Plant performance under thermal stress: strategies and trade-offs, and their potential role in determining species distribution

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Summary

The distribution of species is often restricted to a particular climatic zone with distribution boundaries following thermal isoclines. What hinders species from expanding their geographic distribution? To answer this question it is important to consider the traits of climate adaptation and their genetic architecture. For this, we used an integrative approach, combining common garden experiments and the analysis of the transcriptome based on RNA-sequencing to explore both phenotypic and genetic aspects of the thermal stress response. Study organism was the plant species *Arabidopsis lyrata* ssp. *lyrata* (Brassicaceae). **Chapter 1** addressed the question of whether populations differed in thermal stress resistance and tolerance along two latitudinal clines and tested for the existence of trade-offs. A main result was that frost tolerance traded off against plant size in the absence of thermal stress. This genetically-based trade-off could be involved in constraining the evolution at the northern species border if selection favors fast development to large size at the cost of less frost tolerance. **Chapter 2** focused on the acclimation process, its impact on thermal stress resistance, the cost and the underlying changes in gene expression. Acclimation increased thermal stress resistance independent of acclimation temperature. Furthermore, the plastic acclimation response did not seem to be costly. But a negative correlation between basal and induced resistance was found, which may constrain the evolution of acclimation. **Chapter 3** explored genetic divergence in thermal resistance and tolerance and fitness related traits in a single population of a heterogeneous sand dune landscape. Overall, the work indicates high lability in the evolution of thermal stress-resistance strategies. Few constraints seem to exist, with the most important probably being one between frost tolerance and fast reproductive development.

General introduction

During the 20th century, biogeographers and ecologists realized the importance of climatic conditions in determining species distributions (Good, 1931) and demonstrated that species distributions often followed climatic isotherms (Uphof, 1920; Salisbury, 1926; Dansereau, 1957; Gaston, 2003). This observation led to the thinking that species are distributed only over limited ranges, greatly determined by temperature, that allows them to survive, grow and reproduce. But what hinders species from evolving their thermal niche and expanding their distribution?

To answer this question it is important to consider the traits implicated in thermal performance and their genetic architecture. There are generally three adaptive strategies that allow plants to cope with thermal stress: escape, resistance and tolerance (Levitt, 1980). Escape strategies allow the completion of the life cycle before the onset of adverse conditions. In plants, escape may be achieved by the timing of stress-sensitive life phases (McKay *et al.*, 2003). An example in plants is early flowering to avoid summer droughts (Kooyers, 2015). Resistance is defined as a defense strategy that prevents or reduces damage by a stressor (Roy & Kirchner, 2000). Resistance to temperature extremes for instance may be the degree that cell membrane injury can be prevented (Cornelissen *et al.*, 2003). Thermal tolerance is defined as a defense strategy that reduces the negative fitness impact of damage (Roy & Kirchner, 2000). These types of strategies may however not all easily evolve to increase stress performance. Life history theory suggests that adaptive strategies have fitness costs and are involved in trade-offs that constrain adaptive evolution (Roff, 1992; Stearns, 1992). This prediction is based on the idea that resistance and tolerance to thermal stress are beneficial under stress exposure, but are costly in the absence of stress. Another theoretical prediction is that resistance and tolerance to the same thermal stress may trade off against each other as they are redundant strategies. The goal of my PhD project was to test these predictions and investigate the genetic basis of thermal adaptation at different spatial scales, considering the entire latitudinal distribution of a species and fine-scale environmental gradients within a population. Study organism was the North American plant species *Arabidops lyrata*. The specific questions addressed were:

1) Is there latitudinal variation in resistance and tolerance to frost and heat? Are these traits involved in trade-offs among themselves? Is it costly for plants to be resistant or tolerant? These questions were studied in **Chapter 1**.

2) What is the role of acclimation in determining frost and heat resistance? What are the genes differentially expressed under cold and heat acclimation? Is acclimation costly? Acclimation was the theme of **Chapter 2**.

3) Has within-population spatial heterogeneity in environmental conditions lead to divergence in resistance and tolerance to frost and heat and fitness related traits? What genes could be involved in genetic divergence? **Chapter 3** addresses these questions over several gradients of a sand dune landscape.

Study organism

Arabidopsis lyrata (Brassicaceae) is an herbaceous plant species of 10 to 45 cm height with leaves forming a rosette at the base where floral stems emerge. This species is a close relative of *Arabidopsis thaliana*, with which it shares a divergence time of about ten million years (Koch & Kiefer, 2005). *Arabidopsis lyrata* differs from *A. thaliana* by its life cycle and its mode of reproduction. *Arabidopsis lyrata* is a perennial plant, while *A. thaliana* is an annual plant. The former species is mainly self-incompatible and requires cross-pollination while *A. thaliana* is an autogamous selfer (Willi & Määttänen, 2010). The species has a circumpolar distribution, but is split in several subspecies (Schmickl et al 2010). The one of North America, subsp. *lyrata*, has a distinct southern and northern distribution limit. Its distribution ends in the south in North Carolina and Missouri and in the north in southern Ontario and New York State (Paccard et al. 2016). Compared to *A. thaliana*, *A. lyrata* ssp. *lyrata* has a more fragmented distribution and populations are geographically isolated (Willi & Määttänen 2010; Griffin & Willi 2013).

Populations occur along a latitudinal gradient with temperatures varying from high in the south to low in the north; along such a considerable latitudinal gradient, anatomical and physiological adaptations to temperature may be expected. Furthermore, the subspecies (from now on commonly described as species) lives in different types of habitats: rocky outcrops, boulders or sand dunes. Also within sites, the species grows at sites that may strongly differ in microclimate. Such environmental heterogeneity may result in different selection pressures among and within populations on traits linked to coping with thermal stress (Hedrick, 2006).

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Chapter 1: **Temperature-stress resistance and tolerance along a latitudinal cline in North American *Arabidopsis lyrata***

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Abstract

The study of latitudinal gradients can yield important insights into adaptation to temperature stress. Two strategies are available: resistance by limiting damage, or tolerance by reducing the fitness consequences of damage. Here we studied latitudinal variation in resistance and tolerance to frost and heat and tested the prediction of a trade-off between the two strategies and their costliness. We raised plants of replicate maternal seed families from eight populations of North American *Arabidopsis lyrata* collected along a latitudinal gradient in climate chambers and exposed them repeatedly to either frost or heat stress, while a set of control plants grew under standard conditions. When control plants reached maximum rosette size, leaf samples were exposed to frost and heat stress, and electrolyte leakage (PEL) was measured and treated as an estimate of resistance. Difference in maximum rosette size between stressed and control plants was used as an estimate of tolerance. Northern populations were more frost resistant, and less heat resistant and less heat tolerant, but – unexpectedly – they were also less frost tolerant. Negative genetic correlations between resistance and tolerance to the same and different thermal stress were generally not significant, indicating only weak trade-offs. However, tolerance to frost was consistently accompanied by small size under control conditions, which may explain the non-adaptive latitudinal pattern for frost tolerance. Our results suggest that adaptation to frost and heat is not constrained by trade-offs between them. But the cost of frost tolerance in terms of plant size reduction may be important for the limits of species distributions and climate niches.

Keywords: abiotic stress, *Arabidopsis lyrata,* latitudinal gradient, life-history evolution, percentage electrolyte leakage, resistance, tolerance, temperature cline, thermal adaptation.

Introduction

The distribution of species may be determined in part by their ability to withstand sources of abiotic and biotic stress that vary clinally [1,2]. Indeed, evidence suggests that abiotic stress imposes strong selection along two widely-studied gradients – latitude and elevation – because populations are often locally adapted to changing thermal conditions along these gradients [3]. Thermal adaptation manifests itself in varying degrees of resistance to, or tolerance of, extreme temperatures. These two traits have rarely been studied simultaneously in the context of latitude mainly reflecting a temperature cline, and their fitness costs have rarely been assessed.

Life history theory predicts that coping with stress is likely to entail costs in other traits related to fitness [4,5]. These costs – referred to as trade-offs – may be important in determining species distribution limits. One trade-off that has been predicted theoretically is that between resistance and tolerance to the same type of stress [6,7]. Resistance is defense that prevents damage or limits its extent, whereas tolerance is defined as defense against stress that reduces the negative fitness impact of damage [8]. In the context of thermal stress in plants, resistance includes reduction in the degree of cell membrane injury [9]. Tolerance reflects the extent to which a plant maintains reproductive output despite sustaining damage from stress. Models of the joint evolution of resistance and tolerance suggest that the two may be alternatives; selection should maximize either strategy, but not both [10]. This is because the benefits of resistance are unnecessary in a highly tolerant individual, and the benefits of tolerance are rarely realized in a highly resistant individual [11]. Maximization of both traits therefore confers limited benefits while causing greater fitness costs than having either resistance or tolerance. This creates a trade-off between resistance and tolerance.

The resistance-tolerance trade-off has been well studied empirically in the context of biotic stressors [10,12]. While the idea that plants respond to biotic enemies with resistance and tolerance has been generally accepted, there is little empirical support for the prediction that the two strategies are negatively correlated. In fact, studies on plant-insect, plant-mammal, and plant-virus systems have often failed to detect phenotypic or genetic trade-offs between resistance and tolerance [13–16]. Instead, plants allocate resources to both strategies and the two can be maintained simultaneously at intermediate levels. Plant-thermal stress responses have rarely been studied in the context of life history evolution and trade-offs. This may stem from the difficulty of assessing tolerance against static stress factors without confounding it with the effect of resistance. For such stress factors – unlike, for example, for herbivory – it is hard to ensure that damage is equal across replicates. Agrawal et al. [17] measured selection acting on resistance and tolerance to frost in *Raphanus raphanistrum* in an outdoor garden experiment, and found that resistance was favored while tolerance was disfavored, most likely due to fitness costs of the latter. However, there was no genetic correlation between resistance and tolerance.

Other trade-offs important for species distribution limits may exist. Resistance and tolerance to different temperature extremes may trade off against one another. Furthermore, thermal-stress resistance and tolerance might trade off against components of fitness in the absence of stress, in which case we refer to costs of resistance/tolerance [18]. And finally, they might trade off against responses to other kinds of stress. Any of these trade-offs could become important for limiting adaptation if selection acting under a current temperature regime is perpendicular to a strong correlation between traits [19,20]. Limits to adaptation may also change with latitude. A species may be well-adapted to conditions at the center of its distribution, yet experience increasing fitness costs of adaptations to coping with increasingly stressful conditions towards the range margins [21]. In general, if adaptive strategies and fitness share a common genetic basis, trade-offs have the potential to limit the optimization of resistance and tolerance and hence species expansion.

In this study, we describe the latitudinal patterns in resistance and tolerance to frost and heat and the genetic trade-off between them within populations of *Arabidopsis lyrata* ssp. *lyrata*. *Arabidopsis lyrata* is a short-lived perennial, herbaceous plant closely related to *A.*

thaliana. The species occurs in eastern North America from North Carolina to New York and in the midwest from Missouri to southwestern Ontario [22]. Eastern and midwestern populations form two ancestral genetic clusters; within these clusters the species has a fragmented distribution and most populations are genetically well isolated from one another [23]. The latitudinal cline is strongly correlated with mean annual temperature (higher temperatures in the south; [24]). This temperature gradient may create a gradient in natural selection, leading to a latitudinal cline in anatomical and physiological adaptations to temperature [25]. Thus, *A. lyrata* ssp. *lyrata* is an appropriate organism for assessing latitudinal gradients in resistance and tolerance to temperature.

In two climate chamber experiments, we assessed resistance and tolerance to frost and heat stress in plants of several seed families from each of multiple populations. We defined resistance as the difference in percentage electrolyte leakage between excised leaves that experienced no stress and leaves that were frost- or heat-stressed (analogous to [9]). Electrolyte leakage is caused by cell damage and therefore this method reflects cell membrane stability under stress [26]. Tolerance was defined as the difference in size between plants treated to regular frost or heat stress and plants experiencing control conditions. Size serves as an indicator of individual fitness in this analysis, which is reasonable for this species because the total size of the plant is correlated with reproductive output (see below). This measure of tolerance may not be completely independent of resistance; some plants may have continued growing well under the stress treatment because they were stress resistant. We addressed the following questions: (1) Do resistance and tolerance to frost and heat co-vary with latitude? (2) Does a negative genetic correlation exist between thermal-stress resistance and tolerance to the same temperature stress, and to different temperature stress? (3) Does a negative genetic correlation exist between thermal-stress resistance or tolerance and plant performance under no stress? Our first experiment compared populations along two parallel latitudinal gradients of 6 and 10° from North Carolina to New York and from Missouri to Ontario (Table S1, Fig. 1).

Family means from this experiment were used to indicate the pattern of genetic correlations. A second experiment included many replicate families from one *A. lyrata* population to provide stronger estimates of genetic correlations observed in the first experiment.

Materials and methods

Plant material

For *Experiment 1*, seeds of eight North American *Arabidopsis lyrata* ssp. *lyrata* populations were collected in 2007 and 2011. The sample included four populations near the northern and southern edges of the species' distribution, and four that are more centrally located (Fig. 1). In each population, several fruits of maternal plants were sampled over an area of about 500 m^2; we used seeds of three maternal lines per population for this study. For *Experiment 2,* seeds of 40 plants were collected in 2010 from an area of about 2.5 ha in one population at Saugatuck Dunes State Park, Michigan, USA (42° 42′ N, 86° 12′ W; population 07L in Fig. 1). All populations were outcrossing, judging from their low inbreeding coefficients [23,27]. Collection permits were granted by: Fort Leonard Wood Army Base; Michigan Department of Natural Resources; Rock Island Lodge, Michipicoten, Ontario; US National Park Service; Virginia Department of Conservation and Recreation.

Experimental design

Field-collected seeds were raised in growth chambers and exposed regularly to three temperature treatments: frost, heat and control. The difference in final plant size between stress treatment and control was used as an estimate of tolerance. We measured resistance by excising leaf disks from control plants and measuring electrolyte leakage after exposing them to frost, heat or control conditions.

Experiment 1. The experimental design involved three spatially separated blocks, with one replicate plant per maternal line-treatment combination per block (8 populations x 3 maternal lines x 3 plant-growth treatments x 3 replicates/blocks = 216 plants). Seeds were haphazardly selected and sown in individual pots (dimension: 7 cm diameter, 5 cm depth; substrate 1:1 sand:peat). Pots were arranged in randomized positions on three holding trays per block. We placed two seeds into each pot, to ensure that we had at least one seedling per pot. Seeds were stratified for one week at 4 °C in dark and kept under wet conditions. Trays were transferred into a growth chamber (Grobank, CLF, Germany) for two weeks during germination (18 °C; 8 h:16 h light:dark; light intensity: 150 µmol m^{-2} s^{-1}; relative humidity, RH: 40-70%). We increased the humidity around the seeds by covering pots with a perforated plastic cloth. At the end of the germination period, 78% of seeds had germinated and 184 pots had at least one seedling. Seedlings were haphazardly thinned to one per pot; some were transplanted into pots with no germinated seeds, so that there were 194 pots with seedlings in the end. Day length was then changed to 12 h:12 h light:dark (20 °C:18 °C day:night; light intensity: 180 µmol m^{-2} s^{-1}; RH: 40-70%).

Experiment 2. The experimental design involved three replicates of each maternal line and treatment, arranged in three blocks (40 maternal lines x 3 plant-growth treatments x 3 replicates/blocks = 360 plants). Sowing procedure and conditions for germination were as in Experiment 1. At the end of the germination period, 81% of seeds had germinated. After thinning and transplantation, 353 pots had one seedling.

Treatment during growth to assess temperature-stress tolerance

To assess tolerance to temperature stress, we exposed plants to one of three treatments during growth: control, frost and heat. Temperatures were chosen based on their relevance in nature. Frost events are not uncommon during the early growth period in spring – from April to May – in most of the locations where *A. lyrata* grows (Table S1). Afternoon summer temperatures can reach 46 °C near the basal rosette in mid-latitude populations (Y. Willi, unpublished data). Treatments were applied two weeks after the end of the germination period, when 80% of the plants were at the 4-leaf stage. In the frost treatment, plants were exposed to frost (-3 °C) at the end of nighttime on three days in succession on each of three successive weeks. On each of these treatment days, we gradually decreased the temperature during the night. Starting at 18°C in the growth chamber, plants were transferred into a smaller cabinet (Sanyo® electric Co., Ltd, Japan, model MLR-351H) with humidity conditions as in the growth chamber, then to a freezer, back to the cabinet, and then returned to the growth chamber. Temperature was decreased and then increased in steps of 1 h, starting at 18 °C, then 0 °C, -3 °C, 0 °C and back to 18 °C. We followed a similar schedule for the heat treatment, except that plants were transferred at midday into a cabinet with similar light and humidity conditions as in the growth chamber. Temperature was increased and then decreased in steps of 1 h, starting at the base temperature of 20 °C, then 30 °C, 46 °C in *Experiment 1* / 47 °C in *Experiment 2*, 30 °C and back to 20 °C.

Growth trajectory parameters. The growth trajectory of plants was estimated from photographs of every holding tray made once a week for five weeks beginning at the end of germination. On each week, we measured the length of the two longest leaves of each plant using the software ImageJ v1.45s [28]. We selected an appropriate growth model for our plants by fitting seven alternative models to the mean leaf length for all weeks, separately for each plant. The models were: (1) linear, (2) exponential, (3) power function, (4) three-parameter logistic, (5) two-parameter logistic, (6) Gompertz and (7) von Bertalanffy. Models were fit in R version 3.0.1 (R Core Team 2013) with the package drc [29]. For both experiments, the best-supported model was the three-parameter logistic, which had the lowest Akaike information criterion value. In *Experiment 1*, average AIC weights for the 7 models were: (1) 0.0023, (2) 0.0214, (3) 0.0341, (4) 0.4975, (5) 0.0222, (6) 0.4217, and (7) 0.0004. In *Experiment 2*, average AIC weights for the 7 models were: (1) 0.0142, (2) 0.0231, (3) 0.0596, (4) 0.4414, (5) 0.1387, (6) 0.3162, and (7) 0.0067. The parameters of the three-parameter logistic model, estimated separately for each plant, are the asymptotic leaf length at the end of the growth period, the scale parameter, and x_{mid} (time until 50% of size is reached). The scale parameter is the inverse of maximum growth rate, *r*, so a large value corresponds to a low rate of growth. Parameter estimates for one plant in *Experiment 1* and for two plants in *Experiment 2* were discarded because they were >5 SD away from the mean; for asymptotic size, the direct measure from the last picture was taken instead. We also counted the number of leaves at the end of the experiment as a fourth measure of plant performance.

Calculating tolerance. Tolerance was calculated as the value of asymptotic rosette size of the stressed plant minus that of the control plant of the same maternal family within a block. We used asymptotic size as a measure of plant performance because it is strongly related with the number of fruits in the European sub-species of *A. lyrata* ssp. *petraea* [30] and with number of flowers in subsp. *lyrata* [31].

Temperature-stress resistance

Resistance to stress in the absence of acclimation came from measures of percent electrolyte leakage (PEL) five weeks after the end of germination on plants growing under control conditions only. PEL measured on freshly collected leaves that are exposed to thermal stress or control conditions for some time reflects direct cell damage [32]. We picked the fifth and sixth rosette leaves from each plant and excised from each leaf three 5-mm diameter fragments. Leaf fragments were gently shaken in de-ionized water for 10 min to remove electrolytes from the surface, dried on a tissue, and then fully submerged in separate 1.5 ml tubes with 200 µl of de-ionized water. We applied one of three treatments to each tube: (1) control: incubation at 20 °C for 1 h; (2) frost stress: incubation at -16 °C in *Experiment 1* and -14 °C in *Experiment 2* for 1 h in a freezer; (3) heat stress: incubation at 46 °C in *Experiment 1* and 47 °C *in Experiment 2* for 1 h in a water bath. Incubations were conducted in darkness. The heat temperature was the same as that applied to whole plants during growth. Both temperatures were selected based on preliminary experiments over a wide range of temperatures. After incubation, the leaf fragments rested at room temperature for one hour, after which conductivity of the solution was measured (Conductivity meter FE30 - FiveEasy® Mettler Toledo). Tubes were then placed in a boiling bath for 30 min and conductivity was measured a second time. PEL was conductivity after treatment relative to conductivity after the boiling bath in percent [32]. Resistance was calculated separately for each leaf as PEL of the control disc minus PEL of the stressed disc; low PEL values correspond to low damage, and low differences correspond to low resistance.

Statistical analysis

Latitudinal variation. We first tested for latitudinal differences in growth parameters, number of leaves and PEL by hierarchical mixed model analysis using restricted maximum likelihood (PROC GLIMMIX, SAS Institute, 2006, 2008). Random effects were plant nested within family and population on the first level, family within population on the second level, and population on the third level; for the analysis of PEL, there was one lower level, the leaf nested within plant, family and population. Treatment was a fixed effect on the level of the plant, and block, ancestral cluster and latitude were fixed effects on the level of the population. Latitude was centered to a mean of 0. Similarly, we tested for latitudinal differences in resistance and tolerance to frost and heat stress with mixed models in which random effects were plant (resistance) or plant pair (tolerance) nested within family and population on the first level, family within population on the second level, and population on the third level. Again, for resistance there was one lower level, the leaf nested within plant, family and population. Block, ancestral cluster and latitude were fixed effects on the level of the population. In both kinds of models, interaction terms of cluster-by-latitude and cluster-by-latitude-by-treatment were never significant ($P > 0.2$) and not included in the final models. Latitude is a good proxy for temperature in this region: both mean minimum temperature during spring and mean maximum temperature during summer were strongly negatively correlated with latitude (mean minimum temperature March-May: $N = 8$, $r = -0.90$; mean maximum temperature June-August: $N = 8$, $r = -0.73$; monthly means from *www.worldclim.org*).

Correlations between resistance and tolerance. A second analysis estimated within-population genetic correlations among resistance, tolerance, and plant size under control conditions across all populations. Family means were taken to reflect genotypic values. For Experiment 1, we standardized family means by population (mean = 0, SD = 1) and calculated Pearson correlation coefficients. For Experiment 2, we calculated Pearson correlation coefficients on untransformed family means.

Results

Latitudinal variation

Percent electrolyte leakage, PEL. Electrolyte leakage did not vary with latitude or ancestral cluster, but increased when leaves were exposed to stressful treatments (Table 1). PEL under control conditions was significantly lower than under frost and heat (least squares means, LSM ± SE control: 4.41 ± 0.39%, frost: 78.07 ± 1.74%, heat: 24.80 ± 4.70%). The treatment effect tended to interact with latitude: while PEL was about the same across latitude for the control treatment, it increased with latitude under heat, and decreased slightly with latitude under frost stress (Table 1, Fig. 2a).

Plant growth. The asymptotic size of plants differed significantly among treatments but not with latitude or ancestral cluster (Table 1). Size was significantly smaller in plants growing in frost and heat treatments than in the control treatment (LSM ± SE control: 49.32 ± 1.72 mm, frost: 42.32 ± 1.63 mm, heat: 39.87 ± 1.88 mm). This indicates that frost and heat were stressful to the plants. The latitude-by-treatment interaction was significant because plants originating from higher-latitude sites grew to a larger size than low-latitude populations under control conditions, while under stressful conditions there were no trends with latitude (Table 1; Fig. 2b). The other two parameters of logistic growth, the scale parameter and x_{mid}, were unaffected by treatment or latitude (Table 1). The number of leaves at the end of the experiment was reduced in plants exposed to frost or heat stress, but was not significantly related to latitude (LSM ± SE control: 18.2 ± 0.9, frost: 16.6 ± 0.8 mm, heat: 16.8 ± 0.8 mm).

Temperature-stress resistance and tolerance. Resistance to frost and heat – calculated based on PEL – varied significantly with latitude, but in opposite directions (Table 2, Fig. 2c). Populations from the north were more frost resistant and populations from the south were more heat resistant. Frost resistance was greater in western populations than eastern populations. (LSM ± SE western populations: -69.96 ± 1.38%, eastern populations: -77.83 ± 1.51%). Tolerance to frost and heat based on asymptotic size declined significantly with latitude (Table 2, Fig. 2d). Populations in the western cluster were less tolerant to heat than eastern populations (LSM ± SE western populations: -14.54 ± 1.75 mm, eastern populations: -4.15 ± 2.20 mm). Results were unchanged when tolerance was standardized by the size under control conditions ([size stress – size control]/size control).

Correlations between resistance and tolerance

Experiment 1. Genetic correlations between resistance and tolerance to the same type of stress were not significant (Table 3). This suggests no genetic trade-off between the two. The fact that the correlations were also not significantly positive suggests that our measure of tolerance was not strongly affected by resistance. Across stress types, resistance and tolerance to frost tended to trade off against heat resistance. Costs of resistance and tolerance, measured as genetic correlations with plant size in the absence of stress, were important only for frost tolerance. Relatively frost-tolerant genotypes were also relatively small. Frost resistance varied positively with plant size.

Experiment 2. Genetic correlations between resistance and tolerance to the same type of stress were not significant (Table 3). Across stress type, there were significant positive correlations between frost and heat resistance, and between frost and heat tolerance. Costs of frost tolerance were also detected, this time along with costs of frost resistance and heat tolerance.

Discussion

Populations of *Arabidopsis lyrata* distributed across two latitudinal clines differ in several traits related to life history and persistence under thermal stress: plant size and resistance and tolerance to frost and heat. Plants from northern populations grew larger under control conditions, were more frost resistant, but less heat resistant and less heat tolerant compared to plants from southern populations. Surprisingly, plants from northern populations were also less tolerant to frost. We also found no evidence for a genetic trade-off between resistance and tolerance for the same type of thermal stress; nor was there consistent evidence for genetic trade-offs between resistance and tolerance for different types of stress. Resistance and tolerance to thermal extremes carried no consistent measurable costs, except that frost tolerance traded off against plant size under control conditions. The latter correlation was due to within-population variation.

The common garden design of this study emphasized genetic contributions to population divergence and variation among seed families within populations. Maternal environmental effects cannot be entirely ruled out, but they seem unlikely to have strongly impacted results. In herbaceous plants, early life-cycle traits such as seed size have been shown to be affected by maternal environmental effects, while later-expressed traits are not significantly impacted [33]. In *A. lyrata*, we have found that seed size is not correlated with a variety of later traits such as rosette size, carbon isotope discrimination, leaf dissection, trichome density, stomata density and length, and flowering time [34]. A few empirical studies specifically investigated the effect of developing seeds or parental exposure to low and high temperature and its carry-over effect to the next generation. In one accession of *A. thaliana*, exposure of parents to warm (25 °C) and cold (15 °C) conditions during flowering and seed development influenced some performance traits in their offspring and the speed of recovery of photosynthesis after frost but not longer-term recovery [35]. In replicate accessions of *A. thaliana*, exposure of parents to heat stress (40 °C) or control conditions during their vegetative growth phase for two generations did not influence final performance traits in their offspring when assessed under heat stress and control conditions [36]. For these reasons, we assume that variation among populations and seed families in this experiment is mostly genetic.

Latitudinal variation

Latitudinal trends in plant size and thermal-stress resistance and tolerance suggest that selection differs along the latitudinal gradient. The alternative – genetic drift – seems unlikely to have driven genetic differentiation because drift is a random force and therefore cannot create systematic differences in expressed traits along environmental gradients. The fact that results were qualitatively the same for the eastern and western clusters strengthens this conclusion. Moreover, latitudinal variation in size is consistent with data from many other plant species [37]. Our results also agree with previous studies on *A. lyrata* ssp. *lyrata* [24] and ssp. *petreae* [38,39], for which common garden experiments reveal that plants from high-latitude populations grow to larger size. In contrast, *A. thaliana*, a close relative of *A. lyrata*, apparently exhibits reduced growth rate, asymptotic size and leaf number at high latitude [40]. In our study, the two parameters reflecting the speed of growth – the scale parameter and x_{mid} – did not significantly vary with latitude. Larger plant size in northern populations of *A. lyrata* may be associated with a generally faster reproductive development [24], possibly in response to more adverse conditions and a shorter vegetation period in the north (i.e., counter-gradient variation; Conover et al. [41]).

Latitude represents a complex environmental gradient strongly associated with temperature. Populations exposed to different temperatures along the gradient are expected to evolve correlated differences in characters related to resisting or tolerating thermal extremes [3,42]. Indeed, we found good evidence for this. Low-latitude populations exhibited elevated resistance and tolerance to heat stress, and this is consistent with the temperatures they experience in nature. High-latitude populations had elevated resistance to frost stress, which agrees with the association between frost resistance and latitudinal in *A. thaliana*, both with and without prior acclimation [43,44]. Unexpectedly, we also found that tolerance to frost declined with latitude; this may be due to trade-offs between frost tolerance and other performance traits, as discussed later.

Correlations between resistance and tolerance

Our data did not support the hypothesis that resistance and tolerance of the same type of thermal extreme trade off against one another, at least in Experiment 1 (analysis of family means across populations). The situation is similar in the study of plant-herbivore interactions, for which evidence of a trade-off between resistance and tolerance is limited [13,15]. Among stress types, we also found no significant evidence for a trade-off between resistance and tolerance. In Experiment 1, coping with frost tended to trade off against heat resistance. And in Experiment 2 (many more families from one population), frost and heat resistance and frost and heat tolerance were positively correlated. Overall, our results provide no indication of constraints on the joint evolution of (increased) resistance and tolerance.

Evidence for costs of resistance and tolerance expressed as reduced performance under benign conditions was inconsistent. Costs of frost resistance and heat tolerance were detected in the experiment on seed families from one populations, but not in the experiment on seed families in multiple populations. An exception here was frost tolerance, for which costs were observed in both experiments (assuming that plant size was costly). The cost of frost tolerance could be an important constraint on adaptation at the northern edge of the distribution. Evidence suggests that selection in the north favors large size and an early switch to sexual reproduction [24], and frost tolerance is presumably also beneficial in cold, northern environments. But the trade-off between them implies that the two cannot evolve adaptively in the same time. This result is based on within-population genetic variation, but it matches exactly the pattern of among-population variation for plant size and frost tolerance. Plants from the north were large under benign conditions but were less frost tolerant. Plants from the south grew to smaller size under control conditions and their frost tolerance was higher. Thus, one explanation for the northern distribution limit of *A. lyrata* may be the combination of a short vegetation period and frequent frosts that delay flowering.

Conclusions

Our study is among the first to systematically investigate the relationship between resistance and tolerance in the context of thermal stress. The rate of reproductive development is a well known mode of adaptation to latitude in plants (reviewed in Paccard et al. [24]), and our results suggest that thermal-stress resistance and tolerance may be important as well. Although there was no evidence for trade-offs between resistance and tolerance to the same thermal stress, we did find that thermal adaptation may be constrained by adaptation to other stress factors, for example the length of the growth and reproductive season. Evolution toward larger size and early reproduction is prevalent in the north, but may be impossible to maintain under frost. Obviously, finding generalities in these patterns across species would be of great interest for many fields, including climate adaptation, understanding species distribution limits and global climate change.

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Table 1. Results of hierarchical mixed model analysis testing the effect of block, ancestral cluster, latitude, treatment and the interaction between the latter two on percentage electrolyte leakage (PEL), three parameters describing plant growth (asymptotic size, scale parameter and mid-point of growth x_{mid}), and the number of leaves of *Arabidopsis lyrata* plants (N = 384, 194, 193, 193, 194). The table shows F values; the last two rows show t values for contrasts between pairs of treatments. Statistics for the random effects are not shown. Significance is indicated in bold: $^{(*)}P < 0.1$, $^{*}P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$

			PEL		Asymptotic size	Scale parameter	x_{mid}	Number of leaves
Dependent variables	df$_{num}$	df$_{den}$	F	df$_{den}$	F	F	F	F
Block	2	14	0.49	14	**3.54**$^{(*)}$	0.19	1.21	1.11
Ancestral cluster	1	5	0.22	5	1.21	0.37	0.37	2.53
Latitude	1	5	3.27	5	2.97	0.05	0.14	0.73
Treatment	2	14	**855.90*** **	14	**21.88*** **	0.34	0.16	**3.80***
Latitude x treatment	2	370	**2.84**$^{(*)}$	179/180	**8.17*** **	1.59	0.25	2.33
		df	t	df	t			t
Frost vs. control		14	**41.22*** **	14	**-5.37*** **			**-2.61***
Heat vs. control		14	**4.32*** **	14	**-5.94*** **			**-2.30***

Table 2. Results of hierarchical mixed model analysis on resistance to frost and heat assessed from percentage electrolyte leakage (PEL), and tolerance to frost and heat stress assessed from asymptotic size AS. Sample sizes were 128 *Arabidopsis lyrata* plants for resistance, and 64 and 61 plant pairs for tolerance to frost and heat, respectively. The table shows *F* values for the fixed effects of block, ancestral cluster and latitude. Statistics for the random effects are not shown. Significance is indicated in bold: $^{(*)}P < 0.1$, * $P < 0.05$, **$P < 0.01$

				Resistance,PEL	Tolerance,AS
Stress	Dependent variables	df_{num}	df_{den}	*F*	*F*
Frost	Block	2	14	**3.15$^{(*)}$**	1.58
	Ancestral cluster	1	5	**12.56***	3.89
	Latitude	1	5	**11.56***	**26.60****
Heat	Block	2	14	0.17	0.85
	Ancestral cluster	1	5	2.41	**10.66***
	Latitude	1	5	**8.62***	**32.21****

Table 3. Correlations between frost/heat resistance (RES_{PEL}), frost/heat tolerance based on asymptotic size (TOL_{AS}), and performance based on asymptotic rosette size of control plants of *Arabidopsis lyrata* ($AS_{control}$) for two experiments. Correlations were performed on family means from eight populations (*Experiment 1*; population-scaled family means, $N = 20$-21) and on family means from one population near the distribution center (*Experiment 2*; $N = 39$-40). Significance is indicated in bold: $^{(*)}P < 0.1$, $*P < 0.05$, $**P < 0.01$, $***P < 0.001$

			Frost		Heat		Performance
Experiment			RES_{PEL}	TOL_{AS}	RES_{PEL}	TOL_{AS}	$AS_{control}$
1	Frost	RES_{PEL}	1	-0.25	**-0.42$^{(*)}$**	0.05	**0.54***
		TOL_{AS}		1	**-0.37$^{(*)}$**	0.02	**-0.50***
	Heat	RES_{PEL}			1	0.02	-0.20
		TOL_{AS}				1	-0.09
2	Frost	RES_{PEL}	1	0.22	**0.45*****	0.22	**-0.34***
		TOL_{AS}		1	0.24	**0.61*****	**-0.77*****
	Heat	RES_{PEL}			1	0.05	-0.18
		TOL_{AS}				1	**-0.67*****

Figure legend

Fig. 1. Locations of the nine North American *Arabidopsis lyrata* populations included in this study. The grey shading indicates the approximate distribution of the species based on herbarium records, regional botanical lists, personal communication with local botanists, and our own field experience. The actual distribution is highly fragmented. The eastern and western regions represent distinct ancestral genetic clusters [23].

Fig. 2. Latitude of origin of *Arabidopsis lyrata* plants differing in electrolyte leakage (a), asymptotic size (b), resistance to frost and heat based on electrolyte leakage (c), and tolerance to frost and heat based on asymptotic size (d). Symbols depict population means based on family means and one-/two-sided bars indicate standard errors. Regression lines on panels a and b represent the significant or close to significant latitude-by-treatment interaction, regression lines on panels c and d represent significant latitude effect. For statistics see Tables 1 and 2. Data for heat tolerance and frost resistance had been corrected for ancestral cluster.

Fig.1

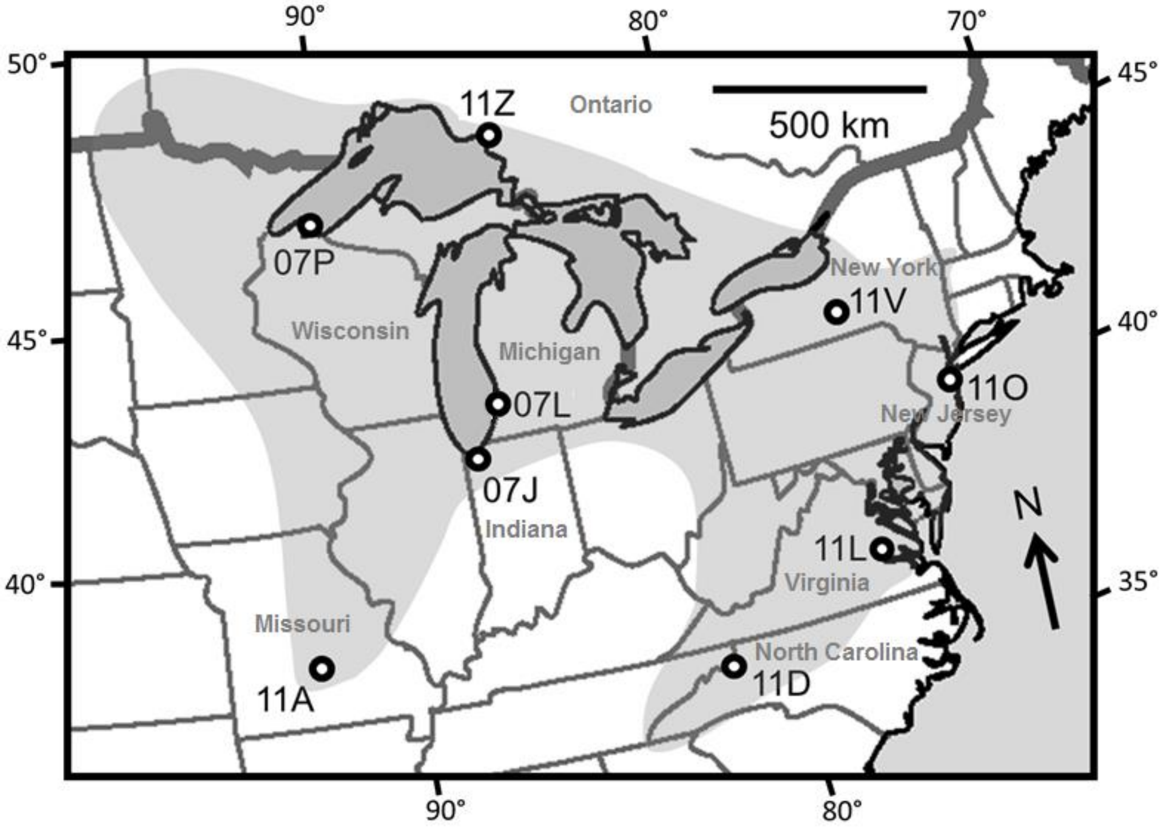
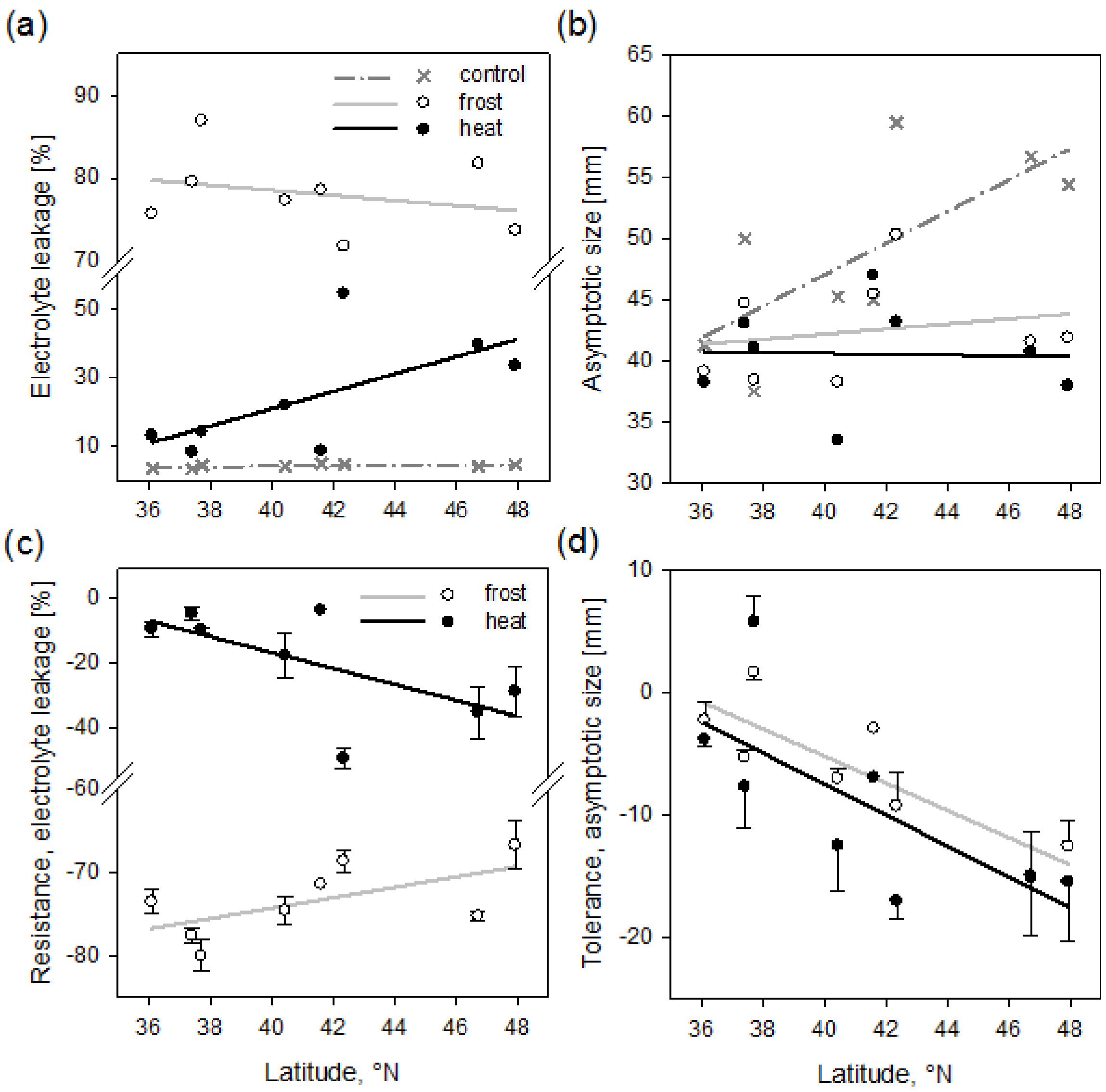

90°
80°
70°
50°
45°
40°
45°
40°
35°
500 km
Ontario
11Z
07P
Wisconsin
Michigan
07L
07J
Indiana
Missouri
11A
New York
11V
11O
New Jersey
11L
Virginia
North Carolina
11D
N
90°
80°

Fig. 2


(a)
(b)
(c)
(d)
control
frost
heat
frost
heat
Electrolyte leakage [%]
Asymptotic size [mm]
Resistance, electrolyte leakage [%]
Tolerance, asymptotic size [mm]
Latitude, °N
Latitude, °N
36
38
40
42
44
46
48
10
30
50
70
80
90
30
35
40
45
50
55
60
65
0
-20
-40
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-80
10
0
-10
-20

Supporting information

S1 Table. Locations of *Arabidopsis lyrata* ssp. *lyrata* populations of this study and average number of days with negative temperatures (Frost days) recorded for April and May over the last 10 years, from 2001 to 2011. Weather records from the closest weather station of the populations studied were downloaded from the National Climatic Data Center webpage (http://www.ncdc.noaa.gov/). For population 11O, data were obtained from the Sandy Hook station for the years 2001, 2005 and 2008-2011, and from the Long Branch Oakhurst station for the other years. For population 11Z, data were obtained from the Wawa Station for the years 2004, 2005 and 2006 and from a weather forecast website for the other years (http://www.wunderground.com/history/)

Pop	**Location**	**Lat. °N**	**Long. °W**	**Weather Station**	**Frost days April**	**Frost days May**
11D	North Carolina	36.11	81.66	Boone, NC	7.45	1.72
11L	Virginia	37.41	77.02	Williamsburg 2 N, VA	0.72	0
11A	Missouri	37.72	92.05	Waynesville 2 W, MO	4.72	0.45
11O	New Jersey	40.44	73.98	Sandy Hook, NJ	1.36	0
07J	Indiana	41.60	87.19	Indiana Dunes NAT LK, IN	4.63	0.27
11V	New York	42.35	76.39	Ithaca Cornell University, NY	12.45	3.63
07P	Wisconsin	46.73	90.80	Madeline Island, WI	21.72	7.81
11Z	Ontario, Lake Superior	47.93	84.85	Wawa AUT	24.18	11.72

Chapter 2: **The evolutionary ecology and transcriptome profiling of thermal acclimation in *Arabidopsis lyrata***

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Summary

Frost and heat events can be challenging for sessile organisms that cannot escape extreme thermal events. However, adverse effects on fitness may be reduced by pre-exposure to cold or heat, a process known as acclimation. To understand the ecological and evolutionary implications of acclimation, we investigated (1) the magnitude of improved thermal stress resistance after acclimation, (2) costs of acclimation, and (3) the genes differing in expression due to acclimation. Plants of *Arabidopsis lyrata* were raised under three acclimation treatments: frost, heat, or none. Resistance of leaves to frost and heat stress was then measured by electrolyte leakage. RNA-seq analysis was performed to examine the genes differentially expressed between acclimated and non-acclimated plants. Acclimation increased thermal resistance independent of acclimation temperature, with the highest increase in resistance to frost after frost acclimation (as a trend) and in heat resistance after heat acclimation. There was no significant evidence of costs of acclimation. RNA-sequencing suggested that increases in resistance after frost and heat acclimation were caused by distinct mechanisms: modification of the chloroplast membrane and modification of the cell wall, respectively. Our results suggest that thermal resistance is a labile complex of traits, strongly affected by the acclimation environment, with undetermined costs.

Keywords: acclimation, adaptive phenotypic plasticity, *Arabidopsis lyrata*, environmental change, temperature stress, thermal adaptation, transcriptome analysis.

Introduction

Coping with temperature extremes represents an ecological challenge for many species, but especially for sessile organisms that have limited options for escape. Temperature extremes can cause adverse effects on metabolism, growth and development, with detrimental consequences for individual fitness (Larcher, 2003; Wahid *et al.*, 2007; Thakur *et al.*, 2010). In many cases, negative effects of thermal stress are moderated by pre-exposure to cold or hot conditions, a process known as acclimation (Levitt, 1980). At the same time, temperature extremes seem to be an evolutionary challenge because many organisms have restricted climatic niches that are often greatly determined by temperature (Gaston, 2003). This fact points to constraints in the evolution of acclimation. Causes of constraints may include different types of costs of acclimation, for example maintenance costs and genetic costs due to genetic non-independence of the acclimation response (*sensu* DeWitt *et al.*, 1998). To fully understand the ecological and evolutionary implications of exposure to temperature extremes, the extent of acclimation, its costs and its genetic basis need to be understood.

Acclimation is a form of presumably adaptive phenotypic plasticity which helps organisms cope with stressful conditions (Levitt, 1980). Exposure to suboptimal conditions triggers rapid and transient physiological modifications that enhance resistance to subsequent stress (Levitt, 1980). As a type of adaptive phenotypic plasticity, acclimation should evolve under environmental conditions that require a rapid response to predictable or unpredictable environmental challenges (Angilletta, 2009). But acclimation may be costly, and this could limit its expression in spite of positive effects on fitness under stress (DeWitt *et al.*, 1998). First, costs could arise from maintaining the capacity to express acclimation (maintenance costs). In this case genotypes that are capable of acclimation will bear its costs regardless of whether they ever express acclimation. Second, costs may arise due to the non-independence of genes responsible for the plastic response via linkage, pleiotropy or epistasis, with the effect of a negative relation between acclimation response and other performance traits relevant to fitness (genetic costs).

Genetic costs can be revealed by looking for genotypic associations between plasticity and performance traits in the presence and absence of acclimation.

Costs of thermal acclimation have been extensively studied in animals, especially in *Drosophila* species (Hoffmann *et al.*, 2003) but to a lesser extent in plants. These studies commonly quantified fitness costs and benefits between acclimated and non-acclimated genotypes. While evidence for costs on fitness, i.e. reduction in fecundity after cold and heat acclimation was demonstrated in *Drosophila* (Hoffmann *et al.*, 2003), no decrease in fitness was shown after a cold acclimation treatment in the plant species *Arabidopsis lyrata* (Zhen *et al.*, 2011). However, most of the studies that estimated costs of acclimation did not distinguish between the different types of costs including maintenance cost or genetic costs. A more detailed understanding of the wider implications of acclimation and genetic integration may arise from understanding the physiological and genetic basis of the acclimation process. For example, these data could indicate connections between pathways that stand in antagonistic interaction and may limits the evolution of acclimation.

The physiological basis of acclimation has been particularly well studied in *Arabidopsis thaliana*. The cold acclimation process in this species was reviewed by (Thomashow, 1999) and (Xin & Browse, 2000). Acclimation by a cold period induces modifications in the structure and the composition of the plasma membrane revealed by microscopy and chromatography analysis (Ristic & Ashworth, 1993; Uemura *et al.*, 1995), in metabolites and soluble carbohydrate content (Ristic & Ashworth, 1993; Kaplan *et al.*, 2007) and in the level of antioxidants (O’Kane *et al.*, 1996). Cold acclimation rapidly increases resistance to cold. The degree of resistance and accompanying physiological modifications occur within one hour and are positively correlated with the duration of the acclimation period (Gilmour *et al.*, 1988). Furthermore, sudden changes in gene expression were observed during acclimation, mostly involving the temperature-stress response and hormone signaling (Hannah *et al.*, 2005).

Heat acclimation in *A. thaliana* involves adjustments of membranes important in protection against thermal stress. For instance, Falcone *et al.* (Falcone *et al.*, 2004) reported a decrease of polyunsaturated lipids in leaf membranes after a heat treatment, as determined by chromatography assay. Expression studies on other Brassicaceae species demonstrated that heat shock proteins (HSPs), hormone response elements and genes involved in cell wall thickness tended to be overexpressed after heat acclimation (Yang *et al.*, 2006; Larkindale & Vierling, 2008). Research so far has focused on particular acclimation temperatures, and it is not known how different temperatures affect the efficacy of acclimation or gene expression during the thermal acclimation process.

The goal of this study was to investigate the acclimation response of plants exposed to frost and heat stress, two prominent abiotic stresses. The specific questions addressed were: (1) How do frost and heat acclimation affect thermal resistance to frost and heat stress? (2) Are there maintenance costs or genetic costs of frost and heat acclimation? (3) Which genes are differentially expressed under frost and heat acclimation relative to control conditions? What are the treatment-specific differences and what are the shared differences? The study was conducted on the perennial plant *Arabidopsis lyrata* ssp. *lyrata*, a close relative of *A. thaliana*. Seeds of several maternal families were collected in one large, outcrossing population in nature. Plants were raised in a climate chamber experiment under frost, heat or no acclimation. Resistance to frost and heat was then measured by the percentage of electrolyte leakage (PEL), a method used to estimate cell membrane stability at extreme temperatures (Cornelissen *et al.*, 2003). Furthermore, a subset of leaf samples was snap-frozen and the transcriptome sequenced by next-generation sequencing.

Material and methods

Experimental design

Arabidopsis lyrata subsp. *lyrata* is a short-lived perennial plant of open habitats, such as sand dunes or rocky outcrops and ledges, in the northeastern and midwestern United States and southern Ontario, Canada (Griffin & Willi, 2014; Paccard *et al.*, 2016). The plant produces basal rosettes and flowers in spring; one or several inflorescences produce many small white flowers. Because *A. lyrata* generally grows where grass and other herbaceous species are not very dense, it is directly exposed to variation in air and substrate temperature.

The experimental design included 40 maternal seed families, each reared with three replicates under three thermal-acclimation treatments (N = 40 families × 3 treatments × 3 replicates [one per block] = 360 plants). The three treatments were frost acclimation, heat acclimation and control. Acclimation temperatures, applied repeatedly but for short duration, were -3 °C and 47 °C, respectively. The low temperature was chosen to reflect short frost events in the early morning phase during late spring, and the high temperature was chosen to reflect short heat events as they can occur close to the soil surface where *A. lyrata* grows in nature in the early afternoon during summer time. Plant material came from *A. lyrata* seed families collected in June 2010, over an area of 2.5 ha at Saugatuck Dunes State Park, Lake Michigan, USA (42°42′ N, 86°12′ W). Progeny array analysis on this population had revealed that it was predominantly outcrossing (Willi & Määttänen, 2010, 2011). The plants were grown in cylindrical tubs (7 cm diameter, 5 cm depth) filled with a 1:1 ratio of peat:sand. We germinated two seeds per tub, and nine tubs for each seed family. Tubs were then arranged in random positions within five trays per block, with three tubs – one for each treatment – per family in a block. There were a total of three blocks. After a stratification period of one week at 4 °C in darkness under wet conditions, plants were transferred to a growth chamber (Grobank, CLF, Germany) with short-day conditions (8 h : 16 h light : dark; light intensity: 150 µmol m-^{2} s^{-1}; 18 °C; relative humidity (RH): 40-70%). Seeds started to germinate five days after the end of stratification, and 80% of seeds had germinated after two week. Day length and temperature were then increased in two steps to reach favorable conditions for plant growth: 12 h : 12 h light : dark, light intensity: 180 µmol m-^{2} s^{-1}, 20 °C : 18 °C day : night, RH: 40-70%. One week after the end of germination, extra seedlings were haphazardly removed from each tub and some seedlings were transplanted into tubs with no germinated seeds. This resulted in 348 tubs with one seedling each.

Acclimation treatments. The three treatments – frost acclimation, heat acclimation and no acclimation – began when plants were in the four-leaf stage, four weeks after the onset of germination. Treatments were applied for three weeks, on three sequential days per week. All tubs in an acclimation treatment were moved into a separate growth chamber, and the temperature was changed in intervals of 1h. For frost acclimation, temperatures were set to 0°C, -3 °C, 0 °C during nighttime. For heat acclimation, temperatures were set to 30 °C, 47 °C, 30 °C during midday. These temperature regimes were neither lethal for *A. lyrata* nor did they cause any visible damage on leaves. At the end of each treatment cycle, plants were returned to their original position in the experiment.

Plant size. Rosette size was used as a component of plant fitness because it is closely associated with reproductive traits such as the number of flowers (Willi, 2013) and the number of fruits (Sandring *et al.*, 2007). Asymptotic rosette size at the end of the growth period was estimated by fitting a logistic growth model to repeated measurements of plant size of each plant. We defined rosette size as the average of the length of the two longest leaves, measured from photographs of entire holding trays taken once a week for five weeks starting when plants were three weeks old. The two-parameter logistic growth model was the best-supported model out of seven that we compared: linear, exponential, power function, two-parameter logistic, three-parameter logistic, Gompertz, and von Bertalanffy (Wos & Willi, 2015). The two parameters of the two-parameter logistic growth model represent asymptotic rosette size and the rate of exponential growth. Parameter estimates for one plant were > 5 SD away from the mean; these were rejected and replaced by the mean length of the two longest leaves on the last round of photography (for rosette size) and a missing value (for growth rate). Tolerance of stress was calculated as the asymptotic rosette size of a stressed plant minus that of the control plant of the same maternal family within a block.

Temperature-stress resistance. Thermal resistance was estimated by measuring percent electrolyte leakage (PEL) when plants were fully grown at about seven weeks of age. For each plant, three 6-mm diameter discs were excised from the fifth rosette leaf. Each disc was gently rinsed in de-ionized water prior measurements to remove electrolytes from the surface and then dried on a tissue. Next, we exposed each disc to one of three treatments: (1) control: incubation of the disc in a plastic tube at 20°C for 1h; (2) frost stress: incubation at -14°C for 1h; (3) heat stress: incubation at 47°C for 1h. Stress temperatures were chosen to achieve approximately 50% electrolyte leakage, or in other words, at which 50% of the damage on leaves occurred (Ehlert & Hincha, 2008; Thalhammer *et al.*, 2014b). After incubation, we measured a first time conductivity (Conductivity Meter FiveEasy FE30, Mettler Toledo, Columbus OH, USA). We then placed the tubes in a boiling bath for 30 min and measured conductivity a second time, assuming that the conductivity after boiling represents complete electrolyte leakage. We measured PEL as the ratio of the conductivity before boiling to that after the boiling bath (Cornelissen *et al.*, 2003). For each acclimation treatment, resistance was calculated as PEL of the control disc minus PEL of the treated disc, so that a low value corresponded to low level of resistance.

Statistical analysis of growth and resistance variables

Effect of acclimation on resistance. Hierarchical mixed model analysis was used for testing the effect of treatment on y-variables of rosette size, exponential growth, PEL, and resistance (SAS Institute, 2011). The random effects were leaf disc or leaf disc pair nested within plant and maternal family (for PEL and resistance, respectively), plant nested within maternal family, and maternal family. Fixed effects were leaf disc treatment on the level of a plant (for PEL and resistance; only one replicate measure per plant), acclimation treatment on the level of the plant, and block. A simple diagonal covariance structure for random effects was assumed, modelling a different variance component for each random effect (SAS Institute, 2011).

Costs of acclimation. Maintenance costs for frost and heat acclimation were estimated by selection-gradient analysis, where residual fitness – after accounting for resistance – should show a negative relationship with the acclimation response if there are significant costs of this type (Van Tienderen, 1991; DeWitt *et al.*, 1998). Family means were calculated for asymptotic rosette size, frost resistance and heat resistance, for the three acclimation treatments separately. The relative asymptotic rosette size for a particular treatment was the family mean of asymptotic rosette size divided by the mean of family means for asymptotic rosette size in that treatment. Acclimation plasticity was calculated as frost or heat resistance under acclimation minus frost or heat resistance under no acclimation. Next, we performed a multiple regression of plant size in the acclimation environment against resistance in the same environment as the first explanatory variable and plasticity in resistance as the second explanatory variable (DeWitt *et al.*, 1998). Type 1 sums of squares statistics were used. We repeated the multiple regression for values of the control environment because costs could also appear in the benign environment.

We tested for genetic costs of cold and heat acclimation by Pearson correlation analysis on family means involving the following traits: acclimation plasticity in resistance, resistance under no acclimation and tolerance as well as plant size with and without acclimation. Negative correlations were interpreted as genetically-based trade-offs. Finally, correlation analysis on family means for resistances under all acclimation treatments was performed to look into their genetic dependence.

Transcriptome analysis

RNA extraction. Transcriptome analysis was performed on 16 randomly chosen maternal families in the first block (16 maternal families x 3 treatments = 48 individuals). Six hours after the acclimation treatment concluded, just before PEL measurements were taken, the seventh rosette leaf was collected and immediately snap-frozen in liquid nitrogen. Total RNA was extracted using the RNeasy® Mini Kit protocol (Qiagen, Hilden, Germany) including the DNase treatment step with the RNase-Free DNase Set (Qiagen, Hilden, Germany) according to the manufacturer's instructions. We checked the purity and quantity of RNA with a Nanodrop 2000 spectrophotometer (Thermo Scientific, Wilmington, DE, United States).

Library construction and sequencing. RNA integrity was assessed on an Agilent 2100 Bioanalyzer (Agilent Technologies, Palo Alto, CA, USA). cDNA libraries for each plant were prepared according to the instructions of the Illumina TruSeq Stranded mRNA Sample Preparation Kit (Catalog # RS-122-2101). Specific TruSeq adapters were ligated on the cDNA for each library for individual sequencing. Sequencing was done on an Illumina NextSeq^{TM} 500 platform (Illumina, San Diego, CA, USA). The 48 plants were sequenced on two lanes (2x24) using 75 bp single-end reads. Raw data was filtered to remove low quality reads. The data are available in EMBL Sequence Read Archive (http://www.ebi.ac.uk/ena) under the accession PRJEB13660.

Data processing and sequence alignment. Sequencing generated 590 and 580 million quality-filtered reads for the two lanes, respectively. Quality of each library was further checked using the software FastQC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/). FastQC reported for each library between 19.1 and 30.9 million reads per plant and an overrepresentation of one sequence, which was the TruSeq adapter. The adapter was then trimmed using the software cutadapt (Martin, 2011) and reads for each individual were aligned on the *A. lyrata* reference genome (Hu *et al.*, 2011) with the version-2 annotation (Rawat *et al.*, 2015) using the TopHat v2.1.0 software (Trapnell *et al.*, 2012). We kept only the uniquely mapped reads (70-75% of the total number of reads).

Gene expression analysis. To compare gene expression after frost and heat acclimation relative to control conditions, the number of reads mapped on each gene was counted with HTSeq-count v0.6.1p2 (Anders *et al.*, 2015) using the union mode. Read counts were analyzed by a generalized linear model using the EdgeR v3.12.0 package (Robinson *et al.*, 2010) in program R (R Core Team, 2013). We scaled the library size with the calcNormFactors function and estimated dispersion using the estimateGLMCommonDisp and estimateGLMTagwiseDisp functions. The model tested for the effect of acclimation treatment and the factor of maternal line and was run twice, for the two acclimation treatments separately. *P*-values were adjusted for multiple testing with the Benjamini and Hochberg false discovery rate correction (FDR). Genes with FDR < 0.05 were considered as differentially expressed. The distinction between down- and up-regulated genes was established based on the log2foldchange (log2FC) ≤ -0.5 and ≥ 0.5, respectively.

Gene ontology analysis. We used the *A. thaliana* annotation for the gene ontology (GO) analysis. Information on homology between *A. lyrata* and *A. thaliana* genes were looked up in the *A. lyrata* version-2 annotation database. Gene description was obtained from The Arabidopsis Information Resource (TAIR) (Berardini *et al.*, 2015). Gene Ontology term enrichment analysis was performed with BiNGO v 3.0.3 in Cytoscape v 3.3.0 (Maere *et al.*, 2005). Gene Ontology terms were considered as significantly enriched if they were represented by at least five genes and if FDR-adjusted *P* value < 0.05.

Results

Effect of acclimation treatment on growth, PEL and resistance

Asymptotic rosette size, but not the exponential growth parameter, was significantly affected by the acclimation treatment during growth (Table S1). Frost and heat acclimation led to smaller plant size (least squares means, LSM ± standard error, SE of control: 49.27 ± 0.67 mm, frost: 42.42 ± 0.68 mm, heat: 41.56 ± 0.68 mm), with the chosen temperatures for frost and heat having similar effect sizes. Acclimation strongly affected PEL and resistance to thermal stress (Table 1, Fig. 1). Frost resistance was significantly enhanced after both frost and heat acclimation compared to non-acclimated control plants, and frost resistance tended to be higher after frost acclimation compared to heat acclimation. Likewise, heat resistance was significantly increased after both frost and heat acclimation, and heat resistance was significantly higher after heat acclimation compared to frost acclimation. Results indicated that acclimation generally triggered resistance, but higher resistance was achieved when acclimation temperature corresponded to the stress temperature.

Costs of acclimation

If maintenance costs are associated with acclimation, maternal families with a higher difference in resistance between acclimated and non-acclimated conditions – higher acclimation plasticity – should have a lower plant size, after accounting for general resistance in that environment. There was no significant negative relationship between plant size (y-variable) in the frost acclimation environment and acclimation plasticity in frost resistance, when the model also contained frost resistance as a first explanatory variable (slope b ± SE: -0.0003 ± 0.0031; Table S2, Fig. S1). Also, there was no significant negative relationship between plant size in the heat acclimation environment and acclimation plasticity in heat resistance, when the model also contained heat resistance as an explanatory variable (b = 0.0011 ± 0.0011; Table S2, Fig. S1). Furthermore, there was no significant negative relationship between plant size in the benign environment and acclimation plasticity for both frost (slope b ± SE: -0.0008 ± 0.0038) and heat acclimation (b = -0.0043 ± 0.0031; Table S2, Fig. S1). The most plastic families did not exhibit higher costs in terms of rosette size reduction.

Genetic costs of acclimation were investigated by correlation analysis on family means (Table 2). Frost resistance plasticity due to frost acclimation, assessed in terms of change in frost resistance between frost-acclimated and non-acclimated plants of the same family, did not significantly trade off against tolerance or rosette sizes expressed after acclimation treatment or no treatment. Similarly, we did not find any significant correlation between heat resistance plasticity due to heat acclimation, assessed in terms of change in heat resistance between heat-acclimated and non-acclimated plants of the same family, and tolerance or rosette sizes. In short, no significant evidence of genetically-based trade-offs was detected. However it was found that the plastic increase in frost resistance after frost acclimation traded off against constitutively expressed frost resistance (frost resistance of non-acclimated plants; Table 2). Likewise, the plastic increase in heat resistance after heat acclimation traded off against constitutively expressed heat resistance. Results suggest that induced protection is an alternative strategy to constitutive protection.

Correlation analysis suggested that the genetic basis of frost and heat resistance – at least the part with variability within population – was strongly dependent on acclimation (Table S3). Of the 15 correlations involving frost and heat resistance assessed in the three growth environments (6 variables), only three were significant and always involved resistance under no acclimation: There were significant positive correlations between frost resistance under no acclimation and frost resistance under acclimation, both for frost (N = 40, r = 0.53, P < 0.001) and heat acclimation (N = 40, r = 0.52, P < 0.001). The third positive correlation was between heat resistance under no acclimation and frost resistance under frost acclimation (N = 40, r = 0.46, P < 0.01). This indicates some common genetic basis with baseline resistances. However, the same type of resistance, frost or heat, of the two acclimation treatments were not significantly correlated, and there was also an absence of significant positive correlations between frost and heat resistance within the same acclimation treatment. These results indicate that 1) acclimation has a crucial impact on the genetic basis of resistance, and that 2) even within acclimation treatment, resistances to different thermal stress – frost and heat – have a strongly different genetic basis. Again, conclusions apply to the part of genetic basis for which there is variation within population.

Transcriptome analysis

We detected 377 differentially expressed genes (DEGs) after frost acclimation compared to control conditions (Table S4) and 1608 DEGs after heat acclimation (Table S5). Of these, 143 DEGs overlapped between acclimation treatments.

Specific responses to frost acclimation. Analysis of enriched Gene Ontology (GO) terms on the 234 DEGs specific to frost acclimation returned eight GO terms associated with biological processes including 'response to stimulus' and 'terpenoid biosynthetic process' and two GO terms associated with 'molecular function' (Figure 2a, Table S6). A total of 13 genes were related to 'response to temperature stimulus' and eight of them were cold responsive genes. Of those, six were up-regulated and included: *DWARD AND DELAY FLOWERING 1*, a C-repeat binding factor/dehydration responsive element binding (CBF/DREB) transcription factor; *GALACTINOL SYNTHASE 3,* involved in the synthesis of osmoprotectants and thylakoid membrane protection; *GERMIN 3*; *CHILLING SENSITIVE 1*; and two cold-regulated (COR) genes: *COR413-TM1* and *COR15b*. The last three genes have their products localized in the chloroplast membrane and are involved in its protection. Two cold-responsive genes were down-regulated and associated with detoxification of carbonyl compounds (*ALDO-KETO REDUCTASE*) and seedling freezing resistance (*OLEOSIN 3*). The five remaining genes from the 'response to temperature stimulus' category were heat shock proteins (HSPs) associated with 'response to heat' and they were down-regulated. No heat-responsive genes were found to be up-regulated after frost acclimation (Table S7a).

Under frost acclimation, another 26 genes were related to 'response to stress' and included 11 genes involved in biotic stress response, four of them were specific to fungi and seven were involved in general defense pathways. Furthermore, within the 'terpenoid metabolic process', five genes were directly associated with the terpenoid metabolism. Three were up-regulated with two genes involved in hormone biosynthesis: *9-CIS-EPOXYCAROTENOID DIOXYGENASE 5* involved in ABA biosynthesis and *GIBBERELLIN-20-OXIDASE 3* involved in gibberellin biosynthesis, and one gene encoding a zeta-carotene desaturase, which is part of the carotenoid biosynthesis pathway. The two genes down-regulated encoded a phytoene desaturase, also part of the carotenoid biosynthesis pathway, and a terpene synthase, involved in the production of volatile defense compounds.

Specific responses to heat acclimation. GO term enrichment analysis on the 1465 DEGs specific to heat acclimation revealed more processes involved (Figure 2b, Table S6). Within ‘biological process’, 21 GO terms were enriched and could be divided in three groups: ‘response to abiotic stimulus’, ‘response to chemical’ and ‘response to biotic stimulus’. Six GO terms were in ‘molecular function’ and three in ‘cellular component’. In the latter category, all GO terms were associated with locations outside of the plasma membrane: ‘cell wall’, ‘external encapsulating structure’ and ‘extracellular region’. Of the 109 DEGs related to ‘response to abiotic stimulus’ 39 were associated with ‘response to heat’. Of these, 34 genes were up-regulated including 24 HSPs. Heat shock proteins are controlled by heat shock factors (HSF). However, no HSF was significantly up-regulated, but two HSFs were found to be significantly down-regulated. Additionally, the category of ‘response to abiotic stimulus’ included 15 differentially expressed cold-responsive genes; nine of them were down-regulated and six up-regulated (Table S7b).

A higher number of 146 DEGs of heat acclimation depicted by the enriched-GO-term analysis were associated with ‘response to chemical’, represented by the ‘response to oxidative stress’ and ‘response to organic substance’. Heat acclimation also strongly impacted the response to biotic stimuli, especially response to bacteria. We identified 60 genes in ‘response to biotic stimulus’; of which 24 were up-regulated, with 15 genes in ‘response to bacterium’. We found 36 genes down-regulated, with 19 genes in ‘response to bacterium’ and the other ones mainly associated with ‘response to fungus’. Finally, 60 DEGs were linked to the cell wall. Among those, 17 genes were cell wall-modifying enzymes, of which 13 were up-regulated: nine genes encoding xyloglucan endotransglucosylase/hydrolase (XTH) enzymes, one beta-xylosidase, one expansin, one xylanase, and one beta-galactosidase. Four genes were down-regulated: one expansin, two pectin methylesterases and one chitinase. These enzymes have a xyloglucan or a hydrolase activity and contributed to the enriched GO terms ‘xyloglucan:xyloglucosyl activity’ and ‘hydrolase activity, hydrolyzing O-glycosyl compounds’ in ‘molecular function’.

Non-specific response to frost and heat acclimation. The GO term enrichment analysis on the 143 overlapping DEGs revealed only three enriched GO terms. None of them was associated with a category of response to stress, rather they were related to general pathways: ‘photosynthesis’, ‘lipid localization’ and ‘lipid transport’ (Table S6). Five genes were associated with ‘photosynthesis’, four were up-regulated after both frost and heat acclimation. Three of these genes belonged to the light-harvesting chlorophyll a/b-binding family, encoding components of the photosynthetic antenna, and one gene was a PsbP-like protein, part of the photosystem II. The down-regulated gene encoded a glucose-6-phosphate/phosphate transporter. Six genes were in ‘lipid localization’ and ‘lipid transport’ each and belonged to the lipid-transfer protein superfamily.

Discussion

Acclimation and its costs

Acclimation is one way organisms can achieve protection against near-term exposure to thermal stress. In this study on *Arabidopsis lyrata,* thermal acclimation via short bouts of frost or heat increased resistance to both frost and heat stress (Fig. 1). Apart from frost acclimation increasing frost resistance and heat acclimation increasing heat resistance, we also found evidence for cross-protection. Frost exposure also increased heat resistance and heat exposure also increased frost resistance, but both were increased to a lesser extent. This result may imply some common genetic basis of both frost and heat resistance under the same acclimation treatment. But there was no significant genotypic correlation between thermal stress resistances within a particular acclimation treatment (Table S3). Also, the same type of thermal stress resistance – resistance to frost or heat – was not correlated between acclimation treatments, indicating that depending on acclimation, the genetic basis of resistance – the one that is variable within population – is strongly dependent on acclimation. In line, transcriptome analysis revealed very little overlap in gene expression differences between acclimation treatments. And for those genes that overlapped in showing differential expression, their grouping in ontology terms did not reveal an obvious association with stress factors.

Our results on acclimation agree with previous work, which showed the ability of plants to harden in response to low or high temperature (Levitt, 1980), including in *Arabidopsis thaliana* and crop species (Chen *et al.*, 1982; Gilmour *et al.*, 1988; Uemura *et al.*, 1995). As far as we are aware of, induced cross-resistance however has never been reported for frost and heat stress. Cross-resistance (defined as cross-tolerance by Sabehat *et al.*, 1998) was demonstrated between several other pairs of abiotic stresses in plants, i.e. between salt and cold stress (Sabehat *et al.*, 1998). These past studies suggested that cross-resistance might be induced by the expression of specific proteins during pre-exposure to one stress, i.e. heat shock proteins that may be also involved in resistance to other stress. Our own results are ambiguous in this regard. On the one hand, genotypic correlation analysis found that frost and heat resistance in the same acclimation environment were not correlated. On the other hand, the transcriptome study did not reveal the upregulation of heat-responsive genes under frost acclimation. Of the 13 genes related to 'response to temperature stimulus' under frost acclimation, five were heat-responsive and they were all down-regulated. Under heat acclimation, we detected only six upregulated cold-responsive genes, and none of them had been shown to be related to cell membrane modifications (Table S7b).

As acclimation plasticity – the change in resistance between acclimated and non-acclimated plants – should help plants cope with more stressful conditions, e.g., at range edges determined by a change in thermal conditions, its evolution may be constrained by costs. With the approaches and variables used, we found no evidence for maintenance costs. Therefore, our results on *A. lyrata* add to the list of studies who detected no significant maintenance costs of acclimation plasticity in response to abiotic factors in plants (Van Kleunen & Fischer, 2005).

This may stem from the difficulty of detecting such costs, for example because the detection seems affected by stress intensity (Van Buskirk & Steiner, 2009). Empirical studies demonstrated that costs were higher under the most unfavourable conditions (Steinger *et al.*, 2003; Bell & Galloway, 2008). But even when significant costs of plasticity were found, they were often low (Van Buskirk & Steiner, 2009). To date, no study is available for comparison in plants, and more data on costs of plasticity are needed that assess them under different environmental regimes.

We also did not detect evidence for genetic costs of acclimation plasticity. None of the genotypic correlations between acclimation plasticity and thermal tolerance or plant performance in the presence or absence of stress were significantly negative. This result implies that the acclimation-induced resistance does not come at the costs of lowered values in other traits likely to be relevant for fitness. These results stand in contrast to those found in *Drosophila serrata* and *Drosophila birchii* and their hybrids, for which negative correlations between heat acclimation and fitness traits were revealed (Berrigan & Hoffmann, 1998). The strongest indication for potentially constrained evolution of acclimation plasticity in our study was the negative genotypic correlation between acclimation plasticity and constitutive resistance (Table 2). This result suggests a trade-off between induced and constitutive protection against abiotic stress. In plants, little is known about the relationship between induced and constitutive resistance in the context of acclimation. In *Drosophila* species it was found that induced and constitutive resistance were not independent (Hoffmann *et al.*, 2003), but both negative (Nyamukondiwa *et al.*, 2011; Gerken *et al.*, 2015) and positive relationships (Kellett *et al.*, 2005; Sgrò *et al.*, 2010) were found. Also here more research is needed to see whether induced and constitutive resistance trade off against each other in plants.

Transcriptome study

By comparing trancriptome profiles of acclimated and non-acclimated plants, we detected a large fraction of differentially expressed genes that were specific to either the frost or the heat acclimation treatment. The focus of the following discussion is on enriched Gene Ontology terms and genes most likely involved in the acclimation response and that had been linked to membrane stability under stress, as this is what we assessed with the PEL-based measure of resistance.

Specific responses to frost acclimation. Several cold-responsive genes were up-regulated after frost acclimation and unique to that treatment. The cold-responsive genes identified were mainly related to chloroplast membrane protection. This was the case for the two COR genes: *COR413 TM1* and *COR15b*, and *CHILLING SENSITIVE 1* (Okawa *et al.*, 2008; Zbierzak *et al.*, 2013; Thalhammer *et al.*, 2014a) and probably *GALACTINOL SYNTHASE 3* (Taji *et al.*, 2002). Protection and stabilization of membranes, both plasma and organelle, against freezing-induced lesions has been considered as one of the primary role of cold acclimation (Thomashow, 1999; Mahajan & Tuteja, 2005). Here, protection seemed to have been highly specific to the chloroplast membrane since no genes related to other membranes were found. In line, previous studies which used the same measure of resistance as we did found a reduction of leakiness linked to the protection of the chloroplast membrane (Thomashow, 1999; Zbierzak *et al.*, 2013; Thalhammer *et al.*, 2014a).

Overall, our gene expression analysis for frost acclimation was consistent with previous transcriptomic studies conducted in *A. thaliana*. Despite the wide variety of approaches, these studies agree in the importance of two functional groups of genes during cold acclimation: the cold-regulated (COR) genes and one of their key regulatory elements, the C-repeat binding factor/dehydration responsive element binding (CBF/DREB) transcription factors (Thomashow, 1999; Seki *et al.*, 2001; Hannah *et al.*, 2005). We found both COR genes and CBF/DREB transcription factors being up-regulated, which indicates that the cold acclimation process involves the same pathways. Cold-regulated genes and CBF/DREB transcription factors have been considered as the main regulatory network for controlling the acclimation process and the some of the associated phenotypic modifications. For instance, expression of COR genes and CBF/DREB factors were found to enhance freezing resistance but to impede growth in *Arabidopsis thaliana* (Chinnusamy *et al.*, 2010; Thalhammer *et al.*, 2014a), in line with our phenotypic measurements. However, some of the cold-responsive genes we detected, down- or up-regulated, were not yet fully characterized and are likely to be more specific of the experimental design.

Specific responses to heat acclimation. Among the abiotic-stimuli-responsive genes that were differentially expressed, the category of heat-responsive elements was represented by a large number of genes encoding heat shock proteins (HSPs). The primary role of HSPs is to protect proteins against denaturation, but they can also act as antioxidants or be involved in lipid membrane protection (Wang *et al.*, 2004). Apart, we found that a significant fraction of genes involved in biotic stress resistance significantly affected by heat acclimation, and some also by frost acclimation. A previous gene expression study in *A. thaliana* on heat acclimation also revelaed a large number of genes involved in biotic stress resistance being mainly down-regulated (Larkindale & Vierling, 2008). This pattern suggests two possible interactions between abiotic and biotic factors. First, a trade-off may exist between acclimation and response to biotic factors due to resource limitation; plants may not be able to maintain a high level of resistance to different stressors. Second, there may be antagonistic interactions between hormone pathways. For instance, it has been demonstrated that a rise of ABA concentration increased disease susceptibility probably due to antagonistic interactions with pathways mediated by jasmonic acid and ethylene, two phytohormones important in plant defense (Anderson *et al.*, 2004). These results stress that future work on the evolutionary ecology of acclimation should focus on trade-offs between thermal acclimation and resistance to biotic stressors.

Interestingly, we identified a total of 17 DEGs related to cell wall modifications specifically expressed after heat acclimation. In line, in *Brassica rapa*, heat acclimation led to the up-regulated expression of many cell wall-modifying enzymes, especially xyloglucan endotransglucosylase/hydrolase (XTHs), and the strengthening of the cell wall (Yang *et al.*, 2006). Based on histological analysis, the authors also demonstrated an increase in the cell wall thickness. In our experiment, most of the differentially expressed genes were part of the XTH gene family. These genes had been related to the formation and strengthening of the cell wall as well as to plant growth and cell elongation (Cosgrove, 2005). Our gene expression results for heat acclimation suggest that the increase in resistance reflected by the decrease in electrolyte leakage may have been caused by a remodeling of the cell wall and changes of its physical properties.

Non-specific response to frost and heat acclimation. We found that few differentially expressed genes overlapped between frost and heat acclimation. Studies that investigated interactions between other abiotic stress responses in *A. thaliana* also demonstrated that expression patterns had mainly significant treatment-specific aspects, e.g., after drought and heat (Rizhsky *et al.*, 2004). In our study, these genes were part of the regulation of general metabolic processes and related to the photosynthetic activity that may impact plant performance during acclimation. Additionally, we found genes from the lipid-transfer protein superfamily previously described to be involved in the transport of cuticle monomers and cuticle thickening, cell wall modifications or defense to pathogens (Pyee *et al.*, 1994; Yeats & Rose, 2008). However due to the few number of genes related with membrane modifications in the non-specific response, it is likely that they play a minor role in the cross-resistance mechanism.

Conclusion

Evidence for constraints to thermal adaptation is ubiquitous e.g., in that many species have geographic distributions that seem to be ultimately limited by temperature. Based on our results, we conclude that the acclimation response measured as increased thermal stress resistance has three important facets. First, cross-resistance for different types of thermal stress is significant.

Second, acclimation works best when the acclimation temperature resembles the later stress temperature. Third, the genetic basis of the acclimation response seems to be highly labile, where neither thermal resistances within acclimation treatment nor the same type of resistance across acclimation treatments seems to be related. A considerable constraint to the evolution of acclimation plasticity in thermal resistance is likely to stem from the genetic trade-off with basal thermal resistance. Based on results of our transcriptome analysis, we suggest to further search for other costs of acclimation plasticity by looking into trade-offs with coping with biotic stressors, e.g., bacteria and fungi.

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Table 1. Results of hierarchical mixed model analysis testing the effect of block, acclimation treatment during growth, disc treatment and their interaction on percent electrolyte leakage (PEL) of *Arabidopsis lyrata* leaf discs (*N* = 1026) and on thermal resistance. Resistance was calculated by subtracting from the PEL of the control disc the PEL of the stress-exposed disc of the same leaf (*N* = 684). The table shows *F* values. Statistics for the random effects are not shown.

			PEL	Resistance
Dependent variables	df_{Num}	df_{Den}	*F*	*F*
Block	2	77	**27.26*** **	**26.48*** **
Acclimation treatment	2	78	**98.39*** **	**99.89*** **
Treatment of disc	2 / 1	78 / 39	**1814.12*** **	**777.30*** **
Acc. treat. * treat. disc	4 / 2	156 / 78	**86.32*** **	**83.51*** **

Significance is indicated in bold: **P* < 0.05, ***P* < 0.01, ****P* < 0.001.

Table 2. Correlation matrices for difference in resistance due to acclimation treatment (acclimation plasticity) under frost acclimation (a) and heat acclimation (b). Correlations were calculated between the acclimation response, estimated for frost resistance and heat resistance, and the following further traits: frost or heat resistance under no acclimation (second column), frost tolerance or heat tolerance (third column), and plant size after frost acclimation, heat acclimation and no acclimation (last three columns). Sample size varied between 39 and 40 maternal families.

(a) Frost acclimation	Frost resistance	Frost tolerance	Plant size		
	no acclimation		frost	heat	control
in frost resistance	**-0.57*****	-0.17	-0.08	-0.10	0.15
in heat resistance	-0.34*	-0.35*	-0.30	0.01	0.19

(b) Heat acclimation	Heat resistance	Heat tolerance	Plant size		
	no acclimation		frost	heat	control
in heat resistance	**-0.93*****	-0.05	-0.29	0.04	0.05
in frost resistance	-0.25	-0.11	0.04	0.07	0.17

Pearson correlation coefficients are given and significance is indicated: *P < 0.05, **P < 0.01, *** < 0.001. When the alpha-value for multiple testing was adjusted (0.05 / 20 = 0.0025), only the two largest correlations remained significant (in bold).

Figure legends

Fig. 1. The effect of the acclimation treatment during growth: control, frost acclimation and heat acclimation, on resistance to frost (a) and heat (b) based on electrolyte leakage of leaf discs. Symbols (filled for frost resistance, open for heat resistance) depict means of family means and two-sided bars represent twice the standard error, which represents about the 95% confidence interval. The dashed lines with *P*-values represent the contrasts performed, the lower ones between no acclimation versus acclimation and the upper ones between the two acclimation treatments.

Fig. 2. Enriched GO terms for the differentially expressed genes (DEGs) after frost and heat acclimation compared to control conditions. Only the DEGs specific of the frost acclimation treatment (a) and specific of the heat acclimation treatment (b) were used in the analysis. The GO term enrichment analysis was performed with BiNGO (Maere *et al.*, 2005). GO terms were considered as significantly enriched if they are represented by at least 5 genes and for FDR-adjusted P-value < 0.05. White nodes indicate GO terms not significantly enriched, colored nodes indicate significantly enriched GO terms according to the color bar. The node areas reflect the relative number of genes associated with each GO term. Additional information can be found in Table S4.

Fig. 1.

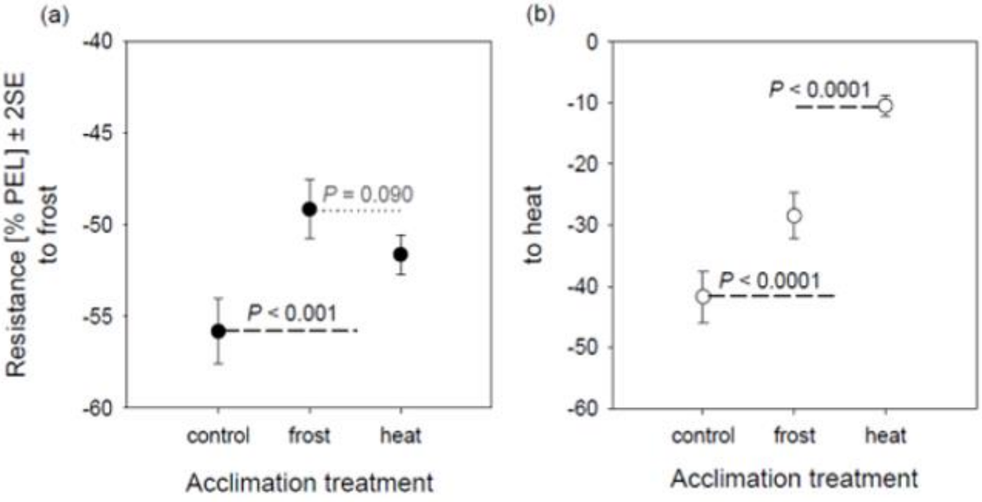
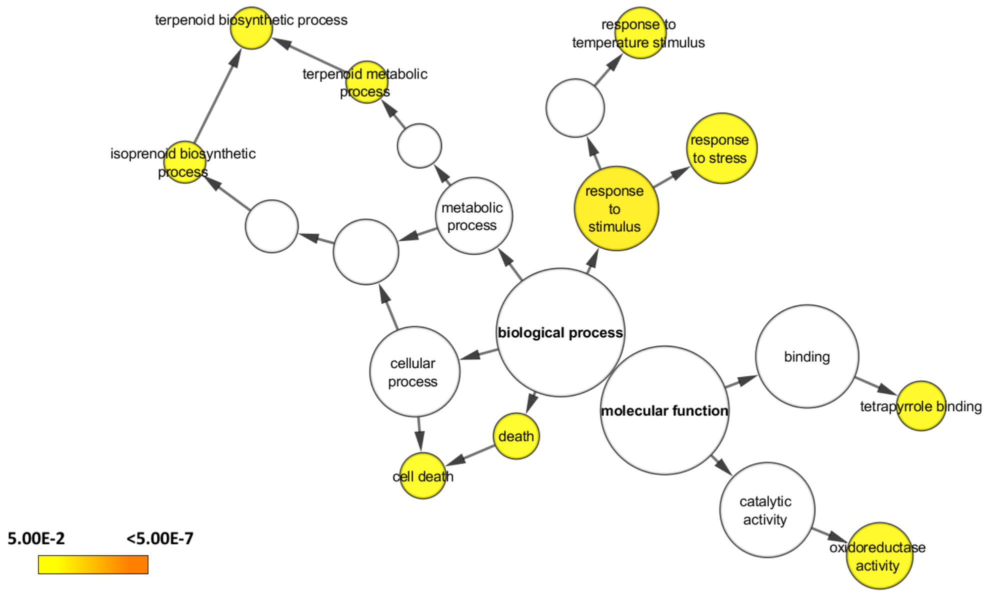
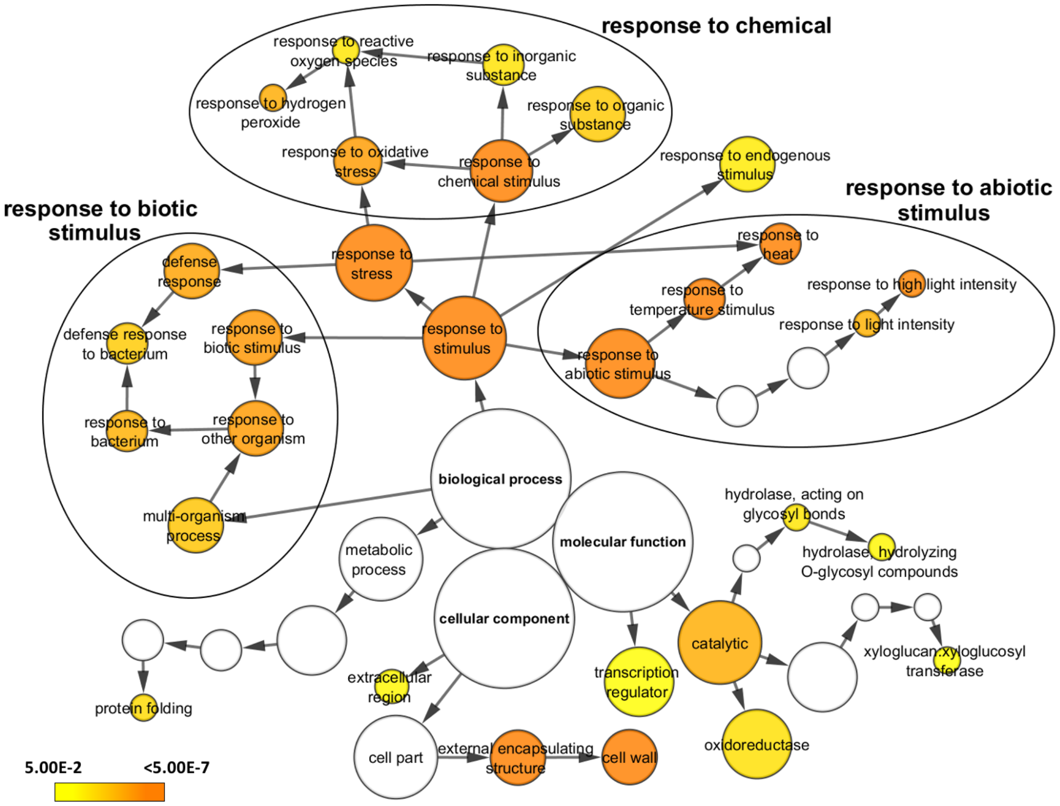

(a)
(b)
Resistance [% PEL] ± 2SE
to frost
to heat
-40
-45
-50
-55
-60
0
-10
-20
-30
-40
-50
-60
P = 0.090
P < 0.001
P < 0.0001
P < 0.0001
control
frost
heat
control
frost
heat
Acclimation treatment
Acclimation treatment

Fig. 2.

(a) Specific to frost acclimation



(b) Specific to heat acclimation



Supporting Information

Fig. S1 Relationship between residual performance under acclimation stress and no acclimation and phenotypic plasticity

Table S1 Results of hierarchical mixed model analysis testing the effect of block and acclimation treatment during growth on the two parameters describing plant growth.

Table S2 Analysis on the maintenance costs of plasticity.

Table S3 Correlation analysis between frost and heat resistance measured under the three acclimation treatments: frost acclimation, heat acclimation and control.

Table S4 Lists of genes differentially expressed (DEGs) after frost acclimation (separate excel file)

Table S5 Lists of genes differentially expressed (DEGs) after heat acclimation (separate excel file)

Table S6 Lists of Gene Ontology (GO) terms significantly enriched after frost and heat acclimation (separate excel file)

Table S7 List of (a) heat-responsive genes differentially expressed after frost acclimation and (b) cold-responsive genes differentially expressed after heat acclimation (separate excel file)

Fig. S1. Relationship between residual performance estimated by plant size under acclimation stress (a, b) and no acclimation (c, d) – after accounting for resistance in that environment – and acclimation plasticity in frost resistance (a, c) and heat resistance (b, d). Symbols (black for frost, white for heat) represent means of maternal families (note the different scales for acclimation plasticity for frost and heat resistance). All panels show that there is no correlation between residual performance and the plastic acclimation response in resistance, indicating no maintenance costs of plasticity.

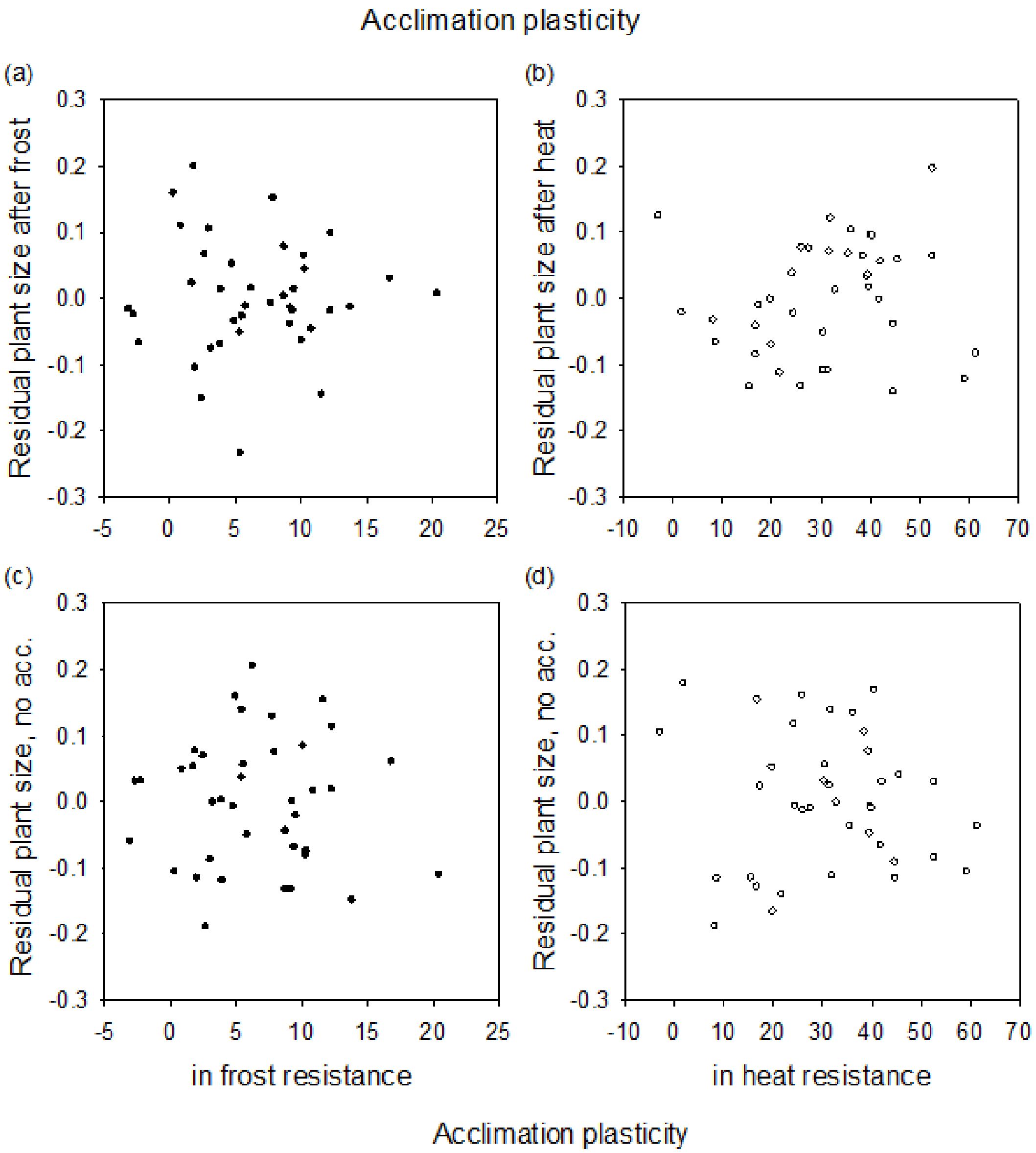


Table S1. Results of hierarchical mixed model analysis testing the effect of block and acclimation treatment during growth on the two parameters describing logistic plant growth: asymptotic size (*N* = 347) and exponential growth (both *N* = 346). The table shows *F* values; the last two rows show *t* values for contrasts between pairs of acclimation treatments. Statistics for the random effects are not shown.

			Asymptotic size	Exponential growth
Dependent variables	df_{Num}	df_{Den}	*F/t*	*F/t*
Block	2	77	**14.00*** **	**9.74*** **
Acclimation treatment	2	78	**41.61*** **	1.48
Frost vs. control	1	78	**-7.39*** **	
Heat vs. control	1	78	**-8.31*** **	

Significance is indicated in bold: *$P < 0.05$, **$P < 0.01$, ***$P < 0.001$.

Table S2. Analysis on the maintenance costs of acclimation plasticity, with the model of relative rosette size in an environment depending on stress resistance in that environment and acclimation plasticity (resistance under the corresponding acclimation treatment minus resistance under no acclimation). Results are shown for the maintenance costs of frost acclimation (a) and heat acclimation (b). Models on the left test costs under the stressful environment, while model on the right test for costs under the benign environment. Sample size varied between 39 and 40.

(a)	Frost acclimation treatment	Control conditions
	Relative rosette size	Relative rosette size
N	39	39
R^2	0.02	0.10
Frost resistance	-0.0025 ± 0.0031	-0.0063 ± 0.0035$^{(*)}$
Acclimation plasticity	-0.0003 ± 0.0031	-0.0008 ± 0.0038

(b)	Heat acclimation treatment	Control conditions
	Relative rosette size	Relative rosette size
N	39	39
R^2	0.08	0.07
Heat resistance	-0.0052 ± 0.0029	-0.0055 ± 0.0034
Acclimation plasticity	0.0011 ± 0.0011	-0.0043 ± 0.0031

Significance of the F-value is indicated: $^{(*)}P < 0.1$.

Table S3. Correlation analysis between frost and heat resistance measured by electrolyte leakage (written in normal text height) under the three acclimation treatments: frost acclimation, heat acclimation and control (subscript text). Sample size was 40 maternal families.

$\text{Resistance}_{\text{acclimation treatment}}$	$\text{frost}_{\text{frost}}$	$\text{frost}_{\text{heat}}$	$\text{frost}_{\text{control}}$	$\text{heat}_{\text{heat}}$	$\text{heat}_{\text{frost}}$
$\text{frost}_{\text{heat}}$	0.30				
$\text{frost}_{\text{control}}$	**0.53*** **	**0.52*** **			
$\text{heat}_{\text{heat}}$	-0.22	-0.05	0.02		
$\text{heat}_{\text{frost}}$	0.27	-0.20	0.02	0.19	
$\text{heat}_{\text{control}}$	**0.46** **	0.39*	0.45**	-0.09	0.10

Pearson correlation coefficients are given and significance is indicated: *P < 0.05, **P < 0.01, ***P < 0.001. When the alpha-value for multiple testing was adjusted (0.05 / 15 = 0.0033), only the three largest correlations remained significant (in bold).

Table S4. List of the differentially expressed genes (DEG) after frost acclimation compared to control conditions. Genes were considered as differentially expressed when false discovery rate (FDR) < 0.05. Genes are sorted by log2FoldChange (log2FC)

Gene_ID_lyrata	log2FC	P-value	FDR	Homolog_thaliana	Gene_name
AL2G23820	6.42	4.90E-11	7.40E-08	AT5G41660	unknown protein
AL8G15120	6.35	4.27E-11	6.76E-08	/	Unknown
AL4G20660	6.06	7.94E-15	3.77E-11	AT2G31470	DOR, F-box and associated interaction domains-containing protein
AL4G33850	5.98	1.49E-17	8.91E-14	AT2G37435	Cystatin/monellin superfamily protein
AL3G44260	5.90	1.90E-13	4.84E-10	AT2G23150	ATNRAMP3, NRAMP3, natural resistance-associated macrophage protein 3
AL3G46710	5.64	1.35E-22	2.25E-18	/	Unknown
AL2G28210	5.63	1.04E-37	3.47E-33	/	Unknown
AL7G31840	5.37	2.04E-13	4.84E-10	AT4G21940	CPK15, calcium-dependent protein kinase 15
AL615U10010	5.25	3.95E-09	3.28E-06	AT3G23955	F-box family protein
AL7G31830	5.01	1.38E-10	1.69E-07	AT4G21940	CPK15, calcium-dependent protein kinase 15
AL1G53170	4.95	6.66E-08	3.88E-05	/	Unknown
AL1G14050	4.80	4.86E-14	1.62E-10	/	Unknown
AL6G36800	4.58	3.58E-07	1.52E-04	AT5G61500	ATATG3, ATG3, autophagy 3 (APG3)
AL1G51800	4.26	1.72E-07	8.30E-05	AT1G01090	PDH-E1 ALPHA, pyruvate dehydrogenase E1 alpha
AL5G27180	4.21	1.02E-07	5.63E-05	AT1G65113	SCRL2, SCR-like 2
AL5G26400	3.95	6.22E-10	5.58E-07	/	Unknown
AL755U10010	3.93	2.33E-08	1.62E-05	/	Unknown
AL1G56780	3.84	9.12E-09	6.89E-06	AT1G02190	Fatty acid hydroxylase superfamily
AL1G20660	3.82	3.57E-06	1.03E-03	AT1G10095	Protein prenylyltransferase superfamily protein
AL7G31820	3.75	6.15E-08	3.65E-05	AT4G21940	CPK15, calcium-dependent protein kinase 15
AL429U10010	3.72	2.81E-13	6.21E-10	/	Unknown
AL3G43140	3.70	5.12E-07	2.05E-04	AT3G54540	ATGCN4, GCN4, general control non-repressible 4
AL7G18500	3.62	1.42E-05	3.09E-03	/	Unknown
AL1G29920	3.61	1.13E-10	1.44E-07	AT1G17600	Disease resistance protein (TIR-NBS-LRR class) family
AL6G44140	3.61	1.48E-05	3.20E-03	AT4G10300	RmlC-like cupins superfamily protein
AL8G16120	3.60	2.64E-08	1.79E-05	/	Unknown
AL6G35870	3.57	2.75E-06	8.29E-04	/	Unknown
AL6G32920	3.55	1.07E-07	5.83E-05	AT5G21960	Integrase-type DNA-binding superfamily protein
AL1G25240	3.55	1.09E-06	3.90E-04	AT1G13470	Protein of unknown function (DUF1262)
AL4G30400	3.46	3.46E-18	3.83E-14	AT2G34430	LHB1B1, LHCB1.4, light-harvesting chlorophyll-protein complex II subunit B1
AL2G29810	3.46	1.14E-06	4.02E-04	AT1G70440	SRO3, similar to RCD one 3
AL1G50890	3.36	1.84E-07	8.75E-05	AT5G27470	seryl-tRNA synthetase / serine--tRNA ligase
AL6G15900	3.32	2.14E-10	2.36E-07	AT5G05965	unknown protein
AL7G31810	3.29	8.68E-07	3.28E-04	AT4G30750	unknown protein
AL1G23960	3.26	3.08E-10	3.10E-07	AT1G12610	DDF1, Integrase-type DNA-binding superfamily protein
AL1G16150	3.18	2.99E-07	1.31E-04	/	Unknown
AL1G36780	3.06	8.86E-05	1.36E-02	AT1G24190	ATSIN3, SIN3, SNL3, SIN3-like 3
AL1G52070	3.02	1.20E-04	1.69E-02	AT1G35617	unknown protein
AL1G22730	3.01	8.05E-05	1.30E-02	AT1G11600	CYP77B1, cytochrome P450, family 77, subfamily B, polypeptide 1
AL8G26360	2.98	1.67E-10	1.92E-07	AT5G52020	Integrase-type DNA-binding superfamily protein
AL6G33330	2.97	6.17E-05	1.04E-02	AT1G17277	transposable element gene
AL1G63660	2.94	1.69E-04	2.13E-02	AT1G55600	ATWRKY10, MINI3, WRKY10, WRKY DNA-binding protein 10
AL8G27740	2.93	3.77E-10	3.68E-07	AT5G50420	O-fucosyltransferase family protein
AL3G45100	2.92	4.73E-06	1.28E-03	/	Unknown
AL4G38190	2.90	1.63E-06	5.36E-04	AT2G40370	LAC5, laccase 5
AL6G49360	2.87	1.20E-06	4.21E-04	AT4G03540	Uncharacterised protein family (UPF0497)
AL7G30360	2.85	5.49E-06	1.44E-03	AT4G23120	Bromo-adjacent homology (BAH) domain-containing protein
AL5G30110	2.85	9.67E-06	2.29E-03	AT5G67360	ARA12, Subtilase family protein
AL6G24550	2.82	7.24E-05	1.20E-02	AT5G13900	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL7G40360	2.81	1.24E-04	1.72E-02	AT4G15250	B-box type zinc finger protein with CCT domain
AL8G21350	2.81	1.89E-14	6.99E-11	AT5G48490	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL2G27840	2.81	2.28E-05	4.62E-03	AT1G68850	Peroxidase superfamily protein
AL136U10020	2.78	4.08E-04	4.04E-02	AT2G30410	KIS, TFCA, tubulin folding cofactor A (KIESEL)
AL5G10900	2.77	3.24E-04	3.47E-02	AT2G01770	ATVIT1, VIT1, vacuolar iron transporter 1
AL6G17980	2.76	5.14E-10	4.88E-07	AT5G07380	unknown protein
AL8G17640	2.75	2.29E-04	2.73E-02	/	Unknown
AL5G23550	2.74	1.97E-04	2.43E-02	AT3G45060	ATNRT2.6, NRT2.6, high affinity nitrate transporter 2.6
AL964U10010	2.72	4.21E-04	4.11E-02	AT5G02230	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
AL6G31880	2.71	3.96E-04	3.95E-02	AT3G48150	APC8, CDC23, anaphase-promoting complex subunit 8
AL52U10030	2.70	3.33E-04	3.55E-02	AT5G56940	Ribosomal protein S16 family protein
AL5G19990	2.66	3.07E-04	3.32E-02	/	Unknown
AL3G20260	2.66	2.44E-04	2.83E-02	AT3G09150	ATHY2, GUN3, HY2, phytochromobilin:ferredoxin oxidoreductase, chloroplast / phytochromobilin synthase (HY2)
AL5G30100	2.60	1.01E-04	1.49E-02	AT5G67360	ARA12, Subtilase family protein
AL1G23100	2.60	3.29E-07	1.42E-04	/	Unknown
AL3G52220	2.59	3.75E-04	3.80E-02	AT2G16120	ATPMT1, PMT1, polyol/monosaccharide transporter 1
AL463U10030	2.58	1.69E-07	8.30E-05	AT2G39450	ATMTP11, MTP11, Cation efflux family protein
AL8G10090	2.57	8.50E-11	1.17E-07	AT4G25340	ATFKBP53, FKBP53, FK506 BINDING PROTEIN 53
AL8G36200	2.57	2.81E-06	8.32E-04	AT5G59680	Leucine-rich repeat protein kinase family protein
AL1G19860	2.55	1.61E-17	8.91E-14	AT1G09350	AtGolS3, GolS3, galactinol synthase 3
AL4G47760	2.54	1.01E-04	1.49E-02	AT2G48130	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL8G11870	2.53	1.84E-06	5.76E-04	AT1G52990	thioredoxin family protein
AL1072U10010	2.48	3.09E-04	3.33E-02	AT5G54190	PORA, protochlorophyllide oxidoreductase A
AL6G44420	2.48	1.66E-06	5.40E-04	/	Unknown

AL8G20800	2.41	5.01E-04	4.56E-02	AT5G48140	Pectin lyase-like superfamily protein
AL2G12560	2.38	3.68E-05	6.72E-03	AT1G63030	ddf2, Integrase-type DNA-binding superfamily protein
AL8G26320	2.36	2.46E-05	4.93E-03	AT5G51990	CBF4, DREB1D, C-repeat-binding factor 4
AL7G16850	2.31	9.95E-07	3.64E-04	AT4G34410	RRTF1, redox responsive transcription factor 1
AL6G41340	2.27	1.15E-04	1.65E-02	AT4G07960	ATCSLC12, CSLC12, CSLC12, Cellulose-synthase-like C12
AL1G59130	2.26	7.05E-05	1.17E-02	AT1G30790	F-box and associated interaction domains-containing protein
AL2G15710	2.25	1.03E-05	2.43E-03	AT5G28740	Tetratricopeptide repeat (TPR)-like superfamily protein
AL1G29930	2.25	1.61E-04	2.06E-02	AT1G17610	Chilling sensitive 1, CHS1
AL3G15120	2.25	7.60E-10	6.65E-07	AT3G04870	PDE181, SPC1, ZDS, zeta-carotene desaturase
AL516U10020	2.25	3.55E-04	3.69E-02	AT5G48810	ATB5-B, ATCB5-D, B5 #3, CB5-D, cytochrome B5 isoform D
AL3G17220	2.24	2.67E-06	8.15E-04	AT1G03710	Cystatin/monellin superfamily protein
AL3G44270	2.21	1.56E-07	7.86E-05	/	Unknown
AL8G22240	2.21	2.89E-04	3.20E-02	AT5G24860	ATFPF1, FPF1, flowering promoting factor 1
AL7G47000	2.16	2.61E-04	2.97E-02	/	Unknown
AL2G24600	2.14	3.68E-04	3.75E-02	AT1G66630	Protein with RING/U-box and TRAF-like domains
AL5G15080	2.11	9.96E-07	3.64E-04	AT1G52390	unknown protein
AL3G53310	2.11	6.29E-06	1.61E-03	AT2G20350	Integrase-type DNA-binding superfamily protein
AL6G47420	2.07	5.75E-05	9.94E-03	AT4G12500	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL1G31790	2.01	1.31E-04	1.78E-02	AT1G19210	DREB subfamily A-5 of ERF/AP2 transcription factor family
AL390U10010	2.01	4.94E-04	4.53E-02	AT5G43650	BHLH92, basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AL2G28230	2.01	5.38E-12	1.12E-08	/	Unknown
AL7G52290	2.00	8.46E-06	2.05E-03	AT5G38350	Disease resistance protein (NBS-LRR class) family
AL608U10010	2.00	2.72E-04	3.07E-02	/	Unknown
AL4G43940	1.98	1.86E-04	2.32E-02	/	Unknown
AL4G33820	1.98	7.37E-05	1.21E-02	/	Unknown
AL8G16540	1.95	2.80E-06	8.32E-04	AT5G43745	Protein of unknown function (DUF1012)
AL5G23330	1.94	1.59E-04	2.03E-02	AT3G44860	FAMT, farnesoic acid carboxyl-O-methyltransferase
AL7G40490	1.92	4.60E-04	4.34E-02	AT4G15200	AFH3, FH3, formin 3
AL2G16640	1.88	2.64E-05	5.09E-03	AT1G60050	Nodulin MtN21 /EamA-like transporter family protein
AL3G47900	1.86	4.23E-06	1.16E-03	/	Unknown
AL4G19130	1.85	2.83E-04	3.16E-02	AT3G62210	EDA32, Putative endonuclease or glycosyl hydrolase
AL6G32170	1.83	1.89E-07	8.84E-05	AT5G20630	ATGER3, GER3, GLP3, GLP3A, GLP3B, germin 3
AL4G30580	1.83	2.92E-04	3.21E-02	AT2G34600	JAZ7, TIFY5B, jasmonate-zim-domain protein 7
AL8G12030	1.81	6.52E-06	1.63E-03	AT5G46380	Kinase-related protein of unknown function (DUF1296)
AL4G13390	1.80	3.44E-04	3.61E-02	/	Unknown
AL1G67310	1.77	3.76E-04	3.80E-02	ATCG00790	RPL16, ribosomal protein L16
AL4G29440	1.75	2.28E-06	7.02E-04	AT2G33750	ATPUP2, PUP2, purine permease 2
AL2G28650	1.73	8.22E-09	6.35E-06	AT1G69526	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AL7G49700	1.72	1.26E-05	2.76E-03	AT5G40270	HD domain-containing metal-dependent phosphohydrolase family protein
AL3G11700	1.72	9.34E-05	1.42E-02	AT3G02410	ICME-LIKE2, alpha/beta-Hydrolases superfamily protein
AL409U10010	1.71	4.29E-05	7.70E-03	AT2G42390	protein kinase C substrate, heavy chain-related
AL3G36910	1.68	1.31E-04	1.78E-02	AT3G22620	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL3G42860	1.68	1.54E-05	3.30E-03	AT2G05380	GRP3S, glycine-rich protein 3 short isoform
AL7G40060	1.68	1.33E-04	1.79E-02	AT4G15480	UGT84A1, UDP-Glycosyltransferase superfamily protein
AL219U10010	1.67	2.19E-04	2.64E-02	AT3G20460	Major facilitator superfamily protein
AL5G17130	1.66	2.77E-08	1.81E-05	AT3G27690	LHCB2, LHCB2.3, LHCB2.4, photosystem II light harvesting complex gene 2.3
AL7G25050	1.66	2.35E-04	2.76E-02	AT4G27657	unknown protein
AL4G18140	1.65	5.90E-05	1.01E-02	AT2G40955	unknown protein
AL1G14790	1.64	4.71E-07	1.93E-04	AT1G05040	unknown protein
AL6G17420	1.62	4.87E-04	4.52E-02	AT5G07200	ATGA20OX3, GA20OX3, YAP169, gibberellin 20-oxidase 3
AL7G32360	1.60	3.44E-06	1.00E-03	AT4G21630	Subtilase family protein
AL2G30550	1.60	7.34E-06	1.79E-03	AT1G71000	Chaperone DnaJ-domain superfamily protein
AL1G60640	1.59	3.01E-06	8.84E-04	AT1G52390	unknown protein
AL735U10010	1.57	5.83E-06	1.51E-03	AT5G65670	IAA9, indole-3-acetic acid inducible 9
AL7G20690	1.57	7.07E-06	1.74E-03	AT4G31380	FLP1, FPF1-like protein 1
AL3G29130	1.56	3.37E-04	3.58E-02	AT4G11630	Ribosomal protein L19 family protein
AL5G41010	1.55	2.72E-05	5.15E-03	AT3G59120	Cysteine/Histidine-rich C1 domain family protein
AL4G39690	1.47	1.18E-04	1.68E-02	AT2G41620	Nucleoporin interacting component (Nup93/Nic96-like) family protein
AL4G19010	1.46	6.16E-05	1.04E-02	AT5G02830	Tetratricopeptide repeat (TPR)-like superfamily protein
AL6G36360	1.43	8.61E-05	1.34E-02	AT5G24780	ATVSP1, VSP1, vegetative storage protein 1
AL7G38820	1.39	2.67E-05	5.09E-03	/	Unknown
AL7G52360	1.38	4.49E-04	4.30E-02	AT5G38350	Disease resistance protein (NBS-LRR class) family
AL8G36160	1.36	1.13E-04	1.64E-02	/	Unknown
AL8G29420	1.36	3.84E-06	1.08E-03	AT5G54190	PORA, protochlorophyllide oxidoreductase A
AL6G47290	1.33	1.72E-04	2.17E-02	AT4G12410	SAUR-like auxin-responsive protein family
AL8G18900	1.33	2.49E-05	4.95E-03	/	Unknown
AL6G44460	1.33	4.90E-04	4.53E-02	AT5G12100	pentatricopeptide (PPR) repeat-containing protein
AL8G26690	1.33	2.05E-04	2.52E-02	AT5G52300	LTI65, RD29B, CAP160 protein
AL4G13760	1.32	3.80E-04	3.82E-02	/	Unknown
AL2G16110	1.31	2.52E-04	2.90E-02	AT1G60500	DRP4C, Dynamin related protein 4C
AL8G33790	1.31	2.34E-04	2.76E-02	AT5G57740	XBAT32, XB3 ortholog 2 in Arabidopsis thaliana
AL3G48860	1.30	8.87E-05	1.36E-02	AT2G22340	unknown protein
AL43U10060	1.29	4.54E-05	8.06E-03	AT5G48580	FKBP15-2, FK506- and rapamycin-binding protein 15 kD-2
AL5G29590	1.26	5.22E-04	4.69E-02	AT3G62090	PIF6, PIL2, phytochrome interacting factor 3-like 2
AL8G36190	1.26	1.30E-04	1.78E-02	/	Unknown
AL8G12750	1.25	4.32E-05	7.72E-03	AT5G45830	ATDOG1, DOG1, GSQ5, delay of germination 1
AL3G29500	1.25	9.84E-05	1.48E-02	AT3G17340	ARM repeat superfamily protein
AL9U10260	1.23	3.40E-04	3.60E-02	AT4G13395	DVL10, RTFL12, ROTUNDIFOLIA like 12
AL2G34560	1.23	9.30E-06	2.22E-03	AT1G74670	Gibberellin-regulated family protein
AL792U10020	1.22	2.99E-05	5.56E-03	/	Unknown

AL6G28210	1.21	1.44E-06	4.89E-04	AT5G17165	unknown protein
AL3G37070	1.20	1.04E-04	1.52E-02	/	Unknown
AL4G36860	1.19	8.35E-05	1.32E-02	AT2G39470	PPL2, PsbP-like protein 2
AL2G32120	1.18	4.37E-04	4.24E-02	/	Unknown
AL1G14520	1.18	2.61E-04	2.97E-02	AT1G04800	glycine-rich protein
AL1G21380	1.15	2.81E-05	5.27E-03	AT1G10560	ATPUB18, PUB18, plant U-box 18
AL3G44750	1.14	2.87E-04	3.18E-02	AT2G10940	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL3G28390	1.12	5.35E-05	9.35E-03	AT3G15720	Pectin lyase-like superfamily protein
AL1G41350	1.10	1.57E-04	2.03E-02	/	Unknown
AL2G34820	1.10	3.68E-04	3.75E-02	AT1G74930	ORA47, Integrase-type DNA-binding superfamily protein
AL3G12680	1.08	7.44E-05	1.21E-02	AT3G03080	Zinc-binding dehydrogenase family protein
AL6G46030	1.07	5.59E-04	4.96E-02	AT4G11530	CRK34, cysteine-rich RLK (RECEPTOR-like protein kinase) 34
AL6G19930	1.06	5.42E-04	4.84E-02	AT5G09530	hydroxyproline-rich glycoprotein family protein
AL1G43190	1.06	1.67E-06	5.40E-04	AT1G29395	COR413-TM1, COR413IM1, COR414-TM1, COLD REGULATED 314 INNER MEMBRANE 1
AL1G21490	1.06	1.82E-04	2.28E-02	AT1G10640	Pectin lyase-like superfamily protein
AL1G56610	1.05	2.38E-05	4.78E-03	AT1G49450	Transducin/WD40 repeat-like superfamily protein
AL1G48120	1.03	3.00E-04	3.28E-02	/	Unknown
AL2G35680	1.03	1.23E-04	1.72E-02	AT1G75700	HVA22G, HVA22-like protein G
AL1G54940	1.03	4.27E-04	4.18E-02	AT1G48330	unknown protein
AL1G18740	0.99	4.21E-04	4.14E-02	AT1G08320	bZIP21, TGA9, bZIP transcription factor family protein
AL2G29550	0.97	3.59E-04	3.70E-02	AT1G70260	nodulin MtN21 /EamA-like transporter family protein
AL6G13810	0.96	4.87E-04	4.52E-02	AT5G04190	PKS4, phytochrome kinase substrate 4
AL4G22230	0.96	5.79E-05	9.96E-03	AT2G27970	CKS2, CDK-subunit 2
AL3G25800	0.96	3.78E-04	3.82E-02	AT3G13750	BGAL1, BGAL1, beta galactosidase 1
AL1G43770	0.94	1.34E-04	1.79E-02	AT1G29930	AB140, CAB1, CAB140, LHCB1.3, chlorophyll A/B binding protein 1
AL1G44000	0.93	1.69E-04	2.13E-02	AT1G30100	ATNCED5, NCED5, nine-cis-epoxycarotenoid dioxygenase 5
AL8G39310	0.90	1.24E-04	1.72E-02	AT5G62430	CDF1, cycling DOF factor 1
AL7G36050	0.88	4.82E-04	4.50E-02	AT4G18340	Glycosyl hydrolase superfamily protein
AL4G41070	0.86	2.50E-04	2.88E-02	AT2G42530	COR15B, cold regulated 15b
AL3G19940	0.85	5.29E-04	4.74E-02	AT3G08940	LHCB4.2, light harvesting complex photosystem II
AL2G29590	0.84	5.18E-04	4.67E-02	AT1G70290	ATTPS8, ATTPSC, TPS8, trehalose-6-phosphatase synthase S8
AL5G21990	-0.78	4.96E-04	4.53E-02	AT3G43960	Cysteine proteinases superfamily protein
AL7G27460	-0.84	4.45E-04	4.27E-02	AT4G25630	ATFIB2, FIB2, fibrillarin 2
AL2G35830	-0.88	1.37E-04	1.82E-02	AT2G26010	PDF1.3, plant defensin 1.3
AL6G19830	-0.90	1.89E-04	2.35E-02	AT5G09440	EXL4, EXORDIUM like 4
AL7G18510	-0.92	3.18E-04	3.42E-02	AT4G33070	Thiamine pyrophosphate dependent pyruvate decarboxylase family protein
AL6G32310	-0.93	3.83E-04	3.85E-02	AT5G20790	unknown protein
AL4G35330	-0.93	4.93E-04	4.53E-02	AT2G38280	ATAMPD, FAC1, AMP deaminase, putative / myoadenylate deaminase, putative
AL2G35740	-0.94	6.74E-05	1.13E-02	AT1G75750	GASA1, GAST1 protein homolog 1
AL6G38820	-0.96	4.55E-04	4.33E-02	AT5G26920	CBP60G, Cam-binding protein 60-like G
AL2G14730	-0.97	4.61E-04	4.34E-02	AT1G61560	ATMLO6, MLO6, Seven transmembrane MLO family protein
AL8G21570	-0.97	2.91E-04	3.20E-02	AT5G48580	FKBP15-2, FK506- and rapamycin-binding protein 15 kD-2
AL2G33610	-0.98	1.04E-04	1.53E-02	AT1G73805	SAR DEFICIENT 1, SARD1
AL4G11840	-0.99	5.62E-04	4.98E-02	AT2G14365	LCR84, low-molecular-weight cysteine-rich 84
AL1G52710	-0.99	1.55E-04	2.01E-02	AT2G14080	Disease resistance protein (TIR-NBS-LRR class) family
AL7G50640	-1.00	4.94E-04	4.53E-02	AT5G39670	Calcium-binding EF-hand family protein
AL6G23770	-1.00	2.08E-04	2.54E-02	AT5G13170	SAG29, senescence-associated gene 29
AL7G18740	-1.01	2.13E-04	2.57E-02	AT4G32950	Protein phosphatase 2C family protein
AL3G13160	-1.02	3.68E-04	3.75E-02	AT3G03480	CHAT, acetyl CoA:(Z)-3-hexen-1-ol acetyltransferase
AL4G44330	-1.02	2.12E-04	2.57E-02	AT2G45210	SAUR-like auxin-responsive protein family
AL8G26600	-1.03	5.13E-04	4.64E-02	AT5G52220	unknown protein
AL6G15320	-1.03	1.97E-04	2.43E-02	AT5G05440	PYL5, RCAR8, Polyketide cyclase/dehydrase and lipid transport superfamily protein
AL3G14520	-1.03	1.58E-04	2.03E-02	AT3G04510	LSH2, Protein of unknown function (DUF640)
AL8G30070	-1.04	3.44E-04	3.61E-02	AT5G54610	ANK, ankyrin
AL4G32180	-1.05	4.53E-04	4.33E-02	AT2G36090	F-box family protein
AL3G37940	-1.05	3.22E-05	5.95E-03	AT3G23290	LSH4, Protein of unknown function (DUF640)
AL3G20850	-1.11	1.76E-05	3.70E-03	AT3G09640	APX1B, APX2, ascorbate peroxidase 2
AL2G33620	-1.13	2.83E-04	3.16E-02	AT1G73810	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein
AL8G12310	-1.13	5.48E-04	4.88E-02	/	Unknown
AL2G11680	-1.14	8.42E-05	1.32E-02	AT1G63530	unknown protein
AL6G45710	-1.15	5.19E-04	4.68E-02	AT4G11310	Papain family cysteine protease
AL1G25640	-1.16	9.50E-05	1.43E-02	AT1G13820	alpha/beta-Hydrolases superfamily protein
AL6G46070	-1.18	4.13E-04	4.08E-02	AT4G11521	Receptor-like protein kinase-related family protein
AL6G42280	-1.20	1.39E-04	1.85E-02	/	Unknown
AL5G38610	-1.21	4.28E-04	4.19E-02	AT3G57130	BOP1, Blade-on-petiol 1, Ankyrin repeat family protein / BTB/POZ domain-containing protein
AL1G34170	-1.22	2.63E-05	5.09E-03	AT1G21120	IGMT2, Indole glucosinolate O-methyltransferase 2, O-methyltransferase family protein
AL6G28960	-1.23	1.76E-06	5.58E-04	AT5G17860	CAX7, calcium exchanger 7
AL8G43280	-1.23	1.08E-04	1.58E-02	/	Unknown
AL7G41310	-1.24	3.03E-04	3.29E-02	AT4G14690	ELIP2, Chlorophyll A-B binding family protein
AL2G15250	-1.28	4.01E-04	3.99E-02	AT1G61120	GES, TPS04, TPS4, terpene synthase 04
AL4G19450	-1.29	2.87E-04	3.18E-02	AT2G26560	PLA IIA, PLA2A, PLP2, PLP2, phospholipase A 2A
AL1G62090	-1.32	8.37E-05	1.32E-02	AT1G53540	HSP20-like chaperones superfamily protein
AL4G38160	-1.32	1.36E-04	1.82E-02	AT2G40330	PYL6, RCAR9, PYR1-like 6
AL8G43300	-1.33	7.30E-05	1.20E-02	/	Unknown
AL6G21620	-1.33	6.12E-06	1.58E-03	AT5G08695	RNA-binding (RRM/RBD/RNP motifs) family protein
AL5G29070	-1.34	2.63E-05	5.09E-03	AT3G49320	Metal-dependent protein hydrolase
AL1G61440	-1.34	2.82E-04	3.16E-02	AT1G53080	Legume lectin family protein
AL8G36240	-1.38	1.65E-04	2.10E-02	AT5G59720	HSP18.2, heat shock protein 18.2
AL5G25020	-1.38	6.98E-06	1.73E-03	AT3G46230	ATHSP17.4, HSP17.4, heat shock protein 17.4
AL7G24210	-1.39	2.14E-05	4.35E-03	AT4G28380	Leucine-rich repeat (LRR) family protein

AL2G13450	-1.39	1.08E-05	2.51E-03	AT1G62420	Protein of unknown function (DUF506)
AL7G36070	-1.39	1.23E-04	1.72E-02	AT4G18330	Translation elongation factor EF1A/initiation factor IF2gamma family protein
AL8G32820	-1.44	3.60E-04	3.70E-02	AT5G56960	basic helix-loop-helix (bHLH) DNA-binding family protein
AL3G44950	-1.44	8.17E-05	1.31E-02	/	Unknown
AL1G21360	-1.47	1.15E-05	2.61E-03	AT1G10550	XET, XTH33, xyloglucan:xyloglucosyl transferase 33
AL5G22420	-1.47	3.59E-04	3.70E-02	AT3G44290	anac060, NAC060, NAC domain containing protein 60
AL3G26970	-1.48	2.44E-04	2.83E-02	AT3G14630	CYP72A9, cytochrome P450, family 72, subfamily A, polypeptide 9
AL6G51320	-1.49	6.38E-06	1.62E-03	AT4G01970	AtSTS, STS, stachyose synthase
AL4G22340	-1.50	5.16E-06	1.37E-03	AT2G27900	unknown protein
AL1G47340	-1.50	4.44E-04	4.27E-02	AT1G33030	O-methyltransferase family protein
AL4G29000	-1.51	1.16E-04	1.65E-02	AT2G33350	CCT motif family protein
AL7G20750	-1.51	1.37E-07	7.24E-05	AT4G31330	Protein of unknown function, DUF599
AL6G32390	-1.53	1.06E-05	2.47E-03	/	Unknown
AL1G53610	-1.54	3.46E-04	3.63E-02	AT1G47390	F-box and associated interaction domains-containing protein
AL7G15780	-1.54	4.14E-05	7.47E-03	AT4G35380	SEC7-like guanine nucleotide exchange family protein
AL2G38780	-1.54	3.60E-06	1.03E-03	AT1G78410	VQ motif-containing protein
AL5G23970	-1.55	1.31E-04	1.78E-02	AT3G45410	Concanavalin A-like lectin protein kinase family protein
AL1G47730	-1.55	2.81E-04	3.16E-02	AT1G33350	Pentatricopeptide repeat (PPR) superfamily protein
AL8G42210	-1.56	3.88E-06	1.08E-03	AT5G64750	ABR1, Integrase-type DNA-binding superfamily protein
AL3G26530	-1.57	1.13E-04	1.64E-02	/	Unknown
AL3G29360	-1.59	5.70E-05	9.91E-03	AT3G16530	Legume lectin family protein
AL2G14290	-1.60	3.49E-08	2.23E-05	AT1G61800	ATGPT2, GPT2, glucose-6-phosphate/phosphate translocator 2
AL2G13080	-1.60	1.39E-07	7.24E-05	AT1G62710	BETA-VPE, BETAVPE, beta vacuolar processing enzyme
AL7G45930	-1.61	1.71E-07	8.30E-05	AT5G37350	Serine/threonine-protein kinase Rio1
AL1G24580	-1.62	5.99E-07	2.37E-04	AT1G12940	ATNRT2.5, NRT2.5, nitrate transporter2.5
AL6G44080	-1.62	1.86E-05	3.86E-03	AT4G10250	ATHSP22.0, HSP20-like chaperones superfamily protein
AL1G54340	-1.63	4.03E-04	4.00E-02	AT1G47890	AtRLP7, RLP7, receptor like protein 7
AL5G44570	-1.66	9.85E-07	3.64E-04	AT1G26762	unknown protein
AL7G35860	-1.67	2.10E-05	4.31E-03	AT4G18430	AtRABA1e, RABA1e, RAB GTPase homolog A1E
AL939U10010	-1.68	4.75E-07	1.93E-04	AT3G19100	Protein kinase superfamily protein
AL1G24210	-1.70	2.73E-05	5.15E-03	AT3G20000	TOM40, translocase of the outer mitochondrial membrane 40
AL1G25950	-1.71	1.43E-04	1.88E-02	AT1G14080	ATFUT6, FUT6, fucosyltransferase 6
AL6G50030	-1.72	2.34E-04	2.76E-02	AT4G05320	UBQ10, polyubiquitin 10
AL4G42400	-1.72	3.80E-06	1.08E-03	AT2G43580	Chitinase family protein
AL2G21040	-1.73	3.82E-08	2.40E-05	AT5G44000	Glutathione S-transferase family protein
AL1G36000	-1.77	8.65E-06	2.08E-03	AT1G22480	Cupredoxin superfamily protein
AL1G23920	-1.79	4.89E-05	8.63E-03	AT1G12570	Glucose-methanol-choline (GMC) oxidoreductase family protein
AL5G17080	-1.80	1.56E-06	5.17E-04	AT3G27660	OLE3, OLEO4, oleosin 4
AL4G34720	-1.82	2.99E-05	5.56E-03	AT2G37770	NAD(P)-linked oxidoreductase superfamily protein
AL7G24740	-1.85	5.37E-06	1.42E-03	AT4G27890	HSP20-like chaperones superfamily protein
AL4G14290	-1.89	3.22E-04	3.45E-02	/	Unknown
AL5G41600	-1.91	1.58E-05	3.37E-03	AT3G59630	diphthamide synthesis DPH2 family protein
AL5G25850	-1.93	3.52E-04	3.67E-02	AT3G46840	Subtilase family protein
AL6G16180	-1.94	1.99E-06	6.18E-04	AT2G40460	Major facilitator superfamily protein
AL5G42930	-1.95	1.01E-04	1.49E-02	/	Unknown
AL8G30960	-1.96	6.43E-06	1.62E-03	AT5G55410	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL1G35670	-1.97	5.85E-05	1.00E-02	AT1G22220	F-box family protein
AL3G30470	-1.98	1.79E-05	3.74E-03	AT3G17400	F-box family protein
AL2G17430	-1.98	1.51E-06	5.08E-04	AT1G59620	CW9, Disease resistance protein (CC-NBS-LRR class) family
AL8G20470	-1.99	4.41E-04	4.26E-02	AT1G79280	AtTPR, NUA, nuclear pore anchor
AL1G32120	-2.00	3.87E-05	7.02E-03	AT1G14830	ADL1C, ADL5, DL1C, DRP1C, DYNAMIN-like 1C
AL5G33780	-2.00	4.57E-04	4.33E-02	AT3G52970	CYP76G1, cytochrome P450, family 76, subfamily G, polypeptide 1
AL9U11830	-2.01	1.44E-04	1.89E-02	/	Unknown
AL3G48170	-2.02	2.63E-05	5.09E-03	AT2G40910	F-box and associated interaction domains-containing protein
AL4G33830	-2.08	2.72E-07	1.20E-04	AT2G37430	C2H2 and C2HC zinc fingers superfamily protein
AL4G33770	-2.08	2.29E-04	2.73E-02	AT2G37390	Chloroplast-targeted copper chaperone protein
AL7G46580	-2.09	1.32E-04	1.78E-02	AT2G32980	unknown protein
AL2G35840	-2.09	1.40E-05	3.06E-03	AT5G44430	PDF1.2c, plant defensin 1.2C
AL8G14330	-2.12	4.32E-04	4.21E-02	AT5G45060	Disease resistance protein (TIR-NBS-LRR class) family
AL6G36530	-2.14	4.96E-04	4.53E-02	AT5G24860	ATFPF1, FPF1, flowering promoting factor 1
AL8G35270	-2.15	1.87E-04	2.32E-02	AT5G64410	ATOPT4, OPT4, oligopeptide transporter 4
AL3G48410	-2.16	1.44E-08	1.02E-05	AT2G19800	MIOX2, myo-inositol oxygenase 2
AL5G23880	-2.17	4.75E-04	4.45E-02	AT3G45280	ATSYP72, SYP72, syntaxin of plants 72
AL2G30020	-2.18	8.19E-05	1.31E-02	AT2G40460	Major facilitator superfamily protein
AL146U10030	-2.18	6.96E-05	1.16E-02	AT2G29020	Rab5-interacting family protein
AL8G13800	-2.20	1.10E-05	2.53E-03	AT2G02360	AtPP2-B10, PP2-B10, phloem protein 2-B10
AL6G40850	-2.22	3.85E-04	3.85E-02	/	Unknown
AL6G42040	-2.26	2.32E-04	2.75E-02	/	Unknown
AL6G41750	-2.28	3.11E-09	2.65E-06	AT1G14570	UBX domain-containing protein
AL34U10120	-2.28	2.20E-04	2.64E-02	AT5G49000	Galactose oxidase/kelch repeat superfamily protein
AL7G18650	-2.29	1.24E-05	2.74E-03	AT4G33020	ATZIP9, ZIP9, ZIP metal ion transporter family
AL5G27690	-2.33	3.95E-06	1.09E-03	AT3G48310	CYP71A22, cytochrome P450, family 71, subfamily A, polypeptide 22
AL8G11130	-2.34	4.58E-04	4.34E-02	/	Unknown
AL3G52710	-2.34	2.40E-04	2.81E-02	/	Unknown
AL1G20890	-2.35	1.45E-04	1.89E-02	AT3G20000	TOM40, translocase of the outer mitochondrial membrane 40
AL7G49510	-2.35	4.70E-04	4.41E-02	AT5G40382	Cytochrome c oxidase subunit Vc family protein
AL1G20960	-2.37	1.22E-04	1.72E-02	AT4G03298	unknown protein
AL41U10050	-2.40	1.21E-05	2.74E-03	AT2G29150	NAD(P)-binding Rossmann-fold superfamily protein
AL6G52880	-2.41	9.45E-05	1.43E-02	AT4G20480	Putative endonuclease or glycosyl hydrolase
AL3G18960	-2.42	1.15E-04	1.65E-02	AT3G07600	Heavy metal transport/detoxification superfamily protein

AL7G38400	-2.44	3.40E-05	6.25E-03	AT4G16530	Family of unknown function (DUF577)
AL6G42050	-2.49	8.91E-05	1.36E-02	/	Unknown
AL1G25670	-2.56	5.10E-04	4.63E-02	/	Unknown
AL7G40540	-2.57	1.08E-08	7.80E-06	AT4G15160	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL9U10430	-2.61	1.70E-06	5.42E-04	/	Unknown
AL2G11470	-2.62	1.09E-07	5.84E-05	AT2G42470	TRAF-like family protein
AL6G19270	-2.66	4.39E-04	4.25E-02	/	Unknown
AL2G13380	-2.66	3.02E-04	3.29E-02	AT1G62500	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL3G32960	-2.68	4.91E-05	8.63E-03	AT3G19550	unknown protein
AL1G57910	-2.69	2.62E-07	1.18E-04	AT4G35260	IDH-I, IDH1, isocitrate dehydrogenase 1
AL1G24250	-2.72	4.87E-08	3.00E-05	AT1G10510	emb2004, RNI-like superfamily protein
AL3G49050	-2.75	6.06E-07	2.37E-04	/	Unknown
AL191U10020	-2.75	8.45E-05	1.32E-02	AT5G56230	PRA1.G2, prenylated RAB acceptor 1.G2
AL3G33370	-2.75	4.88E-04	4.47E-02	AT3G20030	F-box and associated interaction domains-containing protein
AL4G10030	-2.79	2.54E-04	2.91E-02	AT4G14210	PDE226, PDS, PDS3, phytoene desaturase 3
AL6G33590	-2.88	2.11E-04	2.57E-02	AT5G22560	Plant protein of unknown function (DUF247)
AL5G16490	-2.89	2.64E-04	3.00E-02	AT3G27290	RNI-like superfamily protein
AL6G34490	-2.91	9.96E-05	1.49E-02	AT5G23260	ABS, AGL32, TT16, K-box region and MADS-box transcription factor family protein
AL5G44200	-2.92	8.46E-05	1.32E-02	/	Unknown
AL1G67270	-2.96	7.89E-05	1.28E-02	AT2G41350	unknown protein
AL1G60810	-2.96	3.48E-04	3.63E-02	AT1G52560	HSP20-like chaperones superfamily protein
AL7G35240	-2.97	2.21E-11	3.86E-08	/	Unknown
AL419U10010	-3.00	3.37E-11	5.60E-08	AT5G56340	ATCRT1, RING/U-box superfamily protein
AL7G39760	-3.01	1.93E-05	3.98E-03	AT4G15670	Thioredoxin superfamily protein
AL5G34210	-3.07	1.28E-04	1.77E-02	AT5G35715	CYP71B8, cytochrome P450, family 71, subfamily B, polypeptide 8
AL3G47620	-3.18	1.41E-04	1.86E-02	AT2G40910	F-box and associated interaction domains-containing protein
AL7G44960	-3.19	2.47E-04	2.86E-02	AT4G38640	Plasma-membrane choline transporter family protein
AL5G20400	-3.21	1.01E-06	3.64E-04	AT1G04985	unknown protein
AL4G32840	-3.22	2.28E-07	1.05E-04	AT2G36660	PAB7, poly(A) binding protein 7
AL5G25310	-3.22	8.11E-08	4.64E-05	AT1G52950	Nucleic acid-binding, OB-fold-like protein
AL1G54150	-3.24	2.64E-05	5.09E-03	AT1G47760	AGL102, AGAMOUS-like 102
AL5G27070	-3.28	1.10E-05	2.53E-03	AT3G47790	ATATH7, ATH7, ABC2 homolog 7
AL2G11070	-3.31	4.66E-06	1.27E-03	AT1G64030	ATSRP3, SRP3, serpin 3
AL5G31070	-3.46	1.52E-07	7.75E-05	/	Unknown
AL5G33280	-3.51	2.65E-05	5.09E-03	AT3G52140	tetratricopeptide repeat (TPR)-containing protein
AL3G26370	-3.59	1.49E-11	2.91E-08	AT3G14130	Aldolase-type TIM barrel family protein
AL7G50590	-3.65	1.43E-06	4.89E-04	AT1G71680	Transmembrane amino acid transporter family protein
AL8G13780	-3.66	1.71E-05	3.62E-03	/	Unknown
AL1G61330	-3.68	9.18E-08	5.17E-05	AT1G52990	thioredoxin family protein
AL1G55760	-3.69	1.22E-05	2.74E-03	AT1G48930	AtGH9C1, GH9C1, glycosyl hydrolase 9C1
AL5G23200	-3.75	1.24E-05	2.74E-03	AT3G44790	TRAF-like family protein
AL6G41500	-3.78	6.21E-07	2.40E-04	AT4G09012	Mitochondrial ribosomal protein L27
AL5G25120	-3.78	1.03E-08	7.58E-06	AT1G53540	HSP20-like chaperones superfamily protein
AL1G36260	-3.85	4.49E-07	1.89E-04	/	Unknown
AL5G30750	-3.86	8.36E-07	3.19E-04	AT3G50610	unknown protein
AL7G45000	-3.93	4.92E-06	1.32E-03	/	Unknown
AL2G16560	-3.98	6.07E-08	3.65E-05	/	Unknown
AL1G64190	-4.26	1.42E-13	4.14E-10	AT1G55940	CYP708A1, cytochrome P450, family 708, subfamily A, polypeptide 1
AL2G22180	-4.41	4.76E-07	1.93E-04	AT1G65480	Flowering locus T, PEBP (phosphatidylethanolamine-binding protein) family protein
AL7G50060	-4.52	4.86E-09	3.94E-06	/	Unknown
AL3G53610	-4.54	1.51E-14	6.27E-11	/	Unknown
AL3G37310	-4.57	2.58E-07	1.17E-04	/	Unknown
AL3G40380	-4.61	1.41E-06	4.89E-04	AT5G58840	Subtilase family protein
AL6G28820	-5.07	7.60E-09	6.01E-06	AT3G01345	Expressed protein
AL1G50770	-5.08	2.73E-08	1.81E-05	/	Unknown
AL5G12390	-5.31	1.49E-13	4.14E-10	/	Unknown
AL3G34090	-5.40	1.38E-17	8.91E-14	AT3G20370	TRAF-like family protein
AL6G31550	-5.79	6.18E-10	5.58E-07	/	Unknown
AL7G44980	-5.86	1.62E-10	1.92E-07	/	Unknown
AL1G50760	-6.09	2.74E-10	2.85E-07	/	Unknown
AL8G13710	-6.12	2.20E-10	2.36E-07	AT5G45050	ATWRKY16, TTR1, WRKY16, Disease resistance protein (TIR-NBS-LRR class)
AL2G13710	-6.27	8.83E-11	1.17E-07	AT1G62210	unknown protein
AL4G25140	-6.50	6.07E-11	8.77E-08	AT2G30290	BP80-1;2, VSR1;2, VSR2, VACUOLAR SORTING RECEPTOR 2
AL8G12660	-8.25	2.20E-11	3.86E-08	AT5G45890	SAG12, senescence-associated gene 12

Table S5. List of the differentially expressed genes (DEG) after heat acclimation compared to control conditions. Genes were considered as differentially expressed when false discovery rate (FDR) < 0.05. Genes are sorted by log2FoldChange (log2FC)

Gene_ID_lyrata	log2FC	P-value	FDR	Homolog_thaliana	Gene_name
AL8G36240	10.64	1.88E-112	6.23E-108	AT5G59720	HSP18.2, heat shock protein 18.2
AL6G44080	9.66	3.39E-92	5.64E-88	AT4G10250	ATHSP22.0, HSP20-like chaperones superfamily protein
AL6G26110	8.67	8.15E-62	6.77E-58	AT5G15250	ATFTSH6, FTSH6, FTSH protease 6
AL7G49510	7.71	5.03E-72	5.56E-68	AT5G40382	Cytochrome c oxidase subunit Vc family protein
AL1G60810	7.39	8.09E-39	2.24E-35	AT1G52560	HSP20-like chaperones superfamily protein
AL1G47730	7.31	5.88E-43	2.79E-39	AT1G33350	Pentatricopeptide repeat (PPR) superfamily protein
AL4G20660	6.46	3.88E-17	3.07E-14	AT2G31470	DOR, F-box and associated interaction domains-containing protein
AL5G25120	6.44	8.92E-43	3.70E-39	AT1G53540	HSP20-like chaperones superfamily protein
AL6G22820	6.39	9.10E-37	2.33E-33	AT5G12030	AT-HSP17.6A, HSP17.6, HSP17.6A, heat shock protein 17.6A
AL1G62090	6.34	5.46E-35	1.30E-31	AT1G53540	HSP20-like chaperones superfamily protein
AL7G24990	6.12	1.95E-61	1.29E-57	AT4G27670	HSP21, heat shock protein 21
AL3G44260	6.09	9.13E-21	1.17E-17	AT2G23150	ATNRAMP3, NRAMP3, natural resistance-associated macrophage protein 3
AL4G17310	5.54	1.34E-43	7.42E-40	/	Unknown
AL7G45780	5.53	8.69E-12	3.14E-09	AT5G37140	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AL6G17600	5.53	6.03E-42	2.00E-38	AT5G07330	unknown protein
AL6G37160	5.43	1.18E-09	2.72E-07	AT5G25415	Protein of Unknown Function (DUF239)
AL3G46710	5.29	6.60E-20	6.85E-17	/	Unknown
AL6G31860	5.24	2.81E-08	4.81E-06	AT5G20310	Adenine nucleotide alpha hydrolases-like superfamily protein
AL8G13700	5.10	6.79E-09	1.37E-06	AT5G45060	Disease resistance protein (TIR-NBS-LRR class) family
AL6G36800	4.96	3.86E-07	4.61E-05	/	Unknown
AL1G12530	4.94	1.94E-41	5.86E-38	AT1G03070	Bax inhibitor-1 family protein
AL615U10010	4.70	7.01E-08	1.08E-05	AT3G23955	F-box family protein
AL1G47160	4.69	1.80E-42	6.63E-39	AT3G03773	HSP20-like chaperones superfamily protein
AL5G25020	4.67	6.58E-26	1.15E-22	AT3G46230	ATHSP17.4, HSP17.4, heat shock protein 17.4
AL2G18760	4.44	1.45E-06	1.45E-04	AT1G57800	ORTH3, VIM5, zinc finger (C3HC4-type RING finger) family protein
AL7G15240	4.43	1.65E-07	2.22E-05	AT4G35830	ACO1, aconitase 1
AL1G16160	4.35	2.40E-07	3.03E-05	AT5G15690	zinc ion binding
AL1G25240	4.35	8.07E-08	1.23E-05	AT1G13470	Protein of unknown function (DUF1262)
AL4G25940	4.15	8.61E-17	6.50E-14	AT5G60600	CLB4, CSB3, GCPE, HDS, ISPG, 4-hydroxy-3-methylbut-2-enyl diphosphate synthase
AL1G20660	4.06	1.28E-06	1.30E-04	AT1G10095	Protein prenylyltransferase superfamily protein
AL7G28880	4.05	2.18E-07	2.80E-05	/	Unknown
AL6G31880	4.01	1.12E-07	1.62E-05	AT3G48150	APC8, CDC23, anaphase-promoting complex subunit 8
AL7G25440	3.93	9.17E-13	4.55E-10	AT4G27360	Dynein light chain type 1 family protein
AL7G30390	3.89	7.57E-07	8.27E-05	AT4G23100	ATECS1, CAD2, GSH1, GSHA, PAD2, RML1, glutamate-cysteine ligase
AL4G46730	3.74	6.65E-27	1.30E-23	AT2G47180	AtGolS1, GolS1, galactinol synthase 1
AL5G27180	3.72	7.74E-07	8.36E-05	AT1G65113	SCRL2, SCR-like 2
AL7G29960	3.68	2.88E-14	1.77E-11	AT4G23496	SP1L5, SPIRAL1-like5
AL2G14580	3.67	2.55E-08	4.51E-06	AT1G80740	CMT1, DMT4, chromomethylase 1
AL1G12070	3.66	1.57E-17	1.37E-14	AT1G02700	unknown protein
AL1G51460	3.58	2.35E-07	2.98E-05	/	Unknown
AL7G46490	3.56	6.33E-30	1.40E-26	AT5G37670	HSP20-like chaperones superfamily protein
AL1G14050	3.55	1.03E-07	1.52E-05	/	Unknown
AL6G44140	3.54	1.25E-05	8.52E-04	AT4G10300	RmlC-like cupins superfamily protein
AL2G32340	3.54	1.07E-29	2.22E-26	AT1G72660	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AL6G22810	3.52	4.72E-19	4.75E-16	AT5G12020	HSP17.6II, 17.6 kDa class II heat shock protein
AL5G23550	3.44	1.39E-05	9.27E-04	AT3G45060	ATNRT2.6, NRT2.6, high affinity nitrate transporter 2.6
AL1G50040	3.42	1.38E-11	4.77E-09	/	Unknown
AL7G15490	3.39	4.12E-08	6.77E-06	AT4G35650	IDH-III, isocitrate dehydrogenase III
AL4G14250	3.38	1.30E-06	1.32E-04	AT2G24130	Leucine-rich receptor-like protein kinase family protein
AL1G56380	3.36	3.26E-09	6.95E-07	AT3G46210	Ribosomal protein S5 domain 2-like superfamily protein
AL8G21550	3.36	4.85E-23	7.68E-20	AT5G48570	ATFKBP65, FKBP65, ROF2, FKBP-type peptidyl-prolyl cis-trans isomerase family protein
AL6G17550	3.33	4.92E-06	3.87E-04	AT5G07310	Integrase-type DNA-binding superfamily protein
AL2G24390	3.30	1.21E-05	8.31E-04	AT1G66560	ATWRKY64, WRKY64, WRKY DNA-binding protein 64
AL8G14350	3.26	9.70E-07	1.01E-04	AT3G47570	Leucine-rich repeat protein kinase family protein
AL2G13360	3.25	5.28E-19	5.16E-16	/	Unknown
AL5G39970	3.21	4.87E-05	2.43E-03	AT3G58260	TRAF-like family protein
AL8G13620	3.21	4.87E-05	2.43E-03	AT5G45260	ATWRKY52, RRS1, SLH1, Disease resistance protein (TIR-NBS-LRR class)
AL463U10030	3.17	1.44E-07	2.02E-05	AT2G39450	ATMTP11, MTP11, Cation efflux family protein
AL3G20260	3.16	1.10E-05	7.65E-04	AT3G09150	ATHY2, GUN3, HY2, phytochromobilin:ferredoxin oxidoreductase, chloroplast / phytochromobilin synthase (HY2)
AL6G29040	3.15	4.75E-05	2.39E-03	/	Unknown
AL1G56780	3.15	6.47E-06	4.89E-04	AT1G02190	Fatty acid hydroxylase superfamily
AL8G34500	3.14	6.52E-05	3.08E-03	AT2G39570	ACT domain-containing protein
AL5G35360	3.11	3.15E-08	5.37E-06	AT3G54310	unknown protein
AL1G63660	3.10	7.36E-05	3.39E-03	AT1G55600	ATWRKY10, MINI3, WRKY10, WRKY DNA-binding protein 10
AL8G13780	3.08	3.40E-06	2.88E-04	/	Unknown
AL8G45480	3.08	1.12E-25	1.85E-22	AT5G66110	Heavy metal transport/detoxification superfamily protein
AL5G19990	3.06	8.48E-05	3.81E-03	/	Unknown
AL7G40360	3.06	2.00E-05	1.23E-03	AT4G15250	B-box type zinc finger protein with CCT domain
AL7G49640	3.06	7.33E-10	1.78E-07	AT5G40270	HD domain-containing metal-dependent phosphohydrolase family protein
AL5G23330	3.05	3.96E-10	1.04E-07	AT3G44860	FAMT, farnesoic acid carboxyl-O-methyltransferase
AL1G33320	3.04	8.99E-07	9.55E-05	AT1G20940	F-box family protein
AL1G52070	3.01	1.03E-04	4.47E-03	AT1G35617	unknown protein

AL8G39700	3.00	1.44E-22	2.17E-19	AT5G62730	Major facilitator superfamily protein
AL6G44600	2.97	4.48E-05	2.27E-03	AT4G10550	Subtilase family protein
AL7G19330	2.97	9.59E-22	1.33E-18	AT4G32480	Protein of unknown function (DUF506)
AL8G43880	2.96	1.63E-07	2.19E-05	AT5G67430	Acyl-CoA N-acyltransferases (NAT) superfamily protein
AL7G19300	2.96	5.31E-09	1.10E-06	AT4G32510	HCO3- transporter family
AL6G37230	2.95	2.83E-20	3.19E-17	AT5G25450	Cytochrome bd ubiquinol oxidase, 14kDa subunit
AL1G60100	2.94	6.40E-08	9.94E-06	AT1G52030	F-ATMBP, MBP1.2, MBP2, myrosinase-binding protein 2
AL645U10010	2.92	3.70E-05	1.95E-03	/	Unknown
AL1G53440	2.91	8.95E-05	3.97E-03	AT1G47280	unknown protein
AL4G31230	2.88	1.24E-09	2.83E-07	/	Unknown
AL7G27950	2.88	8.19E-17	6.33E-14	AT4G25200	ATHSP23.6-MITO, HSP23.6-MITO, mitochondrion-localized small heat shock protein 23.6
AL1G33450	2.86	1.74E-05	1.10E-03	AT1G20520	Arabidopsis protein of unknown function (DUF241)
AL6G41770	2.85	4.88E-16	3.52E-13	AT4G08040	ACS11, 1-aminocyclopropane-1-carboxylate synthase 11
AL4G47120	2.85	6.49E-05	3.08E-03	AT2G47540	Pollen Ole e 1 allergen and extensin family protein
AL1G27740	2.83	1.71E-04	6.67E-03	AT1G15620	unknown protein
AL5G22390	2.83	1.39E-14	9.06E-12	AT1G49500	unknown protein
AL4G47390	2.82	3.23E-05	1.76E-03	AT2G47810	NF-YB5, nuclear factor Y, subunit B5
AL7G29780	2.77	4.12E-05	2.11E-03	AT4G23590	Tyrosine transaminase family protein
AL3G51350	2.77	4.51E-06	3.65E-04	AT2G09388	unknown protein
AL1G23100	2.74	1.29E-05	8.78E-04	/	Unknown
AL1G16150	2.72	2.62E-05	1.51E-03	/	Unknown
AL3G47660	2.72	1.80E-06	1.73E-04	AT5G43070	WPP1, WPP domain protein 1
AL7G32800	2.72	3.90E-20	4.18E-17	AT4G21320	HSA32, Aldolase-type TIM barrel family protein
AL4G19130	2.71	6.37E-07	7.18E-05	AT3G62210	EDA32, Putative endonuclease or glycosyl hydrolase
AL8G13610	2.70	3.51E-04	1.15E-02	AT5G45275	Major facilitator superfamily protein
AL7G30360	2.68	6.88E-06	5.19E-04	AT4G23120	Bromo-adjacent homology (BAH) domain-containing protein
AL6G35870	2.67	3.27E-04	1.09E-02	/	Unknown
AL3G11190	2.67	9.85E-12	3.52E-09	AT3G01070	AtENODL16, ENODL16, early nodulin-like protein 16
AL1G64200	2.66	3.67E-04	1.19E-02	AT2G01370	DNA-binding storekeeper protein-related transcriptional regulator
AL7G39720	2.65	1.77E-05	1.11E-03	AT4G15680	Thioredoxin superfamily protein
AL7G15330	2.65	8.97E-17	6.62E-14	AT4G35770	ATSEN1, DIN1, SEN1, SEN1, Rhodanese/Cell cycle control phosphatase superfamily protein
AL6G31650	2.64	3.07E-05	1.69E-03	AT5G20100	unknown protein
AL6G49770	2.63	2.09E-04	7.74E-03	AT4G03153	Kinase interacting (KIP1-like) family protein
AL4G15910	2.61	4.49E-04	1.37E-02	AT2G24850	TAT, TAT3, tyrosine aminotransferase 3
AL4G16980	2.61	3.30E-11	1.07E-08	AT2G25540	CESA10, cellulose synthase 10
AL1G65650	2.60	2.26E-04	8.19E-03	AT1G58390	Disease resistance protein (CC-NBS-LRR class) family
AL3G11800	2.60	5.81E-10	1.46E-07	AT3G02480	Late embryogenesis abundant protein (LEA) family protein
AL6G49360	2.60	1.35E-05	9.01E-04	AT4G03540	Uncharacterised protein family (UPF0497)
AL6G28630	2.59	8.19E-06	5.96E-04	AT5G17540	HXXXD-type acyl-transferase family protein
AL4G25290	2.58	3.61E-04	1.18E-02	AT2G30420	ETC2, Homeodomain-like superfamily protein
AL1G67430	2.57	1.94E-04	7.33E-03	AT1G57730	RING/U-box superfamily protein
AL4G33850	2.57	5.75E-05	2.79E-03	AT2G37435	Cystatin/monellin superfamily protein
AL5G21170	2.56	3.95E-04	1.26E-02	/	Unknown
AL7G40510	2.56	5.12E-04	1.52E-02	AT1G51405	myosin-related
AL7G28870	2.54	4.18E-04	1.31E-02	AT4G24340	Phosphorylase superfamily protein
AL6G20350	2.52	8.48E-21	1.13E-17	AT5G09930	ATGCN2, GCN2, ABC transporter family protein
AL5G22470	2.49	4.55E-04	1.39E-02	AT3G44326	F-box family protein
AL8G16830	2.49	7.22E-04	1.97E-02	AT5G23290	PFD5, prefoldin 5
AL3G25870	2.48	6.16E-22	8.90E-19	AT3G13784	AtcwINV5, CWINV5, cell wall invertase 5
AL1G54470	2.46	9.32E-07	9.81E-05	/	Unknown
AL8G38490	2.45	4.02E-05	2.08E-03	AT5G61730	ATATH11, ATH11, ABC2 homolog 11
AL8G23480	2.45	2.05E-03	4.43E-02	/	Unknown
AL3G32420	2.45	1.74E-14	1.11E-11	AT3G19030	unknown protein
AL2G28210	2.45	1.94E-07	2.53E-05	/	Unknown
AL103U10030	2.44	4.88E-08	7.91E-06	AT2G32100	ATOFP16, OFP16, ovate family protein 16
AL7G35610	2.44	1.13E-05	7.83E-04	AT4G18650	transcription factor-related
AL1G45940	2.43	6.69E-04	1.87E-02	/	Unknown
AL6G19010	2.42	1.98E-04	7.43E-03	AT5G08500	Transmembrane CLPTM1 family protein
AL6G39780	2.42	1.27E-03	3.05E-02	/	Unknown
AL3G28600	2.42	4.82E-04	1.45E-02	AT3G15960	mismatched DNA binding;ATP binding
AL3G40560	2.42	6.80E-04	1.89E-02	AT3G24790	Protein kinase superfamily protein
AL7G30200	2.41	2.06E-04	7.66E-03	AT4G23160	CRK8, cysteine-rich RLK (RECEPTOR-like protein kinase) 8
AL4G30840	2.39	7.77E-04	2.09E-02	/	Unknown
AL2G38750	2.39	2.76E-05	1.55E-03	AT3G14420	Aldolase-type TIM barrel family protein
AL3G43140	2.38	1.10E-03	2.73E-02	AT3G54540	ATGCN4, GCN4, general control non-repressible 4
AL8G38810	2.37	1.03E-10	3.07E-08	AT5G62040	PEBP (phosphatidylethanolamine-binding protein) family protein
AL4G27770	2.36	5.95E-04	1.71E-02	AT2G37435	Cystatin/monellin superfamily protein
AL6G19290	2.36	1.94E-04	7.32E-03	AT5G08565	Transcription initiation Spt4-like protein
AL8G16300	2.34	4.10E-08	6.77E-06	AT5G43840	AT-HSFA6A, HSFA6A, heat shock transcription factor A6A
AL6G14650	2.34	4.91E-12	1.90E-09	AT5G04950	ATNAS1, NAS1, nicotianamine synthase 1
AL2G28650	2.34	1.08E-12	5.19E-10	AT1G69526	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AL1G44890	2.33	1.02E-03	2.58E-02	AT1G30790	F-box and associated interaction domains-containing protein
AL1G26990	2.33	1.26E-03	3.02E-02	AT4G19640	ARA-7, ARA7, ATRAB-F2B, ATRAB5B, ATRABF2B, RAB-F2B, RABF2B, Ras-related small GTP-binding family protein
AL5G18290	2.33	1.05E-03	2.63E-02	AT3G28650	Cysteine/Histidine-rich C1 domain family protein
AL5G21460	2.31	1.21E-03	2.93E-02	AT4G25210	DNA-binding storekeeper protein-related transcriptional regulator
AL1G28930	2.30	8.66E-04	2.28E-02	AT1G16760	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain
AL5G45710	2.30	2.88E-10	7.84E-08	AT3G62930	Thioredoxin superfamily protein
AL1G46760	2.30	1.43E-03	3.35E-02	AT1G32510	ANAC011, NAC011, NAC domain containing protein 11

AL7G34530	2.29	1.18E-03	2.88E-02	AT4G19570	Chaperone DnaJ-domain superfamily protein
AL4G26130	2.29	7.96E-06	5.81E-04	AT3G10060	FKBP-like peptidyl-prolyl cis-trans isomerase family protein
AL6G32920	2.29	3.62E-05	1.93E-03	AT5G21960	Integrase-type DNA-binding superfamily protein
AL7G43430	2.29	1.56E-03	3.59E-02	AT5G56500	TCP-1/cpn60 chaperonin family protein
AL4G44510	2.28	1.15E-17	1.03E-14	AT2G45380	unknown protein
AL3G28360	2.28	8.82E-07	9.43E-05	/	Unknown
AL3G14770	2.27	2.77E-11	9.19E-09	AT4G01380	plastocyanin-like domain-containing protein
AL9U10170	2.27	2.71E-08	4.71E-06	/	Unknown
AL5G29480	2.27	9.43E-05	4.16E-03	AT3G49620	DIN11, 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AL65U10040	2.27	1.61E-03	3.66E-02	AT5G45070	AtPP2-A8, PP2-A8, phloem protein 2-A8
AL3G54100	2.26	2.05E-03	4.43E-02	AT2G20850	SRF1, STRUBBELIG-receptor family 1
AL3G35520	2.25	3.02E-04	1.03E-02	AT3G21450	Protein kinase superfamily protein
AL9U11340	2.25	1.68E-03	3.78E-02	AT4G13030	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AL7G39740	2.24	3.57E-10	9.48E-08	AT4G15690	Thioredoxin superfamily protein
AL667U10010	2.24	5.24E-13	2.76E-10	/	Unknown
AL4G42600	2.24	9.31E-04	2.41E-02	AT2G43740	Mannose-binding lectin superfamily protein
AL4G27490	2.24	4.87E-12	1.90E-09	AT2G32120	HSP70T-2, heat-shock protein 70T-2
AL1G28200	2.24	6.28E-08	9.79E-06	AT1G16030	Hsp70b, heat shock protein 70B
AL5G17730	2.23	1.10E-06	1.13E-04	AT3G28220	TRAF-like family protein
AL4G39610	2.23	5.53E-08	8.79E-06	/	Unknown
AL755U10010	2.23	2.00E-03	4.35E-02	/	Unknown
AL6G11620	2.22	4.51E-05	2.28E-03	AT5G02390	Protein of unknown function (DUF3741)
AL5G35920	2.22	3.06E-13	1.64E-10	AT3G54830	Transmembrane amino acid transporter family protein
AL7G51030	2.22	9.76E-04	2.49E-02	AT1G54680	unknown protein
AL1G64230	2.22	1.13E-05	7.85E-04	AT1G55970	HAC04, HAC4, HAC6, HAG04, HAG4, histone acetyltransferase of the CBP family 4
AL6G20700	2.22	2.69E-10	7.39E-08	AT5G10210	unknown protein
AL8G38500	2.22	1.68E-03	3.78E-02	AT5G61740	ATATH14, ATH14, ABC2 homolog 14
AL3G18400	2.22	2.07E-12	8.95E-10	AT3G07150	unknown protein
AL5G30110	2.20	3.81E-04	1.23E-02	AT5G67360	ARA12, Subtilase family protein
AL1G58760	2.20	2.19E-03	4.64E-02	AT1G51035	unknown protein.
AL8G42570	2.19	1.56E-04	6.20E-03	/	Unknown
AL1G25390	2.19	2.06E-09	4.53E-07	AT1G13610	alpha/beta-Hydrolases superfamily protein
AL667U10020	2.19	5.66E-13	2.89E-10	/	Unknown
AL5G25060	2.19	1.96E-03	4.29E-02	AT3G46240	unknown protein
AL1G61570	2.18	2.35E-08	4.21E-06	/	Unknown
AL8G33850	2.18	9.42E-04	2.43E-02	AT5G57810	TET15, tetraspanin15
AL4G38680	2.17	4.99E-05	2.47E-03	AT2G40790	ATCXXS2, CXXS2, C-terminal cysteine residue is changed to a serine 2
AL5G36210	2.15	1.05E-03	2.63E-02	AT3G55090	ABC-2 type transporter family protein
AL7G29970	2.13	5.93E-15	4.10E-12	AT4G23493	unknown protein
AL6G36360	2.13	5.22E-09	1.08E-06	AT5G24780	ATVSP1, VSP1, vegetative storage protein 1
AL7G47890	2.13	8.26E-08	1.25E-05	AT5G41550	Disease resistance protein (TIR-NBS-LRR class) family
AL3G20850	2.11	9.72E-14	5.77E-11	AT3G09640	APX1B, APX2, ascorbate peroxidase 2
AL7G39750	2.10	2.34E-06	2.13E-04	AT4G15680	Thioredoxin superfamily protein
AL1G17680	2.10	1.27E-10	3.74E-08	/	Unknown
AL3G30590	2.08	4.39E-06	3.57E-04	AT3G17520	Late embryogenesis abundant protein (LEA) family protein
AL7G13150	2.07	1.31E-10	3.82E-08	AT4G37610	BT5, BTB and TAZ domain protein 5
AL4G28750	2.06	9.65E-04	2.48E-02	/	Unknown
AL2G24600	2.06	4.69E-04	1.42E-02	AT1G66630	Protein with RING/U-box and TRAF-like domains
AL7G36520	2.06	9.85E-04	2.51E-02	AT4G17980	anac071, NAC071, NAC domain containing protein 71
AL103U10020	2.06	4.52E-14	2.73E-11	AT2G32120	HSP70T-2, heat-shock protein 70T-2
AL2G10570	2.05	1.87E-13	1.05E-10	AT3G60040	F-box family protein
AL7G47000	2.05	5.35E-04	1.58E-02	AT5G61500	ATATG3, ATG3, autophagy 3 (APG3)
AL4G24200	2.05	4.59E-08	7.51E-06	AT2G29500	HSP20-like chaperones superfamily protein
AL1G30230	2.04	8.15E-15	5.52E-12	AT1G17870	ATEGY3, EGY3, ethylene-dependent gravitropism-deficient and yellow-green-like 3
AL6G38340	2.04	2.13E-03	4.55E-02	AT5G26594	ARR24, RR24, response regulator 24
AL1G62490	2.04	4.24E-04	1.32E-02	/	Unknown
AL6G50340	2.03	6.56E-10	1.64E-07	AT4G02690	Bax inhibitor-1 family protein
AL8G27110	2.02	6.15E-12	2.29E-09	AT5G52640	ATHS83, AtHsp90-1, ATHSP90.1, HSP81-1, HSP81.1, HSP83, HSP90.1, heat shock protein 90.1
AL3G52510	2.01	2.23E-08	4.04E-06	/	Unknown
AL8G32990	2.00	2.82E-07	3.50E-05	AT5G57090	AGR, AGR1, ATPIN2, EIR1, PIN2, WAV6, Auxin efflux carrier family protein
AL8G36200	1.99	4.15E-06	3.40E-04	AT5G59680	Leucine-rich repeat protein kinase family protein
AL5G18280	1.99	4.79E-04	1.45E-02	/	Unknown
AL8G16730	1.98	4.64E-04	1.41E-02	AT5G43570	Serine protease inhibitor, potato inhibitor I-type family protein
AL983U10010	1.98	2.25E-04	8.19E-03	/	Unknown
AL7G41470	1.98	1.91E-05	1.18E-03	/	Unknown
AL5G44670	1.98	7.04E-04	1.94E-02	/	Unknown
AL8G38510	1.97	6.91E-05	3.24E-03	AT5G61750	RmlC-like cupins superfamily protein
AL4G36890	1.97	4.31E-04	1.33E-02	AT2G39260	binding;RNA binding
AL4G45510	1.95	7.16E-10	1.76E-07	AT2G46240	ATBAG6, BAG6, BCL-2-associated athanogene 6
AL1G52300	1.94	1.00E-10	3.00E-08	AT1G44414	unknown protein
AL3G42970	1.92	3.14E-05	1.72E-03	AT3G23960	F-box and associated interaction domains-containing protein
AL8G35750	1.90	8.43E-06	6.08E-04	AT5G59310	LTP4, lipid transfer protein 4
AL6G21730	1.90	2.28E-13	1.24E-10	AT5G11100	ATSYTD, NTMC2T2.2, NTMC2TYPE2.2, SYT4, SYTD, Calcium-dependent lipid-binding (CaLB domain) family protein
AL6G46290	1.90	1.74E-06	1.69E-04	AT3G05770	unknown protein
AL7G45270	1.90	5.94E-05	2.87E-03	AT5G61530	small G protein family protein / RhoGAP family protein
AL4G34810	1.89	8.72E-15	5.79E-12	AT2G37870	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein

AL4G43940	1.89	1.16E-03	2.85E-02	/	Unknown
AL7G32790	1.89	6.65E-11	2.05E-08	AT4G21323	Subtilase family protein
AL1G21540	1.88	1.76E-03	3.91E-02	AT1G10680	PGP10, P-glycoprotein 10
AL1G60110	1.88	1.89E-06	1.79E-04	AT1G52030	F-ATMBP, MBP1.2, MBP2, myrosinase-binding protein 2
AL1G35900	1.88	2.07E-04	7.69E-03	/	Unknown
AL6G23770	1.88	8.78E-13	4.42E-10	AT5G13170	SAG29, senescence-associated gene 29
AL3G37530	1.87	1.08E-03	2.69E-02	AT4G02580	NADH-ubiquinone oxidoreductase 24 kDa subunit, putative
AL2G14840	1.86	7.32E-05	3.39E-03	AT1G61415	unknown protein
AL8G10090	1.85	3.25E-07	3.99E-05	AT5G05420	FKBP-like peptidyl-prolyl cis-trans isomerase family protein
AL7G23180	1.85	4.67E-04	1.42E-02	AT4G29270	HAD superfamily, subfamily IIIB acid phosphatase
AL8G16120	1.84	5.57E-05	2.72E-03	/	Unknown
AL4G36860	1.84	1.92E-13	1.06E-10	AT2G39470	PPL2, PsbP-like protein 2
AL6G23990	1.84	4.88E-12	1.90E-09	AT5G13370	Auxin-responsive GH3 family protein
AL8G15670	1.83	1.05E-04	4.52E-03	AT5G44310	Late embryogenesis abundant protein (LEA) family protein
AL1G19610	1.82	9.51E-05	4.19E-03	AT5G39650	Protein of unknown function (DUF679)
AL5G28960	1.81	1.73E-05	1.10E-03	AT3G49270	unknown protein
AL3G36270	1.81	3.99E-04	1.26E-02	AT3G22090	unknown protein
AL7G39770	1.80	1.66E-06	1.63E-04	AT4G15700	Thioredoxin superfamily protein
AL7G48680	1.80	7.30E-10	1.78E-07	AT5G40890	ATCLC-A, ATCLCA, CLC-A, CLC-A, CLCA, chloride channel A
AL6G35100	1.79	3.27E-11	1.07E-08	AT5G23820	MD-2-related lipid recognition domain-containing protein
AL5G25350	1.79	7.39E-07	8.13E-05	AT3G46490	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AL4G18140	1.79	8.33E-06	6.04E-04	AT2G40955	unknown protein
AL2G38400	1.79	8.91E-05	3.96E-03	AT1G78090	ATTPPB, TPPB, trehalose-6-phosphate phosphatase
AL3G29130	1.78	6.42E-05	3.06E-03	AT4G11630	Ribosomal protein L19 family protein
AL5G17550	1.78	8.75E-04	2.30E-02	/	Unknown
AL8G27740	1.78	6.18E-04	1.76E-02	/	Unknown
AL7G47200	1.76	4.17E-05	2.14E-03	AT1G22090	emb2204, Protein of unknown function (DUF626)
AL8G16020	1.76	2.50E-05	1.44E-03	AT5G44050	MATE efflux family protein
AL4G16220	1.76	3.27E-07	3.99E-05	AT2G25090	CIPK16, SnRK3.18, CBL-interacting protein kinase 16
AL6G17980	1.75	1.00E-04	4.38E-03	AT5G07380	unknown protein
AL429U10010	1.74	1.64E-03	3.72E-02	/	Unknown
AL7G14130	1.74	1.67E-05	1.07E-03	AT4G36850	PQ-loop repeat family protein / transmembrane family protein
AL6G44090	1.74	1.07E-03	2.67E-02	AT4G10260	pfkB-like carbohydrate kinase family protein
AL5G25320	1.73	1.45E-07	2.02E-05	/	Unknown
AL6G27270	1.73	1.82E-04	6.96E-03	AT5G16350	O-acyltransferase (WSD1-like) family protein
AL3G53750	1.72	4.33E-10	1.13E-07	AT2G20670	Protein of unknown function (DUF506)
AL6G45170	1.72	1.64E-05	1.05E-03	AT4G05470	RNI-like superfamily protein
AL5G14890	1.72	1.38E-08	2.63E-06	AT3G26140	Cellulase (glycosyl hydrolase family 5) protein
AL8G34170	1.71	2.06E-12	8.95E-10	AT5G58070	ATTIL, TIL, temperature-induced lipocalin
AL3G45000	1.71	2.24E-07	2.85E-05	AT2G12480	SCPL43, serine carboxypeptidase-like 43
AL6G21700	1.71	1.52E-07	2.08E-05	AT5G11080	Ubiquitin-like superfamily protein
AL2G24930	1.70	1.03E-09	2.39E-07	AT1G66760	MATE efflux family protein
AL1G60080	1.70	1.23E-05	8.42E-04	AT1G52040	ATMBP, MBP1, myrosinase-binding protein 1
AL8G42130	1.70	2.39E-10	6.61E-08	AT2G18465	Chaperone DnaJ-domain superfamily protein
AL8G23190	1.69	3.12E-04	1.05E-02	/	Unknown
AL7G21870	1.68	5.80E-08	9.18E-06	AT4G30280	ATXTH18, XTH18, xyloglucan endotransglucosylase/hydrolase 18
AL7G11210	1.67	8.61E-12	3.14E-09	AT4G39235	unknown protein
AL1G54270	1.67	4.43E-04	1.36E-02	/	Unknown
AL8G26360	1.66	2.32E-04	8.40E-03	AT5G52020	Integrase-type DNA-binding superfamily protein
AL5G44250	1.66	9.26E-08	1.39E-05	AT2G25410	RING/U-box superfamily protein
AL3G32530	1.66	3.11E-04	1.05E-02	AT3G19160	ATIPT8, IPT8, IPT8, PGA22, ATP/ADP isopentenyltransferases
AL7G27050	1.65	1.33E-05	8.92E-04	AT4G25950	VATG3, vacuolar ATP synthase G3
AL3G44270	1.65	2.68E-05	1.53E-03	/	Unknown
AL8G33530	1.65	7.26E-05	3.37E-03	AT5G57550	XTH25, XTR3, xyloglucan endotransglucosylase/hydrolase 25
AL7G21700	1.65	7.81E-10	1.87E-07	AT4G30450	glycine-rich protein
AL8G20960	1.65	1.43E-05	9.43E-04	AT5G48220	Aldolase-type TIM barrel family protein
AL6G47270	1.64	1.47E-09	3.30E-07	AT4G12400	stress-inducible protein, putative
AL8G16540	1.64	1.06E-04	4.55E-03	AT5G43745	Protein of unknown function (DUF1012)
AL6G51270	1.64	6.06E-11	1.90E-08	AT4G01985	unknown protein
AL1G48030	1.64	6.00E-04	1.72E-02	AT1G33610	Leucine-rich repeat (LRR) family protein
AL4G46120	1.63	6.97E-04	1.93E-02	/	Unknown
AL1G16040	1.63	1.90E-03	4.18E-02	AT1G06090	Fatty acid desaturase family protein
AL4G30580	1.63	3.33E-04	1.10E-02	AT2G34600	JAZ7, TIFY5B, jasmonate-zim-domain protein 7
AL3G43850	1.63	1.33E-03	3.15E-02	AT1G22400	ATUGT85A1, UGT85A1, UDP-Glycosyltransferase superfamily protein
AL7G45920	1.62	8.87E-10	2.09E-07	AT5G37340	ZPR1 zinc-finger domain protein
AL5G32600	1.62	7.35E-05	3.39E-03	AT1G45063	copper ion binding;electron carriers
AL3G30090	1.62	8.49E-09	1.69E-06	AT3G17110	pseudogene, glycine-rich protein
AL8G45500	1.62	6.35E-11	1.97E-08	AT5G66090	unknown protein
AL8G10870	1.62	1.70E-03	3.80E-02	AT3G55780	Glycosyl hydrolase superfamily protein
AL7G13220	1.61	5.18E-08	8.32E-06	AT4G37540	LBD39, LOB domain-containing protein 39
AL3G28610	1.60	1.10E-04	4.70E-03	AT2G13720	DNA topoisomerase (ATP-hydrolyzing)s;ATP binding;DNA binding
AL3G30190	1.60	2.12E-10	5.92E-08	AT3G17180	scpl33, serine carboxypeptidase-like 33
AL6G43060	1.60	7.84E-04	2.10E-02	AT4G09500	UDP-Glycosyltransferase superfamily protein
AL5G13010	1.59	9.89E-04	2.52E-02	AT2G03320	unknown protein
AL1G36560	1.59	3.42E-04	1.12E-02	AT1G22990	Heavy metal transport/detoxification superfamily protein
AL7G31430	1.59	8.35E-06	6.04E-04	AT4G22217	Arabidopsis defensin-like protein
AL463U10020	1.58	7.75E-04	2.09E-02	AT2G39460	ATRPL23A, RPL23A, RPL23AA, ribosomal protein L23AA
AL2G31800	1.58	4.94E-05	2.45E-03	AT1G72140	Major facilitator superfamily protein
AL3G45920	1.58	1.01E-06	1.05E-04	AT2G14247	Expressed protein
AL1025U10010	1.58	3.39E-07	4.11E-05	/	Unknown

AL1G12470	1.58	2.26E-05	1.35E-03	AT1G03020	Thioredoxin superfamily protein
AL3G11700	1.57	6.52E-05	3.08E-03	AT3G02410	ICME-LIKE2, alpha/beta-Hydrolases superfamily protein
AL7G32580	1.57	1.28E-03	3.06E-02	AT4G21490	NDB3, NAD(P)H dehydrogenase B3
AL6G48660	1.57	4.45E-05	2.26E-03	AT4G05060	PapD-like superfamily protein
AL6G15290	1.57	1.78E-04	6.83E-03	AT5G05390	LAC12, laccase 12
AL6G12880	1.56	4.05E-05	2.08E-03	AT5G03480	RNA-binding (RRM/RBD/RNP motifs) family protein
AL4G38220	1.56	5.67E-10	1.44E-07	AT2G40400	Protein of unknown function (DUF399 and DUF3411)
AL2G32670	1.56	9.91E-04	2.52E-02	AT3G30820	Arabidopsis retrotransposon ORF-1 protein
AL5G45850	1.56	3.70E-04	1.20E-02	AT3G63052	unknown protein
AL7G40590	1.55	4.10E-04	1.29E-02	AT4G15120	VQ motif-containing protein
AL7G27230	1.55	1.12E-07	1.62E-05	AT4G25810	XTH23, XTR6, xyloglucan endotransglycosylase 6
AL7G46160	1.54	1.52E-04	6.10E-03	AT5G37470	Family of unknown function (DUF577)
AL1G61180	1.54	1.69E-03	3.78E-02	/	Unknown
AL3G37150	1.53	2.83E-04	9.82E-03	AT3G22830	AT-HSFA6B, HSFA6B, heat shock transcription factor A6B
AL6G51960	1.53	8.40E-08	1.27E-05	AT4G01430	nodulin MtN21 /EamA-like transporter family protein
AL5G30030	1.53	6.87E-04	1.91E-02	AT5G61180	Putative endonuclease or glycosyl hydrolase
AL304U10020	1.52	7.76E-04	2.09E-02	AT5G17140	Cysteine proteinases superfamily protein
AL1G56280	1.52	2.13E-08	3.88E-06	AT1G49320	ATUSPL1, USPL1, unknown seed protein like 1
AL2G15520	1.52	2.51E-05	1.45E-03	AT1G60970	SNARE-like superfamily protein
AL6G42420	1.51	2.82E-09	6.05E-07	AT4G08570	Heavy metal transport/detoxification superfamily protein
AL4G35810	1.51	8.18E-07	8.77E-05	AT2G38530	cdf3, LP2, LTP2, lipid transfer protein 2
AL3G18650	1.51	1.08E-06	1.11E-04	AT3G07350	Protein of unknown function (DUF506)
AL3G31860	1.50	9.05E-06	6.47E-04	AT3G18550	ATTCP18, BRC1, TCP18, TCP family transcription factor
AL5G30300	1.49	1.19E-03	2.90E-02	AT3G50170	Plant protein of unknown function (DUF247)
AL4G32170	1.48	6.12E-06	4.66E-04	AT2G36080	AP2/B3-like transcriptional factor family protein
AL7G40060	1.48	6.42E-04	1.82E-02	AT4G15480	UGT84A1, UDP-Glycosyltransferase superfamily protein
AL2G36290	1.47	1.57E-03	3.60E-02	AT1G76220	Arabidopsis protein of unknown function (DUF241)
AL8G21350	1.47	2.35E-04	8.45E-03	AT5G48490	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL7G27200	1.47	1.01E-08	1.95E-06	AT4G25835	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AL7G28800	1.46	1.28E-07	1.83E-05	/	Unknown
AL5G17680	1.46	1.63E-03	3.69E-02	AT3G28190	unknown protein
AL8G10590	1.46	5.74E-06	4.42E-04	AT5G47440	Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region
AL1G49860	1.46	3.63E-07	4.35E-05	AT1G35140	EXL7, PHI-1, Phosphate-responsive 1 family protein
AL1G39900	1.45	2.31E-08	4.14E-06	AT3G20370	TRAF-like family protein
AL3G40520	1.44	2.07E-08	3.80E-06	AT5G13210	Uncharacterised conserved protein UCP015417, vWA
AL8G11730	1.44	2.08E-03	4.49E-02	AT5G46610	Aluminium activated malate transporter family protein
AL1G29540	1.44	1.19E-04	5.03E-03	AT1G17285	unknown protein
AL2G14990	1.44	2.03E-07	2.62E-05	AT1G61340	F-box family protein
AL8G26690	1.44	1.86E-07	2.44E-05	AT5G52300	LTI65, RD29B, CAP160 protein
AL7G29940	1.44	3.60E-05	1.92E-03	AT4G23510	Disease resistance protein (TIR-NBS-LRR class) family
AL3G21100	1.43	9.79E-05	4.30E-03	AT3G09870	SAUR-like auxin-responsive protein family
AL6G35930	1.43	3.72E-04	1.20E-02	/	Unknown
AL6G37680	1.43	2.37E-09	5.11E-07	AT5G25810	tny, Integrase-type DNA-binding superfamily protein
AL1G37510	1.43	7.27E-05	3.37E-03	AT1G23760	JP630, PG3, BURP domain-containing protein
AL5G23450	1.43	8.00E-08	1.22E-05	AT3G44990	ATXTR8, XTH31, XTR8, xyloglucan endo-transglycosylase-related 8
AL3G47900	1.42	9.31E-05	4.11E-03	/	Unknown
AL6G17820	1.42	2.93E-05	1.62E-03	/	Unknown
AL7G28970	1.42	1.61E-07	2.19E-05	AT4G24275	Identified as a screen for stress-responsive genes.
AL4G30400	1.41	6.92E-05	3.24E-03	AT2G34430	LHB1B1, LHCB1.4, light-harvesting chlorophyll-protein complex II subunit B1
AL2G15710	1.41	5.45E-04	1.60E-02	AT5G28740	Tetratricopeptide repeat (TPR)-like superfamily protein
AL4G11130	1.40	2.77E-08	4.77E-06	AT2G21820	unknown protein
AL8G23150	1.40	9.66E-06	6.86E-04	/	Unknown
AL1G18740	1.40	3.10E-07	3.82E-05	AT1G08320	bZIP21, TGA9, bZIP transcription factor family protein
AL7G44940	1.40	4.94E-09	1.03E-06	/	Unknown
AL3G36910	1.40	2.28E-03	4.78E-02	AT3G22620	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL3G35530	1.39	5.82E-05	2.82E-03	AT3G21460	Glutaredoxin family protein
AL4G45900	1.39	6.38E-07	7.18E-05	AT2G46495	RING/U-box superfamily protein
AL1G39840	1.39	2.33E-04	8.42E-03	AT1G25460	NAD(P)-binding Rossmann-fold superfamily protein
AL3G52480	1.39	3.03E-04	1.04E-02	/	Unknown
AL7G25450	1.38	3.76E-05	1.97E-03	AT4G27350	Protein of unknown function (DUF1223)
AL8G10350	1.38	2.48E-08	4.40E-06	AT5G47610	RING/U-box superfamily protein
AL3G36540	1.38	2.30E-03	4.81E-02	AT3G22275	unknown protein
AL3G34400	1.38	3.22E-05	1.76E-03	AT3G44770	Protein of unknown function (DUF626)
AL1G30570	1.37	1.32E-04	5.40E-03	AT1G18200	AtRABA6b, RABA6b, RAB GTPase homolog A6B
AL6G33860	1.37	5.28E-05	2.59E-03	AT1G30790	F-box and associated interaction domains-containing protein
AL6G15060	1.37	2.45E-04	8.72E-03	AT5G05220	unknown protein
AL1G11450	1.37	1.82E-07	2.41E-05	AT1G01070	nodulin MtN21 /EamA-like transporter family protein
AL7G19100	1.37	1.97E-04	7.43E-03	/	Unknown
AL3G26760	1.37	1.65E-07	2.22E-05	AT3G14395	unknown protein
AL5G42680	1.36	2.50E-04	8.86E-03	AT3G50050	Eukaryotic aspartyl protease family protein
AL6G12410	1.36	5.96E-07	6.83E-05	AT1G79640	Protein kinase superfamily protein
AL5G31980	1.35	1.56E-03	3.60E-02	AT3G51540	unknown protein
AL8G15890	1.35	1.73E-06	1.68E-04	AT5G44130	FLA13, FASCICLIN-like arabinogalactan protein 13 precursor
AL4G30570	1.35	1.36E-09	3.10E-07	AT2G34590	Transketolase family protein
AL3G13920	1.35	1.61E-06	1.59E-04	AT3G04010	O-Glycosyl hydrolases family 17 protein
AL2G12760	1.35	2.92E-06	2.55E-04	AT1G62935	unknown protein
AL4G43410	1.34	4.46E-04	1.37E-02	AT3G04610	FLK, RNA-binding KH domain-containing protein
AL8G13930	1.34	5.98E-04	1.72E-02	AT4G36140	disease resistance protein (TIR-NBS-LRR class), putative
AL2G23260	1.34	2.67E-08	4.67E-06	AT1G65880	BZO1, benzoyloxyglucosinolate 1
AL6G45190	1.34	1.32E-03	3.14E-02	AT4G11050	AtGH9C3, GH9C3, glycosyl hydrolase 9C3

AL7G25050	1.33	9.60E-04	2.46E-02	AT4G27657	unknown protein
AL4G36670	1.33	2.34E-05	1.38E-03	AT2G39330	JAL23, jacalin-related lectin 23
AL363U10010	1.33	1.20E-03	2.92E-02	AT5G50090	unknown protein
AL5G17130	1.32	2.21E-06	2.05E-04	AT3G27690	LHCB2, LHCB2.3, LHCB2.4, photosystem II light harvesting complex gene 2.3
AL1G10830	1.32	1.02E-04	4.42E-03	AT1G01570	Protein of unknown function (DUF604)
AL2G37220	1.32	1.85E-06	1.76E-04	AT1G77060	Phosphoenolpyruvate carboxylase family protein
AL226U10010	1.32	8.22E-04	2.19E-02	AT5G53045	unknown protein
AL8G23010	1.32	1.47E-07	2.04E-05	AT5G49360	ATBXL1, BXL1, beta-xylosidase 1
AL7G52950	1.31	1.53E-04	6.11E-03	AT5G38010	UDP-Glycosyltransferase superfamily protein
AL7G38180	1.31	1.30E-04	5.34E-03	AT5G66510	GAMMA CA3, gamma carbonic anhydrase 3
AL3G26490	1.31	1.12E-07	1.62E-05	AT3G14210	ESM1, epithiospecifier modifier 1
AL3G12220	1.31	2.36E-03	4.90E-02	AT3G02810	Protein kinase superfamily protein
AL2G32120	1.31	2.47E-04	8.80E-03	/	Unknown
AL8G37810	1.31	2.26E-06	2.09E-04	AT5G61160	AACT1, anthocyanin 5-aromatic acyltransferase 1
AL5G24610	1.31	2.23E-06	2.07E-04	AT2G39570	ACT domain-containing protein
AL7G27250	1.31	5.09E-04	1.52E-02	AT4G25790	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein
AL6G10020	1.30	1.28E-06	1.31E-04	AT5G01015	unknown protein
AL2G37850	1.30	1.03E-04	4.47E-03	AT1G77640	Integrase-type DNA-binding superfamily protein
AL4G31770	1.30	1.04E-04	4.49E-03	AT2G35690	ACX5, acyl-CoA oxidase 5
AL3G12980	1.29	1.34E-03	3.18E-02	AT3G03341	unknown protein
AL5G27770	1.29	7.10E-04	1.96E-02	AT3G48360	ATBT2, BT2, BTB and TAZ domain protein 2
AL8G25140	1.28	3.37E-07	4.10E-05	AT5G50950	FUM2, FUMARASE 2
AL1G47890	1.28	9.06E-04	2.36E-02	AT1G33500	unknown protein
AL6G32660	1.28	4.66E-06	3.72E-04	AT5G21080	Uncharacterized protein
AL1G47370	1.28	2.94E-06	2.56E-04	AT1G33055	unknown protein
AL4G19710	1.28	3.08E-06	2.65E-04	/	Unknown
AL7G31160	1.28	5.86E-05	2.84E-03	AT4G22460	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL1G58780	1.27	1.02E-03	2.56E-02	AT1G51000	unknown protein
AL3G37800	1.27	2.11E-03	4.53E-02	AT3G23175	HR-like lesion-inducing protein-related
AL2G24250	1.27	3.88E-04	1.24E-02	AT1G59930	MADS-box family protein
AL1G52490	1.27	1.06E-04	4.56E-03	AT1G44830	Integrase-type DNA-binding superfamily protein
AL4G25930	1.27	1.06E-03	2.66E-02	AT5G60590	DHBP synthase RibB-like alpha/beta domain
AL6G47290	1.26	1.55E-04	6.18E-03	AT4G12410	SAUR-like auxin-responsive protein family
AL2G33100	1.26	1.39E-03	3.26E-02	AT1G73330	ATDR4, DR4, drought-repressed 4
AL5G31020	1.26	1.71E-06	1.67E-04	AT3G50800	unknown protein
AL7G21850	1.25	2.96E-05	1.63E-03	AT4G30290	ATXTH19, XTH19, xyloglucan endotransglucosylase/hydrolase 19
AL8G12560	1.25	7.19E-06	5.32E-04	AT5G45960	GDSL-like Lipase/Acylhydrolase superfamily protein
AL8G16100	1.24	2.40E-03	4.98E-02	AT5G44000	Glutathione S-transferase family protein
AL6G22890	1.24	1.74E-07	2.31E-05	AT5G12110	Glutathione S-transferase, C-terminal-like;Translation elongation factor EF1B/ribosomal protein S6
AL3G40550	1.23	6.74E-04	1.88E-02	AT3G24780	Uncharacterised conserved protein UCP015417, vWA
AL2G27080	1.23	5.85E-04	1.69E-02	AT1G68238	unknown protein
AL8G41020	1.23	1.56E-08	2.96E-06	AT5G63800	BGAL6, MUM2, Glycosyl hydrolase family 35 protein
AL1G15590	1.23	2.22E-03	4.69E-02	AT1G05680	UGT74E2, Uridine diphosphate glycosyltransferase 74E2
AL6G13110	1.23	9.16E-05	4.05E-03	AT5G03600	SGNH hydrolase-type esterase superfamily protein
AL6G35280	1.22	2.77E-08	4.77E-06	AT5G23950	Calcium-dependent lipid-binding (CaLB domain) family protein
AL8G17090	1.22	7.67E-07	8.33E-05	AT5G43300	PLC-like phosphodiesterases superfamily protein
AL7G51480	1.22	6.77E-04	1.89E-02	AT5G38940	RmlC-like cupins superfamily protein
AL8G36400	1.22	2.37E-05	1.39E-03	AT5G59845	Gibberellin-regulated family protein
AL2G21000	1.22	9.42E-09	1.85E-06	ATCG00080	PSBI, photosystem II reaction center protein I
AL3G35680	1.22	6.61E-05	3.11E-03	AT3G21570	unknown protein
AL8G19800	1.22	1.15E-07	1.66E-05	AT5G47830	unknown protein
AL3G12940	1.21	1.21E-07	1.73E-05	AT3G03310	ATLCAT3, LCAT3, lecithin:cholesterol acyltransferase 3
AL5G20030	1.21	1.55E-03	3.57E-02	/	Unknown
AL1G56080	1.20	3.62E-07	4.35E-05	AT1G49210	RING/U-box superfamily protein
AL8G36190	1.20	1.43E-04	5.78E-03	/	Unknown
AL8G10930	1.20	9.72E-05	4.27E-03	AT5G47160	YDG/SRA domain-containing protein
AL1G56190	1.19	1.11E-07	1.62E-05	AT1G49320	ATUSPL1, USPL1, unknown seed protein like 1
AL5G24680	1.19	5.12E-07	5.97E-05	AT3G45970	ATEXLA1, ATEXPL1, ATHEXP BETA 2.1, EXLA1, EXPL1, expansin-like A1
AL8G33540	1.19	2.73E-06	2.42E-04	AT5G57560	TCH4, XTH22, Xyloglucan endotransglucosylase/hydrolase family protein
AL8G31680	1.19	3.90E-05	2.03E-03	AT5G56100	glycine-rich protein / oleosin
AL1G31160	1.19	1.83E-04	7.00E-03	AT1G18710	AtMYB47, MYB47, myb domain protein 47
AL6G26230	1.19	7.17E-07	7.91E-05	AT5G15350	AtENODL17, ENODL17, early nodulin-like protein 17
AL6G42680	1.18	1.24E-05	8.47E-04	AT4G08870	Arginase/deacetylase superfamily protein
AL3G31410	1.18	1.16E-03	2.85E-02	/	Unknown
AL2G13430	1.18	6.62E-05	3.12E-03	AT1G62440	LRX2, leucine-rich repeat/extensin 2
AL6G28380	1.18	2.03E-05	1.23E-03	AT5G17300	RVE1, Homeodomain-like superfamily protein
AL8G15170	1.17	8.14E-05	3.68E-03	/	Unknown
AL1G41350	1.17	1.25E-05	8.53E-04	/	Unknown
AL7G21220	1.17	1.96E-03	4.28E-02	AT4G30880	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL1G39750	1.17	6.28E-06	4.77E-04	AT1G25550	myb-like transcription factor family protein
AL6G37560	1.17	4.34E-04	1.34E-02	AT1G65790	ARK1, RK1, receptor kinase 1
AL7G39730	1.15	9.67E-04	2.48E-02	AT4G15700	Thioredoxin superfamily protein
AL6G42390	1.15	9.26E-07	9.80E-05	AT4G08590	ORL1, ORL1, ORTHL, VIM6, ORTHRUS-like
AL6G27250	1.15	5.47E-04	1.60E-02	AT5G16350	O-acyltransferase (WSD1-like) family protein
AL4G18160	1.15	1.87E-03	4.13E-02	AT2G26000	BRIZ2, zinc finger (C3HC4-type RING finger) family protein
AL1G64600	1.15	5.73E-07	6.58E-05	AT5G48920	TED7, tracheary element differentiation-related 7
AL4G12300	1.15	4.93E-06	3.87E-04	AT2G22770	NAI1, basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AL7G13980	1.15	7.89E-06	5.77E-04	AT4G37180	Homeodomain-like superfamily protein

AL6G11470	1.15	2.41E-07	3.04E-05	AT5G02230	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
AL5G25090	1.14	1.87E-03	4.13E-02	/	Unknown
AL1G56180	1.14	9.45E-06	6.72E-04	AT1G49310	unknown protein
AL1G41840	1.14	8.18E-07	8.77E-05	AT1G28290	AGP31, arabinogalactan protein 31
AL1G37720	1.14	2.41E-06	2.19E-04	AT1G23970	Protein of unknown function (DUF626)
AL7G46600	1.13	1.68E-05	1.07E-03	AT2G32400	ATGLR3.7, GLR3.7, GLR5, glutamate receptor 5
AL6G42730	1.13	1.58E-05	1.03E-03	AT4G08870	Arginase/deacetylase superfamily protein
AL5G42350	1.12	1.55E-06	1.53E-04	AT3G60130	BGLU16, beta glucosidase 16
AL8G30590	1.12	1.17E-04	4.93E-03	AT5G55090	MAPKKK15, mitogen-activated protein kinase kinase kinase 15
AL6G46450	1.12	1.78E-06	1.71E-04	AT4G11740	SAY1, Ubiquitin-like superfamily protein
AL7G37190	1.12	1.17E-03	2.87E-02	AT4G17470	alpha/beta-Hydrolases superfamily protein
AL7G10330	1.12	2.68E-06	2.38E-04	AT4G38470	ACT-like protein tyrosine kinase family protein
AL1G60070	1.11	1.84E-04	7.02E-03	AT1G52030	F-ATMBP, MBP1.2, MBP2, myrosinase-binding protein 2
AL1G49700	1.10	4.62E-06	3.71E-04	AT1G31335	unknown protein
AL2G19220	1.10	1.14E-03	2.81E-02	AT1G64790	ILA, ILITYHIA
AL5G43730	1.10	4.49E-07	5.26E-05	AT3G61430	ATPIP1, PIP1, PIP1;1, PIP1A, plasma membrane intrinsic protein 1A
AL5G16510	1.10	1.27E-05	8.60E-04	AT3G27290	RNI-like superfamily protein
AL7G37690	1.09	6.38E-07	7.18E-05	AT4G17030	AT-EXPR, ATEXLB1, ATEXPR1, ATHEXP BETA 3.1, EXLB1, EXPR, expansin-like B1
AL2G10940	1.09	2.20E-05	1.33E-03	AT1G64110	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AL6G19930	1.09	3.86E-04	1.24E-02	AT5G09530	hydroxyproline-rich glycoprotein family protein
AL5G23740	1.09	7.18E-05	3.34E-03	AT5G58670	ATPLC, ATPLC1, PLC1, PLC1, phospholipase C1
AL5G26740	1.09	4.41E-06	3.59E-04	AT3G47510	unknown protein
AL6G11940	1.08	3.14E-04	1.06E-02	AT5G02640	unknown protein
AL9U11560	1.08	7.57E-06	5.55E-04	AT4G12970	EPFL9, STOMAGEN, stomagen
AL1G39920	1.08	5.25E-04	1.55E-02	AT1G25400	unknown protein
AL8G13770	1.07	1.95E-03	4.27E-02	AT5G45240	Disease resistance protein (TIR-NBS-LRR class)
AL8G25530	1.07	1.95E-05	1.20E-03	AT5G51270	U-box domain-containing protein kinase family protein
AL7G14390	1.07	8.44E-06	6.08E-04	/	Unknown
AL1G23520	1.07	4.43E-07	5.20E-05	AT1G12240	ATBETAFRUCT4, VAC-INV, Glycosyl hydrolases family 32 protein
AL4G24070	1.07	4.86E-05	2.43E-03	AT2G29470	ATGSTU3, GST21, GSTU3, glutathione S-transferase tau 3
AL2G34280	1.07	2.34E-04	8.45E-03	AT1G74430	ATMYB95, ATMYBCP66, MYB95, myb domain protein 95
AL6G30540	1.07	5.44E-05	2.66E-03	AT5G19120	Eukaryotic aspartyl protease family protein
AL1G56030	1.07	2.11E-06	1.98E-04	AT1G49160	WNK7, Protein kinase superfamily protein
AL3G33760	1.07	1.19E-05	8.21E-04	AT3G20100	CYP705A19, cytochrome P450, family 705, subfamily A, polypeptide 19
AL2G13190	1.07	2.13E-06	1.99E-04	AT1G62660	Glycosyl hydrolases family 32 protein
AL7G21250	1.06	1.73E-04	6.71E-03	AT4G30860	ASHR3, SDG4, SET domain group 4
AL8G29170	1.05	5.70E-04	1.65E-02	AT5G65600	Concanavalin A-like lectin protein kinase family protein
AL5G40850	1.05	7.09E-06	5.28E-04	/	Unknown
AL6G13800	1.05	2.25E-03	4.73E-02	AT5G04180	ACA3, ATACA3, alpha carbonic anhydrase 3
AL6G27780	1.05	1.62E-04	6.37E-03	/	Unknown
AL5G37570	1.05	5.65E-06	4.35E-04	AT3G56250	unknown protein
AL6G29530	1.05	1.93E-03	4.22E-02	AT5G18300	anac088, NAC088, NAC domain containing protein 88
AL4G27480	1.05	2.51E-05	1.45E-03	AT2G32100	ATOFP16, OFP16, ovate family protein 16
AL1G53690	1.04	8.05E-05	3.67E-03	/	Unknown
AL3G16650	1.04	1.87E-05	1.16E-03	AT3G05890	RCI2B, RARE-COLD-INDUCIBLE 2B, Low temperature and salt responsive protein family
AL7G17970	1.04	2.38E-06	2.17E-04	AT4G33550	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL7G36050	1.04	3.16E-05	1.73E-03	AT4G18340	Glycosyl hydrolase superfamily protein
AL6G46000	1.04	1.09E-04	4.66E-03	AT4G11470	CRK31, cysteine-rich RLK (RECEPTOR-like protein kinase) 31
AL8G10360	1.03	1.94E-03	4.24E-02	AT5G47590	Heat shock protein HSP20/alpha crystallin family
AL5G33030	1.03	7.21E-04	1.97E-02	AT3G52320	F-box and associated interaction domains-containing protein
AL4G36120	1.03	4.33E-06	3.54E-04	AT2G38820	Protein of unknown function (DUF506)
AL6G48300	1.03	6.00E-06	4.59E-04	AT4G04810	ATMSRB4, MSRB4, methionine sulfoxide reductase B4
AL3G45790	1.03	3.58E-05	1.91E-03	AT2G14095	unknown protein
AL5G19720	1.03	8.80E-04	2.31E-02	AT3G29635	HXXXD-type acyl-transferase family protein
AL3G27080	1.03	2.62E-06	2.34E-04	AT3G14770	Nodulin MtN3 family protein
AL9U10260	1.02	1.09E-03	2.71E-02	AT4G13395	DVL10, RTFL12, ROTUNDIFOLIA like 12
AL3G25800	1.02	2.42E-05	1.41E-03	AT3G13750	BGAL1, BGAL1, beta galactosidase 1
AL4G44170	1.02	1.21E-04	5.09E-03	AT2G45080	cycp3;1, cyclin p3;1
AL3G47370	1.02	7.09E-06	5.28E-04	AT2G15620	ATHNIR, NIR, NIR1, nitrite reductase 1
AL5G46170	1.02	6.46E-06	4.89E-04	AT3G63310	BIL4, Bax inhibitor-1 family protein
AL1G25990	1.02	9.91E-04	2.52E-02	AT1G14120	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AL4G28330	1.02	1.28E-04	5.29E-03	AT2G32830	PHT1;5, PHT5, phosphate transporter 1;5
AL7G30430	1.02	3.99E-04	1.26E-02	AT4G23070	ATRBL7, RBL7, RHOMBOID-like protein 7
AL5G36960	1.02	4.25E-04	1.32E-02	AT3G55710	UDP-Glycosyltransferase superfamily protein
AL8G35470	1.01	2.33E-05	1.38E-03	AT5G59220	HAI1, highly ABA-induced PP2C gene 1
AL2G37620	1.01	2.34E-03	4.88E-02	AT1G77410	BGAL16, beta-galactosidase 16
AL1G12730	1.01	4.78E-05	2.40E-03	AT1G03220	Eukaryotic aspartyl protease family protein
AL1G47870	1.01	5.50E-06	4.26E-04	AT1G33480	RING/U-box superfamily protein
AL4G12100	1.01	4.64E-06	3.72E-04	AT2G22560	Kinase interacting (KIP1-like) family protein
AL7G33290	1.01	6.83E-05	3.20E-03	AT4G20860	FAD-binding Berberine family protein
AL3G39970	1.00	3.72E-05	1.96E-03	AT3G24500	ATMBF1C, MBF1C, multiprotein bridging factor 1C
AL7G45400	1.00	8.68E-05	3.89E-03	AT2G26010	PDF1.3, plant defensin 1.3
AL6G26300	1.00	1.58E-05	1.03E-03	AT5G15450	APG6, CLPB-P, CLPB3, casein lytic proteinase B3
AL1G44130	0.99	4.90E-06	3.87E-04	AT1G30220	ATINT2, INT2, inositol transporter 2
AL2G27520	0.99	2.23E-05	1.34E-03	AT1G68600	Aluminium activated malate transporter family protein
AL3G12870	0.99	1.38E-05	9.24E-04	AT3G03270	Adenine nucleotide alpha hydrolases-like superfamily protein
AL6G13700	0.99	2.33E-05	1.38E-03	AT5G04070	NAD(P)-binding Rossmann-fold superfamily protein
AL2G37800	0.99	7.50E-06	5.53E-04	AT1G77590	LACS9, long chain acyl-CoA synthetase 9
AL8G38780	0.99	2.29E-05	1.36E-03	AT5G62020	AT-HSFB2A, HSFB2A, heat shock transcription factor B2A
AL7G16160	0.98	1.54E-04	6.14E-03	AT4G35060	Heavy metal transport/detoxification superfamily protein

AL6G37000	0.98	6.03E-05	2.90E-03	/	Unknown
AL3G15950	0.98	3.74E-05	1.97E-03	AT3G05400	Major facilitator superfamily protein
AL4G10310	0.98	1.01E-03	2.56E-02	AT2G21200	SAUR-like auxin-responsive protein family
AL1G36920	0.98	2.73E-04	9.50E-03	AT1G23205	Plant invertase/pectin methylesterase inhibitor superfamily protein
AL3G21670	0.97	3.26E-05	1.77E-03	AT3G10340	PAL4, phenylalanine ammonia-lyase 4
AL4G43210	0.97	1.17E-03	2.87E-02	AT2G44250	Protein of Unknown Function (DUF239)
AL5G20580	0.97	3.88E-06	3.21E-04	AT3G32980	Peroxidase superfamily protein
AL3G43930	0.97	1.31E-04	5.36E-03	AT5G35320	unknown protein
AL7G28790	0.96	2.33E-05	1.38E-03	AT4G24430	Rhamnogalacturonate lyase family protein
AL1G46160	0.96	4.99E-06	3.91E-04	AT1G32090	early-responsive to dehydration stress protein (ERD4)
AL2G35680	0.96	1.00E-04	4.38E-03	AT1G75700	HVA22G, HVA22-like protein G
AL6G14240	0.96	3.07E-04	1.04E-02	AT5G04610	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AL7G35870	0.96	1.35E-05	9.01E-04	AT4G18425	Protein of unknown function (DUF679)
AL2G10920	0.96	2.28E-03	4.77E-02	AT1G64110	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AL1G23220	0.95	4.16E-04	1.31E-02	AT1G12010	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AL8G37120	0.95	4.05E-04	1.28E-02	AT5G60530	late embryogenesis abundant protein-related / LEA protein-related
AL1G46170	0.95	3.15E-06	2.69E-04	AT1G32100	ATPRR1, PRR1, pinoresinol reductase 1
AL2G35740	0.95	2.67E-05	1.52E-03	AT1G75750	GASA1, GAST1 protein homolog 1
AL7G20690	0.95	3.68E-04	1.20E-02	AT4G31380	FLP1, FPF1-like protein 1
AL7G32170	0.95	1.23E-04	5.13E-03	AT4G21760	BGLU47, beta-glucosidase 47
AL1G19600	0.95	6.41E-04	1.82E-02	AT1G09155	AtPP2-B15, PP2-B15, phloem protein 2-B15
AL2G37990	0.95	8.45E-04	2.24E-02	AT1G77760	GNR1, NIA1, NR1, nitrate reductase 1
AL5G17900	0.95	1.74E-04	6.77E-03	AT3G28340	GATL10, galacturonosyltransferase-like 10
AL3G11240	0.94	1.58E-03	3.62E-02	AT3G01030	C2H2 and C2HC zinc fingers superfamily protein
AL3G28790	0.94	8.23E-05	3.71E-03	AT3G24600	Late embryogenesis abundant protein, group 2
AL7G34250	0.94	1.64E-05	1.06E-03	AT4G19830	FKBP-like peptidyl-prolyl cis-trans isomerase family protein
AL3G44300	0.94	1.24E-04	5.17E-03	/	Unknown
AL1G33000	0.94	1.46E-05	9.57E-04	AT1G20160	ATSBT5.2, Subtilisin-like serine endopeptidase family protein
AL8G45580	0.94	1.55E-05	1.01E-03	AT5G66040	STR16, sulfurtransferase protein 16
AL6G25520	0.94	1.23E-04	5.12E-03	AT5G14740	BETA CA2, CA18, CA2, carbonic anhydrase 2
AL6G14010	0.93	3.96E-05	2.05E-03	AT5G04370	NAMT1, S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AL7G29690	0.93	2.05E-04	7.64E-03	AT4G23670	Polyketide cyclase/dehydrase and lipid transport superfamily protein
AL3G23350	0.93	7.18E-04	1.97E-02	AT3G11773	Thioredoxin superfamily protein
AL7G28960	0.93	8.03E-06	5.85E-04	AT4G24280	cpHsc70-1, chloroplast heat shock protein 70-1
AL8G25730	0.93	4.10E-04	1.29E-02	AT5G51440	HSP20-like chaperones superfamily protein
AL3G53590	0.93	1.85E-05	1.15E-03	AT2G20560	DNAJ heat shock family protein
AL3G30400	0.93	1.74E-05	1.10E-03	AT3G17350	unknown protein
AL792U10010	0.93	1.44E-03	3.35E-02	AT5G51960	unknown protein
AL3G19990	0.92	4.79E-05	2.40E-03	AT3G08970	ATERDJ3A, TMS1, DNAJ heat shock N-terminal domain-containing protein
AL1G17500	0.92	2.34E-05	1.38E-03	AT1G07350	RNA-binding (RRM/RBD/RNP motifs) family protein
AL4G19700	0.92	2.46E-05	1.43E-03	AT2G26690	Major facilitator superfamily protein
AL1G63220	0.92	2.76E-05	1.55E-03	AT1G55180	PLDALPHA4, PLDEPSILON, phospholipase D alpha 4
AL5G35380	0.92	3.72E-04	1.20E-02	AT3G54340	AP3, ATAP3, K-box region and MADS-box transcription factor family protein
AL7G12870	0.92	2.63E-05	1.51E-03	AT4G37800	XTH7, xyloglucan endotransglucosylase/hydrolase 7
AL3G24230	0.92	5.97E-05	2.88E-03	AT3G12580	ATHSP70, HSP70, heat shock protein 70
AL6G10310	0.92	2.84E-04	9.83E-03	AT5G01740	Nuclear transport factor 2 (NTF2) family protein
AL6G32580	0.92	6.58E-04	1.85E-02	AT5G21030	PAZ domain-containing protein / piwi domain-containing protein
AL1G62750	0.91	2.24E-04	8.18E-03	AT1G54050	HSP20-like chaperones superfamily protein
AL5G27940	0.91	8.81E-04	2.31E-02	AT3G48510	unknown protein
AL1G37620	0.91	3.22E-05	1.76E-03	AT1G23870	ATTPS9, TPS9, TPS9, trehalose-phosphatase/synthase 9
AL2G28320	0.91	1.48E-05	9.71E-04	AT1G69230	SP1L2, SPIRAL1-like2
AL6G48310	0.91	1.63E-04	6.40E-03	AT4G04830	ATMSRB5, MSRB5, methionine sulfoxide reductase B5
AL4G30790	0.91	1.99E-04	7.45E-03	AT2G34810	FAD-binding Berberine family protein
AL6G32910	0.91	3.70E-04	1.20E-02	AT5G21950	alpha/beta-Hydrolases superfamily protein
AL1G54510	0.91	2.53E-04	8.93E-03	AT1G48000	AtMYB112, MYB112, myb domain protein 112
AL1G36390	0.91	1.74E-05	1.10E-03	AT1G22850	SNARE associated Golgi protein family
AL7G34410	0.91	3.40E-04	1.12E-02	AT4G19645	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein
AL5G28590	0.91	7.36E-05	3.39E-03	AT3G49070	Protein of unknown function (DUF677)
AL1G47090	0.90	1.29E-04	5.33E-03	AT1G32780	GroES-like zinc-binding dehydrogenase family protein
AL7G45600	0.90	6.59E-04	1.85E-02	AT5G36970	NHL25, NDR1/HIN1-like 25
AL6G42070	0.90	1.80E-04	6.90E-03	AT4G08300	nodulin MtN21 /EamA-like transporter family protein
AL6G26220	0.90	5.45E-05	2.66E-03	AT5G15340	Pentatricopeptide repeat (PPR) superfamily protein
AL6G32720	0.90	2.02E-05	1.23E-03	AT5G21105	Plant L-ascorbate oxidase
AL6G36670	0.89	2.92E-04	1.00E-02	/	Unknown
AL6G28390	0.89	2.72E-05	1.54E-03	AT5G17310	AtUGP2, UGP2, UDP-glucose pyrophosphorylase 2
AL5G31060	0.89	2.47E-05	1.43E-03	AT3G50820	OEC33, PSBO-2, PSBO2, photosystem II subunit O-2
AL8G37980	0.89	1.92E-03	4.22E-02	AT5G61320	CYP89A3, cytochrome P450, family 89, subfamily A, polypeptide 3
AL7G13710	0.89	3.56E-05	1.90E-03	AT4G36945	PLC-like phosphodiesterases superfamily protein
AL4G42320	0.89	1.73E-03	3.85E-02	AT2G43535	Scorpion toxin-like knottin superfamily protein
AL6G23980	0.89	9.97E-05	4.36E-03	AT5G13360	Auxin-responsive GH3 family protein
AL2G33060	0.88	2.44E-04	8.71E-03	AT1G73260	ATKTI1, KTI1, kunitz trypsin inhibitor 1
AL1G56260	0.88	8.96E-04	2.34E-02	AT1G49320	ATUSPL1, USPL1, unknown seed protein like 1
AL4G30950	0.88	3.83E-04	1.23E-02	AT2G34930	disease resistance family protein / LRR family protein
AL8G18360	0.88	4.70E-05	2.37E-03	AT5G42760	Leucine carboxyl methyltransferase
AL6G18820	0.88	8.10E-05	3.68E-03	AT5G08380	AGAL1, AtAGAL1, alpha-galactosidase 1
AL6G32690	0.88	1.29E-03	3.07E-02	AT5G21080	Uncharacterized protein
AL1G40040	0.88	1.76E-04	6.80E-03	AT5G05020	Pollen Ole e 1 allergen and extensin family protein
AL7G44130	0.88	6.47E-05	3.08E-03	AT5G35320	unknown protein
AL7G33330	0.88	9.32E-04	2.41E-02	AT4G20820	FAD-binding Berberine family protein
AL8G31730	0.88	1.11E-03	2.73E-02	AT5G56100	glycine-rich protein / oleosin

AL3G21500	0.88	1.91E-03	4.20E-02	AT3G10185	Gibberellin-regulated family protein
AL1G29190	0.88	6.02E-04	1.73E-02	AT1G17030	unknown protein
AL1G43470	0.88	1.62E-04	6.38E-03	AT1G29640	Protein of unknown function, DUF584
AL7G25380	0.88	4.40E-05	2.24E-03	AT4G27410	ATRD26, RD26, Responsive to dessication 26, NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
AL3G44750	0.87	1.81E-03	4.01E-02	AT2G10940	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL1G57610	0.87	5.85E-04	1.69E-02	AT1G50040	Protein of unknown function (DUF1005)
AL7G17030	0.87	1.12E-04	4.76E-03	AT4G34260	FUC95A, 1,2-alpha-L-fucosidases
AL6G26100	0.87	1.01E-04	4.41E-03	AT5G15240	Transmembrane amino acid transporter family protein
AL7G25250	0.87	2.85E-05	1.58E-03	AT4G27520	AtENODL2, ENODL2, early nodulin-like protein 2
AL5G15240	0.87	2.90E-04	9.96E-03	AT3G26460	Polyketide cyclase/dehydrase and lipid transport superfamily protein
AL1G34700	0.86	6.80E-04	1.89E-02	AT1G21550	Calcium-binding EF-hand family protein
AL6G11950	0.86	1.91E-03	4.20E-02	AT5G02710	unknown protein
AL8G23990	0.86	1.91E-03	4.20E-02	AT5G50010	sequence-specific DNA binding transcription factors;transcription regulators
AL5G26800	0.86	1.29E-04	5.33E-03	AT3G47560	alpha/beta-Hydrolases superfamily protein
AL1G43770	0.86	1.28E-04	5.29E-03	AT1G29930	AB140, CAB1, CAB140, LHCB1.3, chlorophyll A/B binding protein 1
AL7G28020	0.85	2.78E-05	1.55E-03	AT4G25130	PMSR4, peptide met sulfoxide reductase 4
AL7G35590	0.85	7.03E-04	1.94E-02	AT4G18670	Leucine-rich repeat (LRR) family protein
AL3G25430	0.85	1.06E-04	4.55E-03	AT3G13520	AGP12, ATAGP12, arabinogalactan protein 12
AL2G31760	0.85	7.46E-04	2.02E-02	AT1G72130	Major facilitator superfamily protein
AL6G17250	0.85	8.08E-05	3.67E-03	AT5G07080	HXXXD-type acyl-transferase family protein
AL5G33110	0.85	6.47E-04	1.83E-02	AT3G52460	hydroxyproline-rich glycoprotein family protein
AL7G22340	0.85	1.59E-04	6.28E-03	AT4G29905	unknown protein
AL6G12600	0.85	1.85E-04	7.03E-03	AT5G03280	ATEIN2, CKR1, EIN2, ERA3, ORE2, ORE3, PIR2, NRAMP metal ion transporter family protein
AL3G11460	0.85	1.55E-04	6.18E-03	AT3G02210	COBL1, COBRA-like protein 1 precursor
AL4G24190	0.85	1.21E-03	2.93E-02	AT2G29490	ATGSTU1, GST19, GSTU1, glutathione S-transferase TAU 1
AL8G39690	0.85	3.97E-04	1.26E-02	AT5G62720	Integral membrane HPP family protein
AL3G32280	0.85	1.77E-04	6.83E-03	AT3G18890	NAD(P)-binding Rossmann-fold superfamily protein
AL7G21690	0.84	3.38E-04	1.12E-02	AT4G30460	glycine-rich protein
AL6G24720	0.84	3.37E-04	1.11E-02	AT5G14060	CARAB-AK-LYS, Aspartate kinase family protein
AL2G33650	0.84	1.52E-04	6.09E-03	AT1G73830	BEE3, BR enhanced expression 3
AL7G13340	0.84	2.15E-04	7.92E-03	AT4G37450	AGP18, ATAGP18, arabinogalactan protein 18
AL8G42510	0.83	1.15E-04	4.85E-03	AT5G65010	ASN2, asparagine synthetase 2
AL1G12210	0.83	6.74E-04	1.88E-02	AT1G02820	Late embryogenesis abundant 3 (LEA3) family protein
AL8G27480	0.83	1.33E-04	5.44E-03	AT5G52970	thylakoid lumen 15.0 kDa protein
AL1G14410	0.83	2.55E-04	8.95E-03	AT1G04700	PB1 domain-containing protein tyrosine kinase
AL1G65300	0.83	1.35E-03	3.19E-02	AT1G54840	HSP20-like chaperones superfamily protein
AL3G39800	0.83	1.76E-04	6.80E-03	AT3G24340	chr40, chromatin remodeling 40
AL7G40230	0.83	2.73E-04	9.50E-03	AT3G30280	HXXXD-type acyl-transferase family protein
AL2G17850	0.83	2.55E-04	8.95E-03	AT1G58370	Arabidopsis thaliana XYLANASE 1, ATXYN1, RXF12
AL4G36480	0.82	2.05E-03	4.43E-02	AT2G39180	ATCRR2, CCR2, CRINKLY4 related 2
AL7G10580	0.82	8.82E-05	3.94E-03	AT4G38690	PLC-like phosphodiesterases superfamily protein
AL2G10030	0.82	1.20E-04	5.05E-03	AT1G64720	CP5, Polyketide cyclase/dehydrase and lipid transport superfamily protein
AL6G52180	0.82	2.53E-04	8.92E-03	AT4G01200	Calcium-dependent lipid-binding (CaLB domain) family protein
AL3G22570	0.82	5.16E-04	1.54E-02	AT3G11020	DREB2, DREB2B, DRE/CRT-binding protein 2B
AL1G41810	0.82	1.16E-04	4.89E-03	AT1G28260	Telomerase activating protein Est1
AL6G41580	0.82	2.15E-04	7.92E-03	AT4G08950	EXO, Phosphate-responsive 1 family protein
AL6G34060	0.82	1.06E-03	2.64E-02	AT5G22920	CHY-type/CTCHY-type/RING-type Zinc finger protein
AL7G46390	0.81	8.91E-04	2.33E-02	AT3G02580	BUL1, DWF7, STE1, sterol 1
AL8G37250	0.81	4.17E-04	1.31E-02	AT5G60660	PIP2;4, PIP2F, plasma membrane intrinsic protein 2;4
AL2G34170	0.81	1.09E-03	2.70E-02	AT1G74310	ATHSP101, HOT1, HSP101, heat shock protein 101
AL8G16060	0.81	5.84E-04	1.69E-02	AT5G44020	HAD superfamily, subfamily IIIB acid phosphatase
AL6G41270	0.81	1.24E-03	2.98E-02	AT4G06744	Leucine-rich repeat (LRR) family protein
AL3G26480	0.81	1.70E-04	6.65E-03	AT1G54030	MVP1, GDSL-like Lipase/Acylhydrolase superfamily protein
AL5G17110	0.81	1.66E-03	3.74E-02	AT3G27690	LHCB2, LHCB2.3, LHCB2.4, photosystem II light harvesting complex gene 2.3
AL6G27980	0.81	1.56E-04	6.19E-03	AT5G16970	AER, AT-AER, alkenal reductase
AL2G37690	0.81	3.03E-04	1.04E-02	AT1G77490	TAPX, thylakoidal ascorbate peroxidase
AL1G66190	0.80	9.55E-04	2.46E-02	AT1G09200	Histone superfamily protein
AL1G23270	0.80	3.37E-04	1.12E-02	AT1G12030	Protein of unknown function (DUF506)
AL5G34980	0.80	1.05E-04	4.52E-03	AT3G53980	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL1G40640	0.80	5.47E-04	1.60E-02	AT1G24280	G6PD3, glucose-6-phosphate dehydrogenase 3
AL4G14090	0.80	3.24E-04	1.08E-02	AT2G24040	Low temperature and salt responsive protein family
AL1G31730	0.80	2.96E-04	1.01E-02	AT1G19150	LHCA2*1, LHCA6, photosystem I light harvesting complex gene 6
AL6G12290	0.80	8.04E-04	2.15E-02	AT5G03000	Galactose oxidase/kelch repeat superfamily protein
AL7G12200	0.80	1.02E-03	2.58E-02	AT4G39950	CYP79B2, cytochrome P450, family 79, subfamily B, polypeptide 2
AL1G63930	0.80	4.31E-04	1.33E-02	AT1G55810	UKL3, uridine kinase-like 3
AL3G43880	0.80	4.93E-04	1.48E-02	AT2G06850	EXGT-A1, EXT, XTH4, xyloglucan endotransglucosylase/hydrolase 4
AL4G12640	0.79	3.49E-04	1.14E-02	AT2G22990	SCPL8, SNG1, sinapoylglucose 1
AL8G43890	0.79	5.60E-04	1.63E-02	AT5G67420	ASL39, LBD37, LOB domain-containing protein 37
AL8G40560	0.79	1.90E-04	7.22E-03	AT5G63500	Protein of unknown function (DUF 3339)
AL3G12780	0.79	8.08E-04	2.16E-02	AT3G03170	unknown protein
AL4G21550	0.79	5.89E-04	1.70E-02	AT2G28470	BGAL8, beta-galactosidase 8
AL7G49980	0.79	6.18E-04	1.76E-02	AT5G40020	Pathogenesis-related thaumatin superfamily protein
AL8G33700	0.79	3.35E-04	1.11E-02	AT5G57670	Protein kinase superfamily protein
AL4G43220	0.79	2.52E-04	8.89E-03	AT2G44260	Plant protein of unknown function (DUF946)
AL6G17000	0.78	4.80E-04	1.45E-02	AT5G06870	ATPGIP2, PGIP2, polygalacturonase inhibiting protein 2
AL7G10590	0.78	1.65E-03	3.73E-02	AT4G38700	Disease resistance-responsive (dirigent-like protein) family protein
AL7G27390	0.78	2.04E-04	7.60E-03	AT4G25690	unknown protein
AL5G30390	0.78	3.87E-04	1.24E-02	AT3G50270	HXXXD-type acyl-transferase family protein

AL7G28030	0.78	2.19E-04	8.03E-03	AT4G25120	ATSRS2, SRS2, P-loop containing nucleoside triphosphate hydrolases superfamily protein
AL1G20450	0.78	1.54E-04	6.16E-03	AT1G09850	XBCP3, xylem bark cysteine peptidase 3
AL6G53520	0.78	2.38E-03	4.93E-02	AT2G44840	ATERF13, EREBP, ERF13, ethylene-responsive element binding factor 13
AL1G29650	0.77	1.62E-03	3.67E-02	AT1G17380	JAZ5, TIFY11A, jasmonate-zim-domain protein 5
AL4G43260	0.77	1.70E-04	6.65E-03	AT2G44300	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL3G12450	0.77	6.65E-04	1.86E-02	AT3G02990	ATHSFA1E, HSFA1E, heat shock transcription factor A1E
AL5G23660	0.77	2.00E-03	4.35E-02	AT3G45140	ATLOX2, LOX2, lipoxygenase 2
AL8G39000	0.77	7.13E-04	1.96E-02	AT5G62180	AtCXE20, CXE20, carboxyesterase 20
AL7G16300	0.77	1.99E-04	7.45E-03	AT4G34920	PLC-like phosphodiesterases superfamily protein
AL1G58470	0.77	7.03E-04	1.94E-02	AT1G50732	unknown protein.
AL5G35300	0.77	5.71E-04	1.66E-02	AT3G54260	TBL36, TRICHOME BIREFRINGENCE-LIKE 36
AL4G40580	0.77	3.56E-04	1.16E-02	AT2G42220	Rhodanese/Cell cycle control phosphatase superfamily protein
AL3G47210	0.76	8.51E-04	2.25E-02	AT2G15490	UGT73B4, UDP-glycosyltransferase 73B4
AL1G62070	0.76	1.75E-03	3.89E-02	AT1G53520	Chalcone-flavanone isomerase family protein
AL1G28300	0.76	3.16E-04	1.06E-02	AT1G16170	unknown protein
AL3G49470	0.76	1.68E-03	3.78E-02	AT4G36580	AAA-type ATPase family protein
AL3G39170	0.76	2.89E-04	9.96E-03	AT3G24100	Uncharacterised protein family SERF
AL4G10330	0.76	9.24E-04	2.39E-02	AT2G21210	SAUR-like auxin-responsive protein family
AL1G13730	0.76	3.86E-04	1.24E-02	AT1G04130	Tetratricopeptide repeat (TPR)-like superfamily protein
AL6G45440	0.76	4.44E-04	1.36E-02	AT4G11220	BTI2, RTNLB2, VIRB2-interacting protein 2
AL4G27930	0.76	1.44E-03	3.36E-02	AT2G32540	ATCSLB04, ATCSLB4, CSLB04, CSLB04, cellulose synthase-like B4
AL6G41510	0.76	3.78E-04	1.22E-02	AT4G09010	APX4, TL29, ascorbate peroxidase 4
AL6G12570	0.76	4.60E-04	1.40E-02	AT5G03260	LAC11, laccase 11
AL5G37520	0.75	8.47E-04	2.24E-02	AT3G56200	Transmembrane amino acid transporter family protein
AL1G52860	0.75	1.38E-03	3.25E-02	AT1G45201	ATTLL1, TLL1, triacylglycerol lipase-like 1
AL2G10800	0.75	8.39E-04	2.23E-02	AT1G64200	VHA-E3, vacuolar H+-ATPase subunit E isoform 3
AL3G19420	0.75	8.21E-04	2.19E-02	AT3G08030	Protein of unknown function, DUF642
AL3G33340	0.75	3.50E-04	1.15E-02	AT3G19830	NTMC2T5.2, NTMC2TYPE5.2, Calcium-dependent lipid-binding (CaLB domain) family protein
AL5G46290	0.75	1.04E-03	2.61E-02	AT3G63430	unknown protein
AL271U10010	0.74	8.88E-04	2.32E-02	/	Unknown
AL1G50570	0.74	6.44E-04	1.82E-02	AT1G35680	Ribosomal protein L21
AL3G10690	0.74	5.46E-04	1.60E-02	AT3G01480	ATCYP38, CYP38, cyclophilin 38
AL8G44470	0.74	5.69E-04	1.65E-02	AT5G66920	sks17, SKU5 similar 17
AL6G13820	0.74	5.66E-04	1.65E-02	AT5G04200	AtMC9, MC9, metacaspase 9
AL6G20970	0.74	3.22E-04	1.08E-02	AT5G10460	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
AL3G27120	0.74	5.68E-04	1.65E-02	AT3G14810	MSL5, mechanosensitive channel of small conductance-like 5
AL5G11380	0.74	4.33E-04	1.34E-02	AT2G02130	LCR68, PDF2.3, low-molecular-weight cysteine-rich 68
AL6G27610	0.74	1.21E-03	2.93E-02	/	Unknown
AL6G24030	0.74	3.20E-04	1.07E-02	AT5G13410	FKBP-like peptidyl-prolyl cis-trans isomerase family protein
AL1G43140	0.74	1.51E-03	3.50E-02	AT1G29320	Transducin/WD40 repeat-like superfamily protein
AL7G25560	0.74	1.13E-03	2.78E-02	AT4G27260	GH3.5, WES1, Auxin-responsive GH3 family protein
AL5G39100	0.73	6.49E-04	1.83E-02	AT3G57520	AtSIP2, SIP2, seed imbibition 2
AL6G48700	0.73	8.80E-04	2.31E-02	AT4G05100	AtMYB74, MYB74, myb domain protein 74
AL1G19680	0.73	6.74E-04	1.88E-02	AT1G09200	Histone superfamily protein
AL1G37120	0.73	7.16E-04	1.97E-02	AT1G23330	alpha/beta-Hydrolases superfamily protein
AL1G51910	0.73	3.94E-04	1.25E-02	AT1G43790	TED6, tracheary element differentiation-related 6
AL1G38770	0.73	5.13E-04	1.53E-02	AT1G26820	RNS3, ribonuclease 3
AL4G24940	0.73	2.11E-03	4.53E-02	/	Unknown
AL7G29230	0.73	1.33E-03	3.16E-02	AT4G24050	NAD(P)-binding Rossmann-fold superfamily protein
AL8G11620	0.73	5.07E-04	1.51E-02	AT5G46730	glycine-rich protein
AL4G11820	0.73	1.48E-03	3.43E-02	AT2G22330	CYP79B3, cytochrome P450, family 79, subfamily B, polypeptide 3
AL2G38310	0.72	5.86E-04	1.69E-02	AT1G77990	AST56, SULTR2;2, STAS domain / Sulfate transporter family
AL2G28960	0.72	8.92E-04	2.33E-02	AT1G69770	CMT3, chromomethylase 3
AL3G28100	0.72	1.45E-03	3.37E-02	AT3G15520	Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein
AL4G45480	0.72	9.18E-04	2.39E-02	AT2G46220	Uncharacterized conserved protein (DUF2358)
AL4G30780	0.72	5.25E-04	1.55E-02	AT2G34790	EDA28, MEE23, FAD-binding Berberine family protein
AL6G53260	0.72	5.44E-04	1.60E-02	AT4G00230	XSP1, xylem serine peptidase 1
AL6G24240	0.72	6.13E-04	1.75E-02	AT5G13630	ABAR, CCH, CCH1, CHLH, GUN5, magnesium-chelatase subunit chlH, chloroplast, putative / Mg-protoporphyrin IX chelatase, putative (CHLH)
AL1G50630	0.72	1.72E-03	3.84E-02	AT1G35720	ANNAT1, ATOXY5, OXY5, annexin 1
AL7G15830	0.72	9.79E-04	2.50E-02	AT4G35320	unknown protein
AL3G19850	0.72	2.36E-03	4.90E-02	AT3G08860	PYD4, PYRIMIDINE 4
AL6G27620	0.72	9.95E-04	2.53E-02	/	Unknown
AL7G35800	0.71	7.38E-04	2.01E-02	AT4G18480	CH-42, CH42, CHL11, CHLI-1, CHLI1, P-loop containing nucleoside triphosphate hydrolases superfamily protein
AL4G28130	0.71	1.33E-03	3.15E-02	AT2G32690	ATGRP23, GRP23, glycine-rich protein 23
AL5G16160	0.71	6.30E-04	1.79E-02	AT3G27050	unknown protein
AL4G20840	0.71	1.67E-03	3.76E-02	AT2G27130	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL6G24790	0.71	7.12E-04	1.96E-02	AT5G14120	Major facilitator superfamily protein
AL1G46800	0.71	5.51E-04	1.61E-02	AT1G32550	2Fe-2S ferredoxin-like superfamily protein
AL4G16310	0.71	2.07E-03	4.47E-02	AT2G25140	CLPB-M, CLPB4, HSP98.7, casein lytic proteinase B4
AL6G17680	0.71	7.15E-04	1.97E-02	AT5G07380	unknown protein
AL1G34520	0.71	5.30E-04	1.57E-02	AT1G21410	SKP2A, F-box/RNI-like superfamily protein
AL5G18400	0.70	1.90E-03	4.18E-02	/	Unknown
AL9U11930	0.70	5.60E-04	1.63E-02	ATCG01010	NDHF, NADH-Ubiquinone oxidoreductase (complex I), chain 5 protein
AL1G36670	0.70	2.21E-03	4.67E-02	AT1G23100	GroES-like family protein
AL7G48440	0.70	5.22E-04	1.55E-02	AT5G41110	unknown protein
AL1G64080	0.70	1.75E-03	3.90E-02	AT2G02770	4'-phosphopantetheinyl transferase superfamily

AL6G11310	0.70	1.11E-03	2.74E-02	AT5G02090	unknown protein
AL3G30990	0.70	1.53E-03	3.53E-02	AT3G17830	Molecular chaperone Hsp40/DnaJ family protein
AL4G27920	0.70	2.21E-03	4.67E-02	AT2G32530	ATCSLB03, ATCSLB3, CSLB03, cellulose synthase-like B3
AL1G45000	0.69	1.11E-03	2.74E-02	AT1G30820	CTP synthase family protein
AL6G22400	0.69	9.48E-04	2.44E-02	AT5G11680	unknown protein
AL8G33710	0.69	8.68E-04	2.29E-02	AT5G57685	ATGDU3, GDU3, LSB1, glutamine dumper 3
AL3G25380	0.69	9.00E-04	2.35E-02	AT3G13470	TCP-1/cpn60 chaperonin family protein
AL9U11050	0.69	9.74E-04	2.49E-02	AT4G15280	UGT71B5, UDP-glucosyl transferase 71B5
AL1G22220	0.69	7.93E-04	2.12E-02	AT1G11190	BFN1, ENDO1, bifunctional nuclease i
AL3G48450	0.69	2.12E-03	4.53E-02	AT2G19780	Leucine-rich repeat (LRR) family protein
AL4G25720	0.69	1.15E-03	2.82E-02	AT1G06680	OE23, OEE2, PSBP-1, PSII-P, photosystem II subunit P-1
AL8G43470	0.68	1.06E-03	2.65E-02	AT5G65750	2-oxoglutarate dehydrogenase, E1 component
AL1G66690	0.68	1.63E-03	3.69E-02	AT1G56720	Protein kinase superfamily protein
AL1G43960	0.68	2.27E-03	4.77E-02	AT1G30070	SGS domain-containing protein
AL5G14580	0.68	1.02E-03	2.58E-02	AT3G25920	RPL15, ribosomal protein L15
AL2G35670	0.68	1.08E-03	2.69E-02	AT1G75690	DnaJ/Hsp40 cysteine-rich domain superfamily protein
AL6G41800	0.68	1.80E-03	3.99E-02	AT4G08160	glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containing protein
AL1G15530	0.68	1.98E-03	4.30E-02	AT1G05620	URH2, uridine-ribohydrolase 2
AL8G43450	0.68	1.17E-03	2.86E-02	AT5G65730	Galactose oxidase/kelch repeat superfamily protein
AL4G35760	0.68	1.39E-03	3.27E-02	AT2G38480	Uncharacterised protein family (UPF0497)
AL3G20560	0.67	9.59E-04	2.46E-02	AT3G09390	ATMT-1, ATMT-K, MT2A, metallothionein 2A
AL2G31240	0.67	1.60E-03	3.64E-02	AT1G71695	Peroxidase superfamily protein
AL8G25220	0.67	1.39E-03	3.26E-02	AT5G51010	Rubredoxin-like superfamily protein
AL6G29930	0.67	1.43E-03	3.34E-02	AT5G18660	PCB2, NAD(P)-binding Rossmann-fold superfamily protein
AL3G33060	0.67	1.16E-03	2.84E-02	AT3G19620	Glycosyl hydrolase family protein
AL4G11860	0.66	1.46E-03	3.40E-02	AT2G22360	DNAJ heat shock family protein
AL1G48900	0.66	2.13E-03	4.54E-02	AT1G34350	unknown protein
AL3G35660	0.66	1.62E-03	3.67E-02	AT3G21550	AtDMP2, DMP2, DUF679 domain membrane protein 2
AL5G23470	0.65	1.04E-03	2.62E-02	AT3G45010	scpl48, serine carboxypeptidase-like 48
AL7G37060	0.65	1.75E-03	3.90E-02	AT4G17560	Ribosomal protein L19 family protein
AL7G26420	0.65	1.88E-03	4.14E-02	AT4G26500	ATSUFE, CPSUFE, EMB1374, SUFE1, chloroplast sulfur E
AL8G40250	0.65	1.89E-03	4.16E-02	AT5G63160	BT1, BTB and TAZ domain protein 1
AL6G47930	0.65	2.04E-03	4.41E-02	AT4G04460	Saposin-like aspartyl protease family protein
AL5G23340	0.65	1.87E-03	4.13E-02	AT3G44880	ACD1, LLS1, PAO, Pheophorbide a oxygenase family protein with Rieske [2Fe-2S] domain
AL6G28800	0.65	1.61E-03	3.66E-02	AT5G17710	EMB1241, Co-chaperone GrpE family protein
AL6G51500	0.65	1.19E-03	2.90E-02	AT4G01800	AGY1, AtcpSecA, Albino or Glassy Yellow 1
AL1G15220	0.64	1.66E-03	3.73E-02	AT1G05385	LPA19, Psb27-H1, photosystem II 11 kDa protein-related
AL4G26300	0.64	2.12E-03	4.53E-02	AT2G31110	TBL40, Plant protein of unknown function (DUF828)
AL4G47140	0.64	1.94E-03	4.24E-02	AT2G47560	RING/U-box superfamily protein
AL3G16090	0.64	2.15E-03	4.58E-02	AT3G05490	RALFL22, ralf-like 22
AL2G10290	0.64	2.10E-03	4.52E-02	AT1G64510	Translation elongation factor EF1B/ribosomal protein S6 family protein
AL7G11930	0.63	1.91E-03	4.19E-02	AT4G39730	Lipase/lipooxygenase, PLAT/LH2 family protein
AL1G62150	0.63	1.84E-03	4.08E-02	AT1G53560	Ribosomal protein L18ae family
AL2G35130	0.63	1.97E-03	4.29E-02	AT1G75220	Major facilitator superfamily protein
AL5G25790	0.63	2.32E-03	4.85E-02	AT3G46780	PTAC16, plastid transcriptionally active 16
AL8G24260	0.62	2.13E-03	4.55E-02	AT5G50240	PIMT2, protein-l-isoaspartate methyltransferase 2
AL5G37460	0.62	2.09E-03	4.49E-02	AT3G56140	Protein of unknown function (DUF399 and DUF3411)
AL2G39010	0.61	2.12E-03	4.53E-02	AT1G78610	MSL6, mechanosensitive channel of small conductance-like 6
AL8G38550	-0.62	1.81E-03	4.01E-02	AT5G61790	ATCNX1, CNX1, calnexin 1
AL7G21090	-0.63	2.09E-03	4.49E-02	AT4G30990	ARM repeat superfamily protein
AL8G13450	-0.63	1.63E-03	3.70E-02	AT5G45350	proline-rich family protein
AL2G31260	-0.63	2.16E-03	4.60E-02	AT1G71697	ATCK1, CK, CK1, choline kinase 1
AL8G45200	-0.64	2.29E-03	4.79E-02	AT5G66320	GATA5, GATA transcription factor 5
AL4G33950	-0.64	1.90E-03	4.18E-02	/	Unknown
AL8G26450	-0.64	2.25E-03	4.74E-02	AT5G52070	Agenet domain-containing protein
AL3G28920	-0.64	2.10E-03	4.52E-02	AT3G16220	Predicted eukaryotic LigT
AL3G26460	-0.64	2.17E-03	4.61E-02	AT3G14200	Chaperone DnaJ-domain superfamily protein
AL7G23260	-0.64	1.81E-03	4.01E-02	AT4G29190	Zinc finger C-x8-C-x5-C-x3-H type family protein
AL5G13300	-0.65	2.35E-03	4.89E-02	AT2G03530	ATUPS2, UPS2, ureide permease 2
AL6G22720	-0.65	1.20E-03	2.91E-02	AT5G11950	Putative lysine decarboxylase family protein
AL8G30430	-0.65	1.36E-03	3.22E-02	AT5G54960	PDC2, pyruvate decarboxylase-2
AL4G30970	-0.66	1.71E-03	3.83E-02	AT2G34960	CAT5, cationic amino acid transporter 5
AL7G30900	-0.67	1.38E-03	3.24E-02	AT4G22690	CYP706A1, cytochrome P450, family 706, subfamily A, polypeptide 1
AL2G25500	-0.67	1.21E-03	2.93E-02	AT1G67120	ATPases;nucleotide binding;ATP binding;nucleoside-triphosphatases;transcription factor binding
AL7G52640	-0.67	2.07E-03	4.47E-02	AT5G38210	Protein kinase family protein
AL7G35100	-0.67	1.33E-03	3.15E-02	AT4G19030	AT-NLM1, ATNLM1, NIP1;1, NLM1, NOD26-like major intrinsic protein 1
AL6G17890	-0.67	1.65E-03	3.73E-02	AT5G07580	Integrase-type DNA-binding superfamily protein
AL8G22370	-0.67	1.54E-03	3.56E-02	AT5G49015	Expressed protein
AL5G37740	-0.67	1.34E-03	3.17E-02	AT3G56410	Protein of unknown function (DUF3133)
AL1G62580	-0.68	2.23E-03	4.71E-02	AT1G53890	Protein of unknown function (DUF567)
AL6G19210	-0.68	1.51E-03	3.50E-02	AT1G76810	eukaryotic translation initiation factor 2 (eIF-2) family protein
AL7G32490	-0.68	1.65E-03	3.72E-02	AT4G21534	Diacylglycerol kinase family protein
AL8G38320	-0.68	2.03E-03	4.39E-02	AT5G61590	Integrase-type DNA-binding superfamily protein
AL7G30170	-0.68	1.11E-03	2.73E-02	AT4G23250	CRK17, DUF26-21, EMB1290, RKC1, kinases;protein kinases
AL1G12690	-0.68	2.15E-03	4.57E-02	AT1G03210	Phenazine biosynthesis PhzC/PhzF protein
AL3G21520	-0.69	1.59E-03	3.63E-02	AT3G10190	Calcium-binding EF-hand family protein
AL4G21310	-0.69	9.41E-04	2.43E-02	AT2G27360	GDSL-like Lipase/Acylhydrolase superfamily protein
AL4G33210	-0.69	7.93E-04	2.12E-02	AT2G36970	UDP-Glycosyltransferase superfamily protein
AL7G21180	-0.70	2.41E-03	4.99E-02	AT4G30910	Cytosol aminopeptidase family protein

AL5G38720	-0.70	7.19E-04	1.97E-02	AT3G57230	AGL16, AGAMOUS-like 16
AL8G29310	-0.70	1.19E-03	2.89E-02	AT5G54160	ATOMT1, OMT1, O-methyltransferase 1
AL4G23490	-0.70	7.57E-04	2.05E-02	AT2G28940	Protein kinase superfamily protein
AL3G47790	-0.70	1.44E-03	3.37E-02	AT2G15960	unknown protein
AL2G29240	-0.70	8.63E-04	2.27E-02	AT1G70000	myb-like transcription factor family protein
AL6G19350	-0.70	9.34E-04	2.41E-02	AT5G08620	ATRH25, STRS2, DEA(D/H)-box RNA helicase family protein
AL8G38690	-0.71	1.68E-03	3.78E-02	AT5G61930	APO3, Arabidopsis thaliana protein of unknown function (DUF794)
AL4G29950	-0.71	2.13E-03	4.54E-02	AT2G34020	Calcium-binding EF-hand family protein
AL1G39720	-0.71	1.03E-03	2.58E-02	AT1G25580	ANAC008, SOG1, NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
AL5G45300	-0.71	2.29E-03	4.79E-02	AT3G62550	Adenine nucleotide alpha hydrolases-like superfamily protein
AL7G50160	-0.71	1.69E-03	3.79E-02	/	Unknown
AL7G47170	-0.71	1.57E-03	3.61E-02	AT5G42010	Transducin/WD40 repeat-like superfamily protein
AL5G10520	-0.71	1.40E-03	3.27E-02	AT2G01520	MLP328, MLP-like protein 328
AL4G24730	-0.72	6.45E-04	1.83E-02	AT2G29980	FAD3, fatty acid desaturase 3
AL3G49630	-0.72	6.79E-04	1.89E-02	AT2G16890	UDP-Glycosyltransferase superfamily protein
AL6G15680	-0.72	5.48E-04	1.61E-02	AT5G05790	Duplicated homeodomain-like superfamily protein
AL1G57800	-0.72	1.38E-03	3.25E-02	AT1G50180	NB-ARC domain-containing disease resistance protein
AL1G27520	-0.72	4.57E-04	1.40E-02	AT1G15410	aspartate-glutamate racemase family
AL7G33580	-0.73	1.25E-03	3.01E-02	AT4G20320	CTP synthase family protein
AL5G22860	-0.73	1.20E-03	2.92E-02	AT3G44480	cog1, RPP1, Disease resistance protein (TIR-NBS-LRR class) family
AL6G44400	-0.73	1.48E-03	3.42E-02	AT4G10450	Ribosomal protein L6 family
AL3G27660	-0.73	1.69E-03	3.79E-02	AT3G15270	SPL5, squamosa promoter binding protein-like 5
AL4G32490	-0.73	6.78E-04	1.89E-02	AT2G36340	DNA-binding storekeeper protein-related transcriptional regulator
AL3G47970	-0.73	1.53E-03	3.53E-02	AT2G20110	Tesmin/TSO1-like CXC domain-containing protein
AL4G24500	-0.73	9.21E-04	2.39E-02	AT2G29720	CTF2B, FAD/NAD(P)-binding oxidoreductase family protein
AL5G15260	-0.73	5.20E-04	1.54E-02	AT3G26500	PIRL2, plant intracellular ras group-related LRR 2
AL2G28670	-0.73	2.27E-03	4.77E-02	AT1G69530	AT-EXP1, ATEXP1, ATEXPA1, ATHEXP ALPHA 1.2, EXP1, EXPA1, expansin A1
AL3G50800	-0.73	9.05E-04	2.36E-02	AT2G17780	MCA2, PLAC8 family protein
AL4G33670	-0.73	1.46E-03	3.38E-02	AT2G37290	Ypt/Rab-GAP domain of gyp1p superfamily protein
AL8G12090	-0.74	8.56E-04	2.26E-02	AT5G46330	Flagellin-sensitive 2, Leucine-rich receptor-like protein kinase family protein
AL8G41250	-0.74	7.18E-04	1.97E-02	AT5G63990	Inositol monophosphatase family protein
AL1G35510	-0.74	5.63E-04	1.64E-02	AT1G22070	TGA3, TGA1A-related gene 3
AL1G41250	-0.74	9.75E-04	2.49E-02	AT1G27720	TAF4, TAF4B, TBP-associated factor 4B
AL8G23560	-0.74	7.46E-04	2.02E-02	AT5G49680	KIP, Golgi-body localisation protein domain ;RNA pol II promoter Fmp27 protein domain
AL6G11810	-0.75	1.14E-03	2.82E-02	AT5G02550	unknown protein
AL3G30740	-0.75	7.20E-04	1.97E-02	AT3G17640	Leucine-rich repeat (LRR) family protein
AL1G24970	-0.75	7.58E-04	2.05E-02	AT1G13260	EDF4, RAV1, related to ABI3/VP1 1
AL1G41780	-0.75	2.63E-04	9.21E-03	AT1G28230	ATPUP1, PUP1, purine permease 1
AL8G11880	-0.75	3.28E-04	1.09E-02	AT2G34690	ACD11, Glycolipid transfer protein (GLTP) family protein
AL3G51420	-0.75	3.38E-04	1.12E-02	AT2G18193	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AL8G15180	-0.75	1.59E-03	3.63E-02	AT5G44568	unknown protein
AL2G41410	-0.75	7.87E-04	2.11E-02	AT1G80120	Protein of unknown function (DUF567)
AL8G34780	-0.75	6.56E-04	1.85E-02	AT5G58540	Protein kinase superfamily protein
AL6G38190	-0.75	6.66E-04	1.87E-02	AT5G26180	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AL4G19800	-0.76	4.93E-04	1.48E-02	AT2G26710	BAS1, CYP72B1, CYP734A1, Cytochrome P450 superfamily protein
AL7G29840	-0.76	4.09E-04	1.29E-02	AT4G23570	SGT1A, phosphatase-related
AL5G29160	-0.76	3.49E-04	1.14E-02	AT3G49400	Transducin/WD40 repeat-like superfamily protein
AL4G45750	-0.76	1.67E-03	3.75E-02	AT2G46450	ATCNGC12, CNGC12, cyclic nucleotide-gated channel 12
AL6G18130	-0.76	9.25E-04	2.39E-02	AT5G07790	unknown protein
AL4G42390	-0.77	2.36E-03	4.90E-02	AT5G52440	HCF106, Bacterial sec-independent translocation protein mttA/Hcf106
AL5G41090	-0.77	3.92E-04	1.25E-02	AT3G59210	F-box/RNI-like superfamily protein
AL6G18340	-0.77	2.14E-03	4.55E-02	AT5G08000	E13L3, PDCB2, glucan endo-1,3-beta-glucosidase-like protein 3
AL2G16230	-0.77	1.18E-03	2.89E-02	AT1G60460	unknown protein
AL3G24530	-0.77	5.37E-04	1.59E-02	AT3G12860	NOP56-like pre RNA processing ribonucleoprotein
AL8G44850	-0.77	1.01E-03	2.55E-02	AT5G17890	CHS3, Chilling sensitive 3, DAR4, DA1-related protein 4
AL4G45760	-0.78	1.57E-03	3.60E-02	AT2G46450	ATCNGC12, CNGC12, cyclic nucleotide-gated channel 12
AL2G30610	-0.78	4.48E-04	1.37E-02	AT1G71040	LPR2, Cupredoxin superfamily protein
AL2G27810	-0.78	4.30E-04	1.33E-02	AT1G68840	EDF2, RAP2.8, RAV2, TEM2, related to ABI3/VP1 2
AL4G27670	-0.78	1.33E-03	3.16E-02	AT2G32280	Protein of unknown function (DUF1218)
AL6G27540	-0.78	5.40E-04	1.59E-02	AT5G16570	GLN1;4, glutamine synthetase 1;4
AL1G15100	-0.78	5.46E-04	1.60E-02	AT1G05300	ZIP5, zinc transporter 5 precursor
AL8G27880	-0.78	9.25E-04	2.39E-02	AT5G53220	unknown protein
AL3G33100	-0.78	1.21E-03	2.92E-02	AT3G19660	unknown protein
AL2G28610	-0.78	1.46E-03	3.38E-02	AT1G69490	ANAC029, ATNAP, NAP, NAC-like, activated by AP3/PI
AL6G28030	-0.78	1.25E-03	3.01E-02	AT5G17030	UGT78D3, UDP-glucosyl transferase 78D3
AL6G12170	-0.79	4.29E-04	1.33E-02	AT5G02890	HXXXD-type acyl-transferase family protein
AL1G37580	-0.79	4.28E-04	1.33E-02	AT1G23830	unknown protein
AL4G23380	-0.79	1.57E-04	6.22E-03	AT2G28840	XBAT31, XB3 ortholog 1 in Arabidopsis thaliana
AL7G15150	-0.79	2.51E-04	8.87E-03	AT4G35900	atbzip14, FD, FD-1, Basic-leucine zipper (bZIP) transcription factor family protein
AL3G40580	-0.79	1.45E-03	3.38E-02	AT3G24810	ICK3, KRP5, Cyclin-dependent kinase inhibitor family protein
AL4G27150	-0.79	2.01E-03	4.37E-02	AT2G31865	PARG2, poly(ADP-ribose) glycohydrolase 2
AL6G33540	-0.80	8.61E-04	2.27E-02	AT5G22540	Plant protein of unknown function (DUF247)
AL3G14910	-0.80	2.80E-04	9.72E-03	AT3G04770	RPSAb, 40s ribosomal protein SA B
AL1G30800	-0.80	3.58E-04	1.17E-02	AT1G18390	Protein kinase superfamily protein
AL7G32890	-0.80	3.68E-04	1.20E-02	AT4G21215	unknown protein
AL1G32350	-0.80	1.21E-04	5.08E-03	AT1G19630	CYP722A1, cytochrome P450, family 722, subfamily A, polypeptide 1
AL4G10020	-0.81	4.15E-04	1.30E-02	AT5G13480	FY, Transducin/WD40 repeat-like superfamily protein
AL5G15630	-0.81	1.68E-03	3.78E-02	AT3G26760	NAD(P)-binding Rossmann-fold superfamily protein
AL1G52460	-0.81	1.67E-04	6.54E-03	AT1G44800	nodulin MtN21 /EamA-like transporter family protein

AL5G30620	-0.81	2.12E-03	4.53E-02	AT3G50470	HR3, MLA10, homolog of RPW8 3
AL6G18410	-0.81	4.72E-04	1.43E-02	AT5G08020	ATRPA70B, RPA70B, RPA70-kDa subunit B
AL1G47960	-0.82	3.16E-04	1.06E-02	/	Unknown
AL8G42930	-0.82	1.40E-03	3.27E-02	AT5G65340	Protein of unknown function, DUF617
AL7G30440	-0.82	2.18E-04	7.98E-03	AT4G23060	IQD22, IQ-domain 22
AL1G16840	-0.82	7.42E-04	2.02E-02	AT1G06830	Glutaredoxin family protein
AL8G44250	-0.82	2.15E-04	7.92E-03	AT5G67110	ALC, basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AL7G27060	-0.82	1.00E-03	2.55E-02	AT4G25940	ENTH/ANTH/VHS superfamily protein
AL5G27340	-0.82	2.07E-03	4.46E-02	AT3G48020	unknown protein
AL1G58230	-0.82	2.11E-03	4.53E-02	AT1G50580	UDP-Glycosyltransferase superfamily protein
AL2G25130	-0.83	1.01E-03	2.56E-02	AT1G66880	Protein kinase superfamily protein
AL2G10060	-0.83	6.78E-04	1.89E-02	AT1G64700	unknown protein
AL6G28980	-0.83	2.28E-03	4.77E-02	AT5G17880	CSA1, disease resistance protein (TIR-NBS-LRR class)
AL7G14920	-0.83	1.17E-04	4.95E-03	AT4G36120	Plant protein of unknown function (DUF869)
AL1G23800	-0.83	2.84E-04	9.84E-03	AT1G12451	unknown protein
AL5G12020	-0.83	1.20E-04	5.06E-03	AT2G02810	ATUTR1, UTR1, UDP-galactose transporter 1
AL7G33940	-0.83	1.04E-03	2.61E-02	AT4G19970	unknown protein
AL8G13390	-0.83	6.48E-04	1.83E-02	AT2G37790	NAD(P)-linked oxidoreductase superfamily protein
AL5G18900	-0.83	1.02E-03	2.56E-02	AT3G29034	unknown protein
AL2G33340	-0.83	8.14E-05	3.68E-03	AT1G73590	ATPIN1, PIN1, Auxin efflux carrier family protein
AL8G43230	-0.84	3.04E-04	1.04E-02	AT5G65640	bHLH093, beta HLH protein 93
AL3G10950	-0.84	3.41E-04	1.12E-02	AT3G01290	SPFH/Band 7/PHB domain-containing membrane-associated protein family
AL5G24270	-0.84	5.22E-04	1.55E-02	AT3G45650	NAXT1, nitrate excretion transporter1
AL5G30990	-0.84	1.25E-03	3.01E-02	AT3G50770	CML41, calmodulin-like 41
AL4G43390	-0.84	1.39E-03	3.27E-02	AT2G44400	Cysteine/Histidine-rich C1 domain family protein
AL4G31620	-0.84	7.57E-05	3.47E-03	AT2G35585	unknown protein
AL1G29370	-0.84	7.77E-04	2.09E-02	AT1G17147	VQ motif-containing protein
AL5G13380	-0.85	2.49E-04	8.84E-03	AT2G03590	ATUPS1, UPS1, ureide permease 1
AL6G29410	-0.85	1.59E-04	6.29E-03	AT3G03960	TCP-1/cpn60 chaperonin family protein
AL1G13230	-0.85	3.80E-04	1.23E-02	AT1G03710	Cystatin/monellin superfamily protein
AL6G11740	-0.85	5.06E-05	2.49E-03	AT5G02500	AT-HSC70-1, HSC70, HSC70-1, HSP70-1, heat shock cognate protein 70-1
AL8G39310	-0.85	3.24E-04	1.08E-02	AT5G62430	CDF1, cycling DOF factor 1
AL6G45770	-0.85	8.59E-05	3.85E-03	AT4G11360	RHA1B, RING-H2 finger A1B
AL2G31890	-0.85	4.02E-04	1.27E-02	AT1G72220	RING/U-box superfamily protein
AL3G16300	-0.85	2.45E-04	8.73E-03	/	Unknown
AL7G12810	-0.85	1.36E-04	5.56E-03	AT4G37870	PCK1, PEPCK, phosphoenolpyruvate carboxykinase 1
AL8G22970	-0.85	6.53E-05	3.08E-03	AT5G49330	ATMYB111, MYB111, PFG3, myb domain protein 111
AL1G35960	-0.86	1.13E-04	4.82E-03	AT1G22440	Zinc-binding alcohol dehydrogenase family protein
AL6G17340	-0.86	6.15E-04	1.76E-02	AT5G07150	Leucine-rich repeat protein kinase family protein
AL6G41590	-0.86	3.17E-04	1.06E-02	/	Unknown
AL9U12090	-0.86	2.53E-04	8.92E-03	/	Unknown
AL1G11800	-0.87	9.05E-04	2.36E-02	AT1G02460	Pectin lyase-like superfamily protein
AL3G28830	-0.87	4.93E-04	1.48E-02	AT3G16150	N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein
AL7G32700	-0.87	4.87E-04	1.46E-02	AT4G21390	B120, S-locus lectin protein kinase family protein
AL3G28150	-0.87	1.74E-04	6.75E-03	AT1G52857	unknown protein
AL5G41510	-0.87	8.12E-05	3.68E-03	AT3G59580	Plant regulator RWP-RK family protein
AL1G36360	-0.87	2.31E-03	4.83E-02	AT1G22810	Integrase-type DNA-binding superfamily protein
AL4G43500	-0.87	7.53E-04	2.04E-02	AT2G44480	BGLU17, beta glucosidase 17
AL7G40320	-0.88	1.28E-03	3.05E-02	AT4G15270	glucosyltransferase-related
AL7G49370	-0.88	2.27E-03	4.77E-02	AT5G40460	unknown protein
AL8G28890	-0.88	8.88E-05	3.96E-03	AT5G53830	VQ motif-containing protein
AL5G22500	-0.88	8.51E-04	2.25E-02	AT3G44350	anac061, NAC061, NAC domain containing protein 61
AL8G36180	-0.88	5.03E-04	1.50E-02	AT5G59660	Leucine-rich repeat protein kinase family protein
AL7G28330	-0.88	4.17E-04	1.31E-02	AT4G24860	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AL2G14960	-0.88	8.08E-05	3.67E-03	AT1G61370	S-locus lectin protein kinase family protein
AL1G64400	-0.88	2.24E-04	8.19E-03	AT1G56120	Leucine-rich repeat transmembrane protein kinase
AL2G31490	-0.88	1.83E-04	7.00E-03	AT1G71880	ATSUC1, SUC1, sucrose-proton symporter 1
AL5G38740	-0.88	7.28E-04	1.99E-02	AT3G62200	Putative endonuclease or glycosyl hydrolase
AL7G47090	-0.88	1.76E-03	3.91E-02	AT4G00695	unknown protein
AL4G32980	-0.88	1.25E-03	3.00E-02	AT2G36780	UDP-Glycosyltransferase superfamily protein
AL4G40700	-0.89	2.41E-03	4.99E-02	AT2G42320	nucleolar protein gar2-related
AL2G27280	-0.89	3.06E-04	1.04E-02	AT5G56680	EMB2755, SYNC1, SYNC1 ARATH, Class II aminoacyl-tRNA and biotin synthetases superfamily protein
AL3G14640	-0.89	1.04E-04	4.50E-03	/	Unknown
AL4G41690	-0.89	1.35E-03	3.19E-02	AT2G43050	ATPMEPCRD, Plant invertase/pectin methylesterase inhibitor superfamily
AL7G16330	-0.90	2.12E-04	7.83E-03	AT4G34880	Amidase family protein
AL2G36400	-0.90	1.09E-03	2.70E-02	/	Unknown
AL6G33400	-0.90	2.11E-03	4.53E-02	AT5G22380	anac090, NAC090, NAC domain containing protein 90
AL4G23150	-0.90	1.02E-03	2.57E-02	AT2G28630	KCS12, 3-ketoacyl-CoA synthase 12
AL3G40730	-0.90	1.42E-04	5.76E-03	/	Unknown
AL68U10050	-0.90	1.49E-03	3.44E-02	AT2G37800	Cysteine/Histidine-rich C1 domain family protein
AL2G11290	-0.91	2.25E-04	8.19E-03	/	Unknown
AL8G34550	-0.91	1.53E-03	3.53E-02	AT5G58390	Peroxidase superfamily protein
AL2G25110	-0.91	3.84E-04	1.23E-02	AT1G66880	Protein kinase superfamily protein
AL8G35410	-0.91	1.37E-03	3.22E-02	/	Unknown
AL6G25700	-0.91	3.16E-05	1.73E-03	AT5G14920	Gibberellin-regulated family protein
AL7G16270	-0.91	2.59E-04	9.10E-03	AT4G34950	Major facilitator superfamily protein
AL1G21260	-0.91	6.42E-05	3.06E-03	AT1G10470	ARR4, ATRR1, IBC7, MEE7, response regulator 4
AL7G34270	-0.92	5.89E-04	1.70E-02	AT4G19820	Glycosyl hydrolase family protein with chitinase insertion domain
AL2G13780	-0.92	8.40E-04	2.23E-02	AT1G62130	AAA-type ATPase family protein

AL6G33310	-0.92	1.85E-04	7.03E-03	AT5G22300	AtNIT4, NIT4, nitrilase 4
AL7G52960	-0.92	1.05E-03	2.63E-02	AT5G38020	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AL3G16840	-0.92	1.97E-03	4.29E-02	AT3G06020	Protein of unknown function (DUF3049)
AL6G25970	-0.92	5.84E-04	1.69E-02	AT5G15150	ATHB-3, ATHB3, HAT7, HB-3, homeobox 3
AL1G32050	-0.92	2.41E-03	4.99E-02	/	Unknown
AL3G49880	-0.92	2.08E-04	7.72E-03	AT2G17040	anac036, NAC036, NAC domain containing protein 36
AL7G10440	-0.92	5.22E-05	2.56E-03	AT4G38550	Arabidopsis phospholipase-like protein (PEARLI 4) family
AL8G43680	-0.92	2.22E-04	8.10E-03	AT5G67620	unknown protein
AL7G22010	-0.92	9.18E-04	2.39E-02	AT4G30180	sequence-specific DNA binding transcription factors;transcription regulators
AL6G51810	-0.92	1.62E-03	3.68E-02	AT4G01540	ANAC068, NTM1, NAC with transmembrane motif1
AL7G39350	-0.93	3.53E-04	1.15E-02	AT4G15920	Nodulin MtN3 family protein
AL5G14040	-0.93	4.22E-04	1.32E-02	AT3G25570	Adenosylmethionine decarboxylase family protein
AL7G11000	-0.93	2.69E-05	1.53E-03	AT4G39070	B-box zinc finger family protein
AL2G27410	-0.93	3.92E-05	2.04E-03	AT2G35630	GEM1, MOR1, ARM repeat superfamily protein
AL4G44010	-0.93	9.46E-04	2.44E-02	AT2G44910	ATHB-4, ATHB4, HB4, homeobox-leucine zipper protein 4
AL371U10010	-0.93	2.25E-03	4.74E-02	AT2G45900	Phosphatidylinositol N-acetyglucosaminlytransferase subunit P-related
AL8G27190	-0.93	2.35E-03	4.89E-02	AT5G52760	Copper transport protein family
AL4G29600	-0.93	7.48E-05	3.44E-03	AT2G33830	Dormancy/auxin associated family protein
AL7G20300	-0.94	1.27E-03	3.04E-02	/	Unknown
AL7G14680	-0.94	2.67E-05	1.52E-03	AT4G36410	UBC17, ubiquitin-conjugating enzyme 17
AL4G23660	-0.94	5.75E-05	2.79E-03	AT2G29090	CYP707A2, cytochrome P450, family 707, subfamily A, polypeptide 2
AL4G38540	-0.94	2.88E-04	9.94E-03	AT2G40670	ARR16, RR16, response regulator 16
AL5G41770	-0.95	5.77E-04	1.67E-02	AT3G59700	ATHLECRK, HLECRK, LECRK1, lectin-receptor kinase
AL2G16660	-0.95	1.74E-03	3.88E-02	/	Unknown
AL4G45610	-0.95	1.40E-05	9.27E-04	AT2G46310	CRF5, cytokinin response factor 5
AL1G49530	-0.95	2.49E-04	8.85E-03	AT5G66620	DAR6, DA1-related protein 6
AL7G27780	-0.95	6.02E-05	2.90E-03	AT4G25350	SHB1, EXS (ERD1/XPR1/SYG1) family protein
AL8G12310	-0.95	4.02E-04	1.27E-02	/	Unknown
AL2G14230	-0.96	1.18E-03	2.89E-02	AT1G61840	Cysteine/Histidine-rich C1 domain family protein
AL2G33620	-0.96	2.12E-03	4.53E-02	AT1G73810	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein
AL4G16580	-0.96	8.86E-05	3.95E-03	AT2G25260	unknown protein
AL3G40700	-0.96	2.21E-03	4.67E-02	AT3G24900	AtRLP39, RLP39, receptor like protein 39
AL5G15010	-0.96	1.92E-06	1.81E-04	AT3G26290	CYP71B26, cytochrome P450, family 71, subfamily B, polypeptide 26
AL6G16590	-0.96	1.69E-05	1.08E-03	AT5G06510	NF-YA10, nuclear factor Y, subunit A10
AL8G15110	-0.96	3.05E-04	1.04E-02	AT5G44575	unknown protein
AL6G29720	-0.96	3.32E-04	1.10E-02	AT5G18470	Curculin-like (mannose-binding) lectin family protein
AL8G30980	-0.97	7.47E-04	2.03E-02	AT5G55440	Protein of unknown function (DUF295)
AL5G42510	-0.97	1.62E-03	3.67E-02	AT3G60290	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AL6G14610	-0.97	3.49E-05	1.88E-03	AT5G04920	EAP30/Vps36 family protein
AL7G49280	-0.97	2.47E-05	1.43E-03	AT5G40540	Protein kinase superfamily protein
AL5G33060	-0.97	1.58E-04	6.26E-03	AT3G52400	ATSYP122, SYP122, syntaxin of plants 122
AL3G41990	-0.97	8.48E-04	2.24E-02	AT2G04300	Leucine-rich repeat protein kinase family protein
AL1G10010	-0.97	4.17E-04	1.31E-02	AT1G02205	CER1, Fatty acid hydroxylase superfamily
AL1G17600	-0.97	1.48E-03	3.42E-02	AT1G07450	NAD(P)-binding Rossmann-fold superfamily protein
AL3G53600	-0.97	9.10E-05	4.03E-03	AT2G20562	unknown protein
AL1G28030	-0.97	1.03E-04	4.46E-03	AT1G15870	Mitochondrial glycoprotein family protein
AL1G23570	-0.97	2.73E-05	1.54E-03	AT1G12270	stress-inducible protein, putative
AL8G42920	-0.97	5.00E-04	1.50E-02	/	Unknown
AL6G12030	-0.97	1.09E-03	2.70E-02	AT5G02780	GSTL1, glutathione transferase lambda 1
AL8G42210	-0.97	1.97E-03	4.29E-02	AT5G64750	ABR1, Integrase-type DNA-binding superfamily protein
AL1G22810	-0.97	2.37E-04	8.52E-03	AT1G11670	MATE efflux family protein
AL3G14520	-0.98	1.28E-04	5.29E-03	AT3G04510	LSH2, Protein of unknown function (DUF640)
AL6G22050	-0.98	1.78E-04	6.83E-03	AT5G11410	Protein kinase superfamily protein
AL6G40320	-0.98	2.37E-04	8.52E-03	/	Unknown
AL6G51120	-0.98	2.16E-04	7.94E-03	/	Unknown
AL3G33500	-0.98	1.04E-05	7.32E-04	AT3G19930	ATSTP4, STP4, sugar transporter 4
AL6G21710	-0.98	1.22E-03	2.95E-02	AT1G23780	F-box family protein
AL4G45110	-0.98	6.57E-04	1.85E-02	AT2G45900	Phosphatidylinositol N-acetyglucosaminlytransferase subunit P-related
AL8G18660	-0.98	1.46E-04	5.87E-03	AT5G42610	Protein of unknown function (DUF607)
AL4G47050	-0.99	1.07E-04	4.57E-03	AT2G47485	unknown protein
AL5G20470	-0.99	3.77E-05	1.97E-03	AT1G52950	Nucleic acid-binding, OB-fold-like protein
AL1G64930	-0.99	1.34E-04	5.49E-03	AT1G47890	AtRLP7, RLP7, receptor like protein 7
AL7G18750	-0.99	4.40E-04	1.35E-02	AT4G32940	GAMMA-VPE, GAMMAVPE, gamma vacuolar processing enzyme
AL1G17040	-0.99	2.88E-04	9.94E-03	AT1G07000	ATEXO70B2, EXO70B2, exocyst subunit exo70 family protein B2
AL7G46360	-0.99	1.31E-05	8.86E-04	AT5G37600	ATGLN1;1, ATGSR1, GLN1;1, GSR 1, glutamine synthase clone R1
AL8G31590	-1.00	2.79E-06	2.45E-04	AT5G56030	AtHsp90.2, ERD8, HSP81-2, HSP90.2, heat shock protein 81-2
AL5G34190	-1.00	7.03E-05	3.29E-03	AT3G53280	CYP71B5, cytochrome p450 71b5
AL7G40420	-1.00	2.67E-05	1.52E-03	AT4G15236	ABC-2 and Plant PDR ABC-type transporter family protein
AL4G23890	-1.00	3.88E-04	1.24E-02	AT2G29340	NAD-dependent epimerase/dehydratase family protein
AL810U10010	-1.00	7.12E-04	1.96E-02	AT3G16030	CES101, lectin protein kinase family protein
AL1G22380	-1.00	4.12E-04	1.30E-02	AT1G11300	protein serine/threonine kinases;protein kinases;ATP binding;sugar binding;kinases;carbohydrate binding
AL8G19840	-1.00	2.11E-03	4.53E-02	AT5G47850	CCR4, CRINKLY4 related 4
AL3G25180	-1.00	2.55E-04	8.95E-03	AT3G13350	HMG (high mobility group) box protein with ARID/BRIGHT DNA-binding domain
AL8G26040	-1.00	7.51E-04	2.04E-02	AT5G50220	F-box family protein
AL4G43460	-1.01	6.21E-05	2.98E-03	AT2G44450	BGLU15, beta glucosidase 15
AL5G22150	-1.01	4.26E-04	1.33E-02	AT3G48650	pseudogene, At14a-related protein, similar to At14a (GI:11994571 and GI:11994573) (Arabidopsis thaliana)
AL8G41780	-1.01	6.32E-06	4.79E-04	AT5G64410	ATOPT4, OPT4, oligopeptide transporter 4
AL5G39900	-1.01	1.90E-04	7.21E-03	AT3G58200	TRAF-like family protein

AL7G18530	-1.01	4.78E-05	2.40E-03	AT4G33050	EDA39, calmodulin-binding family protein
AL8G42690	-1.01	2.21E-05	1.34E-03	AT5G65170	VQ motif-containing protein
AL3G10550	-1.01	3.05E-05	1.68E-03	AT3G01600	anac044, NAC044, NAC domain containing protein 44
AL8G37520	-1.01	7.69E-04	2.07E-02	AT5G60900	RLK1, receptor-like protein kinase 1
AL5G34140	-1.01	4.55E-06	3.67E-04	AT3G53235	unknown protein
AL1G63450	-1.02	2.26E-05	1.35E-03	AT1G55450	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AL5G35470	-1.02	1.69E-04	6.61E-03	AT3G54420	ATCHITIV, ATEP3, CHIV, EP3, homolog of carrot EP3-3 chitinase
AL7G36920	-1.02	1.76E-06	1.70E-04	AT4G17670	Protein of unknown function (DUF581)
AL6G33550	-1.02	1.48E-03	3.43E-02	AT5G22545	unknown protein
AL1G37960	-1.02	1.96E-04	7.38E-03	AT1G24147	unknown protein
AL2G32620	-1.02	3.91E-05	2.04E-03	AT5G28823	unknown protein
AL6G38820	-1.02	5.56E-04	1.63E-02	AT5G26920	CBP60G, Cam-binding protein 60-like G
AL5G13940	-1.02	8.99E-04	2.35E-02	AT2G04038	AtbZIP48, bZIP48, basic leucine-zipper 48
AL5G16480	-1.02	1.45E-04	5.85E-03	AT5G11250	Disease resistance protein (TIR-NBS-LRR class)
AL5G45800	-1.03	2.59E-06	2.32E-04	AT3G63010	ATGID1B, GID1B, alpha/beta-Hydrolases superfamily protein
AL4G42440	-1.03	5.60E-04	1.63E-02	AT2G43620	Chitinase family protein
AL5G38750	-1.03	6.53E-04	1.84E-02	AT3G57260	BG2, BGL2, PR-2, PR2, beta-1,3-glucanase 2
AL7G30640	-1.03	4.04E-04	1.28E-02	AT4G22880	ANS, LDOX, TDS4, TT18, leucoanthocyanidin dioxygenase
AL8G16390	-1.04	5.66E-05	2.75E-03	AT5G43780	APS4, Pseudouridine synthase/archaeosine transglycosylase-like family protein
AL5G26150	-1.04	4.39E-04	1.35E-02	AT3G46930	Protein kinase superfamily protein
AL3G15050	-1.04	6.06E-05	2.91E-03	/	Unknown
AL5G24040	-1.04	2.04E-04	7.60E-03	AT3G56730	Putative endonuclease or glycosyl hydrolase
AL5G27410	-1.04	1.63E-04	6.41E-03	AT3G48080	alpha/beta-Hydrolases superfamily protein
AL61U10020	-1.04	2.36E-03	4.90E-02	AT5G42800	DFR, M318, TT3, dihydroflavonol 4-reductase
AL5G11210	-1.04	6.47E-04	1.83E-02	AT2G02010	GAD4, glutamate decarboxylase 4
AL8G26150	-1.04	2.17E-04	7.97E-03	AT5G51850	unknown protein
AL4G46070	-1.04	1.76E-05	1.11E-03	AT2G46640	unknown protein
AL6G25030	-1.05	4.80E-04	1.45E-02	AT5G14330	unknown protein
AL6G44610	-1.05	3.20E-04	1.07E-02	AT4G10560	MEE53, Cysteine/Histidine-rich C1 domain family protein
AL1G27770	-1.05	4.77E-06	3.79E-04	AT1G15670	Galactose oxidase/kelch repeat superfamily protein
AL6G16260	-1.05	3.04E-04	1.04E-02	AT5G06250	AP2/B3-like transcriptional factor family protein
AL1G32110	-1.06	1.47E-04	5.91E-03	AT1G14830	ADL1C, ADL5, DL1C, DRP1C, DYNAMIN-like 1C
AL3G38500	-1.06	7.55E-05	3.47E-03	/	Unknown
AL3G46430	-1.06	2.33E-03	4.87E-02	AT3G53610	ATRAB8, AtRab8B, AtRABE1a, RAB8, RAB GTPase homolog 8
AL8G42410	-1.06	1.67E-05	1.07E-03	AT5G64910	unknown protein
AL7G33000	-1.06	3.88E-05	2.03E-03	AT4G21120	AAT1, CAT1, amino acid transporter 1
AL5G37170	-1.06	8.62E-06	6.20E-04	AT3G55880	SUE4, Alpha/beta hydrolase related protein
AL4G38470	-1.06	3.39E-05	1.82E-03	AT2G40600	appr-1-p processing enzyme family protein
AL1G19360	-1.06	3.24E-06	2.75E-04	AT1G08930	ERD6, Major facilitator superfamily protein
AL2G30070	-1.07	8.26E-04	2.20E-02	AT1G70640	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein
AL1G44780	-1.07	1.14E-04	4.85E-03	AT1G30720	FAD-binding Berberine family protein
AL1G15640	-1.07	2.43E-04	8.70E-03	AT1G05730	Eukaryotic protein of unknown function (DUF842)
AL1G64390	-1.07	1.49E-04	6.01E-03	AT1G56120	Leucine-rich repeat transmembrane protein kinase
AL5G38730	-1.07	3.17E-04	1.06E-02	AT3G57240	BG3, beta-1,3-glucanase 3
AL7G29330	-1.08	5.53E-07	6.38E-05	AT4G23990	ATCSLG3, CSLG3, cellulose synthase like G3
AL5G26860	-1.08	4.53E-05	2.29E-03	AT3G47570	Leucine-rich repeat protein kinase family protein
AL8G30490	-1.08	7.17E-04	1.97E-02	AT5G55190	ATRAN3, RAN3, RAN GTPase 3
AL1G52710	-1.08	2.84E-05	1.58E-03	AT2G14080	Disease resistance protein (TIR-NBS-LRR class) family
AL7G38870	-1.08	9.74E-04	2.49E-02	AT1G31970	STRS1, DEA(D/H)-box RNA helicase family protein
AL6G51320	-1.08	3.05E-04	1.04E-02	AT4G01970	AtSTS, STS, stachyose synthase
AL4G29720	-1.08	1.75E-04	6.79E-03	AT2G33980	atnudt22, NUDT22, nudix hydrolase homolog 22
AL5G26340	-1.08	2.63E-04	9.21E-03	AT3G47570	Leucine-rich repeat protein kinase family protein
AL4G41450	-1.08	1.18E-03	2.88E-02	AT2G42840	PDF1, protodermal factor 1
AL4G13670	-1.09	2.25E-04	8.19E-03	AT2G23680	Cold acclimation protein WCOR413 family
AL2G22380	-1.09	2.80E-05	1.56E-03	AT1G65490	unknown protein
AL1G39120	-1.09	8.43E-04	2.24E-02	AT1G26610	C2H2-like zinc finger protein
AL5G35190	-1.09	9.87E-04	2.52E-02	AT3G54150	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AL7G27540	-1.09	6.49E-04	1.83E-02	AT4G25560	AtMYB18, MYB18, myb domain protein 18
AL3G44840	-1.09	4.08E-06	3.36E-04	AT2G11810	ATMGD3, MGD3, MGDC, monogalactosyldiacylglycerol synthase type C
AL3G20620	-1.09	7.75E-07	8.36E-05	AT3G09440	Heat shock protein 70 (Hsp 70) family protein
AL3G48080	-1.10	2.23E-05	1.34E-03	/	Unknown
AL2G23580	-1.10	4.03E-05	2.08E-03	AT1G65985	Plant protein of unknown function (DUF247)
AL1G56980	-1.10	1.45E-03	3.37E-02	AT1G49610	F-box family protein
AL5G29640	-1.10	5.04E-05	2.49E-03	AT3G49690	ATMYB84, MYB84, RAX3, myb domain protein 84
AL1G46300	-1.10	2.45E-05	1.43E-03	AT1G32190	alpha/beta-Hydrolases superfamily protein
AL2G16980	-1.10	1.67E-04	6.55E-03	AT1G58390	Disease resistance protein (CC-NBS-LRR class) family
AL1G38450	-1.10	1.32E-03	3.15E-02	AT1G27045	Homeobox-leucine zipper protein family
AL4G35790	-1.11	2.02E-04	7.56E-03	AT2G38500	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AL5G45360	-1.11	1.26E-04	5.23E-03	AT3G62610	ATMYB11, MYB11, PFG2, myb domain protein 11
AL4G25230	-1.11	1.23E-03	2.98E-02	AT2G30370	CHAL, EPFL6, allergen-related
AL4G33110	-1.11	3.85E-04	1.24E-02	AT2G36890	ATMYB38, BIT1, MYB38, RAX2, Duplicated homeodomain-like superfamily protein
AL4G39480	-1.11	1.48E-06	1.48E-04	AT2G41410	Calcium-binding EF-hand family protein
AL4G41800	-1.11	7.14E-05	3.33E-03	AT2G43140	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AL2G19750	-1.11	6.37E-04	1.81E-02	/	Unknown
AL7G19230	-1.11	4.42E-05	2.25E-03	AT3G26480	Transducin family protein / WD-40 repeat family protein
AL8G11850	-1.12	3.26E-05	1.77E-03	AT2G34690	ACD11, Glycolipid transfer protein (GLTP) family protein
AL3G49610	-1.12	4.41E-07	5.20E-05	AT2G16890	UDP-Glycosyltransferase superfamily protein
AL5G12290	-1.12	1.26E-04	5.23E-03	AT4G13510	AMT1;1, ATAMT1, ATAMT1;1, ammonium transporter 1;1
AL6G24580	-1.12	1.62E-05	1.04E-03	AT5G13930	ATCHS, CHS, TT4, Chalcone and stilbene synthase family protein
AL41U10010	-1.13	1.30E-03	3.11E-02	AT2G29110	ATGLR2.8, GLR2.8, GLR2.8, glutamate receptor 2.8

AL1G19060	-1.13	5.34E-06	4.15E-04	AT1G08630	THA1, threonine aldolase 1
AL6G48570	-1.13	2.19E-03	4.64E-02	AT4G04990	Protein of unknown function (DUF761)
AL6G51620	-1.13	2.84E-06	2.49E-04	AT4G01720	AtWRKY47, WRKY47, WRKY family transcription factor
AL8G16880	-1.13	7.12E-06	5.28E-04	AT5G43420	RING/U-box superfamily protein
AL3G47945	-1.14	2.01E-05	1.23E-03	AT2G20142	Toll-Interleukin-Resistance (TIR) domain family protein
AL2G37370	-1.14	6.33E-05	3.03E-03	AT1G77200	Integrase-type DNA-binding superfamily protein
AL6G22690	-1.14	2.19E-07	2.80E-05	AT5G11930	Thioredoxin superfamily protein
AL8G25190	-1.14	2.00E-04	7.49E-03	AT5G51000	F-box and associated interaction domains-containing protein
AL4G22130	-1.14	3.20E-06	2.73E-04	/	Unknown
AL8G42550	-1.14	6.04E-07	6.89E-05	AT5G65040	Protein of unknown function (DUF581)
AL8G37070	-1.14	2.41E-05	1.41E-03	AT5G60470	C2H2 and C2HC zinc fingers superfamily protein
AL4G37150	-1.15	1.21E-05	8.31E-04	AT2G39705	DVL11, RTFL8, ROTUNDIFOLIA like 8
AL4G38160	-1.15	3.21E-04	1.07E-02	AT2G40330	PYL6, RCAR9, PYR1-like 6
AL3G30840	-1.15	1.73E-05	1.10E-03	AT3G17700	ATCNGC20, CNBT1, CNGC20, cyclic nucleotide-binding transporter 1
AL5G31370	-1.15	5.02E-05	2.48E-03	AT3G50970	Low temperature induced30, XERO2, dehydrin family protein
AL5G20420	-1.15	2.82E-07	3.50E-05	AT3G30775	AT-POX, ATPDH, ATPOX, ERD5, PRO1, PRODH, Methylenetetrahydrofolate reductase family protein
AL8G21710	-1.15	2.26E-05	1.35E-03	AT5G48657	defense protein-related
AL8G15090	-1.15	3.25E-05	1.77E-03	AT5G44578	unknown protein
AL2G25120	-1.15	1.40E-05	9.31E-04	AT1G66880	Protein kinase superfamily protein
AL2G41490	-1.16	8.64E-06	6.20E-04	AT1G80050	APT2, ATAPT2, PHT1.1, adenine phosphoribosyl transferase 2
AL1G27190	-1.16	7.67E-04	2.07E-02	AT1G15125	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AL1G23350	-1.16	1.99E-05	1.22E-03	AT1G12080	Vacuolar calcium-binding protein-related
AL6G39590	-1.16	2.76E-05	1.55E-03	AT5G27420	ATL31, CNI1, carbon/nitrogen insensitive 1
AL6G40390	-1.16	8.74E-05	3.91E-03	AT5G28080	WNK9, Protein kinase superfamily protein
AL7G20320	-1.16	1.03E-03	2.58E-02	AT4G31680	Transcriptional factor B3 family protein
AL8G10780	-1.17	1.59E-04	6.29E-03	AT5G47260	ATP binding;GTP binding;nucleotide binding;nucleoside-triphosphatases
AL6G43450	-1.17	3.94E-05	2.04E-03	AT4G09820	BHLH42, TT8, basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AL6G44540	-1.17	3.79E-04	1.22E-02	AT4G10500	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AL1G52720	-1.17	7.55E-04	2.04E-02	AT2G14080	Disease resistance protein (TIR-NBS-LRR class) family
AL6G40620	-1.17	2.38E-04	8.54E-03	AT5G28610	unknown protein
AL8G31690	-1.17	2.05E-03	4.43E-02	AT5G56090	COX15, cytochrome c oxidase 15
AL7G48940	-1.17	2.49E-06	2.25E-04	AT5G40780	LHT1, lysine histidine transporter 1
AL3G31690	-1.18	2.35E-03	4.89E-02	AT3G18400	anac058, NAC058, NAC domain containing protein 58
AL7G33710	-1.18	1.04E-04	4.50E-03	AT4G20110	BP80-3;1, VSR3;1, VSR7, VACUOLAR SORTING RECEPTOR 7
AL4G37700	-1.18	7.58E-05	3.47E-03	AT2G40080	ELF4, Protein of unknown function (DUF1313)
AL4G15620	-1.18	1.58E-03	3.62E-02	AT1G64840	Protein of unknown function (DUF295)
AL595U10010	-1.18	2.38E-04	8.53E-03	/	Unknown
AL1G22870	-1.18	1.65E-03	3.72E-02	AT1G11730	Galactosyltransferase family protein
AL6G33490	-1.18	7.43E-05	3.42E-03	AT5G22470	NAD+ ADP-ribosyltransferases;NAD+ ADP-ribosyltransferases
AL1G11290	-1.18	5.04E-05	2.49E-03	AT1G01190	CYP78A8, cytochrome P450, family 78, subfamily A, polypeptide 8
AL1G30320	-1.19	4.25E-05	2.17E-03	AT1G17960	Threonyl-tRNA synthetase
AL1G22440	-1.19	6.99E-06	5.24E-04	AT1G11350	CBRLK1, RKS2, SD1-13, S-domain-1 13
AL5G32880	-1.19	1.29E-03	3.09E-02	AT3G52270	Transcription initiation factor IIF, beta subunit
AL5G40690	-1.19	1.31E-05	8.86E-04	/	Unknown
AL848U10010	-1.19	1.77E-04	6.82E-03	AT5G55570	unknown protein
AL1G11110	-1.19	2.13E-06	1.99E-04	AT1G01340	ACBK1, ATCNGC10, CNGC10, cyclic nucleotide gated channel 10
AL5G46240	-1.20	3.10E-04	1.05E-02	AT3G63380	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein
AL7G10450	-1.20	3.48E-04	1.14E-02	AT4G38560	Arabidopsis phospholipase-like protein (PEARLI 4) family
AL1G31620	-1.20	4.77E-06	3.79E-04	AT1G19050	ARR7, response regulator 7
AL6G18330	-1.21	7.52E-06	5.53E-04	AT5G07990	CYP75B1, D501, TT7, Cytochrome P450 superfamily protein
AL1G28270	-1.21	1.52E-04	6.10E-03	AT1G16110	WAKL6, wall associated kinase-like 6
AL6G52770	-1.21	1.14E-04	4.85E-03	AT4G00700	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein
AL5G13290	-1.21	7.19E-04	1.97E-02	AT2G03520	ATUPS4, UPS4, ureide permease 4
AL1G40340	-1.21	3.32E-08	5.59E-06	AT1G24575	unknown protein
AL4G38550	-1.21	1.80E-04	6.92E-03	/	Unknown
AL4G13590	-1.22	3.00E-05	1.65E-03	AT2G23620	ATMES1, MES1, methyl esterase 1
AL8G10320	-1.22	1.10E-03	2.73E-02	AT5G47635	Pollen Ole e 1 allergen and extensin family protein
AL1G27530	-1.22	2.19E-04	8.03E-03	AT1G15415	Encodes protein phosphatase 2A (PP2A) B'gamma subunit.
AL1G17410	-1.22	2.22E-03	4.69E-02	AT1G07260	UGT71C3, UDP-glucosyl transferase 71C3
AL2G24270	-1.22	3.69E-05	1.95E-03	AT1G01530	AGL28, AGAMOUS-like 28
AL1G61090	-1.22	3.71E-06	3.09E-04	AT1G52770	Phototropic-responsive NPH3 family protein
AL3G13800	-1.23	3.12E-06	2.68E-04	AT3G03910	GDH3, glutamate dehydrogenase 3
AL7G29540	-1.23	3.44E-06	2.90E-04	AT4G23810	ATWRKY53, WRKY53, WRKY family transcription factor
AL6G45710	-1.23	8.45E-05	3.80E-03	AT4G11310	Papain family cysteine protease
AL1G14710	-1.23	6.62E-07	7.43E-05	AT1G04980	ATPDI10, ATPDIL2-2, PDI10, PDIL2-2, PDI-like 2-2
AL1G59800	-1.23	1.41E-05	9.31E-04	AT1G51790	Leucine-rich repeat protein kinase family protein
AL2G16160	-1.24	8.16E-05	3.68E-03	AT1G60500	DRP4C, Dynamin related protein 4C
AL2G28640	-1.24	2.74E-06	2.43E-04	AT1G69520	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AL3G36330	-1.24	2.28E-06	2.09E-04	AT3G22142	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL3G43460	-1.25	2.36E-03	4.90E-02	/	Unknown
AL7G26330	-1.26	1.06E-08	2.04E-06	AT5G56030	AtHsp90.2, ERD8, HSP81-2, HSP90.2, heat shock protein 81-2
AL3G37430	-1.26	7.83E-05	3.58E-03	/	Unknown
AL3G52040	-1.27	2.42E-05	1.41E-03	AT2G18660	PNP-A, plant natriuretic peptide A
AL6G48650	-1.27	3.77E-06	3.13E-04	AT4G05320	UBQ10, polyubiquitin 10
AL3G16310	-1.27	5.13E-06	4.01E-04	AT3G05660	AtRLP33, RLP33, receptor like protein 33
AL383U10010	-1.27	6.18E-04	1.76E-02	AT2G28470	BGAL8, beta-galactosidase 8
AL1G28380	-1.27	9.08E-06	6.47E-04	AT1G16260	Wall-associated kinase family protein
AL7G46250	-1.28	1.63E-03	3.69E-02	AT5G37490	ARM repeat superfamily protein
AL1G30440	-1.28	1.50E-07	2.07E-05	/	Unknown

AL6G45210	-1.28	2.77E-05	1.55E-03	AT4G11070	AtWRKY41, WRKY41, WRKY family transcription factor
AL2G28890	-1.28	1.20E-04	5.03E-03	AT1G69720	HO3, heme oxygenase 3
AL8G38970	-1.28	1.30E-04	5.36E-03	AT5G62165	AGL42, AGAMOUS-like 42
AL5G37720	-1.29	3.92E-05	2.04E-03	AT2G40740	ATWRKY55, WRKY55, WRKY DNA-binding protein 55
AL1G32130	-1.29	8.35E-04	2.22E-02	AT1G14820	Sec14p-like phosphatidylinositol transfer family protein
AL6G23220	-1.29	9.61E-08	1.44E-05	AT5G12420	O-acyltransferase (WSD1-like) family protein
AL6G16180	-1.29	6.25E-04	1.78E-02	AT2G40460	Major facilitator superfamily protein
AL4G45130	-1.29	1.92E-04	7.27E-03	AT2G45920	U-box domain-containing protein
AL3G41650	-1.29	2.04E-04	7.60E-03	AT3G25490	Protein kinase family protein
AL3G34060	-1.30	1.03E-05	7.24E-04	AT3G20340	Expression of the gene is downregulated in the presence of paraquat, an inducer of photoxidative stress.
AL1G34330	-1.30	1.75E-04	6.79E-03	AT1G21245	Protein kinase superfamily protein
AL1G30060	-1.30	2.41E-06	2.19E-04	AT1G17710	Pyridoxal phosphate phosphatase-related protein
AL6G18200	-1.31	4.22E-04	1.32E-02	AT5G07870	HXXXD-type acyl-transferase family protein
AL6G38300	-1.31	2.04E-07	2.63E-05	AT5G26340	ATSTP13, MSS1, STP13, Major facilitator superfamily protein
AL6G53130	-1.31	1.01E-06	1.05E-04	AT4G00350	MATE efflux family protein
AL22U10100	-1.31	8.19E-05	3.69E-03	AT1G69880	ATH8, TH8, thioredoxin H-type 8
AL7G41820	-1.31	2.04E-04	7.60E-03	AT4G14390	Ankyrin repeat family protein
AL7G36070	-1.31	4.57E-04	1.39E-02	AT4G18330	Translation elongation factor EF1A/initiation factor IF2gamma family protein
AL8G14690	-1.31	1.09E-03	2.70E-02	AT5G44820	Nucleotide-diphospho-sugar transferase family protein
AL5G28360	-1.32	5.24E-06	4.08E-04	AT3G48850	PHT3;2, phosphate transporter 3;2
AL5G28870	-1.32	3.35E-05	1.81E-03	AT3G49160	pyruvate kinase family protein
AL6G21320	-1.32	2.77E-06	2.44E-04	AT5G10760	Eukaryotic aspartyl protease family protein
AL8G35640	-1.32	6.03E-06	4.61E-04	AT5G59070	UDP-Glycosyltransferase superfamily protein
AL2G17800	-1.32	1.94E-07	2.53E-05	AT1G58420	Uncharacterised conserved protein UCP031279
AL4G10840	-1.33	1.86E-06	1.76E-04	AT2G21640	Encodes a protein of unknown function that is a marker for oxidative stress response.
AL8G30960	-1.33	8.86E-04	2.32E-02	AT5G55410	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL6G48930	-1.33	3.64E-05	1.93E-03	AT4G05320	UBQ10, polyubiquitin 10
AL1G36690	-1.33	7.82E-04	2.10E-02	AT1G23120	Polyketide cyclase/dehydrase and lipid transport superfamily protein
AL8G30970	-1.33	1.17E-05	8.08E-04	AT5G55420	Encodes a Protease inhibitor/seed storage/LTP family protein [pseudogene]
AL5G39980	-1.34	1.84E-05	1.15E-03	AT3G58270	Arabidopsis phospholipase-like protein (PEARLI 4) with TRAF-like domain
AL7G14930	-1.34	4.13E-07	4.90E-05	AT4G36110	SAUR-like auxin-responsive protein family
AL7G41860	-1.35	3.52E-05	1.88E-03	AT4G14365	XBAT34, XB3 ortholog 4 in Arabidopsis thaliana
AL1010U10010	-1.35	3.88E-04	1.24E-02	AT5G58730	pfkB-like carbohydrate kinase family protein
AL1G34180	-1.35	1.97E-06	1.86E-04	AT1G21130	IGMT4, Indole glucosinolate O-methyltransferase 4, O-methyltransferase family protein
AL6G44110	-1.35	1.85E-05	1.15E-03	AT4G10270	Wound-responsive family protein
AL8G15490	-1.35	2.62E-04	9.18E-03	AT5G44380	FAD-binding Berberine family protein
AL2G19210	-1.36	4.36E-04	1.34E-02	/	Unknown
AL5G39760	-1.36	2.24E-03	4.71E-02	AT3G58090	Disease resistance-responsive (dirigent-like protein) family protein
AL4G23220	-1.36	6.51E-05	3.08E-03	AT2G28680	RmlC-like cupins superfamily protein
AL6G52310	-1.36	4.14E-07	4.90E-05	AT4G01060	CPL3, ETC3, CAPRICE-like MYB3
AL5G32010	-1.37	6.05E-04	1.73E-02	AT3G51570	Disease resistance protein (TIR-NBS-LRR class) family
AL2G38130	-1.37	1.78E-08	3.34E-06	AT1G77580	Plant protein of unknown function (DUF869)
AL70U10040	-1.37	7.30E-05	3.38E-03	AT5G33330	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
AL3G46670	-1.38	1.73E-05	1.10E-03	AT5G25600	unknown protein
AL6G46070	-1.38	8.03E-05	3.67E-03	AT4G11521	Receptor-like protein kinase-related family protein
AL3G29370	-1.38	6.68E-07	7.47E-05	AT3G16540	DegP11, DegP protease 11
AL6G50520	-1.38	2.81E-07	3.50E-05	AT4G02520	ATGSTF2, ATPM24, ATPM24.1, GST2, GSTF2, glutathione S-transferase PHI 2
AL3G51590	-1.38	4.99E-10	1.29E-07	AT2G18328	ATRL4, RL4, RAD-like 4
AL1G12370	-1.38	6.97E-06	5.24E-04	AT1G02930	ATGST1, ATGSTF3, ATGSTF6, ERD11, GST1, GSTF6, glutathione S-transferase 6
AL4G32560	-1.38	6.04E-08	9.52E-06	AT2G36400	AtGRF3, GRF3, growth-regulating factor 3
AL3G43450	-1.39	9.96E-04	2.53E-02	AT3G48860	unknown protein
AL7G19630	-1.39	2.37E-05	1.39E-03	AT4G32200	ASY2, DNA-binding HORMA family protein
AL3G48140	-1.40	6.95E-07	7.73E-05	AT1G72600	hydroxyproline-rich glycoprotein family protein
AL6G52680	-1.40	4.31E-04	1.33E-02	AT4G00770	unknown protein
AL3G11860	-1.40	9.39E-04	2.42E-02	AT3G02500	unknown protein
AL5G14130	-1.40	2.84E-07	3.50E-05	AT3G25610	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein
AL3G46130	-1.40	2.24E-03	4.72E-02	AT2G14580	ATPRB1, PRB1, basic pathogenesis-related protein 1
AL1G31580	-1.41	2.74E-04	9.53E-03	AT1G19020	unknown protein
AL7G30260	-1.41	4.09E-06	3.36E-04	AT4G23210	CRK13, cysteine-rich RLK (RECEPTOR-like protein kinase) 13
AL6G11850	-1.41	6.68E-08	1.03E-05	AT5G02580	Plant protein 1589 of unknown function
AL3G37940	-1.41	3.24E-08	5.49E-06	AT3G23290	LSH4, Protein of unknown function (DUF640)
AL481U10010	-1.42	2.34E-03	4.89E-02	/	Unknown
AL6G26020	-1.42	1.79E-05	1.12E-03	/	Unknown
AL6G47960	-1.43	2.86E-06	2.50E-04	AT4G04490	CRK36, cysteine-rich RLK (RECEPTOR-like protein kinase) 36
AL7G52480	-1.43	3.73E-06	3.11E-04	AT5G38310	unknown protein
AL7G35740	-1.44	5.08E-08	8.20E-06	AT4G18540	unknown protein
AL3G20390	-1.44	3.64E-04	1.18E-02	AT3G09270	ATGSTU8, GSTU8, glutathione S-transferase TAU 8
AL6G28960	-1.44	2.61E-08	4.58E-06	AT5G17860	CAX7, calcium exchanger 7
AL7G48030	-1.44	1.60E-03	3.64E-02	AT5G41390	PLAC8 family protein
AL6G23500	-1.45	5.22E-10	1.33E-07	AT5G12930	unknown protein
AL1G67280	-1.45	1.71E-06	1.67E-04	AT3G44480	cog1, RPP1, Disease resistance protein (TIR-NBS-LRR class) family
AL3G26070	-1.45	1.59E-06	1.57E-04	AT3G13898	unknown protein
AL1G62100	-1.45	4.24E-05	2.17E-03	AT2G06845	Beta-galactosidase related protein
AL1G13970	-1.45	1.77E-03	3.93E-02	AT1G04370	ATERF14, ERF14, Ethylene-responsive element binding factor 14
AL1G20540	-1.45	1.62E-05	1.04E-03	AT1G09932	Phosphoglycerate mutase family protein
AL6G16610	-1.45	1.24E-06	1.26E-04	AT5G12280	SWAP (Suppressor-of-White-APricot)/surp RNA-binding domain-containing protein
AL3G28090	-1.45	3.69E-06	3.08E-04	AT3G15518	unknown protein
AL5G22430	-1.46	7.01E-07	7.77E-05	AT3G44300	AtNIT2, NIT2, nitrilase 2
AL4G26350	-1.47	2.09E-05	1.27E-03	AT2G31160	LSH3, Protein of unknown function (DUF640)

AL68U10030	-1.48	1.13E-04	4.82E-03	/	Unknown
AL1G34170	-1.48	7.50E-07	8.22E-05	AT1G21120	IGMT2, Indole glucosinolate O-methyltransferase 2, O-methyltransferase family protein
AL8G45180	-1.48	3.92E-07	4.67E-05	AT5G66350	SHI, Lateral root primordium (LRP) protein-related
AL6G50670	-1.48	1.46E-05	9.57E-04	AT4G02420	Concanavalin A-like lectin protein kinase family protein
AL6G12500	-1.48	2.06E-05	1.26E-03	AT5G03210	ATDIP2, DBP-INTERACTING PROTEIN 2, DIP2
AL4G19190	-1.48	3.45E-08	5.73E-06	AT2G26440	Plant invertase/pectin methylesterase inhibitor superfamily
AL7G14140	-1.50	3.95E-04	1.26E-02	AT4G36840	Galactose oxidase/kelch repeat superfamily protein
AL1G26100	-1.50	3.23E-04	1.08E-02	AT1G14210	Ribonuclease T2 family protein
AL8G27170	-1.50	2.79E-05	1.56E-03	AT5G52740	Copper transport protein family
AL1G28250	-1.50	7.09E-06	5.28E-04	AT1G16090	WAKL7, wall associated kinase-like 7
AL1G22240	-1.51	3.38E-08	5.64E-06	AT1G11210	Protein of unknown function (DUF761)
AL6G50030	-1.52	4.71E-04	1.43E-02	AT4G05320	UBQ10, polyubiquitin 10
AL2G14290	-1.52	8.37E-09	1.67E-06	AT1G61800	ATGPT2, GPT2, glucose-6-phosphate/phosphate translocator 2
AL3G48150	-1.52	9.96E-05	4.36E-03	AT1G62220	unknown protein
AL4G13360	-1.52	1.23E-03	2.97E-02	/	Unknown
AL2G22200	-1.52	2.82E-04	9.78E-03	AT1G65481	unknown protein
AL6G35600	-1.52	2.77E-06	2.44E-04	AT5G24210	alpha/beta-Hydrolases superfamily protein
AL4G32080	-1.52	3.37E-04	1.11E-02	AT2G35980	ATNHL10, NHL10, YLS9, Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
AL3G18190	-1.53	1.29E-03	3.09E-02	AT3G06040	Ribosomal protein L12/ ATP-dependent Clp protease adaptor protein ClpS family protein
AL1G35090	-1.53	5.00E-04	1.50E-02	AT1G21890	nodulin MtN21 /EamA-like transporter family protein
AL5G22420	-1.53	1.33E-04	5.46E-03	AT3G44290	anac060, NAC060, NAC domain containing protein 60
AL6G18640	-1.54	4.55E-06	3.67E-04	AT5G08240	unknown protein
AL60U10040	-1.54	5.58E-05	2.72E-03	AT1G78290	SNRK2-8, SNRK2.8, SRK2C, Protein kinase superfamily protein
AL6G35620	-1.55	3.81E-04	1.23E-02	AT5G24220	Lipase class 3-related protein
AL5G26520	-1.55	1.08E-06	1.11E-04	AT3G47360	ATHSD3, HSD3, hydroxysteroid dehydrogenase 3
AL5G12280	-1.56	2.67E-04	9.31E-03	/	Unknown
AL6G51580	-1.56	5.15E-07	5.98E-05	AT4G01750	RGXT2, rhamnogalacturonan xylosyltransferase 2
AL89U10020	-1.56	2.21E-06	2.05E-04	/	Unknown
AL7G52300	-1.57	6.58E-05	3.10E-03	AT5G38350	Disease resistance protein (NBS-LRR class) family
AL4G23310	-1.57	1.80E-05	1.13E-03	AT2G28780	unknown protein
AL4G35170	-1.57	8.75E-04	2.30E-02	AT2G38152	alpha 1,4-glycosyltransferase family protein
AL8G22630	-1.57	1.04E-05	7.32E-04	AT5G49120	Protein of unknown function (DUF581)
AL3G37610	-1.58	2.87E-04	9.92E-03	AT3G23172	unknown protein
AL7G51240	-1.58	1.62E-07	2.19E-05	AT5G39220	alpha/beta-Hydrolases superfamily protein
AL4G41640	-1.58	3.34E-06	2.83E-04	AT2G43000	anac042, NAC042, NAC domain containing protein 42
AL2G24170	-1.58	1.49E-06	1.49E-04	AT1G66390	ATMYB90, MYB90, PAP2, myb domain protein 90
AL6G46190	-1.59	2.94E-04	1.01E-02	AT4G11610	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein
AL3G44950	-1.59	4.09E-05	2.10E-03	/	Unknown
AL3G48170	-1.59	2.12E-05	1.29E-03	/	Unknown
AL3G10640	-1.60	1.44E-03	3.35E-02	AT3G01516	unknown protein
AL7G10150	-1.60	1.09E-11	3.85E-09	AT4G38230	ATCPK26, CPK26, calcium-dependent protein kinase 26
AL3G42610	-1.60	8.24E-09	1.66E-06	AT3G16580	F-box and associated interaction domains-containing protein
AL5G16850	-1.60	1.58E-03	3.62E-02	AT3G27440	UKL5, uridine kinase-like 5
AL4G41630	-1.61	2.37E-04	8.52E-03	AT2G42990	GDSL-like Lipase/Acylhydrolase superfamily protein
AL5G32400	-1.61	2.67E-05	1.52E-03	AT3G51910	AT-HSFA7A, HSFA7A, heat shock transcription factor A7A
AL2G33680	-1.61	6.28E-04	1.79E-02	AT1G73860	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AL2G19450	-1.62	2.33E-04	8.42E-03	AT1G64940	CYP89A6, cytochrome P450, family 87, subfamily A, polypeptide 6
AL4G14290	-1.62	1.58E-03	3.62E-02	/	Unknown
AL4G21130	-1.63	1.45E-07	2.02E-05	AT2G27220	BLH5, BEL1-like homeodomain 5
AL8G32440	-1.63	2.33E-04	8.42E-03	AT5G56620	anac099, NAC099, NAC domain containing protein 99
AL8G15190	-1.63	6.67E-04	1.87E-02	/	Unknown
AL8G20470	-1.64	2.37E-03	4.92E-02	/	Unknown
AL3G52030	-1.64	1.39E-07	1.97E-05	AT2G18650	MEE16, RING/U-box superfamily protein
AL8G14260	-1.64	6.55E-04	1.84E-02	AT1G33920	ATPP2-A4, PP2-A4, phloem protein 2-A4
AL3G29360	-1.64	3.44E-05	1.85E-03	AT3G16530	Legume lectin family protein
AL1G47540	-1.64	3.10E-04	1.05E-02	AT1G33220	Glycosyl hydrolase superfamily protein
AL6G30850	-1.65	2.17E-03	4.61E-02	AT5G19360	CPK34, calcium-dependent protein kinase 34
AL6G25070	-1.65	1.99E-08	3.70E-06	AT5G14360	Ubiquitin-like superfamily protein
AL2G24780	-1.65	6.78E-05	3.19E-03	/	Unknown
AL4G41090	-1.65	1.37E-12	6.52E-10	AT2G42540	COR15, COR15A, cold-regulated 15a
AL4G29650	-1.66	4.84E-06	3.84E-04	AT2G33850	unknown protein
AL3G26510	-1.67	1.39E-06	1.40E-04	AT3G14225	GLIP4, GDSL-motif lipase 4
AL8G35270	-1.67	2.19E-03	4.65E-02	AT5G64410	ATOPT4, OPT4, oligopeptide transporter 4
AL2G34480	-1.67	2.24E-08	4.05E-06	AT1G74590	ATGSTU10, GSTU10, glutathione S-transferase TAU 10
AL3G29960	-1.67	1.22E-04	5.12E-03	AT3G16980	NRPB9A, NRPD9A, NRPE9A, RNA polymerases M/15 Kd subunit
AL4G31340	-1.68	1.41E-03	3.31E-02	AT2G35310	Transcriptional factor B3 family protein
AL6G42280	-1.68	1.93E-08	3.59E-06	/	Unknown
AL4G33830	-1.68	1.45E-05	9.57E-04	AT2G37430	C2H2 and C2HC zinc fingers superfamily protein
AL1G36030	-1.68	4.91E-05	2.44E-03	AT1G22500	RING/U-box superfamily protein
AL1G47760	-1.68	8.92E-06	6.38E-04	AT4G10265	Wound-responsive family protein
AL2G35840	-1.68	1.83E-04	7.00E-03	AT5G44430	PDF1.2c, plant defensin 1.2C
AL1G52220	-1.69	7.07E-05	3.30E-03	AT1G44180	Peptidase M20/M25/M40 family protein
AL7G48560	-1.69	6.84E-07	7.63E-05	AT5G40990	GLIP1, GDSL lipase 1
AL8G11860	-1.71	2.61E-06	2.34E-04	AT1G37020	Cysteine proteinases superfamily protein
AL1G25250	-1.71	1.46E-03	3.38E-02	AT1G13470	Protein of unknown function (DUF1262)
AL68U10040	-1.72	1.07E-12	5.19E-10	/	Unknown
AL1G62230	-1.72	8.18E-04	2.18E-02	AT1G53610	unknown protein
AL6G42600	-1.72	4.37E-05	2.23E-03	AT4G08780	Peroxidase superfamily protein
AL5G22700	-1.73	1.22E-06	1.25E-04	AT3G44550	FAR5, fatty acid reductase 5

AL8G32820	-1.73	1.61E-05	1.04E-03	AT5G56960	basic helix-loop-helix (bHLH) DNA-binding family protein
AL7G47020	-1.73	4.84E-04	1.46E-02	AT2G18196	Heavy metal transport/detoxification superfamily protein
AL6G46610	-1.74	8.19E-10	1.94E-07	AT4G11890	Protein kinase superfamily protein
AL8G19350	-1.74	9.93E-11	3.00E-08	AT5G42250	Zinc-binding alcohol dehydrogenase family protein
AL2G18200	-1.74	9.19E-10	2.15E-07	AT1G58225	unknown protein
AL1G32100	-1.75	1.02E-04	4.45E-03	AT1G14840	ATMAP70-4, MAP70-4, microtubule-associated proteins 70-4
AL4G18400	-1.75	3.76E-11	1.20E-08	AT2G26150	ATHSFA2, HSFA2, heat shock transcription factor A2
AL5G31070	-1.76	6.13E-04	1.75E-02	/	Unknown
AL2G22190	-1.76	6.08E-08	9.53E-06	/	Unknown
AL2G14850	-1.77	1.94E-04	7.33E-03	/	Unknown
AL3G16790	-1.78	1.92E-05	1.19E-03	AT3G05980	unknown protein
AL3G47130	-1.78	3.45E-07	4.17E-05	AT2G15390	atfut4, FUT4, fucosyltransferase 4
AL8G42900	-1.78	1.32E-05	8.89E-04	AT5G65320	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AL6G46230	-1.79	9.85E-08	1.46E-05	AT4G11650	ATOSM34, OSM34, osmotin 34
AL7G19360	-1.79	7.11E-06	5.28E-04	AT3G55260	ATHEX2, HEXO1, beta-hexosaminidase 1
AL7G51220	-1.79	4.85E-06	3.84E-04	AT5G39240	unknown protein
AL7G43190	-1.79	4.03E-06	3.33E-04	AT1G44810	DNA-binding storekeeper protein-related transcriptional regulator
AL7G29660	-1.80	1.05E-07	1.54E-05	AT4G23700	ATCHX17, CHX17, cation/H+ exchanger 17
AL1G17310	-1.80	2.07E-08	3.80E-06	AT1G07390	AtRLP1, RLP1, receptor like protein 1
AL6G21340	-1.81	7.51E-11	2.29E-08	AT5G10770	Eukaryotic aspartyl protease family protein
AL8G41260	-1.81	1.71E-10	4.88E-08	AT5G64000	ATSAL2, SAL2, Inositol monophosphatase family protein
AL1G39380	-1.81	1.58E-06	1.56E-04	AT1G26380	FAD-binding Berberine family protein
AL5G26290	-1.81	2.72E-05	1.54E-03	AT3G47050	Glycosyl hydrolase family protein
AL8G15380	-1.82	2.28E-04	8.28E-03	AT5G44480	DUR, NAD(P)-binding Rossmann-fold superfamily protein
AL5G17510	-1.82	4.87E-04	1.46E-02	AT3G27970	Exonuclease family protein
AL8G31660	-1.84	1.19E-03	2.91E-02	AT5G56080	ATNAS2, NAS2, nicotianamine synthase 2
AL6G52790	-1.84	4.42E-12	1.79E-09	AT4G00670	Remorin family protein
AL3G41420	-1.85	1.82E-05	1.13E-03	AT1G27150	Tetratricopeptide repeat (TPR)-like superfamily protein
AL8G22270	-1.86	2.40E-04	8.59E-03	AT3G59070	Cytochrome b561/ferric reductase transmembrane with DOMON related domain
AL3G33580	-1.86	1.45E-05	9.57E-04	AT4G00260	MEE45, Transcriptional factor B3 family protein
AL7G28310	-1.87	3.20E-06	2.73E-04	AT4G24890	ATPAP24, PAP24, purple acid phosphatase 24
AL3G24660	-1.88	1.62E-03	3.68E-02	AT3G12970	unknown protein
AL5G23110	-1.88	8.98E-05	3.98E-03	AT3G44780	Cysteine proteinases superfamily protein
AL1G36790	-1.88	2.88E-04	9.94E-03	AT1G23130	Polyketide cyclase/dehydrase and lipid transport superfamily protein
AL6G47140	-1.89	6.45E-12	2.38E-09	AT4G12290	Copper amine oxidase family protein
AL41U10020	-1.90	1.98E-10	5.57E-08	AT2G29120	ATGLR2.7, GLR2.7, GLR2.7, glutamate receptor 2.7
AL6G47980	-1.90	2.24E-05	1.34E-03	AT4G04510	CRK38, cysteine-rich RLK (RECEPTOR-like protein kinase) 38
AL1G19860	-1.91	1.03E-08	1.99E-06	AT1G09350	AtGolS3, GolS3, galactinol synthase 3
AL7G37960	-1.91	1.32E-11	4.63E-09	AT4G16745	Exostosin family protein
AL1G25950	-1.92	3.29E-05	1.78E-03	AT1G14080	ATFUT6, FUT6, fucosyltransferase 6
AL9U10390	-1.92	2.94E-04	1.01E-02	AT4G13290	CYP71A19, cytochrome P450, family 71, subfamily A, polypeptide 19
AL1G32120	-1.93	2.49E-05	1.44E-03	AT1G14830	ADL1C, ADL5, DL1C, DRP1C, DYNAMIN-like 1C
AL4G36140	-1.93	1.37E-03	3.22E-02	AT2G38830	Ubiquitin-conjugating enzyme/RWD-like protein
AL4G31880	-1.93	1.42E-04	5.76E-03	AT2G35770	scpl28, serine carboxypeptidase-like 28
AL3G36480	-1.95	2.14E-04	7.90E-03	AT3G22231	PCC1, pathogen and circadian controlled 1
AL2G37100	-1.95	1.45E-12	6.71E-10	AT1G76955	Expressed protein
AL6G42570	-1.96	9.88E-04	2.52E-02	AT4G08770	Peroxidase superfamily protein
AL8G14340	-1.96	1.07E-05	7.48E-04	AT2G32140	transmembrane receptors
AL6G51310	-1.97	1.07E-03	2.67E-02	/	Unknown
AL7G21600	-1.98	4.13E-05	2.12E-03	AT4G30540	Class I glutamine amidotransferase-like superfamily protein
AL7G52750	-1.98	2.51E-04	8.88E-03	AT5G38130	HXXXD-type acyl-transferase family protein
AL7G36480	-1.98	1.11E-05	7.73E-04	AT4G17990	unknown protein
AL3G38410	-1.99	1.20E-03	2.91E-02	AT2G46760	D-arabinono-1,4-lactone oxidase family protein
AL5G20940	-2.00	2.24E-03	4.72E-02	/	Unknown
AL2G39110	-2.02	1.92E-03	4.20E-02	AT1G78710	TBL42, TRICHOME BIREFRINGENCE-LIKE 42
AL1G23980	-2.02	2.86E-05	1.59E-03	AT1G12630	Integrase-type DNA-binding superfamily protein
AL6G37120	-2.02	2.99E-10	8.00E-08	AT5G25390	SHN2, Integrase-type DNA-binding superfamily protein
AL5G29090	-2.02	1.81E-07	2.40E-05	AT2G27420	Cysteine proteinases superfamily protein
AL4G18410	-2.02	4.59E-09	9.64E-07	/	Unknown
AL7G14660	-2.03	4.61E-04	1.40E-02	AT4G36430	Peroxidase superfamily protein
AL1G53950	-2.05	2.70E-05	1.53E-03	AT1G47603	ATPUP19, PUP19, purine permease 19
AL7G30310	-2.05	2.91E-10	7.86E-08	AT4G23130	CRK5, RLK6, cysteine-rich RLK (RECEPTOR-like protein kinase) 5
AL5G38610	-2.06	1.61E-09	3.57E-07	AT3G57130	BOP1, Blade-on-petiol 1, Ankyrin repeat family protein / BTB/POZ domain-containing protein
AL8G33190	-2.07	3.63E-06	3.04E-04	AT5G57220	CYP81F2, cytochrome P450, family 81, subfamily F, polypeptide 2
AL7G40540	-2.07	2.58E-07	3.23E-05	AT4G15160	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL1G35500	-2.07	4.02E-09	8.50E-07	AT1G22065	unknown protein
AL34U10120	-2.08	4.63E-04	1.41E-02	AT5G49000	Galactose oxidase/kelch repeat superfamily protein
AL6G21330	-2.08	1.42E-12	6.67E-10	AT5G10770	Eukaryotic aspartyl protease family protein
AL3G33420	-2.08	1.29E-04	5.31E-03	/	Unknown
AL4G19450	-2.09	7.74E-10	1.86E-07	AT2G26560	PLA IIA, PLA2A, PLP2, PLP2, phospholipase A 2A
AL8G29940	-2.09	4.27E-04	1.33E-02	AT5G54550	Protein of unknown function (DUF295)
AL3G24130	-2.10	1.59E-05	1.03E-03	AT3G12500	ATHCHIB, B-CHI, CHI-B, HCHIB, PR-3, PR3, basic chitinase
AL3G26370	-2.10	1.93E-04	7.30E-03	AT3G14130	Aldolase-type TIM barrel family protein
AL1G23200	-2.11	4.74E-04	1.43E-02	AT1G11990	O-fucosyltransferase family protein
AL7G30250	-2.11	3.67E-12	1.52E-09	AT4G23220	CRK14, cysteine-rich RLK (RECEPTOR-like protein kinase) 14
AL3G22350	-2.11	5.29E-05	2.59E-03	AT3G10830	Unknown
AL481U10020	-2.12	5.75E-04	1.67E-02	/	Unknown
AL6G40690	-2.13	2.27E-06	2.09E-04	AT2G07760	Zinc knuckle (CCHC-type) family protein
AL6G21820	-2.14	3.67E-05	1.94E-03	AT5G11210	ATGLR2.5, GLR2.5, glutamate receptor 2.5

AL2G17640	-2.14	2.73E-11	9.19E-09	AT1G58936	Inositol-pentakisphosphate 2-kinase family protein
AL8G27310	-2.14	1.70E-12	7.76E-10	AT5G52860	ABC-2 type transporter family protein
AL3G33570	-2.16	2.96E-06	2.56E-04	AT4G00260	MEE45, Transcriptional factor B3 family protein
AL3G46510	-2.17	2.28E-06	2.09E-04	/	Unknown
AL8G17290	-2.18	1.31E-05	8.86E-04	AT5G43230	unknown protein
AL5G25650	-2.19	2.27E-09	4.92E-07	AT3G46690	UDP-Glycosyltransferase superfamily protein
AL3G45910	-2.20	1.47E-04	5.91E-03	AT2G14210	AGL44, ANR1, AGAMOUS-like 44
AL6G42290	-2.20	1.96E-10	5.57E-08	/	Unknown
AL191U10030	-2.21	3.36E-05	1.81E-03	AT5G56240	unknown protein
AL2G30020	-2.22	3.05E-06	2.63E-04	AT2G40460	Major facilitator superfamily protein
AL2G33800	-2.22	1.99E-03	4.32E-02	AT1G73965	CLE13, CLAVATA3/ESR-RELATED 13
AL1G12360	-2.23	5.00E-12	1.91E-09	AT1G02920	ATGST11, ATGSTF7, ATGSTF8, GST11, GSTF7, glutathione S-transferase 7
AL3G22850	-2.25	1.48E-06	1.48E-04	AT3G11340	UDP-Glycosyltransferase superfamily protein
AL1G52030	-2.26	1.20E-03	2.91E-02	AT1G43800	Plant stearoyl-acyl-carrier-protein desaturase family protein
AL1G48080	-2.26	7.36E-04	2.00E-02	AT1G33670	Leucine-rich repeat (LRR) family protein
AL6G42650	-2.27	2.43E-05	1.42E-03	AT4G08840	APUM11, PUM11, pumilio 11
AL96U10010	-2.28	1.24E-03	2.98E-02	AT5G18880	RNA-directed DNA polymerase (reverse transcriptase)-related family protein
AL1G46220	-2.34	1.83E-03	4.05E-02	AT1G32140	F-box family protein
AL6G22680	-2.34	2.90E-12	1.22E-09	AT5G11920	AtcwINV6, cwINV6, 6-&1-fructan exohydrolase
AL8G27540	-2.35	4.28E-06	3.50E-04	AT5G53000	TAP46, 2A phosphatase associated protein of 46 kD
AL1G43700	-2.35	6.90E-04	1.91E-02	AT1G29860	ATWRKY71, WRKY71, WRKY DNA-binding protein 71
AL2G31310	-2.37	1.05E-03	2.63E-02	AT1G71740	unknown protein
AL6G33590	-2.37	2.01E-03	4.37E-02	AT5G22560	Plant protein of unknown function (DUF247)
AL6G51550	-2.37	9.93E-06	7.01E-04	AT4G01770	RGXT1, rhamnogalacturonan xylosyltransferase 1
AL3G46350	-2.37	1.26E-03	3.02E-02	AT5G27910	NF-YC8, nuclear factor Y, subunit C8
AL7G31650	-2.38	1.36E-03	3.22E-02	AT4G04910	NSF, AAA-type ATPase family protein
AL6G13740	-2.39	3.53E-06	2.97E-04	AT5G04120	Phosphoglycerate mutase family protein
AL5G23650	-2.40	4.56E-05	2.30E-03	AT4G21700	Protein of unknown function (DUF2921)
AL7G30210	-2.40	2.21E-12	9.41E-10	AT4G23160	CRK8, cysteine-rich RLK (RECEPTOR-like protein kinase) 8
AL1G35710	-2.42	9.84E-08	1.46E-05	AT1G22250	unknown protein
AL7G11230	-2.42	5.99E-18	5.53E-15	AT4G39250	ATRL1, RL1, RSM2, RAD-like 1
AL2G39420	-2.45	7.28E-04	1.98E-02	AT1G78970	ATLUP1, LUP1, lupeol synthase 1
AL6G42410	-2.46	1.99E-07	2.59E-05	AT5G28712	transposable element gene
AL1G66220	-2.47	6.66E-09	1.36E-06	AT3G59990	MAP2B, methionine aminopeptidase 2B
AL2G25450	-2.49	1.12E-03	2.77E-02	/	Unknown
AL3G30470	-2.52	1.50E-07	2.07E-05	AT3G17400	F-box family protein
AL5G16490	-2.53	8.27E-04	2.20E-02	AT3G27290	RNI-like superfamily protein
AL8G30500	-2.54	5.36E-04	1.58E-02	/	Unknown
AL7G15980	-2.59	3.34E-08	5.61E-06	/	Unknown
AL831U10010	-2.61	4.34E-04	1.34E-02	AT3G06050	ATPRXIIF, PRXIIF, peroxiredoxin IIF
AL6G24210	-2.62	3.09E-04	1.05E-02	AT5G13600	Phototropic-responsive NPH3 family protein
AL6G11730	-2.66	2.82E-20	3.19E-17	AT5G02490	Heat shock protein 70 (Hsp 70) family protein
AL7G37970	-2.66	2.50E-06	2.25E-04	AT4G16740	ATTPS03, TPS03, terpene synthase 03
AL3G18960	-2.68	3.52E-05	1.89E-03	AT3G07600	Heavy metal transport/detoxification superfamily protein
AL2G24790	-2.68	3.69E-05	1.95E-03	AT5G24740	Protein of unknown function (DUF1162)
AL8G11360	-2.69	5.33E-08	8.52E-06	AT2G16210	Transcriptional factor B3 family protein
AL4G10030	-2.70	3.19E-04	1.07E-02	/	Unknown
AL6G34000	-2.70	5.00E-04	1.50E-02	AT5G22860	Serine carboxypeptidase S28 family protein
AL5G28080	-2.71	9.36E-07	9.81E-05	AT1G80700	unknown protein
AL1G25670	-2.72	2.72E-04	9.50E-03	/	Unknown
AL4G16330	-2.72	2.33E-04	8.42E-03	AT2G25150	HXXXD-type acyl-transferase family protein
AL5G27070	-2.72	4.43E-04	1.36E-02	AT3G47790	ATATH7, ATH7, ABC2 homolog 7
AL1G65180	-2.75	2.04E-04	7.60E-03	AT1G54730	Major facilitator superfamily protein
AL5G34710	-2.76	1.35E-04	5.51E-03	/	Unknown
AL5G15780	-2.80	4.72E-08	7.69E-06	AT3G26830	CYP71B15, PAD3, Cytochrome P450 superfamily protein
AL2G13380	-2.81	1.60E-04	6.33E-03	AT1G62500	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL8G44620	-2.84	2.36E-05	1.39E-03	AT5G66816	unknown protein
AL1G24580	-2.84	1.76E-11	6.03E-09	AT1G12940	ATNRT2.5, NRT2.5, nitrate transporter2.5
AL2G11070	-2.84	9.83E-06	6.95E-04	AT1G64030	ATSRP3, SRP3, serpin 3
AL3G41580	-2.85	6.16E-07	7.01E-05	AT1G14610	TWN2, VALRS, valyl-tRNA synthetase / valine--tRNA ligase (VALRS)
AL7G15990	-2.85	1.51E-09	3.36E-07	/	Unknown
AL8G11420	-2.88	5.18E-05	2.55E-03	AT5G46871	Putative membrane lipoprotein
AL8G41130	-2.88	1.35E-04	5.52E-03	AT5G63900	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain
AL7G14500	-2.91	9.56E-19	9.08E-16	AT4G39250	ATRL1, RL1, RSM2, RAD-like 1
AL2G24140	-2.91	1.17E-05	8.09E-04	AT1G66370	AtMYB113, MYB113, myb domain protein 113
AL5G12390	-2.92	1.66E-05	1.06E-03	/	Unknown
AL4G44090	-2.94	1.27E-04	5.28E-03	AT2G44990	ATCCD7, CCD7, MAX3, carotenoid cleavage dioxygenase 7
AL6G51710	-2.94	1.72E-04	6.70E-03	AT4G01630	ATEXP17, ATEXPA17, ATHEXP ALPHA 1.13, EXPA17, expansin A17
AL4G35600	-2.96	1.43E-04	5.78E-03	AT2G38380	Peroxidase superfamily protein
AL3G47620	-2.97	1.94E-04	7.32E-03	AT2G40910	F-box and associated interaction domains-containing protein
AL8G20770	-2.98	1.42E-04	5.76E-03	AT1G21720	PBC1, proteasome beta subunit C1
AL5G45740	-3.01	1.47E-20	1.80E-17	AT3G62960	Thioredoxin superfamily protein
AL1G38320	-3.04	5.24E-07	6.07E-05	/	Unknown
AL2G13080	-3.05	2.88E-20	3.19E-17	AT1G62710	BETA-VPE, BETAVPE, beta vacuolar processing enzyme
AL4G43200	-3.05	2.14E-09	4.67E-07	AT2G44240	Protein of Unknown Function (DUF239)
AL7G38240	-3.10	5.55E-06	4.29E-04	/	Unknown
AL4G15520	-3.12	1.77E-06	1.70E-04	AT1G66235	unknown protein
AL4G25680	-3.15	5.69E-09	1.17E-06	AT2G30770	CYP71A13, cytochrome P450, family 71, subfamily A, polypeptide 13
AL4G36650	-3.17	2.98E-06	2.58E-04	AT2G39310	JAL22, jacalin-related lectin 22
AL3G34480	-3.19	9.72E-05	4.27E-03	/	Unknown

AL1G47080	-3.20	3.84E-05	2.01E-03	AT1G32770	ANAC012, NAC012, NST3, SND1, NAC domain containing protein 12
AL5G34210	-3.26	6.22E-05	2.98E-03	AT5G35715	CYP71B8, cytochrome P450, family 71, subfamily B, polypeptide 8
AL7G16100	-3.27	1.38E-09	3.12E-07	AT4G35120	Galactose oxidase/kelch repeat superfamily protein
AL8G10760	-3.27	9.34E-07	9.81E-05	/	Unknown
AL191U10020	-3.32	4.57E-06	3.67E-04	AT5G56230	PRA1.G2, prenylated RAB acceptor 1.G2
AL2G16560	-3.39	1.33E-06	1.34E-04	/	Unknown
AL4G46210	-3.41	9.79E-09	1.91E-06	AT2G46740	D-arabinono-1,4-lactone oxidase family protein
AL7G24740	-3.41	2.72E-14	1.71E-11	AT4G27890	HSP20-like chaperones superfamily protein
AL1G38230	-3.52	5.95E-06	4.56E-04	/	Unknown
AL5G14020	-3.68	4.51E-12	1.80E-09	AT3G25550	F-box family protein
AL5G22230	-3.68	1.66E-08	3.14E-06	AT3G44190	FAD/NAD(P)-binding oxidoreductase family protein
AL5G28430	-3.70	5.16E-06	4.02E-04	AT3G48920	AtMYB45, MYB45, myb domain protein 45
AL5G33280	-3.77	9.77E-06	6.92E-04	AT3G52140	tetratricopeptide repeat (TPR)-containing protein
AL1G53680	-3.79	7.65E-07	8.33E-05	/	Unknown
AL4G10850	-3.84	1.29E-26	2.37E-23	AT2G21650	ATRL2, MEE3, RSM1, Homeodomain-like superfamily protein
AL5G23200	-3.87	7.38E-06	5.45E-04	AT3G44790	TRAF-like family protein
AL9U11830	-3.93	1.26E-13	7.21E-11	/	Unknown
AL5G30750	-4.09	1.68E-07	2.24E-05	AT3G50610	unknown protein
AL8G40150	-4.11	5.15E-10	1.33E-07	AT5G63090	LOB, Lateral organ boundaries (LOB) domain family protein
AL8G18270	-4.24	8.91E-07	9.48E-05	AT3G26670	Protein of unknown function (DUF803)
AL6G41500	-4.27	1.58E-07	2.16E-05	AT4G09012	Mitochondrial ribosomal protein L27
AL3G26060	-4.33	5.82E-12	2.20E-09	AT3G13890	ATMYB26, MS35, MYB26, myb domain protein 26
AL7G16090	-4.35	2.74E-11	9.19E-09	AT4G35120	Galactose oxidase/kelch repeat superfamily protein
AL2G24530	-4.40	5.61E-13	2.89E-10	/	Unknown
AL6G21110	-4.44	1.46E-10	4.22E-08	AT5G10580	Protein of unknown function, DUF599
AL2G13710	-4.56	1.81E-06	1.73E-04	AT1G62210	unknown protein
AL5G26400	-4.58	9.32E-09	1.84E-06	/	Unknown
AL2G22180	-4.65	1.31E-07	1.86E-05	AT1G65480	Flowering locus T, PEBP (phosphatidylethanolamine-binding protein) family protein
AL8G23530	-4.73	2.09E-17	1.74E-14	AT4G39753	Galactose oxidase/kelch repeat superfamily protein
AL1G48610	-4.83	5.75E-11	1.82E-08	/	Unknown
AL1G36260	-5.33	3.66E-11	1.18E-08	/	Unknown
AL6G42040	-5.37	1.25E-13	7.21E-11	/	Unknown
AL6G28820	-5.56	6.84E-10	1.70E-07	AT3G01345	Expressed protein
AL3G53610	-5.58	1.90E-17	1.62E-14	/	Unknown
AL6G42050	-5.62	5.20E-15	3.67E-12	/	Unknown
AL1G63670	-5.86	3.95E-12	1.62E-09	/	Unknown
AL3G40380	-6.66	1.89E-12	8.50E-10	AT5G58840	Subtilase family protein
AL4G25140	-7.08	1.96E-12	8.70E-10	AT2G30290	BP80-1;2, VSR1;2, VSR2, VACUOLAR SORTING RECEPTOR 2
AL8G12660	-9.51	3.30E-17	2.67E-14	AT5G45890	SAG12, senescence-associated gene 12

Table S6. List of enriched Gene Ontology (GO) terms for the differentially expressed genes specific of the frost (a) and heat acclimation treatment (b), and shared between the two treatments (c) . Only GO terms with adjusted P-value < 0.05 and represented by at least 5 genes are shown. Enriched GO terms are sorted by the adjusted P-value.

(a) Specific to frost acclimation	**Main Category**	**Name**	**GO term**	**Cluster freq.**	**Adj. P-value**
	Biological process	response to stimulus	GO:0050896	42/182 23.0%	8.66E-03
		terpenoid biosynthetic process	GO:0016114	5/182 2.7%	3.18E-02
		response to temperature stimulus	GO:0071502	13/182 7.1%	3.29E-02
		response to stress	GO:0006950	26/182 14.2%	3.65E-02
		terpenoid metabolic process	GO:0006721	5/182 2.7%	3.65E-02
		cell death	GO:0008219	7/182 3.8%	4.03E-02
		death	GO:0016265	7/182 3.8%	4.03E-02
		isoprenoid biosynthetic process	GO:0008299	5/182 2.7%	4.44E-02
	Molecular function	oxidoreductase activity	GO:0016491	22/182 12.0%	3.07E-02
		tetrapyrrole binding	GO:0046906	9/182 4.9%	3.65E-02

(b) Specific to heat acclimation	**Main Category**	**Name**	**GO term**	**Cluster freq.**	**Adj. P-value**
	Biological process	response to stimulus	GO:0050896	265/1269 20.8%	7.29E-18
		response to heat	GO:0009408	39/1269 3.0%	4.82E-16
		response to stress	GO:0006950	175/1269 13.7%	7.20E-16
		response to temperature stimulus	GO:0071502	53/1269 4.1%	9.38E-10
		response to chemical stimulus	GO:0042221	146/1269 11.5%	2.14E-09
		response to abiotic stimulus	GO:0009628	109/1269 8.5%	1.35E-08
		response to high light intensity	GO:0009644	16/1269 1.2%	7.68E-07
		response to biotic stimulus	GO:0009607	60/1269 4.7%	3.98E-06
		response to other organism	GO:0051707	58/1269 4.5%	5.80E-06
		response to oxidative stress	GO:0006979	36/1269 2.8%	7.05E-06
		defense response	GO:0006952	65/1269 5.1%	1.08E-05
		response hydrogen peroxide	GO:0042542	14/1269 1.1%	2.73E-05
		response to bacterium	GO:0009617	34/1269 2.6%	4.11E-05
		response to light intensity	GO:0009642	18/1269 1.4%	4.41E-05
		multi-organism process	GO:0051704	65/1269 5.1%	2.38E-04
		defense response to bacterium	GO:0042742	28/1269 2.2%	4.08E-04
		response to organic substance	GO:0010033	86/1269 6.7%	4.25E-04
		protein folding	GO:0006457	26/1269 2.0%	1.77E-03
		response to inorganic substance	GO:0010035	44/1269 3.4%	3.70E-03
		response to reactive oxygen species	GO:0000302	14/1269 1.1%	5.30E-03
		response to endogenous stimulus	GO:0009719	69/1269 5.4%	7.66E-03
	Molecular function	catalytic activity	GO:0003824	438/1269 34.5%	2.93E-05
		oxidoreductase activity	GO:0016491	100/1269 7.8%	3.05E-03
		hydrolase activity, acting on glycosyl bonds	GO:0016798	43/1269 3.3%	5.37E-03
		hydrolase activity, hydrolyzing O-glycosyl compounds	GO:0004553	39/1269 3.0%	2.50E-02
		transcription regulator activity	GO:0030528	119/1269 9.3%	4.34E-02
		xyloglucan:xyloglucosyl activity	GO:0016762	9/1269 0.7%	4.74E-02
	Cellular component	cell wall	GO:0005618	60/1269 4.7%	3.69E-09
		external encapsulating structure	GO:0030312	60/1269 4.7%	5.23E-09
		extracellular region	GO:0005576	39/1269 3.0%	2.24E-02

(c) Shared between acclimation treatments	**Main Category**	**Name**	**GO term**	**Cluster freq.**	**Adj. P-value**
	Biological process	photosynthesis	GO:0015979	5/109 4.5%	2.25E-02
		lipid transport	GO:0006869	6/109 5.5%	3.41E-02
		lipid localization	GO:0010876	6/109 5.5%	3.76E-02

Table S7. List of (a) heat-responsive genes differentially expressed after frost acclimation and (b) cold-responsive genes differentially expressed after heat acclimation. In all cases, the comparison was made relative to control conditions, and the listed genes were part of the Gene Ontology category of "response to temperature stimulus". Genes were considered as differentially expressed when false discovery rate (FDR) < 0.05. Genes are sorted by log2FoldChange (log2FC)

(a)

Gene_ID_lyrata	expression change	log2FC	P-value	FDR	Homolog_thaliana	Gene_name
AL5G25120	down-regulated	-3.78	1.03E-08	7.58E-06	AT1G53540	HSP20-like chaperones superfamily protein
AL1G60810	down-regulated	-2.96	3.48E-04	3.63E-02	AT1G52560	HSP20-like chaperones superfamily protein
AL6G44080	down-regulated	-1.62	1.86E-05	3.86E-03	AT4G10250	ATHSP22.0, HSP20-like chaperones superfamily protein
AL5G25020	down-regulated	-1.38	6.98E-06	1.73E-03	AT3G46230	ATHSP17.4, HSP17.4, heat shock protein 17.4
AL8G36240	down-regulated	-1.38	1.65E-04	2.10E-02	AT5G59720	HSP18.2, heat shock protein 18.2

(b)

Gene_ID_lyrata	expression change	log2FC	P-value	FDR	Homolog_thaliana	Gene_name
AL8G27540	down-regulated	-2.35	4.28E-06	3.50E-04	AT5G53000	TAP46, 2A phosphatase associated protein of 46 kD
AL1G19860	down-regulated	-1.91	1.03E-08	1.99E-06	AT1G09350	AtGolS3, GolS3, galactinol synthase 3
AL4G41090	down-regulated	-1.65	1.37E-12	6.52E-10	AT2G42540	COR15, COR15A, cold-regulated 15a
AL6G50520	down-regulated	-1.38	2.81E-07	3.50E-05	AT4G02520	ATGSTF2, ATPM24, ATPM24.1, GST2, GSTF2, glutathione S-transferase PHI 2
AL5G31370	down-regulated	-1.15	5.02E-05	2.48E-03	AT3G50970	Low temperature induced30, XERO2, dehydrin family protein
AL5G38750	down-regulated	-1.03	6.53E-04	1.84E-02	AT3G57260	BG2, BGL2, PR-2, PR2, beta-1,3-glucanase 2
AL6G11740	down-regulated	-0.85	5.06E-05	2.49E-03	AT5G02500	AT-HSC70-1, HSC70, HSC70-1, HSP70-1, heat shock cognate protein 70-1
AL8G44850	down-regulated	-0.77	1.01E-03	2.55E-02	AT5G17890	CHS3, DAR4, DA1-related protein 4
AL6G19350	down-regulated	-0.70	9.34E-04	2.41E-02	AT5G08620	ATRH25, STRS2, DEA(D/H)-box RNA helicase family protein
AL4G14090	up-regulated	0.80	3.24E-04	1.08E-02	AT2G24040	Low temperature and salt responsive protein family
AL7G28960	up-regulated	0.93	8.03E-06	5.85E-04	AT4G24280	cpHsc70-1, chloroplast heat shock protein 70-1
AL3G16650	up-regulated	1.04	1.87E-05	1.16E-03	AT3G05890	RCI2B, RARE-COLD-INDUCIBLE 2B, Low temperature and salt responsive protein family
AL5G23740	up-regulated	1.09	7.18E-05	3.34E-03	AT5G58670	ATPLC, ATPLC1, PLC1, PLC1, phospholipase C1
AL3G26490	up-regulated	1.31	1.12E-07	1.62E-05	AT3G14210	ESM1, epithiospecifier modifier 1
AL463U10020	up-regulated	1.58	7.75E-04	2.09E-02	AT2G39460	ATRPL23A, RPL23A, RPL23AA, ribosomal protein L23AA

Chapter 3: **Genetic divergence in life history traits and thermal stress performance across a heterogeneous dune landscape in *Arabidopsis lyrata***

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Running title: Ecotype formation in a heterogeneous landscape

Abstract

Over spatial scale of a few meters, the habitat of a species can differ in abiotic and biotic conditions that may lead to adaptive differentiation and ecotype formation within populations. In this study we tested whether over a heterogeneous dune landscape (i) plants differ in life history traits and thermal stress performance and (ii) whether phenotypic differences were associated with changes in gene expression? Seeds of *Arabidopsis lyrata* from one population of an active sand dune landscape were collected and raised in a common garden experiment. Plants of replicate seed families were repeatedly exposed to one of three treatments: frost, heat or constant control conditions. The following traits were assessed: plant growth and size, flowering time, frost resistance, heat resistance and tolerance to frost and heat. RNA-seq analysis was performed to examine the genes differentially expressed along several environmental gradients. Two strong associations were detected, the first between the distance from the crown edge of the nearest trees and frost tolerance and the second between the relative position on the dunes and flowering time. Gene expression analysis along these environmental variables revealed candidate genes involved in the cold response and in the circadian rhythm, respectively. These results indicate that spatial heterogeneity likely led to divergent adaptation and ecotype formation, which contribute to genetic diversity within populations.

Keywords: *Arabidopsis lyrata*, fine-scale adaptation, thermal stress resistance, spatial heterogeneity, thermal adaptation, thermal tolerance, transcriptome analysis.

Introduction

Environmental heterogeneity in both abiotic and biotic factors may result in varying patterns of selection and be the source of divergence within populations (Hutchings *et al.*, 2000). Investigating the adaptive potential of plants to environmental stress on a local scale is a crucial aspect underlying community structure and the functioning of ecosystem (Menge *et al.*, 2002; Fenu *et al.*, 2012). Due to their sessile nature, plants may be particularly prone to experiencing divergent natural selection on a very fine spatial scale (Schmitt & Gamble, 1990; Knight & Miller, 2004). Such fine-scale adaptive divergence has been detected in plants for shady versus sunny places (Donohue *et al.*, 2000), exposure to pathogens (Thrall *et al.*, 2002). Environmental conditions may actually change in a multivariate manner, which requires the depicting of many environmental variables, their importance in explaining phenotypic and genotypic divergence as observed in common garden settings. Furthermore, gene expression differences can give an indication of the candidate genes and pathways involved in divergence and in ecotype formation.

Spatially heterogeneous environments often lead to different selective pressures between microhabitats (Kawecki & Ebert, 2004). Along steep ecological gradients and in the presence of ecological barriers that limit gene flow, divergent selection may contribute to the maintenance of genetic diversity and lead to local adaptation (Lenormand, 2002). Studies of local adaptation provides important insight on how organisms are shaped by their environments and into evolutionary processes that occur with population. A lot of efforts have been made to identify the traits under selection and their genetic architecture, for this latter aspect studies provided mixed results with adaptive traits that may be determined by a few number of genes of larger effects or by multiple genes with smaller effects (Howe *et al.*, 2003; Yeaman & Whitlock, 2011). However the precise nature of the genes remain largely unknown.

Habitats of plants commonly differ over scales of meters in temperature, soil composition, water availability and intra-and interspecific competition (Hutchings *et al.*, 2000). Since an environment is heterogeneous, plant performance, reproductive traits or stress response were likely to differ between individuals (Hutchings *et al.*, 2000). Some common garden experiments studies provided evidence for this. For instance, it has been demonstrated, in several plant species, differences in flowering time between plants from two microhabitats which differed soil temperature, with plants from hotter soils flowering earlier than plant from cooler soils (Tercek & Whitbeck, 2004; Lekberg *et al.*, 2012). Ravenscroft *et al.*, (2014) showed that edaphic heterogeneity may lead to differences in coping with drought stress in *Plantago lanceolata*. Paccard *et al.*, (2013) found than plants from bottom of dunes flowered earlier and had fewer stomata than plant in top of dunes experiencing dryer conditions in *Arabidopsis lyrata*. Finally, variations in plant growth and response to far red light have been observed between *Festuca rubra* plants originating from a grassland that varied in vegetation density (Skálová *et al.*, 1997). So far, variations in plant performance and reproductive traits received much more attention, only few studies investigated how the stress response vary in a contrasting environment.

Here, we studied influences of spatial heterogeneity in a dune landscape on life history traits and stress response with particular interest for frost and heat adaptation in the perennial plant *Arabidopsis lyrata* ssp. *lyrata*, a close relative to *Arabidopsis thaliana*. We focused on one population inhabiting a sand dune landscape on the shore of Lake Michigan, Saugatuck Dune Sand Park, USA. Coastal dunes have been previously described as variable in many respects. Dune top and lakeward parts of the dune are frequently exposed to strong wind, dryer conditions, strong temperature variations and higher temperatures. Bottom of dunes and leeward part of the dune provided a more sheltered environment, higher moisture content and less exposed to temperature variations (Hesp, 1991; Leege & Murphy, 2001; Maun, 2009). Its distribution ranged from open to forested habitats. Plants in open habitats experienced dryer conditions and higher temperatures since soil warmed up faster especially in summer while plants in the understorey experiencing lower air and soil temperature and lower light intensity (Puerta-Piñero *et al*., 2007; Maun, 2009). Finally, *A. lyrata* typically exhibited a clumped distribution that varied in density and likely to affect growth and reproductive traits (Miller & Schemske, 1990). Therefore, Saugatuck Dune Sand Park differed in microhabitat conditions (Peterson & Dersch, 1981) which could have led to differential imprinting on seeds or past divergent selection and evolutionary differences between plants. For this experiment, we collected seeds from 40 maternal lines on the field and raised plants in common garden experiment. Assuming that many dune gradients would be linked to differences in temperature exposure, we repeatedly exposed plants to either frost, heat or control conditions. We assessed resistance to frost and heat stress using percentage of electrolyte leakage (Cornelissen *et al.*, 2003). Electrolyte leakage is caused by cell damage and therefore this method reflects cell membrane stability under stress. Tolerance was defined as the difference in growth performance between plants treated to regular frost or heat stress and plants experiencing control conditions. The specific questions we addressed were: (i) what are the environmental variables that are linked with differences in life history traits and thermal performance? (ii) What are the genes differentially expressed along the most relevant environmental variables?

Material and methods

Sampling design and rearing plants. In June 2010, 2 healthy siliques filled with seeds of 40 plants of *Arabidopsis lyrata* ssp. *lyrata* of the same outcrossing population (Willi & Määttänen, 2010, 2011) were collected at Saugatuck Dune State Park, Lake Michigan, USA (42°42′ N, 86°12′ W) over an area of 2.5 ha (Fig.1). In order to test whether habitat heterogeneity were linked with vegetative and reproductive traits as well as resistance and tolerance to thermal stress, data on local environmental conditions of each field-samples plant was collected. The environmental data were:

distance from the crown of the nearest trees (distance from trees, in meter), which usually corresponds to a gradient of closed to open habitat, fraction down from the dune top (dune position), that corresponds to the position on the dune ranging from 0 (top of dune) to 1 (bottom of dune), wind exposure indicating the position of plants on the windward or leeward part of the dune (wind exposure), number of *A. lyrata* plants on ¼ m^2 quadrat with the maternal plant in the center as an indication of intraspecific competition (intraspecific density).

We raised 40 maternal lines under three experimental treatments: frost stress, heat stress and control, with three replicates each (N = 40 families × 3 treatments × 3 blocks = 360 plants). We planted two seeds per pot (7 cm diameter, 5 cm depth; 1:1 peat:sand ratio) to ensure that at least one seed germinated and pots were arranged in random positions within five trays per block. Seeds were then stratified for one week (4 °C in darkness under wet conditions). After stratification, plants were transferred into a growth chamber (Grobank, CLF Germany) for germination. Raising conditions were chosen to mimic the natural life cycle of *A. lyrata*. Germination occurs in late fall on short day length, conditions for initiating germination were set up to 18° C constant, 8 h : 16 h light : dark; light intensity: 150 µmol m^{-2} s-1; 18 °C; relative humidity (RH): 40-70%. Germination was scored every day for two weeks. After germination, we gradually increased day length and temperature to mimic spring conditions that corresponds to the growing period of *A. lyrata* and is reflected by an increase in rosette size (12 h : 12 h light : dark, light intensity: 180 µmol m^{-2} s-1, 20 °C : 18 °C day : night, RH: 40-70%). At the same time, we haphazardly removed extra seedlings from each pot and transplanted into pots, of the corresponding maternal line, with no germinated seeds. At the end, we had 348 pots with one seedling each.

Stress treatments. When plants were at the four leaf stage, four weeks after germination, one of these three following treatments were applied: frost stress, heat stress or control. Stress temperatures were chosen to reflect short frost or heat events that can occur in nature during the nighttime or the midday of the growing period. Frost and heat stress were applied using the same sequence. All pots in one stress treatment were moved into a separate climate chamber. The temperature, initially set up to 20 °C, was gradually decreased during nighttime by steps of 1h, to 0 °C and to -3 °C and then back to 0 °C and 20 °C for frost stress. The temperature was gradually increased by steps of 1h, to 30 °C and to 47 °C and then back to 30 °C and 20 °C during midday for heat stress. At the end of each treatment application, plants were placed in the growth chamber. Stress temperatures were applied three subsequent days per week, for three weeks.

Phenotypic trait assessment

Vegetative traits. To estimate the growth parameters of *A. lyrata*, we tested which of seven growth models (linear, exponential, power function, two-parameter logistic, three-parameter logistic, Gompertz, and von Bertalanffy) were best supported by the sequential size data for all the plants of the experiment. Plant size was depicted by the average length of the two longest leaves. We measured the leaf length starting one week before the treatment application, when plants were three weeks old, and for five weeks. The two-parameter logistic best explained the growth trajectory of *A. lyrata* based on its weighted AIC value (0.306). The two parameters of the two-parameter logistic growth model were asymptotic rosette size (Rosette_size) and exponential growth (Exp_growth) that corresponds to the speed of growth. We further used these two growth parameters to estimate thermal tolerance. Parameter estimates for one plant were discarded because > 5 SD away from the mean and were replaced by the mean length of the two longest leaves on the last round of photography for rosette size and a missing value for growth rate. We also measured the number of leaves (Nb_leaves) at the end of the treatment.

Temperature-stress resistance. Thermal resistance was estimated by measuring percentage of electrolyte leakage (PEL) seven weeks after germination according to the protocol described in

Wos & Willi (2015). Electrolyte leakage was measured on plants raised under control conditions only. Briefly, for each control plant, three discs were excised from the fifth rosette leaf and put in three separate tubes. We exposed each disc to one of three treatments: (1) control: incubation at 20°C for 1h; (2) frost stress: incubation at -14°C for 1h; (3) heat stress: incubation at 47°C for 1h. After incubation, we measured a first time conductivity (Conductivity Meter FiveEasy FE30, Mettler Toledo, Columbus OH, USA). We then placed the tubes in a boiling bath for 30 minutes and measured conductivity a second time. We measured PEL as the ratio of the conductivity before boiling to that after the boiling bath (Cornelissen et al., 2003). We calculated resistance as PEL of the control disc minus PEL of the treated disc, for each treatment, so that a low value corresponded to low level of resistance.

Temperature-stress tolerance. We used both rosette size and exponential growth as an estimate of tolerance. We calculated the difference in asymptotic rosette size of a stressed plant minus that of the control plant of the same maternal family within a block ($\mathrm{Tol}_{\mathrm{rosette\_size}}$). Similarly, we calculated the difference in exponential growth of a control plant minus that of the stressed plant of the same maternal family within a block ($\mathrm{Tol}_{\mathrm{exp\_growth}}$) so that low value reflected low level of tolerance.

Flowering traits. We used flowering traits as an estimate of fitness. In *A. lyrata* flowering is induced by long days exposure, we gradually increased the day length and temperature regime two weeks after the end of treatments (16 h:8 h light:dark; 22 °C:18 °C day:night; light intensity: 240 µmol m-² s-1; RH: 40-70%). We recorded the following flowering traits every 2 days: The appearance of the first inflorescence defined as the number of days between germination and the appearance of the inflorescence bud (Bolting_time). The flowering time defined as the number of days between germination and the appearance of the first open flower (Flower_time). For the plant that flowered, we counted the number of pedicels, buds and open flowers as an indicator of flower production (Nb_flowers) and the number of inflorescences (Nb_inflorescences) four weeks after the flowering start that corresponds to the length of the flowering period in nature.

We tested whether the phenotypic variables were spatially independent. For this we computed a Geary's C test that measures the similarity between observations to detect spatial autocorrelation (Geary, 1954). Typically, Geary's C statistic ranges between 0 and 2, a value of 1 indicates spatial randomness. Geary's C statistics for each vegetative and reproductive traits varied between 0.918 and 1.088, indicating no significant relationship between the traits in neighbouring maternal lines.

Statistical analysis.

To determine the most relevant environmental variables we, first, run a mixed model analysis to test for the effects of treatments and environmental variables for each phenotypic traits independently. Then, we performed a multivariate analysis by canonical correlation analysis (CCA, Hotelling, 1936), for exploring the relationships between two sets of phenotypic and environmental variables and identified the variables that were the most correlated.

Mixed model analysis. Mixed model analysis was used for testing effects on phenotypic traits (Package lme, R core team). The phenotypic traits, except flowering time and number of leaves, were log-transformed to approach the normal distribution. Fixed effects were leaf disc treatment (only applicable for percent electrolyte leakage), growth treatment on the level of the plant, block and the four environmental variables: distance from the crown edge of the nearest tree, fraction down from the dune top and density of *A. lyrata* plants were considered as continuous variables whereas wind exposure was considered as factorial. The random effects were plant nested within seed family and seed family.

Canonical correlation analysis. Canonical correlation analysis is a type of multivariate analysis for studying linear relationships between two sets of variables. The principle is based on the creation of canonical variates, each consisting of a linear combination of one set of variables (Hair *et al.*, 2010). The canonical correlation coefficient represents the optimal linear combination between the two canonical variates. Canonical correlation analysis create as many canonical correlation coefficients as there are variables in the smaller set. In our study, the first set of variables contained the phenotypic variables including number of leaves, appearance of the first inflorescence (bolting time), time to flowering, number of flowers and number of inflorescences measured on control plants as well as resistance and the two measures of tolerance to thermal stress. Because rosette size and exponential growth were used to calculate the tolerance traits, to avoid redundancy and multicollinearity issues, these two variables were not include in the analysis. In total the first set contained 11 phenotypic variables. The second set included the four environmental variables. The analysis was based at the individual level (N = 40 maternal lines x 3 replicates = 120 individuals for each original variable). We used F-approximation of Wilks' lambda to test for the significance of the canonical correlation coefficients (Hair *et al.*, 2010).

To determine the relative importance of each original variable to the canonical correlation it has been suggested to use the canonical loadings or the canonical cross-loadings (Hair *et al.*, 2010). Canonical loadings represents the measure of the simple linear correlation between the variables and their respective canonical variates. For the canonical loadings, the contribution of a variable is considered as significant if the canonical loading is greater than |0.30|. Canonical cross-loadings, calculated by the product of the canonical loadings by the canonical coefficient, is the simple linear correlation between the variables with the opposite canonical variates and represent a more direct measure of the relationship between the phenotypic and environmental variables. Here, we reported both loadings and cross-loadings. The analysis was run with the package CCA in R (González *et al.*, 2008).

Transcriptome analysis

RNA extraction, library construction and sequencing. For each treatment, leaf tissue from 16 randomly chosen maternal lines, of the first block only, were collected seven weeks after germination, prior PEL measurement (Fig.1). Samples were immediately snap-frozen in liquid nitrogen for RNA extraction (RNeasy® Mini Kit protocol, Qiagen, Hilden, Germany). RNA samples were subjected to a DNase treatment (RNase-Free DNase Set, Qiagen, Hilden, Germany), RNA concentration and integrity were checked using a Nanodrop 2000 (Thermo Scientific, Wilmington, DE, United States) and a Bioanalyzer 2100 (Agilent Technologies, Palo Alto, CA, USA). cDNA libraries for each individual were prepared using the Illumina TruSeq Stranded mRNA Sample Preparation Kit (Catalog #: RS-122-2101) using specific TruSeq adapters for individual sequencing. Sequencing was done on an Illumina NextSeq^{TM} 500 platform (Illumina, San Diego, CA, USA) using 75pb single-end reads. Raw data was filtered to remove low quality reads.

Read alignment. Quality of the sequence data was checked with the software FastQC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) and the software cutadapt (Martin, 2011) was used to trim the TruSeq adapter for each library. We used the read-mapping tool TopHat v2.1.0 (Trapnell *et al.*, 2012) for read alignment on the *A. lyrata* genome (Hu *et al.*, 2011) with the version-2 annotation (Rawat *et al.*, 2015).

Gene expression analysis and enrichment analysis. To compare gene expression along environmental gradients, we first split the two following continuous environmental variables into categorical variables: distance from the crown edge and fraction down from the dune top, so that each category contained between 3 and 6 individuals (Schurch *et al.*, 2016). We split distance from the crown edge into three categories along a closed- to open-habitat gradient: < 1 meter, from 1 to 2 meters, > 2 meters from the crown edge. Fraction down from the dune top were split into four categories: top, top-middle, bottom-middle and bottom of dunes. The number of reads mapped on each gene was counted with HTSeq-count v0.6.1p2 (Anders *et al.*, 2015) and used in EdgeR v3.12.0 (Robinson *et al.*, 2010) for gene expression analysis. Distinct models were run for each environmental variable based on the generalized linear model approach. *P*-values was adjusted for multiple testing with the Benjamini and Hochberg false discovery rate correction (FDR), we considered genes as differentially expressed (DEGs) using a conservative approach with FDR < 0.01.

The DEGs were further used for the gene ontology (GO) term enrichment analysis, performed with the Cytoscape application ClueGO (Bindea *et al.*, 2009). We limited our GO term enrichment analysis to the category "biological process". *P*-values were adjusted using Benjamini and Hochberg false discovery rate correction; GO terms were considered as significantly enriched if they were represented by at least five genes and for adjusted $P < 0.05$. Gene description was obtained from The Arabidopsis Information Resource (Berardini *et al.*, 2015).

Results

Effect of treatment and spatial heterogeneity on vegetative traits. Results of the mixed model analysis is shown in Table S1. We observed no difference in timing of germination along the environmental variables. Among the three phenotypic traits: only asymptotic rosette size (least squares means, LSM ± SE control: 49.27 ± 0.68 mm, frost: 42.37 ± 0.69 mm, heat: 41.57 ± 0.69 mm) and number of leaves (LSM ± SE control: 13.91 ± 0.21, frost: 12.20 ± 0.21, heat: 12.85 ± 0.21) showed a significant treatment effect. However, the three variables exhibited a significant treatment-by-distance from the crown edge of the nearest tree interaction. Plants close to the trees had larger rosette size and faster growth when exposed to frost (Fig. 2A and B) and they had fewer leaves under control conditions (Fig. 2C). In addition, the interaction treatment-by-density of *A.*

lyrata plants was significant for exponential growth, as a trend, frost-exposed plants grew faster (t = 1.59, df = 294) and heat-exposed plants grew slower when the density was low (t = -1.61, df = 294). Percentage of electrolyte leakage did not vary between microhabitats, but increased when leaves were exposed to treatments (LSM ± SE control: 4.11 ± 0.19 %, frost: 59.96 ± 0.19 %, heat: 45.98 ± 0.19 %).

Effects of treatments and spatial heterogeneity on flowering traits. Results of the mixed model analysis is shown in Table S2. Among the flowering traits, propensity to flower was not affected by any of the environmental variables. The time between germination and appearance of the first inflorescence and flowering time were significantly affected by the treatment, but only the contrast heat vs control was significant ($\text{LSM}_{\text{Bolting\_time}}$ ± SE control: 93.33 ± 4.41 days, frost: 99.50 ± 4.42 days, heat: 116.55 ± 4.55 days; $\text{LSM}_{\text{flower\_time}}$ ± SE control: 167.61 ± 5.88 days, frost: 173.54 ± 6.14 days, heat: 188.50 ± 5.79 days. Flowering time and number of inflorescences were also significantly and strongly affected by the dune position, with plants flowering earlier but producing less stems in bottom of dunes, independently of the treatments (Fig. 3A and B). Flowering time showed an additional significant treatment-by-wind exposure interaction, as a trend, frost-stressed plants growing on the leeward side flowered 20 days after those growing on the windward side (t = -1.75, df = 237, $P < 0.1$, LSM ± SE $\text{frost}_{\text{windward}}$: 160.39 ± 10.43 days, $\text{frost}_{\text{leeward}}$: 180.46 ± 7.56 days). The number of stems showed a significant interaction treatment-by-distance from the crown edge, under frost (t = -1.67, df = 237, $P < 0.1$) or heat stress (t = -2.61, df = 237, $P < 0.01$) plants produced more stems near the trees.

Effects of spatial heterogeneity on thermal resistance and tolerance. Resistance to frost and heat did not show variation along the environmental variables (Table 1). Tolerance to frost and heat –based on asymptotic size– varied significantly depending on the position of the plants on the windward or leeward side of the dunes with a higher tolerance to frost and heat on the leeward side. Tolerance to frost –based on asymptotic size and exponential growth– varied significantly along the distance from the crown edge of the nearest tree, with plants being more frost tolerant near the trees.

Canonical correlation analysis

Canonical correlation analysis revealed two significant correlations (Table 2). The first canonical correlation (Correlation coefficient $R = 0.51$, Wilk's Lambda = 0.49, $DF_{num} = 44$, $DF_{den} = 403.66$, $P < 0.01$) accounted for 26.01 % ($R^2 = 0.2601$) of the total variance and the second (Correlation coefficient $R = 0.46$, Wilk's Lambda = 0.66, $DF_{num} = 30$, $DF_{den} = 311.81$, $P < 0.05$) accounted for 21.16 % ($R^2 = 0.2116$) of the total variance.

Analysis of the first canonical correlation. Loadings indicate the relative proportion of each variable to the canonical correlation. The phenotypic variable that accounted the most for canonical correlation were the two estimates of frost tolerance ($Frost_{rosette\_size} = 0.67$ and $Frost_{expGrowth =}$ 0.51), heat tolerance based on rosette size ($Heat_{rosette\_size} = 0.33$), number of stems (-0.52) and flowering time (-0.43). The environmental variables that accounted the most for the canonical correlation were, in descending order, distance from the crown edge (-0.84), fraction down from the dune top (-0.70) and wind exposure (-0.48). Based on the cross-loadings, frost tolerance based on rosette size exhibited the highest correlation coefficient with the canonical variate on the environmental data (0.34). Similarly, the two environmental variables the most correlated with the opposite canonical variate were distance from the crown edge (-0.43) and fraction down from the dune top (0.36). The sign of the correlation coefficient indicated a negative correlation between frost tolerance and distance from the crown edge with plants and a positive correlation with fraction down from the dune top. Analysis of the first canonical correlation, in line with the mixed model analysis, showed that distance from the crown edge of the nearest tree was the most important predictor of phenotypic traits variation, especially those related to frost tolerance. Based on these results, we conducted a gene expression analysis on the frost-exposed plants along the distance from the crown edge of the nearest tree in order to test whether differences in frost tolerance was reflected at the gene expression level.

Gene expression analysis – distance from the crown edge. The gene expression analysis along the distance from the crown edge on the frost-exposed plants revealed 166 DEGs (Table S3). Analysis of enriched GO terms returned nine GO terms (Fig. 4). We identified 20 genes associated with “response to stress” and 14 genes with “response to abiotic stimulus”. Among these, six genes were in “response to temperature” including five genes described as cold-responsive: *COLD REGULATED 27* (*COR27*), *GLUTATHIONE S-TRANSFERASE PHI 2*, *CHILLING SENSITIVE 1*, *ZAT10* and *ZAT12*. The last gene was a heat shock factor involved in response to heat. Another six genes were in “response to osmotic stress” and included genes involved in salt tolerance and five genes were in “response to oxidative stress”. The enriched GO term “defense response” contained nine genes involved in response to pathogens, especially bacteria. The three closely related GO terms “catabolic process”, “cellular catabolic process” and “single-organism catabolic process” that contained 10 genes in total included various classes of genes i.e. ubiquitin, genes involved in oxidoreduction process or lipid catabolism. We found 13 genes related to the GO term “Response to endogeneous stimulus” which were hormone-responsive element, especially abscisic acid and ethylene.

Analysis of the second canonical correlation. The phenotypic variables that accounted the most for the second canonical correlation were number of stems (0.33) and flowering time (0.71), number of leaves (-0.33) and frost tolerance based on exponential growth (0.39), and the environmental variables were fraction down from the dune top (-0.66) and intraspecific density (-0.50). The cross-loadings were very low for most of the variables except for flowering time (0.33) and fraction down from the dune top (-0.31), indicating that the second canonical correlation was mainly represented by the correlation between these two variables. Therefore, this result confirmed the significant effect of dune position on flowering time identified by mixed model analysis. To investigate the genetic basis of this correlation, we conducted a gene expression analysis along the dune gradient on plants raised under control conditions.

Gene expression analysis – fraction down from the dune top. Gene expression analysis along the dune gradient on control plants revealed in total 435 DEGs (table S4). The GO term enrichment analysis detected 6 enriched GO term (Fig. 5). Among the 12 genes involved in "response to temperature", nine were related to "response to heat". These nine genes belonged to various gene families including heat shock proteins, heat shock factors, abscisic acid responsive elements or cell wall modifactory enzyme. We detected 17 genes in "secondary metabolic process" with seven genes part of the *CYTOCHROME P450* gene family. Seven genes were in the "phenylpropanoid metabolic process" category with genes involved in lignin catabolism, flavonoid and carotenoid production. We found nine genes associated with "rhythmic process" with six genes part of the circadian clock: *CCR2*, *TOC1*, *PHYTOCLOCK 1*, *PSEUDO-RESPONSE REGULATOR 5*, *EARLY FLOWERING 3* (*ELF3*) and *JUMONJI C DOMAIN-CONTAINING 30*. One gene part of the germination process *BME3* and two genes part of the floral development: *CONSTANS-LIKE 9* and *FKF1*. Finally, six genes were related to "regulation of reproductive process" and involved in floral transition: *CONSTANS-LIKE 9*, *FLOWERING LOCUS T* (*FT*), *FLOWERING LOCUS KH*, *FKF1*, *TOUCH 2* and *ELF3*.

Discussion

Microhabitat divergence has often been studied along single environmental gradients. Here we investigated four environmental gradients over a dune landscape and linked them with genotypic differences in a climate chamber experiment with three thermal treatments. Two associations were found to be significant: a first between frost tolerance and distance from the crown edge of the nearest tree that accounted for 26.01 % variation in the first canonical correlation. Transcriptome analysis along this gradient revealed differential expression of genes involved in the cold response. The second association that accounted for 21.16 % of variation in the second canonical correlation was between flowering time and position on the dune. Transcriptome analysis revealed differential expression of genes involved in floral transition and the circadian rhythm along this gradient.

Effects of spatial heterogeneity on vegetative and flowering traits.

We found that spatial heterogeneity had more impact on reproductive than vegetative traits in our population of *A. lyrata* inhabiting a sand dune landscape. An anterior study in *A. lyrata* also showed minor impact of dune position on vegetative traits like rosette size or trichome density (Paccard *et al.*, 2013). However, our results contrasted with field studies where authors found a significant effects of the closed- to open-habitat gradient on growth performance and survival in *Quercus ilex* (Puerta-Piñero *et al.*, 2007) or of the dune position on plant performance in *Hydrocotyle bonariensis* (Knight & Miller, 2004).

We showed that flowering time was strongly associated with position on the dune with plants flowering earlier in bottom of dune. This finding was consistent with a previous common garden study in *A. lyrata* that demonstrated local adaptation in regards to flowering traits with plants at the bottom of dunes flowering up to 4 weeks earlier compared to plants at top of dunes (Paccard *et al.*, 2013). Plants at top of dunes experienced drier and hotter conditions than plants at bottom of dunes and difference in the timing of flowering may reflect different strategies in coping with drought stress. Plants can cope with drought either through escape strategy defined as the completion of the life cycle before the onset of adverse conditions (Franks, 2011; Kooyers, 2015) or through tolerance mechanism by maintaining high fitness despite drought stress (Franks, 2011). Selection in flowering time within populations has been also demonstrated in field-conducted studies in the context plant-pollinator interaction (Moreira *et al.*, 2015). In plants, the transition from vegetative to reproductive phase is a crucial aspect in response to complex natural environments. Because the timing of flowering has major fitness consequences for out-crossing species, probably more than the other flowering traits we measured i.e. number of flowers, it needed to be adjusted to environmental conditions so that plant can reproduce and seeds disperse when conditions are favorable (Putterill *et al.*, 2004).

In that sense, our gene expression analysis provided consistent results for explaining differences in flowering time. Some genes differentially expressed between top and bottom of dunes were involved in floral transition (Levy & Dean, 1998) or part of the circadian rhythm. The circadian clock is at the interface between environment and internal physiological processes and flowering was largely dependent on the circadian clock. Some flowering genes we detected were directly controlled by the circadian clock especially *FT*, *CO*, *ELF3* and *FKF1* (Hayama & Coupland, 2004). Genetic variation in the circadian rhythm within populations has already been shown in *Boechera stricta* (Salmela *et al.*, 2016) and, interestingly, seemed to be predominant in field conducted studies for controlling timing of flowering in *A. thaliana* (Brachi *et al.*, 2010). In nature, the circadian clock is synchronized by numerous environmental factors to adjust the timing of biological activities including flowering (Harmer *et al.*, 2000). Light intensity and cold temperature, are among the most prominent synchronizers (Rensing & Ruoff, 2002; Bünning, 2013) but recent studies demonstrated also the importance of drought (Marcolino-Gomes *et al.*, 2014). The different environmental conditions experienced by plant between top and bottom of dunes probably led to different synchronization of the circadian clock and flowering time divergences. However the abiotic factors that precisely drive the genetic differentiation of the circadian clock remain unknown.

The circadian clock controls many other physiological processes such as plant growth (Farré, 2012) or the response to abiotic stress (Grundy *et al.*, 2015). While we did not observe variation in growth along the dune gradient, we detected some genes involved in the abiotic stress response differentially expressed. In addition, we identified some genes from the Cytochrome P450 family, involved in the secondary metabolism, also controlled by the circadian clock (Pan *et al.*, 2009) suggesting that, in our study, influence of the circadian clock was probably not limited to flowering.

Effects of spatial heterogeneity on thermal adaptation.

Our results highlighted that frost tolerance was more affected by spatial heterogeneity than frost resistance or heat resistance and tolerance. We demonstrated a significant relationship between the distance from trees and frost tolerance, with plants growing faster and reached bigger rosette size close to the trees or in the understorey than plants in open habitat. This pattern was consistent with the environmental conditions experienced by plants in nature and the lower air and soil temperature in the understorey. However we did not find any effect of spatial heterogeneity on frost resistance while differences in frost resistance was shown in yellow cedar between open and closed canopy, indicating that hardening capacity may also occur at very fine spatial scale (Schaberg *et al.*, 2005). Here, we provided another evidence that within population, over very short distances (< 15 meters), individuals may be locally adapted to their abiotic environment. Previous studies on forest trees highlighted the strong selection acting on cold adaptation traits, especially those related cold hardening and bud flushing, among and within populations (Howe *et al.*, 2003). They demonstrated that the cold adaptive traits were likely to be controlled by multiple genes of smaller effects, however the nature of these genes were not yet characterized. Using gene expression analysis, we explored this aspect and identified cold-response genes that might be of particular interest for local cold adaptation.

The cold-responsive genes found to be differentially expressed belonged to various signalling pathways. The most represented pathway was the ZAT regulon with two genes differentially expressed *ZAT 10* and *ZAT 12*. The ZAT regulon was a signalling pathway involved in the cold response and increased freezing tolerance and survival under frost stress (Vogel *et al.*, 2005; van Buer *et al.*, 2016). Additionally, the ZAT regulon affected, positively and negatively, the expression of some genes involved in defense pathways (Vogel *et al.*, 2005) and in the response of oxidative stress (Davletova *et al.*, 2005). The other cold-responsive genes, *CHILLING SENSITIVE 1* and *COLD REGULATED 27* were part of other pathways and were described to be involved in cell membrane hardening while we did not observed variations in freezing resistance measured by electrolyte leakage (Mikkelsen & Thomashow, 2009; Zbierzak *et al.*, 2013). Our results demonstrated that differences in abiotic conditions between microhabitats may lead to divergent selection toward thermal adaptation likely to be triggered by changes in gene expression.

Finally, we found minor impacts of the four environmental variables on heat resistance and tolerance. Plants inhabiting sand dune habitats experienced extreme high soil temperature (Maun, 2009). Physiological studies on several sand-dune plants demonstrated high concentrations of sugars and polyols, compounds that increased cell membrane stability, independently of their position on the dune (Smirnoff & Stewart, 1985). Plants in such habitats may exhibit naturally high degree of heat resistance or tolerance with minor differences between microhabitats. However, only few studies are available for comparison more data on thermal adaptation at very fine spatial scale are needed.

Conclusion

Sand dune landscape provided an ideal system for investigating the adaptive evolution at very fine spatial scale because associated with sharp environmental gradients. Our results illustrated that spatial heterogeneity can lead to phenotypic differentiation and contribute to genetic diversity within populations over very short distances. Based on our results, we concluded that the response to spatial heterogeneity seems to involve markedly traits related to cold adaptation and to the timing of flowering. Finally, our gene expression analysis along the relevant environmental variables highlighted some candidate genes that might be of interest for local adaptation studies.

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Table 1

Results of mixed model analysis testing the effect of distance from the crown of the nearest tree (Distance from trees), fraction down from the dune top (Dune position), wind exposure (Wind exposure) and number of A. lyrata plants on ¼ m^2 quadrat (Intraspecific density) on resistance to frost and heat assessed from percentage electrolyte leakage (PEL), and tolerance to frost and heat stress assessed from asymptotic size ($Tol_{rosette\_size}$) and exponential growth (Tol_{exp_growth}) of *Arabidopsis lyrata* plants (N = 117, 113, 112). The table shows *F* values. Statistic for the random effects are not shown. Significance is indicated in bold: * $P < 0.05$, ** $P < 0.01$.

				Resistance		$Tol_{rosette\_size}$	Tol_{exp_growth}
Stress	Dependent Variables	DF_{num}	DF_{den}	*F*	DF_{den}	*F*	*F*
Frost	Block	2	75	**5.45****	71	0.04	1.27
	Intraspecific density	1	35	0.19	35	0.11	1.50
	Wind exposure	1	35	0.02	35	**5.09***	0.11
	Distance from trees	1	35	0.02	35	**12.81****	**10.21***
	Dune position	1	35	1.40	35	0.41	0.09
Heat	Block	2	75	**6.85****	71	0.85	1.23
	Intraspecific density	1	35	0.85	35	1.01	2.70
	Wind exposure	1	35	0.71	35	**5.91***	0.04
	Distance from trees	1	35	0.23	35	1.50	0.12
	Dune position	1	35	0.36	35	0.03	1.08

Table 2

Canonical loadings and cross-loadings for the 1st and 2st canonical correlation. The phenotypic variables were: number of leaves (Nb_leaves), the time to produce an inflorescence (Bolting_time), flowering time (Flower_time), number of flowers (Nb_flowers) and number of stems (Nb_inflorescences) measured plants raised under control conditions. The environmental variables were distance from the crown of the nearest tree (Distance from trees), fraction down from the dune top (Dune position), wind exposure (Wind exposure) and number of *A. lyrata* plants on ¼ m^2 quadrat (Intraspecific density). *N* = 120. Canonical loadings and cross-loadings were considered as significant if they are greater than |0.30| as indicated in bold.

1st canonical correlation

Phenotypic variables		Loadings	Cross-loadings
	Nb_leaves	-0.17	-0.09
	Bolting_time	0.13	0.06
	Flower_time	**-0.44**	-0.22
	Nb_flowers	-0.12	-0.06
	Nb_inflorescences	**-0.52**	-0.27
Resistance	Frost	0.12	0.06
	Heat	0.02	0.01
Tolerance	Frost$_{\text{rosette size}}$	**0.67**	**0.34**
	Frost$_{\text{exp\_growth}}$	**0.51**	0.26
	Heat$_{\text{rosette size}}$	**0.34**	0.17
	Heat$_{\text{exp\_growth}}$	-0.21	-0.11

Environmental variables		Loadings	Cross-loadings
	Intraspecific density	-0.13	0.07
	Wind exposure	**-0.47**	-0.24
	Distance from trees	**-0.84**	**-0.43**
	Dune position	**0.70**	**0.36**

2st canonical correlation

Phenotypic variables		Loadings	Cross-loadings
	Nb_leaves	-0.33	-0.15
	Bolting_time	0.23	0.11
	Flower_time	**0.71**	**0.33**

	Nb_flowers	0.09	0.04
	Nb_inflorescences	**0.32**	0.15
Resistance	Frost	-0.20	-0.09
	Heat	0.12	-0.05
Tolerance	$\text{Frost}_{\text{rosette size}}$	0.19	0.08
	$\text{Frost}_{\text{exp\_growth}}$	**0.39**	0.18
	$\text{Heat}_{\text{rosette size}}$	-0.02	-0.01
	$\text{Heat}_{\text{exp\_growth}}$	0.10	0.04
Environmental variables			
	Intraspecific density	**-0.50**	-0.23
	Wind exposure	0.15	0.07
	Distance from trees	-0.22	-0.10
	Dune position	**-0.66**	**-0.31**

Fig.1

Location of the 40 seed families of *Arabidopsis lyrata* collected in Saugatuck Dunes State Park, Michigan, USA. Dots filled in black represent the maternal lines randomly chosen for the gene expression analysis.

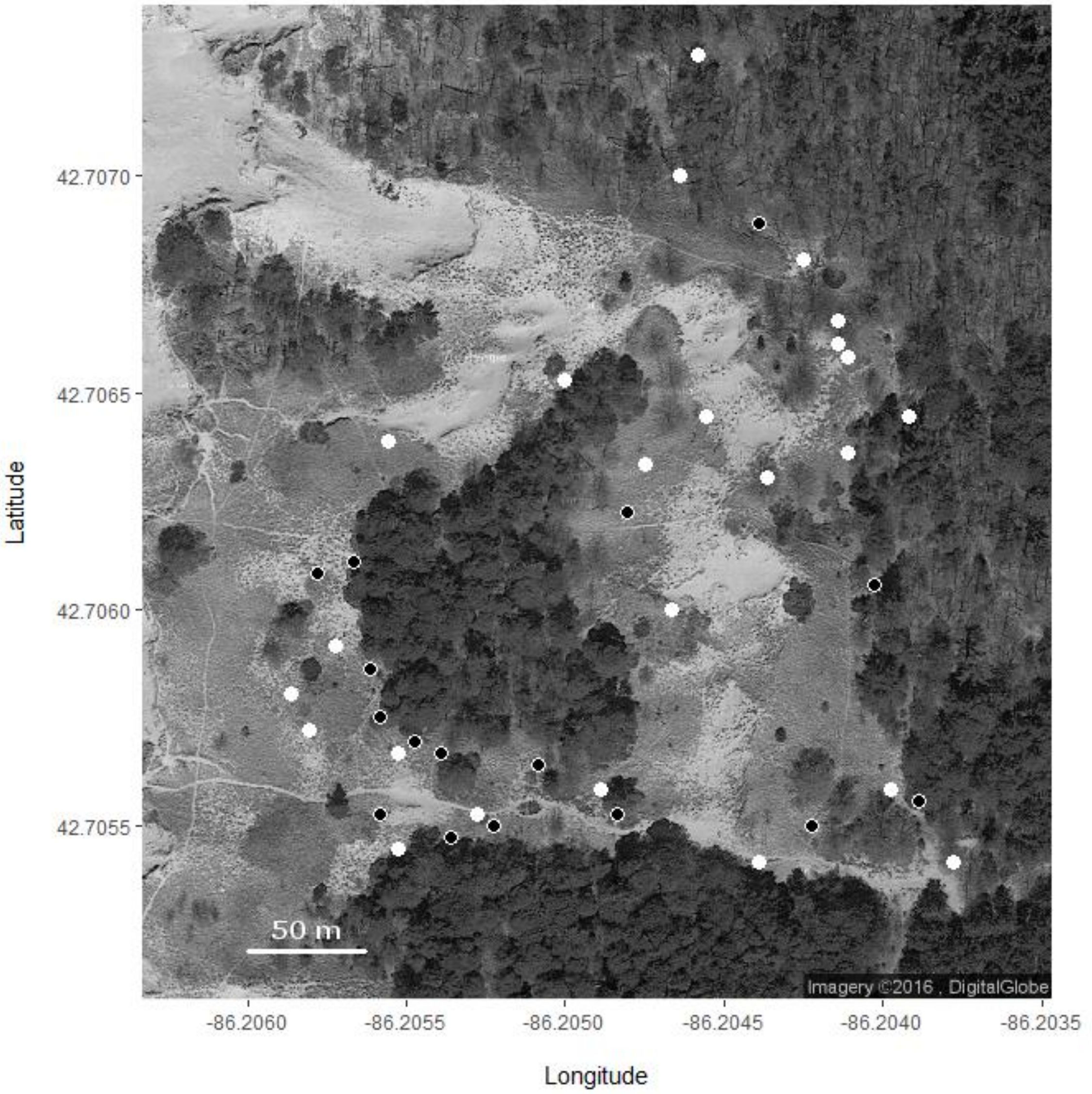

Fig. 2

Effect of distance from the crown edge of the nearest tree on asymptotic rosette size (A), exponential growth (B) and number of leaves (C). Symbols depict family mean. Color code is: light grey circles and full line for control plants, grey circles and dashed line for frost-exposed plants and black circles and dash-dot line for heat-exposed plants.

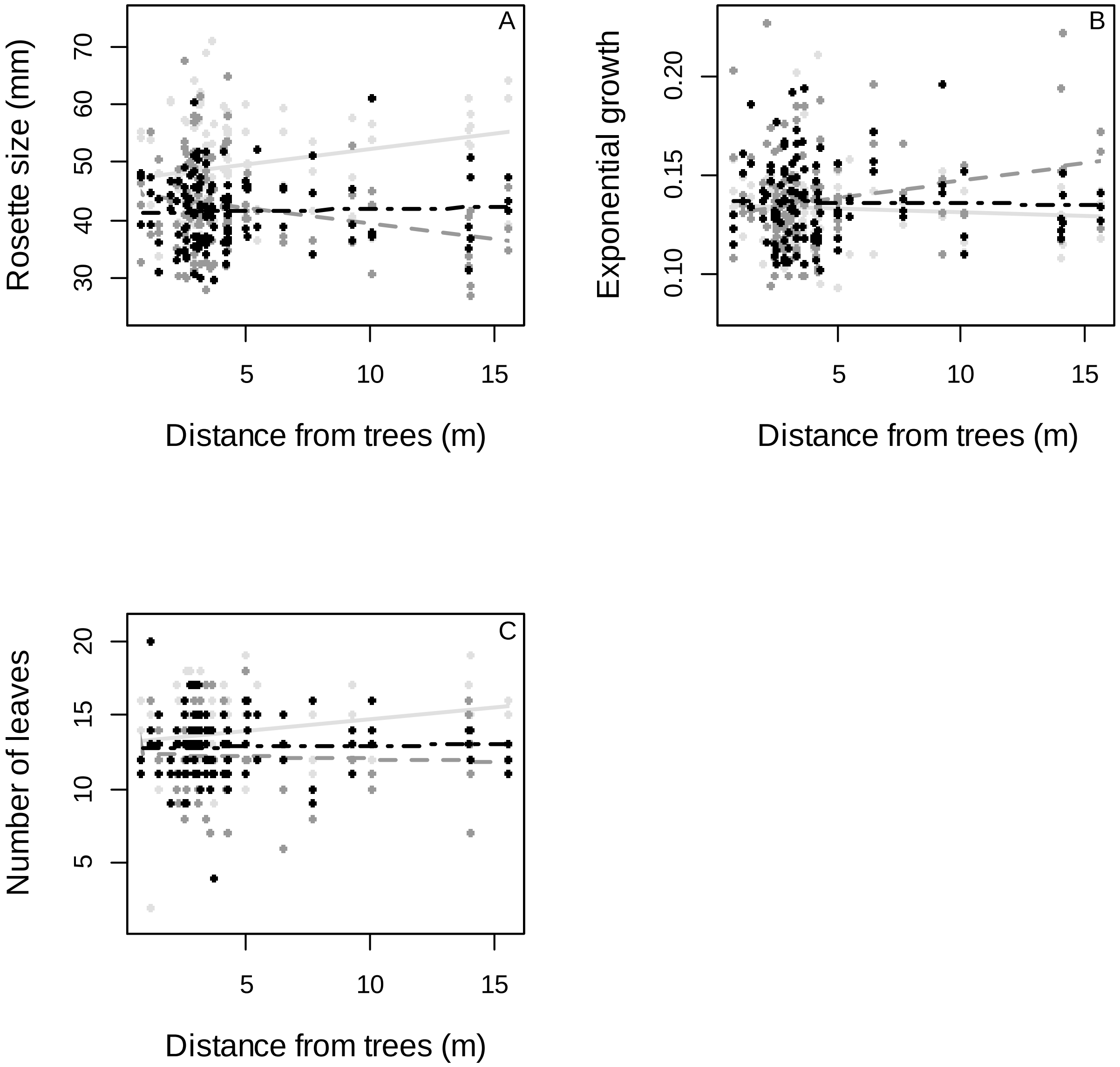

Fig. 3

Effect of position on the dune on flowering time (A) and number of stems (B). Symbols depict family mean. Color code is: light grey circles and full line for control plants, grey circles and dashed line for frost-exposed plant, black circles and dash-dot line for heat-exposed plants.

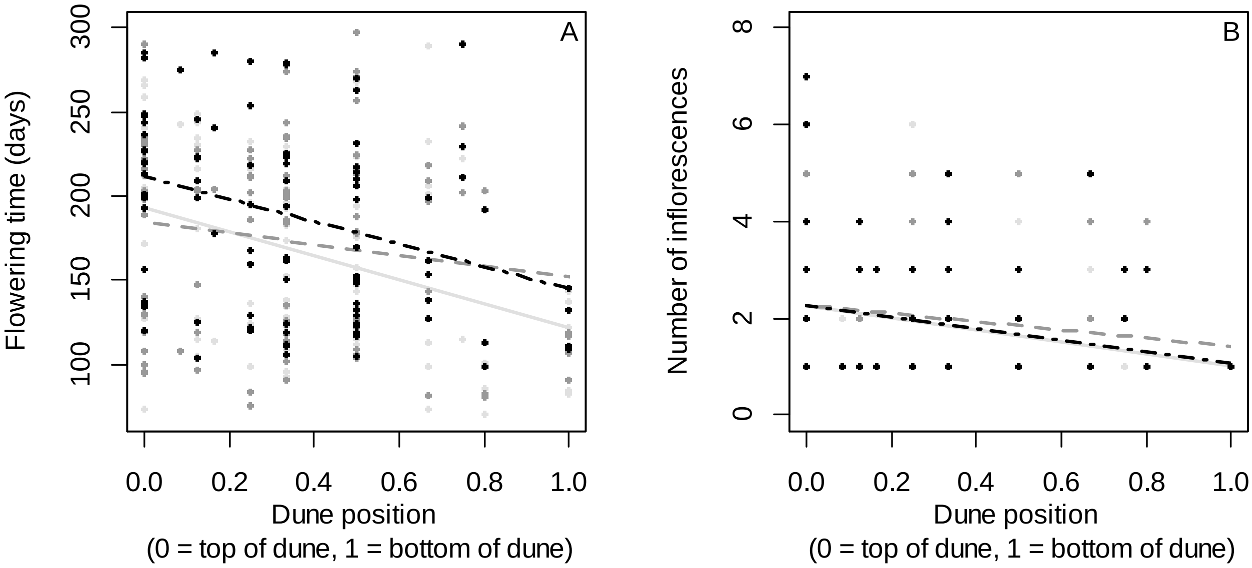

Fig 4.

Enriched GO terms for the differentially expressed genes (DEGs) along the distance from the crown edge of the nearest tree on frost exposed plant only. The GO term enrichment analysis was performed with CLUEGO (Bindea *et al.*, 2009). GO terms were considered as significantly enriched if they are represented by at least 5 genes and for FDR-adjusted P-value < 0.05. A link between two nodes indicates that more than 50% of the genes are shared. Colored nodes indicate significantly enriched GO terms according to the color scale. The node areas reflect the relative number of genes associated with each GO term.

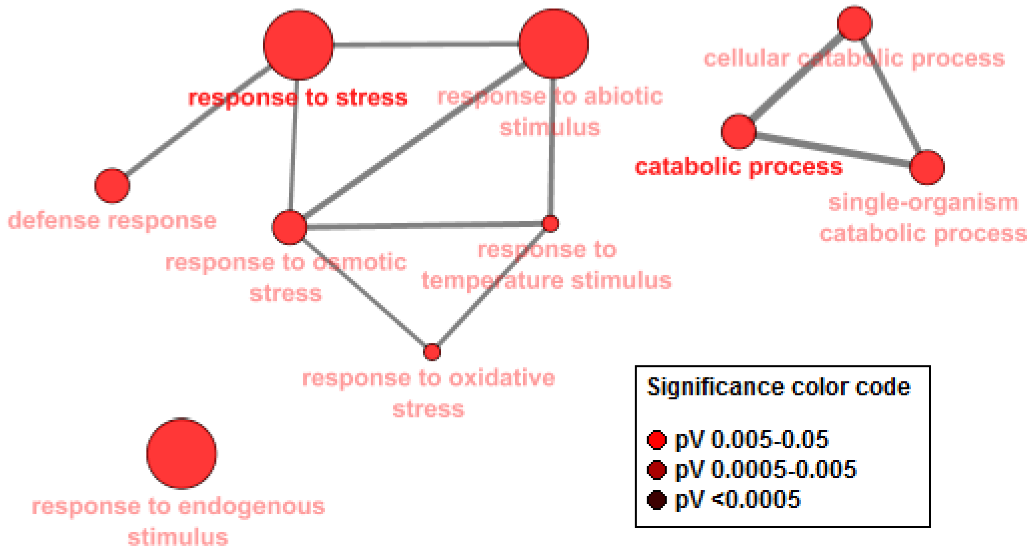

Fig. 5.

Enriched GO terms for the differentially expressed genes (DEGs) along the dune gradient on plant growing under control conditions. The GO term enrichment analysis was performed with CLUEGO (Bindea *et al.*, 2009). GO terms were considered as significantly enriched if they are represented by at least 5 genes and for FDR-adjusted P-value < 0.05. A link between two nodes indicates that more than 50% of the genes are shared. Colored nodes indicate significantly enriched GO terms according to the color scale. The node areas reflect the relative number of genes associated with each GO term.

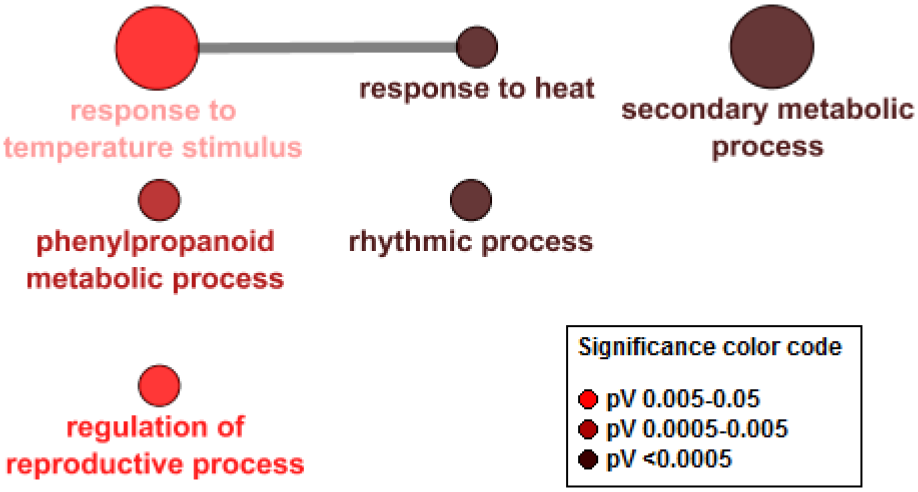

Table S1

Results of the mixed model analysis testing the effect of treatment, distance from the crown of the nearest tree (Distance from trees, in meter), fraction down from the dune top (Dune position), wind exposure (Wind exposure) and number of A. lyrata plants on ¼ m^2 quadrat (Intraspecific density) and their interactions on germination date (Germdate), the two growth parameters (Rosette_size and exponential growth, Exp_growth), number of leaves and percentage electrolyte leakage (PEL) of *Arabidopsis lyrata* plants (N = 350, 347, 346, 349, 351). The table shows *F* values, the last two rows show contrasts between pairs of treatments. Statistic for the random effects are not shown. Significance is indicated in bold: $^{(*)}$ $P < 0.1$, * $P < 0.05$ and *** $P < 0.001$.

			Germdate		Rosette_size	Exp_growth	Nb_leaves	PEL
DependentVariables	DF$_{num}$	DF$_{den}$	*F*	DF$_{den}$	*F*	*F*	*F*	*F*
Block	1	311	0.03	295/294/297/299	**14.80*** **	**10.43*** **	2.90$^{(*)}$	**12.57*** **
Treatment	2	/	/	295/294/297/299	**42.56*** **	1.00	**17.22*** **	**727.50*** **
Intraspecific density	1	35	1.14	35	0.50	0.09	0.02	0.04
Wind exposure	1	35	0.38	35	0.01	0.27	1.12	0.04
Distance from trees	1	35	0.00	35	0.62	0.16	0.28	0.07
Dune position	1	35	0.04	35	0.02	0.17	0.79	0.30
Treatment*Intraspecific density	2		/	295/294/297/299	2.06	**3.61***	1.65	0.65
Treatment*Wind exposure	2		/	295/294/297/299	2.87$^{(*)}$	0.19	1.45	0.40
Treatment*Dune position	2		/	295/294/297/299	0.74	0.77	0.05	0.22
Treatment*Distance from trees	2		/	295/294/297/299	**7.71*****	**6.96***	**3.80***	0.17
				df	*t*		*t*	*t*
Frost vs control				344	**-7.11*** **		**-5.70*** **	**33.23*** **
Heat vs control				344	**-7.94*** **		**-3.51*** **	**24.91*** **

Table S2

Results of the mixed model analysis testing the effect of treatment, distance from the crown of the nearest tree (Distance from trees, in meter), fraction down from the dune top (Dune position), wind exposure (Wind exposure) and number of A. lyrata plants on ¼ m^2 quadrat (Intraspecific density) and their interactions on the propensity to flower, the time to produce a stem (Bolting_time), flowering time (Flower_time), number of flowers (Nb_flower) and number of stems (Nb_inflorescences) of *Arabidopsis lyrata* plants (N = 331, 289, 289, 289). The table shows *F* values, the last two rows show contrasts between pairs of treatments. Statistic for the random effects are not shown. Significance is indicated in bold: * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$.

			Bolting_time		Flower_time	Nb_flower	Nb_inflorescences
Dependent Variables	DF_{num}	DF_{den}	*F*	DF_{den}	*F*	*F*	*F*
Block	2	279	**4.91****	237	**8.30*****	0.98	**5.47****
Treatment	2	279	**13.04*****	237	**4.10***	1.06	0.09
Intraspecific density	1	35	0.27	35	0.29	2.61	0.83
Wind exposure	1	35	0.50	35	0.00	0.64	1.18
Distance from trees	1	35	0.10	35	0.05	0.02	0.97
Dune position	1	35	1.04	35	**13.19*****	2.85	**5.52***
Treatment*Intraspecific density	2	279	1.52	237	1.14	0.37	0.18
Treatment*Wind exposure	2	279	0.03	237	**4.22***	0.49	1.49
Treatment*Dune position	2	279	1.34	237	0.26	0.52	0.02
Treatment*Distance from trees	2	279	0.88	237	0.54	0.62	**3.63***
		df	*t*	df	*t*		
Frost vs control		328	0.99	286	0.70		
Heat vs control		328	**3.66*****	286	**2.53***		

Table S3. List of the differentially expressed genes (DEG) along the distance from thecrown edge of the nearest tree on frost-exposed plants. Genes were considered as differentially expressed when false discovery rate (FDR) < 0.01. Genes are sorted by FDR values.

Gene_ID_lyrata	logFC1	logFC2	PValue	FDR	Homolog_thaliana	Gene_name
AL4G34580	8.36	-0.18	1.01E-25	3.35E-21	/	Unknown
AL1G56380	9.66	0.00	5.76E-17	9.56E-13	AT3G46210	Ribosomal protein S5 domain 2-like superfamily protein
AL4G33850	10.02	10.85	5.68E-15	6.29E-11	AT2G37435	Cystatin/monellin superfamily protein
AL6G36800	8.00	-0.29	2.38E-14	1.98E-10	/	Unknown
AL1G36260	0.00	8.99	2.13E-13	1.17E-09	/	Unknown
AL2G23820	0.00	9.07	2.47E-13	1.17E-09	AT5G41660	Unknown
AL8G21750	8.71	3.05	1.97E-13	1.17E-09	AT5G56350	Pyruvate kinase family protein
AL1G36300	-7.97	-8.08	7.02E-12	2.91E-08	AT1G22760	PAB3, poly(A) binding protein 3
AL7G43480	10.64	6.85	1.09E-11	4.01E-08	/	Unknown
AL2G19210	-0.27	-9.68	1.47E-11	4.87E-08	/	Unknown
AL2G22370	1.89	4.29	1.89E-11	5.69E-08	AT1G65486	Unknown
AL1G53170	2.80	8.88	4.01E-11	1.05E-07	/	Unknown
AL2G34820	-4.76	-6.70	4.12E-11	1.05E-07	AT1G74930	ORA47, Integrase-type DNA-binding superfamily protein
AL6G47410	3.78	7.58	5.62E-11	1.33E-07	AT4G12480	pEARLI 1, Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL3G15350	7.81	0.00	7.95E-11	1.65E-07	/	Unknown
AL7G19760	-8.49	-8.49	7.69E-11	1.65E-07	AT4G32620	Enhancer of polycomb-like transcription factor protein
AL3G34730	0.10	4.54	8.92E-11	1.74E-07	AT3G20810	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AL1G31790	-7.91	-7.21	1.33E-10	2.45E-07	AT1G19210	Integrase-type DNA-binding superfamily protein
AL7G20820	-8.43	-8.43	2.21E-10	3.86E-07	AT4G17750	ATHSF1, ATHSFA1A, HSF1, HSFA1A, heat shock factor 1
AL1G53820	5.21	4.89	3.93E-10	6.40E-07	/	Unknown
AL1G56400	5.04	-1.82	4.05E-10	6.40E-07	AT3G46200	aTNUDT9, NUDT9, nudix hydrolase homolog 9
AL2G18150	-3.22	3.37	9.39E-10	1.42E-06	/	Unknown
AL2G17320	4.57	-3.28	1.20E-09	1.74E-06	AT1G59650	CW14, Protein of unknown function (DUF1336)
AL6G39150	5.95	1.58	1.45E-09	2.00E-06	/	Unknown
AL7G50060	-8.99	-7.66	1.66E-09	2.21E-06	/	Unknown
AL1G51800	1.51	7.67	1.99E-09	2.47E-06	AT1G01090	PDH-E1 ALPHA, pyruvate dehydrogenase E1 alpha
AL8G36980	2.29	0.29	2.00E-09	2.47E-06	AT5G60370	Unknown
AL6G32920	-6.98	-6.99	2.88E-09	3.42E-06	AT5G21960	Integrase-type DNA-binding superfamily protein
AL755U10010	-8.43	-6.24	4.22E-09	4.83E-06	/	Unknown
AL1G26460	7.06	6.07	4.91E-09	5.27E-06	/	Unknown
AL1G58440	0.41	7.03	4.81E-09	5.27E-06	AT5G22030	UBP8, ubiquitin-specific protease 8
AL5G25600	-0.42	3.52	7.69E-09	7.98E-06	/	Unknown
AL8G15120	-8.60	-7.30	1.18E-08	1.19E-05	/	Unknown
AL1G31350	0.79	-5.70	1.22E-08	1.19E-05	AT1G18830	Transducin/WD40 repeat-like superfamily protein
AL3G14830	3.19	-1.69	1.63E-08	1.55E-05	AT3G04720	HEL, PR-4, PR4, pathogenesis-related 4
AL7G19230	-3.77	-0.26	3.04E-08	2.81E-05	AT3G26480	Transducin family protein / WD-40 repeat family protein
AL4G33820	5.73	7.65	3.44E-08	3.09E-05	/	Unknown
AL1G16150	6.73	2.89	3.90E-08	3.41E-05	/	Unknown
AL6G33490	-0.19	-8.47	5.88E-08	5.01E-05	AT5G22470	NAD+ ADP-ribosyltransferases;NAD+ ADP-ribosyltransferases
AL7G22470	-5.18	-3.06	6.80E-08	5.65E-05	AT4G29780	Unknown
AL6G38410	6.71	1.45	7.01E-08	5.68E-05	/	Unknown
AL350U10020	0.00	7.05	7.49E-08	5.69E-05	AT2G46520	cellular apoptosis susceptibility protein, putative / importin-alpha re-exporter, putative
AL6G45170	9.08	6.06	7.39E-08	5.69E-05	/	Unknown
AL7G34280	2.81	-1.78	7.54E-08	5.69E-05	AT4G19810	Glycosyl hydrolase family protein with chitinase insertion domain
AL3G46130	4.13	-0.65	8.34E-08	6.16E-05	AT2G14580	ATPRB1, PRB1, basic pathogenesis-related protein 1
AL1G29920	-4.61	-6.57	1.21E-07	8.74E-05	AT1G17600	Disease resistance protein (TIR-NBS-LRR class) family
AL7G48880	-4.52	-5.51	1.34E-07	9.48E-05	/	Unknown
AL4G19950	-1.26	-7.40	1.39E-07	9.59E-05	/	Unknown
AL7G45350	6.50	0.00	1.70E-07	1.15E-04	/	Unknown
AL4G34590	5.04	-0.68	2.07E-07	1.38E-04	AT2G37670	Transducin/WD40 repeat-like superfamily protein
AL7G28630	-4.29	-2.46	2.39E-07	1.56E-04	AT4G24570	DIC2, dicarboxylate carrier 2
AL7G43410	8.63	7.57	2.60E-07	1.66E-04	/	Unknown
AL6G53520	-3.99	-4.11	2.94E-07	1.84E-04	AT2G44840	ATERF13, EREBP, ERF13, ethylene-responsive element binding factor 13
AL5G17900	-4.04	-2.62	3.26E-07	2.00E-04	AT3G28340	GATL10, galacturonosyltransferase-like 10
AL5G19840	-0.96	5.29	3.31E-07	2.00E-04	AT2G10440	Unknown
AL1G29930	-6.52	-6.52	4.24E-07	2.49E-04	AT1G17610	Disease resistance protein (TIR-NBS class)
AL1G53140	0.00	6.74	4.35E-07	2.49E-04	/	Unknown
AL1G55850	4.01	4.71	4.29E-07	2.49E-04	AT1G48980	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AL7G52950	3.82	-0.41	4.49E-07	2.53E-04	AT5G38010	UDP-Glycosyltransferase superfamily protein
AL1G25240	0.43	-9.52	4.75E-07	2.63E-04	AT1G13470	Protein of unknown function (DUF1262)
AL409U10010	5.95	5.24	4.97E-07	2.71E-04	AT2G42390	protein kinase C substrate, heavy chain-related
AL6G12890	-1.34	3.41	5.52E-07	2.96E-04	AT5G03495	RNA-binding (RRM/RBD/RNP motifs) family protein
AL7G30360	8.07	6.86	5.97E-07	3.15E-04	AT4G23120	Bromo-adjacent homology (BAH) domain-containing protein
AL1G30680	-3.12	-2.88	6.31E-07	3.27E-04	AT1G18300	atnudt4, NUDT4, nudix hydrolase homolog 4
AL1G62480	-6.17	-6.17	6.64E-07	3.34E-04	/	Unknown
AL6G44140	6.37	0.00	6.55E-07	3.34E-04	AT4G10300	RmlC-like cupins superfamily protein
AL7G21220	4.20	-0.40	7.15E-07	3.55E-04	AT4G30880	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL7G24570	-2.56	-8.33	7.74E-07	3.78E-04	AT4G28040	nodulin MtN21 /EamA-like transporter family protein
AL9U11830	-7.25	-5.80	8.25E-07	3.97E-04	/	Unknown
AL3G28060	3.74	-2.79	1.06E-06	5.04E-04	/	Unknown
AL1G33320	-7.22	-5.15	1.42E-06	6.66E-04	AT1G20940	F-box family protein
AL5G41100	-0.57	3.84	1.60E-06	7.38E-04	AT3G59220	ATPIRIN1, PRN, PRN1, pirin

AL189U10010	-6.92	-6.92	1.98E-06	8.94E-04	/	Unknown
AL9U10260	-3.84	-3.64	1.99E-06	8.94E-04	AT4G13395	DVL10, RTFL12, ROTUNDIFOLIA like 12
AL1G64190	-5.05	-7.36	2.03E-06	8.97E-04	AT1G55940	CYP708A1, cytochrome P450, family 708, subfamily A, polypeptide 1
AL6G43060	4.92	-0.31	2.15E-06	9.41E-04	AT4G09500	UDP-Glycosyltransferase superfamily protein
AL6G28420	-3.88	-2.51	2.29E-06	9.89E-04	AT5G17350	Unknown
AL3G53610	1.65	-8.35	2.36E-06	1.00E-03	/	Unknown
AL964U10010	5.99	0.00	2.51E-06	1.06E-03	AT5G02230	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
AL2G17430	-1.01	3.46	2.64E-06	1.10E-03	AT1G59620	CW9, Disease resistance protein (CC-NBS-LRR class) family
AL59U10010	-7.34	1.52	2.95E-06	1.21E-03	AT2G30120	Unknown
AL1G63670	-7.75	-5.32	3.03E-06	1.23E-03	/	Unknown
AL1G24000	4.27	0.96	3.12E-06	1.25E-03	/	Unknown
AL8G18050	0.09	3.71	3.28E-06	1.30E-03	AT5G42900	COR27, cold regulated gene 27
AL4G25940	5.59	5.16	3.94E-06	1.54E-03	/	Unknown
AL3G18020	-3.92	-2.97	4.08E-06	1.58E-03	AT3G06890	Unknown
AL136U10020	0.00	5.95	4.26E-06	1.63E-03	AT2G30410	KIS, TFCA, tubulin folding cofactor A (KIESEL)
AL3G14820	2.54	-0.50	4.71E-06	1.78E-03	AT3G04720	HEL, PR-4, PR4, pathogenesis-related 4
AL8G35270	5.67	2.22	4.84E-06	1.81E-03	AT5G64410	ATOPT4, OPT4, oligopeptide transporter 4
AL1G52070	5.70	0.00	5.26E-06	1.90E-03	/	Unknown
AL4G42410	2.61	-0.16	5.19E-06	1.90E-03	AT2G43590	Chitinase family protein
AL5G22170	-1.85	0.84	5.24E-06	1.90E-03	AT3G48640	Unknown
AL4G15180	-4.34	0.08	5.33E-06	1.90E-03	AT2G24600	Ankyrin repeat family protein
AL1G55260	1.87	2.06	5.58E-06	1.95E-03	AT1G48605	ATHAL3B, HAL3, HAL3B, Flavoprotein
AL7G34390	-3.86	2.11	5.53E-06	1.95E-03	AT3G18100	AtMYB4R1, MYB4R1, myb domain protein 4r1
AL2G34310	-3.09	-1.78	5.69E-06	1.97E-03	AT1G74450	Protein of unknown function (DUF793)
AL5G25850	-7.18	1.83	5.74E-06	1.97E-03	AT3G46840	Subtilase family protein
AL3G46510	7.21	6.33	6.13E-06	2.08E-03	/	Unknown
AL6G39780	-6.62	-6.62	6.49E-06	2.18E-03	/	Unknown
AL1G56460	-6.39	-3.28	6.60E-06	2.19E-03	AT1G52420	UDP-Glycosyltransferase superfamily protein
AL4G30580	-8.00	-2.87	6.70E-06	2.20E-03	AT2G34600	JAZ7, TIFY5B, jasmonate-zim-domain protein 7
AL7G14130	-1.61	-7.37	7.78E-06	2.53E-03	AT4G36850	PQ-loop repeat family protein / transmembrane family protein
AL4G13390	-3.71	3.25	8.18E-06	2.61E-03	/	Unknown
AL5G25530	-1.27	3.57	8.14E-06	2.61E-03	AT3G46640	LUX, PCL1, Homeodomain-like superfamily protein
AL6G50030	-0.30	-4.90	8.42E-06	2.66E-03	AT4G05320	UBQ10, polyubiquitin 10
AL5G22380	-3.74	-1.53	8.78E-06	2.75E-03	AT3G44260	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
AL7G10270	-2.92	-1.57	9.03E-06	2.80E-03	AT4G38400	ATEXLA2, ATEXPL2, ATHEXP BETA 2.2, EXLA2, EXPL2, expansin-like A2
AL8G21160	-8.30	0.61	9.41E-06	2.89E-03	/	Unknown
AL6G23940	0.32	2.86	1.10E-05	3.34E-03	AT5G13320	GDG1, GH3.12, PBS3, WIN3, Auxin-responsive GH3 family protein
AL2G17080	-0.10	-3.01	1.13E-05	3.40E-03	AT1G59780	NB-ARC domain-containing disease resistance protein
AL2G38750	5.41	0.00	1.14E-05	3.41E-03	AT3G14420	Aldolase-type TIM barrel family protein
AL1G56780	3.96	6.18	1.19E-05	3.52E-03	AT1G02190	Fatty acid hydroxylase superfamily
AL2G32120	2.91	0.87	1.21E-05	3.52E-03	/	Unknown
AL8G35170	-7.43	-1.57	1.20E-05	3.52E-03	AT3G62850	zinc finger protein-related
AL8G35760	1.79	-1.11	1.22E-05	3.53E-03	AT5G59320	LTP3, lipid transfer protein 3
AL3G44260	7.17	7.11	1.30E-05	3.71E-03	AT2G23150	ATNRAMP3, NRAMP3, natural resistance-associated macrophage protein 3
AL9U10430	-9.49	-0.73	1.33E-05	3.77E-03	/	Unknown
AL3G52480	-7.87	0.04	1.41E-05	3.98E-03	/	Unknown
AL615U10010	-7.05	-4.97	1.45E-05	4.05E-03	AT3G23955	F-box family protein
AL6G45660	-2.38	-2.05	1.51E-05	4.15E-03	AT4G11280	ACS6, ATACS6, 1-aminocyclopropane-1-carboxylic acid (acc) synthase 6
AL6G50790	-3.89	-0.31	1.50E-05	4.15E-03	AT4G02330	ATPMEPCRB, Plant invertase/pectin methylesterase inhibitor superfamily
AL8G41670	-2.93	-2.28	1.57E-05	4.27E-03	AT5G64310	AGP1, ATAGP1, arabinogalactan protein 1
AL1G51570	-0.11	5.15	1.58E-05	4.27E-03	AT1G43160	RAP2.6, related to AP2 6
AL1G41260	-3.50	-1.70	1.60E-05	4.27E-03	AT1G27730	STZ, ZAT10, salt tolerance zinc finger
AL6G50520	1.38	-0.97	1.70E-05	4.49E-03	AT4G02520	ATGSTF2, ATPM24, ATPM24.1, GST2, GSTF2, glutathione S-transferase PHI 2
AL7G25030	-2.62	-2.11	1.70E-05	4.49E-03	AT4G27657	Unknown
AL4G12820	3.65	4.46	1.75E-05	4.57E-03	AT1G06900	Insulinase (Peptidase family M16) family protein
AL350U10010	0.00	5.63	1.87E-05	4.85E-03	/	Unknown
AL6G42050	-6.14	-6.14	1.93E-05	4.98E-03	/	Unknown
AL1G63660	5.28	0.00	1.98E-05	5.06E-03	AT1G55600	ATWRKY10, MINI3, WRKY10, WRKY DNA-binding protein 10
AL5G38270	-2.24	-1.06	2.08E-05	5.26E-03	AT3G56880	VQ motif-containing protein
AL372U10020	5.29	0.00	2.13E-05	5.37E-03	AT5G64210	AOX2, alternative oxidase 2
AL8G10090	-0.73	-5.46	2.15E-05	5.38E-03	/	Unknown
AL2G17290	0.21	-8.64	2.19E-05	5.42E-03	AT1G59650	CW14, Protein of unknown function (DUF1336)
AL2G10940	0.69	-3.01	2.26E-05	5.56E-03	AT1G64110	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AL2G17330	2.74	-1.48	2.32E-05	5.66E-03	AT1G59650	CW14, Protein of unknown function (DUF1336)
AL7G25060	-2.55	-2.36	2.34E-05	5.66E-03	AT4G27652	Unknown
AL1G51460	6.51	7.03	2.36E-05	5.67E-03	/	Unknown
AL5G30180	-4.13	-0.86	2.47E-05	5.90E-03	AT3G50060	MYB77, myb domain protein 77
AL5G15050	1.63	4.64	2.52E-05	5.99E-03	AT3G26300	CYP71B34, cytochrome P450, family 71, subfamily B, polypeptide 34
AL2G33290	-2.61	-2.00	2.61E-05	6.15E-03	AT1G73540	atnudt21, NUDT21, nudix hydrolase homolog 21
AL1G57700	-7.66	-3.64	2.63E-05	6.16E-03	AT1G50090	D-aminoacid aminotransferase-like PLP-dependent enzymes superfamily protein
AL4G12970	-2.91	-2.14	2.69E-05	6.21E-03	AT2G23130	AGP17, ATAGP17, arabinogalactan protein 17
AL8G23530	0.87	-6.34	2.68E-05	6.21E-03	/	Unknown
AL3G48410	-3.43	-4.03	2.71E-05	6.22E-03	AT2G19800	MIOX2, myo-inositol oxygenase 2
AL4G20640	-3.76	-1.43	2.77E-05	6.30E-03	AT2G27080	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
AL4G33860	6.18	2.44	2.80E-05	6.32E-03	AT2G37435	Cystatin/monellin superfamily protein
AL5G18750	-6.50	2.39	2.99E-05	6.71E-03	/	Unknown
AL1G41980	-3.33	-1.77	3.15E-05	6.99E-03	AT1G28370	ATERF11, ERF11, ERF domain protein 11
AL6G23700	-2.86	-1.85	3.16E-05	6.99E-03	AT5G13100	Unknown
AL3G34190	-0.20	-2.00	3.26E-05	7.17E-03	AT3G20470	ATGRP-5, ATGRP5, GRP-5, GRP5, glycine-rich protein 5
AL6G42680	1.74	1.87	3.30E-05	7.22E-03	AT4G08870	Arginase/deacetylase superfamily protein
AL8G36370	-3.05	-2.04	3.55E-05	7.72E-03	AT5G59820	RHL41, ZAT12, C2H2-type zinc finger family protein
AL8G11160	-1.20	-2.39	3.59E-05	7.74E-03	/	Unknown

AL1G49860	-4.75	-1.51	3.76E-05	7.95E-03	AT1G35140	EXL7, PHI-1, Phosphate-responsive 1 family protein
AL5G22780	-0.53	-3.28	3.74E-05	7.95E-03	AT3G42050	vacuolar ATP synthase subunit H family protein
AL8G19120	-3.81	-2.47	3.75E-05	7.95E-03	AT5G42380	CML37, CML39, calmodulin like 37
AL1G60320	-0.78	2.70	3.99E-05	8.30E-03	AT1G51800	Leucine-rich repeat protein kinase family protein
AL215U10020	-5.06	-0.43	4.01E-05	8.30E-03	AT3G46020	RNA-binding (RRM/RBD/RNP motifs) family protein
AL6G19830	0.12	1.84	4.02E-05	8.30E-03	AT5G09440	EXL4, EXORDIUM like 4
AL7G18550	-3.00	-6.54	3.95E-05	8.30E-03	/	Unknown
AL2G13640	-0.55	-2.44	4.17E-05	8.56E-03	AT1G62290	Saposin-like aspartyl protease family protein
AL1G25390	4.97	0.34	4.21E-05	8.58E-03	AT1G13610	alpha/beta-Hydrolases superfamily protein
AL6G48480	3.02	5.53	4.89E-05	9.90E-03	AT1G05080	F-box/RNI-like/FBD-like domains-containing protein
AL3G28690	0.14	-7.30	4.98E-05	9.98E-03	AT3G16040	Translation machinery associated TMA7
AL8G35690	6.18	5.79	4.98E-05	9.98E-03	/	Unknown

Table S4. List of the differentially expressed genes (DEG) along the fraction down from the dune top on control plants. Genes were considered as differentially expressed when false discovery rate (FDR) < 0.01. Genes are sorted by FDR values.

Gene_ID_lyrata	logFC2	logFC3	logFC4	PValue	FDR	Homolog_thaliana	Gene_name
AL8G12660	0.00	0.00	12.85	1.28E-32	4.26E-28	AT5G45890	SAG12, senescence-associated gene 12
AL8G36240	-8.98	-8.26	-7.89	8.28E-20	1.37E-15	AT5G59720	HSP18.2, heat shock protein 18.2
AL1G63670	10.21	0.00	2.46	4.27E-19	4.63E-15	/	Unknown
AL8G10760	-11.98	-7.66	-9.55	5.58E-19	4.63E-15	/	Unknown
AL1G36300	8.90	2.00	-0.35	3.23E-18	2.14E-14	AT1G22760	PAB3, poly(A) binding protein 3
AL6G44080	-9.02	-8.07	-6.77	4.99E-18	2.76E-14	AT4G10250	ATHSP22.0, HSP20-like chaperones superfamily protein
AL3G44570	0.00	9.25	0.00	2.01E-16	9.52E-13	/	Unknown
AL4G33850	-4.03	-4.03	6.37	2.90E-16	1.20E-12	AT2G37435	Cystatin/monellin superfamily protein
AL8G10090	3.17	0.68	8.38	7.20E-16	2.66E-12	AT5G48570	ATFKBP65, FKBP65, ROF2, FKBP-type peptidyl-prolyl cis-trans isomerase family protein
AL1G47730	-8.86	-5.22	-6.65	4.90E-15	1.63E-11	AT1G33350	Pentatricopeptide repeat (PPR) superfamily protein
AL6G45170	-8.85	-11.06	-6.62	6.74E-15	2.04E-11	AT4G05497	RNI-like superfamily protein
AL2G13710	1.60	0.00	9.34	1.01E-14	2.78E-11	AT1G62210	Unknown
AL6G39150	6.43	-3.44	-0.06	2.30E-14	5.89E-11	/	Unknown
AL1G24000	0.20	5.68	-0.55	2.69E-14	6.39E-11	/	Unknown
AL9U11830	9.28	1.68	5.24	4.07E-14	9.00E-11	/	Unknown
AL1G62090	-6.37	-4.48	-5.78	5.29E-14	1.10E-10	AT1G53540	HSP20-like chaperones superfamily protein
AL1G56380	9.24	0.00	0.00	1.50E-13	2.81E-10	AT3G46210	Ribosomal protein S5 domain 2-like superfamily protein
AL3G44590	-1.50	6.11	0.01	1.52E-13	2.81E-10	AT2G07669	Unknown
AL8G13800	0.49	-9.14	-9.14	2.18E-13	3.81E-10	AT2G02360	AtPP2-B10, PP2-B10, phloem protein 2-B10
AL5G19840	0.24	0.05	6.66	3.20E-13	5.32E-10	AT2G10440	Unknown
AL8G13710	9.11	0.00	0.00	6.50E-13	1.03E-09	AT4G19520	disease resistance protein (TIR-NBS-LRR class) family
AL4G32840	-1.41	5.95	7.76	7.33E-13	1.11E-09	AT2G36660	PAB7, poly(A) binding protein 7
AL1G25240	-8.53	-8.55	-10.12	2.09E-12	3.03E-09	AT1G13470	Protein of unknown function (DUF1262)
AL6G26110	-7.56	-7.05	-6.13	2.34E-12	3.24E-09	AT5G15250	ATFTSH6, FTSH6, FTSH protease 6
AL6G31550	-1.42	7.63	-1.42	2.45E-12	3.26E-09	/	Unknown
AL7G10480	6.30	0.35	-0.85	2.85E-12	3.64E-09	AT4G38590	BGAL14, beta-galactosidase 14
AL7G30390	-8.42	-0.05	-9.36	3.11E-12	3.83E-09	AT4G23100	ATECS1, CAD2, GSH1, GSHA, PAD2, RML1, glutamate-cysteine ligase
AL4G25140	-9.35	-9.35	-9.35	5.49E-12	6.52E-09	AT2G30290	BP80-1;2, VSR1;2, VSR2, VACUOLAR SORTING RECEPTOR 2
AL4G22940	-8.50	-8.34	-10.10	6.94E-12	7.95E-09	AT4G01560	MEE49, Ribosomal RNA processing Brix domain protein
AL1G18640	3.24	0.12	0.39	9.06E-12	1.00E-08	AT1G08230	ATGAT1, GAT1, Transmembrane amino acid transporter family protein
AL6G47420	5.01	-5.00	-1.17	9.71E-12	1.04E-08	AT4G12500	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL3G34090	0.00	9.44	8.30	1.13E-11	1.17E-08	AT3G20370	TRAF-like family protein
AL8G35750	-7.58	-7.02	-6.76	2.25E-11	2.26E-08	AT5G59310	LTP4, lipid transfer protein 4
AL6G30200	-6.33	-4.57	-3.33	2.35E-11	2.29E-08	AT5G18840	Major facilitator superfamily protein
AL5G31070	-8.94	1.16	-8.94	3.53E-11	3.36E-08	/	Unknown
AL63U10060	5.92	-0.08	-0.80	3.75E-11	3.46E-08	AT5G50740	Heavy metal transport/detoxification superfamily protein
AL2G17260	-6.92	-1.69	-9.81	7.41E-11	6.66E-08	AT4G19500	nucleoside-triphosphatases;transmembrane receptors;nucleotide binding;ATP binding
AL8G21350	-0.43	4.70	-3.27	8.53E-11	7.46E-08	AT5G48490	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL4G44090	-2.55	-0.89	6.07	9.56E-11	8.15E-08	AT2G44990	ATCCD7, CCD7, MAX3, carotenoid cleavage dioxygenase 7
AL9U10170	-1.73	0.32	5.97	1.20E-10	9.97E-08	/	Unknown
AL7G22610	2.01	6.51	-3.43	1.31E-10	1.06E-07	AT4G29700	Alkaline-phosphatase-like family protein
AL7G23180	-7.81	-6.18	-9.44	2.21E-10	1.75E-07	AT4G29270	HAD superfamily, subfamily IIIB acid phosphatase
AL3G22850	6.59	1.01	2.17	2.59E-10	2.00E-07	AT3G11340	UDP-Glycosyltransferase superfamily protein
AL5G18230	4.57	-0.85	-0.60	3.16E-10	2.39E-07	AT3G28580	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AL7G49510	-7.38	-7.40	-6.53	3.42E-10	2.52E-07	AT5G40382	Cytochrome c oxidase subunit Vc family protein
AL1G20790	-5.41	-7.38	-6.39	3.94E-10	2.85E-07	AT1G10095	Protein prenylyltransferase superfamily protein
AL1G34320	5.24	-0.16	1.06	4.41E-10	3.11E-07	AT1G21240	WAK3, wall associated kinase 3
AL4G36930	-6.94	-9.27	-6.86	5.60E-10	3.88E-07	AT2G39510	nodulin MtN21 /EamA-like transporter family protein
AL8G14180	6.69	6.05	-0.05	6.37E-10	4.32E-07	AT3G23890	ATTOPII, TOPII, topoisomerase II
AL1G50760	-8.30	-8.30	-8.30	7.80E-10	5.19E-07	/	Unknown
AL7G24990	-3.10	-4.83	-3.80	9.38E-10	6.11E-07	AT4G27670	HSP21, heat shock protein 21
AL8G21750	1.08	7.23	0.01	1.01E-09	6.47E-07	AT5G56350	Pyruvate kinase family protein
AL7G14130	-6.93	-5.09	-7.28	1.07E-09	6.69E-07	AT4G36850	PQ-loop repeat family protein / transmembrane family protein
AL7G43480	-7.37	3.14	-5.57	1.32E-09	8.11E-07	/	Unknown
AL2G19210	9.84	9.36	9.67	1.39E-09	8.40E-07	/	Unknown
AL3G40380	-9.27	-6.82	-7.47	1.53E-09	9.06E-07	AT5G58840	Subtilase family protein
AL4G23910	5.62	-1.51	1.46	1.59E-09	9.20E-07	AT2G29350	SAG13, senescence-associated gene 13
AL5G25020	-3.79	-4.02	-3.94	1.61E-09	9.20E-07	AT3G46230	ATHSP17.4, HSP17.4, heat shock protein 17.4
AL8G16820	1.01	2.31	-1.87	1.77E-09	9.94E-07	AT5G43500	ARP9, ATARP9, actin-related protein 9
AL350U10020	0.00	7.84	0.00	6.13E-09	3.39E-06	AT2G46520	cellular apoptosis susceptibility protein, putative / importin-alpha re-exporter, putative
AL7G30360	7.63	0.00	0.00	7.50E-09	4.09E-06	AT4G23120	Bromo-adjacent homology (BAH) domain-containing protein
AL1G36260	-8.35	1.77	-8.35	9.60E-09	5.06E-06	/	Unknown
AL7G22470	3.04	0.73	-1.09	9.56E-09	5.06E-06	AT4G29780	Unknown
AL8G20560	1.19	-9.65	1.28	1.06E-08	5.52E-06	AT3G24080	KRR1 family protein
AL463U10030	9.53	8.74	7.67	1.28E-08	6.56E-06	AT2G39450	ATMTP11, MTP11, Cation efflux family protein
AL6G47440	5.96	1.08	-0.64	1.39E-08	7.00E-06	AT4G12500	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL8G21450	0.00	7.73	4.45	1.42E-08	7.03E-06	/	Unknown
AL3G37310	7.53	0.00	0.00	1.54E-08	7.50E-06	/	Unknown
AL3G39890	2.88	-0.40	0.33	2.25E-08	1.08E-05	AT3G24460	Serinc-domain containing serine and sphingolipid biosynthesis protein
AL2G11070	-9.22	0.49	-7.42	2.49E-08	1.17E-05	AT1G64030	ATSRP3, SRP3, serpin 3

AL8G35760	-2.13	-5.48	-2.56	2.47E-08	1.17E-05	AT5G59320	LTP3, lipid transfer protein 3
AL8G17640	0.00	7.46	0.00	2.59E-08	1.19E-05	/	Unknown
AL1G26460	-0.72	-8.39	-8.39	2.74E-08	1.23E-05	/	Unknown
AL1G56400	6.82	2.55	1.25	2.70E-08	1.23E-05	AT3G46200	aTNUDT9, NUDT9, nudix hydrolase homolog 9
AL3G36900	4.72	-2.47	1.55	3.09E-08	1.37E-05	AT3G22600	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL7G39760	-6.44	-5.14	-9.26	3.13E-08	1.37E-05	AT4G15670	Thioredoxin superfamily protein
AL1G40130	5.44	5.85	-1.13	3.31E-08	1.43E-05	/	Unknown
AL8G41390	3.29	0.32	-1.55	3.36E-08	1.43E-05	AT5G64120	Peroxidase superfamily protein
AL1G32050	0.73	-3.84	-4.78	3.72E-08	1.54E-05	AT3G19515	Unknown
AL5G32900	-7.64	-7.64	1.89	3.71E-08	1.54E-05	AT3G56590	hydroxyproline-rich glycoprotein family protein
AL7G39750	-6.33	-2.81	-10.25	4.01E-08	1.64E-05	AT4G15680	Thioredoxin superfamily protein
AL1G60060	-0.78	4.35	-4.46	4.32E-08	1.75E-05	AT1G52000	Mannose-binding lectin superfamily protein
AL6G46200	7.80	2.88	5.40	4.45E-08	1.78E-05	/	Unknown
AL1G47160	-2.97	-4.28	-3.82	4.57E-08	1.81E-05	AT3G03773	HSP20-like chaperones superfamily protein
AL1G36560	-1.84	-4.15	4.07	4.90E-08	1.91E-05	AT1G22990	Heavy metal transport/detoxification superfamily protein
AL5G25530	-7.76	-2.82	-2.08	4.94E-08	1.91E-05	AT3G46640	LUX, PCL1, Homeodomain-like superfamily protein
AL3G46710	8.78	9.39	1.72	5.17E-08	1.98E-05	/	Unknown
AL8G18270	0.00	7.44	0.00	5.68E-08	2.14E-05	AT3G26670	Protein of unknown function (DUF803)
AL6G21160	1.85	1.70	5.51	6.68E-08	2.49E-05	AT5G10625	Unknown
AL3G15490	1.97	3.89	1.28	8.08E-08	2.98E-05	AT3G05110	Domain of unknown function (DUF3444)
AL5G25120	-5.29	-4.33	-8.10	8.39E-08	3.06E-05	AT1G53540	HSP20-like chaperones superfamily protein
AL6G46640	2.73	6.39	7.01	8.50E-08	3.07E-05	AT4G11910	Unknown
AL8G25100	0.97	-3.60	-4.26	9.00E-08	3.22E-05	AT5G50915	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AL2G28230	-3.47	1.49	2.28	9.50E-08	3.32E-05	/	Unknown
AL8G13740	-1.56	1.86	1.74	9.39E-08	3.32E-05	AT5G45275	Major facilitator superfamily protein
AL1G32120	1.03	-5.61	-8.03	1.00E-07	3.47E-05	AT1G14830	ADL1C, ADL5, DL1C, DRP1C, DYNAMIN-like 1C
AL5G16560	6.97	0.00	0.00	1.08E-07	3.71E-05	AT3G27320	alpha/beta-Hydrolases superfamily protein
AL2G37060	1.34	-4.67	-3.24	1.16E-07	3.93E-05	AT1G76930	ATEXT1, ATEXT4, EXT1, EXT4, ORG5, extensin 4
AL6G42410	7.46	3.05	5.37	1.18E-07	3.96E-05	AT5G28712	transposable element gene
AL8G26410	7.87	0.00	5.96	1.24E-07	4.11E-05	/	Unknown
AL7G25540	1.95	-0.15	-1.10	1.28E-07	4.20E-05	AT4G27280	Calcium-binding EF-hand family protein
AL6G44600	-6.08	-7.67	-7.67	1.38E-07	4.48E-05	AT4G10550	Subtilase family protein
AL3G33370	0.00	2.41	7.31	1.40E-07	4.52E-05	AT3G20030	F-box and associated interaction domains-containing protein
AL3G15350	0.00	7.10	0.00	1.42E-07	4.54E-05	/	Unknown
AL5G22780	4.74	3.78	3.46	1.43E-07	4.54E-05	AT3G42050	vacuolar ATP synthase subunit H family protein
AL2G32340	1.31	-3.68	-2.58	1.52E-07	4.75E-05	AT1G72660	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AL1G50770	-7.28	-7.28	-7.28	1.53E-07	4.76E-05	/	Unknown
AL7G14660	-3.61	-9.45	-6.55	1.63E-07	5.00E-05	AT4G36430	Peroxidase superfamily protein
AL1G59780	-5.38	-2.39	-5.09	1.68E-07	5.06E-05	AT1G51780	ILL5, IAA-leucine resistant (ILR)-like gene 5
AL7G47000	-2.13	-2.13	5.31	1.68E-07	5.06E-05	AT5G61500	ATATG3, ATG3, autophagy 3 (APG3)
AL3G40440	1.68	-6.51	-6.51	1.79E-07	5.37E-05	AT3G24715	Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain
AL1G55760	0.00	6.91	0.00	1.86E-07	5.49E-05	AT1G48930	AtGH9C1, GH9C1, glycosyl hydrolase 9C1
AL7G44980	-6.39	-6.31	-7.99	1.87E-07	5.49E-05	/	Unknown
AL6G36020	-0.61	5.20	0.06	2.17E-07	6.34E-05	AT5G24440	CID13, CTC-interacting domain 13
AL189U10010	7.09	0.00	0.00	2.21E-07	6.37E-05	/	Unknown
AL5G25600	-3.09	1.08	-3.61	2.28E-07	6.51E-05	/	Unknown
AL8G21550	-1.39	-4.47	-3.65	2.29E-07	6.51E-05	AT5G48570	ATFKBP65, FKBP65, ROF2, FKBP-type peptidyl-prolyl cis-trans isomerase family protein
AL5G28640	5.12	4.57	1.33	2.32E-07	6.54E-05	AT3G49110	ATPCA, ATPRX33, PRX33, PRXCA, peroxidase CA
AL8G19650	-3.36	-9.37	-6.12	2.35E-07	6.55E-05	AT5G42180	Peroxidase superfamily protein
AL6G19060	-8.39	0.09	-8.39	2.62E-07	7.25E-05	AT1G76810	eukaryotic translation initiation factor 2 (eIF-2) family protein
AL1G65910	-6.11	-0.06	-0.26	2.99E-07	8.16E-05	AT1G56300	Chaperone DnaJ-domain superfamily protein
AL6G27350	-3.02	4.09	-3.02	2.99E-07	8.16E-05	AT5G16410	HXXXD-type acyl-transferase family protein
AL9U10040	0.00	6.81	0.00	3.18E-07	8.58E-05	AT4G13490	RING/U-box superfamily protein
AL2G31800	-1.29	1.24	-5.06	3.32E-07	8.89E-05	AT1G72140	Major facilitator superfamily protein
AL8G33540	2.42	-0.90	-2.81	3.69E-07	9.80E-05	AT5G57560	TCH4, XTH22, Xyloglucan endotransglucosylase/hydrolase family protein
AL1G64230	-0.49	5.47	-2.09	3.94E-07	1.04E-04	AT1G55970	HAC04, HAC4, HAC6, HAG04, HAG4, histone acetyltransferase of the CBP family 4
AL2G22180	-7.24	-7.24	-7.24	4.08E-07	1.05E-04	AT1G65480	FT, PEBP (phosphatidylethanolamine-binding protein) family protein
AL7G13020	-4.89	3.27	1.03	4.06E-07	1.05E-04	/	Unknown
AL7G25000	3.75	-1.75	0.62	4.02E-07	1.05E-04	AT5G54160	ATOMT1, OMT1, O-methyltransferase 1
AL4G36670	-0.44	0.50	-5.00	4.19E-07	1.07E-04	AT2G39330	JAL23, jacalin-related lectin 23
AL3G38410	0.88	-7.91	-6.13	4.25E-07	1.08E-04	AT2G46760	D-arabinono-1,4-lactone oxidase family protein
AL5G20050	0.00	7.38	4.94	4.28E-07	1.08E-04	AT3G43833	Unknown
AL1G29400	4.53	7.61	9.74	4.42E-07	1.09E-04	AT1G17170	ATGSTU24, GST, GSTU24, glutathione S-transferase TAU 24
AL350U10010	0.00	7.05	0.00	4.37E-07	1.09E-04	AT3G20490	Unknown
AL3G38800	3.67	7.53	5.74	4.40E-07	1.09E-04	/	Unknown
AL5G27070	-7.07	-8.68	-0.20	5.30E-07	1.29E-04	AT3G47790	ATATH7, ATH7, ABC2 homolog 7
AL7G40550	4.41	-0.59	1.29	5.78E-07	1.40E-04	/	Unknown
AL6G42290	5.54	2.72	4.45	6.26E-07	1.50E-04	/	Unknown
AL7G48300	-0.41	2.66	4.58	6.22E-07	1.50E-04	AT5G41150	ATRAD1, RAD1, UVH1, Restriction endonuclease, type II-like superfamily protein
AL1G49860	2.22	-1.83	-4.41	6.45E-07	1.53E-04	AT1G35140	EXL7, PHI-1, Phosphate-responsive 1 family protein
AL5G30180	2.50	-0.42	-1.91	6.96E-07	1.64E-04	AT3G50060	MYB77, myb domain protein 77
AL1G11690	-1.44	0.01	1.91	7.17E-07	1.67E-04	AT4G01690	HEMG1, PPO1, PPOX, Flavin containing amine oxidoreductase family
AL7G47600	2.51	0.30	-0.18	7.15E-07	1.67E-04	AT5G41750	Disease resistance protein (TIR-NBS-LRR class) family
AL6G52880	2.16	6.51	1.98	7.42E-07	1.71E-04	AT3G62850	zinc finger protein-related
AL6G28820	-7.77	-7.77	-4.52	7.59E-07	1.74E-04	AT3G01345	Expressed protein
AL7G16160	3.08	-1.04	-0.63	7.69E-07	1.75E-04	AT4G35060	Heavy metal transport/detoxification superfamily protein
AL6G17600	-3.24	-4.78	-4.13	7.93E-07	1.79E-04	AT5G07330	Unknown

AL3G12910	6.77	0.00	0.00	8.00E-07	1.80E-04	AT3G03290	Adenine nucleotide alpha hydrolases-like superfamily protein
AL3G31480	6.04	0.76	2.09	8.11E-07	1.81E-04	AT3G18250	Putative membrane lipoprotein
AL1G57700	-7.39	-7.39	1.05	8.56E-07	1.90E-04	AT1G50090	D-aminoacid aminotransferase-like PLP-dependent enzymes superfamily protein
AL3G34480	-5.47	-6.24	-7.81	8.71E-07	1.92E-04	/	Unknown
AL7G29320	2.23	-0.33	1.61	9.13E-07	2.00E-04	AT4G24000	ATCSLG2, CSLG2, cellulose synthase like G2
AL1G53670	-7.72	-5.14	-7.72	9.72E-07	2.11E-04	/	Unknown
AL6G33740	2.90	3.00	-8.76	1.01E-06	2.18E-04	/	Unknown
AL5G23200	6.78	0.00	0.00	1.05E-06	2.25E-04	AT3G44790	TRAF-like family protein
AL2G33610	2.04	-0.58	0.04	1.10E-06	2.29E-04	AT1G73805	Calmodulin binding protein-like
AL6G19510	2.72	-1.98	-0.87	1.08E-06	2.29E-04	AT5G08760	Unknown
AL7G32520	0.88	0.31	3.82	1.09E-06	2.29E-04	AT4G21540	SPHK1, sphingosine kinase 1
AL7G49110	2.30	7.10	0.00	1.09E-06	2.29E-04	AT5G40640	Unknown
AL1G51460	0.00	6.69	0.00	1.12E-06	2.32E-04	/	Unknown
AL8G14260	6.89	7.17	0.00	1.13E-06	2.33E-04	AT4G19840	ATPP2-A1, ATPP2A-1, PP2-A1, phloem protein 2-A1
AL7G43410	-6.96	1.65	-6.96	1.17E-06	2.40E-04	/	Unknown
AL1G17160	-9.23	-1.05	-0.58	1.18E-06	2.41E-04	AT1G07050	CCT motif family protein
AL7G45150	-1.50	2.49	0.61	1.20E-06	2.44E-04	AT5G36220	CYP81D1, CYP91A1, cytochrome p450 81d1
AL1G16360	-7.05	-7.05	-5.33	1.22E-06	2.47E-04	AT1G06350	Fatty acid desaturase family protein
AL6G22820	-3.35	-5.81	-5.39	1.25E-06	2.51E-04	AT5G12030	AT-HSP17.6A, HSP17.6, HSP17.6A, heat shock protein 17.6A
AL8G23010	0.74	2.02	3.16	1.27E-06	2.52E-04	AT5G49360	ATBXL1, BXL1, beta-xylosidase 1
AL1G20960	4.68	-2.61	5.68	1.30E-06	2.56E-04	AT4G03298	Unknown
AL4G43470	0.93	1.76	-6.30	1.36E-06	2.67E-04	AT2G44460	BGLU28, beta glucosidase 28
AL6G30220	1.91	-1.00	-0.24	1.38E-06	2.69E-04	AT5G18860	inosine-uridine preferring nucleoside hydrolase family protein
AL6G31800	-5.06	-0.58	-2.86	1.49E-06	2.89E-04	AT5G20250	DIN10, Raffinose synthase family protein
AL8G18050	-5.78	-2.78	-1.84	1.52E-06	2.93E-04	AT5G42900	COR27, cold regulated gene 27
AL2G11520	1.22	-6.45	-6.45	1.55E-06	2.97E-04	AT1G63710	CYP86A7, cytochrome P450, family 86, subfamily A, polypeptide 7
AL6G15210	-1.58	-6.97	-4.78	1.55E-06	2.97E-04	AT5G05340	Peroxidase superfamily protein
AL6G41120	3.81	-0.46	-0.21	1.66E-06	3.15E-04	AT2G29380	HAI3, highly ABA-induced PP2C gene 3
AL4G30400	-0.52	3.16	-1.50	1.70E-06	3.21E-04	AT2G34430	LHB1B1, LHCB1.4, light-harvesting chlorophyll-protein complex II subunit B1
AL1G32090	0.06	-8.27	-4.63	1.71E-06	3.22E-04	AT1G14840	ATMAP70-4, MAP70-4, microtubule-associated proteins 70-4
AL4G28630	0.50	-1.63	-3.64	1.73E-06	3.24E-04	/	Unknown
AL2G10230	-1.34	5.61	3.28	1.82E-06	3.38E-04	AT2G25130	ARM repeat superfamily protein
AL1G48060	8.02	3.44	6.63	1.84E-06	3.39E-04	AT1G33612	Leucine-rich repeat (LRR) family protein
AL1G48040	4.50	-0.91	5.92	1.85E-06	3.40E-04	AT1G33610	Leucine-rich repeat (LRR) family protein
AL8G13780	6.66	0.00	0.00	1.88E-06	3.43E-04	/	Unknown
AL1G60810	-6.67	-6.67	-6.67	1.90E-06	3.44E-04	AT1G52560	HSP20-like chaperones superfamily protein
AL1G13240	-7.42	-4.32	-7.42	1.93E-06	3.48E-04	AT1G03710	Cystatin/monellin superfamily protein
AL3G11700	0.00	3.87	-3.70	2.01E-06	3.60E-04	AT3G02410	ICME-LIKE2, alpha/beta-Hydrolases superfamily protein
AL5G35890	1.75	-0.44	-1.16	2.25E-06	4.03E-04	AT3G54810	BME3, BME3-ZF, GATA8, Plant-specific GATA-type zinc finger transcription factor family protein
AL6G11620	1.60	2.43	7.08	2.32E-06	4.13E-04	AT5G02390	Protein of unknown function (DUF3741)
AL3G52610	0.00	6.53	0.00	2.35E-06	4.16E-04	AT3G03640	BGLU25, GLUC, beta glucosidase 25
AL7G13460	5.81	1.45	2.25	2.59E-06	4.55E-04	AT4G37370	CYP81D8, cytochrome P450, family 81, subfamily D, polypeptide 8
AL8G13460	1.41	-0.62	-1.63	2.72E-06	4.75E-04	AT5G45340	CYP707A3, cytochrome P450, family 707, subfamily A, polypeptide 3
AL8G12980	-2.78	-1.99	-7.49	2.74E-06	4.76E-04	AT5G45670	GDSL-like Lipase/Acylhydrolase superfamily protein
AL7G52770	-0.54	3.41	-3.01	2.81E-06	4.86E-04	AT5G38120	4CL8, AMP-dependent synthetase and ligase family protein
AL7G15780	3.85	2.81	6.05	3.10E-06	5.33E-04	AT4G35380	SEC7-like guanine nucleotide exchange family protein
AL6G23420	-1.59	3.63	0.54	3.24E-06	5.54E-04	/	Unknown
AL2G26860	-9.12	-0.66	-0.10	3.25E-06	5.54E-04	AT1G68050	ADO3, FKF1, flavin-binding, kelch repeat, f box 1
AL7G20820	0.86	-7.82	-7.82	3.50E-06	5.93E-04	AT4G17750	ATHSF1, ATHSFA1A, HSF1, HSFA1A, heat shock factor 1
AL3G27910	-4.70	2.38	-3.76	3.52E-06	5.93E-04	AT3G15380	Plasma-membrane choline transporter family protein
AL1G29930	0.00	0.00	6.24	3.57E-06	5.94E-04	AT1G17610	Disease resistance protein (TIR-NBS class)
AL2G16290	-6.71	-6.71	-6.71	3.57E-06	5.94E-04	AT1G60410	F-box family protein
AL2G33100	-5.65	-2.74	-5.67	3.57E-06	5.94E-04	AT1G73330	ATDR4, DR4, drought-repressed 4
AL6G44710	-6.33	-6.33	-6.33	3.59E-06	5.94E-04	/	Unknown
AL5G13060	-0.88	-7.18	-7.18	3.64E-06	5.98E-04	/	Unknown
AL5G40550	8.48	5.55	3.51	3.95E-06	6.47E-04	AT5G42850	Thioredoxin superfamily protein
AL1G52030	-6.10	-6.10	-6.10	4.03E-06	6.56E-04	AT1G43800	Plant stearoyl-acyl-carrier-protein desaturase family protein
AL1G60110	-2.95	0.93	-3.67	4.43E-06	7.15E-04	AT1G52030	F-ATMBP, MBP1.2, MBP2, myrosinase-binding protein 2
AL3G47945	2.59	0.28	0.36	4.43E-06	7.15E-04	AT2G20142	Toll-Interleukin-Resistance (TIR) domain family protein
AL1G27480	2.32	4.34	7.72	4.60E-06	7.34E-04	AT1G15380	Lactoylglutathione lyase / glyoxalase I family protein
AL1G56460	6.09	1.12	4.32	4.61E-06	7.34E-04	AT1G52420	UDP-Glycosyltransferase superfamily protein
AL5G26400	-6.53	1.88	-6.53	4.62E-06	7.34E-04	/	Unknown
AL6G48480	-4.56	-7.70	-6.02	4.80E-06	7.59E-04	AT1G05080	F-box/RNI-like/FBD-like domains-containing protein
AL1G41960	-3.57	-5.84	-1.77	4.85E-06	7.64E-04	/	Unknown
AL1G54270	-1.71	-9.75	-2.43	5.07E-06	7.87E-04	/	Unknown
AL1G62230	2.18	-5.23	-5.23	5.06E-06	7.87E-04	AT1G53610	Unknown
AL4G10860	-4.72	-0.18	-0.05	5.04E-06	7.87E-04	AT2G21660	ATGRP7, CCR2, GR-RBP7, GRP7, cold, circadian rhythm, and rna binding 2
AL3G34730	-4.46	-3.35	-2.50	5.34E-06	8.26E-04	AT3G20810	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AL6G20350	0.03	-2.12	-3.82	5.48E-06	8.44E-04	AT5G09930	ATGCN2, GCN2, ABC transporter family protein
AL3G36480	-7.64	-3.12	-3.19	5.53E-06	8.46E-04	AT3G22240	Unknown
AL2G37740	-5.07	-1.18	-5.89	5.66E-06	8.62E-04	AT1G77530	O-methyltransferase family protein
AL8G10590	-6.09	2.03	-0.17	5.80E-06	8.80E-04	AT5G47440	Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region
AL4G17940	2.50	-6.95	-0.15	6.05E-06	9.14E-04	AT2G44220	Protein of Unknown Function (DUF239)
AL7G10860	2.71	0.98	-1.19	6.11E-06	9.18E-04	AT4G38960	B-box type zinc finger family protein
AL6G36050	-6.60	-0.04	0.16	6.22E-06	9.31E-04	AT5G24470	APRR5, PRR5, pseudo-response regulator 5
AL1G16370	-2.69	3.80	-4.28	6.32E-06	9.42E-04	AT1G06360	Fatty acid desaturase family protein
AL6G42280	4.02	1.45	3.24	6.48E-06	9.61E-04	/	Unknown
AL3G46510	0.60	-6.06	3.21	6.61E-06	9.67E-04	/	Unknown
AL4G39740	2.55	-0.17	0.27	6.58E-06	9.67E-04	AT2G41640	Glycosyltransferase family 61 protein

AL6G41460	2.21	0.15	-0.82	6.61E-06	9.67E-04	AT4G09030	AGP10, ATAGP10, arabinogalactan protein 10
AL5G33280	0.00	6.20	0.00	6.75E-06	9.84E-04	/	Unknown
AL7G46640	1.96	0.18	-1.26	6.83E-06	9.91E-04	AT5G37770	CML24, TCH2, EF hand calcium-binding protein family
AL4G23190	-2.18	0.80	0.83	6.89E-06	9.95E-04	AT2G28660	Chloroplast-targeted copper chaperone protein
AL1G25420	-3.51	-3.87	-4.14	7.17E-06	1.03E-03	AT1G13635	DNA glycosylase superfamily protein
AL6G26830	1.93	-0.24	-1.11	7.30E-06	1.04E-03	AT5G15950	Adenosylmethionine decarboxylase family protein
AL8G23580	-3.69	-4.45	2.46	7.31E-06	1.04E-03	AT1G51600	GATA28, TIFY2A, ZML2, ZIM-LIKE 2
AL1G50890	0.00	6.16	0.00	8.26E-06	1.17E-03	AT5G27470	seryl-tRNA synthetase / serine--tRNA ligase
AL1G64210	3.02	0.83	0.92	8.50E-06	1.20E-03	AT1G55960	Polyketide cyclase/dehydrase and lipid transport superfamily protein
AL2G40370	9.02	7.21	7.58	8.61E-06	1.21E-03	/	Unknown
AL3G46130	-2.19	-6.22	-6.91	8.83E-06	1.23E-03	AT2G14580	ATPRB1, PRB1, basic pathogenesis-related protein 1
AL7G52990	-1.98	-1.06	-5.38	8.86E-06	1.23E-03	AT5G37970	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AL8G39190	-3.61	-0.69	-1.65	8.82E-06	1.23E-03	AT5G62360	Plant invertase/pectin methylesterase inhibitor superfamily protein
AL1G35110	2.63	-0.09	-1.52	8.96E-06	1.24E-03	AT1G21910	Integrase-type DNA-binding superfamily protein
AL1G65520	6.15	0.00	0.00	9.01E-06	1.24E-03	AT1G54970	ATPRP1, PRP1, RHS7, proline-rich protein 1
AL3G27390	-3.70	-4.29	-4.40	9.42E-06	1.29E-03	AT3G15050	IQD10, IQ-domain 10
AL6G15290	-4.71	-4.74	-6.54	9.63E-06	1.32E-03	AT5G05390	LAC12, laccase 12
AL4G16860	6.71	2.28	3.30	1.00E-05	1.37E-03	AT2G32680	AtRLP23, RLP23, receptor like protein 23
AL8G39700	-2.40	-2.53	-3.93	1.02E-05	1.38E-03	AT5G62730	Major facilitator superfamily protein
AL7G10460	7.04	1.57	4.09	1.06E-05	1.43E-03	AT4G38570	PIS2, probable CDP-diacylglycerol--inositol 3-phosphatidyltransferase 2
AL7G24740	2.16	-0.03	4.56	1.06E-05	1.43E-03	AT4G27890	HSP20-like chaperones superfamily protein
AL1G10890	2.60	-0.94	0.81	1.08E-05	1.44E-03	AT1G01520	Homeodomain-like superfamily protein
AL3G39970	1.35	-2.90	-1.00	1.10E-05	1.46E-03	AT3G24500	ATMBF1C, MBF1C, multiprotein bridging factor 1C
AL6G11800	-3.07	1.45	1.11	1.12E-05	1.49E-03	AT5G02540	NAD(P)-binding Rossmann-fold superfamily protein
AL8G23270	2.05	-0.31	-1.68	1.13E-05	1.50E-03	AT5G49520	ATWRKY48, WRKY48, WRKY DNA-binding protein 48
AL1G23920	-0.33	-4.63	-7.11	1.14E-05	1.50E-03	AT1G12570	Glucose-methanol-choline (GMC) oxidoreductase family protein
AL3G42970	-6.43	-6.43	-4.63	1.15E-05	1.51E-03	/	Unknown
AL7G15330	-3.00	1.88	2.14	1.17E-05	1.53E-03	AT4G35770	ATSEN1, DIN1, SEN1, SEN1, Rhodanese/Cell cycle control phosphatase superfamily protein
AL1G17790	-2.30	2.22	-0.61	1.19E-05	1.55E-03	/	Unknown
AL70U10050	-6.26	-6.26	-6.26	1.20E-05	1.56E-03	AT3G15351	Unknown
AL3G53610	-8.40	1.65	0.27	1.28E-05	1.66E-03	/	Unknown
AL6G16780	-3.20	0.32	-0.01	1.31E-05	1.68E-03	AT5G06690	WCRKC1, WCRKC thioredoxin 1
AL4G19940	1.26	-0.89	-4.24	1.33E-05	1.70E-03	AT2G26760	CYCB1;4, Cyclin B1;4
AL6G11730	2.46	-0.52	2.13	1.33E-05	1.70E-03	AT5G02490	Heat shock protein 70 (Hsp 70) family protein
AL4G37570	-3.55	1.04	1.05	1.37E-05	1.75E-03	AT2G39980	HXXXD-type acyl-transferase family protein
AL9U10340	1.31	-0.41	-2.41	1.38E-05	1.75E-03	AT4G13340	Leucine-rich repeat (LRR) family protein
AL1G21360	1.95	-1.27	-2.44	1.40E-05	1.77E-03	AT1G10550	XET, XTH33, xyloglucan:xyloglucosyl transferase 33
AL1G39990	4.19	-0.26	-0.98	1.43E-05	1.80E-03	AT1G25340	AtMYB116, MYB116, myb domain protein 116
AL1G32390	-0.13	2.11	-0.10	1.45E-05	1.81E-03	AT1G19670	ATCLH1, ATHCOR1, CLH1, CORI1, chlorophyllase 1
AL2G31960	-3.85	-1.90	-7.93	1.45E-05	1.81E-03	AT1G72290	Kunitz family trypsin and protease inhibitor protein
AL41U10050	3.01	1.81	6.07	1.45E-05	1.81E-03	AT2G29150	NAD(P)-binding Rossmann-fold superfamily protein
AL103U10010	-2.13	-2.13	3.67	1.46E-05	1.81E-03	/	Unknown
AL1G42710	0.00	5.92	0.00	1.58E-05	1.96E-03	AT1G29020	Calcium-binding EF-hand family protein
AL7G19760	0.66	-6.44	-8.13	1.60E-05	1.97E-03	AT4G32620	Enhancer of polycomb-like transcription factor protein
AL3G46040	-5.03	-0.24	-0.28	1.70E-05	2.06E-03	AT2G14520	CBS domain-containing protein with a domain of unknown function (DUF21)
AL3G47680	-4.75	-0.53	-0.55	1.68E-05	2.06E-03	AT2G15890	MEE14, maternal effect embryo arrest 14
AL4G35600	-6.11	-6.11	-6.11	1.71E-05	2.06E-03	AT2G38380	Peroxidase superfamily protein
AL6G42680	-1.62	0.10	-2.40	1.69E-05	2.06E-03	AT4G08870	Arginase/deacetylase superfamily protein
AL7G22020	-2.72	-6.87	-5.48	1.70E-05	2.06E-03	AT4G30170	Peroxidase family protein
AL5G34790	-4.04	-0.39	-1.92	1.71E-05	2.06E-03	AT3G53800	Fes1B, Fes1B
AL6G41580	1.44	-1.41	-3.12	1.80E-05	2.15E-03	AT4G08950	EXO, Phosphate-responsive 1 family protein
AL6G53050	-0.04	1.21	-1.97	1.80E-05	2.15E-03	AT4G00400	AtGPAT8, GPAT8, glycerol-3-phosphate acyltransferase 8
AL608U10010	7.11	6.71	8.63	1.88E-05	2.24E-03	/	Unknown
AL6G24370	1.55	-0.01	-0.10	1.94E-05	2.30E-03	AT5G13750	ZIFL1, zinc induced facilitator-like 1
AL1G29920	0.00	1.57	6.19	1.94E-05	2.30E-03	AT1G17600	Disease resistance protein (TIR-NBS-LRR class) family
AL2G15170	7.24	5.24	0.00	1.96E-05	2.31E-03	AT1G61310	LRR and NB-ARC domains-containing disease resistance protein
AL7G45000	-6.13	-6.13	-6.13	1.97E-05	2.31E-03	/	Unknown
AL2G22370	3.07	0.23	0.50	2.02E-05	2.36E-03	AT1G65486	Unknown
AL7G17410	-7.36	-0.93	0.01	2.03E-05	2.36E-03	AT4G33980	Unknown
AL8G19010	-7.00	-5.32	1.32	2.03E-05	2.36E-03	/	Unknown
AL3G38970	-7.57	-4.31	-5.77	2.04E-05	2.36E-03	/	Unknown
AL2G32680	1.17	-1.11	-0.86	2.14E-05	2.46E-03	AT1G72940	Toll-Interleukin-Resistance (TIR) domain-containing protein
AL8G10790	-1.92	0.95	0.29	2.14E-05	2.46E-03	AT5G47240	atnudt8, NUDT8, nudix hydrolase homolog 8
AL1014U10010	-1.12	-2.75	4.03	2.24E-05	2.56E-03	/	Unknown
AL3G43990	-4.49	1.38	1.41	2.24E-05	2.56E-03	AT3G25270	Ribonuclease H-like superfamily protein
AL2G25430	-0.19	1.79	2.14	2.27E-05	2.57E-03	AT1G53480	ATMRD1, MRD1, mto 1 responding down 1
AL4G45550	2.22	-0.59	1.16	2.26E-05	2.57E-03	AT2G46270	GBF3, G-box binding factor 3
AL1G48610	6.24	0.00	6.21	2.34E-05	2.64E-03	/	Unknown
AL3G44960	-6.83	0.00	-6.83	2.35E-05	2.65E-03	/	Unknown
AL4G25940	-5.99	-5.36	0.96	2.40E-05	2.67E-03	AT5G60600	CLB4, CSB3, GCPE, HDS, ISPG, 4-hydroxy-3-methylbut-2-enyl diphosphate synthase
AL6G52770	3.30	0.17	1.78	2.39E-05	2.67E-03	AT4G00700	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein
AL7G44960	-5.28	-5.32	-6.88	2.39E-05	2.67E-03	AT4G38640	Plasma-membrane choline transporter family protein
AL7G48550	3.22	1.90	4.16	2.43E-05	2.71E-03	AT1G22410	Class-II DAHP synthetase family protein
AL5G24540	-4.75	-0.77	1.04	2.44E-05	2.71E-03	AT3G45860	CRK4, cysteine-rich RLK (RECEPTOR-like protein kinase) 4
AL1G18840	-3.00	-1.36	-7.02	2.50E-05	2.76E-03	AT1G08430	ALMT1, ATALMT1, aluminum-activated malate transporter 1
AL8G27540	-0.80	-5.90	-7.56	2.51E-05	2.76E-03	AT5G53000	TAP46, 2A phosphatase associated protein of 46 kD
AL7G13580	1.38	-0.93	-1.45	2.58E-05	2.82E-03	AT4G37260	ATMYB73, MYB73, myb domain protein 73
AL8G29420	-3.19	0.97	-0.12	2.58E-05	2.82E-03	AT5G54190	PORA, protochlorophyllide oxidoreductase A
AL4G33370	1.51	-0.27	-1.61	2.66E-05	2.90E-03	AT2G37040	ATPAL1, PAL1, PHE ammonia lyase 1

AL1G55850	3.35	-0.18	-0.35	2.70E-05	2.93E-03	AT1G48980	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AL2G25090	0.55	4.56	0.79	2.71E-05	2.93E-03	AT1G66860	Class I glutamine amidotransferase-like superfamily protein
AL2G24790	-0.55	0.17	-11.93	2.78E-05	2.99E-03	/	Unknown
AL3G42860	6.92	4.90	2.59	2.77E-05	2.99E-03	AT2G05380	GRP3S, glycine-rich protein 3 short isoform
AL3G34910	1.20	4.53	5.91	2.81E-05	3.01E-03	AT1G14850	NUP155, nucleoporin 155
AL5G23420	-6.21	-1.03	-0.95	2.83E-05	3.02E-03	/	Unknown
AL3G33150	1.89	-0.09	-1.10	2.85E-05	3.04E-03	AT3G19680	Protein of unknown function (DUF1005)
AL7G52410	5.59	2.86	3.66	2.86E-05	3.04E-03	AT5G38340	Disease resistance protein (TIR-NBS-LRR class) family
AL6G19010	-6.46	-0.64	-8.07	2.93E-05	3.10E-03	/	Unknown
AL4G18010	-2.31	0.21	-0.22	2.94E-05	3.10E-03	AT2G25930	ELF3, PYK20, hydroxyproline-rich glycoprotein family protein
AL7G15500	2.59	1.51	-1.53	2.95E-05	3.11E-03	AT4G35640	ATSERAT3;2, SERAT3;2, serine acetyltransferase 3;2
AL5G45510	1.31	-1.46	-2.05	3.21E-05	3.36E-03	AT3G62740	BGLU7, beta glucosidase 7
AL7G27520	3.69	5.13	6.91	3.24E-05	3.39E-03	AT4G25580	CAP160 protein
AL1G38640	-0.09	1.71	1.65	3.29E-05	3.41E-03	/	Unknown
AL4G46900	4.74	4.72	-2.09	3.28E-05	3.41E-03	AT2G47340	Plant invertase/pectin methylesterase inhibitor superfamily protein
AL6G42540	0.00	0.00	5.54	3.30E-05	3.41E-03	/	Unknown
AL2G19700	1.96	-0.17	-1.45	3.31E-05	3.42E-03	AT1G65060	4CL3, 4-coumarate:CoA ligase 3
AL6G41500	4.90	0.00	7.02	3.34E-05	3.44E-03	AT4G09012	Mitochondrial ribosomal protein L27
AL1G57190	1.84	-8.11	0.33	3.36E-05	3.44E-03	/	Unknown
AL8G38050	-4.27	-1.21	-1.07	3.37E-05	3.44E-03	AT5G61380	APRR1, AtTOC1, PRR1, TOC1, CCT motif -containing response regulator protein
AL5G20940	3.16	2.34	6.70	3.41E-05	3.47E-03	/	Unknown
AL1G35990	2.54	-1.07	-2.33	3.44E-05	3.49E-03	AT1G22470	Unknown
AL4G18580	-1.46	3.47	5.73	3.53E-05	3.58E-03	AT5G42660	Protein of unknown function (DUF616)
AL5G26710	3.00	0.39	-0.02	3.55E-05	3.59E-03	AT3G47480	Calcium-binding EF-hand family protein
AL1G39350	2.89	6.36	6.89	3.62E-05	3.63E-03	AT3G55960	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
AL2G32660	1.29	-1.00	-1.23	3.61E-05	3.63E-03	AT1G72910	Toll-Interleukin-Resistance (TIR) domain-containing protein
AL5G15230	3.52	-3.47	4.27	3.80E-05	3.81E-03	AT1G12990	beta-1,4-N-acetylglucosaminyltransferase family protein
AL6G18330	2.04	-1.59	-0.27	3.81E-05	3.81E-03	AT5G07990	CYP75B1, D501, TT7, Cytochrome P450 superfamily protein
AL4G44300	-2.10	-0.39	-2.59	3.84E-05	3.82E-03	AT2G45180	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AL8G16990	5.67	0.00	0.00	3.85E-05	3.82E-03	AT5G43370	APT1, PHT1;2, PHT2, phosphate transporter 2
AL2G34560	-3.49	-0.55	-1.08	3.97E-05	3.91E-03	AT1G74670	Gibberellin-regulated family protein
AL4G33820	-1.32	3.16	5.86	3.99E-05	3.91E-03	/	Unknown
AL8G19120	2.45	0.14	-0.33	3.99E-05	3.91E-03	AT5G42380	CML37, CML39, calmodulin like 37
AL8G26400	3.16	0.50	0.40	3.96E-05	3.91E-03	AT5G52050	MATE efflux family protein
AL4G20740	2.91	-1.62	-1.13	4.21E-05	4.11E-03	AT2G27080	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
AL5G18750	-6.46	-1.18	-8.79	4.29E-05	4.18E-03	/	Unknown
AL1G60050	0.91	-6.46	-6.46	4.43E-05	4.29E-03	AT1G51990	O-methyltransferase family protein
AL4G24920	-7.16	-2.00	0.63	4.44E-05	4.29E-03	/	Unknown
AL9U11030	1.78	-4.36	0.00	4.43E-05	4.29E-03	/	Unknown
AL1G15950	1.79	1.04	-0.98	4.49E-05	4.32E-03	AT1G06000	UDP-Glycosyltransferase superfamily protein
AL3G44930	1.15	-1.10	-1.96	4.59E-05	4.41E-03	AT2G12462	Unknown
AL4G43200	0.97	-5.40	-2.15	4.68E-05	4.48E-03	AT2G44240	Protein of Unknown Function (DUF239)
AL2G18740	-5.42	-5.42	0.66	4.74E-05	4.53E-03	AT2G05642	Nucleic acid-binding, OB-fold-like protein
AL5G20040	0.00	6.07	5.74	4.80E-05	4.55E-03	AT3G26800	Unknown
AL6G11500	5.66	6.65	0.31	4.80E-05	4.55E-03	AT2G40360	Transducin/WD40 repeat-like superfamily protein
AL6G44070	-5.52	0.23	0.51	4.82E-05	4.56E-03	AT4G10240	B-box zinc finger family protein
AL6G36900	4.89	1.71	2.51	4.85E-05	4.58E-03	AT5G25260	SPFH/Band 7/PHB domain-containing membrane-associated protein family
AL1G26470	1.28	-4.60	-4.60	4.89E-05	4.60E-03	/	Unknown
AL2G30610	1.00	-1.10	-0.80	4.90E-05	4.60E-03	AT1G71040	LPR2, Cupredoxin superfamily protein
AL6G46650	1.63	3.91	-4.07	5.01E-05	4.69E-03	AT4G11911	Unknown
AL6G23770	1.14	-1.21	-2.91	5.16E-05	4.82E-03	AT5G13170	SAG29, senescence-associated gene 29
AL7G38270	1.70	-0.51	-0.55	5.26E-05	4.90E-03	AT4G16563	Eukaryotic aspartyl protease family protein
AL8G10470	-0.83	-2.98	-4.66	5.30E-05	4.92E-03	AT5G47500	Pectin lyase-like superfamily protein
AL3G45650	5.20	0.00	0.00	5.37E-05	4.97E-03	AT2G13810	ALD1, AGD2-like defense response protein 1
AL6G34460	-3.01	0.36	0.03	5.43E-05	5.01E-03	AT5G23240	DNAJ heat shock N-terminal domain-containing protein
AL4G25490	-1.55	0.49	-0.75	5.45E-05	5.02E-03	AT2G30600	BTB/POZ domain-containing protein
AL1G64800	-0.46	4.94	0.48	5.47E-05	5.02E-03	/	Unknown
AL2G12080	0.77	-0.92	-2.82	5.57E-05	5.10E-03	AT1G63240	Unknown
AL6G36840	-4.54	-0.97	-0.92	5.67E-05	5.18E-03	AT5G25180	CYP71B14, cytochrome P450, family 71, subfamily B, polypeptide 14
AL4G39780	-3.31	1.85	3.36	5.70E-05	5.19E-03	AT2G41640	Glycosyltransferase family 61 protein
AL5G22740	6.71	3.29	2.97	5.72E-05	5.19E-03	AT5G11250	Disease resistance protein (TIR-NBS-LRR class)
AL1G17520	0.00	2.56	-0.95	5.82E-05	5.25E-03	AT1G07370	ATPCNA1, PCNA1, proliferating cellular nuclear antigen 1
AL7G39880	-2.50	0.21	-8.58	5.80E-05	5.25E-03	/	Unknown
AL1G57240	1.74	-0.06	-0.78	5.86E-05	5.27E-03	AT1G49780	PUB26, plant U-box 26
AL7G39770	-4.69	-2.45	-6.06	5.87E-05	5.27E-03	AT4G15700	Thioredoxin superfamily protein
AL2G11240	2.82	-0.89	1.75	5.99E-05	5.36E-03	AT1G63870	Disease resistance protein (TIR-NBS-LRR class) family
AL7G48670	1.02	-2.25	-4.85	6.08E-05	5.43E-03	/	Unknown
AL4G33860	-6.79	-6.79	-2.11	6.20E-05	5.52E-03	AT2G37435	Cystatin/monellin superfamily protein
AL8G36840	-1.34	0.68	1.09	6.28E-05	5.58E-03	AT5G60230	ATSEN2, SEN2, splicing endonuclease 2
AL983U10010	-0.02	2.78	-7.87	6.38E-05	5.65E-03	/	Unknown
AL6G48330	1.68	-3.49	-2.08	6.41E-05	5.66E-03	AT4G04840	ATMSRB6, MSRB6, methionine sulfoxide reductase B6
AL1G53760	1.56	-0.03	0.15	6.48E-05	5.71E-03	AT1G47530	MATE efflux family protein
AL4G23740	0.62	-0.68	-8.13	6.53E-05	5.74E-03	AT2G29180	Unknown
AL7G25330	-2.30	0.63	-0.94	6.55E-05	5.74E-03	AT4G27440	PORB, protochlorophyllide oxidoreductase B
AL2G30270	-1.64	0.59	-0.07	6.58E-05	5.75E-03	AT1G70820	phosphoglucomutase, putative / glucose phosphomutase, putative
AL5G14900	5.21	1.20	3.45	6.59E-05	5.75E-03	AT3G26150	CYP71B16, cytochrome P450, family 71, subfamily B, polypeptide 16
AL6G49710	4.31	6.15	2.46	6.61E-05	5.75E-03	AT4G03220	Protein with RNI-like/FBD-like domains
AL6G38220	1.55	1.70	-1.23	7.03E-05	6.09E-03	AT5G26220	ChaC-like family protein
AL3G18220	-2.48	-1.47	-2.24	7.09E-05	6.12E-03	AT3G07010	Pectin lyase-like superfamily protein

AL5G17130	-0.16	1.47	-3.06	7.09E-05	6.12E-03	AT3G27690	LHCB2, LHCB2.3, LHCB2.4, photosystem II light harvesting complex gene 2.3
AL3G48410	1.54	-2.16	-2.59	7.13E-05	6.14E-03	AT2G19800	MIOX2, myo-inositol oxygenase 2
AL3G12320	-1.39	-4.87	-6.57	7.19E-05	6.17E-03	AT3G02885	GASA5, GAST1 protein homolog 5
AL5G37260	1.05	-0.67	-1.39	7.20E-05	6.17E-03	AT3G55980	ATSZF1, SZF1, salt-inducible zinc finger 1
AL3G41500	1.73	3.05	-2.55	7.26E-05	6.20E-03	AT1G24070	ATCSLA10, CSLA10, CSLA10, cellulose synthase-like A10
AL8G12110	4.95	0.00	0.00	7.31E-05	6.23E-03	AT5G46320	MADS-box family protein
AL1G61070	-5.60	-0.61	-5.51	7.33E-05	6.23E-03	AT1G52750	alpha/beta-Hydrolases superfamily protein
AL1G28200	-2.06	-2.12	-2.01	7.40E-05	6.25E-03	AT1G16030	Hsp70b, heat shock protein 70B
AL6G27550	0.46	0.37	-2.37	7.39E-05	6.25E-03	AT4G22100	BGLU3, beta glucosidase 2
AL2G37650	1.83	-0.02	0.36	7.51E-05	6.33E-03	AT1G77450	anac032, NAC032, NAC domain containing protein 32
AL4G19950	-5.75	-0.13	1.81	7.56E-05	6.36E-03	/	Unknown
AL5G14910	2.73	1.49	1.94	7.77E-05	6.52E-03	AT3G26160	CYP71B17, cytochrome P450, family 71, subfamily B, polypeptide 17
AL1G33320	0.16	4.97	-1.41	8.00E-05	6.69E-03	AT1G20940	F-box family protein
AL3G26060	-0.89	-7.09	-5.41	8.02E-05	6.70E-03	AT3G13890	ATMYB26, MS35, MYB26, myb domain protein 26
AL4G11210	-5.69	1.17	0.09	8.72E-05	7.26E-03	AT2G21910	CYP96A5, cytochrome P450, family 96, subfamily A, polypeptide 5
AL2G10900	-5.18	-4.66	-4.48	8.92E-05	7.41E-03	AT1G64130	Polyketide cyclase/dehydrase and lipid transport superfamily protein
AL5G34210	-5.73	-5.73	-5.73	9.01E-05	7.46E-03	AT5G35715	CYP71B8, cytochrome P450, family 71, subfamily B, polypeptide 8
AL8G30800	2.53	0.15	0.30	9.12E-05	7.54E-03	AT5G55250	IAMT1, IAA carboxylmethyltransferase 1
AL1G38230	3.42	0.00	6.18	9.30E-05	7.66E-03	/	Unknown
AL3G52040	1.55	-1.24	-0.89	9.46E-05	7.78E-03	AT2G18660	PNP-A, plant natriuretic peptide A
AL3G38240	-1.64	-6.88	-1.36	9.60E-05	7.88E-03	AT3G23570	alpha/beta-Hydrolases superfamily protein
AL6G35480	1.62	-0.71	-0.35	9.71E-05	7.95E-03	AT5G24120	ATSIG5, SIG5, SIGE, sigma factor E
AL8G10380	0.63	-2.93	-3.02	9.75E-05	7.96E-03	AT5G47590	Heat shock protein HSP20/alpha crystallin family
AL1G41920	-3.72	-0.66	-0.56	9.93E-05	8.08E-03	AT1G28330	DRM1, DYL1, dormancy-associated protein-like 1
AL201U10030	-4.63	1.03	0.86	1.00E-04	8.14E-03	AT2G30110	ATUBA1, MOS5, UBA1, ubiquitin-activating enzyme 1
AL3G19010	-3.72	-0.63	-0.90	1.01E-04	8.20E-03	AT3G07650	COL9, CONSTANS-like 9
AL3G46250	-4.92	-4.92	-4.92	1.02E-04	8.23E-03	/	Unknown
AL5G12400	0.27	-4.50	-5.68	1.02E-04	8.26E-03	AT2G02850	ARPN, plantacyanin
AL3G39840	-1.40	1.34	1.56	1.03E-04	8.28E-03	AT3G24550	ATPERK1, PERK1, proline extensin-like receptor kinase 1
AL7G48880	3.17	5.39	3.07	1.04E-04	8.33E-03	/	Unknown
AL293U10020	3.33	-3.34	2.37	1.08E-04	8.58E-03	/	Unknown
AL429U10010	1.60	5.82	0.00	1.08E-04	8.58E-03	/	Unknown
AL516U10020	0.00	5.30	0.00	1.07E-04	8.58E-03	AT5G48810	ATB5-B, ATCB5-D, B5 #3, CB5-D, cytochrome B5 isoform D
AL5G25980	0.64	1.56	-7.88	1.08E-04	8.58E-03	AT2G39330	JAL23, jacalin-related lectin 23
AL6G31220	-4.08	-1.90	-6.66	1.08E-04	8.58E-03	AT3G16360	AHP4, HPT phosphotransmitter 4
AL3G47620	-5.55	-5.55	-5.55	1.09E-04	8.66E-03	AT2G40910	F-box and associated interaction domains-containing protein
AL4G43410	-5.50	-0.85	-6.15	1.11E-04	8.75E-03	AT3G04610	FLK, RNA-binding KH domain-containing protein
AL3G12640	-3.10	0.17	3.38	1.12E-04	8.78E-03	AT5G17570	TatD related DNase
AL3G49880	1.51	-0.52	-0.16	1.12E-04	8.81E-03	AT2G17040	anac036, NAC036, NAC domain containing protein 36
AL7G30460	-3.47	-0.14	-0.40	1.12E-04	8.81E-03	AT4G23040	Ubiquitin-like superfamily protein
AL3G28310	0.33	-1.62	-3.15	1.14E-04	8.93E-03	AT3G15650	alpha/beta-Hydrolases superfamily protein
AL1G14520	0.39	1.34	-2.79	1.15E-04	8.95E-03	AT1G04800	glycine-rich protein
AL5G23980	-6.37	1.40	0.55	1.17E-04	9.10E-03	AT3G45420	Concanavalin A-like lectin protein kinase family protein
AL3G47660	-4.25	-4.94	-6.62	1.19E-04	9.21E-03	AT5G43070	WPP1, WPP domain protein 1
AL7G18920	0.07	-0.63	2.88	1.22E-04	9.45E-03	AT4G32810	ATCCD8, CCD8, MAX4, carotenoid cleavage dioxygenase 8
AL1G62070	-1.22	1.03	-0.86	1.23E-04	9.47E-03	AT1G53520	Chalcone-flavanone isomerase family protein
AL1G13910	-1.57	1.64	1.24	1.26E-04	9.65E-03	AT1G04310	ERS2, ethylene response sensor 2
AL6G39800	-2.32	-2.93	-4.95	1.25E-04	9.65E-03	AT3G49120	ATPCB, ATPERX34, PERX34, PRX34, PRXCB, peroxidase CB
AL7G12650	2.56	0.29	1.27	1.26E-04	9.65E-03	AT4G37990	ATCAD8, CAD-B2, ELI3, ELI3-2, elicitor-activated gene 3-2
AL7G39740	-5.15	-0.47	-4.18	1.26E-04	9.65E-03	AT4G15690	Thioredoxin superfamily protein
AL8G19070	-2.71	0.10	-0.47	1.30E-04	9.95E-03	AT5G42420	Nucleotide-sugar transporter family protein

Conclusions

The goal of my PhD was to conduct a comprehensive study on the adaptive potential of plants to cope with thermal stress. Based on climate chamber experiments on different populations of *Arabidopsis lyrata*, we found phenotypic differentiation along a latitudinal cline and potential constraints acting on thermal adaptation, in particular a genetically based trade-off between frost tolerance and plant size under no stress. This trade off may be involved in constraining niche evolution at the northern distribution limit. This is indicated by another result, that plants from the north grew to large size but were less frost tolerant than plants from the south, which were actually more frost tolerant. No such trade-offs or costs were detected in traits related to coping with heat stress. At very fine spatial scale, we showed that spatial heterogeneity led to within-population differentiation but only in regards to frost tolerance. Therefore, we demonstrated that thermal adaptation may occur from global to local scale, and, overall, heat stress adaptation seemed to be less constrained than cold stress adaptation. However the gene expression analysis after heat acclimation revealed numerous genes involved in biotic stress resistance suggesting that the two were probably not independent. And one of the major open question that arose from my PhD is to what extent thermal adaptation may impede or favor resistance to biotic stress. Further work is needed to disentangle the nature of the relationship between thermal adaptation and resistance to pathogens. This outcome leads us to further consider thermal adaptation at a more integrated level and to focus on interactions between environmental factors.

Finally, my thesis addressed not only fundamental aspects of thermal adaptation but has also practical application in the fields of conservation biology, environmental science and crop science. In the current context of climatic change and the predicted increase of unexpected and extreme events, understanding whether organisms can respond to environmental stress in a plastic way by acclimation or by means of adaptive evolution is crucial for predicting population and species persistence. Global climate change represents also an increasing threat to agricultural productivity with a need to assess the impacts of temperature on plant performance. My thesis provides several important inputs to those fields. First, the threat that represents the increase in frequency of extreme events may be particularly challenging and unable plants to achieve developmental processes, i.e. flowering. Secondly, the apparent trade-off between frost and heat acclimation and basal resistance may limit the hardening capacity of plants to face sudden rises of temperature or strong temperature variations.