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Jonathan Thomas Vogel

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TRANSCRIPTION FACTORS THAT CONFIGURE THE LOW TEMPERATURE
TRANSCRIPTOME OF ARABIDOPSIS THALIANA

By

Jonathan Thomas Vogel

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ABSTRACT

TRANSCRIPTION FACTORS THAT CONFIGURE THE LOW TEMPERATURE TRANSCRIPTOME OF ARABIDOPSIS THALIANA

By

Jonathan Thomas Vogel

Many plants can sense low temperature and respond by altering gene expression. These changes in gene expression can ultimately lead to increased freezing tolerance as part of a dynamic physiological process known as cold acclimation. One well known pathway that contributes to cold acclimation is the CBF/DREB1 cold response pathway. This pathway includes the action of the transcriptional activators *CBF1*, 2, and 3 (also known as *DREB1b*, *c*, and *a*, respectively) that are rapidly induced in response to low temperature and activate the expression of a suite of target genes, known as the CBF regulon. The CBF regulon gene products act in concert to increase plant freezing tolerance. Work in this dissertation focused on gaining a better understanding of the changes in gene expression that occur in response to low temperature, the extent to which the CBF pathway contributes to these changes, and whether six other transcription factors that were coordinately regulated with *CBF2* affected cold-responsive genes.

In this work, the Affymetrix GeneChip containing probe sets for approximately 24,000 genes was used to define a core set of cold-responsive transcripts. A total of 514 transcripts were found to have altered transcript accumulation, 302 of which were up-regulated and 212 down-regulated, in plants grown in two commonly used growth conditions (soil and solid media). These genes were termed the COS (cold standard) gene set. Hierarchical clustering assigned each transcript to one of seven expression classes and bioinformatic analysis revealed multiple novel potential *cis*-elements present

in the promoters of genes in each expression class. Further bioinformatic analysis revealed additional motifs among one of these expression classes, cluster III, but experiments indicated no evidence that any of the novel motifs in clusters III or IV were cold-responsive. One element, GTGATCAC, conferred constitutive GUS activity when fused as a tetramer in front of the reporter. A functional analysis of the COS transcripts revealed how the plants might be globally altering their metabolism in order to cope with low temperature, which has generated a number of new hypotheses that can be tested.

Plants overexpressing *CBF2* or one of six transcription factors that were coordinately regulated with *CBF2* were also profiled using the GeneChips. The *CBF2* regulon was comprised of 85 cold-induced and eight cold-repressed genes. Of the six genes that were induced in parallel with *CBF2* only one, *ZAT12*, influenced cold-responsive genes when constitutively expressed. The *ZAT12* regulon contained nine cold-induced genes and 15 cold-repressed genes. Constitutive expression of *ZAT12* resulted in a small, but reproducible increase in freezing tolerance, indicating a role for *ZAT12* in cold acclimation. *ZAT12* also appeared to have a role in a negative regulatory circuit that dampened expression of the *CBF* genes. Constitutive expression of *ZAT12* dampened *CBF* transcript accumulation in response to low temperature, while decreased levels of *ZAT12* resulted in higher levels of *CBF* transcript accumulation.

The definition of the COS genes provides a framework on which the low temperature regulatory networks of Arabidopsis can be constructed and this dissertation begins this process by defining two regulons, the *CBF2* and *ZAT12* regulons. Future experiments will expand our knowledge of these and other networks and could eventually lead to novel strategies for engineering plants with increased stress tolerance.

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CHAPTER ONE

LITERATURE REVIEW

Introduction

Photosynthesis, the overall process of using light energy to synthesize organic compounds, allows plants to maintain an autotrophic lifestyle. This autotrophic lifestyle includes remaining rooted in place, which is fine most of the time but prevents plants from evading environmental stress. However, evasion is not the only method of dealing with stress. Plants have evolved a number of effective mechanisms to cope with multiple biotic and abiotic environmental stresses while remaining sessile.

One abiotic stress plants must deal with is temperature fluctuation. Cold or freezing temperatures can significantly limit plant growth or result in damage or death. Plants exhibit a wide range in their ability to survive freezing temperatures. Plants from the tropics have essentially no capacity for surviving even a mild freeze and are damaged by chilling temperatures in the range of 0°C to 12°C. Some examples include tomato, maize (Taylor et al., 1974), and rice (Tajima et al., 1983). Other plants, such as the cultivated potato (*Solanum tuberosum*), exhibit chilling resistance, but are still injured or killed by any ice formation (Sukumaran and Weiser, 1972). There are other plants that are killed by temperatures in the range of -6°C to -1°C. Most *Citrus* is killed in this range (-6°C to -3°C) (Yelenosky and Guy, 1989). Depending on the species, herbaceous plants from temperate regions (wheat, canola, *Arabidopsis*) generally survive freezing in the range of -5°C to -30°C (Fowler and Gusta, 1979; Gilmour et al., 1988). The record holders for freezing tolerance include tree species from boreal forests that regularly survive winters with temperatures below -30°C and can even survive immersion in liquid

nitrogen when fully cold-acclimated (Sakai and Larcher, 1987). The level of freezing tolerance achieved is not constitutive, but induced in response to low, non-freezing temperatures (below approximately 10°C), in a process known as cold acclimation (Guy, 1990; Thomashow, 1998). Cold acclimation allows plants that would normally be killed by mild freezing conditions (-5°C) to survive at much lower temperatures (-20°C).

The study of cold acclimation in plants is important. Not only does understanding conditional freezing tolerance (or lack of it) further science, it has practical applications for agricultural production. Freezing temperatures negatively impact crop productivity and limit the geographical locations where plants are grown (Thomashow, 1998). Understanding the molecular basis of cold acclimation and freezing tolerance could lead to new strategies of improving crop productivity through increased freezing tolerance. Much research has focused on how freezing damages plant cells, what mechanisms exist to protect the plant, and how plants sense and respond to low temperatures in order to activate protective mechanisms.

Freezing-Induced Damage

Water, while essential to life, forms ice crystals spontaneously (homogeneous nucleation) or when catalyzed by another substance (heterogeneous nucleation) that can kill or damage a cell. At temperatures just below 0°C, homogeneous ice formation is unlikely and nucleation is needed. In the absence of any nucleator, a single cell will freeze only when the temperature falls below -38.5°C, the point of spontaneous nucleation (Franks, 1985). Otherwise, water can remain in a supercooled state. Many substances can act as nucleators including ice nucleation-active bacteria,

organic/inorganic debris, and biological molecules (Pearce, 2001). In plants, freezing temperatures generally first induce ice formation in intercellular spaces because these spaces have a higher freezing point due to a lower solute concentration and contain ice nucleating agents (Brush et al., 1994). Ice formation in intercellular spaces has the potential to physically disrupt cells (Levitt, 1980). However, most damage results from severe cellular dehydration associated with freezing (Levitt, 1980; Steponkus and Webb, 1992). Since the chemical potential of ice at a given temperature is lower than liquid water, extracellular ice formation results in a decrease in water potential outside the cell and a consequent movement of water through the plasma membrane to the extracellular space, leading to the dehydration of the cell. The amount of dehydration is dependent on both the temperature and the initial solute concentration of the cytoplasm. Cellular dehydration also occurs in drought and salinity stress, which suggest that the mechanisms that protect a plant from freezing-induced dehydration should also protect the plant from the dehydration caused by drought or salinity stress.

Cellular dehydration during freezing can potentially have numerous deleterious effects, including protein denaturation, the precipitation of molecules, and membrane damage. Since 1912, the plasma membrane has been thought to be a primary site of freeze-induced injury (Levitt, 1980). Studies done with rye protoplasts have shown that freezing-induced dehydration can result in three main membrane lesions (Webb et al., 1994; Uemura et al., 1995). In the range of -2°C to -4°C , expansion-induced lysis can occur, caused by osmotic expansion and contraction cycles (during freeze/thaw cycles). The contraction of the plasma membrane during freezing results in the endocytic vesiculation of the plasma membrane, which decreases plasma membrane surface area. If

sufficient membrane is lost, water re-entering the cell during expansion can lyse the membrane. Cold acclimation prevents this type of lesion from occurring, as the plasma membrane is retained in exocytotic extrusions that allow expansion.

Between -4°C and -10°C, freezing can induce lamellar-to-hexagonal II phase transitions, which involves the fusion of various membranes. In this type of damage, a lamellar membrane, when brought into close apposition with another membrane due to cellular dehydration, can form non-bilayer Hex II phase lipids. This results in a loss of membrane integrity. The chloroplast envelope is particularly susceptible to this type of damage (Steponkus et al., 1993). Again, protoplasts isolated from cold-acclimated leaves generally do not suffer this type of damage.

Fracture jump lesions can occur at temperatures below -10°C with cold acclimation. This lesion was observed as a localized deviation in the fracture plane of the plasma membrane during cryoelectron microscopy and is likely due to localized fusion of the plasma membrane with other cellular membranes (Webb *et al.*, 1994). This type of lesion has only been observed with cold acclimation and varies greatly between plant species (Webb et al., 1994; Uemura et al., 1995). While little is known about why variation exists, fracture jump lesions appear to be a relative measure of the potential freezing tolerance that can be achieved.

In addition to dehydration induced damage, cold temperatures can generate reactive oxygen species (ROS) which can contribute to membrane damage (McKersie and Bowley, 1997). Low temperature causes a decrease in the turnover rate of components of photosystem II, leading to excess excitation energy and the generation of reactive oxygen species, including hydrogen peroxide (Huner et al., 1998). ROS not only

damages membrane lipids, but can also harm carbohydrates, proteins, and nucleic acids (McKersie and Bowley, 1997). Additionally, ROS species generated at low temperature could be activating a programmed cell death response (Wagner et al., 2004), which evidence suggests occurs in plants exposed to low temperature (reviewed in Kratsch and Wise, 2000).

Mechanisms for Freezing Tolerance

The mechanisms involved in freezing tolerance are not well understood, but numerous studies have identified physiological and biochemical changes that occur during cold acclimation. Some of these changes include reduced growth rates, decreased water content (Levitt, 1980), altered membrane lipid composition (Uemura and Steponkus, 1994), the production of new proteins (including membrane stabilizers, antifreeze proteins, and chaperones) (Smallwood and Bowles, 2002), transient increases in abscisic acid (Chen et al., 1983), increased levels of antioxidants (McKersie and Bowley, 1997), and the accumulation of compatible osmolytes (proline, betaine, polyols, and soluble sugars) (Levitt, 1980; Yancey et al., 1982). Given the many changes that occur during cold acclimation, it is hard to discern those changes that contribute to freezing tolerance from those that simply occur in response to low temperature. Nevertheless, the multitude of changes indicate that cold acclimation is a dynamic event, requiring multiple biochemical, metabolic, and cellular changes to occur in order to achieve freezing tolerance.

Given that cell membranes appear to be a primary site of freezing damage, protecting membranes at freezing temperatures seems essential. In fact, alterations in

membrane lipid composition and structure are some of the best documented changes that occur during cold acclimation (reviewed in Nishida and Murata, 1996). While not completely understood, ultrastructural changes in the membrane become apparent within 6 h of cold treatment in *Arabidopsis* (Ristic and Ashworth, 1993). Moreover, the changes in membrane lipid composition that occur during cold acclimation correlate with membrane cryostability (Steponkus, 1984; Uemura et al., 1995). Direct evidence also exists for membrane lipid composition playing a direct role in freezing tolerance. Increased levels of mono- and di-unsaturated species of phosphatidylcholine can prevent membranes from forming endocytotic vesicles during hyperosmotic stress, while disaturated species of phosphatidylcholine can not (Steponkus et al., 1988).

These *in vitro* experiments are complemented by experiments *in planta*, as alterations in lipid composition have been shown to influence chilling tolerance in *Arabidopsis* and tobacco. After prolonged exposure to chilling temperatures (2°C to 5°C), *Arabidopsis* mutants with diminished levels of unsaturated lipids become chlorotic (Wu et al., 1997; Vijayan and Browse, 2002). At low temperature, these mutants, *fad5*, *fad6*, and the *fad3-2 fad7-2 fad8* triple mutant were found to be more susceptible to photoinhibition than wild type *Arabidopsis* (Vijayan and Browse, 2002). Additionally, experiments in tobacco revealed that some of this plant's chilling sensitivity can be alleviated if the level of membrane unsaturation is increased (Moon et al., 1995).

Plants increase the levels of a number of low molecular weight organic solutes upon cold acclimation, including proline, glycine betaine, and sugars (raffinose, sucrose, and trehalose). These molecules are known as compatible solutes or compatible osmolytes, as they are highly soluble and their accumulation does not interfere with

cellular metabolism. While their main role in freezing tolerance is thought to be in maintaining cellular osmotic balance, this is not the only role they play. Some compatible solutes stabilize membranes (Hinch and Crowe, 1998; Hinch et al., 1999), while others serve as enzyme cryoprotectants (reviewed in Sakamoto and Murata, 2001). Many compatible solutes accumulate to high levels during cold acclimation, which correlates well with increased freezing tolerance. For example, increased levels of proline (30-fold higher) have been found in the constitutively freezing tolerant mutant *eskimo1* (Xin and Browse, 1998). Conversely, a lack of sugar accumulation during cold acclimation in the *Arabidopsis sfr4* mutant correlates with its sensitivity to freezing (Warren et al., 1996). Still, the specific role of each osmolyte in freezing tolerance is unclear. Dissection of osmolyte function has been complicated by their metabolic roles, which are generally essential.

Freezing tolerant plants can withstand ice formation in their apoplast (Griffith and Yaish, 2004), thought to be due in part to the production of a number of anti-freeze proteins (AFPs) that prevent or alter ice formation in this compartment (Urrutia et al., 1992; Duman, 1994; Hon et al., 1995; Hinch et al., 1997; Worrall et al., 1998; Smallwood et al., 1999; Yeh et al., 2000). Antifreeze proteins interact with ice crystals and inhibit their growth. They do so through two mechanisms. First, they can prevent the accretion of water molecules to the growing face of an ice crystal. Secondly, AFPs can depress the freezing point of water through binding to the surface of ice crystals, without affecting the melting point of the solution (this is known as thermal hysteresis activity). Most plant AFPs are homologous to pathogenesis-related proteins and also provide protection against psychrophilic pathogens (Griffith and Yaish, 2004). Given the

difficulty of mounting a defense response in sub-zero conditions, accumulating proteins during cold acclimation that serve a dual purpose could be advantageous for the plant. Unfortunately, there is no consensus sequence for identifying an AFP through a database search, so they must be identified experimentally. While *in vitro* data firmly confirms the thermal hysteresis activity of AFPs identified in plants, *in vivo* data for their function is limited (Griffith and Yaish, 2004). Still, their widespread occurrence and expression at low temperature in diverse plant species suggest they play a role in freezing tolerance.

Plants produce numerous small, highly hydrophilic polypeptides during cold acclimation. These proteins have a relatively simple amino acid composition, have repeated amino acid motifs, are generally predicted to form amphipathic α -helices, and remain soluble upon boiling in a dilute aqueous buffer (reviewed in Thomashow, 1999). These proteins have been identified by a number of researchers and hence possess multiple designations, including COR (cold-regulated), LTI (low temperature induced), KIN (cold-inducible), RD (responsive to desiccation), and ERD (early dehydration-inducible). Additionally, some of these proteins are homologs of the LEA (late embryogenesis abundant) proteins, which are produced just before seed desiccation during embryogenesis (Dure et al., 1981). The exact function of these proteins is unknown. They are, however, also expressed in response to dehydration and ABA. Given the similarities between freezing and dehydration injuries and the similar biochemical properties of these proteins, one hypothesis is that they function in mitigating dehydration-induced damage. This hypothesis is supported by work on the COR15a protein from Arabidopsis.

COR15a is a 15 kDa polypeptide that is targeted to chloroplasts, where it is processed to a mature 9.4 kDa protein (COR15am). Regions of the polypeptide are predicted to form amphipathic α -helices. In order to determine its role in freezing tolerance, Artus et al. (1996) created transgenic plants constitutively expressing *COR15a*. The chloroplasts of nonacclimated transgenic plants were 1°C to 2°C more freezing tolerant than wild type chloroplasts in the range of -4°C to -8°C. Additionally, protoplasts isolated from the leaves of nonacclimated transgenic plants were 1°C more freezing tolerant in the same temperature range (Steponkus et al., 1998).

One hypothesis concerning how COR15a brings about increased chloroplast freezing tolerance is that COR15a stabilizes membranes. Steponkus et al. (1998) showed that in the temperature range of -4.5°C to -7°C, COR15am decreased the incidence of HexII phase lipid formation in regions where the plasma membrane was brought into close apposition with the chloroplast envelope during freezing-induced dehydration. COR15am is thought to decrease the incidence of HexII lipid formation by altering the intrinsic curvature of the inner membrane of the chloroplast envelope, thereby lowering the temperature at which HexII lipids form. *In vitro* data supports this hypothesis, as COR15am increased the lamellar-to-hexagonal II phase transition temperature of dioleoylphosphatidylethanolamine (this is a sensitive test for an effect on monolayer curvature) and promoted formation of the lamellar phase in a lipid mixture composed of the major lipid species of the chloroplast envelope (Steponkus *et al.*, 1998). Given that other COR proteins are predicted to form similar structures (amphipathic α -helices), the possibility exists that these proteins also help stabilize membranes against freezing-induced dehydration injury by altering the intrinsic curvature of membranes. Indeed,

work on a LEA II protein (CAP85) and a novel COR-like protein (CAP160) from spinach indicate they may also play a role in stabilizing membranes (Kaye et al., 1998), as might the dehydrins (members of the LEA II protein family) RAB18, COR47/RD17, LTI29/ERD10, and LTI30/XERO2 (Puhakainen et al., 2004).

Low Temperature Perception

The mechanism by which plants sense low temperature is unknown. While the nature of this “thermometer” is a mystery, low temperature alters a number of physiological processes that could act as the initial transducer of a cold stimulus. Low temperature can alter RNA and DNA secondary structure and the enzymatic activity of proteins. Changes such as these could function as the sensor. The photosynthetic apparatus itself may act as the sensor, detecting changes in temperature through increased energy imbalances and photoinhibition (Huner *et al.*, 1998).

One of the earliest and most direct effects of low temperature on a cell is a decrease in membrane fluidity (Levitt, 1980). The idea that changes in membrane fluidity could act as the initial cold sensor is supported by a number of studies. Initial observations in *Synechocystis* revealed that rigidification of membranes could induce the expression of cold-regulated genes (Vigh et al., 1993). Murata and Los (1997) hypothesized that the sensor is found in microdomains of the plasma membrane and senses physical alterations in membrane phase transitions, leading to conformational changes or alterations in the phosphorylation state of the sensor. Studies in alfalfa also support the hypothesis that the sensor works through interpreting membrane fluidity (Orvar et al., 2000). Treatment of alfalfa cells at warm temperatures with benzyl alcohol

increases membrane fluidity and inhibits the accumulation of the cold-responsive transcript *CAS30* in response to low temperature. Conversely, treatment of cells with dimethyl sulfoxide, which reduces membrane fluidity, increased *CAS30* levels at warm temperatures. The authors also showed that actin microfilament reorganization and an influx of calcium was required for cold-responsive expression of *CAS30*. This work provided a model where upon cold treatment membrane fluidity decreases, followed by a downstream reorganization of actin microfilaments, and finally by an influx of calcium.

A number of studies have shown a rapid and transient increase in cytosolic calcium upon cold treatment (Knight et al., 1991; Monroy et al., 1993; Knight and Knight, 2000), that comes both from apoplastic and vacuolar stores (Knight et al., 1996). Calcium is required for maximal expression of the cold-responsive transcripts *KIN1* and *CAS30* (Knight et al., 1996; Tahtiharju et al., 1997; Orvar et al., 2000) and the acquisition of freezing tolerance in response to low temperature (Monroy et al., 1993; Monroy and Dhindsa, 1995). Plants that have been cold-acclimated display an altered calcium transient upon subsequent cold treatment (Knight et al., 1996; Plieth et al., 1999; Knight and Knight, 2000). Knight et al. (1996) has shown that the peak levels and duration of the calcium transient becomes diminished in magnitude and prolonged in length upon cold acclimation, indicating that the sensor likely possesses the ability to “remember” the cold. Due to such evidence, the suggestion has been made that the sensor is one or more of the calcium channels located in the plasma membrane. In fact, some membrane bound mechano-sensitive calcium channels are activated by low temperature (Ding and Pickard, 1993).

The thermometer could also resemble low temperature sensors found in other species. In *Synechocystis*, evidence points towards the role of two-component regulators as temperature sensors. Mutations in the *Hik33* or *Hik19* (histidine kinase) genes greatly reduced the expression of a number of low temperature inducible genes (Suzuki et al., 2001; Mikami et al., 2002). Further, microarray analysis on the Δ *Hik33* mutant reveal that at least one additional cold sensor exists in *Synechocystis* (Mikami et al., 2002; Inaba et al., 2003). Two-component systems exist in plants, but these two *Hik* genes have no plant homologs and, to date, there is no evidence that such a system functions as the temperature sensor in plants.

In mammalian systems, two TRP (transient receptor potential) nonselective cation channels have been identified that are responsive to cold (Peier et al., 2002; Story et al., 2003). One, TRPM8, is a methanol and cold-responsive TRPM-class channel that was discovered in sensory neurons (Peier *et al.*, 2002). The other, ANKTM1, is distantly related to TRP channels and possesses very little amino acid similarity to TRPM8 (Peier *et al.*, 2002). ANKTM1 was cold-responsive and also found in sensory neurons, but was not responsive to methanol.

Low Temperature Signal Transduction

The initial temperature sensing event has to be transmitted to downstream effectors in order for the plant to respond. Cold-responsive signaling cascades are poorly understood in plants. Only recently have studies elucidated some of these signaling events, but most of the players have not been placed into coherent pathways.

As stated earlier, low temperature signaling involves transient calcium accumulation. A number of proteins can be involved in detecting and responding to calcium, including calmodulin (CaM), calcium dependent protein kinases (CDPKs), and calcium-regulated phosphatases (Knight and Knight, 2001). Overexpression of a calmodulin gene in *Arabidopsis* resulted in decreased levels of expression of the cold and ABA responsive *COR* genes, suggesting that CaM plays a role as a negative regulator (Townley and Knight, 2002). Calmodulin is not the only player to be implicated in calcium mediated cold signaling. In *Arabidopsis*, there are approximately 40 CDPKs, some of which have been proposed to play a role in ABA, drought, cold, and salinity responses (Sheen, 1996). Serine/threonine phosphatases (PPases) can also interact with calcium and regulate signaling pathways. The activity of protein phosphatase 2A increases in alfalfa in response to cold and this activity depends on calcium influx. Additionally, inhibiting protein kinases with staurosporine inhibits the low temperature induction of the *CAS15* gene, while inhibiting protein phosphatase activity with okadaic acid induces *CAS15* at 25°C (Monroy et al., 1998). Type-2C PPases include a sub-group of proteins with properties similar to the calcium sensor protein calcineurin B. The expression of one calcineurin B-like (CBLs) calcium sensor, *CBL1*, is induced by drought, salt, ABA, and cold (Albrecht et al., 2003; Cheong et al., 2003). Studies on *CBL1* reveal that it plays a role in drought, salt, and cold stress signaling. A calcium sensor-associated protein kinase, CIPK3, was also found to modulate cold and salinity gene expression, but not drought-induced gene expression (Kim et al., 2003). The authors propose that CIPK3 functions as a cross-talk node between ABA and abiotic stress signaling.

The levels of phosphatidic acid (PtdOH) and inositol triphosphate (InsP₃) increase in plants upon cold shock, along with activation of phospholipase C and D activity (Ruelland et al., 2002). These events are dependent upon calcium, as chemically blocking calcium influx inhibited PtdOH and InsP₃ formation. These results indicate that cold signaling may involve one or more phosphoinositide signaling pathways. Further support comes from a study where the plasma membrane bound phospholipase D δ (PLD δ) was either knocked out or overexpressed in Arabidopsis (Li et al., 2004). Plants with no PLD δ activity displayed sensitivity to freezing at -7°C at the whole plant level, while overexpression of PLD δ resulted in plants that were more freezing tolerant (at -10°C) than wild type plants. These two mutant plants did not impact COR proteins, soluble sugar levels, or proline accumulation. This suggests that the alteration in freezing tolerance brought about by altering PLD δ represents a separate signaling pathway from the pathway that activates *COR* genes, proline, and soluble sugars.

MAPK cascades have also been implicated in cold signal transduction. In these cascades, a MAPK kinase kinase (MAPKKK) phosphorylates a MAPK kinase, (MAPKK), which in turn phosphorylates a MAPK. These MAPK's then activate or inactivate a transcription factor through phosphorylation. Introduction of a tobacco MAPKKK (NPK1) into maize enhanced cold tolerance by 2°C (Shou et al., 2004), indicating it may play a role in cold signaling pathways. Cold activated MAP kinases have also been found in alfalfa (Jonak et al., 1996) and Arabidopsis (Mizoguchi et al., 1996). Recently, a more detailed study on the MAPKK MKK2 in Arabidopsis revealed its role in cold and salt stress signaling. Teige et al. (2004) reported that MKK2 is activated by salt and cold stress, which in turn activates MPK2 and MPK4 through

phosphorylation. MEKK1 (a MAPKKK) was found to regulate MKK2. A null mutation of *MKK2* resulted in plants that were hypersensitive to cold shock or germination on media containing salt, while *MKK2* overexpression lead to increased tolerance to cold shock and increased germination on media containing salt. RT-PCR analysis revealed altered levels of several cold- and salt-responsive transcripts in the *MKK2* constitutive expression lines. The study by Teige et al. (2004) was the first report of an entire MAPK cascade involved in both cold and salt signaling.

Cold-Responsive Gene Expression

Signal transduction cascades generally result in the activation of transcriptional regulators that influence the expression of multiple genes in response to a given stimulus. During cold acclimation, multiple changes in gene expression occur. The transcripts for COR proteins, antioxidants, enzymes involved in cryoprotectant production, and many other gene products are induced in response to low temperature (Thomashow, 1998). While few transcriptional regulators involved in modifying cold-responsive genes are known, one pathway is now well established.

The previously mentioned COR proteins were first identified by their high transcript accumulation in response to cold (Hajela et al., 1990). Studies on the regulation of *COR15a* transcription resulted in the isolation of a fragment of the *COR15a* promoter that could drive expression of a reporter gene in response to low temperature (Baker et al., 1994; Yamaguchi-Shinozaki and Shinozaki, 1994). One sequence of interest in this promoter fragment was the C-repeat (TGGCCGAC), also known as the DRE (dehydration responsive element). The core sequence of the C-repeat, CCGAC,

was also found in the promoters of other *COR* genes. Using a yeast one-hybrid approach, Stockinger et al. (1997) isolated a protein that could bind to the C-repeat and activate transcription. This protein was named CBF1 (C-repeat binding factor 1). Since overexpression of *COR15a* led to only a modest improvement in chloroplast freezing tolerance, a question arose as to whether the simultaneous expression of multiple *COR* genes could alter the freezing tolerance of Arabidopsis. The discovery of CBF1 provided a tool to answer this question. Arabidopsis overexpressing *CBF1* were found to accumulate levels of *COR* transcripts similar to cold-acclimated plants and were constitutively freezing tolerant without a period of cold acclimation (Jaglo-Ottosen et al., 1998). This and other studies (Liu et al., 1998; Kasuga et al., 1999; Gilmour et al., 2000; Gilmour et al., 2004) have revealed that *CBF* expression has a significant impact on plant freezing and chilling tolerance (Gong et al., 2002).

The Arabidopsis genome encodes three cold-responsive CBF transcriptional activators CBF1, CBF2, and CBF3 (Stockinger et al., 1997; Gilmour et al., 1998; Medina et al., 1999), which are also known as DREB1b, DREB1c, and DREB1a (Liu et al., 1998; Kasuga et al., 1999), respectively. The CBF transcription factors are members of the AP2/EREBP family of DNA-binding proteins (Riechmann and Meyerowitz, 1998). The CBF proteins bind to the CRT (C-repeat)/DRE (dehydration responsive element) (Baker et al., 1994; Yamaguchi-Shinozaki and Shinozaki, 1994). *In vitro* studies on the binding of CBF to the CRT/DRE element defined (A/G)CCGAC as the consensus binding sequence (Sakuma et al., 2002). The *CBF1-3* genes are induced within 15 min of plants being exposed to cold temperatures followed at about 2 h by induction of a group of genes that contain the CRT/DRE-regulatory element, known as the “CBF regulon”

(Gilmour et al., 1988; Liu et al., 1998). The level of freezing tolerance observed by expression of the CBF regulon is substantial; constitutive expression of the *CBF1-3* genes increases the freezing tolerance of nonacclimated plants 3.5-7.5°C (Gilmour et al., 2000; Gilmour et al., 2004). While the exact mechanisms by which the CBF regulon enhances freezing and chilling tolerance are not known, it is clear that multiple mechanisms are involved. This includes the synthesis of low molecular weight cryoprotective molecules such as proline, sucrose, and raffinose (Gilmour et al., 2000; Taji et al., 2002) and the production of proteins with cryoprotective properties such as COR15a (Artus et al., 1996; Steponkus et al., 1998).

The CBF cold response pathway is conserved across plant species (Jaglo et al., 2001). Cold-responsive CBF orthologs have been found in freezing tolerant and chilling-sensitive plants, including wheat, rye, barley, oat, *Brassica napus*, rice, maize, tomato, and others (Jaglo et al., 2001; Choi et al., 2002; Chen et al., 2003; Dubouzet et al., 2003; Shen et al., 2003; Qin et al., 2004; Zhang et al., 2004). The existence of cold-responsive CBFs in chilling-sensitive species leads to fundamental questions on the nature of cold acclimation and chilling-sensitivity. Do these chilling-sensitive plants contain a complete CBF cold response pathway? Are they deficient in an important component(s) of the CBF pathway? Work in chilling-sensitive tomato indicates that tomato has a functional CBF cold response pathway, but the CBF regulon of tomato differs dramatically from *Arabidopsis* (Zhang *et al.*, 2004). This study suggests that tomato either lacks a co-activator activity required for CBF function that is present in *Arabidopsis* or lacks functional CRT/DRE elements within the genome.

While the CBF cold response pathway is conserved across plant species and increases the freezing tolerance of some plants, it is unknown whether additional cold response pathways exist in *Arabidopsis*. Studies with *Arabidopsis* mutants suggest that additional pathways do exist. The *eskimo1* mutant of *Arabidopsis* is constitutively more freezing tolerant than wild type plants, but *COR* genes are not constitutively expressed indicating that the mutation activated a freezing tolerance pathway outside the CBF system (Xin and Browse, 1998). Similarly, *ada2* mutants of *Arabidopsis* (*ADA2* encodes a transcriptional adaptor protein) are constitutively more freezing tolerant than wild type plants, but *COR* genes are not constitutively induced suggesting that the *ADA2* protein is involved in inhibiting expression of a freezing tolerance pathway that is distinct from the CBF cold response pathway (Vlachonasios et al., 2003). Microarray studies profiling roughly one-third of *Arabidopsis* genes in response to low temperature also indicate the existence of additional low temperature pathways (Seki et al., 2001; Fowler and Thomashow, 2002; Kreps et al., 2002; Seki et al., 2002).

No study has yet defined the low temperature transcriptome for *Arabidopsis* on a whole genome level, nor the extent to which the CBF transcription factors influence these genes. Also unknown are the identities of additional transcription factors that configure the low temperature transcriptome. To further understand the roles of the CBF proteins in configuring the low temperature transcriptome and to identify additional transcription factors with roles in cold acclimation, work in this dissertation aimed to define a low temperature transcriptome for *Arabidopsis*, to determine the contribution of the CBF transcription factors to the cold transcriptome, and to determine the regulons of other cold-responsive transcription factors.

CHAPTER TWO

ROLES OF THE CBF2 AND ZAT12 TRANSCRIPTION FACTORS IN CONFIGURING THE LOW TEMPERATURE TRANSCRIPTOME OF ARABIDOPSIS

The majority of work in this chapter was published in the Plant Journal.

Vogel, Jonathan T., Zarka, Daniel G., Van Buskirk, Heather A., Fowler, Sarah G., and Thomashow, Michael F. (2005) Roles of the CBF2 and ZAT12 transcription factors in configuring the low temperature transcriptome of Arabidopsis. Plant J. 41, 195-211.

SUMMARY

The CBF cold response pathway has a prominent role in cold acclimation. The pathway includes action of three transcription factors, CBF1, 2, and 3 (also known as DREB1b, c, and a, respectively), that are rapidly induced in response to low temperature followed by expression of the CBF-targeted genes (the CBF regulon) that act in concert to increase plant freezing tolerance. Results of transcriptome profiling and mutagenesis experiments, however, indicate that additional cold-response pathways exist and may have important roles in life at low temperature. To further understand the roles that the CBF proteins play in configuring the low temperature transcriptome and to identify additional transcription factors with roles in cold acclimation, the Affymetrix GeneChip® containing probe sets for approximately 24,000 Arabidopsis genes was used to define a core set of cold-responsive genes and to determine which genes were targets of CBF2 and six other transcription factors that appeared to be coordinately regulated with *CBF2*. A total of 514 genes were placed in the core set of cold-responsive genes, 302 of which were up-regulated and 212 down-regulated. Hierarchical clustering and bioinformatic analysis indicated that the 514 cold-responsive transcripts could be assigned to one of seven distinct expression classes and identified multiple potential novel *cis*-acting cold-regulatory elements. Eighty-five cold-induced genes and eight cold-repressed genes were assigned to the CBF2 regulon. An additional nine cold-induced genes and 15 cold-repressed genes were assigned to a regulon controlled by ZAT12. Of the 25 core cold-induced genes that were most highly up-regulated (induced over 15-fold), 19 genes (84%) were induced by CBF2 and another two genes (8%) were regulated by both CBF2 and ZAT12. Thus, the large majority (92%) of the most highly induced genes belong to

the CBF2 and ZAT12 regulons. Constitutive expression of *ZAT12* in Arabidopsis caused a small, but reproducible, increase in freezing tolerance, indicating a role for the ZAT12 regulon in cold acclimation. In addition, ZAT12 was found to down-regulate expression of the *CBF* genes indicating a role for ZAT12 in a negative regulatory circuit that dampens expression of the CBF cold response pathway.

INTRODUCTION

Many plants increase in freezing tolerance in response to low nonfreezing temperature, a phenomenon known as “cold acclimation” (Thomashow, 1999; Smallwood and Bowles, 2002). Cold acclimation in *Arabidopsis* involves action of the CBF cold response pathway (Thomashow, 2001). The pathway includes the *CBF1*, *CBF2*, and *CBF3* genes (Gilmour et al., 1998; Medina et al., 1999; Jaglo et al., 2001), also known as *DREB1b*, *DREB1c*, and *DREB1a*, respectively (Liu et al., 1998), which encode transcriptional activators that bind to the CRT (C-repeat)/DRE (dehydration response element) regulatory element present in the promoters of *COR* and other cold-responsive genes (Baker et al., 1994; Yamaguchi-Shinozaki and Shinozaki, 1994; Stockinger et al., 1997; Gilmour et al., 1998). Transcripts for *CBF1*, 2, and 3 accumulate rapidly (within 15 min) upon exposing plants to low temperature followed by induction of the CBF-targeted genes known as the CBF regulon. Constitutive expression of the *CBF* genes results in constitutive expression of the CBF regulon and increased freezing tolerance without a low temperature stimulus (Jaglo-Ottosen et al., 1998; Liu et al., 1998; Gilmour et al., 2000; Gilmour et al., 2004). The freezing tolerance conferred by the CBF regulon involves the production of cryoprotective polypeptides such as COR15a (Artus et al., 1996; Steponkus et al., 1998) and the accumulation of compatible solutes such as sucrose, raffinose, and proline (Nanjo et al., 1999; Gilmour et al., 2000; Gilmour et al., 2004).

The CBF cold response pathway is currently the best understood genetic system with a role in cold acclimation. However, it does not appear to be the sole pathway with a role in freezing tolerance. The *eskimo1* mutant of *Arabidopsis* described by Xin and

Browse (1998) is constitutively more freezing tolerant than wild type plants, but the *COR* genes are not constitutively expressed indicating that the mutation activated a freezing tolerance pathway outside the CBF system. Similarly, *ada2* mutants of Arabidopsis (*ADA2* encodes a transcriptional adaptor protein) are constitutively more freezing tolerant than wild type plants, but *COR* genes are not constitutively induced suggesting that the ADA2 protein is involved in inhibiting expression of a freezing tolerance pathway that is distinct from the CBF cold response pathway (Vlachonasios *et al.*, 2003).

To more fully understand the role of the CBF cold response pathway in cold acclimation, investigators have examined the changes that occur in the Arabidopsis transcriptome in response to low temperature and overexpression of the CBF transcription factors. Fowler and Thomashow (2002) surveyed the expression of about 8,000 Arabidopsis genes in response to low temperature. The results indicated that extensive changes occur in the transcriptome during cold acclimation. In particular, 306 (~4%) genes were found to be either up- or down-regulated at least 3-fold in response to low temperature. However, only 12% of these genes could be assigned to the CBF regulon (i.e., were both cold- and CBF-responsive); at least 28% of the cold-responsive genes were not affected by expression of the CBF transcription factors, including 15 encoding known or putative transcription factors. Thus, it was concluded that cold acclimation is associated with the activation of multiple low temperature regulatory pathways. Similar conclusions have been reached by others studying the Arabidopsis low temperature transcriptome (Seki *et al.*, 2001; Kreps *et al.*, 2002; Seki *et al.*, 2002).

Here, the regulation of the low temperature transcriptome of Arabidopsis was further explored. Using the Affymetrix GeneChip® containing probe sets for

approximately 24,000 genes, I defined a core set of cold-responsive genes and determined whether they were targets of CBF2 or six other transcription factors that appeared to be coordinately regulated with *CBF2*. I conclude that the majority of genes that are most highly induced in response to low temperature are part of the CBF2 regulon; that the ZAT12 transcription factor participates in the induction and repression of cold-responsive genes; and that the ZAT12 regulon contributes to an increase in freezing tolerance. The results also indicate that certain cold-responsive genes are members of both the ZAT12 and CBF2 regulons and that ZAT12 has a role in a negative regulatory circuit that dampens expression of the CBF cold response pathway.

RESULTS

Identification of a Core Set of Cold-Responsive Genes

The first objective was to identify a core set of cold-responsive genes that could be used to further our understanding of the low temperature regulons and regulatory networks of Arabidopsis. The goal was not to identify all genes that were cold-responsive, but to identify a set of genes that were reproducibly cold-responsive using two common lab conditions, plants grown on soil in pots and plants grown on plates containing solid culture medium. This was accomplished using the Arabidopsis Affymetrix GeneChip® ATH1 array, which contains probes for approximately 24,000 genes, to compare the transcriptomes of plants grown in soil and on plates at “warm” temperatures (22°C soil, 24°C plates) with those of plants that had been transferred to low temperature (4°C) for 1 h, 24 h, and 7 d. In the plate experiments both root and shoot tissue was harvested, while in the soil experiments, shoot tissue was harvested. Pooled RNA from multiple samples at each time-point was labeled and hybridized to the arrays. A probe set was designated as being up-regulated if, in both biological samples for a given time-point, the detection algorithm assigned a call of “present” in the cold-treated sample, the change algorithm assigned a call of “increased,” and the signal log ratio was greater than or equal to 1.3. A probe set was designated as being down-regulated if, in both biological samples for a given time-point, the detection algorithm assigned a call of “present” in the warm sample, the change algorithm assigned a call of “decreased,” and the signal log ratio was less than or equal to -1.3. The signal log ratio cutoffs used corresponded to approximately a 2.5-fold change.

Using these criteria, 1,295 probe sets were cold-responsive in the plate experiments and 938 probe sets were cold-responsive in the soil experiments (the complete “raw” data sets for these experiments are posted at the TAIR website “www.arabidopsis.org” and the cold-responsive probe sets are listed in Appendices A-D). In the plate experiments, 673 probe sets were up-regulated, 627 were down-regulated and five were both up- and down-regulated at different times in the experiment. In the soil experiments, 557 probe sets were up-regulated, 382 were down-regulated and one was both up- and down-regulated at different times in the experiment. A comparison of the probe sets that were cold-responsive in the plate and soil experiments indicated that 302 were up-regulated in both experiments and that 212 were down-regulated in both experiments (Figure 2.1a; Appendices E and F), with the largest number of changes occurring at 24 h (Figure 2.1b). These changes in gene expression were statistically significant at a $p < 0.05$, with 95% (490/514) statistically significant at a $p < 0.005$ (see Materials and Methods). Many of the probe sets that were categorized as not being responsive in both soil- and plate-grown plants showed a corresponding increase or decrease in both experiments, but did not meet the strict criteria used for designating cold-responsiveness in both experiments. Some probe sets, however, were only responsive in either the soil or plate experiments. The reason for these differences is currently unknown, but is likely to reflect, in part, the differences in the culture conditions and tissues harvested in the experiments. Exploring these differences will be the subject of future study. The goal accomplished here was the identification of 514 probe sets that were cold-responsive in four experiments using two different culture conditions; i.e., an identification of a robust set of cold-responsive genes that could be

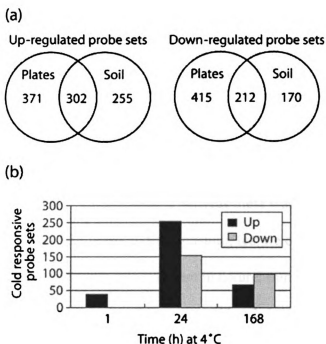


Figure 2.1. Low temperature responsive probe sets.

- (a) Probe sets differentially regulated (2.5-fold cutoff, $p \leq 0.05$) at low temperature in plants grown in soil (soil) and on solid medium (plates).
- (b) Number of probe sets with altered accumulation at 1 h, 24 h, and 168 h after transfer to low temperature in both soil and solid medium.

used in deciphering the low temperature regulatory network of Arabidopsis. I refer to these genes as a “cold standard” (COS) set of cold-responsive genes.

Members of the COS Gene Set can be Assigned to One of Seven Expression Clusters

The 514 COS genes were subjected to hierarchical clustering based on their relative transcript levels in plants after 1 h, 24 h, and 7 d of cold treatment (Figure 2.2a). Each gene was assigned to one of seven expression clusters (Figure 2.2b). Expression clusters I and II comprised down-regulated transcripts and clusters III to VII comprised up-regulated transcripts. The major difference between clusters I and II was that the

transcripts in the former cluster continued to decrease in levels between 24 h and 7 d whereas those in cluster II showed some recovery over this time interval. A major difference between the up-regulated transcripts in clusters III and IV, as compared to those in clusters V, VI, and VII, was that those in the former two clusters were delayed in response; i.e., there was little increase in the levels of the transcripts in clusters III and IV after 1 h of cold treatment whereas there was an increase for the transcripts in clusters V, VI, and VII. Also, a distinguishing feature of cluster V was that the cold-response for these transcripts was transient in nature; transcript levels increased dramatically by 1 h, but returned to near “un-stressed” levels by 24 h.

The clustering of genes with similar expression patterns raises the possibility of using bioinformatic approaches to identify potential *cis*-acting regulatory elements involved in coordinate gene regulation (reviewed in Rombauts et al., 2003). In this regard, MotifSampler (Thijs et al., 2002) was used to search for 8 bp sequences that were significantly overrepresented in the promoter regions of the COS genes that comprised the different expression clusters. Those elements that were enriched 5-fold or more (as compared to all genes on the array) are listed in Table 2.1. No potential cold-regulatory elements were identified for the genes in clusters I and II, the cold-repressed genes, but many were identified for the up-regulated genes in clusters III to VII. Most of these potential regulatory sequences were novel. However, an analysis of the genes comprising cluster III lead to the identification of the motif krCCGAC which contains the CRT/DRE element, (A/G)CCGAC, the element to which the CBF transcriptional activators bind (Sakuma *et al.*, 2002). The sequence (A/G)CCGAC was present within 1kb upstream of 123 (53%) of the 233 genes included in the cluster (as shown below, most of the genes

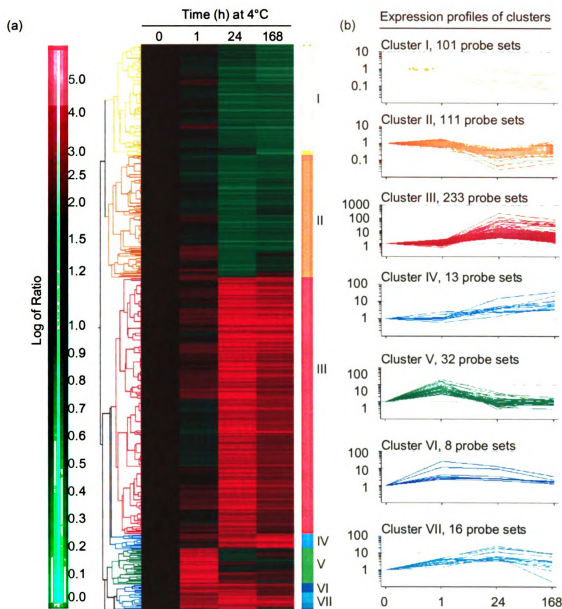


Figure 2.2. Hierarchical cluster and expression profiles of the 514 COS genes.

- (a) Hierarchical cluster analysis of the 514 COS genes. Log of ratio values for each probe set responding to low temperature at 1 h, 24 h, or 168 h was used to generate the cluster (see Materials and Methods). Down-regulated probe sets ($n=212$, green) consisted of two sub-clusters (yellow and orange side bars). Up-regulated probe sets ($n=302$, red) comprised five sub-clusters (red, blue, green, navy, and light blue side bars).
- (b) Expression profiles for the genes in each cluster are presented in a graph format. The graphs plot log of ratio values over time (h). Images in this figure are presented in color.

Table 2.1. Potential low temperature regulatory elements I^a

Class	Motif	PlantCARE	Class (%)	GeneChip (%)
Class I	None			
Class II	None			
Class III	krCCGAC	CRT/DRE	33	6
Class IV	CAATGAGG	Novel	23	0.8
	GTGATCAC	Novel	8	0.4
	GnATTGAC	Novel	39	4
	TGTATACA	Novel	23	2
Class V	AGCGCGTG	Novel	16	0.9
	mrCGCGTG	Novel	22	2
	mrCGCGTk	Novel	25	3
	AGCCGmCC	Novel	9	0.5
	ACCGmGT	Novel	22	3
	rCCGCsT	JERE	25	4
	GAGAArGG	Novel	25	4
Class VI	CTCTCACT	Novel	38	3
	kTrGCTGT	Novel	50	4
	yTkCCTCT	Novel	63	12
	AGkyTACG	Novel	38	2
	yAnCTTCC	Novel	63	11
	GsCTCGTG	Novel	13	0.8
Class VII	rAGnCGAC	Novel	38	6
	AACGCGTT	Novel	13	0.5
	GCTTCGTC	Novel	6	1
	GCyTCGTC	Novel	6	1
	CArAGsCk	Novel	38	6

^a All 8bp motifs overrepresented in the promoters of a given class of transcripts are shown. The motifs were queried to PlantCARE (<http://oberon.fvms.ugent.be:8080/PlantCARE/index.html>) to determine if they were similar to any known *cis*-element. The percent of promoters in each class containing the motifs and for all transcripts on the GeneChip was calculated.

assigned to the CBF regulon were members of this cluster). In addition, a potential jasmonic acid responsive element along with three other novel elements, having in common the sequence CGCGT, were enriched in cluster V.

The CBF2 Regulon Comprises 93 COS Genes

Previous transcriptome profiling experiments that surveyed about one-third of the Arabidopsis transcriptome indicated that: 1) the CBF transcription factors controlled

expression of about 30 cold-regulated genes (Seki et al., 2001; Fowler and Thomashow, 2002); and 2), that there were no obvious differences in the genes that were affected by overexpression of either *CBF1*, 2, or 3 (Gilmour *et al.*, 2004). Here these previous findings were extended by profiling two independent transgenic lines overexpressing *CBF2* using the “full genome” ATH1 Affymetrix array. Probe sets were designated CBF2 up-regulated if, in both biological samples, the detection algorithm assigned a call of “present” in the transgenic line, the change algorithm assigned a call of “increased,” and the signal log ratio was greater than or equal to 1.3. A probe set was labeled as down-regulated by CBF2 if, in both biological samples, the detection algorithm assigned a call of “present” in the wild type sample, the change algorithm assigned a call of “decreased,” and the signal log ratio was less than or equal to -1.3.

Of the 302 COS genes that were up-regulated in response to low temperature, 85 were also up-regulated in response to *CBF2* expression at control temperature (Appendix G). These genes were assigned to the CBF regulon. Analysis of the promoter regions of these genes using MotifSampler identified six versions of the CRT/DRE element (Table 2.2). Alignment of all six motifs revealed a consensus of (A/G)CCGACnT. Additionally, when the sequence 1kb upstream of these genes was examined for longer motifs (n=10), the most conserved sequence in the CBF regulon was found to be krCCGACnTm. Further analysis indicated that of these 85 genes, 68 (80%) had at least one potential CRT/DRE element (A/GCCGAC) within 1 kb upstream of the start of the protein coding sequence and thus, were likely to be direct targets of the CBF transcription factors. All but three of these 68 genes fell into expression cluster III (Figure 2.3), the expression cluster for which the bioinformatic analysis described above identified the

Table 2.2. Potential low temperature regulatory elements II^a

Class	Motif	PlantCARE	Class (%)	GeneChip (%)
CBF2 and cold up	ACCGACrT	CRT/DRE	28	1
	krCCGAC	CRT/DRE	60	6
	rCCGACnT	CRT/DRE	55	4
	GACCGAC	CRT/DRE	24	2
	GCCGAC	CRT/DRE	40	5
	GyCGrC	CRT/DRE	47	10
	CCGACrT	CRT/DRE	44	4
CBF2 and cold down	AGnCGnCT	Novel	40	3
	CACmACAC	Novel	25	4
	CAAGTTGr	Novel	50	4
	CGAwCyAG	Novel	25	2
	CTTTGCCT	Novel	25	2
	TTCnGAGT	Novel	50	5
	TCsnCTCs	Novel	50	9
Zat12 and cold up	GCATTGAC	Novel	44	0.8
	yCTCTTCA	Novel	44	6
	CAATGmkG	Unnamed	44	3
	TGAGGTCA	Novel	22	0.7
	rsAATGAG	Novel	56	6
	mCAACTTs	Novel	56	8
	AwGAkGwC	OCS	67	11
Zat12 and cold down	ACAwmTTC	Novel	67	12
	TATCCAAA	Novel	40	5
	GAmTAAGA	Novel	33	5
	TAyGCCAG	Novel	13	0.4

^a All 8bp motifs overrepresented in the promoters of a given class of transcripts are shown. The motifs were queried to PlantCARE (<http://oberon.fvms.ugent.be:8080/PlantCARE/index.html>) to determine if they were similar to any known *cis*-element. The percent of promoters in each class containing the motifs and for all transcripts on the GeneChip was calculated.

CRT/DRE element. The 17 genes that were both cold- and CBF-regulated, but did not have potential CRT/DRE elements within 1 kb of the start of the coding sequence, might have active CRT/DRE elements elsewhere within or surrounding the gene coding sequence or might have been targets of transcription factors that were up-regulated in response to CBF2; such factors include RAP2.1 (At1g46768) (Okamuro et al., 1997), a putative zinc finger (At5g04340), a CONSTANS B-box zinc finger (At2g47890), and a protein related to squamosa promoter binding protein (At1g76580).

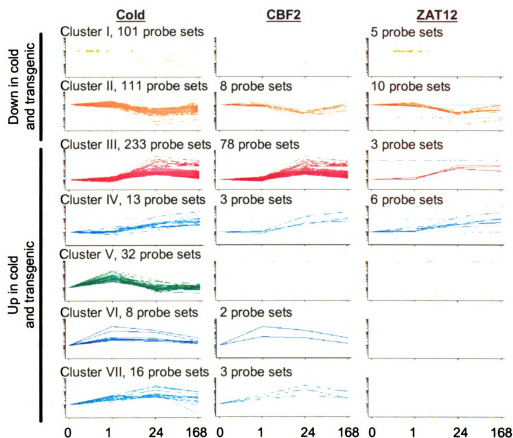


Figure 2.3. Expression profiles of the COS genes and those that comprise the CBF2 and ZAT12 regulons.

The expression profiles for all of the COS genes are presented in the panel labeled “Cold.” In the panels labeled “CBF2” and “ZAT12” are the cold-regulation profiles for those genes that comprise the CBF2 and ZAT12 regulons, respectively. In each graph, log of ratio values are plotted versus time (h). Images in this figure are presented in color.

Of the 212 genes that were down-regulated in response to low temperature, eight (4%) were down-regulated in response to *CBF2* overexpression (Appendix H). These genes, which belong to expression cluster II (Figure 2.3), were also assigned to the CBF regulon. The promoter regions of these genes did not have potential CRT/DRE elements, but an analysis using MotifSampler identified a number of potential novel elements (Table 2.2). These genes are not likely to be direct targets of the CBF transcription factors, but could be repressed by the expression of genes that are members of the CBF regulon.

The effects of *CBF2* overexpression were not limited to cold-responsive genes. Transcripts for 66 cold non-responsive genes were up-regulated and 35 were down-regulated by *CBF2* overexpression. Assignment of many of these genes to the cold-nonresponsive class, however, was due to the strict criteria used to designate a gene as being cold-responsive. In fact, many of these transcripts were increased or decreased in the cold, but not to the same level used for selecting the COS transcripts. There were, however, some *CBF2*-regulated transcripts that showed no sign of cold-responsiveness. The altered expression of these genes likely resulted from the secondary effects that *CBF2* overexpression has on plant growth and development, including stunted growth and a delay in flowering (Gilmour et al., 1998; Liu et al., 1998). A question thus raised was whether it was valid to assign a gene to the CBF regulon based on the criterion of the gene being both cold- and *CBF2*-responsive. Statistical analysis supported such assignments. In particular, the transcript levels for 151 genes were up-regulated and 43 genes down-regulated in the *CBF2* overexpressing plants which corresponded, respectively, to 0.66% and 0.34% of the total genes assayed on the array. Thus, by

chance, one would expect two of the 302 cold-induced COS genes to be up-regulated in response to *CBF2* overexpression and less than one of the 212 cold-repressed COS genes to be down-regulated in response to low temperature (Table 2.3). Instead, 85 of the cold-induced genes and eight of the cold-repressed genes were up- and down-regulated, respectively, in response to *CBF2* overexpression (Table 2.3). The large differences between expected and observed genes argued strongly against the hypothesis that the observed regulation of the COS genes by both cold and *CBF2* was due to chance ($p < 0.0001$).

CBF2 Regulates a Majority of Highly Induced COS Genes

The results presented above indicated that the CBF regulon included a significant portion (28%) of the cold-induced COS genes. Further analysis indicated that of the genes that were most highly induced in response to low temperature, the large majority were members of the CBF regulon. Shown in Figure 2.4 is a ranking of the 302 cold-induced transcripts ordered from the most highly induced to the least highly induced based on the average fold-change at 24 h. All 13 transcripts that increased 25-fold or more in response to low temperature were induced in response to *CBF2* expression. Of those transcripts that increased more than 15-fold, 84% increased in response to *CBF2* expression. In contrast, about 90% of the transcripts that accumulated less than 5-fold in response to low temperature fell outside of the CBF regulon.

Table 2.3. Chi-square analysis of expected and observed changes in gene expression in response to low temperature and transcription factor overexpression

Transgenic	Total changes ^a		Total possible ^b		Expected ^c		Observed ^d		Chi-square p-value	
	Up	Down	Up	Down	Up	Down	Up	Down	Up	Down
CBF2	151	43	22746	12726	2	0.7	85	8	<0.0001	<0.0001
ZAT12	47	158	22746	13320	0.6	2.5	9	15	<0.0001	<0.0001
RAV1	83	63	22746	14884	1.1	0.9	1	0	0.7	0.7
STZ	58	11	22746	13922	0.8	0.2	2	0	0.4	5
MYB73	28	2	22746	14198	0.4	0	0	0	0.9	n/a
CZF2	36	24	22746	14198	0.5	0.4	1	1	1	0.9

^a The number of probe sets up- or down-regulated by expression of each transcription factor (see Materials and Methods).

^b The number of probe sets that could possibly be up- or down-regulated by each transcription factor. Every probe set on the GeneChip had an equal probability of being up-regulated in a transgenic line, but only those probe sets “present” in the control samples could be down-regulated and this number fluctuated between the various controls.

^c The number of probe sets expected to be regulated by a transcription factor and the cold (see Materials and Methods).

^d The actual number of probe sets that were both cold and transcription factor regulated.

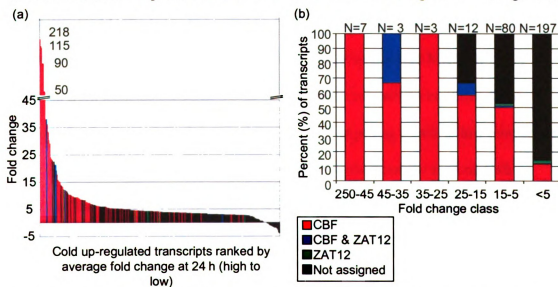


Figure 2.4. CBF2 and ZAT12 induce a majority of the most highly cold-induced transcripts.

- (a) Cold up-regulated transcripts were ranked by average fold change at 24 h and colored red if they were responsive to CBF2, green if responsive to ZAT12, and blue if responsive to both CBF2 and ZAT12.
- (b) Cold up-regulated transcripts were placed into classes defined by fold-change and the percentage of transcripts responsive to CBF2, ZAT12, both, or neither (not assigned) are indicated. The number of transcripts in each fold-change class is indicated above each bar. Images in this figure are presented in color.

Candidate Transcription Factors for Regulating COS Gene Expression

The experiments described above indicated that 70% of the cold-induced COS genes, and more than 95% of the cold-repressed COS genes, remained unassigned to a regulon. The challenge was to determine which of the more than 1,700 transcription factors encoded by the Arabidopsis genome (Riechmann, 2002) might have roles in controlling expression of these genes. It was hypothesized that transcription factors that were coordinately regulated with *CBF2* might be involved in regulating expression of these genes. Genes encoding transcription factors that were candidates for being coordinately regulated with *CBF2* included six that were previously identified as being up-regulated within 1 h of transferring plants to low temperature (Fowler and Thomashow, 2002). These genes were *ZAT12*, *RAV1*, *MYB73*, *STZ/ZAT10*, and two genes designated *CZF1* (cold-induced zinc finger proteins) (At2g40140) and *CZF2* (At5g04340) [*CZF2* is likely to correspond to *ZAT6* (Meissner and Michael, 1997) designated from a partial sequence of the gene]. Northern analysis confirmed that transcripts for these six genes increased within 1 h of exposing plants to low temperature (Figure 2.5a). Gene fusion experiments indicated that the promoter regions (1kb upstream of the ATG) of each of these genes, with the exception (for unknown reasons) of *RAV1*, were responsive to low temperature (D. Zarka, J. Vogel, H. Van Buskirk, M.F. Thomashow, unpublished).

Additional experiments indicated that transcripts for all six genes, like those for *CBF2* (Zarka et al., 2003), increased in response to both mechanical agitation and treatment with cycloheximide (Figure 2.5b). This was not true of all cold-inducible

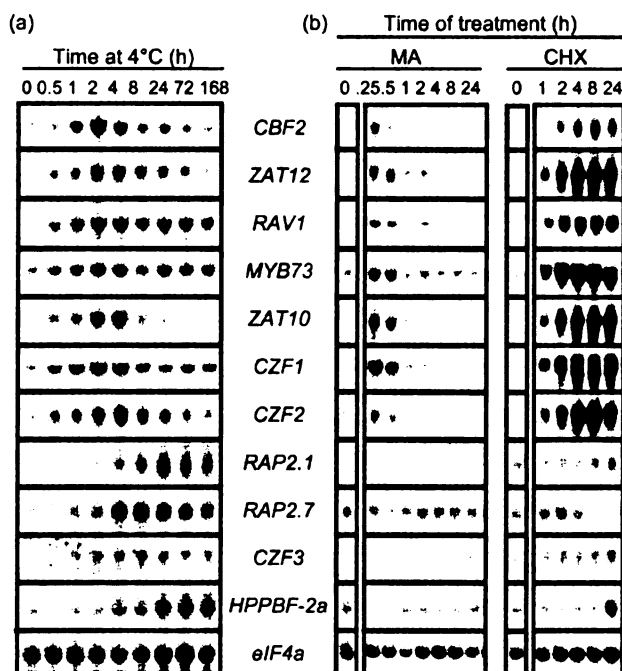


Figure 2.5. Expression of transcription factors that are candidates for configuring the low temperature transcriptome.

RNA was isolated from plants that were exposed to low temperature, mechanical agitation, or treatment with cycloheximide for various times and the transcript levels for the indicated genes was determined by RNA blot hybridization. *eIF4a* was used as a loading control on each blot and a representative blot is shown.

(a) Transcript accumulation in response to low temperature. Plants were grown at 24°C and then exposed to 4°C for the indicated times.

(b) Transcript accumulation in response to mechanical agitation (MA) and treatment with cycloheximide (CHX). Plants were grown at 24°C and then treated with mechanical agitation (MA) or cycloheximide (CHX) for the times indicated (see Materials and Methods for details).

genes that encode transcription factors. For instance, *RAP2.1*, *RAP2.7* (At2g28550), *CZF3* (At4g38960), and *HPPBF-2a* (At3g47500), which are induced after two hours of cold-treatment (Figure 2.5a), were not induced in response to mechanical agitation or treatment with cycloheximide (Figure 2.5b). The link between cold, mechanical, and cycloheximide regulation of *CBF2* is not known. However, two regulatory regions within the *CBF2* promoter, designated ICer1 (induction of *CBF* expression region 1) and ICer2, have been shown to be involved in gene induction by each of these three stimuli,

indicating a regulatory link between them (Zarka *et al.*, 2003). A question thus raised was whether ICer1 or ICer2 sequences were present in the promoters of *ZAT12*, *MYB73*, *ZAT10*, *CZF1*, and *CZF2*. Searches indicated that the promoters of each of these genes had four sequences that overlapped with ICer1, and a fifth sequence that overlapped with ICer2 (Figure 2.6).

(a)

Sequence	PlantCARE	% Genome
<u>ICE region 1</u>		
<u>ACACGTGT</u>	G-box	3%
<u>AArGAAAs</u>	MPE	44%
<u>AGAwTCT</u>	light responsive	25%
<u>CCTTyCTC</u>	novel	8%
<u>ICE region 2</u>		
<u>CCsAAACG</u>	novel	3%

(b)

~~ICer1~~ ATGGGTCAAAGGACACATGTCAGATTCTCAGTGA
 ACACGTGT
 AArGAAAs AGAwTCT
 GAGrAAGG

~~ICer2~~ AGAGACAGAAACTCCGCGTTCGACCC
 CCsAAACG

Figure 2.6. Potential regulatory sequences common to the promoter regions of *CBF2*, *ZAT12*, *ZAT10/STZ*, *MYB73*, *CZF1*, and *CZF2*.

- (a) Motifs that overlap the *CBF2* ICer1 or ICer2 sequences that are conserved in the promoter regions of *ZAT12*, *ZAT10/STZ*, *MYB73*, *CZF1*, and *CZF2* (see Materials and Methods for details). Base pairs of the motifs that are perfectly conserved in all the promoters analyzed are underlined. The sequences were queried to PlantCARE (<http://oberon.fvms.ugent.be:8080/PlantCARE/index.html>) to determine if they were similar to known *cis*-acting regulatory elements. All promoters in the Arabidopsis genome were examined for the presence of these motifs and the percent containing the motif is given.
- (b) Position of motifs aligned to the ICer1 and ICer2 (underlined) sequences.

Transgenic plants that constitutively expressed *RAV1*, *MYB73*, *ZAT10*, *CZF2*, or *ZAT12* under control of the CaMV 35S promoter were generated and the transcriptomes profiled to determine whether any of these transcription factors controlled expression of COS genes. Results with plants overexpressing *RAV1*, *MYB73*, *ZAT10/STZ*, or *CZF2*, using one GeneChip per line, indicated that the expression of few, if any, COS genes were affected by these transcription factors (northern analysis indicated that the transcript levels for each of the transgenes was equal to or greater than the maximum level for the corresponding endogenous gene attained upon cold treatment; data not shown). *RAV1* up-regulated one COS transcript (At1g35140), *STZ/ZAT10* up-regulated two COS transcripts (At4g22470 and At4g12490), and *CZF2* up-regulated one COS transcript (At4g12490) and down-regulated one COS transcript (At2g40610). These effects were confirmed by northern analysis (data not shown). However, the chance of observing up- or down-regulation of the COS genes by this group of transcription factors was no greater than expected by random occurrence; i.e., the extent to which COS genes were affected by expression of the transcription factors was no greater than that observed for non-COS genes (Table 2.3). Thus, no COS genes could be confidently assigned to regulons for *RAV1*, *MYB73*, *STZ/ZAT10*, or *CZF2*. As described in the next section, COS genes could be assigned to the *ZAT12* regulon.

The ZAT12 Regulon Comprises 24 COS Genes

Transgenic plants that constitutively expressed *ZAT12* under control of the CaMV 35S promoter were generated (Figure 2.7) and the transcriptome profiled using the Affymetrix array. An examination of two independent transgenic lines indicated that 24

COS genes were responsive to *ZAT12* overexpression (Appendices I and J). Of the 302 COS genes that were up-regulated in response to low temperature, nine were also up-regulated in response to *ZAT12* overexpression and fell into expression clusters III and IV (Figure 2.3). Of the 212 COS genes that were down-regulated by low temperature, 15 were also down-regulated by *ZAT12* overexpression and fell into expression clusters I and II (Figure 2.3). Significantly, seven of the *ZAT12* responsive genes were also responsive to *CBF2* overexpression (Figure 2.8), indicating the possibility that these two transcription factors coordinately regulate expression of these COS genes.

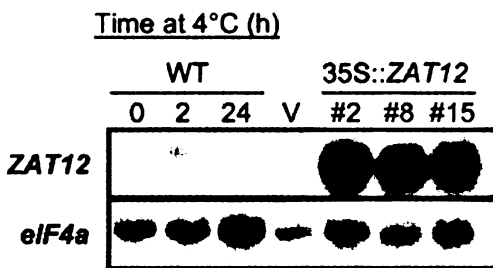


Figure 2.7. *ZAT12* transcript levels in transgenic Arabidopsis plants.

Transgenic lines expressing *ZAT12* under control of the CaMV 35S promoter (#2, #8 and #15) or carrying an empty vector (V) were grown at 24°C and the levels of *ZAT12* transcripts determined by RNA blot analysis. For comparison, wild type (WT) plants were exposed to low temperature (4°C) for 0 h, 2 h, and 24 h and *ZAT12* transcript accumulation was determined by RNA blot analysis. *eIF4a* was used as a loading control.

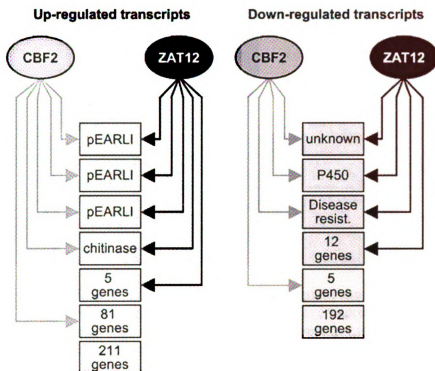


Figure 2.8. Regulation of COS genes by CBF2 and ZAT12.

Cold-responsive transcripts are indicated by boxes. Arrows indicate transcripts also responsive to *CBF2* or *ZAT12* expression.

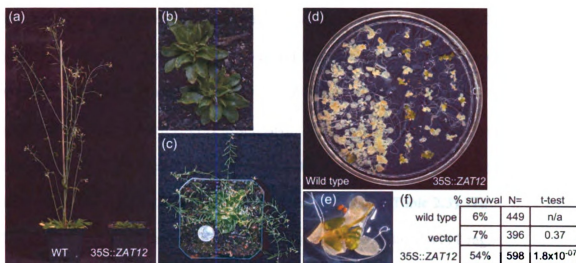


Figure 2.9. Effect of *ZAT12* expression on plant morphology and freezing tolerance.

- Six week old wild type (WT) and *ZAT12* overexpressing (35S::*ZAT12*) plants.
- Magnified view of six week old *ZAT12* overexpressing plants.
- Mature eleven week old *ZAT12* overexpressing plants. A U.S. dime (17mm) is shown for size comparison.
- Effect of freezing on nonacclimated ten day old wild type and *ZAT12* expressing plants.
- Magnified view of nonacclimated *ZAT12* plant after freezing.
- Table of results of multiple freeze tests, including the percentage of plants scored as surviving (% survival), the number of plants examined (N=), and the p-value from a t-test.

Images in this figure are presented in color.

A number of genes that were not cold-regulated were responsive to *ZAT12* expression; 38 were up-regulated and 143 were down-regulated. As with *CBF2* overexpression, assignment of many of these genes to the cold-nonresponsive class was due to the strict criteria used to designate a gene as being cold-responsive and a number were either increased or decreased to a lower extent than the *COS* genes. Expression of the remaining genes was likely a consequence of the effects that *ZAT12* expression had on growth and development (Figure 2.9). *ZAT12* overexpressing plants were smaller

than wild type plants and had curled leaves, short petioles, short bolts, and downward pointing siliques. As with the *CBF2* overexpression experiments, the question raised was whether it was valid to assign a gene to the *ZAT12* regulon based on the criterion of the gene being both cold- and *ZAT12*-responsive. Again, statistical analysis supported such assignments. Chi-square analysis indicated that it was highly unlikely for a given gene to be both cold- and *ZAT12*-responsive by chance ($p < 0.0001$) (Table 2.3). Thus, the 24 *COS* genes that were responsive to *ZAT12* were assigned to the *ZAT12* regulon.

The binding site for *ZAT12* is unknown, and thus I was unable to tentatively assign genes to being direct targets for the *ZAT12* protein. However, bioinformatic analysis of the promoter regions of the genes that were up-regulated in response to both cold and *ZAT12* expression identified multiple novel sequences that were overrepresented, three of which had CATTG as a core sequence suggesting that this may be a part of the *ZAT12* binding site (Table 2.2). Three additional novel elements were detected in the genes that were down-regulated in response to both cold and *ZAT12*.

The ZAT12 Regulon Contributes to Freezing Tolerance

Whole plant freeze assays indicated that *ZAT12* expression resulted in a slight, but detectable, increase in freezing tolerance. Whereas nonacclimated control plants were killed by freezing to -5°C , the innermost and youngest leaves of the rosettes in 54% of the *ZAT12* overexpressing plants survived (Figure 2.9). No difference in freezing tolerance was observed between cold-acclimated control and cold-acclimated *ZAT12* overexpressing plants (not shown).

ZAT12 Negatively Regulates CBF Gene Expression

The level of *CBF1*, 2, and 3 transcripts peaks at about 2 h after shifting plants to low temperature and then, as the *COR* gene transcripts begin to accumulate, the *CBF* transcripts begin to decrease. It was of interest to determine whether *ZAT12* might have a role in this down-regulation of *CBF* gene expression as the *ZAT12* protein can function as a transcriptional repressor (Hiratsu et al., 2002) and its induction kinetics (Figure 2.5) were consistent with this possibility. To test this hypothesis, the kinetics of low temperature induction of the *CBF1-3* genes in wild type plants and in transgenic plants overexpressing *ZAT12* was compared. The results indicated that the *CBF1*, 2, and 3 transcripts accumulated to much lower levels in response to low temperature in the *ZAT12* overexpressing plants as compared to the control plants (Figure 2.10). Transcript levels of the *CBF*-targeted genes *COR78* and *COR6.6*, however, were only slightly lower in the *ZAT12* transgenic plants.

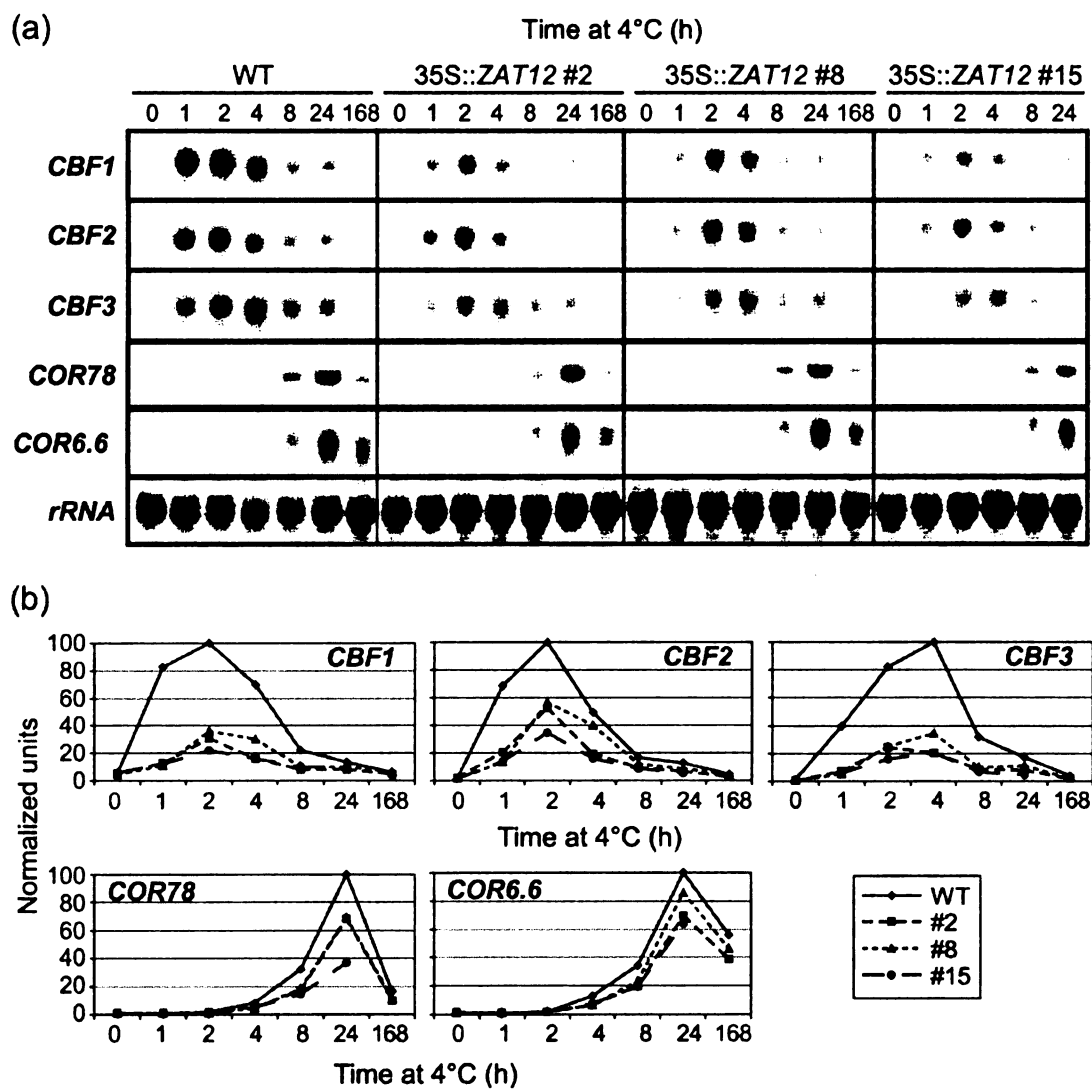


Figure 2.10. ZAT12 overexpression dampens cold induction of *CBF1*, 2, and 3. Wild type (WT) or *ZAT12* overexpressing (35S::*ZAT12*) plants were grown at 24°C and then exposed to 4°C for the times indicated. RNA was isolated and *CBF1*, 2, and 3 transcript levels were determined by RNA blot hybridization using gene specific probes. *rRNA* was used as a loading control.

- (a) Transcript accumulation in response to low temperature. Plants were grown at 24°C and then exposed to 4°C for the indicated times.
- (b) Quantitative transcript accumulation in response to low temperature. The highest transcript level after normalization was set to 100 and all other values are shown proportionally.

Since constitutive expression of *ZAT12* resulted in lower *CBF* transcript accumulation, loss of *ZAT12* would likely result in higher *CBF* transcript accumulation.

To test this hypothesis, two independent T-DNA insertions in the *ZAT12* locus were ordered from public collections (Alonso et al., 2003; Mario et al., 2003). These lines were then screened by PCR for plants homozygous for the insertion and sequenced to verify the insertion site. The T-DNA in SALK line 037357 was 294 bp upstream of the ATG and the T-DNA in GABI-Kat line 348H06 was inserted after 326 bp of the coding region (Figure 2.11). Given the location of the insertion in the SALK line, these plants might still express *ZAT12* at low levels, while the GABI-Kat line appeared to be a null mutation. RT-PCR results show that after 2 h at low temperature, wild type plants exhibited increased accumulation of *ZAT12*, while the SALK line displayed reduced *ZAT12* accumulation (Figure 2.12). RNA blot analysis resulted in similar results (Figure 2.13). No full length *ZAT12* transcript could be detected in the GABI-Kat line by RT-PCR analysis (Figure 2.12), however, RNA blot analysis revealed high levels of two products lower in size than the full length *ZAT12* transcript (Figure 2.13). This discrepancy is likely due to the CaMV 35S promoter present in the T-DNA used to create the GABI-Kat population, as the plasmid used was originally designed for activation tagged screens (Mario *et al.*, 2003). The sizes of the transcripts detected by RNA blot analysis would indicate that the transcripts are truncated, so if they are being translated, they may not be fully functional.

In response to low temperature, the accumulation of *CBF1*, 2, and 3 transcripts was higher in both *ZAT12* insertion lines compared to wild type plants at the 2 h time-point (Figure 2.13). *CBF* levels were slightly higher in the GABI-Kat line compared to the SALK line. As in the *ZAT12* overexpressing lines, expression of *COR6.6* and *COR78* was little, if at all, impacted.

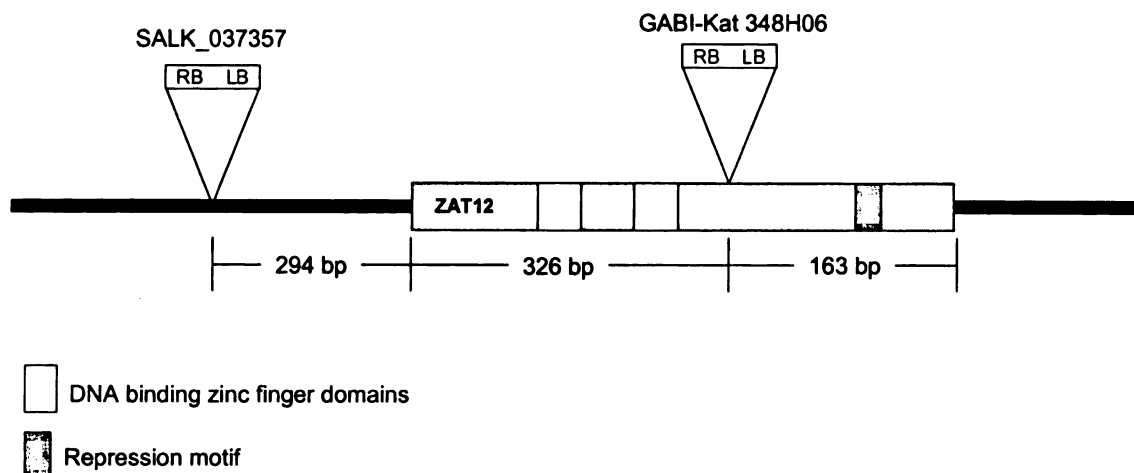


Figure 2.11. T-DNA insertion lines in the *ZAT12* locus.

This figure depicts the two T-DNA insertion lines available from the public collections with insertions in the *ZAT12* locus. The dark line indicates the upstream and downstream regions, while the box indicates the *ZAT12* protein coding sequence. The two zinc fingers of *ZAT12* are represented by white boxes, while the EAR-like repression motif is indicated by the dark box. T-DNA insertions are represented by the triangles, with the right and left borders (RB, LB) of the T-DNA indicated.

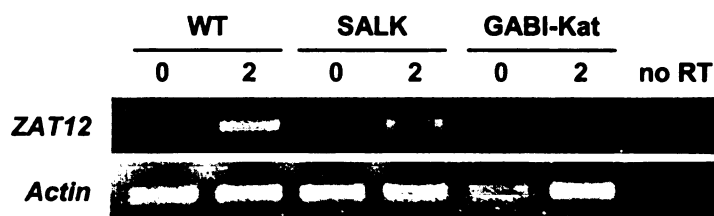


Figure 2.12. RT-PCR analysis of *ZAT12* expression in the two T-DNA insertion lines.

Total RNA was isolated from warm grown (0) plants or plants cold shocked at 4°C for two hours (2). The plants used were Col-0 (WT), SALK_037357 (SALK), and GABI-Kat 348H06 (GABI-Kat). PCR was performed on cDNA reverse transcribed from 5 µg of total RNA (see Materials and Methods) with primers specific to *ZAT12* or actin. A sample of RNA which was not reversed transcribed was also used to control for contaminating genomic DNA.

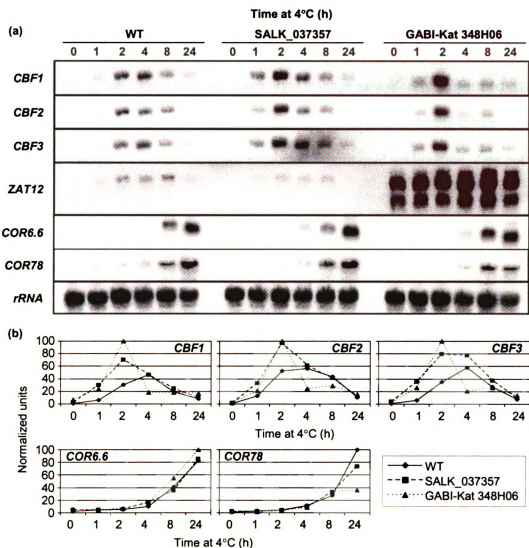


Figure 2.13. Decreased *ZAT12* expression enhances cold induction of *CBF1*, 2, and 3.

Wild type (WT) or *ZAT12* T-DNA insertion lines (SALK_037357 and GABI-Kat 348H06) plants were grown at 24°C and then exposed to 4°C for the times indicated. RNA was isolated and *CBF1*, 2, and 3 transcript levels were determined by RNA blot hybridization using gene specific probes. Transcript accumulation for *ZAT12*, *COR6.6*, and *COR78* were also monitored and *rRNA* was used as a loading control.

- (a) Transcript accumulation in response to low temperature. Plants were grown at 24°C and then exposed to 4°C for the indicated times.
- (b) Quantitative transcript accumulation in response to low temperature. The highest transcript level after normalization was set to 100 and all other values are shown proportionally.

Since the level of *COR* gene mRNA accumulation was little affected by loss of ZAT12, one would not expect to see a change in the freezing tolerance of these lines. To test this, whole plant freeze tests and electrolyte leakage assays were performed on the two T-DNA insertion lines. No effect was seen on whole plant freezing tolerance or electrolyte leakage for either line (both with and without cold acclimation, data not shown).

DISCUSSION

The objectives of this study were to determine more completely the role of the CBF transcriptional activators in configuring the low temperature transcriptome and to identify additional transcription factors that participate in this process (the functional roles of the cold-responsive genes identified in this study are considered in Chapter 3). To begin, I used the “full genome” Affymetrix GeneChip® array to define a core set of cold-responsive genes that were reproducibly up- or down-regulated in response to low temperature in plants grown both in soil and on solid culture medium, two commonly used growth conditions. The experiments resulted in the identification of 514 such cold-responsive genes, referred to as COS (“cold standard”) genes, 302 of which were up-regulated and 212 down-regulated at least 2.5-fold after either 1 h, 24 h, or 7 d of exposing plants to low temperature. This gene set does not contain all cold-responsive genes as the tissue harvested from the soil-grown plants was primarily foliar, whereas both root and shoot tissue was harvested from the plate-grown plants. In addition, many genes were not designated as COS genes due to the strict signal log ratio cutoff imposed in the analysis. Over 80% of the up-regulated genes that were designated as being “present,” “increased” and had a signal log ratio of ≥ 1.3 in both replicates for a given growth condition, were also “present” and “increased” under the other growth condition. The same situation held for approximately 70% of the down-regulated genes. However, the objective here was not to identify all cold-responsive genes, but to generate a robust gene set that could be used in efforts to decipher the low temperature regulatory network of Arabidopsis. The COS gene set should have considerable utility in this regard.

To assess the extent to which the low temperature transcriptome falls under control of the CBF1-3 transcription factors, I determined which cold-induced and cold-repressed COS genes were up-regulated and down-regulated, respectively, at least 2.5-fold in response to constitutive *CBF2* expression. Those genes that were both cold- and CBF2-responsive were assigned to the CBF regulon. The analysis indicated that 93 of the 514 COS genes were members of the regulon, 85 of which were cold-induced. Significantly, these 85 genes included the majority of those genes that were the most highly induced in response to low temperature; i.e., 84% of the genes induced more than 15-fold, and 50% of those induced between five to 10-fold, were found to belong to the CBF regulon. In addition, greater than 50% (37/67) of the COS genes that continued to be up-regulated after 7 d of cold-treatment were members of the CBF regulon. Taken together, these results indicate that the CBF transcription factors have a prominent role in regulating the expression of those cold-responsive genes that are both highly and stably induced in response to low temperature.

In a newly published study, Maruyama et al. (2004) also presented results identifying genes that are members of the CBF/DREB1 regulon. In these experiments, both the Affymetrix AtGenome1 GeneChip and a RIKEN Arabidopsis full-length cDNA array (Seki *et al.*, 2001) were used. The two arrays combined represented approximately 12,000 different genes. Of these, 38 were found to be responsive to both low temperature and *DREB1A/CBF3* overexpression. In these experiments, 22 of these 38 genes were also assigned to the CBF regulon. Of the 16 genes that not assigned to the CBF regulon, one was not represented on the array used (there was no probe for the *KIN2* gene) and seven others fell short of the 2.5-fold cutoff used in one or more samples from either the

cold-treated plants or plants overexpressing *CBF2*. The remaining eight genes (At4g14000, At4g15910, At5g17460, At1g29390, At2g43510, At1g27730, At2g31360, and At2g33830) showed “no change” in these experiments in both transgenic lines overexpressing *CBF2*. One possibility that could potentially explain this difference in the two studies is that *CBF2* and *DREB1A/CBF3* might have somewhat different target-gene specificities. Though this possibility cannot be ruled out at present, the recent findings of Gilmour et al. (2004) argue against it. In particular, these investigators used the Affymetrix AtGenome1 GeneChip to compare the transcriptomes of transgenic *Arabidopsis* lines overexpressing either *CBF1*, 2, or 3 and found no qualitative differences in target gene specificity between the three transcription factors. Other possible explanations for the observed differences include differences in the probe sets used to represent genes in the Affymetrix AtGenome1 GeneChip and the Affymetrix *Arabidopsis* ATH1 GeneChip, potential cross hybridization of probes on the cDNA arrays, and differences in growth conditions.

The CBF proteins are transcriptional activators that bind to the CRT/DRE DNA regulatory element. Thus, it was not surprising that of the 85 CBF regulon genes that were cold-induced, 68 (80%) had at least one putative CRT/DRE element within the 1 kb upstream region of the gene coding sequence. It is likely that most, if not all, of these genes are direct targets of the CBF transcription factors. The other 17 cold-induced genes that belong to the CBF regulon might have active CRT/DRE elements elsewhere within or surrounding their coding sequences. Alternatively, these genes could be targets of one or more of the transcription factors that belong to the CBF regulon, such as RAP2.1 (Appendix G), or their regulation might be affected by expression of other CBF

regulon genes. Similarly, down-regulation of the eight CBF regulon genes is likely to involve the action of regulatory or other proteins induced by the CBF transcription factors as the CBF1-3 proteins have not been reported to act as repressors.

Previous transcript profiling and mutagenesis experiments suggested the existence of cold regulatory pathways in addition to the CBF cold response pathway in Arabidopsis and that such putative pathways might have roles in freezing tolerance (Xin and Browse, 1998; Fowler and Thomashow, 2002; Kreps et al., 2002; Seki et al., 2002; Vlachonasios et al., 2003). This hypothesis was confirmed here. A new low temperature regulatory pathway, the ZAT12 cold-response pathway, was defined and evidence presented indicating that it has a role in cold acclimation. In particular, I show that *ZAT12* is induced in parallel with the *CBF1-3* transcription factors; that it regulates expression of 24 COS genes, nine of which were cold-induced genes and 15 cold-repressed; and that expression of the ZAT12 regulon results in a limited, but reproducible, increase in freezing tolerance. Additionally, the results indicated that the ZAT12 cold response pathway interacts in at least two fundamental ways with the CBF cold response pathway. First, there is overlap in the genes that comprise the ZAT12 and CBF2 regulons (Figure 2.8); four genes were up-regulated and three down-regulated in response to both transcription factors and low temperature. Thus, the ZAT12 and CBF cold response pathways appear to coordinately regulate the expression of certain COS genes. Moreover, constitutive *ZAT12* expression was found to dampen induction of the *CBF1-3* genes in response to low temperature (Figure 2.10), while decreased expression of *ZAT12* increased levels of *CBF1-3* after 2 h at low temperature (Figure 2.13). Thus, the ZAT12 regulon appears to be involved in negative regulation of the CBF cold response pathway.

Precisely how ZAT12 controls expression of the 24 COS genes and suppresses induction of the *CBF1-3* genes remains to be determined. However, ZAT12 has an EAR (ERF-associated amphiphilic repression)-like repressor domain (Ohta et al., 2001) and can act as a repressor (Hiratsu *et al.*, 2002). Thus, a simple scenario would be that ZAT12 directly represses expression of *CBF1-3* and the 15 down-regulated COS genes that belong to the ZAT12 regulon, the consequences of which include induction of the cold-induced COS genes that belong to the ZAT12 regulon. It must be stressed, however, that this scenario is highly speculative and that its central tenet, that ZAT12 binds to a *cis*-acting regulatory element in promoters of the cold- and ZAT12 repressed genes, cannot be assessed at present as the putative DNA binding site of the ZAT12 protein has not been reported.

In addition to a role for ZAT12 in cold acclimation reported here, ZAT12 has been implicated in multiple other abiotic stress responses. Transcripts for *ZAT12* have been shown to increase in response to high light (Iida et al., 2000), wounding (Chen et al., 2002; Cheong et al., 2002; Rizhsky et al., 2004), low-oxygen (Klok et al., 2002), hydrogen peroxide (Desikan et al., 2001), heat, and treatment with paraquat (Rizhsky *et al.*, 2004). Also, overexpression of *ZAT12* in transgenic Arabidopsis plants has been shown to result in increased tolerance to high light (Iida *et al.*, 2000) and oxidative stress caused by application of paraquat (Rizhsky *et al.*, 2004). As both high light (Demmigadams and Adams, 1992) and cold (Wise and Naylor, 1987) are associated with the formation of reactive oxygen species, the role of the ZAT12 regulon may be to help plants cope with oxidative stress. In this regard, it is of interest that *ZAT12* expression resulted in down-regulation of transcripts encoding a putative L-ascorbate oxidase

(At5g21100; Appendix J). This down-regulation could account, at least in part, for the increased levels of ascorbic acid, a potent antioxidant (Noctor and Foyer, 1998; Sanmartin et al., 2003), observed in cold-acclimated Arabidopsis plants (Cook et al., 2004). In addition, *ZAT12* expression resulted in accumulation of transcripts encoding arginine decarboxylase (At4g34710; Appendix I) which is involved in the production of putrescine, a polyamine that appears to have protective roles against abiotic stress, including oxidative stress (Ye et al., 1997; Bouchereau et al., 1999).

Transgenic Arabidopsis plants overexpressing *ZAT12* have been described in two previous studies (Iida et al., 2000; Rizhsky et al., 2004) in which different effects on plant morphology were noted. Rizhsky et al. (2004) reported that *ZAT12* overexpression had no effect on plant growth and development while Iida et al. (2000) found that *ZAT12* overexpressing plants had leaves that were thicker, rounder, and darker green than the control plants. The *ZAT12* expressing plants in this study had curled leaves, short petioles, short bolts, and downward pointing siliques. A simple explanation for these different observations is that the levels of *ZAT12* expression attained in the three studies were different. It is more difficult, however, to explain the differences observed in the makeup of the *ZAT12* regulon reported by Rizhsky et al. (2004) and that reported here. Rizhsky et al. (2004) reported up-regulated expression of 67 genes using a SLR cutoff of 0.8. Of these, only two were up-regulated in these experiments (“P,” “I” in both *ZAT12* lines) and of these only one was up-regulated at least 2.5-fold. Moreover, of the nine genes that were found to be up-regulated in response to both low temperature and *ZAT12* expression, none were found to be induced in response to *ZAT12* by Rizhsky et al. (2004). No data are available for a comparison of down-regulated transcripts.

While the CBF and ZAT12 regulons include the majority of the highly and stably expressed cold-regulated genes, most of the COS genes remain to be assigned to regulons. Determining which of the approximately 1,700 transcription factors encoded by the Arabidopsis genome have roles in regulating expression of these genes is now the challenge. As hypothesized above, transcription factors that are up-regulated in parallel with the *CBF1-3* transcription factors seem to be logical candidates, and proved to be true for *ZAT12*. However, I was unable to assign COS genes to regulons controlled by any of the other genes encoding known or putative transcription factors that were up-regulated along with the *CBF* genes; namely *RAV1*, *MYB73*, *STZ/ZAT10*, or *CZF2*. One interpretation of these results is that these transcription factors simply do not have a role in configuring the low temperature transcriptome. However, the results obtained with *DREB2a* (Liu *et al.*, 1998) suggest that it may be premature to draw this conclusion. *DREB2a* is a dehydration-induced gene that encodes an AP2-domain transcription factor that binds to the CRT/DRE element. Expression of the DREB2a protein in transient assays activates expression of reporter genes containing the CRT/DRE sequence. However, constitutive overexpression of the *DREB2a* gene in transgenic plants does not result in constitutive expression of CRT/DRE containing genes. Thus, it has been proposed that the DREB2a protein must undergo posttranslational modification induced by dehydration stress to be active (Liu *et al.*, 1998). Similarly, the RAV1, MYB73, STZ/ZAT10, and CZF2 proteins could be activated at low temperature to regulate expression of bona fide target genes. Another possibility is that the proteins cannot work alone, but must function in conjunction with other cold-regulated proteins.

A final point regards the potential *cis*-acting regulatory elements that were identified for the COS genes. In using MotifSampler (Thijs *et al.*, 2002) to analyze the promoter regions of COS genes included in the seven cold-regulated expression clusters (Figure 2.2), I was able to identify a number of potential *cis*-acting regulatory elements involved in cold-regulated gene expression. Most of these potential elements were novel. However, the fact that the CRT/DRE element was identified as a potential element for genes in expression cluster III, which includes the large majority of CBF regulon genes (Figure 2.3), lends credence to the hypothesis that at least some of the sequences are active. If this can be verified, the elements could then be used in biochemical and genetic approaches to identify additional transcription factors involved in shaping the low temperature transcriptome.

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MATERIALS AND METHODS

Constructs and Plant Transformation

Plasmids were constructed using PCR (polymerase chain reaction) and standard molecular biological techniques (Sambrook and Russell, 2001). Primers used to amplify the coding regions of each transcription factor from either genomic DNA or cDNA contained sites for unique restriction enzymes. PCR fragments were cloned into the pGEM-T easy vector (Promega, Madison, WI). The inserts were excised using restriction enzymes for the sites present in the primers and then cloned into a plant expression vector. The following primers and restriction enzymes were used: ZAT12 Spe I 5'-ACTAGTCAGAAGAAAAATGGTTGCGATA-3', BamH I 5'-GGATCCGAAAAATTCAAAGAATGAGAGAAACA-3'; RAV1 Xba I 5'-CTAGACAGATTAAATGGAATCGAGTAGC-3', BamH I 5'-GGATCCGAGTTGTTACGAGGCGTGAA-3'; CZF2 Xba I 5'-TCTAGATCTTCAAGATAATGGCACTTGAAA-3', BamH I 5'-GGATCCTCCTAGGTTTATGTTTAGGGTTTCTC-3'; MYB73 Xba I 5'-TCTAGATAAAAAGATCCGGCGATGTC-3', BamH I 5'-GGATCCCACTCTACTCCATCTTCCCAAT-3'; STZ/ZAT10 Xba I 5'-TCTAGACGAGAGACAAGAAATCCTCAGAA-3', BamH I 5'-GGATCCTTTCCTTAAAGTTGAAGTTTGACC-3'.

The DNAs were transferred to *Arabidopsis thaliana* (L.) Heynh. ecotype Columbia (Col-0 or *gll* Col-PRL) via a whole plant dipping method similar to that described by Clough and Bent (1998). Seed germination on medium containing kanamycin (50 mg/L) (Sigma-Aldrich, St. Louis, MO) was used to identify plants

containing transferred DNA. Expression of the transgene was monitored via RNA blot analysis and T3 lines homozygous for the transferred DNA were used in all experiments.

Plant Growth and Experimental Treatments

Arabidopsis thaliana constitutively expressing *ZAT12*, *RAV1*, *MYB73*, *CZF2*, or *STZ/ZAT10* (this study) or *CBF2* (Gilmour *et al.*, 2004) were grown in controlled environment chambers at 22°C under constant illumination from cool-white fluorescent lights ($\sim 100 \mu\text{mol m}^{-2}\text{s}^{-1}$) in Baccto planting mix (Michigan Peat, Houston). Pots were subirrigated with deionized water as needed. Plants were also grown on solid agar medium which contained Gamborg's B5 nutrients (Caisson Laboratories, Inc., Rexburg, ID) and 0.8% phytagar (Life Technologies Inc., Gaithersburg, MD) at 24°C under constant illumination from cool-white fluorescent lights ($\sim 100 \mu\text{mol m}^{-2}\text{s}^{-1}$). Seeds were stratified four days at 4°C before being grown at warm temperatures.

Experiments were performed on seedlings that were 10-12 days old. Treatments with cycloheximide (Sigma-Aldrich, St. Louis, MO) were performed by growing seedlings on filter papers that had been placed on top of the agar so that the seedlings could be lifted off the plate with minimal damage or mechanical stress. The seedlings were then floated on a solution of cycloheximide (10 $\mu\text{g/ml}$) in covered dishes for various times. Mechanical treatment involved tapping plates on a bench top for 15 minutes before harvesting tissue. All transgenic lines for the transcriptome analysis were grown in plates on solid media. Cold shock treatments involved transfer of plants (in the plate experiment, 10 day old plants were used with ~ 100 per plate; in the soil experiment 18 day old plants had been grown one plant per pot, 50 per flat) to a 4°C chamber with

constant dim light ($\sim 25 \mu\text{mol m}^{-2} \text{s}^{-1}$). Two biological duplicates of both the plate and soil experiments were performed for profiling.

Affymetrix GeneChip Hybridization and Data Collection

RNA isolation, probe labeling, hybridization, and data collection were performed as described (Fowler and Thomashow, 2002) with the following modifications. For the plate grown transgenic and wild type *Arabidopsis*, approximately 100 plants grown on a single plate were collected and total RNA was extracted using the Qiagen RNeasy Plant Mini Kits (Qiagen Inc., Valencia, CA) with modifications. To obtain adequate and consistent yields with the kit, the amount of starting plant tissue was doubled.

Subsequently the amount of extraction buffer (RLT) was also doubled. The remaining procedure was performed as described in the Qiagen manual. Biotinylated target RNA was prepared from 16 μg of total RNA equally pooled from two to four plates. For the soil grown plants, aerial parts of twelve plants were harvested from various parts of a flat for each time-point. Total RNA was extracted from two seedlings at once as described above. All samples for a given time-point were then pooled and precipitated.

Biotinylated target RNA was prepared from 16 μg of total RNA. The samples were hybridized to the Affymetrix *Arabidopsis* ATH1 GeneChip (Affymetrix, Santa Clara, CA) representing $\sim 24,000$ *Arabidopsis* genes. Two biological replicates were analyzed per growth condition, for a total of four samples per time-point.

The results from the microarray experiments have been submitted to TAIR (www.arabidopsis.org) according to MAIME guidelines under the accession numbers ME00320, ME00321, ME00322, and ME00323.

Affymetrix GeneChip Data Analysis

The Affymetrix Microarray Suite 5.0 statistical algorithms were used for microarray data analysis. Output from all GeneChip hybridizations was scaled globally such that its average intensity was equal to an arbitrary target intensity of 500 allowing comparisons between GeneChips. Signal (gene expression) and Signal Log Ratios (SLR) were calculated from the GeneChip fluorescence intensity data. The software was also used to determine whether each gene was present or absent (Detection) and whether the SLR represented a genuine change in mRNA accumulation (Change). SLRs and Change calls were determined for each transgenic line or cold sample compared to its corresponding wild type sample. Microsoft Access was used as the database management software and to filter and query the data.

Probe sets that met the following criteria were selected for further analysis. Those determined to be up-regulated by the cold treatment were selected as having, at any time-point, an absolute call of present in both cold samples (soil or plates), difference calls of increase, and SLRs of at least 1.3 for both change comparisons. Those determined to be down-regulated by the cold treatment were selected as having, at any time-point, an absolute call of present in both warm samples, difference calls of decrease, and SLRs of at least -1.3 for both change comparisons. Those probe sets meeting the above criteria in both the soil and plate experiments at any time-point were analyzed. Statistically significant changes in mRNA abundance were determined using the statistical package with GeneSpring 6.0 (Silicon Genetics, Redwood City, CA). The GeneChip data was imported into GeneSpring and normalized to respective control samples as specified by

the manufacturer for single color array data. The 3,178 transcripts with reliably altered levels (probe sets with an absolute call of “present” in all four cold samples and four difference calls of “increase” for a given timepoint or an absolute call of “present” in all four warm samples and four difference calls of “decrease” for a given timepoint) were analyzed using ANOVA (p-value cutoff 0.05 or 0.005) and the Benjamini and Hochberg False Discovery Rate multiple testing correction.

Genes up-regulated by *CBF2* (lines E2 and E24) or *ZAT12* (lines p15-8 and p15-15) expression were selected as having an absolute call of present in both transgenic samples, difference calls of increase, and a SLR of at least 1.3 for both change comparisons between wild type and transgenic lines. Those determined to be down-regulated were selected as having an absolute call of present in both wild type samples, difference calls of decrease, and a SLR of at least -1.3 for both change comparisons between wild type and *CBF* transgenic lines. Probe sets changing in the *RAV1*, *MYB73*, *CZF2*, or *STZ/ZAT10* expressing lines were selected in the same manner, but with data from only one GeneChip experiment per line.

Statistical analysis of the probe sets changing in a given overexpression line compared to the cold-responsive transcripts was performed by chi-square analysis using Yate’s correction, $\chi^2 = \sum(|O-E|-0.5)^2 / E$. The expected number of cold-responsive probe sets was calculated by dividing the number of probe sets changing in a transgenic line by the total number of possible probe sets that could change in the cold and multiplying by the number of cold-responsive probe sets (302 or 212). Every probe set on the GeneChip had an equal probability of being up-regulated in a transgenic line, but only

those probe sets “present” in the control samples for each transgenic line could be down-regulated hence this number could fluctuate between various controls.

Hierarchical clustering was performed with GeneSpring 6.0, using data normalized as described previously. Hierarchical clustering was done using the log of ratios (i.e., the ratio of the signal to the control, not their logs) of both the soil and plate experiment data using a standard correlation (separation ratio of 1 and a minimum distance of 0.001).

Whole Plant Freeze Test

Arabidopsis plants were grown on plates as described above. Cold- and non-acclimated plants were placed at -2°C in the dark for three hours after which freezing of the plates was nucleated with ice chips. The plants were incubated an additional 21 h at -2°C, followed by -5°C for 24h. The temperature was then raised to 4°C for 24 h. The plants were allowed to recover at 24°C for 48 h in continuous light and then scored for survival. A t-test was used to assess difference in the mean survival between control and experimental plants. In most experiments, the control and test plants were grown on separate plates (data presented in Figure 2.9f), but similar results were obtained when control and test plants were grown on the same plate (Figure 2.9d).

RNA Blot Analysis

RNA blots were prepared (10 µg of total RNA was loaded) and hybridized as described (Hajela *et al.*, 1990) using normal high stringency wash conditions (Stockinger

et al., 1997). Quantitation of mRNA abundance was performed with a Molecular Imager FX Pro multi-imager system (Bio-Rad Laboratories, Hercules, CA).

Probes for *CBF* (Gilmour *et al.*, 1998), *COR6.6*, *COR78* (Hajela *et al.*, 1990), *eIF4a* (Taylor *et al.*, 1993), *ZAT12* (Fowler and Thomashow, 2002), 25S rRNA (Delseny *et al.*, 1983), *RAP2.1* and *RAP2.7* (Okamuro *et al.*, 1997) were prepared as previously described. Probes for *MYB73*, *STZ/ZAT10*, *CZF1*, *CZF2*, *CZF3*, and *HPPBF-2a* were PCR amplified from cDNAs using the primer pairs used in “Constructs and Plant Transformation” except for the following: *CZF1* (At2g40140) 5’-TCTAGACACTTTTGAATCACAGGcAAGA-3’, 5’-GGATCCGCTTCTTATGCCACAATCTGC-3’; *CZF3* (At4g38960) 5’-TCTAGAGAAAAAGCAAGATGCGGATT-3’, 5’-GGATCCTTATCACTTCTCAGACTCTCG-3’; *HPPBF-2a* 5’-TCTAGAAAAATGATGATGGAGACTAGAGA-3’, 5’-AGATCTCATATGTA ACTCTAAATCTGTTCATGG-3’. The *RAV1* probe was isolated from an *AclI* and *BamHI* digest using an *AclI* site present in the *RAV1* coding region and the *BamHI* site in the PCR primer used for amplifying the coding region. Probes for genes up- or down-regulated in the cold and in one of the single GeneChip experiments profiling transgenic lines were performed with restriction enzyme digests of ESTs available from the Arabidopsis Biological Resource Center at Ohio State University (Columbus). Probes were labeled with ³²P by random priming (Feinberg and Vogelstein, 1983).

RT-PCR

Total RNA was extracted using the Qiagen RNeasy Plant Mini Kits (Qiagen Inc., Valencia, CA) with modifications. To obtain adequate and consistent yields with the kit, the amount of starting plant tissue was doubled. Subsequently the amount of extraction buffer (RLT) was also doubled. The remaining procedure was performed as described in the Qiagen manual. The reverse transcription reaction was performed with 5 µg of total RNA which was first treated with 10 U of RNase-free DNase I (Roche, Indianapolis, IN) for 15 min at room temperature in 1x RT buffer (Invitrogen, Carlsbad, CA), and heat inactivated for 10 min at 70°C. The rest of the reverse transcription procedure was carried out using the SuperScript First-Strand Synthesis System for RT-PCR (Invitrogen, Carlsbad, CA) as described in the manual (primed with random hexamers). PCR was performed using *Actin3* primers (forward 5'-GGTCGTACTACCGGTATTGTGCT-3', reverse 5'-TGACAATTTACGCTCTGCT-3') to standardize the amount of DNA to add to each reaction and *ZAT12* transcript accumulation was monitored using the following primers (forward 5'-CCTTAGGAGGTCACCGTGC-3', reverse 5'-CAAGCCACTCTCTTCCCACT-3').

Motif Analysis

Motif searches were performed with the command line version of MotifSampler v3.0 (<http://www.esat.kuleuven.ac.be/~thijs/Work/MotifSampler.html>). The dataset searched was the 500 bp locus upstream sequence downloaded from TAIR (<http://www.arabidopsis.org>) on March 17, 2003. Arabidopsis intergenic regions were used as a background model with the order set to 3. The motif length was set to 8bp,

with the prior probability of finding 1 motif instance set to 0.3. No limit was set for the number of motif instances that could be found per sequence, the maximum overlap between different motifs was set to 1, the number of motifs per run to be found was set to 3, and the total number of runs was set to 100. The highest scoring motifs were then ranked by MotifRanking using Arabidopsis intergenic sequence as a background model and the Kullback-Liebr distance to score the top ten motifs. Those motifs greater than 5-fold overrepresented in a class compared to the rest of the promoters on the GeneChip were analyzed. The number of motifs present in the upstream regions of Arabidopsis genes was determined using Patmatch at TAIR or a set of custom PERL scripts (Appendix M). All PERL scripts are available upon request. All motifs were queried at PlantCARE (Lescot et al., 2002) to determine if they were similar to any known sequence.

MotifSampler was also used to identify motifs present in the 1000 bp locus upstream sequence (downloaded from TAIR) of CZF1, CZF2, MYB73, ZAT12, STZ/ZAT10 and the ICE regions (including flanking sequences) of the CBF2 promoter. The ICE regions searched were ICer1: atgggtcaaaGGACACATGTCAGAttctcagtga and ICer2: agagacagaaACTCCGcggttcgaccc (Zarka *et al.*, 2003). The defined ICE regions are capitalized. Only motifs common among all the promoters were analyzed.

CHAPTER THREE

A FUNCTIONAL ANALYSIS OF THE ARABIDOPSIS COLD TRANSCRIPTOME

SUMMARY

The experiments described in Chapter 2 resulted in the identification of a set of transcripts that change in plants grown under two common laboratory conditions (solid medium and soil) at low temperature. This set was designated the COS (cold standard) transcripts. The experiments in Chapter 2 also indicated that the transcription factor CBF2 affected the levels of a majority of the most highly cold-induced COS transcripts. Another transcription factor, ZAT12, was found to contribute to the low temperature transcriptome and alter the stress tolerance of Arabidopsis. Work presented here furthers our understanding of Arabidopsis cold acclimation through a functional analysis of the COS transcripts and the CBF2 and ZAT12 regulons. The COS gene set contained transcripts of diverse biological functions, which changed with time at low temperature. Several categories of transcripts were found to be overrepresented among the COS genes compared to all transcripts in the genome. Transcripts encoding four new COR-like proteins were identified, along with transcripts that are likely involved in protecting cells from the damage associated with cold and freezing stress. Analysis of the CBF2 and ZAT12 regulons revealed enrichment for stress-related transcripts. Additionally, the ZAT12 regulon contained transcripts likely involved in protecting the plant from oxidative stress and putative antifreeze proteins that could alter ice formation.

INTRODUCTION

Temperature fluctuation is a significant stress experienced by plants, including agricultural crops that are grown in temperate climates. Many plants increase in freezing tolerance in response to low nonfreezing temperature, a phenomenon known as “cold acclimation”. Cold acclimation involves the action of the CBF/DREB1 cold response pathway (Thomashow, 1999; Smallwood and Bowles, 2002). Transcripts for *CBF1*, *CBF2*, and *CBF3* (Gilmour et al., 1998; Jaglo-Ottosen et al., 1998; Medina et al., 1999), also known as *DREB1b*, *DREB1c*, and *DREB1a*, respectively (Liu *et al.*, 1998), accumulate rapidly in response to low temperature and encode transcriptional activators that bind to the CRT (C-repeat)/DRE (dehydration response element) regulatory element present in the promoters of *COR* and other cold-responsive genes (Baker et al., 1994; Yamaguchi-Shinozaki and Shinozaki, 1994; Stockinger et al., 1997; Gilmour et al., 1998). Constitutive expression of the CBF regulon results in increased freezing tolerance without a low temperature stimulus (Jaglo-Ottosen et al., 1998; Liu et al., 1998; Gilmour et al., 2000; Gilmour et al., 2004). The CBF regulon increases freezing tolerance in part through the production of cryoprotective polypeptides such as COR15a (Artus et al., 1996; Steponkus et al., 1998) and the accumulation of compatible solutes such as sucrose, raffinose, and proline (Nanjo et al., 1999; Gilmour et al., 2000; Gilmour et al., 2004).

While best understood, the CBF pathway does not appear to be solely responsible for freezing tolerance. The mutants *eskimo1* (Xin and Browse, 1998) and *ada2* (*ADA2* encodes a transcriptional adaptor protein) (Vlachonasios *et al.*, 2003) are both constitutively more freezing tolerant than wild type plants, but the *COR* genes are not constitutively expressed. This suggests that the mutations activated freezing tolerance

pathways outside the CBF system, indicating that other pathways may be active at low temperature.

Changes in the *Arabidopsis* transcriptome and metabolome at low temperature also indicate the existence of additional pathways for cold acclimation. Studies investigating changes in transcript abundance during cold acclimation and with overexpression of the CBF transcription factors have revealed: 1), that cold acclimation involves many changes in gene expression; and 2), that the CBF pathway does not mediate all of these changes (Seki et al., 2001; Fowler and Thomashow, 2002; Kreps et al., 2002; Seki et al., 2002; Maruyama et al., 2004). Besides altering gene expression, low temperature significantly reconfigures the metabolome (Cook et al., 2004; Kaplan et al., 2004). The CBF cold response pathway was found to have a prominent role in configuring these metabolic changes, but at least 20% of the alterations could not be attributed to CBF (Cook *et al.*, 2004).

In Chapter 2, a more global survey of the low temperature transcriptome was conducted using the Affymetrix GeneChip® containing probe sets for approximately 24,000 genes. In this work, a core set of cold-responsive genes was defined, as were the regulons of the cold-responsive transcription factors *CBF2* and *ZAT12*. The goal of the study was not to define every cold-responsive transcript, but to define a set of transcripts that could be used to understand low temperature regulatory networks of *Arabidopsis*. To this end, a total of 514 transcripts were found to be altered in accumulation after 1 h, 24 h, or 7 d at low temperature in two growth conditions (soil or solid media, 2.5-fold cutoff, $p < 0.05$), defined as COS (cold standard) transcripts (Chapter 2).

In order to gain a better understanding of what types of transcripts are altered by low temperature and how those changes could influence freezing tolerance, a functional analysis of the COS transcripts, including the CBF2 and ZAT12 regulons, was performed. This analysis revealed that the COS genes have diverse biological functions and that the types of functions represented are different after various times at low temperature. Transcripts encoding four new *COR*-like genes were identified, along with transcripts likely involved in protecting cells from the damage associated with cold and freezing stress. Analyses of the CBF2 and ZAT12 regulons revealed they were enriched for stress-related transcripts and provided insight into how the ZAT12 regulon might impact freezing tolerance. Finally, the co-regulation of transcripts by CBF2, ZAT12, and other transcription factors reveals the complexity of low temperature regulatory networks.

RESULTS

The COS Gene Set Comprise Diverse Biological Functions

The 514 COS transcripts were manually classified into exclusive functional categories and sub-roles using annotation available at TAIR, MIPS, and TIGR (Appendices E and F). This allowed each transcript to be placed into a single functional category. Examination of the 302 up-regulated and 212 down-regulated transcripts revealed that they encoded proteins of diverse biological function (Figures 3.1). In comparing percentages, more stress-related, RNA processing and translation, protein processing and fate, and transcription transcripts were up-regulated than down-regulated and more metabolism and energy transcripts were down-regulated than up-regulated (Figure 3.1). While this analysis provides a simple and understandable summary of the data, transcripts can fit into multiple functional categories.

In order to address the issue of transcripts fitting multiple categories, a second classification method was also used. The COS transcripts were classified into gene ontology (GO) functional categories using the GO functional categorization tool available at TAIR (<http://www.arabidopsis.org/tools/bulk/go/>). The gene ontology system divides transcripts into multiple non-exclusive categories under three organizing principles (molecular function, biological process, and cellular component). GeneMerge (Castillo-Davis and Hartl, 2003) was then used to determine if any GO categories were statistically overrepresented compared to the rest of the genome. One caveat of this analysis is that all the transcripts analyzed were cold-responsive, yet the GO ontology only classified 15 transcripts as cold-responsive. One problem with relying on automated annotation is that

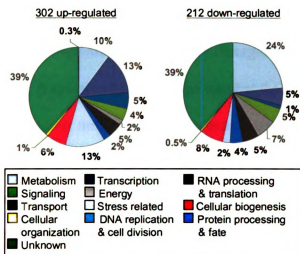


Figure 3.1. Functional categories of the 514 COS transcripts.

Each of the COS transcripts was placed into an exclusive functional category based on annotations available at TAIR, TIGR, MIPS, and in published literature (see Materials and Methods). Images in this figure are presented in color.

the annotation for each transcript has not been examined individually by a person hence they are not always up-to-date. Among the up-regulated transcripts, transcription factors and several categories of stress responsive genes were over-represented, i.e. had an E-score ≤ 0.05 (Table 3.1). Among the down-regulated genes, water transporters, oligopeptide transporters, oxidoreductases, carbonate dehydratases, and phosphoethanolamine N-methyltransferases were overrepresented (Table 3.1). The manual and automated analysis revealed that the COS gene set contains transcripts of diverse biological functions and is enriched for stress responsive transcripts.

The Functional Classes of COS Genes Differ Over Time Indicating that Changes Early in the Cold Response Influence Later Changes

A question that arose was whether the types of cold-responsive transcripts changed over time or whether the overall composition of the up- or down-regulated transcripts remained constant. Hierarchical clustering of COS transcript accumulation after 1 h, 24 h, and 7 d of cold treatment resulted in the assignment of the transcripts to one of seven expression clusters (Vogel et al., 2005). These clusters were used to examine the functional categories of the transcripts over time.

The seven expression clusters were comprised of COS transcripts with different functional profiles (Figure 3.2 and Table 3.2). The overall picture which emerged from this analysis was that early in the cold response (clusters V-VII) there was considerable enrichment for transcription factors and signaling molecules compared to the overall composition of the COS gene set. At later times (clusters I-IV and VII), the composition of the COS transcripts was more diverse. These later changes included transcripts whose function is thought to be involved in protecting the plant from stress (COR proteins, sucrose synthase, raffinose synthase, etc.). This is consistent with the current model of how the CBF cold response pathway functions, where the CBF transcription factors are induced quickly upon cold stress (within 15 min) and then regulate the expression of genes later in the cold response. The analysis presented below reveals that this paradigm occurs on a genome-wide level.

Table 3.1. Overrepresented GO terms among the COS transcripts

Class	GO Ontology	Frequency in genome	Frequency in class	E-score	GO Term
302 up-regulated genes	Biological Process	63/27627	15/302	8.14E-14	response to cold
		109/27627	15/302	4.32E-10	response to temperature
		66/27627	12/302	2.71E-09	response to water
		59/27627	11/302	1.55E-08	response to water deprivation
		590/27627	26/302	8.71E-07	response to abiotic stimulus
		930/27627	33/302	1.32E-06	response to external stimulus
		889/27627	31/302	6.11E-06	response to stress
		11/27627	5/302	2.63E-05	cold acclimation
		39/27627	7/302	7.89E-05	salinity response
		64/27627	8/302	1.93E-04	response to abscisic acid stimulus
		54/27627	7/302	7.90E-04	response to osmotic stress
		1841/27627	40/302	1.06E-02	response to stimulus
		13743/27627	184/302	2.22E-02	physiological processes
		22/27627	4/302	3.49E-02	hyperosmotic salinity response
		23/27627	4/302	4.19E-02	hyperosmotic response
		344/27627	13/302	4.71E-02	response to hormone stimulus
	Molecular	1847/27627	39/302	1.60E-02	transcription regulator activity
	Function	42/27627	5/302	2.35E-02	transcriptional activator activity
		1734/27627	36/302	4.35E-02	transcription factor activity
				4.49E-02	oligopeptide transport
212 down-regulated genes	Biological Process	65/27627	5/212	4.49E-02	oligopeptide transport
	Cellular Component	6642/27627	78/212	9.96E-04	membrane
		4520/27627	57/212	3.17E-03	endomembrane system
		18/27627	3/212	1.57E-02	vacuole (sensu Streptophyta)
		15445/27627	143/212	1.75E-02	cell
	Molecular Function	35/27627	5/212	1.39E-03	water channel activity
		17/27627	4/212	1.51E-03	oligopeptide transporter activity
		1237/27627	25/212	2.11E-03	oxidoreductase activity
		22/27627	4/212	4.51E-03	peptide transporter activity
		141/27627	7/212	2.29E-02	oxidoreductase activity
		14/27627	3/212	3.11E-02	carbonate dehydratase activity
		3/27627	2/212	3.57E-02	phosphoethanolamine N-methyltransferase activity

The 514 COS transcripts (Appendices E and F) were classified into gene ontology (GO) categories using the functional categorization tool at TAIR. The categories represented among the COS transcripts were then compared to those for all genes in the Arabidopsis genome using GeneMerge. Overrepresented terms among the up- or down-regulated COS genes as compared to the rest of the genome ($E \leq 0.05$) are shown. Each term is associated with an organizing principle (biological process, cellular component, or molecular function) listed under “GO ontology” in the table.

Table 3.2. Overrepresented GO terms among COS transcript expression clusters

Class	GO Ontology	Frequency in genome	Frequency in class	E-score	GO Term
1	Cellular Component	18/27627	3/101	1.12E-03	vacuole (sensu Streptophyta)
		36/27627	3/101	9.31E-03	vacuole
		15/27627	2/101	4.04E-02	vacuolar membrane (sensu Streptophyta)
	Molecular Function	35/27627	5/101	2.43E-05	water channel activity
		3/27627	2/101	5.47E-03	phosphoethanolamine N-methyltransferase activity
		141/27627	5/101	2.38E-02	oxidoreductase activity
		154/27627	5/101	3.58E-02	alpha-type channel activity
		7/27627	2/101	3.79E-02	squalene monooxygenase activity
		158/27627	5/101	4.03E-02	channel/pore class transporter activity
		8/27627	2/101	5.04E-02	hydrolase activity\acting on acid halide bonds\in C-halide compounds
2	Cellular Component	15445/27627	79/111	1.94E-02	cell
	Component	6642/27627	42/111	2.35E-02	membrane
3	Biological Process	63/27627	12/233	6.05E-11	response to cold
		66/27627	11/233	2.94E-09	response to water
		59/27627	10/233	2.23E-08	response to water deprivation
		109/27627	12/233	5.05E-08	response to temperature
		11/27627	5/233	6.16E-06	cold acclimation
		590/27627	21/233	1.19E-05	response to abiotic stimulus
		64/27627	8/233	2.27E-05	response to abscisic acid stimulus
		39/27627	6/233	2.97E-04	salinity response
		930/27627	24/233	4.48E-04	response to external stimulus
		889/27627	23/233	7.23E-04	response to stress
		54/27627	6/233	2.11E-03	response to osmotic stress
		22/27627	4/233	1.09E-02	hyperosmotic salinity response
		23/27627	4/233	1.31E-02	hyperosmotic response
	Cellular Component	80/27627	5/233	3.11E-02	heterotrimeric G-protein complex
		82/27627	5/233	3.49E-02	extrinsic to plasma membrane
		86/27627	5/233	4.33E-02	extrinsic to membrane
4	Biological Process	104/27627	4/13	7.00E-06	lipid transport
	Cellular Component	4520/27627	8/13	3.61E-03	endomembrane system
	Molecular Function	143/27627	4/13	1.09E-05	lipid binding
		55/27627	2/13	6.88E-03	structural constituent of cell wall
		144/27627	2/13	4.66E-02	rhodopsin-like receptor activity
5	Biological Process	1412/27627	9/32	2.28E-03	regulation of transcription\DNA-dependent
		1437/27627	9/32	2.62E-03	transcription\DNA-dependent
		2303/27627	11/32	3.33E-03	regulation of biological process
		1957/27627	10/32	4.82E-03	regulation of transcription
		1967/27627	10/32	5.03E-03	regulation of nucleobase \nucleoside \nucleotide and nucleic acid metabolism

		2032/27627	10/32	6.63E-03	regulation of physiological process
		2032/27627	10/32	6.63E-03	regulation of metabolism
		2035/27627	10/32	6.71E-03	transcription
6	Molecular Function	1847/27627	12/32	1.92E-05	transcription regulator activity
		1734/27627	11/32	8.49E-05	transcription factor activity
		293/27627	4/32	1.38E-02	calcium ion binding
		3025/27627	11/32	1.50E-02	DNA binding
		63/27627	2/8	4.83E-03	response to cold
	Biological Process	109/27627	2/8	1.45E-02	response to temperature
		1957/27627	4/8	4.74E-02	regulation of transcription
		1967/27627	4/8	4.83E-02	regulation of nucleobase\nucleoside\nucleotide and nucleic acid metabolism
		1734/27627	5/8	9.70E-04	transcription factor activity
	Molecular Function	1847/27627	5/8	1.32E-03	transcription regulator activity
		42/27627	2/8	1.32E-03	transcriptional activator activity
		3025/27627	5/8	1.39E-02	DNA binding

The 514 COS transcripts were binned into their respective expression classes (see Chapter 2, Appendices E and F) and classified into gene ontology (GO) categories using the functional categorization tool at TAIR (<http://www.arabidopsis.org/tools/bulk/go/>). The categories represented among the various classes of COS transcripts were then compared to those for all genes in the Arabidopsis genome using GeneMerge. Overrepresented terms among the classes of COS genes as compared to the rest of the genome ($E \leq 0.05$) are shown. Each term is associated with an organizing principle (biological process, cellular component, or molecular function) listed under “GO ontology” in the table.

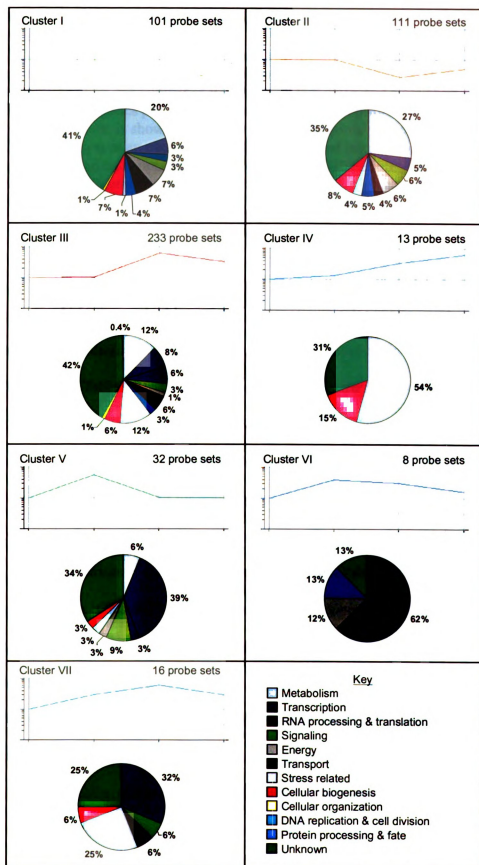


Figure 3.2. Functional categories represented in each expression class of the COS transcripts.

The 514 COS transcripts were analyzed with hierarchical clustering which allowed visualization of transcripts with expression profiles (see Chapter 2). Each box shows the expression class, the number of transcripts in that class, and a pie chart summarizing the functional categories present. The average expression profile for all transcripts in a particular cluster is shown in each graph (log of ratio values versus time). Each of the COS transcripts in an expression profile were placed into an exclusive functional category based on annotations available at TAIR, TIGR, MIPS, and in published literature (see Materials and Methods). Images in this figure are presented in color.

The transcripts that were rapidly up-regulated in response to low temperature (clusters V-VII) were highly enriched in genes with roles in transcription; 50% of the transcripts in these three clusters encoded proteins involved in the production of mRNA (Figure 3.2, Table 3.2). Cluster VII contained many transcription factors, but unlike clusters V and VI, analysis with GeneMerge did not find enrichment in any given category in this cluster (possibly due to the small sample size for this group of genes). In addition to the enrichment for transcription factors in clusters V and VI, transcripts with potential roles in signaling (e.g. calcium ion binding) were also enriched.

The classes of transcripts present at later times during the cold response were more diverse. Cluster III contained the most transcripts overall and the most functional categories of overrepresented transcripts (Figure 3.2, Table 3.2). This group of genes, which peaked in expression after 24 h, contained enrichment for stress-related transcripts, five transcripts annotated as components of heterotrimeric G-protein complexes, and transcripts that were membrane associated. Cluster III contained all of the previously described *COR* genes except for *COR28* (Fowler and Thomashow, 2002) and *COR35* (this paper, described in a later section). Class III also contained all of the cold-induced

transcripts for enzymes involved in the production of known cryoprotectants (ex: sucrose, proline, and raffinose). All of this is consistent with the idea that the transcripts in this class function in protecting the plant from freezing stress.

Cluster IV contained transcripts whose accumulation only increased with time and was enriched for lipid transport and lipid binding proteins (Figure 3.2, Table 3.2). Four protease inhibitor/seed storage/lipid transfer protein (LTP) family members were in this cluster. Given that these transcripts increase with time, one might expect the gene products perform important protective roles during cold acclimation. One attractive hypothesis for their function would be that of membrane stabilization. Overexpression of pEARLI1, an LTP family member, does not increase whole plant freezing tolerance, but does protect cells from freezing damage as measured by a decrease in electrolyte leakage in the range of -2 to -4°C (Bubier and Schlappi, 2004). Recent work on cryoprotectin, a lipid-transfer protein family member isolated from cold-acclimated cabbage (*Brassica oleracea*), revealed that it stabilized thylakoid membranes during freezing (Hincha et al., 2001; Hincha, 2002). It is possible that the pEARLI-like proteins could be playing a similar role in Arabidopsis.

Cluster IV contained other transcripts with potential roles in cold acclimation, including a thaumatin-like transcript, polygalacturonase inhibitors, a LEA, and a pectinesterase (Figure 3.2, Table 3.2). The accumulation of these transcripts increases with time. One hypothesis concerning the function of these transcripts is that they encode antifreeze proteins. A number of studies have identified potential antifreeze proteins from different plant species that contain similarity to β -1,3-glucanases, thaumatin like proteins, polygalacturonase inhibitor proteins, and endochitinases (Hon et

al., 1995; Hinch et al., 1997; Worrall et al., 1998; Meyer et al., 1999; Smallwood et al., 1999; Yeh et al., 2000). Cold up-regulated transcripts in cluster IV and in other clusters contained thaumatin like proteins (At1g20030, cluster VII; At1g75040, cluster IV), a polygalacturonase inhibiting protein (At5g06860, cluster IV), an endochitinase (At2g43620, cluster III), and β -1,3-glucanases (At1g32860, At3g04010, At5g55180, cluster III).

A number of categories of transcripts were enriched among the down-regulated genes (clusters I and II, Figure 3.2, Table 3.2) including products located in the vacuole, water channels, oxidoreductases, peptide transporters, carbonate dehydratases, and phosphoethanolamine N-methyltransferases. One hypothesis for why transcripts are down-regulated at low temperature would be that they are simply not needed during cold acclimation. Another hypothesis would be that they are inherently problematic for the plant at low temperatures and need to be down-regulated.

Transcripts for five water channels (At2g36830, At2g37180, At3g16240, At4g17340, and At4g23400) were down-regulated in the cold and enriched in cluster I. During freezing stress, intracellular ice formation results in a water gradient and water will move down that chemical gradient and out of the cell (Thomashow, 1999). Aquaporins are thought to allow water flow in either direction, down its potential gradient (Maurel, 1997). Down-regulation of these water channels may help regulate the cell's osmotic homeostasis.

Among the down-regulated transcripts, oxidoreductases (involved in a variety of metabolic pathways), and carbonate dehydratases (involved in photosynthetic carbon assimilation) were identified as overrepresented. Plants need to adjust their energy

production and metabolism to cope with low temperature. This is consistent with the number of metabolites that change in response to low temperature, including those involved in the TCA cycle (Stitt and Hurry, 2002; Cook et al., 2004). The decrease in energy related transcripts mainly concerned transcripts encoding proteins involved in photosynthesis. This has been observed in previous microarray experiments (Fowler and Thomashow, 2002; Kreps et al., 2002; Seki et al., 2002) and elsewhere (reviewed in Huner *et al.*, 1998). Such a decrease may be a result of the lower light levels used during the cold treatment, but other studies have shown that exposure to low temperature leads to inhibition of photosynthesis and a concurrent decrease in transcript levels for photosynthetic components (Krapp and Stitt, 1995; Strand et al., 1997).

Also enriched among the down-regulated transcripts were peptide/oligopeptide transporters and phosphoethanolamine N-methyltransferases. Peptide transporters could be involved in either signaling or transporting small peptides that are to be metabolized and used as a source of amino acids, nitrogen, or carbon (Koh et al., 2002). Phosphoethanolamine N-methyltransferase is the key step in the production of phosphocholine and then choline, which is the precursor of the osmoprotectant glycine betaine (McNeil et al., 2001). Since the transcripts for this enzyme decreased, it seems unlikely they are involved in producing higher levels of glycine betaine. Rather, the enzyme may be involved in changing the phosphocholine pool available for producing lipids, such as phosphatidylcholine, that are then incorporated into cellular membranes (Lynch and Steponkus, 1987). Changes such as these may be important for signaling or altering the membrane lipid composition.

Given the enrichment for stress-related transcripts in clusters III and IV, and the number of transcription factors that are up-regulated early in the cold response, the picture emerges that those changes that occur later in the cold response are involved in protecting the plant from possible future freezing stress or coping with life at low temperature, while those that occur early are involved in signaling or gene regulation to bring about those changes. Since transcriptome profiling only measures steady state transcript levels, one does not know which transcripts are regulated at the transcriptional level, post-transcriptional level, or both. However, the above analysis supports the idea that the initial increase in transcriptional regulators influences downstream changes in gene expression. The idea that changes in gene expression that occur early in the cold response impact the expression of later changes in gene expression is not new (Gilmour *et al.*, 1998), but this analysis demonstrates the cold transcriptome behaves in a similar manner at the whole-genome level.

The Early Cold-Induced Transcription Factors CBF2 and ZAT12 Control Regulons Enriched in Stress-Related Transcripts, Including Novel COR-Like Genes

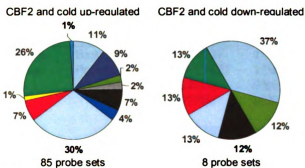
Examination of the regulons of cold-inducible transcription factors, such as *CBF1*, 2, and 3 and *ZAT12*, that are up-regulated quickly in response to low temperature, further strengthens the idea that early changes in the transcriptome influence later changes during cold acclimation. The CBF2 and ZAT12 regulons have been shown to regulate 94 and 24 COS transcripts, respectively (Chapter 2) and most of the cold-responsive genes that CBF2 and ZAT12 affect are cold-responsive at later times in the cold (24 h or 7 d). A more thorough understanding of the functions of downstream genes

that are controlled by CBF2 and ZAT12 could provide insight into how each regulon alters freezing tolerance.

The CBF2 regulon was determined by profiling changes in plants constitutively expressing *CBF2* and comparing these genes to the COS transcripts (see Chapter 2 for details). The functional roles of the CBF regulon were diverse (including cyroprotectant production, lipid and cell wall modification, and transcription), with many of the up-regulated transcripts involved in stress responses and the down-regulated transcripts enriched for transcripts annotated with oxygen binding activity or membrane localization (Figure 3.3a and Table 3.3). Interestingly, 91% of the up-regulated transcripts fell into cluster III, reinforcing the idea that the early cold-responsive CBF transcription factors play important roles in regulating the expression of genes that are induced at later times. Since the functional roles of CBF2 and cold up-regulated transcripts revealed significant enrichment for transcripts encoding stress-related proteins (Table 3.3) which fall into cluster III, this again strengthens the idea that changes occurring later in the cold are responsible for increased freezing tolerance. Additionally, at least 26% of the up-regulated transcripts had unknown roles.

The unknown transcripts in the CBF2 regulon were examined to determine if any could be novel *COR* genes (transcripts encoding small, highly hydrophilic polypeptides). A search of the unclassified highly up-regulated transcripts revealed four new COR/LEA-like proteins based on their highly hydrophilic character and were designated COR35 (At1g11210), COR17 (At1g16850), COR33.5 (At1g80130), and COR42 (At4g30830) (Figure 3.4). COR35 and COR17 both possess predicted target peptides based on

(a)



(b)

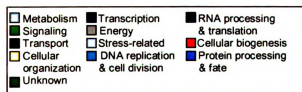
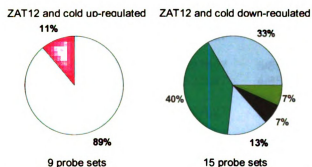


Figure 3.3. Functional categories of the CBF2 and ZAT12 regulons.

Members of the CBF2 and ZAT12 regulons were placed into an exclusive functional category based on annotations available at TAIR, TIGR, MIPS, and in published literature (see Materials and Methods). Images in this figure are presented in color.

Table 3.3. Overrepresented GO terms in the CBF2 regulon

Class	GO Ontology	Frequency in genome	Frequency in class	E-score	GO Term
CBF2 & cold up	Biological Process	63/27627	11/85	1.01E-14	response to cold
		109/27627	11/85	5.64E-12	response to temperature
		66/27627	9/85	8.05E-11	response to water
		59/27627	8/85	1.76E-09	response to water deprivation
		590/27627	16/85	4.85E-09	response to abiotic stimulus
		11/27627	5/85	1.75E-08	cold acclimation
		889/27627	18/85	2.88E-08	response to stress
		930/27627	18/85	5.93E-08	response to external stimulus
		64/27627	7/85	1.72E-07	response to abscisic acid stimulus
		39/27627	5/85	2.04E-05	salinity response
		22/27627	4/85	9.19E-05	hyperosmotic salinity response
		54/27627	5/85	1.08E-04	response to osmotic stress
		23/27627	4/85	1.11E-04	hyperosmotic response
		1841/27627	19/85	3.90E-04	response to stimulus
		3/27627	2/85	4.40E-03	cellular response to water deprivation
		344/27627	7/85	1.47E-02	response to hormone stimulus
	Cellular Component	6642/27627	33/85	4.26E-02	membrane
CBF2 & cold down	Cellular Component	6642/27627	6/8	1.70E-02	membrane
	Molecular Function	229/27627	2/8	4.45E-02	oxygen binding

CBF2 regulon members (Appendices G and H) were classified into gene ontology (GO) categories using the functional categorization tool at TAIR (<http://www.arabidopsis.org/tools/bulk/go/>). Overrepresented terms among transcripts in the CBF2 regulon as compared to the rest of the genome ($E \leq 0.05$) are shown. Each term is associated with an organizing principle (biological process, cellular component, or molecular function) listed under “GO ontology” in the table.

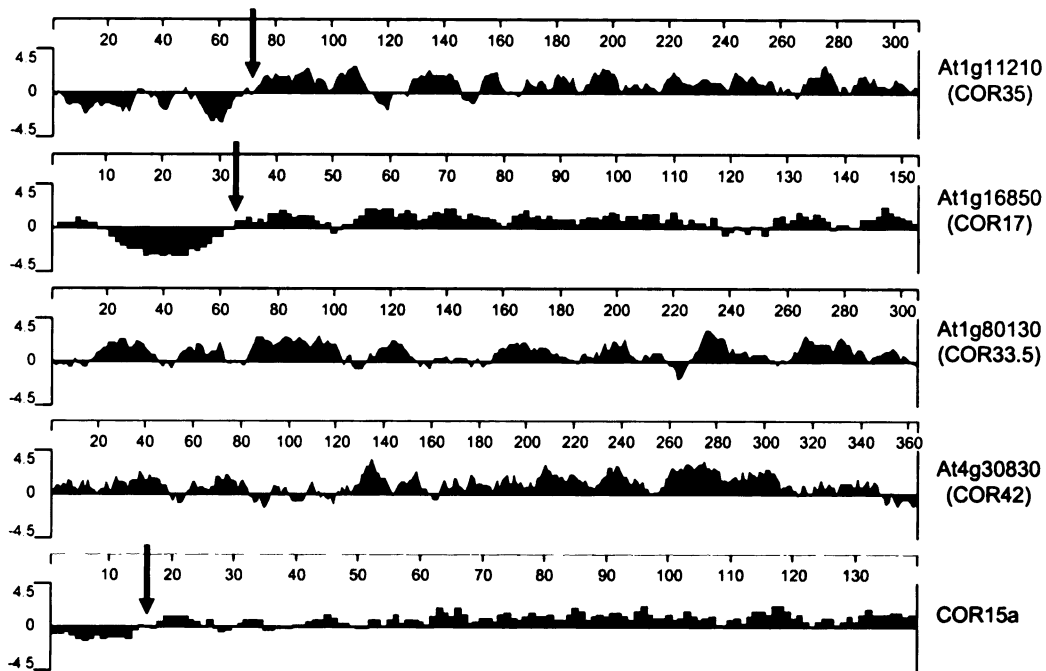


Figure 3.4. Hydropathy plots for novel COR-like peptides in the CBF2 regulon.

The hydropathic character of the COR-like proteins was analyzed using the methods of Kyte and Doolittle (1982). The x-axis of each plot represents regions with hydrophilic or hydrophobic character; values > 0 represent hydrophilic regions, while values < 0 are hydrophobic. The length of the protein (number of amino acids) is indicated along the top of each plot. TargetP (<http://www.cbs.dtu.dk/services/TargetP/>) was used to deduce potential signal peptides and the predicted cleavage sites are indicated by arrows. COR15a is shown for comparison.

sequence analysis using TargetP (Nielsen et al., 1997; Emanuelsson et al., 2000), suggesting they are targeted to cellular organelles. Of these four, *COR17* was the most highly up-regulated (>375 fold) by *CBF2* expression and contained 3 CRT/DRE elements within 500 bp of the 5' UTR, likely making it a direct target of the CBFs. *COR17* contained a group 3 LEA domain (Dure et al., 1989) and the mature peptide was rich in Ser, Val, Thr, Ala, Glu, and Lys (51% of the amino acid residues). *COR17* was also the most highly up-regulated transcript at any time (>390 -fold at 24 h) in the experiment examining cold-responsive genes in plate grown plants. *COR17* lies on chromosome 1

next to another gene (At1g16840), also predicted to encode a highly hydrophilic peptide possessing a targeting peptide (At1g16840 was not cold-regulated). This type of chromosomal arrangement is similar to that described for other *COR* gene pairs (Thomashow et al., 1997). Given the high level of expression and predicted domains in the protein, it seems likely that COR17 plays a protective role during freezing stress, perhaps in a fashion similar to COR15a (Artus *et al.*, 1996). Future experiments will be needed to confirm this hypothesis.

The ZAT12 regulon was enriched for transcripts annotated with the biological processes of lipid transport and binding, transport, and cell growth (Figure 3.3b and Table 3.4). Among the down-regulated transcripts, there was no enrichment for any biological processes or molecular function, but further examination showed that six transcripts encoded proteins of unknown function and five encoded proteins potentially involved in metabolism. The other four transcripts were classified as signaling, transport, and stress.

ZAT12 overexpression results in altered freezing tolerance, but to a much lesser degree than overexpression of *CBF*. The mechanism for this change in freezing tolerance is not known, but the putative functions of the proteins encoded by transcripts altered by *ZAT12* reveal some possibilities. I previously speculated on the role of two transcripts, L-ascorbate oxidase (At5g21100) and arginine decarboxylase (At4g34710), in protecting the plant from damage during cold stress (Chapter 2). Additional transcripts influenced by *ZAT12* have stress-related roles. *ZAT12* up-regulated five members of the protease inhibitor/seed storage/lipid transfer protein family, which may stabilize or remodel membranes, as hypothesized by Wilkosz and Schlappi (2000). Transcripts for potential antifreeze proteins (At2g43620 and At5g06860) were also up-regulated by *ZAT12*.

Table 3.4. Overrepresented GO terms in the ZAT12 regulon

Class	GO Ontology	Frequency in genome	Frequency in class	E-score	GO Term
ZAT12 & cold up	Cellular Component	4520/27627	8/9	4.32E-05	endomembrane system
		6642/27627	8/9	8.66E-04	membrane
	Biological Process	104/27627	5/9	2.31E-09	lipid transport
		4687/27627	7/9	2.84E-03	cellular process
		3237/27627	6/9	4.26E-03	cell growth and/or maintenance
		1987/27627	5/9	5.10E-03	transport
		3592/27627	6/9	7.67E-03	cellular physiological process
	Molecular Function	143/27627	5/9	1.12E-08	lipid binding
		115/27627	2/9	1.58E-02	nutrient reservoir activity
ZAT12 & cold down	Cellular Component	6642/27627	10/15	3.96E-03	membrane
		4520/27627	7/15	4.15E-02	endomembrane system

ZAT12 regulon members (Appendices G and H) were classified into gene ontology (GO) categories using the functional categorization tool at TAIR (<http://www.arabidopsis.org/tools/bulk/go/>). Overrepresented terms among transcripts in the ZAT12 regulon as compared to the rest of the genome ($E \leq 0.05$) are shown. Each term is associated with an organizing principle (biological process, cellular component, or molecular function) listed under “GO ontology” in the table.

Transcripts for proteins likely involved in protecting the plant from oxidative stress were up-regulated, including a putative anthocyanidin synthase (At4g22870) and a dihydroflavanol 4-reductase (At5g42800), both of which are involved in anthocyanin production, but neither is a COS transcript.

The Co-Regulation of Transcripts by Multiple Transcription Factors Indicates Many of the Early Cold-Responsive Transcription Factors May Co-Regulate Cold-Responsive Transcripts

The co-regulation of transcripts by CBF2 and ZAT12 (Chapter 2) is of interest, as it reveals the complexity of the networks of gene expression that occur at low temperature. The *pEARLI* transcripts are a case in point. These proteins of unknown function are members of the protease inhibitor/seed storage/lipid transfer protein family and were first identified as transcripts responding to toxic levels of aluminum (Richards and Gardner, 1995) and, more recently, vernalization (Wilkosz and Schlappi, 2000). Of the five *pEARLI*-like genes identified as COS genes, four occur in tandem on chromosome 4. Interestingly, all of the cold-regulated transcripts belonging to this family were placed into either the CBF2 or ZAT12 regulons. In addition to being affected by expression of *CBF2* or *ZAT12* (Figure 2.8, Chapter 2), the transcription factors *STZ/ZAT10* and *CZF2* (At5g04340) also altered the expression of one or more of the *pEARLIs* (J.T. Vogel, unpublished data). Even though *STZ/ZAT10* and *CZF2* did not contribute significantly to the cold transcriptome (Chapter 2), it seems unlikely that these cold inducible transcription factors would influence *pEARLI* expression by chance. A question that arises is why such redundancy would be needed. These proteins could be playing a critical role in freezing tolerance, vernalization, or life at low temperature. Whatever their role, the identification of cold-regulated genes that appear to be influenced by multiple transcription factors reveals the complexity of signaling events at low temperature and may denote factors with critical roles in cold acclimation.

CONCLUSION

The Arabidopsis cold transcriptome is composed of transcripts encoding myriad functions, as one would expect given the number of physiological changes that occur

during cold acclimation. As the work here demonstrates, those transcripts induced quickly in the cold are enriched for signaling molecules and transcription factors, which presumably influence downstream changes in gene expression and, ultimately, freezing tolerance. Examination of the CBF2 and ZAT12 regulons also supports this model. The CBF cold response pathway regulates genes with altered accumulation at later times in the cold, but that picture has been expanded upon here. The CBF regulon is enriched in stress-related transcripts, the majority of which fall into cluster III. The ZAT12 regulon is also composed of transcripts that are highly up-regulated later in the cold response (24 h or 7 d). The co-regulation of a number of transcripts by multiple transcription factors only adds to the apparent complexity of cold signaling pathways.

The analysis presented in this work generates new hypotheses that can be tested experimentally. The need exists to continue studying the functions of both the downstream genes in order to assess their roles in cold acclimation and the upstream factors that regulate them. This will include biochemical and physiological studies of gene products such as the COR peptides and molecular genetic studies on the transcription factors and *cis*-elements responsible for cold-regulated gene expression. This will result in a greater understanding of Arabidopsis low temperature regulatory networks and how plants increase their freezing tolerance during cold acclimation.

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MATERIALS AND METHODS

Functional Classification of Transcripts

COS probe sets were assigned AGI locus identities derived from TAIR's annotation of the ATH1 GeneChip using the TIGR v 5.0 annotation of the Arabidopsis genome. COS genes were placed into functional categories manually using annotation available at TAIR (The Arabidopsis Information Resource, www.arabidopsis.org), TIGR (The Institute for Genomic Research, www.tigr.org), and MIPS (Munich Information Center for Protein Sequences, <http://mips.gsf.de>). The transcripts were then placed into sub-roles based primarily on this annotation and on published literature. A full description of the microarray datasets and tables of the COS genes can be found in Chapter 2 and Appendices E and F. The COS genes were also automatically classified into gene ontology (GO) functional categories using the functional categorization tool available at TAIR (<http://www.arabidopsis.org/tools/bulk/go/>). GeneMerge was then used to find categories of transcripts statistically ($E\text{-score} \leq 0.05$) overrepresented in a given class compared to the rest of the genome as described by Castillo-Davis and Hartl (2003).

CHAPTER FOUR

THE IDENTIFICATION OF SIX NOVEL MOTIFS IN THE PROMOTERS OF COLD-REGULATED GENES AND THE DETERMINATION OF THEIR COLD-RESPONSIVENESS

SUMMARY

The definition of the COS (cold standards) gene set (Chapter 2), transcripts that change in plants grown in either soil or solid media in response to low temperature, provides the framework with which the low temperature regulatory networks of Arabidopsis can be constructed. Understanding Arabidopsis low temperature regulatory networks will lead to a greater understanding of how plants cold acclimate and may ultimately result in genetic methods of increasing the freezing tolerance of agricultural crops. One component of these regulatory networks comprises the *cis*-elements present in the promoters of cold-responsive genes. Studies on the COS gene set has led to the identification of several motifs in the promoters of genes with similar expression profiles (Chapter 2). These motifs could be binding sites for transcription factors that regulate transcription in a cold dependent manner. The studies presented here aimed to identify additional motifs present in the promoters of the COS genes and to determine their cold-responsiveness. To this end, two new novel motifs were identified in the promoters of COS genes with the highest expression after 24 h at low temperature and that were outside of the CBF regulon. These two novel motifs, along with four motifs previously found to be overrepresented in the promoters of COS genes (Chapter 2), were each fused as a tetramer in front of the GUS reporter gene, transformed into Arabidopsis, and assayed for the activity of the reporter. None of the six motifs were found to confer cold-responsiveness to the reporter. However, fusion of a tetramer of the sequence

GTGATCAC in front of the *GUS* reporter gene resulted in GUS activity in both warm and cold treated plants.

INTRODUCTION

Cold acclimation is the process by which plants increase their freezing tolerance through exposure to low non-freezing temperatures (Thomashow, 1999; Smallwood and Bowles, 2002). Understanding how plants cold acclimate not only furthers science, but may ultimately lead to novel methods of engineering increased freezing tolerance in crop species. Such an understanding includes deciphering the low temperature transcriptome, those genes whose expression is altered in response to low temperature.

In order to more fully understand the gene networks involved in regulating the low temperature transcriptome, it is necessary to identify transcription factors that regulate cold-responsive transcripts and identify the *cis*-elements they bind. Given that the *Arabidopsis* genome encodes more than 1,700 transcription factors (Riechmann, 2002), the question becomes which regulate cold-responsive transcripts. One approach is to constitutively express transcription factors whose mRNA levels accumulate in response to low temperature and determine if the expression of any cold-responsive transcripts is altered. This approach led to limited success, as one out of five transcription factors whose mRNA accumulated in response to low temperature was found to influence a significant number of cold-responsive transcripts (Chapter 2). This approach is limited to only those transcription factors whose transcripts increase in the cold and that can function independently of other cold-responsive factors and/or modifications. Alternatively, a mutational approach can be taken. Studies using the *RD29a/COR78* or *CBF3* promoter fused to luciferase have identified transcription factors such as *HOS9* and *ICE1*, whose expression is not altered by low temperatures, which influence cold-responsive genes (Chinnusamy et al., 2003; Zhu et al., 2004). This

mutational approach has the drawback of taking longer to isolate, characterize, and clone the mutated gene which may or may not be involved in cold-responsive transcription. Additional approaches are needed in order to define novel cold response pathways in *Arabidopsis*.

A more direct approach to define novel pathways is to first determine the cold-responsive elements present in the promoters of cold-regulated genes and then isolate the factor(s) that bind them. Such an approach was successfully used to identify the CRT/DRE element in the promoters of certain cold-responsive genes (Baker et al., 1994; Yamaguchi-Shinozaki and Shinozaki, 1994) and the CBF/DREB1 transcription factors that bind to this element (Stockinger *et al.*, 1997). Constitutive expression of *CBF1*, 2, or 3 in plants leads to activation of genes containing the CRT/DRE element in their promoter and increases freezing tolerance (Jaglo-Ottosen et al., 1998; Gilmour et al., 2004). The success of these experiments may have lain, in part, with the gene used in the promoter-deletion experiments (*COR15a*), which has a high level of expression in response to low temperature.

Current work suggests that had global gene expression data and computational approaches been available when experiments studying the *COR15a* promoter began, the CRT/DRE element would have quickly been identified as it has recently (Kreps et al., 2003; Vogel et al., 2005). Fusion of the CRT/DRE motif as a tetramer in front of a reporter gene such as *GUS* or *LUC* would have resulted in the reporter's expression after cold treatment. This computational approach would have saved time and effort put into creating multiple promoter-reporter deletion constructs in stably transformed transgenic

plants. In fact, this exact type of bioinformatic approach was used to rapidly identify the circadian responsive evening element in *Arabidopsis* (Harmer et al., 2000).

Here, I apply the above approach to the study of cold-regulated gene expression to identify non-CBF cold response pathways. Transcriptome profiling experiments examining transcripts with altered accumulation after 1 h, 24 h, or 7 d at low temperature in two growth conditions (soil or solid media, 2.5-fold cutoff, $p < 0.05$), resulted in the identification of 514 transcripts changing in both culture conditions, defined as COS (cold standard) transcripts (Chapter 2). Hierarchical clustering revealed seven expression classes among the COS genes. Additionally, bioinformatics analysis revealed DNA motifs that were overrepresented in the promoters of each cluster of up-regulated genes. Elements identified in the promoters of genes whose transcripts increased the most after 24 h or 7 d of exposure to low temperature should be good candidates for testing the motifs identified, as these motifs might confer a high level of cold-responsiveness to a reporter gene. Among those genes that increased to the highest levels after 24 h at low temperature, clusters III and IV, the CRT/DRE motif was identified in cluster III and four novel motifs were found in cluster IV.

In this study, cluster III promoters were found to contain the evening element, ABREs, and two novel motifs. The cold-responsiveness of these novel motifs, along with the motifs previously identified in cluster IV, was tested by fusing a tetramer of each motif in front of the *GUS* reporter gene and monitoring for cold induction of the reporter. When placed as a tetramer in front of *GUS*, none of the motifs conferred cold-responsive *GUS* activity. One element, GTGATCAC, resulted in constitutive activation of the reporter gene. Future work that could reveal the function of these elements is discussed.

RESULTS

The Circadian Evening Element and the ABRE are Present in the Promoters of the Most Highly Cold-Induced Transcripts Outside of the CBF Regulon

In an effort to decipher Arabidopsis low temperature regulatory networks, the promoters of the 25 transcripts with the highest average fold change after 24 h of cold treatment that were not CBF regulon members were examined. Should a cold-responsive element be present in this group of genes, one might expect such an element to be easier to discover if the high expression level is due to multiple copies of that element. The 500 bp upstream regions of these transcripts was searched for overrepresented motifs using MotifSampler (Thijs *et al.*, 2002). MotifSampler is a statistical program based on Gibbs sampling (Thijs *et al.*, 2001; Thijs *et al.*, 2002). Gibbs sampling is a stochastic variant of the expectation-maximization (EM) method (reviewed in Rombauts *et al.*, 2003). Due to the stochastic nature of Gibbs sampling, a detected motif can be replaced by another with a higher score. This results in different outputs from the algorithm each time it is run. However, motifs that are more conserved and overrepresented in a group of sequences will be retrieved more frequently over different runs. Statistically analyzing the output of multiple runs allows one to find the highest scoring motifs. Here, the program was run 100 times and the results were then searched for the highest scoring motifs.

Two motifs, CACGTGM and AAATATCT, were identified that were statistically overrepresented and approximately 2-fold enriched in the promoters of these genes compared to the rest of the promoters for genes on the GeneChip. Each is a known *cis*-element, CACGTGM is an ABRE (abscisic acid response element) (Guiltinan *et al.*, 1990) and AAATATCT is the evening element (Harmer *et al.*, 2000). Both elements

have been previously identified in the promoters of cold-regulated genes (Baker et al., 1994; Yamaguchi-Shinozaki and Shinozaki, 1994; Kreps et al., 2002; Kreps et al., 2003), but this is the first report of their occurrence in the promoters of the most highly cold-induced genes not part of the CBF regulon. MotifSampler previously found the CRT/DRE element in the promoters of cold-regulated genes (Chapter 2). The program has now successfully found two other *cis*-elements present in the promoters of cold-responsive genes. This indicates that the program can find overrepresented motifs which can play a role in gene expression.

Novel Potential cis-Elements are Revealed in Cluster III Promoters when CBF Regulon Members are Removed

In order to find additional overrepresented motifs, another approach was taken to analyze the promoters of cold-responsive genes. Cluster III represents a group of good candidate genes for identifying cold-responsive *cis*-elements, as their expression is high at 24 h and elements found in these promoters might impart high levels of cold-responsiveness to a reporter gene. Since the CRT/DRE element was the only motif identified as ≥ 5 -fold enriched in cluster III, these genes were further analyzed to determine if the presence of the CRT/DRE could be masking additional motifs that were not as greatly enriched. By removing all the CBF regulon members and genes containing an (A/G)CCGAC within 1kb upstream among the 233 cluster III genes, 96 remained. Analysis of these 96 promoters (500 bp upstream) with MotifSampler uncovered one known motif, WNGMCACGTG (ABRE), and one novel element, AGGCCCAWNA, that

were both approximately 2-fold enriched in cluster III (Table 4.1). Each motif was present in over 20 of the promoters of cluster III genes.

Since removal of CRT/DRE and CBF regulon member genes from the analysis allowed the identification of a new overrepresented motif, cluster III promoters that contained WNGMCACGTG or AGGCCCAWNA were removed and the remaining promoters analyzed. Among these promoters, one novel motif, AAAACCCTA, was discovered as overrepresented and 2-fold enriched (Table 4.1). Again, this motif was present in over 20 promoters of cluster III genes.

A question arose as to whether these novel elements occurred in promoters with CRT/DRE elements, by themselves, or in some combination. To address this question, the promoter region queried was expanded to 1kb upstream and cluster III transcripts were examined for promoters with each of the motifs (Table 4.2). Besides examining promoters with at least two motifs, Figure 4.1 depicts the overlap between cluster III genes with the CRT/DRE and either of the two novel elements. The results indicate that no cluster III gene promoter possesses all four of the motifs. Promoters with the two novel elements also contain a CRT/DRE element more often than each other or WNGMCACGTG. Given the number of promoters containing one or more of these different motifs, multiple transcription factors are likely acting on the promoters of cluster III genes.

Some of the Base Pairs Flanking the Motifs in Cluster III Appear to be Conserved

When MotifSampler searches for motifs among a group of sequences, the length of the motif to be searched for must be pre-set. To determine whether any of the novel

Table 4.1. Overrepresented motifs in cluster III

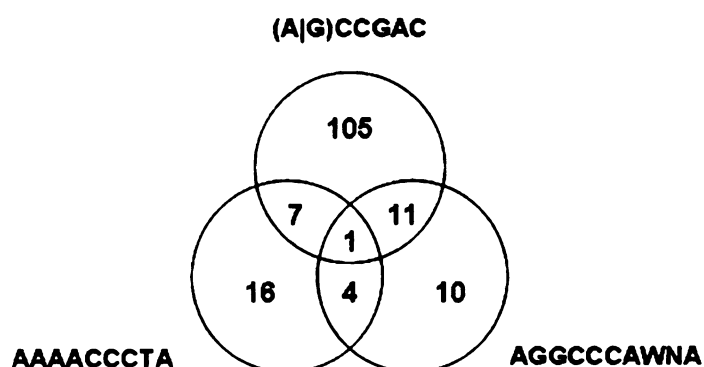
Motif	PlantCARE	500bp upstream		1000bp upstream	
		Class (%)	GeneChip (%)	Class (%)	GeneChip (%)
AGGCCCAWNA	novel	21/233 (9%)	1159/22746 (5%)	26/233 (11%)	1483/22746 (6.5%)
WNGMCACGTG	ABRE	27/233 (11.6%)	888/22746 (3.9%)	30/233 (13%)	1245/22746 (5.5%)
AAAACCCTA	novel	21/233 (9%)	1036/22746 (4.5%)	28/233 (12%)	1486/22746 (6.5%)

Overrepresented motifs discovered in the promoters of cluster III genes that do not have CRT/DRE elements (1kb upstream) and are not CBF regulon members. Each motif was queried to the PlantCARE database to determine if it was a known or novel element. The numbers of promoters in cluster III or for promoters from genes on the ATH1 GeneChip that contain the element (in the 500 bp or 1000 bp upstream regions) are shown. ABRE: abscisic acid responsive element.

Table 4.2. Number of promoters with each pair-wise motif combination

Element	CRT/DRE	WNGMCACGTG	AGGCCCAWNA	AAAACCCTA
CRT/DRE	124			
WNGMCACGTG	18	30		
AGGCCCAWNA	12	3	26	
AAAACCCTA	8	1	5	28

This table depicts the number of promoters of the 233 cluster III (1kb upstream) genes that contain each motif in any given pair-wise combination. To be identified in the promoter of a gene, the element had to be present exactly as shown.

**Figure 4.1. Overlap of the two novel motifs and the CRT/DRE element in cluster III promoters.**

This figure depicts the number of promoters (1kb upstream sequence) of the 233 cluster III genes with the CRT/DRE element and the two novel motifs. To be identified in the promoter of a gene, the element had to be present exactly as shown.

motifs identified might be part of a larger consensus, a custom PERL script was written and used to extract the 4 bp flanking sequence around each motif present within 500 bp of the start of transcription for cluster III genes. The conservation at each position in the aligned sequences was visualized using WebLogo (Crooks et al., 2004), which can reveal significant features of an alignment (Figure 4.2). The alignments revealed no conserved base pairs flanking AGGCCCAWNA. The motif WNGMCACGTG had a conserved T/G (indicated by the arrow in Figure 4.2) and AAAACCCTA had three positions outside of the core motif that appear to be conserved. As a comparison, the flanking sequences of CBF regulon members containing (A/G)CCGAC were analyzed in the same fashion, revealing a previously identified conserved T (Maruyama et al., 2004; Vogel et al., 2005). Since flanking base pairs might be important for the binding of a transcription factor, any analysis of these motifs should include flanking sequence.

Cluster IV Contains Novel Potential cis-elements, Including Palindromic Sequences

Cluster IV represents a second cluster of good candidate genes for discovering and testing promoter elements, as the expression of genes in this class continues to increase the entire time the plants are at low temperature (7 d in this experiment). Work presented in Chapter 2 identified four novel motifs among cluster IV genes, which are listed in Table 4.3. Two of the sequences, TGTATACA and GTGATCAC, are palindromes.

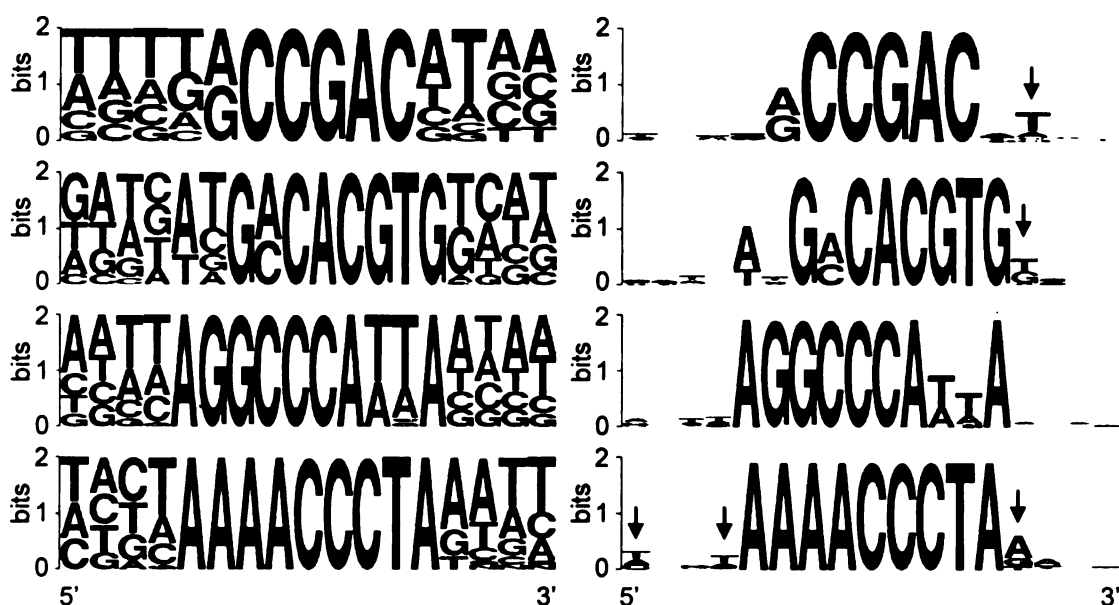


Figure 4.2. WebLogos depicting conserved sequences flanking the CRT/DRE, ABRE, and two novel motifs in cluster III genes.

Each element from all cluster III promoters (500 bp upstream) was extracted, along with 4bp of flanking sequence, and aligned. Weblogo (<http://weblogo.berkeley.edu/>) was used to visualize these alignments. The left side of the figure depicts each alignment with a uniform logo height, while the right side depicts the conservation of each position by height (the height of the y-axis is the maximum entropy for DNA, $\log_2 4 = 2$ bits). Residues that appear to be conserved outside of the core motifs are indicated by arrows.

Table 4.3. Overrepresented motifs in cluster IV

Motif	PlantCARE	500bp upstream		1000bp upstream	
		Class (%)	GeneChip (%)	Class (%)	GeneChip (%)
CAATGAGG	Novel	3/13 (23%)	176/22746 (0.8%)	3/13 (23%)	379/22746 (1.6%)
GTGATCAC	Novel	1/13 (8%)	96/22746 (0.4%)	1/13 (8%)	199/22746 (0.9%)
GnATTGAC	Novel	5/13 (38%)	937/22746 (4.1%)	5/13 (38%)	1808/22746 (8%)
TGTATACA	Novel	3/13 (23%)	327/22746 (1.4%)	4/13 (31%)	647/22746 (2.8%)

Overrepresented motifs discovered in the promoters of cluster IV genes. Each motif was queried to the PlantCARE database to determine if it was a known or novel element. The numbers of promoters in cluster IV or for promoters from genes on the ATH1 GeneChip that contain the element (in the 500 bp or 1000 bp upstream regions) are shown.

A Tetramer of the Novel Motif GTGATCAC Fused in Front of the GUS Reporter Gene Results in GUS Activity in both Warm and Cold Temperatures

In order to determine whether any of the newly identified novel elements from cluster III and those previously found in cluster IV (Table 4.3) were cold-responsive, a tetramer of each motif was fused in front of the β -glucuronidase (*GUS*) reporter gene, and transformed into *Arabidopsis*. Each tetramer contained 6 bp of flanking sequence, since some of the motifs in cluster III possessed conserved residues outside of the identified motif. The motifs, along with flanking sequence, were taken from the context of the promoter of the cold-responsive gene in either cluster III or IV with the highest level of cold-regulated expression (Appendix L). T_1 plants were assayed for expression of *GUS* in response to low temperature by histochemical staining. After 48 h or 7 d at 4°C, none of the lines stained blue for cold-responsive *GUS* activity (data not shown, >20 T_1 plants screened per condition). However, plants expressing the motif GTGATCAC fused in front of *GUS* stained blue in both the warm and the cold (Figure 4.3). *GUS* activity was seen with both plate and soil grown plants. These preliminary results indicate that this motif is likely a *cis*-acting element involved in transcriptional activation.

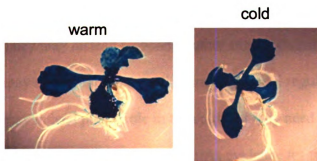


Figure 4.3. The motif GTGATCAC confers activity to a *GUS* reporter.

A tetramer of GTGATCAC confers activity to a *GUS* reporter in both warm (24°C) grown and cold (7 d at 4°C) treated plants. Approximately 10 plants were screened in the warm and in the cold. Bar = 5mm. Images in this figure are presented in color.

DISCUSSION

In an effort to identify non-CBF cold response pathways, the objective of this study was to use a bioinformatics approach to discover novel potential *cis*-elements in the promoters of highly cold-inducible genes. This goal was accomplished, as use of MotifSampler on non-CBF regulon COS genes revealed the presence of two novel motifs among cluster III promoters, those transcripts induced to the highest levels after 24 h at low temperature. In addition to these two novel motifs, two known motifs, the ABRE and the evening element, were found in the promoters of the 25 non-CBF regulon genes with the highest fold-change at 24 h.

It was then hypothesized that these two novel elements and those identified previously in cluster IV were cold-responsive elements. To address this question, constructs were created where a tetramer of each motif along with flanking sequence was fused in front of the *GUS* reporter gene. Plants containing these constructs were tested for cold-inducible reporter activity. While the motif GTGATCAC conferred activity on the *GUS* reporter gene, none of the other constructs tested displayed any GUS activity in the warm or after 48 h at 4°C. This result could be due to a number of possibilities. One explanation is that none of these elements play a role in cold-responsive gene expression. They may instead respond to other stimuli (hormones, circadian rhythm, light, etc.) or may not be involved at all in transcriptional regulation. Alternatively, these elements may indeed play a role in the cold, but may need to work in combination with additional elements to function properly. As evidence for this hypothesis, each novel element was found in a number of promoters containing CRT/DRE elements. While none of the elements were sufficient for cold-responsiveness, further experiments would be needed to

test each of the above possibilities and to determine if any of the elements were necessary for cold-responsiveness. Furthermore, the use of RT-PCR or RNA blot analysis might reveal changes in *GUS* transcript accumulation which might not be reflected by the intensity of the staining. An additional possibility is that the program used to discover these novel motifs may have not worked optimally, resulting in the identification of motifs that were not the most overrepresented. This seems unlikely since MotifSampler found three motifs known to be present in the promoters of cold-responsive genes, including the CRT/DRE.

Since the initial work done here to discover the motifs in clusters III and IV, a study assessing the ability of 13 motif discovery tools to find statistically overrepresented motifs was published (Tompa et al., 2005). This study revealed a number of interesting findings. No program worked very well on all the datasets or conditions tested and the longer the binding site, the less likely a program was to find it. Based on their results, the authors recommend that researchers pursue the top several motifs, not just the “best” one and to use other data (such as chromatin IP, global expression studies, etc.) or multiple programs when available. MotifSampler, the program used here, was found to perform the best of all 13 programs on a dataset consisting of actual data. While the work presented here used global expression studies and focused on the top several motifs, future motif searches should be performed using a second program, such as Weeder (Pavesi et al., 2004), to confirm the results of the first algorithm.

There is only one other published study that identified novel motifs in the promoters of cold-responsive genes (Kreps *et al.*, 2003). The study by Kreps et al. did not use a statistical algorithm, but pattern enumeration. This method takes longer and

needs more computing power than statistical methods, but its advantage lies in that it requires no statistical assumptions to be made. Kreps et al. (2003) searched the promoter regions of cold-responsive transcripts identified in experiments using the 8K GeneChip (Kreps *et al.*, 2002) and found the CRT/DRE element and ABRE as the top scoring motifs. As found in this study, their work also identified the evening element as overrepresented among cold-responsive promoters. Kreps et al. (2003) speculate the evening element could possess a dual role, functioning both in circadian rhythms and the cold response. Additionally, Kreps et al. (2003) found numerous novel motifs, none of which were the same as those analyzed in this paper. It will be interesting to see if future experimental evidence points towards a role in cold-responsive gene expression for any of the novel motifs they identified.

While the motif GTGATCAC did not confer cold-responsiveness to the *GUS* reporter gene, fusion of this element in front of *GUS* resulted in GUS activity in both warm and cold treated plants. The level of staining observed was similar to plants expressing *GUS* under control of the CMV 35S promoter. This preliminary data indicates that this motif likely constitutively stimulates transcription. These results need to be confirmed in the T2 generation and by testing a mutated version of the element. This element is present within 500 bp of the start of transcription for 114/27,186 Arabidopsis genes. Only two of the COS genes have this element in their promoters (500 bp upstream), the up-regulated gene At4g22470 and the down-regulated gene At2g33480. While it may or may not play role in cold-responsive gene expression, this element could be used in a yeast one-hybrid to identify the transcription factor which binds to it and stimulates expression of the reporter gene.

While no study has yet identified a new cold-responsive *cis*-element through bioinformatic means, this event is still a strong possibility. The use of additional computer programs and more extensive global expression datasets could lead to their discovery. Chromatin IP experiments could also be used to reveal promoters that contain acetylated histones, revealing which genes are most likely to be transcriptionally active, which would help to refine any bioinformatic analysis. Additionally, a number of motifs were identified among the cold-responsive genes that have not yet been tested experimentally (Chapter 2, Table 2.1). In the study presented here, one of the elements discovered was constitutively active and this element could play a role in the regulation of genes possessing the motif in its promoter. The computational discovery of motifs among co-regulated genes holds the possibility of greatly reducing the time and effort currently involved in uncovering *cis*-elements through traditional promoter bashing experiments.

MATERIALS AND METHODS

Constructs and Plant Transformation

Plasmids were constructed using standard molecular biological techniques (Sambrook and Russell, 2001). Synthetic double stranded tetramers of each motif (along with mutated versions of each motif) were created by annealing single stranded oligos synthesized at the Michigan State University Macromolecular Synthesis Facility (E. Lansing, MI) by heating at 94°C for 5 min and cooling to room temperature. Each double stranded oligo had a 5' EcoR I overhang, followed by an Xma I site, followed by four copies of the motif taken from the context of a promoter containing that motif with 6 bp of sequence flanking either side, and a 3' Xma I site that would be destroyed by ligation into an Xma I site. Mutant versions of each motif retained the 6 bp flanking sequence as was found in the context of the actual promoter. Oligos were then ligated into the pBS SK⁻ vector (Clontech, Palo Alto, CA) cut with EcoR I and Xma I. The oligo was then cut from pBS SK⁻ using Hind III and Xba I and ligated into the plant binary transformation vector pBI101 plus (Clontech, Palo Alto, CA) cut with the same enzymes. The genes from which the motifs were taken and the sequence of each tetramer are listed in Appendix L.

The DNAs were transferred to *Arabidopsis thaliana* (L.) Heynh. ecotype Wassilewskija-2 (WS-2) via a whole plant dipping method similar to that described by Clough and Bent (1998). Seed germination on medium containing kanamycin (50 mg/L) (Sigma-Aldrich, St. Louis, MO) was used to identify plants containing transferred DNA. Kanamycin resisitant seedlings were grown and T₁ plants were used in all experiments.

Plant Growth and Experimental Treatments

All *Arabidopsis* plants were grown in controlled environmental chambers at 22°C under constant illumination from cool-white fluorescent lights ($100 \mu\text{mol m}^{-2} \text{s}^{-1}$) in Baccto planting mix (Michigan Peat, Houston). Pots were subirrigated with deionized water. After four days stratification at 4°C, plants were also grown for 10-12 days in Petri plates containing Gamborg's B5 nutrients (Caisson Laboratories, Inc., Rexburg, ID) and 0.8% phytagar (Life Technologies Inc., Gaithersburg, MD) at 22°C under constant illumination from cool-white fluorescent lights (approximately $100 \mu\text{mol m}^{-2} \text{s}^{-1}$). The plates of plants were then transferred to 4°C under constant illumination from cool-white fluorescent lights (approximately $30 \mu\text{mol m}^{-2} \text{s}^{-1}$) and harvested at the indicated times.

Staining for GUS Activity

Staining of plant tissue for GUS activity was performed on plants grown at 22°C and those transferred to 4°C for 24 h, 48 h, or 7 d. Plants were immersed in a GUS staining solution (Jefferson et al., 1987) and incubated overnight at 37°C. The tissue was then cleared by several rinses of 70% (v/v) ethanol to assist in revealing the staining.

Motif Analysis

Motif searches were performed using the command line version of MotifSampler v3.0 (<http://www.esat.kuleuven.ac.be/~thijs/Work/MotifSampler.html>). Motifs were identified from various sub-groups of the 500 bp locus upstream sequence (TIGR v5.0 annotation of the *Arabidopsis* genome) downloaded from TAIR

(<http://www.arabidopsis.org>) on February 28, 2004. Arabidopsis intergenic regions were used as a background model with the order set to 3. The motif length was set to 8 or 10bp, with the prior probability of finding 1 motif instance set to 0.3. No limit was set for the number of motif instances that could be found per sequence, the maximum overlap between different motifs was set to 1, the number of motifs to be found per run was set to 4, and the total number of runs was set to 100. The highest scoring motifs were then ranked by the command line version of MotifRanking v3.0 (<http://www.esat.kuleuven.ac.be/~thijs/Work/MotifSampler.html>) using Arabidopsis intergenic sequence as a background model and the Kullback-Liebr distance to score the top ten motifs. The Patmatch program at TAIR or a PERL script (Appendix M) was used to identify all promoters in the genome that contained each motif. Those motifs approximately 2-fold enriched compared to all promoters in the genome were chosen for further analysis. Motifs were queried at PlantCARE (Lescot *et al.*, 2002) to determine if they were similar to any known *cis*-element.

The 4 bp flanking either side of the identified motifs was extracted from the 500 bp locus upstream sequence for cluster III genes (Appendix E) using a custom PERL script (Appendix M). The alignment of these sequences was then used to identify potentially conserved residues flanking a motif through the creation of WebLogos (<http://weblogo.berkeley.edu/>).

CHAPTER FIVE

A SUMMARY OF THE GENE REGULONS THAT CONTRIBUTE TO THE ARABIDOPSIS COLD TRANSCRIPTOME

The goal of identifying cold-responsive genes, the *cis*-elements within their promoters, and the transcription factors that bind to those elements, is to understand the gene networks contributing to cold acclimation in Arabidopsis. Such knowledge not only furthers science, but could provide the genetic means of improving the freezing tolerance of agriculturally important crops. The identification of the COS gene set, as described in this dissertation, should serve as a robust resource to begin to decipher the low temperature regulatory network of Arabidopsis. Indeed, the work described in this dissertation represents the start of this work. Using the COS gene set as a guide, this chapter summarizes what is currently known about the low temperature regulatory networks of Arabidopsis.

While transcriptome profiling experiments have led to the definition of the COS gene set, the regulatory networks cannot be properly explained without knowledge of the *cis*-elements present in the promoters of the COS genes and the transcription factors that bind to those elements. The CBF transcription factors, which bind to the CRT/DRE element, play a major role in configuring the low temperature transcriptome of Arabidopsis. The CBF transcription factors each appear to regulate the same suite of target genes (Gilmour et al., 2004). Of the 514 COS genes, 93 were CBF2 regulon members and of these 93, the large majority, 85 (91%), were cold-induced. The promoters of 68 (80%) of these 85 genes had one or more CRT/DRE elements, (A/G)CCGAC, present within 1 kb upstream of the start of the protein coding sequence.

Thus, these genes were likely to be direct targets of CBF2. CBF2-regulated COS genes without CRT/DRE elements in their promoters were presumably regulated by other genes controlled by CBF2 though this remains to be established.

The 85 cold-induced CBF regulon members represented a diverse range of functional roles, including metabolism, transcription, intercellular communication and signaling, transport, energy, protein processing, and cellular biogenesis. The largest group of transcripts (30%) in the CBF2 up-regulated regulon were stress-related transcripts. A further distinguishing characteristic of these genes was that they comprised the majority of genes that were most highly-induced in response to low temperature. Of the 25 COS genes that were up-regulated at least 15-fold at 24 h, 21 (84%) were members of the CBF regulon and nearly half of those up-regulated 5- to 10-fold, 32/66 (49%), were also assigned to the CBF regulon. Conversely, approximately 90% of the COS genes that were induced less than 5-fold were not assigned to the CBF regulon. Finally, an additional distinguishing feature of the CBF regulon COS genes was the enrichment for genes that remained up-regulated at 7 d. Of these 67 “long-term” up-regulated COS genes (≥ 2.5 -fold increase at 7 d), 37 (55%) were members of the CBF regulon.

Taken together, the above results indicate that the CBF transcription factors have a prominent role in regulating the expression of those cold-responsive COS genes that are both highly-induced and long-term up-regulated in response to low temperature. However, it is also clear that additional cold-response pathways participate in configuring the low temperature transcriptome, indicated by the finding that the transcript levels for 112 (22%) of the total 302 up-regulated COS genes showed no detectable change in either

of the *CBF2* overexpressing transgenic lines profiled. Thus, it would appear that these cold-regulated genes fall outside of the CBF regulon. While most of these genes are induced less than 5-fold in response to low temperature, 33 were induced more than 5-fold. Identifying the transcription factors that regulate the expression of these genes is required to more completely define the low temperature regulatory network of *Arabidopsis*.

ZAT12, a C2H2 zinc finger transcription factor (Meissner and Michael, 1997), was found to define an additional cold response pathway. *ZAT12* is cold-induced in parallel with *CBF2* and shares two additional features with *CBF2*; it is responsive to mechanical agitation and treatment with cycloheximide. Analysis of the *ZAT12* promoter indicates that this regulation may occur at a transcriptional level, as two regions were found to be similar to the ICer1 and ICer2 cold-, mechanical-, and cycloheximide-responsive regions in the *CBF2* promoter (Zarka *et al.*, 2003). Constitutive expression of *ZAT12* influenced a statistically significant number of COS genes (24) and caused a limited, but reproducible, increase in the freezing tolerance of *Arabidopsis*. In addition, *ZAT12* interacted with the CBF cold response pathway in two significant ways. First, constitutive expression of *ZAT12* influenced some of the same genes as *CBF2*. Secondly, constitutive expression of *ZAT12* resulted in lower cold-induced levels of *CBF* transcripts, while two independent T-DNA insertions in the *ZAT12* locus resulted in higher levels of *CBF* transcripts in response to low temperature. However, constitutive expression of *ZAT12* or lower levels of *ZAT12* expression did not impact the levels of the *COR* genes as severely as the *CBFs*. In summary, *ZAT12* represents a new cold response pathway in *Arabidopsis* that has a negative regulatory role in *CBF* expression.

Another transcription factor has also recently been shown to alter the expression of cold-regulated genes outside of the CBF cold response pathway. The *hos9-1* mutant displays hyperactivation of an *RD29A* promoter luciferase fusion in response to low temperature, but not in response to ABA treatment or salinity stress. Additionally, this mutation altered freezing tolerance (Zhu *et al.*, 2004). *HOS9* was found to encode a putative homeodomain transcription factor that was constitutively expressed and did not increase in response to low temperature. *CBF* transcripts were not affected by *hos9-1*, but since the promoter from the reporter gene construct contained CRT/DRE elements, this gene might be affected by the CBF pathway in some manner. Microarray experiments performed on cold treated *hos9-1* plants by Zhu *et al.* (2004) revealed that a number of cold-responsive genes were affected in their expression, but only one GeneChip experiment was performed, so these results should be viewed as preliminary. In comparing these genes to the COS gene set, 13 COS genes were found to be cold up-regulated and *hos9-1* up-regulated, one gene was cold down-regulated and *hos9-1* up-regulated, and one COS gene was cold down-regulated and *hos9-1* down-regulated and none were members of the CBF regulon. Interestingly, all 13 of the up-regulated COS genes influenced by *hos9-1* fell into expression class V, those genes up-regulated transiently in the cold. The majority of these 13 transcripts encoded either transcription factors or enzymes for signaling molecules. This indicated that HOS9 may play a role in regulating some of the earliest events during cold acclimation.

In addition to ZAT12 and HOS9, ICE1 (a MYC-like basic helix loop helix transcription factor) impacts the expression of cold-regulated genes (Chinnusamy *et al.*, 2003). A dominant mutation of ICE1, *ice1*, results in loss of *CBF3* transcript

accumulation in response to low temperature, but does not impact accumulation of *CBF1* or *CBF2* transcripts. The mutation also alters freezing tolerance and a preliminary microarray experiment performed without replication revealed that the expression of a number of cold-responsive transcripts was altered in response to low temperature. A comparison of these transcripts to the COS genes revealed that none of the down-regulated COS genes were impacted by *ice1*, but 78 of the up-regulated genes displayed lower cold induction in the mutant than in wild type plants (13 were in class V, 5 in class VI, 9 in class VII, and 51 in class III). It is interesting to note that *ice1* affected some, but not all of the CBF regulon members (51 of the 85 CBF regulon members displayed altered cold-induction in *ice1*). This could possibly be due to the fold-change cutoff used by Chinnusamy et al (2003). Alternatively, this could indicate that some genes are more greatly impacted by *CBF3* expression, while others are more responsive to *CBF1* or *2*. Finally, this result could be due to the action of additional transcription factors acting on these CBF regulon members. Regardless of the reason, ICE1 seems to play a role in regulating cold-responsive genes.

In order to complete the low temperature regulatory network of Arabidopsis (Figure 5.1), approximately 70% of the cold up-regulated COS genes still need to be assigned to a regulon. In this study (Chapter 2) *RAV1*, *MYB73*, *STZ/ZAT10*, and *CZF2* were overexpressed in Arabidopsis, but were not found to affect the expression of a statistically significant number of cold-regulated genes. It is possible that these transcription factors may need to act in concert with other factors or be modified posttranslationally in the cold, similar to the mechanism proposed for DREB2 (Liu *et al.*, 1998), in order to function properly. Chromatin immunoprecipitation experiments could

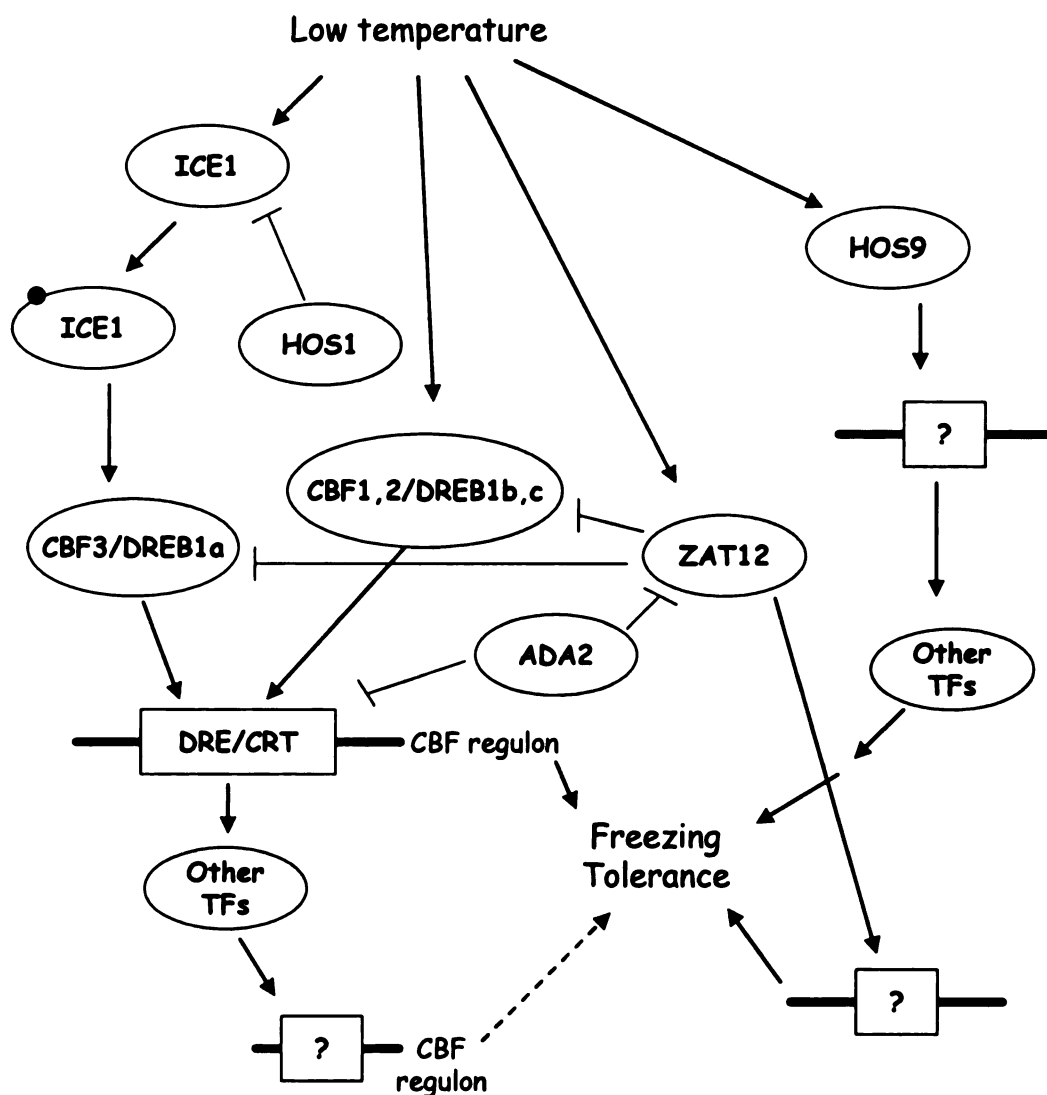


Figure 5.1. The low temperature regulatory networks of Arabidopsis.

Shown above is a summary of the transcriptional regulators currently known to be involved in the configuring the low temperature regulatory networks of *Arabidopsis thaliana*. HOS1 is an E3 ubiquitin conjugating enzyme (Ishitani *et al.*, 1998). The rest of the proteins listed are described in the text. Other TFs stands for other transcription factors. Boxes with lines behind them represent genes with specific *cis* regulatory elements, while the ovals represent proteins.

be used to test whether any of these transcription factors actually bind to the promoters of COS genes. Work on *RAV1*, *MYB73*, *STZ/ZAT10*, *CZF1*, *CZF2* and other cold-induced transcription factors will be needed to determine if they play a role in cold-responsive gene expression. Other transcription factors that regulate the COS genes could be found by first identifying the *cis*-elements in the promoters of these genes, either through the use of bioinformatic means or promoter bashing experiments, and then isolating the transcription factors that bind to these elements. Regardless of the methods used, much work still needs to be done in order to define all the regulons that comprise the Arabidopsis low temperature transcriptome. The work presented in this dissertation provides both a set of genes which can be used to characterize these regulons and defines two of these regulons, the CBF2 and ZAT12 regulons.

APPENDIX A

TABLE A.1. PROBE SETS UP-REGULATED BY LOW TEMPERATURE IN THE PLATE EXPERIMENT

Probe set	AGI	1h			24h			168h			Cold responsive			Annotation
		A	B		A	B		A	B		A	B		
261048_at	At1g01420	1.0	1.3		3.5	5.7		1.9	3.0		x			similar to UTP-glucose glucosyltransferases
259426_at	At1g01470	-1.1	-1.1		9.2	8.6		3.5	3.0		x			Lea protein (LEA14)
259442_at	At1g02310	-1.1	1.1		3.0	2.6		1.3	1.3		x			glycosyl hydrolase family 5/cellulase ((1-4)-beta-mannan endohydrolase)
259444_at	At1g02370	1.6	1.5		4.0	4.3		2.1	2.5		x			pentatricopeptide (PPR) repeat-containing protein
260903_at	At1g02460	-1.1	1.1		4.3	4.9		4.6	2.6		x			putative polygalacturonase
262112_at	At1g02870	-1.1	1.0		3.5	3.2		2.6	2.5		x			expressed protein
262119_s_at	At1g02930	1.1	1.3		2.0	2.0		2.5	3.0		x			glutathione transferase, putative
264357_at	At1g03360	1.1	1.5		2.8	2.6		1.3	2.1		x			hypothetical protein
264818_at	At1g03530	1.0	-1.1		6.1	4.9		3.0	1.6		x			expressed protein
265093_at	At1g03905	-1.7	1.0		4.0	3.0		2.0	1.9		x			ABC transporter family protein
263656_at	At1g04240	1.5	1.9		2.8	2.8		-1.3	2.1		x			putative auxin-induced protein AUX2-11
261130_at	At1g04870	-1.1	-1.1		2.5	3.2		2.5	2.5		x			expressed protein
261168_at	At1g04940	-1.1	1.3		3.5	3.0		1.2	1.9		x			Tic20 family
263182_at	At1g05575	3.5	4.9		-2.1	-1.6		1.4	1.4		x			expressed protein
260955_at	At1g06000	1.0	1.2		3.0	5.7		-1.4	2.0		x			similar to UDPG glucosyltransferase
260824_at	At1g06720	-1.2	-1.1		4.3	4.3		2.8	3.0		x			expressed protein
260832_at	At1g06780	1.1	-1.3		3.2	2.6		1.6	1.3		x			glycosyltransferase family 8
256065_at	At1g07070	-1.6	1.0		2.3	3.0		4.6	6.1		x			60S ribosomal protein L35a (RPL35aA)
264803_at	At1g08580	-1.5	1.0		4.0	4.0		4.0	3.5		x			expressed protein
264806_at	At1g08610	1.1	1.3		2.6	2.6		1.4	2.0		x			hypothetical protein
264652_at	At1g08920	1.1	1.1		2.8	2.5		1.1	-1.1		x			putative sugar transport protein
264261_at	At1g09240	1.4	1.3		4.6	2.8		3.7	3.7		x			nicotianamine synthase, putative
264511_at	At1g09350	-1.3	1.4		147.0	97.0		52.0	34.3		x			putative galactinol synthase
264668_at	At1g09780	-1.1	1.1		2.1	2.6		2.5	3.5		x			putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
264515_at	At1g10080	-1.1	1.1		3.7	2.6		1.4	1.4		x			hypothetical protein
264516_at	At1g10090	-1.1	1.2		4.6	2.8		1.2	1.3		x			expressed protein

264452_at	At1g10270	1.1	1.2	5.7	4.3	2.6	1.2	x	pentatricopeptide (PPR) repeat-containing protein
264436_at	At1g10370	1.1	-1.1	3.5	7.0	-1.7	1.4	x	glutathione S-transferase (ERD9)
264458_at	At1g10410	1.1	1.0	6.5	4.0	2.0	1.9	x	expressed protein
263255_at	At1g10490	1.0	1.0	3.7	3.7	2.3	2.1	x	WD-40 repeat protein family
262452_at	At1g11210	4.9	3.2	78.8	8.0	42.2	3.2	x	expressed protein (COR35)
262777_at	At1g13030	1.0	1.2	2.8	2.6	1.1	2.1	x	hypothetical protein
262766_at	At1g13160	-1.2	1.1	3.7	3.7	1.9	2.3	x	expressed protein
259364_at	At1g13260	3.0	5.7	3.5	3.5	2.8	4.3	x	RAV1
262611_at	At1g14050	1.0	1.1	2.6	2.8	2.0	1.4	x	Expressed protein
260776_at	At1g14580	1.2	-1.1	8.0	4.6	4.3	1.3	x	zinc finger (C2H2 type) protein family
262832_s_at	At1g14870	1.0	1.1	-1.6	-1.2	14.9	13.9	x	expressed protein (similar to PGPS/D12)
262544_at	At1g15425	-1.3	1.3	3.5	3.7	1.3	2.5	x	expressed protein
262584_at	At1g15440	-1.3	1.0	4.6	4.0	1.7	2.5	x	WD-40 repeat protein family
259503_at	At1g15870	-1.2	3.5	2.6	6.5	1.3	4.0	x	expressed protein
262706_at	At1g16280	-1.5	1.0	3.2	2.8	1.1	2.5	x	DEAD/DEAH box RNA helicase, putative
256114_at	At1g16850	-1.1	2.8	238.9	548.7	55.7	137.2	x	expressed protein (COR17)
262517_at	At1g17180	-2.1	-1.1	6.5	3.0	3.0	3.2	x	glutathione transferase, putative
256077_at	At1g18090	1.2	1.2	2.5	2.6	1.6	2.8	x	expressed protein
261664_s_at	At1g18320	-1.6	-1.1	3.0	4.0	1.7	5.7	x	expressed protein
261377_at	At1g18850	-1.1	1.2	4.9	4.9	1.3	2.8	x	expressed protein
259466_at	At1g19050	5.7	4.9	-2.0	-1.5	1.2	1.7	x	response regulator 7
256017_at	At1g19180	2.8	3.5	4.0	2.5	3.0	2.1	x	expressed protein
260674_at	At1g19370	-1.2	1.3	2.6	2.5	1.2	1.1	x	expressed protein
261221_at	At1g19960	-1.2	1.2	-4.0	-2.3	3.5	4.0	x	expressed protein
261248_at	At1g20030	1.3	1.1	5.3	3.2	-4.9	-6.1	x	thaumatin family
261226_at	At1g20190	-3.7	1.1	1.2	-1.4	4.9	2.8	x	expansin, putative
259570_at	At1g20440	-1.2	-1.1	8.6	9.2	4.9	2.6	x	dehydrin (COR47)
259516_at	At1g20450	1.1	1.4	17.1	17.1	12.1	6.1	x	dehydrin (ERD10)
256091_at	At1g20693	-1.1	1.2	5.7	4.9	3.7	2.8	x	high mobility group (HMG) protein beta1 (HMGbeta1)
262496_at	At1g21790	-1.1	1.3	4.3	4.0	1.2	1.9	x	expressed protein
260856_at	At1g21910	4.0	5.3	1.7	1.7	1.5	-1.1	x	TINY-like protein
264211_at	At1g22770	1.3	1.0	11.3	3.5	6.5	2.8	x	GIGANTEA
264895_at	At1g23100	-1.2	1.3	3.7	4.0	2.8	7.0	x	10kDa chaperonin (CPN10), putative
264893_at	At1g23140	-1.1	1.4	1.9	2.6	3.2	3.5	x	C2 domain-containing protein family

263039_at	At1g23280	-1.1	1.1	2.6	4.0	-1.1	2.3	x	mak16-like protein-related
265184_at	At1g23710	2.6	3.0	-1.1	-1.5	1.2	-1.3	x	expressed protein
264864_at	At1g24310	-1.1	-1.2	2.6	2.6	2.0	2.3	x	hypothetical protein
265028_at	At1g24530	1.6	1.7	3.7	3.7	2.3	2.5	x	expressed protein
265025_at	At1g24575	1.3	1.7	6.1	8.0	6.1	3.2	x	expressed protein
255733_at	At1g25400	3.5	2.6	-1.1	-1.7	1.0	-1.1	x	expressed protein
255734_at	At1g25550	3.2	3.2	1.5	1.2	2.0	1.5	x	MYB family transcription factor
261263_at	At1g26790	3.0	2.5	4.6	6.1	2.3	3.0	x	H-protein promoter binding factor-2b like
263691_at	At1g26880	-1.1	-1.1	1.7	2.0	2.8	2.8	x	60s ribosomal protein L34
264989_at	At1g27200	1.2	1.5	6.5	7.0	3.5	3.2	x	expressed protein
264438_at	At1g27400	-1.1	-1.2	1.6	2.0	2.5	2.5	x	putative 60S ribosomal protein L17
261648_at	At1g27730	8.6	14.9	2.5	2.5	2.1	1.9	x	ZAT10/STZ
261651_at	At1g27760	1.0	1.0	7.0	5.7	2.5	2.8	x	expressed protein
259605_at	At1g27910	1.2	-1.1	2.5	2.5	1.2	-1.2	x	U-box domain protein
245662_at	At1g28190	5.7	4.0	1.9	2.5	1.4	-1.1	x	expressed protein
245670_at	At1g28210	2.3	1.3	2.8	3.5	4.0	1.7	x	mitochondrial protein (AtJ1), putative
260896_at	At1g29310	1.1	1.0	1.6	1.9	2.5	2.8	x	flower pigmentation protein ATAN11
259789_at	At1g29395	1.1	1.1	13.0	10.6	10.6	5.3	x	similar to cold acclimation protein WCOR414 (WCOR414-TM1)
260049_at	At1g29940	1.1	1.1	2.6	2.5	-1.1	1.2	x	DNA-directed RNA polymerase subunit, putative
245770_at	At1g30240	-1.1	1.1	3.2	3.5	1.3	2.0	x	expressed protein
256310_at	At1g30360	1.1	1.0	2.8	2.5	1.3	-1.1	x	dehydrin (ERD4)
263221_at	At1g30620	1.1	1.1	3.0	2.5	1.6	2.0	x	UDP-galactose 4-epimerase-like protein
265154_at	At1g30960	-1.6	1.3	5.3	8.0	4.3	2.6	x	GTP-binding protein
246575_at	At1g31660	-1.3	-1.1	3.5	4.0	1.7	2.6	x	putative bystin
260653_at	At1g32440	1.1	-1.1	2.5	2.8	1.4	1.2	x	pyruvate kinase, plastid isozyme, putative
261187_at	At1g32860	-1.1	1.3	7.0	5.7	-1.2	1.1	x	beta-1,3-glucanase precursor, putative
261193_at	At1g32920	3.0	3.5	1.1	-1.6	-2.0	-1.5	x	expressed protein
261566_at	At1g33230	-1.2	-1.1	3.7	2.5	1.4	1.4	x	expressed protein
261986_s_at	At1g33720	-1.1	1.4	1.7	1.4	3.0	2.6	x	cytochrome P450 monooxygenase
262412_at	At1g34760	-1.6	2.0	-1.3	1.4	2.5	3.5	x	14-3-3 protein GF14 omicron (grf11)
245757_at	At1g35140	6.1	24.3	5.3	11.3	1.1	1.2	x	phosphate-induced (phi-1) protein
259550_at	At1g35230	3.7	2.6	4.3	-2.1	32.0	10.6	x	arabinogalactan-protein (AGP5)
262272_at	At1g42440	-1.1	1.0	2.6	2.8	1.3	1.9	x	expressed protein

260868_at	At1g43860	1.0	1.0	3.5	2.6	1.6	1.9	x	expressed protein
245807_at	At1g46768	-1.1	4.0	6.5	19.7	7.5	9.2	x	AP2 domain transcription factor (RAP2.1)
262440_at	At1g47710	-1.1	-1.1	4.9	4.3	1.5	1.6	x	serpin, putative
260727_at	At1g48100	1.6	1.1	11.3	9.8	3.0	2.6	x	expressed protein (putative splicing domain)
261301_at	At1g48570	-1.1	1.0	3.5	3.5	2.8	2.5	x	expressed protein
246623_at	At1g48920	-1.1	1.1	3.5	3.5	1.7	2.8	x	nucleolin, putative
260753_at	At1g49230	2.5	2.6	2.8	2.0	-1.1	1.1	x	zinc finger (C3HC4-type RING finger) protein family
261610_at	At1g49560	1.1	-1.3	4.0	2.6	2.0	1.1	x	expressed protein
261613_at	At1g49720	1.3	1.9	8.0	5.3	3.5	2.6	x	abscisic acid responsive element-binding factor 1 (ABF1)
245749_at	At1g51090	-1.1	1.1	27.9	14.9	4.0	2.0	x	similar to proline-rich protein
265147_at	At1g51380	-1.9	1.0	6.1	4.3	2.6	3.5	x	expressed protein
260489_at	At1g51610	1.1	1.5	8.0	5.7	3.0	2.8	x	cation efflux family
260157_at	At1g52930	-1.1	-1.1	3.5	4.0	2.6	3.2	x	expressed protein
261318_at	At1g53035	1.2	1.3	9.2	6.5	2.5	3.5	x	expressed protein
264186_at	At1g54570	1.1	1.1	3.0	3.2	1.7	1.3	x	esterase/lipase/thioesterase family
265078_at	At1g55500	-1.1	1.1	2.8	4.0	1.1	1.6	x	expressed protein
260596_at	At1g55900	1.0	1.0	3.7	3.2	2.5	2.3	x	expressed protein
262094_at	At1g56110	-1.2	1.0	4.0	4.9	2.5	4.0	x	nucleolar protein Nop56, putative
245628_at	At1g56650	1.4	1.4	2.5	3.0	1.6	2.1	x	MYB family transcription factor (MYB75)
246405_at	At1g57630	1.4	1.9	2.8	1.0	9.2	5.3	x	disease resistance protein (TIR class), putative
263679_at	At1g59990	-1.1	1.1	2.8	3.2	2.5	3.7	x	DEAD/DEAH box RNA helicase protein, putative
264940_at	At1g60470	-1.2	1.3	8.0	7.0	1.9	3.2	x	galactinol synthase, putative
259908_at	At1g60850	-1.1	-1.1	2.5	3.0	1.3	1.7	x	RNA polymerase subunit
265032_at	At1g61580	-1.5	1.2	1.2	2.0	2.6	7.0	x	ribosomal protein
265061_at	At1g61640	1.1	1.0	3.2	3.0	2.5	2.3	x	expressed protein (similar to ABC transporter protein)
264400_at	At1g61800	1.5	3.0	8.0	24.3	3.0	22.6	x	glucose-6-phosphate/phosphate-translocator, putative
265119_at	At1g62570	-1.2	1.1	17.1	17.1	8.0	5.7	x	flavin-containing monooxygenase (similar to glutamate synthase)
262644_at	At1g62710	1.0	-1.1	8.0	9.8	3.7	4.3	x	vaucular cystein proteinase (beta-VPE)
262691_at	At1g62740	-1.1	-1.2	2.6	2.8	2.3	1.5	x	TPR-repeat protein
260323_at	At1g63780	-1.1	-1.1	2.6	3.2	1.7	2.1	x	putative U3 small nucleolar ribonucleoprotein protein
260316_at	At1g63810	1.0	1.1	3.5	3.7	1.9	2.0	x	Nrap protein family
262336_at	At1g64220	-1.9	-1.1	4.3	4.0	3.0	1.9	x	hypothetical protein
261972_at	At1g64600	1.0	1.1	2.6	2.6	2.1	1.7	x	hypothetical protein

262881_at	At1g64890	1.0	1.2	13.0	8.0	3.2	3.2	x	x	expressed protein (integral membrane/transporter family)
264638_at	At1g65480	1.4	1.1	1.2	1.6	3.7	3.2	x	x	flowering locus T protein (FT)
260135_at	At1g66400	2.8	3.0	1.4	1.1	1.6	1.6			calmodulin-related protein, putative
264471_at	At1g67120	1.1	-1.4	3.5	2.6	2.3	2.1	x		hypothetical protein
264968_at	At1g67360	-1.4	-1.3	3.0	4.0	2.1	3.0	x		stress related protein
245200_at	At1g67850	1.1	1.2	3.0	3.7	2.8	2.6	x	x	expressed protein
260264_at	At1g68500	1.0	1.5	8.6	4.9	1.7	2.0	x		expressed protein
260209_at	At1g68550	1.2	1.2	2.5	2.5	1.2	1.7	x		AP2 domain transcription factor, putative
259672_at	At1g68990	1.1	1.2	2.8	2.6	1.1	1.6	x		DNA-directed RNA polymerase
259367_at	At1g69070	1.1	1.1	3.7	3.0	2.6	1.7	x		expressed protein
260343_at	At1g69200	1.1	1.1	2.1	2.6	2.5	2.5		x	fructokinase (Fk1), putative
260338_at	At1g69250	-1.1	1.0	4.0	4.6	2.3	2.5	x		putative RNA-binding protein
259834_at	At1g69570	1.9	1.1	5.3	5.7	6.1	4.6	x	x	H-protein promoter binding factor-2b like
260410_at	At1g69870	1.4	1.5	8.0	6.5	2.0	2.6	x		putative proton-dependent oligopeptide transport (POT) protein
260365_at	At1g70630	2.1	-1.1	3.0	2.5	3.0	1.5	x		hypothetical protein
257487_at	At1g71850	1.1	-1.1	2.6	2.6	-1.1	1.4	x		hypothetical protein
260398_at	At1g72320	-1.1	-1.1	3.2	2.5	1.7	2.0	x		pumilio-family RNA-binding protein, putative
260425_at	At1g72440	1.1	1.2	3.2	3.2	1.3	2.1	x		CCAAT-box-binding transcription factor related
262383_at	At1g72940	2.5	5.7	-1.5	1.0	-2.5	2.0	x		disease resistance protein (TIR-NBS class), putative
245734_at	At1g73480	1.5	1.3	11.3	7.0	6.5	3.0	x	x	putative lysophospholipase
260076_at	At1g73630	1.2	1.1	3.5	2.8	1.7	2.0	x		putative calmodulin protein
260062_at	At1g73710	1.0	1.2	2.5	3.0	2.0	1.1	x		hypothetical protein
260046_at	At1g73800	1.5	2.0	-1.3	1.9	3.5	4.0		x	calmodulin-binding protein
260068_at	At1g73805	1.6	2.1	-1.1	1.5	4.0	3.5		x	calmodulin-binding protein
262219_at	At1g74750	1.1	-1.3	3.5	2.6	2.3	1.3	x		hypothetical protein
262212_at	At1g74890	4.0	3.7	-1.7	1.1	-1.1	1.7			response regulator 15 (ARR15)
259925_at	At1g75040	1.9	1.1	7.5	8.6	13.0	18.4	x		thaumatin-like protein
256505_at	At1g75200	1.1	1.0	2.5	2.5	3.2	2.5	x	x	flavodoxin family
261116_at	At1g75370	1.1	1.1	3.2	2.5	1.0	1.1	x		SEC14 cytosolic factor, putative / phosphatidylinositol transfer-like protein
261114_at	At1g75390	-1.2	1.1	3.0	2.5	-1.6	-1.3	x		bZIP transcription factor ATB2, putative
262953_at	At1g75670	-1.1	-1.1	3.0	3.2	1.5	2.1	x		expressed protein
262677_at	At1g75860	1.2	1.5	3.0	2.6	1.7	1.3	x		unknown protein

262682_at	At1g75900	-1.1	1.1	3.2	3.2	2.5	4.3	x	family II extracellular lipase 3 (EXL3)
261728_at	At1g76160	1.1	1.1	3.0	3.0	1.7	1.7	x	pectinesterase (pectin methylesterase), putative
259971_at	At1g76580	1.1	1.3	4.3	5.3	1.4	1.3	x	squamosa promoter binding protein -related
259977_at	At1g76590	1.9	1.6	5.3	3.2	2.5	-1.1	x	expressed protein
259979_at	At1g76600	2.6	2.8	-2.0	-1.5	-1.5	-1.6	x	expressed protein
264948_at	At1g77050	1.0	1.6	4.6	6.5	2.3	3.2	x	DEAD/DEAH box helicase, putative
264953_at	At1g77120	-1.4	1.0	4.9	8.0	-1.1	2.8	x	alcohol dehydrogenase
262164_at	At1g78070	1.1	-1.3	4.6	4.0	3.0	1.7	x	expressed protein
260804_at	At1g78410	4.0	2.6	1.3	-4.3	8.0	7.0	x	VQ motif-containing protein family
263134_at	At1g78570	-1.1	1.1	3.0	4.0	1.3	2.5	x	trehalose-6-phosphate synthase, putative
263127_at	At1g78610	1.1	1.4	2.6	2.6	1.9	1.2	x	hypothetical protein
264118_at	At1g79140	-1.1	-1.1	4.6	5.7	3.7	2.8	x	expressed protein
264131_at	At1g79150	1.0	1.1	3.7	3.2	1.6	2.6	x	hypothetical protein
262946_at	At1g79390	-1.2	1.0	1.4	2.0	2.8	2.6	x	expressed protein
262943_at	At1g79470	-1.4	-1.9	2.5	3.0	1.7	1.7	x	inosine-5'-monophosphate dehydrogenase, putative
262050_at	At1g80130	1.2	1.1	24.3	45.3	27.9	45.3	x	expressed protein (COR33.5)
260331_at	At1g80270	-1.3	1.2	4.9	6.5	2.0	3.2	x	DNA binding protein, putative
260287_at	At1g80440	2.8	2.5	-3.5	-4.9	-1.9	-3.0	x	Kelch repeat containing F-box protein family
261911_at	At1g80750	-1.5	1.1	3.2	3.2	1.9	3.0	x	60S ribosomal protein L7 (RPL7A)
261892_at	At1g80840	4.0	4.0	1.3	1.1	1.9	1.1	x	WRKY family transcription factor (WRKY40)
266119_at	At2g02100	1.0	1.3	2.8	3.2	2.8	3.0	x	putative plant defensin protein putative (PDF2.2)
266141_at	At2g02120	-1.3	-1.5	5.7	6.1	8.0	12.1	x	putative plant defensin protein putative (PDF2.1)
263334_at	At2g03820	1.1	1.2	3.0	3.0	1.3	1.9	x	nonsense mediated mRNA decay protein NMD3 family
263854_at	At2g04430	-1.1	-1.3	1.2	2.0	2.6	2.6	x	putative muT domain protein
263852_at	At2g04450	1.0	1.2	1.1	1.1	3.7	5.7	x	MutT/nudix family protein
263864_at	At2g04530	1.1	1.2	1.6	2.1	2.8	4.0	x	hypothetical protein
265561_s_at	At2g05510	-1.1	-1.9	1.5	1.5	4.3	4.0	x	putative glycine-rich protein
266932_s_at	At2g07750	1.6	1.7	6.5	5.3	1.6	3.5	x	DEAD/DEAH box helicase, putative
265837_at	At2g14560	-1.1	1.1	-3.0	-2.6	3.2	3.5	x	expressed protein
266385_at	At2g14610	1.7	1.3	2.1	1.3	48.5	48.5	x	pathogenesis-related protein 1 (PR-1)
265474_at	At2g15690	1.1	1.1	4.3	3.2	2.1	1.7	x	expressed protein
265480_at	At2g15970	-1.1	-1.1	4.9	4.9	4.0	2.6	x	similar to cold acclimation protein WCOR413 (WCOR413-PM1)
266532_at	At2g16890	1.1	2.5	13.0	14.9	3.5	9.8	x	putative phenylpropanoid glucosyltransferase

263574_at	A12g16990	-1.3	-1.1	3.2	3.2	1.5	1.5	x	putative tetracycline transporter protein
263421_at	A2g17230	1.1	2.6	3.5	3.2	1.7	1.9	x	phosphate-induced protein 1 family
263415_at	A2g17250	-1.1	1.1	2.5	3.0	1.6	1.9	x	hypothetical protein
264907_at	A2g17280	-1.1	1.2	3.0	4.6	1.1	1.5	x	expressed protein
264787_at	A2g17840	-1.2	-1.1	8.6	7.5	3.5	2.5	x	ERD7
265326_at	A2g18220	1.1	-1.4	4.3	3.7	1.7	2.3	x	expressed protein
265931_at	A2g18520	1.1	1.3	4.3	6.5	1.4	3.7	x	pentatricopeptide (PPR) repeat-containing protein
266946_at	A2g18890	1.4	1.3	4.3	3.7	2.8	1.5	x	putative protein kinase
266934_at	A2g18900	-1.1	1.3	4.9	4.6	1.7	2.1	x	WD-40 repeat protein family
267309_at	A2g19385	1.0	-1.1	3.2	3.2	2.0	2.3	x	expressed protein
267280_at	A2g19450	-1.2	1.3	3.0	2.5	1.2	1.4	x	diacylglycerol O-acyltransferase (TAG1)
265387_at	A2g20670	3.5	4.6	-2.5	-3.0	-1.9	-1.6	x	expressed protein
264019_at	A2g21130	-1.1	-1.1	3.5	2.5	2.0	1.2	x	peptidyl-prolyl cis-trans isomerase (cyclophilin/CYP2)
263739_at	A2g21320	1.2	-1.5	4.9	4.9	2.8	2.6	x	CONSTANS B-box zinc finger family protein
263766_at	A2g21440	1.0	-1.1	3.0	3.2	2.3	1.9	x	RNA recognition motif (RRM) - containing protein
263517_at	A2g21620	-1.1	-1.1	3.2	3.2	2.3	2.0	x	responsive to dessiccation protein (RD2) family
263548_at	A2g21660	1.0	1.1	3.5	2.5	2.6	1.7	x	glycine-rich RNA binding protein AtGRP7
263352_at	A2g22080	-1.2	1.5	3.0	4.9	-1.1	2.5	x	related to En/Spm transposon family of maize
263452_at	A2g22190	1.1	1.1	4.0	2.8	1.7	1.2	x	putative trehalose-6-phosphate phosphatase
264000_at	A2g22500	1.7	2.8	2.6	3.0	1.1	2.6	x	mitochondrial carrier protein family
265290_at	A2g22590	-1.4	-1.2	17.1	8.0	2.6	2.1	x	putative anthocyanidin-3-glucoside rhamnosyltransferase
266830_at	A2g22810	1.3	1.9	3.7	9.2	1.5	3.5	x	1-aminocyclopropane-1-carboxylate synthase 4 (ACC synthase 4)
266797_at	A2g22840	1.4	1.2	2.8	2.5	2.3	1.1	x	expressed protein
267261_at	A2g23120	1.2	1.1	6.5	5.7	5.3	2.6	x	expressed protein (COR8.5)
245076_at	A2g23170	1.1	1.3	3.5	2.5	1.1	2.1	x	unknown protein
245078_at	A2g23340	1.0	-1.2	2.8	2.8	-1.5	1.1	x	AP2 domain transcription factor (RAP2.6)
266578_at	A2g23910	-1.4	1.1	4.9	4.3	1.2	1.1	x	putative cinnamoyl CoA reductase
266567_at	A2g24050	-1.1	1.0	4.0	3.5	3.0	2.3	x	putative eukaryotic initiation factor 4 (eIF4)
265999_at	A2g24100	1.2	-1.2	3.2	2.5	4.0	2.3	x	expressed protein
265662_at	A2g24500	1.0	1.0	3.7	3.0	1.3	1.9	x	C2H2-type zinc finger protein (FZF)
263789_at	A2g24560	1.1	1.5	48.5	12.1	-1.1	-1.3	x	putative GDSL-motif lipase/hydrolase
257435_at	A2g24590	-1.1	1.1	2.6	2.5	2.0	3.0	x	putative RSZp22 splicing factor
263585_at	A2g25210	-1.3	-1.1	1.4	1.4	2.5	2.5	x	60S ribosomal protein L39

266656_at	At2g25900	2.5	2.8	-2.0	-3.5	-1.4	-1.6	x	putative CCH-type zinc finger protein
245035_at	At2g26400	1.1	2.5	-1.5	1.1	3.2	11.3	x	acireductone dioxygenase (ARD) family
266253_at	At2g27840	-1.7	1.0	2.8	4.0	1.6	4.9	x	unknown protein
264057_at	At2g28550	1.4	1.1	3.0	2.8	2.8	1.6	x	AP2 domain protein RAP2.7
263435_at	At2g28600	1.1	-1.1	2.8	2.5	1.5	2.1	x	putative ATP-dependent RNA helicase
263412_at	At2g28720	-1.1	1.4	3.5	2.6	2.1	1.9	x	putative histone H2B
266225_at	At2g28900	-1.3	1.0	8.0	7.0	4.9	3.5	x	putative membrane channel protein
266778_at	At2g29090	2.5	2.3	3.2	2.8	1.2	1.4	x	taxane 13-alpha-hydroxylase(cytochrome p450 family), putative
255866_at	At2g30350	-1.2	1.3	1.9	3.2	3.2	3.0	x	hypothetical protein
267201_at	At2g31010	1.1	1.2	4.3	3.7	2.0	1.3	x	putative protein kinase
266471_at	At2g31060	-1.1	1.1	2.8	2.5	1.9	2.1	x	putative GTP-binding protein
263249_at	At2g31360	1.0	1.3	4.9	4.0	3.2	2.1	x	delta 9 desaturase (ADS2)
267004_at	At2g34260	-1.1	-1.1	2.6	3.5	1.9	2.1	x	G-protein beta-subunit (transducin) family
267044_at	At2g34350	-1.1	1.2	3.2	6.1	1.5	2.8	x	nodulin-like protein
266903_at	At2g34570	-1.1	-1.5	4.0	3.5	2.8	2.8	x	expressed protein
266908_at	At2g34650	-2.3	1.3	3.0	9.8	-1.6	8.0	x	protein kinase (PINOID/PID)
267411_at	At2g34930	-1.1	1.6	5.7	4.3	3.7	2.0	x	putative disease resistance protein
263951_at	At2g35960	1.1	1.0	4.6	5.7	3.7	2.3	x	putative harpin-induced protein
263931_at	At2g36220	1.9	1.9	3.2	2.8	3.0	1.1	x	expressed protein
265210_at	At2g36620	-1.1	-1.1	1.5	1.6	2.5	3.2	x	60S ribosomal protein L24
265962_at	At2g37460	1.2	1.3	2.5	3.0	2.3	2.1	x	nodulin-like protein
267162_s_at	At2g37690	-1.3	-1.1	3.5	3.5	2.0	3.0	x	phosphoribosylaminoimidazole carboxylase (AIR carboxylase), putative
267165_at	At2g37710	1.2	1.2	1.7	1.5	3.2	3.2	x	putative receptor-like protein kinase
266093_at	At2g37990	-1.1	-1.1	3.0	3.2	2.0	2.1	x	expressed protein
267028_at	At2g38470	3.5	4.0	-1.6	-1.1	1.5	1.1	x	WRKY family transcription factor (WRKY33)
266980_at	At2g39390	-1.4	1.0	1.5	1.9	3.0	3.0	x	60S ribosomal protein L35 (RPL35B)
266965_at	At2g39510	1.3	1.7	3.2	5.3	4.9	10.6	x	nodulin MtN21 family protein
267592_at	At2g39710	1.3	1.3	4.6	3.7	2.3	2.8	x	expressed protein
267361_at	At2g39920	1.4	1.3	3.2	2.3	6.1	2.8	x	expressed protein
267357_at	At2g40000	2.6	3.0	-5.7	-3.0	-1.6	-2.6	x	unknown protein
267349_at	At2g40010	1.0	1.1	2.5	2.8	2.1	4.0	x	60S acidic ribosomal protein P0
263384_at	At2g40130	1.7	2.0	2.6	3.0	-1.3	1.0	x	expressed protein

263379_at	At2g40140	3.5	2.5	2.5	1.9	2.5	1.4	x	putative CCCH-type zinc finger protein
263824_at	At2g40360	-1.1	-1.1	2.5	2.5	1.2	1.5	x	putative WD-40 repeat protein
263802_at	At2g40430	1.0	1.0	3.0	2.6	2.5	2.0	x	expressed protein
255877_at	At2g40460	1.3	1.5	3.5	4.3	1.0	1.5	x	putative PTR2 family peptide transporter
266076_at	At2g40700	1.0	1.1	2.6	3.2	1.4	2.0	x	DEAD/DEAH box RNA helicase protein, putative
266049_at	At2g40780	1.0	-1.9	2.6	3.0	2.3	1.7	x	putative translation initiation factor
263495_at	At2g42530	1.0	2.0	78.8	39.4	59.7	26.0	x	COR15b
263497_at	At2g42540	-2.6	5.3	137.2	294.1	168.9	157.6	x	COR15a
260560_at	At2g43590	-1.2	-1.1	1.3	-1.2	3.0	2.8	x	glycosyl hydrolase family 19 (chitinase)
260556_at	At2g43620	1.3	1.3	7.0	5.7	3.2	3.0	x	putative endochitinase
260585_at	At2g43650	1.1	1.5	3.5	3.2	-1.3	2.0	x	expressed protein
267371_at	At2g44510	-1.2	-1.1	2.8	2.6	2.1	1.6	x	Expressed protein
267509_at	At2g45660	1.4	1.2	3.7	3.2	1.7	1.4	x	MADS-box protein (AGL20)
266916_at	At2g45860	1.0	-1.1	2.3	1.9	3.2	2.5	x	hypothetical protein
266720_s_at	At2g46790	-1.2	-1.4	6.1	4.3	5.7	2.8	x	pseudo-response regulator (APRR9/TL1)
266719_at	At2g46830	1.5	1.1	2.6	4.0	1.5	1.9	x	MYB-related transcription factor (CCA1)
263320_at	At2g47180	1.3	-1.2	8.0	3.2	4.6	1.7	x	galactinol synthase
266514_at	At2g47890	-1.2	1.1	4.0	3.7	1.7	1.2	x	CONSTANS B-box zinc finger family protein
266510_at	At2g47990	-1.2	1.1	4.9	4.3	1.4	2.6	x	WD-40 repeat protein family
265771_at	At2g48030	-1.1	1.0	2.6	2.5	2.5	1.5	x	expressed protein
259278_at	At3g01160	1.0	1.1	3.7	3.2	2.5	2.0	x	expressed protein
258996_at	At3g01800	-1.5	1.1	3.0	3.0	1.9	2.1	x	putative ribosome recycling factor
258998_at	At3g01820	1.1	1.2	3.5	3.5	1.3	1.6	x	putative adenylate kinase
259132_at	At3g02250	1.0	1.9	2.6	3.5	1.4	2.1	x	similar to auxin-independent growth promoter
258871_at	At3g03060	-1.2	1.1	4.0	5.3	2.0	2.8	x	putative 26S proteasome regulatory subunit
259173_at	At3g03640	-1.5	1.0	4.9	3.7	1.6	2.3	x	beta-glucosidase (GLUC)
258805_at	At3g04010	-1.4	1.0	4.0	3.0	1.3	1.4	x	putative beta-1,3-glucanase
258800_at	At3g04550	-1.1	1.1	2.5	2.1	3.2	2.5	x	expressed protein
258792_at	At3g04640	2.5	3.7	1.1	1.3	1.9	1.2	x	glycine-rich protein
259096_at	At3g04840	1.1	1.0	1.6	1.9	2.6	2.6	x	putative 40S ribosomal protein S3A (S phase specific)
259311_at	At3g05060	-1.2	-1.1	3.2	4.3	1.9	2.8	x	putative SAR DNA-binding protein
259105_at	At3g05500	-1.1	1.3	3.0	3.2	1.6	3.0	x	putative stress related protein
258893_at	At3g05660	1.0	-1.1	8.6	7.0	7.0	2.5	x	disease resistance protein
258742_at	At3g05800	1.7	2.8	4.3	3.2	3.5	2.5	x	hypothetical protein

258505_at	At3g06530	-1.1	1.1	4.9	4.9	2.3	2.8	x	expressed protein
258532_at	At3g06700	-1.1	-1.1	1.6	1.9	3.0	3.7	x	60S ribosomal protein L29 (RPL29A)
258545_at	At3g07050	-1.6	1.1	3.5	6.5	1.9	4.9	x	putative GTPase
259018_at	At3g07390	-1.1	1.2	3.0	3.2	2.6	2.3	x	auxin-induced protein (AIR12)
259227_at	At3g07750	-1.4	-1.2	2.6	3.5	1.6	2.0	x	putative 3' exonuclease
258692_at	At3g08640	-1.1	1.3	2.5	2.6	2.0	2.8	x	unknown protein
258979_at	At3g09440	-1.2	-1.4	3.2	2.8	1.2	1.1	x	heat-shock protein (At-hsc70-3)
258719_at	At3g09540	-1.3	1.1	7.0	9.2	2.3	3.7	x	putative pectate lyase
258965_at	At3g10530	1.1	1.2	7.5	6.1	3.5	3.0	x	WD-40 repeat protein family
256442_at	At3g10930	4.0	16.0	-7.5	-1.3	1.2	5.3	x	expressed protein
256438_s_at	At3g11120	-1.1	1.1	1.6	2.0	3.5	3.2	x	60S ribosomal protein L41 (RPL41E)
256661_at	At3g11964	-1.2	1.0	3.5	4.0	2.5	3.5	x	putative pre-rRNA processing protein
256288_at	At3g12270	-1.1	-1.1	4.3	4.9	3.0	2.6	x	putative arginine N-methyltransferase
256266_at	At3g12320	1.4	1.1	3.2	3.0	3.0	2.5	x	expressed protein
257702_at	At3g12670	-1.2	-1.1	3.7	3.5	1.4	1.5	x	CTP synthase (UTP-ammonia ligase), putative
257694_at	At3g12860	1.1	1.1	4.0	4.6	1.9	1.9	x	putative nucleolar protein
257188_at	At3g13150	1.0	1.4	3.5	4.9	2.1	2.8	x	pentatricopeptide (PPR) repeat-containing protein
257658_at	At3g13230	-1.3	-1.1	3.5	3.2	1.9	2.3	x	expressed protein
256649_at	At3g13570	-1.1	-1.1	2.6	2.8	2.1	1.7	x	arginine/serine-rich splicing factor SCL30a
256779_at	At3g13784	1.0	-1.2	3.2	3.2	18.4	17.1	x	similar to beta-fructofuranosidase
258202_at	At3g13940	-1.1	1.4	3.5	3.7	1.1	1.6	x	expressed protein
258204_at	At3g13960	1.4	1.6	2.6	2.6	2.1	1.2	x	hypothetical protein
257280_at	At3g14440	2.5	-2.1	4.0	3.0	3.0	-1.1	x	9-cis-epoxycarotenoid dioxygenase (NCED3)
258094_at	At3g14690	1.1	-1.1	2.5	2.6	1.5	1.1	x	putative cytochrome P450
257237_at	At3g14890	-1.1	-1.1	7.5	8.0	2.3	3.2	x	DNA nick sensor, putative
257218_at	At3g15000	1.0	1.0	2.6	2.6	2.1	1.6	x	expressed protein
257267_at	At3g15030	1.2	1.3	3.7	3.0	2.6	1.1	x	TCP family transcription factor, putative
257211_at	At3g15080	-1.2	1.2	3.7	3.5	1.7	2.1	x	exonuclease, putative
258396_at	At3g15460	1.0	1.0	4.0	4.0	2.6	3.2	x	expressed protein
258270_at	At3g15650	-1.9	1.1	3.2	4.0	-1.6	1.5	x	putative lysophospholipase
257652_at	At3g16810	-1.1	1.1	4.6	4.6	1.7	2.8	x	expressed protein
257876_at	At3g17130	1.0	-1.1	8.0	10.6	2.6	3.0	x	hypothetical protein, similar to invertase/pectin methylesterase inhibitor
258220_at	At3g17830	1.3	2.0	2.8	4.3	4.3	4.9	x	heat shock protein dnaJ family

258215_at	At3g17970	1.1	1.1	2.6	2.5	1.5	2.3	x	phosphoprotein phosphatase, putative
258217_at	At3g17990	-1.1	1.1	1.9	2.8	3.7	6.5	x	phosphoethanolamine N-methyltransferase 1 (AtNMT1)
258218_at	At3g18000	-1.1	1.0	2.1	3.0	5.3	5.7	x	phosphoethanolamine N-methyltransferase 1 (AtNMT1)
258155_at	At3g18130	-1.1	1.1	2.5	3.2	2.0	4.6	x	protein kinase C-receptor/G-protein, putative
256797_at	At3g18600	-1.3	-1.1	4.6	5.3	2.8	3.5	x	DEAD/DEAH box helicase, putative
256891_at	At3g19030	2.6	2.6	-1.9	-1.7	1.1	1.1	x	expressed protein
258009_at	At3g19440	1.2	1.3	3.7	3.0	2.6	1.5	x	pseudouridine synthase family
257076_at	At3g19680	2.0	2.6	3.0	2.5	1.5	1.1	x	expressed protein
256627_at	At3g19970	2.1	1.6	3.0	2.5	2.5	1.9	x	expressed protein
257667_at	At3g20440	1.2	-1.1	2.6	2.6	4.9	3.7	x	similar to 1,4-alpha-glucan branching enzyme
258166_at	At3g21540	-1.1	1.2	6.1	5.7	2.0	2.5	x	WD-40 repeat protein family
258167_at	At3g21560	-1.1	1.0	2.6	2.5	-1.2	1.2	x	UDP-glucosyltransferase, putative
256766_at	At3g22231	-1.1	1.0	-1.3	1.1	2.6	3.0	x	pathogen and circadian controlled 1 (PCC1)
258449_s_at	At3g22310	-1.2	1.1	3.0	3.7	-1.4	2.5	x	putative RNA helicase
258316_at	At3g22660	-1.3	1.1	4.3	4.9	2.5	4.3	x	expressed protein
258321_at	At3g22840	1.2	1.3	26.0	32.0	7.0	7.5	x	early light-induced protein (ELIP)
258104_at	At3g23620	-1.4	-1.1	4.0	4.0	2.6	3.0	x	expressed protein
257173_at	At3g23810	1.1	-1.1	2.8	4.0	1.5	1.9	x	S-adenosyl-L-homocysteinas, putative
256910_at	At3g24080	1.1	1.3	2.6	2.6	1.1	1.9	x	hypothetical protein
256911_at	At3g24090	1.0	5.7	1.9	9.2	3.0	12.1	x	similar to glutamine-fructose-6-phosphate amidotransferase
257253_at	At3g24190	1.1	-1.1	2.8	3.5	-1.1	-1.2	x	expressed protein
256881_at	At3g26410	1.0	-1.1	3.2	3.2	2.6	1.9	x	expressed protein
257154_at	At3g27210	-1.1	1.0	3.7	3.7	3.7	2.5	x	expressed protein
257968_at	At3g27550	1.1	-1.3	3.2	2.8	1.3	1.4	x	expressed protein
256601_s_at	At3g28290	-1.3	1.1	3.5	2.0	29.9	21.1	x	integrin like protein (similar to At14a)
256595_x_at	At3g28530	1.3	2.1	4.0	5.7	-1.2	3.2	x	hypothetical protein
252679_at	At3g44260	3.2	3.0	-1.5	-1.4	-1.3	-1.5	x	CCR4-NOT complex protein, putative
252661_at	At3g44450	1.2	-1.1	2.5	2.5	1.7	1.7	x	putative protein
252639_at	At3g44550	1.3	1.6	3.2	4.3	2.6	3.0	x	acyl CoA reductase -like protein
252625_at	At3g44750	-1.4	-1.3	3.5	4.9	3.0	4.0	x	putative histone deacetylase
252563_at	At3g45970	2.0	3.5	4.0	2.6	1.3	-2.1	x	expansin protein family (EXPL1)
252417_at	At3g47480	-1.1	-1.4	-1.4	-1.6	3.7	2.5	x	putative calcium-binding protein
252429_at	At3g47500	2.0	1.1	4.3	2.8	3.5	1.7	x	H-protein promoter binding factor-2a

252374_at	At3g48100	6.1	4.9	-1.6	-2.8	1.6	1.1	x	response regulator 2 (ATTR2)
252355_at	At3g48250	1.0	-1.1	3.7	2.6	1.2	1.1	x	putative protein
252367_at	At3g48360	4.9	4.9	-4.6	-78.8	-1.6	-3.5	x	speckle-type POZ protein-related
252305_at	At3g49240	1.5	1.3	5.3	4.3	1.6	2.0	x	pentatricopeptide (PPR) repeat-containing protein
252239_at	At3g49990	-1.1	1.0	2.8	2.6	1.5	1.4	x	putative protein
252102_at	At3g50970	1.0	2.3	26.0	48.5	13.9	22.6	x	dehydrin (Xero2)
252123_at	At3g51240	-1.1	-1.2	4.3	5.3	1.0	1.5	x	flavanone 3-hydroxylase (FH3)
252034_at	At3g52040	-1.1	-1.1	3.0	2.6	3.0	2.1	x	putative protein
251984_at	At3g53260	1.4	1.4	3.0	3.2	1.1	2.0	x	phenylalanine ammonia-lyase 2 (PAL2)
251915_at	At3g53940	1.2	1.7	2.5	3.7	1.5	2.5	x	mitochondrial carrier protein family
251927_at	At3g53990	1.0	1.1	3.5	3.2	2.6	1.6	x	expressed protein
251899_at	At3g54400	-1.1	1.1	5.7	5.3	3.5	3.0	x	aspartyl protease family
251827_at	At3g55120	-1.1	1.0	5.7	5.3	1.9	2.6	x	chalcone-flavanone isomerase
251783_at	At3g55280	-1.2	-1.2	1.9	2.3	2.5	2.8	x	ribosomal L23a - like protein
251800_at	At3g55510	-1.1	1.1	7.0	8.6	4.0	4.6	x	expressed protein
251793_at	At3g55580	1.6	9.8	27.9	84.4	22.6	119.4	x	regulator of chromosome condensation RCC1 family
251775_s_at	At3g55610	1.1	-1.1	4.3	3.7	1.9	1.7	x	delta-1-pyrroline-5-carboxylate synthetase (P5CS2)
251776_at	At3g55620	-1.1	-1.1	2.5	2.5	1.5	1.7	x	putative eukaryotic translation initiation factor 6 (EIF-6)
251753_at	At3g55760	-1.1	-1.5	13.0	13.0	2.0	1.3	x	expressed protein
251768_at	At3g55940	-1.7	1.5	3.2	11.3	1.7	4.9	x	phosphoinositide-specific phospholipase C
251745_at	At3g55980	4.9	7.0	-1.1	1.1	1.2	1.0	x	zinc finger (CCH type) protein family
251735_at	At3g56090	-1.5	-1.1	3.0	4.3	5.3	7.0	x	putative protein ferritin 2 precursor
251705_at	At3g56400	2.0	4.3	-3.7	-2.1	2.6	3.2	x	WRKY family transcription factor (WRKY70)
246293_at	At3g56710	2.3	2.8	-1.5	-1.7	4.0	2.8	x	SigA binding protein
251678_at	At3g56990	-1.5	1.1	3.7	5.3	1.6	2.6	x	glycine-rich protein
251657_at	At3g57000	-1.2	-1.1	2.5	2.5	1.2	2.1	x	putative protein
251667_at	At3g57150	-1.1	1.1	2.6	3.5	1.7	3.5	x	putative protein
251673_at	At3g57240	1.4	1.0	1.7	2.5	19.7	9.8	x	glycosyl hydrolase family 17 (beta-1,3-glucanase bg3)
251625_at	At3g57260	1.4	1.2	-1.1	1.0	3.5	3.7	x	beta-1,3-glucanase 2 (BG2)
251593_at	At3g57660	1.1	1.2	4.0	3.7	1.9	2.0	x	DNA-directed RNA polymerase I
251611_at	At3g57940	-1.1	-1.2	4.6	4.0	2.6	1.7	x	expressed protein
251538_at	At3g58660	-1.4	1.3	4.3	5.3	-1.1	3.7	x	expressed protein
251494_at	At3g59350	1.2	2.1	3.7	2.5	1.6	-1.1	x	putative serine/threonine protein kinase (similar to Pto1)
251476_at	At3g59670	1.0	-1.1	3.2	2.6	1.9	2.6	x	putative protein

251432_at	At3g59820	1.1	-1.1	6.1	4.9	3.7	2.0	x	putative leucine zipper-EF-hand containing transmembrane protein
251371_at	At3g60360	-1.1	1.1	2.5	4.0	1.5	1.6	x	putative protein
251190_at	At3g62690	1.0	1.5	3.0	4.9	1.4	1.1	x	zinc finger (C3HC4-type RING finger) protein (ATL5)
251227_at	At3g62700	1.0	1.1	3.0	2.6	1.7	1.7	x	ABC transporter, glutathione-conjugate transporter, putative
251229_at	At3g62740	-1.9	1.0	4.0	5.3	4.3	3.7	x	beta-glucosidase-like protein
251197_at	At3g62960	1.4	2.8	2.1	7.0	2.5	4.9	x	glutaredoxin -like protein
255685_s_at	At4g00600	-1.1	1.0	2.5	3.0	1.4	2.1	x	putative tetrahydrofolate synthase
255568_at	At4g01250	2.6	2.8	-1.2	1.4	1.6	-1.1	x	WRKY family transcription factor (WRKY31)
255586_at	At4g01560	-1.2	-1.1	2.6	2.5	1.7	2.0	x	expressed protein
255524_at	At4g02330	2.0	2.5	6.1	5.7	5.7	8.0	x	pectinesterase family
255479_at	At4g02380	1.4	2.8	1.2	1.4	3.5	4.3	x	late embryogenesis abundant protein (SAG21)
255501_at	At4g02400	-1.1	-1.2	4.0	3.7	1.6	1.9	x	expressed protein
255403_at	At4g03400	1.7	1.2	4.9	2.6	4.3	1.3	x	auxin responsive protein, putative (GH3 family)
255278_at	At4g04940	-1.2	1.3	6.1	7.0	2.6	4.3	x	WD-40 repeat protein family
255259_at	At4g05020	-1.3	-1.3	3.7	3.5	1.9	2.6	x	NADH dehydrogenase - related
255225_at	At4g05410	-1.1	-1.1	4.9	4.6	2.1	3.2	x	WD-40 repeat protein family
255070_at	At4g09020	1.0	1.0	2.8	2.5	3.5	2.6	x	isoamylase-like protein
254963_at	At4g11060	-1.6	-1.1	2.8	2.5	1.5	1.7	x	putative protein
254926_at	At4g11280	2.6	2.8	1.2	1.2	1.1	1.1	x	ACC synthase (AtACS-6)
254850_at	At4g12000	1.0	-1.1	3.0	2.8	1.2	1.1	x	expressed protein
254857_at	At4g12120	1.4	-1.1	2.5	2.5	2.3	1.2	x	putative protein
254818_at	At4g12470	1.0	1.1	9.8	18.4	14.9	17.1	x	pEARLI 1-like protein
254805_at	At4g12480	-1.1	1.1	5.3	6.1	14.9	13.0	x	pEARLI 1
254832_at	At4g12490	-1.4	1.3	3.0	3.0	8.0	13.9	x	pEARLI 1-like protein
254819_at	At4g12500	-1.4	-1.1	3.0	3.2	5.7	5.7	x	pEARLI 1-like protein
254778_at	At4g12750	1.0	1.0	3.2	2.6	1.4	1.5	x	expressed protein
254740_s_at	At4g13890	-1.1	1.1	2.5	3.2	-1.2	1.9	x	glycine hydroxymethyltransferase - like protein
245311_at	At4g14320	-1.1	1.0	1.3	1.5	2.5	3.5	x	ribosomal protein
245306_at	At4g14690	1.6	1.6	27.9	32.0	2.8	3.5	x	early light-inducible protein like
245533_at	At4g15130	1.1	1.6	6.1	7.5	2.8	5.3	x	putative phosphocholine cytidyltransferase (AtCCT2)
245392_at	At4g15680	2.5	2.6	-2.5	-4.9	-10.6	1.4	x	glutaredoxin protein family
245505_at	At4g15690	2.5	3.2	-84.4	-11.3	-2.8	1.1	x	glutaredoxin

245512_at	At4g15770	-1.3	1.2	2.8	3.2	1.1	3.0	x	expressed protein
245494_at	At4g16390	1.1	1.1	2.0	2.1	2.8	3.2	x	salt-inducible protein homolog
245336_at	At4g16515	1.2	1.4	4.0	4.0	1.9	1.7	x	expressed protein
245437_at	At4g16630	-1.1	1.3	3.0	4.9	1.6	2.5	x	RNA helicase like protein
245346_at	At4g17090	1.4	1.2	5.3	7.5	3.2	2.1	x	glycosyl hydrolase family 14 (beta-amylase)
245250_at	At4g17490	9.2	8.6	-2.8	1.1	-1.9	-4.6	x	ethylene responsive element binding factor (AtERF6)
245427_at	At4g17550	1.0	1.0	14.9	13.9	3.5	2.8	x	glycerol-3-phosphate permease like protein
254656_at	At4g18070	-1.1	1.0	2.5	2.6	1.4	1.6	x	putative protein
254662_at	At4g18270	1.1	1.3	3.0	2.5	1.4	1.1	x	glycosyltransferase family 4 (ATTRANS11)
254667_at	At4g18280	1.2	1.2	4.0	3.5	3.7	2.3	x	glycine-rich cell wall protein
254670_at	At4g18390	1.1	1.1	4.6	3.2	2.0	1.0	x	TCP family transcription factor, putative
254563_at	At4g19120	1.1	1.2	4.9	4.0	2.6	3.2	x	early-responsive to dehydration protein (ERD3)
254446_at	At4g20890	-1.1	1.0	3.0	3.2	1.5	1.9	x	tubulin beta-9 chain (TUB9)
254355_at	At4g22380	-1.1	1.1	3.0	2.8	1.6	2.5	x	Ribosomal protein L7Ae - like
254314_at	At4g22470	2.1	1.3	2.5	1.7	4.6	3.0	x	protease inhibitor/seed storage/lipid transfer protein (LTP) family
254321_at	At4g22590	1.1	1.0	2.6	2.5	1.7	1.5	x	trehalose-6-phosphate phosphatase-like protein
254271_at	At4g23150	1.3	-1.1	1.1	2.0	3.7	3.2	x	serine/threonine protein kinase, putative
254243_at	At4g23210	1.0	1.3	-1.1	1.3	2.5	2.6	x	serine/threonine kinase - like protein
254255_at	At4g23220	1.6	1.1	1.2	1.1	4.9	2.5	x	serine/threonine kinase - like protein
254238_at	At4g23540	1.4	-1.1	4.6	3.0	4.6	2.5	x	expressed protein
254227_at	At4g23630	1.0	-1.2	2.5	3.2	1.4	1.7	x	expressed protein
254215_at	At4g23700	-1.6	-2.5	-1.1	1.5	2.5	2.6	x	putative Na ⁺ /H ⁺ -exchanging protein
254235_at	At4g23750	2.8	3.7	1.9	2.0	-1.9	1.1	x	AP2 domain transcription factor, putative
254188_at	At4g23920	-1.1	-1.3	3.5	2.8	1.2	1.2	x	putative UDP-glucose 4-epimerase
254120_at	At4g24570	11.3	17.1	3.0	2.8	1.5	2.1	x	mitochondrial carrier protein family
254085_at	At4g24960	-1.1	1.1	8.6	9.2	1.2	2.8	x	similar to abscisic acid-induced protein (HVA22D)
254076_at	At4g25340	-1.2	-1.1	4.3	6.5	2.3	3.7	x	expressed protein
254075_at	At4g25470	9.8	16.0	7.0	8.0	2.6	3.5	x	CBF2/DREB1c
254066_at	At4g25480	7.0	18.4	9.8	9.8	2.5	3.0	x	CBF3/DREB1a
254073_at	At4g25500	1.1	1.1	4.3	3.7	2.6	2.3	x	splicing factor (At-SRp40)
254080_at	At4g25630	-1.3	1.1	5.7	7.5	3.7	9.2	x	fibrillarin 2 (AtFib2)
254079_at	At4g25730	1.0	1.4	5.3	6.5	3.2	3.5	x	expressed protein
254043_at	At4g25990	2.8	2.5	5.7	3.0	3.7	3.2	x	weak similarity to CONSTANS-like 1 protein (CIL)

253975_at	At4g26600	1.0	1.3	7.5	6.5	2.0	3.5	x	expressed protein
253949_at	At4g26780	-1.3	1.4	3.0	3.5	1.7	2.6	x	co-chaperone grpE protein family
253915_at	At4g27280	2.8	4.3	-1.3	-1.1	-1.1	-1.1	x	calcium-binding EF-hand family protein
253917_at	At4g27380	-1.1	-1.3	3.2	3.7	3.2	3.7	x	expressed protein
253875_at	At4g27520	1.1	1.0	3.7	3.7	2.8	1.9	x	putative protein ENOD20 predicted GPI-anchored protein
253879_s_at	At4g27570	1.1	1.3	8.6	9.8	2.8	3.0	x	UDP rhamnose-anthocyanidin-3-glucoside rhamnosyltransferase
253892_at	At4g27620	1.1	1.1	2.5	2.5	2.6	1.6	x	expressed protein
253891_at	At4g27720	1.1	1.2	2.6	2.6	2.0	2.8	x	putative protein
253835_at	At4g27820	-1.1	1.1	4.0	3.5	1.0	1.2	x	putative beta-glucosidase beta-glucosidase
253841_at	At4g27830	1.1	1.0	4.6	3.0	1.5	1.1	x	putative beta-glucosidase
253828_at	At4g27970	1.2	1.4	3.0	2.5	1.9	1.7	x	putative protein
253848_at	At4g28020	1.1	1.2	2.1	2.6	3.2	2.8	x	putative protein
253777_at	At4g28450	-1.4	-1.1	3.7	2.8	2.3	2.1	x	WD-40 repeat protein family
253794_at	At4g28720	1.7	2.0	2.8	3.2	2.3	2.1	x	putative protein
253722_at	At4g29190	2.3	2.6	3.5	3.0	2.8	1.7	x	zinc finger (CCCH type) protein family
253695_at	At4g29510	-1.1	1.0	5.3	4.0	2.6	2.1	x	arginine methyltransferase (PAM1)
253643_at	At4g29780	3.2	4.9	1.1	1.7	1.0	1.0	x	expressed protein
253627_at	At4g30650	-1.4	1.5	13.0	11.3	9.8	9.8	x	hydrophobic protein (LT16A/RIC12A)
253585_at	At4g30720	1.0	1.1	1.9	1.9	4.3	2.5	x	expressed protein
253595_at	At4g30830	-1.3	-1.1	128.0	36.8	32.0	8.6	x	expressed protein (COR42)
253603_at	At4g30935	-1.1	-1.1	2.5	2.5	1.9	1.3	x	WRKY family transcription factor
253559_at	At4g31140	1.1	1.2	2.8	3.5	1.1	1.7	x	glycosyl hydrolase family 17
253490_at	At4g31790	-1.1	1.1	3.0	3.2	2.0	2.5	x	methyltransferase - like protein
253485_at	At4g31800	2.6	4.3	1.6	2.0	2.5	2.6	x	WRKY family transcription factor (WRKY18)
253482_at	At4g31985	-1.1	-1.1	1.3	1.5	2.8	2.6	x	Expressed protein
253425_at	At4g32190	1.1	1.1	3.7	3.7	1.5	1.1	x	expressed protein
253423_at	At4g32280	1.5	1.2	7.5	6.1	7.5	3.2	x	auxin-responsive protein AUX/IAA family
253405_at	At4g32800	2.5	4.3	5.3	5.7	3.0	11.3	x	AP2 domain transcription factor TINY, putative
253416_at	At4g33070	-1.3	1.1	9.8	13.9	2.3	7.0	x	pyruvate decarboxylase-1 (Pdc1)
253323_at	At4g33920	1.6	2.6	2.8	2.6	2.0	1.5	x	putative protein phosphatase
253322_at	At4g33980	1.9	4.0	5.7	4.3	3.5	1.9	x	expressed protein (COR28)
253254_at	At4g34650	-1.1	-1.6	4.9	3.7	1.1	1.1	x	squalene synthase (SQS2)
253203_at	At4g34710	-1.1	1.4	3.7	3.7	2.3	2.8	x	arginine decarboxylase (SPE2)

253252_at	At4g34740	1.1	1.4	4.9	5.3	2.0	3.5	x	amidophosphoribosyltransferase 2 precursor
253213_at	At4g34910	-1.4	-1.4	4.0	3.7	4.6	2.3	x	RNA helicase (RH16)
253219_at	At4g34990	-1.1	-1.1	3.2	2.6	1.1	1.0	x	MYB family transcription factor (MYB32)
253188_at	At4g35300	1.0	1.1	3.2	3.0	1.7	1.6	x	putative sugar transporter protein
253156_at	At4g35730	1.1	1.5	3.0	4.6	1.9	2.0	x	expressed protein
253104_at	At4g36010	2.5	3.5	17.1	12.1	2.6	2.5	x	thaumatin-like protein
253129_at	At4g36020	1.1	1.4	2.6	3.0	-1.1	2.0	x	glycine-rich protein
246282_at	At4g36580	-2.8	1.1	6.5	5.7	2.8	3.2	x	ATPase-like protein
246249_at	At4g36680	1.0	-1.2	3.2	2.5	1.7	1.9	x	salt-inducible like protein
246196_at	At4g37090	-1.1	-1.3	3.0	2.8	2.8	2.3	x	expressed protein
246253_at	At4g37260	2.0	3.7	2.5	2.5	1.2	1.6	x	MYB family transcription factor (MYB73)
253097_at	At4g37320	-1.1	-1.2	2.6	3.0	-1.2	1.9	x	cytochrome P450 family
253005_at	At4g38100	-1.3	-1.2	1.7	2.3	2.6	4.0	x	expressed protein
253027_at	At4g38150	1.0	1.3	2.8	2.8	1.1	1.6	x	putative protein
252986_at	At4g38380	1.0	1.1	4.6	4.6	4.0	5.7	x	hypothetical protein
252997_at	At4g38400	1.2	4.0	13.9	17.1	4.3	4.6	x	expansin protein family (EXPL2)
252956_at	At4g38580	1.0	1.1	8.6	6.1	4.0	4.3	x	farnesylated protein (ATFP6)
252952_at	At4g38710	-1.1	1.1	2.5	2.5	1.2	1.2	x	putative protein
252885_at	At4g39260	1.0	1.2	3.7	2.6	-1.4	-1.4	x	glycine-rich RNA-binding protein 8 (GRP8)
252880_at	At4g39730	-1.1	-1.1	3.2	3.5	3.0	2.1	x	expressed protein
252863_at	At4g39800	1.0	-1.1	3.5	4.9	1.7	2.0	x	myo-inositol-1-phosphate synthase
252871_at	At4g40000	1.6	1.3	3.2	3.5	2.1	2.3	x	proliferating-cell nucleolar antigen - like protein
251109_at	At5g01600	-1.1	-1.1	1.1	1.3	2.8	2.6	x	ferritin 1 precursor
251058_at	At5g01790	1.1	-1.2	3.0	2.5	2.5	1.6	x	putative protein
251029_at	At5g02050	-1.1	-1.1	3.0	3.2	2.1	2.8	x	expressed protein
251017_at	At5g02760	1.2	-1.1	2.3	3.0	5.3	3.2	x	protein phosphatase 2C (PP2C) family
250974_at	At5g02820	-1.2	1.2	4.0	4.6	2.5	4.0	x	brassinosteroid insensitive 5 (BRI5/RHL2)
250942_at	At5g03350	1.2	2.5	1.0	1.9	8.0	16.0	x	legume lectin protein family (protein kinase family)
245714_at	At5g04280	1.0	1.1	2.5	3.0	-1.2	1.3	x	glycine-rich RNA-binding protein
245711_at	At5g04340	2.6	3.5	2.8	2.6	1.7	-1.1	x	putative c2h2 zinc finger transcription factor
250825_at	At5g05210	-1.2	1.1	4.0	3.5	2.5	2.1	x	expressed protein
250758_at	At5g06000	1.2	1.1	2.8	2.5	2.3	2.5	x	eukaryotic translation initiation factor 3 subunit, putative
250711_at	At5g06110	1.2	1.1	4.0	3.7	1.9	1.6	x	cell division related protein-like
250679_at	At5g06550	-1.3	1.1	3.0	3.0	1.6	2.1	x	hypothetical protein

250670_at	At5g06860	1.1	1.5	1.7	1.6	3.7	3.2	x	polygalacturonase inhibiting protein (PGIP1)
250665_at	At5g06980	1.2	1.1	4.0	3.7	2.0	2.5	x	expressed protein
250558_at	At5g07990	-1.1	1.2	3.5	2.8	1.0	-1.1	x	flavonoid 3'-hydroxylase (F3'H)
250517_at	At5g08260	-1.1	1.1	1.5	1.9	2.5	4.0	x	serine-type carboxypeptidase II-like protein
246055_at	At5g08380	-1.1	1.0	1.1	1.3	2.5	2.6	x	glycosyl hydrolase family 27 (alpha-galactosidase/melibiose)
246057_at	At5g08400	-1.2	-1.1	1.1	1.2	2.6	2.5	x	putative protein
250529_at	At5g08610	1.0	1.1	3.0	3.2	2.8	3.7	x	DEAD box RNA helicase, putative
250538_at	At5g08620	-1.1	1.1	3.2	3.2	1.6	2.3	x	DEAD box RNA helicase (RH25)
250533_at	At5g08640	1.0	-1.1	3.2	3.7	1.0	1.5	x	flavonol synthase (FLS)
245879_at	At5g09420	1.1	1.4	3.7	3.7	1.9	1.6	x	putative subunit of TOC complex chloroplast gene (Toc64)
245886_at	At5g09510	-1.1	1.0	2.0	2.1	2.8	2.5	x	ribosomal protein S15-like
250502_at	At5g09590	-1.1	-1.3	2.6	2.5	1.9	1.2	x	heat shock protein 70 (Hsc70-5)
250504_at	At5g09840	-1.3	-1.3	3.5	4.3	-2.5	1.7	x	expressed protein
250445_at	At5g10760	1.1	1.4	1.1	1.0	3.0	3.7	x	nucleoid DNA-binding protein cnd41-like protein
245904_at	At5g11110	-1.1	-1.1	8.6	5.3	2.1	1.3	x	sucrose-phosphate synthase, putative
250418_at	At5g11240	-1.1	1.5	4.3	4.9	1.7	3.0	x	WD-40 repeat protein family
250379_at	At5g11590	1.3	1.4	4.9	3.5	2.5	1.6	x	AP2 domain transcription factor TINY, putative
250309_at	At5g12220	1.0	1.1	5.3	2.6	1.5	1.5	x	expressed protein
250279_at	At5g13200	1.4	1.5	4.9	6.1	4.9	2.1	x	like ABA-responsive protein
250207_at	At5g13930	1.1	-1.2	3.0	5.7	1.6	2.6	x	chalcone synthase (naringenin-chalcone synthase)
250222_at	At5g14050	-1.2	-1.1	3.5	3.7	1.6	2.8	x	WD-40 repeat protein family
250192_at	At5g14520	-1.1	1.0	2.8	2.5	1.1	2.1	x	pescadillo - like protein
250151_at	At5g14570	-1.3	1.2	5.3	4.9	1.9	2.3	x	similar to trans-membrane nitrate transporter protein
250196_at	At5g14580	-1.4	1.1	3.0	3.5	1.1	2.1	x	polynucleotide phosphorylase
246550_at	At5g14920	-1.1	1.1	3.5	2.5	5.7	3.2	x	expressed protein
246566_at	At5g14940	1.1	1.4	2.6	2.6	3.0	2.6	x	oligopeptide transporter family
246559_at	At5g15550	-1.2	1.1	2.8	3.5	1.1	2.0	x	WD-40 repeat protein family
246527_at	At5g15750	-1.3	1.1	4.0	4.6	1.9	3.7	x	ribosomal protein-like
246490_at	At5g15950	1.2	1.1	4.9	6.1	2.5	3.7	x	S-adenosylmethionine decarboxylase (adoMetDC2)
246481_s_at	At5g15960	1.0	1.1	13.0	10.6	16.0	6.5	x	KIN1
246484_at	At5g16040	-1.2	1.2	3.5	4.3	2.8	2.8	x	regulator of chromosome condensation RCC1 family
246457_at	At5g16750	-1.3	-1.1	2.8	3.5	1.6	1.9	x	WD40-repeat protein

246461_at	At5g16930	1.0	-1.1	4.6	4.3	1.9	2.6	x	ATPase AAA family protein
246419_at	At5g17030	-1.6	-5.7	18.4	5.3	4.6	1.4	x	UDP glucose:flavonoid 3-o-glucosyltransferase family
246468_at	At5g17050	1.2	1.4	3.0	4.0	-1.5	1.4	x	similar to UDP glucose:flavonoid 3-o-glucosyltransferase
250062_at	At5g17760	-1.2	-1.1	3.0	3.7	1.4	2.6	x	putative AAA-type ATPase
250053_at	At5g17850	5.7	2.0	24.3	4.9	6.5	2.8	x	similar to sodium/calcium exchanger protein
250009_at	At5g18440	1.0	1.0	3.2	2.8	1.6	1.3	x	putative protein
249983_at	At5g18470	-1.1	1.5	-1.1	1.1	4.9	3.5	x	agglutinin (lectin) family
249977_at	At5g18820	-1.3	-2.3	3.5	1.7	7.0	2.6	x	chaperonin 60 alpha chain - like protein
245941_at	At5g19820	-1.1	-1.1	2.6	2.5	1.4	1.6	x	putative protein
246125_at	At5g19875	1.2	-1.1	3.5	2.5	1.4	1.2	x	expressed protein
246070_at	At5g20160	-1.2	-1.1	2.8	3.7	3.0	4.0	x	ribosomal protein L7Ae family
246073_at	At5g20180	-1.4	1.1	2.5	3.5	3.0	4.3	x	ribosomal protein family
246088_at	At5g20600	1.1	1.1	3.7	2.8	1.9	1.9	x	putative protein
245998_at	At5g20830	-1.1	1.1	7.5	7.0	3.0	3.0	x	sucrose synthase I (SUS1)
249938_at	At5g22330	-1.1	-1.1	2.6	2.6	2.1	2.0	x	Ruv DNA-helicase-like protein
249890_at	At5g22570	1.6	1.9	-2.5	-1.7	4.6	4.3	x	WRKY family transcription factor
249894_at	At5g22580	1.1	-1.1	-1.3	-1.4	2.8	3.5	x	expressed protein
249901_at	At5g22650	-1.1	-1.2	2.5	2.8	2.1	2.0	x	histone deacetylase-like protein
249859_at	At5g22840	-1.1	1.0	2.6	2.8	1.7	1.4	x	serine protein kinase-like protein
249916_at	At5g22880	1.0	1.3	1.1	1.9	2.6	2.8	x	histone H2B like protein
249848_at	At5g23220	-1.4	-1.2	6.1	4.3	2.8	2.5	x	expressed protein
249830_at	At5g23300	1.0	-1.1	2.6	2.6	2.0	2.0	x	dihydroorotate dehydrogenase precursor (dihydroorotate oxidase)
249806_at	At5g23850	-1.1	1.1	2.6	3.5	1.6	2.0	x	putative protein
249741_at	At5g24470	2.8	4.3	13.0	6.1	7.0	3.5	x	pseudo-response regulator (APRR5)
249750_at	At5g24570	-1.1	1.0	2.8	3.2	3.5	2.0	x	expressed protein
246965_at	At5g24840	-1.2	1.2	2.6	2.8	1.5	2.8	x	methyltransferase-like protein
246922_at	At5g25110	-1.4	1.1	7.0	7.0	3.5	5.7	x	serine/threonine protein kinase-like
246809_s_at	At5g27140	-1.1	-1.1	3.0	3.7	1.7	3.5	x	NOP58-like protein
246756_at	At5g27930	-1.1	1.0	3.2	2.5	1.6	1.1	x	protein phosphatase 2C (PP2C), putative
246178_s_at	At5g28430	3.0	5.7	5.7	7.5	2.8	5.3	x	hypothetical protein
249528_at	At5g38720	-1.3	1.1	4.0	5.3	1.9	3.5	x	expressed protein
249475_at	At5g38890	1.4	1.4	3.7	3.2	3.2	3.5	x	exoribonuclease-related
249454_at	At5g39520	-4.3	-2.0	1.1	2.1	2.6	2.6	x	expressed protein

249426_at	At5g39840	1.1	2.0	3.0	4.6	-1.4	2.0	x	putative ATP-dependent mitochondrial RNA helicase
249411_at	At5g40390	-1.1	-1.1	4.3	3.7	2.3	2.3	x	raffinose synthase
249354_at	At5g40480	-1.2	1.1	2.6	3.2	2.1	2.8	x	nuclear pore protein -like
249364_at	At5g40590	-1.3	-1.1	1.6	1.9	4.0	3.7	x	CHP-rich zinc finger protein, putative
249315_at	At5g41190	1.0	1.1	3.5	3.2	1.4	1.9	x	hypothetical protein
249303_at	At5g41460	1.4	-1.1	2.8	3.5	1.6	1.9	x	putative protein
249233_at	At5g42150	1.0	1.1	2.6	2.5	1.1	2.0	x	expressed protein
249204_at	At5g42570	-1.1	-1.1	5.3	4.6	2.5	2.1	x	expressed protein
249174_at	At5g42900	1.2	2.0	10.6	5.3	9.2	2.5	x	expressed protein
249091_at	At5g43860	1.1	-1.1	3.2	3.2	2.3	1.7	x	chlorophyllase (CLH2)
249011_at	At5g44670	1.2	1.3	3.5	3.2	1.0	2.1	x	expressed protein
254521_at	At5g44810	1.4	1.0	1.5	-6.1	4.9	3.2	x	expressed protein
248964_at	At5g45340	3.0	6.5	1.2	2.0	-2.8	1.1	x	cytochrome P450 family
248895_at	At5g46330	2.0	1.3	3.7	1.9	4.9	2.8	x	leucine-rich repeat transmembrane protein kinase, putative
248870_at	At5g46710	1.5	2.5	4.6	5.3	1.6	1.5	x	expressed protein
248820_at	At5g47060	1.2	1.1	3.5	2.8	1.6	1.2	x	expressed protein
248799_at	At5g47230	2.6	2.5	1.9	1.4	-1.2	1.1	x	ethylene responsive element binding factor 5 (AtERF5)
248762_at	At5g47455	-1.1	-1.1	3.7	3.5	4.0	3.0	x	expressed protein
248753_at	At5g47630	-1.4	1.3	2.0	3.5	2.8	4.0	x	acyl carrier protein-like
248749_at	At5g47880	1.1	1.3	3.5	3.5	1.2	2.3	x	eukaryotic release factor 1 (ERF1)
248732_at	At5g48070	-1.5	1.3	6.5	9.2	7.0	10.6	x	xyloglucan endo-1,4-beta-D-glucanase
248743_at	At5g48240	1.1	-1.1	3.7	3.0	1.9	2.3	x	hypothetical protein
248744_at	At5g48250	1.2	1.5	5.3	3.2	3.7	1.2	x	CONSTANS B-box zinc finger family protein
248625_at	At5g48880	1.0	1.0	3.5	3.7	1.3	1.4	x	acetyl-CoA C-acyltransferase 1 (3-ketoacyl-CoA thiolase 1)
248614_at	At5g49560	-1.3	1.1	3.0	2.5	2.6	4.0	x	expressed protein
248509_at	At5g50335	1.4	1.4	2.3	1.5	5.3	2.5	x	expressed protein
248496_at	At5g50790	1.2	1.4	3.2	2.6	-1.1	1.2	x	nodulin MtN3 family protein
248467_at	At5g50800	-1.1	1.1	4.9	5.3	4.3	5.3	x	nodulin MtN3-like protein
248448_at	At5g51190	4.0	6.1	-1.6	1.6	-1.4	-1.3	x	AP2 domain transcription factor, putative
248337_at	At5g52310	-1.1	2.0	68.6	78.8	36.8	32.0	x	COR78
248357_at	At5g52380	-1.1	-1.1	3.0	3.2	2.0	2.3	x	expressed protein
248326_at	At5g52820	-1.3	-1.1	3.2	2.8	1.9	2.1	x	Notchless protein homolog

248197_at	At5g54190	-4.0	-1.1	2.5	1.5	6.1	2.5	x	protochlorophyllide reductase A (PCRA/PORA)
248160_at	At5g54470	2.3	1.5	13.9	5.3	4.3	3.5	x	CONSTANS B-box zinc finger family protein
248164_at	At5g54490	2.5	2.5	1.2	1.4	2.5	1.1	x	calcium-binding EF-hand protein (PBP1)
248136_at	At5g54910	-1.1	-1.1	3.7	3.2	1.2	1.5	x	DEAD/DEAH box helicase, putative
248100_at	At5g55180	-1.1	1.2	5.3	4.6	1.1	2.0	x	beta-1,3-glucanase-like protein
248105_at	At5g55280	1.0	1.0	2.6	2.8	2.5	2.3	x	cell division protein FtsZ chloroplast homolog precursor
248062_at	At5g55450	-1.2	1.3	2.3	2.6	8.0	5.7	x	protease inhibitor/seed storage/lipid transfer protein (LTP) family
248036_at	At5g55920	-1.3	1.4	3.5	4.9	1.4	3.2	x	nucleolar protein-like
248045_at	At5g56030	-1.1	-1.2	2.8	2.6	1.1	1.7	x	HEAT SHOCK PROTEIN 81-2 (HSP81-2)
247968_at	At5g56670	-1.2	-1.1	1.3	1.5	2.8	2.6	x	40S ribosomal protein S30 homolog
247959_at	At5g57080	-2.0	-1.1	1.0	1.4	3.7	2.8	x	unknown protein
247937_at	At5g57110	-1.2	1.0	7.0	6.5	3.0	3.0	x	Ca ²⁺ -transporting ATPase (ACA8)
247942_at	At5g57120	-1.3	1.1	2.6	3.0	-1.2	2.0	x	putative protein
247949_at	At5g57220	3.2	7.5	-1.6	-2.1	-3.2	2.5	x	cytochrome P450, putative
247926_at	At5g57280	-1.3	1.2	4.0	4.3	1.4	2.5	x	protein carboxyl methylase-like
247900_at	At5g57290	-1.2	-1.1	1.3	1.6	2.5	2.5	x	60S acidic ribosomal protein P3
247871_at	At5g57530	-1.4	-1.1	3.5	2.0	3.5	3.0	x	xyloglucan endotransglycosylase, putative
247925_at	At5g57560	3.7	6.1	2.3	2.1	1.0	-1.6	x	TCH4
247921_at	At5g57660	1.6	1.4	6.1	3.7	5.7	2.6	x	CONSTANS B-box zinc finger family protein
247878_at	At5g57760	1.2	1.9	2.3	3.0	7.0	2.8	x	unknown protein
247838_at	At5g57990	1.2	-1.1	2.6	2.5	1.7	1.5	x	ubiquitin-specific protease 23 (UBP23), putative
247851_at	At5g58070	1.1	-1.3	4.6	3.5	2.6	1.6	x	outer membrane lipoprotein - like
247818_at	At5g58370	1.1	1.3	3.2	2.5	2.6	2.0	x	contains similarity to GTP-binding protein CGPA
247786_at	At5g58600	1.0	1.2	4.0	3.2	2.0	2.5	x	expressed protein
247774_at	At5g58660	-1.6	1.1	3.0	3.2	3.5	3.5	x	oxidoreductase, 2OG-Fe(II) oxygenase family
247776_at	At5g58700	1.0	1.0	4.3	3.2	1.2	1.3	x	phosphoinositide specific phospholipase C family
247797_at	At5g58780	1.3	-5.7	34.3	4.3	34.3	1.7	x	dehydrodichyl diphosphate synthase
247739_at	At5g59240	-1.5	1.2	2.8	7.5	1.6	3.0	x	40S ribosomal protein S8 (RPS8B)
247676_at	At5g59980	2.6	1.7	8.0	2.6	4.6	2.1	x	putative protein
247555_at	At5g61020	-1.3	-1.1	2.5	2.8	1.5	2.1	x	putative protein
247575_at	At5g61030	-1.4	1.4	2.8	5.7	2.0	4.6	x	glycine-rich RNA-binding protein
247566_at	At5g61170	-1.1	-1.1	1.9	1.9	2.5	3.0	x	40S ribosomal protein S19 - like
247580_at	At5g61330	1.2	-1.1	2.8	2.6	1.7	1.6	x	putative protein

247543_at	At5g61600	3.0	4.0	-1.7	-1.2	-1.3	-1.6	x	ethylene responsive element binding factor family
247541_at	At5g61660	-1.1	1.1	3.2	3.0	2.1	3.0	x	glycine-rich protein
247497_at	At5g61770	1.0	-1.1	4.0	3.7	2.5	2.6	x	like protein Peter Pan, <i>Drosophila melanogaster</i>
247498_at	At5g61810	1.0	1.0	3.5	3.0	1.4	1.3	x	peroxisomal Ca-dependent solute carrier - like protein
247463_at	At5g62210	1.0	1.4	7.5	10.6	1.2	3.0	x	contains similarity to embryo-specific protein 3
247474_at	At5g62280	1.1	1.3	3.5	4.6	5.3	3.7	x	expressed protein
247478_at	At5g62360	1.1	1.1	10.6	3.5	3.2	-1.4	x	similar to pectinesterase
247453_at	At5g62440	-1.2	1.1	2.8	2.8	1.6	2.5	x	expressed protein
247454_at	At5g62450	-1.3	-1.1	3.0	2.8	1.6	2.0	x	unknown protein
247406_at	At5g62920	4.0	3.7	-1.7	-3.0	-1.7	1.1	x	ARR6
247378_at	At5g63120	1.0	1.1	3.5	2.6	1.7	1.7	x	ethylene-responsive DEAD box RNA helicase, putative
247348_at	At5g63810	-1.3	1.2	2.0	2.5	3.2	2.8	x	glycosyl hydrolase family 35 (beta-galactosidase)
247277_at	At5g64420	1.0	1.1	3.5	3.5	1.6	1.9	x	DNA polymerase V family
247241_at	At5g64680	-1.1	1.0	2.6	2.5	2.3	2.1	x	unknown protein
247101_at	At5g66530	-1.1	1.1	1.4	1.4	2.8	3.0	x	apospory-associated protein C-like
247046_at	At5g66540	-1.4	1.2	4.6	4.0	3.0	2.6	x	expressed protein
244937_at	ndhH	5.7	2.3	2.6	2.6	1.6	1.9	x	NADH dehydrogenase 49KDa protein
245015_at	rbcl	6.5	1.5	4.3	6.1	8.0	4.3	x	large subunit of ribose-1,5-bisphosphate carboxylase/oxygenase
244998_at	rpoC1	3.5	1.4	2.6	1.7	4.0	2.8	x	RNA polymerase beta' subunit-1
244997_at	rpoC2	2.8	2.1	2.0	2.5	4.6	3.5	x	RNA polymerase beta' subunit-2
244996_at	rps2	2.1	1.9	1.6	1.7	2.6	2.8	x	ribosomal protein S2

The AGI identifier, the fold change values for each biological duplicate at each time (h), and the annotation for each probe set is shown. An "x" indicates times at which the probe set met the criteria (see Chapter 2) for being labeled cold responsive at a 2.5-fold level.

APPENDIX B

TABLE B.1. PROBE SETS DOWN-REGULATED BY LOW TEMPERATURE IN THE PLATE EXPERIMENT

Probe set	AGI	1h		24h		168h		Cold responsive			Annotation
		A	B	A	B	A	B	1h	24h	168h	
261570_at	At1g01120	-1.1	1.1	-1.5	-1.5	-2.8	-2.6			x	fatty acid elongase 3-ketoacyl-CoA synthase 1 (KCS1)
261572_at	At1g01170	-1.1	-1.2	-2.6	-2.8	-1.1	-2.0		x		unknown protein
262118_at	At1g02850	1.1	-1.3	-2.0	-2.8	-3.2	-6.1			x	glycosyl hydrolase family 1
263118_at	At1g03090	1.3	1.0	-4.6	-29.9	-1.3	-2.8		x		putative 3-methylcrotonyl-CoA carboxylase
263114_at	At1g03130	1.2	-1.1	-2.8	-3.0	-1.1	-1.9		x		photosystem I reaction center subunit II precursor
264365_s_at	At1g03220	-1.1	1.0	-2.8	-4.0	-1.9	-2.0		x		unknown protein
264354_s_at	At1g03240	-2.8	-2.1	-4.0	-2.1	-2.8	-3.5			x	unknown protein
265067_at	At1g03850	1.3	1.3	-4.0	-2.6	1.2	2.0		x		expressed protein
263668_at	At1g04350	-1.1	-1.4	-3.7	-4.0	-10.6	-12.1		x	x	putative 2-oxoglutarate-dependent dioxygenase
263184_at	At1g05560	1.0	1.0	-4.9	-3.2	-9.2	-8.0		x	x	UDP-glucose transferase(UGT1)
262626_at	At1g06430	1.1	1.0	1.2	1.2	-2.5	-3.7			x	FtsH protease, putative
262637_at	At1g06640	-1.1	-1.1	-1.7	-2.5	-3.0	-2.8			x	2-oxoglutarate-dependent dioxygenase
261081_at	At1g07350	-1.5	-2.5	-3.7	-4.3	-2.3	-4.9		x		putative transformer serine/arginine-rich ribonucleoprotein
261084_at	At1g07440	-1.1	-1.1	-3.2	-3.5	-2.6	-3.2		x	x	tropinone reductase, putative
260619_at	At1g08110	-1.1	-1.1	-2.5	-3.0	-4.9	-3.0		x	x	glyoxalase I, putative (lactoylglutathione lyase)
264255_at	At1g09140	-1.2	-1.5	-2.5	-2.6	-2.5	-3.5		x	x	arginine/serine-rich splicing factor, atSRp30
264507_at	At1g09415	1.3	-1.1	-3.7	-3.7	-1.3	-2.5		x		expressed protein
264463_at	At1g10150	-1.1	1.0	-3.0	-2.5	-3.5	-2.8		x	x	expressed protein
264435_at	At1g10360	-1.1	-1.2	-5.3	-4.6	-2.6	-2.6		x	x	glutathione S-transferase (GST29)
263236_at	At1g10470	1.5	1.9	-2.6	-3.0	-2.0	-1.1		x	x	putative response regulator 3
260481_at	At1g10960	1.3	-1.4	-1.9	-2.1	-4.6	-8.6			x	ferredoxin
262455_at	At1g11310	1.1	1.1	-3.0	-2.8	1.1	1.0		x		Mlo protein, putative
261868_s_at	At1g11460	1.0	-1.1	-1.6	-1.5	-16.0	-4.6			x	hypothetical protein
261826_at	At1g11580	-1.3	-1.3	-2.5	-4.9	-3.7	-3.2		x	x	pectin methylesterase
264342_at	At1g12080	-2.0	-1.3	-4.9	-3.0	-3.2	-3.7		x	x	expressed protein
260969_at	At1g12240	1.1	1.0	-2.8	-4.9	-1.4	-2.3		x		beta-fructosidase
260968_at	At1g12250	1.1	-1.1	-2.5	-3.5	-2.5	-3.0		x	x	chloroplast lumen pentapeptide protein, putative

261211_at	At1g12780	1.3	1.1	-3.2	-2.5	-1.6	-3.2	x	uridine diphosphate glucose epimerase
262826_at	At1g13080	-1.1	-1.3	-3.7	-3.0	-2.8	-2.3	x	putative cytochrome P450
256096_at	At1g13650	-1.2	-1.2	-17.1	-17.1	-29.9	-8.0	x	expressed protein
262615_at	At1g13950	-1.3	-1.6	-2.5	-9.2	-1.1	-2.0	x	initiation factor 5A-4
262607_at	At1g13990	1.3	-1.2	-2.8	-4.3	-2.6	-5.3	x	expressed protein
262608_at	At1g14120	1.1	-2.3	-14.9	-21.1	-29.9	-6.5	x	2-oxoglutarate-dependent dioxygenase, putative
262830_at	At1g14700	1.0	1.0	-5.7	-4.3	-3.5	-4.0	x	putative purple acid phosphatase
262603_at	At1g15380	-1.7	-1.6	-4.0	-2.8	-1.7	-3.2	x	expressed protein
259500_at	At1g15740	1.1	-1.1	-4.6	-4.0	-1.4	-2.5	x	expressed protein
261788_at	At1g15980	1.1	-1.1	-2.6	-2.8	-4.3	-3.5	x	expressed protein
261793_at	At1g16080	1.1	-1.4	-1.9	-1.7	-3.0	-3.2	x	expressed protein
262522_at	At1g17120	-1.1	-1.1	-2.0	-2.0	-2.8	-2.5	x	putative amino acid transporter
255895_at	At1g17990	1.2	1.2	-13.0	-6.1	-3.2	-2.8	x	similar to 12-oxophytodienoate reductase OPR1
255779_at	At1g18650	-1.1	-1.1	-3.0	-2.3	-2.5	-2.5	x	similar to beta-1,3-glucanase
259476_at	At1g19000	1.2	-1.4	-4.9	-4.3	-1.3	-3.5	x	MYB family transcription factor
256015_at	At1g19150	1.0	-1.1	-4.3	-4.9	-3.7	-4.9	x	PSI type II chlorophyll a/b-binding protein
260668_at	At1g19530	-1.4	-1.6	-4.3	-5.7	1.6	-1.1	x	expressed protein
261144_s_at	At1g19660	1.5	1.1	-4.6	-7.5	-4.3	-3.2	x	expressed protein
255786_at	At1g19670	-1.1	-1.7	-6.1	-7.0	-3.0	-3.7	x	chlorophyllase/coronatine-induced protein 1 (COR11)
261143_at	At1g19770	1.5	1.9	-2.8	-3.0	-2.8	-2.6	x	unknown protein
259545_at	At1g20560	1.0	1.2	-3.0	-2.6	-3.0	-3.0	x	expressed protein
262796_at	At1g20850	-1.1	-1.1	-1.1	-1.4	-2.8	-4.0	x	cysteine proteinase XCP2
261459_at	At1g21100	1.5	-1.1	-68.6	-97.0	-10.6	-27.9	x	O-methyltransferase 1, putative
260872_at	At1g21350	-1.1	-1.1	-2.8	-1.7	-3.5	-2.8	x	expressed protein
260877_at	At1g21500	1.1	1.0	-2.6	-3.5	-2.0	-2.6	x	expressed protein
261931_at	At1g22430	1.0	1.0	-3.0	-3.7	-2.5	-2.0	x	alcohol dehydrogenase ADH, putative
264774_at	At1g22890	1.1	-1.1	-3.5	-4.6	-2.6	-9.2	x	hypothetical protein
264751_at	At1g23020	1.0	-1.1	-3.2	-5.7	-21.1	-5.7	x	putative ferric-chelate reductase
264898_at	At1g23205	-1.2	-1.5	-1.9	-1.1	-3.2	-2.8	x	pectinesterase
262986_at	At1g23390	1.6	1.1	-7.5	-13.0	-1.9	-3.7	x	Kelch repeat containing F-box protein family
265175_at	At1g23480	-1.1	1.0	-3.0	-4.3	-2.3	-1.6	x	similar to cellulose synthase (AtCSLA03)
265182_at	At1g23740	1.1	-1.1	-2.3	-1.9	-4.6	-3.0	x	putative auxin-induced protein
263035_at	At1g23860	1.0	-1.5	-3.0	-3.7	-6.1	-11.3	x	splicing factor (SRZ_21)
263019_at	At1g23870	1.5	1.2	-3.0	-4.3	-1.5	-3.7	x	trehalose 6-phosphate synthase, putative

245637_at	At1g25230	-1.1	1.1	-3.7	-3.5	-1.6	-2.8	x	purple acid phosphatase family
245642_at	At1g25275	1.1	-1.1	-3.2	-4.0	1.3	-1.6	x	expressed protein
261016_at	At1g26560	1.1	1.1	-4.3	-3.7	-4.9	-3.0	x	glycosyl hydrolase family 1
261276_at	At1g26670	1.1	-1.3	-4.0	-4.3	-2.1	-5.3	x	v-SNARE protein (VT112/AtVT11b)
261265_at	At1g26800	-1.4	-1.5	-3.0	-4.0	-2.0	-2.8	x	expressed protein
264985_at	At1g27150	-1.3	-1.1	-2.5	-2.5	-1.2	1.0	x	expressed protein
264445_at	At1g27290	1.1	1.5	-3.2	-3.7	-2.1	-1.6	x	expressed protein
245668_at	At1g28330	1.0	1.0	-4.0	-4.9	-2.8	-4.9	x	dormancy-associated protein
262749_at	At1g28580	1.0	-1.1	-4.3	-4.0	-1.9	-1.5	x	putative lipase
262733_s_at	At1g28670	-1.3	-1.2	-3.5	-3.5	-3.7	-3.0	x	lipase (ARAB-1)
259791_at	At1g29700	1.1	-1.1	-1.4	-1.5	-2.6	-2.6	x	expressed protein
245776_at	At1g30260	-1.2	-1.3	-4.6	-6.1	-1.1	-2.0	x	expressed protein
261801_at	At1g30520	-1.3	-1.1	-6.1	-3.2	-2.5	-2.1	x	expressed protein
264497_at	At1g30840	-1.1	-1.2	-2.8	-4.3	-2.6	-3.2	x	expressed protein
263703_at	At1g31170	-1.1	-1.1	-2.8	-2.6	-2.1	-2.6	x	expressed protein
255718_at	At1g32070	-1.1	1.0	-2.1	-2.1	-2.8	-2.8	x	expressed protein
255719_at	At1g32080	1.1	-1.2	-1.3	-1.5	-2.6	-3.0	x	expressed protein
245792_at	At1g32100	1.0	-1.1	-2.0	-1.7	-5.7	-4.3	x	pinorensinol-lariciresinol reductase, putative
260651_at	At1g32460	1.0	1.0	-2.8	-2.6	-1.4	-2.5	x	expressed protein
261713_at	At1g32640	1.2	1.4	-2.5	-3.0	-4.0	-4.0	x	bHLH protein (RAP-1)
261982_at	At1g33780	1.0	-1.2	-2.5	-2.5	-1.6	-2.0	x	chloroplast lumen common protein family
261981_at	At1g33811	1.1	1.1	-2.5	-2.3	-4.9	-4.3	x	GDSL-motif lipase/hydrolase protein
256008_s_at	At1g34040	1.0	-1.3	-3.5	-2.8	-3.5	-6.5	x	allinase family
262407_at	At1g34630	1.1	1.3	-3.5	-3.5	-1.9	-2.6	x	hypothetical protein
262411_at	At1g34640	-1.3	-1.2	-4.0	-3.0	-1.7	-1.4	x	expressed protein
245783_s_at	At1g35180	-1.5	-1.1	-4.0	-22.6	-13.9	-45.3	x	expressed protein
260079_s_at	At1g35460	-1.2	1.1	-3.5	-2.5	-2.1	-1.7	x	bHLH protein
262725_at	At1g43580	-1.1	-1.1	-2.8	-3.2	-2.3	-1.6	x	expressed protein
260869_at	At1g43800	-1.6	-1.3	-32.0	-55.7	-59.7	-5.7	x	putative stearoyl acyl carrier protein desaturase
261324_at	At1g44770	-1.1	-1.1	-2.8	-3.0	-2.0	-2.1	x	unknown protein
260730_at	At1g48030	1.0	-1.1	-1.5	-1.9	-2.8	-2.5	x	lipamide dehydrogenase precursor
261309_at	At1g48600	1.0	-1.1	-1.9	-2.3	-3.5	-3.5	x	phosphoethanolamine N-methyltransferase
262473_at	At1g50250	1.0	-1.1	-1.5	-1.5	-2.8	-2.6	x	chloroplast FtsH protease
245745_at	At1g51115	-1.1	1.1	-1.4	-1.5	-3.5	-2.8	x	unknown protein

265149_at	At1g51400	1.3	-1.2	-8.6	-10.6	-2.1	-3.7	x	photosystem II 5 KD protein
265053_at	At1g52000	1.3	-1.3	-7.0	-4.9	-3.5	-2.8	x	myrosinase binding protein
265049_at	At1g52060	-2.6	-1.4	-1.9	-3.0	-8.0	-3.5	x	jasmonate inducible protein, putative
265050_at	At1g52070	-2.3	-1.6	-1.4	-1.9	-4.3	-4.0	x	jasmonate inducible protein, putative
265051_at	At1g52100	1.0	1.1	-22.6	-10.6	-8.0	-3.2	x	jasmonate inducible protein, putative
259839_at	At1g52190	-1.1	1.1	-3.2	-5.7	-1.6	-1.4	x	proton-dependent oligopeptide transport protein family
259669_at	At1g52340	-1.1	-1.1	-2.6	-17.1	-2.8	-1.1	x	dehydrogenase/reductase family protein (ABA2)
262151_at	At1g52510	1.0	-1.1	-1.5	-1.3	-2.8	-2.8	x	hypothetical protein
262159_at	At1g52720	-1.3	-1.5	-4.6	-3.2	-2.5	-2.5	x	expressed protein
260983_at	At1g53560	-1.1	-1.2	-4.6	-4.0	-3.0	-5.7	x	expressed protein
263174_at	At1g54040	-1.1	1.0	-3.7	-2.3	-4.0	-2.8	x	Kelch repeats protein family (TASTY/ESP)
256353_at	At1g55000	1.1	1.0	-3.7	-4.3	-2.5	-2.8	x	expressed protein
259664_at	At1g55330	1.1	1.0	-2.3	-3.5	-3.0	-2.5	x	arabinogalactan-protein (AGP21)
257510_at	At1g55360	-1.2	-1.1	-5.3	-4.0	-2.8	-2.8	x	expressed protein
265075_at	At1g55450	1.4	1.9	-2.8	-4.0	-1.2	-1.1	x	expressed protein
260592_at	At1g55850	1.0	-1.2	-7.5	-7.0	-5.7	-6.1	x	cellulose synthase family (CSLE1)
260603_at	At1g55960	1.2	-1.2	-6.1	-3.7	-4.3	-3.5	x	membrane related protein CP5, putative
256225_at	At1g56220	1.1	-1.3	-4.3	-6.1	1.2	-2.3	x	expressed protein
256226_at	At1g56280	1.1	-1.5	-2.0	-3.5	-2.6	-8.0	x	expressed protein
259603_at	At1g56500	1.0	1.0	-1.6	-1.9	-3.5	-2.6	x	haloacid dehalogenase family
245866_s_at	At1g57990	1.9	2.6	-3.2	-9.8	-2.3	-3.7	x	unknown protein
245868_at	At1g58032	-1.1	-1.1	-4.0	-3.7	-2.6	-2.3	x	amino acid permease family
246396_at	At1g58180	1.2	1.1	-4.3	-3.2	-1.1	-2.6	x	carbonic anhydrase, putative
256025_at	At1g58370	-1.2	1.3	-4.3	-1.3	-3.2	-2.5	x	glycosyl hydrolase family 10
262076_at	At1g59580	1.0	-1.3	-4.3	-3.5	-2.0	-2.8	x	mitogen-activated protein kinase (MPK2)
262913_at	At1g59960	-1.3	-1.1	-2.6	-2.8	-2.0	-1.9	x	aldo/keto reductase, putative
264244_at	At1g60440	-1.1	-1.3	-3.0	-2.6	-1.1	-1.7	x	pantothenate kinase, putative
264923_s_at	At1g60740	-1.2	1.0	-2.5	-4.9	-29.9	-21.1	x	peroxiredoxin, putative
264280_at	At1g61820	-1.1	-1.2	-4.9	-13.9	-3.7	-3.0	x	glycosyl hydrolase family 1
264736_at	At1g62200	-1.2	-1.2	-2.8	-3.5	-1.5	-2.5	x	oligopeptide transporter, putative
265116_at	At1g62480	-1.2	-1.3	-4.0	-3.7	-2.1	-3.2	x	expressed protein
265111_at	At1g62510	1.2	-1.7	-2.0	-2.5	-3.5	-5.7	x	similar to 14KD proline-rich protein DC2.15 precursor
259685_at	At1g63090	1.1	-1.2	-1.7	-1.7	-2.8	-3.2	x	unknown protein
260317_at	At1g63800	-1.1	-1.1	-8.0	-5.7	-6.1	-2.8	x	ubiquitin-conjugating enzyme 5 (UBC5)

262354_at	At1g64200	-1.2	-1.4	-4.9	-2.5	-3.7	-6.5	x	x	H+-transporting ATPase protein, putative
262884_at	At1g64720	1.2	-1.1	-4.9	-7.0	-3.5	-4.9	x	x	membrane related protein CP5, putative
262883_at	At1g64780	-1.1	-1.4	-1.4	1.1	-9.2	-3.2	x	x	ammonium transporter, putative
263142_at	At1g65230	1.0	-1.3	-2.8	-3.7	-2.6	-4.0	x	x	unknown protein
259822_at	At1g66230	1.3	1.1	-4.9	-2.5	-9.2	-11.3	x	x	MYB family transcription factor (MYB20)
256383_at	At1g66820	-1.4	-1.2	-2.8	-2.5	-1.2	-1.4	x	x	glycine rich protein
255857_at	At1g67080	1.0	-1.1	-4.0	-4.9	-1.7	-2.8	x	x	expressed protein
245196_at	At1g67750	-1.3	-1.1	-3.7	-2.6	-2.5	-1.9	x	x	pectate lyase
260014_at	At1g68010	1.2	-1.3	-2.3	-2.8	-2.5	-4.3	x	x	hydroxypyruvate reductase (HPR)
260431_at	At1g68190	1.4	-1.1	-18.4	-13.0	-8.0	-24.3	x	x	CONSTANS B-box zinc finger family protein
259856_at	At1g68440	1.5	1.4	-3.7	-2.3	-4.9	-4.6	x	x	expressed protein
260267_at	At1g68530	1.1	-1.1	-2.8	-3.2	-1.6	-2.1	x	x	very-long-chain fatty acid condensing enzyme (CUT1)
260350_at	At1g69410	1.0	-1.1	-1.3	-1.7	-2.6	-3.0	x	x	Eukaryotic initiation factor 5A, putative
256299_at	At1g69530	1.2	-1.3	-8.6	-11.3	-1.9	-2.8	x	x	expansin (EXP1)
260409_at	At1g69935	-1.1	1.0	-2.5	-2.8	-2.8	-2.0	x	x	expressed protein
264339_at	At1g70290	1.9	1.7	-2.8	-2.8	-1.2	-2.1	x	x	trehalose-6-phosphate synthase, putative
264313_at	At1g70410	1.1	-1.1	-2.5	-2.5	-2.1	-2.0	x	x	carbonic anhydrase, putative
260205_at	At1g70700	1.4	1.1	-2.3	-2.0	-2.5	-3.2	x	x	hypothetical protein
262312_at	At1g70830	1.0	1.0	-2.0	-2.6	-2.8	-4.9	x	x	Bet v I allergen family
262260_at	At1g70850	-1.3	-1.5	-2.6	-4.3	-2.1	-2.8	x	x	Csf-2-related
259853_at	At1g72300	1.1	1.1	-2.8	-2.6	-2.1	-2.3	x	x	leucine-rich repeat transmembrane protein kinase, putative
260427_at	At1g72430	-1.3	-1.5	-3.7	-4.0	-8.6	-6.5	x	x	auxin-induced protein-related
260453_s_at	At1g72510	-1.2	-1.3	-2.1	-4.3	-5.3	-2.8	x	x	expressed protein
262366_at	At1g72890	1.3	1.2	-3.0	-12.1	-2.6	-2.0	x	x	disease resistance protein (TIR-NBS class), putative
262374_s_at	At1g72930	1.0	1.1	-5.7	-3.7	-1.4	1.0	x	x	disease resistance protein (TIR class), putative
245736_at	At1g73330	-1.1	-1.6	-3.5	-6.5	-12.1	-24.3	x	x	protease inhibitor (ATDR4)
259842_at	At1g73600	1.1	1.3	-1.9	-1.6	-4.3	-2.5	x	x	phosphoethanolamine N-methyltransferase
260048_at	At1g73750	1.2	-1.1	-2.8	-2.6	-1.7	-2.8	x	x	expressed protein
260393_at	At1g73920	1.1	1.0	-3.2	-3.0	-2.1	-2.6	x	x	putative lipase
260388_at	At1g74070	-1.1	-1.1	-4.3	-3.0	-2.0	-1.9	x	x	expressed protein
260231_at	At1g74410	1.0	-1.1	-2.5	-2.6	-2.0	-1.7	x	x	putative RING zinc finger protein
260221_at	At1g74670	1.1	1.1	-18.4	-39.4	-4.6	-8.0	x	x	GAST1-like protein
256458_at	At1g75220	1.1	1.0	-3.0	-4.3	-4.0	-3.5	x	x	integral membrane protein

256454_at	At1g75280	1.2	1.0	-2.0	-2.0	-6.1	-3.2	x	isoflavone reductase homolog P3
261118_at	At1g75460	1.0	-1.1	-2.6	-3.2	-1.6	-2.5	x	protease, putative
262678_at	At1g75810	-1.1	-1.4	-1.4	-1.6	-3.0	-2.5	x	expressed protein
261751_at	At1g76080	1.2	-1.1	-2.8	-4.3	-4.0	-7.5	x	thioredoxin family
261769_at	At1g76100	1.1	1.1	-2.6	-3.2	-1.7	-1.7	x	plastocyanin
264958_at	At1g76960	-1.2	-1.3	-8.6	-39.4	-1.4	-3.5	x	expressed protein
262194_at	At1g77930	1.0	-1.2	-3.0	-3.7	-2.8	-3.2	x	expressed protein
264250_at	At1g78680	-1.1	-1.1	-3.0	-4.3	-2.5	-3.7	x	gamma-glutamyl hydrolase
264279_s_at	At1g78820	1.6	1.6	-3.5	-6.1	-1.6	-1.6	x	glycoprotein(EP1), putative
262049_at	At1g80180	1.0	-1.4	-6.5	-5.3	-1.7	-4.9	x	expressed protein
260287_at	At1g80440	2.8	2.5	-3.5	-4.9	-1.9	-3.0	x	Kelch repeat containing F-box protein family
261893_at	At1g80690	-1.5	1.1	-2.6	-2.5	-1.7	-1.9	x	expressed protein
261901_at	At1g80920	1.7	1.2	-10.6	-13.9	-3.2	-6.5	x	J8-like protein similar to DnaJ
266353_at	At2g01520	-1.4	-1.7	-2.3	-3.0	-2.5	-4.9	x	major latex protein (MLP)-related
266330_at	At2g01530	-1.6	-2.0	-5.3	-6.1	-2.6	-4.9	x	major latex protein (MLP)-related
266235_at	At2g02360	-1.1	1.0	-2.8	-3.0	-1.5	-1.3	x	putative phloem-specific lectin
267477_at	At2g02710	1.4	1.2	-3.2	-4.0	-1.7	-2.6	x	putative receptor-like protein kinase
267485_at	At2g02820	-1.1	-1.5	-3.0	-2.5	-1.7	-2.1	x	myb family transcription factor (myb88)
266707_at	At2g03310	1.1	-1.3	-3.2	-4.3	-2.5	-7.0	x	hypothetical protein
265713_at	At2g03530	1.0	-1.2	-3.0	-3.0	-1.9	-1.7	x	putative integral membrane protein
264037_at	At2g03750	1.1	1.1	-3.5	-3.0	-1.5	-1.1	x	similar to steroid sulfotransferase
263647_at	At2g04690	-1.1	-1.1	-4.0	-3.7	-1.7	-1.7	x	expressed protein
263674_at	At2g04790	-1.1	-1.1	-5.7	-2.3	-2.8	-3.0	x	expressed protein
263048_s_at	At2g05310	1.1	-1.2	-2.5	-2.8	-1.9	-3.0	x	expressed protein
265511_at	At2g05540	1.1	-1.4	-13.9	-19.7	-9.2	-14.9	x	putative glycine-rich protein
265974_at	At2g11260	-1.1	-1.4	-2.6	-2.8	1.0	-1.6	x	unknown protein
265837_at	At2g14560	-1.1	1.1	-3.0	-2.6	3.2	3.5	x	expressed protein
266614_at	At2g14910	1.2	-1.2	-1.9	-2.8	-2.5	-4.6	x	unknown protein
265892_at	At2g15020	-1.1	-1.3	-2.6	-2.3	-4.6	-3.7	x	hypothetical protein
265894_at	At2g15050	-1.3	-1.5	-5.3	-3.5	-2.5	-2.6	x	putative lipid transfer protein
265481_at	At2g15960	1.1	1.3	-2.6	-3.2	-2.6	-4.0	x	expressed protein
263096_at	At2g16060	-1.7	-1.1	-8.6	-4.3	1.2	2.6	x	class 1 non-symbiotic hemoglobin (AHB1)
263584_at	At2g17040	1.9	1.6	-3.5	-3.0	1.0	-1.5	x	NAM (no apical meristem)-like protein
263073_at	At2g17500	-1.2	-1.4	-1.2	-2.1	-4.3	-6.5	x	expressed protein

264590_at	At2g17710	-1.1	-1.3	-2.6	-3.2	-1.3	-1.7	x	expressed protein
266941_at	At2g18980	-1.3	-1.4	-1.4	-1.9	-4.6	-2.6	x	peroxidase, putative
267336_at	At2g19310	-1.1	-1.7	-5.7	-8.0	-2.0	-6.1	x	putative small heat shock protein
266693_at	At2g19800	1.1	-1.1	-6.1	-4.9	-1.6	-2.3	x	expressed protein
265387_at	At2g20670	3.5	4.6	-2.5	-3.0	-1.9	-1.6	x	expressed protein
265417_at	At2g20920	1.0	1.1	-1.7	-1.9	-2.6	-2.5	x	unknown protein
264014_at	At2g21210	1.4	-1.1	-3.5	-4.3	-2.0	-2.5	x	putative auxin-regulated protein
263545_at	At2g21560	1.0	-1.5	-1.6	-2.3	-2.6	-2.5	x	unknown protein
263898_at	At2g21950	1.0	-1.2	-2.8	-3.5	-3.7	-2.3	x	SKP1 interacting partner 6 (SKIP6), putative
265344_at	At2g22660	-1.4	-1.1	-3.2	-3.7	-2.1	-1.7	x	unknown protein
266827_at	At2g22920	1.1	1.0	-2.6	-2.0	-3.7	-3.7	x	putative serine carboxypeptidase I
267265_at	At2g22980	-1.1	-1.3	-2.8	-9.8	-1.9	-7.5	x	putative serine carboxypeptidase I
267262_at	At2g22990	1.2	-1.1	-2.8	-5.7	-4.3	-6.1	x	putative serine carboxypeptidase I
267297_at	At2g23780	1.0	-1.3	-2.8	-3.2	-2.1	-2.3	x	putative RING zinc finger protein
266572_at	At2g23840	-1.1	1.0	-1.4	-1.9	-2.5	-2.8	x	unknown protein
263799_at	At2g24550	1.3	1.3	-4.3	-3.7	-2.1	-3.0	x	expressed protein
264379_at	At2g25200	1.1	1.1	-4.0	-2.1	-3.0	-3.5	x	hypothetical protein
265902_at	At2g25590	-2.3	-2.5	-3.7	-13.0	-3.5	-4.6	x	hypothetical protein
267607_s_at	At2g26740	1.1	1.0	-2.8	-3.2	-3.5	-4.0	x	epoxide hydrolase (ATsEH)
266313_at	At2g26980	1.3	1.1	-2.5	-4.6	-3.0	-4.0	x	putative protein kinase
265665_at	At2g27420	-1.1	-1.4	-6.5	-3.7	-90.5	-7.0	x	cysteine proteinase, putative
265572_at	At2g28210	1.1	-1.1	-2.8	-1.7	-3.5	-4.9	x	carbonic anhydrase
263442_at	At2g28605	-1.1	-1.1	-2.5	-2.8	-3.0	-2.5	x	hypothetical protein
266781_at	At2g28940	-1.2	1.2	-3.5	-2.6	-1.4	1.2	x	protein kinase family
266279_at	At2g29290	1.1	-1.1	-6.5	-6.5	-2.3	-5.3	x	putative tropinone reductase
266278_at	At2g29300	1.1	1.1	-4.3	-3.0	-1.1	-1.9	x	putative tropinone reductase
266277_at	At2g29310	1.1	1.1	-3.2	-4.0	-1.6	-3.7	x	putative tropinone reductase
266265_at	At2g29340	1.1	1.0	-7.5	-4.0	-1.9	-2.1	x	similar to tropinone reductase-I
266238_at	At2g29400	-1.2	-1.1	-2.5	-2.5	-1.9	-2.0	x	phosphoprotein phosphatase-type 1 catalytic subunit
266296_at	At2g29420	-1.2	-1.6	-3.2	-5.7	-4.6	-6.5	x	glutathione transferase, putative
267518_at	At2g30500	1.1	1.1	-2.6	-2.8	-1.4	-1.5	x	unknown protein
267516_at	At2g30520	1.2	-1.2	-2.6	-2.5	-1.5	-1.9	x	unknown protein
266476_at	At2g31090	-1.3	1.1	-2.6	-3.2	-3.5	-1.5	x	expressed protein
263449_at	At2g31670	1.0	-1.1	-2.1	-2.8	-3.0	-2.5	x	unknown protein

265680_at	At2g32150	1.0	1.3	-4.9	-7.5	-2.5	-2.8	x	x	putative hydrolase
266357_at	At2g32290	1.2	-1.2	-9.2	-2.5	-5.7	-78.8	x	x	beta-amylase
267057_at	At2g32500	-1.1	-1.1	-1.7	-1.1	-2.8	-3.0	x	x	expressed protein
267115_s_at	At2g32540	1.3	-1.1	-3.7	-3.2	-1.9	-1.1	x	x	putative cellulose synthase
267644_s_at	At2g32880	-1.1	1.1	-3.7	-4.6	-119.4	-119.4	x	x	expressed protein
255793_at	At2g33250	1.1	-1.1	-2.1	-2.6	-2.8	-2.8	x	x	expressed protein
255794_at	At2g33480	-1.3	-1.2	-2.8	-3.2	-2.0	-1.4	x	x	No apical meristem (NAM) protein family
266899_at	At2g34620	-1.1	-1.4	-8.6	-4.0	-3.2	-2.6	x	x	expressed protein
263867_at	At2g36830	1.1	-1.2	-2.0	-2.8	-3.2	-3.7	x	x	putative aquaporin (tonoplast intrinsic protein gamma)
265471_at	At2g37130	-1.4	-1.4	-3.7	-9.2	1.4	-1.4	x	x	peroxidase, putative (ATP2a)
265444_s_at	At2g37180	-1.2	-1.3	-3.7	-6.5	-5.3	-4.3	x	x	aquaporin (plasma membrane intrinsic protein 2C)
266005_at	At2g37340	-1.1	-1.2	-1.5	-1.9	-4.0	-4.0	x	x	splicing factor RSZ33, putative
265952_at	At2g37480	-1.1	1.1	-3.2	-3.7	-3.5	-2.5	x	x	expressed protein
265953_at	At2g37490	1.1	-1.3	-2.6	-2.8	-1.7	-3.5	x	x	expressed protein
267178_at	At2g37750	-1.6	-1.6	-5.7	-7.5	-1.5	-2.0	x	x	expressed protein
267168_at	At2g37770	1.5	-1.1	1.5	-1.3	-2.6	-4.0	x	x	aldo/keto reductase family
266091_at	At2g37920	-1.1	1.1	-2.8	-3.0	-1.6	-1.9	x	x	expressed protein
263265_at	At2g38820	1.2	1.1	-3.0	-3.5	-1.6	-1.7	x	x	expressed protein
266168_at	At2g38870	1.0	-1.1	-3.7	-4.9	-3.7	-3.2	x	x	putative protease inhibitor
266188_at	At2g39000	1.1	-1.3	-3.2	-3.0	-1.3	-2.5	x	x	unknown protein
266988_at	At2g39310	-1.1	1.0	-3.5	-6.5	-7.5	-5.7	x	x	jacalin lectin family
266984_at	At2g39570	-1.1	-1.1	-5.3	-4.6	-7.0	-5.7	x	x	ACT domain-containing protein
245088_at	At2g39850	1.5	1.2	-1.5	-1.3	-10.6	-6.5	x	x	subtilisin-like serine protease
267357_at	At2g40000	2.6	3.0	-5.7	-3.0	-1.6	-2.6	x	x	unknown protein
265722_at	At2g40100	1.1	-1.2	-1.6	-1.7	-6.1	-7.5	x	x	chlorophyll a/b binding protein (LHCB4.3)
265720_at	At2g40110	-1.1	1.0	-3.0	-3.2	-1.9	-1.7	x	x	expressed protein
255822_at	At2g40610	-1.1	-2.0	-11.3	-11.3	-1.4	-5.3	x	x	expansin, putative (EXP8)
267083_at	At2g41100	1.6	2.5	-3.2	-3.0	-1.3	1.1	x	x	calmodulin-like protein (TCH3)
267063_at	At2g41120	1.2	-1.2	-2.0	-1.1	-3.0	-2.5	x	x	hypothetical protein
266372_at	At2g41310	1.1	1.7	-3.5	-2.6	-4.6	-1.3	x	x	two-component response regulator (ARR8/ATRR3)
263987_at	At2g42690	-1.1	-1.1	-4.9	-4.0	-2.1	-1.9	x	x	putative lipase
267385_at	At2g44380	-1.3	1.1	-4.0	-4.6	-2.1	-1.5	x	x	CHIP-rich zinc finger protein, putative
266106_at	At2g45170	1.2	1.2	-3.2	-3.7	-1.5	-2.0	x	x	putative microtubule-associated protein
245131_s_at	At2g45330	1.0	1.2	-2.8	-3.2	-3.7	-1.7	x	x	unknown protein

267500_s_at	At2g45510	-1.3	-1.2	-3.2	-14.9	-1.6	-2.8	x	cytochrome p450, putative
267511_at	At2g45670	-1.1	-1.1	-1.4	-1.9	-3.0	-2.6	x	unknown protein
266925_at	At2g45740	-1.1	-1.1	-4.0	-3.7	-3.2	-3.7	x	expressed protein
266604_at	At2g46030	-1.1	-1.2	-3.0	-2.6	-2.3	-2.0	x	E2, ubiquitin-conjugating enzyme 6 (UBC6)
266583_at	At2g46220	1.2	-1.1	-2.6	-3.0	-1.5	-2.1	x	expressed protein
265451_at	At2g46490	1.0	-1.2	-2.8	-3.2	-1.9	-3.2	x	expressed protein
259272_at	At3g01290	1.4	1.3	-2.5	-4.0	1.9	1.1	x	expressed protein
258957_at	At3g01420	-1.3	-1.2	-1.6	-1.9	-3.5	-2.6	x	feebly-like protein
259163_at	At3g01490	1.0	-1.1	-3.7	-2.5	-1.1	-2.6	x	putative protein kinase
259161_at	At3g01500	1.5	-1.1	-1.1	-1.7	-4.3	-8.0	x	carbonic anhydrase (CA1)
259181_at	At3g01690	1.0	-1.1	-2.6	-2.8	-1.1	-1.9	x	unknown protein
258976_at	At3g01980	-1.2	-1.1	-3.5	-2.5	-1.7	-1.3	x	short-chain dehydrogenase/reductase family
259131_at	At3g02180	1.1	-1.1	-3.2	-4.0	-2.1	-3.0	x	expressed protein
258487_at	At3g02550	-1.2	-2.3	-7.5	-3.2	-3.2	-1.9	x	expressed protein
258623_at	At3g02790	-1.2	-1.1	-1.5	-1.1	-2.8	-3.5	x	C2H2-type zinc finger protein family
258618_at	At3g02885	1.0	-1.1	-4.3	-2.1	-3.0	-3.0	x	gibberellin-regulated protein 5 (GASA5)
258609_at	At3g02910	-1.2	-1.3	-1.9	-2.0	-2.5	-2.8	x	expressed protein
258617_at	At3g03000	-1.4	-1.1	-4.3	-4.3	-1.9	-2.3	x	putative calmodulin protein
258537_at	At3g04210	1.4	1.4	-3.0	-3.5	1.2	-1.2	x	disease resistance protein (TIR-NBS class), putative
258791_at	At3g04720	-1.1	-1.2	-4.3	-7.5	-1.5	-2.3	x	hevein-like protein precursor (PR-4)
259310_s_at	At3g05165	-1.1	1.0	-2.6	-3.2	-2.3	-2.1	x	expressed protein
258468_at	At3g06070	2.0	2.0	-3.7	-3.7	1.1	-2.6	x	expressed protein
258535_at	At3g06750	1.4	1.3	-2.8	-2.5	-2.0	-1.7	x	expressed protein
258501_at	At3g06780	-1.1	-1.9	-2.5	-2.6	-1.6	-3.2	x	expressed protein
258527_at	At3g06850	1.0	-1.2	-3.5	-2.5	-2.1	-2.1	x	branched chain alpha-keto acid dehydrogenase E2 subunit (DIN3/LTA1)
259017_at	At3g07310	1.1	-1.1	-3.7	-2.8	-1.7	-3.5	x	expressed protein
259061_at	At3g07410	-1.1	-1.1	-2.6	-2.5	-1.5	-1.6	x	GTP-binding protein, putative
259068_at	At3g07560	-1.1	-1.1	-3.0	-2.6	-3.2	-2.6	x	unknown protein
259009_at	At3g09260	-1.1	-1.2	-1.4	-2.3	-2.5	-2.6	x	beta-glucosidase (PSR3.1/PYK10)
258708_at	At3g09580	1.1	-1.3	-4.3	-3.0	-2.1	-2.8	x	putative oxidoreductase
258723_at	At3g09600	1.1	1.1	-4.9	-19.7	-4.6	-42.2	x	MYB family transcription factor
258724_at	At3g09610	-1.3	1.2	-4.3	-5.7	-7.0	-2.6	x	unknown protein
258774_at	At3g10740	1.1	1.0	-2.8	-2.6	-2.6	-3.5	x	glycosyl hydrolase family 51

256441_at	At3g10940	-1.2	-1.1	-2.8	-2.1	-3.7	-4.9	x	expressed protein
256427_at	At3g11090	-1.1	-1.1	-7.0	-4.6	-2.3	-3.7	x	expressed protein
256413_at	At3g11100	-1.4	1.2	-2.6	-6.5	-2.5	-1.5	x	expressed protein
256256_at	At3g11230	-1.4	-1.2	-5.7	-2.8	-2.6	-2.0	x	expressed protein
258727_at	At3g11930	1.1	-1.1	-3.7	-4.6	1.0	-1.6	x	ethylene-responsive protein, putative
256245_at	At3g12580	-2.1	-1.7	3.0	1.3	-3.0	-3.7	x	heat shock protein (hsp70)
256772_at	At3g13750	1.5	1.0	-6.5	-8.6	-2.5	-5.7	x	putative beta-galactosidase (BGAL1)
258063_at	At3g14620	1.0	-1.3	-6.5	-3.7	-1.9	-3.2	x	cytochrome P450, putative
258225_at	At3g15630	1.4	1.5	-4.6	-6.1	-1.1	-2.8	x	expressed protein
258275_at	At3g15760	1.5	1.1	-22.6	-6.5	-1.7	-2.0	x	expressed protein
258263_at	At3g15780	-1.1	-1.1	-2.6	-3.5	-1.3	-3.0	x	unknown protein
258052_at	At3g16190	1.0	-1.3	-3.0	-2.5	-1.4	-2.6	x	putative hydrolase
258049_at	At3g16220	1.1	-1.3	-2.5	-3.5	-1.6	-3.2	x	hypothetical protein
258053_at	At3g16230	-1.1	1.0	-4.6	-4.6	-2.6	-1.7	x	expressed protein
258054_at	At3g16240	1.4	-1.1	-2.8	-6.1	-3.2	-4.9	x	delta tonoplast integral protein (delta-TIP)
258055_at	At3g16250	-1.1	-1.1	-3.7	-4.0	-2.8	-3.2	x	ferredoxin related
259382_s_at	At3g16430	-1.1	-1.1	-2.8	-5.3	-2.6	-3.0	x	putative myrosinase binding protein
259384_at	At3g16450	-1.1	-1.2	-3.5	-7.0	-3.0	-4.6	x	putative lectin
257206_at	At3g16530	1.1	1.1	-4.9	-5.7	-4.3	-8.0	x	legume lectin protein family
258434_at	At3g16770	1.1	-1.3	-2.5	-3.7	2.6	-1.4	x	AP2 domain protein RAP2.3
257880_at	At3g16910	-1.2	-1.3	-8.0	-5.3	-5.7	-4.3	x	AMP-dependent synthetase and ligase family
257896_at	At3g16920	1.1	1.0	-1.4	-2.5	-12.1	-3.5	x	glycosyl hydrolase family 19 (chitinase)
257801_at	At3g18750	-1.1	-1.2	-2.8	-1.2	-3.2	-4.6	x	WNK protein family kinases (WNK6/ZIK5)
256892_at	At3g19000	-1.1	-1.2	-4.3	-3.7	-4.0	-3.2	x	similar to flavanone-3-hydroxylase
257966_at	At3g19800	1.1	-1.2	-7.0	-7.5	-2.8	-5.7	x	expressed protein
257673_at	At3g20370	-1.6	-1.4	-2.6	-3.2	-3.7	-2.5	x	expressed protein
257985_at	At3g20810	-1.3	-1.3	-2.3	-3.2	-3.7	-3.5	x	expressed protein
257264_at	At3g22060	1.2	1.0	-4.0	-3.2	-1.7	-1.6	x	receptor kinase common family, putative
258452_at	At3g22370	1.1	1.1	1.3	1.5	-4.6	-3.0	x	alternative oxidase 1a precursor
258456_at	At3g22420	1.1	-1.1	-3.0	-2.8	-3.2	-2.8	x	putative protein kinase
256935_at	At3g22570	-2.0	-1.3	-2.0	-1.9	-8.0	-6.1	x	expressed protein
257772_at	At3g23080	1.0	1.0	-4.6	-4.9	-1.9	-2.8	x	similar to phosphatidylcholine transfer
258299_at	At3g23410	1.0	-1.1	-1.6	-2.0	-3.2	-4.0	x	alcohol oxidase-related
257175_s_at	At3g23470	-2.0	-1.1	-7.5	-8.0	-3.7	-5.3	x	cyclopropane-fatty-acyl-phospholipid synthase, putative

258100_at	At3g23550	1.1	1.4	-2.6	-3.7	-1.9	-2.6	x	MATE efflux protein family
258108_at	At3g23570	-1.1	-1.1	-2.5	-2.5	-2.1	-2.3	x	expressed protein
257239_at	At3g24100	-1.2	-1.1	-2.0	-3.7	-7.0	-48.5	x	expressed protein
256621_at	At3g24450	-1.1	-1.3	-2.8	-2.6	1.2	-1.4	x	expressed protein
258133_at	At3g24500	-2.5	-4.0	-5.7	-21.1	-8.6	-4.6	x	putative ethylene-responsive transcriptional coactivator
256994_s_at	At3g25830	-1.6	-2.1	-1.9	-2.1	-2.8	-4.6	x	myrcene/ocimene synthase, putative
258080_at	At3g25930	-2.3	-1.4	-2.8	-3.0	-1.6	-1.5	x	expressed protein
258085_at	At3g26100	-1.2	-1.3	-3.2	-3.0	-1.6	-2.6	x	expressed protein
257634_s_at	At3g26170	1.0	-1.1	-3.5	-4.6	-1.2	-1.5	x	cytochrome p450 family
257625_at	At3g26230	-1.1	1.5	-29.9	-3.2	-4.3	-1.9	x	cytochrome p450 family
256880_at	At3g26450	-1.1	-1.3	-6.1	-6.1	-2.5	-3.7	x	putative major latex protein
257615_at	At3g26510	1.1	-2.3	-4.6	-4.6	-1.7	-5.7	x	expressed protein
257611_at	At3g26580	1.1	-1.1	-2.8	-4.6	-2.3	-5.3	x	unknown protein
257832_at	At3g26740	1.3	-1.2	-2.5	-5.7	-2.0	-7.5	x	light regulated protein, putative
258256_at	At3g26890	1.2	-1.1	-3.5	-3.0	-1.2	-2.5	x	expressed protein
257789_at	At3g27020	1.0	-1.2	-3.5	-3.2	-3.2	-3.5	x	putative oligopeptide transporter
257153_at	At3g27220	-1.6	-2.1	-4.6	-6.1	-3.2	-2.6	x	expressed protein
257227_at	At3g27820	1.1	-1.1	-1.7	-2.1	-2.5	-2.5	x	monodehydroascorbate reductase, putative
257299_at	At3g28050	-1.1	1.0	-3.7	-4.9	-2.8	-2.0	x	nodulin MtN21 family protein
256603_at	At3g28270	-1.1	-1.2	-27.9	-19.7	-32.0	-9.8	x	At14a-related protein
256589_at	At3g28740	1.1	-1.1	-1.9	-8.6	-3.7	-3.0	x	cytochrome p450 family
258002_at	At3g28930	-2.1	1.0	-4.0	-13.9	-1.3	1.0	x	AIG2-like protein
258000_at	At3g28940	-1.1	-1.1	-3.5	-4.6	-1.5	-1.4	x	AIG2-like protein
257745_at	At3g29240	1.3	1.1	-5.3	-4.0	-1.6	-1.4	x	chloroplast lumen common protein family
257315_at	At3g30775	1.3	1.4	-2.8	-2.8	-2.6	-3.5	x	proline dehydrogenase (ERD5/PRO1/AT-POX)
256607_at	At3g32930	-1.1	1.0	-2.6	-2.8	-1.9	-1.9	x	expressed protein
252746_at	At3g43190	-1.3	-1.1	-5.7	-3.5	-4.6	-2.1	x	sucrose synthase
252612_at	At3g45160	-1.2	1.0	-3.7	-4.0	-1.9	-1.6	x	hypothetical protein
252570_at	At3g45300	-1.1	1.0	-2.6	-2.8	-1.9	-1.9	x	isovaleryl-CoA-dehydrogenase precursor (IVD)
252537_at	At3g45710	-1.4	-1.3	-3.5	-7.5	-1.6	-3.2	x	putative transporter protein
252511_at	At3g46280	-1.2	-1.4	-5.7	-3.2	-2.6	-3.5	x	putative protein
252411_at	At3g47430	-1.1	-1.6	-2.5	-2.5	-2.0	-2.6	x	putative protein
252433_at	At3g47560	1.1	1.3	-7.0	-3.7	-1.9	-1.5	x	putative hydrolase
252353_at	At3g48200	1.1	-1.1	-2.6	-2.6	-1.3	-1.9	x	putative protein

252365_at	At3g48350	-1.1	-1.1	-2.0	-1.6	-4.0	-2.6	x	expressed protein
252367_at	At3g48360	4.9	4.9	-4.6	-78.8	-1.6	-3.5	x	speckle-type POZ protein-related
252366_at	At3g48420	1.2	-1.1	-1.4	-1.4	-3.5	-3.5	x	haloacid dehalogenase family
252315_at	At3g48690	1.1	-1.1	-1.9	-2.8	-2.8	-3.5	x	putative protein
252317_at	At3g48720	-1.1	-1.2	-4.3	-3.7	-2.1	-2.5	x	expressed protein
252250_at	At3g49790	1.1	1.3	-4.3	-4.3	-2.3	-5.3	x	putative protein
252213_at	At3g50210	-1.1	1.0	-2.0	-2.5	-2.6	-2.8	x	oxidoreductase (din11), putative
252170_at	At3g50480	1.0	1.3	-4.3	-3.7	-1.2	1.1	x	expressed protein
252154_at	At3g50880	-1.3	-1.3	-3.5	-3.7	-2.3	-2.6	x	putative DNA-3-methyladenine glycosidase
252095_at	At3g51000	1.1	-1.1	-3.0	-2.6	1.1	-1.9	x	epoxide hydrolase-like protein
252092_at	At3g51420	1.1	-1.2	-2.8	-3.0	-2.1	-2.5	x	strictosidine synthase-related
246304_at	At3g51840	1.0	-1.1	-3.0	-4.0	-1.6	-2.5	x	acyl-coA dehydrogenase
252040_at	At3g52060	1.2	1.0	-3.5	-2.6	-1.3	-2.5	x	putative protein
256674_at	At3g52360	-1.1	-1.1	-6.1	-4.0	-2.5	-4.0	x	expressed protein
252011_at	At3g52720	1.1	-1.1	-45.3	-22.6	-6.1	-2.1	x	carbonic anhydrase (CAH1)
251886_at	At3g54260	-1.1	-1.2	-7.0	-9.2	-3.2	-5.3	x	expressed protein
251867_at	At3g54480	-1.2	-1.1	-2.8	-2.5	-2.5	-2.3	x	SKP1 interacting partner 5 (SKIP5)
251759_at	At3g55630	-1.1	-1.3	-9.8	-4.9	-2.6	-2.6	x	folypolyglutamate-dihydrofolate synthase (dhfs/fpgs4)
251704_at	At3g56360	1.0	-1.5	-2.5	-3.0	-6.5	-8.6	x	expressed protein
251517_at	At3g59370	-2.0	-3.0	-27.9	-3.2	-7.5	-4.3	x	putative protein
251438_s_at	At3g59930	-2.5	-1.5	-3.0	-2.6	-14.9	-119.4	x	expressed protein
251403_at	At3g60300	-1.1	-1.4	-2.5	-3.2	-1.1	-2.8	x	putative protein
251408_at	At3g60340	-1.1	1.1	-2.8	-3.2	-1.9	-2.3	x	palmitoyl-protein thioesterase precursor - like
251369_at	At3g60480	-1.1	-1.1	-2.6	-3.7	-1.2	-1.3	x	putative protein
251342_at	At3g60690	1.3	-1.1	-2.5	-2.5	-1.5	-2.5	x	putative protein
251391_at	At3g60910	-1.1	-1.4	-4.0	-3.0	-3.2	-3.7	x	expressed protein
251324_at	At3g61430	1.1	-1.1	-3.7	-5.7	-2.5	-3.5	x	plasma membrane intrinsic protein 1a
251218_at	At3g62410	1.1	-1.3	-3.7	-3.7	-1.3	-3.2	x	CP12 protein precursor-like protein
255671_at	At4g00355	-1.1	1.0	-3.2	-3.7	-1.2	-1.5	x	expressed protein
255626_at	At4g00780	1.0	-1.2	-3.0	-2.6	-3.2	-5.3	x	expressed protein
255617_at	At4g01330	1.2	1.1	-4.9	-4.6	-4.0	-3.2	x	putative protein kinase
255561_at	At4g02050	-1.1	1.0	-2.8	-2.5	-1.3	-1.5	x	putative hexose transporter
255517_at	At4g02290	1.1	-1.1	-4.9	-4.9	-2.8	-3.0	x	glycosyl hydrolase family 9
255487_at	At4g02610	-1.3	-1.1	-3.0	-2.5	-1.1	1.0	x	tryptophan synthase alpha 1-like protein

255365_at	At4g04040	-1.1	1.0	-4.3	-4.0	-1.6	-1.5	x	putative phosphofructokinase beta subunit
255302_at	At4g04830	-1.2	-1.2	-2.5	-3.7	-3.0	-2.6	x	similar to transcriptional regulator
255298_at	At4g04840	1.0	-1.1	1.3	-1.2	-4.0	-4.9	x	expressed protein
255008_at	At4g10060	1.1	-1.1	-5.3	-3.7	-3.7	-3.2	x	expressed protein
255807_at	At4g10270	-1.5	-1.9	-12.1	-3.7	-5.7	-1.6	x	probable wound-induced protein
254938_at	At4g10770	1.0	-1.1	-3.2	-3.2	-4.6	-4.0	x	oligopeptide transporter (AtOPT7)
254914_at	At4g11290	-1.3	-1.6	-3.0	-9.2	-3.2	-2.3	x	peroxidase, putative
254915_s_at	At4g11310	-1.4	-1.1	-2.5	-3.5	-2.3	-1.9	x	cysteine proteinase
254931_at	At4g11460	-1.2	1.5	-6.1	-8.6	-12.1	-3.0	x	serine/threonine kinase-like protein
254874_at	At4g11570	1.1	-1.1	-2.1	-2.5	-3.0	-3.5	x	putative protein
254870_at	At4g11900	1.1	-1.5	-17.1	-11.3	-1.5	-1.7	x	KI domain interacting kinase 1 -like protein
254848_at	At4g11960	-1.1	-1.2	-4.3	-4.0	-4.3	-6.1	x	putative protein
254853_at	At4g12080	-1.3	-1.2	-2.1	-4.6	-3.5	-3.5	x	putative DNA-binding protein
254820_s_at	At4g12510	-1.6	-1.5	-1.4	-3.0	-4.6	-4.9	x	pEARL1 1-like protein
254798_at	At4g13050	1.0	-1.1	-2.5	-2.6	-1.9	-2.5	x	oleoyl-(acyl-carrier-protein) hydrolase-like protein
254722_at	At4g13530	-1.1	-1.1	-3.2	-3.0	-2.5	-3.7	x	putative protein
254718_at	At4g13580	-1.9	-1.3	-3.5	-6.5	-3.5	-2.3	x	disease resistance response protein-related
254688_at	At4g13830	1.5	-1.1	-4.0	-3.7	-1.7	-5.7	x	DnaJ-like protein
245310_at	At4g13950	-1.3	-1.1	-2.8	-2.6	-1.7	-1.9	x	expressed protein
245386_at	At4g14010	-1.3	-1.1	-2.6	-2.8	-2.0	-2.0	x	expressed protein
245265_at	At4g14400	-1.3	-1.1	-7.0	-3.5	1.4	1.7	x	hypothetical protein
245592_at	At4g14540	-1.1	-1.2	-3.0	-2.6	-1.9	-1.7	x	CCAAAT-binding transcription factor subunit A (CBF-A)
245396_at	At4g14870	1.0	1.0	-2.6	-2.8	-2.1	-3.0	x	expressed protein
245330_at	At4g14930	1.1	1.2	-7.0	-2.6	-1.9	-1.7	x	expressed protein
245555_at	At4g15390	-1.7	-2.0	-4.0	-3.2	-1.1	-1.3	x	acyltransferase family
245352_at	At4g15490	1.6	1.2	1.7	-1.1	-2.6	-4.0	x	UDP-glycosyltransferase, putative
245321_at	At4g15545	1.1	-1.2	-2.5	-2.5	-1.5	-2.0	x	expressed protein
245281_at	At4g15560	1.1	1.0	-2.6	-2.8	-1.7	-2.0	x	DEF (CLA1) protein
245501_at	At4g15620	-1.1	1.1	-2.6	-1.5	-6.1	-2.8	x	hypothetical protein
245513_at	At4g15780	-1.2	-1.2	-2.6	-3.0	-1.9	-2.6	x	SYBL1 like protein
245524_at	At4g15920	1.1	1.1	-2.0	-2.6	-2.5	-3.7	x	nodulin MtN3 family protein
245393_at	At4g16260	-1.4	-1.1	-2.5	-10.6	-2.1	-4.0	x	glycosyl hydrolase family 17
245391_at	At4g16520	1.1	1.1	-3.5	-4.0	-2.1	-2.0	x	symbiosis-related like protein
245399_at	At4g17340	-1.2	-1.2	-3.7	-4.6	-19.7	-16.0	x	membrane channel like protein

245308_at	At4g17486	-1.1	-1.1	-2.8	-3.2	-2.0	-2.6	x	putative protein
254705_at	At4g17870	1.1	-1.2	-3.2	-3.7	-3.2	-4.9	x	expressed protein
254624_at	At4g18580	-1.2	-1.3	-3.2	-2.6	-1.9	-1.6	x	expressed protein
254573_at	At4g19420	1.1	1.1	-3.2	-2.6	-2.3	-2.8	x	pectinacetylerase family
254553_at	At4g19530	1.1	1.1	-2.0	-1.7	-3.5	-2.6	x	disease resistance protein (TIR-NBS-LRR class)
254532_at	At4g19660	1.0	1.0	-2.8	-2.8	1.2	-1.2	x	putative protein
254547_at	At4g19860	1.2	-1.1	-2.8	-2.6	-1.1	-2.5	x	putative protein
254549_at	At4g19880	-1.2	-1.1	-3.0	-3.5	-1.7	-1.9	x	putative protein
254430_at	At4g20820	-1.1	1.0	-2.5	-10.6	-11.3	-36.8	x	FAD-linked oxidoreductase family
254378_at	At4g21810	1.0	-1.2	-3.0	-2.6	-1.6	-1.4	x	putative protein
254385_s_at	At4g21830	-1.5	-1.5	-4.0	-8.6	-3.7	-1.6	x	putative protein
254387_at	At4g21850	-1.5	-1.1	-6.5	-12.1	-6.1	-2.6	x	expressed protein
254384_at	At4g21870	1.1	1.1	-7.0	-7.0	-68.6	-17.1	x	heat shock protein
254361_at	At4g22212	-2.1	-1.5	-2.0	-2.8	-4.0	-3.5	x	expressed protein
254327_at	At4g22490	1.1	1.0	-1.1	-1.1	-2.5	-3.5	x	RCc3- like protein
254331_s_at	At4g22710	1.1	1.1	-4.6	-4.9	-2.1	-3.5	x	cytochrome P450 family
254280_at	At4g22756	-1.2	1.0	-3.2	-2.5	-2.5	-1.4	x	putative sterol 4-alpha-methyl-oxidase
254256_at	At4g23180	1.5	1.9	-4.0	-4.0	-1.2	-1.2	x	serine/threonine protein kinase (RLK4)
254239_at	At4g23400	1.1	-1.1	-3.2	-4.9	-3.0	-4.3	x	major intrinsic protein (MIP) family
254225_at	At4g23670	1.0	1.1	-3.0	-5.7	-7.0	-3.7	x	putative major latex protein
254119_at	At4g24780	-1.1	-1.1	-3.2	-2.8	-2.0	-1.1	x	putative pectate lyase
254020_at	At4g25700	1.1	1.0	-1.5	-1.1	-4.3	-3.0	x	beta-carotene hydroxylase
254082_at	At4g25720	-1.4	-1.1	-2.8	-2.6	-1.3	1.1	x	glutamine cyclotransferase precursor - like protein
253957_at	At4g26320	-2.1	-1.7	-1.2	-1.9	-6.1	-2.5	x	arabinogalactan-protein (AGP13)
253973_at	At4g26555	-1.2	-1.1	-2.1	-2.6	-2.8	-3.5	x	peptidylprolyl isomerase, putative
253943_at	At4g27030	1.2	-1.1	-1.1	1.0	-4.0	-4.6	x	hypothetical protein
253874_at	At4g27450	1.0	-1.2	-18.4	-13.0	-12.1	-7.0	x	expressed protein
253886_at	At4g27710	1.1	-1.1	-3.7	-2.8	-1.4	-2.3	x	cytochrome P450, member of CYP709B
253842_at	At4g27860	-1.2	-1.3	-3.2	-16.0	-2.6	-3.0	x	putative protein
253806_at	At4g28270	1.1	-1.4	-4.9	-4.3	-4.6	-2.6	x	C3HC4-type zinc finger protein family
253814_at	At4g28290	1.4	1.1	-3.2	-3.5	-4.0	-3.5	x	putative protein
253709_at	At4g29220	1.0	-1.1	-3.7	-2.8	-1.5	-2.5	x	pyrophosphate-dependent phosphofructo-1-kinase-like protein
253701_at	At4g29890	-1.6	-1.5	-3.5	-3.7	-3.2	-4.9	x	choline monooxygenase

253597_at	At4g30690	1.0	1.0	-3.7	-4.3	-2.6	-3.7	x	putative protein
253548_at	At4g30993	-1.1	1.0	-4.3	-3.7	-2.1	-2.3	x	expressed protein
253534_at	At4g31500	1.1	1.1	-2.8	-2.6	1.1	1.1	x	cytochrome P450 (ATR4/CYP83B1)
253496_at	At4g31870	1.3	-1.3	1.2	1.0	-2.8	-3.0	x	glutathione peroxidase, putative
253412_at	At4g33000	-1.1	-1.3	-3.0	-3.0	-1.9	-2.3	x	calcineurin B-like protein (fragment)
253373_at	At4g33150	1.0	-1.1	-3.0	-3.7	-1.7	-2.5	x	lysine-ketoglutarate reductase/saccharopine
253332_at	At4g33420	-1.1	-1.1	-3.2	-3.2	-2.1	-5.3	x	peroxidase, putative
253298_at	At4g33560	1.1	-2.8	-2.3	-5.7	-2.8	-2.6	x	expressed protein
253302_at	At4g33660	-1.3	-1.1	-8.6	-34.3	-10.6	-5.3	x	expressed protein
253305_at	At4g33666	1.0	-1.4	-10.6	-13.9	-7.5	-11.3	x	expressed protein
253281_at	At4g34138	1.1	1.1	-3.2	-2.1	-2.8	-2.6	x	similar to glucosyltransferase -like protein
253269_at	At4g34140	-1.3	-1.3	-2.8	-6.5	-1.2	-2.0	x	hypothetical protein
253245_at	At4g34590	1.2	1.0	-1.4	-1.6	-3.0	-3.0	x	bZIP transcription factor (GBF6)
253228_at	At4g34630	1.0	-1.2	-4.6	-3.2	-2.0	-1.6	x	putative protein
253220_s_at	At4g34920	1.0	-1.4	-4.3	-5.3	-2.3	-6.1	x	putative protein
253191_at	At4g35350	-1.2	-1.1	-1.5	-1.6	-5.7	-3.0	x	cysteine protease (XCP1)
253163_at	At4g35750	-1.1	-1.4	-3.2	-3.2	1.1	-2.1	x	putative protein
253161_at	At4g35770	1.2	-1.2	-13.9	-16.0	-2.0	-7.5	x	senescence-associated protein (SEN1)
246275_at	At4g36540	1.5	1.1	-3.5	-3.2	-1.4	-1.9	x	putative protein
246197_at	At4g37010	-1.4	-1.6	-6.5	-18.4	-1.7	-2.5	x	caltractin-like protein
253049_at	At4g37300	1.1	-1.1	-4.0	-3.0	-1.3	-3.7	x	expressed protein
253099_s_at	At4g37530	-1.2	-1.1	-3.7	-3.5	-2.0	-2.0	x	peroxidase, putative
253061_at	At4g37610	2.6	2.3	-6.5	-18.4	-1.7	-2.6	x	p300/CBP acetyltransferase-related protein
253040_at	At4g37800	1.1	-1.1	-2.6	-3.0	-2.1	-2.8	x	putative endo-xyloglucan transferase
252983_at	At4g37980	1.1	1.0	-1.7	-1.3	-3.5	-3.5	x	mannitol dehydrogenase (ELI3-1), putative
252972_at	At4g38840	1.3	-1.4	-4.0	-3.7	-1.4	-2.3	x	auxin-induced protein
252882_at	At4g39675	-2.0	-2.0	-137.2	-42.2	-17.1	-16.0	x	expressed protein
251024_at	At5g02180	1.1	1.1	1.3	1.1	-2.5	-3.2	x	putative protein
251028_at	At5g02230	-1.1	-1.1	-2.6	-3.7	-4.3	-7.0	x	haloacid dehalogenase-like hydrolase family
251011_at	At5g02560	-1.1	-1.4	-2.6	-2.5	-2.1	-3.2	x	putative protein
250937_at	At5g03230	1.3	-1.4	-2.8	-4.3	-1.7	-2.8	x	putative protein
250916_at	At5g03630	-1.4	-1.3	-2.5	-3.0	-2.1	-2.1	x	monodehydroascorbate reductase, putative
250828_at	At5g05250	-1.4	-1.1	-7.0	-2.3	-8.6	-2.8	x	expressed protein
250549_at	At5g07860	1.0	-1.1	-6.1	-2.6	-2.5	-2.5	x	N-hydroxycinnamoyl/benzoyltransferase

246034_at	At5g08350	1.6	1.1	-2.5	-3.0	1.1	-1.5	x	putative protein
245906_at	At5g11070	2.0	2.5	-2.6	-3.0	-1.6	-1.4	x	expressed protein
250318_at	At5g12200	-1.2	-1.2	-3.7	-3.2	-2.1	-1.9	x	dihydropyrimidinase
250217_at	At5g14120	1.4	1.1	-8.6	-17.1	-5.3	-7.0	x	nodulin-related protein
250180_at	At5g14450	1.1	1.0	-2.3	-2.1	-3.7	-3.2	x	GDSL-motif lipase/hydrolase protein
250152_at	At5g15120	-1.3	-1.3	-8.0	-16.0	-1.6	-1.4	x	putative protein
250160_at	At5g15210	-1.1	-1.1	-3.2	-3.2	-1.7	-2.0	x	putative protein
246565_at	At5g15530	-1.3	1.0	-1.7	-2.1	-3.2	-2.6	x	biotin carboxyl carrier protein 2 (BCCP2)
246540_at	At5g15600	1.2	-1.3	-4.3	-2.1	-3.5	-3.0	x	nitrilase associated protein
246487_at	At5g16030	1.3	1.1	-4.0	-2.5	-1.9	-1.2	x	expressed protein
250114_s_at	At5g16340	1.4	1.3	-5.3	-11.3	-4.9	-4.0	x	AMP-binding protein
250133_at	At5g16400	1.1	1.1	-2.1	-3.0	-3.2	-3.0	x	thioredoxin f2
250079_at	At5g16650	-1.1	1.0	-3.2	-2.8	-2.1	-2.6	x	putative protein
250017_at	At5g18140	1.1	1.0	-4.0	-4.0	-2.3	-3.2	x	unknown protein
250032_at	At5g18170	1.0	-1.1	-3.7	-2.5	1.1	-2.0	x	glutamate dehydrogenase (GDH1)
249996_at	At5g18600	1.2	1.5	-3.7	-2.6	1.0	1.3	x	glutaredoxin -like protein
250008_at	At5g18630	1.1	-1.1	-5.3	-3.7	-2.3	-2.8	x	triacylglycerol lipase-like protein
250007_at	At5g18670	2.0	1.1	-7.5	-4.6	-1.6	-3.7	x	glycosyl hydrolase family 14 (beta-amylase)
249978_at	At5g18850	1.0	-1.1	-2.8	-4.9	-1.6	-2.0	x	putative protein
249923_at	At5g19120	2.0	1.9	-6.5	-12.1	-4.3	-13.0	x	conglutin gamma - like protein
245957_at	At5g19590	1.0	-1.2	-2.6	-2.6	-1.2	-2.0	x	putative protein
245913_at	At5g19860	-1.1	-1.1	-4.0	-4.6	-2.8	-3.7	x	unknown protein
246146_at	At5g20050	-1.1	-1.1	-2.5	-2.6	-3.2	-2.0	x	receptor-like protein kinase - like protein
246114_at	At5g20250	1.4	1.1	-7.5	-8.6	-8.6	-13.9	x	glycosyl hydrolase family (DIN10)
246021_at	At5g21100	-1.1	-1.1	-3.5	-3.0	-3.0	-5.7	x	L-ascorbate oxidase, putative
246028_at	At5g21170	1.1	-1.1	-5.3	-4.6	-1.7	-3.7	x	AKIN beta1
249941_at	At5g22270	1.1	1.0	-3.5	-3.5	1.3	-1.1	x	putative protein
249914_at	At5g22850	-1.1	-1.1	-2.8	-2.6	-3.0	-2.0	x	protease-like protein
249862_at	At5g22920	2.3	3.2	-17.1	-19.7	-3.5	-4.6	x	zinc finger protein (RING family)
249869_at	At5g23050	1.1	1.0	-2.8	-2.5	-2.5	-2.8	x	AMP-dependent synthetase and ligase family
249835_s_at	At5g23510	-1.2	1.3	-2.5	-2.5	-2.0	-1.1	x	putative protein
249798_at	At5g23730	1.2	1.1	-1.1	-1.2	-18.4	-3.0	x	G-protein beta-subunit (transducin) family
249797_at	At5g23750	-1.2	1.3	-1.5	1.2	-4.9	-2.6	x	putative protein
249817_at	At5g23820	-1.1	-1.1	-3.0	-4.0	-2.8	-1.6	x	expressed protein

249812_at	At5g23830	-1.5	-1.6	-1.7	-4.3	-68.6	-2.5	x	putative protein	
249769_at	At5g24120	1.1	-1.2	1.2	1.2	-2.5	-4.0	x	sigma-like factor	
249774_at	At5g24150	1.3	-1.4	-6.1	-5.7	-39.4	-32.0	x	squalene monooxygenase (SQP1,1)	
249775_at	At5g24160	1.2	-1.1	-5.7	-52.0	-11.3	-24.3	x	squalene monooxygenase (SQP1,2)	
249732_at	At5g24420	-1.1	-1.1	-3.5	-1.6	-4.0	-3.5	x	6-phosphogluconolactonase-like protein	
249742_at	At5g24490	1.2	1.1	-2.6	-6.1	-1.1	-2.6	x	expressed protein	
245928_s_at	At5g24780	1.4	1.1	-3.5	-6.1	-4.3	-9.2	x	vegetative storage protein (VSP1)	
246962_s_at	At5g24800	1.1	-1.5	-3.5	-4.3	-4.0	-7.5	x	bZIP protein, G/HBF-1-related	
246901_at	At5g25630	1.1	-1.1	-3.5	-3.5	-2.0	-1.7	x	putative protein	
246909_at	At5g25770	-1.2	-1.3	-4.3	-6.1	-2.1	-3.5	x	expressed protein	
246825_at	At5g26260	-2.0	-1.1	-1.9	-3.7	-7.5	-9.8	x	putative protein	
246855_at	At5g26280	-1.9	-1.1	-4.6	-10.6	-8.6	-4.9	x	putative protein	
246832_at	At5g26595	-1.2	-1.1	-3.7	-2.6	-3.2	-2.1	x	putative protein	
246781_at	At5g27350	1.1	1.1	-4.3	-5.7	-2.3	-2.8	x	sugar transporter-like protein	
246783_at	At5g27360	-1.1	1.1	-4.3	-2.5	-3.2	-2.3	x	sugar-porter family protein 2 (SFP2)	
246768_at	At5g27400	-1.2	-1.2	-4.0	-2.8	-3.2	-2.3	x	expressed protein	
246651_at	At5g35170	-1.1	-1.1	-2.0	-2.3	-2.8	-3.5	x	adenylate kinase -like protein	
246607_at	At5g35370	-1.3	-1.4	-4.3	-4.9	-3.0	-1.6	x	receptor-like protein kinase - like protein	
249694_at	At5g35790	1.0	1.0	-4.3	-3.7	-1.4	-2.3	x	glucose-6-phosphate dehydrogenase	
249658_s_at	At5g36700	1.1	-1.1	-1.7	-2.0	-3.0	-2.5	x	N-glyceraldehyde-2-phosphotransferase-like	
249580_at	At5g37740	-1.1	-1.3	-2.5	-2.5	-1.6	-1.9	x	C2 domain-containing protein	
249599_at	At5g37990	-1.1	1.0	1.0	-1.7	-4.0	-7.0	x	methyltransferase-related	
249545_at	At5g38030	-1.4	1.1	-1.4	-1.6	-2.8	-3.5	x	putative transmembrane protein	
249482_at	At5g38980	1.1	-1.2	-3.2	-3.7	-1.5	-1.6	x	putative protein	
249480_s_at	At5g38990	1.1	1.1	-2.6	-2.5	1.2	1.0	x	protein kinase - like protein	
249493_at	At5g39080	-1.1	-1.4	-3.0	-2.8	-2.3	-1.9	x	acyltransferase -like protein	
249439_at	At5g40020	1.1	1.0	-5.3	-7.0	-3.7	-27.9	x	thauromatin-like protein	
249355_at	At5g40500	1.1	-1.2	-3.0	-3.5	-3.0	-5.7	x	expressed protein	
249325_at	At5g40850	1.4	1.7	-4.0	-2.6	-2.6	-1.5	x	urophorphyrin III methylase (UPM1)	
249327_at	At5g40890	1.1	-1.1	-2.6	-3.5	-1.1	-2.1	x	CLC-a chloride channel protein	
249299_at	At5g41340	1.0	-1.1	-3.0	-2.8	-2.5	-2.3	x	E2, ubiquitin-conjugating enzyme 4 (UBC4)	
249191_at	At5g42760	1.5	-1.1	-1.2	-1.1	-2.6	-2.8	x	putative protein	
249177_at	At5g42850	-1.1	-1.2	-2.5	-3.5	-1.5	-2.3	x	expressed protein	
249122_at	At5g43850	-1.1	-1.4	-5.7	-4.6	-2.8	-3.2	x	putative protein	

249073_at	At5g44020	1.1	-1.1	-2.6	-3.7	-1.3	-2.8	x	vegetative storage protein-related
249045_at	At5g44380	-1.7	-1.3	-2.6	-4.0	-2.3	-2.6	x	FAD-linked oxidoreductase family
249002_at	At5g44520	1.1	1.0	-1.1	-1.9	-3.2	-2.5	x	putative protein
248994_at	At5g45250	1.1	1.1	-2.5	-2.5	-1.5	-2.0	x	disease resistance protein RPS4 (TIR-NBS-LRR class), putative
248793_at	At5g47240	1.2	1.4	-1.6	-3.7	-3.7	-5.7	x	mutT domain protein-like
248787_at	At5g47420	-1.3	-1.3	-2.5	-2.6	1.1	1.1	x	putative protein
248790_at	At5g47450	-1.9	-1.1	-4.9	-2.3	-6.1	-4.6	x	membrane channel protein-like, aquaporin
248657_at	At5g48570	-1.1	1.1	-2.6	-29.9	-3.5	-2.1	x	peptidylprolyl isomerase
248622_at	At5g49360	1.7	1.2	-16.0	-21.1	-8.6	-27.9	x	beta-xylosidase (BXL1)
248606_at	At5g49450	1.4	1.4	-3.5	-3.2	-3.0	-3.0	x	bZIP family transcription factor
248566_s_at	At5g49730	1.4	-1.4	-11.3	-13.0	-1.3	-3.5	x	FRO2-like protein
248382_at	At5g51890	1.3	1.0	1.0	-1.3	-3.5	-6.5	x	peroxidase, putative
248398_at	At5g51970	-1.1	-1.3	-3.7	-4.3	-2.3	-3.0	x	sorbitol dehydrogenase-like protein
248401_at	At5g52110	-1.1	-1.1	-2.8	-6.1	-1.5	-1.1	x	putative protein
248353_at	At5g52320	-1.3	-1.6	-3.0	-3.5	-1.6	-1.1	x	putative cytochrome P450
248332_at	At5g52640	-1.1	-1.1	1.1	-2.1	-4.6	-6.5	x	heat-shock protein
248329_at	At5g52780	-1.2	-1.5	-3.7	-3.0	-1.5	-2.1	x	expressed protein
248287_at	At5g52970	-1.1	1.1	-2.5	-2.5	-3.0	-2.0	x	thylakoid lumen 15.0-kDa protein
248252_at	At5g53250	-2.5	-1.6	-7.5	-6.1	-11.3	-14.9	x	arabinogalactan-protein, putative (AGP22)
248193_at	At5g54080	1.1	-1.1	-4.0	-4.6	-2.3	-2.6	x	homogentisate 1,2-dioxygenase
248037_at	At5g55930	1.2	1.0	-2.8	-3.2	-2.0	-2.3	x	oligopeptide transporter (AtOPT1)
248050_at	At5g56100	1.2	1.1	-3.5	-2.5	-1.7	-2.6	x	unknown protein
247977_at	At5g56850	-1.1	-1.1	-6.1	-4.6	-2.8	-3.0	x	putative protein
247954_at	At5g56870	1.4	1.1	-9.8	-14.9	-4.6	-3.0	x	beta-galactosidase
247931_at	At5g57040	1.1	-1.1	-1.1	-1.3	-2.5	-4.0	x	putative protein
247943_at	At5g57170	-1.1	-1.1	-2.8	-2.6	-1.7	-1.6	x	Macrophage migration inhibitory factor (MIF) family
247899_at	At5g57345	1.1	-1.2	-1.5	-1.4	-2.6	-3.0	x	expressed protein
247882_at	At5g57785	-1.3	-1.1	-4.9	-4.0	-2.5	-2.5	x	expressed protein
247884_at	At5g57800	1.1	1.0	-1.5	-1.5	-2.8	-2.6	x	lipid transfer protein
247863_at	At5g57900	-1.2	-1.4	-4.0	-21.1	-2.1	-4.6	x	SKIP1 interacting partner 1 (SKIP1)
247816_at	At5g58260	-1.1	-1.2	-2.5	-2.0	-2.6	-3.2	x	similar to unknown protein
247817_at	At5g58375	-1.1	-1.1	-2.6	-3.2	-1.4	-1.7	x	expressed protein
247828_at	At5g58510	-1.4	-1.3	-2.5	-5.7	-1.1	-1.1	x	putative protein

247780_at	At5g58770	-1.1	-1.5	-7.0	-8.6	-222.9	-362.0	x	x	dehydrodolichyl diphosphate synthase (DEDOL-PP synthase), putative expressed protein
247792_at	At5g58787	-1.1	1.0	-2.5	-2.6	-2.1	-2.0	x		subtilisin-like serine protease
247755_at	At5g59090	-1.6	-1.6	-2.5	-4.3	-5.7	-7.5	x	x	thymidylate kinase - like protein
247735_at	At5g59440	-1.3	-1.1	-2.3	-2.6	-2.6	-2.5	x		putative protein
247650_at	At5g59960	-1.1	1.0	-3.7	-2.6	-1.5	-1.9	x		cysteine proteinase AALP
247627_at	At5g60360	1.0	-1.1	-3.2	-4.0	-1.6	-2.1	x	x	anthocyanin 5-aromatic acyltransferase like
247573_at	At5g61160	1.1	1.5	-11.3	-21.1	-3.5	-36.8	x	x	putative protein
247522_at	At5g61340	-1.2	-1.4	-3.0	-1.6	-2.5	-2.6	x		putative protein
247443_at	At5g62720	1.1	1.1	-3.0	-3.5	-2.0	-2.6	x	x	GDSL-motif lipase/hydrolase protein
247396_at	At5g62930	-1.1	-1.2	-8.6	-32.0	-4.0	-2.8	x		topoisomerase, putative
247374_at	At5g63190	1.1	-1.3	-3.2	-4.0	-2.1	-2.8	x		transcription factor Hap5a-like protein
247388_s_at	At5g63470	1.2	1.1	-2.8	-3.2	-1.2	-1.9	x		1-aminocyclopropane-1-carboxylic acid oxidase-like protein
247333_at	At5g63600	-1.6	-1.4	-3.2	-3.7	-2.8	-2.5	x		serine/threonine-protein kinase
247352_at	At5g63650	-1.4	-1.4	-2.8	-11.3	-1.7	-1.1	x		putative protein
247347_at	At5g63780	1.1	-1.1	-1.6	-3.0	-2.8	-2.5	x	x	expressed protein
247282_at	At5g64240	1.1	1.1	-2.5	-2.6	-3.0	-3.5	x		2-oxoglutarate/malate translocator
247286_at	At5g64280	-1.1	1.0	-2.8	-2.5	-2.1	-2.1	x		beta-ureidopropionase
247275_at	At5g64370	-1.2	-1.3	-2.8	-3.2	1.3	-1.4	x		oligopeptide transporter (AtOPT4)
247284_at	At5g64410	1.0	1.1	-3.5	-3.0	1.3	1.3	x		glycosyl hydrolase family 3
247266_at	At5g64570	1.1	1.2	-3.2	-4.0	-1.6	-1.9	x		COP1-interacting protein CIP8
247219_at	At5g64920	1.1	1.2	-2.6	-2.5	-2.5	-1.7	x		acyl-CoA oxidase
247176_at	At5g65110	1.1	1.0	-3.0	-3.7	-2.0	-1.5	x		putative protein
247193_at	At5g65380	-1.1	-1.1	-1.7	-2.3	-4.0	-4.6	x	x	putative protein
247072_at	At5g66490	-1.1	-1.3	-5.7	-4.6	-1.1	-2.3	x		serine/threonine protein kinase
247043_at	At5g66880	1.1	1.0	-2.6	-2.5	-2.1	-3.7	x		ATPase subunit 9
257339_s_at	AtMg01080	1.3	-1.1	-1.2	-1.7	-3.7	-2.8	x		

The AGI identifier, the fold change values for each biological duplicate at each time (h), and the annotation for each probe set is shown. An "x" indicates times at which the probe set met the criteria (see Chapter 2) for being labeled cold responsive at a 2.5-fold level.

APPENDIX C

TABLE C.1. PROBE SETS UP-REGULATED BY LOW TEMPERATURE IN THE SOIL EXPERIMENT

Probe set	AGI	1h			24h			168h			Cold responsive			Annotation
		A	B		A	B		A	B		A	B		
261048_at	At1g01420	1.2	-1	6.5	3.7	4	2.5				x	x		similar to UTP-glucose glucosyltransferases
259426_at	At1g01470	1.4	1.3	7.5	9.2	3.2	3.7				x	x		Lea protein (LEA14)
260903_at	At1g02460	-2	1	2.1	5.7	2.8	4.9						x	putative polygalacturonase
260915_at	At1g02660	4.3	2.5	1.6	1.4	-1	1.3			x				expressed protein
262113_at	At1g02820	1.1	1	5.7	4.9	-2	-3				x			late embryogenesis abundant (LEA) protein family
262112_at	At1g02870	-1	1	2.6	2.5	2	1.4				x			expressed protein
264824_at	At1g03420	-1	-1	1.4	1.3	2.6	2.5						x	unknown protein
264818_at	At1g03530	-1	-1	3.5	4	1.7	1.2				x			expressed protein
263182_at	At1g05575	6.5	4.6	-1	-2	-3	1.7			x				expressed protein
260824_at	At1g06720	-1	-1	3.5	3	2.5	1.7				x			expressed protein
260832_at	At1g06780	-1	-1	3	2.6	1.5	1.3				x			glycosyltransferase family 8
261745_at	At1g08500	-1	1.3	2	3.2	3.7	6.5						x	expressed protein
264803_at	At1g08580	1	1.2	2.8	2.6	2	1.5				x			expressed protein
264652_at	At1g08920	1.3	1.2	3.7	4.9	1.9	2.3				x			putative sugar transport protein
264655_at	At1g09070	3.2	2.6	1.1	1.2	-2	1			x				expressed protein
264261_at	At1g09240	1.1	1.1	2.8	2.8	1.1	2				x			nicotianamine synthase, putative
264511_at	At1g09350	-1	-1	91	119	34	42				x			putative galactinol synthase
264515_at	At1g10080	1	1	2.8	3.2	1.5	1.5				x			hypothetical protein
264516_at	At1g10090	-1	-1	2.6	3.7	1.2	1.6				x			expressed protein
264458_at	At1g10410	1.1	1.4	7	8	3.7	4.3				x			expressed protein
263210_at	At1g10585	1.1	-3	4	5.7	1.4	7				x			Expressed protein
262452_at	At1g11210	5.7	3.2	17	30	3.2	7.5			x				expressed protein (COR35)
255931_at	At1g12710	1.2	1.1	2.6	2.6	2	1.7				x			hypothetical protein
262766_at	At1g13160	-1	1.3	2.8	3.2	1.5	1.3				x			expressed protein
259364_at	At1g13260	5.7	3.5	6.5	3.5	4.3	3.5			x				RAV1
260776_at	At1g14580	1.1	-1	5.3	3.2	2.8	1.7				x			zinc finger (C2H2 type) protein family
260744_at	At1g15010	8	3.2	1.6	1.2	1.1	1.1			x				expressed protein
262584_at	At1g15440	-1	1	2.8	3.5	2.1	1.6				x			WD-40 repeat protein family

256114_at	At1g16850	1.1	-1	42	42	26	24	x	x	expressed protein (COR17)
262518_at	At1g17170	-10	2.1	2.1	6.1	2.6	17		x	glutathione transferase, putative
261664_s_at	At1g18320	1.1	-1	3	2.6	2.3	1.3	x		expressed protein
261431_at	At1g18710	1.1	1.1	-1	1.1	3.7	3.7		x	MYB family transcription factor (MYB47)
261405_at	At1g18740	4	3.5	-1	-1	1.1	-1	x		expressed protein
261377_at	At1g18850	-1	-1	3.2	3.2	1.6	1.5		x	expressed protein
261428_at	At1g18870	1.5	-2	3.5	2.6	2.5	2.1	x		isochorismate synthase 1 (ICS1), putative
259479_at	At1g19020	4.6	2.6	-1	-1	-2	1.4	x		expressed protein
256017_at	At1g19180	6.5	5.3	3	3	1.6	4	x		expressed protein
260674_at	At1g19370	1.4	1	2.5	2.8	2.3	1.7	x		expressed protein
260656_at	At1g19380	6.1	2.6	-1	-3	-1	-2	x		hypothetical protein
261248_at	At1g20030	1.5	1.3	5.7	3.5	-1	-14		x	thaumatin family
259570_at	At1g20440	1.3	1.4	12	24	4.6	7	x	x	dehydrin (COR47)
259516_at	At1g20450	1.9	1.9	9.8	17	3.7	5.7	x	x	dehydrin (ERD10)
256091_at	At1g20693	1	1	2.6	4	1.7	2.5	x		high mobility group (HMG) protein beta1 (HMGbeta1)
256093_at	At1g20823	4.3	4	-1	-2	-1	-2	x		similar to putative RING zinc finger protein
259553_x_at	At1g21310	1.5	-1	1.7	1.9	2.5	2.5		x	hypothetical protein
260876_at	At1g21460	1.1	-1	3	2.8	2	1.7	x		nodulin MtN3 family protein
260921_at	At1g21540	3.2	-2	9.8	8	15	7.5		x	amp-binding protein, putative
262503_at	At1g21670	1.1	1.2	3.2	6.1	2	2.5	x		expressed protein
262496_at	At1g21790	1.1	-1	8	7	3.2	2.1	x		expressed protein
260856_at	At1g21910	14	9.8	1.4	-1	1.5	-1	x		TINY-like protein
255926_at	At1g22190	3.7	3	-2	-2	-2	-1	x		AP2 domain containing protein
264211_at	At1g22770	1	1	3.7	4.9	4.9	4.9	x		GIGANTEA
265184_at	At1g23710	5.7	3.7	1.3	-1	-1	-1	x		expressed protein
264866_at	At1g24140	7	2.6	1.6	-4	-1	-1	x		putative metalloproteinase
255733_at	At1g25400	11	3.7	1.9	-15	1.4	-2	x		expressed protein
255742_at	At1g25560	3.5	2.6	1.4	1.1	1.2	2.1	x		AP2 domain transcription factor (RAV2)
261263_at	At1g26790	1.1	2.6	3.5	4.9	3.7	3		x	H-protein promoter binding factor-2b like
264989_at	At1g27200	2.3	1.5	9.8	6.5	5.3	3.5		x	expressed protein
261648_at	At1g27730	17	9.2	2	1.3	-1	1.7	x		ZAT10/STZ
261651_at	At1g27760	-1	-1	3.7	4.3	2.6	2.5		x	expressed protein
261470_at	At1g28370	6.1	4.9	1.2	1.1	-1	1.6	x		ethylene responsive element binding factor 11
262747_at	At1g28540	-1	1.3	1.5	2.1	2.6	2.5		x	expressed protein

259789_at	At1g29395	-1	-1	5.7	8.6	5.3	8	x	similar to WCOR414 (WCOR414-TM1)
245770_at	At1g30240	-1	1	2.5	2.6	1.6	1.4	x	expressed protein
256310_at	At1g30360	1.1	1	2.8	3.2	1.3	1.2	x	dehydrin (ERD4)
264529_at	At1g30820	1.1	1.1	2.5	2.8	1	-1	x	CTP synthase-like protein
265154_at	At1g30960	1.5	1	4.3	3.2	2.6	-1	x	GTP-binding protein
261187_at	At1g32860	-1	-1	7	8	1.4	1.5	x	beta-1,3-glucanase precursor, putative
261192_at	At1g32870	-1	-1	2.5	2.5	1.2	1.3	x	NAM protein, putative
261193_at	At1g32920	8	4.3	-1	-2	-2	-2	x	expressed protein
261240_at	At1g32940	1.4	1.3	2.5	2	2.8	3	x	subtilisin-like serine protease
261566_at	At1g33230	1.1	1	5.7	4	3.7	2.3	x	expressed protein
261984_at	At1g33760	69	45	-2	-2	-1	-2	x	TINY-like protein
245757_at	At1g35140	49	17	4	-2	-2	-1	x	phosphate-induced (phi-1) protein
245755_at	At1g35210	4.9	2.8	-3	-2	1.3	-1	x	expressed protein
260870_at	At1g43890	1	-1	3.5	3.2	1.9	1.5	x	GTP-binding protein(RAB1Y), putative
245807_at	At1g46768	-2	-24	8	7.5	3.2	2.5	x	AP2 domain transcription factor (RAP2.1)
262440_at	At1g47710	-1	-1	5.7	6.5	2.5	2.3	x	serpin, putative
260727_at	At1g48100	-1	1	21	21	4.6	3	x	expressed protein (putative splicing domain)
262448_at	At1g49450	4.6	5.7	14	30	11	12	x	En/Spm-like transposon protein, putative
261613_at	At1g49720	-1	1.1	4.6	5.7	2.6	3.2	x	abscisic acid responsive elements binding factor 1 (ABF1)
245749_at	At1g51090	2.1	3	23	52	3.7	8	x	similar to proline-rich protein
265147_at	At1g51380	-1	1.1	3.7	7.5	2.3	2.1	x	expressed protein
260489_at	At1g51610	1	-1	3	4.6	2	3	x	cation efflux family
259841_at	At1g52200	1.3	1.4	3.2	2.3	2.8	3.7	x	expressed protein
260157_at	At1g52930	-1	1.1	3	2.8	2.5	1.7	x	expressed protein
261318_at	At1g53035	1.1	1.2	8	11	4.9	7.5	x	expressed protein
260589_at	At1g53400	1.1	-1	2.8	2.5	1.4	1.3	x	expressed protein
262259_s_at	At1g53870	1.5	-1	4	3	3.2	1.7	x	expressed protein
262094_at	At1g56110	-1	1	3	2.8	1.9	1.4	x	nucleolar protein Nop56, putative
245677_at	At1g56660	3.5	5.3	1.1	1.7	1.5	3.7	x	hypothetical protein
245866_s_at	At1g57990	6.1	3.7	-2	-3	-1	-2	x	unknown protein
256021_at	At1g58270	1.1	1.1	1.9	2.6	3.5	3.2	x	expressed protein
245840_at	At1g58420	4.3	3	1.3	-1	-1	-2	x	expressed protein
262099_s_at	At1g59500	1	-4	9.8	6.5	1.7	1.9	x	auxin-regulated protein GH3, putative
264246_at	At1g60140	1.4	1	6.1	3.7	2.5	1.9	x	trehalose-6-phosphate synthase, putative

264217_at	At1g60190	12	3.7	17	24	6.5	4.6	x	x	hypothetical protein
264758_at	At1g61340	4.6	4.6	1.5	1.6	1.9	1.3	x	x	late embryogenesis abundant protein, putative
264767_at	At1g61380	1.1	1.1	3	2.6	2.6	3.7	x	x	expressed protein
265119_at	At1g62570	-1	-1	42	45	13	12	x	x	flavin-containing monooxygenase (similar to glutamate synthase)
262644_at	At1g62710	-1	1	8	9.8	7	5.7	x	x	vaoluar cystein proteinase (beta-VPE)
259793_at	At1g64380	1.3	1.9	1.5	2	2.8	4.3	x	x	AP2-containing DNA-binding protein
262881_at	At1g64890	-1	-1	7	11	3.5	3.7	x	x	expressed protein (integral membrane/transporter family)
264153_at	At1g65390	28	4	-1	-3	2.1	-1	x	x	disease resistance protein (TIR class), putative
264213_at	At1g65400	7.5	4.6	1.5	-1	1.1	-2	x	x	hypothetical protein
256526_at	At1g66090	4.6	2.6	-1	-2	-2	1.1	x	x	disease resistance protein (TIR-NBS class), putative
256522_at	At1g66160	9.2	3.7	2.1	-3	1.1	-2	x	x	expressed protein
260135_at	At1g66400	2.5	2.8	-1	-1	-2	1	x	x	calmodulin-related protein, putative
256376_s_at	At1g66690	3.5	2.3	17	5.3	11	11	x	x	methyltransferase-related
264968_at	At1g67360	-1	-1	2.5	3.7	2.5	3	x	x	stress related protein
245200_at	At1g67850	1.2	1	4.3	3.7	3.2	2.3	x	x	expressed protein
260264_at	At1g68500	1.2	1.2	30	28	5.3	3.7	x	x	expressed protein
262281_at	At1g68570	-1	1	2.5	3	2.8	2.3	x	x	peptide transporter, putative
260338_at	At1g69250	-1	-1	3.2	3.2	1.5	1.5	x	x	putative RNA-binding protein
260357_at	At1g69260	-2	1.1	4.6	4.6	2.1	1.2	x	x	expressed protein
256300_at	At1g69490	2	1.3	4.6	4.3	-1	3.2	x	x	no apical meristem (NAM) protein family
259834_at	At1g69570	1.9	2.5	4.9	3.5	4.9	3.7	x	x	H-protein promoter binding factor-2b like
260410_at	At1g69870	1.1	-1	6.1	8.6	2.6	3.7	x	x	putative proton-dependent oligopeptide transport (POT) protein
260411_at	At1g69890	2.8	2.5	1.1	-1	-2	1	x	x	expressed protein
262313_at	At1g70900	1.2	1.1	3.5	4.3	1.9	1.6	x	x	expressed protein
261522_at	At1g71710	1.1	1	2.5	3	1.4	1.2	x	x	RIBOSOMAL PROTEIN, putative
260176_at	At1g71950	1.2	1.3	2.8	3.2	1.9	2	x	x	expressed protein
260399_at	At1g72520	5.7	3.5	1	-3	-2	1.9	x	x	putative lipoxxygenase
262382_at	At1g72920	15	4.3	-2	-8	-1	1.4	x	x	disease resistance protein (TIR-NBS class), putative
262383_at	At1g72940	7	4	-2	-2	-3	1.3	x	x	disease resistance protein (TIR-NBS class), putative
245724_at	At1g73390	1.5	1.1	2.6	3.5	1.5	1.9	x	x	hypothetical protein
245734_at	At1g73480	1.1	1.4	13	13	5.3	4.9	x	x	putative lysophospholipase
245731_at	At1g73500	4.3	2.8	1.5	1.2	1.7	2	x	x	mitogen-activated protein kinase kinase (MAPKK), putative
245777_at	At1g73540	14	5.7	-2	-3	-2	-2	x	x	unknown protein
260076_at	At1g73630	1.2	1.3	2.5	2.5	1.5	1.6	x	x	putative calmodulin protein

260227_at	At1g74450	8.6	4.6	-1	-2	1.2	-1	x	expressed protein
262166_at	At1g74840	1.2	1.1	4.3	2.6	2.1	1.1	x	myb family transcription factor
259925_at	At1g75040	1.1	1.6	1.9	2.5	3.5	3.5	x	thaumatin-like protein
261116_at	At1g75370	-1	-1	2.8	3.5	1.6	1.4	x	SEC14 cytosolic factor, putative
262682_at	At1g75900	-1	-1	2.5	2.5	2.5	2.5	x	family II extracellular lipase 3 (EXL3)
261749_at	At1g76180	1.3	1.1	3.2	3.7	1.4	1.4	x	dehydrin, putative
259971_at	At1g76580	1.1	-1	4.6	4	2.5	2.5	x	squamosa promoter binding protein -related
259977_at	At1g76590	1.4	1.1	8	11	2.5	3	x	expressed protein
259979_at	At1g76600	5.7	4.3	1.1	-1	-1	1	x	expressed protein
259879_at	At1g76650	56	17	1.1	-1	1.3	1.3	x	calcium-binding EF-hand family protein
264960_at	At1g76930	1.6	1.1	2.5	1.7	8.6	6.1	x	expressed protein
264953_at	At1g77120	-1	-1	18	16	7.5	2.5	x	alcohol dehydrogenase
259729_at	At1g77640	3.2	3.5	1.4	-2	1.1	1.3	x	AP2 domain transcription factor, putative
262164_at	At1g78070	1.4	1.1	6.1	5.7	3.2	2.6	x	expressed protein
264118_at	At1g79140	-1	1	3.2	3.5	2	1.6	x	expressed protein
264102_at	At1g79270	1.1	-1	4.6	3.7	1.6	1	x	expressed protein
261356_at	At1g79660	-1	1.1	2.8	2.6	1.2	1.2	x	unknown protein
262050_at	At1g80130	-1	1.2	15	12	17	15	x	expressed protein (COR33.5)
260331_at	At1g80270	-1	-1	2.5	2.6	1.4	1.3	x	DNA binding protein, putative
261892_at	At1g80840	16	6.1	-1	-1	-1	3	x	WRKY family transcription factor (WRKY40)
266119_at	At2g02100	1.1	1.1	3.2	5.3	2.5	3.7	x	putative plant defensin protein putative (PDF2.2)
266141_at	At2g02120	1.1	4	3.5	34	5.7	20	x	putative plant defensin protein putative (PDF2.1)
264042_at	At2g03760	1.2	1.9	2.6	5.7	-1	2.8	x	putative steroid sulfotransferase
263334_at	At2g03820	1	1.1	2.8	2.8	1.9	1.4	x	nonsense mediated mRNA decay protein NMD3 family
263046_at	At2g05380	-1	1.1	1.3	1.9	2.6	3.7	x	expressed protein (COR8.6)
265480_at	At2g15970	-1	-1	3.7	6.5	2.6	3.7	x	similar to cold acclimation protein WCOR413 (WCOR413-PM1)
265354_at	At2g16700	-1	1.3	3.7	4	-1	1.2	x	actin depolymerizing factor 5 (ADF5)
266532_at	At2g16890	1.3	3	14	16	8.6	9.8	x	putative phenylpropanoid glucosyltransferase
263574_at	At2g16990	-1	-1	3	3.7	2.3	2.3	x	putative tetracycline transporter protein
264787_at	At2g17840	3	2.3	8.6	13	2.5	4.3	x	ERD7
266934_at	At2g18900	-1	-1	2.5	2.8	1.3	1	x	WD-40 repeat protein family
267280_at	At2g19450	1.1	-1	3	4	2	2.1	x	diacylglycerol O-acyltransferase (TAG1)
264019_at	At2g21130	-1	-1	2.6	4.3	1.5	2.3	x	peptidyl-prolyl cis-trans isomerase (cyclophilin/CYP2)
263739_at	At2g21320	1.1	1.1	5.3	4	4.3	1.9	x	CONSTANS B-box zinc finger family protein

263517_at	A12g21620	1	1.1	4.6	5.7	2.6	3.2	x	x	responsive to dessication protein (RD2) family
263352_at	A12g22080	1.1	1	4.9	4.3	3.2	2.8	x	x	related to En/Spm transposon family of maize
263452_at	A12g22190	1.1	1.1	2.6	4	1.5	1.9	x		putative trehalose-6-phosphate phosphatase
264000_at	A12g22500	4.9	2.6	1.9	1.7	-1	1.4	x		mitochondrial carrier protein family
266797_at	A12g22840	1.2	1.7	2.5	3.2	2	2	x		expressed protein
267261_at	A12g23120	1.7	1.7	6.5	6.1	3	2.8	x	x	expressed protein (COR8.5)
267293_at	A12g23810	4.9	2.6	-1	-1	1.1	1.4	x		hypothetical protein
266567_at	A12g24050	-1	1.1	2.6	2.5	1.5	1.4	x		putative eukaryotic initiation factor 4 (eIF4)
265999_at	A12g24100	1.1	1.2	6.1	3.5	3.7	2.6	x	x	expressed protein
265662_at	A12g24500	-1	1	2.6	2.6	1.6	1.3	x		C2H2-type zinc finger protein (FZF)
263789_at	A12g24560	-5	7	7.5	26	1.7	17	x		putative GDSL-motif lipase/hydrolase
245041_at	A12g26530	5.7	2.8	1.1	-2	-1	1.1	x		expressed protein (similar to yeast pheromone receptor)
266861_at	A12g26830	1.1	1	2.6	3	1.5	1.5	x		putative choline kinase
266316_at	A12g27080	11	6.1	-2	-2	1	-1	x		unknown protein
266259_at	A12g27830	2	2	3.7	5.3	1.5	2.5	x		expressed protein
265276_at	A12g28400	3	1.3	6.1	4	2	2.1	x		hypothetical protein
266225_at	A12g28900	1	-1	3.2	6.1	2	3.7	x		putative membrane channel protein
266834_s_at	A12g30020	8.6	4.9	-2	-1	-1	-1	x		protein phosphatase 2C (PP2C)
266832_at	A12g30040	11	7	1.1	-1	1	-1	x		protein kinase family
267567_at	A12g30770	1.1	1.3	3	2.5	2.6	3.7	x		cytochrome p450 family
263249_at	A12g31360	1	1.2	3.5	4.6	1.7	2.1	x		delta 9 desaturase (ADS2)
263252_at	A12g31380	1.2	1.3	3.7	2.6	3.2	1.5	x		salt tolerance-like protein
265670_s_at	A12g32210	2.8	1.9	2.5	2.5	1.1	1.3	x		expressed protein
255795_at	A12g33380	-1	-1	3.2	6.5	1.6	2	x		RD20
267461_at	A12g33830	1.3	1.1	3.7	5.7	2.3	4.3	x		auxin-regulated protein
267315_at	A12g34720	-1	1.1	2.8	3.2	1.9	1.7	x		putative CCAAT-binding transcription factor subunit
266545_at	A12g35290	13	4.9	2	1.7	1.9	-1	x		hypothetical protein
265841_at	A12g35710	18	4	3.7	-1	-1	-1	x		putative glycogenin
263935_at	A12g35930	8.6	4	-1	-5	-1	1.1	x		unknown protein
263951_at	A12g35960	-1	1	3.2	4.3	2.1	2.5	x		putative harpin-induced protein
263931_at	A12g36220	4.3	2.8	4.3	4.6	1.7	2.3	x		expressed protein
263907_at	A12g36270	2.5	5.3	9.2	11	11	13	x		abscisic acid insensitive 5 (ABI5)
267036_at	A12g38465	1	-2	2.8	2.8	2.6	2.8	x	x	Expressed protein
267028_at	A12g38470	6.1	3.7	-1	-2	-2	1.5	x		WRKY family transcription factor (WRKY33)

267592_at	At2g39710	1.1	1.9	1.9	2.5	4.6	4	x	expressed protein
267361_at	At2g39920	1.1	1.1	2.8	3	1.9	2.8	x	expressed protein
267357_at	At2g40000	11	5.3	1.3	-2	-2	-1	x	unknown protein
263384_at	At2g40130	1.4	1.1	2.5	2.8	1.9	1.9	x	expressed protein
263379_at	At2g40140	5.7	3.5	2.6	2.3	1.6	2.1	x	putative CCH-type zinc finger protein
245096_at	At2g40880	1	1.1	4	3	1.5	1.3	x	putative cysteine proteinase inhibitor B (cystatin B)
267069_at	At2g41010	3.5	2.6	-1	-2	1.1	1.3	x	unknown protein
267080_at	At2g41190	1	1.1	3.2	7	1.7	1.4	x	expressed protein
245119_at	At2g41640	30	7	1.1	-8	1.9	-1	x	expressed protein
267534_at	At2g41900	1	1	2.5	3.2	1.4	1.7	x	putative CCH-type zinc finger protein
263495_at	At2g42530	-1	-1	9.8	17	6.1	11	x	COR15b
263497_at	At2g42540	-1	-1	14	18	9.8	15	x	COR15a
260556_at	At2g43620	2.1	1.4	18	17	15	16	x	putative endochitinase
260585_at	At2g43650	1.3	1.7	2.8	2.6	2.1	1.3	x	expressed protein
267509_at	At2g45660	1.1	1	4.3	2.8	2.8	1.9	x	MADS-box protein (AGL20)
263783_at	At2g46400	4.3	2.5	-2	-3	-2	1	x	WRKY family transcription factor
266720_s_at	At2g46790	1.2	-1	11	5.3	11	1.7	x	pseudo-response regulator (APRR9/TL1)
266719_at	At2g46830	1	1.1	7	2.8	3.5	1.2	x	MYB-related transcription factor (CCA1)
263320_at	At2g47180	-1	-1	11	11	7	6.5	x	galactinol synthase
266462_at	At2g47770	1.7	-3	4.6	5.3	4.6	1.1	x	expressed protein
266514_at	At2g47890	1	-1	5.3	9.2	3.7	4.3	x	CONSTANS B-box zinc finger family protein
266510_at	At2g47990	-1	1.1	3	3.5	1.9	1.5	x	WD-40 repeat protein family
258947_at	At3g01830	9.2	2.8	-1	-3	-2	1.4	x	expressed protein
259077_s_at	At3g02230	-1	-1	2.8	2.6	2	1.9	x	reversibly glycosylated polypeptide-1
259132_at	At3g02250	1.1	1	2.6	2.6	1.9	1.5	x	similar to auxin-independent growth promoter
258606_at	At3g02840	9.8	3	-2	-2	1.4	1.2	x	expressed protein
258603_at	At3g02990	2.3	1.1	6.1	2.1	6.1	3.7	x	putative heat shock transcription factor
259173_at	At3g03640	1.1	1.1	4	4	1.9	1.5	x	beta-glucosidase (GLUC)
258805_at	At3g04010	3.7	4.3	18	30	4	11	x	putative beta-1,3-glucanase
258792_at	At3g04640	11	7	1.2	-1	-1	-1	x	glycine-rich protein
258893_at	At3g05660	1.1	1.1	7.5	6.1	7	6.5	x	disease resistance protein
258735_at	At3g05880	1	-1	2.8	3.7	1.5	1.9	x	low temperature and salt responsive protein LT16A
258505_at	At3g06530	-1	-1	2.8	3	1.9	1.5	x	expressed protein
258545_at	At3g07050	1.1	1	4.3	3	3.5	2	x	putative GTPase

258979_at	At3g09440	-1	-1	2.6	2.8	1	1.5	x	heat-shock protein (At-hsc70-3)
258719_at	At3g09540	-1	-1	5.7	5.7	3.5	2.6	x	putative pectate lyase
259137_at	At3g10300	2	1.1	2.8	2.5	2.5	2.6	x	unknown protein
258965_at	At3g10530	-1	-1	3.5	3.7	2.1	1.7	x	WD-40 repeat protein family
256442_at	At3g10930	74	4.6	-1	-4	1.1	-1	x	expressed protein
256430_at	At3g11020	1.2	1.2	3.2	3	1.7	2.6	x	DREB2B
256288_at	At3g12270	-1	1.1	2.8	4.9	2.5	1.9	x	putative arginine N-methyltransferase
256266_at	At3g12320	1.1	1.4	5.7	2.5	4.3	1.2	x	expressed protein
257702_at	At3g12670	-1	1	3	3	2.1	1.4	x	CTP synthase (UTP-ammonia ligase), putative
257654_at	At3g13310	1.2	1.2	2.8	3.2	2	1.4	x	DnaJ protein, putative
257708_at	At3g13330	-1	1.1	2	2.5	2.8	2.6	x	expressed protein
257610_at	At3g13810	1.2	1.3	2.6	3.5	3.5	2.6	x	zinc finger protein, putative
258370_at	At3g14395	2.3	1	2	-5	13	2.8	x	Expressed protein
257280_at	At3g14440	2.3	2.8	4	9.2	2.8	2.6	x	9-cis-epoxycarotenoid dioxygenase (NCED3)
258094_at	At3g14690	1.1	1	3.7	4.6	2.1	1.9	x	putative cytochrome P450
257237_at	At3g14890	-1	-1	8	7	3	2.6	x	DNA nick sensor, putative
257053_at	At3g15210	4.3	2.8	1.9	2.3	1.2	1.5	x	ethylene responsive element binding factor 4 (AtERF4)
258402_at	At3g15450	2.5	1.7	5.7	3.2	1.4	1.3	x	expressed protein
258437_at	At3g16560	1.3	1.3	3	2.6	1.7	1.4	x	expressed protein
258436_at	At3g16720	2.6	2.5	-1	-1	-2	-1	x	zinc finger (C3HC4-type RING finger) protein family
257650_at	At3g16800	1.1	1.1	2.8	3	2.6	1.9	x	protein phosphatase 2C (PP2C)
257652_at	At3g16810	1	1.3	2.8	3	1.6	1.3	x	expressed protein
257876_at	At3g17130	-2	-1	9.2	9.8	2.8	1.6	x	similar to invertase/pectin methylesterase inhibitor
256797_at	At3g18600	-1	1.1	3	2.6	2.1	1.2	x	DEAD/DEAH box helicase, putative
256891_at	At3g19030	4.3	3	1.5	1.1	1.3	1.1	x	expressed protein
258016_at	At3g19350	-2	1.1	2.8	3.2	4.9	4.9	x	hypothetical protein
257076_at	At3g19680	2.6	3	1.6	-1	1.3	1	x	expressed protein
257083_s_at	At3g20590	3	2.5	-2	-2	-2	-1	x	non-race specific disease resistance protein, putative
258166_at	At3g21540	-1	-1	3.5	3.2	2	1.5	x	WD-40 repeat protein family
258316_at	At3g22660	-1	1.2	3.7	3.7	2.8	2.1	x	expressed protein
258321_at	At3g22840	1	1.1	13	6.5	5.7	3.2	x	early light-induced protein (ELIP)
257771_at	At3g23000	1.6	1.2	4.3	2.8	1.7	1.1	x	SNF1 related protein kinase (ATSRPK1)
257925_at	At3g23170	4	3.5	-1	-1	-1	1	x	expressed protein
258104_at	At3g23620	-1	1.2	3	3	2.3	1.7	x	expressed protein

256890_at	At3g23830	-1	-1	2.8	2.5	2.3	1.4	x	glycine-rich RNA-binding protein
257253_at	At3g24190	-1	1	2.5	2.5	1.2	1.1	x	expressed protein
258139_at	At3g24520	4.6	2.5	6.5	7	1.9	1.3	x	heat shock transcription factor family
256755_at	At3g25600	4	3	-2	-2	1	1.2	x	calmodulin, putative
258078_at	At3g25870	1.1	1.2	4.3	7	1.4	2.8	x	expressed protein
256881_at	At3g26410	-1	-1	2.5	2.6	2	1.6	x	expressed protein
257154_at	At3g27210	1.9	1.5	6.5	6.1	4	4	x	expressed protein
257968_at	At3g27550	1.1	-1	2.5	3.7	-1	1.3	x	expressed protein
257226_at	At3g27880	-1	1.1	2.6	3.7	1.6	1.3	x	expressed protein
257271_at	At3g28007	-2	-1	2.8	3.7	4.9	4.3	x	Expressed protein
256577_at	At3g28220	1.3	-1	3	1.9	7.5	4.6	x	expressed protein
256601_s_at	At3g28290	1.2	-1	3	4	16	20	x	integrin like protein (similar to At14a)
256633_at	At3g28340	11	4.6	1.9	-1	1.1	-1	x	unknown protein
256595_x_at	At3g28530	1.1	1	3.7	3.2	2.1	1.7	x	hypothetical protein
256589_at	At3g28740	1	1	3.7	8.6	7	24	x	cytochrome p450 family
265941_s_at	At3g32920	1.2	-1	4	2.8	2.6	1.5	x	recA, putative
252679_at	At3g44260	21	7.5	-1	-2	-2	-1	x	CCR4-NOT complex protein, putative
252625_at	At3g44750	-1	1	2.8	2.5	1.7	1.1	x	putative histone deacetylase
252591_at	At3g45600	1	-1	4.3	4.6	2.8	2.8	x	senescence-associated protein family
252563_at	At3g45970	4.9	4.3	4.3	4.9	-2	-2	x	expansin protein family (EXPL1)
252474_at	At3g46620	9.2	5.3	1.1	1	1.1	1.1	x	zinc finger (C3HC4-type RING finger) protein family
252374_at	At3g48100	3.5	3.7	-1	-1	1	-1	x	response regulator 2 (ATR2)
252323_at	At3g48530	1	-1	2.8	2.6	1.6	1.3	x	putative protein
252346_at	At3g48650	9.8	4.3	-3	-2	1.5	1.5	x	hypothetical protein
252305_at	At3g49240	-1	-1	2.5	3.2	1.4	1.4	x	pentatricopeptide (PPR) repeat-containing protein
252193_at	At3g50060	4.9	4	-1	-2	-1	-2	x	MYB transcription factor (MYB77)
252214_at	At3g50260	1.2	2.1	6.1	3.7	1.2	1.5	x	EREBP-3 homolog
252131_at	At3g50930	5.7	2.8	-2	-3	-1	1.1	x	BCS1 protein-like protein
252102_at	At3g50970	1	-1	56	79	28	37	x	dehydrin (Xero2)
252053_at	At3g52400	4.9	3.5	1.1	-1	-1	1.6	x	syntaxin SYP122
251984_at	At3g53260	1.4	1.1	4	2.5	2.5	1.4	x	phenylalanine ammonia-lyase 2 (PAL2)
251910_at	At3g53810	1.2	1.5	3.2	2.8	2.1	1.7	x	serine/threonine-specific kinase like protein
251928_at	At3g53980	-1	-6	4.3	-1	16	3.5	x	putative protein
251927_at	At3g53990	1.1	1.3	4.3	6.5	1.4	2.6	x	expressed protein

251922_at	At3g54030	1.2	-1	2.8	2.5	2.8	2.3	x	protein kinase -like protein
251899_at	At3g54400	1	-1	4.3	4	2.3	2.3	x	aspartyl protease family
251800_at	At3g55510	1.1	-1	4.3	3.7	2.8	1.6	x	expressed protein
251793_at	At3g55580	-2	1.1	24	16	15	11	x	regulator of chromosome condensation RCC1 family
251775_s_at	At3g55610	1	-1	8	8.6	3	2.5	x	delta-1-pyrroline-5-carboxylate synthetase (P5CS2)
251776_at	At3g55620	-1	-1	2.5	2.8	1.2	1.2	x	putative eukaryotic translation initiation factor 6 (EIF-6)
251753_at	At3g55760	1.1	1	8	7.5	2.6	2.3	x	expressed protein
251745_at	At3g55980	11	5.7	1	-2	-1	-1	x	zinc finger (CCCH type) protein family
246289_at	At3g56880	4.6	3.2	1.7	1.6	1.7	1.5	x	VQ motif-containing protein family
251658_at	At3g57020	-1	-1	4.3	2.6	3.5	1.9	x	putative protein stricosidine synthase
251538_at	At3g58660	1	-1	3	2.8	1.7	1.1	x	expressed protein
251507_at	At3g59080	3.2	2.6	-1	-2	-1	-2	x	chloroplast nucleoid DNA binding protein family
251494_at	At3g59350	2.5	2	2.5	3	1.1	1.9	x	putative serine/threonine protein kinase (similar to Pto1)
251432_at	At3g59820	-1	-1	4.6	5.3	2.5	2.3	x	putative leucine zipper-EF-hand containing transmembrane protein
251402_at	At3g60290	1.3	1	1	-2	2.6	3.2	x	2-oxoglutarate-dependent dioxygenase family
251372_at	At3g60520	1.4	1.2	3.2	2.6	2.3	2.3	x	putative protein
251336_at	At3g61190	18	4	4.9	1.2	1.7	1.3	x	BON1-associated protein 1 (BAP1)
251272_at	At3g61890	1.2	1.7	3.2	6.1	2.8	2.1	x	homeobox-leucine zipper protein ATHB-12
251221_at	At3g62550	1.1	1.4	3.7	7	1.6	3.5	x	putative protein
251227_at	At3g62700	-1	-1	2.5	3.2	2.1	2.5	x	ABC transporter, glutathione-conjugate transporter, putative
251229_at	At3g62740	1.3	-1	37	2.5	39	1.4	x	beta-glucosidase-like protein
251196_at	At3g62950	3	2.6	2.1	-1	2	2.6	x	glutaredoxin -like protein
255625_at	At4g01120	1.2	1.1	2.8	2.8	1.4	-1	x	G-box binding factor(bZIP protein), putative
255568_at	At4g01250	3.5	3	1.1	-1	-1	-1	x	WRKY family transcription factor (WRKY31)
255543_at	At4g01870	1.5	1.5	11	11	4.3	7	x	hypothetical protein
255549_at	At4g01950	2.8	2.6	-1	-2	1.1	-2	x	unknown protein
255524_at	At4g02330	3	2.5	3.2	2	3	3.2	x	pectinesterase family
255479_at	At4g02380	3.2	2.1	4	2.5	2.1	3.2	x	late embryogenesis abundant protein (SAG21)
255494_at	At4g02710	-1	1.1	2.3	2.1	2.8	2.5	x	unknown protein
255452_at	At4g02880	1	-1	2.6	2.6	1.6	1.4	x	hypothetical protein
255403_at	At4g03400	1.2	1.3	3	2.5	2.8	2.6	x	auxin responsive protein, putative (GH3 family)
255331_at	At4g04330	1.1	-1	2.5	3.5	1.2	2	x	expressed protein
255278_at	At4g04940	-2	1.1	2.8	3.7	1.5	1.7	x	WD-40 repeat protein family
255259_at	At4g05020	-1	1.2	2.5	3	2.6	4	x	NADH dehydrogenase - related

255255_at	At4g05070	1.9	1.6	4	2.6	2.1	1.1	x	coded for by A. thaliana cDNA T44741
255225_at	At4g05410	-1	1	2.8	3.2	1.9	1.5	x	WD-40 repeat protein family
254926_at	At4g11280	7.5	4.6	1.1	1.1	-1	1.6	x	ACC synthase (AtACS-6)
254850_at	At4g12000	1.1	1.1	4.3	4.9	2.5	1.9	x	expressed protein
254818_at	At4g12470	1.1	1.2	56	69	49	56	x	pEARLI 1-like protein
254805_at	At4g12480	1.1	1.2	32	42	64	97	x	pEARLI 1
254832_at	At4g12490	1	-1	3.5	2.5	7.5	11	x	pEARLI 1-like protein
254819_at	At4g12500	-1	1.3	4.3	7.5	9.8	21	x	pEARLI 1-like protein
254778_at	At4g12750	-1	1	2.8	2.6	1.6	1.3	x	expressed protein
245306_at	At4g14690	1.2	1.5	14	12	3.7	2.3	x	early light-inducible protein like
245533_at	At4g15130	1.1	1.1	7	6.1	3.5	3.5	x	putative phosphocholine cytidyltransferase (AtCCT2)
245352_at	At4g15490	-1	-1	3.5	5.7	-1	1.2	x	UDP-glycosyltransferase, putative
245512_at	At4g15770	1	1.1	2.8	2.6	2	1.4	x	expressed protein
245523_at	At4g15910	1.1	-1	2.5	4.6	1.7	-1	x	drought-induced protein (DI21)
245336_at	At4g16515	1.1	1	4	3.7	1.3	1	x	expressed protein
245437_at	At4g16630	1.1	1.1	3.2	2.6	1.7	1.1	x	RNA helicase like protein
245346_at	At4g17090	1.3	1.3	4.3	4.9	1.9	2.3	x	glycosyl hydrolase family 14 (beta-amylase)
245250_at	At4g17490	12	13	-7	-2	-2	-10	x	ethylene responsive element binding factor (AtERF6)
245427_at	At4g17550	2	-1	20	12	9.2	3.7	x	glycerol-3-phosphate permease like protein
254707_at	At4g18010	2.8	2.6	1.7	1.4	1.2	1.1	x	putative protein
254662_at	At4g18270	-1	-1	2.5	3.7	2	1.7	x	glycosyltransferase family 4 (ATTRANS11)
254667_at	At4g18280	1.9	1.6	4	4.3	2.8	3	x	glycine-rich cell wall protein
254670_at	At4g18390	1	1	2.6	3	1.6	1.6	x	TCP family transcription factor, putative
254639_at	At4g18750	1.9	3	2	8.6	2.8	5.7	x	putative protein
254592_at	At4g18880	3	2.6	1.2	1	1.9	1.9	x	heat shock transcription factor - like protein
254543_at	At4g19810	1.7	1.1	2.5	2.6	1.9	2.1	x	glycosyl hydrolase family 18
254457_at	At4g21170	1.4	-1	2.6	3	1.5	1.9	x	putative protein
254314_at	At4g22470	1.6	2.1	2	4.6	2.5	6.5	x	protease inhibitor/seed storage/lipid transfer protein (LTP) family
254210_at	At4g23450	2.6	-1	17	2.5	4.6	1.1	x	putative protein
254227_at	At4g23630	-1	1.1	3.7	3.2	2.1	1.9	x	expressed protein
254231_at	At4g23810	7	3.2	-2	-2	-1	2.5	x	WRKY family transcription factor (WRKY53)
254178_at	At4g23880	1.5	2	3	2.8	2.3	1.7	x	hypothetical protein
254188_at	At4g23920	1.1	1.2	3.5	4.9	2.1	2.1	x	putative UDP-glucose 4-epimerase
254197_at	At4g24040	1.1	1.2	2.5	3	3	3.5	x	glycosyl hydrolase family 37 (trehalase)

254157_at	At4g24220	1.1	1.1	2.5	2.8	1.4	1.7	x	putative protein
254120_at	At4g24570	34	11	1.1	-2	1.1	-1	x	mitochondrial carrier protein family
254085_at	At4g24960	1.1	-1	8.6	8	2.5	2	x	similar to abscisic acid-induced protein (HVA22D)
254076_at	At4g25340	-1	-1	3.2	2.8	1.9	1.4	x	expressed protein
254075_at	At4g25470	37	26	14	8	4.6	2.1	x	CBF2/DREB1c
254066_at	At4g25480	16	24	8.6	13	2	2.1	x	CBF3/DREB1a
254074_at	At4g25490	74	315	14	30	5.3	12	x	CBF1/DREB1b
254073_at	At4g25500	-1	1.1	3.2	4.3	2.1	2.5	x	splicing factor (At-SRp40)
254080_at	At4g25630	-1	-1	4	3.2	3.5	2.1	x	fibrillarin 2 (AtFib2)
254079_at	At4g25730	-1	1	3.2	3.5	1.9	1.4	x	expressed protein
253975_at	At4g26600	4.9	1.2	5.7	4	3.2	1	x	expressed protein
253915_at	At4g27280	11	4.3	-2	-2	-2	1	x	calcium-binding EF-hand family protein
253872_at	At4g27410	1.1	1.5	11	13	1.7	2.8	x	no apical meristem (NAM) protein family (RD26)
253875_at	At4g27520	1	1.1	3.2	4	1.6	1.9	x	putative protein ENOD20 predicted GPI-anchored protein
253879_s_at	At4g27570	-1	1	4.6	6.1	2.1	2	x	UDP rhamnose-anthocyanidin-3-glucoside rhamnosyltransferase
253830_at	At4g27652	5.3	3.7	-1	1	-2	1.1	x	Expressed protein
253859_at	At4g27657	6.1	3.7	2.5	1.9	2.6	1.5	x	expressed protein
253841_at	At4g27830	1	1.1	7	5.7	3.7	2.6	x	putative beta-glucosidase
253813_at	At4g28150	1.2	-1	3.2	2.6	2.1	1.7	x	putative protein
253777_at	At4g28450	-1	1.1	2.5	2.8	1.4	1.3	x	WD-40 repeat protein family
253722_at	At4g29190	1.9	2	4.6	5.3	2.6	3	x	zinc finger (CCH type) protein family
253695_at	At4g29510	-1	1	2.6	2.8	1.4	1.3	x	arginine methyltransferase (PAM1)
253643_at	At4g29780	26	9.2	1.1	-2	-1	-1	x	expressed protein
253627_at	At4g30650	1.1	-1	3.5	8	2.6	6.5	x	hydrophobic protein (LT16A/RC12A)
253585_at	At4g30720	1	1.1	1.2	1.4	2.8	2.5	x	expressed protein
253595_at	At4g30830	7.5	-2	128	74	97	26	x	expressed protein (COR42)
253559_at	At4g31140	1.1	-1	3	2.6	2	1.7	x	glycosyl hydrolase family 17
253485_at	At4g31800	2.8	2.5	1.1	-2	1.1	1.1	x	WRKY family transcription factor (WRKY18)
253455_at	At4g32020	3.2	2.8	2.3	2.6	1.2	1.6	x	putative protein
253425_at	At4g32190	1	-1	5.7	3.7	2	1.2	x	expressed protein
253423_at	At4g32280	-1	1	6.1	4.3	3.5	2.1	x	auxin-responsive protein AUX/IAA family
253416_at	At4g33070	-1	-2	30	37	11	8	x	pyruvate decarboxylase-1 (Pdc1)
253343_at	At4g33540	-1	1.1	1.9	3.5	3.5	5.7	x	putative protein
253323_at	At4g33920	3.5	4.3	1.7	2.8	1.1	1.6	x	putative protein phosphatase

253322_at	At4g33980	2.1	1.5	4.6	9.2	2.5	3.5	x	x	expressed protein (COR28)
253268_s_at	At4g34135	1.3	1.5	1.5	3.2	2.8	4.6		x	glucosyltransferase -like protein
253259_at	At4g34410	3.5	4.3	-1	1.5	-2	2	x		AP2 domain transcription factor, putative
253254_at	At4g34650	1	-3	8	17	4.3	4.3	x	x	squalene synthase (SQS2)
253252_at	At4g34740	-1	1	2.6	2.6	1.4	1.4	x		amidophosphoribosyltransferase 2 precursor
253213_at	At4g34910	-2	-1	2.8	3	2.1	1.6	x		RNA helicase (RH16)
253219_at	At4g34990	-2	-1	2.6	2.5	2.1	1.5	x		MYB family transcription factor (MYB32)
253188_at	At4g35300	-1	-1	2.5	3.2	2.8	2.5	x	x	putative sugar transporter protein
253104_at	At4g36010	4	3	11	12	3	1.9	x	x	thaumatin-like protein
253125_at	At4g36040	1.5	1.6	3.5	2.5	1.3	1.1	x		DnaJ-like protein
253103_at	At4g36110	1.4	1.1	3.2	2.8	1.3	-1	x		putative auxin-induced protein
246200_at	At4g37240	2.5	2.5	-1	-2	-1	1.1	x		putative protein
246253_at	At4g37260	3.2	3	1.9	1.9	1.6	1.7	x		MYB family transcription factor (MYB73)
253097_at	At4g37320	1.3	-1	4	3.5	2.3	2	x		cytochrome P450 family
253054_at	At4g37580	1	-1	2.6	2.5	2.1	1.7	x		probable N-acetyltransferase hookless 1
253061_at	At4g37610	4.9	2.8	-2	-3	-3	-2	x		p300/CBP acetyltransferase-related protein
252982_at	At4g38130	1	1.1	1.5	1.6	2.5	2.5		x	Histone deacetylase
252986_at	At4g38380	1.3	-1	8	2.3	11	3		x	hypothetical protein
252997_at	At4g38400	1.3	1	4	3.5	1.9	-1	x		expansin protein family (EXPL2)
252956_at	At4g38580	1.1	1.1	9.2	16	3.7	6.1	x	x	farnesylated protein (ATFP6)
252908_at	At4g39670	3.7	2.8	1.6	1.5	1.1	2.6	x		putative protein
252880_at	At4g39730	-1	-1	2.5	2.6	1.9	1.9	x		expressed protein
252863_at	At4g39800	-1	-1	3.2	3.7	2.1	2.3	x		myo-inositol-1-phosphate synthase
251084_at	At5g01520	-1	1.1	4.3	4.9	2.5	2.1	x		zinc finger (C3HC4-type RING finger) protein family
251060_at	At5g01820	1.1	1.1	2.5	2.6	1.3	1.5	x		putative protein
251039_at	At5g02020	1.6	1.5	5.3	6.5	1.6	2.5	x		putative protein
250971_at	At5g02810	-1	1	2.8	2.1	4.6	3.7		x	pseudo-response regulator (APRR7)
245702_at	At5g04220	1	-1	3	2.3	2.6	2.5		x	C2 domain-containing protein
245699_at	At5g04250	-1	1.3	5.7	9.2	1.9	1.7	x		putative protein
245711_at	At5g04340	9.8	7	4.9	4.3	1.2	1.9	x		putative c2h2 zinc finger transcription factor
250825_at	At5g05210	1.1	1.1	3.2	2.5	1.5	1.2	x		expressed protein
250781_at	At5g05410	3.7	3.2	2.8	7.5	1.1	2.3	x		DREB2A
250690_at	At5g06530	1	1	1.9	1.5	4	2.5		x	ABC transporter family protein
250648_at	At5g06760	-2	1.1	34	239	6.5	13	x		late embryogenesis abundant protein LEA like

250670_at	At5g06860	1.9	2.1	7.5	5.3	6.5	9.2	x	x	polygalacturonase inhibiting protein (PGIP1)
250665_at	At5g06980	-1	1.2	7	2.8	4	1.1	x	x	expressed protein
250662_at	At5g07010	-2	1.1	20	39	28	137	x	x	steroid sulfotransferase-like protein
245885_at	At5g09440	1.7	1.3	3	2.8	3	1.7	x	x	putative protein
246018_at	At5g10695	3.5	2.8	-1	-1	-2	-2	x		Expressed protein
245904_at	At5g11110	-1	1.3	2.5	4.3	2	2.5	x	x	sucrose-phosphate synthase, putative
250418_at	At5g11240	-1	1	3.2	2.6	2.1	1.5	x	x	WD-40 repeat protein family
250309_at	At5g12220	-1	1.2	2.5	2.5	1.7	1.4	x	x	expressed protein
250279_at	At5g13200	1.6	1.3	3.7	3	2.1	1.7	x	x	like ABA-responsive protein
250252_at	At5g13750	-2	-1	2.5	3	2.5	2.5	x	x	transporter-like protein
250151_at	At5g14570	1.1	1.1	4.9	5.7	3.2	3.7	x	x	similar to trans-membrane nitrate transporter protein
246550_at	At5g14920	1.1	1	1.9	2.3	2.5	4.3	x	x	expressed protein
246566_at	At5g14940	-1	1.1	3	2.5	3	3.7	x	x	oligopeptide transporter family
250158_at	At5g15190	1.5	1.3	2.8	3.5	2	1.1	x	x	putative protein
246559_at	At5g15550	1	1.2	2.8	3.2	1.5	1.4	x	x	WD-40 repeat protein family
246527_at	At5g15750	1	1.1	3.2	2.8	1.7	1.5	x	x	ribosomal protein-like
246523_at	At5g15850	1.4	1.3	6.1	4.3	3.7	1.9	x	x	CONSTANS-like 1
246490_at	At5g15950	1	1.1	3	3	1.7	2	x	x	S-adenosylmethionine decarboxylase (adoMetDC2)
246481_s_at	At5g15960	-1	-1	3.7	6.1	2.8	4.3	x	x	KIN1
246484_at	At5g16040	1.1	1	3	3.5	3.2	2.6	x	x	regulator of chromosome condensation RCC1 family
246495_at	At5g16200	4.6	3.5	-2	1	1.3	-1	x		putative protein
246419_at	At5g17030	-8	7.5	13	56	3	15	x	x	UDP glucose:flavonoid 3-o-glucosyltransferase family
250087_at	At5g17270	1.3	1.1	6.1	2.6	2.1	-1	x	x	putative protein
250098_at	At5g17350	6.1	4	-1	-2	-11	-1	x		putative protein
250053_at	At5g17850	5.3	2.8	9.8	7.5	7.5	3.5	x	x	similar to sodium/calcium exchanger protein
249984_at	At5g18400	1.2	1.3	2.6	2.6	1.7	1.7	x	x	putative protein
246125_at	At5g19875	1.2	1.1	4.3	4.3	3.7	2.6	x	x	expressed protein
246070_at	At5g20160	1	1	2.8	2.5	2.5	1.9	x	x	ribosomal protein L7Ae family
246099_at	At5g20230	3.2	2.6	3.5	3.2	-1	2	x		plastocyanin-like domain containing protein
245998_at	At5g20830	1.1	-1	15	12	7.5	6.1	x	x	sucrose synthase I (SUS1)
249928_at	At5g22250	4.6	2.6	1.1	-2	-2	1.2	x		CCR4-associated factor-like protein
249940_at	At5g22380	4.6	2.8	1.5	-2	1.1	1	x		NAC-domain protein-like
249769_at	At5g24120	-1	1.1	2.8	2.8	-1	-2	x	x	sigma-like factor (emb CAA77213.1)
249741_at	At5g24470	2.5	4	6.5	12	4	6.1	x	x	pseudo-response regulator (APRR5)

249750_at	At5g24570	1	-1	5.3	4	2.1	2.3	x	expressed protein
246922_at	At5g25110	-2	4.3	111	239	45	137	x	serine/threonine protein kinase-like
246831_at	At5g26340	1.4	1.4	3.2	3.5	1.7	2.5	x	hexose transporter - like protein
246796_at	At5g26770	1.9	1.9	4.6	3.2	3.2	2.1	x	putative protein
246821_at	At5g26920	3.7	2.6	-1	1.2	-1	1.4	x	calmodulin-binding protein
246809_s_at	At5g27140	-1	1.1	2.6	2.8	1.9	1.5	x	NOP58-like protein
246756_at	At5g27930	-1	1.1	2.8	3	2	2	x	protein phosphatase 2C (PP2C), putative
246708_at	At5g28150	-1	-1	2.5	2.6	1.5	1.6	x	expressed protein
246178_s_at	At5g28430	1.6	8.6	2.5	11	1.1	3.5	x	hypothetical protein
246108_at	At5g28630	11	3	1.9	-26	-2	-32	x	putative protein
249619_at	At5g37500	-2	-3	4.3	4.9	2.3	3.2	x	guard cell outward rectifying K+ channel (GORK)
249583_at	At5g37770	4.6	2.8	-2	-3	-1	-2	x	calmodulin-related protein 2, touch-induced (TCH2)
249528_at	At5g38720	-1	1.1	2.6	2.6	2	1.5	x	expressed protein
249411_at	At5g40390	-1	1	8	8	3.2	2.6	x	raffinose synthase
249264_s_at	At5g41740	6.1	2.5	-2	-2	-1	1.2	x	disease resistance protein (TIR-NBS-LRR class), putative
249197_at	At5g42380	16	2.6	2.3	1.4	3	1.1	x	putative protein
249204_at	At5g42570	1.2	1.1	6.5	6.1	4.6	3.5	x	expressed protein
249174_at	At5g42900	1.4	1.4	6.1	16	4.3	8	x	expressed protein
249134_at	At5g43150	1.1	-1	4	3.2	2.1	1.1	x	unknown protein
249148_at	At5g43260	1.1	1.3	2.6	3	1.3	1.4	x	expressed protein
249125_at	At5g43450	1.1	1.2	3.2	3	2	2.6	x	1-aminocyclopropane-1-carboxylate oxidase
249063_at	At5g44110	1.1	1	2.8	2.5	2	1.5	x	ABC transporter family protein
249065_at	At5g44260	1.4	1.1	2.8	13	1.1	6.1	x	expressed protein
248964_at	At5g45340	26	12	1	-2	-1	-2	x	cytochrome P450 family
248870_at	At5g46710	3.5	2.3	5.7	3.7	1.5	1.5	x	expressed protein
248820_at	At5g47060	1	1.3	3.2	4	1.4	1.4	x	expressed protein
248794_at	At5g47220	4.9	2.6	1.4	-1	2.3	3.5	x	ethylene responsive element binding factor 2 (EREBP-2)
248799_at	At5g47230	8.6	4.3	2.8	1.5	1.3	-1	x	ethylene responsive element binding factor 5 (AtERF5)
248801_at	At5g47370	1	1.1	2.5	2.5	-1	-1	x	homeobox-leucine zipper protein-like
248762_at	At5g47455	1.1	-1	2.5	2.8	2.5	2.5	x	expressed protein
248756_at	At5g47560	1.1	1.2	3.2	2.8	1.5	1.2	x	sodium-dicarboxylate cotransporter-like
248765_at	At5g47650	1.1	1.1	4.6	3	2.8	1.9	x	MutT/nudix family protein
248749_at	At5g47880	1.1	1.2	3.2	3.2	1.9	1.5	x	eukaryotic release factor 1 (ERF1)
248744_at	At5g48250	1.1	1.3	2.6	5.7	1.7	3.5	x	CONSTANS B-box zinc finger family protein

248686_at	At5g48540	2.3	1.6	2.5	2.1	3.2	2.6	x	33 kDa secretory protein-like
248607_at	At5g49480	2.1	1.7	4.3	4	3.7	2.6	x	NaCl-inducible Ca2+-binding protein-like
248611_at	At5g49520	4	3.5	1.6	1.4	2.3	1.4	x	WRKY family transcription factor (WRKY48)
248466_at	At5g50720	1.1	1	8	8.6	2.5	1.6	x	abscisic acid-induced-like protein (AtHVA22e)
248467_at	At5g50800	-1	1	3.2	4.3	9.8	8.6	x	nodulin MtN3-like protein
248451_at	At5g51180	-1	1.1	3.2	3	1.5	1.5	x	putative protein
248448_at	At5g51190	18	7	1.7	-2	1.3	-2	x	AP2 domain transcription factor, putative
248410_at	At5g51570	1.1	-1	2.6	2.8	2.3	2.6	x	putative protein
248381_at	At5g51830	1.1	1.1	3	2.6	1.9	3.7	x	fructokinase 1
248389_at	At5g51990	2.5	3	-4	2	-9	1.1	x	DRE binding protein
248392_at	At5g52050	52	18	4.9	1.1	1.3	4	x	integral membrane protein-like
248352_at	At5g52300	-2	-1	16	8	7.5	1.4	x	RD29B
248337_at	At5g52310	1.1	1.1	18	39	9.2	18	x	COR78
248326_at	At5g52820	1	1.1	2.5	2.8	1.9	1.9	x	Notchless protein homolog
248236_at	At5g53870	-2	1.3	3.5	6.5	2.5	3.2	x	putative protein
248207_at	At5g53970	1.4	1.1	4.6	3.2	2.1	1.3	x	tyrosine aminotransferase
248197_at	At5g54190	1	-1	1.4	-2	7.5	5.3	x	protochlorophyllide reductase A (PCRAPORA)
248160_at	At5g54470	16	2.5	64	7	39	3.2	x	CONSTANS B-box zinc finger family protein
248164_at	At5g54490	7	4.6	-1	-1	-1	1.4	x	calcium-binding EF-hand protein (PBP1)
248136_at	At5g54910	-1	-1	2.5	3.5	1.2	1.1	x	DEAD/DEAH box helicase, putative
248100_at	At5g55180	1	-1	3.5	4.3	1.5	1.2	x	beta-1,3-glucanase-like protein
248040_at	At5g55970	1.5	1.1	3.5	3	1.1	-2	x	putative protein
247957_at	At5g57050	-1	1	3.2	4.3	1.3	1.7	x	protein phosphatase 2C, ABI2
247937_at	At5g57110	1	-1	7	9.8	4	4.3	x	Ca2+-transporting ATPase (ACA8)
247925_at	At5g57560	18	9.8	1.7	-1	-2	-2	x	TCH4
247867_at	At5g57630	1.6	1.5	4.3	4.6	2.6	3.2	x	SNF1 related protein kinase-like protein
247921_at	At5g57660	1.1	1.1	7	4.3	4.6	2.6	x	CONSTANS B-box zinc finger family protein
247851_at	At5g58070	-1	1.1	4.6	4.9	2.3	2.1	x	outer membrane lipoprotein - like
247795_at	At5g58620	1.1	1.1	2.8	3.5	1.6	2.1	x	putative protein
247776_at	At5g58700	1.1	-1	5.3	6.1	2.6	1.7	x	phosphoinositide specific phospholipase C family
247739_at	At5g59240	1.2	4	2.8	11	1.7	6.5	x	40S ribosomal protein S8 (RPS8B)
247718_at	At5g59310	-1	-2	-1	2	12	11	x	nonspecific lipid-transfer protein precursor - like
247717_at	At5g59320	-1	1.1	1.9	2.6	18	8.6	x	nonspecific lipid-transfer protein precursor - like
247708_at	At5g59550	3.2	2.5	-1	1	-1	1	x	putative protein

247655_at	At5g59820	11	6.5	3.2	3	1.3	2	x	x	ZAT12
247585_at	At5g60680	2.5	2.1	4.9	3.7	2	1.3		x	putative protein
247528_at	At5g61460	1.2	1.1	1.6	1.6	2.5	2.8			MIM protein
247543_at	At5g61600	11	4.6	-1	-2	1	-2	x		ethylene responsive element binding factor family
247498_at	At5g61810	-1	-1	2.5	3.5	1.4	1.9	x	x	peroxisomal Ca-dependent solute carrier - like protein
247488_at	At5g61820	-1	1.1	5.3	11	3.7	5.7	x	x	putative protein
247463_at	At5g62210	1.2	1.1	4.3	3.5	1.4	-1	x		contains similarity to embryo-specific protein 3
247474_at	At5g62280	-2	-2	8.6	4.3	3.7	4	x	x	expressed protein
247450_at	At5g62350	1.1	1	3	4	1.1	1.1	x		pectinesterase family
247478_at	At5g62360	1.9	1.5	9.2	9.8	2.5	3.7	x	x	similar to pectinesterase
247453_at	At5g62440	1.1	1.1	2.6	2.5	2	1.2	x		expressed protein
247318_at	At5g63990	1.1	1.2	2.8	4.3	3.5	4.6	x	x	3(2),5-bisphosphate nucleotidase
247323_at	At5g64170	-1	1.1	4.6	2.8	4	2.1	x		putative protein
247280_at	At5g64260	2.5	1.7	5.7	4.3	2.3	1.1	x		phi-1-like protein
247137_at	At5g66210	4.6	2.6	-1	-1	1.4	1.3	x		calcium-dependent protein kinase
247046_at	At5g66540	-1	-1	2.8	2.5	1.9	1.2	x		expressed protein
246987_at	At5g67300	3	2.6	2	1.3	1.2	1.1	x		myb family transcription factor
246993_at	At5g67450	3.7	3.2	-1	-9	-1	1.1	x		Cys2 His2-type zinc finger protein
247013_at	At5g67480	1.3	1.6	2.5	3	1.6	2.5	x		putative protein

The AGI identifier, the fold change values for each biological duplicate at each time (h), and the annotation for each probe set is shown. An "x" indicates times at which the probe set met the criteria (see Chapter 2) for being labeled cold responsive at a 2.5-fold level.

APPENDIX D

TABLE D.1. PROBE SETS DOWN-REGULATED BY LOW TEMPERATURE IN THE SOIL EXPERIMENT

Probe set	AGI	1h			24h			168h			Cold responsive			Annotation
		A	B	1	A	B	1	A	B	1	1h	24h	168h	
260904_at	At1g02450	2.6	1.1	-3	-3	-3	1.07	2.14			x			unknown protein
262113_at	At1g02820	1.1	1	5.7	4.9	-2.5	-3.5					x		late embryogenesis abundant (LEA) protein family
263114_at	At1g03130	-1	-1	-2	-3	-1.9	-2				x			photosystem I reaction center subunit II precursor
265066_at	At1g03870	1.1	-1	-3	-5	-3.7	-5.7				x			fasciclin-like arabinogalactan-protein (FLA9)
263668_at	At1g04350	-1	-1	-3	-4	-4.9	-6.1				x			putative 2-oxoglutarate-dependent dioxygenase
262637_at	At1g06640	1	1	-2	-2	-2.5	-2.6				x			2-oxoglutarate-dependent dioxygenase
256050_at	At1g07000	1.9	1.6	-2	-3	-1.7	-1.1				x			leucine zipper protein, putative
261081_at	At1g07350	-1	-1	-3	-2	-4	-2.5					x		putative transformer serine/arginine-rich ribonucleoprotein
261084_at	At1g07440	-1	-1	-5	-3	-2.8	-1.9				x			tropinone reductase, putative
261747_at	At1g08350	-1	-1	-3	-3	1.41	1				x			syntaxin SYP111
264648_at	At1g09080	-1	1.3	-2	-37	-2.5	-3				x			putative luminal binding protein
264264_at	At1g09250	-1	-1	-3	-3	-2.5	-1.6				x			bHLH protein
264507_at	At1g09415	1.2	-1	-3	-5	-1.3	-1.5				x			expressed protein
264522_at	At1g10050	-2	1	-15	-7	-42	-1.1				x			glycosyl hydrolase family 10
264435_at	At1g10360	-1	-1	-4	-5	-1.9	-2.3				x			glutathione S-transferase (GST29)
260481_at	At1g10960	-1	1	-2	-2	-5.3	-4.6					x		ferredoxin
262811_at	At1g11700	-1	-1	-5	-4	-1.4	-1.4				x			unknown protein
264342_at	At1g12080	1.1	-2	-1	-1	-2.6	-8					x		expressed protein
264348_at	At1g12110	1.1	-1	-4	-4	-2	-1.6				x			putative NPK1-related protein kinase 2
260969_at	At1g12240	-1	1	-3	-3	-2.5	-2.5				x			beta-fructosidase
262826_at	At1g13080	-1	-1	-3	-5	-1.6	-3				x			putative cytochrome P450
259385_at	At1g13470	1.5	1.1	-3	-2	-1.6	1.32				x			hypothetical protein
256096_at	At1g13650	-1	-1	-23	-23	-13	-21				x			expressed protein
262830_at	At1g14700	-1	1.1	-5	-5	-3.2	-4.9				x			putative purple acid phosphatase
262850_at	At1g14920	-1	-1	-3	-3	-1.9	-1.4				x			signal response protein (GAI)
260739_at	At1g15000	-1	-1	-3	-4	-1.9	-2				x			serine carboxypeptidase precursor, putative
262598_at	At1g15260	-1	-1	-2	-3	-1.3	-1.6				x			expressed protein
261793_at	At1g16080	1	-1	-2	-2	-2.8	-3.5					x		expressed protein

262705_at	At1g16260	-1	1	-3	-3	-1.5	-1.3	x	putative wall-associated kinase
255760_at	At1g16780	-1	1.1	-3	-3	-1.4	-2	x	vacuolar-type H ⁺ -translocating inorganic pyrophosphatase, putative
261032_at	At1g17430	-1	1.1	-6	-4	-1.6	-1.2	x	expressed protein
260735_at	At1g17610	-1	-1	-3	-3	-4.9	-1.4	x	disease resistance protein, putative
255895_at	At1g17990	1.1	1.1	-3	-3	-1.1	-1.1	x	similar to 12-oxophytodienoate reductase OPR1
255908_s_at	At1g18010	1.1	-1	-3	-2	-1.3	-1.4	x	expressed protein
255779_at	At1g18650	1	-1	-3	-3	-2	-2.8	x	similar to beta-1,3-glucanase
259476_at	At1g19000	-1	-1	-3	-2	-2.3	-2.3	x	MYB family transcription factor
256015_at	At1g19150	-1	-1	-5	-4	-4.3	-3.5	x	PSI type II chlorophyll a/b-binding protein
255786_at	At1g19670	-1	-1	-7	-6	-9.2	-3.5	x	chlorophyllase/coronatine-induced protein 1 (COR11)
259560_at	At1g21270	1	1	-3	-4	-1.7	-1.2	x	wall-associated kinase 2
260872_at	At1g21350	1	-1	-2	-2	-2.8	-3	x	expressed protein
260877_at	At1g21500	-1	-1	-2	-3	-2.5	-3.5	x	expressed protein
255957_at	At1g22160	1.3	-1	-5	-3	-1.5	-1.5	x	senescence-associated protein
255969_at	At1g22330	-1	-1	-14	-15	-11	-3.7	x	RRM-containing protein
255962_at	At1g22335	1.2	-1	-3	-6	-1.6	-1.9	x	glycine-rich RNA-binding protein, putative
264774_at	At1g22890	1.3	1.4	-2	-3	-3.5	-3.7	x	hypothetical protein
264751_at	At1g23020	1	-1	-17	-4	-4.6	-4	x	putative ferric-chelate reductase
264898_at	At1g23205	-1	-2	-3	-3	-5.3	-4.9	x	pectinesterase
265175_at	At1g23480	1.1	1.1	-3	-7	-1.9	-3	x	similar to cellulose synthase (AtCSLA03)
263035_at	At1g23860	-1	-1	-2	-3	-4.6	-4.6	x	splicing factor (SRZ_21)
245638_s_at	At1g24996	-2	-2	-3	-2	-3	-2.6	x	unknown protein
245637_at	At1g25230	1	-1	-3	-4	-2.1	-2.6	x	purple acid phosphatase family
245816_at	At1g26210	-1	-2	-3	-5	-1.6	-2.3	x	expressed protein
261016_at	At1g26560	-1	-1	-3	-4	-2	-3.2	x	glycosyl hydrolase family 1
261276_at	At1g26670	-1	-1	-2	-2	-2.1	-2.3	x	v-SNARE protein (VT112/AtVT11b)
264987_at	At1g27030	-1	-1	-1	1.1	-2.5	-2.6	x	expressed protein
262749_at	At1g28580	-1	1.1	-3	-3	-1.4	-1.1	x	putative lipase
262733_s_at	At1g28670	1	-1	-6	-6	-3.5	-4	x	lipase (ARAB-1)
261801_at	At1g30520	-1	-1	-5	-6	-2.6	-3.7	x	expressed protein
261712_at	At1g32780	-1	1	-3	-9	-1.9	-2	x	alcohol dehydrogenase, putative
261981_at	At1g33811	1.1	-1	-2	-4	-2.6	-3.2	x	GDSL-motif lipase/hydrolase protein
245783_s_at	At1g35180	1.1	-1	-5	-5	-17	-20	x	expressed protein

260869_at	At1g43800	-1	-1	-7	-39	-8	-12	x	putative stearoyl acyl carrier protein desaturase
259507_at	At1g43910	1.4	1.1	-2	-2	-1.1	-1.1	x	unknown protein
261308_at	At1g48480	1	1	-3	-2	-1.7	-2.5	x	leucine-rich repeat transmembrane protein kinase, putative
261309_at	At1g48600	1	-1	-2	-2	-3.7	-3	x	phosphoethanolamine N-methyltransferase
265149_at	At1g51400	-1	-1	-5	-6	-3.2	-3	x	photosystem II 5 KD protein
257497_at	At1g51430	-1	-1	-3	-3	-2.3	-2.5	x	hypothetical protein
256186_at	At1g51680	-1	-1	-3	-4	-2	-1.9	x	4-coumarate:CoA ligase 1
265053_at	At1g52000	-1	-1	-3	-4	2.14	1.74	x	myrosinase binding protein
259839_at	At1g52190	-1	-2	-3	-7	-1.5	-2	x	proton-dependent oligopeptide transport (POT) protein family
259671_at	At1g52290	-1	1	-3	-3	-1.6	-1.1	x	protein kinase
259669_at	At1g52340	-1	-1	-2	-3	-1.1	-1.7	x	dehydrogenase/reductase family protein (ABA2)
262159_at	At1g52720	-1	-1	-3	-3	-2.8	-1.9	x	expressed protein
260983_at	At1g53560	-1	-1	-3	-4	-2.1	-3.5	x	expressed protein
259960_at	At1g53710	-1	-1	-3	-5	-1.7	-1.7	x	cell division control protein, putative
263174_at	At1g54040	-1	-1	-3	-2	-4	-3.7	x	Kelch repeats protein family (TASTY/ESP)
264240_at	At1g54820	-1	-1	-4	-3	1.07	1.15	x	protein kinase, putative
259664_at	At1g55330	-1	-1	-3	-5	-2.8	-4.6	x	arabinogalactan-protein (AGP21)
257510_at	At1g55360	1.1	-1	-3	-5	-2	-2.6	x	expressed protein
265075_at	At1g55450	2.1	1.5	-2	-3	-1.4	1.15	x	expressed protein
260592_at	At1g55850	-1	1	-5	-4	-1.9	-1.3	x	cellulose synthase family (CSLE1)
259603_at	At1g56500	-1	-1	-2	-1	-2.8	-2.8	x	haloacid dehalogenase family
262076_at	At1g59580	1.1	1	-3	-3	-2.5	-1.7	x	mitogen-activated protein kinase (MPK2)
265116_at	At1g62480	-1	1	-2	-2	-5.3	-5.3	x	expressed protein
265118_at	At1g62660	-1	-1	-3	-3	-3.7	-4.3	x	glycosyl hydrolase family 32
260109_at	At1g63260	1.1	-1	-2	-4	-1.3	-2.3	x	hypothetical protein
260317_at	At1g63800	1.1	-1	-3	-5	-2	-2.5	x	ubiquitin-conjugating enzyme 5 (UBC5)
262871_at	At1g65010	1.2	-1	-2	-3	-1.2	-1.2	x	hypothetical protein
259822_at	At1g66230	-2	1.1	-2	-4	-1.6	-3.2	x	MYB family transcription factor (MYB20)
260141_at	At1g66350	-1	-1	-3	-2	-2.1	-1.6	x	gibberellin regulatory protein, putative
256383_at	At1g66820	1	1	-3	-3	-1.6	-1.3	x	glycine rich protein
255857_at	At1g67080	-1	-1	-3	-3	-1.5	-2	x	expressed protein
245196_at	At1g67750	1	-1	-6	-4	-3.5	-4	x	pectate lyase
260431_at	At1g68190	1.2	-1	-5	-7	-2.1	-4	x	CONSTANS B-box zinc finger family protein
262232_at	At1g68600	1.1	-2	-4	-5	-1.4	1.41	x	expressed protein

256299_at	At1g69530	-1	-1	-7	-9	-6.1	-3.2	x	x	expansin (EXP1)
260427_at	At1g72430	1.1	-1	-3	-7	-4.6	-7	x	x	auxin-induced protein-related
260453_s_at	At1g72510	-1	-2	-3	-3	-2	-3.2	x		expressed protein
262374_s_at	At1g72930	1.5	1.2	-6	-6	-2.6	-1.2	x		disease resistance protein (TIR class), putative
245736_at	At1g73330	1.5	-2	-2	-2	-6.1	-4.3		x	protease inhibitor (ATDR4)
259842_at	At1g73600	-1	-1	-1	-2	-5.7	-4.6		x	phosphoethanolamine N-methyltransferase
260388_at	At1g74070	-1	-1	-3	-3	-2.3	-2.3	x		expressed protein
260221_at	At1g74670	1.1	-1	-14	-34	-11	-13	x	x	GAST1-like protein
256458_at	At1g75220	-1	-1	-3	-3	-4	-3.7	x	x	integral membrane protein
262698_at	At1g75960	-1	1.1	-3	-8	-2	-2.3	x		AMP-binding protein, putative
261751_at	At1g76080	-1	-1	-3	-3	-4.3	-4.9	x	x	thioredoxin family
261727_at	At1g76090	1.1	-1	-1	-2	-2.5	-4.9		x	S-adenosyl-methionine-sterol-C-methyltransferase, putative
261769_at	At1g76100	-1	-1	-3	-4	-1.7	-2.3		x	plastocyanin
259875_s_at	At1g76690	1.2	1.2	-3	-3	1.15	1.41	x		12-oxophytodienoate reductase (OPR2)
262134_at	At1g77990	1	-1	-3	-4	-1.1	-1.2	x		sulfate transporter, putative
264250_at	At1g78680	-1	-1	-5	-3	-2.5	-2.1	x		gamma-glutamyl hydrolase
261346_at	At1g79720	-1	-1	-3	-3	-1.6	-2.3	x		putative aspartyl protease
262049_at	At1g80180	-1	1	-3	-3	-2	-2	x		expressed protein
261893_at	At1g80690	1.1	1	-2	-2	-1.4	-1.4	x		expressed protein
261901_at	At1g80920	1.3	1.1	1.1	-2	-2.6	-2.6		x	J8-like protein similar to DnaJ
264037_at	At2g03750	1	-1	-3	-3	-1.2	-1.6	x		similar to steroid sulfotransferase
263647_at	At2g04690	1	-1	-2	-3	-1.2	-1.4	x		expressed protein
263674_at	At2g04790	1.1	1	-3	-5	-1.5	-2.1	x		expressed protein
265893_at	At2g15040	1	-1	-2	-3	-1.3	1	x		putative disease resistance protein
265894_at	At2g15050	-1	-1	-3	-4	-2.3	-2.8	x		putative lipid transfer protein
265494_at	At2g15680	-1	1	-8	-5	-2.1	-1.4	x		putative calmodulin-like protein
267336_at	At2g19310	-1	-1	-4	-3	-4.3	-2	x		putative small heat shock protein
265948_at	At2g19590	1.1	-2	-4	-6	-8	-4	x	x	1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase), putative
265394_at	At2g20725	-1	-1	-3	-3	-1.9	-1.9		x	unknown protein
265443_at	At2g20750	-2	-1	-4	-5	-1.7	-1.7	x		beta-expansin pollen allergen protein
263549_at	At2g21650	1.1	-1	-2	-5	-5.3	-4.6	x	x	MYB family transcription factor
264052_at	At2g22330	1.1	1	-3	-3	-1.3	-1.2	x		putative cytochrome P450
266001_at	At2g24150	1	-1	-3	-3	-1.6	-2.1	x		expressed protein

265902_at	At2g25590	-2	1.1	-3	-4	-4	-3.2	x	hypothetical protein
266893_at	At2g26070	-1	1.1	-3	-2	-1.7	-1.2	x	hypothetical protein
267380_at	At2g26170	1.1	1.1	-3	-3	-2	-2.5	x	thromboxane-A synthase(cytochrome p450 family), putative
265572_at	At2g28210	-1	1	-2	-2	-3	-2.8	x	carbonic anhydrase
263443_at	At2g28630	1.6	1.2	-3	-3	-3.7	-8	x	beta-ketoacyl-CoA synthase family
266781_at	At2g28940	1.1	1.2	-3	-3	-1.3	1	x	protein kinase family
266790_at	At2g28950	1	-1	-3	-3	-1.5	-1.7	x	expansin, putative
266279_at	At2g29290	-1	-1	-4	-5	-3.2	-3.2	x	putative tropinone reductase
266265_at	At2g29340	1.1	1.1	-3	-3	-1.1	-1.3	x	similar to tropinone reductase-I
266357_at	At2g32290	-2	-2	-12	-4	-4.6	-26	x	beta-amylase
267057_at	At2g32500	-1	-1	-2	-2	-3.5	-3	x	expressed protein
267116_at	At2g32560	-1	-1	-3	-3	-1.5	-1.9	x	unknown protein
267546_at	At2g32680	1.1	1.1	-5	-3	-2.3	-1.3	x	disease resistance protein family
267644_s_at	At2g32880	-1	1.1	-3	-2	-16	-7	x	expressed protein
255794_at	At2g33480	-1	-2	-2	-3	-1.4	-1.9	x	No apical meristem (NAM) protein family
266899_at	At2g34620	-1	-2	-7	-11	-2.8	-3.2	x	expressed protein
267425_at	At2g34810	-1	1	-3	-2	-1.7	-1.7	x	FAD-linked oxidoreductase family
263947_at	At2g35820	-2	-1	-3	-2	-2.8	-2.1	x	expressed protein
263867_at	At2g36830	-1	-1	-2	-2	-3	-3	x	putative aquaporin (tonoplast intrinsic protein gamma)
265444_s_at	At2g37180	1	-1	-5	-6	-4	-4.6	x	aquaporin (plasma membrane intrinsic protein 2C)
266005_at	At2g37340	-1	-1	-1	-1	-2.8	-4	x	splicing factor RSZ33, putative
265952_at	At2g37480	1.1	-1	-3	-4	-2.1	-2.1	x	expressed protein
265953_at	At2g37490	1	-1	-3	-3	-2.5	-2	x	expressed protein
267034_at	At2g38310	1.1	1	-5	-9	-3.7	-3.7	x	expressed protein
266988_at	At2g39310	-1	1	-4	-1	-2.6	-6.5	x	jacalin lectin family
266989_at	At2g39330	-1	1.1	-3	-2	-4.3	-4	x	putative myrosinase-binding protein
266977_at	At2g39420	1	-1	-3	-2	-1.3	-1.6	x	putative phospholipase
266984_at	At2g39570	1.4	1.1	-4	-5	-3.2	-2.6	x	ACT domain-containing protein
245088_at	At2g39850	-1	-1	-2	-2	-3	-2.6	x	subtilisin-like serine protease
265722_at	At2g40100	-1	-1	-2	-2	-7.5	-7	x	chlorophyll a/b binding protein (LHCb4.3)
265720_at	At2g40110	1	-1	-2	-3	-1.3	-1.3	x	expressed protein
255822_at	At2g40610	-2	-2	-12	-16	-12	-5.7	x	expansin, putative (EXP8)
266078_at	At2g40670	1	-1	-5	-5	-1.9	1.15	x	putative two-component response regulator protein
267083_at	At2g41100	2.3	1.4	-3	-4	-3	-1.2	x	calmodulin-like protein (TCH3)

266372_at	At2g41310	1	-1	-3	-3	-1.6	-2.5	x	two-component response regulator (ARR8/ATRR3)
263987_at	At2g42690	-1	-1	-4	-5	-1.7	-1.7	x	putative lipase
263972_at	At2g42760	-1	1	-4	-2	-2.1	-5.3	x	unknown protein
267367_at	At2g44210	-1	-1	-3	-4	-2.6	-2.5	x	expressed protein
267393_at	At2g44500	3	1.7	-3	-4	-1.2	-1.5	x	similar to axi 1 protein from Nicotiana tabacum
266581_at	At2g46140	-1	-1	-2	-2	-3.5	-2.6	x	putative desiccation related protein
266552_at	At2g46330	1.1	1.1	-3	-4	-1.5	-1.7	x	arabinogalactan-protein (AGP16)
265451_at	At2g46490	1	-1	-2	-2	-2	-1.7	x	expressed protein
266749_at	At2g47060	1.9	1.3	-2	-3	-1.5	-2.1	x	putative protein kinase
266460_at	At2g47930	-1	-1	-3	-3	-1.9	-2.6	x	expressed protein
259272_at	At3g01290	2.1	1.6	-3	-4	-2.5	-1.1	x	expressed protein
259115_at	At3g01360	-1	-1	-2	-2	-1.9	-1.6	x	hypothetical protein
259161_at	At3g01500	-1	-1	-1	-1	-3.7	-3.2	x	carbonic anhydrase (CA1)
258976_at	At3g01980	-1	-1	-3	-3	-1.1	-1.1	x	short-chain dehydrogenase/reductase family
259104_at	At3g02170	1.2	1.1	-3	-3	-1.1	-1.1	x	expressed protein
259131_at	At3g02180	-1	-1	-3	-3	-2.6	-2.1	x	expressed protein
258484_at	At3g02580	1	1	-3	-2	-2.5	-2.6	x	sterol-C5-desaturase
258623_at	At3g02790	1.2	-1	-1	-2	-4.6	-1.1	x	C2H2-type zinc finger protein family
258609_at	At3g02910	1.2	-1	-4	-3	-2.6	-2.6	x	expressed protein
258537_at	At3g04210	1.5	1.2	-6	-9	-1.4	1.07	x	disease resistance protein (TIR-NBS class), putative
258527_at	At3g06850	1	1	-3	-4	-1.6	-2.1	x	branched chain alpha-keto acid dehydrogenase E2 subunit (DIN3/LTA1)
258552_at	At3g07010	-1	-1	-3	-4	-2.5	-2.3	x	polysaccharide lyase family 1 (pectate lyase)
259010_at	At3g07340	-1	-1	-3	-3	-1.4	-2	x	bHLH protein
259211_at	At3g09020	2.3	1.3	-11	-5	-9.8	-1.6	x	unknown protein
259009_at	At3g09260	1.1	1.1	-1	-2	-7	-8	x	beta-glucosidase (PSR3.1/PYK10)
258723_at	At3g09600	-1	-1	-4	-4	-3.5	-4.9	x	MYB family transcription factor
258935_at	At3g10120	-2	-3	-3	-3	-1.4	-2.6	x	unknown protein
258764_at	At3g10720	1.6	1.5	-2	-3	-1.9	-1.6	x	putative pectinesterase
256441_at	At3g10940	-1	-1	-3	-2	-4	-3.7	x	expressed protein
256433_at	At3g10980	1.6	1.2	-1	-1	-2.6	-2.6	x	unknown protein
256431_s_at	At3g11010	1.3	1.2	-4	-3	-1.3	-1.1	x	disease resistance protein family
256427_at	At3g11090	1	1	-4	-4	-3.7	-3.5	x	expressed protein
258782_at	At3g11750	1.3	1	-4	-3	-1.7	-1.6	x	putative dihydroneopterin aldolase

258787_at	At3g11840	1.1	1	-3	-3	-1.7	-1.3	x	expressed protein
256275_at	At3g12110	-1	-1	-2	-3	-2.5	-5.7	x	actin 11 (ACT11)
256237_at	At3g12610	-1	-1	-2	-3	-1.6	-1.7	x	DNA-damage-repair/tolerance protein, putative (DRT100)
256772_at	At3g13750	1.1	-1	-2	-5	-2.5	-3	x	putative beta-galactosidase (BGAL1)
258275_at	At3g15760	1.5	1.7	-2	-3	-3	-1.9	x	expressed protein
257798_at	At3g15950	1	1.2	-3	-1	-3.7	-3	x	unknown protein
258053_at	At3g16230	-1	-1	-2	-2	-2.8	-1.7	x	expressed protein
258054_at	At3g16240	-1	-1	-3	-5	-4	-5.7	x	delta tonoplast integral protein (delta-TIP)
258055_at	At3g16250	-1	-1	-3	-4	-3.5	-2.6	x	ferredoxin related
259382_s_at	At3g16430	1.1	1.2	-3	-2	-6.1	-5.3	x	putative myrosinase binding protein
259327_at	At3g16460	1.1	1	-2	-2	-2.8	-4	x	putative lectin
257880_at	At3g16910	-1	-1	-5	-3	-4	-2.8	x	AMP-dependent synthetase and ligase family
258156_at	At3g18050	-1	-1	-2	-2	-1.5	-1.6	x	expressed protein
257801_at	At3g18750	-1	1	-2	-3	-2.6	-5.3	x	WNK protein family kinases (WNK6/ZIK5)
256655_at	At3g18890	-1	-1	-2	-2	-2.8	-2.5	x	hypothetical protein
256892_at	At3g19000	-1	-1	-2	-3	-2	-2.1	x	similar to flavanone-3-hydroxylase
258006_at	At3g19400	-1	-1	-3	-2	-1.7	-1.7	x	cysteine proteinase
257966_at	At3g19800	-1	1	-3	-4	-2.6	-3	x	expressed protein
257964_at	At3g19850	1.1	-1	-3	-7	-1.7	-2	x	hypothetical protein
256832_at	At3g22880	1.1	-1	-2	-3	-2.6	-3	x	meiotic recombination protein (AtDMC1)
257772_at	At3g23080	-1	-1	-2	-5	-1.3	-2.1	x	similar to phosphatidylcholine transfer
257763_s_at	At3g23110	-1	-1	-5	-4	-3.7	-2	x	disease resistance protein family
258299_at	At3g23410	-1	-1	-2	-3	-2.8	-3.7	x	alcohol oxidase-related
258125_s_at	At3g23520	-1	-1	-3	-6	-2.5	-1.9	x	unknown protein
258100_at	At3g23550	-1	1.3	-3	-3	-11	1.87	x	MATE efflux protein family
257239_at	At3g24100	-1	1	-1	-2	-18	-4.6	x	expressed protein
258133_at	At3g24500	-1	-2	-3	-6	-5.7	-3.7	x	putative ethylene-responsive transcriptional coactivator
256869_at	At3g26430	-1	-2	-4	-3	1	-1.1	x	nodulin, putative
256880_at	At3g26450	-1	-1	-4	-4	-3	-3	x	putative major latex protein
257615_at	At3g26510	-2	-2	-5	-6	-3	-2.6	x	expressed protein
257789_at	At3g27020	-1	1.1	-4	-3	-2.6	-2	x	putative oligopeptide transporter
257299_at	At3g28050	1.1	1.1	-4	-3	-2.1	-1.5	x	nodulin MtN21 family protein
257300_at	At3g28080	-1	-2	-4	-3	-1.2	-1.5	x	expressed protein
256603_at	At3g28270	-1	-2	-28	-4	-9.2	-3.5	x	At14a-related protein

258003_at	At3g29030	-1	-1	-3	-3	-1.7	-3.5	x	expansin (At-EXP5)
256940_at	At3g30720	-2	-3	-2	-3	-2.5	-3	x	unknown protein
257315_at	At3g30775	2	1.1	-3	-4	-2.8	-3.5	x	proline dehydrogenase (ERD5/PRO1/AT-POX)
252712_at	At3g43800	-1	-1	-3	-3	-1.1	1	x	glutathione transferase, putative
252607_at	At3g44990	-1	1.1	-4	-3	-2.8	-2.3	x	xyloglucan endotransglycosylase, putative
252529_at	At3g46490	-1	1	-5	-3	-2.3	-2.5	x	putative oxidoreductase
252478_at	At3g46540	-1	1	-3	-3	-1.6	-1.5	x	expressed protein
252433_at	At3g47560	1	1	-5	-8	-2.1	-2.5	x	putative hydrolyse
252366_at	At3g48420	-1	1	-2	-2	-3	-3	x	haloacid dehalogenase family
252154_at	At3g50880	-1	-1	-4	-5	-2.5	-2.6	x	putative DNA-3-methyladenine glycosidase
256674_at	At3g52360	1.1	-1	-3	-4	-3	-2.8	x	expressed protein
252011_at	At3g52720	-1	-1	-5	-9	-4.3	-8	x	carbonic anhydrase (CAH1)
251982_at	At3g53190	1	-1	-3	-3	-2.6	-2.5	x	polysaccharide lyase family 1 (pectate lyase)
251964_at	At3g53370	-1	-1	-3	-2	-2.6	-1.5	x	expressed protein
251886_at	At3g54260	1.1	-1	-4	-3	-3	-9.2	x	expressed protein
251759_at	At3g55630	-1	-1	-6	-3	-3.5	-2.1	x	folylpolyglutamate-dihydrofolate synthase (dhfs/fpgs4)
251746_at	At3g56060	-1	-2	-2	-3	-4	-4.6	x	mandelonitrile lyase-like protein
251704_at	At3g56360	-1	-1	-2	-2	-2.6	-2.8	x	expressed protein
251705_at	At3g56400	2.3	1.6	-3	-3	-1.4	1.52	x	WRKY family transcription factor (WRKY70)
251649_at	At3g57330	1.1	1.1	-3	-2	-1.9	-1.4	x	potential calcium-transporting ATPase 11, plasma membrane-type (Ca2+-ATPase, isoform 11)
251575_at	At3g58120	1.1	1.3	-3	-12	-1.9	-2.8	x	transcription factor bZIP61 (BZIP61)
251516_s_at	At3g59310	1.1	1	-3	-4	-1.1	-1.2	x	putative protein
251391_at	At3g60910	-1	1	-3	-3	-3	-4	x	expressed protein
251360_at	At3g61210	-1	1	-2	-4	-3	-2.8	x	putative protein
255626_at	At4g00780	1	1.1	-2	-2	-4	-3	x	expressed protein
255645_at	At4g00880	-1	1	-3	-3	-1.9	-1.3	x	coded for by A. thaliana cDNA T43845
255604_at	At4g01080	-1	-1	-3	-2	-1.6	-1.7	x	hypothetical protein
255517_at	At4g02290	1.2	-1	-3	-3	-3.2	-4.3	x	glycosyl hydrolase family 9
255294_at	At4g04750	1	-1	-3	-3	-1.5	-1.6	x	putative sugar transporter
255302_at	At4g04830	1.2	-1	-3	-3	-1.6	-1.6	x	similar to transcriptional regulator
255298_at	At4g04840	1	-1	-1	1	-4.9	-4.3	x	expressed protein
255008_at	At4g10060	-1	-1	-3	-4	-2.6	-3.7	x	expressed protein
254938_at	At4g10770	-1	-1	-3	-3	-3.2	-3	x	oligopeptide transporter (AtOPT7)

245265_at	At4g14400	-1	1	-5	-3	-1.4	1.32	x	hypothetical protein
245592_at	At4g14540	-1	-1	-3	-3	-2.3	-2.1	x	CCAAT-binding transcription factor subunit A(CBF-A)
245281_at	At4g15560	-1	-1	-2	-2	-1.7	-1.6	x	DEF (CLA1) protein
245524_at	At4g15920	-1	1	-3	-3	-4.3	-9.2	x	nodulin MtN3 family protein
245463_at	At4g17030	-1	1.1	-3	-3	1	-1.6	x	allergen like protein
245266_at	At4g17070	-1	1	-3	-3	-1.2	-1.4	x	expressed protein
245399_at	At4g17340	-1	1	-3	-2	-5.7	-4.3	x	membrane channel like protein
245362_at	At4g17460	1.9	1.7	-4	-17	-2.6	-2.6	x	homeobox-leucine zipper protein HAT1 (HD-Zip protein 1)
254705_at	At4g17870	1	-1	-3	-5	-4	-5.3	x	expressed protein
254609_at	At4g18970	-1	-1	-2	-2	-2.5	-2.5	x	expressed protein
254561_at	At4g19160	-1	-1	-3	-2	-1.1	-1.1	x	putative protein
254574_at	At4g19430	-2	-2	-2	-4	-3.2	-4.3	x	expressed protein
254553_at	At4g19530	1	-1	-3	-5	-3.5	-4.9	x	disease resistance protein (TIR-NBS-LRR class)
254505_at	At4g19985	-1	-1	-3	-4	-1.9	-2.3	x	expressed protein
254387_at	At4g21850	1.4	1.2	-4	-3	-2.3	1.07	x	expressed protein
254384_at	At4g21870	1.6	-1	-4	-5	-23	-7.5	x	heat shock protein
254328_at	At4g22570	1.1	1	-3	-4	-1.7	-2.6	x	adenine phosphoribosyltransferase like protein
254331_s_at	At4g22710	1.2	1.2	-4	-6	-3.5	-2	x	cytochrome P450 family
254333_at	At4g22753	1	1.1	-3	-4	-1.3	-1.7	x	similar to putative C-4 sterol methyl oxidase
254280_at	At4g22756	1.1	-1	-3	-3	-1.4	-1.6	x	putative sterol 4-alpha-methyl-oxidase
254283_s_at	At4g22870	1	1.1	-1	-2	-2.5	-9.2	x	putative anthocyanidin synthase
254266_at	At4g23130	-1	-1	-3	-6	-1.2	1.07	x	protein kinase - like protein
254256_at	At4g23180	2.1	1.7	-3	-3	-1.3	1	x	serine/threonine protein kinase (RLK4)
254239_at	At4g23400	1	-1	-3	-3	-2.8	-3	x	major intrinsic protein (MIP) family
254225_at	At4g23670	-1	-1	-3	-3	-6.5	-8.6	x	putative major latex protein
254119_at	At4g24780	-1	-1	-4	-3	-1.7	-1.7	x	putative pectate lyase
254024_at	At4g25780	-1	-1	-3	-2	-2.3	-1.6	x	putative pathogenesis-related protein
253874_at	At4g27450	1.3	1.1	-2	-6	-4.3	-7	x	expressed protein
253886_at	At4g27710	-1	1.1	-3	-4	-1.9	-2.3	x	cytochrome P450, member of CYP709B
253815_at	At4g28250	-1	-1	-2	-2	-1.6	-2.1	x	putative beta-expansin (EXPB3)
253806_at	At4g28270	-1	1.1	-4	-3	-5.3	-2	x	C3HC4-type zinc finger protein family
253697_at	At4g29700	1.2	1.1	-3	-3	-20	-3.7	x	nucleotide pyrophosphatase -like protein
253701_at	At4g29890	-1	-1	-2	-2	-2.6	-2.5	x	choline monoxygenase
253548_at	At4g30993	1	-1	-4	-4	-2.1	-2.3	x	expressed protein

253534_at	At4g31500	-1	1.1	-5	-3	-1.3	1.07	x	cytochrome P450 (ATR4/CYP83B1)
253412_at	At4g33000	-1	-1	-2	-5	-1.2	-1.7	x	calcineurin B-like protein (fragment)
253302_at	At4g33660	-1	-1	-6	-4	-5.3	-5.3	x	expressed protein
253305_at	At4g33666	-1	-1	-4	-9	-3.5	-7	x	expressed protein
253245_at	At4g34590	1.1	-1	-2	-2	-4.6	-2.6	x	bZIP transcription factor (GBF6)
253191_at	At4g35350	-1	1	-2	-2	-3.5	-3.2	x	cysteine protease (XCP1)
246195_at	At4g36410	1.1	-1	-3	-3	-2.5	-1.7	x	E2, ubiquitin-conjugating enzyme 17 (UBC17)
253049_at	At4g37300	-1	1	-3	-3	-2.6	-2.3	x	expressed protein
253073_at	At4g37410	1.2	1.1	-2	-3	-8.6	-3.7	x	cytochrome p450, putative
253040_at	At4g37800	1	-1	-2	-3	-7	-6.1	x	putative endo-xyloglucan transferase
252949_at	At4g38670	1	-1	-4	-3	-1.3	-1.9	x	putative thaumatin-like protein
252950_at	At4g38690	-1	-1	-2	-2	-2.6	-2.6	x	1-phosphatidylinositol phosphodiesterase-related
252972_at	At4g38840	-2	-2	-2	-4	-1.5	-2	x	auxin-induced protein
252916_at	At4g38950	-1	-1	-3	-3	-1.9	-1.5	x	kinesin like protein
251142_at	At5g01015	-1	-1	-2	-4	-2.5	-3.7	x	expressed protein
251028_at	At5g02230	-1	-1	-9	-18	-4.6	-6.1	x	haloacid dehalogenase-like hydrolase family
250828_at	At5g05250	-1	-1	-4	-3	-3.7	-2.6	x	expressed protein
250777_at	At5g05440	1.4	1.6	-1	-5	-2.8	-2.6	x	putative protein
250582_at	At5g07580	1.1	1.1	-2	-4	-1.4	-1.7	x	ethylene-responsive element-binding family protein
250549_at	At5g07860	-1	-1	-3	-4	-2.8	-1.3	x	N-hydroxycinnamoyl/benzoyltransferase
250471_at	At5g10170	-1	-1	-2	-1	-4.9	-3.2	x	myo-inositol-1-phosphate synthase -like protein
250277_at	At5g12940	1.5	1	-3	-5	-2.1	1.07	x	leucine rich repeat protein family
250217_at	At5g14120	1	-1	-2	-6	-3	-4.6	x	nodulin-related protein
250180_at	At5g14450	-1	-1	-3	-3	-2.5	-2.8	x	GDSL-motif lipase/hydrolase protein
246540_at	At5g15600	-1	-1	-1	-2	-5.7	-7	x	nitrilase associated protein
246522_at	At5g15830	-1	-1	-4	-3	-1.9	-1.7	x	bZIP family transcription factor
246487_at	At5g16030	1	-1	-4	-8	-1.6	-2.3	x	expressed protein
246494_at	At5g16190	1.1	-1	-1	-2	-6.1	-2.6	x	putative protein
246462_at	At5g16940	1	-1	-3	-5	-1.7	-1.2	x	putative protein
250016_at	At5g18100	1.1	-1	-2	-3	-1.4	-1.7	x	copper/zinc superoxide dismutase (CSD3)
250032_at	At5g18170	-1	1	-3	-2	-1.5	-1.4	x	glutamate dehydrogenase (GDH1)
249923_at	At5g19120	1.4	1.1	-3	-6	-4	-5.7	x	conglutin gamma - like protein
246114_at	At5g20250	1.6	1.2	-3	-6	-6.5	-16	x	glycosyl hydrolase family (DIN10)
246021_at	At5g21100	-1	-1	-5	-3	-3	-4.6	x	L-ascorbate oxidase, putative

249917_at	At5g22460	1	1	-2	-4	-1.1	-1.9	x	putative protein
249862_at	At5g22920	2	1.2	-3	-7	-3.2	-5.7	x	zinc finger protein (RING family)
249869_at	At5g23050	1.1	-1	-4	-2	-1.7	-1.3	x	AMP-dependent synthetase and ligase family
249847_at	At5g23210	-1	-1	-3	-3	-1.2	-1.1	x	serine carboxypeptidase II-like protein
249817_at	At5g23820	1	1.1	-2	-2	-2.5	-3.2	x	expressed protein
249818_at	At5g23860	-1	-1	-2	-3	-2.8	-2.8	x	expressed protein
249774_at	At5g24150	-1	-1	-3	-3	-4.5	-4.2	x	squalene monooxygenase (SQP1,1)
249775_at	At5g24160	-1	-1	-3	-7	-1.19	-20	x	squalene monooxygenase (SQP1,2)
245928_s_at	At5g24780	-1	-1	-2	-1	-4.9	-5.7	x	vegetative storage protein (VSP1)
246909_at	At5g25770	-1	1	-24	-21	-7.5	-3.5	x	expressed protein
246768_at	At5g27400	1	-1	-3	-3	-1.7	-2.8	x	expressed protein
249694_at	At5g35790	-1	-1	-2	-4	-1.7	-2.3	x	glucose-6-phosphate dehydrogenase
249485_at	At5g39020	2.3	1.2	-3	-4	-1.2	-1.4	x	receptor protein kinase - like protein
249378_at	At5g40450	-1	-1	-2	-3	-5.7	-5.3	x	putative protein
249355_at	At5g40500	1	-1	-3	-3	-2.6	-2.3	x	expressed protein
249325_at	At5g40850	1.6	1.3	-2	-2	-3.5	-3	x	uroporphyrin III methylase (UPM1)
249215_at	At5g42800	1.1	-1	-2	-3	-4.9	-4.9	x	dihydroflavonol 4-reductase (dihydrokaempferol 4-reductase) (DFR)
249188_at	At5g42830	1.2	1.1	-3	-3	-1.9	1.15	x	N-hydroxycinnamoyl benzoyltransferase-like protein
249073_at	At5g44020	-1	-1	-3	-5	-3.5	-3	x	vegetative storage protein-related
249072_at	At5g44060	1.1	1	-3	-3	-2.1	-2.1	x	putative protein
249078_at	At5g44070	1.2	1.2	-3	-3	-1.5	1.07	x	phytochelatin synthase (gb AAD41794.1)
249008_at	At5g44680	-1	-2	-3	-3	-1.9	-1.9	x	putative protein
254521_at	At5g44810	1.2	1.1	-11	-3	-1.3	1.07	x	expressed protein
248942_at	At5g45480	1	1.1	-3	-3	-1.5	-1.1	x	putative protein
248961_at	At5g45650	-1	-1	-2	-3	-1.1	-1.5	x	subtilisin-like protease
248868_at	At5g46780	1.9	1.9	-3	-3	-1.4	-1.4	x	expressed protein
248865_at	At5g46790	1	-1	-2	-3	-2.3	-2.5	x	putative protein
248719_at	At5g47910	1.7	1.9	-4	-3	-2.3	-1.4	x	respiratory burst oxidase protein
248622_at	At5g49360	1.5	1.1	-3	-11	-8	-15	x	beta-xylosidase (BXL1)
248353_at	At5g52320	-1	-1	-4	-3	-1.4	-1.4	x	putative cytochrome P450
248329_at	At5g52780	-1	-1	-3	-3	-1.7	-1.5	x	expressed protein
248246_at	At5g53200	-2	-1	-17	-5	-2.3	-7.5	x	putative protein
248153_at	At5g54250	-1	-1	-5	-4	-4.9	-3.5	x	cyclic nucleotide-regulated ion channel (CNGC4)

248091_at	At5g55120	-1	-1	-3	-3	-1.5	-1.3	x	putative protein
248092_at	At5g55170	-1	1	-3	-3	-2.1	-1.6	x	ubiquitin-like protein
248037_at	At5g55930	-1	-1	-3	-3	-1.7	-1.4	x	oligopeptide transporter (AtOPT1)
247880_at	At5g57780	-2	-2	-5	-3	-1.5	-1.9	x	putative protein
247882_at	At5g57785	1	1.1	-3	-3	-1.7	-2.8	x	expressed protein
247814_at	At5g58310	-1	-1	-5	-4	-4.6	-2.5	x	polynuridine aldehyde esterase-like
247780_at	At5g58770	-1	-1	-3	-2	-69	-223	x	dehydrodichyl diphosphate synthase (DEDOL-PP synthase), putative
247782_at	At5g58790	-11	-1	-2	-2	-2.8	-17	x	putative protein
247684_at	At5g59670	1.1	1.1	-5	-3	-1.5	1.23	x	leucine rich repeat protein kinase
247594_at	At5g60800	1.2	1.1	-2	-3	-1.6	-1.4	x	expressed protein
247524_at	At5g61440	1.7	1.2	-6	-4	-2.3	-1.6	x	thioredoxin-like 3
247396_at	At5g62930	1.2	-1	-3	-3	-4.3	-2.6	x	GDSL-motif lipase/hydrolase protein
247377_at	At5g63180	-1	1	-2	-3	-1.6	-1.5	x	polysaccharide lyase family 1 (pectate lyase)
247282_at	At5g64240	-1	1	-2	-2	-3.2	-2.6	x	expressed protein
247284_at	At5g64410	1.2	1.1	-2	-3	1.32	1.52	x	oligopeptide transporter (AtOPT4)
247266_at	At5g64570	1.2	1.1	-3	-4	-2	-2.3	x	glycosyl hydrolase family 3
247043_at	At5g66880	1	-1	-4	-3	-3.2	-2.3	x	serine/threonine protein kinase
245047_at	psbA	-3	-3	1	-2	-2	-1.7	x	PSII 32 KDa protein
244974_at	psbN	-3	-4	-1	-2	-2.5	-1.4	x	PSII low MW protein

The AGI identifier, the fold change values for each biological duplicate at each time (h), and the annotation for each probe set is shown. An "x" indicates times at which the probe set met the criteria (see Chapter 2) for being labeled cold responsive at a 2.5-fold level.

APPENDIX E

TABLE E.1. PROBE SETS UP-REGULATED BY LOW TEMPERATURE IN BOTH THE PLATE AND SOIL EXPERIMENTS

Probe set	AGI	Annotation	Sub-role	Avg. fold change			Expression	ANOVA	
				1h	24h	168h	class	1kb upstream	p-value
<i>Metabolism</i>									
265119_at	At1g62570	flavin-containing monooxygenase (similar to glutamate synthase)	amino acid	-0.6	30.4	9.7	3	0	1.02E-06
251775_s_at	At3g55610	delta-1-pyrroline-5-carboxylate synthetase (P5CS2)	amino acid	0.0	6.1	2.3	3	1	5.56E-06
253695_at	At4g29510	arginine methyltransferase (PAM1)	amino acid	0.0	3.7	1.9	3	1	7.37E-05
246490_at	At5g15950	S-adenosylmethionine decarboxylase (adoMetDC2)	amino acid	1.1	4.3	2.5	3	0	9.48E-05
264511_at	At1g09350	putative galactinol synthase	carbohydrate	-0.6	113.5	40.7	3	3	1.35E-08
263452_at	At2g22190	putative trehalose-6-phosphate phosphatase	carbohydrate	1.1	3.4	1.6	3	0	5.10E-07
263320_at	At2g47180	galactinol synthase	carbohydrate	-0.5	8.3	4.9	3	1	2.58E-04
257876_at	At3g17130	hypothetical protein, similar to invertase/pectin methylesterase inhibitor	carbohydrate	-0.7	9.4	2.5	3	1	4.06E-07
245346_at	At4g17090	glycosyl hydrolase family 14 (beta-amylase)	carbohydrate	1.3	5.5	2.4	3	0	3.25E-06
254188_at	At4g23920	putative UDP-glucose 4-epimerase	carbohydrate	0.0	3.7	1.7	3	1	5.74E-06
253559_at	At4g31140	glycosyl hydrolase family 17	carbohydrate	0.5	3.0	1.7	3	1	2.38E-04
252863_at	At4g39800	myo-inositol-1-phosphate synthase	carbohydrate	-0.6	3.8	2.0	3	0	5.76E-08
245904_at	At5g11110	sucrose-phosphate synthase, putative	carbohydrate	-0.5	5.2	2.0	3	0	2.41E-04
245998_at	At5g20830	sucrose synthase I (SUS1)	carbohydrate	0.0	10.4	4.9	3	1	8.41E-06
249411_at	At5g40390	raffinose synthase	carbohydrate	-0.6	6.0	2.6	3	1	1.21E-05
267280_at	At2g19450	diacylglycerol O-acyltransferase (TAG1)	lipid	0.0	3.1	1.7	3	1	1.47E-05
263789_at	At2g24560	putative GDSL-motif lipase/hydrolase	lipid	1.2	23.5	4.1	3	2	1.86E-02
245533_at	At4g15130	putative phosphocholine cytidyltransferase (AtCCT2)	lipid	1.2	6.6	3.8	3	1	1.41E-07
253254_at	At4g34650	squalene synthase (SQS2)	lipid	-1.1	8.5	2.7	3	1	3.73E-03

257702_at	At3g12670	CTP synthase (UTP--ammonia ligase), putative	nucleotide	-0.6	3.3	1.6	3	1	1.33E-06
253252_at	At4g34740	amidophosphoribosyltransferase 2 precursor	nucleotide	0.6	3.9	2.1	3	1	3.91E-04
261048_at	At1g01420	similar to UTP-glucose glucosyltransferases	secondary	0.6	4.8	2.8	3	1	8.25E-06
264261_at	At1g09240	nicotianamine synthase, putative	secondary	1.3	3.3	2.6	3	0	2.63E-03
266532_at	At2g16890	putative phenylpropanoid glucosyltransferase	secondary	2.0	14.5	7.9	3	0	7.54E-06
257280_at	At3g14440	9-cis-epoxycarotenoid dioxygenase (NCED3)	secondary	1.4	5.1	1.9	3	0	9.77E-03
258094_at	At3g14690	putative cytochrome P450	secondary	0.5	3.4	1.6	3	0	1.85E-05
251984_at	At3g53260	phenylalanine ammonia-lyase 2 (PAL2)	secondary	1.3	3.2	1.8	3	0	1.50E-05
254926_at	At4g11280	ACC synthase (AtACS-6)	secondary	4.4	1.2	0.7	5	0	2.48E-04
253879_s_at	At4g27570	UDP rhamnose--anthocyanidin-3-glucoside rhamnosyltransferase	secondary	0.6	7.3	2.5	3	0	6.41E-06
253097_at	At4g37320	cytochrome P450 family	secondary	-0.6	3.3	1.2	3	1	4.89E-04
246419_at	At5g17030	UDP glucose:flavonoid 3-O-glucosyltransferase family	secondary	-2.0	23.1	6.0	3	1	5.43E-03
248964_at	At5g45340	cytochrome P450 family	secondary	11.9	0.7	-1.4	5	0	2.99E-04
<i>Transcription</i>									
252625_at	At3g44750	putative histone deacetylase	chromatin modification	-0.7	3.4	2.5	3	0	1.37E-03
259364_at	At1g13260	RAV1	mRNA synthesis	4.5	4.2	3.7	7	0	2.75E-04
260776_at	At1g14580	zinc finger (C2H2 type) protein family	mRNA synthesis	0.0	5.3	2.5	3	0	1.03E-05
260856_at	At1g21910	TINY-like protein	mRNA synthesis	8.3	0.9	0.2	5	0	1.28E-04
261263_at	At1g26790	H-protein promoter binding factor-2b like	mRNA synthesis	2.3	4.8	3.0	7	0	3.82E-05
261648_at	At1g27730	ZAT10/STZ	mRNA synthesis	12.5	2.1	1.1	5	1	1.23E-04
245807_at	At1g46768	AP2 domain transcription factor (RAP2.1)	mRNA synthesis	-5.8	10.4	5.6	3	2	7.95E-03
261613_at	At1g49720	abscisic acid responsive elements-binding factor 1 (ABF1)	mRNA synthesis	0.8	5.9	3.0	3	0	6.25E-07
259834_at	At1g69570	H-protein promoter binding factor-2b like	mRNA synthesis	1.8	4.8	4.8	3	0	4.09E-06
259971_at	At1g76580	squamosa promoter binding protein - related	mRNA synthesis	0.6	4.5	1.9	3	1	3.27E-06

261892_at	At1g80840	WRKY family transcription factor (WRKY40)	mRNA synthesis	7.5	0.0	1.2	5	0	3.26E-03
263739_at	At2g21320	CONSTANS B-box zinc finger family protein	mRNA synthesis	0.5	4.8	2.9	3	0	1.86E-05
265662_at	At2g24500	C2H2-type zinc finger protein (FZF)	mRNA synthesis	0.5	3.0	1.5	3	1	6.24E-07
267028_at	At2g38470	WRKY family transcription factor (WRKY33)	mRNA synthesis	4.3	-1.4	0.6	5	0	6.13E-05
263379_at	At2g40140	putative CCCH-type zinc finger protein	mRNA synthesis	3.8	2.3	1.9	6	0	7.00E-04
267509_at	At2g45660	MADS-box protein (AGL20)	mRNA synthesis	1.2	3.5	2.0	3	0	1.83E-04
266719_at	At2g46830	MYB-related transcription factor (CCA1)	mRNA synthesis	1.2	4.1	2.0	3	0	8.15E-04
266514_at	At2g47890	CONSTANS B-box zinc finger family protein	mRNA synthesis	0.0	5.5	2.7	3	1	1.84E-04
252374_at	At3g48100	response regulator 2 (ATR2)	mRNA synthesis	4.6	-1.8	0.6	5	0	2.36E-05
251793_at	At3g55580	regulator of chromosome condensation RCC1 family	mRNA synthesis	2.6	38.1	41.9	3	0	4.64E-05
251745_at	At3g55980	zinc finger (CCCH type) protein family	mRNA synthesis	7.2	-0.3	0.0	5	0	8.35E-06
255568_at	At4g01250	WRKY family transcription factor (WRKY31)	mRNA synthesis	3.0	0.0	-0.5	5	0	3.91E-05
245250_at	At4g17490	ethylene responsive element binding factor (AtERF6)	mRNA synthesis	10.7	-2.8	-4.6	5	0	7.08E-05
254670_at	At4g18390	TCP family transcription factor, putative	mRNA synthesis	1.1	3.4	1.6	3	0	5.40E-06
254075_at	At4g25470	CBF2/DREB1c	mRNA synthesis	22.1	9.2	3.2	6	0	8.68E-06
254066_at	At4g25480	CBF3/DREB1a	mRNA synthesis	16.4	10.3	2.4	6	0	6.70E-06
253722_at	At4g29190	zinc finger (CCCH type) protein family	mRNA synthesis	2.2	4.1	2.6	7	1	4.73E-06
253485_at	At4g31800	WRKY family transcription factor (WRKY18)	mRNA synthesis	3.1	0.7	1.8	5	0	3.91E-02
253423_at	At4g32280	auxin-responsive protein AUX/IAA family	mRNA synthesis	0.6	6.0	4.1	3	1	1.83E-05
253219_at	At4g34990	MYB family transcription factor (MYB32)	mRNA synthesis	-1.3	2.7	1.5	3	0	3.13E-04
246253_at	At4g37260	MYB family transcription factor (MYB73)	mRNA synthesis	3.0	2.2	1.6	6	0	3.18E-05
245711_at	At5g04340	putative c2h2 zinc finger transcription factor	mRNA synthesis	5.7	3.7	0.9	6	2	3.61E-03
246484_at	At5g16040	regulator of chromosome condensation RCC1 family	mRNA synthesis	0.5	3.6	2.9	3	0	2.23E-05
249741_at	At5g24470	pseudo-response regulator (APRR5)	mRNA synthesis	3.4	9.4	5.1	7	0	8.18E-05

248799_at	At5g47230	ethylene responsive element binding factor 5 (AtERF5)	mRNA synthesis	4.5	1.9	0.0	5	1	3.36E-03
248744_at	At5g48250	CONSTANS B-box zinc finger family protein	mRNA synthesis	1.3	4.2	2.5	3	0	8.20E-04
248448_at	At5g51190	AP2 domain transcription factor, putative	mRNA synthesis	8.9	-0.1	-0.8	5	0	2.19E-03
248160_at	At5g54470	CONSTANS B-box zinc finger family protein	mRNA synthesis	5.6	22.5	12.6	7	0	2.32E-02
247921_at	At5g57660	CONSTANS B-box zinc finger family protein	mRNA synthesis	1.3	5.3	3.9	3	2	8.75E-05
247543_at	At5g61600	ethylene responsive element binding factor family	mRNA synthesis	5.5	-1.7	-0.9	5	0	5.57E-06
<u>RNA processing and translation</u>									
263334_at	At2g03820	nonsense mediated mRNA decay protein NMD3 family	mRNA processing	1.1	2.9	1.6	3	0	6.41E-06
256797_at	At3g18600	DEAD/DEAH box helicase, putative	mRNA processing	-0.6	3.9	2.4	3	0	5.38E-05
245437_at	At4g16630	RNA helicase like protein	mRNA processing	0.6	3.5	1.7	3	1	5.52E-05
254080_at	At4g25630	fibrillarin 2 (AtFib2)	mRNA processing	-0.6	5.1	4.6	3	0	2.19E-05
253213_at	At4g34910	RNA helicase (RH16)	mRNA processing	-1.4	3.4	2.7	3	0	2.77E-05
246809_s_at	At5g27120	NOP58-like protein	mRNA processing	-0.6	3.1	2.2	3	1	2.01E-05
252679_at	At3g44260	CCR4-NOT complex protein, putative	mRNA turnover	8.7	-1.5	-1.5	5	0	1.15E-03
254073_at	At4g25500	splicing factor (At-SRp40)	RNA processing	0.6	3.9	2.4	3	0	1.08E-06
248136_at	At5g54910	DEAD/DEAH box helicase, putative	RNA processing	-1.1	3.2	1.3	3	0	3.97E-06
262094_at	At1g56110	nucleolar protein Nop56, putative	RNA processing	-0.1	3.7	2.4	3	1	1.80E-05
266567_at	At2g24050	putative eukaryotic initiation factor 4 (eIF4)	translation	0.0	3.1	2.1	3	0	9.07E-05
251776_at	At3g55620	putative eukaryotic translation initiation factor 6 (EIF-6)	translation	-1.1	2.6	1.4	3	0	3.25E-06
246527_at	At5g15750	ribosomal protein-like	translation	0.5	3.7	2.2	3	1	9.59E-05
246070_at	At5g20160	ribosomal protein L7Ae family	translation	-0.1	3.0	2.8	3	2	1.57E-05

248749_at	At5g47880	eukaryotic release factor 1 (ERF1)	translation	1.2	3.4	1.7	3	1	8.45E-05
247739_at	At5g59240	40S ribosomal protein S8 (RPS8B)	translation	1.2	5.9	3.2	3	1	7.32E-03
<u>Intercellular communication and signal transduction</u>									
245734_at	At1g73480	putative lysophospholipase	intracellular signaling	1.3	11.1	4.9	3	1	3.25E-06
246922_at	At5g25110	serine/threonine protein kinase-like	intracellular signaling	0.5	91.1	47.9	3	0	5.60E-03
260135_at	At1g66400	calmodulin-related protein, putative	signal	2.8	0.0	0.6	5	0	4.47E-03
260076_at	At1g73630	putative calmodulin protein	transduction	1.2	2.8	1.7	3	0	4.54E-05
266720_s_at	At2g46790	pseudo-response regulator (APRR9/TL1)	transduction	-0.7	6.5	5.2	3	0	8.23E-05
251494_at	At3g59350	putative serine/threonine protein kinase (similar to Pto1)	signal	2.0	2.9	0.9	7	2	1.60E-03
251432_at	At3g59820	putative leucine zipper-EF-hand containing transmembrane protein	transduction	-0.6	5.2	2.6	3	0	3.15E-07
253915_at	At4g27280	calcium-binding EF-hand family protein	signal	5.5	-1.6	-0.8	5	1	8.91E-05
246756_at	At5g27930	protein phosphatase 2C (PP2C), putative	transduction	0.0	2.9	1.7	3	0	8.33E-05
248164_at	At5g54490	calcium-binding EF-hand protein (PBP1)	signal	4.1	0.0	0.9	5	1	7.63E-04
247776_at	At5g58700	phosphoinositide specific phospholipase C family	transduction	0.5	4.7	1.7	3	0	1.06E-04
248326_at	At5g52820	Notchless protein homolog	transduction	-0.1	2.8	1.9	3	1	1.70E-05
<u>Energy</u>									
264953_at	At1g77120	alcohol dehydrogenase	fermentation	-0.7	11.8	2.9	3	1	2.34E-04
253416_at	At4g33070	pyruvate decarboxylase-1 (Pdc1)	fermentation	-0.9	22.6	7.1	3	1	2.96E-05
264000_at	At2g22500	mitochondrial carrier protein family	respiration	3.0	2.3	1.0	6	0	3.30E-03
255259_at	At4g05020	NADH dehydrogenase - related	respiration	-0.6	3.2	2.8	3	0	5.38E-05
254120_at	At4g24570	mitochondrial carrier protein family	transport	18.5	1.3	0.9	5	0	4.43E-05
<u>Transport</u>									
247937_at	At5g57110	Ca2+-transporting ATPase (ACA8)	calcium transport	-0.2	7.6	3.6	3	1	2.06E-07

246566_at	At5g14940	oligopeptide transporter family	peptide transport	0.6	2.7	3.1	3	0	1.18E-06
264652_at	At1g08920	putative sugar transport protein	sugar transport	1.2	3.5	1.0	3	1	8.67E-05
245427_at	At4g17550	glycerol-3-phosphate permease like protein	sugar transport	0.7	15.2	4.8	3	2	4.06E-07
253188_at	At4g35300	putative sugar transporter protein	sugar transport	-0.1	3.0	2.2	3	1	5.82E-06
260489_at	At1g51610	cation efflux family	transport	0.6	5.3	2.7	3	0	5.27E-06
260410_at	At1g69870	putative proton-dependent oligopeptide transport (POT) protein	transport	0.8	7.3	2.8	3	1	5.04E-07
261116_at	At1g75370	SEC14 cytosolic factor, putative/phosphatidylinositol transfer-like protein	transport	0.0	3.0	1.3	3	1	4.08E-05
263574_at	At2g16990	putative tetracycline transporter protein	transport	-1.2	3.3	1.9	3	2	4.49E-06
266225_at	At2g28900	putative membrane channel protein	transport	-0.1	6.1	3.5	3	2	2.07E-06
251227_at	At3g62700	ABC transporter, glutathione-conjugate transporter, putative	transport	0.0	2.8	2.0	3	1	1.98E-04
250151_at	At5g14570	similar to trans-membrane nitrate transporter protein	transport	0.6	5.2	2.8	3	1	1.88E-06
250053_at	At5g17850	similar to sodium/calcium exchanger protein	transport	3.9	11.6	5.1	7	1	1.62E-03
247498_at	At5g61810	peroxisomal Ca-dependent solute carrier - like protein	transport	-0.1	3.1	1.5	3	1	8.30E-06
<u>Protein processing and fate</u>									
264019_at	At2g21130	peptidyl-prolyl cis-trans isomerase (cyclophilin/CYP2)	protein folding	-1.1	3.2	1.8	3	0	1.27E-04
258979_at	At3g09440	heat-shock protein (At-hsc70-3)	protein folding	-1.3	2.9	1.2	3	2	6.41E-06
262440_at	At1g47710	serpin, putative	protein modification	-1.1	5.3	2.0	3	2	2.12E-07
256288_at	At3g12270	putative arginine N-methyltransferase	protein modification	-0.6	4.2	2.5	3	0	1.17E-05
253323_at	At4g33920	putative protein phosphatase	protein modification	3.0	2.5	1.6	6	0	7.38E-04
251899_at	At3g54400	aspartyl protease family	proteolysis	0.0	4.8	2.8	3	1	9.53E-07
262644_at	At1g62710	vaoular cystein proteinase (beta-VPE)	targeting and sorting	-0.1	8.9	5.2	3	0	3.32E-05

Stress related									
264787_at	At2g17840	ERD7	aging	0.8	9.4	3.2	3	1	5.13E-05
261248_at	At1g20030	thaumatin family	defense	1.3	4.4	-6.6	7	1	1.31E-05
262383_at	At1g72940	disease resistance protein (TIR-NBS class), putative	defense	4.8	-1.1	-0.5	5	1	4.34E-03
259925_at	At1g75040	thaumatin-like protein	defense	1.4	5.1	9.6	4	0	2.20E-03
266119_at	At2g02100	putative plant defensin protein putative (PDF2.2)	defense	1.1	3.7	3.0	3	1	1.03E-05
266141_at	At2g02120	putative plant defensin protein putative (PDF2.1)	defense	0.6	12.4	11.4	3	2	2.17E-04
263951_at	At2g35960	putative harpin-induced protein	defense	0.5	4.4	2.7	3	0	1.02E-06
260556_at	At2g43620	putative endochitinase	defense	1.5	12.0	9.3	3	1	1.16E-03
250670_at	At5g06860	polygalacturonase inhibiting protein (PGIP1)	defense	1.6	4.0	5.7	4	1	5.43E-03
258893_at	At3g05660	disease resistance protein	defense	0.5	7.3	5.7	3	2	4.73E-06
259426_at	At1g01470	Lea protein (LEA14)	LEA/dehydrin	0.1	8.6	3.4	3	3	2.06E-07
259570_at	At1g20440	dehydrin (COR47)	LEA/dehydrin	0.1	13.5	4.8	3	3	8.21E-06
259516_at	At1g20450	dehydrin (ERD10)	LEA/dehydrin	1.6	15.3	6.9	3	3	4.73E-06
256310_at	At1g30360	dehydrin (ERD4)	LEA/dehydrin	1.1	2.8	0.7	3	1	2.08E-06
263495_at	At2g42530	COR15b	LEA/dehydrin	0.2	36.3	25.8	3	2	4.75E-05
263497_at	At2g42540	COR15a	LEA/dehydrin	0.0	115.9	87.8	3	2	7.25E-04
252102_at	At3g50970	dehydrin (Xero2)	LEA/dehydrin	0.7	52.3	25.3	3	3	5.10E-07
255479_at	At4g02380	late embryogenesis abundant protein (SAG21)	LEA/dehydrin	2.4	2.3	3.3	4	0	4.58E-03
246481_s_at	At5g15960	KIN1	LEA/dehydrin	0.0	8.3	7.4	3	1	1.92E-04
248337_at	At5g52310	COR78	LEA/dehydrin	0.8	51.3	24.1	3	4	1.18E-05
258321_at	At3g22840	early light-induced protein (ELIP)	photoprotective	1.2	19.4	5.8	3	0	1.31E-05
245306_at	At4g14690	early light-inducible protein like	photoprotective	1.5	21.5	3.1	3	1	1.68E-07
253104_at	At4g36010	thaumatin-like protein	stress	3.2	13.2	2.5	7	3	3.63E-07
262452_at	At1g11210	expressed protein (COR35)	unknown	4.3	33.4	14.0	7	0	6.51E-04
256114_at	At1g16850	expressed protein (COR17)	unknown	0.4	218.0	60.8	3	3	2.83E-05
259789_at	At1g29395	similar to cold acclimation protein WCOR414 (WCOR414-TM1)	unknown	-0.1	9.4	7.3	3	1	9.53E-07
264968_at	At1g67360	stress related protein	unknown	-1.2	3.3	2.7	3	1	1.87E-06

262050_at	At1g80130	expressed protein (COR33.5)	unknown	0.6	24.1	26.3	3	1	2.12E-06
265480_at	At2g15970	similar to cold acclimation protein WCOR413 (WCOR413-PM1)	unknown	-1.1	5.0	3.3	3	2	4.28E-06
263517_at	At2g21620	responsive to desiccation protein (RD2) family	unknown	0.0	4.2	2.5	3	1	2.08E-06
267261_at	At2g23120	expressed protein (COR8.5)	unknown	1.4	6.2	3.4	3	1	2.30E-06
254818_at	At4g12470	pEARLI 1-like protein	unknown	1.1	38.1	34.1	3	0	4.86E-06
254805_at	At4g12480	pEARLI 1	unknown	0.6	21.4	47.2	4	0	3.54E-04
254832_at	At4g12490	pEARLI 1-like protein	unknown	-0.1	3.0	10.2	4	0	2.19E-05
254819_at	At4g12500	pEARLI 1-like protein	unknown	-0.6	4.5	10.6	4	0	2.28E-05
254314_at	At4g22470	protease inhibitor/seed storage/lipid transfer protein (LTP) family	unknown	1.8	2.7	4.1	4	0	3.38E-03
253627_at	At4g30650	hydrophobic protein (LT16A/RC12A)	unknown	0.0	8.9	7.2	3	1	6.26E-05
253595_at	At4g30830	expressed protein (COR42)	unknown	0.8	91.6	40.9	3	2	2.51E-05
253322_at	At4g33980	expressed protein (COR28)	unknown	2.4	5.9	2.8	7	0	1.68E-04
<i>Cellular biogenesis</i>									
260903_at	At1g02460	putative polygalacturonase	cell wall	-0.1	4.3	3.7	3	0	2.70E-06
260832_at	At1g06780	glycosyltransferase family 8	cell wall	-0.7	2.9	1.4	3	2	1.28E-04
261187_at	At1g32860	beta-1,3-glucanase precursor, putative	cell wall	-0.6	6.9	0.7	3	2	5.56E-06
259173_at	At3g03640	beta-glucosidase (GLUC)	cell wall	0.4	4.2	1.8	3	2	1.84E-06
258805_at	At3g04010	putative beta-1,3-glucanase	cell wall	1.9	13.8	4.3	3	1	2.32E-02
258719_at	At3g09540	putative pectate lyase	cell wall	-0.6	6.9	3.0	3	2	5.57E-06
252563_at	At3g45970	expansin protein family (EXPL1)	cell wall	3.7	4.0	-1.1	7	1	2.24E-04
251229_at	At3g62740	beta-glucosidase-like protein	cell wall	-0.2	12.1	12.2	3	1	4.22E-02
255524_at	At4g02330	pectinesterase family	cell wall	2.5	4.2	5.0	4	0	1.39E-03
254662_at	At4g18270	glycosyltransferase family 4 (ATTRANS11)	cell wall	0.0	2.9	1.6	3	1	4.68E-05
253841_at	At4g27830	putative beta-glucosidase	cell wall	1.1	5.1	2.2	3	1	6.49E-04
252997_at	At4g38400	expansin protein family (EXPL2)	cell wall	1.9	9.6	2.4	3	3	3.39E-03
248100_at	At5g55180	beta-1,3-glucanase-like protein	cell wall	0.0	4.4	1.5	3	0	6.28E-05
247925_at	At5g57560	TCH4	cell wall	9.5	1.2	-1.1	5	1	6.07E-05
247478_at	At5g62360	similar to pectinesterase	cell wall	1.4	8.3	2.0	3	1	5.54E-04
248197_at	At5g54190	protochlorophyllide reductase A (PCRA/PORA)	chloroplast	-1.3	1.0	5.3	4	0	8.92E-04

263249_at	At2g31360	delta 9 desaturase (ADS2)	plasma membrane	1.1	4.3	2.3	3	0	1.78E-06
247851_at	At5g58070	outer membrane lipoprotein - like	plasma membrane	0.0	4.4	2.2	3	0	1.02E-07
<u>Cellular organization</u>									
256091_at	At1g20693	high mobility group (HMG) protein beta 1 (HMGbeta1)	chromatin binding	0.5	4.3	2.7	3	1	3.09E-05
254085_at	At4g24960	similar to abscisic acid-induced protein (HVA22D)	vesicular trafficking	0.0	8.6	2.1	3	3	5.10E-07
<u>DNA replication and cell division</u>									
257237_at	At3g14890	DNA nick sensor, putative	DNA synthesis	-1.1	7.6	2.8	3	2	1.65E-07
<u>Unknown role</u>									
262584_at	At1g15440	WD-40 repeat protein family	unknown	-0.1	3.7	2.0	3	0	1.78E-06
264211_at	At1g22770	GIGANTEA	unknown	1.1	5.9	4.8	3	0	7.75E-05
265154_at	At1g30960	GTP-binding protein	unknown	0.6	5.2	2.1	3	0	4.28E-04
245757_at	At1g35140	phosphate-induced (phi-1) protein	unknown	24.0	4.6	-0.1	5	0	2.01E-03
260727_at	At1g48110	expressed protein (putative splicing domain)	unknown	0.6	15.8	3.3	3	0	1.78E-06
245749_at	At1g51090	similar to proline-rich protein	unknown	1.3	29.3	4.4	3	2	1.21E-05
262881_at	At1g64890	expressed protein (integral membrane/transporter family)	unknown	0.0	9.6	3.4	3	1	1.85E-05
260338_at	At1g69250	putative RNA-binding protein	unknown	-0.6	3.8	1.9	3	1	3.04E-06
262682_at	At1g75900	family II extracellular lipase 3 (EXL3)	unknown	-0.6	2.9	2.9	3	0	9.15E-06
260331_at	At1g80270	DNA binding protein, putative	unknown	-0.6	4.1	2.0	3	0	1.71E-04
266934_at	At2g18900	WD-40 repeat protein family	unknown	-0.5	3.7	1.6	3	0	1.73E-04
263352_at	At2g22080	related to En/Spm transposon family of maize	unknown	0.6	4.3	1.8	3	1	2.77E-04
266510_at	At2g47990	WD-40 repeat protein family	unknown	0.0	3.9	1.9	3	0	1.32E-05
259132_at	At3g02250	similar to auxin-independent growth promoter	unknown	1.2	2.8	1.7	3	1	2.66E-04
258792_at	At3g04640	glycine-rich protein	unknown	6.1	0.6	0.1	5	1	3.54E-05
258545_at	At3g07050	putative GTPase	unknown	0.4	4.3	3.1	3	0	8.41E-05
258965_at	At3g10530	WD-40 repeat protein family	unknown	0.0	5.2	2.6	3	0	5.65E-06
258166_at	At3g21540	WD-40 repeat protein family	unknown	-0.5	4.6	2.0	3	0	3.31E-05

256601_s_at	At3g28290	integrin like protein (similar to At14a)	unknown	-0.1	3.1	21.7	4	0	2.06E-07
252305_at	At3g49240	pentatricopeptide (PPR) repeat-containing protein	unknown	0.1	3.8	1.6	3	0	1.19E-05
255403_at	At4g03400	auxin responsive protein, putative (GH3 family)	unknown	1.4	3.3	2.8	3	0	1.56E-04
255278_at	At4g04940	WD-40 repeat protein family	unknown	-0.1	4.9	2.5	3	0	9.14E-05
255225_at	At4g05410	WD-40 repeat protein family	unknown	-0.6	3.9	2.2	3	2	1.63E-05
254667_at	At4g18280	glycine-rich cell wall protein	unknown	1.5	3.9	3.0	3	1	6.00E-06
253875_at	At4g27520	putative protein ENOD20 predicted GPI-anchored protein	unknown	1.1	3.7	2.0	3	1	4.88E-06
253777_at	At4g28450	WD-40 repeat protein family	unknown	-0.6	3.0	1.8	3	0	1.12E-04
252956_at	At4g38580	farnesylated protein (ATFP6)	unknown	1.1	10.0	4.5	3	2	1.10E-06
250418_at	At5g11240	WD-40 repeat protein family	unknown	0.1	3.8	2.1	3	1	2.34E-04
250279_at	At5g13200	like ABA-responsive protein	unknown	1.5	4.4	2.7	3	1	3.70E-05
246559_at	At5g15550	WD-40 repeat protein family	unknown	0.5	3.1	1.5	3	0	4.20E-04
249750_at	At5g24570	expressed protein	unknown	-0.1	3.8	2.5	3	1	5.85E-06
248467_at	At5g50800	nodulin MtN3-like protein	unknown	-0.1	4.4	7.0	4	0	1.78E-06
247463_at	At5g62210	contains similarity to embryo-specific protein 3	unknown	1.2	6.4	1.1	3	0	3.86E-04
<u>Unknown protein</u>									
262112_at	At1g02870	expressed protein	unknown	-0.1	3.0	2.1	3	0	2.37E-05
264818_at	At1g03530	expressed protein	unknown	-0.6	4.6	1.9	3	0	4.73E-06
263182_at	At1g05575	expressed protein	unknown	4.9	-1.7	0.5	5	0	4.69E-04
260824_at	At1g06720	expressed protein	unknown	-1.1	3.8	2.5	3	0	4.06E-07
264803_at	At1g08580	expressed protein	unknown	0.4	3.4	2.7	3	0	6.42E-05
264515_at	At1g10080	hypothetical protein	unknown	0.5	3.1	1.5	3	0	1.38E-07
264516_at	At1g10090	expressed protein	unknown	-0.6	3.4	1.4	3	2	5.84E-05
264458_at	At1g10410	expressed protein	unknown	1.2	6.4	3.0	3	1	2.47E-05
262766_at	At1g13160	expressed protein	unknown	0.0	3.4	1.7	3	0	2.47E-05
261664_s_at	At1g18320	expressed protein	unknown	-0.7	3.2	2.8	3	0	1.74E-03
261377_at	At1g18850	expressed protein	unknown	-0.5	4.1	1.8	3	0	7.04E-05
256017_at	At1g19180	expressed protein	unknown	4.5	3.1	2.7	7	0	1.21E-03
260674_at	At1g19370	expressed protein	unknown	0.6	2.6	1.6	3	0	2.02E-04
262496_at	At1g21790	expressed protein	unknown	0.1	5.8	2.1	3	2	2.41E-04

265184_at	At1g23710	expressed protein	unknown	3.8	-0.7	-0.6	5	0	1.88E-03
255733_at	At1g25400	expressed protein	unknown	5.3	-4.0	0.0	5	1	1.84E-02
264989_at	At1g27200	expressed protein	unknown	1.6	7.5	3.9	3	1	1.02E-06
261651_at	At1g27760	expressed protein	unknown	-0.2	5.2	2.6	3	1	1.35E-05
245770_at	At1g30240	expressed protein	unknown	-0.1	3.0	1.6	3	0	5.56E-06
261193_at	At1g32920	expressed protein	unknown	4.7	-0.9	-1.7	5	0	1.62E-05
261566_at	At1g33230	expressed protein	unknown	-0.1	4.0	2.2	3	1	1.92E-04
265147_at	At1g51380	expressed protein	unknown	-0.2	5.4	2.6	3	1	3.35E-05
260157_at	At1g52930	expressed protein	unknown	-0.6	3.3	2.5	3	0	1.50E-05
261318_at	At1g53035	expressed protein	unknown	1.2	8.6	4.6	3	0	9.53E-07
245200_at	At1g67850	expressed protein	unknown	1.1	3.7	2.8	3	0	4.06E-07
260264_at	At1g68500	expressed protein	unknown	1.2	17.8	3.2	3	1	2.20E-04
259977_at	At1g76590	expressed protein	unknown	1.5	6.8	1.7	3	2	5.24E-04
259979_at	At1g76600	expressed protein	unknown	3.9	-0.9	-0.8	5	0	5.02E-05
262164_at	At1g78070	expressed protein	unknown	0.6	5.1	2.7	3	2	1.20E-05
264118_at	At1g79140	expressed protein	unknown	-0.6	4.2	2.5	3	0	5.74E-06
266797_at	At2g22840	expressed protein	unknown	1.4	2.8	1.9	3	0	1.41E-04
265999_at	At2g24100	expressed protein	unknown	0.6	3.8	3.2	3	0	1.47E-04
263931_at	At2g36220	expressed protein	unknown	2.7	3.7	2.1	7	0	9.19E-05
267592_at	At2g39710	expressed protein	unknown	1.4	3.2	3.4	3	2	5.97E-05
267361_at	At2g39920	expressed protein	unknown	1.2	2.9	3.4	3	0	1.97E-04
267357_at	At2g40000	expressed protein	unknown	5.4	-2.2	-1.8	5	1	8.21E-04
263384_at	At2g40130	expressed protein	unknown	1.6	2.7	0.9	3	1	6.37E-03
260585_at	At2g43650	expressed protein	unknown	1.4	3.0	1.0	3	0	4.32E-04
258505_at	At3g06530	expressed protein	unknown	-0.6	3.9	2.1	3	0	3.07E-06
256442_at	At3g10930	expressed protein	unknown	24.5	-3.5	1.5	5	0	7.26E-03
256266_at	At3g12320	expressed protein	unknown	1.3	3.6	2.8	3	1	6.38E-04
257652_at	At3g16810	expressed protein	unknown	0.6	3.8	1.9	3	0	2.40E-06
256891_at	At3g19030	expressed protein	unknown	3.1	-0.3	1.1	5	0	4.02E-04
257076_at	At3g19680	expressed protein	unknown	2.6	1.5	1.2	6	2	4.22E-03
258316_at	At3g22660	expressed protein	unknown	-0.1	4.2	2.9	3	0	9.98E-06
258104_at	At3g23620	expressed protein	unknown	-0.6	3.5	2.4	3	0	8.80E-06
257253_at	At3g24190	expressed protein	unknown	0.0	2.8	0.0	3	2	8.87E-07
256881_at	At3g26410	expressed protein	unknown	-0.6	2.9	2.0	3	0	4.06E-07

257154_at	At3g27210	expressed protein	unknown	0.8	5.0	3.5	3	0	2.54E-05
257968_at	At3g27550	expressed protein	unknown	-0.1	3.1	0.7	3	0	4.85E-05
256595_x_at	At3g28530	hypothetical protein	unknown	1.4	4.2	1.5	3	0	9.74E-04
251927_at	At3g53990	expressed protein	unknown	1.1	4.4	2.1	3	2	5.25E-04
251800_at	At3g55510	expressed protein	unknown	0.0	5.9	3.3	3	0	2.36E-05
251753_at	At3g55760	expressed protein	unknown	-0.1	10.4	2.1	3	1	1.02E-07
251538_at	At3g58660	expressed protein	unknown	-0.1	3.9	1.4	3	0	5.21E-04
254850_at	At4g12000	expressed protein	unknown	0.5	3.8	1.7	3	1	4.76E-04
254778_at	At4g12750	expressed protein	unknown	0.4	2.8	1.5	3	0	1.02E-06
245512_at	At4g15770	expressed protein	unknown	0.5	2.9	1.9	3	0	8.09E-05
245336_at	At4g16515	expressed protein	unknown	1.2	3.9	1.5	3	3	1.33E-04
254227_at	At4g23630	expressed protein	unknown	-0.1	3.2	1.8	3	1	4.06E-07
254076_at	At4g25340	expressed protein	unknown	-1.1	4.2	2.3	3	0	1.60E-04
254079_at	At4g25730	expressed protein	unknown	0.6	4.6	2.5	3	0	6.70E-05
253975_at	At4g26600	expressed protein	unknown	2.1	5.9	2.4	3	0	1.12E-04
253643_at	At4g29780	expressed protein	unknown	10.8	0.4	-0.1	5	0	7.59E-04
253585_at	At4g30720	expressed protein	unknown	1.0	1.6	3.0	4	0	3.16E-06
253425_at	At4g32190	expressed protein	unknown	0.5	4.2	1.5	3	2	1.18E-06
252986_at	At4g38380	hypothetical protein	unknown	0.5	4.9	5.8	3	0	3.71E-03
252880_at	At4g39730	expressed protein	unknown	-1.1	3.0	2.2	3	1	2.06E-07
250825_at	At5g05210	expressed protein	unknown	0.5	3.3	1.8	3	0	5.81E-05
250665_at	At5g06980	expressed protein	unknown	0.6	4.4	2.4	3	2	9.23E-04
250309_at	At5g12220	expressed protein	unknown	0.5	3.2	1.5	3	1	8.53E-05
246550_at	At5g14920	expressed protein	unknown	0.5	2.5	3.9	4	0	8.23E-06
246125_at	At5g19875	expressed protein	unknown	0.6	3.6	2.3	3	1	4.26E-05
246178_s_at	At5g28430	hypothetical protein	unknown	4.7	6.5	3.2	7	3	5.31E-03
249528_at	At5g38720	expressed protein	unknown	0.0	3.6	2.2	3	0	2.48E-04
249204_at	At5g42570	expressed protein	unknown	0.0	5.6	3.2	3	2	1.02E-06
249174_at	At5g42900	expressed protein	unknown	1.5	9.5	6.0	3	0	6.60E-05
248870_at	At5g46710	expressed protein	unknown	2.4	4.8	1.5	7	1	7.94E-06
248820_at	At5g47060	expressed protein	unknown	1.2	3.4	1.4	3	0	3.43E-05
248762_at	At5g47455	expressed protein	unknown	-0.5	3.1	3.0	3	1	2.48E-06
247474_at	At5g62280	expressed protein	unknown	-0.2	5.2	4.2	3	0	5.56E-06
247453_at	At5g62440	expressed protein	unknown	0.5	2.7	1.8	3	0	1.14E-04

247046_at	At5g66540	expressed protein	unknown	-0.7	3.5	2.2	3	0	4.68E-05
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AGI identifiers, annotations, and role assignments were derived from data provided by Affymetrix (<http://www.affymetrix.com/>), TAIR (<http://www.arabidopsis.org/>), TIGR (<http://www.tigr.org/tdb/e2k1/ath1/>), and MIPS (<http://mips.gsf.de/proj/thal/db/index.html>). The mean fold change values were calculated from the individual fold change values at each time in both duplicates of the plate (solid media) and soil experiments. Values in bold indicate times at which the probe set was labeled cold-responsive in both the soil and solid media experiments. The expression class of each transcript from hierarchical clustering analysis (Chapter 2), the number of CRT/DRE elements present in the sequence 1kb upstream (<http://www.arabidopsis.org/tools/bulk/sequences/index.jsp>) of the transcript, and the p-value from ANOVA analysis (see Materials and Methods, Chapter 2) are given.

APPENDIX F

TABLE F.1. PROBE SETS DOWN-REGULATED BY LOW TEMPERATURE IN BOTH THE PLATE AND SOIL EXPERIMENTS

Probe set	AGI	Annotation	Sub-role	Avg. fold change			Expression	(A G)CCGAC	ANOVA
				1h	24h	168h	class	1kb upstream	p-value
<i>Metabolism</i>									
261309_at	At1g48600	phosphoethanolamine N-methyltransferase	amino acid	-0.1	-1.9	-3.4	1	0	5.56E-06
259603_at	At1g56500	haloacid dehalogenase family	amino acid	0.0	-1.6	-2.9	1	0	1.78E-06
259842_at	At1g73600	phosphoethanolamine N-methyltransferase	amino acid	0.1	-1.7	-4.3	1	0	2.96E-05
257315_at	At3g30775	proline dehydrogenase (ERD5/PRO1/AT-POX)	amino acid	1.5	-3.2	-3.1	2	0	5.03E-06
252366_at	At3g48420	haloacid dehalogenase family	amino acid	0.0	-1.5	-3.3	1	0	1.78E-06
251028_at	At5g02230	haloacid dehalogenase-like hydrolase family	amino acid	-1.1	-8.3	-5.5	1	0	1.20E-04
250032_at	At5g18170	glutamate dehydrogenase (GDH1)	amino acid	-0.1	-2.8	-1.0	2	0	4.06E-05
261016_at	At1g26560	glycosyl hydrolase family 1	carbohydrate	0.0	-3.8	-3.3	1	0	2.05E-05
256772_at	At3g13750	putative beta-galactosidase (BGAL1)	carbohydrate	0.6	-5.5	-3.4	2	0	5.81E-05
255517_at	At4g02290	glycosyl hydrolase family 9	carbohydrate	0.0	-4.2	-3.3	2	0	1.60E-05
246114_at	At5g20250	glycosyl hydrolase family (DIN10)	carbohydrate	1.4	-6.2	-11.3	1	0	2.58E-05
247266_at	At5g64570	glycosyl hydrolase family 3	carbohydrate	1.2	-3.6	-1.9	2	0	2.37E-06
255786_at	At1g19670	chlorophyllase/coronatine-induced protein 1 (COR1)	chlorophyll	-1.3	-6.5	-4.9	2	0	3.75E-05
263668_at	At1g04350	putative 2-oxoglutarate-dependent dioxygenase	ethylene	-1.2	-3.8	-8.4	1	0	7.54E-06
262637_at	At1g06640	2-oxoglutarate-dependent dioxygenase	ethylene	-0.1	-1.9	-2.7	1	1	3.35E-05
253701_at	At4g29890	choline monooxygenase	glycine betaine	-1.4	-3.0	-3.3	2	0	8.40E-05
262749_at	At1g28580	putative lipase	lipid	0.0	-3.6	-1.5	2	0	2.36E-05
262733_s_at	At1g28670	lipase (ARAB-1)	lipid	-0.7	-4.8	-3.6	2	0	3.87E-05
261981_at	At1g33811	GDSL-motif lipase/hydrolase protein	lipid	0.6	-2.7	-3.8	1	0	4.69E-05
260869_at	At1g43800	putative stearyl acyl carrier protein desaturase	lipid	-1.4	-33.5	-21.4	2	0	3.90E-04
264037_at	At2g03750	similar to steroid sulfotransferase	lipid	0.5	-3.2	-1.4	2	0	9.52E-06

265894_at	At2g15050	putative lipid transfer protein	lipid	-1.4	-4.0	-2.6	2	0	1.82E-05
263987_at	At2g42690	putative lipase	lipid	-1.1	-4.3	-1.9	2	1	1.43E-05
257772_at	At3g23080	similar to phosphatidylcholine transfer	lipid	-0.1	-4.1	-2.0	2	0	1.81E-05
254280_at	At4g22756	putative sterol 4-alpha-methyl-oxidase	lipid	-0.1	-2.9	-1.7	2	0	1.38E-03
250180_at	At5g14450	GDSL-motif lipase/hydrolase protein	lipid	-0.1	-2.7	-3.1	1	2	1.50E-05
249774_at	At5g24150	squalene monooxygenase (SQP1,1)	lipid	-0.6	-4.6	-39.7	1	1	1.38E-07
249775_at	At5g24160	squalene monooxygenase (SQP1,2)	lipid	-0.5	-16.8	-43.7	1	0	3.51E-04
247780_at	At5g58770	dehydrodolicyl diphosphate synthase (DEDOL-PP synthase), putative	lipid	-1.3	-5.3	-219.1	1	1	1.94E-07
247396_at	At5g62930	GDSL-motif lipase/hydrolase protein	lipid	-0.6	-11.8	-3.4	2	1	1.03E-03
246540_at	At5g15600	nitrilase associated protein	nitrogen	-0.6	-2.5	-4.8	1	0	6.49E-04
261084_at	At1g07440	tropinone reductase, putative	secondary	-1.2	-3.8	-2.6	2	0	5.67E-05
262826_at	At1g13080	putative cytochrome P450	secondary	-1.2	-3.7	-2.4	2	0	9.17E-05
255895_at	At1g17990	similar to 12-oxophytodienoate reductase OPR1	secondary	1.2	-6.3	-2.1	2	0	7.68E-04
259669_at	At1g52340	dehydrogenase/reductase family protein (ABA2)	secondary	-1.2	-6.2	-1.7	2	1	3.87E-02
263174_at	At1g54040	Kelch repeats protein family (TASTY/ESP)	secondary	-0.6	-2.9	-3.6	1	0	4.02E-06
264250_at	At1g78680	gamma-glutamyl hydrolase	secondary	-1.2	-3.9	-2.7	1	0	5.06E-06
266279_at	At2g29290	putative tropinone reductase	secondary	-0.6	-5.4	-3.5	2	0	2.28E-06
266265_at	At2g29340	similar to tropinone reductase-I	secondary	1.1	-4.5	-1.6	2	0	1.73E-05
258976_at	At3g01980	short-chain dehydrogenase/reductase family	secondary	-1.2	-2.9	-1.3	2	0	2.88E-04
256892_at	At3g19000	similar to flavanone-3-hydroxylase	secondary	-1.2	-3.3	-2.8	1	0	3.31E-05
258299_at	At3g23410	alcohol oxidase-related	secondary	-0.6	-2.2	-3.5	1	0	3.85E-04
251759_at	At3g55630	folylpolyglutamate-dihydrofolate synthase (dhfs/fpgs4)	secondary	-1.2	-6.0	-2.7	2	0	1.42E-04
254331_s_at	At4g22710	cytochrome P450 family	secondary	1.2	-4.8	-2.8	2	0	2.28E-06
253886_at	At4g27710	cytochrome P450, member of CYP709B	secondary	0.0	-3.3	-2.0	2	0	2.54E-05
253534_at	At4g31500	cytochrome P450 (ATR4/CYP83B1)	secondary	0.6	-3.3	0.5	2	0	4.54E-05
250549_at	At5g07860	N-hydroxycinnamoyl/ benzoyltransferase	secondary	-0.6	-3.8	-2.3	2	0	7.65E-04
246021_at	At5g21100	L-ascorbate oxidase, putative	secondary	-1.1	-3.8	-4.1	1	0	4.14E-06
249869_at	At5g23050	AMP-dependent synthetase and ligase family	secondary	0.5	-3.0	-2.1	2	0	2.98E-04

248353_at	At5g52320	putative cytochrome P450	secondary	-1.4	-3.4	-1.4	2	1	1.34E-02
<u>Transcription</u>									
259476_at	At1g19000	MYB family transcription factor	mRNA synthesis	-0.6	-3.6	-2.3	2	0	2.67E-03
259822_at	At1g66230	MYB family transcription factor (MYB20)	mRNA synthesis	0.5	-3.5	-6.3	1	0	9.84E-03
260431_at	At1g68190	CONSTANS B-box zinc finger family protein	mRNA synthesis	0.1	-10.9	-9.6	1	1	8.06E-04
255794_at	At2g33480	No apical meristem (NAM) protein family	mRNA synthesis	-1.4	-2.9	-1.7	2	0	3.44E-04
258623_at	At3g02790	C2H2-type zinc finger protein family	mRNA synthesis	-0.6	-1.4	-5.6	1	1	4.99E-05
258723_at	At3g09600	MYB family transcription factor	mRNA synthesis	-0.1	-8.2	-13.8	1	0	5.76E-03
258133_at	At3g24500	putative ethylene-responsive transcriptional coactivator	mRNA synthesis	-2.6	-9.0	-5.6	2	0	7.18E-03
255302_at	At4g04830	similar to transcriptional regulator	mRNA synthesis	-0.6	-3.1	-2.2	2	1	1.20E-03
245592_at	At4g14540	CCAAT-binding transcription factor subunit A (CBF-A)	mRNA synthesis	-1.2	-3.0	-2.0	2	1	4.35E-06
253806_at	At4g28270	C3HC4-type zinc finger protein family	mRNA synthesis	-0.2	-4.1	-3.6	1	0	1.38E-03
253245_at	At4g34590	bZIP transcription factor (GBF6)	mRNA synthesis	0.6	-1.7	-3.3	1	0	2.02E-05
<u>RNA processing and translation</u>									
263035_at	At1g23860	splicing factor (SRZ_21)	mRNA processing	-0.7	-3.0	-6.6	1	0	9.48E-06
266005_at	At2g37340	splicing factor RSZ33, putative	mRNA processing	-1.1	-1.4	-3.7	1	1	9.53E-07
261081_at	At1g07350	putative transformer serine/arginine-rich ribonucleoprotein	RNA processing	-1.6	-3.1	-3.4	1	0	2.45E-03
<u>Intercellular communication and signal transduction</u>									
266372_at	At2g41310	two-component response regulator (ARR8/ATR3)	signal transduction	0.7	-2.9	-2.5	2	0	9.07E-04
262830_at	At1g14700	putative purple acid phosphatase	signaling	0.5	-4.8	-3.9	1	0	8.15E-06
245637_at	At1g25230	purple acid phosphatase family	signaling	-0.1	-3.6	-2.3	2	0	2.12E-07
262076_at	At1g59580	mitogen-activated protein kinase (MPK2)	signaling	0.4	-3.3	-2.3	2	0	1.71E-04
266781_at	At2g28940	protein kinase family	signaling	0.6	-2.9	-0.1	2	0	3.99E-02
267083_at	At2g41100	calmodulin-like protein (TCH3)	signaling	1.9	-3.5	-1.1	2	0	9.99E-05
257801_at	At3g18750	WNK protein family kinases (WNK6/ZIK5)	signaling	-0.6	-2.4	-3.9	1	0	1.79E-05
254256_at	At4g23180	serine/threonine protein kinase (RLK4)	signaling	1.8	-3.5	-0.7	2	0	2.33E-06
253412_at	At4g33000	calliceurin B-like protein (fragment)	signaling	-1.2	-3.4	-1.8	2	1	3.31E-05

247043_at	At5g66880	serine/threonine protein kinase	signaling	0.5	-3.0	-2.9	1	1	8.18E-05
<u>Energy</u>									
265572_at	At2g28210	carbonic anhydrase	carbon fixation	0.0	-2.3	-3.6	1	1	1.10E-05
259161_at	At3g01500	carbonic anhydrase (CA1)	carbon fixation	-0.5	-1.3	-4.8	1	0	1.99E-05
252011_at	At3g52720	carbonic anhydrase (CAH1)	carbon fixation	-0.5	-20.3	-5.1	2	0	8.40E-04
264751_at	At1g23020	putative ferric-chelate reductase	electron transport	-0.1	-7.4	-8.8	1	0	1.60E-03
261751_at	At1g76080	thioredoxin family	electron transport	-0.6	-3.3	-5.2	1	0	4.14E-06
263114_at	At1g03130	photosystem I reaction center subunit II precursor	photosynthesis	-0.5	-2.9	-1.7	2	0	4.49E-05
260481_at	At1g10960	ferredoxin	photosynthesis	-0.1	-2.0	-5.8	1	0	3.61E-06
256015_at	At1g19150	PSI type II chlorophyll a/b-binding protein	photosynthesis	-0.6	-4.5	-4.1	1	2	6.25E-07
265149_at	At1g51400	photosystem II 5 KD protein	photosynthesis	-0.6	-7.7	-3.0	2	0	5.84E-06
261769_at	At1g76100	plastocyanin	photosynthesis	0.0	-3.1	-1.9	2	0	4.06E-07
265722_at	At2g40100	chlorophyll a/b binding protein (LHCB4.3)	photosynthesis	-0.6	-1.7	-7.0	1	0	4.42E-07
258055_at	At3g16250	ferredoxin related	photosynthesis	-1.1	-3.7	-3.0	2	1	5.79E-07
258527_at	At3g06850	branched chain alpha-keto acid dehydrogenase E2 subunit (DIN3/LTA1)	respiration	0.4	-3.3	-2.0	2	0	8.26E-06
249694_at	At5g35790	glucose-6-phosphate dehydrogenase	respiration	-0.1	-3.6	-1.9	2	0	1.10E-06
<u>Transport</u>									
259839_at	At1g52190	proton-dependent oligopeptide transport (POT) protein family	transport	-0.6	-4.9	-1.6	2	0	2.04E-04
258100_at	At3g23550	MATE efflux protein family	transport	0.7	-3.1	-3.5	2	1	3.02E-02
257789_at	At3g27020	putative oligopeptide transporter	transport	-0.1	-3.4	-2.8	1	0	2.70E-06
254938_at	At4g10770	oligopeptide transporter (AtOPT7)	transport	-0.6	-3.0	-3.7	1	0	6.90E-04
248037_at	At5g55930	oligopeptide transporter (AtOPT1)	transport	0.0	-3.0	-1.9	2	1	2.88E-05
247284_at	At5g64410	oligopeptide transporter (AtOPT4)	transport	1.1	-3.1	1.4	2	0	6.00E-06
263867_at	At2g36830	putative aquaporin (tonoplast intrinsic protein gamma)	water transport	-0.6	-2.1	-3.3	1	1	6.13E-06
265444_s_at	At2g37180	aquaporin (plasma membrane intrinsic protein 2C)	water transport	-0.7	-5.2	-4.5	1	0	1.78E-06
258054_at	At3g16240	delta tonoplast integral protein (delta-TIP)	water transport	-0.5	-4.2	-4.5	1	1	8.59E-05
245399_at	At4g17340	membrane channel like protein	water transport	-0.6	-3.6	-11.4	1	0	2.47E-05
254239_at	At4g23400	major intrinsic protein (MIP) family	water transport	0.0	-3.7	-3.3	1	0	1.19E-05
<u>Protein processing and fate</u>									

261901_at	At1g80920	J8-like protein similar to DnaJ	protein folding	1.4	-6.2	-3.8	2	0	2.32E-02
267336_at	At2g19310	putative small heat shock protein	protein folding	-1.4	-5.2	-3.6	2	0	3.50E-03
254384_at	At4g21870	heat shock protein	protein folding	0.7	-5.7	-29.0	1	0	2.19E-05
249862_at	At5g22920	zinc finger protein (RING family)	protein	2.2	-11.8	-4.2	2	0	1.11E-04
252433_at	At3g47560	putative hydrolase	interaction						
			protein	1.1	-5.9	-2.0	2	0	2.09E-06
260317_at	At1g63800	ubiquitin-conjugating enzyme 5 (UBC5)	processing						
245736_at	At1g73330	protease inhibitor (ATDR4)	proteolysis	-0.5	-5.3	-3.3	2	0	6.32E-05
245088_at	At2g39850	subtilisin-like serine protease	proteolysis	-0.9	-3.6	-11.7	1	0	4.48E-04
253191_at	At4g35350	cysteine protease (XCP1)	proteolysis	0.0	-1.6	-5.7	1	0	1.73E-03
			proteolysis	-0.6	-1.6	-3.9	1	0	1.85E-05
<u>Stress related</u>									
262374_s_at	At1g72930	disease resistance protein (TIR class), putative	defense	1.2	-5.2	-1.1	2	0	1.33E-05
258537_at	At3g04210	disease resistance protein (TIR-NBS class), putative	defense	1.4	-5.6	-0.1	2	0	3.35E-05
254553_at	At4g19530	disease resistance protein (TIR-NBS-LRR class)	defense	0.5	-3.0	-3.6	1	0	1.01E-04
264435_at	At1g10360	glutathione S-transferase (GST29)	detoxification	-1.2	-4.5	-2.4	2	1	5.74E-06
252154_at	At3g50880	putative DNA-3-methyladenine glycosidase	DNA repair	-1.2	-3.9	-2.5	2	0	1.03E-05
<u>Cellular biogenesis</u>									
260969_at	At1g12240	beta-fructosidase	cell wall	0.5	-3.6	-2.2	2	0	1.78E-06
255779_at	At1g18650	similar to beta-1,3-glucanase	cell wall	-0.6	-3.0	-2.4	1	0	1.02E-06
264898_at	At1g23205	pectinesterase	cell wall	-1.4	-2.3	-4.1	1	0	4.65E-03
265175_at	At1g23480	similar to cellulose synthase (AtCSLA03)	cell wall	0.5	-4.3	-2.2	2	0	7.00E-06
259664_at	At1g55330	arabinogalactan-protein (AGP21)	cell wall	-0.1	-3.3	-3.2	1	0	3.10E-05
260592_at	At1g55850	cellulose synthase family (CSLE1)	cell wall	-0.1	-5.8	-3.7	2	0	6.51E-04
245196_at	At1g67750	pectate lyase	cell wall	-0.7	-4.2	-3.0	2	0	4.02E-04
256299_at	At1g69530	expansin (EXP1)	cell wall	-0.7	-9.0	-3.5	2	0	3.91E-05
266357_at	At2g32290	beta-amylase	cell wall	-0.9	-7.0	-28.8	1	1	8.89E-04
255822_at	At2g40610	expansin, putative (EXP8)	cell wall	-1.6	-12.7	-6.1	2	0	7.20E-05
259009_at	At3g09260	beta-glucosidase (PSR3.1/PYK10)	cell wall	0.0	-1.7	-5.0	1	0	9.74E-04

254119_at	At4g24780	putative pectate lyase	cell wall	-1.2	-3.4	-1.7	2	1	5.06E-06
253040_at	At4g37800	putative endo-xyloglucan transferase	cell wall	0.0	-2.8	-4.5	1	0	2.89E-04
248622_at	At5g49360	beta-xylosidase (BXL1)	cell wall	1.4	-12.6	-14.8	1	0	4.90E-05
245281_at	At4g15560	DEF (CLA1) protein	chloroplast	0.0	-2.6	-1.8	2	0	2.12E-06
249325_at	At5g40850	urophorphyrin III methylase (UPM1)	chloroplast	1.5	-2.7	-2.7	2	0	1.09E-04
<u>Cellular organization</u>									
261276_at	At1g26670	v-SNARE protein (VT112/AVT11b)	vesicular trafficking	-0.6	-3.3	-3.0	1	0	2.89E-04
<u>Unknown role</u>									
265053_at	At1g52000	myrosinase binding protein	unknown	-0.7	-4.6	-0.6	2	1	2.04E-03
256383_at	At1g66820	glycing rich protein	unknown	-0.2	-2.7	-1.4	2	0	1.89E-05
260427_at	At1g72430	auxin-induced protein-related	unknown	-0.7	-4.5	-6.7	1	0	4.65E-05
260221_at	At1g74670	GAST1-like protein	unknown	0.6	-26.5	-9.0	2	0	1.78E-06
256458_at	At1g75220	integral membrane protein	unknown	0.0	-3.4	-3.8	1	0	3.25E-06
266988_at	At2g39310	jacalin lectin family	unknown	0.0	-3.8	-5.6	1	0	4.93E-04
266984_at	At2g39570	ACT domain-containing protein	unknown	0.1	-4.5	-4.6	1	0	5.65E-06
259382_s_at	At3g16430	putative myrosinase binding protein	unknown	0.0	-3.1	-4.3	1	0	8.71E-05
257880_at	At3g16910	AMP-dependent synthetase and ligase family	unknown	-1.2	-5.3	-4.2	1	0	1.40E-05
256880_at	At3g26450	putative major latex protein	unknown	-1.1	-4.9	-3.1	2	0	4.14E-06
257299_at	At3g28050	nodulin MtN21 family protein	unknown	0.5	-3.9	-2.1	2	0	3.41E-05
256603_at	At3g28270	At14a-related protein	unknown	-1.3	-19.9	-13.6	1	0	1.07E-03
245524_at	At4g15920	nodulin MtN3 family protein	unknown	0.5	-2.6	-4.9	1	0	2.33E-04
254225_at	At4g23670	putative major latex protein	unknown	0.0	-3.7	-6.4	1	0	1.19E-05
252972_at	At4g38840	auxin-induced protein	unknown	-0.8	-3.5	-1.8	2	0	5.56E-05
250217_at	At5g14120	nodulin-related protein	unknown	0.6	-8.3	-5.0	1	0	4.29E-04
249923_at	At5g19120	conglutin gamma - like protein	unknown	1.6	-6.8	-6.7	2	2	5.01E-05
245928_s_at	At5g24780	vegetative storage protein (VSP1)	unknown	0.0	-3.1	-6.0	1	0	1.23E-03
249073_at	At5g44020	vegetative storage protein-related	unknown	-0.6	-3.6	-2.7	2	0	6.54E-05
<u>Unknown protein</u>									
264507_at	At1g09415	expressed protein	unknown	0.0	-3.8	-1.7	2	0	2.88E-05
264342_at	At1g12080	expressed protein	unknown	-0.9	-2.6	-4.4	1	0	2.08E-02
256096_at	At1g13650	expressed protein	unknown	-1.2	-19.9	-18.0	1	0	1.02E-06
261793_at	At1g16080	expressed protein	unknown	-0.1	-1.7	-3.1	1	0	5.53E-06

260872_at	At1g21350	expressed protein	unknown	-0.6	-2.0	-3.0	1	1	3.73E-05
260877_at	At1g21500	expressed protein	unknown	0.0	-2.9	-2.6	1	0	1.80E-05
264774_at	At1g22890	hypothetical protein	unknown	0.7	-3.3	-4.8	1	1	2.68E-04
261801_at	At1g30520	expressed protein	unknown	-1.2	-5.2	-2.7	2	0	5.67E-06
245783_s_at	At1g35180	expressed protein	unknown	-0.7	-9.1	-24.0	1	1	2.19E-06
262159_at	At1g52720	expressed protein	unknown	-1.3	-3.5	-2.4	2	1	4.59E-06
260983_at	At1g53560	expressed protein	unknown	-1.2	-3.9	-3.6	1	0	4.73E-06
257510_at	At1g55360	expressed protein	unknown	-0.6	-4.3	-2.6	2	0	1.35E-08
265075_at	At1g55450	expressed protein	unknown	1.7	-3.2	-0.6	2	0	1.50E-05
265116_at	At1g62480	expressed protein	unknown	-0.7	-2.9	-4.0	1	0	3.07E-04
255857_at	At1g67080	expressed protein	unknown	-0.6	-3.9	-2.0	2	0	5.49E-06
260453_s_at	At1g72510	expressed protein	unknown	-1.3	-3.0	-3.3	2	1	1.28E-04
260388_at	At1g74070	expressed protein	unknown	-1.2	-3.5	-2.1	2	0	2.70E-06
262049_at	At1g80180	expressed protein	unknown	-0.2	-4.4	-2.7	2	0	5.41E-04
261893_at	At1g80690	expressed protein	unknown	0.4	-2.5	-1.6	2	0	3.35E-03
263647_at	At2g04690	expressed protein	unknown	-0.6	-3.4	-1.5	2	0	1.73E-05
263674_at	At2g04790	expressed protein	unknown	0.0	-4.0	-2.4	2	0	2.11E-05
265902_at	At2g25590	hypothetical protein	unknown	-1.4	-5.9	-3.8	2	0	2.31E-03
267057_at	At2g32500	expressed protein	unknown	-1.1	-1.7	-3.1	1	0	1.43E-04
267644_s_at	At2g32880	expressed protein	unknown	0.0	-3.3	-65.5	1	0	5.51E-04
266899_at	At2g34620	expressed protein	unknown	-1.3	-7.8	-3.0	2	0	1.84E-06
265952_at	At2g37480	expressed protein	unknown	-0.1	-3.4	-2.6	2	2	5.38E-05
265953_at	At2g37490	expressed protein	unknown	-0.1	-2.9	-2.4	1	0	6.98E-05
265720_at	At2g40110	expressed protein	unknown	0.0	-3.1	-1.6	2	0	5.31E-04
265451_at	At2g46490	expressed protein	unknown	-0.1	-2.8	-2.2	2	0	1.15E-04
259272_at	At3g01290	expressed protein	unknown	1.6	-3.3	-0.1	2	0	2.00E-03
259131_at	At3g02180	expressed protein	unknown	-0.6	-3.3	-2.5	2	0	3.54E-06
258609_at	At3g02910	expressed protein	unknown	-0.6	-2.7	-2.6	1	0	2.31E-04
256441_at	At3g10940	expressed protein	unknown	-1.2	-2.4	-4.1	1	0	1.38E-07
256427_at	At3g11090	expressed protein	unknown	-0.1	-4.9	-3.3	2	0	5.74E-06
258275_at	At3g15760	expressed protein	unknown	1.5	-8.6	-2.2	2	1	1.85E-03
258053_at	At3g16230	expressed protein	unknown	-0.6	-3.5	-2.2	2	0	4.07E-05
257966_at	At3g19800	expressed protein	unknown	-0.1	-5.5	-3.5	1	0	2.93E-05
257239_at	At3g24100	expressed protein	unknown	-0.7	-2.1	-19.6	1	0	2.98E-04

257615_at	At3g26510	expressed protein	unknown	-1.3	-5.2	-3.3	2	0	1.85E-04
256674_at	At3g52360	expressed protein	unknown	-0.6	-4.4	-3.1	1	0	3.94E-05
251886_at	At3g54260	expressed protein	unknown	-0.6	-5.7	-5.2	1	0	2.02E-04
251704_at	At3g56360	expressed protein	unknown	-0.8	-2.4	-5.1	1	0	9.00E-05
251391_at	At3g60910	expressed protein	unknown	-0.7	-3.5	-3.5	1	0	2.39E-07
255626_at	At4g00780	expressed protein	unknown	0.5	-2.5	-3.9	1	0	8.04E-06
255298_at	At4g04840	expressed protein	unknown	0.0	0.0	-4.5	1	0	5.60E-07
255008_at	At4g10060	expressed protein	unknown	-0.6	-4.1	-3.3	1	0	2.01E-05
245265_at	At4g14400	hypothetical protein	unknown	-0.6	-4.5	0.8	2	0	2.89E-04
254705_at	At4g17870	expressed protein	unknown	-0.1	-3.9	-4.4	1	0	2.34E-06
254387_at	At4g21850	expressed protein	unknown	0.0	-6.5	-2.5	2	0	4.34E-03
253874_at	At4g27450	expressed protein	unknown	0.5	-10.0	-7.6	1	0	1.98E-04
253548_at	At4g30993	expressed protein	unknown	0.0	-4.0	-2.2	2	0	1.65E-07
253302_at	At4g33660	expressed protein	unknown	-1.2	-13.3	-6.6	1	0	4.43E-04
253305_at	At4g33666	expressed protein	unknown	-0.7	-9.5	-7.3	1	1	1.06E-05
253049_at	At4g37300	expressed protein	unknown	0.0	-3.2	-2.5	1	1	3.23E-04
250828_at	At5g05250	expressed protein	unknown	-1.3	-4.3	-4.4	2	0	4.25E-05
246487_at	At5g16030	expressed protein	unknown	0.6	-4.6	-1.8	2	0	2.93E-05
249817_at	At5g23820	expressed protein	unknown	0.0	-2.7	-2.5	1	0	5.70E-04
246909_at	At5g25770	expressed protein	unknown	-0.7	-13.9	-4.1	2	0	1.12E-03
246768_at	At5g27400	expressed protein	unknown	-0.6	-3.2	-2.5	2	0	2.06E-07
249355_at	At5g40500	expressed protein	unknown	0.0	-3.0	-3.4	1	0	9.66E-05
248329_at	At5g52780	expressed protein	unknown	-1.3	-3.3	-1.7	2	0	2.01E-05
247882_at	At5g57785	expressed protein	unknown	-0.1	-3.6	-2.4	2	0	8.59E-05
247282_at	At5g64240	expressed protein	unknown	0.5	-2.2	-3.1	1	0	1.41E-05

AGI identifiers, annotations, and role assignments were derived from data provided by Affymetrix (<http://www.affymetrix.com/>), TAIR (<http://www.arabidopsis.org/>), TIGR (<http://www.tigr.org/tdb/e2k1/ath1/>), and MIPS (<http://mips.gsf.de/proj/thal/db/index.html>). The mean fold change values were calculated from the individual fold change values at each time in both duplicates of the plate (solid media) and soil experiments. Values in bold indicate times at which the probe set was labeled cold-responsive in both the soil and solid media experiments. The expression class of each transcript from hierarchical clustering analysis (Chapter 2), the number of CRT/DRE elements present in the sequence 1kb upstream (<http://www.arabidopsis.org/tools/bulk/sequences/index.jsp>) of the transcript, and the p-value from ANOVA analysis (see Materials and Methods, Chapter 2) are given.

APPENDIX G

TABLE G.1. PROBE SETS UP-REGULATED IN RESPONSE TO CBF2 EXPRESSION

Probe Set	AGI	Annotation	Sub-role	35S::CBF2 E2	Cold E24 responsive	Expression class	(A G)CCGAC 1kb upstream
<i>Metabolism</i>							
265119_at	At1g62570	flavin-containing monooxygenase (similar to glutamate synthase)	amino acid	10.6	x	3	0
251775_s_at	At3g55610	delta-1-pyrroline-5-carboxylate synthetase (P5CS2)	amino acid	3.5	x	3	1
264583_at	At1g05170	galactosyltransferase family	carbohydrate	6.1	5.3		0
264511_at	At1g09350	putative galactinol synthase	carbohydrate	512.0	181.0	x	3
262784_at	At1g10760	starch excess 1 protein (sex1)	carbohydrate	3.0	3.5		0
264940_at	At1g60470	galactinol synthase, putative	carbohydrate	7.5	4.6		0
267429_at	At2g34850	putative UDP-galactose-4-epimerase	carbohydrate	9.8	5.3		1
250467_at	At5g10100	trehalose-6-phosphate phosphatase, putative	carbohydrate	7.5	11.3		2
245998_at	At5g20830	sucrose synthase I (SUS1)	carbohydrate	2.5	2.8	x	1
249785_at	At5g24300	starch synthase	carbohydrate	2.5	2.8		1
266830_at	At2g22810	1-aminocyclopropane-1-carboxylate synthase 4 (ACC synthase 4)	ethylene biosynthesis	2.8	3.7		2
263789_at	At2g24560	putative GDSL-motif lipase/hydrolase	lipid	294.1	222.9	x	3
251780_s_at	At3g55310	beta-ketoacyl-ACP reductase - like protein	lipid	2.6	5.7		0
245533_at	At4g15130	putative phosphocholine cytidylyltransferase (AtCCT2)	lipid	5.7	3.7	x	1
261048_at	At1g01420	similar to UTP-glucose glucosyltransferases	secondary	7.0	5.7	x	1
262482_at	At1g17020	Fe(II)/ascorbate oxidase gene family; senescence-related gene (SRG1)	secondary	5.7	2.6		1
266532_at	At2g16890	putative phenylpropanoid glucosyltransferase	secondary	2.5	2.6	x	0
265290_at	At2g22590	putative anthocyanidin-3-glucoside rhamnosyltransferase	secondary	16.0	3.0		1
258113_at	At3g14650	putative cytochrome P450 (CYP72A11)	secondary	3.0	2.5		0

258064_at	At3g14680	putative cytochrome P450	secondary	3.5	8.0		0
251658_at	At3g57020	putative protein strictosidine synthase	secondary	3.5	3.2		1
254232_at	At4g23600	tyrosine transaminase like protein (COR13/JR2)	secondary	5.7	3.5		1
253879_s_at	At4g27570	UDP rhamnose–anthocyanidin-3-glucoside rhamnosyltransferase	secondary	6.5	2.5	x	0
253277_at	At4g34230	cinnamyl alcohol dehydrogenase - like protein	secondary	4.9	3.0		1
247577_at	At5g61290	putative protein flavin-containing monooxygenase	secondary	2.8	4.3		0
<u>Transcription</u>							
266142_at	At2g39030	GCN5-related N-acetyltransferase (GNAT) family	chromatin modification	13.0	13.9		2
260776_at	At1g14580	zinc finger (C2H2 type) protein family	mRNA synthesis	3.2	3.5	x	0
245807_at	At1g46768	AP2 domain transcription factor (RAP2.1)	mRNA synthesis	7.0	3.7	x	2
257471_at	At1g59530	bZIP protein	mRNA synthesis	32.0	29.9		0
259971_at	At1g76580	squamosa promoter binding protein -related	mRNA synthesis	3.0	3.5	x	1
245078_at	At2g23340	AP2 domain transcription factor (RAP2.6)	mRNA synthesis	6.5	4.9		1
266514_at	At2g47890	CONSTANS B-box zinc finger family protein	mRNA synthesis	4.3	2.8	x	1
252573_at	At3g45260	zinc finger (C2H2 type) protein family	mRNA synthesis	3.5	3.0		2
251793_at	At3g55580	regulator of chromosome condensation RCC1 family	mRNA synthesis	5.3	5.7	x	0
254075_at	At4g25470	CBF2/DREB1c	mRNA synthesis	157.6	207.9	x	0
253872_at	At4g27410	no apical meristem (NAM) protein family (RD26)	mRNA synthesis	2.6	4.9		1
253722_at	At4g29190	zinc finger (CCCH type) protein family	mRNA synthesis	2.5	3.2	x	1
253219_at	At4g34990	MYB family transcription factor (MYB32)	mRNA synthesis	3.2	3.0	x	0
251084_at	At5g01520	zinc finger (C3HC4-type RING finger) protein family	mRNA synthesis	2.6	13.9		1
245711_at	At5g04340	putative c2h2 zinc finger transcription factor	mRNA synthesis	2.6	4.3	x	2
246432_at	At5g17490	DELLA subfamily member involved in GA signal transduction (RGL3)	mRNA synthesis	3.5	24.3		0

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246922_at	At5g25110	serine/threonine protein kinase-like	intracellular signaling	7.0	16.0	x	3	0
251768_at	At3g55940	phosphoinositide-specific phospholipase C	signal transduction	14.9	17.1			1
246756_at	At5g27930	protein phosphatase 2C (PP2C), putative	signal transduction	4.3	3.0	x	3	0
258300_at	At3g23340	putative casein kinase	signaling	2.6	2.6			1
252872_at	At4g40010	putative serine/threonine protein kinase	signaling	2.6	2.8			0
<i>Energy</i>								
264953_at	At1g77120	alcohol dehydrogenase	fermentation	7.0	5.3	x	3	1
253416_at	At4g33070	pyruvate decarboxylase-1 (Pdc1)	fermentation	4.3	3.0	x	3	1
<i>Transport</i>								
247937_at	At5g57110	Ca ²⁺ -transporting ATPase (ACA8)	calcium transport	2.8	2.5	x	3	1
264654_s_at	At1g08900	putative sugar transport protein	sugar transport	2.6	2.6			0
245427_at	At4g17550	glycerol-3-phosphate permease like protein	sugar transport	6.5	7.0	x	3	2
256022_at	At1g58360	amino acid permease I (AAP1)	transport	3.7	3.2			0
260410_at	At1g69870	putative proton-dependent oligopeptide transport (POT) protein	transport	4.3	3.0	x	3	1
263574_at	At2g16990	putative tetracycline transporter protein	transport	14.9	14.9	x	3	2
266225_at	At2g28900	putative membrane channel protein	transport	9.2	6.5	x	3	2
250151_at	At5g14570	similar to trans-membrane nitrate transporter protein	transport	3.2	3.0	x	3	1
249619_at	At5g37500	guard cell outward rectifying K ⁺ channel (GORK)	transport	5.7	3.2			1
248932_at	At5g46050	proton-dependent oligopeptide transport (POT) protein family	transport	3.5	2.6			1
248700_at	At5g48400	glutamate receptor family (ATGLR1.2)	transport/signaling	2.6	2.6			1
<i>Protein processing and fate</i>								
256245_at	At3g12580	heat shock protein (hsp70)	protein folding	10.6	2.6			1
262440_at	At1g47710	serpin, putative	protein modification	4.3	3.2	x	3	2
250316_at	At5g12140	cysteine protease inhibitor (cystatin), putative	protein modification	3.2	2.8			1
251899_at	At3g54400	aspartyl protease family	proteolysis	2.8	3.2	x	3	1

262644_at	At1g62710	vacuolar cysteine proteinase (beta-VPE)	3.0	2.5	x	3	0
<u>Stress related</u>							
264787_at	At2g17840	senescence-associated protein 12, similar to ERD7	3.7	3.5	x	3	1
252591_at	At3g45600	senescence-associated protein family	2.5	2.6			1
263951_at	At2g35960	putative harpin-induced protein	2.8	2.6	x	3	0
260556_at	At2g43620	putative endochitinase	59.7	21.1	x	3	1
258894_at	At3g05650	putative disease resistance protein	3.7	4.6			2
258893_at	At3g05660	putative disease resistance protein	26.0	14.9	x	3	2
264779_at	At1g08570	putative thioredoxin	3.5	3.2			1
259426_at	At1g01470	Lea protein (LEA14)	12.1	8.6	x	3	3
262113_at	At1g02820	late embryogenesis abundant (LEA) protein family	6.1	3.2			1
259570_at	At1g20440	dehydrin (COR47)	4.9	6.5	x	3	3
259516_at	At1g20450	dehydrin (ERD10)	8.6	8.6	x	3	3
256310_at	At1g30360	dehydrin (ERD4)	2.5	2.6	x	3	1
263495_at	At2g42530	COR15b	55.7	52.0	x	3	2
263497_at	At2g42540	COR15a	294.1	675.6	x	3	2
252102_at	At3g50970	dehydrin (Xero2)	73.5	84.4	x	3	3
252137_at	At3g50980	dehydrin (Xero1)	22.6	2.5			0
246481_s_at	At5g15960	KIN1	21.1	21.1	x	3	1
248352_at	At5g52300	RD29B	27.9	13.9			1
248337_at	At5g52310	COR78	59.7	55.7	x	3	4
253104_at	At4g36010	thumatin-like protein	5.7	4.3	x	7	3
262452_at	At1g11210	expressed protein (COR35)	4.0	3.0	x	7	0
256114_at	At1g16850	expressed protein (COR17)	445.7	315.2	x	3	3
259789_at	At1g29395	similar to cold acclimation protein WCOR414 (WCOR414-TM1)	13.9	26.0	x	3	1
262050_at	At1g80130	expressed protein (COR33.5)	6.5	5.7	x	3	1
265480_at	At2g15970	similar to cold acclimation protein WCOR413 (WCOR413-PM1)	4.0	4.0	x	3	2
267261_at	At2g23120	expressed protein (COR8.5)	8.6	8.6	x	3	1
255795_at	At2g33380	RD20	3.5	2.6			2

254818_at	At4g12470	pEARL1 1-like protein	unknown	11.3	12.1	x	3	0
254805_at	At4g12480	pEARL1 1	unknown	16.0	3.5	x	4	0
254832_at	At4g12490	pEARL1 1-like protein	unknown	4.9	3.2	x	4	0
253627_at	At4g30650	hydrophobic protein (LTI6A/RIC2A)	unknown	16.0	7.5	x	3	1
253595_at	At4g30830	expressed protein (COR42)	unknown	64.0	68.6	x	3	2
<u>Cellular biogenesis</u>								
261834_at	At1g10640	polygalacturonase, putative	cell wall	3.7	2.5			0
259173_at	At3g03640	beta-glucosidase (GLUC)	cell wall	3.7	2.6	x	3	2
258719_at	At3g09540	putative pectate lyase	cell wall	4.9	4.0	x	3	2
251229_at	At3g62740	beta-glucosidase-like protein	cell wall	9.8	5.7	x	3	1
254662_at	At4g18270	glycosyltransferase family 4 (ATTRANS11)	cell wall	2.5	2.6	x	3	1
252997_at	At4g38400	expansin protein family (EXPL2)	cell wall	3.5	3.0	x	3	3
247450_at	At5g62350	pectinesterase family	cell wall	3.0	2.8			3
247478_at	At5g62360	similar to pectinesterase	cell wall	3.2	4.6	x	3	1
<u>Cellular organization</u>								
265354_at	At2g16700	actin depolymerizing factor 5 (ADF5)	cytoskeleton	2.8	2.5			2
259606_at	At1g27920	microtubule associated protein (MAP65/ASE1) family	unknown	6.1	4.6			0
254085_at	At4g24960	similar to abscisic acid-induced protein (HVA22D)	vesicular trafficking	14.9	11.3	x	3	3
<u>DNA replication and cell division</u>								
248765_at	At5g47650	MutT/nudix family protein	DNA repair	2.5	3.0			2
257237_at	At3g14890	DNA nick sensor, putative	DNA synthesis	3.5	2.6	x	3	2
<u>Unknown role</u>								
260876_at	At1g21460	nodulin MtN3 family protein	unknown	4.0	2.5			1
259605_at	At1g27910	U-box domain protein	unknown	3.2	2.8			1
245749_at	At1g51090	similar to proline-rich protein	unknown	34.3	78.8	x	3	2
260238_at	At1g74520	AtHVA22a	unknown	2.5	2.5			1
265561_s_at	At2g05510	putative glycine-rich protein	unknown	14.9	9.2			1
263352_at	At2g22080	related to En/Spm transposon family of maize	unknown	3.2	2.6	x	3	1
267538_at	At2g41870	putative DNA binding protein	unknown	3.5	4.6			1
256603_at	At3g28270	At14a-related protein	unknown	12.1	3.2	x	1	0

255364_s_at	At4g04020	plastid-lipid associated protein PAP/fibrillin, putative	unknown	4.0	2.5				1
252956_at	At4g38580	farnesylated protein (ATFP6)	unknown	4.0	2.5	x	3		2
250279_at	At5g13200	like ABA-responsive protein	unknown	7.5	6.5	x	3		1
249750_at	At5g24570	expressed protein	unknown	5.7	4.3	x	3		1
248466_at	At5g50720	abscisic acid-induced-like protein (AtHVA22e)	unknown	29.9	29.9				2
248496_at	At5g50790	nodulin MtN3 family protein	unknown	17.1	10.6				1
248467_at	At5g50800	nodulin MtN3-like protein	unknown	3.2	3.0	x	4		0
<u>Unknown protein</u>									
264516_at	At1g10090	expressed protein	unknown	3.5	2.6	x	3		2
264458_at	At1g10410	expressed protein	unknown	3.2	2.6	x	3		1
262760_at	At1g10770	expressed protein	unknown	4.0	13.0				0
262496_at	At1g21790	expressed protein	unknown	3.7	4.3	x	3		2
264989_at	At1g27200	expressed protein	unknown	4.3	6.1	x	3		1
261566_at	At1g33230	expressed protein	unknown	2.8	3.2	x	3		1
260727_at	At1g48100	expressed protein	unknown	18.4	13.9	x	3		0
245743_at	At1g51080	hypothetical protein	unknown	4.0	3.0				0
262881_at	At1g64890	expressed protein	unknown	2.8	2.8	x	3		1
264636_at	At1g65490	expressed protein	unknown	4.6	2.8				2
245200_at	At1g67850	expressed protein	unknown	4.3	3.0	x	3		0
260264_at	At1g68500	expressed protein	unknown	19.7	9.8	x	3		1
262313_at	At1g70900	expressed protein	unknown	3.0	2.5				1
262164_at	At1g78070	expressed protein	unknown	4.0	5.7	x	3		2
266259_at	At2g27830	expressed protein	unknown	3.2	3.7				1
257876_at	At3g17130	hypothetical protein	unknown	14.9	13.9	x	3		1
258078_at	At3g25870	expressed protein	unknown	8.0	4.0				2
256577_at	At3g28220	expressed protein	unknown	9.8	5.7				1
252127_at	At3g50960	expressed protein	unknown	2.8	3.2				3
251927_at	At3g53990	expressed protein	unknown	3.2	3.5	x	3		2
251753_at	At3g55760	expressed protein	unknown	9.2	10.6	x	3		1
254850_at	At4g12000	expressed protein	unknown	4.0	4.6	x	3		1
253425_at	At4g32190	expressed protein	unknown	2.6	2.8	x	3		2
246125_at	At5g19875	expressed protein	unknown	5.7	2.6	x	3		1

249848_at	At5g23220	expressed protein	unknown	68.6	12.1	1
246708_at	At5g28150	expressed protein	unknown	3.2	2.8	1
247754_at	At5g59080	expressed protein	unknown	3.7	6.1	1
247399_at	At5g62960	hypothetical protein	unknown	4.6	6.1	0

AGI identifiers, annotations, and role assignments were derived from data provided by Affymetrix (<http://www.affymetrix.com/>), TAIR (<http://www.arabidopsis.org/>), TIGR (<http://www.tigr.org/tdb/e2k1/ath1/>), and MIPS (<http://mips.gsf.de/proj/thal/db/index.html>). Fold change values in the two lines profiled (E2 and E24) are shown. An "x" in the cold responsive column indicates that the probe set met the criteria (see Chapter 2) for being labeled cold responsive at a 2.5-fold level in both the soil and solid media experiments. The expression class of each transcript from hierarchical clustering analysis (Chapter 2) and the number of CRT/DRE elements present in the sequence 1kb upstream (<http://www.arabidopsis.org/tools/bulk/sequences/index.jsp>) of the transcript is shown.

APPENDIX H

TABLE H.1. PROBE SETS DOWN-REGULATED IN RESPONSE TO CBF2 EXPRESSION

Probe Set	AGI	Annotation	Sub-role	35S::CBF2 E2	Cold E24 responsive	Expression class	(A G)CCGAC 1kb upstream
<u>Metabolism</u>							
249867_at	At5g23020	2-isopropylmalate synthase (IMS2)	amino acid	-2.8 -2.6			0
259640_at	At1g52400	beta-glucosidase (BG1)	carbohydrate	-6.1 -2.8			0
247954_at	At5g56870	beta-galactosidase	carbohydrate	-7.5 -2.6			0
255786_at	At1g19670	chlorophyllase/coronatine-induced protein 1 (COR11)	chlorophyll	-7.5 -3.0	x	2	0
			catabolism				
263443_at	At2g28630	beta-ketoacyl-CoA synthase family	lipid	-3.7 -3.5			0
249777_at	At5g24210	putative lipase	lipid	-2.8 -2.8			0
261453_at	At1g21130	O-methyltransferase 1, putative	secondary	-3.2 -2.5			0
252529_at	At3g46490	putative oxidoreductase	secondary	-2.8 -2.6			1
254331_s_at	At4g22710	cytochrome P450 family	secondary	-4.9 -4.0	x	2	0
253534_at	At4g31500	cytochrome P450 (ATR4/CYP83B1)	secondary	-2.5 -2.5	x	2	0
245690_at	At5g04230	phenylalanine ammonia-lyase (PAL3)	secondary	-4.0 -3.2			0
248728_at	At5g48000	cytochrome P450-like protein (CYP708A2)	secondary	-34.3 -9.2			0
248729_at	At5g48010	pentacyclic triterpene synthase, putative	secondary	-2.5 -4.0			0
247684_at	At5g59670	leucine rich repeat protein kinase	signaling	-18.4 -14.9			0
<u>Transcription</u>							
264872_at	At1g24260	MADS-box protein (SEP3)	mRNA synthesis	-5.3 -2.8			0
<u>Intercellular communication and signal transduction</u>							
267083_at	At2g41100	calmodulin-like protein (TCH3)	signaling	-3.0 -3.5	x	2	0
254247_at	At4g23260	receptor protein kinase	signaling	-3.2 -2.6			1
<u>Transport</u>							
264901_at	At1g23090	sulphate transporter (AST91)	transport	-3.0 -3.0			1
259839_at	At1g52190	proton-dependent oligopeptide transport (POT) protein family	transport	-7.5 -2.6	x	2	0
251248_at	At3g62150	putative ABC transporter	transport	-29.9 -12.1			0
247447_at	At5g62730	nitrate transporter	transport	-8.6 -2.8			0
<u>Stress related</u>							

266385_at	At2g14610	pathogenesis-related protein 1 (PR-1)	defense	-2.8	-2.5	0
257365_x_at	At2g26020	plant defensin protein, putative	defense	-8.6	-64.0	0
258537_at	At3g04210	putative disease resistance protein (TIR-NBS class)	defense	-36.8	-3.2	0
				x	2	0
249052_at	At5g44420	antifungal protein-like (PDF1.2)	defense	-13.9	-9.8	1
266746_s_at	At2g02930	glutathione transferase (GST16)	detoxification	-3.5	-4.6	0
<u>Cellular biogenesis</u>						
256299_at	At1g69530	expansin (EXP1)	cell wall	-4.0	-2.6	0
				x	2	0
<u>Cellular organization</u>						
253911_at	At4g27300	S-locus protein kinase, putative	cytoskeleton	-4.6	-2.5	0
<u>Unknown role</u>						
265511_at	At2g05540	putative glycine-rich protein	unknown	-3.5	-3.0	0
257206_at	At3g16530	legume lectin protein family	unknown	-8.0	-13.0	1
256766_at	At3g22231	pathogen and circadian controlled 1 (PCC1)	unknown	-3.0	-5.7	0
250445_at	At5g10760	nucleoid DNA-binding protein cnd41-like	unknown	-2.8	-4.3	0
<u>Unknown protein</u>						
261247_at	At1g20070	expressed protein	unknown	-3.7	-2.8	2
260919_at	At1g21520	expressed protein	unknown	-4.6	-3.7	0
245866_s_at	At1g57990	expressed protein	unknown	-4.3	-2.6	0
259076_at	At3g02140	expressed protein	unknown	-3.7	-11.3	0
258419_at	At3g16670	expressed protein	unknown	-39.4	-3.2	0
252317_at	At3g48720	expressed protein	unknown	-2.6	-2.5	0
251438_s_at	At3g59930	expressed protein	unknown	-3.2	-5.7	0
245265_at	At4g14400	hypothetical protein	unknown	-3.0	-3.7	0
253414_at	At4g33050	expressed protein	unknown	-2.6	-3.7	0
249894_at	At5g22580	expressed protein	unknown	-4.9	-3.5	0
249726_at	At5g35480	expressed protein	unknown	-3.5	-3.0	1

AGI identifiers, annotations, and role assignments were derived from data provided by Affymetrix (<http://www.affymetrix.com/>), TAIR (<http://www.arabidopsis.org/>), TIGR (<http://www.tigr.org/tdb/e2k1/ath1/>), and MIPS (<http://mips.gsf.de/proj/thal/db/index.html>). Fold change values in the two lines profiled (E2 and E24) are shown. An "x" in the cold responsive column indicates that the probe set met the criteria (see Chapter 2) for being labeled cold responsive at a 2.5-fold level in both the soil and solid media experiments. The expression class of each transcript from hierarchical clustering analysis (Chapter 2) and the number of CRT/DRE elements present in the sequence 1kb upstream (<http://www.arabidopsis.org/tools/bulk/sequences/index.jsp>) of the transcript is shown.

APPENDIX I

TABLE I.1. PROBE SETS UP-REGULATED IN RESPONSE TO ZAT12 EXPRESSION

Probe Set	AGI	Annotation	Sub-role	35S::ZAT12 p15-8 p15-15	Cold responsive	Expression class
<u>Metabolism</u>						
265221_s_at	At2g02010	putative glutamate decarboxylase	amino acid	3.5	4.6	
253203_at	At4g34710	arginine decarboxylase (SPE2/ADC2)	amino acid	4.3	4.0	
260399_at	At1g72520	putative lipoxigenase	lipid	6.5	3.7	
253285_at	At4g34250	fatty acid elongase 1 (FAE1), putative	lipid	2.6	2.8	
245422_at	At4g17470	palmitoyl protein thioesterase precursor, putative	lipid	18.4	7.0	
257641_s_at	At3g25760	allene oxide cyclase (AOC1, ERD12)	lipid	2.6	3.5	
254234_at	At4g23680	putative major latex protein	secondary	13.9	11.3	
254283_s_at	At4g22870	putative anthocyanidin synthase	secondary	4.9	6.5	
251124_s_at	At5g01040	laccase (diphenol oxidase) family	secondary	2.6	2.8	
258299_at	At3g23410	alcohol oxidase-related	secondary	2.8	2.5	1
249215_at	At5g42800	dihydroflavonol 4-reductase (dihydrokaempferol 4-reductase) (DFR)	secondary	5.7	4.9	
248185_at	At5g54060	flavonol 3-O-glucosyltransferase-like	secondary	6.5	5.7	
265208_at	At2g36690	oxidoreductase, 2OG-Fe(II) oxygenase family protein	secondary	3.5	2.5	
245624_at	At4g14090	putative glucosyltransferase	secondary	3.2	7.0	
265091_s_at	At1g03495	similar to anthocyanin 5-aromatic acyltransferase	secondary	7.5	9.2	
<u>Transcription</u>						
247655_at	At5g59820	ZAT12	mRNA synthesis	111.4	97.0	
245628_at	At1g56650	MYB family transcription factor (MYB75)	mRNA synthesis	4.6	3.0	
251677_at	At3g56980	bHLH protein family	mRNA synthesis	2.8	3.0	
263549_at	At2g21650	MYB family transcription factor	mRNA synthesis	3.2	2.8	
<u>Intercellular communication and signal transduction</u>						
254242_at	At4g23200	putative serine/threonine protein kinase	signal transduction	3.0	3.2	
257294_at	At3g15570	phototropic response protein family	signal transduction	3.5	3.0	
248270_at	At5g53450	protein kinase (ORG1)	signaling	2.5	2.5	
<u>Energy</u>						
246099_at	At5g20230	plastocyanin-like domain containing protein	photosynthesis	4.9	2.5	

(<http://www.arabidopsis.org/>), TIGR (<http://www.tigr.org/tdb/e2k1/ath1/>), and MIPS (<http://mips.gsf.de/proj/thal/db/index.html>). Fold change values in the two lines profiled (p15-8 and p15-15) are shown. An "x" in the cold responsive column indicates that the probe set met the criteria (see Chapter 2) for being labeled cold responsive at a 2.5-fold level in both the soil and solid media experiments. The expression class of each transcript from hierarchical clustering analysis (Chapter 2) is shown.

APPENDIX J

TABLE J.1. PROBE SETS DOWN-REGULATED IN RESPONSE TO ZAT12 EXPRESSION

Probe Set	AGI	Annotation	Sub-role	35S::ZAT12 p15-8 p15-15	Cold responsive	Expression class
<i>Metabolism</i>						
255778_at	At1g18640	3-phosphoserine phosphatase (PSP)	amino acid	-3.7	-3.0	
252983_at	At4g37980	mannitol dehydrogenase (ELI3-1), putative	carbohydrate	-6.5	-4.6	
261191_at	At1g32900	starch synthase, putative	carbohydrate	-4.6	-6.5	
252746_at	At3g43190	sucrose synthase	carbohydrate	-4.6	-7.5	
252446_at	At3g47010	glycosyl hydrolase family 3 protein	carbohydrate	-8.6	-2.5	
250142_at	At5g14650	polygalacturonase, putative	carbohydrate	-2.6	-3.0	
255517_at	At4g02290	glycosyl hydrolase family 9	carbohydrate	-2.5	-3.2	2
259786_at	At1g29660	GDSL-motif lipase/hydrolase protein	lipid	-5.7	-6.5	
263443_at	At2g28630	beta-ketoacyl-CoA synthase family	lipid	-3.2	-2.5	
250891_at	At5g04530	fatty acid elongase 3-ketoacyl-CoA synthase 1 (KCS1)	lipid	-2.5	-2.5	
260869_at	At1g43800	putative stearoyl acyl carrier protein desaturase	lipid	-6.5	-16.0	2
261420_at	At1g07720	beta-ketoacyl-CoA synthase family	lipid	-3.0	-3.2	
261570_at	At1g01120	fatty acid elongase 3-ketoacyl-CoA synthase 1 (KCS1)	lipid	-2.5	-3.2	
263096_at	At2g16060	class 1 non-symbiotic hemoglobin (AHB1)	nitrogen	-2.8	-2.8	
249942_at	At5g22300	nitrilase 4	nitrogen	-4.0	-3.0	
254331_s_at	At4g22710	cytochrome P450 family	secondary	-3.2	-3.2	2
262875_at	At1g64970	gamma-tocopherol methyltransferase (VTE4)	secondary	-3.0	-2.5	
257938_at	At3g19820	cell elongation protein (DWARF1, DIMINUTO, DIM)	secondary	-2.6	-3.0	
262913_at	At1g59960	aldo/keto reductase, putative	secondary	-4.6	-2.6	
265948_at	At2g19590	1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase), putative	secondary	-3.5	-4.3	
254833_s_at	At4g12280	copper amine oxidase like protein	secondary	-3.5	-3.2	
246021_at	At5g21100	L-ascorbate oxidase, putative	secondary	-3.0	-3.2	1
248311_at	At5g52570	beta-carotene hydroxylase	secondary	-2.8	-2.5	
248353_at	At5g52320	putative cytochrome P450	secondary	-5.7	-2.5	2
267307_at	At2g30210	laccase (diphenol oxidase), putative	secondary	-2.8	-2.8	

261804_at	At1g30530	UDP-glucoronosyl/UDP-glucosyl transferase family protein	secondary	-2.6	-2.6	
266996_at	At2g34490	cytochrome P450 family	secondary	-5.3	-4.3	
<u>Transcription</u>						
260664_at	At1g19510	myb family transcription factor	mRNA synthesis	-4.3	-3.7	
253749_at	At4g29080	auxin-responsive AUX/IAA family protein	mRNA synthesis	-2.5	-2.5	
251575_at	At3g58120	transcription factor bZIP61 (BZIP61)	mRNA synthesis	-4.9	-3.7	
251705_at	At3g56400	WRKY family transcription factor (WRKY70)	mRNA synthesis	-2.6	-3.5	
252534_at	At3g46130	Myb family transcription factor (MYB111)	mRNA synthesis	-4.3	-2.5	
257051_at	At3g15270	squamosa promoter binding protein-related 5 (SPL5)	mRNA synthesis	-7.5	-14.9	
256300_at	At1g69490	no apical meristem (NAM) protein family	mRNA synthesis	-22.6	-3.0	
255694_at	At4g00050	bHLH protein family	mRNA synthesis	-4.3	-2.8	
250582_at	At5g07580	ethylene-responsive element-binding family protein	mRNA synthesis	-4.6	-2.8	
265573_at	At2g28200	putative zinc-finger protein	mRNA synthesis	-8.0	-55.7	
267509_at	At2g45660	MADS-box protein (AGL20)	mRNA synthesis	-3.7	-2.8	x 3
<u>Intercellular communication and signal transduction</u>						
258617_at	At3g03000	putative calmodulin protein	signal transduction	-2.5	-2.5	
262451_at	At1g11140	LRR receptor-like protein kinase strubbelig (SUB)	signal transduction	-3.5	-2.8	
249410_at	At5g40380	protein kinase family protein	signaling	-3.5	-14.9	
252950_at	At4g38690	1-phosphatidylinositol phosphodiesterase-related	signaling	-3.2	-2.6	
246633_at	At1g29720	protein kinase family	signaling	-90.5	-39.4	
245637_at	At1g25230	purple acid phosphatase family	signaling	-4.0	-3.2	x 2
247362_at	At5g63140	calcineurin-like phosphoesterase family	signaling	-7.0	-5.3	
<u>Energy</u>						
253971_at	At4g26530	fructose-bisphosphate aldolase	energy	-8.0	-4.9	
253416_at	At4g33070	pyruvate decarboxylase-1 (Pdc1)	fermentation	-3.0	-13.0	x 3
264953_at	At1g77120	alcohol dehydrogenase	fermentation	-4.6	-5.3	x 3
259801_at	At1g72230	plastocyanin-like domain-containing protein	photosynthesis	-2.6	-3.0	
<u>Transport</u>						
258100_at	At3g23550	MATE efflux protein family	transport	-4.0	-4.0	x 2
252377_at	At3g47960	peptide transporter family	transport	-2.6	-2.8	
265768_at	At2g48020	sugar transporter, putative, similar to ERD6	transport	-3.7	-5.3	
247439_at	At5g62670	ATPase, plasma membrane-type, putative	transport	-3.7	-4.3	
251133_at	At5g01240	amino acid permease, putative	transport	-2.5	-4.0	

260623_at	At1g08090	high-affinity nitrate transporter (NRT2)	transport	-6.5	-11.3	
261937_at	At1g22570	peptide transporter family	transport	-2.8	-2.6	
248566_s_at	At5g49730	FRO2-like protein	transport	-12.1	-6.1	
246783_at	At5g27360	sugar-porter family protein 2 (SFP2)	transport	-2.5	-2.5	
<u>Protein processing and fate</u>						
259671_at	At1g52290	protein kinase	protein modification	-2.8	-2.6	
258633_at	At3g07990	serine carboxypeptidase S10 family protein	proteolysis	-2.5	-3.2	
265665_at	At2g27420	cysteine proteinase, putative	proteolysis	-10.6	-9.8	
265795_at	At2g35780	serine carboxypeptidase S10 family protein	proteolysis	-3.0	-2.6	
247760_at	At5g59130	subtilisin-like serine protease	proteolysis	-3.5	-4.0	
<u>Stress related</u>						
263951_at	At2g35960	putative harpin-induced protein	defense	-3.7	-4.0	x 3
257365_x_at	At2g26020	plant defensin protein, putative	defense	-42.2	-17.1	
253545_at	At4g31310	avirulence-responsive protein-related	defense	-13.9	-6.5	
262374_s_at	At1g72930	disease resistance protein (TIR class), putative	defense	-14.9	-16.0	x 2
258537_at	At3g04210	disease resistance protein (TIR-NBS class), putative	defense	-5.3	-4.9	x 2
262381_at	At1g72900	putative disease resistance protein	defense	-4.3	-3.0	
249052_at	At5g44420	antifungal protein-like (PDF1.2)	defense	-36.8	-12.1	
253998_at	At4g26010	putative peroxidase	detoxification	-4.6	-3.2	
264567_s_at	At1g05250	putative peroxidase	detoxification	-4.9	-3.7	
254386_at	At4g21960	peroxidase (PRXR1)	detoxification	-2.8	-2.6	
266516_at	At2g47880	glutaredoxin protein family	detoxification	-3.2	-3.2	
246991_at	At5g67400	putative peroxidase	detoxification	-11.3	-29.9	
257952_at	At3g21770	putative peroxidase	detoxification	-3.7	-2.8	
255637_at	At4g00750	dehydration-responsive family protein	unknown	-2.6	-2.6	
<u>Cellular biogenesis</u>						
254044_at	At4g25820	xyloglucan endotransglycosylase (XTR9)	cell wall	-6.5	-3.0	
255433_at	At4g03210	xyloglucan endotransglycosylase (XTH9)	cell wall	-4.3	-6.5	
254773_at	At4g13410	similar to cellulose synthase (CSLA15)	cell wall	-4.6	-4.0	
261826_at	At1g11580	pectin methylesterase	cell wall	-3.0	-2.6	
253815_at	At4g28250	putative beta-expansin (EXPB3)	cell wall	-2.8	-2.8	
250892_at	At5g03760	similar to cellulose synthase (CSLA9)	cell wall	-3.0	-3.7	
255591_at	At4g01630	expansin, putative (EXP17)	cell wall	-6.5	-3.5	
264611_at	At1g04680	pectate lyase family protein	cell wall	-4.3	-3.0	

250801_at	At5g04960	pectinesterase family	cell wall	-5.3	-3.0	
247162_at	At5g65730	xyloglucan endotransglycosylase, putative	cell wall	-18.4	-19.7	
251226_at	At3g62680	proline rich protein (PRP3)	cell wall	-6.5	-7.5	
<u>Cellular organization</u>						
247964_at	At5g56600	profilin (PRF3)	cytoskeleton	-4.0	-4.3	
255632_at	At4g00680	actin-depolymerizing factor, putative	cytoskeleton	-6.5	-3.2	
261562_at	At1g01750	actin-depolymerizing factor, putative	cytoskeleton	-3.0	-4.3	
<u>Unknown role</u>						
265511_at	At2g05540	putative glycine-rich protein	unknown	-22.6	-39.4	
262947_at	At1g75750	similar to GAST1	unknown	-4.9	-4.6	
245479_at	At4g16140	proline-rich family protein	unknown	-3.5	-2.6	
251395_at	At2g45470	fasciclin-like arabinogalactan-protein (FLA8)	unknown	-3.5	-4.9	
250942_at	At5g03350	legume lectin protein family (protein kinase family)	unknown	-2.5	-6.5	
246652_at	At5g35190	proline-rich family protein	unknown	-6.1	-9.2	
260770_at	At1g49200	zinc finger (C3HC4-type RING finger) family protein	unknown	-6.1	-3.0	
262312_at	At1g70830	Bet v I allergen family	unknown	-3.5	-2.6	
247470_at	At5g62220	exostosin family	unknown	-2.6	-2.5	
249474_s_at	At5g39190	germin-like protein (GLP2a)	unknown	-2.8	-2.8	
262682_at	At1g75900	family II extracellular lipase 3 (EXL3)	unknown	-3.0	-3.2	x 3
267461_at	At2g33830	auxin-regulated protein	unknown	-5.7	-2.5	
265066_at	At1g03870	fasciclin-like arabinogalactan-protein (FLA9)	unknown	-3.5	-2.8	
247463_at	At5g62210	contains similarity to embryo-specific protein 3	unknown	-2.5	-3.0	x 3
260007_at	At1g67870	glycine rich protein	unknown	-13.0	-9.8	
255957_at	At1g22160	senescence-associated protein	unknown	-6.1	-3.0	
256766_at	At3g22231	pathogen and circadian controlled 1 (PCC1)	unknown	-2.8	-4.0	
262290_at	At1g70985	proline-rich family protein	unknown	-16.0	-17.1	
264016_at	At2g21220	similar to auxin-induced protein	unknown	-4.6	-2.6	
255807_at	At4g10270	probable wound-induced protein	unknown	-4.3	-13.0	
254785_at	At4g12730	fasciclin-like arabinogalactan-protein (FLA2)	unknown	-2.5	-3.0	
253754_at	At4g29020	glycine rich protein	unknown	-2.6	-4.0	
256603_at	At3g28270	At14a-related protein	unknown	-13.9	-59.7	x 1
265042_at	At1g04040	acid phosphatase class B family protein	unknown	-4.6	-4.0	
253255_at	At4g34760	auxin-induced protein	unknown	-3.2	-2.6	
<u>Unknown protein</u>						

248190_at	At5g54120	expressed protein	unknown	-2.5	-2.5	
267459_at	At2g33850	expressed protein	unknown	-4.6	-3.7	
264909_at	At2g17300	expressed protein	unknown	-2.6	-2.5	
248377_at	At5g51720	expressed protein	unknown	-3.7	-3.0	
255298_at	At4g04840	expressed protein	unknown	-4.6	-2.8	x 1
254574_at	At4g19430	expressed protein	unknown	-9.8	-52.0	
248526_at	At5g50730	hypothetical protein	unknown	-2.5	-2.6	
261221_at	At1g19960	expressed protein	unknown	-26.0	-17.1	
255310_at	At4g04955	expressed protein	unknown	-3.7	-2.6	
255516_at	At4g02270	expressed protein	unknown	-6.1	-3.5	
245265_at	At4g14400	hypothetical protein	unknown	-3.0	-6.5	x 2
246371_at	At1g51940	expressed protein	unknown	-2.6	-3.5	
246159_at	At5g20935	expressed protein	unknown	-2.8	-2.6	
261926_at	At1g22530	expressed protein	unknown	-2.8	-3.0	
245906_at	At5g11070	expressed protein	unknown	-10.6	-12.1	
262232_at	At1g68600	expressed protein	unknown	-4.9	-6.5	
267644_s_at	At2g32880	expressed protein	unknown	-3.7	-3.7	x 1
262598_at	At1g15260	expressed protein	unknown	-2.5	-3.2	
260004_at	At1g67860	expressed protein	unknown	-4.6	-3.2	
258736_at	At3g05900	expressed protein	unknown	-9.8	-8.6	
253298_at	At4g33560	expressed protein	unknown	-3.7	-27.9	
252478_at	At3g46540	expressed protein	unknown	-2.6	-3.5	
258879_at	At3g03270	expressed protein	unknown	-4.9	-4.3	
259775_at	At1g29530	expressed protein	unknown	-2.6	-2.5	
252317_at	At3g48720	expressed protein	unknown	-3.5	-4.3	
258275_at	At3g15760	expressed protein	unknown	-3.5	-4.0	x 2
265698_at	At2g32160	expressed protein	unknown	-3.5	-8.6	
255876_at	At2g40480	hypothetical protein	unknown	-4.0	-2.5	
249347_at	At5g40830	expressed protein	unknown	-3.0	-4.3	
253874_at	At4g27450	expressed protein	unknown	-4.3	-2.5	x 1
260668_at	At1g19530	expressed protein	unknown	-9.2	-2.5	
250936_at	At5g03120	expressed protein	unknown	-4.3	-3.5	
263498_at	At2g42610	expressed protein	unknown	-4.3	-2.8	
250741_at	At5g05790	hypothetical protein	unknown	-2.5	-2.6	

260012_at	At1g67865	expressed protein	unknown	-14.9	-8.6
260353_at	At1g69230	expressed protein	unknown	-4.6	-3.5
267209_at	At2g30930	expressed protein	unknown	-3.2	-2.5
249742_at	At5g24490	expressed protein	unknown	-2.6	-2.5
257875_at	At3g17120	expressed protein	unknown	-3.2	-4.3
260495_at	At2g41810	expressed protein	unknown	-6.5	-12.1
251400_at	At3g60420	expressed protein	unknown	-2.6	-2.8
264958_at	At1g76960	expressed protein	unknown	-2.8	-3.2

AGI identifiers, annotations, and role assignments were derived from data provided by Affymetrix (<http://www.affymetrix.com/>), TAIR (<http://www.arabidopsis.org/>), TIGR (<http://www.tigr.org/db/e2k1/ath1/>), and MIPS (<http://mips.gsf.de/proj/thal/db/index.html>). Fold change values in the two lines profiled (p15-8 and p15-15) are shown. An "x" in the cold responsive column indicates that the probe set met the criteria (see Chapter 2) for being labeled cold responsive at a 2.5-fold level in both the soil and solid media experiments. The expression class of each transcript from hierarchical clustering analysis (Chapter 2) is shown.

THE BEST BLAST HITS FOR ZAT12 IN ARABIDOPSIS

(a)

```

AT3G46080  WAKCEPVEVEEDTAKCLMLLSRVGEGGCGDERVFRCKTCLKEFSSFQALGGH
AT3G46090  WAKCEPVEVEEDTAKCLMLLSRVGEGGCGDERVFRCKTCLKEFSSFQALGGH
AT3G46070  WAKCEPVEVEEDTAKCLMLLSRVGEGGCGDERVFRCKTCLKEFSSFQALGGH
AT5G59820  WAKCEPVEVEEDTAKCLMLLSRVGEGGCGDERVFRCKTCLKEFSSFQALGGH
*****

AT3G46080  LHKKLINSDFNGLGNN--SFAALSRPPIGVEVFMGQALGGHKKHHSFA
AT3G46090  LHKKLINSDFNGLGNN--SFA--TSHPCPICGVKFFPMQALGGHMRHRHNEFV
AT3G46070  LHKKLINSDFNGLGNN--SFA--TSHPCPICGVKFFPMQALGGHMRHRHNEFV
AT5G59820  LHKKLINSDFNGLGNN--SFA--TSHPCPICGVKFFPMQALGGHMRHRHNEFV
****
*****

AT3G46080  P---TTPRSEFLPETTTVTTLKKSSSGKRVACLDLDDMDLIVNKKLELGRIS--
AT3G46090  ----SFWIRSEFLPETTTVTTLKKSSSGKRVACLDLDDMDLIVNKKLELGRISWS
AT3G46070  EKASNVVTHSEFLPETTTVTTLKKSSSGKRVACLDLDDMDLIVNKKLELGRIMY--
AT5G59820  AG--A--SEFLPETTTVTTLKKSSSGKRVACLDLDDMDLIVNKKLELGRIVY--
*****

```

(b)

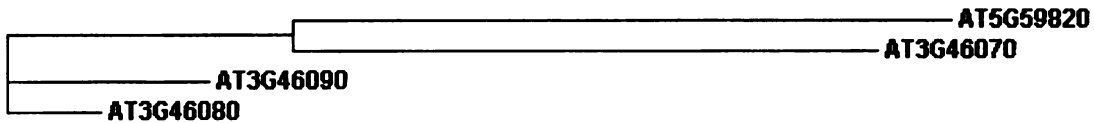


Figure K.1. Amino acid alignment and relationship tree of the best BLAST hits for ZAT12 in the Arabidopsis genome.

- (a) The ZAT12 (At5g59820) protein sequence was used in a BLAST search against all Arabidopsis proteins. The best BLAST hits are shown in an amino acid alignment created with ClustalW v1.82 (add webpage). The C2H2 zinc fingers are indicated by asterisks (*). The EAR-like domain is indicated by colored circles (●). The three best BLAST hits for ZAT12 are located one after the other on chromosome 3 and are the only C2H2 zinc fingers in the Arabidopsis genome with this chromosomal arrangement.
- (b) A relationship tree that depicts the relative relatedness and distance of each sequence is shown. The tree was generated by ClustalW v1.82.

APPENDIX L SUPPLEMENTARY MATERIAL FOR CHAPTER FOUR

Table L.1. The genes which were used to create a tetramer of each motif.

Motif	AGI	Annotation
AGGCCCAWNA	At4G26600	putative nucleolar protein
AAAACCCCTA	At3G10530	WD-40 repeat protein family
GNATTGAC	At4G12480	pEARL1
TGTATACA	At4G02330	pectinesterase family protein
GTGATCAC	At4G22470	pEARL1-like protein
CAATGAGG	At4G12480	pEARL1

The motif is shown in the first column, followed by the AGI locus identifier for the promoter of the gene from which the tetramer containing the motif in the first column was taken. The description of each gene is listed in the column labeled "Annotation".

(a)

AGGCCCwAwA

5' -AATTCCCCGGGTAGTCAGGCCCATTAGTTAGTTAGTCAGGCCCATTAGTTAGTTAGTCAGGCCCATTAGTTAGTA-3'
3' -GGGGCCCCAATCAGTCGGGTAATCAATCAAATCAGTCGGGTAATCAATCAAATCAGTCGGGTAATCAATCATGGCC-5'

Mutant AGGCCCwAwA

5' -AATTCGCCGGGTAGTCCTTAAACGGCGTTAGTTAGTCCTTAAACGGCGTTAGTTAGTCCTTAAACGGCGTTAGTA-3'
3' -GGGGCCCCAATCAGGAATTTGCCGCAATCAAATCAGGAATTTGCCGCAATCAAATCAGGAATTTGCCGCAATCATGGCC-5'

AAAACCCCTA

5' -AATTCGCCGGGTCTCGTAAACCCCTAAAATATTCTCGTAAACCCCTAAAATATTCTCGTAAACCCCTAAAATATA-3'
3' -GGGGCCCCAGAGCATTTTGGGATTTTATAAGAGCATTTTGGGATTTTATAAGAGCATTTTGGGATTTTATATATGGCC-5'

Mutant AAAACCCCTA

5' -AATTCGCCGGGTCTCGTCCCCAAGCAAAATATTCTCGTCCCCAAGCAAAATATTCTCGTCCCCAAGCAAAATATA-3'
3' -GGGGCCCCAGAGCAGGGGTTTCGTTTATAAGAGCAGGGGTTTCGTTTATAAGAGCAGGGGTTTCGTTTATATATGGCC-5'

(b)

GnATTGAC

5' -AATTCCCCGGGTTAAACAGCATTGACAAATTTGTTAACAGCATTGACAAATTTGTTAACAGCATTGACAAATTTGA -3'
3' -GGGGCCCCAATTGTTCGTAACAAATTTGTTAAACAATTTGTTAAACAATTTGTTAAACAATTTGTTAAACTGGCC-5'

Mutant GnATTGAC

5' -AATTCCCCGGGTTAAACATACGGTCAAAATTTGTTAAACATACGGTCAAAATTTGTTAAACATACGGTCAAAATTTGA -3'
3' -GGGGCCCCAATTGTATGCCCTGTTTAAACAATTTGTTAAACAATTTGTTAAACAATTTGTTAAACAATTTGTTAAACTGGCC-5'

TGTATACA

5' -AATTCCCCGGGATAGAATGTATACAGTCTCAATAGAAATGTATACAGTCTCAATAGAAATGTATACAGTCTCAA -3'
3' -GGGGCCCCATCTTACATATGTCAGAGTTATCTTACATATGTCAGAGTTATCTTACATATGTCAGAGTTGGCC-5'

Mutant TGTATACA

5' -AATTCCCCGGGATAGAAGACGCTCGTCTCAATAGAAAGACGCTCGTCTCAATAGAAAGACGCTCGTCTCAA -3'
3' -GGGGCCCCATCTTGGGAGCAGAGTTATCTTCTTGGAGCAGAGTTATCTTCTTGGAGCAGAGTTGGCC-5'

GTGATCAC

5' -AATTCCCCGGGCTTCTCGTGATCACAAAATGCTTCTCGTGATCACAAAATGCTTCTCGTGATCACAAAATGA -3'
3' -GGGGCCCCGAAGACACTAGTGTTTTACGAAGACACTAGTGTTTTACGAAGACACTAGTGTTTTACTGGCC-5'

Mutant GTGATCAC

5' -AATTCCCCGGGCTTCTTAACGACGAAAATGCTTCTTAACGACGAAAATGCTTCTTAACGACGAAAATGA -3'
3' -GGGGCCCCGAAGAGATTGCTGCGTTTACGAAGAATTGCTGCGTTTACGAAGAATTGCTGCTTTACTGGCC-5'

CAATGAGG

5' -AATTCCCCGGGTATGTGCAATGAGTCAATGATATGTGCAATGAGTCAATGATATGTGCAATGAGTCAATGAA -3'
3' -GGGGCCCCATACACGTTACTCCAGTACTATACACGTTACTCCAGTACTATACACGTTACTCCAGTACTTGGCC-5'

Mutant CAATGAGG

5' -AATTCCCCGGGTATGTGACCGTCTTTTCATGATATGTGACCGTCTTTTCATGATATGTGACCGTCTTTTCATGAA -3'
3' -GGGGCCCCATACACTGGCAGAAAGTACTATACACTGGCAGAAAGTACTATACACTGGCAGAAAGTACTTGGCC-5'

Figure L.1. Sequences of the tetramers created from motifs found in clusters III and IV

The above DNA sequences are the tetramers created using each of the novel motifs (Chapter 4) found in cluster III (a) or cluster IV (b) which were fused in front of the GUS reporter gene. See Materials and Methods in Chapter 4 for details.

APPENDIX M

PERL SCRIPTS

Unwrap_fasta.pl PERL script

```
#!/usr/bin/perl -w
```

#This script is from Rob Halgren, MSU-GTSF. It makes fasta files usable for PERL scripts.

```
use strict;
$/=">";
<>;
while (<>){
    chomp;
    my ($name,@array)=split("\n",$_);
    my $sequence=join(" ",@array);
    print uc">$name\t$sequence\n";
}
```

CRT_counter.pl PERL script

```
#!/usr/bin/perl -w
```

#This script takes as input a fasta sequence file in the form of ">AT1G01010 ATCTGTG...", after it has been run through the unwrap_fasta.pl script. It then counts the number of CRT/DRE elements present in the DNA sequence and returns the AGI number followed by the number of CRT/DRE elements present.

```
use strict;
print "AGI (A/G)CCGAC\n";
while (<>){
    chomp;
    my ($acc,$seq) = split "\t";
    ($acc) = $acc =~ />(AT[\d\w]\w\d{5})/;
    my $count=0;

    while ($seq =~ /[A|G]CCGAC)(GTCGG[C|T])/g){
        $count++;
    }

    print "Sacc $count\n"
}
```

CRT_distance_counter.pl PERL script

```
#!/usr/bin/perl -w
```

#This script finds the distances between CRTs in all promoters that contain one, even overlapping ones, in either orientation. It does not return a value if there is no CRT in that promoter. The sequences used as input must go through unwrap_fasta.pl first.

```
use strict;
```

```
print "AGI\tdistance_between_CRTs\n";
```

```
while (<){  
  chomp;  
  my ($agi,$seq) = split "\t";
```

#This finds all the AGI numbers and makes a list of them.

```
($agi) = $agi =~ />(AT[d\w]\w\d{5})/;
```

#This finds all sequences between CRTs in the sequence (in both orientations) and makes an array of them.

```
my (@seqs) = ($seq =~  
/(?=(?:[A|G]CCGAC)|(?:GTCGG[C|T]))(.+?)(?:[A|G]CCGAC)|(?:GTCGG[C|T]))/g);
```

#This takes each element in the above array and determines its length. I am replacing the sequences in the @seqs array with the length of each sequence. The foreach loop allows me to do this for each element in the array.

```
foreach $_ (@seqs){  
  $_ = length $_;  
}
```

#This will print out the AGI followed by the lengths of any sequences between CRTs, separate by tabs.

```
print "$agi\t".join("\t",@seqs);  
print "\n";
```

```
}
```

CRT_to_start_counter.pl PERL script

```
#!/usr/bin/perl -w
```

#This script finds the distance from the bp after the last C in (A|G)CCGAC to the end of the sequence. When using the 1kb upstream dataset from TAIR, this corresponds to the beginning to the 5' UTR. Some genes don't have annotated UTRs, in which case the script finds the distance to the ATG. Transcripts without annotated UTRs can be flagged manually.

```
use strict;
print "AGI\tdistance_to_start\n";
while (<>){
  chomp;
  my ($agi,$seq) = split "\t";
```

#This finds all the AGI numbers and makes a list of them.

```
($agi) = $agi =~ />(AT[\d\w]\w\d{5})/;
```

#This finds all sequences from the end of one CRT (starts after last "C" of (A|G)CCGAC) to the end of the sequence (on either strand) and makes an array of them.

```
my (@seqs)=$seq =~ /(?(?:[A|G]CCGAC|GTCGG[C|T])(.+))/g;
```

#This takes each element in the above array and determines its length. I am replacing the sequences in the @seqs array with the length of each sequence. The foreach loop allows me to do this for each element in the array.

```
foreach $_ (@seqs){
  $_ = length $_;
}
```

#This will print out the AGI followed by the lengths of any sequences between CRTs, separate by tabs.

```
print "$agi\t",join("\t",@seqs);
print "\n";
}
```

Motif_extractor.pl PERL script

```
#!/usr/bin/perl -w
```

#This script takes as input a fasta file that has been run through unwrap_fasta.pl. It searches for a given element, CCGAC, and extracts the 5bp upstream and downstream of the element, if it is there. The script takes the element from either strand of the DNA.

```
use strict;
```

```
while (<>){
  chomp;
  my ($agi) = />(AT[\d\w]\w\d{5})/;
  my (@watson) = /\w{0,4}[A|G]CCGAC\w{0,4})/g;
  my (@crick) = /\w{0,4}GTCGG[C|T]\w{0,4})/g;
  my $reverse = reverse ("@crick");
  $reverse =~ tr/ATGC/TACG/;
  print "$agi @watson $reverse\n";
}
```

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