Genetic regulation of transcriptional variation in natural *Arabidopsis thaliana* accessions

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Abstract

An increased knowledge of the genetic regulation of expression in *Arabidopsis thaliana* is likely to provide important insights about the basis of the plant's extensive phenotypic variation. Here, we reanalysed two publicly available datasets with genome-wide data on genetic and transcript variation in large collections of natural *A. thaliana* accessions. Transcripts from more than half of all genes were detected in the leaf of all accessions, and from nearly all annotated genes in at least one accession. Thousands of genes had high transcript levels in some accessions but no transcripts at all in others and this pattern was correlated with the genome-wide genotype. In total, 2,669 eQTL were mapped in the largest population, and 717 of them were replicated in the other population. 646 cis-eQTLs regulated genes that lacked detectable transcripts in some accessions, and for 159 of these we identified one, or several, common structural variants in the populations that were shown to be likely contributors to the lack of detectable RNA-transcripts for these genes. This study thus provides new insights on the overall genetic regulation of global gene-expression diversity in the leaf of natural *A. thaliana* accessions. Further, it also shows that strong cis-acting polymorphisms, many of which are likely to be structural variations, make important contributions to the transcriptional variation in the worldwide *A. thaliana* population.

Key words: eQTL mapping, RNA sequencing, Gene Expression, *Arabidopsis thaliana*, structural variation.

Introduction

Several earlier studies have utilized genome-wide data to explore the link between genetic and phenotypic diversity in natural *Arabidopsis thaliana* populations [1-10]. Some of this phenotypic variation was found to be caused by regulatory genetic variants that lead to differences in gene expression (Expression Level Polymorphisms or ELPs for short), underlying, for example, semi-dwarfism [11], changes in flowering-time [5, 12], changes in seed flotation [13], and changes in self-incompatibility [14]. By extending efforts to scan for ELPs to the whole genome and transcriptome level in large collections of natural *A. thaliana* accessions, useful insights might be gained about the link between genetic and expression level variation in the worldwide population. This may ultimately reveal interesting candidate genes and mechanisms that have contributed to adaptation to the natural environment.

Earlier studies have shown that there is a considerable transcriptional variation amongst natural *A. thaliana* accessions. A comparison of expression in shoot-tissue from two accessions, Sha and Bay-0, found that (i) 15,352 genes (64% of all tested) were expressed in the shoot in the field, (ii) 3,344 genes (14% of all tested) were differentially expressed between the accessions and (iii) 53 genes were uniquely expressed in Sha/Bay-0, respectively [15]. Later, Gan *et al.* [16] studied the seedling transcriptome from 18 natural accessions and found that 75% (20,550) of the protein-coding genes, 21% of the non-coding RNAs and 21% of the pseudogenes were expressed in the seeding tissue of at least one of the accessions. Further, they also found that 46% (9,360) of the expressed protein-coding genes were differently expressed between at least one pair of accessions [16]. Kliebenstein *et al.* [17] found that, on average, 2,234 genes were differently expressed among 7 natural accessions when treated with salicylic acid and, in the same accessions, Leeuwen *et al.* [18] found that gene-network level expression responses were genotype dependent. There are also numerous other studies that have illustrated the importance of naturally occurring ELPs (e.g. [19-21]) for the transcriptional variation among natural *A.* thaliana accessions. It is therefore expected that there will be an extensive, and genetically controlled, transcriptional variation in the worldwide *A. thaliana* population, although its extent remains to be shown.

Expression quantitative trait loci (eQTL) mapping is a useful approach to link genetic and expression variation. It has been successfully applied in many organisms, including yeast [22], plants [23], as well as animals and humans [24]. Most eQTLs are detected in the close vicinity of the gene itself (cis-eQTL) and these often explain a large proportion of the observed expression variation [25-27]. Fewer eQTL (from 20-50% reported in various organisms [25, 28, 29]) are located in the remainder of the genome (trans-eQTL). Using eQTL mapping, the genetic regulation of expression variation has been dissected in *A. thaliana* using recombinant inbred lines (RIL) [20, 23, 29] and other experimental crosses [30]. These initial studies have revealed that the majority of the ELPs in *A. thaliana* are heritable, that most of the detected eQTLs are located in cis and that structural variations are a common mechanism contributing to this variation [20]. The data generated within the *A. thaliana* 1001 genomes projects now provides an opportunity to explore this expression variation also in larger collections of natural *A. thaliana* accessions that better cover the worldwide distribution of the plant [2, 32, 33].

Here, we explored the genome-wide expression variation, and the genetic regulation of gene expression, using a dataset generated from 144 natural *Arabidopsis thaliana* accessions (*SCHMITZ-data*; [32]) and replicated some of our findings in a second dataset with 107 natural *A. thaliana* accessions (*DUBIN-data*; [33]). Transcripts from a core-set of genes were present in the leaf in all accessions, but thousands of genes showed a different pattern with high transcript levels in some accessions, but no transcripts at all in others. RNA sequencing bias was a concern for lowly expressed genes, but focusing on the highly expressed genes we found a large overall contribution by genetics to this variation. Hundreds of cis-eQTL contributing to the lack of transcripts in some accessions were mapped in the larger dataset [32] and many of these replicated in the independent smaller dataset [33]. For about one quarter of the cis-eQTL genes one, or in many cases several, common structural variants were significantly associated with the lack of reads in the transcriptome analyses. This indicates that the lack of transcripts observed for many accessions in the worldwide *A.* thaliana population is often due to common deletions of transcription start sites or the whole genes. Our results thus provides an overall perspective on the transcript-level variation in natural *A. thaliana* accessions and

dissect the genetics underlying the presence or absence of transcripts for individual genes in individual accessions. Overall, our results confirm that lack-of-function alleles [5, 31, 34-38], often due to structural variations [16, 20], are important contributors to the overall transcriptional variation also in the worldwide *A. thaliana* population.

Results

RNA sequencing detects transcripts from nearly all TAIR10 annotated genes in the leaf of natural A. thaliana *accessions*

We downloaded publicly available RNA-seq [32] and whole-genome SNP genotype data [2] for a population of 144 natural *A. thaliana* accessions (*SCHMITZ-data*). In this data, we first explored the variability in RNA-seq scored expression-values across 33,554 genes and 140 accessions that passed quality control (see Materials and Methods). A gene was considered as expressed if it had a normalized FPKM (Fragment Per Kilobase of exon per Million fragments mapped) value greater than zero. The available RNA-seq data was generated from a single tissue (leaf) and we therefore expected that a considerable proportion of the genes would be transcriptionally inactive due to tissue specific expression. The data, however, showed that among the 33,554 genes in the *SCHMITZ* data, only 289 lacked transcripts across all the accessions in the population (i.e. had a normalized FPKM = 0 in all accessions).

A core-set of genes has detectable transcripts in the leaf of all the evaluated natural A. thaliana *accessions*

In the *SCHMIZ-data*, transcripts were detected (Normalized FPKM > 0) in all accessions for a large set of genes (18,289; Figure 1). In the *DUBIN-data*, 12,927 genes had detectable transcripts in all accessions and all of these transcripts, except 79, had detectable transcripts in all of the accession in the *SCHMITZ-data* [32] (Figure 1). Of the 10,549 genes for which transcripts were detected (RPKM > 0) only in some accessions in the *DUBIN*-data, transcripts were detected for 4,129 in all and 6,393 in some (RPKM > 0) accessions in the *SCHMITZ-data* (Figure 1). Hence, for only 27 genes with transcripts detected in at least one of the accessions in the *DUBIN*-data, no transcripts were detected in any of the accessions in the *SCHMITZ-data* (Figure 1).

The lower sequencing coverage, and more stringent filtering of the sequence reads in the *DUBIN-data* [33], likely explains why transcripts were detected for more genes in more accessions in the *SCHMITZ-data*. Few (27) genes were uniquely expressed in the *DUBIN-data*, but it is noteworthy that 13 of these are t-RNA genes and that 9 of these code for proline (Table S1).

The number of genes with detected transcripts in the leaf of individual* A. thaliana *accessions is highly variable

Within the individual accessions of the *SCHMITZ-data* [32] we found transcripts (Normalized FPKM > 0) for a considerably lower number of genes than the total number of genes with detected transcripts across the entire population. The number of genes with RNA-seq detected transcripts in the individual accessions (Normalized FPKM > 0) varied from 22,574 to 26,967 with an average of 24,565 (Figure 2A). The proportion of genes with detected transcripts was thus higher in this dataset than that what has earlier been reported for shoots in two natural accessions [39], but similar to that in the study of 18 natural accessions [16] (73% in the *SCHMITZ-data*, 64% in [39] and about 70% in [16]). A similar pattern of variability in the number of genes with detected transcripts was also found in the DUBIN-data (Figure 2C).

RNA-seq bias likely explains part of the variability in detected transcripts of the individual* A. thaliana *accessions for lowly expressed genes

RNA-seq detects transcripts from nearly all genes in the genome in at least one of the accessions in the *SCHMITZ-data*. In addition to a core set of genes with transcripts in all accessions, there is a large set of genes (on average 6,256 per accession) for which transcripts are detected only in some of the accessions. A possible explanation for this might be that RNA-seq is unable to reliably detect low levels of transcripts in the samples. Such RNA-seq introduced bias would result in a random detection of transcripts for individual accessions (i.e. produce a score = 0) for lowly expressed genes, and lead to a similar variability in the presence or absence of transcripts among the accessions as when there is a true accession-specific expression. To evaluate the potential contribution of RNA-seq bias to the results, we first evaluated the relationship between the rank of the transcript-levels across the genes and the number of accessions in which transcripts were detected (Figure 2B). There was a clear

overall trend in the data that transcripts were detected in fewer accessions for genes with lower overall transcript-levels. A similar trend was observed also in the *DUBIN-data* (Figure 2D). Based on this, we conclude that RNA-seq bias contributes to the observed variation in presence or absence of transcripts among the accessions. However, transcripts were missing in a large fraction of the studied accessions also for many of the genes with high rank/overall transcript level. As RNA-seq bias is an unlikely explanation in these cases, it suggests that at least part of the variability in the presence or absence of transcripts might be due to accession-specific expression, or structural variations leading to different sets of genes in divergent accessions [16]. Thus, our overall results agree across the two datasets in that i) the number of genes expressed in the leaf of an individual plant is large, and ii) that the actual set of genes that are present or expressed varies between the individual accessions.

Genetics contributes to the variability in detected transcripts of the individual* A. thaliana *accessions

The observed variability in the RNA-seq scored presence or absence of transcripts for individual genes between accessions could also be caused by experiment specific environmental factors affecting e.g. plant growth or sample treatments. As transcript variability due to such effects on plants and samples are expected to be experiment-specific, they should not replicate across experiments. We therefore used the data from a second publicly available RNA-seq dataset from 107 natural Swedish accessions, with fully sequenced genomes and transcriptomes (*DUBIN-data*; [33]), to explore whether a similar pattern of accession-specific transcripts was present also in this data among the genes with high transcript levels. In the *DUBIN*-data, the number of genes with detected transcripts were lower both when measured within any accession (23,478 with RPKM - Reads Per Kilobase per Million mapped reads - > 0), or within the individual accessions (16,136 to 20,109 with an average of 18,663; Figure 2C). The core set of genes expressed in all accessions contained 12,927 genes. The lower number of genes with transcripts is likely a result of the lower sequencing depth (~1/4 of the *SCHMITZ-data*) and the more stringent filtering of the reads. However, the overall trend in the results is the same as in the *SCHMITZ-data*: genes with lower transcript-levels had transcripts detected in fewer accessions, but transcripts for many genes with high overall transcript levels were also found only in

a few accessions (Figure 2D). This overlap between the results from the two datasets suggests that the variation in which transcripts are highly expressed in the leaf of several, but not all, accessions is unlikely to be due to either technical bias or experimental specific errors as described above.

To explore whether there was a genetic basis for the presence or absence of transcripts for individual genes, we studied a set of 4,317 genes in the *SCHMITZ-data* in more detail. These genes were selected to i) have detected transcripts in more than 14 (10%), but fewer than 126 (90%), of the accessions and ii) have transcript levels that were higher than the 2nd lowest expressed gene with transcripts in all accessions (Materials and Methods; Figure 2B). This subset was chosen to remove most of the genes influenced by the RNA-seq bias for lowly expressed genes (as discussed above). To estimate the genetic basis for the transcriptome variation, we first created a covariance matrix for the proportion of transcript sharing among all pairs of accessions based on the average number of shared genes with detected transcripts (FPKM > 0). Then, we created a covariance matrix for the relationship between the accessions based on the genome-wide genotype as a genetic kinship matrix weighted by allele frequencies based on all SNPs with MAF > 0.05. As illustrated in Figure 3, there was a highly significant correlation between the genetic and transcriptome covariances for this set of genes ($r = 0.035$, $p = 1.0 \times 10^{-16}$; Figure 3). Although the correlation is low, it indicates that plants that are genetically identical (i.e. the same accession), on average share $4{,}317 \times 0.035 = 151$ transcripts more than they would with a genetically unrelated accession. This shows that there is a significant genetic contribution to the sharing of transcripts between accessions, suggesting that the accession-specificity of the transcripts has a genetic basis.

cis-eQTL contribute to the accession-specific patterns in the transcriptome

Loss-of-function alleles are known to be important contributors to natural trait-variation in *A. thaliana* [5, 7, 8, 11, 31, 34-38, 40]. Earlier works on the genetic regulation of expression-variation in an *A. thaliana* have also shown that cis-eQTL have a larger effect on expression than trans-eQTL [23, 29]. It is also known that many such ELP genes carry deletions in the regulatory region [20], but in some cases the transcriptional variation is also due to large structural variations leading to, for

example, loss of entire genes [16]. To maximize eQTL-mapping power, we therefore screened the 4,317 genes that are most likely to have a genetically controlled accession-specific expression in the *SCHMITZ-data* (i.e. that are the least likely to be affected by RNA-seq bias as discussed above) for cis-eQTL alleles affecting the presence or absence of transcripts in the accessions. A customized eQTL-mapping approach designed for this scenario was developed and used for this analysis (see Materials and Methods for details).

For each of the 4,317 genes, we first binarized (0/1) the phenotype to indicate presence (1; Normalized FPKM > 0) or absence (0; Normalized FPKM = 0) of transcripts for the assayed gene in each accession. Then, we performed an association analysis to all SNP markers in a 1 Mb region around the evaluated gene. For each SNP marker in this region, a logistic regression was fitted to the genotype of the marker with the binarized phenotype as response. Significant associations are interpreted as detection of a cis-eQTL contributing to the presence or absence of transcripts for the studied gene. In total, 349 such cis-eQTLs were detected (FDR=12.3%). For 172 of the 349 genes, whose transcript-levels were affected by these cis-eQTL, transcripts were also detected in some, but not all, of the accessions of the *DUBIN-data* [33]. By performing the same cis-eQTL analysis for the presence or absence of transcripts for these 172 genes, 81 of the cis-eQTL (FDR = 0.1) could be replicated (Table S2). Given that the collections of accessions in the *SCHMITZ-* and *DUBIN-data* were obtained from non-overlapping geographical locations, it is striking that so many of the cis-eQTL with the ability of almost shutting off the expression are present in, and could be replicated across, such diverse datasets.

Mapping of eQTL for genes with transcripts in most accessions

The majority of the genes in the *SCHMITZ-data* (20,610) [32] were expressed in more than 90% of the accessions. The transcript-levels (Normalized FPKM) for these genes were quantile-transformed and used as phenotypes in linear mixed model based, kinship corrected genome-wide eQTL scans. In total, these analyses revealed 2,320 eQTL (FDR = 0.09), with 1,844 (79.5%) of the associations in cis (within a ±1 Mb window around the mapped gene) and 476 (20.5%) eQTL in trans affecting the expression of 2,240 genes (Table S4). All eQTLs were significant after correction for

genome-wide analyses across multiple expression traits. Out of the 2,320 genes with eQTL in the *SCHMITZ-data*, 2,006 had transcripts in all accessions of the *DUBIN-data* [33], and 649 of the eQTL affecting 636 genes could be replicated at a 0.01 Bonferroni threshold correcting for the number of tested markers in the replication region (FDR = 0.031; Table S5). Among the 2,240 genes with eQTL in the *SCHMITZ-data*, 175 have earlier been shown to have an altered phenotype from loss-of-function alleles [41] and 38 of these were among those replicated in the *DUBIN*-data. As many of these genes have strong effects on potentially adaptive traits, including development, hormone pathways and stress responses, they are plausible functional candidate adaptive genes in *A. thaliana*. These genes are listed in Table S6.

Significant contribution by common structural variants to many of the eQTL

Structural variations, including regulatory unit deletions [20] and larger genome rearrangements [16] have been found to contribute to the transcriptional variation in natural *A. thaliana* population both for individual genes [2, 16, 42, 43] and on a whole transcriptome level [16, 20]. We evaluated the contribution of common structural variations to the presence or absence of transcripts in individual accessions by quantifying the overlap of mapped reads in the genome and transcriptome sequencing to the 646 detected eQTL genes that completely lacked transcripts across the gene body of at least one accession. Using the genome re-sequencing data, we first identified a set of putative structural variants by identifying the individual genes and accessions where no reads were mapped to either the transcription start site (TSS) or the entire gene body of these eQTL genes. Since the probability of observing a lack of mapped reads at the exact same region in multiple accessions by chance is very low, we compiled a high-confidence set of common structural variants by retaining only those where reads were lacking in the TSS or gene body of the same gene in more than 5 accessions. In total, 155 of the 349 cis-eQTL genes showed this pattern. On average, each accession carried 58 genes with such structural variations and each gene was disrupted in 52 accessions (Figure S2). To quantify the contribution of these structural variants to the expression variation observed in the RNA-seq analysis, we tested for association between the presence/absence of the structural variation and the presence/absence of RNA-seq reads in the accessions using a Fisher exact test. This association was significant on a nominal level ($P < 0.05$) for 122 of these genes, and

94 of them passed a significance-threshold that was Bonferroni corrected for testing 155 genes. This suggests that the accession-specific transcript pattern observed is often due to structural variations (Table S2) and our eQTL approach is efficient in detecting such segregating variants. In the standard eQTL analysis that was used to map genes that had transcripts in >90% of the accessions, 297 genes lacked transcripts in at least one accession. By conducting the same structural-variant analysis for these genes, we identified an additional 93 genes with common high-confidence structural variations. In total, 37 of these were significantly associated with the transcript-levels in the accessions on a nominal level ($P < 0.05$) and 17 passed a multiple-testing corrected significance threshold. Thus, in total 248 genes were found to carry at least one common structural variation and for 159 of these, the variants were associated with the transcript-levels in the accessions. Of the 248 genes with common structural variations, 85 contained at least two common structural variants and 60 of the genes with two variants were significantly associated with the presence/absence of transcripts in the accessions. Our results show that structural variations are common, and often multi-allelic, in natural *A. thaliana* accessions and make important contributions to the observed transcriptome variation.

Identification of functional candidate genes with cis-eQTL contributing to the accession specific presence or absence of transcripts

12 of the 349 genes affected by the cis-eQTL mapped in our study had earlier been subjected to functional studies in which the gene had a distinct phenotypic effect (Table 1). The cis-eQTL-mapping result for one of these genes (*AT2G21045*; High Arsenic Content 1; *HAC1*) is illustrated in Figure 4. *HAC1* has a skewed distribution of RNA-seq scored transcript levels (Figure 4A/4C) and a highly significant cis-eQTL signal in both the *SCHMITZ* and *DUBIN-data* (Figure 2B/2D; $p = 1.75 \times 10^{-10}$/ $p = 9.32 \times 10^{-11}$, respectively). It has been shown that loss of *HAC1* expression increases the amount of Arsenic in the leaf and that several functional polymorphisms might be present in natural *Arabidopsis thaliana* population [3][4]. Here, we detected a cis-eQTL for the expression of *HAC1* with the top SNP located within an exon of *HAC1* (Figure 4B; top SNP Chromosome 2 at 9,028,685bp) in the *SCHMITZ-data*. This signal was replicated with a high significance also in the *DUBIN-data* (Figure 4D). This gene is thus a highly interesting functional candidate adaptive gene as i) it

has earlier confirmed effects on Arsenic-levels in the plant, ii) there is a strong cis-eQTL regulating presence or absence of transcript for the gene segregating in natural *A. thaliana* accessions, and iii) effect of the polymorphisms could be replicated at high significance in both analysed populations. Further experimental studies are, however, needed to functionally replicate the effect of the remaining 11 polymorphisms on expression and the indicated phenotype. This to clarify whether such a link, together with the segregation in the worldwide *A. thaliana* population, means that it has contributed to adaptation.

Table 1. Genes with cis-eQTL detected in the population of 140 natural A. thaliana accessions (SCHMITZ-data) contributing to the accession specific presence or absence of transcripts and earlier reported biological function.

Locus	*Gene*	[a]*SNP*	[b]*MAF*	[c]*Log odds ratio±SE*	[d]*P-value*	[e]*Replicated*	*Reference*
AT2G21045	*HAC1*	chr2_9028685	0.14	4.84±0.76	1.75×10^{-10}	Yes-GBF	[3]
AT5G59340	*WOX2*	chr5_23935224	0.43	2.82±0.54	1.83×10^{-7}	Yes	[44]
AT1G77235	*MIR402*	chr1_29007464	0.46	7.07±1.02	5.18×10^{-12}	No.e	[45]
AT2G38220	*APD3*	chr2_16017043	0.29	0.37±0.07	3.64×10^{-7}	No.e	[46]
AT1G13430	*ATST4C*	chr1_4601762	0.51	0.36±0.06	3.87×10^{-10}	No	[47]
AT1G66600	*WRKY63*	chr1_24217798	0.06	0.14±0.02	3.22×10^{-10}	No	[48]
AT2G19500	*ATCKX2*	chr2_8168512	0.07	0.18±0.03	6.13×10^{-9}	No	[49]
AT3G27620	*AOX1C*	chr3_10230473	0.39	0.4±0.07	6.45×10^{-8}	No	[50]
AT3G57270	*BG1*	chr3_22031771	0.06	0.15±0.02	1.09×10^{-9}	No	[51]
AT4G01420	*CBL5*	chr4_583422	0.12	0.2±0.03	7.48×10^{-12}	No	[52]
AT4G02850	*DAAR1*	chr4_597373	0.06	0.15±0.02	1.41×10^{-9}	No	[53]
AT4G29340	*PRF4*	chr4_14639984	0.21	0.36±0.07	2.32×10^{-7}	No	[54]

[a]SNP: Top SNP in association analysis; [b]MAF: Minor allele frequency of the top associated SNP in the *SCHMITZ-data*; [c]Log odds ratio of the top associated SNP ± Standard Error; [d]P-value: Nominal p-value for the top associated SNP; [e]Replicated: Could the original association in the *SCHMITZ-data* be replicated in the *DUBIN-data*, Yes-GBF: Replicated at Genome Wide Bonferroni threshold, Yes, replicated at Bonferroni threshold correcting for number of markers in ± 1 Mb window of the peak SNP in *Dubin-data* No.e: not expressed in *DUBIN-data* so could not be tested for replication. No: Non-significant in replication analysis.

Discussion

Arabidopsis thaliana is a small flowering plant that has colonized a wide range of habitats, and while adapting to these it has evolved a remarkable genotypic and phenotypic variation in the world-wide population [1, 2]. Genetic regulation of gene expression is known to be an important mechanism underlying adaptation [38, 56-58] and many studies have been conducted to investigate the gene expression variation in natural *A. thaliana* accessions [16-18, 20, 21, 23, 39]. These earlier studies have provided valuable insights to the general characteristics of expression variation in *A. thaliana*. Here, we extend these studies by exploring the whole transcriptome in a considerably larger set of natural accessions from the worldwide population.

We have studied the transcript variation in the leaf of natural *A. thaliana* accessions by analyzing data from two large sets of natural accessions from the global *A. thaliana* population. We find that the transcript variation correlates with the genome divergence between the accessions and map thousands of individual eQTL that contribute to the variation in leaf transcript-levels across the accessions. These extensive and genetically controlled differences in expression-levels controlled by alleles that segregate in the wild are a useful resource to explore how selection might have acted on different regulatory variants of genes important for the adaptation of *A. thaliana* to diverse living conditions. Several functional candidate adaptive genes were identified among the eQTL, for which further experimental validation would be highly motivated.

We found that the average proportion of genes with detected transcripts in the leaf within the individual accessions was slightly higher in this study, than in earlier studies based on smaller numbers of accessions (73% here vs 64% in [39]). In the seedling, Gan *et al.* [16] report a slightly higher estimate for protein-coding genes, but lower if all genes are considered. A large core-set of genes (61% of all with scored transcripts) was detected with transcripts in nearly all (>90%) of the accessions. The genes in this core-set overlapped to a great extent between the two independent collections of natural *A. thaliana* accessions studied here, suggesting that these genes include both basal, and leaf-specifically, expressed genes.

When analysing the deep-coverage RNA-seq from the largest collection of natural accessions, we detected transcripts in the leaf from nearly all genes in the genome in at least one of the accessions. Further, a large number of apparently accession-specific transcripts were also detected due to high sensitivity of the RNA-seq approach. The majority of the accession-specific transcripts were found at low levels in only a few accessions, making it difficult to separate true accession specific expression from bias in the RNA-seq analysis. For example, some genes are known to vary their transcripts levels in a circadian manner (2% according to [59] or 6% according to [60]), which might reduce the expression of these genes to a lower level in all accessions and lead to random detection in RNA sequencing. However, transcripts from a relatively large number of genes were abundant in some accessions, and completely absent in others. This suggests that these genes are more likely to be expressed, or lost, in an accession-specific manner, which is supported by the highly significant correlation between the genetic and transcriptome covariances amongst the accessions.

Here, we developed an approach to map cis-eQTL affecting the presence or absence of transcripts in the accessions motivated by earlier findings that illustrated the importance of strong loss-of-function alleles for adaptation in *A. thaliana* [5, 7, 8, 11, 31, 34, 35, 37, 38]. Given that phenotypes of many mutant alleles are already described in the literature, our aim was to identify new functional candidate adaptive genes by screening for cis-eQTL where alleles contributing to the presence or absence of transcripts for the studied genes segregated in populations of natural *A. thaliana* accessions. If these cis-eQTL affect a gene with a known phenotype, it can then be considered as a strong candidate adaptive gene. Among our results, we find a particularly interesting example of where our approach is able to detect adaptive genes that have been studied in detail. *HAC1* [3, 4] was detected by our approach in the larger collection [32] and replicated in the smaller [33], and its role in the reduction of Arsenik has earlier been described in the literature. We find this to be a useful proof-of-principle finding suggesting that at least some of the highlighted functional candidate adaptive genes might be found important for adaption in future studies.

Earlier studies have shown that utilization of several natural *A. thaliana* accessions, in

addition to Col-0, is useful for uncovering biologically important genetic and phenotypic variations that are not present in this reference accession [5, 7, 8, 11, 16, 31, 34-36]. Our results further support this as 5% (111) of the cis-eQTL genes lacked transcripts in the leaf of *Col-0*. The fact that half of them (53) also lacked transcripts in *Col-0* seedling and pollen [61](Table S7) suggests that these genes are not expressed at all in this accession [16].

Structural variations have earlier been found to be common in the genome and make a significant contribution to the transcriptional variation in *A. thaliana* genes (see for example [2, 16, 20, 36, 42, 43]). We found that 248 of the 646 genes that lacked transcripts in one or more accessions, and for which eQTL were mapped, also lacked reads that covered the transcription start site, or the entire gene, in the available whole-genome sequencing data. For about one third of the genes (80), both types of structural variants were common. For a majority (159) of these genes, the structural variants were significantly associated with the presence or absence of the transcript. This result confirms that structural variations regulated transcript variation are relatively common in *A. thaliana* [16, 20], that they are often multi-allelic, and are likely to make significant contributions to the transcriptome variation in the worldwide population.

When there is a leap in technology, it is important to adapt the existing analytical methods to better utilize the additional information. In our particular case, we make use of the information about expression-traits where the transcript distributions for the assayed genes are heavily zero-inflated (i.e. contain many accessions with no detectable transcripts). We show that these distributions, in many cases, are influenced by cis-eQTL with strong effects on the transcript levels. These distributions are too skewed to be appropriately transformed or modelled using other distributions such as a negative binomial [62]. Earlier eQTL-mapping studies based on RNA-seq data have therefore either removed genes whose transcript levels were zero-inflated [63], utilized non parametric testing to avoid the assumption of normality [64] or utilized regression without first addressing the potential issues arising from the non-normality of the transcript-levels [65]. Our approach to, based on the observed distribution properties, propose and test for a particular type of genetic

effects causing accession-specific expression, we could reveal many new cis-eQTL that in many cases are likely to be due to structural variants that either delete important regulatory regions for the genes, or the entire gene. Many of these associations replicated in an independent dataset and several genes were promising functional candidate adaptive genes. Although the proposed cis-eQTL-mapping approach is not a general framework for mapping all eQTL, it illustrates the value of developing and utilizing analysis methods for genome and transcriptome data to test well-defined biological hypotheses.

Materials and methods

Whole genome re-sequencing and RNA-seq data for a population of 144 natural A. thaliana *accessions*

In an earlier study, Schmitz *et al.* [32] RNA-sequenced a collection of 144 natural *Arabidopsis thaliana* accessions. We downloaded this data together with their corresponding whole-genome SNP genotypes made available as part of the 1001 Genomes project [2]. According to the author's description and the original publication [32] , the plants were grown in 22℃ and leaves had been collected from rosettes prior to flowering. Further, RNA reads had been aligned to SNP-substituted reference genomes for each accession using Bioscope version 1.3 with default parameters. Cufflinks version 1.1 had been used to quantify Transcript levels using the following parameters: '–F' 0; '–b'; '–N'; '–library-type' fr-secondstrand; '–G' TAIR10.gtf. Raw FPKM values were quantile normalized by the 75th percentile and multiplied by 1,000,000 to be transformed to a comfortable scale. We removed two accessions from the data (Alst_1 and Ws_2) due to missing genotype data and two accessions (Ann_1 and Got_7) due to their low transcript Call Rate (16,861 and 18,693 genes with transcripts as compared to the range of 22,574 to 26,967 for the other the accessions). The final dataset used for eQTL mapping (*SCHMITZ-data*) included 1,347,036 SNPs with MAF above 0.05, a call-rate above 0.95 and RNA-seq derived FPKM-values for 33,554 genes. For identifying regions without mapped reads in the genome re-sequencing, we used the information about this that was available on the SALK webpage (http://signal.salk.edu/atg1001/download.php).

Whole genome re-sequencing and RNA-seq data for a population of 107 Swedish

natural* A. thaliana *accessions

We downloaded a second public dataset of 107 Swedish *A. thaliana* lines with fully sequenced genomes and transcriptomes [33] from plants grown in 10℃ and 16℃. Here, RNA had been prepared from whole rosettes collected at the 9-true-leaf stage. RNA reads had been aligned using PALMapper aligner using a variant-aware alignment strategy. Reads that were longer than 24 bp and uniquely mapped into the exonic regions had been used to quantify expression. Further details about reads filtering and transcripts quantification can be found in [33]. We used the same quality control procedures for this dataset as for the larger dataset described above. We compared the data from the experiments done at 10℃ and 16℃ and found that they were quantitatively similar and therefore only used the data generated at 10℃ (*DUBIN*-data) for further analysis. In total, this data contained 1,785,214 SNPs with MAF above 0.05, a call-rate above 0.95, and RNA-seq derived RPKM-values for 33,322 genes.

Cis-eQTL mapping to detect polymorphisms contributing to the accession specific presence of gene-transcripts

First, we selected the 4,317 genes in the *SCHMITZ-data* that i) had transcripts in more than 14 (10%), but fewer than 126 (90%), of the accessions and ii) had transcript-levels higher than the 2nd lowest expressed gene with transcripts in all accessions. Then, we binarized the transcript-level phenotype by assigning values zero or one for each accession depending on whether transcripts for the gene were present (Normalized FPKM > 0) or not (Normalized FPKM < 0). Then, a logistic regression approach was used to perform an analysis across the SNP markers in a ±1Mb region around each of the tested genes using the *qtsore (family = binomial)* function in GenABEL [66].

For significance testing, we first applied a Bonferroni corrected significance threshold correcting for the number of SNPs tested in the ±1Mb region around the gene. Second, we accounted for the potential noise in the transcript measurements by applying a second filtering based on a permutation test performed as follows. Under the assumption that all the 0 values (lack of transcripts) resulted from non-biological noise, the binarized phenotypes were randomly shuffled with respect to the cis-SNP

genotypes 1,000 times and an association scan performed in each of these datasets as described above. In each scan, the minimum p-value was saved to provide an empirical null-distribution for every trait. Trait-specific significance-thresholds were obtained by taking the 1% cut off from these distributions. To account for multiple testing across all tested traits (genes), the FDR was calculated as the expected number of significant traits with eQTL at the given significance-threshold under the null hypothesis, divided by the number of traits where significant eQTL were detected.

Mapping of eQTLs for genes with transcripts in most accessions

For the 20,610 genes in the *SCHMITZ-data* where transcripts were detected in more than 90% of the accessions, a standard eQTL mapping approach was used by performing a GWA analysis fitting inverse-Gaussian transformed expression values to the genome-wide SNP genotypes in a linear mixed model (1) using the *polygenic* and *mmscore* functions in GenABEL package [66].

$$Y = X\beta + Zu + e \qquad (1)$$

Y is here the transformed expression phenotype, which is normally distributed with mean 0. *X* is the design matrix with one column containing the allele-count of the tested SNP (0,1,2 for minor-allele homozygous, heterozygous and major-allele homozygous genotypes, respectively). β is a vector of the additive allele-substitution effect for the SNP. *Z* is the design matrix obtained from a Cholesky decomposition of the kinship matrix *G* estimated from the whole-genome, MAF-filtered SNP data with the *ibs* function (option weight = 'freq') in the GenABEL package [66]. The Z matrix satisfies $ZZ' = G$, and thus, the random effect vector *u* is normally distributed, $u \sim N(0, I\sigma_g^2)$. *e* is the normally distributed residual variance with $e \sim N(0, I\sigma_e^2)$. The GWA results were visualized using the *cgmisc* R-package [55].

A permutation test was used to set the significance threshold in the analysis [67, 68]. As the number of traits was too large to derive a trait-specific threshold, a GWA-scan was performed across all traits to identify those with at least one SNP with $p < 1\times10^{-6}$. Among the genes that passed this threshold, a random set of 200 traits was selected.

For each of these traits, GWA were performed in two hundred permuted datasets where GRAMMAR+ transformed residuals [7, 69] were used as phenotype, resulting in 40,000 permutations in total. Based on this total distribution, we derived a 1% significance threshold ($-\log_{10}$(p-value) = 6.84).

Replication of detected eQTLs

As 26/38% the SNPs in the *SCHMITZ-data* were missing from the *DUBIN-data* (before/after filtering for MAF), we replicated our findings by testing for associations to SNPs in the *DUBIN*-data that were physically close to the detected top SNP in the SCHMITZ-*data*. The average expected LD-block size in Arabidopsis is about 10 kb [70], and therefore we performed the replication analysis to SNPs located in a ±10 kb region around the eQTL peaks in the *SCHMITZ-data* and associate their genotypes to the transcript level of the corresponding genes in the *DUBIN-data*. We considered a cis-eQTL replicated if i) the significance for any of the SNPs tested in this region passed a significance threshold corrected for the number of tested SNPs in this region using Bonferroni correction, and ii) the overlapping SNPs show effects in the same direction. FDR was calculated for the results across the trait as the expected number of false positives (0.05 * the number of tested regions) divided by the number of regions with significant eQTL.

Calculating covariances between transcriptome variation and genome variation

Based on the binarized expression values of the 4,317 selected genes (selection procedure described above), we created a relationship matrix following the same approach as when calculating the genomic IBS matrix (see details above). The correlation between the transcriptome and genome variation was calculated as the correlation between elements in these two relationship matrixes.

Definition of cis and trans eQTL peaks

For each gene with a significant GWA, the SNP with the lowest P-value was selected as the peak location for the eQTL. When the leading SNPs had been defined for each trait, SNPs were considered to represent the same eQTL if they were located within 1 Mb of each other in the TAIR10 reference genome. eQTL peaks located within 1Mb up- or downstream of the genes whose expression was used as phenotype were

classified as cis-eQTL, while the remaining eQTL peaks were classified as trans-eQTL.

Supplementary Material

Table S1. 27 genes for which transcripts were only detected in the collection of 107 Swedish *A. thaliana* accessions.

Table S2. 349 cis-eQTL detected in the population of 140 natural *A. thaliana* accessions.

Table S3. 81 cis-eQTL detected in the population of 140 natural *A. thaliana* accessions that were replicated in the population of 107 natural Swedish *A. thaliana* accessions.

Table S4. 2,320 eQTL regulating the expression of 2,240 genes expressed in most of the 140 natural *A. thaliana* accessions

Table S5. 175 genes affected by eQTL in the population of 140 natural *A. thaliana* accessions for which strong phenotypic effect have already been described in Lloyd et al. [41].

Table S6. 649 cis-eQTL detected in the population of 140 natural *A. thaliana* accessions that were replicated in the population of 107 Swedish natural *A. thaliana* accessions.

Table S7. Tissue specific expression pattern for 111 genes with loss-of-expression cis-QTL and no transcripts in the leaf of *Col-0*.

Figure S1: Illustration of the geographical locations for the 140 natural *Arabidopsis thaliana* accessions utilized in the eQTL analyses.

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Availability of data

Whole genome re-sequencing data for a population of 144 natural A. thaliana accessions (http://signal.salk.edu/atg1001/download.php)
Whole genome RNA sequencing data for a population of 144 natural A. thaliana accessions (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE43858)
Whole genome re-sequencing data for a Swedish population (https://github.com/Gregor-Mendel-Institute/swedish-genomes)
Whole genome RNA sequencing data for a Swedish population (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE54680)

Abbreviations

ELPs: Expression Level Polymorphisms; eQTL: expression quantitative trait locus; FPKM: fragment per kilo base of exon per million fragments mapped; RPKM: Reads per kilobase per million reads mapped; HAC1: High Arsenic Content 1.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

ÖC and XS initiated the study; ÖC and YZ developed the study, designed the analyses and summarised the results; YZ performed the analysis with support from SKGF and XS; ÖC and YZ wrote the manuscript. All authors read, commented and approved the final manuscript.

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Figure legends

Figure 1. Overlap of RNA-seq scored transcripts in the leaf of 140 natural A. thaliana accessions [32] (SCHMITZ-data; Normalized FPKM > 0) and 107 Swedish natural A. thaliana accessions [33] (DUBIN-data; RPKM > 0). The numbers of detected transcripts in all accessions of the respective datasets are shown in yellow. The numbers of detected transcripts in at least one, but not all, of the accessions in the respective datasets are shown in purple.

Figure 2. **(A)** Distribution of the number of genes with transcripts in the leaf of 140 natural A. thaliana accessions [32] scored by RNA-seq (Normalized FPKM > 0). **(B)** Relationship between the ranks of the average transcript levels for all genes with transcripts detected in at least one accession (y-axis) and the number of accessions in [32] where transcripts for the gene is found (x-axis). Each dot in the plot represent one of the 33,265 genes with FPKM > 0 in at least one accession of [32]. The transcript-level rank is based on average transcript levels in the accessions where transcripts for a particular gene are detected. Due to this, the ranks are less precise for transcripts present in fewer accessions. **(C)** Distribution of the number of genes with detected transcripts in the leaf of 107 Swedish natural A. thaliana accessions [33] scored by RNA-sequencing (RPKM > 0). **(D)** Relationship between the ranks of the average transcript levels for all genes with detected transcripts in at least one accession and the number of accessions in [33] where the gene is expressed. Each dot

in the plot represent one of the 25,382 genes with RPKM > 0 in at least one accession of [33].

Figure 3. Correlation between the genetic and transcriptome covariances among 4,317 genes with transcripts detected in between 14 and 126 of the accessions in the SCHMITZ-data and that are expressed above a level where transcripts RNA-seq have been able to detect transcripts for a gene in all accessions. Each dot in the figure represents a pairwise relationship between two accessions, with the transcript covariance on the y-axis and the genetic covariance on the y-axis.

Figure 4. The eQTL analysis detects a highly significant, replicable association for the expression of the gene HAC1 (AT2G21045). The peak SNP is located in an exon of HAC1. (A/C) Distributions of transcript-levels for the 140/107 accessions (FPKM/RPKM-values from RNA-sequencing) in the SCHMITZ-data (A) and DUBIN-data (C) [32, 33], respectively. (B/D) Illustrations of the association-profiles [55] for expression of the gene AT2G21045 (HAC1) in the SCHMITZ-data (B) and the DUBIN-data (D) ([32]/[33]), respectively. There is a highly significant cis-eQTL to a SNP located in an exon of HAC1.

Table legend

Table 1. Genes with cis-eQTL detected in the population of 140 natural A. thaliana accessions (SCHMITZ-data) contributing to the accession specific presence or absence of transcripts and earlier reported biological function.

Supplementary Figure legends

Figure S1 Geographical locations of 140 accessions in Schmitz-data

Figure S2. Illustration of 155 genes with detected cis-eQTLs and no mapped reads. A) Histogram of the number of genes with no mapped reads in genome sequencing for each accession. B) Histogram of the number of accessions for genes with no mapped reads.

1 Figure 1

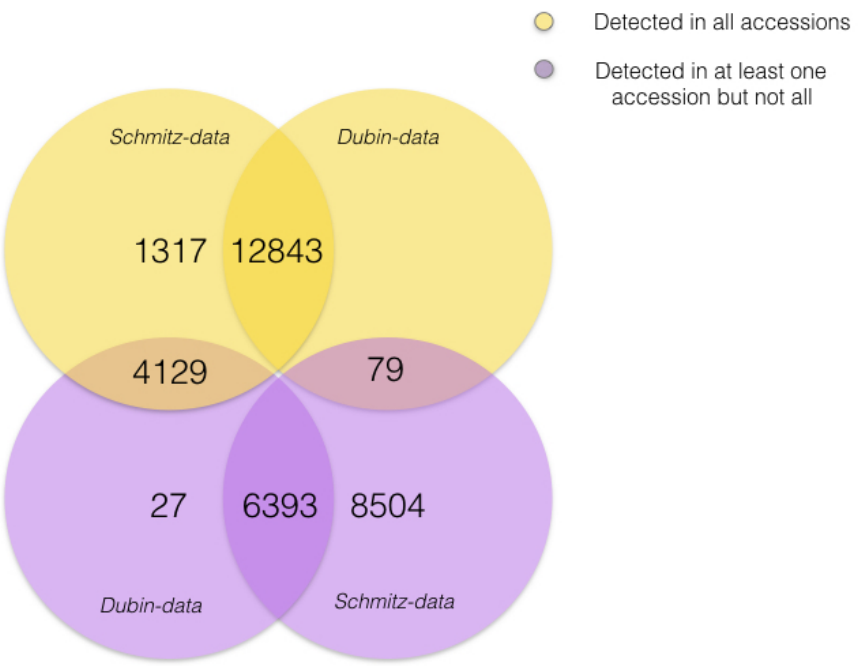

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Figure 2

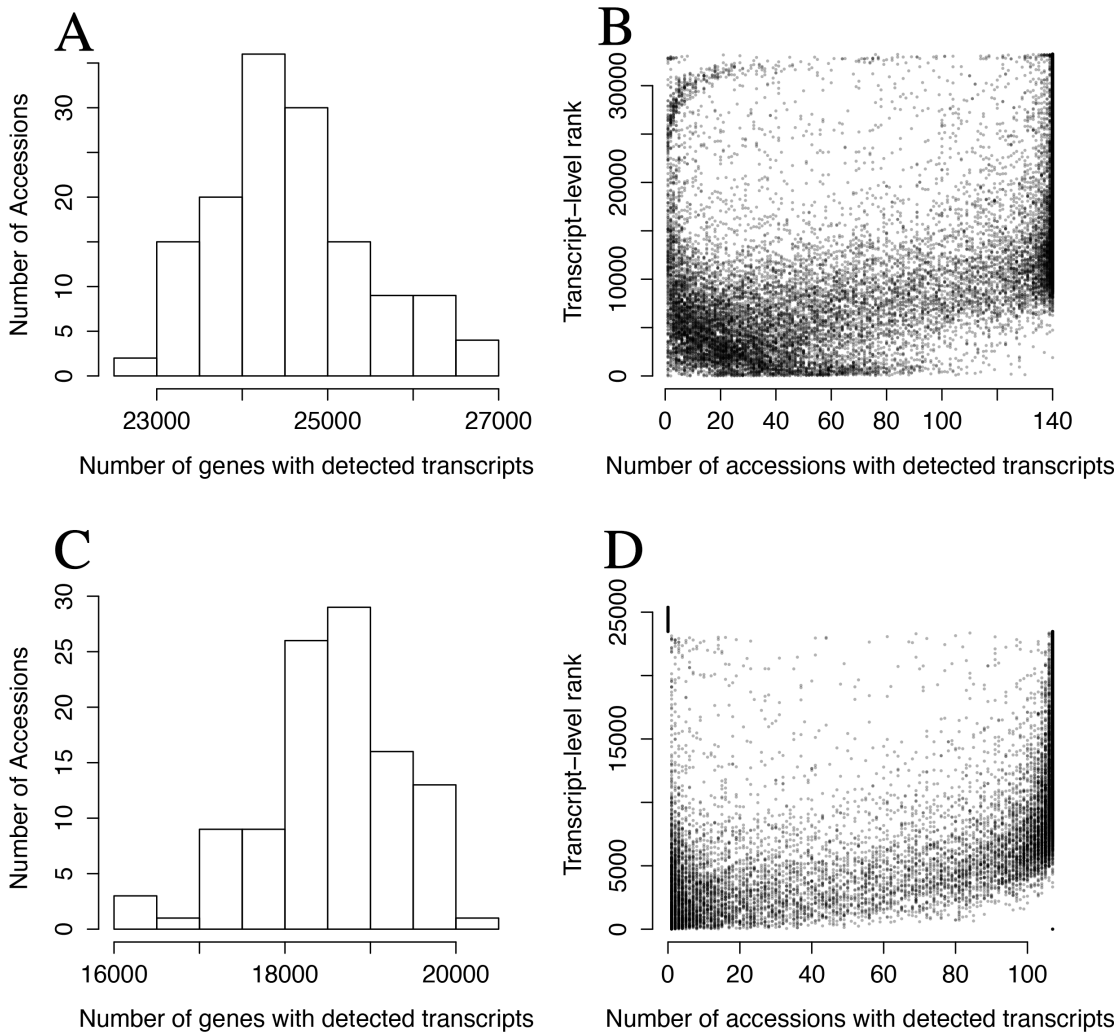
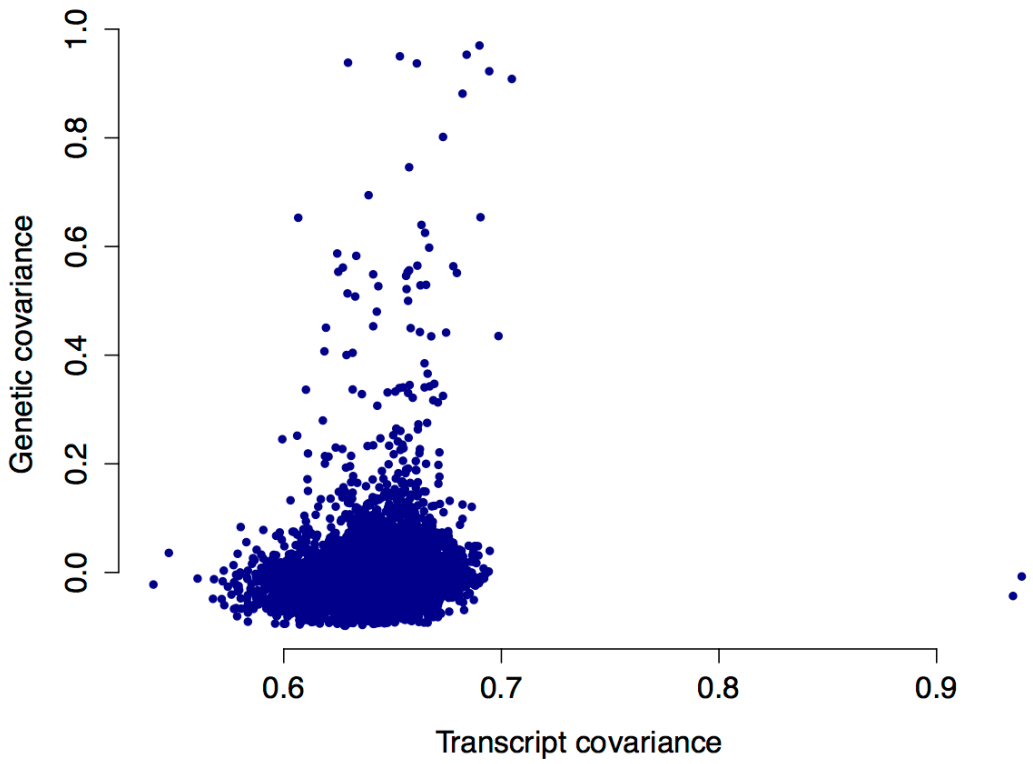
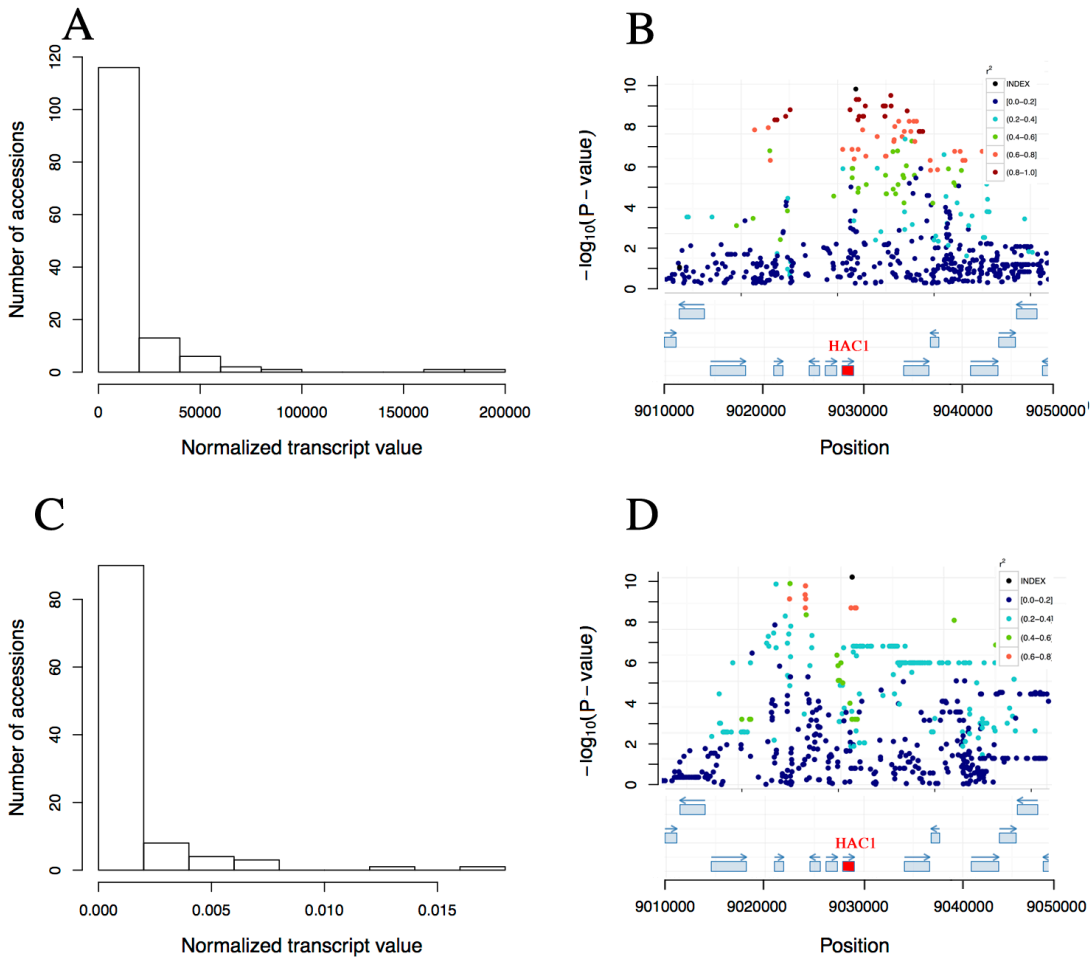

A
Number of Accessions
0
5
10
20
30
23000
25000
27000
Number of genes with detected transcripts
B
Transcript−level rank
0
10000
20000
30000
0
20
40
60
80
100
140
Number of accessions with detected transcripts
C
Number of Accessions
0
5
10
15
20
25
30
16000
18000
20000
Number of genes with detected transcripts
D
Transcript−level rank
0
5000
15000
25000
0
20
40
60
80
100
Number of accessions with detected transcripts

Figure 3


Genetic covariance
0.0
0.2
0.4
0.6
0.8
1.0
0.6
0.7
0.8
0.9
Transcript covariance

1 Figure 4


A
Number of accessions
Normalized transcript value
B
−log10(P−value)
Position
HAC1
INDEX
[0.0–0.2]
(0.2–0.4]
(0.4–0.6]
(0.6–0.8]
(0.8–1.0]
C
Number of accessions
Normalized transcript value
D
−log10(P−value)
Position
HAC1

2

Table S1. 27 genes for which transcripts were only detected in the collection of 107 Swedish *A. thaliana* accessions.

Locus	*Annotation*
AT1G11640	tRNA-Trp
AT1G20210	tRNA-Asp
AT1G22651	Unknown
AT1G28740	tRNA-Pro
AT1G28750	tRNA-Pro
AT1G28790	tRNA-Pro
AT1G28810	tRNA-Pro
AT1G28830	tRNA-Pro
AT1G28840	tRNA-Pro
AT1G28910	tRNA-Pro
AT1G28990	tRNA-Pro
AT1G57710	tRNA-Undet
AT1G80831	Unknown
AT2G01667	Unknown
AT2G16016	Unknown
AT2G16881	Unknown
AT2G34202	MIR399D
AT2G40802	Unknown
AT3G04732	Unknown
AT3G06335	tRNA-Pro
AT3G29195	Unknown
AT3G29633	Unknown
AT3G49051	Unknown
AT3G50651	Unknown
AT5G41774	Unknown
AT5G65445	tRNA-Ser
AT5G66211	Unknown

Table S2. 349 cis-eQTL detected in the population of 140 wild-collected *A. thaliana* accessions

Locus	*Peak SNP*	[a]*MAF*	[b]*Odds ratio±SE*	[c]*P-value*	[d]*Replicated*	[e]*SV*	[f]*Num*	[g]*Deletion*	*Annotation*
AT2G05117	chr2_1830148	0.36	0.21±0.02	1,59E-20	Yes-GBF	No	19	No	SCR-like-9
AT4G22390	chr4_11828893	0.25	0.21±0.02	1,32E-18	Yes-GBF	No	19	No	F-box-associated-ubiquitination-effector-family-protein
AT5G08460	chr5_2734328	0.51	20±2.28	2,04E-18	Yes-GBF	No	19	No	GDSL-like-Lipase/Acylhydrolase-superfamily-protein
AT1G34100	chr1_12399605	0.48	19.39±2.32	6,09E-17	Yes-GBF	No	18	No	unknow function
AT1G05780	chr1_1727506	0.19	0.2±0.03	3,27E-15	Yes-GBF	No	19	No	Vacuolar-ATPase-assembly-integral-membrane-protein-VMA21-like-domain
AT2G04830	chr2_1694433	0.11	6.17±0.82	4,00E-14	Yes-GBF	No	19	No	Protein-of-unknown-function-(DUF295)
AT1G64235	chr1_23835317	0.1	6.83±0.9	4,28E-14	Yes-GBF	No	19	No	Bifunctional-inhibitor/lipid-transfer-protein/seed-storage-2S-albumin-superfamily-protein
AT2G15930	chr2_6938326	0.22	4.11±0.56	2,75E-13	Yes-GBF	No	19	No	unknow function
AT1G33930	chr1_12308998	0.3	0.28±0.04	4,41E-13	Yes-GBF	No	19	No	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT3G25720	chr3_9381875	0.39	3.27±0.46	1,06E-12	Yes-GBF	No	17	No	RNA-directed-DNA-polymerase-(reverse-transcriptase)-related-family-protein
AT1G11370	chr1_3824839	0.26	4.3±0.61	1,25E-12	Yes-GBF	No	19	No	Pectin-lyase-like-superfamily-protein
AT1G67148	chr1_25121971	0.2	0.26±0.04	3,53E-12	Yes-GBF	Yes	16	No	unknow function
AT4G15053	chr4_8578153	0.07	7.03±1.02	5,47E-12	Yes-GBF	No	19	No	Protein-of-Unknown-Function-(DUF239)
AT4G01190	chr4_506690	0.54	42.47±6.2	7,44E-12	Yes-GBF	No	19	No	phosphatidylinositol-phosphate-kinase-10
AT1G76830	chr1_28791638	0.07	7.05±1.05	1,90E-11	Yes-GBF	No	19	No	F-box-and-associated-interaction-domains-containing-protein
AT5G24206	chr5_8195618	0.37	0.33±0.05	3,10E-11	Yes-GBF	No	18	No	other-RNA
AT3G25719	chr3_9381875	0.39	3.01±0.46	4,17E-11	Yes-GBF	No	19	No	unknow function
AT1G78030	chr1_29344914	0.35	5.37±0.82	7,22E-11	Yes-GBF	No	18	No	unknow function
AT2G24165	chr2_10272756	0.26	0.28±0.04	8,64E-11	Yes-GBF	No	19	No	unknow function
AT1G22090	chr1_7795619	0.46	0.35±0.05	9,70E-11	Yes-GBF	No	19	No	Protein-of-unknown-function-(DUF626)
AT2G21045	chr2_9028685	0.14	4.84±0.76	1,76E-10	Yes-GBF	No	19	No	HAC1
AT1G70870	chr1_26720882	0.24	0.3±0.05	4,39E-10	Yes-GBF	No	19	No	Polyketide-cyclase/dehydrase-and-lipid-transport-superfamily-protein
AT4G09012	chr4_5783151	0.51	13.02±2.12	7,81E-10	Yes-GBF	No	19	No	Mitochondrial-ribosomal-protein-L27
AT3G46482	chr3_17116461	0.22	3.49±0.58	1,44E-09	Yes-GBF	No	19	No	unknow function
AT3G53840	chr3_19946789	0.55	53.73±8.95	1,93E-09	Yes-GBF	No	19	No	Protein-kinase-superfamily-protein
AT3G59180	chr3_21880703	0.13	4.56±0.78	5,78E-09	Yes-GBF	No	18	No	Protein-with-RNI-like/FBD-like-domains
AT3G58480	chr3_21625946	0.31	0.35±0.06	8,47E-09	Yes-GBF	No	19	No	calmodulin-binding-family-protein
AT5G67040	chr5_26759092	0.17	3.37±0.59	1,29E-08	Yes-GBF	No	19	No	Protein-of-unknown-function-(DUF295)
AT5G40050	chr5_16033293	0.31	4.35±0.78	2,26E-08	Yes-GBF	No	19	No	F-box/FBD-like-domains-containing-protein
AT5G48350	chr5_19593564	0.27	3.98±0.72	3,61E-08	Yes-GBF	No	19	No	Polynucleotidyl-transferase,-ribonuclease-H-like-superfamily-protein
AT1G50050	chr1_18548772	0.33	0.31±0.06	8,79E-08	Yes-GBF	No	19	No	CAP-(Cysteine-rich-secretory-proteins,-Antigen-5,-and-Pathogenesis-related-1-protein)-superfamily-protein
AT1G51990	chr1_19330953	0.37	0.34±0.06	1,21E-07	Yes-GBF	No	19	No	O-methyltransferase-family-protein
AT5G36240	chr5_14280170	0.12	0.28±0.05	1,63E-07	Yes-GBF	No	19	No	zinc-knuckle-(CCHC-type)-family-protein
AT1G73120	chr1_27496441	0.26	3.8±0.73	1,74E-07	Yes-GBF	No	19	No	unknow function
AT5G24040	chr5_8122802	0.1	4.43±0.85	1,89E-07	Yes-GBF	No	19	No	Protein-of-unknown-function-(DUF295)
AT4G01335	chr4_525881	0.3	2.93±0.56	1,93E-07	Yes-GBF	No	19	No	unknow function
AT2G10260	chr2_3235177	0.22	2.87±0.56	2,92E-07	Yes-GBF	No	19	No	unknow function
AT5G22680	chr5_7539592	0.32	2.63±0.51	3,07E-07	Yes-GBF	No	19	No	unknow function
AT2G29000	chr2_12676615	0.37	0.42±0.08	3,23E-07	Yes-GBF	Not found	19	No	Leucine-rich-repeat-protein-kinase-family-protein
AT2G45940	chr2_18981758	0.41	0.43±0.09	4,90E-07	Yes-GBF	No	19	No	Protein-of-unknown-function-(DUF295)
AT2G13128	chr2_5419483	0.31	0.23±0.03	8,63E-18	Yes	No	19	No	
AT5G54206	chr5_22001192	0.17	0.18±0.02	1,17E-16	Yes	No	19	No	
AT3G59190	chr3_21877104	0.12	0.16±0.02	1,05E-15	Yes	No	19	No	F-box/RNI-like-superfamily-protein
AT5G34830	chr5_12253016	0.57	4.32±0.56	1,48E-14	Yes	No	19	No	
AT5G47130	chr5_19138652	0.39	0.29±0.04	2,31E-14	Yes	No	19	No	Bax-inhibitor-1-family-protein
AT5G49420	chr5_20036165	0.25	0.25±0.03	4,32E-14	Yes	No	19	No	MADS-box-transcription-factor-family-protein
AT5G03820	chr5_1016502	0.49	0.24±0.03	1,06E-13	Yes	No	19	No	GDSL-like-Lipase/Acylhydrolase-family-protein
AT5G14290	chr5_4618808	0.21	3.88±0.56	3,94E-12	Yes	No	16	No	Mitochondrial-ribosomal-protein-L37

AT1G61070	chr1_22493111	0.24	3.97±0.58	8,08E-12	Yes	No	19	No	low-molecular-weight-cysteine-rich-66
AT4G06536	chr4_3043219	0.1	0.19±0.03	3,72E-11	Yes	Not found	19	No	SPla/RYanodine-receptor-(SPRY)-domain-containing-protein
AT2G12935	chr2_5094798	0.09	5.47±0.83	5,21E-11	Yes	No	18	No	
AT4G28790	chr4_14228260	0.07	0.16±0.03	1,95E-10	Yes	No	19	No	basic-helix-loop-helix-(bHLH)-DNA-binding-superfamily-protein
AT5G41650	chr5_15873336	0.06	0.14±0.02	2,77E-10	Yes	No	19	No	Lactoylglutathione-lyase-/-glyoxalase-I-family-protein
AT1G48390	chr1_17880215	0.11	0.21±0.03	3,91E-10	Yes	Not found	19	No	RNI-like-superfamily-protein
AT1G03660	chr1_911682	0.06	0.14±0.02	4,17E-10	Yes	No	19	No	Ankyrin-repeat-containing-protein
AT3G17150	chr3_5846031	0.11	4.82±0.77	4,18E-10	Yes	No	19	No	Plant-invertase/pectin-methylesterase-inhibitor-superfamily-protein
AT5G66970	chr5_26734708	0.19	3.69±0.6	5,57E-10	Yes	No	19	No	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT2G25169	chr2_10687471	0.06	6.8±1.12	1,10E-09	Yes	No	19	No	
AT1G27045	chr1_9458354	0.1	0.21±0.03	1,36E-09	Yes	No	19	No	Homeobox-leucine-zipper-protein-family
AT1G51520	chr1_19034219	0.11	0.22±0.04	1,91E-09	Yes	No	19	No	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT5G22555	chr5_7487426	0.51	0.34±0.06	3,14E-09	Yes	No	13	No	
AT1G70020	chr1_26377295	0.35	0.36±0.06	4,15E-09	Yes	No	19	No	Protein-of-unknown-function-(DUF1163)
AT3G30214	chr3_11852746	0.58	11.15±1.9	4,74E-09	Yes	No	18	No	
AT3G59620	chr3_22023014	0.42	0.33±0.06	5,01E-09	Yes	No	19	No	Mannose-binding-lectin-superfamily-protein
AT1G62410	chr1_23092977	0.19	3.33±0.57	5,32E-09	Yes	No	19	No	MIF4G-domain-containing-protein
AT3G22940	chr3_8127537	0.26	0.34±0.06	5,99E-09	Yes	No	19	No	F-box-associated-ubiquitination-effector-family-protein
AT3G42786	chr3_15007014	0.06	6.18±1.06	6,05E-09	Yes	No	19	No	
AT2G24735	chr2_10527160	0.36	2.8±0.48	6,49E-09	Yes	No	19	No	
AT1G67010	chr1_24960535	0.49	0.39±0.07	1,36E-08	Yes	No	19	No	
AT5G38750	chr5_15516051	0.54	0.39±0.07	1,37E-08	Yes	Yes	19	No	asparaginyl-tRNA-synthetase-family
AT5G37280	chr5_14761553	0.1	4.8±0.85	1,72E-08	Yes	No	19	No	RING/U-box-superfamily-protein
AT4G09600	chr4_6073004	0.33	0.38±0.07	2,80E-08	Yes	No	19	No	GAST1-protein-homolog-3
AT5G60220	chr5_23949615	0.18	0.31±0.06	3,45E-08	Yes	No	19	No	tetraspanin4
AT3G21570	chr3_7601585	0.37	2.81±0.51	3,60E-08	Yes	No	19	No	
AT3G62760	chr3_23218672	0.19	3.08±0.56	3,78E-08	Yes	No	19	No	Glutathione-S-transferase-family-protein
AT2G36550	chr2_15327657	0.56	0.33±0.06	4,13E-08	Yes	No	19	No	
AT1G19410	chr1_6711880	0.28	3.59±0.67	1,01E-07	Yes	No	19	No	FBD-/-Leucine-Rich-Repeat-domains-containing-protein
AT5G59340	chr5_23935224	0.43	2.82±0.54	1,83E-07	Yes	No	19	No	WUSCHEL-related-homeobox-2
AT4G01925	chr4_929945	0.07	0.2±0.04	2,12E-07	Yes	No	19	No	Cysteine/Histidine-rich-C1-domain-family-protein
AT1G02830	chr1_625899	0.13	3.35±0.66	3,76E-07	Yes	No	19	No	Ribosomal-L22e-protein-family
AT1G14688	chr1_5049711	0.33	2.53±0.5	4,09E-07	Yes	No	19	No	
AT1G61542	chr1_22703776	0.16	7.51±0.76	3,34E-23	No.e	No	19	No	unknow function
AT2G16520	chr2_7160242	0.27	5.29±0.56	3,86E-21	No.e	No	19	No	unknow function
AT5G09445	chr5_2943446	0.1	0.12±0.01	6,46E-19	No.e	No	19	No	
AT1G58150	chr1_21522140	0.15	6.29±0.71	1,29E-18	No.e	No	19	Yes	unknow function
AT2G07110	chr2_2932104	0.12	0.14±0.02	1,86E-18	No.e	No	19	No	unknow function
AT3G28193	chr3_10515364	0.23	5.06±0.58	2,09E-18	No.e	No	14	No	
AT1G58130	chr1_21522140	0.15	6.57±0.75	2,13E-18	No.e	No	19	Yes	unknow function
AT5G38275	chr5_15284919	0.34	0.24±0.03	2,42E-18	No.e	No	19	No	
AT1G64260	chr1_23845471	0.21	0.2±0.02	4,47E-18	No.e	No	15	Yes	MuDR-family-transposase
AT5G34810	chr5_12972884	0.59	8.23±0.95	6,41E-18	No.e	No	17	No	transposable-element-gene
AT5G42965	chr5_17235489	0.19	5.39±0.63	1,86E-17	No.e	No	10	No	Polynucleotidyl-transferase,-ribonuclease-H-like-superfamily-protein
AT2G12460	chr2_5029104	0.22	0.2±0.02	2,16E-17	No.e	No	16	No	transposable-element-gene
AT5G35800	chr5_13976331	0.65	0.12±0.01	2,18E-17	No.e	No	19	No	transposable-element-gene
AT5G11290	chr5_3581269	0.44	7.35±0.87	2,77E-17	No.e	No	10	No	Plant-protein-of-unknown-function-(DUF247)
AT5G53815	chr5_21851007	0.26	0.23±0.03	3,14E-17	No.e	No	16	No	transposable-element-gene
AT2G07667	chr2_3377361	0.48	6.57±0.79	7,90E-17	No.e	Not found	19	No	unknow function
AT1G70885	chr1_26723607	0.46	8.16±0.98	9,40E-17	No.e	No	13	No	unknow function

AT5G45080	chr5_18192961	0.16	5.49±0.68	6,21E-16	No.e	No	19	No	phloem-protein-2-A6
AT1G62835	chr1_23267657	0.29	0.22±0.03	8,95E-16	No.e	No	15	Yes	unknow function
AT1G50530	chr1_18726662	0.18	5.49±0.69	1,93E-15	No.e	No	17	Yes	unknow function
AT3G13335	chr3_4340453	0.17	0.2±0.02	2,11E-15	No.e	No	19	No	pre-tRNA
AT5G35710	chr5_13877980	0.21	5.07±0.64	2,92E-15	No.e	No	19	No	transposable-element-gene
AT5G35420	chr5_13656899	0.39	0.26±0.03	3,91E-15	No.e	No	19	No	transposable-element-gene
AT5G45090	chr5_18185205	0.3	3.97±0.51	5,83E-15	No.e	No	19	No	phloem-protein-2-A7
AT5G45469	chr5_18418449	0.39	5.03±0.65	7,58E-15	No.e	No	18	No	
AT3G60972	chr3_22225185	0.29	0.26±0.03	9,56E-15	No.e	No	19	No	other-RNA
AT1G72850	chr1_27408422	0.21	4.77±0.62	1,10E-14	No.e	No	16	Yes	Disease-resistance-protein-(TIR-NBS-class)
AT3G32904	chr3_13450087	0.18	4.58±0.6	3,47E-14	No.e	No	15	No	
AT2G11280	chr2_4474960	0.28	5.65±0.75	3,86E-14	No.e	No	19	No	unknow function
AT4G01910	chr4_327944	0.06	0.11±0.01	5,27E-14	No.e	No	15	No	Cysteine/Histidine-rich-C1-domain-family-protein
AT4G01490	chr4_637062	0.26	0.26±0.03	5,83E-14	No.e	No	15	No	transposable-element-gene
AT5G34800	chr5_12151563	0.36	0.29±0.04	6,90E-14	No.e	No	18	No	transposable-element-gene
AT5G59616	chr5_24046162	0.44	0.24±0.03	1,00E-13	No.e	No	19	No	Interleukin-1-receptor-associated-kinase-4-protein
AT5G34795	chr5_12251538	0.6	347.46±46.76	1,08E-13	No.e	No	14	No	
AT3G44444	chr3_16069748	0.12	5.43±0.74	2,42E-13	No.e	No	14	No	MIR849a;-miRNA
AT1G60110	chr1_22174815	0.13	0.19±0.03	3,26E-13	No.e	Yes	19	Yes	Mannose-binding-lectin-superfamily-protein
AT5G28440	chr5_10367582	0.23	3.93±0.54	3,79E-13	No.e	No	16	No	unknown-protein
AT5G27250	chr5_9583825	0.15	5.15±0.71	5,86E-13	No.e	No	16	No	transposable-element-gene
AT2G05995	chr2_2328708	0.15	0.21±0.03	6,38E-13	No.e	No	18	No	other-RNA
AT4G32212	chr4_15552870	0.06	0.13±0.02	1,86E-12	No.e	Not found	18	No	
AT2G15770	chr2_6871331	0.17	0.23±0.03	2,12E-12	No.e	Not found	19	No	Cupredoxin-superfamily-protein
AT2G44390	chr2_18329124	0.39	3.69±0.53	2,21E-12	No.e	No	12	No	Cysteine/Histidine-rich-C1-domain-family-protein
AT1G52100	chr1_19386721	0.06	0.13±0.02	2,44E-12	No.e	No	19	Yes	Mannose-binding-lectin-superfamily-protein
AT3G50450	chr3_18722203	0.25	0.26±0.04	2,74E-12	No.e	No	19	No	homolog-of-RPW8-1
AT3G53080	chr3_19676397	0.09	6.29±0.9	3,13E-12	No.e	No	19	No	D-galactoside/L-rhamnose-binding-SUEL-lectin-protein
AT3G14540	chr3_4879136	0.34	0.29±0.04	3,40E-12	No.e	No	19	No	Terpenoid-cyclases/Protein-prenyltransferases-superfamily-protein
AT3G28170	chr3_10496945	0.21	3.78±0.55	4,00E-12	No.e	No	14	No	
AT2G06917	chr2_1927857	0.06	8.53±1.23	4,09E-12	No.e	No	15	No	transposable-element-gene
AT1G77235	chr1_29007464	0.46	7.07±1.02	5,18E-12	No.e	No	19	No	MICRORNA402 (MIR402)
AT4G29300	chr4_14433095	0.08	6.52±0.95	5,78E-12	No.e	No	18	No	low-molecular-weight-cysteine-rich-27
AT5G59662	chr5_24046162	0.44	5.08±0.74	5,92E-12	No.e	No	19	No	other-RNA
AT3G26539	chr3_9744326	0.1	0.17±0.03	6,62E-12	No.e	No	15	No	
AT1G25141	chr1_8794957	0.09	6.25±0.91	7,75E-12	No.e	Not found	18	No	F-box-associated-ubiquitination-effector-family-protein
AT4G12520	chr4_7412141	0.25	0.26±0.04	8,41E-12	No.e	No	18	No	Bifunctional-inhibitor/lipid-transfer-protein/seed-storage-2S-albumin-superfamily-protein
AT1G35280	chr1_12946221	0.28	3.85±0.56	8,56E-12	No.e	Yes	18	No	transposable-element-gene
AT3G13270	chr3_4294833	0.2	4.34±0.64	9,00E-12	No.e	No	18	No	transposable-element-gene
AT3G54363	chr3_20133288	0.53	0.33±0.05	9,17E-12	No.e	No	9	Yes	
AT1G19070	chr1_6584881	0.19	0.23±0.03	9,78E-12	No.e	No	19	No	F-box-family-protein
AT2G04380	chr2_1523480	0.15	4.33±0.64	1,42E-11	No.e	No	8	Yes	unknow function
AT4G09840	chr4_6189560	0.19	0.25±0.04	1,61E-11	No.e	No	19	No	
AT3G29764	chr3_11613507	0.06	7.87±1.17	1,81E-11	No.e	No	19	No	
AT2G11270	chr2_4476413	0.34	5.38±0.8	1,82E-11	No.e	No	19	No	citrate-synthase-related
AT4G05631	chr4_3313308	0.32	4.32±0.64	1,88E-11	No.e	No	9	No	
AT2G05950	chr2_2298593	0.34	0.29±0.04	2,25E-11	No.e	No	19	No	transposable-element-gene
AT4G09250	chr4_5924252	0.51	6.37±0.96	2,80E-11	No.e	Yes	18	No	SPla/RYanodine-receptor-(SPRY)-domain-containing-protein
AT5G28860	chr5_10697614	0.06	7.43±1.12	2,90E-11	No.e	No	8	No	transposable-element-gene
AT5G43040	chr5_17258020	0.27	3.63±0.55	3,07E-11	No.e	No	14	No	Cysteine/Histidine-rich-C1-domain-family-protein

AT4G12382	chr4_7327127	0.07	0.15±0.02	4,62E-11	No.e	No	19	No	F-box-family-protein
AT5G54040	chr5_21920938	0.42	0.34±0.05	6,25E-11	No.e	No	19	No	Cysteine/Histidine-rich-C1-domain-family-protein
AT5G16486	chr5_5384684	0.26	3.27±0.5	7,19E-11	No.e	Not found	17	No	RNA-directed-DNA-polymerase-(reverse-transcriptase)-related-family-protein
AT5G23065	chr5_7736999	0.41	2.97±0.46	7,64E-11	No.e	No	19	No	MIR162B;-miRNA
AT1G15885	chr1_5459026	0.09	5.8±0.89	8,53E-11	No.e	No	17	Yes	unknow function
AT4G03811	chr4_1772158	0.26	0.28±0.04	1,26E-10	No.e	No	19	No	other-RNA
AT1G20520	chr1_7104762	0.15	0.24±0.04	1,34E-10	No.e	No	19	No	Arabidopsis-protein-of-unknown-function-(DUF241)
AT3G24929	chr3_9120303	0.15	0.25±0.04	1,65E-10	No.e	Not found	16	No	
AT3G25014	chr3_9296271	0.07	6.2±0.97	1,95E-10	No.e	No	16	No	
AT5G34790	chr5_13043021	0.07	0.16±0.03	1,95E-10	No.e	No	14	No	transposable-element-gene
AT5G05282	chr5_1565256	0.39	0.35±0.05	2,04E-10	No.e	No	19	No	conserved-peptide-upstream-open-reading-frame-64
AT1G31900	chr1_11462269	0.18	0.25±0.04	2,28E-10	No.e	No	19	Yes	unknow function
AT5G28913	chr5_11295973	0.5	0.36±0.06	2,53E-10	No.e	No	19	No	transposable-element-gene
AT1G35750	chr1_13253071	0.25	0.3±0.05	2,72E-10	No.e	No	19	Yes	pumilio-10
AT2G27000	chr2_11519531	0.17	0.26±0.04	2,93E-10	No.e	No	19	No	cytochrome-P450,-family-705,-subfamily-A,-polypeptide-8
AT2G27850	chr2_12470885	0.26	3.33±0.53	3,49E-10	No.e	No	19	No	pre-tRNA
AT3G33145	chr3_14056096	0.15	4.26±0.68	4,58E-10	No.e	No	19	No	transposable-element-gene
AT2G15940	chr2_6947019	0.29	0.33±0.05	4,59E-10	No.e	No	18	No	transposable-element-gene
AT1G72870	chr1_27425514	0.21	3.94±0.63	5,60E-10	No.e	No	19	Yes	Disease-resistance-protein-(TIR-NBS-class)
AT1G25180	chr1_9184262	0.08	0.18±0.03	6,41E-10	No.e	No	18	Yes	unknow function
AT1G30935	chr1_11015394	0.32	0.33±0.05	7,40E-10	No.e	No	19	No	unknow function
AT4G03490	chr4_1544498	0.43	0.36±0.06	8,22E-10	No.e	Not found	18	No	Ankyrin-repeat-family-protein
AT5G48780	chr5_19769664	0.22	4.49±0.73	8,66E-10	No.e	No	7	No	disease-resistance-protein-(TIR-NBS-class)
AT3G43303	chr3_15221988	0.1	4.79±0.79	1,36E-09	No.e	No	16	No	transposable-element-gene
AT1G61688	chr1_23114405	0.07	5.84±0.97	1,53E-09	No.e	No	19	No	Defensin-like-(DEFL)-family-protein
AT4G09745	chr4_5151551	0.07	5.84±0.97	1,53E-09	No.e	No	19	No	transposable-element-gene
AT4G19090	chr4_10425735	0.06	0.16±0.03	1,80E-09	No.e	No	10	No	Protein-of-unknown-function-(DUF594)
AT4G20230	chr4_10918811	0.06	0.16±0.03	1,80E-09	No.e	No	19	No	Terpenoid-cyclases/Protein-prenyltransferases-superfamily-protein
AT4G27220	chr4_13637554	0.49	0.38±0.06	1,87E-09	No.e	No	19	Yes	NB-ARC-domain-containing-disease-resistance-protein
AT4G07408	chr4_4190993	0.3	2.87±0.48	2,07E-09	No.e	No	7	No	
AT4G12990	chr4_7592733	0.38	5.6±0.94	2,19E-09	No.e	No	11	No	
AT2G13660	chr2_5690457	0.44	0.36±0.06	2,32E-09	No.e	No	14	No	unknow function
AT4G04680	chr4_2368681	0.39	2.8±0.47	2,41E-09	No.e	No	12	No	
AT5G48775	chr5_19769604	0.26	4.56±0.77	2,83E-09	No.e	No	7	No	other-RNA
AT3G29786	chr3_12432899	0.06	6.36±1.07	2,87E-09	No.e	Not found	16	Yes	transposable-element-gene
AT2G07777	chr2_2322938	0.08	0.19±0.03	3,04E-09	No.e	No	19	No	ATP-synthase-9-mitochondrial
AT4G03292	chr4_1446046	0.38	2.69±0.45	3,13E-09	No.e	No	18	No	Polynucleotidyl-transferase,-ribonuclease-H-like-superfamily-protein
AT2G17160	chr2_7437677	0.12	4.15±0.7	3,19E-09	No.e	No	19	No	Interleukin-1-receptor-associated-kinase-4-protein
AT3G27809	chr3_10296836	0.06	0.15±0.03	3,33E-09	No.e	No	19	No	
AT1G72852	chr1_27408381	0.26	3.34±0.56	3,34E-09	No.e	No	12	Yes	unknow function
AT3G21030	chr3_7367733	0.3	3.74±0.63	3,76E-09	No.e	No	19	No	transposable-element-gene
AT5G43770	chr5_17588945	0.38	3.99±0.68	3,95E-09	No.e	No	19	No	proline-rich-family-protein
AT2G16550	chr2_7172407	0.09	0.19±0.03	4,04E-09	No.e	Not found	19	No	unknow function
AT4G03500	chr4_1557953	0.36	0.36±0.06	4,63E-09	No.e	No	19	No	Ankyrin-repeat-family-protein
AT3G62490	chr3_22225372	0.14	0.25±0.04	4,74E-09	No.e	No	18	No	transposable-element-gene
AT4G09300	chr4_5896840	0.26	3.07±0.53	4,79E-09	No.e	Yes	19	No	LisH-and-RanBPM-domains-containing-protein
AT4G07820	chr4_4702825	0.34	0.37±0.06	5,02E-09	No.e	No	19	No	CAP-(Cysteine-rich-secretory-proteins,-Antigen-5,-and-Pathogenesis-related-1-protein)-superfamily-protein
AT3G45851	chr3_16861459	0.44	0.28±0.05	5,20E-09	No.e	Not found	19	No	
AT1G23935	chr1_8466494	0.42	0.36±0.06	5,75E-09	No.e	Yes	19	Yes	unknow function
AT3G15320	chr3_5152829	0.34	3.12±0.54	5,87E-09	No.e	Yes	19	No	transposable-element-gene

AT5G03377	chr5_817193	0.06	0.16±0.03	5,88E-09	No.e	No	18	No	
AT2G17043	chr2_7404804	0.11	4.7±0.81	6,95E-09	No.e	No	19	No	unknow function
AT5G23955	chr5_8104721	0.09	0.22±0.04	8,95E-09	No.e	No	16	No	transposable-element-gene
AT5G29560	chr5_11044218	0.06	6.24±1.09	9,16E-09	No.e	No	10	No	caleosin-related-family-protein
AT2G15350	chr2_5697276	0.06	0.16±0.03	9,16E-09	No.e	No	19	No	fucosyltransferase-10
AT1G47915	chr1_17983412	0.09	4.78±0.84	1,02E-08	No.e	No	19	No	F-box-family-protein
AT1G50550	chr1_18718957	0.44	0.33±0.06	1,02E-08	No.e	No	19	No	unknow function
AT1G44940	chr1_16994763	0.37	2.65±0.46	1,13E-08	No.e	No	16	No	unknow function
AT1G32010	chr1_11505353	0.23	3.34±0.58	1,16E-08	No.e	Yes	16	Yes	myosin-heavy-chain-related
AT4G09200	chr4_5850272	0.46	4.08±0.72	1,21E-08	No.e	No	19	No	SPla/RYanodine-receptor-(SPRY)-domain-containing-protein
AT5G26642	chr5_9271988	0.12	4.08±0.72	1,21E-08	No.e	Yes	8	No	transposable-element-gene
AT3G44470	chr3_16389683	0.18	3.33±0.59	1,29E-08	No.e	No	18	No	transposable-element-gene
AT4G01930	chr4_823407	0.29	0.36±0.06	1,46E-08	No.e	No	19	No	Cysteine/Histidine-rich-C1-domain-family-protein
AT2G11300	chr2_4475297	0.26	3.33±0.59	1,51E-08	No.e	No	19	No	transposable-element-gene
AT2G46455	chr2_19072315	0.37	0.38±0.07	1,56E-08	No.e	No	19	No	OxaA/YidC-like-membrane-insertion-protein
AT1G22720	chr1_7447447	0.13	4.43±0.78	1,60E-08	No.e	Not found	19	No	Protein-kinase-superfamily-protein
AT5G50665	chr5_20664184	0.11	0.25±0.04	1,63E-08	No.e	Not found	16	No	
AT5G44569	chr5_17963028	0.36	3.09±0.55	1,66E-08	No.e	No	19	No	
AT1G43590	chr1_16413361	0.21	0.33±0.06	1,71E-08	No.e	No	19	Yes	transposable-element-gene
AT1G16620	chr1_6529298	0.2	3.19±0.57	1,73E-08	No.e	No	13	No	transposable-element-gene
AT4G08430	chr4_5322669	0.11	4.56±0.81	1,97E-08	No.e	No	19	No	Ulp1-protease-family-protein
AT5G42092	chr5_16407954	0.06	0.18±0.03	2,05E-08	No.e	No	19	No	
AT5G36185	chr5_14243034	0.11	0.23±0.04	2,06E-08	No.e	Not found	19	No	
AT2G44800	chr2_18465031	0.06	0.17±0.03	2,07E-08	No.e	No	19	No	2-oxoglutarate-(2OG)-and-Fe(II)-dependent-oxygenase-superfamily-protein
AT1G33950	chr1_12308998	0.3	0.35±0.06	2,27E-08	No.e	No	19	No	Avirulence-induced-gene-(AIG1)-family-protein
AT5G59060	chr5_23844434	0.14	3.66±0.66	2,35E-08	No.e	Yes	6	No	
AT3G29636	chr3_11469465	0.06	6.27±1.12	2,44E-08	No.e	No	8	No	transferase-related
AT2G05185	chr2_2222789	0.09	0.23±0.04	3,20E-08	No.e	No	17	No	unknow function
AT5G22608	chr5_7501851	0.5	Inf±Inf	3,45E-08	No.e	No	13	No	
AT3G26235	chr3_9632586	0.6	0.3±0.06	3,94E-08	No.e	Not found	19	No	
AT5G48210	chr5_20062490	0.08	4.76±0.87	4,35E-08	No.e	No	19	No	Protein-of-unknown-function-(DUF1278)
AT5G55790	chr5_22571442	0.07	0.2±0.04	4,42E-08	No.e	No	16	No	
AT5G12090	chr5_3911124	0.1	4.32±0.8	6,31E-08	No.e	No	19	No	Protein-kinase-superfamily-protein
AT2G13760	chr2_5714445	0.41	2.46±0.46	6,50E-08	No.e	No	12	No	unknow function
AT3G43826	chr3_15671078	0.24	0.36±0.07	6,55E-08	No.e	Yes	19	Yes	
AT5G46010	chr5_18653506	0.14	3.47±0.65	7,89E-08	No.e	Yes	18	No	Homeodomain-like-superfamily-protein
AT3G30812	chr3_11740096	0.1	4.04±0.75	8,32E-08	No.e	Not found	6	No	
AT2G14020	chr2_6293350	0.09	4.56±0.85	8,33E-08	No.e	No	18	No	transposable-element-gene
AT3G23085	chr3_8209322	0.5	3.54±0.66	9,21E-08	No.e	No	15	No	transposable-element-gene
AT5G28671	chr5_10690624	0.59	2.83±0.53	9,64E-08	No.e	No	19	No	transposable-element-gene
AT2G01360	chr2_174116	0.28	2.81±0.53	1,01E-07	No.e	No	19	No	pentatricopeptide-(PPR)-repeat-containing-protein
AT5G32434	chr5_11657908	0.11	3.89±0.73	1,01E-07	No.e	No	18	No	transposable-element-gene
AT4G04409	chr4_1610995	0.21	0.35±0.07	1,05E-07	No.e	No	19	No	
AT5G20750	chr5_7031063	0.48	0.42±0.08	1,23E-07	No.e	No	14	No	transposable-element-gene
AT1G57850	chr1_21424565	0.3	3.68±0.7	1,25E-07	No.e	No	19	Yes	Toll-Interleukin-Resistance-(TIR)-domain-family-protein
AT4G19095	chr4_10458746	0.3	0.39±0.07	1,26E-07	No.e	No	18	No	
AT4G17512	chr4_9464355	0.19	3.15±0.6	1,57E-07	No.e	No	18	No	
AT5G05400	chr5_1596755	0.44	0.42±0.08	1,60E-07	No.e	No	8	No	LRR-and-NB-ARC-domains-containing-disease-resistance-protein
AT5G32436	chr5_11621803	0.13	3.66±0.7	1,71E-07	No.e	No	19	No	transposable-element-gene
AT2G07000	chr2_2902135	0.53	4.77±0.92	1,94E-07	No.e	No	19	No	unknow function

AT3G44805	chr3_16349893	0.29	0.39±0.08	2,52E-07	No.e	Yes	16	No	TRAF-like-superfamily-protein
AT2G06550	chr2_2732433	0.41	4.25±0.83	2,55E-07	No.e	No	19	No	transposable-element-gene
AT5G39070	chr5_15636156	0.3	0.37±0.07	2,87E-07	No.e	Yes	19	No	transposable-element-gene
AT4G04110	chr4_2230922	0.16	3.26±0.64	3,04E-07	No.e	No	19	No	Toll-Interleukin-Resistance-(TIR)-domain-family-protein
AT5G27889	chr5_9903730	0.14	3.34±0.65	3,11E-07	No.e	No	16	No	
AT4G06551	chr4_3757309	0.07	4.98±0.98	3,41E-07	No.e	Not found	19	No	transposable-element-gene
AT3G25573	chr3_8551425	0.09	4.6±0.9	3,47E-07	No.e	No	19	No	
AT2G38220	chr2_16017043	0.29	0.37±0.07	3,65E-07	No.e	No	18	No	ABERRANT POLLEN DEVELOPMENT 3, APD3
AT1G24388	chr1_8641496	0.2	3.55±0.7	3,70E-07	No.e	No	19	No	unknow function
AT3G62475	chr3_23091510	0.27	3.13±0.64	8,82E-07	No.e	No	18	No	transposable-element-gene
AT3G48346	chr3_17899107	0.34	5.43±0.59	2,54E-20	No	No	19	No	unknow function
AT3G47410	chr3_17469057	0.26	0.19±0.02	4,93E-19	No	No	19	No	unknow function
AT3G20935	chr3_7329829	0.09	0.11±0.01	1,14E-18	No	No	19	No	cytochrome-P450,-family-705,-subfamily-A,-polypeptide-28
AT2G13130	chr2_5419483	0.31	0.25±0.03	2,85E-16	No	No	19	No	unknow function
AT5G09490	chr5_2952537	0.17	0.2±0.02	2,11E-15	No	No	19	No	Ribosomal-protein-S19-family-protein
AT3G03280	chr3_765798	0.37	4.53±0.57	3,23E-15	No	No	19	No	unknow function
AT2G03360	chr2_1024173	0.09	0.15±0.02	4,53E-13	No	No	19	No	Glycosyltransferase-family-61-protein
AT4G01230	chr4_528694	0.06	0.11±0.02	4,78E-13	No	No	19	No	Reticulon-family-protein
AT4G01420	chr4_583422	0.12	0.2±0.03	7,49E-12	No	No	19	No	CALCINEURIN B-LIKE PROTEIN 5 (CBL5)
AT4G28365	chr4_14033745	0.24	0.29±0.04	1,14E-11	No	Not found	19	No	early-nodulin-like-protein-3
AT1G05770	chr1_1727707	0.2	0.27±0.04	1,50E-11	No	No	19	No	Mannose-binding-lectin-superfamily-protein
AT2G05300	chr2_1931621	0.07	0.15±0.02	4,62E-11	No	No	19	No	unknow function
AT5G46915	chr5_18857822	0.06	0.13±0.02	8,27E-11	No	Not found	19	No	transcriptional-factor-B3-family-protein
AT1G32570	chr1_11777767	0.14	4.92±0.76	9,13E-11	No	No	19	No	unknow function
AT3G16440	chr3_5591618	0.06	0.15±0.02	9,96E-11	No	No	19	No	myrosinase-binding-protein-like-protein-300B
AT4G19080	chr4_10446003	0.3	0.33±0.05	1,42E-10	No	No	18	No	Protein-of-unknown-function-(DUF594)
AT3G16590	chr3_5650988	0.44	7.03±1.1	1,47E-10	No	No	19	No	F-box-and-associated-interaction-domains-containing-protein
AT3G03230	chr3_748863	0.13	0.23±0.04	1,56E-10	No	No	19	No	alpha/beta-Hydrolases-superfamily-protein
AT4G19829	chr4_10769359	0.35	0.33±0.05	1,82E-10	No	No	19	No	unknow function
AT1G66600	chr1_24217798	0.06	0.14±0.02	3,22E-10	No	No	19	No	AtWRKY63
AT2G44383	chr2_18330255	0.6	3.92±0.62	3,50E-10	No	No	19	No	unknow function
AT3G28060	chr3_10446335	0.31	0.34±0.05	3,51E-10	No	No	17	No	Nodulin-MtN21-/EamA-like-transporter-family-protein
AT1G13430	chr1_4601762	0.51	0.36±0.06	3,87E-10	No	No	19	No	sulfotransferase-4C
AT1G22680	chr1_7537404	0.06	0.14±0.02	4,17E-10	No	No	19	No	unknow function
AT5G22490	chr5_7491397	0.27	0.32±0.05	5,02E-10	No	No	19	No	O-acyltransferase-(WSD1-like)-family-protein
AT4G12510	chr4_7419182	0.31	0.32±0.05	5,37E-10	No	No	19	No	Bifunctional-inhibitor/lipid-transfer-protein/seed-storage-2S-albumin-superfamily-protein
AT1G60750	chr1_21859114	0.11	0.22±0.04	5,87E-10	No	No	19	No	NAD(P)-linked-oxidoreductase-superfamily-protein
AT3G57270	chr3_22031771	0.06	0.15±0.02	1,10E-09	No	No	19	No	BETA-1,3-GLUCANASE 1
AT5G04210	chr5_546273	0.1	0.21±0.03	1,36E-09	No	No	19	No	CCCH-type-zinc-fingerfamily-protein-with-RNA-binding-domain
AT4G02850	chr4_597373	0.06	0.15±0.02	1,41E-09	No	No	19	No	D-AMINO ACID RACEMASE1, DAAR1
AT3G06545	chr3_2568920	0.06	6.14±1.02	1,80E-09	No	No	19	No	unknow function
AT4G16105	chr4_9048095	0.06	6.85±1.15	2,54E-09	No	Not found	19	No	pre-tRNA
AT2G28440	chr2_12732439	0.07	0.18±0.03	4,06E-09	No	No	19	No	proline-rich-family-protein
AT3G26480	chr3_9690338	0.39	0.37±0.06	4,30E-09	No	No	19	No	Transducin-family-protein-/-WD-40-repeat-family-protein
AT4G27890	chr4_13885908	0.24	0.33±0.06	5,05E-09	No	No	19	No	HSP20-like-chaperones-superfamily-protein
AT5G28230	chr5_10193083	0.5	6.37±1.09	5,09E-09	No	No	19	No	unknow function
AT5G17110	chr5_5895166	0.11	0.24±0.04	5,09E-09	No	No	19	No	Cystatin/monellin-superfamily-protein
AT2G15610	chr2_6812189	0.09	4.68±0.8	5,28E-09	No	No	19	No	Protein-of-unknown-function-(DUF1685)
AT4G20420	chr4_11015485	0.44	3.02±0.52	5,67E-09	No	No	19	No	Tapetum-specific-protein-TAP35/TAP44
AT1G44674	chr1_17468129	0.06	6.65±1.14	5,69E-09	No	Not found	18	No	Protein-of-unknown-function-(DUF1664)

AT3G59460	chr3_22174226	0.56	0.24±0.04	6,08E-09	No	No	15	No	unknow function
AT2G19500	chr2_8168512	0.07	0.18±0.03	6,14E-09	No	No	19	No	CYTOKININ OXIDASE 2 (CKX2)
AT4G22460	chr4_11839617	0.29	0.32±0.06	6,44E-09	No	No	19	No	Bifunctional-inhibitor/lipid-transfer-protein/seed-storage-2S-albumin-superfamily-protein
AT1G50520	chr1_18724446	0.45	0.37±0.06	6,64E-09	No	No	19	No	cytochrome-P450,-family-705,-subfamily-A,-polypeptide-27
AT4G36740	chr4_17549071	0.13	0.26±0.04	6,95E-09	No	No	19	No	homeobox-protein-40
AT1G48180	chr1_17797167	0.18	0.29±0.05	7,56E-09	No	No	19	No	unknow function
AT3G50373	chr3_19561243	0.08	5.11±0.89	7,91E-09	No	No	19	No	unknow function
AT4G22230	chr4_10808675	0.08	0.2±0.03	7,92E-09	No	No	19	No	Arabidopsis-defensin-like-protein
AT2G44780	chr2_17926729	0.06	6.24±1.09	9,16E-09	No	No	19	No	unknow function
AT4G29305	chr4_14044368	0.06	6.24±1.09	9,16E-09	No	No	19	No	low-molecular-weight-cysteine-rich-25
AT3G55590	chr3_20700450	0.06	0.16±0.03	9,16E-09	No	No	18	No	Glucose-1-phosphate-adenylyltransferase-family-protein
AT5G60140	chr5_24954904	0.06	0.16±0.03	9,16E-09	No	Not found	19	No	AP2/B3-like-transcriptional-factor-family-protein
AT2G17080	chr2_7433437	0.54	0.27±0.05	1,21E-08	No	No	19	No	Arabidopsis-protein-of-unknown-function-(DUF241)
AT2G40440	chr2_15976280	0.06	0.17±0.03	1,22E-08	No	No	19	No	BTB/POZ-domain-containing-protein
AT5G48050	chr5_19465476	0.3	0.36±0.06	1,25E-08	No	No	19	No	unknow function
AT5G10880	chr5_3431828	0.1	0.23±0.04	1,34E-08	No	No	19	No	tRNA-synthetase-related-/-tRNA-ligase-related
AT3G09240	chr3_2073507	0.13	0.26±0.05	1,43E-08	No	No	19	No	Protein-kinase-protein-with-tetratricopeptide-repeat-domain
AT5G56368	chr5_22822204	0.09	4.73±0.84	1,95E-08	No	No	19	No	unknow function
AT3G26742	chr3_9836139	0.07	0.19±0.03	2,02E-08	No	Yes	19	No	unknow function
AT2G23970	chr2_10862861	0.08	0.2±0.04	2,33E-08	No	No	19	No	Class-I-glutamine-amidotransferase-like-superfamily-protein
AT1G61160	chr1_22544801	0.21	0.33±0.06	2,44E-08	No	No	19	No	unknow function
AT1G15772	chr1_4560811	0.12	0.26±0.05	2,83E-08	No	No	19	No	unknow function
AT4G13860	chr4_8024486	0.67	49.54±8.95	3,07E-08	No	No	7	No	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT5G37072	chr5_14654563	0.1	0.23±0.04	3,60E-08	No	No	19	No	unknow function
AT1G32710	chr1_11832701	0.16	3.38±0.61	3,63E-08	No	No	19	No	Cytochrome-c-oxidase,-subunit-Vib-family-protein
AT5G52600	chr5_21155836	0.08	0.21±0.04	4,35E-08	No	No	19	No	myb-domain-protein-82
AT4G05497	chr4_2779656	0.21	0.34±0.06	4,61E-08	No	No	19	No	RNI-like-superfamily-protein
AT4G33930	chr4_16270624	0.51	4.77±0.87	4,92E-08	No	No	19	No	Cupredoxin-superfamily-protein
AT2G47660	chr2_18957842	0.06	5.35±0.98	4,96E-08	No	Not found	19	No	unknow function
AT2G26211	chr2_11160207	0.14	0.27±0.05	5,00E-08	No	No	19	No	MIR825a;-miRNA
AT3G27440	chr3_9690941	0.11	0.25±0.05	5,06E-08	No	No	19	No	uridine-kinase-like-5
AT1G69990	chr1_26363570	0.34	5.3±0.98	6,19E-08	No	No	19	No	Leucine-rich-repeat-protein-kinase-family-protein
AT3G27620	chr3_10230473	0.39	0.4±0.07	6,46E-08	No	No	19	No	ALTERNATIVE OXIDASE 1C (AOX1C)
AT3G28310	chr3_10557784	0.24	4.2±0.78	7,03E-08	No	Not found	19	No	Protein-of-unknown-function-(DUF677)
AT4G05170	chr4_2660358	0.26	0.37±0.07	8,27E-08	No	No	19	No	basic-helix-loop-helix-(bHLH)-DNA-binding-superfamily-protein
AT3G13432	chr3_4841943	0.19	0.33±0.06	8,89E-08	No	No	17	No	unknow function
AT2G03972	chr2_1256591	0.24	0.35±0.07	9,56E-08	No	Yes	19	No	unknow function
AT5G44065	chr5_17732661	0.31	0.37±0.07	1,04E-07	No	No	19	No	unknow function
AT4G34800	chr4_16598096	0.17	0.32±0.06	1,04E-07	No	Not found	19	No	SAUR-like-auxin-responsive-protein-family-
AT4G12530	chr4_7403214	0.28	2.75±0.52	1,17E-07	No	No	19	No	Bifunctional-inhibitor/lipid-transfer-protein/seed-storage-2S-albumin-superfamily-protein
AT1G24010	chr1_8524105	0.29	2.95±0.56	1,31E-07	No	No	19	No	Polyketide-cyclase/dehydrase-and-lipid-transport-superfamily-protein
AT5G37050	chr5_14641068	0.31	0.38±0.07	1,32E-07	No	No	19	No	unknow function
AT1G33500	chr1_12158521	0.11	0.25±0.05	1,36E-07	No	No	19	No	unknow function
AT4G01260	chr4_823678	0.09	4.1±0.78	1,52E-07	No	No	19	No	DNA-binding-storekeeper-protein-related-transcriptional-regulator
AT5G03860	chr5_896614	0.09	0.24±0.05	1,52E-07	No	No	19	No	malate-synthase
AT1G36340	chr1_13654375	0.32	2.74±0.52	1,61E-07	No	No	19	No	ubiquitin-conjugating-enzyme-31
AT2G38830	chr2_15979271	0.15	0.31±0.06	1,61E-07	No	No	19	No	Ubiquitin-conjugating-enzyme/RWD-like-protein
AT4G34810	chr4_16578580	0.06	0.2±0.04	1,82E-07	No	No	19	No	SAUR-like-auxin-responsive-protein-family-
AT4G29340	chr4_14639984	0.21	0.36±0.07	2,32E-07	No	No	19	No	profilin-4
AT1G70840	chr1_26737635	0.15	0.31±0.06	3,59E-07	No	No	19	No	MLP-like-protein-31

AT4G37230	chr4_17519865	0.39	2.35±0.47	5,44E-07	No	No	19	No	Photosystem-II-manganese-stabilising-protein-(PsbO)-family

region surrounding peak SNP(Yes); No.e: Gene could not be tested as no expression in replication dataset; No: No significance after Bonferroni correction);[c]SV: Yes, this SNP is located in a deletion region in Cao et al.(2011,Nature genetics), Not found, this pisition is not polymophic in Cao et al.(2011,Nature genetics), NO, This position is no located in the deletion region in Cao et al.(2011,Nature genetics);[f]Num:The number of appearing in denovo assembled genome for 19 natural accessions(Gan et al.(2011,Nature));[g]Deletion:No, whole gene are not deleted in at least one of the

Table S3: 81 cis-eQTL detected in the population of 140 wild-collected *A. thaliana* accessions that were replicated in the population of 107 wild-collected Swedish *A. thaliana* accessions.

			Schmitz-data			*Dubin-data*		
Locus	[a]***SNP***	[b]***Genotype***	[c]***Odds ratio±SE***	[d]***MAF***	[e]***P-value***	[c]***Odds ratio±SE***	[d]***MAF***	[e]***P-value***
AT1G02830	chr1_624687	C/C	2.97±0.59	0.29	5.51E-07	1.89±0.61	0.2	1.82E-03
AT1G03660	chr1_926200	A/A	0.33±0.09	0.32	1.29E-04	0.45±0.13	0.5	4.35E-04
AT1G05780	chr1_1730502	C/C	0.32±0.07	0.06	8.55E-07	0.18±0.02	0.29	5.01E-14
AT1G11370	chr1_3828411	T/T	3.79±0.61	0.06	3.77E-10	4.94±0.78	0.1	2.48E-10
AT1G14688	chr1_5130918	C/C	0.57±0.25	0.09	2.09E-02	2.23±0.74	0.28	2.67E-03
AT1G19410	chr1_6703778	A/A	3.29±0.62	0.06	1.33E-07	1.99±0.65	0.2	2.23E-03
AT1G22090	chr1_7796024	T/T	3.02±0.68	0.39	8.90E-06	0.19±0.02	0.38	1.52E-15
AT1G27045	chr1_9947683	A/A	2.19±1.1	0.33	4.71E-02	2.06±0.67	0.07	2.02E-03
AT1G33930	chr1_12308998	T/T	0.28±0.04	0.06	4.41E-13	0.22±0.03	0.23	1.01E-13
AT1G34100	chr1_12399605	A/A	19.39±2.32	0.07	6.09E-17	0.27±0.05	0.06	1.30E-07
AT1G48390	chr1_17879580	A/A	0.32±0.07	0.42	8.55E-07	0.55±0.17	0.31	1.63E-03
AT1G50050	chr1_18564085	C/C	2.13±0.97	0.2	2.86E-02	3.44±1.29	0.25	7.68E-03
AT1G51520	chr1_19053511	T/T	0.49±0.15	0.12	8.64E-04	2.01±0.63	0.21	1.34E-03
AT1G51990	chr1_19304765	G/G	2.35±0.5	0.16	2.09E-06	0.36±0.08	0.21	4.87E-06
AT1G61070	chr1_22320587	A/A	0.56±0.27	0.09	4.08E-02	6.46±1.53	0.5	2.47E-05
AT1G62410	chr1_23196263	T/T	2.01±0.58	0.09	5.16E-04	2.75±1.04	0.2	8.20E-03
AT1G64235	chr1_23877480	T/T	3±0.6	0.16	4.59E-07	9.26±1	0.27	1.58E-20
AT1G67010	chr1_24961784	A/A	3.1±0.88	0.26	4.00E-04	0.38±0.13	0.07	4.54E-03
AT1G67148	chr1_25121971	A/A	0.26±0.04	0.53	3.53E-12	2.08±0.65	0.24	1.52E-03
AT1G70020	chr1_26377468	C/C	0.33±0.06	0.06	1.05E-08	2.48±0.52	0.08	1.85E-06
AT1G70870	chr1_26719733	G/G	0.3±0.05	0.12	1.55E-09	0.24±0.05	0.36	5.33E-07
AT1G73120	chr1_27497719	G/G	3.33±0.73	0.06	4.61E-06	4.2±0.75	0.11	2.33E-08
AT1G76830	chr1_28830886	A/A	1.71±0.7	0.26	1.38E-02	6.46±1.53	0.38	2.47E-05
AT1G78030	chr1_29342131	A/A	0.43±0.09	0.32	9.54E-07	4.65±0.64	0.2	3.34E-13
AT2G04830	chr2_1693588	A/A	5.52±0.76	0.19	4.84E-13	2.5±0.73	0.31	5.95E-04
AT2G05117	chr2_1831031	T/T	0.27±0.04	0.19	4.86E-13	0.11±0.02	0.1	1.12E-09
AT2G10260	chr2_3235727	G/G	2.63±0.54	0.19	1.08E-06	0.35±0.13	0.36	7.31E-03
AT2G12935	chr2_5190356	A/A	2.34±0.57	0.3	3.86E-05	2.4±1.07	0.42	2.58E-02
AT2G13128	chr2_5108880	T/T	0.3±0.05	0.64	1.52E-08	0.6±0.29	0.27	3.64E-02
AT2G15930	chr2_6939722	A/A	3.32±0.54	0.06	9.21E-10	4.18±0.82	0.24	3.36E-07
AT2G21045	chr2_8997433	A/A	4.56±0.81	0.06	1.97E-08	4.3±0.76	0.09	1.50E-08
AT2G24165	chr2_10272982	A/A	0.27±0.04	0.05	2.17E-10	0.16±0.02	0.07	3.45E-12
AT2G24735	chr2_10523189	C/C	3.73±0.65	0.06	8.47E-09	3.18±0.61	0.36	2.12E-07
AT2G25169	chr2_10851248	T/T	0.92±6.21	0.29	8.82E-01	5.64±2.05	0.28	5.88E-03
AT2G29000	chr2_12631021	A/A	2.11±0.6	0.42	4.49E-04	2.51±0.77	0.25	1.15E-03
AT2G36550	chr2_15327657	A/A	0.33±0.06	0.53	4.13E-08	0.2±0.05	0.27	9.16E-05
AT2G45940	chr2_18902487	C/C	0.46±0.11	0.12	3.75E-05	0.29±0.08	0.47	5.08E-04
AT3G17150	chr3_5842339	G/G	2.38±0.63	0.46	1.60E-04	2.25±0.89	0.24	1.12E-02
AT3G21570	chr3_7727067	A/A	3.44±0.97	0.54	3.78E-04	1.92±0.58	0.5	8.59E-04
AT3G22940	chr3_8127537	G/G	0.34±0.06	0.21	5.99E-09	0.57±0.2	0.21	4.31E-03
AT3G25719	chr3_9381875	G/G	3.01±0.46	0.22	4.17E-11	0.11±0.01	0.35	4.19E-14
AT3G25720	chr3_9381875	G/G	3.27±0.46	0.22	1.06E-12	0.12±0.02	0.35	1.91E-15
AT3G30214	chr3_11891239	T/T	0.43±0.09	0.43	6.08E-07	3.83±1.08	0.15	3.78E-04
AT3G42786	chr3_14917003	G/G	1.52±0.67	0.38	2.41E-02	4.29±1.41	0.26	2.38E-03
AT3G46482	chr3_17105125	C/C	4.67±0.93	0.06	5.45E-07	3.67±0.61	0.1	1.92E-09
AT3G53840	chr3_19949277	C/C	0.52±0.14	0.39	1.79E-04	0.38±0.08	0.13	1.51E-06
AT3G58480	chr3_21628568	T/T	0.39±0.08	0.31	2.28E-06	0.23±0.03	0.21	2.70E-11
AT3G59180	chr3_21760130	A/A	2.22±0.57	0.07	1.05E-04	1.64±0.7	0.07	1.90E-02
AT3G59190	chr3_22175616	T/T	0.23±0.04	0.22	1.45E-08	0.54±0.27	0.28	4.75E-02
AT3G59620	chr3_22023014	C/C	0.33±0.06	0.06	5.01E-09	0.2±0.08	0.06	1.76E-02
AT3G62760	chr3_23189064	T/T	0.43±0.14	0.11	1.80E-03	1.96±0.9	0.1	2.86E-02
AT4G01190	chr4_506690	C/C	42.47±6.2	0.54	7.44E-12	3.96±0.55	0.36	4.88E-13
AT4G01335	chr4_463836	T/T	2.42±0.97	0.56	1.29E-02	8.81±1.75	0.45	5.11E-07
AT4G01925	chr4_822143	A/A	4.16±0.89	0.08	3.32E-06	2.51±0.63	0.43	6.66E-05
AT4G06536	chr4_3334822	C/C	0.34±0.07	0.09	3.68E-06	0.57±0.26	0.34	2.85E-02
AT4G09012	chr4_5784087	G/G	0.47±0.11	0.29	8.72E-06	3.63±0.86	0.44	2.47E-05
AT4G09600	chr4_6074156	T/T	6.75±1.31	0.2	2.67E-07	1.73±0.64	0.49	6.64E-03

AT4G15053	chr4_8598649	T/T	6.51±1.1	0.57	3.33E-09	5.89±1.02	0.31	8.31E-09
AT4G22390	chr4_11846652	G/G	0.24±0.03	0.06	3.33E-16	0.32±0.07	0.29	1.38E-06
AT4G28790	chr4_14357466	A/A	0.32±0.09	0.4	4.82E-04	3.56±1.79	0.25	4.62E-02
AT5G03820	chr5_1016604	G/G	0.24±0.03	0.2	1.06E-13	0.31±0.1	0.08	2.64E-03
AT5G08460	chr5_2734328	T/T	20±2.28	0.39	2.04E-18	6.24±0.93	0.29	1.62E-11
AT5G14290	chr5_5004746	T/T	1.65±0.58	0.34	4.34E-03	1.7±0.84	0.2	4.21E-02
AT5G22555	chr5_7487426	A/A	0.34±0.06	0.11	3.14E-09	0.38±0.09	0.28	1.33E-05
AT5G22680	chr5_7625326	G/G	0.52±0.15	0.24	5.32E-04	2.56±1.28	0.28	4.50E-02
AT5G24040	chr5_8150163	C/C	3.67±0.79	0.1	3.75E-06	9.03±1.34	0.08	1.74E-11
AT5G24206	chr5_8210609	A/A	4.59±0.9	0.59	3.04E-07	0.14±0.02	0.39	2.96E-09
AT5G34830	chr5_12151563	G/G	0.2±0.03	0.06	7.97E-13	2.26±0.79	0.16	4.03E-03
AT5G36240	chr5_14277903	G/G	3.33±0.89	0.56	1.83E-04	4.52±0.75	0.17	2.17E-09
AT5G37280	chr5_14761553	T/T	4.8±0.85	0.06	1.72E-08	3.66±0.96	0.38	1.32E-04
AT5G38750	chr5_15513299	G/G	0.39±0.08	0.11	2.57E-07	0.38±0.11	0.35	6.96E-04
AT5G40050	chr5_16033285	C/C	2.15±0.57	0.06	1.73E-04	2.12±0.69	0.07	1.99E-03
AT5G41650	chr5_16309822	T/T	0.3±0.08	0.06	1.31E-04	0.35±0.16	0.49	2.82E-02
AT5G47130	chr5_19140035	T/T	0.29±0.04	0.29	5.54E-14	0.51±0.2	0.29	9.35E-03
AT5G48350	chr5_19591922	G/G	3.79±0.72	0.08	1.23E-07	0.26±0.04	0.25	1.38E-12
AT5G49420	chr5_20036039	G/G	21.25±4.8	0.24	9.51E-06	0.4±0.13	0.35	2.81E-03
AT5G54206	chr5_21999241	A/A	0.23±0.03	0.32	2.06E-13	0.36±0.08	0.38	1.09E-05
AT5G59340	chr5_24032779	A/A	0.53±0.16	0.13	1.19E-03	2.03±0.79	0.21	9.83E-03
AT5G60220	chr5_24003551	G/G	0.53±0.15	0.09	6.16E-04	2±0.62	0.23	1.27E-03
AT5G66970	chr5_26741775	C/C	2.02±0.48	0.16	2.56E-05	2.65±0.83	0.21	1.43E-03
AT5G67040	chr5_26756966	C/C	0.53±0.24	0.11	2.80E-02	5.53±0.98	0.22	1.41E-08

[a]SNP: Overlapping SNP between the two datasets; [b]Genotype: Genotype at the coding allele from SCHMITZ data; [c]odds ratio ±SE: log odds ration ± Standard Error from the logistic regression;[d]MAF: Minor Allele Frequency; [e]P-value: nominal P-value from single-SNP association

Table S4: 2,320 eQTL regulating the expression of 2,240 genes expressed in most of the 140 wild-collected *A. thaliana* accessions

Locus	[a]*SNP*	[b]*Type*	[c]*a±SE*	[d]*P-value*	[e]*MAF*	*Annotation*
AT1G80555	chr1_30287050	cis	-0,83±0,09	4,05E-19	0,36	Isocitrate/isopropylmalate-dehydrogenase-family-protein
AT5G28350	chr5_10323384	cis	-0,83±0,09	6,45E-19	0,61	Quinoprotein-amine-dehydrogenase,-beta-chain-like;-RIC1-like-guanyl-nucleotide-exchange-factor
AT3G11220	chr3_3513881	cis	0,78±0,09	1,11E-18	0,46	Paxneb-protein-related
AT5G44570	chr5_17962791	cis	-0,75±0,08	1,48E-18	0,37	
AT3G43210	chr3_15190921	cis	0,77±0,09	3,02E-18	0,36	ATP-binding-microtubule-motor-family-protein
AT3G57460	chr3_21268732	cis	-0,84±0,1	3,39E-18	0,28	catalytics;metal-ion-binding
AT3G61020	chr3_22577967	cis	0,75±0,09	3,67E-18	0,48	
AT3G55170	chr3_20446391	cis	-0,77±0,09	7,02E-18	0,34	Ribosomal-L29-family-protein-
AT5G38260	chr5_15284589	cis	-0,79±0,09	7,25E-18	0,29	Protein-kinase-superfamily-protein
AT3G27997	chr3_10406021	cis	0,77±0,09	1,10E-17	0,41	
AT5G37530	chr5_14906626	cis	-0,76±0,09	1,11E-17	0,34	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT4G17180	chr4_9645974	cis	0,82±0,1	1,17E-17	0,26	O-Glycosyl-hydrolases-family-17-protein
AT4G28220	chr4_13995497	cis	0,75±0,09	1,24E-17	0,41	NAD(P)H-dehydrogenase-B1
AT1G31580	chr1_11313660	cis	-0,73±0,09	1,28E-17	0,52	ECS1
AT4G17240	chr4_9668653	cis	0,74±0,09	1,77E-17	0,47	
AT1G64270	chr1_23852426	cis	-0,86±0,1	1,97E-17	0,25	transposable-element-gene
AT2G38780	chr2_16206381	cis	0,8±0,09	3,19E-17	0,29	
AT4G14590	chr4_8374711	cis	-0,73±0,09	4,30E-17	0,39	embryo-defective-2739
AT1G12790	chr1_4361386	cis	-0,74±0,09	4,91E-17	0,39	
AT3G46710	chr3_17212160	cis	0,75±0,09	5,10E-17	0,39	NB-ARC-domain-containing-disease-resistance-protein
AT5G27110	chr5_9540150	cis	0,74±0,09	6,91E-17	0,36	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT2G39110	chr2_16319245	cis	-0,85±0,1	7,48E-17	0,27	Protein-kinase-superfamily-protein
AT2G21640	chr2_9249267	cis	0,72±0,09	8,01E-17	0,45	
AT2G44690	chr2_18428322	cis	0,72±0,09	1,09E-16	0,42	Arabidopsis-RAC-like-9
AT2G28460	chr2_12166333	cis	-0,71±0,09	1,20E-16	0,50	Cysteine/Histidine-rich-C1-domain-family-protein
AT4G21460	chr4_11429464	cis	0,79±0,1	1,24E-16	0,27	Ribosomal-protein-S24/S35,-mitochondrial
AT5G36930	chr5_14590245	cis	0,88±0,11	1,32E-16	0,22	Disease-resistance-protein-(TIR-NBS-LRR-class)-family
AT3G54366	chr3_20133288	cis	0,77±0,09	1,84E-16	0,53	
AT1G49630	chr1_18368655	cis	0,74±0,09	2,64E-16	0,47	presequence-protease-2
AT3G46658	chr3_17189218	cis	-0,76±0,09	2,68E-16	0,31	other-RNA
AT3G44280	chr3_15968886	cis	-0,79±0,1	3,03E-16	0,29	
AT1G13780	chr1_4725940	cis	0,8±0,1	3,04E-16	0,30	F-box/RNI-like/FBD-like-domains-containing-protein
AT2G19400	chr2_8403801	cis	-0,71±0,09	3,07E-16	0,44	AGC-(cAMP-dependent,-cGMP-dependent-and-protein-kinase-C)-kinase-family-protein
AT5G51470	chr5_20906654	cis	0,73±0,09	3,18E-16	0,34	Auxin-responsive-GH3-family-protein
AT3G59600	chr3_22018007	cis	-0,75±0,09	3,60E-16	0,32	RNA-polymerase-Rpb8
AT4G22960	chr4_12033401	cis	0,81±0,1	3,86E-16	0,30	Protein-of-unknown-function-(DUF544)-----
AT5G45428	chr5_18408354	cis	-0,72±0,09	4,06E-16	0,46	conserved-peptide-upstream-open-reading-frame-24
AT4G37170	chr4_17502758	cis	0,72±0,09	4,53E-16	0,31	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT3G21100	chr3_7401258	cis	0,76±0,09	5,18E-16	0,29	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT4G18750	chr4_10304955	cis	0,71±0,09	5,24E-16	0,46	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT1G66930	chr1_24960780	cis	0,71±0,09	5,30E-16	0,51	Protein-kinase-superfamily-protein
AT1G30420	chr1_10748282	cis	-0,72±0,09	6,06E-16	0,42	multidrug-resistance-associated-protein-12
AT1G73940	chr1_27798005	cis	0,75±0,09	6,25E-16	0,29	
AT5G45480	chr5_18427115	cis	0,73±0,09	6,57E-16	0,41	Protein-of-unknown-function-(DUF594)
AT4G16710	chr4_9397913	cis	0,72±0,09	7,87E-16	0,33	glycosyltransferase-family-protein-28
AT3G07525	chr3_2398863	cis	-0,68±0,08	8,25E-16	0,51	autophagocytosis-associated-family-protein
AT3G08980	chr3_2740857	cis	0,79±0,1	8,88E-16	0,29	Peptidase-S24/S26A/S26B/S26C-family-protein
AT1G22440	chr1_7922907	cis	0,7±0,09	1,12E-15	0,46	Zinc-binding-alcohol-dehydrogenase-family-protein
AT2G23672	chr2_10063693	cis	0,72±0,09	1,13E-15	0,39	other-RNA
AT2G13665	chr3_11216048	trans	0,71±0,09	1,24E-15	0,45	other-RNA
AT2G01870	chr2_389440	cis	-0,73±0,09	1,45E-15	0,37	
AT2G05755	chr2_2171352	cis	0,72±0,09	1,48E-15	0,33	Nodulin-MtN21-/EamA-like-transporter-family-protein
AT5G08120	chr5_2596249	cis	0,71±0,09	1,60E-15	0,49	movement-protein-binding-protein-2C
AT1G48740	chr1_18025758	cis	-0,67±0,08	1,63E-15	0,46	2-oxoglutarate-(2OG)-and-Fe(II)-dependent-oxygenase-superfamily-protein
AT4G27370	chr4_13697729	cis	-0,7±0,09	1,65E-15	0,36	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT1G67365	chr1_25237465	cis	-0,82±0,1	1,82E-15	0,24	other-RNA
AT5G21060	chr5_7150004	cis	-0,82±0,1	1,86E-15	0,24	Glyceraldehyde-3-phosphate-dehydrogenase-like-family-protein
AT4G19830	chr4_10773603	cis	-0,69±0,09	1,86E-15	0,37	FKBP-like-peptidyl-prolyl-cis-trans-isomerase-family-protein
AT2G04170	chr2_1422823	cis	0,75±0,09	1,92E-15	0,34	TRAF-like-family-protein
AT5G45510	chr5_18425889	cis	0,77±0,1	1,93E-15	0,31	Leucine-rich-repeat-(LRR)-family-protein
AT2G16530	chr2_7161753	cis	-0,8±0,1	1,97E-15	0,31	3-oxo-5-alpha-steroid-4-dehydrogenase-family-protein
AT2G30480	chr2_12982265	cis	-0,84±0,11	2,02E-15	0,24	
AT1G12340	chr1_4220424	cis	0,77±0,1	2,04E-15	0,32	Cornichon-family-protein
AT2G35810	chr2_15044781	cis	-0,75±0,09	2,10E-15	0,34	
AT4G21900	chr4_11614996	cis	0,76±0,1	2,26E-15	0,33	proteinaceous-RNase-P-3
AT3G12040	chr3_3837428	cis	-0,74±0,09	2,41E-15	0,39	DNA-3-methyladenine-glycosylase-(MAG)
AT3G29290	chr3_11238348	cis	-0,81±0,1	2,42E-15	0,25	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT2G40240	chr2_16810960	cis	-0,77±0,1	2,75E-15	0,28	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT1G03905	chr1_993375	cis	0,79±0,1	2,87E-15	0,26	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT4G09680	chr4_6119455	cis	0,71±0,09	2,95E-15	0,37	conserved-telomere-maintenance-component-1
AT5G37410	chr5_14835977	cis	-0,72±0,09	3,00E-15	0,29	Family-of-unknown-function-(DUF577)
AT1G63210	chr1_23443274	cis	0,74±0,09	3,19E-15	0,32	Transcription-elongation-factor-Spt6
AT3G44100	chr3_15866682	cis	-0,69±0,09	3,22E-15	0,50	MD-2-related-lipid-recognition-domain-containing-protein
AT5G42460	chr5_16978784	cis	-0,82±0,1	3,47E-15	0,22	F-box-and-associated-interaction-domains-containing-protein
AT1G11320	chr1_3808391	cis	-0,69±0,09	3,65E-15	0,52	
AT1G11800	chr1_3987293	cis	-0,79±0,1	3,74E-15	0,26	endonuclease/exonuclease/phosphatase-family-protein
AT3G09680	chr5_695868	trans	0,74±0,09	3,92E-15	0,38	Ribosomal-protein-S12/S23-family-protein

AT5G28390	chr5_10348548	cis	0,89±0,11	4,03E-15	0,18	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT2G22905	chr2_9748570	cis	0,67±0,09	4,06E-15	0,51	Expressed-protein
AT4G39660	chr4_18406370	cis	0,83±0,11	4,38E-15	0,23	alanine:glyoxylate-aminotransferase-2
AT2G18100	chr2_7868173	cis	-0,7±0,09	4,42E-15	0,51	Protein-of-unknown-function-(DUF726)
AT4G16990	chr4_9568061	cis	-0,87±0,11	4,55E-15	0,17	disease-resistance-protein-(TIR-NBS-class),-putative
AT4G36650	chr4_17286479	cis	0,69±0,09	4,57E-15	0,46	plant-specific-TFIIB-related-protein
AT5G50350	chr5_20499378	cis	-0,74±0,09	5,12E-15	0,33	
AT5G17060	chr5_5610876	cis	-0,78±0,1	5,21E-15	0,24	ADP-ribosylation-factor-B1B
AT5G43660	chr5_17538051	cis	0,68±0,09	5,30E-15	0,41	2-oxoglutarate-(2OG)-and-Fe(II)-dependent-oxygenase-superfamily-protein
AT3G43430	chr3_15355282	cis	0,71±0,09	5,40E-15	0,34	RING/U-box-superfamily-protein
AT5G23235	chr5_7826249	cis	-0,67±0,09	5,55E-15	0,41	
AT3G47290	chr3_17392402	cis	0,7±0,09	5,63E-15	0,46	phosphatidylinositol-speciwc-phospholipase-C8
AT1G58270	chr1_21607764	cis	0,71±0,09	5,64E-15	0,35	TRAF-like-family-protein
AT1G45616	chr1_17186607	cis	0,7±0,09	5,73E-15	0,57	receptor-like-protein-6
AT4G19520	chr4_10655911	cis	-0,67±0,09	5,87E-15	0,44	disease-resistance-protein-(TIR-NBS-LRR-class)-family
AT2G14285	chr2_6054717	cis	-0,7±0,09	5,88E-15	0,46	Small-nuclear-ribonucleoprotein-family-protein
AT4G00980	chr4_421194	cis	0,81±0,1	5,90E-15	0,33	zinc-knuckle-(CCHC-type)-family-protein
AT4G03635	chr4_1610306	cis	0,81±0,1	6,09E-15	0,27	
AT4G03635	chr4_2782400	trans	0,81±0,1	6,09E-15	0,27	
AT3G27883	chr3_10969380	trans	-0,89±0,11	6,59E-15	0,16	transposable-element-gene
AT3G20130	chr3_7026006	cis	0,76±0,1	6,93E-15	0,30	cytochrome-P450,-family-705,-subfamily-A,-polypeptide-22
AT1G33990	chr1_12356041	cis	0,71±0,09	7,10E-15	0,36	methyl-esterase-14
AT4G11630	chr4_7023030	cis	0,7±0,09	7,56E-15	0,31	Ribosomal-protein-L19-family-protein
AT1G23470	chr1_8330782	cis	0,68±0,09	7,92E-15	0,51	
AT5G66960	chr5_26739679	cis	0,7±0,09	8,96E-15	0,51	Prolyl-oligopeptidase-family-protein
AT1G19396	chr1_6703658	cis	-0,77±0,1	8,97E-15	0,31	
AT1G57590	chr1_21330272	cis	-0,68±0,09	9,15E-15	0,36	Pectinacetylesterase-family-protein
AT1G23940	chr1_8441984	cis	0,68±0,09	9,18E-15	0,55	ARM-repeat-superfamily-protein
AT5G25230	chr5_8742785	cis	0,81±0,1	9,34E-15	0,25	Ribosomal-protein-S5/Elongation-factor-G/III/V-family-protein
AT5G45040	chr5_18174178	cis	-0,71±0,09	1,07E-14	0,40	Cytochrome-c
AT1G23960	chr1_8481111	cis	0,69±0,09	1,08E-14	0,36	Protein-of-unknown-function-(DUF626)
AT3G45860	chr3_16867335	cis	-0,75±0,1	1,13E-14	0,29	cysteine-rich-RLK-(RECEPTOR-like-protein-kinase)-4
AT5G15760	chr5_5142587	cis	-0,7±0,09	1,20E-14	0,59	Ribosomal-protein-PSRP-3/Ycf65
AT4G01915	chr4_833857	cis	0,72±0,09	1,22E-14	0,34	
AT1G04090	chr1_1056228	cis	0,7±0,09	1,44E-14	0,32	Plant-protein-of-unknown-function-(DUF946)
AT4G19500	chr4_10619181	cis	0,8±0,1	1,50E-14	0,22	nucleoside-triphosphatases;transmembrane-receptors;nucleotide-binding;ATP-binding
AT1G23140	chr1_8202964	cis	-0,74±0,1	1,53E-14	0,29	Calcium-dependent-lipid-binding-(CaLB-domain)-family-protein
AT4G19510	chr4_10622367	cis	0,67±0,09	1,59E-14	0,56	Disease-resistance-protein-(TIR-NBS-LRR-class)
AT3G30875	chr3_12655676	cis	0,71±0,09	1,72E-14	0,46	
AT5G54290	chr5_22054713	cis	-0,72±0,09	1,73E-14	0,31	cytochrome-c-biogenesis-protein-family
AT4G16800	chr4_9455662	cis	0,69±0,09	1,76E-14	0,34	ATP-dependent-caseinolytic-(Clp)-protease/crotonase-family-protein
AT1G65540	chr1_24365326	cis	0,69±0,09	1,86E-14	0,37	LETM1-like-protein
AT5G10400	chr5_3272353	cis	-0,81±0,11	1,88E-14	0,26	Histone-superfamily-protein
AT5G45730	chr5_18552017	cis	0,76±0,1	1,90E-14	0,24	Cysteine/Histidine-rich-C1-domain-family-protein
AT3G61480	chr5_10323384	trans	-0,71±0,09	1,98E-14	0,61	Quinoprotein-amine-dehydrogenase,-beta-chain-like;-RIC1-like-guanyl-nucleotide-exchange-factor
AT1G02050	chr1_360888	cis	-0,75±0,1	2,03E-14	0,29	Chalcone-and-stilbene-synthase-family-protein
AT5G42930	chr5_17213357	cis	0,69±0,09	2,04E-14	0,35	alpha/beta-Hydrolases-superfamily-protein
AT5G42730	chr5_7888582	trans	0,72±0,09	2,07E-14	0,39	
AT4G27585	chr4_13770278	cis	0,66±0,09	2,11E-14	0,50	SPFH/Band-7/PHB-domain-containing-membrane-associated-protein-family
AT1G35112	chr5_18407914	trans	0,78±0,1	2,28E-14	0,20	transposable-element-gene
AT5G27230	chr5_9589751	cis	0,7±0,09	2,36E-14	0,30	Frigida-like-protein
AT5G41580	chr5_16635453	cis	0,66±0,09	2,47E-14	0,49	RING/U-box-superfamily-protein
AT3G44430	chr3_16071143	cis	0,71±0,09	2,55E-14	0,32	
AT5G44582	chr5_17980151	cis	0,71±0,09	2,55E-14	0,29	
AT5G17900	chr5_5907963	cis	-0,66±0,09	2,79E-14	0,51	microfibrillar-associated-protein-related
AT1G02300	chr1_449560	cis	-0,82±0,11	2,81E-14	0,24	Cysteine-proteinases-superfamily-protein
AT1G77960	chr1_29313634	cis	0,67±0,09	2,97E-14	0,41	
AT5G35930	chr5_14074359	cis	-0,66±0,09	3,41E-14	0,51	AMP-dependent-synthetase-and-ligase-family-protein
AT5G44870	chr5_18135644	cis	-0,91±0,12	3,45E-14	0,16	Disease-resistance-protein-(TIR-NBS-LRR-class)-family
AT4G13920	chr4_8043290	cis	-0,71±0,09	3,54E-14	0,29	receptor-like-protein-50
AT5G20580	chr5_6963670	cis	0,79±0,1	3,55E-14	0,50	
AT1G55000	chr1_20513401	cis	-0,81±0,11	3,65E-14	0,21	peptidoglycan-binding-LysM-domain-containing-protein
AT5G28442	chr5_10322650	cis	0,7±0,09	4,07E-14	0,36	
AT5G28340	chr5_10348548	cis	0,83±0,11	4,40E-14	0,18	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT5G41260	chr5_16503811	cis	-0,8±0,11	4,52E-14	0,20	Protein-kinase-protein-with-tetratricopeptide-repeat-domain
AT4G11000	chr4_6731977	cis	0,74±0,1	4,53E-14	0,25	Ankyrin-repeat-family-protein
AT5G11580	chr5_3721190	cis	-0,87±0,12	4,61E-14	0,18	Regulator-of-chromosome-condensation-(RCC1)-family-protein
AT5G28330	chr5_10348548	cis	0,84±0,11	4,62E-14	0,18	
AT3G28715	chr3_10773240	cis	0,8±0,11	4,75E-14	0,20	ATPase,-V0/A0-complex,-subunit-C/D
AT3G02700	chr3_582610	cis	0,76±0,1	5,43E-14	0,24	NC-domain-containing-protein-related
AT1G49980	chr1_18507818	cis	-0,69±0,09	5,59E-14	0,35	DNA/RNA-polymerases-superfamily-protein
AT1G04590	chr1_1259655	cis	0,66±0,09	5,89E-14	0,43	
AT5G23410	chr5_7888582	cis	0,7±0,09	6,48E-14	0,39	
AT4G26170	chr4_13258607	cis	0,72±0,1	6,59E-14	0,27	
AT4G21480	chr4_11434031	cis	-0,66±0,09	6,60E-14	0,39	sugar-transporter-protein-12
AT5G27210	chr5_9575184	cis	-0,75±0,1	6,65E-14	0,24	Protein-of-unknown-function,-transmembrane-40
AT5G41950	chr5_16783931	cis	-0,93±0,12	6,71E-14	0,16	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT3G52950	chr3_19634392	cis	0,66±0,09	7,21E-14	0,44	CBS-/-octicosapeptide/Phox/Bemp1-(PB1)-domains-containing-protein
AT5G05230	chr5_1551994	cis	-0,73±0,1	7,46E-14	0,31	RING/U-box-superfamily-protein

AT1G35560	chr1_13116559	cis	0,68±0,09	7,48E-14	0,31	TCP-family-transcription-factor-
AT5G49970	chr5_20333567	cis	-0,81±0,11	7,55E-14	0,22	pyridoxin-(pyrodoxamine)-5'-phosphate-oxidase
AT5G02740	chr5_616527	cis	-0,65±0,09	7,82E-14	0,43	Ribosomal-protein-S24e-family-protein
AT4G14400	chr4_8297587	cis	-0,67±0,09	7,82E-14	0,33	ankyrin-repeat-family-protein
AT4G14030	chr4_8098226	cis	-0,71±0,09	7,95E-14	0,33	selenium-binding-protein-1
AT5G41850	chr5_16757604	cis	-0,64±0,09	8,16E-14	0,41	alpha/beta-Hydrolases-superfamily-protein
AT3G44740	chr3_16298344	cis	0,82±0,11	8,21E-14	0,19	Class-II-aaRS-and-biotin-synthetases-superfamily-protein
AT5G33400	chr5_12360116	trans	0,76±0,1	8,56E-14	0,44	
AT5G03420	chr5_845287	cis	-0,7±0,09	8,64E-14	0,31	5'-AMP-activated-protein-kinase-related
AT4G20920	chr4_11201042	cis	0,75±0,1	8,82E-14	0,25	double-stranded-RNA-binding-domain-(DsRBD)-containing-protein
AT1G31910	chr1_11458878	cis	0,61±0,08	8,83E-14	0,49	GHMP-kinase-family-protein
AT1G19485	chr1_6744457	cis	0,81±0,11	1,10E-13	0,29	Transducin/WD40-repeat-like-superfamily-protein
AT2G41460	chr2_17288582	cis	-0,8±0,11	1,14E-13	0,20	apurinic-endonuclease-redox-protein
AT3G25440	chr3_9224929	cis	0,76±0,1	1,20E-13	0,31	RNA-binding-CRS1-/-YhbY-(CRM)-domain-protein
AT1G69485	chr1_26119245	cis	-0,72±0,1	1,25E-13	0,29	Ribosomal-L32p-protein-family
AT3G22850	chr3_8087828	cis	-0,92±0,12	1,36E-13	0,19	Aluminium-induced-protein-with-YGL-and-LRDR-motifs
AT5G45490	chr5_18425889	cis	0,7±0,09	1,37E-13	0,31	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT5G45500	chr5_18425889	cis	0,7±0,09	1,37E-13	0,31	RNI-like-superfamily-protein
AT3G47300	chr3_17437885	cis	0,69±0,09	1,38E-13	0,32	SELT-like-protein-precursor
AT4G15330	chr4_8753954	cis	-0,78±0,11	1,39E-13	0,23	cytochrome-P450,-family-705,-subfamily-A,-polypeptide-1
AT1G61980	chr1_22909598	cis	0,84±0,11	1,40E-13	0,16	Mitochondrial-transcription-termination-factor-family-protein
AT5G58980	chr5_23812400	cis	0,74±0,1	1,48E-13	0,25	Neutral/alkaline-non-lysosomal-ceramidase
AT3G60980	chr3_22577967	cis	0,61±0,08	1,52E-13	0,48	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT5G20450	chr5_6919465	cis	0,64±0,09	1,53E-13	0,39	
AT4G31530	chr4_15284066	cis	-0,69±0,09	1,54E-13	0,34	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT4G21760	chr4_11561162	cis	0,65±0,09	1,56E-13	0,50	beta-glucosidase-47
AT2G27960	chr2_11910888	cis	-0,81±0,11	1,62E-13	0,22	cyclin-dependent-kinase-subunit-1
AT5G45050	chr5_18187250	cis	0,8±0,11	1,62E-13	0,22	Disease-resistance-protein-(TIR-NBS-LRR-class)
AT2G15042	chr2_6508008	cis	-0,75±0,1	1,71E-13	0,27	Leucine-rich-repeat-(LRR)-family-protein
AT2G47210	chr2_19378842	cis	0,69±0,09	1,71E-13	0,38	myb-like-transcription-factor-family-protein
AT2G25580	chr2_10887602	cis	-0,71±0,1	1,74E-13	0,45	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT5G28320	chr5_10348548	cis	0,83±0,11	1,83E-13	0,18	
AT5G16220	chr5_5301375	cis	-0,66±0,09	1,85E-13	0,44	Octicosapeptide/Phox/Bem1p-family-protein
AT1G19070	chr1_6584025	cis	-0,67±0,09	1,89E-13	0,31	F-box-family-protein
AT4G03060	chr4_1341870	cis	-0,68±0,09	2,07E-13	0,26	AOP2-(ALKENYL-HYDROXALKYL-PRODUCING-2);-oxidoreductase,-acting-on-paired-donors,-with-incorporation-or-reduction-of-molecular-oxygen,-2-oxoglutarate-as-one-donor,-and-incorporation-of-one-atom-each-of-oxygen-into-both-donors
AT3G06145	chr3_1861208	cis	0,66±0,09	2,07E-13	0,39	
AT5G25640	chr5_8968191	cis	0,76±0,1	2,19E-13	0,21	Rhomboid-related-intramembrane-serine-protease-family-protein
AT5G28400	chr5_10348548	cis	0,82±0,11	2,25E-13	0,18	
AT1G25260	chr1_8855262	cis	0,65±0,09	2,25E-13	0,44	Ribosomal-protein-L10-family-protein
AT1G09995	chr1_3257815	cis	-0,74±0,1	2,27E-13	0,30	DNA-repair-DEAD-helicase-RAD3/XP-D-subfamily-protein
AT4G21880	chr4_11607385	cis	0,73±0,1	2,37E-13	0,26	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT5G42920	chr5_17206718	cis	0,67±0,09	2,38E-13	0,29	THO-complex,--subunit-5
AT2G02590	chr2_702791	cis	0,7±0,1	2,38E-13	0,27	
AT1G14700	chr1_5057590	cis	-0,79±0,11	2,41E-13	0,26	purple-acid-phosphatase-3
AT5G45720	chr5_18549293	cis	0,73±0,1	2,43E-13	0,27	AAA-type-ATPase-family-protein
AT1G27560	chr1_9566485	cis	-0,6±0,08	2,69E-13	0,40	
AT5G45130	chr5_18245912	cis	0,69±0,09	2,69E-13	0,32	RAB-homolog-1
AT5G43940	chr5_17684842	cis	-0,62±0,08	2,73E-13	0,51	GroES-like-zinc-binding-dehydrogenase-family-protein
AT3G21080	chr3_7384837	cis	-0,77±0,1	2,74E-13	0,23	ABC-transporter-related
AT4G01270	chr4_531859	cis	0,88±0,12	2,74E-13	0,17	RING/U-box-superfamily-protein
AT4G03230	chr4_1424372	cis	0,63±0,09	2,85E-13	0,47	S-locus-lectin-protein-kinase-family-protein
AT5G25910	chr5_9037698	cis	0,77±0,1	2,87E-13	0,21	receptor-like-protein-52
AT1G09830	chr1_3192604	cis	0,64±0,09	2,92E-13	0,45	Glycinamide-ribonucleotide-(GAR)-synthetase
AT5G41910	chr5_16779280	cis	-0,62±0,09	3,00E-13	0,48	Mediator-complex,-subunit-Med10
AT2G24690	chr2_10499307	cis	-0,72±0,1	3,04E-13	0,29	Transcriptional-factor-B3-family-protein
AT1G63855	chr1_23699933	cis	-0,78±0,11	3,09E-13	0,20	Putative-methyltransferase-family-protein
AT5G33400	chr5_13020995	trans	0,75±0,1	3,11E-13	0,44	
AT1G03410	chr1_821772	cis	0,69±0,1	3,12E-13	0,34	2-oxoglutarate-(2OG)-and-Fe(II)-dependent-oxygenase-superfamily-protein
AT3G49180	chr3_18229388	cis	-0,64±0,09	3,29E-13	0,41	Transducin/WD40-repeat-like-superfamily-protein
AT4G19410	chr4_10582176	cis	-0,67±0,09	3,49E-13	0,36	Pectinacetylesterase-family-protein
AT1G14520	chr1_4969398	cis	-0,9±0,12	3,51E-13	0,15	myo-inositol-oxygenase-1
AT2G46930	chr2_19283244	cis	0,73±0,1	3,78E-13	0,22	Pectinacetylesterase-family-protein
AT1G66860	chr1_24943021	cis	-0,65±0,09	3,79E-13	0,41	Class-I-glutamine-amidotransferase-like-superfamily-protein
AT1G30740	chr1_10902868	cis	-0,62±0,09	3,81E-13	0,51	FAD-binding-Berberine-family-protein
AT4G12670	chr4_7468587	cis	-0,61±0,08	3,81E-13	0,49	Homeodomain-like-superfamily-protein
AT1G01690	chr1_249475	cis	-0,66±0,09	3,83E-13	0,48	putative-recombination-initiation-defects-3
AT5G47510	chr5_19280615	cis	-0,64±0,09	3,89E-13	0,37	Sec14p-like-phosphatidylinositol-transfer-family-protein
AT4G27080	chr4_13553783	cis	0,74±0,1	3,94E-13	0,26	PDI-like-5-4
AT1G19690	chr1_6810785	cis	0,66±0,09	4,00E-13	0,41	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT2G25510	chr2_10856538	cis	-0,65±0,09	4,16E-13	0,41	
AT4G09430	chr4_5974237	cis	-0,78±0,11	4,21E-13	0,20	Disease-resistance-protein-(TIR-NBS-LRR-class)-family
AT4G38100	chr4_17886975	cis	0,65±0,09	4,36E-13	0,46	
AT1G29820	chr1_10433128	cis	-0,71±0,1	4,61E-13	0,30	Magnesium-transporter-CorA-like-family-protein
AT3G02900	chr3_647521	cis	0,69±0,1	4,67E-13	0,42	
AT5G26160	chr5_9142426	cis	0,62±0,09	4,76E-13	0,57	
AT5G23010	chr5_7700167	cis	-0,67±0,09	4,86E-13	0,25	methylthioalkylmalate-synthase-1
AT2G38720	chr2_16167438	cis	0,78±0,11	4,90E-13	0,20	microtubule-associated-protein-65-5
AT3G56460	chr3_20923532	cis	-0,73±0,1	4,99E-13	0,25	GroES-like-zinc-binding-alcohol-dehydrogenase-family-protein
AT2G43920	chr2_18191504	cis	-0,69±0,09	5,02E-13	0,31	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein

AT1G66100	chr1_24609666	cis	0,79±0,11	5,10E-13	0,21	Plant-thionin
AT1G77720	chr1_29210222	cis	0,8±0,11	5,30E-13	0,19	putative-protein-kinase-1
AT1G01355	chr1_136383	cis	-0,67±0,09	5,35E-13	0,48	Putative-endonuclease-or-glycosyl-hydrolase
AT1G59780	chr1_21994094	cis	0,82±0,11	5,63E-13	0,15	NB-ARC-domain-containing-disease-resistance-protein
AT1G16820	chr1_5756373	cis	-0,81±0,11	5,80E-13	0,19	vacuolar-ATP-synthase-catalytic-subunit-related-/-V-ATPase-related-/-vacuolar-proton-pump-related
AT5G63620	chr5_25468341	cis	-0,68±0,09	5,91E-13	0,47	GroES-like-zinc-binding-alcohol-dehydrogenase-family-protein
AT2G26750	chr2_11393446	cis	-0,62±0,09	5,94E-13	0,38	alpha/beta-Hydrolases-superfamily-protein
AT1G02260	chr1_442418	cis	-0,67±0,09	5,97E-13	0,33	Divalent-ion-symporter
AT1G66530	chr1_24823755	cis	0,61±0,08	5,99E-13	0,46	Arginyl-tRNA-synthetase,-class-Ic
AT1G58280	chr1_21614442	cis	0,66±0,09	5,99E-13	0,39	Phosphoglycerate-mutase-family-protein
AT2G46450	chr2_19069130	cis	-0,72±0,1	6,43E-13	0,23	cyclic-nucleotide-gated-channel-12
AT4G18930	chr4_10370636	cis	-0,85±0,12	6,48E-13	0,18	RNA-ligase/cyclic-nucleotide-phosphodiesterase-family-protein
AT5G48020	chr5_19470007	cis	-0,72±0,1	6,70E-13	0,31	2-oxoglutarate-(2OG)-and-Fe(II)-dependent-oxygenase-superfamily-protein
AT4G13918	chr4_8047254	cis	-0,59±0,08	6,79E-13	0,43	
AT2G45150	chr2_18613863	cis	0,81±0,11	6,95E-13	0,21	cytidinediphosphate-diacylglycerol-synthase-4
AT3G48260	chr3_17875002	cis	0,61±0,09	7,22E-13	0,45	with-no-lysine-(K)-kinase-3
AT4G12680	chr4_7467417	cis	-0,61±0,09	7,32E-13	0,45	
AT1G24240	chr1_8586603	cis	0,65±0,09	7,66E-13	0,34	Ribosomal-protein-L19-family-protein
AT4G12520	chr4_7415194	cis	-0,69±0,1	7,71E-13	0,24	Bifunctional-inhibitor/lipid-transfer-protein/seed-storage-2S-albumin-superfamily-protein
AT1G28620	chr1_10062524	cis	-0,94±0,13	7,75E-13	0,14	
AT3G28140	chr3_10469441	cis	0,69±0,1	7,79E-13	0,29	RNA-ligase/cyclic-nucleotide-phosphodiesterase-family-protein
AT4G20340	chr4_10983382	cis	-0,68±0,09	7,83E-13	0,31	Transcription-factor-TFIIE,-alpha-subunit
AT2G04800	chr2_1688172	cis	-0,7±0,1	7,85E-13	0,24	
AT1G12390	chr1_4222207	cis	-0,67±0,09	7,88E-13	0,34	Cornichon-family-protein
AT1G53830	chr1_20101000	cis	-0,64±0,09	8,01E-13	0,40	pectin-methylesterase-2
AT5G10600	chr5_3352806	cis	-0,75±0,11	8,05E-13	0,22	cytochrome-P450,-family-81,-subfamily-K,-polypeptide-2
AT1G65200	chr1_24222811	cis	-0,91±0,13	8,14E-13	0,14	Ubiquitin-carboxyl-terminal-hydrolase-related-protein
AT2G35520	chr2_14920429	cis	-0,68±0,09	8,23E-13	0,36	Defender-against-death-(DAD-family)-protein
AT3G46530	chr3_17133077	cis	-0,62±0,09	8,62E-13	0,40	NB-ARC-domain-containing-disease-resistance-protein
AT2G21860	chr2_9305442	cis	0,88±0,12	8,62E-13	0,14	violaxanthin-de-epoxidase-related
AT1G51538	chr1_19112612	cis	0,91±0,13	8,64E-13	0,12	Aminotransferase-like,-plant-mobile-domain-family-protein
AT4G00650	chr4_259252	cis	-0,83±0,12	8,78E-13	0,22	FRIGIDA-like-protein
AT2G29570	chr2_12641575	cis	-0,61±0,08	8,87E-13	0,37	proliferating-cell-nuclear-antigen-2
AT3G61010	chr3_22577967	cis	0,62±0,09	8,92E-13	0,48	Ferritin/ribonucleotide-reductase-like-family-protein
AT1G16130	chr1_5520044	cis	-0,9±0,13	8,97E-13	0,14	wall-associated-kinase-like-2
AT3G49050	chr3_18179526	cis	-0,65±0,09	9,14E-13	0,32	alpha/beta-Hydrolases-superfamily-protein
AT5G41960	chr5_16780285	cis	-0,83±0,12	9,17E-13	0,17	
AT5G42530	chr5_17002945	cis	-0,92±0,13	9,22E-13	0,14	
AT5G25800	chr5_8982250	cis	0,71±0,1	9,35E-13	0,26	Polynucleotidyl-transferase,-ribonuclease-H-like-superfamily-protein
AT5G48340	chr5_19591922	cis	-0,75±0,1	9,87E-13	0,26	
AT1G74280	chr1_27930080	cis	-0,62±0,09	1,02E-12	0,39	alpha/beta-Hydrolases-superfamily-protein
AT1G65370	chr1_24285650	cis	0,59±0,08	1,03E-12	0,44	TRAF-like-family-protein
AT4G19070	chr4_10451283	cis	-0,72±0,1	1,04E-12	0,29	Putative-membrane-lipoprotein
AT5G38020	chr5_15165080	cis	-0,62±0,09	1,05E-12	0,44	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein
AT5G03495	chr5_16706120	trans	0,6±0,08	1,05E-12	0,51	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT4G05530	chr4_2817353	cis	-0,67±0,09	1,07E-12	0,39	indole-3-butyric-acid-response-1
AT5G38860	chr5_15559675	cis	-0,74±0,1	1,09E-12	0,24	BES1-interacting-Myc-like-protein-3
AT1G05830	chr1_1753743	cis	-0,65±0,09	1,12E-12	0,50	trithorax-like-protein-2
AT4G37120	chr4_17489547	cis	-0,77±0,11	1,12E-12	0,19	Pre-mRNA-splicing-Prp18-interacting-factor
AT3G60480	chr3_22348103	cis	-0,67±0,09	1,12E-12	0,29	
AT4G15960	chr4_9047223	cis	0,82±0,12	1,15E-12	0,16	alpha/beta-Hydrolases-superfamily-protein
AT5G24310	chr5_8273614	cis	-0,62±0,09	1,15E-12	0,47	ABL-interactor-like-protein-3
AT5G47810	chr5_19348410	cis	0,63±0,09	1,21E-12	0,44	phosphofructokinase-2
AT1G48960	chr1_18112039	cis	-0,73±0,1	1,22E-12	0,26	Adenine-nucleotide-alpha-hydrolases-like-superfamily-protein
AT3G04181	chr3_1099944	cis	-0,84±0,12	1,24E-12	0,16	
AT2G42160	chr2_17574128	cis	0,77±0,11	1,26E-12	0,19	zinc-finger-(ubiquitin-hydrolase)-domain-containing-protein
AT1G26200	chr1_9064978	cis	0,72±0,1	1,29E-12	0,24	TRAM,-LAG1-and-CLN8-(TLC)-lipid-sensing-domain-containing-protein
AT5G35796	chr5_13969400	cis	-0,64±0,09	1,29E-12	0,58	
AT2G40570	chr2_16940810	cis	0,85±0,12	1,34E-12	0,18	initiator-tRNA-phosphoribosyl-transferase-family-protein
AT2G02770	chr2_772832	cis	-0,64±0,09	1,46E-12	0,37	4'-phosphopantetheinyl-transferase-superfamily
AT5G35530	chr5_13711886	cis	-0,71±0,1	1,49E-12	0,32	Ribosomal-protein-S3-family-protein
AT5G43830	chr5_17624441	cis	0,55±0,08	1,53E-12	0,50	Aluminium-induced-protein-with-YGL-and-LRDR-motifs
AT5G53220	chr5_21595969	cis	-0,7±0,1	1,57E-12	0,29	
AT5G59770	chr5_24080644	cis	-0,75±0,11	1,61E-12	0,22	Protein-tyrosine-phosphatase-like,-PTPLA
AT4G19100	chr4_10453802	cis	0,82±0,12	1,63E-12	0,21	Protein-of-unknown-function-(DUF3464)
AT4G13640	chr4_7939172	cis	-0,87±0,12	1,65E-12	0,14	Homeodomain-like-superfamily-protein
AT2G09970	chr1_27304145	trans	-0,62±0,09	1,66E-12	0,41	Protein-of-unknown-function-(DUF1677)
AT1G52980	chr1_19738355	cis	0,61±0,09	1,70E-12	0,44	GTP-binding-family-protein
AT4G29550	chr4_14497223	cis	0,83±0,12	1,76E-12	0,15	Protein-of-unknown-function-(DUF626)
AT4G11640	chr4_7024518	cis	0,74±0,1	1,79E-12	0,21	serine-racemase
AT3G46580	chr3_17139514	cis	-0,84±0,12	1,83E-12	0,14	methyl-CPG-binding-domain-protein-5
AT4G08250	chr4_5195761	cis	0,62±0,09	1,85E-12	0,38	GRAS-family-transcription-factor
AT4G02120	chr4_942894	cis	0,65±0,09	1,90E-12	0,30	CTP-synthase-family-protein
AT4G25340	chr4_12962704	cis	0,78±0,11	1,91E-12	0,23	FK506-BINDING-PROTEIN-53
AT4G07410	chr4_4203200	cis	0,74±0,1	1,92E-12	0,30	Transducin-family-protein-/-WD-40-repeat-family-protein
AT1G19397	chr1_6703658	cis	-0,68±0,1	1,98E-12	0,31	
AT5G45560	chr5_18465446	cis	0,63±0,09	2,03E-12	0,36	Pleckstrin-homology-(PH)-domain-containing-protein-/-lipid-binding-START-domain-containing-protein
AT4G39240	chr4_18269285	cis	-0,67±0,09	2,05E-12	0,37	Galactose-oxidase/kelch-repeat-superfamily-protein
AT3G23560	chr3_8456447	cis	-0,69±0,1	2,08E-12	0,25	MATE-efflux-family-protein

AT3G25490	chr1_7447447	trans	0,87±0,12	2,12E-12	0,13	Protein-kinase-family-protein
AT5G14210	chr5_4578361	cis	-0,64±0,09	2,30E-12	0,43	Leucine-rich-repeat-protein-kinase-family-protein
AT5G43070	chr5_17289785	cis	-0,61±0,09	2,35E-12	0,40	WPP-domain-protein-1
AT3G57430	chr3_21255050	cis	0,68±0,1	2,42E-12	0,32	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT5G26180	chr5_9149412	cis	-0,63±0,09	2,46E-12	0,33	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein
AT1G65520	chr1_24359557	cis	-0,8±0,11	2,55E-12	0,19	delta(3),-delta(2)-enoyl-CoA-isomerase-1
AT3G59380	chr3_21945839	cis	-0,61±0,09	2,60E-12	0,52	farnesyltransferase-A
AT1G48380	chr1_17879415	cis	0,76±0,11	2,61E-12	0,21	root-hair-initiation-protein-root-hairless-1-(RHL1)
AT1G31150	chr1_11120051	cis	0,61±0,09	2,64E-12	0,40	Domain-of-unknown-function-(DUF1985)
AT1G72890	chr1_27430024	cis	0,64±0,09	2,67E-12	0,39	Disease-resistance-protein-(TIR-NBS-class)
AT2G32830	chr2_13930701	cis	-0,73±0,11	2,70E-12	0,27	phosphate-transporter-1;5
AT3G15590	chr3_5289455	cis	0,67±0,1	2,76E-12	0,39	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT4G23200	chr4_12145728	cis	-0,76±0,11	2,79E-12	0,21	cysteine-rich-RLK-(RECEPTOR-like-protein-kinase)-12
AT5G44010	chr5_17711255	cis	0,67±0,1	2,83E-12	0,26	
AT4G25770	chr4_13120538	cis	-0,69±0,1	2,91E-12	0,29	alpha/beta-Hydrolases-superfamily-protein
AT5G41170	chr5_16480617	cis	0,68±0,1	2,95E-12	0,28	Pentatricopeptide-repeat-(PPR-like)-superfamily-protein
AT2G30960	chr2_13170243	cis	-0,81±0,12	3,07E-12	0,19	
AT5G54064	chr5_21939485	cis	-0,81±0,12	3,12E-12	0,19	
AT4G07868	chr4_4692338	cis	0,65±0,09	3,14E-12	0,31	
AT2G36680	chr2_15370601	cis	-0,66±0,09	3,22E-12	0,30	Modifier-of-rudimentary-(Mod(r))-protein
AT3G23109	chr3_8218794	cis	0,62±0,09	3,24E-12	0,39	
AT3G24255	chr3_8793946	cis	-0,66±0,1	3,29E-12	0,36	RNA-directed-DNA-polymerase-(reverse-transcriptase)-related-family-protein
AT1G34110	chr1_12417145	cis	-0,59±0,09	3,31E-12	0,42	Leucine-rich-receptor-like-protein-kinase-family-protein
AT1G67850	chr1_25442185	cis	0,68±0,1	3,32E-12	0,36	Protein-of-unknown-function-(DUF707)
AT3G56680	chr3_20991323	cis	0,61±0,09	3,36E-12	0,50	Single-stranded-nucleic-acid-binding-R3H-protein
AT3G60965	chr3_22593699	cis	0,64±0,09	3,36E-12	0,28	transposable-element-gene
AT2G35830	chr2_15050779	cis	0,74±0,11	3,37E-12	0,25	
AT3G50210	chr3_18617672	cis	0,64±0,09	3,41E-12	0,37	2-oxoglutarate-(2OG)-and-Fe(II)-dependent-oxygenase-superfamily-protein
AT1G17240	chr1_5898135	cis	0,69±0,1	3,45E-12	0,29	receptor-like-protein-2
AT4G28740	chr4_14201805	cis	-0,94±0,14	3,47E-12	0,11	
AT1G11280	chr1_3785997	cis	-0,67±0,1	3,48E-12	0,33	S-locus-lectin-protein-kinase-family-protein
AT1G18773	chr1_6473466	cis	0,74±0,11	3,51E-12	0,22	
AT1G22650	chr1_8016139	cis	0,68±0,1	3,56E-12	0,28	Plant-neutral-invertase-family-protein
AT4G23310	chr4_12137949	cis	0,65±0,09	3,64E-12	0,39	cysteine-rich-RLK-(RECEPTOR-like-protein-kinase)-23
AT1G21210	chr1_7447447	cis	0,88±0,13	3,66E-12	0,13	wall-associated-kinase-4
AT3G25400	chr3_9213250	cis	-0,59±0,08	3,92E-12	0,40	
AT1G18410	chr1_21500435	trans	0,62±0,09	3,95E-12	0,36	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT3G29390	chr3_11290769	cis	-0,71±0,1	3,97E-12	0,26	RS2-interacting-KH-protein
AT5G56370	chr5_22842831	cis	-0,7±0,1	4,07E-12	0,19	F-box/RNI-like/FBD-like-domains-containing-protein
AT1G24100	chr1_8527073	cis	-0,68±0,1	4,17E-12	0,32	UDP-glucosyl-transferase-74B1
AT5G08565	chr5_2775823	cis	0,85±0,12	4,17E-12	0,18	Transcription-initiation-Spt4-like-protein
AT4G24175	chr4_12546464	cis	0,61±0,09	4,22E-12	0,41	
AT2G29910	chr2_12747060	cis	-0,89±0,13	4,23E-12	0,14	F-box/RNI-like-superfamily-protein
AT5G38980	chr5_15616106	cis	-0,97±0,14	4,26E-12	0,11	
AT2G18210	chr2_7925812	cis	-0,58±0,08	4,27E-12	0,56	
AT3G60150	chr3_22225185	cis	-0,68±0,1	4,39E-12	0,29	Protein-of-unknown-function-(DUF498/DUF598)
AT3G17626	chr3_6027963	cis	-0,61±0,09	4,40E-12	0,53	structural-constituent-of-ribosome
AT5G38590	chr5_15460933	cis	0,67±0,1	4,50E-12	0,30	F-box/RNI-like/FBD-like-domains-containing-protein
AT3G06110	chr3_1843238	cis	0,67±0,1	4,67E-12	0,38	MAPK-phosphatase-2
AT4G10810	chr4_6645980	cis	-0,61±0,09	4,68E-12	0,43	
AT5G05890	chr5_1770444	cis	0,64±0,09	4,77E-12	0,44	UDP-Glycosyltransferase-superfamily-protein
AT2G16850	chr2_7306624	cis	0,68±0,1	4,77E-12	0,30	plasma-membrane-intrinsic-protein-2;8
AT5G66455	chr5_26538158	cis	0,61±0,09	4,98E-12	0,48	
AT2G27402	chr2_11711907	cis	0,69±0,1	5,02E-12	0,31	
AT1G52800	chr1_19661599	cis	-0,64±0,09	5,09E-12	0,39	2-oxoglutarate-(2OG)-and-Fe(II)-dependent-oxygenase-superfamily-protein
AT2G41600	chr2_17347276	cis	-0,82±0,12	5,18E-12	0,17	Mitochondrial-glycoprotein-family-protein
AT3G43610	chr3_15524846	cis	0,7±0,1	5,30E-12	0,22	Spc97-/-Spc98-family-of-spindle-pole-body-(SBP)-component
AT3G49340	chr3_18295338	cis	0,62±0,09	5,46E-12	0,38	Cysteine-proteinases-superfamily-protein
AT1G61500	chr1_22689801	cis	-0,59±0,09	5,60E-12	0,44	S-locus-lectin-protein-kinase-family-protein
AT1G65280	chr1_24245770	cis	0,59±0,09	5,63E-12	0,51	DNAJ-heat-shock-N-terminal-domain-containing-protein
AT4G04402	chr4_2164811	cis	-0,67±0,1	5,74E-12	0,34	two-component-phosphorelay-mediator,-putative
AT5G40405	chr5_16166653	cis	0,72±0,1	5,80E-12	0,20	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT1G13790	chr1_4726993	cis	0,68±0,1	6,14E-12	0,34	XH/XS-domain-containing-protein
AT5G38060	chr5_15189750	cis	0,62±0,09	6,17E-12	0,33	
AT1G04360	chr1_1175561	cis	-0,87±0,13	6,30E-12	0,14	RING/U-box-superfamily-protein
AT4G15420	chr4_8824699	cis	0,69±0,1	6,34E-12	0,26	Ubiquitin-fusion-degradation-UFD1-family-protein
AT4G02660	chr4_1158571	cis	-0,6±0,09	6,35E-12	0,49	Beige/BEACH-domain-;WD-domain,-G-beta-repeat-protein
AT3G32920	chr3_13442123	cis	0,91±0,13	6,70E-12	0,14	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT5G49555	chr5_20110273	cis	0,71±0,1	6,75E-12	0,21	FAD/NAD(P)-binding-oxidoreductase-family-protein
AT1G23120	chr1_8198583	cis	0,87±0,13	6,76E-12	0,16	Polyketide-cyclase/dehydrase-and-lipid-transport-superfamily-protein
AT4G32950	chr4_15911442	cis	0,64±0,09	6,94E-12	0,37	Protein-phosphatase-2C-family-protein
AT5G01970	chr5_374088	cis	-0,64±0,09	7,04E-12	0,51	
AT1G12230	chr1_4152530	cis	-0,61±0,09	7,10E-12	0,52	Aldolase-superfamily-protein
AT5G16350	chr5_5353646	cis	0,66±0,1	7,17E-12	0,29	O-acyltransferase-(WSD1-like)-family-protein
AT5G11910	chr5_3837551	cis	-0,84±0,12	7,19E-12	0,14	alpha/beta-Hydrolases-superfamily-protein
AT4G36280	chr4_17170011	cis	-0,69±0,1	7,20E-12	0,25	Histidine-kinase-,-DNA-gyrase-B-,-and-HSP90-like-ATPase-family-protein
AT2G15310	chr2_6660296	cis	0,6±0,09	7,21E-12	0,39	ADP-ribosylation-factor-B1A
AT5G42660	chr5_17104571	cis	-0,66±0,1	7,55E-12	0,30	Protein-of-unknown-function-(DUF616)
AT1G12350	chr1_4202765	cis	0,63±0,09	7,58E-12	0,35	4-phospho-panto-thenoylcysteine-synthetase

AT3G25010	chr3_9108946	cis	0,62±0,09	7,59E-12	0,49	receptor-like-protein-41
AT1G64150	chr1_23811306	cis	0,6±0,09	7,64E-12	0,41	Uncharacterized-protein-family-(UPF0016)
AT4G13150	chr4_7649774	cis	-0,93±0,14	7,69E-12	0,12	
AT2G16370	chr2_7085202	cis	0,61±0,09	7,83E-12	0,39	thymidylate-synthase-1
AT2G37680	chr2_15803792	cis	-0,73±0,11	7,90E-12	0,20	
AT1G24793	chr1_8839098	trans	0,59±0,09	7,96E-12	0,44	UDP-3-O-acyl-N-acetylglycosamine-deacetylase-family-protein
AT2G45920	chr2_18895426	cis	-0,63±0,09	7,98E-12	0,32	U-box-domain-containing-protein
AT4G37150	chr4_17494759	cis	0,72±0,1	8,06E-12	0,27	methyl-esterase-9
AT2G22410	chr2_9507478	cis	0,63±0,09	8,08E-12	0,47	SLOW-GROWTH-1
AT5G24750	chr5_8490354	cis	0,78±0,11	8,40E-12	0,19	UDP-Glycosyltransferase-superfamily-protein
AT1G12620	chr1_4296754	cis	-0,71±0,1	8,55E-12	0,24	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT1G03180	chr1_779349	cis	0,68±0,1	8,69E-12	0,31	
AT4G23300	chr4_12178057	cis	-0,88±0,13	8,74E-12	0,13	cysteine-rich-RLK-(RECEPTOR-like-protein-kinase)-22
AT1G72130	chr1_27137072	cis	0,59±0,09	9,13E-12	0,54	Major-facilitator-superfamily-protein
AT1G36980	chr1_14065468	cis	0,59±0,09	9,47E-12	0,44	
AT4G37410	chr4_17591119	cis	-0,61±0,09	9,60E-12	0,51	cytochrome-P450,-family-81,-subfamily-F,-polypeptide-4
AT5G35730	chr5_13896253	cis	0,69±0,1	9,61E-12	0,24	EXS-(ERD1/XPR1/SYG1)-family-protein
AT3G03070	chr3_695184	cis	-0,66±0,1	9,79E-12	0,28	NADH-ubiquinone-oxidoreductase-related
AT4G13170	chr4_7655449	cis	0,61±0,09	1,00E-11	0,41	Ribosomal-protein-L13-family-protein
AT3G63480	chr3_23440586	cis	0,66±0,1	1,00E-11	0,26	ATP-binding-microtubule-motor-family-protein
AT1G54217	chr1_20243752	cis	-0,61±0,09	1,03E-11	0,40	Ribosomal-protein-L18ae-family
AT2G04550	chr2_1579467	cis	-0,6±0,09	1,04E-11	0,46	indole-3-butyric-acid-response-5
AT2G14800	chr2_6349052	cis	-0,62±0,09	1,06E-11	0,33	
AT2G04520	chr2_1574787	cis	0,6±0,09	1,07E-11	0,51	Nucleic-acid-binding,-OB-fold-like-protein
AT5G28050	chr5_10047341	cis	-0,65±0,1	1,08E-11	0,35	Cytidine/deoxycytidylate-deaminase-family-protein
AT3G20040	chr3_6994828	cis	0,65±0,1	1,09E-11	0,35	Hexokinase
AT3G24982	chr3_9108946	cis	0,6±0,09	1,09E-11	0,49	receptor-like-protein-40
AT4G01040	chr4_453349	cis	0,64±0,09	1,10E-11	0,55	Glycosyl-hydrolase-superfamily-protein
AT5G63030	chr5_25287390	cis	-0,63±0,09	1,10E-11	0,44	Thioredoxin-superfamily-protein
AT4G14410	chr4_8301179	cis	0,61±0,09	1,10E-11	0,33	basic-helix-loop-helix-(bHLH)-DNA-binding-superfamily-protein
AT4G16180	chr4_9168218	cis	-0,59±0,09	1,12E-11	0,48	
AT3G48820	chr3_18102517	cis	-0,57±0,08	1,14E-11	0,44	Glycosyltransferase-family-29-(sialyltransferase)-family-protein
AT1G22403	chr5_26850990	trans	0,91±0,13	1,14E-11	0,11	other-RNA
AT5G52190	chr5_21202402	cis	-0,82±0,12	1,14E-11	0,16	Sugar-isomerase-(SIS)-family-protein
AT4G00420	chr4_181765	cis	-0,65±0,1	1,17E-11	0,27	Double-stranded-RNA-binding-domain-(DsRBD)-containing-protein
AT4G12200	chr4_7280607	cis	-0,61±0,09	1,18E-11	0,36	transposable-element-gene
AT1G63870	chr1_23712636	cis	0,59±0,09	1,21E-11	0,44	Disease-resistance-protein-(TIR-NBS-LRR-class)-family
AT5G03360	chr5_814645	cis	0,58±0,09	1,23E-11	0,49	DC1-domain-containing-protein
AT1G72930	chr1_27438135	cis	-0,89±0,13	1,24E-11	0,15	toll/interleukin-1-receptor-like
AT3G05685	chr3_1672952	cis	01,±0,15	1,24E-11	0,09	Cystatin/monellin-superfamily-protein
AT5G61550	chr5_24747219	cis	-0,67±0,1	1,25E-11	0,29	U-box-domain-containing-protein-kinase-family-protein
AT2G36500	chr2_15317806	cis	-0,74±0,11	1,31E-11	0,19	CBS-/-octicosapeptide/Phox/Bemp1-(PB1)-domains-containing-protein
AT5G58575	chr5_23674026	cis	-0,61±0,09	1,33E-11	0,53	
AT2G21840	chr2_9318420	cis	-0,62±0,09	1,33E-11	0,29	Cysteine/Histidine-rich-C1-domain-family-protein
AT2G22482	chr2_9548445	cis	-0,82±0,12	1,34E-11	0,16	
AT5G17040	chr5_5607110	cis	0,97±0,14	1,39E-11	0,10	UDP-Glycosyltransferase-superfamily-protein
AT3G16700	chr3_5688040	cis	0,73±0,11	1,41E-11	0,22	Fumarylacetoacetate-(FAA)-hydrolase-family
AT4G05060	chr4_2590490	cis	0,64±0,09	1,43E-11	0,35	PapD-like-superfamily-protein
AT1G31500	chr1_11275511	cis	-0,64±0,09	1,46E-11	0,25	DNAse-I-like-superfamily-protein
AT2G02960	chr2_864047	cis	0,67±0,1	1,48E-11	0,24	RING/FYVE/PHD-zinc-finger-superfamily-protein
AT1G75100	chr1_28192328	cis	-0,67±0,1	1,52E-11	0,27	J-domain-protein-required-for-chloroplast-accumulation-response-1
AT2G03760	chr2_1150723	cis	0,74±0,11	1,52E-11	0,20	sulphotransferase-12
AT1G23130	chr1_8198411	cis	-0,9±0,13	1,54E-11	0,11	Polyketide-cyclase/dehydrase-and-lipid-transport-superfamily-protein
AT1G60220	chr1_22212081	cis	0,7±0,1	1,54E-11	0,21	UB-like-protease-1D
AT3G18165	chr3_6222138	cis	-0,67±0,1	1,54E-11	0,23	modifier-of-snc1,4
AT3G47220	chr3_17387327	cis	0,58±0,09	1,57E-11	0,46	phosphatidylinositol-speciwc-phospholipase-C9
AT1G20050	chr1_6947020	cis	0,68±0,1	1,62E-11	0,33	C-8,7-sterol-isomerase
AT1G03220	chr1_786874	cis	-0,63±0,09	1,63E-11	0,41	Eukaryotic-aspartyl-protease-family-protein
AT1G08530	chr1_2700642	cis	-0,65±0,1	1,63E-11	0,34	
AT1G79529	chr1_29920199	cis	-0,78±0,12	1,65E-11	0,16	other-RNA
AT5G07000	chr5_2172553	cis	-0,78±0,12	1,65E-11	0,17	sulfotransferase-2B
AT1G47625	chr1_17510207	cis	0,6±0,09	1,69E-11	0,43	
AT3G27430	chr3_10156913	cis	-0,61±0,09	1,72E-11	0,35	N-terminal-nucleophile-aminohydrolases-(Ntn-hydrolases)-superfamily-protein
AT5G24450	chr5_8348974	cis	-0,62±0,09	1,72E-11	0,40	Transcription-factor-IIIC,-subunit-5
AT1G02020	chr1_353313	cis	0,59±0,09	1,73E-11	0,48	nitroreductase-family-protein
AT4G33945	chr4_16274000	cis	-0,64±0,1	1,74E-11	0,34	ARM-repeat-superfamily-protein
AT1G60700	chr1_22355520	cis	0,62±0,09	1,75E-11	0,33	SMAD/FHA-domain-containing-protein-
AT4G00620	chr4_261007	cis	0,74±0,11	1,82E-11	0,26	Amino-acid-dehydrogenase-family-protein
AT3G21580	chr3_7602812	cis	-0,84±0,13	1,87E-11	0,14	cobalt-ion-transmembrane-transporters
AT2G23110	chr2_9840409	cis	0,74±0,11	1,88E-11	0,24	Late-embryogenesis-abundant-protein,-group-6
AT3G16640	chr3_5669704	cis	-0,63±0,09	1,90E-11	0,29	translationally-controlled-tumor-protein
AT4G02425	chr4_1063049	cis	-0,62±0,09	1,95E-11	0,39	
AT2G39230	chr2_16387379	cis	0,83±0,12	1,95E-11	0,14	LATERAL-ORGAN-JUNCTION
AT1G58410	chr1_21702313	cis	0,58±0,09	2,01E-11	0,43	Disease-resistance-protein-(CC-NBS-LRR-class)-family
AT3G54420	chr3_20145503	cis	-0,61±0,09	2,01E-11	0,41	homolog-of-carrot-EP3-3-chitinase
AT4G39235	chr4_18268432	cis	-0,67±0,1	2,01E-11	0,23	
AT5G41000	chr3_18025128	trans	-0,68±0,1	2,02E-11	0,30	YELLOW-STRIPE-like-4
AT5G04220	chr5_1159530	cis	-0,86±0,13	2,11E-11	0,13	Calcium-dependent-lipid-binding-(CaLB-domain)-family-protein
AT1G28670	chr1_10077576	cis	0,75±0,11	2,13E-11	0,20	GDSL-like-Lipase/Acylhydrolase-superfamily-protein

AT2G01400	chr2_175191	cis	-0,68±0,1	2,16E-11	0,23	
AT1G18940	chr1_6530366	cis	0,63±0,09	2,17E-11	0,39	Nodulin-like-/-Major-Facilitator-Superfamily-protein
AT4G29050	chr4_14317089	cis	0,68±0,1	2,17E-11	0,29	Concanavalin-A-like-lectin-protein-kinase-family-protein
AT3G14160	chr3_4689076	cis	0,86±0,13	2,27E-11	0,14	2-oxoglutarate-dependent-dioxygenase-family-protein
AT1G09820	chr1_3192055	cis	-0,57±0,09	2,29E-11	0,45	Pentatricopeptide-repeat-(PPR-like)-superfamily-protein
AT2G21870	chr2_9321894	cis	-0,63±0,09	2,33E-11	0,31	copper-ion-binding;cobalt-ion-binding;zinc-ion-binding
AT1G19750	chr1_6832148	cis	0,71±0,11	2,36E-11	0,24	Transducin/WD40-repeat-like-superfamily-protein
AT5G37130	chr5_14680473	cis	0,69±0,1	2,38E-11	0,22	Protein-prenylyltransferase-superfamily-protein
AT2G19910	chr2_8600617	cis	-0,64±0,1	2,40E-11	0,32	RNA-dependent-RNA-polymerase-family-protein
AT5G40880	chr5_16378279	cis	0,6±0,09	2,43E-11	0,44	WD-40-repeat-family-protein-/-zfwd3-protein-(ZFWD3)
AT4G14490	chr4_8333079	cis	0,73±0,11	2,43E-11	0,19	SMAD/FHA-domain-containing-protein-
AT4G04790	chr4_2437780	cis	0,63±0,09	2,43E-11	0,32	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT1G71330	chr1_26879415	cis	0,66±0,1	2,50E-11	0,26	non-intrinsic-ABC-protein-5
AT4G38300	chr4_17946830	cis	0,62±0,09	2,55E-11	0,30	glycosyl-hydrolase-family-10-protein
AT3G53100	chr3_19687722	cis	-0,61±0,09	2,59E-11	0,45	GDSL-like-Lipase/Acylhydrolase-superfamily-protein
AT2G48120	chr2_19683015	cis	0,58±0,09	2,64E-11	0,44	pale-cress-protein-(PAC)
AT4G31540	chr4_15278621	cis	-0,64±0,1	2,65E-11	0,37	exocyst-subunit-exo70-family-protein-G1
AT1G69450	chr1_26110274	cis	-0,57±0,08	2,70E-11	0,49	Early-responsive-to-dehydration-stress-protein-(ERD4)
AT5G43600	chr5_17512663	cis	0,85±0,13	2,70E-11	0,14	ureidoglycolate-amidohydrolase
AT5G24660	chr1_14308406	trans	-0,73±0,11	2,71E-11	0,31	response-to-low-sulfur-2
AT5G50340	chr5_20492993	cis	-0,57±0,09	2,72E-11	0,31	ATP-dependent-peptidases;nucleotide-binding;serine-type-endopeptidases;DNA-helicases;ATP-binding;damaged-DNA-binding;nucleoside-triphosphatases
AT3G05530	chr3_1599235	cis	-0,63±0,1	2,74E-11	0,36	regulatory-particle-triple-A-ATPase-5A
AT2G29950	chr2_12767693	cis	-0,77±0,12	2,74E-11	0,16	ELF4-like-1
AT5G47940	chr5_19405610	cis	-0,59±0,09	2,74E-11	0,45	
AT2G19670	chr2_8500807	cis	0,87±0,13	2,75E-11	0,13	protein-arginine-methyltransferase-1A
AT2G27760	chr2_11823627	cis	-0,91±0,14	2,80E-11	0,11	tRNAisopentenyltransferase-2
AT1G07660	chr1_2378193	cis	0,85±0,13	2,84E-11	0,16	Histone-superfamily-protein
AT3G05140	chr3_1438382	cis	-0,62±0,09	2,84E-11	0,29	ROP-binding-protein-kinases-2
AT5G27780	chr1_10304618	trans	0,62±0,09	2,86E-11	0,31	SAUR-like-auxin-responsive-protein-family-
AT4G22280	chr4_11781527	cis	-0,62±0,09	2,91E-11	0,33	F-box/RNI-like-superfamily-protein
AT3G45430	chr3_16668483	cis	-0,67±0,1	2,93E-11	0,22	Concanavalin-A-like-lectin-protein-kinase-family-protein
AT1G23970	chr1_8484262	cis	-0,6±0,09	2,96E-11	0,34	Protein-of-unknown-function-(DUF626)
AT1G21260	chr1_7450625	cis	-0,87±0,13	2,96E-11	0,11	transposable-element-gene
AT3G44840	chr3_16380533	cis	0,62±0,09	2,97E-11	0,33	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein
AT3G18070	chr3_6188404	cis	0,67±0,1	3,02E-11	0,27	beta-glucosidase-43
AT1G76705	chr1_28787300	cis	-0,69±0,1	3,03E-11	0,22	calmodulin-binding
AT3G24070	chr3_8693279	cis	-0,62±0,09	3,07E-11	0,40	Zinc-knuckle-(CCHC-type)-family-protein
AT1G43640	chr1_16441368	cis	0,64±0,1	3,12E-11	0,19	tubby-like-protein-5
AT1G62085	chr1_22958193	cis	0,8±0,12	3,12E-11	0,19	Mitochondrial-transcription-termination-factor-family-protein
AT5G60250	chr5_24252041	cis	-0,64±0,1	3,20E-11	0,27	zinc-finger-(C3HC4-type-RING-finger)-family-protein
AT1G20270	chr1_7012941	cis	0,7±0,11	3,20E-11	0,29	2-oxoglutarate-(2OG)-and-Fe(II)-dependent-oxygenase-superfamily-protein
AT1G03950	chr1_1013305	cis	-0,61±0,09	3,24E-11	0,49	vacuolar-protein-sorting-associated-protein-2.3
AT3G03720	chr3_929830	cis	-0,6±0,09	3,25E-11	0,44	cationic-amino-acid-transporter-4
AT4G29540	chr4_14498589	cis	-0,82±0,12	3,26E-11	0,14	bacterial-transferase-hexapeptide-repeat-containing-protein
AT4G31350	chr4_15212436	cis	0,58±0,09	3,33E-11	0,54	Core-2/I-branching-beta-1,6-N-acetylglucosaminyltransferase-family-protein
AT1G03430	chr1_846368	cis	0,68±0,1	3,34E-11	0,32	histidine-containing-phosphotransfer-factor-5
AT1G67460	chr1_25271417	cis	01,03±0,15	3,37E-11	0,07	Minichromosome-maintenance-(MCM2/3/5)-family-protein
AT3G44850	chr3_16377086	cis	-0,58±0,09	3,37E-11	0,36	Protein-kinase-superfamily-protein
AT5G38250	chr5_15282333	cis	-0,68±0,1	3,38E-11	0,29	Protein-kinase-family-protein
AT5G02230	chr5_448353	cis	-0,62±0,09	3,45E-11	0,36	Haloacid-dehalogenase-like-hydrolase-(HAD)-superfamily-protein
AT1G63860	chr1_23699948	cis	-0,72±0,11	3,48E-11	0,18	Disease-resistance-protein-(TIR-NBS-LRR-class)-family
AT3G05520	chr3_1597217	cis	0,72±0,11	3,49E-11	0,21	Subunits-of-heterodimeric-actin-filament-capping-protein-Capz-superfamily
AT1G47480	chr1_17417234	cis	0,59±0,09	3,49E-11	0,40	alpha/beta-Hydrolases-superfamily-protein
AT1G10350	chr1_3394361	cis	-0,63±0,09	3,52E-11	0,27	DNAJ-heat-shock-family-protein
AT4G10970	chr4_6723527	cis	0,58±0,09	3,61E-11	0,38	
AT2G41160	chr2_17158899	cis	0,64±0,1	3,70E-11	0,33	Ubiquitin-associated-(UBA)-protein
AT5G03690	chr5_965085	cis	0,63±0,1	3,76E-11	0,31	Aldolase-superfamily-protein
AT1G01670	chr1_245885	cis	0,74±0,11	3,85E-11	0,19	RING/U-box-superfamily-protein
AT1G63900	chr1_23717698	cis	-0,58±0,09	3,86E-11	0,54	E3-Ubiquitin-ligase-family-protein
AT3G08800	chr3_2695806	cis	0,76±0,12	3,91E-11	0,16	ARM-repeat-superfamily-protein
AT1G43245	chr1_16399107	trans	-0,6±0,09	3,96E-11	0,43	SET-domain-containing-protein
AT5G23570	chr5_7938150	cis	-0,76±0,12	3,96E-11	0,19	XS-domain-containing-protein-/-XS-zinc-finger-domain-containing-protein-related
AT1G32210	chr1_11608838	cis	-0,56±0,09	3,97E-11	0,39	Defender-against-death-(DAD-family)-protein
AT5G45610	chr5_18496799	cis	-0,59±0,09	4,04E-11	0,42	protein-dimerizations
AT1G56130	chr1_20990846	cis	-0,59±0,09	4,13E-11	0,49	Leucine-rich-repeat-transmembrane-protein-kinase
AT3G49510	chr3_18353953	cis	0,85±0,13	4,16E-11	0,15	F-box-family-protein
AT5G43460	chr5_17459417	cis	-0,81±0,12	4,22E-11	0,15	HR-like-lesion-inducing-protein-related
AT5G57230	chr5_23190534	cis	0,56±0,09	4,25E-11	0,39	Thioredoxin-superfamily-protein
AT3G50430	chr3_18713181	cis	0,61±0,09	4,25E-11	0,39	
AT1G34570	chr1_12656236	cis	-0,64±0,1	4,25E-11	0,27	Essential-protein-Yae1,-N-terminal
AT3G18520	chr3_6360408	cis	-0,97±0,15	4,28E-11	0,12	histone-deacetylase-15
AT4G38280	chr4_17952125	cis	-0,81±0,12	4,31E-11	0,14	
AT3G27930	chr3_10375644	cis	-0,71±0,11	4,35E-11	0,22	
AT1G75620	chr1_28398064	cis	0,61±0,09	4,44E-11	0,33	glyoxal-oxidase-related-protein
AT1G37150	chr1_14205440	cis	-0,6±0,09	4,46E-11	0,35	holocarboxylase-synthetase-2
AT2G16595	chr2_7198233	cis	0,97±0,15	4,55E-11	0,10	Translocon-associated-protein-(TRAP),-alpha-subunit
AT4G08540	chr4_5431654	cis	0,66±0,1	4,56E-11	0,25	DNA-directed-RNA-polymerase-II-protein
AT4G01883	chr4_802185	cis	-0,61±0,09	4,61E-11	0,36	Polyketide-cyclase-/-dehydrase-and-lipid-transport-protein
AT3G47990	chr3_17715309	cis	-0,69±0,1	4,62E-11	0,22	SUGAR-INSENSITIVE-3

AT4G12760	chr4_7505406	cis	-0,67±0,1	4,66E-11	0,21	
AT5G66840	chr5_26695453	cis	0,6±0,09	4,66E-11	0,27	SAP-domain-containing-protein
AT4G35785	chr4_16955002	cis	-0,6±0,09	4,67E-11	0,32	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT1G24120	chr1_8532808	cis	0,65±0,1	4,73E-11	0,32	ARG1-like-1
AT5G22860	chr5_7650977	cis	0,64±0,1	4,74E-11	0,36	Serine-carboxypeptidase-S28-family-protein
AT1G20225	chr1_7008332	cis	0,63±0,1	4,75E-11	0,34	Thioredoxin-superfamily-protein
AT4G37110	chr4_17489547	cis	0,71±0,11	4,78E-11	0,19	Zinc-finger-domain-of-monoamine-oxidase-A-repressor-R1
AT1G56120	chr1_20993126	cis	-0,66±0,1	4,79E-11	0,49	Leucine-rich-repeat-transmembrane-protein-kinase
AT2G42450	chr2_17686212	cis	0,6±0,09	4,85E-11	0,41	alpha/beta-Hydrolases-superfamily-protein
AT2G02470	chr2_655171	cis	-0,57±0,09	4,88E-11	0,46	alfin-like-6
AT3G14940	chr3_5025461	cis	-0,7±0,11	4,89E-11	0,21	phosphoenolpyruvate-carboxylase-3
AT3G03850	chr3_981957	cis	-0,81±0,12	4,91E-11	0,15	SAUR-like-auxin-responsive-protein-family-
AT5G23020	chr5_7703372	cis	0,59±0,09	4,97E-11	0,37	2-isopropylmalate-synthase-2
AT2G25420	chr2_10799197	cis	-0,7±0,11	4,98E-11	0,41	transducin-family-protein-/-WD-40-repeat-family-protein
AT5G35430	chr5_13662860	cis	0,6±0,09	5,16E-11	0,36	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT1G60730	chr1_22359534	cis	0,65±0,1	5,26E-11	0,19	NAD(P)-linked-oxidoreductase-superfamily-protein
AT2G21830	chr2_9303757	cis	-0,65±0,1	5,27E-11	0,36	Cysteine/Histidine-rich-C1-domain-family-protein
AT4G07810	chr4_11390461	trans	-0,58±0,09	5,29E-11	0,44	transposable-element-gene
AT3G46980	chr3_17309471	cis	0,82±0,13	5,33E-11	0,18	phosphate-transporter-4;3
AT1G21480	chr1_7521814	cis	0,78±0,12	5,35E-11	0,13	Exostosin-family-protein
AT4G07868	chr5_24731389	trans	0,57±0,09	5,43E-11	0,58	
AT4G39930	chr4_18518933	cis	0,67±0,1	5,49E-11	0,25	
AT1G22590	chr1_7981208	cis	0,55±0,08	5,56E-11	0,47	AGAMOUS-like-87
AT4G12020	chr4_7201310	cis	-0,93±0,14	5,64E-11	0,09	protein-kinase-family-protein
AT1G03230	chr1_786874	cis	-0,62±0,1	5,67E-11	0,41	Eukaryotic-aspartyl-protease-family-protein
AT1G51480	chr5_17564586	trans	0,58±0,09	5,69E-11	0,46	Disease-resistance-protein-(CC-NBS-LRR-class)-family
AT3G16170	chr3_5478668	cis	-0,83±0,13	5,90E-11	0,17	AMP-dependent-synthetase-and-ligase-family-protein
AT2G30820	chr2_13129360	cis	0,77±0,12	5,90E-11	0,16	
AT2G16895	chr2_7319981	cis	0,57±0,09	5,95E-11	0,51	
AT5G23390	chr5_7870343	cis	0,58±0,09	6,02E-11	0,41	Plant-protein-of-unknown-function-(DUF639)
AT1G67910	chr1_25472493	cis	-0,96±0,15	6,04E-11	0,11	
AT4G28085	chr4_13966410	cis	0,67±0,1	6,09E-11	0,24	
AT5G40820	chr5_16363727	cis	0,75±0,11	6,30E-11	0,19	Ataxia-telangiectasia-mutated-and-RAD3-related
AT2G22482	chr3_129672	trans	-0,85±0,13	6,31E-11	0,14	
AT4G07950	chr4_4800152	cis	-0,61±0,09	6,34E-11	0,39	DNA-directed-RNA-polymerase,-subunit-M,-archaeal
AT1G26530	chr1_9166436	cis	-0,85±0,13	6,39E-11	0,13	PIN-domain-like-family-protein
AT1G32310	chr1_11653587	cis	0,58±0,09	6,43E-11	0,31	
AT5G38280	chr5_15292221	cis	-0,57±0,09	6,43E-11	0,34	PR5-like-receptor-kinase
AT5G47760	chr5_19342075	cis	0,57±0,09	6,44E-11	0,46	2-phosphoglycolate-phosphatase-2
AT4G31870	chr4_15409973	cis	-0,66±0,1	6,45E-11	0,31	glutathione-peroxidase-7
AT1G65700	chr1_24435496	cis	-0,79±0,12	6,46E-11	0,16	Small-nuclear-ribonucleoprotein-family-protein
AT4G19460	chr4_10610785	cis	-0,58±0,09	6,46E-11	0,36	UDP-Glycosyltransferase-superfamily-protein
AT4G07950	chr4_3904715	trans	-0,9±0,14	6,47E-11	0,12	DNA-directed-RNA-polymerase,-subunit-M,-archaeal
AT1G24340	chr1_8635114	cis	0,81±0,12	6,56E-11	0,19	FAD/NAD(P)-binding-oxidoreductase-family-protein
AT1G65130	chr1_24197451	cis	-0,89±0,14	6,57E-11	0,11	Ubiquitin-carboxyl-terminal-hydrolase-related-protein
AT4G09420	chr4_5932389	cis	-0,78±0,12	6,60E-11	0,16	Disease-resistance-protein-(TIR-NBS-class)
AT3G44120	chr3_15875158	cis	0,59±0,09	6,61E-11	0,34	F-box-and-associated-interaction-domains-containing-protein
AT5G45475	chr5_18424570	cis	-0,84±0,13	6,63E-11	0,14	
AT4G01880	chr4_812373	cis	-0,72±0,11	6,65E-11	0,21	methyltransferases
AT3G53210	chr3_19720549	cis	0,67±0,1	6,67E-11	0,23	nodulin-MtN21-/EamA-like-transporter-family-protein
AT2G44360	chr2_18321698	cis	0,58±0,09	6,97E-11	0,53	
AT1G48240	chr1_17811939	cis	0,63±0,1	6,98E-11	0,31	novel-plant-snare-12
AT5G23380	chr5_7868418	cis	-0,57±0,09	7,02E-11	0,44	Protein-of-unknown-function-(DUF789)
AT1G29960	chr1_10496204	cis	0,58±0,09	7,06E-11	0,49	Peptidase-S24/S26A/S26B/S26C-family-protein
AT3G58940	chr3_21783678	cis	0,97±0,15	7,07E-11	0,11	F-box/RNI-like-superfamily-protein
AT1G25210	chr1_8842441	cis	0,91±0,14	7,10E-11	0,12	UDP-3-O-acyl-N-acetylglycosamine-deacetylase-family-protein
AT2G27330	chr2_11695193	cis	0,65±0,1	7,23E-11	0,35	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT2G36590	chr2_15345697	cis	-0,75±0,11	7,33E-11	0,21	proline-transporter-3
AT5G36940	chr5_14590286	cis	-0,62±0,1	7,41E-11	0,35	cationic-amino-acid-transporter-3
AT2G28560	chr2_12237067	cis	01,02±0,16	7,66E-11	0,08	DNA-repair-(Rad51)-family-protein
AT1G65080	chr1_24176095	cis	0,56±0,09	7,71E-11	0,49	Membrane-insertion-protein,-OxaA/YidC-with-tetratricopeptide-repeat-domain
AT2G31250	chr2_13321609	cis	0,68±0,1	7,84E-11	0,22	Glutamyl-tRNA-reductase-family-protein
AT5G24660	chr1_15491836	trans	-0,71±0,11	8,04E-11	0,32	response-to-low-sulfur-2
AT1G44910	chr1_16971689	cis	-0,6±0,09	8,21E-11	0,34	pre-mRNA-processing-protein-40A
AT4G36515	chr4_17226130	cis	-0,86±0,13	8,25E-11	0,11	
AT1G15280	chr1_5249719	cis	0,6±0,09	8,34E-11	0,46	CASC3/Barentsz-eIF4AIII-binding
AT5G48670	chr5_19739149	cis	-0,72±0,11	8,47E-11	0,20	AGAMOUS-like-80
AT2G02880	chr2_841410	cis	0,59±0,09	8,62E-11	0,29	mucin-related
AT5G03250	chr5_774497	cis	-0,57±0,09	8,63E-11	0,49	Phototropic-responsive-NPH3-family-protein
AT4G23290	chr4_12184127	cis	-0,81±0,12	8,68E-11	0,14	cysteine-rich-RLK-(RECEPTOR-like-protein-kinase)-21
AT4G02430	chr4_1075423	cis	-0,61±0,09	8,70E-11	0,36	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT5G03285	chr5_793000	cis	-0,6±0,09	8,90E-11	0,40	other-RNA
AT3G26380	chr3_9662059	cis	-0,81±0,13	8,91E-11	0,16	Melibiase-family-protein
AT2G41830	chr2_17458181	cis	0,88±0,14	8,92E-11	0,17	Uncharacterized-protein
AT1G14040	chr1_4790675	cis	-0,56±0,09	9,03E-11	0,43	EXS-(ERD1/XPR1/SYG1)-family-protein
AT2G21130	chr2_9056486	cis	0,59±0,09	9,06E-11	0,42	Cyclophilin-like-peptidyl-prolyl-cis-trans-isomerase-family-protein
AT5G26240	chr5_9190048	cis	0,58±0,09	9,08E-11	0,35	chloride-channel-D
AT3G02790	chr3_616719	cis	-0,91±0,14	9,18E-11	0,11	zinc-finger-(C2H2-type)-family-protein
AT1G52290	chr1_19471163	cis	-0,59±0,09	9,27E-11	0,39	Protein-kinase-superfamily-protein

AT3G54160	chr3_20053329	cis	0,58±0,09	9,34E-11	0,34	RNI-like-superfamily-protein
AT1G05350	chr1_1562537	cis	0,6±0,09	9,43E-11	0,41	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT2G45510	chr2_18755446	cis	0,57±0,09	9,61E-11	0,46	cytochrome-P450,-family-704,-subfamily-A,-polypeptide-2
AT5G10610	chr5_3355152	cis	0,76±0,12	9,71E-11	0,16	cytochrome-P450,-family-81,-subfamily-K,-polypeptide-1
AT3G27860	chr3_10325509	cis	0,91±0,14	1,02E-10	0,10	Tudor/PWWP/MBT-superfamily-protein
AT4G36420	chr4_17202791	cis	0,67±0,1	1,03E-10	0,22	Ribosomal-protein-L12-family-protein
AT1G65070	chr1_24174627	cis	0,59±0,09	1,04E-10	0,34	DNA-mismatch-repair-protein-MutS,-type-2
AT4G18400	chr4_10169909	cis	-0,57±0,09	1,05E-10	0,39	
AT4G19560	chr4_10661099	cis	0,56±0,09	1,07E-10	0,48	Cyclin-family-protein
AT4G31990	chr4_15471552	cis	-0,78±0,12	1,07E-10	0,17	aspartate-aminotransferase-5
AT2G17320	chr2_7534189	cis	0,73±0,11	1,08E-10	0,21	Uncharacterised-conserved-protein-(UCP030210)
AT1G48605	chr1_17968019	cis	0,94±0,15	1,08E-10	0,09	Flavoprotein
AT3G30875	chr1_15752864	trans	0,58±0,09	1,09E-10	0,45	
AT3G43340	chr3_15284517	cis	0,6±0,09	1,11E-10	0,40	Pseudouridine-synthase-family-protein
AT3G03330	chr3_788485	cis	0,66±0,1	1,12E-10	0,34	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT1G05030	chr1_1438483	cis	-0,57±0,09	1,13E-10	0,36	Major-facilitator-superfamily-protein
AT1G72200	chr1_27172376	cis	0,66±0,1	1,15E-10	0,22	RING/U-box-superfamily-protein
AT2G25270	chr2_10759702	cis	-0,62±0,1	1,15E-10	0,36	
AT5G41690	chr5_16675076	cis	-0,61±0,09	1,18E-10	0,27	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT1G60620	chr1_22329166	cis	0,67±0,1	1,19E-10	0,21	RNA-polymerase-I-subunit-43
AT5G51640	chr5_20975731	cis	-0,59±0,09	1,19E-10	0,34	Plant-protein-of-unknown-function-(DUF828)
AT2G29370	chr2_12605976	cis	0,86±0,13	1,19E-10	0,13	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT3G28900	chr3_10900646	cis	-0,59±0,09	1,21E-10	0,31	Ribosomal-protein-L34e-superfamily-protein
AT4G15260	chr4_8717138	cis	0,66±0,1	1,22E-10	0,23	UDP-Glycosyltransferase-superfamily-protein
AT5G53970	chr5_21911490	cis	-0,6±0,09	1,23E-10	0,30	Tyrosine-transaminase-family-protein
AT2G32940	chr2_13973428	cis	-0,62±0,1	1,24E-10	0,39	Argonaute-family-protein
AT5G60340	chr5_24275857	cis	-0,65±0,1	1,24E-10	0,29	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT5G64630	chr5_25833185	cis	0,78±0,12	1,25E-10	0,16	Transducin/WD40-repeat-like-superfamily-protein
AT4G19540	chr4_10657339	cis	0,62±0,1	1,25E-10	0,29	IND1(iron-sulfur-protein-required-for-NADH-dehydrogenase)-like
AT1G04425	chr1_1194246	cis	0,58±0,09	1,27E-10	0,40	other-RNA
AT2G43280	chr2_17989969	cis	-0,71±0,11	1,29E-10	0,21	Far-red-impaired-responsive-(FAR1)-family-protein
AT5G22840	chr5_7627056	cis	-0,73±0,11	1,29E-10	0,24	Protein-kinase-superfamily-protein
AT4G13885	chr4_8028708	cis	-0,64±0,1	1,29E-10	0,24	Polynucleotidyl-transferase,-ribonuclease-H-like-superfamily-protein
AT1G08640	chr1_2749318	cis	-0,75±0,12	1,31E-10	0,24	Chloroplast-J-like-domain-1
AT3G19860	chr3_6910797	cis	0,64±0,1	1,32E-10	0,26	basic-helix-loop-helix-(bHLH)-DNA-binding-superfamily-protein
AT5G28897	chr3_9723545	trans	0,58±0,09	1,33E-10	0,31	
AT1G62820	chr1_23263842	cis	0,79±0,12	1,35E-10	0,14	Calcium-binding-EF-hand-family-protein
AT1G12550	chr1_4275390	cis	-0,6±0,09	1,38E-10	0,41	D-isomer-specific-2-hydroxyacid-dehydrogenase-family-protein
AT3G62890	chr3_23246117	cis	0,57±0,09	1,42E-10	0,41	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT1G27560	chr2_4222984	trans	0,64±0,1	1,43E-10	0,23	
AT4G26555	chr4_13407581	cis	-0,84±0,13	1,44E-10	0,14	FKBP-like-peptidyl-prolyl-cis-trans-isomerase-family-protein
AT2G25590	chr2_10886589	cis	-0,59±0,09	1,46E-10	0,44	Plant-Tudor-like-protein
AT4G27070	chr4_13588063	cis	0,61±0,09	1,47E-10	0,29	tryptophan-synthase-beta-subunit-2
AT4G22285	chr4_11781726	cis	0,58±0,09	1,49E-10	0,37	Ubiquitin-C-terminal-hydrolases-superfamily-protein
AT4G02730	chr4_1207780	cis	-0,61±0,1	1,50E-10	0,36	Transducin/WD40-repeat-like-superfamily-protein
AT5G22530	chr5_7480836	cis	0,59±0,09	1,51E-10	0,41	
AT3G54910	chr3_20342213	cis	-0,63±0,1	1,53E-10	0,23	RNI-like-superfamily-protein
AT1G61960	chr1_22903135	cis	-0,88±0,14	1,54E-10	0,11	Mitochondrial-transcription-termination-factor-family-protein
AT1G11270	chr1_3790577	cis	01,06±0,17	1,54E-10	0,08	F-box-and-associated-interaction-domains-containing-protein
AT1G35320	chr1_12957347	cis	-0,65±0,1	1,55E-10	0,23	
AT1G78750	chr1_29614181	cis	-0,66±0,1	1,59E-10	0,21	F-box/RNI-like-superfamily-protein
AT4G20400	chr4_11015485	cis	-0,54±0,09	1,60E-10	0,44	JUMONJI-14
AT5G53920	chr5_21892406	cis	-0,74±0,12	1,61E-10	0,16	ribosomal-protein-L11-methyltransferase-related
AT1G52590	chr1_19588597	cis	0,55±0,09	1,61E-10	0,48	Putative-thiol-disulphide-oxidoreductase-DCC
AT3G24340	chr3_8837356	cis	0,57±0,09	1,62E-10	0,37	chromatin-remodeling-40
AT1G23360	chr1_8296501	cis	0,6±0,09	1,63E-10	0,34	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein
AT1G29500	chr1_10315428	cis	-0,73±0,11	1,64E-10	0,17	SAUR-like-auxin-responsive-protein-family-
AT1G32540	chr1_11770333	cis	-0,58±0,09	1,67E-10	0,31	lsd-one-like-1
AT3G26100	chr3_9537065	cis	-0,79±0,12	1,68E-10	0,16	Regulator-of-chromosome-condensation-(RCC1)-family-protein
AT2G22970	chr2_9774878	cis	-0,65±0,1	1,69E-10	0,24	serine-carboxypeptidase-like-11
AT1G63350	chr1_23494652	cis	-0,57±0,09	1,76E-10	0,36	Disease-resistance-protein-(CC-NBS-LRR-class)-family
AT2G43490	chr2_18053906	cis	-0,55±0,09	1,77E-10	0,43	Ypt/Rab-GAP-domain-of-gyp1p-superfamily-protein
AT1G34210	chr1_12459119	cis	-0,69±0,11	1,78E-10	0,20	somatic-embryogenesis-receptor-like-kinase-2
AT3G07200	chr3_2290749	cis	-0,58±0,09	1,79E-10	0,48	RING/U-box-superfamily-protein
AT2G23620	chr2_10047637	cis	0,59±0,09	1,79E-10	0,33	methyl-esterase-1
AT5G12980	chr2_1833581	trans	-0,56±0,09	1,80E-10	0,37	Cell-differentiation,-Rcd1-like-protein
AT4G33370	chr4_16070698	cis	0,62±0,1	1,81E-10	0,28	DEA(D/H)-box-RNA-helicase-family-protein
AT5G45260	chr5_18327098	cis	-0,58±0,09	1,81E-10	0,36	Disease-resistance-protein-(TIR-NBS-LRR-class)
AT3G23740	chr3_8555055	cis	-0,7±0,11	1,83E-10	0,19	
AT4G11150	chr4_6801368	cis	0,57±0,09	1,86E-10	0,46	vacuolar-ATP-synthase-subunit-E1
AT1G11240	chr1_3764300	cis	-0,85±0,13	1,87E-10	0,14	
AT5G01180	chr5_45229	cis	-0,87±0,14	1,87E-10	0,14	peptide-transporter--5
AT2G28070	chr2_11958613	cis	-0,69±0,11	1,90E-10	0,24	ABC-2-type-transporter-family-protein
AT1G58300	chr1_21628676	cis	-0,58±0,09	1,91E-10	0,39	heme-oxygenase-4
AT5G03350	chr5_816975	cis	-0,68±0,11	1,91E-10	0,27	Legume-lectin-family-protein
AT3G14710	chr3_4939889	cis	0,6±0,09	1,94E-10	0,32	RNI-like-superfamily-protein
AT1G73860	chr1_27777739	cis	0,56±0,09	1,97E-10	0,49	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT4G07410	chr3_13806264	trans	0,68±0,11	1,98E-10	0,30	Transducin-family-protein-/-WD-40-repeat-family-protein
AT4G05390	chr4_2738807	cis	0,58±0,09	1,98E-10	0,36	root-FNR-1

AT5G52420	chr5_21282509	cis	0,61±0,1	2,00E-10	0,45	
AT3G03970	chr3_1030187	cis	-0,88±0,14	2,01E-10	0,09	ARM-repeat-superfamily-protein
AT1G61620	chr1_22739696	cis	-0,51±0,08	2,01E-10	0,42	phosphoinositide-binding
AT1G28640	chr1_10077576	cis	0,68±0,11	2,07E-10	0,20	GDSL-like-Lipase/Acylhydrolase-superfamily-protein
AT1G12160	chr1_4126364	cis	0,93±0,15	2,07E-10	0,09	Flavin-binding-monooxygenase-family-protein
AT3G09960	chr3_3061969	cis	0,93±0,15	2,13E-10	0,11	Calcineurin-like-metallo-phosphoesterase-superfamily-protein
AT4G27080	chr1_11505353	trans	0,7±0,11	2,14E-10	0,23	PDI-like-5-4
AT4G10420	chr4_6453774	cis	0,54±0,09	2,16E-10	0,39	FBD-/-Leucine-Rich-Repeat-domains-containing-protein
AT4G15165	chr4_8649777	cis	0,8±0,13	2,16E-10	0,12	N-terminal-nucleophile-aminohydrolases-(Ntn-hydrolases)-superfamily-protein
AT3G30875	chr3_13158367	trans	0,64±0,1	2,23E-10	0,32	
AT5G23890	chr5_8050126	cis	0,77±0,12	2,26E-10	0,16	
AT5G57880	chr5_23449524	cis	0,68±0,11	2,30E-10	0,21	multipolar-spindle-1
AT4G12010	chr4_7199993	cis	-0,55±0,09	2,34E-10	0,40	Disease-resistance-protein-(TIR-NBS-LRR-class)-family
AT4G21326	chr4_11346540	cis	0,78±0,12	2,37E-10	0,14	subtilase-3.12
AT5G27660	chr5_9792918	cis	-0,53±0,08	2,39E-10	0,49	Trypsin-family-protein-with-PDZ-domain
AT4G19060	chr4_10447444	cis	-0,6±0,09	2,39E-10	0,36	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT1G33060	chr1_11985485	cis	-0,64±0,1	2,40E-10	0,26	NAC-014
AT4G39925	chr4_18518933	cis	0,64±0,1	2,44E-10	0,25	AT-hook-motif-DNA-binding-family-protein
AT2G27360	chr2_11705507	cis	0,63±0,1	2,44E-10	0,60	GDSL-like-Lipase/Acylhydrolase-superfamily-protein
AT1G56510	chr1_21171909	cis	-0,64±0,1	2,46E-10	0,23	Disease-resistance-protein-(TIR-NBS-LRR-class)
AT1G72020	chr1_27110298	cis	0,55±0,09	2,52E-10	0,46	
AT3G52670	chr3_19526591	cis	-0,61±0,1	2,52E-10	0,32	FBD,-F-box,-Skp2-like-and-Leucine-Rich-Repeat-domains-containing-protein
AT4G15270	chr4_8717696	cis	-0,54±0,09	2,55E-10	0,51	glucosyltransferase-related
AT1G12013	chr1_4057189	cis	-0,55±0,09	2,57E-10	0,45	SNOR111;-snoRNA
AT1G20600	chr1_7122124	cis	0,74±0,12	2,59E-10	0,19	AP2/B3-like-transcriptional-factor-family-protein
AT4G29860	chr4_14605507	cis	-0,77±0,12	2,59E-10	0,16	Transducin/WD40-repeat-like-superfamily-protein
AT3G06470	chr3_1984116	cis	0,73±0,11	2,63E-10	0,19	GNS1/SUR4-membrane-protein-family
AT4G10955	chr4_6715832	cis	0,6±0,1	2,66E-10	0,30	alpha/beta-Hydrolases-superfamily-protein
AT5G44230	chr5_17819248	cis	0,55±0,09	2,66E-10	0,55	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT2G42240	chr2_17590200	cis	0,77±0,12	2,71E-10	0,18	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT3G60300	chr3_22281512	cis	-0,84±0,13	2,71E-10	0,11	RWD-domain-containing-protein
AT2G05140	chr2_15808355	trans	0,56±0,09	2,76E-10	0,44	phosphoribosylaminoimidazole-carboxylase-family-protein-/-AIR-carboxylase-family-protein
AT1G65950	chr1_24551091	cis	0,59±0,09	2,81E-10	0,37	Protein-kinase-superfamily-protein
AT2G24010	chr2_10216288	cis	-0,56±0,09	2,81E-10	0,48	serine-carboxypeptidase-like-23
AT4G18230	chr4_10080045	cis	0,72±0,11	2,85E-10	0,18	
AT3G58020	chr3_21479339	cis	-0,55±0,09	2,88E-10	0,43	Chaperone-DnaJ-domain-superfamily-protein
AT1G65260	chr1_24237544	cis	0,55±0,09	2,89E-10	0,44	plastid-transcriptionally-active-4
AT2G40290	chr2_16836053	cis	-0,58±0,09	2,90E-10	0,29	Eukaryotic-translation-initiation-factor-2-subunit-1
AT3G45890	chr3_16877300	cis	0,61±0,1	2,90E-10	0,27	Protein-of-unknown-function,-DUF647
AT2G39910	chr2_16660660	cis	0,74±0,12	3,01E-10	0,18	ARM-repeat-superfamily-protein
AT5G17680	chr5_5819976	cis	0,55±0,09	3,04E-10	0,35	disease-resistance-protein-(TIR-NBS-LRR-class),-putative
AT2G44280	chr2_18293820	cis	-0,57±0,09	3,06E-10	0,34	Major-facilitator-superfamily-protein
AT5G04000	chr5_1080007	cis	0,85±0,13	3,08E-10	0,12	
AT4G00880	chr4_271105	trans	0,66±0,1	3,09E-10	0,35	SAUR-like-auxin-responsive-protein-family-
AT1G69540	chr1_26147426	cis	0,73±0,12	3,12E-10	0,16	AGAMOUS-like-94
AT1G31600	chr1_11314592	cis	0,52±0,08	3,15E-10	0,52	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT1G30550	chr1_10820932	cis	0,66±0,11	3,16E-10	0,21	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein
AT5G24155	chr5_8176641	cis	-0,69±0,11	3,17E-10	0,19	FAD/NAD(P)-binding-oxidoreductase-family-protein
AT1G80560	chr1_30287050	cis	-0,57±0,09	3,17E-10	0,36	isopropylmalate-dehydrogenase-2
AT4G14900	chr4_8522304	cis	0,56±0,09	3,27E-10	0,33	FRIGIDA-like-protein
AT4G33700	chr4_16177030	cis	0,82±0,13	3,36E-10	0,14	CBS-domain-containing-protein-with-a-domain-of-unknown-function-(DUF21)
AT5G17780	chr5_5868804	cis	0,6±0,1	3,38E-10	0,31	alpha/beta-Hydrolases-superfamily-protein
AT3G32920	chr3_12934421	trans	0,86±0,14	3,38E-10	0,13	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT4G39390	chr4_18316245	cis	0,58±0,09	3,38E-10	0,35	nucleotide-sugar-transporter-KT-1
AT3G48680	chr3_18034930	cis	-0,62±0,1	3,39E-10	0,30	gamma-carbonic-anhydrase-like-2
AT5G55840	chr5_22597960	cis	-0,72±0,11	3,40E-10	0,16	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT3G07580	chr3_2433900	cis	-0,69±0,11	3,41E-10	0,21	
AT2G32910	chr2_13959650	cis	0,91±0,14	3,44E-10	0,11	DCD-(Development-and-Cell-Death)-domain-protein
AT4G27540	chr4_13753849	cis	-0,92±0,15	3,46E-10	0,09	prenylated-RAB-acceptor-1.H
AT1G05200	chr1_1505613	cis	0,61±0,1	3,47E-10	0,26	glutamate-receptor-3.4
AT3G59190	chr3_21877104	cis	-0,92±0,15	3,47E-10	0,12	F-box/RNI-like-superfamily-protein
AT5G28010	chr5_10032888	cis	-0,55±0,09	3,50E-10	0,35	Polyketide-cyclase/dehydrase-and-lipid-transport-superfamily-protein
AT3G08920	chr3_2711620	cis	0,55±0,09	3,55E-10	0,40	Rhodanese/Cell-cycle-control-phosphatase-superfamily-protein
AT5G01595	chr5_221671	cis	0,56±0,09	3,65E-10	0,54	other-RNA
AT5G59720	chr5_24034956	cis	-0,7±0,11	3,72E-10	0,19	heat-shock-protein-18.2
AT5G24660	chr5_8443580	cis	-0,69±0,11	3,81E-10	0,29	response-to-low-sulfur-2
AT1G52550	chr1_19573429	cis	0,65±0,1	3,85E-10	0,23	
AT1G48400	chr1_17882506	cis	0,53±0,08	3,88E-10	0,49	F-box/RNI-like/FBD-like-domains-containing-protein
AT1G25380	chr1_8904072	cis	-0,61±0,1	3,99E-10	0,26	NAD+-transporter-2
AT4G31110	chr4_15127463	cis	-0,75±0,12	4,01E-10	0,15	Wall-associated-kinase-family-protein
AT2G41340	chr2_17235505	cis	-0,61±0,1	4,04E-10	0,30	RNA-polymerase-II-fifth-largest-subunit,-D
AT1G64970	chr1_24135673	cis	-0,57±0,09	4,14E-10	0,48	gamma-tocopherol-methyltransferase
AT5G59600	chr5_24012782	cis	-0,59±0,09	4,14E-10	0,33	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT3G07300	chr3_2327628	cis	0,55±0,09	4,15E-10	0,50	NagB/RpiA/CoA-transferase-like-superfamily-protein
AT4G16570	chr4_9336847	cis	0,66±0,11	4,18E-10	0,23	protein-arginine-methyltransferase-7
AT5G24150	chr5_8180451	cis	0,77±0,12	4,18E-10	0,14	FAD/NAD(P)-binding-oxidoreductase-family-protein
AT3G56990	chr3_21087135	cis	-0,68±0,11	4,19E-10	0,21	embryo-sac-development-arrest-7
AT1G37150	chr1_14893683	trans	-0,6±0,1	4,21E-10	0,40	holocarboxylase-synthetase-2
AT1G78940	chr1_29684120	cis	0,76±0,12	4,23E-10	0,14	Protein-kinase-protein-with-adenine-nucleotide-alpha-hydrolases-like-domain

AT5G50940	chr5_20724966	cis	-0,61±0,1	4,29E-10	0,34	RNA-binding-KH-domain-containing-protein
AT1G78860	chr1_29646578	cis	-0,56±0,09	4,30E-10	0,47	D-mannose-binding-lectin-protein-with-Apple-like-carbohydrate-binding-domain
AT4G14630	chr4_8390580	cis	-0,74±0,12	4,34E-10	0,15	germin-like-protein-9
AT1G45170	chr1_17094706	cis	-0,63±0,1	4,36E-10	0,28	
AT2G32340	chr2_13732366	cis	-0,59±0,09	4,37E-10	0,32	TraB-family-protein
AT2G38980	chr2_16282870	cis	-0,56±0,09	4,39E-10	0,46	
AT2G20130	chr2_8687834	cis	0,54±0,09	4,39E-10	0,55	like-COV-1
AT1G20590	chr1_7132765	cis	-0,62±0,1	4,40E-10	0,42	Cyclin-family-protein
AT5G56100	chr5_22703218	cis	-0,83±0,13	4,41E-10	0,11	glycine-rich-protein-/-oleosin
AT1G77230	chr1_29009432	cis	0,58±0,09	4,42E-10	0,47	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT1G27530	chr1_9565203	cis	-0,56±0,09	4,45E-10	0,41	
AT5G16790	chr5_5523941	cis	0,92±0,15	4,50E-10	0,11	Tho-complex-subunit-7/Mft1p
AT4G19490	chr4_10616870	cis	-0,54±0,09	4,51E-10	0,37	VPS54
AT1G68940	chr1_25918515	cis	-0,79±0,13	4,53E-10	0,14	Armadillo/beta-catenin-like-repeat-family-protein
AT1G64230	chr1_23846006	cis	-0,58±0,09	4,54E-10	0,36	ubiquitin-conjugating-enzyme-28
AT5G54400	chr5_22088472	cis	0,57±0,09	4,60E-10	0,47	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein
AT4G05450	chr4_2759845	cis	-0,56±0,09	4,62E-10	0,47	mitochondrial-ferredoxin-1
AT5G18750	chr5_6254423	cis	0,67±0,11	4,81E-10	0,20	DNAJ-heat-shock-N-terminal-domain-containing-protein
AT5G20420	chr5_6887510	cis	-0,66±0,11	4,82E-10	0,28	chromatin-remodeling-42
AT2G31530	chr2_13436307	cis	-0,65±0,11	4,89E-10	0,25	SecY-protein-transport-family-protein
AT2G28130	chr2_11989124	cis	-0,56±0,09	4,89E-10	0,39	
AT3G18870	chr3_6508974	cis	-0,66±0,11	5,00E-10	0,20	Mitochondrial-transcription-termination-factor-family-protein
AT2G39100	chr2_16312091	cis	0,58±0,09	5,11E-10	0,36	RING/U-box-superfamily-protein
AT1G16150	chr1_5531987	cis	0,8±0,13	5,15E-10	0,13	wall-associated-kinase-like-4
AT1G31750	chr1_11372296	cis	-0,6±0,1	5,19E-10	0,26	proline-rich-family-protein
AT5G37350	chr5_14794054	cis	0,63±0,1	5,22E-10	0,22	Serine/threonine-protein-kinase-Rio1
AT1G33490	chr1_12172603	cis	-0,87±0,14	5,23E-10	0,10	
AT1G29320	chr1_10247985	cis	0,81±0,13	5,33E-10	0,13	Transducin/WD40-repeat-like-superfamily-protein
AT5G42670	chr5_17108205	cis	0,62±0,1	5,33E-10	0,29	Agenet-domain-containing-protein
AT3G03480	chr3_830684	cis	0,59±0,09	5,46E-10	0,29	acetyl-CoA:(Z)-3-hexen-1-ol-acetyltransferase
AT5G39380	chr5_15762102	cis	0,56±0,09	5,54E-10	0,52	Plant-calmodulin-binding-protein-related
AT5G46500	chr5_18853814	cis	0,96±0,15	5,55E-10	0,09	
AT4G12120	chr4_7260781	cis	-0,73±0,12	5,57E-10	0,16	Sec1/munc18-like-(SM)-proteins-superfamily
AT1G29785	chr1_10430531	cis	0,73±0,12	5,58E-10	0,19	other-RNA
AT4G21940	chr4_11638383	cis	-0,65±0,11	5,66E-10	0,21	calcium-dependent-protein-kinase-15
AT4G01600	chr4_693151	cis	-0,57±0,09	5,71E-10	0,36	GRAM-domain-family-protein
AT5G66080	chr5_26424978	cis	-0,54±0,09	5,71E-10	0,49	Protein-phosphatase-2C-family-protein
AT5G62480	chr5_25089660	cis	-0,6±0,1	5,72E-10	0,31	glutathione-S-transferase-tau-9
AT4G30390	chr4_14863146	cis	0,68±0,11	5,73E-10	0,20	
AT4G16330	chr4_9227540	cis	-0,72±0,12	5,74E-10	0,16	2-oxoglutarate-(2OG)-and-Fe(II)-dependent-oxygenase-superfamily-protein
AT2G25220	chr2_10747302	cis	0,55±0,09	5,75E-10	0,46	Protein-kinase-superfamily-protein
AT4G37680	chr4_17707596	cis	-0,64±0,1	5,88E-10	0,24	heptahelical-protein-4
AT1G02680	chr1_582044	cis	0,59±0,1	5,92E-10	0,26	TBP-associated-factor-13
AT5G56950	chr5_23033330	cis	0,68±0,11	5,92E-10	0,22	nucleosome-assembly-protein-1;3
AT4G25780	chr4_13099081	cis	-0,58±0,09	5,93E-10	0,29	CAP-(Cysteine-rich-secretory-proteins,-Antigen-5,-and-Pathogenesis-related-1-protein)-superfamily-protein
AT1G22500	chr1_7957563	cis	-0,59±0,1	5,95E-10	0,31	RING/U-box-superfamily-protein
AT2G35950	chr2_15102717	cis	0,57±0,09	6,01E-10	0,30	embryo-sac-development-arrest-12
AT2G14260	chr2_6042140	cis	-0,79±0,13	6,01E-10	0,15	proline-iminopeptidase
AT1G32220	chr1_11607120	cis	0,56±0,09	6,03E-10	0,46	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT2G29440	chr2_12622339	cis	0,54±0,09	6,06E-10	0,54	glutathione-S-transferase-tau-6
AT3G25060	chr3_9128896	cis	-0,53±0,09	6,08E-10	0,44	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT4G09750	chr4_6146593	cis	-0,56±0,09	6,09E-10	0,41	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT5G49650	chr5_20154335	cis	-0,83±0,13	6,13E-10	0,11	xylulose-kinase-2
AT5G60430	chr5_24304209	cis	-0,71±0,11	6,18E-10	0,18	drug-transmembrane-transporters;antiporters
AT3G49410	chr3_18329902	cis	0,59±0,09	6,22E-10	0,47	Transcription-factor-IIIC,-subunit-5
AT5G40700	chr5_16293488	cis	0,78±0,13	6,27E-10	0,14	
AT5G42310	chr5_16913465	cis	0,55±0,09	6,30E-10	0,41	Pentatricopeptide-repeat-(PPR-like)-superfamily-protein
AT2G44290	chr2_18290320	cis	-0,54±0,09	6,36E-10	0,45	Bifunctional-inhibitor/lipid-transfer-protein/seed-storage-2S-albumin-superfamily-protein
AT5G44568	chr5_17966184	cis	-0,57±0,09	6,36E-10	0,35	
AT5G19180	chr5_6453495	cis	-0,64±0,1	6,47E-10	0,24	E1-C-terminal-related-1
AT3G14550	chr3_4874896	cis	0,68±0,11	6,52E-10	0,22	geranylgeranyl-pyrophosphate-synthase-3
AT1G63230	chr1_23448744	cis	0,56±0,09	6,62E-10	0,42	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT1G71350	chr1_26891020	cis	0,63±0,1	6,66E-10	0,24	eukaryotic-translation-initiation-factor-SUI1-family-protein
AT1G05430	chr1_1590032	cis	-0,79±0,13	6,69E-10	0,14	
AT3G56690	chr3_20998587	cis	-0,63±0,1	6,75E-10	0,25	Cam-interacting-protein-111
AT5G38030	chr5_15174498	cis	-0,57±0,09	6,75E-10	0,34	MATE-efflux-family-protein
AT1G11870	chr1_4004173	cis	-0,57±0,09	6,79E-10	0,31	Seryl-tRNA-synthetase
AT5G60410	chr5_24292611	cis	0,77±0,13	6,83E-10	0,15	DNA-binding-protein-with-MIZ/SP-RING-zinc-finger,-PHD-finger-and-SAP-domain
AT1G77765	chr1_29244015	cis	-0,53±0,09	6,90E-10	0,39	
AT5G05760	chr5_1728894	cis	0,55±0,09	7,11E-10	0,41	syntaxin-of-plants-31
AT1G61390	chr1_21928292	trans	0,72±0,12	7,12E-10	0,16	S-locus-lectin-protein-kinase-family-protein
AT2G46440	chr2_19092333	cis	0,53±0,09	7,16E-10	0,41	cyclic-nucleotide-gated-channels
AT1G70500	chr1_26568399	cis	-0,74±0,12	7,40E-10	0,14	Pectin-lyase-like-superfamily-protein
AT5G25490	chr5_8875445	cis	-0,68±0,11	7,46E-10	0,19	Ran-BP2/NZF-zinc-finger-like-superfamily-protein
AT5G67290	chr5_26850045	cis	-0,84±0,14	7,61E-10	0,13	FAD-dependent-oxidoreductase-family-protein
AT1G50700	chr1_18787783	cis	0,76±0,12	7,67E-10	0,11	calcium-dependent-protein-kinase-33
AT3G61200	chr3_22657467	cis	-0,57±0,09	7,72E-10	0,40	Thioesterase-superfamily-protein
AT1G29590	chr1_10354583	cis	0,61±0,1	7,75E-10	0,26	Eukaryotic-initiation-factor-4E-protein
AT1G25054	chr1_8842441	cis	0,85±0,14	7,85E-10	0,12	UDP-3-O-acyl-N-acetylglycosamine-deacetylase-family-protein

AT3G47730	chr3_17598994	cis	-0,53±0,09	7,87E-10	0,53	ATP-binding-cassette-A2
AT5G38340	chr5_15321266	cis	0,86±0,14	7,88E-10	0,10	Disease-resistance-protein-(TIR-NBS-LRR-class)-family
AT3G32410	chr3_13368834	cis	0,68±0,11	7,90E-10	0,19	
AT3G46440	chr3_17091869	cis	0,53±0,09	7,93E-10	0,39	UDP-XYL-synthase-5
AT1G64840	chr1_24092660	cis	-0,53±0,09	8,00E-10	0,40	Protein-of-unknown-function-(DUF295)
AT3G59750	chr3_22078350	cis	0,55±0,09	8,03E-10	0,45	Concanavalin-A-like-lectin-protein-kinase-family-protein
AT1G52100	chr1_19361404	cis	-0,6±0,1	8,08E-10	0,24	Mannose-binding-lectin-superfamily-protein
AT1G63000	chr1_23342609	cis	0,57±0,09	8,08E-10	0,46	nucleotide-rhamnose-synthase/epimerase-reductase
AT5G48160	chr5_19528651	cis	-0,65±0,11	8,18E-10	0,22	Protein-of-unknown-function-(DUF1423)
AT2G43720	chr2_18129783	cis	-0,88±0,14	8,34E-10	0,11	Eukaryotic-protein-of-unknown-function-(DUF842)
AT3G18940	chr3_6527040	cis	-0,62±0,1	8,39E-10	0,27	clast3-related
AT5G21950	chr5_7255900	cis	-0,59±0,1	8,40E-10	0,51	alpha/beta-Hydrolases-superfamily-protein
AT1G15890	chr1_5459026	cis	0,94±0,15	8,43E-10	0,09	Disease-resistance-protein-(CC-NBS-LRR-class)-family
AT3G60880	chr3_22494822	cis	0,62±0,1	8,44E-10	0,24	dihydrodipicolinate-synthase-1
AT4G26550	chr4_13403992	cis	-0,76±0,12	8,48E-10	0,16	Got1/Sft2-like-vescicle-transport-protein-family
AT4G23230	chr4_12153793	cis	-0,66±0,11	8,49E-10	0,41	cysteine-rich-RLK-(RECEPTOR-like-protein-kinase)-15
AT3G08880	chr3_2704353	cis	0,7±0,11	8,50E-10	0,19	
AT5G17840	chr5_5896262	cis	-0,7±0,11	8,56E-10	0,19	DnaJ/Hsp40-cysteine-rich-domain-superfamily-protein
AT5G03770	chr5_995194	cis	0,56±0,09	8,58E-10	0,36	KDO-transferase-A
AT3G46900	chr3_17271482	cis	-0,61±0,1	8,65E-10	0,26	copper-transporter-2
AT2G23360	chr5_14311152	trans	0,71±0,12	8,74E-10	0,15	Plant-protein-of-unknown-function-(DUF869)
AT3G56320	chr3_20882460	cis	0,87±0,14	8,84E-10	0,12	PAP/OAS1-substrate-binding-domain-superfamily
AT3G25470	chr3_9233282	cis	-0,54±0,09	8,84E-10	0,52	bacterial-hemolysin-related
AT5G45220	chr5_18299834	cis	-01,01±0,16	8,85E-10	0,09	Disease-resistance-protein-(TIR-NBS-LRR-class)-family
AT5G09443	chr5_2943446	cis	-0,84±0,14	8,89E-10	0,10	other-RNA
AT1G10110	chr1_3274595	cis	0,94±0,15	8,91E-10	0,09	F-box-family-protein
AT1G57600	chr1_21334193	cis	-0,58±0,09	8,94E-10	0,31	MBOAT-(membrane-bound-O-acyl-transferase)-family-protein
AT2G43990	chr2_18212140	cis	0,52±0,08	8,97E-10	0,56	
AT1G31190	chr1_11141205	cis	0,56±0,09	9,06E-10	0,38	myo-inositol-monophosphatase-like-1
AT4G14660	chr4_8407709	cis	0,51±0,08	9,25E-10	0,54	RNA-polymerase-Rpb7-like,-N-terminal-domain
AT3G44716	chr3_16263695	cis	-0,53±0,09	9,31E-10	0,39	
AT3G28880	chr3_10891692	cis	-0,69±0,11	9,37E-10	0,19	Ankyrin-repeat-family-protein
AT1G55550	chr1_20749194	cis	0,59±0,1	9,39E-10	0,31	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT3G26280	chr3_9632640	cis	-0,52±0,09	9,55E-10	0,38	cytochrome-P450,-family-71,-subfamily-B,-polypeptide-4
AT1G80570	chr1_30288235	cis	-0,66±0,11	9,56E-10	0,23	RNI-like-superfamily-protein
AT1G04390	chr1_1196560	cis	0,76±0,12	9,56E-10	0,18	BTB/POZ-domain-containing-protein
AT4G22350	chr4_11781527	cis	-0,59±0,1	9,58E-10	0,33	Ubiquitin-C-terminal-hydrolases-superfamily-protein
AT5G55810	chr5_22585634	cis	-0,82±0,13	9,73E-10	0,10	nicotinate/nicotinamide-mononucleotide-adenyltransferase
AT2G27190	chr2_11623555	cis	0,54±0,09	9,74E-10	0,54	purple-acid-phosphatase-12
AT2G45490	chr2_18745425	cis	01,05±0,17	9,85E-10	0,06	ataurora3
AT5G21274	chr5_7215584	cis	0,67±0,11	9,93E-10	0,22	calmodulin-6
AT1G51965	chr1_19314183	cis	-0,54±0,09	1,00E-09	0,36	ABA-Overly-Sensitive-5
AT1G18540	chr1_6376763	cis	0,55±0,09	1,01E-09	0,50	Ribosomal-protein-L6-family-protein
AT3G30415	chr3_12040229	cis	-0,61±0,1	1,02E-09	0,28	
AT5G46020	chr5_18671090	cis	0,6±0,1	1,04E-09	0,26	
AT2G18560	chr2_8059975	cis	0,56±0,09	1,04E-09	0,31	UDP-Glycosyltransferase-superfamily-protein
AT1G16445	chr1_5619023	cis	0,56±0,09	1,06E-09	0,33	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein
AT1G55060	chr4_2591900	trans	0,93±0,15	1,07E-09	0,09	ubiquitin-12
AT3G24030	chr3_8680846	cis	0,66±0,11	1,08E-09	0,19	hydroxyethylthiazole-kinase-family-protein
AT1G23465	chr1_8327189	cis	0,53±0,09	1,09E-09	0,53	Peptidase-S24/S26A/S26B/S26C-family-protein
AT2G43550	chr2_18073286	cis	0,59±0,1	1,09E-09	0,28	Scorpion-toxin-like-knottin-superfamily-protein
AT4G13270	chr4_7731923	cis	-0,62±0,1	1,11E-09	0,21	Late-embryogenesis-abundant-(LEA)-hydroxyproline-rich-glycoprotein-family
AT2G01090	chr2_80380	cis	-0,54±0,09	1,11E-09	0,53	Ubiquinol-cytochrome-C-reductase-hinge-protein
AT1G66990	chr1_24998798	cis	0,62±0,1	1,12E-09	0,26	
AT2G31900	chr2_13569505	cis	-0,8±0,13	1,13E-09	0,12	myosin-like-protein-XIF
AT4G02070	chr4_908938	cis	0,58±0,1	1,13E-09	0,35	MUTS-homolog-6
AT1G66980	chr1_24996712	cis	-0,77±0,13	1,15E-09	0,13	suppressor-of-npr1-1-constitutive-4
AT2G44530	chr2_18385999	cis	-0,53±0,09	1,15E-09	0,44	Phosphoribosyltransferase-family-protein
AT5G63580	chr5_25432318	cis	-0,62±0,1	1,15E-09	0,36	flavonol-synthase-2
AT5G50950	chr5_20727510	cis	0,59±0,1	1,15E-09	0,47	FUMARASE-2
AT5G52547	chr5_21326420	cis	-01,03±0,17	1,17E-09	0,09	
AT1G65220	chr1_24227508	cis	0,57±0,09	1,18E-09	0,31	ARM-repeat-superfamily-protein
AT3G09310	chr3_2860339	cis	0,74±0,12	1,18E-09	0,15	
AT2G35690	chr2_14996156	cis	0,56±0,09	1,19E-09	0,31	acyl-CoA-oxidase-5
AT1G63050	chr1_23378719	cis	0,56±0,09	1,19E-09	0,31	MBOAT-(membrane-bound-O-acyl-transferase)-family-protein
AT5G42990	chr5_17246025	cis	0,66±0,11	1,20E-09	0,21	ubiquitin-conjugating-enzyme-18
AT5G56020	chr5_22689265	cis	-0,64±0,1	1,20E-09	0,21	Got1/Sft2-like-vescicle-transport-protein-family
AT1G15250	chr1_5249719	cis	0,55±0,09	1,20E-09	0,46	Zinc-binding-ribosomal-protein-family-protein
AT2G21620	chr2_9251171	cis	-0,53±0,09	1,20E-09	0,52	Adenine-nucleotide-alpha-hydrolases-like-superfamily-protein
AT5G05750	chr5_1730564	cis	-0,67±0,11	1,20E-09	0,24	DNAJ-heat-shock-N-terminal-domain-containing-protein
AT1G69800	chr1_26288176	cis	-0,54±0,09	1,21E-09	0,37	Cystathionine-beta-synthase-(CBS)-protein
AT5G02820	chr5_638795	cis	-0,59±0,1	1,21E-09	0,59	Spo11/DNA-topoisomerase-VI,-subunit-A-protein
AT4G07410	chr4_4738380	trans	0,64±0,11	1,22E-09	0,29	Transducin-family-protein-/-WD-40-repeat-family-protein
AT3G01920	chr3_315601	cis	0,81±0,13	1,22E-09	0,18	DHBP-synthase-RibB-like-alpha/beta-domain
AT3G26240	chr3_9628252	cis	-0,54±0,09	1,24E-09	0,54	Cysteine/Histidine-rich-C1-domain-family-protein
AT5G03390	chr5_855311	cis	0,53±0,09	1,24E-09	0,41	Protein-of-unknown-function-(DUF295)
AT5G24060	chr5_8123401	cis	0,95±0,16	1,26E-09	0,09	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT3G43610	chr5_9604488	trans	0,65±0,11	1,29E-09	0,19	Spc97-/-Spc98-family-of-spindle-pole-body-(SBP)-component
AT4G00270	chr4_123214	cis	-0,6±0,1	1,29E-09	0,29	DNA-binding-storekeeper-protein-related-transcriptional-regulator

AT5G26680	chr5_9317120	cis	01,06±0,17	1,29E-09	0,08	5'-3'-exonuclease-family-protein
AT1G14640	chr1_5038823	cis	0,57±0,09	1,32E-09	0,34	SWAP-(Suppressor-of-White-APricot)/surp-domain-containing-protein
AT1G31970	chr1_11479866	cis	-0,7±0,11	1,33E-09	0,16	DEA(D/H)-box-RNA-helicase-family-protein
AT5G37055	chr5_14642272	cis	0,61±0,1	1,36E-09	0,21	HIT-type-Zinc-finger-family-protein
AT2G24310	chr2_10341522	cis	0,56±0,09	1,36E-09	0,38	
AT3G43400	chr1_25248868	trans	-0,53±0,09	1,37E-09	0,41	ELMO/CED-12-family-protein
AT2G36305	chr2_15215901	cis	0,88±0,15	1,37E-09	0,11	farnesylated-protein-converting-enzyme-2
AT1G22370	chr1_7900160	cis	-0,61±0,1	1,39E-09	0,24	UDP-glucosyl-transferase-85A5
AT2G31490	chr2_13411014	cis	0,88±0,15	1,39E-09	0,09	
AT5G51620	chr5_20975575	cis	-0,72±0,12	1,40E-09	0,19	Uncharacterised-protein-family-(UPF0172)
AT4G28900	chr4_14258824	cis	0,78±0,13	1,40E-09	0,13	transposable-element-gene
AT3G61030	chr3_22577967	cis	0,52±0,09	1,41E-09	0,48	Calcium-dependent-lipid-binding-(CaLB-domain)-family-protein
AT5G40400	chr5_16169885	cis	-0,66±0,11	1,42E-09	0,19	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT4G01525	chr4_664689	cis	-0,58±0,1	1,42E-09	0,21	transposable-element-gene
AT3G21690	chr3_7635436	cis	-0,78±0,13	1,42E-09	0,14	MATE-efflux-family-protein
AT1G24148	chr1_8544275	cis	-0,64±0,11	1,42E-09	0,20	
AT4G13495	chr4_7845665	cis	-0,52±0,09	1,43E-09	0,49	other-RNA
AT5G23405	chr5_7884380	cis	0,51±0,08	1,45E-09	0,44	HMG-box-(high-mobility-group)-DNA-binding-family-protein
AT1G07960	chr1_2471021	cis	0,51±0,08	1,45E-09	0,43	PDI-like-5-1
AT1G17820	chr1_6097465	cis	0,9±0,15	1,45E-09	0,10	Putative-integral-membrane-protein-conserved-region-(DUF2404)
AT2G35635	chr2_14981947	cis	-0,6±0,1	1,48E-09	0,22	ubiquitin-7
AT3G02710	chr3_618249	cis	0,54±0,09	1,49E-09	0,45	ARM-repeat-superfamily-protein
AT3G43600	chr3_15517078	cis	-0,61±0,1	1,50E-09	0,23	aldehyde-oxidase-2
AT4G16845	chr4_9475749	cis	0,5±0,08	1,51E-09	0,53	VEFS-Box-of-polycomb-protein
AT1G02520	chr1_523780	cis	-0,69±0,11	1,52E-09	0,20	P-glycoprotein-11
AT5G48660	chr5_19736200	cis	-0,69±0,11	1,53E-09	0,17	B-cell-receptor-associated-protein-31-like-
AT3G48320	chr3_17891171	cis	-0,53±0,09	1,53E-09	0,34	cytochrome-P450,-family-71,-subfamily-A,-polypeptide-21
AT5G47960	chr5_19410732	cis	0,54±0,09	1,58E-09	0,47	RAB-GTPase-homolog-A4C
AT3G45410	chr3_16655687	cis	0,55±0,09	1,58E-09	0,36	Concanavalin-A-like-lectin-protein-kinase-family-protein
AT2G43540	chr2_18070625	cis	-0,66±0,11	1,61E-09	0,19	
AT1G74780	chr1_28095806	cis	-0,95±0,16	1,62E-09	0,08	Nodulin-like-/-Major-Facilitator-Superfamily-protein
AT2G41050	chr2_17125850	cis	-0,57±0,09	1,63E-09	0,31	PQ-loop-repeat-family-protein-/-transmembrane-family-protein
AT1G59840	chr1_22026485	cis	0,92±0,15	1,65E-09	0,09	cofactor-assembly-of-complex-C
AT1G66690	chr1_24877851	cis	0,52±0,09	1,66E-09	0,46	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein
AT4G34900	chr4_16629287	cis	-0,59±0,1	1,66E-09	0,24	xanthine-dehydrogenase--2
AT3G14700	chr3_4943857	cis	0,6±0,1	1,67E-09	0,25	SART-1-family
AT1G05720	chr1_1716782	cis	-0,67±0,11	1,67E-09	0,21	selenoprotein-family-protein
AT4G36130	chr4_17096933	cis	0,62±0,1	1,68E-09	0,25	Ribosomal-protein-L2-family
AT1G17260	chr1_5898135	cis	0,57±0,09	1,70E-09	0,29	autoinhibited-H(+)-ATPase-isoform-10
AT3G19390	chr3_6722728	cis	0,57±0,09	1,71E-09	0,36	Granulin-repeat-cysteine-protease-family-protein
AT5G03180	chr5_767404	cis	-0,67±0,11	1,72E-09	0,20	RING/U-box-superfamily-protein
AT5G56900	chr5_23019431	cis	0,81±0,13	1,74E-09	0,12	CwfJ-like-family-protein-/-zinc-finger-(CCCH-type)-family-protein
AT4G04490	chr4_2238541	cis	-0,55±0,09	1,75E-09	0,43	cysteine-rich-RLK-(RECEPTOR-like-protein-kinase)-36
AT1G11420	chr1_3852453	cis	-0,75±0,12	1,75E-09	0,15	DOMAIN-OF-UNKNOWN-FUNCTION-724-2
AT4G27740	chr4_13838610	cis	-0,52±0,09	1,78E-09	0,46	Yippee-family-putative-zinc-binding-protein
AT2G11000	chr2_4347440	cis	0,79±0,13	1,80E-09	0,18	MAK10-homologue
AT1G08350	chr1_2658328	cis	-0,67±0,11	1,80E-09	0,28	Endomembrane-protein-70-protein-family
AT1G15000	chr1_5139089	cis	0,69±0,12	1,81E-09	0,21	serine-carboxypeptidase-like-50
AT5G55460	chr5_22470885	cis	-0,93±0,15	1,81E-09	0,08	Bifunctional-inhibitor/lipid-transfer-protein/seed-storage-2S-albumin-superfamily-protein
AT4G07950	chr2_1267472	trans	-0,87±0,14	1,82E-09	0,11	DNA-directed-RNA-polymerase,-subunit-M,-archaeal
AT1G56440	chr1_21137671	cis	-0,52±0,09	1,82E-09	0,46	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT5G43822	chr5_17615905	cis	-0,52±0,09	1,82E-09	0,42	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT1G63245	chr1_23460503	cis	0,65±0,11	1,84E-09	0,19	CLAVATA3/ESR-RELATED-14
AT1G08030	chr1_2492448	cis	-0,61±0,1	1,86E-09	0,24	tyrosylprotein-sulfotransferase
AT2G02400	chr2_630968	cis	-0,64±0,11	1,86E-09	0,19	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT5G45520	chr5_18453651	cis	0,55±0,09	1,87E-09	0,34	Leucine-rich-repeat-(LRR)-family-protein
AT1G72030	chr1_27110891	cis	-0,54±0,09	1,87E-09	0,42	Acyl-CoA-N-acyltransferases-(NAT)-superfamily-protein
AT1G16310	chr1_5577794	cis	-0,54±0,09	1,91E-09	0,37	Cation-efflux-family-protein
AT1G65610	chr1_24395482	cis	0,78±0,13	1,91E-09	0,14	Six-hairpin-glycosidases-superfamily-protein
AT4G17010	chr4_9576056	cis	0,56±0,09	1,91E-09	0,31	
AT2G19310	chr2_8370278	cis	0,57±0,1	1,93E-09	0,31	HSP20-like-chaperones-superfamily-protein
AT4G15200	chr4_8666801	cis	-0,87±0,14	1,99E-09	0,09	formin-3
AT1G29150	chr1_10178929	cis	-0,53±0,09	2,00E-09	0,43	non-ATPase-subunit-9
AT1G76300	chr1_28610141	cis	-0,55±0,09	2,01E-09	0,34	snRNP-core-protein-SMD3
AT1G63110	chr1_23404953	cis	0,61±0,1	2,02E-09	0,21	GPI-transamidase-subunit-PIG-U
AT1G22403	chr1_7907579	cis	-01,02±0,17	2,04E-09	0,06	other-RNA
AT1G14900	chr1_5138651	cis	-0,56±0,09	2,04E-09	0,39	high-mobility-group-A
AT5G48560	chr5_19688512	cis	0,53±0,09	2,05E-09	0,45	basic-helix-loop-helix-(bHLH)-DNA-binding-superfamily-protein
AT2G30280	chr2_12910878	cis	-0,54±0,09	2,08E-09	0,38	RNA-directed-DNA-methylation-4
AT1G58122	chr5_9764016	trans	-0,69±0,12	2,09E-09	0,16	conserved-peptide-upstream-open-reading-frame-45
AT2G21080	chr2_9038933	cis	-0,8±0,13	2,09E-09	0,14	
AT1G53790	chr1_20083314	cis	-0,81±0,14	2,09E-09	0,14	F-box-and-associated-interaction-domains-containing-protein
AT5G20730	chr5_7044231	cis	-0,75±0,13	2,12E-09	0,14	Transcriptional-factor-B3-family-protein-/-auxin-responsive-factor-AUX/IAA-related
AT5G36260	chr5_14291357	cis	0,51±0,08	2,12E-09	0,49	Eukaryotic-aspartyl-protease-family-protein
AT5G61865	chr5_24848242	cis	-0,87±0,15	2,13E-09	0,09	
AT4G37970	chr4_17850377	cis	-0,62±0,1	2,13E-09	0,21	cinnamyl-alcohol-dehydrogenase-6
AT4G25020	chr4_12862378	cis	-0,51±0,09	2,16E-09	0,46	D111/G-patch-domain-containing-protein
AT5G64440	chr5_25766681	cis	0,6±0,1	2,17E-09	0,24	fatty-acid-amide-hydrolase
AT2G29480	chr2_12631663	cis	-0,51±0,09	2,20E-09	0,41	glutathione-S-transferase-tau-2

AT5G21070	chr5_7150277	cis	-0,62±0,1	2,24E-09	0,23	
AT4G21630	chr4_11487432	cis	0,88±0,15	2,25E-09	0,09	Subtilase-family-protein
AT1G21270	chr1_7447447	cis	-0,75±0,13	2,26E-09	0,13	wall-associated-kinase-2
AT1G05730	chr1_1719028	cis	-0,68±0,11	2,27E-09	0,24	Eukaryotic-protein-of-unknown-function-(DUF842)
AT1G10095	chr1_3314223	cis	0,87±0,15	2,27E-09	0,10	Protein-prenylyltransferase-superfamily-protein
AT5G46390	chr5_18819603	cis	0,8±0,13	2,27E-09	0,12	Peptidase-S41-family-protein
AT3G48850	chr5_19013106	trans	-0,75±0,13	2,27E-09	0,14	phosphate-transporter-3;2
AT4G39366	chr4_18305704	cis	-0,79±0,13	2,30E-09	0,11	snoRNA
AT1G21120	chr1_7399114	cis	-0,64±0,11	2,30E-09	0,21	O-methyltransferase-family-protein
AT4G10620	chr4_6564358	cis	-0,52±0,09	2,35E-09	0,54	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT5G66490	chr5_26547716	cis	-0,98±0,16	2,37E-09	0,08	
AT5G59210	chr5_23893941	cis	-0,71±0,12	2,39E-09	0,15	myosin-heavy-chain-related
AT2G22980	chr2_9779362	cis	-0,53±0,09	2,42E-09	0,46	serine-carboxypeptidase-like-13
AT1G71920	chr4_11121261	trans	0,87±0,15	2,45E-09	0,11	HISTIDINE-BIOSYNTHESIS-6B
AT2G18990	chr2_8235442	cis	0,64±0,11	2,48E-09	0,18	thioredoxin-domain-containing-protein-9-homolog
AT3G62400	chr3_23089676	cis	-0,69±0,11	2,48E-09	0,15	
AT3G18535	chr3_6375145	cis	0,69±0,12	2,48E-09	0,17	tubulin-tyrosine-ligases
AT1G61230	chr1_22577460	cis	0,54±0,09	2,48E-09	0,31	Mannose-binding-lectin-superfamily-protein
AT1G20490	chr1_7098732	cis	-0,85±0,14	2,50E-09	0,11	AMP-dependent-synthetase-and-ligase-family-protein
AT1G69430	chr1_26098393	cis	-0,53±0,09	2,52E-09	0,40	
AT2G43190	chr2_17956198	cis	0,89±0,15	2,56E-09	0,10	ribonuclease-P-family-protein
AT3G52072	chr3_19311464	cis	0,83±0,14	2,57E-09	0,11	other-RNA
AT3G07570	chr3_2420114	cis	0,58±0,1	2,60E-09	0,31	Cytochrome-b561/ferric-reductase-transmembrane-with-DOMON-related-domain
AT3G21300	chr3_7498122	cis	0,87±0,15	2,61E-09	0,09	RNA-methyltransferase-family-protein
AT1G69750	chr1_26228492	cis	-0,73±0,12	2,63E-09	0,15	cytochrome-c-oxidase-19-2
AT2G32430	chr2_13770653	cis	-0,58±0,1	2,63E-09	0,27	Galactosyltransferase-family-protein
AT1G59950	chr1_22070099	cis	-0,54±0,09	2,64E-09	0,32	NAD(P)-linked-oxidoreductase-superfamily-protein
AT4G13460	chr4_7823970	cis	0,57±0,1	2,67E-09	0,27	SU(VAR)3-9-homolog-9
AT4G14610	chr4_8383533	cis	0,73±0,12	2,69E-09	0,31	
AT1G27190	chr1_9448006	cis	-0,52±0,09	2,70E-09	0,51	Leucine-rich-repeat-protein-kinase-family-protein
AT5G20720	chr5_7017067	cis	0,77±0,13	2,70E-09	0,14	chaperonin-20
AT4G04293	chr4_2078441	cis	-0,91±0,15	2,72E-09	0,11	transposable-element-gene
AT4G31100	chr4_15116617	cis	0,63±0,11	2,72E-09	0,19	wall-associated-kinase,-putative
AT4G24026	chr4_12486594	cis	-0,63±0,11	2,74E-09	0,24	
AT4G18593	chr4_10238041	cis	0,5±0,08	2,76E-09	0,43	dual-specificity-protein-phosphatase-related
AT4G18220	chr4_10086984	cis	-0,51±0,09	2,78E-09	0,44	Drug/metabolite-transporter-superfamily-protein
AT1G10865	chr1_3614901	cis	0,51±0,09	2,80E-09	0,51	
AT2G22140	chr2_9400342	cis	0,66±0,11	2,80E-09	0,19	essential-meiotic-endonuclease-1B
AT5G40290	chr5_16093847	cis	0,54±0,09	2,83E-09	0,31	HD-domain-containing-metal-dependent-phosphohydrolase-family-protein
AT4G35520	chr4_16865237	cis	0,53±0,09	2,84E-09	0,40	MUTL-protein-homolog-3
AT3G10530	chr3_3285914	cis	0,81±0,14	2,85E-09	0,14	Transducin/WD40-repeat-like-superfamily-protein
AT1G16210	chr1_5586883	cis	-0,83±0,14	2,86E-09	0,14	
AT4G11830	chr4_7126483	cis	-0,7±0,12	2,86E-09	0,15	phospholipase-D-gamma-2
AT1G61990	chr1_22910904	cis	0,74±0,12	2,87E-09	0,14	Mitochondrial-transcription-termination-factor-family-protein
AT2G27650	chr2_11794485	cis	-0,5±0,08	2,87E-09	0,51	Ubiquitin-carboxyl-terminal-hydrolase-related-protein
AT4G38170	chr4_17904846	cis	-0,52±0,09	2,90E-09	0,34	FAR1-related-sequence-9
AT2G31141	chr2_13271870	cis	0,67±0,11	2,93E-09	0,19	
AT1G69680	chr1_26203727	cis	0,97±0,16	2,94E-09	0,07	Mog1/PsbP/DUF1795-like-photosystem-II-reaction-center-PsbP-family-protein
AT1G74290	chr1_27934467	cis	-0,82±0,14	2,95E-09	0,11	alpha/beta-Hydrolases-superfamily-protein
AT1G76050	chr1_28534028	cis	-0,68±0,11	2,95E-09	0,19	Pseudouridine-synthase-family-protein
AT2G34585	chr2_14569936	cis	-0,68±0,11	2,98E-09	0,18	
AT1G69290	chr1_26050455	cis	0,66±0,11	3,00E-09	0,20	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT3G47010	chr3_17319204	cis	-0,58±0,1	3,04E-09	0,35	Glycosyl-hydrolase-family-protein
AT3G25013	chr3_9114019	cis	-0,53±0,09	3,05E-09	0,33	Synaptobrevin-family-protein
AT5G36120	chr5_14196522	cis	-0,56±0,09	3,06E-09	0,45	cofactor-assembly,-complex-C-(B6F)
AT4G16060	chr4_9099903	cis	-0,52±0,09	3,11E-09	0,50	
AT1G15080	chr1_5171876	cis	0,56±0,09	3,12E-09	0,38	lipid-phosphate-phosphatase-2
AT2G13100	chr2_5390318	cis	-0,75±0,13	3,15E-09	0,15	Major-facilitator-superfamily-protein
AT5G02450	chr5_534379	cis	-0,58±0,1	3,17E-09	0,29	Ribosomal-protein-L36e-family-protein
AT5G23850	chr5_8038046	cis	-0,87±0,15	3,18E-09	0,11	Arabidopsis-thaliana-protein-of-unknown-function-(DUF821)
AT3G46450	chr3_17093682	cis	0,56±0,09	3,24E-09	0,29	SEC14-cytosolic-factor-family-protein-/-phosphoglyceride-transfer-family-protein
AT1G61440	chr1_22673235	cis	0,73±0,12	3,24E-09	0,14	S-locus-lectin-protein-kinase-family-protein
AT5G47550	chr5_19287775	cis	-0,52±0,09	3,25E-09	0,38	Cystatin/monellin-superfamily-protein
AT5G48530	chr5_19668014	cis	-0,53±0,09	3,25E-09	0,40	
AT3G20660	chr3_7219123	cis	0,92±0,16	3,26E-09	0,08	organic-cation/carnitine-transporter4
AT1G07420	chr1_2290662	cis	-0,7±0,12	3,26E-09	0,16	sterol-4-alpha-methyl-oxidase-2-1
AT4G14965	chr4_8550431	cis	-0,52±0,09	3,27E-09	0,50	membrane-associated-progesterone-binding-protein-4
AT2G15050	chr2_6512033	cis	-0,79±0,13	3,28E-09	0,11	lipid-transfer-protein
AT2G43745	chr2_18121519	cis	-0,77±0,13	3,29E-09	0,15	
AT2G43535	chr2_18076562	cis	-0,83±0,14	3,30E-09	0,11	Scorpion-toxin-like-knottin-superfamily-protein
AT3G27925	chr3_10365435	cis	-0,53±0,09	3,35E-09	0,40	DegP-protease-1
AT4G03415	chr4_1471041	cis	-0,82±0,14	3,35E-09	0,13	Protein-phosphatase-2C-family-protein
AT2G19490	chr3_13440600	trans	0,77±0,13	3,37E-09	0,13	recA-DNA-recombination-family-protein
AT1G54260	chr1_20255602	cis	-0,93±0,16	3,38E-09	0,09	winged-helix-DNA-binding-transcription-factor-family-protein
AT1G33480	chr1_12150056	cis	-0,71±0,12	3,39E-09	0,19	RING/U-box-superfamily-protein
AT3G55700	chr3_20671176	cis	-0,53±0,09	3,43E-09	0,39	UDP-Glycosyltransferase-superfamily-protein
AT3G30875	chr4_4508615	trans	0,6±0,1	3,44E-09	0,26	
AT5G37000	chr5_14618076	cis	-0,84±0,14	3,45E-09	0,13	Exostosin-family-protein
AT3G23610	chr3_8479578	cis	-0,59±0,1	3,46E-09	0,28	dual-specificity-protein-phosphatase-1

AT1G31360	chr1_11236608	cis	0,8±0,14	3,51E-09	0,11	RECQ-helicase-L2
AT1G35670	chr1_13203648	cis	-0,73±0,12	3,51E-09	0,13	calcium-dependent-protein-kinase-2
AT4G01350	chr5_24128930	trans	0,98±0,17	3,52E-09	0,08	Cysteine/Histidine-rich-C1-domain-family-protein
AT1G36622	chr1_13829306	cis	-0,62±0,1	3,53E-09	0,21	
AT4G13345	chr4_7762558	cis	-0,54±0,09	3,53E-09	0,37	Serinc-domain-containing-serine-and-sphingolipid-biosynthesis-protein
AT4G13100	chr4_7638618	cis	-0,55±0,09	3,54E-09	0,32	RING/U-box-superfamily-protein
AT5G58595	chr5_23677967	cis	0,6±0,1	3,54E-09	0,26	snoRNA
AT1G62010	chr1_22908815	cis	-0,87±0,15	3,55E-09	0,09	Mitochondrial-transcription-termination-factor-family-protein
AT2G44210	chr2_18281511	cis	0,82±0,14	3,55E-09	0,11	Protein-of-Unknown-Function-(DUF239)
AT4G00970	chr4_420840	cis	-0,54±0,09	3,55E-09	0,38	cysteine-rich-RLK-(RECEPTOR-like-protein-kinase)-41
AT5G10620	chr5_3351841	cis	0,64±0,11	3,56E-09	0,16	methyltransferases
AT1G78780	chr1_29615953	cis	0,64±0,11	3,61E-09	0,19	pathogenesis-related-family-protein
AT4G34550	chr4_16496186	cis	0,58±0,1	3,68E-09	0,31	
AT4G22720	chr4_11939573	cis	-0,5±0,09	3,70E-09	0,46	Actin-like-ATPase-superfamily-protein
AT1G55720	chr1_20822857	cis	-0,99±0,17	3,77E-09	0,08	cation-exchanger-6
AT3G60950	chr3_22544900	cis	0,67±0,11	3,81E-09	0,16	C2-calcium/lipid-binding-endonuclease/exonuclease/phosphatase
AT5G34850	chr5_13108258	cis	-0,53±0,09	3,84E-09	0,45	purple-acid-phosphatase-26
AT5G04320	chr5_1212665	cis	-0,51±0,09	3,85E-09	0,39	Shugoshin-C-terminus
AT1G66700	chr1_24876630	cis	0,48±0,08	3,86E-09	0,33	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein
AT4G01460	chr4_616803	cis	0,53±0,09	3,86E-09	0,44	basic-helix-loop-helix-(bHLH)-DNA-binding-superfamily-protein
AT5G62575	chr5_25117753	cis	-0,58±0,1	3,87E-09	0,26	
AT1G65590	chr1_24387301	cis	-0,63±0,11	3,88E-09	0,22	beta-hexosaminidase-3
AT5G04710	chr5_1360240	cis	0,71±0,12	3,95E-09	0,16	Zn-dependent-exopeptidases-superfamily-protein
AT2G43500	chr2_18060212	cis	0,58±0,1	3,96E-09	0,25	Plant-regulator-RWP-RK-family-protein
AT3G48650	chr3_18028229	cis	-0,91±0,16	3,96E-09	0,11	
AT2G24650	chr2_10466568	cis	0,52±0,09	3,97E-09	0,40	DNA-binding;DNA-binding;sequence-specific-DNA-binding-transcription-factors
AT5G42690	chr5_17120893	cis	-0,63±0,11	3,99E-09	0,18	Protein-of-unknown-function,-DUF547
AT3G26922	chr3_9925133	cis	0,52±0,09	4,01E-09	0,43	F-box/RNI-like-superfamily-protein
AT1G70985	chr1_26766121	cis	0,59±0,1	4,02E-09	0,35	hydroxyproline-rich-glycoprotein-family-protein
AT1G52910	chr1_19695673	cis	0,62±0,11	4,06E-09	0,21	Protein-of-unknown-function-(DUF1218)
AT3G15260	chr3_5127140	cis	-0,91±0,15	4,06E-09	0,10	Protein-phosphatase-2C-family-protein
AT4G19010	chr4_10413907	cis	-0,51±0,09	4,09E-09	0,54	AMP-dependent-synthetase-and-ligase-family-protein
AT4G13120	chr4_7646168	cis	-0,96±0,16	4,12E-09	0,08	transposable-element-gene
AT4G01860	chr4_817109	cis	-0,58±0,1	4,18E-09	0,28	Transducin-family-protein-/-WD-40-repeat-family-protein
AT2G21260	chr2_9106508	cis	-0,57±0,1	4,21E-09	0,29	NAD(P)-linked-oxidoreductase-superfamily-protein
AT2G24680	chr2_10497318	cis	0,79±0,14	4,21E-09	0,11	transcriptional-factor-B3-family-protein
AT1G74180	chr1_27900760	cis	-0,7±0,12	4,23E-09	0,15	receptor-like-protein-14
AT5G28080	chr5_10117026	cis	0,6±0,1	4,23E-09	0,26	Protein-kinase-superfamily-protein
AT1G02850	chr1_628630	cis	0,61±0,1	4,25E-09	0,26	beta-glucosidase-11
AT5G56130	chr5_22722445	cis	-0,54±0,09	4,32E-09	0,29	Transducin/WD40-repeat-like-superfamily-protein
AT1G06640	chr1_2051561	cis	-0,75±0,13	4,37E-09	0,12	2-oxoglutarate-(2OG)-and-Fe(II)-dependent-oxygenase-superfamily-protein
AT2G34840	chr2_14700261	cis	-0,89±0,15	4,40E-09	0,10	Coatomer-epsilon-subunit
AT5G53830	chr5_21857638	cis	-0,57±0,1	4,41E-09	0,27	VQ-motif-containing-protein
AT4G27060	chr4_13571868	cis	0,58±0,1	4,44E-09	0,26	ARM-repeat-superfamily-protein
AT1G50500	chr1_18716339	cis	0,51±0,09	4,45E-09	0,46	Membrane-trafficking-VPS53-family-protein
AT4G27070	chr1_11506651	trans	0,66±0,11	4,47E-09	0,21	tryptophan-synthase-beta-subunit-2
AT2G35075	chr2_14776040	cis	0,54±0,09	4,47E-09	0,34	
AT4G11410	chr4_6946044	cis	0,82±0,14	4,48E-09	0,11	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT3G50100	chr3_18578397	cis	0,88±0,15	4,49E-09	0,09	small-RNA-degrading-nuclease-1
AT5G43330	chr5_17391678	cis	0,58±0,1	4,49E-09	0,25	Lactate/malate-dehydrogenase-family-protein
AT2G24040	chr2_10225798	cis	0,63±0,11	4,56E-09	0,27	Low-temperature-and-salt-responsive-protein-family
AT1G63390	chr1_23493092	cis	-0,5±0,09	4,59E-09	0,45	FAD/NAD(P)-binding-oxidoreductase-family-protein
AT2G06510	chr2_2336551	trans	01,07±0,18	4,59E-09	0,10	replication-protein-A-1A
AT2G37050	chr2_15566680	cis	0,55±0,09	4,59E-09	0,33	Leucine-rich-repeat-protein-kinase-family-protein
AT5G39940	chr5_15987774	cis	-0,74±0,13	4,59E-09	0,12	FAD/NAD(P)-binding-oxidoreductase-family-protein
AT5G27220	chr5_9580241	cis	-0,57±0,1	4,62E-09	0,26	Frigida-like-protein
AT3G32920	chr1_10156018	trans	0,9±0,15	4,63E-09	0,10	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT1G60000	chr1_22094609	cis	-0,86±0,15	4,64E-09	0,09	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT5G23950	chr5_8082568	cis	0,57±0,1	4,65E-09	0,56	Calcium-dependent-lipid-binding-(CaLB-domain)-family-protein
AT1G17790	chr1_6122391	cis	-0,73±0,12	4,66E-09	0,14	DNA-binding-bromodomain-containing-protein
AT1G67440	chr1_25265828	cis	0,5±0,09	4,68E-09	0,49	Minichromosome-maintenance-(MCM2/3/5)-family-protein
AT5G48480	chr5_19664194	cis	0,53±0,09	4,68E-09	0,39	Lactoylglutathione-lyase-/-glyoxalase-I-family-protein
AT5G46260	chr5_18853814	trans	0,88±0,15	4,70E-09	0,09	disease-resistance-protein-(TIR-NBS-LRR-class)-family
AT5G27860	chr5_9874674	cis	0,71±0,12	4,74E-09	0,16	
AT1G62305	chr1_23026723	cis	-0,66±0,11	4,75E-09	0,19	Core-2/I-branching-beta-1,6-N-acetylglucosaminyltransferase-family-protein
AT2G43950	chr3_17419622	trans	0,54±0,09	4,75E-09	0,31	chloroplast-outer-envelope-protein-37
AT4G13660	chr4_7943892	cis	01,06±0,18	4,75E-09	0,06	pinoresinol-reductase-2
AT1G51830	chr5_24043295	trans	0,5±0,09	4,75E-09	0,44	Leucine-rich-repeat-protein-kinase-family-protein
AT2G46490	chr2_19078005	cis	-0,5±0,09	4,76E-09	0,46	
AT5G01040	chr5_33234	cis	-0,63±0,11	4,88E-09	0,19	laccase-8
AT2G29160	chr2_12504339	cis	0,71±0,12	4,88E-09	0,15	
AT3G25900	chr3_9480243	cis	0,66±0,11	4,89E-09	0,19	Homocysteine-S-methyltransferase-family-protein
AT4G27060	chr1_11506730	trans	0,63±0,11	4,90E-09	0,24	ARM-repeat-superfamily-protein
AT1G62040	chr1_22932927	cis	0,52±0,09	4,91E-09	0,66	Ubiquitin-like-superfamily-protein
AT4G19380	chr4_10573108	cis	0,5±0,09	4,92E-09	0,39	Long-chain-fatty-alcohol-dehydrogenase-family-protein
AT5G09840	chr5_3058074	cis	0,55±0,09	4,97E-09	0,41	Putative-endonuclease-or-glycosyl-hydrolase
AT3G51880	chr3_19248505	cis	-0,57±0,1	5,03E-09	0,28	high-mobility-group-B1
AT3G23480	chr3_8431540	cis	0,71±0,12	5,03E-09	0,17	Cyclopropane-fatty-acyl-phospholipid-synthase
AT3G13845	chr3_4559312	cis	0,51±0,09	5,04E-09	0,37	

AT3G05230	chr3_1492253	cis	0,5±0,09	5,06E-09	0,44	Signal-peptidase-subunit
AT5G14680	chr1_3359097	trans	-0,62±0,11	5,10E-09	0,21	Adenine-nucleotide-alpha-hydrolases-like-superfamily-protein
AT1G16635	chr1_5686292	cis	-0,51±0,09	5,14E-09	0,56	
AT3G53370	chr3_19779802	cis	0,53±0,09	5,14E-09	0,54	S1FA-like-DNA-binding-protein
AT2G12550	chr2_5118537	cis	0,54±0,09	5,18E-09	0,51	ubiquitin-associated-(UBA)/TS-N-domain-containing-protein
AT1G16340	chr1_5521223	trans	-0,91±0,16	5,21E-09	0,09	Aldolase-superfamily-protein
AT1G52710	chr1_19639432	cis	-0,98±0,17	5,26E-09	0,07	Rubredoxin-like-superfamily-protein
AT3G57990	chr3_21470658	cis	-0,53±0,09	5,27E-09	0,51	
AT5G43725	chr5_17560200	cis	0,54±0,09	5,29E-09	0,33	other-RNA
AT3G17250	chr3_5894722	cis	0,72±0,12	5,30E-09	0,14	Protein-phosphatase-2C-family-protein
AT3G23110	chr3_8227670	cis	0,61±0,1	5,36E-09	0,20	receptor-like-protein-37
AT2G26980	chr2_11518603	cis	0,61±0,11	5,40E-09	0,24	CBL-interacting-protein-kinase-3
AT4G04830	chr4_2445653	cis	-0,61±0,11	5,43E-09	0,29	methionine-sulfoxide-reductase-B5
AT4G07825	chr4_3274080	trans	0,61±0,1	5,46E-09	0,27	
AT3G50845	chr3_18901574	cis	-0,52±0,09	5,46E-09	0,42	Protein-of-unknown-function-(DUF59)
AT2G02240	chr2_593420	cis	0,51±0,09	5,55E-09	0,39	F-box-family-protein
AT3G17590	chr3_6019674	cis	-01,18±0,2	5,55E-09	0,06	transcription-regulatory-protein-SNF5,-putative-(BSH)
AT1G13270	chr1_4544969	cis	0,59±0,1	5,62E-09	0,27	methionine-aminopeptidase-1B
AT5G38840	chr5_15547507	cis	0,51±0,09	5,65E-09	0,44	SMAD/FHA-domain-containing-protein-
AT5G39710	chr5_15895781	cis	0,63±0,11	5,68E-09	0,22	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT2G14835	chr2_6381561	cis	0,5±0,09	5,68E-09	0,55	RING/U-box-superfamily-protein
AT5G25450	chr5_8855080	cis	0,77±0,13	5,69E-09	0,12	Cytochrome-bd-ubiquinol-oxidase,-14kDa-subunit
AT3G01790	chr3_260335	cis	0,87±0,15	5,73E-09	0,09	Ribosomal-protein-L13-family-protein
AT3G26150	chr3_9567178	cis	0,55±0,09	5,74E-09	0,34	cytochrome-P450,-family-71,-subfamily-B,-polypeptide-16
AT1G15880	chr1_5459026	cis	0,87±0,15	5,78E-09	0,09	golgi-snare-11
AT1G14490	chr1_4959533	cis	-0,52±0,09	5,80E-09	0,42	Predicted-AT-hook-DNA-binding-family-protein
AT3G23470	chr3_8431540	cis	0,72±0,12	5,81E-09	0,17	Cyclopropane-fatty-acyl-phospholipid-synthase
AT3G59410	chr3_21950171	cis	0,63±0,11	5,83E-09	0,21	protein-kinase-family-protein
AT1G26920	chr1_9328093	cis	0,55±0,1	5,88E-09	0,33	
AT2G47370	chr2_19443291	cis	-0,52±0,09	5,89E-09	0,46	Calcium-dependent-phosphotriesterase-superfamily-protein
AT2G41650	chr2_17359821	cis	-0,52±0,09	5,96E-09	0,36	
AT1G66540	chr1_24825520	cis	-0,59±0,1	5,99E-09	0,21	Cytochrome-P450-superfamily-protein
AT1G25083	chr1_8838392	cis	-0,49±0,08	6,02E-09	0,49	Glutamine-amidotransferase-type-1-family-protein
AT1G05550	chr1_1641888	cis	0,54±0,09	6,09E-09	0,47	Protein-of-unknown-function-(DUF295)
AT3G61560	chr3_22777968	cis	-0,62±0,11	6,10E-09	0,24	Reticulon-family-protein
AT3G60164	chr3_22231957	cis	-0,54±0,09	6,11E-09	0,50	
AT4G02460	chr4_1074131	cis	0,81±0,14	6,13E-09	0,11	DNA-mismatch-repair-protein,-putative
AT5G22510	chr5_7476949	cis	-0,55±0,09	6,13E-09	0,38	alkaline/neutral-invertase
AT4G13630	chr4_7937315	cis	0,53±0,09	6,17E-09	0,30	Protein-of-unknown-function,-DUF593
AT3G23100	chr3_8218557	cis	-0,51±0,09	6,22E-09	0,36	homolog-of-human-DNA-ligase-iv-binding-protein-XRCC4
AT2G36050	chr2_15138413	cis	0,5±0,09	6,29E-09	0,50	ovate-family-protein-15
AT3G26070	chr3_9527159	cis	-0,54±0,09	6,30E-09	0,34	Plastid-lipid-associated-protein-PAP-/-fibrillin-family-protein
AT1G49930	chr1_18484994	cis	-0,79±0,14	6,35E-09	0,11	
AT1G64600	chr1_23995767	cis	0,52±0,09	6,35E-09	0,42	methyltransferases;copper-ion-binding
AT1G04985	chr1_1418552	cis	-0,86±0,15	6,54E-09	0,09	
AT1G63420	chr1_23517242	cis	0,55±0,1	6,58E-09	0,29	Arabidopsis-thaliana-protein-of-unknown-function-(DUF821)
AT4G27852	chr4_13869975	cis	-0,88±0,15	6,61E-09	0,09	
AT4G36840	chr4_17354710	cis	-0,8±0,14	6,63E-09	0,11	Galactose-oxidase/kelch-repeat-superfamily-protein
AT1G76530	chr1_28720156	cis	-0,49±0,08	6,64E-09	0,45	Auxin-efflux-carrier-family-protein
AT4G12300	chr4_7310109	cis	0,56±0,1	6,67E-09	0,33	cytochrome-P450,-family-706,-subfamily-A,-polypeptide-4
AT3G01740	chr3_269343	cis	-0,73±0,13	6,76E-09	0,15	Mitochondrial-ribosomal-protein-L37
AT5G07880	chr3_10393637	trans	0,5±0,09	6,83E-09	0,38	synaptosomal-associated-protein-SNAP25-like-29
AT5G23070	chr5_7645645	trans	0,64±0,11	6,87E-09	0,25	Thymidine-kinase
AT3G26165	chr3_9571909	cis	0,55±0,09	6,93E-09	0,31	
AT2G20650	chr2_8909014	cis	0,52±0,09	7,02E-09	0,40	RING/U-box-superfamily-protein
AT3G21790	chr1_3859014	trans	0,51±0,09	7,03E-09	0,66	UDP-Glycosyltransferase-superfamily-protein
AT5G49510	chr5_20080369	cis	-0,79±0,14	7,04E-09	0,11	prefoldin-3
AT3G21100	chr1_28105103	trans	0,54±0,09	7,06E-09	0,29	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT4G19350	chr4_10562571	cis	-0,56±0,1	7,09E-09	0,28	embryo-defective-3006
AT1G78915	chr1_29658052	cis	0,83±0,14	7,10E-09	0,10	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT1G32910	chr1_11924416	cis	-0,52±0,09	7,10E-09	0,38	HXXXD-type-acyl-transferase-family-protein
AT5G14250	chr5_4600661	cis	0,55±0,09	7,15E-09	0,32	Proteasome-component-(PCI)-domain-protein
AT1G33140	chr1_12024011	cis	-0,7±0,12	7,18E-09	0,14	Ribosomal-protein-L6-family
AT5G19350	chr5_6519290	cis	0,53±0,09	7,20E-09	0,48	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT5G44730	chr5_18046985	cis	0,53±0,09	7,28E-09	0,36	Haloacid-dehalogenase-like-hydrolase-(HAD)-superfamily-protein
AT4G02725	chr4_1220128	cis	0,62±0,11	7,28E-09	0,22	
AT1G26900	chr1_9322541	cis	-0,52±0,09	7,30E-09	0,41	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT2G37370	chr2_15679136	cis	0,55±0,09	7,33E-09	0,50	
AT2G38370	chr2_16068570	cis	-0,8±0,14	7,38E-09	0,12	Plant-protein-of-unknown-function-(DUF827)
AT2G25350	chr2_10797830	cis	-0,59±0,1	7,39E-09	0,38	Phox-(PX)-domain-containing-protein
AT2G34790	chr2_14679048	cis	-0,5±0,09	7,39E-09	0,42	FAD-binding-Berberine-family-protein
AT3G08885	chr3_2704556	cis	0,86±0,15	7,42E-09	0,10	
AT5G45400	chr5_18398980	cis	0,71±0,12	7,51E-09	0,15	Replication-factor-A-protein-1-related
AT1G30835	chr1_10964549	cis	-0,54±0,09	7,52E-09	0,34	transposable-element-gene
AT1G24880	chr1_8842441	trans	0,83±0,14	7,55E-09	0,12	UDP-3-O-acyl-N-acetylglycosamine-deacetylase-family-protein
AT4G37210	chr4_17514967	cis	-0,56±0,1	7,58E-09	0,35	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT5G41240	chr5_16501243	cis	0,66±0,11	7,58E-09	0,28	glutathione-S-transferase-THETA-2
AT1G33970	chr1_12350213	cis	-0,51±0,09	7,68E-09	0,34	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT4G14103	chr4_8148790	cis	0,57±0,1	7,70E-09	0,29	F-box/RNI-like-superfamily-protein

AT2G21800	chr2_9293627	cis	0,9±0,16	7,74E-09	0,09	essential-meiotic-endonuclease-1A
AT1G64350	chr1_23881942	cis	0,53±0,09	7,78E-09	0,46	Transducin/WD40-repeat-like-superfamily-protein
AT2G41660	chr2_17409805	cis	0,61±0,11	7,79E-09	0,21	Protein-of-unknown-function,-DUF617
AT1G74240	chr1_27917198	cis	0,55±0,1	7,82E-09	0,28	Mitochondrial-substrate-carrier-family-protein
AT1G23850	chr1_8426708	cis	-0,67±0,12	7,84E-09	0,19	
AT5G59250	chr5_23903147	cis	0,8±0,14	7,85E-09	0,11	Major-facilitator-superfamily-protein
AT5G04880	chr5_1456665	cis	-0,94±0,16	7,86E-09	0,07	
AT3G54460	chr3_20182082	cis	0,85±0,15	7,87E-09	0,08	SNF2-domain-containing-protein-/-helicase-domain-containing-protein-/-F-box-family-protein
AT3G11210	chr3_3512810	cis	-0,55±0,1	7,87E-09	0,26	SGNH-hydrolase-type-esterase-superfamily-protein
AT2G25310	chr2_10777579	cis	0,58±0,1	7,91E-09	0,29	Protein-of-unknown-function-(DUF2012)
AT1G31910	chr5_11642972	trans	-0,54±0,09	7,98E-09	0,42	GHMP-kinase-family-protein
AT2G25355	chr2_10801269	cis	0,59±0,1	8,04E-09	0,41	PNAS-3-related
AT3G28300	chr3_10561937	cis	0,82±0,14	8,06E-09	0,11	Protein-of-unknown-function-(DUF677)
AT1G47840	chr1_17618965	cis	0,57±0,1	8,10E-09	0,24	hexokinase-3
AT5G18840	chr5_6282597	cis	-0,69±0,12	8,11E-09	0,16	Major-facilitator-superfamily-protein
AT3G47390	chr3_17461680	cis	-0,51±0,09	8,18E-09	0,37	cytidine/deoxycytidylate-deaminase-family-protein
AT2G30230	chr2_12892570	cis	0,53±0,09	8,18E-09	0,31	
AT2G25510	chr1_2030563	trans	-0,62±0,11	8,22E-09	0,21	
AT3G32920	chr1_11308596	trans	0,84±0,15	8,23E-09	0,10	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT4G09432	chr4_5932389	cis	-0,71±0,12	8,41E-09	0,16	
AT1G12200	chr1_4135556	cis	0,71±0,12	8,44E-09	0,17	Flavin-binding-monooxygenase-family-protein
AT2G01720	chr4_613562	trans	-0,73±0,13	8,49E-09	0,14	Ribophorin-I
AT5G18060	chr5_5978226	cis	0,56±0,1	8,54E-09	0,28	SAUR-like-auxin-responsive-protein-family-
AT4G37270	chr4_17552077	cis	0,54±0,09	8,57E-09	0,31	heavy-metal-atpase-1
AT3G26800	chr2_10613173	trans	-0,6±0,1	8,63E-09	0,18	
AT1G13580	chr1_4646940	cis	-0,6±0,1	8,69E-09	0,25	LAG1-longevity-assurance-homolog-3
AT3G59330	chr3_21917869	cis	-0,64±0,11	8,70E-09	0,17	Eukaryotic-protein-of-unknown-function-(DUF914)
AT2G35160	chr2_14822819	cis	-0,59±0,1	8,70E-09	0,29	SU(VAR)3-9-homolog-5
AT4G31877	chr4_15415403	cis	-0,53±0,09	8,74E-09	0,32	MIR156C;-miRNA
AT1G23900	chr1_8442838	cis	0,52±0,09	8,84E-09	0,57	gamma-adaptin-1
AT5G38780	chr5_15550869	cis	0,57±0,1	8,93E-09	0,25	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein
AT5G45460	chr5_18423609	cis	0,77±0,13	8,94E-09	0,11	
AT1G25145	chr1_8842441	cis	0,77±0,13	9,01E-09	0,12	UDP-3-O-acyl-N-acetylglycosamine-deacetylase-family-protein
AT1G55890	chr1_20897112	cis	0,53±0,09	9,02E-09	0,45	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT5G58130	chr5_23506858	cis	-0,68±0,12	9,05E-09	0,16	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT3G03520	chr3_840539	cis	0,6±0,1	9,07E-09	0,30	non-specific-phospholipase-C3
AT2G29300	chr2_12586091	cis	-0,83±0,14	9,08E-09	0,09	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT5G66130	chr5_26430031	cis	0,72±0,13	9,10E-09	0,14	RADIATION-SENSITIVE-17
AT4G22470	chr4_11846652	cis	-0,52±0,09	9,12E-09	0,28	protease-inhibitor/seed-storage/lipid-transfer-protein-(LTP)-family-protein
AT2G26220	chr2_11169276	cis	0,57±0,1	9,13E-09	0,31	
AT5G42470	chr5_16978784	cis	0,59±0,1	9,16E-09	0,22	
AT3G03560	chr3_872072	cis	-0,49±0,09	9,26E-09	0,37	
AT2G33600	chr2_14226753	cis	-0,97±0,17	9,28E-09	0,07	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT1G16160	chr1_5538867	cis	0,61±0,11	9,29E-09	0,20	wall-associated-kinase-like-5
AT4G02405	chr4_1059368	cis	-0,85±0,15	9,35E-09	0,09	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein
AT2G30460	chr2_12978858	cis	-0,57±0,1	9,36E-09	0,34	Nucleotide/sugar-transporter-family-protein
AT1G73670	chr1_27699959	cis	-0,94±0,16	9,44E-09	0,07	MAP-kinase-15
AT1G09500	chr1_3067045	cis	-0,79±0,14	9,44E-09	0,12	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT2G24190	chr2_10283196	cis	-0,48±0,08	9,47E-09	0,50	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT5G23980	chr5_8104296	cis	0,77±0,13	9,50E-09	0,12	ferric-reduction-oxidase-4
AT5G01450	chr1_22594423	trans	0,62±0,11	9,55E-09	0,19	RING/U-box-superfamily-protein
AT1G26440	chr1_9148650	cis	-0,53±0,09	9,62E-09	0,31	ureide-permease-5
AT5G05430	chr5_1594615	cis	-0,54±0,09	9,64E-09	0,33	RNA-binding-protein
AT3G50420	chr3_18713181	cis	0,53±0,09	9,67E-09	0,39	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT1G72920	chr1_27444328	cis	0,49±0,09	9,83E-09	0,44	Toll-Interleukin-Resistance-(TIR)-domain-family-protein
AT1G53320	chr1_19889747	cis	-0,75±0,13	9,84E-09	0,12	tubby-like-protein-7
AT5G67540	chr5_26919119	cis	0,75±0,13	9,87E-09	0,12	Arabinanase/levansucrase/invertase
AT1G16900	chr1_5780205	cis	0,95±0,17	9,99E-09	0,10	Alg9-like-mannosyltransferase-family
AT1G73490	chr1_27639200	cis	-0,88±0,15	1,00E-08	0,09	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT1G11880	chr1_4009452	cis	-0,56±0,1	1,00E-08	0,27	transferases,-transferring-hexosyl-groups
AT1G25098	chr1_8842441	cis	0,81±0,14	1,00E-08	0,12	other-RNA
AT3G16390	chr3_5583592	cis	0,94±0,16	1,01E-08	0,08	nitrile-specifier-protein-3
AT1G12600	chr1_4273340	cis	0,85±0,15	1,02E-08	0,10	UDP-N-acetylglucosamine-(UAA)-transporter-family
AT5G15520	chr5_5034307	cis	0,54±0,09	1,02E-08	0,40	Ribosomal-protein-S19e-family-protein
AT5G24330	chr3_9639176	trans	0,66±0,12	1,02E-08	0,15	ARABIDOPSIS-TRITHORAX-RELATED-PROTEIN-6
AT1G65420	chr1_23055533	trans	-0,77±0,13	1,03E-08	0,11	Protein-of-unknown-function-(DUF565)
AT5G06060	chr5_1817325	cis	-0,83±0,14	1,03E-08	0,10	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT1G68110	chr1_25525707	cis	-0,56±0,1	1,06E-08	0,20	ENTH/ANTH/VHS-superfamily-protein
AT3G18530	chr3_6375145	cis	0,67±0,12	1,07E-08	0,17	ARM-repeat-superfamily-protein
AT3G55530	chr3_20593930	cis	0,79±0,14	1,08E-08	0,11	RING/U-box-superfamily-protein
AT4G11460	chr4_6964866	cis	0,53±0,09	1,08E-08	0,31	cysteine-rich-RLK-(RECEPTOR-like-protein-kinase)-30
AT1G63120	chr1_18905855	trans	0,87±0,15	1,08E-08	0,09	RHOMBOID-like-2
AT5G11540	chr3_3555309	trans	-0,65±0,11	1,09E-08	0,15	D-arabinono-1,4-lactone-oxidase-family-protein
AT1G17270	chr1_5905175	cis	0,84±0,15	1,10E-08	0,09	O-fucosyltransferase-family-protein
AT5G66480	chr5_26547716	cis	-0,88±0,15	1,10E-08	0,08	
AT5G13970	chr5_4489231	cis	0,93±0,16	1,13E-08	0,08	
AT3G46060	chr3_16918799	cis	-0,5±0,09	1,13E-08	0,44	RAB-GTPase-homolog-8A
AT4G03440	chr4_1514386	cis	-0,58±0,1	1,13E-08	0,28	Ankyrin-repeat-family-protein
AT5G27010	chr5_9500086	cis	0,58±0,1	1,14E-08	0,29	ARM-repeat-superfamily-protein

AT3G49220	chr5_13313436	trans	0,6±0,11	1,15E-08	0,21	Plant-invertase/pectin-methylesterase-inhibitor-superfamily
AT1G17860	chr1_6140944	cis	0,57±0,1	1,16E-08	0,28	Kunitz-family-trypsin-and-protease-inhibitor-protein
AT4G34660	chr4_16551820	cis	-0,61±0,11	1,16E-08	0,35	SH3-domain-containing-protein
AT3G20310	chr3_7087448	cis	-0,56±0,1	1,17E-08	0,26	ethylene-response-factor-7
AT3G25020	chr3_9119626	cis	-0,54±0,09	1,18E-08	0,61	receptor-like-protein-42
AT3G62860	chr3_23240879	cis	0,62±0,11	1,19E-08	0,22	alpha/beta-Hydrolases-superfamily-protein
AT3G57200	chr3_21169754	cis	-0,94±0,17	1,19E-08	0,07	
AT1G20160	chr1_6993390	cis	-0,63±0,11	1,19E-08	0,19	Subtilisin-like-serine-endopeptidase-family-protein
AT2G47500	chr2_19475452	cis	0,88±0,15	1,19E-08	0,09	P-loop-nucleoside-triphosphate-hydrolases-superfamily-protein-with-CH-(Calponin-Homology)-domain
AT1G24265	chr1_8600456	cis	0,52±0,09	1,20E-08	0,32	Protein-of-unknown-function-(DUF1664)
AT5G23330	chr5_7855094	cis	-0,62±0,11	1,21E-08	0,24	Nucleotidylyl-transferase-superfamily-protein
AT5G19750	chr5_6673627	cis	0,77±0,14	1,22E-08	0,12	Peroxisomal-membrane-22-kDa-(Mpv17/PMP22)-family-protein
AT1G10990	chr1_3633414	cis	-0,94±0,17	1,22E-08	0,07	
AT5G05350	chr5_1585297	cis	0,5±0,09	1,22E-08	0,48	PLAC8-family-protein
AT1G78450	chr1_29513534	cis	-0,58±0,1	1,23E-08	0,24	SOUL-heme-binding-family-protein
AT2G39750	chr3_10273905	trans	-0,64±0,11	1,23E-08	0,17	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein
AT1G71040	chr1_26800400	cis	-0,53±0,09	1,23E-08	0,30	Cupredoxin-superfamily-protein
AT3G25220	chr3_9183287	cis	-0,61±0,11	1,24E-08	0,20	FK506-binding-protein-15-kD-1
AT4G37925	chr4_17830243	cis	0,62±0,11	1,24E-08	0,24	subunit-NDH-M-of-NAD(P)H:plastoquinone-dehydrogenase-complex
AT1G52700	chr1_19608287	cis	0,77±0,14	1,25E-08	0,11	alpha/beta-Hydrolases-superfamily-protein
AT3G24300	chr3_873521	trans	0,54±0,1	1,26E-08	0,26	ammonium-transporter-1;3
AT2G38430	chr2_16094147	cis	-0,58±0,1	1,27E-08	0,28	
AT2G33240	chr2_14097649	cis	-0,58±0,1	1,28E-08	0,23	myosin-XI-D
AT3G32920	chr2_3105959	trans	0,82±0,14	1,28E-08	0,11	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT3G16710	chr3_5690265	cis	-0,61±0,11	1,28E-08	0,21	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT4G33360	chr4_16069056	cis	-0,79±0,14	1,29E-08	0,13	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT5G20810	chr5_7044231	cis	-0,75±0,13	1,29E-08	0,14	SAUR-like-auxin-responsive-protein-family-
AT1G47578	chr1_17484722	cis	0,6±0,11	1,30E-08	0,21	Biotin/lipoate-A/B-protein-ligase-family
AT2G39850	chr2_16630326	cis	-0,75±0,13	1,30E-08	0,14	Subtilisin-like-serine-endopeptidase-family-protein
AT4G26570	chr4_13404089	cis	-0,69±0,12	1,30E-08	0,14	calcineurin-B-like-3
AT3G27470	chr3_10163601	cis	-0,55±0,1	1,31E-08	0,29	Protein-of-unknown-function-(DUF707)
AT5G41150	chr5_16469400	cis	-0,6±0,1	1,32E-08	0,25	Restriction-endonuclease,-type-II-like-superfamily-protein
AT2G03710	chr2_1127824	cis	0,82±0,14	1,32E-08	0,11	K-box-region-and-MADS-box-transcription-factor-family-protein-
AT1G72190	chr1_27168598	cis	-0,65±0,11	1,33E-08	0,16	D-isomer-specific-2-hydroxyacid-dehydrogenase-family-protein
AT5G47800	chr5_19354265	cis	-0,48±0,08	1,33E-08	0,41	Phototropic-responsive-NPH3-family-protein
AT2G39890	chr2_16652965	cis	0,73±0,13	1,34E-08	0,19	proline-transporter-1
AT1G09920	chr1_3215190	cis	0,57±0,1	1,35E-08	0,29	TRAF-type-zinc-finger-related
AT1G10330	chr1_3393212	cis	0,83±0,15	1,35E-08	0,10	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT4G14548	chr4_8348045	cis	-0,92±0,16	1,35E-08	0,06	other-RNA
AT1G54040	chr1_20170832	cis	-0,73±0,13	1,37E-08	0,16	epithiospecifier-protein
AT1G50575	chr1_18726991	cis	0,62±0,11	1,37E-08	0,17	Putative-lysine-decarboxylase-family-protein
AT2G24440	chr2_10391465	cis	0,54±0,09	1,37E-08	0,34	selenium-binding
AT3G13640	chr3_4461578	cis	0,78±0,14	1,37E-08	0,11	RNAse-l-inhibitor-protein-1
AT4G01200	chr4_506690	cis	0,54±0,1	1,38E-08	0,54	Calcium-dependent-lipid-binding-(CaLB-domain)-family-protein
AT1G15210	chr1_5234896	cis	-0,72±0,13	1,38E-08	0,14	pleiotropic-drug-resistance-7
AT3G20420	chr3_7119760	cis	0,57±0,1	1,39E-08	0,23	RNAse-THREE-like-protein-2
AT1G60630	chr1_22341230	cis	0,49±0,09	1,40E-08	0,41	Leucine-rich-repeat-protein-kinase-family-protein
AT4G05130	chr4_2639087	cis	-0,81±0,14	1,40E-08	0,10	equilibrative-nucleoside-transporter-4
AT1G07020	chr1_16973461	trans	-0,64±0,11	1,40E-08	0,19	
AT1G60740	chr1_24560818	trans	0,51±0,09	1,41E-08	0,37	Thioredoxin-superfamily-protein
AT5G15920	chr4_6804353	trans	-0,54±0,1	1,41E-08	0,34	structural-maintenance-of-chromosomes-5
AT4G23140	chr4_12114095	cis	-0,57±0,1	1,41E-08	0,24	cysteine-rich-RLK-(RECEPTOR-like-protein-kinase)-6
AT5G42530	chr1_26288716	trans	0,56±0,1	1,42E-08	0,24	
AT4G12110	chr4_7254085	cis	-0,73±0,13	1,42E-08	0,12	sterol-4alpha-methyl-oxidase-1-1
AT3G50810	chr3_18890045	cis	0,56±0,1	1,42E-08	0,29	Uncharacterised-protein-family-(UPF0497)
AT1G04250	chr1_1134230	cis	0,54±0,09	1,43E-08	0,30	AUX/IAA-transcriptional-regulator-family-protein
AT4G17710	chr4_9859327	cis	-0,66±0,12	1,43E-08	0,15	homeodomain-GLABROUS-4
AT5G15510	chr5_5032483	cis	0,51±0,09	1,43E-08	0,36	TPX2-(targeting-protein-for-Xklp2)-protein-family
AT2G28570	chr5_10076415	trans	-0,48±0,08	1,45E-08	0,61	
AT2G21070	chr2_9049079	cis	0,52±0,09	1,45E-08	0,56	methyltransferases
AT4G38800	chr4_18114982	cis	-0,7±0,12	1,47E-08	0,14	methylthioadenosine-nucleosidase-1
AT2G17250	chr2_7502298	cis	-0,63±0,11	1,47E-08	0,20	CCAAT-binding-factor
AT5G49880	chr5_20283201	cis	-0,52±0,09	1,48E-08	0,43	mitotic-checkpoint-family-protein
AT4G27060	chr5_15241492	trans	0,66±0,12	1,49E-08	0,19	ARM-repeat-superfamily-protein
AT1G03687	chr1_911035	cis	0,73±0,13	1,49E-08	0,14	DTW-domain-containing-protein
AT3G12500	chr3_3961589	cis	0,73±0,13	1,49E-08	0,14	basic-chitinase
AT2G27340	chr2_11749813	trans	0,55±0,1	1,49E-08	0,40	N-acetylglucosaminylphosphatidylinositol-de-N-acetylase-family-protein
AT1G35710	chr1_13217203	cis	-0,49±0,09	1,50E-08	0,41	Protein-kinase-family-protein-with-leucine-rich-repeat-domain
AT5G56990	chr5_23061966	cis	0,86±0,15	1,51E-08	0,09	
AT2G26355	chr2_11211668	cis	0,54±0,1	1,51E-08	0,41	other-RNA
AT3G01920	chr1_11108688	trans	-0,74±0,13	1,52E-08	0,11	DHBP-synthase-RibB-like-alpha/beta-domain
AT3G11440	chr3_3602192	cis	-0,51±0,09	1,52E-08	0,44	myb-domain-protein-65
AT5G63520	chr5_25423865	cis	-0,96±0,17	1,52E-08	0,07	
AT3G01320	chr3_106640	cis	-0,55±0,1	1,52E-08	0,28	SIN3-like-1
AT1G25155	chr1_8838392	cis	-0,48±0,09	1,53E-08	0,49	Glutamine-amidotransferase-type-1-family-protein
AT4G27080	chr5_15243254	trans	0,67±0,12	1,54E-08	0,19	PDI-like-5-4
AT3G30885	chr3_12656772	cis	-0,79±0,14	1,54E-08	0,10	
AT5G46720	chr5_18959636	cis	-0,56±0,1	1,56E-08	0,31	AIG2-like-(avirulence-induced-gene)-family-protein
AT4G29890	chr4_14536920	trans	-0,69±0,12	1,57E-08	0,16	choline-monooxygenase,-putative-(CMO-like)

AT1G79950	chr1_30058921	cis	-0,67±0,12	1,59E-08	0,16	RAD3-like-DNA-binding-helicase-protein
AT1G63460	chr1_23539579	cis	-0,68±0,12	1,59E-08	0,16	glutathione-peroxidase-8
AT4G14580	chr4_8369338	cis	-0,91±0,16	1,60E-08	0,08	CBL-interacting-protein-kinase-4
AT5G44080	chr5_17739427	cis	0,52±0,09	1,60E-08	0,39	Basic-leucine-zipper-(bZIP)-transcription-factor-family-protein
AT5G58600	chr5_23680788	cis	-0,61±0,11	1,60E-08	0,23	Plant-protein-of-unknown-function-(DUF828)
AT2G19240	chr2_8349464	cis	0,56±0,1	1,61E-08	0,26	Ypt/Rab-GAP-domain-of-gyp1p-superfamily-protein
AT3G53650	chr3_19885798	cis	-0,77±0,14	1,61E-08	0,09	Histone-superfamily-protein
AT2G30270	chr2_12905734	cis	0,5±0,09	1,63E-08	0,53	Protein-of-unknown-function-(DUF567)
AT4G00975	chr5_7918293	trans	0,84±0,15	1,63E-08	0,09	other-RNA
AT1G55420	chr1_20693672	cis	0,96±0,17	1,63E-08	0,06	Cysteine/Histidine-rich-C1-domain-family-protein
AT5G16540	chr5_5405112	cis	0,56±0,1	1,65E-08	0,25	zinc-finger-nuclease-3
AT5G21030	chr5_7140817	cis	0,5±0,09	1,65E-08	0,50	PAZ-domain-containing-protein-/-piwi-domain-containing-protein
AT1G66590	chr1_26235271	trans	-0,5±0,09	1,66E-08	0,46	cytochrome-c-oxidase-19-1
AT1G72950	chr1_27441129	cis	0,7±0,12	1,68E-08	0,14	Disease-resistance-protein-(TIR-NBS-class)
AT5G25770	chr5_8970186	cis	-0,93±0,16	1,68E-08	0,07	alpha/beta-Hydrolases-superfamily-protein
AT2G18410	chr3_15611343	trans	-0,52±0,09	1,69E-08	0,31	
AT4G14147	chr5_17997128	trans	0,54±0,1	1,70E-08	0,24	protein-binding
AT1G53460	chr1_19948118	cis	-0,9±0,16	1,71E-08	0,09	
AT3G30200	chr1_27556182	trans	-0,63±0,11	1,73E-08	0,18	Plant-transposase-(Ptta/En/Spm-family)
AT3G48330	chr3_17891002	cis	-0,49±0,09	1,74E-08	0,46	protein-l-isoaspartate-methyltransferase-1
AT5G47440	chr5_19237562	cis	0,77±0,14	1,75E-08	0,12	Plant-protein-of-unknown-function-(DUF828)-with-plant-pleckstrin-homology-like-region
AT3G54280	chr2_5407788	trans	0,52±0,09	1,75E-08	0,39	DNA-binding;ATP-binding;nucleic-acid-binding;binding;helicases;ATP-binding;DNA-binding;helicases
AT5G10800	chr5_3410379	cis	-0,67±0,12	1,77E-08	0,15	RNA-recognition-motif-(RRM)-containing-protein
AT3G59710	chr3_22059222	cis	-0,57±0,1	1,77E-08	0,26	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT4G00230	chr4_97499	cis	-0,67±0,12	1,78E-08	0,16	xylem-serine-peptidase-1
AT2G35738	chr2_15023025	cis	0,57±0,1	1,79E-08	0,21	other-RNA
AT4G02460	chr5_14985436	trans	-0,46±0,08	1,80E-08	0,46	DNA-mismatch-repair-protein,-putative
AT2G42810	chr3_7511056	trans	0,61±0,11	1,80E-08	0,18	protein-phosphatase-5.2
AT5G22545	chr5_7483918	cis	-0,65±0,12	1,81E-08	0,19	
AT2G14090	chr2_5925301	cis	-0,56±0,1	1,82E-08	0,26	
AT5G55130	chr5_22441845	NA	0,91±0,16	1,82E-08	0,09	co-factor-for-nitrate,-reductase-and-xanthine-dehydrogenase-5
AT5G03830	chr5_1017018	cis	0,51±0,09	1,83E-08	0,48	CDK-inhibitor-P21-binding-protein
AT5G10080	chr1_24538442	trans	-0,5±0,09	1,83E-08	0,37	Eukaryotic-aspartyl-protease-family-protein
AT5G03300	chr5_796262	cis	0,49±0,09	1,85E-08	0,33	adenosine-kinase-2
AT1G11860	chr1_4006487	cis	0,52±0,09	1,86E-08	0,32	Glycine-cleavage-T-protein-family
AT1G68935	chr1_25921536	cis	-0,85±0,15	1,87E-08	0,09	
AT3G13438	chr3_4378113	cis	-0,93±0,17	1,88E-08	0,11	transposable-element-gene
AT1G03300	chr1_807780	cis	-0,67±0,12	1,89E-08	0,19	DOMAIN-OF-UNKNOWN-FUNCTION-724-1
AT5G09960	chr5_3101648	cis	0,58±0,1	1,89E-08	0,24	
AT5G52820	chr5_21396010	cis	0,58±0,1	1,92E-08	0,24	WD-40-repeat-family-protein-/-notchless-protein,-putative
AT2G31940	chr2_13582422	cis	-0,67±0,12	1,92E-08	0,20	
AT3G19440	chr3_6742417	cis	-0,5±0,09	1,93E-08	0,35	Pseudouridine-synthase-family-protein
AT5G23520	chr5_7931777	cis	0,57±0,1	1,93E-08	0,39	smr-(Small-MutS-Related)-domain-containing-protein
AT1G70505	chr1_26569272	cis	0,56±0,1	1,94E-08	0,26	
AT1G75990	chr1_28524806	cis	-0,52±0,09	1,94E-08	0,34	PAM-domain-(PCI/PINT-associated-module)-protein
AT1G49245	chr1_18219075	cis	-0,68±0,12	1,95E-08	0,19	Prefoldin-chaperone-subunit-family-protein
AT2G28670	chr2_12301537	cis	0,48±0,09	1,96E-08	0,41	Disease-resistance-responsive-(dirigent-like-protein)-family-protein
AT1G09010	chr1_2899517	cis	0,53±0,09	1,97E-08	0,31	glycoside-hydrolase-family-2-protein
AT3G04000	chr3_1036834	cis	0,52±0,09	1,97E-08	0,30	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT2G37150	chr1_27132704	trans	0,47±0,08	1,99E-08	0,44	RING/U-box-superfamily-protein
AT1G24909	chr1_8838392	trans	-0,48±0,09	1,99E-08	0,49	Glutamine-amidotransferase-type-1-family-protein
AT3G51820	chr3_19215689	cis	0,67±0,12	2,00E-08	0,19	UbiA-prenyltransferase-family-protein
AT4G36880	chr4_17377498	cis	0,56±0,1	2,01E-08	0,25	cysteine-proteinase1
AT3G29250	chr5_20942173	trans	0,6±0,11	2,01E-08	0,20	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT3G28290	chr3_10561937	cis	0,79±0,14	2,02E-08	0,11	Protein-of-unknown-function-(DUF677)
AT1G07790	chr1_2389507	cis	0,75±0,13	2,03E-08	0,15	Histone-superfamily-protein
AT2G38610	chr2_16137736	cis	-0,47±0,08	2,03E-08	0,45	RNA-binding-KH-domain-containing-protein
AT2G45560	chr2_18778754	cis	-0,52±0,09	2,04E-08	0,40	cytochrome-P450,-family-76,-subfamily-C,-polypeptide-1
AT3G07500	chr3_2395955	cis	0,48±0,09	2,04E-08	0,49	Far-red-impaired-responsive-(FAR1)-family-protein
AT3G27120	chr3_10008757	cis	01,02±0,18	2,06E-08	0,06	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT2G44670	chr4_7756752	trans	0,44±0,08	2,06E-08	0,50	Protein-of-unknown-function-(DUF581)
AT5G02170	chr5_428888	cis	-0,63±0,11	2,07E-08	0,19	Transmembrane-amino-acid-transporter-family-protein
AT1G53340	chr1_19897175	cis	0,5±0,09	2,07E-08	0,44	Cysteine/Histidine-rich-C1-domain-family-protein
AT2G35060	chr2_14753584	cis	0,5±0,09	2,08E-08	0,44	K+-uptake-permease-11
AT5G10010	chr5_3128050	cis	-0,56±0,1	2,09E-08	0,29	
AT2G30140	chr2_12891166	cis	0,59±0,11	2,09E-08	0,23	UDP-Glycosyltransferase-superfamily-protein
AT1G60610	chr1_22329998	cis	-0,51±0,09	2,09E-08	0,31	SBP-(S-ribonuclease-binding-protein)-family-protein
AT5G10510	chr5_3319849	cis	0,58±0,1	2,10E-08	0,29	AINTEGUMENTA-like-6
AT5G01340	chr5_190469	cis	0,71±0,13	2,11E-08	0,16	Mitochondrial-substrate-carrier-family-protein
AT1G20620	chr1_7124385	cis	0,72±0,13	2,11E-08	0,12	catalase-3
AT3G10730	chr3_3361393	cis	0,61±0,11	2,14E-08	0,21	SAD1/UNC-84-domain-protein-2
AT1G79520	chr1_29915150	cis	0,49±0,09	2,14E-08	0,44	Cation-efflux-family-protein
AT1G02770	chr1_607355	cis	0,53±0,09	2,15E-08	0,32	Protein-of-unknown-function-(DUF626)
AT5G63970	chr3_7011617	trans	0,54±0,1	2,16E-08	0,25	Copine-(Calcium-dependent-phospholipid-binding-protein)-family
AT4G31790	chr4_15373256	cis	-0,63±0,11	2,17E-08	0,19	Tetrapyrrole-(Corrin/Porphyrin)-Methylases
AT3G07080	chr3_2238593	cis	-0,67±0,12	2,17E-08	0,15	EamA-like-transporter-family
AT5G40080	chr5_15935609	trans	0,49±0,09	2,17E-08	0,36	Mitochondrial-ribosomal-protein-L27
AT5G10810	chr5_3415555	cis	-0,58±0,1	2,20E-08	0,22	enhancer-of-rudimentary-protein,-putative
AT3G53890	chr3_19955946	cis	-0,58±0,1	2,20E-08	0,23	Ribosomal-protein-S21e-

AT5G32440	chr5_11618157	trans	0,53±0,09	2,20E-08	0,41	Ubiquitin-system-component-Cue-protein
AT4G36150	chr4_12112307	trans	0,59±0,11	2,21E-08	0,21	Disease-resistance-protein-(TIR-NBS-LRR-class)-family
AT2G16400	chr2_7103052	cis	-0,65±0,12	2,23E-08	0,24	BEL1-like-homeodomain-7
AT5G08360	chr5_2688664	cis	-01,01±0,18	2,24E-08	0,06	Protein-of-unknown-function-(DUF789)
AT3G26430	chr3_9675361	cis	0,52±0,09	2,25E-08	0,37	GDSL-like-Lipase/Acylhydrolase-superfamily-protein
AT2G41830	chr3_7410921	trans	-0,63±0,11	2,25E-08	0,17	Uncharacterized-protein
AT1G69400	chr1_26087154	cis	-0,7±0,13	2,26E-08	0,13	Transducin/WD40-repeat-like-superfamily-protein
AT5G26220	chr5_9162525	cis	-0,74±0,13	2,27E-08	0,14	ChaC-like-family-protein
AT5G51590	chr2_17487927	trans	0,68±0,12	2,27E-08	0,14	AT-hook-motif-DNA-binding-family-protein
AT1G07780	chr1_2411504	cis	0,62±0,11	2,27E-08	0,20	phosphoribosylanthranilate-isomerase-1
AT5G43780	chr5_17592204	cis	0,49±0,09	2,27E-08	0,55	Pseudouridine-synthase/archaeosine-transglycosylase-like-family-protein
AT5G39960	chr5_15993334	cis	0,61±0,11	2,33E-08	0,19	GTP-binding;GTP-binding
AT5G47730	chr5_19342075	cis	-0,48±0,09	2,33E-08	0,46	Sec14p-like-phosphatidylinositol-transfer-family-protein
AT3G23260	chr3_8313341	cis	-0,54±0,1	2,33E-08	0,27	F-box-and-associated-interaction-domains-containing-protein
AT4G36970	chr1_21358004	trans	0,62±0,11	2,34E-08	0,17	Remorin-family-protein
AT1G64355	chr1_23890668	cis	-0,5±0,09	2,34E-08	0,40	
AT5G26330	chr5_9243151	cis	-0,52±0,09	2,34E-08	0,57	Cupredoxin-superfamily-protein
AT5G19151	chr5_6424256	cis	-0,95±0,17	2,34E-08	0,07	
AT3G28730	chr3_10776224	cis	0,75±0,13	2,34E-08	0,11	high-mobility-group
AT3G02850	chr3_627697	cis	-0,59±0,11	2,34E-08	0,31	STELAR-K+-outward-rectifier
AT1G17890	chr1_6155204	cis	0,49±0,09	2,35E-08	0,42	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT5G18640	chr5_6212879	cis	-0,67±0,12	2,35E-08	0,15	alpha/beta-Hydrolases-superfamily-protein
AT3G02515	chr1_19317553	trans	0,52±0,09	2,35E-08	0,30	transposable-element-gene
AT4G25160	chr4_12901908	cis	-0,57±0,1	2,35E-08	0,26	U-box-domain-containing-protein-kinase-family-protein
AT5G20590	chr5_6976013	cis	0,56±0,1	2,36E-08	0,51	TRICHOME-BIREFRINGENCE-LIKE-5
AT4G14970	chr4_8549663	cis	0,63±0,11	2,37E-08	0,17	
AT5G10700	chr5_3378136	cis	0,52±0,09	2,37E-08	0,32	Peptidyl-tRNA-hydrolase-II-(PTH2)-family-protein
AT1G34630	chr1_12663560	cis	-0,53±0,1	2,38E-08	0,29	
AT2G02061	chr2_497693	cis	-0,54±0,1	2,40E-08	0,25	Nucleotide-diphospho-sugar-transferase-family-protein
AT5G08370	chr5_2692864	cis	0,99±0,18	2,40E-08	0,07	alpha-galactosidase-2
AT1G09410	chr1_3029542	cis	-0,88±0,16	2,40E-08	0,08	pentatricopeptide-(PPR)-repeat-containing-protein
AT3G30300	chr3_11977788	trans	01,01±0,18	2,42E-08	0,06	O-fucosyltransferase-family-protein
AT3G21750	chr2_13921849	trans	-0,61±0,11	2,43E-08	0,19	UDP-glucosyl-transferase-71B1
AT1G30860	chr1_10989031	cis	0,62±0,11	2,43E-08	0,19	RING/U-box-superfamily-protein
AT5G50130	chr5_20402588	cis	0,58±0,1	2,44E-08	0,24	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT1G22350	chr1_7893594	cis	-0,46±0,08	2,45E-08	0,53	
AT3G09480	chr3_2914935	cis	0,58±0,1	2,45E-08	0,21	Histone-superfamily-protein
AT5G56190	chr5_22741453	cis	0,49±0,09	2,45E-08	0,44	Transducin/WD40-repeat-like-superfamily-protein
AT3G03600	chr2_19503336	trans	0,79±0,14	2,46E-08	0,09	ribosomal-protein-S2
AT2G39250	chr2_16409973	cis	0,66±0,12	2,47E-08	0,16	Integrase-type-DNA-binding-superfamily-protein
AT1G49720	chr1_18400592	cis	0,53±0,1	2,48E-08	0,34	abscisic-acid-responsive-element-binding-factor-1
AT3G23325	chr3_8345695	cis	-0,61±0,11	2,48E-08	0,24	Splicing-factor-3B-subunit-5/RDS3-complex-subunit-10
AT5G60700	chr5_24404922	cis	0,52±0,09	2,49E-08	0,52	glycosyltransferase-family-protein-2
AT3G06180	chr4_2412418	trans	-0,73±0,13	2,49E-08	0,10	Ribosomal-protein-L34e-superfamily-protein
AT1G78476	chr1_29524227	cis	-0,53±0,1	2,50E-08	0,24	
AT2G46290	chr1_19690189	trans	0,89±0,16	2,51E-08	0,07	Transducin/WD40-repeat-like-superfamily-protein
AT5G47660	chr5_23344738	trans	-0,74±0,13	2,52E-08	0,12	Homeodomain-like-superfamily-protein
AT1G10230	chr1_3396134	cis	-0,6±0,11	2,52E-08	0,19	SKP1-like-18
AT1G31910	chr4_9528845	trans	-0,5±0,09	2,54E-08	0,49	GHMP-kinase-family-protein
AT2G45670	chr1_16935634	trans	-0,48±0,09	2,54E-08	0,47	calcineurin-B-subunit-related
AT2G27970	chr2_11913129	cis	-0,5±0,09	2,55E-08	0,53	CDK-subunit-2
AT1G66340	chr1_24734188	cis	0,59±0,11	2,59E-08	0,23	Signal-transduction-histidine-kinase,-hybrid-type,-ethylene-sensor
AT1G01240	chr1_100027	cis	0,62±0,11	2,59E-08	0,17	
AT3G57740	chr3_21437509	cis	0,7±0,13	2,59E-08	0,14	Protein-kinase-superfamily-protein
AT5G10260	chr2_2419382	trans	0,75±0,13	2,60E-08	0,11	RAB-GTPase-homolog-H1E
AT5G27630	chr5_9766989	cis	0,73±0,13	2,60E-08	0,15	acyl-CoA-binding-protein-5
AT5G44520	chr5_17932027	cis	-0,81±0,15	2,60E-08	0,10	NagB/RpiA/CoA-transferase-like-superfamily-protein
AT1G63770	chr1_4473727	trans	0,55±0,1	2,62E-08	0,22	Peptidase-M1-family-protein
AT4G01320	chr4_549506	cis	-0,69±0,12	2,62E-08	0,14	Peptidase-family-M48-family-protein
AT2G05590	chr2_2064956	cis	0,53±0,1	2,62E-08	0,29	TLD-domain-containing-nucleolar-protein
AT3G57120	chr3_21140914	cis	0,68±0,12	2,64E-08	0,16	Protein-kinase-superfamily-protein
AT5G10330	chr4_11121261	trans	0,81±0,15	2,64E-08	0,11	histidinol-phosphate-aminotransferase-1
AT2G31910	chr1_21850510	trans	0,46±0,08	2,64E-08	0,44	cation/H+-exchanger-21
AT2G02955	chr2_860116	cis	0,96±0,17	2,64E-08	0,06	maternal-effect-embryo-arrest-12
AT3G05570	chr3_1613760	cis	0,92±0,16	2,65E-08	0,07	
AT2G14285	chr4_4788804	trans	-0,64±0,12	2,66E-08	0,20	Small-nuclear-ribonucleoprotein-family-protein
AT4G10920	chr4_6699117	cis	0,55±0,1	2,67E-08	0,24	transcriptional-coactivator-p15-(PC4)-family-protein-(KELP)
AT2G04540	chr2_1579288	cis	0,79±0,14	2,68E-08	0,11	Beta-ketoacyl-synthase
AT3G57140	chr4_11589080	trans	-0,45±0,08	2,71E-08	0,46	sugar-dependent-1-like
AT4G01575	chr4_688298	cis	0,55±0,1	2,71E-08	0,24	serine-protease-inhibitor,-Kazal-type-family-protein
AT1G55320	chr1_20635146	cis	-0,54±0,1	2,74E-08	0,32	acyl-activating-enzyme-18
AT5G60370	chr5_24281843	cis	0,5±0,09	2,75E-08	0,60	
AT2G30330	chr2_12929033	cis	0,53±0,1	2,75E-08	0,32	GCN5L1-family-protein
AT4G02195	chr4_974563	cis	0,95±0,17	2,78E-08	0,06	syntaxin-of-plants-42
AT3G53680	chr3_19898140	cis	-0,55±0,1	2,78E-08	0,34	Acyl-CoA-N-acyltransferase-with-RING/FYVE/PHD-type-zinc-finger-domain
AT1G13670	chr3_13803064	trans	-0,49±0,09	2,79E-08	0,66	
AT2G32840	chr2_13923281	cis	-0,48±0,09	2,80E-08	0,39	proline-rich-family-protein
AT1G43180	chr1_18587810	trans	0,63±0,11	2,81E-08	0,16	
AT5G57345	chr5_23227828	cis	0,68±0,12	2,83E-08	0,18	

ATMG00640	chr3_19051497	trans	0,5±0,09	2,84E-08	0,28	hydrogen-ion-transporting-ATP-synthases,-rotational-mechanism;zinc-ion-binding
AT1G12250	chr1_4158507	cis	-0,96±0,17	2,85E-08	0,06	Pentapeptide-repeat-containing-protein
AT4G32730	chr4_13252657	trans	-0,71±0,13	2,86E-08	0,13	Homeodomain-like-protein
AT5G46270	chr1_19328809	trans	-0,53±0,09	2,87E-08	0,25	Disease-resistance-protein-(TIR-NBS-LRR-class)-family
AT4G19840	chr4_10774639	cis	0,54±0,1	2,88E-08	0,24	phloem-protein-2-A1
AT2G39130	chr2_16328361	cis	-0,47±0,08	2,88E-08	0,44	Transmembrane-amino-acid-transporter-family-protein
AT5G64050	chr5_25633453	cis	-0,59±0,11	2,89E-08	0,25	glutamate-tRNA-synthetase
AT2G32810	chr2_13928359	cis	-0,61±0,11	2,92E-08	0,18	beta-galactosidase-9
AT3G55060	chr3_20419609	cis	0,53±0,1	2,93E-08	0,29	
AT2G23100	chr2_9839691	cis	-0,56±0,1	2,97E-08	0,23	Cysteine/Histidine-rich-C1-domain-family-protein
AT3G25990	chr3_22169625	trans	-0,56±0,1	2,97E-08	0,23	Homeodomain-like-superfamily-protein
AT5G20940	chr5_7114734	cis	-0,56±0,1	2,97E-08	0,27	Glycosyl-hydrolase-family-protein
AT3G45940	chr3_16889397	cis	0,69±0,13	2,98E-08	0,15	Glycosyl-hydrolases-family-31--protein
AT4G13190	chr4_7662128	cis	-0,65±0,12	2,98E-08	0,14	Protein-kinase-superfamily-protein
AT5G55170	chr4_616041	trans	-0,77±0,14	2,98E-08	0,10	small-ubiquitin-like-modifier-3
AT1G65970	chr1_24571257	cis	0,56±0,1	2,99E-08	0,25	thioredoxin-dependent-peroxidase-2
AT5G53730	chr5_21807548	cis	-0,69±0,12	3,00E-08	0,14	Late-embryogenesis-abundant-(LEA)-hydroxyproline-rich-glycoprotein-family
AT3G12510	chr3_3950102	cis	0,61±0,11	3,02E-08	0,23	MADS-box-family-protein
AT2G01640	chr2_288906	cis	0,87±0,16	3,02E-08	0,08	
AT3G23020	chr3_8177200	cis	0,53±0,1	3,03E-08	0,31	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT5G27610	chr5_9764697	cis	-0,66±0,12	3,03E-08	0,15	DIRP-;Myb-like-DNA-binding-domain
AT1G74680	chr1_28063927	cis	0,58±0,1	3,08E-08	0,22	Exostosin-family-protein
AT5G20350	chr5_6876585	cis	-0,5±0,09	3,08E-08	0,35	Ankyrin-repeat-family-protein-with-DHHC-zinc-finger-domain
AT3G52420	chr3_19429961	cis	-0,53±0,1	3,08E-08	0,26	outer-envelope-membrane-protein-7
AT5G56130	chr3_18598374	trans	-0,6±0,11	3,09E-08	0,21	Transducin/WD40-repeat-like-superfamily-protein
AT5G12930	chr5_4085323	cis	-0,67±0,12	3,09E-08	0,21	
AT2G31910	chr2_13572549	cis	0,62±0,11	3,12E-08	0,16	cation/H+-exchanger-21
AT1G30620	chr1_10864371	cis	0,53±0,1	3,15E-08	0,29	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT5G33300	chr5_12450869	trans	0,92±0,17	3,17E-08	0,08	chromosome-associated-kinesin-related
AT4G09670	chr4_6108822	cis	0,54±0,1	3,17E-08	0,24	Oxidoreductase-family-protein
AT2G37860	chr2_15852326	cis	0,99±0,18	3,18E-08	0,06	Protein-of-unknown-function-(DUF3411)
AT2G40240	chr5_15481306	trans	-0,64±0,11	3,18E-08	0,16	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT4G37030	chr4_17447506	cis	-0,61±0,11	3,22E-08	0,19	
AT1G71440	chr1_26921006	cis	0,82±0,15	3,24E-08	0,09	tubulin-folding-cofactor-E-/-Pfifferling-(PFI)
AT5G38360	chr5_15332018	cis	-0,67±0,12	3,27E-08	0,16	alpha/beta-Hydrolases-superfamily-protein
AT2G18710	chr2_8112156	cis	-0,49±0,09	3,28E-08	0,47	SECY-homolog-1
AT1G32928	chr1_11930336	cis	-0,48±0,09	3,28E-08	0,40	
AT5G66360	chr4_6690528	trans	-0,49±0,09	3,29E-08	0,56	Ribosomal-RNA-adenine-dimethylase-family-protein
AT1G14730	chr1_5069662	cis	-0,94±0,17	3,29E-08	0,06	Cytochrome-b561/ferric-reductase-transmembrane-protein-family
AT3G20975	chr3_7329829	cis	0,92±0,17	3,29E-08	0,09	transposable-element-gene
AT5G01090	chr1_1926622	trans	-0,73±0,13	3,33E-08	0,11	Concanavalin-A-like-lectin-family-protein
AT2G39570	chr2_16507683	cis	-0,66±0,12	3,34E-08	0,14	ACT-domain-containing-protein
AT5G01810	chr5_311371	cis	0,49±0,09	3,35E-08	0,46	CBL-interacting-protein-kinase-15
AT2G21970	chr1_7336537	trans	-0,73±0,13	3,35E-08	0,11	stress-enhanced-protein-2
AT1G54050	chr1_20170832	cis	0,78±0,14	3,36E-08	0,16	HSP20-like-chaperones-superfamily-protein
AT5G28340	chr4_2873038	trans	-0,95±0,17	3,37E-08	0,06	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT4G03820	chr2_9283891	trans	-0,67±0,12	3,37E-08	0,13	Protein-of-unknown-function-(DUF3537)
AT3G23910	chr3_8793946	trans	-0,51±0,09	3,41E-08	0,36	
AT3G26040	chr3_9530571	cis	-0,77±0,14	3,42E-08	0,11	HXXXD-type-acyl-transferase-family-protein
AT4G11310	chr4_6879549	cis	-0,52±0,09	3,42E-08	0,31	Papain-family-cysteine-protease
AT5G66630	chr5_26588890	cis	-0,52±0,09	3,43E-08	0,33	DA1-related-protein-5
AT2G04340	chr2_1498237	cis	-0,76±0,14	3,43E-08	0,11	
AT4G01580	chr4_687044	cis	0,5±0,09	3,43E-08	0,38	AP2/B3-like-transcriptional-factor-family-protein
AT5G42230	chr5_16879527	cis	0,9±0,16	3,44E-08	0,07	serine-carboxypeptidase-like-41
AT2G17280	chr1_13461629	trans	-0,62±0,11	3,44E-08	0,16	Phosphoglycerate-mutase-family-protein
AT1G02000	chr1_346022	cis	0,53±0,1	3,45E-08	0,26	UDP-D-glucuronate-4-epimerase-2
AT4G14455	chr4_8309045	cis	-0,48±0,09	3,45E-08	0,45	Target-SNARE-coiled-coil-domain-protein
AT1G53080	chr1_19779839	cis	-0,51±0,09	3,49E-08	0,34	Legume-lectin-family-protein
AT1G33290	chr1_12077757	cis	0,55±0,1	3,49E-08	0,25	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT5G24660	chr3_15302783	trans	-0,73±0,13	3,50E-08	0,12	response-to-low-sulfur-2
AT5G02270	chr5_467255	cis	0,47±0,09	3,51E-08	0,49	non-intrinsic-ABC-protein-9
AT4G36750	chr4_17326398	cis	0,57±0,1	3,52E-08	0,27	Quinone-reductase-family-protein
AT5G64830	chr5_25916033	cis	-0,98±0,18	3,53E-08	0,06	programmed-cell-death-2-C-terminal-domain-containing-protein
AT5G41970	chr5_16791339	cis	-0,71±0,13	3,54E-08	0,15	Metal-dependent-protein-hydrolase
AT5G50450	chr1_18170823	trans	0,51±0,09	3,55E-08	0,33	HCP-like-superfamily-protein-with-MYND-type-zinc-finger
AT1G04030	chr1_1049948	cis	0,48±0,09	3,56E-08	0,46	
AT2G25430	chr3_18761539	trans	0,48±0,09	3,57E-08	0,29	epsin-N-terminal-homology-(ENTH)-domain-containing-protein-/-clathrin-assembly-protein-related
AT3G03360	chr3_764333	cis	-0,53±0,1	3,58E-08	0,39	F-box/RNI-like-superfamily-protein
AT1G35230	chr1_12918273	cis	0,5±0,09	3,58E-08	0,57	arabinogalactan-protein-5
AT1G72330	chr1_27237295	cis	0,49±0,09	3,59E-08	0,48	alanine-aminotransferase-2
AT1G80750	chr1_30348415	cis	0,49±0,09	3,59E-08	0,44	Ribosomal-protein-L30/L7-family-protein
AT4G27560	chr4_13759116	cis	-0,52±0,09	3,59E-08	0,36	UDP-Glycosyltransferase-superfamily-protein
AT5G15920	chr5_5208450	cis	-0,82±0,15	3,60E-08	0,13	structural-maintenance-of-chromosomes-5
AT1G22540	chr1_10151342	trans	0,66±0,12	3,61E-08	0,14	Major-facilitator-superfamily-protein
AT3G50790	chr4_5607625	trans	0,7±0,13	3,62E-08	0,12	esterase/lipase/thioesterase-family-protein
AT1G70430	chr1_26545813	cis	0,5±0,09	3,63E-08	0,35	Protein-kinase-superfamily-protein
AT5G66930	chr5_26736168	cis	0,58±0,11	3,63E-08	0,26	
AT1G32375	chr1_11676019	cis	0,98±0,18	3,63E-08	0,06	F-box/RNI-like/FBD-like-domains-containing-protein
AT4G09500	chr4_6017910	cis	-0,51±0,09	3,64E-08	0,48	UDP-Glycosyltransferase-superfamily-protein

AT3G26340	chr3_9652112	cis	0,67±0,12	3,64E-08	0,13	N-terminal-nucleophile-aminohydrolases-(Ntn-hydrolases)-superfamily-protein
AT5G11780	chr1_16840961	trans	-0,95±0,17	3,64E-08	0,06	
AT4G31520	chr4_15281562	cis	0,73±0,13	3,66E-08	0,11	SDA1-family-protein
AT3G55860	chr3_20729596	cis	-0,51±0,09	3,68E-08	0,29	
AT3G08930	chr3_2713870	cis	0,51±0,09	3,68E-08	0,32	LMBR1-like-membrane-protein
AT3G17710	chr3_6089215	cis	0,57±0,1	3,69E-08	0,24	F-box-and-associated-interaction-domains-containing-protein
AT2G43940	chr2_18197881	cis	0,48±0,09	3,70E-08	0,54	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein
AT2G34655	chr1_8321934	trans	0,48±0,09	3,70E-08	0,41	
AT3G02520	chr3_525833	cis	0,53±0,1	3,70E-08	0,43	general-regulatory-factor-7
AT3G44660	chr3_16232070	cis	-0,66±0,12	3,70E-08	0,16	histone-deacetylase-10
AT2G47980	chr5_26359562	trans	0,75±0,14	3,71E-08	0,11	sister-chromatid-cohesion-protein-3
AT5G27750	chr5_9831277	cis	0,61±0,11	3,75E-08	0,19	F-box/FBD-like-domains-containing-protein
AT2G05100	chr2_1830877	cis	0,78±0,14	3,78E-08	0,11	photosystem-II-light-harvesting-complex-gene-2.1
AT5G02430	chr5_530113	cis	0,65±0,12	3,78E-08	0,16	Transducin/WD40-repeat-like-superfamily-protein
AT2G46890	chr2_11722565	trans	0,8±0,15	3,78E-08	0,08	Protein-of-unknown-function-(DUF1295)
AT2G31980	chr2_13590583	cis	-0,84±0,15	3,81E-08	0,09	PHYTOCYSTATIN-2
AT5G20550	chr5_6958246	cis	-0,53±0,1	3,83E-08	0,48	2-oxoglutarate-(2OG)-and-Fe(II)-dependent-oxygenase-superfamily-protein
AT5G14710	chr4_4437048	trans	-0,89±0,16	3,83E-08	0,07	
AT1G23750	chr1_8401967	cis	0,61±0,11	3,86E-08	0,19	Nucleic-acid-binding,-OB-fold-like-protein
AT4G21410	chr4_11405085	cis	0,63±0,11	3,87E-08	0,20	cysteine-rich-RLK-(RECEPTOR-like-protein-kinase)-29
AT3G01130	chr5_11755315	trans	-0,62±0,11	3,88E-08	0,14	
AT1G20480	chr1_7097121	cis	0,83±0,15	3,88E-08	0,09	AMP-dependent-synthetase-and-ligase-family-protein
AT3G55140	chr3_20407685	cis	-0,81±0,15	3,88E-08	0,09	Pectin-lyase-like-superfamily-protein
AT4G19985	chr4_10833135	cis	0,63±0,12	3,88E-08	0,16	Acyl-CoA-N-acyltransferases-(NAT)-superfamily-protein
AT5G49015	chr5_19868135	cis	-0,48±0,09	3,89E-08	0,36	Expressed-protein
AT4G02890	chr4_2720901	trans	-0,48±0,09	3,89E-08	0,60	Ubiquitin-family-protein
AT3G15710	chr1_8350453	trans	0,73±0,13	3,90E-08	0,11	Peptidase-S24/S26A/S26B/S26C-family-protein
AT1G63180	chr1_23417693	cis	0,94±0,17	3,90E-08	0,06	UDP-D-glucose/UDP-D-galactose-4-epimerase-3
AT5G57270	chr1_28930265	trans	0,47±0,09	3,90E-08	0,38	Core-2/I-branching-beta-1,6-N-acetylglucosaminyltransferase-family-protein
AT4G22270	chr4_11777311	cis	-0,52±0,09	3,93E-08	0,33	Protein-of-unknown-function-(DUF3537)
AT4G23130	chr4_12119508	cis	-0,51±0,09	3,94E-08	0,42	cysteine-rich-RLK-(RECEPTOR-like-protein-kinase)-5
AT3G23080	chr3_8209226	cis	-0,84±0,15	3,95E-08	0,10	Polyketide-cyclase/dehydrase-and-lipid-transport-superfamily-protein
AT2G33820	chr2_14305380	cis	-0,56±0,1	3,95E-08	0,23	Mitochondrial-substrate-carrier-family-protein
AT4G01060	chr4_448429	cis	-0,59±0,11	3,95E-08	0,24	CAPRICE-like-MYB3
AT2G14170	chr2_5991119	cis	0,47±0,09	3,96E-08	0,45	aldehyde-dehydrogenase--6B2
AT4G32970	chr5_10138211	trans	-0,74±0,14	3,96E-08	0,11	
AT4G26530	chr2_6149075	trans	-0,5±0,09	3,98E-08	0,29	Aldolase-superfamily-protein
AT5G47380	chr5_19233935	cis	-0,93±0,17	4,00E-08	0,08	Protein-of-unknown-function,-DUF547
AT3G11530	chr3_3634582	cis	-0,8±0,15	4,00E-08	0,11	Vacuolar-protein-sorting-55-(VPS55)-family-protein
AT1G05310	chr1_1551431	cis	-0,65±0,12	4,01E-08	0,19	Pectin-lyase-like-superfamily-protein
AT5G41685	chr5_16669310	cis	0,58±0,11	4,01E-08	0,21	Mitochondrial-outer-membrane-translocase-complex,-subunit-Tom7
AT4G15950	chr4_9036335	cis	-0,48±0,09	4,02E-08	0,36	RNA-polymerase-II,-Rpb4,-core-protein
AT5G54260	chr5_1280017	trans	-0,76±0,14	4,07E-08	0,11	DNA-repair-and-meiosis-protein-(Mre11)
AT3G20090	chr3_7016612	cis	0,62±0,11	4,07E-08	0,16	cytochrome-P450,-family-705,-subfamily-A,-polypeptide-18
AT3G45440	chr3_16659722	cis	0,51±0,09	4,07E-08	0,34	Concanavalin-A-like-lectin-protein-kinase-family-protein
AT5G35840	chr5_14009659	cis	0,51±0,09	4,07E-08	0,35	phytochrome-C
AT5G53940	chr5_21897559	cis	-0,71±0,13	4,08E-08	0,11	Yippee-family-putative-zinc-binding-protein
AT1G13570	chr1_4647283	cis	-0,47±0,09	4,10E-08	0,48	F-box/RNI-like-superfamily-protein
AT4G18960	chr4_10381453	cis	0,55±0,1	4,10E-08	0,24	K-box-region-and-MADS-box-transcription-factor-family-protein-
AT4G00234	chr4_124226	cis	0,81±0,15	4,10E-08	0,10	
AT1G19480	chr1_6746695	cis	-0,86±0,16	4,12E-08	0,10	DNA-glycosylase-superfamily-protein
AT5G37780	chr5_15004448	cis	-0,51±0,09	4,13E-08	0,32	calmodulin-1
AT3G15920	chr3_5393567	cis	0,76±0,14	4,13E-08	0,13	Phox-(PX)-domain-containing-protein
AT5G12140	chr5_3923131	cis	0,49±0,09	4,13E-08	0,39	cystatin-1
AT1G57770	chr1_21394811	cis	0,68±0,12	4,14E-08	0,14	FAD/NAD(P)-binding-oxidoreductase-family-protein
AT3G21110	chr1_11165270	trans	0,69±0,13	4,17E-08	0,13	purin-7
AT1G36060	chr1_13328534	trans	0,55±0,1	4,18E-08	0,30	Integrase-type-DNA-binding-superfamily-protein
AT1G34010	chr1_12355872	cis	-0,67±0,12	4,19E-08	0,14	
AT4G02290	chr3_20966251	trans	0,63±0,12	4,20E-08	0,17	glycosyl-hydrolase-9B13
AT4G39920	chr4_18519040	cis	0,92±0,17	4,21E-08	0,07	C-CAP/cofactor-C-like-domain-containing-protein
AT1G16830	chr5_16642012	trans	-0,66±0,12	4,21E-08	0,14	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT1G05835	chr1_1761767	cis	-0,51±0,09	4,21E-08	0,32	PHD-finger-protein
AT2G11891	chr2_4804747	cis	-0,55±0,1	4,22E-08	0,24	
AT4G28706	chr4_14168669	cis	0,53±0,1	4,23E-08	0,28	pfkB-like-carbohydrate-kinase-family-protein
AT1G55270	chr3_11813635	trans	0,67±0,12	4,27E-08	0,11	Galactose-oxidase/kelch-repeat-superfamily-protein
AT2G23110	chr1_11782965	trans	0,68±0,12	4,27E-08	0,16	Late-embryogenesis-abundant-protein,-group-6
AT3G55830	chr1_12244325	trans	0,49±0,09	4,27E-08	0,31	Nucleotide-diphospho-sugar-transferases-superfamily-protein
AT3G29000	chr3_11000751	cis	-0,95±0,17	4,27E-08	0,06	Calcium-binding-EF-hand-family-protein
AT4G24240	chr4_12506621	trans	-0,79±0,14	4,31E-08	0,10	WRKY-DNA-binding-protein-7
AT3G48770	chr3_18088378	cis	0,51±0,09	4,36E-08	0,33	DNA-binding;ATP-binding
AT1G67870	chr3_18783571	trans	0,69±0,13	4,38E-08	0,14	glycine-rich-protein
AT5G47720	chr5_19342075	cis	0,45±0,08	4,38E-08	0,46	Thiolase-family-protein
AT5G67488	chr1_20695617	trans	-0,45±0,08	4,39E-08	0,43	other-RNA
ATCG00270	chr4_6933846	trans	0,93±0,17	4,40E-08	0,94	photosystem-II-reaction-center-protein-D
AT3G06125	chr3_1842299	cis	-0,5±0,09	4,41E-08	0,44	other-RNA
AT2G32140	chr2_13656947	cis	-0,49±0,09	4,41E-08	0,40	transmembrane-receptors
AT5G47320	chr5_19203832	cis	-0,81±0,15	4,42E-08	0,09	ribosomal-protein-S19
AT1G60545	chr1_22304145	cis	-0,49±0,09	4,49E-08	0,46	other-RNA
AT4G38545	chr4_18025338	cis	0,89±0,16	4,49E-08	0,08	other-RNA

AT5G48490	chr5_19651751	cis	0,52±0,09	4,50E-08	0,34	Bifunctional-inhibitor/lipid-transfer-protein/seed-storage-2S-albumin-superfamily-protein
AT4G01500	chr1_516502	trans	0,6±0,11	4,51E-08	0,21	AP2/B3-like-transcriptional-factor-family-protein
AT2G11000	chr3_11690914	trans	0,79±0,15	4,53E-08	0,12	MAK10-homologue
AT3G06210	chr3_1954194	trans	0,68±0,12	4,54E-08	0,16	ARM-repeat-superfamily-protein
AT2G38530	chr5_25213415	trans	0,49±0,09	4,56E-08	0,52	lipid-transfer-protein-2
AT1G13970	chr1_4789634	cis	-0,55±0,1	4,56E-08	0,24	Protein-of-unknown-function-(DUF1336)
AT1G61240	chr1_22580363	cis	0,57±0,1	4,57E-08	0,24	Protein-of-unknown-function-(DUF707)
AT4G02900	chr4_1267655	cis	0,59±0,11	4,58E-08	0,26	ERD-(early-responsive-to-dehydration-stress)-family-protein
AT3G17510	chr3_5993315	cis	-0,5±0,09	4,62E-08	0,42	CBL-interacting-protein-kinase-1
AT4G10610	chr4_6557083	cis	0,52±0,1	4,62E-08	0,26	CTC-interacting-domain-12
AT5G09930	chr5_3100426	cis	-0,7±0,13	4,64E-08	0,15	ABC-transporter-family-protein
AT1G12750	chr1_4323408	cis	-0,58±0,11	4,64E-08	0,32	RHOMBOID-like-protein-6
AT1G61280	chr1_22603684	cis	-0,48±0,09	4,64E-08	0,42	Phosphatidylinositol-N-acetylglucosaminyltransferase,-GPI19/PIG-P-subunit
AT5G42250	chr5_16895056	cis	0,47±0,09	4,65E-08	0,53	Zinc-binding-alcohol-dehydrogenase-family-protein
AT1G20380	chr1_7061163	cis	0,64±0,12	4,65E-08	0,16	Prolyl-oligopeptidase-family-protein
AT1G75560	chr1_28373198	cis	0,57±0,1	4,67E-08	0,21	zinc-knuckle-(CCHC-type)-family-protein
AT3G57680	chr3_21385591	cis	-0,57±0,1	4,68E-08	0,27	Peptidase-S41-family-protein
AT5G05240	chr4_6150083	trans	0,73±0,13	4,69E-08	0,11	Uncharacterised-conserved-protein-(UCP030365)
AT5G42570	chr5_17022679	cis	-0,49±0,09	4,69E-08	0,48	B-cell-receptor-associated-31-like
AT3G18880	chr3_6511656	cis	0,67±0,12	4,70E-08	0,15	Nucleic-acid-binding,-OB-fold-like-protein
AT4G14590	chr5_14551793	trans	0,72±0,13	4,71E-08	0,12	embryo-defective-2739
AT5G48790	chr5_19781596	cis	0,53±0,1	4,72E-08	0,29	Domain-of-unknown-function-(DUF1995)
AT1G76850	chr1_28854365	cis	0,62±0,11	4,73E-08	0,18	exocyst-complex-component-sec5
AT2G07727	chr2_15109656	trans	-0,58±0,11	4,78E-08	0,16	Di-haem-cytochrome,-transmembrane;Cytochrome-b/b6,-C-terminal
AT4G28500	chr1_17370274	trans	-0,49±0,09	4,79E-08	0,36	NAC-domain-containing-protein-73
AT2G16630	chr5_7783637	trans	-0,67±0,12	4,80E-08	0,14	Pollen-Ole-e-1-allergen-and-extensin-family-protein
AT5G04510	chr5_10076415	trans	0,47±0,09	4,82E-08	0,61	3'-phosphoinositide-dependent-protein-kinase-1
AT3G46740	chr4_12536294	trans	0,91±0,17	4,86E-08	0,07	translocon-at-the-outer-envelope-membrane-of-chloroplasts-75-III
AT1G71730	chr1_26984099	cis	-0,5±0,09	4,88E-08	0,31	
AT5G66180	chr1_24769415	trans	-0,48±0,09	4,89E-08	0,34	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein
AT3G26744	chr3_9833104	cis	-0,53±0,1	4,90E-08	0,31	basic-helix-loop-helix-(bHLH)-DNA-binding-superfamily-protein
AT4G14420	chr4_8301491	cis	0,69±0,13	4,91E-08	0,13	HR-like-lesion-inducing-protein-related
AT1G65420	chr1_24290690	cis	-0,57±0,11	4,92E-08	0,23	Protein-of-unknown-function-(DUF565)
AT5G49780	chr5_20471774	trans	-0,47±0,09	4,92E-08	0,43	Leucine-rich-repeat-protein-kinase-family-protein
AT1G66510	chr1_24821866	cis	0,66±0,12	4,95E-08	0,15	AAR2-protein-family
AT1G19080	chr1_6586637	cis	-0,78±0,14	4,95E-08	0,09	GINS-complex-protein
AT4G17190	chr4_9648315	cis	-0,57±0,11	4,96E-08	0,21	farnesyl-diphosphate-synthase-2
AT4G09920	chr4_6224093	cis	0,69±0,13	5,01E-08	0,11	FBD,-F-box-and-Leucine-Rich-Repeat-domains-containing-protein
AT3G32410	chr2_10654331	trans	0,51±0,09	5,03E-08	0,31	
AT3G50820	chr4_5706995	trans	0,49±0,09	5,03E-08	0,44	photosystem-II-subunit-O-2
AT2G26460	chr2_11264873	cis	-0,5±0,09	5,03E-08	0,36	RED-family-protein
AT1G31200	chr1_11147801	cis	01,±0,18	5,04E-08	0,06	phloem-protein-2-A9
AT1G65520	chr5_798776	trans	0,46±0,08	5,05E-08	0,44	delta(3),-delta(2)-enoyl-CoA-isomerase-1
AT2G28140	chr1_29869612	trans	-0,65±0,12	5,06E-08	0,15	Protein-of-unknown-function-(DUF1635)
AT1G25375	chr1_8906159	cis	0,46±0,08	5,06E-08	0,42	Metallo-hydrolase/oxidoreductase-superfamily-protein
AT1G29370	chr1_17275275	trans	-0,69±0,13	5,06E-08	0,14	Kinase-related-protein-of-unknown-function-(DUF1296)
AT3G19260	chr3_6672304	cis	01,11±0,2	5,06E-08	0,06	LAG1-homologue-2
AT5G53020	chr5_21484313	cis	-01,±0,18	5,06E-08	0,06	Ribonuclease-P-protein-subunit-P38-related
AT3G50880	chr3_18914843	cis	-0,5±0,09	5,07E-08	0,37	DNA-glycosylase-superfamily-protein
AT2G43080	chr1_1291559	trans	0,51±0,09	5,08E-08	0,27	P4H-isoform-1
AT3G43540	chr3_15405270	cis	0,47±0,09	5,08E-08	0,43	Protein-of-unknown-function-(DUF1350)
AT5G43570	chr5_17507130	cis	-0,47±0,09	5,10E-08	0,50	Serine-protease-inhibitor,-potato-inhibitor-I-type-family-protein
AT2G04850	chr2_1704360	cis	-0,72±0,13	5,10E-08	0,13	Auxin-responsive-family-protein
AT4G35070	chr2_11761904	trans	0,54±0,1	5,14E-08	0,24	SBP-(S-ribonuclease-binding-protein)-family-protein
AT1G07180	chr2_11761927	trans	-0,61±0,11	5,14E-08	0,18	alternative--NAD(P)H-dehydrogenase-1
AT1G01610	chr5_13313436	trans	0,57±0,1	5,16E-08	0,21	glycerol-3-phosphate-acyltransferase-4
AT1G70950	chr1_26759495	cis	0,55±0,1	5,18E-08	0,27	TPX2-(targeting-protein-for-Xklp2)-protein-family
AT4G14720	chr4_8435420	cis	-0,46±0,09	5,19E-08	0,54	TIFY-domain/Divergent-CCT-motif-family-protein
AT4G07825	chr4_1821236	trans	0,75±0,14	5,20E-08	0,16	
AT4G00180	chr2_11761927	trans	-0,6±0,11	5,24E-08	0,18	Plant-specific-transcription-factor-YABBY-family-protein
AT4G16970	chr4_9554731	cis	0,5±0,09	5,26E-08	0,31	Protein-kinase-superfamily-protein
AT2G04795	chr2_1656543	cis	-0,71±0,13	5,26E-08	0,11	
AT1G78970	chr1_29703723	cis	0,58±0,11	5,28E-08	0,20	lupeol-synthase-1
AT2G40970	chr2_17098828	cis	0,49±0,09	5,28E-08	0,49	Homeodomain-like-superfamily-protein
AT4G10930	chr4_6714161	cis	0,69±0,13	5,30E-08	0,14	
AT1G07230	chr2_1136489	trans	-0,65±0,12	5,31E-08	0,14	non-specific-phospholipase-C1
AT1G51390	chr1_19049510	cis	-0,7±0,13	5,32E-08	0,11	NFU-domain-protein-5
AT4G31130	chr2_8285903	trans	-0,71±0,13	5,32E-08	0,14	Protein-of-unknown-function-(DUF1218)
AT3G61620	chr3_22801958	cis	0,55±0,1	5,32E-08	0,24	3'-5'-exoribonuclease-family-protein
AT4G38460	chr4_17984808	cis	-0,86±0,16	5,34E-08	0,09	geranylgeranyl-reductase
AT5G49930	chr5_20314076	cis	-0,52±0,1	5,37E-08	0,33	zinc-knuckle-(CCHC-type)-family-protein
AT2G13600	chr2_5671648	cis	0,58±0,11	5,38E-08	0,22	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT5G24280	chr5_8262612	cis	0,65±0,12	5,38E-08	0,16	gamma-irradiation-and-mitomycin-c-induced-1
AT2G35340	chr2_16507075	trans	01,16±0,21	5,39E-08	0,05	helicase-domain-containing-protein
AT2G28870	chr1_19250971	trans	-0,48±0,09	5,39E-08	0,34	
AT3G48300	chr3_17885422	cis	-0,65±0,12	5,39E-08	0,17	cytochrome-P450,-family-71,-subfamily-A,-polypeptide-23
AT2G35859	chr1_14188364	trans	-0,5±0,09	5,39E-08	0,24	
AT1G15910	chr1_5468316	cis	-0,54±0,1	5,39E-08	0,31	XH/XS-domain-containing-protein
AT5G47770	chr5_19338000	cis	-0,49±0,09	5,40E-08	0,38	farnesyl-diphosphate-synthase-1

AT3G46900	chr4_10861994	trans	0,89±0,16	5,41E-08	0,07	copper-transporter-2
AT1G35710	chr2_4042995	trans	-0,85±0,16	5,41E-08	0,10	Protein-kinase-family-protein-with-leucine-rich-repeat-domain
AT4G17910	chr4_9950250	cis	0,57±0,1	5,43E-08	0,23	transferases,-transferring-acyl-groups
AT5G03795	chr5_1010033	cis	-0,46±0,08	5,44E-08	0,51	Exostosin-family-protein
AT5G37360	chr5_14836321	cis	-0,51±0,09	5,45E-08	0,31	
AT5G22875	chr5_7652304	cis	0,53±0,1	5,45E-08	0,33	
AT4G00780	chr5_20301461	trans	-0,64±0,12	5,46E-08	0,16	TRAF-like-family-protein
AT5G41800	chr5_16733689	cis	-0,53±0,1	5,47E-08	0,28	Transmembrane-amino-acid-transporter-family-protein
AT1G59970	chr4_6432632	trans	-0,86±0,16	5,47E-08	0,09	Matrixin-family-protein
AT5G47310	chr5_19200283	cis	-0,5±0,09	5,47E-08	0,33	PPPDE-putative-thiol-peptidase-family-protein
AT1G09480	chr1_3060171	cis	-0,5±0,09	5,49E-08	0,30	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT3G48410	chr3_17927998	cis	0,46±0,09	5,50E-08	0,44	alpha/beta-Hydrolases-superfamily-protein
AT3G08970	chr3_2737991	cis	0,55±0,1	5,51E-08	0,24	DNAJ-heat-shock-N-terminal-domain-containing-protein
AT5G10390	chr5_3281886	cis	0,58±0,11	5,52E-08	0,22	Histone-superfamily-protein
AT3G01170	chr1_27132991	trans	0,47±0,09	5,53E-08	0,43	Ribosomal-protein-L34e-superfamily-protein
AT3G15534	chr5_2832203	trans	0,75±0,14	5,55E-08	0,09	
AT1G30320	chr5_22536612	trans	-0,55±0,1	5,56E-08	0,26	Remorin-family-protein
AT4G17245	chr4_9668933	cis	-0,57±0,11	5,57E-08	0,20	RING/U-box-superfamily-protein
AT4G15620	chr4_8913888	cis	-0,48±0,09	5,60E-08	0,34	Uncharacterised-protein-family-(UPF0497)
AT3G20150	chr4_12325778	trans	0,45±0,08	5,62E-08	0,48	Kinesin-motor-family-protein
AT3G27730	chr3_10279321	cis	0,61±0,11	5,62E-08	0,16	ATP-binding;ATP-dependent-helicases;DNA-helicases
AT1G05710	chr1_1715035	cis	-0,48±0,09	5,62E-08	0,41	basic-helix-loop-helix-(bHLH)-DNA-binding-superfamily-protein
AT4G37310	chr4_17551488	cis	0,87±0,16	5,64E-08	0,10	cytochrome-P450,-family-81,-subfamily-H,-polypeptide-1
AT1G05630	chr1_1681154	cis	-0,67±0,12	5,65E-08	0,16	Endonuclease/exonuclease/phosphatase-family-protein
AT4G03038	chr3_23145836	trans	0,6±0,11	5,65E-08	0,17	other-RNA
AT2G05120	chr2_1761985	trans	-0,61±0,11	5,68E-08	0,17	Nucleoporin,-Nup133/Nup155-like
AT2G27920	chr2_11890106	cis	0,85±0,16	5,69E-08	0,09	serine-carboxypeptidase-like-51
AT1G63660	chr1_23603515	cis	0,6±0,11	5,70E-08	0,19	GMP-synthase-(glutamine-hydrolyzing),-putative-/-glutamine-amidotransferase,-putative
AT5G53000	chr1_22688724	trans	0,47±0,09	5,71E-08	0,36	2A-phosphatase-associated-protein-of-46-kD
AT1G21190	chr1_7419967	cis	0,48±0,09	5,75E-08	0,41	Small-nuclear-ribonucleoprotein-family-protein
AT1G10740	chr1_3570713	cis	-0,89±0,16	5,76E-08	0,07	alpha/beta-Hydrolases-superfamily-protein
AT3G17450	chr3_5976256	cis	0,84±0,15	5,76E-08	0,09	hAT-dimerisation-domain-containing-protein
AT1G30050	chr3_18941904	trans	-0,45±0,08	5,80E-08	0,39	
AT1G63260	chr1_23468482	cis	-0,55±0,1	5,81E-08	0,25	tetraspanin10
AT1G28340	chr1_9940044	cis	0,68±0,12	5,85E-08	0,13	receptor-like-protein-4
AT5G54165	chr5_22001192	cis	-0,69±0,13	5,91E-08	0,17	
AT1G63770	chr1_23656988	cis	-0,45±0,08	5,92E-08	0,41	Peptidase-M1-family-protein
AT4G22380	chr4_11866232	trans	0,63±0,12	5,93E-08	0,16	Ribosomal-protein-L7Ae/L30e/S12e/Gadd45-family-protein
AT3G14395	chr3_4816176	cis	0,5±0,09	5,95E-08	0,34	
AT1G80860	chr1_30400563	cis	0,48±0,09	5,97E-08	0,54	phospholipid-N-methyltransferase
AT2G17880	chr4_14837841	trans	0,48±0,09	5,97E-08	0,36	Chaperone-DnaJ-domain-superfamily-protein
AT2G33000	chr2_14010015	cis	-0,78±0,14	5,98E-08	0,09	ubiquitin-associated-(UBA)/TS-N-domain-containing-protein-related
AT5G05230	chr1_14941234	trans	0,89±0,16	5,99E-08	0,06	RING/U-box-superfamily-protein
AT1G53910	chr5_14063988	trans	-0,67±0,12	6,00E-08	0,14	related-to-AP2-12
AT1G16250	chr1_5556456	cis	-0,47±0,09	6,01E-08	0,49	Galactose-oxidase/kelch-repeat-superfamily-protein
AT5G03870	chr5_17815863	trans	0,5±0,09	6,01E-08	0,31	Glutaredoxin-family-protein
AT2G17630	chr2_7666708	cis	0,49±0,09	6,01E-08	0,35	Pyridoxal-phosphate-(PLP)-dependent-transferases-superfamily-protein
AT5G43150	chr5_17319150	cis	0,47±0,09	6,01E-08	0,43	
AT5G25020	chr5_8610661	cis	-0,47±0,09	6,03E-08	0,43	Protein-of-unknown-function-(DUF1336)
AT3G46290	chr4_7306359	trans	-0,77±0,14	6,05E-08	0,11	hercules-receptor-kinase-1
AT3G18485	chr3_6347954	cis	0,6±0,11	6,06E-08	0,18	iaa-leucine-resistant-2
AT5G51460	chr5_20900660	cis	-0,7±0,13	6,09E-08	0,15	Haloacid-dehalogenase-like-hydrolase-(HAD)-superfamily-protein
AT1G32090	chr1_11544946	cis	0,5±0,09	6,10E-08	0,34	early-responsive-to-dehydration-stress-protein-(ERD4)
AT4G36195	chr5_15502500	trans	0,54±0,1	6,10E-08	0,22	Serine-carboxypeptidase-S28-family-protein
AT3G53490	chr3_19829246	cis	0,81±0,15	6,12E-08	0,09	
AT1G06570	chr3_13898892	trans	0,64±0,12	6,13E-08	0,14	phytoene-desaturation-1
AT1G11180	chr1_3747109	cis	-0,77±0,14	6,13E-08	0,11	Secretory-carrier-membrane-protein-(SCAMP)-family-protein
AT1G34340	chr1_12533162	cis	0,78±0,14	6,14E-08	0,09	alpha/beta-Hydrolases-superfamily-protein
AT1G20693	chr1_7177247	cis	-0,51±0,09	6,15E-08	0,31	high-mobility-group-B2
AT1G70830	chr1_26712764	cis	0,5±0,09	6,16E-08	0,31	MLP-like-protein-28
AT2G35090	chr2_14783232	cis	0,46±0,09	6,18E-08	0,49	Protein-of-unknown-function-(DUF1640)
AT1G22470	chr2_1700789	trans	0,82±0,15	6,20E-08	0,09	
AT1G07350	chr1_2260475	cis	0,48±0,09	6,20E-08	0,45	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT5G15750	chr5_5142587	cis	-0,48±0,09	6,21E-08	0,59	Alpha-L-RNA-binding-motif/Ribosomal-protein-S4-family-protein
AT4G25490	chr3_17166734	trans	-0,55±0,1	6,22E-08	0,20	C-repeat/DRE-binding-factor-1
AT4G02360	chr4_1042631	cis	0,54±0,1	6,22E-08	0,26	Protein-of-unknown-function,-DUF538
AT1G65110	chr1_24189970	cis	-0,59±0,11	6,23E-08	0,20	Ubiquitin-carboxyl-terminal-hydrolase-related-protein
AT5G02620	chr5_590556	cis	0,48±0,09	6,33E-08	0,40	ankyrin-like1
AT2G20850	chr2_9019507	cis	-0,86±0,16	6,33E-08	0,14	STRUBBELIG-receptor-family-1
AT3G51350	chr3_19061350	cis	-0,72±0,13	6,38E-08	0,12	Eukaryotic-aspartyl-protease-family-protein
AT1G45000	chr1_16980716	cis	0,47±0,09	6,39E-08	0,35	AAA-type-ATPase-family-protein
AT4G21320	chr4_11340530	cis	-0,79±0,15	6,39E-08	0,09	Aldolase-type-TIM-barrel-family-protein
AT2G25260	chr2_10760230	cis	-0,54±0,1	6,40E-08	0,34	
AT5G24020	chr5_8143249	cis	0,58±0,11	6,42E-08	0,20	septum-site-determining-protein-(MIND)
AT1G75440	chr1_28305576	cis	-0,8±0,15	6,44E-08	0,11	ubiquitin-conjugating-enzyme-16
AT1G14185	chr4_6606970	trans	0,46±0,08	6,44E-08	0,40	Glucose-methanol-choline-(GMC)-oxidoreductase-family-protein
AT3G21950	chr1_8057048	trans	-0,58±0,11	6,44E-08	0,20	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein
AT2G20560	chr3_17642577	trans	-0,49±0,09	6,46E-08	0,34	DNAJ-heat-shock-family-protein
AT5G16080	chr2_1190927	trans	0,6±0,11	6,48E-08	0,20	carboxyesterase-17

AT3G56220	chr3_20854013	cis	0,47±0,09	6,49E-08	0,39	transcription-regulators
AT2G46290	chr2_19007924	cis	0,77±0,14	6,50E-08	0,10	Transducin/WD40-repeat-like-superfamily-protein
AT5G25470	chr5_8867659	cis	-0,75±0,14	6,52E-08	0,11	AP2/B3-like-transcriptional-factor-family-protein
AT3G22880	chr3_8085466	cis	0,63±0,12	6,54E-08	0,16	DNA-repair-(Rad51)-family-protein
AT3G54600	chr3_20210243	cis	0,77±0,14	6,55E-08	0,11	Class-I-glutamine-amidotransferase-like-superfamily-protein
AT2G46240	chr4_10473876	trans	0,84±0,16	6,55E-08	0,08	BCL-2-associated-athanogene-6
AT1G12530	chr1_4270479	cis	-0,49±0,09	6,56E-08	0,39	
AT3G07800	chr3_2491135	cis	0,61±0,11	6,58E-08	0,19	Thymidine-kinase
AT4G36620	chr1_22073816	trans	0,47±0,09	6,60E-08	0,34	GATA-transcription-factor-19
AT5G64240	chr1_12455969	trans	0,52±0,1	6,62E-08	0,24	metacaspase-3
AT3G51100	chr3_803907	trans	0,51±0,1	6,63E-08	0,34	
AT5G47280	chr5_19207371	cis	0,94±0,17	6,64E-08	0,06	ADR1-like-3
AT4G38330	chr4_17952125	cis	-0,66±0,12	6,65E-08	0,14	Integral-membrane-protein-hemolysin-III-homolog
AT4G17510	chr4_9768732	cis	0,51±0,09	6,65E-08	0,29	ubiquitin-C-terminal-hydrolase-3
AT4G12390	chr4_7338121	cis	0,45±0,08	6,68E-08	0,51	pectin-methylesterase-inhibitor-1
AT3G04181	chr5_525023	trans	-0,82±0,15	6,69E-08	0,09	
AT5G42950	chr4_10249006	trans	0,8±0,15	6,69E-08	0,09	GYF-domain-containing-protein
AT4G00430	chr4_188619	cis	-0,67±0,12	6,71E-08	0,14	plasma-membrane-intrinsic-protein-1;4
AT2G45520	chr3_19499785	trans	-0,53±0,1	6,72E-08	0,27	
AT5G44750	chr5_18049110	cis	-0,88±0,16	6,73E-08	0,09	DNA-directed-DNA-polymerases
AT1G33790	chr1_12236202	cis	-0,47±0,09	6,73E-08	0,46	jacalin-lectin-family-protein
AT1G21240	chr1_7447447	cis	0,68±0,13	6,75E-08	0,13	wall-associated-kinase-3
AT4G33410	chr4_16068297	cis	-0,74±0,14	6,76E-08	0,11	SIGNAL-PEPTIDE-PEPTIDASE-LIKE-1
AT5G24210	chr5_21443089	trans	0,62±0,12	6,77E-08	0,16	alpha/beta-Hydrolases-superfamily-protein
AT1G64640	chr1_24025567	cis	0,53±0,1	6,77E-08	0,24	early-nodulin-like-protein-8
AT2G18260	chr3_8435111	trans	0,5±0,09	6,80E-08	0,74	syntaxin-of-plants-112
AT1G21220	chr1_7428601	cis	0,76±0,14	6,80E-08	0,11	transposable-element-gene
AT3G10572	chr3_3305801	cis	0,65±0,12	6,82E-08	0,16	3-phosphoinositide-dependent-protein-kinase-1,-putative
AT3G16390	chr5_5637212	trans	0,62±0,11	6,82E-08	0,19	nitrile-specifier-protein-3
AT5G08520	chr5_18775630	trans	0,61±0,11	6,82E-08	0,16	Duplicated-homeodomain-like-superfamily-protein
AT5G36210	chr5_14266897	cis	0,49±0,09	6,83E-08	0,35	alpha/beta-Hydrolases-superfamily-protein
AT3G51910	chr3_19266344	cis	-0,49±0,09	6,87E-08	0,43	heat-shock-transcription-factor--A7A
AT5G08010	chr5_2571805	cis	0,52±0,1	6,88E-08	0,29	
AT4G27640	chr4_13796410	cis	0,53±0,1	6,90E-08	0,24	ARM-repeat-superfamily-protein
AT1G32190	chr5_3215635	trans	-0,45±0,08	6,90E-08	0,44	alpha/beta-Hydrolases-superfamily-protein
AT5G62300	chr5_25022670	cis	0,54±0,1	6,91E-08	0,31	Ribosomal-protein-S10p/S20e-family-protein
AT3G14172	chr3_4698372	cis	0,66±0,12	6,91E-08	0,16	
AT2G42800	chr4_11025667	trans	0,84±0,15	6,92E-08	0,08	receptor-like-protein-29
AT2G17700	chr2_7690887	cis	-0,56±0,1	6,95E-08	0,26	ACT-like-protein-tyrosine-kinase-family-protein
AT3G48210	chr3_17851438	cis	0,53±0,1	6,95E-08	0,29	
AT3G22520	chr3_7974995	cis	-0,7±0,13	6,98E-08	0,12	
AT1G78820	chr1_29636012	cis	0,47±0,09	7,01E-08	0,39	D-mannose-binding-lectin-protein-with-Apple-like-carbohydrate-binding-domain
AT1G06310	chr1_18905090	trans	0,72±0,13	7,02E-08	0,12	acyl-CoA-oxidase-6
AT1G13550	chr1_4638319	cis	-0,45±0,08	7,02E-08	0,43	Protein-of-unknown-function-(DUF1262)
AT4G25610	chr3_14029684	trans	-0,52±0,1	7,03E-08	0,27	C2H2-like-zinc-finger-protein
AT1G32740	chr4_11304047	trans	0,67±0,12	7,05E-08	0,14	SBP-(S-ribonuclease-binding-protein)-family-protein
AT3G57950	chr3_8150023	trans	-0,94±0,18	7,05E-08	0,07	
AT3G27906	chr3_10356114	cis	-0,83±0,15	7,09E-08	0,08	
AT4G14350	chr4_8256892	cis	-0,58±0,11	7,11E-08	0,19	AGC-(cAMP-dependent,-cGMP-dependent-and-protein-kinase-C)-kinase-family-protein
AT1G14660	chr1_5030827	cis	-0,98±0,18	7,13E-08	0,06	Na+/H+-exchanger-8
AT3G18930	chr3_6523804	cis	0,52±0,1	7,16E-08	0,29	RING/U-box-superfamily-protein
AT1G33080	chr1_11984792	cis	0,64±0,12	7,17E-08	0,14	MATE-efflux-family-protein
AT5G25570	chr5_8901472	cis	-0,96±0,18	7,18E-08	0,09	
AT5G42770	chr5_11410551	trans	0,72±0,13	7,19E-08	0,11	Maf-like-protein
AT2G15430	chr2_6738364	cis	0,61±0,11	7,20E-08	0,21	DNA-directed-RNA-polymerase-family-protein
AT1G74800	chr1_28097847	cis	0,49±0,09	7,20E-08	0,41	Galactosyltransferase-family-protein
AT3G59190	chr3_4928651	trans	-0,79±0,15	7,21E-08	0,11	F-box/RNI-like-superfamily-protein
AT4G37553	chr4_17645278	cis	-0,48±0,09	7,21E-08	0,42	
AT2G32180	chr1_8548969	trans	-0,77±0,14	7,22E-08	0,09	plastid-transcriptionally-active-18
AT5G62980	chr3_22382411	trans	0,6±0,11	7,22E-08	0,19	Dihydroneopterin-aldolase
AT3G06780	chr5_8362024	trans	-0,62±0,12	7,23E-08	0,16	glycine-rich-protein
AT5G13500	chr1_17588496	trans	0,51±0,1	7,28E-08	0,28	
AT2G41470	chr2_17337187	cis	-0,89±0,17	7,28E-08	0,08	
AT1G75220	chr1_2320563	trans	0,48±0,09	7,29E-08	0,45	Major-facilitator-superfamily-protein
AT3G24200	chr2_29717	trans	-0,71±0,13	7,31E-08	0,11	FAD/NAD(P)-binding-oxidoreductase-family-protein
AT3G17650	chr3_10273905	trans	-0,61±0,11	7,32E-08	0,17	YELLOW-STRIPE-like-5
AT1G62480	chr1_23128164	cis	-0,47±0,09	7,35E-08	0,42	Vacuolar-calcium-binding-protein-related
AT1G17145	chr5_20067627	trans	-0,67±0,13	7,38E-08	0,14	RING/U-box-superfamily-protein
AT2G45510	chr1_14941234	trans	0,9±0,17	7,38E-08	0,06	cytochrome-P450,-family-704,-subfamily-A,-polypeptide-2
AT5G23330	chr3_12094818	trans	0,73±0,14	7,39E-08	0,10	Nucleotidylyl-transferase-superfamily-protein
AT5G02560	chr5_577807	cis	0,59±0,11	7,41E-08	0,19	histone-H2A-12
AT5G60335	chr5_24274906	cis	-0,46±0,09	7,43E-08	0,43	Thioesterase-superfamily-protein
AT1G77140	chr4_6758588	trans	-0,52±0,1	7,47E-08	0,27	vacuolar-protein-sorting-45
AT1G51630	chr1_19152171	cis	0,52±0,1	7,51E-08	0,29	O-fucosyltransferase-family-protein
AT3G17820	chr3_6156010	trans	-0,74±0,14	7,52E-08	0,11	glutamine-synthetase-1.3
AT2G44270	chr2_18268606	cis	-0,56±0,1	7,54E-08	0,26	repressor-of-lrx1
AT5G65000	chr5_25973993	cis	-0,64±0,12	7,62E-08	0,16	Nucleotide-sugar-transporter-family-protein
AT5G47680	chr5_19354016	cis	-0,48±0,09	7,62E-08	0,46	
AT2G38070	chr2_15928646	cis	-0,84±0,16	7,64E-08	0,08	Protein-of-unknown-function-(DUF740)

AT2G29020	chr2_12469946	cis	-0,47±0,09	7,65E-08	0,46	Rab5-interacting-family-protein
AT1G72140	chr1_27141526	cis	0,53±0,1	7,65E-08	0,25	Major-facilitator-superfamily-protein
AT1G65810	chr1_24481267	cis	0,79±0,15	7,65E-08	0,09	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT4G02230	chr1_16973461	trans	-0,61±0,11	7,66E-08	0,19	Ribosomal-protein-L19e-family-protein
AT3G11780	chr5_13542679	trans	-0,64±0,12	7,66E-08	0,15	MD-2-related-lipid-recognition-domain-containing-protein-/-ML-domain-containing-protein
AT5G27240	chr5_9594001	cis	0,66±0,12	7,67E-08	0,14	DNAJ-heat-shock-N-terminal-domain-containing-protein
AT1G58350	chr1_21666910	cis	0,5±0,09	7,72E-08	0,28	Putative-serine-esterase--family-protein
AT2G22140	chr5_17292018	trans	0,7±0,13	7,73E-08	0,14	essential-meiotic-endonuclease-1B
AT4G06534	chr2_19352303	trans	0,64±0,12	7,76E-08	0,14	
AT4G14150	chr2_11394858	trans	0,69±0,13	7,77E-08	0,12	phragmoplast-associated-kinesin-related-protein-1
AT1G08010	chr5_13313436	trans	0,56±0,1	7,80E-08	0,21	GATA-transcription-factor-11
AT4G13560	chr4_7921402	cis	0,61±0,11	7,82E-08	0,18	Late-embryogenesis-abundant-protein-(LEA)-family-protein
AT4G20410	chr4_11014210	cis	-0,53±0,1	7,83E-08	0,25	gamma-soluble-NSF-attachment-protein
AT3G13060	chr4_7711468	trans	0,62±0,11	7,84E-08	0,17	evolutionarily-conserved-C-terminal-region-5
AT5G45430	chr5_18425889	cis	-0,52±0,1	7,85E-08	0,31	Protein-kinase-superfamily-protein
AT1G20120	chr1_7147321	trans	-0,57±0,11	7,86E-08	0,20	GDSL-like-Lipase/Acylhydrolase-superfamily-protein
AT5G38710	chr5_15624451	trans	0,73±0,14	7,88E-08	0,11	Methylenetetrahydrofolate-reductase-family-protein
AT2G43535	chr1_22581233	trans	0,49±0,09	7,89E-08	0,31	Scorpion-toxin-like-knottin-superfamily-protein
AT1G22380	chr2_15597312	trans	0,58±0,11	7,92E-08	0,19	UDP-glucosyl-transferase-85A3
AT5G03450	chr5_863684	cis	0,71±0,13	7,92E-08	0,11	Transducin/WD40-repeat-like-superfamily-protein
AT1G14680	chr1_5040765	cis	0,49±0,09	7,92E-08	0,35	
AT3G07050	chr3_2224259	cis	0,56±0,1	7,95E-08	0,29	GTP-binding-family-protein
AT4G14500	chr3_7012334	trans	0,66±0,12	7,98E-08	0,14	Polyketide-cyclase/dehydrase-and-lipid-transport-superfamily-protein
AT1G79640	chr2_16846203	trans	-0,73±0,14	7,99E-08	0,10	Protein-kinase-superfamily-protein
AT3G56030	chr3_20791163	cis	-0,9±0,17	7,99E-08	0,07	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT5G23660	chr4_180885	trans	0,74±0,14	8,03E-08	0,11	homolog-of-Medicago-truncatula-MTN3
AT2G34050	chr4_18392988	trans	0,43±0,08	8,03E-08	0,40	
AT5G18290	chr5_6092863	cis	0,56±0,1	8,03E-08	0,36	Aquaporin-like-superfamily-protein
AT2G36240	chr2_15195216	cis	-0,64±0,12	8,04E-08	0,19	pentatricopeptide-(PPR)-repeat-containing-protein
AT1G04430	chr4_766684	trans	0,71±0,13	8,08E-08	0,11	S-adenosyl-L-methionine-dependent-methyltransferases-superfamily-protein
AT3G47050	chr3_17330476	cis	0,48±0,09	8,08E-08	0,44	Glycosyl-hydrolase-family-protein
AT1G10095	chr5_15388675	trans	0,58±0,11	8,08E-08	0,19	Protein-prenylyltransferase-superfamily-protein
AT2G29580	chr2_12646813	cis	-0,48±0,09	8,12E-08	0,40	CCCH-type-zinc-fingerfamily-protein-with-RNA-binding-domain
AT4G11320	chr1_25787334	trans	-0,6±0,11	8,14E-08	0,18	Papain-family-cysteine-protease
AT4G03240	chr4_1479106	trans	0,46±0,09	8,14E-08	0,42	frataxin-homolog
AT4G35680	chr4_687919	trans	0,53±0,1	8,14E-08	0,26	Arabidopsis-protein-of-unknown-function-(DUF241)
AT5G01410	chr3_13292224	trans	-0,71±0,13	8,16E-08	0,11	Aldolase-type-TIM-barrel-family-protein
AT2G47630	chr2_19535380	cis	-0,53±0,1	8,16E-08	0,29	alpha/beta-Hydrolases-superfamily-protein
AT5G20850	chr1_11531283	trans	-0,44±0,08	8,17E-08	0,48	RAS-associated-with-diabetes-protein-51
AT3G55490	chr1_16965374	trans	0,67±0,13	8,19E-08	0,13	GINS-complex-protein
AT3G24740	chr3_10618296	trans	0,53±0,1	8,22E-08	0,25	Protein-of-unknown-function-(DUF1644)
AT5G49990	chr5_20340531	cis	-0,48±0,09	8,24E-08	0,34	Xanthine/uracil-permease-family-protein
AT5G50680	chr1_13335389	trans	-0,47±0,09	8,25E-08	0,50	SUMO-activating-enzyme-1B
AT5G15010	chr5_4858188	cis	0,51±0,09	8,25E-08	0,45	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT4G33220	chr5_13313436	trans	0,57±0,11	8,25E-08	0,21	pectin-methylesterase-44
AT3G47833	chr5_19780435	trans	0,46±0,09	8,30E-08	0,53	
AT5G62310	chr5_25075437	trans	0,96±0,18	8,30E-08	0,06	AGC-(cAMP-dependent,-cGMP-dependent-and-protein-kinase-C)-kinase-family-protein
AT2G02750	chr5_17936884	trans	0,51±0,1	8,33E-08	0,69	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT2G42730	chr2_17790805	cis	-0,7±0,13	8,37E-08	0,14	F-box-family-protein
AT1G72060	chr1_27116153	cis	0,52±0,1	8,39E-08	0,35	serine-type-endopeptidase-inhibitors
AT2G39400	chr2_16452208	cis	-0,58±0,11	8,39E-08	0,22	alpha/beta-Hydrolases-superfamily-protein
AT3G14170	chr3_4691463	cis	0,67±0,12	8,41E-08	0,15	Plant-protein-of-unknown-function-(DUF936)
AT1G73570	chr1_27650106	cis	0,66±0,12	8,42E-08	0,15	HCP-like-superfamily-protein
AT4G31010	chr2_11326579	trans	0,44±0,08	8,45E-08	0,42	RNA-binding-CRS1-/-YhbY-(CRM)-domain-containing-protein
AT3G47810	chr3_17639369	cis	-0,66±0,12	8,45E-08	0,16	Calcineurin-like-metallo-phosphoesterase-superfamily-protein
AT4G23630	chr4_7755336	trans	-0,46±0,09	8,46E-08	0,46	VIRB2-interacting-protein-1
AT3G28080	chr3_10453238	cis	0,73±0,14	8,47E-08	0,12	nodulin-MtN21-/EamA-like-transporter-family-protein
AT5G47750	chr5_19341840	cis	-0,44±0,08	8,49E-08	0,44	D6-protein-kinase-like-2
AT4G26490	chr2_16030260	trans	-0,83±0,15	8,50E-08	0,07	Late-embryogenesis-abundant-(LEA)-hydroxyproline-rich-glycoprotein-family
AT5G54650	chr5_21426099	NA	-0,87±0,16	8,52E-08	0,11	formin-homology5
AT4G00650	chr1_16822116	trans	-0,53±0,1	8,53E-08	0,26	FRIGIDA-like-protein
AT1G75880	chr4_5464467	trans	-0,5±0,09	8,55E-08	0,31	SGNH-hydrolase-type-esterase-superfamily-protein
AT5G20240	chr3_12987992	trans	0,63±0,12	8,56E-08	0,15	K-box-region-and-MADS-box-transcription-factor-family-protein-
AT2G01870	chr4_12687112	trans	0,47±0,09	8,56E-08	0,38	
AT1G04900	chr5_22746815	trans	0,56±0,1	8,57E-08	0,22	Protein-of-unknown-function-(DUF185)
AT3G09920	chr3_3014408	cis	0,49±0,09	8,59E-08	0,48	phosphatidyl-inositol-monophosphate-5-kinase
AT3G63510	chr5_17913612	trans	0,46±0,09	8,64E-08	0,54	FMN-linked-oxidoreductases-superfamily-protein
AT1G29830	chr1_10438010	cis	-0,46±0,09	8,65E-08	0,59	Magnesium-transporter-CorA-like-family-protein
AT3G62290	chr4_6690528	trans	-0,44±0,08	8,68E-08	0,56	ADP-ribosylation-factor-A1E
AT1G01140	chr1_78272	cis	0,48±0,09	8,72E-08	0,32	CBL-interacting-protein-kinase-9
AT1G70890	chr1_26726124	cis	-0,91±0,17	8,72E-08	0,07	MLP-like-protein-43
AT4G38020	chr3_14908489	trans	-0,71±0,13	8,74E-08	0,11	tRNA/rRNA-methyltransferase-(SpoU)-family-protein
AT1G63310	chr2_13787318	trans	-0,47±0,09	8,74E-08	0,48	
AT3G12965	chr3_4166759	cis	0,6±0,11	8,75E-08	0,21	other-RNA
AT1G18382	chr4_5665889	trans	0,49±0,09	8,83E-08	0,28	other-RNA
AT5G66658	chr5_26833923	trans	0,6±0,11	8,84E-08	0,20	
AT3G02680	chr3_582584	cis	0,57±0,11	8,85E-08	0,19	nijmegen-breakage-syndrome-1
AT5G03340	chr5_806859	cis	-0,57±0,11	8,87E-08	0,21	ATPase,-AAA-type,-CDC48-protein
AT4G01900	chr5_16334322	trans	0,64±0,12	8,89E-08	0,14	GLNB1-homolog

AT1G50840	chr1_18839088	cis	0,7±0,13	8,89E-08	0,11	polymerase-gamma-2
AT3G17280	chr3_5907053	cis	0,49±0,09	8,89E-08	0,45	F-box-and-associated-interaction-domains-containing-protein
AT3G13210	chr1_12762755	trans	-0,69±0,13	8,93E-08	0,12	crooked-neck-protein,-putative-/-cell-cycle-protein,-putative
AT1G72960	chr1_27444543	cis	0,53±0,1	8,94E-08	0,26	Root-hair-defective-3-GTP-binding-protein-(RHD3)
AT2G22740	chr4_18516461	trans	-0,99±0,19	8,95E-08	0,06	SU(VAR)3-9-homolog-6
AT5G43950	chr5_17688733	cis	0,5±0,09	8,96E-08	0,28	Plant-protein-of-unknown-function-(DUF946)
AT3G15020	chr5_19780435	trans	0,46±0,09	8,97E-08	0,53	Lactate/malate-dehydrogenase-family-protein
AT4G21530	chr4_11450465	cis	-0,45±0,09	9,00E-08	0,45	Transducin/WD40-repeat-like-superfamily-protein
AT2G30000	chr2_12804858	cis	-0,83±0,16	9,02E-08	0,07	PHF5-like-protein
AT3G57580	chr3_21320119	cis	-0,68±0,13	9,05E-08	0,14	F-box-and-associated-interaction-domains-containing-protein
AT3G48710	chr3_18039834	cis	-0,55±0,1	9,06E-08	0,26	DEK-domain-containing-chromatin-associated-protein
AT3G05790	chr3_1726470	cis	-0,48±0,09	9,07E-08	0,44	lon-protease-4
AT3G49900	chr1_19060201	trans	-0,5±0,09	9,09E-08	0,29	Phototropic-responsive-NPH3-family-protein
AT3G59680	chr1_28598165	trans	-0,6±0,11	9,09E-08	0,17	
AT1G58410	chr1_9062115	trans	-0,46±0,09	9,10E-08	0,56	Disease-resistance-protein-(CC-NBS-LRR-class)-family
AT3G57030	chr1_25096888	trans	-0,6±0,11	9,12E-08	0,16	Calcium-dependent-phosphotriesterase-superfamily-protein
AT4G00290	chr4_125450	cis	0,48±0,09	9,12E-08	0,43	Mechanosensitive-ion-channel-protein
AT1G29290	chr1_24056703	trans	0,77±0,14	9,13E-08	0,10	
AT3G07510	chr3_2394408	cis	-0,46±0,09	9,14E-08	0,57	
AT5G67200	chr1_19060201	trans	-0,5±0,09	9,17E-08	0,29	Leucine-rich-repeat-protein-kinase-family-protein
AT4G26310	chr2_6860880	trans	0,48±0,09	9,19E-08	0,34	elongation-factor-P-(EF-P)-family-protein
AT5G13430	chr2_4540219	trans	-0,86±0,16	9,19E-08	0,06	Ubiquinol-cytochrome-C-reductase-iron-sulfur-subunit
AT2G31725	chr5_8355621	trans	-0,6±0,11	9,20E-08	0,18	Eukaryotic-protein-of-unknown-function-(DUF842)
AT5G47930	chr5_19422086	cis	0,59±0,11	9,20E-08	0,22	Zinc-binding-ribosomal-protein-family-protein
AT1G16240	chr1_5556456	cis	-0,48±0,09	9,20E-08	0,49	syntaxin-of-plants-51
AT1G68470	chr5_633813	trans	0,61±0,11	9,23E-08	0,17	Exostosin-family-protein
AT1G16550	chr2_1870568	trans	-0,83±0,16	9,24E-08	0,10	
AT5G13690	chr3_16326916	trans	-0,48±0,09	9,26E-08	0,34	alpha-N-acetylglucosaminidase-family-/-NAGLU-family
AT5G03720	chr5_11908724	trans	0,85±0,16	9,26E-08	0,06	heat-shock-transcription-factor-A3
AT1G11630	chr3_9122297	trans	0,7±0,13	9,27E-08	0,11	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT1G54660	chr5_15364544	trans	-0,49±0,09	9,27E-08	0,39	
AT3G47295	chr3_17442953	cis	0,48±0,09	9,31E-08	0,34	
AT5G24680	chr5_8460672	cis	0,51±0,1	9,32E-08	0,36	Peptidase-C78,-ubiquitin-fold-modifier-specific-peptidase-1/-2
AT1G34770	chr1_12746729	cis	0,47±0,09	9,34E-08	0,35	
AT5G11540	chr2_11798291	trans	-0,44±0,08	9,35E-08	0,59	D-arabinono-1,4-lactone-oxidase-family-protein
AT1G19400	chr1_6701737	cis	-0,54±0,1	9,38E-08	0,27	Erythronate-4-phosphate-dehydrogenase-family-protein
AT3G51260	chr1_17022453	trans	0,44±0,08	9,39E-08	0,50	20S-proteasome--alpha-subunit-PAD1
AT3G52310	chr1_16671060	trans	-0,6±0,11	9,40E-08	0,18	ABC-2-type-transporter-family-protein
AT3G05560	chr3_1632697	cis	-0,49±0,09	9,41E-08	0,38	Ribosomal-L22e-protein-family
AT2G07140	chr3_15875158	trans	0,48±0,09	9,41E-08	0,34	F-box-and-associated-interaction-domains-containing-protein
AT1G24610	chr1_8703503	cis	-0,84±0,16	9,43E-08	0,08	Rubisco-methyltransferase-family-protein
AT3G26420	chr3_9674892	cis	-0,49±0,09	9,43E-08	0,49	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein-with-retrovirus-zinc-finger-like-domain
AT5G28380	chr5_10348548	cis	0,56±0,1	9,46E-08	0,18	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT3G52500	chr5_13313436	trans	0,57±0,11	9,46E-08	0,21	Eukaryotic-aspartyl-protease-family-protein
AT1G64385	chr1_23900037	cis	0,52±0,1	9,47E-08	0,34	
AT3G55910	chr3_20741076	cis	-0,54±0,1	9,47E-08	0,24	
AT5G18255	chr5_6037590	cis	-0,73±0,14	9,52E-08	0,11	other-RNA
AT4G04221	chr2_12424986	trans	0,66±0,12	9,54E-08	0,12	other-RNA
AT5G38690	chr5_15504983	cis	-0,48±0,09	9,55E-08	0,35	Zinc-finger-domain-of-monoamine-oxidase-A-repressor-R1-protein
AT5G66910	chr5_26720691	cis	-0,51±0,1	9,55E-08	0,39	Disease-resistance-protein-(CC-NBS-LRR-class)-family
AT1G14970	chr1_5182982	cis	0,61±0,11	9,59E-08	0,19	O-fucosyltransferase-family-protein
AT4G37682	chr4_17824214	trans	0,47±0,09	9,59E-08	0,46	Protein-of-unknown-function-(DUF1399)
AT3G25290	chr3_9208737	cis	-0,49±0,09	9,60E-08	0,31	Auxin-responsive-family-protein
AT2G16390	chr2_7093811	cis	0,53±0,1	9,61E-08	0,31	SNF2-domain-containing-protein-/-helicase-domain-containing-protein
AT5G60490	chr3_10273905	trans	-0,59±0,11	9,65E-08	0,17	FASCICLIN-like-arabinogalactan-protein-12
AT3G18145	chr3_6215458	cis	0,89±0,17	9,66E-08	0,06	
AT5G14080	chr5_4543368	cis	-0,73±0,14	9,70E-08	0,09	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT5G40760	chr4_7668010	trans	0,68±0,13	9,71E-08	0,13	glucose-6-phosphate-dehydrogenase-6
AT3G42150	chr3_14311162	cis	-0,57±0,11	9,72E-08	0,20	
AT4G01660	chr4_708558	cis	-0,46±0,09	9,72E-08	0,42	ABC-transporter-1
AT3G25700	chr5_13313436	trans	0,57±0,11	9,73E-08	0,21	Eukaryotic-aspartyl-protease-family-protein
AT4G12120	chr2_3103492	trans	-0,77±0,14	9,76E-08	0,09	Sec1/munc18-like-(SM)-proteins-superfamily
AT3G06430	chr5_10045758	trans	0,55±0,1	9,87E-08	0,21	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT1G67600	chr5_8316373	trans	0,55±0,1	9,89E-08	0,80	Acid-phosphatase/vanadium-dependent-haloperoxidase-related-protein
AT1G13630	chr5_18779372	trans	0,46±0,09	9,95E-08	0,40	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT5G43620	chr5_17522428	cis	0,48±0,09	9,96E-08	0,34	Pre-mRNA-cleavage-complex-II
AT2G20560	chr2_8834265	cis	0,52±0,1	1,00E-07	0,33	DNAJ-heat-shock-family-protein
AT1G47420	chr1_17396251	cis	-0,58±0,11	1,00E-07	0,21	succinate-dehydrogenase-5
AT2G27460	chr5_6821780	trans	0,52±0,1	1,00E-07	0,38	sec23/sec24-transport-family-protein
AT2G21420	chr2_9168970	cis	-0,48±0,09	1,01E-07	0,36	IBR-domain-containing-protein
AT5G52980	chr5_21454704	cis	0,93±0,17	1,01E-07	0,06	
AT5G15030	chr5_4869269	cis	0,47±0,09	1,01E-07	0,51	Paired-amphipathic-helix-(PAH2)-superfamily-protein
AT4G22756	chr5_9384664	trans	0,75±0,14	1,01E-07	0,09	sterol-C4-methyl-oxidase-1-2
AT4G31480	chr4_15266990	cis	-0,46±0,09	1,01E-07	0,37	Coatomer,-beta-subunit
AT5G54960	chr5_22310442	NA	0,45±0,08	1,01E-07	0,44	pyruvate-decarboxylase-2
AT1G49850	chr2_3098610	trans	-0,49±0,09	1,01E-07	0,27	RING/U-box-superfamily-protein
AT1G31935	chr1_11469268	cis	-0,51±0,1	1,01E-07	0,30	other-RNA
AT2G20420	chr1_17022453	trans	0,47±0,09	1,02E-07	0,50	ATP-citrate-lyase-(ACL)-family-protein
AT1G11730	chr1_3956855	cis	0,58±0,11	1,02E-07	0,21	Galactosyltransferase-family-protein

AT3G59710	chr1_18007764	trans	-0,48±0,09	1,02E-07	0,35	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT5G47570	chr5_19293407	cis	-0,48±0,09	1,02E-07	0,39	
AT1G44920	chr1_16976331	cis	-0,46±0,09	1,02E-07	0,64	
AT2G25560	chr2_3603231	trans	-01,±0,19	1,02E-07	0,06	DNAJ-heat-shock-N-terminal-domain-containing-protein
AT1G31820	chr1_11423409	cis	0,88±0,17	1,02E-07	0,07	Amino-acid-permease-family-protein
AT2G35500	chr4_5706995	trans	0,48±0,09	1,02E-07	0,44	shikimate-kinase-like-2
AT4G16120	chr2_1688213	trans	0,45±0,09	1,02E-07	0,51	COBRA-like-protein-7-precursor
AT5G60460	chr5_24317327	cis	-0,53±0,1	1,03E-07	0,26	Preprotein-translocase-Sec,-Sec61-beta-subunit-protein
AT4G17390	chr1_7365759	trans	0,45±0,09	1,03E-07	0,43	Ribosomal-protein-L23/L15e-family-protein
AT2G01480	chr2_215194	cis	0,64±0,12	1,03E-07	0,17	O-fucosyltransferase-family-protein
AT3G49940	chr1_11421011	trans	0,58±0,11	1,03E-07	0,19	LOB-domain-containing-protein-38
AT2G41780	chr2_17439085	cis	-0,47±0,09	1,04E-07	0,59	
AT1G09490	chr1_3067045	cis	-0,72±0,14	1,04E-07	0,12	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT1G32120	chr4_7196901	trans	0,42±0,08	1,04E-07	0,54	
AT1G47056	chr1_516944	trans	-0,55±0,1	1,05E-07	0,24	VIER-F-box-proteine-1
AT4G10845	chr4_6650465	cis	-0,6±0,11	1,06E-07	0,17	
AT3G30740	chr3_12361180	cis	0,52±0,1	1,06E-07	0,24	
AT1G05135	chr5_13241678	trans	0,51±0,1	1,06E-07	0,28	
AT2G36810	chr2_15439825	cis	0,51±0,1	1,06E-07	0,30	ARM-repeat-superfamily-protein
AT5G39995	chr5_23834426	trans	-0,65±0,12	1,07E-07	0,15	
AT5G49540	chr2_1220507	trans	-0,66±0,13	1,07E-07	0,14	Rab5-interacting-family-protein
AT1G69460	chr1_26112852	cis	-0,47±0,09	1,07E-07	0,42	emp24/gp25L/p24-family/GOLD-family-protein
AT3G12780	chr1_17095651	trans	-0,71±0,13	1,07E-07	0,11	phosphoglycerate-kinase-1
AT2G27385	chr2_11707418	cis	-0,46±0,09	1,07E-07	0,38	Pollen-Ole-e-1-allergen-and-extensin-family-protein
ATMG01330	chr3_4119827	trans	0,46±0,09	1,07E-07	0,56	
AT2G23290	chr3_21497245	trans	-0,72±0,14	1,07E-07	0,11	myb-domain-protein-70
AT1G28110	chr1_9806790	cis	0,53±0,1	1,08E-07	0,28	serine-carboxypeptidase-like-45
AT4G21585	chr1_13723742	trans	-0,45±0,09	1,08E-07	0,46	endonuclease-4
AT2G44180	chr2_18255185	cis	-0,81±0,15	1,08E-07	0,09	methionine-aminopeptidase-2A
AT1G19420	chr1_6855013	trans	0,51±0,1	1,08E-07	0,51	
AT2G31560	chr2_13435705	cis	0,55±0,1	1,08E-07	0,24	Protein-of-unknown-function-(DUF1685)
AT4G04950	chr1_11606838	trans	0,6±0,11	1,08E-07	0,15	thioredoxin-family-protein
AT3G07730	chr3_10618296	trans	0,53±0,1	1,09E-07	0,25	
AT2G18910	chr2_8190531	cis	-0,63±0,12	1,09E-07	0,16	hydroxyproline-rich-glycoprotein-family-protein
AT3G01690	chr3_258525	cis	0,5±0,09	1,09E-07	0,38	alpha/beta-Hydrolases-superfamily-protein
AT4G24530	chr4_12664107	cis	0,96±0,18	1,10E-07	0,06	O-fucosyltransferase-family-protein
AT2G27420	chr2_11674816	trans	-0,51±0,1	1,10E-07	0,39	Cysteine-proteinases-superfamily-protein
AT3G27580	chr3_10234350	cis	0,65±0,12	1,10E-07	0,16	Protein-kinase-superfamily-protein
AT1G27620	chr1_9608120	cis	0,54±0,1	1,10E-07	0,23	HXXXD-type-acyl-transferase-family-protein
AT1G28410	chr1_9989731	cis	0,47±0,09	1,10E-07	0,41	
AT1G12700	chr1_4310313	cis	-0,6±0,11	1,10E-07	0,29	ATP-binding;nucleic-acid-binding;helicases
AT5G15140	chr5_4909111	cis	-0,45±0,09	1,11E-07	0,57	Galactose-mutarotase-like-superfamily-protein
AT4G01595	chr1_19974260	trans	0,49±0,09	1,11E-07	0,31	Protein-kinase-superfamily-protein
AT5G07880	chr5_2525053	cis	0,46±0,09	1,11E-07	0,51	synaptosomal-associated-protein-SNAP25-like-29
AT1G52000	chr1_19336176	cis	-0,49±0,09	1,11E-07	0,39	Mannose-binding-lectin-superfamily-protein
AT4G19040	chr4_10430162	cis	0,48±0,09	1,11E-07	0,34	ENHANCED-DISEASE-RESISTANCE-2
AT1G11070	chr1_3699590	cis	0,51±0,1	1,12E-07	0,33	
AT1G61380	chr1_21928292	trans	0,62±0,12	1,12E-07	0,16	S-domain-1-29
AT3G61260	chr1_16626320	trans	0,75±0,14	1,12E-07	0,10	Remorin-family-protein
AT5G35360	chr2_3110136	trans	-0,72±0,13	1,13E-07	0,11	acetyl-Co-enzyme-a-carboxylase-biotin-carboxylase-subunit
AT1G68600	chr5_21397497	trans	-0,69±0,13	1,13E-07	0,15	Aluminium-activated-malate-transporter-family-protein
AT5G50010	chr5_17652059	trans	-0,63±0,12	1,13E-07	0,15	sequence-specific-DNA-binding-transcription-factors;transcription-regulators
AT4G28450	chr4_14061957	cis	0,96±0,18	1,13E-07	0,06	nucleotide-binding;protein-binding
AT2G38695	chr2_16160135	cis	-0,65±0,12	1,14E-07	0,15	
AT4G27820	chr4_13859640	cis	0,76±0,14	1,14E-07	0,10	beta-glucosidase-9
AT3G59360	chr5_593516	trans	0,49±0,09	1,14E-07	0,34	UDP-galactose-transporter-6
AT3G06010	chr5_9427561	trans	-0,48±0,09	1,14E-07	0,36	Homeotic-gene-regulator
AT4G16765	chr4_9443280	cis	0,96±0,18	1,15E-07	0,06	2-oxoglutarate-(2OG)-and-Fe(II)-dependent-oxygenase-superfamily-protein
AT1G53780	chr1_20080144	cis	0,54±0,1	1,15E-07	0,26	peptidyl-prolyl-cis-trans-isomerases;hydrolases;nucleoside-triphosphatases;ATP-binding;nucleotide-binding;ATPases
AT1G26940	chr1_9340882	cis	0,47±0,09	1,15E-07	0,45	Cyclophilin-like-peptidyl-prolyl-cis-trans-isomerase-family-protein
AT4G27070	chr4_4400300	trans	0,66±0,12	1,15E-07	0,14	tryptophan-synthase-beta-subunit-2
AT3G05420	chr1_11139970	trans	-0,44±0,08	1,15E-07	0,37	acyl-CoA-binding-protein-4
AT1G64360	chr1_23888299	cis	-0,48±0,09	1,15E-07	0,32	
AT3G44380	chr3_11081145	trans	-0,45±0,09	1,16E-07	0,48	Late-embryogenesis-abundant-(LEA)-hydroxyproline-rich-glycoprotein-family
AT5G19830	chr5_6702507	cis	0,87±0,16	1,16E-07	0,07	Peptidyl-tRNA-hydrolase-family-protein
AT4G09510	chr4_6023926	cis	0,77±0,15	1,16E-07	0,10	cytosolic-invertase-2
AT1G16330	chr4_9168761	trans	0,48±0,09	1,16E-07	0,33	cyclin-b3;1
AT3G12230	chr2_8797313	trans	-0,58±0,11	1,16E-07	0,19	serine-carboxypeptidase-like-14
AT1G53580	chr1_19989116	cis	-0,76±0,14	1,16E-07	0,11	glyoxalase-II--3
AT3G19570	chr5_25494317	trans	0,67±0,13	1,17E-07	0,12	Family-of-unknown-function-(DUF566)-
AT2G31320	chr2_13359519	cis	-0,72±0,14	1,18E-07	0,12	poly(ADP-ribose)-polymerase-2
AT1G17470	chr5_15951787	trans	0,46±0,09	1,18E-07	0,39	developmentally-regulated-G-protein-1
AT1G16960	chr1_5143991	trans	-0,49±0,09	1,18E-07	0,35	Ubiquitin-domain-containing-protein
AT5G18040	chr5_5952479	cis	0,52±0,1	1,19E-07	0,24	
AT1G50180	chr1_18466810	trans	-0,74±0,14	1,19E-07	0,10	NB-ARC-domain-containing-disease-resistance-protein
AT1G52570	chr1_19587948	cis	0,46±0,09	1,19E-07	0,37	phospholipase-D-alpha-2
AT3G13570	chr3_11081145	trans	-0,46±0,09	1,19E-07	0,48	SC35-like-splicing-factor-30A
AT1G55100	chr1_5098226	trans	-0,46±0,09	1,19E-07	0,35	transposable-element-gene
AT3G21755	chr3_7666792	cis	-0,81±0,15	1,19E-07	0,08	other-RNA

AT3G24615	chr1_22974129	trans	0,84±0,16	1,20E-07	0,06	snoRNA
AT3G44280	chr1_2399042	trans	-0,69±0,13	1,20E-07	0,12	
AT3G50880	chr1_5929751	trans	0,56±0,1	1,21E-07	0,21	DNA-glycosylase-superfamily-protein
AT2G34240	chr2_8300520	trans	0,84±0,16	1,21E-07	0,08	Protein-with-domains-of-unknown-function-DUF627-and-DUF632
AT5G11140	chr4_7752692	trans	-0,45±0,08	1,21E-07	0,44	Arabidopsis-phospholipase-like-protein-(PEARLI-4)-family
AT3G12460	chr3_3955504	cis	-0,73±0,14	1,21E-07	0,11	Polynucleotidyl-transferase,-ribonuclease-H-like-superfamily-protein
AT3G54180	chr5_22816629	trans	-0,84±0,16	1,21E-07	0,08	cyclin-dependent-kinase-B1;1
AT5G17420	chr1_29311910	trans	-0,47±0,09	1,22E-07	0,37	Cellulose-synthase-family-protein
AT1G12390	chr2_15955410	trans	-0,45±0,09	1,22E-07	0,55	Cornichon-family-protein
AT2G04390	chr2_7255221	trans	-0,46±0,09	1,22E-07	0,39	Ribosomal-S17-family-protein
AT3G14020	chr3_4644022	cis	-0,47±0,09	1,22E-07	0,40	nuclear-factor-Y,-subunit-A6
AT3G47670	chr1_10708763	trans	0,49±0,09	1,23E-07	0,32	Plant-invertase/pectin-methylesterase-inhibitor-superfamily-protein
AT5G64830	chr1_15499724	trans	-0,78±0,15	1,23E-07	0,09	programmed-cell-death-2-C-terminal-domain-containing-protein
AT4G39550	chr3_18516310	trans	-0,69±0,13	1,23E-07	0,11	Galactose-oxidase/kelch-repeat-superfamily-protein
AT2G42270	chr2_17601926	cis	-0,63±0,12	1,23E-07	0,16	U5-small-nuclear-ribonucleoprotein-helicase
AT1G51860	chr1_19260731	cis	-0,69±0,13	1,23E-07	0,13	Leucine-rich-repeat-protein-kinase-family-protein
AT1G72800	chr1_27396416	cis	0,48±0,09	1,24E-07	0,39	RNA-binding-(RRM/RBD/RNP-motifs)-family-protein
AT2G22450	chr4_18256161	trans	-0,45±0,09	1,24E-07	0,43	riboflavin-biosynthesis-protein,-putative
AT5G12390	chr5_3837785	trans	-0,6±0,11	1,25E-07	0,16	Tetratricopeptide-repeat-(TPR)-like-superfamily-protein
AT4G36810	chr1_16671064	trans	-0,76±0,14	1,25E-07	0,11	geranylgeranyl-pyrophosphate-synthase-1
AT2G15820	chr2_6888822	cis	-0,61±0,12	1,25E-07	0,16	endonucleases
AT1G76110	chr1_28560286	cis	-0,48±0,09	1,25E-07	0,43	HMG-(high-mobility-group)-box-protein-with-ARID/BRIGHT-DNA-binding-domain
AT5G47420	chr5_19225274	cis	0,84±0,16	1,25E-07	0,09	Tryptophan-RNA-binding-attenuator-protein-like
AT3G57590	chr5_23153505	trans	-0,57±0,11	1,26E-07	0,20	F-box-and-associated-interaction-domains-containing-protein
AT5G23450	chr1_23725854	trans	0,69±0,13	1,26E-07	0,11	long-chain-base-(LCB)-kinase-1
AT2G18390	chr2_7987752	cis	-0,47±0,09	1,26E-07	0,45	ADP-ribosylation-factor-family-protein
AT2G26830	chr2_11419578	cis	0,48±0,09	1,26E-07	0,36	Protein-kinase-superfamily-protein
AT5G44570	chr3_15766547	trans	-0,43±0,08	1,27E-07	0,47	
AT4G39740	chr4_18434250	cis	-0,73±0,14	1,27E-07	0,11	Thioredoxin-superfamily-protein
AT4G09160	chr3_10279428	trans	-0,82±0,16	1,27E-07	0,08	SEC14-cytosolic-factor-family-protein-/-phosphoglyceride-transfer-family-protein
AT4G13180	chr4_7661956	cis	0,44±0,08	1,27E-07	0,44	NAD(P)-binding-Rossmann-fold-superfamily-protein
AT5G07810	chr5_2494833	cis	0,63±0,12	1,27E-07	0,16	SNF2-domain-containing-protein-/-helicase-domain-containing-protein-/-HNH-endonuclease-domain-containing-protein
AT2G16500	chr2_7146401	cis	0,56±0,11	1,27E-07	0,21	arginine-decarboxylase-1
AT5G62220	chr2_11761927	trans	-0,59±0,11	1,27E-07	0,18	glycosyltransferase-18
AT2G04650	chr5_5926526	trans	-0,87±0,16	1,27E-07	0,07	ADP-glucose-pyrophosphorylase-family-protein
AT3G56300	chr3_20874671	cis	-0,95±0,18	1,27E-07	0,06	Cysteinyl-tRNA-synthetase,-class-Ia-family-protein
AT2G39180	chr5_19661348	trans	-0,49±0,09	1,27E-07	0,29	CRINKLY4-related-2
AT1G28060	chr3_11124668	trans	-0,77±0,15	1,28E-07	0,10	Pre-mRNA-splicing-factor-3
AT1G78750	chr2_6495746	trans	0,64±0,12	1,29E-07	0,14	F-box/RNI-like-superfamily-protein
AT3G48730	chr5_10045758	trans	0,54±0,1	1,30E-07	0,21	glutamate-1-semialdehyde-2,1-aminomutase-2
AT3G49640	chr3_18402861	cis	0,49±0,09	1,30E-07	0,53	Aldolase-type-TIM-barrel-family-protein
AT5G42450	chr5_17969122	trans	0,47±0,09	1,30E-07	0,67	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT5G03020	chr5_9013543	trans	-0,47±0,09	1,30E-07	0,49	Galactose-oxidase/kelch-repeat-superfamily-protein
AT3G14070	chr3_4662808	cis	-0,55±0,1	1,30E-07	0,21	cation-exchanger-9
AT5G48450	chr4_7684380	trans	-01,04±0,2	1,31E-07	0,06	SKU5--similar-3
AT5G40510	chr3_18890129	trans	-0,58±0,11	1,31E-07	0,21	Sucrase/ferredoxin-like-family-protein
AT3G24200	chr2_3974783	trans	-0,91±0,17	1,31E-07	0,08	FAD/NAD(P)-binding-oxidoreductase-family-protein
AT1G13145	chr3_16129687	trans	0,91±0,17	1,31E-07	0,06	
AT5G23150	chr1_22581176	trans	-0,57±0,11	1,31E-07	0,19	Tudor/PWWP/MBT-domain-containing-protein
AT3G46690	chr3_17199333	cis	-0,47±0,09	1,31E-07	0,37	UDP-Glycosyltransferase-superfamily-protein
AT1G33960	chr1_12349665	cis	0,46±0,09	1,31E-07	0,56	P-loop-containing-nucleoside-triphosphate-hydrolases-superfamily-protein
AT2G47600	chr2_19529195	cis	-0,53±0,1	1,31E-07	0,32	magnesium/proton-exchanger
AT1G47530	chr1_17454430	cis	0,5±0,1	1,31E-07	0,26	MATE-efflux-family-protein
AT5G48040	chr5_19471168	cis	-0,51±0,1	1,32E-07	0,36	Ubiquitin-carboxyl-terminal-hydrolase-family-protein
AT2G22122	chr2_9405329	cis	-0,47±0,09	1,32E-07	0,35	
AT1G75370	chr1_22705764	trans	0,54±0,1	1,32E-07	0,21	Sec14p-like-phosphatidylinositol-transfer-family-protein
AT4G34620	chr1_29284466	trans	-0,49±0,09	1,32E-07	0,28	small-subunit-ribosomal-protein-16
AT1G77680	chr1_516944	trans	-0,55±0,1	1,32E-07	0,24	Ribonuclease-II/R-family-protein
AT5G06660	chr3_10089517	trans	-0,66±0,12	1,32E-07	0,14	Protein-of-unknown-function-DUF106,-transmembrane
AT1G49780	chr2_5693939	trans	-0,61±0,11	1,33E-07	0,20	plant-U-box-26
AT5G48730	chr1_9233315	trans	-0,68±0,13	1,33E-07	0,14	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT4G31420	chr4_10164510	trans	0,6±0,11	1,33E-07	0,16	Zinc-finger-protein-622
AT5G62740	chr2_16145887	trans	0,79±0,15	1,33E-07	0,09	SPFH/Band-7/PHB-domain-containing-membrane-associated-protein-family
AT3G18215	chr1_24056703	trans	-0,77±0,15	1,33E-07	0,10	Protein-of-unknown-function,-DUF599
AT5G17150	chr5_5641884	cis	0,47±0,09	1,33E-07	0,36	Cystatin/monellin-superfamily-protein
AT5G46740	chr1_29648907	trans	-0,51±0,1	1,34E-07	0,36	ubiquitin-specific-protease-21
AT2G04530	chr3_16228923	trans	0,56±0,11	1,34E-07	0,20	Metallo-hydrolase/oxidoreductase-superfamily-protein
AT3G45730	chr4_14861925	trans	-0,49±0,09	1,34E-07	0,28	
AT1G70518	chr1_26583389	cis	-0,82±0,16	1,34E-07	0,09	
AT3G27340	chr3_10118104	cis	0,46±0,09	1,34E-07	0,39	
AT4G14050	chr4_8104584	cis	-0,48±0,09	1,35E-07	0,31	Pentatricopeptide-repeat-(PPR)-superfamily-protein
AT4G15530	chr5_7349392	trans	-0,73±0,14	1,35E-07	0,11	pyruvate-orthophosphate-dikinase
AT1G34480	chr1_12607163	cis	-0,49±0,09	1,36E-07	0,29	Cysteine/Histidine-rich-C1-domain-family-protein
AT2G27350	chr4_8855279	trans	-0,73±0,14	1,36E-07	0,10	OTU-like-cysteine-protease-family-protein
AT5G38610	chr5_15458592	cis	-0,49±0,09	1,36E-07	0,40	Plant-invertase/pectin-methylesterase-inhibitor-superfamily-protein
AT1G12460	chr1_19060201	trans	-0,5±0,09	1,36E-07	0,29	Leucine-rich-repeat-protein-kinase-family-protein
AT1G22000	chr1_7746843	cis	-0,63±0,12	1,37E-07	0,15	FBD,-F-box-and-Leucine-Rich-Repeat-domains-containing-protein
AT1G13820	chr1_4738415	cis	0,7±0,13	1,37E-07	0,12	alpha/beta-Hydrolases-superfamily-protein
AT5G33210	chr1_22741687	trans	-0,68±0,13	1,37E-07	0,09	SHI-related-sequence-8

AT1G16010	chr1_5497248	cis	0,58±0,11	1,37E-07	0,18	magnesium-transporter-2
AT5G27990	chr2_1847927	trans	0,63±0,12	1,37E-07	0,15	Pre-rRNA-processing-protein-TSR2,-conserved-region
AT1G74390	chr1_27963851	cis	0,86±0,16	1,38E-07	0,07	Polynucleotidyl-transferase,-ribonuclease-H-like-superfamily-protein
AT3G60200	chr5_10018614	trans	0,49±0,09	1,38E-07	0,36	
AT4G21730	chr1_12852388	trans	-0,79±0,15	1,38E-07	0,09	
AT5G08290	chr5_15481637	trans	-0,7±0,13	1,38E-07	0,11	mRNA-splicing-factor,-thioredoxin-like-U5-snRNP
AT1G66380	chr2_9986904	trans	0,54±0,1	1,38E-07	0,21	myb-domain-protein-114
AT5G67230	chr5_26822334	cis	-0,63±0,12	1,38E-07	0,15	Nucleotide-diphospho-sugar-transferases-superfamily-protein
AT1G04820	chr1_1364944	cis	-0,48±0,09	1,39E-07	0,33	tubulin-alpha-4-chain
AT1G17200	chr5_22110954	trans	-0,58±0,11	1,39E-07	0,18	Uncharacterised-protein-family-(UPF0497)
AT1G22020	chr2_3563096	trans	-0,67±0,13	1,39E-07	0,16	serine-hydroxymethyltransferase-6
AT2G20790	chr2_8995610	cis	0,76±0,14	1,40E-07	0,11	clathrin-adaptor-complexes-medium-subunit-family-protein
AT5G38590	chr1_19716111	trans	-0,45±0,09	1,40E-07	0,56	F-box/RNI-like/FBD-like-domains-containing-protein
AT3G62430	chr3_23097357	cis	-0,84±0,16	1,40E-07	0,93	Protein-with-RNI-like/FBD-like-domains
AT3G48190	chr1_20829477	trans	0,45±0,09	1,40E-07	0,64	ataxia-telangiectasia-mutated
AT1G71980	chr2_10851297	trans	0,7±0,13	1,40E-07	0,11	Protease-associated-(PA)-RING/U-box-zinc-finger-family-protein
AT5G66658	chr1_13148503	trans	0,53±0,1	1,41E-07	0,23	
AT1G27900	chr1_9705362	cis	0,93±0,18	1,41E-07	0,06	RNA-helicase-family-protein
AT4G09340	chr4_5924677	cis	0,96±0,18	1,41E-07	0,06	SPla/RYanodine-receptor-(SPRY)-domain-containing-protein
AT4G23870	chr2_1115475	trans	0,83±0,16	1,41E-07	0,07	
AT1G26300	chr1_21309404	trans	-0,76±0,15	1,42E-07	0,09	BSD-domain-containing-protein
AT4G37020	chr5_6722955	trans	0,59±0,11	1,42E-07	0,16	
AT2G23330	chr2_9942448	cis	0,76±0,14	1,42E-07	0,09	transposable-element-gene
AT3G05410	chr5_20068108	trans	-0,67±0,13	1,42E-07	0,13	Photosystem-II-reaction-center-PsbP-family-protein
AT5G40570	chr4_11421007	trans	-0,43±0,08	1,42E-07	0,43	Surfeit-locus-protein-2-(SURF2)
AT5G43260	chr5_17360038	cis	-0,7±0,13	1,43E-07	0,11	chaperone-protein-dnaJ-related
AT2G29910	chr2_19384823	trans	0,45±0,09	1,43E-07	0,52	F-box/RNI-like-superfamily-protein
AT3G08740	chr1_12934923	trans	0,55±0,1	1,43E-07	0,21	elongation-factor-P-(EF-P)-family-protein
AT4G02040	chr4_892628	cis	0,46±0,09	1,44E-07	0,49	
AT5G42790	chr3_15887691	trans	-0,82±0,16	1,44E-07	0,07	proteasome-alpha-subunit-F1
AT5G57190	chr3_6714518	trans	-0,52±0,1	1,45E-07	0,23	phosphatidylserine-decarboxylase-2

[a]SNP: Top SNP in eQTL; [b]Type: cis/trans (</>1 Mb from peak association to expressed gene); [c]a±SE: Additive effect ± Standard Error; [d]P-value: nominal P-value in expression Genome-Wide Association analysis; [e]MAF: Minor Allele Frequency

Table S5. 175 genes affected by eQTL in the population of 140 wild-collected *A. thaliana* accessions for which strong phenotypic effect have already been described in the literature

Locus	*Gene*	*[a]SNP*	*[b]Type*	*[c]Replicated*	*Short description*	*[d]Description of mutant phenotype*	*[e]Reference*	*[f]Year*
AT1G02050	LAP6	chr1_360888	cis	Yes	Less Adhesive Pollen	Abnormal pollen exine layer	C. Douglas	2010
AT1G11870	OVA7	chr1_4004173	cis	Yes	Ovule Abortion	Ovule abortion; Gametophyte defective; Early embryo defective (inferred)	D. Meinke	2005
AT1G12550	HPR3	chr1_4275390	cis	Yes	Hydroxypyruvate Reductase	Slightly elevated levels of photorespiratory intermediates; No other phenotypes detected	H. Bauwe	2011
AT1G48380	RHL1	chr1_17879415	cis	Yes	Root Hairless	Complete loss of root hairs on primary root	L. Dolan	1998
AT1G54040	TASTY	chr1_20170832	cis	Yes	Tasty	Abnormal glucosinolate composition	F. Ausubel	2001
AT1G55320	AAE18	chr1_20635146	cis	Yes	Acyl-Activation Enzyme	Insensitive to pro-auxins	J. Bussell	2009
AT1G63000	UER1	chr1_23342609	cis	Yes	UDP-4-Keto-6-Deoxy-D-Glucose-3,5-Epimerase-4-Reductase	Short root hairs	Y. Zhu	2010
AT1G63900	DAL1	chr1_23717698	cis	Yes	DIAP1-Like Protein	Susceptible to avirulent bacteria	F. Song	2011
AT1G64970	TMT1	chr1_24135673	cis	Yes	Tocopherol Methyltransferase	Slightly reduced fresh weight; Low alpha and beta tocopherol levels	P. Doermann	2003
AT2G28560	RAD51B	chr2_12237067	cis	Yes	Rad51 Paralog	Sensitive to mitomycin C (DNA cross-linking agent)	C. White	2005
AT2G32940	AGO6	chr2_13973428	cis	Yes	Argonaute	Decreased DNA methylation	J. Zhu	2007
AT2G41660	MIZ1	chr2_17409805	cis	Yes	Mizu-Kussei	Reduced hydrotropism	H. Takahashi	2007
AT3G07525	ATG10	chr3_2398863	cis	Yes	Autophagy	Slightly slower rosette growth; Reduced fertility; Late flowering; Early senescence; Sensitive to carbon starvation and limited nitrogen	R. Vierstra	2008
AT3G08970	AtERdj3A	chr3_2737991	cis	Yes		Male gametophyte defective; Homozygotes are viable: Severely reduced male fertility at high temperature; Fertility phenotype rescued at low temperature	D. Ye	2009
AT3G11220	ELO1	chr3_3513881	cis	Yes	Elongata	Very low germination rate; Slow seedling growth; Narrow leaves; Short primary root; Short inflorescence stems with abnormal architecture	M. Van Lijsebettens	2005
AT3G18165	MOS4	chr3_6222138	cis	Yes	Modifier of snc1, 4	Reduced fertility; Late flowering	X. Li	2007
AT3G23560	ALF5	chr3_8456447	cis	Yes	Aberrant Lateral Root Formation	Root growth sensitive to toxic compounds (including one in Bacto agar)	G. Fink	2001
AT3G29290	EMB2076	chr3_11238348	cis	Yes	Embryo Defective	Embryo defective; Transition	D. Meinke	2003
AT3G43210	TES	chr3_15190921	cis	Yes	Tetraspore	Reduced fertility due to defects in meiosis; Large pollen	H. Dickinson	2003
AT3G45890	RUS1	chr3_16877300	cis	Yes	Root UV-B Sensitive	Short roots; Seedling lethal when roots are exposed to UV-B light	Z. He	2009
AT3G55530	SDIR1	chr3_20593930	cis	Yes	Salt- and Drought-Induced RING Finger	Long primary root	Q. Xie	2007
AT3G59380	FTA	chr3_21945839	cis	Yes	Farnesyltransferase	Dwarf; Slow growth; Low penetrance of fasciated stems and inflorescences; Increased floral organ number; Reduced fertility; Late flowering; Large shoot meristem	S. Yalovsky	2004
AT4G00620	EMB3127	chr4_261007	cis	Yes	Embryo Defective	Embryo defective; Preglobular	D. Meinke	2011
AT4G01060	CPL3	chr4_448429	cis	Yes	Caprice-Like MYB	Increased trichome density; Abnormal root hairs	T. Wada	2008
AT4G02460	PMS1	chr4_1074131\chr5_14985436	cis/trans	Yes	Post Meiotic Segregation	Male and female gametophyte defective; Homozygotes are viable: Reduced fertility	F. Belzile	2009
AT4G19100	PAM68	chr4_10453802	cis	Yes	Photosynthesis Affected Mutant	Pale green cotyledons and leaves; Slow growth	D. Leister	2010
AT4G21320	Hsa32	chr4_11340530	cis	Yes	Heat-Stress-Associated	Sensitive to high temperature	S. Ko	2006
AT4G27060	TOR1	chr1_11506730\chr4_13571868	trans/cis	Yes	Tortifolia	Abnormal root gravitropism; Anti-clockwise twisting rosette leaves, cauline leaves, and petals	T. Hashimoto	2000
AT4G31870	GPX7	chr4_15409973	cis	Yes	Glutathione Peroxidase	Sensitive to photooxidative stress	S. Karpinski	2009
AT4G33360	FLDH	chr4_16069056	cis	Yes	Farnesol Dehydrogenase	Germination and stomatal closure insensitive to ABA	D. Crowell	2010
AT4G37925	NDH-M	chr4_17830243	cis	Yes	Subunit NDH-M of NAD(P)H:Plastoquinone Dehydrogenase Complex	Complete loss of post-illumination chlorophyll fluorescence; Slightly increased non-photochemical quenching	G. Peltier	2005
AT4G38800	MTN1	chr4_18114982	cis	Yes	Methylthioadenosine Nucleosidase	Reduced growth with MTA as source of nitrogen	M. Sauter	2010
AT4G39920	POR	chr4_18519040	cis	Yes	Porcino	Embryo defective; Preglobular; Enlarged embryo cells and endosperm nuclei	U. Mayer	2002
AT5G23020	IMS2	chr5_7703372	cis	Yes	2-Isopropylmalate Synthase	Low C8 glucosinolate levels	J. Gershenzon	2007
AT5G45610	HUS2	chr5_18496799	cis	Yes	Hydroxyurea Sensitive	Sensitive to genotoxic stress	A. Tanaka	2009
AT5G49970	AtPPOX	chr5_20333567	cis	Yes	Pyridoxin (Pyrodoxamine) 5'-phosphate Oxidase	Small root system; Reduced fertility; Sensitive to high light; Increased growth in response to sucrose; Resistant to salt	M. Daub	2007
AT5G50950	FUM2	chr5_20727510	cis	Yes	Fumarase	Low fumarate levels; Low amino acid levels in the daytime; Elevated amino acid levels at night	S. Smith	2010
AT5G64630	FAS2	chr5_25833185	cis	Yes	Fasciata	Slow growth; Short roots; Fasciated stems and inflorescences; Abnormal leaf morphology; Abnormal phyllotaxy; Reduced petal and stamen number; Narrow sepals and petals; Reduced fertility; Abnormal SAM and RAM morphology	T. Araki	2001
AT1G01690	PRD3	chr1_249475	cis	No	Putative Recombination Initiation Defect	Reduced fertility due to defects in meiosis	M. Grelon	2009
AT1G04250	AXR3	chr1_1134230	cis	No	Auxin Resistant	Complete loss of root gravitropism	O. Leyser	1998
AT1G04820	TOR2	chr1_1364944	cis	No	Tortifolia	Short, thick hypocotyl; Helical growth; Right-handed petiole torsions; Sensitive to microtubule-disrupting drugs	A. Schaffner	2009
AT1G05630	At5PT13	chr1_1681154	cis	No	Inositol Polyphosphate 5' Phosphatase	Altered vein patterning in cotyledons	H. Xue	2005
AT1G06570	PDS1	chr3_13898892	trans	No	Phytoene Desaturase	Seedling lethal (inferred from pigment defect)	D. DellaPenna	1998
AT1G08030	TPST	chr1_2492448	cis	No	Tyrosylprotein Sulfotransferase	Small cotyledons; Small, pale green leaves; Short roots and inflorescence stems; Early senescence; Abnormal vein morphology; Disorganized RAM	Y. Matsubayashi	2009

AT1G14660	AtNHX8	chr1_5030827	cis	No	Sodium Hydrogen Exchanger	Sensitive to lithium	X. Wang	2007
AT1G16150	WAKL4	chr1_5531987	cis	No	Wall-Associated Kinase-Like	Short roots; Sensitive to sodium, potassium, copper, and zinc; Resistant to nickel	Z. He	2005
AT1G19080	TTN10	chr1_6586637	cis	No	Titan	Embryo defective; Preglobular	D. Meinke	2003
AT1G19750	CSAat1B	chr1_6832148	cis	No	Cockayne Syndrome A-like Protein	Sensitive to genotoxic stress	T. Guo	2010
AT1G20050	HYD1	chr1_6947020	cis	No	Hydra	Embryo and seedling defective	K. Lindsey	2002
AT1G21270	WAK2	chr1_7447447	cis	No	Wall-Associated Kinase	Incomplete penetrance of seedling lethality; Slow growth; Small seedlings; Short roots	N. Byers	2006
AT1G24340	EMB2421	chr1_8635114	cis	No	Embryo Defective	Embryo defective; Globular	D. Meinke	2003
AT1G30620	MUR4	chr1_10864371	cis	No	Murus	Abnormal starch, anthocyanin, and chlorophyll levels; Sensitive to sugar	M. Bevan	2007
AT1G35670	AtCDPK2	chr1_13203648	cis	No	Calcium-Dependent Protein Kinase	Sensitive to drought and salt; Insensitive to ABA	D. Zhang	2007
AT1G49720	ABF1	chr1_18400592	cis	No	ABRE Binding Factor	Sensitive to freezing when not acclimated	T. Palva	2002
AT1G50500	HIT1	chr1_18716339	cis	No	Heat-Intolerant	Null: Male gametophyte defective; Embryo defective (inferred); Knockdown: Sensitive to high temperature and osmotic stress	S. Wu	2006
AT1G51965	ABO5	chr1_19314183	cis	No	ABA Overly-Sensitive	Seedling and root growth sensitive to ABA	Z. Gong	2010
AT1G53580	ETHE1	chr1_19989116	cis	No	Similar to Human ETHE1	Embryo defective; Transition	C. Makaroff	2007
AT1G56510	WRR4	chr1_21171909	cis	No	White Rust Resistance	Susceptible to Albugo candida	E. Holub	2008
AT1G65420	NPQ7	chr1_23055533/chr1_24290690	trans/cis	No	Nonphotochemical Quenching	Reduced non-photochemical quenching	K. Niyogi	2010
AT1G66340	EIN1	chr1_24734188	cis	No	Ethylene Insensitive	Sensitive to ethylene	P. Larsen	2002
AT1G67440	EMB1688	chr1_25265828	cis	No	Embryo Defective	Embryo defective; Cotyledon	D. Meinke	2002
AT1G71440	PFI	chr1_26921006	cis	No	Pfifferling	Embryo defective; Preglobular; Enlarged embryo cells and endosperm nuclei	U. Mayer	2002
AT1G75100	JAC1	chr1_28192328	cis	No	J-Domain Protein Required for Chloroplast Accumulation Response	Abnormal chloroplast movement under weak blue light and in the dark	M. Wada	2005
AT1G77140	VPS45	chr4_6758588	trans	No	Vacuolar Sorting Protein	Null: Complete male gametophyte defective; Female gametophyte defective; Knockdown: Severe dwarf	D. Bassham	2009
AT2G02955	MEE12	chr2_860116	cis	No	Maternal Effect Embryo Arrest	Female gametophyte defective; Embryo defective (inferred)	W. Yang	2007
AT2G03760	SOT12	chr2_1150723	cis	No	Sulphotransferase	Germination sensitive to ABA and salt; Seedling growth sensitive to SA; Susceptible to bacterial infection	H. Shi	2010
AT2G04530	TRZ2	chr3_16228923	trans	No	tRNase Z	Embryo defective; Globular	A. Marchfelder	2009
AT2G04550	IBR5	chr2_1579467	cis	No	Indole-3-Butyric Acid Response	Long primary root; Few, short lateral roots; Short hypocotyl; Serrated leaves; Abnormal vascular patterning	B. Bartel	2003
AT2G06510	RPA70a	chr2_2336551	trans	No	Replication Protein A	Reduced fertility due to defects in meiosis; Sensitive to genotoxic stress	K. Tamura	2009
AT2G15820	OTP51	chr2_6888822	cis	No	Organelle Transcript Processing	Lethal on soil or in normal light; Pale yellow; With exogenous sucrose under low light: Pale green; Dwarf; Slow growth	I. Small	2008
AT2G16390	DRD1	chr2_7093811	cis	No	Defective in RNA-Directed DNA Methylation	Reduced RNA-directed DNA methylation	A. Matzke	2004
AT2G17250	EMB2762	chr2_7502298	cis	No	Embryo Defective	Embryo defective; Globular	D. Meinke	2007
AT2G18390	TTN5	chr2_7987752	cis	No	Titan	Embryo defective; Preglobular; Enlarged embryo cells and endosperm nuclei	D. Meinke	2002
AT2G18710	SCY1	chr2_8112156	cis	No	SecY Homolog	Seedling lethal; Albino embryos	D. Fernandez	2011
AT2G21070	FIO1	chr2_9049079	cis	No	Fiona	Early flowering; Abnormal circadian rhythms	H. Nam	2008
AT2G21870	MGP1	chr2_9321894	cis	No	Male Gametophyte Defective	Complete male gametophyte defective; Female gametophyte defective	D. Ye	2010
AT2G22410	SLO1	chr2_9507478	cis	No	Slow Growth	Dwarf; Slow growth	M. Hsieh	2010
AT2G26460	SMU2	chr2_11264873	cis	No	Suppressors of MEC-8 and UNC-52	Slow growth; Incomplete penetrance of abnormal cotyledon number and heavy seeds	B. Larkins	2009
AT2G26830	EMB1187	chr2_11419578	cis	No	Embryo Defective	Embryo defective; Globular	D. Meinke	2002
AT2G28670	ESB2	chr2_12301537	cis	No	Enhanced Suberin	Resistant to drought; Elevated suberin levels in roots	D. Salt	2009
AT2G30280	RDM4	chr2_12910878	cis	No	RNA-Directed DNA Methylation	Increased seed dormancy; Pale green seedlings; Slow growth; Dwarf; Abnormal phyllotaxy; Abnormal rosette leaf morphology; Reduced fertility; Late flowering; Altered DNA methylation	M. Matzke	2009
AT2G31530	EMB2289	chr2_13436307	cis	No	Embryo Defective	Embryo defective; Globular	D. Meinke	2002
AT2G34790	EDA28	chr2_14679048	cis	No	Embryo Sac Development Arrest	Female gametophyte defective; Embryo defective (inferred)	V. Sundaresan	2005
AT2G37680	PAT3	chr2_15803792	cis	No	Phytochrome A Transduction	Long hypocotyl under far-red light	N. Chua	2001
AT2G37860	LCD1	chr2_15852326	cis	No	Lower Cell Density	Pale plants in response to ozone	P. Conklin	2002
AT2G40970	MYBC1	chr2_17098828	cis	No	MYB transcription factor	Resistant to freezing	J. Li	2010
AT2G42160	BRIZ1	chr2_17574128	cis	No	BRAP2 RING ZnUBP Domain-Containing Protein	Seedling lethal; Pale embryos; Delayed germination	J. Callis	2010
AT2G46240	AtBAG6	chr4_10473876	trans	No	BCL-2-Associated Athanogene	Heterozygotes: Increased branching and lateral root number; Early flowering and senescence; Incomplete penetrance of purple leaves; Homozygotes not mentioned	M. Dickman	2006
AT2G47980	SCC3	chr5_26359562	trans	No	Sister-Chromatid Cohesion Protein	No homozygous mutant plants recovered; Heterozygotes: Reduced sister chromatid alignment	I. Schubert	2009
AT2G48120	PAC	chr2_19683015	cis	No	Pale Cress	Seedling lethal (inferred from pigment defect)	P. Scolnik	1994
AT3G02680	NBS1	chr3_582584	cis	No	Nijmegen Breakage Syndrome	Sensitive to MMS (inducer of genotoxic stress) and mitomycin C (DNA cross-linking agent)	C. West	2007
AT3G02850	SKOR	chr3_627697	cis	No	Defect in SKOR K+ Channel	Low potassium levels in shoot and xylem sap	H. Sentenac	1998

AT3G05530	RPT5a	chr3_1599235	cis	No	Regulatory Particle	Null: Complete male gametophyte defective; Female gametophyte defective; Knockdown: Male gametophyte defective; Homozygotes are viable: Dwarf; Short roots; Reduced fertility	P. Guerche	2009
AT3G06430	EMB2750	chr5_10045758	trans	No	Embryo Defective	Embryo defective; Globular	D. Meinke	2003
AT3G16640	TCTP	chr3_5669704	cis	No	Translationally Controller Tumor Protein	Male gametophyte defective; Embryo defective (inferred)	J. Masle	2008
AT3G17650	PDE321	chr3_10273905	trans	No	Pigment Defective Embryo	Seedling lethal (inferred from pigment defect)	D. Meinke	2003
AT3G19570	SCO3	chr5_25494317	trans	No	Snowy Cotyledon	Null: No homozygous mutant plants recovered; Knockdown: Chlorotic cotyledons; Slight delay in growth	B. Pogson	2010
AT3G22880	DMC1	chr3_8085466	cis	No	Homolog of Yeast DMC 1	Reduced fertility due to defects in meiosis	M. Doutriaux	1999
AT3G23110	EMB2800	chr3_8227670	cis	No	Embryo Defective	Embryo defective; Cotyledon	D. Meinke	2008
AT3G26420	AtRZ-1a	chr3_9674892	cis	No		Germination and seedling growth sensitive to low temperature	H. Kang	2005
AT3G26744	ICE1	chr3_9833104	cis	No	Inducer of CBF Expression	Abnormal stomata morphology	K. Torii	2008
AT3G27730	RCK	chr3_10279321	cis	No	Rock-N-Rollers	Reduced fertility due to defects in meiosis	H. Ma	2005
AT3G28730	SSRP1	chr3_10776224	cis	No		Increased branching and leaf number; Abnormal flower and leaf morphology; Reduced fertility; Early flowering	K. Grasser	2009
AT3G46530	RPP13	chr3_17133077	cis	No	Recognition of Peronospora parasitica	Altered response to fungal infection	J. Benyon	2000
AT3G46740	TOC75	chr4_12536294	trans	No	Translocon at outer envelope membrane of chloroplasts	Embryo defective; Preglobular	P. Jarvis	2007
AT3G47390	PHS1	chr3_17461680	cis	No	Photosensitive	Dwarf; Bleached leaves; Phenotype enhanced under high light	L. Zhang	2010
AT3G47990	SIS3	chr3_17715309	cis	No	Sugar Insensitive	Insensitive to elevated sugar	S. Gibson	2010
AT3G48190	ATM	chr1_20829477	trans	No	Ataxia-Telangiectasia Mutated	Reduced female fertility	A. Tissier	2003
AT3G49180	RID3	chr3_18229388	cis	No	Root Initiation Defective	Shoots fail to regenerate from callus at high temperature	M. Sugiyama	2009
AT3G49940	LBD38	chr1_11421011	trans	No	LOB Domain-Containing Protein	Elevated anthocyanin levels in response to nitrogen	W. Scheible	2009
AT3G50820	PsbO2	chr4_5706995	trans	No	Photosystem II Subunit	Slow growth; Long, dark green leaves with bent margins	C. Spetea	2007
AT3G51820	PDE325	chr3_19215689	cis	No	Pigment Defective Embryo	Pale green seeds and seedlings	D. Meinke	2008
AT3G54280	RGD3	chr2_5407788	trans	No	Root Growth Defective	Unable to regenerate shoots from callus; Phenotype enhanced at high temperature	M. Sugiyama	2009
AT3G55830	EPC1	chr1_12244325	trans	No	Ectopically Parting Cells	High penetrance of seedling lethality on soil; Curled, thick cotyledons; Short hypocotyls; Short roots; Increased lateral root number; Pale, bleached, small rosette leaves; Complete loss of branching; Severely reduced fertility; Fragile cotyledons	A. Marchant	2005
AT4G00650	FRI	chr1_16822116/chr4_259252	trans/cis	No	Frigida	Altered vernalization requirement for flowering	C. Dean	2000
AT4G01500	NGA4	chr1_516502	trans	No	Ngatha	Altered pistil morphology	C. Ferrandiz	2009
AT4G02195	SYP42	chr4_974563	cis	No	Syntaxin of Plants	Complete male gametophyte defective	N. Raikhel	2001
AT4G03240	AtFH	chr4_1479106	trans	No	Frataxin	Embryo defective; Preglobular	D. Gomez-Casati	2007
AT4G05450	PGD6	chr4_2759845	cis	No	Pollen Germination Defective	Male and female gametophyte defective; Rare embryo defective (inferred)	S. McCormick	2009
AT4G05530	IBR1	chr4_2817353	cis	No	Indole-3-Butyric Acid Response	Insensitive to IBA	J. Bussell	2009
AT4G11150	EMB2448	chr4_6801368	cis	No	Embryo Defective	Embryo defective; Globular	D. Meinke	2003
AT4G14590	EMB2739	chr4_8374711/chr5_14551793	cis/trans	No	Embryo Defective	Embryo defective; Globular	D. Meinke	2003
AT4G15950	RDM2	chr4_9036335	cis	No	RNA-Directed DNA Methylation	Decreased DNA methylation	J. Zhu	2008
AT4G16845	VRN2	chr4_9475749	cis	No	Reduced Vernalization Response	Altered vernalization response	C. Dean	2001
AT4G16990	RLM3	chr4_9568061	cis	No	Resistance to Leptosphaeria Maculans	Susceptible to necrotrophic fungi	C. Dixelius	2008
AT4G18750	DOT4	chr4_10304955	cis	No	Defectively Organized Tributaries	Short roots; Small rosette; Abnormal leaf morphology	T. Nelson	2008
AT4G18960	AG	chr4_10381453	cis	No	Agamous	Homeotic floral transformations	E. Meyerowitz	1990
AT4G19040	EDR2	chr4_10430162	cis	No	Enhanced Disease Resistance	Resistant to powdery mildew	R. Innes	2005
AT4G19350	EMB3006	chr4_10562571	cis	No	Embryo Defective	Embryo defective; Preglobular / Globular	D. Meinke	2004
AT4G19490	AtVPS54	chr4_10616870	cis	No	VPS54 Homolog	Male and female gametophyte defective; Embryo defective (inferred)	S. Bonhomme	2008
AT4G20400	AtJmj4	chr4_11015485	cis	No	Jumonji	Early flowering independent of photoperiod	Y. Noh	2009
AT4G29860	EMB2757	chr4_14605507	cis	No	Embryo Defective	Embryo defective; Cotyledon	D. Meinke	2004
AT4G34620	SSR16	chr1_29284466	trans	No	Small Subunit Ribosomal Protein	Embryo defective; Transition	N. Fedoroff	1996
AT4G35520	MLH3	chr4_16865237	cis	No	MutL Protein Homolog	Reduced fertility	F. Franklin	2006
AT4G37270	HMA1	chr4_17552077	cis	No	Heavy Metal ATPase	Variegated leaves under high light	N. Rolland	2006
AT5G01410	RSR4	chr3_13292224	trans	No	Reduced Sugar Response	Pale green, slightly chlorotic rosette leaves; Short roots; Reduced fertility	T. Fitzpatrick	2006
AT5G02820	BIN5	chr5_638795	cis	No	Brassinosteroid Insensitive	Dwarf; Increased branching; Downward-bending leaves; Short petioles; Dark-grown seedlings are de-etiolated; Insensitive to brassinosteroids	J. Chory	2002
AT5G08370	AtAGAL2	chr5_2692864	cis	No	Alpha-Galactosidase	Curly rosette leaves: Late flowering	K. Krupinska	2007
AT5G10330	HISN6A	chr4_11121261	trans	No	Histidine Auxotroph	Null: Embryo defective; Preglobular; Knockdown: Short roots	D. Meinke	2003
AT5G12390	FIS1B	chr5_3837785	trans	No	Fission	Semi-dwarf; Abnormal mitochondria and peroxisome morphology	J. Hu	2008
AT5G13690	CYL1	chr3_16326916	trans	No	Cyclops	Embryo defective; Preglobular	M. Devic	2008
AT5G14250	FUS11	chr5_4600661	cis	No	Fusca	Seedling lethal; Red seedlings due anthocyanin accumulation	X. Deng	2001
AT5G15920	EMB2782	chr4_6804353/chr5_5208450	trans/cis	No	Embryo Defective	Embryo defective; Preglobular	D. Meinke	2008
AT5G17420	IRX3	chr1_29311910	trans	No	Irregular Xylem	Collapsed xylem; Cellulose-deficient secondary walls	S. Turner	1999
AT5G20240	PI	chr3_12987992	trans	No	Pistillata	Homeotic floral transformations	E. Meyerowitz	1994
AT5G20350	TIP1	chr5_6876585	cis	No	Tip Growth Defective	Male gametophyte defective; Homozygotes are viable: Semi-dwarf; Small rosette; Reduced male fertility; Late flowering; Early senescence; Short, branched root hairs	S. Ford	1993

AT5G20730	NPH4	chr5_7044231	cis	No	Non-Phototropic Hypocotyl	Altered inflorescence gravitropism; Reduced phototropism	E. Liscum	2000
AT5G20850	AtRAD51	chr1_11531283	trans	No	RAS Associated with Diabetes Protein	Completely male and female sterile due to defects in meiosis	B. Reiss	2004
AT5G23010	MAM1	chr5_7700167	cis	No	Methylthioalkylmalate Synthase	Abnormal glucosinolate composition	T. Mitchell-Olds	2001
AT5G23570	SGS3	chr5_7938150	cis	No	Suppressor of Gene Silencing	Susceptible to viral infection	H. Vaucheret	2000
AT5G24310	ABIL3	chr5_8273614	cis	No	ABL Interactor-Like Protein	Distorted trichomes	J. Uhrig	2010
AT5G26240	CLC-D	chr5_9190048	cis	No	Chloride Channel D	Short roots; Sensitive to concanamycin A (vacuole proton pump inhibitor)	U. Ludwig	2007
AT5G34850	PAP26	chr5_13108258	cis	No	Purple Acid Phosphatase	Low phosphate levels; Sensitive to phosphate starvation	W. Plaxton	2010
AT5G35840	PHYC	chr5_14009659	cis	No	Phytochrome C	Long hypocotyl under red light	P. Quail	2002
AT5G37055	SEF	chr5_14642272	cis	No	Serrated Leaves and Early Flowering	Serrated leaves; Increased petal number; Small siliques; Early flowering	I. Lee	2007
AT5G39710	EMB2745	chr5_15895781	cis	No	Embryo Defective	Embryo defective; Cotyledon	D. Meinke	2003
AT5G41150	UVH1	chr5_16469400	cis	No	Ultraviolet Hypersensitive	Early senescence; Sensitive to UV light and ionizing radiation	D. Mount	2000
AT5G42790	ARS5	chr3_15887691	trans	No	Arsenic Tolerance	Resistant to arsenic	J. Schroeder	2009
AT5G43940	HOT5	chr5_17684842	cis	No	Sensitive to Hot Temperatures	Semi-dwarf; Increased branching; Few rosette leaves; Distorted, pale green leaves; Reduced fertility; Sensitive to high temperature; Lethal when grown on nutrient plates	E. Vierling	2008
AT5G44750	REV1	chr5_18049110	cis	No	Reversionless	Sensitive to UV-B light	S. Takahashi	2008
AT5G45260	RRS1	chr5_18327098	cis	No	Resistance to Ralstonia solanacearum	Susceptible to fungal infection	Y. Narusaka	2009
AT5G48670	FEM111	chr5_19739149	cis	No		Complete female gametophyte defective	G. Drews	2006
AT5G49510	PFD3	chr5_20080369	cis	No	Prefoldin	Dwarf; Slow growth; Slightly darker green; Short hypocotyl; Late flowering; Abnormal pavement cell morphology and microtubule development; Sensitive to salt	J. Salinas	2009
AT5G49930	EMB1441	chr5_20314076	cis	No	Embryo Defective	Embryo defective; Globular	D. Meinke	2002
AT5G54260	MRE11	chr5_1280017	trans	No	Meiotic Recombination	Dwarf; Sterile; Long telomeres; Sensitive to genotoxic stress	P. Bundock	2002
AT5G54650	FH5	chr5_21426099	NA	No	Formin Homology	Delayed endosperm cellularization; No other phenotypes detected	F. Berger	2005
AT5G55170	SUM3	chr4_616041	trans	No	Small Ubiquitin-Like Modifier	Late flowering independent of photoperiod	F. Takken	2010
AT5G55810	AtNMNAT	chr5_22585634	cis	No	Nicotinate/Nicotinamide Mononucleotide Adenyltransferase	Male gametophyte defective; Rare embryo defective	H. Uchimiya	2007
AT5G57880	MPS1	chr5_23449524	cis	No	Multipolar Spindle	Reduced male and female fertility	Z. Yang	2009
AT5G58600	PMR5	chr5_23680788	cis	No	Powdery Mildew Resistant	Short, rounded leaves; Elevated pectin and uronic acid levels in cell wall; Resistant to fungal infection	S. Sommerville	2004
AT5G60410	AtSIZ1	chr5_24292611	cis	No		Sensitive to phosphate starvation	P. Hasegawa	2005
AT5G62310	IRE	chr5_25075437	trans	No	Incomplete Root Hair Elongation	Short root hairs	K. Okada	2002
AT5G64050	OVA3	chr5_25633453	cis	No	Ovule Abortion	Ovule abortion; Male and female gametophyte defective; Early embryo defective (inferred)	D. Meinke	2005
AT5G64440	AtFAAH	chr5_25766681	cis	No	Fatty Acid Amide Hydrolase	Short primary root; Narrow cotyledons; Short hypocotyl	E. Blancaflor	2006
AT5G66130	RAD17	chr5_26430031	cis	No	Radiation Sensitive	Sensitive to DNA damaging agents; Increased intrachromosomal recombination frequency	H. Puchta	2004

[a]SNP: Peak SNP in eQTL analysis; [b]Type: cis/trans = peak SNP located <>1Mb from expressed gene; [c]Replicated: eQTL replicated in Dubin collection of Swedish Accessions ; [d] Description of mutant phenotype: Description of the mutant phenotype from relevant publication; [e-f]: Individual involved with identification of gene responsible for mutant phenotype, along with date of publication or database release. See Materials and Methods section of Lloyd et al (2012).t for further clarification.

Table S6. 649 cis-eQTL detected in the population of 140 wild-collected *A. thaliana* accessions that were replicated in the population of 107 wild-collected Swedish *A. thaliana* accessions.

			Schmitz-data			*Dubin-data*		
Locus	[a]***SNP***	[b]***Genotype***	[c]***a±SE***	[d]***MAF***	[e]***P-value***	[c]***a±SE***	[d]***MAF***	[e]***P-value***
AT1G01355	chr1_133794	A/A	-0,51±0,09	0,14	2,24E-09	-0.36±0.09	0,07	2,94E-05
AT1G02000	chr1_346016	T/T	-0,52±0,09	0,44	9,38E-10	-0.53±0.1	0,18	6,45E-08
AT1G02050	chr1_360888	C/C	-0,79±0,09	0,35	1,60E-17	-0.77±0.11	0,30	5,43E-12
AT1G02260	chr1_442418	T/T	-0,66±0,09	0,08	1,14E-13	-0.62±0.1	0,40	1,49E-10
AT1G02300	chr1_454505	T/T	-0,35±0,08	0,20	4,13E-05	-0.42±0.1	0,22	1,63E-05
AT1G02770	chr1_474285	A/A	0,49±0,11	0,11	6,33E-06	0.3±0.1	0,31	2,72E-03
AT1G02850	chr1_677970	A/A	0,26±0,09	0,09	2,18E-03	0.46±0.1	0,07	1,99E-06
AT1G03180	chr1_794740	G/G	0,42±0,09	0,06	1,88E-06	0.41±0.1	0,12	2,08E-05
AT1G03230	chr1_787587	A/A	0,38±0,08	0,57	6,46E-06	0.61±0.1	0,22	2,86E-10
AT1G03430	chr1_847854	A/A	-0,65±0,11	0,11	2,50E-09	-0.61±0.11	0,07	5,02E-08
AT1G03905	chr1_993375	G/G	0,8±0,1	0,06	9,48E-17	0.79±0.11	0,48	1,33E-13
AT1G04090	chr1_926370	T/T	0,32±0,1	0,06	1,02E-03	0.44±0.1	0,37	4,45E-06
AT1G04425	chr1_1193354	T/T	0,59±0,08	0,27	2,52E-12	0.73±0.1	0,33	2,53E-14
AT1G05550	chr1_1737628	T/T	0,51±0,12	0,46	1,97E-05	0.52±0.1	0,06	1,09E-07
AT1G05720	chr1_1717336	A/A	-0,49±0,09	0,44	2,43E-07	-0.68±0.12	0,40	8,48E-09
AT1G05835	chr1_1762555	G/G	-0,44±0,08	0,08	1,98E-07	-0.6±0.1	0,40	1,01E-09
AT1G06640	chr1_2034485	G/G	-0,58±0,14	0,17	3,90E-05	-0.92±0.17	0,06	2,24E-08
AT1G07350	chr1_2260475	G/G	0,51±0,08	0,22	1,62E-09	0.42±0.1	0,30	1,59E-05
AT1G07660	chr1_2378193	A/A	0,79±0,12	0,08	7,30E-12	0.52±0.1	0,26	6,99E-08
AT1G07780	chr1_2378193	A/A	0,45±0,12	0,06	9,11E-05	0.51±0.09	0,38	5,49E-08
AT1G07790	chr1_2382624	T/T	0,65±0,12	0,06	2,19E-08	0.49±0.1	0,26	5,37E-07
AT1G09490	chr1_3075310	C/C	-0,39±0,1	0,59	2,06E-04	-0.44±0.13	0,19	4,27E-04
AT1G09500	chr1_3131332	C/C	0,22±0,1	0,16	2,27E-02	0.67±0.18	0,21	1,76E-04
AT1G10230	chr1_3405791	A/A	0,31±0,1	0,11	1,40E-03	0.86±0.19	0,48	1,08E-05
AT1G10865	chr1_3616706	A/A	-0,52±0,08	0,09	7,65E-10	-0.6±0.11	0,06	7,23E-08
AT1G11070	chr1_3693829	A/A	-0,71±0,13	0,12	3,15E-08	-0.27±0.11	0,22	9,74E-03
AT1G11180	chr1_3714563	C/C	0,34±0,12	0,49	5,06E-03	0.74±0.17	0,50	8,02E-06
AT1G11240	chr1_3758989	A/A	-0,62±0,1	0,11	1,74E-10	-0.45±0.1	0,08	1,22E-05
AT1G11280	chr1_3772921	T/T	-0,43±0,08	0,11	4,71E-07	-0.48±0.11	0,08	5,59E-06
AT1G11420	chr1_3850062	A/A	-0,68±0,13	0,43	1,17E-07	-0.4±0.1	0,38	2,76E-05
AT1G11800	chr1_3936486	T/T	-0,43±0,09	0,08	3,10E-06	-0.37±0.1	0,16	1,68E-04
AT1G11870	chr1_4002668	A/A	0,41±0,08	0,60	1,33E-06	0.45±0.1	0,29	1,73E-05
AT1G11880	chr1_4022150	A/A	-0,42±0,08	0,51	4,48E-07	-0.28±0.12	0,07	1,83E-02
AT1G12200	chr1_4132980	G/G	0,68±0,11	0,08	1,07E-09	0.69±0.1	0,21	1,61E-12
AT1G12230	chr1_4149174	G/G	0,68±0,13	0,15	3,05E-07	0.82±0.11	0,06	6,00E-14
AT1G12350	chr1_4207654	C/C	0,67±0,09	0,11	3,08E-14	0.44±0.1	0,07	4,68E-06
AT1G12530	chr1_4272302	G/G	-0,42±0,1	0,36	1,49E-05	-0.44±0.1	0,07	2,64E-05
AT1G12550	chr1_4273859	A/A	-0,54±0,08	0,08	1,93E-10	-0.73±0.1	0,07	3,11E-12
AT1G12750	chr1_4353910	C/C	-0,48±0,09	0,27	2,11E-07	-0.64±0.1	0,14	9,62E-11
AT1G12790	chr1_4361418	G/G	-0,77±0,09	0,26	3,29E-18	-0.67±0.1	0,29	1,28E-11
AT1G13580	chr1_4640900	G/G	-0,37±0,09	0,21	1,25E-05	-0.6±0.1	0,32	6,32E-10
AT1G13780	chr1_4735035	G/G	0,78±0,09	0,09	2,46E-17	0.73±0.11	0,21	3,07E-11
AT1G13820	chr1_4738415	G/G	0,68±0,13	0,07	1,48E-07	0.72±0.15	0,31	9,77E-07
AT1G14520	chr1_4972842	A/A	-0,82±0,17	0,17	1,85E-06	-0.67±0.12	0,38	5,37E-08
AT1G14700	chr1_5056701	T/T	-0,77±0,09	0,37	3,23E-16	-0.73±0.1	0,27	1,74E-14
AT1G15280	chr1_5261771	C/C	0,57±0,08	0,06	1,09E-11	0.36±0.11	0,07	5,69E-04
AT1G16160	chr1_5305118	T/T	-0,29±0,08	0,07	4,81E-04	-0.27±0.07	0,37	3,19E-05
AT1G16210	chr1_5602451	T/T	-0,53±0,1	0,55	5,37E-08	-0.46±0.13	0,25	3,67E-04
AT1G16340	chr1_5631781	G/G	-0,33±0,08	0,07	7,32E-05	-0.25±0.1	0,36	1,50E-02
AT1G16445	chr1_5632013	G/G	0,43±0,09	0,15	7,34E-07	0.33±0.12	0,49	4,45E-03
AT1G16900	chr1_6103841	A/A	0,71±0,14	0,06	2,04E-07	0.4±0.12	0,08	4,48E-04
AT1G17240	chr1_5897950	G/G	0,42±0,08	0,27	4,31E-07	0.31±0.08	0,37	1,39E-04
AT1G17270	chr1_5918999	C/C	0,4±0,09	0,48	4,65E-06	0.54±0.1	0,08	4,47E-08

AT1G17890	chr1_6155204	A/A	0,48±0,09	0,49	1,31E-08	0.47±0.1	0,07	1,33E-06
AT1G18773	chr1_6473466	C/C	0,76±0,1	0,10	6,20E-14	0.68±0.1	0,39	5,78E-12
AT1G18940	chr1_6554452	G/G	0,66±0,11	0,06	1,85E-09	0.67±0.13	0,35	1,80E-07
AT1G19400	chr1_6701737	T/T	-0,5±0,09	0,30	1,14E-07	-0.79±0.1	0,10	1,02E-15
AT1G20225	chr1_7012120	G/G	0,72±0,1	0,55	4,59E-12	0.52±0.15	0,11	7,08E-04
AT1G20490	chr1_7165949	T/T	-0,47±0,09	0,51	1,12E-07	-0.45±0.1	0,34	2,18E-06
AT1G20620	chr1_7198841	T/T	0,4±0,12	0,16	8,77E-04	0.29±0.1	0,44	2,46E-03
AT1G20693	chr1_7177247	A/A	-0,52±0,09	0,41	1,33E-08	-0.25±0.1	0,29	8,07E-03
AT1G21120	chr1_7398878	T/T	-0,42±0,09	0,10	1,43E-06	-0.6±0.09	0,38	2,02E-10
AT1G21210	chr1_7443462	G/G	0,84±0,13	0,37	8,55E-11	0.7±0.1	0,08	7,75E-13
AT1G22370	chr1_7901643	C/C	-0,3±0,09	0,24	3,57E-04	-0.41±0.1	0,41	4,35E-05
AT1G22440	chr1_7923369	G/G	0,52±0,1	0,34	4,16E-07	0.57±0.09	0,42	2,10E-10
AT1G22650	chr1_7991470	T/T	-0,26±0,09	0,31	4,58E-03	-0.58±0.1	0,21	1,45E-08
AT1G23120	chr1_8203729	A/A	0,22±0,09	0,11	1,48E-02	0.44±0.1	0,19	4,12E-06
AT1G23130	chr1_8264101	G/G	-0,26±0,09	0,54	3,93E-03	-0.56±0.11	0,50	1,44E-07
AT1G23140	chr1_8203853	C/C	-0,77±0,12	0,27	1,65E-10	-0.7±0.11	0,15	1,36E-10
AT1G23750	chr1_8402914	G/G	-0,37±0,09	0,38	2,11E-05	-0.4±0.1	0,27	8,24E-05
AT1G23850	chr1_8426708	G/G	-0,74±0,11	0,45	9,22E-12	-0.82±0.12	0,37	4,96E-12
AT1G23970	chr1_8481515	A/A	0,48±0,1	0,08	5,65E-07	0.4±0.1	0,39	4,11E-05
AT1G24240	chr1_8588436	C/C	0,61±0,09	0,08	2,19E-12	0.67±0.1	0,07	6,69E-12
AT1G24265	chr1_8622211	T/T	0,53±0,11	0,16	1,10E-06	0.47±0.12	0,21	4,93E-05
AT1G26200	chr1_8664505	G/G	0,41±0,1	0,27	6,27E-05	0.33±0.12	0,28	6,05E-03
AT1G26530	chr1_9200314	T/T	-0,26±0,09	0,51	3,29E-03	-0.66±0.13	0,06	1,25E-07
AT1G26920	chr1_9328434	A/A	0,47±0,09	0,09	6,41E-08	0.54±0.1	0,23	1,64E-07
AT1G26940	chr1_9340882	C/C	0,49±0,08	0,51	7,88E-09	0.32±0.1	0,06	7,32E-04
AT1G27190	chr1_9439514	G/G	0,5±0,09	0,24	4,71E-09	0.4±0.1	0,21	3,42E-05
AT1G27530	chr1_9559801	T/T	-0,46±0,1	0,26	4,14E-06	-0.2±0.1	0,07	4,11E-02
AT1G28620	chr1_10048508	C/C	-0,59±0,12	0,09	3,95E-07	-0.69±0.12	0,28	2,37E-09
AT1G28670	chr1_10077700	T/T	-0,32±0,14	0,43	1,97E-02	-0.65±0.12	0,23	6,76E-08
AT1G30050	chr3_18913580	C/C	-0,38±0,17	0,36	2,46E-02	-0.25±0.08	0,36	1,57E-03
AT1G30860	chr1_10985838	A/A	0,59±0,1	0,09	5,29E-09	0.45±0.1	0,20	5,29E-06
AT1G31200	chr1_11586591	A/A	-0,36±0,11	0,34	1,56E-03	-0.49±0.15	0,35	1,52E-03
AT1G31600	chr1_11314334	T/T	-0,62±0,11	0,06	5,73E-09	-0.6±0.1	0,31	7,41E-10
AT1G31750	chr1_11292268	T/T	0,33±0,1	0,36	8,99E-04	0.28±0.09	0,17	3,03E-03
AT1G32090	chr1_11540381	G/G	0,46±0,09	0,44	1,68E-07	0.3±0.1	0,38	3,11E-03
AT1G33080	chr1_11964044	G/G	-0,39±0,09	0,55	2,40E-05	-0.34±0.1	0,07	1,10E-03
AT1G33480	chr1_12150508	A/A	0,57±0,11	0,21	6,43E-07	0.54±0.11	0,35	6,92E-07
AT1G33790	chr1_12244324	T/T	0,39±0,09	0,51	5,72E-06	0.49±0.1	0,30	2,87E-07
AT1G33990	chr1_12351037	G/G	0,65±0,08	0,11	1,14E-14	0.45±0.1	0,23	4,62E-06
AT1G34210	chr1_12459258	C/C	0,51±0,09	0,09	5,89E-09	0.4±0.1	0,14	3,40E-05
AT1G34340	chr1_12533162	T/T	0,78±0,14	0,39	6,62E-08	0.53±0.13	0,06	2,48E-05
AT1G34480	chr1_12555439	G/G	0,25±0,09	0,21	9,43E-03	0.43±0.1	0,35	7,75E-06
AT1G34570	chr1_12656117	C/C	-0,69±0,11	0,14	3,67E-10	-0.65±0.11	0,07	7,31E-10
AT1G34630	chr1_12690160	A/A	-0,51±0,09	0,37	3,03E-08	-0.29±0.11	0,06	9,38E-03
AT1G35230	chr1_12808695	G/G	0,44±0,13	0,19	9,18E-04	0.68±0.16	0,42	1,13E-05
AT1G35320	chr1_12957332	G/G	-0,63±0,1	0,31	5,40E-10	-0.4±0.07	0,11	5,96E-08
AT1G35560	chr1_13117589	C/C	-0,5±0,09	0,24	5,13E-09	-0.67±0.13	0,31	9,24E-08
AT1G43245	chr1_16310196	A/A	-0,6±0,08	0,06	7,41E-13	-0.56±0.1	0,10	6,43E-09
AT1G43640	chr1_16441326	T/T	0,77±0,1	0,20	3,33E-14	0.72±0.1	0,43	1,74E-12
AT1G45170	chr1_17070377	T/T	0,31±0,1	0,14	2,24E-03	0.45±0.1	0,16	2,87E-06
AT1G47420	chr1_17396376	T/T	-0,55±0,1	0,07	1,09E-07	-0.34±0.12	0,46	4,55E-03
AT1G47480	chr1_17418151	G/G	-0,51±0,09	0,85	5,34E-08	-0.4±0.1	0,15	3,79E-05
AT1G47530	chr1_17454430	G/G	0,52±0,1	0,19	5,27E-08	0.44±0.1	0,07	1,98E-05
AT1G48380	chr1_17879580	A/A	0,71±0,11	0,19	3,06E-11	0.41±0.1	0,13	2,25E-05
AT1G48605	chr1_18011492	C/C	0,37±0,09	0,09	3,77E-05	0.36±0.1	0,07	2,48E-04
AT1G48740	chr1_18026575	G/G	0,46±0,1	0,19	1,01E-05	0.47±0.09	0,45	3,88E-07
AT1G49630	chr1_18370101	G/G	-0,66±0,08	0,10	5,11E-15	-0.61±0.1	0,37	1,04E-09

AT1G49980	chr1_18507818	T/T	-0,74±0,09	0,27	5,46E-17	-0.71±0.1	0,14	1,90E-13
AT1G51860	chr1_19395243	G/G	-0,58±0,14	0,52	3,59E-05	-0.41±0.09	0,23	8,43E-06
AT1G52290	chr1_19459971	A/A	-0,62±0,12	0,44	3,10E-07	-0.6±0.1	0,08	1,22E-08
AT1G52550	chr1_19574670	C/C	0,74±0,14	0,27	5,44E-08	0.78±0.12	0,17	1,38E-11
AT1G52590	chr1_19553810	A/A	0,51±0,11	0,09	7,98E-06	0.56±0.13	0,28	2,08E-05
AT1G52710	chr1_19414665	A/A	-0,38±0,1	0,49	8,93E-05	-0.35±0.11	0,08	2,22E-03
AT1G52800	chr1_19659309	A/A	-0,58±0,08	0,11	9,00E-12	-0.58±0.09	0,27	7,95E-11
AT1G53080	chr1_19738403	C/C	0,32±0,08	0,07	1,26E-04	0.24±0.09	0,17	9,05E-03
AT1G53830	chr1_20100295	C/C	-0,66±0,09	0,25	2,83E-14	-0.51±0.12	0,47	1,07E-05
AT1G54040	chr1_20157965	T/T	-0,8±0,16	0,09	1,00E-06	-0.79±0.12	0,46	1,84E-10
AT1G54050	chr1_20176520	A/A	0,49±0,09	0,08	8,60E-08	0.79±0.11	0,21	6,19E-12
AT1G54260	chr1_20588156	A/A	-0,83±0,18	0,09	4,49E-06	-0.4±0.2	0,49	4,80E-02
AT1G55320	chr1_20635146	A/A	-0,54±0,09	0,06	1,58E-09	-0.29±0.1	0,37	3,65E-03
AT1G56120	chr1_20993126	G/G	-0,66±0,08	0,21	3,70E-15	-0.51±0.1	0,29	1,29E-07
AT1G56130	chr1_20985936	A/A	-0,54±0,08	0,08	1,92E-10	-0.4±0.09	0,20	1,96E-05
AT1G57600	chr1_21335444	G/G	0,63±0,12	0,10	2,72E-07	0.4±0.1	0,36	2,95E-05
AT1G57770	chr1_21394855	C/C	0,68±0,13	0,07	6,95E-08	0.42±0.1	0,28	2,13E-05
AT1G58270	chr1_21614442	C/C	0,66±0,09	0,36	1,36E-14	0.78±0.09	0,46	2,35E-18
AT1G58280	chr1_21614442	C/C	0,65±0,09	0,54	5,45E-14	0.61±0.11	0,39	8,45E-09
AT1G58300	chr1_21674226	C/C	-0,57±0,11	0,31	4,06E-07	-0.3±0.09	0,13	1,12E-03
AT1G59840	chr1_22029068	T/T	-0,35±0,09	0,24	6,54E-05	-0.51±0.11	0,07	2,40E-06
AT1G60620	chr1_22292954	T/T	-0,27±0,08	0,47	1,74E-03	-0.47±0.11	0,47	9,54E-06
AT1G60630	chr1_22341984	C/C	-0,39±0,08	0,52	3,73E-06	-0.47±0.1	0,46	1,08E-06
AT1G60700	chr1_22359845	G/G	-0,34±0,09	0,09	9,47E-05	-0.42±0.11	0,08	7,78E-05
AT1G60730	chr1_22358494	A/A	0,49±0,09	0,06	1,75E-08	0.47±0.1	0,30	3,07E-06
AT1G60740	chr1_24559034	A/A	-0,48±0,1	0,11	7,98E-07	-0.61±0.11	0,06	1,50E-08
AT1G61230	chr1_22577822	A/A	0,46±0,09	0,37	6,90E-08	0.37±0.08	0,36	1,41E-05
AT1G61280	chr1_22703776	C/C	-0,41±0,11	0,08	3,22E-04	-0.47±0.14	0,47	1,07E-03
AT1G61380	chr1_21966164	C/C	-0,27±0,08	0,06	1,18E-03	-0.22±0.1	0,40	3,22E-02
AT1G61500	chr1_22686463	A/A	-0,5±0,09	0,06	6,18E-09	-0.4±0.09	0,49	8,95E-06
AT1G63000	chr1_23342373	G/G	0,41±0,13	0,11	9,83E-04	0.53±0.12	0,35	6,57E-06
AT1G63110	chr1_23408542	G/G	0,55±0,14	0,06	1,60E-04	0.42±0.12	0,36	5,92E-04
AT1G63180	chr1_23461440	T/T	-0,2±0,09	0,11	2,48E-02	-0.62±0.13	0,07	2,38E-06
AT1G63855	chr1_23701054	G/G	-0,67±0,11	0,11	1,52E-10	-0.25±0.1	0,07	8,63E-03
AT1G63900	chr1_23718116	T/T	0,66±0,1	0,43	3,18E-12	0.43±0.1	0,06	2,20E-05
AT1G64150	chr1_23813948	A/A	0,63±0,09	0,43	2,46E-13	0.6±0.1	0,07	2,73E-09
AT1G64355	chr1_23887201	G/G	-0,47±0,09	0,09	1,95E-07	-0.35±0.1	0,37	5,26E-04
AT1G64840	chr1_24090730	C/C	0,44±0,1	0,08	2,11E-05	0.39±0.1	0,13	1,06E-04
AT1G64970	chr1_24136076	G/G	0,5±0,09	0,09	1,82E-08	0.46±0.1	0,06	1,86E-06
AT1G65080	chr1_24176717	T/T	0,53±0,09	0,24	4,23E-09	0.52±0.1	0,39	6,46E-08
AT1G65200	chr1_24223190	T/T	0,41±0,09	0,11	3,90E-06	0.43±0.09	0,46	3,94E-06
AT1G66700	chr1_24878797	T/T	-0,62±0,1	0,40	1,28E-10	-0.55±0.12	0,06	2,38E-06
AT1G66860	chr1_24948678	T/T	0,63±0,09	0,06	1,51E-13	0.47±0.09	0,28	3,17E-08
AT1G66930	chr1_24948678	T/T	0,58±0,09	0,24	1,05E-11	0.11±0.05	0,07	3,02E-02
AT1G66980	chr1_24998827	G/G	0,45±0,09	0,18	2,99E-07	0.43±0.1	0,49	1,63E-05
AT1G67460	chr1_25276982	G/G	0,45±0,11	0,06	8,05E-05	0.26±0.07	0,38	9,15E-05
AT1G69400	chr1_26088853	T/T	0,39±0,08	0,33	4,35E-06	0.39±0.1	0,21	7,35E-05
AT1G69485	chr1_26117628	T/T	-0,56±0,09	0,14	9,09E-10	-0.41±0.09	0,29	1,10E-05
AT1G69540	chr1_26147776	A/A	-0,55±0,1	0,09	3,22E-08	-0.28±0.12	0,23	1,91E-02
AT1G70830	chr1_26742845	T/T	-0,38±0,1	0,12	2,12E-04	-0.3±0.1	0,30	1,65E-03
AT1G70890	chr1_26712510	G/G	0,21±0,09	0,09	2,60E-02	0.38±0.1	0,17	2,46E-04
AT1G70985	chr1_26766444	A/A	0,56±0,12	0,13	3,56E-06	0.29±0.09	0,06	2,43E-03
AT1G72020	chr1_27109058	T/T	-0,32±0,09	0,08	4,88E-04	-0.34±0.1	0,43	4,05E-04
AT1G72030	chr1_27109250	A/A	0,41±0,09	0,08	1,17E-05	0.43±0.1	0,43	9,01E-06
AT1G72130	chr1_27136812	G/G	0,57±0,09	0,10	1,68E-09	0.72±0.13	0,15	1,16E-08
AT1G72140	chr1_27171837	T/T	0,27±0,08	0,22	1,53E-03	0.36±0.11	0,24	8,83E-04
AT1G72190	chr1_27203172	A/A	-0,31±0,08	0,11	2,16E-04	-0.3±0.1	0,06	3,99E-03

AT1G72800	chr1_27396038	G/G	0,48±0,09	0,76	3,20E-08	0.46±0.11	0,50	1,24E-05
AT1G73570	chr1_27648874	G/G	-0,23±0,08	0,09	7,18E-03	-0.37±0.12	0,25	1,48E-03
AT1G74280	chr1_27934205	T/T	0,48±0,08	0,46	1,57E-08	0.43±0.1	0,07	6,09E-06
AT1G74290	chr1_27934467	A/A	-0,83±0,14	0,06	1,08E-09	-0.51±0.12	0,36	1,96E-05
AT1G74780	chr1_28105706	G/G	-0,64±0,14	0,06	2,34E-06	-0.21±0.1	0,34	3,28E-02
AT1G75560	chr1_28371780	T/T	-0,4±0,08	0,51	2,61E-06	-0.29±0.1	0,10	2,41E-03
AT1G76300	chr1_28639230	A/A	0,54±0,13	0,27	3,79E-05	0.45±0.1	0,38	7,42E-06
AT1G76530	chr1_28714983	T/T	0,43±0,09	0,56	3,74E-07	0.38±0.1	0,34	1,16E-04
AT1G76850	chr1_28859683	G/G	0,36±0,09	0,94	3,98E-05	0.44±0.1	0,11	4,78E-06
AT1G77230	chr1_28965278	G/G	0,55±0,08	0,06	9,09E-11	0.23±0.1	0,30	1,99E-02
AT1G77720	chr1_29210222	G/G	0,81±0,11	0,16	6,47E-14	0.41±0.1	0,28	3,48E-05
AT1G78450	chr1_29511437	A/A	-0,71±0,11	0,05	1,63E-10	-0.37±0.1	0,37	4,31E-04
AT1G78820	chr1_29638971	G/G	0,33±0,09	0,11	3,23E-04	0.37±0.1	0,48	1,10E-04
AT1G78970	chr1_29703723	C/C	0,57±0,11	0,12	7,56E-08	0.42±0.13	0,22	1,61E-03
AT1G79529	chr1_29915978	G/G	-0,69±0,11	0,08	1,35E-10	-0.48±0.1	0,26	1,84E-06
AT1G80555	chr1_30287050	G/G	-0,79±0,09	0,54	1,66E-19	-0.73±0.1	0,25	2,81E-13
AT1G80860	chr1_30383702	A/A	-0,43±0,08	0,54	3,52E-07	-0.39±0.1	0,46	5,18E-05
AT2G01090	chr2_81914	T/T	0,52±0,09	0,07	3,21E-09	0.72±0.09	0,06	3,32E-14
AT2G02240	chr2_593637	A/A	0,33±0,11	0,31	2,27E-03	0.5±0.1	0,17	1,70E-07
AT2G02590	chr2_705249	A/A	0,65±0,09	0,43	1,56E-12	0.55±0.11	0,09	2,89E-07
AT2G02770	chr2_761410	A/A	0,42±0,1	0,21	5,32E-05	0.47±0.11	0,07	9,06E-06
AT2G02960	chr2_861154	G/G	-0,19±0,08	0,11	2,28E-02	-0.53±0.1	0,41	1,06E-07
AT2G04170	chr2_1424281	A/A	0,71±0,09	0,10	2,73E-15	0.6±0.1	0,17	6,11E-10
AT2G04800	chr2_1688388	T/T	-0,57±0,12	0,06	1,17E-06	-0.44±0.09	0,24	6,05E-07
AT2G14090	chr2_5930277	C/C	0,52±0,1	0,26	1,78E-07	0.37±0.09	0,38	4,69E-05
AT2G15042	chr2_6511737	T/T	-0,79±0,1	0,79	7,85E-16	-0.43±0.08	0,14	1,72E-08
AT2G15310	chr2_6655004	G/G	-0,57±0,08	0,15	9,22E-12	-0.39±0.1	0,42	4,00E-05
AT2G16530	chr2_7163650	G/G	-0,78±0,09	0,07	1,24E-17	-0.71±0.1	0,08	2,15E-13
AT2G16595	chr2_7197748	A/A	-0,41±0,08	0,46	1,18E-06	-0.36±0.1	0,07	4,30E-04
AT2G17320	chr2_7549380	C/C	0,7±0,11	0,44	2,83E-11	0.55±0.1	0,17	9,82E-09
AT2G17630	chr2_7666708	T/T	0,51±0,09	0,44	1,00E-08	0.72±0.1	0,17	2,02E-13
AT2G18100	chr2_7863028	A/A	0,51±0,09	0,08	1,69E-09	0.46±0.11	0,47	1,72E-05
AT2G18210	chr2_7923730	C/C	-0,73±0,12	0,16	7,45E-10	-0.5±0.17	0,21	3,55E-03
AT2G19240	chr2_8349464	G/G	0,56±0,1	0,51	6,51E-09	0.45±0.09	0,32	1,27E-06
AT2G19310	chr2_8372701	T/T	-0,45±0,13	0,08	2,99E-04	-0.8±0.12	0,49	1,50E-11
AT2G19400	chr2_8403801	A/A	-0,73±0,08	0,30	4,91E-18	-0.76±0.14	0,32	4,48E-08
AT2G19910	chr2_8600731	A/A	-0,66±0,1	0,14	1,94E-11	-0.17±0.08	0,07	2,32E-02
AT2G21080	chr2_9036397	A/A	-0,63±0,11	0,13	3,95E-09	-0.79±0.13	0,42	3,68E-09
AT2G21130	chr2_9060377	C/C	0,52±0,09	0,32	2,57E-08	0.41±0.1	0,06	3,32E-05
AT2G21830	chr2_9322464	G/G	-0,53±0,1	0,45	3,05E-08	-0.26±0.11	0,21	1,92E-02
AT2G21840	chr2_9323098	C/C	0,37±0,08	0,17	1,38E-05	0.4±0.1	0,21	3,30E-05
AT2G21860	chr2_9521419	T/T	-0,43±0,08	0,06	4,09E-07	-0.37±0.1	0,11	2,30E-04
AT2G22905	chr2_9752751	A/A	0,53±0,08	0,36	2,88E-10	0.39±0.09	0,38	1,75E-05
AT2G22970	chr2_9774878	A/A	-0,66±0,1	0,18	2,48E-11	-0.51±0.11	0,34	3,24E-06
AT2G22980	chr2_9773888	A/A	-0,57±0,08	0,18	1,33E-11	-0.62±0.12	0,20	5,60E-07
AT2G23620	chr2_10049585	T/T	0,61±0,09	0,08	4,89E-11	0.45±0.1	0,43	7,32E-06
AT2G24040	chr2_10224549	T/T	-0,52±0,09	0,10	1,71E-09	-0.37±0.1	0,15	2,73E-04
AT2G24190	chr2_10282817	A/A	-0,5±0,08	0,44	3,07E-09	-0.48±0.1	0,07	1,14E-06
AT2G25220	chr2_10744960	C/C	0,48±0,08	0,31	1,10E-08	0.43±0.1	0,22	6,49E-06
AT2G25260	chr2_10758402	G/G	-0,49±0,08	0,31	1,02E-08	-0.41±0.1	0,11	2,67E-05
AT2G25310	chr2_10775680	G/G	0,55±0,09	0,19	1,94E-09	0.61±0.1	0,33	3,09E-10
AT2G25355	chr2_10801269	T/T	0,59±0,09	0,11	7,00E-12	0.69±0.11	0,30	1,21E-09
AT2G25590	chr2_10892004	T/T	-0,49±0,09	0,07	6,60E-08	-0.39±0.1	0,21	4,62E-05
AT2G27190	chr2_11622390	A/A	-0,63±0,09	0,18	1,54E-13	-0.43±0.1	0,08	8,85E-06
AT2G27360	chr2_11689092	G/G	0,46±0,09	0,14	4,96E-08	0.32±0.1	0,07	1,17E-03
AT2G27385	chr2_11707680	T/T	-0,47±0,09	0,36	4,95E-07	-0.27±0.1	0,38	4,56E-03
AT2G27650	chr2_11797697	T/T	-0,53±0,08	0,32	1,56E-10	-0.61±0.13	0,44	3,66E-06

AT2G27960	chr2_11920870	G/G	-0,71±0,1	0,14	4,06E-13	-0.42±0.1	0,29	2,77E-05
AT2G28130	chr2_11993201	G/G	-0,6±0,12	0,11	5,89E-07	-0.54±0.11	0,14	4,79E-07
AT2G28560	chr2_12239210	C/C	0,97±0,16	0,10	4,87E-10	0.41±0.09	0,23	1,07E-05
AT2G29160	chr2_12623091	G/G	0,42±0,09	0,18	5,59E-06	0.62±0.13	0,26	7,29E-07
AT2G29370	chr2_12200958	C/C	-0,31±0,14	0,13	2,39E-02	-0.45±0.13	0,30	4,71E-04
AT2G29440	chr2_12622677	T/T	0,5±0,09	0,29	7,81E-09	0.56±0.1	0,32	2,81E-08
AT2G29580	chr2_12646569	A/A	-0,42±0,09	0,47	4,79E-06	-0.44±0.12	0,29	1,87E-04
AT2G29950	chr2_12786863	T/T	-0,34±0,09	0,09	8,42E-05	-0.5±0.12	0,07	2,54E-05
AT2G30230	chr2_12893401	T/T	-0,18±0,09	0,14	3,93E-02	-0.36±0.1	0,16	4,47E-04
AT2G30480	chr2_12986516	T/T	-0,83±0,1	0,06	2,54E-17	-0.59±0.11	0,37	3,15E-07
AT2G31250	chr2_13255966	A/A	-0,45±0,12	0,08	2,27E-04	-0.49±0.09	0,42	2,74E-07
AT2G31560	chr2_13426709	C/C	0,46±0,12	0,06	1,38E-04	0.53±0.1	0,26	6,47E-08
AT2G32340	chr2_13732366	T/T	-0,63±0,09	0,06	3,26E-12	-0.46±0.09	0,13	1,02E-06
AT2G32840	chr2_13915905	G/G	0,5±0,13	0,13	7,90E-05	0.43±0.1	0,34	6,16E-06
AT2G32940	chr2_13977350	A/A	-0,54±0,08	0,31	1,62E-10	-0.53±0.1	0,20	1,66E-07
AT2G33600	chr2_14484119	T/T	-0,5±0,14	0,10	2,72E-04	-0.48±0.12	0,15	8,42E-05
AT2G34840	chr2_14700261	T/T	-0,94±0,14	0,24	2,18E-11	-0.83±0.12	0,09	7,61E-12
AT2G35060	chr2_14782595	T/T	-0,57±0,12	0,07	8,30E-07	-0.54±0.1	0,20	2,01E-08
AT2G35520	chr2_14920429	G/G	-0,69±0,09	0,08	2,04E-15	-0.51±0.13	0,09	4,72E-05
AT2G35635	chr2_14982465	G/G	-0,53±0,11	0,06	1,08E-06	-0.75±0.11	0,15	9,90E-12
AT2G35690	chr2_14999577	A/A	0,46±0,09	0,16	4,24E-07	0.22±0.1	0,42	2,46E-02
AT2G35738	chr2_15026659	G/G	0,7±0,12	0,06	1,57E-09	0.49±0.11	0,26	1,61E-05
AT2G35810	chr2_15002274	T/T	-0,46±0,09	0,07	3,68E-07	-0.62±0.15	0,28	4,30E-05
AT2G35830	chr2_15028694	A/A	0,55±0,1	0,07	1,18E-08	0.25±0.12	0,32	4,07E-02
AT2G36050	chr2_15138413	C/C	0,51±0,08	0,47	1,87E-09	0.33±0.1	0,27	7,76E-04
AT2G36590	chr2_15345697	C/C	-0,71±0,1	0,29	5,13E-12	-0.43±0.11	0,49	1,09E-04
AT2G37370	chr2_15679172	T/T	-0,5±0,08	0,09	3,22E-09	-0.66±0.1	0,07	3,50E-11
AT2G38430	chr2_16056730	A/A	0,38±0,09	0,22	1,36E-05	0.45±0.09	0,20	9,00E-07
AT2G38610	chr2_16145325	G/G	-0,46±0,13	0,55	3,63E-04	-0.46±0.1	0,07	7,70E-06
AT2G38720	chr2_16159606	G/G	0,51±0,1	0,06	1,43E-07	0.56±0.12	0,29	1,64E-06
AT2G38780	chr2_16205849	C/C	0,61±0,08	0,09	5,34E-13	0.42±0.1	0,29	2,08E-05
AT2G39110	chr2_16294335	C/C	0,41±0,08	0,06	1,66E-06	0.35±0.09	0,26	1,83E-04
AT2G40570	chr2_16940810	G/G	0,81±0,11	0,07	1,89E-13	0.52±0.12	0,10	9,76E-06
AT2G41050	chr2_17121356	G/G	-0,33±0,08	0,07	7,70E-05	-0.47±0.1	0,28	9,95E-07
AT2G41160	chr2_17150460	G/G	0,49±0,08	0,21	5,22E-09	0.31±0.1	0,19	1,78E-03
AT2G41340	chr2_17243707	T/T	-0,69±0,14	0,07	4,17E-07	-0.52±0.11	0,07	2,23E-06
AT2G41470	chr2_17299327	G/G	0,36±0,13	0,19	4,11E-03	0.48±0.1	0,36	6,76E-07
AT2G41650	chr2_17363240	C/C	-0,49±0,1	0,34	9,17E-07	-0.53±0.1	0,28	2,85E-08
AT2G41660	chr2_17381872	C/C	0,6±0,11	0,11	1,85E-08	0.52±0.12	0,32	2,87E-05
AT2G41780	chr2_17439085	G/G	-0,51±0,09	0,19	3,07E-09	-0.44±0.1	0,29	5,78E-06
AT2G42240	chr2_17639893	G/G	-0,34±0,12	0,06	5,88E-03	-0.63±0.19	0,22	1,21E-03
AT2G43500	chr2_18060212	C/C	0,65±0,1	0,07	2,73E-11	0.6±0.1	0,20	9,13E-09
AT2G43540	chr2_18071235	T/T	-0,67±0,11	0,14	1,07E-09	-0.47±0.1	0,49	4,38E-06
AT2G43720	chr2_18117794	G/G	-0,41±0,1	0,07	2,72E-05	-0.42±0.1	0,42	1,71E-05
AT2G43920	chr2_18173085	G/G	-0,44±0,09	0,21	5,08E-07	-0.55±0.09	0,29	4,93E-09
AT2G44210	chr2_18281511	G/G	0,82±0,13	0,06	5,88E-10	0.59±0.1	0,42	1,12E-08
AT2G44290	chr2_18305617	A/A	0,43±0,08	0,06	3,54E-07	0.44±0.1	0,21	7,45E-06
AT2G44360	chr2_18321698	A/A	0,63±0,08	0,06	1,06E-13	0.48±0.1	0,07	6,44E-07
AT2G44530	chr2_18395070	A/A	-0,38±0,09	0,39	7,61E-06	-0.49±0.11	0,08	8,84E-06
AT2G44690	chr2_18429206	G/G	0,69±0,08	0,06	3,10E-16	0.48±0.1	0,16	8,57E-07
AT2G45150	chr2_18613825	T/T	0,42±0,09	0,59	1,87E-06	0.61±0.11	0,06	5,13E-08
AT2G45920	chr2_18895426	T/T	-0,63±0,09	0,13	2,65E-12	-0.45±0.1	0,39	2,49E-06
AT2G46450	chr2_19084290	G/G	-0,31±0,09	0,11	6,15E-04	-0.43±0.1	0,06	2,61E-05
AT2G46930	chr2_19304723	T/T	-0,58±0,18	0,43	1,45E-03	-0.33±0.11	0,14	2,74E-03
AT2G47600	chr2_19519015	A/A	0,48±0,09	0,65	1,61E-08	0.56±0.1	0,25	5,19E-09
AT2G47630	chr2_19535380	T/T	-0,5±0,09	0,24	1,05E-07	-0.59±0.1	0,18	6,77E-10
AT3G01790	chr3_602512	A/A	-0,54±0,17	0,38	1,54E-03	-0.24±0.11	0,10	3,55E-02

AT3G02520	chr3_629989	A/A	-0,55±0,13	0,06	1,23E-05	-0.48±0.1	0,31	1,67E-06
AT3G02790	chr3_629989	A/A	-0,38±0,13	0,43	2,63E-03	-0.64±0.1	0,23	2,06E-10
AT3G02900	chr3_649418	C/C	0,49±0,08	0,06	4,98E-09	0.55±0.1	0,33	9,24E-09
AT3G03330	chr3_785985	G/G	0,38±0,08	0,48	5,59E-06	0.42±0.1	0,22	1,24E-05
AT3G04000	chr3_1037014	C/C	0,44±0,09	0,07	3,05E-07	0.43±0.1	0,31	9,22E-06
AT3G05140	chr3_1438382	T/T	-0,7±0,09	0,06	8,01E-15	-0.43±0.09	0,07	1,39E-06
AT3G05230	chr3_1484026	C/C	0,32±0,09	0,41	3,51E-04	0.38±0.1	0,07	7,31E-05
AT3G05685	chr3_1674158	T/T	0,98±0,14	0,48	1,14E-11	0.85±0.12	0,06	1,33E-12
AT3G06110	chr3_1842274	A/A	0,55±0,09	0,09	6,68E-10	0.52±0.1	0,08	3,72E-07
AT3G06145	chr3_1861208	C/C	0,67±0,09	0,32	1,23E-14	0.66±0.1	0,25	7,86E-12
AT3G06210	chr3_1916844	C/C	0,59±0,14	0,06	5,14E-05	0.67±0.15	0,48	5,53E-06
AT3G07200	chr3_2254013	A/A	-0,36±0,09	0,06	3,99E-05	-0.53±0.1	0,11	4,13E-08
AT3G07500	chr3_2392142	A/A	0,5±0,08	0,06	3,63E-09	0.43±0.1	0,27	4,94E-06
AT3G07525	chr3_2392193	C/C	-0,63±0,08	0,21	9,00E-14	-0.52±0.1	0,19	5,33E-08
AT3G08920	chr3_2719090	C/C	0,35±0,09	0,06	7,53E-05	0.49±0.1	0,32	4,35E-07
AT3G08970	chr3_2742245	C/C	0,3±0,09	0,08	9,02E-04	0.51±0.1	0,42	5,40E-07
AT3G08980	chr3_2742245	C/C	0,52±0,09	0,36	8,93E-09	0.64±0.1	0,33	3,26E-10
AT3G09480	chr3_2909694	G/G	0,31±0,15	0,06	3,85E-02	0.67±0.13	0,09	3,23E-07
AT3G09960	chr3_3061942	T/T	-0,54±0,1	0,06	9,14E-08	-0.28±0.09	0,14	2,34E-03
AT3G11210	chr3_3447117	A/A	-0,39±0,16	0,08	1,24E-02	-0.34±0.11	0,42	1,85E-03
AT3G11220	chr3_3517660	C/C	-0,54±0,09	0,46	2,58E-10	-0.34±0.1	0,37	4,30E-04
AT3G11530	chr3_3628662	G/G	-0,72±0,12	0,16	5,32E-09	-0.59±0.14	0,41	2,27E-05
AT3G12040	chr3_3838989	C/C	-0,58±0,13	0,19	4,02E-06	-0.62±0.15	0,25	1,99E-05
AT3G12460	chr3_3961828	A/A	-0,44±0,11	0,19	9,92E-05	-0.54±0.13	0,08	2,08E-05
AT3G12500	chr3_3958518	T/T	0,73±0,13	0,51	6,58E-09	0.79±0.14	0,07	3,10E-08
AT3G13640	chr3_4461443	C/C	0,61±0,14	0,08	8,29E-06	0.47±0.11	0,06	9,32E-06
AT3G13845	chr3_4559312	A/A	0,51±0,09	0,08	4,61E-09	0.4±0.1	0,06	2,98E-05
AT3G14020	chr3_4644022	C/C	-0,49±0,09	0,16	1,17E-08	-0.42±0.1	0,08	1,36E-05
AT3G14160	chr3_4697541	T/T	-0,48±0,09	0,08	2,59E-07	-0.26±0.1	0,11	8,43E-03
AT3G14172	chr3_4525271	A/A	-0,27±0,09	0,10	2,32E-03	-0.29±0.1	0,32	3,50E-03
AT3G14940	chr3_4988187	T/T	-0,36±0,08	0,92	1,51E-05	-0.46±0.1	0,07	2,16E-06
AT3G16700	chr3_5688112	G/G	0,73±0,1	0,07	4,94E-13	0.63±0.1	0,07	1,55E-10
AT3G17280	chr3_5888492	C/C	0,26±0,11	0,16	1,78E-02	0.55±0.12	0,09	2,04E-06
AT3G17450	chr3_5953850	A/A	0,33±0,1	0,12	1,72E-03	0.37±0.12	0,21	1,70E-03
AT3G18070	chr3_6179175	A/A	0,35±0,14	0,22	1,03E-02	0.58±0.17	0,41	4,24E-04
AT3G18145	chr3_6243655	A/A	-0,26±0,11	0,42	1,76E-02	-0.77±0.13	0,32	3,66E-09
AT3G18165	chr3_6193227	A/A	-0,48±0,09	0,59	1,63E-07	-0.33±0.1	0,06	7,93E-04
AT3G18485	chr3_6840933	A/A	-0,28±0,1	0,05	5,77E-03	-0.42±0.11	0,06	1,07E-04
AT3G18880	chr3_6513592	T/T	-0,75±0,14	0,53	1,55E-07	-0.39±0.11	0,25	4,49E-04
AT3G19390	chr3_6713747	T/T	0,42±0,12	0,11	3,86E-04	0.24±0.1	0,45	1,52E-02
AT3G20130	chr3_7026006	G/G	0,75±0,09	0,06	4,22E-16	0.73±0.11	0,14	3,27E-11
AT3G20420	chr3_7119760	C/C	0,57±0,1	0,06	1,30E-08	0.36±0.11	0,20	1,26E-03
AT3G21580	chr3_7608987	G/G	-0,82±0,12	0,17	1,92E-11	-0.36±0.11	0,28	1,60E-03
AT3G21690	chr3_7635436	A/A	-0,8±0,12	0,16	3,53E-11	-0.68±0.13	0,13	5,44E-07
AT3G22850	chr3_7946890	T/T	-0,64±0,13	0,07	1,11E-06	-0.43±0.19	0,20	2,75E-02
AT3G23100	chr3_8218794	T/T	0,44±0,09	0,12	3,40E-07	0.56±0.1	0,29	1,00E-08
AT3G23260	chr3_8325788	T/T	-0,47±0,12	0,06	8,74E-05	-0.36±0.11	0,40	1,83E-03
AT3G23325	chr3_8341521	C/C	-0,48±0,1	0,10	7,67E-07	-0.53±0.1	0,06	1,85E-07
AT3G23480	chr3_8476343	G/G	0,42±0,09	0,06	5,52E-06	0.42±0.11	0,17	6,69E-05
AT3G23560	chr3_8456654	G/G	-0,75±0,12	0,34	8,67E-10	-0.59±0.13	0,45	1,31E-05
AT3G24030	chr3_8346687	T/T	0,33±0,11	0,10	1,76E-03	0.33±0.12	0,42	3,99E-03
AT3G24070	chr3_8693279	C/C	-0,62±0,09	0,29	7,01E-13	-0.4±0.1	0,10	7,56E-05
AT3G24255	chr3_8802794	T/T	0,41±0,09	0,19	7,54E-06	0.27±0.09	0,21	2,70E-03
AT3G25010	chr3_9110240	C/C	0,25±0,11	0,14	2,40E-02	0.45±0.09	0,43	5,88E-07
AT3G25400	chr3_9212043	C/C	0,42±0,09	0,21	6,32E-07	0.32±0.1	0,17	8,73E-04
AT3G26165	chr3_9570707	G/G	-0,29±0,09	0,06	6,45E-04	-0.4±0.1	0,06	3,07E-05
AT3G26240	chr3_9629719	C/C	0,6±0,1	0,09	2,75E-09	0.4±0.09	0,36	1,74E-05

AT3G26280	chr3_9630842	C/C	-0,46±0,1	0,06	1,30E-06	-0.44±0.1	0,35	5,27E-06
AT3G26922	chr3_9930640	A/A	-0,39±0,09	0,17	1,48E-05	-0.33±0.1	0,07	6,93E-04
AT3G27340	chr3_10045557	A/A	0,2±0,08	0,37	2,00E-02	0.48±0.1	0,43	7,17E-07
AT3G27470	chr3_10163151	C/C	0,44±0,09	0,36	3,89E-07	0.36±0.1	0,19	2,66E-04
AT3G27930	chr3_9961973	G/G	-0,41±0,16	0,15	1,28E-02	-0.86±0.21	0,12	4,00E-05
AT3G28140	chr3_10472339	A/A	0,63±0,1	0,10	1,72E-10	0.54±0.13	0,12	2,69E-05
AT3G28880	chr3_10889704	C/C	-0,54±0,11	0,06	5,81E-07	-0.69±0.15	0,47	4,99E-06
AT3G29290	chr3_11245075	T/T	-0,61±0,11	0,12	8,37E-09	-0.39±0.11	0,25	4,85E-04
AT3G43210	chr3_15190906	A/A	-0,8±0,13	0,12	6,05E-10	-0.58±0.13	0,26	3,67E-06
AT3G43600	chr3_15534068	A/A	-0,58±0,14	0,06	4,06E-05	-0.4±0.1	0,12	3,94E-05
AT3G44100	chr3_15869786	T/T	0,43±0,09	0,24	3,73E-07	0.34±0.1	0,07	4,21E-04
AT3G45860	chr3_16867335	A/A	-0,76±0,09	0,12	1,36E-16	-0.65±0.09	0,06	1,72E-13
AT3G45890	chr3_16886045	A/A	0,82±0,17	0,24	1,53E-06	0.74±0.13	0,16	1,59E-08
AT3G46690	chr3_17199333	A/A	-0,46±0,09	0,09	9,61E-08	-0.43±0.09	0,33	1,06E-06
AT3G46710	chr3_17212160	T/T	0,73±0,08	0,24	8,06E-18	0.42±0.08	0,33	9,08E-08
AT3G47010	chr3_17310993	C/C	-0,33±0,11	0,06	2,99E-03	-0.53±0.12	0,10	6,26E-06
AT3G47050	chr3_17330843	G/G	0,38±0,1	0,24	2,51E-04	0.35±0.09	0,41	2,12E-04
AT3G47220	chr3_17423375	C/C	-0,45±0,09	0,06	6,52E-07	-0.59±0.09	0,10	7,44E-12
AT3G47730	chr3_17598837	G/G	-0,49±0,08	0,09	7,89E-09	-0.47±0.1	0,35	1,82E-06
AT3G48260	chr3_18362640	T/T	-0,38±0,09	0,09	1,74E-05	-0.24±0.09	0,40	7,14E-03
AT3G48680	chr3_18042587	A/A	-0,55±0,09	0,06	1,42E-10	-0.21±0.1	0,35	2,60E-02
AT3G49340	chr3_18295338	G/G	0,65±0,09	0,24	4,13E-14	0.64±0.09	0,28	1,35E-12
AT3G49510	chr3_18365410	G/G	0,7±0,14	0,36	1,35E-06	0.5±0.14	0,38	2,50E-04
AT3G50210	chr3_18639772	A/A	-0,44±0,08	0,14	1,60E-07	-0.41±0.1	0,38	2,29E-05
AT3G50845	chr3_18900203	A/A	-0,5±0,08	0,20	3,00E-09	-0.39±0.1	0,49	7,31E-05
AT3G53370	chr3_19772576	A/A	-0,53±0,09	0,66	6,18E-10	-0.4±0.1	0,24	7,49E-05
AT3G53650	chr3_19884568	A/A	-0,42±0,12	0,26	5,19E-04	-0.44±0.11	0,42	3,65E-05
AT3G54160	chr3_20045512	G/G	-0,53±0,09	0,18	5,68E-10	-0.32±0.09	0,35	4,65E-04
AT3G54366	chr3_20157830	A/A	-0,54±0,09	0,11	8,14E-09	-0.3±0.1	0,06	1,95E-03
AT3G54420	chr3_20378592	A/A	-0,51±0,09	0,08	1,95E-08	-0.67±0.19	0,07	6,08E-04
AT3G55170	chr3_20449055	G/G	-0,61±0,12	0,48	1,16E-07	-0.66±0.1	0,07	1,92E-11
AT3G55530	chr3_20593930	T/T	0,78±0,13	0,15	3,12E-09	0.51±0.1	0,40	1,19E-06
AT3G56680	chr3_20986847	C/C	-0,53±0,08	0,52	3,89E-10	-0.26±0.1	0,09	7,51E-03
AT3G57460	chr3_21217502	C/C	0,27±0,09	0,07	3,57E-03	0.32±0.09	0,07	6,98E-04
AT3G57680	chr3_21400980	T/T	-0,52±0,1	0,39	6,56E-08	-0.44±0.11	0,38	4,47E-05
AT3G57990	chr3_21470658	T/T	-0,49±0,08	0,59	6,66E-09	-0.65±0.1	0,08	1,02E-11
AT3G58940	chr3_21783695	A/A	-0,46±0,1	0,14	2,01E-06	-0.44±0.1	0,20	1,03E-05
AT3G59380	chr3_21942854	T/T	0,36±0,09	0,05	5,95E-05	0.56±0.11	0,06	2,67E-07
AT3G60150	chr3_22225185	C/C	-0,72±0,09	0,18	2,39E-15	-0.68±0.08	0,44	9,06E-17
AT3G60164	chr3_22225185	C/C	0,49±0,09	0,41	1,03E-07	0.39±0.08	0,07	1,03E-06
AT3G60300	chr3_22277820	G/G	-0,49±0,09	0,31	2,25E-07	-0.22±0.1	0,29	2,68E-02
AT3G60480	chr3_22348322	C/C	-0,58±0,11	0,06	4,41E-08	-0.68±0.1	0,21	7,20E-12
AT3G60880	chr3_22476682	T/T	0,52±0,12	0,51	2,19E-05	0.34±0.1	0,06	4,11E-04
AT3G61560	chr3_22777968	G/G	-0,61±0,1	0,11	4,48E-10	-0.39±0.1	0,07	7,01E-05
AT3G63480	chr3_23441032	A/A	0,55±0,09	0,07	8,81E-10	0.51±0.12	0,36	1,73E-05
AT4G00230	chr4_91149	A/A	-0,67±0,11	0,08	1,04E-09	-0.67±0.13	0,43	2,88E-07
AT4G00234	chr4_18776	G/G	0,35±0,09	0,06	3,74E-05	0.12±0.06	0,06	4,82E-02
AT4G00270	chr4_80055	T/T	-0,47±0,09	0,15	5,12E-08	-0.24±0.1	0,13	1,44E-02
AT4G00620	chr4_617140	A/A	0,45±0,13	0,14	2,95E-04	0.53±0.17	0,21	1,20E-03
AT4G00970	chr4_417205	T/T	0,38±0,09	0,22	9,24E-06	0.4±0.1	0,16	3,51E-05
AT4G01060	chr4_460817	T/T	0,48±0,08	0,43	1,15E-08	0.44±0.1	0,08	4,06E-06
AT4G01200	chr4_506690	C/C	0,48±0,08	0,54	1,69E-08	0.37±0.1	0,36	1,80E-04
AT4G01320	chr4_549347	A/A	-0,52±0,09	0,14	4,01E-08	-0.58±0.1	0,20	1,39E-08
AT4G01600	chr4_693045	T/T	0,39±0,09	0,07	5,75E-06	0.68±0.1	0,47	1,54E-12
AT4G01660	chr4_708594	A/A	0,57±0,13	0,19	6,31E-06	0.53±0.12	0,13	1,05E-05
AT4G01883	chr4_807179	A/A	-0,59±0,09	0,14	1,09E-11	-0.42±0.1	0,30	3,16E-05
AT4G02360	chr4_1380375	T/T	-0,3±0,08	0,23	4,32E-04	-0.34±0.11	0,06	1,90E-03

AT4G02430	chr4_1074953	A/A	-0,6±0,09	0,22	5,85E-12	-0.4±0.1	0,39	2,71E-05
AT4G02660	chr4_1158571	C/C	-0,61±0,08	0,07	4,47E-13	-0.44±0.1	0,45	7,29E-06
AT4G02725	chr4_1210485	A/A	0,44±0,09	0,20	8,16E-07	0.43±0.1	0,10	1,33E-05
AT4G03060	chr4_1356510	T/T	-0,74±0,1	0,24	5,83E-14	-0.81±0.14	0,27	4,06E-09
AT4G03230	chr4_1441524	C/C	0,49±0,08	0,11	4,81E-09	0.26±0.09	0,26	5,05E-03
AT4G04402	chr4_2151088	G/G	0,3±0,11	0,38	6,07E-03	0.67±0.11	0,27	2,35E-09
AT4G04830	chr4_2417084	G/G	-0,28±0,09	0,36	3,19E-03	-0.47±0.1	0,17	1,10E-06
AT4G05060	chr4_2564748	T/T	0,6±0,09	0,34	6,35E-11	0.25±0.11	0,36	2,16E-02
AT4G05130	chr4_2662846	T/T	-0,55±0,1	0,06	1,82E-08	-0.47±0.09	0,40	1,81E-07
AT4G05390	chr4_2737877	T/T	0,5±0,09	0,43	5,62E-08	0.67±0.1	0,16	6,53E-12
AT4G08250	chr4_5196072	A/A	0,61±0,09	0,57	6,08E-13	0.41±0.09	0,31	6,52E-06
AT4G09680	chr4_6113352	A/A	0,69±0,09	0,36	1,99E-15	0.38±0.09	0,17	3,19E-05
AT4G09750	chr4_6146859	T/T	0,42±0,08	0,21	4,78E-07	0.45±0.1	0,37	5,93E-06
AT4G09920	chr4_6228870	G/G	0,31±0,09	0,06	2,64E-04	0.23±0.08	0,09	4,69E-03
AT4G11000	chr4_6732770	A/A	-0,63±0,09	0,48	1,53E-13	-0.64±0.11	0,07	1,30E-09
AT4G11410	chr4_6971346	A/A	0,42±0,08	0,36	6,50E-07	0.28±0.11	0,06	1,02E-02
AT4G11460	chr4_6964745	T/T	-0,25±0,08	0,23	3,39E-03	-0.48±0.1	0,28	7,45E-07
AT4G11630	chr4_7017986	C/C	-0,63±0,09	0,16	2,21E-13	-0.59±0.1	0,47	3,14E-09
AT4G12110	chr4_7194682	G/G	0,34±0,09	0,31	8,45E-05	0.29±0.1	0,40	2,41E-03
AT4G12200	chr4_7281602	G/G	-0,45±0,08	0,06	4,80E-08	-0.24±0.08	0,06	1,93E-03
AT4G12300	chr4_7309739	G/G	0,42±0,11	0,28	1,06E-04	0.83±0.11	0,45	7,18E-15
AT4G13150	chr4_7649860	T/T	-0,93±0,13	0,09	2,40E-12	-0.73±0.11	0,12	1,34E-10
AT4G13170	chr4_7649375	T/T	0,49±0,09	0,30	1,44E-08	0.43±0.1	0,26	1,35E-05
AT4G13180	chr4_7659927	G/G	0,61±0,11	0,08	7,31E-08	0.57±0.1	0,24	1,14E-08
AT4G13630	chr4_7937622	A/A	0,54±0,09	0,10	5,89E-09	0.4±0.1	0,35	1,08E-04
AT4G13660	chr4_7944003	G/G	0,41±0,11	0,12	1,61E-04	0.5±0.13	0,07	2,30E-04
AT4G13885	chr4_8030070	G/G	0,46±0,08	0,34	4,81E-08	0.33±0.08	0,14	6,08E-05
AT4G14030	chr4_8098585	C/C	-0,58±0,1	0,06	3,61E-09	-0.53±0.12	0,49	9,40E-06
AT4G14400	chr4_8300954	G/G	-0,59±0,09	0,31	1,79E-11	-0.32±0.1	0,13	9,12E-04
AT4G14610	chr4_8384144	A/A	-0,43±0,09	0,12	3,82E-07	-0.59±0.09	0,06	2,49E-10
AT4G14970	chr4_8553355	A/A	0,58±0,11	0,13	9,51E-08	0.49±0.11	0,12	2,93E-06
AT4G15165	chr4_8648283	A/A	0,54±0,09	0,26	9,47E-10	0.48±0.1	0,17	2,81E-06
AT4G15260	chr4_8726585	G/G	0,42±0,09	0,24	2,66E-06	0.74±0.12	0,30	5,81E-10
AT4G15330	chr4_8750023	T/T	0,56±0,08	0,17	1,11E-11	0.48±0.08	0,40	1,50E-08
AT4G15620	chr4_8964655	G/G	-0,28±0,08	0,06	8,73E-04	-0.37±0.1	0,43	1,24E-04
AT4G15960	chr4_9047261	A/A	0,74±0,11	0,12	1,79E-11	0.55±0.1	0,30	4,37E-08
AT4G16765	chr4_9449963	T/T	0,37±0,11	0,21	4,08E-04	0.36±0.1	0,17	5,11E-04
AT4G17010	chr4_9577903	G/G	0,79±0,16	0,35	4,26E-07	0.34±0.12	0,36	5,29E-03
AT4G17240	chr4_9669316	A/A	-0,64±0,08	0,10	2,63E-14	-0.47±0.1	0,15	9,33E-07
AT4G18220	chr4_10086984	A/A	-0,5±0,08	0,28	3,52E-09	-0.36±0.1	0,41	3,01E-04
AT4G18930	chr4_10370636	G/G	-0,85±0,11	0,15	1,27E-14	-0.62±0.11	0,29	7,72E-09
AT4G19100	chr4_10453802	C/C	0,77±0,1	0,23	8,46E-14	0.64±0.15	0,07	1,21E-05
AT4G19410	chr4_10585609	C/C	0,54±0,09	0,06	2,99E-10	0.42±0.11	0,08	1,54E-04
AT4G19510	chr4_10621807	T/T	-0,7±0,09	0,37	2,71E-15	-0.21±0.1	0,29	3,53E-02
AT4G19830	chr4_10774193	G/G	-0,66±0,08	0,11	8,27E-15	-0.62±0.1	0,35	2,61E-10
AT4G21320	chr4_11374140	T/T	-0,49±0,12	0,35	5,72E-05	-0.37±0.1	0,28	1,40E-04
AT4G21410	chr4_11392164	G/G	0,25±0,09	0,25	4,60E-03	0.46±0.1	0,07	1,90E-06
AT4G21460	chr4_11432573	T/T	0,59±0,14	0,24	1,37E-05	0.68±0.1	0,07	4,06E-12
AT4G21480	chr4_11432573	T/T	-0,57±0,14	0,06	2,62E-05	-0.43±0.09	0,43	3,57E-06
AT4G21630	chr4_11464339	T/T	0,21±0,1	0,38	3,18E-02	0.48±0.09	0,20	4,52E-08
AT4G21760	chr4_11556660	T/T	-0,58±0,08	0,09	5,39E-12	-0.5±0.09	0,27	2,00E-08
AT4G21900	chr4_11621849	T/T	0,66±0,09	0,38	3,21E-14	0.48±0.1	0,14	7,30E-07
AT4G22280	chr4_11781527	G/G	-0,6±0,09	0,28	2,93E-11	-0.73±0.1	0,34	4,55E-13
AT4G22960	chr4_12030325	A/A	-0,5±0,09	0,26	4,59E-09	-0.42±0.09	0,29	1,70E-06
AT4G23140	chr4_12111816	A/A	-0,57±0,12	0,19	9,53E-07	-0.45±0.1	0,37	2,95E-06
AT4G23200	chr4_12145728	C/C	-0,73±0,1	0,18	8,82E-13	-0.68±0.1	0,34	5,23E-12
AT4G23290	chr4_11865007	G/G	-0,64±0,15	0,07	2,05E-05	-0.56±0.16	0,15	6,40E-04

AT4G23300	chr4_12173034	T/T	0,36±0,09	0,17	3,68E-05	0.24±0.1	0,43	1,42E-02
AT4G23310	chr4_12139678	T/T	-0,43±0,08	0,21	2,69E-07	-0.55±0.13	0,32	2,51E-05
AT4G24175	chr4_12703822	T/T	-0,52±0,17	0,07	2,60E-03	-0.46±0.13	0,36	4,44E-04
AT4G25020	chr4_12863500	A/A	0,48±0,09	0,08	2,64E-07	0.43±0.1	0,30	8,81E-06
AT4G26170	chr4_13290066	C/C	0,4±0,08	0,39	1,57E-06	0.18±0.09	0,29	4,92E-02
AT4G26550	chr4_13405154	A/A	-0,64±0,17	0,55	1,73E-04	-0.4±0.1	0,47	1,05E-04
AT4G26555	chr4_13407368	G/G	-0,72±0,12	0,17	2,39E-09	-0.48±0.11	0,28	5,06E-06
AT4G27820	chr4_13890471	C/C	0,34±0,12	0,08	3,74E-03	0.29±0.11	0,26	1,13E-02
AT4G28220	chr4_13985272	A/A	-0,57±0,08	0,08	1,37E-11	-0.47±0.1	0,10	5,14E-06
AT4G28706	chr4_14169692	A/A	0,45±0,09	0,06	1,25E-06	0.4±0.1	0,40	3,75E-05
AT4G29050	chr4_14267639	A/A	-0,41±0,09	0,19	2,34E-06	-0.52±0.11	0,20	1,58E-06
AT4G29540	chr4_14499217	T/T	0,41±0,08	0,16	1,12E-06	0.24±0.1	0,17	1,11E-02
AT4G29550	chr4_14496442	G/G	-0,46±0,08	0,39	2,82E-08	-0.31±0.1	0,38	2,24E-03
AT4G29890	chr4_14584638	G/G	0,38±0,08	0,32	5,98E-06	0.52±0.1	0,30	6,68E-08
AT4G31870	chr4_15409973	C/C	-0,67±0,09	0,06	1,25E-13	-0.5±0.1	0,30	2,36E-07
AT4G33360	chr4_16069056	T/T	-0,73±0,13	0,12	7,24E-09	-0.72±0.1	0,37	1,02E-13
AT4G33370	chr4_15723466	A/A	0,34±0,09	0,08	4,95E-05	0.17±0.08	0,10	3,71E-02
AT4G33410	chr4_16084591	A/A	-0,91±0,16	0,36	2,30E-08	-0.6±0.1	0,09	7,66E-10
AT4G36880	chr4_17377423	C/C	0,43±0,09	0,54	2,01E-06	0.59±0.09	0,20	2,67E-10
AT4G37150	chr4_17494470	T/T	0,53±0,12	0,08	1,51E-05	0.76±0.1	0,42	1,57E-15
AT4G37310	chr4_17542308	A/A	0,77±0,13	0,06	6,48E-09	0.6±0.11	0,10	4,02E-08
AT4G37925	chr4_17842697	A/A	0,45±0,1	0,11	5,97E-06	0.27±0.12	0,29	2,39E-02
AT4G38100	chr4_17886739	C/C	0,58±0,08	0,49	5,57E-12	0.44±0.1	0,08	4,89E-06
AT4G38460	chr4_17799227	A/A	-0,65±0,16	0,07	7,84E-05	-0.76±0.13	0,48	1,41E-08
AT4G38800	chr4_18081582	G/G	-0,4±0,12	0,06	9,79E-04	-0.3±0.12	0,46	1,09E-02
AT4G39390	chr4_18316203	T/T	0,57±0,09	0,06	8,03E-11	0.48±0.1	0,33	9,02E-07
AT4G39740	chr4_18434232	T/T	-0,68±0,16	0,07	1,41E-05	-0.74±0.13	0,29	3,50E-08
AT4G39920	chr4_18528826	T/T	0,52±0,13	0,26	8,29E-05	0.42±0.11	0,22	2,15E-04
AT5G01040	chr5_33234	A/A	-0,63±0,11	0,14	4,19E-09	-0.47±0.11	0,32	2,08E-05
AT5G02230	chr5_448353	T/T	-0,62±0,09	0,09	1,52E-12	-0.63±0.1	0,28	8,00E-11
AT5G02430	chr5_526258	T/T	0,51±0,18	0,45	4,56E-03	0.44±0.13	0,33	4,46E-04
AT5G02560	chr5_575922	T/T	0,24±0,08	0,63	4,84E-03	0.45±0.1	0,41	3,56E-06
AT5G02740	chr5_621000	C/C	-0,48±0,1	0,49	9,96E-07	-0.55±0.1	0,18	1,85E-07
AT5G03285	chr5_793000	G/G	-0,61±0,09	0,18	1,53E-12	-0.32±0.1	0,17	1,86E-03
AT5G03300	chr5_798261	T/T	0,65±0,12	0,08	1,09E-07	0.53±0.14	0,17	2,20E-04
AT5G03350	chr5_818236	T/T	0,24±0,09	0,21	6,20E-03	0.43±0.1	0,15	2,11E-05
AT5G03390	chr5_839822	G/G	-0,26±0,08	0,23	2,31E-03	-0.56±0.1	0,28	2,45E-08
AT5G03495	chr5_16706938	G/G	0,43±0,1	0,06	5,27E-06	0.41±0.08	0,12	1,53E-06
AT5G04000	chr5_1024769	A/A	0,56±0,11	0,55	8,73E-07	0.58±0.18	0,06	1,03E-03
AT5G04220	chr5_1288875	G/G	-0,49±0,13	0,24	1,12E-04	-0.28±0.1	0,07	5,90E-03
AT5G05430	chr5_1605316	T/T	-0,49±0,08	0,41	2,21E-09	-0.2±0.07	0,09	8,33E-03
AT5G05890	chr5_1771593	C/C	-0,54±0,09	0,61	1,09E-08	-0.39±0.1	0,39	4,90E-05
AT5G06060	chr5_1728043	C/C	-0,43±0,14	0,07	1,69E-03	-0.31±0.1	0,28	1,45E-03
AT5G07000	chr5_2182218	G/G	-0,3±0,08	0,38	4,23E-04	-0.37±0.11	0,36	1,04E-03
AT5G08010	chr5_2574913	C/C	0,4±0,09	0,45	3,22E-06	0.4±0.1	0,20	4,63E-05
AT5G08360	chr5_2762078	T/T	0,26±0,09	0,49	2,06E-03	0.25±0.1	0,11	1,20E-02
AT5G08565	chr5_2630270	T/T	0,43±0,11	0,55	6,22E-05	0.38±0.13	0,21	3,33E-03
AT5G09840	chr5_3058931	C/C	0,51±0,08	0,50	1,52E-09	0.36±0.1	0,13	3,43E-04
AT5G10390	chr5_3281886	A/A	0,61±0,1	0,08	1,93E-09	0.69±0.12	0,42	1,37E-08
AT5G10400	chr5_3272353	A/A	-0,8±0,1	0,08	7,85E-17	-0.85±0.12	0,42	9,51E-13
AT5G10610	chr5_3359832	G/G	-0,4±0,08	0,57	2,79E-06	-0.53±0.1	0,29	5,55E-07
AT5G10620	chr5_3356691	A/A	-0,17±0,08	0,08	4,10E-02	-0.59±0.11	0,29	4,19E-08
AT5G11580	chr5_3719036	G/G	-0,85±0,12	0,31	6,39E-13	-0.57±0.1	0,21	5,61E-08
AT5G14680	chr1_3381420	T/T	-0,23±0,09	0,14	8,82E-03	-0.48±0.1	0,07	5,07E-07
AT5G15520	chr5_5031656	A/A	0,47±0,14	0,42	1,20E-03	0.57±0.12	0,29	2,05E-06
AT5G15760	chr5_5142437	G/G	0,65±0,09	0,08	1,24E-12	0.42±0.1	0,42	1,00E-05
AT5G16220	chr5_5291565	C/C	-0,61±0,08	0,63	4,67E-13	-0.49±0.1	0,12	2,44E-06

AT5G16350	chr5_5554397	A/A	0,42±0,1	0,54	1,60E-05	0.3±0.11	0,43	4,93E-03
AT5G17040	chr5_5586708	C/C	0,81±0,14	0,50	6,95E-09	0.65±0.11	0,06	2,26E-09
AT5G17780	chr5_5868804	A/A	0,61±0,09	0,11	1,26E-11	0.45±0.1	0,21	2,71E-06
AT5G18040	chr5_5962646	A/A	-0,21±0,09	0,14	1,38E-02	-0.51±0.1	0,39	9,93E-08
AT5G18290	chr5_5939680	A/A	-0,37±0,09	0,55	1,06E-05	-0.24±0.11	0,06	2,64E-02
AT5G18840	chr5_6249990	C/C	-0,45±0,1	0,08	4,07E-06	-0.71±0.11	0,34	1,55E-11
AT5G19180	chr5_6454534	A/A	-0,62±0,1	0,07	2,34E-10	-0.41±0.11	0,44	2,08E-04
AT5G19350	chr5_6518623	C/C	-0,57±0,09	0,26	2,77E-10	-0.46±0.1	0,29	2,93E-06
AT5G20420	chr5_6960707	T/T	-0,54±0,09	0,09	7,45E-10	-0.31±0.09	0,28	6,25E-04
AT5G20580	chr5_6969298	T/T	0,69±0,08	0,09	1,68E-16	0.52±0.1	0,07	1,16E-07
AT5G20810	chr5_6602468	A/A	-0,63±0,16	0,06	6,28E-05	-0.42±0.1	0,38	2,89E-05
AT5G21060	chr5_7157944	A/A	-0,78±0,11	0,09	6,69E-12	-0.73±0.1	0,09	3,43E-14
AT5G22545	chr5_7636152	T/T	-0,66±0,16	0,40	4,87E-05	-0.71±0.16	0,08	4,76E-06
AT5G23020	chr5_7718472	G/G	-0,49±0,09	0,18	9,63E-09	-0.4±0.1	0,44	4,24E-05
AT5G23405	chr5_7913147	G/G	-0,63±0,09	0,09	5,03E-12	-0.28±0.1	0,36	3,08E-03
AT5G23850	chr5_8046976	G/G	-0,64±0,14	0,08	4,38E-06	-0.39±0.17	0,06	2,53E-02
AT5G23980	chr5_8100470	C/C	0,67±0,13	0,11	1,66E-07	0.37±0.1	0,33	9,43E-05
AT5G24450	chr5_8346726	T/T	-0,48±0,09	0,45	3,17E-07	-0.41±0.1	0,25	2,30E-05
AT5G24680	chr5_8522452	T/T	0,52±0,11	0,06	1,65E-06	0.34±0.1	0,06	4,62E-04
AT5G25230	chr5_8736804	G/G	0,59±0,09	0,30	3,72E-11	0.34±0.08	0,27	1,76E-05
AT5G25450	chr5_8857203	G/G	0,85±0,13	0,25	5,34E-11	0.76±0.11	0,06	1,03E-11
AT5G25470	chr5_8815941	T/T	0,29±0,09	0,09	7,89E-04	0.45±0.09	0,17	8,26E-07
AT5G25570	chr5_8904831	T/T	-01,±0,16	0,12	1,10E-09	-0.81±0.14	0,27	4,52E-09
AT5G25640	chr5_8968191	G/G	0,82±0,1	0,09	3,18E-16	0.72±0.1	0,47	6,50E-14
AT5G26330	chr5_9243133	A/A	0,45±0,09	0,21	9,81E-08	0.51±0.1	0,35	7,97E-08
AT5G27010	chr5_9499588	T/T	0,57±0,11	0,35	8,34E-08	0.57±0.08	0,49	1,77E-12
AT5G27110	chr5_9533635	G/G	-0,45±0,09	0,09	1,93E-07	-0.5±0.11	0,22	5,11E-06
AT5G27210	chr5_9559987	C/C	-0,53±0,09	0,26	1,86E-09	-0.41±0.1	0,23	9,90E-05
AT5G27220	chr5_9578927	G/G	-0,44±0,09	0,42	2,06E-06	-0.46±0.1	0,44	7,62E-06
AT5G27230	chr5_9600085	T/T	0,64±0,09	0,06	9,25E-12	0.46±0.1	0,09	2,38E-06
AT5G27660	chr5_9793385	T/T	0,4±0,09	0,08	1,16E-05	0.5±0.11	0,39	6,65E-06
AT5G28010	chr5_10018839	A/A	0,52±0,09	0,06	6,47E-09	0.32±0.1	0,36	6,60E-04
AT5G28080	chr5_10127627	T/T	0,48±0,09	0,12	1,65E-07	0.47±0.1	0,07	1,76E-06
AT5G36260	chr5_14288615	C/C	-0,62±0,13	0,20	1,11E-06	-0.47±0.09	0,45	4,59E-07
AT5G36930	chr5_14586136	G/G	0,67±0,16	0,20	3,08E-05	0.52±0.11	0,12	4,46E-06
AT5G36940	chr5_14626995	T/T	0,36±0,12	0,08	2,59E-03	0.64±0.11	0,06	8,70E-09
AT5G37410	chr5_14835977	A/A	-0,75±0,09	0,28	6,76E-16	-0.43±0.09	0,08	1,86E-06
AT5G37530	chr5_14906498	A/A	-0,75±0,09	0,19	2,02E-17	-0.42±0.1	0,25	1,26E-05
AT5G38020	chr5_15185253	A/A	0,53±0,09	0,08	1,21E-09	0.28±0.1	0,18	3,52E-03
AT5G38060	chr5_15189206	G/G	0,53±0,09	0,11	2,22E-09	0.4±0.1	0,26	2,90E-05
AT5G38250	chr5_15282467	A/A	-0,65±0,09	0,21	3,78E-12	-0.56±0.1	0,35	1,75E-08
AT5G38260	chr5_15284523	G/G	-0,6±0,09	0,14	1,99E-12	-0.53±0.09	0,35	1,81E-08
AT5G38280	chr5_15284523	G/G	-0,36±0,09	0,11	2,42E-05	-0.39±0.1	0,45	6,30E-05
AT5G40290	chr5_16094398	A/A	-0,3±0,09	0,18	6,65E-04	-0.12±0.05	0,11	7,87E-03
AT5G40820	chr5_16363472	G/G	0,65±0,1	0,61	2,77E-10	0.55±0.1	0,11	1,54E-07
AT5G41580	chr5_16627887	C/C	0,64±0,09	0,14	1,39E-12	0.64±0.1	0,28	3,31E-11
AT5G41690	chr5_16674846	A/A	-0,4±0,09	0,11	2,65E-06	-0.39±0.09	0,28	2,36E-05
AT5G41910	chr5_16778517	G/G	-0,63±0,08	0,09	1,41E-13	-0.45±0.1	0,21	7,47E-06
AT5G41950	chr5_16780665	T/T	-0,66±0,11	0,11	5,44E-10	-0.4±0.11	0,21	2,09E-04
AT5G42230	chr5_16938554	T/T	0,31±0,12	0,10	8,83E-03	0.35±0.1	0,06	7,10E-04
AT5G42250	chr5_16911504	C/C	-0,25±0,09	0,12	4,64E-03	-0.36±0.1	0,08	1,90E-04
AT5G42670	chr5_17108687	G/G	0,61±0,1	0,24	2,31E-10	0.45±0.11	0,33	5,42E-05
AT5G43070	chr5_17290556	A/A	0,37±0,08	0,07	1,21E-05	0.31±0.1	0,23	1,55E-03
AT5G43150	chr5_17328573	A/A	0,44±0,09	0,06	1,25E-06	0.4±0.1	0,21	3,25E-05
AT5G43620	chr5_17521121	T/T	-0,35±0,11	0,09	1,19E-03	-0.36±0.09	0,06	1,35E-04
AT5G43660	chr5_17541491	A/A	-0,59±0,09	0,06	3,51E-12	-0.27±0.09	0,28	1,78E-03
AT5G43725	chr5_17560566	G/G	0,45±0,09	0,08	1,32E-06	0.24±0.1	0,45	1,52E-02

AT5G44080	chr5_17826554	A/A	-0,32±0,13	0,06	1,17E-02	-0.71±0.16	0,14	6,36E-06
AT5G44568	chr5_17961505	A/A	0,47±0,09	0,16	3,20E-08	0.58±0.1	0,41	1,64E-09
AT5G44582	chr5_17979016	G/G	0,63±0,1	0,11	8,96E-10	0.38±0.19	0,49	4,78E-02
AT5G45040	chr5_18173199	G/G	-0,67±0,09	0,25	2,09E-14	-0.6±0.1	0,28	1,16E-09
AT5G45510	chr5_18428369	A/A	-0,6±0,08	0,29	8,88E-13	-0.46±0.1	0,28	1,82E-06
AT5G45610	chr5_18503730	C/C	-0,58±0,09	0,26	9,59E-12	-0.39±0.1	0,26	5,85E-05
AT5G45730	chr5_18557137	A/A	0,7±0,12	0,23	2,16E-09	0.44±0.1	0,35	4,58E-06
AT5G46720	chr5_19422222	G/G	-0,27±0,09	0,09	2,62E-03	-0.51±0.15	0,50	7,06E-04
AT5G47310	chr5_19191911	A/A	-0,39±0,09	0,41	4,90E-06	-0.62±0.15	0,06	4,32E-05
AT5G47510	chr5_19280669	T/T	-0,63±0,1	0,31	3,94E-10	-0.61±0.14	0,25	5,80E-06
AT5G47760	chr5_19356640	G/G	-0,44±0,08	0,08	1,68E-07	-0.55±0.1	0,43	1,52E-07
AT5G47770	chr5_19351286	T/T	0,33±0,09	0,08	1,63E-04	0.45±0.1	0,34	4,35E-06
AT5G47810	chr5_19348410	T/T	0,64±0,08	0,09	5,91E-14	0.7±0.1	0,17	6,36E-12
AT5G48020	chr5_19520266	A/A	-0,44±0,09	0,60	1,88E-06	-0.41±0.1	0,14	1,92E-05
AT5G48340	chr5_19586453	C/C	-0,76±0,1	0,46	1,07E-14	-0.39±0.1	0,19	4,46E-05
AT5G48530	chr5_19669066	T/T	-0,57±0,09	0,14	3,06E-11	-0.47±0.1	0,21	8,53E-06
AT5G48560	chr5_19688573	G/G	0,51±0,09	0,18	5,83E-08	0.32±0.1	0,36	2,06E-03
AT5G49970	chr5_20343995	A/A	-0,42±0,09	0,05	6,35E-07	-0.43±0.1	0,21	8,95E-06
AT5G50350	chr5_20495953	T/T	-0,68±0,1	0,16	2,02E-12	-0.41±0.1	0,36	2,71E-05
AT5G50950	chr5_20802283	C/C	-0,36±0,09	0,05	6,26E-05	-0.42±0.1	0,07	1,52E-05
AT5G51470	chr5_20906654	G/G	0,75±0,09	0,46	1,94E-17	0.62±0.09	0,42	2,45E-12
AT5G52190	chr5_21202402	G/G	-0,88±0,12	0,13	2,46E-14	-0.78±0.1	0,08	1,49E-14
AT5G53970	chr5_21914245	A/A	-0,54±0,08	0,16	2,08E-10	-0.46±0.11	0,06	1,90E-05
AT5G54400	chr5_22092370	G/G	0,32±0,09	0,08	1,52E-04	0.25±0.1	0,16	9,68E-03
AT5G54960	chr5_22310411	A/A	0,36±0,09	0,07	4,63E-05	0.52±0.11	0,36	1,82E-06
AT5G55460	chr5_22460639	A/A	-0,95±0,16	0,24	6,82E-09	-0.9±0.16	0,07	4,66E-08
AT5G56020	chr5_22689472	T/T	-0,71±0,16	0,09	1,56E-05	-0.6±0.13	0,09	5,40E-06
AT5G56100	chr5_22707349	G/G	-0,49±0,1	0,42	4,34E-07	-0.49±0.1	0,36	6,06E-07
AT5G56370	chr5_22860221	G/G	-0,52±0,09	0,06	5,09E-09	-0.47±0.09	0,25	4,27E-08
AT5G57230	chr5_23193315	G/G	0,49±0,09	0,10	3,80E-08	0.33±0.1	0,16	6,38E-04
AT5G58980	chr5_23809336	C/C	0,72±0,1	0,07	1,76E-13	0.52±0.13	0,10	1,18E-04
AT5G60340	chr5_24275857	G/G	-0,61±0,09	0,41	5,63E-11	-0.61±0.1	0,43	2,45E-10
AT5G61550	chr5_24747219	T/T	-0,69±0,09	0,11	9,29E-14	-0.44±0.09	0,31	6,04E-07
AT5G63520	chr5_25435104	G/G	-0,64±0,13	0,56	1,08E-06	-0.54±0.18	0,11	2,94E-03
AT5G63580	chr5_25468341	G/G	0,43±0,08	0,44	4,34E-07	0.53±0.09	0,44	2,30E-09
AT5G64630	chr5_25833100	G/G	0,75±0,11	0,39	3,31E-12	0.57±0.1	0,18	1,35E-08
AT5G66080	chr5_26424978	G/G	-0,52±0,08	0,08	8,13E-10	-0.44±0.1	0,25	1,59E-05
AT5G66480	chr5_26549786	T/T	-0,82±0,17	0,06	1,87E-06	-0.44±0.12	0,07	2,12E-04
AT5G66490	chr5_26549786	T/T	-0,83±0,17	0,06	1,18E-06	-0.81±0.12	0,07	2,35E-11
AT5G66840	chr5_26746223	T/T	0,62±0,1	0,07	2,03E-10	0.63±0.17	0,32	2,91E-04
AT5G67290	chr5_26846358	A/A	-0,62±0,1	0,33	2,22E-09	-0.45±0.1	0,36	5,74E-06
AT5G67540	chr5_26944169	A/A	0,7±0,12	0,35	1,06E-08	0.47±0.1	0,46	2,72E-06
AT3G16390	chr3_5568916	C/C	0,99±0,16	0,31	1,39E-09	0.83±0.11	0,29	2,94E-14
AT3G16390	chr5_5855701	T/T	0,32±0,09	0,08	3,66E-04	0.33±0.1	0,07	5,11E-04
AT3G32920	chr1_10008048	A/A	0,28±0,12	0,15	2,21E-02	0.17±0.07	0,25	1,53E-02
AT3G32920	chr3_13416069	A/A	0,93±0,12	0,24	6,77E-14	0.57±0.08	0,28	3,51E-14
AT3G32920	chr3_13416069	A/A	0,93±0,12	0,16	6,77E-14	0.57±0.08	0,30	3,51E-14
AT3G43610	chr3_15531245	C/C	0,63±0,1	0,20	6,09E-11	0.38±0.1	0,07	1,02E-04
AT3G46900	chr3_17269895	A/A	-0,52±0,1	0,08	2,91E-07	-0.48±0.09	0,24	2,94E-07
AT3G50880	chr3_18936789	C/C	-0,39±0,09	0,07	2,57E-05	-0.49±0.1	0,44	8,40E-07
AT3G59190	chr3_21884602	T/T	0,65±0,11	0,48	1,62E-08	0.7±0.13	0,06	7,86E-08
AT4G02460	chr4_1058973	G/G	0,59±0,11	0,47	4,22E-08	0.44±0.1	0,16	9,19E-06
AT4G07410	chr4_4214036	A/A	-0,51±0,08	0,14	1,70E-09	-0.43±0.1	0,29	3,83E-05
AT4G27060	chr4_13571820	C/C	0,63±0,11	0,54	2,64E-09	0.39±0.1	0,35	4,44E-05
AT4G27070	chr1_11506730	C/C	0,62±0,1	0,09	4,30E-10	0.61±0.1	0,35	2,33E-10
AT4G27070	chr4_13553783	T/T	0,66±0,1	0,19	6,14E-12	0.72±0.1	0,27	1,08E-13
AT4G27080	chr1_11506730	C/C	0,66±0,1	0,11	2,90E-11	0.41±0.1	0,06	2,44E-05

AT4G27080	chr4_13553783	T/T	0,7±0,1	0,49	3,56E-13	0.48±0.1	0,21	7,09E-07
AT4G27080	chr5_15243278	T/T	0,6±0,11	0,24	1,49E-07	0.49±0.1	0,12	4,12E-07
AT5G24660	chr1_14600466	T/T	-0,7±0,09	0,06	2,86E-14	-0.79±0.16	0,10	6,53E-07
AT5G24660	chr1_15575602	G/G	0,49±0,08	0,13	7,58E-09	0.74±0.15	0,16	1,21E-06
AT5G24660	chr5_8442551	T/T	0,3±0,1	0,43	1,97E-03	0.37±0.1	0,31	1,23E-04
AT5G38590	chr5_15453373	C/C	0,61±0,09	0,36	5,44E-12	0.55±0.11	0,06	9,03E-07
AT5G44570	chr5_17961505	A/A	0,37±0,08	0,08	1,24E-05	0.48±0.09	0,26	4,91E-07
AT1G22403	chr5_26850990	T/T	0,91±0,13	0,08	5,78E-12	0.56±0.1	0,33	9,28E-09
AT5G66658	chr1_13323173	T/T	-0,2±0,1	0,06	4,55E-02	-0.36±0.08	0,18	5,19E-06
AT5G66658	chr5_26609368	C/C	-0,55±0,11	0,13	2,46E-07	-0.43±0.08	0,07	3,55E-08
AT1G27560	chr1_9570009	A/A	-0,4±0,09	0,07	4,74E-06	-0.31±0.07	0,08	1,17E-05
AT1G31910	chr1_11458878	A/A	0,65±0,08	0,09	7,18E-15	0.49±0.1	0,35	1,64E-06
AT1G31910	chr5_11997528	A/A	-0,45±0,08	0,31	1,05E-07	-0.43±0.1	0,35	9,55E-06
AT1G65520	chr1_24361666	A/A	0,28±0,09	0,38	1,21E-03	0.36±0.1	0,35	2,35E-04
AT2G11000	chr2_4347440	G/G	0,75±0,11	0,18	1,15E-11	0.66±0.1	0,44	2,25E-11
AT2G20560	chr2_8883614	A/A	0,39±0,09	0,08	4,57E-06	0.34±0.11	0,22	2,21E-03
AT2G23110	chr2_9840140	T/T	0,38±0,08	0,08	4,38E-06	0.45±0.1	0,23	1,14E-05
AT2G25510	chr1_2031544	T/T	-0,54±0,1	0,41	1,15E-08	-0.63±0.12	0,10	7,39E-08
AT2G25510	chr2_10847006	C/C	-0,49±0,12	0,08	4,07E-05	-0.51±0.1	0,24	8,59E-07
AT2G29910	chr2_12666437	C/C	-0,49±0,12	0,31	7,17E-05	-0.6±0.15	0,35	7,18E-05
AT2G40240	chr2_16810569	A/A	-0,47±0,09	0,35	3,50E-08	-0.52±0.1	0,20	5,84E-08
AT2G41830	chr2_17458181	T/T	0,74±0,11	0,19	3,93E-11	0.57±0.11	0,39	1,91E-07
AT2G43535	chr2_18071235	T/T	-0,6±0,11	0,06	4,21E-08	-0.53±0.1	0,06	2,39E-07
AT3G01920	chr3_319854	A/A	0,46±0,08	0,19	3,53E-08	0.44±0.1	0,27	3,79E-06
AT3G04181	chr3_1099944	A/A	-0,82±0,11	0,31	2,30E-13	-0.57±0.09	0,18	2,12E-10
AT3G04181	chr5_525023	G/G	-0,8±0,15	0,09	6,74E-08	-0.24±0.11	0,36	3,50E-02

[a]SNP: Overlapping SNP between the two datasets; [b]Genotype: Genotype at the coding allele in Schmitz-data; [c]a±SE: Additive effect ± Standard Error;[d]MAF: Minor Allele Frequency; [e]P-value: nominal P-value from single-SNP association

Table S7. Tissue specific expression of the 111 genes do not expressed in leaf of Col-0

Locus	Tissue
AT2G05117	No
AT5G08460	pollen/seedling
AT2G04830	No
AT1G64235	pollen
AT2G15930	No
AT3G25720	No
AT1G11370	pollen/seedling
AT4G15053	No
AT1G76830	No
AT3G25719	pollen
AT3G46482	No
AT5G67040	No
AT5G40050	pollen
AT5G48350	pollen/seedling
AT1G50050	pollen/seedling
AT1G51990	No
AT5G36240	pollen/seedling
AT5G22680	pollen/seedling
AT2G29000	No
AT5G54206	No
AT5G03820	pollen
AT5G14290	pollen/seedling
AT2G12935	pollen
AT3G17150	No
AT5G66970	pollen
AT2G25169	pollen/seedling
AT5G22555	No
AT1G62410	No
AT3G42786	No
AT1G67010	No
AT5G37280	pollen/seedling
AT3G21570	pollen/seedling
AT2G36550	No
AT4G01925	pollen/seedling
AT1G02830	No
AT1G14688	pollen
AT2G16520	pollen
AT3G28193	No
AT5G38275	No
AT5G35800	No
AT1G50530	pollen/seedling
AT3G32904	No
AT2G11280	pollen/seedling
AT5G59616	No

AT3G44444	No
AT3G53080	pollen
AT2G06917	No
AT4G29300	No
AT1G35280	No
AT3G29764	No
AT5G23065	No
AT1G20520	pollen/seedling
AT3G25014	pollen/seedling
AT2G27850	No
AT3G33145	pollen
AT3G43303	No
AT1G61688	No
AT4G09745	No
AT4G04680	pollen/seedling
AT3G29786	No
AT4G03292	pollen/seedling
AT2G17160	No
AT5G43770	pollen/seedling
AT3G15320	pollen/seedling
AT2G17043	No
AT5G29560	pollen
AT1G47915	No
AT1G44940	pollen
AT1G32010	No
AT5G26642	No
AT1G22720	pollen
AT2G44800	pollen/seedling
AT3G29636	No
AT5G48210	No
AT5G12090	No
AT5G46010	No
AT3G30812	No
AT2G14020	No
AT5G28671	No
AT2G01360	No
AT5G32434	No
AT5G20750	No
AT4G17512	pollen/seedling
AT4G04110	No
AT3G25573	No
AT3G48346	pollen
AT2G44383	pollen/seedling
AT1G22680	pollen/seedling
AT3G06545	pollen
AT4G16105	No

AT4G27890	pollen
AT5G17110	pollen
AT2G15610	No
AT4G20420	pollen/seedling
AT1G44674	No
AT3G59460	pollen/seedling
AT1G48180	pollen/seedling
AT4G22230	pollen/seedling
AT2G44780	pollen/seedling
AT4G29305	pollen
AT2G17080	No
AT5G56368	pollen
AT1G32710	No
AT2G47660	pollen
AT2G26211	pollen/seedling
AT3G28310	pollen/seedling
AT5G44065	pollen/seedling
AT1G24010	No
AT4G01260	No
AT2G38830	pollen/seedling
AT4G29340	pollen/seedling