357 | 1.59 | 0.04 | 0.21 | 0.03 | -2.89 | 1.68E-02 | NO | NO | NO | NO |
| AT3G15460 | 19.88 | 0.71 | 14.01 | 0.43 | -0.50 | 4.51E-02 | NO | NO | NO | NO |
| AT3G16140 | 858.71 | 6.55 | 562.03 | 5.84 | -0.61 | 2.52E-03 | NO | NO | NO | NO |
| AT3G16670 | 151.47 | 3.78 | 90.51 | 3.67 | -0.74 | 7.43E-05 | NO | NO | NO | NO |
| AT3G17120 | 17.75 | 0.13 | 11.82 | 0.62 | -0.59 | 2.60E-03 | NO | NO | NO | NO |
| AT3G17998 | 67.66 | 0.67 | 33.05 | 2.28 | -1.03 | 1.13E-09 | NO | NO | NO | NO |
| AT3G18090 | 1.72 | 0.02 | 0.62 | 0.06 | -1.47 | 8.10E-04 | NO | NO | NO | NO |
| AT3G18420 | 97.34 | 3.08 | 46.79 | 1.01 | -1.06 | 1.59E-09 | NO | NO | NO | NO |
| AT3G18490 | 204.13 | 1.77 | 146.43 | 1.98 | -0.48 | 2.08E-02 | NO | NO | NO | NO |
| AT3G18500 | 16.81 | 0.35 | 12.18 | 0.30 | -0.47 | 2.93E-02 | NO | NO | NO | NO |
| AT3G19800 | 60.07 | 0.55 | 36.03 | 0.96 | -0.74 | 6.52E-06 | NO | NO | DOWN | NO |
| AT3G19820 | 162.19 | 1.79 | 117.02 | 2.96 | -0.47 | 7.85E-05 | NO | NO | NO | NO |
| AT3G20300 | 13.84 | 0.93 | 9.15 | 0.27 | -0.60 | 1.36E-02 | NO | NO | NO | NO |
| AT3G20470 | 12.86 | 0.97 | 6.78 | 0.20 | -0.92 | 1.44E-02 | NO | NO | NO | NO |
| AT3G21870 | 47.52 | 0.39 | 31.29 | 0.51 | -0.60 | 8.81E-03 | NEGATIVE | NO | NO | NO |
| AT3G22150 | 14.86 | 0.43 | 9.59 | 0.27 | -0.63 | 1.55E-03 | NO | NO | NO | NO |
| AT3G22200 | 86.31 | 0.81 | 65.14 | 0.82 | -0.41 | 5.30E-03 | POSITIVE | NO | NO | NO |
| AT3G23570 | 35.98 | 0.54 | 26.35 | 0.56 | -0.45 | 4.87E-02 | NO | NO | NO | NO |
| AT3G23580 | 31.55 | 0.31 | 19.44 | 0.82 | -0.70 | 3.93E-04 | NO | NO | NO | NO |
| AT3G23640 | 24.94 | 0.34 | 17.78 | 0.42 | -0.49 | 9.54E-04 | NO | NO | NO | NO |
| AT3G23940 | 76.05 | 1.43 | 61.22 | 0.32 | -0.31 | 3.96E-02 | NO | NO | NO | NO |
| AT3G24420 | 20.37 | 2.34 | 11.95 | 0.81 | -0.77 | 2.11E-03 | NO | NO | NO | NO |
| AT3G24590 | 56.38 | 0.64 | 37.88 | 0.64 | -0.57 | 4.77E-03 | NO | NO | NO | NO |
| AT3G25770 | 495.10 | 1.10 | 352.86 | 7.04 | -0.49 | 1.75E-02 | NO | NO | NO | NO |

**Table A3.3 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G26290 | 35.84 | 0.13 | 20.30 | 0.34 | -0.82 | 1.07E-05 | NO | NO | NO | NO |
| AT3G26300 | 58.94 | 0.52 | 41.05 | 0.14 | -0.52 | 7.50E-03 | NO | NO | NO | NO |
| AT3G26450 | 49.29 | 1.06 | 24.14 | 0.64 | -1.03 | 5.97E-07 | NO | NO | DOWN | NO |
| AT3G26900 | 54.10 | 0.68 | 39.69 | 0.63 | -0.45 | 1.59E-02 | NO | NO | NO | NO |
| AT3G27180 | 49.64 | 1.28 | 35.96 | 0.63 | -0.47 | 1.92E-02 | NO | NO | NO | NO |
| AT3G27690 | 622.51 | 11.88 | 312.38 | 7.42 | -0.99 | 1.37E-07 | NO | NO | NO | NO |
| AT3G29320 | 107.63 | 1.08 | 61.50 | 0.61 | -0.81 | 1.24E-05 | NO | NO | NO | NO |
| AT3G29390 | 9.87 | 0.21 | 5.84 | 0.04 | -0.76 | 2.19E-03 | NO | NO | NO | NO |
| AT3G46780 | 320.82 | 3.82 | 219.87 | 1.36 | -0.55 | 9.05E-03 | NO | NO | NO | NO |
| AT3G46970 | 413.39 | 5.52 | 211.20 | 0.97 | -0.97 | 1.20E-05 | NO | NO | NO | NO |
| AT3G47160 | 49.82 | 0.74 | 36.99 | 0.96 | -0.43 | 4.32E-02 | NO | NO | NO | NO |
| AT3G47860 | 255.85 | 0.78 | 136.79 | 1.99 | -0.90 | 1.35E-07 | NO | NO | NO | NO |
| AT3G48460 | 23.89 | 0.69 | 15.27 | 1.51 | -0.65 | 3.40E-03 | NO | NO | NO | NO |
| AT3G48610 | 23.50 | 0.46 | 15.44 | 0.65 | -0.61 | 2.93E-03 | NO | NO | NO | NO |
| AT3G48700 | 3.15 | 0.48 | 0.82 | 0.13 | -1.93 | 1.83E-03 | NO | NO | NO | NO |
| AT3G49560 | 171.74 | 0.51 | 123.01 | 2.72 | -0.48 | 1.18E-02 | NO | NO | NO | NO |
| AT3G49910 | 1235.69 | 9.19 | 887.91 | 12.03 | -0.48 | 4.98E-02 | NO | NO | NO | NO |
| AT3G50500 | 31.10 | 0.08 | 20.57 | 0.31 | -0.60 | 2.41E-03 | NO | NO | NO | NO |
| AT3G50740 | 19.33 | 1.25 | 13.74 | 0.42 | -0.49 | 3.10E-02 | NO | NO | NO | NO |
| AT3G52070 | 26.66 | 2.64 | 15.97 | 1.15 | -0.74 | 3.34E-02 | NO | NO | NO | NO |
| AT3G52390 | 34.31 | 0.74 | 20.61 | 0.11 | -0.74 | 5.88E-05 | NO | NO | NO | NO |
| AT3G53000 | 18.41 | 0.22 | 12.50 | 0.29 | -0.56 | 2.17E-02 | NO | NO | NO | NO |
| AT3G53530 | 17.90 | 0.42 | 11.74 | 0.93 | -0.61 | 2.38E-02 | NO | NO | NO | NO |
| AT3G54050 | 1147.94 | 11.42 | 836.04 | 5.08 | -0.46 | 3.00E-02 | NO | NO | NO | NO |
| AT3G55120 | 95.30 | 1.72 | 64.13 | 1.81 | -0.57 | 4.25E-03 | NO | NO | NO | NO |
| AT3G55580 | 87.91 | 1.88 | 40.95 | 0.93 | -1.10 | 1.72E-10 | NO | NO | UP | NO |
| AT3G55610 | 306.79 | 5.19 | 173.37 | 2.72 | -0.82 | 3.00E-07 | NO | NO | UP | NO |
| AT3G56490 | 131.05 | 0.44 | 96.96 | 1.71 | -0.43 | 3.12E-02 | NO | NO | NO | NO |
| AT3G57030 | 97.85 | 0.36 | 63.76 | 1.80 | -0.62 | 7.39E-04 | NO | NO | NO | NO |

**Table A3.3 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G57062 | 51.13 | 1.30 | 35.45 | 1.02 | -0.53 | 3.99E-02 | NO | NO | NO | NO |
| AT3G58010 | 59.01 | 0.74 | 40.30 | 0.56 | -0.55 | 5.71E-03 | NO | NO | NO | NO |
| AT3G58070 | 21.20 | 0.51 | 13.84 | 0.64 | -0.61 | 1.55E-02 | NO | YES | NO | NO |
| AT3G59980 | 126.01 | 1.31 | 91.51 | 1.92 | -0.46 | 1.76E-02 | NEGATIVE | NO | NO | NO |
| AT3G60530 | 31.80 | 0.22 | 20.07 | 1.03 | -0.66 | 2.12E-03 | NO | YES | NO | NO |
| AT3G61080 | 41.04 | 0.22 | 20.25 | 0.31 | -1.02 | 1.23E-07 | NO | NO | NO | NO |
| AT3G62750 | 9.31 | 0.16 | 6.14 | 0.08 | -0.60 | 4.31E-02 | NO | NO | NO | NO |
| AT3G63160 | 4669.45 | 13.44 | 2926.92 | 14.12 | -0.67 | 8.93E-03 | NO | NO | NO | NO |
| AT4G00310 | 11.29 | 0.23 | 6.19 | 0.41 | -0.87 | 1.60E-03 | NO | NO | NO | NO |
| AT4G00670 | 0.32 | 0.07 | 0.05 | 0.03 | -2.60 | 1.47E-02 | NO | NO | NO | NO |
| AT4G00810 | 390.27 | 2.31 | 290.01 | 4.20 | -0.43 | 2.63E-02 | NO | NO | NO | NO |
| AT4G01130 | 18.25 | 0.13 | 6.22 | 0.28 | -1.55 | 1.97E-09 | NO | NO | NO | NO |
| AT4G01460 | 12.04 | 0.29 | 7.81 | 1.05 | -0.63 | 2.20E-02 | NO | YES | NO | NO |
| AT4G01670 | 17.36 | 0.08 | 9.26 | 0.26 | -0.91 | 3.65E-04 | NO | NO | NO | NO |
| AT4G01940 | 336.24 | 0.38 | 190.23 | 2.93 | -0.82 | 2.64E-06 | NO | NO | NO | NO |
| AT4G02920 | 396.75 | 3.16 | 265.80 | 1.68 | -0.58 | 2.87E-04 | NO | NO | NO | NO |
| AT4G04330 | 118.04 | 0.56 | 74.91 | 0.38 | -0.66 | 3.64E-04 | NO | NO | NO | NO |
| AT4G04470 | 53.27 | 0.63 | 39.34 | 0.30 | -0.44 | 4.54E-02 | NO | NO | NO | NO |
| AT4G04630 | 9.18 | 0.03 | 4.29 | 0.71 | -1.10 | 1.98E-03 | NO | NO | NO | NO |
| AT4G04840 | 14.78 | 0.57 | 8.56 | 0.80 | -0.79 | 1.81E-02 | NEGATIVE | NO | DOWN | NO |
| AT4G09970 | 28.64 | 1.28 | 20.16 | 0.93 | -0.51 | 3.23E-02 | NO | NO | NO | NO |
| AT4G10380 | 13.18 | 0.61 | 8.80 | 0.54 | -0.58 | 2.69E-02 | NO | NO | NO | NO |
| AT4G12000 | 19.93 | 0.49 | 11.64 | 0.56 | -0.78 | 6.39E-04 | POSITIVE | NO | UP | NO |
| AT4G12470 | 1853.39 | 67.10 | 1159.34 | 45.80 | -0.68 | 8.50E-03 | NO | NO | UP | UP |
| AT4G12600 | 273.29 | 5.11 | 190.84 | 3.16 | -0.52 | 6.55E-03 | NO | NO | NO | NO |
| AT4G12900 | 33.53 | 0.88 | 19.01 | 0.19 | -0.82 | 1.09E-03 | NO | NO | NO | NO |
| AT4G13150 | 33.31 | 0.05 | 20.37 | 0.19 | -0.71 | 5.84E-04 | NO | NO | NO | NO |
| AT4G13220 | 126.85 | 1.96 | 94.97 | 0.55 | -0.42 | 4.24E-02 | NEGATIVE | NO | NO | NO |
| AT4G13493 | 338.15 | 0.56 | 222.03 | 1.90 | -0.61 | 4.49E-02 | NO | NO | NO | NO |

**Table A3.3 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | | DOW |
| AT4G13840 | 59.95 | 0.59 | 30.00 | 0.47 | -1.00 | 7.31E-09 | NO | NO | NO | N |
| AT4G14020 | 167.14 | 2.61 | 70.37 | 1.95 | -1.25 | 1.79E-11 | NO | NO | NO | NO |
| AT4G14105 | 1.06 | 0.84 | 0.55 | 0.38 | -0.94 | 4.13E-06 | NO | NO | NO | NO |
| AT4G14605 | 45.34 | 1.17 | 27.90 | 0.20 | -0.70 | 1.68E-04 | NO | NO | NO | NO |
| AT4G15510 | 91.04 | 1.31 | 69.27 | 0.47 | -0.39 | 3.95E-02 | NO | NO | NO | NO |
| AT4G16060 | 37.62 | 0.67 | 20.73 | 0.53 | -0.86 | 2.11E-05 | NO | NO | NO | NO |
| AT4G17090 | 1829.44 | 6.20 | 912.16 | 11.92 | -1.00 | 1.04E-03 | NO | NO | UP | NO |
| AT4G17550 | 60.35 | 1.96 | 34.18 | 0.87 | -0.82 | 2.90E-06 | NO | NO | UP | UP |
| AT4G17730 | 90.08 | 0.57 | 68.08 | 1.10 | -0.40 | 4.27E-02 | NO | NO | NO | NO |
| AT4G17770 | 34.77 | 1.66 | 16.44 | 0.76 | -1.08 | 2.66E-10 | NO | NO | NO | NO |
| AT4G18670 | 13.97 | 0.48 | 10.34 | 0.25 | -0.44 | 4.68E-02 | NEGATIVE | NO | NO | NO |
| AT4G18700 | 105.13 | 1.34 | 69.84 | 0.88 | -0.59 | 1.67E-03 | NO | NO | NO | NO |
| AT4G19120 | 123.77 | 0.93 | 85.47 | 1.30 | -0.53 | 6.11E-04 | NO | NO | NO | NO |
| AT4G19410 | 85.26 | 1.17 | 56.20 | 0.46 | -0.60 | 6.08E-04 | NO | NO | NO | NO |
| AT4G20170 | 33.27 | 0.09 | 18.15 | 0.18 | -0.87 | 1.52E-06 | NO | NO | NO | NO |
| AT4G21215 | 50.47 | 0.34 | 20.32 | 0.52 | -1.31 | 1.53E-13 | NO | NO | NO | NO |
| AT4G22890 | 240.03 | 1.93 | 182.99 | 2.69 | -0.39 | 1.18E-03 | NO | NO | NO | NO |
| AT4G23630 | 353.03 | 2.56 | 246.82 | 2.95 | -0.52 | 1.87E-02 | POSITIVE | NO | UP | UP |
| AT4G24010 | 4.40 | 0.07 | 2.06 | 0.16 | -1.10 | 8.23E-04 | NO | NO | NO | NO |
| AT4G24930 | 124.10 | 1.51 | 88.81 | 0.88 | -0.48 | 1.01E-02 | NO | NO | NO | NO |
| AT4G24960 | 78.24 | 1.44 | 51.39 | 1.56 | -0.61 | 1.76E-03 | NO | NO | UP | UP |
| AT4G25470 | 45.16 | 0.68 | 30.27 | 0.13 | -0.58 | 8.06E-03 | NO | YES | UP | UP |
| AT4G25910 | 83.37 | 0.41 | 58.94 | 1.60 | -0.50 | 1.19E-02 | NO | NO | NO | NO |
| AT4G26530 | 147.61 | 1.37 | 98.04 | 1.27 | -0.59 | 7.07E-04 | NO | NO | NO | NO |
| AT4G26555 | 35.33 | 0.47 | 22.77 | 0.79 | -0.63 | 6.71E-03 | NO | NO | NO | NO |
| AT4G26670 | 80.33 | 1.74 | 51.52 | 1.11 | -0.64 | 5.13E-04 | NO | NO | NO | NO |
| AT4G26950 | 19.08 | 0.69 | 11.05 | 0.85 | -0.79 | 2.74E-02 | NO | NO | NO | NO |
| AT4G27440 | 1757.23 | 14.33 | 765.72 | 10.88 | -1.20 | 2.50E-06 | NO | NO | NO | NO |

**Table A3.3 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT4G27520 | 417.18 | 7.47 | 256.97 | 2.89 | -0.70 | 3.76E-04 | NO | NO | UP | NO |
| AT4G27560 | 26.69 | 0.49 | 19.70 | 0.70 | -0.44 | 4.33E-02 | NO | NO | NO | NO |
| AT4G27570 | 6.79 | 0.09 | 3.52 | 0.19 | -0.95 | 4.41E-03 | POSITIVE | NO | UP | NO |
| AT4G27800 | 135.76 | 1.46 | 103.14 | 0.39 | -0.40 | 4.10E-02 | NO | NO | NO | NO |
| AT4G28706 | 30.01 | 0.17 | 16.80 | 0.42 | -0.84 | 1.79E-06 | NO | NO | NO | NO |
| AT4G28750 | 902.84 | 5.77 | 658.46 | 5.73 | -0.46 | 3.40E-02 | NO | NO | NO | NO |
| AT4G29490 | 22.58 | 0.42 | 16.51 | 0.26 | -0.45 | 4.23E-02 | NO | NO | NO | NO |
| AT4G30710 | 7.60 | 0.21 | 4.02 | 0.10 | -0.92 | 4.71E-05 | NO | NO | NO | NO |
| AT4G31780 | 86.15 | 1.80 | 61.32 | 0.70 | -0.49 | 1.25E-02 | NO | NO | NO | UP |
| AT4G31810 | 29.04 | 0.38 | 21.09 | 0.55 | -0.46 | 3.12E-02 | NO | NO | NO | NO |
| AT4G32520 | 82.38 | 1.40 | 58.89 | 0.48 | -0.48 | 1.07E-03 | NO | NO | NO | NO |
| AT4G32590 | 123.17 | 1.51 | 98.43 | 1.10 | -0.32 | 2.59E-02 | NO | NO | NO | NO |
| AT4G32950 | 2.98 | 0.00 | 0.79 | 0.22 | -1.91 | 7.88E-03 | NO | NO | NO | NO |
| AT4G33480 | 67.68 | 1.35 | 47.50 | 0.31 | -0.51 | 8.13E-03 | NO | NO | NO | NO |
| AT4G33490 | 22.09 | 0.29 | 15.51 | 0.47 | -0.51 | 6.67E-03 | NO | NO | NO | NO |
| AT4G33520 | 65.85 | 0.59 | 33.09 | 0.57 | -0.99 | 1.69E-13 | NEGATIVE | NO | NO | NO |
| AT4G33905 | 5.26 | 0.37 | 1.70 | 0.34 | -1.63 | 1.64E-03 | POSITIVE | NO | NO | NO |
| AT4G33980 | 90.40 | 1.76 | 67.35 | 1.26 | -0.42 | 2.81E-02 | NO | NO | UP | NO |
| AT4G34560 | 10.01 | 0.46 | 5.55 | 0.50 | -0.85 | 1.22E-02 | NO | NO | NO | NO |
| AT4G34950 | 270.64 | 0.74 | 165.98 | 1.53 | -0.71 | 3.14E-04 | NO | NO | NO | NO |
| AT4G34990 | 17.70 | 0.31 | 7.96 | 0.27 | -1.15 | 4.92E-05 | NO | YES | UP | UP |
| AT4G35450 | 404.87 | 3.60 | 335.41 | 4.30 | -0.27 | 8.71E-03 | NO | NO | NO | NO |
| AT4G36240 | 12.02 | 0.14 | 3.79 | 0.68 | -1.67 | 1.23E-05 | NO | YES | NO | NO |
| AT4G36570 | 24.70 | 1.42 | 12.03 | 0.97 | -1.04 | 3.28E-02 | NO | NO | NO | NO |
| AT4G37320 | 25.27 | 0.44 | 8.77 | 0.19 | -1.53 | 1.85E-14 | NO | NO | UP | NO |
| AT4G37330 | 14.23 | 0.11 | 9.79 | 0.34 | -0.54 | 2.89E-02 | NO | NO | NO | NO |
| AT4G37470 | 112.63 | 1.04 | 72.40 | 1.12 | -0.64 | 3.71E-04 | NO | NO | NO | NO |
| AT4G37660 | 46.33 | 0.80 | 31.63 | 0.98 | -0.55 | 1.57E-02 | NO | NO | NO | NO |
| AT4G38050 | 4.99 | 0.10 | 3.05 | 0.07 | -0.71 | 2.60E-02 | NO | NO | NO | NO |

**Table A3.3 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT4G39260 | 253.08 | 5.38 | 170.07 | 3.23 | -0.57 | 1.07E-08 | NO | NO | NO | NO |
| AT4G39510 | 16.21 | 0.42 | 11.05 | 1.06 | -0.55 | 1.37E-02 | NO | NO | NO | NO |
| AT4G39540 | 31.11 | 0.54 | 22.28 | 0.16 | -0.48 | 2.50E-02 | NO | NO | NO | NO |
| AT4G40065 | 63.05 | 0.41 | 31.93 | 0.50 | -0.98 | 9.46E-08 | NO | NO | NO | NO |
| AT5G01520 | 15.75 | 0.44 | 4.32 | 0.29 | -1.87 | 7.72E-12 | NO | NO | NO | NO |
| AT5G02190 | 11.45 | 0.66 | 7.93 | 0.28 | -0.53 | 4.54E-02 | NO | NO | NO | NO |
| AT5G02240 | 661.26 | 3.99 | 396.65 | 0.69 | -0.74 | 1.37E-04 | NO | NO | NO | NO |
| AT5G02790 | 206.73 | 0.43 | 143.53 | 0.10 | -0.53 | 4.85E-03 | NO | NO | NO | NO |
| AT5G03230 | 20.02 | 0.42 | 11.76 | 0.52 | -0.77 | 6.75E-03 | NO | NO | NO | NO |
| AT5G03670 | 6.61 | 0.19 | 3.65 | 0.26 | -0.86 | 3.68E-03 | NO | NO | NO | NO |
| AT5G06530 | 66.07 | 0.74 | 45.83 | 1.12 | -0.53 | 3.16E-03 | NO | NO | NO | NO |
| AT5G07580 | 53.96 | 0.80 | 37.87 | 1.23 | -0.51 | 1.06E-02 | NO | YES | NO | NO |
| AT5G07690 | 57.12 | 1.04 | 27.38 | 1.51 | -1.06 | 1.81E-09 | NO | YES | NO | NO |
| AT5G08030 | 3.70 | 0.28 | 1.13 | 0.13 | -1.71 | 2.22E-03 | NO | NO | NO | NO |
| AT5G08100 | 35.93 | 0.22 | 26.49 | 0.80 | -0.44 | 4.09E-02 | NO | NO | NO | NO |
| AT5G08260 | 137.93 | 0.92 | 95.57 | 1.34 | -0.53 | 6.21E-03 | NO | NO | NO | NO |
| AT5G08410 | 380.19 | 2.36 | 287.35 | 1.14 | -0.40 | 4.39E-02 | NO | NO | NO | NO |
| AT5G09672 | 5.57 | 1.39 | 2.65 | 0.59 | -1.07 | 3.51E-04 | NO | NO | NO | NO |
| AT5G10170 | 4.62 | 0.11 | 1.95 | 0.02 | -1.24 | 9.25E-04 | NO | NO | NO | NO |
| AT5G11110 | 12.76 | 0.72 | 8.00 | 0.14 | -0.67 | 5.34E-04 | NO | NO | UP | NO |
| AT5G11310 | 7.07 | 0.08 | 2.65 | 0.27 | -1.41 | 1.06E-06 | NO | NO | NO | NO |
| AT5G11450 | 255.86 | 0.78 | 182.63 | 2.88 | -0.49 | 1.18E-02 | NO | NO | NO | NO |
| AT5G11790 | 53.17 | 0.81 | 39.02 | 1.09 | -0.45 | 2.93E-02 | NO | NO | NO | NO |
| AT5G11840 | 44.16 | 0.24 | 31.62 | 0.38 | -0.48 | 2.92E-02 | NO | NO | NO | NO |
| AT5G13930 | 643.47 | 16.94 | 222.62 | 3.79 | -1.53 | 0.00E+00 | NO | NO | NO | NO |
| AT5G14090 | 9.91 | 0.74 | 4.73 | 0.30 | -1.07 | 6.12E-04 | NO | NO | NO | NO |
| AT5G14545 | 3469.79 | 48.24 | 606.23 | 4.05 | -2.52 | 5.50E-07 | NO | NO | NO | NO |
| AT5G14565 | 53.30 | 1.68 | 20.90 | 0.40 | -1.35 | 0.00E+00 | NO | NO | NO | NO |
| AT5G14570 | 32.90 | 0.35 | 21.95 | 0.28 | -0.58 | 2.58E-03 | NO | NO | UP | UP |

**Table A3.3 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G15160 | 9.81 | 0.13 | 4.03 | 0.23 | -1.28 | 1.85E-02 | NO | NO | NO | NO |
| AT5G15190 | 19.10 | 1.07 | 9.97 | 0.18 | -0.94 | 2.84E-03 | NO | NO | NO | NO |
| AT5G15360 | 80.07 | 1.93 | 50.32 | 0.93 | -0.67 | 7.02E-04 | NO | NO | NO | NO |
| AT5G15650 | 517.49 | 9.35 | 340.35 | 2.74 | -0.60 | 6.11E-03 | NO | NO | NO | NO |
| AT5G16010 | 154.66 | 2.62 | 111.70 | 1.10 | -0.47 | 1.81E-02 | NO | NO | NO | NO |
| AT5G16290 | 43.91 | 0.94 | 30.25 | 0.44 | -0.54 | 3.87E-03 | NO | NO | NO | NO |
| AT5G17840 | 65.80 | 0.82 | 40.85 | 0.20 | -0.69 | 7.49E-04 | NO | NO | NO | NO |
| AT5G18680 | 18.33 | 0.14 | 12.50 | 0.13 | -0.55 | 2.10E-02 | NO | YES | NO | NO |
| AT5G19090 | 38.88 | 0.34 | 23.06 | 1.18 | -0.75 | 1.30E-08 | NO | NO | NO | NO |
| AT5G19150 | 31.04 | 0.05 | 23.37 | 0.27 | -0.41 | 3.20E-02 | NO | NO | NO | NO |
| AT5G19460 | 32.24 | 0.65 | 22.62 | 0.40 | -0.51 | 1.44E-02 | NO | NO | NO | NO |
| AT5G20280 | 129.33 | 2.10 | 86.86 | 0.54 | -0.57 | 6.47E-03 | POSITIVE | NO | NO | NO |
| AT5G20700 | 901.96 | 9.56 | 620.43 | 2.19 | -0.54 | 2.36E-02 | NO | NO | NO | NO |
| AT5G21020 | 196.73 | 1.04 | 127.91 | 1.72 | -0.62 | 5.07E-04 | NO | NO | NO | NO |
| AT5G21100 | 6.66 | 0.06 | 4.05 | 0.53 | -0.72 | 1.39E-02 | NO | NO | DOWN | NO |
| AT5G22020 | 27.41 | 0.63 | 20.13 | 0.34 | -0.45 | 4.64E-02 | NO | NO | NO | NO |
| AT5G22070 | 32.55 | 0.61 | 21.75 | 0.32 | -0.58 | 2.63E-03 | NO | NO | NO | NO |
| AT5G22650 | 254.73 | 2.29 | 187.60 | 3.36 | -0.44 | 2.09E-02 | NO | NO | NO | NO |
| AT5G22880 | 253.00 | 1.73 | 161.08 | 3.85 | -0.65 | 4.14E-04 | NO | NO | NO | NO |
| AT5G24300 | 157.63 | 1.66 | 108.50 | 0.63 | -0.54 | 7.17E-03 | NO | NO | NO | UP |
| AT5G24490 | 429.59 | 1.89 | 247.88 | 0.76 | -0.79 | 1.80E-05 | NO | NO | NO | NO |
| AT5G25890 | 22.52 | 0.63 | 14.95 | 0.10 | -0.59 | 3.32E-02 | NO | YES | NO | NO |
| AT5G26570 | 173.21 | 2.26 | 84.75 | 0.16 | -1.03 | 8.40E-08 | NO | NO | NO | NO |
| AT5G28150 | 28.30 | 0.82 | 14.78 | 0.37 | -0.94 | 2.14E-06 | NO | NO | NO | UP |
| AT5G28300 | 53.64 | 1.63 | 29.25 | 1.23 | -0.87 | 4.43E-07 | NO | YES | NO | NO |
| AT5G37360 | 52.59 | 0.34 | 31.46 | 0.51 | -0.74 | 9.76E-05 | NO | NO | NO | NO |
| AT5G39240 | 274.06 | 2.87 | 158.24 | 5.08 | -0.79 | 1.25E-04 | NO | NO | NO | NO |
| AT5G39350 | 4.44 | 0.23 | 2.50 | 0.14 | -0.83 | 2.14E-02 | NO | NO | NO | NO |
| AT5G42420 | 49.40 | 0.24 | 37.08 | 0.65 | -0.41 | 4.47E-02 | NO | NO | NO | NO |

**Table A3.3 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G42530 | 3652.28 | 130.06 | 1728.50 | 9.29 | -1.08 | 2.54E-06 | NO | NO | NO | NO |
| AT5G42900 | 200.37 | 3.24 | 157.06 | 0.76 | -0.35 | 5.63E-03 | NO | NO | UP | NO |
| AT5G43150 | 70.15 | 1.13 | 33.67 | 0.91 | -1.06 | 1.21E-06 | NO | NO | NO | NO |
| AT5G43400 | 1.17 | 0.10 | 0.43 | 0.05 | -1.44 | 3.44E-02 | NO | NO | NO | NO |
| AT5G43850 | 101.90 | 0.30 | 70.42 | 1.53 | -0.53 | 6.66E-03 | NO | NO | NO | NO |
| AT5G44005 | 34.19 | 0.58 | 13.55 | 0.71 | -1.34 | 7.59E-07 | NO | NO | NO | NO |
| AT5G44530 | 12.75 | 0.29 | 8.85 | 0.16 | -0.53 | 1.40E-02 | NO | NO | NO | UP |
| AT5G45680 | 279.32 | 1.44 | 142.13 | 1.01 | -0.97 | 7.27E-09 | NO | NO | NO | NO |
| AT5G45930 | 178.18 | 1.66 | 93.94 | 1.35 | -0.92 | 6.20E-08 | NO | NO | NO | NO |
| AT5G46160 | 84.25 | 1.38 | 52.30 | 1.64 | -0.69 | 7.77E-05 | NO | NO | NO | NO |
| AT5G46600 | 13.77 | 0.30 | 7.64 | 0.29 | -0.85 | 1.42E-04 | NO | NO | NO | NO |
| AT5G46710 | 30.15 | 0.53 | 15.99 | 0.46 | -0.91 | 1.74E-05 | NO | YES | UP | NO |
| AT5G47060 | 66.36 | 1.15 | 29.78 | 0.89 | -1.16 | 3.09E-10 | NO | NO | UP | NO |
| AT5G47540 | 28.64 | 0.41 | 18.57 | 0.61 | -0.63 | 1.93E-03 | NEGATIVE | NO | NO | NO |
| AT5G47700 | 460.51 | 2.63 | 317.94 | 9.62 | -0.53 | 3.40E-03 | NO | NO | NO | NO |
| AT5G48630 | 37.21 | 0.85 | 26.28 | 0.41 | -0.50 | 3.38E-02 | NO | NO | NO | NO |
| AT5G48790 | 55.97 | 0.42 | 28.74 | 0.45 | -0.96 | 1.83E-07 | NO | NO | NO | NO |
| AT5G49190 | 3.15 | 0.26 | 1.55 | 0.03 | -1.02 | 7.50E-03 | NO | NO | NO | NO |
| AT5G50240 | 14.84 | 0.17 | 8.63 | 0.44 | -0.78 | 8.58E-03 | NO | NO | NO | NO |
| AT5G50250 | 179.70 | 1.35 | 130.69 | 2.00 | -0.46 | 1.88E-02 | NO | NO | NO | NO |
| AT5G50360 | 22.39 | 0.45 | 11.93 | 0.22 | -0.91 | 7.07E-05 | NO | NO | NO | NO |
| AT5G51820 | 150.21 | 1.44 | 89.79 | 0.62 | -0.74 | 4.52E-05 | NO | NO | NO | NO |
| AT5G54580 | 63.49 | 0.89 | 46.48 | 1.70 | -0.45 | 3.67E-02 | NO | NO | NO | NO |
| AT5G55280 | 177.75 | 2.58 | 125.73 | 1.13 | -0.50 | 9.98E-03 | NEGATIVE | NO | NO | NO |
| AT5G57345 | 205.84 | 2.27 | 147.91 | 0.85 | -0.48 | 1.26E-02 | NO | NO | NO | NO |
| AT5G57760 | 35.34 | 4.42 | 14.51 | 2.76 | -1.28 | 2.01E-05 | NO | NO | NO | NO |
| AT5G58490 | 128.35 | 1.49 | 71.78 | 0.87 | -0.84 | 1.27E-06 | NO | NO | NO | NO |
| AT5G58700 | 14.42 | 0.58 | 5.98 | 0.36 | -1.27 | 2.18E-09 | NO | NO | UP | NO |
| AT5G59080 | 20.23 | 0.26 | 9.75 | 0.59 | -1.05 | 2.01E-04 | NO | NO | NO | NO |

**Table A3.3 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G59680 | 1.00 | 0.16 | 0.28 | 0.05 | -1.82 | 9.25E-03 | NO | NO | NO | NO |
| AT5G59700 | 2.08 | 0.08 | 0.97 | 0.08 | -1.10 | 1.40E-02 | NO | NO | NO | NO |
| AT5G59950 | 79.63 | 0.18 | 53.71 | 1.11 | -0.57 | 1.48E-04 | POSITIVE | NO | NO | NO |
| AT5G60540 | 94.80 | 0.50 | 51.24 | 0.66 | -0.89 | 3.14E-07 | NO | NO | NO | NO |
| AT5G61520 | 30.16 | 0.18 | 20.95 | 0.22 | -0.53 | 6.38E-04 | NO | NO | NO | NO |
| AT5G61660 | 145.45 | 1.28 | 106.65 | 2.18 | -0.45 | 2.71E-02 | NO | NO | NO | NO |
| AT5G61810 | 39.39 | 0.22 | 26.32 | 0.72 | -0.58 | 2.24E-03 | NO | NO | UP | UP |
| AT5G62360 | 149.35 | 2.66 | 97.20 | 3.60 | -0.62 | 7.36E-04 | NO | NO | UP | NO |
| AT5G62960 | 12.13 | 1.00 | 4.77 | 0.23 | -1.35 | 2.43E-06 | NO | NO | NO | UP |
| AT5G63810 | 44.33 | 0.39 | 31.87 | 0.39 | -0.48 | 1.43E-02 | NO | NO | NO | NO |
| AT5G64040 | 3250.16 | 81.42 | 1924.23 | 33.98 | -0.76 | 5.00E-03 | NO | NO | NO | NO |
| AT5G64240 | 11.61 | 0.28 | 7.14 | 0.08 | -0.70 | 6.58E-03 | NO | NO | DOWN | NO |
| AT5G64350 | 330.08 | 0.58 | 247.18 | 3.57 | -0.42 | 3.42E-02 | NO | NO | NO | NO |
| AT5G64460 | 104.70 | 0.94 | 76.87 | 0.87 | -0.45 | 1.25E-03 | NO | NO | NO | NO |
| AT5G64550 | 19.16 | 0.19 | 11.35 | 0.76 | -0.76 | 7.49E-05 | NO | NO | NO | NO |
| AT5G65220 | 1230.84 | 17.13 | 737.48 | 17.73 | -0.74 | 4.90E-04 | NEGATIVE | NO | NO | NO |
| AT5G65420 | 8.51 | 0.21 | 4.92 | 0.14 | -0.79 | 1.49E-02 | NO | NO | NO | NO |
| AT5G65480 | 95.46 | 1.35 | 65.95 | 0.29 | -0.53 | 5.62E-03 | NO | NO | NO | NO |
| AT5G66420 | 25.91 | 0.49 | 19.23 | 0.42 | -0.43 | 1.99E-02 | NO | NO | NO | NO |
| AT5G66530 | 271.43 | 2.45 | 192.21 | 2.00 | -0.50 | 9.57E-03 | NO | NO | NO | NO |
| AT5G66610 | 4.51 | 0.15 | 2.31 | 0.17 | -0.97 | 6.22E-03 | NO | YES | NO | NO |
| AT5G66720 | 118.40 | 0.94 | 81.66 | 1.59 | -0.54 | 1.84E-03 | NO | NO | NO | NO |

**Table A3.4**. 1656 Category 1 FTD Candidate Genes with higher expression in IT at 2 weeks of cold-acclimation. Genes are ordered by their AGI numbers. FPKM values are the average of three biological replicates (n=3). Standard error (SE) values are also given for each FPKM value. Genes were considered significantly different between SW and IT under non-acclimated conditions if they had a Benjamini-Hochberg corrected p-value (FDR P-VALUE) of <0.05 and a minimum of ≥3FPKM in IT. The differential expression of each gene is also represented by the logarithm (base=2) of the fold change (LOG2.FC). This table also denotes if a gene was previously described as positively or negatively correlating with freezing tolerance (HANNAH;(6)), a transcription factor (TF), a gene previously described as up- or down-regulated by 1 week of cold (COS, (25)), identified as an up- or down-regulated component of the CBF regulon (CBF REGULON; (25)).

| AGI | SW.2WK FPKM | SW.2WK SE | IT.2WK FPKM | IT.2WK SE | SW.IT.2WK LOG2FC | SW.IT.2WK FDR P-VALUE | HANNAH? | TF? | COS? | CBF REG? |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G01180 | 3.95 | 0.21 | 11.81 | 0.30 | 1.58 | 7.19E-07 | NO | NO | NO | NO |
| AT1G01240 | 12.36 | 0.26 | 17.96 | 0.17 | 0.54 | 2.13E-02 | NO | NO | NO | NO |
| AT1G01340 | 1.05 | 0.18 | 11.58 | 0.46 | 3.46 | 0.00E+00 | NO | NO | NO | NO |
| AT1G01440 | 5.27 | 0.06 | 8.17 | 0.14 | 0.63 | 1.71E-02 | NO | NO | NO | NO |
| AT1G01490 | 31.27 | 0.73 | 46.49 | 0.39 | 0.57 | 1.57E-03 | NO | NO | NO | NO |
| AT1G01560 | 3.21 | 0.76 | 22.16 | 0.42 | 2.79 | 0.00E+00 | NO | NO | NO | NO |
| AT1G02335 | 4.60 | 0.26 | 8.63 | 0.13 | 0.91 | 4.10E-02 | NO | NO | NO | NO |
| AT1G02450 | 2.66 | 0.39 | 28.09 | 1.90 | 3.40 | 7.37E-13 | NO | NO | NO | NO |
| AT1G02500 | 49.68 | 1.00 | 139.80 | 2.80 | 1.49 | 0.00E+00 | NO | NO | NO | NO |
| AT1G02640 | 1.31 | 0.04 | 2.49 | 0.25 | 0.93 | 2.73E-02 | NEGATIVE | NO | NO | NO |
| AT1G02920 | 113.78 | 4.47 | 449.52 | 0.57 | 1.98 | 0.00E+00 | NO | NO | NO | NO |
| AT1G02930 | 207.21 | 14.24 | 1012.24 | 4.71 | 2.29 | 0.00E+00 | NO | NO | NO | NO |
| AT1G03060 | 4.82 | 0.20 | 7.04 | 0.26 | 0.55 | 4.99E-03 | NO | NO | NO | NO |
| AT1G03210 | 21.79 | 0.75 | 31.44 | 0.35 | 0.53 | 3.63E-02 | NO | NO | NO | NO |
| AT1G03290 | 20.73 | 0.70 | 45.39 | 0.30 | 1.13 | 0.00E+00 | POSITIVE | NO | NO | NO |
| AT1G03370 | 11.32 | 0.61 | 19.25 | 0.41 | 0.77 | 3.27E-05 | NO | NO | NO | NO |
| AT1G03400 | 27.38 | 0.96 | 43.81 | 0.16 | 0.68 | 6.71E-04 | NO | NO | NO | NO |
| AT1G03730 | 6.51 | 0.21 | 10.90 | 0.38 | 0.74 | 2.74E-02 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G04140 | 18.15 | 0.43 | 23.81 | 0.27 | 0.39 | 1.35E-02 | NO | NO | NO | NO |
| AT1G04425 | 30.21 | 0.54 | 63.27 | 3.12 | 1.07 | 5.43E-05 | NO | NO | NO | NO |
| AT1G04530 | 34.88 | 0.58 | 77.34 | 1.48 | 1.15 | 1.85E-11 | NO | NO | NO | NO |
| AT1G04770 | 8.61 | 0.44 | 21.16 | 0.86 | 1.30 | 4.52E-08 | NO | NO | NO | NO |
| AT1G04780 | 20.89 | 0.32 | 39.76 | 0.39 | 0.93 | 7.32E-08 | NO | NO | NO | NO |
| AT1G04980 | 8.28 | 0.38 | 32.65 | 0.84 | 1.98 | 0.00E+00 | NO | NO | NO | NO |
| AT1G05000 | 3.05 | 0.34 | 6.33 | 0.65 | 1.05 | 7.42E-03 | NO | NO | NO | NO |
| AT1G05010 | 96.25 | 0.92 | 193.56 | 0.98 | 1.01 | 3.09E-09 | NO | NO | NO | DOWN |
| AT1G05230 | 6.76 | 0.24 | 9.59 | 0.39 | 0.50 | 1.06E-02 | NO | YES | NO | NO |
| AT1G05570 | 12.02 | 0.43 | 20.02 | 0.31 | 0.74 | 2.55E-05 | NO | NO | NO | NO |
| AT1G05630 | 5.93 | 0.24 | 10.10 | 0.23 | 0.77 | 1.44E-05 | NO | NO | NO | NO |
| AT1G05880 | 0.33 | 0.14 | 5.50 | 0.14 | 4.07 | 0.00E+00 | NO | NO | NO | NO |
| AT1G05910 | 14.38 | 0.27 | 20.19 | 0.23 | 0.49 | 1.20E-02 | NO | NO | NO | NO |
| AT1G06410 | 26.90 | 0.39 | 43.52 | 0.29 | 0.69 | 1.08E-04 | NO | NO | NO | NO |
| AT1G06430 | 55.48 | 0.90 | 86.22 | 1.44 | 0.64 | 4.06E-04 | NO | NO | NO | NO |
| AT1G06620 | 1.91 | 0.33 | 5.83 | 0.24 | 1.61 | 1.27E-04 | NO | NO | NO | NO |
| AT1G06645 | 8.20 | 0.40 | 15.11 | 0.19 | 0.88 | 6.60E-04 | NO | NO | NO | NO |
| AT1G06650 | 52.94 | 0.09 | 75.50 | 0.52 | 0.51 | 6.95E-04 | NO | NO | NO | NO |
| AT1G07000 | 7.43 | 1.16 | 22.05 | 0.53 | 1.57 | 1.93E-14 | NO | NO | NO | NO |
| AT1G07128 | 2.12 | 0.11 | 5.22 | 0.14 | 1.30 | 2.64E-02 | NO | NO | NO | NO |
| AT1G07135 | 9.88 | 1.10 | 24.64 | 0.26 | 1.32 | 6.79E-06 | NO | NO | NO | NO |
| AT1G07590 | 141.59 | 1.64 | 208.87 | 1.46 | 0.56 | 1.16E-02 | NO | NO | NO | NO |
| AT1G07600 | 4144.39 | 75.33 | 6055.84 | 37.14 | 0.55 | 1.62E-02 | NO | NO | NO | NO |
| AT1G07620 | 5.92 | 0.72 | 18.54 | 0.49 | 1.65 | 0.00E+00 | NO | NO | NO | NO |
| AT1G07640 | 5.78 | 0.28 | 10.15 | 0.08 | 0.81 | 2.26E-03 | NO | YES | NO | NO |
| AT1G07650 | 19.03 | 0.32 | 31.75 | 0.41 | 0.74 | 1.02E-08 | NO | NO | NO | NO |
| AT1G07900 | 3.75 | 0.97 | 9.84 | 1.08 | 1.39 | 1.11E-02 | NO | YES | NO | NO |
| AT1G08050 | 1.68 | 0.17 | 13.21 | 0.54 | 2.98 | 0.00E+00 | NO | NO | NO | NO |
| AT1G08060 | 3.04 | 0.08 | 4.42 | 0.32 | 0.54 | 5.85E-03 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G08450 | 41.91 | 1.71 | 157.81 | 2.45 | 1.91 | 0.00E+00 | NO | NO | NO | NO |
| AT1G08600 | 5.08 | 0.18 | 7.18 | 0.23 | 0.50 | 3.07E-03 | NO | NO | NO | NO |
| AT1G08620 | 5.50 | 0.17 | 7.58 | 0.19 | 0.46 | 4.15E-02 | NO | YES | NO | NO |
| AT1G08650 | 31.91 | 0.91 | 43.35 | 0.75 | 0.44 | 3.67E-02 | NO | NO | NO | NO |
| AT1G08830 | 215.63 | 0.76 | 418.66 | 6.35 | 0.96 | 3.24E-08 | NO | NO | NO | NO |
| AT1G08930 | 70.02 | 0.64 | 95.18 | 0.93 | 0.44 | 2.20E-02 | NO | NO | NO | NO |
| AT1G08940 | 2.45 | 0.33 | 15.47 | 0.03 | 2.66 | 6.78E-12 | NO | NO | NO | NO |
| AT1G09180 | 1.80 | 0.12 | 9.33 | 0.99 | 2.38 | 3.46E-06 | NO | NO | NO | NO |
| AT1G09210 | 159.65 | 2.84 | 360.11 | 5.38 | 1.17 | 3.99E-10 | NO | NO | NO | NO |
| AT1G09415 | 24.92 | 0.72 | 40.42 | 1.17 | 0.70 | 5.69E-03 | NO | NO | DOWN | NO |
| AT1G09560 | 62.06 | 1.61 | 221.01 | 1.82 | 1.83 | 0.00E+00 | NO | NO | NO | NO |
| AT1G09850 | 28.52 | 0.84 | 43.26 | 0.56 | 0.60 | 1.87E-03 | NO | NO | NO | NO |
| AT1G09970 | 28.73 | 0.71 | 89.69 | 2.41 | 1.64 | 0.00E+00 | NO | NO | NO | NO |
| AT1G10020 | 7.35 | 0.02 | 13.02 | 0.70 | 0.83 | 2.52E-04 | NO | NO | NO | NO |
| AT1G10050 | 3.83 | 0.30 | 5.97 | 0.40 | 0.64 | 1.39E-02 | NO | NO | NO | NO |
| AT1G10140 | 6.55 | 0.30 | 14.11 | 0.39 | 1.11 | 2.78E-03 | NO | NO | NO | NO |
| AT1G10155 | 29.68 | 0.41 | 59.89 | 0.46 | 1.01 | 1.39E-05 | NO | NO | NO | NO |
| AT1G10170 | 8.59 | 0.17 | 12.58 | 0.29 | 0.55 | 6.96E-03 | NO | NO | NO | NO |
| AT1G10550 | 5.43 | 0.78 | 14.71 | 0.53 | 1.44 | 1.35E-06 | NO | NO | NO | NO |
| AT1G10920 | 4.66 | 0.19 | 7.46 | 0.37 | 0.68 | 3.21E-03 | NO | NO | NO | NO |
| AT1G10960 | 121.53 | 1.38 | 167.31 | 2.05 | 0.46 | 1.95E-02 | NEGATIVE | NO | DOWN | NO |
| AT1G11050 | 3.59 | 0.37 | 11.14 | 0.56 | 1.63 | 1.16E-11 | NO | NO | NO | NO |
| AT1G11190 | 0.93 | 0.22 | 3.11 | 0.63 | 1.74 | 2.16E-03 | NO | NO | NO | NO |
| AT1G11310 | 35.64 | 0.34 | 66.00 | 0.67 | 0.89 | 5.82E-08 | NO | NO | NO | NO |
| AT1G11410 | 2.23 | 0.12 | 3.74 | 0.23 | 0.75 | 2.66E-02 | NO | NO | NO | NO |
| AT1G11790 | 15.75 | 0.69 | 21.96 | 0.05 | 0.48 | 2.99E-02 | NO | NO | NO | NO |
| AT1G11905 | 27.86 | 0.87 | 41.86 | 1.08 | 0.59 | 2.10E-03 | NO | NO | NO | NO |
| AT1G12110 | 25.71 | 0.17 | 35.47 | 0.43 | 0.46 | 2.09E-02 | NO | NO | NO | NO |
| AT1G12140 | 18.41 | 0.08 | 28.13 | 0.67 | 0.61 | 2.27E-03 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G12240 | 20.47 | 0.28 | 30.92 | 0.62 | 0.59 | 1.59E-03 | NEGATIVE | NO | DOWN | NO |
| AT1G12290 | 2.66 | 0.17 | 5.24 | 0.29 | 0.98 | 1.73E-04 | NO | NO | NO | NO |
| AT1G12360 | 24.86 | 0.12 | 39.12 | 0.14 | 0.65 | 3.36E-04 | NO | NO | NO | NO |
| AT1G12420 | 8.25 | 0.23 | 17.87 | 0.30 | 1.12 | 1.14E-07 | NO | NO | NO | NO |
| AT1G12440 | 144.56 | 1.06 | 209.85 | 1.45 | 0.54 | 3.32E-03 | NO | NO | NO | NO |
| AT1G12520 | 37.47 | 0.20 | 60.71 | 0.78 | 0.70 | 3.88E-05 | NO | NO | NO | NO |
| AT1G12990 | 13.24 | 0.33 | 24.86 | 0.25 | 0.91 | 1.82E-06 | NO | NO | NO | NO |
| AT1G13210 | 16.94 | 0.87 | 44.47 | 0.86 | 1.39 | 0.00E+00 | NO | NO | NO | NO |
| AT1G13245 | 47.19 | 1.42 | 107.41 | 2.25 | 1.19 | 2.44E-09 | NO | NO | NO | NO |
| AT1G13260 | 61.71 | 1.05 | 92.94 | 1.26 | 0.59 | 1.32E-03 | NO | YES | UP | NO |
| AT1G13950 | 2.37 | 0.25 | 6.15 | 0.28 | 1.38 | 1.53E-02 | NO | NO | NO | NO |
| AT1G14010 | 33.14 | 0.33 | 64.06 | 0.45 | 0.95 | 5.13E-07 | NO | NO | NO | NO |
| AT1G14330 | 4.07 | 0.19 | 9.15 | 0.38 | 1.17 | 3.19E-06 | NO | NO | NO | NO |
| AT1G14360 | 18.38 | 0.48 | 50.23 | 1.00 | 1.45 | 0.00E+00 | NO | NO | NO | NO |
| AT1G14370 | 7.13 | 0.35 | 17.52 | 0.60 | 1.30 | 2.38E-09 | NO | NO | NO | NO |
| AT1G14820 | 40.45 | 0.40 | 54.23 | 0.57 | 0.42 | 3.67E-02 | NO | NO | NO | NO |
| AT1G14870 | 1.17 | 0.34 | 8.73 | 0.38 | 2.91 | 5.19E-07 | NO | NO | NO | NO |
| AT1G14890 | 4.94 | 0.11 | 9.45 | 0.16 | 0.94 | 1.56E-02 | NO | NO | NO | NO |
| AT1G15020 | 8.43 | 0.12 | 11.66 | 0.16 | 0.47 | 4.70E-02 | NO | NO | NO | NO |
| AT1G15340 | 52.61 | 0.62 | 82.58 | 1.26 | 0.65 | 3.16E-04 | NO | NO | NO | NO |
| AT1G15430 | 5.88 | 0.48 | 9.48 | 0.40 | 0.69 | 4.31E-02 | NO | NO | NO | NO |
| AT1G15520 | 2.98 | 1.38 | 76.00 | 2.25 | 4.67 | 0.00E+00 | NO | NO | NO | NO |
| AT1G15670 | 1.05 | 0.22 | 4.62 | 0.57 | 2.14 | 2.25E-06 | NO | NO | NO | NO |
| AT1G15750 | 32.47 | 0.41 | 43.96 | 0.27 | 0.44 | 3.40E-04 | NO | NO | NO | NO |
| AT1G15860 | 44.88 | 0.67 | 65.95 | 0.99 | 0.56 | 3.90E-04 | NO | NO | NO | NO |
| AT1G15950 | 54.65 | 0.85 | 101.87 | 0.98 | 0.90 | 1.58E-07 | NO | NO | NO | NO |
| AT1G16090 | 3.95 | 0.15 | 11.99 | 0.69 | 1.60 | 7.17E-08 | NO | NO | NO | NO |
| AT1G16110 | 3.08 | 0.31 | 4.95 | 0.24 | 0.69 | 3.19E-02 | NO | NO | NO | NO |
| AT1G16260 | 6.19 | 0.12 | 9.59 | 0.33 | 0.63 | 5.35E-03 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G16270 | 4.23 | 0.10 | 6.10 | 0.12 | 0.53 | 1.20E-02 | NO | NO | NO | NO |
| AT1G16420 | 0.97 | 0.49 | 15.44 | 0.82 | 3.99 | 0.00E+00 | NO | NO | NO | NO |
| AT1G16670 | 7.14 | 0.48 | 18.33 | 0.03 | 1.36 | 4.88E-10 | NO | NO | NO | NO |
| AT1G17070 | 4.09 | 0.12 | 6.35 | 0.32 | 0.63 | 1.60E-02 | NO | NO | NO | NO |
| AT1G17330 | 11.06 | 0.33 | 25.29 | 0.11 | 1.19 | 1.14E-06 | NO | NO | NO | NO |
| AT1G17340 | 3.04 | 0.15 | 6.18 | 0.08 | 1.02 | 5.23E-05 | NO | NO | NO | NO |
| AT1G17360 | 11.15 | 0.32 | 19.29 | 0.47 | 0.79 | 1.67E-05 | NO | NO | NO | NO |
| AT1G17380 | 1.70 | 0.37 | 8.78 | 0.49 | 2.37 | 1.59E-08 | NO | YES | NO | NO |
| AT1G17430 | 5.31 | 0.35 | 8.83 | 0.33 | 0.73 | 4.24E-02 | NO | NO | NO | NO |
| AT1G17440 | 20.43 | 0.13 | 30.36 | 0.70 | 0.57 | 5.83E-05 | NO | NO | NO | NO |
| AT1G17550 | 16.07 | 0.24 | 25.23 | 0.71 | 0.65 | 6.09E-04 | NO | NO | NO | NO |
| AT1G17600 | 2.33 | 0.15 | 6.35 | 0.33 | 1.45 | 5.11E-09 | NO | NO | NO | NO |
| AT1G17620 | 13.67 | 0.24 | 27.82 | 0.84 | 1.03 | 3.46E-06 | NO | NO | NO | NO |
| AT1G17745 | 80.82 | 1.50 | 152.73 | 3.89 | 0.92 | 1.97E-07 | POSITIVE | NO | NO | NO |
| AT1G18210 | 116.67 | 1.37 | 156.06 | 1.16 | 0.42 | 5.02E-03 | NO | NO | NO | NO |
| AT1G18260 | 15.39 | 0.12 | 26.32 | 0.77 | 0.77 | 4.14E-05 | NO | NO | NO | NO |
| AT1G18300 | 2.23 | 0.25 | 8.91 | 0.64 | 2.00 | 7.29E-07 | NO | NO | NO | NO |
| AT1G18370 | 6.90 | 0.14 | 9.69 | 0.45 | 0.49 | 3.28E-02 | NO | NO | NO | NO |
| AT1G18390 | 6.18 | 0.48 | 9.98 | 0.89 | 0.69 | 1.91E-03 | NO | NO | NO | NO |
| AT1G18570 | 5.38 | 0.46 | 22.46 | 1.50 | 2.06 | 0.00E+00 | NO | YES | NO | NO |
| AT1G19000 | 40.63 | 0.56 | 55.29 | 1.61 | 0.44 | 8.55E-03 | NO | YES | DOWN | NO |
| AT1G19020 | 5.24 | 1.34 | 73.67 | 1.47 | 3.81 | 0.00E+00 | NO | NO | NO | NO |
| AT1G19180 | 34.47 | 0.30 | 78.94 | 1.22 | 1.20 | 1.08E-12 | NO | YES | UP | NO |
| AT1G19250 | 0.17 | 0.13 | 13.41 | 0.91 | 6.32 | 0.00E+00 | NO | NO | NO | NO |
| AT1G19300 | 2.84 | 0.24 | 8.02 | 0.41 | 1.50 | 4.47E-06 | NO | NO | NO | NO |
| AT1G19350 | 59.81 | 1.67 | 73.70 | 1.89 | 0.30 | 2.43E-02 | NO | YES | NO | NO |
| AT1G19360 | 22.54 | 0.18 | 33.82 | 0.35 | 0.59 | 2.66E-03 | NO | NO | NO | NO |
| AT1G19380 | 1.98 | 0.39 | 17.52 | 1.11 | 3.14 | 2.59E-11 | NO | NO | NO | NO |
| AT1G19490 | 6.86 | 0.10 | 11.08 | 0.25 | 0.69 | 7.79E-03 | NO | YES | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G19660 | 27.48 | 0.52 | 36.45 | 0.59 | 0.41 | 4.42E-02 | NO | NO | NO | NO |
| AT1G19670 | 49.97 | 0.99 | 66.34 | 1.59 | 0.41 | 4.80E-02 | NO | NO | DOWN | NO |
| AT1G19835 | 15.87 | 0.60 | 25.56 | 0.42 | 0.69 | 2.22E-06 | NO | NO | NO | NO |
| AT1G20100 | 47.59 | 0.42 | 100.82 | 0.42 | 1.08 | 1.91E-10 | NO | NO | NO | NO |
| AT1G20330 | 40.01 | 0.51 | 65.93 | 1.50 | 0.72 | 8.88E-05 | NO | NO | NO | NO |
| AT1G20510 | 38.11 | 0.92 | 63.52 | 1.86 | 0.74 | 1.86E-05 | NO | NO | NO | NO |
| AT1G20630 | 32.92 | 0.69 | 45.92 | 0.44 | 0.48 | 1.52E-02 | NO | NO | NO | NO |
| AT1G20780 | 11.23 | 0.37 | 18.02 | 0.15 | 0.68 | 4.74E-04 | NO | NO | NO | NO |
| AT1G20920 | 8.87 | 0.23 | 14.13 | 0.41 | 0.67 | 4.75E-05 | NO | NO | NO | NO |
| AT1G21100 | 1.06 | 0.23 | 4.42 | 0.16 | 2.06 | 2.15E-05 | NO | NO | NO | NO |
| AT1G21240 | 3.98 | 0.42 | 21.69 | 0.53 | 2.45 | 0.00E+00 | NO | NO | NO | NO |
| AT1G21250 | 56.92 | 2.59 | 182.09 | 1.04 | 1.68 | 0.00E+00 | NO | NO | NO | DOWN |
| AT1G21310 | 88.27 | 2.04 | 618.14 | 18.55 | 2.81 | 0.00E+00 | NO | NO | NO | NO |
| AT1G21370 | 7.89 | 0.07 | 15.55 | 0.40 | 0.98 | 8.84E-06 | NO | NO | NO | NO |
| AT1G21450 | 10.27 | 0.18 | 15.51 | 0.19 | 0.59 | 5.75E-03 | NO | YES | NO | NO |
| AT1G21460 | 53.05 | 0.87 | 86.84 | 0.84 | 0.71 | 8.57E-05 | NO | NO | NO | UP |
| AT1G21520 | 15.09 | 1.33 | 51.82 | 2.07 | 1.78 | 1.26E-12 | NO | NO | NO | NO |
| AT1G21580 | 8.55 | 0.12 | 11.65 | 0.53 | 0.45 | 2.74E-02 | NO | NO | NO | NO |
| AT1G21900 | 82.80 | 0.14 | 146.27 | 2.08 | 0.82 | 2.83E-06 | NO | NO | NO | NO |
| AT1G21910 | 0.78 | 0.17 | 2.36 | 0.26 | 1.61 | 1.55E-02 | NO | YES | UP | NO |
| AT1G21920 | 15.55 | 0.25 | 22.03 | 1.01 | 0.50 | 2.15E-02 | NO | NO | NO | NO |
| AT1G22280 | 28.43 | 0.95 | 66.30 | 1.41 | 1.22 | 1.04E-13 | NO | NO | NO | NO |
| AT1G22330 | 1.28 | 0.16 | 2.81 | 0.51 | 1.14 | 4.96E-02 | NO | NO | NO | NO |
| AT1G22410 | 42.80 | 0.86 | 99.73 | 1.71 | 1.22 | 1.20E-13 | NO | NO | NO | NO |
| AT1G22500 | 2.04 | 0.17 | 7.62 | 0.43 | 1.90 | 2.07E-07 | NO | NO | NO | NO |
| AT1G22650 | 3.06 | 0.11 | 8.12 | 0.39 | 1.41 | 9.89E-07 | NO | NO | NO | NO |
| AT1G22750 | 56.76 | 0.59 | 78.97 | 0.62 | 0.48 | 4.23E-04 | NO | NO | NO | NO |
| AT1G22930 | 33.99 | 0.27 | 62.71 | 0.30 | 0.88 | 3.73E-13 | NO | NO | NO | NO |
| AT1G23000 | 0.81 | 0.10 | 2.13 | 0.43 | 1.40 | 2.17E-02 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G23020 | 0.92 | 0.32 | 2.07 | 0.14 | 1.17 | 8.78E-03 | NO | NO | DOWN | NO |
| AT1G23030 | 5.88 | 0.05 | 8.87 | 0.42 | 0.59 | 2.30E-02 | NO | NO | NO | NO |
| AT1G23140 | 21.76 | 0.69 | 37.15 | 0.38 | 0.77 | 3.25E-03 | NO | NO | NO | NO |
| AT1G23170 | 2.25 | 0.05 | 5.09 | 0.20 | 1.18 | 1.23E-04 | NO | NO | NO | NO |
| AT1G23390 | 15.44 | 0.57 | 41.67 | 0.29 | 1.43 | 0.00E+00 | NO | NO | NO | NO |
| AT1G23440 | 47.02 | 0.54 | 92.47 | 0.93 | 0.98 | 1.64E-08 | NO | NO | NO | NO |
| AT1G23480 | 4.12 | 0.15 | 6.96 | 0.35 | 0.75 | 4.12E-03 | NO | NO | DOWN | NO |
| AT1G23710 | 6.60 | 0.24 | 13.41 | 0.92 | 1.02 | 2.89E-04 | NO | NO | DOWN | NO |
| AT1G24100 | 32.76 | 0.29 | 63.52 | 0.79 | 0.96 | 4.34E-08 | NEGATIVE | NO | NO | NO |
| AT1G24140 | 1.07 | 0.30 | 10.30 | 0.42 | 3.27 | 1.85E-14 | NO | NO | NO | NO |
| AT1G24147 | 29.36 | 3.05 | 149.55 | 1.42 | 2.35 | 0.00E+00 | NO | NO | NO | NO |
| AT1G24150 | 5.42 | 0.43 | 14.65 | 0.63 | 1.43 | 2.05E-11 | NO | NO | NO | NO |
| AT1G24265 | 1.77 | 0.10 | 3.71 | 0.12 | 1.07 | 1.88E-02 | NO | NO | NO | NO |
| AT1G24340 | 4.26 | 0.07 | 9.23 | 0.26 | 1.12 | 1.75E-06 | NO | NO | NO | NO |
| AT1G24350 | 19.19 | 0.26 | 25.97 | 0.19 | 0.44 | 3.92E-02 | NO | NO | NO | NO |
| AT1G24460 | 11.27 | 0.43 | 15.81 | 0.64 | 0.49 | 1.11E-03 | NO | NO | NO | NO |
| AT1G24530 | 17.87 | 0.37 | 26.44 | 0.49 | 0.57 | 9.37E-03 | NO | NO | NO | NO |
| AT1G25220 | 7.66 | 0.28 | 21.53 | 0.21 | 1.49 | 1.62E-10 | NO | NO | NO | NO |
| AT1G25280 | 17.68 | 0.36 | 25.03 | 0.34 | 0.50 | 2.21E-03 | NO | YES | NO | NO |
| AT1G25390 | 7.64 | 0.13 | 16.16 | 0.49 | 1.08 | 2.00E-07 | NO | NO | NO | NO |
| AT1G25400 | 1.95 | 0.06 | 6.52 | 0.16 | 1.74 | 3.64E-06 | NO | NO | DOWN | NO |
| AT1G25550 | 17.05 | 0.99 | 24.01 | 0.77 | 0.49 | 3.11E-02 | NO | YES | NO | NO |
| AT1G26130 | 5.90 | 0.18 | 10.52 | 0.33 | 0.84 | 4.15E-06 | NO | NO | NO | NO |
| AT1G26270 | 18.16 | 0.46 | 29.43 | 0.65 | 0.70 | 1.62E-04 | NO | NO | NO | NO |
| AT1G26380 | 2.49 | 0.81 | 10.94 | 0.67 | 2.13 | 2.81E-13 | NO | NO | NO | NO |
| AT1G26390 | 2.41 | 1.65 | 41.54 | 1.24 | 4.11 | 0.00E+00 | NO | NO | NO | NO |
| AT1G26420 | 0.58 | 0.21 | 5.66 | 0.16 | 3.27 | 1.66E-11 | NO | NO | NO | NO |
| AT1G27020 | 18.94 | 1.51 | 37.27 | 1.25 | 0.98 | 6.62E-07 | NO | NO | NO | NO |
| AT1G27100 | 19.70 | 0.04 | 30.91 | 0.70 | 0.65 | 5.28E-04 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G27290 | 16.41 | 0.51 | 35.53 | 0.16 | 1.11 | 8.73E-08 | NO | NO | NO | NO |
| AT1G27340 | 27.18 | 0.64 | 36.64 | 0.15 | 0.43 | 3.86E-02 | NO | NO | NO | NO |
| AT1G27730 | 9.11 | 0.77 | 39.18 | 0.28 | 2.11 | 0.00E+00 | NO | YES | UP | NO |
| AT1G27770 | 14.85 | 0.17 | 33.85 | 0.60 | 1.19 | 1.85E-12 | NO | NO | NO | NO |
| AT1G27980 | 16.07 | 0.55 | 23.30 | 0.24 | 0.54 | 1.12E-02 | NO | NO | NO | NO |
| AT1G28010 | 1.48 | 0.06 | 2.97 | 0.11 | 1.00 | 1.04E-03 | NO | NO | NO | NO |
| AT1G28240 | 8.42 | 0.08 | 11.70 | 0.29 | 0.47 | 4.92E-02 | NO | NO | NO | NO |
| AT1G28280 | 27.00 | 0.39 | 48.95 | 0.84 | 0.86 | 4.86E-07 | NO | NO | NO | NO |
| AT1G28370 | 5.35 | 0.72 | 9.51 | 0.61 | 0.83 | 3.00E-02 | NO | YES | NO | NO |
| AT1G28380 | 22.00 | 0.43 | 34.86 | 0.81 | 0.66 | 3.79E-04 | NO | NO | NO | NO |
| AT1G28480 | 1.52 | 0.54 | 29.91 | 0.99 | 4.30 | 0.00E+00 | NO | NO | NO | NO |
| AT1G28680 | 12.05 | 0.37 | 19.91 | 0.33 | 0.72 | 8.04E-04 | NO | NO | NO | NO |
| AT1G29290 | 0.77 | 0.37 | 6.16 | 0.29 | 2.99 | 7.65E-05 | NO | NO | NO | NO |
| AT1G29310 | 32.29 | 0.45 | 65.61 | 0.77 | 1.02 | 7.40E-09 | NO | NO | NO | NO |
| AT1G29690 | 5.04 | 0.09 | 11.90 | 0.58 | 1.24 | 3.42E-08 | NO | NO | NO | NO |
| AT1G30040 | 1.26 | 0.02 | 3.65 | 0.22 | 1.54 | 9.63E-04 | NO | NO | NO | NO |
| AT1G30420 | 1.43 | 0.11 | 4.00 | 0.21 | 1.49 | 2.15E-08 | NO | NO | NO | NO |
| AT1G30450 | 8.68 | 0.05 | 11.61 | 0.22 | 0.42 | 1.55E-02 | NO | NO | NO | NO |
| AT1G30470 | 15.22 | 0.13 | 24.99 | 0.50 | 0.72 | 6.31E-05 | NO | NO | NO | NO |
| AT1G30590 | 8.21 | 0.38 | 13.06 | 0.30 | 0.67 | 2.54E-03 | NO | NO | NO | NO |
| AT1G30720 | 0.73 | 0.11 | 3.14 | 0.64 | 2.11 | 2.01E-05 | NO | NO | NO | NO |
| AT1G30755 | 6.87 | 0.32 | 13.91 | 0.64 | 1.02 | 2.76E-06 | NO | NO | NO | NO |
| AT1G30810 | 6.01 | 0.17 | 9.25 | 0.19 | 0.62 | 5.66E-03 | NO | YES | NO | NO |
| AT1G30850 | 0.09 | 0.03 | 4.89 | 0.52 | 5.78 | 1.04E-09 | NO | NO | NO | NO |
| AT1G31130 | 39.25 | 0.33 | 87.80 | 0.46 | 1.16 | 3.59E-12 | NO | NO | NO | NO |
| AT1G31710 | 2.61 | 0.33 | 6.21 | 0.46 | 1.25 | 2.03E-05 | NO | NO | NO | NO |
| AT1G32100 | 1.01 | 0.16 | 2.84 | 0.37 | 1.49 | 1.74E-02 | NO | NO | NO | NO |
| AT1G32230 | 87.88 | 0.67 | 132.58 | 0.41 | 0.59 | 3.61E-07 | NO | NO | NO | NO |
| AT1G32460 | 26.02 | 0.27 | 47.11 | 0.56 | 0.86 | 2.06E-04 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G32640 | 20.26 | 0.09 | 28.10 | 0.51 | 0.47 | 2.17E-02 | NO | YES | NO | NO |
| AT1G32700 | 18.62 | 0.32 | 46.25 | 0.18 | 1.31 | 4.90E-12 | NO | YES | NO | NO |
| AT1G32750 | 5.36 | 0.17 | 7.84 | 0.29 | 0.55 | 7.40E-03 | NO | NO | NO | NO |
| AT1G32928 | 1.00 | 0.24 | 3.72 | 0.35 | 1.90 | 1.99E-02 | NO | NO | NO | NO |
| AT1G32960 | 1.74 | 0.63 | 37.61 | 1.51 | 4.43 | 0.00E+00 | NO | NO | NO | NO |
| AT1G33030 | 1.34 | 0.40 | 11.21 | 0.45 | 3.06 | 2.96E-13 | NO | NO | NO | NO |
| AT1G33240 | 12.97 | 0.18 | 21.71 | 0.28 | 0.74 | 8.57E-05 | NO | YES | NO | NO |
| AT1G33360 | 7.30 | 0.19 | 12.56 | 0.10 | 0.78 | 2.66E-04 | NO | NO | NO | NO |
| AT1G33560 | 3.29 | 0.15 | 10.91 | 0.01 | 1.73 | 1.86E-14 | NO | NO | NO | NO |
| AT1G33700 | 0.73 | 0.06 | 4.13 | 0.07 | 2.51 | 0.00E+00 | NO | NO | NO | NO |
| AT1G33811 | 6.68 | 0.54 | 12.26 | 0.76 | 0.88 | 1.15E-03 | NEGATIVE | NO | DOWN | NO |
| AT1G33950 | 2.01 | 0.24 | 30.88 | 4.65 | 3.94 | 0.00E+00 | NO | NO | NO | NO |
| AT1G34180 | 3.81 | 0.38 | 8.79 | 0.32 | 1.21 | 3.51E-06 | NO | YES | NO | NO |
| AT1G34190 | 52.30 | 0.43 | 73.09 | 0.84 | 0.48 | 1.35E-02 | NO | YES | NO | NO |
| AT1G34300 | 7.59 | 0.13 | 13.47 | 0.62 | 0.83 | 8.23E-05 | NO | NO | NO | NO |
| AT1G34420 | 0.63 | 0.11 | 3.69 | 0.27 | 2.55 | 1.52E-10 | NO | NO | NO | NO |
| AT1G34750 | 9.81 | 0.83 | 29.35 | 0.28 | 1.58 | 0.00E+00 | NO | NO | NO | NO |
| AT1G35210 | 3.84 | 1.01 | 12.01 | 0.74 | 1.64 | 8.16E-05 | NO | NO | NO | NO |
| AT1G35220 | 7.02 | 0.19 | 9.60 | 0.23 | 0.45 | 4.77E-02 | NO | NO | NO | NO |
| AT1G35230 | 1.60 | 0.55 | 17.74 | 0.67 | 3.47 | 5.86E-11 | NO | NO | NO | NO |
| AT1G35350 | 4.59 | 0.11 | 9.90 | 0.54 | 1.11 | 3.67E-06 | NO | NO | NO | NO |
| AT1G35580 | 22.66 | 0.00 | 42.71 | 0.33 | 0.91 | 1.04E-08 | NO | NO | NO | NO |
| AT1G35670 | 8.89 | 0.08 | 18.79 | 0.20 | 1.08 | 2.74E-07 | NO | NO | NO | NO |
| AT1G36160 | 12.12 | 0.30 | 18.05 | 0.09 | 0.57 | 1.36E-04 | NO | NO | NO | NO |
| AT1G36370 | 15.59 | 0.66 | 33.71 | 1.58 | 1.11 | 3.37E-10 | NO | NO | NO | NO |
| AT1G37130 | 102.67 | 0.90 | 191.77 | 0.18 | 0.90 | 3.64E-06 | NO | NO | NO | NO |
| AT1G42990 | 68.33 | 0.49 | 197.75 | 2.59 | 1.53 | 0.00E+00 | NO | YES | NO | NO |
| AT1G43710 | 39.21 | 0.26 | 53.39 | 1.68 | 0.45 | 2.62E-02 | NO | NO | NO | NO |
| AT1G47128 | 173.90 | 1.83 | 346.49 | 7.44 | 0.99 | 2.91E-07 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G48090 | 8.71 | 0.41 | 12.79 | 0.45 | 0.56 | 3.71E-03 | NO | NO | NO | NO |
| AT1G48120 | 2.51 | 0.07 | 3.67 | 0.08 | 0.55 | 4.96E-02 | NO | NO | NO | NO |
| AT1G48320 | 9.72 | 0.23 | 28.33 | 0.63 | 1.54 | 4.12E-09 | NO | NO | NO | NO |
| AT1G48370 | 5.46 | 0.04 | 8.18 | 0.58 | 0.58 | 2.46E-02 | NO | NO | NO | NO |
| AT1G48490 | 5.76 | 0.07 | 7.78 | 0.21 | 0.43 | 4.41E-02 | NO | NO | NO | NO |
| AT1G48605 | 5.47 | 0.33 | 13.66 | 0.45 | 1.32 | 1.68E-03 | NO | NO | NO | NO |
| AT1G49050 | 9.11 | 0.74 | 24.43 | 0.35 | 1.42 | 2.16E-13 | NO | NO | NO | NO |
| AT1G49450 | 8.47 | 0.44 | 13.78 | 0.73 | 0.70 | 2.05E-03 | NO | NO | NO | NO |
| AT1G49750 | 126.99 | 0.31 | 175.49 | 1.10 | 0.47 | 1.98E-02 | NO | NO | NO | NO |
| AT1G50140 | 11.04 | 0.25 | 14.70 | 0.17 | 0.41 | 1.36E-02 | NO | NO | NO | NO |
| AT1G50740 | 15.79 | 0.28 | 33.18 | 0.47 | 1.07 | 8.24E-06 | NO | NO | NO | NO |
| AT1G51350 | 7.22 | 0.04 | 10.72 | 0.22 | 0.57 | 1.61E-02 | NO | NO | NO | NO |
| AT1G51620 | 1.15 | 0.29 | 3.71 | 0.50 | 1.69 | 2.59E-04 | NO | NO | NO | NO |
| AT1G51660 | 15.55 | 0.25 | 25.44 | 0.53 | 0.71 | 4.93E-04 | NO | NO | NO | NO |
| AT1G51680 | 31.66 | 1.52 | 63.96 | 0.51 | 1.01 | 4.40E-11 | NO | NO | NO | NO |
| AT1G51760 | 19.06 | 0.33 | 50.79 | 0.50 | 1.41 | 0.00E+00 | NO | NO | NO | NO |
| AT1G51790 | 0.24 | 0.10 | 3.31 | 0.54 | 3.78 | 4.95E-13 | NO | NO | NO | NO |
| AT1G51805 | 26.84 | 0.67 | 51.90 | 0.54 | 0.95 | 0.00E+00 | NO | NO | NO | NO |
| AT1G51860 | 0.74 | 0.20 | 2.19 | 0.19 | 1.56 | 5.49E-04 | NO | NO | NO | NO |
| AT1G52030 | 5.95 | 1.21 | 8.86 | 1.22 | 0.58 | 2.09E-02 | NO | NO | NO | NO |
| AT1G52340 | 12.27 | 0.37 | 20.38 | 0.79 | 0.73 | 2.28E-03 | NO | NO | DOWN | NO |
| AT1G52780 | 11.10 | 0.21 | 19.04 | 0.63 | 0.78 | 2.75E-05 | NO | NO | NO | NO |
| AT1G52800 | 0.44 | 0.11 | 2.88 | 0.36 | 2.70 | 3.95E-04 | NO | NO | NO | NO |
| AT1G53920 | 5.93 | 0.30 | 10.91 | 0.13 | 0.88 | 5.11E-03 | NO | NO | NO | NO |
| AT1G54115 | 9.90 | 0.20 | 15.87 | 0.17 | 0.68 | 1.73E-03 | NO | NO | NO | NO |
| AT1G55210 | 120.70 | 3.07 | 227.86 | 4.26 | 0.92 | 6.42E-09 | NO | NO | NO | NO |
| AT1G55310 | 3.99 | 0.18 | 6.76 | 0.08 | 0.76 | 4.53E-02 | NO | NO | NO | NO |
| AT1G55325 | 5.48 | 0.11 | 8.70 | 0.27 | 0.67 | 5.48E-06 | NO | NO | NO | NO |
| AT1G55350 | 10.50 | 0.27 | 13.42 | 0.33 | 0.35 | 4.31E-03 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G55450 | 36.73 | 1.10 | 73.87 | 0.94 | 1.01 | 3.64E-14 | NO | NO | DOWN | DOWN |
| AT1G55850 | 7.76 | 0.27 | 19.33 | 0.56 | 1.32 | 1.35E-11 | NO | NO | DOWN | NO |
| AT1G55910 | 20.07 | 1.18 | 48.57 | 0.66 | 1.28 | 1.02E-11 | NO | NO | NO | NO |
| AT1G55915 | 3.87 | 0.07 | 6.74 | 0.05 | 0.80 | 2.00E-02 | NO | NO | NO | NO |
| AT1G55960 | 12.85 | 0.27 | 23.11 | 0.44 | 0.85 | 2.60E-05 | NO | NO | NO | NO |
| AT1G56060 | 1.83 | 0.54 | 32.49 | 1.92 | 4.15 | 9.76E-13 | NO | NO | NO | NO |
| AT1G56120 | 3.27 | 0.37 | 10.13 | 0.08 | 1.63 | 1.84E-13 | NO | NO | NO | NO |
| AT1G56145 | 3.41 | 0.12 | 6.81 | 0.20 | 1.00 | 1.41E-05 | NO | NO | NO | NO |
| AT1G56150 | 3.44 | 0.12 | 7.98 | 0.46 | 1.22 | 4.58E-02 | NO | NO | NO | NO |
| AT1G56330 | 212.73 | 1.10 | 308.75 | 4.47 | 0.54 | 6.42E-03 | NO | NO | NO | NO |
| AT1G56340 | 112.05 | 1.76 | 246.84 | 3.89 | 1.14 | 0.00E+00 | NO | NO | NO | NO |
| AT1G56460 | 19.98 | 0.24 | 26.83 | 0.40 | 0.43 | 3.95E-02 | NO | NO | NO | NO |
| AT1G56550 | 0.45 | 0.15 | 4.16 | 0.36 | 3.20 | 7.62E-09 | NO | NO | NO | NO |
| AT1G56610 | 10.03 | 0.36 | 14.14 | 0.16 | 0.50 | 2.81E-02 | NO | NO | NO | NO |
| AT1G57990 | 2.84 | 0.30 | 11.19 | 0.32 | 1.98 | 3.41E-10 | NO | NO | NO | NO |
| AT1G58070 | 0.69 | 0.11 | 2.37 | 0.27 | 1.78 | 8.54E-03 | NO | NO | NO | NO |
| AT1G58440 | 10.41 | 0.39 | 15.72 | 0.39 | 0.59 | 8.72E-03 | NO | NO | NO | NO |
| AT1G59580 | 10.95 | 0.59 | 16.37 | 0.30 | 0.58 | 7.49E-03 | NO | NO | DOWN | NO |
| AT1G59620 | 4.73 | 0.36 | 12.79 | 0.53 | 1.43 | 6.19E-12 | NO | NO | NO | NO |
| AT1G59710 | 17.03 | 0.20 | 38.13 | 0.46 | 1.16 | 1.02E-10 | NO | NO | NO | NO |
| AT1G59870 | 166.74 | 1.91 | 315.07 | 5.44 | 0.92 | 1.85E-04 | NO | NO | NO | NO |
| AT1G59910 | 5.40 | 0.12 | 7.73 | 0.32 | 0.52 | 3.68E-02 | NO | NO | NO | NO |
| AT1G60270 | 3.30 | 0.13 | 5.60 | 0.32 | 0.76 | 4.17E-02 | NO | NO | NO | NO |
| AT1G60420 | 25.83 | 0.04 | 34.77 | 0.40 | 0.43 | 3.74E-02 | POSITIVE | NO | NO | NO |
| AT1G60490 | 15.97 | 0.19 | 27.19 | 0.40 | 0.77 | 2.54E-05 | NO | NO | NO | NO |
| AT1G60610 | 2.30 | 0.74 | 4.72 | 0.00 | 1.04 | 1.21E-02 | NO | NO | NO | NO |
| AT1G61100 | 12.10 | 0.29 | 17.64 | 0.23 | 0.54 | 6.67E-03 | NO | NO | NO | NO |
| AT1G61120 | 0.25 | 0.19 | 4.64 | 0.33 | 4.18 | 0.00E+00 | NO | NO | NO | NO |
| AT1G61140 | 5.83 | 0.23 | 8.57 | 0.39 | 0.56 | 7.28E-03 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G61250 | 28.81 | 0.30 | 61.10 | 0.71 | 1.08 | 5.79E-10 | NO | NO | NO | NO |
| AT1G61260 | 2.53 | 0.43 | 6.91 | 0.29 | 1.45 | 6.66E-05 | NO | NO | NO | NO |
| AT1G61360 | 3.85 | 0.06 | 7.39 | 0.30 | 0.94 | 4.48E-05 | NO | NO | NO | NO |
| AT1G61370 | 1.39 | 0.10 | 3.25 | 0.02 | 1.22 | 1.30E-03 | NO | NO | NO | NO |
| AT1G61470 | 0.63 | 0.18 | 2.08 | 0.14 | 1.72 | 4.40E-02 | NO | NO | NO | NO |
| AT1G61560 | 1.43 | 0.00 | 4.06 | 0.13 | 1.50 | 4.77E-06 | NO | NO | NO | NO |
| AT1G61660 | 19.45 | 0.28 | 26.03 | 0.27 | 0.42 | 2.19E-02 | NO | NO | NO | NO |
| AT1G62300 | 4.75 | 0.23 | 19.07 | 0.78 | 2.01 | 0.00E+00 | NO | YES | NO | NO |
| AT1G62360 | 0.48 | 0.07 | 2.15 | 0.44 | 2.16 | 1.00E-03 | NO | YES | NO | NO |
| AT1G62422 | 4.33 | 0.63 | 18.22 | 0.37 | 2.07 | 4.14E-10 | NO | NO | NO | NO |
| AT1G62500 | 3.68 | 0.10 | 13.31 | 1.12 | 1.86 | 4.37E-11 | NO | NO | NO | DOWN |
| AT1G62630 | 7.04 | 0.10 | 12.85 | 0.04 | 0.87 | 2.86E-05 | NO | NO | NO | NO |
| AT1G62660 | 1.62 | 0.23 | 6.23 | 0.26 | 1.94 | 3.90E-10 | NO | NO | NO | NO |
| AT1G62790 | 60.31 | 1.34 | 85.19 | 1.05 | 0.50 | 2.54E-03 | NO | NO | NO | NO |
| AT1G62840 | 0.58 | 0.23 | 3.26 | 0.09 | 2.48 | 4.30E-04 | NO | NO | NO | NO |
| AT1G63010 | 22.58 | 0.13 | 31.26 | 0.33 | 0.47 | 4.00E-04 | NO | NO | NO | NO |
| AT1G63100 | 5.42 | 0.31 | 8.32 | 0.29 | 0.62 | 2.62E-02 | NO | YES | NO | NO |
| AT1G63220 | 16.24 | 0.35 | 35.16 | 0.87 | 1.11 | 4.98E-06 | NO | NO | NO | NO |
| AT1G63670 | 19.21 | 0.46 | 24.89 | 0.76 | 0.37 | 1.11E-02 | NO | NO | NO | NO |
| AT1G63720 | 1.93 | 0.26 | 6.51 | 0.04 | 1.75 | 2.40E-06 | NO | NO | NO | NO |
| AT1G63750 | 1.68 | 0.04 | 3.49 | 0.57 | 1.06 | 1.03E-04 | NO | NO | NO | NO |
| AT1G63840 | 8.39 | 0.69 | 45.30 | 1.16 | 2.43 | 0.00E+00 | NO | NO | NO | NO |
| AT1G64050 | 8.49 | 0.37 | 12.13 | 0.37 | 0.51 | 2.04E-02 | NO | NO | NO | NO |
| AT1G64060 | 3.02 | 0.06 | 7.80 | 0.13 | 1.37 | 1.62E-10 | NO | NO | NO | NO |
| AT1G64280 | 17.27 | 0.52 | 31.50 | 0.31 | 0.87 | 8.28E-07 | NO | NO | NO | NO |
| AT1G64400 | 15.23 | 0.75 | 28.03 | 1.06 | 0.88 | 1.79E-06 | NO | NO | NO | NO |
| AT1G64460 | 6.29 | 0.44 | 16.73 | 1.02 | 1.41 | 3.87E-07 | NO | NO | NO | NO |
| AT1G64470 | 6.26 | 0.26 | 16.82 | 0.60 | 1.43 | 4.80E-07 | NO | NO | NO | NO |
| AT1G64490 | 38.19 | 0.24 | 56.43 | 1.51 | 0.56 | 2.26E-02 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G64600 | 7.71 | 0.30 | 11.88 | 0.13 | 0.62 | 1.40E-02 | NO | NO | NO | NO |
| AT1G64620 | 1.51 | 0.14 | 3.22 | 0.20 | 1.09 | 2.43E-02 | NO | YES | NO | NO |
| AT1G65040 | 13.10 | 0.18 | 37.17 | 1.55 | 1.50 | 0.00E+00 | NO | NO | NO | NO |
| AT1G65200 | 2.08 | 0.04 | 3.73 | 0.00 | 0.85 | 4.84E-03 | NO | NO | NO | NO |
| AT1G65481 | 0.48 | 0.24 | 10.67 | 1.25 | 4.47 | 7.37E-07 | NO | NO | NO | NO |
| AT1G65800 | 5.50 | 0.59 | 12.33 | 0.15 | 1.17 | 2.47E-08 | NO | NO | NO | NO |
| AT1G65820 | 220.36 | 3.01 | 302.72 | 2.46 | 0.46 | 1.74E-02 | POSITIVE | NO | NO | NO |
| AT1G65845 | 13.41 | 1.52 | 76.46 | 3.60 | 2.51 | 0.00E+00 | NO | NO | NO | NO |
| AT1G66090 | 0.50 | 0.15 | 6.32 | 0.20 | 3.67 | 3.27E-12 | NO | NO | NO | NO |
| AT1G66330 | 45.08 | 0.34 | 62.31 | 0.73 | 0.47 | 1.28E-03 | NO | NO | NO | NO |
| AT1G66760 | 5.72 | 0.22 | 9.08 | 1.29 | 0.67 | 1.33E-02 | NO | NO | NO | NO |
| AT1G66840 | 11.73 | 0.26 | 16.27 | 0.41 | 0.47 | 3.91E-02 | NO | NO | NO | NO |
| AT1G66850 | 0.00 | 0.00 | 6.95 | 3.60 | Inf | 2.55E-04 | NO | NO | NO | NO |
| AT1G66910 | 3.01 | 0.08 | 8.41 | 0.48 | 1.48 | 1.12E-07 | NO | NO | NO | NO |
| AT1G66920 | 4.87 | 0.06 | 12.22 | 1.06 | 1.33 | 8.40E-10 | NO | NO | NO | NO |
| AT1G67195 | 28.24 | 0.46 | 62.11 | 1.61 | 1.14 | 3.52E-07 | NO | NO | NO | NO |
| AT1G67260 | 2.66 | 0.11 | 5.37 | 3.57 | 1.02 | 2.01E-02 | NO | NO | NO | NO |
| AT1G67490 | 4.47 | 0.10 | 6.44 | 0.08 | 0.53 | 4.23E-02 | NO | NO | NO | NO |
| AT1G67560 | 5.96 | 0.14 | 13.05 | 0.01 | 1.13 | 1.63E-08 | NO | NO | NO | NO |
| AT1G67800 | 23.19 | 0.31 | 36.85 | 0.80 | 0.67 | 4.73E-07 | NO | NO | NO | NO |
| AT1G67865 | 8.39 | 1.27 | 45.30 | 2.21 | 2.43 | 1.10E-10 | NO | NO | NO | NO |
| AT1G67900 | 12.04 | 0.25 | 20.96 | 0.29 | 0.80 | 1.47E-07 | NO | NO | NO | NO |
| AT1G67920 | 9.36 | 0.94 | 30.74 | 0.59 | 1.71 | 6.60E-08 | NO | NO | NO | NO |
| AT1G68290 | 1.28 | 0.17 | 5.30 | 0.84 | 2.05 | 4.01E-05 | NO | NO | NO | NO |
| AT1G68440 | 5.40 | 0.07 | 23.20 | 1.57 | 2.10 | 0.00E+00 | NO | NO | NO | NO |
| AT1G68670 | 9.16 | 0.71 | 14.72 | 0.92 | 0.68 | 4.28E-03 | NO | YES | NO | NO |
| AT1G68690 | 0.98 | 0.07 | 4.93 | 0.04 | 2.33 | 1.96E-12 | NO | NO | NO | NO |
| AT1G68710 | 2.96 | 0.06 | 4.91 | 0.10 | 0.73 | 3.17E-03 | NO | NO | NO | NO |
| AT1G68840 | 14.66 | 0.31 | 23.43 | 1.32 | 0.68 | 2.01E-03 | NO | YES | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G68910 | 11.17 | 0.24 | 17.68 | 0.10 | 0.66 | 2.01E-04 | NO | NO | NO | NO |
| AT1G69160 | 9.16 | 0.08 | 19.64 | 0.83 | 1.10 | 1.07E-06 | NO | NO | NO | NO |
| AT1G69440 | 1.83 | 0.14 | 3.48 | 0.12 | 0.92 | 3.56E-03 | NO | NO | NO | NO |
| AT1G69520 | 3.39 | 0.40 | 9.06 | 0.57 | 1.42 | 1.55E-03 | NO | NO | NO | NO |
| AT1G69570 | 6.71 | 0.08 | 12.19 | 0.52 | 0.86 | 4.95E-04 | NO | YES | UP | NO |
| AT1G69572 | 9.00 | 0.15 | 14.98 | 0.65 | 0.74 | 1.13E-02 | NO | NO | NO | NO |
| AT1G69780 | 7.58 | 0.10 | 12.68 | 0.80 | 0.74 | 5.68E-03 | NEGATIVE | YES | NO | NO |
| AT1G69840 | 24.97 | 0.20 | 60.13 | 0.88 | 1.27 | 0.00E+00 | NO | NO | NO | NO |
| AT1G69900 | 0.99 | 0.16 | 3.16 | 0.24 | 1.67 | 2.01E-03 | NO | NO | NO | NO |
| AT1G69920 | 0.56 | 0.29 | 2.96 | 0.85 | 2.40 | 1.33E-03 | NO | NO | NO | NO |
| AT1G70140 | 0.83 | 0.10 | 3.27 | 0.19 | 1.99 | 1.10E-06 | NO | NO | NO | NO |
| AT1G70160 | 60.58 | 0.30 | 92.33 | 0.98 | 0.61 | 1.12E-03 | NO | NO | NO | NO |
| AT1G70180 | 7.76 | 0.09 | 12.89 | 0.06 | 0.73 | 3.89E-04 | NO | NO | NO | NO |
| AT1G70250 | 8.15 | 0.40 | 14.29 | 0.93 | 0.81 | 1.45E-04 | NO | NO | NO | NO |
| AT1G70290 | 4.07 | 0.27 | 7.71 | 0.24 | 0.92 | 6.30E-05 | NO | NO | NO | NO |
| AT1G70520 | 12.40 | 0.45 | 29.39 | 0.63 | 1.25 | 7.05E-12 | NO | NO | NO | NO |
| AT1G70530 | 10.56 | 0.45 | 19.52 | 0.37 | 0.89 | 1.55E-05 | NO | NO | NO | NO |
| AT1G70620 | 12.58 | 0.16 | 17.19 | 0.55 | 0.45 | 3.03E-03 | NO | NO | NO | NO |
| AT1G70700 | 35.34 | 0.46 | 82.14 | 1.30 | 1.22 | 6.92E-13 | NO | YES | NO | DOWN |
| AT1G70710 | 4.54 | 0.15 | 7.86 | 0.59 | 0.79 | 6.88E-03 | NO | NO | NO | NO |
| AT1G70740 | 3.87 | 0.25 | 7.69 | 0.21 | 0.99 | 6.68E-04 | NO | NO | NO | NO |
| AT1G70782 | 42.74 | 0.80 | 78.56 | 2.38 | 0.88 | 1.05E-06 | NO | NO | NO | NO |
| AT1G71010 | 7.52 | 0.10 | 12.16 | 0.17 | 0.69 | 2.62E-04 | NO | NO | NO | NO |
| AT1G71030 | 61.57 | 0.94 | 100.03 | 0.90 | 0.70 | 9.97E-05 | NO | YES | NO | NO |
| AT1G71140 | 3.76 | 0.32 | 7.41 | 0.55 | 0.98 | 2.33E-03 | NO | NO | NO | NO |
| AT1G71220 | 25.23 | 0.68 | 41.06 | 0.72 | 0.70 | 1.06E-08 | NO | NO | NO | NO |
| AT1G71390 | 0.10 | 0.06 | 4.21 | 0.55 | 5.33 | 5.10E-12 | NO | NO | NO | NO |
| AT1G71840 | 36.83 | 0.82 | 48.79 | 0.97 | 0.41 | 4.99E-02 | NO | NO | NO | NO |
| AT1G71970 | 9.75 | 0.20 | 15.27 | 0.77 | 0.65 | 3.41E-02 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G72150 | 54.88 | 0.86 | 73.07 | 1.05 | 0.41 | 4.25E-02 | NO | NO | NO | NO |
| AT1G72240 | 0.96 | 0.16 | 5.14 | 0.61 | 2.42 | 1.78E-03 | NO | NO | NO | NO |
| AT1G72280 | 7.89 | 0.83 | 29.39 | 1.71 | 1.90 | 0.00E+00 | NO | NO | NO | NO |
| AT1G72450 | 28.86 | 0.47 | 64.54 | 0.66 | 1.16 | 5.44E-11 | NO | YES | NO | NO |
| AT1G72680 | 26.54 | 0.59 | 75.99 | 1.46 | 1.52 | 0.00E+00 | NO | NO | NO | NO |
| AT1G72700 | 10.69 | 0.29 | 25.14 | 0.12 | 1.23 | 2.96E-13 | NO | NO | NO | NO |
| AT1G72770 | 15.99 | 0.16 | 23.55 | 0.56 | 0.56 | 7.45E-04 | NO | NO | NO | NO |
| AT1G72900 | 6.70 | 0.90 | 41.84 | 0.76 | 2.64 | 0.00E+00 | NO | NO | NO | NO |
| AT1G72910 | 3.63 | 0.55 | 16.88 | 0.69 | 2.22 | 0.00E+00 | NO | NO | NO | NO |
| AT1G72920 | 1.32 | 0.14 | 8.66 | 0.56 | 2.71 | 2.64E-09 | NO | NO | NO | NO |
| AT1G72930 | 70.95 | 0.77 | 146.22 | 1.42 | 1.04 | 1.22E-10 | NO | NO | DOWN | NO |
| AT1G72940 | 3.54 | 0.20 | 13.44 | 0.82 | 1.92 | 5.51E-12 | NO | NO | DOWN | NO |
| AT1G73030 | 72.42 | 0.75 | 100.93 | 1.05 | 0.48 | 1.74E-02 | NO | NO | NO | NO |
| AT1G73540 | 4.91 | 0.31 | 11.44 | 0.66 | 1.22 | 5.28E-04 | NO | NO | NO | NO |
| AT1G73650 | 54.96 | 0.23 | 71.97 | 0.31 | 0.39 | 3.96E-03 | NO | NO | NO | NO |
| AT1G73740 | 5.97 | 0.13 | 9.95 | 0.53 | 0.74 | 7.91E-03 | NO | NO | NO | NO |
| AT1G74020 | 19.30 | 0.78 | 35.90 | 1.25 | 0.89 | 5.42E-06 | NO | NO | NO | NO |
| AT1G74030 | 5.05 | 0.28 | 8.05 | 0.59 | 0.67 | 2.16E-02 | NO | NO | NO | NO |
| AT1G74080 | 0.25 | 0.09 | 2.77 | 0.19 | 3.49 | 2.01E-06 | NO | YES | NO | NO |
| AT1G74090 | 54.16 | 0.86 | 75.83 | 1.79 | 0.49 | 1.64E-02 | NEGATIVE | NO | NO | NO |
| AT1G74100 | 38.77 | 0.58 | 96.33 | 1.64 | 1.31 | 1.88E-14 | NO | NO | NO | NO |
| AT1G74210 | 5.24 | 0.24 | 13.56 | 0.39 | 1.37 | 1.94E-07 | NO | NO | NO | NO |
| AT1G74360 | 2.32 | 0.24 | 9.32 | 0.06 | 2.01 | 0.00E+00 | NO | NO | NO | NO |
| AT1G75000 | 1.07 | 0.06 | 5.23 | 1.00 | 2.28 | 9.82E-05 | NO | NO | NO | NO |
| AT1G75130 | 6.35 | 0.02 | 9.87 | 0.25 | 0.64 | 2.35E-02 | NO | NO | NO | NO |
| AT1G75220 | 5.01 | 0.33 | 11.36 | 0.05 | 1.18 | 7.79E-07 | NEGATIVE | NO | DOWN | NO |
| AT1G75280 | 20.83 | 0.30 | 29.41 | 1.56 | 0.50 | 2.52E-02 | NO | NO | NO | NO |
| AT1G75380 | 52.08 | 0.71 | 88.51 | 0.67 | 0.76 | 1.86E-07 | NO | NO | NO | NO |
| AT1G75410 | 13.39 | 0.10 | 28.60 | 0.55 | 1.10 | 2.74E-10 | NO | YES | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G75440 | 8.63 | 0.68 | 17.36 | 0.77 | 1.01 | 1.87E-03 | NO | NO | NO | NO |
| AT1G75960 | 0.53 | 0.05 | 2.22 | 0.17 | 2.06 | 2.01E-04 | NO | NO | NO | NO |
| AT1G76040 | 4.58 | 0.25 | 20.15 | 0.60 | 2.14 | 0.00E+00 | NO | NO | NO | NO |
| AT1G76070 | 1.97 | 0.24 | 4.88 | 0.16 | 1.31 | 4.27E-03 | NO | NO | NO | NO |
| AT1G76090 | 4.80 | 0.04 | 8.15 | 0.42 | 0.76 | 2.16E-02 | NO | NO | NO | NO |
| AT1G76240 | 4.44 | 0.23 | 16.52 | 0.32 | 1.90 | 1.63E-10 | NO | NO | NO | NO |
| AT1G76320 | 6.97 | 0.09 | 9.43 | 0.07 | 0.43 | 4.35E-02 | NO | NO | NO | NO |
| AT1G76390 | 6.04 | 0.23 | 12.52 | 0.15 | 1.05 | 9.33E-09 | NO | NO | NO | NO |
| AT1G76640 | 0.18 | 0.08 | 3.26 | 0.73 | 4.14 | 5.42E-03 | NO | NO | NO | NO |
| AT1G76690 | 3.56 | 0.41 | 6.15 | 0.54 | 0.79 | 4.44E-02 | NO | NO | NO | NO |
| AT1G76760 | 4.20 | 0.15 | 9.80 | 0.42 | 1.22 | 3.11E-03 | NO | NO | NO | NO |
| AT1G76890 | 3.09 | 0.23 | 6.13 | 0.25 | 0.99 | 1.32E-03 | NO | YES | NO | NO |
| AT1G76892 | 5.86 | 0.29 | 9.19 | 0.42 | 0.65 | 3.30E-02 | NO | NO | NO | NO |
| AT1G76980 | 14.44 | 0.86 | 48.59 | 1.24 | 1.75 | 0.00E+00 | NO | NO | NO | NO |
| AT1G77300 | 7.22 | 0.36 | 9.53 | 0.16 | 0.40 | 2.41E-02 | NO | YES | NO | NO |
| AT1G77320 | 3.01 | 0.16 | 4.38 | 0.12 | 0.54 | 4.64E-02 | NO | NO | NO | NO |
| AT1G77380 | 1.91 | 0.30 | 6.72 | 0.24 | 1.81 | 4.58E-08 | NO | NO | NO | NO |
| AT1G77420 | 7.25 | 0.16 | 11.79 | 0.21 | 0.70 | 8.11E-03 | NO | NO | NO | NO |
| AT1G77460 | 2.07 | 0.63 | 3.52 | 0.17 | 0.76 | 1.49E-04 | NO | NO | NO | NO |
| AT1G77770 | 9.44 | 0.18 | 17.39 | 0.27 | 0.88 | 2.18E-04 | NO | NO | NO | NO |
| AT1G77800 | 10.18 | 0.45 | 13.22 | 0.34 | 0.38 | 2.97E-02 | NO | YES | NO | NO |
| AT1G77810 | 13.90 | 0.36 | 28.27 | 1.20 | 1.02 | 7.96E-10 | NO | NO | NO | NO |
| AT1G77990 | 3.42 | 0.33 | 6.50 | 0.50 | 0.92 | 1.15E-03 | NO | NO | NO | NO |
| AT1G78000 | 0.66 | 0.07 | 3.96 | 0.50 | 2.57 | 2.84E-11 | NO | NO | NO | NO |
| AT1G78150 | 71.75 | 0.57 | 102.22 | 2.06 | 0.51 | 1.29E-04 | NO | NO | NO | NO |
| AT1G78200 | 35.34 | 0.41 | 49.03 | 0.88 | 0.47 | 4.41E-03 | NO | NO | NO | NO |
| AT1G78230 | 11.55 | 0.74 | 19.67 | 1.06 | 0.77 | 7.53E-05 | NO | NO | NO | NO |
| AT1G78280 | 6.25 | 0.04 | 10.27 | 0.31 | 0.72 | 6.13E-04 | NO | YES | NO | NO |
| AT1G78460 | 38.86 | 1.85 | 53.12 | 1.03 | 0.45 | 4.50E-02 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G78510 | 48.67 | 0.00 | 80.65 | 0.00 | 0.73 | 4.70E-09 | NO | NO | NO | NO |
| AT1G78850 | 51.94 | 1.45 | 80.70 | 0.76 | 0.64 | 4.07E-04 | NO | NO | NO | DOWN |
| AT1G78920 | 22.55 | 0.29 | 36.65 | 0.89 | 0.70 | 1.05E-04 | NO | NO | NO | NO |
| AT1G79000 | 8.19 | 0.32 | 11.65 | 0.33 | 0.51 | 5.87E-03 | NO | YES | NO | NO |
| AT1G79380 | 27.31 | 0.36 | 43.40 | 0.34 | 0.67 | 3.25E-04 | NO | NO | NO | NO |
| AT1G79680 | 0.55 | 0.20 | 4.61 | 0.20 | 3.06 | 1.14E-12 | NO | NO | NO | NO |
| AT1G79830 | 27.19 | 0.45 | 33.59 | 0.35 | 0.30 | 6.42E-03 | NO | NO | NO | NO |
| AT1G79990 | 52.87 | 0.77 | 69.11 | 0.86 | 0.39 | 4.45E-03 | NO | NO | NO | NO |
| AT1G80020 | 8.31 | 0.22 | 11.29 | 0.17 | 0.44 | 4.85E-02 | NO | NO | NO | NO |
| AT1G80280 | 8.66 | 0.30 | 16.01 | 0.44 | 0.89 | 5.01E-06 | NO | NO | NO | NO |
| AT1G80420 | 10.74 | 0.52 | 19.24 | 0.38 | 0.84 | 1.09E-05 | NO | NO | NO | NO |
| AT1G80440 | 1.71 | 0.35 | 7.94 | 0.57 | 2.21 | 3.05E-09 | NO | NO | NO | NO |
| AT1G80460 | 21.73 | 0.33 | 52.88 | 0.58 | 1.28 | 1.87E-14 | NO | NO | NO | NO |
| AT1G80490 | 7.49 | 0.10 | 11.39 | 0.26 | 0.61 | 3.81E-04 | NO | NO | NO | NO |
| AT1G80510 | 7.73 | 0.03 | 11.07 | 0.14 | 0.52 | 4.71E-02 | NO | NO | NO | NO |
| AT1G80610 | 1.61 | 0.16 | 4.11 | 0.08 | 1.35 | 8.15E-03 | NO | NO | NO | NO |
| AT1G80840 | 2.27 | 0.57 | 30.31 | 1.33 | 3.74 | 0.00E+00 | NO | YES | UP | NO |
| AT1G80960 | 1.53 | 0.16 | 4.80 | 0.13 | 1.65 | 1.88E-05 | NO | NO | NO | NO |
| AT2G01180 | 4.94 | 0.35 | 10.49 | 0.16 | 1.09 | 1.94E-05 | NO | NO | NO | NO |
| AT2G01190 | 6.00 | 0.20 | 12.54 | 0.42 | 1.06 | 4.32E-07 | NO | NO | NO | NO |
| AT2G01450 | 29.04 | 0.39 | 55.21 | 0.69 | 0.93 | 4.43E-10 | NO | NO | NO | NO |
| AT2G01650 | 11.99 | 0.14 | 19.87 | 0.25 | 0.73 | 7.01E-04 | NO | YES | NO | NO |
| AT2G01680 | 11.26 | 0.23 | 17.92 | 0.29 | 0.67 | 1.42E-03 | NO | NO | NO | NO |
| AT2G01850 | 34.08 | 1.42 | 47.71 | 0.71 | 0.49 | 1.79E-02 | NO | NO | NO | NO |
| AT2G01860 | 14.53 | 0.84 | 22.19 | 0.38 | 0.61 | 3.30E-03 | NO | NO | NO | NO |
| AT2G02010 | 1.38 | 0.37 | 4.93 | 0.57 | 1.84 | 3.56E-06 | NO | NO | NO | NO |
| AT2G02220 | 6.33 | 0.34 | 16.64 | 0.72 | 1.39 | 2.00E-13 | NO | NO | NO | NO |
| AT2G02810 | 13.92 | 0.36 | 50.41 | 1.65 | 1.86 | 0.00E+00 | NO | NO | NO | NO |
| AT2G02870 | 15.85 | 0.30 | 25.73 | 0.48 | 0.70 | 7.78E-05 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT2G02930 | 48.69 | 2.21 | 157.33 | 3.60 | 1.69 | 0.00E+00 | NO | NO | NO | DOWN |
| AT2G02990 | 2.27 | 1.61 | 6.85 | 1.18 | 1.59 | 5.34E-04 | NO | NO | NO | NO |
| AT2G03120 | 106.40 | 1.10 | 199.87 | 1.76 | 0.91 | 2.55E-07 | NO | NO | NO | NO |
| AT2G03730 | 19.71 | 0.45 | 26.76 | 0.12 | 0.44 | 3.25E-02 | NO | NO | NO | NO |
| AT2G04160 | 16.32 | 1.86 | 31.34 | 1.51 | 0.94 | 4.98E-08 | NO | NO | NO | NO |
| AT2G04390 | 34.13 | 0.63 | 48.88 | 0.91 | 0.52 | 3.32E-02 | NO | NO | NO | NO |
| AT2G04400 | 40.68 | 0.67 | 81.01 | 0.75 | 0.99 | 5.44E-09 | NO | NO | NO | NO |
| AT2G04430 | 5.79 | 0.28 | 29.57 | 0.35 | 2.35 | 0.00E+00 | NO | NO | NO | NO |
| AT2G04515 | 0.44 | 0.11 | 5.32 | 0.47 | 3.60 | 6.56E-07 | NO | NO | NO | NO |
| AT2G04650 | 2.87 | 0.09 | 8.95 | 0.21 | 1.64 | 2.03E-07 | NO | NO | NO | NO |
| AT2G04780 | 19.58 | 1.00 | 31.59 | 1.26 | 0.69 | 3.75E-04 | NEGATIVE | NO | NO | NO |
| AT2G05320 | 8.68 | 0.39 | 15.12 | 0.46 | 0.80 | 1.11E-03 | NO | NO | NO | NO |
| AT2G06050 | 23.06 | 0.72 | 36.66 | 0.69 | 0.67 | 1.98E-04 | NO | NO | NO | NO |
| AT2G07180 | 37.77 | 0.33 | 47.71 | 0.71 | 0.34 | 3.17E-02 | NO | NO | NO | NO |
| AT2G11520 | 11.05 | 0.19 | 18.43 | 0.14 | 0.74 | 4.21E-04 | NO | NO | NO | NO |
| AT2G13790 | 3.27 | 0.29 | 8.92 | 0.18 | 1.45 | 1.88E-08 | NO | NO | NO | NO |
| AT2G14740 | 7.51 | 0.18 | 10.52 | 0.13 | 0.49 | 4.79E-02 | NO | NO | NO | NO |
| AT2G15042 | 15.65 | 0.63 | 31.61 | 1.29 | 1.01 | 5.08E-08 | NO | NO | NO | NO |
| AT2G15580 | 15.41 | 0.26 | 32.54 | 0.19 | 1.08 | 7.58E-07 | NO | NO | NO | NO |
| AT2G15760 | 1.37 | 0.39 | 3.12 | 0.15 | 1.18 | 3.55E-02 | NO | NO | NO | NO |
| AT2G16280 | 49.01 | 1.20 | 70.84 | 1.54 | 0.53 | 6.05E-03 | NO | NO | NO | NO |
| AT2G16430 | 33.55 | 0.38 | 65.81 | 0.97 | 0.97 | 1.91E-08 | NO | NO | NO | NO |
| AT2G16500 | 104.26 | 0.71 | 240.53 | 1.43 | 1.21 | 1.21E-10 | NO | NO | NO | NO |
| AT2G16890 | 19.67 | 0.30 | 37.07 | 1.18 | 0.91 | 1.41E-07 | NO | NO | UP | NO |
| AT2G16900 | 8.40 | 0.13 | 39.31 | 0.93 | 2.23 | 0.00E+00 | NO | NO | NO | NO |
| AT2G17130 | 39.13 | 0.37 | 57.83 | 0.96 | 0.56 | 1.27E-03 | NO | NO | NO | NO |
| AT2G17220 | 9.88 | 0.23 | 21.25 | 0.22 | 1.10 | 1.16E-10 | NO | NO | NO | NO |
| AT2G17230 | 28.33 | 0.49 | 42.44 | 0.94 | 0.58 | 2.76E-03 | NO | NO | NO | NO |
| AT2G17290 | 16.44 | 0.46 | 26.81 | 0.18 | 0.71 | 1.62E-04 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT2G17520 | 15.79 | 0.33 | 24.02 | 0.55 | 0.60 | 1.58E-03 | NO | NO | NO | NO |
| AT2G17560 | 121.90 | 2.40 | 148.76 | 2.93 | 0.29 | 3.52E-02 | NO | YES | NO | NO |
| AT2G17710 | 20.34 | 1.29 | 32.91 | 0.45 | 0.69 | 2.63E-03 | NO | NO | NO | NO |
| AT2G17720 | 46.21 | 0.46 | 81.83 | 0.77 | 0.82 | 3.46E-06 | NO | NO | NO | NO |
| AT2G17730 | 12.62 | 0.15 | 25.63 | 0.10 | 1.02 | 5.76E-07 | NO | NO | NO | NO |
| AT2G17740 | 4.19 | 1.84 | 17.39 | 1.17 | 2.05 | 3.15E-10 | NO | NO | NO | NO |
| AT2G17790 | 15.64 | 0.27 | 22.37 | 0.23 | 0.52 | 9.85E-03 | NO | NO | NO | NO |
| AT2G17930 | 6.19 | 0.18 | 9.17 | 0.49 | 0.57 | 2.71E-03 | NO | NO | NO | NO |
| AT2G18160 | 22.86 | 0.67 | 34.43 | 0.11 | 0.59 | 5.15E-03 | NO | YES | NO | NO |
| AT2G18280 | 41.81 | 0.47 | 54.36 | 0.50 | 0.38 | 2.68E-02 | NO | YES | NO | NO |
| AT2G18660 | 38.78 | 2.20 | 135.92 | 2.62 | 1.81 | 0.00E+00 | NO | NO | NO | NO |
| AT2G19130 | 8.32 | 0.62 | 22.48 | 0.52 | 1.43 | 1.85E-14 | NO | NO | NO | NO |
| AT2G19190 | 2.31 | 0.85 | 19.87 | 1.54 | 3.11 | 0.00E+00 | NO | NO | NO | NO |
| AT2G19710 | 3.49 | 0.06 | 9.62 | 0.45 | 1.46 | 7.95E-12 | NO | NO | NO | NO |
| AT2G20010 | 7.25 | 0.08 | 13.07 | 0.35 | 0.85 | 1.89E-07 | NO | NO | NO | NO |
| AT2G20142 | 7.52 | 0.58 | 33.62 | 1.95 | 2.16 | 0.00E+00 | NO | NO | NO | NO |
| AT2G20570 | 88.36 | 1.33 | 122.65 | 2.08 | 0.47 | 1.43E-02 | NO | YES | NO | NO |
| AT2G20610 | 60.51 | 0.92 | 84.20 | 1.01 | 0.48 | 8.66E-03 | NEGATIVE | NO | NO | NO |
| AT2G20720 | 1.86 | 0.08 | 3.38 | 0.44 | 0.86 | 2.90E-02 | NO | NO | NO | NO |
| AT2G20870 | 4.49 | 0.46 | 9.65 | 5.37 | 1.10 | 1.88E-02 | NO | NO | NO | NO |
| AT2G20960 | 17.39 | 0.09 | 29.38 | 0.70 | 0.76 | 4.15E-05 | NO | NO | NO | NO |
| AT2G21140 | 23.67 | 0.49 | 36.05 | 2.73 | 0.61 | 2.90E-03 | NO | NO | NO | NO |
| AT2G21470 | 14.57 | 0.17 | 21.23 | 0.29 | 0.54 | 1.77E-03 | NO | NO | NO | NO |
| AT2G21500 | 8.20 | 0.36 | 13.05 | 0.91 | 0.67 | 2.25E-03 | NO | NO | NO | NO |
| AT2G22300 | 18.06 | 0.38 | 30.80 | 0.45 | 0.77 | 4.77E-09 | NO | YES | NO | NO |
| AT2G22420 | 10.29 | 0.16 | 15.50 | 0.59 | 0.59 | 3.39E-02 | NO | NO | NO | NO |
| AT2G22480 | 10.26 | 0.22 | 15.30 | 0.40 | 0.58 | 1.19E-02 | NO | NO | NO | NO |
| AT2G22500 | 21.82 | 1.09 | 57.11 | 0.55 | 1.39 | 0.00E+00 | NO | NO | UP | NO |
| AT2G22560 | 1.65 | 0.09 | 4.05 | 0.42 | 1.29 | 3.86E-05 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT2G23140 | 6.61 | 0.10 | 10.60 | 0.06 | 0.68 | 6.13E-04 | NO | NO | NO | NO |
| AT2G23170 | 1.31 | 0.05 | 15.67 | 0.62 | 3.58 | 0.00E+00 | NO | NO | NO | NO |
| AT2G23200 | 10.21 | 0.46 | 17.81 | 0.50 | 0.80 | 3.77E-05 | NO | NO | NO | NO |
| AT2G23270 | 0.14 | 0.04 | 3.59 | 0.20 | 4.65 | 2.64E-04 | NO | NO | NO | NO |
| AT2G23290 | 1.71 | 0.12 | 9.32 | 0.34 | 2.44 | 2.49E-09 | NO | YES | NO | NO |
| AT2G23320 | 11.48 | 0.54 | 31.47 | 0.92 | 1.45 | 2.07E-12 | NO | YES | NO | NO |
| AT2G23380 | 7.91 | 0.41 | 10.83 | 0.24 | 0.45 | 4.97E-02 | NO | YES | NO | NO |
| AT2G23450 | 7.44 | 0.16 | 14.47 | 0.10 | 0.96 | 9.48E-08 | NO | NO | NO | NO |
| AT2G23680 | 5.31 | 0.92 | 12.60 | 0.58 | 1.25 | 5.01E-05 | NO | NO | NO | NO |
| AT2G23770 | 1.67 | 0.24 | 4.82 | 0.31 | 1.53 | 4.75E-05 | NO | NO | NO | NO |
| AT2G23810 | 42.29 | 0.61 | 122.74 | 1.44 | 1.54 | 0.00E+00 | NO | NO | NO | NO |
| AT2G24200 | 198.37 | 1.31 | 287.46 | 2.07 | 0.54 | 1.91E-04 | NO | NO | NO | NO |
| AT2G24360 | 62.41 | 0.52 | 90.15 | 1.31 | 0.53 | 4.82E-03 | NO | NO | NO | NO |
| AT2G24550 | 1.52 | 0.05 | 5.44 | 0.15 | 1.84 | 1.13E-04 | NO | NO | NO | NO |
| AT2G24590 | 55.96 | 0.72 | 77.22 | 1.19 | 0.46 | 2.44E-02 | NO | NO | NO | NO |
| AT2G24600 | 2.04 | 0.89 | 7.22 | 0.00 | 1.82 | 9.47E-13 | NO | NO | NO | NO |
| AT2G24650 | 1.79 | 0.10 | 3.81 | 0.11 | 1.09 | 3.43E-04 | NO | YES | NO | NO |
| AT2G25000 | 8.43 | 0.34 | 20.64 | 0.19 | 1.29 | 5.47E-08 | NO | YES | NO | NO |
| AT2G25110 | 48.87 | 0.82 | 116.75 | 1.84 | 1.26 | 2.48E-13 | NO | NO | NO | NO |
| AT2G25735 | 2.79 | 0.19 | 7.09 | 0.26 | 1.34 | 1.36E-02 | NO | NO | NO | NO |
| AT2G26190 | 18.32 | 1.15 | 45.86 | 0.61 | 1.32 | 5.36E-14 | NO | NO | NO | NO |
| AT2G26300 | 18.57 | 0.31 | 30.66 | 0.36 | 0.72 | 1.12E-04 | NO | NO | NO | NO |
| AT2G26400 | 6.87 | 1.35 | 52.83 | 1.90 | 2.94 | 0.00E+00 | NO | NO | NO | NO |
| AT2G26440 | 18.44 | 1.48 | 35.79 | 1.12 | 0.96 | 3.65E-07 | NO | NO | NO | NO |
| AT2G26530 | 4.99 | 0.24 | 20.76 | 0.76 | 2.06 | 0.00E+00 | NO | NO | NO | DOWN |
| AT2G26540 | 19.68 | 0.60 | 27.38 | 0.16 | 0.48 | 3.22E-02 | NO | NO | NO | NO |
| AT2G26800 | 15.31 | 0.47 | 23.16 | 0.36 | 0.60 | 5.81E-04 | NO | NO | NO | NO |
| AT2G26980 | 8.98 | 0.38 | 20.12 | 0.74 | 1.16 | 2.43E-12 | NEGATIVE | NO | NO | NO |
| AT2G27200 | 12.49 | 0.03 | 18.07 | 0.19 | 0.53 | 1.69E-02 | POSITIVE | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT2G27310 | 4.95 | 0.27 | 10.14 | 0.16 | 1.03 | 2.31E-03 | NO | NO | NO | NO |
| AT2G27350 | 20.11 | 0.15 | 28.01 | 0.19 | 0.48 | 3.80E-04 | NO | NO | NO | NO |
| AT2G27510 | 15.98 | 0.53 | 23.88 | 1.07 | 0.58 | 4.88E-02 | NO | NO | NO | NO |
| AT2G27690 | 1.11 | 0.06 | 3.52 | 0.38 | 1.67 | 1.11E-04 | NO | NO | NO | NO |
| AT2G28190 | 280.95 | 1.46 | 413.77 | 6.23 | 0.56 | 4.68E-03 | NO | NO | NO | NO |
| AT2G28210 | 0.38 | 0.07 | 1.74 | 0.24 | 2.19 | 3.39E-02 | NO | NO | DOWN | NO |
| AT2G28290 | 8.69 | 0.36 | 11.69 | 0.40 | 0.43 | 1.32E-02 | NO | NO | NO | NO |
| AT2G28570 | 1.71 | 0.33 | 10.48 | 0.69 | 2.62 | 2.62E-09 | NO | NO | NO | NO |
| AT2G28760 | 2.25 | 0.69 | 9.05 | 0.46 | 2.01 | 5.59E-11 | NO | NO | NO | NO |
| AT2G28890 | 13.21 | 0.72 | 22.90 | 0.44 | 0.79 | 3.57E-05 | NO | NO | NO | NO |
| AT2G28910 | 104.84 | 0.50 | 141.36 | 0.78 | 0.43 | 2.77E-02 | NO | NO | NO | NO |
| AT2G28950 | 29.43 | 0.82 | 50.30 | 1.83 | 0.77 | 2.62E-05 | NO | NO | NO | NO |
| AT2G29070 | 11.22 | 0.27 | 16.14 | 0.44 | 0.52 | 3.61E-02 | NO | NO | NO | NO |
| AT2G29110 | 0.84 | 0.19 | 8.37 | 1.01 | 3.31 | 0.00E+00 | NO | NO | NO | NO |
| AT2G29460 | 5.67 | 1.46 | 87.94 | 0.69 | 3.96 | 0.00E+00 | NO | NO | NO | NO |
| AT2G29510 | 12.13 | 0.17 | 16.77 | 0.44 | 0.47 | 2.57E-02 | NO | NO | NO | NO |
| AT2G29720 | 15.84 | 1.43 | 24.09 | 0.74 | 0.60 | 5.73E-03 | NO | NO | NO | NO |
| AT2G29990 | 11.48 | 0.19 | 26.53 | 0.57 | 1.21 | 3.27E-10 | NO | NO | NO | NO |
| AT2G30040 | 3.00 | 0.32 | 5.65 | 0.29 | 0.91 | 1.78E-02 | NO | NO | NO | NO |
| AT2G30140 | 9.33 | 0.83 | 44.26 | 0.37 | 2.25 | 0.00E+00 | NO | NO | NO | NO |
| AT2G30250 | 15.25 | 0.75 | 53.08 | 0.64 | 1.80 | 0.00E+00 | NO | YES | NO | NO |
| AT2G30395 | 0.54 | 0.07 | 2.74 | 0.08 | 2.34 | 3.20E-03 | NO | NO | NO | NO |
| AT2G30520 | 38.44 | 0.74 | 71.03 | 1.21 | 0.89 | 3.56E-08 | NO | NO | NO | NO |
| AT2G30640 | 1.79 | 0.03 | 3.65 | 0.12 | 1.03 | 5.81E-03 | NO | NO | NO | NO |
| AT2G30720 | 14.64 | 0.11 | 21.65 | 0.40 | 0.56 | 8.61E-03 | NO | NO | NO | NO |
| AT2G30750 | 3.00 | 0.98 | 30.63 | 1.26 | 3.35 | 0.00E+00 | NO | NO | NO | NO |
| AT2G30840 | 0.88 | 0.15 | 2.21 | 0.11 | 1.32 | 4.45E-02 | NO | NO | NO | NO |
| AT2G31090 | 22.99 | 0.51 | 41.51 | 0.62 | 0.85 | 4.77E-03 | NO | NO | NO | NO |
| AT2G31110 | 2.78 | 0.08 | 10.16 | 0.52 | 1.87 | 2.47E-08 | NO | NO | NO | DOWN |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT2G31260 | 5.08 | 0.17 | 7.76 | 0.15 | 0.61 | 9.51E-03 | NO | NO | NO | NO |
| AT2G31490 | 232.93 | 0.66 | 313.37 | 4.02 | 0.43 | 3.24E-02 | NO | NO | NO | NO |
| AT2G31570 | 99.84 | 0.20 | 197.37 | 2.32 | 0.98 | 3.36E-09 | NO | NO | NO | NO |
| AT2G31750 | 16.83 | 0.75 | 27.57 | 1.80 | 0.71 | 3.02E-04 | NO | NO | NO | NO |
| AT2G31865 | 5.46 | 0.71 | 30.21 | 1.57 | 2.47 | 0.00E+00 | NO | NO | NO | NO |
| AT2G31870 | 4.44 | 0.40 | 6.89 | 0.15 | 0.63 | 3.12E-02 | NO | NO | NO | NO |
| AT2G31970 | 5.06 | 0.26 | 8.96 | 0.25 | 0.82 | 3.92E-05 | NO | NO | NO | NO |
| AT2G32020 | 0.62 | 0.17 | 2.91 | 0.04 | 2.22 | 8.20E-03 | NO | NO | NO | NO |
| AT2G32030 | 1.56 | 0.44 | 5.87 | 0.15 | 1.91 | 4.97E-04 | NO | NO | NO | NO |
| AT2G32130 | 0.61 | 0.17 | 8.33 | 0.35 | 3.78 | 1.95E-07 | NO | NO | NO | NO |
| AT2G32190 | 1.39 | 0.60 | 18.06 | 0.32 | 3.69 | 1.99E-11 | NO | NO | NO | NO |
| AT2G32210 | 6.41 | 0.45 | 17.48 | 0.63 | 1.45 | 3.46E-04 | NO | NO | NO | NO |
| AT2G32400 | 4.96 | 0.14 | 8.14 | 0.23 | 0.72 | 1.55E-03 | NO | NO | NO | NO |
| AT2G32800 | 3.94 | 0.33 | 12.58 | 0.17 | 1.68 | 0.00E+00 | NO | NO | NO | NO |
| AT2G33170 | 9.79 | 0.23 | 14.35 | 0.64 | 0.55 | 6.15E-03 | NO | NO | NO | NO |
| AT2G33580 | 1.28 | 0.23 | 6.50 | 0.21 | 2.34 | 6.53E-12 | NO | NO | NO | NO |
| AT2G33620 | 12.12 | 0.41 | 16.70 | 0.77 | 0.46 | 3.49E-02 | NO | NO | NO | NO |
| AT2G33770 | 29.24 | 0.35 | 39.34 | 0.53 | 0.43 | 3.46E-02 | NO | NO | NO | NO |
| AT2G34250 | 203.22 | 2.69 | 323.41 | 5.27 | 0.67 | 1.33E-03 | NO | NO | NO | NO |
| AT2G34300 | 6.92 | 0.24 | 12.49 | 0.27 | 0.85 | 1.66E-05 | NO | NO | NO | NO |
| AT2G34780 | 4.19 | 0.12 | 6.11 | 0.11 | 0.54 | 6.21E-03 | NO | NO | NO | NO |
| AT2G34810 | 3.30 | 0.64 | 7.20 | 2.19 | 1.13 | 2.04E-04 | NO | NO | NO | NO |
| AT2G34940 | 1.23 | 0.24 | 5.37 | 0.22 | 2.12 | 1.69E-08 | NO | NO | NO | NO |
| AT2G34960 | 4.97 | 0.29 | 8.13 | 0.24 | 0.71 | 1.19E-02 | NO | NO | NO | NO |
| AT2G35020 | 5.21 | 0.25 | 11.05 | 0.15 | 1.09 | 1.24E-05 | NO | NO | NO | NO |
| AT2G35070 | 0.71 | 0.12 | 3.15 | 0.15 | 2.14 | 4.36E-03 | NO | NO | NO | NO |
| AT2G35110 | 8.43 | 0.14 | 12.54 | 0.35 | 0.57 | 3.63E-03 | NO | NO | NO | NO |
| AT2G35930 | 1.33 | 0.23 | 10.61 | 0.88 | 3.00 | 0.00E+00 | NO | NO | NO | NO |
| AT2G36080 | 3.47 | 0.31 | 13.32 | 0.33 | 1.94 | 8.21E-11 | NO | YES | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT2G36310 | 20.22 | 0.13 | 32.47 | 0.73 | 0.68 | 6.52E-04 | NEGATIVE | NO | NO | NO |
| AT2G36580 | 24.04 | 0.56 | 55.34 | 0.70 | 1.20 | 1.32E-12 | NO | NO | NO | NO |
| AT2G36630 | 29.47 | 0.40 | 40.75 | 0.84 | 0.47 | 1.79E-02 | NO | NO | NO | NO |
| AT2G36792 | 0.26 | 0.02 | 0.97 | 0.18 | 1.89 | 1.86E-02 | NO | NO | NO | NO |
| AT2G36800 | 3.45 | 0.29 | 22.96 | 1.13 | 2.73 | 0.00E+00 | NO | NO | NO | NO |
| AT2G36880 | 168.28 | 2.63 | 282.61 | 3.02 | 0.75 | 9.87E-05 | NO | NO | NO | NO |
| AT2G36895 | 43.63 | 0.15 | 64.98 | 0.72 | 0.57 | 5.69E-04 | NO | NO | NO | NO |
| AT2G37080 | 14.74 | 0.26 | 22.79 | 0.58 | 0.63 | 1.34E-03 | NO | NO | NO | NO |
| AT2G37100 | 2.29 | 0.03 | 5.33 | 0.26 | 1.22 | 1.39E-02 | NO | NO | NO | NO |
| AT2G37110 | 68.58 | 0.67 | 151.89 | 1.06 | 1.15 | 3.63E-12 | NO | NO | NO | NO |
| AT2G37150 | 3.93 | 0.14 | 7.07 | 0.41 | 0.85 | 6.30E-04 | NO | NO | NO | NO |
| AT2G37970 | 131.20 | 0.47 | 303.93 | 4.83 | 1.21 | 2.17E-13 | NO | NO | NO | NO |
| AT2G38250 | 0.72 | 0.22 | 9.21 | 0.70 | 3.69 | 1.24E-10 | NO | YES | NO | NO |
| AT2G38290 | 27.76 | 0.60 | 49.21 | 1.17 | 0.83 | 3.34E-06 | NO | NO | NO | NO |
| AT2G38310 | 6.32 | 0.34 | 17.45 | 0.18 | 1.47 | 7.35E-08 | NO | NO | NO | DOWN |
| AT2G38360 | 8.11 | 0.34 | 13.92 | 0.38 | 0.78 | 1.26E-02 | NO | NO | NO | NO |
| AT2G38410 | 6.05 | 0.11 | 9.24 | 0.09 | 0.61 | 1.23E-02 | NO | NO | NO | NO |
| AT2G38470 | 17.35 | 1.37 | 77.52 | 1.54 | 2.16 | 0.00E+00 | NO | YES | UP | NO |
| AT2G38750 | 5.31 | 0.15 | 11.45 | 1.66 | 1.11 | 9.62E-05 | NEGATIVE | NO | NO | NO |
| AT2G38790 | 13.08 | 0.81 | 29.23 | 0.84 | 1.16 | 1.41E-07 | NO | NO | NO | NO |
| AT2G38860 | 32.96 | 1.10 | 106.55 | 0.48 | 1.69 | 0.00E+00 | NO | NO | NO | NO |
| AT2G38940 | 4.27 | 0.80 | 9.96 | 0.57 | 1.22 | 2.64E-06 | NO | NO | NO | NO |
| AT2G39200 | 0.92 | 0.29 | 5.03 | 0.58 | 2.45 | 5.89E-09 | NO | NO | NO | NO |
| AT2G39250 | 12.96 | 0.13 | 21.81 | 1.01 | 0.75 | 1.08E-03 | NO | YES | NO | NO |
| AT2G39350 | 0.86 | 0.07 | 3.34 | 0.46 | 1.96 | 1.19E-06 | NO | NO | NO | NO |
| AT2G39360 | 4.85 | 0.11 | 9.62 | 0.14 | 0.99 | 8.57E-06 | NO | NO | NO | NO |
| AT2G39420 | 17.28 | 0.87 | 35.19 | 0.76 | 1.03 | 3.41E-07 | NO | NO | NO | NO |
| AT2G39518 | 1.81 | 1.38 | 7.65 | 1.07 | 2.08 | 3.43E-04 | NO | NO | NO | NO |
| AT2G39570 | 6.28 | 0.15 | 11.83 | 0.52 | 0.91 | 2.22E-04 | NO | NO | DOWN | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT2G39660 | 9.61 | 0.41 | 21.59 | 0.36 | 1.17 | 1.15E-08 | NO | NO | NO | NO |
| AT2G39770 | 139.53 | 0.48 | 191.92 | 4.48 | 0.46 | 1.58E-02 | NO | NO | NO | NO |
| AT2G39870 | 5.40 | 0.16 | 9.86 | 0.63 | 0.87 | 9.48E-04 | NO | NO | NO | NO |
| AT2G40140 | 35.89 | 0.65 | 93.13 | 1.01 | 1.38 | 0.00E+00 | NO | YES | UP | NO |
| AT2G40330 | 1.60 | 0.23 | 7.25 | 0.52 | 2.18 | 1.29E-06 | NO | NO | NO | DOWN |
| AT2G40520 | 16.28 | 0.23 | 29.18 | 0.21 | 0.84 | 2.38E-08 | NO | NO | NO | NO |
| AT2G40540 | 17.17 | 0.43 | 27.62 | 0.24 | 0.69 | 1.26E-06 | NO | NO | NO | NO |
| AT2G40570 | 4.69 | 0.06 | 8.78 | 0.27 | 0.90 | 4.65E-04 | NO | NO | NO | NO |
| AT2G40610 | 3.34 | 0.24 | 10.47 | 1.40 | 1.65 | 2.35E-06 | NO | NO | DOWN | NO |
| AT2G40750 | 16.88 | 2.29 | 48.35 | 1.61 | 1.52 | 0.00E+00 | NO | YES | NO | NO |
| AT2G40940 | 29.33 | 0.05 | 40.32 | 0.33 | 0.46 | 1.94E-02 | NO | NO | NO | NO |
| AT2G41100 | 0.00 | 4.11 | 234.53 | 7.88 | 3.38 | 0.00E+00 | NO | NO | DOWN | DOWN |
| AT2G41110 | 71.91 | 1.07 | 186.57 | 3.05 | 1.38 | 0.00E+00 | NO | NO | NO | NO |
| AT2G41220 | 6.27 | 0.10 | 10.50 | 0.12 | 0.74 | 7.66E-05 | NO | NO | NO | NO |
| AT2G41250 | 153.48 | 1.75 | 203.76 | 1.22 | 0.41 | 4.59E-02 | NO | NO | NO | NO |
| AT2G41410 | 42.98 | 1.35 | 137.98 | 1.80 | 1.68 | 0.00E+00 | NO | NO | NO | NO |
| AT2G41430 | 342.70 | 7.21 | 447.09 | 2.18 | 0.38 | 4.67E-02 | NO | NO | NO | NO |
| AT2G41700 | 6.15 | 0.14 | 11.99 | 0.90 | 0.96 | 1.43E-07 | NO | NO | NO | NO |
| AT2G41730 | 2.37 | 0.31 | 26.37 | 2.36 | 3.48 | 5.57E-11 | NO | NO | NO | NO |
| AT2G41835 | 4.00 | 0.29 | 9.50 | 0.08 | 1.25 | 1.56E-04 | NO | YES | NO | NO |
| AT2G41850 | 1.65 | 1.03 | 7.44 | 2.86 | 2.18 | 8.32E-09 | NO | NO | NO | NO |
| AT2G41880 | 6.02 | 0.25 | 10.35 | 0.05 | 0.78 | 4.89E-03 | NO | NO | NO | NO |
| AT2G42330 | 2.79 | 0.24 | 4.24 | 0.31 | 0.61 | 3.73E-02 | NO | NO | NO | NO |
| AT2G42360 | 2.46 | 0.38 | 12.73 | 0.92 | 2.37 | 6.41E-10 | NO | NO | NO | NO |
| AT2G42380 | 1.45 | 0.10 | 3.88 | 0.48 | 1.42 | 8.73E-04 | NO | YES | NO | NO |
| AT2G42490 | 16.22 | 0.19 | 23.33 | 0.43 | 0.52 | 7.23E-03 | NO | NO | NO | NO |
| AT2G42610 | 20.53 | 0.54 | 30.95 | 1.34 | 0.59 | 4.23E-03 | NO | NO | NO | NO |
| AT2G42840 | 105.50 | 1.30 | 143.75 | 5.27 | 0.45 | 2.31E-02 | NO | NO | NO | NO |
| AT2G42890 | 11.08 | 0.25 | 15.79 | 0.23 | 0.51 | 1.52E-03 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT2G43000 | 2.28 | 0.58 | 15.57 | 0.64 | 2.77 | 9.57E-12 | NO | YES | NO | NO |
| AT2G43140 | 0.79 | 0.17 | 3.14 | 0.76 | 1.98 | 1.08E-03 | NO | YES | NO | NO |
| AT2G43160 | 47.80 | 0.40 | 64.40 | 0.29 | 0.43 | 1.34E-04 | NO | NO | NO | NO |
| AT2G43210 | 20.69 | 0.37 | 28.41 | 0.48 | 0.46 | 1.80E-02 | NO | NO | NO | NO |
| AT2G43320 | 7.50 | 0.41 | 22.48 | 0.34 | 1.58 | 0.00E+00 | NO | NO | NO | NO |
| AT2G43680 | 44.11 | 0.35 | 67.27 | 0.24 | 0.61 | 6.84E-07 | NO | NO | NO | NO |
| AT2G44280 | 1.46 | 0.03 | 4.12 | 0.03 | 1.49 | 2.13E-05 | NO | NO | NO | NO |
| AT2G44370 | 0.79 | 0.29 | 3.02 | 0.61 | 1.93 | 2.35E-03 | NO | NO | NO | NO |
| AT2G44500 | 2.01 | 0.28 | 6.55 | 0.30 | 1.70 | 2.71E-09 | NO | NO | NO | NO |
| AT2G45000 | 7.18 | 0.26 | 10.87 | 0.29 | 0.60 | 1.09E-02 | NO | NO | NO | NO |
| AT2G45010 | 19.57 | 0.57 | 30.58 | 0.44 | 0.64 | 1.76E-03 | NO | NO | NO | NO |
| AT2G45030 | 7.17 | 0.23 | 10.29 | 0.17 | 0.52 | 3.00E-02 | NO | NO | NO | NO |
| AT2G45070 | 330.68 | 4.89 | 498.26 | 13.95 | 0.59 | 4.39E-07 | NO | NO | NO | NO |
| AT2G45170 | 18.47 | 0.57 | 38.79 | 0.25 | 1.07 | 7.81E-06 | NO | NO | NO | NO |
| AT2G45280 | 4.72 | 0.13 | 8.68 | 0.36 | 0.88 | 3.15E-03 | NO | NO | NO | NO |
| AT2G45290 | 10.39 | 0.51 | 14.20 | 0.47 | 0.45 | 4.29E-02 | NO | NO | NO | NO |
| AT2G45540 | 9.31 | 0.37 | 14.32 | 0.32 | 0.62 | 1.27E-05 | NO | NO | NO | NO |
| AT2G45590 | 14.98 | 0.49 | 21.73 | 0.37 | 0.54 | 8.51E-03 | NO | NO | NO | NO |
| AT2G45680 | 3.72 | 0.19 | 9.38 | 0.38 | 1.33 | 2.89E-06 | NO | YES | NO | NO |
| AT2G45700 | 7.18 | 0.13 | 10.18 | 0.24 | 0.50 | 3.97E-02 | NO | NO | NO | NO |
| AT2G45790 | 126.47 | 0.65 | 199.15 | 3.30 | 0.66 | 4.11E-04 | NO | NO | NO | NO |
| AT2G45910 | 7.67 | 0.10 | 11.31 | 0.32 | 0.56 | 1.02E-02 | NO | NO | NO | NO |
| AT2G45960 | 239.62 | 19.48 | 352.32 | 26.16 | 0.56 | 4.15E-03 | NO | NO | NO | NO |
| AT2G46020 | 10.43 | 0.26 | 14.55 | 0.34 | 0.48 | 4.60E-04 | NO | NO | NO | NO |
| AT2G46150 | 1.21 | 0.17 | 7.43 | 0.22 | 2.61 | 1.61E-07 | NO | NO | NO | NO |
| AT2G46270 | 1.97 | 0.26 | 10.45 | 0.08 | 2.41 | 0.00E+00 | NO | YES | NO | NO |
| AT2G46330 | 57.26 | 0.24 | 101.27 | 1.02 | 0.82 | 6.51E-06 | NO | NO | NO | NO |
| AT2G46420 | 9.51 | 0.30 | 17.94 | 0.15 | 0.92 | 7.04E-06 | NO | NO | NO | NO |
| AT2G46500 | 15.49 | 0.56 | 31.20 | 0.76 | 1.01 | 1.48E-10 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT2G46600 | 146.49 | 1.59 | 303.78 | 2.59 | 1.05 | 1.08E-09 | NO | NO | NO | UP |
| AT2G47130 | 5.18 | 1.71 | 27.68 | 0.47 | 2.42 | 0.00E+00 | NO | NO | NO | NO |
| AT2G47470 | 137.45 | 1.77 | 319.71 | 3.25 | 1.22 | 2.78E-11 | NO | NO | NO | NO |
| AT2G47730 | 154.03 | 1.69 | 290.59 | 0.72 | 0.92 | 4.69E-07 | NO | NO | NO | NO |
| AT2G47800 | 5.79 | 0.21 | 14.09 | 0.09 | 1.28 | 4.04E-13 | NO | NO | NO | NO |
| AT2G48030 | 7.45 | 0.41 | 15.60 | 0.41 | 1.07 | 1.67E-06 | NO | NO | NO | NO |
| AT3G01290 | 32.29 | 2.41 | 182.61 | 1.90 | 2.50 | 0.00E+00 | NO | NO | DOWN | NO |
| AT3G01650 | 2.23 | 0.16 | 5.06 | 0.05 | 1.18 | 1.12E-03 | NO | NO | NO | NO |
| AT3G01720 | 10.57 | 0.05 | 19.99 | 0.52 | 0.92 | 6.64E-07 | NO | NO | NO | NO |
| AT3G01830 | 2.56 | 1.17 | 31.33 | 1.06 | 3.61 | 0.00E+00 | NO | NO | NO | NO |
| AT3G02040 | 4.01 | 0.39 | 6.98 | 0.61 | 0.80 | 1.76E-02 | NO | NO | NO | NO |
| AT3G02050 | 12.32 | 0.12 | 22.38 | 0.14 | 0.86 | 2.00E-06 | NO | NO | NO | NO |
| AT3G02170 | 3.47 | 0.24 | 11.01 | 0.13 | 1.67 | 0.00E+00 | NO | NO | NO | NO |
| AT3G02260 | 11.00 | 0.37 | 15.17 | 0.43 | 0.46 | 2.22E-02 | NO | NO | NO | NO |
| AT3G02770 | 53.96 | 0.57 | 86.76 | 0.83 | 0.69 | 3.71E-04 | NO | NO | NO | NO |
| AT3G02840 | 0.42 | 0.18 | 4.45 | 0.22 | 3.41 | 1.97E-08 | NO | NO | NO | NO |
| AT3G02880 | 7.25 | 0.42 | 11.85 | 0.44 | 0.71 | 1.48E-03 | NO | NO | NO | NO |
| AT3G02885 | 0.28 | 0.12 | 1.51 | 0.35 | 2.44 | 3.43E-02 | NO | NO | NO | NO |
| AT3G03440 | 13.69 | 0.50 | 22.16 | 0.35 | 0.69 | 1.37E-03 | NO | NO | NO | NO |
| AT3G03640 | 25.52 | 1.56 | 39.14 | 1.96 | 0.62 | 1.54E-03 | NO | NO | UP | NO |
| AT3G03680 | 2.47 | 0.04 | 3.78 | 0.13 | 0.61 | 4.62E-02 | NO | NO | NO | NO |
| AT3G03990 | 30.28 | 0.89 | 45.27 | 0.51 | 0.58 | 4.72E-03 | NO | NO | NO | UP |
| AT3G04010 | 4.60 | 0.27 | 7.09 | 0.45 | 0.63 | 4.98E-02 | NO | NO | UP | NO |
| AT3G04110 | 12.57 | 0.21 | 17.39 | 0.36 | 0.47 | 2.98E-02 | NO | NO | NO | NO |
| AT3G04210 | 64.89 | 2.90 | 111.38 | 0.45 | 0.78 | 8.16E-06 | NO | NO | DOWN | NO |
| AT3G04240 | 41.06 | 0.54 | 62.70 | 0.47 | 0.61 | 1.22E-03 | POSITIVE | NO | NO | NO |
| AT3G04300 | 0.16 | 0.02 | 1.37 | 0.20 | 3.10 | 1.44E-02 | NO | NO | NO | NO |
| AT3G04580 | 11.41 | 0.11 | 18.27 | 0.39 | 0.68 | 7.41E-06 | NO | NO | NO | NO |
| AT3G04640 | 10.01 | 1.25 | 24.97 | 0.98 | 1.32 | 3.40E-05 | NO | NO | UP | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G04670 | 14.68 | 0.01 | 25.52 | 0.63 | 0.80 | 2.98E-05 | NO | YES | NO | NO |
| AT3G04720 | 99.75 | 5.32 | 154.11 | 2.36 | 0.63 | 4.27E-04 | NO | NO | NO | NO |
| AT3G05165 | 2.39 | 0.12 | 6.25 | 0.45 | 1.39 | 3.09E-05 | NO | NO | NO | NO |
| AT3G05320 | 1.46 | 0.14 | 4.82 | 0.48 | 1.72 | 7.04E-05 | NO | NO | NO | NO |
| AT3G05360 | 0.77 | 0.02 | 2.28 | 0.08 | 1.57 | 4.99E-04 | NO | NO | NO | NO |
| AT3G05500 | 85.31 | 0.90 | 125.89 | 1.55 | 0.56 | 3.79E-03 | NO | NO | NO | NO |
| AT3G05680 | 5.52 | 0.16 | 7.39 | 0.22 | 0.42 | 4.55E-02 | NO | NO | NO | NO |
| AT3G05830 | 6.18 | 0.22 | 12.00 | 0.25 | 0.96 | 6.76E-04 | NO | NO | NO | NO |
| AT3G05970 | 34.76 | 0.35 | 51.79 | 0.20 | 0.58 | 2.14E-03 | NO | NO | NO | NO |
| AT3G06070 | 4.91 | 0.54 | 9.65 | 0.98 | 0.98 | 2.49E-02 | NO | NO | NO | NO |
| AT3G06330 | 6.38 | 0.30 | 9.32 | 0.37 | 0.55 | 4.73E-02 | NO | NO | NO | NO |
| AT3G06500 | 25.30 | 0.45 | 51.47 | 0.36 | 1.02 | 1.58E-09 | NO | NO | NO | DOWN |
| AT3G06890 | 3.56 | 0.27 | 7.96 | 0.29 | 1.16 | 2.09E-02 | NO | NO | NO | NO |
| AT3G07010 | 9.44 | 0.32 | 16.92 | 1.17 | 0.84 | 1.54E-04 | NO | NO | NO | NO |
| AT3G07270 | 23.67 | 0.13 | 39.14 | 0.41 | 0.73 | 1.31E-06 | NO | NO | NO | NO |
| AT3G07340 | 1.55 | 0.07 | 4.29 | 0.03 | 1.47 | 1.87E-04 | NO | YES | NO | NO |
| AT3G07525 | 13.45 | 0.84 | 22.11 | 1.20 | 0.72 | 4.13E-03 | NO | NO | NO | NO |
| AT3G07690 | 13.59 | 0.12 | 20.16 | 0.63 | 0.57 | 1.01E-02 | NO | NO | NO | NO |
| AT3G07700 | 37.50 | 0.22 | 69.92 | 0.84 | 0.90 | 1.37E-13 | NO | NO | NO | NO |
| AT3G07720 | 44.16 | 0.48 | 105.81 | 1.02 | 1.26 | 7.04E-14 | NO | NO | NO | NO |
| AT3G08650 | 30.41 | 0.22 | 42.23 | 0.15 | 0.47 | 1.40E-03 | NO | NO | NO | NO |
| AT3G08670 | 7.73 | 0.16 | 11.36 | 0.31 | 0.56 | 2.37E-02 | NO | NO | NO | NO |
| AT3G08760 | 10.23 | 0.29 | 22.01 | 0.20 | 1.11 | 8.30E-09 | NO | NO | NO | NO |
| AT3G08850 | 8.30 | 0.25 | 11.17 | 0.25 | 0.43 | 4.39E-02 | NO | NO | NO | NO |
| AT3G09010 | 5.01 | 0.59 | 9.78 | 0.17 | 0.96 | 3.96E-04 | NO | NO | NO | NO |
| AT3G09020 | 1.63 | 0.34 | 6.68 | 0.17 | 2.03 | 8.38E-07 | NO | NO | NO | NO |
| AT3G09490 | 1.31 | 0.26 | 4.88 | 0.25 | 1.90 | 2.06E-04 | NO | NO | NO | NO |
| AT3G09520 | 1.75 | 0.56 | 6.04 | 0.67 | 1.79 | 2.20E-07 | NO | NO | NO | NO |
| AT3G09560 | 7.92 | 2.23 | 12.02 | 0.30 | 0.60 | 1.76E-04 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G09830 | 15.28 | 0.22 | 30.38 | 0.49 | 0.99 | 2.34E-09 | NO | NO | NO | NO |
| AT3G09920 | 12.33 | 0.11 | 20.52 | 0.48 | 0.73 | 9.98E-08 | NO | NO | NO | NO |
| AT3G10010 | 4.55 | 0.23 | 6.61 | 0.18 | 0.54 | 2.27E-02 | NO | NO | NO | NO |
| AT3G10070 | 9.75 | 0.47 | 13.97 | 0.09 | 0.52 | 2.80E-02 | NO | NO | NO | NO |
| AT3G10130 | 25.62 | 0.26 | 39.01 | 0.27 | 0.61 | 4.34E-03 | NO | NO | NO | NO |
| AT3G10250 | 6.05 | 0.20 | 9.84 | 0.17 | 0.70 | 1.45E-02 | NO | NO | NO | NO |
| AT3G10420 | 48.35 | 0.45 | 84.02 | 0.54 | 0.80 | 1.54E-06 | NO | NO | NO | NO |
| AT3G10500 | 6.25 | 0.21 | 14.72 | 0.20 | 1.24 | 1.14E-08 | NO | YES | NO | NO |
| AT3G10640 | 8.42 | 0.18 | 18.34 | 0.29 | 1.12 | 1.08E-05 | NO | NO | NO | NO |
| AT3G10720 | 6.64 | 0.28 | 11.78 | 0.43 | 0.83 | 2.37E-04 | NO | NO | NO | NO |
| AT3G10740 | 9.91 | 0.24 | 15.48 | 0.05 | 0.64 | 2.03E-03 | NO | NO | NO | NO |
| AT3G10930 | 0.39 | 0.19 | 3.30 | 0.29 | 3.10 | 8.10E-04 | NO | NO | UP | NO |
| AT3G10985 | 11.41 | 0.41 | 37.33 | 0.22 | 1.71 | 8.76E-14 | NO | NO | NO | NO |
| AT3G11090 | 8.88 | 0.91 | 18.11 | 0.45 | 1.03 | 6.92E-03 | NO | YES | DOWN | NO |
| AT3G11330 | 8.64 | 0.17 | 12.79 | 0.35 | 0.57 | 1.84E-02 | NO | NO | NO | NO |
| AT3G11700 | 27.19 | 0.55 | 36.20 | 0.79 | 0.41 | 4.78E-02 | NO | NO | NO | NO |
| AT3G11820 | 18.56 | 0.57 | 45.73 | 0.44 | 1.30 | 0.00E+00 | NO | NO | NO | NO |
| AT3G11840 | 4.31 | 0.79 | 11.25 | 0.17 | 1.38 | 3.03E-07 | NO | NO | NO | NO |
| AT3G12145 | 5.67 | 0.37 | 10.74 | 1.26 | 0.92 | 1.10E-03 | NO | NO | NO | NO |
| AT3G12150 | 3.34 | 0.12 | 5.59 | 0.07 | 0.74 | 4.08E-02 | NO | NO | NO | NO |
| AT3G12360 | 24.84 | 0.54 | 38.71 | 0.48 | 0.64 | 6.05E-04 | NO | NO | NO | NO |
| AT3G12520 | 1.49 | 0.10 | 4.34 | 0.60 | 1.54 | 1.00E-05 | NO | NO | NO | NO |
| AT3G12600 | 15.38 | 0.19 | 26.10 | 0.45 | 0.76 | 5.36E-04 | NO | NO | NO | NO |
| AT3G12610 | 24.66 | 0.76 | 34.85 | 1.91 | 0.50 | 1.71E-02 | NEGATIVE | NO | NO | NO |
| AT3G12710 | 1.99 | 0.27 | 5.32 | 0.27 | 1.42 | 7.53E-04 | NEGATIVE | NO | NO | NO |
| AT3G12740 | 42.66 | 0.57 | 91.40 | 0.77 | 1.10 | 3.60E-11 | NO | NO | NO | NO |
| AT3G12830 | 3.60 | 0.02 | 15.41 | 0.43 | 2.10 | 1.05E-09 | NO | NO | NO | NO |
| AT3G13060 | 25.20 | 0.12 | 33.87 | 0.19 | 0.43 | 3.60E-02 | NO | NO | NO | NO |
| AT3G13061 | 7.24 | 0.06 | 14.99 | 0.14 | 1.05 | 5.87E-03 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G13062 | 32.12 | 0.55 | 47.36 | 0.28 | 0.56 | 2.58E-03 | NO | NO | NO | NO |
| AT3G13080 | 14.02 | 0.14 | 57.64 | 0.39 | 2.04 | 0.00E+00 | NO | NO | NO | NO |
| AT3G13430 | 9.49 | 0.26 | 13.46 | 0.64 | 0.50 | 4.90E-02 | NO | NO | NO | NO |
| AT3G13437 | 0.55 | 0.25 | 2.60 | 0.04 | 2.26 | 4.92E-02 | NO | NO | NO | NO |
| AT3G13445 | 8.14 | 0.22 | 12.02 | 0.19 | 0.56 | 4.32E-02 | NO | NO | NO | NO |
| AT3G13670 | 41.70 | 0.56 | 55.39 | 0.32 | 0.41 | 4.26E-02 | NO | NO | NO | NO |
| AT3G13720 | 18.66 | 0.87 | 27.56 | 0.99 | 0.56 | 2.33E-02 | NO | NO | NO | NO |
| AT3G13810 | 23.49 | 0.60 | 33.83 | 0.38 | 0.53 | 6.62E-04 | NO | YES | NO | NO |
| AT3G13910 | 34.83 | 0.91 | 63.83 | 1.13 | 0.87 | 1.33E-04 | NO | NO | NO | NO |
| AT3G14050 | 14.65 | 0.54 | 24.76 | 0.17 | 0.76 | 5.00E-05 | NO | NO | NO | NO |
| AT3G14060 | 2.63 | 0.75 | 9.81 | 0.47 | 1.90 | 8.58E-04 | POSITIVE | NO | NO | NO |
| AT3G14067 | 39.58 | 0.89 | 65.62 | 0.58 | 0.73 | 3.83E-05 | NO | NO | NO | NO |
| AT3G14090 | 5.31 | 0.06 | 8.95 | 0.17 | 0.75 | 2.48E-03 | NO | NO | NO | NO |
| AT3G14230 | 97.59 | 0.95 | 132.75 | 0.65 | 0.44 | 7.01E-03 | NO | YES | NO | NO |
| AT3G14270 | 3.95 | 0.17 | 6.82 | 0.23 | 0.79 | 7.26E-05 | NO | NO | NO | NO |
| AT3G14470 | 2.08 | 0.09 | 5.85 | 0.33 | 1.49 | 7.81E-09 | NO | NO | NO | NO |
| AT3G14610 | 1.52 | 0.08 | 4.09 | 0.08 | 1.42 | 4.78E-04 | NO | NO | NO | NO |
| AT3G14770 | 7.69 | 0.11 | 12.28 | 0.05 | 0.68 | 7.57E-03 | NO | NO | NO | NO |
| AT3G14790 | 16.84 | 0.46 | 30.71 | 0.23 | 0.87 | 1.51E-06 | NO | NO | NO | NO |
| AT3G14840 | 16.57 | 0.87 | 45.40 | 0.44 | 1.45 | 0.00E+00 | NO | NO | NO | DOWN |
| AT3G14920 | 7.72 | 0.06 | 11.54 | 0.18 | 0.58 | 1.81E-02 | NO | NO | NO | NO |
| AT3G15353 | 1634.45 | 24.92 | 2244.20 | 9.07 | 0.46 | 3.74E-02 | NO | NO | NO | NO |
| AT3G15400 | 2.19 | 0.18 | 7.90 | 3.71 | 1.85 | 1.92E-07 | NO | NO | NO | NO |
| AT3G15430 | 24.66 | 0.22 | 37.49 | 0.60 | 0.60 | 1.81E-05 | POSITIVE | NO | NO | NO |
| AT3G15540 | 1.88 | 0.12 | 8.58 | 0.21 | 2.19 | 6.78E-07 | NEGATIVE | YES | NO | NO |
| AT3G15650 | 1.51 | 0.17 | 6.15 | 0.28 | 2.03 | 1.71E-05 | NO | NO | NO | NO |
| AT3G15760 | 0.73 | 0.23 | 3.15 | 0.07 | 2.10 | 4.65E-03 | NO | NO | DOWN | NO |
| AT3G15770 | 8.41 | 0.53 | 21.36 | 0.17 | 1.34 | 1.53E-06 | NO | NO | NO | NO |
| AT3G15790 | 30.43 | 0.68 | 45.80 | 1.02 | 0.59 | 3.14E-03 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G15810 | 36.24 | 1.14 | 77.21 | 0.71 | 1.09 | 1.01E-09 | NO | NO | NO | NO |
| AT3G15820 | 4.77 | 0.33 | 17.65 | 0.13 | 1.89 | 9.76E-12 | NO | NO | NO | NO |
| AT3G15880 | 14.80 | 0.28 | 18.71 | 0.33 | 0.34 | 2.85E-02 | NO | NO | NO | NO |
| AT3G15980 | 22.16 | 0.48 | 47.71 | 2.17 | 1.11 | 0.00E+00 | NO | NO | NO | NO |
| AT3G16230 | 12.74 | 0.35 | 17.54 | 0.10 | 0.46 | 2.29E-02 | NO | NO | DOWN | NO |
| AT3G16370 | 115.85 | 0.52 | 168.84 | 5.24 | 0.54 | 4.27E-03 | NO | NO | NO | NO |
| AT3G16460 | 2.03 | 0.22 | 5.50 | 0.53 | 1.44 | 3.29E-07 | NO | NO | NO | NO |
| AT3G16720 | 2.85 | 0.32 | 11.68 | 0.56 | 2.03 | 1.26E-10 | NO | NO | NO | NO |
| AT3G16857 | 8.09 | 0.24 | 12.85 | 0.05 | 0.67 | 3.17E-04 | NO | YES | NO | NO |
| AT3G16910 | 12.17 | 0.25 | 19.30 | 0.57 | 0.67 | 1.56E-03 | NO | NO | DOWN | NO |
| AT3G16950 | 3.72 | 0.15 | 5.87 | 0.24 | 0.66 | 2.78E-02 | NO | NO | NO | NO |
| AT3G17000 | 26.38 | 0.06 | 39.01 | 0.50 | 0.56 | 6.32E-03 | NO | NO | NO | NO |
| AT3G17050 | 1.54 | 0.19 | 5.40 | 0.22 | 1.81 | 1.02E-06 | NO | NO | NO | NO |
| AT3G17205 | 12.33 | 0.20 | 18.11 | 0.24 | 0.55 | 1.01E-04 | NO | NO | NO | NO |
| AT3G17240 | 93.11 | 1.26 | 141.89 | 1.73 | 0.61 | 1.08E-03 | NO | NO | NO | NO |
| AT3G17420 | 5.33 | 0.11 | 11.65 | 0.48 | 1.13 | 2.52E-06 | NO | NO | NO | NO |
| AT3G17609 | 75.03 | 1.66 | 147.59 | 0.82 | 0.98 | 6.47E-13 | NO | YES | NO | NO |
| AT3G17700 | 7.52 | 0.29 | 15.78 | 0.60 | 1.07 | 7.74E-08 | NO | NO | NO | NO |
| AT3G17770 | 10.87 | 0.63 | 17.19 | 0.31 | 0.66 | 1.28E-03 | NO | NO | NO | NO |
| AT3G17800 | 81.99 | 1.04 | 159.86 | 1.29 | 0.96 | 1.14E-08 | NO | NO | NO | NO |
| AT3G17820 | 43.96 | 0.43 | 64.82 | 1.68 | 0.56 | 3.66E-03 | NO | NO | NO | NO |
| AT3G18280 | 46.02 | 1.13 | 104.69 | 2.34 | 1.19 | 1.21E-09 | NEGATIVE | NO | NO | NO |
| AT3G18773 | 0.39 | 0.05 | 1.24 | 0.03 | 1.66 | 4.24E-02 | NO | NO | NO | NO |
| AT3G18930 | 3.10 | 0.05 | 6.23 | 0.17 | 1.01 | 5.63E-04 | NO | NO | NO | NO |
| AT3G19010 | 63.75 | 2.07 | 169.09 | 1.70 | 1.41 | 0.00E+00 | NO | NO | NO | NO |
| AT3G19260 | 5.64 | 0.14 | 20.03 | 0.15 | 1.83 | 1.92E-14 | NO | NO | NO | NO |
| AT3G19870 | 8.64 | 0.02 | 12.89 | 0.35 | 0.58 | 4.61E-03 | NO | NO | NO | NO |
| AT3G19970 | 4.11 | 0.20 | 9.01 | 0.01 | 1.13 | 2.77E-05 | NO | NO | NO | NO |
| AT3G20250 | 14.39 | 0.39 | 24.04 | 0.25 | 0.74 | 5.45E-05 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G20280 | 0.88 | 0.02 | 3.37 | 0.06 | 1.93 | 7.54E-08 | NO | YES | NO | NO |
| AT3G20600 | 7.82 | 0.93 | 20.46 | 0.54 | 1.39 | 9.92E-07 | NO | NO | NO | NO |
| AT3G20830 | 1.72 | 0.15 | 4.17 | 0.04 | 1.28 | 7.46E-03 | NO | NO | NO | NO |
| AT3G21080 | 0.83 | 0.03 | 6.53 | 0.13 | 2.98 | 1.61E-08 | NO | NO | NO | NO |
| AT3G21200 | 53.96 | 0.97 | 73.14 | 1.81 | 0.44 | 3.15E-02 | NEGATIVE | NO | NO | NO |
| AT3G21230 | 1.82 | 0.18 | 7.79 | 0.49 | 2.10 | 6.97E-11 | NO | NO | NO | NO |
| AT3G21520 | 0.31 | 0.14 | 5.02 | 0.56 | 4.00 | 4.86E-07 | NO | NO | NO | NO |
| AT3G21560 | 73.70 | 0.41 | 106.05 | 0.28 | 0.52 | 5.21E-03 | NO | NO | NO | NO |
| AT3G21630 | 11.90 | 0.25 | 18.51 | 0.25 | 0.64 | 2.38E-03 | NO | NO | NO | NO |
| AT3G21780 | 2.70 | 0.48 | 9.07 | 0.26 | 1.75 | 6.53E-08 | NO | NO | NO | NO |
| AT3G21810 | 6.90 | 0.26 | 13.47 | 0.17 | 0.96 | 2.37E-05 | NO | YES | NO | NO |
| AT3G22060 | 18.17 | 2.02 | 87.21 | 3.19 | 2.26 | 0.00E+00 | NO | NO | NO | NO |
| AT3G22160 | 6.19 | 0.13 | 20.09 | 0.76 | 1.70 | 9.72E-11 | NO | NO | NO | NO |
| AT3G22170 | 16.38 | 0.07 | 23.31 | 0.38 | 0.51 | 7.79E-04 | NO | NO | NO | NO |
| AT3G22190 | 28.77 | 0.32 | 41.33 | 0.62 | 0.52 | 4.79E-04 | NO | NO | NO | NO |
| AT3G22400 | 1.01 | 0.08 | 6.33 | 0.09 | 2.65 | 0.00E+00 | NO | NO | NO | NO |
| AT3G22420 | 9.98 | 0.32 | 26.13 | 0.27 | 1.39 | 0.00E+00 | NO | NO | NO | NO |
| AT3G22460 | 0.99 | 0.14 | 2.66 | 0.17 | 1.43 | 2.46E-02 | NO | NO | NO | NO |
| AT3G22550 | 9.48 | 0.41 | 14.25 | 1.06 | 0.59 | 2.02E-02 | NEGATIVE | NO | NO | NO |
| AT3G22620 | 1.20 | 0.15 | 10.61 | 2.92 | 3.14 | 3.14E-10 | NO | NO | NO | NO |
| AT3G22890 | 222.31 | 0.52 | 362.29 | 1.47 | 0.70 | 4.46E-04 | NO | NO | NO | NO |
| AT3G23010 | 0.22 | 0.05 | 0.82 | 0.09 | 1.91 | 2.77E-02 | NO | NO | NO | NO |
| AT3G23030 | 42.97 | 0.75 | 73.77 | 1.58 | 0.78 | 3.57E-05 | NO | YES | NO | NO |
| AT3G23050 | 33.27 | 0.28 | 52.85 | 2.17 | 0.67 | 4.29E-05 | NEGATIVE | YES | NO | NO |
| AT3G23110 | 0.94 | 0.04 | 2.89 | 0.30 | 1.62 | 7.62E-05 | NO | NO | NO | NO |
| AT3G23250 | 0.38 | 0.27 | 2.93 | 0.30 | 2.94 | 1.89E-06 | NO | YES | NO | NO |
| AT3G23280 | 63.10 | 0.35 | 80.83 | 0.69 | 0.36 | 9.98E-03 | POSITIVE | NO | NO | NO |
| AT3G23530 | 4.24 | 0.11 | 6.43 | 0.10 | 0.60 | 1.62E-02 | NO | NO | NO | NO |
| AT3G23750 | 12.27 | 0.35 | 16.91 | 0.14 | 0.46 | 2.78E-02 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G24090 | 8.20 | 0.26 | 17.92 | 0.66 | 1.13 | 3.04E-08 | NO | NO | NO | NO |
| AT3G24180 | 23.41 | 0.08 | 32.38 | 0.20 | 0.47 | 4.26E-03 | NO | NO | NO | NO |
| AT3G24480 | 34.11 | 0.87 | 50.20 | 0.13 | 0.56 | 3.94E-03 | NO | NO | NO | NO |
| AT3G24503 | 71.74 | 0.41 | 149.00 | 5.00 | 1.05 | 5.55E-10 | NO | NO | NO | NO |
| AT3G24550 | 9.81 | 0.34 | 16.11 | 0.07 | 0.72 | 4.48E-04 | NO | NO | NO | NO |
| AT3G24560 | 4.57 | 0.28 | 8.69 | 0.14 | 0.93 | 5.76E-05 | NO | NO | NO | NO |
| AT3G25110 | 2.69 | 0.08 | 7.36 | 0.35 | 1.45 | 7.62E-06 | NO | NO | NO | NO |
| AT3G25180 | 0.56 | 0.37 | 2.61 | 0.61 | 2.22 | 5.80E-05 | NO | NO | NO | NO |
| AT3G25220 | 73.17 | 1.96 | 135.94 | 2.00 | 0.89 | 9.47E-07 | NO | NO | NO | NO |
| AT3G25600 | 7.95 | 0.60 | 27.62 | 0.74 | 1.80 | 2.23E-09 | NO | NO | NO | NO |
| AT3G25610 | 5.88 | 0.36 | 18.68 | 0.31 | 1.67 | 0.00E+00 | NO | NO | NO | NO |
| AT3G25780 | 4.32 | 0.59 | 21.18 | 0.33 | 2.29 | 5.41E-14 | NO | NO | NO | NO |
| AT3G25882 | 24.94 | 3.43 | 140.67 | 1.76 | 2.50 | 0.00E+00 | NO | NO | NO | NO |
| AT3G25890 | 20.41 | 0.53 | 28.58 | 0.30 | 0.49 | 1.22E-02 | NO | YES | NO | NO |
| AT3G26210 | 15.74 | 2.31 | 66.62 | 0.45 | 2.08 | 0.00E+00 | NO | NO | NO | NO |
| AT3G26220 | 5.11 | 0.62 | 13.47 | 0.48 | 1.40 | 2.01E-08 | NO | NO | NO | NO |
| AT3G26440 | 2.46 | 0.44 | 8.58 | 0.26 | 1.80 | 9.93E-11 | NO | NO | NO | NO |
| AT3G26500 | 3.56 | 0.61 | 17.18 | 1.28 | 2.27 | 0.00E+00 | NO | NO | NO | NO |
| AT3G26510 | 1.63 | 0.23 | 9.47 | 0.92 | 2.54 | 8.31E-12 | NO | NO | DOWN | NO |
| AT3G26910 | 2.48 | 0.20 | 5.73 | 0.43 | 1.21 | 2.29E-05 | NO | NO | NO | NO |
| AT3G27020 | 6.17 | 0.17 | 10.57 | 0.56 | 0.78 | 5.18E-04 | NO | NO | DOWN | NO |
| AT3G28340 | 2.59 | 0.29 | 9.31 | 0.78 | 1.85 | 3.06E-09 | NO | NO | NO | NO |
| AT3G28450 | 12.87 | 0.23 | 23.07 | 0.31 | 0.84 | 1.18E-05 | NO | NO | NO | NO |
| AT3G28500 | 1.81 | 0.27 | 11.02 | 4.80 | 2.61 | 1.49E-06 | NO | NO | NO | NO |
| AT3G28540 | 22.33 | 1.30 | 32.28 | 1.27 | 0.53 | 7.34E-03 | NO | NO | NO | NO |
| AT3G28580 | 1.74 | 0.61 | 27.19 | 1.50 | 3.97 | 0.00E+00 | NO | NO | NO | NO |
| AT3G28850 | 1.67 | 0.12 | 3.89 | 0.12 | 1.22 | 8.55E-03 | NO | NO | NO | NO |
| AT3G28890 | 1.26 | 0.44 | 3.06 | 0.43 | 1.28 | 6.52E-04 | NO | NO | NO | NO |
| AT3G28930 | 48.95 | 0.51 | 92.09 | 1.36 | 0.91 | 7.88E-07 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G29000 | 2.46 | 0.91 | 14.32 | 0.97 | 2.54 | 2.92E-07 | NO | NO | NO | NO |
| AT3G29034 | 6.96 | 0.91 | 21.81 | 0.99 | 1.65 | 1.49E-05 | NO | NO | NO | NO |
| AT3G29290 | 11.22 | 0.32 | 17.16 | 0.16 | 0.61 | 4.53E-03 | NO | NO | NO | NO |
| AT3G29400 | 8.67 | 0.46 | 12.73 | 0.34 | 0.55 | 1.77E-02 | NO | NO | NO | NO |
| AT3G44260 | 3.59 | 0.29 | 13.39 | 0.24 | 1.90 | 1.93E-08 | NO | NO | DOWN | NO |
| AT3G44320 | 1.45 | 0.13 | 7.13 | 1.39 | 2.30 | 1.17E-08 | NO | NO | NO | NO |
| AT3G44350 | 1.11 | 0.52 | 5.79 | 0.21 | 2.38 | 2.13E-04 | NO | YES | NO | NO |
| AT3G44400 | 7.81 | 0.20 | 14.19 | 0.34 | 0.86 | 2.89E-06 | NO | NO | NO | NO |
| AT3G44480 | 4.50 | 0.11 | 7.84 | 0.22 | 0.80 | 1.61E-04 | NO | NO | NO | NO |
| AT3G44720 | 12.30 | 0.57 | 28.97 | 0.20 | 1.24 | 1.15E-10 | NO | NO | NO | NO |
| AT3G45440 | 1.71 | 0.10 | 3.37 | 0.12 | 0.98 | 1.87E-02 | NO | NO | NO | NO |
| AT3G45620 | 48.94 | 0.69 | 64.58 | 1.58 | 0.40 | 4.82E-02 | POSITIVE | NO | NO | NO |
| AT3G45640 | 81.58 | 1.32 | 148.74 | 1.93 | 0.87 | 5.43E-07 | NO | NO | NO | NO |
| AT3G45730 | 1.90 | 0.19 | 15.46 | 1.04 | 3.03 | 3.43E-09 | NO | NO | NO | NO |
| AT3G45970 | 8.52 | 0.79 | 22.70 | 0.25 | 1.41 | 2.90E-08 | NO | NO | DOWN | NO |
| AT3G46080 | 1.46 | 0.56 | 43.03 | 1.10 | 4.88 | 0.00E+00 | NO | YES | NO | NO |
| AT3G46090 | 0.79 | 0.09 | 8.96 | 0.15 | 3.50 | 1.49E-07 | NO | YES | NO | NO |
| AT3G46110 | 4.62 | 0.41 | 9.59 | 0.39 | 1.05 | 4.82E-04 | NO | NO | NO | NO |
| AT3G46190 | 0.11 | 0.01 | 4.45 | 0.35 | 5.38 | 1.14E-06 | NO | NO | NO | NO |
| AT3G46510 | 28.10 | 0.32 | 45.40 | 0.32 | 0.69 | 1.10E-04 | NO | NO | NO | NO |
| AT3G46600 | 6.77 | 0.20 | 20.71 | 0.43 | 1.61 | 0.00E+00 | NO | YES | NO | NO |
| AT3G46620 | 29.52 | 0.18 | 47.10 | 0.84 | 0.67 | 3.97E-04 | NO | NO | NO | NO |
| AT3G46920 | 2.15 | 0.10 | 3.83 | 0.16 | 0.83 | 4.03E-03 | NO | NO | NO | NO |
| AT3G47090 | 1.44 | 0.18 | 5.25 | 0.45 | 1.86 | 4.41E-10 | NO | NO | NO | NO |
| AT3G47250 | 44.56 | 0.13 | 57.74 | 0.41 | 0.37 | 5.91E-03 | NEGATIVE | NO | NO | NO |
| AT3G47480 | 36.53 | 2.04 | 257.43 | 2.68 | 2.82 | 0.00E+00 | NO | NO | NO | NO |
| AT3G47590 | 23.80 | 0.34 | 34.67 | 0.96 | 0.54 | 1.06E-02 | NO | NO | NO | NO |
| AT3G47780 | 2.36 | 0.15 | 7.42 | 0.25 | 1.65 | 7.42E-11 | NO | NO | NO | NO |
| AT3G47800 | 56.55 | 0.11 | 121.47 | 1.05 | 1.10 | 6.15E-11 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G47820 | 7.28 | 0.50 | 15.19 | 0.22 | 1.06 | 2.82E-06 | NO | NO | NO | NO |
| AT3G48090 | 29.43 | 1.33 | 61.61 | 0.83 | 1.07 | 2.01E-11 | NO | NO | NO | NO |
| AT3G48100 | 5.82 | 0.20 | 10.52 | 0.51 | 0.85 | 3.88E-03 | NO | NO | UP | NO |
| AT3G48310 | 11.26 | 0.13 | 24.78 | 0.15 | 1.14 | 7.33E-09 | NO | NO | NO | NO |
| AT3G48320 | 21.30 | 0.05 | 36.37 | 0.86 | 0.77 | 4.80E-05 | NO | NO | NO | NO |
| AT3G48360 | 0.71 | 0.15 | 1.82 | 0.21 | 1.36 | 4.12E-02 | NO | NO | NO | NO |
| AT3G49060 | 6.09 | 0.11 | 9.46 | 0.20 | 0.64 | 4.77E-03 | NO | NO | NO | NO |
| AT3G49120 | 220.37 | 6.97 | 441.30 | 8.66 | 1.00 | 3.12E-07 | NO | NO | NO | NO |
| AT3G49210 | 2.25 | 0.31 | 8.29 | 0.19 | 1.88 | 1.61E-09 | NO | NO | NO | NO |
| AT3G49350 | 7.77 | 0.29 | 13.02 | 0.35 | 0.74 | 8.31E-04 | NO | NO | NO | NO |
| AT3G49530 | 11.31 | 0.17 | 30.26 | 0.88 | 1.42 | 1.04E-13 | NO | YES | NO | NO |
| AT3G49800 | 24.10 | 0.20 | 41.05 | 0.62 | 0.77 | 3.26E-05 | NO | NO | NO | NO |
| AT3G49970 | 1.42 | 0.25 | 3.79 | 0.41 | 1.41 | 1.79E-03 | NO | NO | NO | NO |
| AT3G50340 | 2.90 | 0.23 | 5.57 | 0.07 | 0.94 | 1.09E-02 | NO | NO | NO | NO |
| AT3G50880 | 3.62 | 0.21 | 9.75 | 0.28 | 1.43 | 6.00E-05 | NO | NO | DOWN | NO |
| AT3G50910 | 14.65 | 0.45 | 23.50 | 0.24 | 0.68 | 6.84E-04 | NO | NO | NO | NO |
| AT3G50930 | 2.83 | 0.86 | 31.13 | 0.51 | 3.46 | 0.00E+00 | NO | NO | NO | NO |
| AT3G50950 | 28.96 | 1.32 | 63.52 | 0.51 | 1.13 | 0.00E+00 | NO | NO | NO | NO |
| AT3G51000 | 35.15 | 0.44 | 48.79 | 0.48 | 0.47 | 2.18E-02 | POSITIVE | NO | NO | NO |
| AT3G51130 | 18.64 | 0.49 | 27.82 | 0.45 | 0.58 | 5.71E-03 | NO | NO | NO | NO |
| AT3G51250 | 23.60 | 0.24 | 32.83 | 0.60 | 0.48 | 2.19E-02 | NO | NO | NO | NO |
| AT3G51330 | 4.80 | 0.56 | 23.84 | 0.33 | 2.31 | 0.00E+00 | NO | NO | NO | NO |
| AT3G51370 | 65.38 | 0.89 | 95.13 | 0.34 | 0.54 | 3.14E-03 | NO | NO | NO | NO |
| AT3G51440 | 3.76 | 0.25 | 15.37 | 0.25 | 2.03 | 6.28E-12 | NO | NO | NO | NO |
| AT3G51450 | 15.39 | 1.50 | 31.51 | 0.84 | 1.03 | 4.42E-07 | NO | NO | NO | NO |
| AT3G51550 | 39.41 | 0.45 | 54.75 | 0.40 | 0.47 | 1.62E-02 | NO | NO | NO | NO |
| AT3G51630 | 28.76 | 0.29 | 36.08 | 0.10 | 0.33 | 3.73E-02 | NO | NO | NO | NO |
| AT3G51670 | 19.49 | 0.28 | 38.29 | 1.33 | 0.97 | 1.10E-07 | NO | NO | NO | NO |
| AT3G51770 | 6.97 | 0.08 | 9.32 | 0.31 | 0.42 | 3.74E-02 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G51895 | 10.62 | 0.27 | 17.80 | 1.28 | 0.74 | 1.79E-04 | NO | NO | NO | NO |
| AT3G51980 | 18.92 | 0.75 | 50.39 | 1.92 | 1.41 | 0.00E+00 | NO | NO | NO | NO |
| AT3G52430 | 18.12 | 1.11 | 66.65 | 0.86 | 1.88 | 0.00E+00 | NO | NO | NO | NO |
| AT3G52605 | 1.28 | 0.08 | 6.70 | 0.07 | 2.39 | 1.49E-07 | NO | NO | NO | NO |
| AT3G52800 | 41.14 | 0.60 | 64.53 | 0.39 | 0.65 | 5.85E-04 | NO | NO | NO | NO |
| AT3G52930 | 188.21 | 3.03 | 378.52 | 6.01 | 1.01 | 2.66E-07 | NO | NO | NO | NO |
| AT3G53180 | 6.18 | 0.26 | 10.92 | 0.62 | 0.82 | 1.25E-04 | NO | NO | NO | NO |
| AT3G53190 | 12.57 | 0.46 | 17.87 | 1.37 | 0.51 | 2.65E-02 | NO | NO | NO | NO |
| AT3G53230 | 11.96 | 0.45 | 17.55 | 0.36 | 0.55 | 6.48E-03 | NO | NO | NO | NO |
| AT3G53280 | 5.88 | 0.21 | 9.25 | 0.41 | 0.65 | 2.20E-02 | NO | NO | NO | NO |
| AT3G53670 | 70.78 | 0.71 | 96.08 | 0.80 | 0.44 | 2.80E-02 | NO | NO | NO | NO |
| AT3G53710 | 17.65 | 0.50 | 24.25 | 0.41 | 0.46 | 8.88E-03 | NO | NO | NO | NO |
| AT3G54100 | 4.44 | 0.02 | 7.92 | 0.35 | 0.83 | 1.17E-03 | NO | NO | NO | NO |
| AT3G54150 | 3.82 | 0.91 | 13.41 | 1.05 | 1.81 | 5.88E-09 | NO | NO | NO | NO |
| AT3G54250 | 9.40 | 0.10 | 13.62 | 0.77 | 0.54 | 4.36E-02 | NO | NO | NO | NO |
| AT3G54300 | 37.42 | 0.24 | 57.84 | 0.85 | 0.63 | 2.81E-04 | NO | NO | NO | NO |
| AT3G54420 | 2.93 | 0.41 | 14.95 | 0.55 | 2.35 | 7.81E-10 | NO | NO | NO | NO |
| AT3G54640 | 51.83 | 0.86 | 86.62 | 0.31 | 0.74 | 2.88E-05 | NO | NO | NO | NO |
| AT3G54810 | 19.70 | 0.53 | 29.03 | 0.61 | 0.56 | 5.22E-03 | NO | YES | NO | NO |
| AT3G54960 | 25.00 | 0.24 | 67.19 | 1.13 | 1.43 | 0.00E+00 | NO | NO | NO | NO |
| AT3G55130 | 26.98 | 0.45 | 39.42 | 1.22 | 0.55 | 4.92E-03 | NO | NO | NO | NO |
| AT3G55430 | 13.48 | 0.71 | 21.61 | 0.57 | 0.68 | 9.38E-04 | NO | NO | NO | NO |
| AT3G55560 | 3.93 | 0.21 | 7.24 | 0.10 | 0.88 | 6.31E-03 | NO | NO | NO | NO |
| AT3G55840 | 0.57 | 0.14 | 4.49 | 0.24 | 2.97 | 2.90E-10 | NO | NO | NO | NO |
| AT3G55890 | 1.62 | 0.27 | 5.70 | 0.88 | 1.81 | 7.45E-03 | NO | NO | NO | NO |
| AT3G55950 | 2.15 | 0.21 | 5.43 | 0.40 | 1.34 | 2.83E-06 | NO | NO | NO | NO |
| AT3G55960 | 23.51 | 0.25 | 34.53 | 0.79 | 0.55 | 7.62E-03 | NO | NO | NO | NO |
| AT3G55980 | 9.43 | 0.58 | 29.22 | 0.80 | 1.63 | 0.00E+00 | NO | YES | DOWN | NO |
| AT3G56050 | 37.78 | 0.36 | 51.60 | 0.19 | 0.45 | 1.77E-03 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G56060 | 3.07 | 0.10 | 5.10 | 0.32 | 0.73 | 3.35E-02 | NO | NO | NO | DOWN |
| AT3G56170 | 15.84 | 0.14 | 34.15 | 0.48 | 1.11 | 5.92E-09 | NO | NO | NO | NO |
| AT3G56190 | 39.81 | 0.04 | 52.32 | 0.84 | 0.39 | 9.06E-03 | NO | NO | NO | NO |
| AT3G56200 | 11.08 | 0.47 | 36.20 | 0.88 | 1.71 | 0.00E+00 | NO | NO | NO | NO |
| AT3G56410 | 4.90 | 0.22 | 8.90 | 0.56 | 0.86 | 5.35E-08 | NO | NO | NO | NO |
| AT3G56590 | 18.37 | 0.18 | 25.89 | 0.33 | 0.49 | 1.98E-03 | NO | NO | NO | NO |
| AT3G56710 | 107.71 | 5.21 | 201.16 | 1.55 | 0.90 | 9.86E-08 | NO | NO | NO | NO |
| AT3G56880 | 33.82 | 0.24 | 57.32 | 0.90 | 0.76 | 8.68E-05 | NO | NO | NO | NO |
| AT3G56891 | 0.45 | 0.11 | 6.02 | 0.37 | 3.76 | 2.61E-05 | NO | NO | NO | NO |
| AT3G57300 | 6.90 | 0.36 | 9.93 | 0.22 | 0.53 | 9.58E-03 | NO | NO | NO | NO |
| AT3G57330 | 14.69 | 0.87 | 35.97 | 0.64 | 1.29 | 3.64E-14 | NO | NO | NO | NO |
| AT3G57450 | 9.23 | 0.20 | 19.55 | 0.74 | 1.08 | 1.06E-03 | NO | NO | NO | NO |
| AT3G57530 | 16.58 | 0.06 | 27.41 | 0.50 | 0.73 | 1.20E-04 | NO | NO | NO | NO |
| AT3G57550 | 22.63 | 0.27 | 44.64 | 0.56 | 0.98 | 7.68E-09 | NO | NO | NO | NO |
| AT3G57630 | 11.29 | 0.52 | 17.43 | 0.29 | 0.63 | 1.32E-04 | NO | NO | NO | NO |
| AT3G57880 | 9.03 | 0.26 | 13.39 | 0.13 | 0.57 | 6.67E-03 | NO | NO | NO | NO |
| AT3G58110 | 21.79 | 0.47 | 29.36 | 0.11 | 0.43 | 3.15E-02 | NO | NO | NO | NO |
| AT3G58640 | 16.97 | 0.05 | 23.73 | 0.30 | 0.48 | 1.03E-03 | NO | NO | NO | NO |
| AT3G58840 | 19.01 | 0.56 | 25.79 | 0.09 | 0.44 | 4.29E-02 | NO | NO | NO | NO |
| AT3G59080 | 2.24 | 0.17 | 6.16 | 0.15 | 1.46 | 1.84E-06 | NO | NO | NO | NO |
| AT3G59570 | 3.25 | 0.08 | 7.15 | 0.18 | 1.14 | 7.32E-06 | NO | NO | NO | NO |
| AT3G59660 | 7.97 | 0.42 | 18.72 | 0.31 | 1.23 | 6.55E-10 | NO | NO | NO | NO |
| AT3G59700 | 1.61 | 0.07 | 3.61 | 0.13 | 1.16 | 2.76E-03 | NO | NO | NO | NO |
| AT3G60260 | 10.80 | 0.41 | 18.88 | 0.76 | 0.81 | 1.06E-04 | NO | NO | NO | NO |
| AT3G60420 | 68.26 | 2.09 | 254.55 | 6.20 | 1.90 | 0.00E+00 | NO | NO | NO | NO |
| AT3G60520 | 123.54 | 0.31 | 185.59 | 2.33 | 0.59 | 1.40E-03 | NO | NO | NO | UP |
| AT3G60600 | 39.89 | 0.52 | 55.89 | 0.72 | 0.49 | 9.07E-03 | NO | NO | NO | NO |
| AT3G60690 | 10.04 | 0.12 | 21.01 | 0.54 | 1.07 | 1.73E-04 | NO | NO | NO | NO |
| AT3G60860 | 11.46 | 0.14 | 15.87 | 0.47 | 0.47 | 1.79E-02 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G61198 | 0.15 | 0.05 | 1.85 | 0.35 | 3.67 | 9.00E-03 | NO | NO | NO | NO |
| AT3G61220 | 24.56 | 0.50 | 54.68 | 0.95 | 1.15 | 9.56E-12 | NO | NO | NO | NO |
| AT3G61240 | 36.09 | 0.54 | 46.17 | 0.48 | 0.36 | 1.40E-02 | NO | NO | NO | NO |
| AT3G61670 | 5.34 | 0.10 | 8.43 | 0.08 | 0.66 | 4.82E-03 | NO | NO | NO | NO |
| AT3G62260 | 3.96 | 0.14 | 10.31 | 0.26 | 1.38 | 1.17E-07 | NO | NO | NO | NO |
| AT3G62422 | 26.13 | 0.54 | 44.30 | 0.29 | 0.76 | 1.06E-04 | NO | NO | NO | NO |
| AT3G62600 | 46.82 | 0.75 | 146.51 | 2.68 | 1.65 | 0.00E+00 | NO | NO | NO | NO |
| AT3G62720 | 5.38 | 0.17 | 8.43 | 0.39 | 0.65 | 1.67E-02 | NO | NO | NO | NO |
| AT3G62860 | 0.90 | 0.04 | 3.03 | 0.09 | 1.75 | 2.03E-03 | NO | NO | NO | NO |
| AT3G63500 | 19.36 | 0.28 | 28.40 | 0.92 | 0.55 | 1.11E-03 | NO | NO | NO | NO |
| AT4G00050 | 15.25 | 0.13 | 23.20 | 0.46 | 0.61 | 6.08E-03 | NO | YES | NO | NO |
| AT4G00750 | 6.53 | 0.24 | 11.37 | 0.56 | 0.80 | 5.43E-04 | NO | NO | NO | NO |
| AT4G00755 | 11.10 | 0.17 | 15.45 | 0.34 | 0.48 | 4.33E-02 | NO | NO | NO | NO |
| AT4G01010 | 3.63 | 0.32 | 10.72 | 0.56 | 1.56 | 4.69E-10 | NO | NO | NO | NO |
| AT4G01320 | 61.84 | 0.98 | 85.85 | 0.68 | 0.47 | 1.60E-02 | NO | NO | NO | NO |
| AT4G01700 | 6.86 | 0.80 | 17.14 | 0.51 | 1.32 | 4.97E-06 | NO | NO | NO | NO |
| AT4G01750 | 4.18 | 0.08 | 11.16 | 0.44 | 1.42 | 4.34E-07 | NO | NO | NO | NO |
| AT4G01950 | 5.98 | 0.44 | 9.75 | 1.14 | 0.71 | 7.44E-03 | NO | NO | NO | NO |
| AT4G02330 | 5.86 | 0.47 | 21.58 | 1.10 | 1.88 | 0.00E+00 | NO | NO | UP | NO |
| AT4G02380 | 311.32 | 23.01 | 975.61 | 23.70 | 1.65 | 0.00E+00 | NO | NO | UP | NO |
| AT4G02520 | 537.35 | 15.15 | 1742.96 | 9.96 | 1.70 | 0.00E+00 | NO | NO | NO | NO |
| AT4G03080 | 15.06 | 0.23 | 24.62 | 0.28 | 0.71 | 1.10E-04 | NO | NO | NO | NO |
| AT4G03110 | 10.74 | 0.38 | 17.16 | 0.02 | 0.68 | 1.23E-03 | NO | NO | NO | NO |
| AT4G03190 | 5.06 | 0.09 | 8.15 | 0.29 | 0.69 | 1.08E-02 | NO | NO | NO | NO |
| AT4G03390 | 6.37 | 0.07 | 13.63 | 0.23 | 1.10 | 9.18E-09 | NO | NO | NO | NO |
| AT4G03400 | 39.83 | 0.31 | 74.63 | 0.77 | 0.91 | 1.79E-07 | NO | NO | UP | NO |
| AT4G03550 | 12.50 | 0.35 | 17.49 | 0.46 | 0.49 | 1.26E-02 | NO | NO | NO | NO |
| AT4G03820 | 3.78 | 0.25 | 9.31 | 0.26 | 1.30 | 1.99E-06 | NO | NO | NO | NO |
| AT4G04220 | 3.05 | 0.13 | 6.56 | 0.24 | 1.10 | 4.57E-05 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT4G04500 | 1.07 | 0.25 | 4.79 | 0.43 | 2.16 | 3.77E-08 | NO | NO | NO | NO |
| AT4G04540 | 0.88 | 0.35 | 9.25 | 0.37 | 3.39 | 0.00E+00 | NO | NO | NO | NO |
| AT4G04570 | 20.78 | 0.52 | 41.11 | 0.59 | 0.98 | 2.08E-09 | NO | NO | NO | NO |
| AT4G04610 | 53.48 | 0.91 | 83.24 | 2.23 | 0.64 | 5.21E-04 | NO | NO | NO | NO |
| AT4G04870 | 9.22 | 0.45 | 14.42 | 0.54 | 0.65 | 1.28E-02 | NO | NO | NO | NO |
| AT4G04880 | 5.81 | 0.11 | 9.88 | 0.20 | 0.77 | 1.32E-02 | NO | NO | NO | NO |
| AT4G04960 | 4.55 | 0.10 | 8.74 | 0.17 | 0.94 | 1.24E-04 | NO | NO | NO | NO |
| AT4G05020 | 29.12 | 0.44 | 50.99 | 1.31 | 0.81 | 2.45E-06 | POSITIVE | NO | UP | NO |
| AT4G05390 | 7.45 | 0.23 | 12.24 | 0.48 | 0.72 | 6.03E-03 | NO | NO | NO | NO |
| AT4G08180 | 7.21 | 0.00 | 9.99 | 0.01 | 0.47 | 2.04E-02 | NO | NO | NO | NO |
| AT4G08480 | 5.71 | 0.26 | 8.11 | 0.11 | 0.50 | 4.44E-02 | NO | NO | NO | NO |
| AT4G08555 | 2.46 | 0.22 | 18.58 | 1.60 | 2.92 | 3.96E-06 | NO | NO | NO | NO |
| AT4G08850 | 25.71 | 0.34 | 71.63 | 1.69 | 1.48 | 0.00E+00 | NO | NO | NO | NO |
| AT4G08870 | 120.96 | 1.75 | 167.30 | 5.08 | 0.47 | 9.11E-03 | NO | NO | NO | NO |
| AT4G08950 | 4.34 | 0.10 | 12.59 | 0.55 | 1.54 | 2.71E-07 | NO | NO | NO | NO |
| AT4G09030 | 9.13 | 0.67 | 27.77 | 0.48 | 1.60 | 1.28E-06 | NO | NO | NO | NO |
| AT4G09670 | 40.62 | 0.51 | 65.48 | 0.55 | 0.69 | 1.45E-04 | NO | NO | NO | NO |
| AT4G09770 | 0.27 | 0.15 | 1.93 | 0.13 | 2.82 | 1.14E-04 | NO | NO | NO | NO |
| AT4G10270 | 1.53 | 0.27 | 6.20 | 0.49 | 2.02 | 9.53E-03 | NO | NO | NO | NO |
| AT4G11280 | 9.28 | 0.99 | 29.42 | 0.50 | 1.67 | 0.00E+00 | NO | NO | UP | NO |
| AT4G11290 | 0.63 | 0.17 | 3.08 | 0.26 | 2.29 | 2.31E-04 | NO | NO | NO | NO |
| AT4G11300 | 4.43 | 0.54 | 9.92 | 0.20 | 1.16 | 1.05E-04 | NO | NO | NO | NO |
| AT4G11350 | 2.71 | 0.16 | 7.59 | 0.31 | 1.48 | 1.00E-06 | NO | NO | NO | NO |
| AT4G11360 | 16.91 | 0.31 | 32.72 | 0.47 | 0.95 | 1.33E-04 | NO | NO | NO | NO |
| AT4G11370 | 2.79 | 0.68 | 9.37 | 1.00 | 1.75 | 3.51E-04 | NO | NO | NO | NO |
| AT4G11530 | 0.80 | 0.10 | 3.10 | 0.17 | 1.95 | 2.17E-05 | NO | NO | NO | NO |
| AT4G11800 | 5.03 | 0.15 | 8.90 | 0.55 | 0.82 | 1.20E-04 | NO | NO | NO | NO |
| AT4G11820 | 21.47 | 0.20 | 32.03 | 0.28 | 0.58 | 3.10E-03 | NO | NO | NO | NO |
| AT4G11850 | 8.66 | 0.30 | 20.28 | 0.33 | 1.23 | 1.00E-11 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT4G11890 | 11.80 | 2.10 | 106.43 | 2.84 | 3.17 | 0.00E+00 | NO | NO | NO | NO |
| AT4G12010 | 4.93 | 0.15 | 9.85 | 0.52 | 1.00 | 1.03E-06 | NO | NO | NO | NO |
| AT4G12120 | 7.43 | 0.16 | 21.02 | 0.46 | 1.50 | 0.00E+00 | NO | NO | NO | NO |
| AT4G12490 | 31.26 | 6.22 | 61.22 | 0.62 | 0.97 | 1.97E-05 | NO | NO | UP | NO |
| AT4G12500 | 14.79 | 5.04 | 63.43 | 3.93 | 2.10 | 0.00E+00 | NO | NO | UP | NO |
| AT4G12720 | 26.23 | 1.12 | 76.56 | 2.34 | 1.55 | 0.00E+00 | NO | NO | NO | NO |
| AT4G12730 | 17.01 | 0.41 | 28.94 | 1.38 | 0.77 | 1.01E-04 | NEGATIVE | NO | NO | DOWN |
| AT4G12770 | 4.87 | 0.15 | 6.75 | 0.19 | 0.47 | 4.55E-02 | NO | NO | NO | NO |
| AT4G13180 | 15.84 | 0.51 | 30.30 | 0.75 | 0.94 | 2.51E-05 | NO | NO | NO | NO |
| AT4G13340 | 6.83 | 0.50 | 23.79 | 0.50 | 1.80 | 0.00E+00 | NO | NO | NO | NO |
| AT4G13510 | 24.86 | 1.24 | 72.10 | 0.37 | 1.54 | 0.00E+00 | NO | NO | NO | NO |
| AT4G13530 | 28.16 | 0.26 | 41.52 | 0.85 | 0.56 | 1.76E-03 | NO | NO | NO | NO |
| AT4G13540 | 1.12 | 0.04 | 4.57 | 0.73 | 2.04 | 1.14E-03 | NO | NO | NO | NO |
| AT4G14365 | 9.19 | 1.74 | 110.64 | 2.11 | 3.59 | 0.00E+00 | NO | NO | NO | NO |
| AT4G14500 | 23.95 | 0.25 | 33.56 | 1.06 | 0.49 | 1.75E-02 | NO | NO | NO | NO |
| AT4G14550 | 2.08 | 0.06 | 4.81 | 0.43 | 1.21 | 3.32E-03 | NO | YES | NO | NO |
| AT4G15440 | 3.11 | 0.57 | 14.68 | 0.36 | 2.24 | 0.00E+00 | NEGATIVE | NO | NO | NO |
| AT4G15620 | 6.50 | 0.05 | 14.32 | 1.17 | 1.14 | 1.07E-03 | NO | NO | NO | NO |
| AT4G15680 | 3.62 | 0.25 | 8.93 | 0.58 | 1.30 | 1.13E-02 | NO | NO | NO | NO |
| AT4G15920 | 4.43 | 0.41 | 9.63 | 0.60 | 1.12 | 2.26E-03 | NO | NO | DOWN | NO |
| AT4G16660 | 49.20 | 0.23 | 128.57 | 1.81 | 1.39 | 0.00E+00 | NO | NO | NO | NO |
| AT4G16780 | 3.33 | 0.21 | 9.86 | 0.49 | 1.56 | 5.84E-06 | NO | YES | NO | NO |
| AT4G16790 | 3.66 | 0.28 | 7.67 | 0.25 | 1.07 | 4.45E-04 | POSITIVE | NO | NO | NO |
| AT4G16990 | 83.84 | 1.22 | 121.59 | 1.58 | 0.54 | 3.45E-05 | NO | NO | NO | NO |
| AT4G17070 | 12.04 | 0.52 | 24.63 | 0.65 | 1.03 | 1.28E-06 | NO | NO | NO | NO |
| AT4G17230 | 17.69 | 0.69 | 29.15 | 0.63 | 0.72 | 1.59E-04 | NO | YES | NO | NO |
| AT4G17245 | 9.88 | 0.51 | 20.65 | 0.97 | 1.06 | 1.92E-03 | NO | NO | NO | NO |
| AT4G17250 | 3.94 | 0.33 | 6.39 | 0.57 | 0.70 | 1.17E-02 | NO | NO | NO | NO |
| AT4G17330 | 13.24 | 0.30 | 25.52 | 0.27 | 0.95 | 2.89E-08 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT4G17420 | 11.41 | 0.32 | 19.50 | 0.21 | 0.77 | 4.81E-04 | NO | NO | NO | NO |
| AT4G17490 | 0.67 | 0.13 | 2.31 | 0.42 | 1.80 | 1.30E-02 | NO | YES | DOWN | NO |
| AT4G17500 | 5.11 | 0.32 | 24.78 | 0.34 | 2.28 | 0.00E+00 | NO | YES | NO | NO |
| AT4G17870 | 8.67 | 0.35 | 14.74 | 0.45 | 0.77 | 2.23E-02 | NO | NO | DOWN | NO |
| AT4G18280 | 25.30 | 1.07 | 45.12 | 1.78 | 0.83 | 2.25E-04 | NO | NO | UP | UP |
| AT4G18430 | 0.95 | 0.27 | 4.87 | 0.32 | 2.35 | 1.07E-04 | NO | NO | NO | NO |
| AT4G18630 | 8.69 | 0.31 | 12.96 | 0.40 | 0.58 | 2.07E-02 | NO | NO | NO | NO |
| AT4G18760 | 4.08 | 0.20 | 7.92 | 0.23 | 0.96 | 5.55E-03 | NO | NO | NO | NO |
| AT4G18880 | 22.63 | 0.83 | 36.35 | 0.50 | 0.68 | 2.65E-04 | NO | YES | NO | NO |
| AT4G18950 | 11.91 | 0.25 | 18.81 | 0.37 | 0.66 | 1.64E-03 | NO | NO | NO | NO |
| AT4G19170 | 77.25 | 1.37 | 119.25 | 1.83 | 0.63 | 6.74E-04 | NO | NO | NO | NO |
| AT4G19180 | 5.69 | 0.16 | 8.50 | 0.14 | 0.58 | 1.71E-02 | NO | NO | NO | NO |
| AT4G19530 | 4.74 | 0.42 | 7.36 | 0.51 | 0.64 | 4.76E-03 | NO | NO | DOWN | NO |
| AT4G19660 | 6.44 | 0.37 | 14.11 | 0.41 | 1.13 | 1.62E-06 | NO | NO | NO | NO |
| AT4G19860 | 22.14 | 0.24 | 30.13 | 0.23 | 0.44 | 3.44E-02 | NO | NO | NO | NO |
| AT4G19880 | 33.11 | 0.15 | 42.31 | 0.40 | 0.35 | 4.13E-02 | NO | NO | NO | NO |
| AT4G20000 | 0.33 | 0.06 | 3.66 | 0.37 | 3.49 | 2.33E-05 | NO | NO | NO | NO |
| AT4G20070 | 26.44 | 0.56 | 36.50 | 0.44 | 0.47 | 2.12E-02 | NO | NO | NO | NO |
| AT4G20110 | 5.29 | 0.45 | 17.43 | 0.23 | 1.72 | 0.00E+00 | NO | NO | NO | NO |
| AT4G20320 | 1.59 | 0.09 | 4.39 | 0.30 | 1.47 | 5.64E-06 | NO | NO | NO | NO |
| AT4G20830 | 32.08 | 1.70 | 101.59 | 2.34 | 1.66 | 0.00E+00 | NO | NO | NO | NO |
| AT4G20860 | 7.87 | 0.70 | 21.89 | 0.48 | 1.48 | 2.80E-13 | NO | NO | NO | NO |
| AT4G21380 | 4.14 | 0.59 | 11.48 | 0.19 | 1.47 | 5.86E-12 | POSITIVE | NO | NO | NO |
| AT4G21400 | 0.32 | 0.04 | 5.55 | 0.48 | 4.09 | 0.00E+00 | NO | NO | NO | NO |
| AT4G21850 | 1.40 | 0.32 | 33.36 | 1.99 | 4.58 | 0.00E+00 | NO | NO | DOWN | NO |
| AT4G22305 | 5.53 | 0.48 | 12.90 | 0.08 | 1.22 | 1.01E-04 | NO | NO | NO | NO |
| AT4G22530 | 3.01 | 0.46 | 10.20 | 0.64 | 1.76 | 1.03E-06 | NO | NO | NO | NO |
| AT4G22590 | 8.10 | 0.07 | 19.09 | 0.74 | 1.24 | 3.00E-09 | NO | NO | NO | NO |
| AT4G22980 | 2.82 | 0.43 | 5.25 | 0.22 | 0.90 | 1.30E-02 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT4G23010 | 42.31 | 0.73 | 61.05 | 0.43 | 0.53 | 3.53E-03 | NO | NO | NO | NO |
| AT4G23030 | 0.53 | 0.19 | 3.42 | 0.25 | 2.68 | 2.68E-06 | NO | NO | NO | NO |
| AT4G23130 | 5.00 | 0.41 | 9.50 | 0.43 | 0.93 | 9.06E-05 | NO | NO | NO | NO |
| AT4G23170 | 49.13 | 1.57 | 118.34 | 0.68 | 1.27 | 3.63E-14 | NO | NO | NO | NO |
| AT4G23180 | 15.42 | 0.24 | 25.48 | 0.95 | 0.72 | 1.97E-04 | NO | NO | DOWN | NO |
| AT4G23190 | 2.37 | 0.35 | 15.89 | 1.09 | 2.74 | 0.00E+00 | NO | NO | NO | NO |
| AT4G23270 | 9.79 | 0.50 | 16.98 | 1.08 | 0.79 | 1.68E-04 | NO | NO | NO | NO |
| AT4G23310 | 0.46 | 0.11 | 4.90 | 0.49 | 3.40 | 3.69E-14 | NO | NO | NO | NO |
| AT4G23320 | 0.73 | 0.21 | 4.00 | 0.22 | 2.45 | 7.51E-06 | NO | NO | NO | NO |
| AT4G23470 | 53.84 | 0.52 | 119.98 | 1.03 | 1.16 | 1.69E-13 | NO | NO | NO | NO |
| AT4G23610 | 2.38 | 0.56 | 12.04 | 0.36 | 2.34 | 6.64E-08 | NO | NO | NO | NO |
| AT4G23730 | 16.44 | 0.16 | 22.95 | 0.87 | 0.48 | 2.84E-02 | NO | NO | NO | NO |
| AT4G23800 | 25.58 | 0.58 | 34.60 | 1.44 | 0.44 | 4.02E-02 | NO | YES | NO | NO |
| AT4G23850 | 77.95 | 0.32 | 134.24 | 0.60 | 0.78 | 1.52E-05 | NO | NO | NO | NO |
| AT4G24020 | 15.56 | 0.38 | 21.62 | 0.33 | 0.47 | 1.90E-02 | NO | YES | NO | NO |
| AT4G24040 | 2.89 | 0.16 | 7.65 | 0.33 | 1.40 | 4.00E-07 | NO | NO | NO | NO |
| AT4G24230 | 5.24 | 0.17 | 15.00 | 0.11 | 1.52 | 2.73E-11 | NO | NO | NO | NO |
| AT4G24690 | 134.45 | 1.04 | 225.21 | 1.97 | 0.74 | 2.38E-04 | POSITIVE | NO | NO | NO |
| AT4G24920 | 54.44 | 0.82 | 104.87 | 0.58 | 0.95 | 3.47E-06 | NO | NO | NO | NO |
| AT4G24970 | 1.34 | 0.14 | 3.77 | 0.30 | 1.50 | 7.39E-05 | NO | NO | NO | NO |
| AT4G25070 | 2.15 | 0.52 | 9.13 | 0.40 | 2.09 | 0.00E+00 | NO | NO | NO | NO |
| AT4G25230 | 11.81 | 0.16 | 17.99 | 0.23 | 0.61 | 2.60E-03 | NO | NO | NO | NO |
| AT4G25290 | 12.98 | 0.24 | 20.89 | 0.17 | 0.69 | 4.81E-04 | NO | NO | NO | NO |
| AT4G25620 | 6.25 | 0.31 | 16.05 | 0.06 | 1.36 | 1.45E-10 | NO | NO | NO | NO |
| AT4G25810 | 0.58 | 0.40 | 7.93 | 0.22 | 3.78 | 3.93E-10 | NO | NO | NO | NO |
| AT4G25880 | 13.50 | 0.10 | 20.83 | 0.20 | 0.62 | 7.99E-06 | NO | NO | NO | NO |
| AT4G25900 | 39.54 | 0.63 | 75.24 | 1.08 | 0.93 | 8.51E-08 | NO | NO | NO | NO |
| AT4G26090 | 2.60 | 0.40 | 4.62 | 0.37 | 0.83 | 1.67E-03 | NO | NO | NO | NO |
| AT4G26120 | 3.37 | 0.29 | 6.75 | 0.36 | 1.00 | 1.29E-03 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT4G26190 | 7.52 | 0.21 | 11.87 | 0.08 | 0.66 | 1.11E-03 | NO | NO | NO | NO |
| AT4G26400 | 21.94 | 0.51 | 29.62 | 0.25 | 0.43 | 1.86E-02 | NO | NO | NO | NO |
| AT4G26470 | 0.96 | 0.33 | 5.40 | 0.20 | 2.49 | 5.19E-06 | NO | NO | NO | NO |
| AT4G26630 | 49.19 | 0.61 | 65.77 | 0.01 | 0.42 | 1.44E-03 | NO | NO | NO | NO |
| AT4G26690 | 12.53 | 0.38 | 21.37 | 0.08 | 0.77 | 3.61E-05 | NO | NO | NO | NO |
| AT4G26910 | 27.91 | 0.36 | 43.80 | 0.25 | 0.65 | 1.71E-06 | NO | NO | NO | NO |
| AT4G26970 | 34.88 | 0.31 | 60.60 | 0.21 | 0.80 | 6.01E-06 | NO | NO | NO | NO |
| AT4G27020 | 4.01 | 0.27 | 9.84 | 0.26 | 1.29 | 9.92E-07 | NO | NO | NO | NO |
| AT4G27040 | 7.64 | 0.05 | 14.12 | 0.31 | 0.89 | 3.14E-05 | NO | NO | NO | NO |
| AT4G27280 | 7.30 | 1.08 | 45.45 | 1.26 | 2.64 | 0.00E+00 | NO | NO | DOWN | NO |
| AT4G27450 | 1.31 | 0.26 | 8.27 | 1.05 | 2.66 | 4.33E-09 | NO | NO | DOWN | NO |
| AT4G27470 | 7.82 | 0.37 | 15.60 | 0.58 | 1.00 | 3.19E-04 | NO | NO | NO | NO |
| AT4G27745 | 8.23 | 0.21 | 14.44 | 0.40 | 0.81 | 2.11E-02 | NO | NO | NO | NO |
| AT4G27830 | 15.73 | 0.17 | 25.60 | 0.57 | 0.70 | 6.24E-04 | NO | NO | UP | NO |
| AT4G27860 | 2.21 | 0.39 | 9.17 | 1.02 | 2.06 | 0.00E+00 | NO | NO | NO | NO |
| AT4G27870 | 12.68 | 0.26 | 18.96 | 0.22 | 0.58 | 4.01E-03 | NO | NO | NO | NO |
| AT4G28300 | 29.77 | 0.33 | 56.43 | 0.46 | 0.92 | 4.25E-11 | NO | NO | NO | NO |
| AT4G28390 | 5.62 | 0.48 | 27.38 | 0.08 | 2.29 | 0.00E+00 | POSITIVE | NO | NO | NO |
| AT4G28395 | 0.00 | 0.00 | 3.72 | 1.30 | Inf | 5.84E-05 | NO | NO | NO | NO |
| AT4G28400 | 17.63 | 0.20 | 40.98 | 0.47 | 1.22 | 9.54E-11 | NO | NO | NO | UP |
| AT4G28490 | 6.52 | 0.53 | 14.29 | 0.53 | 1.13 | 5.95E-09 | NO | NO | NO | NO |
| AT4G28570 | 7.90 | 0.20 | 18.11 | 0.11 | 1.20 | 2.10E-10 | NO | NO | NO | NO |
| AT4G28710 | 4.74 | 0.25 | 7.24 | 0.29 | 0.61 | 3.83E-03 | NO | NO | NO | NO |
| AT4G29160 | 36.01 | 0.51 | 74.53 | 0.74 | 1.05 | 3.29E-11 | NO | NO | NO | NO |
| AT4G29210 | 9.94 | 0.44 | 14.81 | 0.65 | 0.57 | 6.00E-03 | NO | NO | NO | NO |
| AT4G29380 | 7.71 | 0.06 | 11.63 | 0.35 | 0.59 | 2.77E-03 | NO | NO | NO | NO |
| AT4G29440 | 4.49 | 0.08 | 8.85 | 0.39 | 0.98 | 2.82E-07 | NO | NO | NO | NO |
| AT4G29740 | 3.33 | 0.31 | 12.73 | 0.90 | 1.93 | 1.03E-13 | NO | NO | NO | NO |
| AT4G29750 | 23.65 | 0.27 | 31.40 | 0.41 | 0.41 | 4.46E-02 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT4G29780 | 1.72 | 0.18 | 4.84 | 0.04 | 1.49 | 3.18E-05 | NO | NO | DOWN | NO |
| AT4G29810 | 64.22 | 0.59 | 87.69 | 1.10 | 0.45 | 1.88E-02 | NO | NO | NO | NO |
| AT4G29900 | 15.26 | 0.40 | 40.90 | 0.57 | 1.42 | 0.00E+00 | NO | NO | NO | NO |
| AT4G29950 | 10.45 | 0.26 | 28.05 | 0.15 | 1.42 | 0.00E+00 | NO | NO | NO | NO |
| AT4G30060 | 2.92 | 0.05 | 7.36 | 0.20 | 1.33 | 4.01E-06 | NO | NO | NO | NO |
| AT4G30190 | 77.72 | 1.20 | 119.44 | 2.45 | 0.62 | 3.97E-05 | NO | NO | NO | NO |
| AT4G30210 | 30.92 | 0.43 | 40.91 | 0.29 | 0.40 | 4.24E-02 | NO | NO | NO | NO |
| AT4G30250 | 1.60 | 0.18 | 3.41 | 0.44 | 1.09 | 2.28E-02 | NO | NO | NO | NO |
| AT4G30270 | 88.47 | 2.47 | 152.43 | 1.59 | 0.78 | 1.33E-05 | NO | NO | NO | NO |
| AT4G30440 | 33.47 | 0.12 | 47.42 | 1.18 | 0.50 | 1.04E-02 | NO | NO | NO | NO |
| AT4G30530 | 169.43 | 0.64 | 283.80 | 4.61 | 0.74 | 3.00E-05 | NO | NO | NO | NO |
| AT4G30640 | 0.52 | 0.09 | 3.17 | 0.34 | 2.62 | 3.71E-04 | NO | NO | NO | NO |
| AT4G31170 | 36.58 | 1.07 | 49.77 | 0.47 | 0.44 | 1.32E-03 | NO | NO | NO | NO |
| AT4G31500 | 98.45 | 0.92 | 264.91 | 8.12 | 1.43 | 0.00E+00 | NO | NO | UP | DOWN |
| AT4G31510 | 11.54 | 0.76 | 18.55 | 0.15 | 0.68 | 3.04E-02 | NO | NO | NO | NO |
| AT4G31800 | 6.95 | 0.53 | 23.26 | 0.22 | 1.74 | 1.20E-13 | NO | YES | UP | NO |
| AT4G31980 | 3.74 | 0.23 | 6.14 | 0.31 | 0.72 | 2.07E-02 | NO | NO | NO | NO |
| AT4G32030 | 11.89 | 0.12 | 16.92 | 0.14 | 0.51 | 4.15E-02 | NO | NO | NO | NO |
| AT4G32060 | 58.70 | 0.60 | 85.81 | 0.18 | 0.55 | 3.71E-03 | NO | NO | NO | NO |
| AT4G32070 | 4.97 | 0.19 | 7.67 | 0.15 | 0.62 | 1.57E-02 | NO | NO | NO | NO |
| AT4G32285 | 29.39 | 0.35 | 38.47 | 0.77 | 0.39 | 1.24E-02 | NO | NO | NO | NO |
| AT4G32480 | 0.69 | 0.14 | 2.13 | 0.12 | 1.62 | 2.11E-02 | NO | NO | NO | NO |
| AT4G32670 | 1.06 | 0.08 | 3.84 | 0.58 | 1.86 | 6.93E-08 | NO | NO | NO | NO |
| AT4G32760 | 27.24 | 0.35 | 43.31 | 0.24 | 0.67 | 4.48E-07 | NO | NO | NO | NO |
| AT4G33050 | 23.67 | 2.55 | 81.98 | 0.99 | 1.79 | 0.00E+00 | NO | NO | NO | DOWN |
| AT4G33220 | 29.73 | 0.49 | 41.33 | 1.05 | 0.48 | 1.89E-02 | NO | NO | NO | NO |
| AT4G33240 | 9.25 | 0.16 | 15.30 | 0.26 | 0.73 | 3.22E-10 | NO | NO | NO | NO |
| AT4G33300 | 22.57 | 0.46 | 60.57 | 0.87 | 1.42 | 0.00E+00 | NO | NO | NO | NO |
| AT4G33540 | 43.43 | 0.66 | 124.57 | 1.97 | 1.52 | 0.00E+00 | POSITIVE | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT4G33565 | 32.20 | 0.64 | 60.79 | 0.91 | 0.92 | 2.56E-07 | NO | NO | NO | NO |
| AT4G33910 | 17.69 | 0.14 | 33.48 | 0.54 | 0.92 | 4.89E-06 | NO | NO | NO | NO |
| AT4G33920 | 36.37 | 0.62 | 76.81 | 0.65 | 1.08 | 1.92E-10 | NO | NO | UP | NO |
| AT4G34050 | 281.78 | 4.13 | 443.63 | 6.28 | 0.65 | 2.31E-07 | NO | NO | NO | NO |
| AT4G34100 | 26.68 | 0.40 | 36.93 | 0.36 | 0.47 | 1.27E-02 | NO | NO | NO | NO |
| AT4G34135 | 22.00 | 0.85 | 28.86 | 3.60 | 0.39 | 3.39E-02 | NO | NO | NO | NO |
| AT4G34150 | 31.66 | 0.25 | 125.67 | 1.34 | 1.99 | 0.00E+00 | NO | NO | NO | NO |
| AT4G34180 | 85.77 | 1.04 | 122.93 | 0.23 | 0.52 | 5.22E-03 | NO | NO | NO | NO |
| AT4G34480 | 23.10 | 0.45 | 31.90 | 0.76 | 0.47 | 2.41E-02 | NO | NO | NO | NO |
| AT4G34630 | 83.64 | 0.43 | 224.25 | 2.05 | 1.42 | 0.00E+00 | NO | NO | NO | NO |
| AT4G35060 | 1.68 | 0.44 | 4.71 | 0.37 | 1.48 | 8.62E-03 | NO | NO | NO | NO |
| AT4G35180 | 1.40 | 0.42 | 13.14 | 0.12 | 3.23 | 0.00E+00 | NO | NO | NO | NO |
| AT4G35500 | 6.22 | 0.11 | 9.39 | 0.06 | 0.60 | 3.31E-02 | NO | NO | NO | NO |
| AT4G35600 | 6.83 | 0.52 | 22.60 | 0.55 | 1.73 | 0.00E+00 | NO | NO | NO | NO |
| AT4G35810 | 0.33 | 0.17 | 1.77 | 0.45 | 2.43 | 1.40E-02 | NO | NO | NO | NO |
| AT4G36030 | 0.70 | 0.16 | 2.35 | 0.35 | 1.75 | 1.79E-04 | NO | NO | NO | NO |
| AT4G36040 | 95.02 | 1.16 | 198.56 | 0.69 | 1.06 | 6.68E-11 | NO | NO | NO | NO |
| AT4G36220 | 69.33 | 1.05 | 142.64 | 1.10 | 1.04 | 1.16E-09 | NO | NO | NO | NO |
| AT4G36430 | 1.48 | 0.14 | 5.05 | 0.35 | 1.77 | 1.47E-04 | NO | NO | NO | NO |
| AT4G36550 | 5.09 | 0.27 | 9.29 | 0.24 | 0.87 | 1.54E-04 | NO | NO | NO | NO |
| AT4G36670 | 15.31 | 0.72 | 28.94 | 2.03 | 0.92 | 2.69E-06 | NO | NO | NO | NO |
| AT4G36760 | 32.53 | 0.73 | 50.65 | 0.09 | 0.64 | 4.41E-04 | NO | NO | NO | NO |
| AT4G36988 | 11.58 | 0.78 | 55.21 | 0.51 | 2.25 | 0.00E+00 | NO | NO | NO | NO |
| AT4G37010 | 0.90 | 0.48 | 4.07 | 0.16 | 2.17 | 8.19E-04 | NO | NO | NO | NO |
| AT4G37290 | 0.29 | 0.11 | 1.67 | 0.26 | 2.51 | 3.63E-02 | NO | NO | NO | NO |
| AT4G37310 | 16.02 | 0.63 | 39.16 | 0.40 | 1.29 | 2.80E-13 | NO | NO | NO | NO |
| AT4G37390 | 1.54 | 0.90 | 4.90 | 0.65 | 1.67 | 2.16E-06 | NO | NO | NO | NO |
| AT4G37520 | 7.80 | 1.84 | 17.26 | 0.46 | 1.14 | 5.50E-06 | NO | NO | NO | NO |
| AT4G37530 | 3.27 | 1.08 | 13.97 | 1.75 | 2.10 | 1.22E-11 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT4G37640 | 26.04 | 0.36 | 48.26 | 0.80 | 0.89 | 4.17E-07 | NO | NO | NO | NO |
| AT4G37870 | 39.15 | 1.13 | 62.11 | 0.41 | 0.67 | 2.22E-04 | NO | NO | NO | NO |
| AT4G37900 | 1.07 | 0.15 | 4.07 | 0.15 | 1.93 | 2.14E-07 | NO | NO | NO | NO |
| AT4G38470 | 10.11 | 0.37 | 17.77 | 0.17 | 0.81 | 1.29E-04 | NO | NO | NO | NO |
| AT4G38480 | 3.69 | 0.20 | 8.49 | 0.06 | 1.20 | 6.06E-05 | NO | NO | NO | NO |
| AT4G38550 | 36.80 | 1.16 | 71.78 | 1.56 | 0.96 | 1.36E-08 | NO | NO | NO | NO |
| AT4G38560 | 0.92 | 0.37 | 12.15 | 0.53 | 3.73 | 0.00E+00 | NO | NO | NO | NO |
| AT4G38620 | 11.26 | 0.37 | 21.77 | 0.59 | 0.95 | 2.63E-05 | NO | YES | NO | NO |
| AT4G39030 | 3.74 | 0.60 | 37.05 | 1.19 | 3.31 | 0.00E+00 | NO | NO | NO | NO |
| AT4G39390 | 15.03 | 0.20 | 21.28 | 0.11 | 0.50 | 9.02E-03 | NO | NO | NO | NO |
| AT4G39580 | 2.44 | 0.17 | 6.20 | 0.23 | 1.35 | 1.74E-03 | NO | NO | NO | NO |
| AT4G39610 | 0.52 | 0.21 | 7.55 | 0.37 | 3.85 | 3.97E-11 | NO | NO | NO | NO |
| AT4G39640 | 16.33 | 0.30 | 32.66 | 1.07 | 1.00 | 1.31E-10 | NO | NO | NO | NO |
| AT4G39670 | 3.51 | 0.90 | 35.79 | 0.88 | 3.35 | 0.00E+00 | NO | NO | NO | NO |
| AT4G39840 | 6.39 | 0.47 | 9.93 | 0.13 | 0.64 | 1.50E-02 | NO | NO | NO | NO |
| AT4G39890 | 11.20 | 0.64 | 18.98 | 0.37 | 0.76 | 6.93E-03 | NO | NO | NO | NO |
| AT4G39950 | 24.06 | 1.00 | 93.40 | 0.71 | 1.96 | 0.00E+00 | NO | NO | NO | NO |
| AT4G40020 | 1.46 | 0.15 | 4.37 | 0.10 | 1.58 | 6.09E-05 | NO | NO | NO | NO |
| AT5G01100 | 0.83 | 0.23 | 4.04 | 0.12 | 2.28 | 1.59E-08 | NO | NO | NO | NO |
| AT5G01210 | 3.03 | 0.28 | 5.17 | 0.55 | 0.77 | 3.24E-02 | NO | NO | NO | NO |
| AT5G01400 | 5.65 | 0.27 | 7.85 | 0.26 | 0.48 | 3.22E-02 | NO | NO | NO | NO |
| AT5G01500 | 16.39 | 0.28 | 24.07 | 0.50 | 0.55 | 1.08E-02 | NO | NO | NO | NO |
| AT5G01540 | 0.33 | 0.14 | 4.05 | 0.34 | 3.63 | 1.69E-13 | NO | NO | NO | NO |
| AT5G01542 | 5.18 | 0.28 | 26.03 | 1.40 | 2.33 | 0.00E+00 | NO | NO | NO | NO |
| AT5G01720 | 6.59 | 0.30 | 12.35 | 0.22 | 0.91 | 1.95E-05 | NO | NO | NO | NO |
| AT5G01770 | 1.80 | 0.04 | 2.90 | 0.17 | 0.69 | 2.06E-02 | NO | NO | NO | NO |
| AT5G01810 | 41.09 | 1.10 | 63.87 | 1.28 | 0.64 | 5.61E-04 | NO | NO | NO | NO |
| AT5G01820 | 23.57 | 0.48 | 54.83 | 1.11 | 1.22 | 6.63E-13 | NO | NO | NO | NO |
| AT5G01830 | 0.81 | 0.04 | 2.20 | 0.13 | 1.45 | 1.66E-03 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G01900 | 0.30 | 0.09 | 2.07 | 0.24 | 2.79 | 1.24E-03 | NO | YES | NO | NO |
| AT5G02230 | 6.94 | 0.55 | 14.12 | 1.00 | 1.03 | 2.06E-04 | NO | NO | DOWN | NO |
| AT5G02270 | 35.04 | 1.02 | 53.66 | 0.38 | 0.61 | 6.75E-04 | NO | NO | NO | NO |
| AT5G02290 | 18.83 | 0.71 | 45.03 | 0.49 | 1.26 | 6.63E-13 | NO | NO | NO | NO |
| AT5G02310 | 8.72 | 0.13 | 11.97 | 0.31 | 0.46 | 2.34E-02 | NO | NO | NO | NO |
| AT5G02620 | 17.09 | 0.28 | 28.86 | 0.43 | 0.76 | 8.23E-05 | NO | NO | NO | NO |
| AT5G02780 | 0.92 | 0.39 | 16.01 | 1.73 | 4.12 | 0.00E+00 | NO | NO | NO | NO |
| AT5G02830 | 48.41 | 0.46 | 64.85 | 0.31 | 0.42 | 3.68E-02 | NO | NO | NO | NO |
| AT5G02880 | 9.31 | 0.24 | 14.38 | 0.40 | 0.63 | 9.97E-04 | NO | NO | NO | NO |
| AT5G03040 | 38.90 | 0.43 | 61.13 | 0.17 | 0.65 | 1.11E-06 | NO | NO | NO | NO |
| AT5G03120 | 22.36 | 0.60 | 45.91 | 1.73 | 1.04 | 5.77E-05 | NO | NO | NO | NO |
| AT5G03160 | 23.51 | 0.41 | 56.61 | 0.92 | 1.27 | 4.04E-13 | NO | NO | NO | NO |
| AT5G03260 | 1.36 | 0.12 | 2.64 | 0.25 | 0.95 | 4.83E-02 | NO | NO | NO | NO |
| AT5G03555 | 25.22 | 0.66 | 40.46 | 0.55 | 0.68 | 2.32E-04 | NO | NO | NO | NO |
| AT5G03610 | 9.87 | 0.79 | 28.49 | 0.61 | 1.53 | 7.08E-14 | NO | NO | NO | NO |
| AT5G04020 | 5.30 | 0.18 | 8.18 | 0.73 | 0.63 | 3.26E-03 | NO | NO | NO | NO |
| AT5G04040 | 7.65 | 0.26 | 11.80 | 0.20 | 0.62 | 2.56E-03 | NO | NO | NO | NO |
| AT5G04160 | 5.62 | 0.23 | 11.18 | 0.36 | 0.99 | 6.17E-04 | NO | NO | NO | NO |
| AT5G04550 | 24.32 | 0.26 | 35.97 | 0.31 | 0.56 | 2.82E-03 | NO | NO | NO | NO |
| AT5G04560 | 6.42 | 0.31 | 10.86 | 0.50 | 0.76 | 4.29E-05 | NO | NO | NO | NO |
| AT5G04720 | 11.94 | 0.55 | 42.09 | 0.52 | 1.82 | 0.00E+00 | NO | NO | NO | NO |
| AT5G04930 | 19.45 | 0.86 | 40.98 | 0.42 | 1.07 | 4.04E-10 | NO | NO | NO | NO |
| AT5G05090 | 7.02 | 0.51 | 11.44 | 0.20 | 0.70 | 1.87E-02 | NO | YES | NO | NO |
| AT5G05100 | 16.21 | 0.39 | 23.58 | 0.23 | 0.54 | 1.21E-02 | NO | NO | NO | NO |
| AT5G05190 | 3.62 | 0.18 | 10.31 | 0.25 | 1.51 | 1.20E-10 | NO | NO | NO | NO |
| AT5G05340 | 1.26 | 0.89 | 4.68 | 0.60 | 1.89 | 2.48E-04 | NO | NO | NO | NO |
| AT5G05410 | 9.06 | 0.42 | 13.13 | 0.15 | 0.54 | 4.27E-02 | NO | YES | NO | NO |
| AT5G05460 | 6.51 | 0.33 | 9.31 | 0.11 | 0.52 | 4.75E-02 | NO | NO | NO | NO |
| AT5G05570 | 6.69 | 0.05 | 10.58 | 0.33 | 0.66 | 1.31E-03 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G05730 | 19.48 | 0.75 | 43.51 | 0.60 | 1.16 | 8.75E-12 | NO | NO | NO | NO |
| AT5G06120 | 7.58 | 0.05 | 10.11 | 0.23 | 0.42 | 1.21E-02 | NO | NO | NO | NO |
| AT5G06750 | 7.34 | 0.39 | 18.87 | 0.34 | 1.36 | 1.16E-10 | NO | NO | NO | NO |
| AT5G07100 | 12.86 | 1.34 | 20.82 | 1.65 | 0.70 | 2.15E-03 | NO | YES | NO | NO |
| AT5G07180 | 1.62 | 0.07 | 2.90 | 0.36 | 0.84 | 1.28E-02 | NO | NO | NO | NO |
| AT5G07350 | 27.22 | 0.55 | 40.98 | 0.66 | 0.59 | 1.23E-05 | NO | NO | NO | NO |
| AT5G07370 | 51.42 | 0.68 | 72.25 | 0.24 | 0.49 | 5.75E-03 | NO | NO | NO | NO |
| AT5G07710 | 3.57 | 0.18 | 6.95 | 0.10 | 0.96 | 1.85E-03 | NO | NO | NO | NO |
| AT5G07770 | 1.76 | 0.14 | 4.52 | 0.38 | 1.36 | 3.34E-06 | NO | NO | NO | NO |
| AT5G07790 | 3.92 | 0.20 | 7.08 | 0.19 | 0.85 | 7.53E-04 | NO | NO | NO | NO |
| AT5G07870 | 4.26 | 0.05 | 7.76 | 0.21 | 0.86 | 6.41E-03 | NO | NO | NO | NO |
| AT5G08130 | 13.92 | 0.15 | 19.29 | 0.60 | 0.47 | 1.18E-03 | NO | YES | NO | NO |
| AT5G08240 | 3.12 | 0.28 | 8.64 | 0.35 | 1.47 | 7.97E-06 | NO | NO | NO | NO |
| AT5G08450 | 17.52 | 0.11 | 23.93 | 0.41 | 0.45 | 6.67E-04 | NO | NO | NO | NO |
| AT5G08790 | 21.50 | 0.64 | 75.26 | 1.28 | 1.81 | 0.00E+00 | NO | YES | NO | NO |
| AT5G09330 | 26.54 | 0.56 | 35.89 | 0.11 | 0.44 | 3.26E-03 | NO | YES | NO | NO |
| AT5G09670 | 10.12 | 1.39 | 18.84 | 0.53 | 0.90 | 8.05E-07 | NO | NO | NO | NO |
| AT5G10250 | 0.67 | 0.09 | 1.63 | 0.16 | 1.29 | 3.80E-02 | NO | NO | NO | NO |
| AT5G10290 | 14.52 | 0.13 | 24.81 | 0.41 | 0.77 | 4.69E-05 | NO | NO | NO | NO |
| AT5G10300 | 2.13 | 0.23 | 5.71 | 0.21 | 1.43 | 3.29E-03 | NO | NO | NO | NO |
| AT5G10490 | 14.09 | 0.13 | 19.50 | 0.20 | 0.47 | 3.66E-03 | NO | NO | NO | NO |
| AT5G10550 | 16.99 | 0.17 | 23.42 | 0.61 | 0.46 | 3.09E-02 | NO | NO | NO | NO |
| AT5G10770 | 3.44 | 0.40 | 9.43 | 0.08 | 1.46 | 2.03E-07 | NO | NO | NO | NO |
| AT5G11000 | 13.55 | 0.92 | 22.84 | 0.44 | 0.75 | 5.70E-04 | NO | NO | NO | NO |
| AT5G11060 | 25.39 | 0.47 | 35.15 | 0.61 | 0.47 | 2.18E-02 | NO | NO | NO | NO |
| AT5G11250 | 4.64 | 0.19 | 7.67 | 0.44 | 0.72 | 1.37E-03 | NO | NO | NO | NO |
| AT5G11650 | 11.35 | 0.29 | 23.91 | 0.21 | 1.07 | 1.19E-07 | NO | NO | NO | NO |
| AT5G11850 | 5.71 | 0.16 | 8.76 | 0.08 | 0.62 | 7.52E-03 | NO | NO | NO | NO |
| AT5G11920 | 2.93 | 0.48 | 4.91 | 0.30 | 0.74 | 3.95E-02 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G11970 | 16.93 | 0.84 | 40.76 | 0.80 | 1.27 | 2.15E-07 | NO | NO | NO | NO |
| AT5G12010 | 18.35 | 0.68 | 32.23 | 0.39 | 0.81 | 1.56E-05 | NO | NO | NO | NO |
| AT5G12300 | 4.48 | 0.14 | 12.83 | 0.62 | 1.52 | 1.93E-08 | NO | NO | NO | NO |
| AT5G12480 | 24.60 | 0.43 | 37.33 | 0.20 | 0.60 | 1.42E-03 | NO | NO | NO | NO |
| AT5G12850 | 10.89 | 0.43 | 16.58 | 0.50 | 0.61 | 2.55E-03 | NO | YES | NO | NO |
| AT5G12940 | 2.86 | 0.26 | 6.46 | 0.39 | 1.17 | 2.26E-03 | NO | NO | NO | NO |
| AT5G12950 | 6.06 | 0.38 | 8.86 | 0.25 | 0.55 | 2.01E-02 | NO | NO | NO | NO |
| AT5G13080 | 1.46 | 1.01 | 21.46 | 1.40 | 3.88 | 1.88E-14 | NO | YES | NO | NO |
| AT5G13190 | 29.01 | 0.51 | 69.41 | 0.85 | 1.26 | 1.76E-10 | NO | NO | NO | NO |
| AT5G13370 | 24.41 | 0.27 | 32.76 | 0.32 | 0.42 | 4.28E-02 | NO | NO | NO | NO |
| AT5G13420 | 51.84 | 1.35 | 71.57 | 0.35 | 0.47 | 1.78E-02 | NO | NO | NO | NO |
| AT5G13490 | 4.15 | 1.09 | 16.33 | 1.39 | 1.98 | 1.89E-14 | NO | NO | NO | NO |
| AT5G13500 | 8.17 | 0.09 | 13.00 | 0.13 | 0.67 | 3.54E-03 | NO | NO | NO | NO |
| AT5G13820 | 1.96 | 0.18 | 4.40 | 0.13 | 1.17 | 2.59E-04 | NO | NO | NO | NO |
| AT5G14120 | 6.66 | 0.18 | 11.77 | 0.44 | 0.82 | 1.74E-04 | NO | NO | DOWN | NO |
| AT5G14780 | 150.00 | 1.98 | 282.61 | 4.38 | 0.91 | 4.57E-07 | NO | NO | NO | NO |
| AT5G14930 | 18.39 | 0.55 | 33.47 | 0.84 | 0.86 | 7.25E-08 | NO | NO | NO | NO |
| AT5G15850 | 76.38 | 1.47 | 106.37 | 0.88 | 0.48 | 1.31E-02 | NO | YES | NO | NO |
| AT5G15870 | 10.05 | 0.15 | 26.15 | 1.00 | 1.38 | 1.53E-13 | NO | NO | NO | NO |
| AT5G15980 | 9.13 | 0.16 | 12.87 | 0.10 | 0.50 | 2.93E-02 | NO | NO | NO | NO |
| AT5G16170 | 1.28 | 0.21 | 4.81 | 0.27 | 1.92 | 3.22E-05 | NO | NO | NO | NO |
| AT5G16190 | 1.17 | 0.05 | 2.61 | 0.26 | 1.16 | 4.14E-02 | NO | NO | NO | NO |
| AT5G16230 | 6.70 | 0.23 | 14.29 | 0.83 | 1.09 | 1.74E-05 | NO | NO | NO | NO |
| AT5G16510 | 37.64 | 0.72 | 51.90 | 1.05 | 0.46 | 1.72E-02 | NO | NO | NO | NO |
| AT5G16800 | 11.32 | 0.26 | 16.09 | 0.18 | 0.51 | 3.19E-02 | NO | NO | NO | NO |
| AT5G16840 | 94.87 | 0.37 | 117.78 | 2.23 | 0.31 | 3.41E-02 | NO | NO | NO | NO |
| AT5G16880 | 46.73 | 0.44 | 78.62 | 1.12 | 0.75 | 5.51E-07 | NO | NO | NO | NO |
| AT5G17020 | 14.44 | 0.28 | 18.28 | 0.29 | 0.34 | 4.60E-02 | NO | NO | NO | NO |
| AT5G17300 | 13.53 | 0.34 | 28.34 | 0.44 | 1.07 | 1.35E-08 | NO | YES | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G17640 | 5.52 | 0.08 | 12.44 | 0.28 | 1.17 | 8.58E-07 | NO | NO | NO | NO |
| AT5G17910 | 4.82 | 0.08 | 8.37 | 0.30 | 0.80 | 4.01E-05 | NO | NO | NO | NO |
| AT5G18480 | 25.23 | 0.12 | 46.82 | 0.80 | 0.89 | 3.45E-07 | NO | NO | NO | NO |
| AT5G18490 | 7.01 | 0.44 | 11.20 | 0.28 | 0.68 | 5.90E-03 | NO | NO | NO | NO |
| AT5G18650 | 11.27 | 0.35 | 19.12 | 0.49 | 0.76 | 6.37E-04 | NO | NO | NO | NO |
| AT5G18670 | 4.26 | 0.13 | 14.71 | 0.78 | 1.79 | 3.67E-14 | NO | NO | NO | NO |
| AT5G18780 | 3.20 | 0.38 | 6.74 | 0.50 | 1.08 | 7.82E-04 | NO | NO | NO | NO |
| AT5G19120 | 1.13 | 0.06 | 3.57 | 0.05 | 1.66 | 8.07E-04 | NO | NO | DOWN | NO |
| AT5G19230 | 0.80 | 0.37 | 4.47 | 0.52 | 2.49 | 2.74E-04 | NO | NO | NO | NO |
| AT5G19290 | 32.36 | 0.88 | 44.93 | 1.36 | 0.47 | 2.33E-02 | NO | NO | NO | NO |
| AT5G19320 | 19.14 | 0.41 | 29.78 | 0.38 | 0.64 | 8.63E-04 | NO | NO | NO | NO |
| AT5G19780 | 41.64 | 0.68 | 58.19 | 0.85 | 0.48 | 1.31E-02 | NO | NO | NO | NO |
| AT5G20350 | 24.08 | 0.20 | 32.74 | 0.37 | 0.44 | 3.09E-02 | NO | NO | NO | NO |
| AT5G20400 | 10.76 | 0.66 | 18.82 | 0.53 | 0.81 | 9.58E-04 | NO | NO | NO | NO |
| AT5G20730 | 11.55 | 0.15 | 16.51 | 0.47 | 0.52 | 4.30E-03 | NO | YES | NO | NO |
| AT5G20960 | 1.40 | 0.14 | 6.67 | 0.08 | 2.26 | 0.00E+00 | NO | NO | NO | NO |
| AT5G21170 | 6.73 | 0.55 | 10.90 | 0.13 | 0.70 | 1.70E-02 | NO | NO | NO | NO |
| AT5G21326 | 21.10 | 0.31 | 31.81 | 0.24 | 0.59 | 2.45E-03 | NO | NO | NO | NO |
| AT5G21940 | 7.19 | 0.55 | 14.14 | 0.59 | 0.98 | 4.89E-04 | NO | NO | NO | NO |
| AT5G22060 | 86.47 | 0.05 | 117.46 | 2.01 | 0.44 | 2.62E-02 | NO | NO | NO | NO |
| AT5G22090 | 32.27 | 0.71 | 54.09 | 0.43 | 0.75 | 4.46E-05 | NO | NO | NO | NO |
| AT5G22380 | 0.88 | 0.16 | 11.33 | 0.79 | 3.70 | 4.20E-12 | NO | YES | NO | NO |
| AT5G22430 | 0.04 | 0.01 | 14.26 | 3.68 | 8.41 | 2.18E-07 | NO | NO | NO | NO |
| AT5G22460 | 0.38 | 0.09 | 3.06 | 0.37 | 3.02 | 2.60E-07 | NO | NO | NO | NO |
| AT5G22510 | 25.19 | 0.26 | 35.74 | 0.27 | 0.50 | 8.71E-03 | NO | NO | NO | NO |
| AT5G22555 | 0.47 | 0.21 | 6.02 | 1.08 | 3.67 | 6.89E-05 | NO | NO | NO | NO |
| AT5G22570 | 1.27 | 0.63 | 7.83 | 0.49 | 2.62 | 2.22E-07 | NO | YES | NO | NO |
| AT5G22580 | 59.10 | 1.15 | 89.04 | 2.02 | 0.59 | 3.85E-03 | NO | NO | NO | DOWN |
| AT5G22850 | 5.51 | 0.05 | 8.15 | 0.04 | 0.57 | 4.53E-02 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G23150 | 5.36 | 0.15 | 8.13 | 0.19 | 0.60 | 3.90E-03 | NO | NO | NO | NO |
| AT5G23510 | 11.61 | 0.32 | 22.53 | 0.30 | 0.96 | 4.27E-06 | NO | NO | NO | NO |
| AT5G23575 | 50.90 | 0.96 | 74.60 | 0.74 | 0.55 | 3.59E-03 | NO | NO | NO | NO |
| AT5G23730 | 3.45 | 0.27 | 5.91 | 0.17 | 0.78 | 4.72E-02 | NO | NO | NO | NO |
| AT5G23860 | 6.72 | 0.59 | 11.26 | 0.71 | 0.75 | 1.48E-03 | NO | NO | NO | NO |
| AT5G24120 | 27.43 | 1.17 | 47.76 | 1.56 | 0.80 | 6.62E-06 | NO | NO | NO | NO |
| AT5G24240 | 30.39 | 0.23 | 42.64 | 0.39 | 0.49 | 1.19E-02 | NO | NO | NO | NO |
| AT5G24590 | 9.87 | 0.29 | 18.51 | 0.22 | 0.91 | 1.40E-05 | NO | YES | NO | NO |
| AT5G24660 | 68.17 | 1.72 | 103.29 | 4.04 | 0.60 | 4.73E-03 | NO | NO | NO | NO |
| AT5G24810 | 16.34 | 0.50 | 38.46 | 0.47 | 1.23 | 0.00E+00 | NO | NO | NO | NO |
| AT5G25130 | 3.27 | 0.17 | 8.32 | 0.08 | 1.35 | 7.81E-06 | NO | NO | NO | NO |
| AT5G25190 | 3.72 | 0.05 | 8.13 | 0.73 | 1.13 | 1.13E-02 | NO | YES | NO | NO |
| AT5G25250 | 5.59 | 0.77 | 21.84 | 0.66 | 1.97 | 0.00E+00 | NO | NO | NO | NO |
| AT5G25265 | 47.02 | 0.29 | 76.78 | 0.53 | 0.71 | 7.08E-05 | NO | NO | NO | NO |
| AT5G25280 | 18.40 | 0.38 | 29.64 | 0.40 | 0.69 | 2.48E-04 | NO | NO | NO | NO |
| AT5G25440 | 2.54 | 0.67 | 9.64 | 0.18 | 1.92 | 1.68E-07 | NO | NO | NO | NO |
| AT5G25770 | 0.00 | 0.55 | 8.01 | 0.91 | 0.58 | 4.85E-02 | NO | NO | DOWN | NO |
| AT5G25820 | 4.24 | 0.21 | 6.42 | 0.15 | 0.60 | 4.32E-02 | NO | NO | NO | NO |
| AT5G25930 | 2.22 | 0.43 | 13.23 | 0.54 | 2.58 | 0.00E+00 | NO | NO | NO | NO |
| AT5G26040 | 4.27 | 0.35 | 7.13 | 0.04 | 0.74 | 3.67E-02 | NO | NO | NO | NO |
| AT5G26170 | 2.04 | 0.55 | 14.47 | 1.18 | 2.83 | 7.48E-07 | NO | YES | NO | NO |
| AT5G26600 | 10.77 | 0.13 | 15.19 | 0.13 | 0.50 | 2.11E-02 | NO | NO | NO | NO |
| AT5G26920 | 8.08 | 1.33 | 47.83 | 0.99 | 2.57 | 0.00E+00 | NO | NO | NO | NO |
| AT5G27420 | 6.14 | 1.44 | 38.70 | 2.04 | 2.65 | 0.00E+00 | NO | NO | NO | NO |
| AT5G27760 | 106.18 | 1.09 | 196.83 | 2.52 | 0.89 | 5.73E-07 | NO | NO | NO | NO |
| AT5G28540 | 66.69 | 1.12 | 106.15 | 2.55 | 0.67 | 3.50E-04 | NO | NO | NO | NO |
| AT5G28640 | 7.62 | 0.19 | 19.13 | 1.97 | 1.33 | 1.03E-07 | NO | YES | NO | NO |
| AT5G28830 | 21.64 | 0.16 | 38.91 | 0.73 | 0.85 | 1.40E-05 | NO | NO | NO | NO |
| AT5G34850 | 39.97 | 0.53 | 57.82 | 1.23 | 0.53 | 5.05E-03 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G34940 | 3.32 | 0.32 | 8.24 | 0.14 | 1.31 | 3.32E-06 | NO | NO | NO | NO |
| AT5G35080 | 17.10 | 0.05 | 33.66 | 0.83 | 0.98 | 1.63E-06 | NO | NO | NO | NO |
| AT5G35200 | 19.06 | 0.36 | 27.50 | 0.27 | 0.53 | 7.60E-03 | NO | NO | NO | NO |
| AT5G35370 | 1.32 | 0.10 | 2.41 | 0.09 | 0.86 | 3.46E-02 | NO | NO | NO | NO |
| AT5G35735 | 52.00 | 0.89 | 101.16 | 0.93 | 0.96 | 2.92E-08 | NO | NO | NO | NO |
| AT5G35950 | 1.23 | 0.04 | 3.53 | 0.19 | 1.52 | 2.96E-03 | NO | NO | NO | NO |
| AT5G35970 | 46.00 | 0.41 | 80.10 | 0.64 | 0.80 | 1.05E-05 | NO | NO | NO | NO |
| AT5G36160 | 36.84 | 0.63 | 50.20 | 0.09 | 0.45 | 2.89E-02 | NO | NO | NO | NO |
| AT5G36880 | 30.56 | 0.44 | 47.60 | 0.49 | 0.64 | 6.57E-07 | NO | NO | NO | NO |
| AT5G36970 | 0.36 | 0.16 | 5.43 | 1.74 | 3.92 | 2.25E-06 | NO | NO | NO | NO |
| AT5G37260 | 62.78 | 1.03 | 87.60 | 1.12 | 0.48 | 1.55E-02 | NO | YES | NO | NO |
| AT5G37540 | 1.98 | 0.09 | 5.50 | 0.53 | 1.48 | 1.04E-04 | NO | NO | NO | NO |
| AT5G37600 | 173.68 | 2.54 | 265.55 | 1.91 | 0.61 | 1.73E-03 | NO | NO | NO | NO |
| AT5G37770 | 11.78 | 0.57 | 24.39 | 1.62 | 1.05 | 1.47E-04 | NO | NO | NO | NO |
| AT5G37830 | 13.66 | 0.29 | 20.05 | 0.29 | 0.55 | 3.39E-03 | NO | NO | NO | NO |
| AT5G38210 | 5.38 | 0.46 | 12.11 | 0.70 | 1.17 | 1.46E-07 | NO | NO | NO | NO |
| AT5G38212 | 2.88 | 0.15 | 7.82 | 0.51 | 1.44 | 4.11E-08 | NO | NO | NO | NO |
| AT5G38310 | 0.84 | 0.18 | 3.85 | 0.26 | 2.20 | 6.13E-04 | NO | NO | NO | NO |
| AT5G38410 | 194.55 | 3.68 | 276.48 | 4.42 | 0.51 | 7.43E-03 | NO | NO | NO | NO |
| AT5G38650 | 60.49 | 0.19 | 81.91 | 2.33 | 0.44 | 3.61E-02 | NO | NO | NO | NO |
| AT5G38900 | 18.06 | 2.04 | 90.89 | 2.33 | 2.33 | 0.00E+00 | NO | NO | NO | NO |
| AT5G38990 | 16.12 | 0.50 | 29.03 | 0.30 | 0.85 | 2.57E-06 | NO | NO | NO | NO |
| AT5G39080 | 3.48 | 0.21 | 9.86 | 0.57 | 1.50 | 5.40E-07 | NO | NO | NO | NO |
| AT5G39110 | 0.93 | 0.29 | 3.06 | 0.75 | 1.71 | 4.15E-02 | NO | NO | NO | NO |
| AT5G39660 | 11.05 | 0.37 | 16.87 | 0.37 | 0.61 | 1.56E-03 | NO | YES | NO | NO |
| AT5G39860 | 2.32 | 0.33 | 6.00 | 1.28 | 1.37 | 1.91E-02 | NEGATIVE | NO | NO | NO |
| AT5G40010 | 0.13 | 0.02 | 3.12 | 0.85 | 4.60 | 7.61E-09 | NO | NO | NO | NO |
| AT5G40230 | 0.60 | 0.04 | 1.91 | 0.26 | 1.68 | 1.57E-02 | NO | NO | NO | NO |
| AT5G40670 | 38.48 | 0.33 | 59.91 | 1.18 | 0.64 | 6.62E-04 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G40690 | 1.88 | 0.39 | 22.81 | 1.32 | 3.60 | 0.00E+00 | NO | NO | NO | NO |
| AT5G40890 | 17.01 | 1.04 | 22.46 | 0.27 | 0.40 | 2.60E-02 | NEGATIVE | NO | NO | NO |
| AT5G41761 | 24.20 | 1.79 | 42.72 | 1.14 | 0.82 | 1.69E-03 | NO | NO | NO | NO |
| AT5G42010 | 2.48 | 0.20 | 5.95 | 0.27 | 1.26 | 1.28E-05 | NO | NO | NO | NO |
| AT5G42090 | 43.55 | 0.94 | 68.20 | 0.56 | 0.65 | 4.06E-04 | NO | NO | NO | NO |
| AT5G42100 | 34.55 | 0.76 | 51.42 | 0.93 | 0.57 | 2.08E-04 | NO | NO | NO | NO |
| AT5G42250 | 12.12 | 0.62 | 18.85 | 0.71 | 0.64 | 6.89E-03 | NO | NO | NO | NO |
| AT5G42380 | 1.30 | 0.36 | 19.82 | 1.20 | 3.93 | 0.00E+00 | NO | NO | NO | NO |
| AT5G42440 | 2.63 | 0.35 | 5.47 | 0.14 | 1.06 | 1.27E-02 | NO | NO | NO | NO |
| AT5G42760 | 22.41 | 0.37 | 42.02 | 0.98 | 0.91 | 4.77E-07 | NO | NO | NO | NO |
| AT5G42790 | 147.36 | 0.14 | 202.35 | 3.53 | 0.46 | 1.90E-02 | NO | NO | NO | NO |
| AT5G42830 | 2.30 | 0.39 | 14.19 | 1.07 | 2.63 | 0.00E+00 | NO | NO | NO | NO |
| AT5G42870 | 8.81 | 0.13 | 14.18 | 0.31 | 0.69 | 1.47E-05 | NO | NO | NO | NO |
| AT5G42990 | 26.96 | 0.09 | 45.86 | 0.74 | 0.77 | 5.46E-04 | NO | NO | NO | NO |
| AT5G43060 | 14.55 | 0.89 | 40.32 | 1.18 | 1.47 | 0.00E+00 | NO | NO | NO | NO |
| AT5G43380 | 3.33 | 0.02 | 6.00 | 0.35 | 0.85 | 1.99E-02 | NO | NO | NO | NO |
| AT5G43470 | 5.52 | 0.20 | 11.55 | 0.06 | 1.07 | 2.01E-09 | NO | NO | NO | NO |
| AT5G43900 | 5.28 | 0.24 | 12.99 | 0.28 | 1.30 | 1.91E-14 | NO | NO | NO | NO |
| AT5G44070 | 21.02 | 0.98 | 42.36 | 0.41 | 1.01 | 1.38E-08 | NO | NO | NO | NO |
| AT5G44240 | 11.73 | 0.28 | 22.23 | 0.26 | 0.92 | 1.81E-07 | NO | NO | NO | NO |
| AT5G44380 | 0.76 | 0.33 | 1.82 | 0.33 | 1.25 | 3.61E-02 | NO | NO | NO | NO |
| AT5G44390 | 5.74 | 0.40 | 15.56 | 0.77 | 1.44 | 2.27E-10 | NO | NO | NO | NO |
| AT5G44480 | 0.72 | 0.36 | 7.79 | 0.11 | 3.42 | 1.27E-11 | NO | NO | NO | NO |
| AT5G44540 | 0.89 | 0.16 | 4.93 | 3.39 | 2.48 | 2.94E-02 | NO | NO | NO | NO |
| AT5G44585 | 5.76 | 0.78 | 19.45 | 1.79 | 1.76 | 1.19E-03 | NO | NO | NO | NO |
| AT5G44720 | 75.31 | 1.76 | 102.84 | 1.44 | 0.45 | 3.54E-03 | NO | NO | NO | NO |
| AT5G44820 | 12.80 | 0.46 | 22.93 | 0.25 | 0.84 | 2.02E-04 | NO | NO | NO | NO |
| AT5G44860 | 9.62 | 0.30 | 15.88 | 0.19 | 0.72 | 3.87E-03 | NO | NO | NO | NO |
| AT5G44870 | 8.04 | 0.20 | 13.27 | 0.66 | 0.72 | 2.53E-04 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G44990 | 0.45 | 0.24 | 9.33 | 0.60 | 4.39 | 0.00E+00 | NO | NO | NO | NO |
| AT5G45000 | 2.17 | 0.47 | 5.34 | 0.20 | 1.30 | 9.13E-04 | NO | NO | NO | NO |
| AT5G45110 | 7.49 | 0.47 | 29.84 | 0.74 | 1.99 | 0.00E+00 | NO | NO | NO | NO |
| AT5G46270 | 6.35 | 0.21 | 10.08 | 0.56 | 0.67 | 1.33E-03 | NO | NO | NO | NO |
| AT5G46330 | 7.58 | 0.30 | 19.24 | 0.29 | 1.34 | 1.91E-14 | NO | NO | NO | NO |
| AT5G46340 | 6.74 | 0.15 | 9.66 | 0.25 | 0.52 | 4.44E-02 | NO | NO | NO | NO |
| AT5G46350 | 2.53 | 0.71 | 15.42 | 1.00 | 2.61 | 0.00E+00 | NO | YES | NO | NO |
| AT5G46450 | 11.96 | 0.51 | 16.70 | 0.69 | 0.48 | 2.13E-02 | NO | NO | NO | NO |
| AT5G46780 | 6.27 | 0.20 | 14.52 | 0.41 | 1.21 | 2.61E-05 | NO | NO | NO | NO |
| AT5G46790 | 16.66 | 0.36 | 28.60 | 0.88 | 0.78 | 1.16E-03 | NO | NO | NO | NO |
| AT5G47050 | 2.88 | 0.34 | 5.14 | 0.42 | 0.84 | 2.52E-02 | NO | NO | NO | NO |
| AT5G47070 | 8.90 | 0.03 | 15.83 | 0.84 | 0.83 | 1.74E-04 | NO | NO | NO | NO |
| AT5G47120 | 113.61 | 0.35 | 277.84 | 3.25 | 1.29 | 5.38E-14 | NO | NO | NO | NO |
| AT5G47220 | 47.67 | 1.40 | 120.04 | 2.42 | 1.33 | 5.37E-14 | NO | YES | NO | NO |
| AT5G47420 | 8.91 | 0.11 | 15.97 | 0.45 | 0.84 | 1.07E-03 | NO | NO | NO | NO |
| AT5G47500 | 14.27 | 0.58 | 21.61 | 0.93 | 0.60 | 7.79E-03 | NO | NO | NO | NO |
| AT5G47560 | 45.16 | 0.37 | 91.77 | 0.97 | 1.02 | 1.29E-09 | NO | NO | NO | NO |
| AT5G47620 | 33.22 | 0.66 | 45.37 | 0.59 | 0.45 | 1.61E-03 | NO | NO | NO | NO |
| AT5G47820 | 13.29 | 0.44 | 17.38 | 0.30 | 0.39 | 1.60E-02 | NO | NO | NO | NO |
| AT5G47960 | 2.07 | 0.17 | 9.10 | 0.40 | 2.13 | 2.06E-06 | NO | NO | NO | NO |
| AT5G48160 | 33.08 | 0.35 | 50.67 | 0.27 | 0.62 | 4.81E-04 | NO | NO | NO | NO |
| AT5G48380 | 26.59 | 0.44 | 67.03 | 0.44 | 1.33 | 0.00E+00 | NO | NO | NO | NO |
| AT5G48540 | 34.05 | 0.52 | 68.48 | 1.51 | 1.01 | 5.75E-08 | NO | NO | NO | NO |
| AT5G48657 | 4.97 | 0.61 | 18.83 | 0.91 | 1.92 | 3.95E-10 | NO | NO | NO | NO |
| AT5G48920 | 1.00 | 0.10 | 3.64 | 0.07 | 1.87 | 6.74E-03 | NO | NO | NO | NO |
| AT5G48930 | 42.90 | 0.92 | 84.59 | 0.44 | 0.98 | 7.58E-09 | NO | NO | NO | NO |
| AT5G49450 | 2.80 | 0.25 | 5.98 | 0.19 | 1.09 | 2.96E-02 | NO | YES | NO | NO |
| AT5G49520 | 1.21 | 0.05 | 5.93 | 0.57 | 2.29 | 3.30E-09 | NO | YES | NO | NO |
| AT5G49555 | 25.80 | 0.41 | 36.93 | 0.42 | 0.52 | 8.03E-03 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G49680 | 1.40 | 0.07 | 4.38 | 0.39 | 1.65 | 1.93E-14 | NO | NO | NO | NO |
| AT5G49730 | 60.45 | 0.74 | 85.67 | 1.71 | 0.50 | 8.12E-03 | NO | NO | NO | NO |
| AT5G49740 | 12.25 | 0.26 | 25.84 | 0.64 | 1.08 | 1.65E-09 | NO | NO | NO | NO |
| AT5G49760 | 21.93 | 0.46 | 48.09 | 0.14 | 1.13 | 8.72E-12 | NO | NO | NO | NO |
| AT5G49810 | 21.93 | 0.26 | 32.02 | 0.21 | 0.55 | 3.65E-03 | NO | NO | NO | NO |
| AT5G50110 | 20.19 | 0.27 | 28.53 | 0.30 | 0.50 | 4.13E-02 | NO | NO | NO | NO |
| AT5G50200 | 42.67 | 1.12 | 82.87 | 1.79 | 0.96 | 1.28E-07 | NO | NO | NO | NO |
| AT5G50210 | 11.33 | 0.10 | 18.56 | 0.24 | 0.71 | 2.71E-04 | NEGATIVE | NO | NO | NO |
| AT5G50460 | 160.23 | 4.09 | 257.73 | 4.63 | 0.69 | 2.77E-04 | NO | NO | NO | NO |
| AT5G51070 | 35.89 | 0.55 | 65.38 | 0.80 | 0.87 | 4.15E-07 | NO | NO | NO | NO |
| AT5G51190 | 1.21 | 0.01 | 4.10 | 0.14 | 1.76 | 5.33E-03 | NO | YES | DOWN | NO |
| AT5G51290 | 10.64 | 0.34 | 18.05 | 0.37 | 0.76 | 1.48E-04 | NO | NO | NO | NO |
| AT5G51630 | 2.22 | 0.09 | 6.54 | 0.51 | 1.56 | 1.89E-14 | NO | NO | NO | NO |
| AT5G51770 | 7.79 | 0.30 | 12.94 | 0.13 | 0.73 | 1.53E-03 | NO | NO | NO | NO |
| AT5G51830 | 45.33 | 1.43 | 84.19 | 1.52 | 0.89 | 2.74E-07 | NO | NO | NO | NO |
| AT5G52160 | 0.00 | 0.00 | 3.03 | 1.77 | Inf | 2.67E-03 | NO | NO | NO | NO |
| AT5G52250 | 0.45 | 0.10 | 2.14 | 0.22 | 2.26 | 7.58E-04 | NO | NO | NO | NO |
| AT5G52390 | 2.13 | 0.13 | 18.68 | 3.91 | 3.13 | 0.00E+00 | NO | NO | NO | NO |
| AT5G52540 | 39.48 | 0.39 | 60.71 | 0.36 | 0.62 | 6.92E-04 | NO | NO | NO | NO |
| AT5G52730 | 0.56 | 0.23 | 4.87 | 0.48 | 3.11 | 6.34E-04 | NO | NO | NO | NO |
| AT5G52760 | 3.72 | 1.12 | 59.88 | 1.50 | 4.01 | 0.00E+00 | NO | NO | NO | NO |
| AT5G52810 | 10.61 | 0.57 | 27.76 | 0.85 | 1.39 | 5.32E-11 | NO | NO | NO | NO |
| AT5G52870 | 4.59 | 0.05 | 8.44 | 0.06 | 0.88 | 8.73E-03 | NO | NO | NO | NO |
| AT5G52900 | 5.43 | 0.27 | 15.64 | 0.42 | 1.53 | 1.20E-08 | NO | NO | NO | NO |
| AT5G53110 | 2.65 | 0.33 | 9.21 | 0.25 | 1.80 | 2.15E-07 | NO | NO | NO | NO |
| AT5G53170 | 30.48 | 0.40 | 41.70 | 0.35 | 0.45 | 2.23E-02 | NO | NO | NO | NO |
| AT5G53370 | 63.42 | 1.14 | 121.27 | 1.21 | 0.94 | 5.31E-08 | NO | NO | NO | NO |
| AT5G53550 | 29.86 | 0.38 | 61.63 | 1.26 | 1.05 | 0.00E+00 | NO | NO | NO | NO |
| AT5G53760 | 2.34 | 0.03 | 4.10 | 0.08 | 0.81 | 1.27E-02 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G53830 | 2.58 | 0.23 | 5.33 | 0.24 | 1.05 | 4.56E-02 | NO | NO | NO | NO |
| AT5G53870 | 0.84 | 0.34 | 3.34 | 0.52 | 2.00 | 3.25E-04 | NO | NO | NO | NO |
| AT5G53890 | 2.71 | 0.08 | 4.17 | 0.14 | 0.62 | 3.27E-02 | NO | NO | NO | NO |
| AT5G53970 | 18.88 | 0.56 | 28.31 | 0.79 | 0.58 | 4.40E-03 | NO | NO | NO | NO |
| AT5G54080 | 11.61 | 0.04 | 16.49 | 0.16 | 0.51 | 2.86E-02 | NO | NO | NO | NO |
| AT5G54100 | 10.82 | 0.35 | 19.21 | 0.66 | 0.83 | 1.59E-04 | NO | NO | NO | NO |
| AT5G54160 | 45.05 | 1.97 | 184.13 | 0.49 | 2.03 | 0.00E+00 | NO | NO | NO | NO |
| AT5G54380 | 4.77 | 0.23 | 9.85 | 0.24 | 1.05 | 1.55E-06 | NO | NO | NO | NO |
| AT5G54470 | 59.49 | 0.39 | 96.58 | 0.22 | 0.70 | 1.03E-04 | NO | NO | UP | NO |
| AT5G54490 | 6.35 | 1.01 | 33.22 | 0.94 | 2.39 | 2.37E-10 | NO | NO | UP | NO |
| AT5G54510 | 7.54 | 0.22 | 11.11 | 0.74 | 0.56 | 2.05E-02 | NO | NO | NO | NO |
| AT5G54690 | 0.44 | 0.05 | 1.22 | 0.10 | 1.46 | 3.65E-02 | NO | NO | NO | NO |
| AT5G54710 | 26.47 | 0.48 | 86.02 | 1.90 | 1.70 | 0.00E+00 | NO | NO | NO | NO |
| AT5G54860 | 8.76 | 0.24 | 29.24 | 1.00 | 1.74 | 0.00E+00 | NO | NO | NO | NO |
| AT5G54920 | 4.63 | 0.09 | 7.21 | 0.12 | 0.64 | 2.36E-02 | NO | NO | NO | NO |
| AT5G55100 | 11.82 | 0.16 | 16.67 | 0.50 | 0.50 | 2.41E-03 | NO | NO | NO | NO |
| AT5G55300 | 13.31 | 0.38 | 17.75 | 0.20 | 0.42 | 2.75E-02 | NO | NO | NO | NO |
| AT5G55520 | 4.46 | 0.15 | 6.81 | 0.29 | 0.61 | 1.43E-02 | NO | NO | NO | NO |
| AT5G55600 | 12.12 | 0.24 | 16.49 | 0.28 | 0.44 | 9.12E-03 | NO | NO | NO | NO |
| AT5G55730 | 12.41 | 0.90 | 18.23 | 1.41 | 0.55 | 7.60E-03 | NEGATIVE | NO | NO | NO |
| AT5G55850 | 86.59 | 0.66 | 133.15 | 0.60 | 0.62 | 1.71E-06 | NO | NO | NO | NO |
| AT5G55860 | 10.59 | 0.29 | 16.58 | 0.24 | 0.65 | 1.60E-03 | NO | NO | NO | NO |
| AT5G56120 | 8.99 | 0.29 | 16.74 | 1.08 | 0.90 | 5.07E-04 | NO | NO | NO | NO |
| AT5G56240 | 12.92 | 0.21 | 20.24 | 0.25 | 0.65 | 7.11E-06 | NO | NO | NO | NO |
| AT5G56250 | 12.38 | 0.40 | 20.21 | 0.86 | 0.71 | 3.80E-06 | NO | NO | NO | NO |
| AT5G56260 | 73.75 | 0.31 | 104.95 | 0.76 | 0.51 | 7.93E-03 | NO | NO | NO | NO |
| AT5G56270 | 8.26 | 0.25 | 11.62 | 0.11 | 0.49 | 3.09E-02 | NO | YES | NO | NO |
| AT5G56350 | 63.22 | 1.28 | 104.84 | 1.08 | 0.73 | 4.28E-05 | NO | NO | NO | NO |
| AT5G56870 | 0.74 | 0.13 | 3.71 | 0.28 | 2.33 | 1.18E-08 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G57010 | 0.38 | 0.11 | 2.01 | 0.08 | 2.41 | 1.21E-04 | NO | NO | NO | NO |
| AT5G57035 | 9.74 | 0.21 | 16.64 | 0.31 | 0.77 | 7.83E-05 | NO | NO | NO | NO |
| AT5G57123 | 2.77 | 0.15 | 6.81 | 0.95 | 1.30 | 1.59E-02 | NO | NO | NO | NO |
| AT5G57220 | 1.61 | 0.32 | 7.79 | 0.77 | 2.27 | 1.21E-10 | NO | NO | NO | NO |
| AT5G57480 | 2.19 | 0.69 | 7.98 | 0.39 | 1.87 | 4.03E-08 | NO | NO | NO | NO |
| AT5G57510 | 0.69 | 0.52 | 4.20 | 0.85 | 2.61 | 4.04E-02 | NO | NO | NO | NO |
| AT5G57560 | 2.45 | 0.79 | 17.16 | 0.33 | 2.81 | 0.00E+00 | NO | NO | DOWN | NO |
| AT5G57710 | 24.78 | 0.40 | 37.24 | 0.16 | 0.59 | 1.43E-03 | NO | NO | NO | NO |
| AT5G57800 | 16.76 | 0.51 | 40.39 | 0.74 | 1.27 | 8.78E-14 | NO | NO | NO | DOWN |
| AT5G58120 | 5.55 | 0.26 | 8.57 | 0.40 | 0.63 | 5.33E-03 | NO | NO | NO | NO |
| AT5G58220 | 35.37 | 0.58 | 45.46 | 0.19 | 0.36 | 4.65E-02 | NO | NO | NO | NO |
| AT5G58350 | 4.95 | 0.37 | 15.75 | 0.37 | 1.67 | 0.00E+00 | NO | NO | NO | NO |
| AT5G58430 | 33.97 | 0.10 | 47.62 | 0.40 | 0.49 | 1.18E-02 | NO | NO | NO | NO |
| AT5G58710 | 192.36 | 2.89 | 337.11 | 4.58 | 0.81 | 6.72E-06 | NO | NO | NO | NO |
| AT5G58940 | 4.04 | 0.14 | 13.82 | 0.83 | 1.77 | 7.17E-12 | NO | NO | NO | NO |
| AT5G59030 | 60.15 | 0.45 | 89.96 | 1.15 | 0.58 | 3.19E-03 | NO | NO | NO | NO |
| AT5G59070 | 0.32 | 0.08 | 1.72 | 0.10 | 2.43 | 5.01E-04 | NO | NO | NO | NO |
| AT5G59820 | 14.00 | 0.11 | 47.12 | 0.66 | 1.75 | 1.85E-14 | NO | YES | NO | NO |
| AT5G59920 | 4.56 | 0.33 | 9.69 | 0.34 | 1.09 | 9.87E-06 | NO | NO | NO | NO |
| AT5G59960 | 14.90 | 0.18 | 20.62 | 0.39 | 0.47 | 4.42E-02 | NO | NO | NO | NO |
| AT5G60280 | 2.60 | 0.16 | 6.12 | 0.27 | 1.23 | 8.51E-05 | NO | NO | NO | NO |
| AT5G60410 | 27.20 | 0.11 | 35.74 | 0.42 | 0.39 | 4.25E-02 | NO | YES | NO | NO |
| AT5G60800 | 6.52 | 0.40 | 24.58 | 1.00 | 1.91 | 0.00E+00 | NO | NO | NO | NO |
| AT5G60840 | 12.25 | 0.45 | 21.14 | 0.97 | 0.79 | 6.24E-03 | NO | NO | NO | NO |
| AT5G60930 | 2.80 | 0.07 | 4.19 | 0.11 | 0.58 | 3.47E-02 | NO | NO | NO | NO |
| AT5G60950 | 10.05 | 1.18 | 32.43 | 0.54 | 1.69 | 3.11E-13 | NO | NO | NO | NO |
| AT5G61010 | 9.72 | 1.22 | 35.25 | 1.48 | 1.86 | 0.00E+00 | NO | NO | NO | NO |
| AT5G61390 | 4.78 | 0.04 | 7.58 | 0.43 | 0.67 | 3.25E-02 | NO | NO | NO | NO |
| AT5G61560 | 3.84 | 0.11 | 7.88 | 0.31 | 1.04 | 9.76E-07 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G61790 | 153.94 | 2.39 | 505.04 | 11.60 | 1.71 | 0.00E+00 | NO | NO | NO | NO |
| AT5G61900 | 4.84 | 0.10 | 15.13 | 0.14 | 1.64 | 0.00E+00 | NO | NO | NO | NO |
| AT5G62000 | 80.93 | 0.77 | 98.93 | 0.27 | 0.29 | 9.09E-03 | NO | YES | NO | NO |
| AT5G62020 | 1.36 | 0.06 | 7.26 | 0.17 | 2.42 | 1.19E-09 | NO | YES | NO | NO |
| AT5G62150 | 3.91 | 0.59 | 19.35 | 1.55 | 2.31 | 6.44E-07 | NO | NO | NO | NO |
| AT5G62390 | 59.05 | 0.91 | 92.43 | 0.94 | 0.65 | 4.67E-04 | NO | NO | NO | NO |
| AT5G62530 | 25.69 | 0.75 | 39.43 | 0.53 | 0.62 | 9.37E-04 | NO | NO | NO | NO |
| AT5G62540 | 5.57 | 0.25 | 16.79 | 0.02 | 1.59 | 6.29E-07 | NO | NO | NO | NO |
| AT5G62560 | 6.11 | 0.42 | 9.77 | 0.12 | 0.68 | 9.43E-03 | NO | NO | NO | NO |
| AT5G62680 | 21.72 | 0.53 | 31.45 | 0.57 | 0.53 | 6.06E-03 | NO | NO | NO | NO |
| AT5G62770 | 1.65 | 0.30 | 4.81 | 0.28 | 1.55 | 1.84E-03 | NO | NO | NO | NO |
| AT5G63225 | 0.61 | 0.14 | 10.03 | 0.77 | 4.04 | 3.15E-08 | NO | NO | NO | NO |
| AT5G63470 | 19.09 | 0.42 | 31.63 | 0.88 | 0.73 | 3.05E-04 | NO | YES | NO | NO |
| AT5G63490 | 9.75 | 0.20 | 15.36 | 0.31 | 0.66 | 4.00E-03 | NO | NO | NO | NO |
| AT5G63530 | 22.08 | 0.81 | 32.01 | 0.68 | 0.54 | 4.80E-03 | NO | NO | NO | NO |
| AT5G63850 | 7.68 | 0.23 | 24.11 | 0.61 | 1.65 | 0.00E+00 | NO | NO | NO | NO |
| AT5G63950 | 5.52 | 0.17 | 7.68 | 0.17 | 0.48 | 4.50E-02 | NO | NO | NO | NO |
| AT5G63970 | 4.51 | 0.12 | 9.46 | 0.34 | 1.07 | 8.01E-05 | NO | NO | NO | NO |
| AT5G64370 | 24.77 | 0.65 | 42.72 | 0.93 | 0.79 | 2.39E-05 | NO | NO | NO | NO |
| AT5G64510 | 2.11 | 0.11 | 12.75 | 1.36 | 2.59 | 0.00E+00 | NO | NO | NO | NO |
| AT5G64570 | 10.17 | 0.32 | 18.18 | 0.74 | 0.84 | 1.36E-05 | NO | NO | DOWN | DOWN |
| AT5G64572 | 4.10 | 0.21 | 10.46 | 0.67 | 1.35 | 6.33E-06 | NO | NO | NO | NO |
| AT5G64810 | 3.43 | 1.51 | 45.84 | 1.66 | 3.74 | 0.00E+00 | NO | YES | NO | NO |
| AT5G64905 | 0.78 | 0.36 | 3.45 | 0.40 | 2.14 | 3.83E-02 | NO | NO | NO | NO |
| AT5G65210 | 6.23 | 0.07 | 12.88 | 0.54 | 1.05 | 1.32E-07 | NO | YES | NO | NO |
| AT5G65360 | 184.80 | 1.71 | 262.28 | 5.90 | 0.51 | 6.93E-03 | NO | NO | NO | NO |
| AT5G65440 | 6.93 | 0.17 | 12.86 | 0.47 | 0.89 | 2.90E-10 | NO | NO | NO | NO |
| AT5G65660 | 17.87 | 0.48 | 26.80 | 0.74 | 0.58 | 4.00E-02 | NO | NO | NO | NO |
| AT5G66210 | 15.29 | 0.17 | 29.58 | 0.89 | 0.95 | 4.58E-12 | NO | NO | NO | NO |

**Table A3.4 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G66250 | 18.38 | 0.72 | 27.67 | 1.01 | 0.59 | 5.36E-04 | NO | NO | NO | NO |
| AT5G66490 | 7.94 | 0.14 | 21.01 | 0.21 | 1.40 | 3.30E-04 | NO | NO | NO | NO |
| AT5G66600 | 1.32 | 0.03 | 2.50 | 0.08 | 0.93 | 2.09E-02 | NO | NO | NO | NO |
| AT5G66650 | 0.98 | 0.11 | 2.48 | 0.17 | 1.34 | 2.99E-02 | NO | NO | NO | NO |
| AT5G66675 | 21.61 | 0.86 | 30.95 | 0.43 | 0.52 | 1.09E-02 | NO | NO | NO | NO |
| AT5G66730 | 15.36 | 0.30 | 25.01 | 0.37 | 0.70 | 2.16E-04 | NO | YES | NO | NO |
| AT5G66850 | 9.67 | 0.09 | 19.04 | 0.17 | 0.98 | 1.75E-07 | NO | NO | NO | NO |
| AT5G66880 | 1.88 | 0.06 | 5.09 | 0.04 | 1.44 | 4.42E-04 | NO | NO | DOWN | NO |
| AT5G66910 | 7.57 | 0.33 | 15.89 | 0.47 | 1.07 | 5.85E-08 | NO | NO | NO | NO |
| AT5G67080 | 0.06 | 0.03 | 1.01 | 0.34 | 4.05 | 7.00E-03 | NO | NO | NO | NO |
| AT5G67340 | 3.51 | 0.34 | 19.90 | 0.38 | 2.50 | 0.00E+00 | NO | NO | NO | NO |
| AT5G67420 | 3.14 | 0.18 | 7.90 | 0.26 | 1.33 | 1.39E-05 | NO | YES | NO | NO |
| AT5G67450 | 0.44 | 0.12 | 2.20 | 0.30 | 2.31 | 1.83E-03 | NO | YES | NO | NO |
| AT5G67470 | 10.22 | 0.27 | 24.74 | 0.53 | 1.27 | 2.95E-13 | NO | NO | NO | NO |

**Table A3.5**. 294 Category 2 FTD Candidate Genes with higher expression in SW at 2 weeks of cold-acclimations. Genes are ordered by their AGI numbers. FPKM values are the average of three biological replicates (n=3). Genes were considered significantly different between SW and IT under non-acclimated conditions if they had a Benjamini-Hochberg corrected p-value (FDR P-VALUE) of <0.05 and a minimum of ≥3FPKM in IT. The differential expression of each gene is also represented by the logarithm (base=2) of the fold change (LOG2.FC). This table also denotes if a gene was previously described as positively or negatively correlating with freezing tolerance (HANNAH;(6)), a transcription factor (TF), a gene previously described as up- or down-regulated by 1 week of cold (COS, (25)), identified as an up- or down-regulated component of the CBF regulon (CBF REGULON; (25)).

| AGI | SW.1WK FPKM | SW.2WK FPKM | IT.1WK FPKM | IT.2WK FPKM | SW.IT.2WK LOG2FC | SW.IT.2 WK. FDR P-VALUE | HANNAH? | TF? | COS? | CBF REG? |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G01470 | 860.51 | 681.04 | 395.24 | 310.44 | -1.13 | 4.71E-11 | POSITIVE | NO | POSITIVE | UP |
| AT1G01670 | 4.42 | 4.79 | 1.48 | 1.77 | -1.44 | 1.32E-03 | NO | NO | NO | NO |
| AT1G02270 | 36.59 | 39.27 | 18.62 | 24.02 | -0.71 | 1.62E-04 | POSITIVE | NO | NO | NO |
| AT1G03420 | 54.53 | 87.54 | 6.17 | 6.24 | -3.81 | 0.00E+00 | NO | NO | NO | NO |
| AT1G04310 | 5.13 | 5.63 | 2.19 | 3.21 | -0.81 | 4.32E-03 | NO | NO | NO | NO |
| AT1G05320 | 0.00 | 12.32 | 7.15 | 6.21 | -0.99 | 1.13E-06 | NO | NO | NO | NO |
| AT1G05560 | 25.14 | 8.34 | 7.14 | 4.73 | -0.82 | 5.34E-03 | NO | NO | NO | NO |
| AT1G07702 | 0.00 | 319.82 | 646.35 | 278.55 | -0.20 | 1.64E-02 | NO | NO | NO | NO |
| AT1G09350 | 206.56 | 355.61 | 20.52 | 25.87 | -3.78 | 0.00E+00 | POSITIVE | NO | POSITIVE | UP |
| AT1G10070 | 31.71 | 20.16 | 3.71 | 7.82 | -1.37 | 1.67E-12 | NO | NO | NO | NO |
| AT1G11580 | 115.76 | 35.72 | 30.41 | 16.33 | -1.13 | 1.92E-10 | NO | NO | NO | NO |
| AT1G11840 | 479.73 | 534.98 | 343.20 | 304.91 | -0.81 | 0.00E+00 | NO | NO | NO | NO |
| AT1G12350 | 39.94 | 41.62 | 18.57 | 20.08 | -1.05 | 2.72E-08 | NO | NO | NO | NO |
| AT1G12470 | 32.76 | 33.36 | 8.40 | 11.38 | -1.55 | 0.00E+00 | NO | NO | NO | NO |
| AT1G12550 | 11.72 | 12.29 | 4.21 | 5.05 | -1.28 | 2.17E-05 | NO | NO | NO | NO |
| AT1G13080 | 8.86 | 9.67 | 2.89 | 2.43 | -1.99 | 3.65E-11 | NO | NO | DOWN | NO |

**Table A3.5 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G15125 | 90.96 | 117.61 | 20.60 | 55.00 | -1.10 | 1.13E-09 | NO | NO | NO | NO |
| AT1G16850 | 248.49 | 276.40 | 117.34 | 48.76 | -2.50 | 0.00E+00 | POSITIVE | NO | POSITIVE | UP |
| AT1G20440 | 1586.75 | 1453.90 | 279.94 | 254.60 | -2.51 | 0.00E+00 | NO | NO | POSITIVE | UP |
| AT1G20450 | 758.00 | 712.70 | 196.22 | 182.55 | -1.96 | 0.00E+00 | NO | NO | POSITIVE | UP |
| AT1G20620 | 1910.93 | 1991.20 | 845.84 | 1107.69 | -0.85 | 8.97E-05 | NO | NO | NO | NO |
| AT1G20693 | 229.74 | 294.79 | 134.25 | 169.80 | -0.80 | 2.94E-09 | POSITIVE | YES | POSITIVE | NO |
| AT1G21130 | 74.08 | 94.42 | 31.10 | 54.55 | -0.79 | 3.87E-06 | NO | NO | NO | NO |
| AT1G22070 | 40.66 | 39.26 | 21.22 | 27.46 | -0.52 | 9.18E-03 | POSITIVE | YES | NO | NO |
| AT1G22090 | 11.46 | 4.70 | 0.06 | 0.00 | #NAME? | 1.01E-09 | NO | NO | NO | NO |
| AT1G22360 | 14.46 | 15.20 | 6.76 | 8.43 | -0.85 | 1.35E-04 | NO | NO | NO | NO |
| AT1G22370 | 4.66 | 6.20 | 0.98 | 1.19 | -2.38 | 2.29E-08 | NO | NO | NO | NO |
| AT1G22403 | 25.06 | 22.12 | 11.54 | 9.38 | -1.24 | 1.13E-07 | NO | NO | NO | NO |
| AT1G23120 | 12.85 | 8.81 | 0.84 | 0.65 | -3.76 | 2.99E-07 | NO | NO | NO | NO |
| AT1G23800 | 30.15 | 19.22 | 8.99 | 9.74 | -0.98 | 9.62E-07 | NO | NO | NO | NO |
| AT1G23950 | 11.82 | 11.84 | 0.91 | 0.93 | -3.68 | 0.00E+00 | NO | NO | NO | NO |
| AT1G24370 | 91.85 | 88.30 | 0.11 | 0.24 | -8.54 | 0.00E+00 | NO | NO | NO | NO |
| AT1G24388 | 266.65 | 258.07 | 0.08 | 0.51 | -8.99 | 0.00E+00 | NO | NO | NO | NO |
| AT1G27200 | 31.50 | 49.45 | 10.57 | 14.74 | -1.75 | 0.00E+00 | POSITIVE | NO | POSITIVE | UP |
| AT1G28330 | 40.21 | 50.56 | 11.34 | 14.56 | -1.80 | 2.09E-12 | NO | NO | NO | NO |
| AT1G28570 | 5.72 | 6.05 | 1.92 | 2.52 | -1.26 | 8.58E-04 | NO | NO | NO | NO |
| AT1G29050 | 19.81 | 14.62 | 8.38 | 8.27 | -0.82 | 8.25E-04 | NO | NO | NO | NO |
| AT1G29395 | 274.36 | 455.70 | 59.17 | 81.93 | -2.48 | 0.00E+00 | POSITIVE | NO | POSITIVE | UP |
| AT1G33170 | 19.38 | 25.16 | 10.34 | 9.93 | -1.34 | 1.53E-13 | NO | NO | NO | NO |
| AT1G33970 | 65.18 | 68.70 | 39.41 | 47.81 | -0.52 | 4.51E-04 | NO | NO | NO | NO |
| AT1G36180 | 3.01 | 2.76 | 0.48 | 0.58 | -2.25 | 0.00E+00 | NO | NO | NO | NO |
| AT1G42705 | 4.43 | 4.66 | 0.02 | 0.03 | -7.35 | 6.20E-11 | NO | NO | NO | NO |
| AT1G46768 | 17.71 | 24.76 | 6.34 | 9.53 | -1.38 | 3.00E-07 | NO | YES | POSITIVE | UP |
| AT1G48100 | 17.68 | 21.78 | 8.46 | 7.98 | -1.45 | 4.19E-13 | NO | NO | NO | UP |
| AT1G48360 | 16.64 | 15.13 | 3.81 | 3.85 | -1.97 | 0.00E+00 | NO | NO | NO | NO |

**Table A3.5 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G52720 | 13.55 | 14.24 | 4.47 | 6.57 | -1.12 | 2.33E-03 | NO | NO | DOWN | NO |
| AT1G53230 | 63.17 | 61.66 | 32.14 | 43.05 | -0.52 | 6.50E-03 | NO | YES | NO | NO |
| AT1G53580 | 61.84 | 51.09 | 27.46 | 29.98 | -0.77 | 1.92E-07 | POSITIVE | NO | NO | NO |
| AT1G54160 | 9.68 | 9.02 | 3.41 | 4.19 | -1.11 | 2.71E-04 | NO | YES | NO | NO |
| AT1G54890 | 5.08 | 0.86 | 0.30 | 0.11 | -2.95 | 2.20E-02 | NO | NO | NO | NO |
| AT1G56650 | 12.38 | 10.34 | 3.80 | 3.04 | -1.77 | 2.03E-05 | POSITIVE | YES | NO | NO |
| AT1G58300 | 3.47 | 8.24 | 0.52 | 2.37 | -1.79 | 2.14E-04 | NO | NO | NO | NO |
| AT1G58602 | 14.28 | 12.14 | 4.84 | 8.79 | -0.47 | 1.91E-02 | NO | NO | NO | NO |
| AT1G59950 | 16.46 | 5.90 | 0.38 | 0.37 | -3.99 | 5.27E-07 | NO | NO | NO | NO |
| AT1G60730 | 62.87 | 38.04 | 12.23 | 20.07 | -0.92 | 9.68E-11 | NO | NO | NO | NO |
| AT1G61800 | 93.26 | 112.94 | 35.70 | 48.16 | -1.23 | 7.05E-14 | NO | NO | NO | NO |
| AT1G62560 | 50.21 | 31.44 | 19.12 | 9.55 | -1.72 | 0.00E+00 | NO | NO | NO | NO |
| AT1G62570 | 49.71 | 82.13 | 14.01 | 13.92 | -2.56 | 0.00E+00 | POSITIVE | NO | POSITIVE | UP |
| AT1G63350 | 4.30 | 3.67 | 0.01 | 0.01 | -8.37 | 2.54E-07 | NO | NO | NO | NO |
| AT1G64660 | 23.05 | 17.76 | 5.64 | 11.60 | -0.61 | 5.86E-03 | NO | NO | NO | NO |
| AT1G64760 | 11.68 | 15.90 | 5.21 | 5.68 | -1.49 | 2.04E-11 | NO | NO | NO | NO |
| AT1G64780 | 8.52 | 6.00 | 2.43 | 1.58 | -1.93 | 1.49E-07 | NO | NO | NO | NO |
| AT1G64890 | 17.73 | 21.38 | 7.90 | 11.83 | -0.85 | 2.63E-05 | NO | NO | POSITIVE | UP |
| AT1G65980 | 236.37 | 270.97 | 105.14 | 134.32 | -1.01 | 8.23E-10 | NO | NO | NO | NO |
| AT1G67265 | 3.90 | 4.83 | 0.87 | 1.67 | -1.54 | 3.73E-02 | NO | NO | NO | NO |
| AT1G68500 | 44.40 | 56.74 | 15.61 | 11.79 | -2.27 | 1.04E-13 | NO | NO | POSITIVE | UP |
| AT1G68600 | 15.27 | 20.41 | 2.30 | 6.53 | -1.64 | 0.00E+00 | NO | NO | NO | NO |
| AT1G69720 | 23.25 | 14.10 | 1.43 | 1.32 | -3.41 | 0.00E+00 | NO | NO | NO | NO |
| AT1G69890 | 21.94 | 20.69 | 4.40 | 6.55 | -1.66 | 1.41E-11 | NO | NO | NO | NO |
| AT1G70260 | 4.97 | 10.70 | 0.88 | 2.85 | -1.91 | 1.81E-09 | NO | NO | NO | NO |
| AT1G70645 | 14.14 | 14.74 | 0.00 | 0.00 | #NAME? | 0.00E+00 | NO | NO | NO | NO |
| AT1G70830 | 159.30 | 82.01 | 59.25 | 51.81 | -0.66 | 1.27E-02 | NO | NO | NO | NO |
| AT1G71340 | 23.51 | 25.02 | 2.21 | 2.47 | -3.34 | 0.00E+00 | NO | NO | NO | NO |
| AT1G71360 | 13.66 | 17.15 | 7.05 | 9.28 | -0.89 | 6.96E-06 | NO | NO | NO | NO |

**Table A3.5 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G72830 | 8.37 | 6.31 | 1.76 | 2.88 | -1.13 | 3.94E-04 | NO | YES | NO | NO |
| AT1G75370 | 50.02 | 63.64 | 25.50 | 36.75 | -0.79 | 9.35E-06 | NO | NO | POSITIVE | UP |
| AT1G76180 | 811.66 | 855.55 | 369.49 | 390.72 | -1.13 | 0.00E+00 | NO | NO | NO | NO |
| AT1G76520 | 111.41 | 68.90 | 34.18 | 45.27 | -0.61 | 6.78E-05 | NO | NO | NO | NO |
| AT1G76530 | 3.57 | 2.97 | 0.89 | 1.28 | -1.22 | 2.82E-02 | NO | NO | NO | NO |
| AT1G76580 | 16.90 | 20.00 | 6.47 | 8.75 | -1.19 | 1.13E-11 | NO | NO | POSITIVE | UP |
| AT1G76590 | 47.44 | 51.12 | 18.99 | 19.72 | -1.37 | 1.04E-13 | POSITIVE | YES | POSITIVE | UP |
| AT1G76820 | 2.76 | 3.58 | 0.16 | 0.23 | -3.95 | 0.00E+00 | NO | NO | NO | NO |
| AT1G77120 | 381.80 | 355.69 | 150.04 | 111.48 | -1.67 | 0.00E+00 | NO | NO | POSITIVE | NO |
| AT1G78070 | 117.52 | 140.91 | 45.46 | 43.89 | -1.68 | 0.00E+00 | NO | NO | POSITIVE | UP |
| AT1G80130 | 293.11 | 554.44 | 153.50 | 213.76 | -1.38 | 3.67E-14 | POSITIVE | NO | POSITIVE | UP |
| AT1G80570 | 3.70 | 4.21 | 0.45 | 0.98 | -2.10 | 4.21E-07 | NO | NO | NO | NO |
| AT2G05380 | 2196.17 | 2680.92 | 529.44 | 1140.20 | -1.23 | 4.18E-09 | POSITIVE | NO | NO | NO |
| AT2G05510 | 25.45 | 8.77 | 3.06 | 0.87 | -3.34 | 5.61E-08 | NO | NO | NO | NO |
| AT2G12190 | 6.12 | 9.06 | 0.78 | 0.93 | -3.29 | 1.87E-14 | NO | NO | NO | NO |
| AT2G15050 | 98.77 | 122.57 | 23.52 | 17.40 | -2.82 | 0.00E+00 | NO | NO | DOWN | NO |
| AT2G15970 | 1564.76 | 1562.47 | 590.27 | 517.44 | -1.59 | 0.00E+00 | NO | NO | POSITIVE | UP |
| AT2G16700 | 140.34 | 151.38 | 42.67 | 37.97 | -2.00 | 0.00E+00 | NO | NO | NO | UP |
| AT2G16790 | 4.99 | 3.53 | 0.84 | 0.91 | -1.96 | 3.37E-03 | POSITIVE | NO | NO | NO |
| AT2G17280 | 25.98 | 31.01 | 11.91 | 13.10 | -1.24 | 3.14E-09 | NO | NO | NO | NO |
| AT2G17840 | 143.48 | 201.80 | 76.61 | 111.57 | -0.86 | 1.10E-06 | POSITIVE | NO | POSITIVE | UP |
| AT2G18110 | 88.39 | 80.23 | 19.27 | 18.10 | -2.15 | 0.00E+00 | NO | NO | NO | NO |
| AT2G19810 | 27.19 | 60.23 | 11.08 | 14.26 | -2.08 | 0.00E+00 | NO | YES | NO | NO |
| AT2G21620 | 384.16 | 262.42 | 144.60 | 155.70 | -0.75 | 2.19E-05 | POSITIVE | NO | POSITIVE | NO |
| AT2G21830 | 1.05 | 1.03 | 0.25 | 0.19 | -2.46 | 3.46E-03 | NO | NO | NO | NO |
| AT2G21860 | 26.96 | 28.21 | 12.70 | 15.56 | -0.86 | 8.85E-06 | NO | NO | NO | NO |
| AT2G22590 | 7.67 | 5.03 | 1.30 | 0.78 | -2.68 | 1.13E-07 | NO | NO | NO | NO |
| AT2G22660 | 39.60 | 42.29 | 14.10 | 21.58 | -0.97 | 6.09E-09 | NO | NO | NO | NO |
| AT2G25510 | 8645.94 | 10643.80 | 25.11 | 40.26 | -8.05 | 0.00E+00 | NO | NO | NO | NO |

**Table A3.5 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT2G26010 | 154.12 | 237.06 | 5.34 | 66.62 | -1.83 | 0.00E+00 | NO | NO | NO | NO |
| AT2G27360 | 16.91 | 13.50 | 5.04 | 5.83 | -1.21 | 3.39E-06 | NO | NO | NO | NO |
| AT2G28550 | 124.43 | 155.52 | 79.16 | 77.01 | -1.01 | 0.00E+00 | NO | YES | NO | NO |
| AT2G28900 | 983.81 | 1399.48 | 424.69 | 418.81 | -1.74 | 0.00E+00 | NO | NO | POSITIVE | UP |
| AT2G29420 | 69.20 | 29.94 | 16.50 | 16.50 | -0.86 | 2.25E-04 | NO | NO | NO | NO |
| AT2G33830 | 770.26 | 840.49 | 310.33 | 457.27 | -0.88 | 4.66E-07 | NO | NO | NO | NO |
| AT2G34655 | 15.00 | 13.25 | 1.64 | 3.16 | -2.07 | 1.31E-07 | NO | NO | NO | NO |
| AT2G36750 | 18.28 | 13.69 | 6.88 | 6.50 | -1.08 | 2.88E-05 | NO | NO | NO | NO |
| AT2G39850 | 18.21 | 5.47 | 9.57 | 2.53 | -1.11 | 8.11E-05 | NO | NO | DOWN | NO |
| AT2G40010 | 19.08 | 15.02 | 0.08 | 0.04 | -8.39 | 0.00E+00 | NO | NO | NO | NO |
| AT2G41010 | 21.54 | 23.95 | 8.92 | 15.99 | -0.58 | 2.54E-02 | NO | NO | NO | NO |
| AT2G43500 | 29.93 | 32.48 | 7.46 | 8.71 | -1.90 | 0.00E+00 | NO | YES | NO | NO |
| AT2G46440 | 10.37 | 12.40 | 0.12 | 0.17 | -6.18 | 0.00E+00 | NO | NO | NO | NO |
| AT2G46640 | 13.72 | 11.32 | 5.53 | 5.66 | -1.00 | 5.32E-04 | NO | NO | NO | NO |
| AT2G47180 | 78.66 | 46.04 | 32.40 | 33.14 | -0.47 | 1.80E-02 | NO | NO | POSITIVE | NO |
| AT2G47890 | 55.55 | 54.56 | 25.76 | 26.51 | -1.04 | 1.43E-09 | NO | YES | POSITIVE | UP |
| AT3G05660 | 12.07 | 17.35 | 4.81 | 8.32 | -1.06 | 9.44E-09 | POSITIVE | NO | POSITIVE | UP |
| AT3G05880 | 500.06 | 397.98 | 255.71 | 207.90 | -0.94 | 5.80E-08 | NO | NO | NO | NO |
| AT3G07320 | 29.83 | 36.52 | 12.44 | 16.28 | -1.17 | 3.73E-11 | NO | NO | NO | NO |
| AT3G09030 | 10.86 | 11.55 | 4.69 | 7.64 | -0.60 | 2.10E-02 | NO | NO | NO | NO |
| AT3G12500 | 88.88 | 14.23 | 2.97 | 2.32 | -2.62 | 3.08E-12 | NO | NO | NO | NO |
| AT3G13310 | 139.98 | 99.33 | 73.66 | 67.80 | -0.55 | 4.37E-03 | NO | NO | NO | NO |
| AT3G14150 | 26.04 | 33.95 | 9.28 | 7.60 | -2.16 | 0.00E+00 | NO | NO | NO | NO |
| AT3G14940 | 2.95 | 3.54 | 0.76 | 0.44 | -3.02 | 6.29E-12 | NO | NO | NO | NO |
| AT3G17130 | 17.49 | 20.53 | 5.51 | 4.50 | -2.19 | 1.29E-06 | NO | NO | POSITIVE | UP |
| AT3G19000 | 10.79 | 9.13 | 0.19 | 0.11 | -6.32 | 7.52E-13 | NO | NO | DOWN | NO |
| AT3G20100 | 50.62 | 49.57 | 9.41 | 13.66 | -1.86 | 0.00E+00 | NO | NO | NO | NO |
| AT3G21500 | 5.26 | 2.57 | 1.11 | 1.21 | -1.09 | 1.66E-02 | NO | NO | NO | NO |
| AT3G22121 | 284.13 | 267.25 | 127.46 | 138.18 | -0.95 | 7.73E-09 | NO | NO | NO | NO |

**Table A3.5 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G22142 | 62.20 | 68.17 | 15.80 | 15.85 | -2.10 | 0.00E+00 | NO | NO | NO | NO |
| AT3G22840 | 290.33 | 502.14 | 155.08 | 275.06 | -0.87 | 9.46E-07 | NO | NO | POSITIVE | NO |
| AT3G26200 | 4.37 | 4.70 | 1.26 | 2.37 | -0.99 | 1.09E-02 | NO | NO | NO | NO |
| AT3G26280 | 21.27 | 30.61 | 4.24 | 5.35 | -2.52 | 0.00E+00 | NO | NO | NO | NO |
| AT3G26460 | 8.02 | 14.62 | 1.96 | 0.56 | -4.71 | 2.35E-10 | NO | NO | NO | NO |
| AT3G26740 | 395.85 | 342.98 | 210.41 | 232.47 | -0.56 | 1.99E-03 | NO | NO | NO | NO |
| AT3G27210 | 61.39 | 59.15 | 33.67 | 31.14 | -0.93 | 5.83E-07 | NO | NO | POSITIVE | UP |
| AT3G28050 | 38.00 | 36.73 | 15.92 | 18.24 | -1.01 | 4.87E-08 | NO | NO | DOWN | NO |
| AT3G28310 | 66.01 | 102.25 | 8.89 | 19.27 | -2.41 | 5.94E-10 | NO | NO | NO | NO |
| AT3G28320 | 66.81 | 100.01 | 8.45 | 20.41 | -2.29 | 0.00E+00 | NO | NO | NO | NO |
| AT3G28740 | 51.78 | 22.67 | 13.17 | 7.37 | -1.62 | 1.86E-14 | NO | NO | NO | NO |
| AT3G28880 | 3.16 | 2.37 | 0.66 | 0.55 | -2.12 | 2.98E-05 | NO | NO | NO | NO |
| AT3G28950 | 21.18 | 22.38 | 3.62 | 6.36 | -1.82 | 8.41E-10 | NO | NO | NO | NO |
| AT3G32230 | 1.01 | 0.86 | 0.07 | 0.14 | -2.66 | 2.85E-05 | NO | NO | NO | NO |
| AT3G42658 | 67.13 | 104.06 | 32.11 | 42.18 | -1.30 | 5.38E-14 | NO | NO | NO | NO |
| AT3G42670 | 4.84 | 6.40 | 1.84 | 2.54 | -1.34 | 3.09E-09 | NO | NO | NO | NO |
| AT3G43270 | 17.69 | 14.11 | 8.23 | 9.50 | -0.57 | 1.07E-02 | NO | NO | NO | NO |
| AT3G43520 | 139.84 | 124.49 | 67.75 | 58.99 | -1.08 | 1.97E-10 | NO | NO | NO | NO |
| AT3G44430 | 56.06 | 48.19 | 23.73 | 15.08 | -1.68 | 0.00E+00 | NO | NO | NO | NO |
| AT3G44620 | 49.51 | 51.93 | 17.68 | 27.22 | -0.93 | 5.26E-08 | NO | NO | NO | NO |
| AT3G44670 | 11.85 | 10.44 | 2.07 | 3.25 | -1.69 | 0.00E+00 | NO | NO | NO | NO |
| AT3G45600 | 195.08 | 188.10 | 67.28 | 62.81 | -1.58 | 0.00E+00 | NO | NO | NO | UP |
| AT3G46370 | 5.16 | 5.55 | 0.02 | 0.03 | -7.76 | 3.32E-12 | NO | NO | NO | NO |
| AT3G46490 | 6.08 | 5.35 | 0.64 | 0.33 | -4.01 | 3.80E-07 | NO | NO | NO | DOWN |
| AT3G46900 | 11.73 | 16.32 | 0.87 | 3.25 | -2.33 | 7.17E-07 | NO | NO | NO | NO |
| AT3G49130 | 6.46 | 0.39 | 0.08 | 0.00 | #NAME? | 4.62E-02 | NO | NO | NO | NO |
| AT3G50660 | 15.34 | 20.44 | 6.46 | 5.65 | -1.85 | 0.00E+00 | NO | NO | NO | NO |
| AT3G50970 | 1609.21 | 1188.91 | 341.83 | 260.26 | -2.19 | 0.00E+00 | POSITIVE | NO | POSITIVE | UP |
| AT3G52180 | 189.78 | 255.58 | 105.04 | 85.09 | -1.59 | 0.00E+00 | POSITIVE | NO | NO | NO |

**Table A3.5 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G52340 | 33.54 | 40.29 | 19.25 | 19.78 | -1.03 | 3.11E-13 | NO | NO | NO | NO |
| AT3G53990 | 279.86 | 311.84 | 114.72 | 174.88 | -0.83 | 1.09E-06 | NO | NO | POSITIVE | UP |
| AT3G55760 | 41.67 | 43.58 | 13.09 | 11.50 | -1.92 | 0.00E+00 | NO | NO | POSITIVE | UP |
| AT3G55940 | 9.05 | 11.01 | 2.48 | 3.51 | -1.65 | 7.06E-10 | POSITIVE | NO | NO | UP |
| AT3G57460 | 3.48 | 1.36 | 0.05 | 0.06 | -4.39 | 6.99E-04 | NO | NO | NO | NO |
| AT3G57470 | 6.32 | 6.45 | 0.01 | 0.01 | -9.02 | 6.31E-11 | NO | NO | NO | NO |
| AT3G61010 | 5.86 | 5.94 | 0.04 | 0.02 | -8.57 | 1.16E-07 | NO | NO | NO | NO |
| AT3G62740 | 11.79 | 8.31 | 2.01 | 1.13 | -2.88 | 2.66E-11 | NO | NO | POSITIVE | UP |
| AT4G01390 | 27.40 | 11.43 | 2.02 | 1.18 | -3.27 | 7.05E-10 | NO | NO | NO | NO |
| AT4G01500 | 3.12 | 3.28 | 0.47 | 0.37 | -3.16 | 2.24E-06 | NO | YES | NO | NO |
| AT4G01883 | 31.74 | 28.09 | 14.55 | 11.71 | -1.26 | 7.97E-09 | NO | NO | NO | NO |
| AT4G01985 | 43.10 | 39.78 | 22.05 | 25.57 | -0.64 | 8.44E-04 | NO | NO | NO | NO |
| AT4G04020 | 140.38 | 104.74 | 64.25 | 46.93 | -1.16 | 2.33E-12 | NO | NO | NO | NO |
| AT4G04340 | 59.98 | 72.58 | 35.33 | 33.33 | -1.12 | 7.37E-13 | NO | NO | NO | NO |
| AT4G04426 | 1.37 | 1.62 | 0.02 | 0.02 | -6.36 | 1.32E-05 | NO | NO | NO | NO |
| AT4G04925 | 35.49 | 48.77 | 10.47 | 14.77 | -1.72 | 7.59E-12 | NO | NO | NO | NO |
| AT4G05090 | 42.87 | 49.63 | 23.20 | 25.25 | -0.97 | 4.92E-08 | NO | NO | NO | NO |
| AT4G06746 | 39.58 | 62.79 | 7.68 | 17.34 | -1.86 | 3.68E-14 | NO | YES | NO | NO |
| AT4G08390 | 366.40 | 269.16 | 178.17 | 195.65 | -0.46 | 2.69E-03 | NO | NO | NO | NO |
| AT4G09020 | 119.34 | 208.91 | 52.11 | 63.04 | -1.73 | 0.00E+00 | POSITIVE | NO | NO | NO |
| AT4G09760 | 42.74 | 51.58 | 20.32 | 23.53 | -1.13 | 1.89E-14 | NO | NO | NO | NO |
| AT4G10955 | 0.18 | 0.85 | 1.88 | 0.17 | -2.36 | 3.35E-03 | NO | NO | NO | NO |
| AT4G11410 | 14.71 | 15.88 | 6.93 | 9.76 | -0.70 | 5.67E-03 | NO | NO | NO | NO |
| AT4G14270 | 73.23 | 97.47 | 22.41 | 34.73 | -1.49 | 0.00E+00 | NO | NO | NO | NO |
| AT4G14580 | 49.50 | 69.76 | 10.86 | 13.06 | -2.42 | 0.00E+00 | NO | NO | NO | NO |
| AT4G15130 | 51.50 | 63.98 | 24.88 | 27.19 | -1.23 | 3.10E-12 | NO | NO | POSITIVE | NO |
| AT4G15450 | 41.96 | 43.04 | 16.95 | 19.21 | -1.16 | 3.94E-10 | NO | NO | NO | NO |
| AT4G15910 | 324.05 | 169.33 | 57.83 | 28.33 | -2.58 | 0.00E+00 | NO | NO | NO | NO |
| AT4G16146 | 71.67 | 76.17 | 35.84 | 33.41 | -1.19 | 2.38E-09 | NO | NO | NO | NO |

**Table A3.5 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT4G16770 | 6.40 | 6.99 | 1.47 | 1.52 | -2.20 | 2.16E-06 | NO | NO | NO | NO |
| AT4G16860 | 10.83 | 11.75 | 3.69 | 5.46 | -1.11 | 1.81E-08 | NO | NO | NO | NO |
| AT4G16890 | 15.95 | 17.33 | 8.26 | 12.80 | -0.44 | 3.18E-02 | NO | NO | NO | NO |
| AT4G18070 | 78.00 | 87.26 | 44.90 | 40.40 | -1.11 | 0.00E+00 | NO | NO | NO | NO |
| AT4G18422 | 432.66 | 441.74 | 214.21 | 128.37 | -1.78 | 0.00E+00 | NO | NO | NO | NO |
| AT4G19500 | 7.58 | 8.92 | 0.29 | 0.28 | -5.01 | 0.00E+00 | NO | NO | NO | NO |
| AT4G19510 | 9.68 | 10.76 | 0.56 | 0.82 | -3.71 | 0.00E+00 | NO | NO | NO | NO |
| AT4G20310 | 6.39 | 6.12 | 3.00 | 2.46 | -1.31 | 1.40E-05 | NO | NO | NO | NO |
| AT4G23600 | 306.42 | 161.04 | 139.73 | 76.29 | -1.08 | 0.00E+00 | NO | NO | NO | NO |
| AT4G23670 | 218.14 | 153.99 | 116.61 | 37.05 | -2.06 | 0.00E+00 | NO | NO | DOWN | NO |
| AT4G23920 | 23.15 | 27.67 | 9.43 | 7.47 | -1.89 | 0.00E+00 | NO | NO | POSITIVE | UP |
| AT4G24220 | 123.54 | 159.79 | 58.60 | 113.38 | -0.49 | 9.56E-03 | NO | NO | NO | UP |
| AT4G25433 | 24.84 | 27.81 | 4.75 | 3.80 | -2.87 | 5.41E-13 | NO | NO | NO | NO |
| AT4G26255 | 13.33 | 12.39 | 1.06 | 1.28 | -3.28 | 1.68E-13 | NO | NO | NO | NO |
| AT4G27050 | 61.39 | 51.93 | 17.22 | 13.57 | -1.94 | 0.00E+00 | NO | NO | NO | NO |
| AT4G27070 | 21.11 | 17.59 | 6.40 | 7.24 | -1.28 | 5.37E-10 | NO | NO | NO | NO |
| AT4G27300 | 38.86 | 42.74 | 17.91 | 22.41 | -0.93 | 3.01E-07 | NO | NO | NO | NO |
| AT4G27820 | 26.99 | 25.91 | 9.04 | 6.87 | -1.91 | 0.00E+00 | NO | NO | NO | NO |
| AT4G27900 | 36.63 | 36.02 | 14.78 | 19.58 | -0.88 | 6.66E-07 | NO | YES | NO | NO |
| AT4G27970 | 7.02 | 7.58 | 2.42 | 2.70 | -1.49 | 7.74E-06 | NO | NO | NO | NO |
| AT4G28220 | 40.47 | 50.86 | 22.04 | 26.26 | -0.95 | 2.72E-08 | NO | NO | NO | NO |
| AT4G30830 | 16.39 | 28.21 | 2.86 | 2.86 | -3.30 | 0.00E+00 | POSITIVE | NO | POSITIVE | UP |
| AT4G31620 | 2.97 | 3.92 | 0.92 | 1.17 | -1.74 | 9.52E-05 | NO | YES | NO | NO |
| AT4G33070 | 34.90 | 33.52 | 6.76 | 7.35 | -2.19 | 0.00E+00 | NO | NO | POSITIVE | NO |
| AT4G33180 | 12.63 | 11.48 | 4.53 | 4.75 | -1.27 | 2.32E-05 | NO | NO | NO | NO |
| AT4G34530 | 7.88 | 10.98 | 3.13 | 1.24 | -3.14 | 4.19E-13 | NO | YES | NO | NO |
| AT4G35300 | 73.80 | 100.64 | 42.49 | 48.10 | -1.07 | 0.00E+00 | POSITIVE | NO | POSITIVE | NO |
| AT4G36010 | 24.92 | 24.96 | 12.24 | 9.93 | -1.33 | 1.82E-11 | NO | NO | POSITIVE | UP |
| AT4G37000 | 51.43 | 60.46 | 25.14 | 27.52 | -1.14 | 4.72E-10 | NO | NO | NO | NO |

**Table A3.5 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT4G38580 | 141.00 | 144.43 | 67.73 | 78.34 | -0.88 | 6.67E-07 | NO | NO | POSITIVE | NO |
| AT4G39210 | 27.59 | 45.44 | 12.45 | 18.03 | -1.33 | 0.00E+00 | POSITIVE | NO | NO | NO |
| AT4G39800 | 406.75 | 514.02 | 199.33 | 216.45 | -1.25 | 3.00E-10 | NO | NO | POSITIVE | NO |
| AT5G01600 | 335.37 | 344.75 | 93.33 | 147.02 | -1.23 | 3.32E-12 | NO | NO | NO | NO |
| AT5G02130 | 29.98 | 29.53 | 13.36 | 13.82 | -1.10 | 1.95E-08 | POSITIVE | NO | NO | NO |
| AT5G03350 | 180.08 | 302.99 | 56.15 | 109.48 | -1.47 | 0.00E+00 | NO | NO | NO | NO |
| AT5G05270 | 96.18 | 104.41 | 56.56 | 46.33 | -1.17 | 0.00E+00 | NO | NO | NO | NO |
| AT5G07010 | 21.10 | 36.05 | 2.52 | 2.44 | -3.88 | 0.00E+00 | NO | NO | NO | NO |
| AT5G08640 | 94.23 | 86.83 | 42.40 | 35.48 | -1.29 | 3.61E-14 | NO | NO | NO | NO |
| AT5G10140 | 145.95 | 86.18 | 41.81 | 28.39 | -1.60 | 0.00E+00 | NO | YES | NO | NO |
| AT5G13750 | 34.18 | 18.68 | 12.68 | 11.19 | -0.74 | 9.00E-05 | POSITIVE | NO | NO | NO |
| AT5G14550 | 51.44 | 98.97 | 32.49 | 43.51 | -1.19 | 0.00E+00 | NO | NO | NO | NO |
| AT5G14920 | 299.20 | 292.91 | 136.81 | 112.41 | -1.38 | 0.00E+00 | NO | NO | POSITIVE | NO |
| AT5G17040 | 4.53 | 5.41 | 0.84 | 1.17 | -2.21 | 2.76E-06 | NO | NO | NO | NO |
| AT5G17190 | 166.31 | 157.65 | 75.06 | 96.36 | -0.71 | 7.05E-05 | NO | NO | NO | NO |
| AT5G17460 | 126.59 | 138.84 | 44.65 | 37.01 | -1.91 | 0.00E+00 | NO | NO | NO | NO |
| AT5G17700 | 20.09 | 20.54 | 5.80 | 5.38 | -1.93 | 0.00E+00 | NO | NO | NO | NO |
| AT5G20750 | 4.35 | 4.06 | 0.01 | 0.02 | -7.84 | 1.84E-10 | NO | NO | NO | NO |
| AT5G20830 | 281.83 | 314.66 | 75.39 | 107.11 | -1.55 | 0.00E+00 | POSITIVE | NO | POSITIVE | NO |
| AT5G23240 | 25.83 | 35.71 | 11.63 | 25.31 | -0.50 | 1.41E-02 | NO | NO | NO | NO |
| AT5G23820 | 50.35 | 23.88 | 15.00 | 10.08 | -1.24 | 4.12E-06 | NO | NO | DOWN | NO |
| AT5G24160 | 17.92 | 34.00 | 1.27 | 3.63 | -3.23 | 0.00E+00 | NO | NO | DOWN | NO |
| AT5G24210 | 69.59 | 52.95 | 7.63 | 26.16 | -1.02 | 2.18E-08 | NO | NO | NO | DOWN |
| AT5G25110 | 184.09 | 334.24 | 11.96 | 13.19 | -4.66 | 0.00E+00 | POSITIVE | NO | POSITIVE | UP |
| AT5G26770 | 18.56 | 18.11 | 8.91 | 11.04 | -0.71 | 4.10E-04 | NO | NO | NO | NO |
| AT5G26970 | 15.23 | 18.89 | 2.70 | 4.84 | -1.96 | 7.92E-03 | NO | NO | NO | NO |
| AT5G26980 | 1.48 | 1.97 | 0.37 | 0.68 | -1.53 | 6.74E-03 | NO | NO | NO | NO |
| AT5G27930 | 28.95 | 31.49 | 15.44 | 14.84 | -1.09 | 1.87E-11 | NO | NO | POSITIVE | UP |
| AT5G28913 | 11.63 | 12.76 | 0.04 | 0.04 | -8.32 | 3.05E-07 | NO | NO | NO | NO |

**Table A3.5 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G30495 | 50.14 | 49.94 | 28.33 | 19.95 | -1.32 | 3.11E-13 | NO | NO | NO | NO |
| AT5G32460 | 4.56 | 2.68 | 0.26 | 0.20 | -3.77 | 1.74E-06 | NO | NO | NO | NO |
| AT5G35935 | 43.62 | 53.82 | 0.12 | 0.13 | -8.66 | 0.00E+00 | NO | NO | NO | NO |
| AT5G38120 | 13.96 | 12.38 | 5.53 | 5.41 | -1.19 | 8.37E-07 | NO | NO | NO | NO |
| AT5G38250 | 2.46 | 1.91 | 0.12 | 0.12 | -4.03 | 8.56E-06 | NO | NO | NO | NO |
| AT5G39340 | 31.94 | 37.62 | 15.21 | 16.11 | -1.22 | 8.04E-08 | NO | NO | NO | NO |
| AT5G39610 | 14.34 | 16.65 | 4.04 | 8.68 | -0.94 | 2.08E-04 | NO | YES | NO | NO |
| AT5G40390 | 33.15 | 39.46 | 16.34 | 17.26 | -1.19 | 1.55E-12 | NO | NO | POSITIVE | NO |
| AT5G41700 | 135.29 | 140.04 | 62.15 | 71.14 | -0.98 | 1.19E-11 | NO | NO | NO | NO |
| AT5G41740 | 3.18 | 3.23 | 0.15 | 0.43 | -2.92 | 7.04E-14 | NO | NO | NO | NO |
| AT5G42570 | 107.31 | 101.15 | 56.93 | 72.73 | -0.48 | 2.02E-02 | POSITIVE | NO | POSITIVE | NO |
| AT5G42825 | 51.11 | 100.46 | 18.94 | 27.90 | -1.85 | 0.00E+00 | NO | NO | NO | NO |
| AT5G43950 | 8.42 | 11.05 | 3.02 | 3.72 | -1.57 | 3.12E-10 | NO | NO | NO | NO |
| AT5G44400 | 41.21 | 26.99 | 11.16 | 10.51 | -1.36 | 9.32E-13 | NO | NO | NO | NO |
| AT5G44565 | 298.94 | 294.16 | 54.54 | 63.70 | -2.21 | 0.00E+00 | NO | NO | NO | NO |
| AT5G44590 | 22.35 | 57.70 | 8.09 | 17.95 | -1.68 | 0.00E+00 | NO | NO | NO | NO |
| AT5G45470 | 10.46 | 13.21 | 5.33 | 9.74 | -0.44 | 4.53E-02 | NO | NO | NO | NO |
| AT5G45490 | 40.54 | 63.06 | 0.12 | 0.25 | -7.97 | 0.00E+00 | NO | NO | NO | NO |
| AT5G45500 | 6.48 | 9.78 | 2.13 | 4.96 | -0.98 | 2.95E-06 | NO | NO | NO | NO |
| AT5G45510 | 47.41 | 65.79 | 8.21 | 13.44 | -2.29 | 0.00E+00 | NO | NO | NO | NO |
| AT5G47130 | 19.94 | 15.92 | 0.79 | 0.87 | -4.19 | 6.92E-09 | NO | NO | NO | NO |
| AT5G47810 | 9.73 | 10.00 | 0.62 | 1.04 | -3.26 | 0.00E+00 | NO | NO | NO | NO |
| AT5G48490 | 550.57 | 566.92 | 280.57 | 166.41 | -1.77 | 0.00E+00 | NEGATIVE | NO | NO | NO |
| AT5G48530 | 5.30 | 2.85 | 0.77 | 0.63 | -2.18 | 1.24E-03 | NO | NO | NO | NO |
| AT5G48670 | 3.90 | 5.05 | 0.69 | 1.10 | -2.20 | 5.75E-05 | NO | YES | NO | NO |
| AT5G48880 | 73.63 | 64.90 | 35.35 | 33.05 | -0.97 | 5.36E-14 | NO | NO | NO | NO |
| AT5G49120 | 3.78 | 6.46 | 0.72 | 2.12 | -1.61 | 8.65E-03 | NO | NO | NO | NO |
| AT5G49330 | 36.66 | 42.76 | 16.80 | 12.22 | -1.81 | 0.00E+00 | NO | YES | NO | NO |
| AT5G49630 | 42.45 | 50.73 | 11.09 | 26.13 | -0.96 | 3.09E-08 | NO | NO | NO | NO |

**Table A3.5 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G49650 | 52.13 | 57.42 | 23.78 | 29.79 | -0.95 | 3.32E-08 | NO | NO | NO | NO |
| AT5G50950 | 18.14 | 21.79 | 8.84 | 8.85 | -1.30 | 1.35E-11 | NO | NO | NO | NO |
| AT5G52310 | 1276.59 | 1702.55 | 232.93 | 238.95 | -2.83 | 0.00E+00 | POSITIVE | NO | POSITIVE | UP |
| AT5G53120 | 34.48 | 25.92 | 16.92 | 17.75 | -0.55 | 2.62E-03 | NO | NO | NO | NO |
| AT5G53420 | 114.21 | 167.27 | 40.23 | 60.66 | -1.46 | 0.00E+00 | NO | YES | NO | NO |
| AT5G54190 | 75.17 | 158.76 | 18.54 | 29.45 | -2.43 | 0.00E+00 | NO | NO | POSITIVE | NO |
| AT5G54960 | 95.77 | 129.97 | 41.06 | 76.58 | -0.76 | 1.27E-05 | NO | NO | NO | NO |
| AT5G55250 | 5.55 | 6.28 | 1.91 | 1.94 | -1.69 | 2.09E-05 | NO | NO | NO | NO |
| AT5G57110 | 62.10 | 71.56 | 33.91 | 38.11 | -0.91 | 2.43E-07 | NO | NO | POSITIVE | NO |
| AT5G57380 | 1.90 | 3.70 | 0.48 | 1.45 | -1.36 | 4.74E-04 | NO | NO | NO | NO |
| AT5G59130 | 6.94 | 5.31 | 1.56 | 0.99 | -2.42 | 4.11E-11 | NO | NO | NO | NO |
| AT5G59320 | 12.57 | 15.11 | 38.55 | 7.70 | -0.97 | 1.20E-02 | NO | NO | NO | NO |
| AT5G59670 | 5.70 | 9.46 | 2.44 | 3.32 | -1.51 | 2.96E-11 | NO | NO | NO | NO |
| AT5G59732 | 3.72 | 3.84 | 0.29 | 0.67 | -2.51 | 4.11E-06 | NO | NO | NO | NO |
| AT5G65060 | 40.27 | 37.23 | 9.41 | 9.32 | -2.00 | 0.00E+00 | NO | YES | NO | NO |
| AT5G66400 | 77.83 | 11.85 | 15.22 | 5.96 | -0.99 | 5.83E-03 | POSITIVE | NO | NO | NO |
| AT5G66480 | 3.41 | 2.61 | 0.87 | 0.93 | -1.48 | 6.49E-03 | NO | NO | NO | NO |

**Table A3.6**. 504 Category 2 FTD Candidate Genes with higher expression in IT at 2 weeks of cold-acclimations. Genes are ordered by their AGI numbers. FPKM values are the average of three biological replicates (n=3). Genes were considered significantly different between SW and IT under non-acclimated conditions if they had a Benjamini-Hochberg corrected p-value (FDR P-VALUE) of <0.05 and a minimum of ≥3FPKM in IT. The differential expression of each gene is also represented by the logarithm (base=2) of the fold change (LOG2.FC). This table also denotes if a gene was previously described as positively or negatively correlating with freezing tolerance (HANNAH;(6)), a transcription factor (TF), a gene previously described as up- or down-regulated by 1 week of cold (COS, (25)), identified as an up- or down-regulated component of the CBF regulon (CBF REGULON; (25)).

| AGI | SW.1WK FPKM | SW.2WK FPKM | IT.1WKF PKM | IT.2WK FPKM | SW.IT.2WK LOG2FC | SW.IT.2WK. FDR P-VALUE | HANNAH? | TF? | COS? | CBF REG? |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G01480 | 8.34 | 0.32 | 1.91 | 2.39 | 2.91 | 2.24E-07 | NO | NO | NO | NO |
| AT1G01620 | 42.30 | 57.78 | 123.45 | 111.61 | 0.95 | 2.17E-08 | NEGATIVE | NO | NO | NO |
| AT1G03870 | 11.15 | 9.32 | 27.33 | 20.77 | 1.16 | 4.74E-06 | NO | NO | NO | NO |
| AT1G03905 | 6.63 | 4.45 | 16.31 | 19.80 | 2.15 | 3.64E-14 | NO | NO | NO | NO |
| AT1G03940 | 0.28 | 0.09 | 1.36 | 0.74 | 3.01 | 3.42E-03 | NO | NO | NO | NO |
| AT1G04250 | 15.91 | 13.52 | 33.42 | 24.95 | 0.88 | 1.22E-04 | NO | YES | NO | NO |
| AT1G04680 | 15.13 | 17.36 | 33.66 | 27.90 | 0.68 | 3.65E-04 | NO | NO | NO | NO |
| AT1G05550 | 0.60 | 0.33 | 2.30 | 2.38 | 2.85 | 2.94E-05 | NO | NO | NO | NO |
| AT1G05680 | 27.57 | 0.28 | 1.84 | 4.26 | 3.92 | 1.85E-09 | NO | NO | NO | NO |
| AT1G07570 | 14.32 | 14.56 | 28.20 | 31.08 | 1.09 | 1.53E-13 | NO | NO | NO | NO |
| AT1G07610 | 23.26 | 13.71 | 96.25 | 59.98 | 2.13 | 9.30E-12 | NO | NO | NO | NO |
| AT1G08610 | 4.53 | 3.76 | 11.30 | 7.03 | 0.90 | 1.37E-03 | NO | NO | NO | NO |
| AT1G09420 | 2.62 | 2.00 | 15.93 | 16.47 | 3.04 | 0.00E+00 | NO | NO | NO | NO |
| AT1G09932 | 10.59 | 3.04 | 47.32 | 52.92 | 4.12 | 0.00E+00 | NO | NO | NO | NO |
| AT1G10340 | 0.04 | 0.04 | 3.04 | 9.81 | 8.12 | 6.32E-13 | NO | NO | NO | NO |
| AT1G10470 | 45.17 | 41.35 | 85.36 | 65.58 | 0.67 | 3.68E-04 | NO | NO | NO | NO |
| AT1G10585 | 31.14 | 2.18 | 7.09 | 9.90 | 2.18 | 5.22E-06 | NO | YES | NO | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G11175 | 0.05 | 0.00 | 6.19 | 9.83 | Inf | 2.31E-11 | NO | NO | NO | NO |
| AT1G12220 | 0.02 | 0.01 | 4.47 | 5.55 | 8.94 | 4.47E-08 | NO | NO | NO | NO |
| AT1G13350 | 1.96 | 1.54 | 11.14 | 10.91 | 2.82 | 0.00E+00 | NO | NO | NO | NO |
| AT1G13470 | 23.26 | 23.68 | 79.09 | 164.60 | 2.80 | 0.00E+00 | NO | NO | NO | NO |
| AT1G13650 | 0.03 | 0.00 | 2.10 | 0.85 | Inf | 3.36E-03 | NO | NO | DOWN | NO |
| AT1G14700 | 0.54 | 0.55 | 6.19 | 4.43 | 3.02 | 3.28E-09 | NEGATIVE | NO | DOWN | NO |
| AT1G14880 | 191.11 | 286.21 | 548.89 | 980.29 | 1.78 | 0.00E+00 | NO | NO | NO | NO |
| AT1G15010 | 7.71 | 0.94 | 1.47 | 5.08 | 2.44 | 4.41E-03 | NO | NO | NO | NO |
| AT1G15870 | 3.63 | 2.49 | 12.68 | 6.98 | 1.48 | 8.34E-04 | NO | NO | NO | NO |
| AT1G15960 | 0.44 | 0.89 | 2.06 | 3.23 | 1.86 | 1.74E-05 | NO | NO | NO | NO |
| AT1G15980 | 64.43 | 79.74 | 121.81 | 118.60 | 0.57 | 1.89E-03 | NO | NO | NO | NO |
| AT1G16510 | 4.82 | 5.13 | 19.10 | 22.54 | 2.13 | 5.36E-12 | NO | NO | NO | NO |
| AT1G16820 | 0.08 | 0.27 | 2.50 | 4.25 | 4.00 | 1.92E-03 | NO | NO | NO | NO |
| AT1G17170 | 315.23 | 64.23 | 71.61 | 137.50 | 1.10 | 1.94E-10 | POSITIVE | NO | NO | NO |
| AT1G17180 | 14.44 | 0.44 | 2.03 | 4.20 | 3.24 | 1.72E-05 | NO | NO | NO | NO |
| AT1G17190 | 4.46 | 8.13 | 18.90 | 17.12 | 1.07 | 2.03E-04 | NEGATIVE | NO | NO | NO |
| AT1G17665 | 20.11 | 20.86 | 39.85 | 35.92 | 0.78 | 1.20E-04 | NO | NO | NO | NO |
| AT1G17880 | 132.66 | 115.11 | 303.81 | 185.93 | 0.69 | 7.84E-05 | NO | NO | NO | NO |
| AT1G18330 | 0.26 | 0.27 | 1.78 | 1.73 | 2.67 | 1.93E-04 | NEGATIVE | YES | NO | NO |
| AT1G18910 | 1.28 | 1.02 | 5.61 | 10.00 | 3.30 | 0.00E+00 | NO | NO | NO | NO |
| AT1G20160 | 1.77 | 1.00 | 7.05 | 5.82 | 2.55 | 1.04E-13 | NO | NO | NO | NO |
| AT1G20190 | 16.22 | 27.07 | 40.89 | 47.79 | 0.82 | 1.66E-05 | NO | NO | NO | NO |
| AT1G20350 | 0.04 | 0.05 | 4.15 | 1.85 | 5.32 | 3.62E-03 | NO | NO | NO | NO |
| AT1G21270 | 1.19 | 1.76 | 40.11 | 69.59 | 5.30 | 0.00E+00 | NO | NO | NO | DOWN |
| AT1G21750 | 153.45 | 119.07 | 255.57 | 386.01 | 1.70 | 0.00E+00 | NO | NO | NO | NO |
| AT1G22400 | 14.75 | 2.31 | 6.24 | 21.78 | 3.24 | 0.00E+00 | NO | NO | NO | NO |
| AT1G23410 | 14.20 | 10.85 | 41.72 | 19.68 | 0.86 | 1.83E-02 | NO | NO | NO | NO |
| AT1G23850 | 1.37 | 0.14 | 11.26 | 16.17 | 6.82 | 0.00E+00 | NO | NO | NO | NO |
| AT1G27330 | 71.88 | 64.60 | 146.63 | 205.94 | 1.67 | 0.00E+00 | NO | NO | NO | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G28670 | 0.56 | 1.06 | 3.04 | 3.42 | 1.69 | 9.07E-04 | NO | NO | DOWN | NO |
| AT1G30700 | 19.20 | 2.23 | 2.83 | 8.76 | 1.98 | 3.35E-10 | NO | NO | NO | NO |
| AT1G30730 | 3.43 | 0.96 | 0.84 | 2.90 | 1.60 | 1.38E-03 | NO | NO | NO | NO |
| AT1G30900 | 8.43 | 5.76 | 20.12 | 25.78 | 2.16 | 0.00E+00 | NO | NO | NO | NO |
| AT1G31540 | 5.28 | 4.94 | 14.14 | 23.47 | 2.25 | 0.00E+00 | NO | NO | NO | NO |
| AT1G32920 | 30.56 | 7.65 | 9.64 | 26.23 | 1.78 | 6.51E-06 | NO | NO | DOWN | NO |
| AT1G32940 | 24.51 | 4.85 | 8.65 | 17.27 | 1.83 | 0.00E+00 | NO | NO | NO | NO |
| AT1G32950 | 4.44 | 0.13 | 0.89 | 1.24 | 3.28 | 1.69E-05 | NO | NO | NO | NO |
| AT1G33610 | 1.57 | 0.97 | 12.98 | 18.93 | 4.29 | 0.00E+00 | NO | NO | NO | NO |
| AT1G33960 | 74.61 | 17.50 | 18.95 | 220.93 | 3.66 | 0.00E+00 | NO | NO | NO | NO |
| AT1G34575 | 0.06 | 0.09 | 22.63 | 25.60 | 8.17 | 0.00E+00 | NO | NO | NO | NO |
| AT1G35710 | 9.96 | 5.45 | 39.22 | 53.32 | 3.29 | 0.00E+00 | NO | NO | NO | NO |
| AT1G36622 | 13.65 | 2.44 | 51.22 | 73.32 | 4.91 | 0.00E+00 | NO | NO | NO | NO |
| AT1G43910 | 12.36 | 9.22 | 5.52 | 26.96 | 1.55 | 0.00E+00 | POSITIVE | NO | NO | NO |
| AT1G44350 | 12.96 | 2.31 | 5.40 | 8.98 | 1.96 | 2.32E-11 | NO | NO | NO | NO |
| AT1G44750 | 15.10 | 15.20 | 30.81 | 38.79 | 1.35 | 0.00E+00 | POSITIVE | NO | NO | NO |
| AT1G45201 | 16.08 | 5.38 | 53.25 | 26.96 | 2.32 | 0.00E+00 | NO | NO | NO | NO |
| AT1G47370 | 0.05 | 0.07 | 1.52 | 1.98 | 4.82 | 1.25E-04 | NO | NO | NO | NO |
| AT1G47510 | 16.58 | 1.04 | 3.00 | 3.72 | 1.83 | 2.24E-04 | NO | NO | NO | NO |
| AT1G47760 | 0.08 | 0.09 | 7.72 | 5.50 | 5.98 | 6.93E-04 | NO | YES | NO | NO |
| AT1G48260 | 0.83 | 0.80 | 3.71 | 4.54 | 2.51 | 6.56E-08 | NO | NO | NO | NO |
| AT1G48460 | 20.68 | 16.50 | 45.61 | 22.96 | 0.48 | 4.56E-02 | NO | NO | NO | NO |
| AT1G48750 | 13.04 | 11.81 | 58.82 | 40.33 | 1.77 | 4.61E-09 | NO | NO | NO | NO |
| AT1G50110 | 1.20 | 1.50 | 7.93 | 4.44 | 1.57 | 7.73E-04 | NO | NO | NO | NO |
| AT1G50520 | 0.02 | 0.03 | 4.99 | 10.09 | 8.59 | 4.26E-10 | NO | NO | NO | NO |
| AT1G51270 | 0.08 | 0.08 | 6.76 | 17.01 | 7.78 | 0.00E+00 | POSITIVE | NO | NO | NO |
| AT1G51430 | 3.33 | 4.41 | 16.09 | 14.93 | 1.76 | 2.87E-07 | POSITIVE | NO | NO | NO |
| AT1G51890 | 4.82 | 1.05 | 10.50 | 17.17 | 4.03 | 0.00E+00 | NO | NO | NO | NO |
| AT1G52040 | 47.33 | 50.83 | 162.86 | 233.88 | 2.20 | 0.00E+00 | NO | NO | NO | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G52200 | 176.46 | 78.73 | 79.71 | 124.75 | 0.66 | 2.38E-04 | NO | NO | NO | NO |
| AT1G52290 | 6.40 | 4.56 | 17.61 | 21.66 | 2.25 | 0.00E+00 | NO | NO | NO | NO |
| AT1G52342 | 3.58 | 3.12 | 14.61 | 19.68 | 2.66 | 7.26E-08 | NO | NO | NO | NO |
| AT1G52400 | 329.62 | 218.65 | 1020.56 | 974.36 | 2.16 | 0.00E+00 | NO | NO | NO | NO |
| AT1G53480 | 8.94 | 5.43 | 83.13 | 61.00 | 3.49 | 0.00E+00 | NO | NO | NO | NO |
| AT1G55330 | 56.02 | 42.22 | 128.20 | 71.21 | 0.75 | 4.96E-03 | NO | NO | DOWN | NO |
| AT1G56510 | 0.19 | 0.17 | 2.21 | 7.04 | 5.34 | 0.00E+00 | NO | NO | NO | NO |
| AT1G56520 | 0.08 | 0.07 | 4.64 | 7.70 | 6.80 | 0.00E+00 | NO | NO | NO | NO |
| AT1G56660 | 6.04 | 4.80 | 20.21 | 48.80 | 3.35 | 0.00E+00 | NO | NO | NO | NO |
| AT1G57630 | 0.00 | 0.00 | 1.28 | 4.69 | Inf | 5.67E-04 | NO | NO | NO | NO |
| AT1G57650 | 0.12 | 0.09 | 2.63 | 7.97 | 6.51 | 0.00E+00 | POSITIVE | NO | NO | NO |
| AT1G57660 | 30.17 | 28.98 | 105.56 | 69.70 | 1.27 | 8.39E-10 | NO | NO | NO | NO |
| AT1G58225 | 43.95 | 12.15 | 187.81 | 104.62 | 3.11 | 0.00E+00 | NO | NO | NO | NO |
| AT1G58380 | 21.08 | 16.63 | 61.75 | 39.80 | 1.26 | 1.84E-10 | NO | NO | NO | NO |
| AT1G58420 | 5.45 | 1.60 | 16.96 | 12.78 | 3.00 | 2.39E-09 | NO | NO | NO | NO |
| AT1G60190 | 7.31 | 15.05 | 17.37 | 20.99 | 0.48 | 2.17E-02 | NO | NO | NO | NO |
| AT1G61820 | 3.18 | 0.41 | 0.72 | 1.65 | 2.03 | 1.34E-03 | NO | NO | NO | NO |
| AT1G61980 | 4.57 | 4.07 | 13.74 | 8.60 | 1.08 | 3.17E-04 | NO | NO | NO | NO |
| AT1G61990 | 8.42 | 7.38 | 23.26 | 16.90 | 1.20 | 3.80E-08 | NO | NO | NO | NO |
| AT1G62355 | 0.00 | 0.00 | 10.98 | 5.62 | Inf | 3.39E-13 | NO | NO | NO | NO |
| AT1G62540 | 0.06 | 0.10 | 0.86 | 0.77 | 2.88 | 4.11E-03 | NO | NO | NO | NO |
| AT1G63160 | 11.31 | 9.71 | 28.43 | 20.83 | 1.10 | 1.59E-06 | NO | NO | NO | NO |
| AT1G63780 | 32.67 | 21.83 | 62.18 | 31.93 | 0.55 | 1.24E-02 | NO | NO | NO | NO |
| AT1G63860 | 0.31 | 0.30 | 4.47 | 7.27 | 4.62 | 0.00E+00 | NO | NO | NO | NO |
| AT1G65150 | 0.35 | 0.34 | 3.18 | 1.32 | 1.97 | 1.67E-02 | NO | NO | NO | NO |
| AT1G65490 | 49.55 | 62.83 | 178.33 | 229.20 | 1.87 | 0.00E+00 | NO | NO | NO | UP |
| AT1G65500 | 34.66 | 23.58 | 134.03 | 294.68 | 3.64 | 0.00E+00 | NO | NO | NO | NO |
| AT1G65790 | 6.35 | 5.29 | 18.60 | 20.61 | 1.96 | 0.00E+00 | NO | NO | NO | NO |
| AT1G66725 | 10.13 | 9.69 | 43.58 | 88.10 | 3.19 | 0.00E+00 | NO | NO | NO | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G66880 | 14.14 | 8.80 | 31.95 | 48.11 | 2.45 | 0.00E+00 | NO | NO | NO | NO |
| AT1G66960 | 0.02 | 0.05 | 7.84 | 10.15 | 7.80 | 0.00E+00 | NO | NO | NO | NO |
| AT1G67365 | 0.00 | 0.05 | 6.89 | 11.59 | 7.96 | 0.00E+00 | NO | NO | NO | NO |
| AT1G67590 | 0.27 | 0.44 | 5.65 | 5.86 | 3.73 | 3.79E-11 | NEGATIVE | NO | NO | NO |
| AT1G67980 | 40.86 | 11.03 | 16.60 | 43.41 | 1.98 | 0.00E+00 | NO | NO | NO | NO |
| AT1G68620 | 8.64 | 0.87 | 22.47 | 24.40 | 4.81 | 0.00E+00 | NO | NO | NO | NO |
| AT1G69530 | 19.91 | 34.29 | 88.43 | 97.64 | 1.51 | 0.00E+00 | NO | NO | DOWN | DOWN |
| AT1G69880 | 19.88 | 2.06 | 2.93 | 7.52 | 1.87 | 1.81E-03 | NO | NO | NO | NO |
| AT1G70090 | 22.24 | 14.81 | 40.78 | 28.19 | 0.93 | 2.41E-08 | NO | NO | NO | NO |
| AT1G70200 | 62.82 | 75.02 | 129.16 | 106.71 | 0.51 | 9.22E-03 | NO | NO | NO | NO |
| AT1G70420 | 18.09 | 22.79 | 79.36 | 58.81 | 1.37 | 3.66E-14 | NO | NO | NO | NO |
| AT1G70985 | 2.74 | 2.78 | 10.64 | 8.66 | 1.64 | 2.90E-03 | NO | NO | NO | NO |
| AT1G71880 | 26.41 | 21.58 | 67.52 | 62.98 | 1.54 | 0.00E+00 | NO | NO | NO | NO |
| AT1G72130 | 4.75 | 3.86 | 12.48 | 12.73 | 1.72 | 1.04E-13 | NO | NO | NO | NO |
| AT1G72430 | 8.93 | 2.64 | 36.31 | 30.88 | 3.55 | 0.00E+00 | NO | NO | DOWN | DOWN |
| AT1G72520 | 8.00 | 3.85 | 3.01 | 7.99 | 1.06 | 4.87E-06 | NO | NO | NO | NO |
| AT1G72970 | 11.58 | 12.72 | 26.39 | 20.79 | 0.71 | 2.86E-04 | NEGATIVE | NO | NO | NO |
| AT1G73260 | 24.81 | 24.99 | 72.52 | 97.23 | 1.96 | 0.00E+00 | NO | NO | NO | NO |
| AT1G73805 | 10.37 | 12.01 | 27.81 | 86.07 | 2.84 | 0.00E+00 | NO | NO | NO | NO |
| AT1G74670 | 14.88 | 8.58 | 70.40 | 51.51 | 2.59 | 0.00E+00 | NO | NO | DOWN | NO |
| AT1G74710 | 6.67 | 6.29 | 14.45 | 27.71 | 2.14 | 0.00E+00 | NO | NO | NO | NO |
| AT1G75030 | 2.70 | 2.13 | 9.56 | 6.90 | 1.69 | 3.81E-04 | NEGATIVE | NO | NO | NO |
| AT1G75040 | 1396.09 | 359.53 | 8818.64 | 8119.78 | 4.50 | 0.00E+00 | NO | NO | POSITIVE | NO |
| AT1G76470 | 30.54 | 0.06 | 0.08 | 0.53 | 3.13 | 3.81E-02 | NO | NO | NO | NO |
| AT1G76650 | 20.07 | 4.03 | 8.36 | 27.88 | 2.79 | 0.00E+00 | NO | NO | NO | NO |
| AT1G76930 | 461.90 | 155.62 | 122.20 | 624.22 | 2.00 | 0.00E+00 | NO | NO | NO | NO |
| AT1G76955 | 22.27 | 27.04 | 55.22 | 43.05 | 0.67 | 9.31E-03 | NO | NO | NO | NO |
| AT1G76970 | 8.86 | 6.20 | 20.65 | 23.37 | 1.92 | 0.00E+00 | NO | NO | NO | NO |
| AT1G77510 | 64.03 | 31.34 | 213.11 | 281.48 | 3.17 | 0.00E+00 | NO | NO | NO | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT1G77630 | 6.48 | 4.41 | 15.64 | 9.92 | 1.17 | 1.64E-05 | NO | NO | NO | NO |
| AT1G77760 | 23.40 | 20.68 | 42.37 | 43.76 | 1.08 | 7.77E-11 | NO | NO | NO | NO |
| AT1G78080 | 14.51 | 18.21 | 27.88 | 39.48 | 1.12 | 3.76E-10 | NO | YES | NO | NO |
| AT1G78290 | 20.46 | 23.90 | 49.12 | 60.90 | 1.35 | 0.00E+00 | NO | NO | NO | NO |
| AT1G78410 | 16.77 | 6.68 | 43.36 | 106.49 | 4.00 | 0.00E+00 | NO | NO | NO | NO |
| AT2G01670 | 28.44 | 13.42 | 79.08 | 68.28 | 2.35 | 0.00E+00 | NO | NO | NO | NO |
| AT2G01890 | 1.94 | 0.81 | 15.20 | 9.88 | 3.60 | 1.91E-14 | NO | NO | NO | NO |
| AT2G03750 | 15.05 | 20.08 | 54.35 | 47.16 | 1.23 | 4.26E-11 | NO | NO | DOWN | NO |
| AT2G04040 | 27.39 | 3.36 | 13.81 | 23.64 | 2.82 | 0.00E+00 | NO | NO | NO | NO |
| AT2G04450 | 38.95 | 17.47 | 14.49 | 112.95 | 2.69 | 0.00E+00 | NO | NO | NO | NO |
| AT2G04495 | 3.49 | 1.14 | 15.43 | 14.71 | 3.69 | 0.00E+00 | NO | NO | NO | NO |
| AT2G07750 | 0.06 | 0.06 | 4.89 | 3.62 | 5.99 | 0.00E+00 | NO | NO | NO | NO |
| AT2G10940 | 641.34 | 427.76 | 1405.64 | 689.21 | 0.69 | 1.39E-03 | NO | NO | NO | NO |
| AT2G14580 | 2.21 | 2.81 | 17.58 | 7.73 | 1.46 | 7.67E-03 | NO | NO | NO | NO |
| AT2G14610 | 1484.66 | 1091.57 | 4492.87 | 15144.50 | 3.79 | 0.00E+00 | NO | NO | NO | NO |
| AT2G15128 | 1.25 | 0.97 | 383.42 | 430.07 | 8.79 | 4.88E-08 | NO | NO | NO | NO |
| AT2G16676 | 0.02 | 0.00 | 1.37 | 1.91 | Inf | 6.92E-07 | NO | NO | NO | NO |
| AT2G16680 | 0.01 | 0.00 | 0.99 | 1.62 | Inf | 7.01E-12 | NO | NO | NO | NO |
| AT2G17040 | 3.95 | 3.31 | 11.63 | 24.66 | 2.90 | 0.00E+00 | NO | YES | NO | NO |
| AT2G17250 | 19.27 | 12.76 | 38.86 | 20.78 | 0.70 | 4.67E-04 | NO | NO | NO | NO |
| AT2G18193 | 3.54 | 0.49 | 0.38 | 1.42 | 1.54 | 2.51E-02 | NO | NO | NO | NO |
| AT2G18300 | 46.62 | 43.56 | 69.80 | 64.40 | 0.56 | 5.40E-06 | NO | YES | NO | NO |
| AT2G18560 | 2.17 | 1.67 | 7.20 | 6.35 | 1.93 | 6.26E-08 | NO | NO | NO | NO |
| AT2G18680 | 3.92 | 0.05 | 12.71 | 9.74 | 7.59 | 7.89E-08 | NO | NO | NO | NO |
| AT2G22330 | 19.52 | 18.36 | 44.94 | 30.13 | 0.72 | 2.14E-04 | NO | NO | NO | NO |
| AT2G22980 | 3.01 | 2.88 | 11.91 | 11.57 | 2.01 | 0.00E+00 | NO | NO | NO | NO |
| AT2G23000 | 1.92 | 1.64 | 6.58 | 4.63 | 1.50 | 3.93E-04 | NO | NO | NO | NO |
| AT2G23110 | 0.36 | 0.07 | 4.54 | 5.90 | 6.42 | 2.31E-04 | NO | NO | NO | NO |
| AT2G23600 | 23.61 | 23.39 | 119.48 | 91.89 | 1.97 | 0.00E+00 | NO | NO | NO | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT2G24850 | 23.62 | 4.61 | 141.32 | 133.81 | 4.86 | 0.00E+00 | NO | NO | NO | NO |
| AT2G25440 | 0.25 | 0.10 | 2.92 | 5.06 | 5.68 | 3.68E-14 | NO | NO | NO | NO |
| AT2G27420 | 1.88 | 0.93 | 7.85 | 2.98 | 1.67 | 3.05E-03 | NO | NO | NO | NO |
| AT2G27660 | 1.09 | 0.45 | 6.04 | 10.82 | 4.60 | 0.00E+00 | NO | NO | NO | NO |
| AT2G29310 | 6.91 | 6.48 | 19.69 | 13.33 | 1.04 | 1.16E-03 | NEGATIVE | NO | NO | NO |
| AT2G29350 | 72.51 | 15.31 | 176.40 | 300.97 | 4.30 | 0.00E+00 | NO | NO | NO | NO |
| AT2G29470 | 30.68 | 3.33 | 8.74 | 25.58 | 2.94 | 0.00E+00 | NO | NO | NO | NO |
| AT2G30010 | 26.75 | 27.35 | 60.60 | 56.11 | 1.04 | 3.90E-09 | NEGATIVE | NO | NO | DOWN |
| AT2G30400 | 8.45 | 0.42 | 1.38 | 2.53 | 2.60 | 6.79E-04 | NO | NO | NO | NO |
| AT2G30550 | 11.60 | 8.20 | 26.05 | 32.67 | 1.99 | 0.00E+00 | NO | NO | NO | NO |
| AT2G30770 | 45.39 | 2.42 | 16.80 | 13.56 | 2.49 | 0.00E+00 | NO | NO | NO | NO |
| AT2G31420 | 4.01 | 0.12 | 0.60 | 1.38 | 3.56 | 2.54E-02 | NO | NO | NO | NO |
| AT2G31880 | 45.23 | 25.29 | 132.42 | 190.79 | 2.92 | 0.00E+00 | NO | NO | NO | NO |
| AT2G32530 | 0.13 | 0.06 | 1.37 | 0.96 | 3.90 | 4.23E-05 | NO | NO | NO | NO |
| AT2G32560 | 8.98 | 8.27 | 22.32 | 19.90 | 1.27 | 2.86E-08 | NO | NO | NO | NO |
| AT2G32680 | 9.55 | 3.84 | 25.99 | 35.79 | 3.22 | 0.00E+00 | NO | NO | NO | NO |
| AT2G32870 | 1.51 | 0.17 | 10.11 | 2.84 | 4.02 | 2.69E-08 | NO | NO | NO | NO |
| AT2G32880 | 2.03 | 0.35 | 9.76 | 3.80 | 3.46 | 1.65E-07 | NO | NO | DOWN | NO |
| AT2G33400 | 2.52 | 5.10 | 7.12 | 10.05 | 0.98 | 3.97E-04 | NO | NO | NO | NO |
| AT2G33710 | 3.87 | 0.19 | 1.11 | 1.20 | 2.63 | 4.83E-03 | NO | YES | NO | NO |
| AT2G34070 | 25.41 | 10.98 | 10.84 | 18.19 | 0.73 | 1.60E-03 | NO | NO | NO | DOWN |
| AT2G35035 | 0.60 | 1.07 | 3.46 | 4.60 | 2.11 | 9.23E-05 | NO | NO | NO | NO |
| AT2G36780 | 3.82 | 0.59 | 0.64 | 2.02 | 1.78 | 2.76E-03 | NO | NO | NO | NO |
| AT2G36790 | 2.66 | 0.45 | 0.29 | 1.23 | 1.46 | 4.72E-02 | NO | NO | NO | NO |
| AT2G36830 | 34.90 | 29.60 | 127.65 | 74.42 | 1.33 | 5.37E-14 | NEGATIVE | NO | DOWN | NO |
| AT2G37710 | 60.27 | 51.54 | 175.02 | 280.31 | 2.44 | 0.00E+00 | NO | NO | NO | NO |
| AT2G37760 | 48.93 | 17.62 | 20.27 | 23.51 | 0.42 | 4.69E-02 | NO | NO | NO | NO |
| AT2G37770 | 37.03 | 7.05 | 16.65 | 24.94 | 1.82 | 1.86E-14 | NO | NO | NO | NO |
| AT2G38240 | 31.81 | 3.82 | 9.22 | 15.75 | 2.04 | 1.53E-11 | NO | NO | NO | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT2G38340 | 4.95 | 0.62 | 1.28 | 4.92 | 2.98 | 3.48E-06 | NO | YES | NO | NO |
| AT2G39030 | 120.09 | 6.08 | 16.25 | 16.77 | 1.46 | 1.43E-06 | NO | NO | NO | NO |
| AT2G39210 | 15.16 | 10.10 | 30.93 | 47.34 | 2.23 | 0.00E+00 | NO | NO | NO | NO |
| AT2G39330 | 24.36 | 5.93 | 11.79 | 10.93 | 0.88 | 8.43E-04 | NO | NO | NO | NO |
| AT2G39390 | 181.59 | 172.65 | 345.16 | 231.96 | 0.43 | 3.18E-02 | NO | NO | NO | NO |
| AT2G39710 | 16.28 | 17.94 | 43.86 | 36.63 | 1.03 | 2.55E-08 | NO | NO | POSITIVE | NO |
| AT2G40000 | 29.40 | 5.70 | 11.23 | 22.99 | 2.01 | 0.00E+00 | NO | NO | DOWN | NO |
| AT2G40205 | 2047.97 | 2835.29 | 8695.17 | 6573.37 | 1.21 | 5.05E-05 | NO | NO | NO | NO |
| AT2G40740 | 0.92 | 0.43 | 3.94 | 3.31 | 2.93 | 1.24E-03 | NO | YES | NO | NO |
| AT2G41120 | 3.40 | 3.64 | 18.19 | 21.68 | 2.57 | 0.00E+00 | NO | NO | NO | NO |
| AT2G42170 | 0.30 | 0.36 | 10.52 | 7.22 | 4.31 | 3.64E-14 | NO | NO | NO | NO |
| AT2G43150 | 228.88 | 58.20 | 77.25 | 103.87 | 0.84 | 1.13E-06 | NO | NO | NO | NO |
| AT2G43530 | 96.10 | 36.88 | 220.75 | 189.27 | 2.36 | 0.00E+00 | NO | NO | NO | NO |
| AT2G43535 | 11.04 | 4.35 | 59.24 | 36.47 | 3.07 | 0.00E+00 | NO | NO | NO | NO |
| AT2G43570 | 99.62 | 10.79 | 737.05 | 418.54 | 5.28 | 0.00E+00 | NO | NO | NO | NO |
| AT2G43820 | 69.95 | 4.43 | 11.09 | 17.38 | 1.97 | 0.00E+00 | POSITIVE | NO | NO | NO |
| AT2G44240 | 0.06 | 0.09 | 30.21 | 55.03 | 9.29 | 0.00E+00 | NO | NO | NO | NO |
| AT2G44290 | 5.60 | 7.85 | 60.45 | 74.46 | 3.25 | 0.00E+00 | NO | NO | NO | NO |
| AT2G44790 | 27.68 | 2.66 | 7.65 | 8.86 | 1.74 | 3.10E-05 | NO | NO | NO | NO |
| AT2G45570 | 27.02 | 1.64 | 4.69 | 7.43 | 2.18 | 8.59E-10 | NO | NO | NO | NO |
| AT2G45660 | 25.94 | 34.57 | 64.51 | 89.14 | 1.37 | 0.00E+00 | NO | YES | POSITIVE | NO |
| AT2G45710 | 31.00 | 24.68 | 92.21 | 46.41 | 0.91 | 4.71E-04 | NO | NO | NO | NO |
| AT2G46430 | 10.76 | 11.01 | 27.25 | 46.16 | 2.07 | 0.00E+00 | NO | NO | NO | NO |
| AT2G46710 | 5.21 | 6.62 | 19.78 | 16.23 | 1.29 | 4.92E-09 | NEGATIVE | NO | NO | NO |
| AT2G47000 | 14.07 | 3.81 | 2.86 | 9.76 | 1.36 | 5.29E-12 | NO | NO | NO | NO |
| AT2G47950 | 4.51 | 0.27 | 0.85 | 1.56 | 2.53 | 3.52E-02 | NO | NO | NO | NO |
| AT3G02790 | 9.84 | 1.94 | 57.45 | 17.65 | 3.19 | 5.75E-10 | NO | YES | DOWN | NO |
| AT3G03030 | 1.41 | 1.65 | 5.78 | 3.91 | 1.25 | 2.16E-03 | NO | NO | NO | NO |
| AT3G03450 | 3.81 | 3.74 | 9.49 | 8.81 | 1.24 | 1.87E-06 | NO | YES | NO | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G03850 | 1.39 | 1.14 | 8.42 | 4.20 | 1.89 | 1.14E-02 | NO | NO | NO | NO |
| AT3G04480 | 8.82 | 13.11 | 17.47 | 19.68 | 0.59 | 3.69E-03 | NO | NO | NO | NO |
| AT3G06145 | 2.58 | 2.47 | 16.48 | 9.97 | 2.01 | 2.38E-05 | NO | NO | NO | NO |
| AT3G06200 | 31.59 | 26.41 | 62.95 | 44.21 | 0.74 | 1.03E-04 | NO | NO | NO | NO |
| AT3G06530 | 17.72 | 10.29 | 29.68 | 13.63 | 0.41 | 3.48E-03 | NO | NO | POSITIVE | NO |
| AT3G07520 | 4.41 | 3.62 | 12.42 | 14.34 | 1.98 | 0.00E+00 | NO | NO | NO | NO |
| AT3G08870 | 1.25 | 0.73 | 6.59 | 10.34 | 3.82 | 0.00E+00 | NO | NO | NO | NO |
| AT3G08970 | 3.41 | 3.13 | 10.83 | 23.42 | 2.90 | 0.00E+00 | NO | NO | NO | NO |
| AT3G09270 | 70.18 | 6.61 | 8.98 | 22.97 | 1.80 | 1.16E-09 | NO | NO | NO | NO |
| AT3G09940 | 2.43 | 0.38 | 17.79 | 33.00 | 6.43 | 0.00E+00 | NO | NO | NO | NO |
| AT3G11000 | 0.08 | 0.05 | 1.87 | 0.81 | 3.88 | 8.26E-05 | NO | NO | NO | NO |
| AT3G11010 | 0.09 | 0.04 | 6.18 | 9.82 | 7.88 | 0.00E+00 | NO | NO | NO | NO |
| AT3G11080 | 0.98 | 0.81 | 11.97 | 16.48 | 4.35 | 0.00E+00 | NO | NO | NO | NO |
| AT3G11280 | 14.36 | 10.47 | 42.95 | 33.84 | 1.69 | 0.00E+00 | NO | YES | NO | NO |
| AT3G11340 | 13.22 | 0.49 | 3.40 | 9.67 | 4.29 | 0.00E+00 | NO | NO | NO | NO |
| AT3G13130 | 2.29 | 1.08 | 8.94 | 8.64 | 3.00 | 2.21E-08 | NO | NO | NO | NO |
| AT3G13433 | 0.92 | 0.67 | 19.18 | 21.88 | 5.02 | 1.53E-10 | NO | NO | NO | NO |
| AT3G13560 | 17.13 | 15.52 | 34.68 | 34.00 | 1.13 | 3.42E-13 | NEGATIVE | NO | NO | NO |
| AT3G13610 | 28.30 | 1.63 | 12.07 | 50.87 | 4.96 | 0.00E+00 | NO | NO | NO | NO |
| AT3G13750 | 18.94 | 24.75 | 43.02 | 57.22 | 1.21 | 2.17E-13 | NEGATIVE | NO | DOWN | NO |
| AT3G14990 | 181.64 | 53.71 | 86.39 | 135.78 | 1.34 | 0.00E+00 | NO | NO | NO | NO |
| AT3G15536 | 8.13 | 2.70 | 72.57 | 73.19 | 4.76 | 0.00E+00 | NO | NO | NO | NO |
| AT3G16240 | 25.22 | 31.18 | 67.21 | 54.88 | 0.82 | 1.18E-05 | NO | NO | DOWN | NO |
| AT3G16470 | 139.59 | 35.68 | 53.09 | 55.60 | 0.64 | 3.12E-04 | NO | NO | NO | NO |
| AT3G17510 | 14.85 | 14.91 | 37.44 | 40.54 | 1.44 | 0.00E+00 | NO | NO | NO | NO |
| AT3G18830 | 86.28 | 49.21 | 40.80 | 66.53 | 0.44 | 2.70E-02 | NO | NO | NO | NO |
| AT3G19515 | 4.82 | 5.09 | 22.10 | 23.36 | 2.20 | 0.00E+00 | NO | NO | NO | NO |
| AT3G19520 | 10.49 | 9.28 | 23.00 | 27.82 | 1.58 | 5.37E-14 | POSITIVE | NO | NO | NO |
| AT3G21150 | 2.99 | 3.14 | 10.78 | 20.55 | 2.71 | 1.92E-14 | NO | NO | NO | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G22370 | 55.20 | 22.25 | 27.15 | 49.59 | 1.16 | 9.80E-11 | NO | NO | NO | NO |
| AT3G22930 | 0.29 | 0.13 | 2.64 | 4.95 | 5.30 | 7.52E-07 | NO | NO | NO | NO |
| AT3G23080 | 10.53 | 9.99 | 20.20 | 19.10 | 0.94 | 2.09E-06 | NO | NO | DOWN | NO |
| AT3G23120 | 1.82 | 1.87 | 6.77 | 9.93 | 2.41 | 0.00E+00 | NO | NO | NO | NO |
| AT3G23240 | 7.29 | 0.86 | 1.77 | 2.93 | 1.77 | 9.62E-03 | NO | YES | NO | NO |
| AT3G23480 | 0.93 | 0.91 | 6.09 | 6.18 | 2.76 | 3.67E-11 | NO | NO | NO | NO |
| AT3G23620 | 88.22 | 68.95 | 204.42 | 94.61 | 0.46 | 2.30E-02 | NO | NO | POSITIVE | NO |
| AT3G23730 | 7.47 | 10.56 | 21.25 | 18.52 | 0.81 | 1.75E-03 | NO | NO | NO | NO |
| AT3G23890 | 2.31 | 4.21 | 4.84 | 6.38 | 0.60 | 1.71E-03 | NO | NO | NO | NO |
| AT3G24516 | 2.27 | 1.54 | 273.52 | 216.80 | 7.13 | 2.15E-05 | NO | NO | NO | NO |
| AT3G24517 | 0.47 | 0.41 | 74.93 | 50.31 | 6.93 | 0.00E+00 | NO | NO | NO | NO |
| AT3G24518 | 1.08 | 1.54 | 15.14 | 9.72 | 2.65 | 1.36E-11 | NO | NO | NO | NO |
| AT3G25010 | 1.46 | 0.65 | 8.62 | 9.03 | 3.80 | 0.00E+00 | NO | NO | NO | NO |
| AT3G25020 | 0.07 | 0.06 | 6.74 | 9.49 | 7.36 | 0.00E+00 | NO | NO | NO | NO |
| AT3G25250 | 5.77 | 0.49 | 1.43 | 4.01 | 3.05 | 6.66E-08 | NO | NO | NO | NO |
| AT3G25572 | 0.77 | 0.88 | 3.52 | 2.78 | 1.67 | 1.04E-03 | NO | NO | NO | NO |
| AT3G26170 | 2.97 | 1.95 | 8.83 | 10.78 | 2.47 | 1.91E-14 | NO | NO | NO | NO |
| AT3G26240 | 0.04 | 0.04 | 2.61 | 2.42 | 6.07 | 3.73E-13 | NO | NO | NO | NO |
| AT3G26520 | 46.81 | 45.98 | 235.68 | 208.37 | 2.18 | 0.00E+00 | NEGATIVE | NO | NO | NO |
| AT3G26830 | 119.27 | 10.37 | 42.52 | 76.07 | 2.88 | 0.00E+00 | NO | NO | NO | NO |
| AT3G28270 | 0.19 | 0.16 | 9.21 | 1.85 | 3.50 | 3.46E-07 | NO | NO | DOWN | NO |
| AT3G28510 | 0.26 | 0.11 | 3.30 | 7.75 | 6.11 | 0.00E+00 | NO | NO | NO | NO |
| AT3G29240 | 41.24 | 43.43 | 79.69 | 110.08 | 1.34 | 0.00E+00 | NO | NO | NO | NO |
| AT3G29575 | 3.71 | 2.33 | 13.02 | 16.42 | 2.82 | 0.00E+00 | NO | NO | NO | NO |
| AT3G29590 | 2.27 | 1.42 | 6.97 | 4.02 | 1.51 | 1.71E-03 | POSITIVE | NO | NO | NO |
| AT3G43670 | 10.19 | 11.54 | 20.39 | 23.48 | 1.02 | 3.15E-08 | NO | NO | NO | NO |
| AT3G43800 | 37.23 | 42.60 | 100.26 | 116.26 | 1.45 | 0.00E+00 | NO | NO | NO | NO |
| AT3G44215 | 0.02 | 0.01 | 7.10 | 10.24 | 9.75 | 0.00E+00 | NO | NO | NO | NO |
| AT3G44300 | 144.08 | 24.36 | 28.96 | 79.80 | 1.71 | 0.00E+00 | NO | NO | NO | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G44310 | 114.22 | 128.73 | 280.91 | 332.51 | 1.37 | 0.00E+00 | NO | NO | NO | NO |
| AT3G44970 | 0.04 | 0.05 | 2.68 | 1.20 | 4.57 | 3.53E-04 | NO | NO | NO | NO |
| AT3G45030 | 161.26 | 131.07 | 307.10 | 186.51 | 0.51 | 1.06E-02 | NO | NO | NO | NO |
| AT3G45290 | 5.34 | 3.34 | 17.72 | 9.90 | 1.57 | 8.92E-08 | NO | NO | NO | NO |
| AT3G45390 | 0.36 | 0.73 | 1.88 | 2.63 | 1.86 | 2.56E-04 | NO | NO | NO | NO |
| AT3G45443 | 1.73 | 2.37 | 7.43 | 7.13 | 1.59 | 3.13E-04 | NO | NO | NO | NO |
| AT3G45446 | 0.02 | 0.02 | 2.33 | 4.81 | 8.18 | 5.25E-07 | NO | NO | NO | NO |
| AT3G45860 | 20.46 | 3.93 | 71.63 | 51.93 | 3.72 | 0.00E+00 | NO | NO | NO | NO |
| AT3G46650 | 0.46 | 0.35 | 4.56 | 1.42 | 2.01 | 8.76E-03 | NO | NO | NO | NO |
| AT3G46668 | 0.00 | 0.00 | 3.18 | 2.83 | Inf | 1.64E-03 | NO | NO | NO | NO |
| AT3G47560 | 4.22 | 4.25 | 12.31 | 12.45 | 1.55 | 8.82E-07 | NO | NO | DOWN | NO |
| AT3G48080 | 4.12 | 8.01 | 11.64 | 24.86 | 1.63 | 0.00E+00 | NO | NO | NO | NO |
| AT3G48640 | 23.78 | 14.19 | 66.49 | 218.10 | 3.94 | 0.00E+00 | NO | NO | NO | NO |
| AT3G48850 | 12.06 | 0.70 | 3.25 | 4.78 | 2.78 | 1.30E-06 | NO | NO | NO | NO |
| AT3G49180 | 15.81 | 13.64 | 37.59 | 21.10 | 0.63 | 4.15E-03 | NO | NO | NO | NO |
| AT3G49340 | 0.50 | 0.16 | 47.82 | 34.60 | 7.74 | 0.00E+00 | NO | NO | NO | NO |
| AT3G49780 | 59.43 | 26.52 | 168.86 | 171.89 | 2.70 | 0.00E+00 | NO | NO | NO | NO |
| AT3G51230 | 0.68 | 1.92 | 5.41 | 8.82 | 2.20 | 3.46E-07 | NO | NO | NO | NO |
| AT3G51860 | 25.18 | 5.37 | 87.42 | 68.76 | 3.68 | 0.00E+00 | NO | NO | NO | NO |
| AT3G53150 | 3.12 | 0.44 | 11.31 | 8.86 | 4.32 | 0.00E+00 | NO | NO | NO | NO |
| AT3G54390 | 1.69 | 1.39 | 5.95 | 4.50 | 1.69 | 2.53E-04 | NO | YES | NO | NO |
| AT3G54830 | 10.87 | 7.84 | 45.73 | 27.79 | 1.83 | 0.00E+00 | NO | NO | NO | NO |
| AT3G56400 | 22.07 | 20.16 | 52.03 | 125.10 | 2.63 | 0.00E+00 | NO | YES | NO | NO |
| AT3G57040 | 7.44 | 9.34 | 17.78 | 14.46 | 0.63 | 1.73E-02 | NEGATIVE | NO | NO | NO |
| AT3G57260 | 552.31 | 123.31 | 3942.03 | 2454.12 | 4.31 | 0.00E+00 | NO | NO | NO | NO |
| AT3G57490 | 39.33 | 25.39 | 74.37 | 35.80 | 0.50 | 2.77E-02 | NO | NO | NO | NO |
| AT3G58120 | 4.42 | 3.29 | 11.94 | 9.16 | 1.48 | 8.90E-07 | NO | YES | NO | NO |
| AT3G59140 | 14.00 | 4.31 | 4.15 | 6.20 | 0.53 | 2.41E-02 | NO | NO | NO | NO |
| AT3G60140 | 19.06 | 2.17 | 1.51 | 19.34 | 3.16 | 0.00E+00 | NO | NO | NO | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT3G60170 | 0.01 | 0.01 | 1.66 | 2.80 | 7.70 | 4.35E-10 | NO | NO | NO | NO |
| AT3G60500 | 16.25 | 13.62 | 27.72 | 18.73 | 0.46 | 2.09E-02 | NO | NO | NO | NO |
| AT3G60540 | 9.28 | 5.86 | 29.19 | 36.38 | 2.63 | 3.36E-12 | NO | NO | NO | NO |
| AT3G62890 | 2.87 | 2.37 | 9.15 | 5.30 | 1.16 | 8.80E-04 | NO | NO | NO | NO |
| AT4G00700 | 4.63 | 1.01 | 15.88 | 16.67 | 4.05 | 0.00E+00 | NO | NO | NO | NO |
| AT4G01490 | 0.03 | 0.02 | 8.29 | 10.52 | 9.03 | 0.00E+00 | NO | NO | NO | NO |
| AT4G01525 | 0.51 | 0.56 | 146.37 | 247.03 | 8.79 | 0.00E+00 | NO | NO | NO | NO |
| AT4G01720 | 2.37 | 1.42 | 6.86 | 8.32 | 2.55 | 5.56E-13 | NO | YES | NO | NO |
| AT4G01870 | 388.35 | 46.12 | 85.28 | 137.91 | 1.58 | 0.00E+00 | NO | NO | NO | NO |
| AT4G03320 | 3.39 | 0.43 | 0.92 | 1.32 | 1.61 | 5.00E-02 | NO | NO | NO | NO |
| AT4G03450 | 5.12 | 2.70 | 12.63 | 22.77 | 3.08 | 0.00E+00 | NO | NO | NO | NO |
| AT4G04510 | 0.77 | 0.32 | 3.89 | 6.23 | 4.28 | 0.00E+00 | NO | NO | NO | NO |
| AT4G05050 | 98.34 | 83.62 | 204.45 | 315.81 | 1.92 | 0.00E+00 | NO | NO | NO | NO |
| AT4G08470 | 5.82 | 6.68 | 21.66 | 33.85 | 2.34 | 0.00E+00 | NO | NO | NO | NO |
| AT4G08770 | 42.17 | 0.59 | 6.17 | 8.50 | 3.84 | 1.07E-12 | NO | NO | NO | NO |
| AT4G08780 | 11.41 | 0.12 | 1.85 | 2.89 | 4.57 | 1.74E-06 | NO | NO | NO | NO |
| AT4G10120 | 23.44 | 39.04 | 42.77 | 65.83 | 0.75 | 1.74E-09 | NO | NO | NO | NO |
| AT4G10500 | 3.49 | 0.55 | 50.01 | 41.30 | 6.24 | 0.00E+00 | NO | NO | NO | NO |
| AT4G10860 | 0.81 | 0.37 | 20.01 | 81.53 | 7.78 | 0.00E+00 | NO | NO | NO | NO |
| AT4G11000 | 1.02 | 0.83 | 14.62 | 26.50 | 4.99 | 0.00E+00 | NO | NO | NO | NO |
| AT4G11170 | 0.07 | 0.06 | 2.91 | 7.09 | 6.98 | 0.00E+00 | NO | NO | NO | NO |
| AT4G11211 | 3.02 | 3.01 | 13.03 | 17.52 | 2.54 | 1.36E-06 | NO | NO | NO | NO |
| AT4G11650 | 8.31 | 2.14 | 2.75 | 4.55 | 1.09 | 4.10E-02 | NO | NO | NO | NO |
| AT4G12320 | 12.34 | 10.46 | 35.67 | 38.43 | 1.88 | 0.00E+00 | NO | NO | NO | NO |
| AT4G12420 | 22.21 | 28.47 | 41.77 | 39.89 | 0.49 | 1.37E-02 | NO | NO | NO | NO |
| AT4G12735 | 24.95 | 1.97 | 3.93 | 8.14 | 2.05 | 1.97E-03 | NO | NO | NO | NO |
| AT4G12880 | 40.19 | 42.77 | 82.31 | 69.19 | 0.69 | 1.06E-04 | NEGATIVE | NO | NO | NO |
| AT4G13810 | 0.65 | 0.49 | 3.13 | 5.05 | 3.35 | 8.78E-14 | NO | NO | NO | NO |
| AT4G13820 | 0.31 | 0.16 | 2.12 | 2.50 | 3.93 | 2.53E-11 | NO | NO | NO | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT4G13890 | 0.22 | 0.11 | 8.62 | 12.83 | 6.87 | 0.00E+00 | NO | NO | NO | NO |
| AT4G14090 | 7.42 | 4.04 | 20.43 | 15.37 | 1.93 | 1.85E-14 | NO | NO | NO | NO |
| AT4G14390 | 0.16 | 0.16 | 30.89 | 43.04 | 8.06 | 0.00E+00 | NO | NO | NO | NO |
| AT4G14400 | 75.26 | 86.66 | 196.22 | 281.37 | 1.70 | 0.00E+00 | NO | NO | POSITIVE | NO |
| AT4G14640 | 1.09 | 0.98 | 6.83 | 7.44 | 2.93 | 1.58E-05 | NO | NO | NO | NO |
| AT4G14750 | 1.40 | 2.61 | 6.10 | 8.91 | 1.77 | 4.16E-08 | NO | NO | NO | NO |
| AT4G15248 | 6.30 | 4.53 | 24.70 | 16.45 | 1.86 | 7.17E-05 | NO | NO | NO | NO |
| AT4G15530 | 81.86 | 47.74 | 47.85 | 81.65 | 0.77 | 0.00E+00 | NO | NO | NO | NO |
| AT4G16000 | 1.31 | 0.12 | 9.07 | 4.30 | 5.18 | 1.45E-04 | NO | NO | NO | NO |
| AT4G16760 | 61.24 | 29.43 | 28.21 | 38.33 | 0.38 | 4.35E-02 | NO | NO | NO | NO |
| AT4G17340 | 1.92 | 0.72 | 18.70 | 9.50 | 3.73 | 5.12E-12 | NO | NO | DOWN | NO |
| AT4G18010 | 19.10 | 11.47 | 31.58 | 50.12 | 2.13 | 0.00E+00 | NO | NO | NO | NO |
| AT4G18170 | 15.76 | 2.40 | 4.86 | 7.16 | 1.58 | 5.15E-05 | NO | YES | NO | NO |
| AT4G18970 | 4.08 | 4.94 | 15.09 | 12.78 | 1.37 | 3.76E-07 | NO | NO | NO | NO |
| AT4G19370 | 2.91 | 0.79 | 10.29 | 17.89 | 4.51 | 0.00E+00 | NO | NO | NO | NO |
| AT4G19420 | 8.35 | 8.56 | 16.19 | 19.29 | 1.17 | 7.18E-10 | NO | NO | NO | NO |
| AT4G19630 | 0.32 | 1.07 | 11.99 | 8.38 | 2.96 | 1.37E-06 | NO | NO | NO | NO |
| AT4G19990 | 4.98 | 5.53 | 9.94 | 14.76 | 1.42 | 0.00E+00 | NO | NO | NO | NO |
| AT4G20960 | 16.54 | 18.25 | 36.04 | 36.11 | 0.98 | 1.80E-07 | NEGATIVE | NO | NO | NO |
| AT4G21390 | 3.99 | 0.88 | 1.37 | 2.88 | 1.72 | 1.51E-05 | NO | NO | NO | NO |
| AT4G21640 | 0.00 | 0.02 | 2.05 | 1.98 | 7.03 | 2.98E-05 | NO | NO | NO | NO |
| AT4G21680 | 25.71 | 2.15 | 1.19 | 4.43 | 1.04 | 2.78E-03 | NO | NO | NO | NO |
| AT4G21750 | 10.66 | 11.42 | 19.72 | 22.57 | 0.98 | 7.15E-09 | NO | YES | NO | NO |
| AT4G21870 | 1.30 | 1.55 | 19.68 | 15.79 | 3.35 | 1.63E-10 | NO | NO | DOWN | NO |
| AT4G22485 | 22.65 | 15.17 | 47.77 | 42.46 | 1.48 | 0.00E+00 | NO | NO | NO | NO |
| AT4G22505 | 23.62 | 15.78 | 46.45 | 32.43 | 1.04 | 4.58E-08 | NO | NO | NO | NO |
| AT4G22570 | 24.92 | 33.82 | 80.97 | 60.33 | 0.84 | 1.86E-05 | NEGATIVE | NO | NO | NO |
| AT4G23150 | 8.73 | 2.59 | 35.84 | 43.22 | 4.06 | 0.00E+00 | NO | NO | NO | NO |
| AT4G23160 | 2.48 | 0.81 | 11.42 | 15.01 | 4.22 | 0.00E+00 | NO | NO | NO | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT4G23200 | 1.57 | 0.18 | 5.09 | 10.00 | 5.83 | 0.00E+00 | NO | NO | NO | NO |
| AT4G23210 | 0.97 | 0.47 | 4.55 | 16.91 | 5.16 | 0.00E+00 | NO | NO | NO | NO |
| AT4G23220 | 0.13 | 0.16 | 22.00 | 33.28 | 7.73 | 0.00E+00 | NO | NO | NO | NO |
| AT4G23230 | 0.37 | 0.13 | 4.68 | 6.03 | 5.56 | 0.00E+00 | NO | NO | NO | NO |
| AT4G23260 | 8.05 | 8.04 | 16.25 | 31.92 | 1.99 | 0.00E+00 | NO | NO | NO | DOWN |
| AT4G23810 | 6.69 | 3.47 | 26.46 | 34.17 | 3.30 | 0.00E+00 | NO | YES | NO | NO |
| AT4G23880 | 13.60 | 9.62 | 38.28 | 24.62 | 1.36 | 1.67E-06 | NO | NO | NO | NO |
| AT4G24780 | 22.92 | 36.43 | 52.97 | 55.53 | 0.61 | 1.13E-03 | NO | NO | DOWN | NO |
| AT4G25000 | 2.39 | 1.11 | 34.11 | 16.94 | 3.93 | 0.00E+00 | NO | NO | NO | NO |
| AT4G25110 | 0.33 | 0.30 | 8.48 | 17.10 | 5.85 | 0.00E+00 | NO | NO | NO | NO |
| AT4G26760 | 4.22 | 6.75 | 9.89 | 11.74 | 0.80 | 4.03E-04 | NO | NO | NO | NO |
| AT4G29520 | 49.07 | 32.64 | 96.39 | 118.75 | 1.86 | 0.00E+00 | NO | NO | NO | NO |
| AT4G29700 | 3.35 | 1.29 | 9.68 | 12.68 | 3.29 | 0.00E+00 | NO | NO | NO | NO |
| AT4G29905 | 55.47 | 48.47 | 148.11 | 71.06 | 0.55 | 1.33E-02 | NO | NO | NO | NO |
| AT4G30720 | 35.61 | 41.66 | 191.54 | 154.76 | 1.89 | 0.00E+00 | NO | NO | POSITIVE | NO |
| AT4G31790 | 28.25 | 16.79 | 49.15 | 25.75 | 0.62 | 1.89E-03 | NO | NO | NO | NO |
| AT4G31870 | 0.15 | 0.10 | 8.52 | 18.24 | 7.48 | 1.76E-09 | NO | NO | NO | NO |
| AT4G32340 | 52.99 | 63.93 | 104.36 | 105.77 | 0.73 | 7.26E-05 | NEGATIVE | NO | NO | NO |
| AT4G33355 | 0.35 | 1.30 | 4.66 | 4.65 | 1.84 | 1.93E-03 | NO | NO | NO | NO |
| AT4G33360 | 1.50 | 1.27 | 28.27 | 35.06 | 4.79 | 0.00E+00 | NO | NO | NO | NO |
| AT4G33560 | 2.57 | 3.57 | 16.73 | 22.73 | 2.67 | 5.96E-09 | NO | NO | NO | NO |
| AT4G34131 | 10.82 | 2.79 | 2.27 | 4.75 | 0.77 | 4.29E-02 | NO | NO | NO | NO |
| AT4G34760 | 20.41 | 30.15 | 50.28 | 46.20 | 0.62 | 9.34E-03 | NO | NO | NO | NO |
| AT4G34930 | 0.30 | 0.28 | 1.68 | 1.20 | 2.10 | 7.51E-03 | NO | NO | NO | NO |
| AT4G36130 | 168.11 | 135.32 | 340.21 | 189.28 | 0.48 | 1.31E-02 | NO | NO | NO | NO |
| AT4G37150 | 0.37 | 0.33 | 8.36 | 7.53 | 4.53 | 2.38E-10 | NO | NO | NO | NO |
| AT4G37370 | 21.47 | 4.72 | 7.09 | 19.85 | 2.07 | 0.00E+00 | NO | NO | NO | NO |
| AT4G37800 | 13.58 | 16.03 | 28.25 | 26.50 | 0.73 | 1.36E-03 | NO | NO | DOWN | NO |
| AT4G37990 | 54.06 | 1.88 | 6.82 | 13.51 | 2.84 | 0.00E+00 | NO | NO | NO | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT4G38540 | 45.54 | 19.59 | 15.45 | 27.95 | 0.51 | 1.83E-02 | NO | NO | NO | NO |
| AT4G38840 | 44.11 | 46.52 | 90.62 | 77.15 | 0.73 | 7.53E-04 | NEGATIVE | NO | DOWN | NO |
| AT4G38850 | 2.78 | 5.66 | 14.53 | 18.83 | 1.73 | 1.05E-04 | NO | NO | NO | NO |
| AT4G39830 | 3.48 | 2.22 | 10.73 | 20.43 | 3.20 | 0.00E+00 | NO | NO | NO | NO |
| AT4G40060 | 4.53 | 4.79 | 22.83 | 23.79 | 2.31 | 0.00E+00 | NO | YES | NO | NO |
| AT5G01290 | 9.47 | 7.84 | 21.66 | 16.99 | 1.12 | 1.53E-08 | NO | NO | NO | NO |
| AT5G01550 | 0.41 | 0.16 | 2.78 | 4.75 | 4.91 | 3.63E-14 | NO | NO | NO | NO |
| AT5G02020 | 35.83 | 0.66 | 3.40 | 2.87 | 2.13 | 7.64E-04 | NO | NO | NO | NO |
| AT5G03380 | 9.37 | 5.61 | 26.68 | 36.04 | 2.68 | 0.00E+00 | NO | NO | NO | NO |
| AT5G03760 | 28.57 | 24.06 | 54.54 | 35.95 | 0.58 | 2.22E-03 | NEGATIVE | NO | NO | NO |
| AT5G05600 | 34.73 | 6.61 | 13.01 | 16.77 | 1.34 | 4.96E-08 | NO | NO | NO | NO |
| AT5G06860 | 111.41 | 24.82 | 24.92 | 36.68 | 0.56 | 8.38E-03 | POSITIVE | NO | POSITIVE | NO |
| AT5G06870 | 6.34 | 2.96 | 31.45 | 33.70 | 3.51 | 0.00E+00 | NO | NO | NO | NO |
| AT5G07440 | 95.06 | 24.31 | 29.15 | 33.46 | 0.46 | 3.45E-03 | NO | NO | NO | NO |
| AT5G08760 | 37.63 | 27.22 | 141.56 | 191.60 | 2.82 | 0.00E+00 | NO | NO | NO | NO |
| AT5G09290 | 0.10 | 0.07 | 4.08 | 10.26 | 7.25 | 3.40E-11 | NO | NO | NO | NO |
| AT5G10380 | 28.68 | 11.78 | 77.88 | 95.21 | 3.01 | 0.00E+00 | NO | NO | NO | NO |
| AT5G10572 | 98.89 | 110.74 | 760.83 | 397.41 | 1.84 | 2.04E-02 | NO | NO | NO | NO |
| AT5G10760 | 176.34 | 39.35 | 736.26 | 639.62 | 4.02 | 0.00E+00 | NO | NO | NO | NO |
| AT5G11580 | 22.24 | 27.12 | 47.35 | 49.09 | 0.86 | 1.27E-06 | NO | NO | NO | NO |
| AT5G11930 | 1.44 | 2.45 | 6.86 | 9.30 | 1.92 | 1.11E-04 | NO | NO | NO | NO |
| AT5G13330 | 18.68 | 1.39 | 2.58 | 5.29 | 1.93 | 9.54E-05 | NO | YES | NO | NO |
| AT5G14800 | 53.65 | 58.66 | 134.11 | 113.66 | 0.95 | 1.61E-08 | NO | NO | NO | NO |
| AT5G15350 | 24.99 | 24.67 | 50.17 | 39.89 | 0.69 | 2.26E-03 | NO | NO | NO | NO |
| AT5G15948 | 2.17 | 1.90 | 7.38 | 7.70 | 2.02 | 8.79E-10 | NO | NO | NO | NO |
| AT5G15950 | 209.86 | 167.81 | 524.89 | 521.42 | 1.64 | 0.00E+00 | NO | NO | POSITIVE | NO |
| AT5G16250 | 9.47 | 16.30 | 28.16 | 38.53 | 1.24 | 1.49E-08 | NO | NO | NO | NO |
| AT5G16960 | 10.89 | 0.52 | 1.16 | 2.74 | 2.40 | 1.45E-04 | NO | NO | NO | NO |
| AT5G17220 | 13.42 | 10.00 | 31.84 | 20.41 | 1.03 | 5.70E-04 | NO | NO | NO | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G17330 | 0.19 | 0.09 | 1.44 | 3.30 | 5.17 | 3.60E-10 | NO | NO | NO | NO |
| AT5G17760 | 27.54 | 20.50 | 13.33 | 31.07 | 0.60 | 1.72E-03 | NO | NO | NO | NO |
| AT5G17860 | 9.24 | 2.12 | 3.47 | 7.35 | 1.80 | 8.77E-09 | NO | NO | NO | NO |
| AT5G18130 | 42.01 | 17.91 | 22.50 | 30.90 | 0.79 | 4.64E-05 | NO | NO | NO | NO |
| AT5G18470 | 26.63 | 16.32 | 100.75 | 112.36 | 2.78 | 0.00E+00 | NO | NO | NO | NO |
| AT5G19190 | 11.17 | 9.65 | 34.82 | 32.59 | 1.76 | 1.42E-09 | NO | NO | NO | NO |
| AT5G19240 | 144.36 | 94.13 | 348.53 | 448.98 | 2.25 | 0.00E+00 | NO | NO | NO | NO |
| AT5G19880 | 0.40 | 0.20 | 3.05 | 6.69 | 5.06 | 1.03E-10 | NO | NO | NO | NO |
| AT5G20480 | 5.04 | 3.18 | 2.10 | 4.76 | 0.58 | 4.25E-02 | NO | NO | NO | NO |
| AT5G21060 | 8.49 | 11.15 | 38.30 | 35.90 | 1.69 | 0.00E+00 | NO | NO | NO | NO |
| AT5G22300 | 62.12 | 19.15 | 12.16 | 29.39 | 0.62 | 3.25E-03 | POSITIVE | NO | NO | NO |
| AT5G22320 | 12.95 | 11.74 | 27.48 | 21.53 | 0.87 | 9.98E-06 | NO | NO | NO | NO |
| AT5G22330 | 27.69 | 22.99 | 55.09 | 38.23 | 0.73 | 8.43E-05 | NO | NO | NO | NO |
| AT5G22390 | 11.93 | 15.89 | 36.79 | 28.81 | 0.86 | 7.94E-05 | NO | NO | NO | NO |
| AT5G22520 | 0.00 | 0.15 | 4.27 | 25.53 | 7.38 | 6.83E-11 | NO | NO | NO | NO |
| AT5G23010 | 254.95 | 112.20 | 598.88 | 236.47 | 1.08 | 1.77E-08 | NO | NO | NO | NO |
| AT5G24110 | 6.01 | 1.92 | 26.95 | 22.99 | 3.58 | 0.00E+00 | NO | YES | NO | NO |
| AT5G24150 | 0.18 | 0.19 | 7.90 | 6.41 | 5.08 | 0.00E+00 | NO | NO | DOWN | NO |
| AT5G24200 | 16.84 | 5.63 | 2.09 | 10.66 | 0.92 | 1.53E-03 | NO | NO | NO | NO |
| AT5G24530 | 36.09 | 12.93 | 267.38 | 257.60 | 4.32 | 0.00E+00 | NO | NO | NO | NO |
| AT5G24655 | 1.12 | 1.74 | 14.39 | 32.58 | 4.22 | 0.00E+00 | NO | NO | NO | NO |
| AT5G24770 | 1.54 | 0.57 | 6.75 | 3.00 | 2.40 | 3.65E-05 | NO | NO | NO | NO |
| AT5G25180 | 0.03 | 0.01 | 3.54 | 3.95 | 8.41 | 0.00E+00 | NO | NO | NO | NO |
| AT5G25220 | 14.99 | 15.06 | 38.23 | 41.50 | 1.46 | 0.00E+00 | NO | NO | NO | NO |
| AT5G25460 | 29.36 | 38.13 | 0.00 | 70.33 | 0.88 | 3.72E-07 | NEGATIVE | NO | NO | NO |
| AT5G26340 | 83.69 | 28.78 | 33.14 | 59.47 | 1.05 | 4.10E-10 | NO | NO | NO | NO |
| AT5G28770 | 14.11 | 10.86 | 26.57 | 18.54 | 0.77 | 3.20E-04 | NO | YES | NO | NO |
| AT5G33290 | 32.79 | 19.84 | 15.41 | 26.90 | 0.44 | 3.94E-02 | POSITIVE | NO | NO | NO |
| AT5G35790 | 28.51 | 33.15 | 55.80 | 54.01 | 0.70 | 8.49E-05 | NO | NO | DOWN | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G36930 | 0.03 | 0.04 | 9.88 | 14.82 | 8.58 | 0.00E+00 | NO | NO | NO | NO |
| AT5G38150 | 2.82 | 3.04 | 7.40 | 10.21 | 1.75 | 6.41E-10 | NO | NO | NO | NO |
| AT5G38430 | 502.18 | 303.86 | 1114.11 | 450.18 | 0.57 | 5.81E-03 | NO | NO | NO | NO |
| AT5G38940 | 2.44 | 1.36 | 8.85 | 5.87 | 2.11 | 2.71E-04 | NO | NO | NO | NO |
| AT5G39050 | 39.29 | 14.02 | 17.57 | 24.86 | 0.83 | 5.97E-05 | NO | NO | NO | UP |
| AT5G39100 | 4.64 | 2.45 | 15.28 | 13.82 | 2.50 | 1.86E-09 | NO | NO | NO | NO |
| AT5G40340 | 9.70 | 8.56 | 18.04 | 18.67 | 1.13 | 7.32E-10 | NO | NO | NO | NO |
| AT5G41590 | 8.78 | 6.79 | 30.90 | 28.87 | 2.09 | 7.83E-13 | NO | NO | NO | NO |
| AT5G42020 | 49.68 | 38.33 | 97.39 | 165.70 | 2.11 | 0.00E+00 | NO | NO | NO | NO |
| AT5G43440 | 5.34 | 4.46 | 19.91 | 27.97 | 2.65 | 0.00E+00 | NO | NO | NO | NO |
| AT5G43450 | 45.30 | 28.89 | 20.52 | 42.35 | 0.55 | 6.21E-03 | NO | NO | NO | NO |
| AT5G43870 | 4.66 | 5.91 | 11.83 | 14.23 | 1.27 | 1.37E-07 | NEGATIVE | NO | NO | NO |
| AT5G44020 | 14.42 | 18.81 | 68.46 | 53.72 | 1.51 | 0.00E+00 | NO | NO | DOWN | NO |
| AT5G44420 | 247.91 | 152.80 | 38.75 | 439.65 | 1.52 | 8.73E-14 | NO | NO | NO | DOWN |
| AT5G44430 | 65.29 | 16.67 | 13.26 | 143.59 | 3.11 | 0.00E+00 | NO | NO | NO | NO |
| AT5G44568 | 7.92 | 7.74 | 91.63 | 213.40 | 4.78 | 0.00E+00 | NO | NO | NO | NO |
| AT5G44570 | 1.01 | 1.66 | 70.24 | 205.43 | 6.95 | 0.00E+00 | NO | NO | NO | NO |
| AT5G45030 | 7.76 | 9.69 | 15.09 | 20.65 | 1.09 | 5.39E-14 | NO | NO | NO | NO |
| AT5G45100 | 14.53 | 12.18 | 32.52 | 33.33 | 1.45 | 9.92E-13 | NO | NO | NO | NO |
| AT5G45380 | 6.08 | 5.31 | 14.72 | 24.19 | 2.19 | 0.00E+00 | NO | NO | NO | NO |
| AT5G45670 | 6.08 | 7.28 | 16.26 | 16.66 | 1.19 | 3.23E-07 | NEGATIVE | NO | NO | NO |
| AT5G45820 | 5.13 | 3.95 | 24.64 | 14.53 | 1.88 | 1.30E-12 | NO | NO | NO | NO |
| AT5G45950 | 19.00 | 19.65 | 37.98 | 31.20 | 0.67 | 1.05E-03 | NO | NO | NO | NO |
| AT5G46050 | 10.26 | 4.17 | 40.63 | 49.94 | 3.58 | 0.00E+00 | NO | NO | NO | UP |
| AT5G46260 | 4.72 | 5.35 | 10.60 | 18.57 | 1.80 | 0.00E+00 | NO | NO | NO | NO |
| AT5G46490 | 0.06 | 0.03 | 3.09 | 5.71 | 7.41 | 0.00E+00 | NO | NO | NO | NO |
| AT5G46500 | 0.38 | 0.30 | 30.99 | 56.23 | 7.57 | 0.00E+00 | NO | NO | NO | NO |
| AT5G47630 | 49.93 | 41.40 | 96.89 | 59.28 | 0.52 | 2.95E-02 | NO | NO | NO | NO |
| AT5G48110 | 0.73 | 1.84 | 8.17 | 13.05 | 2.83 | 0.00E+00 | NO | NO | NO | NO |

**Table A3.6 (cont'd)**

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| AT5G48620 | 4.61 | 4.51 | 10.10 | 14.20 | 1.66 | 0.00E+00 | NO | NO | NO | NO |
| AT5G48960 | 4.94 | 3.71 | 32.53 | 23.14 | 2.64 | 0.00E+00 | NO | NO | NO | NO |
| AT5G49360 | 0.96 | 1.14 | 4.55 | 6.88 | 2.60 | 0.00E+00 | NO | NO | DOWN | NO |
| AT5G50915 | 3.20 | 2.03 | 8.64 | 6.95 | 1.77 | 7.91E-07 | NO | YES | NO | NO |
| AT5G51460 | 3.26 | 3.50 | 6.92 | 7.05 | 1.01 | 4.99E-04 | NO | NO | NO | NO |
| AT5G52750 | 18.24 | 12.67 | 47.35 | 76.53 | 2.59 | 0.00E+00 | NO | NO | NO | NO |
| AT5G53460 | 50.53 | 36.75 | 87.25 | 63.80 | 0.80 | 1.38E-07 | NO | NO | NO | NO |
| AT5G54610 | 10.49 | 10.41 | 65.06 | 95.39 | 3.20 | 0.00E+00 | NO | NO | NO | NO |
| AT5G54720 | 3.54 | 3.20 | 17.20 | 37.96 | 3.57 | 0.00E+00 | NO | NO | NO | NO |
| AT5G55450 | 429.86 | 232.46 | 1212.13 | 1217.23 | 2.39 | 0.00E+00 | NO | NO | NO | NO |
| AT5G55460 | 21.38 | 17.30 | 50.62 | 48.44 | 1.48 | 1.09E-07 | NO | NO | NO | NO |
| AT5G55510 | 17.65 | 15.66 | 45.22 | 27.38 | 0.81 | 1.27E-03 | NO | NO | NO | NO |
| AT5G57180 | 20.19 | 19.02 | 55.08 | 41.30 | 1.12 | 0.00E+00 | NO | YES | NO | NO |
| AT5G57700 | 2.23 | 3.73 | 6.77 | 9.50 | 1.35 | 1.92E-06 | NO | NO | NO | NO |
| AT5G60900 | 7.85 | 6.90 | 16.51 | 30.42 | 2.14 | 0.00E+00 | NO | NO | NO | NO |
| AT5G62630 | 14.13 | 16.33 | 35.41 | 40.32 | 1.30 | 3.66E-14 | NO | NO | NO | NO |
| AT5G63120 | 16.93 | 12.95 | 36.74 | 26.45 | 1.03 | 4.00E-09 | NO | NO | NO | NO |
| AT5G64000 | 10.02 | 2.43 | 23.80 | 17.27 | 2.83 | 0.00E+00 | NO | NO | NO | NO |
| AT5G65730 | 39.44 | 44.38 | 79.15 | 68.68 | 0.63 | 1.16E-03 | NEGATIVE | NO | NO | NO |
| AT5G66052 | 0.05 | 0.05 | 10.64 | 13.49 | 8.05 | 8.75E-07 | NO | NO | NO | NO |
| AT5G66053 | 4.51 | 0.00 | 120.50 | 146.67 | Inf | 3.87E-03 | NO | NO | NO | NO |
| AT5G66630 | 0.08 | 0.14 | 2.07 | 4.36 | 4.97 | 0.00E+00 | NO | YES | NO | NO |
| AT5G66690 | 0.38 | 0.12 | 10.26 | 9.50 | 6.28 | 0.00E+00 | NO | NO | NO | NO |

**Table A3.7.** Primer pairs used for qRT-PCR and sequencing. QRT-PCR Primers used in this study were designed with Primer Express 3.0.

EQTL PRIMERS

| AGI | NAME | FW | RV |
|---|---|---|---|
| AT1G27730 | ZAT10 | TCGAGCACTGGACAAAGGGTAAGC | CCTGAGTGAGGTTTTGGTGGTGGA |
| AT1G29390 | COR314 | CCAGGTGAACTTGAGCTTCCA | TGATATGGCGCCACAATCA |
| AT2G42540 | COR15A | CGTTGATCTACGCCGCTAAAG | TGGCCTCGTTGAGGTCATC |
| AT3G55980 | STZ1 | TGTCCCCTGTCCCGAGTTC | CGTGAGCATACTCGCAAGAATC |
| AT5G59820 | ZAT12 | GTGCGAGTCACAAGAAGCCTAACA | GCGACGACGTTTTCACCTTCTTCA |
| AT1G20440 | COR47 | CGGTACCAGTGTCGGAGAGT | ACAGCTGGTGAATCCTCTGC |
| AT1G20450 | ERD10 | TTCCAGGCCACAGCAAGAA | CAACCAGCGGTGTGGTGTT |
| AT1G75040 | PR5 | AACGGCGGCGGAGTTC | CGCCATCGCCTACTAGAGTGA |
| AT4G15910 | DI21 | TGGCCGCTCGTTCACTCT | TGCGGCGGAGCAAAGA |
| AT5G52310 | COR78 | GAAAGGAGGAGGAGGAATGG | AACCAGCCAGATGATTTTGG |
| AT3G02780 | IPP2 | ATTTGCCCATCGTCCTCTGT | GAGAAAGCACGAAAATTCGGTAA |
| AT2G41100 | TCH3 | CAATATCATCGCTTCGCCAAT | ATAACAGCGCTTCGAACAAATCT |

SEQUENCING PRIMERS

| AGI | NAME | FW | RV |
|---|---|---|---|
| AT4G25490 | CBF1 | GGGATTGCTTCGCTATGTACTATACACGTGTC | TCCACATATTTTGCCTTGAAAGCAACTACAATATGAC |
| AT4G25470 | CBF2 | ATCCAAATATCTTCCGGCCAATATAAACAGCAAGCT | AGCAGAAAGGCAGAAACTGTTGCTATCAACCAAC |
| AT4G25480 | CBF3 | CCGCCATTATAAAACAGCATGCTCTCACTCC | GCTGAATCGGTTGTTTCGGTTTTATACTCTAATTTAAAC |
| AT2G42540 | COR15A | GGCCTGAAAAGAACGAACAGAAACTCGGTAATG | GGTACAACAATGTATCATACCAATTCGATGTCATAC |
| AT1G20440 | COR47 | GTTACCTCCGCGTTGGCCTGGACCCTTCTC | CCTAAGAAGCCAGATGGCGAAATATTGAAATATTCG |
| AT5G52310 | COR78 | CCCTCCTCTGTTTTACTCACAAATATGCAAACTAG | CTTTAACGATAGAGACAACACCTCAACAAGTCAC |

**Table A3.8**. Number of reads passing the Illumina purity filter for each RNA-seq sample. The lane name represents the lane in which each sample was run. 'PF clusters' indicates reads passing Illumina purity filters, while 'Raw Clusters' denotes all reads. For the sample names: 'SW' indicates the Swedish accession; 'IT' indicates the Italian accession; 'NONACC' indicates the samples not cold-acclimated, '1WK' indicates samples cold-acclimated for 1 week; '2WK' indicates samples cold-acclimated for 2 weeks; the last number in the sample name indicates biological replicate number.

| Lane | Sample | Raw Clusters | PF Clusters | Sample % PF |
|---|---|---|---|---|
| 1 | SW-NONACC-1 | 29,958,443 | 24,697,162 | 82.4% |
| 4 | SW-NONACC-1 | 29,918,355 | 24,249,872 | 81.1% |
| | **SW-NONACC-1 Total** | **59,876,798** | **48,947,034** | **81.7%** |
| 1 | SW-NONACC-2 | 25,139,472 | 20,662,571 | 82.2% |
| 4 | SW-NONACC-2 | 25,085,948 | 20,259,178 | 80.8% |
| | **SW-NONACC-2 Total** | **50,225,420** | **40,921,749** | **81.5%** |
| 1 | SW-NONACC-3 | 24,918,522 | 20,505,290 | 82.3% |
| 4 | SW-NONACC-3 | 24,880,981 | 20,140,545 | 80.9% |
| | **SW-NONACC-3 Total** | **49,799,503** | **40,645,835** | **81.6%** |
| 1 | IT-NONACC-1 | 28,636,037 | 23,420,339 | 81.8% |
| 4 | IT-NONACC-1 | 28,552,106 | 22,949,660 | 80.4% |
| | **IT-NONACC-1 Total** | **57,188,143** | **46,369,999** | **81.1%** |
| 1 | IT-NONACC-2 | 24,842,595 | 20,467,125 | 82.4% |
| 4 | IT-NONACC-2 | 24,815,959 | 20,088,847 | 81.0% |
| | **IT-NONACC-2 Total** | **49,658,554** | **40,555,972** | **81.7%** |
| 1 | IT-NONACC-3 | 31,151,487 | 25,609,805 | 82.2% |
| 4 | IT-NONACC-3 | 31,118,564 | 25,143,267 | 80.8% |
| | **IT-NONACC-3 Total** | **62,270,051** | **50,753,072** | **81.5%** |
| 2 | SW-1WK-1 | 28,952,674 | 23,350,344 | 80.7% |
| 5 | SW-1WK-1 | 28,715,485 | 22,777,897 | 79.3% |
| | **SW-1WK Total** | **57,668,159** | **46,128,241** | **80.0%** |
| 2 | SW-1WK-2 | 26,129,644 | 21,279,472 | 81.4% |

**Table A3.8 cont'd**

| | | | | |
|---|---|---|---|---|
| 5 | SW-1WK-2 | 25,897,791 | 20,772,596 | 80.2% |
| | **SW-1WK-2 Total** | **52,027,435** | **42,052,068** | **80.8%** |
| 2 | SW-1WK-3 | 29,760,111 | 24,072,758 | 80.9% |
| 5 | SW-1WK-3 | 29,565,270 | 23,523,986 | 79.6% |
| | **SW-1WK-3 Total** | **59,325,381** | **47,596,744** | **80.2%** |
| 2 | IT-1WK-1 | 29,677,878 | 24,017,917 | 80.9% |
| 5 | IT-1WK-1 | 29,401,956 | 23,424,329 | 79.7% |
| | **IT-1WK-1 Total** | **59,079,834** | **47,442,246** | **80.3%** |
| 2 | IT-1WK-2 | 29,822,085 | 24,213,801 | 81.2% |
| 5 | IT-1WK-2 | 29,615,504 | 23,659,830 | 79.9% |
| | **IT-1WK-2 Total** | **59,437,589** | **47,873,631** | **80.5%** |
| 2 | IT-1WK-3 | 23,782,918 | 19,711,843 | 82.9% |
| 5 | IT-1WK-3 | 23,506,197 | 19,220,083 | 81.8% |
| | **IT-1WK-3 Total** | **47,289,115** | **38,931,926** | **82.3%** |
| 3 | SW-2WK-1 | 28,637,922 | 23,936,002 | 83.6% |
| 6 | SW-2WK-1 | 28,377,699 | 23,775,237 | 83.8% |
| | **SW-2WK-1 Total** | **57,015,621** | **47,711,239** | **83.7%** |
| 3 | SW-2WK-2 | 25,168,550 | 21,001,016 | 83.4% |
| 6 | SW-2WK-2 | 24,935,016 | 20,853,600 | 83.6% |
| | **SW-2WK-2 Total** | **50,103,566** | **41,854,616** | **83.5%** |
| 3 | SW-2WK-3 | 25,484,480 | 21,280,683 | 83.5% |
| 6 | SW-2WK-3 | 25,236,381 | 21,125,228 | 83.7% |
| | **SW-2WK-3 Total** | **50,720,861** | **42,405,911** | **83.6%** |
| 3 | IT-2WK-1 | 32,233,028 | 26,752,432 | 83.0% |
| 6 | IT-2WK-1 | 31,955,554 | 26,583,643 | 83.2% |
| | **IT-2WK-1 Total** | **64,188,582** | **53,336,075** | **83.1%** |
| 3 | IT-2WK-2 | 26,054,424 | 21,749,785 | 83.5% |
| 6 | IT-2WK-2 | 25,813,016 | 21,599,147 | 83.7% |

**Table A3.8 cont'd**

| | | | | |
|---|---|---|---|---|
| | **IT-2WK-2 Total** | **51,867,440** | **43,348,932** | **83.6%** |
| 3 | IT-2WK-3 | 28,738,532 | 23,962,836 | 83.4% |
| 6 | IT-2WK-3 | 28,468,237 | 23,789,534 | 83.6% |
| | **IT-2WK-3 Total** | **57,206,769** | **47,752,370** | **83.5%** |
| | Grand Total | 994,948,821 | 814,627,660 | 81.9% |

**Table A3.9.** Summary of SW and IT RNA-seq samples. 'Average PF Clusters' indicates the average number of reads passing the Illumina purity filters for each sample. '# Genes' indicates the number of genes in each sample. 'Average R2' indicates the average correlation of genes for each biological replicate when all comparisons are made (i.e. replicate 1 to 2, replicate 2 to 3, and replicate 1 to 3) ± the standard error. While calculating the correlation ($R^2$) for each sample genes that were outliers were removed, none of the outliers removed from cold samples were genes found to be cold regulated and none of the outliers removed from non-acclimated samples were included in the list of genes differentially regulated between SW and IT. The total number of genes removed from calculating correlation was small (18 genes total) in comparison to the number of genes analyzed ('# Genes'). Genes removed were: AT1G15800, AT1G26240, AT1G50310, AT1G71070, AT2G19790, AT2G23740, AT2G30370, AT3G13061, AT4G08109, AT4G15020, AT4G15620, AT5G07720, AT5G08480, AT5G20620, AT5G27450, AT5G35900, AT5G47450, and AT5G58787.

| Sample | Average PF Clusters | # GENES | Average R2 | Maximum FPKM |
|---|---|---|---|---|
| **SW-NONACC Average** | 43,504,873 | 23,127 | 0.90 ± 0.015 | 28,114 |
| **IT-NONACC Average** | 45,893,014 | 23,429 | 0.90 ± 0.032 | 24,553 |
| **SW-1WK Average** | 45,259,018 | 23,303 | 0.88 ± 0.022 | 42,983 |
| **IT-1WK Average** | 44,749,268 | 23,123 | 0.91 ± 0.012 | 18,584 |
| **SW-2WK Average** | 43,990,589 | 22,818 | 0.90 ± 0.015 | 35,927 |
| **IT-2WK Average** | 48,145,792 | 23,785 | 0.90 ± 0.013 | 20,597 |

## LITERATURE CITED

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1. Fournier-Level A, Korte A, Cooper MD, Nordborg M, Schmitt J, & Wilczek AM (2011) A Map Of Local Adaptation In Arabidopsis Thaliana. *Science* 334(6052):86-89.

2. Gaut B (2012) Arabidopsis Thaliana As A Model For The Genetics Of Local Adaptation. *Nat Genet* 44(2):115-116.

3. Leimu R & Fischer M (2008) A Meta-Analysis Of Local Adaptation In Plants. *Plos One* 3(12):e4010.

4. Li Y, Huang Y, Bergelson J, Nordborg M, & Borevitz JO (2010) Association Mapping Of Local Climate-Sensitive Quantitative Trait Loci In Arabidopsis Thaliana. *Proceedings of the National Academy of Sciences* 107(49):21199-21204.

5. Barrett RDH & Hoekstra HE (2011) Molecular Spandrels: Tests Of Adaptation At The Genetic Level. *Nature Reviews Genetics* 12(11):767-780.

6. Hannah MA, Wiese D, Freund S, Fiehn O, Heyer AG, & Hincha DK (2006) Natural Genetic Variation Of Freezing Tolerance In Arabidopsis. *Plant Physiology* 142(1):98-112.

7. Koornneef M, Alonso-Blanco C, & Vreugdenhil D (2004) Naturally Occurring Genetic Variation In Arabidopsis Thaliana. *Annual Review of Plant Biology* 55:141-172.

8. Agren J & Schemske DW (2012) Reciprocal Transplants Demonstrate Strong Adaptive Differentiation Of The Model Organism *Arabidopsis Thaliana* In Its Native Range. *New Phytologist* In Press.

9. Keurentjes JJB, Bentsink L, Alonso-Blanco C, Hanhart CJ, Blankestijn-De Vries H, Effgen S, Vreugdenhil D, & Koornneef M (2007) Development Of A Near-Isogenic Line Population Of Arabidopsis Thaliana And Comparison Of Mapping Power With A Recombinant Inbred Line Population. *Genetics* 175(2):891-905.

10. Alonso-Blanco C, Gomez-Mena C, Llorente F, Koornneef M, Salinas J, & Martínez-Zapater JM (2005) Genetic And Molecular Analyses Of Natural Variation Indicate CBF2 As A Candidate Gene For Underlying A Freezing Tolerance Quantitative Trait Locus In Arabidopsis. *Plant Physiology* 139(3):1304-1312.

11. Hammond JP, Mayes S, Bowen HC, Graham NS, Hayden RM, Love CG, Spracklen WP, Wang J, Welham SJ, White PJ, King GJ, & Broadley MR (2011) Regulatory Hotspots Are Associated With Plant Gene Expression Under Varying Soil Phosphorus Supply In Brassica Rapa. *Plant Physiology* 156(3):1230-1241.

12. Kliebenstein D (2009) Quantitative Genomics: Analyzing Intraspecific Variation Using Global Gene Expression Polymorphisms Or EQTL. *Annual Review of Plant Biology* 60(1):93-114.

13. Keurentjes JJB, Fu JY, Terpstra IR, Garcia JM, van den Ackerveken G, Snoek LB, Peeters AJM, Vreugdenhil D, Koornneef M, & Jansen RC (2007) Regulatory Network Construction In Arabidopsis By Using Genome-Wide Gene Expression Quantitative Trait Loci. *Proceedings of the National Academy of Sciences of the United States of America* 104(5):1708-1713.

14. Majewski J & Pastinen T (2011) The Study Of EQTL Variations By RNA-Seq: From SNPs To Phenotypes. *Trends in Genetics* 27(2):72-79.

15. Broman KW, Wu H, Sen Ś, & Churchill GA (2003) R/qtl: QTL mapping in experimental crosses. *Bioinformatics* 19(7):889-890.

16. Dong MA, Farre EM, & Thomashow MF (2011) CIRCADIAN CLOCK-ASSOCIATED 1 And LATE ELONGATED HYPOCOTYL Regulate Expression Of The C-REPEAT BINDING FACTOR (CBF) Pathway In Arabidopsis. *Proceedings of the National Academy of Sciences of the United States of America* 108(17):7241-7246.

17. Zhen Y & Ungerer MC (2008) Clinal Variation In Freezing Tolerance Among Natural Accessions Of Arabidopsis Thaliana. *New Phytologist* 177(2):419-427.

18. Trapnell C, Williams BA, Pertea G, Mortazavi A, Kwan G, van Baren MJ, Salzberg SL, Wold BJ, & Pachter L (2010) Transcript Assembly And Quantification By RNA-Seq Reveals Unannotated Transcripts And Isoform Switching During Cell Differentiation. *Nat Biotechnol* 28(5):511-515.

19. Deng X, Gu L, Liu C, Lu T, Lu F, Lu Z, Cui P, Pei Y, Wang B, Hu S, & Cao X (2010) Arginine Methylation Mediated By The Arabidopsis Homolog Of PRMT5 Is Essential For Proper Pre-Mrna Splicing. *Proceedings of the National Academy of Sciences of the United States of America* 107(44):19114-19119.

20. Mortazavi A, Williams BA, McCue K, Schaeffer L, & Wold B (2008) Mapping And Quantifying Mammalian Transcriptomes By RNA-Seq. *Nat Methods* 5(7):621-628.

21. Jaglo-Ottosen KR, Gilmour SJ, Zarka DG, Schabenberger O, & Thomashow MF (1998) Arabidopsis CBF1 Overexpression Induces COR Genes And Enhances Freezing Tolerance. *Science* 280(5360):104-106.

22. Liu Q, Kasuga M, Sakuma Y, Abe H, Miura S, Yamaguchi-Shinozaki K, & Shinozaki K (1998) Two Transcription Factors, DREB1 And DREB2, With An EREBP/AP2 DNA Binding Domain Separate Two Cellular Signal Transduction Pathways In Drought- And Low-Temperature-Responsive Gene Expression, Respectively, In Arabidopsis. *Plant Cell* 10(8):1391-1406.

23. Gilmour SJ, Sebolt AM, Salazar MP, Everard JD, & Thomashow MF (2000) Overexpression Of The Arabidopsis CBF3Transcriptional Activator Mimics Multiple Biochemical Changes Associated With Cold Acclimation. *Plant Physiology* 124(4):1854-1865.

24. Gilmour SJ, Fowler SG, & Thomashow MF (2004) Arabidopsis Transcriptional Activators CBF1, CBF2, And CBF3 Have Matching Functional Activities. *Plant Molecular Biology* 54(5):767-781.

25. Vogel JT, Zarka DG, Van Buskirk HA, Fowler SG, & Thomashow MF (2005) Roles Of The CBF2 And ZAT12 Transcription Factors In Configuring The Low Temperature Transcriptome Of Arabidopsis. *Plant Journal* 41(2):195-211.

26. Hon WC, Griffith M, Mlynarz A, Kwok YC, & Yang D (1995) Antifreeze Proteins In Winter Rye Are Similar To Pathogenesis-Related Proteins. *Plant Physiology* 109(3):879-889.

27. Dennis G, Sherman BT, Hosack DA, Yang J, Gao W, Lane HC, & Lempicki RA (2003) DAVID: Database For Annotation, Visualization, And Integrated Discovery. *Genome Biology* 4(9).

28. Tarca AL, Romero R, & Draghici S (2006) Analysis Of Microarray Experiments Of Gene Expression Profiling. *American Journal of Obstetrics and Gynecology* 195(2):373-388.

29. Gilmour SJ, Zarka DG, Stockinger EJ, Salazar MP, Houghton JM, & Thomashow MF (1998) Low Temperature Regulation Of Thearabidopsiscbf Family Of AP2 Transcriptional Activators As An Early Step In Cold-Induced COR gene Expression. *The Plant Journal* 16(4):433-442.

30. Howard BE & Heber S (2010) Towards Reliable Isoform Quantification Using RNA-SEQ Data. *BMC Bioinformatics* 11 Suppl 3:S6.

31. Thomashow MF (1998) Role Of Cold-Responsive Genes In Plant Freezing Tolerance. *Plant Physiology* 118(1):1-8.

32. Thomashow MF (2001) So What's New In The Field Of Plant Cold Acclimation? Lots! *Plant Physiology* 125(1):89-93.

33. Thomashow MF (1999) Plant Cold Acclimation: Freezing Tolerance Genes And Regulatory Mechanisms. *Annual Review of Plant Physiology and Plant Molecular Biology* 50(1):571-599.

34. Hughes MA & Dunn MA (1996) The Molecular Biology Of Plant Acclimation To Low Temperature. *Journal of Experimental Botany* 47(3):291-305.

35. Huner N, Öquist G, Hurry V, Krol M, Falk S, & Griffith M (1993) Photosynthesis, Photoinhibition And Low Temperature Acclimation In Cold Tolerant Plants. *Photosynthesis Research* 37(1):19-39.

36. Savitch LV, Allard G, Seki M, Robert LS, Tinker NA, Huner NPA, Shinozaki K, & Singh J (2005) The Effect Of Overexpression Of Two Brassica CBF/DREB1-Like Transcription Factors On Photosynthetic Capacity And Freezing Tolerance In Brassica Napus. *Plant and Cell Physiology* 46(9):1525-1539.

37. Artus NN, Uemura M, Steponkus PL, Gilmour SJ, Lin C, & Thomashow MF (1996) Constitutive Expression Of The Cold-Regulated Arabidopsis Thaliana COR15a Gene Affects Both Chloroplast And Protoplast Freezing Tolerance. *Proceedings of the National Academy of Sciences of the United States of America* 93(23):13404-13409.

38. Jiang H, Howell GS, & Flore JA (1999) Efficacy Of Chlorophyll Fluorescence As A Viability Test For Freeze-Stressed Woody Grape Tissues. *Canadian Journal of Plant Science* 79(3):401-409.

39. Ehlert B & Hincha DK (2008) Chlorophyll Fluorescence Imaging Accurately Quantifies Freezing Damage And Cold Acclimation Responses In Arabidopsis Leaves. *Plant Methods* 4.

40. Eisen MB, Spellman PT, Brown PO, & Botstein D (1998) Cluster Analysis And Display Of Genome-Wide Expression Patterns. *Proceedings of the National Academy of Sciences* 95(25):14863-14868.

41. Jimenez-Gomez JM, Wallace AD, & Maloof JN (2010) Network Analysis Identifies ELF3 As A QTL For The Shade Avoidance Response In Arabidopsis. *Plos Genetics* 6(9).

42. Fowler S & Thomashow MF (2002) Arabidopsis Transcriptome Profiling Indicates That Multiple Regulatory Pathways Are Activated During Cold Acclimation In Addition To The CBF Cold Response Pathway. *The Plant Cell* 14(8):1675-1690.

43. Xu S (2003) Theoretical Basis Of The Beavis Effect. *Genetics* 165(4):2259-2268.

44. West MAL, Kim K, Kliebenstein DJ, van Leeuwen H, Michelmore RW, Doerge RW, & St. Clair DA (2007) Global Eqtl Mapping Reveals The Complex Genetic Architecture Of Transcript-Level Variation In Arabidopsis. *Genetics* 175(3):1441-1450.

45. Polashock JJ, Arora R, Peng YH, Naik D, & Rowland LJ (2010) Functional Identification Of A C-Repeat Binding Factor Transcriptional Activator From Blueberry Associated With Cold Acclimation And Freezing Tolerance. *Journal of the American Society for Horticultural Science* 135(1):40-48.

46. Rekarte-Cowie I, Ebshish OS, Mohamed KS, & Pearce RS (2008) Sucrose Helps Regulate Cold Acclimation Of Arabidopsis Thaliana. *Journal of Experimental Botany* 59(15):4205-4217.

47. Narusaka Y, Nakashima K, Shinwari ZK, Sakuma Y, Furihata T, Abe H, Narusaka M, Shinozaki K, & Yamaguchi-Shinozaki K (2003) Interaction Between Two Cis-Acting Elements, ABRE And DRE, In ABA-Dependent Expression Of Arabidopsis Rd29a Gene In Response To Dehydration And High-Salinity Stresses. *Plant Journal* 34(2):137-148.

48. Waterer D, Benning NT, Wu GH, Luo XM, Liu XJ, Gusta M, McHughen A, & Gusta LV (2010) Evaluation Of Abiotic Stress Tolerance Of Genetically Modified Potatoes (Solanum Tuberosum Cv. Desiree). *Molecular Breeding* 25(3):527-540.

49. Watanabe KN, Kikuchi A, Shimazaki T, & Asahina M (2011) Salt And Drought Stress Tolerances In Transgenic Potatoes And Wild Species. *Potato Research* 54(4):319-324.

50. Devi MJ, Bhatnagar-Mathur P, Sharma KK, Serraj R, Anwar SY, & Vadez V (2011) Relationships Between Transpiration Efficiency And Its Surrogate Traits In The RD29A:DREB1A Transgenic Lines Of Groundnut. *Journal of Agronomy and Crop Science* 197(4):272-283.

51. Bihani P, Char B, & Bhargava S (2011) Transgenic Expression Of Sorghum DREB2 In Rice Improves Tolerance And Yield Under Water Limitation. *Journal of Agricultural Science* 149:95-101.

52. Kasuga M, Miura S, Shinozaki K, & Yamaguchi-Shinozaki K (2004) A Combination Of The Arabidopsis DREB1A Gene And Stress-Inducible RD29A Promoter Improved Drought- And Low-Temperature Stress Tolerance In Tobacco By Gene Transfer. *Plant and Cell Physiology* 45(3):346-350.

53. Msanne J, Lin JS, Stone JM, & Awada T (2011) Characterization Of Abiotic Stress-Responsive Arabidopsis Thaliana RD29A And RD29B Genes And Evaluation Of Transgenes. *Planta* 234(1):97-107.

54. Haake V, Cook D, Riechmann J, Pineda O, Thomashow MF, & Zhang JZ (2002) Transcription Factor CBF4 Is A Regulator Of Drought Adaptation In Arabidopsis. *Plant Physiology* 130(2):639-648.

55. Maruyama K, Sakuma Y, Kasuga M, Ito Y, Seki M, Goda H, Shimada Y, Yoshida S, Shinozaki K, & Yamaguchi-Shinozaki K (2004) Identification Of Cold-Inducible Downstream Genes Of The Arabidopsis DREB1A/CBF3 Transcriptional Factor Using Two Microarray Systems. *The Plant Journal* 38(6):982-993.

56. Gery C, Zuther E, Schulz E, Legoupi J, Chauveau A, McKhann H, Hincha DK, & Téoulé E (2011) Natural Variation In The Freezing Tolerance Of Arabidopsis Thaliana: Effects Of Rnai-Induced CBF Depletion And QTL Localisation Vary Among Accessions. *Plant Science* 180(1):12-23.

57. McKhann HI, Gery C, Berard A, Leveque S, Zuther E, Hincha DK, De Mita S, Brunel D, & Teoule E (2008) Natural Variation In CBF Gene Sequence, Gene Expression And Freezing Tolerance In The Versailles Core Collection Of Arabidopsis Thaliana. *Bmc Plant Biology* 8.

58. Zhen Y & Ungerer MC (2008) Relaxed Selection On The CBF/DREB1 Regulatory Genes And Reduced Freezing Tolerance In The Southern Range Of Arabidopsis Thaliana. *Molecular Biology and Evolution* 25(12):2547-2555.

59. Carvallo MA, Pino M-T, Jeknić Z, Zou C, Doherty CJ, Shiu S-H, Chen THH, & Thomashow MF (2011) A Comparison Of The Low Temperature Transcriptomes And CBF Regulons Of Three Plant Species That Differ In Freezing Tolerance: Solanum Commersonii, Solanum Tuberosum, And Arabidopsis Thaliana. *Journal of Experimental Botany* 62(11):3807-3819.

60. Sakuma Y, Maruyama K, Osakabe Y, Qin F, Seki M, Shinozaki K, & Yamaguchi-Shinozaki K (2006) Functional Analysis Of An Arabidopsis Transcription Factor, DREB2A, Involved In Drought-Responsive Gene Expression. *The Plant Cell Online* 18(5):1292-1309.

61. Stockinger EJ, Gilmour SJ, & Thomashow MF (1997) Arabidopsis Thaliana CBF1 Encodes An AP2 Domain-Containing Transcriptional Activator That Binds To The C-Repeat/DRE, A Cis-Acting DNA Regulatory Element That Stimulates Transcription In Response To Low Temperature And Water Deficit. *Proceedings of the National Academy of Sciences of the United States of America* 94(3):1035-1040.

62. Lefebvre V, Kiani SP, & Durand-Tardif M (2009) A Focus On Natural Variation For Abiotic Constraints Response In The Model Species Arabidopsis Thaliana. *International Journal of Molecular Sciences* 10(8):3547-3582.

63. Treangen TJ & Salzberg SL (2012) Repetitive DNA And Next-Generation Sequencing: Computational Challenges And Solutions. *Nat Rev Genet* 13(1):36-46.

64. Fury W, Batliwalla F, Gregersen PK, & Li W (2006) Overlapping Probabilities Of Top Ranking Gene Lists, Hypergeometric Distribution, And Stringency Of Gene Selection Criterion. *Conference proceedings : Annual International Conference of the IEEE Engineering in Medicine and Biology Society. IEEE Engineering in Medicine and Biology Society. Conference* 1:5531-5534.

# CHAPTER FOUR

## INTERESTING OBSERVATIONS AND FUTURE DIRECTIONS

# CHAPTER FOUR

## INTERESTING OBSERVATIONS AND FUTURE DIRECTIONS

### SUMMARY

The following represents results and preliminary results from several experiments that were conducted during the course of research described in Chapters Two and Three. These experiments produced interesting results that require further research and may be of value to continue as full focused projects. Preliminary results for additional mechanisms of circadian and gated cold-induced expression are described for the *CBFs* and the CBF-independent gene, *COR27*. Temperature-entrained circadian and gated cold-induced expression of *CBF* genes are also examined in this section, as well as the disruption of the circadian clock by extended cold temperatures. Lastly, morphological differences between SW and IT ecotypes used in Chapter Three are documented, and future construction of a low-temperature network using eQTL and RNA-seq data is discussed.

## RESULTS AND DISCUSSION

***Regulation of CBF genes by the REVEILLES, CK2, and CAMTAS, and circadian regulation of CBF-independent gene, COR27.*** In Chapter Two of this study, we show that EE-binding transcription factors CCA1 and LHY are major positive regulators of *CBF* genes under both circadian and gated (circadian with cold-treatment) conditions (Fig 2.1 and 2.4). ChIP experiments seem to suggest that this interaction is direct. CBF-target gene expression is also affected by mutations in CCA1 and LHY and electrolyte leakage assays indicate that these central clock genes impact freezing tolerance. CCA1 and LHY are thus components of the CBF pathway upstream of the CBFs. Doherty et al. 2009 determined that CAMTA3 is a transcription factor that also positively regulates *CBF* genes (1). In Chapter Two we present a model that suggests, CCA1, LHY and CATMA transcription factors (1) work synergistically to increase expression of CBF genes (Fig 2.5).

The CAMTAs are hypothesized to be a connection between calcium and CBF signaling (1). Cellular calcium levels also oscillate with circadian rhythms (2). Therefore, the CAMTAs may be a second connection between the clock and *CBF* genes. As a first step CAMTA mutants were tested to see if they affect basal circadian and gated cold-induction of *CBF* genes. There are a total of six CAMTAs in *Arabidopsis,* some of which have been shown to have overlapping function ((1) and Kim and Thomashow, unpublished). Preliminary results indicate that peak expression of *CBF1* and *2* is reduced under circadian conditions in a *camta3/camta2* double mutant (mutant constructed by Kim and Thomashow, unpublished), which is consistent with the

CAMTAs acting as activators of *CBF1* and *2* (1). This also suggests that CAMTAs influence basal expression of *CBF* genes. The reduction of *CBF* expression in *camta3/camta2* was not as severe as in *cca1-11/lhy-21 mutants*. Gated cold-induced expression of *CBF1-3* also appears to be reduced though the reduction is greater for *CBF1* and *CBF2* than *CBF3*. The reduction of gated *CBF* expression in *camta3/camta2* was not as severe as in *cca1-11/lhy-21 mutants*. This result needs to be repeated, but does support the model proposed in Chapter Two.

Although *CBF1* and *CBF3* expression is essentially knocked-out under both circadian and gated conditions in the *cca1-11/lhy-21* double mutant, there is some residual (~20%) expression of *CBF2* (Fig. 2.1 and 2.4). In Chapter Two we suggest that the CCA1-like REVEILLE (RVE) genes may play a role in the remaining induction of *CBF2*. Like CCA1 and LHY, the RVEs bind to the EE and are circadian regulated. Preliminary results indicate that *rve2*, *rve3*, *rve4*, and an additional EE-binding *tcp2* mutant do not significantly affect *CBF* expression, under both circadian and gated conditions, though higher order mutants would need to be constructed since there may be redundancy between these genes.

Preliminary results show that the *rve8-1* mutant may have altered *CBF* expression in comparison to wild-type. However, *CBF* expression appears to be elevated in *rve8-1* rather than reduced. This would suggest that RVE8 functions as a repressor rather than an activator of *CBF* expression like CCA1 and LHY. *RVE8* transcripts peak at the same time as *CCA1* and *LHY*, but Rawat et al. 2011 demonstrated that the RVE8 protein does not accumulate until after subjective noon (3),

when *CBF* expression levels drop off (Fig. 2.1). Therefore, circadian oscillations of RVE8 are consistent with RVE8 functioning as a repressor of *CBF* expression. Interestingly, RVE8 was recently found to promote expression of *PRR5* (3), which has previously been implicated as a repressor of *CBF* expression (4). Therefore, RVE8 may potentially acts as a direct or indirect regulator of *CBF* expression.

CCA1 and LHY are controlled by transcriptional as well as post-translational mechanisms (5, 6). Phosphorylation of CCA1 and LHY by CASEIN KINASE 2 (CK2) is necessary for normal clock function and can affect DNA binding (6, 7). Therefore, CK2 was tested to determine if it is necessary for induction of the *CBF* genes. Preliminary time-course experiments using the ck2*β3* mutant indicate that circadian expression, as well as gated cold-induction of *CBF1-3*, and *CBF*-target genes are not strongly affected. This suggests that post-translational modification of CCA1 and LHY is not necessary for binding to the *CBF* locus, but experiments need to be repeated.

The CBF regulon only comprises 12% of cold-regulated genes (8). Therefore, it is of interest to determine if CCA1 and LHY also regulate CBF-independent pathways of cold-signaling. The cold regulated gene, *COR27,* is independent of the CBF pathway, and also gated by the circadian clock (9). Promoter analysis of *COR27* demonstrated that the EE has a role in the cold-induction of *COR27* (9). However, the transcription factors mediating cold-induction through the COR27-EEs have yet to be identified (9). EE-binding transcription factors CCA1 and LHY seem like especially good candidates because of their role in the induction of *CBF* genes (10).

Under circadian conditions, peak *COR27* expression in the *cca1-11/lhy-21* double mutant is not reduced nearly as much as that of the *CBF* genes (Fig 4.1; Fig A4.1; Fig. 2.1). Although more biological replicates may be necessary, five independent biological replicates of ChIP experiments did not find statistically significant enrichment of CCA1 on the *COR27* promoter or coding region (Fig 4.2). Gated cold-induced expression of *COR27* is also not strongly reduced in *cca1-11/lhy-21* in comparison to wild-type (Fig. 4.1). Therefore, CCA1 and LHY do not appear to play a major role in circadian regulation or gated cold-induction of *COR27* (Fig. 4.1). This suggests that there is specificity for CCA1 and LHY in the regulation of *CBF* signaling and that there are multiple mechanisms for gating cold gene expression.

Contrary to previous reports that *CBF* and *COR27* genes have similar peaks and troughs of expression (9), data from this study suggests that *COR27* peaks in expression a few hours after *CBF* genes (Fig 4.1; Fig 2.1 and 2.4). The shift in peak expression is most likely due to the greater number of time-points used in this study. The difference in expression pattern between *CBF* and *COR27* seems significant and may be the foundation for differing modes of circadian regulation. Further work must be conducted in order to determine the major mechanism of circadian and gated cold-expression of COR27. The previously mentioned RVE genes are known to bind to the EE (11). Many of these genes peak in expression before *COR27*, and thus are good first candidates for regulating *COR27* expression.

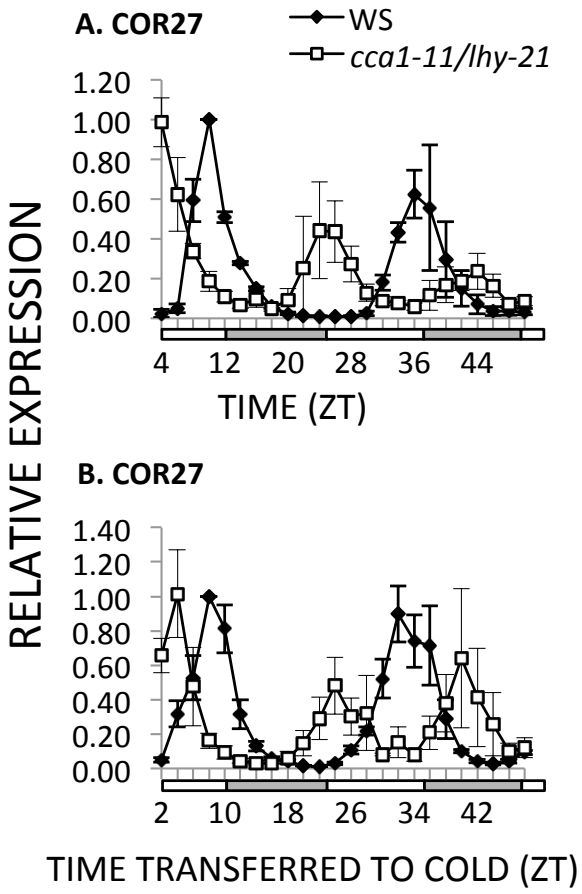


**Figure 4.1.** Effects of the *cca1-11/lhy*-21double mutation on circadian and gated cold-induction of *COR27*. Expression for *COR27* was relative to one wild-type sample (WS) set to a value of 1 in each biological replicate. Values are averages from three independent experiments (n=3); error bars indicate ± SEM. (A) Plants were grown with a 12 h photoperiod at 22$^{0}$C to the four leaf stage and transferred to constant light at ZT0 (subjective day and night are indicated by white and gray bars, respectively). Plants were harvested every 2 h and the transcript levels for *COR27* were determined by qRT-PCR. Gene expression was normalized to IPP2 for each sample. (B) Plants were grown with a 12 h photoperiod at 22$^{0}$C to the four leaf stage and transferred to constant light at ZT0 (subjective day and night are indicated by white and gray bars, respectively). Plants were transferred to cold temperature (4$^{0}$C) for 2 h, every 2 h, for 48 h at the start of constant light conditions and the transcript levels for *COR27* were determined by qRT-PCR. Horizontal axis represents time (ZT) when plants were dropped to cold temperature. Gene expression was normalized to UBQ10 for each sample. See Table A4.1 for primer pair sequences.

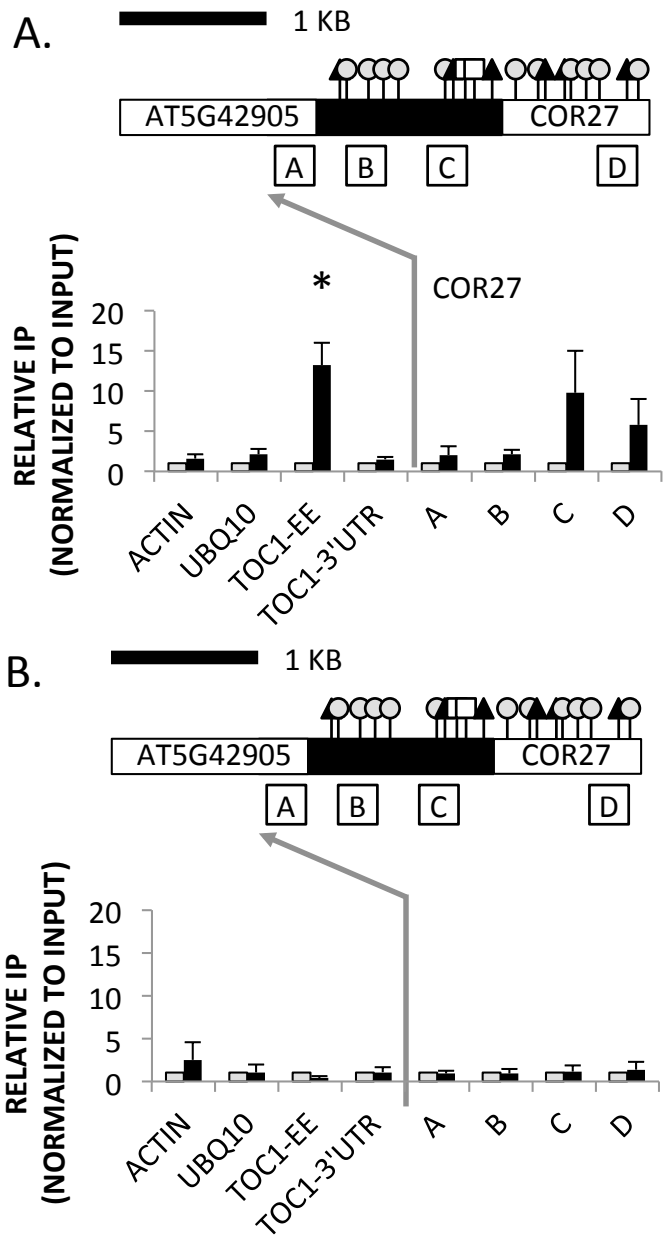


**Figure 4.2.** Binding of CCA1 on COR27. *cca1-1* and *cca1-1 CCA1p:CCA1-GFP* plants were grown at 22$^0$C under a 12 h photoperiod to the four leaf stage. Tissue was fixed at ZT4 and ChIP was performed using an anti-GFP (A) or mock IgG (B) antibody. Immunoprecipitated DNA was quantified by qRT-PCR with primers on COR27 (boxes A through D). Levels of immunoprecipitated DNA were normalized to input DNA. Immunoprecipitation in *cca1-1 CCA1p:CCA1-GFP* plants (black bars) is relative to *cca1-1* plants (gray bars) set to 1. Primers TOC1-3'UTR, *ACTIN7* (ACTIN) and *UBIQUITIN10* (UBQ10) were negative controls. TOC1-EE was a positive control. Values are the average of five independent experiments (n=5). Error bars indicate ± SEM. *=$p<0.05$ using a paired, one-tailed t-test. In the *COR27* diagram, the transcribed regions are indicted with white boxes and the approximate positions of CBS (AATCT), and EE (AAAATATCT) motifs are indicated by gray circles, and white squares respectively.

***Temperature-entrained circadian regulation and gated cold-induction of CBF genes.*** Both light and temperature cues entrain the circadian clock to its external environment (12, 13). *CBF2*, *CBF3* and the CBF-independent cold-regulated gene, *COR27*, all oscillate under temperature-entrained circadian conditions (Fig. 4.3). Temperature-entrained circadian oscillations of *CBF1* do not appear regular and therefore are not as robust as under light-entrained circadian conditions (Fig 4.3; Fig 2.1). This is interesting and may suggest that *CBF1* is distinctively regulated by light in comparison to *CBF2* and *CBF3*. In Chapter Two we establish that CCA1 and LHY play a major role in the induction of *CBF* genes under light-entrained circadian conditions. Consequently, it is of interest to determine if CCA1 and LHY also play a major role in the induction of *CBF* genes under temperature-entrained circadian conditions.

Peak expression of *CBF1-3* is significantly reduced in the *cca1-11/lhy-21* double mutant under temperature-entrained circadian conditions (Fig 4.3). CBF-target genes, *COR15A*, *COR47* and *COR78* also have reduced peak expression in *cca1-11/lhy-21* in comparison to wild-type (Fig 4.4). This suggests that CCA1 and LHY play a major role in the basal induction of *CBF* genes under temperature-entrained circadian conditions. This also would suggest a similar mechanistic model for circadian regulation under temperature-entrained and light entrained conditions (Fig 2.5). However, analysis of clock and cycling genes reveals that there may be a more widespread reduction of rhythmicity in *cca1-11/lhy-21* under temperature-entrained circadian conditions in comparison to light entrained conditions.

*COR27* expression is significantly reduced in *cca1-11/lhy-21* under temperature-entrained conditions (Fig 4.3), which is interesting considering that *COR27* expression is not strongly reduced in *cca1-11/lhy-21* under light-entrained circadian conditions (Fig. 4.1 and 4.3). Moreover, cycling control gene, *LHCB1.4*, also has significantly reduced peak expression in the *cca1-11/lhy-21* under temperature-entrained conditions (Fig. 4.4), which is not the case under light-entrained conditions (Fig A2.3). Therefore expression of clock components, *TOC1*, *PRR3*, *PRR5*, *PRR7* and *PRR9,* were further tested in *cca1-11/lhy-21* under temperature-entrained circadian conditions (Fig. 4.5). Previous literature has shown that the *cca1-11/lhy-21* mutant has robust oscillations of *TOC1* under light-entrained conditions (14). Under temperature-entrained circadian conditions *TOC1*, *PRR3*, *PRR5*, and *PRR7* have significantly reduced peak expression in *cca1-11/lhy-21* in comparison to WT (Fig 4.5). Conversely, *PRR9* maintains robust oscillations in *cca1-11/lhy-21* under temperature-entrained conditions (Fig. 4.5). Previous literature has shown robust cycling of clock-output genes *CAB2 (15, 16)* and *CCR2* (14) in *cca1-11/lhy-21,* under light-entrained conditions. Therefore, expression of cycling control genes, *CAB2* and *CCR2*, were tested under temperature-entrained circadian conditions. *CAB2* and *CCR2*, did show robust oscillations in *cca1-11/lhy-21,* with peak levels similar to wild-type (WS-2) under temperature-entrained conditions (Fig 4.4). Therefore, not all oscillations are knocked-out in *cca1-11/lhy-21* under temperature-entrained conditions. Consequently, there is some specificity for the reduction in *CBF* gene expression under temperature-entrained conditions by CCA1 and LHY, in support of a mechanistic model similar to light-entrained conditions (Fig

2.5). But a more general clock question also seems to emerge from this data. To what extent to do CCA1 and LHY function differently under light- and temperature-entrained circadian conditions? To determine the extent of these differences, light and temperature cycling time-course microarrays or RNA-seq data would have to be performed for *cca1-11/lhy-21* and wild-type (WS-2) plants. This type of data for *cca1-11/lhy-21* does not appear to be publicly available, though there are light and temperature-entrained arrays publically available for wild-type plants.

Significant progress has been made in determining the targets of light input into the clock (17-21), and temperature entrainment of the circadian clock is well established (12). However, mechanisms underlying temperature entrainment are still largely unknown (13, 22). Previous literature suggests that PRR7 and PRR9 are important for temperature-entrainment (22). This was shown through arrhythmic *CCA1* and *TOC1* expression as well as arrhythmic hypocotyl movement in *prr7-3/prr9-1* under temperature-entrained conditions (22). The *cca1-11/lhy-21* mutant also fails to maintain circadian oscillations of several clock genes, as well as cycling control gene *LHCB1.4* under temperature-entrained conditions. CCA1 and LHY have been previously connected to temperature compensation of the clock (23). But data from this study suggests that CCA1 and LHY are also important for temperature entrainment of the circadian clock. This hypothesis should be further tested using other clock-output measurements such as hypocotyl movement.

Fowler et al. 2005 demonstrated that cold-induced expression of *CBF* genes is gated by a light-entrained circadian clock (24). Therefore cold-induced gene expression

was tested under temperature-entrained circadian conditions to see if it is gated as well. Indeed, cold-induced expression of *CBF1-3*, CBF-target genes and *COR27* is gated under temperature-entrained circadian conditions (Fig 4.6 and 4.7). In Chapter Two we show that CCA1 and LHY play a major role in the gated cold-induced expression of *CBF* genes. Therefore, it is of interest to determine if CCA1 and LHY influence gated cold-induction of *CBF* genes under temperature-entrained circadian conditions. The peak cold-induced expression of *CBF1-3* and CBF-target genes is significantly reduced in *cca1-11/lhy-21* under temperature-entrained conditions (Fig. 4.6 and 4.7), similar to light-entrained conditions (Fig 2.4), which suggests that CCA1 and LHY also are vital for the gated cold-induction of *CBF* genes under temperature-entrained conditions and might imply a similar gating mechanism to the one proposed for gated cold-induced *CBF* expression under light-entrained circadian conditions (Fig. 2.5). However, there again appears to be a general reduction in rhythmicity as well as expression level in *cca1-11/lhy-21* under gated temperature-entrained conditions.

Under both basal temperature-entrained circadian conditions and gated temperature-entrained conditions the *cca1-11/lhy-21* double mutant appears to have a more generalized reduction in gene expression in comparison to light-entrained conditions. This sensitivity seems to be intensified with the addition of a cold treatment (gated conditions) since *COR27* and all cycling control genes had significantly reduced peak expression in comparison to wild-type (Fig 4.7). Clock genes *TOC1*, *PRR3*, *PRR5*, and *PRR7,* are arrhythmic in *cca1-11/lhy-21* under gated temperature-entrained circadian conditions, similar to basal temperature-entrained circadian conditions.

However, *PRR9* is also arrhythmic under gated temperature-entrained circadian conditions (Fig 4.8), which was not the case under basal temperature-entrained circadian conditions (Fig. 4.5). CCA1 and LHY have previously been shown to be important for temperature compensation of the clock under light-entrained conditions (23). The increased arrhythmia seen with the addition of a cold treatment under temperature-entrained conditions may be due to the role of CCA1 and LHY in temperature compensation of the clock under temperature-entrained conditions. However, further experiments would need to be conducted to support this claim.

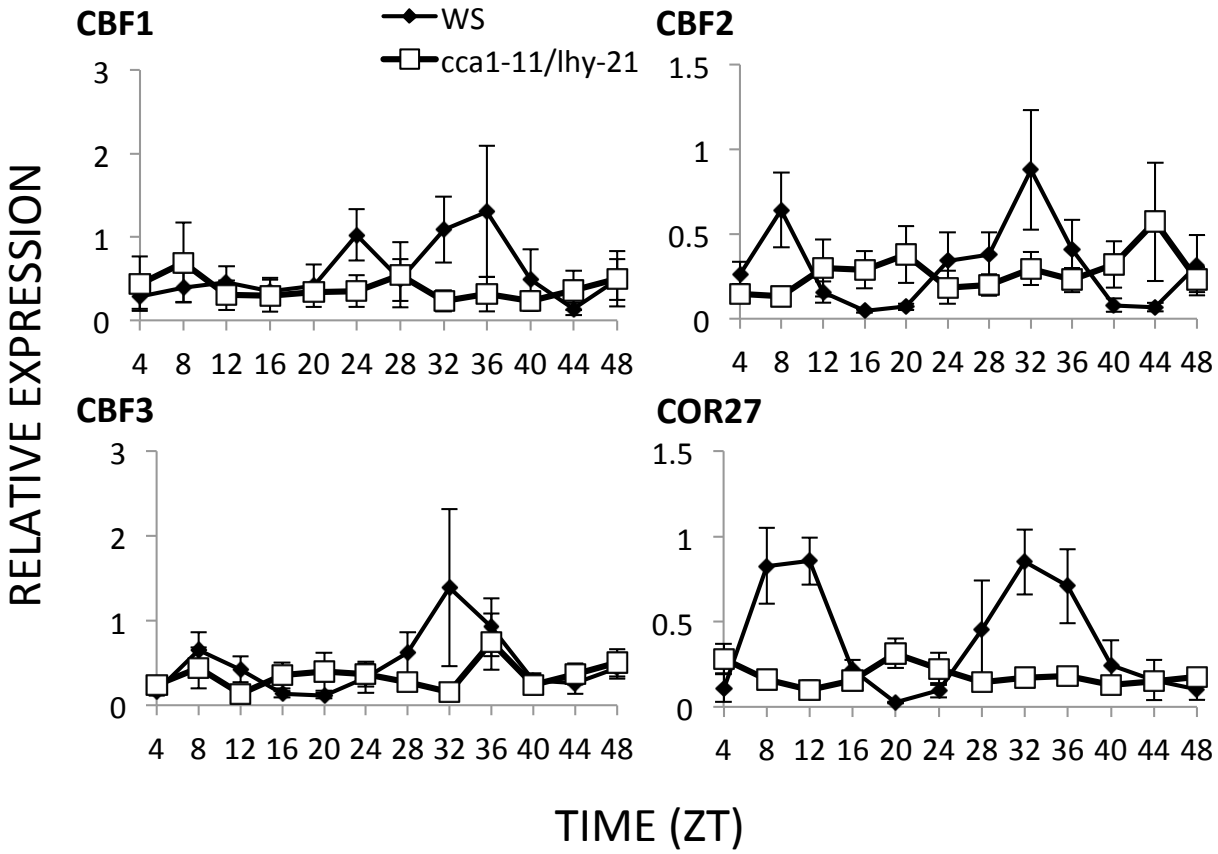


**Figure 4.3.** Effects of the *cca1-11/lhy-*21double mutation on temperature-entrained circadian regulation of *CBF1*, *CBF2*, *CBF3* and *COR27*. Wild-type Ws-2 (WS) and *cca111/lhy-21* double mutant plants were grown at constant light under a 12 h temperature period (22$^0$C day/ 12$^0$C night) to the four leaf stage and transferred to constant temperature (22$^0$C) at ZT0. Plants were harvested every 4 h and the transcript levels for the indicated genes were determined by qRT-PCR. Gene expression was normalized to IPP2 for each sample. Gene expression is relative to one wild-type sample set to a value of 1 for each biological replicate. Values are averages from four independent biological experiments (n=4). Error bars indicate ±SEM. Please see Table A4.1 for primer pair sequences.

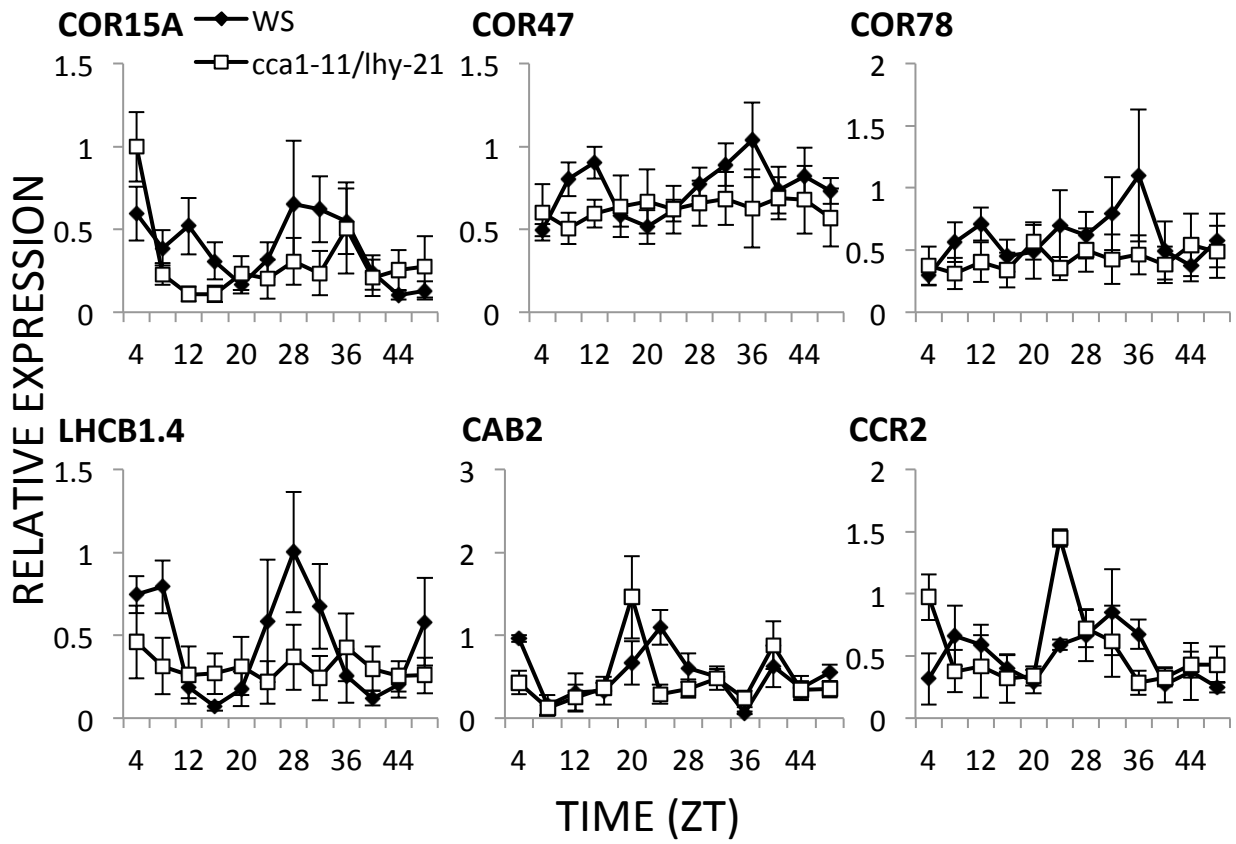


**Figure 4.4.** Effects of the *cca1-11/lhy-*21double mutation on temperature-entrained circadian regulation of CBF target genes, *COR15A*, *COR47* and *COR78*, and cycling control genes *LHCB1.4*, *CAB2* and *CCR2*. Wild-type Ws-2 (WS) and *cca111/lhy-21* double mutant plants were grown at constant light under a 12 h temperature period (22$^0$C day/ 12$^0$C night) to the four leaf stage and transferred to constant temperature (22$^0$C) at ZT0. Plants were harvested every 4 h and the transcript levels for the indicated genes were determined by qRT-PCR. Gene expression was normalized to IPP2 for each sample. Gene expression is relative to one wild-type sample set to a value of 1 for each biological replicate. Values are averages from four independent biological experiments (n=4). Error bars indicate ±SEM. Please see Table A4.1 for primer pair sequences.

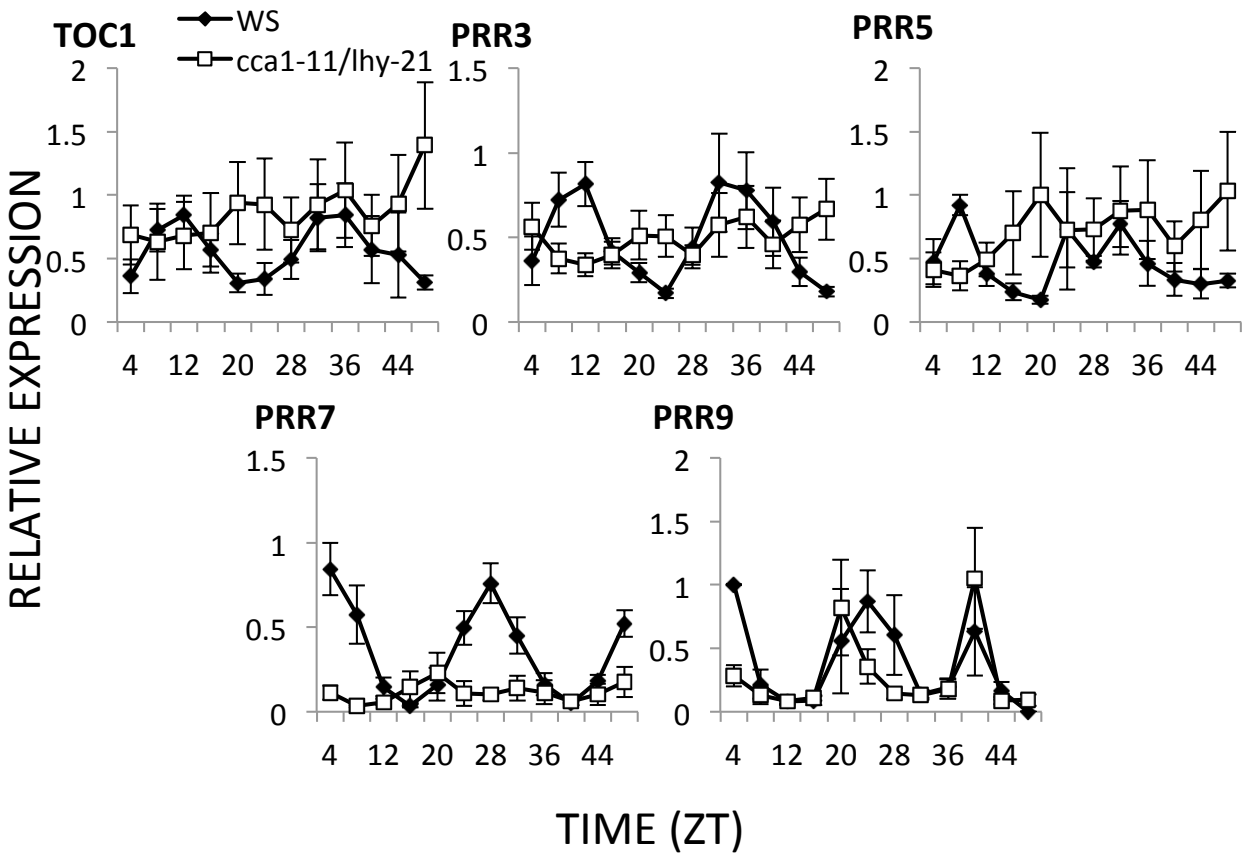


**Figure 4.5.** Effects of the *cca1-11/lhy*-21double mutation on temperature-entrained circadian regulation of clock genes *TOC1, PRR3, PRR5, PRR7* and *PRR9*. Wild-type Ws-2 (WS) and *cca111/lhy-21* double mutant plants were grown at constant light under a 12 h temperature period (22$^0$C day/ 12$^0$C night) to the four leaf stage and transferred to constant temperature (22$^0$C) at ZT0. Plants were harvested every 4 h and the transcript levels for the indicated genes were determined by qRT-PCR. Gene expression was normalized to IPP2 for each sample. Gene expression is relative to one wild-type sample set to a value of 1 for each biological replicate. Values are averages from four independent biological experiments (n=4). Error bars indicate ±SEM. Please see Table A4.1 for primer pair sequences.

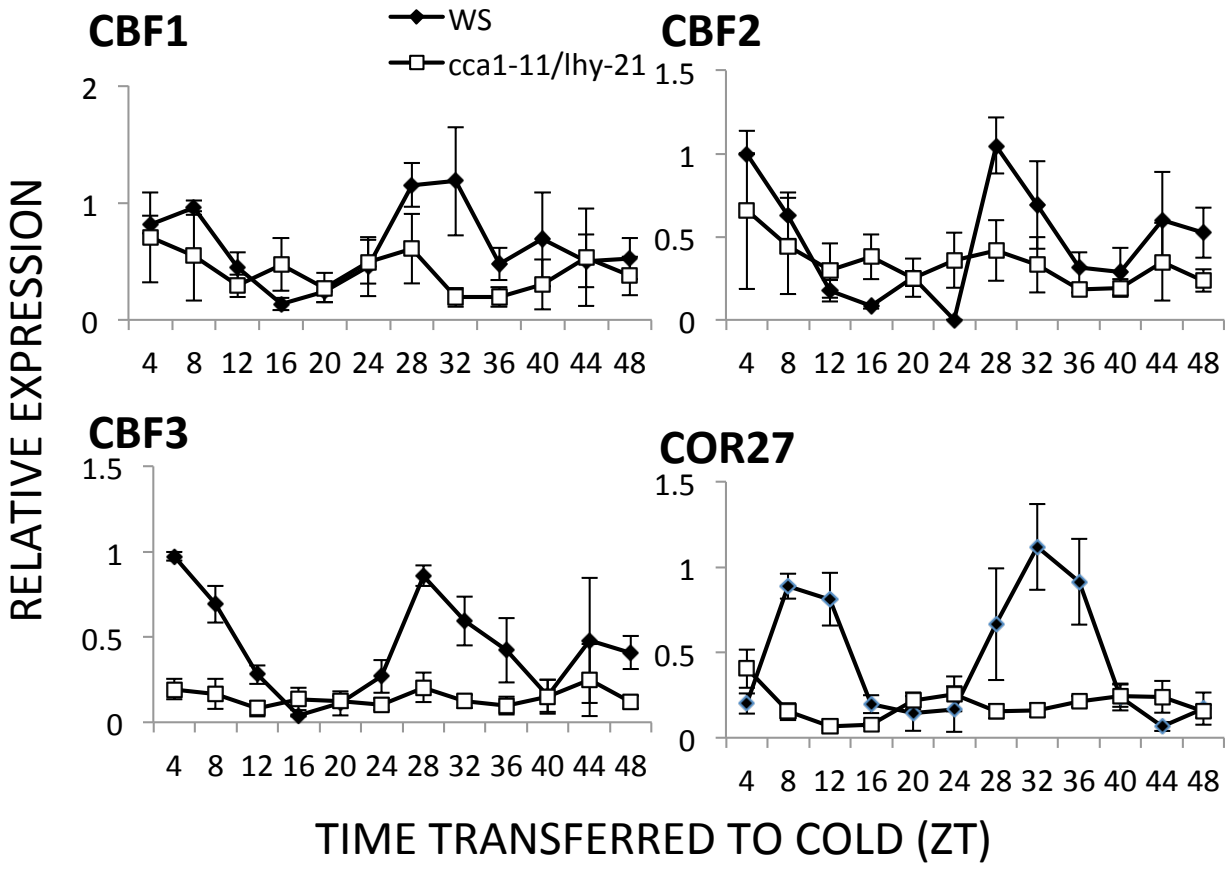


**Figure 4.6.** Effects of the *cca1-11/lhy*-21double mutation on temperature-entrained cold-induction of *CBF1*, *CBF2*, *CBF3* and *COR27*. Wild-type Ws-2 (WS) and *cca1-11/lhy*-21 double mutant plants were grown under constant light with a 12 h temperature period (22$^0$C day/ 12$^0$C night) to the four leaf stage and transferred to constant light at ZT0. Plants were transferred to cold temperature (4$^0$C) for 2 h, every 4 h at the start of constant temperature conditions. Transcript levels for the indicated genes were determined by qRT-PCR. Horizontal axis represents time (ZT) when plants were transferred to cold temperature. Gene expression was normalized to UBQ10 for each sample. Gene expression is relative to one wild-type sample set to a value of 1 for each biological replicate. Values are averages from four independent biological experiments (n=3). Error bars indicate ±SEM. Please see Table A4.1 for primer pair sequences.

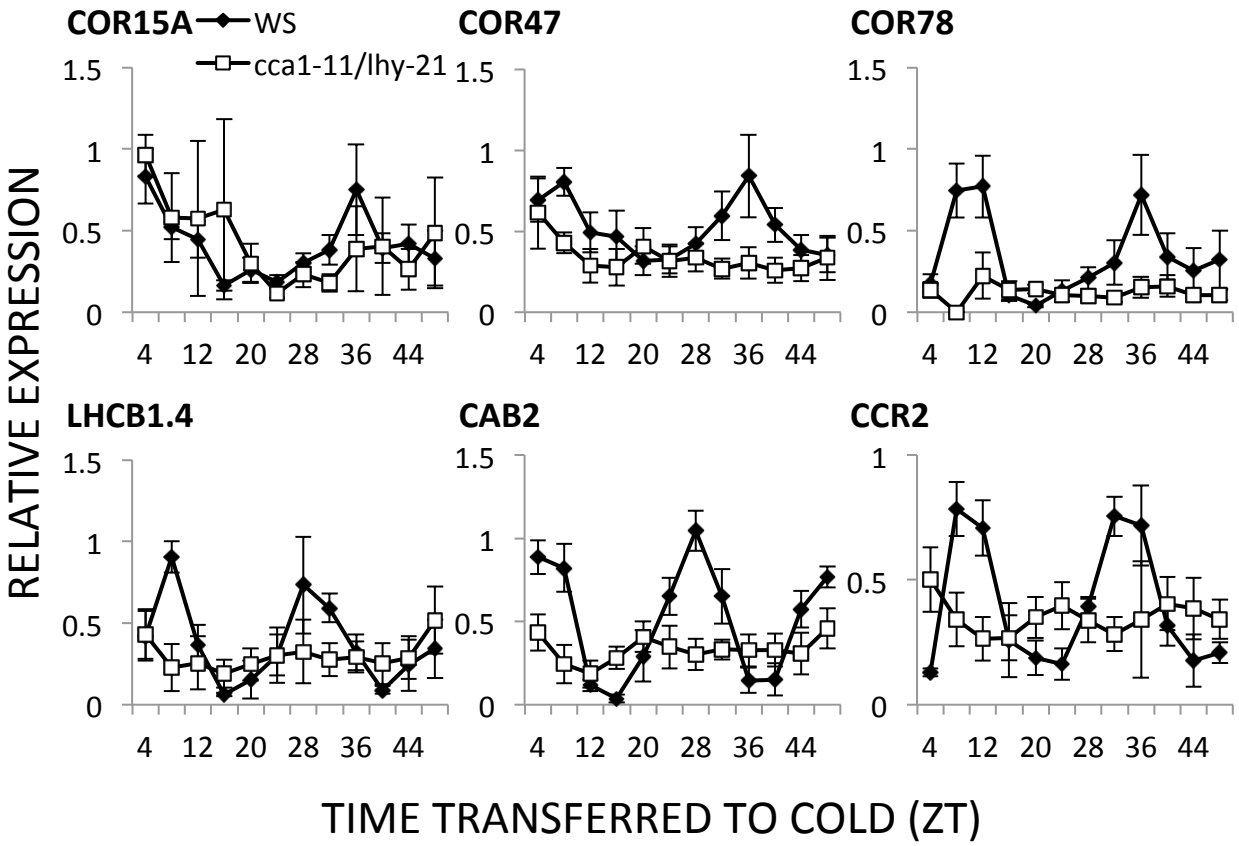


**Figure 4.7.** Effects of the *cca1-11/lhy*-21double mutation on temperature-entrained cold-induction of CBF target genes, *COR15A*, *COR47* and *COR78*, and cycling control genes *LHCB1.4*, *CAB2* and *CCR2*. Wild-type Ws-2 (WS) and *cca1*-11*/lhy*-21 double mutant plants were grown under constant light with a 12 h temperature period (22$^{0}$C day/ 12$^{0}$C night) to the four leaf stage and transferred to constant light at ZT0. Plants were transferred to cold temperature (4$^{0}$C) for 2 h, every 4 h at the start of constant temperature conditions. Transcript levels for the indicated genes were determined by qRT-PCR. Horizontal axis represents time (ZT) when plants were transferred to cold temperature. Gene expression was normalized to UBQ10 for each sample. Gene expression is relative to one wild-type sample set to a value of 1 for each biological replicate. Values are averages from four independent biological experiments (n=3). Error bars indicate ±SEM. Please see Table A4.1 for primer pair sequences.

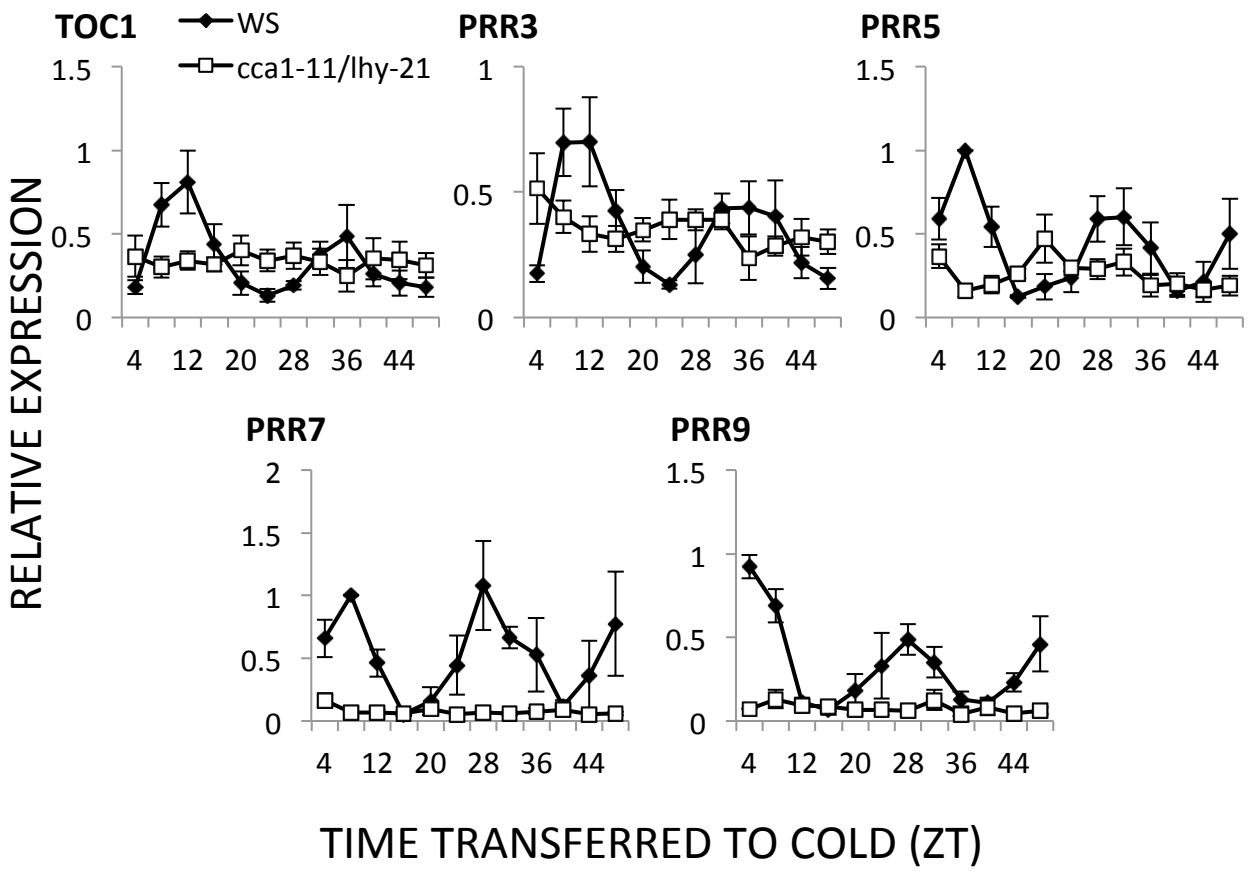


**Figure 4.8.** Effects of the *cca1-11/lhy-*21double mutation on temperature-entrained cold-induction of PRR clock genes *TOC1, PRR3, PRR5, PRR7* and *PRR9*. Wild-type Ws-2 (WS) and *cca1*-11*/lhy*-21 double mutant plants were grown under constant light with a 12 h temperature period (22$^0$C day/ 12$^0$C night) to the four leaf stage and transferred to constant light at ZT0. Plants were transferred to cold temperature (4$^0$C) for 2 h, every 4 h at the start of constant temperature conditions. Transcript levels for the indicated genes were determined by qRT-PCR. Horizontal axis represents time (ZT) when plants were transferred to cold temperature. Gene expression was normalized to UBQ10 for each sample. Gene expression is relative to one wild-type sample set to a value of 1 for each biological replicate. Values are averages from four independent biological experiments (n=3). Error bars indicate ±SEM. Please see Table A4.1 for primer pair sequences.

***Disruption of the circadian clock by low-temperature.*** In 2005, Ramos et al. concluded that the chestnut tree circadian clock was disrupted with extended cold treatment (25). Bieniawska et al. 2008 further explored the disruption of circadian and diurnal oscillations by extended cold in *Arabidopsis* (26). They showed that extended cold treatment disrupts circadian and diurnal oscillations of all clock output genes (*CCR1*, *CCR2*, *CAB2*, *CAT3*), clock components (*PRR3*, *PRR5*, *PRR7*, *PRR9*, *ELF3*, *ELF4*, *GI*, *TOC1*, *CCA1*, *LHY*), and cold-genes (*CBF1-3*, *COR15A*, *COR47*, *COR78*) tested (26). These results are very interesting, but the reported induction pattern of *CBF1-3* genes was also surprising (26). Bieniawska et al. 2008 show *CBF* expression quickly increasing within 2 h of cold treatment then staying at this maximal level for over 2 days (26). In previous experiments performed under constant-light conditions in constant-light grown plants, *CBF* genes also consistently reached maximal levels of cold-induced expression by 2 h (27-29). However, this maximum *CBF* expression level is then reduced significantly (though still higher than warm expression levels) by 24 h in cold (27-29) and remains down for at least 3 weeks (28). Experiments were conducted similar to Bieniawska et al. 2008 to determine if cold-induced *CBF* kinetics in plants grown under entrained conditions is significantly different from previously reported constant-light experiments (27-29). Preliminary experiments (2 biological reps; Fig. 4.9) indicate very different cold-induced *CBF* kinetics from Bieniawska et al. 2008 (26), but similar kinetics to previous constant-light experiments (27-29). There are some differences experimental set-up in comparison to Bieniawska et al. 2008. For example, plants were entrained under a 12 h photoperiod rather than long day condition (26)

before release into constant light conditions. Plants were also transferred to cold temperature at ZT4, rather than at ZT14 (26). These differences in experimental set up could be significant so future experiments should be conducted exactly as they were described in Bieniawska et al. 2008. Yet, more significant might be technical differences in the amount of RNA used for qRT-PCR. Bieniawska et al. 2008, used 2500ng of RNA to synthesize cDNA for expression analysis of *CBF* genes by qRT-PCR. The 25ng-200ng of RNA, used in this study, fell well into the dynamic range of *CBF* genes, whereas 2500ng did not. Therefore, it is possible that differences seen in kinetics of *CBF* genes are the result of technical rather than biological differences, but further experiments are required.

Ramos et al. 2005 used northern blots to show that circadian oscillations of clock genes, *TOC1* and *LHY*, were disrupted with extended cold treatment in chestnut trees (25). These experiments used plants grown in natural winter conditions with both cycling light and temperature (25). Consequently, Ramos et al. concluded that circadian clocks do not function during winter months (25). Although this may be the case in chestnut trees, *Arabidopsis* carrying null mutations in either *TOC1* (30) or *LHY*(31) can continue to have robust rhythms. Furthermore, *Arabidopsis* carrying null mutations in both *TOC1* and *LHY* also have continued rhythmicity (32). In a more extensive analysis of clock gene disruption by cold, Bieniawska et al. 2008 also saw interrupted oscillations of many clock genes (26). However, clock component *LUX* continued to cycle under diurnal conditions (26). This indicates that there is continued rhythmicity under extended cold and thus the possibility of a functioning 'low-temperature' oscillator.

Furthermore, *LUX* may not be the only cold oscillating gene in the *Arabidopsis* transcriptome (26). Therefore, the extent to which genes oscillate under these low-temperature conditions should continue to be examined. Moreover, Ramos et al. 2005 sampled plants in natural conditions with both diurnal cycles and changing day and night temperature, whereas Bieniawska et al. 2008 sampled plants only under circadian and diurnal conditions (25, 26). Both light and temperature entrain the circadian clock and temperature oscillations could be especially important under low-temperature conditions. Accordingly, it is of interest to determine if the disruption of clock gene oscillations by cold also occurs in plants sampled under temperature cycles (comparable to a diurnal treatment; Fig. 4.10).

In preliminary experiments, robust rhythms of central clock component, *CCA1*, were observed in samples without cold treatment ('WARM'), similar to Bieniawska et al. 2008. Disrupted rhythmicity of *CCA1* with extended cold treatment ('COLD') was also observed, similar to Bieniawska et al. 2008 (Fig 4.10). Interestingly, plants sampled under thermocycles ('TEMP CYCLING'), continued to show regular though widened oscillations (Fig. 4.10). However one caveat for these experiments is that plants were grown under 12 h photoperiods then transferred to12 h thermocycles ($9^{o}$C day and $4^{o}$C night) for sampling (Fig. 4.10). Previously, $8^{o}$C treatments have been used for chilling-stress in peppers (33), $7^{o}$C treatments for wheat (34), $6^{o}$C treatments for soybean (35), and $5^{o}$C treatments for tomato (36). Consequently, future experiments should be set up using colder temperature cycles such as a $6^{o}$C day with $2^{o}$C night, or $4^{o}$C day with $0^{o}$C night. Nevertheless, preliminary results suggest the possibility that the circadian clock

functions under low-temperature conditions, which should be further explored in the future.

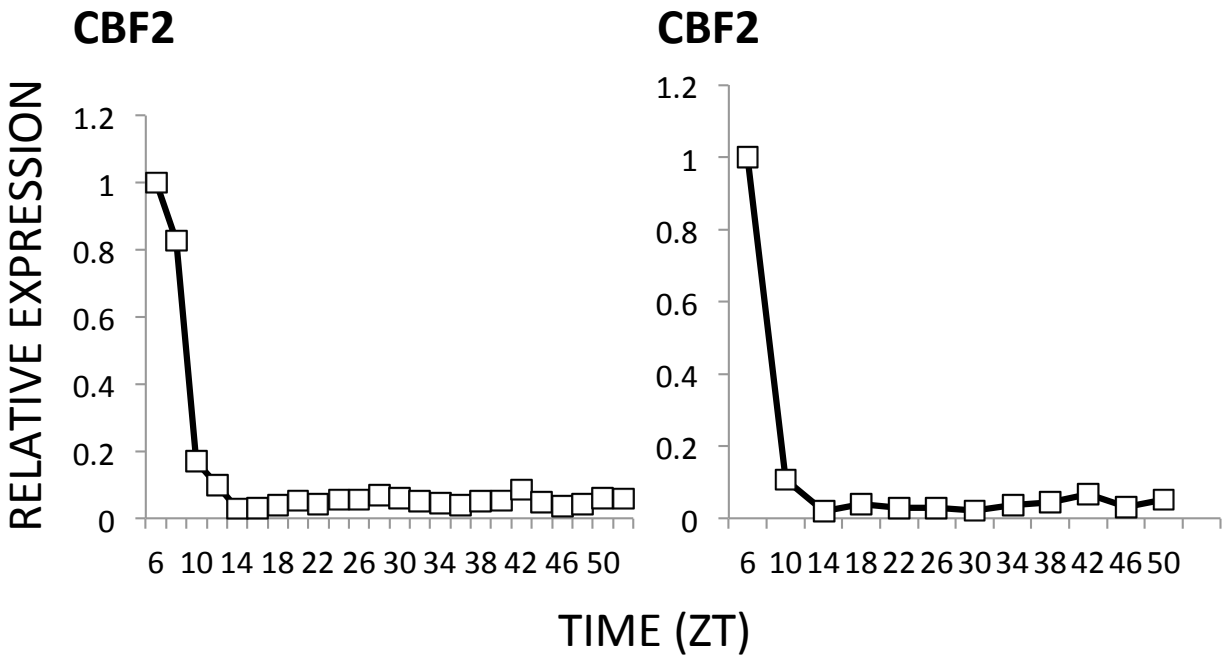


**Figure 4.9.** Cycling of *CBF2* expression in plants grown under light-entrained conditions then sampled in constant-cold conditions. Wild-type, Ws-2, plants were grown at 22°C with a 12 h photoperiod to the four leaf stage and then transferred to constant light and constant cold (4°C) conditions at ZT4. Transcript levels for the indicated genes were determined by qRT-PCR. Gene expression was normalized to UBQ10 for each sample. Gene expression is relative to one sample set to a value of 1 in each experiment. Two biological replications are shown (left graph and right graph). Please see Table A4.1 for primer pair sequences.

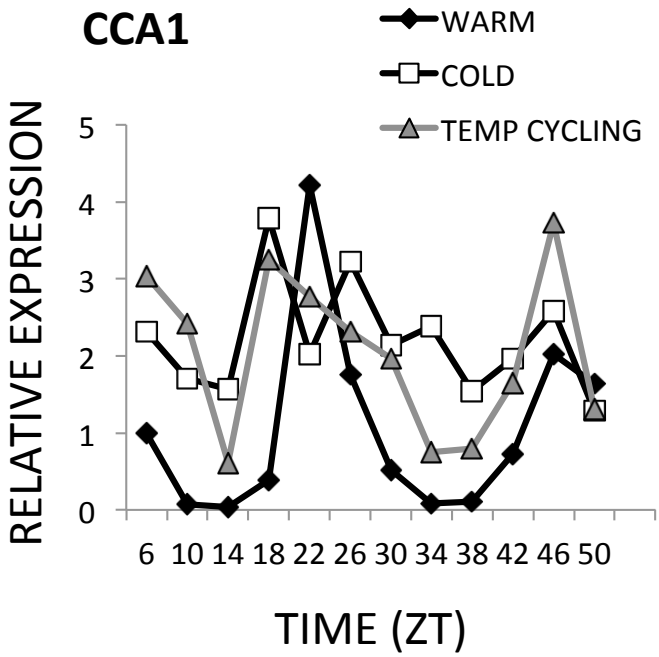


**Figure 4.10.** Cycling of *CCA1* under warm, temperature cycling or constant-cold conditions. Wild-type, Ws-2, plants were grown at 22$^0$C with a 12 h photoperiod to the four leaf stage and then transferred to one of three conditions at ZT4. 'WARM' plants were transferred to constant light and constant temperature (22$^0$C) conditions. 'TEMP CYLING' plants were transferred to constant light with a 12 h cold temperature period (9$^0$C day/ 4$^0$C night). 'COLD' plants were transferred to constant light and constant cold (4$^0$C) conditions. Transcript levels for CCA1 were determined by qRT-PCR. Gene expression was normalized to UBQ10 for each sample. Gene expression is relative to one sample set to a value of 1 for each condition. Values are from one experiment (n=1). Please see Table A4.1 for primer pair sequences.

***Morphological differences between SW and IT.*** Morphological differences between the SW and IT ecotypes, used in Chapter Three of this study, were observed but not quantified. SW leaf edges were rounded, whereas IT leaf edges were variegated. SW and IT plants also appear to grow at different rates, since IT has more leaves than SW at the same number of days in age. SW leaves seem to be thicker than IT at all time-points examined (non-acclimated, 1 week, 2 weeks and 3 weeks cold-acclimated). Interestingly, plants overexpressing *CBF* genes have thicker leaves than wild-type plants and are constitutively freezing tolerant, (37). There is also a strong positive correlation between leaf thickness and photosynthetic capacity (38). Increased photosynthetic capacity is also associated with cold-acclimation (39). This is especially interesting because RNA-seq data in Chapter Three shows that the majority of differentially expressed photosynthesis genes have higher expression in SW (Fig. 3.33). SW leaf thickness also seemed to increase with cold, which is a change associated with cold-acclimation (40-43) and cold developed leaves (43). However, these morphological changes and differences between SW and IT will have to be measured experimentally.

***Low-temperature network construction using SW and IT RILs.*** In Chapter Three of this study, eQTL mapped for genes associated with differences in freezing tolerance (FTD genes), which also fall under fitness QTL, were detailed. The gene hypothesized to be under the FTD eQTL on chromosome 4, which overlaps with a fitness QTL, is CBF2. The FTD eQTL on chromosome 5, overlapping with a fitness

QTL, may be a cis-eQTL, implicating COR78 as the underlying gene. Alternatively, the eQTL on chromosome 5 may be a trans-eQTL, which is postulated to be CBF4. As stated in Chapter Three, near-isogenic lines and complementation lines will need to be made for candidate genes underlying these eQTL, to establish their importance for differential expression of cold-regulated genes in SW and IT. These lines will also be employed to ascertain the role of these genes in freezing tolerance and fitness.

There were also eQTL mapped for genes associated with differences in freezing tolerance that did not fall under fitness QTL (Table 3.18 and 3.19). These genes are not included in the CBF-regulon and for most of these genes specific roles in cold-acclimation are yet to be established. Many of the eQTL were located trans- to the gene they were mapped for and thus potentially represent regulatory loci for CBF-independent cold-regulated genes (Table 3.18 and 3.19), which is especially interesting because relatively little is known about CBF-independent pathways of cold acclimation (44).

Hundreds of genes underlie these trans-eQTL. However, RNA-seq data described in detail in Chapter Three can be used to define a smaller set of candidate regulatory genes. For example, SALT-INDUCIBLE ZINC FINGER 1 (SZF1) is a cold-regulated transcription factor previously described as down-regulated at 1 week of cold-acclimation in *Arabidopsis* (29). Indeed, RNA-seq data from this study also shows SW and IT both down-regulating SZF1 with 1 week of cold-acclimation (Fig 4.11). But SW and IT have significantly different *SZF1* expression at 2 weeks of cold-acclimation, when eQTL were mapped (Fig. 4.11). The trans-eQTL mapped for *SZF1* on chromosome 5

encompasses 805 genes. Of these 805 genes, 108 are differentially regulated between SW and IT at 2 weeks of cold-acclimation, which is when *SZF1* expression is significantly different between SW and IT (Fig. 4.11). There are limitations to this candidate gene list, for instance it would not include genes that have differences in post-transcriptional regulation between SW and IT. Nevertheless, these 108 genes seem like a good starting point for regulation of *SZF1*. Since this is a trans-eQTL, the transcription factors in this list of 108 genes were determined. There were a total of 11 transcription factors among these 108 candidate regulatory genes (Table 4.1). Using the RNA-seq data from all time points, expression patterns for *SZF1* and the 11 transcription factors can be compared (Fig. 4.11). Based on these data, AT5G26170 (WRKY50; Table 4.1) is the transcription factor with an expression pattern that best parallels *SZF1* expression and analysis of the SZF1-500 bp promoter reveals two known WRKY binding sites (Fig. 4.11). Again, near-isogenic lines and complementation lines will need to made for WRKY50 to establish its importance in regulation of *SZF1* expression. These lines would also be tested for differences in freezing tolerance. This method of network construction is a rather tedious process, especially for a single gene that may or may not largely contribute to differences in freezing tolerance. Consequently, future efforts for low-temperature network construction should include transcriptomic analysis of the RILs used for mapping.

It is fiscally daunting to do microarray or RNA-seq eQTL analysis on 544 RILs. However, the minimum number of randomly selected RILs necessary to get similar eQTL results to 544 RILs can be determined through analysis of eQTL mapped for the

10 FTD genes in 544 RILs (described in Chapter Three). The same RIL RNA samples used in eQTL analysis can be submitted for transcriptomic analysis by either RNA-seq or Affymetrix arrays. Genome-wide eQTL would thus be mapped for this subset of RILs and trans-regulatory hotspots (45-48) can be identified at a time-point where there are differences in freezing tolerance (2 weeks of cold-acclimation; Fig 3.2). Accordingly, efforts to find the genes responsible for these trans-eQTL will be focused on major regulatory hubs. It is clear that there is much future effort needed to determine the genes responsible for differences in freezing tolerance between the SW and IT ecotypes, especially for CBF-independent pathways. Nevertheless, data from this study provides a necessary backbone for future studies.

**Table 4.1.** Candidate cold-regulated transcription factors for SZF1 trans-QTL on chromosome 5 (between RIL markers 20.0 and 36.7). The SeqViewer tool on TAIR (www.arabidopsis.org) was used to determine within SZF1 trans-QTL on chromosome 5. From this list SW and IT cold-regulated transcription factors were identified using merge function in R. The comparison of SW and IT expression at 2 weeks of cold-acclimation for each gene, was measured by RNA-seq and is represented by the logarithm (base=2) of the fold change (LOG2FC). The FDR corrected P-value is given for each comparison. The results presented are based on averages from three independent experiments (n=3). The shaded transcription factor is located closest to the peak RIL marker for the SZF1-QTL (marker 22.0).

| AGI | SHORT DESCRIPTION | 2WK.SW.IT | 2WK.LOG2FC | FDR P-VALUE |
|---|---|---|---|---|
| AT5G24110 | WRKY DNA-BINDING PROTEIN 30 | ITHIGH | 3.58 | 0.00E+00 |
| AT5G24590 | TCV-INTERACTING PROTEIN | ITHIGH | 0.91 | 1.40E-05 |
| AT5G25190 | INTEGRASE-TYPE DNA-BINDING | ITHIGH | 1.13 | 1.13E-02 |
| AT5G25390 | INTEGRASE-TYPE DNA-BINDING | SWHIGH | -1.20 | 5.15E-05 |
| AT5G25810 | INTEGRASE-TYPE DNA-BINDING | SWHIGH | -1.92 | 2.21E-03 |
| AT5G25890 | INDOLE-3-ACETIC ACID INDUCIBLE 28 | SWHIGH | -0.59 | 3.32E-02 |
| AT5G26170 | WRKY DNA-BINDING PROTEIN 50 | ITHIGH | 2.83 | 7.48E-07 |
| AT5G27610 | DIRP; MYB-LIKE DNA-BINDING DOMAIN | ITHIGH | 0.74 | 2.60E-02 |
| AT5G28300 | SUPERFAMILY PROTEIN | SWHIGH | -0.87 | 4.43E-07 |
| AT5G28640 | SSXT FAMILY PROTEIN | ITHIGH | 1.33 | 1.03E-07 |
| AT5G28770 | BZIP TRANSCRIPTION FACTOR FAMILY | ITHIGH | 0.77 | 3.20E-04 |

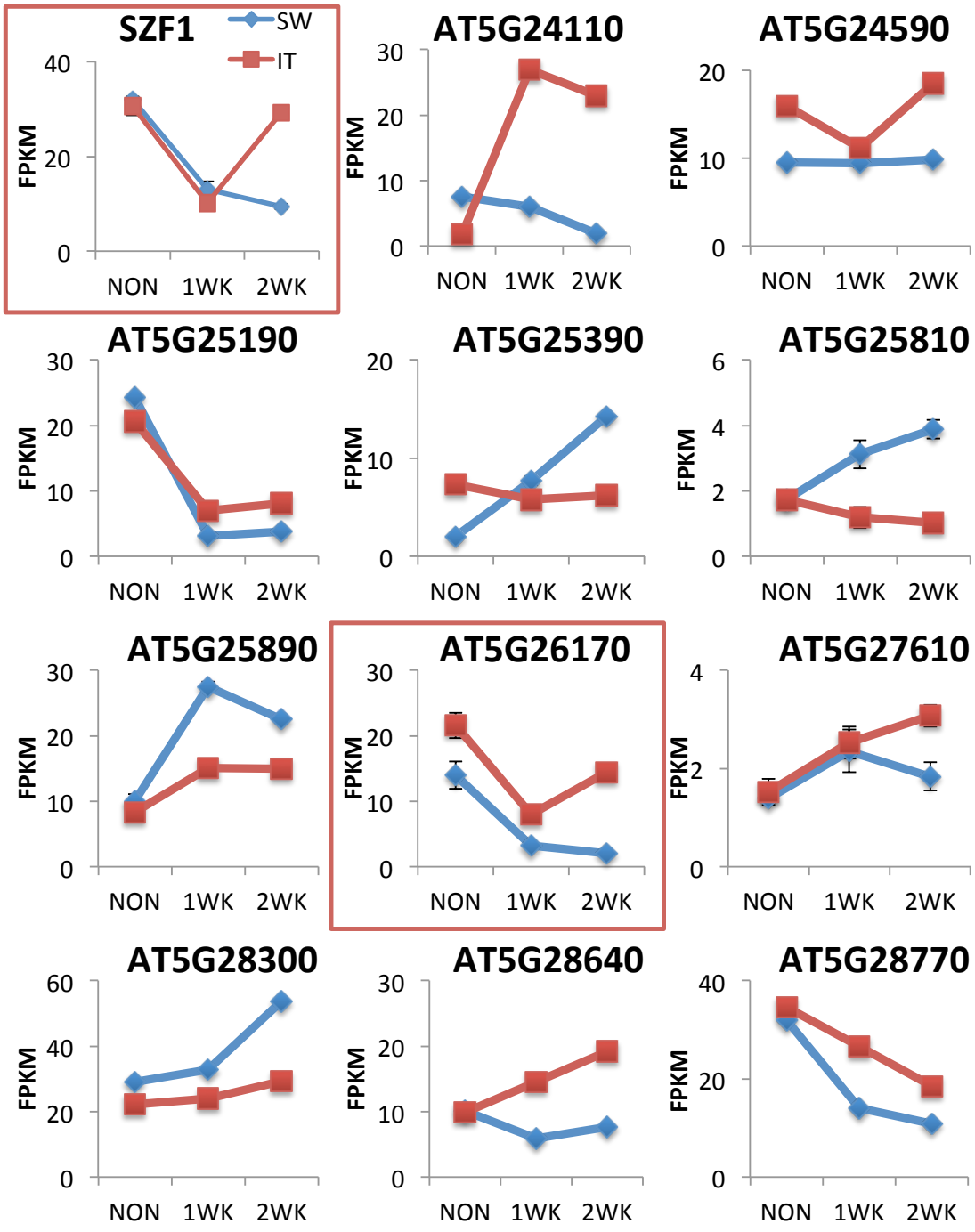


**Figure 4.11.** *SZF1*-regulation candidate gene expression. IT samples are shown in red, and SW in blue. Gene expression was measured by RNA-seq (FPKM). The results presented are average values from three independent experiments (n=3). Error bars indicate ±SEM. Plants were grown at 22$^{0}$C under a 12 h photoperiod and sampled directly or transferred to 4$^{0}$C for 1 or 2 weeks under a 12 h photoperiod then sampled.

## MATERIALS AND METHODS

**Regulation of CBF genes by the REVEILLES, CKβ3, and CAMTAS and circadian regulation of CBF-independent gene, COR27**: Plants were grown and experiments were conducted as described in Chapter Two of this study. Please see Table A4.1and A4.2 for primers.

**Temperature-entrained circadian regulation and gated cold-induction of CBF genes:** Plants were grown and experiments were conducted as described in Chapter Two of this study, except that instead of entrainment with a 12 h photoperiod, plants were entrained with 12 h thermocycles (22$^0$C day/ 12$^0$C night) under constant light, then sampled under constant light and constant temperature conditions (22$^0$C). Please see Table A4.1 for primers.

**Disruption of the circadian clock by low-temperature:** Experiments were conducted as described in Chapter Two of this study. Wild-type Ws-2 plants were grown at 22$^0$C with a 12 h photoperiod to the four leaf stage and then transferred to one of three conditions at ZT4: 'WARM' plants were transferred to constant light and constant temperature (22$^0$C) conditions. 'TEMP CYLING' plants were transferred to constant light with a 12 h cold temperature period (9$^0$C day/ 4$^0$C night). 'COLD' plants were transferred to constant light and constant cold (4$^0$C) conditions. Please see Table A4.1 for primers.

**Low-temperature network construction using SW and IT RILs:** Experiments were conducted as described in Chapter Three of this study.

# APPENDIX

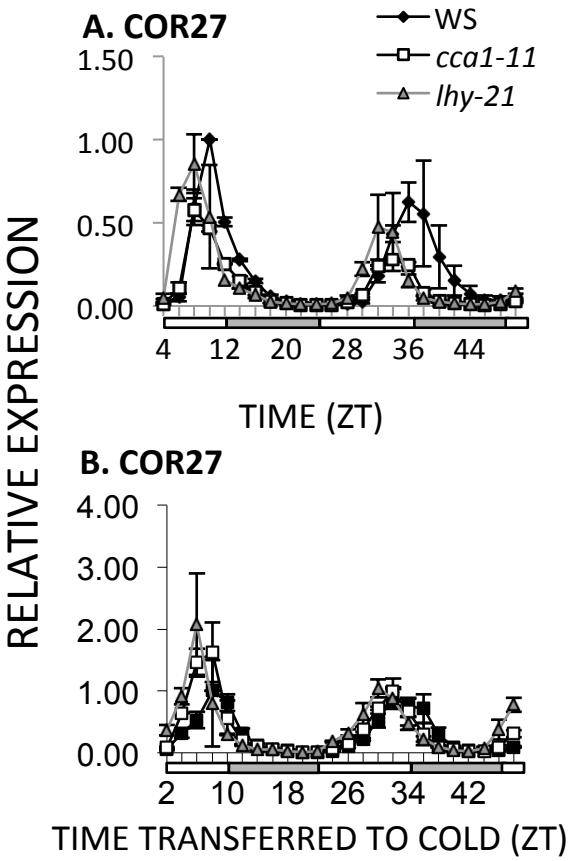


**Figure A4.1.** Effects of the *cca1-11* and *lhy*-21 single mutants on circadian and gated cold-induction of *COR27*. Expression for *COR27* was relative to one wild-type sample WS-2 (WS) set to a value of 1 in each biological replicate. Values for WS-2 are averages from three independent experiments (n=3). Values for *cca1-11* and *lhy-21* are averages from two independent experiments (n=2). Error bars indicate ± SEM. (A) Plants were grown with a 12 h photoperiod at 22$^{0}$C to the four leaf stage and transferred to constant light at ZT0 (subjective day and night are indicated by white and gray bars, respectively). Plants were harvested every 2 h and the transcript levels for *COR27* were determined by qRT-PCR. Gene expression was normalized to IPP2 for each sample. (B) Plants were grown with a 12 h photoperiod at 22$^{0}$C to the four leaf stage and transferred to constant light at ZT0 (subjective day and night are indicated by white and gray bars, respectively). Plants were transferred to cold temperature (4$^{0}$C) for 2 h, every 2 h, for 48 h at the start of constant light conditions and the transcript levels for *COR27* were determined by qRT-PCR. Horizontal axis represents time (ZT) when plants were dropped to cold temperature. Gene expression was normalized to UBQ10 for each sample. Please see Table A4.1 for primer pair sequences.

**Table A4.1.** Primer pairs used for qRT-PCR. Primers used in this study were designed with Primer Express 3.0.

qRT-PCR Primers

| Name | Forward | Reverse | ATG |
|---|---|---|---|
| CAB2 | CCGGAAAGGCTGTGAACCT | CACACGGCCGCTTCCA | AT1G29920 |
| CBF1 | GGAGACAATGTTTGGGATGC | CGACTATCGAATATTAGTAACTCC | AT4G25490 |
| CBF2 | CGACGGATGCTCATGGTCTT | TCTTCATCCATATAAAACGCATCTTG | AT4G25470 |
| CBF2 | CGACGGATGCTCATGGTCTT | TCTTCATCCATATAAAACGCATCTTG | AT4G25470 |
| CBF3 | TTCCGTCCGTACAGTGGAAT | AACTCCATAACGATACGTCGTC | AT4G25480 |
| CCA1 | CCGCAACTTTCGCCTCAT | GCCAGATTCGGAGGTGAGTTC | AT2G46830 |
| CCR2 | TAGGGCGACGTTATTGATTCC | CCCTCAATCGCATCCTTCA | AT1G06820 |
| COR15A | GAAAAAAACAGTGAAACCGCAGAT | CCACATACGCCGCAGCTT | AT2G42540 |
| COR27 | GCTCTGGCTCAGCCTCTAGTCT | GGTCGTGGTCACGCGAAT | AT5G42900 |
| COR47 | CGGTACCAGTGTCGGAGAGT | ACAGCTGGTGAATCCTCTGC | AT1G20440 |
| COR78 | GAAAGGAGGAGGAGGAATGG | AACCAGCCAGATGATTTTGG | AT5G52310 |
| IPP2 | ATTTGCCCATCGTCCTCTGT | GAGAAAGCACGAAAATTCGGTAA | AT3G02780 |
| LHCB1.4 | GCCTTCGCTACCAACTTCGTC | AACCGGATACACACAACTCGATC | AT2G34430 |
| PRR3 | GTGGGAGTAGTGGTGGTTTGAGTA | TTTGTCCAAGAACTCTGAGTTCCA | AT5G60100 |
| PRR5 | CGAGAAGCCGCTTTAACCAA | CGGCTCTCGTAACGAACCTT | AT5G24470 |
| PRR7 | CCACGAGCGGTATCTCTATGG | ACTTGGAAACTCAGGGTTAGAA | AT5G02810 |
| PRR9 | GCCAGAGAGAAGCTGCATTGA | CCTGCTCTGGTACCGAACCTT | AT2G46790 |
| TOC1 | TCTTCGCAGAATCCCTGTGAT | GCTGCACCTAGCTTCAAGCA | AT5G61380 |
| UBQ10 | GGCCTTGTATAATCCCTGATGAATAAG | AAAGAGATAACAGGAACGGAAACATAGT | AT4G05320 |

**Table A4.2.** Primer pairs used for ChIP qRT-PCR. Primers used in this study were designed with Primer Express 3.0.

ChIP PRIMERS

| Name | Forward | Reverse | ATG |
|---|---|---|---|
| ACTIN2 | CGTTTCGCTTTCCTTAGTGTTA | AGCGAACGGATCTAGAGACTC | AT3G18780 |
| COR27-A | TTCGCATGGGAGAAGAAGGT | CCACTATCGCCTCTGAATCCA | AT5G42900 |
| COR27-B | AGTTACAACAATCAATAAGCA | GAGAAGGGTGAGTAATTATGTGAATATACAA | AT5G42900 |
| COR27-C | TCTTCCAAAAGAGACATGTAATAGTCAA | TGGGACGATTCACTTTTCTTATTAGA | AT5G42900 |
| COR27-D | GCTCTGGCTCAGCCTCTAGTCT | GGTCGTGGTCACGCGAAT | AT5G42900 |
| TOC1 | TTTTATGGCCTGCACTTTTTATTG | GGTGGGACTTGGGATATTTTAGG | AT5G61380 |
| TOC1 3'UTR | GCTACAGCCAAAAAAACATCGA | GAGCCGCAAGAGCCAACAT | AT5G61380 |
| UBQ10 | TCCAGGACAAGGAGGTATTCCTCCG | CCACCAAAGTTTTACATGAAACGAA | AT4G05320 |

## LITERATURE CITED

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1. Doherty CJ, Van Buskirk HA, Myers SJ, & Thomashow MF (2009) Roles For Arabidopsis CAMTA Transcription Factors In Cold-Regulated Gene Expression And Freezing Tolerance. *Plant Cell* 21(3):972-984.

2. Johnson CH, Knight MR, Kondo T, Masson P, Sedbrook J, Haley A, & Trewavas A (1995) Circadian Oscillations Of Cytosolic And Chloroplastic Free Calcium In Plants. *Science* 269(5232):1863-1865.

3. Rawat R, Takahashi N, Hsu PY, Jones MA, Schwartz J, Salemi MR, Phinney BS, & Harmer SL (2011) REVEILLE8 And PSEUDO-REPONSE REGULATOR5 Form A Negative Feedback Loop Within The Arabidopsis Circadian Clock. *Plos Genetics* 7(3).

4. Nakamichi N, Kusano M, Fukushima A, Kita M, Ito S, Yamashino T, Saito K, Sakakibara H, & Mizuno T (2009) Transcript Profiling Of An Arabidopsis PSEUDO RESPONSE REGULATOR Arrhythmic Triple Mutant Reveals A Role For The Circadian Clock In Cold Stress Response. *Plant and Cell Physiology* 50(3):447-462.

5. Mas P, Kim WY, Somers DE, & Kay SA (2003) Targeted Degradation Of TOC1 By ZTL Modulates Circadian Function In Arabidopsis Thaliana. *Nature* 426(6966):567-570.

6. Daniel X, Sugano S, & Tobin EM (2004) CK2 Phosphorylation Of CCA1 Is Necessary For Its Circadian Oscillator Function In Arabidopsis. *Proceedings of the National Academy of Sciences of the United States of America* 101(9):3292-3297.

7. Sugano S, Andronis C, Green RM, Wang ZY, & Tobin EM (1998) Protein Kinase CK2 Interacts With And Phosphorylates The Arabidopsis Circadian Clock-Associated 1 Protein. *Proceedings of the National Academy of Sciences of the United States of America* 95(18):11020-11025.

8. Fowler S & Thomashow MF (2002) Arabidopsis Transcriptome Profiling Indicates That Multiple Regulatory Pathways Are Activated During Cold Acclimation In Addition To The CBF Cold Response Pathway. *The Plant Cell* 14(8):1675-1690.

9. Mikkelsen MD & Thomashow MF (2009) A Role For Circadian Evening Elements In Cold-Regulated Gene Expression In Arabidopsis. *Plant Journal* 60(2):328-339.

10. Dong MA, Farre EM, & Thomashow MF (2011) CIRCADIAN CLOCK-ASSOCIATED 1 And LATE ELONGATED HYPOCOTYL Regulate Expression Of The C-REPEAT BINDING FACTOR (CBF) Pathway In Arabidopsis. *Proceedings of the National Academy of Sciences of the United States of America* 108(17):7241-7246.

11. Gong W, He K, Covington M, Dinesh-Kumar SP, Snyder M, Harmer SL, Zhu YX, & Deng XW (2008) The Development Of Protein Microarrays And Their Applications In DNA-Protein And Protein-Protein Interaction Analyses Of Arabidopsis Transcription Factors. *Molecular Plant* 1(1):27-41.

12. Rensing L & Ruoff P (2002) Temperature Effect On Entrainment, Phase Shifting, And Amplitude Of Circadian Clocks And Its Molecular Bases. *Chronobiology International* 19(5):807-864.

13. Salome PA & McClung CR (2005) What Makes The Arabidopsis Clock Tick On Time? A Review On Entrainment. *Plant Cell and Environment* 28(1):21-38.

14. Locke JCW, Kozma-Bognar L, Gould PD, Feher B, Kevei E, Nagy F, Turner MS, Hall A, & Millar AJ (2006) Experimental Validation Of A Predicted Feedback Loop In The Multi-Oscillator Clock Of Arabidopsis Thaliana. *Mol Syst Biol* 2.

15. Pruneda-Paz JL, Breton G, Para A, & Kay SA (2009) A Functional Genomics Approach Reveals CHE As A Component Of The Arabidopsis Circadian Clock. *Science* 323(5920):1481-1485.

16. Wenden B, Kozma-Bognár L, Edwards KD, Hall AJW, Locke JCW, & Millar AJ (2011) Light Inputs Shape The Arabidopsis Circadian System. *The Plant Journal* 66(3):480-491.

17. Millar AJ & Kay SA (1996) Integration Of Circadian And Phototransduction Pathways In The Network Controlling CAB Gene Transcription In Arabidopsis. *Proceedings of the National Academy of Sciences of the United States of America* 93(26):15491-15496.

18. Wang ZY & Tobin EM (1998) Constitutive Expression Of The CIRCADIAN CLOCK ASSOCIATED 1 (CCA1) Gene Disrupts Circadian Rhythms And Suppresses Its Own Expression. *Cell* 93(7):1207-1217.

19. McWatters HG, Bastow RM, Hall A, & Millar AJ (2000) The ELF3 Zeitnehmer Regulates Light Signalling To The Circadian Clock. *Nature* 408(6813):716-720.

20. Farre EM & Kay SA (2007) PRR7 Protein Levels Are Regulated By Light And The Circadian Clock In Arabidopsis. *Plant Journal* 52(3):548-560.

21. Yakir E, Hilman D, Hassidim M, & Green RM (2007) CIRCADIAN CLOCK ASSOCIATED1 Transcript Stability And The Entrainment Of The Circadian Clock In Arabidopsis. *Plant Physiology* 145(3):925-932.

22. Salome PA & McClung CR (2005) PSEUDO-RESPONSE REGULATOR 7 And 9 Are Partially Redundant Genes Essential For The Temperature Responsiveness Of The Arabidopsis Circadian Clock. *Plant Cell* 17(3):791-803.

23. Gould PD, Locke JCW, Larue C, Southern MM, Davis SJ, Hanano S, Moyle R, Milich R, Putterill J, Millar AJ, & Hall A (2006) The Molecular Basis Of Temperature Compensation In The Arabidopsis Circadian Clock. *Plant Cell* 18(5):1177-1187.

24. Fowler SG, Cook D, & Thomashow MF (2005) Low Temperature Induction Of Arabidopsis CBF1, 2, And 3 Is Gated By The Circadian Clock.*Plant Physiology* 137:961-968.

25. Ramos A, Perez-Solis E, Ibanez C, Casado R, Collada C, Gomez L, Aragoncillo C, & Allona I (2005) Winter Disruption Of The Circadian Clock In Chestnut. *Proceedings of the National Academy of Sciences of the United States of America* 102(19):7037-7042.

26. Bieniawska Z, Espinoza C, Schlereth A, Sulpice R, Hincha DK, & Hannah MA (2008) Disruption Of The Arabidopsis Circadian Clock Is Responsible For Extensive Variation In The Cold-Responsive Transcriptome. *Plant Physiology* 147(1):263-279.

27. Gilmour SJ, Zarka DG, Stockinger EJ, Salazar MP, Houghton JM, & Thomashow MF (1998) Low Temperature Regulation Of The Arabidopsiscbf Family Of AP2 Transcriptional Activators As An Early Step In Cold-Induced COR Gene Expression. *The Plant Journal* 16(4):433-442.

28. Zarka DG, Vogel JT, Cook D, & Thomashow MF (2003) Cold Induction Of Arabidopsis CBF Genes Involves Multiple ICE (Inducer Of CBF Expression) Promoter Elements And A Cold-Regulatory Circuit That Is Desensitized By Low Temperature. *Plant Physiology* 133(2):910-918.

29. Vogel JT, Zarka DG, Van Buskirk HA, Fowler SG, & Thomashow MF (2005) Roles Of The CBF2 And ZAT12 Transcription Factors In Configuring The Low Temperature Transcriptome Of Arabidopsis. *Plant Journal* 41(2):195-211.

30. Somers DE, Webb AAR, Pearson M, & Kay SA (1998) The Short-Period Mutant, Toc1-1, Alters Circadian Clock Regulation Of Multiple Outputs Throughout Development In Arabidopsis Thaliana. *Development* 125(3):485-494.

31. Mizoguchi T, Wheatley K, Hanzawa Y, Wright L, Mizoguchi M, Song H-R, CarrÈ IA, & Coupland G (2002) LHY And CCA1 Are Partially Redundant Genes Required To Maintain Circadian Rhythms In Arabidopsis. *Developmental cell* 2(5):629-641.

32. Niwa Y, Ito S, Nakamichi N, Mizoguchi T, Niinuma K, Yamashino T, & Mizuno T (2007) Genetic Linkages Of The Circadian Clock-Associated Genes, TOC1, CCA1 And LHY, In The Photoperiodic Control Of Flowering Time In Arabidopsis Thaliana. *Plant and Cell Physiology* 48(7):925-937.

33. Airaki M, Leterrier M, Mateos RM, Valderrama R, Chaki M, Barroso JB, Del Rio LA, Palma JM, & Corpas FJ (2012) Metabolism Of Reactive Oxygen Species And Reactive Nitrogen Species In Pepper (Capsicum Annuum L.) Plants Under Low Temperature Stress. *Plant Cell and Environment* 35(2):281-295.

34. Mohanty S & Tripathy BC (2011) Early And Late Plastid Development In Response To Chill Stress And Heat Stress In Wheat Seedlings. *Protoplasma* 248(4):725-736.

35. Strauss AJ, Kruger GHJ, Strasser RJ, & Van Heerden PDR (2006) Ranking Of Dark Chilling Tolerance In Soybean Genotypes Probed By The Chlorophyll A Fluorescence Transient O-J-I-P. *Environmental and Experimental Botany* 56(2):147-157.

36. Venema JH, Linger P, van Heusden AW, van Hasselt PR, & Bruggemann W (2005) The Inheritance Of Chilling Tolerance In Tomato (Lycopersicon Spp.). *Plant Biology* 7(2):118-130.

37. Gilmour SJ, Fowler SG, & Thomashow MF (2004) Arabidopsis Transcriptional Activators CBF1, CBF2, And CBF3 Have Matching Functional Activities. *Plant Molecular Biology* 54(5):767-781.

38. Oguchi R, Hikosaka K, & Hirose T (2003) Does The Photosynthetic Light-Acclimation Need Change In Leaf Anatomy? *Plant, Cell & Environment* 26(4):505-512.

39. Savitch LV, Allard G, Seki M, Robert LS, Tinker NA, Huner NPA, Shinozaki K, & Singh J (2005) The Effect Of Overexpression Of Two Brassica CBF/DREB1-Like Transcription Factors On Photosynthetic Capacity And Freezing Tolerance In Brassica Napus. *Plant and Cell Physiology* 46(9):1525-1539.

40. Palta JP & Li PH (1979) Frost-Hardiness In Relation To Leaf Anatomy And Natural Distribution Of Several Solanum Species. *Crop Science* 19(5):665-671.

41. Huner NPA, Palta JP, Li PH, & Carter JV (1981) Anatomical Changes In Leaves Of Puma Rye In Response To Growth At Cold-Hardening Temperatures. *Botanical Gazette* 142(1):55-62.

42. Stefanowska M, Kuras M, Kubacka-Zebalska M, & Kacperska A (1999) Low Temperature Affects Pattern Of Leaf Growth And Structure Of Cell Walls In Winter Oilseed Rape (Brassica Napus L., Var. Oliefera L.). *Annals of Botany* 84(3):313-319.

43. Gorsuch PA, Pandey S, & Atkin OK (2010) Temporal Heterogeneity Of Cold Acclimation Phenotypes In Arabidopsis Leaves. *Plant Cell and Environment* 33(2):244-258.

44. Chinnusamy V, Zhu J, & Zhu JK (2007) Cold Stress Regulation Of Gene Expression In Plants. *Trends in Plant Science* 12(10):444-451.

45. Keurentjes JJB, Fu JY, Terpstra IR, Garcia JM, van den Ackerveken G, Snoek LB, Peeters AJM, Vreugdenhil D, Koornneef M, & Jansen RC (2007) Regulatory Network Construction In Arabidopsis By Using Genome-Wide Gene Expression Quantitative Trait Loci. *Proceedings of the National Academy of Sciences of the United States of America* 104(5):1708-1713.

46. Potokina E, Druka A, Luo ZW, Wise R, Waugh R, & Kearsey M (2008) Gene Expression Quantitative Trait Locus Analysis Of 16,000 Barley Genes Reveals A Complex Pattern Of Genome-Wide Transcriptional Regulation. *Plant Journal* 53(1):90-101.

47. Kliebenstein D (2009) Quantitative Genomics: Analyzing Intraspecific Variation Using Global Gene Expression Polymorphisms Or Eqtls. *Annual Review of Plant Biology* 60(1):93-114.

48. Majewski J & Pastinen T (2011) The Study Of Eqtl Variations By RNA-Seq: From Snps To Phenotypes. *Trends in Genetics* 27(2):72-79.