

Dissection of floral induction pathways using global expression analysis

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Summary

Flowering of the reference plant *Arabidopsis thaliana* is controlled by several signaling pathways, which converge on a small set of genes that function as pathway integrators. We have analyzed the genomic response to one type of floral inductive signal, photoperiod, to dissect the function of several genes transducing this stimulus, including *CONSTANS*, thought to be the major output of the photoperiod pathway. Comparing the effects of *CONSTANS* with those of *FLOWERING LOCUS T*, which integrates inputs from *CONSTANS* and other floral inductive pathways, we find that expression profiles of shoot apices from plants with mutations in either gene are very similar. In contrast, a mutation in *LEAFY*, which also acts downstream of *CONSTANS*, has much more limited effects. Another pathway integrator, *SUPPRESSOR OF OVEREXPRESSION OF CO 1*, is responsive to acute

induction by photoperiod even in the presence of the floral repressor encoded by *FLOWERING LOCUS C*. We have discovered a large group of potential floral repressors that are down-regulated upon photoperiodic induction. These include two AP2 domain-encoding genes that can repress flowering. The two paralogous genes, *SCHLAFMÜTZE* and *SCHNARCHZAPFEN*, share a signature with partial complementarity to the miR172 microRNA, whose precursor we show to be induced upon flowering. These and related findings on *SPL* genes suggest that microRNAs play an important role in the regulation of flowering.

Supplemental data available online

Key words: *Arabidopsis*, Floral induction, Flower development, Floral homeotic genes, Microarrays

Introduction

In contrast to animals, postembryonic development of many plants is highly plastic. A particularly dramatic example is the timing of the transition from vegetative to reproductive growth. In some species, the formation of the reproductive structures, the flowers, begins within a few days after the seedling has emerged from the seed, while in others it can take years or decades. Even within a species, the onset of flowering can vary tremendously, either because of differences in the environment or because of genetic differences.

Flowering is being studied extensively in the reference plant *Arabidopsis thaliana*, an ephemeral weed of the crucifer family (Lohmann and Weigel, 2002; Simpson and Dean, 2002). Many wild *Arabidopsis* strains flower only after several months unless they have experienced an extended period of cold, called vernalization. The vernalization requirement is conferred by a pair of epistatic loci, *FRIGIDA* (*FRI*) and *FLOWERING LOCUS C* (*FLC*), with *FLC* acting downstream of *FRI*. In plants with functional *FRI*, RNA levels of the floral repressor *FLC* are high unless the plants have been vernalized. *FLC* is also upregulated when genes of the so-called autonomous pathway are defective (Michaels and Amasino, 1999; Sheldon et al., 1999).

When *FLC* is only weakly active, *Arabidopsis* strains typically flower within a few weeks under long days, but considerably later when days are short. The effects of photoperiod variation are mediated by a signaling cascade that converges on the *CONSTANS* (*CO*) transcription factor (Suárez-López et al., 2001; Yanovsky and Kay, 2002), so named because *co* mutants are much less responsive to changes in day length than wild-type plants are (Redeí, 1962). *CO* acts redundantly with a pathway that requires the phytohormone gibberellin, and gibberellin-deficient *co* mutants often do not flower at all, even under long days (Reeves and Coupland, 2001).

The different floral induction pathways are integrated by a small set of genes, including *FLOWERING LOCUS T* (*FT*), *SUPPRESSOR OF OVEREXPRESSION OF CO 1* (*SOC1*) and *LEAFY* (*LFY*) (Blázquez and Weigel, 2000; Borner et al., 2000; Lee et al., 2000; Samach et al., 2000). *LFY*, together with another transcription factor, *APETALA1* (*AP1*), activates homeotic genes such as *APETALA3* (*AP3*) and *AGAMOUS* (*AG*), which specify the identity of the different organ types in newly arising floral primordia (Busch et al., 1999; Lamb et al., 2002; Ng and Yanofsky, 2001).

The critical events of early flower development are confined

to a small part of the plant, the shoot apex, where flowers are initiated. To dissect the interactions between several of the floral regulators on a genome-wide scale, we have used global transcriptional profiling to investigate the response to photoperiod induction at the shoot apex. Our results reveal not only a molecular picture of the interplay between the floral repressor *FLC* and the photoperiod pathway, but also reveal discrete steps in the acquisition of floral identity. Finally, we identify a large class of genes that are repressed upon floral induction by photoperiod. Potential microRNA targets are found among both the induced and repressed genes.

Materials and methods

Plant material

Plants were grown under a 3:1 or 1:1 mixture of Cool White and Gro-Lux (Wide Spectrum) fluorescent lights, with a fluence rate of 125 to 175 $\mu\text{mol}/\text{m}^2/\text{s}$ and a temperature of about 21°C. Plants were grown initially in short days (9 hours light, 15 hours dark) and then transferred to long days (16 hours light, 8 hours dark).

Wild type was either Landsberg *erecta* (*Ler*) or Columbia (Col-0, Col-7). In experiments II and III, *Ler* and Col-7 contained *AG::GUS* transgenes (Busch et al., 1999). *lfy-12* is a strong allele in the Col-0 background (Huala and Sussex, 1992; Weigel et al., 1992) and *co-2* and *ft-2* are strong alleles in the *Ler* background (Kardailsky et al., 1999; Kobayashi et al., 1999; Koornneef et al., 1991; Putterill et al., 1995). The *FLC FRI-Sf2* strain contains the *FRI* allele of the San Feliu-2 (*Sf-2*) accession introgressed into Col-0 (Lee et al., 1993). *flc-3* is a strong loss-of-function allele induced in the *FLC FRI-Sf2* strain (Michaels and Amasino, 1999).

Scanning electron microscopy (SEM)

After fixation in methanol for 5 minutes, apices were transferred to 100% ethanol. Further preparation for SEM was as described previously (Weigel and Glazebrook, 2002). Images were acquired on a Hitachi S800 electron microscope, at an accelerating voltage of 20 kV.

RNA isolation and labeling

For RNA isolation from shoot apices, plants were dissected with razor blades under the dissecting microscope at 30 \times magnification. Shoot apices with floral primordia up to about stage 6 (Smyth et al., 1990), or with equivalently sized leaf primordia, were frozen in liquid nitrogen. Because the expression of many floral regulators is under circadian control, shoot apices were harvested starting 1 hour after subjective dawn in about five groups of five from each genotype, and genotypes were rotated during the collection (it takes about 1 minute to dissect a shoot apex). Frozen tissue was stored at -80°C, and RNA was extracted with the Plant RNeasy Mini kit (Qiagen). 5 μg total RNA was used as starting material to synthesize double stranded cDNA using the Superscript Choice System (Invitrogen) and an oligo(dT)-T7 primer (Genset). The cDNA served as a template for synthesis of biotinylated cRNA using the BioArray High Yield Transcript Labeling kit (Enzo). Biotinylated cRNA was cleaned with RNeasy columns (Qiagen) according to the manufacturer's protocol, with the following modifications. First, the cRNA was passed through the column twice to increase binding. Second, the eluate was re-applied to the column once to increase yield. Usually, 50 to 100 μg biotinylated cRNA were obtained. 20 μg of concentration-adjusted cRNA were fragmented according to the GeneChip protocol (Affymetrix).

DNA isolation and labeling

Genomic DNA was isolated by a modified CTAB method. 2 g of tissue frozen in liquid nitrogen was ground up and suspended in 30 ml

extraction buffer (0.35 M sorbitol, 0.1 M Tris pH 8.0, 50 mM EDTA). After centrifugation, the pellet was resuspended in 2 ml extraction buffer and carefully mixed with 2 ml lysis buffer (20 mM Tris pH 7.5, 50 mM EDTA, 2 M NaCl, 2% CTAB) and 150 μl N-laurylsarcosine. Incubation at 65°C for 20 minutes was followed by extraction with 8 ml chloroform. After precipitation with isopropanol and sodium acetate, DNA was extracted three times with phenol:chloroform:isoamylalcohol (25:24:1) and once with chloroform, precipitated again with ethanol, and resuspended in 100 μl TE buffer. DNA was fragmented by overnight digestion at 37°C using restriction enzymes *AluI* and *MseI*, followed by heat inactivation of the enzymes at 65°C for 20 minutes. DNA was extracted with phenol:chloroform:isoamylalcohol and precipitated with ethanol and sodium acetate. DNA fragments were labeled using the BioPrime System (Invitrogen) according to the manufacturer's protocol. Labeled DNA was resuspended in 30 μl nuclease-free water and quantified by spectrophotometry. After DNA quality was determined by agarose gel electrophoresis, four individual labeling reactions were pooled to yield at least 30 μg of DNA for hybridization.

Array hybridization

Hybridization of GeneChip arrays was done according to the manufacturer's protocol (Affymetrix). For washing and staining, protocol EukGe-WS2v4 (Affymetrix) was used. Because there was considerable variation between DNA hybridization experiments, only arrays hybridized with DNA extracted and labeled at the same time were compared (two each for Col and *Ler*). Using previously described algorithms (Borevitz et al., 2003), all unique features were evaluated for differential hybridization. With 3,806 single feature polymorphisms (SFPs) detected among 92,924 unique features, a false discovery rate of 5.4% was estimated, a number similar to the one reported before (Borevitz et al., 2003).

Analysis of expression data

Expression levels were estimated from Affymetrix hybridization intensity data using the robust multi array analysis (RMA) package implemented in R (Irizarry et al., 2003), or MicroArray Suite 5.0 (Affymetrix, 2001). Expression values were imported into GeneSpring 5.1 (Silicon Genetics) and normalized to the 50th percentile of each array for further analysis.

Analysis of DNA hybridization

Scanned images were saved as .CEL files using default settings of MicroArray Suite 5.0 (Affymetrix). Numeric values representing the signal of each feature were analyzed using scripts and statistical methods developed by Borevitz and colleagues (Borevitz et al., 2003) and implemented in R.

Identification of Col/*Ler* length polymorphisms

Primers located in the 5' and 3' UTRs of candidate polymorphic genes are listed in Table S1 at <http://dev.biologists.org/supplemental>. Genomic DNA was purified with the DNeasy Plant Mini kit (Qiagen). PCR was carried out using a 1:10 mixture of ExTaq (Takara) and Taq polymerase in ExTaq buffer with 10 pmol of each primer and 50 ng of DNA in 20 μl volume. PCR reactions were cycled for 41 times at 94°C for 20 seconds, 51°C for 30 seconds and 72°C for 5 minutes.

Real time and semi-quantitative RT-PCR

Total RNA was extracted from apices of plants grown in an independent experiment using RNeasy Mini columns with on-column DNase digestion (Qiagen). Reverse transcription was performed with 1 μg of total RNA, using a Reverse Transcription Kit (Promega). PCR amplification was carried out in the presence of the double-strand DNA-specific dye SYBR Green (Molecular Probes). Amplification was monitored in real time with the Opticon Continuous Fluorescence Detection System (MJR). A list of primers used is shown in Table S2 (<http://dev.biologists.org/supplemental>).

Identification and analysis of the ALF7 mutant

Arabidopsis plants of the Col strain were transformed with the pSKI015 activation-tagging vector (Weigel et al., 2000) and several Activation-tagged Late-Flowering (ALF) lines were selected in the T₁ generation. Plasmid rescue was used to identify the insertion point in one of these lines, ALF7. The corresponding cDNA and that of its paralog were PCR-amplified from first-strand cDNA generated from shoot apex RNA, and placed behind the CaMV 35S promoter in the pART27 derivative pMLBART (Gleave, 1992). The resulting constructs were introduced into Col wild type by *Agrobacterium tumefaciens*-mediated transformation (Weigel and Glazebrook, 2002).

Results and discussion

Experimental design and availability of data

To monitor global changes in gene expression, we used photolithographically produced microarrays in which each gene is represented as a probe set with several oligonucleotide features (Affymetrix GeneChips). Initial experiments were done with the *Arabidopsis* Genome 1 (AtGenome1) array, which contains 8,297 probe sets; the final experiment was performed with the newer *Arabidopsis* ATH1 array, which represents 22,810 probe sets (Table 1). For comparison across different arrays, raw data were scaled using the global intensity of all probe sets on each array. Signal intensities for each probe set were estimated from .CEL files using Affymetrix Microarray Suite (MAS) 5.0 (Affymetrix, 2001) or the log-scale robust multi array analysis (RMA) package implemented in R (Irizarry et al., 2003). The analysis presented here is based on RMA, because it produces fewer false positives when using single arrays than MAS or dChip (Li and Wong, 2001). Microarray data discussed here have been deposited with the Gene Expression Omnibus database at the NCBI (<http://www.ncbi.nlm.nih.gov/geo/>; series accession number GSE576 and GSE577; sample accession numbers GSM8827-8866 and GSM8868-8879). See Table S3

Table 1. Experiments and arrays probed

Experiment I (AtGenome 1; 30 SD)						
Genotype	+ 0 LD	+ 2 LD	+ 4 LD			
Col (<i>FLC fri-Col</i>)	1	1	1			
<i>FLC FRI-Sf2</i>	1	1	1			
<i>flc-3 fri-Col</i>	1	1	1			
<i>flc-3FRI-Sf2</i>	1	1	1			
Experiment II (AtGenome 1; 30 SD)						
Genotype	+ 0 LD	+ 1 LD	+ 2 LD	+ 3 LD	+ 4 LD	+ 5 LD
Col	2	2	2	2	2	2
<i>lfy-12</i> (Col)	1	1	1	1	1	1
<i>Ler</i>	2	2	2	2	2	2
<i>co-2</i> (<i>Ler</i>)	1	1	1	1	1	–
<i>ft-2</i> (<i>Ler</i>)	1	1	1	–	1	–
Experiment III (ATH1; 30 SD)						
Genotype	+ 0 LD	+ 3 LD	+ 5 LD	+ 7 LD		
Col	2	2	2	2		
<i>lfy-12</i> (Col)	2	2	2	2		
<i>Ler</i>	2	2	2	2		
<i>co-2</i> (<i>Ler</i>)	2	2	2	2		
<i>ft-2</i> (<i>Ler</i>)	2	2	2	2		

Numbers indicate arrays probed. In each experiment, plants were grown at the same time, but shoot apices for each array were isolated independently. The array type for each experiment is indicated.

LD, long days; SD, short days; Col, Col; *Ler*, *Ler*.

(<http://dev.biologists.org/supplemental>) for locus identifiers of genes discussed in this work.

Because many floral regulators are expressed exclusively or predominantly at the shoot apex, the site of flower formation, we first compared the sensitivity of the arrays in detecting such genes between whole 30-day-old seedlings and dissected shoot apices. The shoot apex includes the growing point of the plant, the shoot meristem, surrounded by young primordia, which before floral induction develop into leaves, and afterwards into flowers. Several meristem-specific genes, such as *CUPSHAPED COTYLEDON 2* (*CUC2*), *SHOOT MERISTEMLESS* (*STM*) and *WUSCHEL* (*WUS*) (Aida et al., 1999; Long et al., 1996; Mayer et al., 1998), were not reliably detected in whole seedlings, but easily detectable in shoot apices (Fig. 1A). Moreover, reproducibility of the results was not compromised by the manipulations of dissection, as demonstrated by comparison of replicate arrays (Fig. 1B).

DNA polymorphisms between two wild-type strains

The probes (25mer oligonucleotides) on the Affymetrix arrays were designed using mostly information from the Columbia (Col) reference strain, whose genome has been sequenced (The *Arabidopsis* Genome Initiative, 2000). Because many flowering time mutants have been induced in Landsberg *erecta* (*Ler*), another commonly used laboratory strain, we evaluated the efficiency of detecting *Ler* sequences by labeling and hybridizing genomic DNA from Col and *Ler* to AtGenome 1 arrays, using procedures similar to those of Borevitz and colleagues (Borevitz et al., 2003). Less than one percent of loci contained more than six single-feature polymorphisms and these were considered as probably highly polymorphic or deleted in *Ler*. 26 of 31 loci that were PCR amplified had indeed *Ler*-specific deletions (see Table S1 at <http://dev.biologists.org/supplemental>). Among the other five,

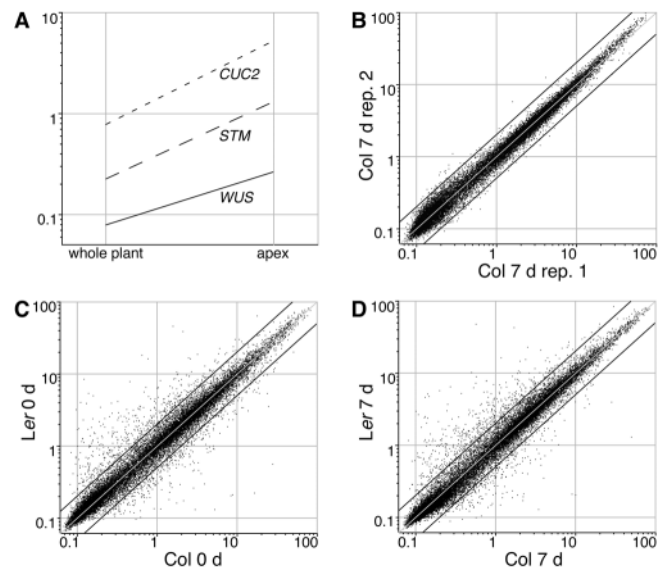


Fig. 1. Characteristics of expression estimates. (A) Expression of marker genes for the shoot apex. (B) Similarity in expression estimates between arrays of duplicate samples. (C,D) Differences in expression estimates for averages from duplicate Col and *Ler* arrays. Numbers indicate relative expression levels. d, days; rep, replicate number.

the RNA signal of 4 genes (At1g60130, At2g15400, At2g21060, At5g26580) was lower in *Ler* than in *Col*, suggesting that these loci are highly polymorphic.

When we used the ATH1 array to compare RNA signals of vegetative shoot apices from *Col* and *Ler*, we found 961 transcripts with at least a two-fold difference in signal intensity between the two accessions. 553 of these had a lower signal in *Ler*, again raising the possibility that some of them might be polymorphic. However, 408 transcripts produced a higher signal in *Ler*, suggesting that these differences are true expression changes (see Fig. S1 at <http://dev.biologists.org/supplemental>). In conclusion, sequence polymorphisms or deletions in the *Ler* sequence should not be a major concern when using Affymetrix arrays for analysis of *Ler*-derived samples. However, there appear to be many genuine expression differences between *Col* and *Ler* (Fig. 1C,D; Fig. S1 at <http://dev.biologists.org/supplemental>), and it is important to consider this fact when comparing non-isogenic strains.

Effect of day length change on two different wild-type strains

To monitor changes in gene expression during floral induction and early flower development, we grew plants under short photoperiods (which delays flowering) for 30 days, and then transferred them to long days. In a pilot experiment, we had found that many flower-specific markers such as homeotic genes were not detected on day 0, but were robustly induced around day 6. Scanning electron microscopy confirmed that the shoot apex was vegetative at the beginning of the experiment (Fig. 2A,C). After wild-type plants had been grown in long photoperiods for 7 days, the oldest floral primordia at the end of our experiments were around stage 7 (Smyth et al., 1990). Importantly, in addition to floral primordia, release of lateral shoot primordia was evident (Hempel and Feldman, 1994). Thus, we can expect to identify in our experiments at least three classes of genes in addition to genes that are expressed in young flowers: genes that characterize young leaf primordia (which should be repressed); genes that mark the formation of side shoots (which should be induced), and genes that distinguish the shoot apical meristem before and after floral induction.

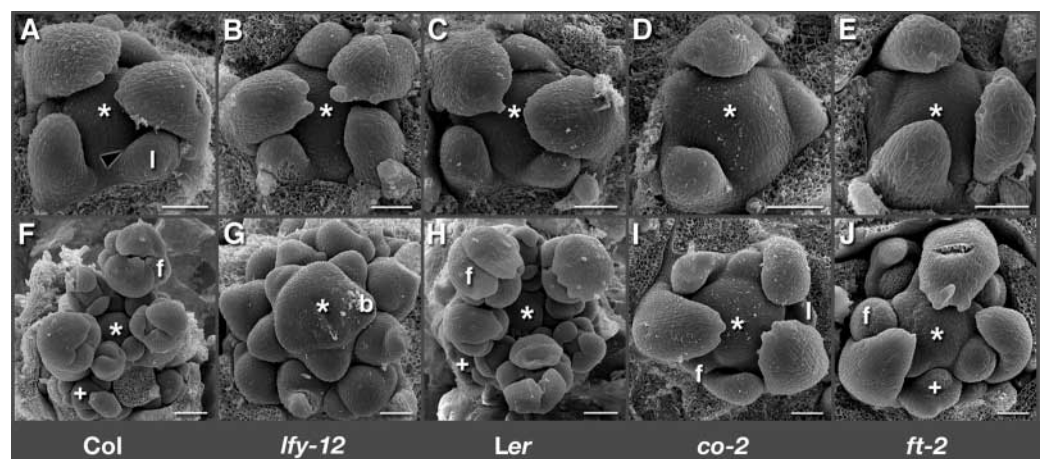
We assayed gene expression changes in the *Col* and *Ler*

wild-type strains at multiple time points in two experiments (Table 1). Both experiments were performed in duplicate, using separately prepared shoot apices from plants grown at the same time. To ensure consistency in the dissection of shoot apices, each investigator performing a specific experiment participated in dissecting plants from all genotypes. Here, we focus on experiment III, in which we used ATH1 arrays.

Several genes are known to be induced in the shoot meristem proper upon floral induction, including the MADS box genes *SOC1* and *FRUITFULL (FUL)*, the *SQUAMOSA PROMOTER BINDING PROTEIN LIKE 3 (SPL3)*, *SPL4* and *SPL5* genes and the *REM1* gene (Borner et al., 2000; Cardon et al., 1999; Cardon et al., 1997; Franco-Zorrilla et al., 2002; Hempel et al., 1997; Lee et al., 2000; Samach et al., 2000). Other genes, such as *FLOWERING PROMOTING FACTOR1 (FPF1)*, are induced at the periphery (Kania et al., 1997). For the floral primordia proper (Smyth et al., 1990), several stage-specific markers are known. During stage 1, the floral meristem identity genes *LFY*, *API* and the *API* paralog *CAULIFLOWER (CAL)* are induced (Gustafson-Brown et al., 1994; Kempin et al., 1995; Weigel et al., 1992). During stage 2, *SEPALLATA1 (SEP1)*, *SEP2* and *SEP3* are activated, and shortly thereafter the homeotic genes *AP3*, *PI* and *AG*, which act in combination with the *SEP* genes (Drews et al., 1991; Flanagan and Ma, 1994; Goto and Meyerowitz, 1994; Jack et al., 1992; Savidge et al., 1995). Upregulation of all genes discussed above was easily detected in both *Col* and *Ler* samples (Fig. 3A-F). For the later time points, the MAS software identified almost all of them 'present', which is an indication of the ease with which these genes are detected.

A sequence of induction of the homeotic genes could be partially resolved in our experiments, with the C function gene *AG*, which is expressed in the center of the flower, being activated last (Fig. 3F). Two other well-studied genes that were robustly detected were *CRABS CLAW (CRC)* and *WUS* (Fig. S2, <http://dev.biologists.org/supplemental>). *CRC* has been reported by in situ hybridization to be activated during stage 6 of flower development, which would be toward the end of our time series (Bowman and Smyth, 1999). This is inconsistent with the profile we observed, suggesting that there is also non-localized induction of *CRC*. *WUS* marks a small group of cells in shoot and floral meristems (Mayer et al., 1998), and its

Fig. 2. Scanning electron micrographs. (A-E) Shoot apices of plants grown for 30 days under short days. (F-J) Shoot apices of plants after 7 additional long days. Axils of leaf primordia appear empty before the shift to long days (A). White asterisks indicate shoot apical meristems, crosses lateral shoot meristems that form in the axils of leaves. The oldest flower primordia (f) are labeled in F and H-J. Note that these are much younger in *co-2* and *ft-2* mutants than in wild type, and that flower-like structures have not yet formed in *lfy-12* mutants, although several bracts (b) that surround the shoot apical meristem are apparent. Scale bars: 50 μ m (A-E,G,I,J); 100 μ m (F,H).



Scale bars: 50 μ m (A-E,G,I,J); 100 μ m (F,H).

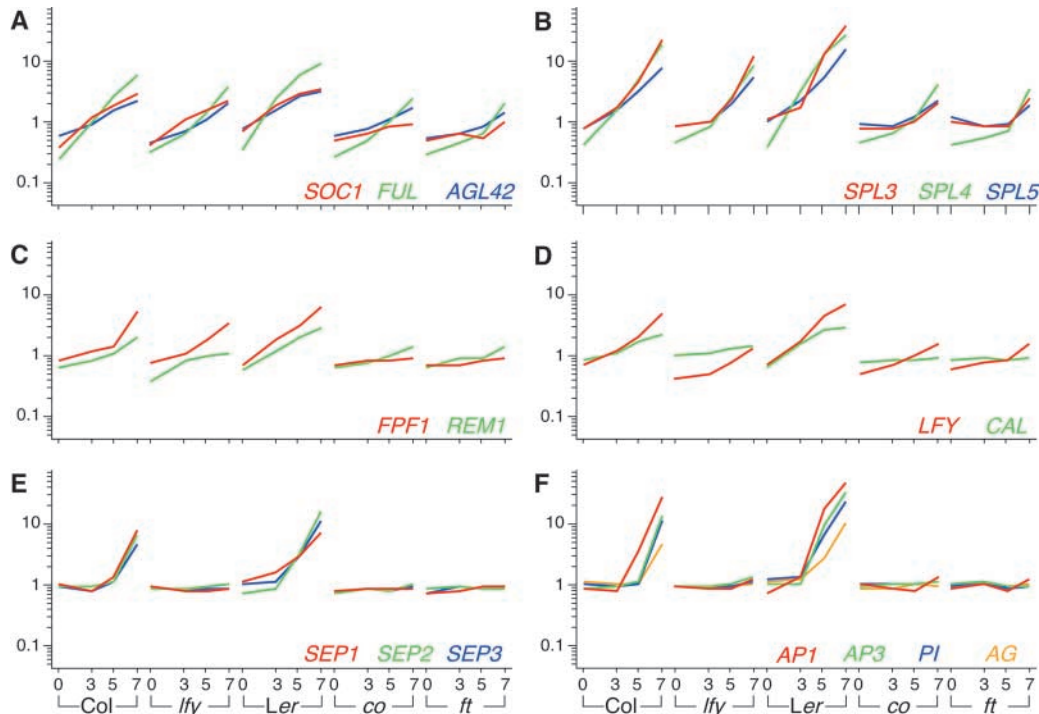


Fig. 3. Expression profiles of known flowering-time and floral genes in wild-type and mutant plants. Signals were normalized to the median for each gene. Numbers on the *x* axis refer to days after transfer to long days. Numbers on the *y* axis indicate relative expression levels. Data are from experiment III, and were analyzed by RMA.

upregulation probably reflects the increase in meristem number after floral induction. Expression of *STM*, which is expressed more widely in the shoot apical meristem, was less markedly changed (Fig. S2, <http://dev.biologists.org/supplemental>).

All floral markers were induced more quickly in *Ler* than in *Col*. Both strains are relatively early flowering compared to many wild accessions, partially because they have null alleles at the *FRIGIDA* (*FRI*) locus, which is required for high expression of the floral repressor *FLC* (Johanson et al., 2000; Michaels and Amasino, 1999; Sheldon et al., 1999). However, *Col* flowers several leaves later than *Ler* under long days (e.g. Kardailsky et al., 1999). One genetic difference between the two strains is that the *Ler* allele of the floral repressor *FLC* is only very weakly active (Koornneef et al., 1994; Lee et al., 1994). Accordingly, we detected lower *FLC* levels in *Ler* than in *Col* (Fig. S3, <http://dev.biologists.org/supplemental>).

CO- and FT-dependent targets of floral induction

Activity of the *CO* gene is essential for perception of photoperiod differences (Koornneef et al., 1991). *CO* acts through at least two other genes with major effects on flowering time, *FT* and *SOC1* (Samach et al., 2000; Suárez-López et al., 2001). Loss-of-function mutations in all three genes delay flowering under long days, with *co* mutations having the strongest and *soc1* the weakest effects (Koornneef et al., 1998; Onouchi et al., 2000). Because *FT* and *SOC1* integrate other cues in addition to photoperiod, mutations in both genes also delay flowering under short days, where *co* mutants are normal (Borner et al., 2000; Koornneef et al., 1991; Lee et al., 2000; Onouchi et al., 2000). To assess whether all effects of day length on gene expression in the shoot apex are transduced by the *CO* pathway, and how much of the *CO* effect is mediated by *FT*, we compared the expression profiles of *Ler* wild-type plants to those of *co-2* and *ft-2* mutants. By the end

of our experiments, floral primordia were just beginning to form in *co-2* and *ft-2* mutants (Fig. 2I,J).

An examination of known floral marker genes revealed that *co* and *ft* had very similar effects (Fig. 3). Overall, the effects of *co* and *ft* reflected the sequence of induction in wild type. That is, early response genes, such as *FUL*, *SOC1* and *SPL3-5*, were attenuated, with *FUL* showing the smallest change compared to wild type (Fig. 3A,B). Induction of *LFY* was only attenuated (Fig. 3D). Interestingly, *FPF1*, which is expressed in a similar temporal pattern as *LFY* in wild type, is affected more strongly than *LFY* by *co* and *ft* (Fig. 3C). There were several other genes whose expression profile across all data sets was highly correlated with that of *FUL* (>90%), including that of the *SOC1* paralog *AGL42* (Fig. 3A). The other floral markers, including *API*, *CAL*, the *SEP* genes and the homeotic genes *AP3*, *PI* and *AG*, were not induced in *co* or *ft* during the time course of the experiment (Fig. 3D-F). Finally, induction of *CRC* was only moderately attenuated in *co* and *ft* mutants (Fig. S2, <http://dev.biologists.org/supplemental>). This observation confirms that the *CRC* expression detected here must be different from the highly localized expression in carpels (Bowman and Smyth, 1999), since neither *co* nor *ft* mutants had produced stage 6 flowers by the end of the experiment.

It is notable that *SOC1* was affected not only by *co*, but to a similar extent by *ft*, indicating cross-regulation between the two *CO* targets, *FT* and *SOC1*. *LFY*, which is expressed weakly during the vegetative phase (Blázquez et al., 1997; Hempel et al., 1997), was identified as 'present' by the MAS software prior to floral induction. The induction of *LFY* is attenuated in *co* mutants, but also in *ft* mutants, even though genetic analyses clearly show *FT* and *LFY* to act in parallel (Kardailsky et al., 1999; Kobayashi et al., 1999; Nilsson et al., 1998; Ruiz-García et al., 1997).

We used reverse transcription followed by quantitative (real-time) PCR to confirm the expression changes of several of these genes in wild type and mutants, using RNAs prepared in a separate experiment from plants at 0 and 7 days after transfer to long days (Fig. S4, <http://dev.biologists.org/supplemental>). All genes tested were induced more strongly in wild-type plants than in the corresponding mutants, confirming the effects. RT-qPCR resulted in higher estimates for induction of the early marker genes (*FUL*, *CAL*, *API*) in *Col* than in *Ler*, which contrasts with the interpretation of the Affymetrix array data. This may either be due to the fact that this was an independent experiment or to differences in amplification efficiencies for *Col* and *Ler* samples.

To compare the effects of *co* and *ft* more broadly, we selected those genes that changed the most during the time course of the experiment. Using RMA, we calculated for all genes the absolute average difference in expression levels between days 0 and 7 for the replicate *Ler* and *Col* sets. We then ranked all genes by expression change and selected the overlap between the top 500 genes in both *Ler* and *Col* ('top 500 list'). This cut-off corresponded to a 2.6-fold change in *Ler* and a 1.9-fold change in *Col*, which reflects the more dramatic responses seen with known flowering genes in *Ler*.

This procedure is conservative, since it removes several genes that are detected robustly in only one of the two accessions. Nevertheless, there was a remarkable overlap between the *Ler* and *Col* sets. For genes with increased expression, the overlapping 101 genes represented 73% and

54% of the corresponding *Ler* and *Col* sets, respectively. For genes with decreased expression, the overlapping 231 genes represented 63% and 74% of the corresponding *Ler* and *Col* sets, respectively. A comparison of results for this list of genes from two replicate arrays for individual genotype-time point combinations demonstrated that the signals for most of these genes are readily reproducible (Fig. 4A). The effects of the filter are obvious in a scatter plot comparing *Ler* (day 0) with *Ler* (day 7) (Fig. 4B).

Comparison of *ft* (day 0) with *Ler* (day 0) showed that *ft* does not have obvious defects in the expression of floral marker genes before transfer to long days (Fig. 4C). Similarly, *ft* (day 0) and *co* (day 0) were very much alike (Fig. 4D). The effects of *FT* and *CO* on global gene expression were apparent when comparing *ft* (day 7) with *Ler* (day 7) (Fig. 4E). Importantly, *ft* (day 7) and *co* (day 7) were also very similar (Fig. 4F), confirming the results seen with a smaller selection of genes. Consistent with the morphological changes (Fig. 2J), we found that *ft* (day 7) was distinct from *ft* (day 0) (Fig. 4G).

In addition to *FT* and *SOCI*, two other *CO* targets, *ACS10* and *P5CS2*, have been found using an inducible form of *CO* (Samach et al., 2000). Both genes were detected at high levels in all genotypes that were analyzed, but their levels did not change during the course of the experiment (Fig. S5, <http://dev.biologists.org/supplemental>). A possible explanation for the discrepancy is that we analyzed only material from the shoot apex, whereas Samach and colleagues (Samach et al., 2000) analyzed whole seedlings.

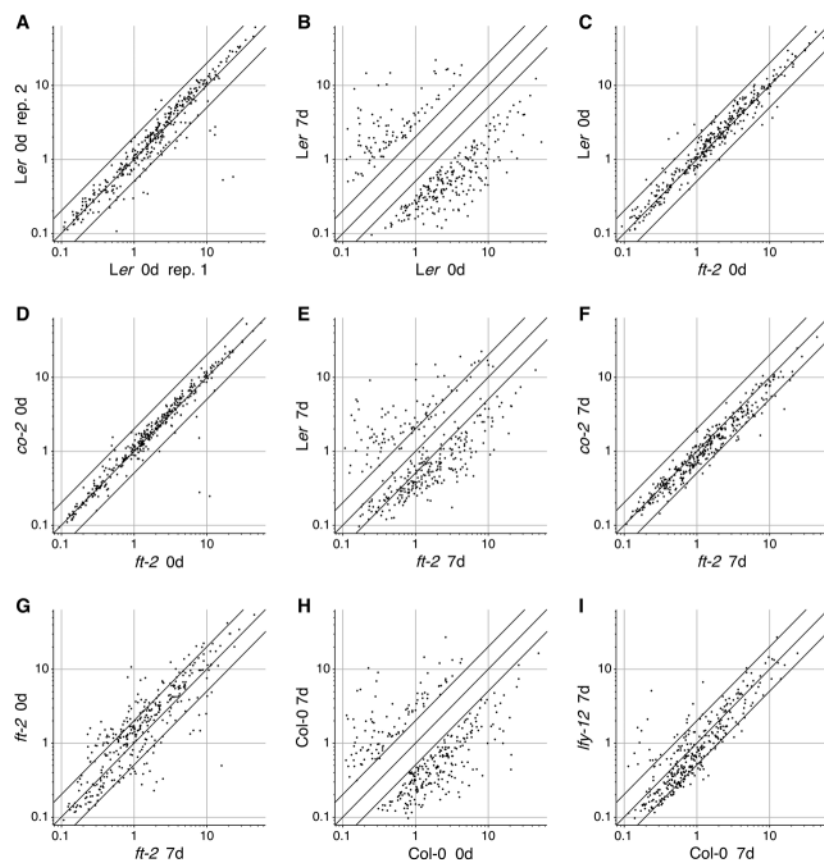


Fig. 4. Correlation analysis of the list of 'top 500 genes in *Col* and *Ler*' (see text for details). d, days; rep, replicate number.

Integration of photoperiod and *FLC* activity

FLC is an important repressor of flowering that acts in parallel with the photoperiod pathway (Borner et al., 2000; Lee et al., 2000; Samach et al., 2000). Because of a deletion in the *FLC* activator *FRI* (Johanson et al., 2000), *FLC* levels are much reduced in *Col* compared to an isogenic strain with the functional *FRI-Sf2* allele (Fig. S3, <http://dev.biologists.org/supplemental>) (Lee et al., 1993). To determine the effects of *FLC* on the acute response to photoperiod induction, we compared the expression of floral markers in the congenic strains *FLC FRI-Sf2*, *FLC fri-Col* (*Col* wild type), *flc-3 FRI-Sf2* and *flc-3 fri-Col* (Michaels and Amasino, 2001). Integration of photoperiod and autonomous pathways appears to be downstream of *CO*, since *CO* displays a similar induction profile in all four genotypes. We found that early induction of *CAL* was only moderately attenuated by *FLC* activity, whereas *SOCI* induction was severely affected, but still detectable. In contrast, *FUL* induction was abolished in *FLC FRI-Sf2* (Fig. 5). Thus, *FLC* appears to act additively with some regulators of the photoperiod pathway and epistatically with others, consistent with the notion that *FLC* and *CO* activities are integrated by the same promoters (Hepworth et al., 2002).

LFY-dependent targets of floral induction

During floral induction, several events can be

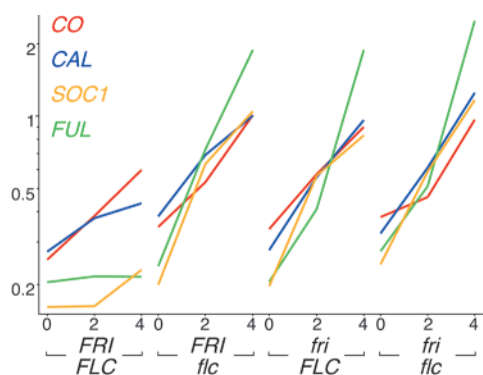


Fig. 5. Effect of *FLC* on the photoperiod response. Induction of *CO* is independent of *FLC* repression. Downstream genes *CAL*, *FUL* and *SOC1* are differentially affected. At the last time point, there was no sign of flower formation in *FRI FLC* plants.

distinguished at the shoot apex. First, expression of genes such as *FUL* or *SOC1*, which act upstream of floral identity genes, changes in the shoot meristem itself. After primordia on the flanks of the shoot meristem have acquired floral identity through the activity of proteins such as *LFY*, genes required for specification of floral organ identity are induced. While mutations in *LFY* affect the formation of individual flowers, *lfy* mutants have only a small effect on other events associated with floral induction, such as stem elongation. To determine which of the genes that are affected by the transfer from short to long days are likely to be flower specific, we compared

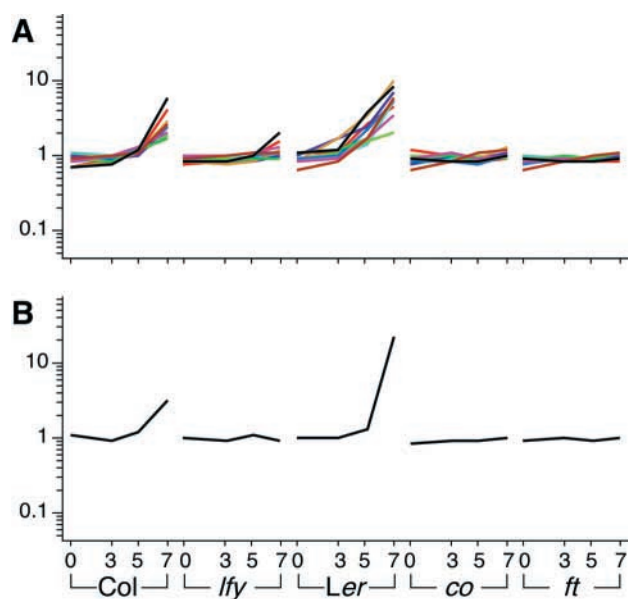


Fig. 6. Expression profiles of new *LFY* candidate targets. Locus identifiers and gene descriptions are listed in Table 2. Signals were normalized to the median for each gene. (A) Expression profiles of genes from Table 2. At2g01520 (tan) At3g04960 (cyan) At4g21590 (brown) At4g27460 (light green) At4g31910 (black) At4g33790 (pink) At5g15150 (red) At5g2390 (purple) At5g22430 (teal). (B) Expression profile of At5g22430, which was identified as a potential *AP3* target by Zik and Irish (Zik and Irish, 2003).

expression profiles in Col wild type and the Col-derived *lfy-12* mutant. In strong *lfy* mutants, the first few flowers are replaced by leaf primordia, in the axils of which lateral shoots arise, while flowers that develop later lack petals and stamens and have some shoot characteristics (Huala and Sussex, 1992; Schultz and Haughn, 1991; Weigel et al., 1992). Scanning electron microscopy showed that, after transfer to long days, *lfy* mutants behaved differently from *co* or *ft* mutants, as many more leaves or bracts with incipient axillary meristems in their axils were apparent (Fig. 2G).

We found that only a minority of substantial expression changes caused by transfer from short to long days was *LFY* dependent. In addition to known *LFY* targets, which are the homeotic genes *API*, *AP3*, *PI* and *AG* (Fig. 3F) (Busch et al., 1999; Lamb et al., 2002; Liljgren et al., 1999; Wagner et al., 1999; Weigel and Meyerowitz, 1993), the group of *LFY*-dependent genes includes the homeotic cofactors *SEPI-3* (Fig. 3E); all 7 genes are also found in the 'Col and Ler top 500' list. A less dramatic effect was seen for the *API* paralog *CAL* (Fig. 3D).

Next, we mined the expression profiles for genes that behaved similarly to the homeotic or the *SEP* genes across all data sets. This procedure resulted in 10 additional genes, of which 6 were again in the 'Col and Ler top 500' list (Fig. 6, Table 2). None of them was as strongly induced as the most obvious *LFY* targets, such as *API*, *AP3* or *PI*. As expected, additional analyses did not identify any genes that were dependent on *LFY*, but not on *CO* or *FT*.

Correlation analysis using the same genes selected for global analysis of *co* and *ft* showed that Col (day 0) and *lfy* (day 0) were very similar, indicating that *LFY* did not affect floral marker gene expression before induction by photoperiod. On day 0, Col and *lfy* are more similar to each other than are Col and *Ler* (not shown). In contrast to *CO* and *FT*, which have dramatic effects on expression of floral marker genes (Fig. 4E, F), a comparison of Col (day 7) and *lfy* (day 7) showed that there were few changes in *lfy* mutants (Fig. 4I), consistent with the finding that only a small number of genes behaved similarly to known *LFY* targets.

Zik and Irish (Zik and Irish, 2003) have recently reported an analysis of the response of about 6,000 genes to changes in activity of the *LFY* targets *AP3* and *PI*. The authors identified 47 potential *AP3/PI* targets, of which 42 are represented on the ATH1 array. Among these, we found only one gene, At5g22430, that is obviously affected in *lfy* mutants (Fig. 6B).

Table 2. Newly identified genes that are activated in a *LFY*-dependent manner

Locus ID	Gene
At2g01520	Major latex protein (MLP)-related
At3g04960	Hypothetical protein
At4g21590	Putative bifunctional nuclease
At4g27460	Hypothetical protein
At4g31910	Putative protein
At4g33790	Male sterility 2-like protein
At5g15150	Homeobox-leucine zipper protein, HAT7
At5g2390	Photoassimilate-responsive protein PAR-like protein
At5g57720	Putative protein
At5g24910	Cytochrome p450, putative

Genes were selected based on 97% correlation in the Col and *lfy* sets with *API*, *SEPI-3*, *PI*, *AP3* or *AG*.

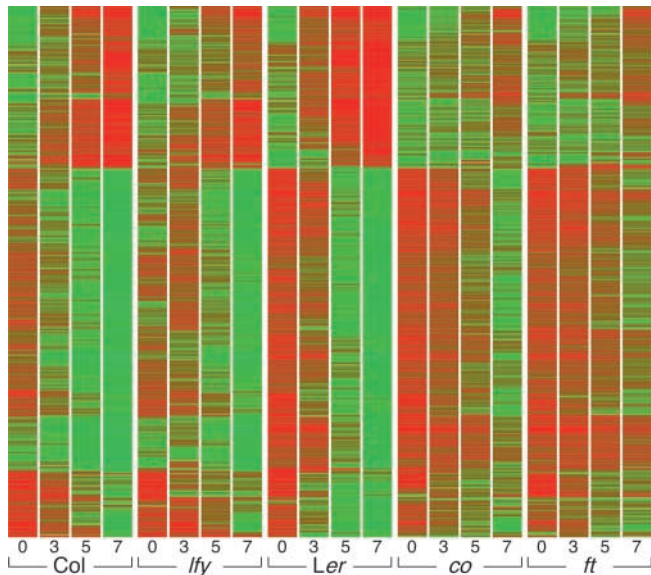


Fig. 7. Hierarchical clustering of ‘top 500 genes in Col and Ler’. Red indicates high expression signal, green low signal. Signals were normalized to the median for each gene.

Genes repressed upon floral induction

An unanticipated finding was that there are considerably more genes that are repressed upon transfer from short to long days than are induced; from our ‘Col and Ler top 500’ list, 101 genes were activated and 231 genes repressed (Fig. 7; see Table S4 at <http://dev.biologists.org/supplemental>, for a list of genes and their expression values). We do not think this is an artifact, because we see a similar ratio if we include a wider range, e.g., top 1000 genes. Previous molecular screens have focused on genes that are activated upon floral induction (e.g. Franco-Zorrilla et al., 1999; Melzer et al., 1990; Samach et al., 2000). Similarly, although forward genetic screens have identified several floral repressors (Mouradov et al., 2002; Simpson and Dean, 2002), only one of them, *FLC*, is known to be down-regulated by vernalization, a treatment that promotes flowering (Michaels and Amasino, 1999; Sheldon et al., 1999), and none has been identified that is repressed by photoperiod. A more

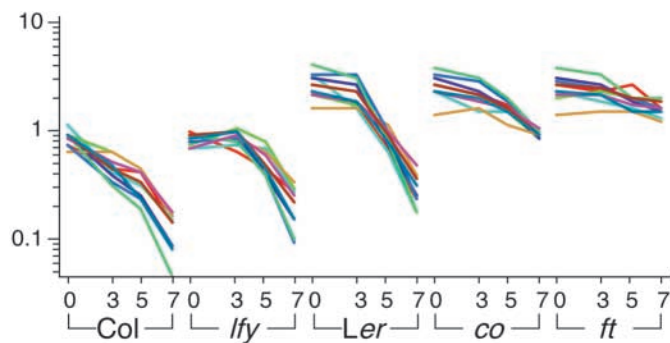


Fig. 8. Expression profiles for a subset of repressed genes, that are expressed more highly in Ler than Col: At3g58990 (green), At2g43100 (blue), At1g47485 (cyan), At3g03190 (purple), At1g74090 (brown), At4g13770 (teal), At2g39310 (pink), At2g37460 (red), At2g46650 (light green), At5g44480 (tan). Signals were normalized to the median for each gene.

detailed inspection of a subset of repressed genes showed that their behavior was opposite to that of the induced genes across all genotypes, i.e., the *Ler* response was faster than that of Col, and repression was not completely absent in *co* and *ft* mutants (Fig. 8).

Many of the genes that are known to be induced during floral induction belong to two classes of transcription factor genes, the MADS box genes and the SBP box (*SPL*) genes, with 69 and 15 members, respectively, represented on the ATH1 array. Among the top 101 induced genes, there were 11 MADS box genes and 5 *SPL* genes. In contrast, among the top 231 repressed genes, there was only one MADS box gene (*AGL14*) and no *SPL* gene. Both the enrichment of MADS box and *SPL* genes in the induced class and the difference between the induced and repressed classes are significant (Fisher’s exact test, $P \leq 0.001$ and $P < 0.003$, respectively).

A pair of paralogous AP2-domain genes that can repress flowering

An important question is, of course, whether any of the repressed genes play an instructive role in flowering. Coincidentally, we isolated a dominant, activation-tagged late-flowering line, ALF7. Plasmid rescue showed that the activation-tagging vector (Weigel et al., 2000) was inserted next to gene At3g54990, which encodes an AP2-domain protein that we named SCHLAFMÜTZE (*SMZ*) (Fig. 9A). Analysis of our expression data showed that this gene was repressed upon photoperiod change in Col and *Ler* wild type as well as *lfy* mutants, but not in *co* or *ft* mutants (Fig. 9B). At3g54990 has a close homolog, At2g39250, which is expressed at lower levels and which was named *SCHNARCHZAPFEN* (*SNZ*). The expression profiles of *SMZ* and *SNZ* were similar when analyzed by MAS, but down-regulation of *SNZ* was less apparent when analyzed by RMA (Fig. 9B). For both genes, we generated several transformants in which the coding sequences were placed behind the constitutive 35S promoter from cauliflower mosaic virus. Several lines in which *SMZ* or *SNZ* were under the control of the 35S promoter flowered much later than wild type (Fig. 9C), confirming that *SMZ* and *SNZ* can repress flowering. Consistent with redundant function of the two genes, *SNZ* knockouts flower normally. Although *SMZ* insertions are available, these do not interfere with RNA expression (data not shown).

Control of microRNA precursor expression by floral induction

Because their gene structure had been wrongly annotated, the phylogenetic affinity of *SMZ* and *SNZ* with AP2 and its close homologs had not been previously recognized. AP2 (At4g36920) and RAP2.7 (At2g28550) form, together with At5g67180 and At5g60120, a clade of proteins that have two AP2 domains. This clade has been identified as having potential target sites for a group of microRNAs (miRNAs) derived from a family of four precursor genes, *MIR172a-1*, *MIR172a-2*, *MIR172b* and *MIR172c* (Park et al., 2002). Although *SMZ* and *SNZ* have only a single AP2 domain, phylogenetic analysis shows that *SMZ* and *SNZ* fall within the clade defined by the other four AP2 domain proteins (not shown).

MiRNA-guided degradation of specific mRNAs has recently

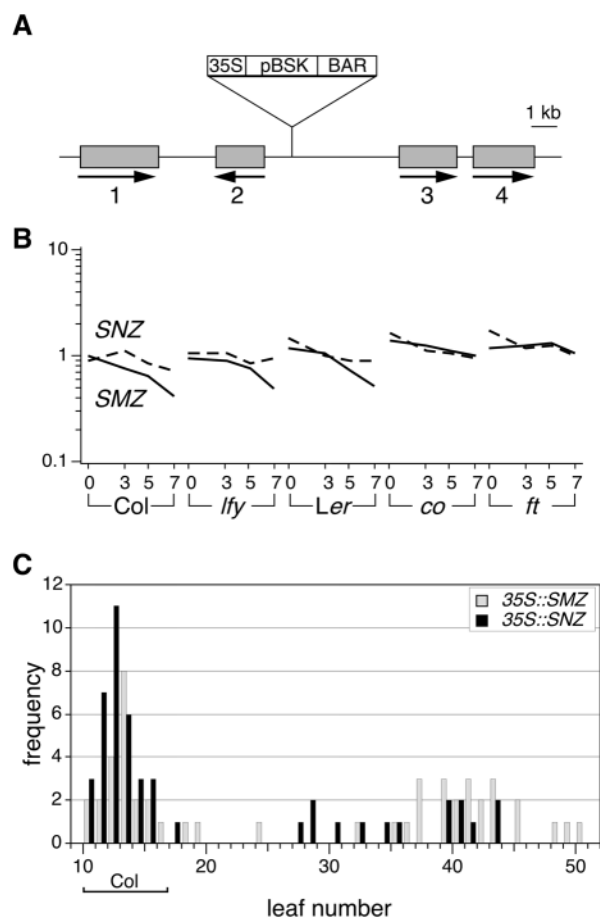


Fig. 9. *SMZ* and *SNZ* characterization. (A) Diagram of ALF7 insertion. The cauliflower mosaic virus 35S enhancers are located approximately 1 kb upstream of *SMZ*, which encodes an AP2-domain protein (2; At3g54990). Other genes in the vicinity of the enhancer are annotated as encoding a putative protein (1; At3g54980), and expressed proteins 3 (At4g55000) and 4 (At3g55005). (B) Expression profiles of *SMZ* and *SNZ*. Signals were normalized to the median for each gene. Numbers on the x axis refer to days after transfer to long days. (C) Histogram of flowering times of primary transformants in long days. Range of flowering time of Columbia wild type is indicated below the histogram.

been demonstrated to be important for plant morphogenesis (Palatnik et al., 2003). For the four *SMZ* and *SNZ*-related genes, Kasschau and colleagues (Kasschau et al., 2003) have shown that at least a fraction of their mRNAs is cleaved in wild-type inflorescences in the middle of the region that is complementary to the miR172 miRNAs. Experiments with *dcl1* mutants and RNA blots indicate that mRNA cleavage is frequent in *RAP2.7* and *At5g60120*, and rarer for *AP2* and *At5g67180* (Kasschau et al., 2003). *SMZ* and *SNZ* share the miR172 complementary motif, but with 3 or 4 mismatches (Fig. S6, <http://dev.biologists.org/supplemental>). Among the other four, only *At5g67180* has also at least 3 mismatches, while the remaining three have 1 or 2 mismatches with at least one miR172 isoform. When we examined the expression profiles of this clade of AP2 domain encoding genes, we found that *AP2*, *RAP2.7* and *At5g60120* are down-regulated similarly to *SMZ*, and that their down-regulation is *CO* and *FT*

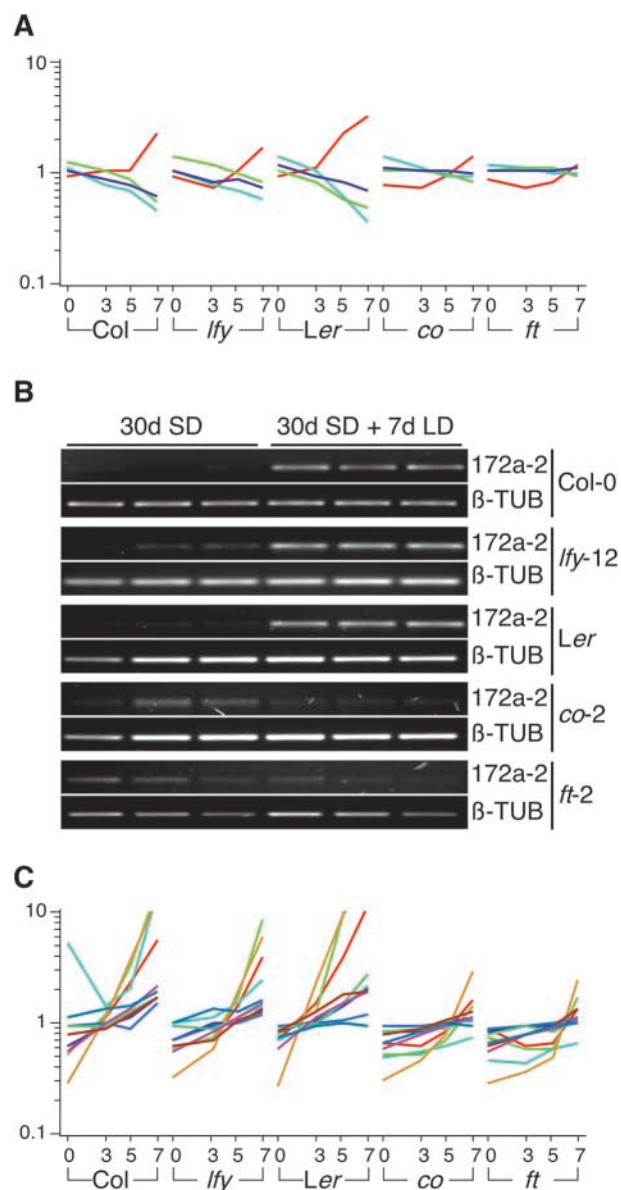


Fig. 10. Expression of putative miRNA target genes and a miRNA precursor in response to photoperiod. (A) *AP2* (purple), *RAP2.7* (cyan), *At5g60120* (green) and *At5g67180* (red). Signals were normalized to the median for each gene. (B) Expression of *MIR172a-2* analyzed by semi-quantitative RT-PCR. Because of background amplification, quantification using SYBR Green and real-time PCR was not possible. β -tubulin was used as a control. (C) Expression profiles of *SPL2* (cyan), *SPL3* (light green), *SPL4* (ochre), *SPL6* (blue), *SPL9* (brown), *SPL10* (dark green), *SPL11* (purple), *SPL13* (teal) and *SPL15* (pink). Signals were normalized to the median for each gene. Numbers on the x axis refer to days after transfer to long days.

dependent. The expression levels of *At5g67180* also responded to floral induction, but in an opposite manner (Fig. 10A).

To determine whether the miR172 miRNAs might mediate transcript accumulation of this clade of AP2-related genes in response to floral induction, we monitored expression of four *MIR172* precursor RNAs by semi-quantitative RT-PCR. We detected PCR products for four precursors and found that at

least one of them, the *MIR172a-2* precursor, was up-regulated after floral induction in a *CO*- and *FT*-dependent manner (Fig. 10B). The miR172 miRNA is detected in young flowers, consistent with a role in down-regulating genes that repress flowering. Furthermore, overexpression of miR172 has the opposite effect to *SMZ* or *SNZ* overexpression, early flowering (Chen, 2003). Interestingly, miR172 appears to act also through translational repression, as deduced from overexpression experiments with one of the targets, *AP2* (Chen, 2003).

The three up-regulated *SPL* genes discussed earlier, *SPL3*, *SPL4* and *SPL5* (Fig. 3B), have also been identified as miRNA targets (Kasschau et al., 2003; Rhoades et al., 2002). When we examined the other *SPL* genes represented on the Affymetrix array, we found that *SPL2*, *SPL6*, *SPL9*, *SPL10*, *SPL11*, *SPL13* and *SPL15* behave similarly to *SPL3*, *SPL4* and *SPL5*, but that they reacted less strongly to floral induction (Fig. 10C). We noted that the latter three are distinguished from the rest by the presence of the miR156 miRNA target motifs in the 3' UTR rather than the coding sequence.

Conclusions

In developmental biology, global expression analysis has been used to date mainly to discover genes or pathways affecting specific processes, but only a few studies (e.g. Hu et al., 2002; Ma et al., 2003; Strand et al., 2003) have exploited this methodology to better understand the effects of mutants with related phenotypes. We have further demonstrated the power of this approach, by analyzing the dynamic behavior of a small organ system, the shoot apex, across multiple time points and multiple genetic backgrounds.

The parallel analysis of many known floral regulatory genes, along with the analysis of a large group of newly identified genes that respond to a change in photoperiod, has allowed us to draw several important conclusions. First, two genes previously identified as *CO* targets by *CO* overexpression, *ACS10* and *PC5S2*, do not change at the shoot apex, implying that *CO* also affects processes outside the region where flowers are formed. Second, consistent with the observation that among the two other known *CO* targets, *FT* has more dramatic effects than *SOCI* (Onouchi et al., 2000; Samach et al., 2000), the very similar expression profiles of *co* and *ft* mutants suggest that, at the shoot apex, *FT* is the major output of *CO*. Third, the effects of the floral repressor *FLC* and photoperiod are additive, resulting in expression profiles of floral marker genes that are similar in plants with and without *FLC*, but with overall much lower levels in the presence of *FLC*. This finding also confirms that the similar expression profiles of *co* and *ft* are not simply due to the fact that flower formation is delayed in both mutants, since plants with high *FLC* levels flower even later than *co* or *ft* mutants. Fourth, compared to *CO* and *FT*, a mutation in *LFY* has much more subtle effects, indicating that *LFY* acts further downstream in the floral induction cascade, even though genetically *FT* and *LFY* act in parallel downstream of *CO*.

There are several additional discoveries that we have made by inspecting our data set for genes without a known role in flowering. First, we found that forward genetic analysis has been very successful in identifying many of the genes that are most strongly activated in response to floral induction. However, an equally important response to floral induction may be the repression of regulatory genes. That at least some

of these repressed genes indeed have a role in flowering is confirmed by the analysis of the *SMZ* and *SNZ* genes. Second, two classes of transcription factor genes, one coding for MADS domain proteins and the other for SBP domain proteins, are highly overrepresented among the genes that are induced in response to photoperiod, both when compared to the overall complement of these families in the genome and when compared to the class of repressed genes. This observation suggests that flower-specific expression is the ancestral state for many genes in these two families. We have also found that there is a large class of genes that produce differential RNA signals between two different wild-type strains, *Col* and *Ler* (Fig. S1, <http://dev.biologists.org/supplemental>), which provides a rich source of candidates controlling phenotypic differences between these two strains.

How floral inductive signals are transmitted from genes such as *CO* and *FT* to downstream effectors such as *LFY* and *API* is not well understood, and the newly discovered set of genes dependent on *CO* and *FT*, but not *LFY*, constitute a source of potential factors playing important roles in this process. We noticed several paralogous gene pairs with very similar *CO* and *FT* responses in this group, which suggests that many of these genes were not identified in forward genetic screens because of redundancy. We have discovered two groups of potential miRNA targets, a clade of AP2-domain-encoding genes and a large group of *SPL* genes, as being regulated by *CO* and *FT*. This observation raises the possibility that miRNAs perform a critical function in mediating the effects of floral induction, which is supported by a recent report on the consequences of miR172 overexpression (Chen, 2003). The analysis of other flowering mutants in a similar experimental design as the one used here should further clarify the regulatory interactions between the many genes already known to play a role in flowering.

This paper is dedicated to the memory of the late François Godard. We thank Justin Borevitz for help with the DNA analysis and the .cdf file translated into the Bioconductor format; Ilha Lee and Rick Amasino for the gift of *FRI-Sf2* and *flc-3* strains; Heinz Schwarz and Jürgen Berger for help with SEM; Norman Warthmann for discussion and help with R. This work was supported by fellowships from the Deutsche Forschungsgemeinschaft (M.S.) and Human Frontiers Science Program (J.L.); by grants from NIH (GM62932) and HFSP to D.W., and by the Max Planck Society. D.W. is a Director of the Max Planck Institute.

Note added in proof

Aukerman and Sakai recently showed that At2g28550 (named TOE1) and At5g60120 (named TOE2) are also floral repressors (Aukerman and Sakai, 2003).

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DEV 0828ER**Dissection of floral induction pathways using global expression analysis**

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Supplementary Material

Supplementary Table 1. Oligonucleotide primers used for confirmation of DNA length polymorphisms (LP) and PCR results for genomic DNA amplification. “+” and “-” indicate whether an amplification product was seen.

Locus ID	Forward primer	Reverse primer	Col	Ler
At1g12010	TCTAAATGACCCAATTATGTGATC	CACACAATTATTGCATAAATAGTC	-	-
At1g31030	TCCAGATTAGTTCCTAACCATAC	AGAAACGTCAGGAGTCAGGTG	-	-
At1g31580	GTCTCAAAGCTCATACGCCAAG	CATACATGATACATTGCAAATATG	+	-
At1g52070	TGCGTGTAAGTGTAGCTAAATAC	ACATCGGAGTAGGTAGTAAATC	+	+
At1g53950	CTCCGTAGCTATCCGATTCAC	GATTAGAAATCGACCATGCCTAG	+	-
At1g53960	CTACATTCGGTCGAGGAACAC	GATAGCTACGGAGCTTCACAG	+	-
At1g60130	ACATGTTCTAGGATGGCTTGC	TCAAACATCAAACCTGCTCGAG	+	+
At1g60310	TGAGTTGGCTAATCATGCATTC	AACTACCCTTTCCTCCGCGG	+	-
At1g62550	CATGGATACCAGAGACTTGTC	GAAGTCGCAGAAGAAGTGTCGTG	+	LP
At1g67240	GAAATCACCTGTTGAGTTGAG	GCCGTTAGAAATAGTAAGATC	+	-
At1g67470	GTTAGATCCGATTTGATCCG	CTTGGCATTGTGTAATCATCTG	+	LP
At2g03560	TGAAATGTTTGATTGAATACAACC	GTATGATTCAAACCTAGCGATTG	-	-
At2g04380	CGTAGGTATGTTCTGGTTAACC	CTCTGTGATAGCTCTCTGGTC	+	-
At2g11140	TCGTTTCTACAGTTTCTGTTC	TTGGACTGTCTTTTGTGTGG	+	-
At2g11150	GTCTCAAAGCTCATACGCCAAG	GTCCATCTAAAACAACCGTCAC	-	-
At2g11250	CAACGGCTGCGTGAGATGC	CAAAGTACGCACCTTAGTGTAG	-	-
At2g13660	CAGACTTTGTGATGGCCAAAC	CCACTAGCCATAGCCCAAG	+	LP
At2g13940	TGGTATCAGAGCTTAAGATCTC	CACTACAACAGAAGTCGGCAC	+	-
At2g13970	GTGACAGTGGTGACGATATCTG	CAATGGTCAACGACATGAAGAC	+	-
At2g15400	CATTACCCTAAGAGTCCCAGAG	TTACCATTGACTCCTAG	+	+

At2g15410	TCAAGTCGGCCCAGATGAAAAG	CTTTGTGAGAGGTTGCCTACG	-	-
At2g16100	CTCTTACCACGGCATTAAAGAG	CAGGTATCGAAACGGATTTCATC	+	-
At2g17590	GACACTCGTATTTGATCTTGATC	GAGATGATCCAGGATATCGAAG	+	-
At2g19230	GTTCCACATGTTGGCAACATGCCTA	GAACAATAGAGCTCAATTGAAG	-	-
At2g21060	CCTATGCCTTTACACACATATC	GATTGTATGAAGGCTTGAAGTAG	+	+
At2g21090	GATTTAGCATTGCTACGAGATG	CTAAAGCTACATCAAATTCATCAC	-	-
At2g31080	TAATCATAGTTATCCACATGAATG	CATGCTAATCAAAGTCGACAATG	-	-
At2g45230	CATTCTGCTCATGTGGCAGC	GAACATCTGCTATATAAGATAGG	-	-
At4g01920	ACTTGAGAGTTAGAAGATACATC	GATAACTAATACATGCCATAAGTAC	+	-
At4g02540	TAATTGGAAGATAGGAGGAGC	TCTCATAACAATATTGGACATATC	+	-
At4g03470	CAAGACCTCACTCACATCGAG	CAACCGTTTGGTGCAAGCTTG	-	-
At4g03480	GCTTGATTTACATAAGTCAATGC	CCAGAGGTCTAATATCTTTCAG	+	-
At4g03500	GATCCTCGGTGCTTTAGCCG	AGGCTCTTGCTAGGATAATAAC	+	-
At4g04390	CACACTGTTTCGATAATGTCTG	GAAGGATCTGCTTAGTATAACCG	+	-
At4g07770	GAATTCCTCCACGCCAACATC	GTAGTCGAATGAGCTGAAGTG	+	-
At4g12180	CGTTTGATGATTCATGAAACGAG	CAAGCTGTTGCTGAAATTAATG	+	LP
At4g20210	CAGCTTTGCTTCGCTCACATTTTCC	CTGGTCCCAATCGAACAGTTA	-	-
At4g23220	GTCTACTGATGGTCCCACTC	CAAAGCTGACCGAGACATCAG	+	-
At4g25420	CTCCATTACAGACTATAGTATTG	CGTACTCACTTGTCATAGTGG	-	-
At4g27190	GAGTCAAGCAACTCGTCTACG	GGCTAAACATTAGTTAGATATCG	+	-
At4g33960	GATATTGTCGGTCGTGTGGAG)	GCGCTACTGCCAAATTACTCAC	+	LP
At5g26580	CTAGCTTACCACAATTTCTATATAC	CGACCTAGGCACTGATTAATCG	+	+
At5g27100	TGAGTGGTCACATGGAATCCG	CTATAGACAATCGGTGCTTTAGG	+	LP
At5g43270	ACATGATAGTTTCTCTCAGACAC	GAAGCTCTCATGTGCTGATGTG	-	-
At5g49440	TCGTTGAGTTAGTGATGCCAC	CTCGTAGTTATCACGATTCATG	+	-

Supplementary Table 2. Oligonucleotide primers used for RT-PCR.

Gene	Forward primer	Reverse primer
<i>FUL</i>	TTGCAAGATCACAACAATTTCGCTTCTC	GAGAGTTTGGTTCCGTCAACGACGATG
<i>CAL</i>	ACTCATGAATGAGTCCCTCAACCACCT	AAAGGAGAAGTCTGATGAGCGATCATG
<i>AP1</i>	AGGGAAAAAATTCTTAGGGCTCAACAG	GCGGCGAAGCAGCCAAGGTTGCAGTTG
<i>AP3</i>	ATACAAAAGAATCTCATAACATGAGCTG	AATGATGTCAGAGGCAGAGGGTGCATG
<i>PI</i>	AAGAAAGAGAATGATAGCTTACAACCTG	CACTCTATATCCAAACTGCCCATCATG
<i>SEP2</i>	ATCAACAGAATATTGCCTATGGACATC	GATGTAGCCGTTTCCTTGTGGGACTG
<i>MIR172a-2</i>	TTTCTCAAGCTTTAGGTATTTGTAG	TCGGCGGATCCATGGAAGAAAGCTC
<i>β-TUB</i>	GAGCCTTACAACGCTACTCTGTCTGTC	ACACCAGACATAGTAGCAGAAATCAAG

Supplementary Table 3. Locus identifiers of genes discussed in this work.

Gene	Locus ID
<i>ACC SYNTHASE 10 (ACS10)</i>	At1g62960
<i>AGAMOUS (AG)</i>	At4g18960
<i>AGL42</i>	At5g62165
<i>AP2-like</i>	At5g67180
<i>AP2-like</i>	At5g60120
<i>APETALA1 (AP1)</i>	At1g69120
<i>APETALA2 (AP2)</i>	At4g36920
<i>APETALA3 (AP3)</i>	At3g54340
<i>CAULIFLOWER (CAL)</i>	At1g26310
<i>CONSTANS (CO)</i>	At5g15840
<i>CRABSCLAW (CRC)</i>	At1g69180
<i>CUPSHAPED COTYLEDON2 (CUC2)</i>	At5g53950
<i>DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHASE (PC5S2)</i>	At3g55610
<i>FLOWERING LOCUS C (FLC)</i>	At5g10140
<i>FLOWERING LOCUS T (FT)</i>	At1g65480
<i>FLOWERING PROMOTING FACTOR1 (FPF1)</i>	At5g24860
<i>FRIGIDA (FRI)</i>	At4g00650
<i>FRUITFULL (FUL)</i>	At5g60910
<i>LEAFY (LFY)</i>	At5g61850
<i>PISTILLATA (PI)</i>	At5g20240
<i>RAP2.7</i>	At2g28550
<i>REM1</i>	At4g31610
<i>SCHLAFMÜTZE (SMZ)</i>	At3g54990
<i>SCHNARCHZAPFEN (SNZ)</i>	At2g39250
<i>SEPELLATA1 (SEP1)</i>	At5g15800
<i>SEPELLATA2 (SEP2)</i>	At3g02310
<i>SEPELLATA3 (SEP3)</i>	At1g24260
<i>SHOOT MERISTEMLESS (STM)</i>	At1g62360
<i>SQUAMOSA PROMOTER BINDING PROTEIN LIKE 2 (SPL2)</i>	At5g43270
<i>SQUAMOSA PROMOTER BINDING PROTEIN LIKE 3 (SPL3)</i>	At2g33810
<i>SQUAMOSA PROMOTER BINDING PROTEIN LIKE 4 (SPL4)</i>	At1g53160
<i>SQUAMOSA PROMOTER BINDING PROTEIN LIKE 5 (SPL5)</i>	At3g15270
<i>SQUAMOSA PROMOTER BINDING PROTEIN LIKE 6 (SPL6)</i>	At1g69170
<i>SQUAMOSA PROMOTER BINDING PROTEIN LIKE 9 (SPL9)</i>	At2g42200
<i>SQUAMOSA PROMOTER BINDING PROTEIN LIKE 10 (SPL10)</i>	At1g27370
<i>SQUAMOSA PROMOTER BINDING PROTEIN LIKE 11 (SPL11)</i>	At1g27360
<i>SQUAMOSA PROMOTER BINDING PROTEIN LIKE 13 (SPL13)</i>	At5g50570
<i>SQUAMOSA PROMOTER BINDING PROTEIN LIKE 15 (SPL15)</i>	At3g57920
<i>SUPPRESSOR OF CONSTANS OVEREXPRESSION 1 (SOC1)</i>	At2g45660
<i>WUSCHEL (WUS)</i>	At2g17950

Supplementary Table 4. Overlap between top 500 genes ranked by change between day 0 and 7 in Col.

Expression estimates from RMA (linear values).

Induced genes:

Rank	Locus ID	Description	Col 0d	Col 3d	Col 5d	Col 7d	Ler 0d	Ler 3d	Ler 5d	Ler 7d	Col change	Ler change
1	At1g53160	transcription factor, putative / similar to GB:X92369 from [Antirrhinum majus];supported by full-length cDNA: Ceres:12071.	27.80	95.02	316.54	1229.98	25.80	226.38	899.64	1823.39	44.2	70.7
2	At1g69120	floral homeotic gene APETALA1 / similar to homeotic protein boi1AP1 GI:1561777 from [Brassica oleracea]; supported by full-length cDNA: Ceres: 39890.	22.59	17.66	84.38	694.03	20.30	36.10	460.64	1272.51	30.7	62.7
3	At2g33810	putative squamosa-promoter binding protein / ;supported by full-length cDNA: Ceres:10375.	44.74	94.19	222.80	1179.71	58.66	94.19	700.70	1916.91	26.4	32.7
4	At5g44630	terpene synthase/cyclase family /	20.98	77.18	185.24	533.26	39.77	253.38	796.59	1324.34	25.4	33.3
5	At5g60910	MADS-box protein / NAP1-1, Nicotiana tabacum, EMBL:AF009126; supported by cDNA: gi_14423383_gb_AF386929.1_AF386929	45.03	159.91	415.45	896.94	58.16	364.35	941.30	1371.92	19.9	23.6
6	At4g14130	xyloglucan endotransglycosylase (XTR7) / almost identical to xyloglucan endotransglycosylase-related protein XTR7 GI:1244760 from [Arabidopsis thaliana], one amino acid difference ;supported by full-length cDNA: Ceres:33554.	34.19	67.25	161.43	572.18	42.22	64.69	274.84	485.21	16.7	11.5
7	At5g37300	putative protein / predicted proteins, Arabidopsis thaliana; supported by cDNA: gi_15810554_gb_AY056316.1_	20.37	41.34	89.45	309.22	21.98	40.49	232.25	597.74	15.2	27.2
8	At3g54340	floral homeotic protein APETALA3 (AP3) / ;supported by full-length cDNA: Ceres:34635.	21.35	23.93	24.67	266.42	23.64	23.46	176.35	705.45	12.5	29.8
9	At3g28500	acidic ribosomal protein P2b (rpp2b), putative / similar to acidic ribosomal protein P2b (rpp2b) GB:U62753 GI:2431770 from [Zea mays];supported by full-length cDNA: Ceres:27571.	203.70	387.98	964.79	2146.27	247.50	615.87	1908.67	2954.93	10.5	11.9
10	At4g19430	expressed protein / supported by cDNA: Ceres:13917.	23.19	48.62	83.32	239.99	27.61	54.75	161.46	282.96	10.3	10.2
11	At3g15270	squamosa promoter binding protein-like 5 / identical to GB:CAB56571 from [Arabidopsis thaliana]	23.87	52.95	91.10	221.11	37.81	81.46	201.70	542.62	9.3	14.4
12	At5g44620	cytochrome p450 family / ; supported by cDNA: gi_16226349_gb_AF428311.1_AF428311	196.63	469.49	987.65	1765.10	248.40	663.48	1471.45	1962.62	9.0	7.9
13	At5g20240	PISTILLATA, MADS-box protein / ; supported by full-length cDNA: Ceres: 1480.	20.65	17.40	20.46	155.78	20.45	20.37	96.20	313.54	7.5	15.3
14	At5g47600	unknown protein /	145.07	366.49	453.05	1046.66	245.55	962.20	1438.03	2222.10	7.2	9.0
15	At3g02310	floral homeotic protein AGL4 / identical to floral homeotic protein AGL4 GB:P29384 [Arabidopsis thaliana], Pfam HMM hit: SRF-type transcription factors (DNA-binding and dimerization domain); supported by cDNA: gi_166592_gb_M55552.1_ATHAGL4A	17.25	21.83	19.90	124.34	16.30	20.03	71.38	374.53	7.2	23.0
16	At5g61850	LFY floral meristem identity control protein /	61.36	113.71	191.52	401.37	61.19	154.58	388.96	625.37	6.5	10.2
17	At5g24860	FPF1 protein /	13.70	22.34	29.47	89.49	15.36	35.98	67.93	138.42	6.5	9.0

18	At4g31910	putative protein / anthranilate N-hydroxycinnamoyl/benzoyltransferase, <i>Dianthus caryophyllus</i> , Z84384; supported by cDNA: gi_15450358_gb_AY052280.1_	39.38	38.60	58.70	232.73	45.53	51.71	156.87	358.66	5.9	7.9
19	At5g15800	MADS-box protein AGL2 / ; supported by cDNA: gi_166589_gb_M55551.1_ATHAGL2A	31.64	28.97	43.15	183.96	26.21	35.51	68.29	161.91	5.8	6.2
20	At3g20100	cytochrome p450 family / contains Pfam profile: PF00067 cytochrome P450; supported by full-length cDNA: Ceres:149380.	58.52	110.37	149.69	334.97	57.43	98.12	166.04	248.09	5.7	4.3
21	At1g02190	hypothetical protein / contains similarity to receptor-like protein glossy1 homolog GI:2213643 from [<i>Oryza sativa</i>]	44.90	65.58	91.32	242.27	44.30	100.37	165.65	466.93	5.4	10.5
22	At5g65730	xyloglucan endotransglycosylase, putative / similar to endo-xyloglucan transferase GI:2244732 from [<i>Gossypium hirsutum</i>]; supported by full-length cDNA: Ceres:12301.	283.80	550.74	680.82	1520.69	572.14	424.26	1364.50	2497.20	5.4	4.4
23	At1g69180	transcription factor CRC / identical to transcription factor CRC GI:4836698 from [<i>Arabidopsis thaliana</i>]; supported by full-length cDNA: Ceres:9132.	61.40	163.42	276.12	326.25	61.97	235.26	456.23	406.14	5.3	6.6
24	At2g45660	MADS-box protein (AGL20) / ; supported by full-length cDNA: Ceres: 5467.	46.73	122.36	188.77	248.10	61.90	149.60	252.13	288.60	5.3	4.7
25	At4g00870	bHLH protein / similar to the myc family of helix-loop-helix transcription factors	28.92	32.20	43.50	149.03	23.62	34.08	103.48	213.86	5.2	9.1
26	At2g03710	MADS-box protein (AGL3) / ; supported by cDNA: gi_1737494_gb_U81369.1_ATU81369	33.99	45.40	65.45	172.37	30.29	57.74	128.34	269.97	5.1	8.9
27	At4g24150	putative protein / various predicted proteins, <i>Arabidopsis thaliana</i>	37.83	42.04	66.40	183.62	35.08	40.58	114.99	221.65	4.9	6.3
28	At4g34400	putative protein / NF-180, <i>Petromyzon marinus</i> , PIR2:I51116	408.97	686.95	1101.57	1948.09	382.54	1061.68	1822.45	2307.00	4.8	6.0
29	At1g54020	myrosinase-associated protein, putative / similar to myrosinase-associated protein GI:1769967 from [<i>Brassica napus</i>]; supported by cDNA: gi_15809979_gb_AY054258.1_	173.61	295.95	644.08	818.90	58.25	94.13	151.23	237.61	4.7	4.1
30	At3g14990	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative / similar to ThiJ GB:AAA82704 [<i>Escherichia coli</i>]; likely encodes two ThiJ subunits within a single polypeptide; supported by cDNA: gi_14517477_gb_AY039574.1_	126.02	277.68	336.83	585.78	162.22	351.35	433.05	675.86	4.6	4.2
31	At2g17280	unknown protein / similar to <i>S.pombe</i> protein C5H10.03	101.52	127.60	179.55	453.82	126.41	237.29	418.59	656.09	4.5	5.2
32	At5g15150	homeobox-leucine zipper protein, HAT7 / <i>Athb-3</i> ; supported by cDNA: gi_527636_gb_U09340.1_ATU09340	14.88	20.08	22.58	66.31	21.18	20.51	52.61	90.96	4.5	4.3
33	At4g39480	cytochrome P450 - like protein / cytochrome P450 CYP86A1, <i>Arabidopsis thaliana</i> , PIR3:JC5965	31.13	39.86	65.76	134.30	27.64	41.15	94.12	172.99	4.3	6.3
34	At1g03170	expressed protein / ; supported by full-length cDNA: Ceres:36143.	30.31	136.73	102.47	125.10	36.47	144.70	193.71	266.28	4.1	7.3
35	At5g09300	branched-chain alpha keto-acid dehydrogenase E1 alpha subunit-like protein / branched-chain alpha keto-acid dehydrogenase E1 alpha subunit - <i>Arabidopsis thaliana</i> , EMBL:AF077955; supported by full-length cDNA: Ceres:3693.	91.82	156.39	189.30	377.47	131.17	210.83	358.61	530.47	4.1	4.0
36	At1g35290	expressed protein / ; supported by full-length cDNA: Ceres:19191.	31.88	44.69	53.16	126.99	34.84	55.79	101.61	190.55	4.0	5.5
37	At3g30775	hypothetical protein / identical to GB:P92983 from [<i>Arabidopsis thaliana</i>] (Plant Cell 8 (8), 1323-1335 (1996)); supported by cDNA: gi_16226334	157.88	442.19	741.39	609.67	82.47	129.49	247.52	328.72	3.9	4.0
38	At1g24260	MADS-box protein / strongly similar to GB:O22456, MADS-box protein, Location of EST gb H37053	18.59	16.95	22.27	70.94	16.20	19.26	44.95	164.16	3.8	10.1

39	At5g59220	protein phosphatase 2C (PP2C) / ABA induced protein phosphatase 2C, <i>Fagus sylvatica</i> , EMBL:FSY277743; supported by cDNA: gi_15809791_gb_AY054163.1_	184.22	294.89	331.14	689.01	159.67	220.41	379.14	637.94	3.7	4.0
40	At1g01140	serine threonine kinase, putative / similar to serine threonine kinase GB:CAA73067.1 GI:2632252 from (<i>Sorghum bicolor</i>); supported by cDNA: gi_14423523_gb_AF386999.1_AF386999	172.39	280.13	317.39	640.79	271.53	413.99	664.67	977.55	3.7	3.6
41	At1g69600	hypothetical protein / predicted by genemark.hmm	46.16	54.43	68.26	170.07	57.95	103.26	156.20	233.92	3.7	4.0
42	At2g01520	major latex protein (MLP)-related / low similarity to major latex protein { <i>Papaver somniferum</i> }[GI:169000]; supported by full-length cDNA: Ceres:17603.	20.50	24.02	27.76	74.67	25.08	44.61	114.01	330.38	3.6	13.2
43	At3g06160	hypothetical protein /	102.33	157.35	228.52	365.57	33.86	62.94	115.12	165.46	3.6	4.9
44	At1g26960	HD-Zip transcription factor / Similar to Homeo Domain proteins from <i>Arabidopsis thaliana</i> GB:S20930, and <i>Helianthus annuus</i> gj 349379, and carrot, gj 1435022. Contains Homeobox domain motif; supported by full-length cDNA: Ceres:121220.	42.09	52.28	66.81	150.23	30.37	49.29	86.15	132.67	3.6	4.4
45	At3g26590	integral membrane protein, putative / contains Pfam profile: PF01554 uncharacterized membrane protein family; supported by cDNA: gi_16323120_gb_AY057664.1_	26.57	31.95	46.63	93.81	30.07	42.71	79.73	128.76	3.5	4.3
46	At4g25830	Expressed protein / ; supported by full-length cDNA: Ceres: 9546.	141.69	184.04	245.57	497.04	88.41	132.78	285.32	462.38	3.5	5.2
47	At5g37260	putative protein / DNA-binding protein CCA1, <i>Arabidopsis thaliana</i> , PIR:T02684	30.06	75.06	61.30	104.28	44.49	85.75	128.03	145.12	3.5	3.3
48	At4g14695	light induced protein like /	17.45	21.80	26.56	59.30	24.28	44.42	93.29	197.50	3.4	8.1
49	At4g31610	putative protein / reproductive meristem gene 1 (REM1), Brassica oleracea, gb:AF051772; supported by cDNA: gi_13604226_gb_AF336344.1_AF336344	48.25	70.00	83.72	163.80	50.60	106.26	166.26	238.89	3.4	4.7
50	At1g72260	thionin / identical to GI:1181531 from [<i>Arabidopsis thaliana</i>] (Plant Physiol. 109 (3), 813-820 (1995)); supported by full-length cDNA: Ceres:26029.	330.65	547.67	812.59	1117.96	84.89	225.61	301.52	363.98	3.4	4.3
51	At4g15480	UDP-glucosyltransferase, putative / similar to UDP-glucose:sinapate glucosyltransferase GI:9794913 from [<i>Brassica napus</i>]	32.51	45.24	63.07	109.57	32.70	59.45	93.69	189.78	3.4	5.8
52	At5g35670	putative protein / similar to unknown protein (pir T00974); supported by full-length cDNA: Ceres:99321.	45.38	71.75	78.71	152.17	65.25	93.77	158.49	230.33	3.4	3.5
53	At3g57920	squamosa promoter-binding protein homolog / spl9 quamosa promoter binding protein-like 9 - <i>Arabidopsis thaliana</i> , EMBL:ATH011639; supported by full-length cDNA: Ceres:247919.	100.00	182.23	232.51	329.29	117.16	217.31	279.02	376.05	3.3	3.2
54	At3g02170	expressed protein / ; supported by full-length cDNA: gi_15810132	145.95	186.67	226.95	480.45	122.15	120.60	247.33	392.62	3.3	3.2
55	At5g62165	MADS-box protein / ; supported by cDNA: gi_15809904_gb_AY054220.1_	72.90	105.83	170.70	234.82	80.07	148.51	278.31	340.41	3.2	4.3
56	At2g31980	putative cysteine proteinase inhibitor B (cystatin B) / ; supported by full-length cDNA: Ceres:35447.	72.04	154.23	164.07	228.85	89.47	145.48	166.21	258.41	3.2	2.9
57	At1g26310	floral regulatory gene CAULIFLOWER / ; supported by full-length cDNA: Ceres: 23736.	21.91	28.12	43.04	68.07	20.20	42.13	67.13	85.95	3.1	4.3
58	At1g01720	NAC domain protein, putative / similar to NAC domain protein NAM GB:AAD17313 GI:4325282 from [<i>Arabidopsis thaliana</i>]; supported by full-length cDNA: Ceres:20909.	104.22	255.50	221.16	321.74	81.82	178.30	192.60	270.66	3.1	3.3
59	At1g03710	hypothetical protein / predicted by genefinder	49.09	71.49	69.74	149.88	90.72	186.30	292.86	445.56	3.1	4.9

60	At2g16210	hypothetical protein / predicted by genscan and genefinder	17.22	19.82	31.07	51.91	16.43	21.95	38.77	64.70	3.0	3.9
61	At3g53310	putative protein / various predicted proteins, Arabidopsis thaliana; supported by full-length cDNA: Ceres: 36830.	75.81	94.46	106.08	227.48	55.58	68.18	118.54	313.07	3.0	5.6
62	At4g23680	major latex protein (MLP)-related / low similarity to major latex protein {Papaver somniferum}[GI:294060]; supported by cDNA: gi_13605713_gb_AF361838.1_AF361838	15.12	27.91	25.76	44.98	15.66	23.80	21.63	69.12	3.0	4.4
63	At1g08630	expressed protein / similar to L-allo-threonine aldolase (D87890); similar to ESTs gb R30517, gb T42772, gb R90493, and gb R90493;supported by full-length cDNA: Ceres:271327.	52.17	64.42	91.94	155.11	96.37	123.79	198.03	290.61	3.0	3.0
64	At4g18960	floral homeotic protein agamous (AGAMOUS) / no suitable start codon could be found; supported by cDNA gi 16155 emb X53579; sequencing gaps exits which are under investigation.	14.12	14.06	13.98	41.98	12.98	13.75	32.46	125.13	3.0	9.6
65	At5g56300	S-adenosyl-L-methionine:carboxyl methyltransferase-related / similar to SAM:jasmonic acid carboxyl methyltransferase (JMT)[GI:13676829] and to SAM:salicylic acid carboxyl methyltransferase (SAMT) [GI:6002712][Clarkia breweri]	34.42	39.93	74.01	102.07	31.09	38.93	92.42	148.06	3.0	4.8
66	At1g69870	putative peptide transporter / similar to peptide transporter GB:AAC32034 [Hordeum vulgare]; supported by full-length cDNA: Ceres: 22243.	27.26	31.32	35.45	80.77	40.19	36.77	57.95	192.90	3.0	4.8
67	At5g10300	alpha-hydroxynitrile lyase-like protein / alpha-hydroxynitrile lyase HNL4 - Manihot esculenta, EMBL:AJ223281; supported by cDNA: gi_15028130_gb_AY046015.1	156.04	245.39	325.89	461.24	93.85	222.21	273.40	380.34	3.0	4.1
68	At2g43520	putative trypsin inhibitor / ;supported by full-length cDNA: Ceres:15927.	581.06	733.92	989.60	1712.88	451.80	963.10	1490.28	1954.53	2.9	4.3
69	At1g75170	unknown protein / ; supported by cDNA: gi_17979168	194.47	247.57	362.65	568.38	281.24	509.08	653.92	859.49	2.9	3.1
70	At5g22430	expressed protein / ;supported by full-length cDNA: Ceres:6519.	19.38	19.99	24.57	56.52	21.17	21.22	28.45	492.01	2.9	23.2
71	At5g24780	vegetative storage protein Vsp1 / ;supported by full-length cDNA: Ceres:32606.	578.05	730.52	1432.60	1663.47	343.89	272.07	810.15	2139.82	2.9	6.2
72	At5g15580	putative protein / unknown protein F14P3.18 - Arabidopsis thaliana, EMBL:AC009755	273.11	353.25	456.52	783.28	259.48	397.86	604.93	873.14	2.9	3.4
73	At4g21590	putative bifunctional nuclease / bifunctional nuclease, Zinnia elegans, gb:U90266;supported by full-length cDNA: Ceres:17760.	60.34	59.06	64.54	171.85	49.67	61.97	130.27	463.49	2.8	9.3
74	At5g37540	putative protein / nucleoid DNA-binding protein cnd41, chloroplast, common tobacco, PIR:T01996; supported by cDNA: gi_15809849_gb_AY054192.1	91.93	116.11	143.95	258.26	82.11	140.93	178.89	299.19	2.8	3.6
75	At1g17745	expressed protein / ; supported by full-length cDNA: Ceres: 20582.	267.11	624.17	480.06	746.62	526.28	1335.81	1172.32	1790.13	2.8	3.4
76	At2g34810	FAD-linked oxidoreductase family / similar to SP P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) [Eschscholzia californica]; contains PF01565 FAD binding domain; supported by cDNA: gi_20466739	71.89	123.44	153.04	198.03	65.76	82.84	185.73	427.49	2.8	6.5
77	At1g30950	unusual floral organ (UFO), AtFBX1 / E3 ubiquitin ligase SCF complex F-box subunit; almost identical to unusual floral organs (UFO)GI:4376159 from [Arabidopsis thaliana] Landsberg-erecta; one amino acid difference	40.72	57.39	46.05	111.92	55.46	78.72	133.50	202.97	2.7	3.7
78	At2g42800	leucine rich repeat protein family / contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; predicted by genefinder and grail	433.69	604.61	770.37	1187.26	450.06	717.95	1093.02	1321.81	2.7	2.9
79	At2g19800	expressed protein / ;supported by full-length cDNA: Ceres:254633.	30.38	40.43	82.52	83.02	27.35	30.58	68.04	84.08	2.7	3.1

80	At1g55850	cellulose synthase catalytic subunit, putative / similar to GB:AAD39534 from [<i>Gossypium hirsutum</i>]; supported by cDNA: gi_17381167	41.70	47.35	60.54	112.67	52.29	50.85	99.12	234.24	2.7	4.5
81	At2g40100	light-harvesting chlorophyll a/b binding protein / ; supported by full-length cDNA: Ceres: 6454.	84.75	174.32	139.49	227.61	131.97	261.49	255.09	394.77	2.7	3.0
82	At2g35820	expressed protein / ;supported by full-length cDNA: Ceres:22535.	30.40	47.74	42.52	80.53	54.10	71.90	105.64	202.59	2.6	3.7
83	At5g24910	cytochrome p450, putative / fatty acid omega-hydroxylase cytochrome P450 4A11 - Homo sapiens, PIR:I53015; supported by cDNA: gi_16604323_gb_AY058060.1_	30.14	32.80	39.99	79.00	30.47	34.33	74.13	183.88	2.6	6.0
84	At1g01120	fatty acid elongase 3-ketoacyl-CoA synthase 1 / identical to GB:AAC99312 GI:4091810 from [<i>Arabidopsis thaliana</i>]; supported by cDNA: gi_18377663	158.66	226.28	244.03	415.72	185.39	221.41	344.68	590.18	2.6	3.2
85	At3g19180	hypothetical protein / predicted by genscan+; supported by cDNA: gi_18377659	57.26	79.25	96.38	149.87	41.02	90.11	123.47	155.02	2.6	3.8
86	At1g07260	UDP-glucose glucosyltransferase, putative / similar to UDP-glucose glucosyltransferase GI:453245 from [<i>Manihot esculenta</i>]	47.05	49.54	73.09	121.23	30.46	50.90	74.05	99.55	2.6	3.3
87	At5g08640	flavonol synthase (FLS) (sp Q96330) / ;supported by full-length cDNA: Ceres:23924.	290.18	365.50	440.59	736.91	165.90	220.25	418.81	1292.18	2.5	7.8
88	At1g22160	expressed protein / ;supported by full-length cDNA: Ceres:23788.	128.01	203.65	147.14	324.99	111.09	214.30	258.45	438.05	2.5	3.9
89	At3g16150	putative L-asparaginase / similar to L-ASPARAGINASE GB:P30364from [<i>Lupinus angustifolius</i>];supported by full-length cDNA: Ceres:21689.	91.98	101.13	133.05	230.16	117.76	170.74	245.29	319.01	2.5	2.7
90	At3g12460	hypothetical protein / predicted by genemark.hmm	37.15	50.00	59.64	91.86	58.58	94.04	133.57	160.10	2.5	2.7
91	At3g58770	putative protein /	184.32	259.37	306.85	442.92	152.89	284.50	370.61	477.05	2.4	3.1
92	At2g03550	putative esterase / (contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187); related to plant sensitive response proteins	151.90	252.25	263.32	360.33	117.30	206.27	233.30	331.40	2.4	2.8
93	At3g06220	hypothetical protein / predicted by genefinder	407.64	530.79	618.76	957.96	375.65	648.42	872.50	1165.52	2.4	3.1
94	At2g20870	expressed protein / ;supported by full-length cDNA: Ceres:2512.	35.99	63.56	81.35	84.25	32.62	42.46	44.84	389.36	2.3	11.9
95	At4g07670	putative peptidase /	82.44	101.89	136.21	189.92	90.12	102.46	189.95	272.79	2.3	3.0
96	At5g64990	GTP-binding protein, putative / similar to GTP-binding protein GI:550072 from [<i>Homo sapiens</i>]	19.88	26.81	29.90	45.23	29.53	40.35	77.38	109.35	2.3	3.7
97	At4g11310	cysteine proteinase / contains similarity to cysteine proteinase RD21A (thiol protease) GI:435619, SP:P43297 from [<i>Arabidopsis thaliana</i>]	64.99	49.85	79.78	146.87	173.77	127.75	282.96	597.79	2.3	3.4
98	At5g43270	squamosa promoter binding protein-like 2 (emb)CAB56576.1) /	168.05	206.69	283.26	379.50	60.99	95.41	203.22	287.55	2.3	4.7
99	At4g33790	male sterility 2-like protein / male sterility protein 2, Brassica napus, gb:X99922; supported by cDNA: gi_16323106_gb_AY057657.1_ ; No start codon identified, may contain anomalous splicing at 5' end.	47.40	51.78	63.12	105.37	45.69	45.29	89.43	195.17	2.2	4.3
100	At2g39330	putative myrosinase-binding protein / ;supported by full-length cDNA: Ceres:39069.	311.74	429.25	737.62	689.93	228.07	387.03	387.26	664.83	2.2	2.9
101	At4g16690	cyanohydrin lyase like protein / ;supported by full-length cDNA: Ceres:5546.	38.62	52.84	52.43	84.82	61.69	46.23	108.83	231.00	2.2	3.7

Repressed genes:

Rank	Locus ID	Description	Col 0d	Col 3d	Col 5d	Col 7d	Ler 0d	Ler 3d	Ler 5d	Ler 7d	Col change	Ler change
1	At3g19710	branched-chain amino acid aminotransferase, putative / similar to branched-chain amino acid aminotransferase GB:AAF07192 from [Solanum tuberosum];supported by full-length cDNA: Ceres:38004.	2750.38	817.21	306.82	55.55	6934.26	4987.29	1444.53	223.93	-49.5	-31.0
2	At5g23010	2-isopropylmalate synthase-like; homocitrate synthase-like / ; supported by cDNA: gi_12330688_gb_AF327648.1_AF327648	2151.33	650.11	336.40	61.18	2410.26	1694.81	515.22	83.13	-35.2	-29.0
3	At1g49320	unknown protein /	489.63	200.67	195.14	24.70	451.07	140.01	58.39	27.42	-19.8	-16.5
4	At3g45160	hypothetical protein /	1177.33	659.67	453.52	68.56	1177.76	796.55	371.44	60.86	-17.2	-19.4
5	At3g58990	3-isopropylmalate dehydratase-like protein (small subunit) / 3-isopropylmalate dehydratase, small subunit - Thermotoga maritima, PIR:A72363; supported by cDNA: gi_17529161	801.50	217.12	127.84	47.97	3064.00	2224.31	591.57	125.81	-16.7	-24.4
6	At1g56300	DnaJ protein, putative / contains Pfam profile: PF00226: DnaJ domain;supported by full-length cDNA: Ceres:25796.	493.41	59.66	28.11	30.12	159.97	34.11	27.84	27.75	-16.4	-5.8
7	At3g25190	integral membrane protein, putative / contains Pfam profile: PF01988 integral membrane protein; similar to nodulin-21 GB:CAA34506 [Glycine max]; supported by cDNA: gi_14030610_gb_AF375396.1_AF375396	955.59	595.33	394.69	64.40	1404.48	1169.21	379.58	67.01	-14.8	-21.0
8	At4g12030	putative transport protein / Na(+) dependent transporter (Sbf family) - Aquifex aeolicus, PIR2:E70482; supported by cDNA: gi_15215838_gb_AY050449.1	862.43	305.00	194.96	59.97	1321.46	842.42	251.58	77.73	-14.4	-17.0
9	At5g59330	putative protein / nonspecific lipid-transfer protein precursor, Brassica napus, EMBL:AF101038	1946.15	1159.01	465.67	138.42	3460.02	3631.88	2803.81	757.30	-14.1	-4.6
10	At3g22740	putative selenocysteine methyltransferase / similar to selenocysteine methyltransferase GB:P56707 from [Astragalus bisulcatus];supported by full-length cDNA: Ceres:36591.	386.48	100.95	43.88	29.00	1195.26	1049.78	229.04	56.03	-13.3	-21.3
11	At5g07690	myb family transcription factor / similar to myb transcription factor GI:3941436 from [Arabidopsis thaliana]; supported by cDNA: gi_14334943_gb_AY035145.1	491.85	190.65	85.97	38.52	338.29	152.44	59.30	34.45	-12.8	-9.8
12	At2g43100	3-isopropylmalate dehydratase, small subunit / ; supported by cDNA: gi_16974632_gb_AY060594.1	473.81	179.80	112.54	38.08	1767.69	1638.82	520.99	123.59	-12.4	-14.3
13	At4g13770	cytochrome p450 family / ; supported by cDNA: gi_3164127_dbj_D78599.1_D78599	1542.23	797.85	389.27	135.57	4129.45	3382.96	1351.29	539.71	-11.4	-7.7
14	At5g64110	peroxidase, putative / similar to peroxidase ATP3a [Arabidopsis thaliana] gj1546698[emb]CAA67340; supported by full-length cDNA: Ceres:2577.	2155.34	900.14	443.55	193.23	1279.32	739.04	545.02	163.81	-11.2	-7.8
15	At1g11080	Serine carboxypeptidase isolog /	248.43	164.42	122.40	22.87	144.09	78.85	34.70	23.10	-10.9	-6.2
16	At1g65860	flavin-containing monooxygenase FMO3, putative / similar to flavin-containing monooxygenase FMO3 GI:349533 from [Oryctolagus cuniculus]	264.93	111.56	72.41	27.23	930.94	577.01	191.45	63.79	-9.7	-14.6
17	At3g23430	unknown protein / ; supported by cDNA: gi_20069031	427.87	255.34	150.70	44.06	743.73	338.45	132.92	47.40	-9.7	-15.7
18	At3g09260	glycosyl hydrolase family 1 / almost identical to beta-glucosidase GI:1732570 from [Arabidopsis thaliana]; supported by cDNA: gi_14423459_gb_AF386967.1_AF386967	1274.78	465.63	425.55	133.40	1806.22	1504.50	749.04	246.84	-9.6	-7.3

19	At3g03190	glutathione transferase, putative / identical to glutathione S-transferase GB:AAB09584 from [Arabidopsis thaliana]; supported by cDNA: gi_1575751_gb_U70672.1_ATU70672	479.88	202.65	126.50	57.69	1649.73	1390.96	384.54	138.73	-8.3	-11.9
20	At5g09220	amino acid transport protein AAP2 / ;supported by full-length cDNA: Ceres:114602.	2719.74	1226.35	891.59	343.83	2778.73	1196.74	471.28	176.51	-7.9	-15.7
21	At4g01430	unknown protein / temporary automated functional assignment	327.26	199.98	141.34	42.39	688.77	413.05	152.92	49.17	-7.7	-14.0
22	At1g44800	nodulin protein, putative / similar to GB:2598575 from [Medicago truncatula];supported by full-length cDNA: Ceres:149985.	850.15	660.18	446.85	115.73	1194.10	993.18	571.88	99.32	-7.3	-12.0
23	At1g62560	similar to flavin-containing monooxygenase (sp)P36366); similar to ESTs gb R30018, gb H36886, gb N37822, and gb T88100 / similar to flavin-containing monooxygenase GB:AAA21178 GI:349534 from [Oryctolagus cuniculus]; supported by cDNA: gi_13877746_gb_AF370136.1_AF370136	436.49	186.45	137.23	59.89	805.17	676.35	287.04	153.22	-7.3	-5.3
24	At1g76800	nodulin-like protein / similar to nodulin GB:P16313 [Glycine max]	402.90	280.29	168.45	55.97	555.15	427.59	156.87	47.73	-7.2	-11.6
25	At3g49620	oxidoreductase (din11), putative / identical to partial cds of 2-oxoacid-dependent oxidase (din11) from GI:10834554 [Arabidopsis thaliana]	283.69	144.74	81.91	42.15	318.59	192.18	114.58	40.85	-6.7	-7.8
26	At1g49470	expressed protein / ;supported by full-length cDNA: Ceres:95546.	324.86	204.09	117.52	48.67	733.34	447.22	160.07	55.31	-6.7	-13.3
27	At2g14580	putative pathogenesis related-1 (PR1) protein / ; supported by cDNA: gi_17529119	1560.54	708.59	492.86	248.32	3500.55	2689.02	1586.58	250.33	-6.3	-14.0
28	At2g28780	hypothetical protein / predicted by genscan and genefinder	122.51	78.12	33.55	20.00	238.53	137.48	34.31	16.84	-6.1	-14.2
29	At1g47400	hypothetical protein / predicted by genemark.hmm	102.43	31.76	22.08	16.83	82.53	30.78	18.65	20.35	-6.1	-4.1
30	At1g62800	aspartate aminotransferase / nearly identical to aspartate aminotransferase, cytoplasmic isozyme 2 SP:P46646 [Arabidopsis thaliana (Mouse-ear cress)]; supported by cDNA: gi_693693_gb_U15035.1_ATU15035	144.58	60.57	42.39	23.84	674.17	489.47	119.00	41.34	-6.1	-16.3
31	At1g74090	putative flavonol sulfotransferase / similar to FLAVONOL 4'-SULFOTRANSFERASE GB:P52837 from [Flaveria chloraefolia];supported by full-length cDNA: Ceres:41006.	1479.76	662.26	448.80	248.99	4058.55	3527.04	1263.86	547.93	-5.9	-7.4
32	At1g16410	putative cytochrome P450 / similar to gb AF069494 cytochrome P450 from Sinapis alba and is a member of the PF 00067 Cytochrome P450 family. EST gb F14190 comes from this gene; supported by cDNA: gi_15208670_gb_AY035021.2_	171.81	37.71	28.13	28.96	444.57	213.94	42.12	26.42	-5.9	-16.8
33	At5g60780	high affinity nitrate transporter protein - like / probable high affinity nitrate transporter protein, Glycine max, PIR:T06237	384.51	252.50	114.11	65.31	436.15	307.39	262.97	69.23	-5.9	-6.3
34	At3g01500	carbonic anhydrase, chloroplast precursor / identical to carbonic anhydrase, chloroplast precursor GB:P27140 [Arabidopsis thaliana]; supported by cDNA: gi_15810272_gb_AY056175.1_	165.43	398.14	47.71	28.17	492.36	72.37	35.28	43.08	-5.9	-11.4
35	At5g61660	structural protein - like / glycine-rich cell wall structural protein 1 precursor, Oryza sativa, PIR:KNRZG1;supported by full-length cDNA: Ceres:9324.	565.07	276.70	200.30	98.50	756.72	222.45	134.66	91.98	-5.7	-8.2
36	At1g07610	metallothionein-like protein / identical to SP:P43392 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:12642.	2407.99	1142.39	1019.08	423.71	3609.71	2132.52	1121.40	608.31	-5.7	-5.9
37	At3g05730	unknown protein /	654.13	598.34	252.81	115.31	819.53	101.97	44.22	35.22	-5.7	-23.3
38	At5g62150	putative protein / predicted protein, Arabidopsis thaliana	604.42	275.63	149.33	107.34	674.25	425.60	268.07	137.85	-5.6	-4.9

39	At4g08290	nodulin-like protein / nodulin gene MtN21 - Medicago truncatula, PID:e1172471;supported by full-length cDNA: Ceres:40485.	386.10	252.14	182.31	68.62	425.39	275.40	131.50	64.51	-5.6	-6.6
40	At2g18570	putative flavonol 3-O-glucosyltransferase / ; supported by cDNA: gi_20260653	158.25	101.70	68.31	28.58	147.40	94.84	51.19	30.50	-5.5	-4.8
41	At5g43180	putative protein / similar to unknown protein (pir T04500)	248.37	171.23	109.19	44.98	476.70	353.33	168.19	53.23	-5.5	-9.0
42	At1g01070	expressed protein / ;supported by full-length cDNA: Ceres:20749.	743.94	764.43	523.34	137.35	1125.39	1495.34	695.22	120.87	-5.4	-9.3
43	At3g54420	glycosyl hydrolase family 19 (class IV chitinase) / almost identical to class IV chitinase from GI:2597826 [Arabidopsis thaliana]	303.18	209.50	128.63	56.23	510.22	315.58	128.04	62.32	-5.4	-8.2
44	At3g25760	hypothetical protein /	110.81	99.07	57.30	20.84	36.39	17.47	12.97	12.87	-5.3	-2.8
45	At5g05960	putative protein / similar to unknown protein (emb CAB88360.1);supported by full-length cDNA: Ceres:29476.	214.80	108.43	75.20	40.75	169.78	52.49	36.39	40.66	-5.3	-4.2
46	At1g80830	metal ion transporter / identical to GB:AAD54417 GI:5853313 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:250751.	1844.73	1040.14	872.72	355.30	1286.79	647.70	325.26	266.81	-5.2	-4.8
47	At1g59740	oligopeptide transporter, putative / similar to oligopeptide transporter GI:510238 from [Arabidopsis thaliana]; supported by cDNA: gi_14334727_gb_AY035037.1_	302.33	198.78	110.53	58.50	718.95	281.81	113.26	55.77	-5.2	-12.9
48	At1g18880	peptide transporter, putative / similar to peptide transporter GI:2655098 from [Hordeum vulgare]; supported by cDNA: gi_17979086	233.48	144.00	111.67	45.44	400.34	292.09	141.06	60.62	-5.1	-6.6
49	At4g37970	cinnamyl alcohol dehydrogenase -like protein, LCADa /	105.89	56.75	40.47	20.75	166.89	102.82	33.06	25.57	-5.1	-6.5
50	At1g02400	dioxygenase, putative / similar to dioxygenase GI:1666096 from [Marah macrocarpus]	265.82	137.15	62.19	52.44	380.94	264.98	148.92	67.55	-5.1	-5.6
51	At1g47485	Expressed protein / ; supported by full-length cDNA: Ceres: 93707.	193.89	73.55	50.78	38.64	673.64	347.55	136.43	41.89	-5.0	-16.1
52	At3g56240	copper homeostasis factor / ;supported by full-length cDNA: Ceres:16647.	963.07	805.90	451.05	193.61	1761.38	1711.86	461.42	142.33	-5.0	-12.4
53	At1g80760	nodulin-like protein / similar to nodulin GB:CAA28471 GI:18710 from [Glycine max]	1076.97	1107.61	540.43	218.81	1220.95	879.85	286.26	100.13	-4.9	-12.2
54	At3g46130	Myb family transcription factor / contains PFAM profile: myb DNA binding domain PF00249; supported by cDNA: gi_9864078_gb_AF272733.1_AF272733	141.27	99.88	49.08	29.32	228.78	121.18	59.65	39.40	-4.8	-5.8
55	At2g37460	nodulin-like protein / ;supported by full-length cDNA: Ceres:16393.	404.63	234.92	173.45	84.32	994.63	742.09	372.10	74.60	-4.8	-13.3
56	At4g08300	nodulin-like protein / nodulin gene MtN21 - Medicago truncatula, PID:e1172471	105.61	79.05	33.05	22.18	73.64	33.53	25.99	21.24	-4.8	-3.5
57	At3g05640	protein phosphatase 2C (PP2C), putative / similar to protein phosphatase-2C GB:AAC36699 from [Mesembryanthemum crystallinum]; supported by cDNA: gi_15215718_gb_AY050388.1_	447.27	263.93	135.71	94.16	614.20	431.69	263.16	142.49	-4.8	-4.3
58	At1g21140	tonoplast intrinsic protein, alpha (alpha-TIP) / similar to GB:X16488 from [Glycine max] (Plant Mol. Biol. 14 (3), 449-451 (1990))	330.59	218.94	176.12	69.86	567.07	506.61	203.38	73.80	-4.7	-7.7
59	At1g01470	hypothetical protein / contains similarity to 1-phosphatidylinositol-4-phosphate 5-kinase(AtPIP5K1) GI:3702691 from [Arabidopsis thaliana]; supported by cDNA: gi_18650613	669.04	403.48	230.79	142.24	1044.63	548.96	190.49	75.68	-4.7	-13.8
60	At5g14740	CARBONIC ANHYDRASE 2 / ; supported by cDNA: gi_13265565_gb_AF324712.2_AF324712	130.37	240.37	51.65	29.50	403.87	63.82	34.35	38.91	-4.4	-10.4
61	At1g13930	expressed protein / ;supported by full-length cDNA: Ceres:1505.	3264.43	1348.61	768.69	739.81	2229.03	861.34	447.92	378.00	-4.4	-5.9

62	At4g34950	putative protein / AT.I.24-7, Arabidopsis thaliana, gb:U63815	402.21	199.83	133.39	91.86	908.05	251.71	126.88	87.15	-4.4	-10.4
63	At5g43580	unknown protein /	315.76	206.88	141.79	72.48	384.30	348.47	291.17	65.36	-4.4	-5.9
64	At1g33440	nitrate transporter NTL1, putative / similar to GI:3377517 from [Arabidopsis thaliana]	102.04	49.71	54.41	23.43	237.56	70.63	40.00	26.50	-4.4	-9.0
65	At5g49630	amino acid permease 6 (emb CAA65051.1) /	384.01	171.28	130.38	88.25	815.30	202.67	95.19	130.79	-4.4	-6.2
66	At4g01720	WRKY family transcription factor / similar to wild oat DNA-binding protein ABF2, GenBank accession number Z48431; supported by cDNA: gi_19172391	188.18	135.96	75.47	43.36	149.78	105.36	72.42	36.57	-4.3	-4.1
67	At5g38320	putative protein /	293.14	212.60	109.30	68.10	445.28	374.06	245.29	87.81	-4.3	-5.1
68	At1g20070	hypothetical protein / predicted by genemark.hmm	378.37	223.32	136.02	88.37	598.44	381.63	164.60	115.18	-4.3	-5.2
69	At2g42540	cold-regulated protein cor15a precursor / ; supported by cDNA: gi_14532457_gb_AY039853.1_	128.96	51.33	29.41	30.20	135.64	32.88	24.06	24.44	-4.3	-5.6
70	At5g40780	amino acid permease / ; supported by cDNA: gi_14194150	555.67	347.18	211.04	130.38	636.71	491.96	353.69	192.82	-4.3	-3.3
71	At2g34700	putative proline-rich glycoprotein /	233.55	146.24	81.14	54.81	338.17	239.56	112.40	54.22	-4.3	-6.2
72	At3g06490	myb family transcription factor (MYB108) / identical to transcription factor MYB108 GI:15375290 from [Arabidopsis thaliana]; supported by cDNA: gi_15375290_gb_AF262733.2_AF262733	216.34	148.75	80.62	50.91	235.57	162.52	107.32	43.85	-4.2	-5.4
73	At1g73600	phosphoethanolamine N-methyltransferase, putative / similar to GI:7407189 from [Spinacia oleracea]	400.21	183.58	151.55	95.07	932.10	181.40	106.48	126.13	-4.2	-7.4
74	At2g18300	expressed protein / ; supported by cDNA: gi_15724317_gb_AF412099.1_AF412099	91.76	61.32	33.34	21.82	202.98	53.51	30.60	20.03	-4.2	-10.1
75	At5g05250	expressed protein / ; supported by cDNA: gi_15810044_gb_AY054291.1_	192.95	158.58	59.44	46.00	217.48	117.74	58.39	58.38	-4.2	-3.7
76	At3g26960	expressed protein / ;supported by full-length cDNA: Ceres:96816.	198.25	127.15	99.20	47.35	608.60	199.37	95.28	99.90	-4.2	-6.1
77	At4g39940	adenosine-5-phosphosulfate-kinase / ; supported by cDNA: gi_18087562	791.83	367.95	289.56	189.91	2343.27	1633.60	555.84	488.73	-4.2	-4.8
78	At4g31330	unknown protein / ; supported by cDNA: gi_15293232_gb_AY051050.1_	239.40	199.90	120.78	57.43	326.24	301.56	121.96	67.38	-4.2	-4.8
79	At2g38940	phosphate transporter (AtPT2) / identical to GB:U62331	278.11	181.72	101.24	66.91	229.13	167.78	101.47	47.83	-4.2	-4.8
80	At2g47180	putative galactinol synthase / ;supported by full-length cDNA: Ceres:124236.	249.71	210.65	113.45	60.22	476.69	288.52	118.13	77.51	-4.1	-6.1
81	At1g06120	delta 9 desaturase, putative / similar to delta 9 desaturase GB:BAA25180 GI:2970034 from [Arabidopsis thaliana]; supported by cDNA: gi_12083275_gb_AF332434.1_AF332434	653.58	422.62	276.23	158.44	655.50	452.62	350.96	140.24	-4.1	-4.7
82	At1g49310	hypothetical protein / predicted by genscan+	63.02	33.74	41.31	15.29	68.10	29.71	20.64	17.05	-4.1	-4.0
83	At1g18590	flavonol 4'-sulfotransferase, putative / similar to flavonol 4'-sulfotransferase GI:168168 from [Flaveria chloraefolia]	522.73	236.40	211.59	126.99	1583.50	997.21	361.74	230.15	-4.1	-6.9
84	At2g02010	glutamate decarboxylase / ; supported by cDNA: gi_13605709_gb_AF361836.1_AF361836	649.04	466.99	282.83	158.25	821.87	659.82	487.61	134.76	-4.1	-6.1
85	At2g30080	putative Fe(II) transport protein /	299.43	191.63	101.76	73.07	333.59	248.43	149.70	61.77	-4.1	-5.4
86	At5g61420	myb-related transcription factor(mixta), putative / similar to myb-related transcription factor(mixta) GI:485867 from [Antirrhinum majus]; supported by cDNA: gi_5823328_gb_AF175998.1_AF175998	424.72	330.27	191.65	103.93	1323.12	810.06	330.75	175.61	-4.1	-7.5

87	At5g50200	putative protein / similar to unknown protein (pir T05562); supported by full-length cDNA: Ceres: 158397.	238.67	144.64	87.46	58.57	275.89	161.19	141.50	63.02	-4.1	-4.4
88	At2g13360	alanine-glyoxylate aminotransferase / ;supported by full-length cDNA: Ceres:8306.	319.32	328.70	115.82	78.42	709.33	222.19	102.48	138.37	-4.1	-5.1
89	At5g07460	peptide methionine sulfoxide reductase-like protein / peptide methionine sulfoxide reductase (msr) - Arabidopsis thaliana, EMBL:AJ133753	381.48	193.85	175.78	95.50	1375.58	1210.76	346.21	158.66	-4.0	-8.7
90	At2g37180	aquaporin (plasma membrane intrinsic protein 2C) / water channel protein in plasma membrane;supported by full-length cDNA: Ceres:11998.	1640.81	1178.06	849.83	414.34	1375.95	1231.65	783.70	344.77	-4.0	-4.0
91	At2g32860	glycosyl hydrolase family 1 /	68.92	34.04	27.46	17.49	304.27	65.18	20.59	16.48	-3.9	-18.5
92	At3g13790	glycosyl hydrolase family 32 / identical to beta-fructofuranosidase Gl:402740 from [Arabidopsis thaliana]; supported by cDNA: gi_15027838_gb_AY045776.1_	663.50	541.32	333.46	168.49	827.64	738.05	466.70	194.80	-3.9	-4.2
93	At3g14560	expressed protein / ;supported by full-length cDNA: Ceres:19279.	172.63	107.04	90.18	44.03	242.09	118.51	52.45	27.60	-3.9	-8.8
94	At2g46650	putative cytochrome b5 / ;supported by full-length cDNA: Ceres:3743.	966.74	620.92	447.73	246.87	2650.27	2286.90	1148.06	606.13	-3.9	-4.4
95	At5g04950	nicotianamine synthase, putative / similar to nicotianamine synthase [Lycopersicon esculentum][Gl:4753801], nicotianamine synthase 2 [Hordeum vulgare][Gl:4894912]; supported by cDNA: gi_18252858	134.96	98.21	64.91	34.52	354.29	122.54	40.69	29.31	-3.9	-12.1
96	At4g30140	putative protein / proline-rich protein APG C-terminus - Arabidopsis thaliana, PIR2:S21961;supported by full-length cDNA: Ceres:21878.	3583.63	1621.83	1132.68	924.48	4926.84	3263.64	2285.04	980.12	-3.9	-5.0
97	At2g39310	putative myrosinase-binding protein / ;supported by full-length cDNA: Ceres:33545.	92.81	52.60	49.50	23.96	281.34	219.71	83.64	31.15	-3.9	-9.0
98	At2g40900	putative integral membrane protein nodulin /	272.07	249.14	162.02	70.82	573.21	389.62	198.79	92.89	-3.8	-6.2
99	At5g38930	germin - like protein / probable germin type 2, Arabidopsis thaliana, PIR:H71408	2325.47	1711.72	1306.60	609.79	1763.21	1707.05	1216.15	372.74	-3.8	-4.7
100	At4g00880	coded for by A. thaliana cDNA T43845 / similar to auxin-induced protein; supported by cDNA: gi_17380987	275.52	126.18	103.28	72.49	316.98	149.03	79.85	53.67	-3.8	-5.9
101	At5g14940	oligopeptide transporter -like protein / oligopeptide transporter (LeOPT1), Lycopersicon esculentum, EMBL:AF016713	103.33	67.43	53.78	27.20	218.40	173.97	74.68	33.55	-3.8	-6.5
102	At1g70410	carbonic anhydrase, putative / similar to carbonic anhydrase Gl:882241 from [Flaveria linearis]; supported by full-length cDNA: Ceres: 38715.	364.05	301.84	183.95	96.84	811.53	366.00	183.72	103.49	-3.8	-7.8
103	At2g46690	putative auxin-regulated protein /	142.85	87.11	82.31	38.82	242.43	93.10	50.58	24.94	-3.7	-9.7
104	At3g11280	MYB-family transcription factor, putative / contains Pfam profile: PF00249 Myb-like DNA-binding domain;supported by full-length cDNA: Ceres:109398.	251.99	186.42	141.35	68.56	320.01	242.47	134.17	73.95	-3.7	-4.3
105	At3g16460	putative lectin / contains Pfam profile: PF01419 jacalin-like lectin domain; similar to jasmonate inducible protein GB:Y11483 (Brassica napus), myrosinase binding protein GB:BAA84545 (Arabidopsis thaliana); supported by cDNA: gi_14334869_gb_AY035108.1_	523.08	326.52	283.66	142.33	594.80	429.65	232.54	100.34	-3.7	-5.9
106	At3g22231	Expressed protein / ; supported by cDNA: gi_14335055_gb_AY037207.1_	517.51	186.32	201.30	141.08	604.65	152.80	153.91	62.97	-3.7	-9.6
107	At1g56430	nicotianamine synthase, putative / similar to nicotianamine synthase [Lycopersicon esculentum][Gl:4753801], nicotianamine synthase 2 [Hordeum vulgare][Gl:4894912]; supported by cDNA: gi_20466583	705.27	522.17	441.54	192.42	1157.04	741.16	367.97	99.51	-3.7	-11.6

108	At5g10180	sulfate transporter / ; supported by cDNA: gi_2114105_dbj_AB003591.1_AB003591	776.58	406.45	369.98	212.84	571.33	83.83	36.65	31.86	-3.6	-17.9
109	At4g32650	potassium channel protein AtKC / potassium channel - Solanum tuberosum, PATX:E264595; supported by cDNA: gi_15529217_gb_AY052233.1_	146.55	87.84	59.28	40.62	150.75	126.40	80.44	33.14	-3.6	-4.5
110	At2g38600	putative acid phosphatase / contains metallo-phosphoesterase motif (PS50185)	117.50	78.10	51.02	32.65	211.86	130.28	52.52	30.52	-3.6	-6.9
111	At2g46790	expressed protein / ; supported by cDNA: gi_10280999_dbj_AB046953.1_AB046953	97.65	49.32	31.06	27.15	119.16	48.52	29.36	24.52	-3.6	-4.9
112	At3g10120	unknown protein / predicted by genscan+, multiple est matches	268.25	173.32	114.10	74.78	209.98	163.34	108.55	56.94	-3.6	-3.7
113	At5g05790	putative protein / contains similarity to I-box binding factor	200.47	161.42	92.71	56.19	315.24	352.93	153.67	44.83	-3.6	-7.0
114	At1g05300	putative zinc transporter / Similar to Arabidopsis Fe(II) transport protein (gb U27590)	253.46	179.95	94.83	71.21	210.50	133.28	90.53	50.83	-3.6	-4.1
115	At2g33830	auxin-regulated protein /	472.89	75.37	67.96	133.58	274.60	33.15	44.79	59.95	-3.5	-4.6
116	At2g30540	putative glutaredoxin / ;supported by full-length cDNA: Ceres:39560.	103.38	56.85	42.52	29.52	135.68	42.64	33.46	27.42	-3.5	-4.9
117	At1g20850	cysteine proteinase XCP2 / identical to papain-type cysteine endopeptidase XCP2 GI:6708183 from [Arabidopsis thaliana]	281.89	234.16	136.26	81.35	527.37	496.05	163.07	163.22	-3.5	-3.2
118	At4g30650	low temperature and salt responsive protein homolog / low temperature and salt responsive protein LTI6A - Arabidopsis thaliana,PID:g4039153	916.36	365.89	254.25	266.80	716.61	235.12	157.65	140.56	-3.4	-5.1
119	At1g67870	expressed protein / contains non-consensus GG donor splice site at exon2; modeled to est match.;supported by full-length cDNA: Ceres:124169.	531.81	284.07	203.62	156.26	796.67	248.12	150.75	95.22	-3.4	-8.4
120	At1g29660	lipase/hydrolase, putative / contains Pfam profile: PF00657 Lipase/Acylhydrolase with GDSL-like motif;supported by full-length cDNA: Ceres:6680.	290.22	244.69	105.89	85.64	359.36	170.43	81.69	58.20	-3.4	-6.2
121	At1g24575	Expressed protein / ; supported by full-length cDNA: Ceres: 38093.	191.24	111.96	90.76	56.55	582.36	244.36	142.33	51.86	-3.4	-11.2
122	At1g19960	hypothetical protein / predicted by genemark.hmm; supported by cDNA: gi_12083285	742.04	340.86	314.34	220.38	873.46	538.67	350.09	108.39	-3.4	-8.1
123	At5g20820	putative protein / predicted proteins, Arabidopsis thaliana;supported by full-length cDNA: Ceres:19897.	198.01	170.96	100.34	59.32	220.87	192.86	83.37	45.36	-3.3	-4.9
124	At3g30340	hypothetical protein / contains Pfam profile: PF00892 Integral membrane protein	315.23	243.03	174.89	94.58	490.59	365.45	177.25	88.51	-3.3	-5.5
125	At3g26770	putative short chain alcohol dehydrogenase / contains Pfam profile: PF00106 short chain dehydrogenase; similar to sex determination protein tasselseed 2 GB:P50160 [Zea mays]; supported by cDNA: gi_15529183_gb_AY052216.1_	175.89	108.88	83.31	53.17	214.94	163.68	106.82	50.84	-3.3	-4.2
126	At3g15840	expressed protein / ; supported by cDNA: gi_13358213_gb_AF325024.2_AF325024	293.11	279.23	115.20	88.66	402.37	185.69	126.05	104.83	-3.3	-3.8
127	At5g26340	hexose transporter - like protein / hexose transporter HT2, Lycopersicon esculentum, EMBL:LES132224; supported by cDNA: gi_15010579_gb_AY045591.1_	132.59	75.08	40.09	40.15	148.26	102.83	60.71	37.20	-3.3	-4.0
128	At3g61380	putative protein / hypothetical protein At2g45900 - Arabidopsis thaliana, EMBL:AC004665	336.12	235.06	137.60	101.90	271.32	260.24	144.75	64.83	-3.3	-4.2
129	At1g06830	glutaredoxin, putative / similar to glutaredoxin GB:CAA89699 GI:1732424 from [Ricinus communis];supported by full-length cDNA: Ceres:125679.	152.92	64.58	77.71	47.02	334.48	81.12	109.98	51.42	-3.3	-6.5

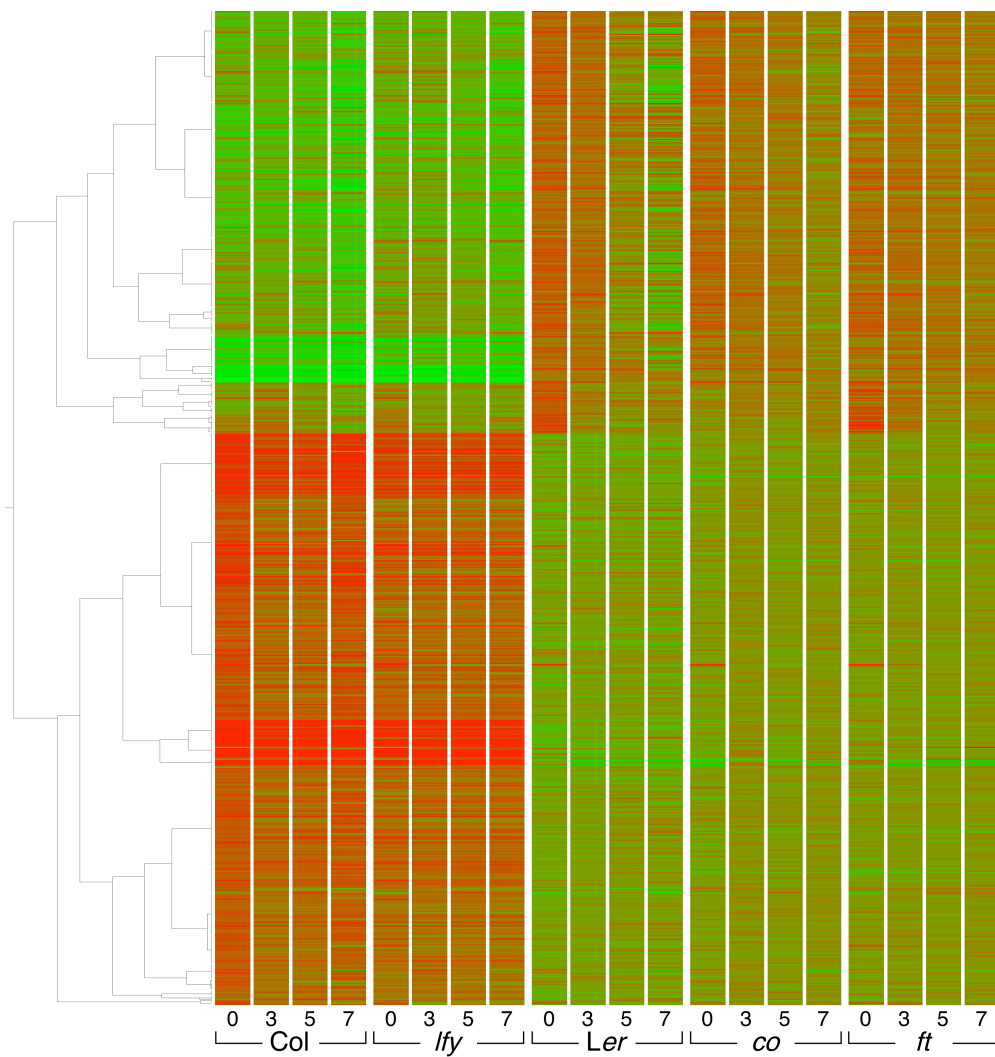
130	At1g71030	myb family transcription factor / similar to MybHv5 GI:19055 from [Hordeum vulgare];supported by full-length cDNA: Ceres:31592.	233.37	139.96	103.26	73.83	379.25	174.39	128.91	76.93	-3.2	-4.9
131	At5g59780	myb family transcription factor / contains PFAM profile: myb DNA binding domain PF00249; supported by cDNA: gi_3941479_gb_AF062894.1_AF062894	101.11	65.29	52.26	32.25	148.97	83.91	42.24	35.52	-3.1	-4.2
132	At5g44480	putative protein / contains similarity to UDP-glucose 4-epimerase	397.43	358.92	217.80	126.95	881.74	758.73	535.63	184.16	-3.1	-4.8
133	At1g62290	aspartic protease, putative / similar to aspartic protease GI:1326164 from [Brassica napus]; supported by cDNA: gi_17979427	379.66	313.80	207.18	121.44	542.46	569.46	248.42	117.24	-3.1	-4.6
134	At4g25100	iron superoxide dismutase (FSD1) / identical to Fe-superoxide dismutase [Arabidopsis thaliana] gi 166700 gb AAA32791; supported by cDNA, Ceres:32935; supported by cDNA: 32935.	135.97	871.00	152.89	43.57	753.58	2336.58	242.84	26.01	-3.1	-29.0
135	At3g57260	glycosyl hydrolase family 17 / similar to glucan endo-1,3-beta-glucosidase, acidic isoform precursor SP:P33157 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:21719.	147.52	55.18	82.46	47.37	309.42	48.21	43.99	75.77	-3.1	-4.1
136	At1g37130	nitrate reductase, putative / similar to nitrate reductase GI:540486 from [Brassica napus]; supported by cDNA: gi_14194132_gb_AF367272.1_AF367272	476.37	419.84	375.95	153.00	1090.71	442.76	259.51	225.49	-3.1	-4.8
137	At4g10500	putative Fe(II)/ascorbate oxidase / SRG1 protein - Arabidopsis thaliana, PIR2:S44261	80.93	43.67	52.68	26.17	74.83	28.45	36.49	21.58	-3.1	-3.5
138	At4g17090	glycosyl hydrolase family 14 (beta-amylase) / identical to beta-amylase enzyme GI:6065749 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:36882.	382.82	242.90	155.43	124.07	485.99	311.38	164.53	102.97	-3.1	-4.7
139	At4g04830	putative protein / similar to transcriptional regulator;supported by full-length cDNA: Ceres:9218.	221.91	45.73	50.56	72.07	76.84	25.98	24.09	22.00	-3.1	-3.5
140	At5g63850	amino acid transporter AAP4 (pir S51169) / ;supported by full-length cDNA: Ceres:116681.	539.02	355.97	304.51	175.83	966.88	622.15	379.88	203.42	-3.1	-4.8
141	At4g23010	putative protein / UDP-galactose transporter related isozyme 3, Homo sapiens, PIR2:JC5026	628.28	433.27	343.20	205.84	874.58	659.33	464.16	257.54	-3.1	-3.4
142	At1g28710	expressed protein / similar to GI:2827651, GI:7527728, GI:4406788, GI:6063544, GI:10764853 from [Arabidopsis thaliana]; supported by cDNA: gi_15027990_gb_AY045852.1_	1635.55	1145.21	866.14	540.97	1321.10	1066.30	790.95	379.80	-3.0	-3.5
143	At1g29280	WRKY family transcription factor / similar to DNA binding protein WRKY3 GB:U56834 GI:1432055 from [Petroselinum crispum]; supported by cDNA: gi_17980955	299.08	195.90	124.21	99.08	260.01	197.64	149.17	88.68	-3.0	-2.9
144	At5g50120	G-protein beta family / contains similarity to GTP-binding regulatory protein and WD-repeat protein	132.94	118.80	63.02	44.05	126.78	98.94	58.08	39.91	-3.0	-3.2
145	At3g47510	putative protein /	71.99	47.96	31.36	23.95	100.24	63.21	33.02	27.98	-3.0	-3.6
146	At3g60520	putative protein / ;supported by full-length cDNA: Ceres:21518.	254.25	129.16	87.56	84.73	285.53	162.12	62.79	44.48	-3.0	-6.4
147	At5g10030	bZIP transcription factor, OBF4 / ocs-element binding factor 4	131.58	75.39	59.54	43.90	178.83	106.77	57.79	40.62	-3.0	-4.4
148	At3g30530	bZIP family transcription factor / similar to bZIP protein(G/HBF-1) GI:1905785 from [Glycine max]; contains PFAM profile: bZIP transcription factor PF00170	216.75	180.60	70.94	72.36	593.66	484.06	303.88	85.21	-3.0	-7.0
149	At2g39350	ABC transporter family protein /	856.43	546.42	463.62	288.27	775.98	565.11	399.62	189.90	-3.0	-4.1
150	At5g20960	aldehyde oxidase AAO1 / ; supported by cDNA: gi_2792301_gb_AF039895.1_AF039895	132.34	74.39	69.69	45.19	265.06	147.73	82.23	47.31	-2.9	-5.6

151	At4g09890	putative protein / Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence, gene T30B22.22, PID:g2529679	95.53	59.92	49.18	32.68	220.24	94.98	69.45	44.32	-2.9	-5.0
152	At5g53320	leucine-rich repeat transmembrane protein kinase, putative /	86.66	62.95	43.98	29.73	94.90	67.80	45.98	31.24	-2.9	-3.0
153	At4g18280	glycine-rich cell wall protein-like / glycine-rich protein 1.0 precursor, Phaseolus vulgaris, PIR1:S01821; supported by cDNA: gi_14030676_gb_AF375429.1_AF375429	158.30	121.22	83.74	54.55	250.55	150.20	64.00	37.75	-2.9	-6.6
154	At3g29590	Anthocyanin 5-aromatic acyltransferase, putative / similar to Anthocyanin 5-aromatic acyltransferase GB:BAA74428 from [Gentiana triflora]	289.68	215.57	163.76	100.62	551.15	439.69	263.45	134.03	-2.9	-4.1
155	At4g26150	GATA zinc finger protein / Arabidopsis thaliana mRNA for GATA transcription factor 3, PID:e1254739	157.08	129.54	75.90	54.67	193.89	113.47	74.66	60.93	-2.9	-3.2
156	At5g01870	lipid-transfer protein-like / lipid-transfer protein - Nicotiana glauca, EMBL:AF151214	6218.09	4333.44	2982.52	2175.91	5831.31	4506.89	3445.49	1565.10	-2.9	-3.7
157	At4g00780	coded for by A. thaliana cDNA T20615 / ;supported by full-length cDNA: Ceres:37305.	185.77	117.07	83.04	65.12	311.83	90.42	59.86	36.33	-2.9	-8.6
158	At1g73630	putative calmodulin / similar to calmodulin GB:P02596 [Renilla reniformis]; contains Pfam profile: PF00036 EF hand (4 copies);supported by full-length cDNA: Ceres:94584.	95.22	60.87	47.81	33.93	228.30	163.89	82.81	41.66	-2.8	-5.5
159	At1g73260	putative trypsin inhibitor / similar to trypsin inhibitor propeptide GB:AAB68964 [Brassica oleracea]; contains Pfam profile: PF00197 Trypsin and protease inhibitors; supported by cDNA: gi_15450971_gb_AY054566.1_	111.66	64.65	53.42	39.84	514.11	314.16	256.42	56.61	-2.8	-9.1
160	At1g31180	3-methyladenine DNA glycosylase, putative / Strong similarity to GB:P29102, 3-isopropylmalate dehydrogenase (IMDH) from Brassica napus. EST gb F14478 comes from this gene;supported by full-length cDNA: Ceres:34420.	763.25	404.03	331.04	275.28	2067.59	1799.29	719.73	311.02	-2.8	-6.6
161	At4g33550	putative protein / predicted protein, Arabidopsis thaliana	54.99	57.03	31.37	19.95	107.47	113.06	28.74	22.71	-2.8	-4.7
162	At3g63160	putative protein / outer envelope membrane protein E 6.7 - chloroplast Spinacia oleracea, PIR:A35958; supported by cDNA: gi_15724349_gb_AF412115.1_AF412115	268.11	216.51	98.37	98.68	245.40	94.00	76.99	82.71	-2.7	-3.0
163	At2g23840	unknown protein /	133.16	71.96	56.79	49.08	175.28	77.41	59.55	58.91	-2.7	-3.0
164	At1g35190	hyoscyamine 6-dioxygenase hydroxylase, putative / similar to hyoscyamine 6-dioxygenase hydroxylase GB:P24397 from [Hyoscyamus niger];supported by full-length cDNA: Ceres:2551.	245.11	215.54	116.26	90.46	266.96	227.74	161.53	87.10	-2.7	-3.1
165	At4g22950	MADS-box protein / MADS-box protein AGL14, Arabidopsis thaliana, gb:U20184; supported by cDNA: gi_11545542_gb_AF312664.1_AF312664	55.14	38.69	34.52	20.48	81.56	45.74	31.03	20.46	-2.7	-4.0
166	At4g20460	UDP-glucose 4-epimerase - like protein / UDP-galactose 4-epimerase, Cyamopsis tetragonoloba, EMBL:AJ005082	226.92	163.54	114.78	84.51	396.05	362.56	271.71	122.84	-2.7	-3.2
167	At4g14040	selenium-binding protein like / ; supported by cDNA: gi_14532843_gb_AY040046.1_	428.53	244.73	213.08	159.74	793.83	678.89	273.76	172.07	-2.7	-4.6
168	At2g31790	UDP-glycosyltransferase family / ; supported by cDNA: gi_15810476_gb_AY056277.1_	614.45	395.08	376.43	230.37	1538.71	1390.17	611.96	355.16	-2.7	-4.3
169	At3g27200	blue copper protein, putative / similar to uclacyanin I GB:AAC32038 from [Arabidopsis thaliana] (Protein Sci (1996) 5(11):2175-83);supported by full-length cDNA: Ceres:15343.	178.98	148.65	106.66	67.13	316.05	230.99	104.89	112.85	-2.7	-2.8

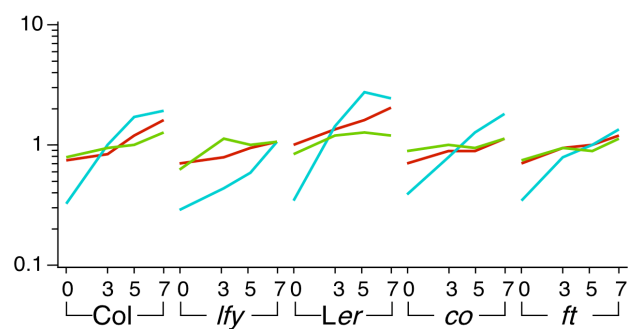
170	At2g38530	putative nonspecific lipid-transfer protein / ;supported by full-length cDNA: Ceres:18328.	3784.58	3243.83	2378.81	1420.11	1900.69	1469.62	833.57	420.02	-2.7	-4.5
171	At4g19810	glycosyl hydrolase family 18 / similar to chitinase/lysozyme GI:467689 from [Nicotiana tabacum]	46.20	38.99	28.89	17.37	61.44	37.42	23.19	18.47	-2.7	-3.3
172	At2g14750	putative adenosine phosphosulfate kinase / identical to GB:U05238;supported by full-length cDNA: Ceres:14216.	1325.69	766.73	680.45	498.59	2928.11	2183.56	1006.94	718.51	-2.7	-4.1
173	At3g01840	putative protein kinase / C-terminal region similar to protein kinases: GB:S71277 [Arabidopsis thaliana], GB:CAB43834 [Arabidopsis thaliana]; Pfam HMM hit: eukaryotic protein kinase domain	137.21	143.13	84.15	51.62	166.02	183.41	103.39	51.89	-2.7	-3.2
174	At5g65210	bZIP transcription factor, TGA1 / ;supported by full-length cDNA: Ceres:31032.	132.78	99.67	64.57	50.12	221.61	148.15	82.21	49.27	-2.6	-4.5
175	At3g52720	carbonic anhydrase (CAH1) / ; supported by cDNA: gi_15450772_gb_AY054466.1_	120.79	69.66	78.06	45.70	309.34	73.37	52.44	41.96	-2.6	-7.4
176	At3g19270	cytochrome P450, putative / similar to cytochrome P450 GB:BAA37167 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:126144.	127.06	142.93	103.85	48.08	360.02	439.74	252.65	72.24	-2.6	-5.0
177	At5g17220	glutathione transferase, putative / ; supported by cDNA: gi_11096011_gb_AF288189.1_AF288189	649.65	618.14	387.01	248.64	1617.66	1388.35	852.51	374.35	-2.6	-4.3
178	At4g31730	hypothetical protein /	122.57	112.88	70.41	47.11	328.78	358.23	168.26	59.16	-2.6	-5.6
179	At2g30670	putative tropinone reductase /	57.79	41.05	41.34	22.30	394.80	169.53	143.47	59.70	-2.6	-6.6
180	At1g61660	expressed protein / ;supported by full-length cDNA: Ceres:159557.	142.43	93.90	73.99	54.97	257.83	134.05	83.56	79.57	-2.6	-3.2
181	At1g15960	metal ion transporter, putative / similar to metal ion transporter GI:5853313 from [Arabidopsis thaliana]; supported by cDNA: gi_18650633	161.97	130.65	78.20	62.67	236.68	119.91	86.40	47.52	-2.6	-5.0
182	At4g04610	5-adenylylsulfate reductase / ;supported by full-length cDNA: Ceres:40330.	836.76	317.21	309.12	323.81	1169.68	767.03	446.60	294.26	-2.6	-4.0
183	At5g19875	Expressed protein / ; supported by full-length cDNA: Ceres: 59.	152.37	159.81	116.80	59.75	139.48	113.89	68.38	36.62	-2.5	-3.8
184	At2g38870	putative protease inhibitor / ;supported by full-length cDNA: Ceres:11662.	1171.25	935.83	512.46	462.35	1500.79	1766.62	1058.48	471.75	-2.5	-3.2
185	At2g39850	subtilisin-like serine protease / contains similarity to subtilisin-like protease C1 GI:13325079 from [Glycine max]	112.40	95.33	63.50	44.41	194.20	108.68	48.86	29.93	-2.5	-6.5
186	At2g24762	Expressed protein / ; supported by full-length cDNA: Ceres: 19631.	269.21	225.23	179.77	106.64	589.78	458.86	249.62	68.21	-2.5	-8.6
187	At5g54060	flavonol 3-O-glucosyltransferase-like /	469.80	400.69	391.87	186.61	1163.49	932.85	677.06	326.98	-2.5	-3.6
188	At1g44100	amino acid permease, putative / almost identical to amino acid permease GI:608673 from [Arabidopsis thaliana]	303.81	194.63	199.51	120.89	493.95	298.00	269.10	153.92	-2.5	-3.2
189	At3g11660	VAMP protein SEC22 / similar to hin1 GB:CAA68848 [Nicotiana tabacum];supported by full-length cDNA: Ceres:8166.	116.51	127.20	83.89	46.61	140.42	119.40	54.67	45.90	-2.5	-3.1
190	At1g20440	hypothetical protein / ; supported by cDNA: gi_18252914	196.41	131.41	106.54	78.66	480.96	161.30	85.21	71.45	-2.5	-6.7
191	At1g70810	expressed protein / contains similarity to zinc finger and C2 domain protein GI:9957238 from [Arabidopsis thaliana];supported by full-length cDNA: Ceres:23322.	141.76	99.73	63.85	56.96	183.32	115.06	74.08	61.54	-2.5	-3.0

192	At5g38780	methyltransferase-related / similar to defense-related protein cjs1 [Brassica carinata][GI:14009292], caffeine synthase [Camellia sinensis][GI:9967143], SAM:benzoic acid carboxyl methyltransferase [Antirrhinum majus][GI:9789277]; supported by cDNA: gi_17380699	46.65	44.63	25.48	18.77	101.07	71.13	47.81	30.92	-2.5	-3.3
193	At5g24660	putative protein / similar to unknown protein (emb CAB62461.1);supported by full-length cDNA: Ceres:268701.	92.79	37.73	32.20	37.37	102.82	31.68	31.35	31.74	-2.5	-3.2
194	At3g08040	MATE efflux family protein, putative / contains TIGRfam profile: TIGR00797: MATE efflux family protein; supported by cDNA: gi_15912322_gb_AY056439.1_	167.67	135.90	116.25	67.93	318.60	280.58	128.92	85.77	-2.5	-3.7
195	At4g19840	lectin like protein / lectin phloem protein PP2, winter squash, PIR2:S38462;supported by full-length cDNA: Ceres:17437.	290.14	231.72	188.64	118.78	369.69	210.91	95.24	45.97	-2.4	-8.0
196	At3g53100	putative protein / proline-rich protein, Raphanus sativa, PIR:S16748	126.06	100.34	73.22	52.04	295.16	200.30	101.74	94.80	-2.4	-3.1
197	At5g38710	proline oxidase, mitochondrial precursor -like protein / PROLINE OXIDASE, MITOCHONDRIAL PRECURSOR, Arabidopsis thaliana, SWISSNEW:PROD	59.96	46.92	30.28	24.76	90.71	64.07	35.12	21.39	-2.4	-4.2
198	At1g09155	Expressed protein / ; supported by full-length cDNA: Ceres: 31022.	69.18	52.21	28.53	28.68	80.81	63.54	46.82	26.75	-2.4	-3.0
199	At5g44400	FAD-linked oxidoreductase family / similar to SPIP30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) [Eschscholzia californica]; contains PF01565 FAD binding domain; supported by cDNA: gi_18176301	660.67	569.68	441.18	274.18	844.69	689.07	447.73	219.61	-2.4	-3.8
200	At3g61880	cytochrome p450 (CYP78A9) / ;supported by full-length cDNA: Ceres:29661.	114.09	85.52	77.85	47.56	152.46	132.33	69.65	47.49	-2.4	-3.2
201	At3g62740	glycosyl hydrolase family 1 / several beta-glucosidases	115.92	79.32	71.33	48.73	212.54	155.28	87.10	58.07	-2.4	-3.7
202	At1g69530	expansin (At-EXP1) / identical to expansin (At-EXP1) [Arabidopsis thaliana] GI:1041702;supported by full-length cDNA: Ceres:255048.	346.07	378.24	239.63	145.54	278.15	298.65	153.28	87.59	-2.4	-3.2
203	At2g43010	expressed protein / ; supported by cDNA: gi_13430617_gb_AF360221.1_AF360221	293.36	254.55	186.95	123.64	283.01	187.20	114.00	69.18	-2.4	-4.1
204	At1g23800	putative aldehyde dehydrogenase / ; supported by cDNA: gi_14334931_gb_AY035139.1_	160.78	136.36	103.73	67.92	324.25	311.74	150.75	85.00	-2.4	-3.8
205	At1g65500	expressed protein / ;supported by full-length cDNA: Ceres:25136.	126.60	109.27	80.81	53.61	138.73	63.41	52.89	43.67	-2.4	-3.2
206	At3g43430	putative protein / RING-H2 zinc finger protein ATL4 - Arabidopsis thaliana, EMBL:AF132014;supported by full-length cDNA: Ceres:3137.	105.56	99.49	66.35	44.74	114.52	107.05	65.24	32.36	-2.4	-3.5
207	At5g27350	sugar transporter-like protein / putative sugar transporter (SUGTL2) - Arabidopsis thaliana, EMBL:AJ249968; supported by cDNA: gi_15294181_gb_AF410282.1_AF410282	84.43	59.38	41.70	36.16	156.90	71.31	43.65	40.24	-2.3	-3.9
208	At4g18640	leucine-rich repeat transmembrane protein kinase, putative /	110.02	88.90	65.99	47.15	277.75	214.34	114.82	74.27	-2.3	-3.7
209	At5g42650	allene oxide synthase / ; supported by cDNA: gi_6002956_gb_AF172727.1_AF172727	196.45	169.30	117.37	84.45	275.92	190.17	105.99	81.64	-2.3	-3.4
210	At2g28550	AP2 domain protein RAP2.7 / identical to GI:2281639 [Arabidopsis thaliana]; supported by cDNA: gi_15292762_gb_AY050815.1_	295.80	212.66	181.27	127.36	401.88	256.57	172.70	80.04	-2.3	-5.0
211	At5g57350	plasma membrane ATPase 3 (proton pump) (sp P20431) / ; supported by cDNA: gi_15982712_gb_AY056780.1_	434.16	401.33	208.26	187.12	841.32	618.34	287.96	168.32	-2.3	-5.0
212	At1g03495	hypothetical protein / similar to Anthocyanin 5-aromatic acyltransferase GB:BAA74428	828.68	680.07	558.61	359.24	1799.64	1582.95	1125.95	539.34	-2.3	-3.3

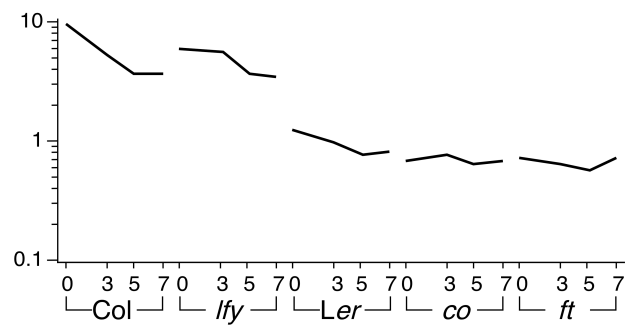
213	At3g62040	hypothetical protein / contains non-consensus GA donor splice site at exon 2	51.12	31.47	32.28	22.20	102.04	30.34	26.19	24.50	-2.3	-4.2
214	At1g14700	purple acid phosphatase, putative / contains Pfam profile: PF02227 Purple acid phosphatase; supported by cDNA: gi_17979080	95.38	85.59	67.40	41.56	204.99	154.58	89.14	69.34	-2.3	-3.0
215	At2g29670	expressed protein / ; supported by cDNA: gi_14030738_gb_AF375460.1_AF375460	142.23	95.74	69.05	62.05	164.98	67.09	54.77	45.71	-2.3	-3.6
216	At3g29030	expansin (At-EXP5) / identical to expansin At-EXP5 GB:AAB38071 from [Arabidopsis thaliana]; supported by cDNA: gi_1041703_gb_U30478.1_ATU30478	675.39	572.70	496.51	296.00	878.89	649.10	385.39	233.74	-2.3	-3.8
217	At1g62570	flavin-containing monooxygenase, putative / similar to flavin-containing monooxygenase GB:AAA21178 GI:349534 from [Oryctolagus cuniculus]; supported by cDNA: gi_15451123_gb_AY054642.1_	118.43	88.56	69.82	52.35	135.45	95.49	57.81	41.04	-2.3	-3.3
218	At3g12890	expressed protein / ;supported by full-length cDNA: Ceres:158736.	166.88	162.88	119.06	74.44	417.44	306.96	167.77	81.89	-2.2	-5.1
219	At1g68150	WRKY family transcription factor / similar to DNA-binding protein ABF2 GI:1159879 from [Avena fatua]; supported by cDNA: gi_15990587_gb_AY052645.1_	36.43	22.51	18.52	16.31	60.04	45.25	27.59	18.00	-2.2	-3.3
220	At1g67865	Expressed protein / ; supported by cDNA: gi_15529158_gb_AY052203.1_	996.20	665.18	595.41	446.49	1594.61	669.15	426.80	194.62	-2.2	-8.2
221	At1g04040	expressed protein / Similar to acid phosphatase; Location of ESTs 110C2T7 , gb T42036, and 110C2XP, gb AI100245; supported by cDNA: gi_13926197_gb_AF370572.1_AF370572	937.79	1027.94	792.52	421.23	528.77	653.18	450.95	149.84	-2.2	-3.5
222	At3g01350	putative peptide transporter / similar to peptide transporter PTR2-B (histidine transporting protein) GB:P46032 (Arabidopsis thaliana)	64.37	51.32	41.82	29.01	90.28	66.69	40.98	31.03	-2.2	-2.9
223	At4g39770	puative protein / various predicted proteins	82.24	50.40	48.97	37.79	194.04	62.16	62.24	38.90	-2.2	-5.0
224	At3g21270	Dof zinc finger protein / identical to Dof zinc finger protein ADOF2 GI:3608263 from [Arabidopsis thaliana]; supported by cDNA: gi_15027980_gb_AY045847.1_	383.11	301.39	222.59	176.21	699.49	541.78	382.42	176.21	-2.2	-4.0
225	At3g20370	expressed protein / similar to GB:BAA87936 (Gene 239 (2), 309-316 (1999)), contains Pfam profile: (2) PF00917 MATH domains;supported by full-length cDNA: Ceres:40420.	84.72	47.65	51.23	38.99	192.54	129.06	90.18	45.63	-2.2	-4.2
226	At1g29395	Expressed protein / ; supported by full-length cDNA: Ceres: 30602.	129.71	97.97	60.53	60.51	191.93	109.94	57.09	45.63	-2.1	-4.2
227	At5g22270	putative protein / similar to unknown protein (gb AAF02129.1);supported by full-length cDNA: Ceres:35419.	144.61	89.86	74.46	68.25	135.29	73.21	56.33	38.00	-2.1	-3.6
228	At4g27830	glycosyl hydrolase family 1 / beta-glucosidase BGQ60 precursor - barley, PIR2:A57512; supported by cDNA: gi_15982821_gb_AY057518.1_	106.05	77.02	60.93	51.20	183.60	93.90	66.79	64.84	-2.1	-2.8
229	At5g63180	pectate lyase / ; supported by cDNA: gi_16648839_gb_AY058197.1_	200.26	186.66	132.56	97.07	237.39	120.57	78.72	85.84	-2.1	-2.8
230	At2g14610	pathogenesis-related PR-1-like protein / identical to GB:M90508; supported by cDNA: gi_166860_gb_M90508.1_ATHRPRP1A	70.34	42.00	53.99	34.40	216.33	74.05	51.51	45.11	-2.0	-4.8
231	At2g21890	putative cinnamyl-alcohol dehydrogenase /	68.34	55.75	44.22	35.21	153.60	67.54	49.01	44.25	-1.9	-3.5



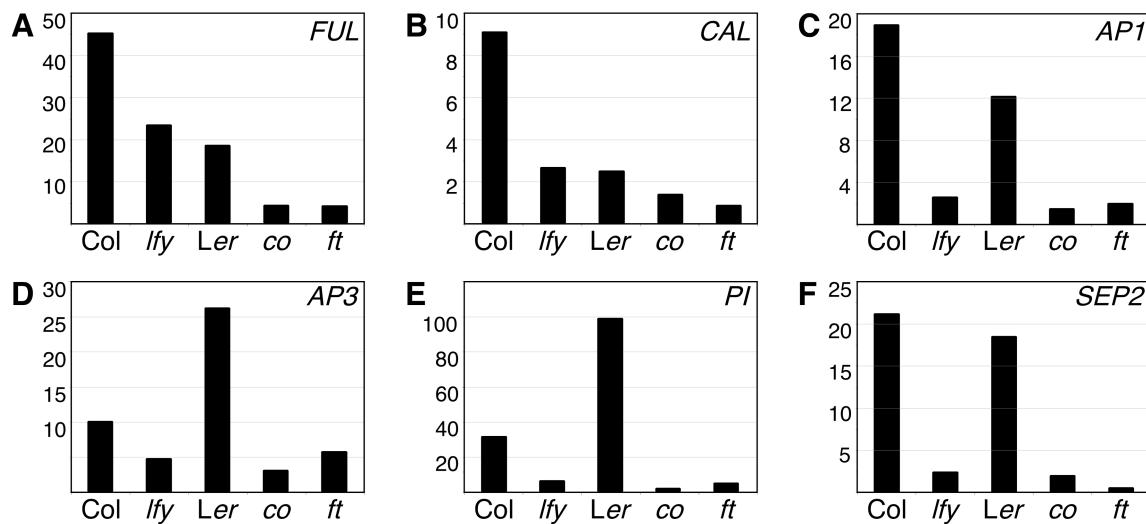
Supplementary Figure 1. Hierarchical clustering of genes differentially expressed between Col and Ler. Signals were normalized to the median for each gene. Red indicates high signal, green low signal.



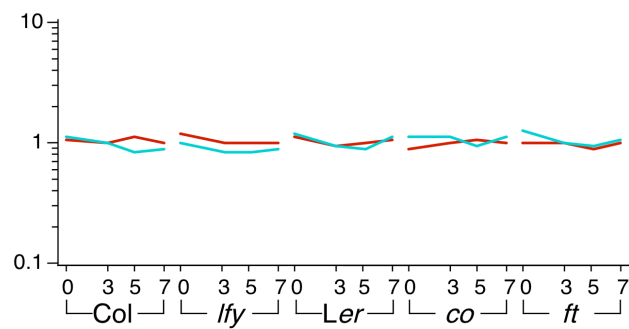
Supplementary Figure 2. Expression of *CRC* (blue), *WUS* (red), and *STM* (green).



Supplementary Figure 3. *FLC* expression across genotypes.



Supplementary Figure 4. Expression changes of selected floral regulators, measured by RT-qPCR. Fold-changes in samples taken 7 and 0 days after transfer to long days are shown.



Supplementary Figure 5. Expression of *ACS10* (At1g6290; red) and *P5CS2* (At3g55610; blue), previously identified as responsive to *CO* overexpression in whole seedlings (Samach et al., 2000).

...	CTG	CAG	CAT	CAT	CAG	GAT	TCT	...	<i>At4g36920 (AP2)</i>
...	TGG	CAG	CAT	CAT	CAG	GAT	TCT	...	<i>At5g67180 (AP2-like)</i>
...	ATG	CAG	CAT	CAT	CAG	GAT	TCT	...	<i>At5g60120 (AP2-like)</i>
...	CAG	CAG	CAT	CAT	CAG	GAT	TCT	...	<i>At2g28550 (RAP2.7)</i>
...	TTG	CAG	CAT	CAT	CAG	GAT	TCC	...	<i>SMZ</i>
...	TTG	TAG	CAT	CAT	CAG	GAT	TCC	...	<i>SNZ</i>
<hr/>									
...	ATG	CAG	CAT	CAT	CAA	GAT	TCT	...	<i>miRNA172a-1/2</i>
...	CTG	CAG	CAT	CAT	CAA	GAT	TCT	...	<i>miRNA172b</i>
...	ATG	CAG	CAT	CAT	CAA	GAT	TCC	...	<i>miRNA172c</i>

reverse complement

Supplementary Figure 6. Alignment of miR172 isoforms with *SMZ*, *SNZ* and homologs.