Effects of a bacterial ACC deaminase on plant growth-promotion

by

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Author's declaration

I hereby declare that I am the sole author of this thesis. This is a true copy of the thesis, including any required final revisions, as accepted by my examiners.

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Abstract

Plants often live in association with growth-promoting bacteria, which provide them with several benefits. One such benefit is the lowering of plant ethylene levels through the action of the bacterial enzyme 1-aminocyclopropane-1-carboxylic acid (ACC) deaminase that cleaves the immediate biosynthetic precursor of ethylene, ACC. The plant hormone ethylene is responsible for many aspects of plant growth and development but under stressful conditions ethylene exacerbates stress symptoms. The ACC deaminase-containing bacterium *Pseudomonas putida* UW4, isolated from the rhizosphere of reeds, is a potent plant growth-promoting strain and as such was used, along with an ACC deaminase minus mutant of this strain, to study the role of ACC deaminase in plant growth-promotion. Also, transgenic plants expressing a bacterial ACC deaminase gene were used to study the role of this enzyme in plant growth and stress tolerance in the presence and absence of nickel. Transcriptional changes occurring within plant tissues were investigated with the use of an Arabidopsis oligonucleotide microarray.

The results showed that transcription of genes involved in hormone regulation, secondary metabolism and the stress response changed in all treatments. In particular, the presence of ACC deaminase caused genes for auxin response factors to be up-regulated in plant tissues suggesting a de-repression of auxin signaling in the absence of high levels of ethylene. Also, transgenic plants had longer roots and grew faster than the non-transformed plants and genes involved in the stress response and secondary metabolism were up-regulated. Plants inoculated with bacteria had lower levels of secondary metabolism gene expression and slightly higher stress response gene expression than uninoculated plants. Yet, inoculation with the ACC deaminase-expressing bacterium caused less up-regulation of plant genes involved in stress and defense responses and the down-regulation of genes involved in nitrogen metabolism in comparison to plants inoculated with the ACC deaminase minus mutant.

Nickel stress caused the down-regulation of genes involved in photosynthesis and carbon fixation and the up-regulation of genes involved in stress responses, and amino acid and lipid breakdown suggesting energy starvation. When transgenic plants expressing ACC deaminase in the roots were exposed to nickel stress, plant stress symptoms were significantly lower and biomass was significantly higher suggesting that lowering the level of ethylene relieved many of the stress symptoms. In fact, genes involved in photosynthesis, secondary metabolism and nitrate assimilation were up-regulated in transgenic plants compared with non-transformed plants in the presence of nickel, suggesting that ACC deaminase is effective at reducing the severe effects of this metal stress.

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Chapter 1

Introduction

1.1 Ethylene

The gaseous plant hormone ethylene is the smallest unsaturated hydrocarbon and is essential for plant growth and development. It regulates many processes including germination, root development, flower and fruit development, senescence and abscission (Jackson and Osborne, 1970; Abeles *et al.*, 1992). It also has roles in cell elongation, cell death, biotic and abiotic stress, nodulation and systemic resistance to pathogens (Bleecker and Kende, 2000). Many of these processes have complex mechanisms and involve processes such as cell wall degradation, cell expansion and cell division (Abeles *et al.*, 1992). Ethylene biosynthesis is relatively straightforward, yet although many components of its signal perception and response have been identified, many parts of the ethylene signal cascade are still not known. Ethylene is thought to initiate a cascade of transcription factors which have widespread effects, and this response is dependent on many variables such as the tissue type, developmental stage and environmental stimuli. The identity of all ethylene effects are not fully known, yet many new insights have been gained due to recent advancements in "omic" studies (i.e. transcriptomics, proteomics), which have illuminated untold numbers of diverse roles for ethylene. It is now believed that $3-7\%$ of all genes investigated in Arabidopsis are regulated by ethylene (Zhong and Burns, 2003).

As early as 1932, ethylene was shown to initiate agravitropic growth and thickening of the stem as well as inhibition of plant stem elongation of seedlings, which was termed the “triple response” (Crocker, 1932). In some plants ethylene is involved in breaking seed dormancy and germination (Gazzarrini and McCourt, 2003) but in others only in germination (Calvo *et al.*, 2004; Gianinetti *et al.*, 2007; Gniazdowska *et al.*, 2007). During germination ethylene promotes the formation of the apical hook, which is necessary for the hypocotyl to emerge from underground. In semi-aquatic plants, such as rice, ethylene is also involved in stem elongation which enables them to rise above water levels to reach air and sunlight (Cohen and Kende, 1987).

The most obvious physiological change which is dependent upon ethylene is the ripening of climacteric fruit. These are fruit in which ripening is accompanied by a steep rise in ethylene production and an increase in respiration. This phenonmenon has been studied in great detail due to the agronomic value of climacteric fruit such as tomato, apple and banana. Ripening begins with loss of chlorophyll, then colour, flavour and texture changes as aromatic and pigment compounds are formed and cell walls lose pectin, ending with abscission of the fruit (Bleecker and Kende, 2000). Plants that produce less ethylene or have a defect in the ethylene perception pathway produce fruit that ripen more slowly or not at all. Ethylene is also responsible for flower wilting and leaf senescence, and the shelf life of economically valuable plants can be lengthened by tempering the ethylene effect.

1.1.1 Ethylene biosynthesis

All plant cells are capable of producing ethylene and its biosynthesis is catalyzed by only two enzymes. The first enzyme, 1-aminocyclopropane-1-carboxylic acid (ACC) synthase, converts S-adenosylmethionine (SAM) to ACC and 5’-methylthioadenosine (MTA). SAM is the major methyl group donor in cells so it is always present and its level remains relatively unchanged throughout the life of the plant. To this end, MTA is diverted back into the methionine cycle (Figure 1.1) to be recycled as L-methionine (Yang and Hoffman, 1984), so that even during high rates of ethylene production, the levels of L-methionine available to produce SAM remains the same (Abeles *et al.*, 1992). The second enzyme, ACC oxidase, catalyzes the conversion of ACC into ethylene in the presence of oxygen. Because it is a gas, ethylene freely diffuses throughout plant tissues, therefore no carrier molecules are required to shuttle it to or into target cells. Not all cells respond to ethylene, however and there may be developmental or environmentally stimulated cues that prime cells to be sensitive to it, but such a mechanism is unknown (Abeles *et al.*, 1992).

Regulation of ethylene biosynthesis

Under certain circumstances, ethylene is known to autocatalyse its own biosynthesis by turning on the transcription of ACC synthase and ACC oxidase genes. This is thought to be how such high levels of ethylene production occur during processes such as fruit ripening, yet other types of regulation are also at work (Yang and Hoffman, 1984; Tsuchisaka and Theologis, 2004). In the model plant Arabidopsis, the ACC synthase multigene family is comprised of 9 members, 8 of which are functional, with subtly different expression patterns and levels of activity (Tsuchisaka and Theologis, 2004). Since ACC is very labile at physiological conditions and ACC oxidase is present at low levels in all cells of the plant, ACC synthase is believed to be the rate limiting step of this reaction (Kende, 1993). ACC oxidase, like ACC synthase, however, is transcribed from a multigene family and exists in several isoforms that are active under different physiological conditions, suggesting more complex control of ethylene biosynthesis (Abeles *et al.*, 1992; Arshad and Frankenberger, 2002; Voesenek *et al.*, 2003). The conjugation of ACC with malonate or glutamate can occur and is thought to proceed via the action of the enzymes ACC N-malonyl transferase and γ-glutamyl transpeptidase, with the production of 1-(malonyl)-ACC (MACC) and 1-(glutamyl)-ACC (GACC), respectively (Peiser and Fa Yang, 1998). Since the K_m of ACC N-malonyl transferase for ACC is much higher than the K_m of ACC oxidase for ACC, the conjugation reaction is

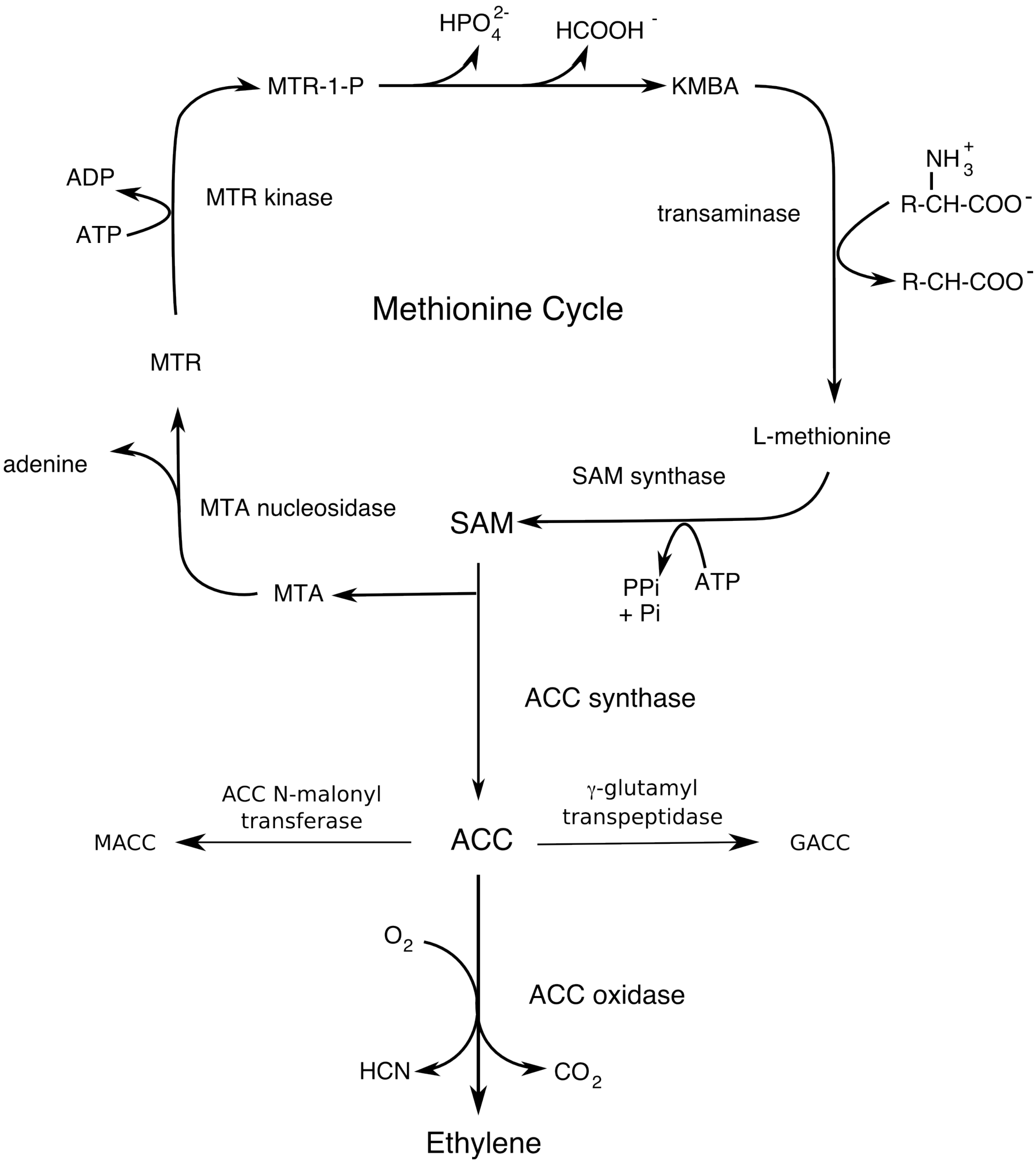

Figure 1.1: Modified methionine cycle and ethylene biosynthesis pathway. ACC: 1-aminocycloproane-1-carboxylic acid; GACC: 1-(glutamyl)-ACC; MACC: 1-(malonyl)-ACC; MTA: 5'-methylthioadenosine; SAM: S-adenosylmethionine.

thought to create a sink for ACC only when it is present in high levels, or when ACC oxidase is saturated or absent (Abeles *et al.*, 1992). It has been suggested that in times of stress MACC may be a source of ACC (Fluhr and Mattoo, 1996), however this suggestion is controversial and has not been proven (Peiser and Fa Yang, 1998).

Recent evidence of post-translational control of ACC synthase suggests a novel method of control over ethylene biosynthesis (Figure 1.2). It involves how the enzyme is tagged for degradation by the ubiquitin 26S proteasome (Chae and Kieber, 2005). An Arabidopsis mutant called *eto1* (for ethylene overproducer) was found to be deficient in its ability to break down ACC synthase, which then accumulates in the tissues. Phosphorylation of the C-terminal end is thought to change the ability of the ACC synthase protein to be complexed with elements of the ubiquitin degradation system through ETO1, hence the enzyme remains active longer (Woeste *et al.*, 1999). The 8 functional ACC synthase proteins differ in their C-terminal amino acid sequences and this is thought to change the ways in which they are tagged for degradation, some remaining active under certain conditions and others being degraded (Chae and Kieber, 2005). This mechanism has been studied for ACC synthase, yet it may also prove true for ACC oxidase. Phosphorylation is known to occur by two distinct mechanisms: mitogen-activated-protein kinase (MAPK) which phosphorylates serine and calcium-dependent protein kinase (CDPK) which also phosphorylates serine but with a different consensus site (Chae and Kieber, 2005). Both CDPK and MAPK cascades have been implicated in ethylene mediated stress responses (Ludwig *et al.*, 2005). The mechanisms of activation of transcription and degradation of active enzyme under diverse conditions and developmental stages illustrate some of the complexity of ethylene signal regulation.

1.1.2 Ethylene perception

Ethylene perception proceeds via a pathway that has been mainly studied in Arabidopsis (Figure 1.3) but appears to be conserved among other plant species. There are five known ethylene receptor proteins in Arabidopsis: ETR1, ETR2, EIN4, ERS1 and ERS2, for ethy-

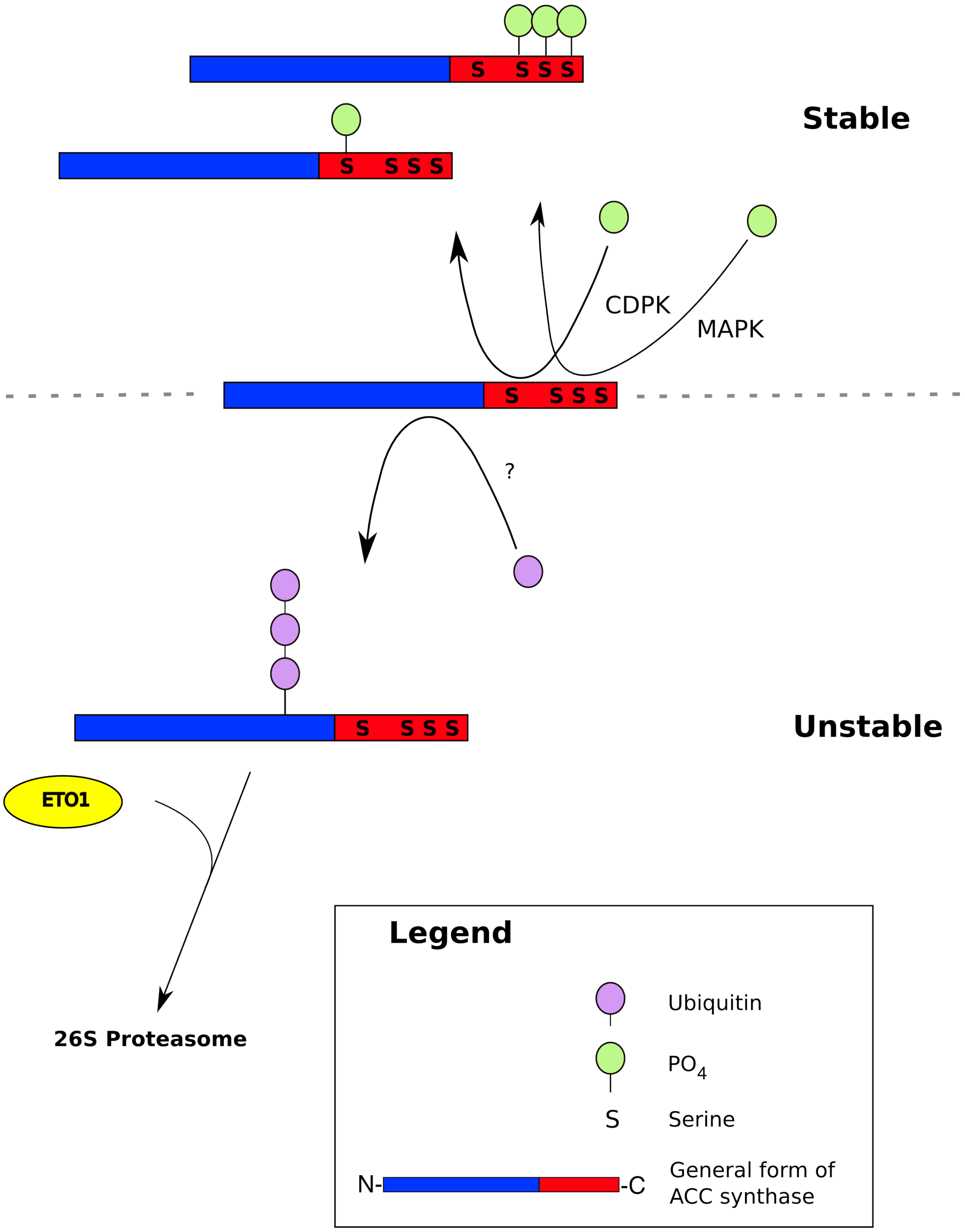

Figure 1.2: Post-translational regulation of ACC synthase (adapted from Chae and Kieber, 2005). CDPK: calcium-dependent protein kinase; ETO1: ethylene overproducer 1; MAPK: mitogen-activated protein kinase

lene receptors 1, 2, ethylene insensitive 4, and ethylene response sensors 1, 2, respectively (reviewed in Guo and Ecker, 2004; Stepanova and Alonso, 2005)). All five receptors bind ethylene and show significant functional redundancy, as illustrated by studies of Arabidopsis receptor mutants, where double and triple mutants are required to see complete loss of ethylene perception. The receptors belong to two groups based on the presence (group I) or lack (group II) of a functional histidine kinase domain, group I includes ETR1 and ERS1; and group II includes: ETR2, EIN4, and ERS2. The receptors resemble the bacterial two component histidine kinases that have a sensor domain, a histidine kinase domain (in the case of group I), and a reciever domain (absent in ERS1 and 2). In many two-component systems, a histidine residue autophosphorylates donating a phosphate to an aspartate residue in the receiver domain (Pirrung, 1999). New evidence casts doubt on the idea of a simple role of phosphotransfer and receiver functions for the histidine kinase and receiver domains as neither has a primary role in ethylene signal transduction. Instead, more complex roles are proposed where repression of the ethylene signal is quantitative and the presence or absence of these domains is a question of efficiency (Chang and Bleecker, 2004). The N-terminal sensor domain binds ethylene and has transmembrane regions that are embeded within the endoplasmic reticulum membrane and form a pocket with the help of a copper cofactor (Figure 1.3). The copper transporter responsive-to-antagonist1 (RAN1) is required for biogenesis of ethylene receptors and is proposed to act in the post-golgi compartment where copper is incorporated into the hydrophobic portion of the receptor protein, which is then able to respond to ethylene. Without a copper ion, the receptor is unable to interact with CTR1 to repress ethylene signaling and a constitutive ethylene response ensues (Hirayama *et al.*, 1999; Woeste and Kieber, 2000).

Downstream of ethylene binding is the protein constitutive triple response 1 (CTR1), a serine-threonine kinase. It is a repressor of downstream signaling and loss of this protein results in a constitutive ethylene-treated phenotype, as there is a derepression of the ethylene signaling cascade, which then stays “on” (much like the left side of Figure 1.3). The

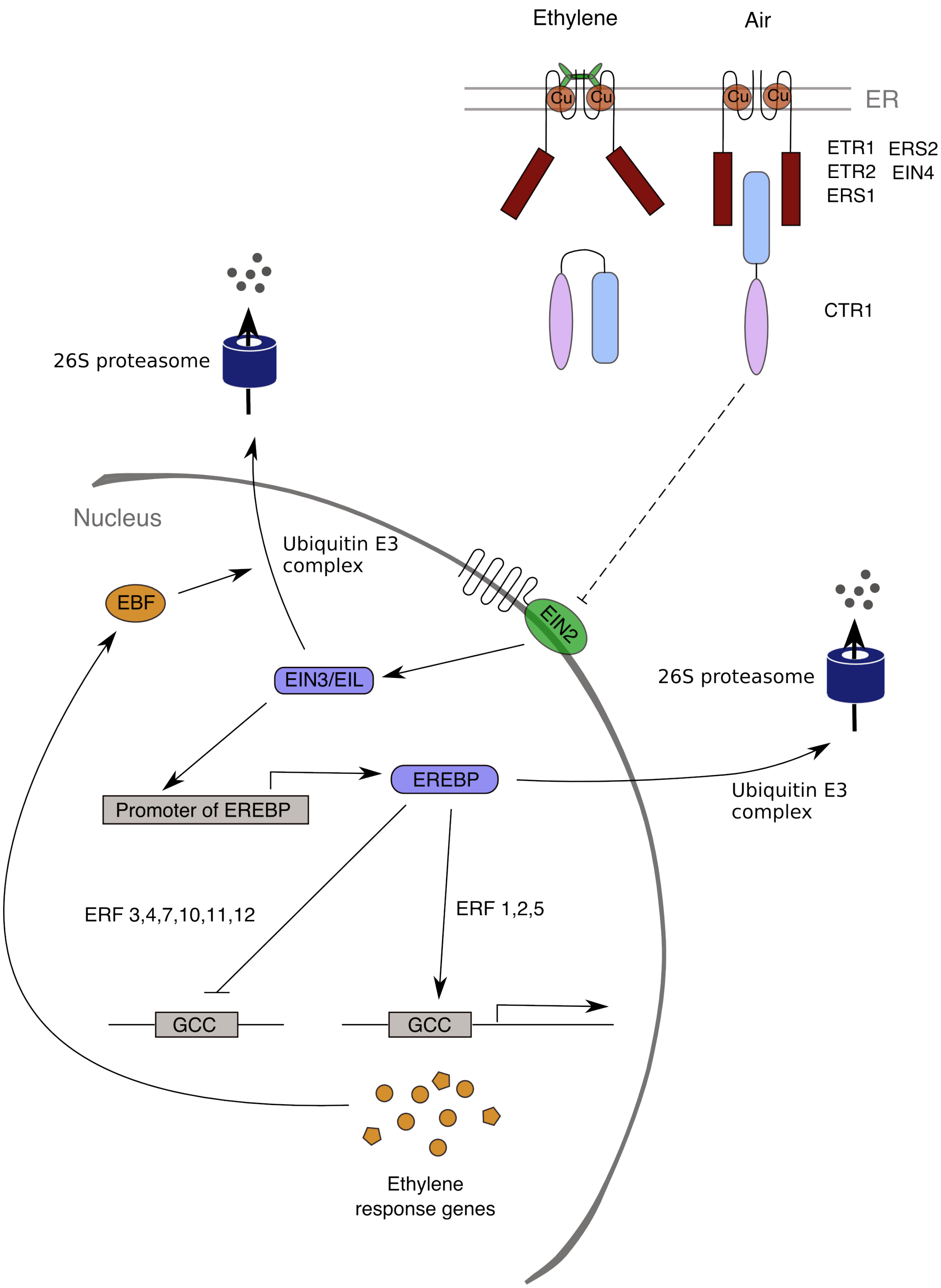

Figure 1.3: Ethylene perception and signal cascade. The dotted line denotes where many steps may be involved. CTR1: constitutive triple response 1; EBF: F-box containing protein; EIL: EIN3-like proteins; EIN2: ethylene insensitive 2; EIN3: ethylene insensitive 3; EIN4: ethylene insensitive 4; EREBP: ethylene response element binding proteins; ERF: ethylene response factor; ERS1: ethylene response sensor 1; ERS2: ethylene response sensor 2; ETR1: ethylene receptor 1; ETR2: ethylene receptor 2.

N-terminal end of CTR1 associates with the ethylene receptors and the whole complex localizes to the endoplasmic reticulum (ER) (Gao *et al.*, 2003). A deletion of the N-terminus of CTR1 confers constitutive ethylene signaling due to its inability to associate with the receptors; the kinetics of how the receptors signal to CTR1, however, is unknown. A MAPK cascade has been postulated to exist within ethylene signaling for some time, and has even recently been implicated to act downstream of CTR1 (Ouaked *et al.*, 2003), however this has yet to be proven and is still debated (Chang, 2003; Ecker, 2004). When ethylene is absent, CTR1 represses ethylene insensitive 2 (EIN2), that is named for the complete loss of ethylene perception which occurs when this protein is mutated or knocked out, illustrating its importance to ethylene signaling and a lack of redundancy at this step. EIN2 is bound within the nuclear membrane and somehow activates ethylene insensitive 3 (EIN3) and EIN3-like proteins (EILs); these have a DNA binding domain and turn on the transcription of ethylene response element binding proteins (EREBP) such as ethylene response factor 1 (ERF1), which are considered the primary ethylene response genes (Stepanova and Alonso, 2005). The expression of EIN3 and EILs does not change in response to ethylene, which suggests that the regulation of these transcription factors is at the protein level, through proteolytic degradation by the 26S proteasome (Gagne *et al.*, 2004). EREBP regulate the ethylene response by binding to the promoters of secondary ethylene response genes, many of which contain a GCC-box within their promoter regions (Broekaert *et al.*, 2006). Secondary ethylene response genes are an area of active research since their functions are largely unknown. van Loon *et al.* (2006b) have done extensive research in the area of ethylene-induced defense-related effector molecules many of which belong to a group called pathogenesis-related (PR) proteins. Classes of PR proteins have been shown to be ethylene responsive due to the GCC-box element within their promoters. These proteins include β-1,3-glucanases, basic-chitinases and plant defensins (PDFs) (Broekaert *et al.*, 2000). The subtleties of this process are not fully understood, however, since some genes with a GCC-box are not ethylene responsive and others without it are ethylene responsive. It suggests complex controls at these deeper levels of the signaling cascade.

1.1.3 Interaction between ethylene and auxin

An interesting characteristic of ethylene is that many of its effects seem contrary to one another. This is because our understanding of ethylene's many effects, and the myriad of conditions that affect it, is not complete. One such contradictory example is that it promotes adventitious rooting and root hair formation (Abeles *et al.*, 1992; Bleecker and Kende, 2000) yet it inhibits root elongation in developing seedlings (Guzman and Ecker, 1990). Very recently, it has been shown that some of this inhibition is due to the up-regulation of auxin biosynthesis (Stepanova *et al.*, 2007). This also illustrates an important point: a balance of ethylene and other plant hormones is essential to feather the physiological response of plants to their environment.

Auxin is known to interact with ethylene at many points, and suspected to interact with it at many others. At the level of biosynthesis, ethylene and auxin each signal the up-regulation of the biosynthesis genes of the other within the root (Stepanova *et al.*, 2005). There is evidence of ethylene inhibition of auxin response factor 2 (ARF2) through the gene hookless 1 (HSL1) in the shoot (Lehman *et al.*, 1996; Li *et al.*, 2004) and evidence of ethylene inhibition of auxin transport (Prayitno *et al.*, 2006). Contrarily, there is increased expression of ARFs in ethylene treated seedling roots (Stepanova *et al.*, 2007; Ruzicka *et al.*, 2007; Swarup *et al.*, 2007). This may seem counterintuitive, however, it is important to note that some auxin response factors are enhancers of the auxin response and other are inhibitors (Ballas *et al.*, 1993; Hagen and Guilfoyle, 2002; Teale *et al.*, 2006).

1.1.4 Stress ethylene

Many biotic and abiotic stresses are accompanied within the plant by a burst of ethylene (Hyodo, 1991; Bleecker and Kende, 2000). Ethylene production has been observed during the following stresses: oxidative stress (Bueso *et al.*, 2007), salt stress (Mayak *et al.*, 2004a; Cao *et al.*, 2006), heat and drought stress (McMichael *et al.*, 1972; Balota *et al.*, 2004; Mayak *et al.*, 2004b; Munne-Bosch *et al.*, 2004), wounding, flooding, mechanical strain (Botella *et al.*, 1995), heavy metal stress (Rodecap *et al.*, 1981; Fuhrer, 1982; Burd *et al.*, 1998; Rodriguez-Serrano *et al.*, 2006) and pathogen infection (Cronshaw and Pegg, 1976; Hyodo, 1991; van Loon, 1984). Stress ethylene, though its role is unclear, is deleterious to plants in many instances and lowering the level or perception of ethylene reduces the severity of the stress. For example, when plants are infected by pathogens, a large portion of the damage that occurs to the plant is due to ethylene synthesis and not from direct pathogen action (van Loon, 1984).

Measurements of ethylene levels in plants undergoing a stress reveal that there are two distinct phases of ethylene evolution (Figure 1.4). The first is a small peak which occurs very near the onset of the stress, is relatively short, and is thought to turn on a protective defense response. The second is a much larger peak which occurs after a lag of a few hours to a few days from when the stress was applied and is so large that processes such as senescence, chlorosis and abscission are initiated, the overall effect of which is inhibitory to plant survival (Stearns and Glick, 2003; Balota *et al.*, 2004). At the time that the stress is applied the level of ACC within plant tissues is very low. Next, ACC oxidase is induced and begins to convert the existing pool of ACC to ethylene, which catalyzes its own biosynthesis by turning on ACC synthase and ACC oxidase gene expression (Kende, 1993; Fluhr and Mattoo, 1996). Once the pool of ACC has been consumed there is a lag in ethylene production until more ACC can be synthesized by the action of ACC synthase. The genes for ACC synthase are regulated by environmental and developmental cues (Tsuchisaka and Theologis, 2004) and its enzymatic action is enhanced during stress conditions (Yang and Hoffman, 1984).

Enzymes that degrade SAM or ACC, the precursors of ethylene, and inhibitors of ethylene synthesis have been shown to effectively reduce ethylene levels without drastically altering the physiology of the plant (Klee *et al.*, 1991; Robison *et al.*, 2001a) and lowering of ethylene levels or perception have conferred stress tolerance. Some examples include: increased drought tolerance in maize (Young *et al.*, 2004) and tomato (Mayak *et al.*, 2004b); salt stress in tomato (Mayak *et al.*, 2004a); oxidative, salt and acid stress in tobacco (Wi and Park, 2002); flooding stress in tomato (Grichko and Glick, 2001); copper and organic contaminants stress in canola (Reed and Glick, 2005); heavy metal stress in tomato (Grichko *et al.*, 2000); arsenic stress in canola (Nie *et al.*, 2002); osmotic stress in tobacco (Mee Park *et al.*, 2001); resistance to the fungal pathogens *Alternaria* (Bashan, 1994), *Fusarium oxysporum* (Cohen *et al.*, 1986), *Colletotrichum lagenarium* (Biles *et al.*, 1990); *Botrytis cinerea* (Elad, 1988, 1990) and *Verticillium* (Robison *et al.*, 2001b); and the bacterial pathogen *Agrobacterium tumefaciens* (Hao *et al.*, 2007).

A review of the literature illustrates that although lowering ethylene levels improves plant survival, mutants with defects in ethylene signal transduction (below EIN2, Figure 1.3) are sometimes more susceptible to pathogen infection. This may be because ERFs are involved in the defense response of various plant species, but the type of defense mounted is entirely dependent on the the specific plant-pathogen interaction. Also, elements of the ethylene signal transduction pathway are involved in a complex set of interactions with other signaling pathways (such as jasmonic acid, salicylic acid and abscisic acid) to mediate the activation of pathogen resistance genes (Alonso *et al.*, 1999; Anderson *et al.*, 2004; Bishopp *et al.*, 2006; van Loon *et al.*, 2006b; Dreher and Callis, 2007; Broekaert *et al.*, 2006). Their removal or inactivation may have unforeseen effects that reduce the ability of plants to respond to a specific pathogen.

1.2 Plant stress

Plants are sessile organisms that have developed unique responses to their environment as compared to their mobile counterparts (animals). Plants are primary producers, meaning that they create organic compounds from CO_2, water and the sun's energy, yet they must also acquire some nutrients from the environment. The plant's environment is full of challenges

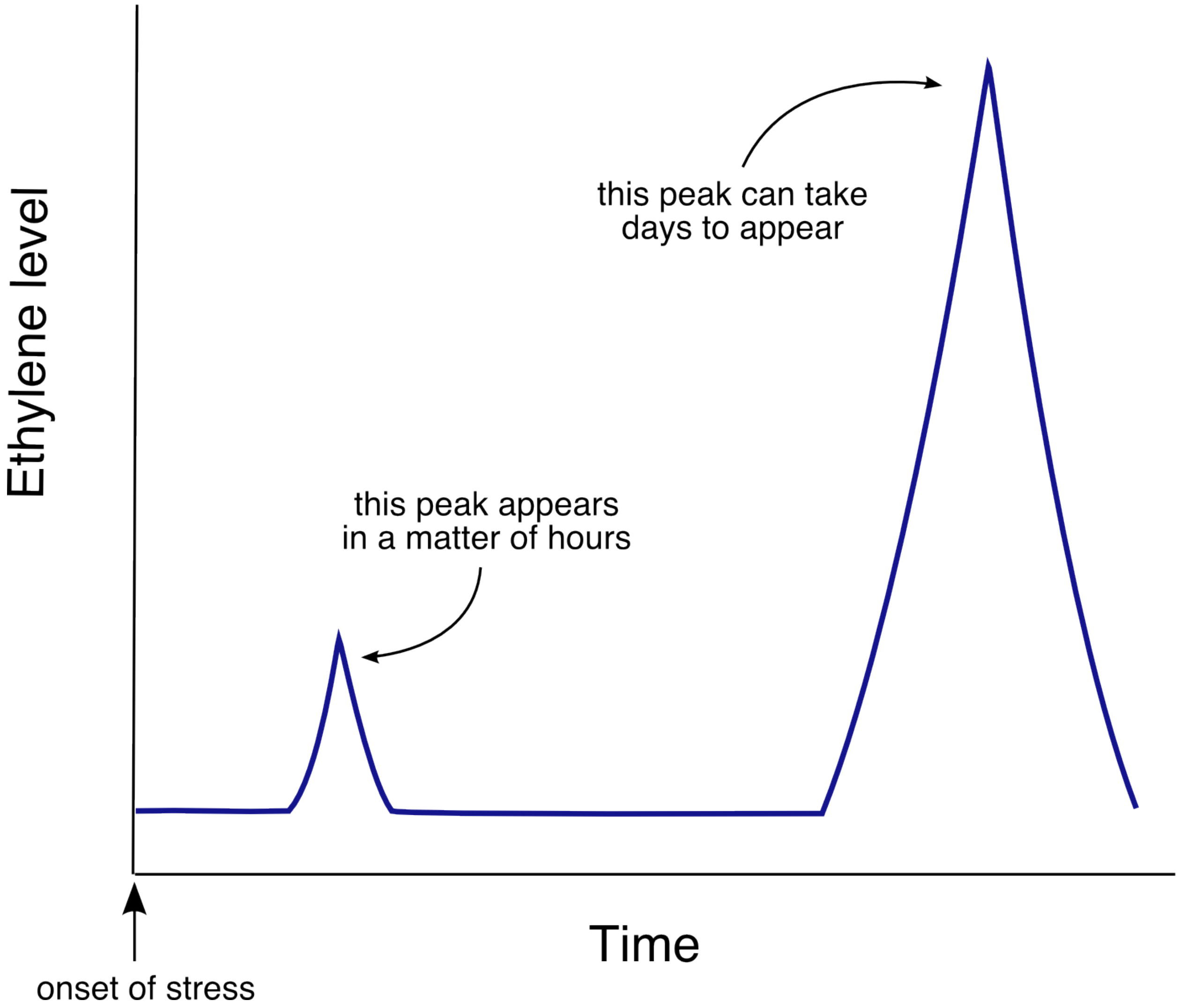

Figure 1.4: Two peaks of ethylene biosynthesis that occur within plants exposed to stressful conditions.

ranging from subtle temperature and nutrient changes, to harsh toxicants and pathogen attack. The complex signaling and response networks that plants have developed to respond appropriately to their environment allow them to survive. When conditions are not favorable, such as in the case of soils contaminated with high salt, heavy metals, or a pathogenic organism, specific stress signals are turned on within the plant. The type of signal varies for each type of stress, yet there is much overlap. In particular, plant stresses can be divided into two categories: biotic and abiotic. The former are cases of fungal, viral, bacterial or insect pathogen ingress and the latter are all other stresses not induced by biological organisms.

1.2.1 Biotic stress

Within the rhizosphere, plant roots are in contact with a myriad of different organisms, many of which are pathogenic. When a biotic stress is sensed, plants mount a defense response which begins with reactive oxygen species (ROS), calcium fluctuations, micro RNAs and many other signaling molecules (Broekaert *et al.*, 2006; Navarro *et al.*, 2006). Even symbiotic plant-microbe relationships induce a defense response within the plant (Timmusk and Wagner, 1999). This may be because the process of beneficial bacteria associating with plant tissues is similar to that which occurs during pathogenic bacterial infection (Haas and Defago, 2005).

Plant responses to biotic stress fall into two categories: local and plant wide. Local responses are limited to the site of infection and include the production of antimicrobial molecules and strengthening of cell walls through the increased synthesis of lignin and callose (Broekaert *et al.*, 2006). Distal, or plant wide, responses involve the triggering of defense signaling through salicylic acid (SA) or ethylene and jasmonic acid (JA), depending on the type of pathogen. Two distinct types of plant wide defense responses have been studied: systemic acquired resistance (SAR), which is triggered by a pathogenic organism; and induced systemic resistance (ISR), which is triggered by beneficial microorganisms. Both pathways protect plants from future pathogen infection, are long lasting, and are effective at sites far from the initial site of infection (Haas and Defago, 2005; van Loon *et al.*, 2006a). Unlike SAR, ISR is not associated with SA signaling but with mainly ethylene and also JA signaling, which is evident from the inability of ethylene or JA signaling mutants to mount an ISR response (Ton *et al.*, 2002). Very little is known about the downstream effects of ISR, despite conclusive evidence that ISR protects against pathogen attack, however, it is known that ethylene response and signaling mutants are unable to mount a significant defense response when colonized by beneficial microorganisms (van Loon *et al.*, 2006a). It has been shown that beneficial microorganisms, which lower plant ethylene levels confer significant advantages to plants under stress as well as inducing ISR. This may be because only small amounts of ethylene are required to mount an ISR or that components downstream of EIN2 are involved in the defense response and these interact with other plant hormones or signals. High levels of ethylene, then, serve only to turn on processes that are deleterious to plant health and survival such as senescence and cell death.

1.2.2 Abiotic stress

Abiotic stresses include heat, drought, cold, salinity, heavy metals, organic contaminants, high light, nutrient stress, and flooding. This study focuses on the response of plants to nickel, therefore, the only abiotic stress that will be discussed here is heavy metal stress. Heavy metals are a widespread contaminant in the environment due mainly to their release from mining and smelting, agriculture, large industries such as textiles and manufacturing, urban development and landfills (Prasad and Strazalka, 2000; Sharma and Agrawal, 2005; Puig *et al.*, 2007).

An important effect on plants of heavy metals in soil is the evolution of reactive oxygen species (ROS), by auto-oxidation and Fenton reactions. Fenton reactions are those in which a transition metal catalyzes the generation of highly reactive hydroxyl radicals from hydrogen peroxide as in the case of iron: $Fe^{2+} + H_2O_2 \longrightarrow Fe^{3+} + {\cdot}OH + OH^-$ (Halliwell and Gutteridge, 1999). ROS cause oxidative damage to proteins, DNA, and lipids as well as disruption of the photosynthetic machinery by interacting with them in a non-specific way. Electron flow can be inhibited in photosystem I (PSI), interrupting the transfer of elections between PSI and PSII, as well as interacting with ferredoxin (the final electron acceptor of PSI). Because of this, non-photochemical quenching is increased which then decreases the efficiency of excitation (electron) capture, and photosynthesis breaks down (Vernay *et al.*, 2007).

Some of the main cellular effects of heavy metals on plants are the displacement of metal ions from biomolecules (competitive inhibition) and functional group blocking by high affinity binding to sulfur-, nitrogen- and oxygen-containing groups, both of which render enzymes inactive (Clemens, 2006). Finally, inhibition of root and shoot development occurs due to reduced photosynthesis and hence reduced carbon fixation and the plant's inability to translocate sugars.

The most obvious effects of heavy metals on plants is the yellowing of leaf tissue, the cause of this is complex and involves a combination of chlorophyll breakdown, iron deficiency and ethylene production. An overall shortage in functional chlorophyll results from the loss of porphyrin, which occurs through the competitive incorporation of a metal ion into protoporphyrin instead of Mg^{2+} by the enzyme Mg^{2+} chelase (Prasad and Strazalka, 2000). Iron deficiency has been observed in many plants when grown in heavy metal contaminated soil (Rmheld and Marschner, 1986; Wallace *et al.*, 1992; Ma and Nomoto, 1993). The exact causes of this deficiency are unknown, but proposed mechanisms include the inhibition of plant iron-deficiency stress response, the competition between metal ions and iron(II), and the effect on the induction or functioning of iron(III) reductase (Alcantara *et al.*, 1994). Heavy metals have been shown to cause increased ethylene production (Goren and Siegel, 1976; Rodecap *et al.*, 1981; Burd *et al.*, 1998; Rodriguez-Serrano *et al.*, 2006). Many of the above symptoms may, in fact be a result of the increased ethylene levels since senescence and cell death processes are known to be activated by ethylene and reduction in ethylene level has been shown to enhance plant survival when exposed to heavy metals (Burd *et al.*, 2000; Grichko *et al.*, 2000; Nie *et al.*, 2002; Stearns *et al.*, 2005).

Plant responses to heavy metals include the initiation of activities that scavenge inactive proteins and free radical species, as well as processes for sequestering and detoxifying contaminants. Glutathione is the major redox buffer within plant cells and other ROS scavenging systems include superoxide dismutase (SOD) (which dismutates superoxide to hydrogen peroxide), ascorbate peroxidase, glutathione peroxidase and catalase (which then detoxify hydrogen peroxide to water). Enzymes such as SOD, metallothionins and phytochelatins (involved in sequestering metals) are among the most commonly over-expressed proteins seen in plants exposed to metals (Prasad and Strazalka, 2000).

1.3 Plant growth-promoting bacteria

The rhizosphere is a diverse ecosystem with a large effect on the health of the plant. This is where plant roots explore in search of nutrients and water, and where both pathogenic and beneficial microorganisms live. It is complex because of the different soil compositions creating uneven nutrient distribution; the varied gradients of water, ions, and even plant exudates; and the microorganisms that colonize this microcosm, which are numerous and respond to the changing soil conditions in the rhizosphere of the plant (Glick *et al.*, 1999). Many organisms, especially fungi, are pathogenic and need only an opportunity, such as a period of environmental stress, to begin infecting the plant. Some, however, are beneficial to plant growth and have evolved to colonize root surfaces or plant tissues. Beneficial rhizosphere bacteria are called plant growth-promoting rhizobacteria (PGPR) and they use direct and indirect methods of promoting plant growth. Indirect methods include competition with pathogenic microorganisms, involving depletion of iron from the soil, production of antibiotics and antifungal molecules, and competition for binding sites on the plant surface (Haas and Defago, 2005). Another indirect method of plant growth promotion, involves the triggering of induced systemic resistance (ISR) in the plant which, as mentioned above, protects them from attack by pathogenic organisms, mainly by inducing the plant-wide production of defense proteins and secondary metabolites that act to deter infection (van Loon *et al.*, 2006a). Direct mechanisms include the production of phytohormones; the lowering of plant ethylene levels; and aid in acquiring nutrients such as phosphorous, nitrogen and iron (Glick *et al.*, 1999). One function in particular, the lowering of plant ethylene levels, has been the focus of this work.

The bacterial enzyme ACC deaminase acts to lower plant ethylene levels by cleaving its biosynthetic precursor ACC. Many PGPR have this enzyme and it has been the subject of much research into its biochemical properties, its action, substrate specificity and even its genetic regulation and mode of heredity (Honma and Shimomura, 1978; Jacobson *et al.*, 1994; Hontzeas *et al.*, 2005; Glick *et al.*, 2007). Plants inoculated with bacteria that possess this enzyme (even *E. coli* containing the transgene) have longer roots than non-inoculated plants, have more nodules or are more tolerant of stress indicating lower ethylene levels (Shah *et al.*, 1998; Mayak *et al.*, 1999; Holguin and Glick, 2003; Ma *et al.*, 2004; Cheng *et al.*, 2007).

1.3.1 ACC deaminase

The ACC deaminase enzyme cleaves the cyclopropane ring of ACC, then deaminates it to ammonia and α-ketobutyrate, which can then be used by the bacterium as a source of both nitrogen and carbon (Honma and Shimomura, 1978). The enzyme was purified and its amino acid sequence determined so that a nucleotide probe could be used to screen libraries of the *Pseudomoas sp.* ACP genome, and in 1991, Sheehy *et al.* determined the complete sequence of the ACC deaminase gene. Since then, ACC deaminase activity has been measured in many other microorganisms, mainly bacteria, and the genes for ACC deaminase in some of these have been sequenced. One such organism, isolated in our lab, is the free-living plant growth-promoting bacterium *Pseudomonas putida* UW4 (Shah *et al.*, 1998). The gene for ACC deaminase from this organism has been extensively studied at both the protein and the regulatory level (Hontzeas *et al.*, 2006). As with other ACC deaminase enzymes, the one from UW4 has a relatively weak K_m of 3.4 mM, a pH optimum of 8, is made up of 3 identical subunits with a mass of 36.8 kDa each and requires a pyridoxal phosphate as a cofactor for each subunit (Hontzeas *et al.*, 2006).

1.3.2 Relief of plant stress by PGPR

ACC deaminase-containing plant growth-promoting bacteria, living in the soil, are attracted to plant exudates such as organic acids, sugars, amino acids, nucleotides and vitamins, then bind to the surface of the plant cell (Figure 1.5). The bacteria produce indole-3-acetic acid (IAA), some of which is taken up into the plant cell and activates the expression of ACC synthase. The bacteria may also activate stress induced MAP-kinases MPK6 and MPK3, which phosphorylate the ACC synthase enzyme stabilizing it (Liu and Zhang, 2004). Due to the increase in both the amount and activity of ACC synthase, more ACC is made in the plant cell and some of it is exuded from the roots into the rhizophere. There it is taken up by the bacterium, where it is broken down by the action of ACC deaminase. As ACC disappears from outside the plant cell, more is exuded from inside the plant cell along its concentration gradient. In this way the bacteria acts as a sink for ACC, thereby reducing the overall concentration available for conversion into ethylene by ACC oxidase within the plant root cells (Glick *et al.*, 1998).

The reduction of plant stress by ACC deaminase containing plant growth-promoting rhizobacteria has been documented in the case of water stress (Mayak *et al.*, 2004b), salt stress (Mayak *et al.*, 2004a) (Cheng *et al.*, 2007), osmotic stress (Sziderics *et al.*, 2007), flooding (Grichko and Glick, 2001; Farwell *et al.*, 2007), copper (Reed *et al.*, 2005), organic contaminants (Reed and Glick, 2005), arsenate (Nie *et al.*, 2002), lead and cadmium (Belimov *et al.*, 2004), nodulation (Ma *et al.*, 2003), and *Agrobacterium tumefaciens* infection (Hao *et al.*, 2007).

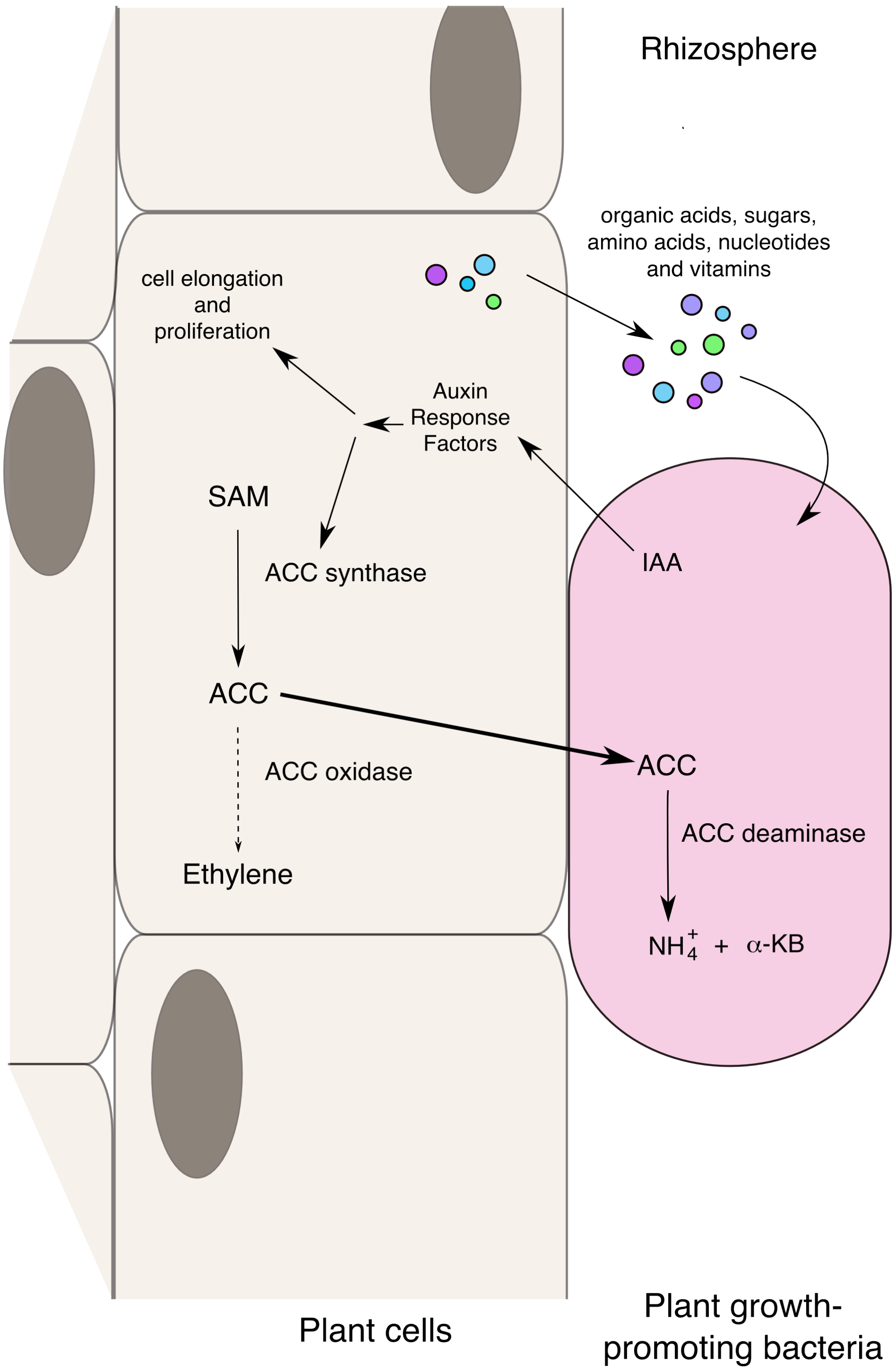

Figure 1.5: Lowering of plant ethylene levels by plant growth-promoting bacteria. α-KB: α-ketobutyrate; ACC: 1-aminocycloproane-1-carboxylic acid; IAA: indole-3-acetic acid; SAM: S-adenosylmethionine.

1.4 Conclusion

Ethylene is an essential plant hormone, which not only has important roles in plant growth and development but is involved in different aspects of plant stress responses. Lowering plant ethylene levels through the action of bacterial ACC deaminase has been shown to improve plant fitness during abiotic and biotic stress. An investigation of the plant response to colonization by plant growth-promoting bacteria and the role of ACC deaminase in plant growth and stress tolerance is presented here. In particular, the transcriptional changes that occur within tissues of *Brassica napus* (canola) were measured with the use of an Arabidopsis oligonucleotide microarray and verified using real-time RT-PCR. Also, the physiological effects of expressing the gene for ACC deaminase from *Pseudomonas putida* UW4 within canola plants, either constitutively or specifically within the roots, and the effects of nickel stress on transgenic and non-transformed plants are considered. The results present a picture of both the physiological and transcriptional effects of ACC deaminase on canola growth in the presence and absence of metal stress. Of particular interest are the changes in gene expression occurring within tissues of transgenic canola expressing ACC deaminase in the roots and the ability of these plants to overcome the effects of nickel stress. Also of interest are the effects of bacterial colonization on plant gene expression, in the presence and absence of bacterial ACC deaminase, and the transcriptional changes induced within non-transformed plants by nickel.

Chapter 2

Materials and Methods

2.1 Plant varieties

This work was performed using *Brassica napus* var. Westar also known as canola. Transgenic lines were created, that contain the ACC deaminase structural gene (AcdS) from *Pseudomonas putida* UW4, by Dr. Saleh Shah at the Alberta Research Council. One transgenic line, designated here as trAcdS-*35S*, contains the ACC deaminase gene under transcriptional control of the constitutively expressed CAMV*35S* promoter from cauliflower mosaic virus (Olszewski *et al.*, 1982). The other line, designated here as trAcdS-*rolD*, contains the ACC deaminase gene under the control of the root specific *rolD* promoter from the *Agrobacterium rhizogenes* Ri plasmid (Elmayan and Tepfer, 1995). These lines were created through *Agrobacterium tumefaciens* transformation of canola callus culture. Both of the transgenic canola lines used in this work were homozygous for the ACC deaminase transgene, the trAcdS-*35S* and trAcdS-*rolD* plants containing one and two copies of the ACC deaminase gene respectively (Sergeeva *et al.*, 2006).

2.2 Plant growth conditions

Prior to planting, all seeds were surface sterilized as follows, regardless of the medium used for growth: first seeds were soaked in 70% ethanol for one minute, then in 1% bleach solution for ten minutes followed by several changes of sterile Milli-Q water. Plants were grown inside of growth chambers with the following parameters: 12-hour photoperiod, light intensities of 50 μmol m^{-2}s^{-1} for the small chamber and 200 μmol m^{-2}s^{-1} for large chambers, and a constant temperature of 20 °C. Four different growth protocols were employed: Murashige and Skoog (MS) growth medium in petri plates, growth pouches, soil and vermiculite; each of which will be described below.

2.2.1 Plate method

To study any differences in the development of non-transformed and trAcdS-*rolD* seedlings, surface sterilized seeds were germinated on one-half concentration MS media in petri plates. Plates were sealed with parafilm, placed in a small growth chamber with the conditions described in Section 2.2 and changes monitored every day for four days.

2.2.2 Growth pouch method

To study germination rates and tolerance of seedlings to nickel, non-transformed, trAcdS-*35S*, and trAcdS-*rolD* seeds were surface sterilized then planted in growth pouches (six per pouch) (Cyg seed germination pouch, Mega International) containing either solutions of $NiSO_4 \cdot 6H_2O$ or pure distilled deionized water with ten pouches per treatment. These growth pouches allow the observation of seed germination, seedling morphology and root and shoot length at all stages of development. After planting, the seeds were covered with aluminum foil, to maintain a dark environment, and placed in a small growth chamber under the conditions described in Section 2.2. Two days after planting, when the cotyledons began to emerge from the seed coat, the aluminum foil was removed and plastic wrap was used to maintain a moist environment for the seedlings. Approximately four days post planting, the plastic wrap was removed to allow elongation of seedling shoots. Root and shoot measurements were made on the fifth day post planting, with 60 seeds per treatment and the experiment was performed in triplicate.

2.2.3 Soil method

Mature plants used in the nickel tolerance studies and expression profiling were grown in soil. Seeds were surface sterilized, as above, then planted in Promix BX greenhouse mix (Premier Horticulture) containing 75-85% (v/v) sphagnum peat moss, perlite, vermiculite, macronutrients (calcium, magnesium, nitrogen, phosphorous, potassium and sulphur), micronutrients (boron, copper, iron, manganese, molybdenum and zinc), dolomitic limestone, calcite limestone and a wetting agent. Thes plants were watered from above with tap water as needed and fertilized once a week, beginning on day 10, with a fertilizer containing 20% nitrogen, 20% phosphorous and 20% potassium (Plant Products). Nickel treated plants were grown in the same manner, yet prior to planting, a solution of $NiSO_4 \cdot 6H_2O$ (approximately 1.874 mM for 2.5 kg of soil) was added to the soil and mixed thoroughly to produce a final concentration of 175 ppm Ni. Plants were grown in a large growth chamber for 21 days under the lighting conditions described in Section 2.2.

2.2.4 Vermiculite method

Seedlings treated with bacteria and used for the expression profiling study were grown in vermiculite. Surface sterilized seeds were inoculated with a bacterial suspension as described in Section 2.3 then planted in vermiculite saturated with a hydroponic solution of 7% nitrogen, 11% phosphorous and 27% potassium at a concentration of 0.63 g/L and solution grade calcium nitrate of 0.43 g/L (Plant Products). Forty seeds were planted per nine inch pan pot and placed in a large growth chamber for six days under the lighting conditions described in Section 2.2. Clear lids were used to retain moisture and were removed after germination.

2.3 Bacterial strains

The two bacterial strains used in this work were the ACC deaminase producing strain *Pseudomonas putida* UW4 (Glick *et al.*, 1995; Shah *et al.*, 1998) and the ACC deaminase minus mutant *Pseudomonas putida* UW4 AcdS$^-$, which has a tetracycline resistance gene inserted within the coding region of the ACC deaminase gene (Li *et al.*, 2000). Both were grown at 30 °C in Bacto tryptic soy broth (TSB) (Becton, Dickinson and Company). The bacterial inoculum, for the treatment of seeds, was prepared as follows: an overnight culture (5 μl frozen stock in 7.5 ml TSB) was centrifuged at $8000\times g$ for 10 minutes at 4 °C; the cells were then resuspended in 5 ml 0.05 M $MgSO_4$ and centrifuged again as above; this step was repeated then the final pellet was resuspended in enough 0.05 M $MgSO_4$ to obtain a final OD_{600} of 0.5. Bacterial inoculation of seeds was performed by soaking surface sterilized seeds in either the bacterial solution or 0.05 M $MgSO_4$ for one hour prior to planting.

2.4 Biomass of plant tissues

To measure the biomass of mature plants in the nickel tolerance study, shoots and roots were detached from one another and washed with 5 mM EDTA, then three changes of Milli-Q water. Fresh weights were recorded after which plant tissues were dried at 80 °C for two to three days to obtain dry weights and for use in the nickel accumulation study. Measurements were made with seven plants per treatment and the experiment was done in triplicate.

2.5 Chlorophyll measurements

Levels of chlorophyll a and b were measured from fresh leaf disks, one centimeter in diameter, using the method outlined in Hiscox and Israelstam (Hiscox and Israelstam, 1979), where DMSO was used to extract total chlorophyll from tissues without maceration. The concentration of chlorophyll was calculated using the method of Moran and Porath (Moran and Porath, 1980). Measurements were taken for one leaf disk from each of five plants per treatment and the experiment was done in duplicate.

2.6 Nickel accumulation

Dried plant material was processed as described in (Stearns *et al.*, 2005), then nickel concentration of tissues was measured using graphite furnace atomic absorption spectrophotometry (Varian SpectrAA 880 spectrophotometer with GTA-100 graphite furnace attachment). These measurements were made with seven samples per treatment and the experiment was done in triplicate.

2.7 RNA isolation

Plant tissues were separated from the whole plant, placed directly into liquid nitrogen, and then stored at $-80\,^{\circ}\mathrm{C}$ until needed. RNA was isolated using the method outlined in (Davis *et al.*, 1986) with a few modifications. GIT buffer was prepared which contains 4 M guanidine isothiocyanate, 3 M NaOAc at pH 6.0 and 8.35 ml β-mercaptoethanol (100%) per liter of buffer (added just prior to use). Frozen tissue was homogenized to a fine powder in a mortar and pestle with liquid nitrogen, then added to 10 ml GIT buffer. This mixture was filtered through two layers of MiraCloth (Calbiochem) then centrifuged at $30{,}000\times g$ in a Sorvall RC 5B Plus centrifuge with an SS-34 rotor. The supernatant was gently layered onto 3.3 ml of 5.7 M CsCl (made without the addition of sodium acetate) in a 30 ml ultracentrifuge tube (Beckman). These were loaded into a SW-41Ti rotor and centrifuged at $116{,}000\times g$ and $10\,^{\circ}\mathrm{C}$ for 23 hours in a Beckman-Coulter Optima L-90K Ultracentrifuge. The supernatant was then removed and the pellet at the bottom of the tube (containing the RNA) was washed with 70% ethanol then suspended in 500 μl of suspension buffer (1:5 3 M NaOAc pH 5.5 to water). Two volumes of ice cold 100% ethanol were added to each tube, which were then stored at $-80\,^{\circ}\mathrm{C}$ for $\geq$1hour, or until needed. Samples were centrifuged at $20{,}000\times g$ in a microcentrifuge at 4 °C for 1 hour, after which the supernatant was removed and the tube refilled with 1 ml 70% ethanol. These were centrifuged again under the same conditions for 30 minutes, after which the supernatant was carefully removed. Pellets were either air dried or dried in a rotary desicator for approximately 10 minutes to remove all traces of ethanol, being careful not to over-dry the samples. Pellets were suspended in between 50 and 500 μl water depending on the size. All buffers and dilutions were performed with RNAse-free water, made either by treatment with diethylpyrocarbonate (DEPC) or purchased from Wisent.

Quantitation was performed by spectrophotometry and the absorbance of each sample was scanned from 230 – 320 nm. The amount of RNA and its purity were estimated as follows:

$$\text{Adjusted OD}_{260} = \text{OD}_{260} - |\text{OD}_{240} - \text{OD}_{280}| - \text{OD}_{320} \tag{2.1}$$

$$\text{Total RNA concentration } (\mu\text{g}/\mu\text{l}) = (\text{Adjusted OD}_{260} \times 40 \times \text{df}) \div 1000 \tag{2.2}$$

$$\text{Protein contamination} = \text{OD}_{260} \div \text{OD}_{280} \tag{2.3}$$

$$\text{Starch contamination} = \text{OD}_{260} \div \text{OD}_{230} \tag{2.4}$$

All RNA used had a value for equation 2.3 of between 1.80 and 2.00, and a value for equation 2.4 >2.00. RNA samples with a value for equation 2.3 below 1.85 were further purified using the Qiagen RNeasy Midi kit, where only 100 μg of RNA was cleaned at a time. RNA samples were then stored at -80 °C until needed.

Upon thawing, the integrity of RNA samples was checked by denaturing formaldehyde gel electrophoresis. Briefly, a denaturing formaldehyde gel, containing MOPS buffer (20 mM 3-N(morpholino) propane sulfonic acid, 5 mM NaOAc and 1 mM EDTA), 1% agarose and 18 ml/L formaldehyde (37%) was loaded with the RNA sample in loading buffer containing 0.25 μg ethidium bromide per sample and run in MOPS buffer, first for 10 minutes at 150 V then for 20 minutes at 75 V.

2.8 Microarray experiments

2.8.1 Experimental design

Two experimental designs were used for the microarray experiments in this work (Figure 2.1). For expression studies of seedlings either treated with bacteria or expressing the ACC deaminase transgene, seeds germinated in vermiculite as described in Section 2.2.4, were compared to controls using the experimental design in Figure 2.1A. In this case C = non-transformed untreated seedlings, tr = trAcdS-*rolD* seedlings, T_1 = non-transformed seedlings inoculated with AcdS^+ bacteria and T_2 = non-transformed seedlings inoculated with AcdS^- bacteria. Each direct comparison (solid arrows) was performed in triplicate where the Cy dyes were swapped for the third replicate. This resulted in a total of 18 hybridizations since the experiment was performed on shoot and root tissues. Data analysis, described in Section 2.8.3, was performed separately for shoot and root tissue and for trAcdS-*rolD* and bacterial treatments.

For expression studies of mature (three week-old) plants expressing the ACC deaminase transgene (trAcdS-*rolD*) and plants exposed to nickel (as described in Section 2.2.3) were compared to control plants using the experimental design in Figure 2.1B. Here C = non-transformed untreated plants, tr = trAcdS-*rolD* plants, and T_1 = plants grown in nickel-spiked soil . Each direct comparison (solid arrows) was done twice where the Cy dyes were swapped for the second replicate. This resulted in a total of 8 slides. Data analysis, described in Section 2.8.3, was performed separately for shoot and root tissues.

2.8.2 Labeling, hybridization and scanning

Arabidopsis II Oligonucleotide arrays and all labeling and hybridizing reagents were purchased from Agilent Technologies, with the exception of the cyanine-3 and cyanine-5 labelled dCTPs which were purchased from Perkin Elmer. The term "probe" refers to the oligonucleotide molecule attached to the solid surface of the slide and "target" refers to the labeled cDNA (made from canola mRNA) in solution (Southern *et al.*, 1999). Target preparation

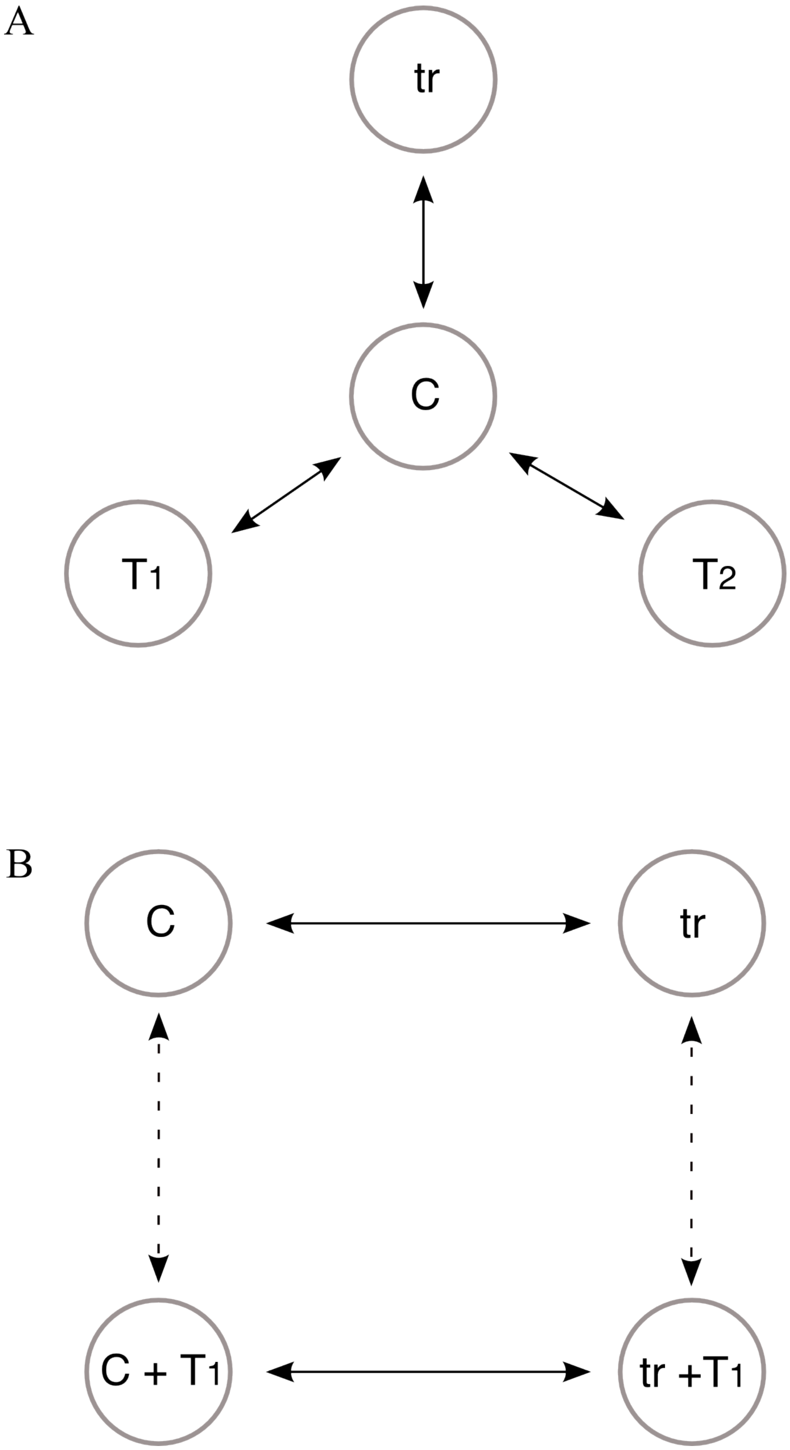

Figure 2.1: The two experimental designs used for microarray experiments. Solid arrows denote direct comparisons made on the same slide, whereas dotted arrows denote indirect comparisons made between treatments not present on the same slide. The scheme represented in (A) was used with seedlings and the scheme represented in (B) was used with mature plants. C: contol; T_1 and T_2: treatments; tr: transgenic plant.

was performed as described in the Agilent Fluorescent Direct Label Kit protocol (v 2.1) and hybridizations were carried out as recommended in the Agilent Oligo Microarray Kit Hybridization Protocol (v 5.0). For the mature plant experiment, hybridized slides were scanned with a ChipReader (Virteck Vision Intl) with software v 2.0. For the seedling experiment scanning was performed on the GenePix Professional 4200A scanner (Molecular Devices) with software v 6.0. For seedling shoots two scans per slide were carried forward for data analysis, whereas one scan per slide was used for all other samples. An example image produced by the GenePix scanner is presented in Figure 2.2.

2.8.3 Data analysis

Background correction and normalization

Raw data was imported into the R environment (v 2.5.0; an open-source project for statistical computing available at www.r-project.org) and analyzed using the LIMMA library (Linear Models for Microarray Data, v 2.10.5) (Smyth, 2004) of the bioconductor package (Gentleman *et al.*, 2004). Due to the different levels of background in each study, two types of background correction were used. For the analysis of seedlings, where background values were uniform and low, pure subtraction of background intensity values from the foreground intensity values was used. For the analysis of mature plants treated with nickel, background was uniform and moderately high throughout most of the signal range, and was extremely high for saturated spots. The assumption was made that the high background estimates were outliers and a 3 by 3 grid smoothing correction was used to replace these with more reasonable values. Specifically, each spot then used, as its background estimate, the minimum of its background and the background of its eight immediate neighbours, an approach called the "moving minimum" in the LIMMA package (Smyth and Speed, 2003). These smoothed background estimates were then subtracted as normal from the signal. This produced many negative and miniscule positive values. In an attempt to estimate a practical minimum intensity, positive signal intensities were rank ordered (on each array) and the bottom 0.1%

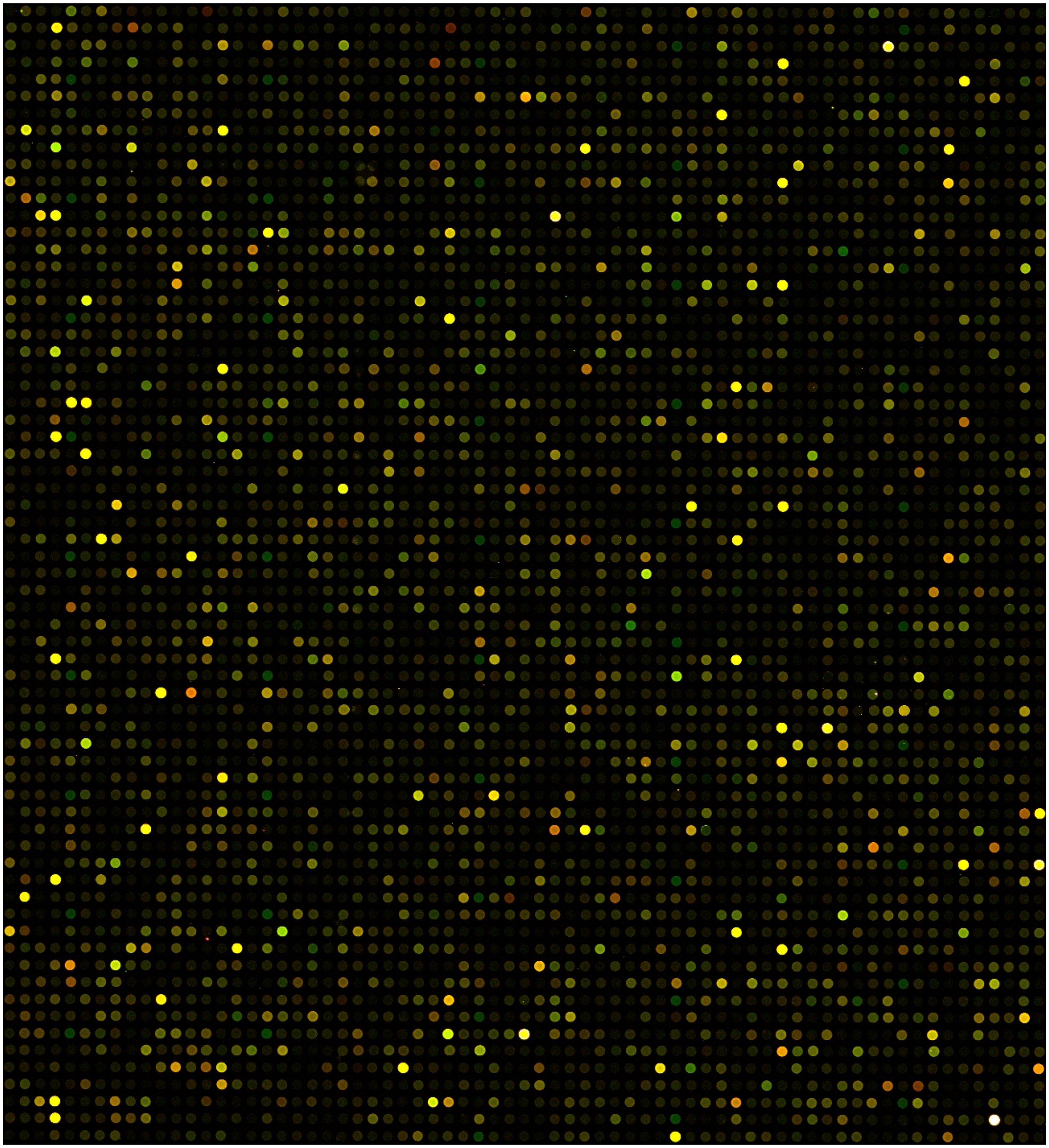

Figure 2.2: Close-up of the fluorescence image of a microarray slide produced with GenePix Pro 4200A scanner. This image represents approximately one-quarter of a whole slide.

quantile was estimated. This value was then used in place of any lower signal.

All other steps were performed the same way for the two studies. LOESS normalization was used to correct for within-array dye and spatial effects then these values were quantile normalized across arrays (Smyth, 2004). The two-replicate scans per slide (for seedling shoots only) were used to maximize the robustness of each gene's differential expression measurement via the lmFit function within LIMMA. This step uses a pooled correlation estimate to generate a more robust estimate of the gene expression across replicates, compared to a straight average of replicates. MvA plots or pre- and post-normalization intensity values are presented in Appendix B. Moderated t-statistics were computed for each gene based on an empirical Bayes method (Smyth, 2004), which shrinks the standard errors towards a common value. Adjustment of p-values was performed using the Benjamini and Hochberg multiple testing procedure (1995). Background correction, LOESS normalization and p-value adjustments were performed by Owen Woody in the Biology Department at the University of Waterloo.

Venn diagrams of total transcriptional changes were created using the online tool VENNY by Oliveros, J.C., 2007 (http://bioinfogp.cnb.csic.es/tools/venny/index.html).

Clustering

Clustering was performed using Cluster v 3.0 for Mac OS X (C Clustering Library 1.36) based on the open source program by the same name (Eisen *et al.*, 1998). Two-dimensional hierarchical clustering of normalized intensity ratios was performed using centered correlation and centroid linkage parameters, where genes and arrays were clustered based on similarity. Clusters were visualized using the open source program Java TreeView v 1.1.1 (Saldanha, 2004). Both Cluster for Mac OS X and Java TreeView are available from (http://bonsai.ims.u-tokyo.ac.jp/˜mdehoon/software/cluster/software.htm#ctv).

Functional categorization

Functional categorization of gene lists was performed using the FatiGO tool from the Babelomics suite of web tools available through the Principe Felipe Centro de Investigacion web site (babelomics2.bioinfo.cipf.es/cgi-bin/tools.cgi) (Al-Shahrour *et al.*, 2004). This tool was used to extract Gene Ontology (GO) terms from the gene lists in Appendix C. The proportion of genes assigned to each GO term was then plotted alongside the proportion of genes for each GO term for all genes on the array (total) and presented graphically using KaleidaGraph v 3.6 (Synergy Software).

Metabolic pathway assignment

Genes from the lists in Appendix C were assigned to biochemical pathways using the AraCyc database v 4.1 and Pathway Tools v 11.0 Omics Viewer (information available at http://bioinformatics.ai.sri.com/ptools/) available through the Arabidopsis information resource website (TAIR, www.arabidopsis.org). This release contained 283 pathways with 1901 unique genes assigned to pathways, 90% of which were experimentally confirmed. The remaining 10% were validated by a curator who assessed that their computational prediction was justified based on a number of cues from the literature. The Pathways Tool Omics Viewer can be used to paint microarray data onto the metabolic overview diagram for Arabidopsis and to visualize individual pathways, however, this data is not presented here.

2.9 Validation of microarray experiments

In order to quantify transcript levels of *Brassica napus* genes which showed differential expression on the Arabidopsis microarray, real-time RT-PCR was used. Since the microarray experiment was heterologous a few extra steps were necessary to ensure that the right transcripts were being quantified. This is summarized in Figure 2.3 and described below.

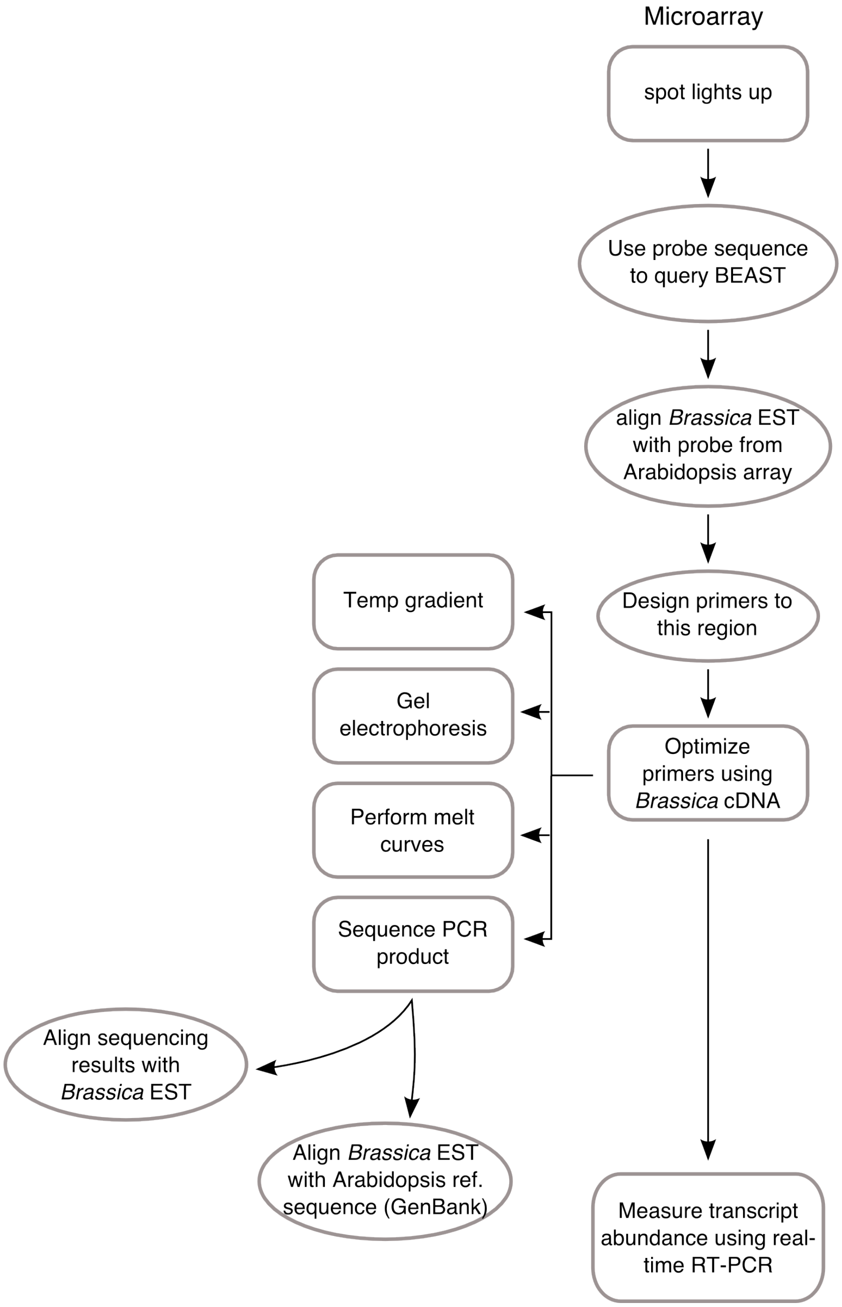

Figure 2.3: Workflow for validation of microarray expression data using real-time RT-PCR. Steps within boxes indicate work done at the bench and steps within ovals indicate work done on the computer.

2.9.1 Primer design

Probe sequences (60-mer oligonucleotides Table 2.1) were chosen for genes which had expression ratios of >2.0 or <0.5 fold then used to query the *Brassica* EST database BEAST, which is housed at the Saskatoon Research Center (Molecular Genetics Section, Agriculture and Agri-Food Canada). This database contained sequences from 31 *Brassica* EST libraries comprising 148,956 sequences and 84,143,936 total letters. The best EST was aligned with the probe from the microarray chip using ClustalW on the EMBL-EBI server (http://www.ebi.ac.uk/Tools/clustalw) and visualized using the open source program JalView v 2.3 (Clamp *et al.*, 2004). Primers were then designed so that part of the PCR product overlapped with the region where the probe aligned with the *Brassica* EST sequence (Table 2.2). Organization and visualization of primers was performed with the help of the open source program AmplifX v 1.4.0 by Nicolas Jullien (http://ifrjr.nord.univ-mrs.fr/AmplifX-Homepage?lang=en). Primer optimization was performed as follows: PCR with each primer set and *Brassica napus* cDNA as the template was performed at five annealing temperatures from 55 to 63 °C, in order to choose the highest temperature which produces one band. Products were separated on 4% agarose gels containing 0.05 μg ethidium bromide (Figure 3.10 in Section 3.1.5) and primers which still produced non-specific binding or primer dimers at the highest temperature were redesigned. RT-PCR products were sequenced at York University's core biological facility which uses the BigDye Terminator chemistry on the Applied Biosystems 337 DNA Sequencer (Heiner *et al.*, 1998). Resulting sequences were used to query the GenBank nt database for Brassicaceae (taxid:3700) and in every case the Arabidopsis ref sequence for the gene of interest appeared in the results list with very low expect scores (Table 3.3 in Section 3.1.5). Ten primer sets were carried forward for use in real-time RT-PCR (Table 2.2).

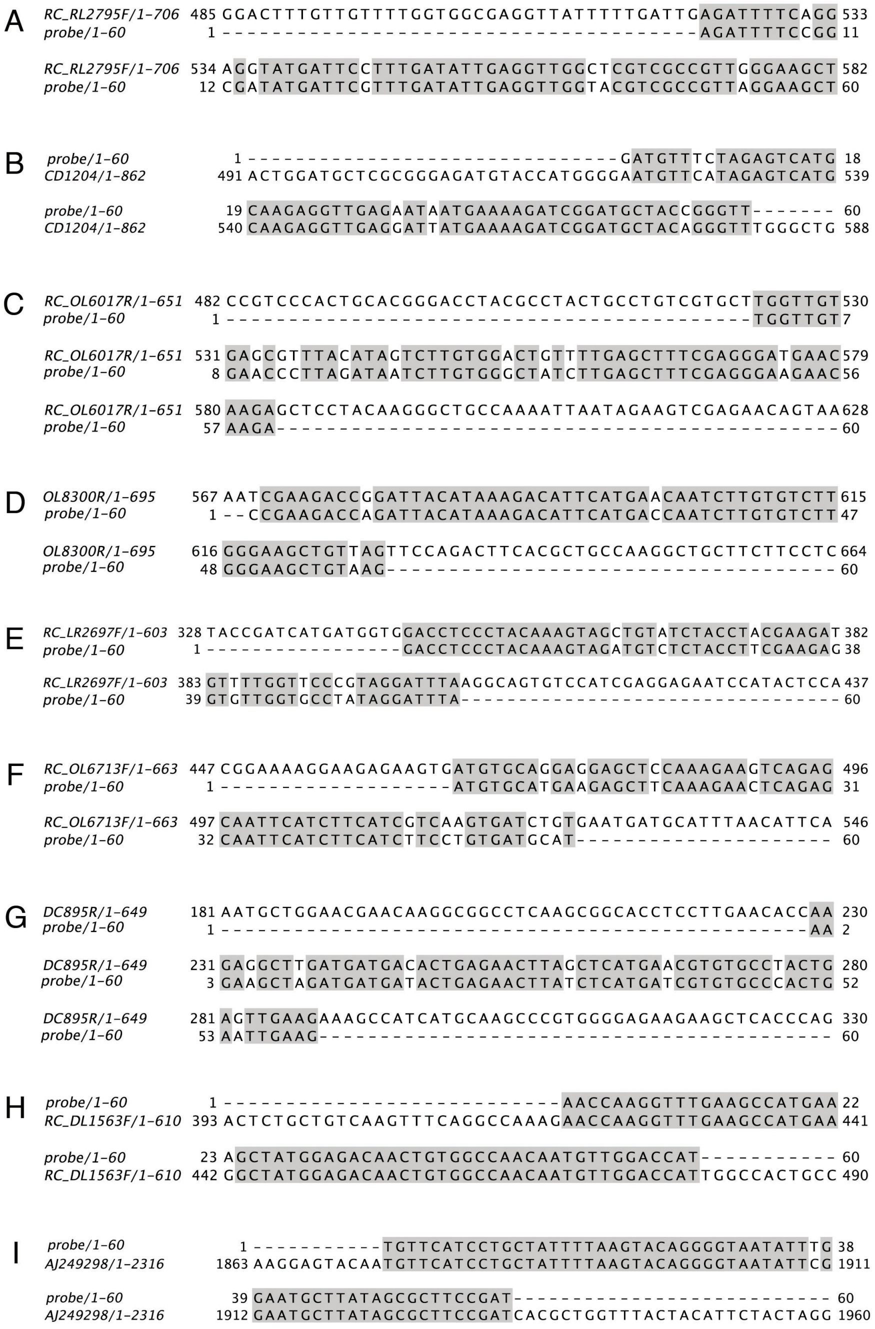

Figure 2.4: Alignments between probes from Arabidopsis microarray and the matching region from *Brassica* ESTs; A) AT5G42650, (B) AT3G15540, (C) AT2G14610, (D) AT4G25100, (E) AT2G43910, (F) AT5G07580, (G) AT3G58680, (H) AT1G05010, (I) AT1G70940.

Table 2.1: The TAIR locus identifiers and microarray probe sequences used to query the *Brassica* EST database (BEAST).

Locus	Probe sequence	Description
AT5G42650	AGATTTTCCGGCGATATGATTCGTTTGATATTGAGGTTGGTACGTCGCCGTTAGGAAGCT	AOS (allene oxide synthase)
AT3G15540	GATGTTTCTAGAGTCATGCAAGAGGTTGAGAATAATGAAAAGATCGGATGCTACCGGGTT	transcription factor (IAA19)
AT2G14610	TCTTGTTCTTCCCTCGAAAGCTCAAGATAGCCCACAAGATTATCTAAGGGTTCACAACCA	PR1 (pathogenesis-related gene 1)
AT4G25100	CCGAAGACCAGATTACATAAAGACATTCATGACCAATCTTGTGTCTTGGGAAGCTGTAAG	FSD1 (Fe superoxide dismutase 1)
AT2G43910	GACCTCCCTACAAAGTAGATGTCTCTACCTTCGAAGAGGTGTTGGTGCCTATAGGATTTA	thiol methyltransferase
AT5G07580	ATGTGCATGAAGAGCTTCAAAGAACTCAGAGCAATTCATCTTCATCTTCCTGTGATGCAT	ERF (ethylene response factor)
AT3G58680	AAGAAGCTAGATGATGATACTGAGAACTTATCTCATGATCGTGTGCCCACTGAATTGAAG	ethylene-responsive transcriptional coactivator
AT1G05010	AACCAAGGTTTGAAGCCATGAAAGCTATGGAGACAACTGTGGCCAACAATGTTGGACCAT	1-aminocyclopropane-1-carboxylate oxidase
AT1G70940	TGTTCATCCTGCTATTTTAAGTACAGGGGTAATATTTGGAATGCTTATAGCGCTTCCGAT	auxin transport protein (PIN3)

Table 2.2: Primer sequences used for real-time RT-PCR. Asterisks denote sequences not present in GenBank and lower case letters denote where the primers overlapped with the probe binding site. AF044573 is *Brassica oleracea* actin (Act1).

Locus	*Brassica* sequence ID	Forward primer	Reverse primer	Product length
AT5G42650	RL2795*	AATAAACAGTGCGCCGGTAAGGAC	TGAATGTAACGGagcttcccaacg	130
AT3G15540	CD1204*	CGACACCGCTTTCACATTGATCAC	TGGACTCGGGCTTGAGATAACTGA	134
AT2G14610	OL6017*	TCCCCGAGGATCATAGTTGCAAGA	ACTACGCTTCGAACACGTGCAT	143
AT4G25100	OL8300*	ATTGACGTCTGGGAGCATGCTTAC	GCAGCGTGAAGTCTGGAACTAACA	119
AT2G43910	LR2697*	TGTGCCATTGAGCCTGAGATGAG	cctacgggaaccaaaacatcttcg	167
AT5G07580	OL6713*	TGACTGTGCAGCTTTCAAGCTC	gacgatgaagatgaattgctctgac	159
AT3G58680	DC895*	catgaacgtgtgcctactgagttg	TCGGTATTGCTTTCCCAGACTCGT	142
AT1G05010	DL1563*	ATAGCTCAAACGGACGGAGAAGG	ttggccacagttgtctccatagc	214
AT1G70940	AJ249298	GAGGGAGAAGGAAGACGAGAATGT	TCTCGTTGCCCCATGTTTTGCT	208
-	AF044573	TTGGGATGAACCAGAAGGACG	GCTCGTTGTAGAAAGTGTGATGCC	147

2.9.2 Real-time RT-PCR

One μg of RNA from each sample was reverse transcribed in a 20 μl volume using SuperscriptIII (Invitrogen) with oligoTd$_{17}$ primers at a concentration of 1 μM (Sigma), then treated with RNAse H (Ambion). The resulting pool of cDNA was then PCR amplified with the iScript master mix (BioRad) in a 20 μl reaction volume containing 2 μl cDNA, and 0.5 μM of both the forward and reverse primers (Sigma). PCR was performed in the BioRad MiniOpticon thermal cycler with the following cycles: denaturation for 10 seconds at 95 °C; annealing for 20 seconds at 62 °C; extention for 20 seconds at 72 °C; for 40 cycles followed by a melting curve measured in 0.5 °C increments. Relative transcript levels were measured, which compares amplification measurements for target genes to that of a reference gene. Actin 1 (AF044573) from *Brassica oleracea* was used as the reference gene and calculations of transcript abundance were performed using the Livak method (Livak and Schmittgen, 2001). Experiments were done in triplicate with mRNA from seperate isolations.

Chapter 3

Results

3.1 The role of ACC deaminase in PGPR-induced plant growth

The bacterium *Pseudomonas putida* UW4 has been studied extensively for its plant growth-promotion and has been shown to produce high levels of ACC deaminase. Inoculation of plant seeds and roots with this microorganism lead to increases in plant biomass, root length (Figure 3.1) and lower stress symptoms. Expression of the ACC deaminase enzyme, by the bacteria, lowers plant ethylene levels which in turn lowers plant stress. In order to study the changes that occur within the plant in response to colonization of the roots by this microorganism, and to gain insight into the function of the ACC deaminase enzyme in this interaction, microarray experiments were performed. Global expression changes that occur within tissues of six day-old seedlings treated with *Pseudomonas putida* UW4, either with or without the ACC deaminase enzyme (AcdS^{+} and AcdS^{-}, respectively) were compared with untreated seedlings.

Microarrays are a powerful tool because they provide a bird's eye view of all expression changes occurring due to a specific treatment or developmental change. However, because of the large amount of data generated and the small number of replicates that can be done,

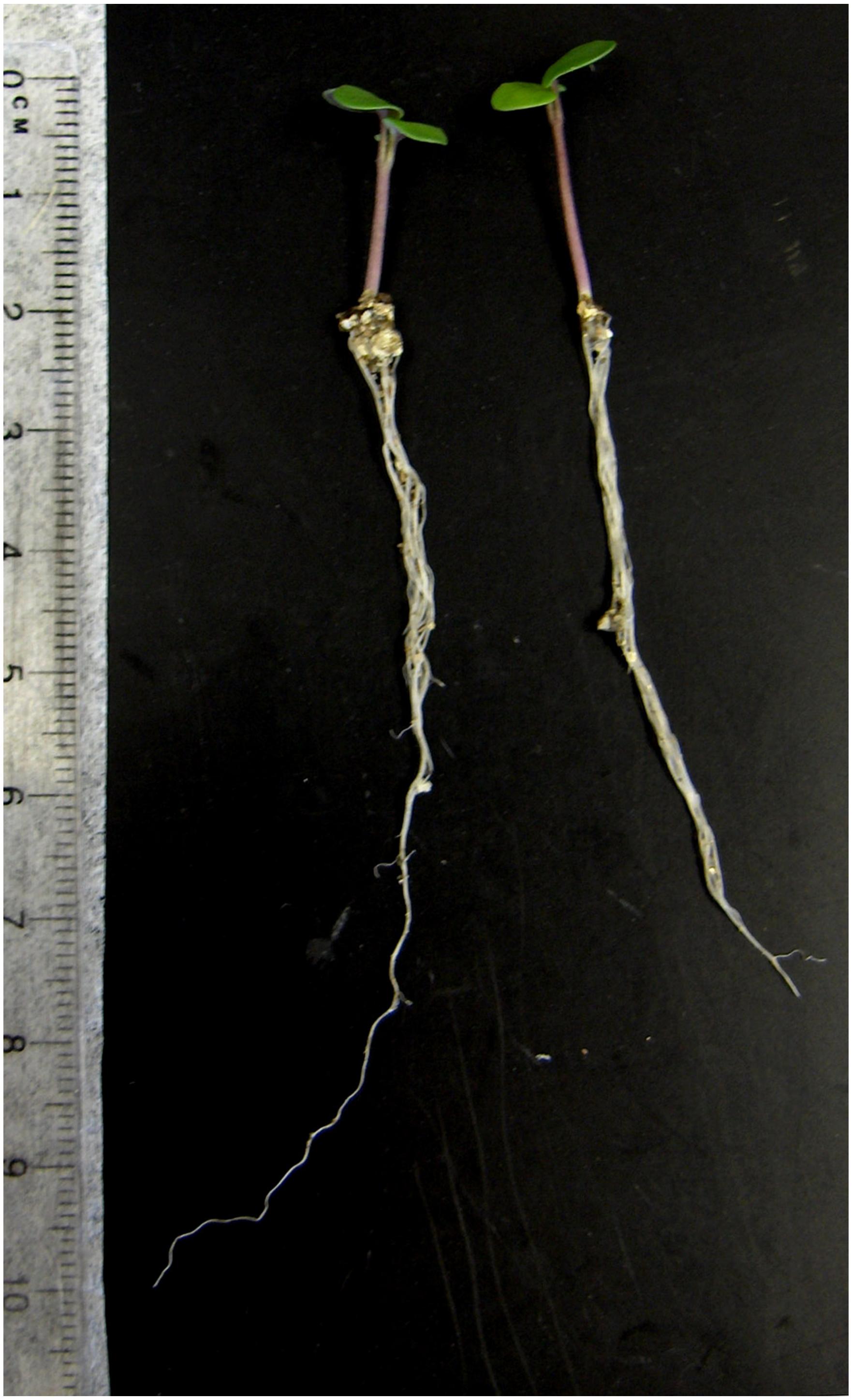

Figure 3.1: Six day-old seedlings inoculated with *Pseudomonas putida* UW4 AcdS$^+$ bacteria (left) and uninoculated (right).

microarrays provide some unique statistical challenges. Correction for type I errors (false-positives) is difficult without good estimates of variance, especially when the data is noisy or the number of replicates is low. To solve for this, multiple testing is used but many of these methods are very conservative. The correction method of Benjamini and Hochberg (1995) is the least conservative and provides an adjusted p-value based on the false discovery rate (FDR). This method, however, still excludes a lot of data since it attempts to maintain control over the FDR while assuming that the t-statistic is independent (Yang and Speed, 2003). Keeping this in mind, the results of this experiment fall into two categories: those genes that pass a cut-off of $p = 0.05$ after FDR correction (denoted as FDR adj. $p < 0.05$); and those which pass a cut off of $p = 0.01$ without FDR correction (denoted as $p < 0.01$). The second group do not quite meet the FDR threshold yet have a significant pattern of expression and biological significance to this study.

The number of changes with FDR adj. $p < 0.05$ are summarized in Figure 3.2 and lists of significant changes are presented in Tables C.1 and C.2 in Appendix C. In shoots of seedlings treated with either AcdS^{+} or AcdS^{-} bacteria, 965 genes showed differential expression (406 of which were common), whereas only 223 genes showed differential expression in the roots (with 128 in common).

3.1.1 Functional categorization of expression data

Genes from Tables C.1 and C.2 were grouped by the functional categorization of their gene ontology (GO) terms. Figure 3.3, 3.4 and 3.5 show the proportion of genes from the two treatments over-represented in each category (biological function level 3) when compared to all the genes represented on the microarray (total). If the number of genes for a particular GO term exceeds the number of genes from the total that fall into that same GO term category, then it is said to be over-represented in that treatment. The number of genes whose expression was up-regulated in the roots of plants with either bacterial treatment was very small, and since functional categorization reports trends in the data as a proportion of genes under each GO term over the total number of genes changed in each treatment, this analysis was not appropriate, therefore only metabolic pathway assignment was performed with root data.

In shoots of plants treated with either *Pseudomonas putida* UW4 AcdS$^+$ or the AcdS$^-$ mutant, genes involved in response to stimuli, catabolic processes and response to stress were up-regulated and over-represented compared to the total (Figure 3.3). Genes involved in biosynthetic process, response to stress, secondary metabolism and defense response were over-represented and down-regulated (Figure 3.4). In roots of plants treated with both bacteria, biosynthetic processes, response to stress, defense response and response to a biotic stimulus were down-regulated and over-represented (Figure 3.5).

In tissues of seedlings treated with AcdS$^+$ bacteria, catabolic processes and nitrogen compound metabolism were down-regulated and over-represented. Aside from the above changes, in shoots of plants treated with the AcdS$^-$ bacteria, genes involved in response to stress, response to stimuli, the defense response, secondary metabolite production and death were up-regulated and over-represented (Figure 3.3). Genes involved in the response to endogenous and external stimuli, cell organization and biogenesis were over-represented and down-regulated in shoots of plants treated with AcdS$^-$ bacteria (Figure 3.4). Genes involved in response to abiotic and chemical stimuli, response to stress and catabolic processes were over-represented and down-regulated in roots and shoots of plants treated with the AcdS$^+$ bacteria (Figures 3.4 and 3.5).

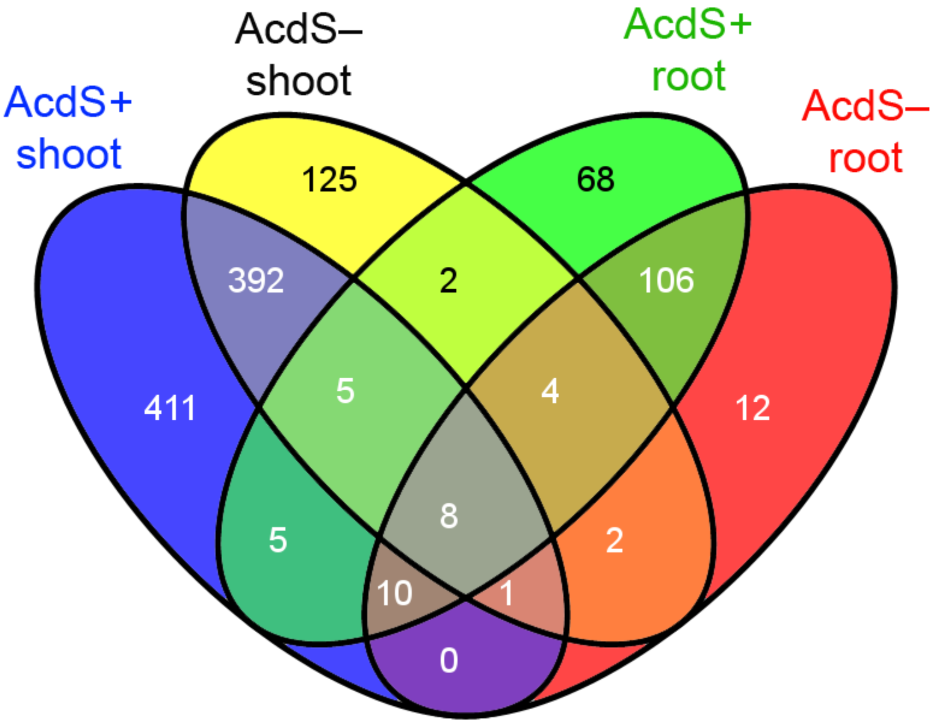

Figure 3.2: Venn diagram representing the number of genes whose expression changed (FDR adj. $p<0.05$) in tissues of plants treated with bacteria.

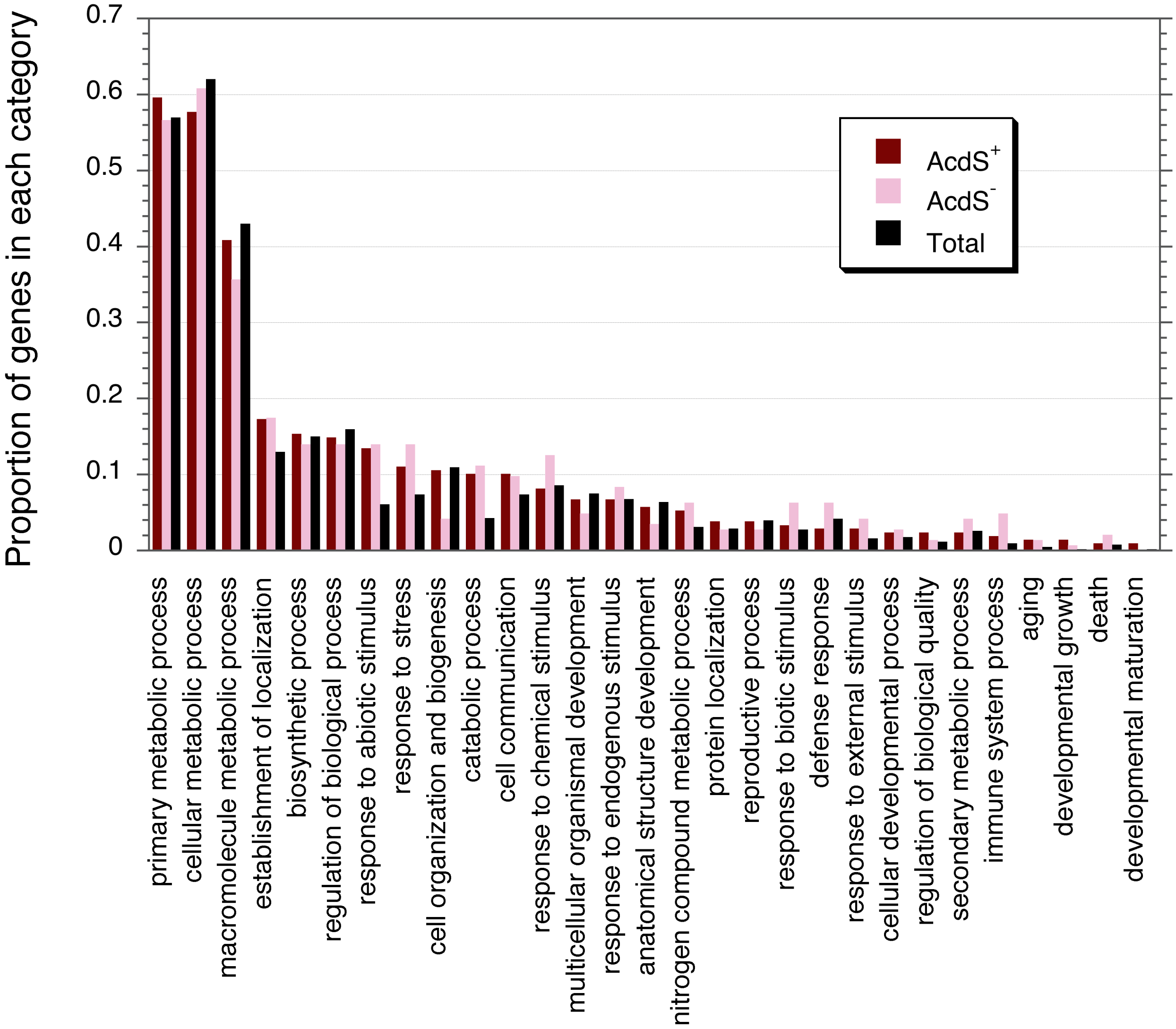

Figure 3.3: Functional categorization of genes up-regulated in the shoots of plants treated with bacteria. Gene Ontology terms, biological process level 3.

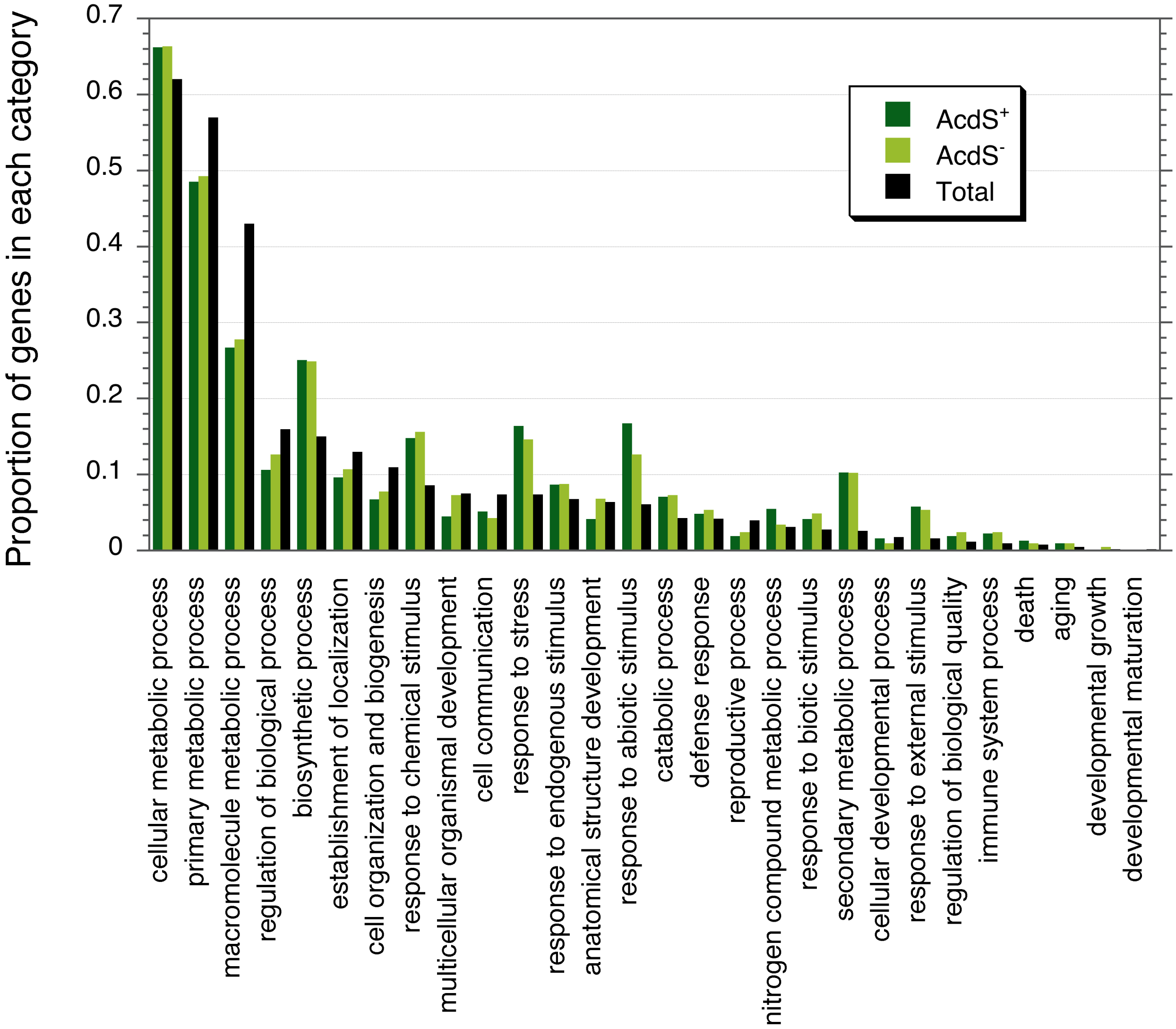

Figure 3.4: Functional categorization of genes down-regulated in the shoots of plants treated with bacteria. Gene Ontology terms, biological process level 3.

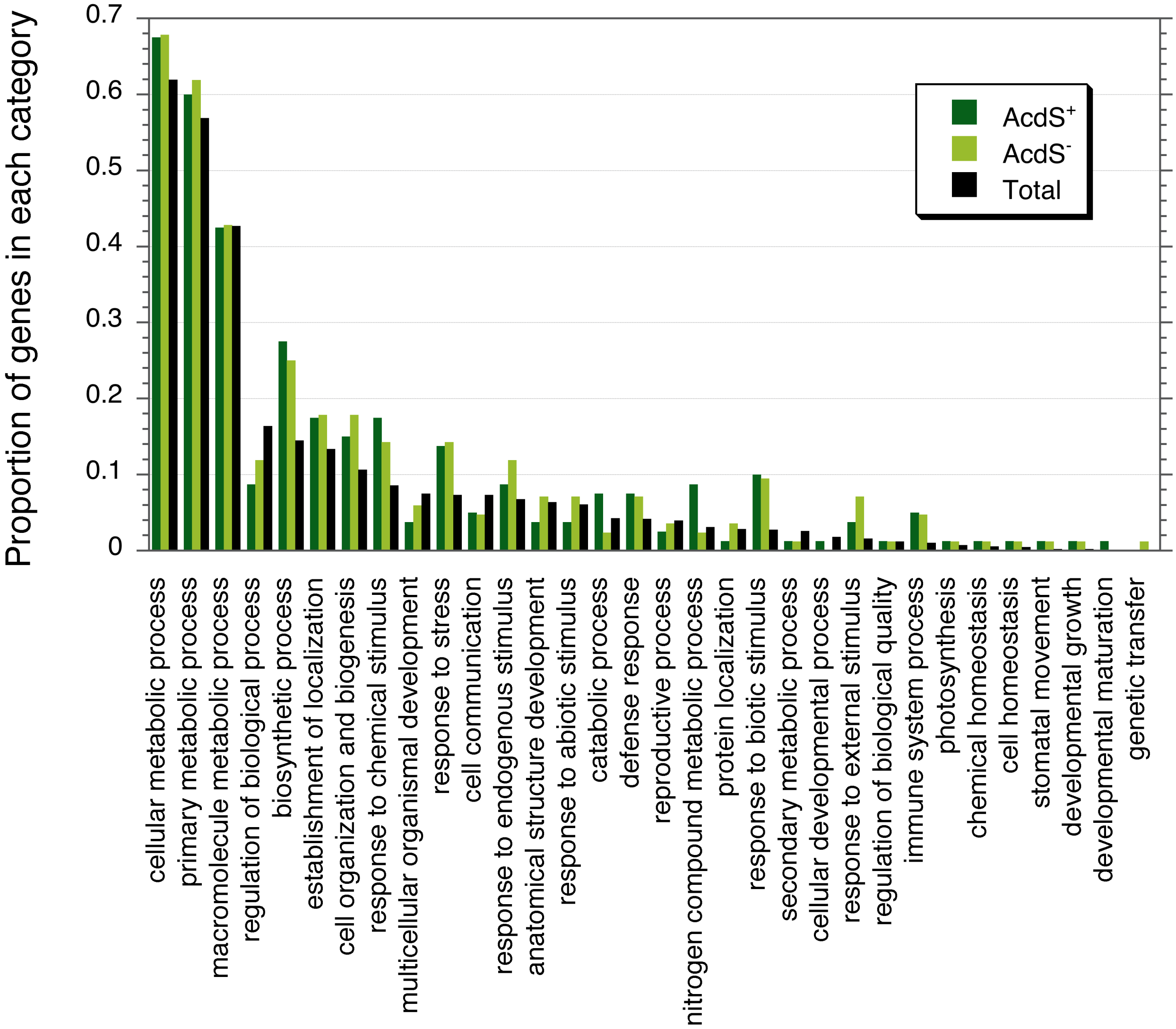

Figure 3.5: Functional categorization of genes down-regulated in the roots of plants treated with bacteria. Gene Ontology terms, biological process level 3.

3.1.2 Metabolic pathways

All genes from Tables C.1 and C.2 were analyzed using the TAIR Pathway Tools Omics Viewer, and any genes for which a biochemical function had been predicted (either biochemically or computationally) were mapped to specific metabolic pathways. These results are presented in Table A.1 in Appendix A and summarized in Table 3.1 and 3.2.

Expression of genes involved in the biosynthesis of phytohormones changed in the presence of bacteria. For instance IAA, cytokinin, ABA (phaseic acid) and the plant signaling molecule salicylic acid (SA) biosynthesis genes were down-regulated in the presence of both bacteria. Ethylene biosynthesis gene expression was different between plants treated with AcdS$^+$ and AcdS$^-$ bacteria (Figure 3.6). For instance, in the presence of the AcdS$^-$ mutant, one ACC oxidase gene was up-regulated (EFE), whereas in the presence of the AcdS$^+$ bacterium one ACC synthase gene (ACS8) and one ACC oxidase gene (EFE) were up-regulated and two other ACC oxidase genes (AT2G30830 and AT2G25450) were down-regulated. The change in expression of the ACC oxidase gene EFE (AT1G05010) was verified through real-time RT-PCR (Figure 3.13). Expression of the jasmonic acid biosynthesis gene (AOS) expression was up-regulated in the presence of the the AcdS$^-$ mutant, which was also verified through real-time RT-PCR (Figure 3.13).

Genes involved in carbon fixation (Calvin cycle) and carbohydrate metabolism (namely gluconeogenesis, glycolysis, lactose degradation and sucrose degradation) were up-regulated whereas trehalose biosynthesis genes were down-regulated, in the presence of both bacteria (Table A.1). Most of these carbohydrate metabolism pathways, however, were more highly up-regulated in plants inoculated with AcdS$^+$ bacteria (Table 3.1). Genes involved in lipid metabolism changed significantly in the presence of both bacteria. Namely there was a down-regulation in choline and sterol biosynthesis and glycolipid desaturation gene expression, the last of which was much more pronounced in plants inoculated with AcdS$^+$ bacteria (Table A.1). Genes involved in the biosynthesis or breakdown of cell wall components also changed significantly in the presence of both bacteria. For example, cellulose and suberin biosynthesis, pectin breakdown (homogalacturonan) and starch degradation gene expression were down-regulated. Of note was the down-regulation of a cellulose synthase-like gene (AT4G16590) by 6.2-fold in the presence of AcdS$^+$ bacteria and only 2.8-fold in the presence of AcdS$^-$ bacteria (Table A.1). Genes involved in secondary metabolism were down-regulated in the presence of bacteria (Table 3.1). For instance, anthocyanin, camalexin, carotenoid, flavonoid, flavonol, geranyldiphosphate and glucosinolate biosynthesis genes as well as glucosinolate breakdown genes were all down-regulated (Table A.1). Expression of genes involved in carbon and nitrogen balance changed in the presence of bacteria, namely glutamate degradation was down-regulated and cyanate degradation was up-regulated. Nitrogen metabolism was highly down-regulated in the presence of AcdS$^+$ bacteria as compared to plants treated with AcdS$^-$ bacteria as was sulfur metabolism but to a lesser extent.

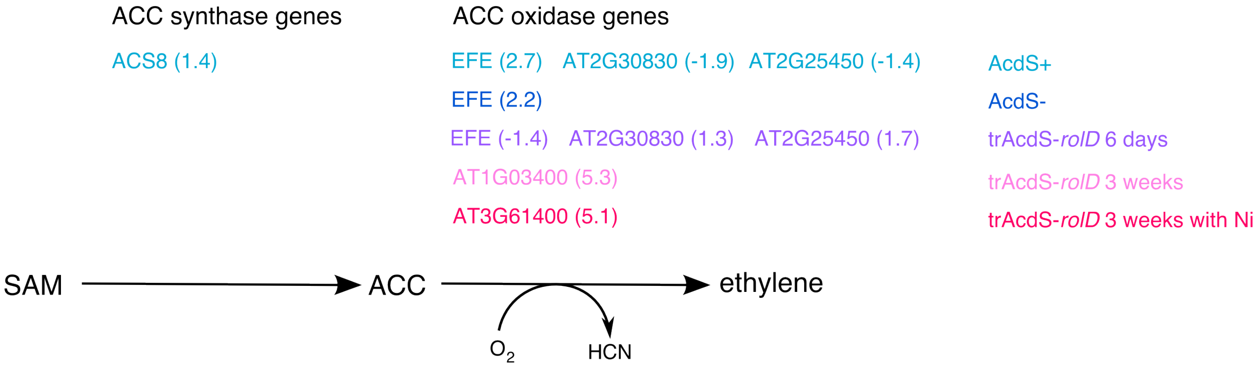

Figure 3.6: Changes in ethylene biosynthesis gene expression. Numbers in brackets signify expression fold change compared to the control.

Table 3.1: Summary of expression changes in shoots of plants treated with bacteria from Table A.1 in Section A and functional categorization data. This summary provides insight into the trends in expression changes across all experimental treatments. Expression changes for all treatments except "trAcdS-*rolD* with Ni" are relative to un-treated, non-transformed controls, whereas expression changes for "trAcdS-*rolD* with Ni" are relative to non-transformed plants with nickel. Plus signs indicate magnitude of up-regulation, minus signs indicate the magnitude of down-regulation and NC stands for "no change".

Pathway	AcdS$^+$	AcdS$^-$	trAcdS-*rolD* seedling	trAcdS-*rolD* mature plant	trAcdS-*rolD* in Ni	Non-transformed in Ni
Ethylene biosynthesis	+/−	+	+	+	+	−
IAA biosynthesis	−	NC	+	+	−	+
JA biosynthesis	−	+/−	+	++	NC	++
Cytokinin biosynthesis	− −	− −	+	+	NC	−
Gibberellin biosynthesis	NC	NC	−	+	+	NC
SA biosynthesis	−	−	+	+	+	NC
Photosynthesis	++	++	+/−	+	+	− − −
Catabolic processes	+	+	+/−	+/−	−	++
Carbohydrate metabolism	+++	++	+/−	++	NC	++
Lipid metabolism	− −	− −	+	−	++	+
Cell wall changes	− − −	− − −	++	+	−	− −
Nitrogen metabolism	− − −	NC	NC	++	+/−	+/−
Sulfur metabolism	− − −	− −	+	++	NC	−
Secondary metabolism	− − −	− − −	+++	+++	+	− − −
Glucosinolate biosynthesis	− −	NC	++	++	NC	+++
Response to stress	+	+	+/−	− − −	NC	+++
Removal of superoxide radicals	−	+/−	+	+	NC	+/−
Defense response	−	+/−	+	+/−	−	+
Response to stimuli	−	+/−	+	+/−	−	+

Table 3.2: Summary of expression changes in roots of plants treated with bacteria from Table A.1 in Section A and functional categorization data. This summary provides insight into the trends in expression changes across all experimental treatments. Expression changes for all treatments except “trAcdS-*rolD* with Ni” are relative to un-treated, non-transformed controls, whereas expression changes for “trAcdS-*rolD* with Ni” are relative to non-transformed plants with nickel. Plus signs indicate magnitude of up-regulation, minus signs indicate the magnitude of down-regulation and NC stands for “no change”.

Pathway	AcdS$^+$	AcdS$^-$	trAcdS-*rolD* seedling	trAcdS-*rolD* mature plant	trAcdS-*rolD* in Ni	Non-transformed in Ni
IAA biosynthesis	NC	NC	− −	− −	NC	NC
SA biosynthesis	NC	NC	NC	NC	NC	− −
Catabolic process	+/−	+/−	− −	−	NC	+/−
Carbohydrate metabolism	NC	− −	NC	NC	NC	− − −
Trehalose biosynthesis	− −	NC	NC	NC	NC	NC
Lipid metabolism	NC	NC	NC	NC	NC	− −
Cell wall changes	+	NC	NC	NC	NC	− − −
Nitrogen compound metabolism	+	+/−	− −	−	NC	+/−
Sulfur metabolism	NC	− −	NC	NC	NC	−
Methionine biosynthesis	NC	NC	NC	NC	NC	− −
Secondary metabolism	+/−	++	− −	− −	NC	+/−
Response to stress	+	− − −	NC	NC	NC	NC
Removal of superoxide radicals	NC	NC	NC	+/−	NC	NC
Defense response	+	+/−	− −	− −	NC	+/−
Response to stimuli	+	−	NC	NC	NC	+/−

3.1.3 Gene lists

An examination of the lists of genes with significant transcriptional changes (Tables C.1 and C.2) reveals a significant number of for genes that would neither fall into the GO categorizations or metabolic pathways. These include genes for zinc finger proteins, MYB transcription factors, PPR proteins, AP2-domain containing transcription factors, LRR proteins, bZIP transcription factors, TCP transcription factors and small ribonucleoprotein. Among this list only genes for AP2-domain containing transcription factors were also differentially expressed in roots of plants treated with bacteria.

Genes whose transcription differed between plants treated with AcdS$^+$ and the AcdS$^-$ bacteria include: ethylene signaling genes and glycine rich RNA binding protein genes which were up-regulated in shoots of plants treated with AcdS$^+$ bacteria; stress responsive genes, FAD binding protein genes and DNAJ heat shock protein genes which were down-regulated in shoots of plants treated with AcdS$^+$ bacteria; and EREBP, oxidoreductase 2OG-Fe(II) and senescence associated genes which were up-regulated in shoots of plants treated with AcdS$^-$ bacteria.

3.1.4 Clustering

When normalized intensity ratios of inoculated versus uninoculated seedlings were clustered, some interesting expression patterns emerged. For instance, the magnitude of expression changes in roots of plants treated with bacteria was much lower than that of shoot tissues (Figure 3.7). This may be due to the lower level of transcriptional activation within root cells. Also, the expression patterns of shoots treated with AcdS$^+$ and AcdS$^-$ bacteria was strikingly similar, as can be seen by the large green and red sections. This suggests that colonization of plant roots by bacteria results in many transcriptional changes within plant cells and that the presence or absence of the ACC deaminase enzyme causes changes that are more subtle. Some interesting differences between the two treatments include the down-regulation of stress genes in plants treated with AcdS$^+$ bacteria (Figure 3.8) and the up-regulation of many auxin response factors (ARF) in the shoots of the AcdS$^+$ treated plants (Figure 3.9). Many ARF are AUX/IAA genes, which are transcription factors known to bind elements within genes that respond to auxin. Also highly represented were small auxin up-regulated (SAUR) (Figure 3.9) genes whose function is largely unknown but are known to only respond to auxin and may play a role in auxin signaling involving calcium and calmodulin (Hagen and Guilfoyle, 2002). Ethylene response and auxin transport genes also appeared and their expression changes clustered with the ARF and SAUR genes.

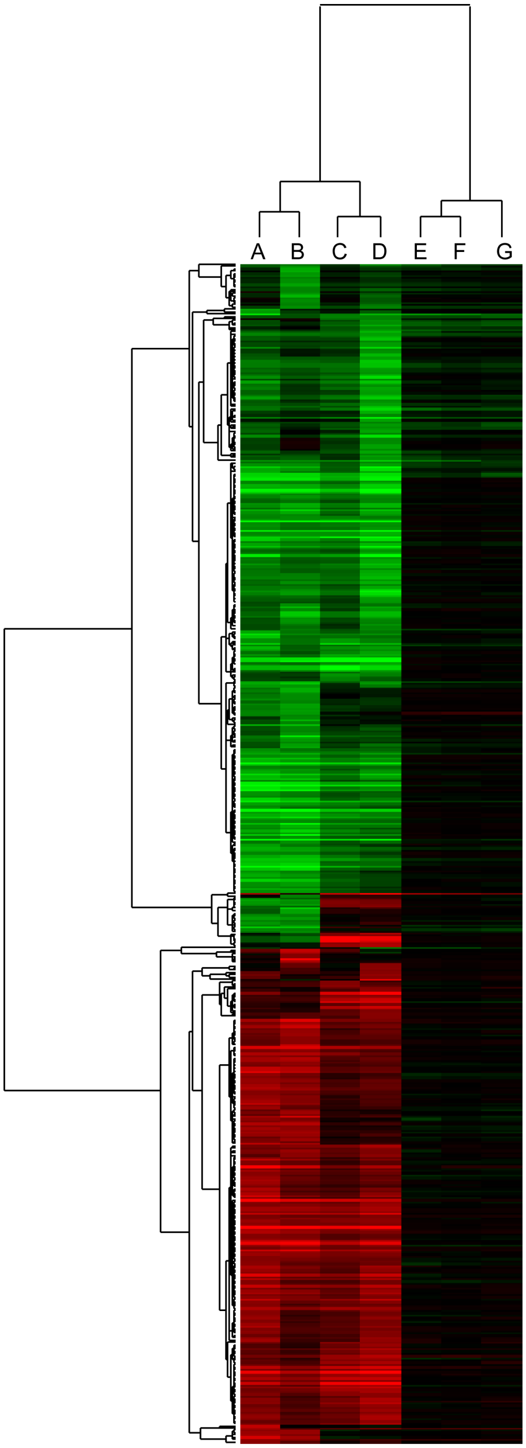

Figure 3.7: Two-dimensional hierarchical clustering performed on a subset of normalized intensity ratios. Green represents down-regulation of a gene in the treatment versus the control and red represents its up-regulation. A) and (B) replicates of seedling shoot inoculated with AcdS$^+$ bacteria, (C) and (D) replicates of seedling shoot inoculated with AcdS$^-$ mutant, (E) and (F) replicates of seedling root inoculated with AcdS$^+$ bacteria, (G) seedling root inoculated with AcdS$^-$ mutant.

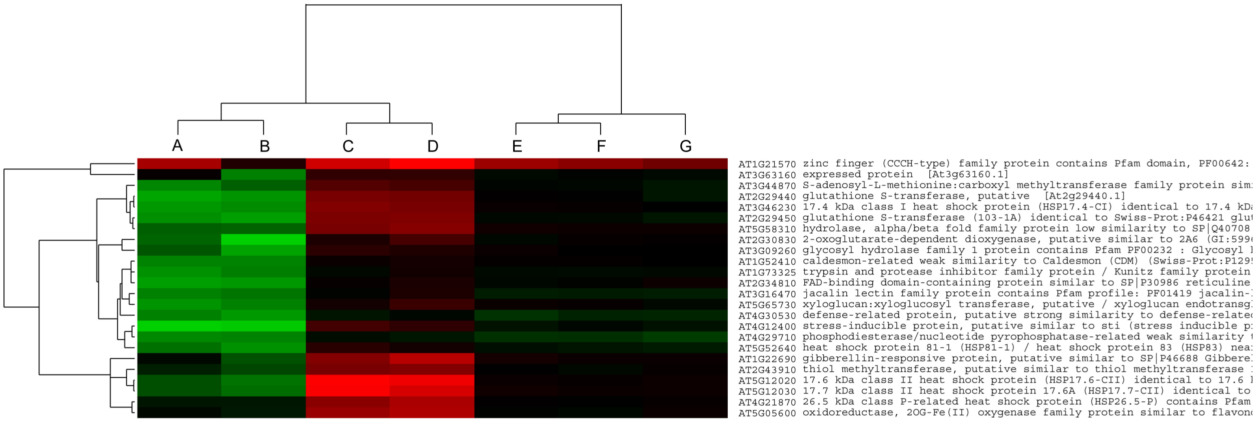

Figure 3.8: Magnified detail of cluster results showing a concentration of genes involved in the stress response. Some stress genes of interest include glutathione S-transferase, defense and stress response genes. A) to (G) same as in Figure 3.7.

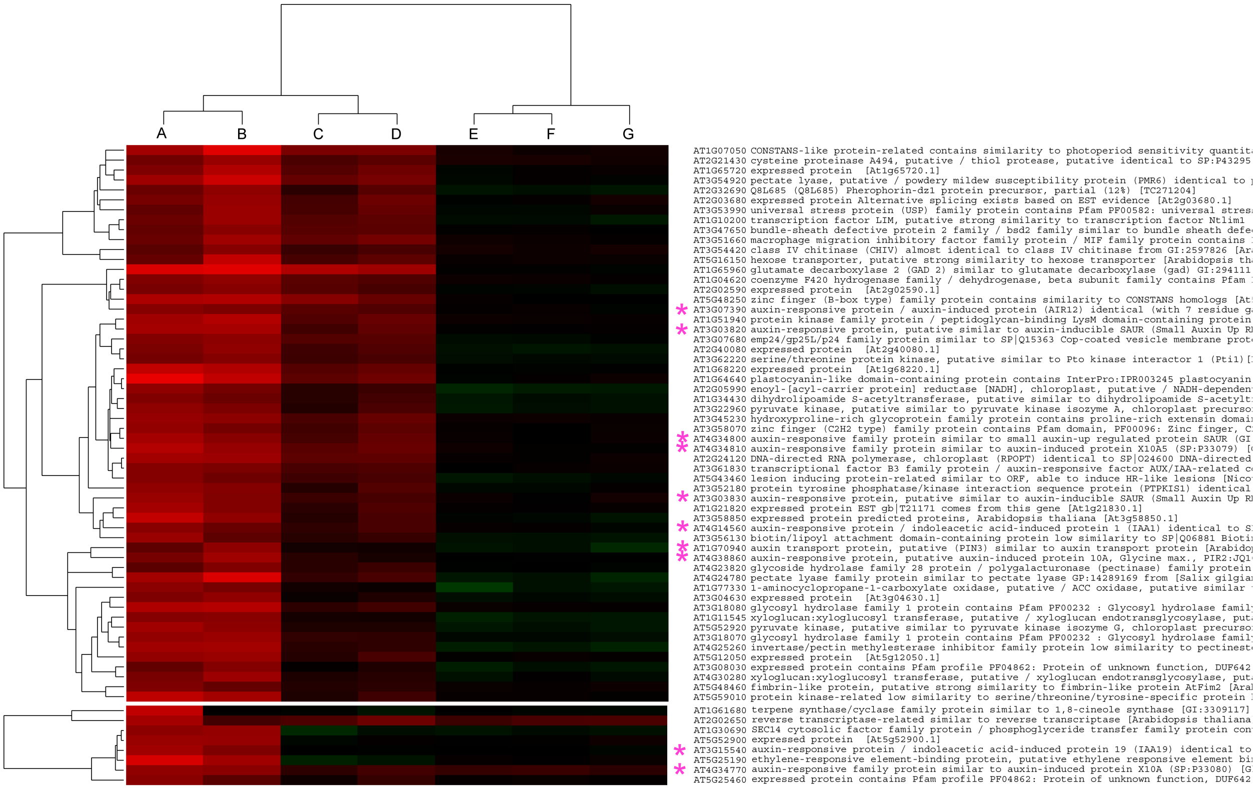

Figure 3.9: Magnified detail of cluster results showing a concentration of auxin response factor (ARF) genes (pink stars). A) to (G) same as in Figure 3.7.

3.1.5 Validation of microarray expression data

In order to confidently say that the heterologous microarray experiment (with probes designed from the coding sequences of Arabidopsis genes) was able to test expression changes occurring within canola (*Brassica napus*) plant tissues, real-time RT-PCR was used. Primers for nine targets were designed based on *Brassica* EST sequences, that corresponded to the sequence of the Arabidopsis probe on the microarray, and used to measure the relative abundance of these transcript within *Brassica napus* tissues compared with the control plants. In order to make accurate measurements of the relative abundance of transcript levels using real-time RT-PCR, it was imperative that primers be specific and that only one product was amplified. One advantage of this technique is the ability to monitor the level of double stranded product present in each cycle, hence at the end of every run of real-time RT-PCR a melting curve was plotted to ensure that there was only one product in each reaction. The melting curves for all ten PCR product are presented in Figure 3.12, with the strong single peak in each graph indicating a single double-stranded product.

The PCR products were then sequenced and the results aligned to the *Brassica* ESTs (from which they were designed) to ensure that the proper product was amplified (Figure 3.11). These sequences were then compared to all sequences within the Brassicaceae family (taxid:3700) using blastn (through NCBI at www.ncbi.nlm.nih.gov/blast/). In every case the results included the corresponding Arabidopsis ref. sequence with high percent identity and expect values (Table 3.3). In fact, the percent identity reported in Table 3.3 under-represents the level of identity between the sequences since there are a number of bases that were not identified during sequencing and were reported as N lowering the percent identity value. This high level of identity between *Brassica* EST and Arabidopsis ref. sequences (from which microarray probes were designed) gives us confidence that cDNA from canola (*Brassica napus*) would have bound to probes on the microarray.

Relative expression values were calculated for nine transcripts using real-time RT-PCR (Figure 3.13). Fold changes are presented for genes that were both up- and down-regulated as well as unchanged, when compared to the control. The expression changes measured with real-time RT-PCR correlate well with those measured with microarrays with an R = 0.93 (Figure 3.14).

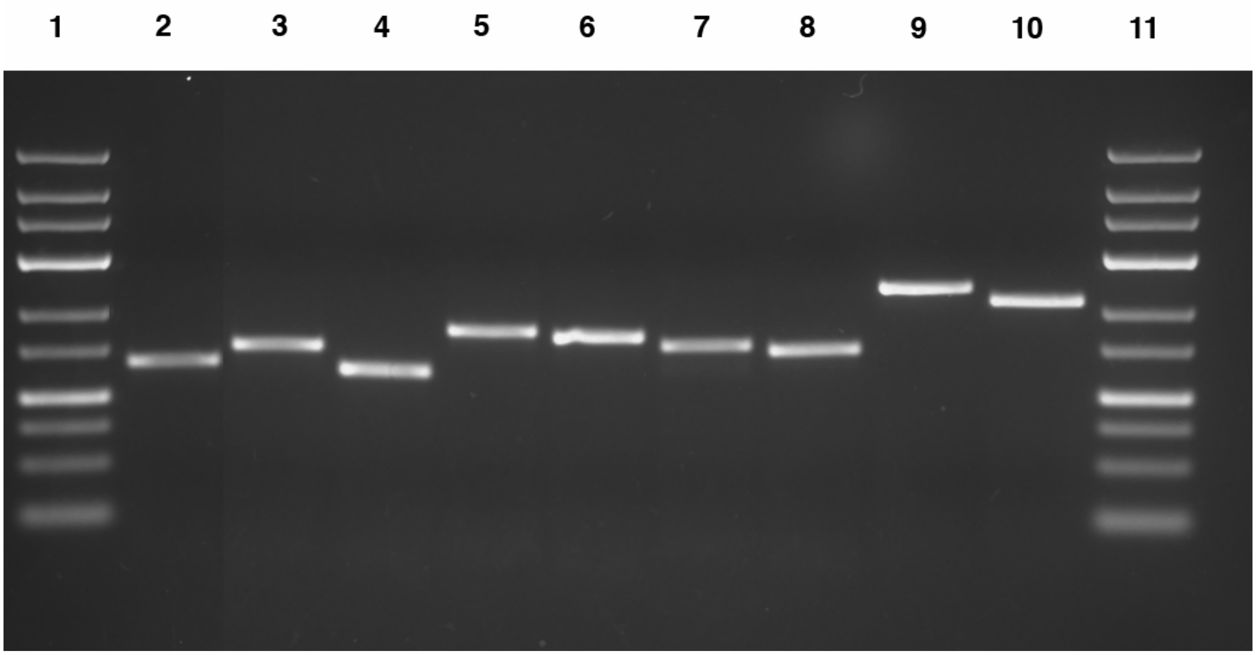

Figure 3.10: An example of RT-PCR products seperated by gel electrophoresis, 5 μl of sample loaded. 1) 100 bp ladder, (2) AT5G42650, (3) AT2G14610, (4) AT4G25100, (5) AT2G43910, (6) AT5G07580, (7) AF044573, (8) AT3G58680, (9) AT1G05010, (10) AT1G70940, (11) 100 bp ladder.

Table 3.3: Blastn results for real-time RT-PCR products. Asterisks denote sequences that do not appear in GenBank. Percent identity reflects the percent of bases that are identical between the sequence of product amplified with RT-PCR (*Brassica napus*) and the GenBank ref. sequence for the corresponding Arabidopsis gene.

Locus	*Brassica* EST	Arabidopsis ref. sequence	Expect value	Identity (%)	
AT5G42650	AOS (ALLENE OXIDE SYNTHASE	RL2795*	NM_123629	4.00E-28	87
AT3G15540	transcription factor (IAA19)	CD1204*	NM_112422	8.00E-39	84
AT2G14610	PR1 (PATHOGENESIS-RELATED GENE 1)	OL6017*	NM_127025	1.00E-37	84
AT4G25100	FSD1 (FE SUPEROXIDE DISMUTASE 1)	OL8300*	NM_179110	9.00E-22	87
AT2G43910	thiol methyltransferase	LR2697*	NM_129953	2.00E-38	86
AT5G07580	ERF (ethylene response factor)	OL6713*	NM_120840	2.00E-38	88
AT3G58680	ethylene-responsive transcriptional coactivator	DC895*	NM_115730	9.00E-30	86
AT1G05010	1-aminocyclopropane-1-carboxylate oxidase	DL1563*	NM_100380	3.00E-72	90
AT1G70940	auxin transport protein, putative (PIN3)	AJ249298	NM_105762	4.00E-44	78

A

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451 ATCCGACGGTGGGGAATAAACAGTGCGCCGGTAAGGACTTTGTTGTTTTG 500
  1 ---------------------------------------TNTTGTTGTTT 11

501 GTGGCGAGGTTATTTTTGATTGAGATTTTCAGGAGGTATGATTCCTTTGA 550
 12 GTGGCGAGGTTATTTTTGATTGAGATTTTCAGGAGGTATGATTCCTTTGA 61

551 TATTGAGGTTGGCTCGTCGCCGTTGGGAAGCTCCGTTACATTCACGTCTC 600
 62 TATTGAGGTTGGCTCNTCGCCGTTGGGAAGCTCCGTTACATTCAANNNNN 111

601 TGAGGAAGGCTAGCTTTTAGAGAGTCAAGGGTAAATTTGTAATGTATGTT 650
112 NNN----------------------------------------------- 114
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B

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  1 --------TCGACACCGCTTTCACATTGATCACTATTACTTCCTGAAGAC 42
401 CTGATGAAACGACACCGCTTTCACATTGATCACTATTACTTCCTGACGAC 450

 43 GCCATGATCATCTCCGTGAAACCTCTCTTCTTCATCATCTTCTCCGTCCC 92
451 GTCATGATCATCTCCGTGAAACCTCTCTTCTTCATCATCTTCTCCGTCCC 500

 93 CGGAAGACCTAGTCTCAGCTCAGTTATCTCAAGCCCGAGTCCAA------ 136
501 CGGAAGACCTAGTCTCAGCTCAGTTATCTCAAGCCCGAGTCCACCTTTCT 550
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C

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129 TATGGCGATGCATAGTAACTCATTAGTAAGGCTTCTCGTTCACATAATTT 178

  3 CCCCGAGGATCATAGTTGCAAGAAATGATGGTTCCACCATTGTTACACCT 52
179 CCCCGAGGATCATAGTTGCAAGAAATGATGGTTCCACCATTGTTACACCT 228

 53 TGCTTTGCCACATCCAATTCTCACAGACTTTCTCCAAACAACCTGAGTAT 102
229 TGCTTTGCCACATCCAATTCTCACAGACTTTCTCCAAACAACCTGAGTAT 278

103 AGTGACGGCATTCTCCATTAATGCACGTGTTCGAAGCGAAGTA------- 145
279 AGTGACGGCATTCTCCATTAATGCACGTGTTCGAAGCGTAGTTATAGTTA 328
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D

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529 TTGACGTCTGGGAGCATGCTTACTATCTAGACTTTCAGAATCGAAGACCG 578
  1 -----------------------NNNNNNNNNNNNNNGAANCGCAGACCG 27

579 GATTACATAAAGACATTCATGAACAATCTTGTGTCTTGGGAAGCTGTTAG 628
 28 GATTACATAAAGACATTCATGAACAATCTTGTGTCTTGGGAGGCTGTTAG 77

629 TTCCAGACTTCACGCTGCCAAGGCTGCTTCTTCCTCTTCTGCTTAAGCAG 678
 78 TTCCAGACTTCACGCTGCANN----------------------------- 98
```

E

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 46 CGAACTCATNACTCTCATGTATCCGATTACCGATCATGATGGTGGACCNC 95

351 CCTACAAAGTAGCTGTATCTACCTACGAAGATGTTTTGGTTCCCGTAGGA 400
 96 CNTACAAAGTAGCTNTNTCTACCTACGAAGATGTTTTGGTTCCCGTAGGA 145

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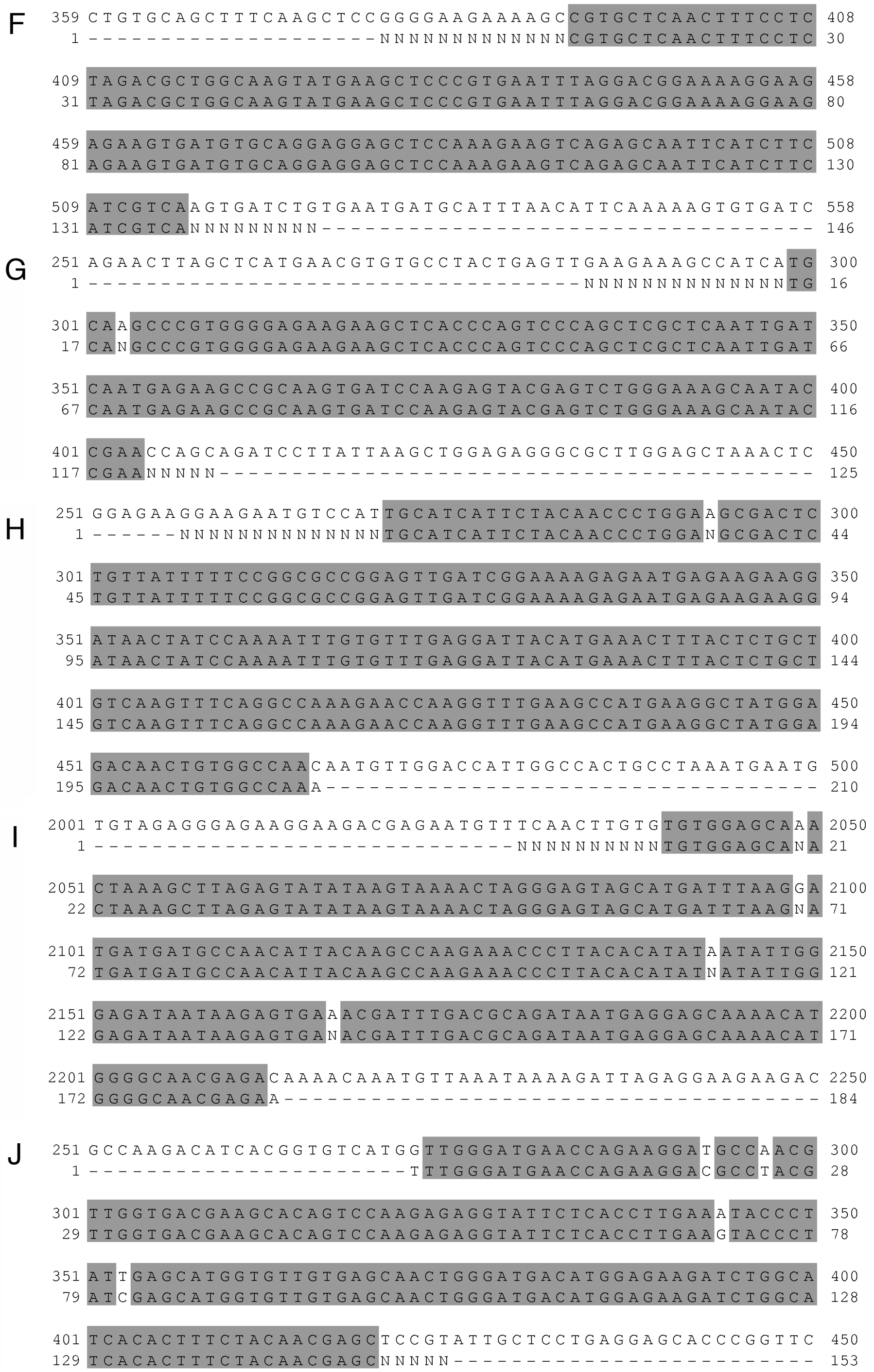

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F
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509 ATCGTCAAGTGATCTGTGAATGATGCATTTAACATTCAAAAAGTGTGATC 558
131 ATCGTCANNNNNNNNN---------------------------------- 146

G
251 AGAACTTAGCTCATGAACGTGTGCCTACTGAGTTGAAGAAAGCCATCATG 300
  1 ----------------------------------NNNNNNNNNNNNNNTG 16

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 17 CANGCCCGTGGGGAGAAGAAGCTCACCCAGTCCCAGCTCGCTCAATTGAT 66

351 CAATGAGAAGCCGCAAGTGATCCAAGAGTACGAGTCTGGGAAAGCAATAC 400
 67 CAATGAGAAGCCGCAAGTGATCCAAGAGTACGAGTCTGGGAAAGCAATAC 116

401 CGAACCAGCAGATCCTTATTAAGCTGGAGAGGGCGCTTGGAGCTAAACTC 450
117 CGAANNNNN----------------------------------------- 125

H
251 GGAGAAGGAAGAATGTCCATTGCATCATTCTACAACCCTGGAAGCGACTC 300
  1 ------NNNNNNNNNNNNNNTGCATCATTCTACAACCCTGGANGCGACTC 44

301 TGTTATTTTTCCGGCGCCGGAGTTGATCGGAAAAGAGAATGAGAAGAAGG 350
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351 ATAACTATCCAAAATTTGTGTTTGAGGATTACATGAAACTTTACTCTGCT 400
 95 ATAACTATCCAAAATTTGTGTTTGAGGATTACATGAAACTTTACTCTGCT 144

401 GTCAAGTTTCAGGCCAAAGAACCAAGGTTTGAAGCCATGAAGGCTATGGA 450
145 GTCAAGTTTCAGGCCAAAGAACCAAGGTTTGAAGCCATGAAGGCTATGGA 194

451 GACAACTGTGGCCAACAATGTTGGACCATTGGCCACTGCCTAAATGAATG 500
195 GACAACTGTGGCCAAA---------------------------------- 210

I
2001 TGTAGAGGGAGAAGGAAGACGAGAATGTTTCAACTTGTGTGTGGAGCAAA 2050
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2151 GAGATAATAAGAGTGAAACGATTTGACGCAGATAATGAGGAGCAAAACAT 2200
 122 GAGATAATAAGAGTGANACGATTTGACGCAGATAATGAGGAGCAAAACAT 171

2201 GGGGCAACGAGACAAAACAAATGTTAAATAAAAGATTAGAGGAAGAAGAC 2250
 172 GGGGCAACGAGAA------------------------------------- 184

J
251 GCCAAGACATCACGGTGTCATGGTTGGGATGAACCAGAAGGATGCCAACG 300
  1 ----------------------TTTGGGATGAACCAGAAGGACGCCTACG 28

301 TTGGTGACGAAGCACAGTCCAAGAGAGGTATTCTCACCTTGAAATACCCT 350
 29 TTGGTGACGAAGCACAGTCCAAGAGAGGTATTCTCACCTTGAAGTACCCT 78

351 ATTGAGCATGGTGTTGTGAGCAACTGGGATGACATGGAGAAGATCTGGCA 400
 79 ATCGAGCATGGTGTTGTGAGCAACTGGGATGACATGGAGAAGATCTGGCA 128

401 TCACACTTTCTACAACGAGCTCCGTATTGCTCCTGAGGAGCACCCGGTTC 450
129 TCACACTTTCTACAACGAGCNNNNN------------------------- 153
```

Figure 3.11: Sequencing results of RT-PCR products. Each sequence is aligned with the *Brassica* EST used to design the primers. A) AT5G42650, (B) AT3G15540, (C) AT2G14610, (D) AT4G25100, (E) AT2G43910, (F) AT5G07580, (G) AT3G58680, (H) AT1G05010, (I) AT1G70940, (J) AF044573.

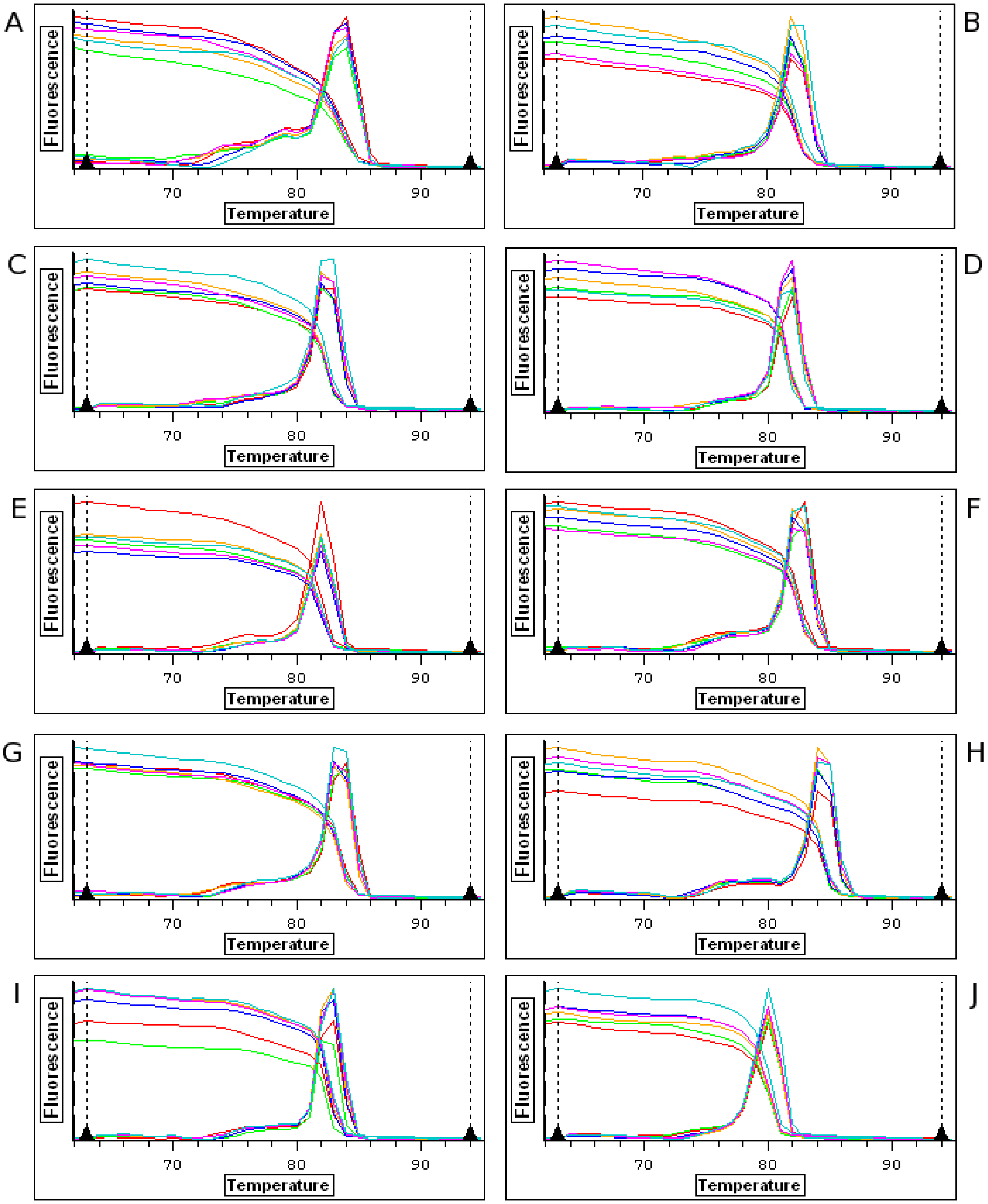

Figure 3.12: Melting curves generated during real-time RT-PCR. A) Actin (AF044573), (B) AT5G42650, (C) AT3G15540, (D) AT2G14610, (E) AT4G25100, (F) AT2G43910, (G) AT5G07580, (H) AT3G58680, (I) AT1G05010, (J) AT1G70940.

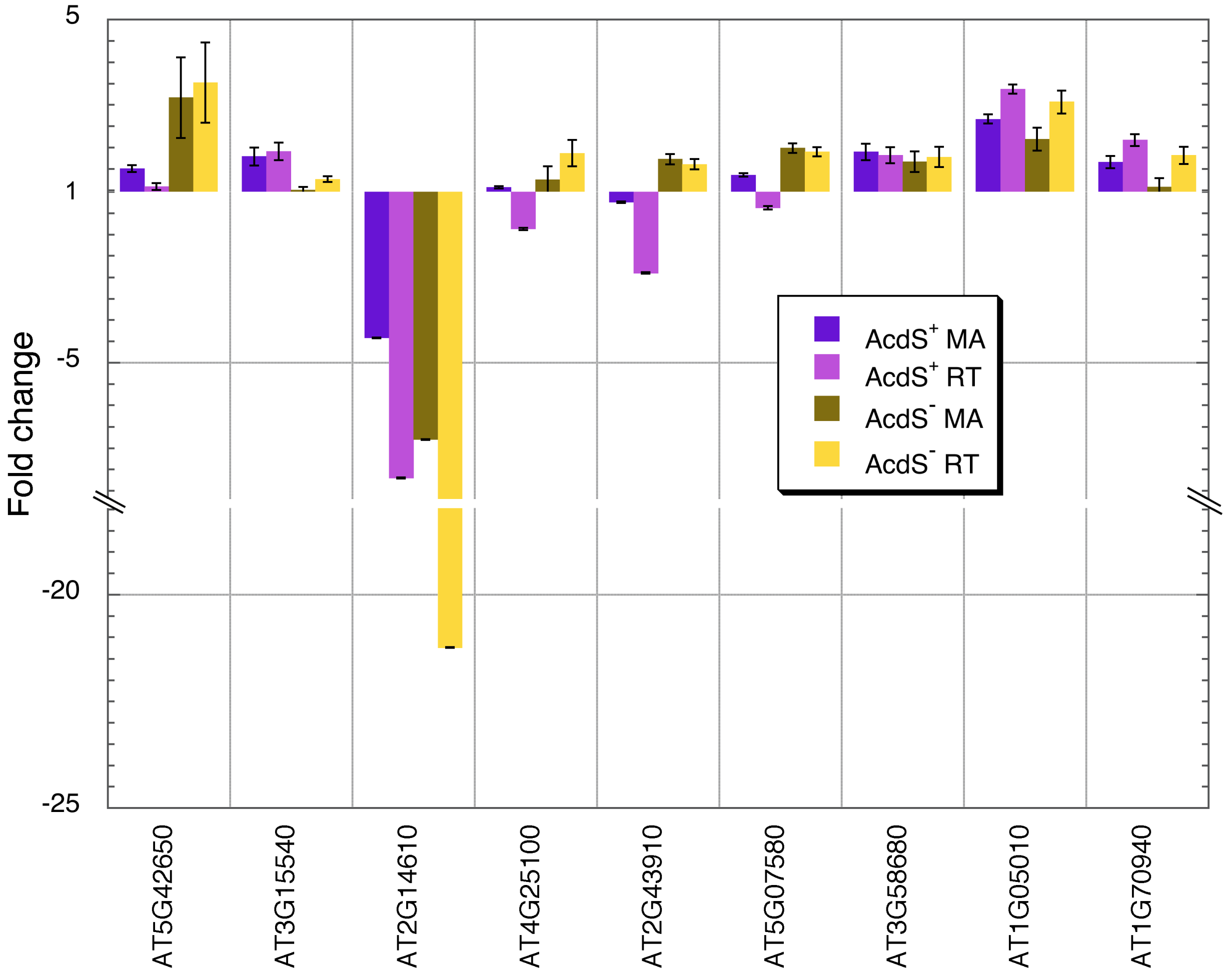

Figure 3.13: Expression changes of select genes measured with real-time RT-PCR (RT) and microarray (MA).

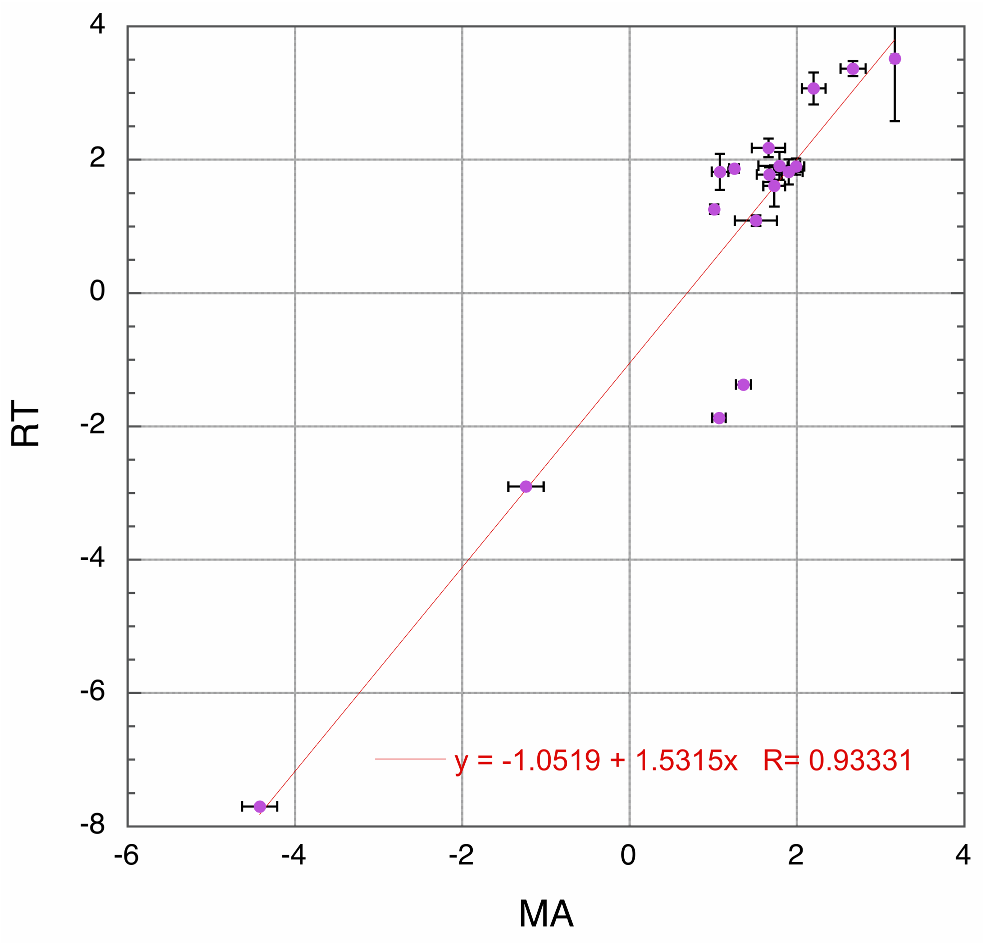

Figure 3.14: Correlation between gene expression measurements (fold change) made with microarray (MA) versus real-time RT-PCR (RT), on plants treated with AcdS^{+} bacteria.

3.2 Transgenic canola expressing bacterial ACC deaminase

3.2.1 Physiological effects of the transgene

To gauge the effect of the bacterial ACC deaminase enzyme alone (without the confounding effects of other compounds produced by PGPR) in the promotion of plant growth, transgenic plants expressing the structural gene from *Pseudomonas putida* UW4 either under the control of the constitutive promoter CAMV*35S* or the root specific promoter *rolD* (trAcdS-*35S* and trAcdS-*rolD*, respectively) were used. Differences in germination rates and root elongation were measured for both transgenic lines, and those plants expressing the transgene in the roots were carried forward for transcriptional profiling of plant tissues during development (this section) and under stress (Section 3.3). The germination rates of transgenic seeds (both trAcdS-*35S* and trAcdS-*rolD*) was faster than non-transformed seeds and the percent of seeds that germinated was slightly higher (Figure 3.15). Five days after seed imbibition, both roots and shoots of transgenic seedlings were longer than those of non-transformed seedlings, with trAcdS-*rolD* showing the most dramatic differences (Figure 3.16). Due to their stress tolerance (Section 3.3), trAcdS-*rolD* were carried forward for further studies.

Early root development was observed for trAcdS-*rolD* and non-transformed plants by germinating seeds on solid medium in the presence and absence of light. As is readily seen by visual inspection, at two days post-germination, trAcdS-*rolD* seedlings had longer roots than non-transformed seedlings and light inhibited the elongation of non-transformed seedling roots to a greater extent than it did for trAcdS-*rolD* roots (Figure 3.17A and 3.17B, respectively). Even when germinated in the dark, trAcdS-*rolD* seedlings had longer roots (Figure 3.17D). At three days post-germination, the longer root phenotype of trAcdS-*rolD* seedlings was much more pronounced (Figure 3.18D), and the root elongation inhibition effect of light was more apparent (Figure 3.18B).

Brassica napus var. Westar began to bolt and then produce flowers between three and four weeks of age. At three weeks, non-transformed and trAcdS-*rolD* were visually indistinguishable from one another (Figure 3.19), however trAcdS-*rolD* bolted one to two days earlier (not shown).

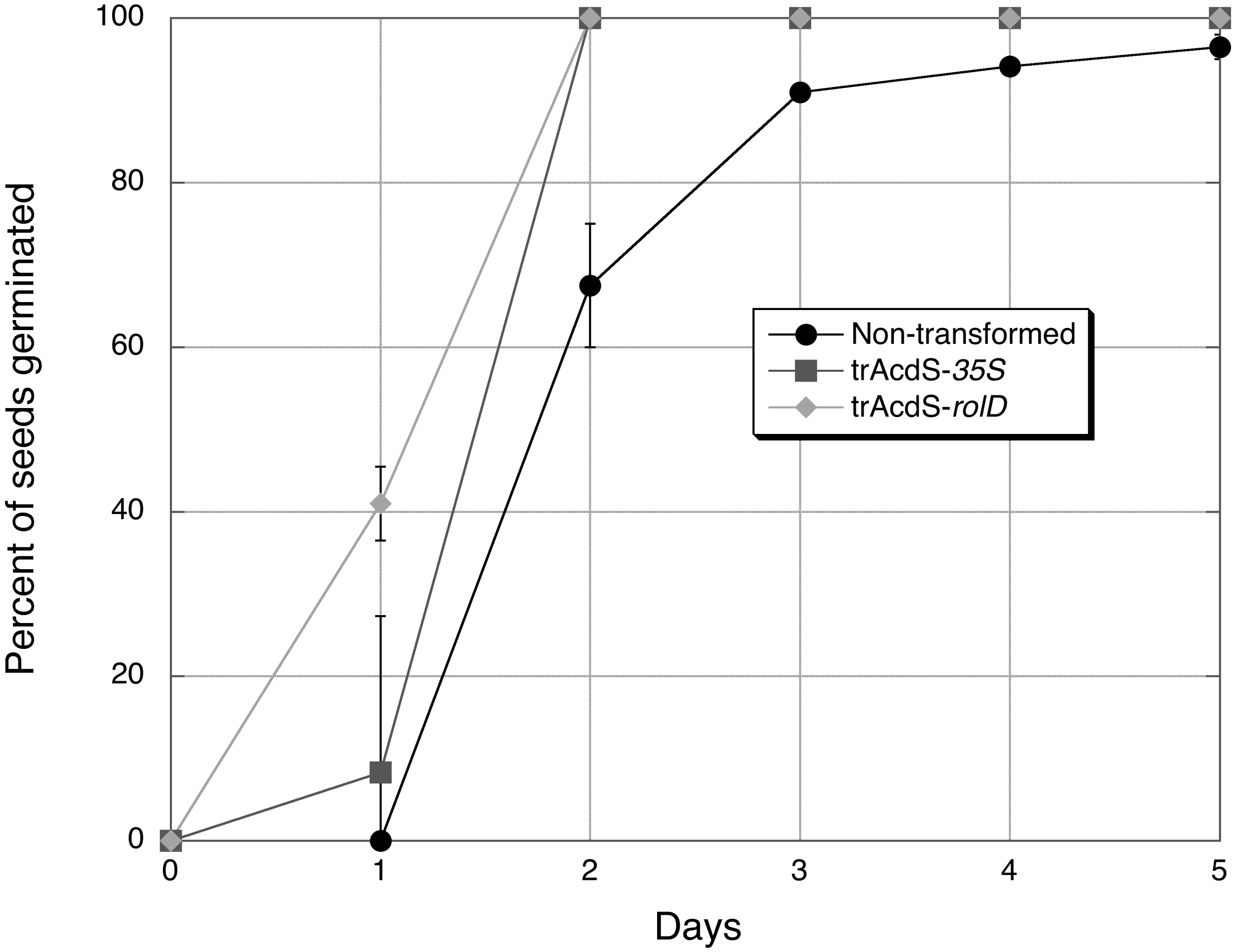

Figure 3.15: Germination rate of transgenic and non-transformed canola seeds.

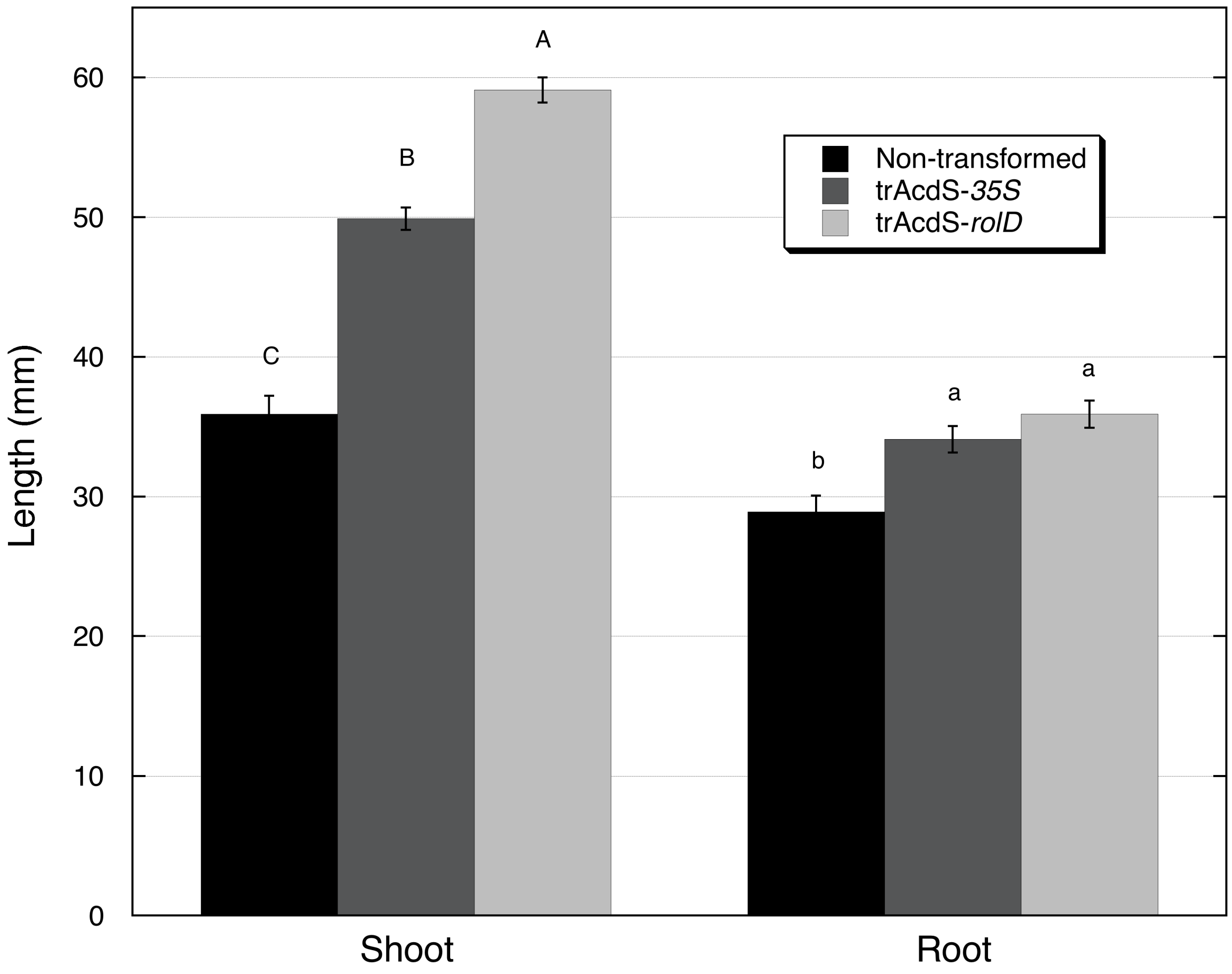

Figure 3.16: Shoot and root elongation of five day-old transgenic and non-transformed seedlings. Capital letters represent results of ANOVA analysis of seedling shoot length, where statistical significance is indicated by a different letter (n=60, $p < 0.001$). Lower case letters represent the same analysis as above on seedling root length.

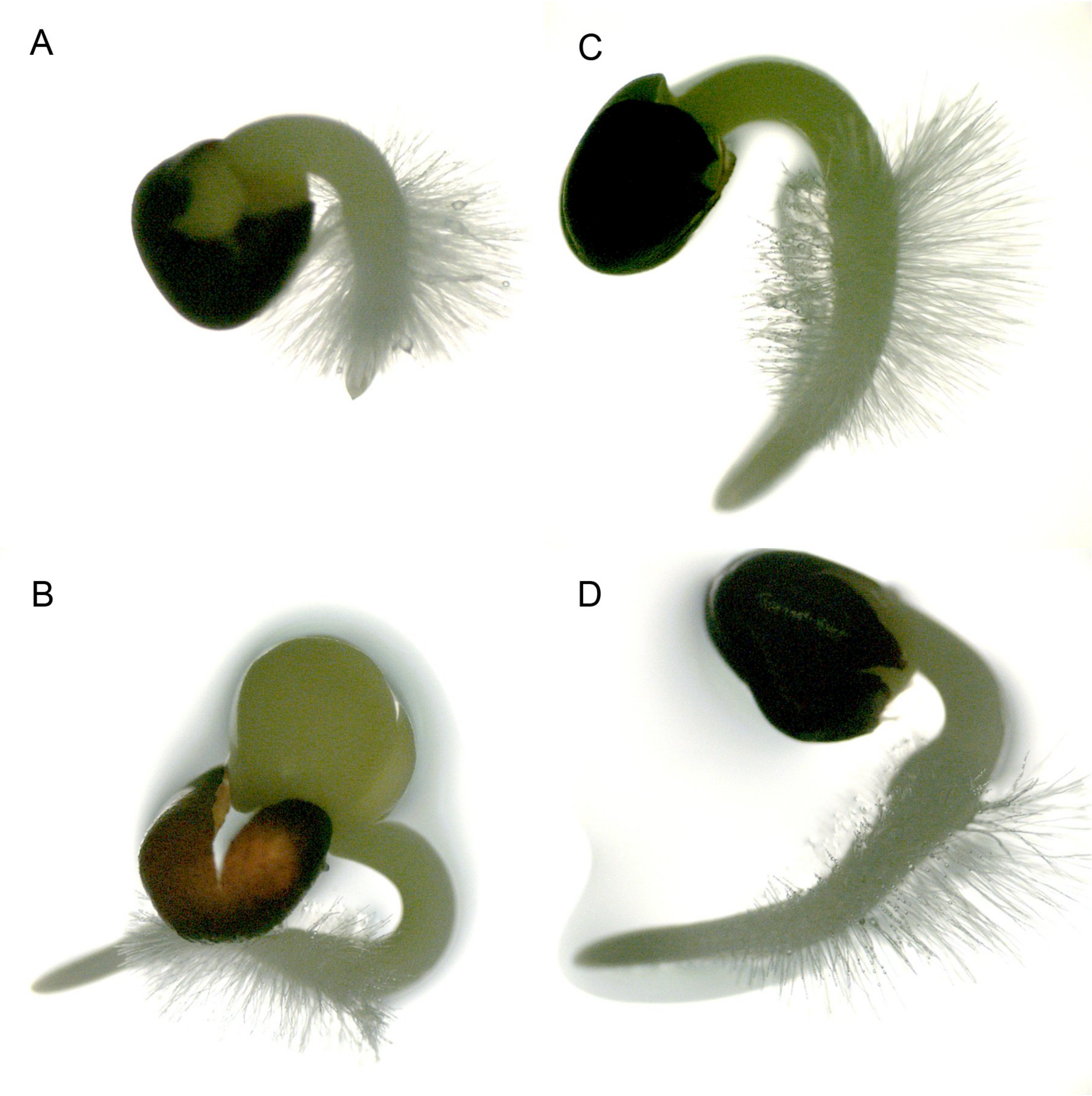

Figure 3.17: Two day-old transgenic and non-transformed seedlings. A) non-transformed and (B) trAcdS-*rolD* seeds germinated in the light. C) non-transformed and (D) trAcdS-*rolD* seeds germinated in the dark.

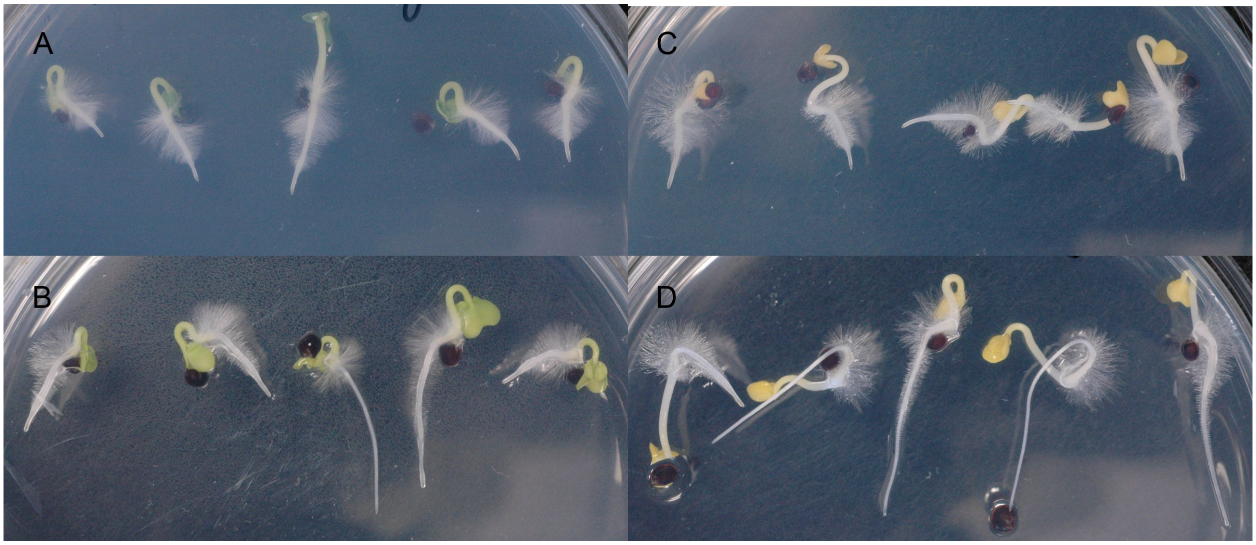

Figure 3.18: Three day-old transgenic and non-transformed seedling. A) non-transformed and (B) trAcdS-*rolD* seeds germinated in the light. C) non-transformed and (D) trAcdS-*rolD* seeds germinated in the dark.

Figure 3.19: Mature (three week-old) canola grown in potting soil. The top image shows non-transformed plants, whereas the bottom shows trAcdS-*rolD* plants.

3.2.2 Transcriptional changes occurring within trAcdS-*rolD* plants

Transcriptional profiling of plant tissues was performed to gain insight into the effect of ACC deaminase on developing plants. Six day-old seedlings and three week-old (mature) trAcdS-*rolD* plants were compared to non-transformed plants at the same stages. Transcriptional changes within both shoots and roots of these two developmental stages were measured in independent experiments and are therefore presented separately. Due to the small number of replicates, false discovery rate (FDR) adjustment of p-values was not informative and Tables C.3, C.4, C.5 and C.6, in Appendix C, lists genes with a $p < 0.01$. Figure 3.20 depicts a summary of transcriptional changes in trAcdS-*rolD* plants. In shoots 762 genes showed differential expression (72 of which were in common between seedlings and mature plants) and in roots 598 genes showed differential expression (25 of which were in common between seedlings and mature plants).

3.2.3 Functional categorization of expression data

Genes from Tables C.3, C.4, C.5 and C.6 were grouped according to their Gene Ontology (GO) terms. Figure 3.21 and 3.22 show the proportion of genes over-represented in each category (biological function level 3) when compared to all the genes represented on the microarray (total). If the number of genes for a particular GO term exceeds the number of genes from the total that fall into that same GO term category, then it is said to be over-represented in that treatment.

In shoots of trAcdS-*rolD* seedlings, genes involved in biosynthetic process, responses to various stimuli, catabolic process, secondary metabolic process, nitrogen compound metabolism, response to stress and sexual reproduction were up-regulated and over-represented (Figure 3.21). The same categories were over-represented in the list of genes which were down-regulated (Figure 3.22) in seedling shoots, but the magnitude of enrichment was much lower. In the roots of seedlings, responses to chemical, endogenous, biotic and external stimuli, response to stress, defense response, cell communication, secondary metabolism and aging

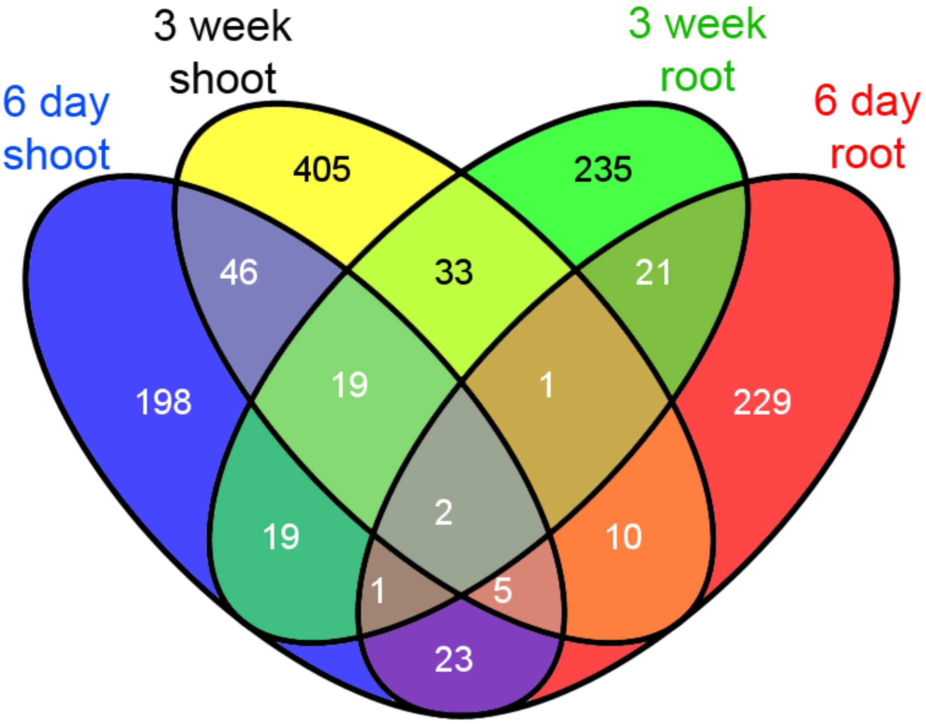

Figure 3.20: Venn diagram of transcriptional changes in trAcdS-*rolD* plants compared to non-transformed plants.

were up-regulated and over-represented (Figure 3.21). The following categories were over-represented in the list of down-regulated genes (Figure 3.22): establishment of localization, response to chemical and biotic stimuli, cell communication, catabolic process, secondary metabolism and regulation of biological quality.

In shoots of mature trAcdS-*rolD* plants, genes involved in processes such as biosynthetic process, the response to stress, responses to stimuli and secondary metabolism were up-regulated and over-represented (Figure 3.21), whereas in the roots many genes involved in biosynthetic process, response to stimuli, development, nitrogen metabolism, defense response and death were up-regulated and over-represented. The list of processes that were down-regulated and over-represented in mature plants include response to stress and stimuli and nitrogen compound metabolism in both tissues, catabolic process and aging in the shoots (Figure 3.22).

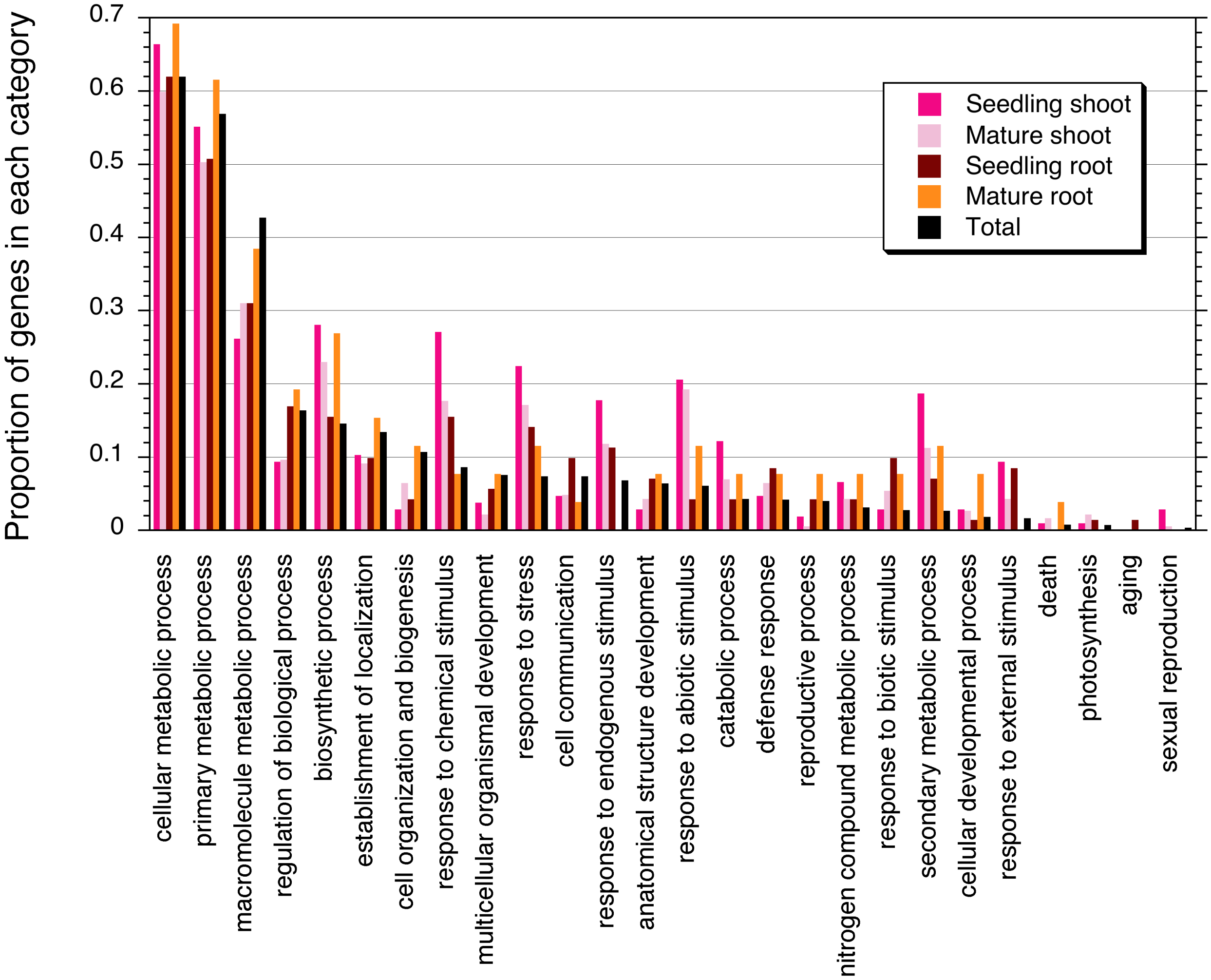

Figure 3.21: Functional categorization of genes up-regulated in trAcdS-*rolD*. Gene Ontology terms, biological process level 3.

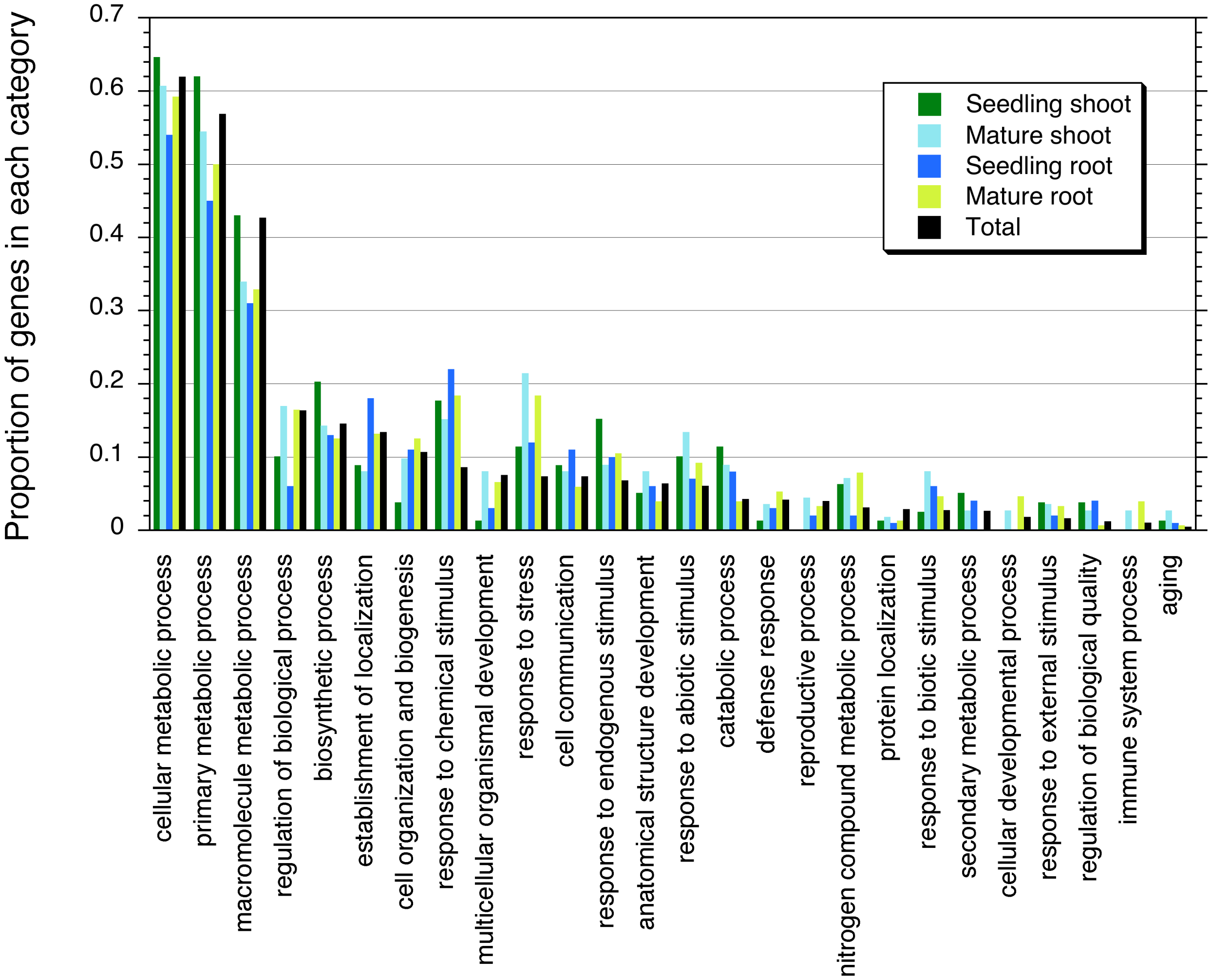

Figure 3.22: Functional categorization of genes down-regulated in trAcdS-*rolD*. Gene Ontology terms, biological process level 3.

3.2.4 Metabolic pathways

All genes whose expression changed with a $p < 0.01$ were analyzed using the TAIR Pathway Tools Omics Viewer, and any genes for which a biochemical function had been predicted (either biochemically or computationally) were mapped to specific metabolic pathways. These results are presented in Table A.1 in Appendix A and summerized in Tables 3.1 and 3.2. This classification revealed that, in shoots of both trAcdS-*rolD* seedlings and mature plants, ethylene biosynthesis genes (ACC oxidases, Figure 3.6) were up-regulated. Also, genes involved in cytokinin, IAA, JA and SA biosynthesis were up-regulated in both seedling and mature plant shoots and genes involved in gibberellin biosynthesis were down-regulated in seedlings, but up-regulated in mature plants.

Carbon fixation was up-regulated in both seedlings and mature plant shoots and carbohydrate metabolism pathways changed (Table 3.1). For instance, in mature trAcdS-*rolD* plants, genes involved in gylcolysis, sucrose degradation and trehalose biosynthesis were up-regulated, whereas genes involved in lactose degradation were down-regulated (Table A.1). In trAcdS-*rolD* seedlings trehalose degradation was down-regulated in the shoot but up-regulated in the root. In trAcdS-*rolD* seedlings, genes involved in some lipid metabolism pathways (namely fatty acid oxidation, sterol biosynthesis and triacylglycerol degradation) were up-regulated, whereas genes involved in the glyoxylate cycle were down-regulated.

Genes involved in cell wall changes, such as cellulose biosynthesis, homogalacturonan degradation and suberin biosynthesis, were up-regulated in trAcdS-*rolD* seedling and mature plant shoots. Genes involved in methionine biosynthesis and nitrate assimilation, were up-regulated in shoots of trAcdS-*rolD* seedling and mature plants, yet genes involved in ammonia assimilation and sulfate reduction were up-regulated in shoots and genes involved in cysteine biosynthesis were down-regulated in roots of mature trAcdS-*rolD* plants (Table A.1).

Genes for many pathways involved in secondary metabolism were up-regulated in both seedlings and mature plants (Table 3.1), including anthocyanin, camalexin, flavonoid, flavonol, glucosinolate, and phenylpropanoid biosynthesis. Some genes involved in stress response pathways were up-regulted in trAcdS-*rolD* seedlings, specifically galactose and glutamate degradation as well as removal of superoxide radicals. In mature trAcdS-*rolD* plants, however, a very large number of genes involved in stress pathways were down-regulated, especially in the roots. These included branched chain amino acid, galactose, glutamate, lysine and tyrosine degradation.

3.2.5 Gene lists

Inspection of the list of genes differentially expressed in trAcdS-*rolD* plants (Tables C.3, C.4, C.5 and C.6) revealed changes in auxin response genes. For instance, in seedling shoots auxin response factors (ARF) were down-regulated whereas in seedling and mature plant tissues auxin response factors were up-regulated. These included ARFs, calmodulin and calcium-binding and auxin biosynthesis. Other expression changes of note were the down-regulation of ethylene response genes (AP2 and ethylene responsive binding proteins) in seedling tissues and their up-regulation in mature plant tissues. Glutathione S-transferases were up-regluated and gibberellin biosynthesis and response genes were down-regulated in seedling shoots, whereas genes known to respond to ethylene such as disease response genes, pathogenesis-related (PR-1) and chitinases were down regulated in seedling tissues.

3.3 Transgenic and non-transformed plants under nickel stress

High levels of nickel in the soil inhibit plant growth and cause symptoms such as chlorosis and necrosis. In order to study the effects of nickel on canola (*Brassica napus*) and to investigate the ability of a bacterial ACC deaminase enzyme to reduce stress syptoms, both seedlings and mature plants of non-transformed and transgenic plants expressing the structural gene from *Pseudomonas putida* UW4 either under the control of the constitutive promoter CAMV*35S* or the root specific promoter *rolD* (trAcdS-*35S* and trAcdS-*rolD*, respectively) were grown in nickel-spiked media.

3.3.1 Physiological effects of excess nickel

Transgenic seedlings expressing ACC deaminase under both promoters had longer roots and shoots than non-transformed seedlings in the presence of nickel (Figure 3.23). Six day-old seedlings of trAcdS-*rolD* plants were healthier and showed significantly longer roots and shoots than either trAcdS-*35S* seedlings or the non-transformed seedlings under high concentrations of nickel (>4.0mM) (Figure 3.23 and 3.24). This effect was magnified when plants were grown to maturity in nickel-spiked soil, where non-transformed and trAcdS-*35S* plants produced severely stunted growth, chlorotic and necrotic patches on the leaves (Figure 3.25) and had significantly lower shoot and root biomass (approximately 85% and 80%, respectively, Figure 3.26) when compared to plants grown in non-spiked soil. On the other hand, trAcdS-*rolD* plants showed less severe stunting and chlorosis and did not exhibit a significant reduction in shoot or root biomass when grown in nickel-spiked soil (Figures 3.25 and 3.26). All plants grown in nickel-spiked soil had higher chlorphyll a/b ratios (Figure 3.27) than plants grown in unspiked soil, indicating chlorophyll b breakdown.

To gauge the suitability of transgenic plants expressing ACC deaminase for phytoremediation studies nickel concentration were calculated for shoot and root tissues (Figure 3.28).

Plants grown in nickel-spiked soil had significantly more nickel within their tissues (approximately 50-fold and 250-fold in shoots and roots, respectively) than did control plants, yet the concentration of nickel accumulated did not increase due to the presence of the transgene. This suggests that nickel from the soil is readily taken into the plant, yet there is a limited amount of translocation of this metal into the above ground tissues. Although the concentration of nickel in plant tissues was similar for non-transformed and transgenic plants, trAcdS-*rolD* plants accumulated a lager amount of nickel in total (Figure 3.29), due to their ability to better tolerate this metal in the soil and hence their much larger biomass.

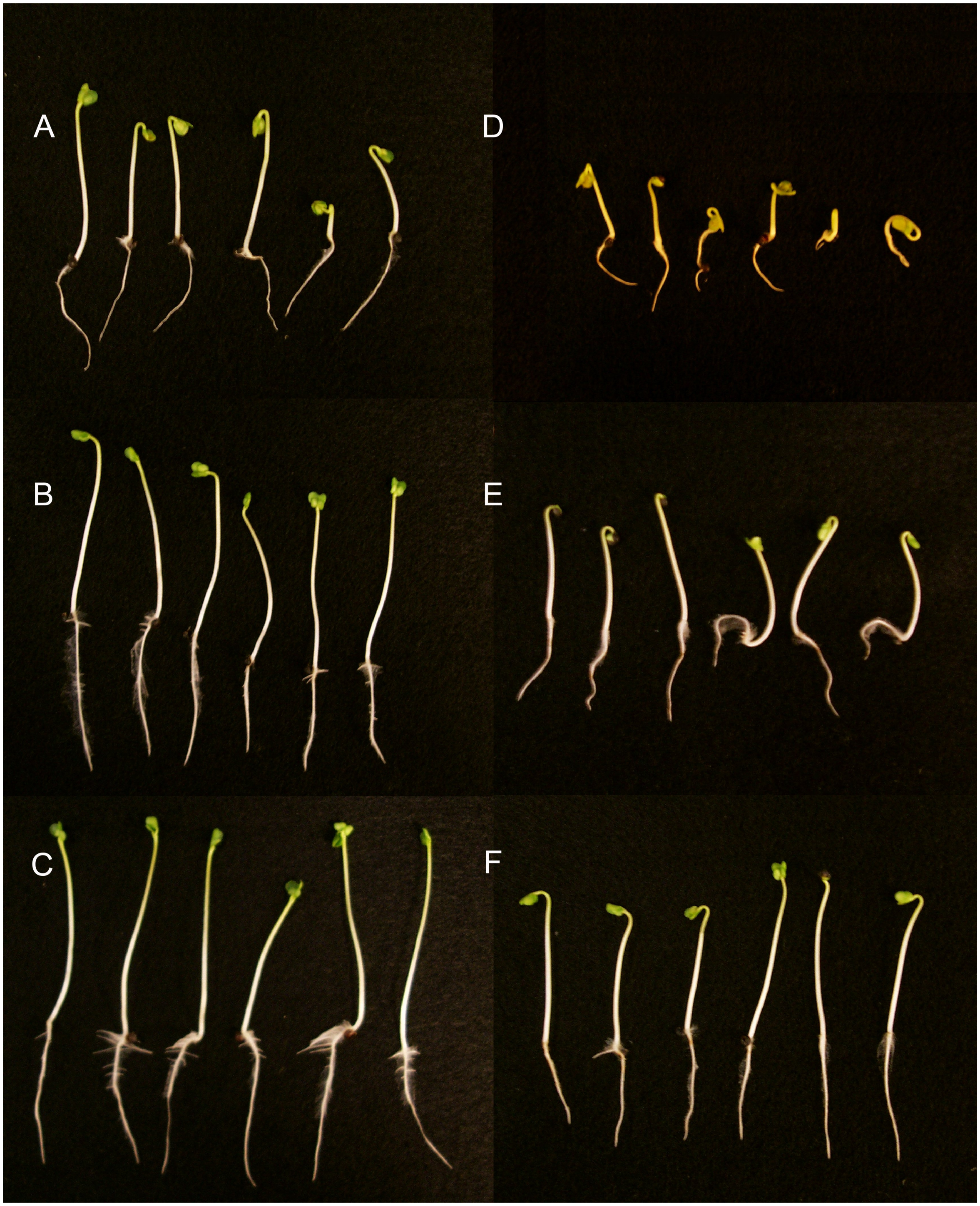

Figure 3.23: Five day-old canola seedlings, Figure from Stearns *et al.* (2005). (A) non-transformed, (B) trAcdS-*35S* and (C) trAcdS-*rolD* grown in water; (D) non-transformed, (E) trAcdS-*35S* and (F) trAcdS-*rolD* grown in 6.0 mM $NiSO_4$ solution.

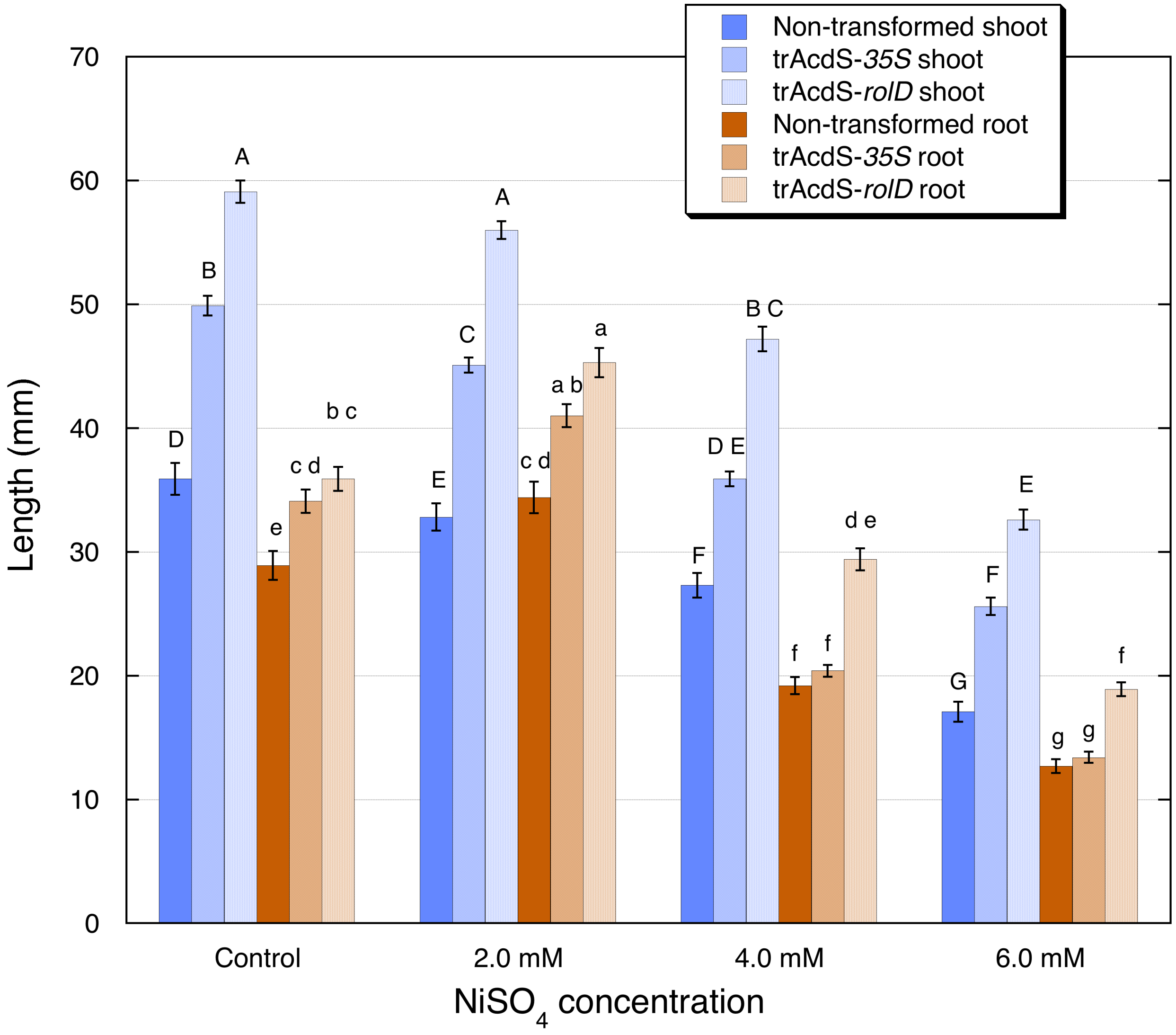

Figure 3.24: Length of five day-old seedlings grown in solutions of $NiSO_4$, Figure from Stearns *et al.* (2005). Capital letters represent results of ANOVA analysis of seedling shoot length, where statistical significance is indicated by a different letter (n = 60, $p < 0.001$). Lower case letters represent the same analysis as above on seedling root length.

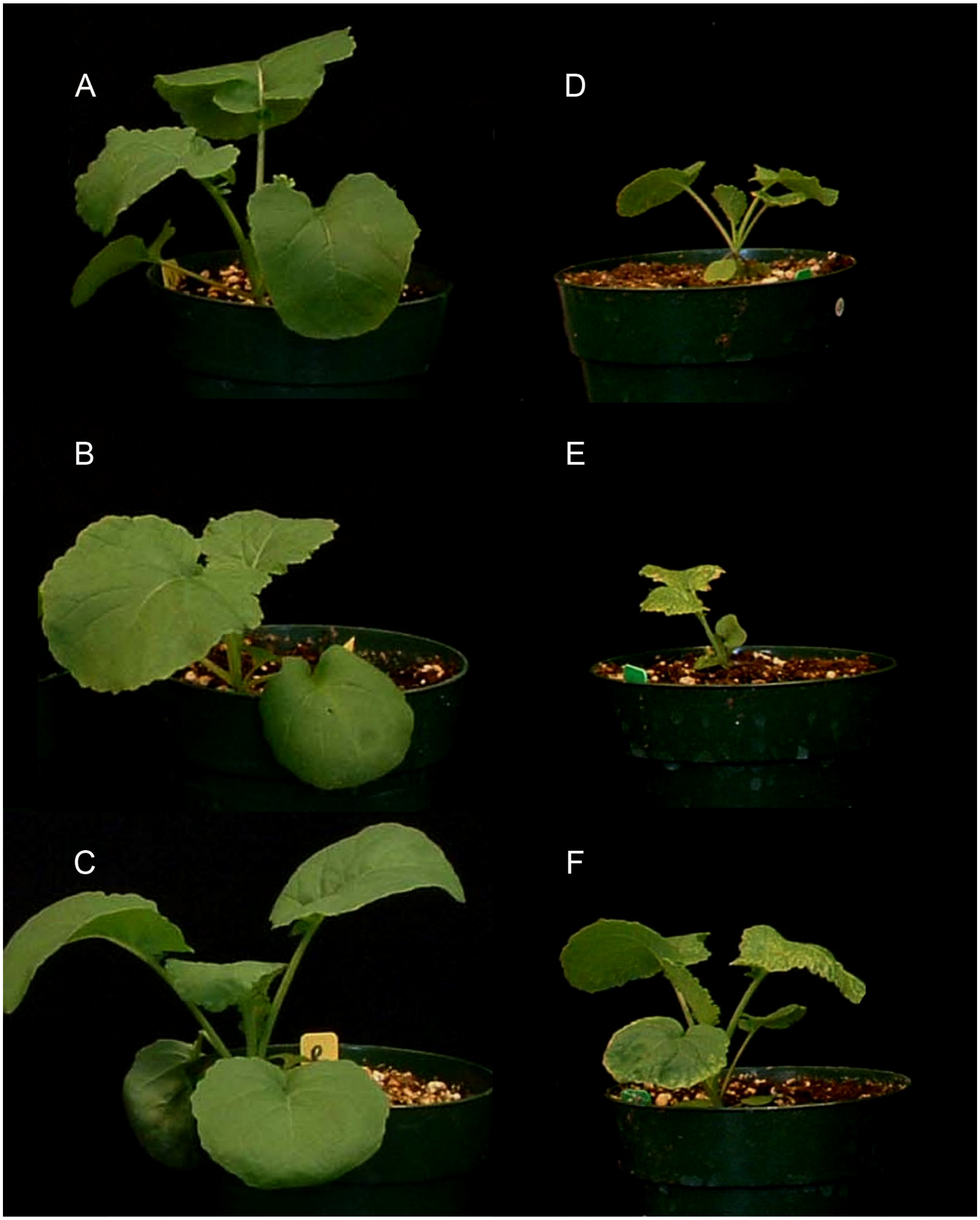

Figure 3.25: Three week-old canola plants, Figure from Stearns *et al.* (2005). (A) non-transformed, (B) trAcdS-*35S* and (C) trAcdS-*rolD* in unspiked soil; (D) non-transformed, (E) trAcdS-*35S* and (F) trAcdS-*rolD* in nickel-spiked soil.

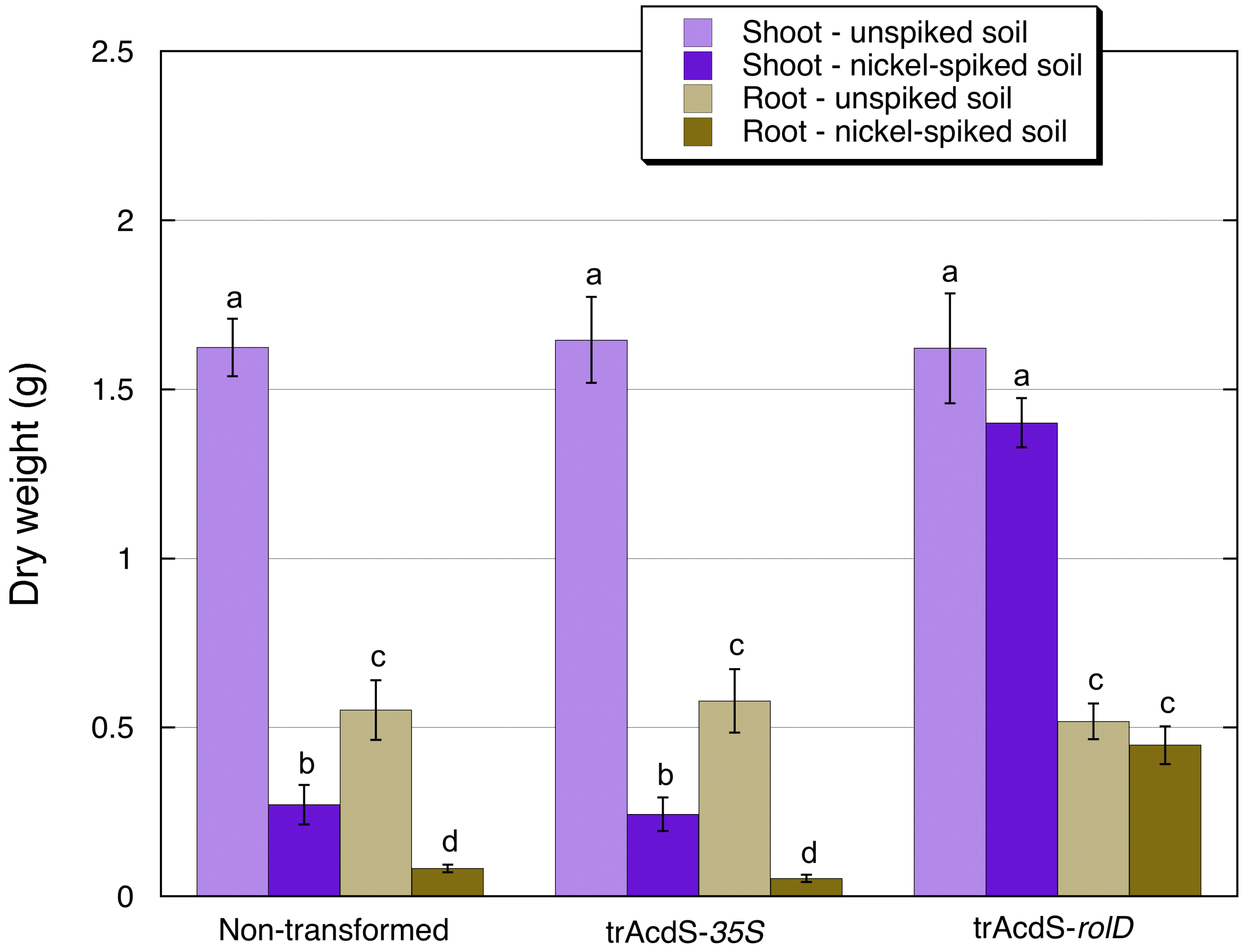

Figure 3.26: Biomass of three week-old transgenic and non-transformed plants in unspiked and nickel-spiked soil, Figure from Stearns *et al.* (2005). Lower case letters represent results of ANOVA analysis where statistical significance is indicated by a different letter (n = 7, $p < 0.001$).

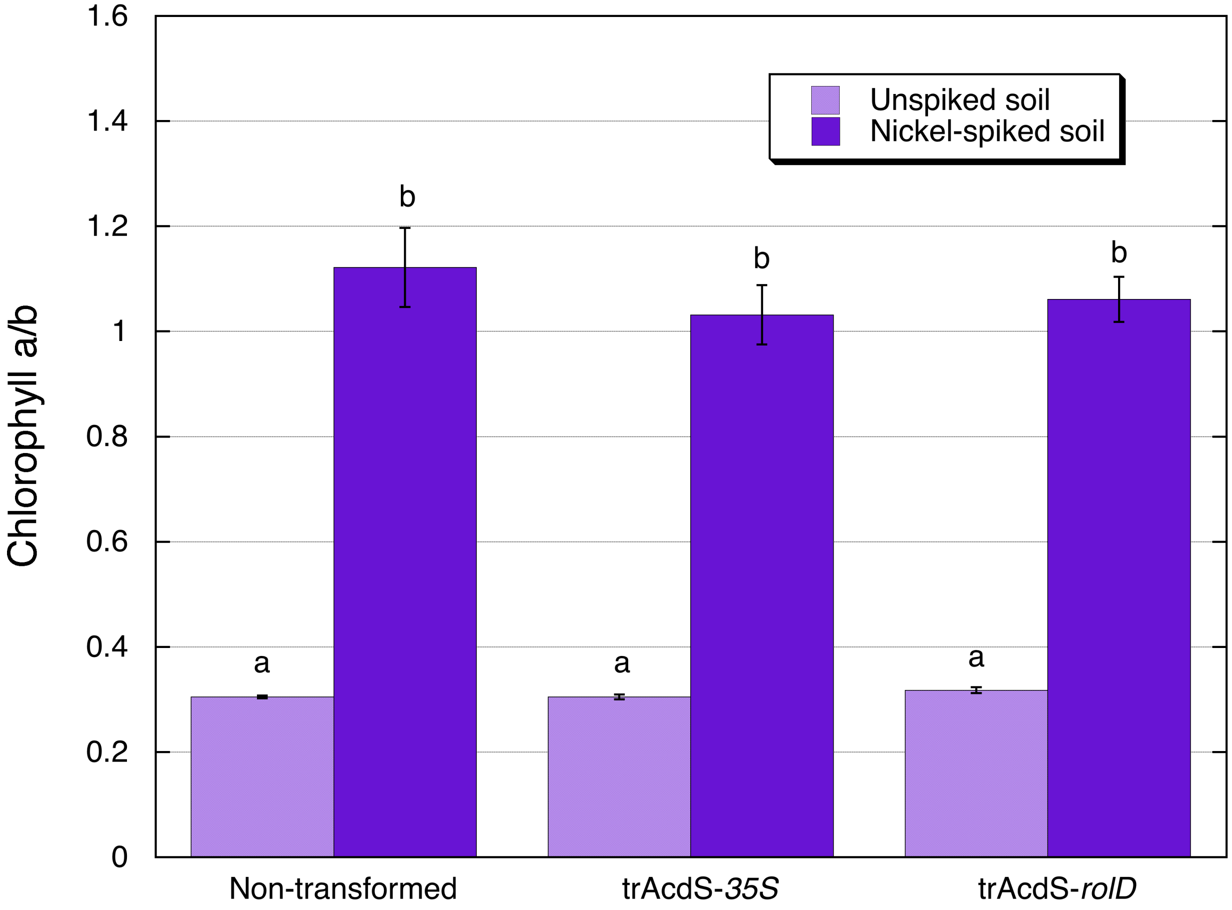

Figure 3.27: Chlorophyll a/b ratios of three week-old transgenic and non-transformed plants in unspiked and nickel-spiked soil, Figure from Stearns *et al.* (2005). Lower case letters represent results of ANOVA analysis of all measurements and statistical significance is indicated by a different letter (n = 5, $p < 0.001$).

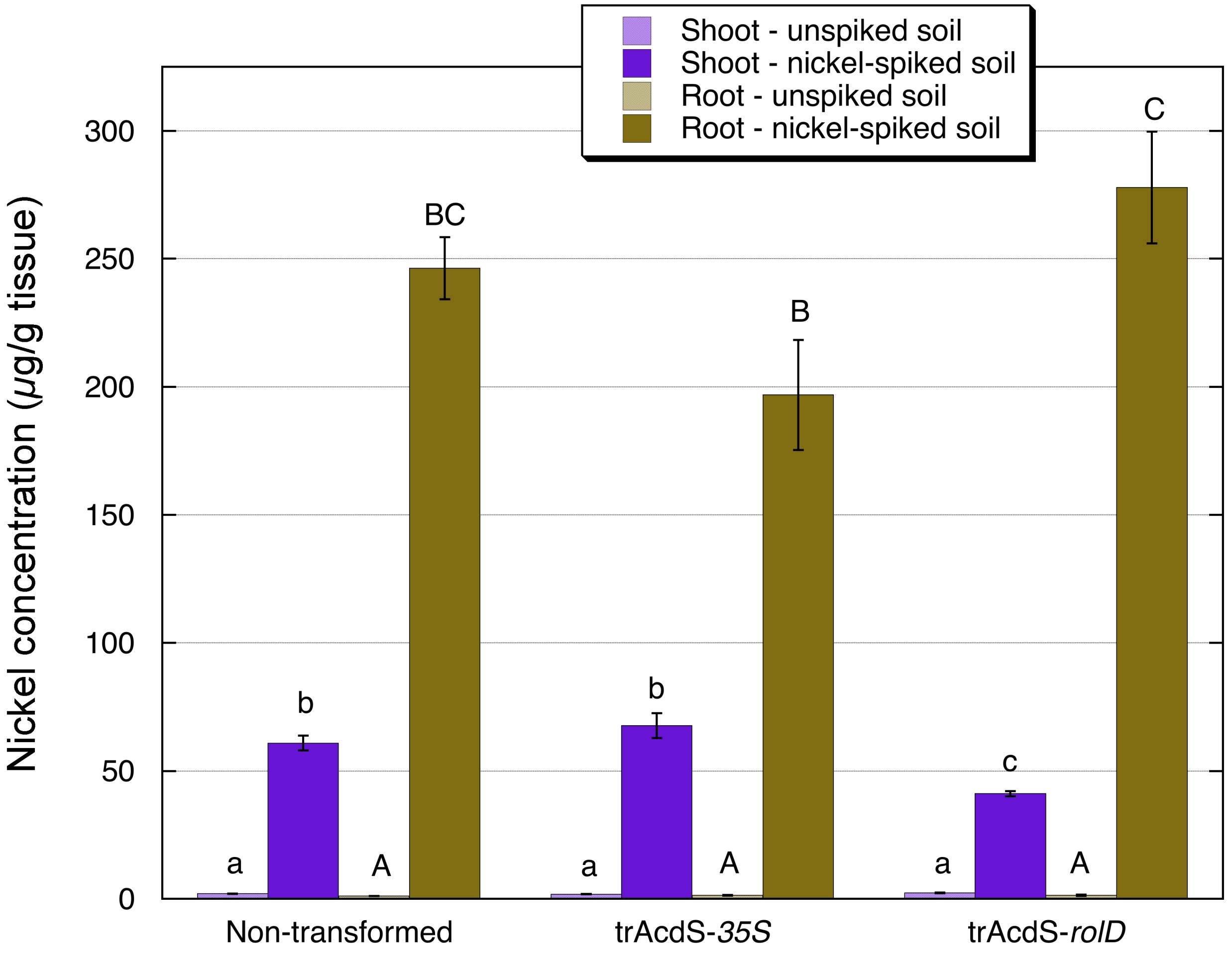

Figure 3.28: Nickel concentration within tissues of three week-old transgenic and non-transformed plants grown in unspiked and nickel-spiked soil, Figure from Stearns *et al.* (2005). Capital letters represent results of ANOVA analysis of seedling root length, where statistical significance is indicated by a different letter (n = 7, $p < 0.001$). Lower case letters represent the same analysis as above on seedling shoot length.

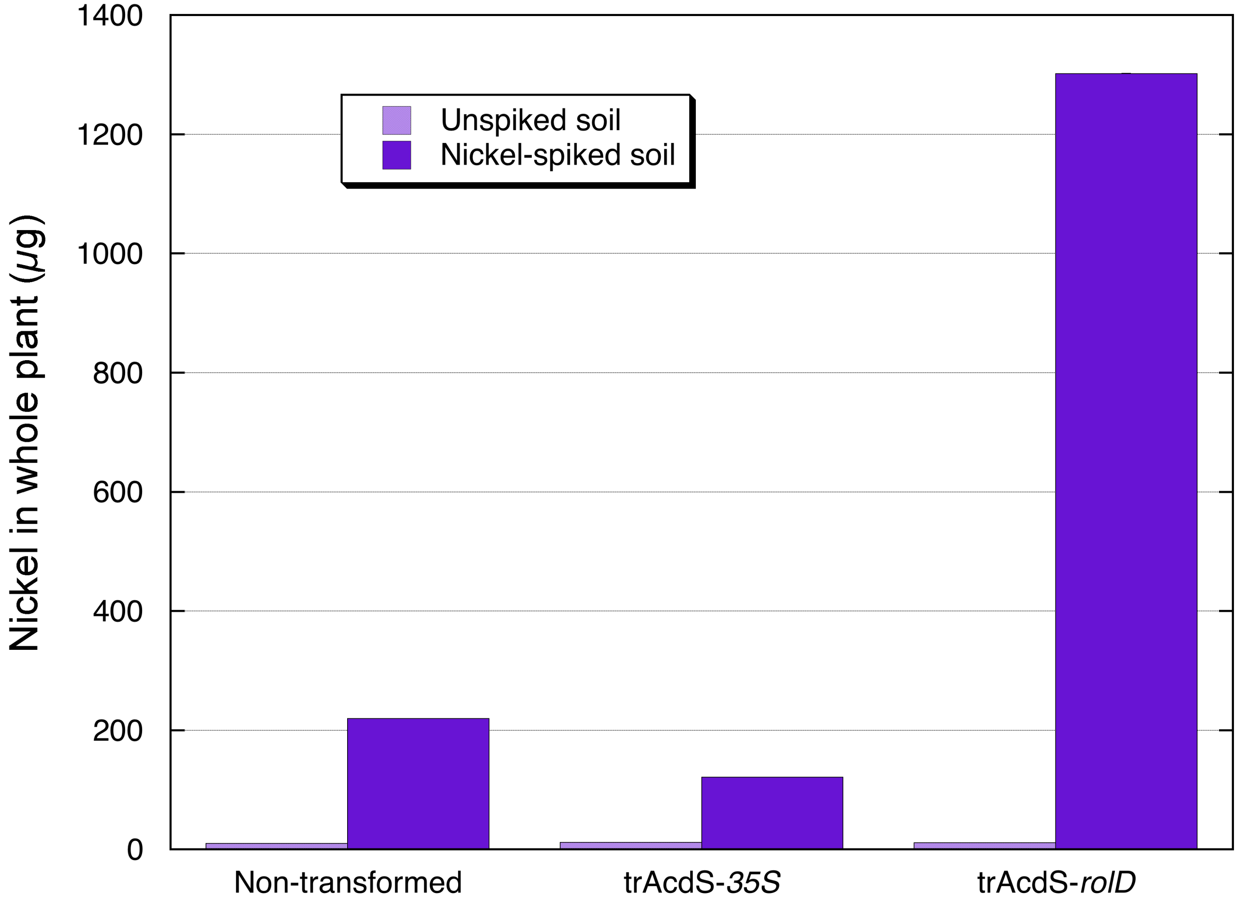

Figure 3.29: Nickel content of three week-old transgenic and non-transformed plants grown in unspiked and nickel-spiked soil (n=5). Average total accumulation of nickel per plant, Figure from Stearns *et al.* (2005).

3.3.2 Transcriptional changes occurring due to the presence of nickel

To gain insight into the response of plants to nickel in the soil, transcriptional profiling was performed on shoots and roots of three week-old trAcdS-*rolD* and non-transformed plants grown in nickel-spiked soil. Due to the small number of replicates, false discovery rate (FDR) adjustment of p-values was not informative and the lists of differentially expressed genes represent those with a $p < 0.01$. In the shoots of non-transformed plants grown in the presence of nickel the expression of 600 genes changed. A list of these changes is presented in Table C.7 in Appendix C, however, since this comparison was not performed on the same chip no fold change values are available. The number of genes which changed in the roots was very small and are discussed in Section 3.3.5.

Because of their nickel tolerance, expression changes within tissues of trAcdS-*rolD* plants grown in nickel-spiked soil were compared to those within non-transformed plants grown in nickel-spiked soil. In the shoots, 79 genes were differentially expressed and a list of these changes is presented in Table C.8. In the roots, 130 genes were differentially expressed a list of which appears in Table C.9.

3.3.3 Functional categorization of expression data

Genes from Table C.7 were grouped according to their Gene Ontology (GO) terms and compared to GO terms for all the genes on the array (total). Functional categorization revealed that in shoots of non-transfromed plants grown in nickel-spiked soil, genes involved in responses to stimuli, response to stress, nitrogen metabolism, secondary metabolite production and catabolic processes were up-regulated and over-represented compared with the total (Figure 3.30). Similarly, genes involved in responses to stimuli and response to stress were down-regulated and over-represented in shoots but to a much lesser degree than the genes which were up-regulated (Figure 3.31).

Functional categorization of genes from Tables C.8 and C.9 is presented in Figures 3.32 and 3.33. In shoots and roots of trAcdS-*rolD* plants grown in nickel-spiked soil, biosynthetic process, nitrogen and secondary metabolism were up-regulated and over-represented (compared to the total). In shoots alone establishment of localization, immune response, sexual reproduction and stomatal movement were up-regulated and over-represented. In roots response to stress and abiotic stimulus were up-regulated and over-represented. In shoot and roots, response to stress and cellular development were down-regulated and over-represented, whereas in the shoots alone response to chemical, endogenous and external stimuli, defense response and aging were down-regulated and over-represented. In the roots alone biosynthetic process, response to abiotic stimulus, nitrogen and secondary metabolism were down-regulated and over-represented.

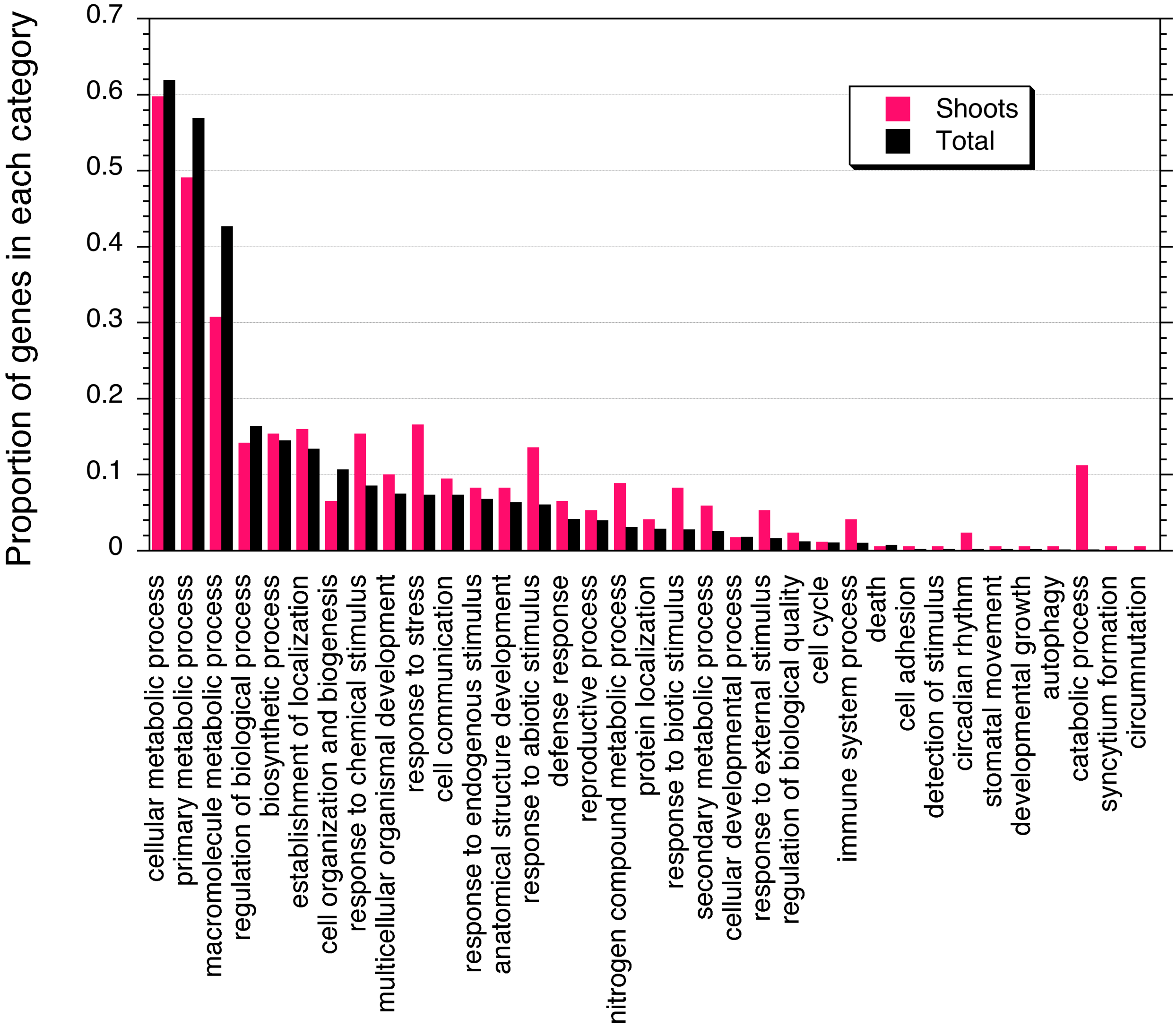

Figure 3.30: Functional categorization of genes up-regulated in shoots of plants grown in nickel-spiked soil. Gene Ontology terms, biological process level 3.

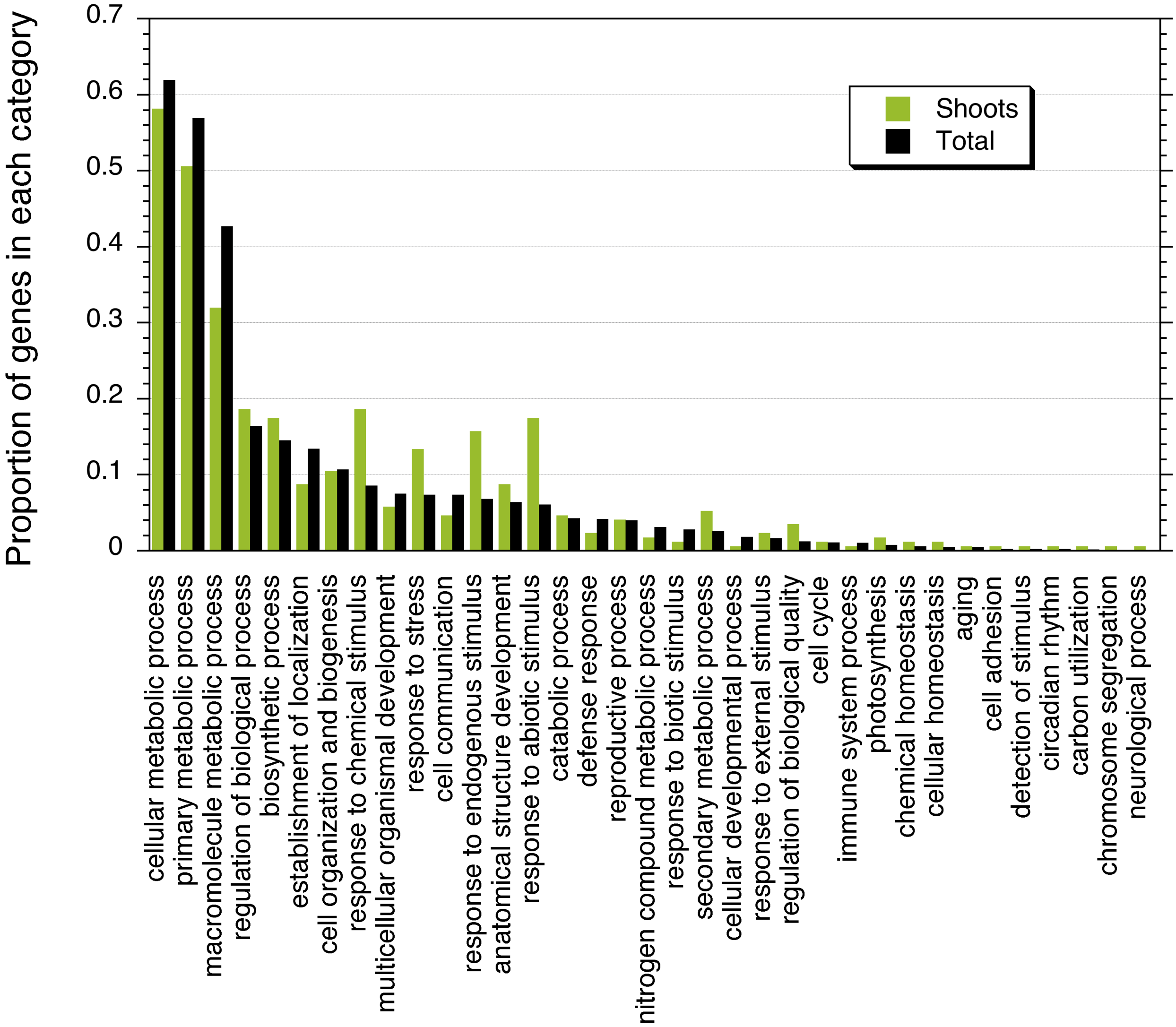

Figure 3.31: Functional categorization of genes down-regulated in shoots of plants grown in nickel-spiked soil. Gene Ontology terms, biological process level 3.

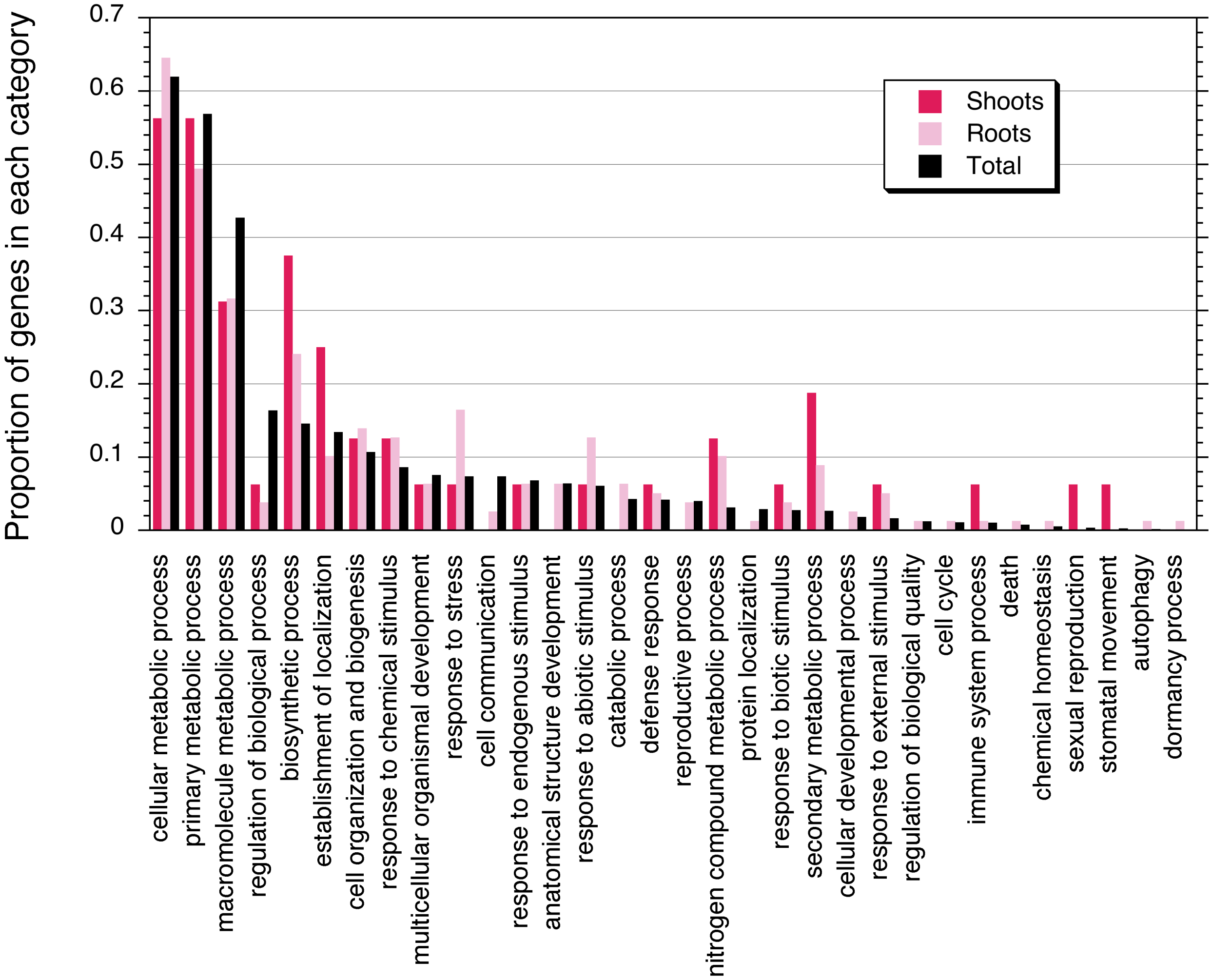

Figure 3.32: Functional categorization of genes up-regulated in trAcdS-*rolD* plants grown in nickel-spiked soil, when compared to non-transformed plants grown in nickel-spiked soil. Gene Ontology terms, biological process level 3.

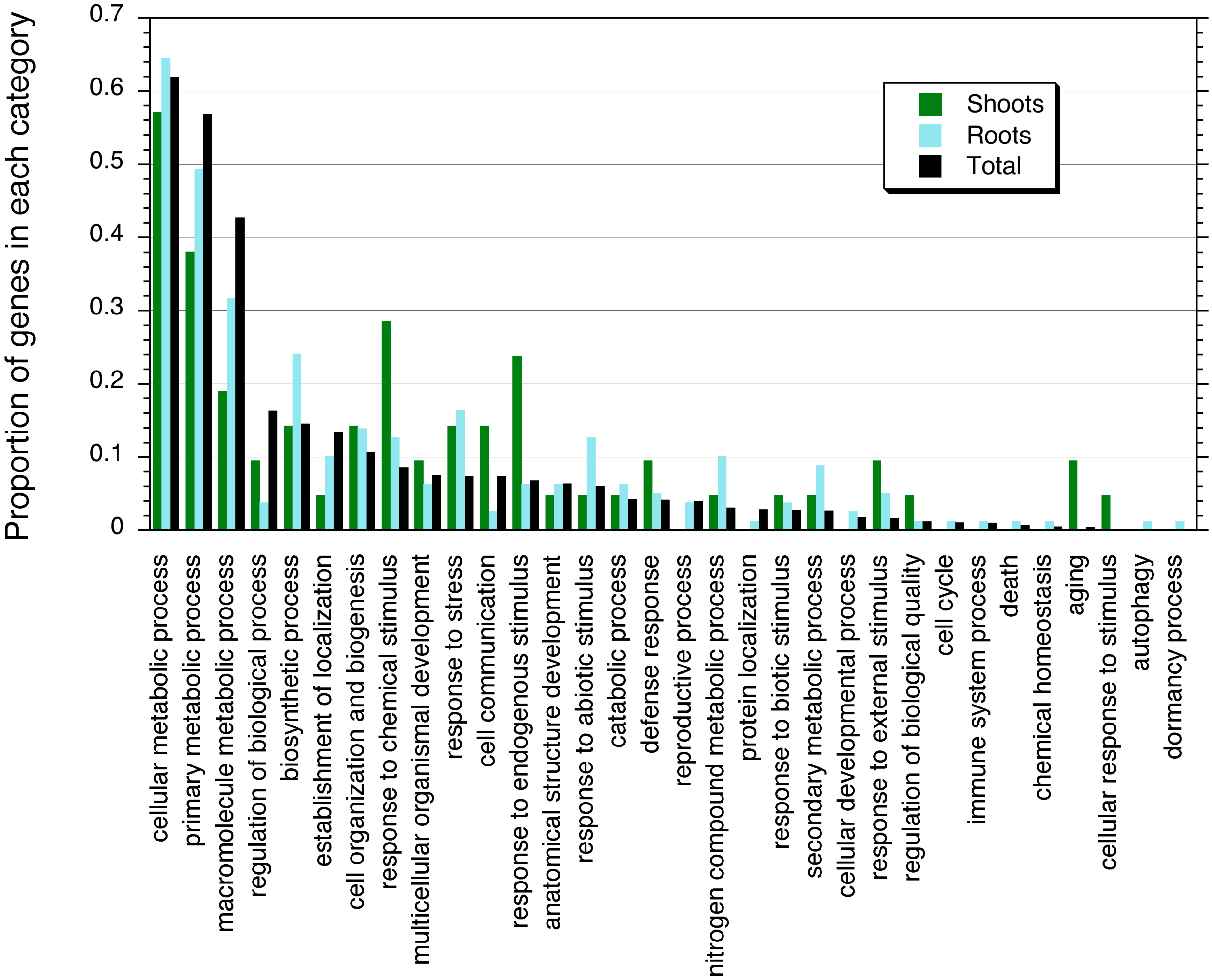

Figure 3.33: Functional categorization of genes down-regulated in trAcdS-*rolD* plants grown in nickel-spiked soil, when compared to non-transformed plants grown in nickel-spiked soil. Gene Ontology terms, biological process level 3.

3.3.4 Metabolic pathways

All genes from Table C.7 were analyzed using the TAIR Pathway Tools Omics Viewer, and any genes for which a biochemical function had been predicted (either biochemically or computationally) were mapped to specific metabolic pathways. These results are presented in Table A.1 in Appendix A and summarized in Tables 3.1 and 3.2. In tissues of non-transformed plants, grown in the presence of nickel, an ACC synthase gene (ACS11) was down-regulated, as were some cytokinin biosynthesis genes. Other genes for cytokinin, IAA and JA biosynthesis were up-regulated. Many genes for photosynthesis were down-regulated (Table 3.1) and genes involved in chlorophyll a degradation were up-regulated. Genes involved in carbohydrate metabolism were up-regulated including those for glycolysis, lactose and sucrose degradation and trehalose biosynthesis. Genes involved in lipid metabolism were both down- and up-regulated. In particular, members of glycolipid desaturation and the glyoxylate cycle were down-regulated, wherease phospholipases and genes involved in triacylglycerol degradation were up-regulated. Fatty acid oxidation genes were both down- and up-regulated (Table A.1). Genes involved in cell wall changes were, for the most part, down-regulated (including cellulose and suberin biosynthesis and homogalacturonan degradation), yet genes for starch degradation were up-regulated. Methionine biosynthesis and sulfate activation genes were up-regulated, yet genes involved in sulfate reduction and the urea cycle were down-regulated (Table A.1). Many genes involved in secondary metabolism were down-regulated (including those involved in anthocyanin, carotenoid, flavonoid, flavonol and phenylpropanoid biosynthesis) with the exception of glucosinolate and tryptophan biosynthesis genes, which were up-regulated. Genes involved in stress responses, such as 4-aminobutyrate, branched chain amino acid and glutamate degradation and glutathione biosynthesis were up-regulated (Table 3.1).

Expression changes of genes from Tables C.8 and C.9 were mapped to the pathways listed in Table A.1 and summarized in Tables 3.1 and 3.2. A few genes for ethylene and gibberellin biosynthesis were up-regulated, whereas genes for IAA and SA biosynthesis were down-regulated. Genes involved in many carbohydrate metabolic pathways were down regulated, including gluconeogenesis and glycolysis, as well as lactose, manose and sucrose degradation. In shoots, genes for sphingolipid biosynthesis and triacylglycerol degradation were up-regulated, whereas genes for the glyoxylate cycle were down-regulated in the roots (Table A.1). Genes involved in cell wall changes were down-regulated mainly in the roots, including homogalacturonan degradation and suberin biosynthesis (Table 3.2). Genes involved in methionine biosynthesis, sulfate reduction and the urea cycle were down-regulated and a gene for nitrate assimilation was up-regulated. Very few genes involved in secondary metabolism pathways changed, with the exception of those involved in phenylpropanoid biosynthesis, which were down-regulated in the roots.

3.3.5 Gene lists

An examination of the list of genes which changed in shoots of non-transformed plants grown in nickel-spiked soil (Table C.7) revealed that genes for AP2-domain containing transcription factor (which are ethylene responsive), auxin response factors, cold-responsive protein, dehydrin, EREBP, expansin family protein, myb family transcription factors, RNA polymerases and WRKY family transcription factors were down-regulated, whereas genes for dormancy associated proteins, F-box proteins, leucine-rich repeat proteins, RNA binding proteins, scarecrow-like transcription factors and WD-40 repeat family proteins were up-regulated. Very few genes were found to change between roots of non-transformed plants grown in nickel-spiked soil compared to the control, among them, however, were, pentatricopeptide (PPR) repeat-containing protein (AT4G20770), glycoside hydrolase family 19 protein (AT2G43610), octicosapeptide/Phox/Bem1p (PB1) domain-containing protein (AT5G20360), and a potassium transporter family protein (AT2G35060) all of which were up-regulated and L-ascorbate peroxidase (AT1G07890), which was down-regulated.

In shoots of trAcdS-*rolD* grown in nickel-spiked soil (Table C.8) genes for auxin response factors, pentatricopeptide (PPR) repeat-containing proteins and WD-40 containing protein (involved in RNA metabolism) were down-regulated and a WRKY transcription factor gene which was up-regulated. In roots (Table C.9), genes for DNAJ heat shock proteins, leucine-rich repeat protein and pathogenesis-related protein were down-regulated.

Chapter 4

Discussion

Some of the most obvious effects of bacterial ACC deaminase on plant development are the increase in root and shoot length, increased biomass and faster development. When stress is added, these effects are magnified and plants are able to thrive where untreated or untransformed plants grow poorly or perish. This advantage, conferred by PGPR, is thought to be due not only to expression of ACC deaminase, but also to the many other biological activities of PGPR including auxin and siderophore production (Glick *et al.*, 1999). When bacterial ACC deaminase is expressed in transgenic plants, a similar level of growth promotion is achieved, suggesting that lowering plant ethylene levels has a powerful effect on plant success. The study described in this thesis provides insight into some of the mechanisms at work in the growth promotion of plants by bacteria and the effects of lowering plant ethylene levels through the action of ACC deaminase.

Gene expression changes, that were observed, fell into three categories: changes in phytohormone biosynthesis and response, plant growth and the stress response. A myriad of other small and large changes in plant gene expression were also observed but upon closer scrutiny many of these were related to one of the above three categories. Changes in phytohormone networks are not surprising since ACC deaminase alters the level of ethylene, a hormone which interacts with many other plant hormones and is central to many plant processes including growth and development. Alterations in genes involved in stress responses are required for the inherent precision with which plants interact with their environments and many parts of the stress response are in fact adaptive changes. Plant responses involve the shifting of the many delicate balances which allow it to cope with changes inside and outside of the plant body.

First, the changes in gene expression of ethylene biosynthesis and response will be examined, followed by changes in auxin and jasmonic acid biosynthesis and response gene expression. Next, the effects of bacterial ACC deminase on growth, development and stress response will be examined in the context of bacterial colonization, ACC deaminase transgene expression and heavy metal stress.

4.1 Phytohormones

Ethylene has direct effects on plant growth, development, maturation and stress and indirect effects on countless other processes through its interaction with other plant hormones. Many of these interactions are not fully understood due to the difficulty in teasing out the action of only one or two elements of a complex network. Much of what is known about ethylene action has been gained through application of exogenous ethylene, whose concentration is often much higher than would naturally occur in the plant, or by characterization of the phenotype of ethylene mutants. These mutants are either constitutive ethylene overproducers (such as *ctr1*) or ethylene insensitive (such as *ein2*). Bacterial ACC deaminase on the other hand, is thought to only lower stress ethylene and not baseline ethylene levels required for regular physiological functions.

4.1.1 Ethylene biosynthesis and response genes

Expression of ethylene biosynthesis and response genes changed in plants treated with bacteria. ACC oxidase, multiple ethylene-response factors and ethylene-inducible stress genes were up-regulated in plants treated with AcdS^{-} bacteria, suggesting that more ethylene was present in these plants. Genes for ACC oxidase, ethylene-inducible stress genes and AP2-domain containing protein genes ((known to be regulated by ethylene response factors Broekaert *et al.*, 2006)) were down-regulated in tissues of plants treated with AcdS^{+} bacteria, lending support to this conclusion. Unexpectedly, some ethylene biosynthesis, signaling and response factor genes were up-regulated in tissues of plants treated with AcdS^{+} bacteria, yet to a lesser extent than in plants treated with AcdS^{-} bacteria and this may be due to the presence of bacterial auxin, which *Pseudomonas putida* UW4 is known to produce. Bacterial auxin has been shown to turn on the transcription of ACC synthase within plant tissues, yet its induction of ACC oxidase has not been shown. Also, transcription of ethylene signaling genes (EIN3 and EIL1) has been shown to not be induced by ethylene (Gagne *et al.*, 2004; Stepanova and Alonso, 2005), suggesting that other factors, such as bacterial colonization or the up-regulation of genes involved in other signaling cascades, may have been responsible for the changes gene expression in plants treated with AcdS^{+} bacteria.

In transgenic plants expressing ACC deaminase, ethylene response factor and DRE-binding protein elements (DREB) containing genes were highly down-regulated. DREB transcription factors are involved in the signaling of many abiotic stresses and members of this family are similar to ethylene response factors (Broekaert *et al.*, 2006). In addition, genes known to respond to ethylene such as disease response, pathogenesis-related protein (PR-1), β-glucanase and chitinase genes were down-regulated in transgenic plants expressing ACC deaminase. This is an indication that plants expressing ACC deaminase have lower levels of ethylene biosynthesis, than do non-transformed plants, since ethylene induced transcription is down-regulated.

In the presence of ACC deaminase, the expression of five different genes for ACC oxidase changed depending on the developmental stage and the treatment (Figure 3.6). When inoculated with AcdS^{+} bacteria, two genes for ACC oxidase were down-regulated and one (EFE) was up-regulated. Interestingly, this same transcript was up-regulated in plants treated with

AcdS^{-} bacteria, suggesting that it is induced by bacteria and not necessarily by ethylene, an observation which is supported by the fact that this same transcript is down-regulated in transgenic seedlings. In transgenic plants expressing ACC deaminase, four different genes for ACC oxidase are up-regulated depending on the develpmental stage and the presence or absence of nickel. Ethylene-responsive gene expression did not increase, however, suggesting that these transcripts are not responsible for higher ethylene biosynthesis. ACC oxidase genes belong to a family comprising many members, yet the gene expression patterns and protein activities have been proven for only two of them (neither of which changed in this study). The genes which were up-regulated here may be expressed as proteins with different enzymatic activities or may be regulated post-transcriptionally. In either case, these genes may be regulated by something other than ethylene in response to bacterial colonization.

4.1.2 Auxin biosynthesis and response genes

One of the most important observations made during this study was that many auxin-responsive protein genes were up-regulated in the presence of ACC deaminase (Figure 3.9, Tables C.1 and C.5). The results presented here offer some evidence about ethylene regulation of auxin action which has also been suggested in recent literature. For example many ARF were up-regulated in shoots of plants treated with AcdS^{+} compared to shoots of plants treated with the AcdS^{-} mutant (Figure 3.9) and in trAcdS-*rolD* plants (Tables C.1 and C.5). Included were representatives from all three major early (or primary) auxin response genes (auxin regulated proteins (AUX/IAA), primary auxin responsive GH3 proteins (GH3), and small auxin up RNA (SAUR). They are called early auxin response genes since they have been shown to be rapidly induced by active auxins (Hagen and Guilfoyle, 2002). All three groups exists as large gene families in Arabidopsis with 28 members for AUX/IAA, 20 for GH3 and 36 for SAUR. AUX/IAAs are involved in regulating the auxin response, but the roles of GH3 and SAUR are still unknown. SAUR, however, are small RNA molecules which are induced within minutes of auxin treatment and are thought to play a role in auxin signal transduction along with Ca^{2+} and calmodulin (Yang and Poovaiah, 2000). Genes for Ca^{2+}- and calmodulin-binding proteins were also up-regulated in tissues of plants treated with $AcdS^+$ bacteria and transgenic plants expressing the bacterial ACC deaminase. This suggests that lowering ethylene levels releases repression of the auxin signaling cascade. The interaction between auxin and ethylene has long been suspected and studied but its intricacies have yet to be elaborated in detail. There is evidence, however, that ethylene acts to inhibit auxin response factors by activating repressors such as hookless1 (HLS1) (Lehman *et al.*, 1996; Li *et al.*, 2004) and that ethylene interacts with auxin transport within different plant species (Suttle, 1988; Lee *et al.*, 1990; Prayitno *et al.*, 2006; Ruzicka *et al.*, 2007). Figure 4.1 illustrates the model of ACC deaminase's role in plant growth promotion, which has been modified to include this new data. This phenomenon occured mainly in the shoots and was a result of lowering ethylene levels in the roots, which suggests that ethylene or some other mobile plant signaling molecule travels up into the shoot from the root to affect auxin responses.

IAA biosynthesis genes were down-regulated both in tissues of plants treated with $AcdS^+$ bacteria and transgenic plants expressing ACC deaminase, but not in tissues of plants treated with the $AcdS^-$ mutant. This observation suggests that ethylene has a role in the regulation of auxin biosynthesis. Some evidence exists for links between ethylene and auxin biosynthesis regulation (Stepanova *et al.*, 2007), however, it has not been studied in great detail due to the difficulty in separating the effects of these two phytohormones. Auxin, like ethylene, is responsible for many physiologically important phenomena including cell elongation and root initiation. In particular, auxin induced cell elongation is of interest since it involves increased cell wall permeability and cell wall synthesis (Delvin, 1966). Changes in the expression of genes involved in cell wall structure, such as pectin breakdown, suberin and cellulose biosynthesis were observed in the presence of bacterial ACC deaminase (Table A.1) and may be due to and increased response to plant or bacterial auxin.

A model of how bacterial ACC deaminase may be contributing to regulation of auxin

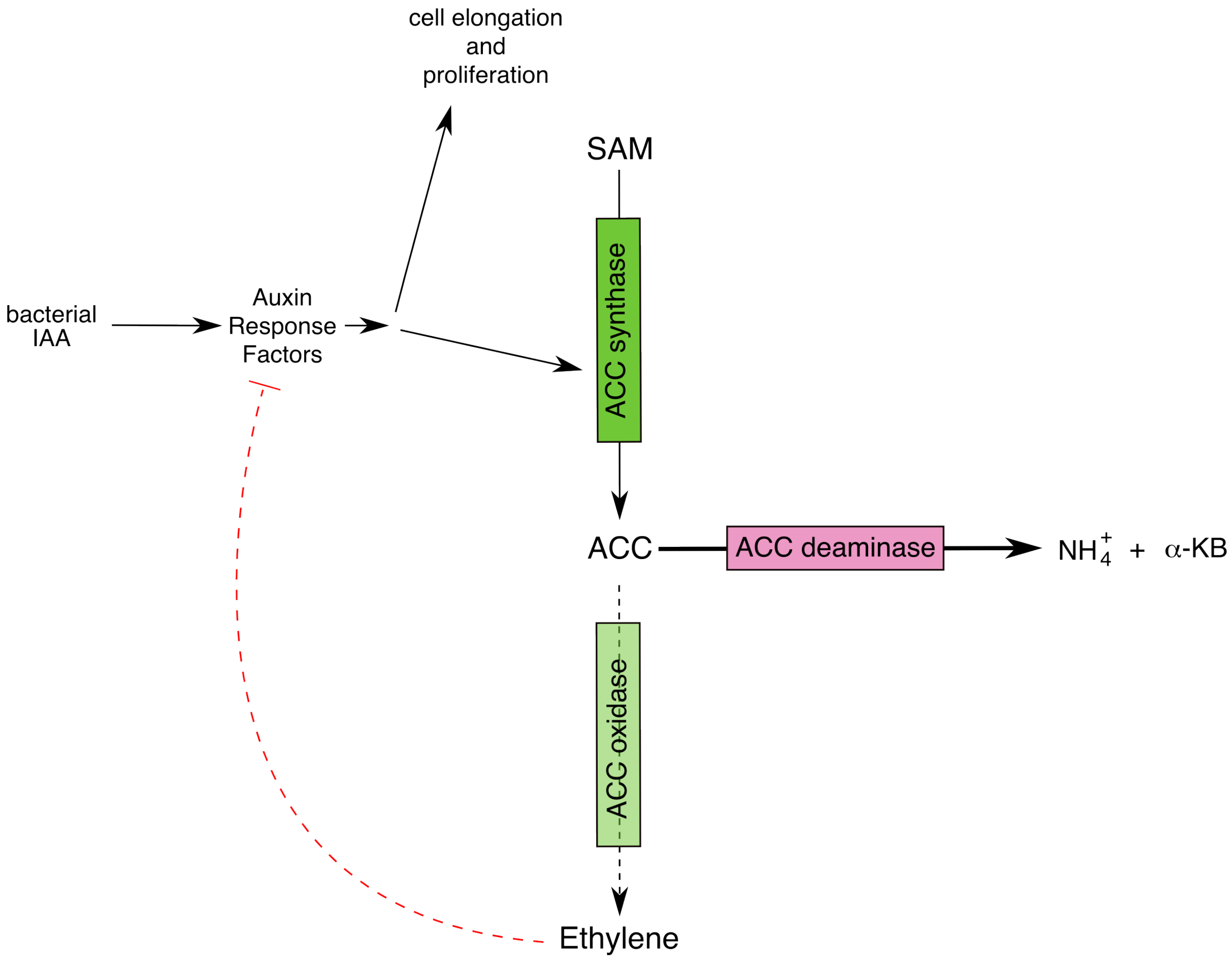

Figure 4.1: Model of the role of ACC deaminase in plant growth promotion. Dotted lines represent steps down-regulated in the presence of ACC deaminase and the red line indicates possible regulatory mechanisms added to the model implied by this work.

response is presented in Figure 4.2. Bacterial pathogen-associated molecular patterns or PAMP (to which *Pseudomonas* flagellin belongs) are small bacterial proteins and secretions which are perceived by plants and cause the down-regulation of auxin signaling in Arabidopsis by targeting auxin receptor transcripts. Bacteria produce auxin which is taken up by the plant and aids some pathogenic bacteria to grow within tissues. Plants are thought to counter-act the effects of auxin produced by pathogenic bacteria by repressing auxin signaling, and this strategy has been shown to restrict growth of some *Pseudomonas* pathogens. Auxin signal repression in this case is thought to occur through activation of microRNA (miRNA), which leads to the degradation of primary auxin response and TIR1 transcripts (Navarro *et al.*, 2006). TIR1 stands for transport inhibitor response 1 and is the auxin receptor in plants. Interestingly, miRNA-mediated regulation of pathogen induced auxin response may have an ethylene component, due to evidence for miRNA mediated regulation of the ethylene response and the fact that ethylene regulates its own signaling. EIN3 is essential to ethylene signaling and is regulated at the protein level by EBF mediated degradation (Figure 1.3). Ethylene insensitive 5 (EIN5) is allelic to the cytoplasmic exoribonuclease 4 (XRN4) (Potuschak *et al.*, 2006), which has recently been implicated in the microRNA (miRNA) mediated turnover of some Arabidopsis transcripts (Souret *et al.*, 2004) and *ein-5* mutants show an accumulation of EBF mRNA and less EIN3 protein. Since neither the regulation of EIN5 nor all of its targets are known, it is possible that it may be involved in ethylene mediated miRNA regulation of auxin response, especially if EIN5 is ethylene induced. MicroRNA are known to co-regulate networks with other miRNA (Mallory and Vaucheret, 2006) and may function to alter a cascade of transcriptional regulation involving ethylene and auxin responses.

4.1.3 Jasmonic acid biosynthesis and response genes

Jasmonic acid (JA) biosynthesis genes were up-regulated to the highest degree within tissues of plants treated with AcdS$^-$ bacteria. The up-regulation of the essential JA biosynthetic

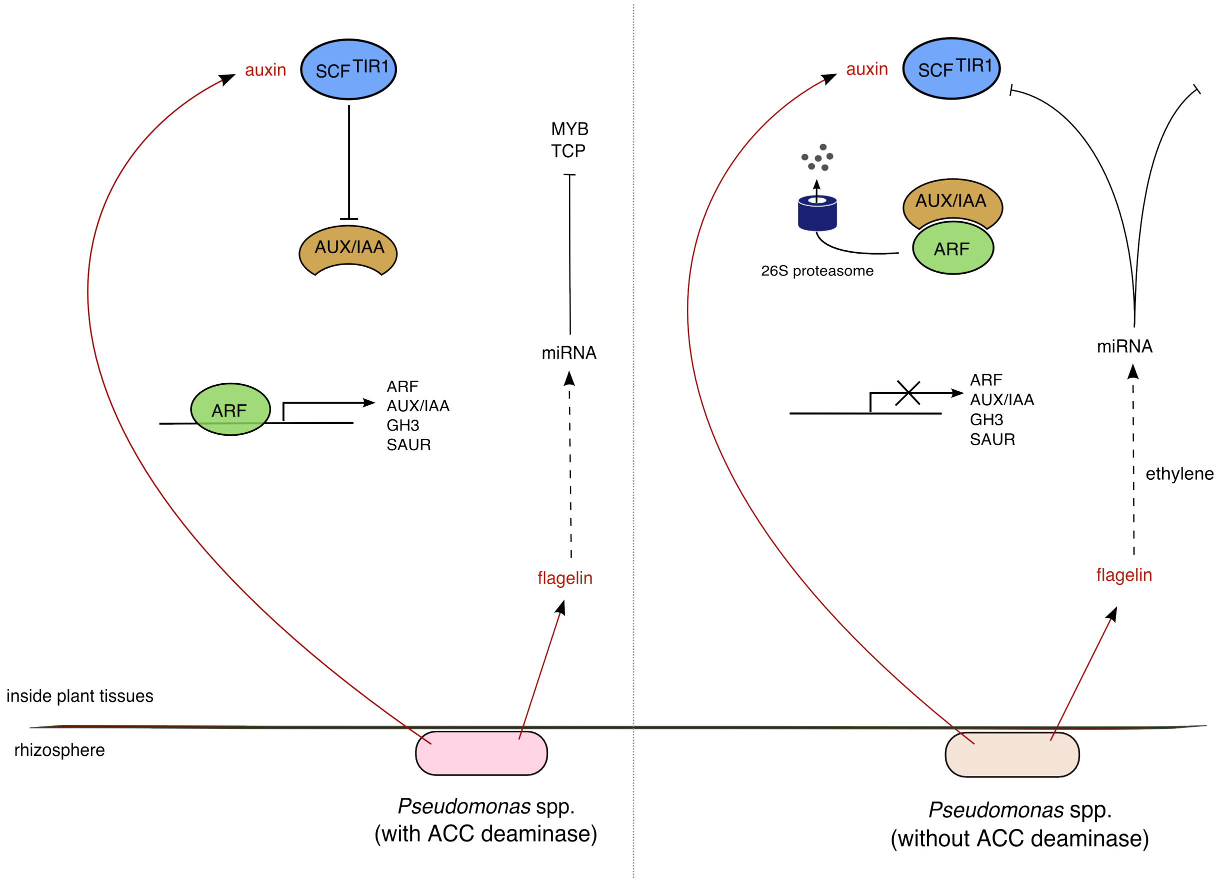

Figure 4.2: Regulation of auxin response by miRNA, proposed role for ethylene. Compounds in red are produced by the bacterium, dotted arrows represent many possible steps, some of which are unknown. Abbreviations include apetala 2 (AP2) , auxin response factors (ARF), auxin regulated proteins (AUX/IAA), primary auxin responsive GH3 proteins (GH3), MYB transcription factors (MYB), pentatricopeptide repeat proteins (PPR), small auxin up RNA (SAUR) and teosinte branched 1, cycloidea and PCF transcription factors (TCP).

enzyme gene allene oxide synthase (AT5G42650) was confirmed with real-time RT-PCR (Figure 3.13). Once it is formed, JA must be conjugated to amino acids by JA-amino synthetases like jasmonate resistant 1 (JAR1) to activate JA signaling. Transcription of JAR1 was up-regulated in plants treated with both AcdS$^+$ and AcdS$^-$ bacteria, yet transcription of the JA responsive gene IAA-Ala resistant 3 (IAR3) and the JA and ethylene responsive gene thionin 2.1 (THI2.1) (Brown *et al.*, 2003) was only present in control plants and those treated with the AcdS$^-$ mutant. JA has been linked to ethylene signaling, and some genes are responsive to JA and ethylene (namely THI2.1), yet it appears from this study that ethylene is required for some forms of JA signaling, namely of pathways that lead to IAR3 expression.

Within the promoter of an ethylene response factor (ERF1) there are elements for both the ethylene signal (EIN3) and the jasmonic acid signaling pathway (Broekaert *et al.*, 2006). This suggests that transcriptional activation of ethylene response factors may be a cross point of these two hormonal systems. One interesting connection between JA and ethylene is the inactive JA conjugate JA-ACC. It has been measured in plant tissues in significant amounts and appears to be the second most abundant JA conjugate in plant tissues (Staswick and Tiryaki, 2004). JA-ACC is thought to act as a form of storage for both JA and ACC and hydrolyis probably proceeds by way of JA-amino synthetases. The only known JA-amino synthetase JAR1, however, inhibits the accumulation of JA-ACC since it catalyzes the formation of JA-Ile (jasmonic acid/isloleucine conjugate), which is the active form of JA. Perhaps the conversion of JA-ACC to JA and ACC causes ethylene and JA responses to be activated simultaneously.

JA responsive genes were found to be up-regulated in nickel-treated plants (ie. IAR3, JAR1, liopxygenase 2 (LOX2), coronatine induced 1 (CORI3) and similar to CORI3 (F9D16.60)) and in trAcdS-*rolD* seedlings (ie. ribonuclease 1 (RNS1), pathogenesis-related 3 (ATHCHIB), COR13 and F9D16.60). Since JA signaling is seen during both botic and abiotic stress, these changes were expected to occur in nickel-stressed plants and in fact the expression of

JA biosynthesis genes was up-regulated in nickel-treated plants as well (Table A.1). The appearance of some JA responsive protein transcripts in trAcdS-*rolD*, however, was surprising as was the up-regulation of a lipoxygenase involved in JA biosynthesis. The biosynthesis of this plant hormone is known to be autocatalytic, yet activation by JA amino synthetases is essential for signaling. JA biosynthesis is not known to be regulated by ethylene, so it is more likely that a difference in ethylene biosynthesis in developing seedling roots turns on JA biosynthesis and signaling due to mild stress.

4.2 Effect of *Pseudomonas putida* UW4 on plant gene expression

The overall expression patterns of plants treated with AcdS$^+$ and AcdS$^-$ bacteria was very similar, which is apparent from the gene tree in Figure 3.8. Colonization of plant roots by growth-promoting bacteria has a profound effect on the transcription of plant genes, so much so that the effect of removing the bacterial ACC deaminase gene is somewhat masked. Below, the effects of bacterial colonization will be discussed as well as the impact of ACC deaminase on plant gene expression.

Timmusk and Wagner (1999) showed that treating plants with PGPR is perceived as a mild stress, where plants inoculated with the bacterium *Paenibacillus polymyxa* in the absence of stress were stunted and markers for both abiotic (drought) and biotic stress were up-regulated. In this study, expression changes within tissues of plants treated with bacteria indicated perception of a mild stress, especially when compared to the stress response of plants treated with nickel described in Section 4.3. This includes the up-regulation of genes involved in response to stimuli, stress and catabolic processes such as glutamate degradation (Figure 3.3 and Tables 3.1, 3.2 and A.1). As illustrated in Section 4.2.1 and noted in (Hontzeas *et al.*, 2004), the presence of ACC deaminase reduces the level of stress perceived by the plant.

4.2.1 Role of ACC deaminase in plant growth-promotion

In this study, plants inoculated with AcdS$^-$ bacteria had a higher stress response than plants inoculated with AcdS$^+$ bacteria. For example in Figure 3.3 genes involved in response to stress, stimuli, defense response, secondary metabolism and immunity were over-represented in tissues of plants treated with AcdS$^-$ bacteria as compared to those treated with AcdS$^+$ bacteria. It is also apparent from this graph that genes involved in development, growth and reproduction were under-represented in tissues of plants treated with AcdS$^-$ bacteria. Nitrogen compound metabolism was down-regulated in tissues of plants treated with AcdS$^+$ bacteria, which indicates that nitrogen uptake was high therefore breakdown of nitrogen stores was not necessary. Also, genes involved in cyanate degradation, nitrate and ammonia assimilation were down-regulated in shoots of plants inoculated with ACC deaminase containing bacteria (Table A.1), suggesting that the carbon/nitrogen balance was different than within control tissues.

A group of genes which clustered together were down-regulated in tissues of plants treated with AcdS$^+$ bacteria and up-regulated in tissues of plants treated with AcdS$^-$ bacteria (Figure 3.8). Among these were genes for glutathione S-transferases, one of which is auxin and pathogen inducible. Also included were genes involved in stress and defense response (i.e. β-glucosidase which is known to be expressed during colonization by fungi). These observations suggests that seedlings inoculated with AcdS$^+$ bacteria had lower stress-induced gene expression and hence lowering ethylene (through ACC deaminase action) reduces the plant stress response which is activated by bacterial colonization of plant roots.

4.2.2 Plants with a bacterial ACC deaminase transgene

Plants expressing ACC deaminase had faster germination, longer roots and shoots and higher biomass than did non-transformed plants. Cellulose biosynthesis was up-regulated in transgenic plants as was the degradation of triacylglycerol and branched-chain amino acid degradation. Since cellulose is important for building new cell walls triacylglycerol is a seed storage oil which is used by the developing seedling and branched chain amino acids promote their own breakdown as a carbon source during seed germination. These observations suggest that transgenic seedlings developed slightly faster than non-transformed seedlings.

In mature transgenic plants, branched chain amino acid breakdown was highly down-regulated and sulfate reduction and nitrate assimilation were up-regulated indicating healthy growth. Sulfate reduction in particular is important since young leaves and shoots have a high demand for cysteine and methionine, the major sulfur-containing compounds in plants. Stress pathways were highly down-regulated in shoots and roots of transgenic plants. Taken together, this data suggests that transgenic plants expressing a bacterial ACC deaminase grow and develop slightly faster than non-transformed plants due to the lower levels of ethylene biosynthesis and de-repression of the auxin response, even in the absence of stress. Since transgenic plants germinate and flower sooner than non-transformed plants (1 – 2 days), many of the the transcriptional changes observed may be due to a slight difference in developmental maturity. In fact, ethylene is involved in aspects of plant development and maturation (Abeles *et al.*, 1992), and is known to interact with other developmentally important phytohormones, such as auxin, jasmonates and giberrellin (Stepanova *et al.*, 2007; Wasternack, 2007; Gazzarrini and McCourt, 2003). It is important to note, therefore, that transcriptional changes occurring within transgenic plants expressing the ACC deaminase transgene may be due primarily to the effect of lowering ethylene and secondarily to a slight mismatch in developmental stage.

4.3 Effects of nickel stress

Some of the effects of nickel in this study include a decrease in biomass, inhibition of root growth, yellowing of leaf tissues, necrosis and death. The transcriptional changes that occurred in tissues of plants grown in nickel-spiked soil included genes involved in growth and development including down-regulation of sulfur reduction, photosynthesis and photorespiration and the up-regulation of branched chain amino acid break down suggesting sugar starvation. Genes involved in cellulose biosynthesis, pectin breakdown and lignin biosynthesis, which are all necessary for growth of new tissues, were also down-regulated in nickel-stressed plant tissues (Table A.1). Finally, genes involved in stress pathways, the breakdown of sucrose and nitrogen storage molecules (such as GABA and 4-aminobutyrate), as well as the biosynthesis of trehalose and glucosinolates were up-regulated. A global view of expression changes on biological function (Figures 3.30 and 3.31) echoes these observations, where response to stress, catabolic processes and secondary metabolism were up-regluated. The biosynthesis of jasmonic acid and IAA was up-regulated in plants under nickel stress, whereas anthocyanin and phenylpropanoid biosynthesis genes were down-regulated. Plants exposed to nickel in the soil were therefore impaired in photosynthesis and carbon fixation, growth and development and had increased stress responses.

4.3.1 Stress tolerance conferred by bacterial ACC deaminse

Huge physiological differences were observed between transgenic plants expressing ACC deaminase and non-transformed plants in the presence of high levels of nickel in the soil. It seems, however, that expressing the transgene constitutively throughout the plant was significantly less effective at protecting plants from stress. When ACC deaminase was expressed solely in the roots there was a dramatic increase in plant fitness. Evidence of this included faster germination and longer roots and shoots of transgenic plants compared to controls when grown in the presence of nickel. There were two different types of plant stresses involved. One was the result of heavy metal specific effects and the other was due to stress ethylene. The first lead to chlorosis and stunting, which was observed in both the transgenic and non-transformed plants however to a lesser extent in trAcdS-*rolD* plants (Figure 3.25). Bacterial ACC deaminase mitigated the effects of stress ethylene by consuming excess ACC and decreasing or abolishing the second, deleterious peak of ethylene synthesis which is usually produced after the onset of stress (Figure 1.4 in Section 1.1.4). Transgenic plants were therefore able to tolerate much higher levels of nickel in the soil than were non-transfored plants. In terms of a phytoremediation strategy, transgenic plants took up the same amount of nickel as did control plants, however they attained higher levels of biomass due to their ability to tolerate nickel stress, so the overall effect was that more total nickel was taken up from the soil (Figure 3.29).

When exposed to nickel, the transcriptional changes occurring within plants expressing the ACC deaminase transgene in their roots were very similar to the response of non-transformed plants. Key differences, however, included the up-regulation of genes involved in nitrate assimilation, sphingolipid and cellulose biosynthesis. Overall, genes involved in the stress response were down-regulated in transgenic plants when compared to non-transformed plants and these included many glutathione S-transferases, cytochrome P450s, and oxidoreductases. Genes involved in biosythetic processes were up-regulated and defense response and aging were down-regulated suggesting that transgenic plants were less stressed than non-transformed plants in the presence of nickel. Also, nitrogen and secondary metabolism and response to abiotic stimuli were up-regulated in transgenic plants, which was likely due to fact that non-transformed plants in the presence of nickel were suffering from necrosis and many metabolic functions were shutting down, especially in the roots.

The effects of nickel were not entirely overcome since the same degree of breakdown in chlorophyll b was observed in all plants in the presence of nickel (Figure 3.27). The chlorophyll a/b ratio is an indication of oxidative plant stress and increases as the level of stress increases. This is because during oxidative stress, the breakdown of chlorophyll b occurs first, due to its higher redox potential compared to chlorophyll a (Huang *et al.*, 2004). In healthy, unstressed canola plants, the chlorophyll a/b ratio was approximately 0.3, whereas, in all cases, plants grown in nickel-spiked soil had a chlorophyll a/b ratio of approximately 1.0. Nevertheless, the survival of these plants was much improved over plants lacking ACC deaminase, illustrating the ability of ACC deaminase to increase plant survival by lowering ethylene levels during abiotic stress.

4.4 Conclusions

Plant growth-promotion by the bacterium *Pseudomonas putida* UW4 has been studied in depth in our lab and in others. The role of ACC deaminase involves lowering of plant ethylene levels, which helps alleviate plant stress symptoms when a stress is present. Bacterial colonization is perceived as a mild stress and colonization of plants by bacteria lacking ACC deaminase leads to a stress response. The effect of an ACC deaminase transgene on plants treated with nickel was to significantly improve plant survival and success. Treatment of the roots of plants with AcdS$^+$ bacteria and expression of the ACC deaminase transgene only in the roots of plants (as opposed to throughout the plant) were effective at conferring stress tolerance to plants suggesting that production of stress ethylene in the roots can cause plant wide effects, and breakdown of ACC in the roots is effective at lowering stress ethylene levels and improving plant fitness.

Some of the more subtle effects of ACC deaminase on plants were studied with the use of expression profiling. In particular, the up-regulation of auxin response factors in the presence of ACC deaminase suggests a link between ethylene and auxin, where repression of the auxin response involves ethylene, either directly or through an intermediate molecule. Evidence for the cross talk between ethylene and jasmonic acid was also observed in this study and may give us better insight into the role of ACC deaminase in plant growth-promotion as do the many other metabolic changes observed during this study. Expression of genes involved in carbohydrate, lipid, nitrogen, sulfur and secondary metabolism as well as cell wall component metabolism and the stress response all changed in the presence of bacterial ACC deaminase, suggesting many different roles for this enzyme in plant growth-promotion.

A large portion of the genes whose expression changed in this study were transcription factors. This suggests that cascades or networks of genes are at work during biotic stimulus and abiotic stress. Future work with this data could include the mapping of transcription factors to target genes using databases such as The Arabidopsis gene regulatory information server (AGRIS) from Ohio State University (http://arabidopsis.med.ohio-state.edu/) which houses the AtTFDB database with information on approximately 1,770 transcription factors. Also, use of the RIKEN Arabidopsis transcription factor database (RARTF) out of the RIKEN Yokohama Institute in Japan. More in depth clustering analysis to find genes that were co-expressed and mapping these to individual plant responses with tools such as The Arabidopsis Co-expression Tool (ACT) from Leeds University (www.Arabidopsis.leeds.ac.uk/ACT) which can be used to provide biological context to clusters of genes with the same r-values.

The use of microarray technology combined with real-time RT-PCR provides large amounts of data with which many important questions may be answered. As is typical with many "omic" technologies, more questions often emerge than are answered, but this only provides the opportunity to approach older problems with a new perspective. The sequencing of model plant genomes such as Arabidopsis have allowed the use of these powerful tools for the study of non-model plant systems in a meaningful way. Sequencing of the *Brassica napus* genome will take time to complete and the use of Arabidopsis for field applications is not practical, therefore the successful use of this heterologous system provides an avenue for studying the deep transcriptional changes occurring within *Brassica* tissues with the full use of the many resources available for Arabidopsis.

Appendix A

Expression data organized by metabolic pathway

Table A.1: Expression changes for each treatment organized by metabolic pathway. Fold change (in relation to untreated control) is reported for each gene in brackets, except for “trAcdS-*rolD* in Ni” which is in relation to non-transformed plants grown with nickel and where the *t*-statistic is reported in brackets. Entries followed by an asterisk are from plant roots and all others are from plant shoots. AcdS$^+$ = canola seedlings treated with *Pseudomonas putida* UW4 AcdS$^+$; AcdS$^-$ = canola seedlings treated with *Pseudomonas putida* UW4 AcdS$^-$; trAcdS-*rolD* = transgenic canola expressing ACC deaminase in the roots.

	Pathway	AcdS$^+$	AcdS$^-$	trAcdS-*rolD* 6 days-old	trAcdS-*rolD* 3 weeks-old	trAcdS-*rolD* in Ni	Non-transformed in Ni
Phytohomones	Cytokinin biosynthesis	AT5G17050 (-1.9) AT4G14090 (-1.5) AT2G31750 (-1.3)	AT5G17050 (-1.8) AT2G31750 (-1.3)	AT5G17050 (1.3) AT1G24100 (1.4)	AT1G24100 (3.9)		AT2G43820 (6.5) AT5G59590 (-3.7) AT2G43840 (4.0) AT2G26480 (-4.6) AT1G22360 (-6.8)
	Ethylene biosynthesis	ACS8 (1.4) EFE (2.7) AT2G30830 (-1.9)	EFE (2.2)	AT2G30830 (1.3) AT2G25450 (1.7) EFE (-1.4)	AT1G03400 (5.3)	AT3G61400 (5.1)	ACS11 (-3.6)

Continued. . .

	Pathway	AcdS$^+$	AcdS$^-$	trAcdS-*rolD* 6 days-old	trAcdS-*rolD* 3 weeks-old	trAcdS-*rolD* in Ni	Non-transformed in Ni
		AT2G25450 (-1.4)					
	Gibberellin biosynthesis			GA20ox4 (-1.6) GA20ox3 (-1.6) GA20ox1 (-1.3)	GA20ox3 (3.5)	GA3ox2 (4.6)	
	IAA biosynthesis	AT5G22300 (-1.6) AO1(-1.6) AT4G39950 (-1.5)* AT2G22330 (-1.2)*	AT4G39950 (-1.5)* AT2G22330 (-1.4)*	AT4G39950 (1.4)	AT4G39950 (3.5)	NCED9 (-3.3)	AT4G39950 (6.7) ill2 (-5.3) iar3 (3.8)
	Jasmonic acid biosynthesis	AT3G01420 (-1.6)	AOS (3.2) AT3G01420 (-1.3)	AT3G01420 (1.6)	AT3G01420 (7.1) AOS (2.8) AT2G06050 (5.5)		LOX2 (4.7) AOS (6.2) AT2G06050 (3.8) AT1G17990 (-4.6)
	Phaseic acid biosynthesis	CYP707A3 (-1.3) CYP707A2 (-2.6)	CYP707A2 (-2.3)				
	Salicylic acid biosynthesis	PAL2 (-2.0) PAL1 (-1.8)	PAL2 (-1.8) PAL1 (-1.6)	PAL2 (1.4) PAL1 (1.3)	PAL1 (2.8)	ICS1 (2.8) PAL2 (-2.2)* PAL1 (-2.0)*	
Photosynthesis	Calvin cycle	AT4G26520 (1.8) AT2G36460 (1.5) AT2G01140 (-2.3) AT2G45290 (-1.4)	AT1G18270 (1.3) AT4G26520 (2.1) AT2G36460 (1.9) AT2G01140 (-1.9)	AT2G01140 (2.4)	GapB (2.9)		AT5G44520 (-4.3)
	Chlorophyll a degradation	RCCR (1.9)	RCCR (1.8)				CLH1 (3.7) PAO (4.3)
	Photorespiration						AT3G14420 (-3.7) AOAT1 (-4.6) AT2G35370 (-7.4)
	Photosynthesis						PSaD-2 (-4.2)
	Phylloquinone biosynthesis					ICS1 (2.8)	
	Tetrapyrrole biosynthesis			AT2G31250 (-1.8)	HEMA1 (3.4)		HEMA1 (-6.0) AT2G31250 (-3.7)
Carbohydrate metabolism	Gluconeogenesis	PCK1 (1.3) GapCp-1 (1.5) GapCp-2 (1.4) AT4G26520 (1.7) AT2G36460 (1.5) AT2G01140 (-2.3) AT5G42740 (-1.3)	AT4G26520 (2.1) AT2G36460 (1.9) AT2G01140 (-1.9) AT1G18270 (1.3)	GapCp-2 (-1.3) AT2G01140 (2.4)	GapB (2.9)	AT2G36530 (-2.1)*	
	Glycolysis	AT5G61580 (1.3) AT5G47810 (2.4) AT4G26520 (1.7) AT2G36460 (1.5) AT2G01140 (-2.3) NP-GAPDH (-2.4) GapCp-1 (1.5) GapCp-2 (1.4)	AT4G26520 (2.1) AT2G36460 (1.9) AT2G01140 (-1.9) AT1G18270 (1.3) NP-GAPDH (-1.9)	AT2G01140 (2.4) GapCp-2 (-1.3) NP-GAPDH (1.4) AT5G52920 (-1.4)	GapB (2.9) AT1G32440 (2.8)	AT3G55440 (-1.6)* AT2G36530 (-2.1)*	AT1G12000 (4.3)

Continued. . .

	Pathway	AcdS^{+}	AcdS^{-}	trAcdS-*rolD* 6 days-old	trAcdS-*rolD* 3 weeks-old	trAcdS-*rolD* in Ni	Non-transformed in Ni
		AT5G42740 (-1.3)					
	Lactose degradation	AT5G63810 (1.5) AT3G52840 (1.6) AT1G45130 (1.5)	AT3G52840 (1.5)	AT5G56870 (1.3) AT5G36800 (-1.4)	AT5G56870 (-9.9) (-5.2)* AT3G13750 (-4.4) (-4.4)*	AT5G56870 (-2.1)*	AT3G13750 (5.1)
	Mannose and mannitol degradation		AT3G02570 (1.7)	AT1G50460 (-1.3)			
	Sucrose degradation	SUS1 (1.5) SUS4 (1.7) AT1G23190 (-1.2) AT5G42740 (-1.3) AT5G61580 (1.3) AT5G47810 (2.4) AT4G26520 (1.7) AT2G36460 (1.5) AT2G01140 (-2.3) GapCp-1 (1.5) GapCp-2 (1.4)	SUS4 (1.4) AT1G23190 (-1.2) AT4G26520 (2.1) AT2G36460 (1.9) AT2G01140 (-1.9) AT1G18270 (1.3)	AT1G12240 (1.3) AT5G17310 (1.2) AT1G50460 (-1.3)		AT3G55440 (-1.6)* AT2G36530 (-2.0)* SUS1 (-1.8)* SUS4 (-1.6)*	SUS1 (4.9) AT3G06500 (4.9)
	Sucrose to degradation (anaerobic)			AT5G17310 (1.2) AT2G01140 (2.4) GapCp-2 (-1.3) AT5G52920 (-1.4)	GapB (2.9) AT1G32440 (2.8)	SUS1 (-1.8)* SUS4 (-1.6)* AT3G55440 (-1.6)* AT2G36530 (-2.1)*	
	Trehalose biosynthesis	TPS8 (-1.8) TPS10 (-1.3) TPS11 (-1.9)	TPS8 (-1.7) TPS11 (-2.4)	TPS11 (-1.4) AT4G12430 (1.2)* AT4G22590 (1.2)*	AT4G39770 (3.3)		AT1G35910 (3.6)
Lipid metabolism	Choline biosynthesis	AT1G73600 (-5.5) PLD gamma (1.5)	AT1G73600 (-3.4) PLD gamma (1.4) PLD alpha (-1.2)		AT1G73600 (6.4)		
	Fatty acid biosynthesis						AT2G38040 (-4.0)
	Fatty acid β-oxidation	KAT5 (-1.5)	AT2G47240 (1.4) KAT5 (-1.4)	AT2G47240 (1.5)	AT3G51840 (-4.0) KAT2 (-3.7) KAT5 (3.9)		AT3G51840 (3.9) KAT2 (3.8) KAT5 (-4.8) KAT1 (3.8)
	Glycolipid desaturation	fad5 (-1.9) fad6 (-1.3) fad7 (-1.5) fad8 (-2.7)	fad8 (-1.9)		fad8 (4.4)		fad8 (-3.9)
	Glyoxylate cycle			AT3G58750 (-1.4) AT3G58740 (-1.4)	AT3G58740 (-2.6) PPC2 (2.9)	AT1G04410 (-2.2)* AT3G61070 (-1.6)*	AT1G53240 (-3.7)
	Phospholipases						AT3G03310 (4.2)
	Sphingolipid biosynthesis					AT5G23670 (20.4)	
	Sterol biosynthesis	AT5G24160 (-2.4) AT5G24150 (-2.4) AT4G37760 (-1.5) SMT1 (1.4)	AT5G24160 (-1.7) AT5G24150 (-1.7) AT4G37760 (-1.5)	AT4G37760 (1.3)			

Continued. . .

	Pathway	$AcdS^+$	$AcdS^-$	trAcdS-*rolD* 6 days-old	trAcdS-*rolD* 3 weeks-old	trAcdS-*rolD* in Ni	Non-transformed in Ni
	Triacylglycerol degradation			AT1G54030 (1.5)	AT5G40990 (-3.2) AT1G75890 (5.3) AT1G53990 (-3.1)	AT1G75880 (6.1)	AT5G10990 (4.7) AT1G53990 (4.1)
Changes in cell walls	Cellulose biosynthesis	AT4G39350 (-1.5) AT5G09870 (-1.4) AT4G24000 (-1.6) AT4G16590 (-6.2) AT4G15290 (-2.5) AT4G13410 (-3.1)	AT3G57260 (-1.6) AT5G09870 (-1.5) AT4G16590 (-2.8) AT4G15290 (-1.9) AT4G13410 (-2.3)	AT4G16590 (1.7) AT4G15290 (1.4) AT4G13410 (1.4)	CesA6 (3.3) AT5G09870 (4.1)		CesA6 (-4.5) AT5G09870 (-3.7)
	Homogalacturonan biosynthesis				GATL (3.0)		
	Homogalacturonan degradation	AT3G49220 (-1.2) AT1G60590 (-1.6)	AT3G49220 (-1.8) AT1G60590 (-2.3)	AT4G32375 (1.3)	AT5G07420 (6.5) AT2G26620 (3.2)	AT3G06830 (-14.3) AT1G11580 (-1.8)* AT1G17150 (-2.0)*	AT3G06830 (-12.0) AT4G32375 (-4.5) AT1G23760 (-5.1) AT3G14310 (4.3)
	Inositol oxidation pathway			MIOX4 (1.5)*	MIOX4 (-7.38)		
	Starch degradation	SEX4 (1.9) DPE1 (1.4) AT4G15210 (-1.7) AT5G18670 (-1.8) AT3G23920 (-1.8) AT2G32290 (-2.0)	AT4G15210 (-1.4) AT5G18670 (-1.5) AT3G46970 (1.3) AT1G23190 (-1.2)	AT4G15210 (1.3) AT1G50460 (-1.3)	AT5G04360 (-3.1)		DPE1 (4.1)
	Suberin biosynthesis	PAL2 (-2.0) PAL1 (-1.8) ATC4H (-1.5) OMT1 (-2.9)	PAL2 (-2.0) PAL1 (-1.8) AT1G67980 (1.4)	PAL2 (1.4) PAL1 (1.3) AT1G67980 (-1.4)	PAL1 (2.8) OMT1 (4.7)	PAL2 (-2.2)* PAL1 (-2.0)* ATC4H (-2.0)* REF8 (-1.7)*	OMT1 (-3.8)
Carbon, Nitrogen and Sulfur metabolism	Ammonia assimilation	GLN1;1 (-2.3) GLN1;2 (-2.2) GLN1;4 (-1.9) AT5G04140 (-1.4)			GLN1-1 (5.2) GLN1-2 (3.0)		GLN1;4 (-5.1) AT3G53180 (4.6)
	Cysteine biosynthesis	SAT1 (-1.6) SAT3 (-1.7) AT3G61440 (-1.3)		SAT3 (1.4) SAT1 (1.4)	SAT3 (-2.0)* AT3G61440 (-2.0)*		
	Methionine biosynthesis	AT3G03780 (-1.8)	AT3G03780 (-1.4)	AT4G23600 (1.6) AT3G03780 (1.4)	AT3G03780 (4.3) AT5G17920 (3.2)	AT2G36880 (-2.2)* AT4G13940 (-1.9)*	AT4G23600 (4.0)
	Nitrate assimilation	NIA1 (-1.5) GLN1;1 (-2.3) GLN1;2 (-2.2) GLN1;4 (-1.9)			NIA1 (6.5) GLN1-1 (5.2) GLN1-2 (3.0)	NIA1 (3.0)	GLN1;4 (-5.1) AT3G53180 (4.6)
	Sulfate activation						AT4G39940 (4.0)
	Sulfate reduction	APS2 (-1.7) APS1 (-2.5) APR3 (-1.6) APR2 (-2.1)	APS2 (-1.6) APS1 (-2.0) APR3 (-1.9) APR2 (-2.3)		APS2 (3.1) APR1 (3.6) APR2 (5.5) APR3 (4.7)	APS4 (-2.0)*	APR3 (-6.4) APR4 (-5.5)

Continued. . .

	Pathway	AcdS$^+$	AcdS$^-$	trAcdS-*rolD* 6 days-old	trAcdS-*rolD* 3 weeks-old	trAcdS-*rolD* in Ni	Non-transformed in Ni
	Urea cycle					AT4G08900 (-11.6)	AT4G08900 (-5.0)
Secondary metabolism	Anthocyanin biosynthesis	AT4G22880 (-1.8) AT4G22870 (-2.9) AT3G51240 (-2.3) AT5G07990 (-1.4) AT5G17050 (-1.9)	AT4G22880 (-1.9) AT4G22870 (-2.5) AT3G51240 (-2.0) AT5G07990 (-1.3) AT5G17050 (-1.8)	AT4G22880 (1.4) AT4G22870 (1.5) AT5G07990 (1.3) AT3G51240 (1.4) AT5G17050 (1.3)	AT3G51240 (4.6)	AT4G22880 (5.3)	AT4G22870 (-4.4)
	Camalexin biosynthesis	AT4G39950 (-1.5)* AT2G22330 (-1.2)*	AT4G39950 (-1.5)* AT2G22330 (-1.4)*	AT4G39950 (1.4)	AT4G39950 (3.5)		AT4G39950 (6.7)
	Carotenoid biosynthesis	LUT2 (-1.4) β-OHase1 (-1.9) β-OHase2 (-1.8) ABA1 (-1.6)	β-OHase1 (-1.8) β-OHase2 (-1.7)	β-Ohase 1 (1.2)	β-Ohase 3 (2.9)		β-Ohase 2 (-4.3)
	Flavonoid biosynthesis	4CL3 (-1.45) AT5G63380 (-1.4) AT1G20490 (-1.3) AT5G13930 (-5.1) AT3G51240 (-2.3)	AT1G20510 (1.8) AT5G13930 (-4.5) AT3G51240 (-2.0)	4CL3 (1.3) AT5G13930 (1.6) AT3G51240 (1.4)	AT4G05160 (-4.0) AT1G20510 (2.5) AT5G13930 (13.6) AT3G51240 (4.6)		AT5G13930 (-3.8) AT3G51240 (-3.6)
	Flavonol biosynthesis	AT5G07990 (-1.4) FLS (-2.0) OMT1 (-2.9)	AT5G07990 (-1.3) FLS (-1.5)	AT5G07990 (1.3)	FLS (7.4) OMT1 (4.7)		OMT1 (-3.8) FLS (-6.7)
	Geranyldiphosphate biosynthesis	SPS1 (-2.1) SPS2 (-1.7)	SPS1 (-1.8) SPS2 (-1.4)				SPS1 (-7.4)
	Glucosinolate biosynthesis	AT4G13770 (-1.7) AT1G06640 (-1.2) AT4G39950 (-1.5)* AT2G22330 (-1.2)*	AT4G39950 (-1.5)* AT2G22330 (-1.4)*	AT4G39950 (1.4) AT4G31500 (1.4) AT4G13770 (2.0) AT1G24100 (1.4)	AT4G39950 (3.5) AT4G31500 (4.8) AT1G24100 (3.9) AT1G74090 (3.0)		AT4G39950 (6.7) AT4G31500 (6.4) AT2G20610 (4.6) AT1G74100 (4.5) AT1G18590 (4.7) AT1G74090 (5.8)
	Glucosinolate breakdown	AT1G54040 (1.6)	AT1G54040 (1.6)				
	Kaempferol glucoside biosynthesis	AT4G01070 (-1.7) AT5G54060 (-1.9) AT2G22930 (-1.4)	AT4G01070 (-1.4) AT5G54060 (-1.8) AT2G22930 (-1.2)				
	Lupeol biosynthesis					AT1G66960 (4.4)	
	Phenylpropanoid biosynthesis	PAL2 (-2.0) PAL1 (-1.8) ATC4H (-1.5) 4CL3 (-1.4) AT5G63380 (-1.4) AT1G20490 (-1.3) AT1G09510 (-1.6) AT1G09500 (-2.5) AT4G36220 (-2.0)	PAL2 (-1.8) PAL1 (-1.6) AT1G20510 (1.8) AT1G09510 (-1.4) AT1G09500 (-1.9) AT1G67980 (1.4)	PAL2 (1.4) PAL1 (1.3) 4CL3 (1.3) AT1G09500 (1.3) AT1G67980 (-1.4) AT4G36220 (1.3)	AT4G05160 (-4.0) AT1G20510 (2.5) AT1G80820 (3.2) AT5G14700 (3.3) AT1G09500 (4.9) AT4G36220 (3.3)	PAL2 (-2.2)* PAL1 (-2.0)* ATC4H (-2.0)*	AT4G30470 (-6.0) AT1G09500 (-5.1) AT4G36220 (-5.2) AT5G19440 (3.9)
	Tryptophan biosynthesis			AT4G02610 (-1.4) AT4G27070 (1.3)	AT2G29690 (-4.2)		AT5G05730 (5.4) AT2G29690 (4.1)

Continued. . .

	Pathway	AcdS$^+$	AcdS$^-$	trAcdS-*rolD* 6 days-old	trAcdS-*rolD* 3 weeks-old	trAcdS-*rolD* in Ni	Non-transformed in Ni
							AT1G25083 (4.3) AT1G24807 (4.9) AT2G04400 (3.6) AT5G54810 (4.2)
	Tryptophan degradation				AT5G47720 (-4.2)		AT5G48230 (3.7)
	Vitamin E biosynthesis				PDS1 (-11)		
Response to stress	Branched chain amino acid degradation (leucine, isoleucine and valine)			AT4G34030 (-1.6) AT2G26800 (1.7) (1.3)*	Atbcat-2 (-12.3) (5.0)* BCE2 (-6.1) (-5.5)* AT3G45300 (-4.7) AT4G34030 (-4.3) (-7.0)* AT1G03090 (-7.5) (-2.4)* KAT2 (-3.7) (-1.8)* KAT5 (3.9)		Atbcat-2 (5.1) AT1G03090 (5.5) KAT2 (3.8) KAT1 (3.8) KAT5 (-4.8)
	Branched-chain α-keto acid dehydrogenase complex				AT1G21400 (-2.0)* AT1G55510 (-5.0) (-2.2)* BCE2 (-6.1) (-5.5)*		
	Galactose degradation			AT5G17310 (1.2) UGE3 (-1.4) UGE1 (-1.3)	AT5G14470 (-4.8) UGE4 (-4.4) UGE3 (-4.4) (-2.2)* UGE2 (-3.1) UGE1 (-3.6) (-1.9)* AT2G28760 (-3.4)* SUS2 (-1.6)*		
	Glutamate degradation	AT1G65960 (3.5) POP2 (1.8) AT1G79440 (1.7)	AT1G65960 (2.7) POP2 (1.8) AT1G79440 (1.6)	AT5G17310 (1.2)	POP2 (-4.0) AT5G07440 (-3.1)* AT5G18170 (-1.8)*		POP2 (5.3) AT1G79440 (4.1) AT5G07440 (5.5)
	Glutathione biosynthesis						GSH2 (3.9)
	Glutathione redox reactions			AT2G30860 (1.3)	AT2G30860 (3.2) AT4G31870 (3.6)		AT2G30860 (4.6) AT4G31870 (-5.5)
	Nitric oxide cycle				AT3G47450 (-23.5)		
	Removal of superoxide radicals	CSD1 (-1.6)	FSD1 (1.6) (1.6)* CSD1 (-2.0) (-1.5)*	FSD1 (1.8)	FDS2 (5.5) CAT2 (3.4)		AT3G56350 (3.9) CAT2 (-4.3)
Other metabolic functions	Acetyl-CoA biosynthesis			AT3G25860 (1.7)			AT1G30120 (-4.8)
	Alanine biosynthesis						AOAT1 (-4.6) AOAT3 (3.7)
	Arginine degradation						AT1G79440 (4.1)
	Ascorbate biosynthesis				VTC4 (3.6)		
	Asparginine biosynthesis				AT3G61440 (-2.0)*		
	β-alanine biosynthesis					AT5G13700 (-8.9)	AT5G13700 (-5.0)
	Cyanate	CA2 (-3.3)	CA2 (-4.0)		AT3G52720 (4.1)		CA2 (-4.0)

Continued. . .

Pathway	AcdS$^+$	AcdS$^-$	trAcdS-*rolD* 6 days-old	trAcdS-*rolD* 3 weeks-old	trAcdS-*rolD* in Ni	Non-transformed in Ni
degradation	AT3G52720 (-1.7) AT1G70410 (-1.5) AT1G23730 (-1.4)	AT3G52720 (-1.6) CA1 (1.8)*		AT1G58180 (-3.0)		
Glycine biosynthesis			THA1 (1.4)	AGT1 (-2.6)* THA1 (-4.8) (-6.2)* AT4G3930 (1.6)*	THA1 (-2.0)*	AOAT1 (-4.6) THA2 (4.1)
Glycine degradation						AT2G35370 (-7.4)
Leucine biosynthesis				ATIMD1 (-2.5)* Atbcat-2 (-12.3) (-5.0)*		Atbcat-2 (5.1)
Lysine degradation				AT4G33150 (-3.9) (-2.2)* AT5G47720 (-4.2) (-1.8)*		AT5G48230 (3.7)
Molybdenum cofactor biosynthesis					Cnx7 (-8.7)	Cnx7 (-5.4)
Phenylalanine biosynthesis						AT1G11790 (5.4) AT2G20610 (4.6)
Proline degradation			AT3G30775 (-1.4)	P5CS2 (2.8)		
Riboflavin biosynthesis	AT5G59750 (-1.3) AT2G22450 (1.4) AT4G21470 (-1.2)				AT5G23330 (-3.6)	
Tyrosine degradation				AT5G53970 (-3.1) PDS1 (-11.0) AT5G54080 (-10.4)		AT5G54080 (4.8)
Valine biosynthesis				AT5G10860 (-2.2)* Atbcat-2 (-12.3) (-5.0)*		

Appendix B

MvA plots

On the x-axis is the average intensity of the red and green channels ($\log_2$) and on the y-axis is the difference in intensity between the two channels.

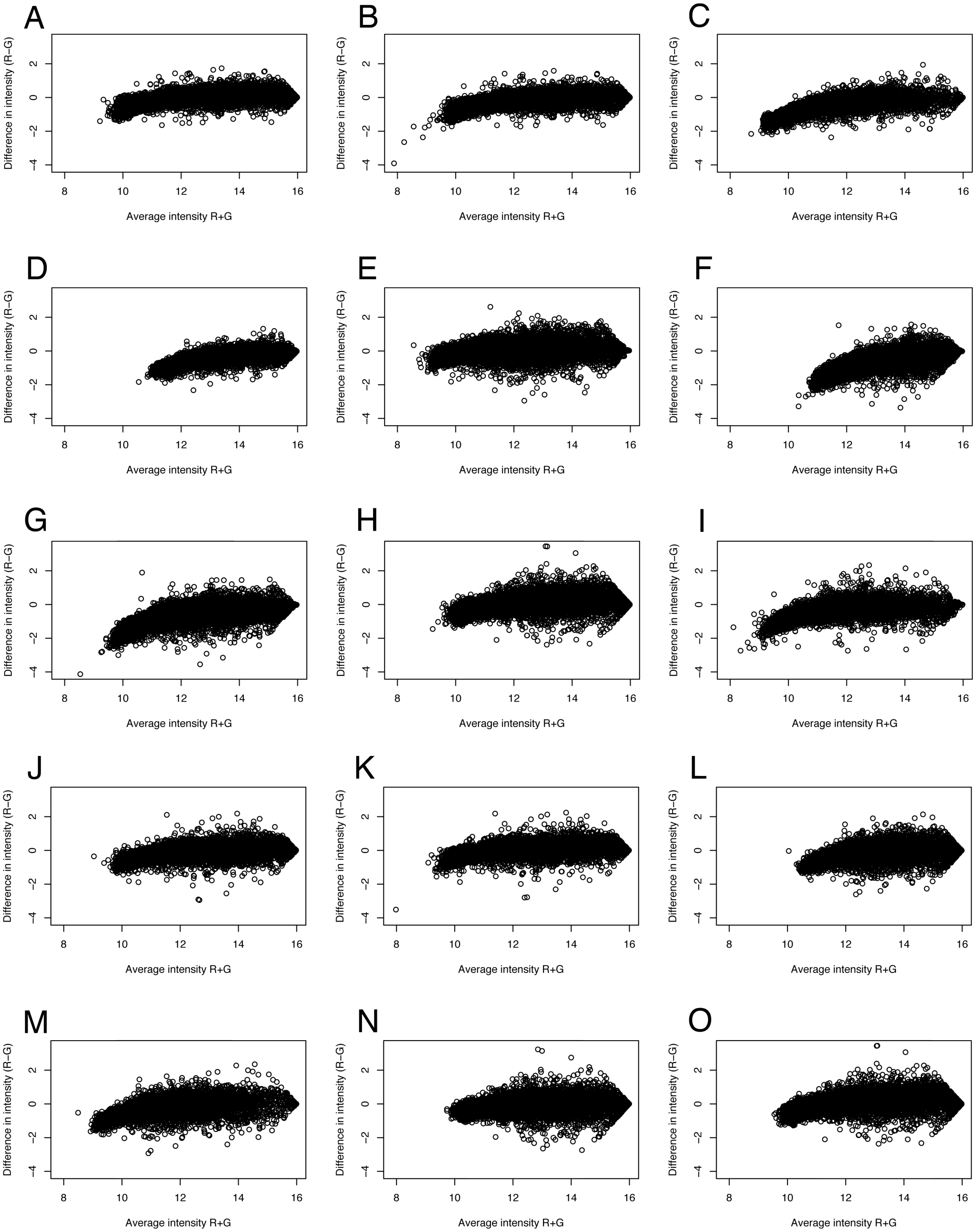

Figure B.1: MvA plots of raw expression data for shoots of 6 day-old seedlings. (A) trAcdS-*rolD* (Cy5) vs. control (Cy3), (B) scan #2 of (A), (C) control (Cy5) vs. trAcdS-*rolD* (Cy3), (D) scan #2 of (C), (E) AcdS$^+$ (Cy5) vs. control (Cy3), (F) second replicate of (E), (G) scan #2 of (F), (H) control (Cy5) vs. AcdS$^+$ (Cy3), (I) scan #2 of (H), (J) AcdS$^-$ (Cy5) vs. control (Cy3), (K) scan #2 of (J), (L) second replicate of (J), (M) scan #2 of (L), (N) control (Cy5) vs. AcdS$^-$(Cy3), (O) scan #2 of (N).

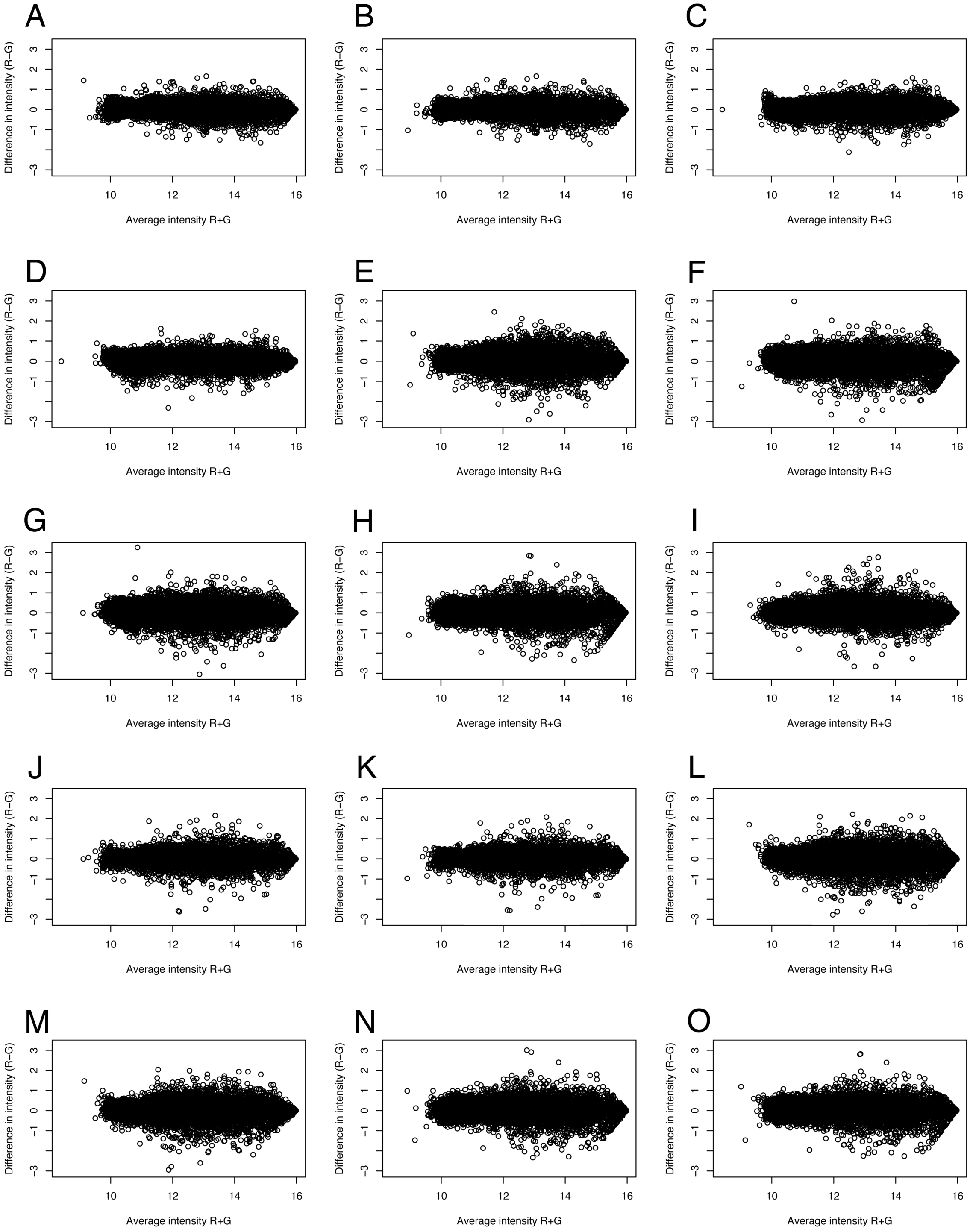

Figure B.2: MvA plots of normalized expression data for shoots of 6 day-old seedlings. (A) to (O) same as for Figure B.1.

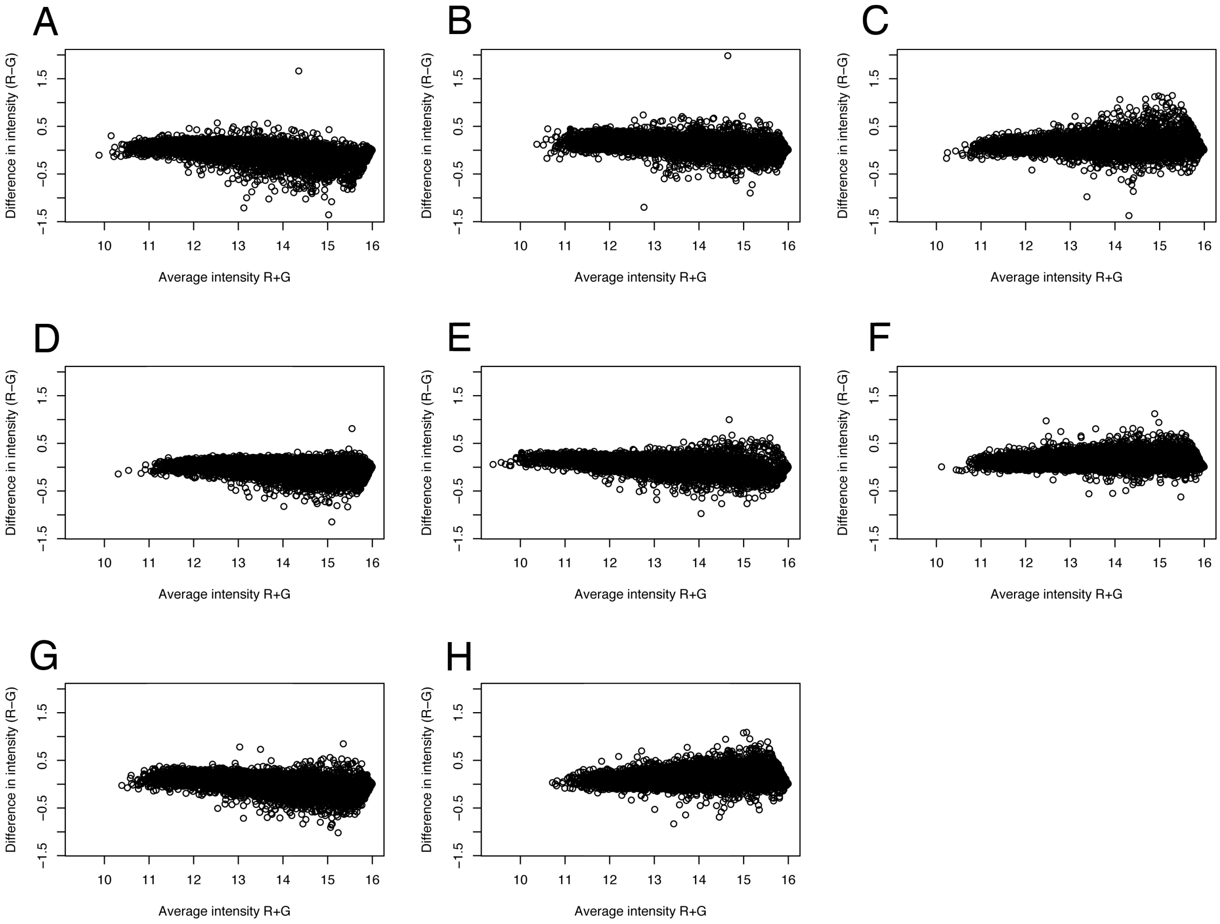

Figure B.3: MvA plots of raw expression data for roots of 6 day-old seedlings. (A) trAcdS-*rolD* (Cy5) vs. control (Cy3), (B) second replicate of (A), (C) control (Cy5) vs. trAcdS-*rolD* (Cy3), (D) AcdS$^+$ (Cy5) vs. control (Cy3), (E) second replicate of (D), (F) control (Cy5) vs. AcdS$^+$ (Cy3), (G) AcdS$^-$ (Cy5) vs. control (Cy3), (H) control (Cy5) vs. AcdS$^-$(Cy3).

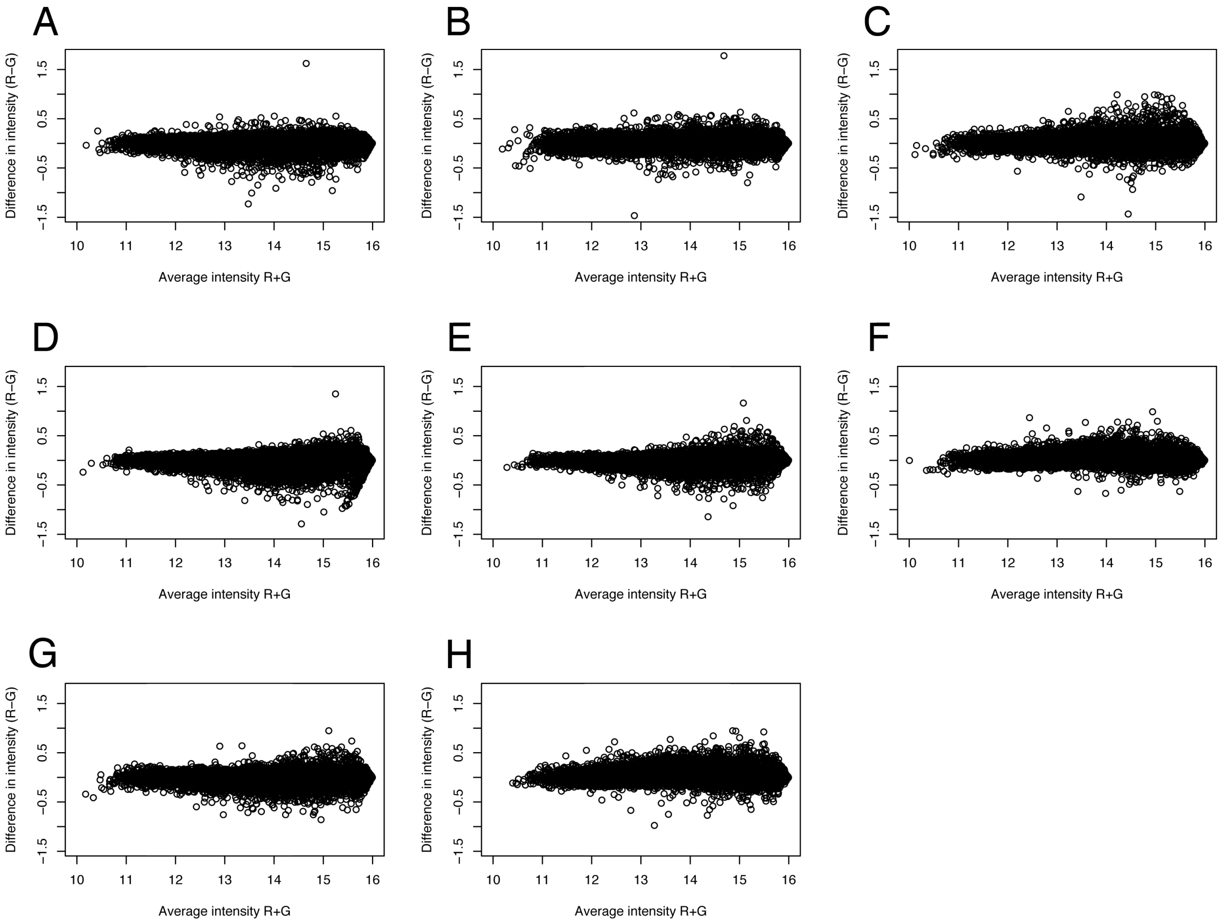

Figure B.4: MvA plots of normalized expression data for roots of 6 day-old seedlings. (A) to (H) same as for Figure B.3.

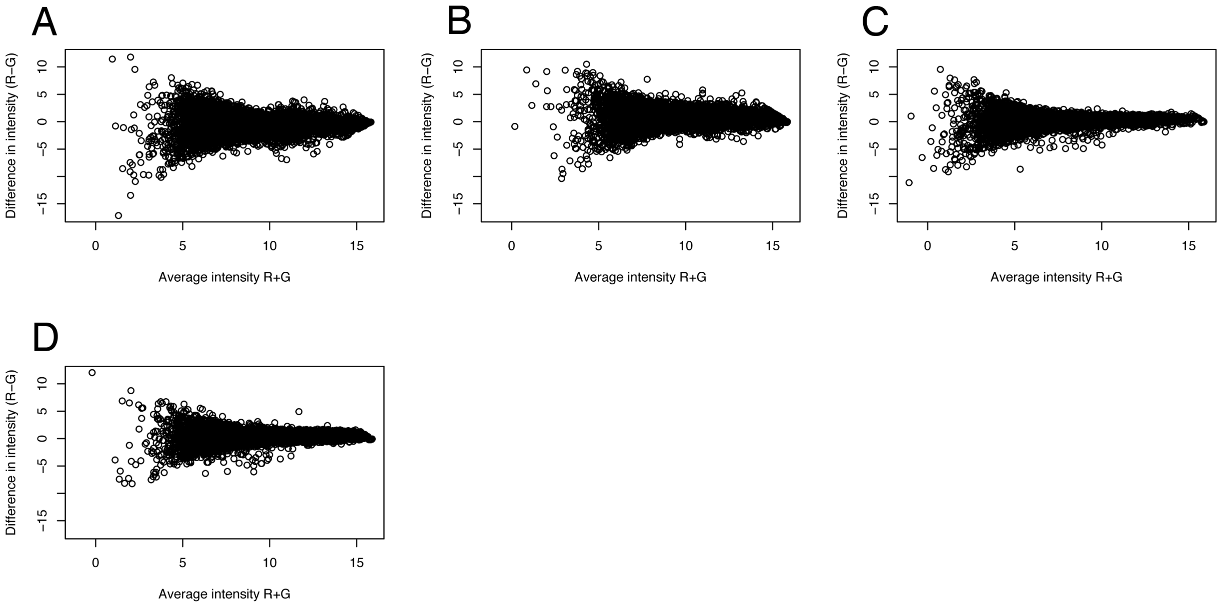

Figure B.5: MvA plots of raw expression data for shoots of 3 week-old plants. (A) non-transformed (Cy5) vs. trAcdS-*rolD* (Cy3), (B) trAcdS-*rolD* (Cy5) vs. non-transformed (Cy3), (C) non-transformed in Ni (Cy5) vs. trAcdS-*rolD* in Ni (Cy3), (D) trAcdS-*rolD* in Ni (Cy5) vs. non-transformed in Ni (Cy3).

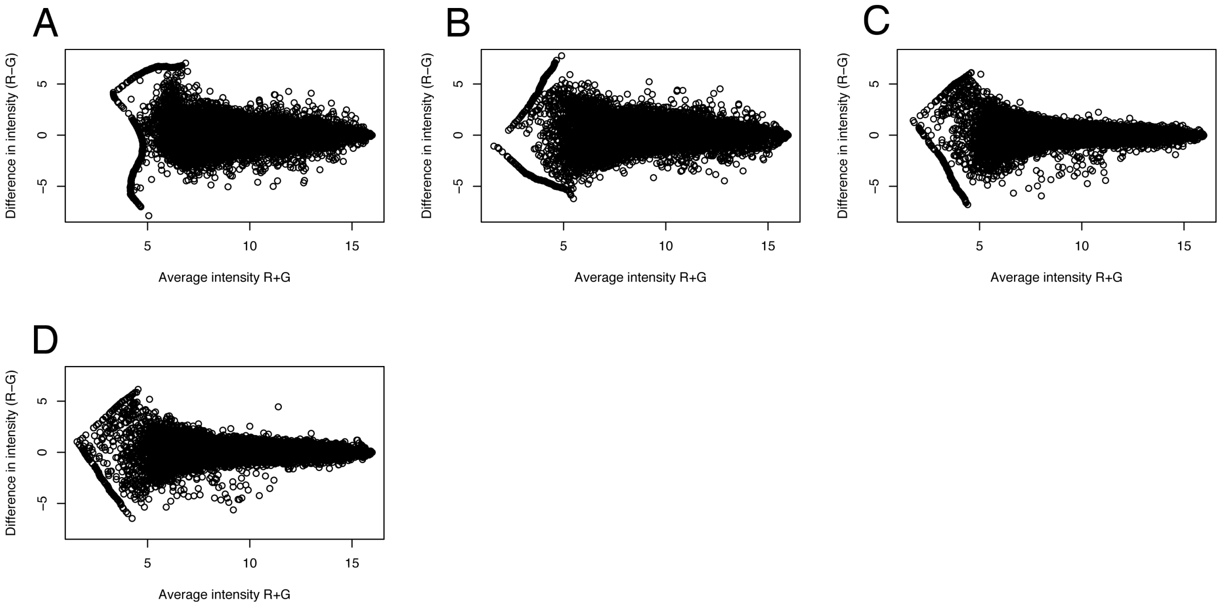

Figure B.6: MvA plots of normalized expression data for shoots of 3 week-old plants. (A) to (D) same as for Figure B.5.

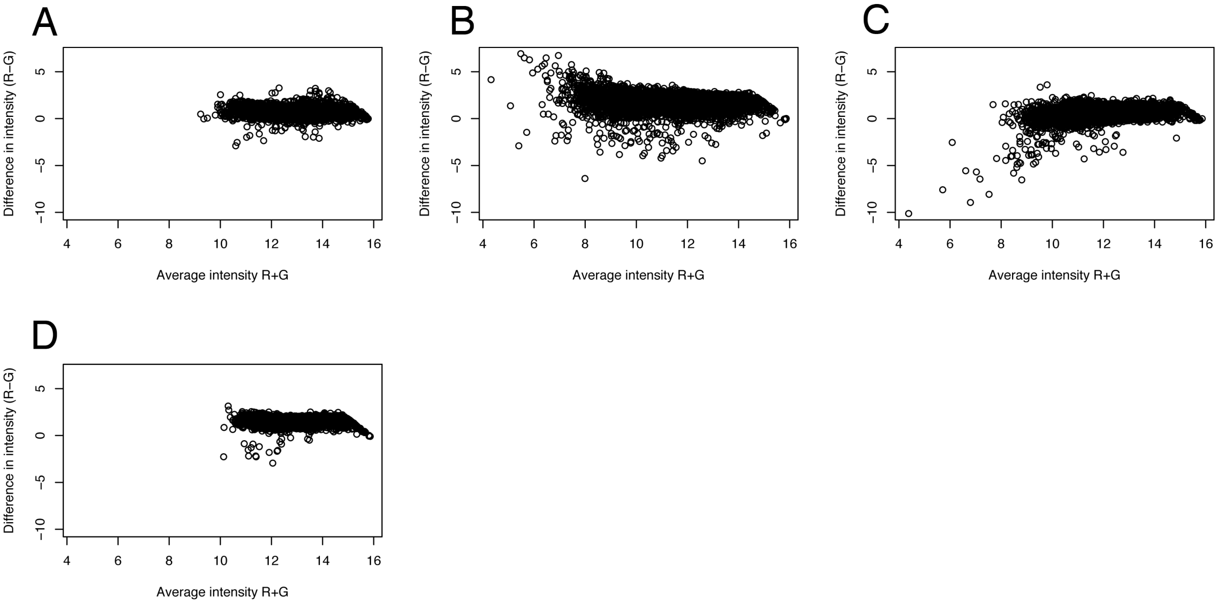

Figure B.7: MvA plots of raw expression data for roots of 3 week-old plants. (A) to (D) same as for Figure B.5.

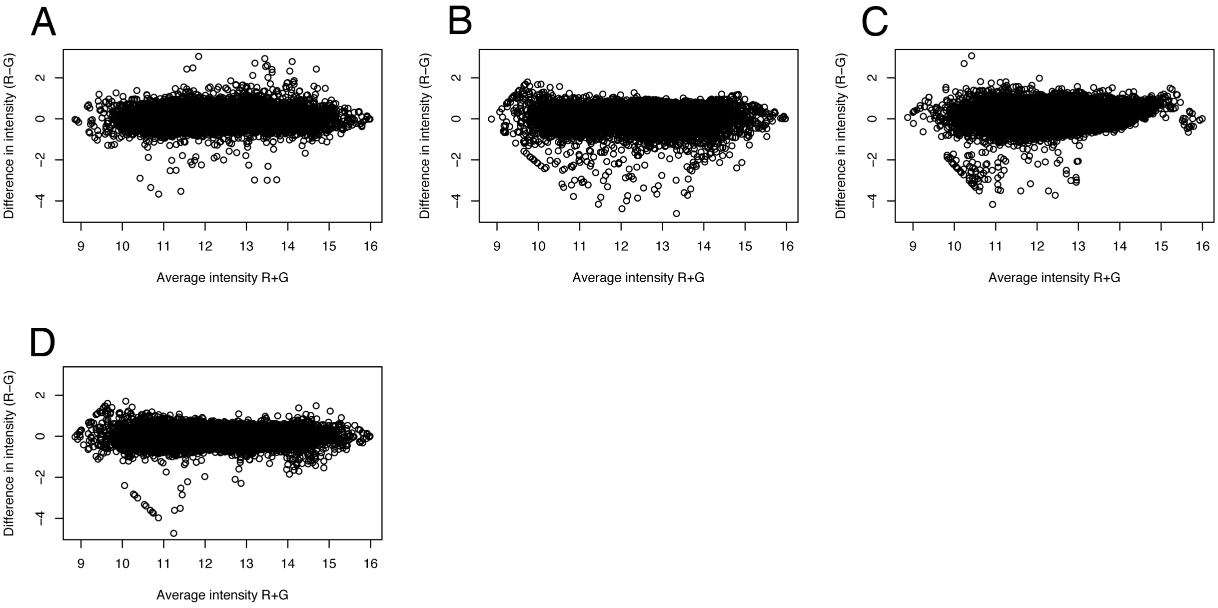

Figure B.8: MvA plots of normalized expression data for roots of 3 week-old plants. (A) to (D) same as for Figure B.5.

Appendix C

Lists of genes with significant expression changes

Table C.1: Significant expression changes in shoots of 6 day-old seedlings treated with bacteria versus untreated seedlings. Numbers in black represent changes with an FDR adjusted $p < 0.05$, whereas numbers in gray represent changes with an FDR adjusted $p > 0.05$. AcdS$^+$ = *Pseudomonas putida* UW4 AcdS$^+$; AcdS$^-$ = *Pseudomonas putida* UW4 AcdS$^-$.

Locus	AcdS$^+$ *t*-statistic	AcdS$^+$ fold change	AcdS$^-$ *t*-statistic	AcdS$^-$ fold change	Description
AT3G14420	-4.83	-1.44	-2.34	-1.19	(S)-2-hydroxy-acid oxidase, peroxisomal, putative glycolate oxidase, putative short chai...
AT2G36390	3.86	1.4	2.89	1.27	1,4-alpha-glucan branching enzyme starch branching enzyme class II (SBE2-1) nearly identi...
AT5G10450	5.58	1.49	4.83	1.41	14-3-3 protein GF14 lambda (GRF6) (AFT1) identical to 14-3-3 GF14lambda GI:1345595 from Ar...
AT1G05010	9.27	2.67	7.56	2.2	1-aminocyclopropane-1-carboxylate oxidase ACC oxidase ethylene-forming enzyme (ACO) (EAT...
AT4G37770	4.81	1.41	0.72	1.06	1-aminocyclopropane-1-carboxylate synthase, putative ACC synthase, putative similar to 1-...
AT3G21500	-5.19	-1.27	-3.33	-1.17	1-deoxy-D-xylulose 5-phosphate synthase, putative 1-deoxyxylulose-5-phosphate synthase, p...
AT4G27670	6.02	1.56	6.88	1.69	25.3 kDa small heat shock protein, chloroplast precursor (HSP25.3-P) identical to small he...
AT4G21870	-0.66	-1.09	4.27	1.8	26.5 kDa class P-related heat shock protein (HSP26.5-P) contains Pfam profile: PF00011 Hsp...
AT4G24820	3.91	1.28	3.07	1.22	26S proteasome regulatory subunit, putative (RPN7) contains similarity to ubiquitin activa...
AT2G37220	4.81	1.5	6.34	1.69	29 kDa ribonucleoprotein, chloroplast, putative RNA-binding protein cp29, putative simila...
AT2G30830	-4.19	-1.89	0.85	1.13	2-oxoglutarate-dependent dioxygenase, putative similar to 2A6 (GI:599622) and tomato ethyl...
AT2G25450	-4.93	-1.44	-2.27	-1.18	2-oxoglutarate-dependent dioxygenase, putative similar to 2A6 (GI:599622) and tomato ethyl...

Continued...

Locus	AcdS$^+$ *t*-statistic	AcdS$^+$ fold change	AcdS$^-$ *t*-statistic	AcdS$^-$ fold change	Description
AT1G06640	-4.52	-1.25	-2.71	-1.14	2-oxoglutarate-dependent dioxygenase, putative similar to 2A6 (GI:599622) and tomato ethyl...
AT1G04350	-12.93	-2.29	-12.95	-2.26	2-oxoglutarate-dependent dioxygenase, putative Similar to Arabidopsis 2A6 (gb—X83096) and ...
AT1G55510	5.11	1.49	3.81	1.34	2-oxoisovalerate dehydrogenase, putative 3-methyl-2-oxobutanoate dehydrogenase, putative ...
AT1G06460	7.33	2.22	6.5	2.02	31.2 kDa small heat shock family protein hsp20 family protein contains Pfam profile: PF00...
AT5G48540	-4.47	-1.78	-1.70	-1.23	33 kDa secretory protein-related contains Pfam PF01657: Domain of unknown function, duplic...
AT1G76490	4.02	1.39	0.63	1.05	3-hydroxy-3-methylglutaryl-CoA reductase 1 HMG-CoA reductase 1 (HMG1) identical to HMG-Co...
AT5G46290	6.38	1.41	3.50	1.21	3-oxoacyl-acyl-carrier-protein synthase I identical to Swiss-Prot:P52410 3-oxoacyl-acyl-ca...
AT2G37270	-0.85	-1.07	-4.39	-1.32	40S ribosomal protein S5 (RPS5A) identical to GP:3043428 At2g37270.1
AT5G64860	5.57	1.43	3.95	1.28	4-alpha-glucanotransferase, putative disproportionating enzyme, putative similar to 4-alp...
AT3G22200	11.22	1.76	11.57	1.79	4-aminobutyrate aminotransferase gamma-amino-N-butyrate transaminase GABA transaminase ...
AT1G65060	-4.92	-1.45	-2.79	-1.21	4-coumarate–CoA ligase 3 4-coumaroyl-CoA synthase 3 (4CL3) identical to SP—Q9S777 4-coum...
AT1G20510	2.15	1.22	6.42	1.77	4-coumarate–CoA ligase family protein 4-coumaroyl-CoA synthase family protein similar to...
AT5G63380	-5.6	-1.35	-2.69	-1.16	4-coumarate–CoA ligase family protein 4-coumaroyl-CoA synthase family protein similar to...
AT3G14990	3.47	1.23	4.41	1.28	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative supportin...
AT1G75210	-5.71	-1.42	-3.40	-1.22	5’ nucleotidase family protein contains Pfam profile: PF05761 5’ nucleotidase family At1g7...
AT4G21990	-4.68	-1.65	-6.7	-1.93	5’-adenylylsulfate reductase (APR3) PAPS reductase homolog (PRH26) identical to 5’-adenyl...
AT1G62180	-9.05	-2.06	-10.35	-2.26	5’-adenylylsulfate reductase 2, chloroplast (APR2) (APSR) adenosine 5’-phosphosulfate 5’-...
AT3G03780	-8.66	-1.76	-5.59	-1.41	5-methyltetrahydropteroyltriglutamate–homocysteine methyltransferase, putative vitamin-B...
AT3G25530	-4	-1.24	-2.12	-1.12	6-phosphogluconate dehydrogenase NAD-binding domain-containing protein low similarity to S...
AT3G63520	-5.04	-1.48	-1.34	-1.11	9-cis-epoxycarotenoid dioxygenase neoxanthin cleavage enzyme NCED1 carotenoid cleavage ...
AT1G24290	3.98	1.25	2.55	1.15	AAA-type ATPase family protein similar to Werner helicase interacting protein Homo sapiens...
AT1G70610	-5.21	-1.86	-2.48	-1.35	ABC transporter (TAP1) contains Pfam profile: PF00005 ABC transporters; similar to TAP1 pr...
AT5G39040	-3.70	-1.20	-4.25	-1.24	ABC transporter (TAP2) TAP-like ABC transporter, Rattus norvegicus, EMBL:AB027520; identic...
AT3G55110	-4.72	-1.36	-2.47	-1.17	ABC transporter family protein ATP-binding cassette-sub-family G-member 2, Mus musculus, E...
AT3G55130	-7.06	-1.5	-4.93	-1.32	ABC transporter family protein breast cancer resistance protein 1 BCRP1, Mus musculus, EMB...
AT2G39480	5.03	1.43	3.01	1.24	ABC transporter family protein related to multi drug resistance proteins and P-glycoprotei...
AT1G17840	5.16	1.59	3.47	1.36	ABC transporter family protein similar to ABC transporter GI:10280532 from Homo sapiens At...
AT3G55320	6.3	1.37	6.56	1.4	ABC transporter family protein similar to multidrug resistant P-glycoprotein pmdr1 GI:4204...
AT1G59870	3.23	1.32	4.16	1.43	ABC transporter family protein similar to PDR5-like ABC transporter GI:1514643 from Spirod...
AT1G04120	2.69	1.16	4.74	1.29	ABC transporter family protein Strong similarity to MRP-like ABC transporter gb—U92650 fro...
AT1G61640	7.57	1.53	6.39	1.41	ABC1 family protein contains Pfam domain, PF03109: ABC1 family At1g61640.1
AT5G64940	-5.28	-1.51	-2.53	-1.21	ABC1 family protein contains Pfam domain, PF03109: ABC1 family At5g64940.1
AT5G61380	19.55	3.23	17.74	2.81	ABI3-interacting protein 1 (AIP1) identical to pseudo-response regulator 1 GI:7576354 from...
AT4G37000	7.5	1.92	6.96	1.82	accelerated cell death 2 (ACD2) identical to accelerated cell death 2 (ACD2) GI:12484129 f...
AT3G48560	-4.39	-1.26	-3.90	-1.23	acetolactate synthase, chloroplast acetohydroxy-acid synthase (ALS) nearly identical to S...
AT5G48880	-5.56	-1.46	-4.77	-1.37	acetyl-CoA C-acyltransferase 1 3-ketoacyl-CoA thiolase 1 (PKT1) identical to 3-keto-acyl-...
AT5G48230	6.53	1.64	3.24	1.27	acetyl-CoA C-acyltransferase, putative 3-ketoacyl-CoA thiolase, putative strong similarit...
AT4G29270	-7.95	-1.87	-2.33	-1.20	acid phosphatase class B family protein similar to acid phosphatase Glycine max GI:3341443...
AT2G43710	-7.76	-1.43	-7.54	-1.4	acyl-acyl-carrier-protein desaturase stearoyl-ACP desaturase (SSI2) identical to gi:15149...
AT3G02630	6.27	1.73	4.44	1.48	acyl-acyl-carrier-protein desaturase, putative stearoyl-ACP desaturase, putative similar ...
AT1G27450	5.73	1.33	5.26	1.29	adenine phosphoribosyltransferase 1 (APT1) nearly identical to SP—P31166 Adenine phosphori...
AT5G35170	-4.57	-1.24	-2.91	-1.14	adenylate kinase family protein contains Pfam profile: PF00406 adenylate kinase At5g35170....
AT3G62290	4.19	1.26	1.87	1.10	ADP-ribosylation factor identical to GP:166586 ADP-ribosylation factor Arabidopsis thalian...
AT3G23410	-8.49	-1.51	-5.86	-1.33	alcohol oxidase-related similar to long chain fatty alcohol oxidase from Candida cloacae G...
AT4G34240	-9.84	-1.85	-8.38	-1.69	aldehyde dehydrogenase (ALDH3) similar to aldehyde dehydrogenase Arabidopsis thaliana gi—1...
AT5G20960	-7.53	-1.56	-4.59	-1.3	aldehyde oxidase 1 (AAO1) identical to aldehyde oxidase AAO1 from Arabidopsis thaliana gi:...

Continued...

Locus	AcdS⁺ *t*-statistic	AcdS⁺ fold change	AcdS⁻ *t*-statistic	AcdS⁻ fold change	Description
AT3G43600	-7.88	-1.54	-6.96	-1.46	aldehyde oxidase, putative identical to gi: 3172025; identical to cDNA putative aldehyde o...
AT4G25900	3.68	1.30	4.23	1.35	aldose 1-epimerase family protein similar to apospory-associated protein C; APOC Chlamydom...
AT5G42650	1.99	1.52	5.89	3.17	allene oxide synthase (AOS) hydroperoxide dehydrase cytochrome P450 74A (CYP74A) identic...
AT1G34060	-6.94	-1.78	-5.7	-1.58	alliinase family protein contains Pfam profiles: PF04864 allinase C-terminal domain, PF048...
AT1G34040	-4.35	-1.62	-3.95	-1.52	alliinase family protein contains Pfam profiles: PF04864 allinase C-terminal domain, PF048...
AT1G65560	-6.73	-1.5	-4.57	-1.31	allyl alcohol dehydrogenase, putative similar to allyl alcohol dehydrogenase from Nicotian...
AT5G08380	-7.02	-1.43	-3.89	-1.22	alpha-galactosidase, putative melibiase, putative alpha-D-galactoside galactohydrolase, ...
AT3G45940	5.42	1.52	2.34	1.19	alpha-xylosidase, putative strong similarity to alpha-xylosidase precursor GI:4163997 from...
AT4G22260	6.34	1.45	6.84	1.49	alternative oxidase, putative immutans protein (IM) identical to IMMUTANS from Arabidopsi...
AT4G34740	-6.95	-1.38	-6.9	-1.37	amidophosphoribosyltransferase glutamine phosphoribosylpyrophosphate amidotransferase ph...
AT2G16570	-3.39	-1.20	-4.31	-1.26	amidophosphoribosyltransferase glutamine phosphoribosylpyrophosphate amidotransferase ph...
AT1G57770	-6.67	-1.37	-5.26	-1.29	amine oxidase family contains similarity to carotenoid isomerase Lycopersicon esculentum G...
AT2G43020	3.46	1.38	4.69	1.51	amine oxidase family protein similar to polyamine oxidase SP:O64411 Zea mays; contains Pfa...
AT1G65840	2.26	1.26	5.29	1.67	amine oxidase family protein similar to polyamine oxidase SP:O64411 Zea mays; contains Pfa...
AT5G36940	3.97	1.21	3.30	1.17	amino acid permease family protein similar to SP—Q09143 High-affinity cationic amino acid ...
AT2G01170	4.87	1.44	3.99	1.33	amino acid permease family protein weak similarity to GABA permease Emericella nidulans GI...
AT5G02180	-4.59	-1.32	-4.77	-1.34	amino acid transporter family protein belongs to INTERPRO:IPR002422 amino acidpolyamine tr...
AT2G39130	4.43	1.32	3.95	1.28	amino acid transporter family protein belongs to INTERPRO:IPR002422 amino acidpolyamine tr...
AT3G56200	3.98	1.33	3.71	1.33	amino acid transporter family protein low similarity to N system amino acids transporter N...
AT1G80510	4.57	1.23	2.69	1.13	amino acid transporter family protein similar to amino acid transporter system N2 Rattus n...
AT2G13810	-6.73	-1.54	-6.43	-1.49	aminotransferase class I and II family protein low similarity to Aromatic Aminotransferase...
AT4G13510	-8.39	-1.49	-6.99	-1.39	ammonium transporter 1, member 1 (AMT1.1) identical to SP—P54144 High affinity ammonium tr...
AT2G38290	5.14	1.34	3.83	1.25	ammonium transporter 2 (AMT2) identical to SP—Q9M6N7 Ammonium transporter 2 (AtAMT2) Arabi...
AT3G16910	-8.9	-1.64	-8.7	-1.6	AMP-dependent synthetase and ligase family protein similar to AMP-binding protein GI:19030...
AT3G48990	9.61	1.72	13.68	2.14	AMP-dependent synthetase and ligase family protein similar to peroxisomal-coenzyme A synth...
AT1G20490	-3.87	-1.29	-1.93	-1.13	AMP-dependent synthetase and ligase family protein similar to SP—Q42524 and SP—Q9S725; con...
AT3G04140	-4.95	-1.37	-5.57	-1.45	ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023 At2g03430.1
AT2G03430	2.00	1.20	5.35	1.68	ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023 At2g28840.1
AT2G28840	12.53	1.96	11.76	1.88	ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023 At3g04140.1
AT2G38750	-4.22	-1.32	-1.61	-1.11	annexin 4 (ANN4) nearly identical to annexin (AnnAt4) Arabidopsis thaliana GI:6503084; con...
AT5G17990	1.76	1.11	4.96	1.35	anthranilate phosphoribosyltransferase identical to anthranilate phosphoribosyltransferase...
AT3G25890	5.05	1.31	5.11	1.3	AP2 domain-containing transcription factor, putative At3g25890.1
AT5G67000	-3.41	-1.57	-5.22	-1.93	AP2 domain-containing transcription factor, putative similar to AP2 domain containing prot...
AT5G67190	-4.62	-1.29	-3.26	-1.19	AP2 domain-containing transcription factor, putative similar to AP2 domain containing prot...
AT4G34710	-9.41	-1.61	-7.58	-1.44	arginine decarboxylase 2 (SPE2) identical to SP—O23141 Arginine decarboxylase 2 (EC 4.1.1....
AT3G53800	1.09	1.10	4.18	1.57	armadillobeta-catenin repeat family protein contains Pfam profile: PF00514 armadillobeta-c...
AT3G09350	-5.08	-1.67	-1.24	-1.14	armadillobeta-catenin repeat family protein contains Pfam profile: PF00514 armadillobeta-c...
AT4G31990	4.53	1.33	2.39	1.16	aspartate aminotransferase, chloroplast transaminase A (ASP5) (AAT1) nearly identical to ...
AT1G62800	5.93	1.34	3.83	1.21	aspartate aminotransferase, cytoplasmic isozyme 2 transaminase A (ASP4) identical to aspa...
AT2G30970	3.85	1.2	4.08	1.21	aspartate aminotransferase, mitochondrial transaminase A (ASP1) identical to SP—P46643 As...
AT1G15410	4.93	1.57	4.00	1.45	aspartate-glutamate racemase family contains Pfam profile PF—01177 Aspartate-glutamate rac...
AT3G61820	5.52	1.42	3.35	1.23	aspartyl protease family protein contains Pfam domain, PF00026: eukaryotic aspartyl protea...
AT1G01300	5.42	1.56	3.71	1.36	aspartyl protease family protein contains Pfam domain, PF00026: eukaryotic aspartyl protea...
AT1G58080	4.03	1.26	4.6	1.3	ATP phosphoribosyl transferase 1 (ATP-PRT1) identical to ATP phosphoribosyl transferase GI...
AT1G80660	4.11	1.22	3.61	1.18	ATPase 9, plasma membrane-type, putative proton pump 9, putative proton-exporting ATPase...
AT3G47950	5.33	1.59	2.24	1.22	ATPase, plasma membrane-type, putative proton pump, putative strong similarity to P-type ...

Continued...

Locus	AcdS$^+$ *t*-statistic	AcdS$^+$ fold change	AcdS$^-$ *t*-statistic	AcdS$^-$ fold change	Description
AT3G42640	5.93	1.63	2.28	1.20	ATPase, plasma membrane-type, putative proton pump, putative strong similarity to P-type . . .
AT5G44316	-9.95	-1.64	-7.84	-1.47	ATP-binding-cassette transporter, putative similar to ATP-binding-cassette transporter (AB. . .
AT1G09430	4.74	1.32	2.69	1.18	ATP-citrate synthase (ATP-citrate (pro-S-)-lyasecitrate cleavage enzyme), putative similar. . .
AT1G70940	4.24	1.66	0.66	1.08	auxin transport protein, putative (PIN3) similar to auxin transport protein Arabidopsis th. . .
AT2G46370	4.49	1.24	4.95	1.25	auxin-responsive GH3 family protein similar to auxin-responsive GH3 product Glycine max GI. . .
AT4G03400	-5.86	-1.42	-2.87	-1.19	auxin-responsive GH3 family protein similar to auxin-responsive GH3 product Glycine max GI. . .
AT3G07390	7.51	1.81	5.12	1.5	auxin-responsive protein auxin-induced protein (AIR12) identical (with 7 residue gap) to . . .
AT5G51570	12.05	1.74	12.29	1.73	band 7 family protein similar to hypersensitive-induced response protein Zea mays GI:77164. . .
AT5G62740	4.75	1.28	4.79	1.27	band 7 family protein strong similarity to hypersensitive-induced response protein Zea may. . .
AT5G46830	-3.96	-1.22	-2.58	-1.14	basic helix-loop-helix (bHLH) family protein At5g46830.1
AT4G00050	-7.21	-1.67	-5.02	-1.41	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-hel. . .
AT1G51070	-4.64	-1.48	-1.96	-1.17	basic helix-loop-helix (bHLH) family protein similar to bHLH transcription factor GI:37575. . .
AT4G15210	-7.58	-1.67	-5.16	-1.4	beta-amylase (BMY1) 1,4-alpha-D-glucan maltohydrolase identical to Beta-amylase (EC 3.2.1. . .
AT5G18670	-6.71	-1.78	-4.67	-1.46	beta-amylase, putative (BMY3) 1,4-alpha-D-glucan maltohydrolase, putative almost identica. . .
AT2G32290	-7.18	-1.95	-3.15	-1.33	beta-amylase, putative 1,4-alpha-D-glucan maltohydrolase, putative similar to beta-amylas. . .
AT4G25700	-11.94	-1.89	-10.54	-1.77	beta-carotene hydroxylase identical to GI:1575296 At4g25700.1
AT5G52570	-13.06	-1.81	-12.38	-1.73	beta-carotene hydroxylase, putative similar to GI:1575296, beta-carotene hydroxylase At5g5. . .
AT4G28250	-5.09	-1.31	-5.01	-1.28	beta-expansin, putative (EXPB3) similar to soybean pollen allergen (cim1) protein - soybea. . .
AT1G12240	-7.54	-1.66	-8.36	-1.75	beta-fructosidase (BFRUCT4) beta-fructofuranosidase invertase, vacuolar identical to bet. . .
AT3G52840	6.23	1.62	4.9	1.47	beta-galactosidase, putative lactase, putative similar to beta-galactosidase Lycopersicon. . .
AT5G63810	4.32	1.51	1.61	1.17	beta-galactosidase, putative lactase, putative similar to beta-galactosidase GI:7939621 f. . .
AT1G45130	4.74	1.46	2.64	1.21	beta-galactosidase, putative lactase, putative similar to beta-galactosidase precursor GI. . .
AT2G35860	-8.12	-1.46	-6.87	-1.37	beta-Ig-H3 domain-containing protein fasciclin domain-containing protein contains Pfam pr. . .
AT4G19710	-3.88	-1.22	-1.47	-1.08	bifunctional aspartate kinasehomoserine dehydrogenase, putative AK-HSDH, putative similar. . .
AT2G26900	-3.99	-1.25	-1.60	-1.09	bile acid:sodium symporter family protein low similarity to SP—Q12908 Ileal sodiumbile aci. . .
AT1G70370	-3.64	-1.19	-6.08	-1.35	BURP domain-containing protein polygalacturonase, putative similar to polygalacturonase i. . .
AT1G23760	-4.85	-1.32	-4.75	-1.32	BURP domain-containing protein polygalacturonase, putative similar to polygalacturonase i. . .
AT5G10030	-3.87	-1.26	-1.18	-1.08	bZIP family transcription factor (OBF4) identical to ocs-element binding factor 4 GI:41461. . .
AT3G62420	-5.9	-1.41	-6.59	-1.43	bZIP transcription factor family protein similar to common plant regulatory factor 6 GI:96. . .
AT5G28770	-5.99	-1.48	-1.93	-1.13	bZIP transcription factor family protein similar to seed storage protein opaque-2(bZIP fam. . .
AT1G67980	2.52	1.17	5.55	1.43	caffeoyl-CoA 3-O-methyltransferase, putative similar to GI:2960356 Populus balsamifera sub. . .
AT5G55990	4.79	1.46	3.52	1.31	calcineurin B-like protein 2 (CBL2) identical to calcineurin B-like protein 2 GI:3309084 f. . .
AT4G24890	3.04	1.22	4.36	1.34	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin. . .
AT1G13900	4.05	1.37	2.25	1.19	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin. . .
AT4G05520	7.43	1.53	6.47	1.46	calcium-binding EF hand family protein similar to EH-domain containing protein 1 from Mus . . .
AT2G33380	-5.24	-1.65	-0.21	-1.02	calcium-binding RD20 protein (RD20) induced by abscisic acid during dehydration PMID:10965. . .
AT5G23580	3.73	1.32	4.65	1.42	calcium-dependent protein kinase 9 (CDPK9) identical to calcium-dependent protein kinase A. . .
AT4G29900	-6.54	-1.52	-6.21	-1.45	calcium-transporting ATPase, plasma membrane-type, putative Ca2+-ATPase, putative (ACA10). . .
AT5G62070	-7.59	-1.59	-6.37	-1.48	calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding mot. . .
AT4G23060	4.69	1.26	4.25	1.22	calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding mot. . .
AT5G09410	6.13	1.4	3.73	1.23	calmodulin-binding protein similar to anther ethylene-upregulated calmodulin-binding prote. . .
AT5G64220	4.84	1.29	4.07	1.22	calmodulin-binding protein similar to anther ethylene-upregulated calmodulin-binding prote. . .
AT2G43290	-4.02	-1.28	-3.28	-1.20	calmodulin-like protein (MSS3) identical to calmodulin-like MSS3 from GI:9965747 Arabidops. . .
AT5G14740	-18.74	-3.29	-22.16	-3.95	carbonic anhydrase 2 carbonate dehydratase 2 (CA2) (CA18) nearly identical to SP—P42737 C. . .
AT3G52720	-6.32	-1.71	-5.86	-1.64	carbonic anhydrase family protein low similarity to storage protein (dioscorin) Dioscorea . . .
AT1G23730	-4.67	-1.45	-3.02	-1.25	carbonic anhydrase, putative carbonate dehydratase, putative similar to SP—P27140 Carboni. . .

Continued. . .

Locus	AcdS^{+} *t*-statistic	AcdS^{+} fold change	AcdS^{-} *t*-statistic	AcdS^{-} fold change	Description
AT1G70410	-5.37	-1.51	-3.31	-1.28	carbonic anhydrase, putative carbonate dehydratase, putative similar to SP—P42737 Carboni. . .
AT4G01610	2.69	1.14	4.35	1.24	cathepsin B-like cysteine protease, putative similar to cathepsin B-like cysteine proteina. . .
AT2G39450	-5.95	-1.48	-2.27	-1.15	cation efflux family protein contains cation efflux family protein domain, Pfam:PF01545 At. . .
AT4G18700	-4.95	-1.38	-2.16	-1.15	CBL-interacting protein kinase 12 (CIPK12) identical to CBL-interacting protein kinase 12 . . .
AT5G57630	6.57	2.65	5.66	2.35	CBL-interacting protein kinase 21, putative (CIPK21) identical to CBL-interacting protein . . .
AT1G01140	-8.53	-2.55	-5.85	-1.87	CBL-interacting protein kinase 9 (CIPK9) identical to CBL-interacting protein kinase 9 Ara. . .
AT4G14230	3.71	1.26	5.6	1.39	CBS domain-containing protein-related contains Pfam profile PF01595: Domain of unknown fun. . .
AT2G34720	-9.2	-1.92	-6.5	-1.56	CCAAT-binding transcription factor (CBF-BNF-YA) family protein contains Pfam profile: PF02. . .
AT5G47640	-3.70	-1.27	-5.07	-1.38	CCAAT-box binding transcription factor subunit B (NF-YB) (HAP3) (AHAP3) family (Hap3b) si. . .
AT4G01330	-3.33	-1.24	-5.94	-1.46	CDC5_YEAST (P32562) Cell cycle serinethreonine-protein kinase CDC5MSD2 , partial (5
AT5G55280	4.5	1.53	2.30	1.23	cell division protein FtsZ, chloroplast, putative (FTSZ) identical to SP—Q42545 Cell divis. . .
AT4G15290	-11.91	-2.48	-8.54	-1.88	cellulose synthase family protein similar to Zea mays cellulose synthase-3 gi:9622878, -2 . . .
AT2G32610	-10.39	-1.96	-7.25	-1.57	cellulose synthase family protein similar to Zea mays cellulose synthase-5 gi:9622882, -4 . . .
AT2G32620	-6.31	-1.83	-4.54	-1.51	cellulose synthase family protein similar to Zea mays cellulose synthase-5 gi:9622882, -4 . . .
AT4G39350	-4.9	-1.54	-1.61	-1.14	cellulose synthase, catalytic subunit (Ath-A) identical to gi:2827141 At4g39350.1
AT5G09870	-6.21	-1.45	-7.11	-1.53	cellulose synthase, catalytic subunit, putative similar to gi:2827141 cellulose synthase c. . .
AT4G32190	-9.87	-2.16	-6.96	-1.7	centromeric protein-related low similarity to SP—Q02224 Centromeric protein E (CENP-E prot. . .
AT5G13930	-8.06	-5.12	-7.38	-4.52	chalcone synthase naringenin-chalcone synthase identical to SP—P13114 At5g13930.1
AT5G05270	-5.63	-1.83	-4.69	-1.62	chalcone-flavanone isomerase family protein contains very low similarity to chalcone-flavo. . .
AT2G43590	-7.65	-1.6	-8.79	-1.66	chitinase, putative similar to basic endochitinase CHB4 precursor SP:Q06209 from Brassica . . .
AT2G43580	-4.75	-1.43	-4.52	-1.39	chitinase, putative similar to basic endochitinase CHB4 precursor SP:Q06209 from Brassica . . .
AT3G22840	-14.65	-3.51	-13.29	-3.13	chlorophyll A-B binding family protein early light-induced protein (ELIP) identical to ea. . .
AT1G15500	9.72	1.78	10.45	1.81	chloroplast ADP, ATP carrier protein, putative ADP, ATP translocase, putative adenine nu. . .
AT2G36250	4.39	1.3	3.56	1.25	chloroplast division protein FtsZ (FtsZ2-1) identical to chloroplast division protein AtFt. . .
AT5G10770	-6.68	-1.77	-3.69	-1.37	chloroplast nucleoid DNA-binding protein, putative similar to CND41, chloroplast nucleoid . . .
AT2G16640	4.01	1.39	2.88	1.26	chloroplast outer membrane protein, putative similar to chloroplast protein import compone. . .
AT2G30440	4.78	1.28	5.52	1.34	chloroplast thylakoidal processing peptidase identical to chloroplast thylakoidal processi. . .
AT3G29200	-3.95	-1.31	-4.26	-1.34	chorismate mutase, chloroplast (CM1) identical to chorismate mutase GB:Z26519 SP—P42738 Ar. . .
AT1G09500	-12.73	-2.51	-9.07	-1.92	cinnamyl-alcohol dehydrogenase family CAD family similar to cinnamyl alcohol dehydrogenas. . .
AT1G09510	-6.36	-1.57	-4.44	-1.35	cinnamyl-alcohol dehydrogenase family CAD family similar to cinnamyl alcohol dehydrogenas. . .
AT3G58750	3.41	1.35	4.2	1.41	citrate synthase, glyoxysomal, putative strong similarity to SP—P49299 Citrate synthase, g. . .
AT1G04620	7.73	2.02	5.1	1.57	coenzyme F420 hydrogenase family dehydrogenase, beta subunit family contains Pfam PF04432. . .
AT2G15970	4.31	1.81	5.51	2.24	cold-acclimation protein, putative (FL3-5A3) similar to cold acclimation WCOR413-like prot. . .
AT1G07050	9.87	2.7	7.88	2.15	CONSTANS-like protein-related contains similarity to photoperiod sensitivity quantitative . . .
AT4G12290	-7.12	-1.48	-2.02	-1.12	copper amine oxidase, putative similar to copper amine oxidase Cicer arietinum gi—3819099—. . .
AT4G08920	-5.39	-1.77	-3.12	-1.39	cryptochrome 1 apoprotein (CRY1) flavin-type blue-light photoreceptor (HY4) contains Pfam. . .
AT5G24850	-7.2	-1.5	-5.63	-1.35	cryptochrome dash (CRYD) nearly identical to cryptochrome dash Arabidopsis thaliana GI:289. . .
AT4G17740	4.74	1.31	3.12	1.19	C-terminal processing protease, putative similar to C-terminal protease precursor Spinacia. . .
AT1G78820	4.48	1.66	6.55	2	curculin-like (mannose-binding) lectin family protein PAN domain-containing protein simil. . .
AT1G78830	3.46	1.60	5.25	1.92	curculin-like (mannose-binding) lectin family protein similar to S glycoprotein Brassica r. . .
AT5G15410	1.93	1.17	5.71	1.59	cyclic nucleotide-regulated ion channel cyclic nucleotide-gated channel (CNGC2) identical. . .
AT2G23980	3.94	1.33	3.45	1.30	cyclic nucleotide-regulated ion channel cyclic nucleotide-gated channel (CNGC6) identical. . .
AT2G28260	-3.86	-1.28	-3.34	-1.25	cyclic nucleotide-regulated ion channel, putative (CNGC15) similar to cyclic nucleotide an. . .
AT1G27630	4.18	1.37	3.20	1.26	cyclin family protein similar to cyclin T1 Homo sapiens GI:2981196; contains Pfam profile . . .
AT3G23510	-6.27	-1.36	-4.52	-1.23	cyclopropane fatty acid synthase, putative CPA-FA synthase, putative similar to cycloprop. . .
AT3G12490	4.15	1.64	3.40	1.45	cysteine protease inhibitor, putative cystatin, putative similar to PRLI-interacting fact. . .

Continued. . .

Locus	AcdS$^+$ *t*-statistic	AcdS$^+$ fold change	AcdS$^-$ *t*-statistic	AcdS$^-$ fold change	Description
AT2G21430	10.9	1.92	8.51	1.64	cysteine proteinase A494, putative thiol protease, putative identical to SP:P43295 Probab...
AT3G49340	-4.67	-1.3	-2.52	-1.15	cysteine proteinase, putative contains PS00640: Eukaryotic thiol (cysteine) proteases aspa...
AT4G16190	8.84	1.56	11.19	1.72	cysteine proteinase, putative contains similarity to papain-like cysteine proteinase isofo...
AT3G61440	-4.63	-1.31	-2.13	-1.13	cysteine synthase, putative O-acetylserine (thiol)-lyase, putative O-acetylserine sulfhy...
AT5G28030	-3.99	-1.26	-3.01	-1.17	cysteine synthase, putative O-acetylserine (thiol)-lyase, putative O-acetylserine sulfhy...
AT5G28050	-4.27	-1.4	-3.53	-1.30	cytidinedeoxycytidylate deaminase family protein similar to SP—O34598 Guanine deaminase (E...
AT5G54290	5.41	1.41	4.17	1.29	cytochrome c biogenesis protein family low similarity to cytochrome c biogenesis protein C...
AT4G10040	-4.4	-1.54	-2.43	-1.25	cytochrome c, putative similar to cytochrome c Pumpkin, Winter squash SWISS-PROT:P00051 At...
AT3G26200	0.71	1.07	4.3	1.45	cytochrome P450 71B22, putative (CYP71B22) Identical to cytochrome P450 71B22 (SP:Q9LTM1)A...
AT3G26290	-3.99	-1.49	-1.93	-1.21	cytochrome P450 71B26, putative (CYP71B26) identical to cytochrome P450 71B26 (SP:Q9LTL0) ...
AT3G26320	-4.15	-1.25	-1.77	-1.11	cytochrome P450 71B36, putative (CYP71B36) identical to Cytochrome P450 71B36 (SP:Q9LIP4) ...
AT1G13110	-5.07	-1.43	-4.69	-1.37	cytochrome P450 71B7 (CYP71B7) identical to (SP:Q96514) cytochrome P450 71B7 Arabidopsis t...
AT4G36220	-4.44	-2.05	-3.01	-1.65	cytochrome P450 84A1 (CYP84A1) ferulate-5-hydroxylase (FAH1) identical to Cytochrome P450...
AT2G02580	-4.2	-1.22	-2.53	-1.12	cytochrome P450 family protein At2g02580.1
AT2G45550	-5.28	-1.37	-4.16	-1.28	cytochrome P450 family protein At2g45550.1
AT4G13770	-6.89	-1.67	-2.82	-1.23	cytochrome P450 family protein At4g13770.1
AT4G37330	-4.22	-1.28	-2.30	-1.14	cytochrome P450 family protein At4g37330.1
AT4G12300	-5.96	-1.32	-5.48	-1.28	cytochrome P450 family protein flavonoid 3',5'-hydroxylase - Campanula medium, PID:d100395...
AT2G29090	-14.23	-2.6	-12.57	-2.28	cytochrome P450 family protein similar to Cytochrome P450 88A3 (SP:O23051) Arabidopsis tha...
AT5G44620	-6.42	-1.51	-6.1	-1.45	cytochrome P450 family protein similar to cytocrhome P450 monooxygenase (GI:14334057) Goss...
AT5G45340	-3.97	-1.31	-3.09	-1.24	cytochrome P450 family protein similar to SP—Q42569—C901_ARATH Cytochrome P450 90A1 (SP:Q...
AT4G12320	-6.9	-1.89	-7.72	-2.05	cytochrome P450, putative Similar to P450 monooxygenase (gi:14334057) Gossypium arboreum A...
AT4G12310	-11.86	-2.02	-13.33	-2.17	cytochrome P450, putative similar to P450 monooxygenase GI:14334057 from Gossypium arboreu...
AT4G30530	-5.71	-1.97	-1.12	-1.14	defense-related protein, putative strong similarity to defense-related protein Brassica ca...
AT5G58770	-8.14	-2.66	-4.23	-1.65	dehydrodolichyl diphosphate synthase, putative DEDOL-PP synthase, putative similar to GI:...
AT2G31360	6.79	1.56	9.86	1.88	delta 9 desaturase (ADS2) identical to delta 9 acyl-lipid desaturase (ADS2) GI:2970036 fro...
AT5G62530	5.06	1.35	7.43	1.52	delta-1-pyrroline-5-carboxylate dehydrogenase (P5CDH) identical to delta-1-pyrroline-5-car...
AT2G29170	-4	-1.29	-5.35	-1.4	DHCA_HUMAN (P16152) Carbonyl reductase NADPH 1 (NADPH-dependent carbonyl reductase 1) (P...
AT4G21540	2.25	1.14	4.28	1.26	diacylglycerol kinase family protein contains INTERPRO domain, IPR001206, DAG-kinase catal...
AT5G06340	5.8	1.38	5.2	1.32	diadenosine 5',5"'-P1,P4-tetraphosphate hydrolase, putative similar to diadenosine 5',5"...
AT1G35420	2.18	1.13	4.47	1.3	dienelactone hydrolase family protein low similarity to dienelactone hydrolase Rhodococcus...
AT3G23600	3.59	1.17	4.49	1.21	dienelactone hydrolase family protein similar to SP—Q9ZT66 Endo-1,3;1,4-beta-D-glucanase p...
AT1G48030	-5.37	-2.01	-4.32	-1.77	dihydrolipoamide dehydrogenase 1, mitochondrial lipoamide dehydrogenase 1 (MTLPD1) identi...
AT3G02770	4.34	1.31	2.55	1.18	dimethylmenaquinone methyltransferase family protein similar to bacterial S-adenosylmethio...
AT1G59620	-3.89	-1.27	-4.73	-1.37	disease resistance protein (CC-NBS class), putative domain signature CC-NBS exists, sugges...
AT1G58848	-5.63	-1.4	-5.86	-1.44	disease resistance protein (CC-NBS-LRR class), putative PRM1 homolog, putative similar to...
AT4G33300	-7.77	-1.63	-6.33	-1.47	disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists...
AT1G59218	-3.75	-1.36	-4.34	-1.46	disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists...
AT1G55210	-3.72	-1.31	-5.07	-1.45	disease resistance response protein-related dirigent protein-related smimilar to dirigent ...
AT1G58170	3.98	1.27	1.91	1.12	disease resistance-responsive protein-related dirigent protein-related similar to dirigen...
AT1G53280	2.53	1.12	4.16	1.2	DJ-1 family protein similar to DJ-1 protein Homo sapiens GI:1780755; similar to DJ-1 beta ...
AT1G63990	4.05	1.27	2.38	1.14	DNA topoisomerase VIA, putative (SPO11-2) similar to topoisomerase 6 subunit A (spo11) Ara...
AT1G13260	-4.99	-1.3	-4.02	-1.25	DNA-binding protein RAV1 (RAV1) identical to SP—Q9ZWM9 DNA-binding protein RAV1 Arabidopsi...
AT2G46870	4.56	1.36	3.69	1.31	DNA-binding protein, putative similar to DNA-binding proteins from Arabidopsis thaliana RA...
AT1G10590	4.39	1.31	2.50	1.16	DNA-binding protein-related contains weak similarity to G-quartet DNA binding protein 3 Te...
AT3G12610	4.24	1.36	2.21	1.18	DNA-damage-repairtoleration protein, putative (DRT100) similar to DNA-damage-repairtolerat...

Continued...

Locus	AcdS$^+$ *t*-statistic	AcdS$^+$ fold change	AcdS$^-$ *t*-statistic	AcdS$^-$ fold change	Description
AT2G24120	10.36	2.06	7.37	1.68	DNA-directed RNA polymerase, chloroplast (RPOPT) identical to SP—O24600 DNA-directed RNA p. . .
AT2G20550	-6.4	-1.75	-1.62	-1.15	DNAJ chaperone C-terminal domain-containing protein contains Pfam profile PF01556: DnaJ C . . .
AT3G62600	-2.10	-1.13	-4.28	-1.28	DNAJ heat shock family protein similar to DnaJ homolog subfamily B member 11 precursor (SP. . .
AT2G20560	-6.17	-2.05	-1.55	-1.19	DNAJ heat shock family protein SP—Q9UDY4 DnaJ homolog subfamily B member 4 (Heat shock 40 . . .
AT4G36040	-6.93	-2.1	-4.75	-1.64	DNAJ heat shock N-terminal domain-containing protein (J11) identical to dnaJ heat shock pr. . .
AT5G23240	20.89	4.23	19.55	3.87	DNAJ heat shock N-terminal domain-containing protein low similarity to SP—O34136 Chaperone. . .
AT4G09350	-7	-1.75	-5.68	-1.56	DNAJ heat shock N-terminal domain-containing protein similar to J11 protein Arabidopsis th. . .
AT3G13310	-5.56	-1.32	-4.17	-1.24	DNAJ heat shock N-terminal domain-containing protein similar to SP—Q45552 Chaperone protei. . .
AT2G17880	-9.19	-1.71	-8.04	-1.58	DNAJ heat shock protein, putative similar to J11 protein Arabidopsis thaliana GI:9843641; . . .
AT1G26790	-5.1	-1.4	-3.73	-1.26	Dof-type zinc finger domain-containing protein similar to H-protein promoter binding facto. . .
AT1G28330	3.91	1.3	3.79	1.29	dormancy-associated protein, putative (DRM1) identical to dormancy-associated protein Arab. . .
AT4G19120	4.15	1.39	3.70	1.34	early-responsive to dehydration stress protein (ERD3) identical to ERD3 protein Arabidopsi. . .
AT3G08950	3.87	1.32	2.69	1.22	electron transport SCO1SenC family protein similar to SP—P23833 SCO1 protein, mitochondria. . .
AT5G13650	-6.39	-1.5	-4.44	-1.33	elongation factor family protein contains Pfam profiles: PF00009 elongation factor Tu GTP . . .
AT2G31060	3.88	1.54	2.05	1.27	elongation factor family protein contains Pfam profiles: PF00009 elongation factor Tu GTP . . .
AT1G62750	-4.07	-1.29	-2.73	-1.19	elongation factor Tu family protein similar to elongation factor G SP:P34811 Glycine max (. . .
AT1G55450	5.9	1.47	7.32	1.58	embryo-abundant protein-related similar to embryo-abundant protein GI:1350531 from Picea g. . .
AT3G07680	4.56	1.65	2.80	1.37	emp24gp25Lp24 family protein similar to SP—Q15363 Cop-coated vesicle membrane protein p24 . . .
AT1G02270	-4	-1.33	-1.28	-1.09	endonucleaseexonucleasephosphatase family protein calcium-binding EF hand family protein . . .
AT4G32285	4.49	1.66	1.27	1.15	epsin N-terminal homology (ENTH) domain-containing protein clathrin assembly protein-rela. . .
AT5G19290	5.22	1.39	3.58	1.25	esteraselipasethioesterase family protein low similarity to monoglyceride lipase Homo sapi. . .
AT3G20770	5.51	1.32	2.44	1.13	ethylene-insensitive 3 (EIN3) identical to ethylene-insensitive3 GI:2224933 from Arabidops. . .
AT2G27050	4.87	1.45	2.10	1.17	ethylene-insensitive3-like1 (EIL1) identical to ethylene-insensitive3-like1 GI:2224927 fro. . .
AT2G22300	3.56	1.20	6.35	1.37	ethylene-responsive calmodulin-binding protein, putative (SR1) identical to partial sequen. . .
AT5G07580	3.06	1.36	6.82	1.99	ethylene-responsive element-binding family protein contains similarity to ethylene respons. . .
AT3G58680	4.67	1.91	3.65	1.67	ethylene-responsive transcriptional coactivator, putative similar to ethylene-responsive t. . .
AT2G27700	-4.54	-1.33	-2.91	-1.21	eukaryotic translation initiation factor 2 family protein eIF-2 family protein similar to. . .
AT5G25820	4.98	1.41	3.95	1.29	exostosin family protein contains Pfam profile: PF03016 exostosin family At5g25820.1
AT3G45970	-10.08	-1.71	-11.49	-1.83	expansin family protein (EXPL1) similar to cim1 induced allergen, Glycine max, EMBL:U03860. . .
AT4G38400	-9.91	-2.06	-13.04	-2.51	expansin family protein (EXPL2) contains Pfam profile: PF01357 pollen allergen; expansin-l. . .
AT3G45960	-8.19	-2.04	-11.2	-2.58	expansin family protein (EXPL3) contains Pfam profile: PF01357 pollen allergen; expansin-l. . .
AT3G29030	-4.2	-1.36	-4.08	-1.32	expansin, putative (EXP5) identical to expansin At-EXP5 GB:AAB38071 from Arabidopsis thali. . .
AT1G73210	1.88	1.09	4.33	1.23	expressed protein At1g73210.1
AT2G01230	3.88	1.33	1.01	1.07	expressed protein At2g01220.1
AT2G34640	4.47	1.24	1.91	1.09	expressed protein At2g34640.1
AT2G41960	2.68	1.17	5.79	1.41	expressed protein At2g41960.1
AT3G54500	-10.56	-2.91	-6.23	-1.85	expressed protein At3g54500.1
AT3G56720	6.24	1.31	4.99	1.24	expressed protein At3g56720.1
AT3G60590	4.31	1.43	3.54	1.37	expressed protein At3g60590.1
AT1G07280	1.34	1.10	5.75	1.42	expressed protein At1g07280.1
AT1G10020	-2.68	-1.20	-4.11	-1.3	expressed protein At1g10020.1
AT1G10690	-4.36	-1.38	-3.02	-1.24	expressed protein At1g10690.1
AT1G13360	6.58	1.46	6.57	1.45	expressed protein At1g13360.1
AT1G17080	4.33	1.65	4.52	1.71	expressed protein At1g17080.1
AT1G19140	-5.43	-1.28	-4.94	-1.26	expressed protein At1g19140.1
AT1G19370	7.14	1.54	2.76	1.18	expressed protein At1g19370.1

Continued. . .

Locus	AcdS$^+$ *t*-statistic	AcdS$^+$ fold change	AcdS$^-$ *t*-statistic	AcdS$^-$ fold change	Description
AT1G19400	-8.64	-1.8	-8	-1.67	expressed protein At1g19400.1
AT1G22850	-8.55	-1.7	-5.4	-1.38	expressed protein At1g22850.1
AT1G23330	-4.82	-1.4	-3.12	-1.23	expressed protein At1g23330.1
AT1G28530	5.03	1.49	1.07	1.09	expressed protein At1g28530.1
AT1G29690	-3.97	-1.31	-4.37	-1.32	expressed protein At1g29690.1
AT1G32520	-4.87	-1.28	-3.07	-1.17	expressed protein At1g32520.1
AT1G44000	-7.83	-1.89	-3.65	-1.33	expressed protein At1g44000.1
AT1G50020	-4.88	-1.74	-2.63	-1.33	expressed protein At1g50020.1
AT1G50040	-4.74	-1.5	-6.2	-1.65	expressed protein At1g50040.1
AT1G50450	-4.21	-1.37	-1.41	-1.11	expressed protein At1g50450.1
AT1G62190	-5.56	-1.47	-2.92	-1.21	expressed protein At1g62190.1
AT1G62220	4.14	1.31	0.06	1.00	expressed protein At1g62220.1
AT1G62250	-8.02	-1.66	-6.57	-1.52	expressed protein At1g62250.1
AT1G64680	-6.49	-1.62	-1.80	-1.14	expressed protein At1g64680.1
AT1G64770	-4.79	-1.34	-1.77	-1.11	expressed protein At1g64770.1
AT1G68220	7.45	2.2	4.15	1.56	expressed protein At1g68220.1
AT1G68440	-5.92	-1.31	-4.37	-1.23	expressed protein At1g68440.1
AT1G68660	-4.62	-1.35	-2.41	-1.17	expressed protein At1g68660.1
AT1G69230	5.83	1.57	3.90	1.36	expressed protein At1g69230.1
AT1G70230	-4.66	-1.55	-2.24	-1.24	expressed protein At1g70230.1
AT1G70780	-8.73	-1.69	-9.07	-1.71	expressed protein At1g70780.1
AT1G75140	4.39	1.29	2.21	1.13	expressed protein At1g75140.1
AT1G76960	3.86	1.9	5.61	2.71	expressed protein At1g76960.1
AT2G02570	3.69	1.21	4.82	1.28	expressed protein At2g02570.1
AT2G02590	6.52	1.68	4.82	1.47	expressed protein At2g02590.1
AT2G04039	-6.28	-1.86	-4.26	-1.49	expressed protein At2g04039.1
AT2G07708	-5.49	-1.49	-4.23	-1.36	expressed protein At2g07708.1
AT2G20495	4	1.21	4.92	1.25	expressed protein At2g20495.1
AT2G22080	1.96	1.19	5.32	1.58	expressed protein At2g22080.1
AT2G23390	-4.05	-1.31	-2.29	-1.16	expressed protein At2g23390.1
AT2G27770	3.34	1.20	5.52	1.36	expressed protein At2g27770.1
AT2G27830	-4.67	-1.42	0.11	1.01	expressed protein At2g27830.1
AT3G12320	-5.18	-1.67	-3.86	-1.44	expressed protein At3g12320.1
AT3G19340	-4.25	-1.41	-2.86	-1.26	expressed protein At3g19340.1
AT4G17870	5.03	1.31	5.25	1.3	expressed protein At4g17870.1
AT4G19400	3.91	1.24	3.31	1.21	expressed protein At4g19400.1
AT4G27030	-11.03	-1.82	-7.95	-1.52	expressed protein At4g27030.1
AT4G28080	-13.87	-2.66	-10.6	-2.09	expressed protein At4g28080.1
AT4G28740	-3.89	-1.4	-2.15	-1.20	expressed protein At4g28740.1
AT4G38060	-3.92	-1.36	-3.56	-1.30	expressed protein At4g38060.2
AT5G04830	-6.68	-1.51	-4.09	-1.28	expressed protein At5g04830.1
AT5G06980	-5.95	-1.68	-4.79	-1.49	expressed protein At5g06980.2
AT5G11070	6.8	2.33	6.86	2.37	expressed protein At5g11070.1
AT5G11480	4.8	1.41	5.2	1.46	expressed protein At5g11480.1
AT5G14240	4.68	1.23	4.45	1.21	expressed protein At5g14240.1
AT5G14390	4.96	1.34	3.87	1.25	expressed protein At5g14390.1

Continued. . .

Locus	AcdS$^+$ *t*-statistic	AcdS$^+$ fold change	AcdS$^-$ *t*-statistic	AcdS$^-$ fold change	Description
AT5G15070	4.27	1.28	6.8	1.5	expressed protein At5g15070.1
AT5G17640	4.21	1.27	1.94	1.12	expressed protein At5g17640.1
AT5G18120	5.86	1.39	6.64	1.47	expressed protein At5g18120.1
AT5G20670	4.71	1.29	5.49	1.37	expressed protein At5g20670.1
AT5G26770	4.04	1.22	2.86	1.15	expressed protein At5g26770.1
AT5G36210	-3.86	-1.24	-2.54	-1.14	expressed protein At5g36210.1
AT5G39570	-3.99	-1.28	-3.07	-1.20	expressed protein At5g39570.1
AT5G41140	3.88	1.55	0.62	1.07	expressed protein At5g41140.1
AT5G51720	-7.75	-3.98	-4.75	-2.32	expressed protein At5g51720.1
AT5G59080	-8.05	-3.13	-5.26	-2.04	expressed protein At5g59080.1
AT5G64510	-4.42	-1.4	-0.11	-1.01	expressed protein At5g64510.1
AT1G55360	4	1.39	1.98	1.17	expressed protein contains Pfam profile PF03080: Arabidopsis proteins of unknown function...
AT2G44240	-5.05	-1.25	-3.88	-1.19	expressed protein contains Pfam profile PF03080: Arabidopsis proteins of unknown function...
AT1G06240	-4.37	-1.3	-3.04	-1.20	expressed protein contains Pfam domain, PF04305: Protein of unknown function (DUF455) At1g...
AT2G41640	-6.56	-1.72	-6.58	-1.7	expressed protein contains Pfam domain, PF04577: Protein of unknown function (DUF563) At2g...
AT5G49820	4.67	1.35	3.40	1.25	expressed protein contains Pfam domain, PF04884: Protein of unknown function, DUF647 At5g4...
AT2G44500	-6.71	-1.59	-8.05	-1.7	expressed protein contains Pfam PF03138: Plant protein family. The function of this family...
AT5G65470	-3.28	-1.29	-4.82	-1.42	expressed protein contains Pfam PF03138: Plant protein family. The function of this family...
AT3G24430	-5.18	-1.42	-2.66	-1.21	expressed protein contains Pfam profile PF01883: Domain of unknown function At3g24430.1
AT4G21570	3.41	1.22	6.91	1.51	expressed protein contains Pfam profile PF03619: Domain of unknown function At4g21570.1
AT1G70750	4.16	1.31	1.15	1.07	expressed protein contains Pfam profile PF04576: Protein of unknown function, DUF593; supp...
AT4G35920	-4.18	-1.28	-2.47	-1.15	expressed protein contains Pfam profile PF04749: Protein of unknown function, DUF614; isof...
AT2G34510	-2.15	-1.21	-5.87	-1.65	expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642 At2g3...
AT1G61740	10.99	1.79	10.23	1.73	expressed protein contains Pfam profile: PF01925 domain of unknown function DUF81; identic...
AT2G32240	2.19	1.29	5.84	2.06	expressed protein contains Pfam profile: PF04508 viral A-type inclusion protein repeat At2...
AT1G52320	4.06	1.24	3.74	1.23	expressed protein contains Pfam profile: PF04782 protein of unknown function (DUF632) At1g...
AT1G64990	4	1.27	2.43	1.16	expressed protein contains similarity to putative G-protein coupled receptor GI:6649579 fr...
AT4G30780	-4.41	-1.44	-3.77	-1.33	expressed protein hypothetical protein F27D4.1 - Arabidopsis thaliana,PID:g4115371 At4g307...
AT4G09620	-5.03	-1.32	-2.95	-1.17	expressed protein hypothetical protein F6E13.15 - Arabidopsis thaliana,PIR2:T00682 At4g096...
AT4G23890	-5.36	-1.33	-1.49	-1.08	expressed protein hypothetical protein, Synechocystis sp., PIR:S76577 At4g23890.1
AT5G39530	-4.01	-1.44	-2.61	-1.25	expressed protein hypothetical protein, Synechocystis sp., PIR:S77152 At5g39530.1
AT5G19120	-6.85	-1.79	-6.4	-1.74	expressed protein low similarity to extracellular dermal glycoprotein EDGP precursor Daucu...
AT5G61820	-4.1	-1.32	-2.78	-1.19	expressed protein MtN19, Medicago truncatula, EMBL:MTY15367 At5g61820.1
AT3G03870	4.14	1.26	5.34	1.37	expressed protein predicted using genefinder At3g03870.2
AT4G24220	4.02	1.36	3.73	1.33	expressed protein protein induced upon wounding - Arabidopsis thaliana, PID:e257749 At4g24...
AT3G29240	0.03	1.01	-4.43	-1.3	expressed protein similar to At1g33780 Arabidopsis thaliana; contains Pfam profile PF02622...
AT3G15000	5.16	2.08	3.72	1.71	expressed protein similar to DAG protein (required for chloroplast differentiation and pal...
AT3G27090	5.44	1.41	4.26	1.29	expressed protein similar to gda-1 Pisum sativum GI:2765418 At3g27090.1
AT1G05960	4.9	1.46	3.44	1.31	expressed protein similar to hypothetical protein GB:AAF80120 GI:8810459 from Arabidopsis ...
AT1G01430	-4.78	-1.91	-1.26	-1.18	expressed protein similar to hypothetical protein GB:CAB80917 GI:7267605 from Arabidopsis ...
AT2G03550	-7.06	-1.62	-5.24	-1.41	expressed protein similar to PrMC3 Pinus radiata GI:5487873; contains an esteraselipasethi...
AT3G12760	5.7	1.37	4.71	1.27	expressed protein similar to RP42 protein Homo sapiens GI:9896486; contains Pfam profile P...
AT1G21680	-6.49	-1.41	-3.86	-1.22	expressed protein similar to TolB protein precursor (SP:Q9ZDM5) Rickettsia prowazekii; EST...
AT5G67370	-7.28	-2.52	-3.57	-1.56	expressed protein similar to unknown protein (gb—AAC18972.1) At5g67370.1
AT5G53160	10.02	1.76	9.39	1.71	expressed protein similar to unknown protein (pir——T02893) At5g53160.1
AT5G44660	-4.06	-1.38	-3.33	-1.28	expressed protein similar to unknown protein (pir——T05327) At5g44660.1

Continued...

Locus	AcdS⁺ *t*-statistic	AcdS⁺ fold change	AcdS⁻ *t*-statistic	AcdS⁻ fold change	Description
AT5G50200	3.83	1.51	5.84	1.93	expressed protein similar to unknown protein (pir——T05562) isoform contains a non-consensu...
AT3G01310	5.42	1.47	5.9	1.54	expressed protein similar to unknown protein GB:BAA24863 Homo sapiens, unknown protein GB:...
AT4G18810	-6.16	-2.05	-2.44	-1.32	expressed protein similar to UV-B and ozone similarly regulated protein 1 UOS1 Pisum sativ...
AT5G21940	-5.32	-1.57	-3.64	-1.35	expressed protein supported by full length cDNA GI:22531282 from Arabidopsis thaliana At5g...
AT5G41620	3.97	1.25	0.91	1.05	expressed protein weak similarity to microtubule binding protein D-CLIP-190 (GI:2773363) D...
AT1G55960	-11.53	-1.87	-9.9	-1.67	expressed protein weak similarity to SP—P53808 Phosphatidylcholine transfer protein (PC-TP...
AT4G25350	-4.03	-1.31	-4.99	-1.36	EXS family protein ERD1XPR1SYG1 family protein similar to PHO1 protein Arabidopsis thalia...
AT3G63440	-2.02	-1.15	-4.91	-1.37	FAD-binding domain-containing protein cytokinin oxidase family protein similar to cytokin...
AT1G75450	4.98	1.35	3.89	1.26	FAD-binding domain-containing protein cytokinin oxidase family protein similar to GB:CAA7...
AT1G26420	-4.46	-1.47	-4.7	-1.47	FAD-binding domain-containing protein similar to SP—P30986 reticuline oxidase precursor (B...
AT2G34810	-4.24	-2.13	-0.06	-1.01	FAD-binding domain-containing protein similar to SP—P30986 reticuline oxidase precursor (B...
AT4G20830	-4.87	-1.47	-1.14	-1.09	FAD-binding domain-containing protein similar to SP—P30986 reticuline oxidase precursor (B...
AT5G44440	-4.81	-1.34	-3.19	-1.21	FAD-binding domain-containing protein similar to SP—P30986 reticuline oxidase precursor (B...
AT1G34575	-4.89	-1.43	-3.46	-1.29	FAD-binding domain-containing protein similar to SP—P30986 reticuline oxidase precursor (B...
AT4G20820	-4.88	-1.27	-3.56	-1.19	FAD-binding domain-containing protein similar to SP—P30986 reticuline oxidase precursor (B...
AT1G06360	4.04	1.4	5.78	1.55	fatty acid desaturase family protein similar to delta 9 acyl-lipid desaturase (ADS1) GI:29...
AT3G15850	-6.25	-1.88	-3.21	-1.39	fatty acid desaturase family protein similar to delta 9 acyl-lipid desaturase (ADS1) GI:29...
AT2G15090	4.04	1.71	0.41	1.05	fatty acid elongase, putative similar to fatty acid elongase 1 GI:881615 At2g15090.1
AT5G18680	4.27	1.33	3.26	1.25	F-box family protein tubby family protein similar to phosphodiesterase (GI:467578) Mus mu...
AT5G67140	2.46	1.31	5.07	1.82	F-box family protein similar to unknown protein (dbj—BAA78736.1) ; similar to SKP1 interac...
AT1G30510	-2.72	-1.13	-4.28	-1.21	ferredoxin–NADP(+) reductase, putative adrenodoxin reductase, putative strong similarity...
AT4G05390	-4.43	-1.24	-4.08	-1.22	ferredoxin–NADP(+) reductase, putative adrenodoxin reductase, putative strong similarity...
AT5G49740	-4.82	-1.41	-4.19	-1.37	ferric reductase-like transmembrane component family protein similar to ferric-chelate red...
AT5G26820	-6.6	-1.36	-4.34	-1.21	ferroportin-related low similarity to ferroportin1 Danio rerio GI:7109245 At5g26820.1
AT5G45680	-3.89	-1.35	-0.93	-1.07	FK506-binding protein 1 (FKBP13) identical to Probable FKBP-type peptidyl-prolyl cis-trans...
AT2G34460	-3.88	-1.61	-0.94	-1.12	flavin reductase-related low similarity to SP—P30043 Flavin reductase Homo sapiens At2g344...
AT1G65860	-6.6	-1.53	-6.4	-1.51	flavin-containing monooxygenase family protein FMO family protein low similarity to FMO3 ...
AT1G62560	-6.35	-1.84	-5.81	-1.74	flavin-containing monooxygenase family protein FMO family protein similar to flavin-conta...
AT5G61290	-4.99	-1.38	-4.3	-1.31	flavin-containing monooxygenase family protein FMO family protein similar to flavin-conta...
AT5G07990	-5.66	-1.41	-4.1	-1.27	flavonoid 3'-monooxygenase flavonoid 3'-hydroxylase (F3'H) cytochrome P450 75B1 (CYP75B1...
AT5G08640	-10.19	-2.04	-5.68	-1.48	flavonol synthase 1 (FLS1) identical to SP—Q96330; contains PF03171 2OG-Fe(II) oxygenase s...
AT1G60700	-5.69	-1.56	-5.78	-1.58	forkhead-associated domain-containing protein FHA domain-containing protein contains simi...
AT4G37560	-4.72	-1.23	-2.61	-1.13	formamidase, putative formamide amidohydrolase, putative similar to SP—Q50228 Formamidase...
AT1G50390	5.96	1.48	3.00	1.20	fructokinase-related similar to fructokinase GI:2102691 from Lycopersicon esculentum At1g5...
AT4G26520	5.66	1.74	8.11	2.08	fructose-bisphosphate aldolase, cytoplasmic identical to SP—P22197 Fructose-bisphosphate a...
AT2G36460	4.37	1.51	6.94	1.89	fructose-bisphosphate aldolase, putative similar to PIR—S65073 fructose-bisphosphate aldol...
AT2G01140	-10.87	-2.29	-8.41	-1.87	fructose-bisphosphate aldolase, putative similar to plastidic aldolase NPALDP1 from Nicoti...
AT5G58870	-7.56	-1.91	-4.85	-1.5	FtsH protease, putative contains similarity to cell division protein FtsH homolog 3 SP:P73...
AT3G47060	-4.52	-1.62	-3.17	-1.41	FtsH protease, putative contains similarity to FtsH protease GI:13183728 from Medicago sat...
AT5G53170	-5.62	-1.33	-3.90	-1.21	FtsH protease, putative similar to ATP-dependent metalloprotease FtsH1 GI:3600100 from Mus...
AT5G42270	-4.35	-1.4	-3.25	-1.31	FtsH protease, putative similar to FtsH protease GI:13183728 from Medicago sativa At5g4227...
AT3G62720	-6.86	-1.4	-7.73	-1.48	galactosyl transferase GMA12MNN10 family protein low similarity to alpha-1,2-galactosyltra...
AT4G36730	-6.55	-1.48	-7.06	-1.5	G-box binding factor 1 (GBF1) identical to G-box binding factor 1 SP:P42774 from Arabidops...
AT1G72030	-8.01	-1.68	-5.79	-1.44	GCN5-related N-acetyltransferase (GNAT) family protein contains Pfam profile PF00583: acet...
AT2G39000	4.68	1.41	7.02	1.67	GCN5-related N-acetyltransferase (GNAT) family protein contains Pfam profile PF00583: acet...
AT2G03980	3.42	1.26	4.57	1.38	GDSL-motif lipasehydrolase family protein similar to Anther-specific proline-rich protein ...

Continued...

Locus	AcdS⁺ *t*-statistic	AcdS⁺ fold change	AcdS⁻ *t*-statistic	AcdS⁻ fold change	Description
AT3G53100	-3.92	-1.18	-2.27	-1.11	GDSL-motif lipasehydrolase family protein similar to family II lipase EXL3 (GI:15054386), . . .
AT3G48460	5.2	1.6	2.83	1.29	GDSL-motif lipasehydrolase family protein similar to lipase Arabidopsis thaliana GI:114562. . .
AT1G53990	-5.91	-1.7	-8.13	-2.04	GDSL-motif lipasehydrolase family protein similar to myrosinase-associated proteins from B. . .
AT5G62930	4.44	1.32	1.61	1.11	GDSL-motif lipasehydrolase family protein similar to SP—P41734 Isoamyl acetate-hydrolyzing. . .
AT1G17050	-7.25	-1.72	-4.91	-1.45	geranyl diphosphate synthase, putative GPPS, putative dimethylallyltransferase, putative. . .
AT5G20630	4.6	1.4	3.45	1.29	germin-like protein (GER3) identical to germin-like protein subfamily 3 member 3 SP—P94072. . .
AT5G07200	5.01	1.38	4.72	1.35	gibberellin 20-oxidase identical to GI:1109699 At5g07200.1
AT1G66350	5.28	1.43	4.08	1.29	gibberellin regulatory protein (RGL1) similar to GB:CAA75492 from Arabidopsis thaliana; co. . .
AT1G22690	-1.34	-1.22	4.26	1.76	gibberellin-responsive protein, putative similar to SP—P46688 Gibberellin-regulated protei. . .
AT1G22770	3.89	1.28	4.34	1.3	gigantea protein (GI) identical to gigantea protein SP:Q9SQI2 from Arabidopsis thaliana At. . .
AT3G29320	1.11	1.06	4.88	1.29	glucan phosphorylase, putative similar to alpha-glucan phosphorylase, L isozyme 1 precurso. . .
AT5G48300	3.95	1.46	1.93	1.21	glucose-1-phosphate adenylyltransferase small subunit 1 (APS1) ADP-glucose pyrophosphoryl. . .
AT1G24280	-4.97	-1.41	-4.13	-1.32	glucose-6-phosphate 1-dehydrogenase, putative G6PD, putative strong similarity to SP—Q438. . .
AT5G42740	-5.2	-1.32	-2.05	-1.11	glucose-6-phosphate isomerase, cytosolic (PGIC) identical to SP—P34795 Glucose-6-phosphate. . .
AT1G61800	-6.31	-1.51	-5.71	-1.44	glucose-6-phosphatephosphate translocator, putative similar to glucose-6-phosphatephosphat. . .
AT3G56060	-4.92	-1.37	-1.87	-1.12	glucose-methanol-choline (GMC) oxidoreductase family protein similar to mandelonitrile lya. . .
AT4G16590	-10.63	-6.21	-6.09	-2.77	glucosyltransferase-related low similarity to beta-(1-3)-glucosyl transferase Bradyrhizobi. . .
AT1G65960	14.33	3.49	11.82	2.72	glutamate decarboxylase 2 (GAD 2) similar to glutamate decarboxylase (gad) GI:294111 from . . .
AT5G07440	3.78	1.30	6.78	1.62	glutamate dehydrogenase 2 (GDH2) identical to glutamate dehydrogenase 2 (GDH 2) Arabidopsi. . .
AT5G04140	-6.34	-1.45	-4.4	-1.3	glutamate synthase (GLU1) ferredoxin-dependent glutamate synthase (Fd-GOGAT 1) identical . . .
AT4G30550	-7.16	-1.77	-2.86	-1.24	glutamine amidotransferase class-I domain-containing protein similar to defense-related pr. . .
AT4G25720	2.86	1.20	4.51	1.33	glutamine cyclotransferase family protein contains Pfam profile: PF05096 glutamine cyclotr. . .
AT5G16570	-8.36	-1.91	-4.32	-1.4	glutamine synthetase, putative similar to glutamine synthetase, cytosolic isozyme (glutama. . .
AT5G37600	-4.02	-2.31	-1.89	-1.50	glutamine synthetase, putative similar to glutamine synthetase, cytosolic isozyme (Glutama. . .
AT1G66200	-4.43	-2.22	-2.75	-1.68	glutamine synthetase, putative similar to glutamine synthetase, cytosolic isozyme (Glutama. . .
AT1G58290	-7.68	-1.65	-5.43	-1.42	glutamyl-tRNA reductase 1 GluTR (HEMA1) identical to glutamyl-tRNA reductase 1, chloropla. . .
AT2G31250	-6.46	-1.58	-3.61	-1.30	glutamyl-tRNA reductase, putative similar to HEMA2 SP—P49294, HEMA1 SP—P42804 At2g31250.1
AT1G64500	-5.32	-1.34	-4.95	-1.32	glutaredoxin family protein At1g64500.1
AT5G13810	-2.69	-1.12	-4.72	-1.23	glutaredoxin family protein At5g13810.1
AT2G34660	-11.35	-1.68	-9.89	-1.57	glutathione S-conjugate ABC transporter (MRP2) almost identical to MgATP-energized glutath. . .
AT2G02930	-4.49	-1.43	-5.89	-1.59	glutathione S-transferase, putative At2g02930.1
AT4G02520	-9.7	-1.96	-12.54	-2.31	glutathione S-transferase, putative At4g02520.1
AT5G17220	-16.59	-3.35	-14.71	-2.81	glutathione S-transferase, putative At5g17220.1
AT1G10370	-4.85	-2.14	-2.94	-1.61	glutathione S-transferase, putative (ERD9) similar to glutathione S-transferase TSI-1 Aegi. . .
AT1G02920	-7.09	-2.26	-7.26	-2.23	glutathione S-transferase, putative similar to glutathione S-transferase GI:860955 from Hy. . .
AT1G02930	-6.78	-1.76	-6.28	-1.64	glutathione S-transferase, putative similar to glutathione S-transferase GI:860955 from Hy. . .
AT1G69920	4.18	1.29	6.82	1.51	glutathione S-transferase, putative similar to glutathione transferase GB:CAA09188 Alopecu. . .
AT1G16300	5.54	1.39	3.36	1.22	glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative NAD-dependent glyceraldehyd. . .
AT1G79530	5.5	1.46	3.80	1.31	glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative NAD-dependent glyceraldehyd. . .
AT5G41080	-3.23	-1.49	-4.58	-1.69	glycerophosphoryl diester phosphodiesterase family protein weak similarity to SP—P37965 Gl. . .
AT1G36370	-5.03	-1.41	-5.26	-1.4	glycine hydroxymethyltransferase, putative serine hydroxymethyltransferase, putative ser. . .
AT5G61660	5.55	1.74	5.45	1.66	glycine-rich protein At5g61660.1
AT4G13850	4.99	1.7	2.38	1.27	glycine-rich RNA-binding protein (GRP2) glycine-rich RNA binding protein 2 AtGRP2 Arabidop. . .
AT2G21660	3.97	1.73	1.64	1.23	glycine-rich RNA-binding protein (GRP7) SP—Q03250 Glycine-rich RNA-binding protein 7 Arabi. . .
AT3G01180	-4.41	-1.39	-1.50	-1.12	glycogen synthase, putative similar to glycogen synthase Q43847 from Solanum tuberosum At3. . .
AT4G23820	5.36	1.76	2.63	1.31	glycoside hydrolase family 28 protein polygalacturonase (pectinase) family protein weak s. . .

Continued. . .

Locus	AcdS⁺ *t*-statistic	AcdS⁺ fold change	AcdS⁻ *t*-statistic	AcdS⁻ fold change	Description
AT5G26570	7.66	1.63	6.72	1.5	glycoside hydrolase starch-binding domain-containing protein similar to SEX1 (starch exces. . .
AT3G18070	4.26	1.81	1.17	1.18	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 do. . .
AT3G18080	4.24	2.05	1.29	1.25	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 do. . .
AT3G06510	-4.27	-1.29	-2.97	-1.19	glycosyl hydrolase family 1 protein similar to Beta-galactosidase (SP:P22498) Sulfolobus s. . .
AT3G57260	-3.47	-1.53	-4.3	-1.65	glycosyl hydrolase family 17 protein similar to glucan endo-1,3-beta-glucosidase, acidic i. . .
AT1G02640	0.69	1.09	4.22	1.64	glycosyl hydrolase family 3 protein similar to beta-xylosidase GB:Z84377 GI:2102655 from A. . .
AT4G13410	-14.84	-3.1	-11	-2.26	glycosyl transferase family 2 protein similar to beta-(1-3)-glucosyl transferase GB:AAC622. . .
AT5G03760	-3.48	-1.27	-6.33	-1.47	glycosyl transferase family 2 protein similar to beta-(1-3)-glucosyl transferase GB:AAC622. . .
AT2G24630	-1.61	-1.10	-4.97	-1.3	glycosyl transferase family 2 protein similar to cellulose synthase from Agrobacterium tum. . .
AT2G18700	-9.01	-1.89	-11.97	-2.36	glycosyl transferase family 20 protein trehalose-phosphatase family protein contains Pfam. . .
AT1G60140	-4.03	-1.33	-2.59	-1.18	glycosyl transferase family 20 protein trehalose-phosphatase family protein similar to tr. . .
AT1G70090	-2.03	-1.15	-4.13	-1.33	glycosyl transferase family 8 protein contains Pfam profile: PF01501 glycosyl transferase . . .
AT2G20810	4.2	1.28	1.69	1.11	glycosyl transferase family 8 protein contains Pfam profile: PF01501 glycosyl transferase . . .
AT3G62660	4.68	1.38	3.76	1.29	glycosyl transferase family 8 protein low similarity to glycosyl transferase lgtC - Neisse. . .
AT5G54060	-8.73	-1.89	-8.23	-1.8	glycosyltransferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP. . .
AT2G22930	-6.47	-1.42	-4.09	-1.24	glycosyltransferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and UDP. . .
AT3G07270	-5.51	-1.29	-4.16	-1.21	GTP cyclohydrolase I identical to GTP cyclohydrolase I GI:19909132 from Arabidopsis thalia. . .
AT2G27200	1.82	1.10	4.89	1.28	GTP-binding family protein contains Pfam domain, PF01926: GTPase of unknown function At2g2. . .
AT1G56050	-4.2	-1.29	-3.11	-1.19	GTP-binding protein-related similar to GTP-binding protein GI:10176676 from Bacillus halod. . .
AT5G02230	-7.55	-2.38	-6.77	-2.11	haloacid dehalogenase-like hydrolase family protein contains InterPro accession IPR005834:. . .
AT2G32150	-5.24	-1.46	-2.14	-1.17	haloacid dehalogenase-like hydrolase family protein contains InterPro accession IPR005834:. . .
AT5G59480	-4.42	-1.48	-3.62	-1.34	haloacid dehalogenase-like hydrolase family protein low similarity to SP—P53078 SSM1 prote. . .
AT1G59820	-4.02	-1.27	-3.49	-1.24	haloacid dehalogenase-like hydrolase family protein similar to Potential phospholipid-tran. . .
AT4G01410	-4.65	-1.29	-4.69	-1.28	harpin-induced family protein HIN1 family protein harpin-responsive family protein simil. . .
AT5G02500	-3.67	-1.47	-4.72	-1.7	heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1) identical to SP—P22953 Heat shock . . .
AT1G56410	-6.6	-2.62	-5.81	-2.34	heat shock cognate 70 kDa protein, putative HSC70, putative HSP70, putative strong simil. . .
AT1G67970	8.8	1.65	7.36	1.5	heat shock factor protein, putative (HSF5) heat shock transcription factor, putative (HST. . .
AT1G74310	-4.61	-1.78	-1.62	-1.22	heat shock protein 101 (HSP101) identical to heat shock protein 101 GI:6715468 GB:AAF26423. . .
AT5G03720	4.4	1.47	3.45	1.34	heat shock transcription factor family protein contains Pfam profile: PF00447 HSF-type DNA. . .
AT1G49420	5.06	1.32	3.22	1.18	heavy-metal-associated domain-containing protein contains Pfam profile PF00403: Heavy-met. . .
AT3G05220	4.46	1.39	5.86	1.54	heavy-metal-associated domain-containing protein similar to farnesylated protein 1 (GI:233. . .
AT5G16150	5.98	1.88	4.01	1.50	hexose transporter, putative strong similarity to hexose transporter Arabidopsis thaliana . . .
AT5G26040	6.43	1.37	5.78	1.31	histone deacetylase family protein (HDA2) identical to HDA2 Arabidopsis thaliana GI:211057. . .
AT4G40060	4.94	1.35	3.20	1.22	homeobox-leucine zipper protein 16 (HB-16) HD-ZIP transcription factor 16 identical to ho. . .
AT5G47370	4.9	1.32	0.82	1.05	homeobox-leucine zipper protein 2 (HAT2) HD-ZIP protein 2 identical to homeobox-leucine z. . .
AT5G65310	6.2	1.5	5.32	1.39	homeobox-leucine zipper protein 5 (HB-5) HD-ZIP transcription factor 5 identical to homeo. . .
AT2G22430	4.93	1.42	5.06	1.45	homeobox-leucine zipper protein 6 (HB-6) HD-ZIP transcription factor 6 identical to homeo. . .
AT4G34610	-9.07	-1.61	-8.26	-1.53	homeodomain-containing protein similaritry to homeotic protein BEL1, Arabidopsis thaliana,. . .
AT5G11650	-4.67	-1.37	-1.39	-1.10	hydrolase, alphabeta fold family protein contains Pfam profile PF00561: hydrolase, alphabe. . .
AT4G10030	3.85	1.39	2.08	1.21	hydrolase, alphabeta fold family protein contains Pfam profile PF00561: hydrolase, alphabe. . .
AT3G10840	-3.64	-1.37	-4.59	-1.43	hydrolase, alphabeta fold family protein low similarity to 3-oxoadipate enol-lactone hydro. . .
AT3G24420	6.02	1.47	4.63	1.34	hydrolase, alphabeta fold family protein low similarity to haloalkane dehalogenase from My. . .
AT5G19850	-4.22	-1.99	-1.25	-1.22	hydrolase, alphabeta fold family protein low similarity to hydrolase Terrabacter sp. DBF63. . .
AT4G12830	-3.94	-1.26	-1.96	-1.11	hydrolase, alphabeta fold family protein low similarity to hydrolase Terrabacter sp. DBF63. . .
AT4G30650	7.11	2.52	8.52	3.11	hydrophobic protein, putative low temperature and salt responsive protein, putative simil. . .
AT1G21090	1.30	1.11	4.14	1.36	hydroxyproline-rich glycoprotein family protein At1g21090.1

Continued. . .

Locus	AcdS⁺ *t*-statistic	AcdS⁺ fold change	AcdS⁻ *t*-statistic	AcdS⁻ fold change	Description
AT4G01050	-3.97	-1.25	-3.19	-1.20	hydroxyproline-rich glycoprotein family protein At4g01050.1
AT4G25620	-5.46	-1.35	-6.3	-1.42	hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains, IN. . .
AT1G05290	8.99	1.61	6.59	1.41	hypothetical protein At1g05290.1
AT5G28940	-5.03	-1.29	-4.55	-1.26	hypothetical protein At5g28940.1
AT2G29650	-6.7	-2.22	-3.59	-1.53	inorganic phosphate transporter, putative similar to brain specific Na+-dependent inorgani. . .
AT2G18230	-6.39	-1.9	-5.54	-1.68	inorganic pyrophosphatase soluble (PPA) pyrophosphate phospho-hydrolase PPase nearly ide. . .
AT4G39800	-12.16	-4.23	-10.17	-3.27	inositol-3-phosphate synthase isozyme 1 myo-inositol-1-phosphate synthase 1 MI-1-P synth. . .
AT2G22240	-13.11	-3.11	-10.91	-2.56	inositol-3-phosphate synthase isozyme 2 myo-inositol-1-phosphate synthase 2 MI-1-P synth. . .
AT5G62720	3.99	1.54	5.49	1.86	integral membrane HPP family protein contains Pfam domain, PF04982: HPP family At5g62720.1
AT2G36330	5.03	1.33	4.37	1.28	integral membrane protein, putative contains 4 transmembrane domains; contains Pfam PF0453. . .
AT1G62763	3.13	1.31	4.25	1.49	invertasepectin methylesterase inhibitor family protein low similarity to extensin Volvox . . .
AT4G25260	3.95	2.08	1.06	1.22	invertasepectin methylesterase inhibitor family protein low similarity to pectinesterase f. . .
AT5G62360	6.44	1.64	5.72	1.55	invertasepectin methylesterase inhibitor family protein similar to pectinesterase from Ara. . .
AT2G27190	-4.23	-1.33	-1.57	-1.10	iron(III)-zinc(II) purple acid phosphatase (PAP12) identical to iron(III)-zinc(II) purple . . .
AT4G35260	5.56	1.33	3.40	1.18	isocitrate dehydrogenase subunit 1 NAD+ isocitrate dehydrogenase subunit 1 nearly identic. . .
AT2G17130	6.4	1.33	4.63	1.22	isocitrate dehydrogenase subunit 2 NAD+ isocitrate dehydrogenase subunit 2 nearly identic. . .
AT5G03290	5.14	1.33	4.88	1.29	isocitrate dehydrogenase, putative NAD+ isocitrate dehydrogenase, putative strong similar. . .
AT1G19720	-5	-1.29	-4.07	-1.23	jacalin lectin family protein similar to agglutinin Castanea crenata GI:25528883; contains. . .
AT1G54040	8.64	1.65	8.14	1.58	kelch repeat-containing protein contains Pfam PF01344: Kelch motif (4 repeats); similar to. . .
AT1G18270	2.01	1.11	5.34	1.29	ketose-bisphosphate aldolase class-II family protein low similarity to KbaY (tagatose-1,6-. . .
AT5G46190	4.7	1.35	3.96	1.27	KH domain-containing protein strong similarity to unknown protein (pir——T04533) At5g46190.. . .
AT3G27960	-4.35	-1.38	-6.19	-1.57	kinesin light chain-related low similarity to kinesin light chain Plectonema boryanum GI:2. . .
AT5G10470	-5.46	-1.58	-4.4	-1.4	kinesin motor protein-related TH65 protein, Arabidopsis thaliana, EMBL:AJ001729; contains . . .
AT1G08630	-7.09	-1.47	-4.52	-1.27	L-allo-threonine aldolase-related similar to L-allo-threonine aldolase (EC 4.1.2.-) (L-all. . .
AT5G21100	-9.33	-1.74	-6.36	-1.46	L-ascorbate oxidase, putative similar to L-ascorbate oxidase Precursor SP:Q40588 from Nico. . .
AT1G02820	-4.06	-1.46	-2.11	-1.21	late embryogenesis abundant 3 family protein LEA3 family protein similar to late embryoge. . .
AT2G46140	3.51	1.45	5.67	1.89	late embryogenesis abundant protein, putative LEA protein, putative similar to SP—P46518 . . .
AT3G54430	6.34	1.49	4.27	1.31	lateral root primordium (LRP) protein-related similar to lateral root primordium 1 (LRP1) . . .
AT5G16000	4.71	1.54	2.37	1.24	leucine-rich repeat family protein protein kinase family protein contains Pfam domains PF. . .
AT1G80080	-2.16	-1.14	-4.09	-1.3	leucine-rich repeat family protein contains leucine rich-repeat domains Pfam:PF00560, INTE. . .
AT1G33670	2.24	1.20	4.48	1.4	leucine-rich repeat family protein contains leucine rich-repeat domains Pfam:PF00560, INTE. . .
AT1G49750	4.76	1.65	4.66	1.68	leucine-rich repeat family protein contains leucine-rich repeats, Pfam:PF00560 At1g49750.1
AT4G35470	-3.12	-1.26	-5.2	-1.43	leucine-rich repeat family protein similar to Leucine-rich repeat protein SHOC-2 (Ras-bind. . .
AT1G51805	-5.44	-1.34	-4.27	-1.26	leucine-rich repeat protein kinase, putative similar to light repressible receptor protein. . .
AT5G06820	1.86	1.20	5.48	1.64	leucine-rich repeat transmembrane protein kinase, putative At5g06820.1
AT5G65710	4.03	1.25	3.77	1.25	leucine-rich repeat transmembrane protein kinase, putative At5g65710.1
AT5G45800	4.21	1.29	3.89	1.26	leucine-rich repeat transmembrane protein kinase, putative At5g45800.1
AT4G22870	-15.54	-2.88	-13.59	-2.47	leucoanthocyanidin dioxygenase, putative anthocyanidin synthase, putative similar to SP—P. . .
AT4G22880	-6.39	-1.79	-6.73	-1.92	leucoanthocyanidin dioxygenase, putative anthocyanidin synthase, putative similar to SP—P. . .
AT3G05790	2.81	1.44	4.64	1.75	Lon protease, putative similar to Lon protease homolog 2 SP:P93655 At3g05790.1
AT2G47240	6.83	1.56	5.31	1.41	long-chain-fatty-acid–CoA ligase family protein long-chain acyl-CoA synthetase family pr. . .
AT1G64400	6.14	1.4	7.08	1.48	long-chain-fatty-acid–CoA ligase, putative long-chain acyl-CoA synthetase, putative simi. . .
AT5G57030	-3.86	-1.36	-2.38	-1.19	lycopene epsilon cyclase identical to lycopene epsilon cyclase GI:1399181 At5g57030.1
AT5G06300	-1.44	-1.08	-5.16	-1.28	lysine decarboxylase family protein contains Pfam profile PF03641: lysine decarboxylase fa. . .
AT3G51660	6.64	1.79	5.86	1.65	macrophage migration inhibitory factor family protein MIF family protein contains Pfam pr. . .
AT4G18480	-4.76	-1.42	-1.08	-1.08	magnesium-chelatase subunit chlI, chloroplast Mg-protoporphyrin IX chelatase (CHLI) (CS) . . .

Continued. . .

Locus	AcdS^{+} *t*-statistic	AcdS^{+} fold change	AcdS^{-} *t*-statistic	AcdS^{-} fold change	Description
AT1G80760	-6.87	-1.48	-4.08	-1.25	major intrinsic family protein MIP family protein contains Pfam profile: MIP PF00230 At1g. . .
AT3G04090	6.66	1.5	7.73	1.58	major intrinsic family protein MIP family protein contains Pfam profile: MIP PF00230 At1g. . .
AT1G52180	4.8	1.59	2.25	1.22	major intrinsic family protein MIP family protein contains Pfam profile: MIP PF00230 At3g. . .
AT4G23680	-7.92	-1.92	-5.99	-1.6	major latex protein-related MLP-related low similarity to major latex protein Papaver som. . .
AT4G23670	-4.53	-1.4	-1.81	-1.13	major latex protein-related MLP-related low similarity to major latex protein Papaver som. . .
AT3G26460	-4.51	-1.62	-2.36	-1.28	major latex protein-related MLP-related low similarity to major latex protein Papaver som. . .
AT1G14950	-4.62	-2.42	-2.87	-1.71	major latex protein-related MLP-related low similarity to major latex protein Papaver som. . .
AT1G79750	4.67	1.34	1.89	1.12	malate oxidoreductase, putative similar to malate oxidoreductase (NADP-dependent malic enz. . .
AT5G25880	8.51	1.63	9.47	1.7	malate oxidoreductase, putative similar to NADP-dependent malic enzyme (EC 1.1.1.40) (NADP. . .
AT5G11670	9.19	1.94	10.6	2.15	malate oxidoreductase, putative similar to NADP-dependent malic enzyme (EC 1.1.1.40) (NADP. . .
AT1G04770	-4.93	-1.47	-5.61	-1.52	male sterility MS5 family protein similar to male sterility MS5 Arabidopsis thaliana GI:38. . .
AT5G48850	-5.23	-1.34	-5.51	-1.35	male sterility MS5 family protein similar to male sterility MS5 Arabidopsis thaliana GI:38. . .
AT4G37980	-4.94	-1.57	-1.64	-1.16	mannitol dehydrogenase, putative (ELI3-1) identical to GI:16267 At4g37980.1
AT4G37990	-3.91	-1.65	-1.65	-1.23	mannitol dehydrogenase, putative (ELI3-2) identical to GI:16269 At4g37990.1
AT1G76150	4.05	1.39	2.09	1.20	maoC-like dehydratase domain-containing protein contains similarity to Swiss-Prot:P51659 e. . .
AT5G17700	-9.26	-2	-4.33	-1.37	MATE efflux family protein similar to ripening regulated protein DDTFR18 Lycopersicon escu. . .
AT3G21690	-5.26	-1.37	-2.66	-1.17	MATE efflux family protein similar to ripening regulated protein DDTFR18 Lycopersicon escu. . .
AT3G16000	-4.04	-1.22	-1.99	-1.10	matrix-localized MAR DNA-binding protein-related similar to matrix-localized MAR DNA bindi. . .
AT1G05140	-4.28	-1.22	-2.48	-1.13	membrane-associated zinc metalloprotease, putative similar to Hypothetical zinc metallopro. . .
AT3G20370	-5.39	-1.89	-2.02	-1.26	meprin and TRAF homology domain-containing protein MATH domain-containing protein similar. . .
AT1G60960	3.42	1.21	5.09	1.31	metal transporter, putative (IRT3) identical to putative metal transporter IRT3 Arabidopsi. . .
AT1G05300	1.61	1.12	5.04	1.4	metal transporter, putative (ZIP5) identical to putative metal transporter ZIP5 Arabidopsi. . .
AT5G63430	7.61	1.76	4.95	1.44	metallo-beta-lactamase family protein At5g63420.1
AT3G25740	5.44	1.37	4.06	1.27	metallopeptidase M24 family protein similar to SP—O33343 Methionine aminopeptidase (EC 3.4. . .
AT1G13270	3.99	1.34	3.22	1.26	metallopeptidase M24 family protein similar to SP—Q01662 Methionine aminopeptidase 1 precu. . .
AT4G29950	-5.52	-1.37	-6.16	-1.4	microtubule-associated protein identical to microtubule-associated protein GI:5032258 from. . .
AT5G46800	-9.79	-2.77	-6.86	-2.02	mitochondrial carnitineacyl carrier, putative a bout de souffle (BOU) CAC-like protein i. . .
AT5G55510	4.82	1.82	4.19	1.72	mitochondrial import inner membrane translocase subunit Tim17Tim22Tim23 family protein con. . .
AT4G26670	6.55	1.89	5.6	1.73	mitochondrial import inner membrane translocase subunit Tim17Tim22Tim23 family protein wea. . .
AT2G28900	12.57	2.21	15.09	2.59	mitochondrial import inner membrane translocase subunit Tim17Tim22Tim23 family protein wea. . .
AT5G26200	-5.55	-1.39	-5.06	-1.35	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondria. . .
AT3G14720	1.32	1.06	4.56	1.29	mitogen-activated protein kinase, putative MAPK, putative (MPK14) mitogen-activated prote. . .
AT4G36450	4.93	1.28	2.26	1.11	mitogen-activated protein kinase, putative MAPK, putative (MPK19) identical to mitogen-ac. . .
AT2G18170	6.44	1.51	3.90	1.28	mitogen-activated protein kinase, putative MAPK, putative (MPK7) identical to mitogen-act. . .
AT1G63680	4.22	1.28	2.04	1.12	Mur ligase family protein contains Pfam profile: PF01225 Mur ligase family, catalytic doma. . .
AT1G73540	-4.3	-1.24	-5.64	-1.32	MutTnudix family protein low similarity to SP—Q09790 Diadenosine 5’,5”’-P1,P6-hexaphospha. . .
AT5G47240	2.24	1.39	6.17	2.44	MutTnudix family protein similar to SP—P53370 Nucleoside diphosphate-linked moiety X motif. . .
AT1G18300	-9.42	-1.57	-9.69	-1.57	MutTnudix family protein similar to SP—Q09790 Diadenosine 5’,5”’-P1,P6-hexaphosphate hydr. . .
AT1G68670	-3.71	-1.53	-4.8	-1.71	myb family transcription factor contains Pfam domain, PF00249: Myb-like DNA-binding domain. . .
AT1G18330	-7.93	-1.79	-8.62	-1.9	myb family transcription factor contains PFAM profile: PF00249 myb-like DNA binding domain. . .
AT1G01060	-7.33	-1.83	-6.27	-1.65	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain. . .
AT3G09600	-7.51	-2.13	-5.64	-1.76	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain. . .
AT5G02840	-6.18	-1.61	-4.2	-1.35	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain. . .
AT5G18240	2.09	1.18	4.73	1.44	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain. . .
AT3G46640	6	1.59	7.18	1.72	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain. . .
AT1G48000	-4.32	-1.56	-2.00	-1.23	myb family transcription factor similar to myb-related transcription factor (cpm10) GB:U33. . .

Continued. . .

Locus	AcdS$^+$ *t*-statistic	AcdS$^+$ fold change	AcdS$^-$ *t*-statistic	AcdS$^-$ fold change	Description
AT2G46830	-12.29	-2.89	-9.7	-2.24	myb-related transcription factor (CCA1) identical to myb-related transcription factor (CCA. . .
AT2G20290	4.61	1.38	3.02	1.25	myosin, putative similar to myosin (GI:499047) Arabidopsis thaliana At2g20290.1
AT2G28760	4.19	1.33	4.11	1.32	NAD-dependent epimerasedehydratase family protein similar to UDP-glucuronic acid decarboxy. . .
AT2G24270	-9.29	-2.4	-7.02	-1.91	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase, putative similar to NADP-dependen. . .
AT4G30210	-5.9	-1.58	-3.51	-1.30	NADPH-cytochrome p450 reductase, putative NADPH-ferrihemoprotein reductase, putative simi. . .
AT1G60550	-8.61	-1.53	-6.62	-1.37	naphthoate synthase, putative dihydroxynaphthoic acid synthetase, putative DHNA syntheta. . .
AT3G51240	-12.47	-2.33	-10.35	-1.97	naringenin 3-dioxygenase flavanone 3-hydroxylase (F3H) identical to GI:3790548 At3g51240.. . .
AT5G11790	-4.47	-1.44	-2.12	-1.18	Ndr family protein similar to SP—O23969 Pollen specific protein SF21 Helianthus annuus; co. . .
AT1G09240	1.75	1.20	5.02	1.73	nicotianamine synthase, putative similar to nicotianamine synthase Lycopersicon esculentum. . .
AT1G77760	-5.35	-1.51	-2.08	-1.17	nitrate reductase 1 (NR1) identical to SP—P11832 Nitrate reductase 1 (formerly EC 1.6.6.1). . .
AT1G12110	5.15	1.39	3.77	1.24	nitratechlorate transporter (NRT1.1) (CHL1) identical to nitratechlorate transporter SP:Q0. . .
AT5G22300	-4.6	-1.65	-0.53	-1.06	nitrilase 4 (NIT4) identical to SP—P46011 Nitrilase 4 (EC 3.5.5.1) Arabidopsis thaliana At. . .
AT4G27410	-8.12	-1.57	-6.46	-1.45	no apical meristem (NAM) family protein (RD26) contains Pfam PF02365: No apical meristem (. . .
AT3G49530	-4.42	-1.28	-5.1	-1.3	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) do. . .
AT2G17040	-1.37	-1.07	-4.26	-1.23	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) do. . .
AT5G63790	-4.96	-1.37	-3.92	-1.28	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) do. . .
AT2G16660	-0.17	-1.02	4.82	1.41	nodulin family protein similar to nodulin-like protein Arabidopsis thaliana GI:3329368, no. . .
AT4G34950	14.37	2.21	18.07	2.64	nodulin family protein similar to nodulin-like protein Arabidopsis thaliana GI:3329368, no. . .
AT1G70260	-11.89	-3.45	-9.24	-2.58	nodulin MtN21 family protein contains similarity to MtN21 Medicago truncatula GI:2598575; . . .
AT3G14770	-4.54	-1.5	-3.08	-1.30	nodulin MtN3 family protein similar to MtN3 GI:1619602 (root nodule development) from Medi. . .
AT4G15540	3.88	1.27	2.76	1.18	nodulin-related low similarity to MtN21 Medicago truncatula GI:2598575 At4g15540.1
AT2G23150	-3.08	-1.18	-4.25	-1.26	NRAMP metal ion transporter 3 (NRAMP3) identical to metal transporter Nramp3 Arabidopsis t. . .
AT5G53400	3.96	1.31	1.49	1.11	nuclear movement family protein contains Pfam profile: PF03593 nuclear movement protein At. . .
AT2G19480	5.31	1.4	1.33	1.09	nucleosome assembly protein (NAP), putative similar to nucleosome assembly protein 1 Glyci. . .
AT5G63310	-3.92	-1.22	-2.17	-1.12	nucleotide diphosphate kinase II, chloroplast (NDPK2) identical to SP—O64903 Nucleoside di. . .
AT5G62290	4.52	1.38	0.70	1.05	nucleotide-sensitive chloride conductance regulator (ICln) family protein contains PF03517. . .
AT4G24000	-5.6	-1.64	-3.85	-1.40	O22989 (O22989) Cellulose synthase isolog, partial (58
AT3G06550	-5.52	-2.61	-3.09	-1.73	O-acetyltransferase-related similar to O-acetyltransferase (GI:17063556) Cryptococcus neof. . .
AT1G07130	-5.44	-1.42	-2.43	-1.16	OB-fold nucleic acid binding domain-containing protein contains InterPro entry IPR004365: . . .
AT1G65730	5.01	1.41	1.96	1.15	oligopeptide transporter OPT family protein similar to iron-phytosiderophore transporter p. . .
AT4G26590	-9.61	-1.72	-6.34	-1.43	oligopeptide transporter OPT family protein similar to SP—P40900 Sexual differentiation pr. . .
AT5G55930	-9.03	-1.61	-6.16	-1.37	oligopeptide transporter OPT family protein similar to SP—P40900 Sexual differentiation pr. . .
AT3G11170	-4.83	-1.53	-1.40	-1.13	omega-3 fatty acid desaturase, chloroplast (FAD7) (FADD) identical to omega-3 fatty acid d. . .
AT5G05580	-11.99	-2.69	-8.12	-1.92	omega-3 fatty acid desaturase, chloroplast, temperature-sensitive (FAD8) identical to SP:4. . .
AT4G30950	-4.7	-1.34	-2.31	-1.15	omega-6 fatty acid desaturase, chloroplast (FAD6) (FADC) identical to GI:493068 At4g30950.. . .
AT4G09670	-6.7	-1.48	-3.41	-1.22	oxidoreductase family protein similar to AX110P Daucus carota GI:285739; contains Pfam pro. . .
AT1G66130	-4.37	-1.26	-2.73	-1.15	oxidoreductase N-terminal domain-containing protein similar to AX110P Daucus carota GI:285. . .
AT5G05600	-0.21	-1.03	4.54	2.11	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to flavonol synthase Citrus un. . .
AT3G11180	1.21	1.21	5.86	2.52	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to leucoanthocyanidin dioxygen. . .
AT3G06300	4	1.3	1.93	1.13	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to prolyl 4-hydroxylase, alpha. . .
AT5G12270	-6.04	-1.35	-3.85	-1.21	oxidoreductase, 2OG-Fe(II) oxygenase family protein similarity to ripening protein E8, tom. . .
AT1G23740	-5	-1.59	-0.77	-1.07	oxidoreductase, zinc-binding dehydrogenase family protein contains Pfam profile PF00107: o. . .
AT4G13010	-6.71	-1.42	-5.05	-1.3	oxidoreductase, zinc-binding dehydrogenase family protein low similarity to probable NADP-. . .
AT3G56460	6.82	1.67	6.8	1.68	oxidoreductase, zinc-binding dehydrogenase family protein low similarity to probable NADP-. . .
AT5G37960	-4.86	-1.43	-4.04	-1.33	oxidoreductase-related At5g37960.1
AT5G64280	-3.89	-1.27	-0.97	-1.06	oxoglutaratemalate translocator, putative similar to SWISS-PROT:Q41364 2-oxoglutaratemalat. . .

Continued. . .

Locus	AcdS⁺ *t*-statistic	AcdS⁺ fold change	AcdS⁻ *t*-statistic	AcdS⁻ fold change	Description
AT1G14150	-4.13	-1.47	-0.74	-1.07	oxygen evolving enhancer 3 (PsbQ) family protein extrinsic pII protein; contains Pfam prof...
AT5G59420	5.18	1.41	2.51	1.18	oxysterol-binding family protein similar to SP—P16258 Oxysterol-binding protein 1 Oryctola...
AT1G70030	4.55	3.42	2.79	1.98	paired amphipathic helix repeat-containing protein similar to Sin3 protein Yarrowia lipoly...
AT2G17340	-3.86	-1.2	-3.88	-1.19	pantothenate kinase-related contains Pfam domain, PF01937: Protein of unknown function; su...
AT2G14610	-11.62	-4.42	-15.79	-6.82	pathogenesis-related protein 1 (PR-1) identical to GB:M90508 SP—P33154 At2g14610.1
AT3G19690	-2.29	-1.16	-4.53	-1.34	pathogenesis-related protein, putative similar to PR-1a protein GI:19944 GB:X06930 from Ni...
AT2G14580	-9.62	-4.19	-13.76	-7.1	pathogenesis-related protein, putative similar to SP—P33154 Pathogenesis-related protein 1...
AT3G01420	-7.69	-1.63	-4.77	-1.34	pathogen-responsive alpha-dioxygenase, putative similar to pathogen-inducible alpha-dioxyg...
AT3G09540	6.3	1.56	5.06	1.44	pectate lyase family protein simliar to style development-specific protein 9612 SP:P24396 ...
AT3G54920	6.9	2.21	4.44	1.66	pectate lyase, putative powdery mildew susceptibility protein (PMR6) identical to powdery...
AT4G19420	-6.19	-1.72	-2.71	-1.26	pectinacetylesterase family protein contains Pfam profile: PF03283 pectinacetylesterase At...
AT2G46930	4.37	1.43	3.81	1.39	pectinacetylesterase, putative similar to pectinacetylesterase precursor GI:1431629 from V...
AT3G49220	-1.91	-1.21	-6.24	-1.78	pectinesterase family protein contains Pfam profile: PF01095 pectinesterase At3g49220.1
AT5G19730	-4.75	-1.38	-2.14	-1.15	pectinesterase family protein contains Pfam profile: PF01095 pectinesterase At5g19730.1
AT1G53830	7.73	1.5	5.13	1.3	pectinesterase family protein identical to pectinesterase 2 (PME2 PE 2) SP:Q42534 from Ara...
AT5G02830	-8.29	-1.43	-7.25	-1.36	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repea...
AT4G31850	4.81	1.26	4.12	1.22	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repea...
AT2G37230	3.91	1.26	1.14	1.07	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repea...
AT5G15980	4.62	1.34	1.30	1.09	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repea...
AT1G31920	-3.85	-1.27	-3.23	-1.21	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repea...
AT1G02370	5.35	1.28	3.56	1.17	pentatricopeptide (PPR) repeat-containing protein low similarity to DNA-binding protein Tr...
AT5G51740	2.57	1.14	4.11	1.24	peptidase M48 family protein contains Pfam domain, PF01435: Peptidase family M48 At3g27110...
AT3G27110	-7.64	-2.07	-3.51	-1.38	peptidase M48 family protein contains Pfam domain, PF01435: Peptidase family M48 At5g51740...
AT3G57680	-6.13	-1.61	-3.88	-1.34	peptidase S41 family protein similar to PSII D1 protein processing enzyme (GI::7268527) Ar...
AT1G73990	-4.67	-1.3	-2.86	-1.17	peptidase U7 family protein similar to protease IV GB:AAA57008 from Escherichia coli; cont...
AT5G35100	3.92	1.52	3.88	1.56	peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein contains Pfam domain, ...
AT2G22420	-4.33	-1.22	-3.51	-1.18	peroxidase 17 (PER17) (P17) identical to SP—Q9SJZ2 Peroxidase 17 precursor (EC 1.11.1.7) (...
AT3G49110	-4.08	-1.38	-2.49	-1.21	peroxidase 33 (PER33) (P33) (PRXCA) neutral peroxidase C (PERC) identical to SP—P24101 Pe...
AT4G08770	-8.24	-1.69	-6.01	-1.45	peroxidase, putative identical to class III peroxidase ATP38 Arabidopsis thaliana gi—17530...
AT2G31390	3.99	1.53	2.95	1.40	pfkB-type carbohydrate kinase family protein contains Pfam profile: PF00294 pfkB family ca...
AT1G06030	6.95	1.48	4.05	1.25	pfkB-type carbohydrate kinase family protein contains Pfam profile: PF00294 pfkB family ca...
AT2G37040	-9.46	-1.84	-7.33	-1.61	phenylalanine ammonia-lyase 1 (PAL1) nearly identical to SP—P35510 At2g37040.1
AT3G53260	-9.43	-2.02	-7.75	-1.78	phenylalanine ammonia-lyase 2 (PAL2) nearly identical to SP—P45724 At3g53260.1
AT3G26570	-7.55	-1.49	-4.97	-1.29	phosphate transporter family protein contains Pfam profile: PF01384 phosphate transporter ...
AT4G08950	-2.44	-1.46	-4.79	-1.99	phosphate-responsive protein, putative (EXO) similar to phi-1 (phosphate-induced gene) Nic...
AT1G71010	4.43	1.24	2.79	1.14	phosphatidylinositol-4-phosphate 5-kinase family protein low similarity to phosphatidylino...
AT4G25970	5.21	1.38	6.74	1.54	phosphatidylserine decarboxylase, putative similar to SP—P53037 Phosphatidylserine decarbo...
AT4G29710	-4.19	-1.78	-0.51	-1.07	phosphodiesterasenucleotide pyrophosphatase-related weak similarity to SP—Q13822 Ectonucle...
AT4G37870	3.93	1.28	3.69	1.23	phosphoenolpyruvate carboxykinase ATP, putative PEP carboxykinase, putative PEPCK, putat...
AT1G73600	-9.59	-5.53	-6.94	-3.4	phosphoethanolamine N-methyltransferase 3, putative (NMT3) strong similarity to SP—Q9FR44 ...
AT5G47810	4.01	2.37	2.56	1.66	phosphofructokinase family protein similar to phosphofructokinase Amycolatopsis methanolic...
AT5G61580	5.12	1.28	3.55	1.19	phosphofructokinase family protein similar to phosphofructokinase Amycolatopsis methanolic...
AT1G23190	-4.11	-1.24	-4.25	-1.25	phosphoglucomutase, cytoplasmic, putative glucose phosphomutase, putative strong similari...
AT3G15730	-3.41	-1.15	-4.18	-1.21	phospholipase D alpha 1 PLD alpha 1 (PLDALPHA1) (PLD1) choline phosphatase 1 identical t...
AT4G11850	5.79	1.48	4.65	1.35	phospholipase D gamma 1 PLD gamma 1 (PLDGAMMA1) identical to phospholipase D gamma 1 SP:Q...
AT3G02570	3.91	1.36	6.68	1.73	phosphomannose isomerase type I family protein contains Pfam profile: PF01238 phosphomanno...

Continued...

Locus	AcdS$^+$ *t*-statistic	AcdS$^+$ fold change	AcdS$^-$ *t*-statistic	AcdS$^-$ fold change	Description
AT2G17630	5.4	1.34	3.82	1.22	phosphoserine aminotransferase, putative similar to Phosphoserine aminotransferase, chloro...
AT3G52430	-6.56	-1.38	-5.66	-1.32	phytoalexin-deficient 4 protein (PAD4) identical to phytoalexin-deficient 4 protein Arabid...
AT3G29810	-3.71	-1.65	-5.97	-2.14	phytochelatin synthetase family protein COBRA cell expansion protein COBL2 similar to phy...
AT2G33430	3.95	1.4	2.74	1.26	plastid developmental protein DAG, putative similar to DAG protein, chloroplast precursor ...
AT4G04020	-5.13	-2.17	-1.02	-1.16	plastid-lipid associated protein PAP, putative fibrillin, putative strong similarity to p...
AT4G22240	-4.1	-1.89	-0.23	-1.04	plastid-lipid associated protein PAP, putative similar to plastid-lipid associated protein...
AT1G08500	3.62	1.41	4.19	1.54	plastocyanin-like domain-containing protein At1g08500.1
AT1G60590	-3.99	-1.69	-6.85	-2.33	polygalacturonase, putative pectinase, putative similar to polygalacturonase PG1 (GI:5669...
AT2G26650	4.04	1.22	3.18	1.18	potassium channel protein 1 (AKT1) identical to AKT1 Arabidopsis thaliana gi—563112—gb—AAA...
AT4G19960	-4.61	-1.39	-4.72	-1.38	potassium transporter family protein similar to potassium transporter Arabidopsis thaliana...
AT4G36850	2.71	1.56	5.73	2.32	PQ-loop repeat family protein transmembrane family protein similar to SP—Q10482 Seven tra...
AT1G08770	4.2	1.24	4.62	1.27	prenylated rab acceptor (PRA1) family protein weak similarity to prenylated Rab acceptor 1...
AT1G64220	4.89	1.41	3.44	1.30	preprotein translocase-related similar to TOM7 protein Solanum tuberosum GI:3319774 At1g64...
AT3G30775	-9.87	-1.89	-6.98	-1.55	proline oxidase, mitochondrial osmotic stress-responsive proline dehydrogenase (POX) (PRO...
AT1G20380	2.96	1.30	7.65	1.86	prolyl oligopeptidase, putative prolyl endopeptidase, putative post-proline cleaving enz...
AT5G49020	4.63	1.29	2.48	1.15	protein arginine N-methyltransferase family protein similar to protein arginine methyltran...
AT4G29510	4.01	1.52	3.81	1.53	protein arginine N-methyltransferase, putative similar to protein arginine N-methyltransfe...
AT5G58140	-4.59	-1.31	-5.4	-1.38	protein kinase family protein non phototropic hypocotyl 1-like protein (NPL1) contains Pf...
AT1G51940	7.87	2.19	4.79	1.61	protein kinase family protein peptidoglycan-binding LysM domain-containing protein contai...
AT4G04570	-6.42	-1.42	-6.03	-1.39	protein kinase family protein contains Pfam domain PF00069: Protein kinase domain At4g0457...
AT4G23290	4.33	1.42	3.24	1.28	protein kinase family protein contains Pfam domain PF00069: Protein kinase domain At4g2329...
AT4G23170	-9.04	-1.9	-7.05	-1.66	protein kinase family protein contains Pfam PF01657: Domain of unknown function; similar t...
AT1G73660	-3.87	-1.35	-2.94	-1.22	protein kinase family protein contains Pfam profile: PF00069 eukaryotic protein kinase dom...
AT5G39000	-3.84	-1.26	-4.83	-1.35	protein kinase family protein contains protein kinase domain, Pfam:PF00069 At1g03740.1
AT1G25390	1.89	1.13	4.75	1.37	protein kinase family protein contains protein kinase domain, Pfam:PF00069 At1g25390.1
AT3G04910	6.82	1.55	4.88	1.36	protein kinase family protein contains protein kinase domain, Pfam:PF00069 At1g30570.1
AT1G03740	4.32	1.35	5.06	1.44	protein kinase family protein contains protein kinase domain, Pfam:PF00069 At3g04910.1
AT5G53450	9.65	1.69	10.52	1.78	protein kinase family protein contains protein kinase domain, Pfam:PF00069 At5g39000.1
AT1G30570	6.04	1.41	4.00	1.24	protein kinase family protein contains protein kinase domain, Pfam:PF00069 At5g53450.1
AT3G50500	3.9	1.35	0.82	1.07	protein kinase, putative similar to abscisic acid-activated protein kinase Vicia faba gi—6...
AT4G26080	4.06	1.32	2.73	1.18	protein phosphatase 2C ABI1 PP2C ABI1 abscisic acid-insensitive 1 (ABI1) nearly identica...
AT1G72770	-4.81	-1.3	-4.57	-1.28	protein phosphatase 2C P2C-HA PP2C P2C-HA (P2C-HA) identical to protein phosphatase 2C (A...
AT3G52180	7.69	1.9	3.93	1.39	protein tyrosine phosphatasekinase interaction sequence protein (PTPKIS1) identical to PTP...
AT5G62730	2.39	1.23	4.34	1.43	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF0085...
AT1G18880	3.74	1.21	6.14	1.39	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF0085...
AT1G22570	5.46	1.43	7.75	1.64	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF0085...
AT5G24470	11.1	2.1	11.23	2.14	pseudo-response regulator 5 (APRR5) identical to pseudo-response regulator 5 GI:10281006 f...
AT2G46790	-4.51	-1.24	-3.17	-1.15	pseudo-response regulator 9 (APRR9) timing of CAB expression 1-like protein (TL1) identic...
AT4G18200	3.77	1.23	5.62	1.37	purine permease family protein similar to purine permease Arabidopsis thaliana GI:7620007;...
AT1G57990	3.10	1.31	5.25	1.52	purine permease-related low similarity to purine permease Arabidopsis thaliana GI:7620007;...
AT1G14700	-9.51	-2.52	-6.79	-1.91	purple acid phosphatase, putative contains Pfam profile: PF00149 calcineurin-like phosphoe...
AT2G11190	4.34	1.44	2.20	1.20	putative retroelement pol polyprotein Arabidopsis thaliana NP454750
AT1G07180	-7.35	-1.53	-9.34	-1.7	pyridine nucleotide-disulphide oxidoreductase family protein contains similarity to altern...
AT2G29990	-6.13	-1.4	-7.05	-1.46	pyridine nucleotide-disulphide oxidoreductase family protein similar to SP—P32340 Rotenone...
AT4G15530	-7.33	-1.74	-4.47	-1.39	pyruvate phosphate dikinase family protein contains Pfam profiles: PF01326 pyruvate phosph...
AT2G32640	-4.94	-1.41	-1.73	-1.12	Q7EYS3 (Q7EYS3) GlycineD-amino acid oxidases-like, partial (67

Continued...

Locus	AcdS$^+$ *t*-statistic	AcdS$^+$ fold change	AcdS$^-$ *t*-statistic	AcdS$^-$ fold change	Description
AT1G03495	-13.85	-3.37	-11.9	-2.72	Q9LR73 (Q9LR73) F21B7.12, complete TC255286
AT5G54160	-7.44	-2.9	-3.92	-1.74	quercetin 3-O-methyltransferase 1 flavonol 3-O-methyltransferase 1 caffeic acid5-hydroxy...
AT4G36750	4.38	1.46	3.76	1.41	quinone reductase family protein similar to 1,4-benzoquinone reductase Phanerochaete chrys...
AT4G27270	5.61	1.5	3.77	1.30	quinone reductase family protein similar to 1,4-benzoquinone reductase Phanerochaete chrys...
AT5G54500	6.18	1.51	4.88	1.4	quinone reductase, putative similar to 1,4-benzoquinone reductase Phanerochaete chrysospor...
AT4G17170	4.38	1.46	1.48	1.13	Rab2-like GTP-binding protein (RAB2) identical to Rab2-like protein (At-RAB2) GI:1765896 f...
AT5G20250	4.6	1.31	7.84	1.56	raffinose synthase family protein seed imbibition protein, putative (din10) similar to se...
AT1G16920	4.2	1.23	3.59	1.18	Ras-related GTP-binding protein, putative similar to GTP binding protein GI:218228 from Vi...
AT5G45750	4.12	1.3	1.84	1.13	Ras-related GTP-binding protein, putative similar to GTP-binding protein GI:303744 from Pi...
AT4G35860	3.22	1.16	4.98	1.26	Ras-related GTP-binding protein, putative similar to Rab2-like GTP-binding protein GI:1765...
AT3G18820	5.35	1.33	3.49	1.20	Ras-related GTP-binding protein, putative similar to Ras-related protein RAB7 GI:1370186 f...
AT1G15530	3.83	1.21	4.49	1.25	receptor lectin kinase, putative similar to receptor lectin kinase 3 Arabidopsis thaliana ...
AT3G53830	-4.29	-1.54	-2.74	-1.31	regulator of chromosome condensation (RCC1) family protein UVB-resistance protein-related...
AT5G23750	5.22	1.5	3.82	1.35	remorin family protein contains Pfam domain, PF03766: Remorin, N-terminal region; contains...
AT4G11220	-4.1	-1.27	-2.43	-1.17	reticulon family protein (RTNLB2) similar to SP—Q64548 Reticulon 1 (Neuroendocrine-specifi...
AT4G27700	-4.7	-1.57	-3.00	-1.32	rhodanese-like domain-containing protein contains rhodanese-like domain PF00581 At4g27700....
AT2G22450	7.29	1.4	5.86	1.29	riboflavin biosynthesis protein, putative similar to SP—P50855 Riboflavin biosynthesis pro...
AT5G59750	-4.03	-1.28	-3.25	-1.22	riboflavin biosynthesis protein, putative similar to SP—P50855 Riboflavin biosynthesis pro...
AT4G21470	-4.28	-1.22	-4.85	-1.26	riboflavin kinaseFAD synthetase family protein contains Pfam profiles PF01687: Riboflavin ...
AT2G42910	4.44	1.49	2.93	1.31	ribose-phosphate pyrophosphokinase 4 phosphoribosyl diphosphate synthetase 4 (PRS4) ident...
AT4G34730	-4.08	-1.25	-2.16	-1.13	ribosome-binding factor A family protein contains PFam PF02033: Ribosome-binding factor A ...
AT2G24820	-4.46	-1.31	-0.80	-1.05	Rieske 2Fe-2S domain-containing protein similar to Rieske iron-sulfur protein Tic55 from P...
AT1G32490	3.9	1.22	3.92	1.23	RNA helicase, putative similar to ATP-dependent RNA helicase #3 Homo sapiens GI:3107913; c...
AT1G64860	-6.77	-1.48	-4.76	-1.32	RNA polymerase sigma subunit SigA (sigA) sigma factor 1 (SIG1) identical to sigma factor ...
AT5G24120	-11.88	-2.13	-7.34	-1.58	RNA polymerase sigma subunit SigE (sigE) sigma-like factor (SIG5) identical to RNA polyme...
AT4G17720	4.47	1.31	2.53	1.17	RNA recognition motif (RRM)-containing protein At4g17720.1
AT5G17520	8.4	1.43	9.93	1.52	root cap 1 (RCP1) identical to GI:6137138 At5g17520.1
AT4G24020	-3.94	-1.26	-2.64	-1.15	RWP-RK domain-containing protein similar to nodule inception protein Lotus japonicus GI:64...
AT5G04780	8.39	1.59	7.07	1.48	SEC14 cytosolic factor-related contains Pfam PF00650 : CRALTRIO domain; contains Pfam PF03...
AT2G15220	-4.66	-1.57	-2.88	-1.33	secretory protein, putative similar to NtPRp27 Nicotiana tabacum GI:5360263; contains Pfam...
AT2G17840	9.25	1.78	9.24	1.79	senescencedehydration-associated protein-related (ERD7) similar to senescence-associated p...
AT5G66040	4.75	1.41	3.25	1.27	senescence-associated family protein almost identical to ketoconazole resistant protein GI...
AT1G66330	-6.08	-1.42	-4.63	-1.28	senescence-associated family protein similar to senescence-associated protein (GI:12836895...
AT3G45600	6.01	1.49	4.27	1.33	senescence-associated family protein similar to senescence-associated protein 5 Hemerocall...
AT5G60220	5.08	1.32	3.82	1.24	senescence-associated family protein similar to senescence-associated protein 5 Hemerocall...
AT4G35770	0.69	1.09	4.25	2.01	senescence-associated protein (SEN1) identical to senescence-associated protein GI:1046270...
AT5G20700	3.60	1.29	4.16	1.34	senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:...
AT1G74940	3.48	1.19	4.43	1.26	senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:...
AT3G22550	7.39	1.55	8.17	1.62	senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:...
AT2G22960	-6.27	-1.47	-4.51	-1.3	serine carboxypeptidase S10 family protein contains Pfam profile: PF00450 serine carboxype...
AT4G30810	-7.06	-1.59	-7.01	-1.6	serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor ...
AT2G23000	-8.82	-2.56	-6.59	-1.95	serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor ...
AT4G30610	-4.07	-1.33	-5.54	-1.46	serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II chains A ...
AT5G23210	-4.86	-1.31	-4.76	-1.28	serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II chains A ...
AT1G73270	-4.71	-1.42	-2.02	-1.15	serine carboxypeptidase S10 family protein similar to serine carboxypeptidase II SP:P08819...
AT3G17180	-4.92	-1.38	-2.76	-1.19	serine carboxypeptidase S10 family protein similar to serine-type carboxypeptidase (SP:P55...

Continued...

Locus	AcdS⁺ *t*-statistic	AcdS⁺ fold change	AcdS⁻ *t*-statistic	AcdS⁻ fold change	Description
AT3G13110	-7.37	-1.66	-3.31	-1.25	serine O-acetyltransferase (SAT-1) identical to serine acetyltransferase (Sat-1) GI:118404...
AT1G55920	-6.73	-1.58	-3.50	-1.26	serine O-acetyltransferase, putative identical to GI:608677 from Arabidopsis thaliana At1g...
AT2G30740	3.71	1.22	5.99	1.39	serinethreonine protein kinase, putative similar to Pto kinase interactor 1 (Pti1)Lycopers...
AT3G62220	5.06	1.79	2.71	1.36	serinethreonine protein kinase, putative similar to Pto kinase interactor 1 (Pti1)Lycopers...
AT5G66880	4.2	1.64	3.39	1.51	serinethreonine protein kinase, putative similar to serine-threonine protein kinase Tritic...
AT5G59160	3.74	1.20	4.13	1.23	serinethreonine protein phosphatase PP1 isozyme 2 (TOPP2) identical to SP—P48482 Serinethr...
AT2G30980	4.06	1.3	2.52	1.18	shaggy-related protein kinase delta ASK-delta ASK-dzeta (ASK4) identical to shaggy-relat...
AT4G24190	-1.78	-1.15	-4.44	-1.41	shepherd protein (SHD) clavata formation protein, putative nearly identical to SHEPHERD A...
AT3G50560	-9.91	-2	-5.92	-1.5	short-chain dehydrogenasereductase (SDR) family protein contains INTERPRO family IPR002198...
AT4G11410	4.37	1.37	2.70	1.23	short-chain dehydrogenasereductase (SDR) family protein contains INTERPRO family IPR002198...
AT5G02540	4.68	1.29	3.80	1.24	short-chain dehydrogenasereductase (SDR) family protein contains INTERPRO family IPR002198...
AT4G09750	-5.68	-2.36	-2.18	-1.35	short-chain dehydrogenasereductase (SDR) family protein similar to 3-beta-hydroxysteroidde...
AT3G29260	-5.78	-1.52	-2.63	-1.21	short-chain dehydrogenasereductase (SDR) family protein similar to androgen-regulated shor...
AT2G29340	-4.58	-1.46	-3.48	-1.31	short-chain dehydrogenasereductase (SDR) family protein similar to carbonyl reductase GI:1...
AT3G61220	-5.13	-1.4	-3.80	-1.26	short-chain dehydrogenasereductase (SDR) family protein similar to tropinone reductase-I G...
AT1G06870	4.49	1.24	3.94	1.21	signal peptidase, putative similar to chloroplast thylakoidal processing peptidase GB:CAA7...
AT1G60270	-4.65	-1.37	-2.71	-1.19	Similar to beta glucosidase (bg1A) gb—X94986 from Manihot esculenta. NP041544
AT1G11330	4.39	1.35	4.95	1.42	S-locus lectin protein kinase family protein contains Pfam domains, PF00954: S-locus glyco...
AT5G47560	-4.83	-1.65	-2.42	-1.27	sodiumdicarboxylate cotransporter, putative similar to SWISS-PROT:Q13183 renal sodiumdicar...
AT1G78510	-7.76	-2.1	-6.23	-1.83	solanesyl diphosphate synthase (SPS) identical to solanesyl diphosphate synthase Arabidops...
AT1G17100	-9.19	-1.96	-7.34	-1.7	SOUL heme-binding family protein similar to SOUL protein Mus musculus GI:4886906; contains...
AT3G48360	3.61	1.58	5.39	1.85	speckle-type POZ protein-related contains Pfam PF00651 : BTBPOZ domain; similar to Speckle...
AT5G24150	-8.58	-2.44	-5.22	-1.68	squalene monooxygenase 1,1 squalene epoxidase 1,1 (SQP1,1) identical to SP—O65404 At5g241...
AT5G24160	-7.82	-2.42	-4.57	-1.66	squalene monooxygenase 1,2 squalene epoxidase 1,2 (SQP1,2) identical to SP—O65402 At5g241...
AT4G37760	-7.23	-1.53	-7.49	-1.54	squalene monooxygenase, putative squalene epoxidase, putative similar to SP—O65404 (SE 1,...
AT2G22830	-5.48	-1.35	-6.11	-1.37	squalene monooxygenase, putative squalene epoxidase, putative similar to SP—O65404 (SE 1,...
AT1G10760	11.99	1.91	14.02	2.13	starch excess protein (SEX1) identical to SEX1 Arabidopsis thaliana GI:12044358; supportin...
AT3G46970	1.85	1.12	5.06	1.33	starch phosphorylase, putative similar to alpha-glucan phosphorylase, H isozyme SP:P32811 ...
AT5G24300	-4.92	-1.39	-2.02	-1.14	starch synthase, putative similar to starch synthase I-1 GI:9369334 from Triticum aestivum...
AT3G02850	-6.88	-1.39	-4.82	-1.25	stelar K+ outward rectifier (SKOR) potassium channel protein identical to SKOR Arabidopsi...
AT2G03760	-4.42	-1.34	-4.27	-1.32	steroid sulfotransferase, putative strong similarity to steroid sulfotransferases from Bra...
AT5G13710	4.8	1.4	1.70	1.12	sterol 24-C-methyltransferase, putative similar to SP:P25087 Sterol 24-C-methyltransferase...
AT2G38230	-3.86	-1.3	-0.83	-1.06	stress-responsive protein, putative similar to ethylene-inducible protein HEVER Hevea bras...
AT5G01410	-5.39	-1.5	-2.57	-1.22	stress-responsive protein, putative similar to ethylene-inducible protein HEVER Hevea bras...
AT4G30020	4.82	1.35	2.49	1.17	subtilase family protein contains similarity to meiotic serine proteinase TMP GI:6468325 f...
AT3G14240	3.98	1.34	0.94	1.07	subtilase family protein contains similarity to SBT1 GI:1771160 from Lycopersicon esculent...
AT1G79440	9.8	1.69	8.87	1.58	succinate-semialdehyde dehydrogenase (SSADH1) similar to succinate-semialdehyde dehydrogen...
AT5G20830	5.14	1.51	3.37	1.29	sucrose synthase sucrose-UDP glucosyltransferase (SUS1) identical to SP—P49040 Sucrose sy...
AT3G43190	7.91	1.68	5.53	1.42	sucrose synthase, putative sucrose-UDP glucosyltransferase, putative strong similarity to...
AT4G10120	-9.15	-1.78	-6.11	-1.47	sucrose-phosphate synthase, putative similar to sucrose-phosphate synthase, Zea mays, PIR2...
AT4G00370	-4.68	-1.51	-2.04	-1.19	sugar transporter family protein contains Pfam profile PF00083: major facilitator superfam...
AT4G04750	-5.13	-1.42	-4.45	-1.34	sugar transporter family protein similar to sugar-porter family proteins 1 and 2 Arabidops...
AT4G04760	-5.29	-1.39	-4.07	-1.27	sugar transporter family protein similar to sugar-porter family proteins 1 and 2 Arabidops...
AT5G18840	1.12	1.13	4.93	1.46	sugar transporter, putative similar to ERD6 protein Arabidopsis thaliana GI:3123712, sugar...
AT2G48020	9.59	1.52	11.03	1.59	sugar transporter, putative similar to ERD6 protein Arabidopsis thaliana GI:3123712, sugar...
AT1G08900	2.70	1.31	5.93	1.7	sugar transporter-related contains similarity to sugar-porter family protein 2 GI:14585701...

Continued...

Locus	AcdS$^+$ *t*-statistic	AcdS$^+$ fold change	AcdS$^-$ *t*-statistic	AcdS$^-$ fold change	Description
AT5G27350	-5.86	-1.36	-5.95	-1.37	sugar-porter family protein 1 (SFP1) identical to sugar-porter family protein 1 Arabidopsi...
AT5G27360	-8.64	-1.51	-8.9	-1.52	sugar-porter family protein 2 (SFP2) identical to sugar-porter family protein 2 Arabidopsi...
AT3G22890	-5.53	-2.49	-4.27	-2.05	sulfate adenylyltransferase 1 ATP-sulfurylase 1 (APS1) nearly identical to ATP sulfurylas...
AT1G19920	-9.51	-1.74	-9.07	-1.65	sulfate adenylyltransferase 2 ATP-sulfurylase 2 (ASA1) (MET3-1) (APS2) identical to ATP s...
AT1G77990	-9.61	-1.66	-8.81	-1.58	sulfate transporter identical to sulfate transporter Arabidopsis thaliana GI:1498120 At1g7...
AT1G08830	-10.32	-1.65	-14.46	-1.97	superoxide dismutase Cu-Zn (SODCC) copperzinc superoxide dismutase (CSD1) identical to SW...
AT4G25100	0.92	1.07	5.18	1.57	superoxide dismutase Fe, chloroplast (SODB) iron superoxide dismutase (FSD1) identical to...
AT5G11150	7.36	1.56	6.99	1.52	synaptobrevin vesicle-associated membrane protein 713 (VAMP713) identified as AtVAMP713 b...
AT2G25340	6.05	1.55	5.4	1.49	synaptobrevin family protein similar to Synaptobrevin-like protein 1 (SP:P51809) Homo sapi...
AT4G32150	7.5	1.81	6.36	1.64	synaptobrevin family protein similar to Synaptobrevin-like protein 1 (SP:P51809) Homo sapi...
AT4G37610	-6.15	-1.99	-6.97	-2.15	TAZ zinc finger family protein BTBPOZ domain-containing protein contains Pfam PF00651 : B...
AT5G67480	5.77	1.81	8.24	2.29	TAZ zinc finger family protein BTBPOZ domain-containing protein contains Pfam PF00651 : B...
AT3G15030	5.93	1.7	5.2	1.61	TCP family transcription factor, putative similar to TCP3 GB:AAC24010 Arabidopsis thaliana...
AT4G18390	4.29	1.39	3.97	1.39	TCP family transcription factor, putative similar to TFPD (GI:6681577) Arabidopsis thalian...
AT5G13820	-4.87	-1.4	-4.39	-1.32	telomeric DNA-binding protein 1 (TBP1) identical to telomeric DNA-binding protein 1 Arabid...
AT4G00600	-7.9	-1.47	-7.88	-1.45	tetrahydrofolate dehydrogenasecyclohydrolase, putative similar to SP—P09440 C-1-tetrahydro...
AT3G17040	-6.14	-1.42	-5.37	-1.37	tetratricopeptide repeat (TPR)-containing protein low similarity to SP—P46825 Kinesin ligh...
AT1G01320	-3.96	-1.47	-3.00	-1.32	tetratricopeptide repeat (TPR)-containing protein low similarity to SP—Q9FNS4 PsbB mRNA ma...
AT1G72260	-5.63	-1.57	-1.31	-1.11	thionin (THI2.1) identical to thionin Arabidopsis thaliana gi—1181531—gb—AAC41678 At1g7226...
AT5G06690	4.08	1.25	4.53	1.28	thioredoxin family protein low similiarity to SP—P34723 Thioredoxin Penicillium chrysogenu...
AT1G11530	5.55	1.55	4.85	1.47	thioredoxin family protein similar to thioredoxin H-type from Arabidopsis thaliana SP—P294...
AT3G02730	-4.86	-1.46	-2.03	-1.16	thioredoxin, putative similar to SP—P29450 Thioredoxin F-type, chloroplast precursor (TRX-...
AT1G77090	-4.96	-1.66	-1.32	-1.14	thylakoid lumenal 29.8 kDa protein identical to SP—O49292—TL30_ARATH (Arabidopsis thalian...
AT5G02120	-4.01	-1.87	-1.57	-1.26	thylakoid membrane one helix protein (OHP) identical to one helix protein GI:3283057 from ...
AT4G01870	-5.22	-1.48	-2.35	-1.17	tolB protein-related contains weak similarity to TolB protein precursor (Swiss-Prot:P44677...
AT5G37770	-5.73	-1.72	-6.89	-1.91	touch-responsive protein calmodulin-related protein 2, touch-induced (TCH2) identical to ...
AT1G12230	3.89	1.4	2.87	1.31	transaldolase, putative similar to Swiss-Prot:P30148 transaldolase B (EC 2.2.1.2) Escheric...
AT2G30490	-7.13	-1.46	-3.90	-1.22	trans-cinnamate 4-monooxygenase cinnamic acid 4-hydroxylase (C4H) (CA4H) cytochrome P450...
AT3G20810	4.83	1.31	3.83	1.23	transcription factor jumonji (jmjC) domain-containing protein contains Pfam domain PF02373...
AT3G61830	6.21	1.71	3.86	1.41	transcriptional factor B3 family protein auxin-responsive factor AUXIAA-related contains ...
AT4G03020	3.29	1.19	4.61	1.26	transducin family protein WD-40 repeat family protein contains 6 WD-40 repeats (PF00400);...
AT2G43770	4.15	1.27	3.50	1.21	transducin family protein WD-40 repeat family protein contains 7 WD-40 repeats (PF00400);...
AT4G32990	4.39	1.77	4.05	1.64	transducin family protein WD-40 repeat family protein HIRA protein, Drosophila melanogast...
AT2G47990	4.01	1.31	0.82	1.06	transducin family protein WD-40 repeat family protein similar to Vegetatible incompatibil...
AT2G39980	-7.18	-1.39	-5.37	-1.28	transferase family protein contains Pfam profile PF02458 transferase family At2g39980.1
AT2G23510	-4.72	-1.26	-4.36	-1.22	transferase family protein low similarity to EIG-I24 from Nicotiana tabacum gi:10798748, 1...
AT5G39090	-4.18	-1.34	-1.82	-1.14	transferase family protein similar to anthocyanin 5-aromatic acyltransferase from Gentiana...
AT5G38130	3.45	1.25	5.46	1.42	transferase family protein similar to anthranilate N-hydroxycinnamoylbenzoyltransferase, D...
AT5G42830	-4.44	-1.34	-4.04	-1.29	transferase family protein similar to anthranilate N-hydroxycinnamoylbenzoyltransferase, D...
AT1G07350	-5.07	-1.38	-3.75	-1.26	transformer serinearginine-rich ribonucleoprotein, putative similar to GB:Y09506 from Nico...
AT2G45290	-4.12	-1.4	-2.80	-1.25	transketolase, putative strong similarity to transketolase 1 Capsicum annuum GI:3559814; c...
AT1G17220	-5.91	-1.54	-2.83	-1.23	translation initiation factor IF-2, chloroplast, putative similar to SP—P57997—IF2C_PHAVU...
AT5G23575	4.96	1.87	4.61	1.84	transmembrane protein, putative similar to cleft lip and palate transmembrane protein 1 Ho...
AT5G58030	4.2	1.27	2.26	1.14	transport protein particle (TRAPP) component Bet3 family protein very strong similarity to...
AT5G53550	5.53	1.3	5.51	1.29	transporter, putative similar to iron-phytosiderophore transporter protein yellow stripe 1...
AT5G42420	4.04	1.27	2.85	1.19	transporter-related low similarity to phosphoenolpyruvatephosphate translocator precursor ...

Continued...

Locus	AcdS⁺ *t*-statistic	AcdS⁺ fold change	AcdS⁻ *t*-statistic	AcdS⁻ fold change	Description
AT1G70290	-11.39	-1.75	-11.33	-1.72	trehalose-6-phosphate synthase, putative similar to Alpha,alpha-trehalose-phosphate syntha...
AT3G01550	-4.27	-1.42	-1.80	-1.15	triose phosphatephosphate translocator, putative similar to SWISS-PROT:P52178 triose phosp...
AT2G29310	-4.85	-1.51	-3.77	-1.37	tropinone reductase, putative tropine dehydrogenase, putative similar to tropinone reduct...
AT1G73325	-4.05	-2.19	-0.71	-1.14	trypsin and protease inhibitor family protein Kunitz family protein similar to Dr4 Arabid...
AT2G43550	3.05	1.51	6.93	2.7	trypsin inhibitor, putative similar to SP—P26780 Trypsin inhibitor 2 precursor (MTI-2) Sin...
AT4G27070	-4.85	-1.5	-3.48	-1.36	tryptophan synthase, beta subunit 2 (TSB2) identical to SP—25269 At4g27070.1
AT5G19500	-5.74	-1.52	-4.3	-1.36	tryptophantyrosine permease family protein contains Pfam profile PF03222: Tryptophantyrosi...
AT1G64740	6.83	1.64	3.96	1.33	tubulin alpha-1 chain (TUA1) nearly identical to SP—P11139 Tubulin alpha-1 chain Arabidops...
AT5G19780	4.2	1.33	1.29	1.09	tubulin alpha-3alpha-5 chain (TUA5) nearly identical to SP—P20363 Tubulin alpha-3alpha-5 c...
AT4G20890	6.39	1.74	3.41	1.32	tubulin beta-9 chain (TUB9) nearly identical to SP—P29517 Tubulin beta-9 chain Arabidopsis...
AT3G57040	-4.34	-1.36	-3.49	-1.27	two-component responsive regulator response reactor 4 (RR4) identical to responce reactor...
AT4G29690	-4	-1.54	0.72	1.08	type I phosphodiesterasenucleotide pyrophosphatase family protein similar to SP—P22413 Ect...
AT1G14400	4.17	1.48	3.85	1.45	ubiquitin-conjugating enzyme 1 (UBC1) E2; identical to gi:431259, SP:P25865 At1g14400.1
AT3G46460	3.13	1.30	4.09	1.44	ubiquitin-conjugating enzyme 13 (UBC13) E2; identical to gi:992706 At3g46460.1
AT2G02760	4.42	1.34	4.3	1.34	ubiquitin-conjugating enzyme 2 (UBC2) E2; identical to gi:2689242, SP:P42745 At2g02760.1
AT5G62540	6.6	2.11	5.86	1.99	ubiquitin-conjugating enzyme 3 (UBC3) E2; identical to gi:431261, SP:P42746 At5g62540.1
AT2G31750	-5.77	-1.34	-5.16	-1.29	UDP-glucoronosylUDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP...
AT4G01070	-7.61	-1.68	-4.79	-1.39	UDP-glucoronosylUDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP...
AT3G11340	-4.34	-1.32	-4.26	-1.31	UDP-glucoronosylUDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP...
AT2G36970	0.12	1.01	4.32	1.33	UDP-glucoronosylUDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP...
AT4G14090	-4.03	-1.46	-2.72	-1.29	UDP-glucoronosylUDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP...
AT1G22370	-4.59	-1.31	-3.78	-1.23	UDP-glucoronosylUDP-glucosyl transferase family protein glycosyltransferase family At1g223...
AT5G17050	-14.17	-1.88	-13.01	-1.78	UDP-glucoronosylUDP-glucosyl transferase family protein similar to UDP glucose:flavonoid 3...
AT3G21560	-4.5	-1.28	-3.72	-1.22	UDP-glucosyltransferase, putative similar to UDP-glucose:sinapate glucosyltransferase GI:9...
AT5G59290	5.43	1.35	5.56	1.34	UDP-glucuronic acid decarboxylase (UXS3) identical to UDP-glucuronic acid decarboxylase Ar...
AT3G17020	3.94	1.42	2.90	1.30	universal stress protein (USP) family protein similar to early nodulin ENOD18 Vicia faba G...
AT1G21390	-5.29	-1.29	-4.63	-1.24	Unknown
AT2G03310	5.65	1.7	7.29	1.99	Unknown
AT2G47220	-4.23	-1.27	-3.27	-1.18	Unknown
AT3G24470	-4.32	-1.31	-3.29	-1.23	Unknown
AT4G26510	5.03	1.37	4.55	1.32	uracil phosphoribosyltransferase UMP pyrophosphorylase (UPT1) nearly identical to SP—O655...
AT2G34470	-6.49	-1.43	-5.91	-1.36	urease accessory protein (UREG) identical to urease accessory protein UREG GI:4324678 from...
AT5G40850	-9.04	-1.61	-6.4	-1.4	urophorphyrin III methylase (UPM1) identical to urophorphyrin III methylase (GI:1146165) A...
AT3G14930	-5.52	-1.29	-3.56	-1.18	uroporphyrinogen decarboxylase, putative UPD, putative similar to uroporphyrinogen decarb...
AT3G03250	-4.28	-1.21	-4.98	-1.25	UTP–glucose-1-phosphate uridylyltransferase, putative UDP-glucose pyrophosphorylase, put...
AT5G63860	5.16	1.42	3.57	1.25	UVB-resistance protein (UVR8) identical to UVB-resistance protein UVR8 (GI:5478530, GB:AAD...
AT1G12840	4.15	1.25	2.97	1.18	vacuolar ATP synthase subunit C (VATC) V-ATPase C subunit vacuolar proton pump C subunit...
AT4G32940	-7.1	-1.67	-5.72	-1.52	vacuolar processing enzyme gamma gamma-VPE nearly identical to SP—Q39119 Vacuolar process...
AT2G16280	-1.76	-1.10	-4.96	-1.3	very-long-chain fatty acid condensing enzyme, putative similar to fatty acid condensing en...
AT1G19440	-5.87	-1.3	-3.80	-1.19	very-long-chain fatty acid condensing enzyme, putative similar to GB:AAD37122 from Arabido...
AT4G35250	-5.75	-1.4	-2.40	-1.15	vestitone reductase-related low similarity to vestitone reductase Medicago sativa subsp. s...
AT3G15354	-4.93	-1.63	-5.86	-1.71	WD-40 repeat family protein phytochrome A-related contains 7 WD-40 repeats (PF00400); phy...
AT5G51980	4.69	1.27	3.35	1.18	WD-40 repeat family protein zfwd2 protein (ZFWD2), putative 99.8
AT1G75380	5.42	1.44	4.83	1.35	wound-responsive protein-related similar to wound inducive gene GI:8096273 from Nicotiana ...
AT4G31800	-3.00	-1.22	-4.19	-1.3	WRKY family transcription factor At4g31800.1
AT4G25820	-10.59	-3.47	-12.87	-4.22	xyloglucan:xyloglucosyl transferase xyloglucan endotransglycosylase endo-xyloglucan tran...

Continued...

Locus	AcdS⁺ *t*-statistic	AcdS⁺ fold change	AcdS⁻ *t*-statistic	AcdS⁻ fold change	Description
AT5G57560	-8.82	-2.86	-9.55	-3.07	xyloglucan:xyloglucosyl transferase xyloglucan endotransglycosylase endo-xyloglucan tran. . .
AT5G48070	-6.44	-2.21	-8.79	-2.77	xyloglucan:xyloglucosyl transferase, putative xyloglucan endotransglycosylase, putative . . .
AT4G14130	-2.17	-1.28	-4.63	-1.62	xyloglucan:xyloglucosyl transferase, putative xyloglucan endotransglycosylase, putative . . .
AT4G37800	-4.14	-1.51	-0.70	-1.07	xyloglucan:xyloglucosyl transferase, putative xyloglucan endotransglycosylase, putative . . .
AT5G67030	-4.29	-1.6	-1.01	-1.12	zeaxanthin epoxidase (ZEP) (ABA1) identical to GI:9857296 AtABA1; controls Pfam profiles P. . .
AT2G47890	9.46	2.07	9.51	2.09	zinc finger (B-box type) family protein At2g47890.1
AT2G31380	-19.91	-3.98	-17.99	-3.37	zinc finger (B-box type) family protein salt tolerance-like protein (STH) contains Pfam p. . .
AT1G06040	-4.84	-1.66	-2.32	-1.26	zinc finger (B-box type) family protein salt-tolerance protein (STO) identical to SP—Q962. . .
AT5G48250	11.02	2.61	9.32	2.21	zinc finger (B-box type) family protein contains similarity to CONSTANS homologs At5g48250. . .
AT3G07650	11.31	3.51	9.52	2.88	zinc finger (B-box type) family protein similar to zinc finger protein GB:BAA33206 Oryza s. . .
AT4G38960	-5.04	-1.3	-3.28	-1.19	zinc finger (B-box type) family protein zinc finger protein - Oryza sativa, PID:d1034167 A. . .
AT4G27310	-4.89	-1.42	-3.99	-1.32	zinc finger (B-box type) family protein zinc-finger protein S3574, Oryza sativa, PIR3:JE01. . .
AT2G02070	3.97	1.21	5.34	1.31	zinc finger (C2H2 type) family protein contains Pfam domain, PF00096: Zinc finger, C2H2 t. . .
AT3G46090	-7.34	-1.52	-8.66	-1.64	zinc finger (C2H2 type) family protein (ZAT7) identical to zinc finger protein ZAT7 Arabid. . .
AT1G13290	-4.52	-1.25	-4.6	-1.26	zinc finger (C2H2 type) family protein contains Pfam domian PF00096: Zinc finger, C2H2 typ. . .
AT4G17910	-5.96	-1.32	-4.22	-1.22	zinc finger (C3HC4-type RING finger) family protein pentatricopeptide (PPR) repeat-contai. . .
AT5G19080	3.29	1.21	4.33	1.31	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc fi. . .
AT1G72175	3.59	1.27	4.88	1.42	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc fi. . .
AT3G11110	10.95	1.9	11.5	1.95	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 Zinc fi. . .
AT5G22920	-4.84	-1.43	-0.26	-1.02	zinc finger (C3HC4-type RING finger) family protein contains Pfam profiles:PF05495 CHY zin. . .
AT3G06410	-5.64	-1.32	-5.45	-1.29	zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x. . .
AT3G55980	-4.43	-1.3	-4.62	-1.3	zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x. . .
AT1G21570	2.92	1.53	5.81	2.57	zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x. . .
AT3G02830	-4.45	-1.4	-3.23	-1.26	zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x. . .
AT3G54810	-1.89	-1.14	-4.35	-1.3	zinc finger (GATA type) family protein GATA transcription factor 3, Arabidopsis thaliana, . . .
AT1G48570	4.84	1.44	2.64	1.23	zinc finger (Ran-binding) family protein contains Pfam domain, PF00641: Zn-finger in Ran b. . .
AT5G15850	-9.46	-1.92	-7.47	-1.68	zinc finger protein CONSTANS-LIKE 1 (COL1) identical to Zinc finger protein CONSTANS-LIKE . . .
AT3G02380	-7.55	-1.69	-5.2	-1.43	zinc finger protein CONSTANS-LIKE 2 (COL2) identical to putative flowering-time gene CONST. . .
AT1G32540	4.01	1.43	4.45	1.5	zinc finger protein, putative similar to zinc-finger protein Lsd1 Arabidopsis thaliana gi—. . .
AT5G43630	-6.68	-1.38	-5.07	-1.27	zinc knuckle (CCHC-type) family protein contains Pfam domain PF00098: Zinc knuckle At5g436. . .
AT2G46800	-3.17	-1.19	-4.15	-1.27	zinc transporter (ZAT) identical to zinc transporter ZAT Arabidopsis thaliana gi—4206640—g. . .
AT3G12750	3.59	1.30	4.16	1.38	zinc transporter (ZIP1) identical to putative zinc transporter GB:AAC24197 from Arabidopsi. . .
AT2G32270	1.96	1.15	5.33	1.46	zinc transporter (ZIP3) identical to zinc transporter Arabidopsis thaliana gi—3252870—gb—A. . .

Table C.2: Significant expression changes in roots of 6 day-old seedlings treated with bacteria versus untreated seedlings. Numbers in black represent changes with an FDR adjusted $p < 0.05$, whereas numbers in gray represent changes with an FDR adjusted $p > 0.05$. AcdS$^+$ = *Pseudomonas putida* UW4 AcdS$^+$; AcdS$^-$ = *Pseudomonas putida* UW4 AcdS$^-$.

Locus	AcdS$^+$ t-statistic	AcdS$^+$ fold change	AcdS$^-$ t-statistic	AcdS$^-$ fold change	Description
AT2G06050	-15.08	-1.45	-10.33	-1.37	12-oxophytodienoate reductase (OPR3) / delayed dehiscence1 (DDE1) nearly identical to D...
AT2G42590	-9.05	-1.17	-6.66	-1.15	14-3-3 protein GF14 mu (GRF9) identical to GF14 mu GI:3551052, SP:Q96299 from Arabidops...
AT4G29040	-10.15	-1.17	-8.24	-1.17	26S proteasome AAA-ATPase subunit (RPT2a) almost identical to 26S proteasome AAA-ATPase...
AT5G05780	-9.67	-1.16	-8.77	-1.17	26S proteasome non-ATPase regulatory subunit 7, putative / 26S proteasome regulatory su...
AT4G24820	-8.35	-1.17	-3.79	-1.09	26S proteasome regulatory subunit, putative (RPN7) contains similarity to ubiquitin act...
AT5G63980	-8.23	-1.13	-10.85	-1.21	3'(2'),5'-bisphosphate nucleotidase / inositol polyphosphate 1-phosphatase / FIERY1 pro...
AT1G07770	-11.62	-1.23	-9.94	-1.24	40S ribosomal protein S15A (RPS15aA) identical to GB:AAA61608 from Arabidopsis thaliana...
AT3G10610	-7.4	-1.16	-7.42	-1.19	40S ribosomal protein S17 (RPS17C) similar to 40S ribosomal protein S17 GB:AAD50774 Lyc...
AT3G47370	-14.92	-1.29	-12.12	-1.28	40S ribosomal protein S20 (RPS20B) 40S RIBOSOMAL PROTEIN S20 - ARABIDOPSIS THALIANA,PID...
AT3G53870	-5.13	-1.09	-8.32	-1.19	40S ribosomal protein S3 (RPS3B) ribosomal protein S3a - Xenopus laevis, PIR:R3XL3A At3...
AT4G21990	-5.35	-1.12	-10.43	-1.32	5'-adenylylsulfate reductase (APR3) / PAPS reductase homolog (PRH26) identical to 5'-ad...
AT1G49820	-10.53	-1.18	-7.23	-1.15	5-methylthioribose kinase family contains TIGRfam TIGR01767: 5-methylthioribose kinase ...
AT2G42740	-11.09	-1.23	-9.67	-1.25	60S ribosomal protein L11 (RPL11A) At2g42740.1
AT1G27400	-9.18	-1.29	-6.65	-1.25	60S ribosomal protein L17 (RPL17A) similar to GB:P51413 from Arabidopsis thaliana; simi...
AT3G05560	-9.99	-1.39	-7.96	-1.38	60S ribosomal protein L22-2 (RPL22B) identical to 60S ribosomal protein L22-2 SP:Q9M9W1...
AT2G32220	-5.89	-1.12	-8.31	-1.22	60S ribosomal protein L27 (RPL27A) At2g32220.1
AT3G28900	-8.37	-1.19	-7.03	-1.20	60S ribosomal protein L34 (RPL34C) similar to 60S ribosomal protein L34 GB:P41098 Nicot...
AT4G34000	-8.07	-1.16	-9.41	-1.24	ABA-responsive element-binding protein / abscisic acid responsive elements-binding fact...
AT4G26970	-8.93	-1.19	-6.55	-1.17	aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative st...
AT3G45990	-9.51	-1.19	-8.99	-1.22	actin-depolymerizing factor, putative similar to SP—Q9ZSK3 Actin-depolymerizing factor ...
AT3G25780	-11.94	-1.27	-11.86	-1.34	allene oxide cyclase, putative / early-responsive to dehydration protein, putative / ER...
AT3G25770	-5.16	-1.1	-9.35	-1.23	allene oxide cyclase, putative / early-responsive to dehydration protein, putative / ER...
AT5G42650	-8.55	-1.25	-8.53	-1.31	allene oxide synthase (AOS) / hydroperoxide dehydrase / cytochrome P450 74A (CYP74A) id...
AT1G17000	-9.19	-1.18	-8.36	-1.21	alpha, alpha-trehalose-phosphate synthase, UDP-forming, putative / trehalose-6-phosphat...
AT4G33680	-8.74	-1.15	-6.47	-1.13	aminotransferase class I and II family protein low similarity to Aromatic Aminotransfer...
AT1G25560	-8.89	-1.19	-3.31	-1.08	AP2 domain-containing transcription factor, putative similar to AP2 domain transcriptio...
AT1G36060	-11.73	-1.3	-7.03	-1.21	AP2 domain-containing transcription factor, putative similar to DNA-binding protein RAV...
AT5G56540	-9.11	-1.16	-6.73	-1.14	arabinogalactan-protein (AGP14) identical to gi—10880505—gb—AAG24282 At5g56540.1
AT3G07360	-9.5	-1.19	-9.1	-1.23	armadillo/beta-catenin repeat family protein / U-box domain-containing protein contains...
AT1G58080	-11.35	-1.24	-4.04	-1.10	ATP phosphoribosyl transferase 1 (ATP-PRT1) identical to ATP phosphoribosyl transferase...
AT5G13450	-8.55	-1.16	-6.27	-1.14	ATP synthase delta chain, mitochondrial, putative / H(+)-transporting two-sector ATPase...
AT5G49460	-9.08	-1.17	-6.03	-1.14	ATP-citrate synthase, putative / ATP-citrate (pro-S-)-lyase, putative / citrate cleavag...
AT1G73590	-5.14	-1.1	-7.71	-1.19	auxin efflux carrier protein, putative (PIN1) identical to putative auxin efflux carrie...
AT4G29930	-8.61	-1.14	-8.35	-1.17	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-...
AT1G35580	-9.7	-1.2	-2.17	-1.05	beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-f...
AT3G62420	-11.5	-1.21	-5.93	-1.13	bZIP transcription factor family protein similar to common plant regulatory factor 6 GI...
AT4G38810	-10.5	-1.19	0.14	1.00	calcium-binding EF hand family protein contains INTERPRO:IPR002048 calcium-binding EF-h...
AT1G76640	-15.76	-1.3	-17.6	-1.43	calmodulin-related protein, putative similar to regulator of gene silencing calmodulin-...
AT3G01500	0.06	1.00	9.68	1.77	carbonic anhydrase 1, chloroplast / carbonate dehydratase 1 (CA1) nearly identical to S...

Continued...

Locus	AcdS⁺ t-statistic	AcdS⁺ fold change	AcdS⁻ t-statistic	AcdS⁻ fold change	Description
AT1G20620	8.88	1.18	1.61	1.04	catalase 3 (SEN2) almost identical to catalase 3 SP:Q42547, GI:3123188 from Arabidopsis. . .
AT5G22250	-4.54	-1.08	-7.69	-1.18	CCR4-NOT transcription complex protein, putative similar to SWISS-PROT:Q60809 CCR4-NOT . . .
AT5G56500	-10.73	-1.25	-8.24	-1.24	chaperonin, putative similar to SWISS-PROT:P08927- RuBisCO subunit binding-protein beta. . .
AT2G43620	-5.58	-1.1	8.69	1.2	chitinase, putative similar to basic endochitinase CHB4 precursor SP:Q06209 from Brassi. . .
AT1G29910	-9.76	-1.46	-9.52	-1.57	chlorophyll A-B binding protein 2, chloroplast / LHCII type I CAB-2 / CAB-140 (CAB2A) i. . .
AT1G71697	-6.94	-1.11	-8.81	-1.18	choline kinase, putative similar to GmCK2p choline kinase gi—1438881—gb—AAC49375 At1g71. . .
AT3G60100	-10.02	-1.28	-4.56	-1.15	citrate synthase, mitochondrial, putative strong similarity to SP—Q43175 Citrate syntha. . .
AT1G10730	-7.91	-1.17	-7.5	-1.2	clathrin adaptor complexes medium subunit family protein contains Pfam profile: PF00928. . .
AT3G01120	-8.84	-1.2	-6.74	-1.18	cystathionine gamma-synthase, chloroplast / O-succinylhomoserine (Thiol)-lyase (CGS) id. . .
AT5G48810	-9.1	-1.15	-6.18	-1.13	cytochrome b5 identical to cytochrome b5 Arabidopsis thaliana GI:4240122; strong simila. . .
AT4G39950	-8.82	-1.53	-7.04	-1.52	cytochrome P450 79B2, putative (CYP79B2) identical to cytochrome P450 (79B2) SP:O81346 . . .
AT4G31500	-7.17	-1.13	-8.27	-1.2	cytochrome P450 83B1 (CYP83B1) Identical to Cytochrome P450 (SP:O65782)Arabidopsis tha. . .
AT3G48520	-8.41	-1.17	-8.5	-1.21	cytochrome P450 family protein similar to Cytochrome P450 94A1 (P450-dependent fatty ac. . .
AT2G22330	-7.59	-1.2	-10.88	-1.37	cytochrome P450, putative similar to cytochrome P450 79B2 (SP:O81346) Arabidopsis thali. . .
AT4G30530	-8.28	-1.23	-7.29	-1.25	defense-related protein, putative strong similarity to defense-related protein Brassica. . .
AT3G23300	-8.69	-1.14	-7.7	-1.15	dehydration-responsive protein-related similar to early-responsive to dehydration stres. . .
AT1G29470	-7.42	-1.16	-7.62	-1.21	dehydration-responsive protein-related similar to early-responsive to dehydration stres. . .
AT5G66400	-14.37	-1.28	-11.66	-1.28	dehydrin (RAB18) nearly identical to SP—P30185 Dehydrin Rab18 Arabidopsis thaliana At5g. . .
AT1G17470	-5.28	-1.09	-7.71	-1.17	developmentally regulated GTP-binding protein (DRG1) identical to developmentally regul. . .
AT3G11750	-5.27	-1.14	-8.47	-1.3	dihydroneopterin aldolase, putative similar to SP—P28823 Dihydroneopterin aldolase (EC . . .
AT1G28330	9.17	1.31	7.4	1.3	dormancy-associated protein, putative (DRM1) identical to dormancy-associated protein A. . .
AT5G12110	-9.68	-1.18	-6.38	-1.14	elongation factor 1B alpha-subunit 1 (eEF1Balpha1) identical to elongation factor 1B al. . .
AT4G02930	-8.29	-1.13	-3.17	-1.06	elongation factor Tu, putative / EF-Tu, putative similar to mitochondrial elongation fa. . .
AT5G10830	-8.09	-1.16	-7.75	-1.19	embryo-abundant protein-related similar to embryo-abundant protein Picea glauca GI:1350. . .
AT4G12230	-9.74	-1.17	-5.35	-1.11	esterase/lipase/thioesterase family protein low similarity to 2-hydroxy-6-ketonona-2,4-. . .
AT3G21360	-10.17	-1.18	-8.62	-1.18	expressed protein At3g21360.1
AT5G60400	-4.95	-1.08	-7.46	-1.14	expressed protein At5g60400.1
AT1G06190	-8.59	-1.14	-4.87	-1.09	expressed protein At1g06190.1
AT1G74950	-14.42	-1.76	-11.21	-1.71	expressed protein At1g74950.1
AT1G76200	-8.7	-1.15	-7.19	-1.15	expressed protein At1g76200.1
AT2G28330	-8.95	-1.16	-5.60	-1.12	expressed protein At2g28330.1
AT2G46890	-3.65	-1.07	-7.38	-1.18	expressed protein At2g46890.1
AT4G03420	-8.88	-1.14	-3.95	-1.08	expressed protein At4g03420.1
AT4G22000	-8.65	-1.14	-7.05	-1.14	expressed protein At4g22000.1
AT5G06980	-8.38	-1.19	-4.55	-1.12	expressed protein At5g06980.2
AT5G13140	-4.01	-1.07	-7.54	-1.16	expressed protein At5g13140.1
AT5G17350	-3.51	-1.09	-9.6	-1.33	expressed protein At5g17350.1
AT5G17640	-5.12	-1.09	-8.59	-1.19	expressed protein At5g17640.1
AT5G24740	-8.38	-1.14	-4.11	-1.08	expressed protein At5g24740.1
AT5G45020	-8.82	-1.16	-5.18	-1.12	expressed protein At5g45020.1
AT5G45100	-3.90	-1.06	-7.4	-1.14	expressed protein At5g45100.1
AT2G41770	-5.83	-1.1	-7.34	-1.16	expressed protein contains Pfam domain PF03385: Protein of unknown function, DUF288 At2. . .
AT1G22270	-6.54	-1.1	-7.57	-1.15	expressed protein contains Pfam domain PF03966: Protein of unknown function (DUF343) At. . .
AT2G41640	-5.75	-1.18	-9.42	-1.39	expressed protein contains Pfam domain, PF04577: Protein of unknown function (DUF563) A. . .
AT5G66650	-7.06	-1.14	-10.92	-1.28	expressed protein contains Pfam domain, PF04678: Protein of unknown function, DUF607 At. . .
AT1G21740	-10.1	-1.21	-9.22	-1.24	expressed protein contains Pfam domains, PF04782: Protein of unknown function (DUF632) . . .

Continued. . .

Locus	AcdS$^+$ t-statistic	AcdS$^+$ fold change	AcdS$^-$ t-statistic	AcdS$^-$ fold change	Description
AT3G21190	-7.44	-1.14	-7.81	-1.18	expressed protein contains Pfam PF03138: Plant protein family. The function of this fam. . .
AT1G25520	-14.04	-1.26	-8.99	-1.2	expressed protein contains Pfam profile PF01169: Uncharacterized protein family UPF0016. . .
AT5G11730	-8.45	-1.13	-5.95	-1.11	expressed protein contains Pfam profile PF03267: Arabidopsis protein of unknown functio. . .
AT4G21570	-9.21	-1.15	-3.55	-1.07	expressed protein contains Pfam profile PF03619: Domain of unknown function At4g21570.1
AT2G32240	-8.33	-1.28	-3.30	-1.13	expressed protein contains Pfam profile: PF04508 viral A-type inclusion protein repeat . . .
AT5G22650	-7.08	-1.15	-10.39	-1.28	expressed protein non-consensus AT donor splice site at exon 3, AC acceptor splice site. . .
AT4G29660	-9.09	-1.15	-4.93	-1.09	expressed protein predicted proteins, Arabidopsis thaliana At4g29660.1
AT4G26260	-12.34	-1.22	1.02	1.02	expressed protein similar to myo-inositol oxygenase Sus scrofa gi—17432544—gb—AAL39076 . . .
AT5G21940	-9.2	-1.19	-8.31	-1.22	expressed protein supported by full length cDNA GI:22531282 from Arabidopsis thaliana A. . .
AT2G24550	-11.03	-1.25	-10.18	-1.29	expressed protein weak similarity to MTD1 Medicago truncatula GI:9294810 At2g24550.1
AT1G47590	-5.47	-1.08	-7.8	-1.15	F16N3.13 NP033834
AT5G04750	-8.52	-1.16	-7.37	-1.17	F1F0-ATPase inhibitor protein, putative similar to F1F0-ATPase inhibitor protein Oryza . . .
AT5G52470	-7.62	-1.26	-8.59	-1.38	fibrillarin 1 (FBR1) (FIB1) (SKIP7) identical to fibrillarin 1 GI:9965653 from Arabidop. . .
AT4G25630	-7.65	-1.29	-7.42	-1.36	fibrillarin 2 (FIB2) identical to fibrillarin 2 GI:9965655 from Arabidopsis thaliana At. . .
AT1G74380	-9.53	-1.22	-8.38	-1.24	galactosyl transferase GMA12/MNN10 family protein very low similarity to alpha-1,2-gala. . .
AT2G23540	-5.29	-1.1	-7.54	-1.17	GDSL-motif lipase/hydrolase family protein similar to family II lipase EXL1 GI:15054382. . .
AT5G55050	-8.86	-1.18	-2.73	-1.07	GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 GI:1505438. . .
AT4G36810	-11.74	-1.24	-10.27	-1.26	geranylgeranyl pyrophosphate synthase (GGPS1) / GGPP synthetase / farnesyltranstransfer. . .
AT5G18170	-23.65	-1.5	-8.63	-1.2	glutamate dehydrogenase 1 (GDH1) identical to glutamate dehydrogenase 1 (GDH 1) Arabido. . .
AT4G30550	-14.07	-1.55	-9.83	-1.45	glutamine amidotransferase class-I domain-containing protein similar to defense-related. . .
AT1G28480	-7.88	-1.48	-7.38	-1.57	glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltran. . .
AT1G69920	-9.34	-1.31	-6.62	-1.26	glutathione S-transferase, putative similar to glutathione transferase GB:CAA09188 Alop. . .
AT5G26780	-11.6	-1.18	-6.26	-1.12	glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative . . .
AT4G30450	-10.75	-1.29	-6.15	-1.20	glycine-rich protein At4g30450.1
AT2G43610	-7.38	-1.15	9.12	1.24	glycoside hydrolase family 19 protein similar to chitinase GI:17799 from Brassica napus. . .
AT1G64760	-8.43	-1.15	-5.24	-1.11	glycosyl hydrolase family 17 protein similar to elicitor inducible chitinase Nt-SubE76 . . .
AT5G03760	-6.35	-1.14	-9.96	-1.29	glycosyl transferase family 2 protein similar to beta-(1-3)-glucosyl transferase GB:AAC. . .
AT3G28180	-7.77	-1.18	-7.57	-1.21	glycosyl transferase family 2 protein similar to beta-(1-3)-glucosyl transferase GB:AAC. . .
AT3G29630	-9.4	-1.18	-5.32	-1.12	glycosyltransferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and . . .
AT2G20570	-7.02	-1.11	-10.11	-1.2	golden2-like transcription factor (GLK1) identical to golden2-like transcription factor. . .
AT5G13200	-9.15	-1.2	-5.29	-1.14	GRAM domain-containing protein / ABA-responsive protein-related similar to ABA-responsi. . .
AT1G56330	-7.01	-1.12	-8.79	-1.2	GTP-binding protein (SAR1B) identical to GTP-binding protein (SAR1B) Arabidopsis thalia. . .
AT3G20670	-9.25	-1.18	-7.25	-1.17	histone H2A, putative strong similarity to histone H2A GB:AAF64418 GI:7595337 from Arab. . .
AT5G59910	-9.4	-1.19	-6.75	-1.17	histone H2B nearly identical to histone H2B Arabidopsis thaliana GI:2407802; contains P. . .
AT1G07790	-8.3	-1.16	-4.62	-1.10	histone H2B, putative strong similarity to histone H2B Arabidopsis thaliana GI:2407802,. . .
AT5G22880	-12.39	-1.27	-12.27	-1.34	histone H2B, putative strong similarity to histone H2B-3 Lycopersicon esculentum GI:302. . .
AT5G10390	-10.63	-1.21	-6.96	-1.16	histone H3 identical to histone H3 from Zea mays SP—P05203, Medicago sativa GI:166384, . . .
AT5G10400	-8.1	-1.2	-7.25	-1.22	histone H3 identical to several histone H3 proteins, including Zea mays SP—P05203, Medi. . .
AT3G53730	-10.29	-1.22	-7.45	-1.19	histone H4 identical to histone H4 from Lycopersicon esculentum GI:297150, Lolium temul. . .
AT1G52150	-7.15	-1.13	-7.5	-1.17	homeobox-leucine zipper family protein / lipid-binding START domain-containing protein . . .
AT1G51760	-9.3	-1.2	-3.75	-1.09	IAA-amino acid hydrolase 3 / IAA-Ala hydrolase 3 (IAR3) identical to IAA-Ala hydrolase . . .
AT1G20810	-8.32	-1.14	-6.77	-1.14	immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein identical t. . .
AT5G43360	2.84	1.08	10.2	1.39	inorganic phosphate transporter (PHT3) identical to inorganic phosphate transporter Ara. . .
AT2G22240	-11.97	-1.22	-9.8	-1.22	inositol-3-phosphate synthase isozyme 2 / myo-inositol-1-phosphate synthase 2 / MI-1-P . . .
AT4G19680	-18.24	-1.48	-3.33	-1.09	iron-responsive transporter (IRT2) member of the Zinc (Zn2+)-Iron (Fe2+) permease (ZIP). . .
AT3G16470	-9.17	-1.17	-6.13	-1.14	jacalin lectin family protein contains Pfam profile: PF01419 jacalin-like lectin domain. . .

Continued. . .

Locus	AcdS⁺ t-statistic	AcdS⁺ fold change	AcdS⁻ t-statistic	AcdS⁻ fold change	Description
AT1G19720	-9.12	-1.19	-12.84	-1.35	jacalin lectin family protein similar to agglutinin Castanea crenata GI:25528883; conta. . .
AT1G08110	-7.74	-1.13	-8.68	-1.19	lactoylglutathione lyase, putative / glyoxalase I, putative similar to lactoylglutathio. . .
AT5G59320	-12.23	-1.38	-13.16	-1.53	lipid transfer protein 3 (LTP3) identical to lipid transfer protein 3 from Arabidopsis . . .
AT5G59310	-6.64	-1.12	-8.49	-1.2	lipid transfer protein 4 (LTP4) identical to lipid transfer protein 4 from Arabidopsis . . .
AT1G49430	-6.5	-1.11	-8.01	-1.16	long-chain-fatty-acid–CoA ligase / long-chain acyl-CoA synthetase nearly identical to . . .
AT4G09960	-13.93	-1.32	-10.5	-1.3	MADS-box protein (AGL11) At4g09960.1
AT1G02140	-6.74	-1.19	-7.9	-1.28	mago nashi family protein similar to Mago Nashi, Genbank Accession Number U03559; conta. . .
AT4G10380	-11.89	-1.19	0.51	1.01	major intrinsic family protein / MIP family protein contains Pfam profile: MIP PF00230 . . .
AT3G26460	-8.96	-1.4	-5.17	-1.27	major latex protein-related / MLP-related low similarity to major latex protein Papaver. . .
AT4G23670	-10.47	-1.41	-6.53	-1.30	major latex protein-related / MLP-related low similarity to major latex protein Papaver. . .
AT1G60960	0.84	1.02	8.41	1.22	metal transporter, putative (IRT3) identical to putative metal transporter IRT3 Arabido. . .
AT1G31260	4.82	1.12	8.12	1.27	metal transporter, putative (ZIP10) identical to putative metal transporter ZIP10 Arabi. . .
AT5G45105	-11.07	-1.43	-1.55	-1.06	metal transporter, putative (ZIP8) similar to putative metal transporter ZIP8 Arabidops. . .
AT4G04830	-9.04	-1.19	-11.03	-1.29	methionine sulfoxide reductase domain-containing protein / SeIR domain-containing prote. . .
AT3G46560	-6.78	-1.14	-7.65	-1.2	mitochondrial import inner membrane translocase (TIM9) identical to mitochondrial impor. . .
AT2G22500	-11.46	-1.28	-11.66	-1.36	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochond. . .
AT2G01450	-10.99	-1.24	-7.89	-1.21	mitogen-activated protein kinase, putative / MAPK, putative (MPK17) mitogen-activated p. . .
AT1G73540	-7.42	-1.16	-7.23	-1.19	MutT/nudix family protein low similarity to SP—Q09790 Diadenosine 5’,5”’-P1,P6-hexapho. . .
AT1G18300	-8.39	-1.17	-11.8	-1.31	MutT/nudix family protein similar to SP—Q09790 Diadenosine 5’,5”’-P1,P6-hexaphosphate . . .
AT4G31340	-9.6	-1.16	-5.07	-1.10	myosin heavy chain-related contains weak similarity to Myosin heavy chain, nonmuscle ty. . .
AT5G17770	-13.06	-1.23	-7.66	-1.16	NADH-cytochrome b5 reductase identical to NADH-cytochrome b5 reductase Arabidopsis thal. . .
AT3G12390	-11.33	-1.23	-9.46	-1.23	nascent polypeptide associated complex alpha chain protein, putative / alpha-NAC, putat. . .
AT3G20610	-9.23	-1.16	-7.29	-1.15	non-race specific disease resistance protein, putative similar to non-race specific dis. . .
AT2G23150	-9.35	-1.21	-8.19	-1.23	NRAMP metal ion transporter 3 (NRAMP3) identical to metal transporter Nramp3 Arabidopsi. . .
AT1G76790	-7.36	-1.16	-9.44	-1.27	O-methyltransferase family 2 protein similar to caffeic acid O-methyltransferase Cathar. . .
AT3G13610	-8.29	-1.44	-1.11	-1.06	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to desacetoxyvindoline 4-hy. . .
AT4G21200	-8.97	-1.15	-6.17	-1.13	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to gibberellin 20-oxidase f. . .
AT5G12860	-10.33	-1.17	-10	-1.2	oxoglutarate/malate translocator, putative similar to 2-oxoglutarate/malate translocato. . .
AT4G24780	-6.31	-1.11	-8.75	-1.19	pectate lyase family protein similar to pectate lyase GP:14289169 from Salix gilgiana A. . .
AT1G11580	-8.58	-1.19	0.09	1.00	pectin methylesterase, putative similar to pectin methylesterase GI:1617583 from Lycope. . .
AT3G49220	-11.36	-1.22	-10.27	-1.24	pectinesterase family protein contains Pfam profile: PF01095 pectinesterase At3g49220.1
AT3G21770	-10.17	-1.24	-11.34	-1.34	peroxidase 30 (PER30) (P30) (PRXR9) identical to SP—Q9LSY7 Peroxidase 30 precursor (EC . . .
AT5G19890	-10.09	-1.16	-0.07	-1.00	peroxidase, putative identical to peroxidase Arabidopsis thaliana gi—1403134—emb—CAA670. . .
AT2G41480	-9	-1.25	-6.60	-1.23	peroxidase, putative similar to peroxidase Spinacia oleracea gi—1781334—emb—CAA71494 At. . .
AT4G29710	-8.82	-1.26	-8.6	-1.32	phosphodiesterase/nucleotide pyrophosphatase-related weak similarity to SP—Q13822 Ecton. . .
AT5G04120	-0.67	-1.01	-12.93	-1.36	phosphoglycerate/bisphosphoglycerate mutase family protein low similarity to SP—P36623 . . .
AT5G58700	-8.37	-1.24	-6.60	-1.23	phosphoinositide-specific phospholipase C family protein contains Pfam profile: PF00388. . .
AT2G25080	-8.44	-1.14	-3.10	-1.06	phospholipid hydroperoxide glutathione peroxidase, chloroplast / PHGPx (GPX1) identical. . .
AT1G78040	-8.94	-1.17	-6.72	-1.15	pollen Ole e 1 allergen and extensin family protein contains Pfam domain, PF01190: Poll. . .
AT1G49760	-9.97	-1.24	-7.62	-1.22	polyadenylate-binding protein, putative / PABP, putative similar to poly(A)-binding pro. . .
AT2G26650	-8.41	-1.15	-2.49	-1.05	potassium channel protein 1 (AKT1) identical to AKT1 Arabidopsis thaliana gi—563112—gb—. . .
AT1G29990	-5.34	-1.17	-7.37	-1.31	prefoldin, putative similar to Swiss-Prot:O15212 prefoldin subunit 6 (Protein Ke2) Homo. . .
AT3G30775	-9.44	-1.5	-4.95	-1.30	proline oxidase, mitochondrial / osmotic stress-responsive proline dehydrogenase (POX) . . .
AT1G67250	-6.71	-1.18	-7.85	-1.27	proteasome maturation factor UMP1 family protein contains Pfam profile PF05348: Proteas. . .
AT1G79570	-8.76	-1.14	-5.20	-1.10	protein kinase family protein low similarity to EDR1 Arabidopsis thaliana GI:11127925 A. . .
AT3G17090	-8.98	-1.15	-6.53	-1.13	protein phosphatase 2C family protein / PP2C family protein similar to Ser/Thr protein . . .

Continued. . .

Locus	AcdS$^+$ t-statistic	AcdS$^+$ fold change	AcdS$^-$ t-statistic	AcdS$^-$ fold change	Description
AT3G16800	-9.86	-1.36	-2.22	-1.09	protein phosphatase 2C, putative / PP2C, putative similar to protein phosphatase-2C GB:...
AT5G62680	-17.35	-1.34	-14.29	-1.35	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF0...
AT4G12610	-7.06	-1.13	-7.44	-1.17	Q6S7B9 (Q6S7B9) Mutant TFIIF-alpha (Fragment), complete TC266769
AT2G30710	-9.7	-1.17	-4.88	-1.10	RabGAP/TBC domain-containing protein similar to SP—Q08484 GTPase-activating protein GYP...
AT2G24490	-5.75	-1.1	-8.02	-1.17	replication protein, putative similar to replication protein A 30kDa Oryza sativa (japo...
AT4G11220	-9.11	-1.18	-8.69	-1.21	reticulon family protein (RTNLB2) similar to SP—Q64548 Reticulon 1 (Neuroendocrine-spec...
AT1G63120	-10.35	-1.17	-10.93	-1.22	rhomboid family protein contains PFAM domain PF01694, Rhomboid family At1g63120.1
AT2G42910	-6.95	-1.12	-7.63	-1.17	ribose-phosphate pyrophosphokinase 4 / phosphoribosyl diphosphate synthetase 4 (PRS4) i...
AT5G64670	-7.25	-1.13	-8.21	-1.19	ribosomal protein L15 family protein At5g64670.1
AT5G55550	-5.95	-1.09	-7.25	-1.14	RNA recognition motif (RRM)-containing protein similar to DAZ associated protein 1 Homo...
AT1G51510	-9.65	-1.16	-10.94	-1.23	RNA-binding protein, putative similar to RNA-binding protein 8 (Ribonucleoprotein RBM8)...
AT1G61250	-8.88	-1.15	-3.76	-1.08	secretory carrier membrane protein (SCAMP) family protein (SC3) contains Pfam domain, P...
AT2G47060	-8.4	-1.19	-8.06	-1.23	serine/threonine protein kinase, putative similar to Pto kinase interactor 1 (Pti1)Lyco...
AT1G25490	-9.1	-1.16	-8.69	-1.19	serine/threonine protein phosphatase 2A (PP2A) regulatory subunit A (RCN1) identical to...
AT1G76860	-6.86	-1.16	-7.72	-1.23	small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative simi...
AT3G50660	-5.21	-1.08	-8.81	-1.17	steroid 22-alpha-hydroxylase (CYP90B1) (DWF4) identical to gi:2935342 At3g50660.1
AT3G57010	-9.39	-1.35	-6.28	-1.28	strictosidine synthase family protein similar to strictosidine synthase Rauvolfia serpe...
AT2G05920	-7.26	-1.14	-7.32	-1.17	subtilase family protein contains similarity to cucumisin-like serine protease GI:31768...
AT5G09600	-8.44	-1.14	-3.04	-1.06	succinate dehydrogenase cytochrome b subunit family protein similar to succinate dehydr...
AT3G27380	-10.83	-1.19	-6.66	-1.14	succinate dehydrogenase, iron-sulphur subunit, mitochondrial (SDH2-1) nearly identical ...
AT1G71880	-10.4	-1.35	-3.93	-1.15	sucrose transporter / sucrose-proton symporter (SUC1) identical to sucrose-proton sympo...
AT1G08920	-11.85	-1.34	-7.67	-1.26	sugar transporter, putative similar to ERD6 protein Arabidopsis thaliana GI:3123712, su...
AT1G77990	-12.88	-1.28	-7.73	-1.2	sulfate transporter identical to sulfate transporter Arabidopsis thaliana GI:1498120 At...
AT1G08830	-7.8	-1.4	-8.08	-1.53	superoxide dismutase Cu-Zn (SODCC) / copper/zinc superoxide dismutase (CSD1) identical ...
AT4G25100	4.40	1.07	24.42	1.6	superoxide dismutase Fe, chloroplast (SODB) / iron superoxide dismutase (FSD1) identica...
AT5G22360	-8.89	-1.14	-8.37	-1.16	synaptobrevin family protein similar to Synaptobrevin-like protein 1 (SP:P51809) Homo s...
AT3G52400	-12.57	-1.23	-10.21	-1.23	syntaxin, putative (SYP122) similar to SP—Q9ZSD4 Syntaxin 121 (AtSYP121) (Syntaxin-rela...
AT1G24510	-13.8	-1.28	-11.72	-1.3	T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative / chaperonin, p...
AT5G54770	13.12	1.27	9.34	1.23	thiazole biosynthetic enzyme, chloroplast (ARA6) (THI1) (THI4) identical to SP—Q38814 T...
AT1G10200	-4.33	-1.07	-7.33	-1.15	transcription factor LIM, putative strong similarity to transcription factor Ntlim1 Nic...
AT4G12430	-9.98	-1.2	-7.72	-1.19	trehalose-6-phosphate phosphatase, putative similar to trehalose-6-phosphate phosphatas...
AT4G22590	-11.56	-1.21	-4.23	-1.09	trehalose-6-phosphate phosphatase, putative similar to trehalose-6-phosphate phosphatas...
AT4G29690	-5.05	-1.13	-7.52	-1.24	type I phosphodiesterase/nucleotide pyrophosphatase family protein similar to SP—P22413...
AT1G23410	-9.42	-1.26	-6.67	-1.22	ubiquitin extension protein, putative / 40S ribosomal protein S27A (RPS27aA) strong sim...
AT3G52450	-8.42	-1.17	-7.96	-1.2	U-box domain-containing protein similar to immediate-early fungal elicitor protein CMPG...
AT1G40124	-5.08	-1.09	-8.16	-1.19	Unknown
AT5G42445	-9.9	-1.26	-8.07	-1.26	Unknown
AT2G40070	-9.45	-1.23	-5.06	-1.14	Unknown
AT5G30584	-9.84	-1.19	-6.81	-1.16	Unknown
AT5G40850	-2.19	-1.04	-7.58	-1.18	urophorphyrin III methylase (UPM1) identical to urophorphyrin III methylase (GI:1146165...
AT2G41740	-9.3	-1.19	-3.78	-1.09	villin 2 (VLN2) nearly identical to villin 2 (VLN2) Arabidopsis thaliana GI:3415115 At2...
AT1G80840	-9.64	-1.24	-11.32	-1.36	WRKY family transcription factor similar to WRKY transcription factor GB:BAA87058 GI:64...
AT1G60030	-4.71	-1.08	-9.27	-1.21	xanthine/uracil permease family protein contains Pfam profile: PF00860 permease family ...
AT5G57560	-7.64	-1.19	-7.27	-1.23	xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan...
AT4G03210	-3.95	-1.07	-7.88	-1.18	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putati...
AT1G06040	-8.25	-1.17	-4.92	-1.12	zinc finger (B-box type) family protein / salt-tolerance protein (STO) identical to SP—...

Table C.3: Significant expression changes in shoots of 6 day-old trAcdS-*rolD* seedlings versus non-transformed seedlings, $p < 0.01$.

Locus	*t*-statistic	Fold change	Description
AT5G10450	-3.91	-1.32	14-3-3 protein GF14 lambda (GRF6) (AFT1) identical to 14-3-3 GF14lambda GI:1345595 from [Arabidopsis thaliana]...
AT3G46230	-3.38	-1.26	17.4 kDa class I heat shock protein (HSP17.4-CI) identical to 17.4 kDa class I heat shock protein SP:P19036 fr...
AT5G12020	-4.00	-1.38	17.6 kDa class II heat shock protein (HSP17.6-CII) identical to 17.6 kDa class II heat shock protein SP:P29830...
AT1G05010	-4.01	-1.35	1-aminocyclopropane-1-carboxylate oxidase / ACC oxidase / ethylene-forming enzyme (ACO) (EAT1) Identical to 1-...
AT5G51440	3.87	1.37	23.5 kDa mitochondrial small heat shock protein (HSP23.5-M) similar to heat shock 22 kDa protein, mitochondria...
AT1G20200	4.63	1.35	26S proteasome regulatory subunit S3, putative (RPN3) similar to SP:Q06364 from [Daucus carota] [At1g20200.1]
AT2G25450	4.66	1.67	2-oxoglutarate-dependent dioxygenase, putative similar to 2A6 (GI:599622) and tomato ethylene synthesis regula...
AT2G30830	4.66	1.34	2-oxoglutarate-dependent dioxygenase, putative similar to 2A6 (GI:599622) and tomato ethylene synthesis regula...
AT5G24490	-6.94	-1.58	30S ribosomal protein, putative similar to SP—P19954 Plastid-specific 30S ribosomal protein 1, chloroplast pre...
AT1G07770	-5.98	-1.57	40S ribosomal protein S15A (RPS15aA) identical to GB:AAA61608 from [Arabidopsis thaliana] (Plant Physiol. 106 ...
AT1G65060	3.85	1.28	4-coumarate–CoA ligase 3 / 4-coumaroyl-CoA synthase 3 (4CL3) identical to SP—Q9S777 4-coumarate–CoA ligase 3...
AT5G21170	-4.38	-1.50	5'-AMP-activated protein kinase beta-2 subunit, putative similar to Swiss-Prot:Q9QZH4 5'-AMP-activated protein...
AT3G03780	3.61	1.37	5-methyltetrahydropteroyltriglutamate–homocysteine methyltransferase, putative / vitamin-B12-independent meth...
AT3G58700	-3.56	-1.34	60S ribosomal protein L11 (RPL11B) ribosomal protein L11, cytosolic, Arabidopsis thaliana, PIR:S49033 [At3g587...
AT5G48760	-3.85	-1.28	60S ribosomal protein L13A (RPL13aD) [At5g48760.1]
AT1G27400	-3.65	-1.42	60S ribosomal protein L17 (RPL17A) similar to GB:P51413 from [Arabidopsis thaliana]; similar to ESTs gb—L33542...
AT1G17650	4.07	1.35	6-phosphogluconate dehydrogenase NAD-binding domain-containing protein low similarity to SP—P23523 2-hydroxy-3...
AT4G29270	14.59	2.72	acid phosphatase class B family protein similar to acid phosphatase [Glycine max] GI:3341443; contains Pfam pr...
AT4G34970	6.12	1.61	actin-depolymerizing factor, putative similar to SP—Q9ZNT3 Actin-depolymerizing factor 5 (ADF-5) (AtADF5) Ara...
AT5G22420	4.50	1.45	acyl CoA reductase, putative similar to acyl CoA reductase [Simmondsia chinensis] GI:5020215; contains Pfam pr...
AT2G38400	-9.11	-1.78	alanine–glyoxylate aminotransferase, putative / beta-alanine-pyruvate aminotransferase, putative / AGT, putat...
AT3G57520	-3.62	-1.26	alkaline alpha galactosidase, putative similar to alkaline alpha galactosidase II [Cucumis melo] GI:29838631; ...
AT4G23590	7.71	1.91	aminotransferase class I and II family protein similar to nicotianamine aminotransferase from Hordeum vulgare ...
AT2G28840	-4.25	-1.35	ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023 [At2g28840.1]
AT1G35720	3.63	1.32	annexin 1 (ANN1) identical to annexin (AnnAt1) [Arabidopsis thaliana] GI:4959106 [At1g35720.1]
AT2G38750	3.38	1.27	annexin 4 (ANN4) nearly identical to annexin (AnnAt4) [Arabidopsis thaliana] GI:6503084; contains Pfam profile...
AT5G67190	-3.80	-1.29	AP2 domain-containing transcription factor, putative similar to AP2 domain containing protein RAP2.1 (GI:21555...
AT5G44316	3.70	1.28	ATP-binding-cassette transporter, putative similar to ATP-binding-cassette transporter (ABC1) described in PMI...
AT1G09430	-3.45	-1.25	ATP-citrate synthase (ATP-citrate (pro-S-)-lyase/citrate cleavage enzyme), putative similar to ATP-citrate-lya...
AT4G03400	6.21	1.50	auxin-responsive GH3 family protein similar to auxin-responsive GH3 product [Glycine max] GI:18591; contains P...
AT3G04730	-5.16	-1.42	auxin-responsive protein / indoleacetic acid-induced protein 16 (IAA16) identical to SP—O24407 Auxin-responsiv...
AT2G22670	-3.63	-1.29	auxin-responsive protein / indoleacetic acid-induced protein 8 (IAA8) identical to SP—Q38826 Auxin-responsive ...
AT3G03830	-4.24	-1.52	auxin-responsive protein, putative similar to auxin-inducible SAUR (Small Auxin Up RNAs) (GI:3043536) [Raphanu...
AT5G18020	-3.78	-1.41	auxin-responsive protein, putative similar to auxin-inducible SAUR (Small Auxin Up RNAs) (GI:3043536) [Raphanu...
AT5G18060	-3.37	-1.58	auxin-responsive protein, putative similar to auxin-inducible SAUR (Small Auxin Up RNAs) GI:3043536 from radis...
AT5G51570	-3.95	-1.39	band 7 family protein similar to hypersensitive-induced response protein [Zea mays] GI:7716468; contains Pfam ...
AT3G01290	-7.10	-1.84	band 7 family protein similar to hypersensitive-induced response protein [Zea mays] GI:7716470; contains Pfam ...

Continued...

Locus	*t*-statistic	Fold change	Description
AT4G17880	5.01	1.37	basic helix-loop-helix (bHLH) family protein bHLH protein, Arabidopsis thaliana, PATCHX:E255557 [At4g17880.1]
AT4G15210	3.31	1.26	beta-amylase (BMY1) / 1,4-alpha-D-glucan maltohydrolase identical to Beta-amylase (EC 3.2.1.2) (1,4-alpha-D-gl. . .
AT4G17090	5.07	1.40	beta-amylase (CT-BMY) / 1,4-alpha-D-glucan maltohydrolase identical to beta-amylase enzyme GI:6065749 from [Ar. . .
AT4G25700	3.39	1.24	beta-carotene hydroxylase identical to GI:1575296 [At4g25700.1]
AT1G62660	3.84	1.37	beta-fructosidase (BFRUCT3) / beta-fructofuranosidase / invertase, vacuolar identical to beta-fructosidase GB:. . .
AT1G12240	3.72	1.26	beta-fructosidase (BFRUCT4) / beta-fructofuranosidase / invertase, vacuolar identical to beta-fructosidase GI:. . .
AT5G56870	4.27	1.32	beta-galactosidase, putative / lactase, putative similar to beta-galactosidase precursor GI:3869280 from [Cari. . .
AT2G35860	3.82	1.29	beta-Ig-H3 domain-containing protein / fasciclin domain-containing protein contains Pfam profile PF02469: Fasc. . .
AT5G43760	4.14	1.38	beta-ketoacyl-CoA synthase, putative similar to beta-ketoacyl-CoA synthase [Simmondsia chinensis][GI:1045614] . . .
AT2G30610	-4.00	-1.34	BTB/POZ domain-containing protein contains Pfam PF00651: BTB/POZ domain; contains Interpro IPR000210/ PS50097:. . .
AT5G28770	-3.44	-1.30	bZIP transcription factor family protein similar to seed storage protein opaque-2(bZIP family)GI:168428 from Z. . .
AT4G34050	3.34	1.34	caffeoyl-CoA 3-O-methyltransferase, putative nearly identical to GI:2960356 [Populus balsamifera subsp. tricho. . .
AT1G67980	-4.47	-1.39	caffeoyl-CoA 3-O-methyltransferase, putative similar to GI:2960356 [Populus balsamifera subsp. trichocarpa], G. . .
AT2G33380	3.62	1.46	calcium-binding RD20 protein (RD20) induced by abscisic acid during dehydration PMID:10965948; putative transm. . .
AT1G52410	8.61	1.74	caldesmon-related weak similarity to Caldesmon (CDM) (Swiss-Prot:P12957) [Gallus gallus] [At1g52410.1]
AT5G57630	-4.04	-1.38	CBL-interacting protein kinase 21, putative (CIPK21) identical to CBL-interacting protein kinase 21 [Arabidops. . .
AT2G26980	-5.82	-1.55	CBL-interacting protein kinase 3 (CIPK3) identical to CBL-interacting protein kinase 3 [Arabidopsis thaliana] . . .
AT1G01140	-3.84	-1.32	CBL-interacting protein kinase 9 (CIPK9) identical to CBL-interacting protein kinase 9 [Arabidopsis thaliana] . . .
AT2G32610	3.40	1.25	cellulose synthase family protein similar to Zea mays cellulose synthase-3 [gi:9622878], -2 [gi:9622876], -1 [. . .
AT4G15290	4.85	1.39	cellulose synthase family protein similar to Zea mays cellulose synthase-5 [gi:9622882], -4 [gi:9622880] [At4g. . .
AT4G32190	3.93	1.31	centromeric protein-related low similarity to SP—Q02224 Centromeric protein E (CENP-E protein) Homo sapiens . . .
AT5G57800	3.60	1.27	CER1 protein, putative (WAX2) similar to maize glossy1 homolog GI:2213643 from [Oryza sativa]; contains Pfam p. . .
AT5G13930	3.84	1.64	chalcone synthase / naringenin-chalcone synthase identical to SP—P13114 [At5g13930.1]
AT2G43580	-3.45	-1.29	chitinase, putative similar to basic endochitinase CHB4 precursor SP:Q06209 from [Brassica napus] [At2g43580.1. . .
AT2G43590	-4.64	-1.40	chitinase, putative similar to basic endochitinase CHB4 precursor SP:Q06209 from [Brassica napus] [At2g43590.1. . .
AT4G02530	4.06	1.65	chloroplast thylakoid lumen protein SP:022773 ;TL16_ARATH [At4g02530.1]
AT1G09500	3.71	1.31	cinnamyl-alcohol dehydrogenase family / CAD family similar to cinnamyl alcohol dehydrogenase, Eucalyptus gunni. . .
AT3G58740	-4.91	-1.41	citrate synthase, glyoxysomal, putative strong similarity to SP—P49299 Citrate synthase, glyoxysomal precursor. . .
AT3G58750	-5.03	-1.37	citrate synthase, glyoxysomal, putative strong similarity to SP—P49299 Citrate synthase, glyoxysomal precursor. . .
AT4G12280	4.43	1.33	copper amine oxidase family protein contains Pfam domain, PF01179: Copper amine oxidase, enzyme domain [At4g12. . .
AT4G12290	3.56	1.26	copper amine oxidase, putative similar to copper amine oxidase [Cicer arietinum] gi—3819099—emb—CAA08855 [At4g. . .
AT1G66240	11.82	2.25	copper homeostasis factor, putative / copper chaperone, putative (CCH) similar to gi:3168840 contains Pfam pro. . .
AT4G23600	6.82	1.61	coronatine-responsive tyrosine aminotransferase / tyrosine transaminase similar to nicotianamine aminotransfer. . .
AT5G67360	6.43	1.53	cucumisin-like serine protease (ARA12) Asp48; almost identical to cucumisin-like serine protease (ARA12) GI:31. . .
AT1G78820	-3.80	-1.43	curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein similar to S locus glyco. . .
AT4G39950	3.81	1.36	cytochrome P450 79B2, putative (CYP79B2) identical to cytochrome P450 (79B2) SP:O81346 from [Arabidopsis thali. . .
AT4G37430	8.13	1.85	cytochrome P450 81F1 (CYP81F1) (CYP91A2) identical to cytochrome P450 81F1 (91A2) (SP:O65790) [Arabidopsis tha. . .
AT4G31500	4.43	1.37	cytochrome P450 83B1 (CYP83B1) Identical to Cytochrome P450 (SP:O65782)[Arabidopsis thaliana] [At4g31500.1]
AT4G36220	3.94	1.29	cytochrome P450 84A1 (CYP84A1) / ferulate-5-hydroxylase (FAH1) identical to Cytochrome P450 84A1 (Ferulate-5-h. . .
AT4G13770	11.38	2.04	cytochrome P450 family protein [At4g13770.1]
AT5G44620	3.65	1.32	cytochrome P450 family protein similar to cytocrhome P450 monooxygenase (GI:14334057) [Gossypium arboreum] [At. . .
AT4G00360	4.06	1.37	cytochrome P450, putative [At4g00360.1]
AT1G57750	7.56	1.84	cytochrome P450, putative similar to cytochrome P450 GI:4688670 from [Catharanthus roseus] [At1g57750.1]
AT4G12320	3.86	1.44	cytochrome P450, putative Similar to P450 monooxygenase (gi:14334057) [Gossypium arboreum] [At4g12320.1]
AT4G12310	4.10	1.41	cytochrome P450, putative similar to P450 monooxygenase GI:14334057 from [Gossypium arboreum] [At4g12310.1]
AT1G44050	3.43	1.31	DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain [At1g44050.1]
AT4G30530	3.39	1.32	defense-related protein, putative strong similarity to defense-related protein [Brassica carinata] GI:14009290. . .

Continued. . .

Locus	*t*-statistic	Fold change	Description
AT3G23300	4.33	1.32	dehydration-responsive protein-related similar to early-responsive to dehydration stress ERD3 protein [Arabido. . .
AT5G58770	8.60	1.80	dehydrodolichyl diphosphate synthase, putative / DEDOL-PP synthase, putative similar to GI:796076 [At5g58770.1. . .
AT3G25860	7.20	1.73	dihydrolipoamide S-acetyltransferase (LTA2) identical to dihydrolipoamide S-acetyltransferase (LTA2) [Arabidop. . .
AT1G58848	-3.95	-1.34	disease resistance protein (CC-NBS-LRR class), putative / PRM1 homolog, putative similar to disease resistance. . .
AT1G59218	-3.70	-1.36	disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a di. . .
AT4G10780	4.64	1.41	disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a di. . .
AT5G46450	5.83	1.77	disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a . . .
AT3G15960	3.31	1.28	DNA mismatch repair MutS family protein contains Pfam profile PF05188: MutS domain II [At3g15960.1]
AT5G56840	5.23	1.60	DNA-binding family protein contains Pfam domains, PF00249: Myb-like DNA-binding domain and PF00098: Zinc knuck. . .
AT4G00238	-4.73	-1.45	DNA-binding storekeeper protein-related contains Pfam PF04504: Protein of unknown function, DUF573; similar to. . .
AT3G12610	-3.82	-1.31	DNA-damage-repair/toleration protein, putative (DRT100) similar to DNA-damage-repair/toleration protein DRT100. . .
AT4G36040	-5.51	-1.53	DNAJ heat shock N-terminal domain-containing protein (J11) identical to dnaJ heat shock protein J11 [Arabidops. . .
AT1G80920	-7.66	-2.14	DNAJ heat shock N-terminal domain-containing protein similar to SP—Q05646 Chaperone protein dnaJ Erysipelothri. . .
AT2G17880	-4.27	-1.33	DNAJ heat shock protein, putative similar to J11 protein [Arabidopsis thaliana] GI:9843641; contains Pfam prof. . .
AT1G59725	-4.50	-1.35	DNAJ heat shock protein, putative similar to SP—Q9QYJ3 DnaJ homolog subfamily B member 1 (Heat shock 40 kDa pr. . .
AT5G62430	-6.53	-1.54	Dof-type zinc finger domain-containing protein similar to H-protein promoter binding factor-2a GI:3386546 from. . .
AT2G33830	-13.70	-2.47	dormancy/auxin associated family protein contains Pfam profile: PF05564 dormancy/auxin associated protein [At2. . .
AT1G56220	-6.47	-1.70	dormancy/auxin associated family protein similar to Auxin-repressed 12.5 kDa protein (Swiss-Prot:Q05349) [Frag. . .
AT1G28330	-16.22	-2.80	dormancy-associated protein, putative (DRM1) identical to dormancy-associated protein [Arabidopsis thaliana] G. . .
AT5G25190	-3.65	-1.38	ethylene-responsive element-binding protein, putative ethylene responsive element binding protein homolog, Sty. . .
AT3G42180	10.53	2.20	exostosin family protein contains Pfam profile: PF03016 Exostosin family [At3g42180.1]
AT5G20260	6.80	1.60	exostosin family protein contains Pfam profile: PF03016 Exostosin family [At5g20260.1]
AT4G38400	-3.69	-1.27	expansin family protein (EXPL2) contains Pfam profile: PF01357 pollen allergen; expansin-like gene, PMID:11641. . .
AT1G20190	-4.72	-1.41	expansin, putative (EXP11) similar to GB:U30460 from [Cucumis sativus]; alpha-expansin gene family, PMID:11641. . .
AT2G39080	-3.49	-1.33	expressed protein [At2g39080.1]
AT4G34260	4.96	1.46	expressed protein [At4g34260.1]
AT1G07280	3.48	1.25	expressed protein [At1g07280.1]
AT1G10740	-3.47	-1.28	expressed protein [At1g10740.1]
AT1G27210	-3.73	-1.33	expressed protein [At1g27210.1]
AT1G50040	3.87	1.31	expressed protein [At1g50040.1]
AT2G02420	3.77	1.28	expressed protein [At2g02410.1]
AT2G30930	-4.67	-1.45	expressed protein [At2g30930.1]
AT3G12570	8.75	2.25	expressed protein [At3g12570.1]
AT3G53320	6.51	1.81	expressed protein [At3g53320.1]
AT3G55840	-4.41	-1.38	expressed protein [At3g55840.1]
AT4G11100	4.14	1.42	expressed protein [At4g11100.1]
AT5G49550	-3.41	-1.24	expressed protein [At5g49550.1]
AT5G59080	-3.71	-1.68	expressed protein [At5g59080.1]
AT3G02910	9.10	1.88	expressed protein contains Pfam domain PF03674: Uncharacterised protein family (UPF0131) [At3g02910.1]
AT1G56580	3.31	1.23	expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538 [At1g56580.1]
AT5G03230	-5.02	-1.70	expressed protein contains Pfam profile PF04520: Protein of unknown function, DUF584 [At5g03230.1]
AT5G25460	-4.25	-1.35	expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642 [At5g25460.1]
AT5G05440	-3.62	-1.25	expressed protein low similarity to cytokinin-specific binding protein [Vigna radiata] GI:4190976 [At5g05440.1. . .
AT5G19120	-4.38	-1.43	expressed protein low similarity to extracellular dermal glycoprotein EDGP precursor [Daucus carota] GI:285741. . .
AT3G03870	-4.68	-1.55	expressed protein predicted using genefinder [At3g03870.2]
AT3G29240	-4.10	-1.32	expressed protein similar to At1g33780 [Arabidopsis thaliana]; contains Pfam profile PF02622: Uncharacterized . . .
AT4G27450	-6.93	-1.74	expressed protein similar to auxin down-regulated protein ARG10 [Vigna radiata] GI:2970051, wali7 (aluminum-in. . .

Continued. . .

Locus	*t*-statistic	Fold change	Description
AT1G73010	3.59	1.34	expressed protein similar to phosphatase, orphan 1 (GI:20196841) [Mus musculus], (GI:20196839) [Homo sapiens];. . .
AT3G12760	-3.61	-1.30	expressed protein similar to RP42 protein [Homo sapiens] GI:9896486; contains Pfam profile PF00627: UBA/TS-N d. . .
AT5G44660	6.87	1.54	expressed protein similar to unknown protein (pir——T05327) [At5g44660.1]
AT1G35350	-3.44	-1.29	EXS family protein / ERD1/XPR1/SYG1 family protein similar to PHO1 protein [Arabidopsis thaliana] GI:20069032;. . .
AT2G34810	6.20	1.56	FAD-binding domain-containing protein similar to SP—P30986 reticuline oxidase precursor (Berberine-bridge-form. . .
AT1G75900	6.60	1.74	family II extracellular lipase 3 (EXL3) EXL3 (PMID:11431566); similar to anter-specific proline-rich protein (. . .
AT5G23440	-3.63	-1.31	ferredoxin-thioredoxin reductase, putative similar to ferredoxin-thioredoxin reductase, variable chain (FTR-V,. . .
AT1G62560	3.37	1.26	flavin-containing monooxygenase family protein / FMO family protein similar to flavin-containing monooxygenase. . .
AT5G07990	3.73	1.31	flavonoid 3'-monooxygenase / flavonoid 3'-hydroxylase (F3'H) / cytochrome P450 75B1 (CYP75B1) / transparent te. . .
AT5G13790	-5.01	-1.54	floral homeotic protein AGL-15 (AGL15) [At5g13790.1]
AT4G37550	-3.47	-1.28	formamidase, putative / formamide amidohydrolase, putative similar to SP—Q50228 Formamidase (EC 3.5.1.49) (For. . .
AT2G01140	13.91	2.43	fructose-bisphosphate aldolase, putative similar to plastidic aldolase NPALDP1 from Nicotiana paniculata [GI:4. . .
AT5G42270	3.57	1.27	FtsH protease, putative similar to FtsH protease GI:13183728 from [Medicago sativa] [At5g42270.1]
AT4G30570	3.77	1.49	GDP-mannose pyrophosphorylase, putative similar to GDP-mannose pyrophosphorylase [Arabidopsis thaliana] GI:359. . .
AT1G54030	6.19	1.54	GDSL-motif lipase, putative similar to myrosinase-associated proteins GI:1769968, GI:1769970, GI:1216391, GI:1. . .
AT1G29660	-3.41	-1.30	GDSL-motif lipase/hydrolase family protein low similarity to family II lipase EXL1 [Arabidopsis thaliana] GI:1. . .
AT4G25420	-3.49	-1.31	gibberellin 20-oxidase identical to GI:1109695 [At4g25420.1]
AT5G07200	-5.60	-1.63	gibberellin 20-oxidase identical to GI:1109699 [At5g07200.1]
AT1G60980	-4.79	-1.55	gibberellin 20-oxidase, putative similar to gibberellin 20-oxidase GB:CAA58295 from [Arabidopsis thaliana] [At. . .
AT3G11540	3.73	1.32	gibberellin signal transduction protein (SPINDLY) identical to spindly GB:AAC49446 (GI:1589778) [Arabidopsis t. . .
AT5G15230	-4.45	-1.63	gibberellin-regulated protein 4 (GASA4) / gibberellin-responsive protein 4 identical to SP—P46690 Gibberellin-. . .
AT1G11260	-4.22	-1.32	glucose transporter (STP1) nearly identical to glucose transporter GB:P23586 SP—P23586 from [Arabidopsis thali. . .
AT1G61800	7.48	1.60	glucose-6-phosphate/phosphate translocator, putative similar to glucose-6-phosphate/phosphate-translocator pre. . .
AT4G16590	6.75	1.69	glucosyltransferase-related low similarity to beta-(1-3)-glucosyl transferase [Bradyrhizobium japonicum] GI:36. . .
AT5G18170	-5.95	-1.47	glutamate dehydrogenase 1 (GDH1) identical to glutamate dehydrogenase 1 (GDH 1) [Arabidopsis thaliana] SWISS-P. . .
AT2G31250	-8.27	-1.83	glutamyl-tRNA reductase, putative similar to HEMA2 [SP—P49294], HEMA1 [SP—P42804] [At2g31250.1]
AT5G18600	-4.22	-1.47	glutaredoxin family protein contains glutaredoxin domain, INTERPRO:IPR002109 [At5g18600.1]
AT5G17220	5.59	1.63	glutathione S-transferase, putative [At5g17220.1]
AT1G10370	5.68	1.52	glutathione S-transferase, putative (ERD9) similar to glutathione S-transferase TSI-1 [Aegilops tauschii] gi:2. . .
AT2G30860	3.52	1.28	glutathione S-transferase, putative identical to GB:Y12295 [At2g30860.1]
AT1G59700	4.24	1.50	glutathione S-transferase, putative similar to glutathione S-transferase GB:AAF29773 GI:6856103 from [Gossypiu. . .
AT1G02930	4.45	1.56	glutathione S-transferase, putative similar to glutathione S-transferase GI:860955 from [Hyoscyamus muticus] [. . .
AT1G02920	4.06	1.54	glutathione S-transferase, putative similar to glutathione S-transferase GI:860955 from [Hyoscyamus muticus]; . . .
AT1G78360	-3.32	-1.25	glutathione S-transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya] [At1g78. . .
AT2G30870	4.74	1.37	glutathione S-transferase, putative supported by cDNA GI:443698 GB:D17673 [At2g30870.1]
AT1G16300	-3.45	-1.26	glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative / NAD-dependent glyceraldehyde-3-phosphate dehyd. . .
AT5G41080	-3.93	-1.49	glycerophosphoryl diester phosphodiesterase family protein weak similarity to SP—P37965 Glycerophosphoryl dies. . .
AT5G61660	-5.29	-1.46	glycine-rich protein [At5g61660.1]
AT4G13850	-4.38	-1.41	glycine-rich RNA-binding protein (GRP2) glycine-rich RNA binding protein 2 AtGRP2 [Arabidopsis thaliana] GI:28. . .
AT4G32375	3.46	1.33	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein similar to polygalacturon. . .
AT1G52400	5.48	1.56	glycosyl hydrolase family 1 protein / beta-glucosidase, putative (BG1) contains Pfam PF00232 : Glycosyl hydrol. . .
AT3G09260	8.72	1.75	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01. . .
AT5G25980	4.49	1.39	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01. . .
AT3G18080	-3.63	-1.29	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01. . .
AT5G49360	-5.64	-1.49	glycosyl hydrolase family 3 protein [At5g49360.1]
AT5G63800	-5.68	-1.42	glycosyl hydrolase family 35 protein similar to beta-galactosidase GI:7939621 from [Lycopersicon esculentum]; . . .
AT4G13410	4.71	1.39	glycosyl transferase family 2 protein similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from [. . .

Continued. . .

Locus	*t*-statistic	Fold change	Description
AT5G03760	3.39	1.24	glycosyl transferase family 2 protein similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from [...
AT2G18700	-4.73	-1.44	glycosyl transferase family 20 protein / trehalose-phosphatase family protein similar to trehalose-6-phosphate...
AT2G32150	-4.36	-1.46	haloacid dehalogenase-like hydrolase family protein contains InterPro accession IPR005834: Haloacid dehalogena...
AT5G59480	4.47	1.37	haloacid dehalogenase-like hydrolase family protein low similarity to SP—P53078 SSM1 protein Saccharomyces ce...
AT5G56000	-4.09	-1.64	heat shock protein 81-4 (HSP81-4) nearly identical to heat shock protein hsp81.4 [Arabidopsis thaliana] GI:190...
AT1G50460	-3.93	-1.32	hexokinase, putative similar to hexokinase 1 [Spinacia oleracea] Swiss-Prot:Q9SEK3 [At1g50460.1]
AT4G16780	-3.69	-1.33	homeobox-leucine zipper protein 4 (HAT4) / HD-ZIP protein 4 SP—Q05466—HAT4_ARATH Homeobox-leucine zipper prote...
AT3G10840	3.32	1.32	hydrolase, alpha/beta fold family protein low similarity to hydrolase [Terrabacter sp. DBF63] GI:14196240; con...
AT5G58310	4.82	1.39	hydrolase, alpha/beta fold family protein low similarity to SP—Q40708 PIR7A protein Oryza sativa, polyneurid...
AT2G26800	6.48	1.69	hydroxymethylglutaryl-CoA lyase, putative / 3-hydroxy-3-methylglutarate-CoA lyase, putative / HMG-CoA lyase, p...
AT1G22420	4.38	1.42	hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains, INTERPRO:IPR002965 [At...
AT5G09530	3.33	1.28	hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains, INTERPRO:IPR002965 [At...
AT3G32904	4.94	1.41	hypothetical protein [At3g32904.1]
AT1G25025	9.99	2.28	hypothetical protein [At1g25025.1]
AT2G22240	5.03	1.39	inositol-3-phosphate synthase isozyme 2 / myo-inositol-1-phosphate synthase 2 / MI-1-P synthase 2 / IPS 2 iden...
AT4G25260	-7.72	-1.82	invertase/pectin methylesterase inhibitor family protein low similarity to pectinesterase from Phaseolus vulga...
AT5G62360	-6.51	-1.52	invertase/pectin methylesterase inhibitor family protein similar to pectinesterase from Arabidosis thaliana SP...
AT3G16470	6.83	1.55	jacalin lectin family protein contains Pfam profile: PF01419 jacalin-like lectin domain; similar to myrosinase...
AT2G39330	4.33	1.35	jacalin lectin family protein similar to myrosinase-binding protein homolog [Arabidopsis thaliana] GI:2997767,...
AT1G80440	-7.76	-1.80	kelch repeat-containing F-box family protein similar to SP—Q9ER30 Kelch-related protein 1 (Sarcosin) Rattus n...
AT1G08630	4.24	1.36	L-allo-threonine aldolase-related similar to L-allo-threonine aldolase (EC 4.1.2.-) (L-allo-TA) (L-allo-threon...
AT5G21100	5.94	1.45	L-ascorbate oxidase, putative similar to L-ascorbate oxidase [Precursor] SP:Q40588 from [Nicotiana tabacum] [A...
AT5G06820	4.27	1.32	leucine-rich repeat transmembrane protein kinase, putative [At5g06820.1]
AT4G22880	4.18	1.39	leucoanthocyanidin dioxygenase, putative / anthocyanidin synthase, putative similar to SP—P51091 [Malus domest...
AT4G22870	5.64	1.49	leucoanthocyanidin dioxygenase, putative / anthocyanidin synthase, putative similar to SP—P51091 [Malus domest...
AT2G42690	-7.49	-1.69	lipase, putative similar to lipase [Dianthus caryophyllus] GI:4103627; contains Pfam profile PF01764: Lipase [...
AT5G59310	3.44	1.39	lipid transfer protein 4 (LTP4) identical to lipid transfer protein 4 from Arabidopsis thaliana [gi:8571923]; ...
AT2G47240	6.46	1.50	long-chain-fatty-acid–CoA ligase family protein / long-chain acyl-CoA synthetase family protein similar to GI...
AT5G63190	-3.37	-1.25	MA3 domain-containing protein low similarity to programmed cell death 4 protein [Gallus gallus] GI:12958564; c...
AT1G52180	-3.46	-1.32	major intrinsic family protein / MIP family protein contains Pfam profile: MIP PF00230 [At1g52180.1]
AT1G14950	3.98	1.30	major latex protein-related / MLP-related low similarity to major latex protein Papaver somniferum[GI:294060...
AT1G61890	4.23	1.32	MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:12231296...
AT1G05300	3.78	1.28	metal transporter, putative (ZIP5) identical to putative metal transporter ZIP5 [Arabidopsis thaliana] gi—1738...
AT4G34030	-6.96	-1.60	methylcrotonyl-CoA carboxylase beta chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 2 (MCCB) identical...
AT5G46800	3.55	1.26	mitochondrial carnitine/acyl carrier, putative / a bout de souffle (BOU) / CAC-like protein identical to SP—Q9...
AT2G28900	-3.71	-1.38	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein contains Pfam PF02466...
AT2G35800	-3.95	-1.28	mitochondrial substrate carrier family protein contains INTERPRO:IPR001993 Mitochondrial substrate carrier fam...
AT3G14720	3.73	1.34	mitogen-activated protein kinase, putative / MAPK, putative (MPK19) identical to mitogen-activated protein kin...
AT1G18100	3.69	1.35	mother of FT and TF1 protein (MFT) identical to SP—Q9XFK7 MOTHER of FT and TF1 protein Arabidopsis thaliana;...
AT5G47240	-3.46	-1.32	MutT/nudix family protein similar to SP—P53370 Nucleoside diphosphate-linked moiety X motif 6 Homo sapiens; ...
AT5G61420	3.48	1.31	myb family transcription factor (MYB28) contains Pfam profile: PF00249 myb-like DNA-binding domain [At5g61420....
AT1G56650	3.54	1.42	myb family transcription factor (MYB75) contains Pfam profile: PF00249 myb-like DNA-binding domain; identical ...
AT1G01060	4.02	1.29	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA ...
AT3G25833	8.15	1.91	myrcene/ocimene synthase, putative similar to GI:9957293; contains Pfam profile: PF01397 terpene synthase fami...
AT1G54020	4.51	1.65	myrosinase-associated protein, putative strong similarity to myrosinase-associated proteins GI:1769968, GI:176...
AT2G24270	4.86	1.35	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase, putative similar to NADP-dependent glyceraldehyde-3-p...
AT3G51240	4.45	1.36	naringenin 3-dioxygenase / flavanone 3-hydroxylase (F3H) identical to GI:3790548 [At3g51240.1]

Continued...

Locus	*t*-statistic	Fold change	Description
AT5G11790	3.93	1.34	Ndr family protein similar to SP—O23969 Pollen specific protein SF21 Helianthus annuus; contains Pfam profil...
AT1G45218	3.41	1.34	O04315 (O04315) Jasmonate inducible protein isolog (Jasmonate inducible protein; myrosinase binding protein-li...
AT1G05130	4.86	1.60	O23054 (O23054) YUP8H12.26 protein, complete [TC265008]
AT3G06550	5.34	1.52	O-acetyltransferase-related similar to O-acetyltransferase (GI:17063556) [Cryptococcus neoformans var. neoform...
AT5G59540	4.54	1.58	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to desacetoxyvindoline-4-hydroxylase [Catharanthus...
AT5G63620	-5.76	-1.48	oxidoreductase, zinc-binding dehydrogenase family protein contains PFAM zinc-binding dehydrogenase domain PF00...
AT1G76450	7.19	1.80	oxygen-evolving complex-related SP:Q9S720; contains a PsbP domain [At1g76450.1]
AT5G03700	4.63	1.33	PAN domain-containing protein contains Pfam profile: PF00024 PAN domain [At5g03700.1]
AT4G25780	-3.71	-1.37	pathogenesis-related protein, putative similar to gene PR-1 protein - Medicago truncatula, SP—Q40374; contains...
AT3G01420	6.14	1.55	pathogen-responsive alpha-dioxygenase, putative similar to pathogen-inducible alpha-dioxygenase [Nicotiana att...
AT4G24780	-5.02	-1.51	pectate lyase family protein similar to pectate lyase GP:14289169 from [Salix gilgiana] [At4g24780.1]
AT5G45280	-4.71	-1.39	pectinacetylesterase, putative similar to pectinacetylesterase precursor GI:1431629 from [Vigna radiata] [At5g...
AT3G27110	4.06	1.40	peptidase M48 family protein contains Pfam domain, PF01435: Peptidase family M48 [At3g27110.1]
AT2G37040	4.25	1.33	phenylalanine ammonia-lyase 1 (PAL1) nearly identical to SP—P35510 [At2g37040.1]
AT3G53260	4.16	1.36	phenylalanine ammonia-lyase 2 (PAL2) nearly identical to SP—P45724 [At3g53260.1]
AT4G29710	5.86	1.44	phosphodiesterase/nucleotide pyrophosphatase-related weak similarity to SP—Q13822 Ectonucleotide pyrophosphata...
AT1G50280	-3.39	-1.24	phototropic-responsive NPH3 family protein contains NPH3 family domain, Pfam:PF03000 [At1g50280.1]
AT1G01620	-5.37	-1.40	plasma membrane intrinsic protein 1C (PIP1C) / aquaporin PIP1.3 (PIP1.3) / transmembrane protein B (TMPB) iden...
AT3G26070	-4.35	-1.33	plastid-lipid associated protein PAP / fibrillin family protein contains Pfam profile PF04755: PAP_fibrillin [...
AT4G04020	6.12	1.60	plastid-lipid associated protein PAP, putative / fibrillin, putative strong similarity to plastid-lipid associ...
AT4G22240	5.02	1.47	plastid-lipid associated protein PAP, putative similar to plastid-lipid associated proteins PAP2 [Brassica rap...
AT4G36850	-4.96	-1.39	PQ-loop repeat family protein / transmembrane family protein similar to SP—Q10482 Seven transmembrane protein ...
AT3G30775	-4.73	-1.41	proline oxidase, mitochondrial / osmotic stress-responsive proline dehydrogenase (POX) (PRO1) (ERD5) nearly id...
AT1G20380	5.07	1.45	prolyl oligopeptidase, putative / prolyl endopeptidase, putative / post-proline cleaving enzyme, putative simi...
AT1G51170	-4.65	-2.16	protein kinase family protein [At1g51170.1]
AT1G77720	-3.41	-1.25	protein kinase family protein contains protein kinase domain, Pfam:PF00069 [At1g77720.1]
AT2G21480	3.62	1.27	protein kinase family protein contains protein kinase domain, Pfam:PF00069 [At2g21480.1]
AT3G04910	-5.52	-1.48	protein kinase family protein contains protein kinase domain, Pfam:PF00069 [At3g04910.1]
AT5G59010	-6.07	-1.51	protein kinase-related low similarity to serine/threonine/tyrosine-specific protein kinase APK1, Arabidopsis t...
AT3G05640	-4.29	-1.34	protein phosphatase 2C, putative / PP2C, putative similar to protein phosphatase-2C GB:AAC36699 from [Mesembry...
AT3G10940	-4.10	-1.44	protein phosphatase-related similar to protein phosphatase PTPKIS1 protein (GI:11595504) [Arabidopsis thaliana...
AT1G68570	3.33	1.24	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family [At1g68...
AT5G13400	4.37	1.39	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family [At5g13...
AT1G65260	3.56	1.28	PspA/IM30 family protein contains Pfam PF04012: PspA/IM30 family profile; similar to Membrane-associated 30 kD...
AT1G25230	-4.12	-1.41	purple acid phosphatase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesterase; simila...
AT5G52920	-5.42	-1.42	pyruvate kinase, putative similar to pyruvate kinase isozyme G, chloroplast precursor [Nicotiana tabacum] SWIS...
AT4G15530	3.79	1.29	pyruvate phosphate dikinase family protein contains Pfam profiles: PF01326 pyruvate phosphate dikinase, PEP/py...
AT1G03495	6.20	1.52	Q9LR73 (Q9LR73) F21B7.12, complete [TC255286]
AT4G27270	-3.37	-1.27	quinone reductase family protein similar to 1,4-benzoquinone reductase [Phanerochaete chrysosporium][GI:445499...
AT4G35750	-5.93	-1.46	Rho-GTPase-activating protein-related contains weak similarity to Rho-GTPase-activating protein 1 (GTPase-acti...
AT3G44870	4.00	1.35	S-adenosyl-L-methionine:carboxyl methyltransferase family protein similar to defense-related protein cjs1 [Bra...
AT1G30690	-3.36	-1.28	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein contains Pfam PF00650 : CRAL/...
AT4G35770	-4.00	-1.71	senescence-associated protein (SEN1) identical to senescence-associated protein GI:1046270 from [Arabidopsis t...
AT5G20700	5.57	1.45	senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:22331931) [Arabidops...
AT2G23000	3.88	1.54	serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza s...
AT5G23210	-3.36	-1.29	serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II chains A and B (SP:P08819) (E...
AT4G30810	3.34	1.25	serine carboxypeptidase S10 family protein similar to serine-type carboxypeptidase (SP:P55748) [Hordeum vulgar...

Continued...

Locus	*t*-statistic	Fold change	Description
AT3G13110	5.25	1.39	serine O-acetyltransferase (SAT-1) identical to serine acetyltransferase (Sat-1) GI:1184048 [Arabidopsis thali…
AT1G55920	4.83	1.37	serine O-acetyltransferase, putative identical to GI:608677 from [Arabidopsis thaliana] [At1g55920.1]
AT3G59960	10.49	2.35	SET domain-containing protein low similarity to huntingtin interacting protein 1 [Homo sapiens] GI:12697196; c…
AT1G60270	6.05	1.48	Similar to beta glucosidase (bg1A) gb—X94986 from Manihot esculenta. [NP041544]
AT1G78510	4.32	1.33	solanesyl diphosphate synthase (SPS) identical to solanesyl diphosphate synthase [Arabidopsis thaliana] GI:199…
AT1G17100	6.60	1.56	SOUL heme-binding family protein similar to SOUL protein [Mus musculus] GI:4886906; contains Pfam profile PF04…
AT1G63010	3.63	1.26	SPX (SYG1/Pho81/XPR1) domain-containing protein contains Pfam profile PF03105: SPX domain [At1g63010.1]
AT4G37760	3.82	1.33	squalene monooxygenase, putative / squalene epoxidase, putative similar to SP—O65404 (SE 1,1), SP—O65402 (SE 1…
AT4G12400	-8.16	-1.66	stress-inducible protein, putative similar to sti (stress inducible protein) [Glycine max] GI:872116; contains…
AT4G37220	-5.94	-1.66	stress-responsive protein, putative similar to cold acclimation WCOR413-like protein gamma form [Hordeum vulga…
AT5G27360	4.14	1.31	sugar-porter family protein 2 (SFP2) identical to sugar-porter family protein 2 [Arabidopsis thaliana] GI:1458…
AT4G25100	6.26	1.84	superoxide dismutase [Fe], chloroplast (SODB) / iron superoxide dismutase (FSD1) identical to Fe-superoxide di…
AT1G05350	-4.10	-1.39	thiF family protein low similarity to SP—P30138 Adenylyltransferase thiF (EC 2.7.7.-) Escherichia coli; cont…
AT1G10200	-3.63	-1.39	transcription factor LIM, putative strong similarity to transcription factor Ntlim1 [Nicotiana tabacum] GI:568…
AT4G29830	3.64	1.26	transducin family protein / WD-40 repeat family protein contains 7 WD-40 repeats (PF00400); G protein beta sub…
AT3G03480	3.86	1.35	transferase family protein similar to hypersensitivity-related gene GB:CAA64636 [Nicotiana tabacum]; contains …
AT1G17220	5.51	1.51	translation initiation factor IF-2, chloroplast, putative similar to SP—P57997—IF2C_PHAVU Translation initiati…
AT1G73325	6.35	2.00	trypsin and protease inhibitor family protein / Kunitz family protein similar to Dr4 [Arabidopsis thaliana] GI…
AT1G72290	3.92	1.34	trypsin and protease inhibitor family protein / Kunitz family protein similar to water-soluble chlorophyll pro…
AT4G02610	-4.70	-1.38	tryptophan synthase, alpha subunit, putative similar to A. thaliana tryptophan synthase alpha chain (EC 4.2.1.…
AT4G27070	3.53	1.31	tryptophan synthase, beta subunit 2 (TSB2) identical to SP—25269 [At4g27070.1]
AT4G29690	5.29	1.45	type I phosphodiesterase/nucleotide pyrophosphatase family protein similar to SP—P22413 Ectonucleotide pyropho…
AT4G29700	3.64	1.30	type I phosphodiesterase/nucleotide pyrophosphatase family protein similar to SP—P22413 Ectonucleotide pyropho…
AT4G28680	6.47	1.72	tyrosine decarboxylase, putative similar to SP—P54768 Tyrosine/DOPA decarboxylase 1 [Includes: DOPA decarboxyl…
AT1G24100	4.96	1.37	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and U…
AT5G17050	3.37	1.26	UDP-glucoronosyl/UDP-glucosyl transferase family protein similar to UDP glucose:flavonoid 3-o-glucosyltransfer…
AT1G12780	-3.92	-1.31	UDP-glucose 4-epimerase / UDP-galactose 4-epimerase / Galactowaldenase identical to SP—Q42605 [GB:CAA90941] fr…
AT1G63180	-4.61	-1.38	UDP-glucose 4-epimerase, putative / UDP-galactose 4-epimerase, putative / Galactowaldenase, putative strong si…
AT3G62550	-3.89	-1.69	universal stress protein (USP) family protein similar to ER6 protein [Lycopersicon esculentum] GI:5669654; con…
AT5G17310	3.42	1.25	UTP–glucose-1-phosphate uridylyltransferase, putative / UDP-glucose pyrophosphorylase, putative / UGPase, put…
AT1G64200	-4.40	-1.33	vacuolar ATP synthase subunit E, putative / V-ATPase E subunit, putative / vacuolar proton pump E subunit, put…
AT1G62480	-5.70	-1.47	vacuolar calcium-binding protein-related contains weak similarity to vacuolar calcium binding protein [Raphanu…
AT1G75380	-3.51	-1.25	wound-responsive protein-related similar to wound inducive gene GI:8096273 from [Nicotiana tabacum] [At1g75380…
AT2G06850	-5.21	-1.41	xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (EXT) (EXG…
AT1G68190	-4.10	-1.41	zinc finger (B-box type) family protein [At1g68190.1]
AT1G27730	3.98	1.32	zinc finger (C2H2 type) family protein (ZAT10) / salt-tolerance zinc finger protein (STZ) identical to salt-to…
AT5G22920	-11.53	-2.13	zinc finger (C3HC4-type RING finger) family protein contains Pfam profiles:PF05495 CHY zinc finger, PF00097 zi…
AT1G21570	-6.14	-1.79	zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and s…
AT3G55980	3.89	1.32	zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and s…
AT5G58620	-4.11	-1.32	zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and s…
AT2G32270	3.76	1.31	zinc transporter (ZIP3) identical to zinc transporter [Arabidopsis thaliana] gi—3252870—gb—AAC24199; member of…

Table C.4: Significant expression changes in roots of 6 day-old trAcdS-*rolD* seedlings versus non-transformed seedlings, $p < 0.01$.

Locus	*t*-statistic	Fold change	Description
AT1G20200	6.30	1.21	26S proteasome regulatory subunit S3, putative (RPN3) similar to SP:Q06364 from [Daucus carota] [At1g20200.1]
AT5G55070	-6.31	-1.26	2-oxoacid dehydrogenase family protein similar to SP—Q01205 Dihydrolipoamide succinyltransferase component of . . .
AT5G59530	-8.56	-1.23	2-oxoglutarate-dependent dioxygenase, putative similar to 2A6 (GI:599622) and tomato ethylene synthesis regula. . .
AT1G52820	-3.85	-1.25	2-oxoglutarate-dependent dioxygenase, putative similar to AOP1 [Arabidopsis lyrata][GI:16118889]; contains Pfa. . .
AT1G07770	-12.53	-1.34	40S ribosomal protein S15A (RPS15aA) identical to GB:AAA61608 from [Arabidopsis thaliana] (Plant Physiol. 106 . . .
AT1G51680	-3.87	-1.10	4-coumarate–CoA ligase 1 / 4-coumaroyl-CoA synthase 1 (4CL1) identical to SP—Q42524 4-coumarate–CoA ligase 1. . .
AT3G14990	7.13	1.32	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative supporting cDNA gi—11908017—g. . .
AT2G44050	-4.36	-1.13	6,7-dimethyl-8-ribityllumazine synthase / DMRL synthase / lumazine synthase / riboflavin synthase identical to. . .
AT5G41670	-4.48	-1.14	6-phosphogluconate dehydrogenase family protein contains Pfam profiles: PF00393 6-phosphogluconate dehydrogena. . .
AT3G28510	7.29	1.19	AAA-type ATPase family protein contains Pfam profile: PF00004 ATPase family [At3g28510.1]
AT4G34970	4.13	1.13	actin-depolymerizing factor, putative similar to SP—Q9ZNT3 Actin-depolymerizing factor 5 (ADF-5) (AtADF5) Ara. . .
AT4G25590	-7.04	-1.18	actin-depolymerizing factor, putative strong similarity to pollen specific actin-depolymerizing factor 2 [Nico. . .
AT5G16230	-4.30	-1.10	acyl-[acyl-carrier-protein] desaturase, putative / stearoyl-ACP desaturase, putative similar to Acyl-[acyl-car. . .
AT1G11930	-4.41	-1.10	alanine racemase family protein contains Pfam domain, PF01168: Alanine racemase, N-terminal domain [At1g11930.. . .
AT5G20960	-4.55	-1.12	aldehyde oxidase 1 (AAO1) identical to aldehyde oxidase AAO1 from Arabidopsis thaliana [gi:3172023] isoform co. . .
AT1G60710	4.62	1.13	aldo/keto reductase family protein contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family [. . .
AT1G55740	3.95	1.12	alkaline alpha galactosidase, putative similar to alkaline alpha galactosidase I [Cucumis melo] GI:29838629; c. . .
AT3G06050	-5.15	-1.13	alkyl hydroperoxide reductase/thiol specific antioxidant (AhpC/TSA)/mal allergen family protein identical to S. . .
AT5G57625	-4.07	-1.32	allergen V5/Tpx-1-related family protein low similarity to SP—Q40374 Pathogenesis-related protein PR-1 precurs. . .
AT1G11860	-3.82	-1.15	aminomethyltransferase, putative similar to aminomethyltransferase, mitochondrial precursor SP:O49849 from [Fl. . .
AT3G48990	-5.35	-1.15	AMP-dependent synthetase and ligase family protein similar to peroxisomal-coenzyme A synthetase (FAT2) [gi:586. . .
AT5G08690	-5.27	-1.18	ATP synthase beta chain 2, mitochondrial identical to SP—P83484 ATP synthase beta chain 2, mitochondrial precu. . .
AT5G13450	-5.10	-1.13	ATP synthase delta chain, mitochondrial, putative / H(+)-transporting two-sector ATPase, delta (OSCP) subunit,. . .
AT3G60330	-4.70	-1.16	ATPase, plasma membrane-type, putative / proton pump, putative similar to P-type H(+)-transporting ATPase from. . .
AT5G19140	-4.93	-1.14	auxin/aluminum-responsive protein, putative strong similarity to auxin down-regulated protein ARG10 [Vigna rad. . .
AT4G02980	3.72	1.11	auxin-binding protein 1 (ABP1) identical to Auxin-binding protein 1 precursor (ABP) (Swiss-Prot:P33487) [Arabi. . .
AT1G48670	4.29	1.10	auxin-responsive GH3 family protein similar to auxin-responsive GH3 product [Glycine max] GI:18591; contains P. . .
AT2G22670	-6.73	-1.18	auxin-responsive protein / indoleacetic acid-induced protein 8 (IAA8) identical to SP—Q38826 Auxin-responsive . . .
AT1G33870	-6.02	-1.26	avirulence-responsive protein, putative / avirulence induced gene protein, putative / AIG protein, putative si. . .
AT5G51570	-4.90	-1.14	band 7 family protein similar to hypersensitive-induced response protein [Zea mays] GI:7716468; contains Pfam . . .
AT3G12500	8.63	1.37	basic endochitinase identical to basic endochitinase precursor SP:P19171 from [Arabidopsis thaliana] [At3g1250. . .
AT2G22770	5.16	1.18	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domai. . .
AT2G46510	5.45	1.13	basic helix-loop-helix (bHLH) family protein contains Pfam profile: PF00010 helix-loop-helix DNA-binding domai. . .
AT1G22650	-4.40	-1.11	beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative s. . .
AT1G35580	3.85	1.11	beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative s. . .
AT1G12240	4.61	1.12	beta-fructosidase (BFRUCT4) / beta-fructofuranosidase / invertase, vacuolar identical to beta-fructosidase GI:. . .
AT1G45130	-4.40	-1.17	beta-galactosidase, putative / lactase, putative similar to beta-galactosidase [Lycopersicon esculentum] GI:79. . .
AT5G39670	5.49	1.36	calcium-binding EF hand family protein contains INTERPRO:IPR002048 calcium-binding EF-hand domain [At5g39670.1. . .
AT1G74740	-4.00	-1.10	calcium-dependent protein kinase, putative / CDPK, putative similar to calcium-dependent protein kinase [Arabi. . .
AT2G27030	-7.84	-1.22	calmodulin-2/3/5 (CAM5) (TCH1) identical to calmodulin GI:474183 from [Arabidopsis thaliana], SP—P25069 Calmod. . .
AT3G51920	-6.45	-1.27	calmodulin-9 (CAM9) identical to calmodulin 9 GI:5825602 from [Arabidopsis thaliana]; contains Pfam profile PF. . .
AT1G76640	7.01	1.18	calmodulin-related protein, putative similar to regulator of gene silencing calmodulin-related protein GI:1296. . .
AT2G34180	3.92	1.10	CBL-interacting protein kinase 13 (CIPK13) identical to CBL-interacting protein kinase 13 [Arabidopsis thalian. . .

Continued. . .

Locus	*t*-statistic	Fold change	Description
AT2G26980	-3.72	-1.13	CBL-interacting protein kinase 3 (CIPK3) identical to CBL-interacting protein kinase 3 [Arabidopsis thaliana] . . .
AT5G22250	9.11	1.23	CCR4-NOT transcription complex protein, putative similar to SWISS-PROT:Q60809 CCR4-NOT transcription complex, . . .
AT5G17420	-4.00	-1.10	cellulose synthase, catalytic subunit (IRX3) identical to gi:5230423 [At5g17420.1]
AT2G21770	-8.45	-1.38	cellulose synthase, catalytic subunit, putative similar to gi:2827141 cellulose synthase catalytic subunit, Ar. . .
AT2G43590	4.26	1.18	chitinase, putative similar to basic endochitinase CHB4 precursor SP:Q06209 from [Brassica napus] [At2g43590.1. . .
AT4G01700	-5.21	-1.13	chitinase, putative similar to peanut type II chitinase GI:1237025 from [Arachis hypogaea] [At4g01700.1]
AT2G34420	5.18	1.13	chlorophyll A-B binding protein / LHCII type I (LHB1B2) identical to GB:X64460 photosystem II type I chlorophy. . .
AT3G60100	-4.82	-1.15	citrate synthase, mitochondrial, putative strong similarity to SP—Q43175 Citrate synthase, mitochondrial precu. . .
AT1G67800	4.89	1.12	copine-related low similarity to SP—Q99829 Copine I Homo sapiens [At1g67800.1]
AT1G66240	6.17	1.26	copper homeostasis factor, putative / copper chaperone, putative (CCH) similar to gi:3168840 contains Pfam pro. . .
AT5G45990	-4.61	-1.13	crooked neck protein, putative / cell cycle protein, putative similar to Swiss-Prot:P17886 crooked neck protei. . .
AT1G30820	5.10	1.13	CTP synthase, putative / UTP–ammonia ligase, putative similar to SP—P17812 CTP synthase (EC 6.3.4.2) (UTP–am. . .
AT5G05110	4.22	1.15	cysteine protease inhibitor, putative / cystatin, putative similar to cysteine proteinase inhibitor [Glycine m. . .
AT5G43060	-3.91	-1.15	cysteine proteinase, putative / thiol protease, putative similar to cysteine proteinase RD21A precursor (thiol. . .
AT2G07727	5.84	1.15	cytochrome b (MTCYB) (COB) (CYTB) contains Pfam profile PF00033: Cytochrome b(N-terminal)/b6/petB; ontains Pfa. . .
AT5G40810	-7.30	-1.23	cytochrome c1, putative cytochrome c1, heme protein, mitochondrial precursor (Clone PC13III) [Solanum tuberosu. . .
AT4G36220	-4.79	-1.13	cytochrome P450 84A1 (CYP84A1) / ferulate-5-hydroxylase (FAH1) identical to Cytochrome P450 84A1 (Ferulate-5-h. . .
AT2G42250	-17.11	-1.48	cytochrome P450 family protein similar to cytochrome P450 93A1 (SP:Q42798) [Glycine max] [At2g42250.1]
AT5G45340	4.11	1.15	cytochrome P450 family protein similar to SP—Q42569—C901_ARATH Cytochrome P450 90A1 (SP:Q42569) [Arabidopsis t. . .
AT5G06905	-4.83	-1.15	cytochrome P450 family protein similar to SP—Q42798—C931_SOYBN Cytochrome P450 93A1 (EC 1.14.-.-) Glycine max. . .
AT2G22330	-6.75	-1.19	cytochrome P450, putative similar to cytochrome P450 79B2 (SP:O81346) [Arabidopsis thaliana] [At2g22330.1]
AT2G17740	-4.31	-1.11	DC1 domain-containing protein [At2g17740.1]
AT1G59990	-3.78	-1.46	DEAD/DEAH box helicase, putative (RH22) similar to RNA helicase GI:3776015 from [Arabidopsis thaliana]; contai. . .
AT2G45750	6.26	1.15	dehydration-responsive family protein similar to early-responsive to dehydration stress ERD3 protein [Arabidop. . .
AT3G25860	6.95	1.25	dihydrolipoamide S-acetyltransferase (LTA2) identical to dihydrolipoamide S-acetyltransferase (LTA2) [Arabidop. . .
AT2G34930	10.79	1.30	disease resistance family protein contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; simil. . .
AT1G64160	4.12	1.21	disease resistance-responsive family protein / dirigent family protein similar to dirigent protein GB:AAF25365. . .
AT2G28670	-5.18	-1.25	disease resistance-responsive family protein / fibroin-related contains similarity to silk fibroin heavy chain. . .
AT4G13580	-6.35	-1.16	disease resistance-responsive family protein contains similarity to pathogenesis-related protein [Pisum sativu. . .
AT3G55230	-7.34	-1.26	disease resistance-responsive family protein low similarity to disease resistance response protein 206-d [Pisu. . .
AT1G53280	4.75	1.14	DJ-1 family protein similar to DJ-1 protein [Homo sapiens] GI:1780755; similar to DJ-1 beta (GI:18642508) [Dro. . .
AT5G22060	-4.39	-1.12	DNAJ heat shock protein, putative strong similarity to SP—O60884 DnaJ homolog subfamily A member 2 (Dnj3) Homo. . .
AT1G28330	-5.94	-1.17	dormancy-associated protein, putative (DRM1) identical to dormancy-associated protein [Arabidopsis thaliana] G. . .
AT5G44610	-6.81	-1.19	DREPP plasma membrane polypeptide-related contains Pfam profile: PF05558 DREPP plasma membrane polypeptide [At. . .
AT2G18110	-3.72	-1.14	elongation factor 1-beta, putative / EF-1-beta, putative nearly identical to eEF-1beta [Arabidopsis thaliana] . . .
AT4G02340	5.23	1.21	epoxide hydrolase, putative similar to epoxide hydrolases from Glycine max GI:2764806, Solanum tuberosum GI:40. . .
AT5G07580	-5.65	-1.17	ethylene-responsive element-binding family protein contains similarity to ethylene responsive element binding . . .
AT5G61600	5.23	1.16	ethylene-responsive element-binding family protein contains similarity to ethylene responsive element binding . . .
AT2G44840	4.69	1.12	ethylene-responsive element-binding protein, putative [At2g44840.1]
AT5G54940	-3.82	-1.19	eukaryotic translation initiation factor SUI1, putative similar to SP—P32911 Protein translation factor SUI1 . . .
AT2G39380	3.91	1.30	exocyst subunit EXO70 family protein contains Pfam domain PF03081: Exo70 exocyst complex subunit; [At2g39380.1. . .
AT5G59730	-4.70	-1.14	exocyst subunit EXO70 family protein leucine zipper-containing protein, Lycopersicon esculentum, PIR:S21495 co. . .
AT3G42180	9.76	1.25	exostosin family protein contains Pfam profile: PF03016 Exostosin family [At3g42180.1]
AT4G38040	-4.15	-1.14	exostosin family protein contains Pfam profile: PF03016 Exostosin family [At4g38040.1]
AT5G20260	10.30	1.30	exostosin family protein contains Pfam profile: PF03016 Exostosin family [At5g20260.1]
AT1G62980	-4.49	-1.14	expansin, putative (EXP18) identical to SWISS-PROT:Q9LQ07 alpha-expansin 18 precursor (At-EXP18)[Arabidopsis t. . .
AT1G12560	-6.15	-1.18	expansin, putative (EXP7) similar to expansin GI:2828241 from [Brassica napus]; alpha-expansin gene family, PM. . .

Continued. . .

Locus	*t*-statistic	Fold change	Description
AT4G34260	-4.83	-1.14	expressed protein [At4g34260.1]
AT5G02090	-4.29	-1.12	expressed protein [At5g02090.1]
AT1G17710	5.03	1.12	expressed protein [At1g17710.1]
AT1G23710	4.04	1.12	expressed protein [At1g23710.1]
AT1G32920	3.83	1.31	expressed protein [At1g32920.1]
AT1G71780	-4.07	-1.14	expressed protein [At1g71780.1]
AT1G72110	-3.69	-1.10	expressed protein [At1g72110.1]
AT1G74950	3.81	1.26	expressed protein [At1g74950.1]
AT2G20360	-5.38	-1.13	expressed protein [At2g20360.1]
AT2G26530	5.24	1.16	expressed protein [At2g26530.1]
AT2G34070	-4.49	-1.11	expressed protein [At2g34070.1]
AT3G12570	11.74	1.38	expressed protein [At3g12570.1]
AT3G29180	-4.05	-1.14	expressed protein [At3g29180.1]
AT3G53320	5.40	1.19	expressed protein [At3g53320.1]
AT4G36500	4.15	1.16	expressed protein [At4g36500.1]
AT4G40070	-6.89	-1.22	expressed protein [At4g40070.1]
AT5G01970	-3.98	-1.13	expressed protein [At5g01970.1]
AT5G17350	7.06	1.28	expressed protein [At5g17350.1]
AT3G02910	9.82	1.36	expressed protein contains Pfam domain PF03674: Uncharacterised protein family (UPF0131) [At3g02910.1]
AT2G41640	7.57	1.28	expressed protein contains Pfam domain, PF04577: Protein of unknown function (DUF563) [At2g41640.1]
AT5G66650	4.31	1.10	expressed protein contains Pfam domain, PF04678: Protein of unknown function, DUF607 [At5g66650.1]
AT1G25520	-5.01	-1.13	expressed protein contains Pfam profile PF01169: Uncharacterized protein family UPF0016 [At1g25520.1]
AT1G68650	-4.00	-1.10	expressed protein contains Pfam profile PF01169: Uncharacterized protein family UPF0016 [At1g68650.1]
AT5G26734	-3.73	-1.10	expressed protein contains Pfam profile PF03619: Domain of unknown function [At5g26740.1]
AT5G44670	-4.47	-1.12	expressed protein contains Pfam:PF01697 Domain of unknown function [At5g44670.1]
AT1G67350	-7.66	-1.21	expressed protein contains similarity to MHC class II antigen GI:9502037 from [Aotus nancymaae] [At1g67350.1]
AT1G80110	4.06	1.10	expressed protein contains similarity to SKP1 interacting partner 3 [Arabidopsis thaliana] GI:10716951 [At1g80. . .
AT5G11680	-3.75	-1.09	expressed protein predicted proteins, Arabidopsis thaliana [At5g11680.1]
AT3G15450	6.06	1.18	expressed protein similar to auxin down-regulated protein ARG10 [Vigna radiata] GI:2970051, wali7 (aluminum-in. . .
AT4G26260	13.18	1.47	expressed protein similar to myo-inositol oxygenase [Sus scrofa] gi—17432544—gb—AAL39076 [At4g26260.1]
AT3G18470	-3.71	-1.10	expressed protein similar to PGPS/D12 [Petunia x hybrida] GI:4105794; contains Pfam profile PF04749: Protein o. . .
AT5G53160	-5.15	-1.18	expressed protein similar to unknown protein (pir——T02893) [At5g53160.1]
AT2G24550	4.65	1.12	expressed protein weak similarity to MTD1 [Medicago truncatula] GI:9294810 [At2g24550.1]
AT1G30700	7.05	1.21	FAD-binding domain-containing protein similar to SP—P30986 reticuline oxidase precursor (Berberine-bridge-form. . .
AT4G20800	-3.76	-1.11	FAD-binding domain-containing protein similar to SP—P93479 Reticuline oxidase precursor (EC 1.5.3.9) (Berberin. . .
AT5G18680	-4.26	-1.12	F-box family protein / tubby family protein similar to phosphodiesterase (GI:467578) [Mus musculus]; similar t. . .
AT5G01600	-4.00	-1.13	ferritin 1 (FER1) identical to ferritin [Arabidopsis thaliana] GI:1246401, GI:8163920 [At5g01600.1]
AT5G63590	5.97	1.18	flavonol synthase, putative similar to SP—Q96330 Flavonol synthase 1 (EC 1.14.11.-) (FLS 1) Arabidopsis thali. . .
AT3G14225	-3.76	-1.10	GDSL-motif lipase/hydrolase family protein contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like . . .
AT5G55050	-5.15	-1.23	GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EX. . .
AT1G18970	-4.99	-1.12	germin-like protein (GLP1) (GLP4) identical to germin-like protein subfamily T member 1 [SP—P92995] [At1g18970. . .
AT5G39150	4.72	1.29	germin-like protein, putative similar to germin -like protein GLP6, Arabidopsis thaliana, EMBL:ATU75194 [SP—P9. . .
AT5G38930	-3.99	-1.10	germin-like protein, putative similar to germin-like portein GLP9 [SP—Q9LEA7]; contains PS00725 Germin family . . .
AT5G39180	6.71	1.26	germin-like protein, putative similar to germin-like protein (GLP6) - Arabidopsis thaliana, EMBL:U75194 [SP—P9. . .
AT3G05950	7.68	1.40	germin-like protein, putative similar to germin-like protein GLP6 [SP—P92997]; contains Pfam profile: PF01072 . . .
AT5G38960	-7.15	-1.38	germin-like protein, putative similar to germin-like protein subfamily 1 member 8 [SP—Q9LEA7]; contains PS0072. . .
AT5G38910	-3.99	-1.11	germin-like protein, putative similar to SP—Q9LEA7; contains PS00725 germin family signature [At5g38910.1]

Continued. . .

Locus	*t*-statistic	Fold change	Description
AT5G17630	-3.88	-1.10	glucose-6-phosphate/phosphate translocator, putative similar to glucose-6-phosphate/phosphate-translocator pre...
AT5G07440	4.43	1.11	glutamate dehydrogenase 2 (GDH2) identical to glutamate dehydrogenase 2 (GDH 2) [Arabidopsis thaliana] SWISS-P...
AT4G30550	4.38	1.11	glutamine amidotransferase class-I domain-containing protein similar to defense-related protein [Brassica cari...
AT5G35630	-4.18	-1.15	glutamine synthetase (GS2) identical to glutamine synthetase, chloroplast precursor (glutamate– ammonia ligas...
AT5G16570	-5.76	-1.16	glutamine synthetase, putative similar to glutamine synthetase, cytosolic isozyme (glutamate– ammonia ligase)...
AT1G28480	6.79	1.22	glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase) [At1g28480.1]
AT2G02930	-5.41	-1.14	glutathione S-transferase, putative [At2g02930.1]
AT1G17170	4.61	1.13	glutathione S-transferase, putative One of three repeated putative glutathione transferases. 72% identical to ...
AT1G78360	-7.49	-1.21	glutathione S-transferase, putative similar to glutathione transferase GI:2853219 from [Carica papaya] [At1g78...
AT5G17650	5.73	1.21	glycine/proline-rich protein glycine/proline-rich protein GPRP - Arabidopsis thaliana, EMBL:X84315 [At5g17650....
AT2G43610	4.43	1.10	glycoside hydrolase family 19 protein similar to chitinase GI:17799 from [Brassica napus]; contains Pfam profi...
AT1G47600	-5.10	-1.24	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01...
AT4G19760	23.05	3.35	glycosyl hydrolase family 18 protein similar to chitinase, class V GI:505267 from [Nicotiana tabacum] [At4g197...
AT4G19750	15.69	1.43	glycosyl hydrolase family 18 protein similar to chitinase, class V GI:899342 from [Nicotiana tabacum] [At4g197...
AT4G19810	3.72	1.13	glycosyl hydrolase family 18 protein similar to chitinase/lysozyme GI:467689 from [Nicotiana tabacum] [At4g198...
AT1G78060	4.04	1.15	glycosyl hydrolase family 3 protein similar to xylosidase GI:2102655 from [Aspergillus niger] [At1g78060.1]
AT3G26720	-3.87	-1.11	glycosyl hydrolase family 38 protein similar to lysosomal alpha-mannosidase GI:3522867 from [Homo sapiens] [At...
AT3G28180	6.24	1.15	glycosyl transferase family 2 protein similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from [...
AT1G19900	-4.55	-1.13	glyoxal oxidase-related contains similarity to glyoxal oxidase precursor [Phanerochaete chrysosporium] gi—1050...
AT2G27200	-4.15	-1.11	GTP-binding family protein contains Pfam domain, PF01926: GTPase of unknown function [At2g27200.1]
AT4G02080	-5.41	-1.17	GTP-binding protein (SAR1A) identical to SP:O04834 GTP-binding protein SAR1A. [Arabidopsis thaliana] [At4g0208...
AT3G28715	-3.84	-1.10	H+-transporting two-sector ATPase, putative similar to SP—P54641 Vacuolar ATP synthase subunit d (EC 3.6.3.14)...
AT4G01410	-4.64	-1.12	harpin-induced family protein / HIN1 family protein / harpin-responsive family protein similar to harpin-induc...
AT5G56000	-5.31	-1.41	heat shock protein 81-4 (HSP81-4) nearly identical to heat shock protein hsp81.4 [Arabidopsis thaliana] GI:190...
AT5G03380	4.82	1.12	heavy-metal-associated domain-containing protein similar to farnesylated protein ATFP2 [GI:4097545]; contains ...
AT2G19860	-4.04	-1.13	hexokinase 2 (HXK2) identical to hexokinase 2 [Arabidopsis thaliana] Swiss-Prot:P93834 [At2g19860.1]
AT5G22880	-4.81	-1.15	histone H2B, putative strong similarity to histone H2B-3 Lycopersicon esculentum GI:3021485, H2B Gossypium hir...
AT2G26800	6.82	1.26	hydroxymethylglutaryl-CoA lyase, putative / 3-hydroxy-3-methylglutarate-CoA lyase, putative / HMG-CoA lyase, p...
AT1G25025	5.24	1.32	hypothetical protein [At1g25025.1]
AT1G33820	-3.84	-1.15	hypothetical protein [At1g33820.1]
AT4G34370	3.79	1.09	IBR domain-containing protein similar to SP—Q94981 Ariadne-1 protein (Ari-1) Drosophila melanogaster; contai...
AT3G02840	5.91	1.14	immediate-early fungal elicitor family protein similar to immediate-early fungal elicitor protein CMPG1 (GI:14...
AT5G43360	-3.78	-1.13	inorganic phosphate transporter (PHT3) identical to inorganic phosphate transporter [Arabidopsis thaliana] GI:...
AT5G51520	-4.03	-1.10	invertase/pectin methylesterase inhibitor family protein low similarity to pectinesterase from Lycopersicon es...
AT4G19680	4.81	1.14	iron-responsive transporter (IRT2) member of the Zinc (Zn2+)-Iron (Fe2+) permease (ZIP) family, PMID:11500563 ...
AT2G17130	-6.50	-1.16	isocitrate dehydrogenase subunit 2 / NAD+ isocitrate dehydrogenase subunit 2 nearly identical to NAD+ dependen...
AT5G03290	-3.80	-1.13	isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative strong similarity to isocitrate d...
AT1G54040	-5.44	-1.16	kelch repeat-containing protein contains Pfam PF01344: Kelch motif (4 repeats); similar to jsimilar to epithio...
AT4G36840	-6.63	-1.19	kelch repeat-containing protein contains Pfam profile PF01344: Kelch motif [At4g36840.1]
AT4G26480	-3.74	-1.10	KH domain-containing protein qkI-7, Mus musculus [At4g26480.1]
AT3G09220	-6.97	-1.17	laccase family protein / diphenol oxidase family protein similar to laccase [Pinus taeda][GI:13661201], laccas...
AT2G30210	-5.26	-1.17	laccase, putative / diphenol oxidase, putative similar to laccase [Populus balsamifera subsp. trichocarpa][GI:...
AT1G08110	-4.67	-1.13	lactoylglutathione lyase, putative / glyoxalase I, putative similar to lactoylglutathione lyase SP:O04885 from...
AT2G44060	-4.68	-1.11	late embryogenesis abundant family protein / LEA family protein similar to ethylene-responsive late embryogene...
AT4G27400	-7.24	-1.18	late embryogenesis abundant protein-related / LEA protein-related similar to late embryogenesis abundant prote...
AT5G60530	-5.89	-1.16	late embryogenesis abundant protein-related / LEA protein-related similar to late embryogenesis abundant prote...
AT5G60300	3.89	1.10	lectin protein kinase family protein contains Pfam domains, PF00069: Protein kinase domain and PF00139: Legume...

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Locus	*t*-statistic	Fold change	Description
AT5G12940	-4.73	-1.17	leucine-rich repeat family protein contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611 [At5g. . .
AT3G20820	-6.22	-1.19	leucine-rich repeat family protein contains similarity to Cf-2.1 [Lycopersicon pimpinellifolium] gi—1184075—gb. . .
AT1G30370	3.80	1.09	lipase class 3 family protein similar to DEFECTIVE IN ANTHER DEHISCENCE1 [Arabidopsis thaliana] GI:16215706; c. . .
AT2G42690	-3.79	-1.11	lipase, putative similar to lipase [Dianthus caryophyllus] GI:4103627; contains Pfam profile PF01764: Lipase [. . .
AT5G59320	-6.82	-1.21	lipid transfer protein 3 (LTP3) identical to lipid transfer protein 3 from Arabidopsis thaliana [gi:8571921]; . . .
AT5G64550	-3.89	-1.10	loricrin-related contains weak similarity to Loricrin (Swiss-Prot:P23490) [Homo sapiens] [At5g64550.1]
AT4G09960	7.35	1.19	MADS-box protein (AGL11) [At4g09960.1]
AT3G04090	-4.12	-1.10	major intrinsic family protein / MIP family protein contains Pfam profile: MIP PF00230 [At3g04090.1]
AT4G10380	-5.84	-1.15	major intrinsic family protein / MIP family protein contains Pfam profile: MIP PF00230 [At4g10380.1]
AT5G45105	4.67	1.14	metal transporter, putative (ZIP8) similar to putative metal transporter ZIP8 [Arabidopsis thaliana] gi—189971. . .
AT4G04830	5.86	1.19	methionine sulfoxide reductase domain-containing protein / SeIR domain-containing protein low similarity to pi. . .
AT4G04810	4.31	1.11	methionine sulfoxide reductase domain-containing protein / SeIR domain-containing protein low similarity to pi. . .
AT3G16480	-4.24	-1.10	mitochondrial processing peptidase alpha subunit, putative similar to mitochondrial processing peptidase alpha. . .
AT2G22500	8.40	1.25	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein [A. . .
AT5G03630	7.48	1.20	monodehydroascorbate reductase, putative monodehydroascorbate reductase (NADH), cucumber, PIR:JU0182 [At5g0363. . .
AT1G73540	5.95	1.15	MutT/nudix family protein low similarity to SP—Q09790 Diadenosine 5’,5”’-P1,P6-hexaphosphate hydrolase (EC 3.. . .
AT1G18300	7.77	1.22	MutT/nudix family protein similar to SP—Q09790 Diadenosine 5’,5”’-P1,P6-hexaphosphate hydrolase (EC 3.6.1.-) . . .
AT5G52260	-7.44	-1.20	myb family transcription factor (MYB19) contains PFAM profile: Myb DNA binding domain PF00249 [At5g52260.1]
AT1G13300	-4.24	-1.12	myb family transcription factor contains Pfam domain, PF00249: Myb-like DNA-binding domain [At1g13300.1]
AT3G25790	-3.90	-1.18	myb family transcription factor contains Pfam domain, PF00249: Myb-like DNA-binding domain [At3g25790.1]
AT5G43900	-4.16	-1.11	myosin heavy chain (MYA2) nearly identical to PIR—S51824 myosin heavy chain MYA2 [Arabidopsis thaliana] [At5g4. . .
AT3G25833	-4.43	-1.11	myrcene/ocimene synthase, putative similar to GI:9957293; contains Pfam profile: PF01397 terpene synthase fami. . .
AT4G30440	4.20	1.17	NAD-dependent epimerase/dehydratase family protein similar to nucleotide sugar epimerase from Vibrio vulnificu. . .
AT1G16700	-3.92	-1.24	NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial, putative very strong similarity to SP—Q42599 NAD. . .
AT5G24530	4.22	1.16	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to flavanone 3-hydroxylase [Persea americana][GI:7. . .
AT1G52800	-4.32	-1.13	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to GS-AOP loci [GI:16118889, GI:16118887, GI:16118. . .
AT4G10500	5.89	1.22	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to hyoscyamine 6 beta-hydroxylase [Atropa belladon. . .
AT4G25780	-9.99	-1.31	pathogenesis-related protein, putative similar to gene PR-1 protein - Medicago truncatula, SP—Q40374; contains. . .
AT5G23870	-4.88	-1.14	pectinacetylesterase family protein contains Pfam profile: PF03283 pectinacetylesterase [At5g23870.1]
AT3G09410	-3.92	-1.09	pectinacetylesterase family protein similar to pectinacetylesterase precursor GB:CAA67728 [Vigna radiata]; con. . .
AT2G45220	-5.84	-1.16	pectinesterase family protein contains Pfam profile: PF01095 pectinesterase [At2g45220.1]
AT3G61540	-9.20	-1.23	peptidase family protein similar to prolyl aminopeptidase (proline iminopeptidase) from Aeromonas sobria SP—P4. . .
AT3G25230	3.95	1.19	peptidyl-prolyl cis-trans isomerase / FK506-binding protein (ROF1) identical to rotamase FKBP (ROF1) GB:U49453. . .
AT5G58710	-4.38	-1.11	peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative (ROC7) similar to c. . .
AT2G38380	-3.89	-1.11	peroxidase 22 (PER22) (P22) (PRXEA) / basic peroxidase E identical to SP—P24102 Peroxidase 22 precursor (EC 1.. . .
AT3G49110	-3.80	-1.16	peroxidase 33 (PER33) (P33) (PRXCA) / neutral peroxidase C (PERC) identical to SP—P24101 Peroxidase 33 precurs. . .
AT5G42180	-3.92	-1.15	peroxidase 64 (PER64) (P64) (PRXR4) identical to SP—Q43872 Peroxidase 64 precursor (EC 1.11.1.7) (Atperox P64). . .
AT5G66390	-3.73	-1.11	peroxidase 72 (PER72) (P72) (PRXR8) identical to SP—Q9FJZ9 Peroxidase 72 precursor (EC 1.11.1.7) (Atperox P72). . .
AT4G33420	3.95	1.28	peroxidase, putative identical to class III peroxidase ATP32 [Arabidopsis thaliana] gi—17530547—gb—AAL40837; i. . .
AT1G49570	5.06	1.12	peroxidase, putative identical to peroxidase ATP5a [Arabidopsis thaliana] gi—1546702—emb—CAA67341; similar to . . .
AT4G26010	-4.41	-1.14	peroxidase, putative peroxidase ATP13a - Arabidopsis thaliana, PID:e264765; identical to cDNA class III peroxi. . .
AT1G44970	-4.10	-1.16	peroxidase, putative similar to peroxidase GI:993004 from [Mercurialis annua] [At1g44970.1]
AT5G58560	-5.18	-1.15	phosphatidate cytidylyltransferase family protein contains Pfam profile: PF01148 phosphatidate cytidylyltransf. . .
AT3G15650	4.05	1.11	phospholipase/carboxylesterase family protein low similarity to lysophospholipase I [Mus musculus] GI:1864159;. . .
AT1G80380	4.18	1.13	phosphoribulokinase/uridine kinase-related [At1g80380.1]
AT4G00430	-4.18	-1.31	plasma membrane intrinsic protein, putative identical to transmembrane protein GI:535780 from [Arabidopsis tha. . .
AT5G06860	3.98	1.10	polygalacturonase inhibiting protein 1 (PGIP1) identical to polygalacturonase inhibiting protein 1 (PGIP1) [Ar. . .

Continued. . .

Locus	*t*-statistic	Fold change	Description
AT4G13420	-3.90	-1.11	potassium transporter (HAK5) identical to K+ transporter HAK5 [Arabidopsis thaliana] gi—7108597—gb—AAF36490; s. . .
AT3G30775	7.18	1.20	proline oxidase, mitochondrial / osmotic stress-responsive proline dehydrogenase (POX) (PRO1) (ERD5) nearly id. . .
AT1G54970	-4.45	-1.22	proline-rich family protein similar to proline-rich protein GI:170048 from [Glycine max] [At1g54970.1]
AT4G03120	-4.76	-1.12	proline-rich family protein similar to U1 small nuclear ribonucleoprotein C; contains proline rich extensin do. . .
AT1G20380	3.84	1.13	prolyl oligopeptidase, putative / prolyl endopeptidase, putative / post-proline cleaving enzyme, putative simi. . .
AT1G12090	-4.64	-1.53	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to 14 kDa polypeptide [Cat. . .
AT3G17090	-3.77	-1.10	protein phosphatase 2C family protein / PP2C family protein similar to Ser/Thr protein phosphatase 2C (PP2C6) . . .
AT1G07160	4.69	1.12	protein phosphatase 2C, putative / PP2C, putative similar to protein phosphatase 2C GI:2582800 from [Medicago . . .
AT5G62680	4.78	1.17	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family [At5g62. . .
AT1G19770	7.56	1.24	purine permease-related low similarity to purine permease [Arabidopsis thaliana] GI:7620007; contains Pfam pro. . .
AT2G16430	4.58	1.11	purple acid phosphatase (PAP10) identical to purple acid phosphatase (PAP10) GI:20257482 from [Arabidopsis tha. . .
AT4G27270	-3.79	-1.09	quinone reductase family protein similar to 1,4-benzoquinone reductase [Phanerochaete chrysosporium][GI:445499. . .
AT5G54500	-5.09	-1.14	quinone reductase, putative similar to 1,4-benzoquinone reductase [Phanerochaete chrysosporium][GI:4454993]; c. . .
AT5G41940	-4.63	-1.11	RabGAP/TBC domain-containing protein similar to GTPase activating protein [Yarrowia lipolytica] GI:2370595; co. . .
AT2G02990	4.60	1.22	ribonuclease 1 (RNS1) identical to ribonuclease SP:P42813 Ribonuclease 1 precursor (EC 3.1.27.1) Arabidopsis . . .
AT3G11480	5.03	1.19	S-adenosyl-L-methionine:carboxyl methyltransferase family protein similar to SAM:benzoic acid carboxyl methylt. . .
AT4G34580	-3.94	-1.11	SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative similar to phosphatidylinositol. . .
AT5G58640	-6.67	-1.18	selenoprotein-related contains weak similarity to Selenoprotein W (Swiss-Prot:P49904) [Rattus norvegicus] [At5. . .
AT5G03730	-3.75	-1.10	serine/threonine protein kinase (CTR1) identical to serine/threonine-protein kinase CTR1 [Arabidopsis thaliana. . .
AT3G25800	8.61	1.23	serine/threonine protein phosphatase 2A (PP2A) 65 KDa regulatory subunit A identical to protein phosphatase 2A. . .
AT5G53360	-3.89	-1.25	seven in absentia (SINA) family protein low similarity to siah-1A protein [Mus musculus] GI:297035; contains P. . .
AT1G06870	-4.97	-1.16	signal peptidase, putative similar to chloroplast thylakoidal processing peptidase GB:CAA71502 GI:2769566 from. . .
AT1G20160	4.62	1.12	subtilase family protein similar to subtilisin-type protease precursor GI:14150446 from [Glycine max] [At1g201. . .
AT3G27380	-5.04	-1.14	succinate dehydrogenase, iron-sulphur subunit, mitochondrial (SDH2-1) nearly identical to mitochondrial succin. . .
AT2G20420	-4.12	-1.10	succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial, putative / succinyl-CoA synthetase, beta chain, p. . .
AT1G71880	4.58	1.13	sucrose transporter / sucrose-proton symporter (SUC1) identical to sucrose-proton symporter SUC1 [Arabidopsis . . .
AT1G22710	4.36	1.14	sucrose transporter / sucrose-proton symporter (SUC2) nearly identical to sucrose-proton symporter SUC2 [Arabi. . .
AT4G37610	4.17	1.21	TAZ zinc finger family protein / BTB/POZ domain-containing protein contains Pfam PF00651 : BTB/POZ domain; con. . .
AT2G43920	4.19	1.10	thiol methyltransferase, putative similar to thiol methyltransferase 1 GI:14583119 from [Brassica oleracea] [A. . .
AT4G01870	3.83	1.19	tolB protein-related contains weak similarity to TolB protein precursor (Swiss-Prot:P44677) [Haemophilus influ. . .
AT3G26040	-7.50	-1.27	transferase family protein similar to deacetylvindoline 4-O-acetyltransferase [Catharanthus roseus][GI:4091808. . .
AT4G15400	-5.08	-1.16	transferase family protein similar to deacetylvindoline 4-O-acetyltransferase [Catharanthus roseus][GI:4091808. . .
AT1G79410	5.52	1.15	transporter-related low similarity to organic anion transporter 3 [Rattus norvegicus] GI:5545293; contains Pfa. . .
AT4G22590	7.69	1.22	trehalose-6-phosphate phosphatase, putative similar to trehalose-6-phosphate phosphatase (AtTPPA) GI:2944178; . . .
AT4G12430	9.56	1.24	trehalose-6-phosphate phosphatase, putative similar to trehalose-6-phosphate phosphatase (AtTPPB) [Arabidopsis. . .
AT1G07440	3.77	1.10	tropinone reductase, putative / tropine dehydrogenase, putative similar to tropinone reductase SP:P50165 from . . .
AT5G64660	5.60	1.14	U-box domain-containing protein similar to immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum. . .
AT1G64440	5.10	1.12	UDP-glucose 4-epimerase, putative / UDP-galactose 4-epimerase, putative / Galactowaldenase, putative similar t. . .
AT5G39320	-3.94	-1.09	UDP-glucose 6-dehydrogenase, putative very strong similarity to SP—Q96558 UDP-glucose 6-dehydrogenase (EC 1.1.. . .
AT3G03250	-3.78	-1.12	UTP–glucose-1-phosphate uridylyltransferase, putative / UDP-glucose pyrophosphorylase, putative / UGPase, put. . .
AT1G12840	-6.22	-1.18	vacuolar ATP synthase subunit C (VATC) / V-ATPase C subunit / vacuolar proton pump C subunit (DET3) identical . . .
AT3G58730	-3.91	-1.17	vacuolar ATP synthase subunit D (VATD) / V-ATPase D subunit / vacuolar proton pump D subunit (VATPD) identical. . .
AT1G64200	-10.50	-1.33	vacuolar ATP synthase subunit E, putative / V-ATPase E subunit, putative / vacuolar proton pump E subunit, put. . .
AT3G56880	7.06	1.21	VQ motif-containing protein contains PF05678: VQ motif [At3g56880.1]
AT4G31550	4.52	1.11	WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA -binding domain [At4g31550.2]
AT2G38470	4.85	1.22	WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA -binding domain; [At2g38470.1]
AT1G80840	9.95	1.34	WRKY family transcription factor similar to WRKY transcription factor GB:BAA87058 GI:6472585 from [Nicotiana t. . .

Continued. . .

Locus	*t*-statistic	Fold change	Description
AT4G28850	-4.79	-1.18	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan tr...
AT4G03210	-8.92	-1.22	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan tr...
AT1G10550	-4.31	-1.10	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan tr...
AT5G57530	-4.04	-1.20	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan tr...
AT1G27730	7.57	1.29	zinc finger (C2H2 type) family protein (ZAT10) / salt-tolerance zinc finger protein (STZ) identical to salt-to...
AT5G59820	4.64	1.16	zinc finger (C2H2 type) family protein (ZAT12) identical to zinc finger protein ZAT12 [Arabidopsis thaliana] g...
AT3G46090	7.70	1.19	zinc finger (C2H2 type) family protein (ZAT7) identical to zinc finger protein ZAT7 [Arabidopsis thaliana] gi—...
AT3G19580	3.97	1.28	zinc finger (C2H2 type) protein 2 (AZF2) identical to Cys2/His2-type zinc finger protein 2 [Arabidopsis thalia...
AT4G03510	6.11	1.16	zinc finger (C3HC4-type RING finger) family protein (RMA1) identical to RING zinc finger protein RMA1 gi:31642...
AT1G76410	4.02	1.13	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RI...
AT3G46620	4.54	1.12	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RI...
AT5G59550	3.77	1.18	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RI...
AT3G55980	7.38	1.26	zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and s...
AT3G12750	-6.78	-1.22	zinc transporter (ZIP1) identical to putative zinc transporter GB:AAC24197 from [Arabidopsis thaliana], (Proc...

Table C.5: Significant expression changes in shoots of 3 week-old trAcdS-*rolD* plants versus non-transformed plants, $p < 0.01$.

Locus	*t*-statistic	Fold change	Description
AT2G06050	8.08	5.51	12-oxophytodienoate reductase (OPR3) / delayed dehiscence1 (DDE1) nearly identical to DELAYED DEHISCENCE1 [GI:…
AT5G12020	6.65	4.12	17.6 kDa class II heat shock protein (HSP17.6-CII) identical to 17.6 kDa class II heat shock protein SP:P29830…
AT1G03410	6.31	3.52	2-oxoglutarate-dependent dioxygenase, putative identical to 2A6 (GI:599622), a homolog of the tomato ethylene …
AT1G03400	4.89	5.28	2-oxoglutarate-dependent dioxygenase, putative similar to 2A6 (GI:599622) and tomato ethylene synthesis regula…
AT1G55510	-6.83	-4.97	2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain al…
AT3G45090	4.48	4.15	2-phosphoglycerate kinase-related contains weak similarity to 2-phosphoglycerate kinase (GI:467751) [Methanoth…
AT1G06460	-6.39	-3.72	31.2 kDa small heat shock family protein / hsp20 family protein contains Pfam profile: PF00011 Hsp20/alpha cry…
AT2G19720	6.29	19.44	40S ribosomal protein S15A (RPS15aB) [At2g19720.1]
AT3G22200	-6.54	-4.05	4-aminobutyrate aminotransferase / gamma-amino-N-butyrate transaminase / GABA transaminase / beta-alanine–oxo…
AT1G20510	4.56	2.48	4-coumarate–CoA ligase family protein / 4-coumaroyl-CoA synthase family protein similar to SP—P14912 and SP—P…
AT4G05160	-5.10	-3.94	4-coumarate–CoA ligase, putative / 4-coumaroyl-CoA synthase, putative similar to 4CL2 [gi:12229665] from Arab…
AT1G06570	-12.52	-11.15	4-hydroxyphenylpyruvate dioxygenase (HPD) identical to 4-hydroxyphenylpyruvate dioxygenase (HPD) SP:P93836 [Ar…
AT3G14990	-5.43	-3.68	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative supporting cDNA gi—11908017—g…
AT4G04610	5.27	3.60	5'-adenylylsulfate reductase (APR1) / PAPS reductase homolog (PRH19) identical to 5'-adenylylsulfate reductase…
AT4G21990	6.51	4.73	5'-adenylylsulfate reductase (APR3) / PAPS reductase homolog (PRH26) identical to 5'-adenylylsulfate reductase…
AT1G62180	6.43	5.51	5'-adenylylsulfate reductase 2, chloroplast (APR2) (APSR) / adenosine 5'-phosphosulfate 5'-adenylylsulfate (AP…
AT5G21170	-6.59	-3.74	5'-AMP-activated protein kinase beta-2 subunit, putative similar to Swiss-Prot:Q9QZH4 5'-AMP-activated protein…
AT5G17920	5.71	3.18	5-methyltetrahydropteroyltriglutamate–homocysteine methyltransferase / vitamin-B12-independent methionine syn…
AT3G03780	7.26	4.26	5-methyltetrahydropteroyltriglutamate–homocysteine methyltransferase, putative / vitamin-B12-independent meth…
AT3G51190	4.86	3.35	60S ribosomal protein L8 (RPL8B) ribosomal protein L8, cytosolic - Arabidopsis thaliana, PIR:T04582 [At3g51190…
AT4G04180	7.11	4.51	AAA-type ATPase family protein contains Pfam domain, PF00004: ATPase, AAA family [At4g04180.1]
AT1G70610	4.67	5.47	ABC transporter (TAP1) contains Pfam profile: PF00005 ABC transporters; similar to TAP1 protein (transporter o…
AT1G65950	4.99	4.15	ABC1 family protein contains Pfam domain, PF03109: ABC1 family [At1g65950.1]
AT3G24190	-7.45	-8.47	ABC1 family protein contains Pfam domain, PF03109: ABC1 family [At3g24190.1]
AT5G61380	-8.42	-10.83	ABI3-interacting protein 1 (AIP1) identical to pseudo-response regulator 1 GI:7576354 from [Arabidopsis thalia…
AT5G48880	6.37	3.89	acetyl-CoA C-acyltransferase 1 / 3-ketoacyl-CoA thiolase 1 (PKT1) identical to 3-keto-acyl-CoA-thiolase 1 [Ara…
AT2G33150	-5.36	-3.74	acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative similar to 3-ketoacyl-CoA thiolase …
AT5G47720	-7.09	-4.22	acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative strong similarity to Acetoacetyl-co…
AT5G56180	-4.83	-2.53	actin-related protein, putative (ARP8) strong similarity to actin-related protein 8A (ARP8) [Arabidopsis thali…
AT5G23050	-8.91	-7.28	acyl-activating enzyme 17 (AAE17) nearly identical to acyl-activating enzyme 17 [Arabidopsis thaliana] GI:2989…
AT4G24230	-4.42	-2.39	acyl-CoA binding protein, putative / ACBP, putative contains similarity to acyl-CoA binding protein 2 [Arabido…
AT5G55600	-4.74	-2.87	agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein contains Pfam profi…
AT2G38400	-7.02	-4.14	alanine–glyoxylate aminotransferase, putative / beta-alanine-pyruvate aminotransferase, putative / AGT, putat…
AT1G54100	-5.42	-5.23	aldehyde dehydrogenase, putative / antiquitin, putative strong similarity to SP—Q41247 Aldehyde dehydrogenase …
AT3G57520	-10.90	-9.88	alkaline alpha galactosidase, putative similar to alkaline alpha galactosidase II [Cucumis melo] GI:29838631; …
AT5G42650	4.42	2.79	allene oxide synthase (AOS) / hydroperoxide dehydrase / cytochrome P450 74A (CYP74A) identical to Allene oxide…
AT5G02730	-5.71	-5.79	allergen V5/Tpx-1-related family protein low similarity to SP—Q05968 Pathogenesis-related protein 1 precursor …
AT3G22820	-6.40	-3.51	allergen-related weak similarity to pollen major allergen 2 protein [Juniperus ashei] gi—9955725—emb—CAC05582 …
AT1G65560	4.61	3.51	allyl alcohol dehydrogenase, putative similar to allyl alcohol dehydrogenase from Nicotiana tabacum [gi:669281…
AT3G22370	5.38	3.12	alternative oxidase 1a, mitochondrial (AOX1A) identical to GB:Q39219 [SP—Q39219] from [Arabidopsis thaliana] […
AT4G23590	6.20	3.63	aminotransferase class I and II family protein similar to nicotianamine aminotransferase from Hordeum vulgare …
AT5G53970	-5.61	-3.13	aminotransferase, putative similar to nicotianamine aminotransferase from Hordeum vulgare [GI:6498122, GI:6469…
AT2G28840	-5.34	-2.88	ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023 [At2g28840.1]

Continued…

Locus	*t*-statistic	Fold change	Description
AT2G38750	7.17	4.01	annexin 4 (ANN4) nearly identical to annexin (AnnAt4) [Arabidopsis thaliana] GI:6503084; contains Pfam profile. . .
AT2G29690	-5.41	-4.22	anthranilate synthase, alpha subunit, component I-2 (ASA2) identical to SP—P32069 [At2g29690.1]
AT5G52020	5.79	5.04	AP2 domain-containing protein low similarity to DREB1B GI:3738226 from [Arabidopsis thaliana]; contains Pfam p. . .
AT5G13330	-5.14	-3.87	AP2 domain-containing transcription factor family protein similar to AP2 domain containing protein RAP2.6, Ara. . .
AT4G31060	4.67	4.10	AP2 domain-containing transcription factor, putative TINY, Arabidopsis thaliana, PID:E218696 [At4g31060.1]
AT5G11740	6.93	4.77	arabinogalactan-protein (AGP15) identical to gi—10880507—gb—AAG24283 [At5g11740.1]
AT1G31450	6.56	11.00	aspartyl protease family protein contains eukaryotic and viral aspartyl proteases active site, PROSITE:PS00141. . .
AT4G16563	-6.15	-3.26	aspartyl protease family protein contains Pfam profile: PF00026 eukaryotic aspartyl protease [At4g16563.1]
AT5G62670	-4.57	-2.45	ATPase, plasma membrane-type, putative / proton pump, putative strong similarity to P-type H(+)-transporting A. . .
AT4G04620	-4.63	-2.44	autophagy 8b (APG8b) identical to autophagy 8b [Arabidopsis thaliana] GI:19912153; contains Pfam profile PF029. . .
AT2G45170	-5.80	-3.09	autophagy 8e (APG8e) identical to autophagy 8e [Arabidopsis thaliana] GI:19912159; contains Pfam profile PF029. . .
AT3G60640	-4.48	-7.80	autophagy 8g (APG8g) identical to autophagy 8g [Arabidopsis thaliana] GI:19912163; contains Pfam profile PF029. . .
AT3G25880	5.97	4.80	auxin-resistance protein, putative similar to Swiss-Prot:P42744 auxin-resistance protein AXR1 [Arabidopsis tha. . .
AT4G03400	6.93	3.81	auxin-responsive GH3 family protein similar to auxin-responsive GH3 product [Glycine max] GI:18591; contains P. . .
AT3G15540	6.54	3.50	auxin-responsive protein / indoleacetic acid-induced protein 19 (IAA19) identical to SP—O24409 Auxin-responsiv. . .
AT1G15580	6.40	4.93	auxin-responsive protein / indoleacetic acid-induced protein 5 (IAA5) / auxin-induced protein (AUX2-27) identi. . .
AT5G51570	-5.71	-3.19	band 7 family protein similar to hypersensitive-induced response protein [Zea mays] GI:7716468; contains Pfam . . .
AT5G55500	-4.84	-2.78	beta-(1,2)-xylosyltransferase (XYLT) identical to SP—Q9LDH0 [At5g55500.1]
AT5G20390	-6.24	-7.46	beta-1,3-glucanase, putative similar to plant beta-1,3-glucanase bg4 GI:2808438 from [Arabidopsis thaliana] [A. . .
AT5G52570	4.95	2.87	beta-carotene hydroxylase, putative similar to GI:1575296, beta-carotene hydroxylase [At5g52570.1]
AT5G56870	-10.53	-9.94	beta-galactosidase, putative / lactase, putative similar to beta-galactosidase precursor GI:3869280 from [Cari. . .
AT3G13750	-7.33	-4.44	beta-galactosidase, putative / lactase, putative similar to beta-galactosidase precursor SP:P48980 from [Lycop. . .
AT3G06850	-5.77	-6.08	branched chain alpha-keto acid dehydrogenase E2 subunit (din3) identical to branched chain alpha-keto acid deh. . .
AT1G10070	-11.00	-12.26	branched-chain amino acid aminotransferase 2 / branched-chain amino acid transaminase 2 (BCAT2) identical to S. . .
AT1G52930	5.10	2.89	brix domain-containing protein contains Pfam domain, PF04427: Brix domain [At1g52930.1]
AT1G09070	4.81	2.62	C2 domain-containing protein / src2-like protein, putative similar to cold-regulated gene SRC2 [Glycine max] G. . .
AT1G13750	-5.20	-3.04	calcineurin-like phosphoesterase family protein contains Pfam profile: PF00149 calcineurin-like phosphoesteras. . .
AT1G76650	5.75	4.30	calcium-binding EF hand family protein similar to regulator of gene silencing calmodulin-related protein GI:12. . .
AT3G56800	4.78	3.12	calmodulin-2/3/5 (CAM3) identical to calmodulin GI:474183 from [Arabidopsis thaliana]; almost identical to cal. . .
AT5G62070	4.85	4.70	calmodulin-binding family protein contains Pfam profile PF00612: IQ calmodulin-binding motif [At5g62070.1]
AT5G62570	5.37	4.78	calmodulin-binding protein similar to calmodulin-binding protein TCB60 GI:1698548 from [Nicotiana tabacum] [At. . .
AT3G03400	-4.70	-2.66	calmodulin-related protein, putative similar to calmodulin-related protein 2, touch-induced SP:P25070 from [Ar. . .
AT1G76640	4.64	4.46	calmodulin-related protein, putative similar to regulator of gene silencing calmodulin-related protein GI:1296. . .
AT1G58180	-4.51	-2.97	carbonic anhydrase family protein / carbonate dehydratase family protein similar to SP—P46512 Carbonic anhydra. . .
AT3G52720	5.76	4.12	carbonic anhydrase family protein low similarity to storage protein (dioscorin) [Dioscorea cayenensis] GI:4334. . .
AT4G35090	5.94	3.39	catalase 2 identical to catalase 2 SP:P25819, GI:17865693 from [Arabidopsis thaliana] [At4g35090.1]
AT1G01140	4.54	2.39	CBL-interacting protein kinase 9 (CIPK9) identical to CBL-interacting protein kinase 9 [Arabidopsis thaliana] . . .
AT1G55930	-6.63	-3.92	CBS domain-containing protein / transporter associated domain-containing protein contains Pfam profiles PF0057. . .
AT2G34720	4.51	3.50	CCAAT-binding transcription factor (CBF-B/NF-YA) family protein contains Pfam profile: PF02045 CCAAT-binding t. . .
AT5G09870	6.96	4.14	cellulose synthase, catalytic subunit, putative similar to gi:2827141 cellulose synthase catalytic subunit (At. . .
AT5G64740	5.49	3.26	cellulose synthase, catalytic subunit, putative similar to gi:2827141 cellulose synthase catalytic subunit (At. . .
AT4G32190	8.77	10.48	centromeric protein-related low similarity to SP—Q02224 Centromeric protein E (CENP-E protein) Homo sapiens . . .
AT5G13930	9.42	13.63	chalcone synthase / naringenin-chalcone synthase identical to SP—P13114 [At5g13930.1]
AT5G05270	6.74	6.55	chalcone-flavanone isomerase family protein contains very low similarity to chalcone-flavonone isomerase (chal. . .
AT2G43590	-5.19	-3.47	chitinase, putative similar to basic endochitinase CHB4 precursor SP:Q06209 from [Brassica napus] [At2g43590.1. . .
AT3G22840	5.98	10.59	chlorophyll A-B binding family protein / early light-induced protein (ELIP) identical to early light-induced p. . .
AT3G27690	5.90	3.10	chlorophyll A-B binding protein (LHCB2:4) nearly identical to Lhcb2 protein [Arabidopsis thaliana] GI:4741950;. . .

Continued. . .

Locus	*t*-statistic	Fold change	Description
AT5G54270	7.38	4.89	chlorophyll A-B binding protein / LHCII type III (LHCB3) identical to Lhcb3 protein [Arabidopsis thaliana] GI:...
AT5G33300	5.60	3.25	chromosome-associated kinesin-related contains weak similarity to chromosome-associated kinesin KIF4A (Chromok...
AT1G80820	4.88	3.22	cinnamoyl-CoA reductase, putative identical to CCR2 (GI:12407990), similar to cinnamoyl CoA reductase from Euc...
AT5G14700	4.51	3.28	cinnamoyl-CoA reductase-related similar to cinnamoyl-CoA reductase from Pinus taeda [GI:17978649], Saccharum o...
AT1G09500	7.54	4.86	cinnamyl-alcohol dehydrogenase family / CAD family similar to cinnamyl alcohol dehydrogenase, Eucalyptus gunni...
AT3G58740	-4.51	-2.61	citrate synthase, glyoxysomal, putative strong similarity to SP—P49299 Citrate synthase, glyoxysomal precursor...
AT1G04620	-6.89	-3.89	coenzyme F420 hydrogenase family / dehydrogenase, beta subunit family contains Pfam PF04432: Coenzyme F420 hyd...
AT2G42530	4.92	3.49	cold-responsive protein / cold-regulated protein (cor15b) nearly identical to cold-regulated gene cor15b [Arab...
AT1G08860	5.71	4.49	copine, putative Similar to BONZAI1 [Arabidopsis thaliana] GI:15487382; contains Pfam profile PF00168: C2 doma...
AT5G24850	5.89	3.93	cryptochrome dash (CRYD) nearly identical to cryptochrome dash [Arabidopsis thaliana] GI:28971609; similar to ...
AT4G17740	-4.69	-3.05	C-terminal processing protease, putative similar to C-terminal protease precursor [Spinacia oleracea] GI:99943...
AT1G78820	-5.57	-3.05	curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein similar to S locus glyco...
AT3G12490	-5.18	-2.95	cysteine protease inhibitor, putative / cystatin, putative similar to PRLI-interacting factor M [Arabidopsis t...
AT4G39090	-4.71	-2.87	cysteine proteinase RD19a (RD19A) / thiol protease identical to cysteine proteinase RD19a, thiol protease SP:P...
AT5G28050	-4.53	-2.83	cytidine/deoxycytidylate deaminase family protein similar to SP—O34598 Guanine deaminase (EC 3.5.4.3) (Guanase...
AT1G14730	4.59	3.77	cytochrome B561 family similar to cytochrome GB:AAD11424 GI:4206110 [Mesembryanthemum crystallinum]; contains ...
AT3G26180	-7.03	-40.96	cytochrome P450 71B20, putative (CYP71B2) identical to cytochrome P450 71B20 (SP:Q9LTM3) [Arabidopsis thaliana...
AT4G39950	5.74	3.51	cytochrome P450 79B2, putative (CYP79B2) identical to cytochrome P450 (79B2) SP:O81346 from [Arabidopsis thali...
AT5G36220	6.01	3.39	cytochrome P450 81D1 (CYP81D1) (CYP91A1) Identical to Cytochrome P450 (SP:Q9FG65) [Arabidopsis thaliana]; [At5...
AT4G31500	4.86	4.78	cytochrome P450 83B1 (CYP83B1) Identical to Cytochrome P450 (SP:O65782)[Arabidopsis thaliana] [At4g31500.1]
AT4G36220	5.91	3.32	cytochrome P450 84A1 (CYP84A1) / ferulate-5-hydroxylase (FAH1) identical to Cytochrome P450 84A1 (Ferulate-5-h...
AT1G12740	5.12	6.27	cytochrome P450 family protein similar to Cytochrome P450 90A1 (SP:Q42569) [Arabidopsis thaliana] [At1g12740.1...
AT1G57750	4.61	2.55	cytochrome P450, putative similar to cytochrome P450 GI:4688670 from [Catharanthus roseus] [At1g57750.1]
AT3G61880	-8.62	-5.71	cytochrome P450, putative similar to cytochrome p450 SP:O48927 from [Arabidopsis thaliana] [At3g61880.1]
AT1G01190	4.90	16.78	cytochrome P450, putative similar to cytochrome P450 SP:O48927 from [Glycine max] [At1g01190.1]
AT3G14660	4.61	2.93	cytochrome P450, putative similar to GB:Q05047 from [Catharanthus roseus] [At3g14660.1]
AT3G43890	4.81	4.53	DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain [At3g43890.1]
AT4G01910	-5.65	-10.72	DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain [At4g01910.1]
AT1G71280	5.74	5.20	DEAD/DEAH box helicase, putative contains Pfam profile: PF00270 DEAD/DEAH box helicase [At1g71280.1]
AT5G58770	8.88	5.97	dehydrodolichyl diphosphate synthase, putative / DEDOL-PP synthase, putative similar to GI:796076 [At5g58770.1...
AT3G55610	4.96	2.79	delta 1-pyrroline-5-carboxylate synthetase B / P5CS B (P5CS2) identical to SP—P54888 [At3g55610.1]
AT5G62530	-5.45	-3.53	delta-1-pyrroline-5-carboxylate dehydrogenase (P5CDH) identical to delta-1-pyrroline-5-carboxylate dehydrogena...
AT2G46210	4.60	2.42	delta-8 sphingolipid desaturase, putative similar to delta-8 sphingolipid desaturase GI:3819708 from [Brassica...
AT4G21540	-4.62	-2.48	diacylglycerol kinase family protein contains INTERPRO domain, IPR001206, DAG-kinase catalytic domain [At4g215...
AT3G56940	4.46	3.08	dicarboxylate diiron protein, putative (Crd1) similar to leucine-containing zipper protein At103 GP:6911864; c...
AT2G45400	5.02	3.60	dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family similar to dihydroflavonol 4-reducta...
AT3G23110	7.92	7.96	disease resistance family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611;...
AT1G15890	4.68	9.25	disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a di...
AT2G17050	4.78	3.81	disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a ...
AT2G28670	-5.05	-3.07	disease resistance-responsive family protein / fibroin-related contains similarity to silk fibroin heavy chain...
AT1G10520	4.66	2.90	DNA polymerase lambda (POLL) identical to DNA polymerase lambda GI:12053869 from [Arabidopsis thaliana] [At1g1...
AT1G44900	8.17	39.06	DNA replication licensing factor, putative similar to DNA replication licensing factor MCM2 from Xenopus laev...
AT5G56840	-7.95	-8.50	DNA-binding family protein contains Pfam domains, PF00249: Myb-like DNA-binding domain and PF00098: Zinc knuck...
AT4G35900	9.02	18.07	DNA-binding protein-related weak similarity to DNA-binding factor gmlip15 [Zea mays] GI:14289167 [At4g35900.1]
AT2G20560	5.08	2.94	DNAJ heat shock family protein SP—Q9UDY4 DnaJ homolog subfamily B member 4 (Heat shock 40 kDa protein 1 homolo...
AT5G23240	-10.53	-10.58	DNAJ heat shock N-terminal domain-containing protein low similarity to SP—O34136 Chaperone protein dnaJ (40 kD...
AT4G21040	-9.59	-25.51	Dof-type zinc finger domain-containing protein finger protein rolB, Arabidopsis thaliana, PID:g1359493 [At4g21...

Continued...

Locus	*t*-statistic	Fold change	Description
AT2G33830	-6.12	-3.35	dormancy/auxin associated family protein contains Pfam profile: PF05564 dormancy/auxin associated protein [At2. . .
AT1G56220	-5.48	-3.27	dormancy/auxin associated family protein similar to Auxin-repressed 12.5 kDa protein (Swiss-Prot:Q05349) [Frag. . .
AT1G28330	-8.82	-5.43	dormancy-associated protein, putative (DRM1) identical to dormancy-associated protein [Arabidopsis thaliana] G. . .
AT2G20160	-7.17	-14.02	E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At17), putative E3 ubiquitin ligase; similar to Skp1 homolo. . .
AT2G43400	-4.65	-3.71	electron transfer flavoprotein-ubiquinone oxidoreductase family protein contains Pfam profile: PF05187 Electro. . .
AT1G09580	-4.84	-2.57	emp24/gp25L/p24 family protein similar to SP—P49755 Transmembrane protein Tmp21 precursor (21 kDa Transmembran. . .
AT4G39030	-8.43	-14.06	enhanced disease susceptibility 5 (EDS5) / salicylic acid induction deficient 1 (SID1) identical to SP—Q945F0;. . .
AT5G54940	4.78	2.70	eukaryotic translation initiation factor SUI1, putative similar to SP—P32911 Protein translation factor SUI1 . . .
AT3G45970	4.96	2.97	expansin family protein (EXPL1) similar to cim1 induced allergen, Glycine max, EMBL:U03860; expansin-like gene. . .
AT4G38400	7.49	6.56	expansin family protein (EXPL2) contains Pfam profile: PF01357 pollen allergen; expansin-like gene, PMID:11641. . .
AT3G45960	9.41	6.70	expansin family protein (EXPL3) contains Pfam profile: PF01357 pollen allergen; expansin-like gene, PMID:11641. . .
AT3G55500	-4.83	-4.79	expansin, putative (EXP16) similar to expansin GI:2828241 from [Brassica napus]; alpha-expansin gene family, P. . .
AT2G39700	-6.35	-3.98	expansin, putative (EXP4) similar to alpha-expansin 6 precursor GI:16923359 from [Cucumis sativus]; alpha-expa. . .
AT1G10080	8.67	5.44	expressed protein [At1g10090.1]
AT2G32180	-5.42	-3.74	expressed protein [At2g32180.1]
AT3G17160	-5.62	-5.64	expressed protein [At3g17160.1]
AT4G01080	6.78	3.79	expressed protein [At4g01080.1]
AT1G15430	-4.59	-3.11	expressed protein [At1g15430.1]
AT1G18380	-6.20	-7.20	expressed protein [At1g18380.1]
AT1G27300	-4.73	-3.09	expressed protein [At1g27300.1]
AT1G29690	4.64	5.22	expressed protein [At1g29690.1]
AT1G44000	5.74	5.12	expressed protein [At1g44000.1]
AT1G53770	4.70	2.65	expressed protein [At1g53770.1]
AT1G55480	4.82	2.55	expressed protein [At1g55480.1]
AT1G63670	-6.21	-4.52	expressed protein [At1g63670.1]
AT1G69230	-5.34	-3.19	expressed protein [At1g69230.1]
AT1G70420	5.12	3.98	expressed protein [At1g70420.1]
AT1G80040	-8.02	-6.42	expressed protein [At1g80040.1]
AT2G07713	-4.91	-10.83	expressed protein [At2g07713.1]
AT2G23120	-8.32	-20.32	expressed protein [At2g23120.1]
AT2G25510	-5.50	-3.64	expressed protein [At2g25510.1]
AT2G29670	5.57	3.10	expressed protein [At2g29670.1]
AT2G35900	5.83	3.13	expressed protein [At2g35900.1]
AT2G39740	4.99	2.89	expressed protein [At2g39740.1]
AT3G12320	7.40	4.79	expressed protein [At3g12320.1]
AT3G19970	5.51	3.98	expressed protein [At3g19970.1]
AT3G47450	-4.97	-23.45	expressed protein [At3g47450.1]
AT3G49720	4.96	3.66	expressed protein [At3g49720.1]
AT3G58010	-4.83	-6.68	expressed protein [At3g58010.1]
AT3G59840	4.51	4.20	expressed protein [At3g59840.1]
AT4G16060	4.58	2.42	expressed protein [At4g16060.1]
AT4G19430	-6.59	-6.81	expressed protein [At4g19430.1]
AT4G26060	5.32	3.46	expressed protein [At4g26060.1]
AT4G27840	-5.30	-26.83	expressed protein [At4g27840.1]
AT4G28025	10.33	35.07	expressed protein [At4g28025.1]
AT5G18120	-5.12	-3.68	expressed protein [At5g18120.1]
AT5G24990	5.69	2.97	expressed protein [At5g24990.1]

Continued. . .

Locus	*t*-statistic	Fold change	Description
AT5G32470	4.51	2.60	expressed protein [At5g32470.1]
AT5G35080	5.84	5.40	expressed protein [At5g35080.1]
AT5G42530	-4.53	-5.11	expressed protein [At5g42530.1]
AT5G51720	6.43	4.40	expressed protein [At5g51720.1]
AT1G27100	5.83	7.17	expressed protein contains Pfam profile: PF04601 protein of unknown function (DUF569 [At1g27100.1]
AT1G26720	4.42	2.38	expressed protein ; expression supported by MPSS [At1g26720.1]
AT2G24020	-7.69	-41.62	expressed protein contains Pfam domain PF02575: Uncharacterized BCR, YbaB family COG0718 [At2g24020.1]
AT5G15740	4.74	2.70	expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins i...
AT3G47680	-4.79	-6.76	expressed protein contains similarity to hypothetical proteins of [Arabidopsis thaliana] [At3g47680.1]
AT5G02720	7.32	4.16	expressed protein predicted protein, Arabidopsis thaliana [At5g02720.1]
AT5G60370	8.46	5.74	expressed protein predicted protein, Arabidopsis thaliana [At5g60370.1]
AT1G10190	-10.68	-30.93	expressed protein similar to hypothetical protein GB:CAB10284 contains Pfam profile PF03080: Arabidopsis prote...
AT1G01430	4.64	2.59	expressed protein similar to hypothetical protein GB:CAB80917 GI:7267605 from [Arabidopsis thaliana] [At1g0143...
AT4G26260	-9.34	-7.38	expressed protein similar to myo-inositol oxygenase [Sus scrofa] gi—17432544—gb—AAL39076 [At4g26260.1]
AT2G03550	5.32	3.00	expressed protein similar to PrMC3 [Pinus radiata] GI:5487873; contains an esterase/lipase/thioesterase active...
AT5G67370	9.22	6.17	expressed protein similar to unknown protein (gb—AAC18972.1) [At5g67370.1]
AT4G18810	14.49	17.37	expressed protein similar to UV-B and ozone similarly regulated protein 1 UOS1 [Pisum sativum] GI:20339364 [At...
AT4G31110	-4.58	-2.63	expressed protein supported by full length cDNA gi:21436034 from [Arabidopsis thaliana] [At4g31115.1]
AT3G23080	-5.22	-2.72	expressed protein weak similarity to SP—Q9UKL6 Phosphatidylcholine transfer protein (PC-TP) Homo sapiens [At...
AT2G34810	4.62	2.80	FAD-binding domain-containing protein similar to SP—P30986 reticuline oxidase precursor (Berberine-bridge-form...
AT1G75890	5.73	5.34	family II extracellular lipase 2 (EXL2) EXL2 (PMID:11431566); similar to anter-specific proline-rich protein (...
AT3G06250	-4.94	-13.66	far-red impaired responsive protein, putative similar to far-red impaired response protein FAR1 [Arabidopsis t...
AT1G06120	4.45	9.05	fatty acid desaturase family protein similar to delta 9 acyl-lipid desaturase GB:BAA25180 GI:2970034 (ADS1) fr...
AT3G49030	4.79	3.04	F-box family protein contains F-box domain Pfam:PF00646 [At3g49030.1]
AT4G09920	6.65	8.06	F-box family protein contains F-box domain Pfam:PF00646 [At4g09920.1]
AT4G29420	5.20	3.64	F-box family protein contains F-box Pfam:PF00646 ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At...
AT1G67390	-6.29	-10.26	F-box family protein contains Pfam PF00646: F-box domain [At1g67390.1]
AT4G09870	-9.10	-5.80	F-box family protein contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640: F-box protein interactio...
AT5G39450	-4.85	-3.52	F-box family protein contains Pfam:PF00646 F-box domain ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_...
AT2G16365	4.78	13.50	F-box family protein contains Pfam:PF00646 F-box domain [At2g16365.1]
AT1G06110	-4.56	-2.45	F-box family protein contains similarity to F-box protein FBX3 GI:6103643 from [Homo sapiens] ; similar to SKP...
AT1G67160	-7.48	-45.24	F-box family protein similar to F-box protein family, AtFBX7 (GI:20197899) [Arabidopsis thaliana] [At1g67160.1...
AT2G34460	5.54	3.82	flavin reductase-related low similarity to SP—P30043 Flavin reductase Homo sapiens [At2g34460.1]
AT5G08640	8.61	7.39	flavonol synthase 1 (FLS1) identical to SP—Q96330; contains PF03171 2OG-Fe(II) oxygenase superfamily [At5g0864...
AT4G37550	-5.95	-3.19	formamidase, putative / formamide amidohydrolase, putative similar to SP—Q50228 Formamidase (EC 3.5.1.49) (For...
AT5G14780	-5.05	-2.77	formate dehydrogenase (FDH) identical to GI:7677266 [At5g14780.1]
AT5G58870	4.73	3.65	FtsH protease, putative contains similarity to cell division protein FtsH homolog 3 SP:P73437 (EC 3.4.24.-) [s...
AT1G06430	4.44	2.36	FtsH protease, putative similar to zinc dependent protease GI:7650138 from [Arabidopsis thaliana] [At1g06430.1...
AT1G56600	5.43	3.88	galactinol synthase, putative similar to galactinol synthase, isoform GolS-1 GI:5608497 from [Ajuga reptans] [...
AT3G62720	4.91	4.33	galactosyl transferase GMA12/MNN10 family protein low similarity to alpha-1,2-galactosyltransferase, Schizosac...
AT4G12960	4.43	3.13	gamma interferon responsive lysosomal thiol reductase family protein / GILT family protein similar to SP—P1328...
AT3G55590	4.53	3.00	GDP-mannose pyrophosphorylase, putative strong similarity to GDP-mannose pyrophosphorylase from Arabidopsis th...
AT5G03600	-8.07	-7.04	GDSL-motif lipase/hydrolase family protein low similarity to family II lipase EXL3 [Arabidopsis thaliana] GI:1...
AT5G45950	6.58	3.53	GDSL-motif lipase/hydrolase family protein similar to family II lipase EXL3 (GI:15054386) and EXL1 (GI:1505438...
AT4G28780	4.68	3.72	GDSL-motif lipase/hydrolase family protein similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382),...
AT2G30310	-4.80	-4.15	GDSL-motif lipase/hydrolase family protein similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382 fro...
AT5G45910	-4.70	-3.05	GDSL-motif lipase/hydrolase family protein similar to lipase [Arabidopsis thaliana] GI:1145627; contains Inter...

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Locus	*t*-statistic	Fold change	Description
AT5G40990	-4.50	-3.19	GDSL-motif lipase/hydrolase family protein similar to lipase [Arabidopsis thaliana] GI:1145627; contains Pfam ...
AT1G53990	-4.78	-3.07	GDSL-motif lipase/hydrolase family protein similar to myrosinase-associated proteins from [Brassica napus] GI:...
AT5G20630	-9.39	-6.46	germin-like protein (GER3) identical to germin-like protein subfamily 3 member 3 [SP—P94072] [At5g20630.1]
AT5G14470	-6.65	-4.80	GHMP kinase-related contains similarity to D-glycero-D-manno-heptose 7-phosphate kinase [Aneurinibacillus ther...
AT5G07200	4.77	3.46	gibberellin 20-oxidase identical to GI:1109699 [At5g07200.1]
AT1G02400	8.24	5.52	gibberellin 2-oxidase, putative / GA2-oxidase, putative similar to GA2ox2 [GI:4678368]; similar to dioxygenase...
AT2G14900	8.42	5.40	gibberellin-regulated family protein similar to SP—P46690 Gibberellin-regulated protein 4 precursor Arabidops...
AT5G15230	-9.15	-6.39	gibberellin-regulated protein 4 (GASA4) / gibberellin-responsive protein 4 identical to SP—P46690 Gibberellin-...
AT5G19220	4.72	2.81	glucose-1-phosphate adenylyltransferase large subunit 1 (APL1) / ADP-glucose pyrophosphorylase (ADG2) identica...
AT1G66200	5.42	2.94	glutamine synthetase, putative similar to glutamine synthetase, cytosolic isozyme (Glutamate– ammonia ligase,...
AT5G37600	8.52	5.16	glutamine synthetase, putative similar to glutamine synthetase, cytosolic isozyme (Glutamate– ammonia ligase,...
AT1G58290	5.81	3.41	glutamyl-tRNA reductase 1 / GluTR (HEMA1) identical to glutamyl-tRNA reductase 1, chloroplast [SP—P42804] [At1...
AT4G31870	6.64	3.62	glutathione peroxidase, putative glutathione peroxidase, Arabidopsis thaliana, PIR2:S71250 [At4g31870.1]
AT2G02930	-6.37	-3.56	glutathione S-transferase, putative [At2g02930.1]
AT2G29440	4.50	2.67	glutathione S-transferase, putative [At2g29440.1]
AT2G29460	4.67	2.61	glutathione S-transferase, putative [At2g29460.1]
AT4G02520	-6.74	-4.92	glutathione S-transferase, putative [At4g02520.1]
AT1G10370	4.68	2.94	glutathione S-transferase, putative (ERD9) similar to glutathione S-transferase TSI-1 [Aegilops tauschii] gi:2...
AT2G30860	6.08	3.25	glutathione S-transferase, putative identical to GB:Y12295 [At2g30860.1]
AT2G30870	4.76	2.64	glutathione S-transferase, putative supported by cDNA GI:443698 GB:D17673 [At2g30870.1]
AT1G42970	5.03	2.90	glyceraldehyde-3-phosphate dehydrogenase B, chloroplast (GAPB) / NADP-dependent glyceraldehydephosphate dehydr...
AT5G40610	4.60	2.61	glycerol-3-phosphate dehydrogenase [NAD+] / GPDH strong similarity to SP—P52425 Glycerol-3-phosphate dehydroge...
AT2G26620	5.20	3.25	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein similar to SP—P35339 Exop...
AT5G49360	-7.48	-4.99	glycosyl hydrolase family 3 protein [At5g49360.1]
AT1G02640	-5.11	-3.76	glycosyl hydrolase family 3 protein similar to beta-xylosidase GB:Z84377 GI:2102655 from [Aspergillus niger] [...
AT1G75680	4.78	4.34	glycosyl hydrolase family 9 protein similar to endo-beta-1,4-glucanase GB:AAC12685 GI:3025470 from [Pinus radi...
AT2G32990	4.63	3.11	glycosyl hydrolase family 9 protein similar to endo-beta-1,4-glucanase GI:4972236 from [Fragaria x ananassa] [...
AT5G03760	6.20	3.62	glycosyl transferase family 2 protein similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from [...
AT1G70090	5.14	3.02	glycosyl transferase family 8 protein contains Pfam profile: PF01501 glycosyl transferase family 8 [At1g70090....
AT5G50440	-4.71	-3.45	Golgi SNARE protein membrin 12 (MEMB12) identical to Membrin 12 (AtMEMB12) (Golgi SNAP receptor complex member...
AT1G08750	-5.43	-3.21	GPI-anchor transamidase, putative similar to SP—P49018 GPI-anchor transamidase (EC 3.-.-.-) (GPI transamidase)...
AT5G02230	5.47	2.98	haloacid dehalogenase-like hydrolase family protein contains InterPro accession IPR005834: Haloacid dehalogena...
AT5G59480	4.42	2.32	haloacid dehalogenase-like hydrolase family protein low similarity to SP—P53078 SSM1 protein Saccharomyces ce...
AT4G39970	4.81	2.56	haloacid dehalogenase-like hydrolase family protein low similarity to SP—P95649 CbbY protein Rhodobacter spha...
AT5G44730	4.88	4.39	haloacid dehalogenase-like hydrolase family protein low similarity to SP—Q94915 Rhythmically expressed gene 2 ...
AT5G06320	5.81	4.43	harpin-induced family protein / HIN1 family protein / harpin-responsive family protein / NDR1/HIN1-like protei...
AT3G13030	5.38	8.05	hAT dimerisation domain-containing protein contains Pfam profile: PF04937 domain of unknown function (DUF659),...
AT5G02500	8.25	5.43	heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1) identical to SP—P22953 Heat shock cognate 70 kDa prote...
AT5G02490	7.14	6.04	heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2) identical to SP—P22954 Heat shock cognate 70 kDa prote...
AT1G56410	7.61	13.27	heat shock cognate 70 kDa protein, putative / HSC70, putative / HSP70, putative strong similarity to heat shoc...
AT3G12580	6.74	4.77	heat shock protein 70, putative / HSP70, putative strong similarity to heat shock protein GI:425194 [Spinacia ...
AT5G52640	5.27	3.12	heat shock protein 81-1 (HSP81-1) / heat shock protein 83 (HSP83) nearly identical to SP—P27323 Heat shock pro...
AT5G56000	7.04	8.31	heat shock protein 81-4 (HSP81-4) nearly identical to heat shock protein hsp81.4 [Arabidopsis thaliana] GI:190...
AT1G67300	4.53	2.39	hexose transporter, putative similar to hexose transporters from Solanum tuberosum [GI:8347246], Nicotiana tab...
AT1G62360	-5.14	-28.39	homeobox protein SHOOT MERISTEMLESS (STM) identical to homeobox protein SHOOT MERISTEMLESS (STM) SP:Q38874 fro...
AT4G34610	4.52	2.49	homeodomain-containing protein similaritry to homeotic protein BEL1, Arabidopsis thaliana, PIR2:A57632 [At4g34...
AT5G54080	-10.54	-10.36	homogentisate 1,2-dioxygenase / homogentisicase/homogentisate oxygenase / homogentisic acid oxidase (HGO) iden...

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Locus	*t*-statistic	Fold change	Description
AT3G24420	-6.61	-3.64	hydrolase, alpha/beta fold family protein low similarity to 3-oxoadipate enol-lactone hydrolase [Pseudomonas s. . .
AT5G58310	5.93	4.40	hydrolase, alpha/beta fold family protein low similarity to SP—Q40708 PIR7A protein Oryza sativa , polyneurid. . .
AT4G30650	-5.70	-3.00	hydrophobic protein, putative / low temperature and salt responsive protein, putative similar to SP—Q9ZNQ7 Hyd. . .
AT5G09480	4.59	14.91	hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains, INTERPRO:IPR002965; Co. . .
AT1G05290	-5.87	-3.27	hypothetical protein [At1g05290.1]
AT1G23270	-5.09	-3.20	hypothetical protein [At1g23270.1]
AT1G37045	7.23	4.26	hypothetical protein [At1g37045.1]
AT1G67635	6.75	4.65	hypothetical protein [At1g67635.1]
AT1G71470	-4.64	-2.72	hypothetical protein [At1g71470.1]
AT2G11830	-5.16	-2.71	hypothetical protein [At2g11830.1]
AT2G13865	-5.09	-3.03	hypothetical protein [At2g13865.1]
AT2G27340	-11.91	-16.93	hypothetical protein [At2g27340.1]
AT3G17200	5.19	3.09	hypothetical protein [At3g17200.1]
AT4G08098	-5.49	-6.17	hypothetical protein [At4g08098.1]
AT5G46875	-9.59	-34.32	hypothetical protein [At5g46875.1]
AT5G37460	5.77	3.03	hypothetical protein contains Pfam PF04510 : Family of unknown function (DUF577)); common family comprised of . . .
AT2G16410	-5.55	-43.68	hypothetical protein similar to zinc finger protein [Arabidopsis thaliana] GI:976277 [At2g16410.1]
AT1G47630	-6.89	-8.07	hypothetical protein this may be a pseudogene. No suitable start codon was identified. [At1g47625.1]
AT3G02410	4.76	2.66	hypothetical protein weak similarity to kynurenine formamidase [Mus musculus] GI:21552719 [At3g02410.1]
AT1G51780	6.12	3.62	IAA-amino acid hydrolase 5 / auxin conjugate hydrolase (ILL5) identical to auxin conjugate hydrolase ILL5 [Ara. . .
AT2G29650	6.98	5.39	inorganic phosphate transporter, putative similar to brain specific Na+-dependent inorganic phosphate cotransp. . .
AT5G09650	4.41	2.40	inorganic pyrophosphatase family protein similar to SP—Q15181 Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophos. . .
AT3G02870	6.42	3.61	inositol-1(or 4)-monophosphatase, putative / inositol monophosphatase, putative / IMPase, putative similar to . . .
AT4G39800	7.76	11.96	inositol-3-phosphate synthase isozyme 1 / myo-inositol-1-phosphate synthase 1 / MI-1-P synthase 1 / IPS 1 iden. . .
AT2G22240	8.42	11.51	inositol-3-phosphate synthase isozyme 2 / myo-inositol-1-phosphate synthase 2 / MI-1-P synthase 2 / IPS 2 iden. . .
AT4G15610	-4.64	-2.95	integral membrane family protein contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; conta. . .
AT2G38480	-4.59	-2.62	integral membrane protein, putative contains 4 transmembrane domains; contains plant integral membrane protein. . .
AT5G46950	4.90	2.65	invertase/pectin methylesterase inhibitor family protein contains Pfam profile PF04043: Plant invertase/pectin. . .
AT1G62763	-4.57	-3.55	invertase/pectin methylesterase inhibitor family protein low similarity to extensin [Volvox carteri] GI:21992 . . .
AT3G45300	-5.20	-4.67	isovaleryl-CoA-dehydrogenase (IVD) identical to isovaleryl-CoA-dehydrogenase precursor [Arabidopsis thaliana] . . .
AT1G80440	-4.80	-2.72	kelch repeat-containing F-box family protein similar to SP—Q9ER30 Kelch-related protein 1 (Sarcosin) Rattus n. . .
AT5G48180	-4.87	-2.81	kelch repeat-containing protein contains Pfam PF01344: Kelch motif (5 repeats) ;similar to Tip elongation aber. . .
AT1G18610	4.91	3.93	kelch repeat-containing protein contains Pfam profile PF01344: Kelch motif [At1g18610.1]
AT5G47820	-4.63	-6.10	kinesin-like protein (FRA1) identical to kinesin-like protein [Arabidopsis thaliana] GI:27260890; contains Pfa. . .
AT1G08630	-6.45	-4.81	L-allo-threonine aldolase-related similar to L-allo-threonine aldolase (EC 4.1.2.-) (L-allo-TA) (L-allo-threon. . .
AT1G79310	6.34	3.69	latex-abundant protein, putative (AMC4) / caspase family protein similar to latex-abundant protein [Hevea bras. . .
AT3G03310	-4.95	-3.47	lecithin:cholesterol acyltransferase family protein / LACT family protein weak similarity to LCAT-like lysopho. . .
AT3G45420	5.37	8.72	lectin protein kinase family protein contains Serine/Threonine protein kinases active-site signature, Prosite:. . .
AT5G37450	5.54	4.36	leucine-rich repeat transmembrane protein kinase, putative [At5g37450.1]
AT3G26740	-5.59	-3.16	light responsive protein-related similar to light regulated protein precursor SP:Q03200 [Oryza sativa] (Plant . . .
AT3G27940	-6.24	-40.58	LOB domain family protein / lateral organ boundaries domain family protein (LBD26) identical to SP—Q9LIJ0 LOB . . .
AT3G05780	4.57	4.14	Lon protease, putative similar to Lon protease homolog 2 SP:P93655 [At3g05780.1]
AT1G64400	-4.65	-2.63	long-chain-fatty-acid–CoA ligase, putative / long-chain acyl-CoA synthetase, putative similar to GI:1617270 (. . .
AT3G01760	4.48	3.00	lysine and histidine specific transporter, putative similar to lysine and histidine specific transporter [Arab. . .
AT5G06300	4.59	3.32	lysine decarboxylase family protein contains Pfam profile PF03641: lysine decarboxylase family [At5g06300.1]
AT4G33150	-7.17	-3.94	lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme identical to lysine-ketoglutarat. . .
AT5G26870	-4.86	-2.56	MADS-box family protein contains similarity to hypothetical proteins of [Arabidopsis thaliana] [At5g26870.1]

Continued. . .

Locus	*t*-statistic	Fold change	Description
AT5G13630	5.62	3.11	magnesium-chelatase subunit chlH, chloroplast, putative / Mg-protoporphyrin IX chelatase, putative (CHLH) near...
AT4G23680	4.86	3.24	major latex protein-related / MLP-related low similarity to major latex protein Papaver somniferum [GI:294060...
AT1G04770	6.91	7.08	male sterility MS5 family protein similar to male sterility MS5 [Arabidopsis thaliana] GI:3859112; contains Pf...
AT5G44330	10.36	28.75	male sterility MS5 family protein similar to male sterility MS5 [Arabidopsis thaliana] GI:3859112; contains Pf...
AT1G61890	5.50	3.38	MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:12231296...
AT1G34490	-4.97	-8.48	membrane bound O-acyl transferase (MBOAT) family protein / wax synthase-related contains similarity to wax syn...
AT1G34500	-4.58	-8.69	membrane bound O-acyl transferase (MBOAT) family protein / wax synthase-related similar to wax synthase [Simmo...
AT1G32080	4.83	2.57	membrane protein, putative contains 12 transmembrane domains; similar to yohK (GI:405873) [Escherichia coli] [...
AT1G58270	-4.56	-2.53	meprin and TRAF homology domain-containing protein / MATH domain-containing protein similar to ubiquitin-speci...
AT3G20370	4.68	2.64	meprin and TRAF homology domain-containing protein / MATH domain-containing protein similar to ubiquitin-speci...
AT4G04830	4.69	2.49	methionine sulfoxide reductase domain-containing protein / SeIR domain-containing protein low similarity to pi...
AT1G03090	-10.18	-7.50	methylcrotonyl-CoA carboxylase alpha chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 1 (MCCA) nearly i...
AT4G34030	-4.79	-4.27	methylcrotonyl-CoA carboxylase beta chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 2 (MCCB) identical...
AT2G14170	-5.35	-4.31	methylmalonate-semialdehyde dehydrogenase, putative similar to methylmalonate-semialdehyde dehydrogenase [acyl...
AT5G46800	5.46	3.97	mitochondrial carnitine/acyl carrier, putative / a bout de souffle (BOU) / CAC-like protein identical to SP—Q9...
AT4G24570	5.45	5.78	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein [A...
AT5G01500	5.21	3.86	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein [A...
AT2G29720	-4.43	-3.92	monooxygenase family protein nearly identical to CTF2B [GI:4164578][Plant Physiol. 119, 364 (1999), PGR99-008]...
AT3G13400	5.56	3.35	multi-copper oxidase type I family protein similar to pollen-specific BP10 protein [SP—Q00624][Brassica napus]...
AT2G15810	4.72	2.71	Mutator-like transposase [Arabidopsis thaliana] [NP454104]
AT3G46200	6.04	3.27	MutT/nudix family protein similar to head organizer protein P17F11 GI:17976973 from [Xenopus laevis]; contains...
AT5G47240	-6.54	-4.63	MutT/nudix family protein similar to SP—P53370 Nucleoside diphosphate-linked moiety X motif 6 Homo sapiens ; ...
AT1G18300	4.97	2.88	MutT/nudix family protein similar to SP—Q09790 Diadenosine 5’,5”’-P1,P6-hexaphosphate hydrolase (EC 3.6.1.-) ...
AT4G25560	5.63	6.84	myb family transcription factor (MYB18) contains PFAM profile: Myb DNA binding domain PF00249 [At4g25560.1]
AT5G14340	-5.78	-4.15	myb family transcription factor (MYB40) contains Pfam profile: PF00249 myb-like DNA-binding domain [At5g14340....
AT1G18710	-5.70	-9.75	myb family transcription factor (MYB47) contains Pfam profile: PF00249 myb-like DNA-binding domain [At1g18710....
AT3G46130	-11.35	-14.14	myb family transcription factor (MYB48) contains Pfam profile: PF00249 myb-like DNA-binding domain [At3g46130....
AT2G26960	-5.75	-5.87	myb family transcription factor (MYB81) contains PFAM profile: myb DNA binding domain PF00249; identical to cD...
AT5G11050	5.78	3.87	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA binding domain; identical to cDNA ...
AT3G46640	-5.92	-3.75	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain [At3g46640.1]
AT1G01060	7.82	5.13	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA ...
AT2G46830	5.60	8.91	myb-related transcription factor (CCA1) identical to myb-related transcription factor (CCA1) GI:4090569 from [...
AT1G77580	-4.64	-4.84	myosin heavy chain-related low similarity to SP—P08799 Myosin II heavy chain, non muscle Dictyostelium discoi...
AT3G25810	-4.72	-44.64	myrcene/ocimene synthase, putative similar to GI:9957293; contains Pfam profile: PF01397 terpene synthase fami...
AT1G54020	7.75	5.39	myrosinase-associated protein, putative strong similarity to myrosinase-associated proteins GI:1769968, GI:176...
AT2G34850	4.74	3.46	NAD-dependent epimerase/dehydratase family protein similar to UDP-galactose 4-epimerase from Cyamopsis tetrago...
AT3G18410	5.74	3.87	NADH-ubiquinone oxidoreductase-related similar to NADH-ubiquinone oxidoreductase 12 kDa subunit, mitochondrial...
AT3G51240	7.51	4.57	naringenin 3-dioxygenase / flavanone 3-hydroxylase (F3H) identical to GI:3790548 [At3g51240.1]
AT2G19620	4.85	3.92	Ndr family protein similar to SP—O23969 Pollen specific protein SF21 Helianthus annuus ; contains Pfam profil...
AT4G31230	-5.49	-2.92	NFL_HUMAN (P07196) Neurofilament triplet L protein (68 kDa neurofilament protein) (Neurofilament light polype...
AT1G77760	8.07	6.52	nitrate reductase 1 (NR1) identical to SP—P11832 Nitrate reductase 1 (formerly EC 1.6.6.1) (NR1)Arabidopsis t...
AT3G15500	-11.23	-13.78	no apical meristem (NAM) family protein (NAC3) identical to AtNAC3 [Arabidopsis thaliana] GI:12060424; contain...
AT5G64060	4.94	3.41	no apical meristem (NAM) family protein similar to NAC1 (GI:7716952) Medicago truncatula ; contains Pfam PF02...
AT4G08290	-5.17	-3.32	nodulin MtN21 family protein similar to MtN21 GI:2598575 (root nodule development) from [Medicago truncatula] ...
AT2G47970	4.99	2.90	NPL4 family protein contains Pfam domain, PF05021: NPL4 family [At2g47970.1]
AT5G05580	7.42	4.39	omega-3 fatty acid desaturase, chloroplast, temperature-sensitive (FAD8) identical to SP:48622 Temperature-sen...
AT1G15140	4.47	2.49	oxidoreductase NAD-binding domain-containing protein Contains Pfam profile PF00175: Oxidoreductase NAD-binding...

Continued...

Locus	*t*-statistic	Fold change	Description
AT3G11180	-5.71	-3.89	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to leucoanthocyanidin dioxygenase GB:BAA20143 [Per…
AT1G23740	6.93	3.82	oxidoreductase, zinc-binding dehydrogenase family protein contains Pfam profile PF00107: oxidoreductase, zinc-…
AT5G37960	4.60	2.74	oxidoreductase-related [At5g37960.1]
AT5G02100	-5.60	-6.55	oxysterol-binding family protein similar to SWH1 [Saccharomyces cerevisiae] GI:402658; contains Pfam profile P…
AT3G63200	6.20	3.74	patatin-related low similarity to patatin-like latex protein allergen Hev b 7 - Hevea brasiliensis, EMBL:AF113…
AT2G14610	6.18	3.95	pathogenesis-related protein 1 (PR-1) identical to GB:M90508 SP—P33154 [At2g14610.1]
AT2G14580	7.31	4.29	pathogenesis-related protein, putative similar to SP—P33154 Pathogenesis-related protein 1 precursor (PR-1) A…
AT3G01420	6.23	7.07	pathogen-responsive alpha-dioxygenase, putative similar to pathogen-inducible alpha-dioxygenase [Nicotiana att…
AT3G58180	6.51	4.46	PBS lyase HEAT-like repeat-containing protein contains Pfam profile: PF03130: PBS lyase HEAT-like repeat; cont…
AT5G07420	5.17	6.47	pectinesterase family protein contains Pfam profile: PF01095 pectinesterase [At5g07420.1]
AT2G01860	-4.43	-3.20	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat [At2g01860.1]
AT3G53360	-5.22	-11.61	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat [At3g53360.1]
AT3G57680	5.30	2.81	peptidase S41 family protein similar to PSII D1 protein processing enzyme (GI::7268527) [Arabidopsis thaliana]…
AT3G49120	4.65	2.67	peroxidase, putative identical to peroxidase [Arabidopsis thaliana] gi—405611—emb—CAA50677 [At3g49120.1]
AT4G17690	-5.93	-4.48	peroxidase, putative similar to peroxidase [Spinacia oleracea] gi—1781336—emb—CAA71495 [At4g17690.1]
AT5G20510	-5.09	-2.75	PHD finger family protein contains Pfam domain, PF00628: PHD-finger [At5g20510.1]
AT2G37040	5.11	2.76	phenylalanine ammonia-lyase 1 (PAL1) nearly identical to SP—P35510 [At2g37040.1]
AT4G08950	6.41	3.85	phosphate-responsive protein, putative (EXO) similar to phi-1 (phosphate-induced gene) [Nicotiana tabacum] GI:…
AT5G01300	-4.51	-2.69	phosphatidylethanolamine-binding family protein similar to cold-regulated protein [Hordeum vulgare subsp. vulg…
AT1G08650	4.73	19.52	phosphoenolpyruvate carboxylase kinase identical to phosphoenolpyruvate carboxylase kinase [Arabidopsis thalia…
AT2G42600	4.55	2.88	phosphoenolpyruvate carboxylase, putative / PEP carboxylase, putative (PPC2) strong similarity to phosphoenolp…
AT1G73600	7.21	6.42	phosphoethanolamine N-methyltransferase 3, putative (NMT3) strong similarity to SP—Q9FR44 Phosphoethanolamine …
AT4G16250	-4.48	-2.45	phytochrome D (PHYD) nearly identical to SP—P42497 Phytochrome D Arabidopsis thaliana [At4g16250.1]
AT2G22860	5.59	4.93	phytosulfokines 2 (PSK2) identical to phytosulfokines 2 (PSK2) from [Arabidopsis thaliana] [At2g22860.1]
AT1G01620	5.91	3.31	plasma membrane intrinsic protein 1C (PIP1C) / aquaporin PIP1.3 (PIP1.3) / transmembrane protein B (TMPB) iden…
AT3G53420	9.30	7.88	plasma membrane intrinsic protein 2A (PIP2A) / aquaporin PIP2.1 (PIP2.1) identical to plasma membrane intrinsi…
AT2G37170	6.14	3.59	plasma membrane intrinsic protein 2B (PIP2B) / aquaporin PIP2.2 (PIP2.2) identical to SP—P43287 Plasma membran…
AT4G04020	6.54	4.26	plastid-lipid associated protein PAP, putative / fibrillin, putative strong similarity to plastid-lipid associ…
AT4G22240	8.77	5.45	plastid-lipid associated protein PAP, putative similar to plastid-lipid associated proteins PAP2 [Brassica rap…
AT5G06870	4.50	2.60	polygalacturonase inhibiting protein 2 (PGIP2) identical to polygalacturonase inhibiting protein 2 (PGIP2) [Ar…
AT4G36850	-7.70	-7.42	PQ-loop repeat family protein / transmembrane family protein similar to SP—Q10482 Seven transmembrane protein …
AT4G15420	4.91	3.64	PRLI-interacting factor K nearly identical to PRLI-interacting factor K [Arabidopsis thaliana] GI:11139266; co…
AT3G43720	4.86	2.56	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/s…
AT4G12510	4.84	14.49	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to 14 kDa polypeptide [Cat…
AT4G12520	5.56	6.21	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to 14 kDa polypeptide [Cat…
AT2G48140	-4.78	-2.76	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to pEARLI 1 (Accession No.…
AT4G28670	4.50	2.68	protein kinase family protein contains Pfam domain, PF00069: Protein kinase domain [At4g28670.1]
AT4G23170	5.17	3.02	protein kinase family protein contains Pfam PF01657: Domain of unknown function; similar to receptor-like prot…
AT4G25160	-6.96	-14.38	protein kinase family protein contains Pfam profile: PF00069 Eukaryotic protein kinase domain [At4g25160.1]
AT4G31220	-4.47	-3.48	protein kinase family protein contains Pfam profiles PF00069: Protein kinase domain, PF00582: universal stress…
AT1G30570	-4.49	-5.50	protein kinase family protein contains protein kinase domain, Pfam:PF00069 [At1g30570.1]
AT1G70430	-4.78	-9.85	protein kinase family protein contains protein kinase domain, Pfam:PF00069 [At1g70430.1]
AT5G53450	-6.44	-3.53	protein kinase family protein contains protein kinase domain, Pfam:PF00069 [At5g53450.1]
AT3G24720	4.73	2.72	protein kinase family protein protein kinase family; similar to tyrosine-protein kinase GB:P18160 from [Dictyo…
AT2G07180	4.60	2.63	protein kinase, putative contains protein kinase domain, Pfam:PF00069 [At2g07180.1]
AT1G63580	-4.42	-2.60	protein kinase-related [At1g63580.1]
AT3G44850	-5.72	-3.09	protein kinase-related contains eukaryotic protein kinase domain, INTERPRO:IPR000719 [At3g44850.1]

Continued…

Locus	*t*-statistic	Fold change	Description
AT4G33920	6.96	5.61	protein phosphatase 2C family protein / PP2C family protein similar to Ser/Thr protein phosphatase 2C (PP2C6) ...
AT5G04360	-5.26	-3.10	pullulanase, putative / starch debranching enzyme, putative similar to pullulanase [Spinacia oleracea] GI:6340...
AT1G19770	5.08	3.51	purine permease-related low similarity to purine permease [Arabidopsis thaliana] GI:7620007; contains Pfam pro...
AT3G52820	6.23	37.01	purple acid phosphatase (PAP22) identical to purple acid phosphatase (PAP22)GI:20257494 from [Arabidopsis thal...
AT1G14700	4.94	5.62	purple acid phosphatase, putative contains Pfam profile: PF00149 calcineurin-like phosphoesterase; similar to ...
AT2G06260	5.24	3.71	putative Athila retroelement ORF1 protein [Arabidopsis thaliana] [NP453772]
AT2G31510	4.91	3.79	putative RING zinc finger protein [Arabidopsis thaliana] [NP453339]
AT1G32440	4.67	2.82	pyruvate kinase, putative similar to pyruvate kinase isozyme G, chloroplast precursor [Nicotiana tabacum] SWIS...
AT2G46630	4.69	2.94	Q960W5 (Q960W5) LD32021p, partial (3%) [TC259244]
AT4G08030	4.72	3.18	Q9LHC7 (Q9LHC7) Retroelement pol polyprotein-like, partial (36%) [TC269123]
AT1G20390	-4.56	-2.57	Q9LMV1 (Q9LMV1) F5M15.26, complete [TC275300]
AT4G08970	7.31	5.54	Q9ZVE2 (Q9ZVE2) Mutator-like transposase, partial (16%) [TC259635]
AT5G54160	7.85	4.71	quercetin 3-O-methyltransferase 1 / flavonol 3-O-methyltransferase 1 / caffeic acid/5-hydroxyferulic acid O-me...
AT5G20250	-9.58	-12.76	raffinose synthase family protein / seed imbibition protein, putative (din10) similar to seed imbibition prote...
AT3G29050	-5.23	-27.75	receptor-like protein kinase-related contains Pfam profile: PF01657 Domain of unknown function that is usually...
AT3G53830	4.69	2.53	regulator of chromosome condensation (RCC1) family protein / UVB-resistance protein-related contains Pfam PF00...
AT3G02300	4.61	3.51	regulator of chromosome condensation (RCC1) family protein weak similarity to UVB-resistance protein UVR8 [Ara...
AT1G64060	4.86	2.55	respiratory burst oxidase protein F (RbohF) (RbohAp108) / NADPH oxidase identical to cytochrome b245 beta chai...
AT4G28430	10.04	12.23	reticulon family protein contains Pfam profile PF02453: Reticulon [At4g28430.1]
AT5G24120	6.63	4.12	RNA polymerase sigma subunit SigE (sigE) / sigma-like factor (SIG5) identical to RNA polymerase sigma subunit ...
AT3G19130	-4.66	-2.54	RNA-binding protein, putative similar to RNA Binding Protein 47 [Nicotiana plumbaginifolia] GI:9663769, DNA bi...
AT5G45160	-6.28	-3.65	root hair defective 3 GTP-binding (RHD3) family protein contains Pfam profile: PF05879 root hair defective 3 G...
AT1G66680	-4.52	-2.68	S locus-linked protein, putative similar to S locus-linked protein SLL2 [Brassica napus] GI:1518113 [At1g66680...
AT3G46600	6.13	3.64	scarecrow transcription factor family protein scarecrow-like 11 - Arabidopsis thaliana, EMBL:AF036307 [At3g466...
AT4G35770	-14.87	-19.51	senescence-associated protein (SEN1) identical to senescence-associated protein GI:1046270 from [Arabidopsis t...
AT5G45890	-7.97	-4.95	senescence-specific SAG12 protein (SAG12) / cysteine proteinase, putative identical to senescence-specific pro...
AT2G22970	-5.37	-2.96	serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza s...
AT2G23000	5.60	3.93	serine carboxypeptidase S10 family protein similar to serine carboxypeptidase I precursor (SP:P37890) [Oryza s...
AT5G66880	-4.47	-3.50	serine/threonine protein kinase, putative similar to serine-threonine protein kinase [Triticum aestivum] gi—20...
AT3G59960	4.92	2.97	SET domain-containing protein low similarity to huntingtin interacting protein 1 [Homo sapiens] GI:12697196; c...
AT3G51840	-6.20	-3.95	short-chain acyl-CoA oxidase identical to Short-chain acyl CoA oxidase [Arabidopsis thaliana] GI:5478795; cont...
AT4G09750	7.05	5.35	short-chain dehydrogenase/reductase (SDR) family protein similar to androgen-regulated short-chain dehydrogena...
AT1G43755	5.86	4.79	Similar to Athila ORF 1 [NP207606]
AT4G21366	4.49	2.38	S-locus protein kinase-related similar to S locus receptor kinase (SRK) GI:13620929 from [Arabidopsis lyrata] ...
AT1G78510	5.40	3.18	solanesyl diphosphate synthase (SPS) identical to solanesyl diphosphate synthase [Arabidopsis thaliana] GI:199...
AT4G37220	-4.49	-2.46	stress-responsive protein, putative similar to cold acclimation WCOR413-like protein gamma form [Hordeum vulga...
AT1G32960	5.80	9.00	subtilase family protein contains similarity to subtilase; SP1 GI:9957714 [Oryza sativa] [At1g32960.1]
AT1G19920	4.90	3.10	sulfate adenylyltransferase 2 / ATP-sulfurylase 2 (ASA1) (MET3-1) (APS2) identical to ATP sulfurylase (APS2) [...
AT1G74090	5.25	2.95	sulfotransferase family protein similar to SP—P52837 Flavonol 4'-sulfotransferase (EC 2.8.2.-) (F4-ST) Flaver...
AT5G51100	5.73	5.46	superoxide dismutase [Fe], putative / iron superoxide dismutase, putative similar to Fe-superoxide dismutase p...
AT4G32150	-5.38	-3.04	synaptobrevin family protein similar to Synaptobrevin-like protein 1 (SP:P51809) [Homo sapiens] [At4g32150.1]
AT3G32030	-5.36	-6.39	terpene synthase/cyclase family protein contains Pfam profile: PF01397 terpene synthase family [At3g32030.1]
AT3G07370	-4.44	-2.40	tetratricopeptide repeat (TPR)-containing protein / U-box domain-containing protein similar to serologically d...
AT2G43910	6.64	4.58	thiol methyltransferase, putative similar to thiol methyltransferase 1 GI:14583119 from [Brassica oleracea] [A...
AT1G76080	8.02	4.62	thioredoxin family protein low similarity to thioredoxin (TRX) [Fasciola hepatica] GI:6687568; contains Pfam p...
AT1G11530	-4.88	-6.60	thioredoxin family protein similar to thioredoxin H-type from Arabidopsis thaliana SP—P29448, Nicotiana tabacu...
AT1G17960	6.19	3.67	threonyl-tRNA synthetase, putative / threonine–tRNA ligase, putative similar to SP—O04630 Threonyl-tRNA synth...

Continued...

Locus	*t*-statistic	Fold change	Description
AT1G77090	5.53	3.61	thylakoid lumenal 29.8 kDa protein identical to SP—O49292—TL30_ARATH (Arabidopsis thaliana);contains a PsbP d...
AT5G02120	5.01	2.71	thylakoid membrane one helix protein (OHP) identical to one helix protein GI:3283057 from [Arabidopsis thalian...
AT1G56010	-4.99	-3.91	transcription activator NAC1 (NAC1) contains Pfam PF02365: No apical meristem (NAM) domain; identical to NAC1 ...
AT1G10200	-4.57	-2.65	transcription factor LIM, putative strong similarity to transcription factor Ntlim1 [Nicotiana tabacum] GI:568...
AT1G53670	7.48	4.74	transcription factor-related similar to pilin-like transcription factor [Homo sapiens] GI:5059062; contains Pf...
AT3G50600	-6.40	-3.65	transducin family protein / WD-40 repeat family protein contains 3 WD-40 repeats (PF00400); some similarity to...
AT1G28680	4.48	2.81	transferase family protein similar to elicitor inducible gene product EIG-I24 [Nicotiana tabacum] [gi:10798748...
AT5G53550	-9.25	-7.03	transporter, putative similar to iron-phytosiderophore transporter protein yellow stripe 1 [Zea mays] GI:10770...
AT1G20840	-4.87	-3.84	transporter-related low similarity to D-xylose proton-symporter [Lactobacillus brevis] GI:2895856; contains Pf...
AT4G39770	5.86	3.26	trehalose-6-phosphate phosphatase, putative similar to trehalose-6-phosphate phosphatase (AtTPPB) [Arabidopsis...
AT3G01550	6.42	3.56	triose phosphate/phosphate translocator, putative similar to SWISS-PROT:P52178 triose phosphate/phosphate tran...
AT1G73325	6.80	3.91	trypsin and protease inhibitor family protein / Kunitz family protein similar to Dr4 [Arabidopsis thaliana] GI...
AT2G18280	-4.59	-2.69	tubby-like protein 2 (TULP2) identical to tubby-like protein 2 (GI:27372512) Arabidopsis thaliana ; similar t...
AT2G42230	-5.41	-8.76	tubulin-specific chaperone C-related weak similarity to Tubulin-specific chaperone C (Tubulin-folding cofactor...
AT5G62540	-6.32	-3.80	ubiquitin-conjugating enzyme 3 (UBC3) E2; identical to gi:431261, SP:P42746 [At5g62540.1]
AT1G01660	4.77	2.93	U-box domain-containing protein [At1g01660.1]
AT1G56040	5.64	3.67	U-box domain-containing protein contains Pfam profile PF04564: U-box domain [At1g56040.1]
AT1G24100	4.43	3.89	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and U...
AT1G12780	-4.75	-3.60	UDP-glucose 4-epimerase / UDP-galactose 4-epimerase / Galactowaldenase identical to SP—Q42605 [GB:CAA90941] fr...
AT1G64440	-7.40	-4.39	UDP-glucose 4-epimerase, putative / UDP-galactose 4-epimerase, putative / Galactowaldenase, putative similar t...
AT4G23920	-5.77	-3.14	UDP-glucose 4-epimerase, putative / UDP-galactose 4-epimerase, putative / Galactowaldenase, putative similar t...
AT1G63180	-5.70	-4.42	UDP-glucose 4-epimerase, putative / UDP-galactose 4-epimerase, putative / Galactowaldenase, putative strong si...
AT3G62550	-7.21	-4.27	universal stress protein (USP) family protein similar to ER6 protein [Lycopersicon esculentum] GI:5669654; con...
AT1G31175	-7.44	-4.35	Unknown
AT5G34845	-6.31	-4.62	Unknown
AT4G03813	5.13	3.22	Unknown
AT1G64200	4.96	2.62	vacuolar ATP synthase subunit E, putative / V-ATPase E subunit, putative / vacuolar proton pump E subunit, put...
AT1G62480	-4.58	-3.33	vacuolar calcium-binding protein-related contains weak similarity to vacuolar calcium binding protein [Raphanu...
AT5G54520	-7.12	-6.72	WD-40 repeat family protein contains 5 WD-40 repeats (PF00400); similar to pre-mRNA splicing factor PRP17 (SP:...
AT3G56440	-4.55	-2.44	WD-40 repeat protein family contains 4 WD-40 repeats (PF00400) (2 weak); PS00778 Histidine acid phosphatases a...
AT3G10980	-5.04	-2.80	wound-responsive protein-related similar to SP—P20144 Wound-induced protein 1 Solanum tuberosum [At3g10985.1...
AT4G28240	-4.54	-2.66	wound-responsive protein-related wound-induced protein - tomato (fragment), PIR2:S19773 [At4g28240.1]
AT1G68150	-6.02	-30.97	WRKY family transcription factor similar to DNA-binding protein ABF2 GI:1159879 from [Avena fatua] [At1g68150....
AT5G57560	6.19	6.45	xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (TCH4) ide...
AT4G25820	14.78	21.83	xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (XTR9) ide...
AT5G65730	10.56	9.73	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan tr...
AT5G48070	16.27	24.03	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan tr...
AT1G65310	5.63	5.09	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan tr...
AT2G31380	9.05	8.20	zinc finger (B-box type) family protein / salt tolerance-like protein (STH) contains Pfam profile PF00643: B-b...
AT1G06040	5.45	3.07	zinc finger (B-box type) family protein / salt-tolerance protein (STO) identical to SP—Q96288 Salt-tolerance p...
AT5G48250	-8.02	-6.20	zinc finger (B-box type) family protein contains similarity to CONSTANS homologs [At5g48250.1]
AT3G07650	-9.12	-8.05	zinc finger (B-box type) family protein similar to zinc finger protein GB:BAA33206 [Oryza sativa] [At3g07650.1...
AT1G78600	5.02	2.61	zinc finger (B-box type) family protein similar to zinc finger protein GI:3618316 from [Oryza sativa] [At1g786...
AT1G27730	5.11	3.83	zinc finger (C2H2 type) family protein (ZAT10) / salt-tolerance zinc finger protein (STZ) identical to salt-to...
AT3G46090	6.30	8.97	zinc finger (C2H2 type) family protein (ZAT7) identical to zinc finger protein ZAT7 [Arabidopsis thaliana] gi—...
AT1G53010	4.88	2.57	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RI...
AT1G74410	4.69	2.69	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RI...

Continued...

Locus	*t*-statistic	Fold change	Description
AT4G38140	5.10	3.03	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RI. . .
AT5G22920	-5.34	-3.27	zinc finger (C3HC4-type RING finger) family protein contains Pfam profiles:PF05495 CHY zinc finger, PF00097 zi. . .
AT3G45555	-5.34	-4.05	zinc finger (C3HC4-type RING finger) family protein low similarity to UbcM4-interacting protein 4 [Mus musculu. . .
AT5G10650	-4.81	-2.78	zinc finger (C3HC4-type RING finger) family protein similar to Pfam domain, PF00097: Zinc finger, C3HC4 type (. . .
AT1G21570	-5.82	-3.73	zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and s. . .
AT4G26150	4.81	8.66	zinc finger (GATA type) family protein Arabidopsis thaliana mRNA for GATA transcription factor 3, PID:e1254739. . .
AT5G41580	5.00	4.23	zinc finger (MIZ type) family protein contains Pfam domain PF02891: MIZ zinc finger [At5g41580.1]
AT3G58810	-15.36	-25.99	zinc transporter, putative similar to zinc transporter 4; ZnT4 [Mus musculus] gi—2582990—gb—AAB82593; similar . . .

Table C.6: Significant expression changes in roots of 3 week-old trAcdS-*rolD* plants versus non-transformed plants, $p < 0.01$.

Locus	*t*-statistic	Fold change	Description
AT5G10450	-3.82	-1.58	14-3-3 protein GF14 lambda (GRF6) (AFT1) identical to 14-3-3 GF14lambda GI:1345595 from Arabidopsis thaliana A. . .
AT1G21400	-4.25	-1.96	2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain al. . .
AT1G55510	-5.23	-2.17	2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain al. . .
AT5G14200	-3.48	-2.45	3-isopropylmalate dehydrogenase, chloroplast, putative strong similarity to SP—P29102 3-isopropylmalate dehydr. . .
AT4G29390	3.60	1.68	40S ribosomal protein S30 (RPS30B) RIBOSOMAL PROTEIN S30 - Arabidopsis thaliana,PID:e1358183 At4g29390.1
AT3G22200	-3.76	-1.75	4-aminobutyrate aminotransferase / gamma-amino-N-butyrate transaminase / GABA transaminase / beta-alanine–oxo. . .
AT5G21170	-8.01	-5.33	5'-AMP-activated protein kinase beta-2 subunit, putative similar to Swiss-Prot:Q9QZH4 5'-AMP-activated protein. . .
AT5G17920	3.52	1.79	5-methyltetrahydropteroyltriglutamate–homocysteine methyltransferase / vitamin-B12-independent methionine syn. . .
AT1G27400	3.80	1.83	60S ribosomal protein L17 (RPL17A) similar to GB:P51413 from Arabidopsis thaliana; similar to ESTs gb—L33542 a. . .
AT1G09690	-3.56	-1.55	60S ribosomal protein L21 (RPL21C) Similar to ribosomal protein L21 (gb—L38826). ESTs gb—AA395597,gb—ATTS5197 . . .
AT3G06700	3.41	1.51	60S ribosomal protein L29 (RPL29A) similar to ribosomal protein L29 GI:7959366 Panax ginseng At3g06700.1
AT5G56710	4.21	1.70	60S ribosomal protein L31 (RPL31C) At5g56710.1
AT2G33150	-3.55	-1.77	acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative similar to 3-ketoacyl-CoA thiolase . . .
AT5G47720	-3.84	-1.76	acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative strong similarity to Acetoacetyl-co. . .
AT1G25260	3.55	1.61	acidic ribosomal protein P0-related contains similarity to 60S acidic ribosomal protein GI:5815233 from Homo s. . .
AT5G23050	-3.39	-1.56	acyl-activating enzyme 17 (AAE17) nearly identical to acyl-activating enzyme 17 Arabidopsis thaliana GI:298932. . .
AT3G06810	-3.89	-1.77	acyl-CoA dehydrogenase-related low similarity to acyl-CoA dehydrogenase Acinetobacter sp. NCIMB9871 GI:1458741. . .
AT3G02470	-4.29	-1.71	adenosylmethionine decarboxylase family protein contains Pfam profile: PF01536 adenosylmethionine decarboxylas. . .
AT5G67520	-4.40	-2.06	adenylylsulfate kinase, putative similar to adenylylsulfate kinase, chloroplast precursor (APS kinase, Adenosi. . .
AT2G38400	-8.15	-5.01	alanine–glyoxylate aminotransferase, putative / beta-alanine-pyruvate aminotransferase, putative / AGT, putat. . .
AT1G23800	-5.64	-2.32	aldehyde dehydrogenase, mitochondrial (ALDH3) nearly identical to mitochondrial aldehyde dehydrogenase ALDH3 A. . .
AT1G54100	-5.05	-2.71	aldehyde dehydrogenase, putative / antiquitin, putative strong similarity to SP—Q41247 Aldehyde dehydrogenase . . .
AT3G01260	-4.39	-1.68	aldose 1-epimerase family protein similar to non-cell-autonomous protein pathway2, plasmodesmal receptor Nicot. . .
AT3G57520	-5.11	-2.07	alkaline alpha galactosidase, putative similar to alkaline alpha galactosidase II Cucumis melo GI:29838631; co. . .
AT3G56200	-5.10	-1.88	amino acid transporter family protein low similarity to N system amino acids transporter NAT-1 Mus musculus GI. . .
AT2G38710	-3.43	-1.54	AMMECR1 family similar to AMMECR1 (GI:6063688) Homo sapiens; contains Pfam profile PF01871: AMMECR1 At2g38710.. . .
AT4G14400	-3.62	-1.63	ankyrin repeat family protein contains ankyrin repeats, Pfam domain PF00023 At4g14400.1
AT2G28840	-4.35	-1.70	ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023 At2g28840.1
AT3G50260	-3.94	-1.97	AP2 domain-containing transcription factor, putative EREBP-3 homolog, Stylosanthes hamata, EMBL:U91982 At3g502. . .
AT5G67190	-3.64	-1.57	AP2 domain-containing transcription factor, putative similar to AP2 domain containing protein RAP2.1 (GI:21555. . .
AT5G56540	-4.34	-1.83	arabinogalactan-protein (AGP14) identical to gi—10880505—gb—AAG24282 At5g56540.1
AT5G11740	4.04	1.63	arabinogalactan-protein (AGP15) identical to gi—10880507—gb—AAG24283 At5g11740.1
AT2G46330	-3.67	-1.56	arabinogalactan-protein (AGP16) identical to gi—10880509—gb—AAG24284 At2g46330.1
AT1G35230	-3.81	-1.98	arabinogalactan-protein (AGP5) identical to gi_3883128_gb_AAC77827 At1g35230.1
AT4G17650	-3.46	-1.60	aromatic-rich family protein contains Pfam PF03654: Aromatic-Rich Protein Family At4g17650.1
AT1G11910	-4.49	-2.50	aspartyl protease family protein contains Pfam profiles: PF00026 eukaryotic aspartyl protease, PF03489 surfact. . .
AT4G21980	-4.33	-1.79	autophagy 8a (APG8a) identical to autophagy 8a Arabidopsis thaliana GI:19912151; contains Pfam profile PF02991. . .
AT4G04620	-6.45	-2.22	autophagy 8b (APG8b) identical to autophagy 8b Arabidopsis thaliana GI:19912153; contains Pfam profile PF02991. . .
AT2G45170	-6.45	-2.82	autophagy 8e (APG8e) identical to autophagy 8e Arabidopsis thaliana GI:19912159; contains Pfam profile PF02991. . .
AT4G16520	-4.06	-1.65	autophagy 8f (APG8f) identical to autophagy 8f Arabidopsis thaliana GI:19912161; contains Pfam profile PF02991. . .
AT5G19140	-5.96	-2.23	auxin/aluminum-responsive protein, putative strong similarity to auxin down-regulated protein ARG10 Vigna radi. . .
AT3G16500	-3.60	-1.66	auxin-responsive AUX/IAA family protein similar to SP—O24408—AXII_ARATH Auxin-responsive protein IAA18 (Indol. . .
AT2G46370	-3.47	-1.59	auxin-responsive GH3 family protein similar to auxin-responsive GH3 product Glycine max GI:18591; contains Pfa. . .

Continued. . .

Locus	*t*-statistic	Fold change	Description
AT2G33310	-3.73	-1.67	auxin-responsive protein / indoleacetic acid-induced protein 13 (IAA13) identical to SP—Q38831 Auxin-responsiv...
AT4G12980	-4.42	-1.76	auxin-responsive protein, putative similar to auxin-induced protein AIR12 GI:11357190 Arabidopsis thaliana At4...
AT2G45190	3.54	1.61	axial regulator YABBY1 (YABBY1) / abnormal floral organs protein (AFO) / filamentous flower protein (FIL) iden...
AT5G51570	-4.16	-1.72	band 7 family protein similar to hypersensitive-induced response protein Zea mays GI:7716468; contains Pfam pr...
AT1G35580	-5.26	-2.49	beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative s...
AT5G56870	-9.50	-5.17	beta-galactosidase, putative / lactase, putative similar to beta-galactosidase precursor GI:3869280 from Caric...
AT3G13750	-9.09	-4.37	beta-galactosidase, putative / lactase, putative similar to beta-galactosidase precursor SP:P48980 from Lycope...
AT5G64370	-4.42	-1.70	beta-ureidopropionase, putative / beta-alanine synthase, putative similar to beta-alanine synthase Dictyosteli...
AT5G39860	3.44	1.60	bHLH protein putative DNA-binding protein - Arabidopsis thaliana, EMBL:AC011765 At5g39860.1
AT3G06850	-9.69	-5.53	branched chain alpha-keto acid dehydrogenase E2 subunit (din3) identical to branched chain alpha-keto acid deh...
AT1G10070	-10.34	-5.01	branched-chain amino acid aminotransferase 2 / branched-chain amino acid transaminase 2 (BCAT2) identical to S...
AT2G30610	-4.23	-3.29	BTB/POZ domain-containing protein contains Pfam PF00651: BTB/POZ domain; contains Interpro IPR000210/ PS50097:...
AT1G77920	-3.78	-1.57	bZIP family transcription factor contains Pfam profile: PF00170 bZIP transcription factor At1g77920.1
AT5G49450	-4.47	-1.83	bZIP family transcription factor similar to bZIP transcription factor GI:1769891 from Arabidopsis thaliana At5...
AT4G34590	-3.74	-1.59	bZIP transcription factor family protein similar to common plant regulatory factor 7 GI:9650828 from Petroseli...
AT1G20620	-6.79	-2.24	catalase 3 (SEN2) almost identical to catalase 3 SP:Q42547, GI:3123188 from Arabidopsis thaliana; identical to...
AT5G10860	-5.28	-2.19	CBS domain-containing protein contains Pfam profile PF00571: CBS domain At5g10860.1
AT3G48530	-5.62	-2.41	CBS domain-containing protein low similarity to SP—Q9UGI9 5'-AMP-activated protein kinase, gamma-3 subunit (AM...
AT4G01330	-3.70	-1.55	CDC5_YEAST (P32562) Cell cycle serine/threonine-protein kinase CDC5/MSD2 , partial (5
AT1G02730	-3.65	-1.58	cellulose synthase family protein similar to cellulose synthase catalytic subunit gi:13925881 from Nicotiana a...
AT4G18780	-3.75	-1.59	cellulose synthase, catalytic subunit (IRX1) nearly identical to gi:12836997 At4g18780.1
AT5G17420	-3.62	-1.75	cellulose synthase, catalytic subunit (IRX3) identical to gi:5230423 At5g17420.1
AT4G31290	-3.42	-1.68	ChaC-like family protein contains Pfam profile: PF04752 ChaC-like protein At4g31290.1
AT1G75690	-3.95	-1.79	chaperone protein dnaJ-related contains Pfam PF00684 : DnaJ central domain (4 repeats); similar to bundle shea...
AT5G14420	-3.39	-1.81	copine-related low similarity to SP—Q99829 Copine I Homo sapiens At5g14420.1
AT5G12140	-4.34	-1.93	cysteine protease inhibitor, putative / cystatin, putative similar to SP—P31726 Cystatin I precursor (CORN ker...
AT4G39090	-3.76	-1.87	cysteine proteinase RD19a (RD19A) / thiol protease identical to cysteine proteinase RD19a, thiol protease SP:P...
AT5G43060	-4.94	-2.38	cysteine proteinase, putative / thiol protease, putative similar to cysteine proteinase RD21A precursor (thiol...
AT4G16190	-7.74	-3.33	cysteine proteinase, putative contains similarity to papain-like cysteine proteinase isoform I GI:7381219 from...
AT3G61440	-5.18	-2.03	cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative ...
AT5G28050	-10.54	-4.19	cytidine/deoxycytidylate deaminase family protein similar to SP—O34598 Guanine deaminase (EC 3.5.4.3) (Guanase...
AT2G24940	-4.78	-1.78	cytochrome b5 domain-containing protein similar to SP—P70580 Membrane associated progesterone receptor compone...
AT4G25570	-3.88	-2.05	cytochrome B561 family protein contains Pfam domain, PF03188: Cytochrome b561 At4g25570.1
AT4G39950	4.80	1.87	cytochrome P450 79B2, putative (CYP79B2) identical to cytochrome P450 (79B2) SP:O81346 from Arabidopsis thalia...
AT1G76180	-3.97	-2.19	dehydrin (ERD14) identical to SP—P42763 Dehydrin ERD14 Arabidopsis thaliana At1g76180.1
AT1G54410	-3.95	-1.89	dehydrin family protein contains Pfam domain, PF00257: Dehydrin At1g54410.1
AT2G21490	-3.89	-1.86	dehydrin family protein contains Pfam domain, PF00257: Dehydrin At2g21490.1
AT2G23400	-4.26	-1.66	dehydrodolichyl diphosphate synthase, putative / DEDOL-PP synthase, putative similar to GI:796076; this may be...
AT5G62530	-3.80	-1.59	delta-1-pyrroline-5-carboxylate dehydrogenase (P5CDH) identical to delta-1-pyrroline-5-carboxylate dehydrogena...
AT4G21540	-3.93	-2.31	diacylglycerol kinase family protein contains INTERPRO domain, IPR001206, DAG-kinase catalytic domain At4g2154...
AT5G12200	-3.64	-1.59	dihydropyrimidinase / DHPase / dihydropyrimidine amidohydrolase / hydantoinase (PYD2) identical to dihydropyri...
AT5G17680	3.45	1.51	disease resistance protein (TIR-NBS-LRR class), putative domain signature TIR-NBS-LRR exists, suggestive of a ...
AT1G13260	-4.22	-1.84	DNA-binding protein RAV1 (RAV1) identical to SP—Q9ZWM9 DNA-binding protein RAV1 Arabidopsis thaliana, RAV1 GI:...
AT2G45820	-4.37	-1.71	DNA-binding protein, putative identical to DNA-binding protein gi—601843—gb—AAA57124 Arabidopsis thaliana; con...
AT3G59600	3.72	1.66	DNA-directed RNA polymerase I, II, and III, putative similar to SP—P52434 DNA-directed RNA polymerases I, II, ...
AT4G36040	-7.72	-2.86	DNAJ heat shock N-terminal domain-containing protein (J11) identical to dnaJ heat shock protein J11 Arabidopsi...
AT4G10130	-4.20	-1.73	DNAJ heat shock N-terminal domain-containing protein low similarity to SP—Q9QYI7 DnaJ homolog subfamily B memb...

Continued...

Locus	*t*-statistic	Fold change	Description
AT1G80920	-6.74	-2.83	DNAJ heat shock N-terminal domain-containing protein similar to SP—Q05646 Chaperone protein dnaJ Erysipelothri. . .
AT2G33830	-8.20	-3.83	dormancy/auxin associated family protein contains Pfam profile: PF05564 dormancy/auxin associated protein At2g. . .
AT1G56220	-9.03	-3.47	dormancy/auxin associated family protein similar to Auxin-repressed 12.5 kDa protein (Swiss-Prot:Q05349) Fraga. . .
AT1G28330	-10.27	-4.85	dormancy-associated protein, putative (DRM1) identical to dormancy-associated protein Arabidopsis thaliana GI:. . .
AT2G35680	-4.14	-1.75	dual specificity protein phosphatase family protein contains Pfam profile: PF00782 dual specificity phosphatas. . .
AT4G04340	-3.62	-1.60	early-responsive to dehydration protein-related / ERD protein-related similar to ERD4 protein (early-responsiv. . .
AT1G30360	-3.46	-1.74	early-responsive to dehydration stress protein (ERD4) nearly identical to ERD4 protein (early-responsive to de. . .
AT1G33580	5.06	1.97	En/Spm-like transposon protein, putative NP273619
AT3G13772	-3.73	-1.75	endomembrane protein 70, putative TM4 family; At3g13772.1
AT4G16690	-3.47	-1.56	esterase/lipase/thioesterase family protein similar to ethylene-induced esterase Citrus sinensis GI:14279437, . . .
AT1G50640	-4.30	-1.67	ethylene-responsive element-binding factor 3 (ERF3) identical to SP—O80339 Ethylene responsive element binding. . .
AT1G69410	-4.76	-1.77	eukaryotic translation initiation factor 5A, putative / eIF-5A, putative strong similarity to eukaryotic initi. . .
AT1G54290	-4.24	-1.80	eukaryotic translation initiation factor SUI1, putative similar to P—P32911 Protein translation factor SUI1 Sa. . .
AT4G27130	-4.39	-1.91	eukaryotic translation initiation factor SUI1, putative similar to SP—P32911 Protein translation factor SUI1 S. . .
AT5G54760	-5.65	-2.08	eukaryotic translation initiation factor SUI1, putative similar to SP—P32911 Protein translation factor SUI1 S. . .
AT5G20260	-3.95	-1.63	exostosin family protein contains Pfam profile: PF03016 Exostosin family At5g20260.1
AT5G02090	-6.28	-2.12	expressed protein At5g02090.1
AT5G23920	-3.51	-1.74	expressed protein At5g23920.1
AT1G17080	-4.69	-1.82	expressed protein At1g17080.1
AT1G19530	-7.76	-2.96	expressed protein At1g19530.1
AT1G32920	4.82	1.78	expressed protein At1g32920.1
AT1G45976	-3.59	-1.61	expressed protein At1g45976.1
AT1G48450	-3.50	-1.58	expressed protein At1g48450.1
AT1G62240	-7.09	-2.89	expressed protein At1g62240.1
AT1G65720	-4.39	-1.73	expressed protein At1g65720.1
AT1G68440	-4.29	-1.88	expressed protein At1g68440.1
AT1G71900	3.81	1.65	expressed protein At1g71900.1
AT2G21290	-4.04	-1.85	expressed protein At2g21290.1
AT2G29510	-3.53	-1.53	expressed protein At2g29510.1
AT2G37920	-3.42	-1.51	expressed protein At2g37920.1
AT3G01730	-3.45	-1.54	expressed protein At3g01730.1
AT3G06840	4.43	1.72	expressed protein At3g06840.1
AT3G10770	-3.74	-1.57	expressed protein At3g10770.1
AT3G11690	-4.11	-1.70	expressed protein At3g11690.1
AT3G12650	-3.71	-1.55	expressed protein At3g12650.1
AT3G15110	3.42	1.54	expressed protein At3g15110.1
AT3G21710	-3.89	-1.66	expressed protein At3g21710.1
AT3G23170	-3.63	-1.54	expressed protein At3g23170.1
AT3G29180	3.80	1.90	expressed protein At3g29180.1
AT3G54880	-3.98	-1.62	expressed protein At3g54880.1
AT4G03420	-4.60	-1.73	expressed protein At4g03420.1
AT4G09890	-3.64	-1.59	expressed protein At4g09890.1
AT4G15830	3.79	1.71	expressed protein At4g15830.1
AT4G17215	-4.13	-1.66	expressed protein At4g17215.1
AT4G19700	-5.07	-2.16	expressed protein At4g19700.1
AT4G26240	4.53	1.76	expressed protein At4g26240.1
AT4G30790	-4.22	-1.78	expressed protein At4g30790.1

Continued. . .

Locus	*t*-statistic	Fold change	Description
AT4G38060	-4.32	-1.88	expressed protein At4g38060.2
AT4G40070	-3.74	-1.78	expressed protein At4g40070.1
AT5G04470	-3.55	-2.07	expressed protein At5g04470.1
AT5G05220	-3.68	-1.56	expressed protein At5g05220.1
AT5G06980	-4.32	-1.77	expressed protein At5g06980.2
AT5G11970	-3.68	-1.61	expressed protein At5g11970.1
AT5G40740	-3.58	-1.53	expressed protein At5g40740.1
AT2G07728	-3.51	-1.61	expressed protein ; expression supported by MPSS At2g07728.1
AT5G19590	-3.46	-1.72	expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538 At5g19590.1
AT5G03230	-6.62	-2.40	expressed protein contains Pfam profile PF04520: Protein of unknown function, DUF584 At5g03230.1
AT1G61740	-4.09	-2.27	expressed protein contains Pfam profile: PF01925 domain of unknown function DUF81; identical to cDNA hypotheti. . .
AT5G05440	-3.69	-1.62	expressed protein low similarity to cytokinin-specific binding protein Vigna radiata GI:4190976 At5g05440.1
AT5G19120	-8.05	-3.14	expressed protein low similarity to extracellular dermal glycoprotein EDGP precursor Daucus carota GI:285741, . . .
AT5G03990	-3.60	-1.66	expressed protein predicted protein, Arabidopsis thaliana At5g03990.1
AT4G24220	-4.07	-1.69	expressed protein protein induced upon wounding - Arabidopsis thaliana, PID:e257749 At4g24220.1
AT3G48710	-3.85	-1.61	expressed protein putative protein - Arabidopsis thaliana, EMBL:AL078465.1 At3g48710.1
AT3G29240	-8.15	-2.85	expressed protein similar to At1g33780 Arabidopsis thaliana; contains Pfam profile PF02622: Uncharacterized AC. . .
AT3G15450	-4.10	-1.85	expressed protein similar to auxin down-regulated protein ARG10 Vigna radiata GI:2970051, wali7 (aluminum-indu. . .
AT4G27450	-10.86	-4.72	expressed protein similar to auxin down-regulated protein ARG10 Vigna radiata GI:2970051, wali7 (aluminum-indu. . .
AT1G10140	-5.72	-2.20	expressed protein similar to EST gb—AA598098 At1g10140.1
AT1G70160	-3.51	-1.58	expressed protein similar to hypothetical protein GI:4455225 from Arabidopsis thaliana At1g70160.1
AT4G26260	-4.68	-1.77	expressed protein similar to myo-inositol oxygenase Sus scrofa gi—17432544—gb—AAL39076 At4g26260.1
AT1G26440	-3.99	-1.65	expressed protein similar to SP—Q41706 A3 protein (unknown function) Vigna unguiculata At1g26440.1
AT5G44040	-4.68	-1.91	expressed protein similar to unknown protein (gb—AAD10667.1) At5g44040.1
AT5G50200	-5.68	-2.47	expressed protein similar to unknown protein (pir——T05562) isoform contains a non-consensus AT acceptor splice. . .
AT5G21940	-7.53	-2.48	expressed protein supported by full length cDNA GI:22531282 from Arabidopsis thaliana At5g21940.1
AT3G54260	-3.94	-1.66	expressed protein various predicted proteins, Arabidopsis thaliana At3g54260.1
AT2G24550	-5.66	-2.31	expressed protein weak similarity to MTD1 Medicago truncatula GI:9294810 At2g24550.1
AT3G23080	-7.31	-2.96	expressed protein weak similarity to SP—Q9UKL6 Phosphatidylcholine transfer protein (PC-TP) Homo sapiens At3g2. . .
AT1G30700	-3.56	-1.60	FAD-binding domain-containing protein similar to SP—P30986 reticuline oxidase precursor (Berberine-bridge-form. . .
AT4G20830	-3.47	-1.64	FAD-binding domain-containing protein similar to SP—P30986 reticuline oxidase precursor (Berberine-bridge-form. . .
AT5G52120	-3.79	-1.86	F-box family protein / SKP1 interacting partner 3-related contains Pfam profile PF00646: F-box domain At5g5212. . .
AT1G43640	-3.99	-2.09	F-box family protein / tubby family protein contains Pfam profile: PF01167: Tub family; contains Pfam PF00646:. . .
AT5G18680	-3.55	-1.67	F-box family protein / tubby family protein similar to phosphodiesterase (GI:467578) Mus musculus; similar to . . .
AT3G06380	-3.38	-1.96	F-box family protein / tubby family protein similar to phosphodiesterase (GI:467578) Mus musculus; similar to . . .
AT1G76900	-3.60	-1.96	F-box family protein / tubby family protein similar to Tubby protein (SP:P50586) Mus musculus; similar to Chai. . .
AT5G01600	-8.50	-3.06	ferritin 1 (FER1) identical to ferritin Arabidopsis thaliana GI:1246401, GI:8163920 At5g01600.1
AT3G21640	-3.54	-1.56	FKBP-type peptidyl-prolyl cis-trans isomerase family protein similar to rof1 Arabidopsis thaliana GI:1354207; . . .
AT4G36920	-3.66	-1.72	floral homeotic protein APETALA2 (AP2) Identical to (SP:P47927) Floral homeotic protein APETALA2. Mouse-ear cr. . .
AT1G43670	-7.60	-2.85	fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, put. . .
AT3G04170	3.73	1.63	germin-like protein, putative contains Pfam profile: PF01072 germin family; similar to germin-like protein typ. . .
AT1G11260	-5.28	-2.23	glucose transporter (STP1) nearly identical to glucose transporter GB:P23586 SP—P23586 from Arabidopsis thalia. . .
AT5G18170	-4.83	-1.78	glutamate dehydrogenase 1 (GDH1) identical to glutamate dehydrogenase 1 (GDH 1) Arabidopsis thaliana SWISS-PRO. . .
AT5G07440	-9.16	-3.13	glutamate dehydrogenase 2 (GDH2) identical to glutamate dehydrogenase 2 (GDH 2) Arabidopsis thaliana SWISS-PRO. . .
AT1G03850	-5.95	-2.67	glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase) At1g03850.2
AT2G30860	3.62	1.71	glutathione S-transferase, putative identical to GB:Y12295 At2g30860.1
AT2G30870	4.70	2.13	glutathione S-transferase, putative supported by cDNA GI:443698 GB:D17673 At2g30870.1

Continued. . .

Locus	*t*-statistic	Fold change	Description
AT4G13930	3.40	1.58	glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldo. . .
AT2G43610	-3.65	-1.67	glycoside hydrolase family 19 protein similar to chitinase GI:17799 from Brassica napus; contains Pfam profile. . .
AT2G44490	-3.52	-1.59	glycosyl hydrolase family 1 protein contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01. . .
AT5G49360	-3.51	-1.53	glycosyl hydrolase family 3 protein At5g49360.1
AT1G02640	-7.09	-3.02	glycosyl hydrolase family 3 protein similar to beta-xylosidase GB:Z84377 GI:2102655 from Aspergillus niger At1. . .
AT3G06460	-3.98	-1.66	GNS1/SUR4 membrane family protein similar to SP—P25358 Elongation of fatty acids protein 2 (GNS1 protein) (V-S. . .
AT1G15880	-3.54	-1.55	Golgi SNARE 11 protein identical to Golgi SNARE 11 protein (GI:13898893) Arabidopsis thaliana; similar to puta. . .
AT3G18130	3.43	1.61	guanine nucleotide-binding family protein / activated protein kinase C receptor (RACK1) identical to guanine n. . .
AT2G32150	-4.65	-1.94	haloacid dehalogenase-like hydrolase family protein contains InterPro accession IPR005834: Haloacid dehalogena. . .
AT5G02500	5.97	2.34	heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1) identical to SP—P22953 Heat shock cognate 70 kDa prote. . .
AT3G12580	5.94	2.49	heat shock protein 70, putative / HSP70, putative strong similarity to heat shock protein GI:425194 Spinacia o. . .
AT3G05220	-3.46	-1.67	heavy-metal-associated domain-containing protein similar to farnesylated protein 1 (GI:23304411) Hordeum vulga. . .
AT5G54640	-3.64	-1.55	histone H2A identical to histone H2A Arabidopsis thaliana GI:7595337 At5g54640.1
AT5G12910	-4.05	-1.68	histone H3, putative similar to histone H3 from Mus musculus GI:51301, Gallus gallus GI:211859, Medicago sativ. . .
AT1G75600	-3.51	-1.71	histone H3.2, putative strong similarity to histone H3.2 SP—P11105 GI:417103 from Lolium temulentum, histone H. . .
AT2G46680	-4.77	-1.79	homeobox-leucine zipper protein 7 (HB-7) / HD-ZIP transcription factor 7 identical to homeobox-leucine zipper . . .
AT5G54080	-11.62	-4.09	homogentisate 1,2-dioxygenase / homogentisicase/homogentisate oxygenase / homogentisic acid oxidase (HGO) iden. . .
AT3G05880	-6.72	-2.39	hydrophobic protein (RCI2A) / low temperature and salt responsive protein (LTI6A) identical to SP—Q9ZNQ7 Hydro. . .
AT1G53580	-7.21	-2.45	hydroxyacylglutathione hydrolase, putative / glyoxalase II, putative similar to glyoxalase II GI:1644427 from . . .
AT2G27340	3.46	1.63	hypothetical protein At2g27340.1
AT5G43350	-4.75	-1.77	inorganic phosphate transporter (PHT1) (PT1) identical to inorganic phosphate transporter Arabidopsis thaliana. . .
AT4G15610	-9.70	-5.51	integral membrane family protein contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; conta. . .
AT1G75220	-3.59	-1.57	integral membrane protein, putative strong similarity to integral membrane protein GI:1209756 from Beta vulgar. . .
AT1G47960	-4.00	-2.17	invertase/pectin methylesterase inhibitor family protein low similarity to SP—P83326 Pectinesterase inhibitor . . .
AT1G32130	-5.41	-1.92	IWS1 C-terminus family protein contains Pfam PF05909: IWS1 C-terminus; At1g32130.1
AT3G06570	-3.47	-1.61	kelch repeat-containing F-box family protein contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344 A. . .
AT1G67480	-8.18	-2.88	kelch repeat-containing F-box family protein similar to SKP1 interacting partner 6 Arabidopsis thaliana GI:107. . .
AT1G80440	-6.70	-2.90	kelch repeat-containing F-box family protein similar to SP—Q9ER30 Kelch-related protein 1 (Sarcosin) Rattus no. . .
AT5G48180	-5.38	-1.94	kelch repeat-containing protein contains Pfam PF01344: Kelch motif (5 repeats) ;similar to Tip elongation aber. . .
AT3G20150	3.78	1.63	kinesin motor family protein contains Pfam domain, PF00225: Kinesin motor domain At3g20150.1
AT1G08630	-9.26	-6.18	L-allo-threonine aldolase-related similar to L-allo-threonine aldolase (EC 4.1.2.-) (L-allo-TA) (L-allo-threon. . .
AT3G16150	-6.58	-2.35	L-asparaginase, putative / L-asparagine amidohydrolase, putative similar to Swiss-Prot:P30364 L-asparaginase (. . .
AT1G15740	-5.43	-1.99	leucine-rich repeat family protein At1g15740.1
AT3G20820	-3.45	-1.61	leucine-rich repeat family protein contains similarity to Cf-2.1 Lycopersicon pimpinellifolium gi—1184075—gb—A. . .
AT3G02880	3.82	1.88	leucine-rich repeat transmembrane protein kinase, putative contains Pfam profiles: PF00069 Eukaryotic protein . . .
AT3G26740	-4.38	-1.80	light responsive protein-related similar to light regulated protein precursor SP:Q03200 Oryza sativa (Plant Mo. . .
AT1G06250	-3.45	-2.46	lipase class 3 family protein similar to lipase GB:AAD01804 GI:4103627 from Dianthus caryophyllus; contains Pf. . .
AT5G40780	-4.00	-1.69	lysine and histidine specific transporter, putative strong similarity to lysine and histidine specific transpo. . .
AT4G33150	-5.62	-2.18	lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme identical to lysine-ketoglutarat. . .
AT5G63190	-4.23	-1.78	MA3 domain-containing protein low similarity to programmed cell death 4 protein Gallus gallus GI:12958564; con. . .
AT1G04410	-4.24	-1.90	malate dehydrogenase, cytosolic, putative strong similarity to malate dehydrogenase from Mesembryanthemum crys. . .
AT5G52050	-3.52	-1.60	MATE efflux protein-related contains Pfam profile PF01554: Uncharacterized membrane protein family At5g52050.1
AT5G26290	-3.84	-1.71	meprin and TRAF homology domain-containing protein / MATH domain-containing protein low similarity to ubiquiti. . .
AT1G03090	-6.79	-2.41	methylcrotonyl-CoA carboxylase alpha chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 1 (MCCA) nearly i. . .
AT4G34030	-13.20	-6.95	methylcrotonyl-CoA carboxylase beta chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 2 (MCCB) identical. . .
AT5G47240	-8.61	-4.08	MutT/nudix family protein similar to SP—P53370 Nucleoside diphosphate-linked moiety X motif 6 Homo sapiens; co. . .
AT3G01140	3.47	1.74	myb family transcription factor (MYB106) similar to transforming protein (myb) homolog GB:S26605 from Petunia . . .

Continued. . .

Locus	*t*-statistic	Fold change	Description
AT3G46130	-3.72	-1.63	myb family transcription factor (MYB48) contains Pfam profile: PF00249 myb-like DNA-binding domain At3g46130.1
AT5G59780	-5.95	-2.46	myb family transcription factor (MYB59) contains PFAM profile: myb DNA binding domain PF00249 At5g59780.1
AT2G28760	-8.87	-3.37	NAD-dependent epimerase/dehydratase family protein similar to UDP-glucuronic acid decarboxylase Uxs1p from Fil...
AT5G55850	-4.38	-1.89	nitrate-responsive NOI protein, putative similar to nitrate-induced NOI protein Zea mays GI:2642213 At5g55850....
AT5G13180	-3.82	-1.97	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; hypothetical p...
AT5G14120	-5.12	-3.05	nodulin family protein similar to nodulin-like protein Arabidopsis thaliana GI:3329368, nodule-specific protei...
AT4G28040	-6.39	-2.27	nodulin MtN21 family protein similar to MtN21 GI:2598575 (root nodule development) from Medicago truncatula At...
AT3G14770	-4.32	-1.85	nodulin MtN3 family protein similar to MtN3 GI:1619602 (root nodule development) from Medicago truncatula At3g...
AT5G45370	4.34	1.84	nodulin-related / integral membrane family protein contains Pfam profile:PF00892 integral membrane protein DUF...
AT3G01630	-3.78	-1.59	nodulin-related weak similarity to nodule-specific protein Nlj70 Lotus japonicus GI:3329366 At3g01630.1
AT5G24530	3.66	1.80	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to flavanone 3-hydroxylase Persea americanaGI:7274...
AT1G11580	-4.70	-1.80	pectin methylesterase, putative similar to pectin methylesterase GI:1617583 from Lycopersicon esculentum At1g1...
AT5G25630	-3.61	-1.58	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat At5g25630.1
AT2G02040	-4.04	-2.30	peptide transporter (PTR2-B) / oligopeptide transporter 1-1, putative (OPT1-1) identical to peptide transporte...
AT5G42180	-3.45	-1.60	peroxidase 64 (PER64) (P64) (PRXR4) identical to SP—Q43872 Peroxidase 64 precursor (EC 1.11.1.7) (Atperox P64)...
AT5G64100	-5.66	-2.20	peroxidase, putative identical to peroxidase ATP3a Arabidopsis thaliana gi—1546698—emb—CAA67340 At5g64100.1
AT5G64110	-4.22	-1.68	peroxidase, putative similar to peroxidase ATP3a Arabidopsis thaliana gi—1546698—emb—CAA67340 At5g64110.1
AT1G01820	-3.41	-1.86	peroxisomal biogenesis factor 11 family protein / PEX11 family protein contains Pfam PF05648: Peroxisomal biog...
AT3G61070	-6.33	-2.15	peroxisomal biogenesis factor 11 family protein / PEX11 family protein contains Pfam PF05648: Peroxisomal biog...
AT3G53260	-3.86	-1.81	phenylalanine ammonia-lyase 2 (PAL2) nearly identical to SP—P45724 At3g53260.1
AT5G64040	-3.83	-1.68	photosystem I reaction center subunit PSI-N, chloroplast, putative / PSI-N, putative (PSAN) SP:P49107; Plant P...
AT2G30570	-4.39	-1.72	photosystem II reaction center W (PsbW) protein-related similar to photosystem II reaction center W protein SP...
AT4G35100	-4.53	-2.19	plasma membrane intrinsic protein (SIMIP) nearly identical to plasma membrane intrinsic protein Arabidopsis th...
AT2G16850	-5.39	-2.02	plasma membrane intrinsic protein, putative very strong similarity to plasma membrane intrinsic protein (SIMIP...
AT1G72230	-4.28	-1.70	plastocyanin-like domain-containing protein similar to blue copper protein SP:Q41001 from Pisum sativum At1g72...
AT3G09000	4.76	1.86	proline-rich family protein At3g09000.1
AT5G46900	3.93	1.90	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/s...
AT1G12090	3.63	1.96	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to 14 kDa polypeptide Cath...
AT2G20630	3.55	1.56	protein phosphatase 2C, putative / PP2C, putative At2g20630.1
AT2G29140	4.16	1.70	pumilio/Puf RNA-binding domain-containing protein At2g29140.1
AT2G05080	-3.81	-1.70	putative helicase Arabidopsis thaliana NP453027
AT3G42210	3.68	1.68	putative protein NP208266
AT4G15530	-3.60	-1.75	pyruvate phosphate dikinase family protein contains Pfam profiles: PF01326 pyruvate phosphate dikinase, PEP/py...
AT4G35860	-4.25	-1.77	Ras-related GTP-binding protein, putative similar to Rab2-like GTP-binding protein GI:1765896 from Arabidopsis...
AT1G63120	-5.20	-2.33	rhomboid family protein contains PFAM domain PF01694, Rhomboid family At1g63120.1
AT3G53780	-3.81	-1.69	rhomboid family protein contains PFAM domain PF01694, Rhomboid family At3g53780.1
AT5G06360	-3.44	-1.58	ribosomal protein S8e family protein contains Pfam profile PF01201: Ribosomal protein S8e At5g06360.1
AT5G59950	-3.72	-1.59	RNA and export factor-binding protein, putative At5g59950.1
AT3G51730	-6.03	-2.26	saposin B domain-containing protein contains Pfam profiles: PF00026 eukaryotic aspartyl protease, PF03489 surf...
AT1G61250	-4.25	-1.70	secretory carrier membrane protein (SCAMP) family protein (SC3) contains Pfam domain, PF04144: SCAMP family At...
AT3G23800	-5.97	-2.10	selenium-binding family protein contains Pfam profile: PF05694 56kDa selenium binding protein (SBP56) At3g2380...
AT4G14030	-3.87	-1.65	selenium-binding protein, putative contains Pfam profile PF05694: 56kDa selenium binding protein (SBP56); iden...
AT4G35770	-5.81	-2.19	senescence-associated protein (SEN1) identical to senescence-associated protein GI:1046270 from Arabidopsis th...
AT2G44670	-3.38	-1.64	senescence-associated protein-related similar to senescence-associated protein SAG102 (GI:22331931) Arabidopsi...
AT1G43780	3.93	1.67	serine carboxypeptidase S10 family protein similar to serine carboxylase II-3 GB:CAA55478 GI:474392 from Horde...
AT3G13110	-4.75	-1.95	serine O-acetyltransferase (SAT-1) identical to serine acetyltransferase (Sat-1) GI:1184048 Arabidopsis thalia...
AT2G13360	-5.94	-2.55	serine-glyoxylate aminotransferase-related similar to serine-glyoxylate aminotransferase (GI:21535798)Methylob...

Continued...

Locus	*t*-statistic	Fold change	Description
AT1G51330	4.89	1.79	serpin-related / serine protease inhibitor-related similar to serpin Hordeum vulgare subsp. vulgare CAA64599.1...
AT5G65970	3.50	1.53	seven transmembrane MLO family protein / MLO-like protein 10 (MLO10) identical to membrane protein Mlo10 Arabi...
AT1G11310	-4.63	-1.81	seven transmembrane MLO family protein / MLO-like protein 2 (MLO2) idenctical to membrane protein Mlo2 Arabido...
AT3G51840	-4.15	-1.65	short-chain acyl-CoA oxidase identical to Short-chain acyl CoA oxidase Arabidopsis thaliana GI:5478795; contai...
AT5G61530	-3.75	-1.60	small G protein family protein / RhoGAP family protein contains Pfam domain, PF00620: RhoGAP domain At5g61530....
AT1G19120	-3.38	-1.50	small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative similar to U6 snRNA-associa...
AT5G47560	-6.28	-2.11	sodium/dicarboxylate cotransporter, putative similar to SWISS-PROT:Q13183 renal sodium/dicarboxylate cotranspo...
AT1G63010	-3.39	-1.57	SPX (SYG1/Pho81/XPR1) domain-containing protein contains Pfam profile PF03105: SPX domain At1g63010.1
AT5G35770	-3.92	-1.63	sterile apetala (SAP) identical to sterile apetala (GI:9758652) Arabidopsis thaliana. At5g35770.1
AT3G50830	-3.50	-2.04	stress-responsive protein, putative similar to cold acclimation WCOR413-like protein gamma form Hordeum vulgar...
AT5G49190	-3.60	-1.57	sucrose synthase / sucrose-UDP glucosyltransferase (SUS2) nearly identical to SP—Q00917 Sucrose synthase (EC 2...
AT1G12520	-4.32	-1.80	superoxide dismutase copper chaperone, putative similar to copper chaperone for superoxide dismutase Homo sapi...
AT2G22540	3.87	1.62	SVP_ARATH (Q9FVC1) SHORT VEGETATIVE PHASE protein, partial (70
AT3G54300	-3.72	-1.59	synaptobrevin family protein similar to vesicle-associated membrane protein 7B (At VAMP7B), Arabidopsis thalia...
AT3G05710	-4.11	-1.71	syntaxin, putative similar to syntaxin of plants 42 Arabidopsis thaliana GI:5059352 At3g05710.1
AT1G69690	-3.55	-1.54	TCP family transcription factor, putative similar to PCF1 (GI:2580438) and PCF2 (GI:2580440) Oryza sativa At1g...
AT1G73190	-4.05	-1.85	tonoplast intrinsic protein, alpha / alpha-TIP (TIP3.1) identical to SP—P26587 Tonoplast intrinsic protein, al...
AT2G25810	3.94	1.71	tonoplast intrinsic protein, putative similar to tonoplast intrinsic protein GI:4584429 from Nicotiana tabacum...
AT3G53310	-3.73	-1.59	transcriptional factor B3 family protein contains Pfam profile PF02362: B3 DNA binding domain At3g53310.1
AT3G18140	-3.90	-1.75	transducin family protein / WD-40 repeat family protein contains 6 WD-40 repeats (PF00400); similar to Pop3 (G...
AT2G43770	-3.92	-1.69	transducin family protein / WD-40 repeat family protein contains 7 WD-40 repeats (PF00400); similar to U5 snRN...
AT1G20840	-4.87	-2.33	transporter-related low similarity to D-xylose proton-symporter Lactobacillus brevis GI:2895856; contains Pfam...
AT1G73260	-5.95	-2.53	trypsin and protease inhibitor family protein / Kunitz family protein similar to trypsin inhibitor propeptide ...
AT2G18280	-5.77	-2.16	tubby-like protein 2 (TULP2) identical to tubby-like protein 2 (GI:27372512) Arabidopsis thaliana; similar to ...
AT3G52560	-4.14	-1.77	ubiquitin-conjugating enzyme family protein similar to DNA-binding protein CROC-1B Homo sapiens GI:1066082; co...
AT1G12780	-5.50	-1.92	UDP-glucose 4-epimerase / UDP-galactose 4-epimerase / Galactowaldenase identical to SP—Q42605 GB:CAA90941 from...
AT1G63180	-4.99	-2.17	UDP-glucose 4-epimerase, putative / UDP-galactose 4-epimerase, putative / Galactowaldenase, putative strong si...
AT5G59290	-4.00	-2.13	UDP-glucuronic acid decarboxylase (UXS3) identical to UDP-glucuronic acid decarboxylase Arabidopsis thaliana G...
AT3G53990	-7.29	-2.46	universal stress protein (USP) family protein contains Pfam PF00582: universal stress protein family At3g53990...
AT3G17020	-5.31	-2.09	universal stress protein (USP) family protein similar to early nodulin ENOD18 Vicia faba GI:11602747; contains...
AT2G40070	-4.09	-1.76	Unknown
AT5G42445	3.81	1.69	Unknown
AT2G05170	-3.68	-1.56	vacuolar protein sorting 11 family protein / VPS11 family protein similar to Vacuolar protein sorting 11 (hVPS...
AT5G52990	-3.85	-1.59	vesicle-associated membrane protein-related contains weak similarity to vesicle-associated membrane protein 72...
AT4G28240	-9.09	-3.14	wound-responsive protein-related wound-induced protein - tomato (fragment), PIR2:S19773 At4g28240.1
AT5G28650	-3.79	-1.66	WRKY family transcription factor DNA-binding protein WRKY3, parsley, PIR:S72445 At5g28650.1
AT1G32230	-4.80	-1.91	WWE domain-containing protein / ceo protein, putative (CEO) contains Pfam domain, PF02825: WWE domain; identic...
AT4G03210	-4.36	-2.38	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan tr...
AT4G12040	-4.65	-1.77	zinc finger (AN1-like) family protein contains Pfam domains, PF01428: AN1-like Zinc finger and PF01754: A20-li...
AT1G67030	3.46	1.56	zinc finger (C2H2 type) family protein (ZFP6) identical to zinc finger protein, ZFP6 gi—790683—gb—AAA87302; co...
AT1G34370	-3.59	-1.95	zinc finger (C2H2 type) family protein contains Pfam domain, PF00096: Zinc finger, C2H2 type At1g34370.1
AT4G31420	-3.83	-1.58	zinc finger (C2H2 type) family protein contains Pfam profile: PF00096 zinc finger, C2H2 type At4g31420.1
AT5G16470	-3.95	-1.63	zinc finger (C2H2 type) family protein contains Pfam profile: PF00096 zinc finger, C2H2 type At5g16470.1
AT3G61460	-6.50	-2.19	zinc finger (C3HC4-type RING finger) family protein (BRH1) identical to BRH1 RING finger protein Arabidopsis t...
AT4G03510	-8.16	-2.64	zinc finger (C3HC4-type RING finger) family protein (RMA1) identical to RING zinc finger protein RMA1 gi:31642...
AT3G23280	-3.94	-1.68	zinc finger (C3HC4-type RING finger) family protein / ankyrin repeat family protein contains Pfam profile: PF0...
AT1G62370	-3.83	-1.62	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RI...

Continued...

Locus	*t*-statistic	Fold change	Description
AT1G18470	-3.74	-1.85	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type At1. . .
AT5G44280	3.63	1.58	zinc finger (C3HC4-type RING finger) family protein contains similarity to polycomb-M33 interacting protein Ri. . .
AT1G21570	-3.66	-1.60	zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and s. . .
AT5G41060	-3.62	-1.54	zinc finger (DHHC type) family protein contains Pfam profile PF01529: DHHC zinc finger domain At5g41060.1
AT1G32540	-4.06	-1.93	zinc finger protein, putative similar to zinc-finger protein Lsd1 Arabidopsis thaliana gi—1872521—gb—AAC49660 . . .
AT1G21000	-4.50	-1.73	zinc-binding family protein similar to zinc-binding protein Pisum sativum GI:16117799; contains Pfam profile P. . .

Table C.7: Significant expression changes in shoots of 3 week-old plants grown in nickel-spiked soil versus plants grown in unspiked soil, $p < 0.01$. Fold change values are not presented since the comparison was made on separate arrays. The sign of the t-statistic denotes the direction of the expression change.

Locus	*t*-statistic	Description
AT3G14420	-3.69	(S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy ac. . .
AT2G06050	3.76	12-oxophytodienoate reductase (OPR3) / delayed dehiscence1 (DDE1) nearly identical to DELAYED DEHISCENCE1 [GI:. . .
AT1G17990	-4.58	12-oxophytodienoate reductase, putative similar to OPR1 [GI:3882355] and OPR2 [GI:3882356] [At1g17990.1]
AT4G08040	-3.60	1-aminocyclopropane-1-carboxylate synthase, putative / ACC synthase, putative similar to ACC synthase from Mal. . .
AT5G20000	3.77	26S proteasome AAA-ATPase subunit, putative almost identical to 26S proteasome AAA-ATPase subunit RPT6a GI:665. . .
AT1G06460	7.33	31.2 kDa small heat shock family protein / hsp20 family protein contains Pfam profile: PF00011 Hsp20/alpha cry. . .
AT5G64860	4.11	4-alpha-glucanotransferase, putative / disproportionating enzyme, putative similar to 4-alpha-glucanotransfera. . .
AT3G22200	5.30	4-aminobutyrate aminotransferase / gamma-amino-N-butyrate transaminase / GABA transaminase / beta-alanine–oxo. . .
AT3G14990	3.90	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative supporting cDNA gi—11908017—g. . .
AT4G21990	-6.38	5'-adenylylsulfate reductase (APR3) / PAPS reductase homolog (PRH26) identical to 5'-adenylylsulfate reductase. . .
AT1G62180	-5.47	5'-adenylylsulfate reductase 2, chloroplast (APR2) (APSR) / adenosine 5'-phosphosulfate 5'-adenylylsulfate (AP. . .
AT4G13170	-3.74	60S ribosomal protein L13A (RPL13aC) ribosomal protein L13a -Lupinus luteus,PID:e1237871 [At4g13170.1]
AT3G50940	-4.38	AAA-type ATPase family protein contains Pfam profile: ATPase family PF00004 [At3g50940.1]
AT2G39480	3.65	ABC transporter family protein related to multi drug resistance proteins and P-glycoproteins [At2g39480.1]
AT3G55320	5.50	ABC transporter family protein similar to multidrug resistant P-glycoprotein pmdr1 GI:4204793 from [Solanum tu. . .
AT3G30842	-7.14	ABC transporter protein, putative similar to pleiotropic drug resistance like protein [Nicotiana tabacum] GI:2. . .
AT1G65950	-3.64	ABC1 family protein contains Pfam domain, PF03109: ABC1 family [At1g65950.1]
AT5G61380	6.24	ABI3-interacting protein 1 (AIP1) identical to pseudo-response regulator 1 GI:7576354 from [Arabidopsis thalia. . .
AT2G38040	-3.95	acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit family contains Pfam profile: PF03255: Acetyl. . .
AT5G48880	-4.75	acetyl-CoA C-acyltransferase 1 / 3-ketoacyl-CoA thiolase 1 (PKT1) identical to 3-keto-acyl-CoA-thiolase 1 [Ara. . .
AT2G33150	3.78	acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative similar to 3-ketoacyl-CoA thiolase . . .
AT1G04710	3.83	acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative similar to 3-ketoacyl-CoA thiolase . . .
AT5G48230	3.69	acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative strong similarity to Acetoacetyl-co. . .
AT5G44020	-3.62	acid phosphatase class B family protein similar to SP—P15490 STEM 28 kDa glycoprotein precursor (Vegetative st. . .
AT1G43800	-4.40	acyl-[acyl-carrier-protein] desaturase, putative / stearoyl-ACP desaturase, putative similar to Acyl-[acyl-car. . .
AT4G39940	4.00	adenylylsulfate kinase 2 (AKN2) identical to adenylylsulfate kinase 2, chloroplast precursor (APS kinase, Aden. . .
AT1G72330	3.69	alanine aminotransferase, putative similar to alanine aminotransferase 2 SP—P34106 from Panicum miliaceum, SP—. . .
AT4G34240	-5.62	aldehyde dehydrogenase (ALDH3) similar to aldehyde dehydrogenase [Arabidopsis thaliana] gi—17065876—emb—CAC849. . .
AT3G57520	6.37	alkaline alpha galactosidase, putative similar to alkaline alpha galactosidase II [Cucumis melo] GI:29838631; . . .
AT5G42650	6.19	allene oxide synthase (AOS) / hydroperoxide dehydrase / cytochrome P450 74A (CYP74A) identical to Allene oxide. . .
AT5G02730	3.70	allergen V5/Tpx-1-related family protein low similarity to SP—Q05968 Pathogenesis-related protein 1 precursor . . .
AT4G23590	6.16	aminotransferase class I and II family protein similar to nicotianamine aminotransferase from Hordeum vulgare . . .
AT2G20610	4.61	aminotransferase, putative similar to nicotianamine aminotransferase from Hordeum vulgare [GI:6498122, GI:6469. . .
AT3G23790	4.49	AMP-binding protein, putative similar to AMP-binding protein GB:CAA96521 from [Brassica napus] (Plant Mol. Bio. . .
AT3G48990	4.22	AMP-dependent synthetase and ligase family protein similar to peroxisomal-coenzyme A synthetase (FAT2) [gi:586. . .
AT1G07710	3.62	ankyrin repeat family protein contains ankyrin repeat domains, Pfam:PF00023 [At1g07710.1]
AT1G11740	3.69	ankyrin repeat family protein contains ankyrin repeats, Pfam domain PF00023 [At1g11740.1]
AT2G28840	4.53	ankyrin repeat family protein contains ankyrin repeats, Pfam:PF00023 [At2g28840.1]
AT5G15500	-4.10	ankyrin repeat family protein contains Pfam domain, PF00023: Ankyrin repeat [At5g15500.1]
AT5G17990	4.22	anthranilate phosphoribosyltransferase identical to anthranilate phosphoribosyltransferase, chloroplast precur. . .

Continued. . .

Locus	*t*-statistic	Description
AT1G24807	4.92	anthranilate synthase beta subunit, putative similar to anthranilate synthase beta chain GI:403434; similar to...
AT1G25083	4.32	anthranilate synthase beta subunit, putative strong similarity to anthranilate synthase beta subunit GI:403434...
AT5G05730	5.35	anthranilate synthase, alpha subunit, component I-1 (ASA1) identical to SP—P32068 [At5g05730.1]
AT2G29690	4.08	anthranilate synthase, alpha subunit, component I-2 (ASA2) identical to SP—P32069 [At2g29690.1]
AT4G31060	-3.89	AP2 domain-containing transcription factor, putative TINY, Arabidopsis thaliana, PID:E218696 [At4g31060.1]
AT4G08900	-5.00	arginase identical to Swiss-Prot:P46637 arginase (EC 3.5.3.1) [Arabidopsis thaliana] [At4g08900.1]
AT1G48410	-3.62	argonaute protein (AGO1) identical to SP—O04379 Argonaute protein (AGO1) Arabidopsis thaliana; contains Pfam p...
AT5G13060	3.75	armadillo/beta-catenin repeat family protein / BTB/POZ domain-containing protein contains armadillo/beta-caten...
AT1G23030	-5.06	armadillo/beta-catenin repeat family protein / U-box domain-containing protein contains Pfam domain, PF00514: ...
AT3G03440	3.99	armadillo/beta-catenin repeat family protein contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat...
AT3G53800	5.81	armadillo/beta-catenin repeat family protein contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat...
AT1G49670	3.78	ARP protein (REF) identical to ARP protein GB:CAA89858 GI:886434 from [Arabidopsis thaliana]; contains Pfam pr...
AT2G03200	3.91	aspartyl protease family protein contains Pfam domain, PF00026: eukaryotic aspartyl protease [At2g03200.1]
AT4G04620	4.77	autophagy 8b (APG8b) identical to autophagy 8b [Arabidopsis thaliana] GI:19912153; contains Pfam profile PF029...
AT2G46370	5.42	auxin-responsive GH3 family protein similar to auxin-responsive GH3 product [Glycine max] GI:18591; contains P...
AT1G04250	-3.95	auxin-responsive protein / indoleacetic acid-induced protein 17 (IAA17) Identical to SP—P93830 Auxin-responsiv...
AT1G04240	-4.09	auxin-responsive protein / indoleacetic acid-induced protein 3 (IAA3) identical to SP—Q38822 Auxin-responsive ...
AT1G15580	-3.66	auxin-responsive protein / indoleacetic acid-induced protein 5 (IAA5) / auxin-induced protein (AUX2-27) identi...
AT5G18020	-6.41	auxin-responsive protein, putative similar to auxin-inducible SAUR (Small Auxin Up RNAs) (GI:3043536) [Raphanu...
AT5G18030	-5.31	auxin-responsive protein, putative similar to auxin-inducible SAUR (Small Auxin Up RNAs) (GI:3043536) [Raphanu...
AT3G03830	-4.34	auxin-responsive protein, putative similar to auxin-inducible SAUR (Small Auxin Up RNAs) (GI:3043536) [Raphanu...
AT5G18010	-3.78	auxin-responsive protein, putative similar to auxin-inducible SAUR (Small Auxin Up RNAs) (GI:3043536) [Raphanu...
AT5G18060	-7.12	auxin-responsive protein, putative similar to auxin-inducible SAUR (Small Auxin Up RNAs) GI:3043536 from radis...
AT5G18080	-4.40	auxin-responsive protein, putative similar to GP:3043536 SAUR Raphanus sativus [At5g18080.1]
AT5G51570	3.63	band 7 family protein similar to hypersensitive-induced response protein [Zea mays] GI:7716468; contains Pfam ...
AT5G28010	-3.92	Bet v I allergen family protein similar to Csf-2 [Cucumis sativus][GI:5762258][J Am Soc Hortic Sci 124, 136-13...
AT5G20390	5.21	beta-1,3-glucanase, putative similar to plant beta-1,3-glucanase bg4 GI:2808438 from [Arabidopsis thaliana] [A...
AT5G52570	-4.31	beta-carotene hydroxylase, putative similar to GI:1575296, beta-carotene hydroxylase [At5g52570.1]
AT3G06500	4.92	beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative s...
AT3G13750	5.13	beta-galactosidase, putative / lactase, putative similar to beta-galactosidase precursor SP:P48980 from [Lycop...
AT5G15160	-6.98	bHLH family protein [At5g15160.1]
AT1G10070	5.09	branched-chain amino acid aminotransferase 2 / branched-chain amino acid transaminase 2 (BCAT2) identical to S...
AT1G23760	-5.10	BURP domain-containing protein / polygalacturonase, putative similar to polygalacturonase isoenzyme 1 beta sub...
AT5G11260	-3.73	bZIP protein HY5 (HY5) identical to HY5 protein GI:2251085 from [Arabidopsis thaliana] [At5g11260.1]
AT5G44090	3.60	calcium-binding EF hand family protein, putative / protein phosphatase 2A 62 kDa B” regulatory subunit, putat...
AT2G46600	-3.72	calcium-binding protein, putative similar to EF-hand Ca2+-binding protein CCD1 [Triticum aestivum] GI:9255753 ...
AT1G18210	3.74	calcium-binding protein, putative similar to SP—Q9M7R0 Calcium-binding allergen Ole e 8 (PCA18/PCA23) Olea eur...
AT2G22950	-3.76	calcium-transporting ATPase, plasma membrane-type, putative / Ca2+-ATPase, putative (ACA7) identical to SP—O64...
AT1G52410	6.26	caldesmon-related weak similarity to Caldesmon (CDM) (Swiss-Prot:P12957) [Gallus gallus] [At1g52410.1]
AT5G09410	4.10	calmodulin-binding protein similar to anther ethylene-upregulated calmodulin-binding protein ER1 GI:11612392 f...
AT4G31000	4.27	calmodulin-binding protein similar to calmodulin-binding protein TCB60 GI:1698548 from [Nicotiana tabacum]; co...
AT2G43290	-3.71	calmodulin-like protein (MSS3) identical to calmodulin-like MSS3 from GI:9965747 [Arabidopsis thaliana] [At2g4...
AT5G14740	-3.98	carbonic anhydrase 2 / carbonate dehydratase 2 (CA2) (CA18) nearly identical to SP—P42737 Carbonic anhydrase 2...
AT4G35090	-4.26	catalase 2 identical to catalase 2 SP:P25819, GI:17865693 from [Arabidopsis thaliana] [At4g35090.1]
AT5G57630	4.31	CBL-interacting protein kinase 21, putative (CIPK21) identical to CBL-interacting protein kinase 21 [Arabidops...
AT2G26980	4.40	CBL-interacting protein kinase 3 (CIPK3) identical to CBL-interacting protein kinase 3 [Arabidopsis thaliana] ...
AT1G01140	-6.10	CBL-interacting protein kinase 9 (CIPK9) identical to CBL-interacting protein kinase 9 [Arabidopsis thaliana] ...

Continued...

Locus	*t*-statistic	Description
AT2G34720	-6.37	CCAAT-binding transcription factor (CBF-B/NF-YA) family protein contains Pfam profile: PF02045 CCAAT-binding t...
AT5G63470	-3.76	CCAAT-box binding transcription factor Hap5a, putative [At5g63470.1]
AT3G53340	-3.76	CCAAT-box binding transcription factor, putative similar to CAAT-box DNA binding protein subunit B (NF-YB) (SP...
AT5G64740	-4.48	cellulose synthase, catalytic subunit, putative similar to gi:2827141 cellulose synthase catalytic subunit (At...
AT5G09870	-3.66	cellulose synthase, catalytic subunit, putative similar to gi:2827141 cellulose synthase catalytic subunit (At...
AT4G32190	-6.28	centromeric protein-related low similarity to SP—Q02224 Centromeric protein E (CENP-E protein) Homo sapiens [A...
AT5G13930	-3.80	chalcone synthase / naringenin-chalcone synthase identical to SP—P13114 [At5g13930.1]
AT5G05270	-4.37	chalcone-flavanone isomerase family protein contains very low similarity to chalcone-flavonone isomerase (chal...
AT2G43580	4.76	chitinase, putative similar to basic endochitinase CHB4 precursor SP:Q06209 from [Brassica napus] [At2g43580.1...
AT1G02360	4.06	chitinase, putative similar to chitinase precursor GI:5880845 from [Petroselinum crispum] [At1g02360.1]
AT3G22840	-4.86	chlorophyll A-B binding family protein / early light-induced protein (ELIP) identical to early light-induced p...
AT1G80300	4.69	chloroplast ADP, ATP carrier protein 1 / ADP, ATP translocase 1 / adenine nucleotide translocase 1 (AATP1) ide...
AT1G15500	6.53	chloroplast ADP, ATP carrier protein, putative / ADP, ATP translocase, putative / adenine nucleotide transloca...
AT5G20300	-6.96	chloroplast outer membrane protein, putative similar to chloroplast protein import component Toc159 [Pisum sat...
AT2G16640	5.28	chloroplast outer membrane protein, putative similar to chloroplast protein import component Toc159 [Pisum sat...
AT5G37630	-3.82	chromosome condensation family protein contains pfam profile: PF04154 chromosome condensation protein 3, C-ter...
AT4G30470	-6.01	cinnamoyl-CoA reductase-related similar to cinnamoyl-CoA reductase from Pinus taeda [GI:17978649], Saccharum o...
AT1G09500	-5.09	cinnamyl-alcohol dehydrogenase family / CAD family similar to cinnamyl alcohol dehydrogenase, Eucalyptus gunni...
AT5G19440	3.89	cinnamyl-alcohol dehydrogenase, putative (CAD) similar to cinnamyl-alcohol dehydrogenase, Eucalyptus gunnii [G...
AT2G27250	-3.70	CLAVATA3 CLAVATA3/ESR-Related (CLE) family of proteins; ligand for CLV1; responsible for negative regulation o...
AT1G04620	7.09	coenzyme F420 hydrogenase family / dehydrogenase, beta subunit family contains Pfam PF04432: Coenzyme F420 hyd...
AT2G42530	-4.86	cold-responsive protein / cold-regulated protein (cor15b) nearly identical to cold-regulated gene cor15b [Arab...
AT3G49190	-4.70	condensation domain-containing protein contains Pfam profile PF00668: Condensation domain [At3g49190.1]
AT1G07050	6.98	CONSTANS-like protein-related contains similarity to photoperiod sensitivity quantitative trait locus (Hd1) GI...
AT1G31710	-4.46	copper amine oxidase, putative similar to copper amine oxidase [Lens culinaris] gi—15451834—gb—AAB34918 [At1g3...
AT3G24450	-4.74	copper-binding family protein similar to copper homeostasis factor gi:3168840 from Arabidopsis thaliana; conta...
AT1G19670	3.72	coronatine-responsive protein / coronatine-induced protein 1 (CORI1) identical to coronatine-induced protein 1...
AT4G23600	4.05	coronatine-responsive tyrosine aminotransferase / tyrosine transaminase similar to nicotianamine aminotransfer...
AT3G22760	5.53	CXC domain containing TSO1-like protein 1 (SOL1) identical to CXC domain containing TSO1-like protein 1 (SOL1)...
AT1G27630	3.64	cyclin family protein similar to cyclin T1 [Homo sapiens] GI:2981196; contains Pfam profile PF00134: Cyclin, N...
AT5G10270	-4.38	cyclin-dependent kinase, putative / CDK, putative similar to cyclin dependent kinase C [Lycopersicon esculentu...
AT4G39090	4.73	cysteine proteinase RD19a (RD19A) / thiol protease identical to cysteine proteinase RD19a, thiol protease SP:P...
AT4G39950	6.69	cytochrome P450 79B2, putative (CYP79B2) identical to cytochrome P450 (79B2) SP:O81346 from [Arabidopsis thali...
AT4G31500	6.45	cytochrome P450 83B1 (CYP83B1) Identical to Cytochrome P450 (SP:O65782)[Arabidopsis thaliana] [At4g31500.1]
AT4G36220	-5.18	cytochrome P450 84A1 (CYP84A1) / ferulate-5-hydroxylase (FAH1) identical to Cytochrome P450 84A1 (Ferulate-5-h...
AT4G39480	3.63	cytochrome P450 family protein contains Pfam profile: PF00067 cytochrome P450 [At4g39480.1]
AT4G15380	5.06	cytochrome P450 family protein similar to CYTOCHROME P450 93A3 (P450 CP5) (SP:O81973) [Glycine max] [At4g15380...
AT3G25180	-5.92	cytochrome P450 family protein similar to cytochrome P450 monooxygenase GB:AAC49188 [Pisum sativum]; contains ...
AT4G39500	-4.79	cytochrome P450, putative simialrity to cytochrome P450 CYP86A1, Arabidopsis thaliana, EMBL:X90458 [At4g39500....
AT3G03470	-4.79	cytochrome P450, putative similar to cytochrome P450 89A2 GB:Q42602 [Arabidopsis thaliana] [At3g03470.1]
AT4G37370	5.60	cytochrome P450, putative similar to Cytochrome P450 91A1 (SP:Q9FG65)[Arabidopsis thaliana]; cytochrome P450,...
AT1G66540	-3.71	cytochrome P450, putative Similar to cytochrome P450 91A1 (SP:Q9FG65)[Arabidopsis thaliana]; contains Pfam pro...
AT1G57750	-3.78	cytochrome P450, putative similar to cytochrome P450 GI:4688670 from [Catharanthus roseus] [At1g57750.1]
AT1G17745	6.35	D-3-phosphoglycerate dehydrogenase / 3-PGDH identical to SP—O04130 [At1g17745.1]
AT2G17740	-4.34	DC1 domain-containing protein [At2g17740.1]
AT1G69150	-4.09	DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain [At1g69150.1]
AT3G26240	3.73	DC1 domain-containing protein contains Pfam profile PF03107: DC1 domain [At3g26240.1]

Continued...

Locus	*t*-statistic	Description
AT1G53340	-4.10	DC1 domain-containing protein contains Pfam protein PF03107 DC1 domain [At1g53340.1]
AT3G06980	5.16	DEAD/DEAH box helicase, putative contains Pfam profile: PF00270 DEAD/DEAH box helicase [At3g06980.1]
AT2G45750	4.06	dehydration-responsive family protein similar to early-responsive to dehydration stress ERD3 protein [Arabidop...
AT5G66400	-3.68	dehydrin (RAB18) nearly identical to SP—P30185 Dehydrin Rab18 Arabidopsis thaliana [At5g66400.1]
AT3G50980	-4.79	dehydrin, putative similar to dehydrin Xero 1 [Arabidopsis thaliana] SWISS-PROT:P25863 [At3g50980.1]
AT5G58770	-14.33	dehydrodolichyl diphosphate synthase, putative / DEDOL-PP synthase, putative similar to GI:796076 [At5g58770.1...
AT5G62530	4.05	delta-1-pyrroline-5-carboxylate dehydrogenase (P5CDH) identical to delta-1-pyrroline-5-carboxylate dehydrogena...
AT1G48430	-4.33	dihydroxyacetone kinase family protein similar to dihydroxyacetone kinases; contains Pfam profiles PF02733: DA...
AT2G15080	3.78	disease resistance family protein contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611;...
AT4G11190	3.69	disease resistance-responsive family protein / dirigent family protein similar to dirigent protein [Forsythia ...
AT3G26680	-3.74	DNA cross-link repair protein-related contains weak similarity to Swiss-Prot:P30620 DNA cross-LINK repair prot...
AT5G06250	-4.59	DNA-binding protein, putative similar to DNA-binding proteins from [Arabidopsis thaliana] RAV1 GI:3868857 and ...
AT5G35970	-3.75	DNA-binding protein, putative similar to SWISS-PROT:Q60560 DNA-binding protein SMUBP-2 (Immunoglobulin MU bind...
AT4G12050	-12.87	DNA-binding protein-related contains Pfam domain PF03479: Domain of unknown function (DUF296), found in AT-hoo...
AT4G00238	-4.85	DNA-binding storekeeper protein-related contains Pfam PF04504: Protein of unknown function, DUF573; similar to...
AT3G59600	-10.78	DNA-directed RNA polymerase I, II, and III, putative similar to SP—P52434 DNA-directed RNA polymerases I, II, ...
AT5G23240	6.30	DNAJ heat shock N-terminal domain-containing protein low similarity to SP—O34136 Chaperone protein dnaJ (40 kD...
AT1G10350	-5.43	DNAJ heat shock protein, putative similar to SP—Q9QYJ3 DnaJ homolog subfamily B member 1 (Heat shock 40 kDa pr...
AT5G62940	3.65	Dof-type zinc finger domain-containing protein Dof zinc finger protein, Oryza sativa, EMBL:AB028129 [At5g62940...
AT5G62430	-5.04	Dof-type zinc finger domain-containing protein similar to H-protein promoter binding factor-2a GI:3386546 from...
AT2G33830	4.18	dormancy/auxin associated family protein contains Pfam profile: PF05564 dormancy/auxin associated protein [At2...
AT1G28330	6.71	dormancy-associated protein, putative (DRM1) identical to dormancy-associated protein [Arabidopsis thaliana] G...
AT4G22530	4.38	embryo-abundant protein-related similar to embryo-abundant protein [Picea glauca] GI:1350531 [At4g22530.1]
AT4G26740	3.63	embryo-specific protein 1 (ATS1) identical to embryo-specific protein 1 [Arabidopsis thaliana] GI:3335169 [At4...
AT2G15060	-4.77	En/Spm-like transposon protein [Arabidopsis thaliana] [NP454953]
AT2G01970	4.70	endomembrane protein 70, putative [At2g01970.1]
AT4G39030	5.72	enhanced disease susceptibility 5 (EDS5) / salicylic acid induction deficient 1 (SID1) identical to SP—Q945F0;...
AT1G54570	5.32	esterase/lipase/thioesterase family protein contains Interpro entry IPR000379 [At1g54570.1]
AT4G17490	-4.13	ethylene-responsive element-binding protein, putative similar to SP—O80341 Ethylene responsive element binding...
AT5G54940	-4.38	eukaryotic translation initiation factor SUI1, putative similar to SP—P32911 Protein translation factor SUI1 S...
AT5G25820	4.58	exostosin family protein contains Pfam profile: PF03016 exostosin family [At5g25820.1]
AT3G45970	-7.99	expansin family protein (EXPL1) similar to cim1 induced allergen, Glycine max, EMBL:U03860; expansin-like gene...
AT4G38400	-6.21	expansin family protein (EXPL2) contains Pfam profile: PF01357 pollen allergen; expansin-like gene, PMID:11641...
AT3G45960	-7.83	expansin family protein (EXPL3) contains Pfam profile: PF01357 pollen allergen; expansin-like gene, PMID:11641...
AT5G39300	-3.93	expansin, putative (EXP25) similar to alpha-expansin 4 precursor GI:16923355 from [Cucumis sativus]; alpha-exp...
AT2G39700	3.69	expansin, putative (EXP4) similar to alpha-expansin 6 precursor GI:16923359 from [Cucumis sativus]; alpha-expa...
AT3G45900	3.63	expressed protein [At3g45900.1]
AT4G18740	-4.82	expressed protein [At4g18740.1]
AT4G34260	-4.12	expressed protein [At4g34260.1]
AT4G35560	5.04	expressed protein [At4g35560.1]
AT1G01180	-4.79	expressed protein [At1g01180.1]
AT1G01840	-6.01	expressed protein [At1g01840.1]
AT1G04960	-4.12	expressed protein [At1g04960.1]
AT1G07280	4.70	expressed protein [At1g07280.1]
AT1G14760	-3.86	expressed protein [At1g14760.1]
AT1G18380	4.73	expressed protein [At1g18380.1]
AT1G18620	5.29	expressed protein [At1g18620.1]

Continued...

Locus	*t*-statistic	Description
AT1G19370	4.70	expressed protein [At1g19370.1]
AT1G27300	6.21	expressed protein [At1g27300.1]
AT1G50020	-3.84	expressed protein [At1g50020.1]
AT1G63670	4.65	expressed protein [At1g63670.1]
AT1G64680	-3.72	expressed protein [At1g64680.1]
AT1G65090	-4.13	expressed protein [At1g65090.1]
AT1G68440	-3.81	expressed protein [At1g68440.1]
AT1G68660	-4.34	expressed protein [At1g68660.1]
AT1G76250	-5.22	expressed protein [At1g76250.1]
AT1G76980	-4.25	expressed protein [At1g76980.1]
AT2G19180	3.72	expressed protein [At2g19180.1]
AT2G19310	-3.80	expressed protein [At2g19310.1]
AT2G20495	-3.72	expressed protein [At2g20495.1]
AT2G25510	4.27	expressed protein [At2g25510.1]
AT2G35470	-4.56	expressed protein [At2g35470.1]
AT3G09180	4.03	expressed protein [At3g09180.1]
AT3G12320	-7.36	expressed protein [At3g12320.1]
AT3G13330	5.82	expressed protein [At3g13330.1]
AT3G24150	5.90	expressed protein [At3g24150.1]
AT3G26670	-4.19	expressed protein [At3g26670.1]
AT3G61270	4.52	expressed protein [At3g61270.1]
AT3G63160	-4.08	expressed protein [At3g63160.1]
AT3G63300	4.03	expressed protein [At3g63300.1]
AT4G08810	-5.25	expressed protein [At4g08810.1]
AT4G19160	-3.93	expressed protein [At4g19160.1]
AT4G24430	3.65	expressed protein [At4g24430.1]
AT4G27380	-4.12	expressed protein [At4g27380.1]
AT4G27580	-3.71	expressed protein [At4g27580.1]
AT4G27840	3.83	expressed protein [At4g27840.1]
AT4G28100	3.67	expressed protein [At4g28100.1]
AT4G38440	4.10	expressed protein [At4g38440.1]
AT5G11480	3.97	expressed protein [At5g11480.1]
AT5G15120	4.23	expressed protein [At5g15120.1]
AT5G18120	3.91	expressed protein [At5g18120.1]
AT5G22310	-3.94	expressed protein [At5g22310.1]
AT5G40690	-4.03	expressed protein [At5g40690.1]
AT5G45590	-3.64	expressed protein [At5g45590.1]
AT5G51720	-12.39	expressed protein [At5g51720.1]
AT5G55640	4.40	expressed protein [At5g55640.1]
AT1G28630	-4.16	expressed protein ; expression supported by MPSS [At1g28630.1]
AT5G65470	-4.64	expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins i. . .
AT1G20550	3.91	expressed protein contains Pfam PF03138: Plant protein family. The function of this family of plant proteins i. . .
AT4G21570	4.83	expressed protein contains Pfam profile PF03619: Domain of unknown function [At4g21570.1]
AT1G56580	-4.16	expressed protein contains Pfam profile PF04398: Protein of unknown function, DUF538 [At1g56580.1]
AT2G41660	-4.07	expressed protein contains Pfam profile PF04759: Protein of unknown function, DUF617 [At2g41660.1]
AT1G43020	-5.24	expressed protein contains Pfam profile PF04784: Protein of unknown function, DUF547 [At1g43020.1]
AT2G34510	-5.07	expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642 [At2g34510.1]

Continued. . .

Locus	*t*-statistic	Description
AT5G11420	-3.71	expressed protein contains Pfam profile PF04862: Protein of unknown function, DUF642 [At5g11420.1]
AT4G30200	-4.69	expressed protein contains weak similarities to Pfam profiles: PF00041 Fibronectin type III domain, PF00628 PH...
AT4G08280	4.15	expressed protein hypothetical protein ssr1391 - Synechocystis sp. (strain PCC 6803),PIR2:S75571 [At4g08280.1]
AT3G49890	3.69	expressed protein lea32, Arabidopsis thaliana, EMBL:ATH131342 [At3g49890.1]
AT1G23060	4.79	expressed protein Location of EST gb—T22158 and gb—AA395675 [At1g23060.1]
AT2G40935	-4.15	expressed protein low similarity to PGPS/D12 [Petunia x hybrida] GI:4105794; contains Pfam profile PF04749: Pr...
AT4G27500	5.33	expressed protein non-consensus GA donor splice site at exon 6 [At4g27500.1]
AT5G59400	-3.79	expressed protein predicted protein, Arabidopsis thaliana [At5g59400.2]
AT5G36920	-5.56	expressed protein predicted protein, Arabidopsis thaliana; expression supported by MPSS [At5g36920.1]
AT1G10190	6.04	expressed protein similar to hypothetical protein GB:CAB10284 contains Pfam profile PF03080: Arabidopsis prote...
AT4G26260	3.74	expressed protein similar to myo-inositol oxygenase [Sus scrofa] gi—17432544—gb—AAL39076 [At4g26260.1]
AT5G66480	-4.17	expressed protein similar to unknown protein (pir——T08412) [At5g66480.1]
AT3G01310	4.02	expressed protein similar to unknown protein GB:BAA24863 [Homo sapiens], unknown protein GB:BAA20831 [Homo sap...
AT3G56360	5.64	expressed protein unknown protein 110K5.12 - Sorghum bicolor, TREMBL:AF124045_5 [At3g56360.1]
AT1G55960	-4.95	expressed protein weak similarity to SP—P53808 Phosphatidylcholine transfer protein (PC-TP) Mus musculus [At1g...
AT5G35730	4.67	EXS family protein / ERD1/XPR1/SYG1 family protein low similarity to xenotropic and polytropic murine leukemia...
AT1G23470	3.71	F28C11.10 [NP221342]
AT5G44440	-4.56	FAD-binding domain-containing protein similar to SP—P30986 reticuline oxidase precursor (Berberine-bridge-form...
AT1G03870	-4.06	fasciclin-like arabinogalactan-protein (FLA9) identical to gi_13377784_gb_AAK20861 [At1g03870.1]
AT4G34510	-6.08	fatty acid elongase, putative similar to fatty acid elongase 1, Arabidopsis thaliana,gb:U29142 [GI:881615] [At...
AT2G39490	4.57	F-box family protein ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250 [At2g39490.1]
AT2G36370	4.43	F-box family protein (FBL11) contains similarity to leucine-rich repeats containing F-box protein FBL3 GI:5919...
AT2G03560	-3.78	F-box family protein (FBX7) identical to F-box protein family, AtFBX7 (GI:20197899) [Arabidopsis thaliana]; co...
AT5G18680	4.22	F-box family protein / tubby family protein similar to phosphodiesterase (GI:467578) [Mus musculus]; similar t...
AT5G22660	4.82	F-box family protein contains F-box domain Pfam:PF00646 [At5g22660.1]
AT5G56420	3.62	F-box family protein contains F-box domain Pfam:PF00646 [At5g56420.1]
AT3G62230	5.99	F-box family protein contains Pfam:PF00646 F-box domain [At3g62230.1]
AT1G06110	4.20	F-box family protein contains similarity to F-box protein FBX3 GI:6103643 from [Homo sapiens] ; similar to SKP...
AT5G27920	4.59	F-box family protein contains similarity to leucine-rich repeats containing F-box protein FBL3 GI:5919219 from...
AT1G67160	3.84	F-box family protein similar to F-box protein family, AtFBX7 (GI:20197899) [Arabidopsis thaliana] [At1g67160.1...
AT5G07670	4.60	F-box family protein similar to unknown protein (pir——C71419) ; similar to SKP1 interacting partner 2 (SKIP2) ...
AT1G80960	4.71	F-box protein-related contains weak hit to Pfam PF00646: F-box domain [At1g80960.1]
AT2G40300	-5.19	ferritin, putative similar to ferritin subunit cowpea2 precursor [Vigna unguiculata] GI:2970654; contains Pfam...
AT5G08640	-6.69	flavonol synthase 1 (FLS1) identical to SP—Q96330; contains PF03171 2OG-Fe(II) oxygenase superfamily [At5g0864...
AT3G62720	-4.26	galactosyl transferase GMA12/MNN10 family protein low similarity to alpha-1,2-galactosyltransferase, Schizosac...
AT1G72030	-4.34	GCN5-related N-acetyltransferase (GNAT) family protein contains Pfam profile PF00583: acetyltransferase, GNAT ...
AT5G11340	-3.65	GCN5-related N-acetyltransferase (GNAT) family protein low similarity to SP—Q03503 L-A virus GAG protein N-ace...
AT5G03600	4.22	GDSL-motif lipase/hydrolase family protein low similarity to family II lipase EXL3 [Arabidopsis thaliana] GI:1...
AT5G45950	-6.23	GDSL-motif lipase/hydrolase family protein similar to family II lipase EXL3 (GI:15054386) and EXL1 (GI:1505438...
AT4G28780	-4.46	GDSL-motif lipase/hydrolase family protein similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382),...
AT5G40990	4.67	GDSL-motif lipase/hydrolase family protein similar to lipase [Arabidopsis thaliana] GI:1145627; contains Pfam ...
AT1G53990	4.13	GDSL-motif lipase/hydrolase family protein similar to myrosinase-associated proteins from [Brassica napus] GI:...
AT1G56670	-3.62	GDSL-motif lipase/hydrolase family protein similarity to early early nodulin ENOD8 [Medicago sativa] GI:304037...
AT5G20630	5.13	germin-like protein (GER3) identical to germin-like protein subfamily 3 member 3 [SP—P94072] [At5g20630.1]
AT2G30810	4.44	gibberellin-regulated family protein similar to GASA5 [Arabidopsis thaliana] GI:1289320; contains Pfam profile...
AT2G14900	-7.61	gibberellin-regulated family protein similar to SP—P46690 Gibberellin-regulated protein 4 precursor Arabidopsi...
AT5G15230	8.62	gibberellin-regulated protein 4 (GASA4) / gibberellin-responsive protein 4 identical to SP—P46690 Gibberellin-...

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Locus	*t*-statistic	Description
AT3G29320	5.80	glucan phosphorylase, putative similar to alpha-glucan phosphorylase, L isozyme 1 precursor GB:P04045 from [So...
AT1G11260	4.29	glucose transporter (STP1) nearly identical to glucose transporter GB:P23586 SP—P23586 from [Arabidopsis thali...
AT5G07440	5.49	glutamate dehydrogenase 2 (GDH2) identical to glutamate dehydrogenase 2 (GDH 2) [Arabidopsis thaliana] SWISS-P...
AT1G23310	-4.63	glutamate:glyoxylate aminotransferase 1 (GGT1) identical to glutamate:glyoxylate aminotransferase 1 [Arabidops...
AT3G53180	4.16	glutamine synthetase, putative similar to glutamine synthetase (glutamate–ammonia ligase) [Bacillus subtilis]...
AT5G16570	-5.14	glutamine synthetase, putative similar to glutamine synthetase, cytosolic isozyme (glutamate– ammonia ligase)...
AT1G58290	-6.05	glutamyl-tRNA reductase 1 / GluTR (HEMA1) identical to glutamyl-tRNA reductase 1, chloroplast [SP—P42804] [At1...
AT2G31250	-3.72	glutamyl-tRNA reductase, putative similar to HEMA2 [SP—P49294], HEMA1 [SP—P42804] [At2g31250.1]
AT1G28480	4.12	glutaredoxin family protein contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase) [At1g28480.1]
AT4G31870	-5.49	glutathione peroxidase, putative glutathione peroxidase, Arabidopsis thaliana, PIR2:S71250 [At4g31870.1]
AT2G02390	3.86	glutathione S-transferase zeta 1 (GSTZ1) (GST18) identical to SP—Q9ZVQ3—GTZ1_ARATH Glutathione S-transferase ...
AT2G02930	3.90	glutathione S-transferase, putative [At2g02930.1]
AT2G29460	-3.66	glutathione S-transferase, putative [At2g29460.1]
AT4G02520	6.52	glutathione S-transferase, putative [At4g02520.1]
AT2G30860	4.65	glutathione S-transferase, putative identical to GB:Y12295 [At2g30860.1]
AT1G27130	4.00	glutathione S-transferase, putative similar to glutathione S-transferase GB: AAF22517 GI:6652870 from [Papaver...
AT1G59700	-5.65	glutathione S-transferase, putative similar to glutathione S-transferase GB:AAF29773 GI:6856103 from [Gossypiu...
AT5G27380	3.91	glutathione synthetase (GSH2) non-consensus AT donor splice site at exon 6, AC acceptor splice site at exon 7;...
AT2G35370	-7.43	glycine cleavage system H protein 1, mitochondrial (GDCSH) (GCDH) identical to SP—P25855 Glycine cleavage syst...
AT3G07560	3.83	glycine-rich protein [At3g07560.1]
AT5G61660	3.69	glycine-rich protein [At5g61660.1]
AT2G21660	3.89	glycine-rich RNA-binding protein (GRP7) SP—Q03250 Glycine-rich RNA-binding protein 7 Arabidopsis thaliana [At2...
AT4G39260	3.89	glycine-rich RNA-binding protein 8 (GRP8) (CCR1) SP—Q03251 Glycine-rich RNA-binding protein 8 (CCR1 protein) (...
AT4G32375	-4.51	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein similar to polygalacturon...
AT1G52400	4.40	glycosyl hydrolase family 1 protein / beta-glucosidase, putative (BG1) contains Pfam PF00232 : Glycosyl hydrol...
AT3G57270	-5.72	glycosyl hydrolase family 17 protein similar to beta-1,3-glucanase GI:16903144 from [Prunus persica] [At3g5727...
AT3G47010	-3.93	glycosyl hydrolase family 3 protein beta-D-glucan exohydrolase, Nicotiana tabacum, TREMBL:AB017502_1 [At3g470...
AT4G09090	-3.79	glycosyl hydrolase family protein 17 similar to glucan endo-1,3-beta-glucosidase precursor SP:P52409 from [Tri...
AT1G73740	3.78	glycosyl transferase family 28 protein similar to UDP-N-acetylglucosamine–N-acetylmuramyl-(pentapeptide)-pyro...
AT4G01210	-5.64	glycosyltransferase family protein 1 contains Pfam profile: PF00534 Glycosyl transferases group 1 [At4g01210.1...
AT5G54840	3.73	GTP-binding family protein similar to SP—P87027 Septum-promoting GTP-binding protein 1 (GTPase spg1)(Sid3 prot...
AT5G02230	-3.78	haloacid dehalogenase-like hydrolase family protein contains InterPro accession IPR005834: Haloacid dehalogena...
AT2G41250	3.74	haloacid dehalogenase-like hydrolase family protein low similarity to SP—Q94915 Rhythmically expressed gene 2 ...
AT5G02490	-4.17	heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2) identical to SP—P22954 Heat shock cognate 70 kDa prote...
AT3G52490	4.77	heat shock protein-related contains similarity to 101 kDa heat shock protein; HSP101 [Triticum aestivum] gi—11...
AT1G51090	-3.63	heavy-metal-associated domain-containing protein contains Pfam profile PF00403: Heavy-metal-associated domain...
AT4G23800	4.97	high mobility group (HMG1/2) family protein similar to HMG2B [Homo sapiens] GI:32335; contains Pfam profile PF...
AT3G12980	4.66	histone acetyltransferase 5 (HAC5) identical to HAC5 (GI:21105780) [Arabidopsis thaliana]; similar to CREB-bin...
AT5G35600	-5.97	histone deacetylase, putative (HDA7) similar to SP—O22446 Histone deacetylase (HD) Arabidopsis thaliana; conta...
AT1G54260	-4.24	histone H1/H5 family protein contains Pfam domain, PF00538: linker histone H1 and H5 family [At1g54260.1]
AT1G62360	3.86	homeobox protein SHOOT MERISTEMLESS (STM) identical to homeobox protein SHOOT MERISTEMLESS (STM) SP:Q38874 fro...
AT5G54080	4.82	homogentisate 1,2-dioxygenase / homogentisicase/homogentisate oxygenase / homogentisic acid oxidase (HGO) iden...
AT5G39220	5.30	hydrolase, alpha/beta fold family protein contains Pfam profile: PF00561 alpha/beta hydrolase fold [At5g39220....
AT5G58310	6.12	hydrolase, alpha/beta fold family protein low similarity to SP—Q40708 PIR7A protein Oryza sativa, polyneuridin...
AT2G39400	-4.25	hydrolase, alpha/beta fold family protein similar to monoglyceride lipase from [Homo sapiens] GI:14594904, [Mu...
AT4G30650	4.22	hydrophobic protein, putative / low temperature and salt responsive protein, putative similar to SP—Q9ZNQ7 Hyd...
AT1G21695	-4.34	hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains, INTERPRO:IPR002965 [At...

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Locus	*t*-statistic	Description
AT1G05040	-5.22	hypothetical protein [At1g05040.1]
AT1G30050	-3.93	hypothetical protein [At1g30050.1]
AT2G01410	4.44	hypothetical protein [At2g01410.1]
AT2G05350	-3.84	hypothetical protein [At2g05350.1]
AT2G27340	10.52	hypothetical protein [At2g27340.1]
AT3G25727	-4.57	hypothetical protein [At3g25727.1]
AT5G46875	3.63	hypothetical protein [At5g46875.1]
AT1G67855	-3.81	hypothetical protein hypothetical protein [At1g67855.1]
AT4G32695	5.87	hypothetical protein hypothetical protein yjbI, Bacillus subtilis, PIR2:A69844 [At4g32695.1]
AT1G47813	-4.59	hypothetical protein similar to hypothetical protein GB:AAF19740 GI:6634732 from [Arabidopsis thaliana] [At1g4. . .
AT1G47630	4.53	hypothetical protein this may be a pseudogene. No suitable start codon was identified. [At1g47625.1]
AT5G56660	-5.27	IAA-amino acid hydrolase 2 (ILL2) identical to IAA-amino acid hydrolase homolog 2 precursor [Arabidopsis thali. . .
AT1G51760	3.83	IAA-amino acid hydrolase 3 / IAA-Ala hydrolase 3 (IAR3) identical to IAA-Ala hydrolase (IAR3) [Arabidopsis tha. . .
AT2G04400	3.64	indole-3-glycerol phosphate synthase (IGPS) nearly identical to SP—P49572 [At2g04400.1]
AT4G01480	-4.10	inorganic pyrophosphatase, putative [soluble] / pyrophosphate phospho-hydrolase, putative / PPase, putative st. . .
AT5G18860	-4.74	inosine-uridine preferring nucleoside hydrolase family protein contains Pfam profile PF01156: Inosine-uridine . . .
AT4G39800	-9.54	inositol-3-phosphate synthase isozyme 1 / myo-inositol-1-phosphate synthase 1 / MI-1-P synthase 1 / IPS 1 iden. . .
AT2G22240	-7.07	inositol-3-phosphate synthase isozyme 2 / myo-inositol-1-phosphate synthase 2 / MI-1-P synthase 2 / IPS 2 iden. . .
AT2G37200	4.34	integral membrane protein, putative contains 4 transmembrane domains; contains Pfam PF04535 : Domain of unknow. . .
AT3G59320	-3.82	integral membrane protein, putative contains Pfam profile PF00892: Integral membrane protein; identical to ant. . .
AT3G16470	3.64	jacalin lectin family protein contains Pfam profile: PF01419 jacalin-like lectin domain; similar to myrosinase. . .
AT3G16440	5.21	jacalin lectin family protein contains Pfam profile: PF01419 jacalin-like lectin domain; similar to myrosinase. . .
AT3G16420	-3.63	jacalin lectin family protein similar to myrosinase binding protein [Brassica napus] GI:1711296; contains Pfam. . .
AT1G26930	3.68	kelch repeat-containing F-box family protein contains Pfam:PF01344 Kelch motif, Pfam:PF00646 F-box domain [At1. . .
AT1G80440	3.70	kelch repeat-containing F-box family protein similar to SP—Q9ER30 Kelch-related protein 1 (Sarcosin) Rattus no. . .
AT2G25970	3.77	KH domain-containing protein [At2g25970.1]
AT4G10070	-4.95	KH domain-containing protein DNA-directed RNA polymerase (EC 2.7.7.6) II largestchain - mouse, PIR2:A28490 [At. . .
AT4G26480	-3.70	KH domain-containing protein qkI-7, Mus musculus [At4g26480.1]
AT5G64390	4.46	KH domain-containing RNA-binding protein (HEN4) contains similarity to RNA-binding protein; identical to cDNA . . .
AT2G32090	3.82	lactoylglutathione lyase family protein / glyoxalase I family protein contains glyoxalase family protein domai. . .
AT4G02380	4.26	late embryogenesis abundant 3 family protein / LEA3 family protein similar to several small proteins (100 aa). . .
AT2G44060	-3.65	late embryogenesis abundant family protein / LEA family protein similar to ethylene-responsive late embryogene. . .
AT1G32560	-4.44	late embryogenesis abundant group 1 domain-containing protein / LEA group 1 domain-containing protein contains. . .
AT3G03310	4.25	lecithin:cholesterol acyltransferase family protein / LACT family protein weak similarity to LCAT-like lysopho. . .
AT1G34420	3.80	leucine-rich repeat family protein / protein kinase family protein contains leucine rich repeat (LRR) domains,. . .
AT1G51850	4.10	leucine-rich repeat protein kinase, putative similar to light repressible receptor protein kinase [Arabidopsis. . .
AT4G20270	3.75	leucine-rich repeat transmembrane protein kinase, putative CLAVATA1 receptor kinase, Arabidopsis th., PATX:G21. . .
AT1G72460	3.68	leucine-rich repeat transmembrane protein kinase, putative contains Pfam profiles: PF00560 leucine rich repeat. . .
AT1G09970	4.02	leucine-rich repeat transmembrane protein kinase, putative Similar to A. thaliana receptor-like protein kinase. . .
AT4G22870	-4.41	leucoanthocyanidin dioxygenase, putative / anthocyanidin synthase, putative similar to SP—P51091 [Malus domest. . .
AT3G26740	5.14	light responsive protein-related similar to light regulated protein precursor SP:Q03200 [Oryza sativa] (Plant . . .
AT5G17690	3.82	like heterochromatin protein (LHP1) identical to like heterochromatin protein LHP1 [Arabidopsis thaliana] GI:1. . .
AT2G45800	-6.33	LIM domain-containing protein similar to PGPS/D1 [Petunia x hybrida] GI:4105772, LIM domain protein PLIM1 [Nic. . .
AT3G45140	4.72	lipoxygenase (LOX2) identical to SP—P38418 [At3g45140.1]
AT3G27940	3.76	LOB domain family protein / lateral organ boundaries domain family protein (LBD26) identical to SP—Q9LIJ0 LOB . . .
AT3G05780	-5.86	Lon protease, putative similar to Lon protease homolog 2 SP:P93655 [At3g05780.1]
AT5G40780	4.42	lysine and histidine specific transporter, putative strong similarity to lysine and histidine specific transpo. . .

Continued. . .

Locus	*t*-statistic	Description
AT3G61120	-4.12	MADS-box protein (AGL13) [At3g61120.1]
AT1G52180	4.15	major intrinsic family protein / MIP family protein contains Pfam profile: MIP PF00230 [At1g52180.1]
AT5G37820	5.14	major intrinsic family protein / MIP family protein contains Pfam profile: PF00230 major intrinsic protein (MI...
AT5G37810	-3.93	major intrinsic family protein / MIP family protein similar to pollen-specific membrane integral protein SP:P4...
AT1G53240	-3.71	malate dehydrogenase [NAD], mitochondrial identical to mitochondrial NAD-dependent malate dehydrogenase GI:392...
AT5G11670	6.73	malate oxidoreductase, putative similar to NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (SP—P12628) Pha...
AT1G04770	-4.49	male sterility MS5 family protein similar to male sterility MS5 [Arabidopsis thaliana] GI:3859112; contains Pf...
AT5G38030	4.39	MATE efflux family protein similar to ripening regulated protein DDTFR18 [Lycopersicon esculentum] GI:12231296...
AT4G30270	-9.34	MERI-5 protein (MERI-5) (MERI5B) / endo-xyloglucan transferase / xyloglucan endo-1,4-beta-D-glucanase (SEN4) i...
AT5G63430	5.27	metallo-beta-lactamase family protein [At5g63420.1]
AT3G25740	4.37	metallopeptidase M24 family protein similar to SP—O33343 Methionine aminopeptidase (EC 3.4.11.18) (Peptidase M...
AT1G03090	5.54	methylcrotonyl-CoA carboxylase alpha chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 1 (MCCA) nearly i...
AT5G46800	-5.92	mitochondrial carnitine/acyl carrier, putative / a bout de souffle (BOU) / CAC-like protein identical to SP—Q9...
AT5G55510	4.38	mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein weak similarity to SP...
AT2G35800	6.15	mitochondrial substrate carrier family protein contains INTERPRO:IPR001993 Mitochondrial substrate carrier fam...
AT5G01500	3.63	mitochondrial substrate carrier family protein contains Pfam profile: PF00153 mitochondrial carrier protein [A...
AT4G10100	-5.41	molybdenum cofactor synthesis family protein similar to Molybdenum cofactor synthesis protein 2 small subunit ...
AT5G03630	-3.85	monodehydroascorbate reductase, putative monodehydroascorbate reductase (NADH), cucumber, PIR:JU0182 [At5g0363...
AT2G29720	3.60	monooxygenase family protein nearly identical to CTF2B [GI:4164578][Plant Physiol. 119, 364 (1999), PGR99-008]...
AT5G47240	7.78	MutT/nudix family protein similar to SP—P53370 Nucleoside diphosphate-linked moiety X motif 6 Homo sapiens; co...
AT3G53200	3.98	myb family transcription factor (MYB27) similar to myb-related DNA-binding protein GI:6467223 from [Arabidopsi...
AT5G14340	3.60	myb family transcription factor (MYB40) contains Pfam profile: PF00249 myb-like DNA-binding domain [At5g14340....
AT1G18710	3.75	myb family transcription factor (MYB47) contains Pfam profile: PF00249 myb-like DNA-binding domain [At1g18710....
AT1G19510	-3.69	myb family transcription factor contains PFAM profile: PF00249 myb-like DNA binding domain [At1g19510.1]
AT5G02840	-3.77	myb family transcription factor contains PFAM profile: PF00249 myb-like DNA binding domain [At5g02840.1]
AT5G11050	-5.00	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA binding domain; identical to cDNA ...
AT3G09600	-5.45	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain [At3g09600.1]
AT1G01060	-9.36	myb family transcription factor contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA ...
AT1G48000	-3.69	myb family transcription factor similar to myb-related transcription factor (cpm10) GB:U33915 GI:1002795 from ...
AT2G46830	-6.33	myb-related transcription factor (CCA1) identical to myb-related transcription factor (CCA1) GI:4090569 from [...
AT1G77580	5.25	myosin heavy chain-related low similarity to SP—P08799 Myosin II heavy chain, non muscle Dictyostelium discoid...
AT3G51240	-3.63	naringenin 3-dioxygenase / flavanone 3-hydroxylase (F3H) identical to GI:3790548 [At3g51240.1]
AT4G31230	4.04	NFL_HUMAN (P07196) Neurofilament triplet L protein (68 kDa neurofilament protein) (Neurofilament light polype...
AT5G13180	4.64	no apical meristem (NAM) family protein contains Pfam PF02365: No apical meristem (NAM) domain; hypothetical p...
AT3G48740	3.92	nodulin MtN3 family protein similar to MtN3 GI:1619602 (root nodule development) from [Medicago truncatula] [A...
AT2G35600	5.48	O82281 (O82281) Expressed protein, complete [TC273944]
AT4G16370	4.15	oligopeptide transporter OPT family protein similar to oligopeptide transporter Opt1p [Candida albicans] GI:23...
AT5G19690	4.20	oligosaccharyl transferase STT3 subunit family protein similar to SP—P39007 Oligosaccharyl transferase STT3 su...
AT1G34130	4.20	oligosaccharyl transferase STT3 subunit, putative similar to SP—P39007 Oligosaccharyl transferase STT3 subunit...
AT5G05580	-3.90	omega-3 fatty acid desaturase, chloroplast, temperature-sensitive (FAD8) identical to SP:48622 Temperature-sen...
AT1G01230	-3.88	ORMDL family protein contains Pfam domain PF04061: ORMDL family [At1g01230.1]
AT2G28790	4.30	osmotin-like protein, putative similar to SP—Q41350 Osmotin-like protein precursor Lycopersicon esculentum; co...
AT5G58360	-3.63	ovate family protein 69% similar to ovate protein (GI:23429649) [Lycopersicon esculentum]; contains TIGRFAM TI...
AT5G05600	3.81	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to flavonol synthase [Citrus unshiu][gi:4126403], ...
AT2G38240	4.10	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to flavonol synthase [Citrus unshiu][gi:4126403], ...
AT3G11180	8.66	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to leucoanthocyanidin dioxygenase GB:BAA20143 [Per...
AT4G10490	3.85	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to naringenin,2-oxoglutarate 3-dioxygenase [Dianth...

Continued...

Locus	*t*-statistic	Description
AT3G19000	-5.28	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to SP—P24397 Hyoscyamine 6-dioxygenase (EC 1.14.11...
AT3G56460	4.02	oxidoreductase, zinc-binding dehydrogenase family protein low similarity to probable NADP-dependent oxidoreduc...
AT3G14310	4.27	pectinesterase family protein contains Pfam profiles: PF01095 pectinesterase, PF04043 plant invertase/pectin m...
AT3G06830	-11.96	pectinesterase family protein contains Pfam profiles: PF01095 pectinesterase,PF04043 plant invertase/pectin me...
AT1G53600	3.74	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat [At1g53600.1]
AT4G32430	-5.40	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat [At4g32430.1]
AT5G61370	4.13	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat [At5g61370.1]
AT1G64580	-4.82	pentatricopeptide (PPR) repeat-containing protein low similarity to fertility restorer [Petunia x hybrida] GI:...
AT2G41790	4.04	peptidase M16 family protein / insulinase family protein contains Pfam domain, PF05193: Peptidase M16 inactive...
AT3G27110	-3.88	peptidase M48 family protein contains Pfam domain, PF01435: Peptidase family M48 [At3g27110.1]
AT2G18040	-3.86	peptidyl-prolyl cis-trans isomerase (PIN1) / cyclophilin / rotamase identical to Chain A, Solution Structure O...
AT3G47430	-3.90	peroxisomal biogenesis factor 11 family protein / PEX11 family protein contains Pfam PF05648: Peroxisomal biog...
AT4G08950	-6.10	phosphate-responsive protein, putative (EXO) similar to phi-1 (phosphate-induced gene) [Nicotiana tabacum] GI:...
AT4G29710	4.81	phosphodiesterase/nucleotide pyrophosphatase-related weak similarity to SP—Q13822 Ectonucleotide pyrophosphata...
AT1G70820	3.90	phosphoglucomutase, putative / glucose phosphomutase, putative similar to phosphoglucomutase GI:534981 from [S...
AT1G03130	-4.24	photosystem I reaction center subunit II, chloroplast, putative / photosystem I 20 kDa subunit, putative / PSI...
AT3G29810	-5.95	phytochelatin synthetase family protein / COBRA cell expansion protein COBL2 similar to phytochelatin syntheta...
AT2G46340	-3.64	phytochrome A supressor spa1 (SPA1) identical to phytochrome A supressor spa1 (GI:4809171) [Arabidopsis thalia...
AT4G16250	3.66	phytochrome D (PHYD) nearly identical to SP—P42497 Phytochrome D Arabidopsis thaliana [At4g16250.1]
AT1G01620	-4.47	plasma membrane intrinsic protein 1C (PIP1C) / aquaporin PIP1.3 (PIP1.3) / transmembrane protein B (TMPB) iden...
AT3G53420	-6.88	plasma membrane intrinsic protein 2A (PIP2A) / aquaporin PIP2.1 (PIP2.1) identical to plasma membrane intrinsi...
AT2G37170	-4.77	plasma membrane intrinsic protein 2B (PIP2B) / aquaporin PIP2.2 (PIP2.2) identical to SP—P43287 Plasma membran...
AT4G04020	-6.41	plastid-lipid associated protein PAP, putative / fibrillin, putative strong similarity to plastid-lipid associ...
AT4G22240	-6.36	plastid-lipid associated protein PAP, putative similar to plastid-lipid associated proteins PAP2 [Brassica rap...
AT5G17870	-4.08	plastid-specific ribosomal protein-related contains similarity to plastid-specific ribosomal protein 6 precurs...
AT5G45880	-4.18	pollen Ole e 1 allergen and extensin family protein contains Pfam domain, PF01190: Pollen proteins Ole e I fam...
AT5G03580	3.90	polyadenylate-binding protein, putative / PABP, putative similar to poly(A)-binding protein [Triticum aestivum...
AT5G13700	-4.99	polyamine oxidase, putative similar to SP—O64411 Polyamine oxidase precursor (EC 1.5.3.11) from Zea mays [At5g...
AT1G11790	5.40	prephenate dehydratase family protein similar to gi—2392772 and is a member of the PF—00800 Prephenate dehydra...
AT4G29350	-3.70	profilin 2 (PRO2) (PFN2) (PRF2) identical to profilin 2 SP:Q42418 GI:1353772 from [Arabidopsis thaliana]; iden...
AT1G76930	4.20	proline-rich extensin-like family protein contains extensin-like region, Pfam:PF04554 [At1g76930.1]
AT5G59170	-4.89	proline-rich family protein contains proline-rich extensin domains, INTERPRO:IPR002965 [At5g59170.1]
AT3G43720	-3.95	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein contains Pfam protease inhibitor/s...
AT4G12550	3.78	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein similar to pEARLI 1 (Accession No....
AT1G01650	5.37	protease-associated (PA) domain-containing protein contains protease associated (PA) domain, Pfam:PF02225 [At1...
AT5G49020	3.66	protein arginine N-methyltransferase family protein similar to protein arginine methyltransferase [Mus musculu...
AT1G72760	4.02	protein kinase family protein contains protein kinase domain, Pfam:PF00069 [At1g72760.1]
AT2G40500	3.71	protein kinase family protein contains protein kinase domain, Pfam:PF00069 [At2g40500.1]
AT5G42440	4.25	protein kinase family protein contains protein kinase domain, Pfam:PF00069 [At5g42440.1]
AT5G53450	11.81	protein kinase family protein contains protein kinase domain, Pfam:PF00069 [At5g53450.1]
AT5G56790	4.37	protein kinase family protein contains protein kinase domain, Pfam:PF00069 [At5g56790.1]
AT5G02290	4.71	protein kinase, putative similar to protein kinase APK1A [Arabidopsis thaliana] SWISS-PROT:Q06548 [At5g02290.1...
AT1G22570	3.62	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family [At1g22...
AT3G53960	3.65	proton-dependent oligopeptide transport (POT) family protein contains Pfam profile: PF00854 POT family [At3g53...
AT5G24470	7.85	pseudo-response regulator 5 (APRR5) identical to pseudo-response regulator 5 GI:10281006 from [Arabidopsis tha...
AT5G02810	3.85	pseudo-response regulator 7 (APRR7) identical to pseudo-response regulator 7 GI:10281004 from [Arabidopsis tha...
AT1G12000	4.34	pyrophosphate–fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-ph...

Continued...

Locus	*t*-statistic	Description
AT1G30120	-4.77	pyruvate dehydrogenase E1 component beta subunit, chloroplast identical to pyruvate dehydrogenase E1 beta subu. . .
AT4G15530	-4.17	pyruvate phosphate dikinase family protein contains Pfam profiles: PF01326 pyruvate phosphate dikinase, PEP/py. . .
AT5G54160	-3.79	quercetin 3-O-methyltransferase 1 / flavonol 3-O-methyltransferase 1 / caffeic acid/5-hydroxyferulic acid O-me. . .
AT5G20250	8.13	raffinose synthase family protein / seed imbibition protein, putative (din10) similar to seed imbibition prote. . .
AT3G22060	-3.92	receptor protein kinase-related contains Pfam profile: PF01657 Domain of unknown function that is usually asso. . .
AT3G14050	4.65	RelA/SpoT protein, putative (RSH2) nearly identical to RelA/SpoT homolog RSH2 [Arabidopsis thaliana] GI:714130. . .
AT5G44520	-4.28	ribose 5-phosphate isomerase-related low similarity to SP—P47968 Ribose 5-phosphate isomerase (EC 5.3.1.6) (Ph. . .
AT2G37990	-4.12	ribosome biogenesis regulatory protein (RRS1) family protein contains Pfam profile PF04939: Ribosome biogenesi. . .
AT3G44880	4.32	Rieske [2Fe-2S] domain-containing protein similar to lethal leaf-spot 1 from Zea mays [gi:1935909]; contains P. . .
AT1G64860	-3.72	RNA polymerase sigma subunit SigA (sigA) / sigma factor 1 (SIG1) identical to sigma factor SigA [Arabidopsis t. . .
AT3G53920	-5.44	RNA polymerase sigma subunit SigC (sigC) / sigma factor 3 (SIG3) identical to sigma factor SigC [Arabidopsis t. . .
AT5G24120	-6.14	RNA polymerase sigma subunit SigE (sigE) / sigma-like factor (SIG5) identical to RNA polymerase sigma subunit . . .
AT5G61960	3.86	RNA recognition motif (RRM)-containing protein Mei2-like protein, Arabidopsis thaliana, EMBL:D86122 [At5g61960. . .
AT2G19380	-5.38	RNA recognition motif (RRM)-containing protein similar to UBP1 interacting protein 1a [Arabidopsis thaliana] G. . .
AT4G27000	3.86	RNA-binding protein 45 (RBP45), putative DNA binding protein ACBF - Nicotiana tabacum, PID:g1899188 [At4g27000. . .
AT1G47490	4.32	RNA-binding protein 47 (RBP47), putative similar to DNA binding protein GI:1899187 from [Nicotiana tabacum] [A. . .
AT2G21690	-3.77	RNA-binding protein, putative similar to Glycine-rich RNA-binding protein from Sinapis alba SP—P49311, Brassic. . .
AT2G04530	4.16	RNase Z 97% identical to RNase Z (GI:20975607) [Arabidopsis thaliana]; similar to RNase Z (GI:20975609) [Arabi. . .
AT5G45160	7.51	root hair defective 3 GTP-binding (RHD3) family protein contains Pfam profile: PF05879 root hair defective 3 G. . .
AT5G12370	3.81	SC10_ARATH (Q8RVQ5) Exocyst complex component Sec10, complete [TC271531]
AT1G21450	4.46	scarecrow-like transcription factor 1 (SCL1) identical to scarecrow-like 1 GB:AAF21043 GI:6644390 from [Arabid. . .
AT2G37650	3.65	scarecrow-like transcription factor 9 (SCL9) identical to cDNA scarecrow-like 9 (SCL9) mRNA, partial cds GI:45. . .
AT3G51670	4.17	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein similar to polyphosphoinositi. . .
AT5G04780	3.67	SEC14 cytosolic factor-related contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-. . .
AT2G15220	-4.23	secretory protein, putative similar to NtPRp27 [Nicotiana tabacum] GI:5360263; contains Pfam profile PF04450: . . .
AT4G30610	-4.87	serine carboxypeptidase S10 family protein similar to Serine carboxypeptidase II chains A and B (SP:P08819) (E. . .
AT5G63650	-4.42	serine/threonine protein kinase, putative similar to serine/threonine-protein kinase ASK2[Arabidopsis thaliana. . .
AT4G30860	4.46	SET domain-containing protein low similarity to IL-5 promoter REII-region-binding protein [Homo sapiens] GI:12. . .
AT3G51840	3.90	short-chain acyl-CoA oxidase identical to Short-chain acyl CoA oxidase [Arabidopsis thaliana] GI:5478795; cont. . .
AT3G50560	-4.96	short-chain dehydrogenase/reductase (SDR) family protein contains INTERPRO family IPR002198 short-chain dehydr. . .
AT4G09750	-3.97	short-chain dehydrogenase/reductase (SDR) family protein similar to androgen-regulated short-chain dehydrogena. . .
AT5G61880	4.35	signaling molecule-related contains similarity to mitochondria-associated granulocyte macrophage CSF signaling. . .
AT1G61420	5.38	S-locus lectin protein kinase family protein contains Pfam domains, PF00954: S-locus glycoprotein family, PF00. . .
AT4G27300	-3.64	S-locus protein kinase, putative similar to receptor protein kinase [Ipomoea trifida] gi—836954—gb—AAC23542; c. . .
AT5G44500	-3.85	small nuclear ribonucleoprotein associated protein B, putative / snRNP-B, putative / Sm protein B, putative si. . .
AT1G33980	-3.90	Smg-4/UPF3 family protein contains Pfam PF03467: Smg-4/UPF3 family; similar to hUPF3B (GI:12232324) [Homo sapi. . .
AT5G47560	-4.18	sodium/dicarboxylate cotransporter, putative similar to SWISS-PROT:Q13183 renal sodium/dicarboxylate cotranspo. . .
AT1G78510	-7.40	solanesyl diphosphate synthase (SPS) identical to solanesyl diphosphate synthase [Arabidopsis thaliana] GI:199. . .
AT1G17100	-4.46	SOUL heme-binding family protein similar to SOUL protein [Mus musculus] GI:4886906; contains Pfam profile PF04. . .
AT1G63010	3.79	SPX (SYG1/Pho81/XPR1) domain-containing protein contains Pfam profile PF03105: SPX domain [At1g63010.1]
AT1G10760	5.33	starch excess protein (SEX1) identical to SEX1 [Arabidopsis thaliana] GI:12044358; supporting cDNA gi—12044357. . .
AT4G37220	-4.82	stress-responsive protein, putative similar to cold acclimation WCOR413-like protein gamma form [Hordeum vulga. . .
AT5G01410	-3.84	stress-responsive protein, putative similar to ethylene-inducible protein HEVER [Hevea brasiliensis] SWISS-PRO. . .
AT1G79440	4.10	succinate-semialdehyde dehydrogenase (SSADH1) similar to succinate-semialdehyde dehydrogenase [NADP+] (SSDH) [. . .
AT5G20830	4.89	sucrose synthase / sucrose-UDP glucosyltransferase (SUS1) identical to SP—P49040 Sucrose synthase (EC 2.4.1.13. . .
AT4G04760	-4.50	sugar transporter family protein similar to sugar-porter family proteins 1 and 2 [Arabidopsis thaliana] GI:145. . .
AT1G18590	4.36	sulfotransferase family protein similar to SP—P52837 Flavonol 4’-sulfotransferase (EC 2.8.2.-) (F4-ST) Flaveri. . .

Continued. . .

Locus	*t*-statistic	Description
AT1G74100	4.47	sulfotransferase family protein similar to SP—P52837 Flavonol 4'-sulfotransferase (EC 2.8.2.-) (F4-ST) Flaveri. . .
AT1G74090	5.75	sulfotransferase family protein similar to SP—P52837 Flavonol 4'-sulfotransferase (EC 2.8.2.-) (F4-ST) Flaveri. . .
AT3G56350	3.91	superoxide dismutase [Mn], putative / manganese superoxide dismutase, putative similar to manganese superoxide. . .
AT1G18050	4.56	SWAP (Suppressor-of-White-APricot)/surp domain-containing protein weak similarity to spliceosome-associated-pr. . .
AT3G03800	3.65	syntaxin, putative (SYP131) similar to SP—Q9ZSD4 Syntaxin 121 (AtSYP121) (Syntaxin-related protein At-Syr1) Ar. . .
AT5G67480	7.89	TAZ zinc finger family protein / BTB/POZ domain-containing protein contains Pfam PF00651 : BTB/POZ domain; con. . .
AT3G54960	-4.31	thioredoxin family protein similar to protein disulfide isomerase GI:5902592 from [Volvox carteri f. nagariens. . .
AT5G60640	4.98	thioredoxin family protein similar to protein disulfide isomerase GI:5902592 from [Volvox carteri f. nagariens. . .
AT3G56420	4.03	thioredoxin family protein similar to thioredoxin [Nicotiana tabacum] GI:20047; contains Pfam profile: PF00085. . .
AT3G04520	4.13	threonine aldolase family protein similar to L-allo-threonine aldolase SP:O07051 from [Aeromonas jandaei] [At3. . .
AT5G02120	-7.12	thylakoid membrane one helix protein (OHP) identical to one helix protein GI:3283057 from [Arabidopsis thalian. . .
AT4G20810	-4.17	transcription initiation factor IIE (TFIIE) alpha subunit family protein / general transcription factor TFIIE . . .
AT4G32990	5.86	transducin family protein / WD-40 repeat family protein HIRA protein, Drosophila melanogaster, PID:e1250847 [A. . .
AT3G03480	7.22	transferase family protein similar to hypersensitivity-related gene GB:CAA64636 [Nicotiana tabacum]; contains . . .
AT1G07350	-5.81	transformer serine/arginine-rich ribonucleoprotein, putative similar to GB:Y09506 from [Nicotiana tabacum] (Pl. . .
AT5G23575	3.85	transmembrane protein, putative similar to cleft lip and palate transmembrane protein 1 [Homo sapiens] GI:4039. . .
AT5G53550	8.34	transporter, putative similar to iron-phytosiderophore transporter protein yellow stripe 1 [Zea mays] GI:10770. . .
AT5G13750	6.33	transporter-related [At5g13750.1]
AT2G28315	4.30	transporter-related low similarity to SP—Q9NTN3 UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter (UDP. . .
AT1G35910	3.63	trehalose-6-phosphate phosphatase, putative similar to trehalose-6-phosphate phosphatase (AtTPPB) [Arabidopsis. . .
AT2G43510	3.76	trypsin inhibitor, putative similar to SP—P26780 Trypsin inhibitor 2 precursor (MTI-2) Sinapis alba [At2g43510. . .
AT5G54810	4.21	tryptophan synthase, beta subunit 1 (TSB1) identical to SP—P14671 [At5g54810.1]
AT2G42230	3.96	tubulin-specific chaperone C-related weak similarity to Tubulin-specific chaperone C (Tubulin-folding cofactor. . .
AT4G20370	-5.24	twin sister of FT protein (TSF) / TFL1 like protein identical to SP—Q9S7R5 TWIN SISTER of FT protein (TFL1 lik. . .
AT4G29690	7.21	type I phosphodiesterase/nucleotide pyrophosphatase family protein similar to SP—P22413 Ectonucleotide pyropho. . .
AT2G43370	-4.10	U1 small nuclear ribonucleoprotein 70 kDa, putative [At2g43370.1]
AT4G10570	-5.57	ubiquitin carboxyl-terminal hydrolase family protein similar to ubiquitin-specific protease UBP5 [Arabidopsis . . .
AT1G53950	-4.48	ubiquitin family protein contains INTERPRO:IPR000626 ubiquitin domain [At1g53950.1]
AT3G46180	-4.48	UDP-galactose/UDP-glucose transporter-related contains weak similarity to UDP-galactose/UDP-glucose transporte. . .
AT1G22360	-6.85	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and U. . .
AT2G26480	-4.64	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and U. . .
AT5G59590	-3.73	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and U. . .
AT2G43840	3.99	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and U. . .
AT2G43820	6.46	UDP-glucoronosyl/UDP-glucosyl transferase family protein contains Pfam profile: PF00201 UDP-glucoronosyl and U. . .
AT2G17570	-3.69	undecaprenyl pyrophosphate synthetase family protein / UPP synthetase family protein contains putative undecap. . .
AT1G21390	-5.48	Unknown
AT4G08596	-4.60	Unknown
AT5G63020	-4.42	Unknown
AT5G35205	-3.82	Unknown
AT1G36480	3.67	Unknown
AT5G59630	3.92	Unknown
AT5G41100	3.96	Unknown
AT1G34110	4.15	Unknown
AT3G43715	4.15	Unknown
AT5G27905	4.18	Unknown
AT5G34845	4.87	Unknown
AT2G41000	4.94	Unknown

Continued. . .

Locus	*t*-statistic	Description
AT3G52850	4.24	vacuolar sorting receptor, putative nearly identical to vacuolar sorting receptor homolog (GP:1737218) [Arabid. . .
AT2G38410	3.76	VHS domain-containing protein / GAT domain-containing protein weak similarity to hepatocyte growth factor-regu. . .
AT3G15354	-5.05	WD-40 repeat family protein / phytochrome A-related contains 7 WD-40 repeats (PF00400); phytochrome A supresso. . .
AT2G41500	4.01	WD-40 repeat family protein / small nuclear ribonucleoprotein Prp4p-related similar to U4/U6 small nuclear rib. . .
AT5G26900	3.96	WD-40 repeat family protein contains 5 WD-40 repeats (PF00400); similar to fizzy1 (GI:3298595) Xenopus laevis;. . .
AT2G37670	-4.75	WD-40 repeat family protein contains 6 WD-40 repeats (PF00400); similiar to rab11 binding protein (GI:4512103). . .
AT3G56440	4.22	WD-40 repeat protein family contains 4 WD-40 repeats (PF00400) (2 weak); PS00778 Histidine acid phosphatases a. . .
AT2G34830	-4.14	WRKY family transcription factor [At2g34830.1]
AT2G25000	-4.54	WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA -binding domain [At2g25000.1]
AT4G34890	5.23	xanthine dehydrogenase, putative similar to xanthine dehydrogenase from Gallus gallus, PIR:XOCHDH [SP—P47990];. . .
AT1G49960	-4.13	xanthine/uracil permease family protein contains Pfam profile: PF00860 permease family [At1g49960.1]
AT2G15390	-3.63	xyloglucan fucosyltransferase, putative (FUT4) identical to SP—Q9SJP2 Probable fucosyltransferase 4 (EC 2.4.1.. . .
AT2G06850	-5.23	xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (EXT) (EXG. . .
AT4G25820	-7.94	xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (XTR9) ide. . .
AT5G65730	-13.20	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan tr. . .
AT5G48070	-8.43	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan tr. . .
AT4G25810	-6.36	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan tr. . .
AT1G65310	-6.23	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan tr. . .
AT4G30280	-4.94	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan tr. . .
AT4G13080	-4.18	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan tr. . .
AT2G47890	4.79	zinc finger (B-box type) family protein [At2g47890.1]
AT2G31380	-6.80	zinc finger (B-box type) family protein / salt tolerance-like protein (STH) contains Pfam profile PF00643: B-b. . .
AT1G06040	-5.09	zinc finger (B-box type) family protein / salt-tolerance protein (STO) identical to SP—Q96288 Salt-tolerance p. . .
AT5G48250	6.24	zinc finger (B-box type) family protein contains similarity to CONSTANS homologs [At5g48250.1]
AT5G54470	-3.63	zinc finger (B-box type) family protein similar to unknown protein (pir——T05755) [At5g54470.1]
AT3G07650	7.39	zinc finger (B-box type) family protein similar to zinc finger protein GB:BAA33206 [Oryza sativa] [At3g07650.1. . .
AT3G29340	3.72	zinc finger (C2H2 type) family protein contains Pfam domain, PF00096: Zinc finger, C2H2 type [At3g29340.1]
AT4G02670	-5.03	zinc finger (C2H2 type) family protein similar to potato PCP1 zinc finger protein, GenBank accession number X8. . .
AT1G24570	-11.12	zinc finger (C3HC4-type RING finger) family protein [At1g24580.1]
AT1G72310	-3.74	zinc finger (C3HC4-type RING finger) family protein (ATL3) identical to RING-H2 zinc finger protein (ATL3) GB:. . .
AT1G49230	-3.60	zinc finger (C3HC4-type RING finger) family protein contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RI. . .
AT2G44580	-4.39	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RI. . .
AT2G15580	-3.95	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RI. . .
AT3G25030	-3.89	zinc finger (C3HC4-type RING finger) family protein contains Pfam profile: PF00097 zinc finger, C3HC4 type (RI. . .
AT4G10160	-4.58	zinc finger (C3HC4-type RING finger) family protein zinc finger protein, Arabidopsis thaliana, gb:L76926 [At4g. . .
AT1G21570	6.58	zinc finger (CCCH-type) family protein contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and s. . .
AT2G45050	4.92	zinc finger (GATA type) family protein identical to cDNA GATA transcription factor 2 GI:2959731 [At2g45050.1]
AT5G25490	3.86	zinc finger (Ran-binding) family protein contains Pfam domain, PF00641: Zn-finger in Ran binding protein and o. . .
AT5G19420	4.38	zinc finger protein, putative / regulator of chromosome condensation (RCC1) family protein similar to zinc fin. . .
AT4G00070	-5.08	zinc finger protein-related contains similarity to zinc finger proteins (C3HC4-type RING finger) [At4g00070.1]
AT3G18290	4.05	zinc finger protein-related weak alignment to Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 . . .
AT1G49920	-3.84	zinc finger protein-related weak similarity to mudrA [Zea mays] GI:540581, MURAZC [Zea mays] GI:1857256; conta. . .
AT3G58810	5.96	zinc transporter, putative similar to zinc transporter 4; ZnT4 [Mus musculus] gi—2582990—gb—AAB82593; similar . . .

Table C.8: Significant expression changes in shoots of 3 week-old trAcdS-*rolD* plants grown in nickel-spiked soil versus non-transformed plants also grown in nickel-spiked soil, $p < 0.01$.

Locus	*t*-statistic	Fold change	Description
AT3G49620	-5.94	-7.44	2-oxoacid-dependent oxidase, putative (DIN11) identical to partial cds of 2-oxoacid-dependent oxidase (din11) . . .
AT3G61400	8.48	5.09	2-oxoglutarate-dependent dioxygenase, putative similar to 2A6 (GI:599622) and tomato ethylene synthesis regula. . .
AT4G30010	6.28	4.22	50-E014660-035-002-D13-T7R MPIZ-ADIS-035 Arabidopsis thaliana cDNA clone MPIZp2000D132Q 5-PRIME, mRNA sequence. . .
AT1G78390	-4.80	-3.26	9-cis-epoxycarotenoid dioxygenase, putative / neoxanthin cleavage enzyme, putative / carotenoid cleavage dioxy. . .
AT3G50940	-9.16	-9.77	AAA-type ATPase family protein contains Pfam profile: ATPase family PF00004 [At3g50940.1]
AT3G30842	-5.16	-3.75	ABC transporter protein, putative similar to pleiotropic drug resistance like protein [Nicotiana tabacum] GI:2. . .
AT4G08900	-6.49	-11.60	arginase identical to Swiss-Prot:P46637 arginase (EC 3.5.3.1) [Arabidopsis thaliana] [At4g08900.1]
AT1G12430	-6.18	-7.42	armadillo/beta-catenin repeat family protein / kinesin motor family protein [At1g12430.1]
AT4G11730	4.84	4.04	ATPase, plasma membrane-type, putative / proton pump, putative similar to plasma membrane-type ATPase SP—P2043. . .
AT1G43950	-4.47	-3.03	auxin-responsive factor, putative similar to auxin response factor 9 [Arabidopsis thaliana] GI:4580575; contai. . .
AT4G17280	-4.70	-5.12	auxin-responsive family protein similar to auxin-induced protein AIR12 (GI:11357190) [Arabidopsis thaliana] [A. . .
AT1G77920	-4.42	-4.47	bZIP family transcription factor contains Pfam profile: PF00170 bZIP transcription factor [At1g77920.1]
AT3G49190	-4.85	-3.49	condensation domain-containing protein contains Pfam profile PF00668: Condensation domain [At3g49190.1]
AT3G25180	-4.89	-2.96	cytochrome P450 family protein similar to cytochrome P450 monooxygenase GB:AAC49188 [Pisum sativum]; contains . . .
AT1G48430	-5.76	-14.32	dihydroxyacetone kinase family protein similar to dihydroxyacetone kinases; contains Pfam profiles PF02733: DA. . .
AT1G63360	-4.63	-4.84	disease resistance protein (CC-NBS-LRR class), putative domain signature CC-NBS-LRR exists, suggestive of a di. . .
AT1G44900	5.18	10.20	DNA replication licensing factor, putative similar to DNA replication licensing factor MCM2 from Xenopus laevi. . .
AT1G14780	5.13	17.40	expressed protein [At1g14780.1]
AT1G66080	-6.43	-4.28	expressed protein [At1g66080.1]
AT1G68680	-7.62	-4.68	expressed protein [At1g68680.1]
AT1G80040	7.64	5.87	expressed protein [At1g80040.1]
AT3G02950	5.96	4.99	expressed protein [At3g02950.1]
AT4G23530	4.55	10.88	expressed protein [At4g23530.1]
AT5G18065	-5.80	-5.16	expressed protein [At5g18065.1]
AT5G40550	-6.06	-4.77	expressed protein [At5g40550.1]
AT5G52900	6.97	13.56	expressed protein [At5g52900.1]
AT5G04520	-4.45	-2.71	expressed protein ; expression supported by MPSS [At5g04520.1]
AT3G04820	9.69	15.01	expressed protein contains PFam profile PF01142: Uncharacterized protein family UPF0024; expression supported . . .
AT1G43020	-6.06	-5.16	expressed protein contains Pfam profile PF04784: Protein of unknown function, DUF547 [At1g43020.1]
AT4G18630	4.76	3.00	expressed protein contains Pfam profile: PF05097 protein of unknown function (DUF688) [At4g18630.1]
AT3G47680	-8.48	-29.51	expressed protein contains similarity to hypothetical proteins of [Arabidopsis thaliana] [At3g47680.1]
AT3G03570	5.65	7.09	expressed protein similar to hypothetical protein GB:CAB38918 [Arabidopsis thaliana] [At3g03570.1]
AT1G75880	8.84	6.13	family II extracellular lipase 1 (EXL1) EXL1 (PMID:11431566); similar to anter-specific proline-rich protein (. . .
AT1G80340	6.60	4.64	gibberellin 3-beta-dioxygenase / gibberellin 3 beta-hydroxylase (GA4H) nearly identical to gibberellin 3 beta-. . .
AT2G44560	4.80	4.05	glycosyl hydrolase family 9 protein [At2g44560.1]
AT4G09090	8.72	11.92	glycosyl hydrolase family protein 17 similar to glucan endo-1,3-beta-glucosidase precursor SP:P52409 from [Tri. . .
AT4G01020	-4.80	-7.41	helicase domain-containing protein / IBR domain-containing protein / zinc finger protein-related similar to SP. . .
AT1G38380	5.23	3.99	hypothetical protein [At1g38380.1]
AT1G50350	5.17	13.70	hypothetical protein [At1g50350.1]
AT1G66045	5.26	4.28	hypothetical protein [At1g66045.1]
AT1G71470	11.30	11.49	hypothetical protein [At1g71470.1]

Continued. . .

Locus	*t*-statistic	Fold change	Description
AT3G25727	-4.60	-3.60	hypothetical protein [At3g25727.1]
AT4G04680	5.89	5.97	hypothetical protein [At4g04680.1]
AT2G25020	15.10	32.78	hypothetical protein [Arabidopsis thaliana] [NP453917]
AT2G16410	-4.49	-21.21	hypothetical protein similar to zinc finger protein [Arabidopsis thaliana] GI:976277 [At2g16410.1]
AT1G74710	5.14	2.76	isochorismate synthase 1 (ICS1) / isochorismate mutase identical to GI:17223087 and GB:AF078080; contains Pfam. . .
AT3G20150	5.42	6.07	kinesin motor family protein contains Pfam domain, PF00225: Kinesin motor domain [At3g20150.1]
AT4G22880	4.82	5.35	leucoanthocyanidin dioxygenase, putative / anthocyanidin synthase, putative similar to SP—P51091 [Malus domest. . .
AT2G45800	-7.54	-7.60	LIM domain-containing protein similar to PGPS/D1 [Petunia x hybrida] GI:4105772, LIM domain protein PLIM1 [Nic. . .
AT1G28590	-4.46	-5.94	lipase, putative similar to lipase [Arabidopsis thaliana] GI:1145627; contains InterPro Entry IPR001087 Lipoly. . .
AT1G66960	4.92	4.40	lupeol synthase, putative / 2,3-oxidosqualene-triterpenoid cyclase, putative similar to lupeol synthase GI:176. . .
AT4G10100	-8.47	-8.67	molybdenum cofactor synthesis family protein similar to Molybdenum cofactor synthesis protein 2 small subunit . . .
AT3G09940	-5.81	-7.24	monodehydroascorbate reductase, putative similar to monodehydroascorbate reductase (NADH) GB:JU0182 (Cucumis s. . .
AT1G02520	5.19	3.62	multidrug resistance P-glycoprotein, putative similar to multidrug-resistant protein CjMDR1 GI:14715462 from [. . .
AT1G77760	4.72	2.99	nitrate reductase 1 (NR1) identical to SP—P11832 Nitrate reductase 1 (formerly EC 1.6.6.1) (NR1)Arabidopsis th. . .
AT3G15500	-6.18	-4.24	no apical meristem (NAM) family protein (NAC3) identical to AtNAC3 [Arabidopsis thaliana] GI:12060424; contain. . .
AT5G23660	6.47	5.59	nodulin MtN3 family protein similar to MtN3 GI:1619602 (root nodule development) from [Medicago truncatula] [A. . .
AT1G11780	-8.74	-6.76	oxidoreductase, 2OG-Fe(II) oxygenase family protein low similarity to alkB proteins from Homo sapiens [SP—Q136. . .
AT3G06830	-8.74	-14.34	pectinesterase family protein contains Pfam profiles: PF01095 pectinesterase,PF04043 plant invertase/pectin me. . .
AT2G15630	-5.48	-4.85	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat [At2g15630.1]
AT5G64320	-5.78	-5.64	pentatricopeptide (PPR) repeat-containing protein contains Pfam profile PF01535: PPR repeat [At5g64320.1]
AT1G64580	-6.59	-6.91	pentatricopeptide (PPR) repeat-containing protein low similarity to fertility restorer [Petunia x hybrida] GI:. . .
AT3G14890	4.64	2.65	phosphoesterase identical to phosphoesterase [Arabidopsis thaliana] GI:21630064; contains Pfam profile PF00645. . .
AT5G13700	-7.76	-8.89	polyamine oxidase, putative similar to SP—O64411 Polyamine oxidase precursor (EC 1.5.3.11) from Zea mays [At5g. . .
AT3G51990	5.26	2.98	protein kinase family protein contains protein kinase domain, PF00069 [At3g51990.1]
AT2G39660	-5.25	-3.30	protein kinase, putative similar to protein kinase gi—166809—gb—AAA18853 [At2g39660.1]
AT3G54840	4.87	14.88	Rab GTPase (ARA6) identical to small GTPase Ara6 [Arabidopsis thaliana] GI:13160603 [At3g54840.1]
AT5G23330	-4.46	-3.65	riboflavin biosynthesis protein-related contains weak similarity to Riboflavin biosynthesis protein ribF. (Swi. . .
AT1G58250	-4.68	-2.49	SABRE, putative similar to SABRE (GI:719291) [Arabidopsis thaliana] [At1g58250.1]
AT4G35770	-5.70	-3.13	senescence-associated protein (SEN1) identical to senescence-associated protein GI:1046270 from [Arabidopsis t. . .
AT5G23670	15.25	20.43	serine C-palmitoyltransferase (LCB2) identical to serine palmitoyltransferase [Arabidopsis thaliana] GI:930938. . .
AT3G42835	4.69	4.03	Unknown
AT5G54520	-9.36	-12.23	WD-40 repeat family protein contains 5 WD-40 repeats (PF00400); similar to pre-mRNA splicing factor PRP17 (SP:. . .
AT2G38470	5.47	3.09	WRKY family transcription factor contains Pfam profile: PF03106 WRKY DNA -binding domain; [At2g38470.1]
AT2G15390	-5.49	-9.14	xyloglucan fucosyltransferase, putative (FUT4) identical to SP—Q9SJP2 Probable fucosyltransferase 4 (EC 2.4.1. . . .
AT5G65730	-5.45	-3.23	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan tr. . .
AT1G24570	-13.70	-35.46	zinc finger (C3HC4-type RING finger) family protein [At1g24580.1]
AT1G72310	-4.48	-9.63	zinc finger (C3HC4-type RING finger) family protein (ATL3) identical to RING-H2 zinc finger protein (ATL3) GB:. . .
AT3G58810	4.98	2.88	zinc transporter, putative similar to zinc transporter 4; ZnT4 [Mus musculus] gi—2582990—gb—AAB82593; similar . . .

Table C.9: Significant expression changes in roots of 3 week-old trAcdS-*rolD* plants grown in nickel-spiked soil versus non-transformed plants also grown in nickel-spiked soil, $p < 0.01$.

Locus	*t*-statistic	Fold change	Description
AT1G22410	-3.76	-1.64	2-dehydro-3-deoxyphosphoheptonate aldolase, putative / 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase, p...
AT1G52820	-3.82	-1.69	2-oxoglutarate-dependent dioxygenase, putative similar to AOP1 [Arabidopsis lyrata][GI:16118889]; contains Pfa...
AT5G15200	-3.83	-1.66	40S ribosomal protein S9 (RPS9B) 40S ribosomal protein S9, Chlamydomonas sp., EMBL:AU066528 [At5g15200.1]
AT1G69620	-4.00	-1.65	60S ribosomal protein L34 (RPL34B) similar to SP:Q42351 from [Arabidopsis thaliana] [At1g69620.1]
AT3G02360	-4.19	-1.67	6-phosphogluconate dehydrogenase family protein contains Pfam profiles: PF00393 6-phosphogluconate dehydrogena...
AT5G09810	-5.78	-2.57	actin 7 (ACT7) / actin 2 identical to SP—P53492 Actin 7 (Actin-2) Arabidopsis thaliana [At5g09810.1]
AT4G13940	-3.80	-1.88	adenosylhomocysteinase / S-adenosyl-L-homocysteine hydrolase / AdoHcyase (SAHH) identical to SP—O23255 Adenosy...
AT3G02470	-4.46	-1.75	adenosylmethionine decarboxylase family protein contains Pfam profile: PF01536 adenosylmethionine decarboxylas...
AT3G01260	-4.81	-1.77	aldose 1-epimerase family protein similar to non-cell-autonomous protein pathway2, plasmodesmal receptor [Nico...
AT3G57690	3.73	1.59	arabinogalactan-protein, putative (AGP23) similar to arabinogalactan protein [Arabidopsis thaliana] gi—1088050...
AT1G11910	-3.44	-2.02	aspartyl protease family protein contains Pfam profiles: PF00026 eukaryotic aspartyl protease, PF03489 surfact...
AT2G45170	-3.75	-1.83	autophagy 8e (APG8e) identical to autophagy 8e [Arabidopsis thaliana] GI:19912159; contains Pfam profile PF029...
AT5G19140	-4.36	-1.80	auxin/aluminum-responsive protein, putative strong similarity to auxin down-regulated protein ARG10 [Vigna rad...
AT4G14410	-4.61	-2.01	basic helix-loop-helix (bHLH) family protein [At4g14410.1]
AT1G70850	-3.38	-1.54	Bet v I allergen family protein similar to Csf-2 [Cucumis sativus][GI:5762258][J Am Soc Hortic Sci 124, 136-13...
AT5G56870	-4.31	-2.11	beta-galactosidase, putative / lactase, putative similar to beta-galactosidase precursor GI:3869280 from [Cari...
AT4G34050	-5.57	-2.23	caffeoyl-CoA 3-O-methyltransferase, putative nearly identical to GI:2960356 [Populus balsamifera subsp. tricho...
AT1G53520	4.40	1.80	chalcone-flavanone isomerase-related low similarity to GI:499036 (Vitis vinifera) [At1g53520.1]
AT1G05850	-3.95	-1.77	chitinase-like protein 1 (CTL1) similar to class I chitinase GI:7798656 from [Halimolobos perplexa var. perple...
AT1G45474	4.72	2.20	chlorophyll A-B binding protein, putative (LHCA5) identical to Lhca5 protein [Arabidopsis thaliana] GI:4741942...
AT1G56590	-3.85	-1.60	clathrin adaptor complexes medium subunit family protein contains Pfam profile: PF00928 adaptor complexes medi...
AT2G20190	-3.75	-1.60	CLIP-associating protein (CLASP) -related similar to CLIP-associating protein CLASP2 (GI:13508651) [Rattus nor...
AT3G17700	-3.39	-1.51	cyclic nucleotide-binding transporter 1 / CNBT1 (CNGC20) identical to cyclic nucleotide-binding transporter 1 ...
AT4G16190	-3.47	-1.72	cysteine proteinase, putative contains similarity to papain-like cysteine proteinase isoform I GI:7381219 from...
AT2G24940	-3.40	-1.50	cytochrome b5 domain-containing protein similar to SP—P70580 Membrane associated progesterone receptor compone...
AT2G46650	-3.75	-1.80	cytochrome b5, putative similar to cytochome b5 GI:2695711 from [Olea europaea] [At2g46650.1]
AT2G40890	-4.04	-1.73	cytochrome P450 98A3, putative (CYP98A3) identical to Cytochrome P450 98A3 (SP—O22203) [Arabidopsis thaliana];...
AT4G13770	-4.30	-1.69	cytochrome P450 family protein [At4g13770.1]
AT2G46960	-3.42	-1.61	cytochrome P450 family protein similar to cytochrome P450 72A1 (SP:Q05047) [Catharanthus roseus]; contains Pfa...
AT2G42250	-3.88	-1.61	cytochrome P450 family protein similar to cytochrome P450 93A1 (SP:Q42798) [Glycine max] [At2g42250.1]
AT5G06905	-4.58	-1.78	cytochrome P450 family protein similar to SP—Q42798—C931_SOYBN Cytochrome P450 93A1 (EC 1.14.-.-) Glycine max...
AT2G23400	-3.55	-1.53	dehydrodolichyl diphosphate synthase, putative / DEDOL-PP synthase, putative similar to GI:796076; this may be...
AT4G36040	-3.49	-1.61	DNAJ heat shock N-terminal domain-containing protein (J11) identical to dnaJ heat shock protein J11 [Arabidops...
AT1G72070	-3.51	-1.62	DNAJ heat shock N-terminal domain-containing protein similar to TCJ2 [Trypanosoma cruzi] GI:886414; contains P...
AT2G33830	-6.45	-2.88	dormancy/auxin associated family protein contains Pfam profile: PF05564 dormancy/auxin associated protein [At2...
AT1G28330	-6.71	-2.81	dormancy-associated protein, putative (DRM1) identical to dormancy-associated protein [Arabidopsis thaliana] G...
AT5G35160	-5.27	-2.21	endomembrane protein 70, putative p76, Homo sapiens, EMBL:HSU81006 [At5g35160.1]
AT2G36530	-4.56	-2.08	enolase identical to SWISS-PROT:P25696 enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase)(2-phospho-D- gly...
AT4G12230	-3.56	-1.60	esterase/lipase/thioesterase family protein low similarity to 2-hydroxy-6-ketonona-2,4-dienedoic acid hydrolas...
AT1G54860	-3.48	-1.52	expressed protein [At1g54860.1]
AT3G10770	-4.94	-1.82	expressed protein [At3g10770.1]

Continued...

Locus	*t*-statistic	Fold change	Description
AT4G20150	3.85	1.61	expressed protein [At4g20150.1]
AT4G36370	3.44	1.78	expressed protein [At4g36370.1]
AT5G13140	3.62	1.67	expressed protein [At5g13140.1]
AT5G59410	3.87	1.59	expressed protein [At5g59410.1]
AT1G25520	-4.59	-1.88	expressed protein contains Pfam profile PF01169: Uncharacterized protein family UPF0016 [At1g25520.1]
AT3G29240	-3.55	-1.58	expressed protein similar to At1g33780 [Arabidopsis thaliana]; contains Pfam profile PF02622: Uncharacterized ...
AT1G70160	-3.39	-1.56	expressed protein similar to hypothetical protein GI:4455225 from [Arabidopsis thaliana] [At1g70160.1]
AT4G26260	-5.60	-1.98	expressed protein similar to myo-inositol oxygenase [Sus scrofa] gi—17432544—gb—AAL39076 [At4g26260.1]
AT1G30700	-4.01	-1.70	FAD-binding domain-containing protein similar to SP—P30986 reticuline oxidase precursor (Berberine-bridge-form...
AT5G45360	-6.05	-2.11	F-box family protein similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250 [At5g45360.1]
AT1G01580	-3.39	-1.54	ferric-chelate reductase, putative similar to ferric-chelate reductase (FRO1) [Pisum sativum] GI:15341529; con...
AT1G48270	-3.45	-1.58	G protein coupled receptor-related identical to putative G protein coupled receptor GI:2104224 from [Arabidops...
AT1G09560	-3.89	-1.69	germin-like protein (GLP4) (GLP5) identical to Arabidopsis germin-like protein subfamily 2 member 1 [SP—P94014...
AT3G05950	-4.90	-2.08	germin-like protein, putative similar to germin-like protein GLP6 [SP—P92997]; contains Pfam profile: PF01072 ...
AT5G07440	-4.37	-1.72	glutamate dehydrogenase 2 (GDH2) identical to glutamate dehydrogenase 2 (GDH 2) [Arabidopsis thaliana] SWISS-P...
AT5G16570	-3.70	-1.60	glutamine synthetase, putative similar to glutamine synthetase, cytosolic isozyme (glutamate– ammonia ligase)...
AT2G30860	-3.46	-1.67	glutathione S-transferase, putative identical to GB:Y12295 [At2g30860.1]
AT5G41080	-3.72	-1.87	glycerophosphoryl diester phosphodiesterase family protein weak similarity to SP—P37965 Glycerophosphoryl dies...
AT2G43610	-4.48	-1.87	glycoside hydrolase family 19 protein similar to chitinase GI:17799 from [Brassica napus]; contains Pfam profi...
AT1G17150	-3.93	-2.01	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein similar to polygalacturon...
AT5G58090	-3.55	-1.58	glycosyl hydrolase family 17 protein similar to 3-glucanase GI:18483232 from [Sorghum bicolor] [At5g58090.1]
AT2G32150	-3.40	-1.62	haloacid dehalogenase-like hydrolase family protein contains InterPro accession IPR005834: Haloacid dehalogena...
AT3G09480	-4.01	-1.71	histone H2B, putative similar to histone from Arabidopsis thaliana GI:2407802, Gossypium hirsutum SP—O22582, H...
AT5G12910	-4.77	-1.84	histone H3, putative similar to histone H3 from Mus musculus GI:51301, Gallus gallus GI:211859, Medicago sativ...
AT3G05880	-3.95	-1.67	hydrophobic protein (RCI2A) / low temperature and salt responsive protein (LTI6A) identical to SP—Q9ZNQ7 Hydro...
AT1G79730	3.57	1.90	hydroxyproline-rich glycoprotein family protein contains proline-rich extensin domains, INTERPRO:IPR002965 [At...
AT1G47813	-4.24	-1.67	hypothetical protein similar to hypothetical protein GB:AAF19740 GI:6634732 from [Arabidopsis thaliana] [At1g4...
AT5G10170	-4.32	-1.83	inositol-3-phosphate synthase, putative / myo-inositol-1-phosphate synthase, putative / MI-1-P synthase, putat...
AT4G15610	-3.56	-1.87	integral membrane family protein contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; conta...
AT4G19680	-4.30	-1.97	iron-responsive transporter (IRT2) member of the Zinc (Zn2+)-Iron (Fe2+) permease (ZIP) family, PMID:11500563 ...
AT5G40680	-3.63	-1.71	kelch repeat-containing F-box family protein contains Pfam:PF01344 Kelch motif [At5g40680.1]
AT1G08630	-3.60	-2.03	L-allo-threonine aldolase-related similar to L-allo-threonine aldolase (EC 4.1.2.-) (L-allo-TA) (L-allo-threon...
AT3G16150	-3.55	-1.59	L-asparaginase, putative / L-asparagine amidohydrolase, putative similar to Swiss-Prot:P30364 L-asparaginase (...
AT3G20820	-4.60	-1.88	leucine-rich repeat family protein contains similarity to Cf-2.1 [Lycopersicon pimpinellifolium] gi—1184075—gb...
AT1G04410	-5.09	-2.15	malate dehydrogenase, cytosolic, putative strong similarity to malate dehydrogenase from Mesembryanthemum crys...
AT4G34030	-4.65	-1.98	methylcrotonyl-CoA carboxylase beta chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 2 (MCCB) identical...
AT5G22640	4.10	1.82	MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein contains Pfam profile PF02493: MORN...
AT5G47240	-3.88	-1.89	MutT/nudix family protein similar to SP—P53370 Nucleoside diphosphate-linked moiety X motif 6 Homo sapiens; co...
AT5G56080	-3.54	-1.73	nicotianamine synthase, putative similar to nicotianamine synthase [Lycopersicon esculentum][GI:4753801], nico...
AT5G14120	-4.06	-2.42	nodulin family protein similar to nodulin-like protein [Arabidopsis thaliana] GI:3329368, nodule-specific prot...
AT3G12120	-3.51	-1.54	omega-6 fatty acid desaturase, endoplasmic reticulum (FAD2) / delta-12 desaturase identical to omega-6 fatty a...
AT3G13610	-5.38	-2.24	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to desacetoxyvindoline 4-hydroxylase [Catharanthus...
AT3G12900	-5.46	-1.95	oxidoreductase, 2OG-Fe(II) oxygenase family protein similar to SP—P10967 1-aminocyclopropane-1-carboxylate oxi...
AT4G33720	-3.90	-1.76	pathogenesis-related protein, putative similar to SP—P33154 Pathogenesis-related protein 1 precursor (PR-1) Ar...
AT1G11580	-4.65	-1.78	pectin methylesterase, putative similar to pectin methylesterase GI:1617583 from [Lycopersicon esculentum] [At...
AT3G03670	-3.53	-1.64	peroxidase, putative similar to peroxidase GB:CAA66966 [Arabidopsis thaliana] [At3g03670.1]
AT3G61070	-3.98	-1.62	peroxisomal biogenesis factor 11 family protein / PEX11 family protein contains Pfam PF05648: Peroxisomal biog...

Continued...

Locus	*t*-statistic	Fold change	Description
AT1G03210	-3.47	-1.55	phenazine biosynthesis PhzC/PhzF family protein contains Pfam profile: PF02567 phenazine biosynthesis-like pro. . .
AT2G37040	-5.24	-1.97	phenylalanine ammonia-lyase 1 (PAL1) nearly identical to SP—P35510 [At2g37040.1]
AT3G53260	-5.28	-2.25	phenylalanine ammonia-lyase 2 (PAL2) nearly identical to SP—P45724 [At3g53260.1]
AT4G05050	-3.39	-2.33	polyubiquitin (UBQ11) identical to GI:304117 [At4g05050.1]
AT1G21310	-5.39	-2.09	proline-rich extensin-like family protein contains extensin-like region, Pfam:PF04554 [At1g21310.1]
AT3G49840	-3.67	-1.57	proline-rich family protein contains proline rich extensin domains, INTERPRO:IPR002965 [At3g49840.1]
AT5G35980	6.80	2.54	protein kinase family protein contains protein kinase domain, Pfam:PF00069 [At5g35980.1]
AT3G12620	-3.93	-1.81	protein phosphatase 2C family protein / PP2C family protein similar to Ser/Thr protein phosphatase 2C (PP2C6) . . .
AT4G33920	-3.60	-1.63	protein phosphatase 2C family protein / PP2C family protein similar to Ser/Thr protein phosphatase 2C (PP2C6) . . .
AT1G63120	-3.92	-1.89	rhomboid family protein contains PFAM domain PF01694, Rhomboid family [At1g63120.1]
AT3G59520	3.42	1.55	rhomboid family protein contains Pfam profile PF01694: Rhomboid family [At3g59520.1]
AT1G32790	-3.60	-1.59	RNA-binding protein, putative similar to RNA-binding protein GB:CAB40027 GI:4539439 from [Arabidopsis thaliana. . .
AT2G36880	-5.05	-2.23	S-adenosylmethionine synthetase, putative similar to S-adenosylmethionine synthetase 3 (Methionine adenosyltra. . .
AT2G27460	-4.42	-1.84	sec23/sec24 transport family protein weak similarity to SP—P53992 Protein transport protein Sec24C (SEC24-rela. . .
AT3G13110	-3.79	-1.71	serine O-acetyltransferase (SAT-1) identical to serine acetyltransferase (Sat-1) GI:1184048 [Arabidopsis thali. . .
AT1G11310	-4.82	-1.85	seven transmembrane MLO family protein / MLO-like protein 2 (MLO2) idenctical to membrane protein Mlo2 [Arabid. . .
AT5G53120	-3.56	-1.60	spermidine synthase, putative / putrescine aminopropyltransferase, putative similar to SP—O82147 Spermidine sy. . .
AT5G20830	-3.97	-1.77	sucrose synthase / sucrose-UDP glucosyltransferase (SUS1) identical to SP—P49040 Sucrose synthase (EC 2.4.1.13. . .
AT3G43190	-3.61	-1.63	sucrose synthase, putative / sucrose-UDP glucosyltransferase, putative strong similarity to SP—P49040 Sucrose . . .
AT5G43780	-5.54	-2.01	sulfate adenylyltransferase 4 / ATP-sulfurylase 4 (APS4) identical to ATP sulfurylase precursor (APS4) [Arabid. . .
AT4G25100	-5.32	-1.90	superoxide dismutase [Fe], chloroplast (SODB) / iron superoxide dismutase (FSD1) identical to Fe-superoxide di. . .
AT4G04150	3.58	1.74	T24H24 T24H24.7 Arabidopsis thaliana; , complete [TC278695]
AT4G37610	-3.84	-1.62	TAZ zinc finger family protein / BTB/POZ domain-containing protein contains Pfam PF00651 : BTB/POZ domain; con. . .
AT1G24510	-3.70	-1.61	T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative / chaperonin, putative identical to SW. . .
AT3G26520	-3.89	-1.64	tonoplast intrinsic protein, putative similar to tonoplast intrinsic protein GI:5081419 from [Brassica napus] . . .
AT2G30490	-5.61	-2.04	trans-cinnamate 4-monooxygenase / cinnamic acid 4-hydroxylase (C4H) (CA4H) / cytochrome P450 73 (CYP73) (CYP73. . .
AT3G16640	-4.62	-1.95	translationally controlled tumor family protein similar to translationally controlled tumor protein GB:AAD1003. . .
AT1G20840	-4.43	-2.16	transporter-related low similarity to D-xylose proton-symporter [Lactobacillus brevis] GI:2895856; contains Pf. . .
AT1G76880	3.44	1.87	trihelix DNA-binding protein, putative similar to DNA-binding protein DF1 [Pisum sativum] GI:13646986 [At1g768. . .
AT3G55440	-4.00	-1.63	triosephosphate isomerase, cytosolic, putative strong similarity to triosephosphate isomerase, cytosolic from . . .
AT1G17860	-4.11	-1.66	trypsin and protease inhibitor family protein / Kunitz family protein similar to LeMir (miraculin homolog) GI:. . .
AT5G05370	-3.65	-1.58	ubiquinol-cytochrome C reductase complex ubiquinone-binding protein, putative / ubiquinol-cytochrome C reducta. . .
AT1G53930	-3.68	-1.64	ubiquitin family protein contains Pfam profile: PF00240 ubiquitin family [At1g53930.1]
AT3G53990	-4.39	-1.72	universal stress protein (USP) family protein contains Pfam PF00582: universal stress protein family [At3g5399. . .
AT3G17020	-3.55	-1.63	universal stress protein (USP) family protein similar to early nodulin ENOD18 [Vicia faba] GI:11602747; contai. . .
AT1G62620	-3.46	-1.54	Unknown
AT5G35607	3.53	1.56	Unknown
AT2G40070	3.60	1.65	Unknown
AT4G17440	4.01	1.73	Unknown
AT4G34720	-4.05	-1.73	vacuolar ATP synthase 16 kDa proteolipid subunit 1 / V-ATPase 16 kDa proteolipid subunit 1 (AVAP1) (AVA-P1) id. . .
AT4G11150	-3.93	-1.80	vacuolar ATP synthase subunit E / V-ATPase E subunit / vacuolar proton pump E subunit (VATE) identical to SP—Q. . .
AT4G03510	-4.53	-1.72	zinc finger (C3HC4-type RING finger) family protein (RMA1) identical to RING zinc finger protein RMA1 gi:31642. . .

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