

1 **Title: Volatile compounds emitted by diverse phytopathogenic microorganisms promote**  
2 **plant growth and flowering through cytokinin action**

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4 **Running Title: VCs from microbial phytopathogens promote growth**

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1 **ABSTRACT**

2 It is known that volatile emissions from some beneficial rhizosphere microorganisms promote  
3 plant growth. Here we show that volatile compounds (VCs) emitted by phylogenetically diverse  
4 rhizosphere and non-rhizosphere bacteria and fungi (including plant pathogens and microbes  
5 that do not normally interact mutualistically with plants) promote growth and flowering of  
6 various plant species, including crops. In *Arabidopsis* plants exposed to VCs emitted by the  
7 phytopathogen *Alternaria alternata*, changes included enhancement of photosynthesis and  
8 accumulation of high levels of cytokinins (CKs) and sugars. Evidence obtained using transgenic  
9 *Arabidopsis* plants with altered CK status show that CKs play essential roles in this phenomenon,  
10 since growth and flowering responses to the VCs were reduced in mutants with CK-deficiency  
11 (35S:AtCKX1) or low receptor sensitivity (*ahk2/3*). Further, we demonstrate that the plant  
12 responses to fungal VCs are light-dependent. Transcriptomic analyses of *Arabidopsis* leaves  
13 exposed to *A. alternata* VCs revealed changes in the expression of light- and CK-responsive  
14 genes involved in photosynthesis, growth and flowering. Notably, many genes differentially  
15 expressed in plants treated with fungal VCs were also differentially expressed in plants exposed  
16 to VCs emitted by the plant growth promoting rhizobacterium *Bacillus subtilis* GB03, suggesting  
17 that plants react to microbial VCs through highly conserved regulatory mechanisms.

18  
19 **Key-words:** cytokinin, flowering, growth promotion, microbial volatile compounds,  
20 photoregulation, photosynthesis, plant-microbe interaction, starch

21

## 1 INTRODUCTION

2 Plants' growth and development are influenced by microorganisms occurring either aboveground  
3 in the phyllosphere, underground in the rhizosphere and/or in the endosphere inside the vascular  
4 transport system and apoplastic space. Microbes synthesize a multitude of substances including  
5 carbohydrates, proteins, lipids, amino acids, hormones, etc., which may act directly or indirectly  
6 to activate plant immunity or regulate plant growth and morphogenesis (De-la-Peña & Loyola-  
7 Vargas 2014). Microbes also synthesize and emit many volatile compounds (VCs) with  
8 molecular masses less than 300 Da, low polarity, and a high vapor pressure (Schulz & Dickschat  
9 2007; Lemfack et al. 2014) that can diffuse far from their point of origin and migrate in soil and  
10 aerial environments as well as through porous wood materials. Hence, VCs may play potentially  
11 important roles as semiochemicals in interspecies communication, participating in countless  
12 interactions among plants and microorganisms, both below and above ground (Kanchiswamy et  
13 al. 2015).

14 Mixtures of VCs emitted by some bacteria and fungi can exert inhibitory effects on plant  
15 growth (Splivallo et al. 2007; Tarkka & Piechulla 2007; Wenke et al. 2012; Weise et al. 2013).  
16 Conversely, depending on microbial culture conditions, volatile emissions from some beneficial  
17 rhizosphere bacteria and fungi can promote plant growth (Ryu et al. 2003; Blom et al. 2011;  
18 Hung et al. 2013; Meldau et al. 2013; Naznin et al. 2013; Bailly et al. 2014). Although these  
19 effects were largely attributed to the two volatiles 3-hydroxybutan-2-one and 2,3-butanediol,  
20 several studies have identified additional microbial bioactive VCs that promote plant growth (von  
21 Rad et al. 2008; Zou et al. 2010; Blom et al. 2011; Velázquez-Becerra et al. 2011; Groenhagen et  
22 al. 2013; Meldau et al. 2013; Naznin et al. 2013; Bailly et al. 2014). Analysis of *Arabidopsis*  
23 mutants with perturbations in hormone production and signaling, in conjunction with analyses of  
24 hormone contents, have indicated that abscisic acid (ABA), auxins and cytokinins (CKs) (but not

1 ethylene, brassinosteroids and gibberellins) may participate in the growth-promoting effect of  
2 VCs emitted by the beneficial *Bacillus subtilis* (strain GB03) bacterium, suggesting the  
3 involvement of complex signaling mechanisms (Ryu et al. 2003; Zhang et al. 2007, 2008).  
4 Microbial VCs can also promote changes in plants' photosynthetic capacity, and transitions from  
5 source to sink status in photosynthetic tissues. For example, volatile emissions from *B. subtilis*  
6 GB03 augment photosynthetic capacity by increasing photosynthetic efficiency and chlorophyll  
7 content in *Arabidopsis* (Zhang et al. 2008). Furthermore, VCs from a number of microorganisms  
8 ranging from Gram-negative and Gram-positive bacteria to different fungi promote accumulation  
9 of exceptionally high levels of starch in leaves of mono- and di-cotyledonous plants (Ezquer et al.  
10 2010; Li et al. 2011).

11 To date, studies on stimulatory effects of microbial VCs on plant growth have mainly  
12 focused on a few beneficial rhizosphere bacteria and fungi, using *Arabidopsis* plants cultured in  
13 Murashige and Skoog (MS) medium supplemented with sucrose as model systems (Ryu et al.  
14 2003; Zhang et al. 2007, 2008; von Rad et al. 2008; Kwon et al. 2010; Zou et al. 2010;  
15 Groenhagen et al. 2013; Hung et al. 2013). Exogenously added sucrose inhibits expression of  
16 photosynthetic genes (Jang & Sheen 1994; Osuna et al. 2007) and may trigger senescence and  
17 growth arrest in plants (Ohto et al. 2001; Teng et al. 2005). To increase knowledge of the extent  
18 and nature of microbial VCs-mediated interactions between plants and microorganisms in this  
19 work we assessed responses of *Arabidopsis* and other plants cultured on sucrose-free medium to  
20 VCs emitted by phylogenetically diverse rhizosphere and non-rhizosphere bacteria and fungi,  
21 including some pathogenic strains. We found that all the tested microorganisms produced VCs  
22 that promoted growth and flowering, suggesting that this action is not restricted to some  
23 beneficial rhizosphere bacteria and fungi, but extends to pathogens and microbes that are not  
24 normally considered to interact mutualistically with plants. Thus, to obtain insights into the

1 mechanisms involved in the microbial VCs-mediated promotion of growth and flowering we also  
2 characterized *Arabidopsis* plants exposed to the VCs emitted by the opportunistic fungal plant  
3 pathogen *Alternaria alternata*. We found that promotion of growth and flowering by VCs emitted  
4 by this fungus involves a highly conserved and complex network of transcriptionally regulated  
5 processes allowing the plant to acclimate to the new environmental conditions imposed by the  
6 VCs treatment wherein light and CK signaling play an important role. The discovery that VCs  
7 from pathogenic microorganisms can have beneficial effects on plant growth and development  
8 extends knowledge of the diversity and complexity of the interactions involved in modulation of  
9 plant physiology, raising questions regarding the evolution of the processes, their ecological  
10 significance and potential applications.

11

## 12 **MATERIALS AND METHODS**

### 13 **Plant and microbial cultures and growth conditions**

14 The work was carried out using *A. thaliana* (Heynh) (ecotypes Col-O and Ws-2) and CK  
15 deficient, CK oxidase/dehydrogenase 1 over-expressing 35S:CKX1 plants (Werner et al. 2003)  
16 and CK signaling *ahk2/3*, *ahk2/4* and *ahk3/4* mutants (Riefler et al. 2006). We also used maize  
17 (*Zea mays*, cv. HiII), and pepper (*Capsicum annuum*, cv. Sweet Italian) plants. Microorganisms  
18 used in this study are listed in Supporting Information Table S1. Unless otherwise indicated  
19 *Arabidopsis* plants were cultured in Petri dishes containing sucrose-free solid MS (Duchefa  
20 Biochemie M0222) medium in growth chambers with a 16 h light ( $90 \mu\text{mol photons sec}^{-1} \text{ m}^{-2}$ )/8  
21 h dark photoperiod (22°C during the light period and 18°C during the dark period). Bacteria were  
22 cultured in Petri dishes containing solid M9 minimal (95 mM  $\text{Na}_2\text{HPO}_4$ /44 mM  $\text{KH}_2\text{PO}_4$ /17 mM  
23  $\text{NaCl}$ /37 mM  $\text{NH}_4\text{Cl}$ /0.1 mM  $\text{CaCl}_2$ /2 mM  $\text{MgSO}_4$ , 1.5% bacteriological agar) medium

1 supplemented with 50 mM glucose. M9 medium for *B. subtilis* culture was supplemented with 7  
2  $\mu\text{M}$  each of  $\text{MnSO}_4$ ,  $\text{FeSO}_4$  and  $\text{ZnSO}_4$ , and 1  $\mu\text{M}$  thiamine. Fungi were cultured in Petri dishes  
3 containing solid MS medium supplemented with 90 mM sucrose. To investigate effects of  
4 microbial VCs on *Arabidopsis* plants cultured in MS medium, microbial and plant cultures  
5 without lids were placed without physical contact into sterile plastic boxes (IT200N Instrument  
6 Try 200 x 150 x 50 mm, AWGregory, UK) and sealed with a plastic film as illustrated in  
7 Supporting Information Fig. S1a. Effects of microbial VCs on plants cultured on soil was  
8 investigated by placing microbial cultures without lids and plants in sealed mini-green houses as  
9 illustrated in Supporting Information Fig. S1b,c. As negative control, plants were cultured  
10 together with adjacent Petri dishes containing sterile microbial culture media. Unless otherwise  
11 indicated microbial VCs treatment started at the 14 days after sowing (DAS) growth stage of  
12 plants.

13

#### 14 **Gas exchange determinations**

15 Changes in photosynthetic capacity and mitochondrial respiration of leaves upon exposure to  
16 microbial VCs were investigated essentially as described by Bahaji et al. (2015b). Briefly, fully  
17 expanded apical leaves were enclosed in a LI-COR 6400 gas exchange portable photosynthesis  
18 system (LI-COR, Lincoln, Nebraska, USA). The gas exchange determinations were conducted at  
19 25°C with a photosynthetic photon flux density of 350  $\mu\text{mol m}^{-2} \text{s}^{-1}$ . Net rates of  $\text{CO}_2$  assimilation  
20 ( $A_n$ ) were calculated using equations developed by von Caemmerer & Farquhar (1981). From the  
21  $A_n/C_i$  curves, the maximum rate of carboxylation by Rubisco ( $V_{\text{cmax}}$ ), triose phosphate use (TPU)  
22 and the maximum electron transport demand for RuBP regeneration ( $J_{\text{max}}$ ) values were calculated  
23 according to Long & Bernacchi (2003). To avoid miscalculation of  $A_n$  and intercellular  $\text{CO}_2$

1 concentration ( $C_i$ ) due to leakage into the gasket of the gas analyzer, we performed CO<sub>2</sub> response  
2 curves using an empty chamber. The values obtained for  $A_n$  and  $C_i$  in the empty chamber were  
3 compared with those of the chamber filled with a leaf and subtracted from the values obtained  
4 with the empty chamber. The photosynthetic electron transport rate (ETR) values were calculated  
5 according to Krall & Edwards (1992) as photosystem II (PSII) operating efficiency ( $\Phi_{PSII}$ ) x  
6 PPFD x 0.84 x 0.5, where PPFD is the photosynthetic photon flux density incident on the leaf,  
7 0.5 was used as the fraction of excitation energy distributed to PSII (Ögren & Evans 1993) and  
8 0.84 as the fractional light absorbance (Morales et al. 1991). The rate of mitochondrial respiration  
9 in the dark was determined by measuring the rate of CO<sub>2</sub> evolution in the dark.

10 Chlorophyll fluorescence emission parameters were determined using a PlantScreen™  
11 XYZ System (Photon Systems Instruments, Brno, Czech Republic). This phenotyping system is  
12 equipped with a FluorCam unit for pulse amplitude modulated measurement of chlorophyll  
13 fluorescence. After 20 min of dark adaptation the standardized measuring protocol was applied,  
14 as described in Humplík et al. (2015). The maximum quantum yields of PSII in the dark-adapted  
15 state ( $\Phi_{Po}$ ) (also referred to as  $F_v/F_m$ ),  $\Phi_{PSII}$  and non-photochemical quenching ( $\Phi_{NPQ}$ ) were  
16 calculated from the measured parameters according to Lazár (2015).

17

## 18 **Analytical methods**

19 Fully expanded source leaves of plants cultured in the absence or presence for 3 days of VCs  
20 were harvested at the end of the light period, freeze-clamped and ground to a fine powder in  
21 liquid nitrogen with a pestle and mortar. For measurement of sucrose, glucose and fructose, a 0.1  
22 g aliquot of the frozen powder was resuspended in 1 ml of 90% ethanol, left at 70°C for 90 min  
23 and centrifuged at 13,000 x g for 10 min. Sugar contents from supernatants were then determined



1 by HPLC with pulsed amperometric detection on a DX-500 Dionex system as described in Bahaji  
2 et al. (2015a). Glyceraldehyde-3 P GAP and 3-phosphoglycerate (3PGA) contents were  
3 determined as described by Vogt et al. (1998) and Lytovchenko et al. (2002), respectively. Starch  
4 was measured by using an amyloglucosydase-based test kit (Boehringer Mannheim, Germany).  
5 Total carotenoid and chlorophyll contents were quantified according to Lichtenthaler (1987). To  
6 determine CKs levels, portions of the frozen leaves (see above) from Ws-2 plants were  
7 lyophilized and CKs were quantified according to the method described in Novák et al. (2008).  
8 ABA content was determined essentially as described by Floková et al. (2014).

9

#### 10 **Gene expression analyses**

11 Total RNA was extracted from frozen *Arabidopsis* leaves of *in vitro* cultured plants using the  
12 Trizol method according to the manufacturer's procedure (Invitrogen), following purification  
13 with RNeasy kit (Qiagen). RNA amplification, labeling and statistical data analysis were  
14 performed basically as described by Adie et al. (2007). The *Arabidopsis* Gene Expression  
15 Microarray 4 x 44K (G2519, Agilent Technologies) was used for hybridization. Labeling and  
16 hybridization conditions were those described in "The manual two color microarray based gene  
17 expression analysis" of Agilent Technologies. Three independent biological replicates were  
18 hybridized for leaves from microbe-treated plants and from controls. Images from Cy3 and  
19 Hyper5 channels were equilibrated for intensity differences and captured with a GenePix 4000B  
20 scanner (Axon). Spots were quantified using GenPix software (Axon) and normalized using the  
21 Lowess method. Means of the three replicate log-ratio intensities and their standard deviations  
22 were calculated, and the expression data were statistically analyzed using the LIMMA Package  
23 (Smyth & Speed 2003). Functional characterization of the differentially expressed genes was  
24 done using the Mapman tool (<http://gabi.rzpd.de/projects/MapMan/>).

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## **Real-time quantitative PCR**

Total RNA was extracted from *Arabidopsis* leaves as described above for the microarray analyses, then treated with RNAase free DNAase (Takara). 1.5 µg RNA was reverse transcribed using polyT primers and an Expand Reverse Transcriptase kit (Roche) according to the manufacturer's instructions. RT-PCR reaction was performed using a 7900HT sequence detector system (Applied Biosystems) with the Premix Ex Tag Mix (Takara RR420A) according to the manufacture's protocol. Each reaction was performed in triplicate with 0.4 µL of the first strand cDNA in a total volume of 20 µL. The specificity of the PCR amplifications was checked by acquiring heat dissociation curves (from 60°C to 95°C). Comparative threshold values were normalized to 18S RNA internal control and compared to obtain relative expression levels. Primers used for RT-PCRs are listed in Supporting Information Table S2, and their specificity was checked by separating the obtained products on 1.8% agarose gels.

## **Statistical analysis**

Presented data are the means ( $\pm$  SE) of four independent experiments, with 3-5 replicates for each experiment. The significance of differences between VCs-treated and non-treated plants was statistically evaluated with Student's t-test using the SPSS software. Differences were considered significant if  $p < 0.05$ . In hormone content analyses, significance was determined by ANOVA for parametric data and Kruskal Wallis for non-parametric data, using the open source R software 2.15.1 (<http://cran.r-project.org/>). Multiple comparisons after ANOVA were calculated using the post hoc Tukey's honestly significant difference test.

## 1 **RESULTS**

### 2 **VCs emitted by phylogenetically diverse microorganisms other than beneficial rhizosphere** 3 **bacteria and fungi promote plant growth and flowering**

4 *Arabidopsis* plants were cultured on sucrose-free solid MS medium in the absence or continuous  
5 presence of adjacent cultures of phylogenetically diverse strains of beneficial and non-beneficial  
6 fungi and bacteria. These experiments were conducted in sterile growth boxes with no physical  
7 contact between the plant and the microbial cultures (Supporting Information Fig. S1a). VCs  
8 emitted by all the tested microorganisms (including plant pathogens) induced 2- to 5-fold  
9 increases in fresh weight (FW) of the *Arabidopsis* plants, relative to controls (Fig. 1a). VCs from  
10 most of microorganisms also induced early flowering (Fig. 1b, c). Consistent with our previous  
11 studies (Ezquer et al. 2010), VCs also promoted the accumulation of exceptionally high levels of  
12 starch (Supporting Information Fig. S2). The strength of the responses to microbial VCs differed  
13 from one microorganism to another (Fig. 1; Supporting Information Fig. S2), which can be  
14 ascribed to activation of different signaling pathways in plants in response to different mixtures  
15 of VCs emitted by the microorganisms.

16 To assess further the generality of these responses we grew *Arabidopsis* and two plant  
17 species of agronomic interest, sweet pepper and maize, on soil (Supporting Information Fig.  
18 S1b,c) and examined their responses to microbial VCs. The microbial VCs-exposed *Arabidopsis*  
19 plants had significantly higher FW than controls within 4 days of the treatment, and twice as high  
20 FW after another seven days (Fig. 2a). In addition, exposed maize and pepper plants were almost  
21 twice as tall as controls from day 22 of the treatment until the end of experiment on day 47 (Fig.  
22 2b,c).

23

### 24 ***A. alternata* VCs increase photosynthetic activities of exposed plants**

1 We measured key parameters of light and dark phases of photosynthesis in plants exposed to *A.*  
2 *alternata* VCs for 3 days. During the light phase  $\Phi_{Po}$  and  $\Phi_{PSII}$  were higher, and  $\Phi_{NPQ}$   
3 significantly weaker, in leaves of the exposed plants than in controls (Table 1). These results  
4 indicate that leaves of VCs-treated plants used the light more efficiently, dissipated less  
5 excitation energy as heat, reduced more  $NADP^+$ , formed more ATP and hence had higher  $A_n$  than  
6 controls. This inference was corroborated by the analysis of the levels of photosynthetic pigments  
7 and  $A_n$  under varying  $C_i$ . As shown in Fig. 3a, total chlorophyll and carotenoid contents in leaves  
8 of VCs-treated *pgi1-2* plants were higher than in controls. Moreover, plants exposed to VCs had  
9 higher  $A_n$  than controls at all  $C_i$  levels (Fig. 3b).  $V_{cmax}$  and  $J_{max}$  determined from the  $A_n/C_i$  curves  
10 were significantly higher in leaves of VCs-treated plants than in controls, as was TPU (Table 1).  
11 Furthermore, ETR was higher in the VCs-treated plants than in controls (Fig. 3c), particularly  
12 under minimal  $C_i$  conditions (in which the ETR was 4-fold higher than in controls). Levels of  
13 soluble carbohydrates, regarded here as primary photosynthates, were significantly up-regulated  
14 by *A. alternata* VCs. As shown in Fig. 4, the contents of sucrose, glucose, fructose and Calvin-  
15 Benson cycle intermediates such as GAP and 3PGA were higher in leaves of VCs-treated plants  
16 than in controls.

17

### 18 ***A. alternata* VCs augment the levels of active forms of plastidic CKs**

19 ABA and CKs are important determinants of photosynthesis. To investigate the possible  
20 involvement of these hormones in the responses to *A. alternata* VCs we measured their levels in  
21 mature leaves of plants cultured in the absence or presence of adjacent cultures of *A. alternata* for  
22 3 days. *A. alternata* VCs promoted a moderate, statistically non-significant reduction of the ABA  
23 content in leaves ( $224.48 \pm 35.31$  and  $299.54 \pm 37.27$  pmol g<sup>-1</sup> DW in leaves of VCs-treated and

1 non-treated plants, respectively). In clear contrast, fungal VCs caused a significant increase of the  
2 total content of plastidic-type, 2-C-methyl-D-erythritol 4-phosphate (MEP) pathway-derived CKs  
3 (Table 2; Supporting Information Fig. S3). The most strongly accumulated CK forms were the  
4 ribosides of isopentenyladenine (iP) and *trans*-zeatin (tZ) (iPR and tZR, respectively) and their  
5 precursors (iPRMP and tZRMP, respectively), levels of which increased 3-fold. Levels of free  
6 bases of the most biologically active iP and tZ increased 1.5-fold (Table 2; Supporting  
7 Information Fig. S3) whereas levels of the less biologically active CKs dihydroxy zeatin (DZ)  
8 and *cis*-zeatin (cZ) were substantially reduced (3- and 2-fold, respectively). Concentrations of  
9 inactive *N*- and *O*-glycosylated forms were not significantly affected by *A. alternata* VCs  
10 exposure, except that iP7G and DZ7G levels were slightly lower in the treated plants. The pool of  
11 glycosylated forms of cZ was 1.5-fold lower, mainly due to reductions in cZ9G and cZOG  
12 concentrations (Table 2).

13

#### 14 **CKs and CK signaling are required for activities of *A. alternata* VCs**

15 We compared responses to VCs between wild type (WT) *Arabidopsis* plants, CK-deficient  
16 35S:CKX1 transgenic plants (Werner et al. 2003), and double CK receptor knock-out mutants  
17 with impaired sensitivity to CKs (*ahk2/3*, *ahk2/4*, *ahk3/4*) (Riefler et al. 2006). As shown in Fig.  
18 5a, VCs-promoted increase of rosette FW in *ahk2/4* and *ahk3/4* plants was comparable to that of  
19 WT plants, implying that, individually or in combination with AHK2 or AHK3, AHK4 plays a  
20 minor role in VCs signaling and subsequent growth promotion. The magnitude of this  
21 phenomenon in 35S:CKX1 and *ahk2/3* plants was markedly reduced when compared with WT  
22 plants (Fig. 5a). Similar to WT plants, the appearance of floral buds in VCs treated *ahk2/4* and  
23 *ahk3/4* plants occurred 3-4 days before non-treated plants (Fig. 5b). In clear contrast, VCs did not  
24 exert any significant effect on the time of floral bud appearance in both *ahk2/3* and 35S:CKX1

1 plants (Fig. 5b). VCs promoted the accumulation of exceedingly high levels of starch in leaves of  
2 *ahk2/4* and *ahk3/4* plants, but their effect was markedly reduced in 35S:CKX1 and *ahk2/3* plants  
3 (Fig. 5c). These findings provide strong evidence that *A. alternata* VCs-promoted enhancement  
4 of aerial growth, early floral bud appearance and starch accumulation is strongly regulated by  
5 CKs, and indicate that these responses are mediated mainly through AHK2 and AHK3 receptors.

6

### 7 **Plant responses to *A. alternata* VCs are light-dependent and subject to photoperiod control**

8 CKs serve as endogenous cues that strongly influence plants' responsiveness to light (Guo et al.  
9 2005; Kieber & Schaller 2013; Cortleven & Schmülling 2015), suggesting that some of the  
10 processes promoted by *A. alternata* VCs might be, at least partially, photoregulated. To test this  
11 hypothesis, we compared the rosette FW, flowering and leaf starch contents of plants cultured  
12 under a 16 h light/8 h dark photoperiod that were exposed to *A. alternata* VCs for one week  
13 either only during the light phases, or only during the dark phases. Exposure to VCs only during  
14 the light phases promoted growth (Fig. 6a), starch over-accumulation (Fig. 6b) and flowering  
15 (Fig. 6c). In clear contrast, exposure to VCs only during the dark phases had no effect on the  
16 plants' external phenotype (Fig. 6a,c) and did not induce starch over-accumulation in their leaves  
17 (Fig. 6b). These findings strongly indicate that *A. alternata* VCs-promoted changes in the treated  
18 plants are light-dependent.

19

### 20 **VCs emitted by *A. alternata* and the plant growth promoting rhizobacterium *B. subtilis*** 21 **induce similar transcriptomic changes in *Arabidopsis* leaves**

22 The next step in the study presented here was a high-throughput transcriptome analysis of leaves  
23 from *Arabidopsis* plants cultured *in vitro* under a 16 h light/8 h dark photoperiod in the absence  
24 or in the presence for 16 h of VCs emitted by *A. alternata*. As shown in Supporting Information

1 Table S3, this analysis using an *Arabidopsis* Gene Expression Microarray 4 x 44K (G2519,  
2 Agilent Technologies) revealed that 530 genes were up-regulated and 496 genes were down-  
3 regulated in the presence of VCs (with a  $\geq 2.0$ -fold difference relative to control;  $p < 0.05$ ).  
4 Quantitative real-time RT-PCR analyses of some of the identified genes (Supporting Information  
5 Fig. S4) validated the results of the array analyses. To determine the biological processes affected  
6 by VCs, an analysis of genes using the MapMan tool (Thimm et al. 2004)  
7 (<http://gabi.rzpd.de/projects/MapMan/>) was carried out. This study revealed that *A. alternata* VCs  
8 promote changes in the expression of *Arabidopsis* genes involved in multiple processes including  
9 light harvesting, starch synthesis and breakdown, flowering, cell wall biosynthesis, anthocyanin  
10 and carotenoid metabolism, protection against oxidative stress, etc. (Fig. 7). Notably, ca. 7% of  
11 the differentially regulated genes are known to be CK responsive (see Supporting Information  
12 Table S3). Furthermore, a significant number of the VCs-responding genes are known to be  
13 regulated by light, auxin, ethylene, jasmonic acid, gibberellin, nitrate and sugars, indicating  
14 intense crosstalk between environmental cues, hormones and metabolites.

15 VCs emitted by the plant growth promoting rhizobacterium (PGPR) *B. subtilis* GB03  
16 promote drastic changes in the transcriptome of *Arabidopsis* (Zhang et al. 2007). As the  
17 volatilomes of bacteria and fungi are very different (Schulz & Dickschat 2007; Lemfack et al.  
18 2014) we hypothesized that changes in the transcriptome of plants triggered by mixtures of VCs  
19 emitted by *B. subtilis* GB03 could differ from those triggered by *A. alternata* VCs. Thus, we  
20 compared the sets of genes differentially expressed in leaves of plants exposed to *A. alternata*  
21 VCs (Supporting Information Table S3) with those of leaves of plants exposed to VCs emitted by  
22 *B. subtilis* GB03 (cf. Supporting Information Table 1 in Zhang et al. 2007). Contrary to our  
23 expectations, we found that 101 out of 254 genes that are down-regulated in leaves of plants  
24 exposed to VCs emitted by *B. subtilis* GB03 (including 85% of the 20 most strongly down-

1 regulated genes) are also down-regulated in leaves of plants exposed to VCs emitted by *A.*  
2 *alternata* (Table 3; Supporting Information Table S4). Furthermore, 99 out of the 378 genes that  
3 are up-regulated in leaves of plants exposed to VCs emitted by *B. subtilis* GB03 (including 70%  
4 of the 20 most strongly up-regulated genes) are also up-regulated in leaves of plants exposed to  
5 VCs emitted by *A. alternata* (Table 3; Supporting Information Table S5). Notably, ca. 25% of the  
6 genes that are differentially regulated in *Arabidopsis* leaves exposed to VCs emitted by both *B.*  
7 *subtilis* and *A. alternata* are CK responsive genes (Table 3).

8

## 9 **DISCUSSION**

10 Many plant pathogenic bacteria and fungi have evolved to interact with plants, exhibiting a  
11 versatile metabolism and ingenious mechanisms tailored to modify the development of their  
12 hosts. Consequently, it has been suggested that phytopathogens or their constituents may provide  
13 opportunities for plant production or be useful for specific biotechnological applications  
14 (Tarkowski & Vereecke 2014). In line with this opinion, in this work we have shown that blends  
15 of VCs emitted by a number of beneficial and non-beneficial, phylogenetically diverse  
16 microorganisms (including plant pathogens) promote growth and flowering in both mono- and di-  
17 cotyledonous plants (Figs 1 & 2). As to the ecological implication of this phenomenon we can  
18 just speculate that plant growth promotion by microbial VCs prepares the plant to host the  
19 microorganism, which in the case of phytopathogenic microorganisms ensures proper  
20 continuation into the pathogenic phase.

21 Bioprospecting of VCs from non-beneficial microorganisms and characterization of their  
22 biological functions and ecological roles could offer valuable new strategies for increasing yield  
23 of horticultural crops or biotechnological products in a sustainable and environmentally benign  
24 manner. We must emphasize that part of our future goal is to identify microbial VCs promoting



1 plant growth. The fact that mixtures of VCs emitted by all microbial species analyzed in this  
2 work promote growth would indicate that plants respond to a wide range of bioactive VCs, as  
3 strongly supported by previous reports using pure VCs emitted by different microbial species  
4 (Ryu et al. 2003; Zou et al. 2010; Blom et al. 2011; Velázquez-Becerra et al. 2011; Groenhagen  
5 et al. 2013; Meldau et al. 2013; Naznin et al. 2013). Alternatively and/or additionally, it is likely  
6 that all microorganisms emit the same VCs promoting plant growth. In this respect, it is worth to  
7 note that all microbial species tested in this work produce CO<sub>2</sub>. Although this would indicate in  
8 principle that VCs-treated plants were exposed to elevated CO<sub>2</sub> (a situation that would favor  
9 growth due to enhanced photosynthetic CO<sub>2</sub> fixation) we failed to detect substantial increases of  
10 CO<sub>2</sub> levels in the growth boxes upon inclusion of cultures of most of microbial species used in  
11 this work (not shown), strongly indicating that the positive effect exerted by microbial VCs on  
12 plant growth is not ascribed to photosynthetic fixation of CO<sub>2</sub> emitted by the microorganisms.

13  
14 **VCs emitted by the fungal phytopathogen *A. alternata* enhance photosynthesis in**  
15 ***Arabidopsis***

16 Physical contact with pathogens very often leads to a decrease in photosynthesis in plants (Berger  
17 et al. 2007). However, surprisingly, in this work we found that VCs emitted by the pathogen *A.*  
18 *alternata* have positive effects on photosynthesis in *Arabidopsis* plants (Fig. 3; Table 1), which  
19 can be ascribed, at least partially, to very efficient use of light as a consequence of enhanced  
20 accumulation of photosynthetic pigments and improved ETR (Fig. 3). Photosynthesis is generally  
21 subject to feedback inhibition by elevated sugar levels through a hexokinase-dependent  
22 mechanism of glucose sensing that requires ABA signaling (Moore et al. 2003; Rolland et al.  
23 2006), although this regulatory mechanism does not apply ubiquitously to all cell types under all  
24 growth and developmental conditions (Granot et al. 2013). Notably, *A. alternata* VCs-promoted

1 enhancement of photosynthesis was accompanied by accumulation of high levels of soluble  
2 sugars (Fig. 4). However, unlike *B. subtilis* VCs promoting the reduction of ABA levels as a  
3 mechanism to suppress sugar sensing inhibition of photosynthesis in *Arabidopsis* (Zhang et al.  
4 2008), *A. alternata* VCs treatment resulted in a moderate, statistically non-significant reduction  
5 of ABA levels. These findings would indicate that VCs-promoted suppression of sugar sensing  
6 inhibition of photosynthesis involves mechanism(s) additional and/or alternative to those  
7 implicating ABA. As *A. alternata* VCs promote accumulation of CKs (Table 2), and CKs and  
8 sugars work antagonistically in gene regulated responses (Kushwah & Laxmi 2014) it is  
9 conceivable that the lack of photosynthetic inhibition by high sugar content in leaves of VCs-  
10 exposed plants is due, at least partly, to enhanced CK production.

11  
12 **Plant responses to VCs of the fungal phytopathogen *A. alternata* involve enhanced CK**  
13 **production**

14 CKs are major determinants of growth, energy status and photosynthesis in mature leaves  
15 (Cortleven & Valcke 2012; Kieber & Schaller 2013; Bahaji et al. 2015b). Furthermore, these  
16 versatile hormones play important roles in flowering (Nishimura et al. 2004; Riefler et al. 2006;  
17 D'Aloia et al. 2011), modulation of sugar-induced anthocyanin accumulation (Guo et al. 2005;  
18 Das et al. 2012) and interaction of the plant with both biotic and abiotic factors (Argueso et al.  
19 2012). Moreover, CKs promote starch accumulation in leaves (Werner et al. 2008) most likely by  
20 regulating the expression of starch metabolism related genes (Miyazawa et al. 1999) and/or  
21 enhancing photosynthetic CO<sub>2</sub> fixation. Results presented in Table 2 showing that levels of  
22 plastidic MEP derived CKs in leaves of plants treated with *A. alternata* VCs are higher than in  
23 non-treated leaves would indicate that enhancement of these CKs is involved in the VCs-

1 promoted changes described in this work. This hypothesis is corroborated by the poor responses  
2 to VCs observed in 35S:CKX1 and *ahk2/3* plants (Fig. 5).

3         Regarding mechanisms that may contribute to the high contents of active and transport  
4 forms of MEP-derived CKs and their precursors in leaves of *A. alternata* VCs-treated plants, it  
5 should be noted that the levels of some inactive glycosylated CKs were lower in VCs-treated  
6 plants than in controls (Table 2; Supporting Information Fig. S3). This would indicate that down-  
7 regulation of enzymes involved in the degradation of plastidic CKs could participate in the VCs-  
8 promoted accumulation of active and transport forms of MEP-derived CKs and their precursors.  
9 No significant changes in the expression of genes encoding CK metabolism enzymes could be  
10 observed in leaves of *A. alternata* VCs-treated plants (Supporting Information Table S3),  
11 strongly indicating that VCs-promoted enhancement of CKs is largely regulated at the post-  
12 transcriptional level. In this respect it should be noted that the first suggested level of diurnal  
13 MEP regulation is related to the Calvin-Benson cycle intermediate GAP (Pulido et al. 2012;  
14 Pokhilko et al. 2015). GAP concentrations in chloroplasts fluctuate between 20  $\mu$ M during the  
15 day and 1  $\mu$ M at night (Arrivault et al. 2009). These concentrations are substantially below the  
16  $K_m$  for GAP (110  $\mu$ M) of the first enzyme of the MEP pathway, 1-deoxy-D-xylulose 5-  
17 phosphate synthase (Ghirardo et al. 2014), resulting in a strong direct dependence of the MEP  
18 pathway flux on the GAP concentration. In VCs-treated leaves, GAP concentration is 2-fold  
19 higher than that of non-treated leaves, likely as a consequence of enhanced photosynthesis. Thus,  
20 as illustrated in Fig. 8 and Supporting Information Fig. S3, accumulation of high levels of active  
21 MEP derived CKs in leaves of VCs-treated plants might be at least partly due to enhanced  
22 photosynthetic production of GAP and subsequent conversion into MEP-derived CKs. A striking  
23 alteration in the transcriptome of *A. alternata* VCs-treated plants involves strong up-regulation of

1 *GPT2* (Supporting Information Table S3; Fig. 7), a CK-induced gene (Bhargava et al. 2013)  
2 encoding a plastidic glucose-6-P (G6P)/Pi transporter, which is necessary for dynamic  
3 photosynthetic and metabolic acclimation to increased irradiance (Athanasίου et al. 2010; Dyson  
4 et al. 2015). Therefore, *GPT2*-mediated incorporation of cytosolic G6P into the chloroplast and  
5 subsequent metabolic conversion into GAP linked to the synthesis of CKs (which in turn further  
6 promotes *GPT2* expression) may also contribute to the high levels of MEP-derived CKs observed  
7 in leaves of VCs-treated plants (Fig. 8). Another mechanism explaining the enhancement of  
8 plastidic CKs in VCs-treated leaves could involve the transport of isopentenyl diphosphate (IPP)  
9 and/or dimethylallyl diphosphate (DMAPP) from the cytosolic mevalonate (MVA) pathway into  
10 the chloroplast to increase the DMAPP pool accessible for plastid localized  
11 isopentenyltransferases (Supporting Information Fig. S3). Such mechanism of IPP and/or  
12 DMAPP exchange between the cytosol and plastids has been proposed to explain MVA-derived  
13 contribution to plastidic biosynthesis of gibberellins (Helliwell et al. 2001).

14  
15 **VCs induce changes in expression of CKs- and light-regulated genes involved in**  
16 **photosynthesis, growth, flowering and starch metabolism**

17 Taken together, data presented in this work strongly indicate that changes in VCs-exposed plants  
18 result from complex, transcriptionally regulated processes allowing the plant to acclimate to new  
19 environmental conditions in which light and CKs play important roles (Fig. 8). *Inter alia*, VCs  
20 treatment strongly promoted the expression of a number of light-inducible genes encoding light-  
21 harvesting proteins, some of which (e.g. *ELIPI*) are up-regulated by CKs (Supporting  
22 Information Table S3; Fig. 7). These proteins have inherently photoprotective properties, and  
23 play an important role in collecting light quanta to deliver them to the reaction centres, where  
24 they are converted into chemical forms of energy (Pascal et al. 2005). Thus, VCs-promoted

1 enhancement of photosynthesis (Table 1; Fig. 3) is probably at least partially due to increases in  
2 levels of light-harvesting proteins (Fig. 8).

3 *A. alternata* VCs promoted increase of ETR (Fig. 3) create conditions for the production  
4 of reactive oxygen species (ROS), which may result in photoinhibition and subsequent  
5 photooxidative damage, a phenomenon that could be prevented by the accumulation of  
6 anthocyanins, carotenoids and ROS scavengers. VCs exerted a positive effect on the expression  
7 of genes coding for enzymatic ROS scavengers (Supporting Information Table S3; Fig. 7).  
8 Furthermore, VCs exerted a negative effect on the expression of the CK-repressed negative  
9 *MYBL2* regulator (Dubos et al. 2008), and a positive effect on the expression of a number of  
10 anthocyanin biosynthesis-related genes including the CK-induced positive regulators  
11 *PAP1/MYB75* and *TT8* (Das et al. 2012) and structural genes *TT4* and *UF3GT* (Supporting  
12 Information Table S3; Fig. 7). Moreover, VCs exerted a negative effect on the expression of the  
13 CK-repressed *NCED4* gene involved in carotenoid degradation (Gonzalez-Jorge et al. 2013)  
14 (Supporting Information Table S3; Fig. 7). Therefore, CK-induced modulation of genes coding  
15 for anthocyanins, ROS scavengers and carotenoid content regulators may contribute to the  
16 enhancement of photosynthetic capacities observed in VCs-treated plants (Fig. 8).

17 Glucosinolates are sulfur-rich amino acid-derived secondary plant products that act as  
18 important determinants of plant growth, development and defense against pathogens  
19 (Tantikanjana et al. 2001; He et al. 2011; Imhof et al. 2014). *A. alternata* VCs promoted the  
20 expression of a number of glucosinolate biosynthesis related genes (Supporting Information  
21 Table S3; Fig. 7). Some of them (e.g. *IPMII* and *GSTU20*) are induced by CKs (Brenner &  
22 Schmülling 2015). Others (e.g. *CYP79F1*) play important roles in modulating the intracellular  
23 levels of CKs (Tantikanjana et al. 2004). Thus, CK-promoted up-regulation of glucosinolate

1 biosynthesis related genes and/or glucosinolate-mediated enhancement of CKs levels probably  
2 contribute to the VCs-promoted early flowering and enhancement of growth.

3 Our transcriptomic analyses revealed that *A. alternata* VCs enhance expression of a  
4 number of genes involved in cell wall composition, strength and extensibility (Supporting  
5 Information Table S3; Fig. 7). Some of them (e.g. *XTR8*, *RHM1*, *BGAL3*, *GH9B8* and  
6 *At3g05910*) are up-regulated by CKs. Since cell wall synthesis and extensibility is a major  
7 determinant of growth, VCs-promoted growth may be at least partly mediated by CK-promoted  
8 induction of cell wall-related genes (Fig. 8).

9 *A. alternata* VCs also promoted the expression of starch biosynthetic genes, such as those  
10 encoding the non-catalytic large subunits of ADPglucose pyrophosphorylase APL3 and APL4,  
11 the granule bound starch synthase (GBSS) and inorganic pyrophosphatase (PS2) (Supporting  
12 Information Table S3; Fig. 7) and starch-degradation related genes such as *DBE1*, *ISA3*, *SEX4*,  
13 *PHS1* and *SBE2*. As mentioned above, a striking alteration in the transcriptome of VCs-treated  
14 plants involves the strong up-regulation of the CK-induced G6P/Pi transporter encoding *GPT2*  
15 gene. Thus, accumulation of exceptionally high levels of starch in leaves of VCs-treated plants  
16 probably involves CK induced GPT2-mediated transport of cytosolic G6P, which once in the  
17 chloroplast, is metabolized into starch (Fig. 8).

18 In *Arabidopsis*, the light-controlled *CONSTANS* (*CO*) plays a central role in the  
19 regulation of flowering (An et al. 2004). Recent studies have shown that *CO*-mediated regulation  
20 of *GBSS* and *PCC1* expression is an important element of the induction of floral transition  
21 (Segarra et al. 2010; Ortiz-Marchena et al. 2014). Notably, VCs stimulated the expression of *CO*,  
22 *PCC1* and *GBSS* (Supporting Information Table S3; Fig. 7). Therefore, it is tempting to speculate  
23 that VCs-promoted floral transition involves stimulation of *CO* expression (Fig. 8).

1 In *Arabidopsis*, nitric oxide (NO) represses floral transition by suppressing *CO* expression  
2 (He et al. 2004). Furthermore, high concentrations of this gaseous compound inhibit the electron  
3 transport activity in PSII and photophosphorylation (Takahashi & Yamasaki 2002). VCs  
4 promoted the expression of the non-symbiotic hemoglobin HB1 (Supporting Information Table  
5 S3; Fig. 7), which together with CKs acts as scavenger and suppressor of NO action (Perazzolli et  
6 al. 2006; Liu et al. 2013). Furthermore, high levels of HB1 expression promote early flowering  
7 and growth (Hunt et al. 2002; Hebelstrup & Jensen 2008). Therefore, it is highly conceivable that  
8 suppression of NO action contributes to VCs-promoted early flowering and enhancement of  
9 photosynthesis (Fig. 8).

10

#### 11 **Plants react to VCs emitted by phylogenetically diverse microorganisms through highly** 12 **conserved mechanisms involving CK signaling**

13 Plants have evolved the capacity to detect VCs released by a plethora of microorganisms. The  
14 findings that mixtures of VCs emitted by all microbial species tested in this work promote  
15 growth, early flowering and accumulation of exceptionally high levels of starch would indicate  
16 that plants respond in a similar manner to diverse microbial VCs. Changes observed in  
17 transcriptomes of leaves of *Arabidopsis* plants exposed to VCs emitted by such phylogenetically  
18 distant microbial species as the beneficial PGPR *B. subtilis* GB03 (Zhang et al. 2007) and fungal  
19 plant pathogen *A. alternata* (this work) were strikingly similar (Table 3, Supporting Information  
20 Tables S4 and S5). Thus, under appropriate culture conditions at least, many microorganisms  
21 (both bacteria and fungi that are beneficial to plants and phyopathogens) can modify plants'  
22 physiology and development by triggering highly conserved molecular mechanisms in response  
23 to a wide range of VCs. Furthermore, the finding that ca. 25% of the most differentially regulated  
24 genes in plants exposed to VCs emitted by *B. subtilis* and *A. alternata* are CK responsive genes

1 (Table 3) strongly indicates that such molecular mechanisms involve CK signaling. Clearly,  
2 further research is needed to identify and characterize the signaling and regulatory mechanisms  
3 involved in plants' responses to VCs emitted by different microbial species, and to understand  
4 their roles in the plant-microbe interactions.

5

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**Table 1.** Photosynthetic parameters of leaves of plants cultured in the absence or presence of VCs emitted by *A. alternata* for 3 days. Values are means  $\pm$  SE from four independent experiments.

Treatment	$\Phi_{P_0}$	$\Phi_{PSII}$	$\Phi_{NPQ}$	$J_{max}$ ( $\mu\text{mol e}^- \text{m}^{-2} \text{s}^{-1}$ )	$V_{cmax}$ ( $\mu\text{mol CO}_2 \text{m}^{-2} \text{s}^{-1}$ )	TPU ( $\mu\text{mol Pi m}^{-2} \text{s}^{-1}$ )
- VCs	0.70 $\pm$ 0.01	0.33 $\pm$ 0.02	0.81 $\pm$ 0.04	45.54 $\pm$ 1.13	18.81 $\pm$ 0.47	2.58 $\pm$ 0.08
+ VCs	0.83 $\pm$ 0.01	0.44 $\pm$ 0.01	0.68 $\pm$ 0.03	56.61 $\pm$ 2.89	29.52 $\pm$ 0.91	3.16 $\pm$ 0.09

**Table 2.** CKs content (pmol g<sup>-1</sup> DW) in leaves of 18 DAS plants cultured in solid MS medium in the absence or presence of VCs emitted by *A. alternata* for 3 days. Levels of CK precursors, transport forms, active forms and glycosylated inactive forms originating from the MEP and MVA pathways are separately shown. Total sums and corresponding percentage is shown for individual forms. Asterisks indicate significant differences according to ANOVA. \* < 0.05; \*\* < 0.01; \*\*\* < 0.001.

	MEP pathway (plastid) derived CKs			MVA pathway (cytosol) derived CKs		
		-VCs	+ VCs		- VCs	+ VCs
Precursors	iPRMP	152.03 ± 16.41	460.71 ± 23.28***			
	tZRMP	104.14 ± 3.43	353.00 ± 25.15***	cZRMP	99.69 ± 15.17	139.67 ± 9.05*
	DZRMP	0.80 ± 0.08	1.84 ± 0.18**			
	∑ (%)	256.98 ± 14.07	815.54 ± 14.12***		99.69 ± 15.17	139.67 ± 9.05*
Transport forms	iPR	16.06 ± 1.06	25.86 ± 2.64**			
	tZR	14.84 ± 2.37	47.77 ± 10.43*	cZR	3.90 ± 0.52	6.55 ± 1.43*
	DZR	0.17 ± 0.03	0.32 ± 0.03**			
	∑ (%)	31.07 ± 2.44	73.95 ± 8.78**		3.90 ± 0.52	6.55 ± 1.43*
Active forms	iP	6.71 ± 0.82	8.44 ± 0.54*			
	tZ	8.71 ± 1.63	11.81 ± 0.92*	cZ	2.96 ± 0.25	1.49 ± 0.05**
	DZ	0.09 ± 0.02	0.03 ± 0.01*			
	∑ (%)	16.51 ± 1.74	20.28 ± 0.32*		2.96 ± 0.25	1.49 ± 0.05**
Glycosylated (inactive) forms	iP7G	137.82 ± 6.92	112.7 ± 6.84*			
	tZ7G	154.48 ± 4.24	155.89 ± 3.64			
	DZ7G	31.76 ± 0.90	23.28 ± 0.19***			
	iP9G	23.51 ± 2.40	19.04 ± 1.15	cZ9G	5.30 ± 0.42	2.78 ± 0.11**
	tZ9G	232.69 ± 15.94	217.87 ± 18.40			
	DZ9G	1.82 ± 0.15	1.09 ± 0.40			
	tZOG	58.10 ± 7.61	53.82 ± 3.84	cZOG	15.72 ± 2.10	9.10 ± 0.84*
	DZOG	4.28 ± 0.43	3.42 ± 0.48			
	tZROG	34.59 ± 7.91	33.17 ± 8.32	cZROG	44.11 ± 3.42	33.82 ± 6.27
	DZROG	5.09 ± 0.46	4.71 ± 1.02			
	∑ (%)	684.14 ± 12.80	625.01 ± 18.52		65.13 ± 3.44	45.71 ± 5.10*
TOTAL	∑ (%)	988.69 ± 11.10	1534.78 ± 23.61***		171.68 ± 13.96	193.41 ± 11.86

**Table 3.** Sets of the 20 most strongly up-regulated and 20 most strongly down-regulated genes in plants exposed to VCs emitted by *B. subtilis* that are also up- and down-regulated by VCs emitted by *A. alternata*. Genes that are up-regulated and down-regulated by CKs are indicated with one and two asterisks, respectively.

**Up-regulated genes**

ID	Description
AT1G61800*	glucose-6-phosphate/phosphate translocator 2 mRNA, complete cds [NM_104862]
AT3G18000	conserved peptide upstream open reading frame 30 mRNA, complete cds [NM_001125181]
AT4G39210	glucose-1-phosphate adenylyltransferase large subunit 3 mRNA, complete cds [NM_120081]
AT5G17220	glutathione S-transferase phi 12 mRNA, complete cds [NM_121728]
AT1G56650	transcription factor MYB75 mRNA, complete cds [NM_104541]
AT2G41090	calmodulin-like protein 10 mRNA, complete cds [NM_129674]
AT4G22870	leucoanthocyanidin dioxygenase-like protein mRNA, complete cds [NM_001160794]
AT1G62560	flavin-containing monooxygenase FMO GS-OX3 mRNA, complete cds [NM_104934]
AT5G48850	protein SULPHUR DEFICIENCY-INDUCED 1 mRNA, complete cds [NM_124262]
AT1G49860	glutathione S-transferase (class phi) 14 mRNA, complete cds [NM_103873]
AT4G22880	leucoanthocyanidin dioxygenase mRNA, complete cds [NM_118417]
AT3G26960*	pollen Ole e 1 allergen and extensin family protein mRNA, complete cds [NM_113610]
AT1G56150	SAUR-like auxin-responsive protein mRNA, complete cds [NM_104494]
AT5G19470	nudix hydrolase 24 mRNA, complete cds [NM_121952]

**Down-regulated genes**

ID	Description
AT4G33150	lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme mRNA, complete cds [NM_001160811]
AT4G36850	PQ-loop repeat family protein / transmembrane family protein mRNA, complete cds [NM_119849]
AT5G17300	myb family transcription factor RVE1 mRNA, complete cds [NM_121736]
AT1G53870	TUB_2 domain-containing protein mRNA, complete cds [NM_104264]
AT2G01530	MLP-like protein 329 mRNA, complete cds [NM_126214]
AT1G73750	uncharacterized protein mRNA, complete cds [NM_106034]
AT3G26740**	CCR-like protein mRNA, complete cds [NM_113585]
AT3G49790	Carbohydrate-binding protein mRNA, complete cds [NM_114839]
AT5G56870	beta-galactosidase 4 mRNA, complete cds [NM_125070]
AT4G16690**	methyl esterase 16 mRNA, complete cds [NM_117770]
AT1G75380**	bifunctional nuclease 1 mRNA, complete cds [NM_179559]
AT3G13750	beta galactosidase 1 mRNA, complete cds [NM_112225]

AT1G80920\*\* chaperone protein dnaJ 8 mRNA, complete cds [NM\_106740]  
AT5G63160\*\* BTB and TAZ domain protein 1 mRNA, complete cds [NM\_125711]  
AT4G35770 senescence-associated protein DIN1 mRNA, complete cds [NM\_119743]  
AT2G05540 glycine-rich protein mRNA, complete cds [NM\_126577]  
AT5G49360 bifunctional {beta}-D-xylosidase/{alpha}-L-arabinofuranosidase mRNA, complete cds [NM\_124313]

## 1 **FIGURE LEGENDS**

2 **Figure 1.** VCs emitted by phylogenetically diverse microorganisms promote plant growth and  
3 flowering. (a) Rosette FW, (b) time of floral bud appearance and (c) external phenotypes of  
4 *Arabidopsis* plants cultured in the absence or continuous presence of adjacent cultures of the  
5 indicated microorganisms for one week. In “a” and “b” values represent the means  $\pm$  SE  
6 determined from four independent experiments using 12 plants in each experiment. Asterisks  
7 indicate significant differences between microbial VCs-treated plants and controls (non-treated  
8 plants) according to Student’s t-tests ( $p < 0.05$ ). The phylogenetic tree was constructed using the  
9 PhyloT phylogenetic tree generator ([www.phyloT.biobyte.de](http://www.phyloT.biobyte.de)).

10

11 **Figure 2.** Microbial VCs promote growth of soil-grown *Arabidopsis*, maize and pepper plants.  
12 (a) Rosette FW of *Arabidopsis* plants cultured on soil in the absence or continuous presence of  
13 adjacent cultures of *A. alternata* for indicated times. Essentially the same results were obtained  
14 using cultures from other bacterial and fungal species (not shown). Height of soil-grown maize  
15 (b) and pepper (c) plants cultured in the absence or continuous presence of adjacent cultures of *A.*  
16 *alternata* for indicated times. Values represent the means  $\pm$  SE determined from four independent  
17 experiments using 12 plants in each experiment. Asterisks indicate significant differences  
18 between VCs-treated and non-treated plants according to Student’s t-tests ( $p < 0.05$ ).

19

20 **Figure 3.** *A. alternata* VCs enhance photosynthesis in exposed plants. (a) Total chlorophyll and  
21 carotenoids contents, curves of (b) net CO<sub>2</sub> assimilation rate ( $A_n$ ), and (c) photosynthetic electron  
22 transport (ETR) versus intercellular CO<sub>2</sub> concentration ( $C_i$ ) in leaves of plants cultured in the  
23 absence or continuous presence of adjacent cultures of *A. alternata* for 3 days. VCs treatment  
24 started at the 18 DAS growth stage of plants. In “a” values represent the means  $\pm$  SE determined



1 from four independent experiments using 12 plants in each experiment. Asterisks indicate  
2 significant differences between leaves of VCs-treated and control (non-treated) plants according  
3 to Student's t-tests ( $p < 0.05$ ).

4  
5 **Figure 4.** *A. alternata* VCs increase soluble sugar levels in leaves. Soluble carbohydrate contents  
6 were estimated in leaves of plants grown in the absence or continuous presence of adjacent  
7 cultures of *A. alternata* for 3 days. Leaves were harvested at the end of the light period. Values  
8 represent the means  $\pm$  SE determined from four independent experiments using 12 plants in each  
9 experiment. Asterisks indicate significant differences between leaves of VCs-treated and control  
10 (non-treated) plants according to Student's t-tests ( $p < 0.05$ ).

11  
12 **Figure 5.** CK signaling is required for activities of *A. alternata* VCs. (a) Rosette FW, (b) time of  
13 floral bud appearance, and (c) leaf starch content in WT, 35S:CKX1, *ahk2/3*, *ahk2/4* and *ahk3/4*  
14 plants cultured in the absence or continuous presence of adjacent cultures of *A. alternata* for 12  
15 days. Values represent the means  $\pm$  SE determined from four independent experiments using 12  
16 plants in each experiment. Asterisks indicate significant differences between VCs-treated and  
17 non-treated plants based on Student's t-tests ( $p < 0.05$ ).

18  
19 **Figure 6.** Plant responses to *A. alternata* VCs are light-dependent. (a) FW of rosettes, (b) starch  
20 content and (c) external phenotypes of plants cultured in the absence or presence of adjacent  
21 cultures of *A. alternata* for one week, either only during the light or only during the dark. In "a"  
22 and "b", values represent the means  $\pm$  SE determined from four independent experiments  
23 conducted using 12 plants in each experiment. Asterisks indicate significant differences between  
24 VCs-treated and non-treated plants according to Student's t-tests ( $p < 0.05$ ).

1  
2 **Figure 7.** Functional categorization of the transcripts differentially expressed in leaves of  
3 *Arabidopsis* plants cultured in the presence of VCs emitted by *A. alternata*. Transcripts were  
4 identified using the *Arabidopsis* Gene Expression Microarray 4 x 44K (G2519, Agilent  
5 Technologies). Significantly down- and up-regulated transcripts in exposed plants, with a 2.0 fold  
6 change relative to non-exposed plants, were sorted according to putative functional category  
7 assigned by MapMan software. Numbers of up- and down-regulated genes in each categorical  
8 group are indicated by grey and black bars, respectively. Genes discussed here are boxed and  
9 CK-regulated genes are indicated with asterisks.

10  
11 **Figure 8.** Suggested model for the regulatory network involving CKs and light in response to *A.*  
12 *alternata* VCs. According to this model VCs interact with as yet unidentified plasma membrane  
13 receptors to produce signals that rapidly promote changes in the expression of light-induced  
14 genes encoding proteins involved in photosynthesis and photoprotection (mainly light harvesting  
15 proteins, anthocyanins, ROS scavengers and carotenoids regulators). Augmentation of the  
16 photosynthetic activity results in enhanced GAP, which enters the MEP pathway fueling  
17 production of plastidic CKs that, once exported to the cytosol and sensed in the ER by AHK  
18 receptors, initiate a cascade of reactions resulting in responses such as production of proteins  
19 involved in light harvesting and photoprotection, cell wall modification, initiation of floral  
20 transition, and GPT2-mediated transport of G6P from cytosol to chloroplast. G6P incorporated  
21 into the chloroplast is utilized for production of starch and/or CKs. According to this suggested  
22 model, VCs-promoted early flowering and enhancement of photosynthesis involves suppression  
23 of NO action through the scavenging of NO molecules by CKs and HB1. Genes up- and down-  
24 regulated by *A. alternata* VCs are indicated in brown and red, respectively.

## 1 SUPPORTING INFORMATION

2 The following materials are available in the online version of this article.

3  
4 **Figure S1.** Photographs illustrating the system for exposing plants to *A. alternata* VCs used in  
5 this study. Exposure systems for investigating effects of *A. alternata* VCs on (a) *Arabidopsis*  
6 plants cultured in MS medium and (b,c) maize and pepper plants cultured in soil. Plants were  
7 cultured in the absence or continuous presence of adjacent microbial cultures with no physical  
8 contact.

9  
10 **Figure S2.** VCs emitted by phylogenetically diverse microorganisms promote accumulation of  
11 exceptionally high levels of starch in *Arabidopsis* leaves. Starch contents in leaves of illuminated  
12 plants cultured in the absence or continuous presence of adjacent cultures of the indicated  
13 microorganisms for one day. Values represent the means  $\pm$  SE determined from four independent  
14 experiments using 12 plants in each experiment. Asterisks indicate significant differences  
15 between VCs-treated and control (non-treated) plants based on Student's t-tests ( $p < 0.05$ ). The  
16 phylogenetic tree was constructed using the PhyloT phylogenetic tree generator  
17 ([www.phyloT.biobyte.de](http://www.phyloT.biobyte.de)).

18  
19 **Figure S3.** VCs emitted by *A. alternata* promote augmentation of the levels of CKs in  
20 *Arabidopsis* leaves. Scheme representing pathways of CK biosynthesis through the plastidic MEP  
21 and cytosolic MVA pathways in leaves of VCs-treated plants. Black arrows show the  
22 biosynthesis, interconversions and metabolic flow of CKs in *Arabidopsis* cell (adapted from  
23 Spichal 2012). Multistep reactions are depicted with hollow arrows. The green arrows indicate a  
24 hypothetical exchange of common precursor(s) between the MEP and MVA pathways (adapted

1 from Kasahara et al. 2004). Metabolites whose levels are enhanced by VCs (cf. Table 2) are  
2 highlighted in blue. CKs whose levels are decreased by VCs (cf. Table 2) are highlighted in red.  
3 iPP, isopentenyl diphosphate; DMAPP, dimethylallyl diphosphate.

4  
5 **Figure S4.** Relative abundance of transcript levels in leaves of illuminated *Arabidopsis* plants in  
6 the presence of VCs emitted by *A. alternata*. Fold change values represent changes in levels of  
7 transcripts (measured by quantitative RT-PCR) in leaves of plants cultured in the presence of  
8 VCs and harvested at the end of the light period for 16 h, relative to those of control leaves of  
9 plants cultured in the absence of VCs. Primers used are listed in Supporting Information Table  
10 S2.

11  
12 **Table S1.** Microorganisms used in this study

13  
14 **Table S2.** Primers used in qRT-PCR

15  
16 **Table S3.** List of genes whose expression is altered by *A. alternata* VCs treatment. Genes that  
17 are up-regulated by CKs are highlighted in blue color. Genes that are down-regulated by CKs are  
18 highlighted in yellow color (Tantikanjana et al. 2004, Das et al. 2012, Bhargava et al. 2013,  
19 Brenner & Schmölling 2012, 2015)

20  
21 **Table S4.** List of genes whose expression is down-regulated by VCs emitted by *A. alternata* (this  
22 work, cf. Supporting Information Table S3) and by *B. subtilis* GB03 (cf. Supporting Information  
23 Table 1 in Zhang et al. 2007)

24

1 **Table S5.** List of genes whose expression is up-regulated by VCs emitted by *A. alternata* (this  
2 work, cf. Supporting Information Table S3) and by *B. subtilis* GB03 (cf. Supporting Information  
3 Table 1 in Zhang et al. 2007)  
4

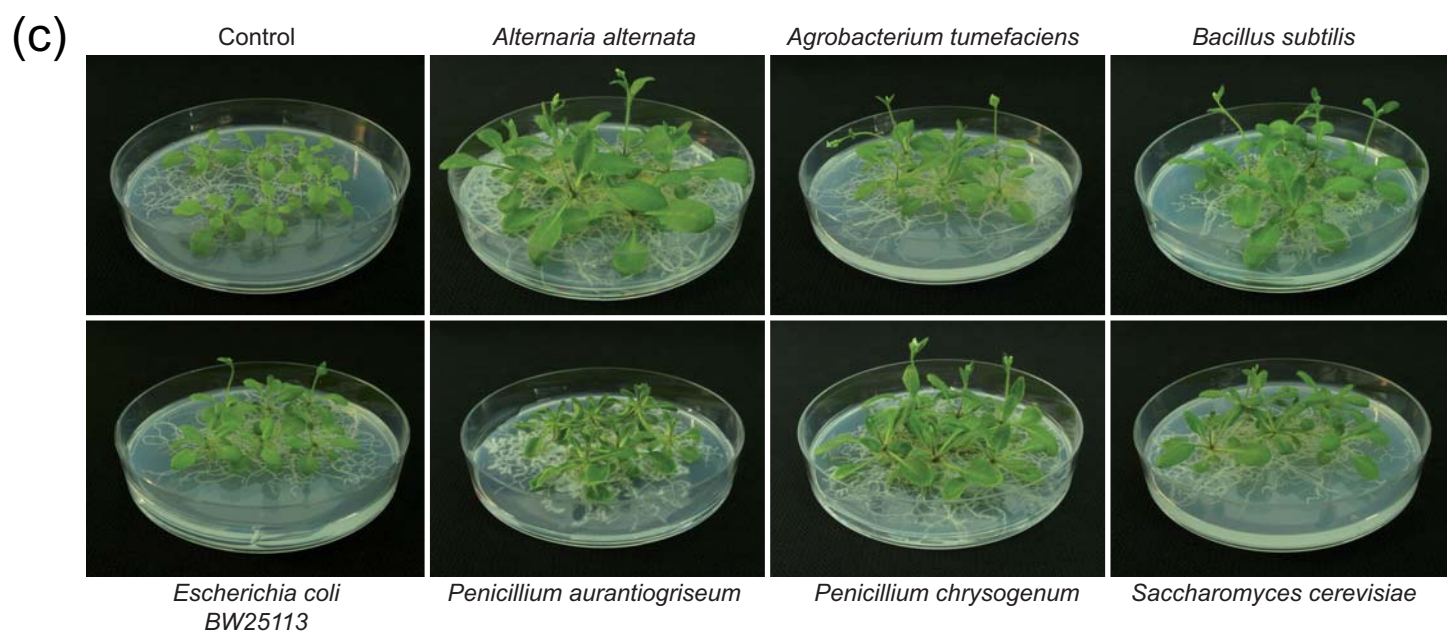
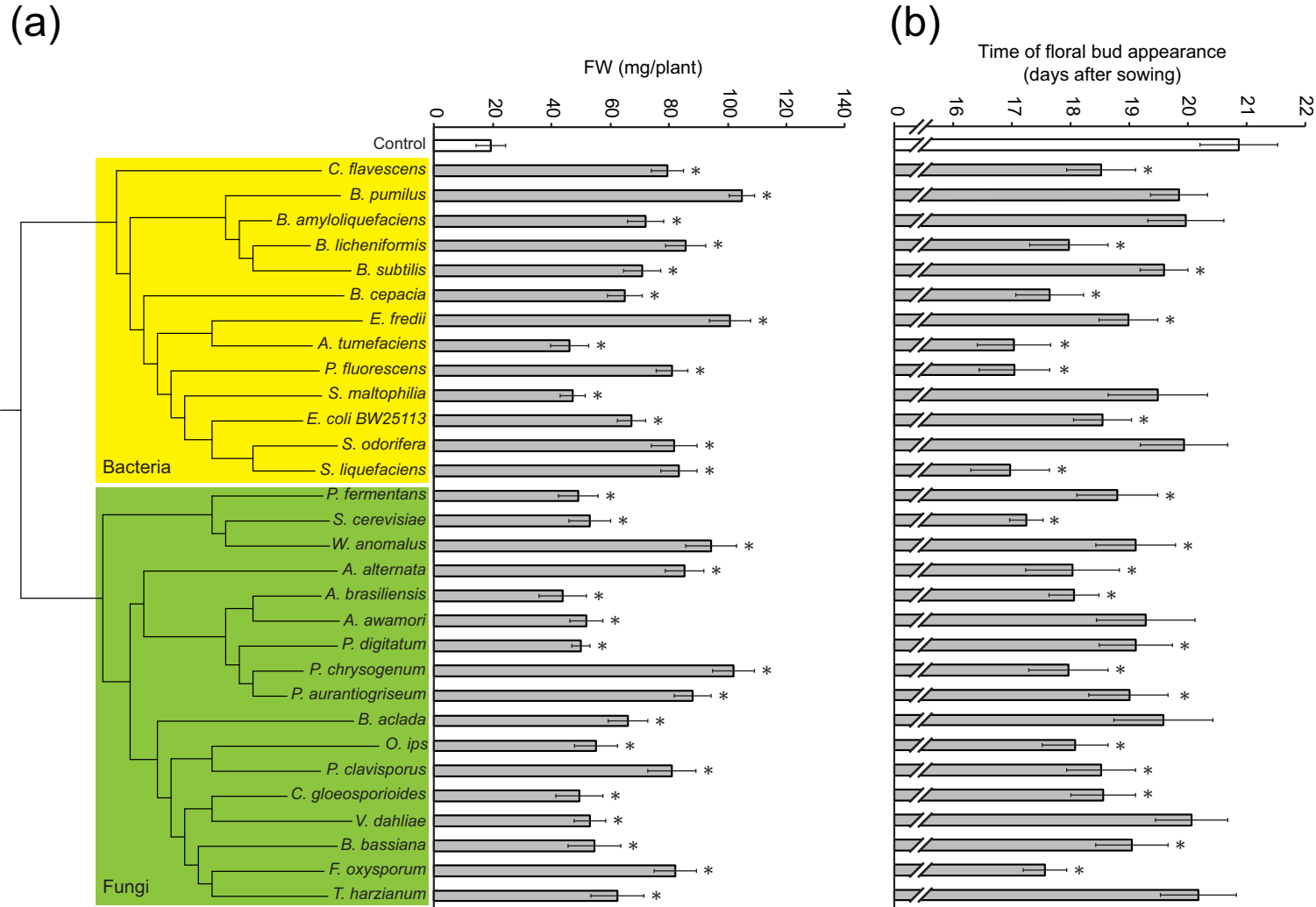


Figure 1

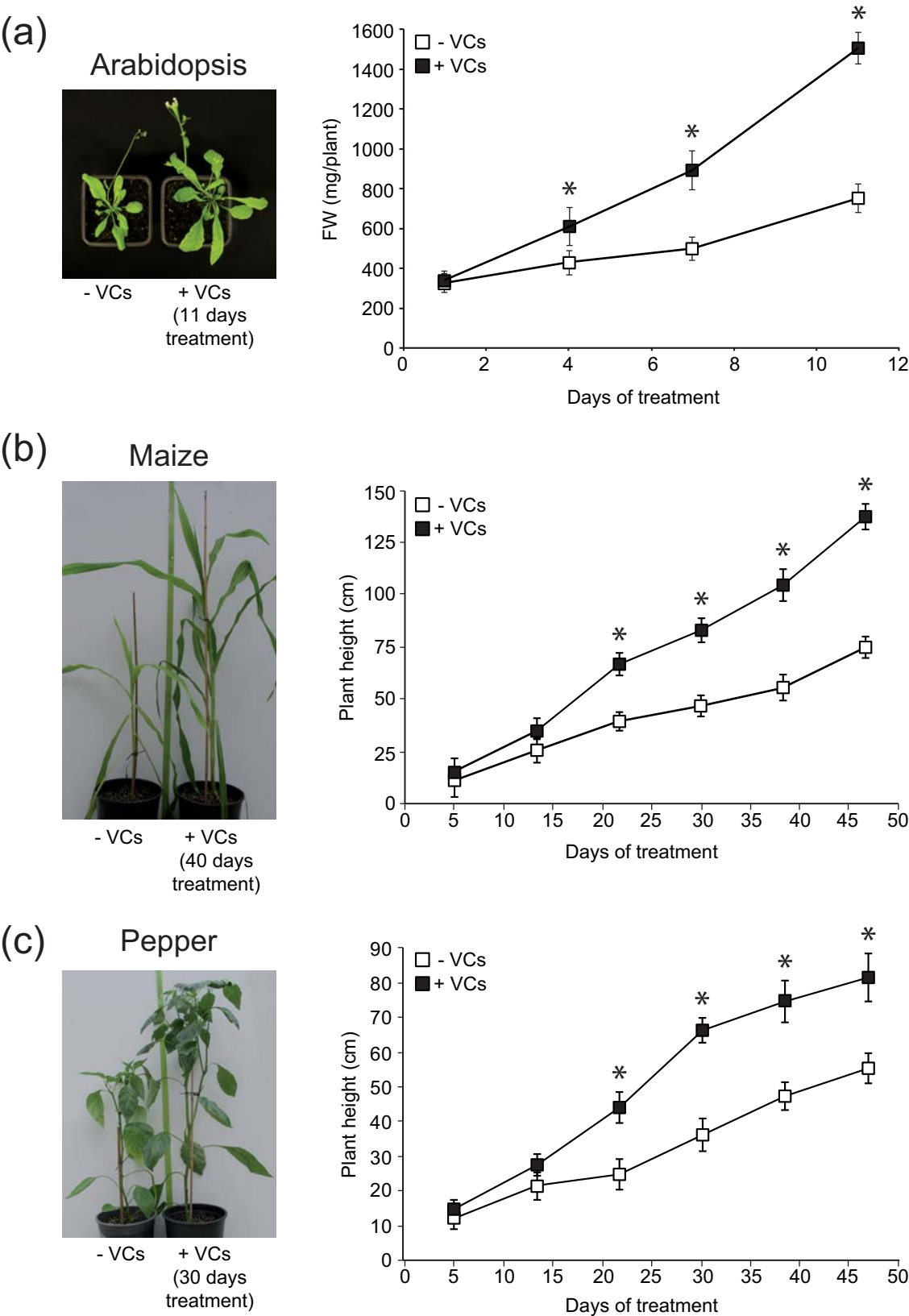


Figure 2

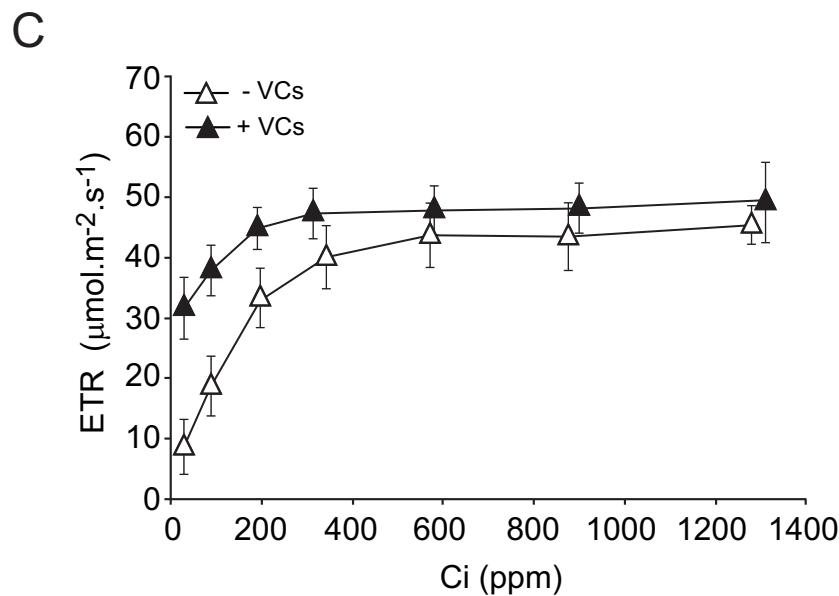
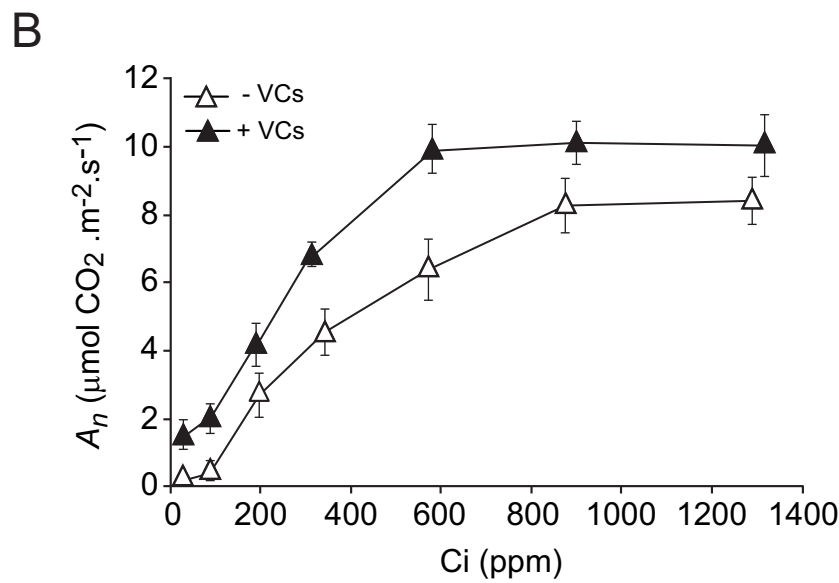
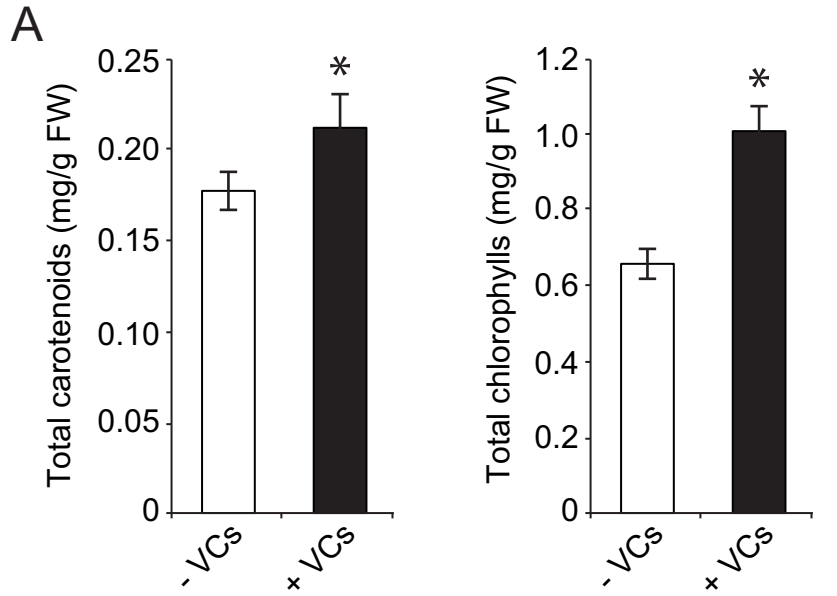


Figure 3



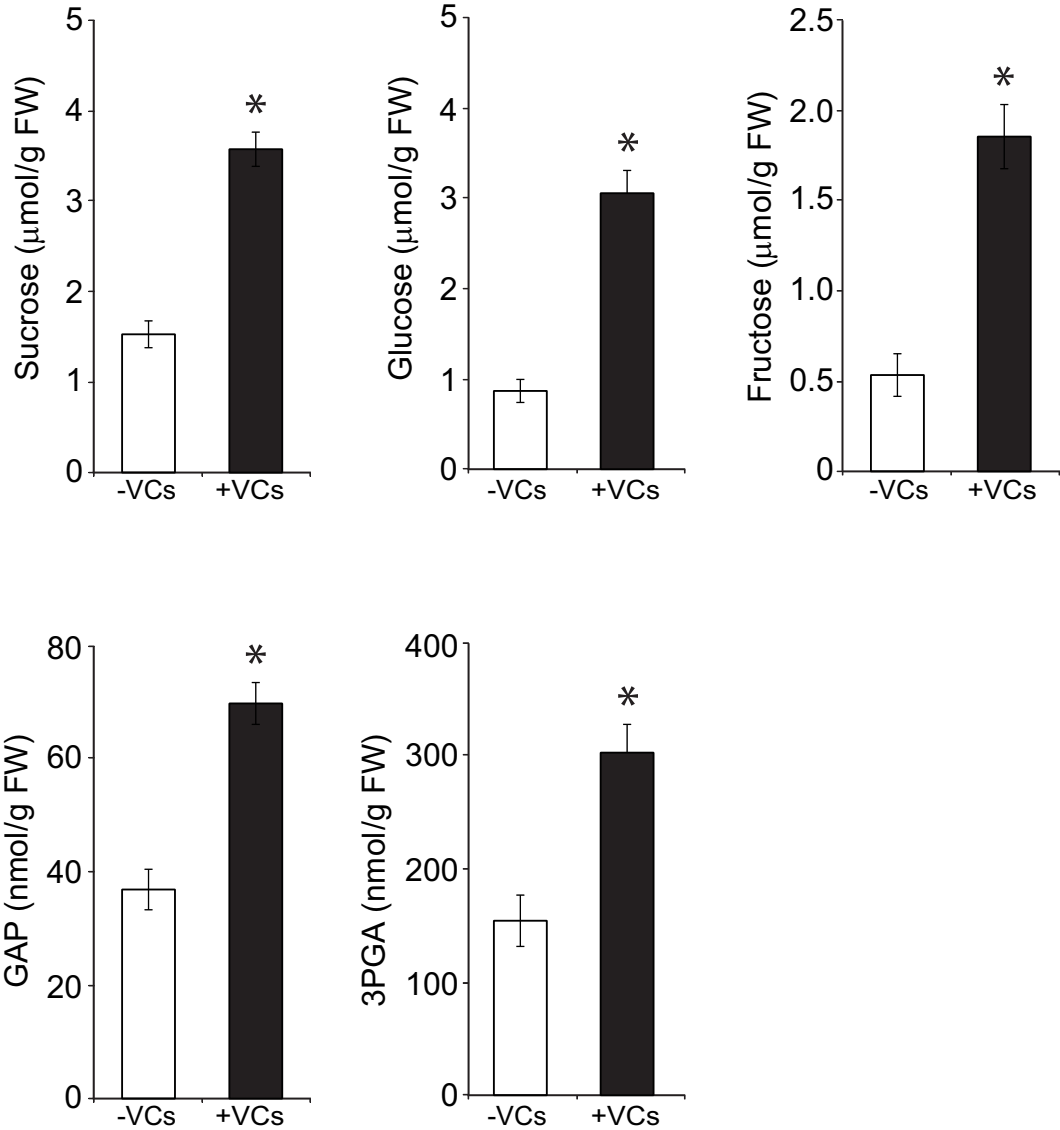


Figure 4

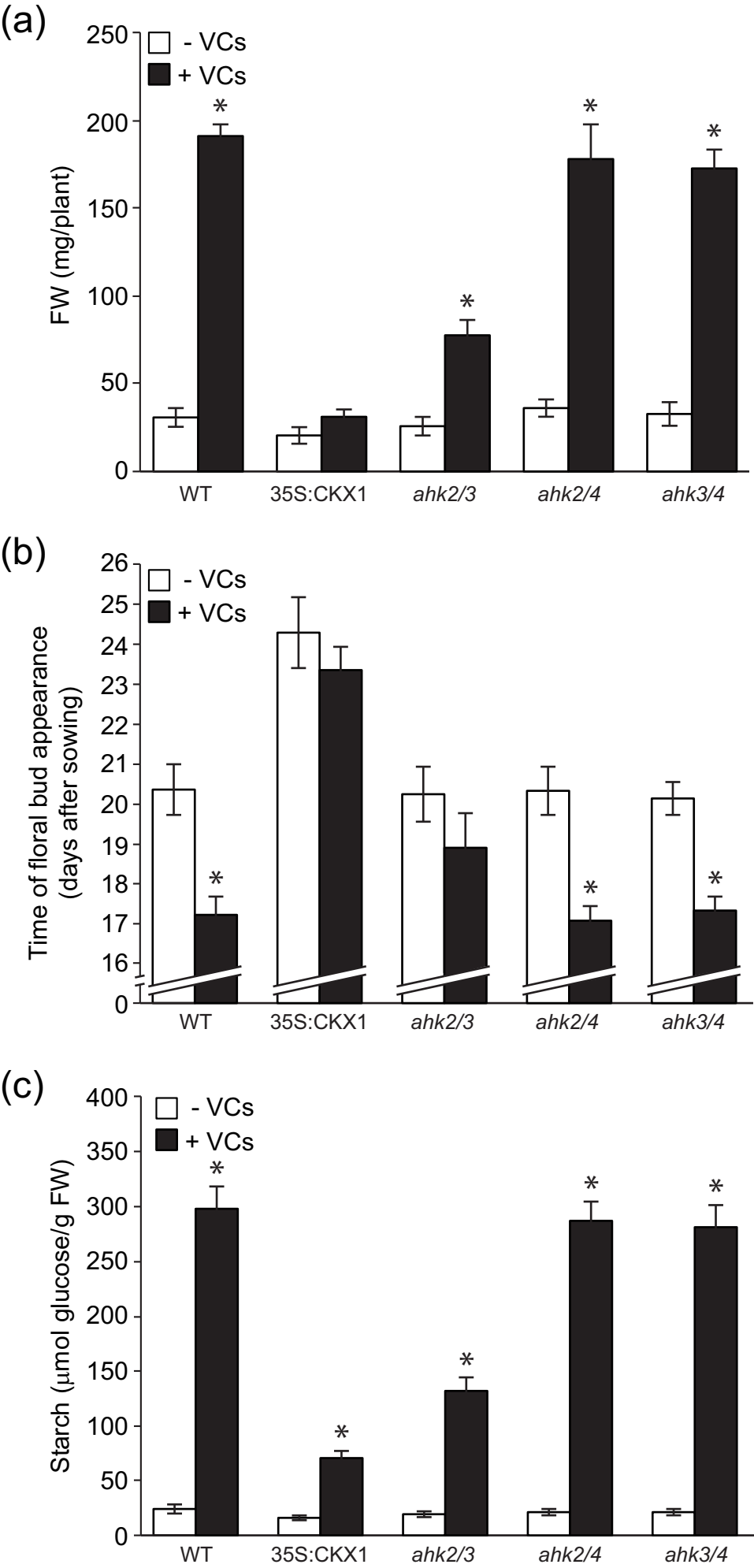
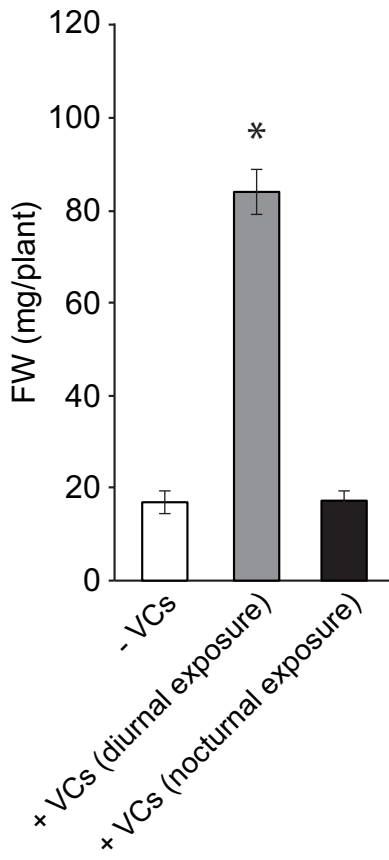
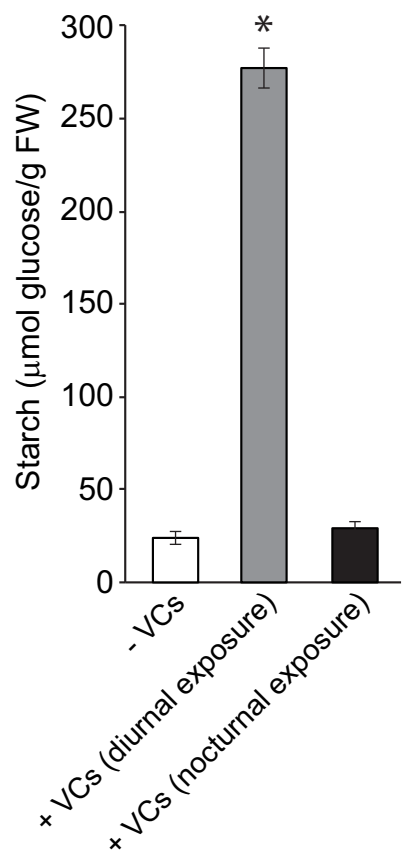


Figure 5

(a)



(b)



(c)

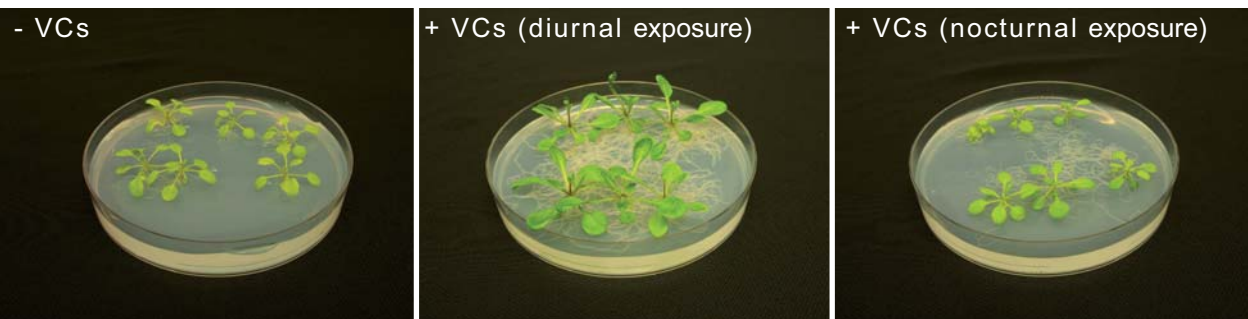


Figure 6

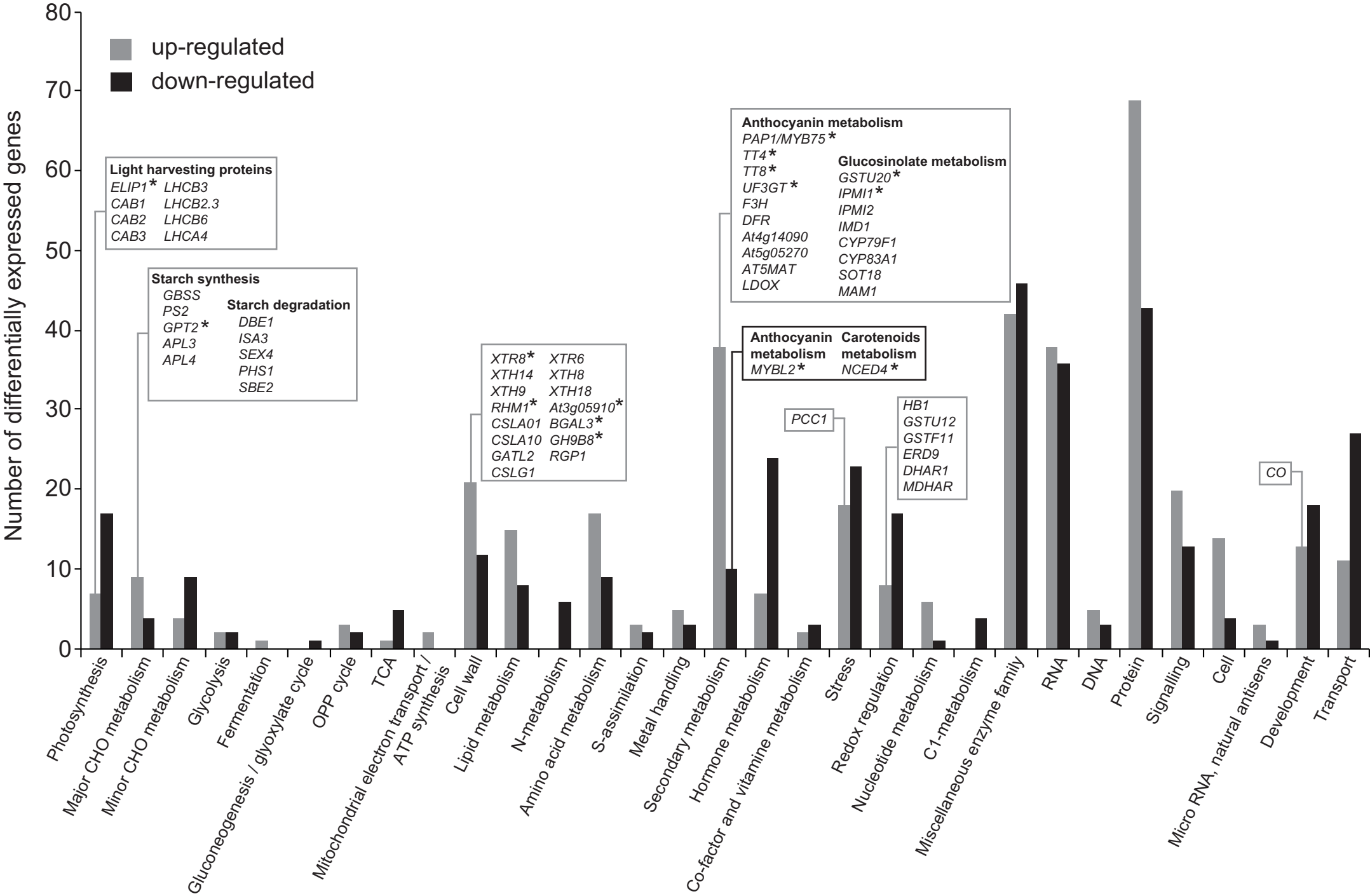


Figure 7

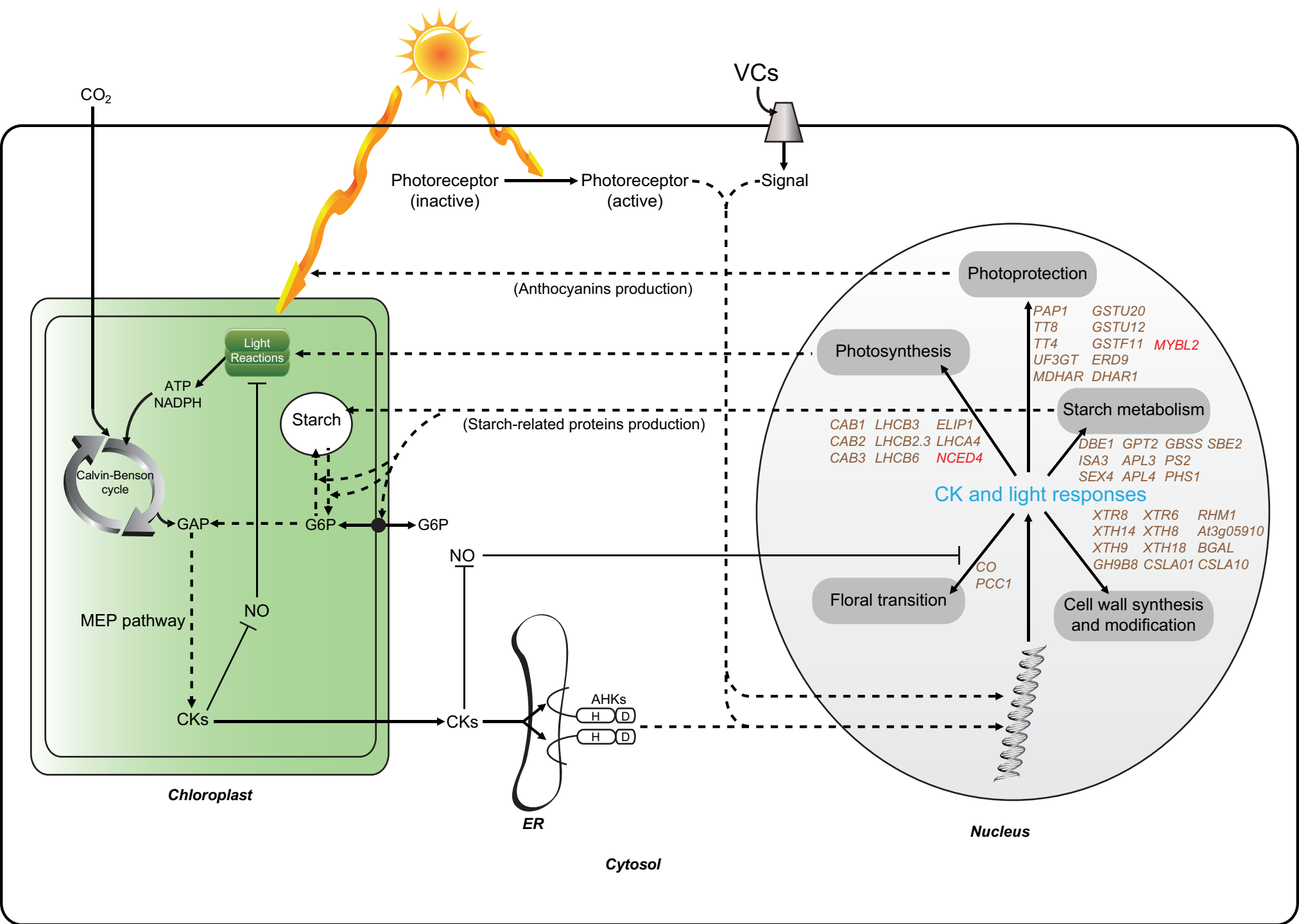
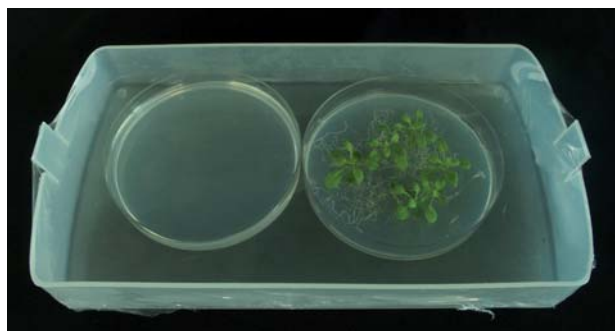


Figure 8

(a)



(b)



(c)



Figure S1

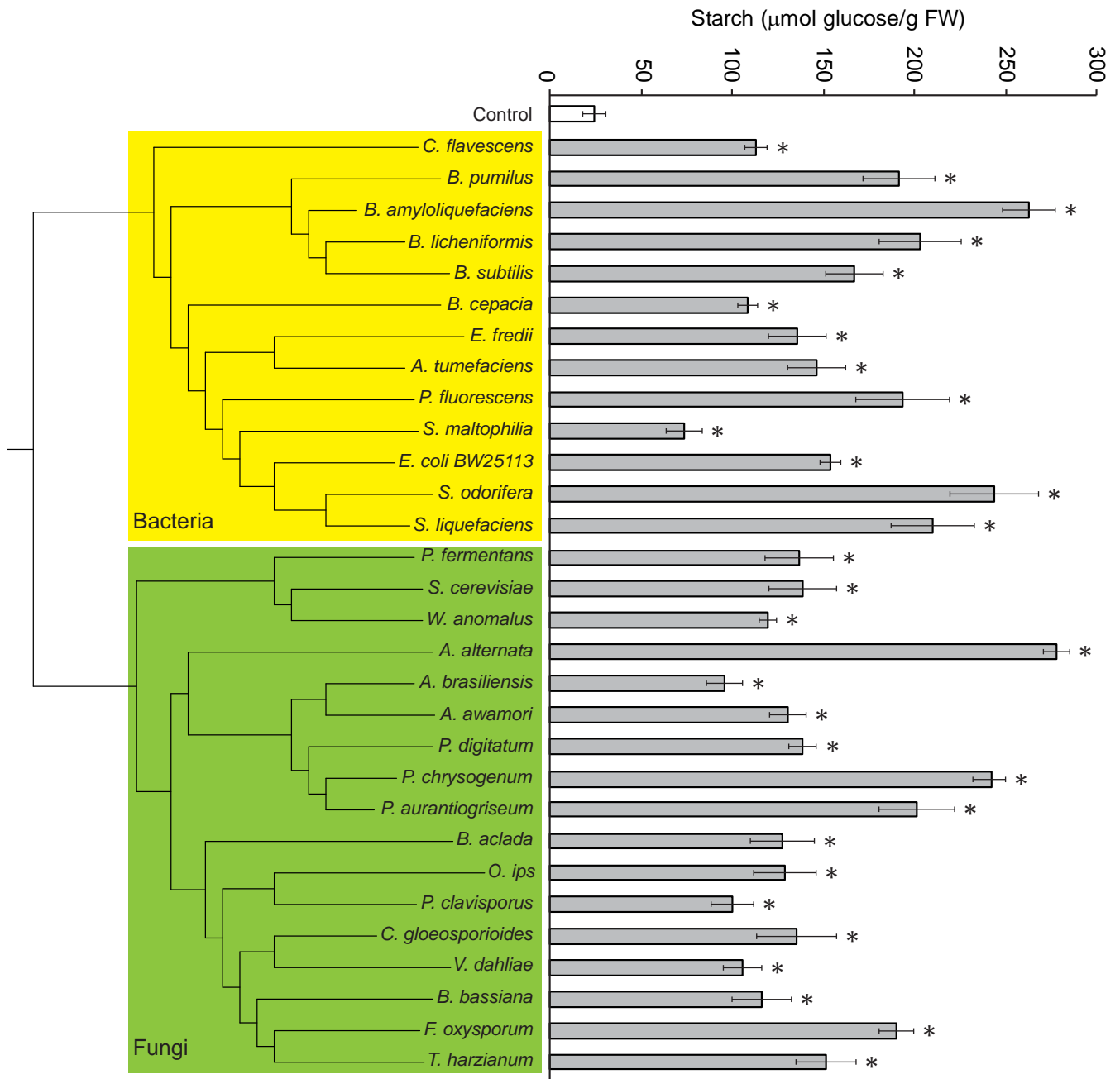


Figure S2

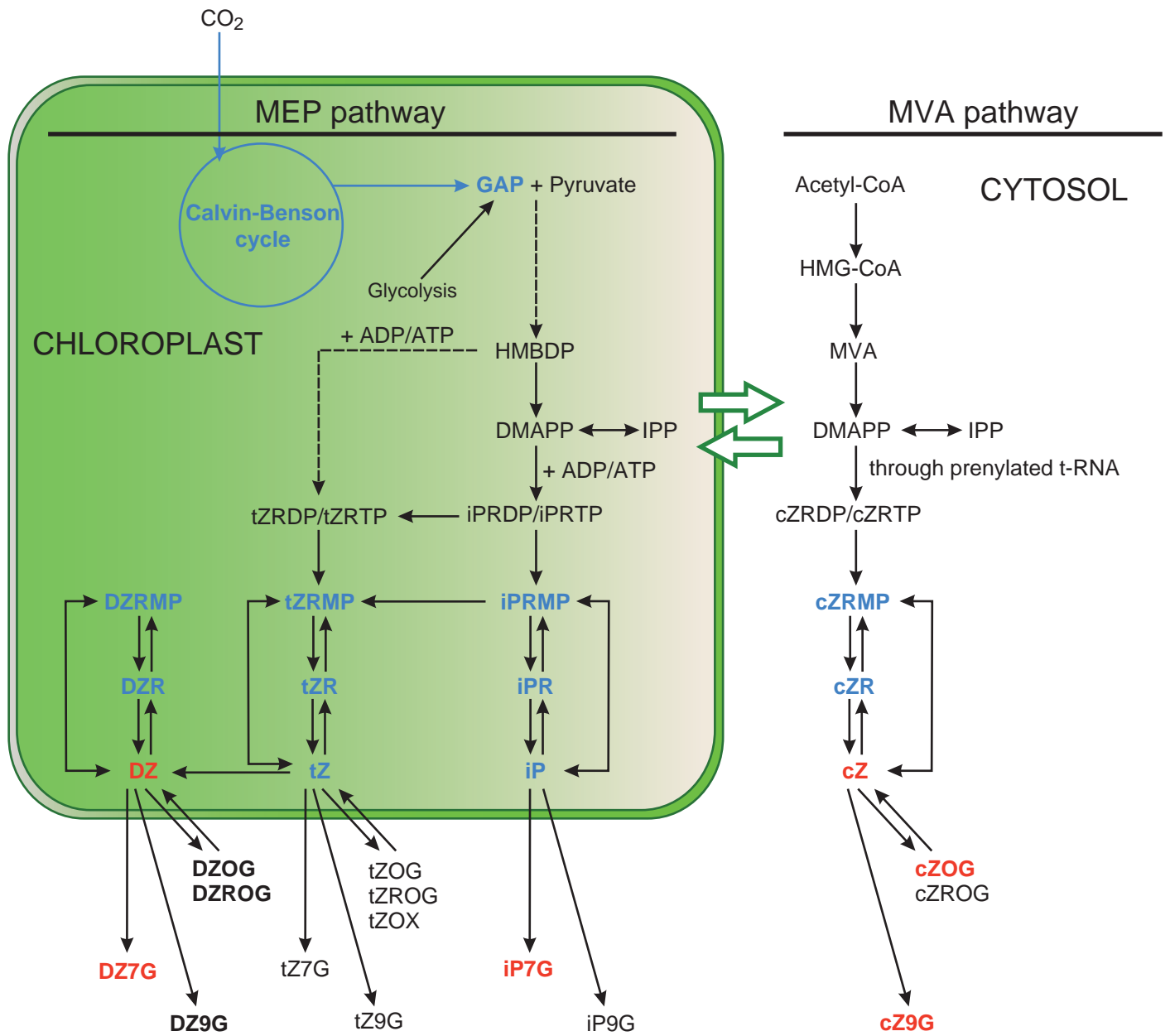


Figure S3



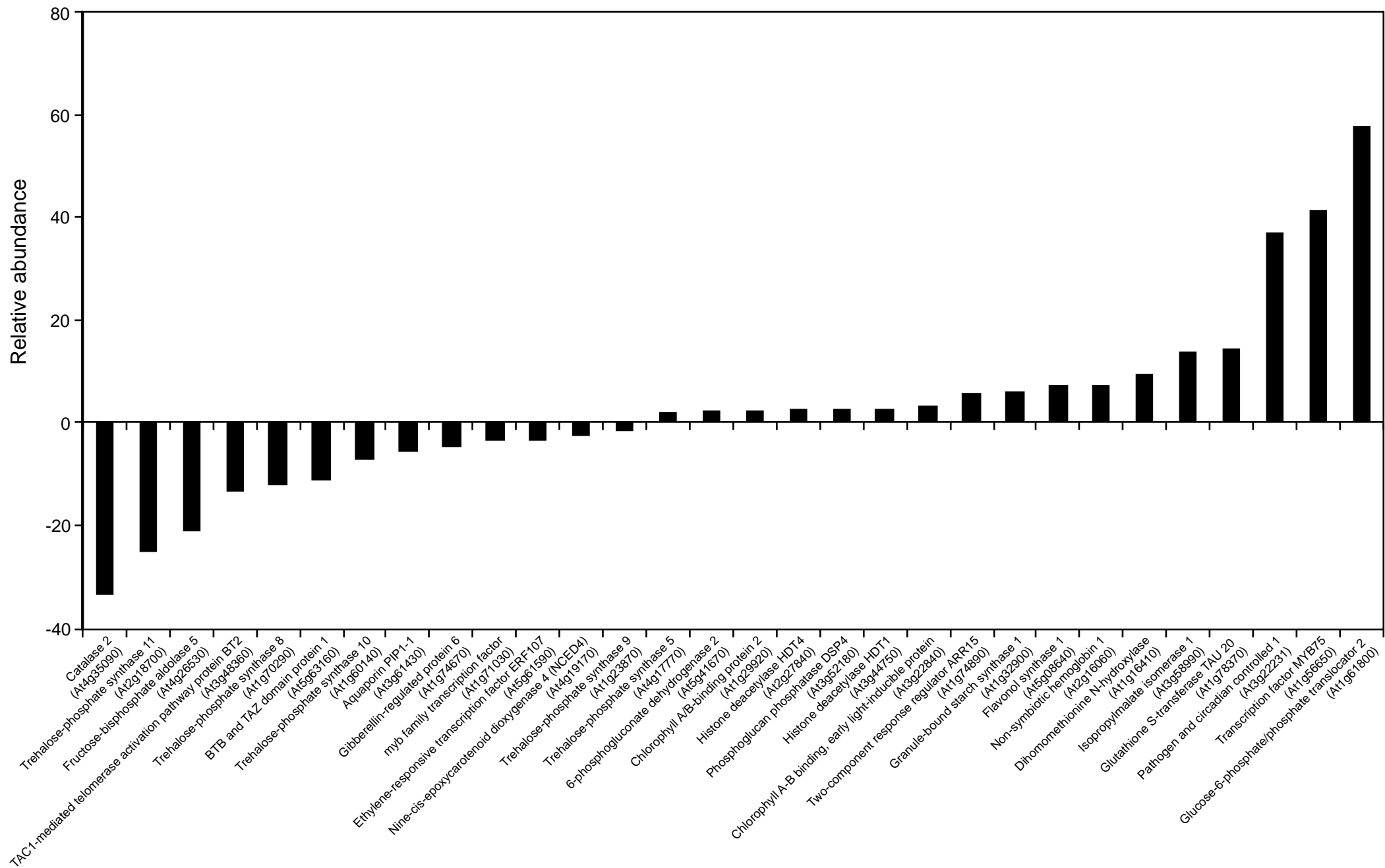


Figure S4

**Table S1:** Microorganisms used in this study

<b>Fungal species</b>	<b>Source</b>	<b>Description</b>
<i>Alternaria alternata</i>	CECT 20192	Filamentous saprophytic fungus. Opportunistic plant pathogen commonly found in soil
<i>Aspergillus awamori</i>	CECT 2907	Filamentous fungus. Plant pathogen, root-associated
<i>Aspergillus brasiliensis</i>	CECT 2091	Filamentous saprophytic fungus. Plant pathogen
<i>Beauveria bassiana</i>	CECT 2704	Filamentous entomopathogenic fungus naturally occurring in soil used as biological insecticide
<i>Botrytis aclada</i>	CECT 2851	Filamentous fungus. Plant pathogen. Can grow saprophytically on decaying plants
<i>Colletotrichum gloeosporioides</i>	CECT 20249	Filamentous fungus. Plant pathogen
<i>Fusarium oxysporum</i>	CECT 20420	Filamentous fungus. Nonpathogenic <i>Fusarium</i> strain, which converts to pathogenic when cured of the bacterial symbionts
<i>Ophiostoma ips</i>	CECT 20676	Filamentous fungus. Plant pathogen
<i>Paecilomyces clavisporus</i>	CECT 20454	Filamentous nematophagous fungus
<i>Penicillium chrysogenum</i>	CECT 2277	Filamentous fungus
<i>Penicillium digitatum</i>	CECT 20796	Filamentous fungus. Plant pathogen
<i>Penicillium aurantiogriseum</i>	CECT 20226	Filamentous fungus. Plant pathogen
<i>Pichia fermentans</i> var. <i>fermentans</i>	CECT 10064	Yeast found in decaying plants
<i>Saccharomyces cerevisiae</i> NA33	CECT 13093	Wine yeast
<i>Trichoderma harzianum</i>	CECT 2413	Filamentous soil fungus used as fungicide
<i>Verticillium dahliae</i>	CECT 2694	Filamentous soil fungus. Plant pathogen
<i>Wickerhamomyces anomalus</i>	CECT 1114	Non-Saccharomyces wine yeast

<b>Bacterial species</b>		
<i>Agrobacterium tumefaciens</i> EHA105	Our laboratory	Plant-growth-promoting soilborne endophytic alphaproteobacterium. Able to induce crown gall tumors on dicotyledonous plants
<i>Bacillus amyloliquefaciens</i>	CECT 493	Non-pathogenic Gram-positive soil bacterium
<i>Bacillus licheniformis</i>	CECT 20	Gram-positive mesophilic bacterium commonly found in the soil
<i>Bacillus pumilus</i>	CECT 29	Plant growth promoting endophytic Gram-positive rhizobacterium naturally occurring in soil

<i>Bacillus subtilis</i> 168	<i>Bacillus</i> Genetic Stock Center, Ohio State University	Plant growth promoting endophytic Gram-positive rhizobacterium naturally occurring in soil
<i>Burkholderia cepacia</i>	CECT 322	Gram-negative endophytic soil-dwelling bacterium
<i>Corynebacterium flavescens</i>	CECT 536	Aerobic Gram-positive bacterium occurring predominantly in dairy products
<i>Ensifer fredii</i>	CECT 4369	Bacterial endophyte
<i>Escherichia coli</i> BW25113	Keio collection (Baba et al. 2006)	Gram-negative bacterium that normally grows in soil and in the intestine of mammals.
<i>Pseudomonas fluorescens</i>	CECT 378	Plant-growth-promoting Gram-negative rhizobacterium occurring in soil that can protect the roots of some plant species against parasitic fungi
<i>Serratia liquefaciens</i>	CECT 483	Widespread Gram-negative facultatively anaerobic rhizobacterium capable of colonizing on soil and plants
<i>Serratia odorifera</i>	CECT 867	Gram-negative facultatively anaerobic rhizobacterium
<i>Stenotrophomonas maltophilia</i>	CECT 7853	Rhizosphere Gram-negative bacterium, ubiquitous in aqueous environments, soils and plants. Grants certain plant species protection against pathogens

**Table S2.** Primers used in qRT-PCR

Gene		Sequence
18S RNA At3g41768	Forward	GGGCATTTCGTATTTTCATAGTCAGAG
	Reverse	CGGTTCTTGATTAATGAAAACATCCT
Glucose-6-phosphate/phosphate translocator At1g61800	Forward	GGTTTCTCAAGTCGGACCAA
	Reverse	TTAACGGCGAAATCTGGTCT
Chlorophyll A-B binding, early light-inducible protein At3g22840	Forward	GTCCAGCACCCAGAGAGGATT
	Reverse	ACCGTCGGAGATCTGAGCTA
Chlorophyll A/B-binding protein At1g29920	Forward	ATTCTTCGTTCAAGCCATCG
	Reverse	AACAAAGTTGGTGGCAAAGG
Transcription factor MYB75 At1g56650	Forward	CTAAACCGGTGCAGGAAAAG
	Reverse	GAAGGCGAAGAAGAAGATCG
Granule-bound starch synthase At1g32900	Forward	CAGCAAAGGCTGTGACAAGA
	Reverse	GGTCCCTTCCAGGAGAAGTC
Phosphoglucan phosphatase DSP4 At3g52180	Forward	CAGCCGTGGTTGGTACTCTT
	Reverse	TGTATGTCAACGCAACAGCA
Dihomomethionine N-hydroxylase At1g16410	Forward	AACGATGGTTGAGAGGTTGG
	Reverse	CTGGACCTCTCGTCGATTA
Pathogen and circadian controlled protein At3g22231	Forward	TCCTCACTCCTCAGCTCCTC
	Reverse	GACTTGTGTACGGCCCTGAT
Non-symbiotic hemoglobin protein At2g16060	Forward	GCCAGCCATTCTAAATACGG
	Reverse	ATCTCCGGTGACCACATCTC
Trehalose-6-phosphate synthase 5 At4g17770	Forward	TCGAATCATCATCGTTGGAA
	Reverse	AGCTGCAAGAGAAGCGAGTC
myb family transcription factor At1g71030	Forward	GGTCATTGATAGCGGGAAGA
	Reverse	TGGGTTCGATTCCCATTTTA
TAC1-mediated telomerase activation pathway BT2 protein At3g48360	Forward	AAGAAAAGAAGGCGACGACA
	Reverse	GGACCGACCAATGTACAACC
Catalase 2 At4g35090	Forward	GTGCTCACCACAACAACCAC
	Reverse	TTCTCAGCATGACGAACCTG
Fructose-bisphosphate aldolase 5 At4g26530	Forward	AAACCCTTCGTTGAGCTCCT
	Reverse	GTAGTGGTCTCGCCATTGGT

Gibberellin-regulated protein 6 AT1G74670	Forward Reverse	AATGTGGAGGACAATGCACA GGGACACAAAGGCATTTAGC
Aquaporin PIP1-1 At3g61430	Forward Reverse	CAAGGGAAGTGGTCTTGGAG GGACATGAGAGTCACGAGCA
Trehalose-6-phosphate synthase 8 At1g70290	Forward Reverse	AATGGTGGAAACCGTTATGA TCAGGATCTGCGTCTTGATG
Trehalose-6-phosphate synthase 9 At1g23870	Forward Reverse	CAGTGATGGATCCTCTGATGTT TGTCCAGTTTCTGTATCTCTCTTAGC
Trehalose-6-phosphate synthase 10 At1g60140	Forward Reverse	GCAAGACGAGGTTTCCATA TGCTGTTTACAAAAGCCAAGG
Trehalose-6-phosphate synthase 11 At2g18700	Forward Reverse	GCAAGCTCAAGGCTCTCTCT CATCATCCGGGTTTAGCACT
Glutathione S-transferase TAU 20 At1g78370	Forward Reverse	TAGAGTTGCGTTGCGAGAGA CGGGATTTTCTTGTGAATGG
Isopropylmalate isomerase 1 At3g58990	Forward Reverse	CAGGCGAGTCAATAACCAGAG GAAGGGATGAGAGTGCCGTA
Flavonol synthase 1 At5g08640	Forward Reverse	ACAACATTCCGAGGTCCAAC AATAGCCCCCATTCTTCACTC
6-phosphogluconate dehydrogenase At5g41670	Forward Reverse	TCAGAACACAGAGCGACGAA GCATAAGAGAAGGACCATTACGA
Histone deacetylase HDT4 At2g27840	Forward Reverse	CGAGCAAAAAGATGCCAAAT AAGAGGGACCACAAGGGAAT
Histone deacetylase HDT1 At3g44750	Forward Reverse	GATGATTCTGATGGTGAGGATTC CAGGTGCTTTAGGGGTAGTTTC
Two-component response regulator ARR15 At1g74890	Forward Reverse	GCTGAAGAAGGAAAAACCAAAA TGAGACGACGATGATGAAGA
Ethylene-responsive transcription factor ERF107 At5g61590	Forward Reverse	TGAAGAAACGAGACATTACAGAGG CAAAGTGCCTAACCAAATCC
Nine-cis-epoxycarotenoid dioxygenase 4 At4g19170	Forward Reverse	AACAAAAGGAGAGCAATGGA CGGAGGAGAGTAGGAGAGGA
BTB and TAZ domain protein 1 At5g63160	Forward Reverse	ATCTTGCCGTGTCCCTCTTT GCAGACGCTACTCTTCTCACC

**Table S3. List of genes whose expression is altered by *A. alternata* VCs treatment. Genes that are up-regulated by CKs are highlighted in blue color. Genes that are down-regulated by CKs are highlighted in yellow color (Tantikanjana et al. 2004; Das et al. 2012; Bhargava et al. 2013; Brenner and Schmülling 2012, 2015)**

Fold Change	pval (LiMMA)	ID	ProbelD	Description
24,26	0.00000025	AT1G61800	GPT2	ref Arabidopsis thaliana glucose-6-phosphate/phosphate translocator 2 mRNA, complete cds [NM_104862]
17,24	0.00000034	AT3G22240	AT3G22240	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_113122]
13,92	0.00000029	AT3G22231	PCC1	ref Arabidopsis thaliana protein PATHOGEN AND CIRCADIAN CONTROLLED 1 mRNA, complete cds [NM_113121]
13,73	0.00000017	AT4G10270	AT4G10270	ref Arabidopsis thaliana putative wound-responsive protein mRNA, complete cds [NM_117095]
13,26	0.00000022	AT1G80130	AT1G80130	ref Arabidopsis thaliana tetratricopeptide repeat domain-containing protein mRNA, complete cds [NM_106662]
12,61	0.00000454	AT2G24850	TAT3	ref Arabidopsis thaliana tyrosine aminotransferase 3 mRNA, complete cds [NM_128044]
11,27	0.00000856	R65132	R65132	tc AAD15384.1 - Arabidopsis thaliana (Mouse-ear cress), partial (68%) [TC400604]
9,98	0.00000457	AT4G36700	AT4G36700	ref Arabidopsis thaliana cupin family protein mRNA, complete cds [NM_119834]
9,66	0.00000027	AT2G14560	LURP1	ref Arabidopsis thaliana protein LURP1 mRNA, complete cds [NM_127019]
9,52	0.00000612	AT3G18000	CPuORF30	ref Arabidopsis thaliana conserved peptide upstream open reading frame 30 mRNA, complete cds [NM_001125181]
9,2	0.00002807	AT3G22235	AT3G22235	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001161166]
8,81	0.00001212	AT5G54060	UF3GT	ref Arabidopsis thaliana anthocyanidin 3-O-glucoside 2 <sup>'''</sup> -O-xylosyltransferase mRNA, complete cds [NM_124785]
8,62	0.00000037	AT4G39210	APL3	ref Arabidopsis thaliana glucose-1-phosphate adenylyltransferase large subunit 3 mRNA, complete cds [NM_120081]
8,41	0.0000045	AT2G16060	HB1	ref Arabidopsis thaliana non-symbiotic hemoglobin 1 mRNA, complete cds [NM_127165]
8,06	0.00000102	AT4G01080	TBL26	ref Arabidopsis thaliana protein TRICHOME BIREFRINGENCE-LIKE 26 mRNA, complete cds [NM_116338]
8,05	0.00000194	AT4G15210	BAM5	ref Arabidopsis thaliana beta-amylase 5 mRNA, complete cds [NM_117609]
7,99	0.00000105	AT1G62420	AT1G62420	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_104922]
7,91	0.00000094	AT1G78370	GSTU20	ref Arabidopsis thaliana glutathione S-transferase TAU 20 mRNA, complete cds [NM_106484]
7,91	0.00000045	AT5G17220	GSTF12	ref Arabidopsis thaliana glutathione S-transferase phi 12 mRNA, complete cds [NM_121728]
7,8	0.00000138	AT1G56650	PAP1	ref Arabidopsis thaliana transcription factor MYB75 mRNA, complete cds [NM_104541]
7,4	0.00000223	AT1G32900	AT1G32900	ref Arabidopsis thaliana granule-bound starch synthase 1 mRNA, complete cds [NM_103023]
7	0.00001879	AT3G10040	AT3G10040	ref Arabidopsis thaliana sequence-specific DNA binding transcription factor mRNA, complete cds [NM_111839]
6,72	0.00000237	EG497537	A_84_P798436	Unknown
6,12	0.00004189	AT2G21590	APL4	ref Arabidopsis thaliana glucose-1-phosphate adenylyltransferase large subunit mRNA, complete cds [NM_001036314]
5,94	0.00000133	AT3G57260	BGL2	ref Arabidopsis thaliana beta 1,3-glucanase 2 mRNA, complete cds [NM_115586]
5,9	0.00000457	AT1G67360	AT1G67360	ref Arabidopsis thaliana REF/SRPP-like protein mRNA, complete cds [NM_179525]
5,72	0.00001041	AT5G20190	AT5G20190	ref Arabidopsis thaliana tetratricopeptide repeat domain-containing protein mRNA, complete cds [NM_122026]
5,61	0.00000855	AT5G15120	AT5G15120	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_121516]
5,11	0.00001222	AT3G56970	BHLH038	ref Arabidopsis thaliana transcription factor ORG2 mRNA, complete cds [NM_115556]
5,1	0.00000305	AT2G41090	AT2G41090	ref Arabidopsis thaliana calmodulin-like protein 10 mRNA, complete cds [NM_129674]
5,04	0.00000428	AT5G14200	IMD1	ref Arabidopsis thaliana isopropylmalate dehydrogenase 1 mRNA, complete cds [NM_001036803]
5,02	0.00000672	AT1G19960	AT1G19960	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_101851]
4,99	0.0000027	AT2G43100	IPMI2	ref Arabidopsis thaliana isopropylmalate isomerase 2 mRNA, complete cds [NM_129871]
4,83	0.00000431	AT1G16410	CYP79F1	ref Arabidopsis thaliana dihomomethionine N-hydroxylase mRNA, complete cds [NM_101507]
4,79	0.00000303	AT3G51240	F3H	ref Arabidopsis thaliana flavanone 3-hydroxylase mRNA, complete cds [NM_114983]
4,77	0.02312371	AT4G27070	TSB2	ref Arabidopsis thaliana tryptophan synthase beta chain mRNA, complete cds [NM_118841]
4,76	0.00002727	AT3G03270	AT3G03270	ref Arabidopsis thaliana adenine nucleotide alpha hydrolases-like protein mRNA, complete cds [NM_180175]
4,66	0.00002262	AT4G22870	AT4G22870	ref Arabidopsis thaliana leucoanthocyanidin dioxygenase-like protein mRNA, complete cds [NM_001160794]
4,65	0.00015214	AT2G39030	AT2G39030	ref Arabidopsis thaliana L-ornithine N5-acetyltransferase NATA1 mRNA, complete cds [NM_129460]
4,6	0.00000391	AT3G56980	BHLH039	ref Arabidopsis thaliana transcription factor ORG3 mRNA, complete cds [NM_115557]
4,54	0.00000783	AT1G47395	AT1G47395	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_179449]
4,54	0.00071237	AT1G68600	AT1G68600	ref Arabidopsis thaliana Aluminum activated malate transporter family protein mRNA, complete cds [NM_105532]
4,51	0.00000533	AT1G06000	AT1G06000	ref Arabidopsis thaliana flavonol-7-O-rhamnosyltransferase mRNA, complete cds [NM_100480]

4,51	0.00000823	AT1G12030	AT1G12030	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_101075]
4,48	0.00000404	AT3G22840	ELIP1	ref Arabidopsis thaliana chlorophyll A-B binding, early light-inducible protein mRNA, complete cds [NM_113183]
4,48	0.00000946	AT5G07990	TT7	ref Arabidopsis thaliana Flavonoid 3'-monooxygenase mRNA, complete cds [NM_120881]
4,46	0.00000591	AT4G23600	CORI3	ref Arabidopsis thaliana cystine lyase CORI3 mRNA, complete cds [NM_179099]
4,44	0.00000484	AT2G29670	AT2G29670	ref Arabidopsis thaliana tetratricopeptide repeat-containing protein mRNA, complete cds [NM_128521]
4,4	0.00383106	AT1G01580	FRO2	ref Arabidopsis thaliana ferric reduction oxidase 2 mRNA, complete cds [NM_100040]
4,24	0.00000876	AT3G58990	IPM1	ref Arabidopsis thaliana isopropylmalate isomerase 1 mRNA, complete cds [NM_115761]
4,18	0.00001156	AT2G41240	BHLH100	ref Arabidopsis thaliana transcription factor bHLH100 mRNA, complete cds [NM_129689]
4,15	0.00001904	AT1G78570	RHM1	ref Arabidopsis thaliana UDP-L-rhamnose synthase mRNA, complete cds [NM_106504]
4,09	0.00007376	AT5G13170	SAG29	ref Arabidopsis thaliana senescence-associated protein 29 mRNA, complete cds [NM_121320]
4,05	0.00041609	AT3G03190	GSTF11	ref Arabidopsis thaliana glutathione S-transferase F11 mRNA, complete cds [NM_111189]
4,05	0.00002311	AT5G42800	DFR	ref Arabidopsis thaliana dihydroflavonol-4-reductase mRNA, complete cds [NM_123645]
4,01	0.000028	AT2G22170	AT2G22170	ref Arabidopsis thaliana PLAT-plant-stress domain-containing protein mRNA, complete cds [NM_127785]
3,99	0.00001164	AT2G28900	OEP16-1	ref Arabidopsis thaliana outer plastid envelope protein 16-1 mRNA, complete cds [NM_128449]
3,96	0.00002718	AT3G19710	BCAT4	ref Arabidopsis thaliana branched-chain aminotransferase4 mRNA, complete cds [NM_112861]
3,95	0.00001151	AT2G46880	PAP14	ref Arabidopsis thaliana purple acid phosphatase 14 mRNA, complete cds [NM_201975]
3,94	0.00000865	AT5G23010	MAM1	ref Arabidopsis thaliana methylthioalkylmalate synthase 1 mRNA, complete cds [NM_122207]
3,89	0.00000673	AT2G27402	AT2G27402	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_201818]
3,87	0.00003971	AT5G54270	LHCB3	ref Arabidopsis thaliana light-harvesting chlorophyll B-binding protein 3 mRNA, complete cds [NM_124807]
3,86	0.0000132	AT1G29920	CAB2	ref Arabidopsis thaliana chlorophyll A/B-binding protein 2 mRNA, complete cds [NM_102732]
3,84	0.00001347	BU917432	BU917432	gb JKHR01A12 Size-selected small cDNAs of Arabidopsis thaliana Arabidopsis thaliana cDNA clone JKHR01A12, mRNA sequence [BU917432]
3,79	0.00003253	AT5G14565	NRT2.7	gb Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL21-90-G19 [AK220694]
3,77	0.00000951	AT3G62820	AT3G62820	ref Arabidopsis thaliana plant invertase/pectin methylesterase inhibitor superfamily protein mRNA, complete cds [NM_116147]
3,76	0.00215854	AT1G28480	GRX480	ref Arabidopsis thaliana glutaredoxin-GRX480 mRNA, complete cds [NM_102616]
3,71	0.00002691	AT3G25795	AK227365	gb Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL14-04-D19 [AK227365]
3,65	0.00154262	AT4G02330	ATPMPECRB	ref Arabidopsis thaliana Probable pectinesterase/pectinesterase inhibitor 41 mRNA, complete cds [NM_116466]
3,61	0.00309877	AT2G29350	SAG13	ref Arabidopsis thaliana senescence-associated protein 13 mRNA, complete cds [NM_201829]
3,61	0.0000125	AT4G17770	TP55	ref Arabidopsis thaliana putative trehalose phosphatase/synthase 5 mRNA, complete cds [NM_117886]
3,56	0.00002026	AT5G03350	AT5G03350	ref Arabidopsis thaliana lectin-like protein mRNA, complete cds [NM_120414]
3,56	0.00001435	AT5G08640	FLS1	ref Arabidopsis thaliana flavonol synthase 1 mRNA, complete cds [NM_001203337]
3,54	0.00052516	AT1G17710	AT1G17710	ref Arabidopsis thaliana phosphoethanolamine/phosphocholine phosphatase mRNA, complete cds [NM_001084087]
3,53	0.00007579	AT4G18440	AT4G18440	ref Arabidopsis thaliana L-aspartase-like family protein mRNA, complete cds [NM_117957]
3,51	0.00003458	AT3G02480	AT3G02480	ref Arabidopsis thaliana Late embryogenesis abundant protein (LEA) family protein mRNA, complete cds [NM_111115]
3,49	0.00002477	AT1G56430	NAS4	ref Arabidopsis thaliana nicotianamine synthase 4 mRNA, complete cds [NM_104521]
3,48	0.0000124	AT4G14090	AT4G14090	ref Arabidopsis thaliana anthocyanin 5-O-glucosyltransferase mRNA, complete cds [NM_117485]
3,47	0.0000176	AT5G67370	AT5G67370	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_126137]
3,45	0.00006529	AT2G26440	AT2G26440	ref Arabidopsis thaliana Probable pectinesterase/pectinesterase inhibitor 12 mRNA, complete cds [NM_128201]
3,44	0.00003334	AT3G03780	MS2	ref Arabidopsis thaliana methionine synthase 2 mRNA, complete cds [NM_111249]
3,44	0.00001917	AT5G05270	AT5G05270	ref Arabidopsis thaliana Chalcone-flavanone isomerase family protein mRNA, complete cds [NM_180439]
3,41	0.00001213	AT1G23020	FRO3	ref Arabidopsis thaliana ferric reduction oxidase 3 mRNA, complete cds [NM_102150]
3,4	0.00026383	AT3G19680	AT3G19680	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_112858]
3,39	0.00092063	AT5G25830	GATA12	ref Arabidopsis thaliana GATA transcription factor 12 mRNA, complete cds [NM_122484]
3,39	0.00135656	AT5G65420	CYCD4;1	ref Arabidopsis thaliana cyclin-D4-1 mRNA, complete cds [NM_001203691]
3,37	0.00001346	AT1G24020	MPL423	ref Arabidopsis thaliana MLP-like protein 423 mRNA, complete cds [NM_102249]
3,37	0.00002103	TC300093	A_84_P847741	Unknown
3,31	0.00016553	AT3G29590	AT5MAT	ref Arabidopsis thaliana malonyl-CoA:anthocyanidin 5-O-glucoside-6-O-malonyltransferase mRNA, complete cds [NM_113880]
3,31	0.00003568	AT4G13770	CYP83A1	ref Arabidopsis thaliana cytochrome P450 83A1 mRNA, complete cds [NM_117451]
3,3	0.00003032	AT1G62560	FMO GS-OX3	ref Arabidopsis thaliana flavin-containing monooxygenase FMO GS-OX3 mRNA, complete cds [NM_104934]

3,3	0.00004299	AT3G13310	AT3G13310	ref Arabidopsis thaliana chaperone DnaJ-domain containing protein mRNA, complete cds [NM_112176]
3,3	0.00001748	AT5G11740	AGP15	ref Arabidopsis thaliana arabinogalactan protein 15 mRNA, complete cds [NM_121212]
3,29	0.00001678	AT4G12030	BAT5	ref Arabidopsis thaliana probable sodium/metabolite cotransporter BASS5 mRNA, complete cds [NM_117273]
3,27	0.00001959	AT1G06830	AT1G06830	ref Arabidopsis thaliana monothiol glutaredoxin-S11 mRNA, complete cds [NM_100560]
3,27	0.00004784	AT3G27220	AT3G27220	ref Arabidopsis thaliana Kelch repeat-containing protein mRNA, complete cds [NM_113636]
3,26	0.00002639	AT3G25882	NIMIN-2	ref Arabidopsis thaliana protein NIM1-INTERACTING 2 mRNA, complete cds [NM_148752]
3,25	0.00001742	AT1G73600	CPuORF32	ref Arabidopsis thaliana conserved peptide upstream open reading frame 32 mRNA, complete cds [NM_001124125]
3,18	0.00002583	AT1G03495	AT1G03495	ref Arabidopsis thaliana coumaroyl-CoA:anthocyanidin 3-O-glucoside-6-O-coumaroyltransferase 2 mRNA, complete cds [NM_100232]
3,18	0.00007772	AT4G16590	CSLA01	ref Arabidopsis thaliana cellulose synthase-like A01 mRNA, complete cds [NM_117760]
3,15	0.00001943	AT1G75040	PR5	ref Arabidopsis thaliana pathogenesis-related protein 5 mRNA, complete cds [NM_106161]
3,14	0.00004517	AT1G18590	SOT17	ref Arabidopsis thaliana sulfotransferase 17 mRNA, complete cds [NM_101717]
3,13	0.00004348	AT3G44860	FAMT	ref Arabidopsis thaliana farnesoic acid carboxyl-O-methyltransferase mRNA, complete cds [NM_114355]
3,11	0.00012443	AT1G73010	PS2	ref Arabidopsis thaliana inorganic pyrophosphatase 1 mRNA, complete cds [NM_105959]
3,11	0.00002351	AT2G46650	CB5-C	ref Arabidopsis thaliana cytochrome B5 isoform C mRNA, complete cds [NM_130230]
3,06	0.00006758	AT3G21560	UGT84A2	ref Arabidopsis thaliana sinapic acid:UDP-glucose glucosyltransferase mRNA, complete cds [NM_113051]
3,06	0.00013786	AT5G54740	SESA5	ref Arabidopsis thaliana seed storage albumin 5 mRNA, complete cds [NM_124855]
3,05	0.00165722	AT5G53048	A_84_P769609	Unknown
3,05	0.00004937	TA26506_3702	TA26506_3702	Unknown
3,04	0.00258018	AT3G17120	AT3G17120	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_112588]
3,03	0.00080709	AT4G28790	AT4G28790	ref Arabidopsis thaliana transcription factor bHLH23 mRNA, complete cds [NM_119023]
3,02	0.00005595	AT4G03060	AF418241	gb Arabidopsis thaliana Col-0 2-oxoglutarate-dependent dioxygenase (AOP2) pseudogene, mRNA sequence [AF418241]
3,01	0.0001084	AT2G35860	FLA16	ref Arabidopsis thaliana fasciclin-like arabinogalactan protein 16 mRNA, complete cds [NM_179922]
3,01	0.00047359	AT3G21600	AT3G21600	ref Arabidopsis thaliana Senescence/dehydration-associated protein-like protein mRNA, complete cds [NM_202620]
3	0.00004891	AT2G46430	CNGC3	ref Arabidopsis thaliana cyclic nucleotide gated channel 3 mRNA, complete cds [NM_130207]
3	0.00003104	AT3G27060	TSO2	ref Arabidopsis thaliana ribonucleoside-diphosphate reductase small chain C mRNA, complete cds [NM_113620]
2,99	0.00005061	AT5G48880	PKT2	ref Arabidopsis thaliana 3-keto-acyl-CoA thiolase 2 mRNA, complete cds [NM_001036960]
2,96	0.00011262	AT1G49700	NP2708883	tc GB NM_103857.1 NP_175392.1 unknown protein;similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G07675.1) [NP2708883]
2,96	0.00005111	AT2G32060	AT2G32060	ref Arabidopsis thaliana 40S ribosomal protein S12-2 mRNA, complete cds [NM_179850]
2,96	0.00002788	AT2G37270	RPS5B	ref Arabidopsis thaliana 40S ribosomal protein S5-1 mRNA, complete cds [NM_001036425]
2,96	0.01061363	AT3G20260	AT3G20260	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_112917]
2,95	0.00004261	AT5G64550	AT5G64550	ref Arabidopsis thaliana loricrin-related protein mRNA, complete cds [NM_125851]
2,95	0.00140346	CB185526	CB185526	Unknown
2,94	0.00023814	AT1G24070	CSLA10	ref Arabidopsis thaliana cellulose synthase-like A10 mRNA, complete cds [NM_102254]
2,93	0.00002984	AT5G20180	AT5G20180	ref Arabidopsis thaliana ribosomal protein L36 mRNA, complete cds [NM_180526]
2,91	0.00004267	AT4G34200	EDA9	ref Arabidopsis thaliana D-3-phosphoglycerate dehydrogenase mRNA, complete cds [NM_119583]
2,9	0.0000344	AT5G67330	NRAMP4	ref Arabidopsis thaliana metal transporter Nramp4 mRNA, complete cds [NM_126133]
2,89	0.00013451	AT2G14750	APK	ref Arabidopsis thaliana Adenylyl-sulfate kinase 1 mRNA, complete cds [NM_127039]
2,89	0.00003798	AT3G56400	WRKY70	ref Arabidopsis thaliana WRKY transcription factor 70 mRNA, complete cds [NM_115498]
2,88	0.00003109	AT1G03470	AT1G03470	ref Arabidopsis thaliana NETWORKED 3A mRNA, complete cds [NM_100229]
2,88	0.0000406	AT1G45191	AT1G45191	ref Arabidopsis thaliana beta-glucosidase 1 mRNA, complete cds [NM_179440]
2,88	0.00018902	AT4G14040	SBP2	ref Arabidopsis thaliana selenium-binding protein 2 mRNA, complete cds [NM_117479]
2,87	0.00003361	AT3G22550	AT3G22550	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_113154]
2,87	0.00003871	AT3G55750	AT3G55750	ref Arabidopsis thaliana 60S ribosomal protein L35a-4 mRNA, complete cds [NM_115433]
2,86	0.00014626	AT3G11010	RLP34	ref Arabidopsis thaliana receptor like protein 34 mRNA, complete cds [NM_111938]
2,85	0.00687353	AT4G21830	MSRB7	ref Arabidopsis thaliana peptide methionine sulfoxide reductase B7 mRNA, complete cds [NM_118303]
2,84	0.00007551	AT2G44670	AT2G44670	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_130031]
2,84	0.00009525	AT4G39940	AKN2	ref Arabidopsis thaliana adenosine-5'-phosphosulfate-kinase 2 mRNA, complete cds [NM_120157]
2,84	0.00752932	AT5G12080	MSL10	ref Arabidopsis thaliana mechanosensitive channel of small conductance-like 10 mRNA, complete cds [NM_180479]



2,83	0.00006187	AT4G09020	ISA3	ref Arabidopsis thaliana isoamylase 3 mRNA, complete cds [NM_116971]
2,81	0.00651667	AT3G60440	AT3G60440	ref Arabidopsis thaliana phosphoglycerate mutase family protein mRNA, complete cds [NM_115908]
2,8	0.02623122	AT5G52540	AT5G52540	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_124633]
2,79	0.00039953	AT1G80120	AT1G80120	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_106661]
2,79	0.00003763	AT3G52180	SEX4	ref Arabidopsis thaliana phosphoglucan phosphatase DSP4 mRNA, complete cds [NM_001035765]
2,78	0.00013806	AT2G43620	AT2G43620	ref Arabidopsis thaliana chitinase family protein mRNA, complete cds [NM_129924]
2,78	0.00004313	AT3G49680	BCAT3	ref Arabidopsis thaliana branched-chain-amino-acid aminotransferase 3 mRNA, complete cds [NM_114828]
2,78	0.00009054	AT5G48850	ATSDI1	ref Arabidopsis thaliana protein SULPHUR DEFICIENCY-INDUCED 1 mRNA, complete cds [NM_124262]
2,77	0.00556886	AT2G32220	AT2G32220	ref Arabidopsis thaliana 60S ribosomal protein L27-1 mRNA, complete cds [NM_128781]
2,77	0.00010385	AT3G27690	LHCB2.3	ref Arabidopsis thaliana photosystem II light harvesting complex protein 2.3 mRNA, complete cds [NM_113685]
2,77	0.00627094	AT3G50760	GATL2	ref Arabidopsis thaliana putative galacturonosyltransferase-like 2 mRNA, complete cds [NM_114936]
2,77	0.00283417	AT4G04745	AT4G04745	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_148231]
2,77	0.00027697	AT4G14400	ACD6	ref Arabidopsis thaliana protein ACCELERATED CELL DEATH 6 mRNA, complete cds [NM_117519]
2,77	0.00010825	AT5G19460	NUDT20	ref Arabidopsis thaliana nudix hydrolase 20 mRNA, complete cds [NM_121951]
2,76	0.00027543	AT5G23020	IMS2	ref Arabidopsis thaliana methylthioalkylmalate synthase 3 mRNA, complete cds [NM_122208]
2,75	0.00942864	AT1G11330	AT1G11330	ref Arabidopsis thaliana G-type lectin S-receptor-like serine/threonine-protein kinase mRNA, complete cds [NM_001198033]
2,75	0.00039369	AT5G44568	AT5G44568	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001085241]
2,74	0.0112407	AT1G03990	AT1G03990	ref Arabidopsis thaliana long-chain-alcohol oxidase FAO1 mRNA, complete cds [NM_100280]
2,74	0.00014982	TA28625_3702	TA28625_3702	Unknown
2,72	0.00155275	AT1G14520	MIOX1	ref Arabidopsis thaliana inositol oxygenase 1 mRNA, complete cds [NM_101319]
2,72	0.00188573	AT1G24580	AT1G24580	ref Arabidopsis thaliana RING/U-box domain-containing protein mRNA, complete cds [NM_202179]
2,72	0.00005532	AT3G02020	AK3	ref Arabidopsis thaliana aspartokinase 3 mRNA, complete cds [NM_111068]
2,72	0.000069	AT3G50440	MES10	ref Arabidopsis thaliana methyl esterase 10 mRNA, complete cds [NM_114904]
2,72	0.00739434	AT5G60900	RLK1	ref Arabidopsis thaliana receptor-like protein kinase 1 mRNA, complete cds [NM_125483]
2,72	0.0030402	TA28146_3702	TA28146_3702	tc Rep: ER lumen protein retaining receptor - Vitis vinifera (Grape), partial (5%) [TC395123]
2,71	0.00005088	AT5G22020	AT5G22020	ref Arabidopsis thaliana strictosidine synthase family protein mRNA, complete cds [NM_147884]
2,7	0.00010403	AT1G79530	GAPCP-1	ref Arabidopsis thaliana glyceraldehyde-3-phosphate dehydrogenase GAPCP1 mRNA, complete cds [NM_106601]
2,7	0.0168803	AT5G01870	AT5G01870	ref Arabidopsis thaliana pathogenesis-related lipid transfer protein mRNA, complete cds [NM_120265]
2,7	0.00031376	AT5G41670	AT5G41670	ref Arabidopsis thaliana 6-phosphogluconate dehydrogenase, decarboxylating 2 mRNA, complete cds [NM_180782]
2,7	0.00012671	AT5G53420	AT5G53420	ref Arabidopsis thaliana CCT motif family protein mRNA, complete cds [NM_124721]
2,69	0.0002344	AT1G74270	AT1G74270	ref Arabidopsis thaliana 60S ribosomal protein L35a-3 mRNA, complete cds [NM_106087]
2,69	0.0000512	AT5G54075	A_84_P767724	Unknown
2,68	0.00026349	AT1G01570	AT1G01570	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_100039]
2,68	0.00179742	AT1G28395	AT1G28395	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_102607]
2,68	0.01555756	AT3G05470	AT3G05470	ref Arabidopsis thaliana Actin-binding protein FH2 mRNA, complete cds [NM_111420]
2,67	0.00024584	AT4G08300	AT4G08300	ref Arabidopsis thaliana nodulin MtN21 /EamA-like transporter family protein mRNA, complete cds [NM_116899]
2,66	0.00013221	AT3G12820	MYB10	ref Arabidopsis thaliana myb domain protein 10 mRNA, complete cds [NM_112118]
2,65	0.00169954	AT2G47010	AT2G47010	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_201976]
2,65	0.00230632	AT5G06270	AT5G06270	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_120710]
2,65	0.00015472	AT5G13930	TT4	ref Arabidopsis thaliana chalcone synthase mRNA, complete cds [NM_121396]
2,64	0.00011113	AT3G56020	AT3G56020	ref Arabidopsis thaliana 60S ribosomal protein L41 mRNA, complete cds [NM_115460]
2,63	0.00006635	AT2G41010	CAMPB25	ref Arabidopsis thaliana calmodulin binding protein 25 mRNA, complete cds [NM_129666]
2,63	0.00375458	AT4G33130	AT4G33130	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_202945]
2,62	0.00048984	AT2G30770	CYP71A13	ref Arabidopsis thaliana cytochrome P450, family 71, subfamily A, polypeptide 13 mRNA, complete cds [NM_128630]
2,62	0.00839797	AT2G37300	AT2G37300	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_129286]
2,62	0.01834754	AT3G07750	AT3G07750	ref Arabidopsis thaliana 3'-5'-exoribonuclease family protein mRNA, complete cds [NM_111654]
2,61	0.00006892	AT1G65060	4CL3	ref Arabidopsis thaliana 4-coumarate--CoA ligase 3 mRNA, complete cds [NM_179513]
2,61	0.0043117	AT3G23990	HSP60	ref Arabidopsis thaliana heat shock protein 60 mRNA, complete cds [NM_113304]

2,61	0.00427971	AT3G60840	MAP65-4	ref Arabidopsis thaliana microtubule-associated protein 65-4 mRNA, complete cds [NM_115948]
2,61	0.00455544	AT5G03120	AT5G03120	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_120390]
2,61	0.00021223	AT5G54610	ANK	ref Arabidopsis thaliana ankyrin repeat family protein mRNA, complete cds [NM_124842]
2,6	0.000059	AY334555	AY334555	gb Arabidopsis thaliana At4-2 mRNA, complete sequence [AY334555]
2,6	0.00136418	TA26504_3702	TA26504_3702	Unknown
2,6	0.02960598	TC314157	TC405945	tc Rep: Ubiquitin extension protein - Pyrus communis (Pear), partial (31%) [TC405945]
2,58	0.0135829	AT1G04010	PSAT1	ref Arabidopsis thaliana phospholipid sterol acyl transferase 1 mRNA, complete cds [NM_100282]
2,58	0.01058687	AT2G27840	HDT4	ref Arabidopsis thaliana histone deacetylase HDT4 mRNA, complete cds [NM_128344]
2,58	0.01475195	AT3G08950	AT3G08950	ref Arabidopsis thaliana copper chaperone SCO1-like protein HCC1 mRNA, complete cds [NM_111729]
2,58	0.01114229	AT5G05590	PAI1	ref Arabidopsis thaliana phosphoribosylanthranilate isomerase mRNA, complete cds [NM_001123771]
2,58	0.00015806	AT5G43150	AT5G43150	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_123681]
2,57	0.00034771	AT1G29930	CAB1	ref Arabidopsis thaliana chlorophyll A/B binding protein 1 mRNA, complete cds [NM_102733]
2,56	0.00029676	AT1G15820	LHCB6	ref Arabidopsis thaliana light harvesting complex photosystem II subunit 6 mRNA, complete cds [NM_101450]
2,55	0.0001476	AT1G21250	WAK1	ref Arabidopsis thaliana wall-associated receptor kinase 1 mRNA, complete cds [NM_101978]
2,55	0.00014918	AT3G14050	RSH2	ref Arabidopsis thaliana RelA-SpoT like protein RSH2 mRNA, complete cds [NM_112259]
2,55	0.00775697	AT4G34580	COW1	ref Arabidopsis thaliana phosphatidylinositol transfer protein COW1 mRNA, complete cds [NM_119624]
2,54	0.00155638	AT1G03820	AT1G03820	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_100261]
2,54	0.00057475	AT2G18730	DGK3	ref Arabidopsis thaliana diacylglycerol kinase 3 mRNA, complete cds [NM_179649]
2,53	0.00007257	AT1G01300	AT1G01300	ref Arabidopsis thaliana aspartyl protease family protein mRNA, complete cds [NM_100012]
2,53	0.00064126	AT1G29660	AT1G29660	ref Arabidopsis thaliana GDSL esterase/lipase mRNA, complete cds [NM_102706]
2,53	0.00025769	AT1G29910	CAB3	ref Arabidopsis thaliana chlorophyll A/B binding protein 3 mRNA, complete cds [NM_102731]
2,53	0.00019548	AT3G28480	AT3G28480	ref Arabidopsis thaliana oxoglutarate/iron-dependent oxygenase mRNA, complete cds [NM_001203065]
2,53	0.01370103	AT5G67100	ICU2	ref Arabidopsis thaliana DNA polymerase alpha catalytic subunit mRNA, complete cds [NM_126110]
2,52	0.01446036	AT2G29260	AT2G29260	ref Arabidopsis thaliana NAD(P)-binding Rossmann-fold superfamily protein mRNA, complete cds [NM_128482]
2,52	0.00174981	AT3G52630	AT3G52630	ref Arabidopsis thaliana Nucleic acid-binding, OB-fold-like protein mRNA, complete cds [NM_115123]
2,52	0.00021233	AT4G12880	ENODL19	ref Arabidopsis thaliana early nodulin-like protein 19 mRNA, complete cds [NM_001203782]
2,51	0.00020277	AT1G31690	AT1G31690	ref Arabidopsis thaliana copper amine oxidase family protein mRNA, complete cds [NM_102904]
2,51	0.00008969	AT2G23350	PAB4	ref Arabidopsis thaliana poly(A) binding protein 4 mRNA, complete cds [NM_127899]
2,51	0.03367699	AT3G56900	AT3G56900	ref Arabidopsis thaliana transducin/WD40 repeat-like superfamily protein mRNA, complete cds [NM_115549]
2,51	0.00283823	AT5G03670	AT5G03670	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_120448]
2,5	0.00018441	AT1G23100	AT1G23100	ref Arabidopsis thaliana GroES-like protein mRNA, complete cds [NM_102158]
2,49	0.00012448	AT4G33560	AT4G33560	ref Arabidopsis thaliana Wound-responsive family protein mRNA, complete cds [NM_119511]
2,49	0.0236102	AT5G60190	AT5G60190	ref Arabidopsis thaliana NEDD8-specific protease 1 mRNA, complete cds [NM_125412]
2,49	0.00138191	EG457990	EG457990	gb AYAWH62TF pooled cDNA populations Arabidopsis thaliana cDNA, mRNA sequence [EG457990]
2,48	0.0001484	AT1G65486	AT1G65486	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001124079]
2,48	0.01144066	AT2G25530	AT2G25530	ref Arabidopsis thaliana AFG1-like ATPase family protein mRNA, complete cds [NM_128110]
2,47	0.00022062	AT5G20740	AT5G20740	ref Arabidopsis thaliana plant invertase/pectin methylesterase inhibitor domain-containing protein mRNA, complete cds [NM_122081]
2,46	0.00027568	AT1G43910	AT1G43910	ref Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA, complete cds [NM_103518]
2,46	0.00149197	AT1G50590	AT1G50590	ref Arabidopsis thaliana Pirin-like protein mRNA, complete cds [NM_103941]
2,46	0.00083462	AT3G23120	RLP38	ref Arabidopsis thaliana receptor like protein 38 mRNA, complete cds [NM_113213]
2,45	0.0001679	AT3G45140	LOX2	ref Arabidopsis thaliana lipoxygenase 2 mRNA, complete cds [NM_114383]
2,45	0.00010041	AT4G36360	BGAL3	ref Arabidopsis thaliana beta-galactosidase 3 mRNA, complete cds [NM_119799]
2,45	0.02161668	AT5G60910	AGL8	ref Arabidopsis thaliana agamous-like MADS-box protein AGL8 mRNA, complete cds [NM_125484]
2,44	0.00567152	AT1G43800	AT1G43800	ref Arabidopsis thaliana acyl-[acyl-carrier-protein] desaturase 6 mRNA, complete cds [NM_103508]
2,44	0.00012238	AT1G73325	AT1G73325	ref Arabidopsis thaliana Kunitz family trypsin and protease inhibitor protein mRNA, complete cds [NM_105992]
2,44	0.00011532	AT1G76960	AT1G76960	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_106347]
2,44	0.00016522	AT2G22240	MIPS2	ref Arabidopsis thaliana myo-inositol-1-phosphate synthase 2 mRNA, complete cds [NM_127790]
2,44	0.00067266	AT5G05365	AT5G05365	ref Arabidopsis thaliana Heavy metal transport/detoxification superfamily protein mRNA, complete cds [NM_001085064]

2,43	0.00050832	AT1G01100	AT1G01100	ref Arabidopsis thaliana 60S acidic ribosomal protein P1-1 mRNA, complete cds [NM_001083970]
2,43	0.00447886	AT2G41340	RPB5D	ref Arabidopsis thaliana RNA polymerase II fifth largest subunit, D mRNA, complete cds [NM_129697]
2,43	0.0001297	AT3G44590	AT3G44590	ref Arabidopsis thaliana 60S acidic ribosomal protein P2-4 mRNA, complete cds [NM_114327]
2,43	0.00080226	AT5G13400	AT5G13400	ref Arabidopsis thaliana putative peptide/nitrate transporter mRNA, complete cds [NM_121343]
2,43	0.00314358	AT5G65880	AT5G65880	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125985]
2,42	0.00009553	AT1G04820	TUA4	ref Arabidopsis thaliana tubulin alpha-4 chain mRNA, complete cds [NM_100360]
2,42	0.00019776	AT1G47400	AT1G47400	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_103634]
2,42	0.02640446	TA46381_3702	TA46381_3702	Unknown
2,41	0.00023652	AT1G31230	AK-HSDH I	ref Arabidopsis thaliana bifunctional aspartokinase/homoserine dehydrogenase 1 mRNA, complete cds [NM_102861]
2,41	0.00049318	AT3G08580	AAC1	ref Arabidopsis thaliana ADP,ATP carrier protein 1 mRNA, complete cds [NM_180210]
2,41	0.00055583	AT4G12600	AT4G12600	ref Arabidopsis thaliana ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein mRNA, complete cds [NM_117330]
2,4	0.01222966	AT1G01710	AT1G01710	ref Arabidopsis thaliana acyl-CoA thioesterase family protein mRNA, complete cds [NM_100053]
2,4	0.00020305	AT1G74090	SOT18	ref Arabidopsis thaliana desulfo-glucosinolate sulfotransferase 18 mRNA, complete cds [NM_106069]
2,4	0.0007839	AT2G20820	AT2G20820	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_179675]
2,4	0.00060967	AT4G35180	LHT7	ref Arabidopsis thaliana LYS/HIS transporter 7 mRNA, complete cds [NM_119684]
2,39	0.00514866	AT1G13830	AT1G13830	ref Arabidopsis thaliana carbohydrate-binding X8 domain-containing protein mRNA, complete cds [NM_101251]
2,39	0.00029046	AT1G15520	PDR12	ref Arabidopsis thaliana ABC transporter G family member 40 mRNA, complete cds [NM_101421]
2,39	0.00412797	AT1G61120	TP504	ref Arabidopsis thaliana terpene synthase 04 mRNA, complete cds [NM_104793]
2,39	0.02272138	AT1G68430	AT1G68430	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_105514]
2,39	0.00862562	AT1G79460	GA2	ref Arabidopsis thaliana Ent-kaur-16-ene synthase mRNA, complete cds [NM_106594]
2,39	0.00942172	AT3G25100	CDC45	ref Arabidopsis thaliana cell division control protein 45 mRNA, complete cds [NM_113414]
2,39	0.00012372	AT4G36010	AT4G36010	ref Arabidopsis thaliana pathogenesis-related thaumatin family protein mRNA, complete cds [NM_001036715]
2,38	0.00128205	AT1G66940	AT1G66940	ref Arabidopsis thaliana protein kinase-related protein mRNA, complete cds [NM_001036167]
2,38	0.0002362	AT3G27570	AT3G27570	ref Arabidopsis thaliana sucrose/ferredoxin-like protein mRNA, complete cds [NM_113673]
2,38	0.00084733	AT4G35850	AT4G35850	ref Arabidopsis thaliana pentatricopeptide repeat-containing protein mRNA, complete cds [NM_119751]
2,37	0.02349645	AT1G13610	AT1G13610	ref Arabidopsis thaliana alpha/beta-hydrolase-like protein mRNA, complete cds [NM_001035965]
2,37	0.0031274	AT1G49860	GSTF14	ref Arabidopsis thaliana glutathione S-transferase (class phi) 14 mRNA, complete cds [NM_103873]
2,37	0.00015764	AT2G27710	AT2G27710	ref Arabidopsis thaliana 60S acidic ribosomal protein P2-2 mRNA, complete cds [NM_128330]
2,37	0.00024184	AT3G61920	AT3G61920	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_116057]
2,37	0.00026985	AT4G22880	LDOX	ref Arabidopsis thaliana leucoanthocyanidin dioxygenase mRNA, complete cds [NM_118417]
2,37	0.01529599	AT5G05680	MOS7	ref Arabidopsis thaliana protein MODIFIER OF SNC1,7 mRNA, complete cds [NM_120650]
2,37	0.0001897	AT5G47700	AT5G47700	ref Arabidopsis thaliana 60S acidic ribosomal protein P1-3 mRNA, complete cds [NM_001085259]
2,36	0.00969772	AT1G03270	AT1G03270	ref Arabidopsis thaliana CBS domain-containing protein mRNA, complete cds [NM_100209]
2,36	0.00017357	AT1G11700	AT1G11700	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_101042]
2,36	0.00011462	AT3G02570	MEE31	ref Arabidopsis thaliana mannose-6-phosphate isomerase mRNA, complete cds [NM_111125]
2,36	0.00151699	AT5G47930	AT5G47930	ref Arabidopsis thaliana 40S ribosomal protein S27-3 mRNA, complete cds [NM_124167]
2,36	0.0004156	AT5G55730	FLA1	ref Arabidopsis thaliana fasciclin-like arabinogalactan protein 1 mRNA, complete cds [NM_001203621]
2,35	0.00016684	AA597599	AA597599	Unknown
2,35	0.00056487	AT1G65290	mtACP2	ref Arabidopsis thaliana acyl carrier protein 2 mRNA, complete cds [NM_105202]
2,35	0.00057425	AT2G38750	ANNAT4	ref Arabidopsis thaliana annexin D4 mRNA, complete cds [NM_129432]
2,35	0.00043142	AT5G08760	AT5G08760	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001085080]
2,34	0.00069616	AT1G44800	AT1G44800	ref Arabidopsis thaliana bidirectional amino acid transporter SIAR1 mRNA, complete cds [NM_103561]
2,34	0.00028798	AT1G67750	AT1G67750	ref Arabidopsis thaliana putative pectate lyase 5 mRNA, complete cds [NM_105443]
2,34	0.00188415	AT2G17630	AT2G17630	ref Arabidopsis thaliana pyridoxal phosphate-dependent transferases superfamily protein mRNA, complete cds [NM_127317]
2,33	0.00798562	AT3G49750	RLP44	ref Arabidopsis thaliana receptor like protein 44 mRNA, complete cds [NM_114835]
2,32	0.00081013	AT1G73940	AT1G73940	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_106053]
2,32	0.02251984	AT2G34900	IMB1	ref Arabidopsis thaliana transcription factor GTE1 mRNA, complete cds [NM_201873]
2,32	0.00037877	AT3G23450	AT3G23450	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_113248]

2,32	0.00042085	AT3G23830	GRP4	ref Arabidopsis thaliana glycine-rich RNA-binding protein 4 mRNA, complete cds [NM_180298]
2,32	0.02169608	AT3G27170	CLC-B	ref Arabidopsis thaliana chloride channel protein CLC-b mRNA, complete cds [NM_113631]
2,32	0.00524152	AT3G58650	AT3G58650	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_115727]
2,32	0.00065315	AT3G61810	AT3G61810	ref Arabidopsis thaliana glycosyl hydrolase family 17 protein mRNA, complete cds [NM_116046]
2,32	0.00017249	AT4G27560	AT4G27560	ref Arabidopsis thaliana UDP-glycosyltransferase 79B2 mRNA, complete cds [NM_118891]
2,32	0.0006194	AT4G31810	AT4G31810	ref Arabidopsis thaliana ATP-dependent caseinolytic (Clp) protease/crotonase family protein mRNA, complete cds [NM_119331]
2,32	0.00228103	AT4G38950	AT4G38950	ref Arabidopsis thaliana ATP binding microtubule motor family protein mRNA, complete cds [NM_120055]
2,32	0.00012904	AT4G39730	AT4G39730	ref Arabidopsis thaliana Lipase/lipooxygenase, PLAT/LH2 family protein mRNA, complete cds [NM_120134]
2,31	0.00035686	AT1G31550	AT1G31550	ref Arabidopsis thaliana GDSL esterase/lipase mRNA, complete cds [NM_102894]
2,31	0.00174088	AT3G12870	AT3G12870	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_112123]
2,31	0.00050732	AT3G26960	AT3G26960	ref Arabidopsis thaliana pollen Ole e 1 allergen and extensin family protein mRNA, complete cds [NM_113610]
2,31	0.00030283	AT4G04570	CRK40	ref Arabidopsis thaliana cysteine-rich receptor-like protein kinase 40 mRNA, complete cds [NM_116695]
2,31	0.00067784	AT4G24010	CSLG1	ref Arabidopsis thaliana cellulose synthase-like protein G1 mRNA, complete cds [NM_118533]
2,31	0.02821422	AT5G43910	AT5G43910	ref Arabidopsis thaliana pfkB-like carbohydrate kinase family protein mRNA, complete cds [NM_123758]
2,3	0.00730231	AT1G74770	AT1G74770	ref Arabidopsis thaliana zinc ion binding protein mRNA, complete cds [NM_106135]
2,3	0.00438784	AT3G13650	AT3G13650	ref Arabidopsis thaliana disease resistance-resistance-responsive, dirigent domain-containing protein mRNA, complete cds [NM_112211]
2,3	0.0001447	AT3G49010	BBC1	ref Arabidopsis thaliana 60S ribosomal protein L13-1 mRNA, complete cds [NM_001035754]
2,3	0.02306009	AT3G49240	emb1796	ref Arabidopsis thaliana pentatricopeptide repeat-containing protein mRNA, complete cds [NM_114783]
2,3	0.00025106	AT3G57150	NAP57	ref Arabidopsis thaliana putative pseudouridine synthase NAP57 mRNA, complete cds [NM_115574]
2,3	0.00632522	AT3G62270	AT3G62270	ref Arabidopsis thaliana putative boron transporter 2 mRNA, complete cds [NM_116092]
2,3	0.00014854	AT4G25890	AT4G25890	ref Arabidopsis thaliana 60S acidic ribosomal protein P3-1 mRNA, complete cds [NM_118722]
2,29	0.01590047	AT1G51660	MKK4	ref Arabidopsis thaliana mitogen-activated protein kinase kinase 4 mRNA, complete cds [NM_104044]
2,29	0.00034657	AT2G25510	AT2G25510	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_128108]
2,29	0.03424227	AT2G43800	AT2G43800	ref Arabidopsis thaliana formin-like protein 2 mRNA, complete cds [NM_129942]
2,29	0.00065552	AT3G14210	ESM1	ref Arabidopsis thaliana epithiospecifier modifier 1 mRNA, complete cds [NM_112278]
2,29	0.00034992	AT3G15020	mMDH2	ref Arabidopsis thaliana malate dehydrogenase 2 mRNA, complete cds [NM_001084687]
2,29	0.00374336	AT3G18850	LPAT5	ref Arabidopsis thaliana lysophosphatidyl acyltransferase 5 mRNA, complete cds [NM_001084714]
2,29	0.00074618	AT3G22310	PMH1	ref Arabidopsis thaliana DEAD-box ATP-dependent RNA helicase mRNA, complete cds [NM_113129]
2,28	0.00377545	AT1G05730	AT1G05730	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_100453]
2,28	0.00067567	AT1G62800	ASP4	ref Arabidopsis thaliana aspartate aminotransferase 4 mRNA, complete cds [NM_179507]
2,28	0.02711816	AT2G14520	AT2G14520	ref Arabidopsis thaliana CBS and transporter associated domain-containing protein mRNA, complete cds [NM_127015]
2,28	0.00027364	AT3G21270	DOF2	ref Arabidopsis thaliana Dof zinc finger protein DOF2 mRNA, complete cds [NM_113022]
2,28	0.00873366	AT4G35840	AT4G35840	ref Arabidopsis thaliana NEP1-interacting protein 1 mRNA, complete cds [NM_119750]
2,28	0.00032037	AT5G07030	AT5G07030	ref Arabidopsis thaliana aspartyl protease family protein mRNA, complete cds [NM_120785]
2,28	0.00106616	AT5G47060	AT5G47060	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_124077]
2,27	0.02833406	AT1G25370	AT1G25370	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_102347]
2,27	0.00018477	AT1G65860	FMO GS-OX1	ref Arabidopsis thaliana flavin-containing monooxygenase FMO GS-OX1 mRNA, complete cds [NM_105258]
2,27	0.02662087	AT1G71100	RSW10	ref Arabidopsis thaliana ribose 5-phosphate isomerase A mRNA, complete cds [NM_105779]
2,27	0.00014831	AT2G36620	RPL24A	ref Arabidopsis thaliana 60S ribosomal protein L24-1 mRNA, complete cds [NM_129217]
2,27	0.00124828	AT4G08570	AT4G08570	ref Arabidopsis thaliana heavy-metal-associated domain-containing protein mRNA, complete cds [NM_116926]
2,27	0.00037563	AT4G21850	MSRB9	ref Arabidopsis thaliana methionine sulfoxide reductase B9 mRNA, complete cds [NM_179087]
2,27	0.00015237	AT4G26780	AR192	ref Arabidopsis thaliana molecular chaperone GrpE mRNA, complete cds [NM_118812]
2,27	0.00757344	AT5G15190	AT5G15190	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_180492]
2,27	0.00512214	AT5G44820	AT5G44820	ref Arabidopsis thaliana Nucleotide-diphospho-sugar transferase family protein mRNA, complete cds [NM_123850]
2,27	0.00049287	AT5G59670	AT5G59670	ref Arabidopsis thaliana Leucine-rich repeat protein kinase family protein mRNA, complete cds [NM_125359]
2,26	0.02743093	AT1G17455	ELF4-L4	ref Arabidopsis thaliana protein ELF4-like 4 mRNA, complete cds [NM_101607]
2,26	0.00507951	AT1G65560	AT1G65560	ref Arabidopsis thaliana zinc-binding dehydrogenase family protein mRNA, complete cds [NM_105230]
2,26	0.00015182	AT5G12110	AT5G12110	ref Arabidopsis thaliana elongation factor 1-beta 1 mRNA, complete cds [NM_121249]

2,26	0.00043298	AT5G25440	AT5G25440	ref Arabidopsis thaliana protein kinase family protein mRNA, complete cds [NM_122454]
2,26	0.00478345	TA28264_3702	TA28264_3702	Unknown
2,25	0.00016561	AT1G19570	DHAR1	ref Arabidopsis thaliana dehydroascorbate reductase mRNA, complete cds [NM_001084095]
2,25	0.00027153	AT1G56150	AT1G56150	ref Arabidopsis thaliana SAUR-like auxin-responsive protein mRNA, complete cds [NM_104494]
2,25	0.00019257	AT1G61580	RPL3B	ref Arabidopsis thaliana 60S ribosomal protein L3-2 mRNA, complete cds [NM_104840]
2,25	0.00029129	AT2G40765	AT2G40765	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_129639]
2,25	0.01057814	AT4G09820	TT8	ref Arabidopsis thaliana transcription factor TT8 mRNA, complete cds [NM_117050]
2,25	0.00016525	AT5G07460	PMSR2	ref Arabidopsis thaliana peptide methionine sulfoxide reductase A2 mRNA, complete cds [NM_120828]
2,25	0.00113371	AT5G20720	CPN20	ref Arabidopsis thaliana chaperonin 20 mRNA, complete cds [NM_180714]
2,25	0.0002675	TA26725_3702	TA26725_3702	tc Rep: LHC II Type III chlorophyll a /b binding protein - Brassica napus (Rape), partial (65%) [TC404282]
2,24	0.04094777	AT1G01260	AT1G01260	ref Arabidopsis thaliana transcription factor bHLH13 mRNA, complete cds [NM_001083971]
2,24	0.00385522	AT1G03310	DBE1	ref Arabidopsis thaliana Isoamylase 2 mRNA, complete cds [NM_202022]
2,24	0.02019373	AT1G13170	ORP1D	ref Arabidopsis thaliana oxysterol binding protein-related protein 1D mRNA, complete cds [NM_101187]
2,23	0.00019441	AT1G10370	ERD9	ref Arabidopsis thaliana glutathione S-transferase U17 mRNA, complete cds [NM_100911]
2,23	0.00021624	AT1G30530	UGT78D1	ref Arabidopsis thaliana UDP-glucosyl transferase 78D1 mRNA, complete cds [NM_102790]
2,23	0.00164649	AT1G74450	AT1G74450	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_106105]
2,23	0.03215644	AT2G33847	AT2G33847	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001084533]
2,23	0.00419552	AT3G24982	RPL40	ref Arabidopsis thaliana receptor like protein 40 mRNA, complete cds [NM_113404]
2,23	0.00021106	AT3G44990	XTR8	ref Arabidopsis thaliana xyloglucan endotransglucosylase/hydrolase mRNA, complete cds [NM_114368]
2,23	0.00018708	AT3G55120	TT5	ref Arabidopsis thaliana chalcone-flavonone isomerase 1 mRNA, complete cds [NM_115370]
2,23	0.0111866	AT4G08850	AT4G08850	ref Arabidopsis thaliana probable LRR receptor-like serine/threonine-protein kinase mRNA, complete cds [NM_116955]
2,23	0.00038796	AT4G12730	FLA2	ref Arabidopsis thaliana fasciclin-like arabinogalactan protein 2 mRNA, complete cds [NM_117342]
2,23	0.00033106	AT5G07690	MYB29	ref Arabidopsis thaliana myb domain protein 29 mRNA, complete cds [NM_120851]
2,23	0.00493549	AT5G08020	RPA70B	ref Arabidopsis thaliana RPA70-kDa subunit B mRNA, complete cds [NM_120884]
2,23	0.00192567	AT5G14700	AT5G14700	ref Arabidopsis thaliana Rossmann-fold NAD(P)-binding domain-containing protein mRNA, complete cds [NM_121474]
2,23	0.00115621	AT5G39580	AT5G39580	ref Arabidopsis thaliana peroxidase 62 mRNA, complete cds [NM_123320]
2,23	0.00033559	AT5G44720	AT5G44720	ref Arabidopsis thaliana molybdenum cofactor sulfurase family protein mRNA, complete cds [NM_123839]
2,23	0.00028772	AT5G60390	AT5G60390	ref Arabidopsis thaliana elongation factor 1-alpha 4 mRNA, complete cds [NM_001125992]
2,23	0.00445283	TC311297	NP230661	tc GB AB016870.1 BAB09313.1 gene_id:K15122.5~pir  T04855~similar to unknown protein [NP230661]
2,22	0.00036406	AT1G21440	AT1G21440	ref Arabidopsis thaliana phosphoenolpyruvate carboxylase family protein mRNA, complete cds [NM_101995]
2,22	0.0049067	AT2G40010	AT2G40010	ref Arabidopsis thaliana 60S acidic ribosomal protein P0-1 mRNA, complete cds [NM_129559]
2,22	0.00092588	AT4G02850	AT4G02850	ref Arabidopsis thaliana phenazine biosynthesis PhzC/PhzF family protein mRNA, complete cds [NM_116519]
2,22	0.00054385	AT4G19430	AT4G19430	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_118063]
2,22	0.00068098	AT5G03545	AT4	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_180427]
2,21	0.00030245	AT1G07000	EXO70B2	ref Arabidopsis thaliana exocyst subunit exo70 family protein B2 mRNA, complete cds [NM_100573]
2,21	0.00019596	AT1G64980	AT1G64980	ref Arabidopsis thaliana putative nucleotide-diphospho-sugar transferase mRNA, complete cds [NM_105172]
2,21	0.00024054	AT2G35190	NPSN11	ref Arabidopsis thaliana novel plant SNARE 11 mRNA, complete cds [NM_129072]
2,21	0.00044276	AT2G37040	PAL1	ref Arabidopsis thaliana phenylalanine ammonia-lyase 1 mRNA, complete cds [NM_129260]
2,21	0.00020601	AT4G02930	AT4G02930	ref Arabidopsis thaliana putative elongation factor Tu mRNA, complete cds [NM_116527]
2,21	0.01529312	AT5G40460	AT5G40460	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_123410]
2,21	0.000231	TC310952	A_84_P857309	Unknown
2,2	0.00156013	AT1G14320	SAC52	ref Arabidopsis thaliana 60S ribosomal protein L10-1 mRNA, complete cds [NM_101298]
2,2	0.00311615	AT1G23290	RPL27AB	ref Arabidopsis thaliana 60S ribosomal protein L27a-2 mRNA, complete cds [NM_102178]
2,2	0.00110778	AT1G55360	AT1G55360	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_104412]
2,2	0.02080813	AT4G25820	XTH14	ref Arabidopsis thaliana xyloglucan endotransglucosylase/hydrolase protein 14 mRNA, complete cds [NM_118714]
2,2	0.00397852	AT5G39790	AT5G39790	ref Arabidopsis thaliana putative starch binding scaffold protein mRNA, complete cds [NM_123342]
2,2	0.02263964	AT5G40540	AT5G40540	ref Arabidopsis thaliana protein kinase family protein mRNA, complete cds [NM_123418]
2,19	0.00042996	AT1G06550	AT1G06550	ref Arabidopsis thaliana 3-hydroxyisobutyryl-CoA hydrolase-like protein 5 mRNA, complete cds [NM_100534]



2,19	0.00121321	AT1G65900	AT1G65900	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_105262]
2,19	0.01911696	AT1G78650	POLD3	ref Arabidopsis thaliana DNA polymerase delta 3 mRNA, complete cds [NM_106512]
2,19	0.00053543	AT3G23810	SAHH2	ref Arabidopsis thaliana adenosylhomocysteinase 2 mRNA, complete cds [NM_113286]
2,19	0.00103605	AT3G62250	UBQ5	ref Arabidopsis thaliana ubiquitin-40S ribosomal protein S27a-3 mRNA, complete cds [NM_116090]
2,19	0.00448417	NP230932	NP230932	tc GB AB012243.1 BAB08891.1 gene_id:MIJ24.9~unknown protein [NP230932]
2,18	0.00026681	AT1G09590	AT1G09590	ref Arabidopsis thaliana 60S ribosomal protein L21-1 mRNA, complete cds [NM_100831]
2,18	0.00030216	AT1G14980	CPN10	ref Arabidopsis thaliana chaperonin 10 mRNA, complete cds [NM_101367]
2,18	0.00858678	AT2G15050	LTP	ref Arabidopsis thaliana non-specific lipid-transfer protein 7 mRNA, complete cds [NM_201737]
2,18	0.00174506	AT2G21870	MGP1	ref Arabidopsis thaliana mitochondrial F1F0-ATP synthase subunit Fad mRNA, complete cds [NM_179687]
2,18	0.00573048	AT3G56030	AT3G56030	ref Arabidopsis thaliana pentatricopeptide repeat-containing protein mRNA, complete cds [NM_115461]
2,17	0.0005025	AT1G29980	AT1G29980	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_202209]
2,17	0.00035683	AT1G41830	SKS6	ref Arabidopsis thaliana SKU5 similar 6 mRNA, complete cds [NM_103408]
2,17	0.00039121	AT3G06680	AT3G06680	ref Arabidopsis thaliana 60S ribosomal protein L29-2 mRNA, complete cds [NM_001125122]
2,17	0.04455145	AT3G12280	RBR1	ref Arabidopsis thaliana Retinoblastoma-related protein 1 mRNA, complete cds [NM_001202939]
2,17	0.00035401	AT3G44750	HDA3	ref Arabidopsis thaliana histone deacetylase HDT1 mRNA, complete cds [NM_114344]
2,17	0.00030415	AT4G03210	XTH9	ref Arabidopsis thaliana xyloglucan endotransglucosylase/hydrolase 9 mRNA, complete cds [NM_116559]
2,17	0.00033022	AT4G03926	PMEPCRA	ref Arabidopsis thaliana methylesterase PCR A mRNA, complete cds [NM_101031]
2,17	0.00071099	AT4G15258	BX841574	gb Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLSIL12ZA11 of Silique of strain col-0 of Arabidopsis thaliana (thale cress) [BX841
2,17	0.00213802	AT4G32800	AT4G32800	ref Arabidopsis thaliana ethylene-responsive transcription factor ERF043 mRNA, complete cds [NM_119433]
2,17	0.00033798	AT5G61170	AT5G61170	ref Arabidopsis thaliana 40S ribosomal protein S19-3 mRNA, complete cds [NM_125510]
2,17	0.01198684	ATMG00040	A_84_P770370	Unknown
2,16	0.00038922	AT1G72370	P40	ref Arabidopsis thaliana 40S ribosomal protein Sa-1 mRNA, complete cds [NM_001036190]
2,16	0.02318294	AT2G07696	AT2G07696	ref Arabidopsis thaliana ribosomal protein S7 mRNA, complete cds [NM_126746]
2,16	0.00082217	AT3G02230	RGP1	ref Arabidopsis thaliana UDP-arabinose mutase 1 mRNA, complete cds [NM_111090]
2,16	0.00053215	AT4G14680	APS3	ref Arabidopsis thaliana ATP sulfurylase mRNA, complete cds [NM_117550]
2,15	0.02885303	AT1G05620	URH2	ref Arabidopsis thaliana inosine nucleoside hydrolase mRNA, complete cds [NM_100442]
2,15	0.02934551	AT1G74890	ARR15	ref Arabidopsis thaliana two-component response regulator ARR15 mRNA, complete cds [NM_106147]
2,15	0.00089838	AT1G77120	ADH1	ref Arabidopsis thaliana alcohol dehydrogenase 1 mRNA, complete cds [NM_106362]
2,15	0.0393282	AT2G25880	AUR2	ref Arabidopsis thaliana serine/threonine-protein kinase aurora-2 mRNA, complete cds [NM_001124914]
2,15	0.00257168	AT3G52370	FLA15	ref Arabidopsis thaliana fasciclin-like arabinogalactan protein 15 mRNA, complete cds [NM_115097]
2,15	0.00039993	AT4G00360	CYP86A2	ref Arabidopsis thaliana cytochrome P450 86A2 mRNA, complete cds [NM_116260]
2,15	0.0037325	AT4G32870	AT4G32870	ref Arabidopsis thaliana SRPBC ligand-binding domain-containing protein mRNA, complete cds [NM_119440]
2,14	0.00074272	AT3G18600	AT3G18600	ref Arabidopsis thaliana DEAD-box ATP-dependent RNA helicase 51 mRNA, complete cds [NM_112746]
2,14	0.00078642	AT4G23810	WRKY53	ref Arabidopsis thaliana putative WRKY transcription factor 53 mRNA, complete cds [NM_118512]
2,14	0.00048372	AT4G37660	AT4G37660	ref Arabidopsis thaliana ribosomal protein L12/ ATP-dependent Clp protease adaptor protein mRNA, complete cds [NM_119929]
2,14	0.0012315	AT5G16250	AT5G16250	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_121630]
2,14	0.03370045	AT5G60930	AT5G60930	ref Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA, complete cds [NM_125486]
2,13	0.01815252	AK227527	AK227527	gb Arabidopsis thaliana mRNA for hypothetical protein, partial cds, clone: RAFL14-14-B17 [AK227527]
2,13	0.00030475	AT3G27230	AT3G27230	ref Arabidopsis thaliana S-adenosyl-L-methionine-dependent methyltransferase-like protein mRNA, complete cds [NM_113637]
2,13	0.00040234	AT4G00810	AT4G00810	ref Arabidopsis thaliana 60S acidic ribosomal protein P1-2 mRNA, complete cds [NM_116307]
2,13	0.03774359	AT4G37750	ANT	ref Arabidopsis thaliana AP2-like ethylene-responsive transcription factor ANT mRNA, complete cds [NM_119937]
2,13	0.027517	AT5G19470	NUDT24	ref Arabidopsis thaliana nudix hydrolase 24 mRNA, complete cds [NM_121952]
2,13	0.00407519	AT5G67150	AT5G67150	ref Arabidopsis thaliana HXXXD-type acyl-transferase-like protein mRNA, complete cds [NM_126115]
2,12	0.00292313	AT1G53645	AT1G53645	ref Arabidopsis thaliana hydroxyproline-rich glycoprotein family protein mRNA, complete cds [NM_104242]
2,12	0.01946319	AT1G72440	EDA25	ref Arabidopsis thaliana protein SLOW WALKER2 mRNA, complete cds [NM_105903]
2,12	0.00035152	AT2G25210	AT2G25210	ref Arabidopsis thaliana 60S ribosomal protein L39-1 mRNA, complete cds [NM_128078]
2,12	0.0160364	AT3G06435	AT3G06435	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_202508]
2,12	0.00571666	AT3G16870	GATA17	ref Arabidopsis thaliana GATA transcription factor 17 mRNA, complete cds [NM_112563]

2,12	0.00041307	AT3G43810	CAM7	ref Arabidopsis thaliana calmodulin 7 mRNA, complete cds [NM_114249]
2,12	0.00072133	AT3G51670	AT3G51670	ref Arabidopsis thaliana patellin-6 mRNA, complete cds [NM_115026]
2,12	0.03142202	AT4G00970	CRK41	ref Arabidopsis thaliana cysteine-rich receptor-like protein kinase 41 mRNA, complete cds [NM_116325]
2,12	0.00459871	AT4G15390	AT4G15390	ref Arabidopsis thaliana HXXXD-type acyl-transferase family protein mRNA, complete cds [NM_117627]
2,12	0.02185499	AT4G21930	AT4G21930	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_118314]
2,12	0.00042461	AT4G29735	AT4G29735	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001160804]
2,12	0.00033145	AT5G19240	AT5G19240	ref Arabidopsis thaliana GPI-anchored glycoprotein membrane precursor mRNA, complete cds [NM_121929]
2,11	0.01785962	AT1G63260	TET10	ref Arabidopsis thaliana tetraspanin10 mRNA, complete cds [NM_202348]
2,11	0.00034045	AT1G73040	AT1G73040	ref Arabidopsis thaliana Mannose-binding lectin superfamily protein mRNA, complete cds [NM_105962]
2,11	0.00065171	AT2G20585	NFD6	ref Arabidopsis thaliana nuclear fusion defective 6 mRNA, complete cds [NM_179671]
2,11	0.02244997	AT5G26680	AT5G26680	ref Arabidopsis thaliana flap endonuclease-1 mRNA, complete cds [NM_180546]
2,11	0.00076729	BP635770	BP635770	tc Rep: Uncharacterized protein At4g15000.2 - Arabidopsis thaliana (Mouse-ear cress), partial (86%) [TC405643]
2,1	0.00031397	AT1G19110	AT1G19110	ref Arabidopsis thaliana inter-alpha-trypsin inhibitor heavy chain-like protein mRNA, complete cds [NM_101769]
2,1	0.00062775	AT2G47880	AT2G47880	ref Arabidopsis thaliana glutaredoxin-C13 mRNA, complete cds [NM_130355]
2,1	0.00027315	AT3G14940	PPC3	ref Arabidopsis thaliana phosphoenolpyruvate carboxylase 3 mRNA, complete cds [NM_112356]
2,1	0.02096336	AT4G10630	AT4G10630	ref Arabidopsis thaliana Glutaredoxin family protein mRNA, complete cds [NM_117131]
2,1	0.00866676	AT4G16780	HB-2	ref Arabidopsis thaliana homeobox protein 2 mRNA, complete cds [NM_117780]
2,1	0.02063505	AT4G21750	ATML1	ref Arabidopsis thaliana homeobox-leucine zipper protein MERISTEM L1 mRNA, complete cds [NM_001036615]
2,1	0.04040983	AT5G20660	AT5G20660	ref Arabidopsis thaliana Zn-dependent exopeptidases superfamily protein mRNA, complete cds [NM_122073]
2,09	0.00037331	AT2G23010	SCPL9	ref Arabidopsis thaliana serine carboxypeptidase-like 9 mRNA, complete cds [NM_127866]
2,09	0.00208657	AT2G43570	CHI	ref Arabidopsis thaliana putative chitinase mRNA, complete cds [NM_129919]
2,09	0.0004624	AT3G54600	AT3G54600	ref Arabidopsis thaliana class I glutamine amidotransferase-like domain-containing protein mRNA, complete cds [NM_115317]
2,08	0.00158486	AT1G41880	AT1G41880	ref Arabidopsis thaliana 60S ribosomal protein L35a-2 mRNA, complete cds [NM_103411]
2,08	0.04050259	AT1G77460	AT1G77460	ref Arabidopsis thaliana armadillo/beta-catenin-like repeat and C2 domain-containing protein mRNA, complete cds [NM_106395]
2,08	0.00144296	AT3G08640	AT3G08640	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_111698]
2,08	0.00097198	AT5G19750	AT5G19750	ref Arabidopsis thaliana Mpv17/PMP22 family protein mRNA, complete cds [NM_121980]
2,08	0.00057325	AT5G56500	AT5G56500	ref Arabidopsis thaliana chaperonin 60 subunit beta 3 mRNA, complete cds [NM_125033]
2,07	0.0020639	AT1G03940	AT1G03940	ref Arabidopsis thaliana coumaroyl-CoA:anthocyanidin 3-O-glucoside-6-O-coumaroyltransferase 1 mRNA, complete cds [NM_100275]
2,07	0.00101107	AT2G43290	MSS3	ref Arabidopsis thaliana calmodulin-like protein MSS3 mRNA, complete cds [NM_129891]
2,07	0.00032401	AT2G44210	AT2G44210	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001036461]
2,07	0.0002987	AT3G05910	AT3G05910	ref Arabidopsis thaliana pectinacetyltransferase family protein mRNA, complete cds [NM_111465]
2,07	0.00078149	AT3G61820	AT3G61820	ref Arabidopsis thaliana aspartyl protease mRNA, complete cds [NM_116047]
2,06	0.00038354	AT2G15000	AT2G15000	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001084423]
2,06	0.00041639	AT2G37400	AT2G37400	ref Arabidopsis thaliana tetratricopeptide repeat domain-containing protein mRNA, complete cds [NM_129295]
2,06	0.0012856	AT2G39870	AT2G39870	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_129545]
2,06	0.00031066	AT3G13110	SERAT2;2	ref Arabidopsis thaliana serine acetyltransferase 2;2 mRNA, complete cds [NM_112150]
2,06	0.00035687	AT4G30800	AT4G30800	ref Arabidopsis thaliana 40S ribosomal protein S11-2 mRNA, complete cds [NM_119226]
2,06	0.00860515	AT5G27660	TC396188	tc Rep: serine-type peptidase/ trypsin - Arabidopsis thaliana, complete [TC396188]
2,06	0.00168653	AT5G49330	MYB111	ref Arabidopsis thaliana myb domain protein 111 mRNA, complete cds [NM_124310]
2,05	0.00143304	AT1G30510	RFNR2	ref Arabidopsis thaliana ferredoxin--NADP reductase, root isozyme 2 mRNA, complete cds [NM_102787]
2,05	0.00156123	AT2G31730	AT2G31730	ref Arabidopsis thaliana basic helix-loop-helix domain-containing protein mRNA, complete cds [NM_128731]
2,05	0.00045261	AT2G37710	RLK	ref Arabidopsis thaliana receptor lectin kinase mRNA, complete cds [NM_129327]
2,05	0.03347114	AT2G46700	CRK3	ref Arabidopsis thaliana CDPK-related kinase 3 mRNA, complete cds [NM_130235]
2,05	0.00045252	AT3G29320	PHS1	ref Arabidopsis thaliana alpha-glucan phosphorylase 1 mRNA, complete cds [NM_113857]
2,05	0.00321302	AT4G25810	XTR6	ref Arabidopsis thaliana probable xyloglucan endotransglucosylase/hydrolase protein 23 mRNA, complete cds [NM_118713]
2,05	0.00036582	AT5G04150	BHLH101	ref Arabidopsis thaliana transcription factor bHLH101 mRNA, complete cds [NM_120497]
2,05	0.01257187	AT5G09420	TOC64-V	ref Arabidopsis thaliana translocon at the outer membrane of chloroplasts 64-V mRNA, complete cds [NM_120979]
2,05	0.04068712	AT5G53570	AT5G53570	ref Arabidopsis thaliana RabGAP/TBC domain-containing protein mRNA, complete cds [NM_124737]

2,04	0.00149354	AT1G03170	AT1G03170	ref Arabidopsis thaliana protein FANTASTIC FOUR 2 mRNA, complete cds [NM_100199]
2,04	0.00038744	AT2G32990	GH9B8	ref Arabidopsis thaliana glycosyl hydrolase 9B8 mRNA, complete cds [NM_128859]
2,04	0.00164862	AT2G35790	AT2G35790	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_129137]
2,04	0.00512039	AT3G18290	BTS	ref Arabidopsis thaliana putative E3 ligase BRUTUS mRNA, complete cds [NM_112713]
2,04	0.02319215	AT3G25180	CYP82G1	ref Arabidopsis thaliana cytochrome P450, family 82, subfamily G, polypeptide 1 mRNA, complete cds [NM_113423]
2,04	0.00161151	AT3G27280	PHB4	ref Arabidopsis thaliana prohibitin 4 mRNA, complete cds [NM_113642]
2,04	0.00546466	AT4G04790	AT4G04790	ref Arabidopsis thaliana pentatricopeptide repeat-containing protein mRNA, complete cds [NM_116717]
2,04	0.00738858	AT5G10080	AT5G10080	ref Arabidopsis thaliana aspartyl protease family protein mRNA, complete cds [NM_121046]
2,04	0.00221288	AT5G15740	AT5G15740	ref Arabidopsis thaliana O-fucosyltransferase family protein mRNA, complete cds [NM_121579]
2,04	0.00138422	AT5G20790	AT5G20790	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_122086]
2,04	0.00323997	AT5G22100	AT5G22100	ref Arabidopsis thaliana RNA 3'-terminal phosphate cyclase-like protein mRNA, complete cds [NM_147891]
2,04	0.02294617	AT5G48240	AT5G48240	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_124199]
2,03	0.00394758	AT1G11545	XTH8	ref Arabidopsis thaliana probable xyloglucan endotransglucosylase/hydrolase protein 8 mRNA, complete cds [NM_101028]
2,03	0.00148733	AT1G15410	AT1G15410	ref Arabidopsis thaliana aspartate-glutamate racemase-like protein mRNA, complete cds [NM_101410]
2,03	0.04565078	AT1G75980	AT1G75980	ref Arabidopsis thaliana biotinyl-lipoyl domain-containing protein mRNA, complete cds [NM_106247]
2,03	0.00076568	AT1G78020	AT1G78020	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_106451]
2,03	0.00050651	AT3G09820	ADK1	ref Arabidopsis thaliana adenosine kinase 1 mRNA, complete cds [NM_202540]
2,03	0.03551466	AT3G09940	MDHAR	ref Arabidopsis thaliana monodehydroascorbate reductase (NADH) mRNA, complete cds [NM_111829]
2,03	0.0007477	AT4G17470	AT4G17470	ref Arabidopsis thaliana putative palmitoyl-protein thioesterase mRNA, complete cds [NM_001203824]
2,03	0.00051705	AT4G34700	AT4G34700	ref Arabidopsis thaliana NADH-ubiquinone oxidoreductase complex 1B22 mRNA, complete cds [NM_119636]
2,03	0.00104221	AT4G39260	CCR1	ref Arabidopsis thaliana glycine-rich RNA-binding protein 8 mRNA, complete cds [NM_179194]
2,03	0.00038404	AT5G15320	AT5G15320	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001085121]
2,03	0.00243973	AT5G39740	RPL5B	ref Arabidopsis thaliana 60S ribosomal protein L5-2 mRNA, complete cds [NM_001203510]
2,03	0.00403704	AT5G42530	AT5G42530	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_123618]
2,02	0.01251627	AT1G17830	AT1G17830	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_101646]
2,02	0.00925601	AT1G18840	IQD30	ref Arabidopsis thaliana protein IQ-domain 30 mRNA, complete cds [NM_101741]
2,02	0.00161575	AT1G22300	GRF10	ref Arabidopsis thaliana 14-3-3-like protein GF14 epsilon mRNA, complete cds [NM_179367]
2,02	0.00722229	AT2G02740	WHY3	ref Arabidopsis thaliana single-stranded DNA-binding protein WHY3 mRNA, complete cds [NM_126329]
2,02	0.0053893	AT2G11810	MGDC	ref Arabidopsis thaliana Monogalactosyldiacylglycerol synthase 3 mRNA, complete cds [NM_001124829]
2,02	0.00043886	AT3G02650	AT3G02650	ref Arabidopsis thaliana pentatricopeptide repeat-containing protein mRNA, complete cds [NM_111133]
2,02	0.03225086	AT3G13860	HSP60-3A	ref Arabidopsis thaliana heat shock protein 60-3A mRNA, complete cds [NM_112240]
2,02	0.00264554	AT3G47470	LHCA4	ref Arabidopsis thaliana chlorophyll a-b binding protein 4 mRNA, complete cds [NM_114615]
2,02	0.00167043	AT4G23130	CRK5	ref Arabidopsis thaliana cysteine-rich receptor-like protein kinase 5 mRNA, complete cds [NM_179094]
2,02	0.0085316	AT4G37170	AT4G37170	ref Arabidopsis thaliana pentatricopeptide repeat-containing protein mRNA, complete cds [NM_119880]
2,02	0.00063318	AT5G03650	SBE2.2	ref Arabidopsis thaliana 1,4-alpha-glucan branching enzyme mRNA, complete cds [NM_120446]
2,02	0.04649271	AT5G54880	AT5G54880	ref Arabidopsis thaliana DTW domain-containing protein mRNA, complete cds [NM_124870]
2,01	0.00050993	AT1G11580	PMEPCRA	ref Arabidopsis thaliana methylesterase PCR A mRNA, complete cds [NM_101031]
2,01	0.00044982	AT1G45201	TLL1	ref Arabidopsis thaliana triacylglycerol lipase-like 1 mRNA, complete cds [NM_179441]
2,01	0.00058315	AT2G29530	TIM10	ref Arabidopsis thaliana mitochondrial import inner membrane translocase subunit Tim10 mRNA, complete cds [NM_001161068]
2,01	0.00063339	AT4G04940	AT4G04940	ref Arabidopsis thaliana transducin/WD40 domain-containing protein mRNA, complete cds [NM_116732]
2,01	0.00691914	AT4G16444	AT4G16444	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_117741]
2,01	0.00319728	AT4G25630	FIB2	ref Arabidopsis thaliana mediator of RNA polymerase II transcription subunit 36a mRNA, complete cds [NM_118695]
2,01	0.01819316	AT4G36150	AT4G36150	ref Arabidopsis thaliana TIR-NBS-LRR class disease resistance protein mRNA, complete cds [NM_119782]
2,01	0.00040691	AT5G11200	AT5G11200	ref Arabidopsis thaliana DEAD-box ATP-dependent RNA helicase 56 mRNA, complete cds [NM_001161234]
2,01	0.04026186	AT5G65158	AT5G65158	ref Arabidopsis thaliana lipase/lipoxygenase, PLAT/LH2 family protein mRNA, complete cds [NM_001037069]
2	0.00064112	AT1G57660	AT1G57660	ref Arabidopsis thaliana 60S ribosomal protein L21-2 mRNA, complete cds [NM_104563]
2	0.00268287	AT2G29980	FAD3	ref Arabidopsis thaliana omega-3 fatty acid desaturase mRNA, complete cds [NM_179808]
2	0.00384509	AT4G17670	AT4G17670	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_117875]



2	0.00666761	AT4G21840	MSRB8	ref Arabidopsis thaliana methionine sulfoxide reductase B8 mRNA, complete cds [NM_118304]
2	0.00071106	AT4G30280	XTH18	ref Arabidopsis thaliana probable xyloglucan endotransglucosylase/hydrolase protein 18 mRNA, complete cds [NM_119174]
2	0.00938622	AT5G15840	CO	ref Arabidopsis thaliana zinc finger protein CONSTANS mRNA, complete cds [NM_001036810]
2	0.00284358	AT5G41140	AT5G41140	ref Arabidopsis thaliana Myosin heavy chain-related protein mRNA, complete cds [NM_001203517]
2	0.00053872	AT5G47870	AT5G47870	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_124161]
2	0.00050288	AT5G63530	FP3	ref Arabidopsis thaliana farnesylated protein 3 mRNA, complete cds [NM_125748]
2	0.00109194	TA28631_3702	TA28631_3702	tc Rep: 60S ribosomal protein L8-3 - Arabidopsis thaliana (Mouse-ear cross), partial (50%) [TC403246]
-2	0.00048291	AT1G21830	AT1G21830	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_102031]
-2	0.00330868	AT1G72610	GER1	ref Arabidopsis thaliana germin-like protein subfamily 3 member 1 mRNA, complete cds [NM_105920]
-2	0.0010663	AT2G01290	RPI2	ref Arabidopsis thaliana ribose 5-phosphate isomerase A mRNA, complete cds [NM_126190]
-2	0.00080248	AT3G52060	AT3G52060	ref Arabidopsis thaliana beta-1,6-N-acetylglucosaminyl transferase-like protein mRNA, complete cds [NM_115065]
-2	0.00041016	AT5G23660	MTN3	ref Arabidopsis thaliana bidirectional sugar transporter SWEET12 mRNA, complete cds [NM_122271]
-2,01	0.00042806	AT1G08550	NPQ1	ref Arabidopsis thaliana Violaxanthin de-epoxidase mRNA, complete cds [NM_100728]
-2,01	0.0003832	AT1G08980	AMI1	ref Arabidopsis thaliana amidase 1 mRNA, complete cds [NM_100769]
-2,01	0.00045785	AT1G20630	CAT1	ref Arabidopsis thaliana catalase 1 mRNA, complete cds [NM_101914]
-2,01	0.00037101	AT1G53210	AT1G53210	ref Arabidopsis thaliana Na <sup>+</sup> /Ca <sup>2+</sup> exchanger-like protein mRNA, complete cds [NM_104200]
-2,01	0.00038672	AT1G71140	AT1G71140	ref Arabidopsis thaliana MATE efflux family protein mRNA, complete cds [NM_105783]
-2,01	0.0014117	AT2G01520	MLP328	ref Arabidopsis thaliana MLP-like protein 328 mRNA, complete cds [NM_126213]
-2,01	0.00101704	AT2G29490	GSTU1	ref Arabidopsis thaliana glutathione S-transferase tau 1 mRNA, complete cds [NM_128503]
-2,01	0.00078038	AT2G30520	RPT2	ref Arabidopsis thaliana Root phototropism protein 2 mRNA, complete cds [NM_001036369]
-2,01	0.00059659	AT3G05160	AT3G05160	ref Arabidopsis thaliana sugar transporter ERD6-like 10 mRNA, complete cds [NM_001084642]
-2,01	0.00084524	AT4G14930	AT4G14930	ref Arabidopsis thaliana survival protein SurE-like phosphatase/nucleotidase mRNA, complete cds [NM_117579]
-2,01	0.0035632	AT4G15690	AT4G15690	ref Arabidopsis thaliana monothiol glutaredoxin-S5 mRNA, complete cds [NM_117660]
-2,01	0.00048619	AT4G33010	GLDP1	ref Arabidopsis thaliana glycine dehydrogenase [decarboxylating] 2 mRNA, complete cds [NM_001125634]
-2,01	0.0006531	AT5G59960	AT5G59960	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125389]
-2,02	0.00046498	AT1G01620	PIP1C	ref Arabidopsis thaliana aquaporin PIP1-3 mRNA, complete cds [NM_100044]
-2,02	0.00110662	AT1G74370	AT1G74370	ref Arabidopsis thaliana RING/U-box domain-containing protein mRNA, complete cds [NM_106097]
-2,02	0.00092568	AT2G21970	sep-02	ref Arabidopsis thaliana stress enhanced protein 2 mRNA, complete cds [NM_127766]
-2,02	0.00093393	AT2G24550	AT2G24550	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_128016]
-2,02	0.00115539	AT2G41100	TCH3	ref Arabidopsis thaliana calmodulin-like protein 4 mRNA, complete cds [NM_001202794]
-2,02	0.00113399	AT3G23170	AT3G23170	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_113218]
-2,02	0.00066098	AT5G05410	DREB2A	ref Arabidopsis thaliana dehydration-responsive element-binding protein 2A mRNA, complete cds [NM_120623]
-2,02	0.00039189	AT5G17000	AT5G17000	ref Arabidopsis thaliana zinc-binding dehydrogenase family protein mRNA, complete cds [NM_121706]
-2,02	0.00040008	AT5G24150	SQP1	ref Arabidopsis thaliana Squalene monooxygenase 5 mRNA, complete cds [NM_122320]
-2,02	0.00112691	AT5G26820	IREG3	ref Arabidopsis thaliana iron-regulated protein 3 mRNA, complete cds [NM_122564]
-2,02	0.0010192	AT5G48545	HINT3	ref Arabidopsis thaliana protein histidine triad nucleotide-binding 3 mRNA, complete cds [NM_203178]
-2,02	0.00037453	AT5G64240	MC3	ref Arabidopsis thaliana metacaspase 3 mRNA, complete cds [NM_180931]
-2,03	0.00038141	AT1G19000	AT1G19000	ref Arabidopsis thaliana myb family transcription factor mRNA, complete cds [NM_101757]
-2,03	0.00057858	AT1G78070	AT1G78070	ref Arabidopsis thaliana transducin/WD40 repeat-like superfamily protein mRNA, complete cds [NM_106456]
-2,03	0.00044104	AT2G28200	AT2G28200	ref Arabidopsis thaliana zinc finger protein ZAT5 mRNA, complete cds [NM_128380]
-2,03	0.00061935	AT3G20060	UBC19	ref Arabidopsis thaliana ubiquitin-conjugating enzyme E2 19 mRNA, complete cds [NM_112897]
-2,03	0.00060144	AT3G61440	CYS1	ref Arabidopsis thaliana cysteine synthase C1 mRNA, complete cds [NM_001084855]
-2,03	0.00557541	AT5G05860	UGT76C2	ref Arabidopsis thaliana cytokinin-N-glucosyltransferase 2 mRNA, complete cds [NM_120668]
-2,03	0.0030552	AT5G20630	GER3	ref Arabidopsis thaliana germin-like protein subfamily 3 member 3 mRNA, complete cds [NM_122070]
-2,04	0.00599604	AT3G15353	MT3	ref Arabidopsis thaliana metallothionein 3 mRNA, complete cds [NM_112401]
-2,04	0.00276094	AT3G25770	AOC2	ref Arabidopsis thaliana allene oxide cyclase 2 mRNA, complete cds [NM_113476]
-2,04	0.00092369	AT3G29035	NAC3	ref Arabidopsis thaliana NAC domain-containing protein 3 mRNA, complete cds [NM_113825]
-2,05	0.00193274	AT1G17990	AT1G18020	ref Arabidopsis thaliana putative 12-oxophytodienoate reductase-like protein 2B mRNA, complete cds [NM_179352]

-2,05	0.00040604	AT1G22370	UGT85A5	ref Arabidopsis thaliana UDP-glucosyl transferase 85A5 mRNA, complete cds [NM_102087]
-2,05	0.00082401	AT1G53280	AT1G53280	ref Arabidopsis thaliana DJ1-like protein B mRNA, complete cds [NM_104206]
-2,05	0.00131056	AT1G70410	BCA4	ref Arabidopsis thaliana beta carbonic anhydrase 4 mRNA, complete cds [NM_202390]
-2,05	0.03639845	AT2G40000	HSPRO2	ref Arabidopsis thaliana HS1 PRO-1 2-like protein mRNA, complete cds [NM_129558]
-2,05	0.00081702	AT3G14690	CYP72A15	ref Arabidopsis thaliana cytochrome P450, family 72, subfamily A, polypeptide 15 mRNA, complete cds [NM_112330]
-2,05	0.00095317	AT4G38810	AT4G38810	ref Arabidopsis thaliana SnRK2-interacting calcium sensor SCS mRNA, complete cds [NM_120041]
-2,06	0.00055096	AT1G03230	AT1G03230	ref Arabidopsis thaliana aspartyl protease-like protein mRNA, complete cds [NM_100205]
-2,06	0.00045491	AT1G73330	DR4	ref Arabidopsis thaliana protein drought-repressed 4 mRNA, complete cds [NM_105993]
-2,06	0.00064606	AT3G12120	FAD2	ref Arabidopsis thaliana omega-6 fatty acid desaturase mRNA, complete cds [NM_001084671]
-2,06	0.0010073	AT3G19850	AT3G19850	ref Arabidopsis thaliana phototropic-responsive NPH3 family protein mRNA, complete cds [NM_112875]
-2,06	0.0008652	AT3G53420	PIP2A	ref Arabidopsis thaliana aquaporin PIP2-1 mRNA, complete cds [NM_001035774]
-2,06	0.00068045	AT5G57345	AT5G57345	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125117]
-2,07	0.00158897	AT1G32540	L0L1	ref Arabidopsis thaliana protein L0L1 mRNA, complete cds [NM_179411]
-2,07	0.00114856	AT1G77210	STP14	ref Arabidopsis thaliana sugar transport protein 14 mRNA, complete cds [NM_106370]
-2,07	0.00053113	AT3G22210	AT3G22210	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_113118]
-2,07	0.00050681	AT3G45780	PHOT1	ref Arabidopsis thaliana phototropin 1 mRNA, complete cds [NM_001035737]
-2,08	0.00038338	AT1G32700	AT1G32700	ref Arabidopsis thaliana PLATZ transcription factor domain-containing protein mRNA, complete cds [NM_202224]
-2,08	0.00158345	AT1G58180	BCA6	ref Arabidopsis thaliana beta carbonic anhydrase 6 mRNA, complete cds [NM_001198330]
-2,08	0.00071952	AT2G45740	PEX11D	ref Arabidopsis thaliana peroxisomal membrane protein 11D mRNA, complete cds [NM_130137]
-2,08	0.00028602	AT3G26510	AT3G26510	ref Arabidopsis thaliana PB1_UP2 domain-containing protein mRNA, complete cds [NM_113558]
-2,08	0.00117034	AT4G25570	ACYB-2	ref Arabidopsis thaliana transmembrane ascorbate ferrireductase 1 mRNA, complete cds [NM_118689]
-2,08	0.00043484	AT5G35790	G6PD1	ref Arabidopsis thaliana glucose-6-phosphate dehydrogenase 1 mRNA, complete cds [NM_122970]
-2,08	0.000349	AT5G59400	AT5G59400	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125331]
-2,09	0.0002964	AT1G21670	AT1G21670	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_102016]
-2,09	0.00033653	AT1G22640	MYB3	ref Arabidopsis thaliana transcription factor MYB3 mRNA, complete cds [NM_102111]
-2,09	0.00247494	AT1G49032	AT1G49032	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001123985]
-2,09	0.00026655	AT2G48020	AT2G48020	ref Arabidopsis thaliana sugar transporter ERD6-like 7 mRNA, complete cds [NM_130369]
-2,09	0.00032933	AT4G34881	AT4G34881	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001125645]
-2,09	0.00035611	AT5G09660	PMDH2	ref Arabidopsis thaliana peroxisomal NAD-malate dehydrogenase 2 mRNA, complete cds [NM_121003]
-2,11	0.00059025	AT2G38230	PDX1.1	ref Arabidopsis thaliana Pyridoxal biosynthesis protein PDX1.1 mRNA, complete cds [NM_129380]
-2,11	0.00150873	AT4G21990	APR3	ref Arabidopsis thaliana 5'-adenylsulfate reductase 3 mRNA, complete cds [NM_118320]
-2,11	0.00718176	AT5G10250	DOT3	ref Arabidopsis thaliana putative BTB/POZ domain-containing protein DOT3 mRNA, complete cds [NM_121063]
-2,12	0.00026918	AT4G33150	AT4G33150	ref Arabidopsis thaliana lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme mRNA, complete cds [NM_001160811]
-2,12	0.00067626	AT5G09440	EXL4	ref Arabidopsis thaliana protein exordium like 4 mRNA, complete cds [NM_120981]
-2,13	0.00033834	AT1G76080	CDSP32	ref Arabidopsis thaliana thioredoxin-like protein CDSP32 mRNA, complete cds [NM_106257]
-2,13	0.00022819	AT1G77450	NAC032	ref Arabidopsis thaliana NAC domain containing protein 32 mRNA, complete cds [NM_106394]
-2,13	0.00721255	AT2G05440	GRP9	ref Arabidopsis thaliana glycine-rich protein 9 mRNA, complete cds [NM_001036253]
-2,13	0.00027248	AT3G01970	WRKY45	ref Arabidopsis thaliana WRKY DNA-binding protein 45 mRNA, complete cds [NM_111063]
-2,13	0.00026883	AT4G20360	RABE1b	ref Arabidopsis thaliana RAB GTPase homolog E1b mRNA, complete cds [NM_118155]
-2,13	0.0003903	AT4G36540	BEE2	ref Arabidopsis thaliana transcription factor BEE 2 mRNA, complete cds [NM_119817]
-2,13	0.00148225	AT5G22270	AT5G22270	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_122132]
-2,13	0.00049079	AT5G56550	OXS3	ref Arabidopsis thaliana protein OXIDATIVE STRESS 3 mRNA, complete cds [NM_125038]
-2,14	0.00044687	AT1G10150	AT1G10150	ref Arabidopsis thaliana Carbohydrate-binding protein mRNA, complete cds [NM_100889]
-2,14	0.00048603	AT1G23040	AT1G23040	ref Arabidopsis thaliana hydroxyproline-rich glycoprotein family protein mRNA, complete cds [NM_102152]
-2,14	0.00103152	AT4G34138	UGT73B1	ref Arabidopsis thaliana UDP-glucosyl transferase 73B1 mRNA, complete cds [NM_119576]
-2,14	0.00105976	AT5G18630	AT5G18630	ref Arabidopsis thaliana putative class 3 lipase mRNA, complete cds [NM_121868]
-2,14	0.00276951	AT5G44572	AT5G44572	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001085242]
-2,14	0.00031794	AT5G45410	AT5G45410	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_148091]

-2,14	0.00022654	AT5G67030	ABA1	ref Arabidopsis thaliana zeaxanthin epoxidase mRNA, complete cds [NM_126103]
-2,14	0.00352027	TA27560_3702	TA27560_3702	Unknown
-2,15	0.000234	AT2G17500	AT2G17500	ref Arabidopsis thaliana auxin efflux carrier family protein mRNA, complete cds [NM_179633]
-2,15	0.00027726	AT5G08410	FTRA2	ref Arabidopsis thaliana ferredoxin/thioredoxin reductase subunit A (variable subunit) 2 mRNA, complete cds [NM_120925]
-2,15	0.00047954	AT5G15850	COL1	ref Arabidopsis thaliana zinc finger protein CONSTANS-LIKE 1 mRNA, complete cds [NM_121590]
-2,16	0.00131557	AT1G22630	AT1G22630	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_102110]
-2,16	0.00040957	AT1G26220	AT1G26220	ref Arabidopsis thaliana GCN5-like N-acetyltransferase mRNA, complete cds [NM_102386]
-2,16	0.00049563	AT1G43790	TED6	ref Arabidopsis thaliana tracheary element differentiation-related 6 protein mRNA, complete cds [NM_103507]
-2,16	0.00048305	AT1G74020	SS2	ref Arabidopsis thaliana strictosidine synthase 2 mRNA, complete cds [NM_106061]
-2,16	0.00027581	AT1G79270	ECT8	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_106577]
-2,16	0.00023124	AT3G44880	ACD1	ref Arabidopsis thaliana pheophorbide A oxygenase mRNA, complete cds [NM_114357]
-2,16	0.00033043	AT5G62020	HSFB2A	ref Arabidopsis thaliana heat stress transcription factor B-2a mRNA, complete cds [NM_125595]
-2,17	0.00021983	AT1G21920	AT1G21920	ref Arabidopsis thaliana Histone H3 K4-specific methyltransferase SET7/9 family protein mRNA, complete cds [NM_102040]
-2,17	0.00101093	AT2G28190	CSD2	ref Arabidopsis thaliana copper/zinc superoxide dismutase 2 mRNA, complete cds [NM_128379]
-2,17	0.00023709	AT2G36895	AT2G36895	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_179941]
-2,17	0.00021811	AT2G37750	AT2G37750	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_129331]
-2,17	0.00033497	AT2G45850	AT2G45850	ref Arabidopsis thaliana AT hook motif DNA-binding family protein mRNA, complete cds [NM_130148]
-2,17	0.00059811	AT3G20340	AT3G20340	ref Arabidopsis thaliana paraquat downregulated protein mRNA, complete cds [NM_112925]
-2,17	0.00055567	AT5G23050	AAE17	ref Arabidopsis thaliana acyl-activating enzyme 17 mRNA, complete cds [NM_122211]
-2,18	0.00061132	AT2G26690	AT2G26690	ref Arabidopsis thaliana nitrate transporter 1.4 mRNA, complete cds [NM_179753]
-2,18	0.00071955	AT2G38210	PDX1L4	ref Arabidopsis thaliana putative PDX1-like protein 4 mRNA, complete cds [NM_129378]
-2,18	0.00035113	AT4G34530	CIB1	ref Arabidopsis thaliana cryptochrome-interacting basic-helix-loop-helix 1 mRNA, complete cds [NM_119618]
-2,18	0.00027334	AT5G24800	BZIP9	ref Arabidopsis thaliana basic leucine zipper 9 mRNA, complete cds [NM_122389]
-2,18	0.0003022	AT5G60360	ALP	ref Arabidopsis thaliana thiol protease aleurain mRNA, complete cds [NM_001085305]
-2,19	0.00025917	AT1G63180	UGE3	ref Arabidopsis thaliana UDP-glucose 4-epimerase mRNA, complete cds [NM_104996]
-2,19	0.00018851	AT2G15480	UGT73B5	ref Arabidopsis thaliana UDP-glucosyl transferase 73B5 mRNA, complete cds [NM_127108]
-2,19	0.00018382	AT3G03470	CYP89A9	ref Arabidopsis thaliana cytochrome P450, family 87, subfamily A, polypeptide 9 mRNA, complete cds [NM_111218]
-2,19	0.00056665	AT4G10120	ATSP54F	ref Arabidopsis thaliana probable sucrose-phosphate synthase 4 mRNA, complete cds [NM_001036532]
-2,19	0.00022557	AT4G36850	AT4G36850	ref Arabidopsis thaliana PQ-loop repeat family protein / transmembrane family protein mRNA, complete cds [NM_119849]
-2,2	0.00021269	AT1G16320	AT1G16320	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_101498]
-2,2	0.00018555	AT1G49650	AT1G49650	ref Arabidopsis thaliana probable carboxylesterase 4 mRNA, complete cds [NM_103853]
-2,2	0.00020812	AT4G32340	AT4G32340	ref Arabidopsis thaliana tetratricopeptide repeat domain-containing protein-like protein mRNA, complete cds [NM_119386]
-2,2	0.00094459	AT5G06860	PGIP1	ref Arabidopsis thaliana polygalacturonase inhibitor 1 mRNA, complete cds [NM_120769]
-2,2	0.00064492	AT5G65380	AT5G65380	ref Arabidopsis thaliana MATE efflux family protein mRNA, complete cds [NM_125936]
-2,21	0.00051958	AT1G13930	AT1G13930	ref Arabidopsis thaliana salt tolerance-related protein mRNA, complete cds [NM_101259]
-2,21	0.00028911	AT1G64380	AT1G64380	ref Arabidopsis thaliana ethylene-responsive transcription factor ERF061 mRNA, complete cds [NM_105113]
-2,21	0.00020474	AT1G65970	TPX2	ref Arabidopsis thaliana thioredoxin-dependent peroxidase 2 mRNA, complete cds [NM_105269]
-2,21	0.00236748	AT3G55630	DFD	ref Arabidopsis thaliana folypolyglutamate synthase 3 mRNA, complete cds [NM_115421]
-2,21	0.00019551	AT3G61060	PP2-A13	ref Arabidopsis thaliana phloem protein 2-A13 mRNA, complete cds [NM_202741]
-2,21	0.00041403	TC310419	TC402207	Unknown
-2,22	0.00030335	AT2G36080	AT2G36080	ref Arabidopsis thaliana B3 DNA-binding domain transcription factor mRNA, complete cds [NM_129167]
-2,22	0.00017695	AT4G05320	UBQ10	ref Arabidopsis thaliana polyubiquitin 10 mRNA, complete cds [NM_001084884]
-2,22	0.00018462	AT5G06690	WCRKC1	ref Arabidopsis thaliana WCRKC thioredoxin 1 mRNA, complete cds [NM_001036767]
-2,22	0.00041493	AT5G38510	AT5G38510	ref Arabidopsis thaliana rhomboid-related intramembrane serine protease-like protein mRNA, complete cds [NM_123212]
-2,23	0.00038564	AT1G52342	AT1G52342	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001123999]
-2,23	0.00046575	AT2G31560	AT2G31560	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_179838]
-2,23	0.00073191	AT3G23700	AT3G23700	ref Arabidopsis thaliana ribosomal protein S1-like RNA-binding domain-containing protein mRNA, complete cds [NM_113274]
-2,23	0.00023035	AT4G11320	AT4G11320	ref Arabidopsis thaliana putative cysteine proteinase mRNA, complete cds [NM_117203]

-2,23	0.00085073	AT5G43580	AT5G43580	ref Arabidopsis thaliana unusual seine protease inhibitor mRNA, complete cds [NM_123724]
-2,24	0.00018353	AT1G65930	ciCDH	ref Arabidopsis thaliana NADP+-dependent isocitrate dehydrogenase mRNA, complete cds [NM_105265]
-2,24	0.00321387	AT2G37130	AT2G37130	ref Arabidopsis thaliana peroxidase mRNA, complete cds [NM_001124989]
-2,24	0.00020567	AT4G18240	SS4	ref Arabidopsis thaliana starch synthase 4 mRNA, complete cds [NM_117934]
-2,24	0.00032223	BP799962	BP799962	gb BP799962 RAFL14 Arabidopsis thaliana cDNA clone RAFL23-13-C23 5', mRNA sequence [BP799962]
-2,25	0.00022038	AT1G19770	PUP14	ref Arabidopsis thaliana purine permease 14 mRNA, complete cds [NM_101833]
-2,25	0.00248907	AT1G26800	AT1G26800	ref Arabidopsis thaliana RING/U-box domain-containing protein mRNA, complete cds [NM_102444]
-2,25	0.00016161	AT1G30360	ERD4	ref Arabidopsis thaliana Early-responsive to dehydration stress protein (ERD4) mRNA, complete cds [NM_102773]
-2,25	0.00082605	AT1G53560	AT1G53560	ref Arabidopsis thaliana ribosomal protein L18ae family mRNA, complete cds [NM_104234]
-2,25	0.00021233	AT2G29310	AT2G29310	ref Arabidopsis thaliana tropinone reductase-like protein mRNA, complete cds [NM_001202703]
-2,26	0.00053186	AT1G09750	AT1G09750	ref Arabidopsis thaliana aspartyl protease-like protein mRNA, complete cds [NM_100847]
-2,26	0.00028671	AT4G15700	AT4G15700	ref Arabidopsis thaliana monothiol glutaredoxin-S3 mRNA, complete cds [NM_117661]
-2,26	0.00017011	AT4G21870	AT4G21870	ref Arabidopsis thaliana heat shock protein class V 15.4 mRNA, complete cds [NM_118308]
-2,26	0.0004374	AT4G34920	AT4G34920	ref Arabidopsis thaliana PLC-like phosphodiesterases superfamily protein mRNA, complete cds [NM_119658]
-2,27	0.0100381	AT1G69490	NAP	ref Arabidopsis thaliana NAC transcription factor protein family mRNA, complete cds [NM_105616]
-2,27	0.00015721	AT3G03150	AT3G03150	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_111185]
-2,27	0.00023474	AT3G16240	DELTA-TIP	ref Arabidopsis thaliana aquaporin TIP2-1 mRNA, complete cds [NM_112495]
-2,27	0.00029658	AT3G16770	EBP	ref Arabidopsis thaliana ethylene-responsive transcription factor RAP2-3 mRNA, complete cds [NM_112550]
-2,27	0.00017994	AT4G15545	AT4G15545	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_117645]
-2,27	0.00069645	AT4G33960	AT4G33960	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_119557]
-2,27	0.00036574	AT5G59540	AT5G59540	ref Arabidopsis thaliana oxidoreductase, 2OG-Fe(II) oxygenase family protein mRNA, complete cds [NM_125346]
-2,27	0.0001657	AT5G63190	AT5G63190	ref Arabidopsis thaliana MA3 domain-containing protein mRNA, complete cds [NM_125714]
-2,28	0.00041534	AT1G15010	AT1G15010	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_101370]
-2,28	0.00026395	AT2G18050	HIS1-3	ref Arabidopsis thaliana histone H1-3 mRNA, complete cds [NM_127361]
-2,29	0.00054426	AT1G70580	AOAT2	ref Arabidopsis thaliana glutamate--glyoxylate aminotransferase 2 mRNA, complete cds [NM_202393]
-2,29	0.00071751	AT1G70790	AT1G70790	ref Arabidopsis thaliana calcium-dependent lipid-binding domain-containing protein mRNA, complete cds [NM_179543]
-2,29	0.00024541	AT1G70850	MLP34	ref Arabidopsis thaliana MLP-like protein 34 mRNA, complete cds [NM_001036188]
-2,29	0.00035827	AT4G28080	AT4G28080	ref Arabidopsis thaliana tetratricopeptide repeat domain protein mRNA, complete cds [NM_118947]
-2,29	0.00047625	AT4G37540	LBD39	ref Arabidopsis thaliana LOB domain-containing protein 39 mRNA, complete cds [NM_119918]
-2,29	0.0001635	AT5G48485	DIR1	ref Arabidopsis thaliana putative lipid-transfer protein DIR1 mRNA, complete cds [NM_124224]
-2,29	0.00023882	AT5G59750	AT5G59750	ref Arabidopsis thaliana monofunctional riboflavin biosynthesis protein RIBA 3 mRNA, complete cds [NM_001203642]
-2,29	0.0002732	AT5G60680	AT5G60680	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125461]
-2,3	0.00019762	AT4G34131	UGT73B3	ref Arabidopsis thaliana UDP-glucosyl transferase 73B3 mRNA, complete cds [NM_119574]
-2,31	0.00074724	AT1G60950	FED A	ref Arabidopsis thaliana ferredoxin-2 mRNA, complete cds [NM_104775]
-2,31	0.00023584	AT2G32540	CSLB04	ref Arabidopsis thaliana cellulose synthase-like protein B4 mRNA, complete cds [NM_128813]
-2,31	0.00013565	AT4G22200	KT2/3	ref Arabidopsis thaliana potassium channel AKT2/3 mRNA, complete cds [NM_118342]
-2,32	0.00016682	AT3G12345	AT3G12345	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001035602]
-2,32	0.00019667	AT4G28240	AT4G28240	ref Arabidopsis thaliana putative wound-responsive protein mRNA, complete cds [NM_118964]
-2,32	0.00203414	AT5G46110	APE2	ref Arabidopsis thaliana triose phosphate/phosphate translocator TPT mRNA, complete cds [NM_001036940]
-2,33	0.00018632	AT1G54500	AT1G54500	ref Arabidopsis thaliana rubredoxin-like protein mRNA, complete cds [NM_104328]
-2,33	0.00033816	AT1G54780	TLP18.3	ref Arabidopsis thaliana thylakoid lumen protein 18.3 mRNA, complete cds [NM_104353]
-2,33	0.00015927	AT3G25690	CHUP1	ref Arabidopsis thaliana protein CHUP1 mRNA, complete cds [NM_113468]
-2,33	0.00040881	AT5G48490	AT5G48490	ref Arabidopsis thaliana bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein mRNA, complete cds [NM_124225]
-2,33	0.00026748	AT5G51070	ERD1	ref Arabidopsis thaliana chaperone protein ClpD mRNA, complete cds [NM_124486]
-2,34	0.00016343	AT1G66330	AT1G66330	ref Arabidopsis thaliana putative senescence-associated protein mRNA, complete cds [NM_202366]
-2,34	0.00019264	AT3G15840	PIFI	ref Arabidopsis thaliana post-illumination chlorophyll fluorescence increase protein mRNA, complete cds [NM_001035630]
-2,34	0.00021753	AT3G53800	Fes1B	ref Arabidopsis thaliana hsp70-interacting protein FES1B-like protein mRNA, complete cds [NM_115240]
-2,35	0.00069438	AT1G09340	CRB	ref Arabidopsis thaliana chloroplast stem-loop binding protein mRNA, complete cds [NM_100804]

-2,35	0.0007816	AT3G05936	AT3G05936	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001125114]
-2,35	0.00028233	AT3G13061	A_84_P762845	Unknown
-2,35	0.00038483	AT5G40450	AT5G40450	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_123409]
-2,36	0.0001392	AT3G23880	AT3G23880	ref Arabidopsis thaliana F-box/kelch-repeat protein mRNA, complete cds [NM_113293]
-2,36	0.0001324	AT5G35630	GS2	ref Arabidopsis thaliana glutamine synthetase 2 mRNA, complete cds [NM_122954]
-2,36	0.00012055	AT5G57655	AT5G57655	ref Arabidopsis thaliana xylose isomerase mRNA, complete cds [NM_180872]
-2,36	0.00107079	DR225970	DR225970	tc Rep: Phospholipid hydroperoxide glutathione peroxidase 1, chloroplast precursor - Arabidopsis thaliana (Mouse-ear cress), partial (53%) [TC391272]
-2,37	0.00038713	AT1G76110	AT1G76110	ref Arabidopsis thaliana high mobility group B protein 9 mRNA, complete cds [NM_106260]
-2,37	0.00011491	AT2G39800	P5CS1	ref Arabidopsis thaliana delta1-pyrroline-5-carboxylate synthase 1 mRNA, complete cds [NM_001202785]
-2,37	0.00065326	AT3G25830	TPS-CIN	ref Arabidopsis thaliana 1,8-cineole synthase mRNA, complete cds [NM_113485]
-2,37	0.00013221	AT3G46130	MYB48	ref Arabidopsis thaliana transcription factor MYB48 mRNA, complete cds [NM_114482]
-2,37	0.00022048	AT4G04040	MEE51	ref Arabidopsis thaliana pyrophosphate--fructose-6-phosphate 1-phosphotransferase mRNA, complete cds [NM_116642]
-2,37	0.00020203	AT5G14570	NRT2.7	ref Arabidopsis thaliana high affinity nitrate transporter 2.7 mRNA, complete cds [NM_121461]
-2,37	0.00029858	AT5G25190	AT5G25190	ref Arabidopsis thaliana ethylene-responsive transcription factor ERF003 mRNA, complete cds [NM_122428]
-2,37	0.00013332	TA30874_3702	TA30874_3702	Unknown
-2,38	0.00047507	AT2G37170	PIP2B	ref Arabidopsis thaliana aquaporin PIP2-2 mRNA, complete cds [NM_129273]
-2,38	0.00010188	AT3G51400	AT3G51400	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_114999]
-2,38	0.00011711	AT5G48180	NSP5	ref Arabidopsis thaliana nitrile specifier protein 5 mRNA, complete cds [NM_124193]
-2,38	0.00040592	AT5G58770	AT5G58770	ref Arabidopsis thaliana dehydrodolichyl diphosphate synthase 2 mRNA, complete cds [NM_125264]
-2,38	0.00012253	AT5G62350	AT5G62350	ref Arabidopsis thaliana plant invertase/pectin methylesterase inhibitor superfamily protein mRNA, complete cds [NM_125629]
-2,39	0.0013498	AT1G21130	AT1G21130	ref Arabidopsis thaliana Indole glucosinolate O-methyltransferase 4 mRNA, complete cds [NM_101967]
-2,39	0.00014297	AT1G60140	TPS10	ref Arabidopsis thaliana putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10 mRNA, complete cds [NM_104705]
-2,39	0.00021209	AT3G12780	PGK1	ref Arabidopsis thaliana phosphoglycerate kinase 1 mRNA, complete cds [NM_112114]
-2,39	0.00023978	AT4G38470	AT4G38470	ref Arabidopsis thaliana ACT-like protein tyrosine kinase family protein mRNA, complete cds [NM_120008]
-2,39	0.00047955	AT5G17310	UGP2	ref Arabidopsis thaliana UTP--glucose-1-phosphate uridylyltransferase 1 mRNA, complete cds [NM_180506]
-2,4	0.00010801	AT1G62180	APR2	ref Arabidopsis thaliana 5'-adenylsulfate reductase 2 mRNA, complete cds [NM_001198364]
-2,4	0.00011643	AT1G73830	BEE3	ref Arabidopsis thaliana transcription factor BEE 3 mRNA, complete cds [NM_106043]
-2,4	0.00015089	AT3G62260	AT3G62260	ref Arabidopsis thaliana putative protein phosphatase 2C 49 mRNA, complete cds [NM_116091]
-2,4	0.00029826	AT4G03280	PETC	ref Arabidopsis thaliana cytochrome b6-f complex iron-sulfur subunit mRNA, complete cds [NM_178964]
-2,4	0.00011338	AT4G36040	AT4G36040	ref Arabidopsis thaliana chaperone protein dnaJ 11 mRNA, complete cds [NM_119771]
-2,4	0.00010023	AT5G67420	LBD37	ref Arabidopsis thaliana LOB domain-containing protein 37 mRNA, complete cds [NM_126142]
-2,4	0.00183026	TA28892_3702	TA28892_3702	Unknown
-2,41	0.00016636	AT3G19800	AT3G19800	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001125194]
-2,41	0.00009428	AT3G53990	AT3G53990	ref Arabidopsis thaliana Adenine nucleotide alpha hydrolases-like superfamily protein mRNA, complete cds [NM_202698]
-2,42	0.00036465	AT3G05880	RCI2A	ref Arabidopsis thaliana Hydrophobic protein RCI2A mRNA, complete cds [NM_111462]
-2,42	0.0002525	AT3G52480	AT3G52480	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_115108]
-2,42	0.00056717	AT4G01026	PYL7	ref Arabidopsis thaliana abscisic acid receptor PYL7 mRNA, complete cds [NM_116332]
-2,42	0.00016303	AT5G11070	AT5G11070	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_121145]
-2,42	0.00038168	TA28495_3702	TA28495_3702	Unknown
-2,43	0.00028675	AT1G20470	AT1G20470	ref Arabidopsis thaliana SAUR-like auxin-responsive protein mRNA, complete cds [NM_101897]
-2,44	0.0001581	AT2G37770	AT2G37770	ref Arabidopsis thaliana aldo-keto reductase family 4 member C9 mRNA, complete cds [NM_001036428]
-2,44	0.00010855	NP229859	NP229859	tc GB AL391141.1 CAC01711.1 quinone oxidoreductase-like protein [NP229859]
-2,46	0.00017105	AT1G55850	CSLE1	ref Arabidopsis thaliana cellulose synthase-like protein E1 mRNA, complete cds [NM_104462]
-2,46	0.00011444	AT1G72680	CAD1	ref Arabidopsis thaliana cinnamyl-alcohol dehydrogenase mRNA, complete cds [NM_105927]
-2,46	0.00013552	AT2G43820	UGT74F2	ref Arabidopsis thaliana UDP-glucosyltransferase 74F2 mRNA, complete cds [NM_129944]
-2,46	0.00019347	AT4G04330	AT4G04330	ref Arabidopsis thaliana Chaperonin-like RbcX protein mRNA, complete cds [NM_116671]
-2,47	0.00015345	AT5G16980	AT5G16980	ref Arabidopsis thaliana zinc-binding dehydrogenase family protein mRNA, complete cds [NM_121704]
-2,48	0.00012328	AT4G02380	SAG21	ref Arabidopsis thaliana senescence-associated protein SAG21 mRNA, complete cds [NM_116471]

-2,49	0.00018426	AT1G25230	AT1G25230	ref Arabidopsis thaliana Calcineurin-like metallo-phosphoesterase superfamily protein mRNA, complete cds [NM_102332]
-2,49	0.00010872	AT4G13830	J20	ref Arabidopsis thaliana chaperone protein dnaJ 20 mRNA, complete cds [NM_117457]
-2,49	0.00045827	AT4G15550	IAGLU	ref Arabidopsis thaliana UDP-glucose:indole-3-acetate beta-D-glucosyltransferase mRNA, complete cds [NM_117646]
-2,49	0.00020584	AT5G06870	PGIP2	ref Arabidopsis thaliana polygalacturonase inhibitor 2 mRNA, complete cds [NM_120770]
-2,49	0.00007716	AT5G14120	AT5G14120	ref Arabidopsis thaliana major facilitator protein mRNA, complete cds [NM_121416]
-2,49	0.00021822	TA43156_3702	TA43156_3702	tc Rep: Nitrile hydratase alpha chain - uncultured bacterium Dr1, partial (18%) [TC397555]
-2,5	0.0001099	AT2G25450	AT2G25450	ref Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate oxidase-like protein mRNA, complete cds [NM_128102]
-2,5	0.00008861	AT3G13062	AT3G13062	ref Arabidopsis thaliana polyketide cyclase/dehydrase and lipid transport superfamily protein mRNA, complete cds [NM_180243]
-2,5	0.00012382	AT3G23080	AT3G23080	ref Arabidopsis thaliana polyketide cyclase/dehydrase and lipid transport superfamily protein mRNA, complete cds [NM_113208]
-2,52	0.00016158	AT1G66200	GSR2	ref Arabidopsis thaliana glutamine synthetase mRNA, complete cds [NM_001198398]
-2,52	0.00008009	AT2G20670	AT2G20670	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_127631]
-2,52	0.00009927	AT3G47430	PEX11B	ref Arabidopsis thaliana peroxisomal membrane protein 11B mRNA, complete cds [NM_114611]
-2,52	0.00023336	AT5G63470	NF-YC4	ref Arabidopsis thaliana nuclear transcription factor Y subunit C-4 mRNA, complete cds [NM_125742]
-2,53	0.00096031	AT3G07350	AT3G07350	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_111614]
-2,53	0.00022658	AT5G24420	PGL5	ref Arabidopsis thaliana 6-phosphogluconolactonase 5 mRNA, complete cds [NM_122350]
-2,54	0.00007583	AT1G64860	SIGA	ref Arabidopsis thaliana RNA polymerase sigma subunit 1 mRNA, complete cds [NM_001198385]
-2,55	0.00009417	AT1G18810	AT1G18810	ref Arabidopsis thaliana protein phytochrome kinase substrate 3 mRNA, complete cds [NM_101739]
-2,55	0.0001087	AT1G72900	AT1G72900	ref Arabidopsis thaliana Toll-Interleukin-Resistance domain-containing protein mRNA, complete cds [NM_105948]
-2,55	0.0023918	AT1G76600	AT1G76600	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_106310]
-2,56	0.00009281	AT2G36950	AT2G36950	ref Arabidopsis thaliana heavy-metal-associated domain-containing protein mRNA, complete cds [NM_129251]
-2,56	0.00008	AT2G41560	ACA4	ref Arabidopsis thaliana autoinhibited Ca(2+)-ATPase 4 mRNA, complete cds [NM_129719]
-2,56	0.00016947	AT4G16190	AT4G16190	ref Arabidopsis thaliana papain family cysteine protease mRNA, complete cds [NM_117715]
-2,56	0.0001301	AT4G26555	AT4G26555	ref Arabidopsis thaliana FKBP-like peptidyl-prolyl cis-trans isomerase family protein mRNA, complete cds [NM_118789]
-2,57	0.00015685	AT2G15020	AT2G15020	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_127064]
-2,58	0.00025913	AT1G62380	ACO2	ref Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate oxidase 2 mRNA, complete cds [NM_104918]
-2,58	0.00009753	AT3G23030	IAA2	ref Arabidopsis thaliana auxin-responsive protein IAA2 mRNA, complete cds [NM_113203]
-2,58	0.00011318	AT4G38540	AT4G38540	ref Arabidopsis thaliana FAD/NAD(P)-binding oxidoreductase family protein mRNA, complete cds [NM_120015]
-2,58	0.00007975	AT5G17300	RVE1	ref Arabidopsis thaliana myb family transcription factor RVE1 mRNA, complete cds [NM_121736]
-2,6	0.0002396	AT3G23550	AT3G23550	ref Arabidopsis thaliana MATE efflux family protein LAL5 mRNA, complete cds [NM_113258]
-2,6	0.00090383	AT4G00750	AT4G00750	ref Arabidopsis thaliana putative methyltransferase PMT15 mRNA, complete cds [NM_116300]
-2,6	0.0000617	AT5G15500	AT5G15500	ref Arabidopsis thaliana ankyrin repeat-containing protein mRNA, complete cds [NM_180494]
-2,61	0.00006225	AT3G26650	GAPA	ref Arabidopsis thaliana glyceraldehyde-3-phosphate dehydrogenase A subunit mRNA, complete cds [NM_113576]
-2,61	0.00006773	AT3G48990	AT3G48990	ref Arabidopsis thaliana 4-coumarate--CoA ligase-like 10 mRNA, complete cds [NM_114758]
-2,61	0.00006701	AT5G65870	PSK5	ref Arabidopsis thaliana putative phytoalkylkinase 5 precursor mRNA, complete cds [NM_125984]
-2,61	0.00036365	AT5G66490	AT5G66490	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_126047]
-2,61	0.00011676	TA37874_3702	TA37874_3702	Unknown
-2,62	0.00020326	AT1G11530	CXXS1	ref Arabidopsis thaliana monocysteinic thioredoxin CXXS1 mRNA, complete cds [NM_101026]
-2,62	0.00005561	AT2G01850	EXGT-A3	ref Arabidopsis thaliana endoxyloglucan transferase A3 mRNA, complete cds [NM_126246]
-2,62	0.00014645	AT2G03310	AT2G03310	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_126382]
-2,62	0.00012093	AT2G29090	CYP707A2	ref Arabidopsis thaliana abscisic acid 8'-hydroxylase 2 mRNA, complete cds [NM_128466]
-2,62	0.00007219	AT5G61440	ACHT5	ref Arabidopsis thaliana atypical CYS HIS rich thioredoxin 5 mRNA, complete cds [NM_125537]
-2,62	0.00033451	T43901	T43901	tc Rep: Uncharacterized protein At2g45960.3 - Arabidopsis thaliana (Mouse-ear cress), partial (26%) [TC397989]
-2,63	0.00046288	AT1G70780	AT1G70780	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_105746]
-2,63	0.00005649	AT3G29240	AT3G29240	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_180317]
-2,65	0.00010726	AT1G13990	AT1G13990	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001160863]
-2,65	0.00033474	AT1G21680	AT1G21680	ref Arabidopsis thaliana DPP6 N-terminal domain-like protein mRNA, complete cds [NM_102017]
-2,65	0.00100242	AT1G32060	PRK	ref Arabidopsis thaliana phosphoribulokinase mRNA, complete cds [NM_102940]
-2,65	0.00220944	AT1G79700	AT1G79700	ref Arabidopsis thaliana AP2-like ethylene-responsive transcription factor WRI4 mRNA, complete cds [NM_001084380]



-2,66	0.00005102	AT1G27290	AT1G27290	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001084133]
-2,66	0.00022177	AT1G53870	AT1G53870	ref Arabidopsis thaliana TUB_2 domain-containing protein mRNA, complete cds [NM_104264]
-2,66	0.00009889	AT5G63790	NAC102	ref Arabidopsis thaliana NAC domain-containing protein 102 mRNA, complete cds [NM_125774]
-2,67	0.00015252	AT2G36320	AT2G36320	ref Arabidopsis thaliana zinc finger A20 and AN1 domain-containing stress-associated protein 4 mRNA, complete cds [NM_129189]
-2,68	0.00005629	AT2G22980	SCPL13	ref Arabidopsis thaliana serine carboxypeptidase-like 13 mRNA, complete cds [NM_001036325]
-2,69	0.00011786	AT1G19740	AT1G19740	ref Arabidopsis thaliana ATP-dependent protease La domain-containing protein mRNA, complete cds [NM_101830]
-2,69	0.00005653	AT1G68190	AT1G68190	ref Arabidopsis thaliana putative zinc finger protein mRNA, complete cds [NM_105490]
-2,69	0.00012306	AT3G50560	AT3G50560	ref Arabidopsis thaliana Rossmann-fold NAD(P)-binding domain-containing protein mRNA, complete cds [NM_114916]
-2,69	0.00011306	AT4G12320	CYP706A6	ref Arabidopsis thaliana cytochrome P450, family 706, subfamily A, polypeptide 6 mRNA, complete cds [NM_117302]
-2,7	0.00020105	AT1G20440	COR47	ref Arabidopsis thaliana dehydrin COR47 mRNA, complete cds [NM_101894]
-2,7	0.0000448	AT1G75460	AT1G75460	ref Arabidopsis thaliana ATP-dependent protease La domain-containing protein mRNA, complete cds [NM_106200]
-2,7	0.00013678	AT2G44920	AT2G44920	ref Arabidopsis thaliana thylakoid lumenal protein 1 mRNA, complete cds [NM_130056]
-2,7	0.00009685	AT4G17340	TIP2;2	ref Arabidopsis thaliana tonoplast intrinsic protein 2;2 mRNA, complete cds [NM_117838]
-2,7	0.00006157	AT5G27350	SFP1	ref Arabidopsis thaliana sugar transporter ERD6-like 17 mRNA, complete cds [NM_122617]
-2,71	0.00005181	AT5G47040	LON2	ref Arabidopsis thaliana lon protease-like 2 mRNA, complete cds [NM_124075]
-2,71	0.00008489	N38085	N38085	tc Rep: Cysteine proteinase - Populus tomentosa (Chinese white poplar), partial (36%) [TC397589]
-2,72	0.00007958	AT1G04280	AT1G04280	ref Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA, complete cds [NM_100309]
-2,73	0.00008805	AT5G51970	AT5G51970	ref Arabidopsis thaliana putative sorbitol dehydrogenase mRNA, complete cds [NM_124576]
-2,74	0.00038441	AT2G27830	AT2G27830	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_128343]
-2,74	0.00017428	AT4G06746	RAP2.9	ref Arabidopsis thaliana ethylene-responsive transcription factor RAP2-9 mRNA, complete cds [NM_179009]
-2,74	0.00006762	AT4G32190	AT4G32190	ref Arabidopsis thaliana myosin heavy chain-related protein mRNA, complete cds [NM_119371]
-2,75	0.00011205	AT1G47128	RD21	ref Arabidopsis thaliana cysteine proteinase RD21a mRNA, complete cds [NM_103612]
-2,76	0.00005641	AT4G37930	SHM1	ref Arabidopsis thaliana serine transhydroxymethyltransferase 1 mRNA, complete cds [NM_119954]
-2,76	0.00005097	AT5G04140	GLU1	ref Arabidopsis thaliana ferredoxin-dependent glutamate synthase 1 mRNA, complete cds [NM_180432]
-2,77	0.00007045	AT1G60590	AT1G60590	ref Arabidopsis thaliana pectin lyase-like protein mRNA, complete cds [NM_104742]
-2,77	0.0000401	AT1G62510	AT1G62510	ref Arabidopsis thaliana bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein mRNA, complete cds [NM_104930]
-2,8	0.00004591	AT3G15770	AT3G15770	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001035628]
-2,81	0.00073152	AT4G39090	RD19	ref Arabidopsis thaliana cysteine proteinase RD19a mRNA, complete cds [NM_120069]
-2,83	0.0000418	AT1G05560	UGT75B1	ref Arabidopsis thaliana UDP-glucosyltransferase 75B1 mRNA, complete cds [NM_100435]
-2,83	0.00006523	AT4G02520	GSTF2	ref Arabidopsis thaliana glutathione S-transferase F2 mRNA, complete cds [NM_116486]
-2,83	0.00003885	AT5G04810	AT5G04810	ref Arabidopsis thaliana pentatricopeptide (PPR) repeat-containing protein mRNA, complete cds [NM_120563]
-2,83	0.00004789	TC304561	TC384346	tc Rep: Xylosidase - Arabidopsis thaliana (Mouse-ear cress), complete [TC384346]
-2,84	0.00004131	AT1G30820	AT1G30820	ref Arabidopsis thaliana CTP synthase-like protein mRNA, complete cds [NM_102819]
-2,84	0.00005557	AT2G04790	AT2G04790	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001084410]
-2,84	0.00018036	AT2G04795	AT2G04795	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_126510]
-2,84	0.00024505	AT2G45960	PIP1B	ref Arabidopsis thaliana aquaporin PIP1-2 mRNA, complete cds [NM_130159]
-2,85	0.00003421	AT1G21100	AT1G21100	ref Arabidopsis thaliana indole glucosinolate o-methyltransferase 1 mRNA, complete cds [NM_101964]
-2,85	0.00005485	AT3G07310	AT3G07310	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_111611]
-2,85	0.00016457	AT5G53460	GLT1	ref Arabidopsis thaliana glutamate synthase 1 [NADH] mRNA, complete cds [NM_001203600]
-2,86	0.00005496	AT2G26980	CIPK3	ref Arabidopsis thaliana CBL-interacting serine/threonine-protein kinase 3 mRNA, complete cds [NM_179763]
-2,86	0.00007419	AT3G14420	AT3G14420	ref Arabidopsis thaliana peroxisomal (S)-2-hydroxy-acid oxidase GLO1 mRNA, complete cds [NM_180254]
-2,86	0.000032	AT5G39050	AT5G39050	ref Arabidopsis thaliana phenolic glucoside malonyltransferase 1 mRNA, complete cds [NM_123267]
-2,87	0.00004288	AT1G12250	AT1G12250	ref Arabidopsis thaliana Pentapeptide repeat-containing protein mRNA, complete cds [NM_101097]
-2,89	0.00013791	AT1G49010	AT1G49010	ref Arabidopsis thaliana myb/SANT-like DNA-binding domain-containing protein mRNA, complete cds [NM_103794]
-2,89	0.00003491	AT2G15960	AT2G15960	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_127155]
-2,89	0.00003242	AT4G29905	AT4G29905	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_148384]
-2,89	0.00003766	AT4G32940	GAMMA-VPE	ref Arabidopsis thaliana vacuolar-processing enzyme gamma mRNA, complete cds [NM_119448]
-2,91	0.00003864	AT4G11360	RHA1B	ref Arabidopsis thaliana E3 ubiquitin-protein ligase RHA1B mRNA, complete cds [NM_117207]

-2,91	0.00006342	AT4G25170	AT4G25170	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001160795]
-2,91	0.00003286	AT5G22140	AT5G22140	ref Arabidopsis thaliana FAD/NAD(P)-binding oxidoreductase family protein mRNA, complete cds [NM_147895]
-2,92	0.00004983	AT2G02710	PLPB	ref Arabidopsis thaliana PAS/LOV protein B mRNA, complete cds [NM_201672]
-2,92	0.00007998	AT5G18670	BMY3	ref Arabidopsis thaliana putative beta-amylase BMY3 mRNA, complete cds [NM_121872]
-2,94	0.00004254	AT1G10585	AT1G10585	ref Arabidopsis thaliana basic helix-loop-helix domain-containing protein mRNA, complete cds [NM_100934]
-2,94	0.00018967	AT2G26500	AT2G26500	ref Arabidopsis thaliana putative cytochrome b6f complex subunit mRNA, complete cds [NM_001084495]
-2,94	0.00003587	AT5G17170	ENH1	ref Arabidopsis thaliana protein ENHANCER OF SOS3-1 mRNA, complete cds [NM_121723]
-2,94	0.00005571	AT5G61590	AT5G61590	ref Arabidopsis thaliana ethylene-responsive transcription factor ERF107 mRNA, complete cds [NM_125552]
-2,95	0.00002657	AT4G33660	AT4G33660	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_119522]
-2,97	0.00003841	AT5G61410	RPE	ref Arabidopsis thaliana D-ribulose-5-phosphate-3-epimerase mRNA, complete cds [NM_125534]
-2,98	0.00003339	AT3G10740	ASD1	ref Arabidopsis thaliana bifunctional alpha-l-arabinofuranosidase/beta-d-xylosidase mRNA, complete cds [NM_111911]
-2,99	0.00002773	AT4G04770	ABC1	ref Arabidopsis thaliana ATP binding cassette protein 1 mRNA, complete cds [NM_116715]
-2,99	0.00005001	TA28320_3702	TA28320_3702	Unknown
-3	0.00003274	AT2G29290	AT2G29290	ref Arabidopsis thaliana tropinone reductase-like protein mRNA, complete cds [NM_001124936]
-3	0.00002555	AT5G28770	BZO2H3	ref Arabidopsis thaliana basic leucine zipper 63 mRNA, complete cds [NM_001036885]
-3	0.00006132	TC312858	TC400435	tc Rep: Chromosome chr8 scaffold_41, whole genome shotgun sequence - Vitis vinifera (Grape), partial (19%) [TC400435]
-3,01	0.00003088	AT2G01530	MLP329	ref Arabidopsis thaliana MLP-like protein 329 mRNA, complete cds [NM_126214]
-3,01	0.00029514	AT2G39400	AT2G39400	ref Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA, complete cds [NM_129497]
-3,02	0.0000256	AT2G25080	GPX1	ref Arabidopsis thaliana phospholipid hydroperoxide glutathione peroxidase 1 mRNA, complete cds [NM_128065]
-3,06	0.00002999	AT1G66760	AT1G66760	ref Arabidopsis thaliana MATE efflux family protein mRNA, complete cds [NM_179523]
-3,07	0.00002177	AT3G59940	AT3G59940	ref Arabidopsis thaliana F-box/kelch-repeat protein SKIP20 mRNA, complete cds [NM_115857]
-3,07	0.00016544	TA28339_3702	TA28339_3702	tc Rep: Carbonic anhydrase, chloroplast precursor - Arabidopsis thaliana (Mouse-ear cress), partial (20%) [TC399157]
-3,09	0.00004499	AT1G22890	AT1G22890	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_102136]
-3,09	0.0001207	AT2G27385	AT2G27385	ref Arabidopsis thaliana pollen Ole e 1 allergen and extensin family protein mRNA, complete cds [NM_179769]
-3,09	0.00003372	AT4G17245	AT4G17245	ref Arabidopsis thaliana RING/U-box domain-containing protein mRNA, complete cds [NM_117830]
-3,09	0.0000225	AT5G21170	AKINBETA1	ref Arabidopsis thaliana SNF1-related protein kinase regulatory subunit beta-1 mRNA, complete cds [NM_001036841]
-3,12	0.00003421	AT3G46600	AT3G46600	ref Arabidopsis thaliana scarecrow-like protein 30 mRNA, complete cds [NM_114527]
-3,12	0.00002299	AT5G16970	AER	ref Arabidopsis thaliana 2-alkenal reductase mRNA, complete cds [NM_121703]
-3,12	0.00008	TA26531_3702	TA26531_3702	Unknown
-3,13	0.00002196	AT4G24972	TPD1	ref Arabidopsis thaliana protein TAPETUM DETERMINANT 1 mRNA, complete cds [NM_202883]
-3,15	0.00021489	TC295612	A_84_P732596	Unknown
-3,18	0.00002873	AT1G71030	MYBL2	ref Arabidopsis thaliana putative myb family transcription factor mRNA, complete cds [NM_105772]
-3,18	0.0000215	AT1G73920	AT1G73920	ref Arabidopsis thaliana alpha/beta-hydrolase domain-containing protein mRNA, complete cds [NM_179552]
-3,18	0.00002085	AT5G65207	AT5G65207	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_148161]
-3,19	0.00124169	AT2G47270	AT2G47270	ref Arabidopsis thaliana transcription factor UPBEAT1 mRNA, complete cds [NM_130295]
-3,2	0.00004014	AT1G23870	TPS9	ref Arabidopsis thaliana putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9 mRNA, complete cds [NM_102235]
-3,2	0.00002864	TA28340_3702	TA28340_3702	Unknown
-3,23	0.00003835	AT1G20620	CAT3	ref Arabidopsis thaliana catalase 3 mRNA, complete cds [NM_001035996]
-3,24	0.00004858	AT1G73750	AT1G73750	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_106034]
-3,24	0.00001839	AT5G47560	TDT	ref Arabidopsis thaliana tonoplast dicarboxylate transporter mRNA, complete cds [NM_124129]
-3,25	0.00019689	AT2G05520	GRP-3	ref Arabidopsis thaliana glycine-rich protein 3 mRNA, complete cds [NM_001036261]
-3,25	0.00002202	AT5G64570	XYL4	ref Arabidopsis thaliana beta-D-xylosidase 4 mRNA, complete cds [NM_125853]
-3,26	0.00001927	AT5G43450	AT5G43450	ref Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate oxidase-like protein mRNA, complete cds [NM_123711]
-3,26	0.00001659	AT5G61820	AT5G61820	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125576]
-3,27	0.00026059	AT1G07890	APX1	ref Arabidopsis thaliana L-ascorbate peroxidase 1 mRNA, complete cds [NM_001123772]
-3,28	0.00003955	AT1G68010	HPR	ref Arabidopsis thaliana hydroxypyruvate reductase mRNA, complete cds [NM_001198420]
-3,31	0.00017932	AT3G26740	CCL	ref Arabidopsis thaliana CCR-like protein mRNA, complete cds [NM_113585]
-3,33	0.00003729	AT3G15630	AT3G15630	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_112433]



-3,33	0.0000138	AT4G05070	AT4G05070	ref Arabidopsis thaliana Wound-responsive family protein mRNA, complete cds [NM_116746]
-3,4	0.00001474	AT3G03990	AT3G03990	ref Arabidopsis thaliana putative strigolactone esterase D14 mRNA, complete cds [NM_111270]
-3,41	0.00002076	AT2G46220	AT2G46220	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_130184]
-3,42	0.03816081	AT2G26530	AR781	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_128210]
-3,42	0.00003624	AT5G62360	AT5G62360	ref Arabidopsis thaliana plant invertase/pectin methylesterase inhibitor superfamily protein mRNA, complete cds [NM_125630]
-3,47	0.00001971	AT1G28330	DYL1	ref Arabidopsis thaliana dormancy-associated protein-like 1 mRNA, complete cds [NM_179389]
-3,48	0.00001348	AT3G47070	AT3G47070	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_114574]
-3,48	0.00003033	AT5G63800	MUM2	ref Arabidopsis thaliana beta-galactosidase 6 mRNA, complete cds [NM_125775]
-3,51	0.00004399	AT3G15760	AT3G15760	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_112446]
-3,52	0.00001431	EQC	EQC	
-3,56	0.00000995	AT2G45170	ATG8E	ref Arabidopsis thaliana autophagy-related protein 8e mRNA, complete cds [NM_180100]
-3,56	0.00001452	AT3G62410	CP12-2	ref Arabidopsis thaliana calvin cycle protein CP12-2 mRNA, complete cds [NM_116106]
-3,56	0.00008724	TA25819_3702	TA25819_3702	Unknown
-3,57	0.00001078	AT1G37130	NIA2	ref Arabidopsis thaliana nitrate reductase [NADH] 2 mRNA, complete cds [NM_103364]
-3,57	0.00004927	AT5G19190	AT5G19190	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_121924]
-3,58	0.0000218	AT2G13360	AGT	ref Arabidopsis thaliana alanine-glyoxylate aminotransferase mRNA, complete cds [NM_126925]
-3,59	0.00001539	TA26581_3702	TA26581_3702	Unknown
-3,6	0.00001152	AT3G19030	AT3G19030	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_112789]
-3,61	0.00001337	AT3G01500	CA1	ref Arabidopsis thaliana carbonic anhydrase 1 mRNA, complete cds [NM_111016]
-3,63	0.00001247	AT3G62550	AT3G62550	ref Arabidopsis thaliana drought responsive ATP-binding motif containing protein mRNA, complete cds [NM_116120]
-3,64	0.00001356	AT2G36780	AT2G36780	ref Arabidopsis thaliana UDP-glucosyl transferase 73C3 mRNA, complete cds [NM_129233]
-3,65	0.00000964	AT1G49500	AT1G49500	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_103838]
-3,65	0.00001011	AT1G76680	OPR1	ref Arabidopsis thaliana 12-oxophytodienoate reductase 1 mRNA, complete cds [NM_106318]
-3,65	0.0000156	AT3G14990	AT3G14990	ref Arabidopsis thaliana protein DJ-1-like A mRNA, complete cds [NM_001035621]
-3,66	0.00002643	AT3G16530	AT3G16530	ref Arabidopsis thaliana legume lectin-like protein mRNA, complete cds [NM_112525]
-3,68	0.00000975	AT5G40890	CLC-A	ref Arabidopsis thaliana chloride channel protein CLC-a mRNA, complete cds [NM_123454]
-3,69	0.00000918	AT1G78830	AT1G78830	ref Arabidopsis thaliana curcumin-like (mannose-binding) lectin-like protein mRNA, complete cds [NM_106531]
-3,73	0.00000892	AT5G37260	RVE2	ref Arabidopsis thaliana MYB family transcription factor Circadian 1 mRNA, complete cds [NM_123085]
-3,74	0.00001367	AT1G72150	PATL1	ref Arabidopsis thaliana patellin-1 mRNA, complete cds [NM_105873]
-3,77	0.00001258	AT1G56220	AT1G56220	ref Arabidopsis thaliana dormancy/auxin associated protein mRNA, complete cds [NM_179488]
-3,78	0.00000964	AT1G23310	GGT1	ref Arabidopsis thaliana glutamate:glyoxylate aminotransferase mRNA, complete cds [NM_001036006]
-3,78	0.00000743	AT5G18600	AT5G18600	ref Arabidopsis thaliana monothiol glutaredoxin-S2 mRNA, complete cds [NM_121865]
-3,81	0.00001348	AT1G01240	AT1G01240	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_202007]
-3,82	0.00005377	AT2G15890	MEE14	ref Arabidopsis thaliana maternal effect embryo arrest 14 protein mRNA, complete cds [NM_127149]
-3,83	0.00001229	AT3G24420	AT3G24420	ref Arabidopsis thaliana hydrolase, alpha/beta fold family protein mRNA, complete cds [NM_113349]
-3,85	0.00003848	AT2G39730	RCA	ref Arabidopsis thaliana ribulose biphosphate carboxylase/oxygenase activase mRNA, complete cds [NM_129531]
-3,86	0.00001215	AT3G57520	SIP2	ref Arabidopsis thaliana putative galactinol--sucrose galactosyltransferase 2 mRNA, complete cds [NM_115612]
-3,88	0.00000857	AT5G24490	AT5G24490	ref Arabidopsis thaliana putative 30S ribosomal protein mRNA, complete cds [NM_122357]
-3,89	0.00015255	AT4G15760	MO1	ref Arabidopsis thaliana monooxygenase 1 mRNA, complete cds [NM_001203809]
-3,9	0.00006756	AT5G21940	AT5G21940	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_147877]
-3,91	0.00000633	AT1G22690	AT1G22690	ref Arabidopsis thaliana gibberellin-regulated protein 9 mRNA, complete cds [NM_001198137]
-3,91	0.00001042	AT3G04000	AT3G04000	ref Arabidopsis thaliana aldehyde reductase mRNA, complete cds [NM_111271]
-3,94	0.00021103	AT1G19660	AT1G19660	ref Arabidopsis thaliana putative wound-responsive protein mRNA, complete cds [NM_001035991]
-3,97	0.00000642	BP660593	BP660593	Unknown
-3,98	0.00004104	AT3G49620	DIN11	ref Arabidopsis thaliana 2-oxoacid-dependent dioxygenase-like protein DIN11 mRNA, complete cds [NM_114822]
-3,99	0.00000979	AT5G26200	AT5G26200	ref Arabidopsis thaliana mitochondrial substrate carrier family protein mRNA, complete cds [NM_122521]
-4,03	0.00018583	TA28344_3702	TA28344_3702	Unknown
-4,04	0.00003115	AT5G25130	CYP71B12	ref Arabidopsis thaliana cytochrome P450 71B12 mRNA, complete cds [NM_122422]

-4,06	0.00001327	AT3G10020	AT3G10020	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001125137]
-4,07	0.00001126	AT1G16720	HCF173	ref Arabidopsis thaliana high chlorophyll fluorescence phenotype 173 protein mRNA, complete cds [NM_101533]
-4,07	0.00000697	AT5G14740	CA2	ref Arabidopsis thaliana carbonic anhydrase 2 mRNA, complete cds [NM_001036806]
-4,07	0.00003316	AT5G14780	FDH	ref Arabidopsis thaliana formate dehydrogenase mRNA, complete cds [NM_121482]
-4,14	0.00000546	AT2G22960	AT2G22960	ref Arabidopsis thaliana putative serine carboxypeptidase-like 52 mRNA, complete cds [NM_127861]
-4,16	0.00001681	AT3G61430	PIP1A	ref Arabidopsis thaliana aquaporin PIP1-1 mRNA, complete cds [NM_001084854]
-4,18	0.00004696	AT1G02820	AT1G02820	ref Arabidopsis thaliana late embryogenesis abundant 3-like protein mRNA, complete cds [NM_100163]
-4,21	0.00010256	TA28693_3702	TA28693_3702	tc Rep: Uncharacterized protein At1g23310.2 - Arabidopsis thaliana (Mouse-ear cress), partial (44%) [TC387783]
-4,25	0.00001691	AT5G49450	bZIP1	ref Arabidopsis thaliana basic leucine-zipper 1 mRNA, complete cds [NM_124322]
-4,26	0.00001816	AT3G11930	AT3G11930	ref Arabidopsis thaliana universal stress protein-like protein mRNA, complete cds [NM_180231]
-4,26	0.00000424	TC309871	TC396686	tc Rep: Conglutin gamma-like protein - Arabidopsis thaliana (Mouse-ear cress), partial (35%) [TC396686]
-4,33	0.00000428	AT2G36800	DOGT1	ref Arabidopsis thaliana UDP-glycosyltransferase 73C5 mRNA, complete cds [NM_129235]
-4,43	0.00000779	TC314163	TC405990	tc Rep: Formate dehydrogenase - Arabidopsis thaliana (Mouse-ear cress), partial (18%) [TC405990]
-4,47	0.00000461	AT3G28270	AT3G28270	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_113746]
-4,49	0.00001339	AT1G73120	AT1G73120	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_105970]
-4,51	0.00000799	AT1G17170	GSTU24	ref Arabidopsis thaliana glutathione S-transferase TAU 24 mRNA, complete cds [NM_101578]
-4,56	0.00000323	AT1G70290	TPS8	ref Arabidopsis thaliana putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 8 mRNA, complete cds [NM_105697]
-4,63	0.00000351	TA26159_3702	TA26159_3702	Unknown
-4,64	0.00001093	AT3G49790	AT3G49790	ref Arabidopsis thaliana Carbohydrate-binding protein mRNA, complete cds [NM_114839]
-4,66	0.00000646	AT5G39610	NAC6	ref Arabidopsis thaliana NAC-domain transcription factor mRNA, complete cds [NM_123323]
-4,67	0.00000379	AT1G08570	ACHT4	ref Arabidopsis thaliana atypical CYS HIS rich thioredoxin 4 mRNA, complete cds [NM_001123776]
-4,67	0.00000565	AT2G05380	GRP3S	ref Arabidopsis thaliana glycine-rich protein 3 short isoform mRNA, complete cds [NM_126561]
-4,67	0.00000453	TA29648_3702	TA29648_3702	Unknown
-4,71	0.00000448	AT2G34430	LHB1B1	ref Arabidopsis thaliana light-harvesting chlorophyll protein complex II subunit B1 mRNA, complete cds [NM_128995]
-4,72	0.00001225	AT5G56870	BGAL4	ref Arabidopsis thaliana beta-galactosidase 4 mRNA, complete cds [NM_125070]
-4,76	0.00000317	AT5G54585	AT5G54585	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_148130]
-4,78	0.0000005	AT1G11260	STP1	ref Arabidopsis thaliana sugar transporter 1 mRNA, complete cds [NM_100998]
-4,84	0.00000254	AT5G02160	AT5G02160	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_120294]
-4,85	0.00000583	AT3G09580	AT3G09580	ref Arabidopsis thaliana FAD/NAD(P)-binding oxidoreductase family protein mRNA, complete cds [NM_111792]
-4,95	0.00000573	AT5G19120	AT5G19120	ref Arabidopsis thaliana aspartyl protease family protein mRNA, complete cds [NM_121917]
-4,95	0.00000265	AT5G51720	AT5G51720	ref Arabidopsis thaliana CDGSH iron-sulfur domain-containing protein NEET mRNA, complete cds [NM_124551]
-4,99	0.00000587	AT4G19170	NCED4	ref Arabidopsis thaliana nine-cis-epoxycarotenoid dioxygenase 4 mRNA, complete cds [NM_118036]
-5,08	0.00000276	AT5G22920	AT5G22920	ref Arabidopsis thaliana ring finger and CHY zinc finger domain-containing protein 1 mRNA, complete cds [NM_122198]
-5,11	0.00000464	AT4G13250	NYC1	ref Arabidopsis thaliana probable chlorophyll(ide) b reductase NYC1 mRNA, complete cds [NM_117396]
-5,15	0.00002203	AT5G39080	AT5G39080	ref Arabidopsis thaliana HXXD-type acyl-transferase-like protein mRNA, complete cds [NM_123270]
-5,36	0.0000031	AT4G16690	MES16	ref Arabidopsis thaliana methyl esterase 16 mRNA, complete cds [NM_117770]
-5,44	0.00000747	AT1G75380	BBD1	ref Arabidopsis thaliana bifunctional nuclease 1 mRNA, complete cds [NM_179559]
-5,69	0.0000144	AT2G18700	TPS11	ref Arabidopsis thaliana putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 11 mRNA, complete cds [NM_127426]
-5,74	0.00050373	AT3G28740	CYP81D1	ref Arabidopsis thaliana cytochrome P450 CYP81D11 mRNA, complete cds [NM_113795]
-5,83	0.00000408	AT1G74670	AT1G74670	ref Arabidopsis thaliana gibberellin-regulated protein 6 mRNA, complete cds [NM_106125]
-5,84	0.00000169	AT5G49740	FRO7	ref Arabidopsis thaliana ferric reduction oxidase 7 mRNA, complete cds [NM_124352]
-5,92	0.00000704	AT4G37610	BT5	ref Arabidopsis thaliana BTB and TAZ domain protein 5 mRNA, complete cds [NM_119924]
-5,97	0.00000335	TA29020_3702	TA29020_3702	Unknown
-6,05	0.0000012	AT5G20250	DIN10	ref Arabidopsis thaliana putative galactinol--sucrose galactosyltransferase 6 mRNA, complete cds [NM_001036833]
-6,05	0.00000151	AT5G49730	FRO6	ref Arabidopsis thaliana ferric reduction oxidase 6 mRNA, complete cds [NM_124351]
-6,1	0.00000202	AT1G23390	AT1G23390	ref Arabidopsis thaliana F-box/kelch-repeat protein mRNA, complete cds [NM_102188]
-6,29	0.00000344	AT3G13750	BGAL1	ref Arabidopsis thaliana beta galactosidase 1 mRNA, complete cds [NM_112225]
-6,37	0.0000011	AT5G02020	AT5G02020	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_180421]

-6,57	0.0000025	AT1G80920	J8	ref Arabidopsis thaliana chaperone protein dnaJ 8 mRNA, complete cds [NM_106740]
-6,94	0.0000008	AT1G69530	EXPA1	ref Arabidopsis thaliana expansin A1 mRNA, complete cds [NM_001124101]
-6,99	0.00000098	AT3G15356	AT3G15356	ref Arabidopsis thaliana lectin-like protein mRNA, complete cds [NM_148726]
-7,31	0.00000088	AT2G22990	SNG1	ref Arabidopsis thaliana sinapoylglucose:malate sinapoyltransferase mRNA, complete cds [NM_127864]
-7,84	0.0000006	AT1G77760	NIA1	ref Arabidopsis thaliana nitrate reductase [NADH] 1 mRNA, complete cds [NM_106425]
-8,23	0.00000079	AT1G05680	UGT74E2	ref Arabidopsis thaliana Uridine diphosphate glycosyltransferase 74E2 mRNA, complete cds [NM_100448]
-8,24	0.00000145	AT5G63160	BT1	ref Arabidopsis thaliana BTB and TAZ domain protein 1 mRNA, complete cds [NM_125711]
-8,26	0.00000067	AT2G40610	EXPA8	ref Arabidopsis thaliana expansin A8 mRNA, complete cds [NM_129623]
-8,58	0.00000119	AT1G09500	AT1G09500	ref Arabidopsis thaliana alcohol dehydrogenase-like protein mRNA, complete cds [NM_001035935]
-9,38	0.00000061	AT1G80440	AT1G80440	ref Arabidopsis thaliana F-box/kelch-repeat protein mRNA, complete cds [NM_106692]
-9,53	0.00000369	AT4G33666	AT4G33666	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_119524]
-9,84	0.00000027	BE039144	BE039144	tc Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vinifera (Grape), partial (59%) [TC393828]
-10,19	0.00000052	AT3G15450	AT3G15450	ref Arabidopsis thaliana aluminum induced protein with YGL and LRDR motif mRNA, complete cds [NM_001035625]
-10,61	0.00000037	TA30818_3702	TA30818_3702	Unknown
-11,04	0.00000021	AT5G66400	RAB18	ref Arabidopsis thaliana dehydrin Rab18 mRNA, complete cds [NM_126038]
-11,56	0.00000124	AT4G01870	AT4G01870	ref Arabidopsis thaliana tolB-related protein mRNA, complete cds [NM_116417]
-12,39	0.00000039	AT4G26530	AT4G26530	ref Arabidopsis thaliana fructose-bisphosphate aldolase 5 mRNA, complete cds [NM_001036644]
-13,38	0.00000057	AT4G35770	SEN1	ref Arabidopsis thaliana senescence-associated protein DIN1 mRNA, complete cds [NM_119743]
-13,6	0.00000011	AT3G48360	BT2	ref Arabidopsis thaliana TAC1-mediated telomerase activation pathway protein BT2 mRNA, complete cds [NM_114697]
-14,33	0.0000001	AT2G05540	AT2G05540	ref Arabidopsis thaliana glycine-rich protein mRNA, complete cds [NM_126577]
-15,72	0.00000031	AT4G35090	CAT2	ref Arabidopsis thaliana catalase 2 mRNA, complete cds [NM_119675]
-19,25	0.00000025	AT5G49360	BXL1	ref Arabidopsis thaliana bifunctional {beta}-D-xylosidase/{alpha}-L-arabinofuranosidase mRNA, complete cds [NM_124313]
-23,93	0.00000021	AT2G33830	AT2G33830	ref Arabidopsis thaliana dormancy/auxin associated protein mRNA, complete cds [NM_179889]

**Table S4. List of genes whose expression is down-regulated by VCs emitted by *A. alternata* (this work, cf. Supporting Information Table S3) and by *B. subtilis* GB03 (cf. Supporting Information Table 1, Zhang et al. 2007)**

ID	Description
AT2G01520	ref Arabidopsis thaliana MLP-like protein 328 mRNA, complete cds [NM_126213]
AT4G15690	ref Arabidopsis thaliana monothiol glutaredoxin-S5 mRNA, complete cds [NM_117660]
AT2G40000	ref Arabidopsis thaliana HS1 PRO-1 2-like protein mRNA, complete cds [NM_129558]
AT1G73330	ref Arabidopsis thaliana protein drought-repressed 4 mRNA, complete cds [NM_105993]
AT1G58180	ref Arabidopsis thaliana beta carbonic anhydrase 6 mRNA, complete cds [NM_001198330]
AT4G33150	ref Arabidopsis thaliana lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme mRNA, complete cds [NM_001160811]
AT5G67030	ref Arabidopsis thaliana zeaxanthin epoxidase mRNA, complete cds [NM_126103]
AT2G17500	ref Arabidopsis thaliana auxin efflux carrier family protein mRNA, complete cds [NM_179633]
AT2G37750	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_129331]
AT4G36850	ref Arabidopsis thaliana PQ-loop repeat family protein / transmembrane family protein mRNA, complete cds [NM_119849]
AT4G32340	ref Arabidopsis thaliana tetratricopeptide repeat domain-containing protein-like protein mRNA, complete cds [NM_119386]
AT3G61060	ref Arabidopsis thaliana phloem protein 2-A13 mRNA, complete cds [NM_202741]
AT5G06690	ref Arabidopsis thaliana WCRKC thioredoxin 1 mRNA, complete cds [NM_001036767]
AT5G38510	ref Arabidopsis thaliana rhomboid-related intramembrane serine protease-like protein mRNA, complete cds [NM_123212]
AT4G11320	ref Arabidopsis thaliana putative cysteine proteinase mRNA, complete cds [NM_117203]
AT5G43580	ref Arabidopsis thaliana unusual seine protease inhibitor mRNA, complete cds [NM_123724]
AT2G37130	ref Arabidopsis thaliana peroxidase mRNA, complete cds [NM_001124989]
AT4G34920	ref Arabidopsis thaliana PLC-like phosphodiesterases superfamily protein mRNA, complete cds [NM_119658]
AT5G63190	ref Arabidopsis thaliana MA3 domain-containing protein mRNA, complete cds [NM_125714]
AT5G48485	ref Arabidopsis thaliana putative lipid-transfer protein DIR1 mRNA, complete cds [NM_124224]
AT5G59750	ref Arabidopsis thaliana monofunctional riboflavin biosynthesis protein RIBA 3 mRNA, complete cds [NM_001203642]
AT5G57655	ref Arabidopsis thaliana xylose isomerase mRNA, complete cds [NM_180872]
AT2G39800	ref Arabidopsis thaliana delta1-pyrroline-5-carboxylate synthase 1 mRNA, complete cds [NM_001202785]
AT3G25830	ref Arabidopsis thaliana 1,8-cineole synthase mRNA, complete cds [NM_113485]
AT1G660140	ref Arabidopsis thaliana putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10 mRNA, complete cds [NM_104705]
AT4G36040	ref Arabidopsis thaliana chaperone protein dnaJ 11 mRNA, complete cds [NM_119771]
AT3G13062	ref Arabidopsis thaliana polyketide cyclase/dehydrase and lipid transport superfamily protein mRNA, complete cds [NM_180243]
AT3G07350	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_111614]
AT4G16190	ref Arabidopsis thaliana papain family cysteine protease mRNA, complete cds [NM_117715]
AT2G15020	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_127064]
AT5G17300	ref Arabidopsis thaliana myb family transcription factor RVE1 mRNA, complete cds [NM_121736]
AT2G03310	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_126382]
AT2G29090	ref Arabidopsis thaliana abscisic acid 8'-hydroxylase 2 mRNA, complete cds [NM_128466]
AT1G79700	ref Arabidopsis thaliana AP2-like ethylene-responsive transcription factor WRI4 mRNA, complete cds [NM_001084380]
AT1G53870	ref Arabidopsis thaliana TUB_2 domain-containing protein mRNA, complete cds [NM_104264]
AT2G22980	ref Arabidopsis thaliana serine carboxypeptidase-like 13 mRNA, complete cds [NM_001036325]
AT4G17340	ref Arabidopsis thaliana tonoplast intrinsic protein 2;2 mRNA, complete cds [NM_117838]
AT5G47040	ref Arabidopsis thaliana lon protease-like 2 mRNA, complete cds [NM_124075]
AT1G47128	ref Arabidopsis thaliana cysteine proteinase RD21a mRNA, complete cds [NM_103612]
AT1G21100	ref Arabidopsis thaliana indole glucosinolate o-methyltransferase 1 mRNA, complete cds [NM_101964]
AT1G12250	ref Arabidopsis thaliana Pentapeptide repeat-containing protein mRNA, complete cds [NM_101097]
AT2G15960	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_127155]
AT4G29905	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_148384]
AT4G25170	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001160795]
AT3G10740	ref Arabidopsis thaliana bifunctional alpha-l-arabinofuranosidase/beta-d-xylosidase mRNA, complete cds [NM_111911]

AT2G29290 ref|Arabidopsis thaliana tropinone reductase-like protein mRNA, complete cds [NM\_001124936]  
AT2G01530 ref|Arabidopsis thaliana MLP-like protein 329 mRNA, complete cds [NM\_126214]  
AT2G39400 ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA, complete cds [NM\_129497]  
AT2G25080 ref|Arabidopsis thaliana phospholipid hydroperoxide glutathione peroxidase 1 mRNA, complete cds [NM\_128065]  
AT1G66760 ref|Arabidopsis thaliana MATE efflux family protein mRNA, complete cds [NM\_179523]  
AT2G27385 ref|Arabidopsis thaliana pollen Ole e 1 allergen and extensin family protein mRNA, complete cds [NM\_179769]  
AT5G21170 ref|Arabidopsis thaliana SNF1-related protein kinase regulatory subunit beta-1 mRNA, complete cds [NM\_001036841]  
AT1G73750 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_106034]  
AT5G64570 ref|Arabidopsis thaliana beta-D-xylosidase 4 mRNA, complete cds [NM\_125853]  
AT5G43450 ref|Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate oxidase-like protein mRNA, complete cds [NM\_123711]  
AT3G26740 ref|Arabidopsis thaliana CCR-like protein mRNA, complete cds [NM\_113585]  
AT1G28330 ref|Arabidopsis thaliana dormancy-associated protein-like 1 mRNA, complete cds [NM\_179389]  
AT3G15760 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_112446]  
AT3G62410 ref|Arabidopsis thaliana calvin cycle protein CP12-2 mRNA, complete cds [NM\_116106]  
AT2G13360 ref|Arabidopsis thaliana alanine--glyoxylate aminotransferase mRNA, complete cds [NM\_126925]  
AT1G49500 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_103838]  
AT5G40890 ref|Arabidopsis thaliana chloride channel protein CLC-a mRNA, complete cds [NM\_123454]  
AT1G72150 ref|Arabidopsis thaliana patellin-1 mRNA, complete cds [NM\_105873]  
AT2G15890 ref|Arabidopsis thaliana maternal effect embryo arrest 14 protein mRNA, complete cds [NM\_127149]  
AT5G24490 ref|Arabidopsis thaliana putative 30S ribosomal protein mRNA, complete cds [NM\_122357]  
AT4G15760 ref|Arabidopsis thaliana monooxygenase 1 mRNA, complete cds [NM\_001203809]  
AT1G19660 ref|Arabidopsis thaliana putative wound-responsive protein mRNA, complete cds [NM\_001035991]  
AT5G25130 ref|Arabidopsis thaliana cytochrome P450 71B12 mRNA, complete cds [NM\_122422]  
AT3G10020 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_001125137]  
AT1G16720 ref|Arabidopsis thaliana high chlorophyll fluorescence phenotype 173 protein mRNA, complete cds [NM\_101533]  
AT5G49450 ref|Arabidopsis thaliana basic leucine-zipper 1 mRNA, complete cds [NM\_124322]  
AT3G11930 ref|Arabidopsis thaliana universal stress protein-like protein mRNA, complete cds [NM\_180231]  
AT1G70290 ref|Arabidopsis thaliana putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 8 mRNA, complete cds [NM\_105697]  
AT3G49790 ref|Arabidopsis thaliana Carbohydrate-binding protein mRNA, complete cds [NM\_114839]  
AT1G08570 ref|Arabidopsis thaliana atypical CYS HIS rich thioredoxin 4 mRNA, complete cds [NM\_001123776]  
AT5G56870 ref|Arabidopsis thaliana beta-galactosidase 4 mRNA, complete cds [NM\_125070]  
AT5G54585 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_148130]  
AT5G02160 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_120294]  
AT5G19120 ref|Arabidopsis thaliana aspartyl protease family protein mRNA, complete cds [NM\_121917]  
AT4G19170 ref|Arabidopsis thaliana nine-cis-epoxycarotenoid dioxygenase 4 mRNA, complete cds [NM\_118036]  
AT4G16690 ref|Arabidopsis thaliana methyl esterase 16 mRNA, complete cds [NM\_117770]  
AT1G75380 ref|Arabidopsis thaliana bifunctional nuclease 1 mRNA, complete cds [NM\_179559]  
AT3G28740 ref|Arabidopsis thaliana cytochrome P450 CYP81D11 mRNA, complete cds [NM\_113795]  
AT1G74670 ref|Arabidopsis thaliana gibberellin-regulated protein 6 mRNA, complete cds [NM\_106125]  
AT4G37610 ref|Arabidopsis thaliana BTB and TAZ domain protein 5 mRNA, complete cds [NM\_119924]  
AT5G20250 ref|Arabidopsis thaliana putative galactinol--sucrose galactosyltransferase 6 mRNA, complete cds [NM\_001036833]  
AT5G49730 ref|Arabidopsis thaliana ferric reduction oxidase 6 mRNA, complete cds [NM\_124351]  
AT1G23390 ref|Arabidopsis thaliana F-box/kelch-repeat protein mRNA, complete cds [NM\_102188]  
AT3G13750 ref|Arabidopsis thaliana beta galactosidase 1 mRNA, complete cds [NM\_112225]  
AT5G02020 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_180421]  
AT1G80920 ref|Arabidopsis thaliana chaperone protein dnaJ 8 mRNA, complete cds [NM\_106740]  
AT2G22990 ref|Arabidopsis thaliana sinapoylglucose:malate sinapoyltransferase mRNA, complete cds [NM\_127864]  
AT1G77760 ref|Arabidopsis thaliana nitrate reductase [NADH] 1 mRNA, complete cds [NM\_106425]  
AT5G63160 ref|Arabidopsis thaliana BTB and TAZ domain protein 1 mRNA, complete cds [NM\_125711]  
AT2G40610 ref|Arabidopsis thaliana expansin A8 mRNA, complete cds [NM\_129623]  
AT1G80440 ref|Arabidopsis thaliana F-box/kelch-repeat protein mRNA, complete cds [NM\_106692]

AT4G01870 ref|Arabidopsis thaliana tolB-related protein mRNA, complete cds [NM\_116417]  
AT4G35770 ref|Arabidopsis thaliana senescence-associated protein DIN1 mRNA, complete cds [NM\_119743]  
AT3G48360 ref|Arabidopsis thaliana TAC1-mediated telomerase activation pathway protein BT2 mRNA, complete cds [NM\_114697]  
AT2G05540 ref|Arabidopsis thaliana glycine-rich protein mRNA, complete cds [NM\_126577]  
AT5G49360 ref|Arabidopsis thaliana bifunctional {beta}-D-xylosidase/{alpha}-L-arabinofuranosidase mRNA, complete cds [NM\_124313]  
AT2G33830 ref|Arabidopsis thaliana dormancy/auxin associated protein mRNA, complete cds [NM\_179889]

**Table S5. List of genes whose expression is up-regulated by VCs emitted by *A. alternata* (this work, cf. Supporting Information Table S3) and by *B. subtilis* GB03 (cf. Supporting Information Table 1, Zhang et al. 2007)**

ID	Description
AT1G61800	ref Arabidopsis thaliana glucose-6-phosphate/phosphate translocator 2 mRNA, complete cds [NM_104862]
AT4G10270	ref Arabidopsis thaliana putative wound-responsive protein mRNA, complete cds [NM_117095]
AT3G18000	ref Arabidopsis thaliana conserved peptide upstream open reading frame 30 mRNA, complete cds [NM_001125181]
AT5G54060	ref Arabidopsis thaliana anthocyanidin 3-O-glucoside 2'''-O-xylosyltransferase mRNA, complete cds [NM_124785]
AT4G39210	ref Arabidopsis thaliana glucose-1-phosphate adenyltransferase large subunit 3 mRNA, complete cds [NM_120081]
AT2G16060	ref Arabidopsis thaliana non-symbiotic hemoglobin 1 mRNA, complete cds [NM_127165]
AT4G01080	ref Arabidopsis thaliana protein TRICHOME BIREFRINGENCE-LIKE 26 mRNA, complete cds [NM_116338]
AT1G78370	ref Arabidopsis thaliana glutathione S-transferase TAU 20 mRNA, complete cds [NM_106484]
AT5G17220	ref Arabidopsis thaliana glutathione S-transferase phi 12 mRNA, complete cds [NM_121728]
AT1G56650	ref Arabidopsis thaliana transcription factor MYB75 mRNA, complete cds [NM_104541]
AT1G32900	ref Arabidopsis thaliana granule-bound starch synthase 1 mRNA, complete cds [NM_103023]
AT1G67360	ref Arabidopsis thaliana REF/SRPP-like protein mRNA, complete cds [NM_179525]
AT2G41090	ref Arabidopsis thaliana calmodulin-like protein 10 mRNA, complete cds [NM_129674]
AT5G14200	ref Arabidopsis thaliana isopropylmalate dehydrogenase 1 mRNA, complete cds [NM_001036803]
AT2G43100	ref Arabidopsis thaliana isopropylmalate isomerase 2 mRNA, complete cds [NM_129871]
AT1G16410	ref Arabidopsis thaliana dihomomethionine N-hydroxylase mRNA, complete cds [NM_101507]
AT3G51240	ref Arabidopsis thaliana flavanone 3-hydroxylase mRNA, complete cds [NM_114983]
AT4G27070	ref Arabidopsis thaliana tryptophan synthase beta chain mRNA, complete cds [NM_118841]
AT4G22870	ref Arabidopsis thaliana leucoanthocyanidin dioxygenase-like protein mRNA, complete cds [NM_001160794]
AT1G68600	ref Arabidopsis thaliana Aluminum activated malate transporter family protein mRNA, complete cds [NM_105532]
AT5G07990	ref Arabidopsis thaliana Flavonoid 3'-monooxygenase mRNA, complete cds [NM_120881]
AT4G23600	ref Arabidopsis thaliana cystine lyase COR13 mRNA, complete cds [NM_179099]
AT3G58990	ref Arabidopsis thaliana isopropylmalate isomerase 1 mRNA, complete cds [NM_115761]
AT3G03190	ref Arabidopsis thaliana glutathione S-transferase F11 mRNA, complete cds [NM_111189]
AT2G28900	ref Arabidopsis thaliana outer plastid envelope protein 16-1 mRNA, complete cds [NM_128449]
AT3G19710	ref Arabidopsis thaliana branched-chain aminotransferase4 mRNA, complete cds [NM_112861]
AT5G23010	ref Arabidopsis thaliana methylthioalkylmalate synthase 1 mRNA, complete cds [NM_122207]
AT2G27402	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_201818]
AT1G29920	ref Arabidopsis thaliana chlorophyll A/B-binding protein 2 mRNA, complete cds [NM_102732]
AT5G08640	ref Arabidopsis thaliana flavonol synthase 1 mRNA, complete cds [NM_001203337]
AT4G14090	ref Arabidopsis thaliana anthocyanin 5-O-glucosyltransferase mRNA, complete cds [NM_117485]
AT1G24020	ref Arabidopsis thaliana MLP-like protein 423 mRNA, complete cds [NM_102249]
AT4G13770	ref Arabidopsis thaliana cytochrome P450 83A1 mRNA, complete cds [NM_117451]
AT1G62560	ref Arabidopsis thaliana flavin-containing monooxygenase FMO GS-OX3 mRNA, complete cds [NM_104934]
AT1G18590	ref Arabidopsis thaliana sulfotransferase 17 mRNA, complete cds [NM_101717]
AT2G46650	ref Arabidopsis thaliana cytochrome B5 isoform C mRNA, complete cds [NM_130230]
AT3G21560	ref Arabidopsis thaliana sinapic acid:UDP-glucose glucosyltransferase mRNA, complete cds [NM_113051]
AT2G35860	ref Arabidopsis thaliana fasciclin-like arabinogalactan protein 16 mRNA, complete cds [NM_179922]
AT5G48880	ref Arabidopsis thaliana 3-keto-acyl-CoA thiolase 2 mRNA, complete cds [NM_001036960]
AT4G14040	ref Arabidopsis thaliana selenium-binding protein 2 mRNA, complete cds [NM_117479]
AT3G22550	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_113154]
AT4G39940	ref Arabidopsis thaliana adenosine-5'-phosphosulfate-kinase 2 mRNA, complete cds [NM_120157]
AT3G60440	ref Arabidopsis thaliana phosphoglycerate mutase family protein mRNA, complete cds [NM_115908]
AT3G52180	ref Arabidopsis thaliana phosphoglucan phosphatase DSP4 mRNA, complete cds [NM_001035765]
AT5G48850	ref Arabidopsis thaliana protein SULPHUR DEFICIENCY-INDUCED 1 mRNA, complete cds [NM_124262]
AT4G04745	ref Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_148231]

AT4G14400 ref|Arabidopsis thaliana protein ACCELERATED CELL DEATH 6 mRNA, complete cds [NM\_117519]  
AT3G02020 ref|Arabidopsis thaliana aspartokinase 3 mRNA, complete cds [NM\_111068]  
AT5G41670 ref|Arabidopsis thaliana 6-phosphogluconate dehydrogenase, decarboxylating 2 mRNA, complete cds [NM\_180782]  
AT5G53420 ref|Arabidopsis thaliana CCT motif family protein mRNA, complete cds [NM\_124721]  
AT5G06270 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_120710]  
AT5G13930 ref|Arabidopsis thaliana chalcone synthase mRNA, complete cds [NM\_121396]  
AT2G37300 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_129286]  
AT1G65060 ref|Arabidopsis thaliana 4-coumarate--CoA ligase 3 mRNA, complete cds [NM\_179513]  
AT5G03120 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_120390]  
AT1G29660 ref|Arabidopsis thaliana GDSL esterase/lipase mRNA, complete cds [NM\_102706]  
AT4G12880 ref|Arabidopsis thaliana early nodulin-like protein 19 mRNA, complete cds [NM\_001203782]  
AT4G33560 ref|Arabidopsis thaliana Wound-responsive family protein mRNA, complete cds [NM\_119511]  
AT1G43910 ref|Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA, complete cds [NM\_103518]  
AT3G45140 ref|Arabidopsis thaliana lipoxygenase 2 mRNA, complete cds [NM\_114383]  
AT4G36010 ref|Arabidopsis thaliana pathogenesis-related thaumatin family protein mRNA, complete cds [NM\_001036715]  
AT1G49860 ref|Arabidopsis thaliana glutathione S-transferase (class phi) 14 mRNA, complete cds [NM\_103873]  
AT4G22880 ref|Arabidopsis thaliana leucoanthocyanidin dioxygenase mRNA, complete cds [NM\_118417]  
AT2G38750 ref|Arabidopsis thaliana annexin D4 mRNA, complete cds [NM\_129432]  
AT1G44800 ref|Arabidopsis thaliana bidirectional amino acid transporter SIAR1 mRNA, complete cds [NM\_103561]  
AT4G27560 ref|Arabidopsis thaliana UDP-glycosyltransferase 79B2 mRNA, complete cds [NM\_118891]  
AT4G39730 ref|Arabidopsis thaliana Lipase/lipoxygenase, PLAT/LH2 family protein mRNA, complete cds [NM\_120134]  
AT1G31550 ref|Arabidopsis thaliana GDSL esterase/lipase mRNA, complete cds [NM\_102894]  
AT3G26960 ref|Arabidopsis thaliana pollen Ole e 1 allergen and extensin family protein mRNA, complete cds [NM\_113610]  
AT3G13650 ref|Arabidopsis thaliana disease resistance-responsive, dirigent domain-containing protein mRNA, complete cds [NM\_112211]  
AT2G25510 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_128108]  
AT3G14210 ref|Arabidopsis thaliana epithiospecifier modifier 1 mRNA, complete cds [NM\_112278]  
AT5G47060 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_124077]  
AT1G65860 ref|Arabidopsis thaliana flavin-containing monooxygenase FMO GS-OX1 mRNA, complete cds [NM\_105258]  
AT4G08570 ref|Arabidopsis thaliana heavy-metal-associated domain-containing protein mRNA, complete cds [NM\_116926]  
AT1G56150 ref|Arabidopsis thaliana SAUR-like auxin-responsive protein mRNA, complete cds [NM\_104494]  
AT1G61580 ref|Arabidopsis thaliana 60S ribosomal protein L3-2 mRNA, complete cds [NM\_104840]  
AT5G07460 ref|Arabidopsis thaliana peptide methionine sulfoxide reductase A2 mRNA, complete cds [NM\_120828]  
AT1G30530 ref|Arabidopsis thaliana UDP-glucoyl transferase 78D1 mRNA, complete cds [NM\_102790]  
AT3G44990 ref|Arabidopsis thaliana xyloglucan endotransglucosylase/hydrolase mRNA, complete cds [NM\_114368]  
AT5G44720 ref|Arabidopsis thaliana molybdenum cofactor sulfurase family protein mRNA, complete cds [NM\_123839]  
AT1G21440 ref|Arabidopsis thaliana phosphoenolpyruvate carboxylase family protein mRNA, complete cds [NM\_101995]  
AT4G02850 ref|Arabidopsis thaliana phenazine biosynthesis PhzC/PhzF family protein mRNA, complete cds [NM\_116519]  
AT4G19430 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_118063]  
AT4G14680 ref|Arabidopsis thaliana ATP sulfurylase mRNA, complete cds [NM\_117550]  
AT1G77120 ref|Arabidopsis thaliana alcohol dehydrogenase 1 mRNA, complete cds [NM\_106362]  
AT3G52370 ref|Arabidopsis thaliana fasciclin-like arabinogalactan protein 15 mRNA, complete cds [NM\_115097]  
AT5G19470 ref|Arabidopsis thaliana nudix hydrolase 24 mRNA, complete cds [NM\_121952]  
AT5G67150 ref|Arabidopsis thaliana HXXXD-type acyl-transferase-like protein mRNA, complete cds [NM\_126115]  
AT3G54600 ref|Arabidopsis thaliana class I glutamine amidotransferase-like domain-containing protein mRNA, complete cds [NM\_115317]  
AT1G03940 ref|Arabidopsis thaliana coumaroyl-CoA:anthocyanidin 3-O-glucoside-6-O-coumaroyltransferase 1 mRNA, complete cds [NM\_100275]  
AT2G44210 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_001036461]  
AT3G61820 ref|Arabidopsis thaliana aspartyl protease mRNA, complete cds [NM\_116047]  
AT2G32990 ref|Arabidopsis thaliana glycosyl hydrolase 9B8 mRNA, complete cds [NM\_128859]  
AT1G78020 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_106451]  
AT4G17470 ref|Arabidopsis thaliana putative palmitoyl-protein thioesterase mRNA, complete cds [NM\_001203824]  
AT5G42530 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_123618]



AT1G45201 ref|Arabidopsis thaliana triacylglycerol lipase-like 1 mRNA, complete cds [NM\_179441]  
AT4G17670 ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM\_117875]