ABSTRACT

A “box-in-box” co-cultivation system was used to investigate plant responses to microbial volatile compounds (VCs), and to evaluate the contributions of organic and inorganic VCs (VOCs and VICs, respectively) to these responses. Arabidopsis plants were exposed to VCs emitted by adjacent *Alternaria alternata* and *Penicillium aurantiogriseum* cultures, with and without charcoal filtration. No VOCs were detected in the headspace of growth chambers containing fungal cultures with charcoal filters. However, these growth chambers exhibited elevated CO_2 and bioactive CO and NO headspace concentrations. Independently of charcoal filtration, VCs from both fungal phytopathogens promoted growth and distinct developmental changes. Plants cultured at CO_2 levels observed in growth boxes containing fungal cultures were identical to those cultured at ambient CO_2. Plants exposed to charcoal-filtered fungal VCs, non-filtered VCs, or super-elevated CO_2 levels exhibited transcriptional changes resembling those induced by increased irradiance. Thus, in the “box-in-box” system, (a) fungal VICs other than CO_2 and/or VOCs not detected by our analytical systems strongly influence the plants´ responses to fungal VCs, (b) different microorganisms release VCs with distinct action potentials, (c) transcriptional changes in VC-exposed plants are mainly due to enhanced photosynthesis signaling, and (d) regulation of some plant responses to fungal VCs is primarily post-transcriptional.

Key-words: Growth promotion, microbial volatile compounds, photosynthesis, plant-microbe interactions.

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INTRODUCTION

The metabolic activity of microorganisms results in the emission of complex mixtures of volatile compounds (VCs). It is well known that beneficial bacteria and fungi can produce volatiles that promote plant growth as well as developmental and metabolic changes (Hung, Lee, & Bennett, 2013; Kanchiswamy, Malnoy, & Maffei, 2015; Ryu et al., 2003). We have recently shown that this capacity is not restricted to beneficial microorganisms, but also extends to phytopathogens (Sánchez-López, Baslam, et al., 2016). When Arabidopsis plants were exposed to airborne signals released by the saprophytic fungus *Alternaria alternata*, growth promotion was accompanied by enhanced photosynthetic electron transport and CO_2 assimilation rates, accelerated flowering, changes in the redox status of enzymes involved in starch metabolism, and starch over-accumulation resulting from the activation of non-canonical starch biosynthetic pathway(s) (Ezquer et al., 2010; Li et al., 2011; Sánchez-López, Bahaji, et al., 2016; Sánchez-López, Baslam, et al., 2016). Short exposure to VCs emitted by *A. alternata* and plant growth-promoting bacteria induced similar transcriptomic changes, indicating that plants react to microbial VCs through highly conserved regulatory mechanisms (Sánchez-López, Baslam, et al., 2016). These findings expanded our knowledge of the diversity and complexity of the mechanisms involved in modulating plant physiology and growth when plants interact with microorganisms, and raised questions about the evolution of the involved processes and their ecological significance.

Growth promotion by microbial VCs has frequently been associated with lipophilic carbon-based compounds with molecular masses less than 300 Da and high vapour pressure, which are known as volatile organic compounds (VOCs) (Kanchiswamy et al., 2015). Nearly 2000 microbial VOCs emitted by 1000 microorganisms are presently registered in the microbial VOC database (Lemfack et al., 2018). Over 50 of these VOCs have been shown to induce changes in the plant´s growth, physiology and/or defence responses (Piechulla, Lemfack, & Kai, 2017). In many cases, exposure of plants to discrete (individual) VOCs or VOC mixtures either failed to reproduce or only partially reproduced the effects induced by the complex blends of VCs emitted by plant growth promoting microorganisms (Cordovez et al., 2017; Groenhagen et al., 2013; Naznin, Kimura, Miyazawa, & Hyakumachi, 2013). This indicates that VOCs not detected by the analytical methods used in these studies may be partly responsible for the growth-promoting effects of microbial VCs. In addition to VOCs, microorganisms also release a limited number of volatile inorganic compounds (VICs) with molecular masses less than 45 Da such as hydrogen sulfide (H_2S), molecular hydrogen (H_2), nitric oxide (NO), nitrogen dioxide (NO_2), nitrous oxide (N_2O), carbon monoxide (CO), carbon dioxide (CO_2), hydrogen cyanide (HCN) and ammonia (NH_3) (Blom, Fabbri, Eberl, & Weisskopf, 2011; Conrath, Amoroso, Köhle, & Sültemeyer, 2004; Engel, Matsen, Chapman, & Schwartz, 1972; Nandi & Sengupta, 1998; Schreiber, Wunderlin, Udert, & Wells, 2012; Shatalin, Shatalina, Mironov, & Nudler, 2011; Siegel & Siegel, 1987; Weise, Kai, & Piechulla, 2013; Wharton & Weintraub, 1980). These compounds can cross biological membranes. Some of them are very reactive with proteins and can act as signalling molecules that promote photosynthesis, growth and developmental changes in plants when exogenously applied in a discrete form and in low concentrations (Chen et al., 2011; Dong, Wu, Kettlewell, Caldwell, & Layzell, 2003; Dooley, Nair, & Ward, 2013; Guo, Kong, & Yang, 2009; He et al., 2004; C. W. Jin, Du, Zhang, Tang, & Lin, 2009; Kong, Zhang, Guo, Liu, & Yang, 2010; Q. Jin et al., 2013; Lin et al., 2014; Lisjak, Teklic, Wilson, Whiteman, & Hancock, 2013; Takahashi et al., 2014; Wang & Liao, 2016; Xu et al., 2010; Zeng, Zhang, & Sun, 2013; Kuruthukulangarakoola et al., 2017). There is also evidence that emissions of some of these compounds from growth-promoting rhizobacteria are an important determinant of root development in their host plants (Boccara et al., 2005; Johnson et al., 2008; Molina-Favero, Creus, Simontacchi, Puntarulo, & Lamattina, 2008).

A number of studies on plant´s responses to microbial VCs have largely relied on the use of sealed dual co-cultivation systems in which plants are exposed to complex mixtures of VICs and VOCs released by nearby microbial cultures (Blom et al., 2011; Casarrubia et al., 2016; Cordovez et al., 2017; Ditengou et al., 2015; Ezquer et al., 2010; Ryu et al., 2003; Sánchez-López, Bahaji, et al., 2016; Sánchez-López, Baslam, et al., 2016; Zhang et al., 2009). All currently known microorganisms that produce plant growth-promoting volatiles are heterotrophic and thus emit respiratory CO_2 and consume O_2 when grown under aerobic conditions. In sealed co-cultivation systems, microbial respiratory CO_2 can accumulate to high levels in the headspace (Kai & Piechulla, 2009) while O_2 levels can fall below the atmospheric O_2 concentrations. Elevated CO_2 and strong reduction of O_2 levels enhance photosynthesis, reduce photorespiration, and promote plant growth, flowering, starch accumulation and changes in root architecture (Ainsworth & Rogers, 2007; Hachiya et al., 2014; Makino & Mae, 1999; Niu et al., 2011; Quebedeaux & Hardy, 1975; Ramonell et al., 2001; Song, Kristie, & Reekie, 2009; Thompson, Gamage, Hirotsu, Martin, & Seneweera, 2017). Therefore, several authors have argued that the responses of plants grown in closely proximity to microbial cultures in sealed containers could be largely due to accumulation of elevated levels of CO_2 from microbial respiration, which calls into question past interpretations of results obtained using sealed co-cultivation systems (Casarrubia et al., 2016; Kai, Effmert, & Piechulla, 2016; Kai & Piechulla, 2009). Consequently, studies using sealed co-cultivation systems should include appropriate CO_2 controls and online monitoring of the levels of this gas in the growth containers. In addition, the design of the test system should be described in detail (Piechulla, 2017; Piechulla et al., 2017).

Our previous studies on plant responses to microbial volatiles were conducted using a “box-in-box” co-cultivation system in which the plant and microbial cultures were placed in a container sealed with a polyvinyl chloride (PVC) plastic wrap (cf. Supporting Information

Figure S2 in Ezquer et al. 2010, cf. Supporting Information Figure S1 in Sánchez-López, Baslam, et al. 2016). In studies using this and other sealed test systems, plants co-cultured with phylogenetically distant microbial species exhibited very similar transcriptomic changes, suggesting that all of the microorganisms emit the same bioactive VC(s) (Sánchez-López, Baslam, et al., 2016). It is thus possible that our observations were due at least in part to elevated CO_2 resulting from microbial respiration. Using the same “box-in-box” test system, here we have conducted new studies to address the question of whether airborne signals from different microorganisms can promote distinct responses in plants. In addition, we evaluated the contribution and mode of action of microbial VOCs and VICs (including respiratory CO_2) in these responses by performing comparative analyses of plants´ developmental, biochemical and molecular responses to (i) CO_2, (ii) complex mixtures of VICs and VOCs, and (iii) VOCs-depleted (VICs-containing) volatile emissions from the fungal phytopathogens *A. alternata* and *Penicillium aurantiogriseum*. Our results show that, in the test system used in this work and our previous studies, respiratory CO_2 plays only a minor role in plant responses to microbial VCs. Moreover, we present evidence that mixtures of VICs from different microorganisms can promote growth and distinct developmental changes in Arabidopsis. We also provide evidence that (a) the highly conserved transcriptional changes occurring in plants exposed to microbial VCs are indirectly due to enhanced photosynthesis, and (b) some plant responses to fungal VOCs-depleted VC mixtures are primarily regulated at the post-transcriptional level.

MATERIAL AND METHODS

Plant and microbial cultures, growth conditions and sampling

The work was carried out using *Arabidopsis thaliana* L. (Heynh) ecotype Columbia (Col-0) and the fungal species *A. alternata* (CECT 20192) and *P. aurantiogriseum* (CECT 20226). Plants were cultured in Petri dishes (92x16mm, Ref. 82.1472.001, Sarstedt) containing sucrose-free solid half strength Murashige and Skoog (MS) (Phytotechlab M519) medium. *A. alternata* and *P. aurantiagriseum* were cultured in Petri dishes (35x10mm, Ref. 82.1135.500, Sarstedt) containing solid MS medium supplemented with 90 mM sucrose. To investigate the plants´ responses to fungal VCs, microbial cultures without lids (with or without filter of charcoal, SIGMA 05105) and plant cultures without lids were placed in sterile boxes without physical contact, and sealed with a PVC film. As negative controls, plant cultures were placed in sealed boxes together with Petri dishes containing sterile MS medium. The sealed boxes containing plants and fungal cultures were placed in CO_2-controlled growth cabinets (Conviron ®, Manitoba, Canada) with a 16 h light (90 µmol photons sec^{-1} m^{-2})/8 h dark photoperiod (22ºC during the light period and 18ºC during the dark period). The growth cabinets were modified including a Vaisala CARBOCAP, Carbon Dioxide Module GMM112 to allow the cabinets to reach 10000 ppm CO_2. Microbial VCs and CO_2 treatments started at the 14th day after sowing. Unless otherwise indicated plants were grown on horizontal plates.

Root morphological analysis

The numbers and lengths of the plants´ roots and root hairs in plants grown on vertical plates were measured using a stereomicroscope Olympus MVX10 (Japan). Microphotographs were captured with a DP72 video camera (Olympus, Japan) and the Cell D software (Olympus, Japan).

Analytical procedures

Fully expanded source leaves of plants cultured in the absence or presence of VCs or exogenously supplied CO_2 were harvested at the end of the light period, freeze-clamped, and ground to a fine powder in liquid nitrogen with a pestle and mortar. Starch was measured using an amyloglucosydase–based test kit (Boehringer Mannheim, Germany). For measurement of sucrose, glucose and fructose levels, a 0.1 g aliquot of the frozen powder was resuspended in 1 ml of 90% ethanol, left at 70 ºC for 90 min, and centrifuged at 13,000 x g for 10 min. Sugar contents from supernatants were then determined by HPLC with pulsed amperometric detection on a ICS-3000 Dionex system.

Gas exchange determinations

Fully expanded apical leaves were enclosed in a LI-COR 6400 gas exchange portable photosynthesis system (LI-COR, Lincoln, Nebraska, USA). The gas exchange determinations were conducted at 25 ºC with a photosynthetic photon flux density of 350 μmol m^{-2} s^{-1}. Net rates of CO_2 assimilation (A_n) were calculated using equations developed by von Caemmerer & Farquhar (1981).

Headspace analysis of microbial VCs

The system to analyse the microbial VCs in the headspace of growth chambers containing fungal cultures is illustrated in Supporting Information Figure S1. The solid-phase microextraction (SPME) technique was selected for gas chromatography-mass spectrometry (GC-MS) analyses of VOCs. The PVC wrap of the sealed growth boxes was carefully drilled with a Divinylbenzene/Carboxen/Polydimethylsiloxane (DVB/CAR/PDMS) coated fiber, and VOCs were adsorbed at 22 ºC for 30 min. The fiber was injected into an Agilent 7890A gas chromatograph containing a 30 m x 0,25 mm fused silica HP-5MS column. The chromatographic conditions used were: inlet 250 ºC; column 40 ºC for 2 min followed by ramping at 5 ºC/min to 250 ºC. Mass spectral analyses were carried out with an Agilent 5975C instrument. The scan mass range extended from m/z 20 to 400. Mass spectra of VCs were compared to those obtained from the NIST library and identifications were confirmed using commercially available standard compounds. High purity chemicals (generally with purities above 99%) were purchased from Sigma-Aldrich to identify some compounds released by the fungi. Kovats retention indices were calculated according to generally accepted standards (van Den Dool & Dec. Kratz, 1963), based on the chromatographic retention times of a saturated alkane mixture (C7 - C30; Sigma-Aldrich) and other alkanes (<C7) occurring in the chromatogram background.

For online monitoring of the CO_2 contents in sealed growth boxes with or without fungal cultures, the sealed growth boxes were connected to a Vaisala CARBOCAP® Carbon Dioxide Probe GMP343 combined with a Vaisala Handheld Measurement Indicator MI70. For O_2 and CO contents analyses, sealed growth boxes were connected to a MX4 portable headspace analyser (Industrial Scientific Corporation, Pennsylvania, United States). For NO analyses, sealed growth boxes were connected to a Ecotec Serinus 40 Oxides Nitrogen Analyser (Ecotech Pty Ltd., Knoxfield, VIC, Australia). The Analyser was used under the conditions needed to meet EN Type approval (TUV 936/21221977/A), which includes enabling Kalman filter in measuring settings.

Textural characterization of activated charcoal

Nitrogen adsorption at -196 ^{o}C was measured using an ASAP 2020 volumetric adsorption analyser from Micromeritics (Norcross, Georgia, USA). Approximately 0.1532 g of sample was weighed in an elongated Pyrex glass tube. Before adsorption analysis, the sample was outgassed for at least 15 h at 573 K at the degassification port of the adsorption apparatus with a residual vacuum of 7 x 10^{-1} Pa. Specific surface areas were calculated from the N_2 adsorption data (molecular cross section 0.162 nm^2) by the Brunauer-Emmett-Teller method.

$$\frac{1}{n^a(1-{}^p/_{p^0})} = \frac{1}{n^a_m} + \frac{1}{n^a_m C} \cdot \frac{1-{}^p/_{p^0}}{{}^p/_{p^0}}$$

where n^a is the amount adsorbed, n^a_m is the monolayer capacity, p/p^0 is the relative pressure, and C is a constant related to the heat of adsorption.

Micropore volume was estimated by applying the DR method to the N_2 ($V_{microDR}$) adsorption data.

$$\log V = \log V^0 - D\log^2\frac{p^0}{p}$$

where V is the volume adsorbed at a given relative pressure, V^0 is the micropore volume and D is a constant characteristic of the adsorbent structure.

Mesopore volume (V_{meso}) values were obtained by subtracting the amount adsorbed at p/p^o 0.80 and 0.30. Macropore volume (V_{macro}) was obtained by difference between V_t and the amount adsorbed at p/p^o 0.80. Pore volumes were calculated using liquid-state density for adsorbate of N_2 at 0.808 g cms.1^{-3} (Garrido et al., 1987; Rodríguez-Reinoso, Garrido, Martín-Martínez, Molina-Sabio, & Torregrosa, 1989).

Gene expression analyses

We proceeded essentially as described in Sánchez-López, Baslam, et al. (2016). Briefly, total RNA was extracted from frozen Arabidopsis leaves of plants cultured *in vitro* using the Trizol method according to the manufacturer's procedure (Invitrogen), and then purified with the RNeasy kit (Qiagen). RNA amplification, labelling and statistical data analysis were performed basically as described by Adie et al. (2007). The Arabidopsis Gene Expression Microarray 4 x 44K (G2519, Agilent Technologies) was used for hybridization. Three independent biological replicates were hybridized for leaves from microbe-treated plants and from controls. Images from Cy3 and Hyper5 channels were equilibrated to compensate for intensity differences and captured with a GenePix 4000B scanner (Axon). Spots were quantified using GenPix software (Axon) and normalized using the Lowess method. Means of the three replicates log-ratio intensities and their standard deviations were calculated, and the expression data were statistically analysed using the LIMMA package (Smyth & Speed, 2003). Functional characterization of the differentially expressed genes was done using the Mapman tool (http://gabi.rzpd.de/projects/MapMan/).

Non-reducing western blot analyses

Fifty mg of the homogenized frozen material (see above) was extracted in cold 16% (w/v) TCA in diethyl ether, mixed, and stored at –20 °C for 2 h. The pellet was collected by centrifugation at 10,000 x g for 5 min at 4 °C, washed 3 times with ice-cold acetone, dried briefly under vacuum, and resuspended in 1x Laemmli sample buffer containing no reductant. Proteins were separated on 10% SDS-PAGE under non-reducing conditions as described by Hendriks, Kolbe, Gibon, Stitt, & Geigenberger (2003), transferred to nitrocellulose filters, and immunodecorated by using the antisera raised against the small subunit of maize AGP, and a goat anti-rabbit IgG alkaline phosphatase conjugate as the secondary antibody (Sigma).

Statistical analysis

The data presented are the means (± SE) from four independent experiments, with 3-5 biological replicates, each biological replicate being a pool of 12 plants. The significance of differences between control and treated was statistically evaluated by means of Student´s t-test using SPSS software. Differences were considered significant if $p<0.05$.

RESULTS

Volatile emissions of *A. alternata* and *P. aurantiogriseum* promote distinct developmental changes in Arabidopsis plants cultured in a “box-in-box” co-cultivation system

Volatiles emitted by *A. alternata* and *P. aurantiogriseum* cultures promoted rosette growth and flowering in adjacent plants (Supporting Information Figure S2), in keeping with the results of Sánchez-López, Baslam, et al. (2016). Furthermore, fungal VCs promoted root growth (Supporting Information Figure S2), root hair proliferation and elongation, and formation of first and second order lateral roots (LRs), thereby increasing the density of the root system (Figure 1).

Volatiles from both microorganisms promoted distinct developmental responses in vicinity plants. Leaves of plants exposed to VCs from *P. aurantiogriseum* were more wrinkled, thicker, and harder than those of plants exposed to VCs from *A. alternata* (Supporting Information Figure S2a and data not shown). Primary roots of plants exposed to *A. alternata* VCs were longer than those of control plants and *P. aurantiogriseum* VC-exposed plants (Figure 1c). Furthermore, whereas *A. alternata* VCs had no effect on the length of first order LRs, *P. aurantiogriseum* VCs inhibited the growth of this root type (Figure 1c). In addition, the root hairs of plants treated with *P. aurantiogriseum* VCs were substantially longer than those of plants treated with *A. alternata* VCs (Figure 1b,c, Supporting Information Figure S2b). *P. aurantiogriseum* VCs also stimulated the formation of second-order LRs more strongly than *A. alternata* VCs (Figure 1c), leading to a higher density of second-order LRs in plants treated with *P. aurantiogriseum* compared to those treated with *A. alternata* VCs (Figure 1a,c). The strong proliferation and elongation of root hairs, combined with the shortening of the LRs induced by *P. aurantiogriseum* VCs led to the formation of peculiar brush-like structures that were not seen in roots of plants exposed to *A. alternata* VCs (Figure 1a,b, Supporting Information Figure S2).

Charcoal-filtered and non-filtered fungal volatile emissions promote similar responses in exposed plants

We next investigated the contribution of fungal VOCs and VICs in the plant responses in the "box-in-box" system used in this work and previous studies. To this end, we characterized Arabidopsis plants grown in the absence or presence for one week of adjacent *A. alternata* and *P. aurantiogriseum* cultures covered with a black, porous nylon mesh, with or without a top layer of VOC-adsorbing activated charcoal (for further details, see Supporting Information Figure S3). According to the adsorption isotherm of N_2 at -196 ^{o}C (Supporting Information Figure S4a) and the porosity distribution (Supporting Information Figure S4b), the type of charcoal used in this study was a micro-meso-porous carbon with specific surface area of 1109 m^2/g, micropores greater than 0.7 nm and mesoproses between 2 and 5 nm (Supporting Information Table S1). Therefore, small molecules such as CO_2 (with a molecular cross section of 0.162 nm^2 and size of 0.33x0.53x0.33 nm), CO, NO, O_2, etc. could cross the porosity of this carbon, especially in the presence of larger molecules that could cover the smallest microporosity. We reasoned that if the plant´s responses to microbial VCs were mainly due to VOCs, charcoal-filtered (VOCs-depleted, VICs-containing) fungal volatile emissions should trigger at most a weak response. Conversely, if the fungal cultures release VICs with high action potentials, charcoal-filtered microbial volatile emissions should still trigger strong responses in plants.

As a first step in these studies, we conducted compositional analyses of the VCs in the headspace of PVC film-sealed growth chambers containing *A. alternata* or *P. aurantiogriseum* cultures with and without charcoal filters. VOCs analyses were done using SPME coupled with GC-MS, a technology that has been widely used to analyse VOCs emitted by microorganisms and to elucidate their potential function in plant-microbe interactions (Contreras-Cornejo, Macías-Rodríguez, Herrera-Estrella, & López-Bucio, 2014; Farag et al., 2017; Garnica-Vergara et al., 2016; Meldau et al., 2013; Naznin et al., 2013; Nieto-Jacobo et al., 2017; Schenkel, Maciá-Vicente, Bissell, & Splivallo, 2018; Velázquez-Becerra et al., 2011; Zou, Li, & Yu, 2010). VOCs extraction was performed using a DVB/CAR/PDMS coated fiber that can capture C3-C20 volatiles and semi-volatiles with molecular masses between 40 and 275 Da. A detailed description of the system used to perform these studies is presented in Supporting Information Figure S1. As shown in Table 1 and Supporting Information Figure S5, SPME GC-MS analyses of VOCs in the headspace of growth chambers containing *A. alternata* or *P. aurantiogriseum* cultures lacking charcoal filters revealed that these microorganisms have different organic volatilomes. Some of the VOCs released by the two fungal phytopathogens have previously been identified among the emissions of plant-growth promoting microorganisms (Table 1). VIC analyses revealed substantially higher levels of CO and NO in the headspace of growth chambers containing the fungal cultures than in controls (Figure 2). No VOCs were detected in the headspace of growth chambers containing fungal cultures covered with charcoal filters (Table 1, Supporting Information Figure S5), showing that this hydrocarbon material captures all VOCs emitted by *A. alternata* and *P. aurantiogriseum* that can be adsorbed by the DVB/CAR/PDMS coated fiber and detected by GC-MS under the conditions used in this study. In contrast, CO and NO levels in the headspace of growth chambers containing fungal cultures covered with charcoal filters where higher than in controls (Figure 2). This shows that the two fungal species emit CO and NO and confirms that the charcoal filter used in this study poorly retains these small VICs.

As expected, plants grown beside fungal cultures not covered with a charcoal filter produced larger rosettes and roots, flowered earlier and developed denser root systems with longer root hairs than control plants (Figure 3a,b). Fungal VCs without charcoal filtration also increased photosynthetic activity in the exposed plants (Figure 4a) and promoted the accumulation of photosynthetic pigments (Figure 4a) and primary photosynthates (*i.e.* sucrose, glucose, fructose and starch) (Figure 4b). Notably, these responses were identical to those of plants grown in the vicinity of fungal cultures covered with a charcoal filter (Figure 3a,b,c, Figure 4).

Respiratory CO_2 makes only a minor contribution to the growth and root architecture changes induced by charcoal-filtered fungal VCs

The results presented above would indicate that, in the box-in-box test system used in this study, VICs could play an important role on plant responses to volatiles emitted by *A. alternata* and *P. aurantiogriseum*. We next investigated the contribution of respiratory CO_2 to the changes in plant growth and root development induced by charcoal-filtered fungal VCs. We also investigated whether strong reduction in the O_2 concentration in the headspace of the co-cultivation system could occur that would account for the observed plant´s responses to the presence of adjacent microbial cultures. To this end, we first measured the CO_2 and O_2 concentrations in the headspace of PVC film-sealed boxes containing fungal cultures covered with charcoal filters using the system illustrated in Supporting Information Figure S1. To test the CO_2-permeability of the PVC film sealant, sealed boxes with or without fungal cultures were placed in a CO_2-controlled growth cabinet, and the CO_2 levels inside the boxes were monitored while manipulating the CO_2 levels in the cabinet.

As shown in Figure 5 the CO_2 and O_2 concentrations in the headspace of the sealed boxes before the addition of the *A. alternata* and *P. aurantiogriseum* cultures were ca. 420 ppm and 21 kPa, respectively. The O_2 concentration in the headspace of the sealed boxes did not change significantly upon addition of the fungal cultures (Figure 5), but the headspace CO_2 concentration oscillated between ca. 550 ppm and 500 ppm during the day and night periods, respectively (Figure 5). This oscillation in the headspace CO_2 concentration can be attributed to the regulation of fungal metabolism by light (Farkas, Gresik, Kolarova, Sulova, & Sestak, 1990; Tisch & Schmoll, 2010). The CO_2 concentrations inside the sealed boxes rapidly changed to match those inside the growth cabinet when the CO_2 level in the cabinet was increased (Figure 5 and Supporting Information Figure S6), showing that the PVC film sealant around the box is highly permeable to CO_2.

We next characterized Arabidopsis plants cultured for one week under 16 h light, 550 ppm CO_2/8 h dark, 500 ppm CO_2 conditions and compared them with plants cultured under the same light/dark cycle with ambient CO_2 levels. As a positive control, we also characterized plants cultured with sustained super-elevated (2000 ppm) CO_2 levels. No differences in shoot fresh weight (FW), root architecture or time of floral bud appearance were detected between plants cultured under ambient CO_2 conditions and plants cultured under 16 h light, 550 ppm CO_2/8 h dark, 500 ppm CO_2 conditions (Figure 6). The 2000 ppm CO_2 treatment caused the FW of the plant´s rosettes to increase approximately two-fold (Figure 6a), which was substantially lower than the 5-fold increase of FW exhibited by plants cultured with adjacent fungal cultures (cf. Figure 3b). The super-elevated CO_2 treatment also promoted early flowering (Figure 6a) and the formation of second order LRs and elongation of root hairs (Figure 6b). However, unlike treatment with fungal volatiles, the super-elevated CO_2 treatment did not promote the formation of first-order LRs, root hair proliferation, or the formation of brush-like root structures (Figure 6b).

Respiratory CO_2 plays a minor role in the accumulation of exceptionally high starch levels in leaves induced by charcoal-filtered fungal VCs

Short-term exposure to microbial VCs promotes the accumulation of exceptionally high levels of starch in leaves (Ezquer et al., 2010; Li et al., 2011; Sánchez-López, Baslam, et al., 2016). The contribution of fungal respiratory CO_2 emissions to this phenomenon was investigated by comparing the starch contents in leaves of Arabidopsis plants grown for 16 h under 550 ppm CO_2 conditions to those of plants cultured for 16 h with adjacent *A. alternata* cultures covered with a layer of activated charcoal. As positive control, we also characterized plants cultured for 16 h under 2000 ppm CO_2. As shown in Figure 7, treatment with 550 ppm and 2000 ppm CO_2 caused a ca. 1.3-fold and 2-fold increases in the leaf starch content, respectively, both of which are much smaller than the ca. 15-fold increase observed in plants cultured with adjacent fungal cultures (cf. Figure 4).

Starch accumulation induced by charcoal-filtered fungal VCs is associated with reductive activation of ADP-glucose pyrophosphorylase, but that induced by super-elevated CO_2 is not

We have shown that short-term exposure to complex mixtures of VICs and VOCs released by *A. alternata* promotes reductive monomerization (activation) of APS1 in leaves (Li et al. 2011). APS1 is the regulatory subunit of ADP-glucose pyrophosphorylase (AGP), which catalyses the first committed step of starch biosynthesis. We therefore proposed that fungal VC-mediated reductive activation of APS1 could at least partly explain the accumulation of high levels of starch in leaves of VCs-exposed plants (Li et al., 2011).

In leaves, APS1 is present as a mixture of 50 kDa active (reduced) monomers and 100 kDa inactive (oxidized) dimers. To determine whether CO_2- and charcoal-filtered fungal VC-promoted starch accumulation involves APS1 reductive monomerization, we conducted non-reducing APS1 immunoblot analyses of proteins extracted from leaves of plants exposed for one day to 2000 ppm CO_2 or charcoal-filtered VCs emitted by *A. alternata* cultures. As shown in Figure 8, exposure of plants to charcoal-filtered fungal VCs promoted reductive APS1 monomerization. Conversely, exposure of plants to 2000 ppm CO_2 did not alter the redox status of APS1 (Figure 8).

Complex mixtures of fungal VCs, charcoal-filtered VCs, super-elevated CO_2 and increased irradiance all induce similar transcriptomic changes in leaves

We finally performed high-throughput transcriptomic analyses of leaves from Arabidopsis plants exposed for 16 h to charcoal-filtered VCs emitted by nearby *A. alternata* cultures, or super-elevated CO_2 levels (2000 ppm CO_2). The sets of genes exhibiting differential expression patterns under these treatments were compared to those previously reported for plants cultured in the absence or in the presence of adjacent *A. alternata* cultures without a covering charcoal filter (cf. Supporting Information Table S3 in Sánchez-López, Baslam, et al. 2016).

As shown in Supporting Information Table S2, 258 genes were up-regulated and 399 genes were down-regulated when plants were exposed to charcoal-filtered fungal VCs (with a > 3.0-fold difference relative to control; $p < 0.05$). Nearly 50% of the genes that were down-regulated in leaves of plants exposed to charcoal-filtered fungal VCs were also down-regulated in leaves of plants exposed to fungal VCs without charcoal filtration (Supporting Information Table S2). Furthermore, 53% of the genes that were up-regulated in leaves of plants exposed to charcoal-filtered fungal VCs were also up-regulated in leaves of plants exposed to fungal VCs not filtered by charcoal (Supporting Information Table S2). Super-elevated CO_2 treatment induced the up-regulation of 217 genes and down-regulation of 401 genes (with a > 3.0-fold difference relative to control; $p < 0.05$) (Supporting Information Table S3). Sixty percent of the genes that were down-regulated in leaves of plants treated with 2000 ppm CO_2 were also down-regulated in leaves of plants exposed to fungal VCs without charcoal filtration (Supporting Information Table S3). Furthermore, 52% of the genes that were up-regulated in leaves of plants exposed to 2000 ppm CO_2 were also up-regulated in leaves of plants exposed to VCs without charcoal filtration (Supporting Information Table S3).

The most strongly up-regulated gene in leaves of plants exposed to fungal volatiles without charcoal filtration was At1g61800 (Sánchez-López, Baslam, et al., 2016), which encodes the GPT2 glucose-6-phosphate (G6P)/phosphate translocator that is necessary for dynamic photosynthetic and metabolic acclimation to increased irradiance (Athanasiou, Dyson, Webster, & Johnson, 2010; Dyson et al., 2015). Notably, 55% of the genes that were down-regulated in plants exposed to increased irradiance (cf. Supporting Information Table S1 in Athanasiou et al. 2010) were also down-regulated in leaves of plants exposed to fungal VCs (Supporting Information Table S4): 80% of the 20 genes exhibiting the strongest down-regulation in plants exposed to increased irradiance were also down-regulated in leaves exposed to fungal VCs (Table 2). Moreover, 25% of the genes that were up-regulated in plants exposed to increased irradiance (cf. Supporting Information Table S1 in Athanasiou et al. 2010) were also up-regulated in leaves of plants treated with fungal VCs (Supporting Information Table S4), 50% of the 20 genes most strongly up-regulated genes in plants exposed to increased irradiance being also up-regulated in leaves exposed to fungal VCs (Table 2).

DISCUSSION

Features and benefits of the “box-in-box” dual co-cultivation system for studying plant responses to microbial volatile emissions

The sealed split Petri dish-based passive diffusion co-cultivation system has frequently been used to investigate the plant´s response to microbial emissions of volatile compounds. Using tri-partite Petri dishes, Casarrubia et al. (2016) analysed the effect of activated charcoal on growth of Arabidopsis plants cultured in the absence or presence of adjacent cultures of the endomycorrhizal fungus *Oidiodendron maius*. Irrespective of the inclusion of activated charcoal in one of the three compartments, fungal cultures promoted plant growth of nearby plants. Because CO_2 levels in the headspace of sealed Petri dishes containing microbial cultures can become extremely high as a result of microbial respiration (Kai & Piechulla, 2009) the authors concluded that the observed growth promotion was mainly due to fungal respiratory CO_2 rather than specific fungal VOC signals (Casarrubia et al., 2016). However, neither the absence of microbial VOCs nor the accumulation of high levels of CO_2 concentrations in the headspace of charcoal-containing Petri dishes was confirmed.

The “box-in-box” system used in this work and our previous studies has a number of advantages over the sealed split Petri dish system when studying plants´ responses to microbial volatile emissions. First, the air diffusion surface of this system is exceedingly larger than that of the sealed Petri dish system (in which air can only diffuse via a slit between the plate and the lid). Second, the sealing wrap used in this experimental setup is highly CO_2- and O_2- permeable PVC, which impedes strong increases in the CO_2/O_2 balance in the headspace of the growth chamber due to respiratory metabolism that would otherwise interfere with the effects of microbial VCs. Third, the system permits easy online monitoring of volatiles in the growth container´s headspace (Figure 5, Supporting Information Figure S1). Fourth, the setup enables the filtration of all VOCs emitted by the microbial cultures, facilitating studies on plant responses to microbial VICs emissions.

Different microbes can release VCs other than CO_2 that promote distinct responses in nearby plants

Results presented here show that diverse microorganisms can release VCs that promote distinct responses in plants. The contribution of VOCs and VICs to plants´ responses to VCs emitted by *A. alternata* and *P. aurantiogriseum* was investigated using a type of charcoal (cf. Supporting Information Figure S4) that captured all VOCs emitted by these fungal species that can be detected by our SPME GC-MS system (Table 1). However, the charcoal did not capture small VICs such as CO, NO and CO_2 (Figure 2 and Figure 5). Therefore, plants grown in the presence of both fungal cultures with charcoal filters were exposed to VOC-depleted volatile emissions. The responses of plants to charcoal-filtered VCs emitted by nearby fungal cultures were identical to those of plants exposed to fungal VCs without charcoal filtration (Figures 3 and 4). Thus, in our experimental system, microbes can release bioactive VICs and/or VOCs that are either poorly captured by the type of micro-meso-porous charcoal used in this study (Supporting Information Figure S4b) or not detected by our SPME GC-MS system. Moreover, these VICs and/or uncaptured VOCs appear to be stronger determinants of the plants´ responses to VCs than the fungal VOCs that are detected by our SPME GC-MS system. Some potentially relevant bioactive VICs are CO and NO, whose concentrations in the headspace of the growth boxes increased in the presence of fungal cultures with charcoal filters (Figure 2). The fact that charcoal-filtered *A. alternata* and *P. aurantiogriseum* VCs promoted distinct changes in the leaves and root architecture of exposed plants (Figure 3) strongly indicates that the charcoal-filtered volatilomes of the two microorganisms have different action potentials. It is evident that further efforts will be necessary to identify all the bioactive VCs of different microorganisms and characterize their action potentials.

We must emphasize that the data obtained in this study do not imply that microbial

VOCs lack bioactivity. In fact, some *A. alternata* and *P. aurantiogriseum* VOCs detected by our SPME GC-MS system (*i.e.* 2-butanol,3-methyl, 1-butanol,2-methyl, tridecane, 3-octanone, β-elemene, γ-muurolene, cis-thujopsene, acoradiene, valencene, α-chamigrene and α-copaene, cf. Table 1) are emitted by plant-growth promoting microorganisms. Moreover, some of these compounds are known to be bioactive when exogenously supplied to plants. For example, discrete application of cis-thujopsene massively stimulated LR formation in Arabidopsis (Ditengou et al., 2015), while 2-butanol,3-methyl promoted plant growth and salinity tolerance (Ledger et al., 2016).

Several factors indicate that plant´s responses to charcoal-filtered microbial VCs were not due to enhanced CO_2/O_2 ratio caused by fungal respiration. First, if the enhanced CO_2/O_2 balance were a major determinant of the plant´s response to nearby microbial cultures, one would expect all microbial cultures to induce similar responses in plants. However, charcoal-filtered VCs from *P. aurantiogriseum* and *A. alternata* induced distinct changes in the leaf morphology and root architecture of Arabidopsis plants (Figure 3, Supporting Information Figure S2). Second, plants grown under CO_2 levels equal to those measured in the headspace of sealed chambers containing fungal cultures (ca. 550 ppm) did not promote growth or changes in the root architecture of the plant or accumulation of starch in leaves (Figures 6 and 7). Third, super-elevated (2000 ppm) CO_2 caused a 2-fold increase in both leaf starch content and FW of exposed plants, which was substantially lower than the 15-fold increase in leaf starch content and 5-fold increase in FW induced by charcoal-filtered microbial VCs (cf. Figures 3b, 6a and 7). Furthermore, unlike treatment with charcoal-filtered fungal VCs, the super-elevated CO_2 treatment did not promote the formation of first-order LRs, root hair proliferation, or the formation of brush-like root structures (Figure 6b). Fourth, charcoal-filtered microbial VCs promoted reductive activation of the starch biosynthetic AGP enzyme, but super-elevated CO_2 conditions did not (Figure 8).

The presence of fungal cultures in the sealed growth chambers increased the headspace CO and NO concentrations (Figure 2), which is consistent with the capacity of fungi to emit these VICs (Conrath et al., 2004; Schreiber et al., 2012; Siegel & Siegel, 1987; Wharton & Weintraub, 1980). Exogenous application of CO promotes growth, chlorophyll accumulation, LR formation and root hair elongation (Guo et al., 2009; Guo, Xia, & Yang, 2008; Han et al., 2012; Kong et al., 2010; Xuan et al., 2008; Yang et al., 2016). Furthermore, exposure to parts per billion levels of NO promotes growth and chlorophyll accumulation (He et al., 2004). Moreover, NO enhances expression of non-symbiotic hemoglobins (nsHB) (Kuruthukulangarakoola et al., 2017), which is known to promote growth (Hebelstrup & Jensen, 2008; Hunt et al. 2002). We observed similar responses in plants exposed to charcoal-filtered fungal VCs (Figures 3 and 4, Supporting Information Table S2) (Sánchez-López, Bahaji, et al., 2016; Sánchez-López, Baslam, et al., 2016). This suggests that enhancement of growth and photosynthesis and promotion of early flowering and changes in the root architecture of plants exposed to charcoal-filtered fungal VCs could be at least partly due to fungal CO and NO emissions.

Many transcriptional changes occurring in leaves after brief exposure to VCs are probably due to enhanced photosynthetic CO_2 fixation signalling

The transcriptomic changes in leaves of Arabidopsis plants shortly exposed to super-elevated CO_2 and VCs emitted by diverse microorganisms, with and without charcoal filtering, are strikingly similar (Supporting Information Table S2, Supporting Information Table S3) (Sánchez-López, Baslam, et al., 2016). These transcriptomic changes are also very similar to those seen in plants shortly exposed to increased irradiance (Table 2, Supporting Information Table S4). All of these treatments promote photosynthetic CO_2 fixation (Figure 4a) (Ainsworth & Rogers, 2007; Athanasiou et al., 2010; Makino & Mae, 1999). We thus propose that many transcriptomic changes in the leaves of plants exposed to super-elevated CO_2, increased irradiance, or microbial VCs indirectly result from signalling of enhanced photosynthetic CO_2 fixation by means of Calvin-Benson cycle (CBC) intermediate(s) or their derivatives. In this respect it should be noted that the production of the CBC intermediate glyceraldehyde 3-phosphate (GAP) is the first point of regulation in the synthesis of isoprenoid compounds derived from the plastidial methylerythritol 4-phosphate (MEP) pathway, including hormones (Pokhilko, Bou-Torrent, Pulido, Rodríguez-Concepción, & Ebenhöh, 2015; Pulido, Perello, & Rodríguez-Concepcion, 2012). Fungal VCs promote the accumulation of high levels of MEP pathway-derived carotenoids and chlorophylls (Figure 4a) (Sánchez-López, Bahaji, et al., 2016), which, in turn, further promote photosynthesis. Moreover, fungal VCs promote the accumulation of MEP pathway-derived CKs and the resulting changes in the expression of a significant number of CK-regulated genes (Sánchez-López, Bahaji, et al., 2016; Sánchez-López, Baslam, et al., 2016). Therefore, as shown schematically in Figure 9, we propose that many transcriptional changes occurring in leaves of plants shortly exposed to microbial VCs, super-elevated CO_2 and increased irradiance are due to signalling involving photosynthetic GAP-derived isoprenoid hormones.

Regulation of some plant responses to fungal VCs is primarily post-transcriptional

The observation of similar transcriptional changes, but distinct developmental and metabolic responses in plants exposed to super-elevated CO_2 levels and VCs emitted by different microorganisms (Figures 3, 4, 6 and 7, Supporting Information Tables S1 and S2, cf. Supporting Information Table S3 in Sánchez-López, Baslam, et al. 2016) suggests that some responses induced by microbial VCs are regulated, at least in part, by different post-transcriptional mechanisms. This hypothesis is supported by the findings that more than 80% of the proteins that are differentially expressed by fungal VCs are encoded by genes whose expression is not altered by this treatment (Sánchez-López, Bahaji, et al., 2016).

Reversible protein thiol redox regulation through mechanisms such as NO-dependent S-nitrosylation, disulfide bond formation, S-sulfenylation and S-glutathionylation is a fundamental switch mechanism of post-translational regulation of metabolism, growth and development, which allows plants to adjust to ever changing environmental constrains (Aroca, Benito, Gotor, & Romero, 2017; Buchanan & Balmer, 2005; Hu et al., 2015). The findings that plants exposed to charcoal-filtered microbial VCs, but not to super-elevated CO_2, exhibit reductive activation of the starch biosynthetic enzyme AGP (Figure 8) further strengthen the idea that some of the plants´ responses to microbial VCs are post-transcriptionally regulated, and suggest that some of these responses are due to post-translational modifications of the thiol redox proteome. Further investigations will be needed to determine whether global post-translational redox modifications of proteins are involved in plant responses to microbial VCs.

AUTHORS´ CONTRIBUTIONS

P G-G, G A and J P-R designed the experiments and analyzed the data; P G-G, G A, AM S-L, A B, K A, A R-B, M B, MC A, A U, FJ M and E B-F performed most of the experiments; F JM, E B-F, A U and J P-R supervised the experiments; P G-G, G A and J P-R wrote the article with contributions from all the authors; J P-R conceived the project and research plans.

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REFERENCES

Adie, B. A. T., Pérez-Pérez, J., Pérez-Pérez, M. M., Godoy, M., Sánchez-Serrano, J.-J., Schmelz, E. a, & Solano, R. (2007). ABA is an essential signal for plant resistance to pathogens affecting JA biosynthesis and the activation of defenses in Arabidopsis. *The Plant Cell*, *19*, 1665–1681.

Ainsworth, E. A., & Rogers, A. (2007). The response of photosynthesis and stomatal conductance to rising [CO_2]: mechanisms and environmental interactions. *Plant, Cell and Environment*, *30,* 258–270

Aroca, A., Benito, J. M., Gotor, C., & Romero, L. C. (2017). Persulfidation proteome reveals the regulation of protein function by hydrogen sulfide in diverse biological processes in Arabidopsis. *Journal of Experimental Botany*, *68*, 4915–4927.

Athanasiou, K., Dyson, B. C., Webster, R. E., & Johnson, G. N. (2010). Dynamic acclimation of photosynthesis increases plant fitness in changing environments. *Plant Physiology*, *152*, 366–373.

Blom, D., Fabbri, C., Eberl, L., & Weisskopf, L. (2011). Volatile-mediated killing of *Arabidopsis thaliana* by bacteria is mainly due to hydrogen cyanide. *Applied and Environmental Microbiology*, *77*, 1000–1008.

Boccara, M., Mills, C. E., Zeier, J., Anzi, C., Lamb, C. Poole, R. K. & Delledonne, M. (2005). Flavohaemoglobin HmpX from *Erwinia chrysanthemi* confers nitrosative stress tolerance and affects the plant hypersensitive reaction by intercepting nitric oxide produced by the host. *The Plant Journal, 43,* 226–237.

Buchanan, B. B., & Balmer, Y. (2005). Redox regulation: a broadening horizon. *Annual Review of Plant Biology*, *56*, 187–220.

Casarrubia, S., Sapienza, S., Fritz, H., Daghino, S., Rosenkranz, M., Schnitzler, J. P., … Martino, E. (2016). Ecologically different fungi affect arabidopsis development: contribution of soluble and volatile compounds. *PLoS ONE*, *11*, e0168236. doi: https://doi.org/10.1371/journal.pone.0168236

Chen, J., Wu, F. H., Wang, W. H., Zheng, C. J., Lin, G. H., Dong, X. J., … Zheng, H. L. (2011). Hydrogen sulphide enhances photosynthesis through promoting chloroplast biogenesis, photosynthetic enzyme expression, and thiol redox modification in *Spinacia oleracea* seedlings. *Journal of Experimental Botany*, *62*, 4481–4493.

Contreras-Cornejo, H. A., Macías-Rodríguez, L., Herrera-Estrella, A., & López-Bucio, J. (2014). The 4-phosphopantetheinyl transferase of *Trichoderma virens* plays a role in plant protection against *Botrytis cinerea* through volatile organic compound emission. *Plant and Soil, 379,* 261–274.

Conrath, U., Amoroso, G., Köhle, H., & Sültemeyer, D. F. (2004). Non-invasive online detection of nitric oxide from plants and some other organisms by mass spectrometry. *The Plant Journal*, *38*, 1015–1022.

Cordovez, V., Mommer, L., Moisan, K., Lucas-Barbosa, D., Pierik, R., Mumm, R., … Raaijmakers, J. M. (2017). Plant phenotypic and transcriptional changes induced by volatiles from the fungal root pathogen *Rhizoctonia solani*. *Frontiers in Plant Science*, *8*. doi: https://doi.org/10.3389/fpls.2017.01262

Ditengou, F. A., Müller, A., Rosenkranz, M., Felten, J., Lasok, H., Van Doorn, M. M., … Polle, A. (2015). Volatile signalling by sesquiterpenes from ectomycorrhizal fungi reprogrammes root architecture. *Nature Communications*. doi: https://doi.org/10.1038/ncomms7279

Dong, Z., Wu, L., Kettlewell, B., Caldwell, C. D., & Layzell, D. B. (2003). Hydrogen fertilization of soils - is this a benefit of legumes in rotation? *Plant, Cell and Environment*, *26*, 1875–1879.

Dooley, F. D., Nair, S. P., & Ward, P. D. (2013). Increased growth and germination success in plants following hydrogen sulfide administration. *PLoS ONE*, *8*, e62048. doi:https://doi.org/10.1371/journal.pone.0062048

Dyson, B. C., Allwood, J. W., Feil, R., Xu, Y. U. N., Miller, M., Bowsher, C. G., … Johnson, G. N. (2015). Acclimation of metabolism to light in *Arabidopsis thaliana*: the glucose 6phosphate/phosphate translocator GPT2 directs metabolic acclimation. *Plant, Cell and Environment*, *38*, 1404–1417.

Engel, R. R., Matsen, J. M., Chapman, S. S., & Schwartz, S. (1972). Carbon monoxide production from heme compounds by bacteria. *Journal of Bacteriology*, *112*, 1310–1315.

Ezquer, I., Li, J., Ovecka, M., Baroja-Fernández, E., Muñoz, F. J., Montero, M., … Pozueta-Romero, J. (2010). Microbial volatile emissions promote accumulation of exceptionally high levels of starch in leaves in mono- and dicotyledonous plants. *Plant and Cell Physiology*, *51*, 1674–1693.

Farag, M. A., Song, G. C., Park, Y. S., Audrain, B., Lee, S., Ghigo, J. M., … Ryu, C. M. (2017). Biological and chemical strategies for exploring inter- and intra-kingdom communication mediated via bacterial volatile signals. *Nature Protocols, 12*, 1359–1377.

Farkas, V., Gresik, M., Kolarova, N., Sulova, Z., & Sestak, S. (1990). Biochemical and physiological changes during photoinduced conidiation and derepression of cellulase synthesis in *Trichoderma*. In *Trichoderma reesei* cellulase: biochemistry, genetics, physiology and application. (eds C.P. Kubicek, D.E. Eveleigh, H. Esterbauer, W. Steiner & E.M. Kubicek-Pranz), pp 139–155. Graham, Cambridge.

Garnica-Vergara, A., Barrera-Ortiz, S., Muñoz-Parra, E., Raya-González, J., Méndez-Bravo, A., Macías-Rodríguez, L., … López-Bucio, J. (2016). The volatile 6-pentyl-2*H*-pyran-2-one from *Trichoderma atroviride* regulates *Arabidopsis thaliana* root morphogenesis via auxin signaling and *ETHYLENE INSENSITIVE 2* functioning. *New Phytologist, 209*, 1496–1512.

Garrido, J., Linares-Solano, A., Martin-Martinez, J. M., Molina-Sabio, M., Rodríguez-Reinoso, F., & Torregrosa, R. (1987). Use of N_2 vs CO_2 in the characterization of activated carbons. *Langmuir*, *3*, 76–81.

Groenhagen, U., Baumgartner, R., Bailly, A., Gardiner, A., Eberl, L., Schulz, S., & Weisskopf, L. (2013). Production of bioactive volatiles by different *Burkholderia ambifaria* strains. *Journal of Chemical Ecology, 39,* 892–906.

Guo, K., Kong, W. W., & Yang, Z. M. (2009). Carbon monoxide promotes root hair development in tomato. *Plant, Cell and Environment*, *32*, 1033–1045.

Guo, K., Xia, K., & Yang, Z. M. (2008). Regulation of tomato lateral root development by carbon monoxide and involvement in auxin and nitric oxide. *Journal of Experimental Botany*, *59*, 3443–3452.

Hachiya, T., Sugiura, D., Kojima, M., Sato, S., Yanagisawa, S., Sakakibara, H., … Noguchi, K. (2014). High CO_2 triggers preferential root growth of *Arabidopsis thaliana* via two distinct systems under low pH and low N stresses. *Plant and Cell Physiology, 55*, 269–280.

Han, B., Xu, S., Xie, Y. J., Huang, J. J., Wang, L. J., Yang, Z., … Xie, G. S. (2012). ZmHO-1, a maize haem oxygenase-1 gene, plays a role in determining lateral root development. *Plant Science*, *184*, 63–74.

He, Y., Tang, R. H., Hao, Y., Stevens, R. D., Cook, C. W., Ahn, S. M., … Pei, Z. M. (2004).

Nitric oxide represses the Arabidopsis floral transition. *Science*, *305*, 1968–1971.

Hebelstrup, K. H., & Jensen, E. O. (2008). Expression of NO scavenging hemoglobin is involved in the timing of bolting in *Arabidopsis thaliana*. *Planta*, *227*, 917–927.

Hendriks, J. H. M., Kolbe, A., Gibon, Y., Stitt, M., & Geigenberger, P. (2003). ADP-glucose pyrophosphorylase is ativated by posttranslational redox-modification in response to light and to sugars in leaves of Arabidopsis and other plant species. *Plant Physiology*, *133*, 838–849.

Hu, J., Huang, X., Chen, L., Sun, X., Lu, C., Zhang, L., … Zuo, J. (2015). Site-specific nitrosoproteomic identification of endogenously S-nitrosylated proteins in Arabidopsis. *Plant Physiology*, *167*, 1731–1746.

Hung, R., Lee, S., & Bennett, J. W. (2013). *Arabidopsis thaliana* as a model system for testing the effect of Trichoderma volatile organic compounds. *Fungal Ecology*, *6*, 19–26.

Hunt, P. W., Klok, E. J., Trevaskis, B., Watts, R. A., Ellis, M. H., Peacock, W. J., & Dennis, E. S. (2002). Increased level of hemoglobin 1 enhances survival of hypoxic stress and promotes early growth in *Arabidopsis thaliana*. *Proceedings of the National Academy of Sciences of the United States of America*, *99*, 17197–17202.

Jin, C. W., Du, S. T., Zhang, Y. S., Tang, C., & Lin, X. Y. (2009). Atmospheric nitric oxide stimulates plant growth and improves the quality of spinach (*Spinacia oleracea*). *Annals of Applied Biology*, *155*, 113–120.

Jin, Q., Zhu, K., Cui, W., Xie, Y., Han, B., & Shen, W. (2013). Hydrogen gas acts as a novel bioactive molecule in enhancing plant tolerance to paraquat-induced oxidative stress via the modulation of heme oxygenase-1 signalling system. *Plant, Cell and Environment*, *36*, 956–969.

Johnson, E., Sparks, J. P., Dzikovski, B., Crane, B. R., Gibson, D. M. & Loria, R. (2008). Plant-pathogenic *Streptomyces* species produce nitric oxide synthase-derived nitric oxide in response to host signals. *Chemistry & Biology, 15,* 43–50.

Kai, M., Effmert, U., & Piechulla, B. (2016). Bacterial-plant-interactions: approaches to unravel the biological function of bacterial volatiles in the rhizosphere. *Frontiers in Microbiology, 9*, 108. doi: https://doi.org/10.3389/fmicb.2016.00108

Kai, M., & Piechulla, B. (2009). Plant growth promotion due to rhizobacterial volatiles - an effect of CO_2? *FEBS Letters*, *583*, 3473–3477.

Kanchiswamy, C. N., Malnoy, M., & Maffei, M. E. (2015). Chemical diversity of microbial volatiles and their potential for plant growth and productivity. *Frontiers in Plant Science*, *6*. https://doi.org/10.3389/fpls.2015.00151

Kong, W. W., Zhang, L. P., Guo, K., Liu, Z. P. & Yang Z. M. (2010). Carbon monoxide improves adaptation of Arabidopsis to iron deficiency. *Plant Biotechnology Journal, 8,* 88–99.

Kuruthukulangarakoola, G. T., Zhang, J., Albert, A., Winkler, B., Lang, H., Buegger, F., … Lindermayr, C. (2017). Nitric oxide-fixation by non-symbiotic haemoglobin proteins in *Arabidopsis thaliana* under N-limited conditions. *Plant, Cell and Environment,* 40, 36–50.

Ledger, T., Rojas, S., Timmermann, T., Pinedo, I., Poupin, M. J., Garrido, T., … Donoso, R. (2016). Volatile-mediated effects predominate in *Paraburkholderia phytofirmans* growth promotion and salt stress tolerance of *Arabidopsis thaliana*. *Frontiers in Microbiology*, *7*. doi: https://doi.org/10.3389/fmicb.2016.01838

Lemfack, M. C., Gohlke, B. O., Toguem, S. M. T., Preissner, S., Piechulla, B., & Preissner, R. (2018). mVOC 2.0: a database of microbial volatiles. *Nucleic Acids Research*, *46*, D1261–

D1265.

Li, J., Ezquer, I., Bahaji, A., Montero, M., Ovecka, M., Baroja-Fernández, E., … Pozueta-Romero, J. (2011). Microbial volatile-induced accumulation of exceptionally high levels of starch in Arabidopsis leaves is a process involving NTRC and starch synthase classes III and IV. *Molecular Plant-Microbe Interactions*, *24*, 1165–1178.

Lin, Y., Zhang, W., Qi, F., Cui, W., Xie, Y., & Shen, W. (2014). Hydrogen-rich water regulates cucumber adventitious root development in a heme oxygenase-1/carbon monoxide-dependent manner. *Journal of Plant Physiology*, *171*, 1–8.

Lisjak, M., Teklic, T., Wilson, I. D., Whiteman, M., & Hancock, J. T. (2013). Hydrogen sulfide: environmental factor or signalling molecule? *Plant, Cell and Environment*, *36*, 1607–1616.

Makino, A., & Mae, T. (1999). Photosynthesis and plant growth at elevated levels of CO_2. *Plant and Cell Physiology*, *40*, 999–1006.

Meldau, D. G., Meldau, S., Hoang, L. H., Underberg, S., Wünsche, H. & Baldwin, I. T. (2013). Dimethyl disulfide produced by the naturally associated bacterium *Bacillus* sp B55 promotes *Nicotiana attenuata* growth by enhancing sulfur nutrition. *The Plant Cell, 25,* 2731–2747.

Molina-Favero, C., Creus, C. M., Simontacchi, M., Puntarulo, S., & Lamattina, L. (2008). Aerobic nitric oxide production by *Azospirillum brasilense* Sp245 and its influence on root architecture in tomato. *Molecular Plant-Microbe Interactions*, *21*, 1001–1009.

Nandi, R., & Sengupta, S. (1998). Microbial production of hydrogen: an overview. *Critical Reviews in Microbiology*, *24*, 61–84.

Naznin, H. A., Kimura, M., Miyazawa, M. & Hyakumachi, M. (2013). Analysis of volatile organic compounds emitted by plant growth-promoting fungus *Phoma* sp. GS8-3 for growth promotion effects on tobacco. *Microbes and Environments, 28*, 42–49.

Nieto-Jacobo, M. F., Steyaert, J. M., Salazar-Badillo, F. B., Nguyen, D. V., Rostás, M., Braithwaite, M., … Mendoza-Mendoza, A. (2017). Environmental growth conditions of *Trichoderma* spp. affects indole acetic acid derivatives, volatile organic compounds, and plant growth promotion. *Frontiers in Plant Science, 8*. doi: 10.3389/fpls.2017.00102

Niu, Y., Jin, C., Jin, G., Zhou, Q., Lin, X., Tang, C., & Zhang, Y. S. (2011). Auxin modulates the enhanced development of root hairs in A*rabidopsis thaliana* (L.) Heynh. under elevated CO_2. *Plant, Cell and Environment*, *34*, 1304–1317.

Piechulla, B. (2017). Considering microbial CO_2 during microbe-plant cocultivation. *Plant Physiology*, *173*, 1529.

Piechulla, B., Lemfack, M. C., & Kai, M. (2017). Effects of discrete bioactive microbial volatiles on plants and fungi. *Plant, Cell and Environment*, *40*, 2042–2067

Pokhilko, A., Bou-Torrent, J., Pulido, P., Rodríguez-Concepción, M., & Ebenhöh, O. (2015). Mathematical modelling of the diurnal regulation of the MEP pathway in Arabidopsis. *New Phytologist*, *206*, 1075–1085.

Pulido, P., Perello, C., & Rodríguez-Concepcion, M. (2012). New insights into plant isoprenoid metabolism. *Molecular Plant*, *5*, 964–967.

Quebedeaux, B., & Hardy, R. W. F. (1975). Reproductive growth and dry matter production of *Glycine max* (L.) Merr. in response to oxygen concentration. *Plant Physiology*, *55*, 102–107.

Ramonell, K. M., Kuang, A., Porterfield, D. M., Crispi, M. L., Xiao, Y., McClure, G., & Musgrave, M. E. (2001). Influence of atmospheric oxygen on leaf structure and starch deposition in *Arabidopsis thaliana. Plant, Cell and Environment*, *24*, 419–428.

Rodríguez-Reinoso, F., Garrido, J., Martín-Martínez, J. M., Molina-Sabio, M., & Torregrosa, R. (1989). The combined use of different approaches in the characterization of microporous carbons. *Carbon* 27, 23–32.

Ryu, C.-M., Farag, M. A., Hu, C.-H., Reddy, M. S., Wei, H.-X., Paré, P. W., & Kloepper, J. W. (2003). Bacterial volatiles promote growth in Arabidopsis. *Proceedings of the National Academy of Sciences*, *100*, 4927–4932.

Sánchez-López, Á. M., Bahaji, A., De Diego, N., Baslam, M., Li, J., Muñoz, F. J., … Pozueta-Romero, J. (2016). Arabidopsis responds to *Alternaria alternata* volatiles by triggering plastid phosphoglucose isomerase-independent mechanisms. *Plant Physiology*, *172*, 1989–2001.

Sánchez-López, Á. M., Baslam, M., De Diego, N., Muñoz, F. J., Bahaji, A., Almagro, G., … Pozueta-Romero, J. (2016). Volatile compounds emitted by diverse phytopathogenic microorganisms promote plant growth and flowering through cytokinin action. *Plant, Cell and Environment*, *39*, 2592–2608.

Schenkel, D., Maciá-Vicente, J. G., Bissell, A., & Splivallo, R. (2018). Fungi indirectly affect plant root architecture by modulating soil volatile organic compounds. *Frontiers in Microbiology, 9*. doi: 10.3389/fmicb.2018.01847.

Schreiber, F., Wunderlin, P., Udert, K. M., & Wells, G. F. (2012). Nitric oxide and nitrous oxide turnover in natural and engineered microbial communities: Biological pathways, chemical reactions, and novel technologies. *Frontiers in Microbiology*. doi: https://doi.org/10.3389/fmicb.2012.00372

Shatalin, K., Shatalina, E., Mironov, A., & Nudler, E. (2011). H_2S: a universal defense against antibiotics in bacteria. *Science*, *334*, 986–990.

Siegel, S. M., & Siegel, B. Z. (1987). Biogenesis of carbon monoxide: production by fungi and seed plants in the dark. *Phytochemistry*, *26*, 3117–3119.

Smyth, G. K., & Speed, T. (2003). Normalization of cDNA microarray data. *Methods*, *31*, 265–273.

Song, X., Kristie, D. N., & Reekie, E. G. (2009). Why does elevated CO_2 affect time of flowering? An exploratory study using the photoperiodic flowering mutants of *Arabidopsis thaliana*. *New Phytologist*, *181*, 339–346.

Takahashi, M., Furuhashi, T., Ishikawa, N., Horiguchi, G., Sakamoto, A., Tsukaya, H., & Morikawa, H. (2014). Nitrogen dioxide regulates organ growth by controlling cell proliferation and enlargement in Arabidopsis. *New Phytologist*, *201*, 1304–1315.

Thompson, M., Gamage, D., Hirotsu, N., Martin, A., & Seneweera, S. (2017). Effects of elevated carbon dioxide on photosynthesis and carbon partitioning: a perspective on root sugar sensing and hormonal crosstalk. *Frontiers in Physiology*, *8,* 578. https://doi.org/10.3389/fphys.2017.00578

Tisch, D., & Schmoll, M. (2010). Light regulation of metabolic pathways in fungi. *Applied Microbiology and Biotechnology*, *85*, 1259–1277

van Den Dool, H., & Dec. Kratz, P. (1963). A generalization of the retention index system including linear temperature programmed gas—liquid partition chromatography. *Journal of Chromatography A*, *11*, 463–471.

Velázquez-Becerra, C., Macías-Rodríguez, L. I., López-Bucio, J., Altamirano-Hernández, J., Flores-Cortez, I. & Valencia-Cantero, E. (2011). A volatile organic compound analysis from *Arthrobacter agilis* identifies dimethylhexadecylamine, an amino-containing lipid modulating bacterial growth and *Medicago sativa* morphogenesis in vitro. *Plant and Soil, 339,* 329–340.

von Caemmerer, S., & Farquhar, G. D. (1981). Some relationships between the biochemistry of photosynthesis and the gas exchange of leaves. *Planta*, *153*, 376–387.

Wang, M., & Liao, W. (2016). Carbon monoxide as a signaling molecule in plants. *Frontiers in Plant Science*. doi: https://doi.org/10.3389/fpls.2016.00572

Weikl, F., Ghirardo, A., Schnitzler, J.-P., & Pritsch, K. (2016). Sesquiterpene emissions from *Alternaria alternata* and *Fusarium oxysporum*: effects of age, nutrient availability, and co-cultivation. *Scientific Reports*, *6*, 2152. doi: https://doi.org/10.1038/srep22152

Weise, T., Kai, M., & Piechulla, B. (2013). Bacterial ammonia causes significant plant growth inhibition. *PLoS ONE*, *8*, e63538. doi: https://doi.org/10.1371/journal.pone.0063538

Wharton, D. C., & Weintraub, S. T. (1980). Identification of nitric oxide and nitrous oxide as products of nitrite reduction by *Pseudomonas* cytochrome oxidase (nitrite reductase). *Biochemical and Biophysical Research Communications*, *97*, 236–242.

Xu, Q., Zhou, B., Ma, C., Xu, X., Xu, J., Jiang, Y., … Hao, L. (2010). Salicylic acid-altering Arabidopsis mutants response to NO_2 exposure. *Bulletin of Environmental Contamination and Toxicology*, *84*, 106–111.

Xuan, W., Zhu, F.-Y., Xu, S., Huang, B.-K., Ling, T.-F., Qi, J.-Y., … Shen, W.-B. (2008). The heme oxygenase/carbon monoxide system is involved in the auxin-induced cucumber adventitious rooting process. *Plant Physiology*, *148*, 881–893.

Yang, L., Ji, J., Wang, H., Harris-Shultz, K. R., Abd Allah, E. F., Luo, Y., … Hu, X. (2016). Carbon monoxide interacts with auxin and nitric oxide to cope with iron deficiency in Arabidopsis. *Frontiers in Plant Science*. doi: https://doi.org/10.3389/fpls.2016.00112

Zeng, J., Zhang, M., & Sun, X. (2013). Molecular hydrogen is involved in phytohormone signaling and stress responses in plants. *PLoS ONE*, *8*, e71038. doi: https://doi.org/10.1371/journal.pone.0071038

Zhang, H., Sun, Y., Xie, X., Kim, M. S., Dowd, S. E., & Paré, P. W. (2009). A soil bacterium regulates plant acquisition of iron via deficiency-inducible mechanisms. *The Plant Journal*, *58*, 568–577.

Zou, C., Li, Z., & Yu, D. (2010). *Bacillus megaterium* strain XTBG34 promotes plant growth by producing 2-pentylfuran. *The Journal of Microbiology, 48*, 460–466.

FIGURE LEGENDS

Figure 1. Volatile emissions of *A. alternata* and *P. aurantiogriseum* promote distinct responses in the root architecture of Arabidopsis plants cultured in a "box-in-box" co-cultivation system. (a) External phenotypes of plants and (b) roots, and (c) root architecture parameters of *Arabidopsis* plants grown on vertical plates in the absence or continuous presence for one week of adjacent cultures of *A. alternata* or *P. aurantiogriseum*. Values given in (c) represent the means ± SE of three biological replicates obtained from three independent experiments, each biological replicate being a pool of 12 plants. Asterisks indicate significant differences relative to plants not cultured with adjacent fungal cultures based on Student´s t-test (p<0.05). Scale bars in a and b = 1 cm and 1 mm, respectively.

Figure 2: CO and NO contents in the headspace of PVC-sealed growth boxes containing *A. alternata* or *P. aurantiogriseum* cultures with or without charcoal filters. Values represent the means ± SE of four biological replicates obtained from four independent experiments, each biological replicate being four growth boxes. Asterisks indicate significant differences relative to controls (fungal cultures lacking growth boxes) based on Student´s t-test (p<0.05).

Figure 3. Charcoal-filtered (VOC-depleted) and non-filtered fungal volatile emissions promote similar growth and root developmental responses in exposed plants. (a) External phenotypes and (b) rosette and root FW and time of floral bud appearance of plants grown with adjacent *A. alternata* and *P. aurantiogriseum* cultures with or without charcoal filter. (c) Root architecture parameters of plants grown with adjacent fungal cultures with charcoal filter. In (a) and (b) plants were grown on horizontal plates, whereas in (c) plants were grown on vertical plates. Values given in (b) and (c) represent the means ± SE of three biological replicates obtained

from three independent experiments, each biological replicate being a pool of 12 plants. Asterisks indicate significant differences relative to plants not cultured with adjacent fungal cultures according to Student´s t-test (p<0.05).

Figure 4. Charcoal-filtered (VOC-depleted) fungal volatile emissions promote photosynthesis in leaves. (a) Net rates of CO_2 assimilation (A_n) and total chlorophyll content, and (b) photosynthate (starch, sucrose, glucose and fructose) levels in leaves of plants cultured with adjacent *A. alternata* and *P. aurantiogriseum* cultures with or without charcoal filter. Values represent means ± SE of three biological replicates obtained from three independent experiments, each biological replicate being a pool of 12 plants. Asterisks indicate significant differences relative to plants not grown with adjacent fungal cultures according to Student´s t-test (p<0.05).

Figure 5. Time-course of CO_2 and O_2 levels in the headspace of PVC-sealed growth boxes containing *A. alternata* or *P. aurantiogriseum* cultures covered with charcoal filters. The sealed boxes were connected to CO_2 and O_2 analysers, and placed in CO_2-controlled growth cabinets with a 16 h light/8 h dark photoperiod (cf. Supporting Information Figure S1). At the indicated time the CO_2 concentration in the cabinet was increased to 1000 ppm.

Figure 6. Respiratory CO_2 plays a minor role in growth and root architecture changes induced by charcoal-filtered fungal VCs in Arabidopsis plants grown in a "box-in-box" co-cultivation system. (a) Rosette FW and time of floral bud appearance and (b) root architecture parameters of plants grown under 550 or 2000 ppm CO_2 conditions. In (a) plants were grown on horizontal plates, whereas in (b) plants were grown on vertical plates. Values are means ± SE of three

biological replicates obtained from three independent experiments, each biological replicate being a pool of 12 plants. Asterisks indicate significant differences from plants cultured under atmospheric CO_2 conditions according to Student´s t-test ($p<0.05$).

Figure 7. Leaf starch levels in *Arabidopsis* plants cultured in the absence or presence for 16 h of 550 ppm CO_2, 2000 ppm CO_2 or adjacent *A. alternata* cultures covered with charcoal filters. Values represent means ± SE of three biological replicates obtained from three independent experiments, each biological replicate being a pool of 12 plants. Asterisks indicate significant differences from plants not cultured with exogenously supplied CO_2 or adjacent fungal cultures according to Student´s t-test ($p<0.05$).

Figure 8. Non-reducing western blot analysis of APS1 in leaves of *Arabidopsis* plants cultured in the absence or presence for 12 h of charcoal-filtered VCs emitted by adjacent *A. alternata* cultures or 2000 ppm CO_2.

Figure 9: Suggested model for the plant´s transcriptional response to short exposure to fungal VCs, super-elevated CO_2 and increased irradiance. According to this model VCs interact with as yet unidentified plasma membrane receptors to produce signals that rapidly promote changes in gene expression. Alternatively and/or additionally, some VCs (especially small and highly reactive VICs) penetrate the cell and modify photosynthesis- and metabolism-related proteins. Increased irradiance and treatment with super-elevated CO_2 promote photosynthesis. Augmentation of the photosynthetic activity induced by these treatments results in enhanced GAP, which enters the MEP pathway to fuel the production of isoprenoid hormones that initiate a cascade of reactions resulting in highly conserved changes in the expression of genes involved

in many different processes.

SUPPORTING INFORMATION

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

Figure S1: System to analyse the microbial VCs in the headspace of growth chambers containing fungal cultures. (A) For VOCs analyses, the PVC wrap of the sealed growth boxes was carefully drilled with a DVB/CAR/PDMS coated fiber, and the adsorbed VOCs were analysed by GC-MS. For online monitoring of the CO_2 contents, the PVC-sealed growth boxes were connected to a Vaisala CARBOCAP® Carbon Dioxide Probe GMP343 combined with a Vaisala Handheld Measurement Indicator MI70. For O_2 and CO contents analyses, sealed growth boxes were connected to a MX4 portable headspace analyser. (B) For NO analyses, sealed growth boxes were connected to a Ecotec Serinus 40 Oxides Nitrogen Analyser (Ecotech Pty Ltd., Knoxfield, VIC, Australia).

Figure S2: Volatile emissions of *A. alternata* and *P. aurantiogriseum* promote rosette and root growth and flowering in Arabidopsis plants cultured in a "box-in-box" co-cultivation system. (a) External phenotypes of plants and (b) roots, and (c) rosette FW, (d) root FW and (e) time of floral bud appearance of *Arabidopsis* plants grown in the absence or continuous presence for one week of adjacent cultures of *A. alternata* or *P. aurantiogriseum*. Values given in (c), (d) and (e) represent the means ± SE of 3 biological replicates obtained from 3 independent experiments, each biological replicate being a pool of 12 plants. Asterisks indicate significant differences relative to plants not cultured with adjacent fungal cultures based on Student´s t-test ($p<0.05$).

Figure S3: Schematic representation of the “box-in-box” co-cultivation system used in this work. Plant cultures were placed in boxes containing *A. alternata* and *P. aurantiogriseum* cultures covered with a porous nylon mesh with or without an upper charcoal filter.

Figure S4: Textural characterization of the charcoal used in this study. (a) N_2 adsorption isotherm at -196 ^{o}C of the charcoal, which according to IUPAC classification, is type I(b)–IV(a). The adsorption branch of this xerogel corresponds to type I(b), and the hysteresis loop is characteristic of type-IV(a) isotherms. Type I(b) isotherms are found with materials having pore size distributions over a broader range including wider micropores and possibly narrow mesopores (< ⍰ 2.5 nm). Type IV isotherms are given by mesoporous adsorbents. In the case of a Type IVa isotherm, capillary condensation is accompanied by hysteresis. This occurs when the pore width exceeds a certain critical width, which is dependent on the adsorption system and temperature. The hysteresis loop is H4. The adsorption branch is a composite of Types I and II, the more pronounced uptake at low p/p0 being associated with the filling of micropores. H4 loops are often found in micro-mesoporous carbons. (b) Porosity distribution of Barret, Joyner and Halenda, which predicts that micropores are greater than 0.7 nm. In the porous texture of the coal there are also present mesopores with sizes ranging between 2 and 5 nm.

Figure S5: SPME GC-MS chromatograms of VOCs in the headspace of growth boxes containing cultures of *A. alternata* and *P. aurantiogriseum* with or without an upper activated charcoal filter.

Figure S6: Time-course of CO_2 levels in the headspace of PVC-sealed growth boxes placed in a CO_2-controlled growth cabinet in which the CO_2 concentrations were increased stepwise from 550 to 700, 1000 and 1500 ppm. The growth boxes did not contain fungal or plant cultures.

Table S1: Textural parameters for the activated charcoal used in this study

Table S2: List of genes whose expression is altered by charcoal-filtered VCs emitted by *A. alternata*.

Table S3: List of genes whose expression is altered by super-elevated CO_2 treatment.

Table S4: List of genes whose expression is altered by high irradiance treatment (Athanasiou et al. 2010) and *A. alternata* VCs.

Table 1. VOCs in the headspace of growth boxes containing *A. alternata* and *P. aurantiogriseum* cultures with or without an upper activated charcoal filter. [a]Compounds identified by comparison of RT and mass spectral data to those of authentic compounds. Other compounds were identified by comparing their mass spectral data to spectra from the NIST library and by comparing their linear retention indices (using an n-alkane scale) to literature values. [b]Compounds emitted by *A. alternata* described in Weikl, Ghirardo, Schnitzler, & Pritsch (2016). [c]Compounds previously reported to affect plant growth (Ditengou et al., 2015; Kanchiswamy et al,. 2015). n.d., not detected. Chromatograms are shown in Supporting Information Figure S4.

Retention time (min)	**Chemical family**	***A. alternata***		***P. aurantiogriseum***	
		- Charcoal	**+Charcoal**	**- Charcoal**	**+ Charcoal**
	Alcohol				
2.099		n.d.	n.d.	3-buten-2-ol,2-methyl[a]	n.d.
2.219		1-propanol,2-methyl[a]	n.d.	n.d.	n.d.
2.777		2-butanol,3-methyl[a]	n.d.	2-butanol,3-methyl[a]	n.d.
3.628		1-butanol,2-methyl[a,b]	n.d.	1-butanol,2-methyl[a]	n.d.
	Aldehyde				
16.783		Decanal[a]	n.d.	n.d.	n.d.
	Alkane				
2.680		hexane,3-methyl	n.d.	n.d	n.d

4.156	heptane,4-methyl	n.d.	n.d	n.d
4.284	heptane,3-methyl	n.d.	n.d	n.d
7.532	n.d.	n.d.	pentane,2-nitro-	n.d.
9.810	octane,2,4,6-trimethyl	n.d.	n.d	n.d
16.608	dodecane[a]	n.d.	n.d	n.d
20.003	tridecane[a]	n.d.	n.d	n.d
Alkene				
3.336	n.d.	n.d.	cyclopentene,3-ethyl	n.d.
3.726	n.d.	n.d.	1-methylcyclohexa-2,4-diene	n.d.
3.970	n.d.	n.d.	1-ethylcyclopentene	n.d.
8.281	n.d.	n.d.	2-butene,1-bromo-3-methyl	n.d.
Aromatic compound				
10.953	n.d.	n.d.	benzene,1-methoxy-3-methyl[a]	n.d.
15.544	benzaldehyde,4-ethyl	n.d.	n.d	n.d
18.491	n.d	n.d	3,5-dimethoxytoluene	n.d.
22.342	n.d	n.d	benzene,1,2,3-trimethoxy-5-methyl	n.d.
Carboxilic acid				

15.867	octanoic acid[a]	n.d.	n.d	n.d.
Ketone				
2.538	n.d.	n.d.	2-butanone,3-methyl	n.d.
4.543	n.d.	n.d.	4(1H)-pyrimidinone[a]	n.d.
10.235	3-octanone[a,c]	n.d.	n.d	n.d.
Monoterpene				
10.116	n.d.	n.d.	2-methylenebornane	n.d.
11.104	n.d.	n.d.	2-methyl-2-bornene	n.d.
16.089	n.d.	n.d.	2-methylisoborneol[a]	n.d.
Nitrile				
2.226	n.d.	n.d.	isobutyronitrile	n.d.
Oxime				
6.433	n.d.	n.d.	butyl aldoxime,2-methyl,syn-	n.d.
6.628	n.d.	n.d.	butyl aldoxime,2-methyl,anti-	n.d.
Sesquiterpene				
21.894	β-elemene[b,c]	n.d.	n.d.	n.d.
22.377	γ-muurolene[a,c]	n.d.	n.d.	n.d.

22.439	α-cedrene[a,b]	n.d.	α-cedrene[a]	n.d.
22.514	n.d.	n.d.	cadina-1,4-diene[c]	n.d.
22.652	β-cedrene[b]	n.d.	β-cedrene	n.d.
22.909	n.d.	n.d.	α-copaene[c]	n.d.
22.913	cis-thujopsene[a,b]	n.d.	n.d.	n.d.
23.219	unknown sesq. 1	n.d.	n.d.	n.d.
23.791	α-longipinene[a,c]	n.d.	n.d.	n.d.
23.999	acoradiene[b,c]	n.d.	n.d.	n.d.
24.238	4,5-di-epi-aristolochene	n.d.	n.d.	n.d.
24.447	valencene[c]	n.d.	n.d.	n.d.
24.708	α-chamigrene[a,b]	n.d.	α-chamigrene[a]	n.d.
24.763	cuparene[a]	n.d.	n.d.	n.d.

Table 2. Sets of the 20 most strongly up-regulated and 20 most strongly down-regulated genes in plants exposed to high irradiance (Athanasiou et al. 2010) that are also up- and down-regulated by VICs emitted by *A. alternata.*

Up-regulated genes

ID	Description
At1g61800	glucose-6-phosphate/phosphate translocator 2, putative mRNA, complete cds
At4g15210	beta-amylase (BMY1) / 1,4-alpha-D-glucan maltohydrolase mRNA, complete cds
At4g25630	fibrillarin 2 (FIB2) mRNA, complete cds
At1g32900	starch synthase, putative mRNA, complete cds
At4g16590	glucosyltransferase-related protein mRNA, complete cds
At2g27840	histone deacetylase-related / HD-related protein mRNA, complete cds
At3g18600	DEAD/DEAH box helicase, putative mRNA, complete cds
At1g06000	UDP-glucoronosyl/UDP-glucosyl transferase family protein mRNA, complete cds
At1g56650	myb family transcription factor (MYB75) mRNA, complete cds
At3g44750	histone deacetylase, putative (HD2A) mRNA, complete cds

Down-regulated genes

ID	Description
At1g74670	gibberellin-responsive protein, putative, complete cds
At2g40610	expansin, putative (EXP8), complete cds
At5g48490	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, complete cds
At3g15450	expressed protein, complete cds
At1g70290	trehalose-6-phosphate synthase, putative, complete cds
At1g23390	kelch repeat-containing F-box family protein, complete cds
At2g22980	serine carboxypeptidase S10 family protein, complete cds
At2g18700	glycosyl transferase family 20 protein / trehalose-phosphatase family protein, complete cds
At2g33830	dormancy/auxin associated family protein, complete cds
At5g61590	AP2 domain-containing transcription factor family protein mRNA, complete cds
At2g15890	expressed protein mRNA, complete cds
At1g80920	DNAJ heat shock N-terminal domain-containing protein mRNA, complete cds
At5g40890	chloride channel protein (CLC-a) mRNA, complete cds
At1g72150	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein mRNA, complete cds
At5g24490	30S ribosomal protein, putative mRNA, complete cds
At5g22920	zinc finger (C3HC4-type RING finger) family protein mRNA, complete cds

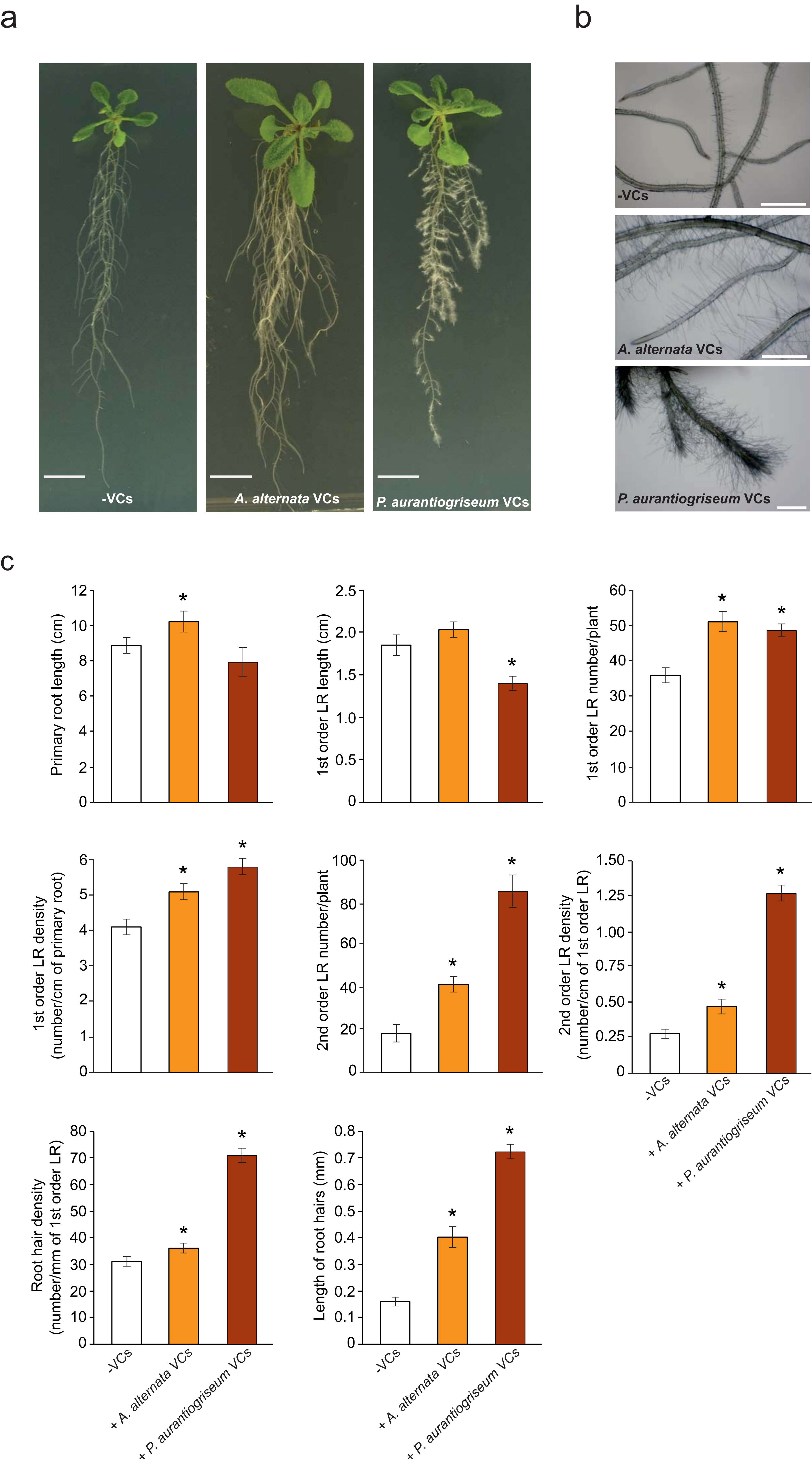

a
b
-VCs
A. alternata VCs
P. aurantiogriseum VCs
-VCs
A. alternata VCs
P. aurantiogriseum VCs
c
Primary root length (cm)
0
2
4
6
8
10
12
*
1st order LR length (cm)
0
0.5
1.0
1.5
2.0
2.5
*
1st order LR number/plant
0
10
20
30
40
50
60
*
*
1st order LR density (number/cm of primary root)
0
1
2
3
4
5
6
*
*
2nd order LR number/plant
0
20
40
60
80
100
*
*
2nd order LR density (number/cm of 1st order LR)
0
0.25
0.50
0.75
1.00
1.25
1.50
*
*
-VCs
+ A. alternata VCs
+ P. aurantiogriseum VCs
Root hair density (number/mm of 1st order LR)
0
10
20
30
40
50
60
70
80
*
*
-VCs
+ A. alternata VCs
+ P. aurantiogriseum VCs
Length of root hairs (mm)
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
*
*
-VCs
+ A. alternata VCs
+ P. aurantiogriseum VCs

Figure 1

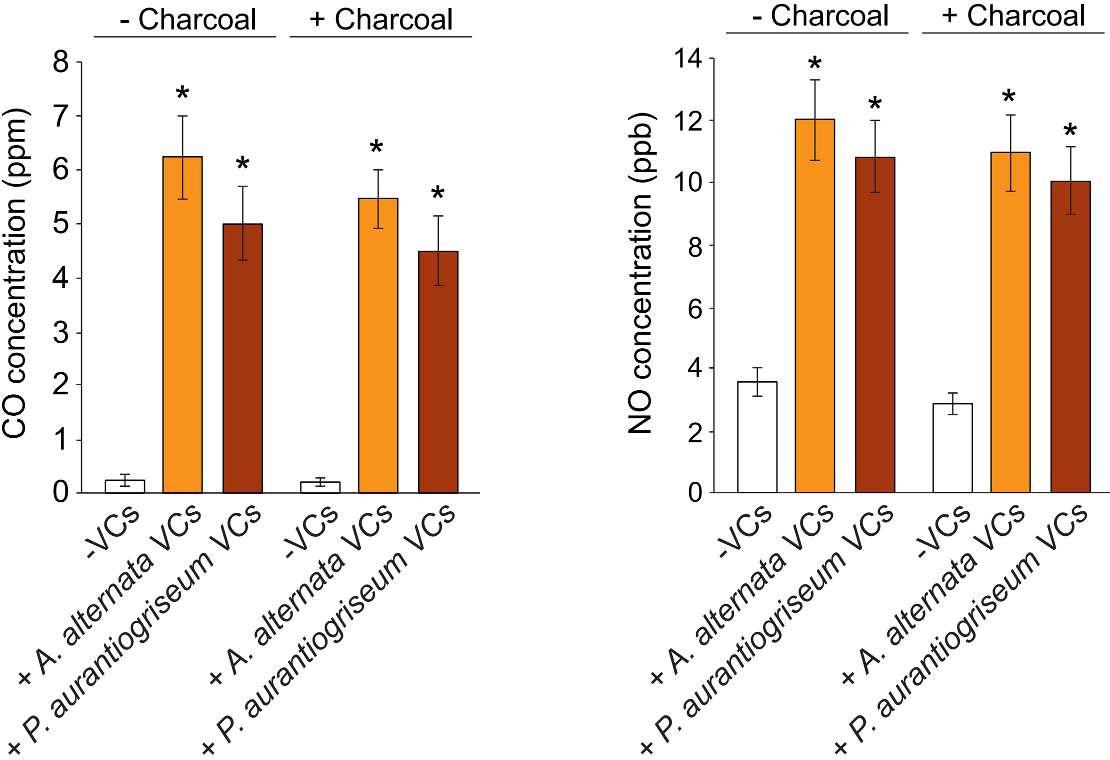

- Charcoal
+ Charcoal
CO concentration (ppm)
0
1
2
3
4
5
6
7
8
*
-VCs
+ A. alternata VCs
+ P. aurantiogriseum VCs
NO concentration (ppb)
0
2
4
6
8
10
12
14

Figure 2

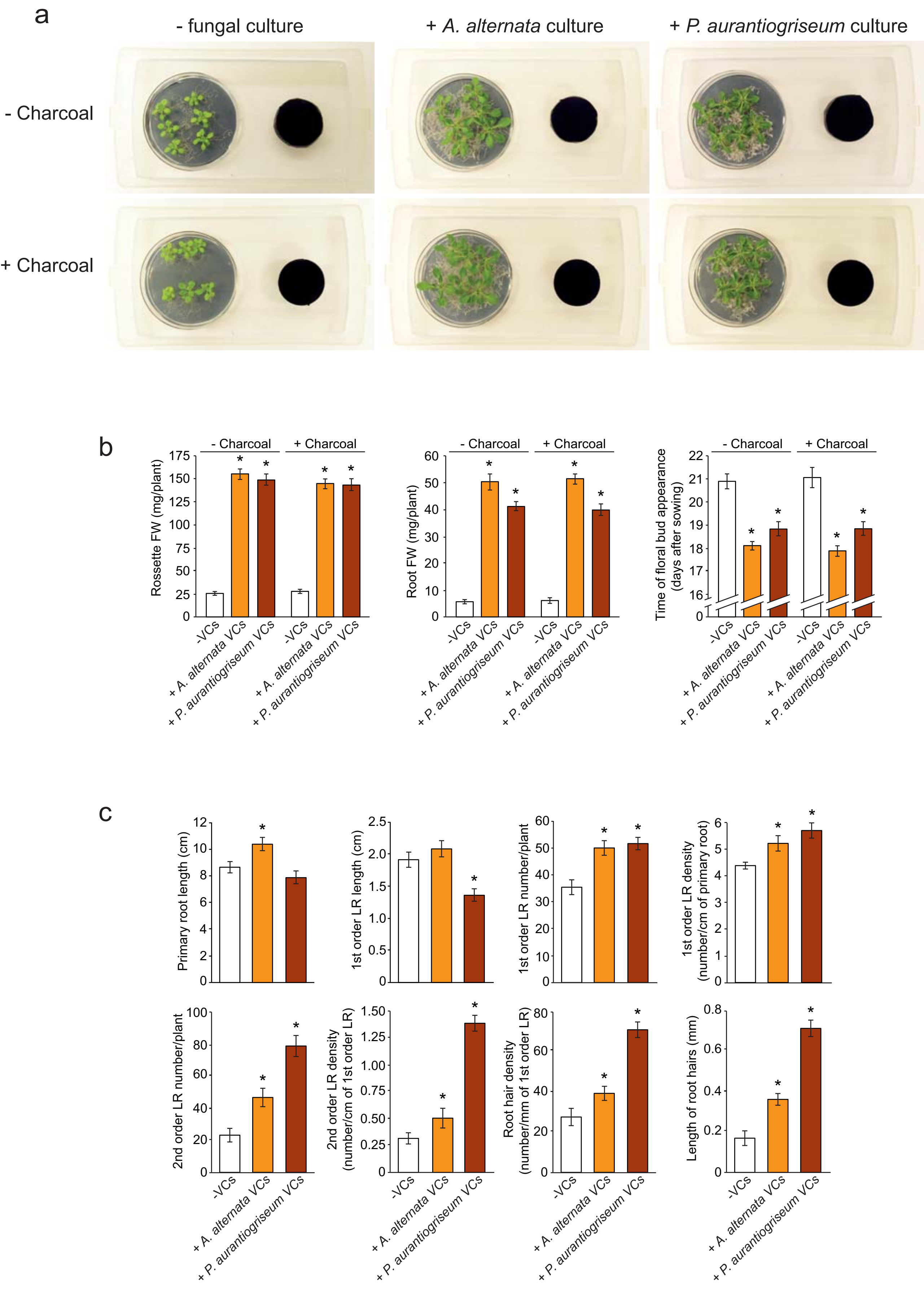

a
- fungal culture
+ A. alternata culture
+ P. aurantiogriseum culture
- Charcoal
+ Charcoal
b
- Charcoal
+ Charcoal
Rossette FW (mg/plant)
0
25
50
75
100
125
150
175
Root FW (mg/plant)
0
10
20
30
40
50
60
Time of floral bud appearance (days after sowing)
0
16
17
18
19
20
21
22
-VCs
+ A. alternata VCs
+ P. aurantiogriseum VCs
*
c
Primary root length (cm)
0
2
4
6
8
10
12
1st order LR length (cm)
0
0.5
1.0
1.5
2.0
2.5
1st order LR number/plant
0
10
20
30
40
50
60
1st order LR density (number/cm of primary root)
0
1
2
3
4
5
6
2nd order LR number/plant
0
20
40
60
80
100
2nd order LR density (number/cm of 1st order LR)
0
0.25
0.50
0.75
1.00
1.25
1.50
Root hair density (number/mm of 1st order LR)
0
20
40
60
80
Length of root hairs (mm)
0
0.2
0.4
0.6
0.8
-VCs
+ A. alternata VCs
+ P. aurantiogriseum VCs
*

Figure 3

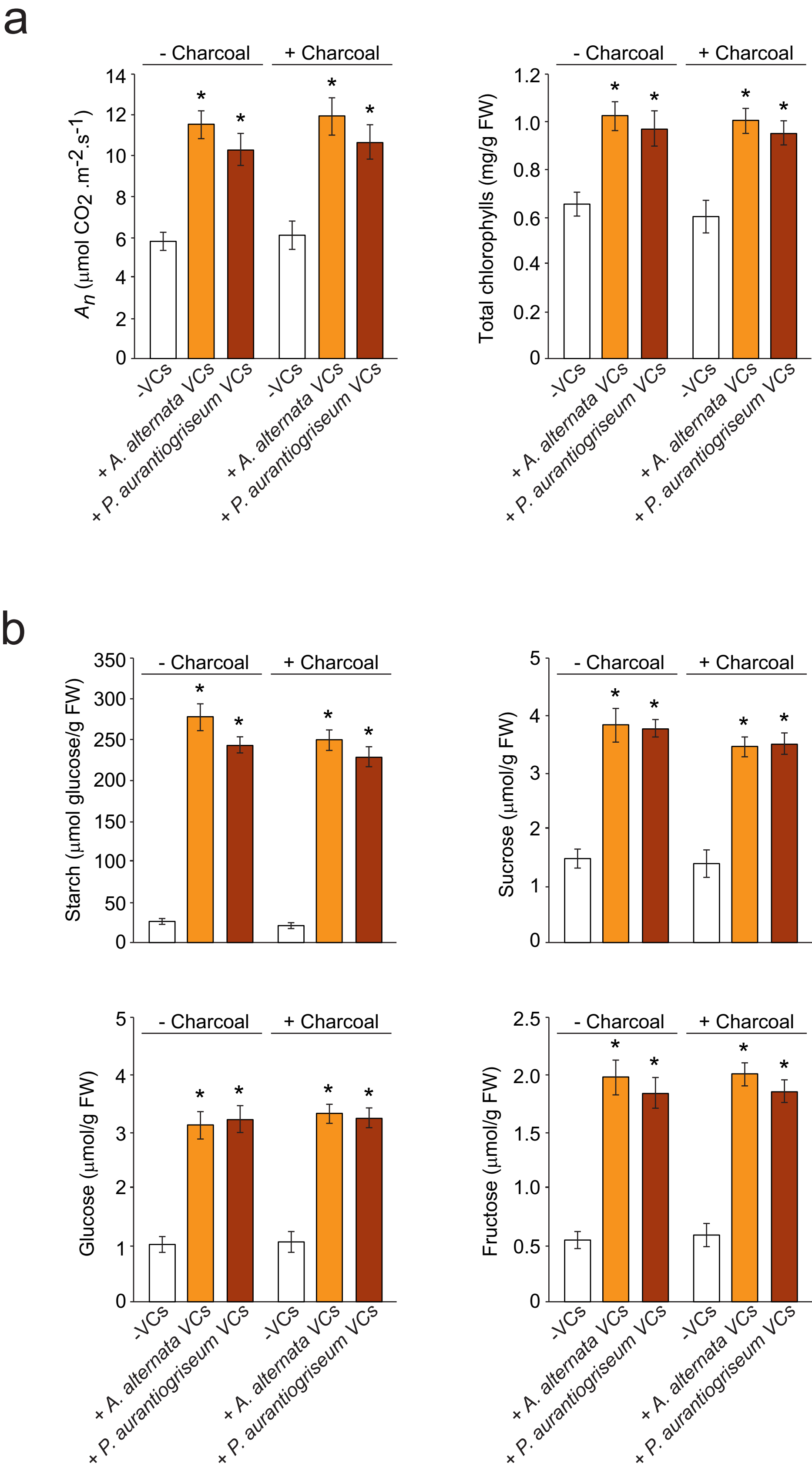
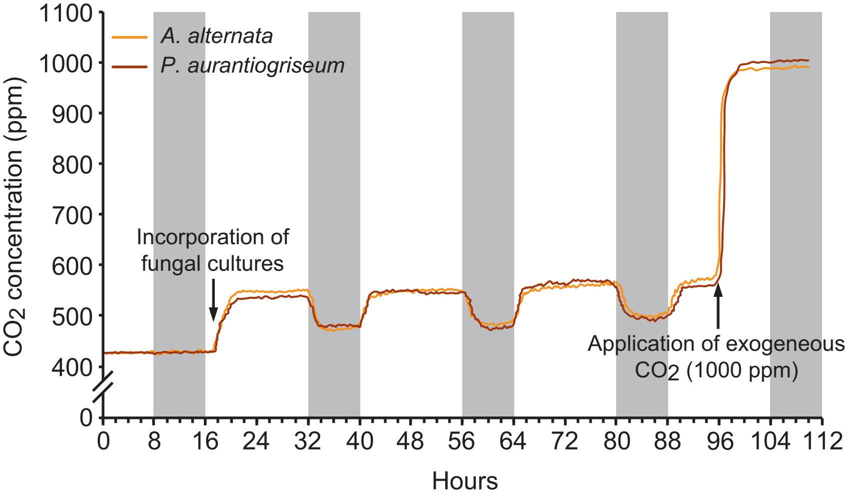

a
- Charcoal
+ Charcoal
A_n (μmol CO$_2$ .m^{-2}.s^{-1})
0
2
4
6
8
10
12
14
Total chlorophylls (mg/g FW)
0
0.2
0.4
0.6
0.8
1.0
1.2
*
-VCs
+ A. alternata VCs
+ P. aurantiogriseum VCs
b
Starch (μmol glucose/g FW)
0
50
100
150
200
250
300
350
Sucrose (μmol/g FW)
0
1
2
3
4
5
Glucose (μmol/g FW)
0
1
2
3
4
5
Fructose (μmol/g FW)
0
0.5
1.0
1.5
2.0
2.5

Figure 4


A. alternata
P. aurantiogriseum
CO2 concentration (ppm)
1100
1000
900
800
700
600
500
400
0
Incorporation of fungal cultures
Application of exogeneous CO2 (1000 ppm)
0 8 16 24 32 40 48 56 64 72 80 88 96 104 112
Hours

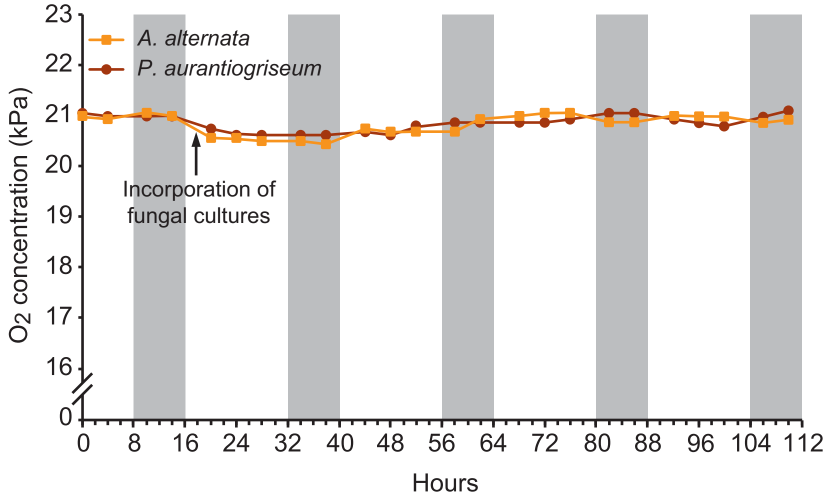

A. alternata
P. aurantiogriseum
O2 concentration (kPa)
23
22
21
20
19
18
17
16
0
Incorporation of fungal cultures
0 8 16 24 32 40 48 56 64 72 80 88 96 104 112
Hours

Figure 5

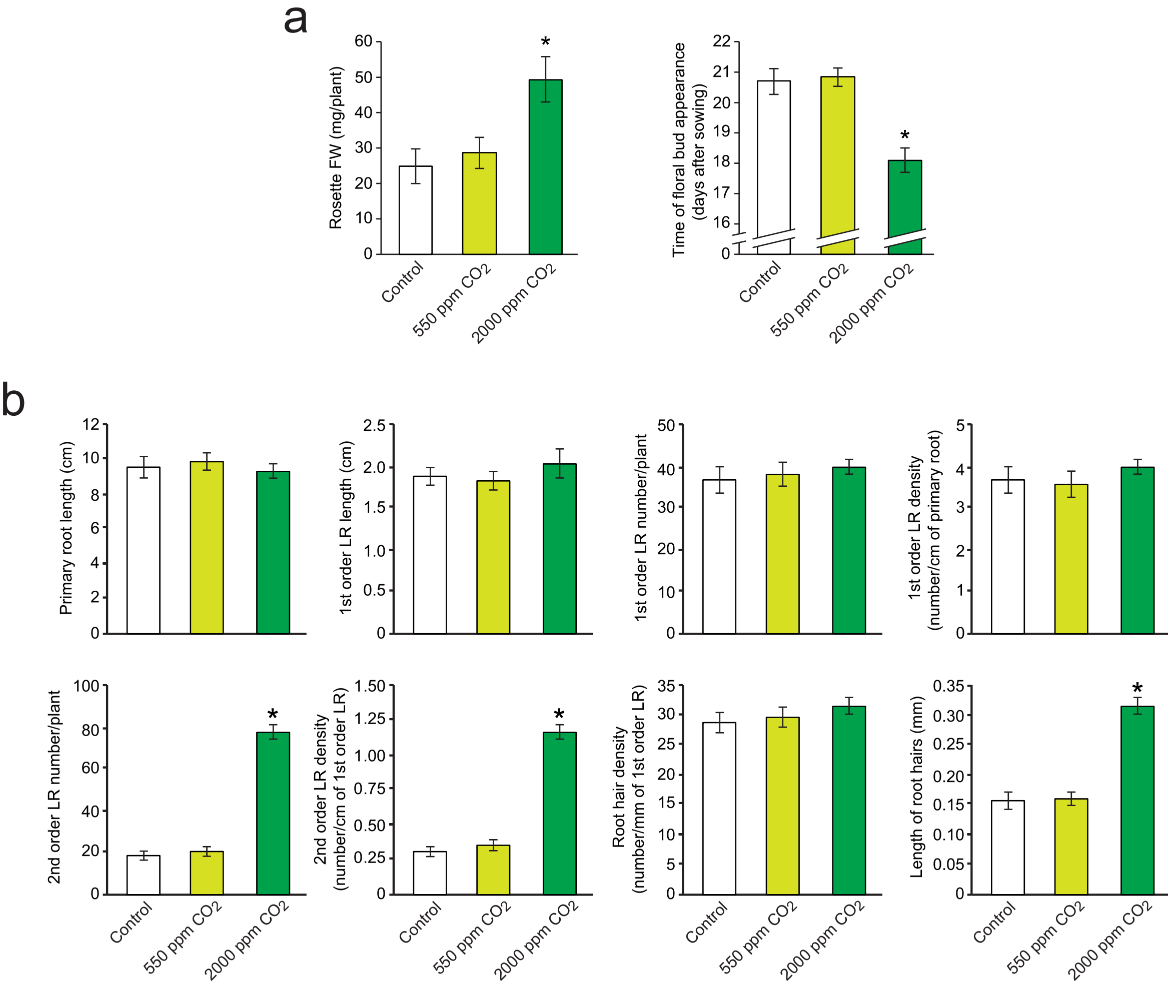
a
Rosette FW (mg/plant)
0
10
20
30
40
50
60
*
Control
550 ppm CO_2
2000 ppm CO_2
Time of floral bud appearance (days after sowing)
0
16
17
18
19
20
21
22
*
Control
550 ppm CO_2
2000 ppm CO_2
b
Primary root length (cm)
0
2
4
6
8
10
12
1st order LR length (cm)
0
0.5
1.0
1.5
2.0
2.5
1st order LR number/plant
0
10
20
30
40
50
1st order LR density (number/cm of primary root)
0
1
2
3
4
5
2nd order LR number/plant
0
20
40
60
80
100
*
2nd order LR density (number/cm of 1st order LR)
0
0.25
0.50
0.75
1.00
1.25
1.50
*
Root hair density (number/mm of 1st order LR)
0
5
10
15
20
25
30
35
Length of root hairs (mm)
0
0.05
0.10
0.15
0.20
0.25
0.30
0.35
*
Control
550 ppm CO_2
2000 ppm CO_2
Control
550 ppm CO_2
2000 ppm CO_2
Control
550 ppm CO_2
2000 ppm CO_2
Control
550 ppm CO_2
2000 ppm CO_2

Figure 6

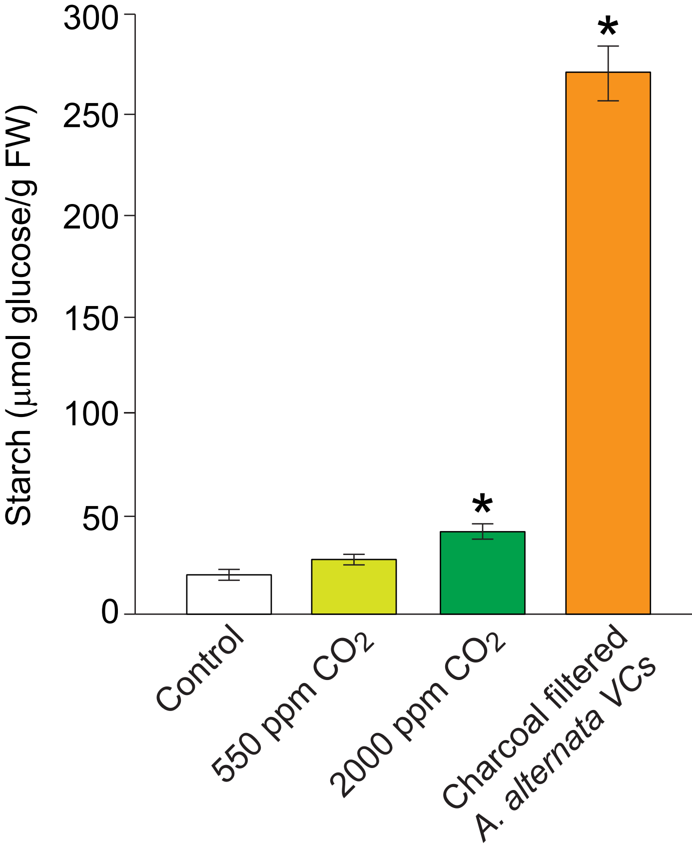

Starch (µmol glucose/g FW)
300
250
200
150
100
50
0
*
*
Control
550 ppm CO2
2000 ppm CO2
Charcoal filtered
A. alternata VCs

Figure 7

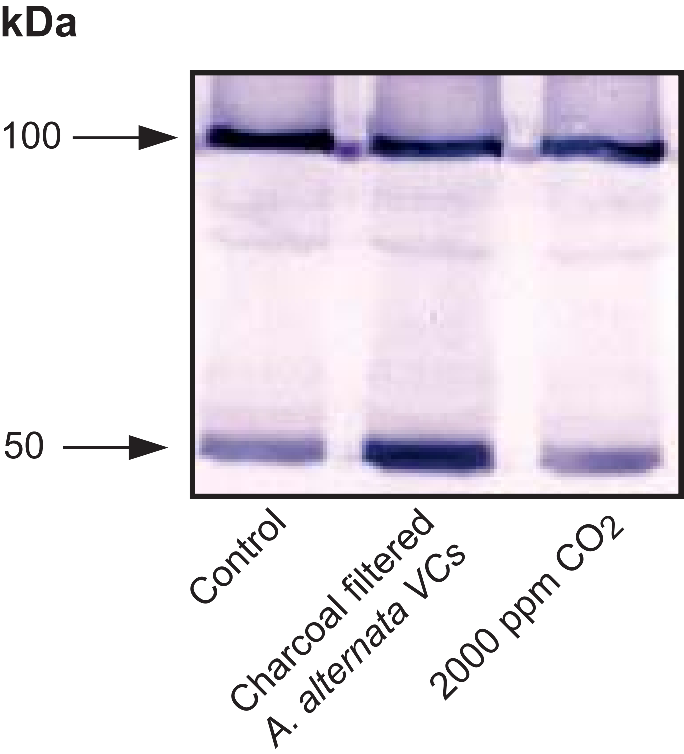

kDa
100
50
Control
Charcoal filtered
A. alternata VCs
2000 ppm CO2

Figure 8

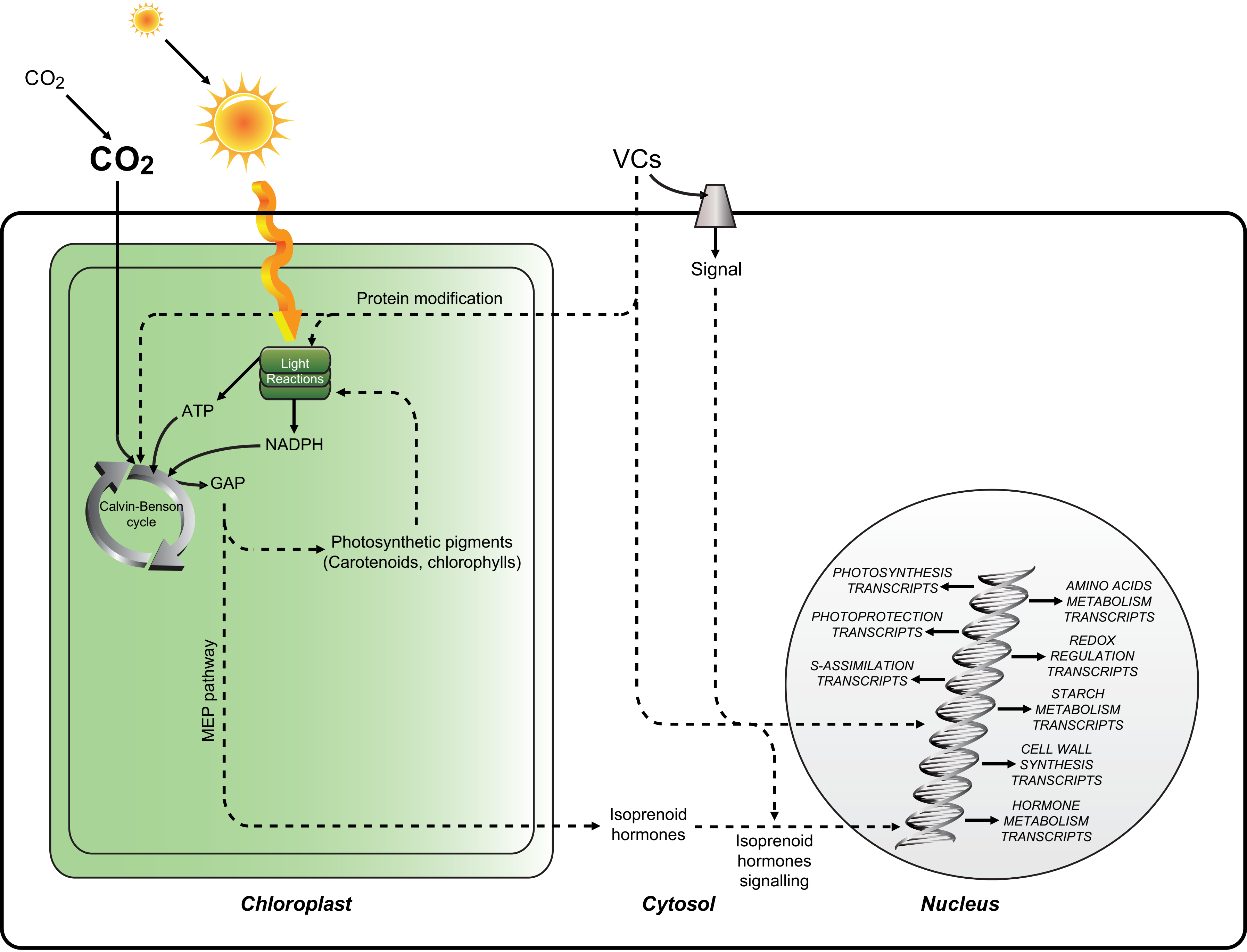
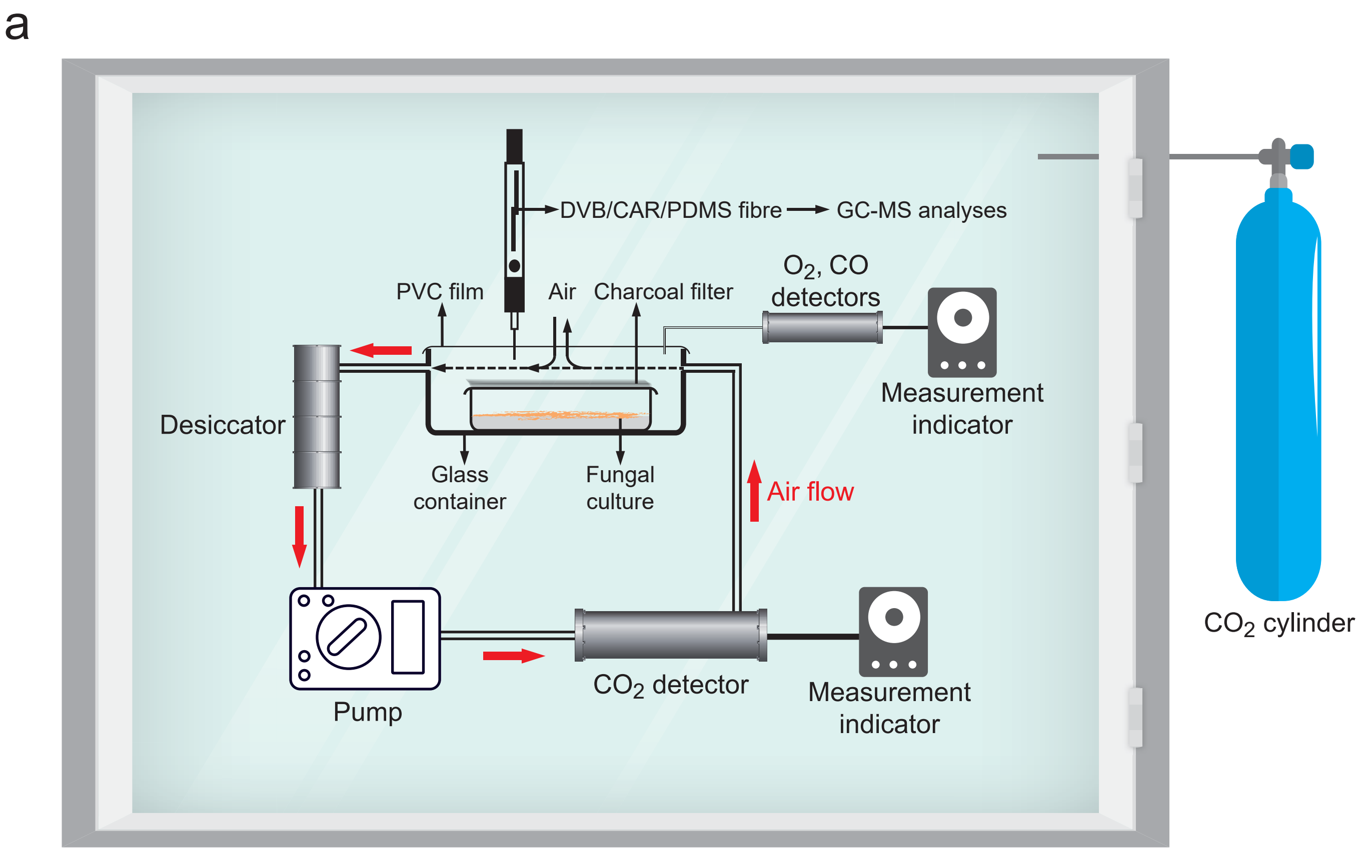
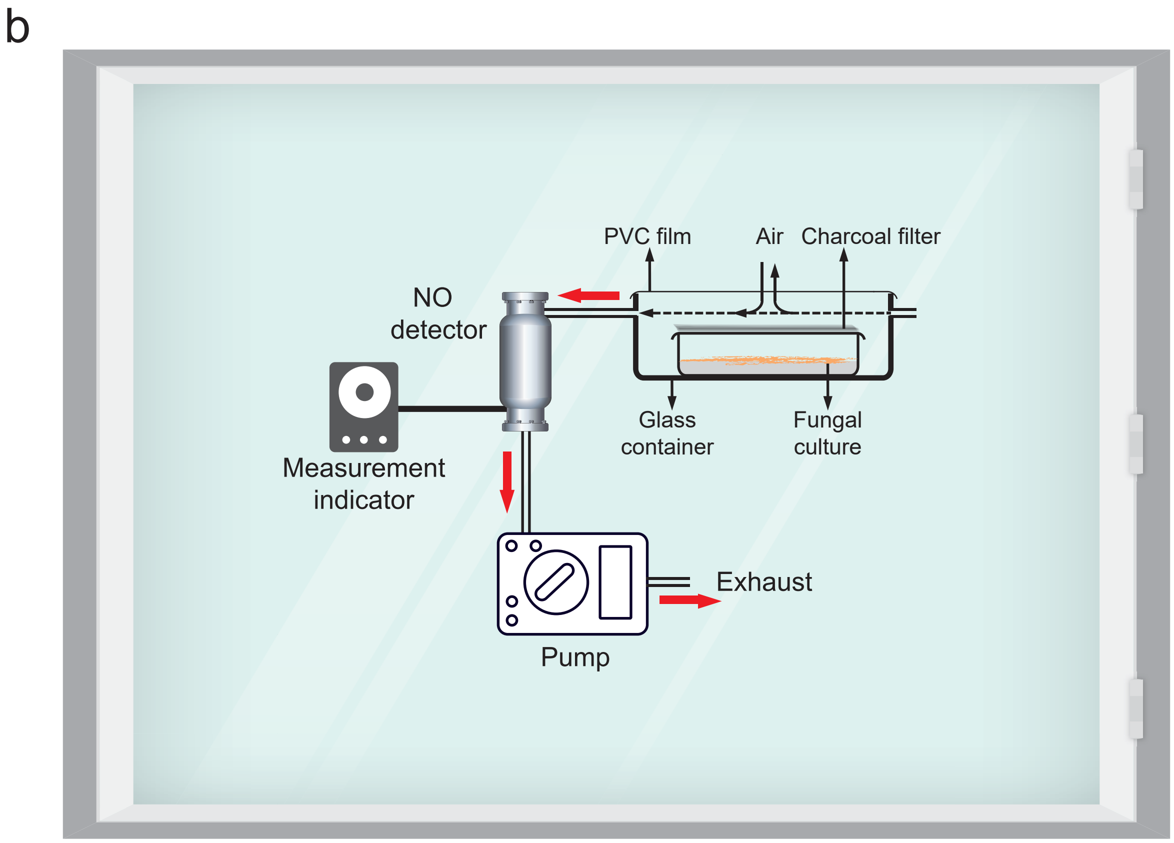

CO_2
CO_2
VCs
Signal
Protein modification
Light Reactions
ATP
NADPH
GAP
Calvin-Benson cycle
Photosynthetic pigments (Carotenoids, chlorophylls)
MEP pathway
Isoprenoid hormones
Isoprenoid hormones signalling
PHOTOSYNTHESIS TRANSCRIPTS
AMINO ACIDS METABOLISM TRANSCRIPTS
PHOTOPROTECTION TRANSCRIPTS
REDOX REGULATION TRANSCRIPTS
S-ASSIMILATION TRANSCRIPTS
STARCH METABOLISM TRANSCRIPTS
CELL WALL SYNTHESIS TRANSCRIPTS
HORMONE METABOLISM TRANSCRIPTS
Chloroplast
Cytosol
Nucleus

Figure 9



CO_2-controlled growth cabinet



Growth cabinet

Figure S1

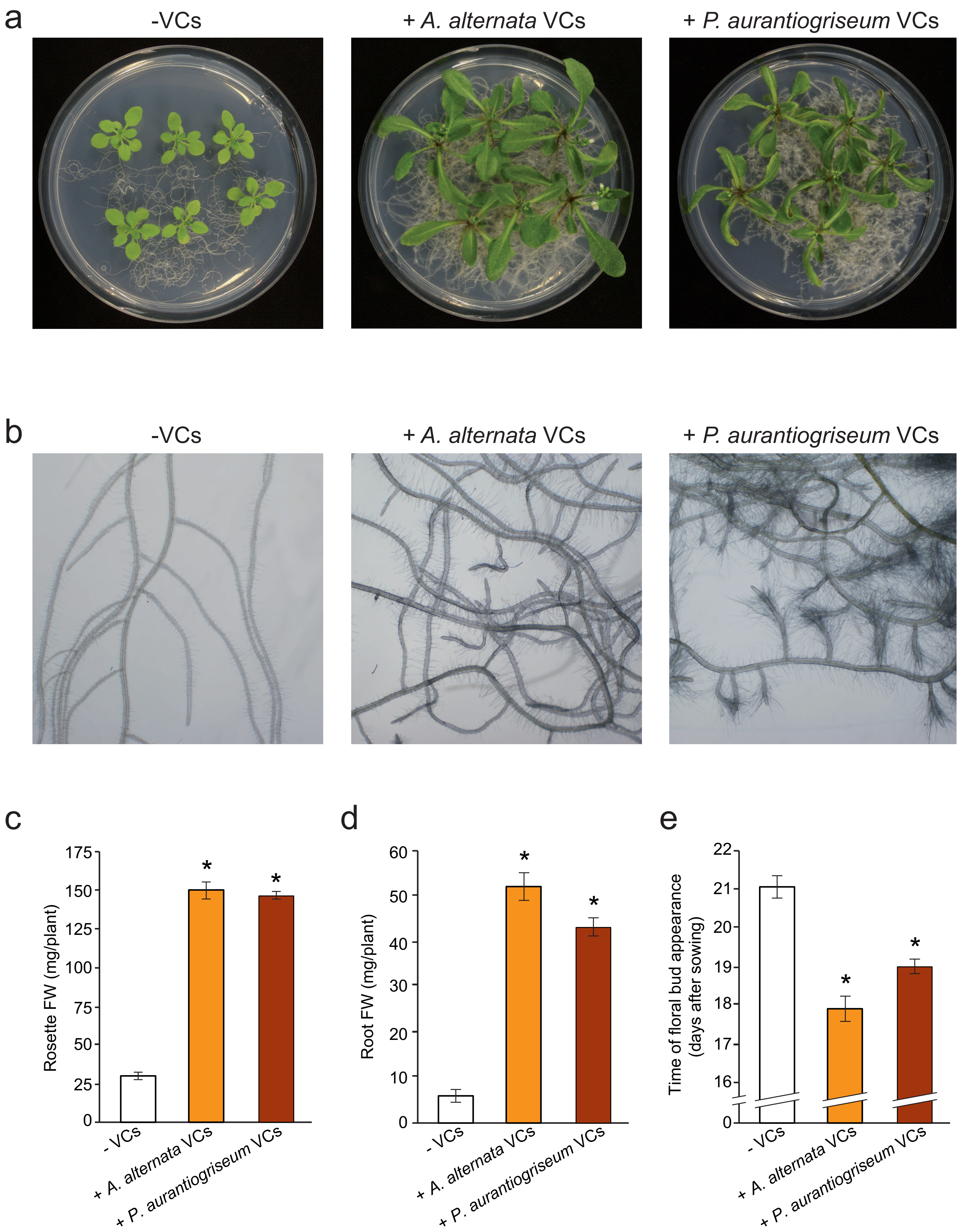

a
-VCs
+ A. alternata VCs
+ P. aurantiogriseum VCs
b
-VCs
+ A. alternata VCs
+ P. aurantiogriseum VCs
c
Rosette FW (mg/plant)
175
150
125
100
75
50
25
0
*
*
- VCs
+ A. alternata VCs
+ P. aurantiogriseum VCs
d
Root FW (mg/plant)
60
50
40
30
20
10
0
*
*
- VCs
+ A. alternata VCs
+ P. aurantiogriseum VCs
e
Time of floral bud appearance (days after sowing)
22
21
20
19
18
17
16
0
*
*
- VCs
+ A. alternata VCs
+ P. aurantiogriseum VCs

Figure S2

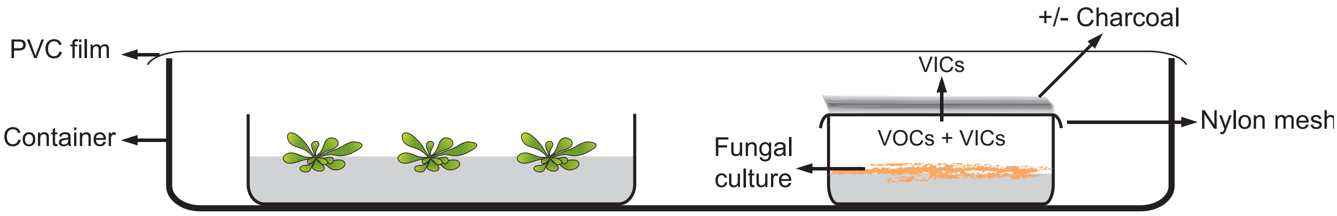

+/- Charcoal
PVC film
VICs
Container
VOCs + VICs
Nylon mesh
Fungal culture

Figure S3

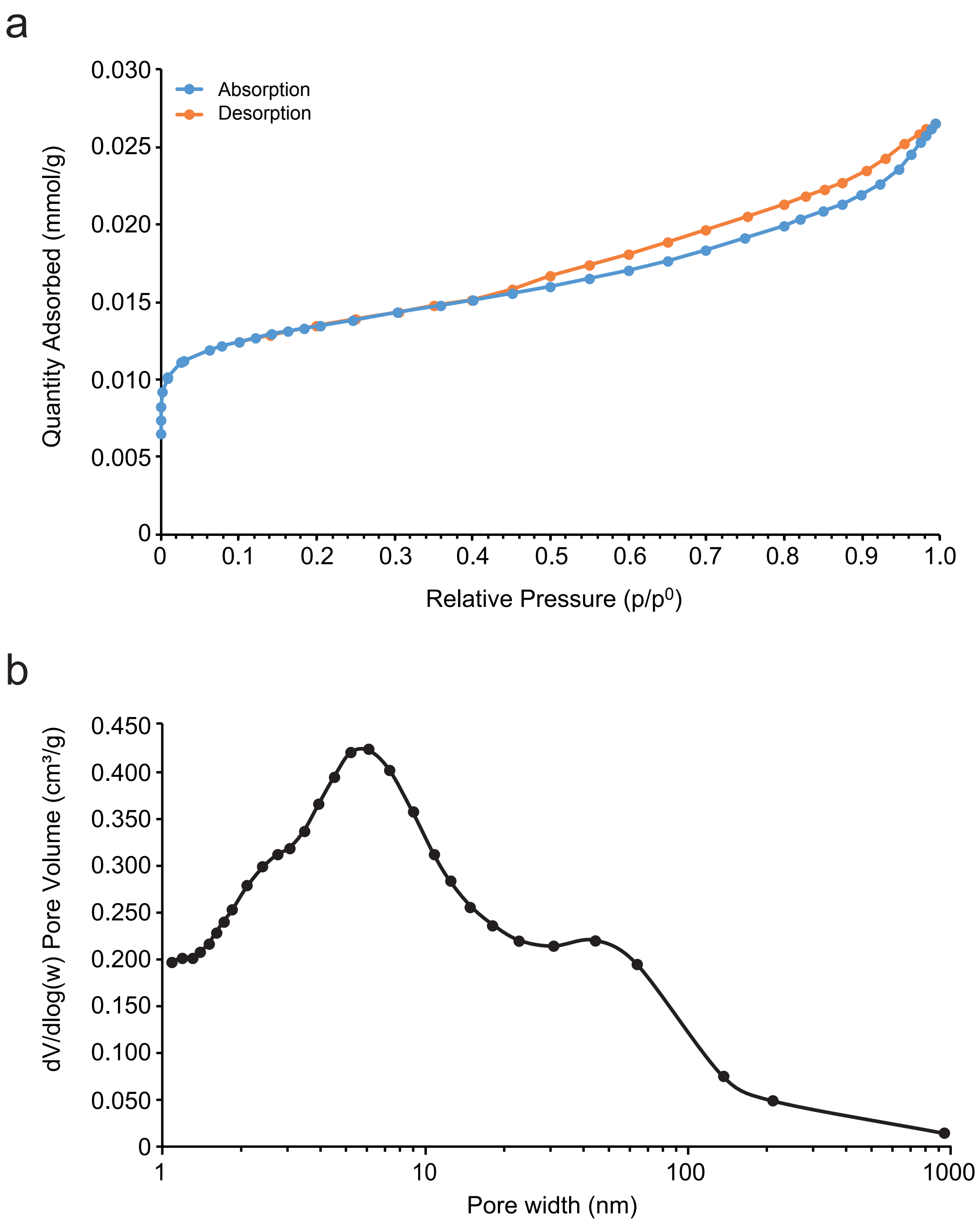

a
0.030
0.025
0.020
0.015
0.010
0.005
0
Quantity Adsorbed (mmol/g)
Absorption
Desorption
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1.0
Relative Pressure (p/p0)
b
0.450
0.400
0.350
0.300
0.250
0.200
0.150
0.100
0.050
0
dV/dlog(w) Pore Volume (cm³/g)
1
10
100
1000
Pore width (nm)

Figure S4

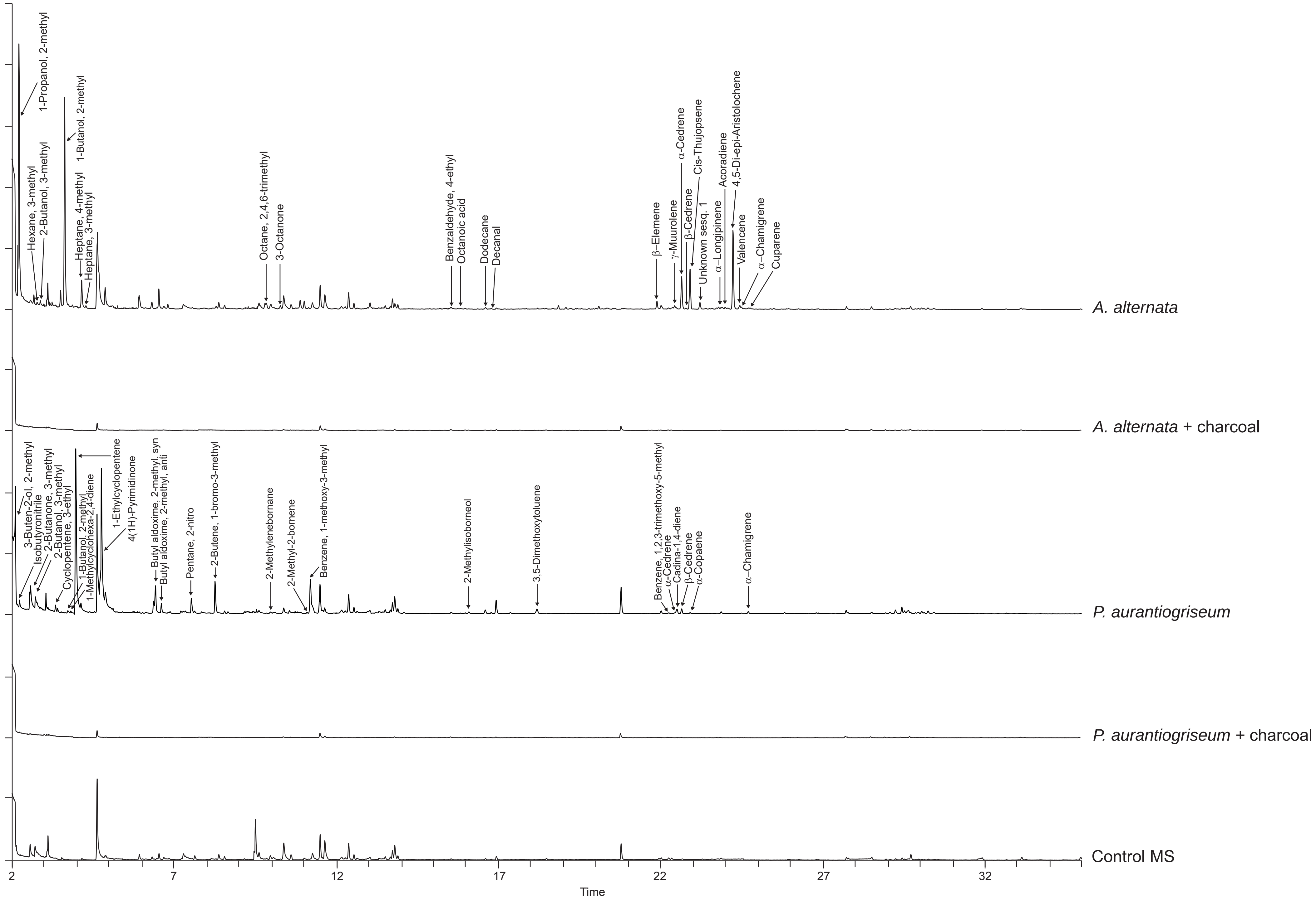

1-Propanol, 2-methyl
Hexane, 3-methyl
2-Butanol, 3-methyl
1-Butanol, 2-methyl
Heptane, 4-methyl
Heptane, 3-methyl
Octane, 2,4,6-trimethyl
3-Octanone
Benzaldehyde, 4-ethyl
Octanoic acid
Dodecane
Decanal
β–Elemene
γ-Muurolene
α-Cedrene
β-Cedrene
Cis-Thujopsene
Unknown sesq. 1
α–Longipinene
Acoradiene
4,5-Di-epi-Aristolochene
Valencene
α–Chamigrene
Cuparene
A. alternata
A. alternata + charcoal
3-Buten-2-ol, 2-methyl
Isobutyronitrile
2-Butanone, 3-methyl
2-Butanol, 3-methyl
Cyclopentene, 3-ethyl
1-Butanol, 2-methyl
1-Methylcyclohexa-2,4-diene
1-Ethylcyclopentene
4(1H)-Pyrimidinone
Butyl aldoxime, 2-methyl, syn
Butyl aldoxime, 2-methyl, anti
Pentane, 2-nitro
2-Butene, 1-bromo-3-methyl
2-Methylenebornane
2-Methyl-2-bornene
Benzene, 1-methoxy-3-methyl
2-Methylisoborneol
3,5-Dimethoxytoluene
Benzene, 1,2,3-trimethoxy-5-methyl
α-Cedrene
Cadina-1,4-diene
β-Cedrene
α-Copaene
α–Chamigrene
P. aurantiogriseum
P. aurantiogriseum + charcoal
Control MS
2
7
12
17
22
27
32
Time

Figure S5

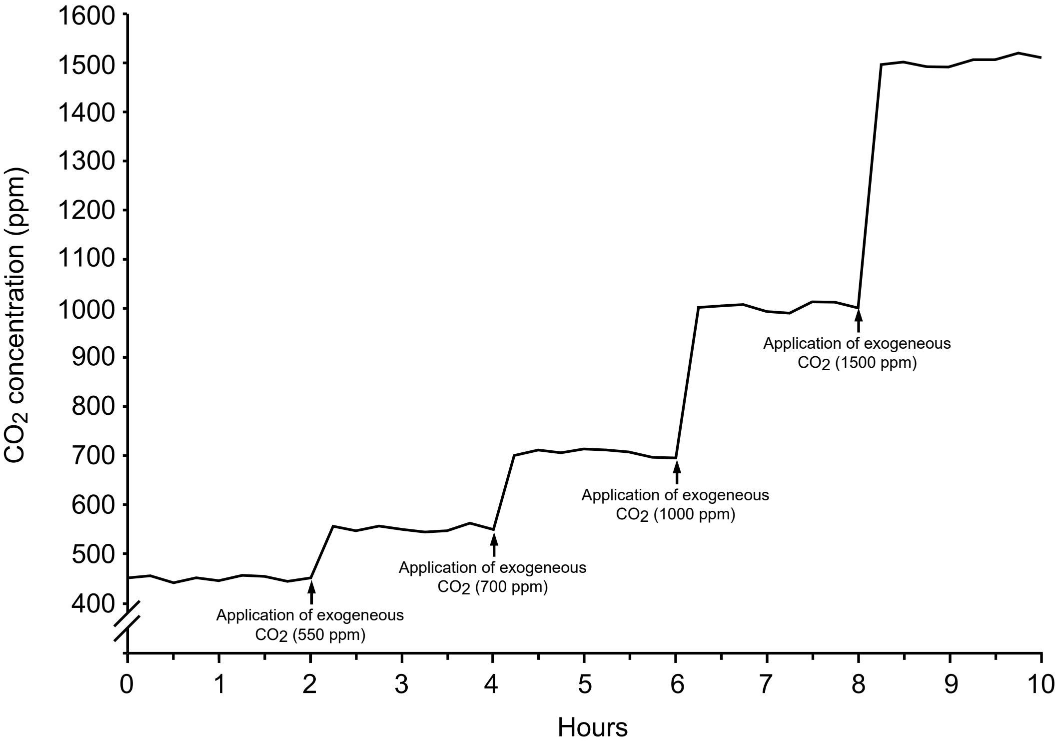

1600
1500
1400
1300
1200
1100
1000
900
800
700
600
500
400
CO$_2$ concentration (ppm)
0
1
2
3
4
5
6
7
8
9
10
Hours
Application of exogeneous CO$_2$ (550 ppm)
Application of exogeneous CO$_2$ (700 ppm)
Application of exogeneous CO$_2$ (1000 ppm)
Application of exogeneous CO$_2$ (1500 ppm)

Figure S6

Table S1. Textural parameters for activated charcoal.

$V_{micro(DR)}$ [a] (cm^3/g)	V_{meso} [b] (cm^3/g)	V_{macro} [c] (cm^3/g)	$a_{BET(N2)}$ (m^2/g)
0.48	0.097	0.115	1109

[a] Micropore volume was deduced by applying the DR.

[b] Deduced by difference between the amount of N_2 adsorbed in the relative pressure range 0.3–0.8.

[c] Deduced by difference between the amount of N_2 adsorbed in the relative pressure range 0.8–1.0.

Table S2: List of genes classified by functional categories whose expression in leaves is altered by charcoal-filtered VCs emitted by A. alternata. Genes that are differentially regulated by total A. alternata VCs (cf. Supplemental Table 3 in Sánchez-López, Baslam, et al., 2016) are highlighted in yelow color. (BY FUNCTIONAL CATEGORIES

Function	Fold Change	pval (LiMMA)	ID	Description
Photosynthesis				
	-4,6	0,00000000	AT4G26530	ref|Arabidopsis thaliana Aldolase superfamily protein (FBA5), mRNA [NM_001036644]
	-31,15	0,00000000	AT2G34430	ref|Arabidopsis thaliana light-harvesting chlorophyll-protein complex II subunit B1 (LHB1B1), mRNA [NM_128995]
Major CHO metabolism				
	4,95	0,00000000	AT4G39210	ref|Arabidopsis thaliana Glucose-1-phosphate adenylyltransferase family protein (APL3), mRNA [NM_001342527]
	4,95	0,00000000	AT4G15210	ref|Arabidopsis thaliana beta-amylase 5 (BAM5), mRNA [NM_179058]
	3,04	0,00000000	AT1G32900	ref|Arabidopsis thaliana UDP-Glycosyltransferase superfamily protein (GBSS1), mRNA [NM_103023]
Minor CHO metabolism				
	3,31	0,00000000	AT4G17770	ref|Arabidopsis thaliana trehalose phosphatase/synthase 5 (TPS5), mRNA [NM_001341241]
	-3,01	0,00000000	AT4G18010	ref|Arabidopsis thaliana myo-inositol polyphosphate 5-phosphatase 2 (IP5PII), mRNA [NM_117911]
	-3,18	0,00000000	AT5G51970	ref|Arabidopsis thaliana GroES-like zinc-binding alcohol dehydrogenase family protein mRNA [NM_124576]
	-3,64	0,00000000	AT2G47180	ref|Arabidopsis thaliana galactinol synthase 1 (GolS1), mRNA [NM_130286]
	-4,76	0,00000000	AT5G57655	ref|Arabidopsis thaliana xylose isomerase family protein mRNA [NM_180872]
	-5,12	0,00000000	AT1G70290	ref|Arabidopsis thaliana trehalose-6-phosphatase synthase S8 (TPS8), mRNA [NM_001334443]
	-5,25	0,00000000	AT1G60140	ref|Arabidopsis thaliana trehalose phosphate synthase (TPS10), mRNA [NM_001333882]
	-6,22	0,00000000	AT3G57520	ref|Arabidopsis thaliana seed imbibition 2 (SIP2), mRNA [NM_180384]
	-6,31	0,00000000	AT2G19800	ref|Arabidopsis thaliana myo-inositol oxygenase 2 (MIOX2), mRNA [NM_127538]
	-7,7	0,00000000	AT1G23870	ref|Arabidopsis thaliana trehalose-phosphatase/synthase 9 (TPS9), mRNA [NM_102235]
	-13,3	0,00000000	AT5G20250	ref|Arabidopsis thaliana Raffinose synthase family protein (DIN10), mRNA [NM_001036833]
	-20,83	0,00000000	AT2G18700	ref|Arabidopsis thaliana trehalose phosphatase/synthase 11 (TPS11), mRNA [NM_127426]
Glycolysis				
	-13,64	0,00000000	AT3G49160	ref|Arabidopsis thaliana pyruvate kinase family protein mRNA [NM_001339402]
Fermentation				
	-5,86	0,00000000	AT1G54100	ref|Arabidopsis thaliana aldehyde dehydrogenase 7B4 (ALDH7B4), mRNA [NM_104287]
Gluconeogenesis				
	-4,91	0,00000000	AT4G15530	ref|Arabidopsis thaliana pyruvate orthophosphate dikinase (PPDK), mRNA [NM_001341051]
OPP				
	3,65	0,00000000	AT1G24280	ref|Arabidopsis thaliana glucose-6-phosphate dehydrogenase 3 (G6PD3), mRNA [NM_102274]
	-3,63	0,00000000	AT1G13700	ref|Arabidopsis thaliana 6-phosphogluconolactonase 1 (PGL1), mRNA [NM_001332083]
	-3,74	0,00000000	AT1G09420	ref|Arabidopsis thaliana glucose-6-phosphate dehydrogenase 4 (G6PD4), mRNA [NM_001198018]
TCA org transformation				
	3,73	0,00000000	AT5G50950	ref|Arabidopsis thaliana FUMARASE 2 (FUM2), mRNA [NM_001344914]
	3,13	0,00000000	AT2G28210	ref|Arabidopsis thaliana alpha carbonic anhydrase 2 (ACA2), mRNA [NM_001336148]
	-4,2	0,00000000	AT1G58180	ref|Arabidopsis thaliana beta carbonic anhydrase 6 (BCA6), mRNA [NM_179492]
Mitochondrial electron transport				
	3,83	0,00000000	AT4G24570	ref|Arabidopsis thaliana dicarboxylate carrier 2 (DIC2), mRNA [NM_118590]
	3,22	0,00000000	AT5G60730	ref|Arabidopsis thaliana Anion-transporting ATPase mRNA [NM_125466]
	-3,24	0,00000000	AT3G22370	ref|Arabidopsis thaliana alternative oxidase 1A (AOX1A), mRNA [NM_113135]
	-3,32	0,00000000	AT2G43400	ref|Arabidopsis thaliana electron-transfer flavoprotein:ubiquinone oxidoreductase (ETFQO), mRNA [NM_129901]
Cell wall				
	6,62	0,00000000	AT3G44990	ref|Arabidopsis thaliana xyloglucan endo-transglycosylase-related 8 (XTH31), mRNA [NM_114368]
	4,48	0,00000000	AT4G28250	ref|Arabidopsis thaliana expansin B3 (EXPB3), mRNA [NM_001341907]
	3,9	0,00000000	AT3G52370	ref|Arabidopsis thaliana FASCICLIN-like arabinogalactan protein 15 precursor (FLA15), mRNA [NM_115097]
	3,58	0,00000000	AT2G26440	ref|Arabidopsis thaliana Plant invertase/pectin methylesterase inhibitor superfamily mRNA [NM_128201]
	3,56	0,00000000	AT1G78570	ref|Arabidopsis thaliana rhamnose biosynthesis 1 (RHM1), mRNA [NM_106504]
	3,54	0,00000000	AT2G18660	ref|Arabidopsis thaliana plant natriuretic peptide A (PNP-A), mRNA [NM_179648]
	3,15	0,00000000	AT5G03760	ref|Arabidopsis thaliana Nucleotide-diphospho-sugar transferases superfamily protein (ATCSLA09), mRNA [NM_120457]
	3,14	0,00000000	AT1G11545	ref|Arabidopsis thaliana xyloglucan endotransglucosylase/hydrolase 8 (XTH8), mRNA [NM_101028]
	3,06	0,00000000	AT2G32990	ref|Arabidopsis thaliana glycosyl hydrolase 9B8 (GH9B8), mRNA [NM_128859]
	3,03	0,00000000	AT1G41830	ref|Arabidopsis thaliana SKU5-similar 6 (SKS6), mRNA [NM_103408]
	-3,05	0,00000000	AT1G55850	ref|Arabidopsis thaliana cellulose synthase like E1 (CSLE1), mRNA [NM_104462]
	-3,26	0,00000000	AT5G64570	ref|Arabidopsis thaliana beta-D-xylosidase 4 (XYL4), mRNA [NM_001345643]
	-3,35	0,00000000	AT2G28110	ref|Arabidopsis thaliana Exostosin family protein (FRA8), mRNA [NM_179782]
	-3,67	0,00000000	AT1G67070	ref|Arabidopsis thaliana Mannose-6-phosphate isomerase, type I (DIN9), mRNA [NM_001334269]
	-3,69	0,00000000	AT3G10740	ref|Arabidopsis thaliana alpha-L-arabinofuranosidase 1 (ASD1), mRNA [NM_001337894]
	-4,08	0,00000000	AT1G63180	ref|Arabidopsis thaliana UDP-D-glucose/UDP-D-galactose 4-epimerase 3 (UGE3), mRNA [NM_104996]
	-4,74	0,00000000	AT1G32170	ref|Arabidopsis thaliana xyloglucan endotransglucosylase/hydrolase 30 (XTH30), mRNA [NM_102950]
	-4,81	0,00000000	AT5G57560	ref|Arabidopsis thaliana Xyloglucan endotransglucosylase/hydrolase family protein (TCH4), mRNA [NM_125137]
	-13,65	0,00000000	AT5G14470	ref|Arabidopsis thaliana GHMP kinase family protein mRNA [NM_121451]

	-16,41	0,00000000	AT5G06860	ref|Arabidopsis thaliana polygalacturonase inhibiting protein 1 (PGIP1), mRNA [NM_120769]
	-33,28	0,00000000	AT4G30270	ref|Arabidopsis thaliana xyloglucan endotransglucosylase/hydrolase 24 (XTH24), mRNA [NM_119173]
	-55,33	0,00000000	AT5G49360	ref|Arabidopsis thaliana beta-xylosidase 1 (BXL1), mRNA [NM_124313]
lipid metabolism				
	12,37	0,00000000	AT1G73600	ref|Arabidopsis thaliana S-adenosyl-L-methionine-dependent methyltransferases superfamily protein mRNA [NM_106018]
	5,32	0,00000000	AT2G11810	ref|Arabidopsis thaliana monogalactosyldiacylglycerol synthase type C (MGDC), mRNA [NM_001124829]
	4,98	0,00000000	AT4G17470	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_001203824]
	3,35	0.00000007	AT1G45201	ref|Arabidopsis thaliana triacylglycerol lipase-like 1 (TLL1), mRNA [NM_179441]
	3,1	0,00000000	AT1G65890	ref|Arabidopsis thaliana acyl activating enzyme 12 (AAE12), mRNA [NM_105261]
	-3,15	0,00000000	AT1G68620	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_105534]
	-3,31	0,00000000	AT5G65110	ref|Arabidopsis thaliana acyl-CoA oxidase 2 (ACX2), mRNA [NM_001037068]
	-3,96	0,00000000	AT5G18630	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_180517]
	-4,1	0,00000000	AT5G16370	ref|Arabidopsis thaliana acyl activating enzyme 5 (AAE5), mRNA [NM_121642]
	-4,18	0,00000000	AT2G39400	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_001336772]
	-5,7	0,00000000	AT5G56100	ref|Arabidopsis thaliana glycine-rich protein / oleosin mRNA [NM_124992]
	-5,71	0,00000000	AT4G24230	ref|Arabidopsis thaliana acyl-CoA-binding domain 3 (ACBP3), mRNA [NM_001084972]
	-6,1	0,00000000	AT5G41080	ref|Arabidopsis thaliana PLC-like phosphodiesterases superfamily protein (GDPD2), mRNA [NM_203136]
	-6,2	0,00000000	AT1G02660	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_100146]
	-16,93	0,00000000	AT5G14180	ref|Arabidopsis thaliana Myzus persicae-induced lipase 1 (MPL1), mRNA [NM_001343319]
N-metabolism				
	-3,41	0,00000000	AT5G18170	ref|Arabidopsis thaliana glutamate dehydrogenase 1 (GDH1), mRNA [NM_121822]
	-6,39	0,00000000	AT1G42490	Unknown
	-6,62	0,00000000	AT5G07440	ref|Arabidopsis thaliana glutamate dehydrogenase 2 (GDH2), mRNA [NM_001125712]
	-8,17	0,00000000	AT1G77760	ref|Arabidopsis thaliana nitrate reductase 1 (NIA1), mRNA [NM_106425]
Aminoacid metabolism				
	59,14	0,00000000	AT2G24850	ref|Arabidopsis thaliana tyrosine aminotransferase 3 (TAT3), mRNA [NM_128044]
	9,13	0,00000000	AT4G23600	ref|Arabidopsis thaliana Tyrosine transaminase family protein (CORI3), mRNA [NM_179099]
	5,44	0,00000000	AT3G03780	ref|Arabidopsis thaliana methionine synthase 2 (MS2), mRNA [NM_111249]
	4,73	0,00000000	AT5G14200	ref|Arabidopsis thaliana isopropylmalate dehydrogenase 1 (IMD1), mRNA [NM_001036803]
	3,5	0,00000000	AT5G48880	ref|Arabidopsis thaliana peroxisomal 3-keto-acyl-CoA thiolase 2 (KAT5), mRNA [NM_001344808]
	3,42	0,00000000	AT1G17745	ref|Arabidopsis thaliana D-3-phosphoglycerate dehydrogenase (PGDH), mRNA [NM_001035984]
	3,35	0,00000000	AT4G34200	ref|Arabidopsis thaliana D-3-phosphoglycerate dehydrogenase (EDA9), mRNA [NM_119583]
	-3,31	0,00000000	AT3G22200	ref|Arabidopsis thaliana Pyridoxal phosphate (PLP)-dependent transferases superfamily protein (POP2), mRNA [NM_001203018]
	-3,9	0,00000000	AT5G53970	ref|Arabidopsis thaliana Tyrosine transaminase family protein (TAT7), mRNA [NM_124776]
	-4,46	0,00000000	AT3G22460	ref|Arabidopsis thaliana O-acetylserine (thiol) lyase (OAS-TL) isoform A2 (OASA2), mRNA [NM_113145]
	-5,08	0,00000000	AT5G38710	ref|Arabidopsis thaliana Methylenetetrahydrofolate reductase family protein mRNA [NM_123232]
	-5,24	0,00000000	AT3G13450	ref|Arabidopsis thaliana Transketolase family protein (DIN4), mRNA [NM_112191]
	-5,76	0,00000000	AT1G21400	ref|Arabidopsis thaliana Thiamin diphosphate-binding fold (THDP-binding) superfamily protein mRNA [NM_001332503]
	-6,26	0,00000000	AT3G45300	ref|Arabidopsis thaliana isovaleryl-CoA-dehydrogenase (IVD), mRNA [NM_114399]
	-7,6	0,00000000	AT4G33150	ref|Arabidopsis thaliana lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme mRNA [NM_001160811]
	-7,65	0,00000000	AT5G54080	ref|Arabidopsis thaliana homogentisate 1,2-dioxygenase (HGO), mRNA [NM_180856]
	-8,73	0,00000000	AT2G38400	ref|Arabidopsis thaliana alanine:glyoxylate aminotransferase 3 (AGT3), mRNA [NM_001202772]
	-10,34	0,00000000	AT1G03090	ref|Arabidopsis thaliana methylcrotonyl-CoA carboxylase alpha chain (MCCA), mRNA [NM_179252]
	-15,04	0,00000000	AT3G30775	ref|Arabidopsis thaliana Methylenetetrahydrofolate reductase family protein (ERD5), mRNA [NM_113981]
	-19,42	0,00000000	AT1G08630	ref|Arabidopsis thaliana threonine aldolase 1 (THA1), mRNA [NM_100736]
	-22,64	0,00000000	AT1G10070	ref|Arabidopsis thaliana branched-chain amino acid transaminase 2 (BCAT-2), mRNA [NM_001035939]
	-107,47	0,00000000	AT3G47340	ref|Arabidopsis thaliana glutamine-dependent asparagine synthase 1 (ASN1), mRNA [NM_180333]
S-assimilation				
	5,09	0,00000000	AT4G39940	ref|Arabidopsis thaliana APS-kinase 2 (AKN2), mRNA [NM_120157]
	4,64	0,00000000	AT4G04610	ref|Arabidopsis thaliana APS reductase 1 (APR1), mRNA [NM_116699]
	3,02	0,00000000	AT4G14680	ref|Arabidopsis thaliana Pseudouridine synthase/archaeosine transglycosylase-like family protein (APS3), mRNA [NM_001340955]
Metal handling				
	5,69	0,00000000	AT1G56430	ref|Arabidopsis thaliana nicotianamine synthase 4 (NAS4), mRNA [NM_104521]
	5,48	0,00000000	AT1G23020	ref|Arabidopsis thaliana ferric reduction oxidase 3 (FRO3), mRNA [NM_001198138]
	-3,32	0.00000001	AT1G09240	ref|Arabidopsis thaliana nicotianamine synthase 3 (NAS3), mRNA [NM_100794]
	-3,4	0,00000000	AT5G49740	ref|Arabidopsis thaliana ferric reduction oxidase 7 (FRO7), mRNA [NM_001344853]
	-3,44	0,00000000	AT5G49730	ref|Arabidopsis thaliana ferric reduction oxidase 6 (FRO6), mRNA [NM_001344852]
	-3,6	0,00000000	AT1G55920	ref|Arabidopsis thaliana serine acetyltransferase 2;1 (SERAT2;1), mRNA [NM_104470]
	-3,85	0,00000000	AT2G40300	ref|Arabidopsis thaliana ferritin 4 (FER4), mRNA [NM_129588]
	-48,13	0,00000000	AT5G01600	ref|Arabidopsis thaliana ferretin 1 (FER1), mRNA [NM_120238]
Secondary metabolism				
	13,38	0,00000000	AT1G61120	ref|Arabidopsis thaliana terpene synthase 04 (TPS04), mRNA [NM_104793]
	8,74	0,00000000	AT5G42800	ref|Arabidopsis thaliana dihydroflavonol 4-reductase (DFR), mRNA [NM_123645]
	8,3	0,00000000	AT4G39950	ref|Arabidopsis thaliana cytochrome P450, family 79, subfamily B, polypeptide 2 (CYP79B2), mRNA [NM_120158]
	7,62	0,00000000	AT4G22870	ref|Arabidopsis thaliana 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein mRNA [NM_001160794]
	7,18	0,00000000	AT1G56650	ref|Arabidopsis thaliana production of anthocyanin pigment 1 (PAP1), mRNA [NM_104541]

	5,69	0,00000000	AT5G54060	ref|Arabidopsis thaliana UDP-glucose:flavonoid 3-o-glucosyltransferase (UF3GT), mRNA [NM_124785]
	5,15	0,00000000	AT5G23020	ref|Arabidopsis thaliana 2-isopropylmalate synthase 2 (IMS2), mRNA [NM_122208]
	4,82	0,00000000	AT1G16410	ref|Arabidopsis thaliana cytochrome p450 79f1 (CYP79F1), mRNA [NM_101507]
	4,44	0,00000000	AT1G06000	ref|Arabidopsis thaliana UDP-Glycosyltransferase superfamily protein mRNA [NM_100480]
	4,35	0,00000000	AT4G03060	gb|Arabidopsis thaliana Col-0 2-oxoglutarate-dependent dioxygenase (AOP2) pseudogene, mRNA sequence [AF418241]
	4,32	0,00000000	AT2G43100	ref|Arabidopsis thaliana isopropylmalate isomerase 2 (IPMI2), mRNA [NM_129871]
	4,32	0,00000000	AT4G22880	ref|Arabidopsis thaliana leucoanthocyanidin dioxygenase (LDOX), mRNA [NM_001036623]
	4,27	0,00000000	AT1G62560	ref|Arabidopsis thaliana flavin-monooxygenase glucosinolate S-oxygenase 3 (FMO GS-OX3), mRNA [NM_001334038]
	4,13	0,00000000	AT2G38240	ref|Arabidopsis thaliana 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein mRNA [NM_129381]
	3,96	0,00000000	AT3G58990	ref|Arabidopsis thaliana isopropylmalate isomerase 1 (IPMI1), mRNA [NM_115761]
	3,91	0,00000000	AT5G05270	ref|Arabidopsis thaliana Chalcone-flavanone isomerase family protein (CHIL), mRNA [NM_180439]
	3,8	0,00000000	AT1G18590	ref|Arabidopsis thaliana sulfotransferase 17 (SOT17), mRNA [NM_101717]
	3,46	0,00000000	AT1G65860	ref|Arabidopsis thaliana flavin-monooxygenase glucosinolate S-oxygenase 1 (FMO GS-OX1), mRNA [NM_105258]
	3,36	0,00000000	AT5G08640	ref|Arabidopsis thaliana flavonol synthase 1 (FLS1), mRNA [NM_001203337]
	3,35	0,00000000	AT1G03495	gb|Arabidopsis thaliana HXXXD-type acyl-transferase-like protein (AT1G03495) mRNA, complete cds [NM_100232]
	3,34	0,00000000	AT3G29590	ref|Arabidopsis thaliana HXXXD-type acyl-transferase family protein (AT5MAT), mRNA [NM_113880]
	3,28	0,00000000	AT3G14210	ref|Arabidopsis thaliana GDSL-like lipase/acylhydrolase superfamily protein (ESM1), mRNA [NM_001338114]
	3,21	0,00000000	AT2G37040	ref|Arabidopsis thaliana PHE ammonia lyase 1 (PAL1), mRNA [NM_129260]
	3,08	0,00000000	AT5G07690	ref|Arabidopsis thaliana myb domain protein 29 (MYB29), mRNA [NM_120851]
	3,04	0,00000000	AT1G20510	ref|Arabidopsis thaliana OPC-8:0 CoA ligase1 (OPCL1), mRNA [NM_202143]
	-3,31	0,00000000	AT2G29290	ref|Arabidopsis thaliana NAD(P)-binding Rossmann-fold superfamily protein mRNA [NM_128483]
	-3,52	0,00000000	AT5G39050	ref|Arabidopsis thaliana HXXXD-type acyl-transferase family protein (PMAT1), mRNA [NM_123267]
	-5,11	0,00000000	AT4G34135	ref|Arabidopsis thaliana UDP-glucosyltransferase 73B2 (UGT73B2), mRNA [NM_179161]
	-5,22	0,00000000	AT1G72680	ref|Arabidopsis thaliana cinnamyl-alcohol dehydrogenase (CAD1), mRNA [NM_105927]
	-7,11	0,00000000	AT1G06570	ref|Arabidopsis thaliana 4-hydroxyphenylpyruvate dioxygenase (PDS1), mRNA [NM_100536]
	-9,33	0,00000000	AT3G44300	ref|Arabidopsis thaliana nitrilase 2 (NIT2), mRNA [NM_114298]
Hormone metabolism				
	18,82	0,00000000	AT3G45140	ref|Arabidopsis thaliana lipoxygenase 2 (LOX2), mRNA [NM_001339198]
	3,76	0,00000000	AT5G13320	ref|Arabidopsis thaliana Auxin-responsive GH3 family protein (PBS3), mRNA [NM_001343268]
	3,51	0,00000000	AT5G42650	ref|Arabidopsis thaliana allene oxide synthase (AOS), mRNA [NM_123629]
	3,13	0,00000000	AT3G09870	ref|Arabidopsis thaliana SAUR-like auxin-responsive protein family mRNA [NM_111822]
	-3,01	0,00000000	AT2G03760	ref|Arabidopsis thaliana sulfotransferase 12 (SOT12), mRNA [NM_126423]
	-3,03	0,00000000	AT2G43820	ref|Arabidopsis thaliana UDP-glucosyltransferase 74F2 (UGT74F2), mRNA [NM_129944]
	-3,13	0,00000000	AT1G18020	ref|Arabidopsis thaliana FMN-linked oxidoreductases superfamily protein mRNA [NM_001035985]
	-3,15	0,00000000	AT1G76690	ref|Arabidopsis thaliana 12-oxophytodienoate reductase 2 (OPR2), mRNA [NM_106319]
	-3,16	0,00000000	AT5G43450	ref|Arabidopsis thaliana 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein mRNA [NM_001344483]
	-3,22	0,00000000	AT5G08350	ref|Arabidopsis thaliana GRAM domain-containing protein / ABA-responsive protein-like protein mRNA [NM_120919]
	-3,48	0,00000000	AT1G17990	ref|Arabidopsis thaliana FMN-linked oxidoreductases superfamily protein mRNA [NM_001035985]
	-4,03	0,00000000	AT2G36750	ref|Arabidopsis thaliana UDP-glucosyl transferase 73C1 (UGT73C1), mRNA [NM_129230]
	-4,95	0,00000000	AT3G61900	ref|Arabidopsis thaliana SAUR-like auxin-responsive protein family mRNA [NM_116055]
	-5,05	0,00000000	AT5G50760	ref|Arabidopsis thaliana SAUR-like auxin-responsive protein family mRNA [NM_124454]
	-5,54	0,00000000	AT2G47770	ref|Arabidopsis thaliana TSPO(outer membrane tryptophan-rich sensory protein)-like protein (TSPO), mRNA [NM_130344]
	-6,11	0,00000000	AT1G05560	ref|Arabidopsis thaliana UDP-glucosyltransferase 75B1 (UGT75B1), mRNA [NM_100435]
	-6,19	0,00000000	AT2G37030	ref|Arabidopsis thaliana SAUR-like auxin-responsive protein family mRNA [NM_129259]
	-6,24	0,00000000	AT1G75750	ref|Arabidopsis thaliana GAST1 protein homolog 1 (GASA1), mRNA [NM_001198478]
	-9,25	0,00000000	AT1G76680	ref|Arabidopsis thaliana 12-oxophytodienoate reductase 1 (OPR1), mRNA [NM_202428]
	-15,78	0,00000000	AT2G33830	ref|Arabidopsis thaliana Dormancy/auxin associated family protein mRNA [NM_001336474]
	-23,82	0,00000000	AT4G27450	ref|Arabidopsis thaliana aluminum induced protein with YGL and LRDR motifs mRNA [NM_118880]
	-30,57	0,00000000	AT3G15450	ref|Arabidopsis thaliana aluminum induced protein with YGL and LRDR motifs mRNA [NM_001035625]
	-35,53	0,00000000	AT1G05680	ref|Arabidopsis thaliana Uridine diphosphate glycosyltransferase 74E2 (UGT74E2), mRNA [NM_100448]
Co-factor and vitamin metabolism				
	-8,45	0,00000000	AT3G14990	ref|Arabidopsis thaliana Class I glutamine amidotransferase-like superfamily protein (DJ1A), mRNA [NM_001035621]
Tetrapyrrole synthesis				
	-3,92	0,00000000	AT1G58290	ref|Arabidopsis thaliana Glutamyl-tRNA reductase family protein (HEMA1), mRNA [NM_104609]
Stress				
	13,06	0,00000000	AT5G44420	ref|Arabidopsis thaliana plant defensin 1.2 (PDF1.2), mRNA [NM_123809]
	11,27	0,00000000	AT3G22231	ref|Arabidopsis thaliana pathogen and circadian controlled 1 (PCC1), mRNA [NM_113121]
	9,18	0,00000000	AT2G43620	ref|Arabidopsis thaliana Chitinase family protein mRNA [NM_129924]
	7,94	0,00000000	AT5G44430	ref|Arabidopsis thaliana plant defensin 1.2C (PDF1.2c), mRNA [NM_123810]
	6,87	0,00000000	AT2G26010	ref|Arabidopsis thaliana plant defensin 1.3 (PDF1.3), mRNA [NM_128160]
	6,79	0,00000000	AT2G43570	ref|Arabidopsis thaliana chitinase (CHI), mRNA [NM_129919]
	6,08	0,00000000	AT4G21830	ref|Arabidopsis thaliana methionine sulfoxide reductase B7 (MSRB7), mRNA [NM_118303]
	5,47	0,00000000	AT2G16367	Unknown
	4,46	0,00000000	AT1G73325	ref|Arabidopsis thaliana Kunitz family trypsin and protease inhibitor protein mRNA [NM_105992]
	4,17	0,00000000	AT2G26020	ref|Arabidopsis thaliana plant defensin 1.2b (PDF1.2b), mRNA [NM_128161]
	4,15	0,00000000	AT4G36010	ref|Arabidopsis thaliana Pathogenesis-related thaumatin superfamily protein mRNA [NM_001036715]
	4,1	0,00000000	AT3G11010	ref|Arabidopsis thaliana receptor like protein 34 (RLP34), mRNA [NM_111938]
	3,99	0,00000000	AT4G39030	ref|Arabidopsis thaliana MATE efflux family protein (EDS5), mRNA [NM_120063]

	3,85	0,00000000	AT3G48080	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_114677]
	3,51	0,00000000	AT4G11190	ref|Arabidopsis thaliana Disease resistance-responsive (dirigent-like protein) family protein mRNA [NM_117190]
	3,39	0,00000000	AT2G41010	ref|Arabidopsis thaliana calmodulin (CAM)-binding protein of 25 kDa (CAMBP25), mRNA [NM_129666]
	3,27	0,00000000	AT1G72910	ref|Arabidopsis thaliana Toll-Interleukin-Resistance (TIR) domain-containing protein mRNA [NM_105949]
	3,22	0,00000000	AT5G42020	ref|Arabidopsis thaliana Heat shock protein 70 (Hsp 70) family protein (BIP2), mRNA [NM_123567]
	3,16	0,00000000	AT5G28540	ref|Arabidopsis thaliana heat shock protein 70 (Hsp 70) family protein (BIP1), mRNA [NM_122737]
	-3,03	0.00000001	AT1G71000	ref|Arabidopsis thaliana Chaperone DnaJ-domain superfamily protein mRNA [NM_001334483]
	-3,04	0.00000002	AT5G36910	ref|Arabidopsis thaliana thionin 2.2 (THI2.2), mRNA [NM_123049]
	-3,14	0,00000000	AT4G13830	ref|Arabidopsis thaliana DNAJ-like 20 (J20), mRNA [NM_117457]
	-3,16	0,00000000	AT2G29500	ref|Arabidopsis thaliana HSP20-like chaperones superfamily protein mRNA [NM_128504]
	-3,27	0,00000000	AT3G03480	ref|Arabidopsis thaliana acetyl CoA:(Z)-3-hexen-1-ol acetyltransferase (CHAT), mRNA [NM_111219]
	-3,35	0.00000001	AT1G75380	ref|Arabidopsis thaliana bifunctional nuclease in basal defense response 1 (BBD1), mRNA [NM_179560]
	-3,46	0,00000000	AT3G59930	ref|Arabidopsis thaliana defensin-like protein mRNA [NM_115856]
	-3,99	0,00000000	AT5G44973	ref|Arabidopsis thaliana defensin-like protein mRNA [NM_001036935]
	-4,24	0,00000000	AT2G26150	ref|Arabidopsis thaliana heat shock transcription factor A2 (HSFA2), mRNA [NM_001336038]
	-4,37	0,00000000	AT3G15620	ref|Arabidopsis thaliana DNA photolyase family protein (UVR3), mRNA [NM_112432]
	-6	0,00000000	AT5G51440	ref|Arabidopsis thaliana HSP20-like chaperones superfamily protein mRNA [NM_124523]
	-6,57	0,00000000	AT2G17880	ref|Arabidopsis thaliana Chaperone DnaJ-domain superfamily protein mRNA [NM_127342]
	-7,31	0,00000000	AT4G36040	ref|Arabidopsis thaliana Chaperone DnaJ-domain superfamily protein (J11), mRNA [NM_119771]
	-7,41	0,00000000	AT2G36800	ref|Arabidopsis thaliana don-glucosyltransferase 1 (DOGT1), mRNA [NM_129235]
	-9,31	0,00000000	AT1G07400	ref|Arabidopsis thaliana HSP20-like chaperones superfamily protein mRNA [NM_100614]
	-9,74	0,00000000	AT5G66400	ref|Arabidopsis thaliana Dehydrin family protein (RAB18), mRNA [NM_126038]
	-14,27	0,00000000	AT1G80920	ref|Arabidopsis thaliana Chaperone DnaJ-domain superfamily protein (J8), mRNA [NM_106740]
	-3,14	0,00000000	AT1G19660	ref|Arabidopsis thaliana Wound-responsive family protein mRNA [NM_001035991]
Redox				
	5,18	0,00000000	AT1G06830	ref|Arabidopsis thaliana Glutaredoxin family protein mRNA [NM_100560]
	4,44	0,00000000	AT1G28480	ref|Arabidopsis thaliana Thioredoxin superfamily protein (GRX480), mRNA [NM_102616]
	3,29	0,00000000	AT2G46650	ref|Arabidopsis thaliana cytochrome B5 isoform C (CB5-C), mRNA [NM_130230]
	3,21	0,00000000	AT1G04980	ref|Arabidopsis thaliana PDI-like 2-2 (PDIL2-2), mRNA [NM_100376]
	3,01	0.00000001	AT2G16060	ref|Arabidopsis thaliana hemoglobin 1 (HB1), mRNA [NM_127165]
	-3,09	0.00000001	AT1G08570	ref|Arabidopsis thaliana atypical CYS HIS rich thioredoxin 4 (ACHT4), mRNA [NM_001123776]
	-3,12	0,00000000	AT4G31870	ref|Arabidopsis thaliana glutathione peroxidase 7 (GPX7), mRNA [NM_001342119]
	-3,22	0,00000000	AT1G20630	ref|Arabidopsis thaliana catalase 1 (CAT1), mRNA [NM_101914]
	-3,35	0,00000000	AT3G62950	ref|Arabidopsis thaliana Thioredoxin superfamily protein mRNA [NM_116160]
	-4,49	0,00000000	AT1G07890	ref|Arabidopsis thaliana ascorbate peroxidase 1 (APX1), mRNA [NM_100663]
	-7,81	0,00000000	AT4G35090	ref|Arabidopsis thaliana catalase 2 (CAT2), mRNA [NM_001342324]
	-23,72	0,00000000	AT1G65970	ref|Arabidopsis thaliana thioredoxin-dependent peroxidase 2 (TPX2), mRNA [NM_105269]
polyamine metabolims				
	-7,88	0,00000000	AT4G34710	ref|Arabidopsis thaliana arginine decarboxylase 2 (ADC2), mRNA [NM_202955]
Nucleotide metabolism				
	5,55	0,00000000	AT3G27060	ref|Arabidopsis thaliana Ferritin/ribonucleotide reductase-like family protein (TSO2), mRNA [NM_113620]
	3,58	0,00000000	AT4G18440	ref|Arabidopsis thaliana L-Aspartase-like family protein mRNA [NM_117957]
	-4,66	0,00000000	AT1G30820	ref|Arabidopsis thaliana CTP synthase family protein mRNA [NM_102819]
Biodegradation of xenobiotics				
	-3,28	0,00000000	AT1G53580	ref|Arabidopsis thaliana glyoxalase II 3 (GLY3), mRNA [NM_202289]
	-27,88	0,00000000	AT1G80160	ref|Arabidopsis thaliana Lactoylglutathione lyase / glyoxalase I family protein (GLYI7), mRNA [NM_001084382]
	-35,27	0,00000000	AT1G15380	ref|Arabidopsis thaliana Lactoylglutathione lyase / glyoxalase I family protein (GLYI4), mRNA [NM_001035972]
Miscellaneous enzyme family				
	27,3	0,00000000	AT2G39030	ref|Arabidopsis thaliana Acyl-CoA N-acyltransferases (NAT) superfamily protein (NATA1), mRNA [NM_129460]
	11,96	0,00000000	AT3G57260	ref|Arabidopsis thaliana beta-1,3-glucanase 2 (BGL2), mRNA [NM_115586]
	11,48	0,00000000	AT3G57240	ref|Arabidopsis thaliana beta-1,3-glucanase 3 (BG3), mRNA [NM_115584]
	10,64	0,00000000	AT3G26830	ref|Arabidopsis thaliana Cytochrome P450 superfamily protein (PAD3), mRNA [NM_113595]
	7,28	0,00000000	AT1G73010	ref|Arabidopsis thaliana inorganic pyrophosphatase 1 (PS2), mRNA [NM_105959]
	7,2	0,00000000	AT3G25180	ref|Arabidopsis thaliana cytochrome P450, family 82, subfamily G, polypeptide 1 (CYP82G1), mRNA [NM_202630]
	7,07	0.00000001	AT2G30770	ref|Arabidopsis thaliana cytochrome P450 family 71 polypeptide (CYP71A13), mRNA [NM_128630]
	6,74	0,00000000	AT5G17220	ref|Arabidopsis thaliana glutathione S-transferase phi 12 (GSTF12), mRNA [NM_121728]
	6,46	0,00000000	AT4G21760	ref|Arabidopsis thaliana beta-glucosidase 47 (BGLU47), mRNA [NM_001341512]
	6,38	0,00000000	AT2G29350	ref|Arabidopsis thaliana senescence-associated gene 13 (SAG13), mRNA [NM_201829]
	5,86	0,00000000	AT5G03350	ref|Arabidopsis thaliana Legume lectin family protein mRNA [NM_120414]
	5,47	0,00000000	AT1G78370	ref|Arabidopsis thaliana glutathione S-transferase TAU 20 (GSTU20), mRNA [NM_106484]
	5,35	0,00000000	AT1G19250	ref|Arabidopsis thaliana flavin-dependent monooxygenase 1 (FMO1), mRNA [NM_101783]
	4,65	0,00000000	AT2G46880	ref|Arabidopsis thaliana purple acid phosphatase 14 (PAP14), mRNA [NM_201975]
	4,4	0,00000000	AT1G29660	ref|Arabidopsis thaliana GDSL-like Lipase/Acylhydrolase superfamily protein mRNA [NM_102706]
	4,27	0,00000000	AT3G11340	ref|Arabidopsis thaliana UDP-Glycosyltransferase superfamily protein (UGT76B1), mRNA [NM_111968]
	4,27	0,00000000	AT3G22600	ref|Arabidopsis thaliana Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein mRNA [NM_113159]
	4,02	0,00000000	AT1G01190	ref|Arabidopsis thaliana cytochrome P450, family 78, subfamily A, polypeptide 8 (CYP78A8), mRNA [NM_100001]
	3,67	0,00000000	AT1G17710	ref|Arabidopsis thaliana Pyridoxal phosphate phosphatase-related protein (PEPC1), mRNA [NM_001084087]

	3,44	0,00000000	AT4G12880	ref|Arabidopsis thaliana early nodulin-like protein 19 (ENODL19), mRNA [NM_001203782]
	3,42	0,00000000	AT1G13750	ref|Arabidopsis thaliana Purple acid phosphatases superfamily protein mRNA [NM_101243]
	3,39	0,00000000	AT3G17790	ref|Arabidopsis thaliana purple acid phosphatase 17 (PAP17), mRNA [NM_112660]
	3,38	0,00000000	AT1G64390	ref|Arabidopsis thaliana glycosyl hydrolase 9C2 (GH9C2), mRNA [NM_105114]
	3,37	0.00000003	AT4G14090	ref|Arabidopsis thaliana UDP-Glycosyltransferase superfamily protein mRNA [NM_117485]
	3,29	0,00000000	AT2G39330	ref|Arabidopsis thaliana jacalin-related lectin 23 (JAL23), mRNA [NM_129490]
	3,11	0,00000000	AT5G64080	ref|Arabidopsis thaliana Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (XYP1), mRNA [NM_125804]
	-3,03	0,00000000	AT2G29480	ref|Arabidopsis thaliana glutathione S-transferase tau 2 (GSTU2), mRNA [NM_128502]
	-3,19	0,00000000	AT4G24050	ref|Arabidopsis thaliana NAD(P)-binding Rossmann-fold superfamily protein mRNA [NM_001341639]
	-3,26	0,00000000	AT2G30140	ref|Arabidopsis thaliana UDP-Glycosyltransferase superfamily protein (UGT87A2), mRNA [NM_001084510]
	-3,26	0,00000000	AT3G55710	ref|Arabidopsis thaliana UDP-Glycosyltransferase superfamily protein mRNA [NM_115429]
	-3,37	0,00000000	AT1G64940	ref|Arabidopsis thaliana cytochrome P450, family 87, subfamily A, polypeptide 6 (CYP89A6), mRNA [NM_105168]
	-3,38	0,00000000	AT1G64950	ref|Arabidopsis thaliana cytochrome P450, family 89, subfamily A, polypeptide 5 (CYP89A5), mRNA [NM_105169]
	-3,43	0.00000001	AT2G32020	ref|Arabidopsis thaliana Acyl-CoA N-acyltransferases (NAT) superfamily protein mRNA [NM_128762]
	-3,45	0,00000000	AT2G37130	ref|Arabidopsis thaliana Peroxidase superfamily protein mRNA [NM_001124989]
	-3,48	0,00000000	AT3G26220	ref|Arabidopsis thaliana cytochrome P450, family 71, subfamily B, polypeptide 3 (CYP71B3), mRNA [NM_113529]
	-3,63	0,00000000	AT3G43670	ref|Arabidopsis thaliana Copper amine oxidase family protein mRNA [NM_114235]
	-3,7	0,00000000	AT1G14130	ref|Arabidopsis thaliana 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein mRNA [NM_101278]
	-3,85	0,00000000	AT4G34138	ref|Arabidopsis thaliana UDP-glucosyl transferase 73B1 (UGT73B1), mRNA [NM_119576]
	-3,92	0,00000000	AT5G16960	ref|Arabidopsis thaliana Zinc-binding dehydrogenase family protein mRNA [NM_001343474]
	-3,93	0,00000000	AT3G03470	ref|Arabidopsis thaliana cytochrome P450, family 87, subfamily A, polypeptide 9 (CYP89A9), mRNA [NM_111218]
	-3,95	0,00000000	AT5G16970	ref|Arabidopsis thaliana alkenal reductase (AER), mRNA [NM_121703]
	-4,01	0,00000000	AT3G14690	ref|Arabidopsis thaliana cytochrome P450, family 72, subfamily A, polypeptide 15 (CYP72A15), mRNA [NM_112330]
	-4,08	0,00000000	AT5G17000	ref|Arabidopsis thaliana Zinc-binding dehydrogenase family protein mRNA [NM_001343476]
	-4,19	0,00000000	AT5G64250	ref|Arabidopsis thaliana Aldolase-type TIM barrel family protein mRNA [NM_125821]
	-4,3	0,00000000	AT3G50560	ref|Arabidopsis thaliana NAD(P)-binding Rossmann-fold superfamily protein mRNA [NM_114916]
	-4,45	0,00000000	AT3G14680	ref|Arabidopsis thaliana cytochrome P450, family 72, subfamily A, polypeptide 14 (CYP72A14), mRNA [NM_112329]
	-4,46	0,00000000	AT4G13250	ref|Arabidopsis thaliana NAD(P)-binding Rossmann-fold superfamily protein (NYC1), mRNA [NM_117396]
	-4,63	0,00000000	AT3G46690	ref|Arabidopsis thaliana UDP-Glycosyltransferase superfamily protein mRNA [NM_114536]
	-4,65	0,00000000	AT1G53100	ref|Arabidopsis thaliana Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein mRNA [NM_104189]
	-4,67	0,00000000	AT1G22380	ref|Arabidopsis thaliana UDP-glucosyl transferase 85A3 (UGT85A3), mRNA [NM_102088]
	-4,76	0,00000000	AT4G37370	ref|Arabidopsis thaliana cytochrome P450, family 81, subfamily D, polypeptide 8 (CYP81D8), mRNA [NM_119900]
	-4,87	0.00000001	AT4G20860	ref|Arabidopsis thaliana FAD-binding Berberine family protein mRNA [NM_118204]
	-5,1	0,00000000	AT4G34131	ref|Arabidopsis thaliana UDP-glucosyl transferase 73B3 (UGT73B3), mRNA [NM_119574]
	-5,15	0,00000000	AT3G14660	ref|Arabidopsis thaliana cytochrome P450, family 72, subfamily A, polypeptide 13 (CYP72A13), mRNA [NM_001338130]
	-5,24	0,00000000	AT3G13750	ref|Arabidopsis thaliana beta galactosidase 1 (BGAL1), mRNA [NM_112225]
	-5,89	0,00000000	AT2G15490	ref|Arabidopsis thaliana UDP-glycosyltransferase 73B4 (UGT73B4), mRNA [NM_127109]
	-5,94	0,00000000	AT2G29420	ref|Arabidopsis thaliana glutathione S-transferase tau 7 (GSTU7), mRNA [NM_128496]
	-6,26	0,00000000	AT1G30720	ref|Arabidopsis thaliana FAD-binding Berberine family protein mRNA [NM_102808]
	-6,96	0,00000000	AT2G36780	ref|Arabidopsis thaliana UDP-Glycosyltransferase superfamily protein mRNA [NM_129233]
	-7,23	0,00000000	AT2G15480	ref|Arabidopsis thaliana UDP-glucosyl transferase 73B5 (UGT73B5), mRNA [NM_127108]
	-7,26	0,00000000	AT4G15760	ref|Arabidopsis thaliana monooxygenase 1 (MO1), mRNA [NM_001203809]
	-7,68	0,00000000	AT5G16980	ref|Arabidopsis thaliana Zinc-binding dehydrogenase family protein mRNA [NM_121704]
	-8,03	0,00000000	AT1G62510	ref|Arabidopsis thaliana Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein mRNA [NM_104930]
	-9,77	0,00000000	AT3G61060	ref|Arabidopsis thaliana phloem protein 2-A13 (PP2-A13), mRNA [NM_202741]
	-10,73	0,00000000	AT4G16690	ref|Arabidopsis thaliana methyl esterase 16 (MES16), mRNA [NM_117770]
	-12,51	0,00000000	AT2G29490	ref|Arabidopsis thaliana glutathione S-transferase TAU 1 (GSTU1), mRNA [NM_128503]
	-12,58	0,00000000	AT1G17170	ref|Arabidopsis thaliana glutathione S-transferase TAU 24 (GSTU24), mRNA [NM_101578]
	-13,3	0,00000000	AT3G60140	ref|Arabidopsis thaliana Glycosyl hydrolase superfamily protein (DIN2), mRNA [NM_001340024]
	-15,3	0,00000000	AT3G04000	ref|Arabidopsis thaliana NAD(P)-binding Rossmann-fold superfamily protein mRNA [NM_111271]
	-15,36	0,00000000	AT5G56870	ref|Arabidopsis thaliana beta-galactosidase 4 (BGAL4), mRNA [NM_125070]
	-17,15	0,00000000	AT1G09500	ref|Arabidopsis thaliana NAD(P)-binding Rossmann-fold superfamily protein mRNA [NM_100821]
	-17,43	0,00000000	AT5G39580	ref|Arabidopsis thaliana Peroxidase superfamily protein mRNA [NM_001036908]
	-45,78	0,00000000	AT3G28740	ref|Arabidopsis thaliana Cytochrome P450 superfamily protein (CYP81D11), mRNA [NM_113795]
RNA				
	42,09	0,00000000	AT2G41240	ref|Arabidopsis thaliana basic helix-loop-helix protein 100 (BHLH100), mRNA [NM_180018]
	20,71	0,00000000	AT3G56970	ref|Arabidopsis thaliana basic helix-loop-helix (bHLH) DNA-binding superfamily protein (bHLH38), mRNA [NM_115556]
	16,45	0,00000000	AT3G56980	ref|Arabidopsis thaliana basic helix-loop-helix (bHLH) DNA-binding superfamily protein (bHLH39), mRNA [NM_115557]
	4,42	0,00000000	AT5G10760	ref|Arabidopsis thaliana Eukaryotic aspartyl protease family protein mRNA [NM_121114]
	4,29	0,00000000	AT3G25882	ref|Arabidopsis thaliana NIM1-interacting 2 (NIMIN-2), mRNA [NM_148752]
	4,11	0,00000000	AT1G02450	ref|Arabidopsis thaliana NIM1-interacting 1 (NIMIN1), mRNA [NM_100126]
	3,95	0,00000000	AT5G61000	ref|Arabidopsis thaliana Replication factor-A protein 1-like protein (RPA70D), mRNA [NM_125493]
	3,64	0,00000000	AT5G04150	ref|Arabidopsis thaliana basic helix-loop-helix (bHLH) DNA-binding superfamily protein (BHLH101), mRNA [NM_120497]
	3,47	0,00000000	AT5G23420	ref|Arabidopsis thaliana high-mobility group box 6 (HMGB6), mRNA [NM_001203442]
	3,43	0,00000000	AT2G40750	ref|Arabidopsis thaliana WRKY DNA-binding protein 54 (WRKY54), mRNA [NM_129637]
	3,36	0,00000000	AT3G56400	ref|Arabidopsis thaliana WRKY DNA-binding protein 70 (WRKY70), mRNA [NM_115498]
	3,25	0,00000000	AT3G44750	ref|Arabidopsis thaliana histone deacetylase 3 (HDA3), mRNA [NM_001203083]
	3,2	0,00000000	AT1G66390	ref|Arabidopsis thaliana myb domain protein 90 (MYB90), mRNA [NM_105310]
	3,11	0,00000000	AT1G04020	ref|Arabidopsis thaliana breast cancer associated RING 1 (BARD1), mRNA [NM_202029]
	3,1	0,00000000	AT5G46830	ref|Arabidopsis thaliana calcium-binding transcription factor NIG1 (NIG1), mRNA [NM_124054]
	3,01	0,00000000	AT5G61030	ref|Arabidopsis thaliana glycine-rich RNA-binding protein 3 (GR-RBP3), mRNA [NM_125496]

	-3,05	0,00000000	AT5G59340	ref|Arabidopsis thaliana WUSCHEL related homeobox 2 (WOX2), mRNA [NM_125325]
	-3,09	0,00000000	AT5G57660	ref|Arabidopsis thaliana CONSTANS-like 5 (COL5), mRNA [NM_125149]
	-3,13	0.00000001	AT5G17300	ref|Arabidopsis thaliana Homeodomain-like superfamily protein (RVE1), mRNA [NM_121736]
	-3,16	0,00000000	AT3G16770	ref|Arabidopsis thaliana ethylene-responsive element binding protein (EBP), mRNA [NM_112550]
	-3,27	0,00000000	AT1G48000	ref|Arabidopsis thaliana myb domain protein 112 (MYB112), mRNA [NM_103696]
	-3,33	0,00000000	AT5G39660	ref|Arabidopsis thaliana cycling DOF factor 2 (CDF2), mRNA [NM_180775]
	-3,44	0,00000000	AT2G30250	ref|Arabidopsis thaliana WRKY DNA-binding protein 25 (WRKY25), mRNA [NM_128578]
	-3,86	0,00000000	AT3G46080	ref|Arabidopsis thaliana C2H2-type zinc finger family protein mRNA [NM_114477]
	-3,97	0,00000000	AT5G28770	ref|Arabidopsis thaliana bZIP transcription factor family protein (BZO2H3), mRNA [NM_001344083]
	-4,2	0,00000000	AT2G25900	ref|Arabidopsis thaliana Zinc finger C-x8-C-x5-C-x3-H type family protein (ATCTH), mRNA [NM_001202675]
	-4,26	0,00000000	AT5G13330	ref|Arabidopsis thaliana related to AP2 6l (Rap2.6L), mRNA [NM_121336]
	-4,38	0,00000000	AT1G75490	ref|Arabidopsis thaliana Integrase-type DNA-binding superfamily protein mRNA [NM_106202]
	-4,42	0,00000000	AT3G15500	ref|Arabidopsis thaliana NAC domain containing protein 3 (NAC3), mRNA [NM_112418]
	-4,49	0,00000000	AT4G16680	ref|Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA [NM_001341126]
	-4,5	0,00000000	AT1G68190	ref|Arabidopsis thaliana B-box zinc finger family protein (BBX27), mRNA [NM_001334353]
	-4,55	0,00000000	AT5G24120	ref|Arabidopsis thaliana sigma factor E (SIGE), mRNA [NM_001343842]
	-4,6	0,00000000	AT1G13300	ref|Arabidopsis thaliana myb-like transcription factor family protein (HRS1), mRNA [NM_101201]
	-5,32	0,00000000	AT5G07100	ref|Arabidopsis thaliana WRKY DNA-binding protein 26 (WRKY26), mRNA [NM_120792]
	-5,4	0,00000000	AT1G71520	ref|Arabidopsis thaliana Integrase-type DNA-binding superfamily protein mRNA [NM_105820]
	-5,41	0,00000000	AT5G49450	ref|Arabidopsis thaliana basic leucine-zipper 1 (bZIP1), mRNA [NM_124322]
	-5,46	0,00000000	AT1G71030	ref|Arabidopsis thaliana MYB-like 2 (MYBL2), mRNA [NM_001334485]
	-5,78	0,00000000	AT5G24800	ref|Arabidopsis thaliana basic leucine zipper 9 (BZIP9), mRNA [NM_122389]
	-5,81	0,00000000	AT5G05410	ref|Arabidopsis thaliana DRE-binding protein 2A (DREB2A), mRNA [NM_001036760]
	-6,92	0,00000000	AT1G79700	ref|Arabidopsis thaliana Integrase-type DNA-binding superfamily protein (WRI4), mRNA [NM_001334913]
	-18,57	0,00000000	AT2G47270	ref|Arabidopsis thaliana transcription factor UPBEAT protein (UPB1), mRNA [NM_130295]
DNA				
	4,11	0,00000000	AT5G59870	ref|Arabidopsis thaliana histone H2A 6 (HTA6), mRNA [NM_125380]
	4,1	0,00000000	AT1G09200	ref|Arabidopsis thaliana Histone superfamily protein mRNA [NM_100790]
	3,75	0,00000000	AT5G65360	ref|Arabidopsis thaliana Histone superfamily protein mRNA [NM_125934]
	3,67	0,00000000	AT5G10390	ref|Arabidopsis thaliana Histone superfamily protein mRNA [NM_121077]
	3,31	0,00000000	AT3G46320	ref|Arabidopsis thaliana Histone superfamily protein mRNA [NM_180329]
	3,29	0,00000000	AT3G45930	ref|Arabidopsis thaliana Histone superfamily protein mRNA [NM_114462]
	3,17	0,00000000	AT5G10400	ref|Arabidopsis thaliana Histone superfamily protein mRNA [NM_121078]
	3,16	0,00000000	AT2G28740	ref|Arabidopsis thaliana histone H4 (HIS4), mRNA [NM_128434]
	3,07	0,00000000	AT3G27360	ref|Arabidopsis thaliana Histone superfamily protein mRNA [NM_113651]
	-4,3	0,00000000	AT5G63190	ref|Arabidopsis thaliana MA3 domain-containing protein mRNA [NM_125714]
	-4,96	0,00000000	AT2G18050	ref|Arabidopsis thaliana histone H1-3 (HIS1-3), mRNA [NM_179639]
Protein				
	8,87	0,00000000	AT4G21840	ref|Arabidopsis thaliana methionine sulfoxide reductase B8 (MSRB8), mRNA [NM_118304]
	5,85	0,00000000	AT5G60900	ref|Arabidopsis thaliana receptor-like protein kinase 1 (RLK1), mRNA [NM_001345434]
	5,5	0,00000000	AT5G53450	ref|Arabidopsis thaliana OBP3-responsive protein 1 (ORG1), mRNA [NM_001345057]
	4,63	0,00000000	AT4G04830	ref|Arabidopsis thaliana methionine sulfoxide reductase B5 (MSRB5), mRNA [NM_001203745]
	4,09	0,00000000	AT3G44870	ref|Arabidopsis thaliana S-adenosyl-L-methionine-dependent methyltransferases superfamily protein mRNA [NM_114356]
	4,07	0,00000000	AT4G25630	ref|Arabidopsis thaliana fibrillarin 2 (FIB2), mRNA [NM_118695]
	4,01	0,00000000	AT5G45650	ref|Arabidopsis thaliana subtilase family protein mRNA [NM_001344636]
	3,79	0,00000000	AT1G43910	ref|Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA [NM_103518]
	3,39	0,00000000	AT3G60540	ref|Arabidopsis thaliana Preprotein translocase Sec, Sec61-beta subunit protein mRNA [NM_202738]
	3,36	0,00000000	AT1G23100	ref|Arabidopsis thaliana GroES-like family protein mRNA [NM_102158]
	3,26	0,00000000	AT3G03060	ref|Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA [NM_111176]
	3,21	0,00000000	AT2G23010	ref|Arabidopsis thaliana serine carboxypeptidase-like 9 (SCPL9), mRNA [NM_201788]
	-3,04	0,00000000	AT4G39090	ref|Arabidopsis thaliana Papain family cysteine protease (RD19), mRNA [NM_120069]
	-3,12	0,00000000	AT3G10910	ref|Arabidopsis thaliana RING/U-box superfamily protein mRNA [NM_111928]
	-3,19	0,00000000	AT2G22960	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_001335830]
	-3,26	0,00000000	AT4G04770	ref|Arabidopsis thaliana ATP binding cassette protein 1 (ABCI8), mRNA [NM_116715]
	-3,27	0,00000000	AT4G25390	ref|Arabidopsis thaliana Protein kinase superfamily protein mRNA [NM_179111]
	-3,31	0,00000000	AT1G06430	ref|Arabidopsis thaliana FTSH protease 8 (FTSH8), mRNA [NM_100523]
	-3,35	0,00000000	AT2G22990	ref|Arabidopsis thaliana sinapoylglucose 1 (SNG1), mRNA [NM_127864]
	-3,4	0,00000000	AT4G16520	ref|Arabidopsis thaliana Ubiquitin-like superfamily protein (ATG8F), mRNA [NM_179064]
	-3,4	0,00000000	AT4G23450	ref|Arabidopsis thaliana RING/U-box superfamily protein (AIRP1), mRNA [NM_001341614]
	-3,42	0,00000000	AT4G37610	ref|Arabidopsis thaliana BTB and TAZ domain protein 5 (BT5), mRNA [NM_119924]
	-3,45	0,00000000	AT4G31860	ref|Arabidopsis thaliana Protein phosphatase 2C family protein mRNA [NM_202927]
	-3,47	0.00000001	AT4G16190	ref|Arabidopsis thaliana Papain family cysteine protease mRNA [NM_117715]
	-3,5	0,00000000	AT2G44130	ref|Arabidopsis thaliana Galactose oxidase/kelch repeat superfamily protein mRNA [NM_129976]
	-3,63	0,00000000	AT1G20350	ref|Arabidopsis thaliana translocase inner membrane subunit 17-1 (TIM17-1), mRNA [NM_101886]
	-3,75	0,00000000	AT4G20070	ref|Arabidopsis thaliana allantoate amidohydrolase (AAH), mRNA [NM_001341398]
	-3,86	0,00000000	AT5G55970	ref|Arabidopsis thaliana RING/U-box superfamily protein mRNA [NM_180866]
	-3,91	0,00000000	AT5G43580	ref|Arabidopsis thaliana Serine protease inhibitor, potato inhibitor I-type family protein (UPI), mRNA [NM_123724]
	-4,01	0,00000000	AT4G32940	ref|Arabidopsis thaliana gamma vacuolar processing enzyme (GAMMA-VPE), mRNA [NM_119448]
	-4,1	0,00000000	AT1G23390	ref|Arabidopsis thaliana Kelch repeat-containing F-box family protein mRNA [NM_102188]
	-4,26	0,00000000	AT5G17170	ref|Arabidopsis thaliana rubredoxin family protein (ENH1), mRNA [NM_001085129]

	-4,37	0,00000000	AT3G19390	ref|Arabidopsis thaliana Granulin repeat cysteine protease family protein mRNA [NM_112826]
	-4,62	0,00000000	AT4G38470	ref|Arabidopsis thaliana ACT-like protein tyrosine kinase family protein (STY46), mRNA [NM_001342498]
	-4,64	0,00000000	AT3G62260	ref|Arabidopsis thaliana Protein phosphatase 2C family protein mRNA [NM_180406]
	-4,74	0,00000000	AT1G63800	ref|Arabidopsis thaliana ubiquitin-conjugating enzyme 5 (UBC5), mRNA [NM_001334127]
	-4,86	0,00000000	AT1G80440	ref|Arabidopsis thaliana Galactose oxidase/kelch repeat superfamily protein mRNA [NM_106692]
	-5,1	0,00000000	AT5G51070	ref|Arabidopsis thaliana Clp ATPase (ERD1), mRNA [NM_124486]
	-5,18	0,00000000	AT5G24490	ref|Arabidopsis thaliana 30S ribosomal protein mRNA [NM_122357]
	-5,28	0,00000000	AT2G45170	ref|Arabidopsis thaliana AUTOPHAGY 8E (ATG8E), mRNA [NM_180100]
	-5,91	0,00000000	AT5G63160	ref|Arabidopsis thaliana BTB and TAZ domain protein 1 (BT1), mRNA [NM_001345581]
	-7,2	0,00000000	AT2G23030	ref|Arabidopsis thaliana SNF1-related protein kinase 2.9 (SNRK2.9), mRNA [NM_127867]
	-7,42	0,00000000	AT5G21170	ref|Arabidopsis thaliana 5'-AMP-activated protein kinase beta-2 subunit protein (AKINBETA1), mRNA [NM_001036841]
	-7,94	0,00000000	AT5G22920	ref|Arabidopsis thaliana CHY-type/CTCHY-type/RING-type Zinc finger protein mRNA [NM_122198]
	-8,56	0,00000000	AT1G66180	ref|Arabidopsis thaliana Eukaryotic aspartyl protease family protein mRNA [NM_105289]
	-12,31	0,00000000	AT1G22500	ref|Arabidopsis thaliana RING/U-box superfamily protein (ATL15), mRNA [NM_102099]
	-12,64	0,00000000	AT1G02610	ref|Arabidopsis thaliana RING/FYVE/PHD zinc finger superfamily protein mRNA [NM_001331347]
	-20,87	0,00000000	AT2G18193	ref|Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA [NM_179641]
Signalling				
	7,58	0,00000000	AT2G41090	ref|Arabidopsis thaliana Calcium-binding EF-hand family protein mRNA [NM_129674]
	6,66	0,00000000	AT3G24982	ref|Arabidopsis thaliana receptor like protein 40 (RLP40), mRNA [NM_113404]
	6,47	0,00000000	AT5G59670	ref|Arabidopsis thaliana Leucine-rich repeat protein kinase family protein mRNA [NM_001345366]
	5,8	0,00000000	AT1G35710	ref|Arabidopsis thaliana kinase family with leucine-rich repeat domain-containing protein mRNA [NM_103273]
	4,32	0,00000000	AT1G21250	ref|Arabidopsis thaliana cell wall-associated kinase (WAK1), mRNA [NM_101978]
	4,03	0,00000000	AT4G23130	ref|Arabidopsis thaliana cysteine-rich RLK (RECEPTOR-like protein kinase) 5 (CRK5), mRNA [NM_001341575]
	3,85	0,00000000	AT3G47480	ref|Arabidopsis thaliana Calcium-binding EF-hand family protein mRNA [NM_114616]
	3,6	0,00000000	AT5G54490	ref|Arabidopsis thaliana pinoid-binding protein 1 (PBP1), mRNA [NM_124829]
	3,36	0,00000000	AT1G73805	ref|Arabidopsis thaliana Calmodulin binding protein-like protein (SARD1), mRNA [NM_106040]
	3,07	0,00000000	AT5G42380	ref|Arabidopsis thaliana calmodulin like 37 (CML37), mRNA [NM_123603]
	3,02	0.00000001	AT4G23140	ref|Arabidopsis thaliana cysteine-rich RLK (RECEPTOR-like protein kinase) 6 (CRK6), mRNA [NM_179095]
	3,01	0,00000000	AT4G23170	ref|Arabidopsis thaliana receptor-like protein kinase-related family protein (EP1), mRNA [NM_118446]
	-3,04	0,00000000	AT1G76650	ref|Arabidopsis thaliana calmodulin-like 38 (CML38), mRNA [NM_001198484]
	-3,67	0,00000000	AT3G13065	ref|Arabidopsis thaliana STRUBBELIG-receptor family 4 (SRF4), mRNA [NM_112145]
	-4,49	0,00000000	AT5G58350	ref|Arabidopsis thaliana with no lysine (K) kinase 4 (WNK4), mRNA [NM_125220]
	-4,85	0,00000000	AT1G35670	ref|Arabidopsis thaliana calcium-dependent protein kinase 2 (CDPK2), mRNA [NM_103271]
	-5,21	0,00000000	AT1G18200	ref|Arabidopsis thaliana Rab GTPase-like A1I protein (RABA6b), mRNA [NM_101680]
	-7,01	0,00000000	AT2G02710	ref|Arabidopsis thaliana PAS/LOV protein B (PLPB), mRNA [NM_179597]
	-8,58	0,00000000	AT4G14690	ref|Arabidopsis thaliana Chlorophyll A-B binding family protein (ELIP2), mRNA [NM_117551]
	-8,58	0,00000000	AT5G09440	ref|Arabidopsis thaliana EXORDIUM like 4 (EXL4), mRNA [NM_120981]
	-9,44	0,00000000	AT5G64260	ref|Arabidopsis thaliana EXORDIUM like 2 (EXL2), mRNA [NM_125822]
Cell				
	10,29	0,00000000	AT5G54610	ref|Arabidopsis thaliana ankyrin (ANK), mRNA [NM_124842]
	6,95	0,00000000	AT4G14400	ref|Arabidopsis thaliana ankyrin repeat family protein (ACD6), mRNA [NM_179051]
	4,03	0,00000000	AT4G14365	ref|Arabidopsis thaliana hypothetical protein (XBAT34), mRNA [NM_117514]
	3,68	0,00000000	AT1G75780	ref|Arabidopsis thaliana tubulin beta-1 chain (TUB1), mRNA [NM_106228]
Micro RNA				
	5,66	0,00000000	AT5G53048	ref|Arabidopsis thaliana other RNA lncRNA [NR_143344]
	3,84	0,00000000	AT3G25795	ref|Arabidopsis thaliana other RNA ncRNA [NR_143943]
	-3,41	0,00000000	AT2G13431	gb|Arabidopsis thaliana clone asmbl_5374 unknown mRNA sequence [EF182961]
	-3,77	0,00000000	AT2G26355	ref|Arabidopsis thaliana other RNA lncRNA [NR_140673]
	-4,63	0,00000000	AT3G13061	ref|Arabidopsis thaliana other RNA lncRNA [NR_141586]
Development				
	5,39	0,00000000	AT2G35980	ref|Arabidopsis thaliana Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (YLS9), mRNA [NM_129157]
	4,92	0,00000000	AT5G48850	ref|Arabidopsis thaliana Tetratricopeptide repeat (TPR)-like superfamily protein (ATSDI1), mRNA [NM_124262]
	3,63	0,00000000	AT1G04770	ref|Arabidopsis thaliana Tetratricopeptide repeat (TPR)-like superfamily protein mRNA [NM_100355]
	3,43	0,00000000	AT2G38860	ref|Arabidopsis thaliana Class I glutamine amidotransferase-like superfamily protein (YLS5), mRNA [NM_129443]
	3,3	0,00000000	AT3G22550	ref|Arabidopsis thaliana NAD(P)H-quinone oxidoreductase subunit, putative (DUF581) mRNA [NM_113154]
	3,21	0,00000000	AT4G08300	ref|Arabidopsis thaliana nodulin MtN21 /EamA-like transporter family protein (UMAMIT17), mRNA [NM_116899]
	-3,05	0,00000000	AT5G39610	ref|Arabidopsis thaliana NAC domain containing protein 6 (NAC6), mRNA [NM_123323]
	-3,09	0,00000000	AT5G65870	ref|Arabidopsis thaliana phytosulfokine 5 precursor (PSK5), mRNA [NM_125984]
	-3,11	0.00000001	AT5G63790	ref|Arabidopsis thaliana NAC domain containing protein 102 (NAC102), mRNA [NM_001345612]
	-3,11	0,00000000	AT5G65380	ref|Arabidopsis thaliana MATE efflux family protein mRNA [NM_125936]
	-3,26	0,00000000	AT3G25190	ref|Arabidopsis thaliana Vacuolar iron transporter (VIT) family protein mRNA [NM_113425]
	-3,7	0,00000000	AT3G04060	ref|Arabidopsis thaliana NAC domain containing protein 46 (NAC046), mRNA [NM_111277]
	-3,94	0,00000000	AT5G19120	ref|Arabidopsis thaliana Eukaryotic aspartyl protease family protein mRNA [NM_121917]
	-4,13	0,00000000	AT5G52250	ref|Arabidopsis thaliana Transducin/WD40 repeat-like superfamily protein (RUP1), mRNA [NM_124604]
	-4,14	0,00000000	AT5G15850	ref|Arabidopsis thaliana CONSTANS-like 1 (COL1), mRNA [NM_121590]
	-4,21	0,00000000	AT2G28120	ref|Arabidopsis thaliana Major facilitator superfamily protein mRNA [NM_128372]
	-4,21	0,00000000	AT5G14120	ref|Arabidopsis thaliana Major facilitator superfamily protein mRNA [NM_121416]
	-4,43	0,00000000	AT1G77450	ref|Arabidopsis thaliana NAC domain containing protein 32 (NAC032), mRNA [NM_106394]

	-5,19	0,00000000	AT1G69490	ref|Arabidopsis thaliana NAC-like, activated by AP3/PI (NAP), mRNA [NM_105616]
	-5,25	0,00000000	AT3G29035	ref|Arabidopsis thaliana NAC domain containing protein 3 (NAC3), mRNA [NM_113825]
	-8,25	0,00000000	AT1G28330	ref|Arabidopsis thaliana dormancy-associated protein-like 1 (DYL1), mRNA [NM_179390]
	-8,45	0,00000000	AT4G28040	ref|Arabidopsis thaliana nodulin MtN21 /EamA-like transporter family protein (UMAMIT33), mRNA [NM_118943]
	-11,55	0,00000000	AT2G41380	ref|Arabidopsis thaliana S-adenosyl-L-methionine-dependent methyltransferases superfamily protein mRNA [NM_129701]
	-305,4	0,00000000	AT4G35770	ref|Arabidopsis thaliana Rhodanese/Cell cycle control phosphatase superfamily protein (SEN1), mRNA [NM_001085028]
Transport				
	9,69	0,00000000	AT1G61800	ref|Arabidopsis thaliana glucose-6-phosphate/phosphate translocator 2 (GPT2), mRNA [NM_001334001]
	7,03	0,00000000	AT1G15520	ref|Arabidopsis thaliana pleiotropic drug resistance 12 (ABCG40), mRNA [NM_001332173]
	4,26	0,00000000	AT2G46430	ref|Arabidopsis thaliana cyclic nucleotide gated channel 3 (CNGC3), mRNA [NM_130207]
	3,85	0,00000000	AT5G13740	ref|Arabidopsis thaliana zinc induced facilitator 1 (ZIF1), mRNA [NM_121377]
	3,77	0,00000000	AT1G79400	ref|Arabidopsis thaliana cation/H+ exchanger 2 (CHX2), mRNA [NM_106588]
	3,43	0.00000001	AT2G46440	ref|Arabidopsis thaliana cyclic nucleotide-gated channels (CNGC11), mRNA [NM_001337191]
	3,15	0,00000000	AT5G26220	ref|Arabidopsis thaliana ChaC-like family protein mRNA [NM_001343968]
	-3,29	0,00000000	AT2G48020	ref|Arabidopsis thaliana Major facilitator superfamily protein mRNA [NM_180152]
	-3,32	0,00000000	AT1G77210	ref|Arabidopsis thaliana sugar transporter 14 (STP14), mRNA [NM_106370]
	-3,64	0,00000000	AT2G36950	ref|Arabidopsis thaliana Heavy metal transport/detoxification superfamily protein mRNA [NM_129251]
	-3,9	0,00000000	AT2G40420	ref|Arabidopsis thaliana Transmembrane amino acid transporter family protein mRNA [NM_129602]
	-4,12	0,00000000	AT5G17860	ref|Arabidopsis thaliana calcium exchanger 7 (CAX7), mRNA [NM_121792]
	-4,19	0,00000000	AT2G17500	ref|Arabidopsis thaliana Auxin efflux carrier family protein mRNA [NM_179633]
	-4,61	0,00000000	AT5G26200	ref|Arabidopsis thaliana Mitochondrial substrate carrier family protein mRNA [NM_122521]
	-4,67	0,00000000	AT5G47560	ref|Arabidopsis thaliana tonoplast dicarboxylate transporter (TDT), mRNA [NM_124129]
	-5,48	0,00000000	AT2G47000	ref|Arabidopsis thaliana ATP binding cassette subfamily B4 (ABCB4), mRNA [NM_001337238]
	-8,88	0,00000000	AT2G23150	ref|Arabidopsis thaliana natural resistance-associated macrophage protein 3 (NRAMP3), mRNA [NM_127879]
	-12,28	0,00000000	AT1G66760	ref|Arabidopsis thaliana MATE efflux family protein mRNA [NM_179523]
	-14,78	0,00000000	AT1G11260	ref|Arabidopsis thaliana sugar transporter 1 (STP1), mRNA [NM_100998]
Not assigned				
	35,34	0,00000000	AT2G14560	ref|Arabidopsis thaliana LURP-one-like protein (DUF567) (LURP1), mRNA [NM_127019]
	19,34	0,00000000	AT3G22235	ref|Arabidopsis thaliana cysteine-rich TM module stress tolerance protein mRNA [NM_180292]
	18,89	0,00000000	AT3G22240	ref|Arabidopsis thaliana cysteine-rich/transmembrane domain PCC1-like protein mRNA [NM_113122]
	17,05	0,00000000	AT2G14247	ref|Arabidopsis thaliana Expressed protein mRNA [NM_201723]
	15,78	0,00000000	AT3G44860	ref|Arabidopsis thaliana farnesoic acid carboxyl-O-methyltransferase (FAMT), mRNA [NM_114355]
	14,81	0,00000000	AT1G47400	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_103634]
	13,64	0,00000000	AT1G47395	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_179449]
	10,49	0,00000000	AT4G01080	ref|Arabidopsis thaliana TRICHOME BIREFRINGENCE-LIKE 26 (TBL26), mRNA [NM_116338]
	10,48	0,00000000	AT1G80130	ref|Arabidopsis thaliana Tetratricopeptide repeat (TPR)-like superfamily protein mRNA [NM_106662]
	10,38	0,00000000	AT2G25510	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_001202672]
	8,9	0.00000001	AT2G30766	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_001336300]
	8,88	0,00000000	AT1G14880	ref|Arabidopsis thaliana PLANT CADMIUM RESISTANCE 1 (PCR1), mRNA [NM_101357]
	7,77	0,00000000	AT3G23120	ref|Arabidopsis thaliana receptor like protein 38 (RLP38), mRNA [NM_113213]
	7,72	0,00000000	AT2G27402	ref|Arabidopsis thaliana plastid transcriptionally active protein mRNA [NM_001336115]
	7,26	0,00000000	AT2G26400	ref|Arabidopsis thaliana acireductone dioxygenase 3 (ARD3), mRNA [NM_001336065]
	7,03	0,00000000	AT1G19960	ref|Arabidopsis thaliana transcription factor mRNA [NM_101851]
	6,84	0,00000000	AT1G76960	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_106347]
	5,88	0,00000000	AT1G12030	ref|Arabidopsis thaliana phosphoenolpyruvate carboxylase, putative (DUF506) mRNA [NM_101075]
	5,8	0,00000000	AT5G19240	ref|Arabidopsis thaliana Glycoprotein membrane precursor GPI-anchored mRNA [NM_121929]
	5,61	0,00000000	AT5G24660	ref|Arabidopsis thaliana response to low sulfur 2 (LSU2), mRNA [NM_122375]
	5,36	0,00000000	AT1G21525	gb|Arabidopsis thaliana clone 31878 mRNA, complete sequence [AY087114]
	5,02	0,00000000	AT5G08760	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_001085080]
	4,65	0,00000000	AT1G67360	ref|Arabidopsis thaliana Rubber elongation factor protein (REF) mRNA [NM_105404]
	4,56	0,00000000	AT4G02850	ref|Arabidopsis thaliana phenazine biosynthesis PhzC/PhzF family protein mRNA [NM_116519]
	4,28	0,00000000	AT5G05250	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_120607]
	4,22	0,00000000	AT3G49580	ref|Arabidopsis thaliana response to low sulfur 1 (LSU1), mRNA [NM_001203113]
	4,1	0,00000000	AT1G68600	ref|Arabidopsis thaliana aluminum activated malate transporter family protein mRNA [NM_105532]
	4,06	0,00000000	AT4G26950	ref|Arabidopsis thaliana senescence regulator (Protein of unknown function, DUF584) mRNA [NM_118829]
	4,02	0,00000000	AT5G52760	ref|Arabidopsis thaliana Copper transport protein family mRNA [NM_001345008]
	3,97	0,00000000	AT1G65486	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_001124079]
	3,94	0.00000001	AT5G20190	ref|Arabidopsis thaliana Tetratricopeptide repeat (TPR)-like superfamily protein mRNA [NM_122026]
	3,94	0,00000000	AT5G44820	ref|Arabidopsis thaliana Nucleotide-diphospho-sugar transferase family protein mRNA [NM_123850]
	3,83	0,00000000	AT1G64980	ref|Arabidopsis thaliana Nucleotide-diphospho-sugar transferases superfamily protein (CDI), mRNA [NM_001334184]
	3,83	0,00000000	AT1G74440	ref|Arabidopsis thaliana ER membrane protein, putative (DUF962) mRNA [NM_106104]
	3,8	0,00000000	AT2G40435	ref|Arabidopsis thaliana transcription factor SCREAM-like protein mRNA [NM_001336840]
	3,77	0,00000000	AT3G52630	ref|Arabidopsis thaliana Nucleic acid-binding, OB-fold-like protein mRNA [NM_115123]
	3,77	0,00000000	AT3G54750	ref|Arabidopsis thaliana downstream neighbor of Son mRNA [NM_115332]
	3,75	0.00000097	AT5G42530	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_123618]
	3,72	0,00000000	AT1G56060	ref|Arabidopsis thaliana cysteine-rich/transmembrane domain protein B mRNA [NM_104484]
	3,7	0,00000000	AT3G49570	ref|Arabidopsis thaliana response to low sulfur 3 (LSU3), mRNA [NM_114817]
	3,69	0,00000000	AT4G26960	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_118830]
	3,67	0,00000000	AT5G54970	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_124879]
	3,61	0,00000000	AT1G13470	ref|Arabidopsis thaliana hypothetical protein (DUF1262) mRNA [NM_101217]

3,57	0.00000001	AT3G26960	ref|Arabidopsis thaliana Pollen Ole e 1 allergen and extensin family protein mRNA [NM_113610]
3,56	0,00000000	AT3G61920	ref|Arabidopsis thaliana UvrABC system protein C mRNA [NM_116057]
3,55	0.00000002	AT2G45760	ref|Arabidopsis thaliana BON association protein 2 (BAP2), mRNA [NM_130139]
3,46	0,00000000	AT3G46880	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_114555]
3,39	0,00000000	AT2G35860	ref|Arabidopsis thaliana FASCICLIN-like arabinogalactan protein 16 precursor (FLA16), mRNA [NM_179922]
3,31	0.00000001	AT5G44568	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_001085241]
3,29	0,00000000	AT1G03820	ref|Arabidopsis thaliana E6-like protein mRNA [NM_100261]
3,21	0.00000001	AT3G60440	ref|Arabidopsis thaliana Phosphoglycerate mutase family protein mRNA [NM_001340043]
3,21	0,00000000	AT5G26690	ref|Arabidopsis thaliana Heavy metal transport/detoxification superfamily protein mRNA [NM_180545]
3,18	0,00000000	AT3G15357	ref|Arabidopsis thaliana phosphopantothenoylcysteine decarboxylase subunit mRNA [NM_112403]
3,18	0.00000001	AT3G44450	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_114313]
3,13	0,00000000	AT5G22460	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_122151]
3,09	0,00000000	AT5G64550	ref|Arabidopsis thaliana loricrin-like protein mRNA [NM_125851]
3,05	0,00000000	AT5G25250	ref|Arabidopsis thaliana SPFH/Band 7/PHB domain-containing membrane-associated protein family (FLOT1), mRNA [NM_122434]
-3,01	0,00000000	AT1G21680	ref|Arabidopsis thaliana DPP6 N-terminal domain-like protein mRNA [NM_102017]
-3,01	0.00000001	AT5G45310	ref|Arabidopsis thaliana coiled-coil protein mRNA [NM_123899]
-3,03	0,00000000	AT1G12250	ref|Arabidopsis thaliana Pentapeptide repeat-containing protein mRNA [NM_001084054]
-3,03	0,00000000	AT1G23040	ref|Arabidopsis thaliana hydroxyproline-rich glycoprotein family protein mRNA [NM_001332581]
-3,03	0,00000000	AT2G46220	ref|Arabidopsis thaliana DUF2358 family protein (DUF2358) mRNA [NM_130184]
-3,04	0,00000000	AT2G25780	ref|Arabidopsis thaliana hypothetical protein (DUF1677) mRNA [NM_128138]
-3,04	0,00000000	AT3G13062	ref|Arabidopsis thaliana Polyketide cyclase/dehydrase and lipid transport superfamily protein mRNA [NM_180243]
-3,06	0,00000000	AT1G04280	ref|Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA [NM_001331471]
-3,08	0,00000000	AT1G18270	ref|Arabidopsis thaliana ketose-bisphosphate aldolase class-II family protein mRNA [NM_001198099]
-3,1	0,00000000	AT4G32480	ref|Arabidopsis thaliana sugar phosphate exchanger, putative (DUF506) mRNA [NM_119400]
-3,12	0,00000000	AT5G06980	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_001203316]
-3,14	0,00000000	AT2G38820	ref|Arabidopsis thaliana DNA-directed RNA polymerase subunit beta-beta protein, putative (DUF506) mRNA [NM_001336739]
-3,14	0,00000000	AT4G25690	ref|Arabidopsis thaliana stress response NST1-like protein mRNA [NM_118701]
-3,2	0,00000000	AT3G07350	ref|Arabidopsis thaliana sulfate/thiosulfate import ATP-binding protein, putative (DUF506) mRNA [NM_111614]
-3,27	0,00000000	AT5G40690	ref|Arabidopsis thaliana histone-lysine N-methyltransferase trithorax-like protein mRNA [NM_123434]
-3,3	0,00000000	AT3G02140	ref|Arabidopsis thaliana AFP2 (ABI five-binding protein 2) family protein (TMAC2), mRNA [NM_111081]
-3,31	0,00000000	AT2G04795	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_126510]
-3,32	0,00000000	AT1G03580	gb|Arabidopsis thaliana unknown protein (At1g03580) mRNA, partial cds [AY091013]
-3,33	0,00000000	AT1G61740	ref|Arabidopsis thaliana Sulfite exporter TauE/SafE family protein mRNA [NM_104856]
-3,35	0,00000000	AT3G10320	ref|Arabidopsis thaliana Glycosyltransferase family 61 protein mRNA [NM_111867]
-3,39	0,00000000	AT3G29240	ref|Arabidopsis thaliana PPR containing protein (DUF179) mRNA [NM_113848]
-3,41	0,00000000	AT5G66480	ref|Arabidopsis thaliana bacteriophage N4 adsorption B protein mRNA [NM_126046]
-3,43	0,00000000	AT2G37750	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_129331]
-3,45	0,00000000	AT1G16720	ref|Arabidopsis thaliana high chlorophyll fluorescence phenotype 173 (HCF173), mRNA [NM_001332253]
-3,46	0,00000000	AT2G42870	ref|Arabidopsis thaliana phy rapidly regulated 1 (PAR1), mRNA [NM_129848]
-3,47	0,00000000	AT1G53280	ref|Arabidopsis thaliana Class I glutamine amidotransferase-like superfamily protein (DJ1B), mRNA [NM_104206]
-3,49	0,00000000	AT4G22920	ref|Arabidopsis thaliana non-yellowing 1 (NYE1), mRNA [NM_001341565]
-3,6	0,00000000	AT5G64230	ref|Arabidopsis thaliana 1,8-cineole synthase mRNA [NM_125819]
-3,61	0.00000001	AT1G10140	ref|Arabidopsis thaliana Uncharacterized conserved protein UCP031279 mRNA [NM_100888]
-3,66	0,00000000	AT2G15890	ref|Arabidopsis thaliana maternal effect embryo arrest 14 (MEE14), mRNA [NM_001084426]
-3,72	0,00000000	AT5G18130	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_203067]
-3,74	0,00000000	AT1G01240	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_001331263]
-3,77	0,00000000	AT4G33660	ref|Arabidopsis thaliana cysteine-rich TM module stress tolerance protein mRNA [NM_119522]
-3,84	0,00000000	AT5G66052	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_148167]
-3,96	0,00000000	AT5G02160	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_120294]
-4,03	0,00000000	AT5G65207	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_148161]
-4,06	0,00000000	AT4G24160	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_202876]
-4,11	0,00000000	AT1G05340	ref|Arabidopsis thaliana cysteine-rich TM module stress tolerance protein mRNA [NM_100413]
-4,19	0,00000000	AT2G27385	ref|Arabidopsis thaliana Pollen Ole e 1 allergen and extensin family protein mRNA [NM_179769]
-4,28	0,00000000	AT3G15770	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_112447]
-4,31	0,00000000	AT3G10020	ref|Arabidopsis thaliana plant/protein mRNA [NM_111837]
-4,36	0,00000000	AT1G76600	ref|Arabidopsis thaliana poly polymerase mRNA [NM_106310]
-4,52	0,00000000	AT1G07040	ref|Arabidopsis thaliana plant/protein mRNA [NM_100578]
-4,57	0,00000000	AT1G14870	ref|Arabidopsis thaliana PLANT CADMIUM RESISTANCE 2 (PCR2), mRNA [NM_101356]
-4,65	0,00000000	AT2G30600	ref|Arabidopsis thaliana BTB/POZ domain-containing protein mRNA [NM_001202713]
-4,66	0,00000000	AT1G79270	ref|Arabidopsis thaliana evolutionarily conserved C-terminal region 8 (ECT8), mRNA [NM_001334878]
-4,84	0,00000000	AT2G39570	ref|Arabidopsis thaliana ACT domain-containing protein (ACR9), mRNA [NM_129515]
-4,96	0,00000000	AT1G72060	ref|Arabidopsis thaliana serine-type endopeptidase inhibitor mRNA [NM_105864]
-5,09	0,00000000	AT4G24972	ref|Arabidopsis thaliana tapetum determinant 1 (TPD1), mRNA [NM_202883]
-5,15	0,00000000	AT3G15630	ref|Arabidopsis thaliana plant/protein mRNA [NM_112433]
-5,37	0,00000000	AT5G61820	ref|Arabidopsis thaliana stress up-regulated Nod 19 protein mRNA [NM_001345498]
-5,4	0,00000000	AT4G12735	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_202810]
-5,6	0,00000000	AT5G14730	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_121477]
-5,64	0,00000000	AT3G10120	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_111847]
-5,69	0,00000000	AT1G13990	ref|Arabidopsis thaliana plant/protein mRNA [NM_001160863]
-5,69	0,00000000	AT5G51720	ref|Arabidopsis thaliana 2 iron, 2 sulfur cluster binding protein (NEET), mRNA [NM_124551]
-5,72	0,00000000	AT5G59400	ref|Arabidopsis thaliana PGR5-like A protein mRNA [NM_180889]
-5,75	0,00000000	AT4G39675	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_120128]

	-5,78	0,00000000	AT4G33666	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_119524]
	-5,84	0,00000000	AT2G20670	ref|Arabidopsis thaliana sugar phosphate exchanger, putative (DUF506) mRNA [NM_127631]
	-5,92	0,00000000	AT2G05380	ref|Arabidopsis thaliana glycine-rich protein 3 short isoform (GRP3S), mRNA [NM_001124801]
	-5,98	0,00000000	AT5G64190	ref|Arabidopsis thaliana neuronal PAS domain protein mRNA [NM_001345621]
	-6,13	0,00000000	AT1G15040	ref|Arabidopsis thaliana Class I glutamine amidotransferase-like superfamily protein (GAT1_2.1), mRNA [NM_101374]
	-6,14	0,00000000	AT2G31945	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_128753]
	-6,18	0,00000000	AT2G15960	ref|Arabidopsis thaliana stress-induced protein mRNA [NM_127155]
	-6,48	0,00000000	AT2G40000	ref|Arabidopsis thaliana ortholog of sugar beet HS1 PRO-1 2 (HSPRO2), mRNA [NM_129558]
	-6,53	0,00000000	AT3G49790	ref|Arabidopsis thaliana Carbohydrate-binding protein mRNA [NM_114839]
	-6,65	0,00000000	AT4G30670	ref|Arabidopsis thaliana Putative membrane lipoprotein mRNA [NM_119213]
	-7,45	0,00000000	AT5G66650	ref|Arabidopsis thaliana calcium uniporter (DUF607) mRNA [NM_126063]
	-8,18	0,00000000	AT1G19530	ref|Arabidopsis thaliana DNA polymerase epsilon catalytic subunit A mRNA [NM_001332396]
	-8,27	0,00000000	AT2G32150	ref|Arabidopsis thaliana Haloacid dehalogenase-like hydrolase (HAD) superfamily protein mRNA [NM_001336371]
	-8,81	0,00000000	AT3G24420	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_113349]
	-9,15	0,00000000	AT5G54585	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_148130]
	-9,26	0,00000000	AT4G36850	ref|Arabidopsis thaliana PQ-loop repeat family protein / transmembrane family protein mRNA [NM_001342421]
	-12,52	0,00000000	AT4G25580	ref|Arabidopsis thaliana CAP160 protein mRNA [NM_001341752]
	-14,84	0,00000000	AT5G02020	ref|Arabidopsis thaliana E3 ubiquitin-protein ligase RLIM-like protein (SIS), mRNA [NM_180421]
	-15,73	0,00000000	AT4G15610	ref|Arabidopsis thaliana Uncharacterized protein family (UPF0497) mRNA [NM_001341066]
	-18,87	0,00000000	AT3G45730	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_114442]
	-20,75	0,00000000	AT5G39520	ref|Arabidopsis thaliana hypothetical protein (DUF1997) mRNA [NM_123314]
	-24,27	0,00000000	AT4G08555	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_179014]
	-30,14	0,00000000	AT4G01870	ref|Arabidopsis thaliana tolB protein-like protein mRNA [NM_001340340]
	-75,94	0,00000000	AT1G73120	ref|Arabidopsis thaliana F-box/RNI superfamily protein mRNA [NM_105970]
	-81,95	0,00000000	AT3G20340	ref|Arabidopsis thaliana protein expression protein mRNA [NM_112925]
Uncategorized				
	10,02	0,00000000	R65132	tc|AAD15384.1 - Arabidopsis thaliana (Mouse-ear cress), partial (68%) [TC400604]
	8,69	0,00000000	TA28146_3702	tc|Rep: ER lumen protein retaining receptor - Vitis vinifera (Grape), partial (5%) [TC395123]
	8,21	0,00000000	EG497537	Unknown
	7,32	0,00000000	CB185526	Unknown
	7,11	0,00000000	CD533642	gb|32O9 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA 3', mRNA sequence [CD533642]
	3,76	0,00000000	NP454661	ref|Arabidopsis thaliana alpha carbonic anhydrase 2 (ACA2), mRNA [NM_001336149]
	3,72	0,00000000	BP783345	Unknown
	3,62	0,00000000	TA29588_3702	tc|Rep: At2g25510/F13B15.17 - Arabidopsis thaliana (Mouse-ear cress), partial (41%) [TC388653]
	3,57	0,00000000	TC300093	Unknown
	3,53	0.00000001	T42092	Unknown
	3,5	0,00000000	BU917432	ref|Arabidopsis thaliana other RNA snoRNA [NR_139469]
	3,22	0,00000000	TA28264_3702	Unknown
	3,21	0,00000000	TA50968_3702	tc|Rep: Eukaryotic translation initiation factor 4E - Cucumis melo (Muskmelon), partial (11%) [TC394106]
	3,12	0.00000869	BP586302	gb|BP586302 RAFL15 Arabidopsis thaliana cDNA clone RAFL15-05-M21 3', mRNA sequence [BP586302]
	3,08	0,00000000	NP335312	tc|GB|AL590346.1|CAC35882.1 putative protein [Arabidopsis thaliana] [NP335312]
	3,03	0,00000000	TA36353_3702	tc|Rep: At5g42860 - Arabidopsis thaliana (Mouse-ear cress), partial (39%) [TC388419]
	-3,02	0,00000000	AK230465	gb|Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL26-03-H08 [AK230465]
	-3,04	0.00000003	TC297782	ref|Arabidopsis thaliana other RNA lncRNA [NR_139108]
	-3,09	0.00000001	CB259684	gb|31-E9537-013-002-M08-T7R MPIZ-ADIS-013 Arabidopsis thaliana cDNA clone MPIZp770M082Q 5-PRIME, mRNA sequence [CB259684]
	-3,09	0,00000000	TA29086_3702	Unknown
	-3,14	0,00000000	BT025685	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_001334179]
	-3,27	0,00000000	TC312617	tc|Rep: Vacuolar-processing enzyme gamma-isozyme precursor - Arabidopsis thaliana (Mouse-ear cress), partial (23%) [TC400087]
	-3,41	0,00000000	BX822927	gb|Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB73ZE03 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress) [BX822927]
	-3,51	0.00000001	AK230421	gb|Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL25-33-B21 [AK230421]
	-3,53	0,00000000	BU917423	ref|Arabidopsis thaliana RING/U-box protein mRNA [NM_112412]
	-3,59	0,00000000	N38085	tc|Rep: Cysteine proteinase - Populus tomentosa (Chinese white poplar), partial (36%) [TC397589]
	-3,61	0.00000001	AV566399	gb|AV566399 Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana cDNA clone SQ242f10F 3', mRNA sequence [AV566399]
	-3,71	0,00000000	TC309871	tc|Rep: Conglutin gamma-like protein - Arabidopsis thaliana (Mouse-ear cress), partial (35%) [TC396686]
	-3,81	0,00000000	TA35940_3702	tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vinifera (Grape), partial (42%) [TC384450]
	-3,84	0.00000001	TA29208_3702	Unknown
	-4,04	0,00000000	TA29997_3702	Unknown
	-4,28	0,00000000	TA26159_3702	Unknown
	-4,33	0,00000000	TA28495_3702	Unknown
	-4,43	0,00000000	TC313866	tc|Rep: Chaperone protein dnaJ 8, chloroplast precursor - Arabidopsis thaliana (Mouse-ear cress), partial (50%) [TC404503]
	-4,66	0,00000000	NP229859	tc|GB|AL391141.1|CAC01711.1 quinone oxidoreductase-like protein [NP229859]
	-4,71	0.00000005	EG427617	gb|AYALO23TFB pooled cDNA populations Arabidopsis thaliana cDNA, mRNA sequence [EG427617]
	-4,72	0,00000000	TC295612	ref|Arabidopsis thaliana other RNA ncRNA [NR_143567]
	-4,73	0,00000000	AV805941	gb|AV805941 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-44-M15 3', mRNA sequence [AV805941]
	-4,79	0,00000000	DR368472	gb|12826078 CERES-AN65 Arabidopsis thaliana cDNA clone 1361839 5', mRNA sequence [DR368472]
	-4,82	0,00000000	DR368506	gb|12842501 CERES-AN65 Arabidopsis thaliana cDNA clone 1366811 5', mRNA sequence [DR368506]
	-4,89	0,00000000	TA30818_3702	Unknown
	-5,01	0,00000000	TA28705_3702	Unknown
	-5,86	0,00000000	TA26531_3702	Unknown
	-7,23	0,00000000	TA27461_3702	Unknown

-9,32	0,00000000	TA30874_3702	Unknown
-10,84	0,00000000	TC309308	tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vinifera (Grape), partial (29%) [TC396119]
-13,62	0,00000000	TA29020_3702	Unknown
-20,29	0,00000000	TC304561	tc|Rep: Xylosidase - Arabidopsis thaliana (Mouse-ear cress), complete [TC384346]
-25,61	0,00000000	BP667596	tc|Rep: Uncharacterized protein At4g35770.3 - Arabidopsis thaliana (Mouse-ear cress), partial (53%) [TC406344]
-27,03	0,00000000	BP660593	Unknown
-28,03	0,00000000	TA25819_3702	Unknown
-30,24	0,00000000	TA29937_3702	Unknown
-30,35	0,00000000	BE039144	tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vinifera (Grape), partial (59%) [TC393828]
-41,86	0,00000000	TA29646_3702	gb|Arabidopsis thaliana AT4G35770 mRNA, complete cds, clone: RAFL24-21-O03 [AK319042]
-336,01	0,00000000	TA29648_3702	Unknown

Table S2: List of genes whose expression in leaves is altered by charcoal-filtered VCs emitted by A. alternata. Genes that are differentially regulated by total A. alternata VCs (cf. Supplemental Table 3 in Sánchez-López, Baslam, et al., 2016) are highlighted in yelow color. (BY FOLD-CHANGE)

Fold Change	pval (LiMMA)	ID	Description
59,14	0,00000000	AT2G24850	ref|Arabidopsis thaliana tyrosine aminotransferase 3 (TAT3), mRNA [NM_128044]
42,09	0,00000000	AT2G41240	ref|Arabidopsis thaliana basic helix-loop-helix protein 100 (BHLH100), mRNA [NM_180018]
35,34	0,00000000	AT2G14560	ref|Arabidopsis thaliana LURP-one-like protein (DUF567) (LURP1), mRNA [NM_127019]
27,3	0,00000000	AT2G39030	ref|Arabidopsis thaliana Acyl-CoA N-acyltransferases (NAT) superfamily protein (NATA1), mRNA [NM_129460]
20,71	0,00000000	AT3G56970	ref|Arabidopsis thaliana basic helix-loop-helix (bHLH) DNA-binding superfamily protein (bHLH38), mRNA [NM_115556]
19,34	0,00000000	AT3G22235	ref|Arabidopsis thaliana cysteine-rich TM module stress tolerance protein mRNA [NM_180292]
18,89	0,00000000	AT3G22240	ref|Arabidopsis thaliana cysteine-rich/transmembrane domain PCC1-like protein mRNA [NM_113122]
18,82	0,00000000	AT3G45140	ref|Arabidopsis thaliana lipoxygenase 2 (LOX2), mRNA [NM_001339198]
17,05	0,00000000	AT2G14247	ref|Arabidopsis thaliana Expressed protein mRNA [NM_201723]
16,45	0,00000000	AT3G56980	ref|Arabidopsis thaliana basic helix-loop-helix (bHLH) DNA-binding superfamily protein (bHLH39), mRNA [NM_115557]
15,78	0,00000000	AT3G44860	ref|Arabidopsis thaliana farnesoic acid carboxyl-O-methyltransferase (FAMT), mRNA [NM_114355]
14,81	0,00000000	AT1G47400	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_103634]
13,64	0,00000000	AT1G47395	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_179449]
13,38	0,00000000	AT1G61120	ref|Arabidopsis thaliana terpene synthase 04 (TPS04), mRNA [NM_104793]
13,06	0,00000000	AT5G44420	ref|Arabidopsis thaliana plant defensin 1.2 (PDF1.2), mRNA [NM_123809]
12,37	0,00000000	AT1G73600	ref|Arabidopsis thaliana S-adenosyl-L-methionine-dependent methyltransferases superfamily protein mRNA [NM_106018]
11,96	0,00000000	AT3G57260	ref|Arabidopsis thaliana beta-1,3-glucanase 2 (BGL2), mRNA [NM_115586]
11,48	0,00000000	AT3G57240	ref|Arabidopsis thaliana beta-1,3-glucanase 3 (BG3), mRNA [NM_115584]
11,27	0,00000000	AT3G22231	ref|Arabidopsis thaliana pathogen and circadian controlled 1 (PCC1), mRNA [NM_113121]
10,64	0,00000000	AT3G26830	ref|Arabidopsis thaliana Cytochrome P450 superfamily protein (PAD3), mRNA [NM_113595]
10,49	0,00000000	AT4G01080	ref|Arabidopsis thaliana TRICHOME BIREFRINGENCE-LIKE 26 (TBL26), mRNA [NM_116338]
10,48	0,00000000	AT1G80130	ref|Arabidopsis thaliana Tetratricopeptide repeat (TPR)-like superfamily protein mRNA [NM_106662]
10,38	0,00000000	AT2G25510	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_001202672]
10,29	0,00000000	AT5G54610	ref|Arabidopsis thaliana ankyrin (ANK), mRNA [NM_124842]
10,02	0,00000000	R65132	tc|AAD15384.1 - Arabidopsis thaliana (Mouse-ear cress), partial (68%) [TC400604]
9,69	0,00000000	AT1G61800	ref|Arabidopsis thaliana glucose-6-phosphate/phosphate translocator 2 (GPT2), mRNA [NM_001334001]
9,18	0,00000000	AT2G43620	ref|Arabidopsis thaliana Chitinase family protein mRNA [NM_129924]
9,13	0,00000000	AT4G23600	ref|Arabidopsis thaliana Tyrosine transaminase family protein (CORI3), mRNA [NM_179099]
8,9	0.00000001	AT2G30766	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_001336300]
8,88	0,00000000	AT1G14880	ref|Arabidopsis thaliana PLANT CADMIUM RESISTANCE 1 (PCR1), mRNA [NM_101357]
8,87	0,00000000	AT4G21840	ref|Arabidopsis thaliana methionine sulfoxide reductase B8 (MSRB8), mRNA [NM_118304]
8,74	0,00000000	AT5G42800	ref|Arabidopsis thaliana dihydroflavonol 4-reductase (DFR), mRNA [NM_123645]
8,69	0,00000000	TA28146_3702	tc|Rep: ER lumen protein retaining receptor - Vitis vinifera (Grape), partial (5%) [TC395123]
8,3	0,00000000	AT4G39950	ref|Arabidopsis thaliana cytochrome P450, family 79, subfamily B, polypeptide 2 (CYP79B2), mRNA [NM_120158]
8,21	0,00000000	EG497537	Unknown
7,94	0,00000000	AT5G44430	ref|Arabidopsis thaliana plant defensin 1.2C (PDF1.2c), mRNA [NM_123810]
7,77	0,00000000	AT3G23120	ref|Arabidopsis thaliana receptor like protein 38 (RLP38), mRNA [NM_113213]
7,72	0,00000000	AT2G27402	ref|Arabidopsis thaliana plastid transcriptionally active protein mRNA [NM_001336115]
7,62	0,00000000	AT4G22870	ref|Arabidopsis thaliana 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein mRNA [NM_001160794]
7,58	0,00000000	AT2G41090	ref|Arabidopsis thaliana Calcium-binding EF-hand family protein mRNA [NM_129674]
7,32	0,00000000	CB185526	Unknown
7,28	0,00000000	AT1G73010	ref|Arabidopsis thaliana inorganic pyrophosphatase 1 (PS2), mRNA [NM_105959]
7,26	0,00000000	AT2G26400	ref|Arabidopsis thaliana acireductone dioxygenase 3 (ARD3), mRNA [NM_001336065]
7,2	0,00000000	AT3G25180	ref|Arabidopsis thaliana cytochrome P450, family 82, subfamily G, polypeptide 1 (CYP82G1), mRNA [NM_202630]
7,18	0,00000000	AT1G56650	ref|Arabidopsis thaliana production of anthocyanin pigment 1 (PAP1), mRNA [NM_104541]
7,11	0,00000000	CD533642	gb|32O9 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA 3', mRNA sequence [CD533642]
7,07	0.00000001	AT2G30770	ref|Arabidopsis thaliana cytochrome P450 family 71 polypeptide (CYP71A13), mRNA [NM_128630]
7,03	0,00000000	AT1G15520	ref|Arabidopsis thaliana pleiotropic drug resistance 12 (ABCG40), mRNA [NM_001332173]
7,03	0,00000000	AT1G19960	ref|Arabidopsis thaliana transcription factor mRNA [NM_101851]
6,95	0,00000000	AT4G14400	ref|Arabidopsis thaliana ankyrin repeat family protein (ACD6), mRNA [NM_179051]
6,87	0,00000000	AT2G26010	ref|Arabidopsis thaliana plant defensin 1.3 (PDF1.3), mRNA [NM_128160]
6,84	0,00000000	AT1G76960	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_106347]
6,79	0,00000000	AT2G43570	ref|Arabidopsis thaliana chitinase (CHI), mRNA [NM_129919]
6,74	0,00000000	AT5G17220	ref|Arabidopsis thaliana glutathione S-transferase phi 12 (GSTF12), mRNA [NM_121728]
6,66	0,00000000	AT3G24982	ref|Arabidopsis thaliana receptor like protein 40 (RLP40), mRNA [NM_113404]
6,62	0,00000000	AT3G44990	ref|Arabidopsis thaliana xyloglucan endo-transglycosylase-related 8 (XTH31), mRNA [NM_114368]
6,47	0,00000000	AT5G59670	ref|Arabidopsis thaliana Leucine-rich repeat protein kinase family protein mRNA [NM_001345366]

6,46	0,00000000	AT4G21760	ref|Arabidopsis thaliana beta-glucosidase 47 (BGLU47), mRNA [NM_001341512]
6,38	0,00000000	AT2G29350	ref|Arabidopsis thaliana senescence-associated gene 13 (SAG13), mRNA [NM_201829]
6,08	0,00000000	AT4G21830	ref|Arabidopsis thaliana methionine sulfoxide reductase B7 (MSRB7), mRNA [NM_118303]
5,88	0,00000000	AT1G12030	ref|Arabidopsis thaliana phosphoenolpyruvate carboxylase, putative (DUF506) mRNA [NM_101075]
5,86	0,00000000	AT5G03350	ref|Arabidopsis thaliana Legume lectin family protein mRNA [NM_120414]
5,85	0,00000000	AT5G60900	ref|Arabidopsis thaliana receptor-like protein kinase 1 (RLK1), mRNA [NM_001345434]
5,8	0,00000000	AT1G35710	ref|Arabidopsis thaliana kinase family with leucine-rich repeat domain-containing protein mRNA [NM_103273]
5,8	0,00000000	AT5G19240	ref|Arabidopsis thaliana Glycoprotein membrane precursor GPI-anchored mRNA [NM_121929]
5,69	0,00000000	AT1G56430	ref|Arabidopsis thaliana nicotianamine synthase 4 (NAS4), mRNA [NM_104521]
5,69	0,00000000	AT5G54060	ref|Arabidopsis thaliana UDP-glucose:flavonoid 3-o-glucosyltransferase (UF3GT), mRNA [NM_124785]
5,66	0,00000000	AT5G53048	ref|Arabidopsis thaliana other RNA lncRNA [NR_143344]
5,61	0,00000000	AT5G24660	ref|Arabidopsis thaliana response to low sulfur 2 (LSU2), mRNA [NM_122375]
5,55	0,00000000	AT3G27060	ref|Arabidopsis thaliana Ferritin/ribonucleotide reductase-like family protein (TSO2), mRNA [NM_113620]
5,5	0,00000000	AT5G53450	ref|Arabidopsis thaliana OBP3-responsive protein 1 (ORG1), mRNA [NM_001345057]
5,48	0,00000000	AT1G23020	ref|Arabidopsis thaliana ferric reduction oxidase 3 (FRO3), mRNA [NM_001198138]
5,47	0,00000000	AT2G16367	Unknown
5,47	0,00000000	AT1G78370	ref|Arabidopsis thaliana glutathione S-transferase TAU 20 (GSTU20), mRNA [NM_106484]
5,44	0,00000000	AT3G03780	ref|Arabidopsis thaliana methionine synthase 2 (MS2), mRNA [NM_111249]
5,39	0,00000000	AT2G35980	ref|Arabidopsis thaliana Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (YLS9), mRNA [NM_129157]
5,36	0,00000000	AT1G21525	gb|Arabidopsis thaliana clone 31878 mRNA, complete sequence [AY087114]
5,35	0,00000000	AT1G19250	ref|Arabidopsis thaliana flavin-dependent monooxygenase 1 (FMO1), mRNA [NM_101783]
5,32	0,00000000	AT2G11810	ref|Arabidopsis thaliana monogalactosyldiacylglycerol synthase type C (MGDC), mRNA [NM_001124829]
5,18	0,00000000	AT1G06830	ref|Arabidopsis thaliana Glutaredoxin family protein mRNA [NM_100560]
5,15	0,00000000	AT5G23020	ref|Arabidopsis thaliana 2-isopropylmalate synthase 2 (IMS2), mRNA [NM_122208]
5,09	0,00000000	AT4G39940	ref|Arabidopsis thaliana APS-kinase 2 (AKN2), mRNA [NM_120157]
5,02	0,00000000	AT5G08760	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_001085080]
4,98	0,00000000	AT4G17470	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_001203824]
4,95	0,00000000	AT4G39210	ref|Arabidopsis thaliana Glucose-1-phosphate adenylyltransferase family protein (APL3), mRNA [NM_001342527]
4,95	0,00000000	AT4G15210	ref|Arabidopsis thaliana beta-amylase 5 (BAM5), mRNA [NM_179058]
4,92	0,00000000	AT5G48850	ref|Arabidopsis thaliana Tetratricopeptide repeat (TPR)-like superfamily protein (ATSDI1), mRNA [NM_124262]
4,82	0,00000000	AT1G16410	ref|Arabidopsis thaliana cytochrome p450 79f1 (CYP79F1), mRNA [NM_101507]
4,73	0,00000000	AT5G14200	ref|Arabidopsis thaliana isopropylmalate dehydrogenase 1 (IMD1), mRNA [NM_001036803]
4,65	0,00000000	AT2G46880	ref|Arabidopsis thaliana purple acid phosphatase 14 (PAP14), mRNA [NM_201975]
4,65	0,00000000	AT1G67360	ref|Arabidopsis thaliana Rubber elongation factor protein (REF) mRNA [NM_105404]
4,64	0,00000000	AT4G04610	ref|Arabidopsis thaliana APS reductase 1 (APR1), mRNA [NM_116699]
4,63	0,00000000	AT4G04830	ref|Arabidopsis thaliana methionine sulfoxide reductase B5 (MSRB5), mRNA [NM_001203745]
4,56	0,00000000	AT4G02850	ref|Arabidopsis thaliana phenazine biosynthesis PhzC/PhzF family protein mRNA [NM_116519]
4,48	0,00000000	AT4G28250	ref|Arabidopsis thaliana expansin B3 (EXPB3), mRNA [NM_001341907]
4,46	0,00000000	AT1G73325	ref|Arabidopsis thaliana Kunitz family trypsin and protease inhibitor protein mRNA [NM_105992]
4,44	0,00000000	AT1G06000	ref|Arabidopsis thaliana UDP-Glycosyltransferase superfamily protein mRNA [NM_100480]
4,44	0,00000000	AT1G28480	ref|Arabidopsis thaliana Thioredoxin superfamily protein (GRX480), mRNA [NM_102616]
4,42	0,00000000	AT5G10760	ref|Arabidopsis thaliana Eukaryotic aspartyl protease family protein mRNA [NM_121114]
4,4	0,00000000	AT1G29660	ref|Arabidopsis thaliana GDSL-like Lipase/Acylhydrolase superfamily protein mRNA [NM_102706]
4,35	0,00000000	AT4G03060	gb|Arabidopsis thaliana Col-0 2-oxoglutarate-dependent dioxygenase (AOP2) pseudogene, mRNA sequence [AF418241]
4,32	0,00000000	AT2G43100	ref|Arabidopsis thaliana isopropylmalate isomerase 2 (IPMI2), mRNA [NM_129871]
4,32	0,00000000	AT4G22880	ref|Arabidopsis thaliana leucoanthocyanidin dioxygenase (LDOX), mRNA [NM_001036623]
4,32	0,00000000	AT1G21250	ref|Arabidopsis thaliana cell wall-associated kinase (WAK1), mRNA [NM_101978]
4,29	0,00000000	AT3G25882	ref|Arabidopsis thaliana NIM1-interacting 2 (NIMIN-2), mRNA [NM_148752]
4,28	0,00000000	AT5G05250	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_120607]
4,27	0,00000000	AT1G62560	ref|Arabidopsis thaliana flavin-monooxygenase glucosinolate S-oxygenase 3 (FMO GS-OX3), mRNA [NM_001334038]
4,27	0,00000000	AT3G11340	ref|Arabidopsis thaliana UDP-Glycosyltransferase superfamily protein (UGT76B1), mRNA [NM_111968]
4,27	0,00000000	AT3G22600	ref|Arabidopsis thaliana Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein mRNA [NM_113159]
4,26	0,00000000	AT2G46430	ref|Arabidopsis thaliana cyclic nucleotide gated channel 3 (CNGC3), mRNA [NM_130207]
4,22	0,00000000	AT3G49580	ref|Arabidopsis thaliana response to low sulfur 1 (LSU1), mRNA [NM_001203113]
4,17	0,00000000	AT2G26020	ref|Arabidopsis thaliana plant defensin 1.2b (PDF1.2b), mRNA [NM_128161]
4,15	0,00000000	AT4G36010	ref|Arabidopsis thaliana Pathogenesis-related thaumatin superfamily protein mRNA [NM_001036715]
4,13	0,00000000	AT2G38240	ref|Arabidopsis thaliana 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein mRNA [NM_129381]
4,11	0,00000000	AT1G02450	ref|Arabidopsis thaliana NIM1-interacting 1 (NIMIN1), mRNA [NM_100126]
4,11	0,00000000	AT5G59870	ref|Arabidopsis thaliana histone H2A 6 (HTA6), mRNA [NM_125380]
4,1	0,00000000	AT3G11010	ref|Arabidopsis thaliana receptor like protein 34 (RLP34), mRNA [NM_111938]

4,1	0,00000000	AT1G09200	ref|Arabidopsis thaliana Histone superfamily protein mRNA [NM_100790]
4,1	0,00000000	AT1G68600	ref|Arabidopsis thaliana aluminum activated malate transporter family protein mRNA [NM_105532]
4,09	0,00000000	AT3G44870	ref|Arabidopsis thaliana S-adenosyl-L-methionine-dependent methyltransferases superfamily protein mRNA [NM_114356]
4,07	0,00000000	AT4G25630	ref|Arabidopsis thaliana fibrillarin 2 (FIB2), mRNA [NM_118695]
4,06	0,00000000	AT4G26950	ref|Arabidopsis thaliana senescence regulator (Protein of unknown function, DUF584) mRNA [NM_118829]
4,03	0,00000000	AT4G23130	ref|Arabidopsis thaliana cysteine-rich RLK (RECEPTOR-like protein kinase) 5 (CRK5), mRNA [NM_001341575]
4,03	0,00000000	AT4G14365	ref|Arabidopsis thaliana hypothetical protein (XBAT34), mRNA [NM_117514]
4,02	0,00000000	AT1G01190	ref|Arabidopsis thaliana cytochrome P450, family 78, subfamily A, polypeptide 8 (CYP78A8), mRNA [NM_100001]
4,02	0,00000000	AT5G52760	ref|Arabidopsis thaliana Copper transport protein family mRNA [NM_001345008]
4,01	0,00000000	AT5G45650	ref|Arabidopsis thaliana subtilase family protein mRNA [NM_001344636]
3,99	0,00000000	AT4G39030	ref|Arabidopsis thaliana MATE efflux family protein (EDS5), mRNA [NM_120063]
3,97	0,00000000	AT1G65486	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_001124079]
3,96	0,00000000	AT3G58990	ref|Arabidopsis thaliana isopropylmalate isomerase 1 (IPMI1), mRNA [NM_115761]
3,95	0,00000000	AT5G61000	ref|Arabidopsis thaliana Replication factor-A protein 1-like protein (RPA70D), mRNA [NM_125493]
3,94	0.00000001	AT5G20190	ref|Arabidopsis thaliana Tetratricopeptide repeat (TPR)-like superfamily protein mRNA [NM_122026]
3,94	0,00000000	AT5G44820	ref|Arabidopsis thaliana Nucleotide-diphospho-sugar transferase family protein mRNA [NM_123850]
3,91	0,00000000	AT5G05270	ref|Arabidopsis thaliana Chalcone-flavanone isomerase family protein (CHIL), mRNA [NM_180439]
3,9	0,00000000	AT3G52370	ref|Arabidopsis thaliana FASCICLIN-like arabinogalactan protein 15 precursor (FLA15), mRNA [NM_115097]
3,85	0,00000000	AT3G48080	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_114677]
3,85	0,00000000	AT3G47480	ref|Arabidopsis thaliana Calcium-binding EF-hand family protein mRNA [NM_114616]
3,85	0,00000000	AT5G13740	ref|Arabidopsis thaliana zinc induced facilitator 1 (ZIF1), mRNA [NM_121377]
3,84	0,00000000	AT3G25795	ref|Arabidopsis thaliana other RNA ncRNA [NR_143943]
3,83	0,00000000	AT4G24570	ref|Arabidopsis thaliana dicarboxylate carrier 2 (DIC2), mRNA [NM_118590]
3,83	0,00000000	AT1G64980	ref|Arabidopsis thaliana Nucleotide-diphospho-sugar transferases superfamily protein (CDI), mRNA [NM_001334184]
3,83	0,00000000	AT1G74440	ref|Arabidopsis thaliana ER membrane protein, putative (DUF962) mRNA [NM_106104]
3,8	0,00000000	AT1G18590	ref|Arabidopsis thaliana sulfotransferase 17 (SOT17), mRNA [NM_101717]
3,8	0,00000000	AT2G40435	ref|Arabidopsis thaliana transcription factor SCREAM-like protein mRNA [NM_001336840]
3,79	0,00000000	AT1G43910	ref|Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA [NM_103518]
3,77	0,00000000	AT1G79400	ref|Arabidopsis thaliana cation/H+ exchanger 2 (CHX2), mRNA [NM_106588]
3,77	0,00000000	AT3G52630	ref|Arabidopsis thaliana Nucleic acid-binding, OB-fold-like protein mRNA [NM_115123]
3,77	0,00000000	AT3G54750	ref|Arabidopsis thaliana downstream neighbor of Son mRNA [NM_115332]
3,76	0,00000000	AT5G13320	ref|Arabidopsis thaliana Auxin-responsive GH3 family protein (PBS3), mRNA [NM_001343268]
3,76	0,00000000	NP454661	ref|Arabidopsis thaliana alpha carbonic anhydrase 2 (ACA2), mRNA [NM_001336149]
3,75	0,00000000	AT5G65360	ref|Arabidopsis thaliana Histone superfamily protein mRNA [NM_125934]
3,75	0.00000097	AT5G42530	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_123618]
3,73	0,00000000	AT5G50950	ref|Arabidopsis thaliana FUMARASE 2 (FUM2), mRNA [NM_001344914]
3,72	0,00000000	AT1G56060	ref|Arabidopsis thaliana cysteine-rich/transmembrane domain protein B mRNA [NM_104484]
3,72	0,00000000	BP783345	Unknown
3,7	0,00000000	AT3G49570	ref|Arabidopsis thaliana response to low sulfur 3 (LSU3), mRNA [NM_114817]
3,69	0,00000000	AT4G26960	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_118830]
3,68	0,00000000	AT1G75780	ref|Arabidopsis thaliana tubulin beta-1 chain (TUB1), mRNA [NM_106228]
3,67	0,00000000	AT1G17710	ref|Arabidopsis thaliana Pyridoxal phosphate phosphatase-related protein (PEPC1), mRNA [NM_001084087]
3,67	0,00000000	AT5G10390	ref|Arabidopsis thaliana Histone superfamily protein mRNA [NM_121077]
3,67	0,00000000	AT5G54970	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_124879]
3,65	0,00000000	AT1G24280	ref|Arabidopsis thaliana glucose-6-phosphate dehydrogenase 3 (G6PD3), mRNA [NM_102274]
3,64	0,00000000	AT5G04150	ref|Arabidopsis thaliana basic helix-loop-helix (bHLH) DNA-binding superfamily protein (BHLH101), mRNA [NM_120497]
3,63	0,00000000	AT1G04770	ref|Arabidopsis thaliana Tetratricopeptide repeat (TPR)-like superfamily protein mRNA [NM_100355]
3,62	0,00000000	TA29588_3702	tc|Rep: At2g25510/F13B15.17 - Arabidopsis thaliana (Mouse-ear cress), partial (41%) [TC388653]
3,61	0,00000000	AT1G13470	ref|Arabidopsis thaliana hypothetical protein (DUF1262) mRNA [NM_101217]
3,6	0,00000000	AT5G54490	ref|Arabidopsis thaliana pinoid-binding protein 1 (PBP1), mRNA [NM_124829]
3,58	0,00000000	AT2G26440	ref|Arabidopsis thaliana Plant invertase/pectin methylesterase inhibitor superfamily mRNA [NM_128201]
3,58	0,00000000	AT4G18440	ref|Arabidopsis thaliana L-Aspartase-like family protein mRNA [NM_117957]
3,57	0.00000001	AT3G26960	ref|Arabidopsis thaliana Pollen Ole e 1 allergen and extensin family protein mRNA [NM_113610]
3,57	0,00000000	TC300093	Unknown
3,56	0,00000000	AT1G78570	ref|Arabidopsis thaliana rhamnose biosynthesis 1 (RHM1), mRNA [NM_106504]
3,56	0,00000000	AT3G61920	ref|Arabidopsis thaliana UvrABC system protein C mRNA [NM_116057]
3,55	0.00000002	AT2G45760	ref|Arabidopsis thaliana BON association protein 2 (BAP2), mRNA [NM_130139]
3,54	0,00000000	AT2G18660	ref|Arabidopsis thaliana plant natriuretic peptide A (PNP-A), mRNA [NM_179648]
3,53	0.00000001	T42092	Unknown
3,51	0,00000000	AT5G42650	ref|Arabidopsis thaliana allene oxide synthase (AOS), mRNA [NM_123629]

3,51	0,00000000	AT4G11190	ref|Arabidopsis thaliana Disease resistance-responsive (dirigent-like protein) family protein mRNA [NM_117190]
3,5	0,00000000	AT5G48880	ref|Arabidopsis thaliana peroxisomal 3-keto-acyl-CoA thiolase 2 (KAT5), mRNA [NM_001344808]
3,5	0,00000000	BU917432	ref|Arabidopsis thaliana other RNA snoRNA [NR_139469]
3,47	0,00000000	AT5G23420	ref|Arabidopsis thaliana high-mobility group box 6 (HMGB6), mRNA [NM_001203442]
3,46	0,00000000	AT1G65860	ref|Arabidopsis thaliana flavin-monooxygenase glucosinolate S-oxygenase 1 (FMO GS-OX1), mRNA [NM_105258]
3,46	0,00000000	AT3G46880	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_114555]
3,44	0,00000000	AT4G12880	ref|Arabidopsis thaliana early nodulin-like protein 19 (ENODL19), mRNA [NM_001203782]
3,43	0,00000000	AT2G40750	ref|Arabidopsis thaliana WRKY DNA-binding protein 54 (WRKY54), mRNA [NM_129637]
3,43	0,00000000	AT2G38860	ref|Arabidopsis thaliana Class I glutamine amidotransferase-like superfamily protein (YLS5), mRNA [NM_129443]
3,43	0.00000001	AT2G46440	ref|Arabidopsis thaliana cyclic nucleotide-gated channels (CNGC11), mRNA [NM_001337191]
3,42	0,00000000	AT1G17745	ref|Arabidopsis thaliana D-3-phosphoglycerate dehydrogenase (PGDH), mRNA [NM_001035984]
3,42	0,00000000	AT1G13750	ref|Arabidopsis thaliana Purple acid phosphatases superfamily protein mRNA [NM_101243]
3,39	0,00000000	AT2G41010	ref|Arabidopsis thaliana calmodulin (CAM)-binding protein of 25 kDa (CAMBP25), mRNA [NM_129666]
3,39	0,00000000	AT3G17790	ref|Arabidopsis thaliana purple acid phosphatase 17 (PAP17), mRNA [NM_112660]
3,39	0,00000000	AT3G60540	ref|Arabidopsis thaliana Preprotein translocase Sec, Sec61-beta subunit protein mRNA [NM_202738]
3,39	0,00000000	AT2G35860	ref|Arabidopsis thaliana FASCICLIN-like arabinogalactan protein 16 precursor (FLA16), mRNA [NM_179922]
3,38	0,00000000	AT1G64390	ref|Arabidopsis thaliana glycosyl hydrolase 9C2 (GH9C2), mRNA [NM_105114]
3,37	0.00000003	AT4G14090	ref|Arabidopsis thaliana UDP-Glycosyltransferase superfamily protein mRNA [NM_117485]
3,36	0,00000000	AT5G08640	ref|Arabidopsis thaliana flavonol synthase 1 (FLS1), mRNA [NM_001203337]
3,36	0,00000000	AT3G56400	ref|Arabidopsis thaliana WRKY DNA-binding protein 70 (WRKY70), mRNA [NM_115498]
3,36	0,00000000	AT1G23100	ref|Arabidopsis thaliana GroES-like family protein mRNA [NM_102158]
3,36	0,00000000	AT1G73805	ref|Arabidopsis thaliana Calmodulin binding protein-like protein (SARD1), mRNA [NM_106040]
3,35	0.00000007	AT1G45201	ref|Arabidopsis thaliana triacylglycerol lipase-like 1 (TLL1), mRNA [NM_179441]
3,35	0,00000000	AT4G34200	ref|Arabidopsis thaliana D-3-phosphoglycerate dehydrogenase (EDA9), mRNA [NM_119583]
3,35	0,00000000	AT1G03495	gb|Arabidopsis thaliana HXXXD-type acyl-transferase-like protein (AT1G03495) mRNA, complete cds [NM_100232]
3,34	0,00000000	AT3G29590	ref|Arabidopsis thaliana HXXXD-type acyl-transferase family protein (AT5MAT), mRNA [NM_113880]
3,31	0,00000000	AT4G17770	ref|Arabidopsis thaliana trehalose phosphatase/synthase 5 (TPS5), mRNA [NM_001341241]
3,31	0,00000000	AT3G46320	ref|Arabidopsis thaliana Histone superfamily protein mRNA [NM_180329]
3,31	0.00000001	AT5G44568	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_001085241]
3,3	0,00000000	AT3G22550	ref|Arabidopsis thaliana NAD(P)H-quinone oxidoreductase subunit, putative (DUF581) mRNA [NM_113154]
3,29	0,00000000	AT2G46650	ref|Arabidopsis thaliana cytochrome B5 isoform C (CB5-C), mRNA [NM_130230]
3,29	0,00000000	AT2G39330	ref|Arabidopsis thaliana jacalin-related lectin 23 (JAL23), mRNA [NM_129490]
3,29	0,00000000	AT3G45930	ref|Arabidopsis thaliana Histone superfamily protein mRNA [NM_114462]
3,29	0,00000000	AT1G03820	ref|Arabidopsis thaliana E6-like protein mRNA [NM_100261]
3,28	0,00000000	AT3G14210	ref|Arabidopsis thaliana GDSL-like lipase/acylhydrolase superfamily protein (ESM1), mRNA [NM_001338114]
3,27	0,00000000	AT1G72910	ref|Arabidopsis thaliana Toll-Interleukin-Resistance (TIR) domain-containing protein mRNA [NM_105949]
3,26	0,00000000	AT3G03060	ref|Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA [NM_111176]
3,25	0,00000000	AT3G44750	ref|Arabidopsis thaliana histone deacetylase 3 (HDA3), mRNA [NM_001203083]
3,22	0,00000000	AT5G60730	ref|Arabidopsis thaliana Anion-transporting ATPase mRNA [NM_125466]
3,22	0,00000000	AT5G42020	ref|Arabidopsis thaliana Heat shock protein 70 (Hsp 70) family protein (BIP2), mRNA [NM_123567]
3,22	0,00000000	TA28264_3702	Unknown
3,21	0,00000000	AT2G37040	ref|Arabidopsis thaliana PHE ammonia lyase 1 (PAL1), mRNA [NM_129260]
3,21	0,00000000	AT1G04980	ref|Arabidopsis thaliana PDI-like 2-2 (PDIL2-2), mRNA [NM_100376]
3,21	0,00000000	AT2G23010	ref|Arabidopsis thaliana serine carboxypeptidase-like 9 (SCPL9), mRNA [NM_201788]
3,21	0,00000000	AT4G08300	ref|Arabidopsis thaliana nodulin MtN21 /EamA-like transporter family protein (UMAMIT17), mRNA [NM_116899]
3,21	0.00000001	AT3G60440	ref|Arabidopsis thaliana Phosphoglycerate mutase family protein mRNA [NM_001340043]
3,21	0,00000000	AT5G26690	ref|Arabidopsis thaliana Heavy metal transport/detoxification superfamily protein mRNA [NM_180545]
3,21	0,00000000	TA50968_3702	tc|Rep: Eukaryotic translation initiation factor 4E - Cucumis melo (Muskmelon), partial (11%) [TC394106]
3,2	0,00000000	AT1G66390	ref|Arabidopsis thaliana myb domain protein 90 (MYB90), mRNA [NM_105310]
3,18	0,00000000	AT3G15357	ref|Arabidopsis thaliana phosphopantothenoylcysteine decarboxylase subunit mRNA [NM_112403]
3,18	0.00000001	AT3G44450	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_114313]
3,17	0,00000000	AT5G10400	ref|Arabidopsis thaliana Histone superfamily protein mRNA [NM_121078]
3,16	0,00000000	AT5G28540	ref|Arabidopsis thaliana heat shock protein 70 (Hsp 70) family protein (BIP1), mRNA [NM_122737]
3,16	0,00000000	AT2G28740	ref|Arabidopsis thaliana histone H4 (HIS4), mRNA [NM_128434]
3,15	0,00000000	AT5G03760	ref|Arabidopsis thaliana Nucleotide-diphospho-sugar transferases superfamily protein (ATCSLA09), mRNA [NM_120457]
3,15	0,00000000	AT5G26220	ref|Arabidopsis thaliana ChaC-like family protein mRNA [NM_001343968]
3,14	0,00000000	AT1G11545	ref|Arabidopsis thaliana xyloglucan endotransglucosylase/hydrolase 8 (XTH8), mRNA [NM_101028]
3,13	0,00000000	AT2G28210	ref|Arabidopsis thaliana alpha carbonic anhydrase 2 (ACA2), mRNA [NM_001336148]
3,13	0,00000000	AT3G09870	ref|Arabidopsis thaliana SAUR-like auxin-responsive protein family mRNA [NM_111822]
3,13	0,00000000	AT5G22460	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_122151]

3,12	0.00000869	BP586302	gb|BP586302 RAFL15 Arabidopsis thaliana cDNA clone RAFL15-05-M21 3', mRNA sequence [BP586302]
3,11	0,00000000	AT5G64080	ref|Arabidopsis thaliana Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (XYP1), mRNA [NM_125804]
3,11	0,00000000	AT1G04020	ref|Arabidopsis thaliana breast cancer associated RING 1 (BARD1), mRNA [NM_202029]
3,1	0,00000000	AT1G65890	ref|Arabidopsis thaliana acyl activating enzyme 12 (AAE12), mRNA [NM_105261]
3,1	0,00000000	AT5G46830	ref|Arabidopsis thaliana calcium-binding transcription factor NIG1 (NIG1), mRNA [NM_124054]
3,09	0,00000000	AT5G64550	ref|Arabidopsis thaliana loricrin-like protein mRNA [NM_125851]
3,08	0,00000000	AT5G07690	ref|Arabidopsis thaliana myb domain protein 29 (MYB29), mRNA [NM_120851]
3,08	0,00000000	NP335312	tc|GB|AL590346.1|CAC35882.1 putative protein [Arabidopsis thaliana] [NP335312]
3,07	0,00000000	AT3G27360	ref|Arabidopsis thaliana Histone superfamily protein mRNA [NM_113651]
3,07	0,00000000	AT5G42380	ref|Arabidopsis thaliana calmodulin like 37 (CML37), mRNA [NM_123603]
3,06	0,00000000	AT2G32990	ref|Arabidopsis thaliana glycosyl hydrolase 9B8 (GH9B8), mRNA [NM_128859]
3,05	0,00000000	AT5G25250	ref|Arabidopsis thaliana SPFH/Band 7/PHB domain-containing membrane-associated protein family (FLOT1), mRNA [NM_122434]
3,04	0,00000000	AT1G32900	ref|Arabidopsis thaliana UDP-Glycosyltransferase superfamily protein (GBSS1), mRNA [NM_103023]
3,04	0,00000000	AT1G20510	ref|Arabidopsis thaliana OPC-8:0 CoA ligase1 (OPCL1), mRNA [NM_202143]
3,03	0,00000000	AT1G41830	ref|Arabidopsis thaliana SKU5-similar 6 (SKS6), mRNA [NM_103408]
3,03	0,00000000	TA36353_3702	tc|Rep: At5g42860 - Arabidopsis thaliana (Mouse-ear cress), partial (39%) [TC388419]
3,02	0,00000000	AT4G14680	ref|Arabidopsis thaliana Pseudouridine synthase/archaeosine transglycosylase-like family protein (APS3), mRNA [NM_001340955]
3,02	0.00000001	AT4G23140	ref|Arabidopsis thaliana cysteine-rich RLK (RECEPTOR-like protein kinase) 6 (CRK6), mRNA [NM_179095]
3,01	0.00000001	AT2G16060	ref|Arabidopsis thaliana hemoglobin 1 (HB1), mRNA [NM_127165]
3,01	0,00000000	AT5G61030	ref|Arabidopsis thaliana glycine-rich RNA-binding protein 3 (GR-RBP3), mRNA [NM_125496]
3,01	0,00000000	AT4G23170	ref|Arabidopsis thaliana receptor-like protein kinase-related family protein (EP1), mRNA [NM_118446]
-3,01	0,00000000	AT4G18010	ref|Arabidopsis thaliana myo-inositol polyphosphate 5-phosphatase 2 (IP5PII), mRNA [NM_117911]
-3,01	0,00000000	AT2G03760	ref|Arabidopsis thaliana sulfotransferase 12 (SOT12), mRNA [NM_126423]
-3,01	0,00000000	AT1G21680	ref|Arabidopsis thaliana DPP6 N-terminal domain-like protein mRNA [NM_102017]
-3,01	0.00000001	AT5G45310	ref|Arabidopsis thaliana coiled-coil protein mRNA [NM_123899]
-3,02	0,00000000	AK230465	gb|Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL26-03-H08 [AK230465]
-3,03	0,00000000	AT2G43820	ref|Arabidopsis thaliana UDP-glucosyltransferase 74F2 (UGT74F2), mRNA [NM_129944]
-3,03	0.00000001	AT1G71000	ref|Arabidopsis thaliana Chaperone DnaJ-domain superfamily protein mRNA [NM_001334483]
-3,03	0,00000000	AT2G29480	ref|Arabidopsis thaliana glutathione S-transferase tau 2 (GSTU2), mRNA [NM_128502]
-3,03	0,00000000	AT1G12250	ref|Arabidopsis thaliana Pentapeptide repeat-containing protein mRNA [NM_001084054]
-3,03	0,00000000	AT1G23040	ref|Arabidopsis thaliana hydroxyproline-rich glycoprotein family protein mRNA [NM_001332581]
-3,03	0,00000000	AT2G46220	ref|Arabidopsis thaliana DUF2358 family protein (DUF2358) mRNA [NM_130184]
-3,04	0.00000002	AT5G36910	ref|Arabidopsis thaliana thionin 2.2 (THI2.2), mRNA [NM_123049]
-3,04	0,00000000	AT4G39090	ref|Arabidopsis thaliana Papain family cysteine protease (RD19), mRNA [NM_120069]
-3,04	0,00000000	AT1G76650	ref|Arabidopsis thaliana calmodulin-like 38 (CML38), mRNA [NM_001198484]
-3,04	0,00000000	AT2G25780	ref|Arabidopsis thaliana hypothetical protein (DUF1677) mRNA [NM_128138]
-3,04	0,00000000	AT3G13062	ref|Arabidopsis thaliana Polyketide cyclase/dehydrase and lipid transport superfamily protein mRNA [NM_180243]
-3,04	0.00000003	TC297782	ref|Arabidopsis thaliana other RNA lncRNA [NR_139108]
-3,05	0,00000000	AT1G55850	ref|Arabidopsis thaliana cellulose synthase like E1 (CSLE1), mRNA [NM_104462]
-3,05	0,00000000	AT5G59340	ref|Arabidopsis thaliana WUSCHEL related homeobox 2 (WOX2), mRNA [NM_125325]
-3,05	0,00000000	AT5G39610	ref|Arabidopsis thaliana NAC domain containing protein 6 (NAC6), mRNA [NM_123323]
-3,06	0,00000000	AT1G04280	ref|Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA [NM_001331471]
-3,08	0,00000000	AT1G18270	ref|Arabidopsis thaliana ketose-bisphosphate aldolase class-II family protein mRNA [NM_001198099]
-3,09	0.00000001	AT1G08570	ref|Arabidopsis thaliana atypical CYS HIS rich thioredoxin 4 (ACHT4), mRNA [NM_001123776]
-3,09	0,00000000	AT5G57660	ref|Arabidopsis thaliana CONSTANS-like 5 (COL5), mRNA [NM_125149]
-3,09	0,00000000	AT5G65870	ref|Arabidopsis thaliana phytosulfokine 5 precursor (PSK5), mRNA [NM_125984]
-3,09	0.00000001	CB259684	gb|31-E9537-013-002-M08-T7R MPIZ-ADIS-013 Arabidopsis thaliana cDNA clone MPIZp770M082Q 5-PRIME, mRNA sequence [CB259684]
-3,09	0,00000000	TA29086_3702	Unknown
-3,1	0,00000000	AT4G32480	ref|Arabidopsis thaliana sugar phosphate exchanger, putative (DUF506) mRNA [NM_119400]
-3,11	0.00000001	AT5G63790	ref|Arabidopsis thaliana NAC domain containing protein 102 (NAC102), mRNA [NM_001345612]
-3,11	0,00000000	AT5G65380	ref|Arabidopsis thaliana MATE efflux family protein mRNA [NM_125936]
-3,12	0,00000000	AT4G31870	ref|Arabidopsis thaliana glutathione peroxidase 7 (GPX7), mRNA [NM_001342119]
-3,12	0,00000000	AT3G10910	ref|Arabidopsis thaliana RING/U-box superfamily protein mRNA [NM_111928]
-3,12	0,00000000	AT5G06980	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_001203316]
-3,13	0,00000000	AT1G18020	ref|Arabidopsis thaliana FMN-linked oxidoreductases superfamily protein mRNA [NM_001035985]
-3,13	0.00000001	AT5G17300	ref|Arabidopsis thaliana Homeodomain-like superfamily protein (RVE1), mRNA [NM_121736]
-3,14	0,00000000	AT4G13830	ref|Arabidopsis thaliana DNAJ-like 20 (J20), mRNA [NM_117457]
-3,14	0,00000000	AT1G19660	ref|Arabidopsis thaliana Wound-responsive family protein mRNA [NM_001035991]
-3,14	0,00000000	AT2G38820	ref|Arabidopsis thaliana DNA-directed RNA polymerase subunit beta-beta protein, putative (DUF506) mRNA [NM_001336739]
-3,14	0,00000000	AT4G25690	ref|Arabidopsis thaliana stress response NST1-like protein mRNA [NM_118701]

-3,14	0,00000000	BT025685	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_001334179]
-3,15	0,00000000	AT1G68620	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_105534]
-3,15	0,00000000	AT1G76690	ref|Arabidopsis thaliana 12-oxophytodienoate reductase 2 (OPR2), mRNA [NM_106319]
-3,16	0,00000000	AT5G43450	ref|Arabidopsis thaliana 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein mRNA [NM_001344483]
-3,16	0,00000000	AT2G29500	ref|Arabidopsis thaliana HSP20-like chaperones superfamily protein mRNA [NM_128504]
-3,16	0,00000000	AT3G16770	ref|Arabidopsis thaliana ethylene-responsive element binding protein (EBP), mRNA [NM_112550]
-3,18	0,00000000	AT5G51970	ref|Arabidopsis thaliana GroES-like zinc-binding alcohol dehydrogenase family protein mRNA [NM_124576]
-3,19	0,00000000	AT4G24050	ref|Arabidopsis thaliana NAD(P)-binding Rossmann-fold superfamily protein mRNA [NM_001341639]
-3,19	0,00000000	AT2G22960	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_001335830]
-3,2	0,00000000	AT3G07350	ref|Arabidopsis thaliana sulfate/thiosulfate import ATP-binding protein, putative (DUF506) mRNA [NM_111614]
-3,22	0,00000000	AT5G08350	ref|Arabidopsis thaliana GRAM domain-containing protein / ABA-responsive protein-like protein mRNA [NM_120919]
-3,22	0,00000000	AT1G20630	ref|Arabidopsis thaliana catalase 1 (CAT1), mRNA [NM_101914]
-3,24	0,00000000	AT3G22370	ref|Arabidopsis thaliana alternative oxidase 1A (AOX1A), mRNA [NM_113135]
-3,26	0,00000000	AT5G64570	ref|Arabidopsis thaliana beta-D-xylosidase 4 (XYL4), mRNA [NM_001345643]
-3,26	0,00000000	AT2G30140	ref|Arabidopsis thaliana UDP-Glycosyltransferase superfamily protein (UGT87A2), mRNA [NM_001084510]
-3,26	0,00000000	AT3G55710	ref|Arabidopsis thaliana UDP-Glycosyltransferase superfamily protein mRNA [NM_115429]
-3,26	0,00000000	AT4G04770	ref|Arabidopsis thaliana ATP binding cassette protein 1 (ABCI8), mRNA [NM_116715]
-3,26	0,00000000	AT3G25190	ref|Arabidopsis thaliana Vacuolar iron transporter (VIT) family protein mRNA [NM_113425]
-3,27	0,00000000	AT3G03480	ref|Arabidopsis thaliana acetyl CoA:(Z)-3-hexen-1-ol acetyltransferase (CHAT), mRNA [NM_111219]
-3,27	0,00000000	AT1G48000	ref|Arabidopsis thaliana myb domain protein 112 (MYB112), mRNA [NM_103696]
-3,27	0,00000000	AT4G25390	ref|Arabidopsis thaliana Protein kinase superfamily protein mRNA [NM_179111]
-3,27	0,00000000	AT5G40690	ref|Arabidopsis thaliana histone-lysine N-methyltransferase trithorax-like protein mRNA [NM_123434]
-3,27	0,00000000	TC312617	tc|Rep: Vacuolar-processing enzyme gamma-isozyme precursor - Arabidopsis thaliana (Mouse-ear cress), partial (23%) [TC400087]
-3,28	0,00000000	AT1G53580	ref|Arabidopsis thaliana glyoxalase II 3 (GLY3), mRNA [NM_202289]
-3,29	0,00000000	AT2G48020	ref|Arabidopsis thaliana Major facilitator superfamily protein mRNA [NM_180152]
-3,3	0,00000000	AT3G02140	ref|Arabidopsis thaliana AFP2 (ABI five-binding protein 2) family protein (TMAC2), mRNA [NM_111081]
-3,31	0,00000000	AT5G65110	ref|Arabidopsis thaliana acyl-CoA oxidase 2 (ACX2), mRNA [NM_001037068]
-3,31	0,00000000	AT3G22200	ref|Arabidopsis thaliana Pyridoxal phosphate (PLP)-dependent transferases superfamily protein (POP2), mRNA [NM_001203018]
-3,31	0,00000000	AT2G29290	ref|Arabidopsis thaliana NAD(P)-binding Rossmann-fold superfamily protein mRNA [NM_128483]
-3,31	0,00000000	AT1G06430	ref|Arabidopsis thaliana FTSH protease 8 (FTSH8), mRNA [NM_100523]
-3,31	0,00000000	AT2G04795	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_126510]
-3,32	0,00000000	AT2G43400	ref|Arabidopsis thaliana electron-transfer flavoprotein:ubiquinone oxidoreductase (ETFQO), mRNA [NM_129901]
-3,32	0.00000001	AT1G09240	ref|Arabidopsis thaliana nicotianamine synthase 3 (NAS3), mRNA [NM_100794]
-3,32	0,00000000	AT1G77210	ref|Arabidopsis thaliana sugar transporter 14 (STP14), mRNA [NM_106370]
-3,32	0,00000000	AT1G03580	gb|Arabidopsis thaliana unknown protein (At1g03580) mRNA, partial cds [AY091013]
-3,33	0,00000000	AT5G39660	ref|Arabidopsis thaliana cycling DOF factor 2 (CDF2), mRNA [NM_180775]
-3,33	0,00000000	AT1G61740	ref|Arabidopsis thaliana Sulfite exporter TauE/SafE family protein mRNA [NM_104856]
-3,35	0,00000000	AT2G28110	ref|Arabidopsis thaliana Exostosin family protein (FRA8), mRNA [NM_179782]
-3,35	0.00000001	AT1G75380	ref|Arabidopsis thaliana bifunctional nuclease in basal defense response 1 (BBD1), mRNA [NM_179560]
-3,35	0,00000000	AT3G62950	ref|Arabidopsis thaliana Thioredoxin superfamily protein mRNA [NM_116160]
-3,35	0,00000000	AT2G22990	ref|Arabidopsis thaliana sinapoylglucose 1 (SNG1), mRNA [NM_127864]
-3,35	0,00000000	AT3G10320	ref|Arabidopsis thaliana Glycosyltransferase family 61 protein mRNA [NM_111867]
-3,37	0,00000000	AT1G64940	ref|Arabidopsis thaliana cytochrome P450, family 87, subfamily A, polypeptide 6 (CYP89A6), mRNA [NM_105168]
-3,38	0,00000000	AT1G64950	ref|Arabidopsis thaliana cytochrome P450, family 89, subfamily A, polypeptide 5 (CYP89A5), mRNA [NM_105169]
-3,39	0,00000000	AT3G29240	ref|Arabidopsis thaliana PPR containing protein (DUF179) mRNA [NM_113848]
-3,4	0,00000000	AT5G49740	ref|Arabidopsis thaliana ferric reduction oxidase 7 (FRO7), mRNA [NM_001344853]
-3,4	0,00000000	AT4G16520	ref|Arabidopsis thaliana Ubiquitin-like superfamily protein (ATG8F), mRNA [NM_179064]
-3,4	0,00000000	AT4G23450	ref|Arabidopsis thaliana RING/U-box superfamily protein (AIRP1), mRNA [NM_001341614]
-3,41	0,00000000	AT5G18170	ref|Arabidopsis thaliana glutamate dehydrogenase 1 (GDH1), mRNA [NM_121822]
-3,41	0,00000000	AT2G13431	gb|Arabidopsis thaliana clone asmbl_5374 unknown mRNA sequence [EF182961]
-3,41	0,00000000	AT5G66480	ref|Arabidopsis thaliana bacteriophage N4 adsorption B protein mRNA [NM_126046]
-3,41	0,00000000	BX822927	gb|Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB73ZE03 of Flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress) [BX822927]
-3,42	0,00000000	AT4G37610	ref|Arabidopsis thaliana BTB and TAZ domain protein 5 (BT5), mRNA [NM_119924]
-3,43	0.00000001	AT2G32020	ref|Arabidopsis thaliana Acyl-CoA N-acyltransferases (NAT) superfamily protein mRNA [NM_128762]
-3,43	0,00000000	AT2G37750	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_129331]
-3,44	0,00000000	AT5G49730	ref|Arabidopsis thaliana ferric reduction oxidase 6 (FRO6), mRNA [NM_001344852]
-3,44	0,00000000	AT2G30250	ref|Arabidopsis thaliana WRKY DNA-binding protein 25 (WRKY25), mRNA [NM_128578]
-3,45	0,00000000	AT2G37130	ref|Arabidopsis thaliana Peroxidase superfamily protein mRNA [NM_001124989]
-3,45	0,00000000	AT4G31860	ref|Arabidopsis thaliana Protein phosphatase 2C family protein mRNA [NM_202927]
-3,45	0,00000000	AT1G16720	ref|Arabidopsis thaliana high chlorophyll fluorescence phenotype 173 (HCF173), mRNA [NM_001332253]

-3,46	0,00000000	AT3G59930	ref|Arabidopsis thaliana defensin-like protein mRNA [NM_115856]
-3,46	0,00000000	AT2G42870	ref|Arabidopsis thaliana phy rapidly regulated 1 (PAR1), mRNA [NM_129848]
-3,47	0.00000001	AT4G16190	ref|Arabidopsis thaliana Papain family cysteine protease mRNA [NM_117715]
-3,47	0,00000000	AT1G53280	ref|Arabidopsis thaliana Class I glutamine amidotransferase-like superfamily protein (DJ1B), mRNA [NM_104206]
-3,48	0,00000000	AT1G17990	ref|Arabidopsis thaliana FMN-linked oxidoreductases superfamily protein mRNA [NM_001035985]
-3,48	0,00000000	AT3G26220	ref|Arabidopsis thaliana cytochrome P450, family 71, subfamily B, polypeptide 3 (CYP71B3), mRNA [NM_113529]
-3,49	0,00000000	AT4G22920	ref|Arabidopsis thaliana non-yellowing 1 (NYE1), mRNA [NM_001341565]
-3,5	0,00000000	AT2G44130	ref|Arabidopsis thaliana Galactose oxidase/kelch repeat superfamily protein mRNA [NM_129976]
-3,51	0.00000001	AK230421	gb|Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL25-33-B21 [AK230421]
-3,52	0,00000000	AT5G39050	ref|Arabidopsis thaliana HXXXD-type acyl-transferase family protein (PMAT1), mRNA [NM_123267]
-3,53	0,00000000	BU917423	ref|Arabidopsis thaliana RING/U-box protein mRNA [NM_112412]
-3,59	0,00000000	N38085	tc|Rep: Cysteine proteinase - Populus tomentosa (Chinese white poplar), partial (36%) [TC397589]
-3,6	0,00000000	AT1G55920	ref|Arabidopsis thaliana serine acetyltransferase 2;1 (SERAT2;1), mRNA [NM_104470]
-3,6	0,00000000	AT5G64230	ref|Arabidopsis thaliana 1,8-cineole synthase mRNA [NM_125819]
-3,61	0.00000001	AT1G10140	ref|Arabidopsis thaliana Uncharacterized conserved protein UCP031279 mRNA [NM_100888]
-3,61	0.00000001	AV566399	gb|AV566399 Arabidopsis thaliana green siliques Columbia Arabidopsis thaliana cDNA clone SQ242f10F 3', mRNA sequence [AV566399]
-3,63	0,00000000	AT1G13700	ref|Arabidopsis thaliana 6-phosphogluconolactonase 1 (PGL1), mRNA [NM_001332083]
-3,63	0,00000000	AT3G43670	ref|Arabidopsis thaliana Copper amine oxidase family protein mRNA [NM_114235]
-3,63	0,00000000	AT1G20350	ref|Arabidopsis thaliana translocase inner membrane subunit 17-1 (TIM17-1), mRNA [NM_101886]
-3,64	0,00000000	AT2G47180	ref|Arabidopsis thaliana galactinol synthase 1 (GolS1), mRNA [NM_130286]
-3,64	0,00000000	AT2G36950	ref|Arabidopsis thaliana Heavy metal transport/detoxification superfamily protein mRNA [NM_129251]
-3,66	0,00000000	AT2G15890	ref|Arabidopsis thaliana maternal effect embryo arrest 14 (MEE14), mRNA [NM_001084426]
-3,67	0,00000000	AT1G67070	ref|Arabidopsis thaliana Mannose-6-phosphate isomerase, type I (DIN9), mRNA [NM_001334269]
-3,67	0,00000000	AT3G13065	ref|Arabidopsis thaliana STRUBBELIG-receptor family 4 (SRF4), mRNA [NM_112145]
-3,69	0,00000000	AT3G10740	ref|Arabidopsis thaliana alpha-L-arabinofuranosidase 1 (ASD1), mRNA [NM_001337894]
-3,7	0,00000000	AT1G14130	ref|Arabidopsis thaliana 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein mRNA [NM_101278]
-3,7	0,00000000	AT3G04060	ref|Arabidopsis thaliana NAC domain containing protein 46 (NAC046), mRNA [NM_111277]
-3,71	0,00000000	TC309871	tc|Rep: Conglutin gamma-like protein - Arabidopsis thaliana (Mouse-ear cress), partial (35%) [TC396686]
-3,72	0,00000000	AT5G18130	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_203067]
-3,74	0,00000000	AT1G09420	ref|Arabidopsis thaliana glucose-6-phosphate dehydrogenase 4 (G6PD4), mRNA [NM_001198018]
-3,74	0,00000000	AT1G01240	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_001331263]
-3,75	0,00000000	AT4G20070	ref|Arabidopsis thaliana allantoate amidohydrolase (AAH), mRNA [NM_001341398]
-3,77	0,00000000	AT2G26355	ref|Arabidopsis thaliana other RNA lncRNA [NR_140673]
-3,77	0,00000000	AT4G33660	ref|Arabidopsis thaliana cysteine-rich TM module stress tolerance protein mRNA [NM_119522]
-3,81	0,00000000	TA35940_3702	tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vinifera (Grape), partial (42%) [TC384450]
-3,84	0,00000000	AT5G66052	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_148167]
-3,84	0.00000001	TA29208_3702	Unknown
-3,85	0,00000000	AT2G40300	ref|Arabidopsis thaliana ferritin 4 (FER4), mRNA [NM_129588]
-3,85	0,00000000	AT4G34138	ref|Arabidopsis thaliana UDP-glucosyl transferase 73B1 (UGT73B1), mRNA [NM_119576]
-3,86	0,00000000	AT3G46080	ref|Arabidopsis thaliana C2H2-type zinc finger family protein mRNA [NM_114477]
-3,86	0,00000000	AT5G55970	ref|Arabidopsis thaliana RING/U-box superfamily protein mRNA [NM_180866]
-3,9	0,00000000	AT5G53970	ref|Arabidopsis thaliana Tyrosine transaminase family protein (TAT7), mRNA [NM_124776]
-3,9	0,00000000	AT2G40420	ref|Arabidopsis thaliana Transmembrane amino acid transporter family protein mRNA [NM_129602]
-3,91	0,00000000	AT5G43580	ref|Arabidopsis thaliana Serine protease inhibitor, potato inhibitor I-type family protein (UPI), mRNA [NM_123724]
-3,92	0,00000000	AT1G58290	ref|Arabidopsis thaliana Glutamyl-tRNA reductase family protein (HEMA1), mRNA [NM_104609]
-3,92	0,00000000	AT5G16960	ref|Arabidopsis thaliana Zinc-binding dehydrogenase family protein mRNA [NM_001343474]
-3,93	0,00000000	AT3G03470	ref|Arabidopsis thaliana cytochrome P450, family 87, subfamily A, polypeptide 9 (CYP89A9), mRNA [NM_111218]
-3,94	0,00000000	AT5G19120	ref|Arabidopsis thaliana Eukaryotic aspartyl protease family protein mRNA [NM_121917]
-3,95	0,00000000	AT5G16970	ref|Arabidopsis thaliana alkenal reductase (AER), mRNA [NM_121703]
-3,96	0,00000000	AT5G18630	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_180517]
-3,96	0,00000000	AT5G02160	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_120294]
-3,97	0,00000000	AT5G28770	ref|Arabidopsis thaliana bZIP transcription factor family protein (BZO2H3), mRNA [NM_001344083]
-3,99	0,00000000	AT5G44973	ref|Arabidopsis thaliana defensin-like protein mRNA [NM_001036935]
-4,01	0,00000000	AT3G14690	ref|Arabidopsis thaliana cytochrome P450, family 72, subfamily A, polypeptide 15 (CYP72A15), mRNA [NM_112330]
-4,01	0,00000000	AT4G32940	ref|Arabidopsis thaliana gamma vacuolar processing enzyme (GAMMA-VPE), mRNA [NM_119448]
-4,03	0,00000000	AT2G36750	ref|Arabidopsis thaliana UDP-glucosyl transferase 73C1 (UGT73C1), mRNA [NM_129230]
-4,03	0,00000000	AT5G65207	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_148161]
-4,04	0,00000000	TA29997_3702	Unknown
-4,06	0,00000000	AT4G24160	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_202876]
-4,08	0,00000000	AT1G63180	ref|Arabidopsis thaliana UDP-D-glucose/UDP-D-galactose 4-epimerase 3 (UGE3), mRNA [NM_104996]

-4,08	0,00000000	AT5G17000	ref|Arabidopsis thaliana Zinc-binding dehydrogenase family protein mRNA [NM_001343476]
-4,1	0,00000000	AT5G16370	ref|Arabidopsis thaliana acyl activating enzyme 5 (AAE5), mRNA [NM_121642]
-4,1	0,00000000	AT1G23390	ref|Arabidopsis thaliana Kelch repeat-containing F-box family protein mRNA [NM_102188]
-4,11	0,00000000	AT1G05340	ref|Arabidopsis thaliana cysteine-rich TM module stress tolerance protein mRNA [NM_100413]
-4,12	0,00000000	AT5G17860	ref|Arabidopsis thaliana calcium exchanger 7 (CAX7), mRNA [NM_121792]
-4,13	0,00000000	AT5G52250	ref|Arabidopsis thaliana Transducin/WD40 repeat-like superfamily protein (RUP1), mRNA [NM_124604]
-4,14	0,00000000	AT5G15850	ref|Arabidopsis thaliana CONSTANS-like 1 (COL1), mRNA [NM_121590]
-4,18	0,00000000	AT2G39400	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_001336772]
-4,19	0,00000000	AT5G64250	ref|Arabidopsis thaliana Aldolase-type TIM barrel family protein mRNA [NM_125821]
-4,19	0,00000000	AT2G17500	ref|Arabidopsis thaliana Auxin efflux carrier family protein mRNA [NM_179633]
-4,19	0,00000000	AT2G27385	ref|Arabidopsis thaliana Pollen Ole e 1 allergen and extensin family protein mRNA [NM_179769]
-4,2	0,00000000	AT1G58180	ref|Arabidopsis thaliana beta carbonic anhydrase 6 (BCA6), mRNA [NM_179492]
-4,2	0,00000000	AT2G25900	ref|Arabidopsis thaliana Zinc finger C-x8-C-x5-C-x3-H type family protein (ATCTH), mRNA [NM_001202675]
-4,21	0,00000000	AT2G28120	ref|Arabidopsis thaliana Major facilitator superfamily protein mRNA [NM_128372]
-4,21	0,00000000	AT5G14120	ref|Arabidopsis thaliana Major facilitator superfamily protein mRNA [NM_121416]
-4,24	0,00000000	AT2G26150	ref|Arabidopsis thaliana heat shock transcription factor A2 (HSFA2), mRNA [NM_001336038]
-4,26	0,00000000	AT5G13330	ref|Arabidopsis thaliana related to AP2 6l (Rap2.6L), mRNA [NM_121336]
-4,26	0,00000000	AT5G17170	ref|Arabidopsis thaliana rubredoxin family protein (ENH1), mRNA [NM_001085129]
-4,28	0,00000000	AT3G15770	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_112447]
-4,28	0,00000000	TA26159_3702	Unknown
-4,3	0,00000000	AT3G50560	ref|Arabidopsis thaliana NAD(P)-binding Rossmann-fold superfamily protein mRNA [NM_114916]
-4,3	0,00000000	AT5G63190	ref|Arabidopsis thaliana MA3 domain-containing protein mRNA [NM_125714]
-4,31	0,00000000	AT3G10020	ref|Arabidopsis thaliana plant/protein mRNA [NM_111837]
-4,33	0,00000000	TA28495_3702	Unknown
-4,36	0,00000000	AT1G76600	ref|Arabidopsis thaliana poly polymerase mRNA [NM_106310]
-4,37	0,00000000	AT3G15620	ref|Arabidopsis thaliana DNA photolyase family protein (UVR3), mRNA [NM_112432]
-4,37	0,00000000	AT3G19390	ref|Arabidopsis thaliana Granulin repeat cysteine protease family protein mRNA [NM_112826]
-4,38	0,00000000	AT1G75490	ref|Arabidopsis thaliana Integrase-type DNA-binding superfamily protein mRNA [NM_106202]
-4,42	0,00000000	AT3G15500	ref|Arabidopsis thaliana NAC domain containing protein 3 (NAC3), mRNA [NM_112418]
-4,43	0,00000000	AT1G77450	ref|Arabidopsis thaliana NAC domain containing protein 32 (NAC032), mRNA [NM_106394]
-4,43	0,00000000	TC313866	tc|Rep: Chaperone protein dnaJ 8, chloroplast precursor - Arabidopsis thaliana (Mouse-ear cress), partial (50%) [TC404503]
-4,45	0,00000000	AT3G14680	ref|Arabidopsis thaliana cytochrome P450, family 72, subfamily A, polypeptide 14 (CYP72A14), mRNA [NM_112329]
-4,46	0,00000000	AT3G22460	ref|Arabidopsis thaliana O-acetylserine (thiol) lyase (OAS-TL) isoform A2 (OASA2), mRNA [NM_113145]
-4,46	0,00000000	AT4G13250	ref|Arabidopsis thaliana NAD(P)-binding Rossmann-fold superfamily protein (NYC1), mRNA [NM_117396]
-4,49	0,00000000	AT1G07890	ref|Arabidopsis thaliana ascorbate peroxidase 1 (APX1), mRNA [NM_100663]
-4,49	0,00000000	AT4G16680	ref|Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA [NM_001341126]
-4,49	0,00000000	AT5G58350	ref|Arabidopsis thaliana with no lysine (K) kinase 4 (WNK4), mRNA [NM_125220]
-4,5	0,00000000	AT1G68190	ref|Arabidopsis thaliana B-box zinc finger family protein (BBX27), mRNA [NM_001334353]
-4,52	0,00000000	AT1G07040	ref|Arabidopsis thaliana plant/protein mRNA [NM_100578]
-4,55	0,00000000	AT5G24120	ref|Arabidopsis thaliana sigma factor E (SIGE), mRNA [NM_001343842]
-4,57	0,00000000	AT1G14870	ref|Arabidopsis thaliana PLANT CADMIUM RESISTANCE 2 (PCR2), mRNA [NM_101356]
-4,6	0,00000000	AT4G26530	ref|Arabidopsis thaliana Aldolase superfamily protein (FBA5), mRNA [NM_001036644]
-4,6	0,00000000	AT1G13300	ref|Arabidopsis thaliana myb-like transcription factor family protein (HRS1), mRNA [NM_101201]
-4,61	0,00000000	AT5G26200	ref|Arabidopsis thaliana Mitochondrial substrate carrier family protein mRNA [NM_122521]
-4,62	0,00000000	AT4G38470	ref|Arabidopsis thaliana ACT-like protein tyrosine kinase family protein (STY46), mRNA [NM_001342498]
-4,63	0,00000000	AT3G46690	ref|Arabidopsis thaliana UDP-Glycosyltransferase superfamily protein mRNA [NM_114536]
-4,63	0,00000000	AT3G13061	ref|Arabidopsis thaliana other RNA lncRNA [NR_141586]
-4,64	0,00000000	AT3G62260	ref|Arabidopsis thaliana Protein phosphatase 2C family protein mRNA [NM_180406]
-4,65	0,00000000	AT1G53100	ref|Arabidopsis thaliana Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein mRNA [NM_104189]
-4,65	0,00000000	AT2G30600	ref|Arabidopsis thaliana BTB/POZ domain-containing protein mRNA [NM_001202713]
-4,66	0,00000000	AT1G30820	ref|Arabidopsis thaliana CTP synthase family protein mRNA [NM_102819]
-4,66	0,00000000	AT1G79270	ref|Arabidopsis thaliana evolutionarily conserved C-terminal region 8 (ECT8), mRNA [NM_001334878]
-4,66	0,00000000	NP229859	tc|GB|AL391141.1|CAC01711.1 quinone oxidoreductase-like protein [NP229859]
-4,67	0,00000000	AT1G22380	ref|Arabidopsis thaliana UDP-glucosyl transferase 85A3 (UGT85A3), mRNA [NM_102088]
-4,67	0,00000000	AT5G47560	ref|Arabidopsis thaliana tonoplast dicarboxylate transporter (TDT), mRNA [NM_124129]
-4,71	0.00000005	EG427617	gb|AYALO23TFB pooled cDNA populations Arabidopsis thaliana cDNA, mRNA sequence [EG427617]
-4,72	0,00000000	TC295612	ref|Arabidopsis thaliana other RNA ncRNA [NR_143567]
-4,73	0,00000000	AV805941	gb|AV805941 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-44-M15 3', mRNA sequence [AV805941]
-4,74	0,00000000	AT1G32170	ref|Arabidopsis thaliana xyloglucan endotransglucosylase/hydrolase 30 (XTH30), mRNA [NM_102950]
-4,74	0,00000000	AT1G63800	ref|Arabidopsis thaliana ubiquitin-conjugating enzyme 5 (UBC5), mRNA [NM_001334127]

-4,76	0,00000000	AT5G57655	ref|Arabidopsis thaliana xylose isomerase family protein mRNA [NM_180872]
-4,76	0,00000000	AT4G37370	ref|Arabidopsis thaliana cytochrome P450, family 81, subfamily D, polypeptide 8 (CYP81D8), mRNA [NM_119900]
-4,79	0,00000000	DR368472	gb|12826078 CERES-AN65 Arabidopsis thaliana cDNA clone 1361839 5', mRNA sequence [DR368472]
-4,81	0,00000000	AT5G57560	ref|Arabidopsis thaliana Xyloglucan endotransglucosylase/hydrolase family protein (TCH4), mRNA [NM_125137]
-4,82	0,00000000	DR368506	gb|12842501 CERES-AN65 Arabidopsis thaliana cDNA clone 1366811 5', mRNA sequence [DR368506]
-4,84	0,00000000	AT2G39570	ref|Arabidopsis thaliana ACT domain-containing protein (ACR9), mRNA [NM_129515]
-4,85	0,00000000	AT1G35670	ref|Arabidopsis thaliana calcium-dependent protein kinase 2 (CDPK2), mRNA [NM_103271]
-4,86	0,00000000	AT1G80440	ref|Arabidopsis thaliana Galactose oxidase/kelch repeat superfamily protein mRNA [NM_106692]
-4,87	0.00000001	AT4G20860	ref|Arabidopsis thaliana FAD-binding Berberine family protein mRNA [NM_118204]
-4,89	0,00000000	TA30818_3702	Unknown
-4,91	0,00000000	AT4G15530	ref|Arabidopsis thaliana pyruvate orthophosphate dikinase (PPDK), mRNA [NM_001341051]
-4,95	0,00000000	AT3G61900	ref|Arabidopsis thaliana SAUR-like auxin-responsive protein family mRNA [NM_116055]
-4,96	0,00000000	AT2G18050	ref|Arabidopsis thaliana histone H1-3 (HIS1-3), mRNA [NM_179639]
-4,96	0,00000000	AT1G72060	ref|Arabidopsis thaliana serine-type endopeptidase inhibitor mRNA [NM_105864]
-5,01	0,00000000	TA28705_3702	Unknown
-5,05	0,00000000	AT5G50760	ref|Arabidopsis thaliana SAUR-like auxin-responsive protein family mRNA [NM_124454]
-5,08	0,00000000	AT5G38710	ref|Arabidopsis thaliana Methylenetetrahydrofolate reductase family protein mRNA [NM_123232]
-5,09	0,00000000	AT4G24972	ref|Arabidopsis thaliana tapetum determinant 1 (TPD1), mRNA [NM_202883]
-5,1	0,00000000	AT4G34131	ref|Arabidopsis thaliana UDP-glucosyl transferase 73B3 (UGT73B3), mRNA [NM_119574]
-5,1	0,00000000	AT5G51070	ref|Arabidopsis thaliana Clp ATPase (ERD1), mRNA [NM_124486]
-5,11	0,00000000	AT4G34135	ref|Arabidopsis thaliana UDP-glucosyltransferase 73B2 (UGT73B2), mRNA [NM_179161]
-5,12	0,00000000	AT1G70290	ref|Arabidopsis thaliana trehalose-6-phosphatase synthase S8 (TPS8), mRNA [NM_001334443]
-5,15	0,00000000	AT3G14660	ref|Arabidopsis thaliana cytochrome P450, family 72, subfamily A, polypeptide 13 (CYP72A13), mRNA [NM_001338130]
-5,15	0,00000000	AT3G15630	ref|Arabidopsis thaliana plant/protein mRNA [NM_112433]
-5,18	0,00000000	AT5G24490	ref|Arabidopsis thaliana 30S ribosomal protein mRNA [NM_122357]
-5,19	0,00000000	AT1G69490	ref|Arabidopsis thaliana NAC-like, activated by AP3/PI (NAP), mRNA [NM_105616]
-5,21	0,00000000	AT1G18200	ref|Arabidopsis thaliana Rab GTPase-like A1I protein (RABA6b), mRNA [NM_101680]
-5,22	0,00000000	AT1G72680	ref|Arabidopsis thaliana cinnamyl-alcohol dehydrogenase (CAD1), mRNA [NM_105927]
-5,24	0,00000000	AT3G13450	ref|Arabidopsis thaliana Transketolase family protein (DIN4), mRNA [NM_112191]
-5,24	0,00000000	AT3G13750	ref|Arabidopsis thaliana beta galactosidase 1 (BGAL1), mRNA [NM_112225]
-5,25	0,00000000	AT1G60140	ref|Arabidopsis thaliana trehalose phosphate synthase (TPS10), mRNA [NM_001333882]
-5,25	0,00000000	AT3G29035	ref|Arabidopsis thaliana NAC domain containing protein 3 (NAC3), mRNA [NM_113825]
-5,28	0,00000000	AT2G45170	ref|Arabidopsis thaliana AUTOPHAGY 8E (ATG8E), mRNA [NM_180100]
-5,32	0,00000000	AT5G07100	ref|Arabidopsis thaliana WRKY DNA-binding protein 26 (WRKY26), mRNA [NM_120792]
-5,37	0,00000000	AT5G61820	ref|Arabidopsis thaliana stress up-regulated Nod 19 protein mRNA [NM_001345498]
-5,4	0,00000000	AT1G71520	ref|Arabidopsis thaliana Integrase-type DNA-binding superfamily protein mRNA [NM_105820]
-5,4	0,00000000	AT4G12735	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_202810]
-5,41	0,00000000	AT5G49450	ref|Arabidopsis thaliana basic leucine-zipper 1 (bZIP1), mRNA [NM_124322]
-5,46	0,00000000	AT1G71030	ref|Arabidopsis thaliana MYB-like 2 (MYBL2), mRNA [NM_001334485]
-5,48	0,00000000	AT2G47000	ref|Arabidopsis thaliana ATP binding cassette subfamily B4 (ABCB4), mRNA [NM_001337238]
-5,54	0,00000000	AT2G47770	ref|Arabidopsis thaliana TSPO(outer membrane tryptophan-rich sensory protein)-like protein (TSPO), mRNA [NM_130344]
-5,6	0,00000000	AT5G14730	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_121477]
-5,64	0,00000000	AT3G10120	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_111847]
-5,69	0,00000000	AT1G13990	ref|Arabidopsis thaliana plant/protein mRNA [NM_001160863]
-5,69	0,00000000	AT5G51720	ref|Arabidopsis thaliana 2 iron, 2 sulfur cluster binding protein (NEET), mRNA [NM_124551]
-5,7	0,00000000	AT5G56100	ref|Arabidopsis thaliana glycine-rich protein / oleosin mRNA [NM_124992]
-5,71	0,00000000	AT4G24230	ref|Arabidopsis thaliana acyl-CoA-binding domain 3 (ACBP3), mRNA [NM_001084972]
-5,72	0,00000000	AT5G59400	ref|Arabidopsis thaliana PGR5-like A protein mRNA [NM_180889]
-5,75	0,00000000	AT4G39675	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_120128]
-5,76	0,00000000	AT1G21400	ref|Arabidopsis thaliana Thiamin diphosphate-binding fold (THDP-binding) superfamily protein mRNA [NM_001332503]
-5,78	0,00000000	AT5G24800	ref|Arabidopsis thaliana basic leucine zipper 9 (BZIP9), mRNA [NM_122389]
-5,78	0,00000000	AT4G33666	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_119524]
-5,81	0,00000000	AT5G05410	ref|Arabidopsis thaliana DRE-binding protein 2A (DREB2A), mRNA [NM_001036760]
-5,84	0,00000000	AT2G20670	ref|Arabidopsis thaliana sugar phosphate exchanger, putative (DUF506) mRNA [NM_127631]
-5,86	0,00000000	AT1G54100	ref|Arabidopsis thaliana aldehyde dehydrogenase 7B4 (ALDH7B4), mRNA [NM_104287]
-5,86	0,00000000	TA26531_3702	Unknown
-5,89	0,00000000	AT2G15490	ref|Arabidopsis thaliana UDP-glycosyltransferase 73B4 (UGT73B4), mRNA [NM_127109]
-5,91	0,00000000	AT5G63160	ref|Arabidopsis thaliana BTB and TAZ domain protein 1 (BT1), mRNA [NM_001345581]
-5,92	0,00000000	AT2G05380	ref|Arabidopsis thaliana glycine-rich protein 3 short isoform (GRP3S), mRNA [NM_001124801]
-5,94	0,00000000	AT2G29420	ref|Arabidopsis thaliana glutathione S-transferase tau 7 (GSTU7), mRNA [NM_128496]

-5,98	0,00000000	AT5G64190	ref|Arabidopsis thaliana neuronal PAS domain protein mRNA [NM_001345621]
-6	0,00000000	AT5G51440	ref|Arabidopsis thaliana HSP20-like chaperones superfamily protein mRNA [NM_124523]
-6,1	0,00000000	AT5G41080	ref|Arabidopsis thaliana PLC-like phosphodiesterases superfamily protein (GDPD2), mRNA [NM_203136]
-6,11	0,00000000	AT1G05560	ref|Arabidopsis thaliana UDP-glucosyltransferase 75B1 (UGT75B1), mRNA [NM_100435]
-6,13	0,00000000	AT1G15040	ref|Arabidopsis thaliana Class I glutamine amidotransferase-like superfamily protein (GAT1_2.1), mRNA [NM_101374]
-6,14	0,00000000	AT2G31945	ref|Arabidopsis thaliana transmembrane protein mRNA [NM_128753]
-6,18	0,00000000	AT2G15960	ref|Arabidopsis thaliana stress-induced protein mRNA [NM_127155]
-6,19	0,00000000	AT2G37030	ref|Arabidopsis thaliana SAUR-like auxin-responsive protein family mRNA [NM_129259]
-6,2	0,00000000	AT1G02660	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_100146]
-6,22	0,00000000	AT3G57520	ref|Arabidopsis thaliana seed imbibition 2 (SIP2), mRNA [NM_180384]
-6,24	0,00000000	AT1G75750	ref|Arabidopsis thaliana GAST1 protein homolog 1 (GASA1), mRNA [NM_001198478]
-6,26	0,00000000	AT3G45300	ref|Arabidopsis thaliana isovaleryl-CoA-dehydrogenase (IVD), mRNA [NM_114399]
-6,26	0,00000000	AT1G30720	ref|Arabidopsis thaliana FAD-binding Berberine family protein mRNA [NM_102808]
-6,31	0,00000000	AT2G19800	ref|Arabidopsis thaliana myo-inositol oxygenase 2 (MIOX2), mRNA [NM_127538]
-6,39	0,00000000	AT1G42490	Unknown
-6,48	0,00000000	AT2G40000	ref|Arabidopsis thaliana ortholog of sugar beet HS1 PRO-1 2 (HSPRO2), mRNA [NM_129558]
-6,53	0,00000000	AT3G49790	ref|Arabidopsis thaliana Carbohydrate-binding protein mRNA [NM_114839]
-6,57	0,00000000	AT2G17880	ref|Arabidopsis thaliana Chaperone DnaJ-domain superfamily protein mRNA [NM_127342]
-6,62	0,00000000	AT5G07440	ref|Arabidopsis thaliana glutamate dehydrogenase 2 (GDH2), mRNA [NM_001125712]
-6,65	0,00000000	AT4G30670	ref|Arabidopsis thaliana Putative membrane lipoprotein mRNA [NM_119213]
-6,92	0,00000000	AT1G79700	ref|Arabidopsis thaliana Integrase-type DNA-binding superfamily protein (WRI4), mRNA [NM_001334913]
-6,96	0,00000000	AT2G36780	ref|Arabidopsis thaliana UDP-Glycosyltransferase superfamily protein mRNA [NM_129233]
-7,01	0,00000000	AT2G02710	ref|Arabidopsis thaliana PAS/LOV protein B (PLPB), mRNA [NM_179597]
-7,11	0,00000000	AT1G06570	ref|Arabidopsis thaliana 4-hydroxyphenylpyruvate dioxygenase (PDS1), mRNA [NM_100536]
-7,2	0,00000000	AT2G23030	ref|Arabidopsis thaliana SNF1-related protein kinase 2.9 (SNRK2.9), mRNA [NM_127867]
-7,23	0,00000000	AT2G15480	ref|Arabidopsis thaliana UDP-glucosyl transferase 73B5 (UGT73B5), mRNA [NM_127108]
-7,23	0,00000000	TA27461_3702	Unknown
-7,26	0,00000000	AT4G15760	ref|Arabidopsis thaliana monooxygenase 1 (MO1), mRNA [NM_001203809]
-7,31	0,00000000	AT4G36040	ref|Arabidopsis thaliana Chaperone DnaJ-domain superfamily protein (J11), mRNA [NM_119771]
-7,41	0,00000000	AT2G36800	ref|Arabidopsis thaliana don-glucosyltransferase 1 (DOGT1), mRNA [NM_129235]
-7,42	0,00000000	AT5G21170	ref|Arabidopsis thaliana 5'-AMP-activated protein kinase beta-2 subunit protein (AKINBETA1), mRNA [NM_001036841]
-7,45	0,00000000	AT5G66650	ref|Arabidopsis thaliana calcium uniporter (DUF607) mRNA [NM_126063]
-7,6	0,00000000	AT4G33150	ref|Arabidopsis thaliana lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme mRNA [NM_001160811]
-7,65	0,00000000	AT5G54080	ref|Arabidopsis thaliana homogentisate 1,2-dioxygenase (HGO), mRNA [NM_180856]
-7,68	0,00000000	AT5G16980	ref|Arabidopsis thaliana Zinc-binding dehydrogenase family protein mRNA [NM_121704]
-7,7	0,00000000	AT1G23870	ref|Arabidopsis thaliana trehalose-phosphatase/synthase 9 (TPS9), mRNA [NM_102235]
-7,81	0,00000000	AT4G35090	ref|Arabidopsis thaliana catalase 2 (CAT2), mRNA [NM_001342324]
-7,88	0,00000000	AT4G34710	ref|Arabidopsis thaliana arginine decarboxylase 2 (ADC2), mRNA [NM_202955]
-7,94	0,00000000	AT5G22920	ref|Arabidopsis thaliana CHY-type/CTCHY-type/RING-type Zinc finger protein mRNA [NM_122198]
-8,03	0,00000000	AT1G62510	ref|Arabidopsis thaliana Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein mRNA [NM_104930]
-8,17	0,00000000	AT1G77760	ref|Arabidopsis thaliana nitrate reductase 1 (NIA1), mRNA [NM_106425]
-8,18	0,00000000	AT1G19530	ref|Arabidopsis thaliana DNA polymerase epsilon catalytic subunit A mRNA [NM_001332396]
-8,25	0,00000000	AT1G28330	ref|Arabidopsis thaliana dormancy-associated protein-like 1 (DYL1), mRNA [NM_179390]
-8,27	0,00000000	AT2G32150	ref|Arabidopsis thaliana Haloacid dehalogenase-like hydrolase (HAD) superfamily protein mRNA [NM_001336371]
-8,45	0,00000000	AT3G14990	ref|Arabidopsis thaliana Class I glutamine amidotransferase-like superfamily protein (DJ1A), mRNA [NM_001035621]
-8,45	0,00000000	AT4G28040	ref|Arabidopsis thaliana nodulin MtN21 /EamA-like transporter family protein (UMAMIT33), mRNA [NM_118943]
-8,56	0,00000000	AT1G66180	ref|Arabidopsis thaliana Eukaryotic aspartyl protease family protein mRNA [NM_105289]
-8,58	0,00000000	AT4G14690	ref|Arabidopsis thaliana Chlorophyll A-B binding family protein (ELIP2), mRNA [NM_117551]
-8,58	0,00000000	AT5G09440	ref|Arabidopsis thaliana EXORDIUM like 4 (EXL4), mRNA [NM_120981]
-8,73	0,00000000	AT2G38400	ref|Arabidopsis thaliana alanine:glyoxylate aminotransferase 3 (AGT3), mRNA [NM_001202772]
-8,81	0,00000000	AT3G24420	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA [NM_113349]
-8,88	0,00000000	AT2G23150	ref|Arabidopsis thaliana natural resistance-associated macrophage protein 3 (NRAMP3), mRNA [NM_127879]
-9,15	0,00000000	AT5G54585	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_148130]
-9,25	0,00000000	AT1G76680	ref|Arabidopsis thaliana 12-oxophytodienoate reductase 1 (OPR1), mRNA [NM_202428]
-9,26	0,00000000	AT4G36850	ref|Arabidopsis thaliana PQ-loop repeat family protein / transmembrane family protein mRNA [NM_001342421]
-9,31	0,00000000	AT1G07400	ref|Arabidopsis thaliana HSP20-like chaperones superfamily protein mRNA [NM_100614]
-9,32	0,00000000	TA30874_3702	Unknown
-9,33	0,00000000	AT3G44300	ref|Arabidopsis thaliana nitrilase 2 (NIT2), mRNA [NM_114298]
-9,44	0,00000000	AT5G64260	ref|Arabidopsis thaliana EXORDIUM like 2 (EXL2), mRNA [NM_125822]
-9,74	0,00000000	AT5G66400	ref|Arabidopsis thaliana Dehydrin family protein (RAB18), mRNA [NM_126038]

-9,77	0,00000000	AT3G61060	ref|Arabidopsis thaliana phloem protein 2-A13 (PP2-A13), mRNA [NM_202741]
-10,34	0,00000000	AT1G03090	ref|Arabidopsis thaliana methylcrotonyl-CoA carboxylase alpha chain (MCCA), mRNA [NM_179252]
-10,73	0,00000000	AT4G16690	ref|Arabidopsis thaliana methyl esterase 16 (MES16), mRNA [NM_117770]
-10,84	0,00000000	TC309308	tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vinifera (Grape), partial (29%) [TC396119]
-11,55	0,00000000	AT2G41380	ref|Arabidopsis thaliana S-adenosyl-L-methionine-dependent methyltransferases superfamily protein mRNA [NM_129701]
-12,28	0,00000000	AT1G66760	ref|Arabidopsis thaliana MATE efflux family protein mRNA [NM_179523]
-12,31	0,00000000	AT1G22500	ref|Arabidopsis thaliana RING/U-box superfamily protein (ATL15), mRNA [NM_102099]
-12,51	0,00000000	AT2G29490	ref|Arabidopsis thaliana glutathione S-transferase TAU 1 (GSTU1), mRNA [NM_128503]
-12,52	0,00000000	AT4G25580	ref|Arabidopsis thaliana CAP160 protein mRNA [NM_001341752]
-12,58	0,00000000	AT1G17170	ref|Arabidopsis thaliana glutathione S-transferase TAU 24 (GSTU24), mRNA [NM_101578]
-12,64	0,00000000	AT1G02610	ref|Arabidopsis thaliana RING/FYVE/PHD zinc finger superfamily protein mRNA [NM_001331347]
-13,3	0,00000000	AT5G20250	ref|Arabidopsis thaliana Raffinose synthase family protein (DIN10), mRNA [NM_001036833]
-13,3	0,00000000	AT3G60140	ref|Arabidopsis thaliana Glycosyl hydrolase superfamily protein (DIN2), mRNA [NM_001340024]
-13,62	0,00000000	TA29020_3702	Unknown
-13,64	0,00000000	AT3G49160	ref|Arabidopsis thaliana pyruvate kinase family protein mRNA [NM_001339402]
-13,65	0,00000000	AT5G14470	ref|Arabidopsis thaliana GHMP kinase family protein mRNA [NM_121451]
-14,27	0,00000000	AT1G80920	ref|Arabidopsis thaliana Chaperone DnaJ-domain superfamily protein (J8), mRNA [NM_106740]
-14,78	0,00000000	AT1G11260	ref|Arabidopsis thaliana sugar transporter 1 (STP1), mRNA [NM_100998]
-14,84	0,00000000	AT5G02020	ref|Arabidopsis thaliana E3 ubiquitin-protein ligase RLIM-like protein (SIS), mRNA [NM_180421]
-15,04	0,00000000	AT3G30775	ref|Arabidopsis thaliana Methylenetetrahydrofolate reductase family protein (ERD5), mRNA [NM_113981]
-15,3	0,00000000	AT3G04000	ref|Arabidopsis thaliana NAD(P)-binding Rossmann-fold superfamily protein mRNA [NM_111271]
-15,36	0,00000000	AT5G56870	ref|Arabidopsis thaliana beta-galactosidase 4 (BGAL4), mRNA [NM_125070]
-15,73	0,00000000	AT4G15610	ref|Arabidopsis thaliana Uncharacterized protein family (UPF0497) mRNA [NM_001341066]
-15,78	0,00000000	AT2G33830	ref|Arabidopsis thaliana Dormancy/auxin associated family protein mRNA [NM_001336474]
-16,41	0,00000000	AT5G06860	ref|Arabidopsis thaliana polygalacturonase inhibiting protein 1 (PGIP1), mRNA [NM_120769]
-16,93	0,00000000	AT5G14180	ref|Arabidopsis thaliana Myzus persicae-induced lipase 1 (MPL1), mRNA [NM_001343319]
-17,15	0,00000000	AT1G09500	ref|Arabidopsis thaliana NAD(P)-binding Rossmann-fold superfamily protein mRNA [NM_100821]
-17,43	0,00000000	AT5G39580	ref|Arabidopsis thaliana Peroxidase superfamily protein mRNA [NM_001036908]
-18,57	0,00000000	AT2G47270	ref|Arabidopsis thaliana transcription factor UPBEAT protein (UPB1), mRNA [NM_130295]
-18,87	0,00000000	AT3G45730	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_114442]
-19,42	0,00000000	AT1G08630	ref|Arabidopsis thaliana threonine aldolase 1 (THA1), mRNA [NM_100736]
-20,29	0,00000000	TC304561	tc|Rep: Xylosidase - Arabidopsis thaliana (Mouse-ear cress), complete [TC384346]
-20,75	0,00000000	AT5G39520	ref|Arabidopsis thaliana hypothetical protein (DUF1997) mRNA [NM_123314]
-20,83	0,00000000	AT2G18700	ref|Arabidopsis thaliana trehalose phosphatase/synthase 11 (TPS11), mRNA [NM_127426]
-20,87	0,00000000	AT2G18193	ref|Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA [NM_179641]
-22,64	0,00000000	AT1G10070	ref|Arabidopsis thaliana branched-chain amino acid transaminase 2 (BCAT-2), mRNA [NM_001035939]
-23,72	0,00000000	AT1G65970	ref|Arabidopsis thaliana thioredoxin-dependent peroxidase 2 (TPX2), mRNA [NM_105269]
-23,82	0,00000000	AT4G27450	ref|Arabidopsis thaliana aluminum induced protein with YGL and LRDR motifs mRNA [NM_118880]
-24,27	0,00000000	AT4G08555	ref|Arabidopsis thaliana hypothetical protein mRNA [NM_179014]
-25,61	0,00000000	BP667596	tc|Rep: Uncharacterized protein At4g35770.3 - Arabidopsis thaliana (Mouse-ear cress), partial (53%) [TC406344]
-27,03	0,00000000	BP660593	Unknown
-27,88	0,00000000	AT1G80160	ref|Arabidopsis thaliana Lactoylglutathione lyase / glyoxalase I family protein (GLYI7), mRNA [NM_001084382]
-28,03	0,00000000	TA25819_3702	Unknown
-30,14	0,00000000	AT4G01870	ref|Arabidopsis thaliana tolB protein-like protein mRNA [NM_001340340]
-30,24	0,00000000	TA29937_3702	Unknown
-30,35	0,00000000	BE039144	tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vinifera (Grape), partial (59%) [TC393828]
-30,57	0,00000000	AT3G15450	ref|Arabidopsis thaliana aluminum induced protein with YGL and LRDR motifs mRNA [NM_001035625]
-31,15	0,00000000	AT2G34430	ref|Arabidopsis thaliana light-harvesting chlorophyll-protein complex II subunit B1 (LHB1B1), mRNA [NM_128995]
-33,28	0,00000000	AT4G30270	ref|Arabidopsis thaliana xyloglucan endotransglucosylase/hydrolase 24 (XTH24), mRNA [NM_119173]
-35,27	0,00000000	AT1G15380	ref|Arabidopsis thaliana Lactoylglutathione lyase / glyoxalase I family protein (GLYI4), mRNA [NM_001035972]
-35,53	0,00000000	AT1G05680	ref|Arabidopsis thaliana Uridine diphosphate glycosyltransferase 74E2 (UGT74E2), mRNA [NM_100448]
-41,86	0,00000000	TA29646_3702	gb|Arabidopsis thaliana AT4G35770 mRNA, complete cds, clone: RAFL24-21-O03 [AK319042]
-45,78	0,00000000	AT3G28740	ref|Arabidopsis thaliana Cytochrome P450 superfamily protein (CYP81D11), mRNA [NM_113795]
-48,13	0,00000000	AT5G01600	ref|Arabidopsis thaliana ferretin 1 (FER1), mRNA [NM_120238]
-55,33	0,00000000	AT5G49360	ref|Arabidopsis thaliana beta-xylosidase 1 (BXL1), mRNA [NM_124313]
-75,94	0,00000000	AT1G73120	ref|Arabidopsis thaliana F-box/RNI superfamily protein mRNA [NM_105970]
-81,95	0,00000000	AT3G20340	ref|Arabidopsis thaliana protein expression protein mRNA [NM_112925]
-107,47	0,00000000	AT3G47340	ref|Arabidopsis thaliana glutamine-dependent asparagine synthase 1 (ASN1), mRNA [NM_180333]
-305,4	0,00000000	AT4G35770	ref|Arabidopsis thaliana Rhodanese/Cell cycle control phosphatase superfamily protein (SEN1), mRNA [NM_001085028]
-336,01	0,00000000	TA29648_3702	Unknown

Table S3: List of genes classified by functional categories whose expression is altered by super-elevated CO2 treatment. Genes that are differentially regulated by A. alternata VCs (cf. Supplemental Table 3 in Sánchez-López, Baslam, et al., 2016) are highlighted in yelow color (BY FUNCTIONAL CATEGORIE

Function	Fold Change	pval (LiMMA)	ID	ProbeID	Description
Photosynthesis					
	-3,36	0.00000000	AT5G61410	RPE	ref|Arabidopsis thaliana D-ribulose-5-phosphate-3-epimerase mRNA, complete cds [NM_125534]
	-3,87	0.00000040	AT2G34430	LHB1B1	ref|Arabidopsis thaliana light-harvesting chlorophyll protein complex II subunit B1 mRNA, complete cds [NM_128995]
	-4,44	0.00000000	AT4G26530	AT4G26530	ref|Arabidopsis thaliana fructose-bisphosphate aldolase 5 mRNA, complete cds [NM_001036644]
Major CHO metabolism					
	9,17	0.00000000	AT4G15210	BAM5	ref|Arabidopsis thaliana beta-amylase 5 mRNA, complete cds [NM_117609]
	8,95	0.00000000	AT4G39210	APL3	ref|Arabidopsis thaliana glucose-1-phosphate adenylyltransferase large subunit 3 mRNA, complete cds [NM_120081]
	4,52	0.00000017	AT1G32900	AT1G32900	ref|Arabidopsis thaliana granule-bound starch synthase 1 mRNA, complete cds [NM_103023]
	-3,07	0.00000000	AT5G18670	BMY3	ref|Arabidopsis thaliana putative beta-amylase BMY3 mRNA, complete cds [NM_121872]
	-4,25	0.00000000	AT3G06500	AT3G06500	ref|Arabidopsis thaliana protein alkaline/neutral invertase C mRNA, complete cds [NM_111526]
Minor CHO metabolism					
	-3,12	0.00000000	AT2G37760	AT2G37760	ref|Arabidopsis thaliana aldo-keto reductase family 4 member C8 mRNA, complete cds [NM_201898]
	-3,47	0.00000000	AT5G51970	AT5G51970	ref|Arabidopsis thaliana putative sorbitol dehydrogenase mRNA, complete cds [NM_124576]
	-3,51	0.00000000	AT4G18010	5PTASE2	ref|Arabidopsis thaliana Type I inositol-1,4,5-trisphosphate 5-phosphatase 2 mRNA, complete cds [NM_179071]
	-4,09	0.00000000	AT2G47180	GolS1	ref|Arabidopsis thaliana galactinol synthase 1 mRNA, complete cds [NM_130286]
	-4,56	0.00000000	AT5G57655	AT5G57655	ref|Arabidopsis thaliana xylose isomerase mRNA, complete cds [NM_180872]
	-5,14	0.00000000	AT1G70290	TPS8	ref|Arabidopsis thaliana putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 8 mRNA, complete cds [NM_105697]
	-5,31	0.00000000	AT1G60140	TPS10	ref|Arabidopsis thaliana putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10 mRNA, complete cds [NM_104705]
	-5,75	0.00000000	AT2G37770	AT2G37770	ref|Arabidopsis thaliana aldo-keto reductase family 4 member C9 mRNA, complete cds [NM_001036428]
	-7,14	0.00000000	AT1G23870	TPS9	ref|Arabidopsis thaliana putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9 mRNA, complete cds [NM_102235]
	-10,72	0.00000000	AT5G20250	DIN10	ref|Arabidopsis thaliana putative galactinol--sucrose galactosyltransferase 6 mRNA, complete cds [NM_001036833]
	-16,16	0.00000000	AT2G18700	TPS11	ref|Arabidopsis thaliana putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 11 mRNA, complete cds [NM_127426]
Glycolysis					
	3,25	0.00000000	AT1G79530	GAPCP-1	ref|Arabidopsis thaliana glyceraldehyde-3-phosphate dehydrogenase GAPCP1 mRNA, complete cds [NM_106601]
	-3,41	0.00000095	AT3G49160	AT3G49160	ref|Arabidopsis thaliana pyruvate kinase-like protein mRNA, complete cds [NM_114775]
Fermentation					
	-5,55	0.00000000	AT1G54100	ALDH7B4	ref|Arabidopsis thaliana aldehyde dehydrogenase 7B4 mRNA, complete cds [NM_104287]
OPP					
	-3,48	0.00000000	AT1G13700	PGL1	ref|Arabidopsis thaliana 6-phosphogluconolactonase 1 mRNA, complete cds [NM_101239]
TCA / Organic transformation					
	4,36	0.00000000	AT5G50950	FUM2	ref|Arabidopsis thaliana fumarate hydratase 2 mRNA, complete cds [NM_124474]
	-3,12	0.00000012	AT1G58180	BCA6	ref|Arabidopsis thaliana beta carbonic anhydrase 6 mRNA, complete cds [NM_179492]
	-3,17	0.00000000	AT5G14740	CA2	ref|Arabidopsis thaliana carbonic anhydrase 2 mRNA, complete cds [NM_001036806]
	-3,31	0.00000000	AT3G01500	CA1	ref|Arabidopsis thaliana carbonic anhydrase 1 mRNA, complete cds [NM_111016]
Mitochondrial electron transport					
	5,15	0.00000000	AT5G60730	AT5G60730	ref|Arabidopsis thaliana Anion-transporting ATPase mRNA, complete cds [NM_125466]
	-3,14	0.00000006	AT3G22370	AOX1A	ref|Arabidopsis thaliana alternative oxidase 1A mRNA, complete cds [NM_113135]
Cell wall					
	4,82	0.00000011	AT4G16590	CSLA01	ref|Arabidopsis thaliana cellulose synthase-like A01 mRNA, complete cds [NM_117760]
	4,29	0.00000000	AT4G02330	ATPMEPCRB	ref|Arabidopsis thaliana Probable pectinesterase/pectinesterase inhibitor 41 mRNA, complete cds [NM_116466]
	3,83	0.00000000	AT4G12730	FLA2	ref|Arabidopsis thaliana fasciclin-like arabinogalactan protein 2 mRNA, complete cds [NM_117342]
	3,77	0.00000000	AT1G11545	XTH8	ref|Arabidopsis thaliana probable xyloglucan endotransglucosylase/hydrolase protein 8 mRNA, complete cds [NM_101028]
	3,58	0.00000000	AT2G26440	AT2G26440	ref|Arabidopsis thaliana Probable pectinesterase/pectinesterase inhibitor 12 mRNA, complete cds [NM_128201]
	3,56	0.00000000	AT3G52370	FLA15	ref|Arabidopsis thaliana fasciclin-like arabinogalactan protein 15 mRNA, complete cds [NM_115097]
	3,5	0.00000000	AT4G28250	EXPB3	ref|Arabidopsis thaliana expansin B3 mRNA, complete cds [NM_118965]
	3,16	0.00000000	AT1G41830	SKS6	ref|Arabidopsis thaliana SKU5 similar 6 mRNA, complete cds [NM_103408]
	3,15	0.00000000	AT1G19940	GH9B5	ref|Arabidopsis thaliana glycosyl hydrolase 9B5 mRNA, complete cds [NM_101849]
	3,12	0.00000000	AT1G24070	CSLA10	ref|Arabidopsis thaliana cellulose synthase-like A10 mRNA, complete cds [NM_102254]
	-3,17	0.00000000	AT2G28110	FRA8	ref|Arabidopsis thaliana probable glucuronoxylan glucuronosyltransferase IRX7 mRNA, complete cds [NM_179782]
	-3,17	0.00000000	AT1G58370	RXF12	ref|Arabidopsis thaliana xylanase 1 mRNA, complete cds [NM_104617]
	-3,41	0.00000000	AT5G57560	TCH4	ref|Arabidopsis thaliana xyloglucan endotransglucosylase/hydrolase protein 22 mRNA, complete cds [NM_125137]
	-3,43	0.00000001	AT1G12780	UGE1	ref|Arabidopsis thaliana bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 1 mRNA, complete cds [NM_101148]

	-3,61	0.00000000	AT1G69530	EXPA1	ref|Arabidopsis thaliana expansin A1 mRNA, complete cds [NM_001124101]
	-3,77	0.00000000	AT5G64570	XYL4	ref|Arabidopsis thaliana beta-D-xylosidase 4 mRNA, complete cds [NM_125853]
	-4,67	0.00000000	AT1G63180	UGE3	ref|Arabidopsis thaliana UDP-glucose 4-epimerase mRNA, complete cds [NM_104996]
	-4,75	0.00000000	AT3G10740	ASD1	ref|Arabidopsis thaliana bifunctional alpha-l-arabinofuranosidase/beta-d-xylosidase mRNA, complete cds [NM_111911]
	-5,71	0.00000000	AT4G30270	XTH24	ref|Arabidopsis thaliana xyloglucan endotransglucosylase/hydrolase protein 24 mRNA, complete cds [NM_119173]
	-5,89	0.00000000	AT5G06860	PGIP1	ref|Arabidopsis thaliana polygalacturonase inhibitor 1 mRNA, complete cds [NM_120769]
	-19,16	0.00000000	AT5G14470	AT5G14470	ref|Arabidopsis thaliana GHMP kinase family protein mRNA, complete cds [NM_121451]
	-41,68	0.00000000	AT5G49360	BXL1	ref|Arabidopsis thaliana bifunctional {beta}-D-xylosidase/{alpha}-L-arabinofuranosidase mRNA, complete cds [NM_124313]
Lipid metabolism					
	7,69	0.00000000	AT3G18000	CPuORF30	ref|Arabidopsis thaliana conserved peptide upstream open reading frame 30 mRNA, complete cds [NM_001125181]
	6,62	0.00000000	AT4G17470	AT4G17470	ref|Arabidopsis thaliana putative palmitoyl-protein thioesterase mRNA, complete cds [NM_001203824]
	3,76	0.00000000	AT1G73600	CPuORF32	ref|Arabidopsis thaliana conserved peptide upstream open reading frame 32 mRNA, complete cds [NM_001124125]
	3,2	0.00000000	AT1G45201	TLL1	ref|Arabidopsis thaliana triacylglycerol lipase-like 1 mRNA, complete cds [NM_179441]
	3,12	0.00000000	AT2G11810	MGDC	ref|Arabidopsis thaliana Monogalactosyldiacylglycerol synthase 3 mRNA, complete cds [NM_001124829]
	-3,23	0.00000000	AT5G18630	AT5G18630	ref|Arabidopsis thaliana putative class 3 lipase mRNA, complete cds [NM_121868]
	-3,34	0.00000000	AT1G73920	AT1G73920	ref|Arabidopsis thaliana alpha/beta-hydrolase domain-containing protein mRNA, complete cds [NM_179552]
	-3,62	0.00000000	AT4G24230	ACBP3	ref|Arabidopsis thaliana acyl-CoA-binding domain 3 mRNA, complete cds [NM_001084972]
	-3,66	0.00000000	AT5G65110	ACX2	ref|Arabidopsis thaliana acyl-coenzyme A oxidase 2 mRNA, complete cds [NM_001037068]
	-3,68	0.00000009	AT1G64720	CP5	ref|Arabidopsis thaliana membrane related protein CP5 mRNA, complete cds [NM_105147]
	-3,85	0.00000000	AT5G59310	LTP4	ref|Arabidopsis thaliana non-specific lipid-transfer protein 4 mRNA, complete cds [NM_125322]
	-4,16	0.00000000	AT3G48990	AT3G48990	ref|Arabidopsis thaliana 4-coumarate--CoA ligase-like 10 mRNA, complete cds [NM_114758]
	-4,49	0.00000000	AT5G56100	AT5G56100	ref|Arabidopsis thaliana glycine-rich protein / oleosin mRNA, complete cds [NM_124992]
	-4,85	0.00000000	AT2G39400	AT2G39400	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA, complete cds [NM_129497]
	-17,51	0.00000000	AT5G14180	MPL1	ref|Arabidopsis thaliana Myzus persicae-induced lipase 1 mRNA, complete cds [NM_121422]
N-metabolism					
	-4,25	0.00000000	AT5G07440	GDH2	ref|Arabidopsis thaliana glutamate dehydrogenase 2 mRNA, complete cds [NM_001125712]
	-4,87	0.00000000	AT1G37130	NIA2	ref|Arabidopsis thaliana nitrate reductase [NADH] 2 mRNA, complete cds [NM_103364]
	-9,32	0.00000000	AT1G77760	NIA1	ref|Arabidopsis thaliana nitrate reductase [NADH] 1 mRNA, complete cds [NM_106425]
Amino acid metabolism					
	6,89	0.00000000	AT4G23600	CORI3	ref|Arabidopsis thaliana cystine lyase CORI3 mRNA, complete cds [NM_179099]
	5,44	0.00000000	AT3G03780	MS2	ref|Arabidopsis thaliana methionine synthase 2 mRNA, complete cds [NM_111249]
	4,93	0.00000000	AT5G14200	IMD1	ref|Arabidopsis thaliana isopropylmalate dehydrogenase 1 mRNA, complete cds [NM_001036803]
	-3,07	0.00000000	AT3G13450	DIN4	ref|Arabidopsis thaliana branched chain alpha-keto acid dehydrogenase E1 beta mRNA, complete cds [NM_112191]
	-3,09	0.00000000	AT2G38400	AGT3	ref|Arabidopsis thaliana alanine:glyoxylate aminotransferase 3 mRNA, complete cds [NM_001202772]
	-3,24	0.00000000	AT3G30775	ERD5	ref|Arabidopsis thaliana proline dehydrogenase 1 mRNA, complete cds [NM_113981]
	-3,33	0.00000000	AT1G21400	AT1G21400	ref|Arabidopsis thaliana thiamin diphosphate-binding fold protein mRNA, complete cds [NM_101992]
	-3,66	0.00000000	AT1G23310	GGT1	ref|Arabidopsis thaliana glutamate:glyoxylate aminotransferase mRNA, complete cds [NM_001036006]
	-3,89	0.00000000	AT4G33150	AT4G33150	ref|Arabidopsis thaliana lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme mRNA, complete cds [NM_001160811]
	-4,17	0.00000000	AT5G53970	AT5G53970	ref|Arabidopsis thaliana tyrosine aminotransferase mRNA, complete cds [NM_124776]
	-4,45	0.00000000	AT3G22460	OASA2	ref|Arabidopsis thaliana O-acetylserine (thiol) lyase (OAS-TL) isoform A2 mRNA, complete cds [NM_113145]
	-5,09	0.00000000	AT5G54080	HGO	ref|Arabidopsis thaliana homogentisate 1,2-dioxygenase mRNA, complete cds [NM_180856]
	-5,49	0.00000000	AT1G10070	BCAT-2	ref|Arabidopsis thaliana branched-chain-amino-acid aminotransferase 2 mRNA, complete cds [NM_001035939]
	-5,67	0.00000000	AT1G03090	MCCA	ref|Arabidopsis thaliana methylcrotonoyl-CoA carboxylase subunit alpha mRNA, complete cds [NM_179252]
	-7,86	0.00000000	AT1G08630	THA1	ref|Arabidopsis thaliana threonine aldolase mRNA, complete cds [NM_100736]
	-8,03	0.00000000	AT3G45300	IVD	ref|Arabidopsis thaliana isovaleryl-CoA-dehydrogenase mRNA, complete cds [NM_114399]
	-48,66	0.00000000	AT3G47340	ASN1	ref|Arabidopsis thaliana asparagine synthetase [glutamine-hydrolyzing] mRNA, complete cds [NM_180333]
S-assimilation					
	4,17	0.00000000	AT4G39940	AKN2	ref|Arabidopsis thaliana adenosine-5'-phosphosulfate-kinase 2 mRNA, complete cds [NM_120157]
Metal handling					
	4,41	0.00000000	AT1G56430	NAS4	ref|Arabidopsis thaliana nicotianamine synthase 4 mRNA, complete cds [NM_104521]
	3,64	0.00000000	AT1G01580	FRO2	ref|Arabidopsis thaliana ferric reduction oxidase 2 mRNA, complete cds [NM_100040]
	3,06	0.00000000	AT1G23020	FRO3	ref|Arabidopsis thaliana ferric reduction oxidase 3 mRNA, complete cds [NM_102150]
	-4,1	0.00000000	AT1G55920	SERAT2;1	ref|Arabidopsis thaliana serine acetyltransferase 1 mRNA, complete cds [NM_104470]
	-4,4	0.00000000	AT5G49740	FRO7	ref|Arabidopsis thaliana ferric reduction oxidase 7 mRNA, complete cds [NM_124352]
	-4,46	0.00000000	AT5G49730	FRO6	ref|Arabidopsis thaliana ferric reduction oxidase 6 mRNA, complete cds [NM_124351]
	-25,49	0.00000000	AT5G01600	FER1	ref|Arabidopsis thaliana ferretin 1 mRNA, complete cds [NM_120238]
Secondary metabolism					
	9,88	0.00000000	AT4G22870	AT4G22870	ref|Arabidopsis thaliana leucoanthocyanidin dioxygenase-like protein mRNA, complete cds [NM_001160794]

	9,73	0.00000000	AT1G56650	PAP1	ref|Arabidopsis thaliana transcription factor MYB75 mRNA, complete cds [NM_104541]
	7,66	0.00000000	AT5G54060	UF3GT	ref|Arabidopsis thaliana anthocyanidin 3-O-glucoside 2'''-O-xylosyltransferase mRNA, complete cds [NM_124785]
	7,25	0.00000000	AT5G42800	DFR	ref|Arabidopsis thaliana dihydroflavonol-4-reductase mRNA, complete cds [NM_123645]
	5,85	0.00000000	AT4G22880	LDOX	ref|Arabidopsis thaliana leucoanthocyanidin dioxygenase mRNA, complete cds [NM_118417]
	5,33	0.00000000	AT1G62560	FMO GS-OX3	ref|Arabidopsis thaliana flavin-containing monooxygenase FMO GS-OX3 mRNA, complete cds [NM_104934]
	5,05	0.00000000	AT4G03060	AF418241	gb|Arabidopsis thaliana Col-0 2-oxoglutarate-dependent dioxygenase (AOP2) pseudogene, mRNA sequence [AF418241]
	4,46	0.00000000	AT3G58990	IPMI1	ref|Arabidopsis thaliana isopropylmalate isomerase 1 mRNA, complete cds [NM_115761]
	4,37	0.00000000	AT2G43100	IPMI2	ref|Arabidopsis thaliana isopropylmalate isomerase 2 mRNA, complete cds [NM_129871]
	4,24	0.00000000	AT1G16410	CYP79F1	ref|Arabidopsis thaliana dihomomethionine N-hydroxylase mRNA, complete cds [NM_101507]
	4,18	0.00000000	AT5G13930	TT4	ref|Arabidopsis thaliana chalcone synthase mRNA, complete cds [NM_121396]
	4,06	0.00000000	AT1G06000	AT1G06000	ref|Arabidopsis thaliana flavonol-7-O-rhamnosyltransferase mRNA, complete cds [NM_100480]
	3,9	0.00000000	AT5G23020	IMS2	ref|Arabidopsis thaliana methylthioalkylmalate synthase 3 mRNA, complete cds [NM_122208]
	3,8	0.00000000	AT5G08640	FLS1	ref|Arabidopsis thaliana flavonol synthase 1 mRNA, complete cds [NM_001203337]
	3,76	0.00000000	AT1G18590	SOT17	ref|Arabidopsis thaliana sulfotransferase 17 mRNA, complete cds [NM_101717]
	3,71	0.00000000	AT1G65860	FMO GS-OX1	ref|Arabidopsis thaliana flavin-containing monooxygenase FMO GS-OX1 mRNA, complete cds [NM_105258]
	3,58	0.00000030	AT3G29590	AT5MAT	ref|Arabidopsis thaliana malonyl-CoA:anthocyanidin 5-O-glucoside-6-O-malonyltransferase mRNA, complete cds [NM_113880]
	3,57	0.00000000	AT3G51240	F3H	ref|Arabidopsis thaliana flavanone 3-hydroxylase mRNA, complete cds [NM_114983]
	3,53	0.00000000	AT4G12030	BAT5	ref|Arabidopsis thaliana probable sodium/metabolite cotransporter BASS5 mRNA, complete cds [NM_117273]
	3,45	0.00000000	AT1G54040	ESP	ref|Arabidopsis thaliana epithiospecifier protein mRNA, complete cds [NM_180632]
	3,33	0.00000009	AT1G52040	MBP1	ref|Arabidopsis thaliana myrosinase-binding protein 1 mRNA, complete cds [NM_104085]
	3,32	0.00000000	AT4G39950	CYP79B2	ref|Arabidopsis thaliana tryptophan N-monooxygenase 1 mRNA, complete cds [NM_120158]
	3,28	0.00000000	AT1G76790	AT1G76790	ref|Arabidopsis thaliana indole glucosinolate o-methyltransferase 5 mRNA, complete cds [NM_106329]
	3,23	0.00000002	AT5G05270	AT5G05270	ref|Arabidopsis thaliana Chalcone-flavanone isomerase family protein mRNA, complete cds [NM_180439]
	3,15	0.00000007	AT1G03495	AT1G03495	ref|Arabidopsis thaliana coumaroyl-CoA:anthocyanidin 3-O-glucoside-6-O-coumaroyltransferase 2 mRNA, complete cds [NM_100232]
	3,04	0.00000000	AT1G30530	UGT78D1	ref|Arabidopsis thaliana UDP-glucosyl transferase 78D1 mRNA, complete cds [NM_102790]
	-3,07	0.00000001	AT3G09580	AT3G09580	ref|Arabidopsis thaliana FAD/NAD(P)-binding oxidoreductase family protein mRNA, complete cds [NM_111792]
	-3,17	0.00000000	AT4G35420	DRL1	ref|Arabidopsis thaliana dihydroflavonol 4-reductase-like1 mRNA, complete cds [NM_119708]
	-3,2	0.00000000	AT2G39980	AT2G39980	ref|Arabidopsis thaliana HXXXD-type acyl-transferase-like protein mRNA, complete cds [NM_129556]
	-3,55	0.00000000	AT5G39080	AT5G39080	ref|Arabidopsis thaliana HXXXD-type acyl-transferase-like protein mRNA, complete cds [NM_123270]
	-3,57	0.00000000	AT3G44300	NIT2	ref|Arabidopsis thaliana nitrilase 2 mRNA, complete cds [NM_114298]
	-4,85	0.00000000	AT5G48180	NSP5	ref|Arabidopsis thaliana nitrile specifier protein 5 mRNA, complete cds [NM_124193]
	-5,14	0.00000000	AT1G72680	CAD1	ref|Arabidopsis thaliana cinnamyl-alcohol dehydrogenase mRNA, complete cds [NM_105927]
	-5,2	0.00000000	AT5G39050	AT5G39050	ref|Arabidopsis thaliana phenolic glucoside malonyltransferase 1 mRNA, complete cds [NM_123267]
	-5,86	0.00000000	AT1G06570	PDS1	ref|Arabidopsis thaliana 4-hydroxyphenylpyruvate dioxygenase mRNA, complete cds [NM_100536]
	-6,7	0.00000000	AT4G34135	UGT73B2	ref|Arabidopsis thaliana UDP-glucosyltransferase 73B2 mRNA, complete cds [NM_179161]
	-7,66	0.00000002	AT5G52570	BETA-OHASE 2	ref|Arabidopsis thaliana beta-carotene hydroxylase 2 mRNA, complete cds [NM_124636]
Hormone metabolism					
	5,41	0.00000000	AT3G45140	LOX2	ref|Arabidopsis thaliana lipoxygenase 2 mRNA, complete cds [NM_114383]
	4,51	0.00000000	AT5G15960	KIN1	ref|Arabidopsis thaliana cold and ABA inducible protein kin1 mRNA, complete cds [NM_121601]
	3,59	0.00000000	AT1G19640	JMT	ref|Arabidopsis thaliana jasmonic acid carboxyl methyltransferase mRNA, complete cds [NM_101820]
	3,28	0.00000000	AT5G11740	AGP15	ref|Arabidopsis thaliana arabinogalactan protein 15 mRNA, complete cds [NM_121212]
	3,18	0.00000000	AT1G56150	AT1G56150	ref|Arabidopsis thaliana SAUR-like auxin-responsive protein mRNA, complete cds [NM_104494]
	3,15	0.00000000	AT2G31230	ERF15	ref|Arabidopsis thaliana ethylene-responsive transcription factor 15 mRNA, complete cds [NM_179831]
	-3,07	0.00000000	AT5G13370	AT5G13370	ref|Arabidopsis thaliana auxin-responsive GH3 family protein mRNA, complete cds [NM_121340]
	-3,08	0.00000000	AT1G62380	ACO2	ref|Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate oxidase 2 mRNA, complete cds [NM_104918]
	-3,26	0.00000000	AT1G76690	OPR2	ref|Arabidopsis thaliana 12-oxophytodienoate reductase 2 mRNA, complete cds [NM_106319]
	-3,35	0.00000000	AT2G03760	SOT12	ref|Arabidopsis thaliana sulphotransferase 12 mRNA, complete cds [NM_126423]
	-3,45	0.00000001	AT3G11930	AT3G11930	ref|Arabidopsis thaliana universal stress protein-like protein mRNA, complete cds [NM_180231]
	-3,46	0.00000000	AT1G52100	AT1G52100	ref|Arabidopsis thaliana jacalin-like lectin domain-containing protein mRNA, complete cds [NM_001198273]
	-3,71	0.00000000	AT5G43450	AT5G43450	ref|Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate oxidase-like protein mRNA, complete cds [NM_123711]
	-4,04	0.00000000	AT1G18020	AT1G18020	ref|Arabidopsis thaliana putative 12-oxophytodienoate reductase-like protein 2B mRNA, complete cds [NM_179352]
	-5,4	0.00000000	AT1G22400	UGT85A1	ref|Arabidopsis thaliana UDP-glycosyltransferase 85A1 mRNA, complete cds [NM_102089]
	-6,02	0.00000000	AT2G43820	UGT74F2	ref|Arabidopsis thaliana UDP-glucosyltransferase 74F2 mRNA, complete cds [NM_129944]
	-6,05	0.00000000	AT2G47770	TSPO	ref|Arabidopsis thaliana tryptophan-rich sensory protein-like protein mRNA, complete cds [NM_130344]
	-7,98	0.00000015	AT2G36750	UGT73C1	ref|Arabidopsis thaliana UDP-glucosyl transferase 73C1 mRNA, complete cds [NM_129230]
	-8,75	0.00000000	AT1G05560	UGT75B1	ref|Arabidopsis thaliana UDP-glucosyltransferase 75B1 mRNA, complete cds [NM_100435]
	-10,8	0.00000000	AT1G76680	OPR1	ref|Arabidopsis thaliana 12-oxophytodienoate reductase 1 mRNA, complete cds [NM_106318]
	-15,89	0.00000000	AT4G27450	AT4G27450	ref|Arabidopsis thaliana aluminum induced protein with YGL and LRDR motifs mRNA, complete cds [NM_118880]
	-16,14	0.00000000	AT2G33830	AT2G33830	ref|Arabidopsis thaliana dormancy/auxin associated protein mRNA, complete cds [NM_179889]
	-41,4	0.00000000	AT3G15450	AT3G15450	ref|Arabidopsis thaliana aluminum induced protein with YGL and LRDR motif mRNA, complete cds [NM_001035625]
	-41,54	0.00000000	AT1G05680	UGT74E2	ref|Arabidopsis thaliana Uridine diphosphate glycosyltransferase 74E2 mRNA, complete cds [NM_100448]
Co-factor and vitamine metabolism					

	-3,15	0.00000000	AT1G67810	SUFE2	ref|Arabidopsis thaliana sulfur E2 mRNA, complete cds [NM_105449]
	-6,73	0.00000000	AT3G14990	AT3G14990	ref|Arabidopsis thaliana protein DJ-1-like A mRNA, complete cds [NM_001035621]
Stress					
	8,19	0.00000000	AT3G22231	PCC1	ref|Arabidopsis thaliana protein PATHOGEN AND CIRCADIAN CONTROLLED 1 mRNA, complete cds [NM_113121]
	5,99	0.00000000	AT2G42540	COR15A	ref|Arabidopsis thaliana cold-regulated protein 15a mRNA, complete cds [NM_001202804]
	5,73	0.00000185	AT1G73325	AT1G73325	ref|Arabidopsis thaliana Kunitz family trypsin and protease inhibitor protein mRNA, complete cds [NM_105992]
	4,62	0.00000000	AT4G10270	AT4G10270	ref|Arabidopsis thaliana putative wound-responsive protein mRNA, complete cds [NM_117095]
	4,27	0.00000000	AT4G11190	AT4G11190	ref|Arabidopsis thaliana disease resistance-responsive, dirigent domain-containing protein mRNA, complete cds [NM_117190]
	4,27	0.00000000	AT1G75040	PR5	ref|Arabidopsis thaliana pathogenesis-related protein 5 mRNA, complete cds [NM_106161]
	4,26	0.00000000	AT4G30650	AT4G30650	ref|Arabidopsis thaliana putative low temperature and salt responsive protein mRNA, complete cds [NM_119211]
	3,23	0.00000000	AT1G24020	MLP423	ref|Arabidopsis thaliana MLP-like protein 423 mRNA, complete cds [NM_102249]
	3,06	0.00000000	AT3G17830	AT3G17830	ref|Arabidopsis thaliana molecular chaperone Hsp40/DnaJ family protein mRNA, complete cds [NM_112664]
	-3,02	0.00000000	AT3G03480	CHAT	ref|Arabidopsis thaliana acetyl CoA:(Z)-3-hexen-1-ol acetyltransferase mRNA, complete cds [NM_111219]
	-3,02	0.00000006	AT4G13830	J20	ref|Arabidopsis thaliana chaperone protein dnaJ 20 mRNA, complete cds [NM_179045]
	-3,03	0.00000001	AT3G10985	SAG20	ref|Arabidopsis thaliana senescence associated protein 20 mRNA, complete cds [NM_202550]
	-3,17	0.00000000	AT5G43570	AT5G43570	ref|Arabidopsis thaliana PR-6 proteinase inhibitor family protein mRNA, complete cds [NM_123723]
	-3,37	0.00000001	AT1G75380	BBD1	ref|Arabidopsis thaliana bifunctional nuclease 1 mRNA, complete cds [NM_179559]
	-3,51	0.00000006	AT5G62520	SRO5	ref|Arabidopsis thaliana probable inactive poly [ADP-ribose] polymerase SRO5 mRNA, complete cds [NM_203252]
	-4,23	0.00000000	AT1G19660	AT1G19660	ref|Arabidopsis thaliana putative wound-responsive protein mRNA, complete cds [NM_001035991]
	-4,26	0.00000000	AT1G71000	AT1G71000	ref|Arabidopsis thaliana chaperone DnaJ-domain containing protein mRNA, complete cds [NM_105769]
	-4,27	0.00000000	AT2G17880	AT2G17880	ref|Arabidopsis thaliana DNAJ heat shock N-terminal domain-containing protein mRNA, complete cds [NM_127342]
	-4,62	0.00000000	AT2G24550	AT2G24550	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_128016]
	-4,66	0.00000044	AT5G44973	AT5G44973	ref|Arabidopsis thaliana defensin-like protein 285 mRNA, complete cds [NM_001036935]
	-4,95	0.00000001	AT1G72900	AT1G72900	ref|Arabidopsis thaliana Toll-Interleukin-Resistance domain-containing protein mRNA, complete cds [NM_105948]
	-5,04	0.00000000	AT5G52640	HSP90.1	ref|Arabidopsis thaliana heat shock protein 90.1 mRNA, complete cds [NM_124642]
	-5,33	0.00000000	AT4G36040	AT4G36040	ref|Arabidopsis thaliana chaperone protein dnaJ 11 mRNA, complete cds [NM_119771]
	-5,61	0.00000000	AT3G12580	HSP70	ref|Arabidopsis thaliana heat shock protein 70-4 mRNA, complete cds [NM_112093]
	-5,81	0.00000000	AT2G26150	HSFA2	ref|Arabidopsis thaliana heat stress transcription factor A-2 mRNA, complete cds [NM_001124916]
	-6,46	0.00000000	AT5G33355	AT5G33355	ref|Arabidopsis thaliana defensin-like protein mRNA, complete cds [NM_147989]
	-6,54	0.00000000	AT3G59930	AT3G59930	ref|Arabidopsis thaliana defensin-like protein 206 mRNA, complete cds [NM_115856]
	-9,94	0.00000000	AT2G36800	DOGT1	ref|Arabidopsis thaliana UDP-glycosyltransferase 73C5 mRNA, complete cds [NM_129235]
	-11,01	0.00000000	AT5G51440	AT5G51440	ref|Arabidopsis thaliana heat shock protein 23.5 mRNA, complete cds [NM_124523]
	-12,03	0.00000000	AT1G80920	J8	ref|Arabidopsis thaliana chaperone protein dnaJ 8 mRNA, complete cds [NM_106740]
	-14,23	0.00000000	AT1G07400	AT1G07400	ref|Arabidopsis thaliana class I heat shock protein mRNA, complete cds [NM_100614]
	-14,85	0.00000000	AT5G66400	RAB18	ref|Arabidopsis thaliana dehydrin Rab18 mRNA, complete cds [NM_126038]
Redox regulation					
	4,65	0.00000000	AT1G06830	AT1G06830	ref|Arabidopsis thaliana monothiol glutaredoxin-S11 mRNA, complete cds [NM_100560]
	3,55	0.00000000	AT2G46650	CB5-C	ref|Arabidopsis thaliana cytochrome B5 isoform C mRNA, complete cds [NM_130230]
	-3,17	0.00000001	AT5G18600	AT5G18600	ref|Arabidopsis thaliana monothiol glutaredoxin-S2 mRNA, complete cds [NM_121865]
	-3,18	0.00000003	AT4G15670	AT4G15670	ref|Arabidopsis thaliana monothiol glutaredoxin-S7 mRNA, complete cds [NM_117658]
	-3,44	0.00000000	AT4G15700	AT4G15700	ref|Arabidopsis thaliana monothiol glutaredoxin-S3 mRNA, complete cds [NM_117661]
	-3,59	0.00000003	AT1G20630	CAT1	ref|Arabidopsis thaliana catalase 1 mRNA, complete cds [NM_101914]
	-3,83	0.00000000	AT1G08570	ACHT4	ref|Arabidopsis thaliana atypical CYS HIS rich thioredoxin 4 mRNA, complete cds [NM_001123776]
	-4,02	0.00000010	AT4G15690	AT4G15690	ref|Arabidopsis thaliana monothiol glutaredoxin-S5 mRNA, complete cds [NM_117660]
	-4,12	0.00000001	AT2G25080	GPX1	ref|Arabidopsis thaliana phospholipid hydroperoxide glutathione peroxidase 1 mRNA, complete cds [NM_128065]
	-4,98	0.00000000	AT1G07890	APX1	ref|Arabidopsis thaliana L-ascorbate peroxidase 1 mRNA, complete cds [NM_001123772]
	-10,12	0.00000000	AT4G35090	CAT2	ref|Arabidopsis thaliana catalase 2 mRNA, complete cds [NM_119675]
	-11,13	0.00000000	AT1G65970	TPX2	ref|Arabidopsis thaliana thioredoxin-dependent peroxidase 2 mRNA, complete cds [NM_105269]
Polyamine metabolism					
	-3,62	0.00000000	AT4G34710	ADC2	ref|Arabidopsis thaliana arginine decarboxylase 2 mRNA, complete cds [NM_119637]
Nucleotide metabolism					
	4,65	0.00000000	AT4G18440	AT4G18440	ref|Arabidopsis thaliana L-aspartase-like family protein mRNA, complete cds [NM_117957]
	4,18	0.00000000	AT3G27060	TSO2	ref|Arabidopsis thaliana ribonucleoside-diphosphate reductase small chain C mRNA, complete cds [NM_113620]
	-3,41	0.00000000	AT1G30820	AT1G30820	ref|Arabidopsis thaliana CTP synthase-like protein mRNA, complete cds [NM_102819]
Biodegradation of xenobiotics					
	-8,71	0.00000000	AT1G15380	AT1G15380	ref|Arabidopsis thaliana Lactoylglutathione lyase / glyoxalase I family protein mRNA, complete cds [NM_101407]
	-14,87	0.00000000	AT1G80160	AT1G80160	ref|Arabidopsis thaliana GLYOXYLASE I 7 mRNA, complete cds [NM_001084382]
C1-metabolism					

-4,35	0.00000000	AT5G14780	FDH	ref|Arabidopsis thaliana formate dehydrogenase mRNA, complete cds [NM_121482]

Miscellaneous enzyme family

11,58	0.00000000	AT2G46880	PAP14	ref|Arabidopsis thaliana purple acid phosphatase 14 mRNA, complete cds [NM_201975]
8,91	0.00000000	AT5G17220	GSTF12	ref|Arabidopsis thaliana glutathione S-transferase phi 12 mRNA, complete cds [NM_121728]
8,59	0.00000000	AT3G57240	BG3	ref|Arabidopsis thaliana beta-1,3-glucanase 3 mRNA, complete cds [NM_115584]
6,95	0.00000000	AT1G78370	GSTU20	ref|Arabidopsis thaliana glutathione S-transferase TAU 20 mRNA, complete cds [NM_106484]
6,48	0.00000000	AT5G03350	AT5G03350	ref|Arabidopsis thaliana lectin-like protein mRNA, complete cds [NM_120414]
6,12	0.00000000	AT4G21760	BGLU47	ref|Arabidopsis thaliana beta-glucosidase 47 mRNA, complete cds [NM_118296]
5,65	0.00000000	AT1G04040	AT1G04040	ref|Arabidopsis thaliana HAD superfamily, subfamily IIIB acid phosphatase mRNA, complete cds [NM_100285]
4,75	0.00000001	AT1G31690	AT1G31690	ref|Arabidopsis thaliana copper amine oxidase family protein mRNA, complete cds [NM_102904]
4,01	0.00000001	AT4G14090	AT4G14090	ref|Arabidopsis thaliana anthocyanin 5-O-glucosyltransferase mRNA, complete cds [NM_117485]
3,92	0.00000000	AT4G15440	HPL1	ref|Arabidopsis thaliana hydroperoxide lyase 1 mRNA, complete cds [NM_117633]
3,91	0.00000000	AT5G20740	AT5G20740	ref|Arabidopsis thaliana plant invertase/pectin methylesterase inhibitor domain-containing protein mRNA, complete cds [NM_122081]
3,85	0.00000000	AT1G29660	AT1G29660	ref|Arabidopsis thaliana GDSL esterase/lipase mRNA, complete cds [NM_102706]
3,49	0.00000003	AT1G66270	BGLU21	ref|Arabidopsis thaliana beta-glucosidase 21 mRNA, complete cds [NM_105298]
3,46	0.00000000	AT2G39030	AT2G39030	ref|Arabidopsis thaliana L-ornithine N5-acetyltransferase NATA1 mRNA, complete cds [NM_129460]
3,42	0.00000000	AT1G01190	CYP78A8	ref|Arabidopsis thaliana cytochrome P450, family 78, subfamily A, polypeptide 8 mRNA, complete cds [NM_100001]
3,33	0.00000000	AT4G00360	CYP86A2	ref|Arabidopsis thaliana cytochrome P450 86A2 mRNA, complete cds [NM_116260]
3,3	0.00000000	AT2G16890	AT2G16890	ref|Arabidopsis thaliana UDP-glycosyltransferase 90A1 mRNA, complete cds [NM_127242]
3,24	0.00000000	AT4G37400	CYP81F3	ref|Arabidopsis thaliana cytochrome P450, family 81, subfamily F, polypeptide 3 mRNA, complete cds [NM_119903]
3,24	0.00000002	AT4G12880	ENODL19	ref|Arabidopsis thaliana early nodulin-like protein 19 mRNA, complete cds [NM_001203782]
3,14	0.00000000	AT4G28780	AT4G28780	ref|Arabidopsis thaliana GDSL esterase/lipase mRNA, complete cds [NM_119022]
3,08	0.00000000	AT1G52400	BGLU18	ref|Arabidopsis thaliana beta glucosidase 18 mRNA, complete cds [NM_104118]
3,03	0.00000002	AT1G45191	AT1G45191	ref|Arabidopsis thaliana beta-glucosidase 1 mRNA, complete cds [NM_179440]
3,03	0.00000000	AT5G64080	AT5G64080	ref|Arabidopsis thaliana Non-specific lipid-transfer protein-like protein mRNA, complete cds [NM_125804]
-3,02	0.00000000	AT1G30720	AT1G30720	ref|Arabidopsis thaliana FAD-binding Berberine family protein mRNA, complete cds [NM_102808]
-3,05	0.00000000	AT3G26200	CYP71B22	ref|Arabidopsis thaliana cytochrome P450 71B22 mRNA, complete cds [NM_113527]
-3,12	0.00000000	AT4G19880	AT4G19880	ref|Arabidopsis thaliana Glutathione S-transferase family protein mRNA, complete cds [NM_118108]
-3,25	0.00000000	AT5G48490	AT5G48490	ref|Arabidopsis thaliana bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein mRNA, complete cds [NM_124225]
-3,25	0.00000001	AT1G02850	BGLU11	ref|Arabidopsis thaliana beta glucosidase 11 mRNA, complete cds [NM_202017]
-3,25	0.00000001	AT2G26740	SEH	ref|Arabidopsis thaliana soluble epoxide hydrolase mRNA, complete cds [NM_128231]
-3,32	0.00000001	AT3G55710	AT3G55710	ref|Arabidopsis thaliana UDP-glycosyltransferase 76F2 mRNA, complete cds [NM_115429]
-3,35	0.00000000	AT1G78830	AT1G78830	ref|Arabidopsis thaliana curculin-like (mannose-binding) lectin-like protein mRNA, complete cds [NM_106531]
-3,37	0.00000000	AT2G30140	AT2G30140	ref|Arabidopsis thaliana UDP-glycosyltransferase 87A2 mRNA, complete cds [NM_128569]
-3,39	0.00000000	AT5G64250	AT5G64250	ref|Arabidopsis thaliana Aldolase-type TIM barrel family protein mRNA, complete cds [NM_125821]
-3,53	0.00000000	AT3G26220	CYP71B3	ref|Arabidopsis thaliana cytochrome P450 71B3 mRNA, complete cds [NM_113529]
-3,59	0.00000000	AT3G04010	AT3G04010	ref|Arabidopsis thaliana O-glycosyl hydrolases family 17 protein mRNA, complete cds [NM_111272]
-3,62	0.00000001	AT4G24050	AT4G24050	ref|Arabidopsis thaliana NAD(P)-binding Rossmann-fold superfamily protein mRNA, complete cds [NM_118537]
-3,64	0.00000001	AT4G20860	AT4G20860	ref|Arabidopsis thaliana FAD-binding Berberine family protein mRNA, complete cds [NM_118204]
-3,64	0.00000000	AT3G53140	LUT1	ref|Arabidopsis thaliana carotene epsilon-monooxygenase mRNA, complete cds [NM_115173]
-3,73	0.00000002	AT3G50560	AT3G50560	ref|Arabidopsis thaliana Rossmann-fold NAD(P)-binding domain-containing protein mRNA, complete cds [NM_114916]
-3,81	0.00000000	AT3G03470	CYP89A9	ref|Arabidopsis thaliana cytochrome P450, family 87, subfamily A, polypeptide 9 mRNA, complete cds [NM_111218]
-3,83	0.00000000	AT4G34138	UGT73B1	ref|Arabidopsis thaliana UDP-glucosyl transferase 73B1 mRNA, complete cds [NM_119576]
-3,92	0.00000011	AT2G02930	GSTF3	ref|Arabidopsis thaliana glutathione S-transferase F3 mRNA, complete cds [NM_126346]
-4,08	0.00000000	AT4G15550	IAGLU	ref|Arabidopsis thaliana UDP-glucose:indole-3-acetate beta-D-glucosyltransferase mRNA, complete cds [NM_117646]
-4,24	0.00000000	AT5G20230	BCB	ref|Arabidopsis thaliana blue-copper-binding protein mRNA, complete cds [NM_122030]
-4,28	0.00000000	AT2G47730	GSTF8	ref|Arabidopsis thaliana glutathione S-transferase phi 8 mRNA, complete cds [NM_180148]
-4,54	0.00000000	AT5G16970	AER	ref|Arabidopsis thaliana 2-alkenal reductase mRNA, complete cds [NM_121703]
-4,57	0.00000000	AT5G16980	AT5G16980	ref|Arabidopsis thaliana zinc-binding dehydrogenase family protein mRNA, complete cds [NM_121704]
-4,63	0.00000000	AT3G61060	PP2-A13	ref|Arabidopsis thaliana phloem protein 2-A13 mRNA, complete cds [NM_202741]
-4,69	0.00000000	AT4G13250	NYC1	ref|Arabidopsis thaliana probable chlorophyll(ide) b reductase NYC1 mRNA, complete cds [NM_117396]
-4,74	0.00000001	AT3G14660	CYP72A13	ref|Arabidopsis thaliana cytochrome P450, family 72, subfamily A, polypeptide 13 mRNA, complete cds [NM_112327]
-4,86	0.00000000	AT3G14630	CYP72A9	ref|Arabidopsis thaliana cytochrome P450, family 72, subfamily A, polypeptide 9 mRNA, complete cds [NM_112324]
-4,87	0.00000000	AT3G46660	UGT76E12	ref|Arabidopsis thaliana UDP-glucosyl transferase 76E12 mRNA, complete cds [NM_114533]
-5,37	0.00000000	AT4G37370	CYP81D8	ref|Arabidopsis thaliana cytochrome P450, family 81, subfamily D, polypeptide 8 mRNA, complete cds [NM_119900]
-5,55	0.00000000	AT3G13750	BGAL1	ref|Arabidopsis thaliana beta galactosidase 1 mRNA, complete cds [NM_112225]
-5,63	0.00000000	AT2G37130	AT2G37130	ref|Arabidopsis thaliana peroxidase mRNA, complete cds [NM_001124989]
-5,81	0.00000000	AT2G29420	GSTU7	ref|Arabidopsis thaliana glutathione S-transferase tau 7 mRNA, complete cds [NM_128496]
-5,87	0.00000000	AT5G25130	CYP71B12	ref|Arabidopsis thaliana cytochrome P450 71B12 mRNA, complete cds [NM_122422]
-6,49	0.00000000	AT2G29490	GSTU1	ref|Arabidopsis thaliana glutathione S-transferase tau 1 mRNA, complete cds [NM_128503]
-6,65	0.00000000	AT4G34131	UGT73B3	ref|Arabidopsis thaliana UDP-glucosyl transferase 73B3 mRNA, complete cds [NM_119574]
-6,79	0.00000000	AT1G62510	AT1G62510	ref|Arabidopsis thaliana bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein mRNA, complete cds [NM_104930]
-7,32	0.00000000	AT2G15490	UGT73B4	ref|Arabidopsis thaliana UDP-glycosyltransferase 73B4 mRNA, complete cds [NM_127109]

-8,64	0.00000000	AT2G15480	UGT73B5	ref|Arabidopsis thaliana UDP-glucosyl transferase 73B5 mRNA, complete cds [NM_127108]
-8,71	0.00000000	AT2G29480	GSTU2	ref|Arabidopsis thaliana glutathione S-transferase tau 2 mRNA, complete cds [NM_128502]
-10,19	0.00000000	AT4G15760	MO1	ref|Arabidopsis thaliana monooxygenase 1 mRNA, complete cds [NM_001203809]
-11,18	0.00000000	AT4G16690	MES16	ref|Arabidopsis thaliana methyl esterase 16 mRNA, complete cds [NM_117770]
-12,2	0.00000000	AT2G36780	AT2G36780	ref|Arabidopsis thaliana UDP-glucosyl transferase 73C3 mRNA, complete cds [NM_129233]
-12,43	0.00000012	AT5G16960	AT5G16960	ref|Arabidopsis thaliana zinc-binding dehydrogenase family protein mRNA, complete cds [NM_121702]
-13,14	0.00000000	AT3G04000	AT3G04000	ref|Arabidopsis thaliana aldehyde reductase mRNA, complete cds [NM_111271]
-13,43	0.00000000	AT1G17170	GSTU24	ref|Arabidopsis thaliana glutathione S-transferase TAU 24 mRNA, complete cds [NM_101578]
-16,74	0.00000000	AT1G09500	AT1G09500	ref|Arabidopsis thaliana alcohol dehydrogenase-like protein mRNA, complete cds [NM_001035935]
-17,72	0.00000000	AT5G56870	BGAL4	ref|Arabidopsis thaliana beta-galactosidase 4 mRNA, complete cds [NM_125070]
-23	0.00000000	AT3G28740	CYP81D1	ref|Arabidopsis thaliana cytochrome P450 CYP81D11 mRNA, complete cds [NM_113795]
-24,7	0.00000000	AT3G60140	DIN2	ref|Arabidopsis thaliana beta-glucosidase 30 mRNA, complete cds [NM_115877]

RNA

13,68	0.00000000	AT2G41240	BHLH100	ref|Arabidopsis thaliana transcription factor bHLH100 mRNA, complete cds [NM_129689]
12,85	0.00000000	AT3G56970	BHLH038	ref|Arabidopsis thaliana transcription factor ORG2 mRNA, complete cds [NM_115556]
9,9	0.00000000	AT3G56980	BHLH039	ref|Arabidopsis thaliana transcription factor ORG3 mRNA, complete cds [NM_115557]
5,04	0.00000000	AT1G66390	MYB90	ref|Arabidopsis thaliana transcription factor MYB90 mRNA, complete cds [NM_105310]
4,87	0.00000000	AT3G25882	NIMIN-2	ref|Arabidopsis thaliana protein NIM1-INTERACTING 2 mRNA, complete cds [NM_148752]
4,08	0.00000000	AT2G40750	WRKY54	ref|Arabidopsis thaliana WRKY DNA-binding protein 54 mRNA, complete cds [NM_129637]
3,99	0.00000000	AT3G44750	HDA3	ref|Arabidopsis thaliana histone deacetylase HDT1 mRNA, complete cds [NM_114344]
3,74	0.00000000	AT3G23830	GRP4	ref|Arabidopsis thaliana glycine-rich RNA-binding protein 4 mRNA, complete cds [NM_180298]
3,71	0.00000000	AT5G61030	GR-RBP3	ref|Arabidopsis thaliana glycine-rich RNA-binding protein 3 mRNA, complete cds [NM_125496]
3,66	0.00000000	AT3G25700	AT3G25700	ref|Arabidopsis thaliana aspartyl protease family protein mRNA, complete cds [NM_113469]
3,6	0.00000000	AT1G80270	PPR596	ref|Arabidopsis thaliana pentatricopeptide repeat-containing protein mRNA, complete cds [NM_001084384]
3,56	0.00000066	AT5G22570	WRKY38	ref|Arabidopsis thaliana putative WRKY transcription factor 38 mRNA, complete cds [NM_122163]
3,5	0.00000000	AT2G27840	HDT4	ref|Arabidopsis thaliana histone deacetylase HDT4 mRNA, complete cds [NM_128344]
3,39	0.00000055	AT1G04240	SHY2	ref|Arabidopsis thaliana auxin-responsive protein IAA3 mRNA, complete cds [NM_100305]
3,34	0.00000000	AT5G61000	RPA70D	ref|Arabidopsis thaliana replication protein A 70 kDa DNA-binding subunit D mRNA, complete cds [NM_125493]
3,26	0.00000001	AT2G37510	AT2G37510	ref|Arabidopsis thaliana RNA recognition motif-containing protein mRNA, complete cds [NM_129306]
3,23	0.00000329	AT3G19350	MPC	ref|Arabidopsis thaliana maternally expressed PAB C-terminal protein mRNA, complete cds [NM_112822]
3,21	0.00000002	AT5G11590	TINY2	ref|Arabidopsis thaliana dehydration-responsive element-binding protein 3 mRNA, complete cds [NM_121197]
3,13	0.00000000	AT5G25830	GATA12	ref|Arabidopsis thaliana GATA transcription factor 12 mRNA, complete cds [NM_122484]
3,12	0.00000000	AT1G02450	NIMIN1	ref|Arabidopsis thaliana protein NIM1-INTERACTING 1 mRNA, complete cds [NM_100126]
3,04	0.00000000	AT5G23420	HMGB6	ref|Arabidopsis thaliana high-mobility group B6 protein mRNA, complete cds [NM_122249]
-3,04	0.00000113	AT1G68320	MYB62	ref|Arabidopsis thaliana R2R3-MYB transcription family mRNA, complete cds [NM_105503]
-3,09	0.00000000	AT2G36320	AT2G36320	ref|Arabidopsis thaliana zinc finger A20 and AN1 domain-containing stress-associated protein 4 mRNA, complete cds [NM_129189]
-3,1	0.00000000	AT1G80840	WRKY40	ref|Arabidopsis thaliana putative WRKY transcription factor 40 mRNA, complete cds [NM_106732]
-3,13	0.00000000	AT3G15500	NAC3	ref|Arabidopsis thaliana ATAF-like NAC-domain transcription factor mRNA, complete cds [NM_112418]
-3,14	0.00000000	AT5G62020	HSFB2A	ref|Arabidopsis thaliana heat stress transcription factor B-2a mRNA, complete cds [NM_125595]
-3,2	0.00000001	AT3G25790	AT3G25790	ref|Arabidopsis thaliana myb-like transcription factor family protein mRNA, complete cds [NM_113478]
-3,25	0.00000000	AT5G04340	ZAT6	ref|Arabidopsis thaliana zinc finger protein ZAT6 mRNA, complete cds [NM_120516]
-3,36	0.00000005	AT5G64750	abr-01	ref|Arabidopsis thaliana ethylene-responsive transcription factor ABR1 mRNA, complete cds [NM_125871]
-3,51	0.00000000	AT4G06746	RAP2.9	ref|Arabidopsis thaliana ethylene-responsive transcription factor RAP2-9 mRNA, complete cds [NM_179009]
-3,55	0.00000001	AT5G59820	RHL41	ref|Arabidopsis thaliana high light responsive zinc finger protein ZAT12 mRNA, complete cds [NM_125374]
-3,56	0.00000000	AT5G28770	BZO2H3	ref|Arabidopsis thaliana basic leucine zipper 63 mRNA, complete cds [NM_001036885]
-3,58	0.00000000	AT3G01970	WRKY45	ref|Arabidopsis thaliana WRKY DNA-binding protein 45 mRNA, complete cds [NM_111063]
-3,68	0.00000000	AT5G59340	WOX2	ref|Arabidopsis thaliana WUSCHEL-related homeobox 2 mRNA, complete cds [NM_125325]
-3,93	0.00000001	AT2G40340	DREB2C	ref|Arabidopsis thaliana dehydration-responsive element-binding protein 2C mRNA, complete cds [NM_129594]
-4,25	0.00000000	AT5G07100	WRKY26	ref|Arabidopsis thaliana WRKY DNA-binding protein 26 mRNA, complete cds [NM_203017]
-4,46	0.00000000	AT1G79700	AT1G79700	ref|Arabidopsis thaliana AP2-like ethylene-responsive transcription factor WRI4 mRNA, complete cds [NM_001084380]
-4,5	0.00000000	AT2G25900	ATCTH	ref|Arabidopsis thaliana putative Cys3His zinc finger protein ATCTH mRNA, complete cds [NM_128150]
-4,56	0.00000000	AT3G46080	AT3G46080	ref|Arabidopsis thaliana zinc finger protein ZAT8 mRNA, complete cds [NM_114477]
-4,73	0.00000010	AT5G13330	Rap2.6L	ref|Arabidopsis thaliana ethylene-responsive transcription factor ERF113 mRNA, complete cds [NM_121336]
-4,74	0.00000000	AT3G16770	EBP	ref|Arabidopsis thaliana ethylene-responsive transcription factor RAP2-3 mRNA, complete cds [NM_112550]
-5,05	0.00000000	AT3G28210	PMZ	ref|Arabidopsis thaliana zinc finger (AN1-like) family protein mRNA, complete cds [NM_113740]
-5,33	0.00000000	AT1G68190	AT1G68190	ref|Arabidopsis thaliana putative zinc finger protein mRNA, complete cds [NM_105490]
-5,33	0.00000000	AT4G16680	AT4G16680	ref|Arabidopsis thaliana putative RNA helicase mRNA, complete cds [NM_117769]
-5,35	0.00000000	AT5G24800	BZIP9	ref|Arabidopsis thaliana basic leucine zipper 9 mRNA, complete cds [NM_122389]
-6,23	0.00000000	AT1G75490	AT1G75490	ref|Arabidopsis thaliana dehydration-responsive element-binding protein 2D mRNA, complete cds [NM_106202]
-6,88	0.00000000	AT1G10585	AT1G10585	ref|Arabidopsis thaliana basic helix-loop-helix domain-containing protein mRNA, complete cds [NM_100934]
-7,03	0.00000000	AT5G05410	DREB2A	ref|Arabidopsis thaliana dehydration-responsive element-binding protein 2A mRNA, complete cds [NM_120623]
-7,1	0.00000000	AT5G49450	bZIP1	ref|Arabidopsis thaliana basic leucine-zipper 1 mRNA, complete cds [NM_124322]
-7,17	0.00000000	AT1G71030	MYBL2	ref|Arabidopsis thaliana putative myb family transcription factor mRNA, complete cds [NM_105772]

	-7,95	0.00000071	AT1G71520	AT1G71520	ref|Arabidopsis thaliana ERF/AP2 transcription factor family protein DREB A-5 mRNA, complete cds [NM_105820]
	-8,61	0.00000003	AT1G43160	RAP2.6	ref|Arabidopsis thaliana ethylene-responsive transcription factor RAP2-6 mRNA, complete cds [NM_103468]
	-11,92	0.00000000	AT2G47270	AT2G47270	ref|Arabidopsis thaliana transcription factor UPBEAT1 mRNA, complete cds [NM_130295]
DNA					
	4,1	0.00000000	AT3G45930	AT3G45930	ref|Arabidopsis thaliana histone H4 mRNA, complete cds [NM_114462]
	3,58	0.00000000	AT5G02570	AT5G02570	ref|Arabidopsis thaliana histone H2B mRNA, complete cds [NM_120335]
	3,51	0.00000000	AT5G12910	AT5G12910	ref|Arabidopsis thaliana histone H3-like 4 mRNA, complete cds [NM_121294]
	3,34	0.00000000	AT3G46320	AT3G46320	ref|Arabidopsis thaliana histone H4 mRNA, complete cds [NM_180329]
	3,23	0.00000000	AT2G28740	HIS4	ref|Arabidopsis thaliana histone H4 mRNA, complete cds [NM_128434]
	3,19	0.00000000	AT5G10390	AT5G10390	ref|Arabidopsis thaliana histone H3 mRNA, complete cds [NM_121077]
	3,01	0.00000000	AT1G09200	AT1G09200	ref|Arabidopsis thaliana histone H3 mRNA, complete cds [NM_100790]
	-4,1	0.00000000	AT5G63190	AT5G63190	ref|Arabidopsis thaliana MA3 domain-containing protein mRNA, complete cds [NM_125714]
Protein					
	5,44	0.00000000	AT1G23100	AT1G23100	ref|Arabidopsis thaliana GroES-like protein mRNA, complete cds [NM_102158]
	4,62	0.00000000	AT4G25630	FIB2	ref|Arabidopsis thaliana mediator of RNA polymerase II transcription subunit 36a mRNA, complete cds [NM_118695]
	4,4	0.00000000	AT2G23010	SCPL9	ref|Arabidopsis thaliana serine carboxypeptidase-like 9 mRNA, complete cds [NM_127866]
	3,73	0.00000001	AT3G03060	AT3G03060	ref|Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA, complete cds [NM_111176]
	3,44	0.00000001	AT4G04940	AT4G04940	ref|Arabidopsis thaliana transducin/WD40 domain-containing protein mRNA, complete cds [NM_116732]
	3,42	0.00000000	AT1G07070	AT1G07070	ref|Arabidopsis thaliana 60S ribosomal protein L35a-1 mRNA, complete cds [NM_100581]
	3,34	0.00000000	AT5G45650	AT5G45650	ref|Arabidopsis thaliana subtilase family protein mRNA, complete cds [NM_123933]
	3,3	0.00000000	AT3G10110	MEE67	ref|Arabidopsis thaliana mitochondrial import inner membrane translocase subunit TIM22-1 mRNA, complete cds [NM_111846]
	3,24	0.00000000	AT2G33210	HSP60-2	ref|Arabidopsis thaliana heat shock protein 60-2 mRNA, complete cds [NM_179872]
	3,2	0.00000000	AT1G23410	AT1G23410	ref|Arabidopsis thaliana 40S ribosomal protein S27a-1 mRNA, complete cds [NM_102190]
	3,12	0.00000000	AT1G61580	RPL3B	ref|Arabidopsis thaliana 60S ribosomal protein L3-2 mRNA, complete cds [NM_104840]
	3,03	0.00000000	AT4G12600	AT4G12600	ref|Arabidopsis thaliana ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein mRNA, complete cds [NM_117330]
	-3,06	0.00000000	AT1G63800	UBC5	ref|Arabidopsis thaliana ubiquitin-conjugating enzyme E2 5 mRNA, complete cds [NM_105055]
	-3,09	0.00000000	AT4G20070	AAH	ref|Arabidopsis thaliana allantoate amidohydrolase mRNA, complete cds [NM_118126]
	-3,09	0.00000002	AT3G60300	AT3G60300	ref|Arabidopsis thaliana RWD domain-containing protein mRNA, complete cds [NM_115894]
	-3,13	0.00000000	AT4G32940	GAMMA-VPE	ref|Arabidopsis thaliana vacuolar-processing enzyme gamma mRNA, complete cds [NM_119448]
	-3,19	0.00000000	AT4G39090	RD19	ref|Arabidopsis thaliana cysteine proteinase RD19a mRNA, complete cds [NM_120069]
	-3,2	0.00000000	AT3G06420	ATG8H	ref|Arabidopsis thaliana autophagy-related protein 8h mRNA, complete cds [NM_111517]
	-3,22	0.00000000	AT1G11080	scpl31	ref|Arabidopsis thaliana serine carboxypeptidase-like 31 mRNA, complete cds [NM_001198028]
	-3,24	0.00000000	AT1G03230	AT1G03230	ref|Arabidopsis thaliana aspartyl protease-like protein mRNA, complete cds [NM_100205]
	-3,29	0.00000000	AT2G22960	AT2G22960	ref|Arabidopsis thaliana putative serine carboxypeptidase-like 52 mRNA, complete cds [NM_127861]
	-3,35	0.00000010	AT2G25090	CIPK16	ref|Arabidopsis thaliana SNF1-related kinase mRNA, complete cds [NM_128066]
	-3,36	0.00000000	AT2G47560	AT2G47560	ref|Arabidopsis thaliana RING-H2 finger protein ATL64 mRNA, complete cds [NM_130324]
	-3,38	0.00000000	AT4G04770	ABC1	ref|Arabidopsis thaliana ATP binding cassette protein 1 mRNA, complete cds [NM_116715]
	-3,48	0.00000008	AT3G57760	AT3G57760	ref|Arabidopsis thaliana protein kinase family protein mRNA, complete cds [NM_001035802]
	-3,56	0.00000001	AT1G66180	AT1G66180	ref|Arabidopsis thaliana aspartyl protease family protein mRNA, complete cds [NM_105289]
	-3,61	0.00000000	AT1G20350	TIM17-1	ref|Arabidopsis thaliana translocase inner membrane subunit 17-1 mRNA, complete cds [NM_101886]
	-3,71	0.00000005	AT1G26800	AT1G26800	ref|Arabidopsis thaliana RING/U-box domain-containing protein mRNA, complete cds [NM_102444]
	-3,75	0.00000013	AT4G17245	AT4G17245	ref|Arabidopsis thaliana RING/U-box domain-containing protein mRNA, complete cds [NM_117830]
	-3,84	0.00000000	AT1G03220	AT1G03220	ref|Arabidopsis thaliana aspartyl protease-like protein mRNA, complete cds [NM_100204]
	-3,9	0.00000001	AT2G18193	AT2G18193	ref|Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA, complete cds [NM_179641]
	-4,06	0.00000000	AT4G03320	tic20-IV	ref|Arabidopsis thaliana translocon at the inner envelope membrane of chloroplasts 20-IV mRNA, complete cds [NM_116570]
	-4,11	0.00000000	AT4G25390	AT4G25390	ref|Arabidopsis thaliana receptor-like serine/threonine-protein kinase mRNA, complete cds [NM_118671]
	-4,21	0.00000000	AT2G26980	CIPK3	ref|Arabidopsis thaliana CBL-interacting serine/threonine-protein kinase 3 mRNA, complete cds [NM_001036350]
	-4,21	0.00000000	AT2G23030	SNRK2.9	ref|Arabidopsis thaliana serine/threonine-protein kinase SNRK2.9 mRNA, complete cds [NM_127867]
	-4,4	0.00000000	AT3G62260	AT3G62260	ref|Arabidopsis thaliana putative protein phosphatase 2C 49 mRNA, complete cds [NM_116091]
	-4,46	0.00000000	AT5G51070	ERD1	ref|Arabidopsis thaliana chaperone protein ClpD mRNA, complete cds [NM_124486]
	-4,48	0.00000000	AT5G24490	AT5G24490	ref|Arabidopsis thaliana putative 30S ribosomal protein mRNA, complete cds [NM_122357]
	-4,49	0.00000000	AT4G38470	AT4G38470	ref|Arabidopsis thaliana ACT-like protein tyrosine kinase family protein mRNA, complete cds [NM_120008]
	-4,82	0.00000000	AT2G45170	ATG8E	ref|Arabidopsis thaliana autophagy-related protein 8e mRNA, complete cds [NM_180100]
	-4,82	0.00000000	AT2G22990	SNG1	ref|Arabidopsis thaliana sinapoylglucose:malate sinapoyltransferase mRNA, complete cds [NM_127864]
	-4,92	0.00000000	AT1G23390	AT1G23390	ref|Arabidopsis thaliana F-box/kelch-repeat protein mRNA, complete cds [NM_102188]
	-5	0.00000000	AT5G22920	AT5G22920	ref|Arabidopsis thaliana ring finger and CHY zinc finger domain-containing protein 1 mRNA, complete cds [NM_122198]
	-5,34	0.00000000	AT5G21170	AKINBETA1	ref|Arabidopsis thaliana SNF1-related protein kinase regulatory subunit beta-1 mRNA, complete cds [NM_001036841]
	-5,91	0.00000000	AT5G17170	ENH1	ref|Arabidopsis thaliana protein ENHANCER OF SOS3-1 mRNA, complete cds [NM_001085129]
	-6,09	0.00000004	AT1G02610	AT1G02610	ref|Arabidopsis thaliana RING/FYVE/PHD zinc finger-containing protein mRNA, complete cds [NM_100141]
	-6,25	0.00000000	AT1G22500	AT1G22500	ref|Arabidopsis thaliana putative C3HC4-type RING zinc finger protein mRNA, complete cds [NM_102099]
	-6,28	0.00000000	AT5G63160	BT1	ref|Arabidopsis thaliana BTB and TAZ domain protein 1 mRNA, complete cds [NM_125711]
	-6,51	0.00000000	AT3G48360	BT2	ref|Arabidopsis thaliana TAC1-mediated telomerase activation pathway protein BT2 mRNA, complete cds [NM_114697]

	-7,04	0.00000000	AT4G37610	BT5	ref|Arabidopsis thaliana BTB and TAZ domain protein 5 mRNA, complete cds [NM_119924]
	-11,06	0.00000000	AT1G80440	AT1G80440	ref|Arabidopsis thaliana F-box/kelch-repeat protein mRNA, complete cds [NM_106692]
Signalling					
	4,94	0.00000000	AT2G41090	AT2G41090	ref|Arabidopsis thaliana calmodulin-like protein 10 mRNA, complete cds [NM_129674]
	4,47	0.00000000	AT5G59670	AT5G59670	ref|Arabidopsis thaliana Leucine-rich repeat protein kinase family protein mRNA, complete cds [NM_125359]
	4,43	0.00000051	AT4G23130	CRK5	ref|Arabidopsis thaliana cysteine-rich receptor-like protein kinase 5 mRNA, complete cds [NM_179094]
	-3,08	0.00000003	AT5G10250	DOT3	ref|Arabidopsis thaliana putative BTB/POZ domain-containing protein DOT3 mRNA, complete cds [NM_121063]
	-3,57	0.00000000	AT2G41100	TCH3	ref|Arabidopsis thaliana calmodulin-like protein 4 mRNA, complete cds [NM_001202794]
	-4,22	0.00000000	AT1G21550	AT1G21550	ref|Arabidopsis thaliana putative calcium-binding protein CML44 mRNA, complete cds [NM_102004]
	-4,66	0.00000000	AT5G64260	EXL2	ref|Arabidopsis thaliana protein EXORDIUM like 2 mRNA, complete cds [NM_125822]
	-4,75	0.00000000	AT5G49480	CP1	ref|Arabidopsis thaliana Ca2+-binding protein 1 mRNA, complete cds [NM_124325]
	-6,36	0.00000000	AT2G02710	PLPB	ref|Arabidopsis thaliana PAS/LOV protein B mRNA, complete cds [NM_201672]
Cell					
	5	0.00000000	AT5G15970	KIN2	ref|Arabidopsis thaliana stress-induced protein KIN2 mRNA, complete cds [NM_121602]
	3,71	0.00000000	AT4G14400	ACD6	ref|Arabidopsis thaliana protein ACCELERATED CELL DEATH 6 mRNA, complete cds [NM_117519]
	-3,68	0.00000000	AT3G53230	AT3G53230	ref|Arabidopsis thaliana cell division control protein 48-B mRNA, complete cds [NM_115183]
Micro RNA					
	5,71	0.00000002	AT3G25795	AK227365	gb|Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL14-04-D19 [AK227365]
	-3,45	0.00000000	AT5G06865	PGIP1	gb|Arabidopsis thaliana clone 108218 mRNA sequence [DQ108691]
Development					
	5,2	0.00000000	AT4G17670	AT4G17670	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_117875]
	5,1	0.00000000	AT2G44670	AT2G44670	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_130031]
	4,26	0.00000000	AT4G08300	AT4G08300	ref|Arabidopsis thaliana nodulin MtN21 /EamA-like transporter family protein mRNA, complete cds [NM_116899]
	4,25	0.00000003	AT5G50800	AT5G50800	ref|Arabidopsis thaliana bidirectional sugar transporter SWEET13 mRNA, complete cds [NM_124458]
	3,71	0.00000000	AT3G22550	AT3G22550	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_113154]
	3,29	0.00000001	AT1G78020	AT1G78020	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_106451]
	-3,01	0.00000000	AT5G65870	PSK5	ref|Arabidopsis thaliana putative phytosulfokines 5 precursor mRNA, complete cds [NM_125984]
	-3,13	0.00000000	AT4G27410	RD26	ref|Arabidopsis thaliana NAC transcription factor RD26 mRNA, complete cds [NM_001084983]
	-3,16	0.00000000	AT1G01720	ATAF1	ref|Arabidopsis thaliana putative transcriptional activator with NAC domain mRNA, complete cds [NM_100054]
	-3,47	0.00000000	AT5G63790	NAC102	ref|Arabidopsis thaliana NAC domain-containing protein 102 mRNA, complete cds [NM_125774]
	-3,47	0.00000000	AT4G02380	SAG21	ref|Arabidopsis thaliana senescence-associated protein SAG21 mRNA, complete cds [NM_116471]
	-3,52	0.00000000	AT3G46600	AT3G46600	ref|Arabidopsis thaliana scarecrow-like protein 30 mRNA, complete cds [NM_114527]
	-3,81	0.00000000	AT5G59510	RTFL5	ref|Arabidopsis thaliana protein rotundifolia like 5 mRNA, complete cds [NM_125343]
	-3,89	0.00000000	AT1G77450	NAC032	ref|Arabidopsis thaliana NAC domain containing protein 32 mRNA, complete cds [NM_106394]
	-3,99	0.00000000	AT1G56220	AT1G56220	ref|Arabidopsis thaliana dormancy/auxin associated protein mRNA, complete cds [NM_104501]
	-4,26	0.00000000	AT2G28120	AT2G28120	ref|Arabidopsis thaliana major facilitator protein mRNA, complete cds [NM_128372]
	-4,72	0.00000000	AT3G49620	DIN11	ref|Arabidopsis thaliana 2-oxoacid-dependent dioxygenase-like protein DIN11 mRNA, complete cds [NM_114822]
	-4,74	0.00000000	AT5G14120	AT5G14120	ref|Arabidopsis thaliana major facilitator protein mRNA, complete cds [NM_121416]
	-4,85	0.00000000	AT5G15850	COL1	ref|Arabidopsis thaliana zinc finger protein CONSTANS-LIKE 1 mRNA, complete cds [NM_121590]
	-5,34	0.00000000	AT2G41380	AT2G41380	ref|Arabidopsis thaliana S-adenosyl-L-methionine-dependent methyltransferase-like protein mRNA, complete cds [NM_129701]
	-5,35	0.00000000	AT1G69490	NAP	ref|Arabidopsis thaliana NAC transcription factor protein family mRNA, complete cds [NM_105616]
	-5,9	0.00000000	AT1G52690	AT1G52690	ref|Arabidopsis thaliana Late embryogenesis abundant protein (LEA) family protein mRNA, complete cds [NM_202280]
	-5,99	0.00000000	AT3G29035	NAC3	ref|Arabidopsis thaliana NAC domain-containing protein 3 mRNA, complete cds [NM_113825]
	-6,16	0.00000000	AT5G39610	NAC6	ref|Arabidopsis thaliana NAC-domain transcription factor mRNA, complete cds [NM_123323]
	-6,63	0.00000000	AT1G02820	AT1G02820	ref|Arabidopsis thaliana late embryogenesis abundant 3-like protein mRNA, complete cds [NM_100163]
	-7,46	0.00000000	AT1G28330	DYL1	ref|Arabidopsis thaliana dormancy-associated protein-like 1 mRNA, complete cds [NM_001160906]
	-7,65	0.00000000	AT5G19120	AT5G19120	ref|Arabidopsis thaliana aspartyl protease family protein mRNA, complete cds [NM_121917]
	-111,32	0.00000000	AT4G35770	SEN1	ref|Arabidopsis thaliana senescence-associated protein DIN1 mRNA, complete cds [NM_119743]
Transport					
	5,8	0.00000000	AT1G61800	GPT2	ref|Arabidopsis thaliana glucose-6-phosphate/phosphate translocator 2 mRNA, complete cds [NM_104862]
	4,52	0.00000000	AT1G18320	AT1G18320	ref|Arabidopsis thaliana mitochondrial import inner membrane translocase subunit TIM22-4 mRNA, complete cds [NM_101690]
	4,43	0.00000000	AT1G79400	CHX2	ref|Arabidopsis thaliana cation/H(+) antiporter 2 mRNA, complete cds [NM_106588]
	4,39	0.00000000	AT1G15150	AT1G15150	ref|Arabidopsis thaliana MATE efflux family protein mRNA, complete cds [NM_101383]
	4,24	0.00000000	AT1G64220	TOM7-2	ref|Arabidopsis thaliana mitochondrial import receptor subunit TOM7-2 mRNA, complete cds [NM_105096]
	3,17	0.00000000	AT4G04750	AT4G04750	ref|Arabidopsis thaliana sugar transporter ERD6-like 14 mRNA, complete cds [NM_116713]
	3,17	0.00000000	AT2G46430	CNGC3	ref|Arabidopsis thaliana cyclic nucleotide gated channel 3 mRNA, complete cds [NM_130207]
	-3,12	0.00000001	AT3G61430	PIP1A	ref|Arabidopsis thaliana aquaporin PIP1-1 mRNA, complete cds [NM_001084854]
	-3,22	0.00000001	AT2G17500	AT2G17500	ref|Arabidopsis thaliana auxin efflux carrier family protein mRNA, complete cds [NM_179633]
	-3,27	0.00000000	AT2G36950	AT2G36950	ref|Arabidopsis thaliana heavy-metal-associated domain-containing protein mRNA, complete cds [NM_129251]

	-3,28	0.00000000	AT2G38170	CAX1	ref|Arabidopsis thaliana vacuolar cation/proton exchanger 1 mRNA, complete cds [NM_201901]
	-3,46	0.00000000	AT4G35440	CLC-E	ref|Arabidopsis thaliana chloride channel protein CLC-e mRNA, complete cds [NM_119709]
	-3,65	0.00000001	AT5G17860	CAX7	ref|Arabidopsis thaliana calcium exchanger 7 mRNA, complete cds [NM_121792]
	-4,38	0.00000004	AT1G66570	SUC7	ref|Arabidopsis thaliana putative sucrose transport protein SUC7 mRNA, complete cds [NM_001036165]
	-4,44	0.00000000	AT1G33110	AT1G33110	ref|Arabidopsis thaliana MATE efflux family protein mRNA, complete cds [NM_103045]
	-5,14	0.00000000	AT2G23150	NRAMP3	ref|Arabidopsis thaliana metal transporter Nramp3 mRNA, complete cds [NM_127879]
	-5,41	0.00000000	AT5G26200	AT5G26200	ref|Arabidopsis thaliana mitochondrial substrate carrier family protein mRNA, complete cds [NM_122521]
	-5,64	0.00000000	AT5G47560	TDT	ref|Arabidopsis thaliana tonoplast dicarboxylate transporter mRNA, complete cds [NM_124129]
	-8,48	0.00000000	AT1G66760	AT1G66760	ref|Arabidopsis thaliana MATE efflux family protein mRNA, complete cds [NM_179523]
	-8,76	0.00000000	AT1G11260	STP1	ref|Arabidopsis thaliana sugar transporter 1 mRNA, complete cds [NM_100998]
Not assigned					
	21,39	0.00000000	AT1G80130	AT1G80130	ref|Arabidopsis thaliana tetratricopeptide repeat domain-containing protein mRNA, complete cds [NM_106662]
	10,94	0.00000000	AT4G01080	TBL26	ref|Arabidopsis thaliana protein TRICHOME BIREFRINGENCE-LIKE 26 mRNA, complete cds [NM_116338]
	10,37	0.00000000	AT3G22240	AT3G22240	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_113122]
	9,37	0.00000000	AT3G22235	AT3G22235	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_180292]
	8,25	0.00000000	AT2G27402	AT2G27402	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_201818]
	7,82	0.00000000	AT4G36700	AT4G36700	ref|Arabidopsis thaliana cupin family protein mRNA, complete cds [NM_119834]
	7,59	0.00000000	AT1G19960	AT1G19960	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_101851]
	7,51	0.00000000	AT1G47395	AT1G47395	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_179449]
	7,14	0.00000000	AT2G26400	ARD3	ref|Arabidopsis thaliana acireductone dioxygenase 3 mRNA, complete cds [NM_128197]
	6,86	0.00000000	AT2G14560	LURP1	ref|Arabidopsis thaliana protein LURP1 mRNA, complete cds [NM_127019]
	5,36	0.00000000	AT1G68600	AT1G68600	ref|Arabidopsis thaliana Aluminum activated malate transporter family protein mRNA, complete cds [NM_105532]
	5,24	0.00000000	AT1G67360	AT1G67360	ref|Arabidopsis thaliana REF/SRPP-like protein mRNA, complete cds [NM_179525]
	4,99	0.00000000	AT3G44450	AT3G44450	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_114313]
	4,94	0.00000000	AT3G61920	AT3G61920	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_116057]
	4,78	0.00000000	AT5G20190	AT5G20190	ref|Arabidopsis thaliana tetratricopeptide repeat domain-containing protein mRNA, complete cds [NM_122026]
	4,76	0.00000000	AT3G26960	AT3G26960	ref|Arabidopsis thaliana pollen Ole e 1 allergen and extensin family protein mRNA, complete cds [NM_113610]
	4,74	0.00000002	AT2G14247	AT2G14247	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_201723]
	4,67	0.00000000	AT2G22170	AT2G22170	ref|Arabidopsis thaliana PLAT-plant-stress domain-containing protein mRNA, complete cds [NM_127785]
	4,6	0.00000002	AT1G47400	AT1G47400	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_103634]
	4,55	0.00000000	AT3G28220	AT3G28220	ref|Arabidopsis thaliana TRAF-like family protein mRNA, complete cds [NM_113741]
	4,51	0.00000000	AT5G63087	NP1655641	tc|GB|NM_001085318.1|NP_001078787.1 unknown protein;similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G63063.1) [NP1655641]
	4,17	0.00000000	AT1G64980	AT1G64980	ref|Arabidopsis thaliana putative nucleotide-diphospho-sugar transferase mRNA, complete cds [NM_105172]
	4,03	0.00000000	AT2G35860	FLA16	ref|Arabidopsis thaliana fasciclin-like arabinogalactan protein 16 mRNA, complete cds [NM_179922]
	3,94	0.00000000	AT5G67370	AT5G67370	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_126137]
	3,73	0.00000001	AT2G30766	AT2G30766	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001124947]
	3,69	0.00000006	AT5G15120	AT5G15120	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_121516]
	3,65	0.00000001	AT2G33847	AT2G33847	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001084533]
	3,62	0.00000003	AT2G07774	AT2G07774	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_147273]
	3,6	0.00000001	AT5G03120	AT5G03120	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_120390]
	3,59	0.00000000	AT3G44860	FAMT	ref|Arabidopsis thaliana farnesoic acid carboxyl-O-methyltransferase mRNA, complete cds [NM_114355]
	3,55	0.00000002	AT2G07815	AT2G07815	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001124814]
	3,54	0.00000000	AT3G17120	AT3G17120	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_202597]
	3,51	0.00000002	AT3G23450	AT3G23450	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_113248]
	3,49	0.00000000	AT4G24265	AT4G24265	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_148370]
	3,46	0.00000000	AT3G52630	AT3G52630	ref|Arabidopsis thaliana Nucleic acid-binding, OB-fold-like protein mRNA, complete cds [NM_115123]
	3,46	0.00000000	AT4G02850	AT4G02850	ref|Arabidopsis thaliana phenazine biosynthesis PhzC/PhzF family protein mRNA, complete cds [NM_116519]
	3,39	0.00000004	AT3G09922	IPS1	ref|Arabidopsis thaliana protein ED BY PHOSPHATE STARVATION1 mRNA, complete cds [NM_180219]
	3,34	0.00000000	AT5G44565	AT5G44565	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_203153]
	3,33	0.00000010	AT1G74770	AT1G74770	ref|Arabidopsis thaliana zinc ion binding protein mRNA, complete cds [NM_106135]
	3,3	0.00000001	AT3G23120	RLP38	ref|Arabidopsis thaliana receptor like protein 38 mRNA, complete cds [NM_113213]
	3,26	0.00000000	AT5G22460	AT5G22460	ref|Arabidopsis thaliana esterase/lipase/thioesterase family protein mRNA, complete cds [NM_180724]
	3,21	0.00000000	AT1G45010	AT1G45010	ref|Arabidopsis thaliana TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein mRNA, complete cds [NM_103581]
	3,18	0.00000000	AT5G14330	AT5G14330	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_121437]
	3,17	0.00000000	AT1G03820	AT1G03820	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_100261]
	3,15	0.00000000	AT5G05365	AT5G05365	ref|Arabidopsis thaliana Heavy metal transport/detoxification superfamily protein mRNA, complete cds [NM_001085064]
	3,13	0.00000000	AT5G44568	AT5G44568	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001085241]
	3,11	0.00000000	AT1G74440	AT1G74440	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_106104]
	3,09	0.00000000	AT2G15000	AT2G15000	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001084423]
	3,07	0.00000000	AT2G18328	RL4	ref|Arabidopsis thaliana protein RADIALIS-like 4 mRNA, complete cds [NM_001084443]
	3,06	0.00000000	AT1G65486	AT1G65486	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001124079]
	3,06	0.00000009	AT3G15357	AT3G15357	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_112403]
	3,03	0.00000000	AT2G40435	AT2G40435	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_129604]

3,03	0.00000003	AT5G41460	AT5G41460	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_123510]
-3,01	0.00000001	AT2G38820	AT2G38820	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_201907]
-3,02	0.00000001	AT1G02470	AT1G02470	ref|Arabidopsis thaliana SRPBCC ligand-binding domain-containing protein mRNA, complete cds [NM_100128]
-3,07	0.00000000	AT5G44572	AT5G44572	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001085242]
-3,08	0.00000000	AT2G27385	AT2G27385	ref|Arabidopsis thaliana pollen Ole e 1 allergen and extensin family protein mRNA, complete cds [NM_179769]
-3,09	0.00000000	AT2G37750	AT2G37750	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_129331]
-3,12	0.00000001	AT5G58570	AT5G58570	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125244]
-3,16	0.00000000	AT2G24100	AT2G24100	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_127972]
-3,16	0.00000000	AT4G25170	AT4G25170	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001160795]
-3,17	0.00000000	AT3G29240	AT3G29240	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_180317]
-3,18	0.00000000	AT5G57910	AT5G57910	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125176]
-3,22	0.00000008	AT5G21940	AT5G21940	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_147877]
-3,23	0.00000002	AT2G41230	AT2G41230	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_180017]
-3,25	0.00000014	AT2G16340	AT2G16340	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_127188]
-3,26	0.00000000	AT1G28260	AT1G28260	ref|Arabidopsis thaliana Telomerase activating protein Est1 mRNA, complete cds [NM_102591]
-3,26	0.00000000	AT3G19615	AT3G19615	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001084720]
-3,26	0.00000000	AT1G16720	HCF173	ref|Arabidopsis thaliana high chlorophyll fluorescence phenotype 173 protein mRNA, complete cds [NM_101533]
-3,27	0.00000000	AT2G36895	AT2G36895	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_179941]
-3,28	0.00000000	AT1G70780	AT1G70780	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_105746]
-3,29	0.00000002	AT5G66480	AT5G66480	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_126046]
-3,3	0.00000000	AT2G04795	AT2G04795	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_126510]
-3,34	0.00000000	AT1G27290	AT1G27290	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001084133]
-3,36	0.00000000	AT5G58770	AT5G58770	ref|Arabidopsis thaliana dehydrodolichyl diphosphate synthase 2 mRNA, complete cds [NM_125264]
-3,37	0.00000001	AT3G52480	AT3G52480	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_115108]
-3,4	0.00000000	AT3G15760	AT3G15760	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_112446]
-3,43	0.00000000	AT3G10120	AT3G10120	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_111847]
-3,46	0.00000000	AT2G46220	AT2G46220	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_130184]
-3,6	0.00000000	AT2G32150	AT2G32150	ref|Arabidopsis thaliana haloacid dehalogenase-like hydrolase domain-containing protein mRNA, complete cds [NM_128774]
-3,64	0.00000000	AT1G49500	AT1G49500	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_103838]
-3,64	0.00000000	AT2G27830	AT2G27830	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_128343]
-3,67	0.00000000	AT5G06570	AT5G06570	ref|Arabidopsis thaliana probable carboxylesterase 15 mRNA, complete cds [NM_120740]
-3,68	0.00000001	AT4G33660	AT4G33660	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_119522]
-3,7	0.00000005	AT2G05380	GRP3S	ref|Arabidopsis thaliana glycine-rich protein 3 short isoform mRNA, complete cds [NM_001124801]
-3,74	0.00000001	AT5G66650	AT5G66650	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_126063]
-3,8	0.00000000	AT1G69260	AFP1	ref|Arabidopsis thaliana ABI five binding protein mRNA, complete cds [NM_105593]
-3,85	0.00000000	AT4G24160	AT4G24160	ref|Arabidopsis thaliana lysophosphatidic acid acyltransferase mRNA, complete cds [NM_202876]
-3,85	0.00000001	AT5G64190	AT5G64190	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125815]
-3,91	0.00000000	AT5G02160	AT5G02160	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_120294]
-4,01	0.00000000	AT5G65207	AT5G65207	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_148161]
-4,06	0.00000001	AT2G41730	AT2G41730	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_129737]
-4,09	0.00000026	AT5G47860	AT5G47860	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_124160]
-4,11	0.00000000	AT3G45730	AT3G45730	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_114442]
-4,13	0.00000109	AT5G14110	AT5G14110	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_121415]
-4,32	0.00000000	AT1G53280	AT1G53280	ref|Arabidopsis thaliana DJ1-like protein B mRNA, complete cds [NM_104206]
-4,38	0.00000004	AT4G25580	AT4G25580	ref|Arabidopsis thaliana CAP160 protein mRNA, complete cds [NM_118690]
-4,45	0.00000000	AT2G15960	AT2G15960	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_127155]
-4,45	0.00000000	AT3G20395	AT3G20395	ref|Arabidopsis thaliana RING-finger domain-containing protein mRNA, complete cds [NM_001084725]
-4,46	0.00000000	AT3G15630	AT3G15630	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_112433]
-4,48	0.00000000	AT1G73750	AT1G73750	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_106034]
-4,51	0.00000000	AT1G01240	AT1G01240	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_202007]
-4,57	0.00000000	AT1G15415	AT1G15415	ref|Arabidopsis thaliana phosphatase 2A B'gamma subunit mRNA, complete cds [NM_101411]
-4,58	0.00000000	AT3G15770	AT3G15770	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001035628]
-4,6	0.00000018	AT1G05340	AT1G05340	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_100413]
-4,77	0.00000000	AT4G12735	AT4G12735	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_202810]
-5,1	0.00000000	AT2G20670	AT2G20670	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_127631]
-5,18	0.00000000	AT1G22890	AT1G22890	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_102136]
-5,29	0.00000002	AT2G31945	AT2G31945	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_128753]
-5,39	0.00000000	AT4G36850	AT4G36850	ref|Arabidopsis thaliana PQ-loop repeat family protein / transmembrane family protein mRNA, complete cds [NM_119849]
-5,42	0.00000000	AT1G15040	AT1G15040	ref|Arabidopsis thaliana putative glutamine amidotransferase mRNA, complete cds [NM_101374]
-5,46	0.00000000	AT5G54165	AT5G54165	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001125962]
-5,82	0.00000000	AT4G17840	AT4G17840	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_117893]
-6,12	0.00000000	AT3G07350	AT3G07350	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_111614]
-6,18	0.00000000	AT4G24972	TPD1	ref|Arabidopsis thaliana protein TAPETUM DETERMINANT 1 mRNA, complete cds [NM_202883]
-6,22	0.00000000	AT1G13990	AT1G13990	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001160863]

	-6,27	0.00000000	AT5G61820	AT5G61820	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125576]
	-6,29	0.00000000	AT4G15610	AT4G15610	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_117652]
	-6,31	0.00000000	AT5G14730	AT5G14730	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_121477]
	-6,34	0.00000000	AT5G59400	AT5G59400	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125331]
	-6,49	0.00000000	AT3G10020	AT3G10020	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_111837]
	-6,52	0.00000000	AT5G64230	AT5G64230	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125819]
	-6,98	0.00000000	AT5G51720	AT5G51720	ref|Arabidopsis thaliana CDGSH iron-sulfur domain-containing protein NEET mRNA, complete cds [NM_124551]
	-7,01	0.00000000	AT4G39675	AT4G39675	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_120128]
	-7,22	0.00000000	AT3G49790	AT3G49790	ref|Arabidopsis thaliana Carbohydrate-binding protein mRNA, complete cds [NM_114839]
	-7,25	0.00000000	AT5G39520	AT5G39520	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_123314]
	-7,29	0.00000005	AT1G19530	AT1G19530	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_101811]
	-7,85	0.00000000	AT1G72060	AT1G72060	ref|Arabidopsis thaliana serine-type endopeptidase inhibitor mRNA, complete cds [NM_105864]
	-8,85	0.00000008	AT1G15010	AT1G15010	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_101370]
	-9,76	0.00000022	AT2G40000	HSPRO2	ref|Arabidopsis thaliana HS1 PRO-1 2-like protein mRNA, complete cds [NM_129558]
	-10,1	0.00000000	AT1G76600	AT1G76600	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_106310]
	-11,56	0.00000000	AT4G33666	AT4G33666	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_119524]
	-12,02	0.00000000	AT5G54585	AT5G54585	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_148130]
	-12,35	0.00000000	AT5G22140	AT5G22140	ref|Arabidopsis thaliana FAD/NAD(P)-binding oxidoreductase family protein mRNA, complete cds [NM_147895]
	-17,67	0.00000000	AT5G02020	AT5G02020	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_180421]
	-19,62	0.00000000	AT2G05540	AT2G05540	ref|Arabidopsis thaliana glycine-rich protein mRNA, complete cds [NM_126577]
	-20,85	0.00000000	AT3G24420	AT3G24420	ref|Arabidopsis thaliana hydrolase, alpha/beta fold family protein mRNA, complete cds [NM_113349]
	-22,75	0.00000000	AT4G08555	AT4G08555	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_179014]
	-31,28	0.00000000	AT1G73120	AT1G73120	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_105970]
	-34,59	0.00000000	AT3G20340	AT3G20340	ref|Arabidopsis thaliana paraquat downregulated protein mRNA, complete cds [NM_112925]
	-41,95	0.00000000	AT4G01870	AT4G01870	ref|Arabidopsis thaliana tolB-related protein mRNA, complete cds [NM_116417]
Uncategorized					
	8,26	0.00000000	R65132	R65132	tc|AAD15384.1 - Arabidopsis thaliana (Mouse-ear cress), partial (68%) [TC400604]
	7,13	0.00000000	CB185526	CB185526	Unknown
	5,22	0.00000000	BU917432	BU917432	gb|JKHR01A12 Size-selected small cDNAs of Arabidopsis thaliana Arabidopsis thaliana cDNA clone JKHR01A12, mRNA sequence [BU917432]
	3,82	0.00000023	BP586302	BP586302	gb|BP586302 RAFL15 Arabidopsis thaliana cDNA clone RAFL15-05-M21 3', mRNA sequence [BP586302]
	3,75	0.00000000	BU917428	BU917428	gb|JK04B05 Size-selected small cDNAs of Arabidopsis thaliana Arabidopsis thaliana cDNA clone JK04B05, mRNA sequence [BU917428]
	3,69	0.00000002	NP226468	NP226468	tc|GB|AB026649.1|BAB01078.1 gene_id:MOJ10.4~unknown protein [NP226468]
	3,63	0.00000000	BP783345	BP783345	Unknown
	3,54	0.00000000	EG453230	AT1G24270	gb|AYARG52TR pooled cDNA populations Arabidopsis thaliana cDNA, mRNA sequence [EG453230]
	3,11	0.00000000	AY334555	AY334555	gb|Arabidopsis thaliana At4-2 mRNA, complete sequence [AY334555]
	-3,51	0.00000000	TC314163	TC405990	tc|Rep: Formate dehydrogenase - Arabidopsis thaliana (Mouse-ear cress), partial (18%) [TC405990]
	-3,57	0.00000006	TA35940_3702	TA35940_3702	tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vinifera (Grape), partial (42%) [TC384450]
	-3,96	0.00000001	AK221828	AK221828	gb|Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL21-96-E04 [AK221828]
	-4,41	0.00000000	BU917423	BU917423	Unknown
	-4,62	0.00000000	CF652575	TA32560_3702	tc|Rep: Beta-glucosidase - Arabidopsis thaliana (Mouse-ear cress), partial (29%) [TC395229]
	-4,72	0.00000000	NP229859	NP229859	tc|GB|AL391141.1|CAC01711.1 quinone oxidoreductase-like protein [NP229859]
	-4,95	0.00000001	TC309308	TC396119	tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vinifera (Grape), partial (29%) [TC396119]
	-5,48	0.00000000	BP660593	BP660593	Unknown
	-5,53	0.00000006	TA32559_3702	TA32559_3702	tc|Rep: AT3g60140/T2O9_120 - Arabidopsis thaliana (Mouse-ear cress), partial (9%) [TC397325]
	-6,56	0.00000000	TC309871	TC396686	tc|Rep: Conglutin gamma-like protein - Arabidopsis thaliana (Mouse-ear cress), partial (35%) [TC396686]
	-6,74	0.00000002	BP667596	BP667596	tc|Rep: Uncharacterized protein At4g35770.3 - Arabidopsis thaliana (Mouse-ear cress), partial (53%) [TC406344]
	-16,54	0.00000000	TC304561	TC384346	tc|Rep: Xylosidase - Arabidopsis thaliana (Mouse-ear cress), complete [TC384346]
	-42,02	0.00000000	BE039144	BE039144	tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vinifera (Grape), partial (59%) [TC393828]

Table S3: List of genes whose expression is altered by super-elevated CO2 treatment. Genes that are differentially regulated by A. alternata VCs (cf. Supplemental Table 3 in Sánchez-López, Baslam, et al., 2016) are highlighted in yelow color. (BY FOLD-CHANGE)

Fold Change	pval (LiMMA)	ID	ProbeID	Description
21,39	0.00000000	AT1G80130	AT1G80130	ref|Arabidopsis thaliana tetratricopeptide repeat domain-containing protein mRNA, complete cds [NM_106662]
13,68	0.00000000	AT2G41240	BHLH100	ref|Arabidopsis thaliana transcription factor bHLH100 mRNA, complete cds [NM_129689]
12,85	0.00000000	AT3G56970	BHLH038	ref|Arabidopsis thaliana transcription factor ORG2 mRNA, complete cds [NM_115556]
11,58	0.00000000	AT2G46880	PAP14	ref|Arabidopsis thaliana purple acid phosphatase 14 mRNA, complete cds [NM_201975]
10,94	0.00000000	AT4G01080	TBL26	ref|Arabidopsis thaliana protein TRICHOME BIREFRINGENCE-LIKE 26 mRNA, complete cds [NM_116338]
10,37	0.00000000	AT3G22240	AT3G22240	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_113122]
9,9	0.00000000	AT3G56980	BHLH039	ref|Arabidopsis thaliana transcription factor ORG3 mRNA, complete cds [NM_115557]
9,88	0.00000000	AT4G22870	AT4G22870	ref|Arabidopsis thaliana leucoanthocyanidin dioxygenase-like protein mRNA, complete cds [NM_001160794]
9,73	0.00000000	AT1G56650	PAP1	ref|Arabidopsis thaliana transcription factor MYB75 mRNA, complete cds [NM_104541]
9,37	0.00000000	AT3G22235	AT3G22235	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_180292]
9,17	0.00000000	AT4G15210	BAM5	ref|Arabidopsis thaliana beta-amylase 5 mRNA, complete cds [NM_117609]
8,95	0.00000000	AT4G39210	APL3	ref|Arabidopsis thaliana glucose-1-phosphate adenylyltransferase large subunit 3 mRNA, complete cds [NM_120081]
8,91	0.00000000	AT5G17220	GSTF12	ref|Arabidopsis thaliana glutathione S-transferase phi 12 mRNA, complete cds [NM_121728]
8,59	0.00000000	AT3G57240	BG3	ref|Arabidopsis thaliana beta-1,3-glucanase 3 mRNA, complete cds [NM_115584]
8,26	0.00000000	R65132	R65132	tc|AAD15384.1 - Arabidopsis thaliana (Mouse-ear cress), partial (68%) [TC400604]
8,25	0.00000000	AT2G27402	AT2G27402	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_201818]
8,19	0.00000000	AT3G22231	PCC1	ref|Arabidopsis thaliana protein PATHOGEN AND CIRCADIAN CONTROLLED 1 mRNA, complete cds [NM_113121]
7,82	0.00000000	AT4G36700	AT4G36700	ref|Arabidopsis thaliana cupin family protein mRNA, complete cds [NM_119834]
7,69	0.00000000	AT3G18000	CPuORF30	ref|Arabidopsis thaliana conserved peptide upstream open reading frame 30 mRNA, complete cds [NM_001125181]
7,66	0.00000000	AT5G54060	UF3GT	ref|Arabidopsis thaliana anthocyanidin 3-O-glucoside 2'''-O-xylosyltransferase mRNA, complete cds [NM_124785]
7,59	0.00000000	AT1G19960	AT1G19960	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_101851]
7,51	0.00000000	AT1G47395	AT1G47395	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_179449]
7,25	0.00000000	AT5G42800	DFR	ref|Arabidopsis thaliana dihydroflavonol-4-reductase mRNA, complete cds [NM_123645]
7,14	0.00000000	AT2G26400	ARD3	ref|Arabidopsis thaliana acireductone dioxygenase 3 mRNA, complete cds [NM_128197]
7,13	0.00000000	CB185526	CB185526	Unknown
6,95	0.00000000	AT1G78370	GSTU20	ref|Arabidopsis thaliana glutathione S-transferase TAU 20 mRNA, complete cds [NM_106484]
6,89	0.00000000	AT4G23600	CORI3	ref|Arabidopsis thaliana cystine lyase CORI3 mRNA, complete cds [NM_179099]
6,86	0.00000000	AT2G14560	LURP1	ref|Arabidopsis thaliana protein LURP1 mRNA, complete cds [NM_127019]
6,62	0.00000000	AT4G17470	AT4G17470	ref|Arabidopsis thaliana putative palmitoyl-protein thioesterase mRNA, complete cds [NM_001203824]
6,48	0.00000000	AT5G03350	AT5G03350	ref|Arabidopsis thaliana lectin-like protein mRNA, complete cds [NM_120414]
6,12	0.00000000	AT4G21760	BGLU47	ref|Arabidopsis thaliana beta-glucosidase 47 mRNA, complete cds [NM_118296]
5,99	0.00000000	AT2G42540	COR15A	ref|Arabidopsis thaliana cold-regulated protein 15a mRNA, complete cds [NM_001202804]
5,85	0.00000000	AT4G22880	LDOX	ref|Arabidopsis thaliana leucoanthocyanidin dioxygenase mRNA, complete cds [NM_118417]
5,8	0.00000000	AT1G61800	GPT2	ref|Arabidopsis thaliana glucose-6-phosphate/phosphate translocator 2 mRNA, complete cds [NM_104862]
5,73	0.00000185	AT1G73325	AT1G73325	ref|Arabidopsis thaliana Kunitz family trypsin and protease inhibitor protein mRNA, complete cds [NM_105992]
5,71	0.00000002	AT3G25795	AK227365	gb|Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL14-04-D19 [AK227365]
5,65	0.00000000	AT1G04040	AT1G04040	ref|Arabidopsis thaliana HAD superfamily, subfamily IIIB acid phosphatase mRNA, complete cds [NM_100285]
5,44	0.00000000	AT3G03780	MS2	ref|Arabidopsis thaliana methionine synthase 2 mRNA, complete cds [NM_111249]
5,44	0.00000000	AT1G23100	AT1G23100	ref|Arabidopsis thaliana GroES-like protein mRNA, complete cds [NM_102158]
5,41	0.00000000	AT3G45140	LOX2	ref|Arabidopsis thaliana lipoxygenase 2 mRNA, complete cds [NM_114383]
5,36	0.00000000	AT1G68600	AT1G68600	ref|Arabidopsis thaliana Aluminum activated malate transporter family protein mRNA, complete cds [NM_105532]
5,33	0.00000000	AT1G62560	FMO GS-OX3	ref|Arabidopsis thaliana flavin-containing monooxygenase FMO GS-OX3 mRNA, complete cds [NM_104934]
5,24	0.00000000	AT1G67360	AT1G67360	ref|Arabidopsis thaliana REF/SRPP-like protein mRNA, complete cds [NM_179525]
5,22	0.00000000	BU917432	BU917432	gb|JKHR01A12 Size-selected small cDNAs of Arabidopsis thaliana Arabidopsis thaliana cDNA clone JKHR01A12, mRNA sequence [BU917432]
5,2	0.00000000	AT4G17670	AT4G17670	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_117875]
5,15	0.00000000	AT5G60730	AT5G60730	ref|Arabidopsis thaliana Anion-transporting ATPase mRNA, complete cds [NM_125466]
5,1	0.00000000	AT2G44670	AT2G44670	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_130031]
5,05	0.00000000	AT4G03060	AF418241	gb|Arabidopsis thaliana Col-0 2-oxoglutarate-dependent dioxygenase (AOP2) pseudogene, mRNA sequence [AF418241]

5,04	0.00000000	AT1G66390	MYB90	ref|Arabidopsis thaliana transcription factor MYB90 mRNA, complete cds [NM_105310]
5	0.00000000	AT5G15970	KIN2	ref|Arabidopsis thaliana stress-induced protein KIN2 mRNA, complete cds [NM_121602]
4,99	0.00000000	AT3G44450	AT3G44450	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_114313]
4,94	0.00000000	AT2G41090	AT2G41090	ref|Arabidopsis thaliana calmodulin-like protein 10 mRNA, complete cds [NM_129674]
4,94	0.00000000	AT3G61920	AT3G61920	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_116057]
4,93	0.00000000	AT5G14200	IMD1	ref|Arabidopsis thaliana isopropylmalate dehydrogenase 1 mRNA, complete cds [NM_001036803]
4,87	0.00000000	AT3G25882	NIMIN-2	ref|Arabidopsis thaliana protein NIM1-INTERACTING 2 mRNA, complete cds [NM_148752]
4,82	0.00000011	AT4G16590	CSLA01	ref|Arabidopsis thaliana cellulose synthase-like A01 mRNA, complete cds [NM_117760]
4,78	0.00000000	AT5G20190	AT5G20190	ref|Arabidopsis thaliana tetratricopeptide repeat domain-containing protein mRNA, complete cds [NM_122026]
4,76	0.00000000	AT3G26960	AT3G26960	ref|Arabidopsis thaliana pollen Ole e 1 allergen and extensin family protein mRNA, complete cds [NM_113610]
4,75	0.00000001	AT1G31690	AT1G31690	ref|Arabidopsis thaliana copper amine oxidase family protein mRNA, complete cds [NM_102904]
4,74	0.00000002	AT2G14247	AT2G14247	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_201723]
4,67	0.00000000	AT2G22170	AT2G22170	ref|Arabidopsis thaliana PLAT-plant-stress domain-containing protein mRNA, complete cds [NM_127785]
4,65	0.00000000	AT1G06830	AT1G06830	ref|Arabidopsis thaliana monothiol glutaredoxin-S11 mRNA, complete cds [NM_100560]
4,65	0.00000000	AT4G18440	AT4G18440	ref|Arabidopsis thaliana L-aspartase-like family protein mRNA, complete cds [NM_117957]
4,62	0.00000000	AT4G10270	AT4G10270	ref|Arabidopsis thaliana putative wound-responsive protein mRNA, complete cds [NM_117095]
4,62	0.00000000	AT4G25630	FIB2	ref|Arabidopsis thaliana mediator of RNA polymerase II transcription subunit 36a mRNA, complete cds [NM_118695]
4,6	0.00000002	AT1G47400	AT1G47400	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_103634]
4,55	0.00000000	AT3G28220	AT3G28220	ref|Arabidopsis thaliana TRAF-like family protein mRNA, complete cds [NM_113741]
4,52	0.00000017	AT1G32900	AT1G32900	ref|Arabidopsis thaliana granule-bound starch synthase 1 mRNA, complete cds [NM_103023]
4,52	0.00000000	AT1G18320	AT1G18320	ref|Arabidopsis thaliana mitochondrial import inner membrane translocase subunit TIM22-4 mRNA, complete cds [NM_101690]
4,51	0.00000000	AT5G15960	KIN1	ref|Arabidopsis thaliana cold and ABA inducible protein kin1 mRNA, complete cds [NM_121601]
4,51	0.00000000	AT5G63087	NP1655641	tc|GB|NM_001085318.1|NP_001078787.1 unknown protein;similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G63063.1) [NP1655641]
4,47	0.00000000	AT5G59670	AT5G59670	ref|Arabidopsis thaliana Leucine-rich repeat protein kinase family protein mRNA, complete cds [NM_125359]
4,46	0.00000000	AT3G58990	IPMI1	ref|Arabidopsis thaliana isopropylmalate isomerase 1 mRNA, complete cds [NM_115761]
4,43	0.00000051	AT4G23130	CRK5	ref|Arabidopsis thaliana cysteine-rich receptor-like protein kinase 5 mRNA, complete cds [NM_179094]
4,43	0.00000000	AT1G79400	CHX2	ref|Arabidopsis thaliana cation/H(+) antiporter 2 mRNA, complete cds [NM_106588]
4,41	0.00000000	AT1G56430	NAS4	ref|Arabidopsis thaliana nicotianamine synthase 4 mRNA, complete cds [NM_104521]
4,4	0.00000000	AT2G23010	SCPL9	ref|Arabidopsis thaliana serine carboxypeptidase-like 9 mRNA, complete cds [NM_127866]
4,39	0.00000000	AT1G15150	AT1G15150	ref|Arabidopsis thaliana MATE efflux family protein mRNA, complete cds [NM_101383]
4,37	0.00000000	AT2G43100	IPMI2	ref|Arabidopsis thaliana isopropylmalate isomerase 2 mRNA, complete cds [NM_129871]
4,36	0.00000000	AT5G50950	FUM2	ref|Arabidopsis thaliana fumarate hydratase 2 mRNA, complete cds [NM_124474]
4,29	0.00000000	AT4G02330	ATPMEPCRB	ref|Arabidopsis thaliana Probable pectinesterase/pectinesterase inhibitor 41 mRNA, complete cds [NM_116466]
4,27	0.00000000	AT4G11190	AT4G11190	ref|Arabidopsis thaliana disease resistance-responsive, dirigent domain-containing protein mRNA, complete cds [NM_117190]
4,27	0.00000000	AT1G75040	PR5	ref|Arabidopsis thaliana pathogenesis-related protein 5 mRNA, complete cds [NM_106161]
4,26	0.00000000	AT4G30650	AT4G30650	ref|Arabidopsis thaliana putative low temperature and salt responsive protein mRNA, complete cds [NM_119211]
4,26	0.00000000	AT4G08300	AT4G08300	ref|Arabidopsis thaliana nodulin MtN21 /EamA-like transporter family protein mRNA, complete cds [NM_116899]
4,25	0.00000003	AT5G50800	AT5G50800	ref|Arabidopsis thaliana bidirectional sugar transporter SWEET13 mRNA, complete cds [NM_124458]
4,24	0.00000000	AT1G16410	CYP79F1	ref|Arabidopsis thaliana dihomomethionine N-hydroxylase mRNA, complete cds [NM_101507]
4,24	0.00000000	AT1G64220	TOM7-2	ref|Arabidopsis thaliana mitochondrial import receptor subunit TOM7-2 mRNA, complete cds [NM_105096]
4,18	0.00000000	AT5G13930	TT4	ref|Arabidopsis thaliana chalcone synthase mRNA, complete cds [NM_121396]
4,18	0.00000000	AT3G27060	TSO2	ref|Arabidopsis thaliana ribonucleoside-diphosphate reductase small chain C mRNA, complete cds [NM_113620]
4,17	0.00000000	AT4G39940	AKN2	ref|Arabidopsis thaliana adenosine-5'-phosphosulfate-kinase 2 mRNA, complete cds [NM_120157]
4,17	0.00000000	AT1G64980	AT1G64980	ref|Arabidopsis thaliana putative nucleotide-diphospho-sugar transferase mRNA, complete cds [NM_105172]
4,1	0.00000000	AT3G45930	AT3G45930	ref|Arabidopsis thaliana histone H4 mRNA, complete cds [NM_114462]
4,08	0.00000000	AT2G40750	WRKY54	ref|Arabidopsis thaliana WRKY DNA-binding protein 54 mRNA, complete cds [NM_129637]
4,06	0.00000000	AT1G06000	AT1G06000	ref|Arabidopsis thaliana flavonol-7-O-rhamnosyltransferase mRNA, complete cds [NM_100480]
4,03	0.00000000	AT2G35860	FLA16	ref|Arabidopsis thaliana fasciclin-like arabinogalactan protein 16 mRNA, complete cds [NM_179922]
4,01	0.00000001	AT4G14090	AT4G14090	ref|Arabidopsis thaliana anthocyanin 5-O-glucosyltransferase mRNA, complete cds [NM_117485]
3,99	0.00000000	AT3G44750	HDA3	ref|Arabidopsis thaliana histone deacetylase HDT1 mRNA, complete cds [NM_114344]
3,94	0.00000000	AT5G67370	AT5G67370	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_126137]

3,92	0.00000000	AT4G15440	HPL1	ref|Arabidopsis thaliana hydroperoxide lyase 1 mRNA, complete cds [NM_117633]
3,91	0.00000000	AT5G20740	AT5G20740	ref|Arabidopsis thaliana plant invertase/pectin methylesterase inhibitor domain-containing protein mRNA, complete cds [NM_122081]
3,9	0.00000000	AT5G23020	IMS2	ref|Arabidopsis thaliana methylthioalkylmalate synthase 3 mRNA, complete cds [NM_122208]
3,85	0.00000000	AT1G29660	AT1G29660	ref|Arabidopsis thaliana GDSL esterase/lipase mRNA, complete cds [NM_102706]
3,83	0.00000000	AT4G12730	FLA2	ref|Arabidopsis thaliana fasciclin-like arabinogalactan protein 2 mRNA, complete cds [NM_117342]
3,82	0.00000023	BP586302	BP586302	gb|BP586302 RAFL15 Arabidopsis thaliana cDNA clone RAFL15-05-M21 3', mRNA sequence [BP586302]
3,8	0.00000000	AT5G08640	FLS1	ref|Arabidopsis thaliana flavonol synthase 1 mRNA, complete cds [NM_001203337]
3,77	0.00000000	AT1G11545	XTH8	ref|Arabidopsis thaliana probable xyloglucan endotransglucosylase/hydrolase protein 8 mRNA, complete cds [NM_101028]
3,76	0.00000000	AT1G73600	CPuORF32	ref|Arabidopsis thaliana conserved peptide upstream open reading frame 32 mRNA, complete cds [NM_001124125]
3,76	0.00000000	AT1G18590	SOT17	ref|Arabidopsis thaliana sulfotransferase 17 mRNA, complete cds [NM_101717]
3,75	0.00000000	BU917428	BU917428	gb|JK04B05 Size-selected small cDNAs of Arabidopsis thaliana Arabidopsis thaliana cDNA clone JK04B05, mRNA sequence [BU917428]
3,74	0.00000000	AT3G23830	GRP4	ref|Arabidopsis thaliana glycine-rich RNA-binding protein 4 mRNA, complete cds [NM_180298]
3,73	0.00000001	AT3G03060	AT3G03060	ref|Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA, complete cds [NM_111176]
3,73	0.00000001	AT2G30766	AT2G30766	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001124947]
3,71	0.00000000	AT1G65860	FMO GS-OX1	ref|Arabidopsis thaliana flavin-containing monooxygenase FMO GS-OX1 mRNA, complete cds [NM_105258]
3,71	0.00000000	AT5G61030	GR-RBP3	ref|Arabidopsis thaliana glycine-rich RNA-binding protein 3 mRNA, complete cds [NM_125496]
3,71	0.00000000	AT4G14400	ACD6	ref|Arabidopsis thaliana protein ACCELERATED CELL DEATH 6 mRNA, complete cds [NM_117519]
3,71	0.00000000	AT3G22550	AT3G22550	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_113154]
3,69	0.00000006	AT5G15120	AT5G15120	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_121516]
3,69	0.00000002	NP226468	NP226468	tc|GB|AB026649.1|BAB01078.1 gene_id:MOJ10.4~unknown protein [NP226468]
3,66	0.00000000	AT3G25700	AT3G25700	ref|Arabidopsis thaliana aspartyl protease family protein mRNA, complete cds [NM_113469]
3,65	0.00000001	AT2G33847	AT2G33847	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001084533]
3,64	0.00000000	AT1G01580	FRO2	ref|Arabidopsis thaliana ferric reduction oxidase 2 mRNA, complete cds [NM_100040]
3,63	0.00000000	BP783345	BP783345	Unknown
3,62	0.00000003	AT2G07774	AT2G07774	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_147273]
3,6	0.00000000	AT1G80270	PPR596	ref|Arabidopsis thaliana pentatricopeptide repeat-containing protein mRNA, complete cds [NM_001084384]
3,6	0.00000001	AT5G03120	AT5G03120	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_120390]
3,59	0.00000000	AT1G19640	JMT	ref|Arabidopsis thaliana jasmonic acid carboxyl methyltransferase mRNA, complete cds [NM_101820]
3,59	0.00000000	AT3G44860	FAMT	ref|Arabidopsis thaliana farnesoic acid carboxyl-O-methyltransferase mRNA, complete cds [NM_114355]
3,58	0.00000000	AT2G26440	AT2G26440	ref|Arabidopsis thaliana Probable pectinesterase/pectinesterase inhibitor 12 mRNA, complete cds [NM_128201]
3,58	0.00000030	AT3G29590	AT5MAT	ref|Arabidopsis thaliana malonyl-CoA:anthocyanidin 5-O-glucoside-6-O-malonyltransferase mRNA, complete cds [NM_113880]
3,58	0.00000000	AT5G02570	AT5G02570	ref|Arabidopsis thaliana histone H2B mRNA, complete cds [NM_120335]
3,57	0.00000000	AT3G51240	F3H	ref|Arabidopsis thaliana flavanone 3-hydroxylase mRNA, complete cds [NM_114983]
3,56	0.00000000	AT3G52370	FLA15	ref|Arabidopsis thaliana fasciclin-like arabinogalactan protein 15 mRNA, complete cds [NM_115097]
3,56	0.00000066	AT5G22570	WRKY38	ref|Arabidopsis thaliana putative WRKY transcription factor 38 mRNA, complete cds [NM_122163]
3,55	0.00000000	AT2G46650	CB5-C	ref|Arabidopsis thaliana cytochrome B5 isoform C mRNA, complete cds [NM_130230]
3,55	0.00000002	AT2G07815	AT2G07815	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001124814]
3,54	0.00000000	AT3G17120	AT3G17120	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_202597]
3,54	0.00000000	EG453230	AT1G24270	gb|AYARG52TR pooled cDNA populations Arabidopsis thaliana cDNA, mRNA sequence [EG453230]
3,53	0.00000000	AT4G12030	BAT5	ref|Arabidopsis thaliana probable sodium/metabolite cotransporter BASS5 mRNA, complete cds [NM_117273]
3,51	0.00000000	AT5G12910	AT5G12910	ref|Arabidopsis thaliana histone H3-like 4 mRNA, complete cds [NM_121294]
3,51	0.00000002	AT3G23450	AT3G23450	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_113248]
3,5	0.00000000	AT4G28250	EXPB3	ref|Arabidopsis thaliana expansin B3 mRNA, complete cds [NM_118965]
3,5	0.00000000	AT2G27840	HDT4	ref|Arabidopsis thaliana histone deacetylase HDT4 mRNA, complete cds [NM_128344]
3,49	0.00000003	AT1G66270	BGLU21	ref|Arabidopsis thaliana beta-glucosidase 21 mRNA, complete cds [NM_105298]
3,49	0.00000000	AT4G24265	AT4G24265	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_148370]
3,46	0.00000000	AT2G39030	AT2G39030	ref|Arabidopsis thaliana L-ornithine N5-acetyltransferase NATA1 mRNA, complete cds [NM_129460]
3,46	0.00000000	AT3G52630	AT3G52630	ref|Arabidopsis thaliana Nucleic acid-binding, OB-fold-like protein mRNA, complete cds [NM_115123]
3,46	0.00000000	AT4G02850	AT4G02850	ref|Arabidopsis thaliana phenazine biosynthesis PhzC/PhzF family protein mRNA, complete cds [NM_116519]
3,45	0.00000000	AT1G54040	ESP	ref|Arabidopsis thaliana epithiospecifier protein mRNA, complete cds [NM_180632]
3,44	0.00000001	AT4G04940	AT4G04940	ref|Arabidopsis thaliana transducin/WD40 domain-containing protein mRNA, complete cds [NM_116732]

3,42	0.00000000	AT1G01190	CYP78A8	ref|Arabidopsis thaliana cytochrome P450, family 78, subfamily A, polypeptide 8 mRNA, complete cds [NM_100001]
3,42	0.00000000	AT1G07070	AT1G07070	ref|Arabidopsis thaliana 60S ribosomal protein L35a-1 mRNA, complete cds [NM_100581]
3,39	0.00000055	AT1G04240	SHY2	ref|Arabidopsis thaliana auxin-responsive protein IAA3 mRNA, complete cds [NM_100305]
3,39	0.00000004	AT3G09922	IPS1	ref|Arabidopsis thaliana protein ED BY PHOSPHATE STARVATION1 mRNA, complete cds [NM_180219]
3,34	0.00000000	AT5G61000	RPA70D	ref|Arabidopsis thaliana replication protein A 70 kDa DNA-binding subunit D mRNA, complete cds [NM_125493]
3,34	0.00000000	AT3G46320	AT3G46320	ref|Arabidopsis thaliana histone H4 mRNA, complete cds [NM_180329]
3,34	0.00000000	AT5G45650	AT5G45650	ref|Arabidopsis thaliana subtilase family protein mRNA, complete cds [NM_123933]
3,34	0.00000000	AT5G44565	AT5G44565	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_203153]
3,33	0.00000009	AT1G52040	MBP1	ref|Arabidopsis thaliana myrosinase-binding protein 1 mRNA, complete cds [NM_104085]
3,33	0.00000000	AT4G00360	CYP86A2	ref|Arabidopsis thaliana cytochrome P450 86A2 mRNA, complete cds [NM_116260]
3,33	0.00000010	AT1G74770	AT1G74770	ref|Arabidopsis thaliana zinc ion binding protein mRNA, complete cds [NM_106135]
3,32	0.00000000	AT4G39950	CYP79B2	ref|Arabidopsis thaliana tryptophan N-monooxygenase 1 mRNA, complete cds [NM_120158]
3,3	0.00000000	AT2G16890	AT2G16890	ref|Arabidopsis thaliana UDP-glycosyltransferase 90A1 mRNA, complete cds [NM_127242]
3,3	0.00000000	AT3G10110	MEE67	ref|Arabidopsis thaliana mitochondrial import inner membrane translocase subunit TIM22-1 mRNA, complete cds [NM_111846]
3,3	0.00000001	AT3G23120	RLP38	ref|Arabidopsis thaliana receptor like protein 38 mRNA, complete cds [NM_113213]
3,29	0.00000001	AT1G78020	AT1G78020	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_106451]
3,28	0.00000000	AT1G76790	AT1G76790	ref|Arabidopsis thaliana indole glucosinolate o-methyltransferase 5 mRNA, complete cds [NM_106329]
3,28	0.00000000	AT5G11740	AGP15	ref|Arabidopsis thaliana arabinogalactan protein 15 mRNA, complete cds [NM_121212]
3,26	0.00000001	AT2G37510	AT2G37510	ref|Arabidopsis thaliana RNA recognition motif-containing protein mRNA, complete cds [NM_129306]
3,26	0.00000000	AT5G22460	AT5G22460	ref|Arabidopsis thaliana esterase/lipase/thioesterase family protein mRNA, complete cds [NM_180724]
3,25	0.00000000	AT1G79530	GAPCP-1	ref|Arabidopsis thaliana glyceraldehyde-3-phosphate dehydrogenase GAPCP1 mRNA, complete cds [NM_106601]
3,24	0.00000000	AT4G37400	CYP81F3	ref|Arabidopsis thaliana cytochrome P450, family 81, subfamily F, polypeptide 3 mRNA, complete cds [NM_119903]
3,24	0.00000002	AT4G12880	ENODL19	ref|Arabidopsis thaliana early nodulin-like protein 19 mRNA, complete cds [NM_001203782]
3,24	0.00000000	AT2G33210	HSP60-2	ref|Arabidopsis thaliana heat shock protein 60-2 mRNA, complete cds [NM_179872]
3,23	0.00000002	AT5G05270	AT5G05270	ref|Arabidopsis thaliana Chalcone-flavanone isomerase family protein mRNA, complete cds [NM_180439]
3,23	0.00000000	AT1G24020	MLP423	ref|Arabidopsis thaliana MLP-like protein 423 mRNA, complete cds [NM_102249]
3,23	0.00000329	AT3G19350	MPC	ref|Arabidopsis thaliana maternally expressed PAB C-terminal protein mRNA, complete cds [NM_112822]
3,23	0.00000000	AT2G28740	HIS4	ref|Arabidopsis thaliana histone H4 mRNA, complete cds [NM_128434]
3,21	0.00000002	AT5G11590	TINY2	ref|Arabidopsis thaliana dehydration-responsive element-binding protein 3 mRNA, complete cds [NM_121197]
3,21	0.00000000	AT1G45010	AT1G45010	ref|Arabidopsis thaliana TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein mRNA, complete cds [NM_103581]
3,2	0.00000000	AT1G45201	TLL1	ref|Arabidopsis thaliana triacylglycerol lipase-like 1 mRNA, complete cds [NM_179441]
3,2	0.00000000	AT1G23410	AT1G23410	ref|Arabidopsis thaliana 40S ribosomal protein S27a-1 mRNA, complete cds [NM_102190]
3,19	0.00000000	AT5G10390	AT5G10390	ref|Arabidopsis thaliana histone H3 mRNA, complete cds [NM_121077]
3,18	0.00000000	AT1G56150	AT1G56150	ref|Arabidopsis thaliana SAUR-like auxin-responsive protein mRNA, complete cds [NM_104494]
3,18	0.00000000	AT5G14330	AT5G14330	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_121437]
3,17	0.00000000	AT4G04750	AT4G04750	ref|Arabidopsis thaliana sugar transporter ERD6-like 14 mRNA, complete cds [NM_116713]
3,17	0.00000000	AT2G46430	CNGC3	ref|Arabidopsis thaliana cyclic nucleotide gated channel 3 mRNA, complete cds [NM_130207]
3,17	0.00000000	AT1G03820	AT1G03820	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_100261]
3,16	0.00000000	AT1G41830	SKS6	ref|Arabidopsis thaliana SKU5 similar 6 mRNA, complete cds [NM_103408]
3,15	0.00000000	AT1G19940	GH9B5	ref|Arabidopsis thaliana glycosyl hydrolase 9B5 mRNA, complete cds [NM_101849]
3,15	0.00000007	AT1G03495	AT1G03495	ref|Arabidopsis thaliana coumaroyl-CoA:anthocyanidin 3-O-glucoside-6-O-coumaroyltransferase 2 mRNA, complete cds [NM_100232]
3,15	0.00000000	AT2G31230	ERF15	ref|Arabidopsis thaliana ethylene-responsive transcription factor 15 mRNA, complete cds [NM_179831]
3,15	0.00000000	AT5G05365	AT5G05365	ref|Arabidopsis thaliana Heavy metal transport/detoxification superfamily protein mRNA, complete cds [NM_001085064]
3,14	0.00000000	AT4G28780	AT4G28780	ref|Arabidopsis thaliana GDSL esterase/lipase mRNA, complete cds [NM_119022]
3,13	0.00000000	AT5G25830	GATA12	ref|Arabidopsis thaliana GATA transcription factor 12 mRNA, complete cds [NM_122484]
3,13	0.00000000	AT5G44568	AT5G44568	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001085241]
3,12	0.00000000	AT1G24070	CSLA10	ref|Arabidopsis thaliana cellulose synthase-like A10 mRNA, complete cds [NM_102254]
3,12	0.00000000	AT2G11810	MGDC	ref|Arabidopsis thaliana Monogalactosyldiacylglycerol synthase 3 mRNA, complete cds [NM_001124829]
3,12	0.00000000	AT1G02450	NIMIN1	ref|Arabidopsis thaliana protein NIM1-INTERACTING 1 mRNA, complete cds [NM_100126]
3,12	0.00000000	AT1G61580	RPL3B	ref|Arabidopsis thaliana 60S ribosomal protein L3-2 mRNA, complete cds [NM_104840]
3,11	0.00000000	AT1G74440	AT1G74440	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_106104]

3,11	0.00000000	AY334555	AY334555	gb|Arabidopsis thaliana At4-2 mRNA, complete sequence [AY334555]
3,09	0.00000000	AT2G15000	AT2G15000	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001084423]
3,08	0.00000000	AT1G52400	BGLU18	ref|Arabidopsis thaliana beta glucosidase 18 mRNA, complete cds [NM_104118]
3,07	0.00000000	AT2G18328	RL4	ref|Arabidopsis thaliana protein RADIALIS-like 4 mRNA, complete cds [NM_001084443]
3,06	0.00000000	AT1G23020	FRO3	ref|Arabidopsis thaliana ferric reduction oxidase 3 mRNA, complete cds [NM_102150]
3,06	0.00000000	AT3G17830	AT3G17830	ref|Arabidopsis thaliana molecular chaperone Hsp40/DnaJ family protein mRNA, complete cds [NM_112664]
3,06	0.00000000	AT1G65486	AT1G65486	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001124079]
3,06	0.00000009	AT3G15357	AT3G15357	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_112403]
3,04	0.00000000	AT1G30530	UGT78D1	ref|Arabidopsis thaliana UDP-glucosyl transferase 78D1 mRNA, complete cds [NM_102790]
3,04	0.00000000	AT5G23420	HMGB6	ref|Arabidopsis thaliana high-mobility group B6 protein mRNA, complete cds [NM_122249]
3,03	0.00000002	AT1G45191	AT1G45191	ref|Arabidopsis thaliana beta-glucosidase 1 mRNA, complete cds [NM_179440]
3,03	0.00000000	AT5G64080	AT5G64080	ref|Arabidopsis thaliana Non-specific lipid-transfer protein-like protein mRNA, complete cds [NM_125804]
3,03	0.00000000	AT4G12600	AT4G12600	ref|Arabidopsis thaliana ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein mRNA, complete cds [NM_117330]
3,03	0.00000000	AT2G40435	AT2G40435	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_129604]
3,03	0.00000003	AT5G41460	AT5G41460	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_123510]
3,01	0.00000000	AT1G09200	AT1G09200	ref|Arabidopsis thaliana histone H3 mRNA, complete cds [NM_100790]
-3,01	0.00000000	AT5G65870	PSK5	ref|Arabidopsis thaliana putative phytosulfokines 5 precursor mRNA, complete cds [NM_125984]
-3,01	0.00000001	AT2G38820	AT2G38820	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_201907]
-3,02	0.00000000	AT3G03480	CHAT	ref|Arabidopsis thaliana acetyl CoA:(Z)-3-hexen-1-ol acetyltransferase mRNA, complete cds [NM_111219]
-3,02	0.00000006	AT4G13830	J20	ref|Arabidopsis thaliana chaperone protein dnaJ 20 mRNA, complete cds [NM_179045]
-3,02	0.00000000	AT1G30720	AT1G30720	ref|Arabidopsis thaliana FAD-binding Berberine family protein mRNA, complete cds [NM_102808]
-3,02	0.00000001	AT1G02470	AT1G02470	ref|Arabidopsis thaliana SRPBCC ligand-binding domain-containing protein mRNA, complete cds [NM_100128]
-3,03	0.00000001	AT3G10985	SAG20	ref|Arabidopsis thaliana senescence associated protein 20 mRNA, complete cds [NM_202550]
-3,04	0.00000113	AT1G68320	MYB62	ref|Arabidopsis thaliana R2R3-MYB transcription family mRNA, complete cds [NM_105503]
-3,05	0.00000000	AT3G26200	CYP71B22	ref|Arabidopsis thaliana cytochrome P450 71B22 mRNA, complete cds [NM_113527]
-3,06	0.00000000	AT1G63800	UBC5	ref|Arabidopsis thaliana ubiquitin-conjugating enzyme E2 5 mRNA, complete cds [NM_105055]
-3,07	0.00000000	AT5G18670	BMY3	ref|Arabidopsis thaliana putative beta-amylase BMY3 mRNA, complete cds [NM_121872]
-3,07	0.00000000	AT3G13450	DIN4	ref|Arabidopsis thaliana branched chain alpha-keto acid dehydrogenase E1 beta mRNA, complete cds [NM_112191]
-3,07	0.00000001	AT3G09580	AT3G09580	ref|Arabidopsis thaliana FAD/NAD(P)-binding oxidoreductase family protein mRNA, complete cds [NM_111792]
-3,07	0.00000000	AT5G13370	AT5G13370	ref|Arabidopsis thaliana auxin-responsive GH3 family protein mRNA, complete cds [NM_121340]
-3,07	0.00000000	AT5G44572	AT5G44572	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001085242]
-3,08	0.00000000	AT1G62380	ACO2	ref|Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate oxidase 2 mRNA, complete cds [NM_104918]
-3,08	0.00000003	AT5G10250	DOT3	ref|Arabidopsis thaliana putative BTB/POZ domain-containing protein DOT3 mRNA, complete cds [NM_121063]
-3,08	0.00000000	AT2G27385	AT2G27385	ref|Arabidopsis thaliana pollen Ole e 1 allergen and extensin family protein mRNA, complete cds [NM_179769]
-3,09	0.00000000	AT2G38400	AGT3	ref|Arabidopsis thaliana alanine:glyoxylate aminotransferase 3 mRNA, complete cds [NM_001202772]
-3,09	0.00000000	AT2G36320	AT2G36320	ref|Arabidopsis thaliana zinc finger A20 and AN1 domain-containing stress-associated protein 4 mRNA, complete cds [NM_129189]
-3,09	0.00000000	AT4G20070	AAH	ref|Arabidopsis thaliana allantoate amidohydrolase mRNA, complete cds [NM_118126]
-3,09	0.00000002	AT3G60300	AT3G60300	ref|Arabidopsis thaliana RWD domain-containing protein mRNA, complete cds [NM_115894]
-3,09	0.00000000	AT2G37750	AT2G37750	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_129331]
-3,1	0.00000000	AT1G80840	WRKY40	ref|Arabidopsis thaliana putative WRKY transcription factor 40 mRNA, complete cds [NM_106732]
-3,12	0.00000000	AT2G37760	AT2G37760	ref|Arabidopsis thaliana aldo-keto reductase family 4 member C8 mRNA, complete cds [NM_201898]
-3,12	0.00000012	AT1G58180	BCA6	ref|Arabidopsis thaliana beta carbonic anhydrase 6 mRNA, complete cds [NM_179492]
-3,12	0.00000000	AT4G19880	AT4G19880	ref|Arabidopsis thaliana Glutathione S-transferase family protein mRNA, complete cds [NM_118108]
-3,12	0.00000001	AT3G61430	PIP1A	ref|Arabidopsis thaliana aquaporin PIP1-1 mRNA, complete cds [NM_001084854]
-3,12	0.00000001	AT5G58570	AT5G58570	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125244]
-3,13	0.00000000	AT3G15500	NAC3	ref|Arabidopsis thaliana ATAF-like NAC-domain transcription factor mRNA, complete cds [NM_112418]
-3,13	0.00000000	AT4G32940	GAMMA-VPE	ref|Arabidopsis thaliana vacuolar-processing enzyme gamma mRNA, complete cds [NM_119448]
-3,13	0.00000000	AT4G27410	RD26	ref|Arabidopsis thaliana NAC transcription factor RD26 mRNA, complete cds [NM_001084983]
-3,14	0.00000006	AT3G22370	AOX1A	ref|Arabidopsis thaliana alternative oxidase 1A mRNA, complete cds [NM_113135]
-3,14	0.00000000	AT5G62020	HSFB2A	ref|Arabidopsis thaliana heat stress transcription factor B-2a mRNA, complete cds [NM_125595]
-3,15	0.00000000	AT1G67810	SUFE2	ref|Arabidopsis thaliana sulfur E2 mRNA, complete cds [NM_105449]

-3,16	0.00000000	AT1G01720	ATAF1	ref|Arabidopsis thaliana putative transcriptional activator with NAC domain mRNA, complete cds [NM_100054]
-3,16	0.00000000	AT2G24100	AT2G24100	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_127972]
-3,16	0.00000000	AT4G25170	AT4G25170	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001160795]
-3,17	0.00000000	AT5G14740	CA2	ref|Arabidopsis thaliana carbonic anhydrase 2 mRNA, complete cds [NM_001036806]
-3,17	0.00000000	AT2G28110	FRA8	ref|Arabidopsis thaliana probable glucuronoxylan glucuronosyltransferase IRX7 mRNA, complete cds [NM_179782]
-3,17	0.00000000	AT1G58370	RXF12	ref|Arabidopsis thaliana xylanase 1 mRNA, complete cds [NM_104617]
-3,17	0.00000000	AT4G35420	DRL1	ref|Arabidopsis thaliana dihydroflavonol 4-reductase-like1 mRNA, complete cds [NM_119708]
-3,17	0.00000000	AT5G43570	AT5G43570	ref|Arabidopsis thaliana PR-6 proteinase inhibitor family protein mRNA, complete cds [NM_123723]
-3,17	0.00000001	AT5G18600	AT5G18600	ref|Arabidopsis thaliana monothiol glutaredoxin-S2 mRNA, complete cds [NM_121865]
-3,17	0.00000000	AT3G29240	AT3G29240	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_180317]
-3,18	0.00000003	AT4G15670	AT4G15670	ref|Arabidopsis thaliana monothiol glutaredoxin-S7 mRNA, complete cds [NM_117658]
-3,18	0.00000000	AT5G57910	AT5G57910	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125176]
-3,19	0.00000000	AT4G39090	RD19	ref|Arabidopsis thaliana cysteine proteinase RD19a mRNA, complete cds [NM_120069]
-3,2	0.00000000	AT2G39980	AT2G39980	ref|Arabidopsis thaliana HXXXD-type acyl-transferase-like protein mRNA, complete cds [NM_129556]
-3,2	0.00000001	AT3G25790	AT3G25790	ref|Arabidopsis thaliana myb-like transcription factor family protein mRNA, complete cds [NM_113478]
-3,2	0.00000000	AT3G06420	ATG8H	ref|Arabidopsis thaliana autophagy-related protein 8h mRNA, complete cds [NM_111517]
-3,22	0.00000000	AT1G11080	scpl31	ref|Arabidopsis thaliana serine carboxypeptidase-like 31 mRNA, complete cds [NM_001198028]
-3,22	0.00000001	AT2G17500	AT2G17500	ref|Arabidopsis thaliana auxin efflux carrier family protein mRNA, complete cds [NM_179633]
-3,22	0.00000008	AT5G21940	AT5G21940	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_147877]
-3,23	0.00000000	AT5G18630	AT5G18630	ref|Arabidopsis thaliana putative class 3 lipase mRNA, complete cds [NM_121868]
-3,23	0.00000002	AT2G41230	AT2G41230	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_180017]
-3,24	0.00000000	AT3G30775	ERD5	ref|Arabidopsis thaliana proline dehydrogenase 1 mRNA, complete cds [NM_113981]
-3,24	0.00000000	AT1G03230	AT1G03230	ref|Arabidopsis thaliana aspartyl protease-like protein mRNA, complete cds [NM_100205]
-3,25	0.00000000	AT5G48490	AT5G48490	ref|Arabidopsis thaliana bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein mRNA, complete cds [NM_124225]
-3,25	0.00000001	AT1G02850	BGLU11	ref|Arabidopsis thaliana beta glucosidase 11 mRNA, complete cds [NM_202017]
-3,25	0.00000001	AT2G26740	SEH	ref|Arabidopsis thaliana soluble epoxide hydrolase mRNA, complete cds [NM_128231]
-3,25	0.00000000	AT5G04340	ZAT6	ref|Arabidopsis thaliana zinc finger protein ZAT6 mRNA, complete cds [NM_120516]
-3,25	0.00000014	AT2G16340	AT2G16340	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_127188]
-3,26	0.00000000	AT1G76690	OPR2	ref|Arabidopsis thaliana 12-oxophytodienoate reductase 2 mRNA, complete cds [NM_106319]
-3,26	0.00000000	AT1G28260	AT1G28260	ref|Arabidopsis thaliana Telomerase activating protein Est1 mRNA, complete cds [NM_102591]
-3,26	0.00000000	AT3G19615	AT3G19615	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001084720]
-3,26	0.00000000	AT1G16720	HCF173	ref|Arabidopsis thaliana high chlorophyll fluorescence phenotype 173 protein mRNA, complete cds [NM_101533]
-3,27	0.00000000	AT2G36950	AT2G36950	ref|Arabidopsis thaliana heavy-metal-associated domain-containing protein mRNA, complete cds [NM_129251]
-3,27	0.00000000	AT2G36895	AT2G36895	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_179941]
-3,28	0.00000000	AT2G38170	CAX1	ref|Arabidopsis thaliana vacuolar cation/proton exchanger 1 mRNA, complete cds [NM_201901]
-3,28	0.00000000	AT1G70780	AT1G70780	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_105746]
-3,29	0.00000000	AT2G22960	AT2G22960	ref|Arabidopsis thaliana putative serine carboxypeptidase-like 52 mRNA, complete cds [NM_127861]
-3,29	0.00000002	AT5G66480	AT5G66480	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_126046]
-3,3	0.00000000	AT2G04795	AT2G04795	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_126510]
-3,31	0.00000000	AT3G01500	CA1	ref|Arabidopsis thaliana carbonic anhydrase 1 mRNA, complete cds [NM_111016]
-3,32	0.00000001	AT3G55710	AT3G55710	ref|Arabidopsis thaliana UDP-glycosyltransferase 76F2 mRNA, complete cds [NM_115429]
-3,33	0.00000000	AT1G21400	AT1G21400	ref|Arabidopsis thaliana thiamin diphosphate-binding fold protein mRNA, complete cds [NM_101992]
-3,34	0.00000000	AT1G73920	AT1G73920	ref|Arabidopsis thaliana alpha/beta-hydrolase domain-containing protein mRNA, complete cds [NM_179552]
-3,34	0.00000000	AT1G27290	AT1G27290	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001084133]
-3,35	0.00000000	AT2G03760	SOT12	ref|Arabidopsis thaliana sulphotransferase 12 mRNA, complete cds [NM_126423]
-3,35	0.00000000	AT1G78830	AT1G78830	ref|Arabidopsis thaliana curculin-like (mannose-binding) lectin-like protein mRNA, complete cds [NM_106531]
-3,35	0.00000010	AT2G25090	CIPK16	ref|Arabidopsis thaliana SNF1-related kinase mRNA, complete cds [NM_128066]
-3,36	0.00000000	AT5G61410	RPE	ref|Arabidopsis thaliana D-ribulose-5-phosphate-3-epimerase mRNA, complete cds [NM_125534]
-3,36	0.00000005	AT5G64750	abr-01	ref|Arabidopsis thaliana ethylene-responsive transcription factor ABR1 mRNA, complete cds [NM_125871]
-3,36	0.00000000	AT2G47560	AT2G47560	ref|Arabidopsis thaliana RING-H2 finger protein ATL64 mRNA, complete cds [NM_130324]
-3,36	0.00000000	AT5G58770	AT5G58770	ref|Arabidopsis thaliana dehydrodolichyl diphosphate synthase 2 mRNA, complete cds [NM_125264]

-3,37	0.00000001	AT1G75380	BBD1	ref|Arabidopsis thaliana bifunctional nuclease 1 mRNA, complete cds [NM_179559]
-3,37	0.00000000	AT2G30140	AT2G30140	ref|Arabidopsis thaliana UDP-glycosyltransferase 87A2 mRNA, complete cds [NM_128569]
-3,37	0.00000001	AT3G52480	AT3G52480	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_115108]
-3,38	0.00000000	AT4G04770	ABC1	ref|Arabidopsis thaliana ATP binding cassette protein 1 mRNA, complete cds [NM_116715]
-3,39	0.00000000	AT5G64250	AT5G64250	ref|Arabidopsis thaliana Aldolase-type TIM barrel family protein mRNA, complete cds [NM_125821]
-3,4	0.00000000	AT3G15760	AT3G15760	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_112446]
-3,41	0.00000095	AT3G49160	AT3G49160	ref|Arabidopsis thaliana pyruvate kinase-like protein mRNA, complete cds [NM_114775]
-3,41	0.00000000	AT5G57560	TCH4	ref|Arabidopsis thaliana xyloglucan endotransglucosylase/hydrolase protein 22 mRNA, complete cds [NM_125137]
-3,41	0.00000000	AT1G30820	AT1G30820	ref|Arabidopsis thaliana CTP synthase-like protein mRNA, complete cds [NM_102819]
-3,43	0.00000001	AT1G12780	UGE1	ref|Arabidopsis thaliana bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 1 mRNA, complete cds [NM_101148]
-3,43	0.00000000	AT3G10120	AT3G10120	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_111847]
-3,44	0.00000000	AT4G15700	AT4G15700	ref|Arabidopsis thaliana monothiol glutaredoxin-S3 mRNA, complete cds [NM_117661]
-3,45	0.00000001	AT3G11930	AT3G11930	ref|Arabidopsis thaliana universal stress protein-like protein mRNA, complete cds [NM_180231]
-3,45	0.00000000	AT5G06865	PGIP1	gb|Arabidopsis thaliana clone 108218 mRNA sequence [DQ108691]
-3,46	0.00000000	AT1G52100	AT1G52100	ref|Arabidopsis thaliana jacalin-like lectin domain-containing protein mRNA, complete cds [NM_001198273]
-3,46	0.00000000	AT4G35440	CLC-E	ref|Arabidopsis thaliana chloride channel protein CLC-e mRNA, complete cds [NM_119709]
-3,46	0.00000000	AT2G46220	AT2G46220	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_130184]
-3,47	0.00000000	AT5G51970	AT5G51970	ref|Arabidopsis thaliana putative sorbitol dehydrogenase mRNA, complete cds [NM_124576]
-3,47	0.00000000	AT5G63790	NAC102	ref|Arabidopsis thaliana NAC domain-containing protein 102 mRNA, complete cds [NM_125774]
-3,47	0.00000000	AT4G02380	SAG21	ref|Arabidopsis thaliana senescence-associated protein SAG21 mRNA, complete cds [NM_116471]
-3,48	0.00000000	AT1G13700	PGL1	ref|Arabidopsis thaliana 6-phosphogluconolactonase 1 mRNA, complete cds [NM_101239]
-3,48	0.00000008	AT3G57760	AT3G57760	ref|Arabidopsis thaliana protein kinase family protein mRNA, complete cds [NM_001035802]
-3,51	0.00000000	AT4G18010	5PTASE2	ref|Arabidopsis thaliana Type I inositol-1,4,5-trisphosphate 5-phosphatase 2 mRNA, complete cds [NM_179071]
-3,51	0.00000006	AT5G62520	SRO5	ref|Arabidopsis thaliana probable inactive poly [ADP-ribose] polymerase SRO5 mRNA, complete cds [NM_203252]
-3,51	0.00000000	AT4G06746	RAP2.9	ref|Arabidopsis thaliana ethylene-responsive transcription factor RAP2-9 mRNA, complete cds [NM_179009]
-3,51	0.00000000	TC314163	TC405990	tc|Rep: Formate dehydrogenase - Arabidopsis thaliana (Mouse-ear cress), partial (18%) [TC405990]
-3,52	0.00000000	AT3G46600	AT3G46600	ref|Arabidopsis thaliana scarecrow-like protein 30 mRNA, complete cds [NM_114527]
-3,53	0.00000000	AT3G26220	CYP71B3	ref|Arabidopsis thaliana cytochrome P450 71B3 mRNA, complete cds [NM_113529]
-3,55	0.00000000	AT5G39080	AT5G39080	ref|Arabidopsis thaliana HXXXD-type acyl-transferase-like protein mRNA, complete cds [NM_123270]
-3,55	0.00000001	AT5G59820	RHL41	ref|Arabidopsis thaliana high light responsive zinc finger protein ZAT12 mRNA, complete cds [NM_125374]
-3,56	0.00000000	AT5G28770	BZO2H3	ref|Arabidopsis thaliana basic leucine zipper 63 mRNA, complete cds [NM_001036885]
-3,56	0.00000001	AT1G66180	AT1G66180	ref|Arabidopsis thaliana aspartyl protease family protein mRNA, complete cds [NM_105289]
-3,57	0.00000000	AT3G44300	NIT2	ref|Arabidopsis thaliana nitrilase 2 mRNA, complete cds [NM_114298]
-3,57	0.00000000	AT2G41100	TCH3	ref|Arabidopsis thaliana calmodulin-like protein 4 mRNA, complete cds [NM_001202794]
-3,57	0.00000006	TA35940_3702	TA35940_3702	tc|Rep: Chromosome chr18 scaffold_1, whole genome shotgun sequence - Vitis vinifera (Grape), partial (42%) [TC384450]
-3,58	0.00000000	AT3G01970	WRKY45	ref|Arabidopsis thaliana WRKY DNA-binding protein 45 mRNA, complete cds [NM_111063]
-3,59	0.00000003	AT1G20630	CAT1	ref|Arabidopsis thaliana catalase 1 mRNA, complete cds [NM_101914]
-3,59	0.00000000	AT3G04010	AT3G04010	ref|Arabidopsis thaliana O-glycosyl hydrolases family 17 protein mRNA, complete cds [NM_111272]
-3,6	0.00000000	AT2G32150	AT2G32150	ref|Arabidopsis thaliana haloacid dehalogenase-like hydrolase domain-containing protein mRNA, complete cds [NM_128774]
-3,61	0.00000000	AT1G69530	EXPA1	ref|Arabidopsis thaliana expansin A1 mRNA, complete cds [NM_001124101]
-3,61	0.00000000	AT1G20350	TIM17-1	ref|Arabidopsis thaliana translocase inner membrane subunit 17-1 mRNA, complete cds [NM_101886]
-3,62	0.00000000	AT4G24230	ACBP3	ref|Arabidopsis thaliana acyl-CoA-binding domain 3 mRNA, complete cds [NM_001084972]
-3,62	0.00000000	AT4G34710	ADC2	ref|Arabidopsis thaliana arginine decarboxylase 2 mRNA, complete cds [NM_119637]
-3,62	0.00000001	AT4G24050	AT4G24050	ref|Arabidopsis thaliana NAD(P)-binding Rossmann-fold superfamily protein mRNA, complete cds [NM_118537]
-3,64	0.00000001	AT4G20860	AT4G20860	ref|Arabidopsis thaliana FAD-binding Berberine family protein mRNA, complete cds [NM_118204]
-3,64	0.00000000	AT3G53140	LUT1	ref|Arabidopsis thaliana carotene epsilon-monooxygenase mRNA, complete cds [NM_115173]
-3,64	0.00000000	AT1G49500	AT1G49500	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_103838]
-3,64	0.00000000	AT2G27830	AT2G27830	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_128343]
-3,65	0.00000001	AT5G17860	CAX7	ref|Arabidopsis thaliana calcium exchanger 7 mRNA, complete cds [NM_121792]
-3,66	0.00000000	AT5G65110	ACX2	ref|Arabidopsis thaliana acyl-coenzyme A oxidase 2 mRNA, complete cds [NM_001037068]
-3,66	0.00000000	AT1G23310	GGT1	ref|Arabidopsis thaliana glutamate:glyoxylate aminotransferase mRNA, complete cds [NM_001036006]

-3,67	0.00000000	AT5G06570	AT5G06570	ref|Arabidopsis thaliana probable carboxylesterase 15 mRNA, complete cds [NM_120740]
-3,68	0.00000009	AT1G64720	CP5	ref|Arabidopsis thaliana membrane related protein CP5 mRNA, complete cds [NM_105147]
-3,68	0.00000000	AT5G59340	WOX2	ref|Arabidopsis thaliana WUSCHEL-related homeobox 2 mRNA, complete cds [NM_125325]
-3,68	0.00000000	AT3G53230	AT3G53230	ref|Arabidopsis thaliana cell division control protein 48-B mRNA, complete cds [NM_115183]
-3,68	0.00000001	AT4G33660	AT4G33660	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_119522]
-3,7	0.00000005	AT2G05380	GRP3S	ref|Arabidopsis thaliana glycine-rich protein 3 short isoform mRNA, complete cds [NM_001124801]
-3,71	0.00000000	AT5G43450	AT5G43450	ref|Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate oxidase-like protein mRNA, complete cds [NM_123711]
-3,71	0.00000005	AT1G26800	AT1G26800	ref|Arabidopsis thaliana RING/U-box domain-containing protein mRNA, complete cds [NM_102444]
-3,73	0.00000002	AT3G50560	AT3G50560	ref|Arabidopsis thaliana Rossmann-fold NAD(P)-binding domain-containing protein mRNA, complete cds [NM_114916]
-3,74	0.00000001	AT5G66650	AT5G66650	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_126063]
-3,75	0.00000013	AT4G17245	AT4G17245	ref|Arabidopsis thaliana RING/U-box domain-containing protein mRNA, complete cds [NM_117830]
-3,77	0.00000000	AT5G64570	XYL4	ref|Arabidopsis thaliana beta-D-xylosidase 4 mRNA, complete cds [NM_125853]
-3,8	0.00000000	AT1G69260	AFP1	ref|Arabidopsis thaliana ABI five binding protein mRNA, complete cds [NM_105593]
-3,81	0.00000000	AT3G03470	CYP89A9	ref|Arabidopsis thaliana cytochrome P450, family 87, subfamily A, polypeptide 9 mRNA, complete cds [NM_111218]
-3,81	0.00000000	AT5G59510	RTFL5	ref|Arabidopsis thaliana protein rotundifolia like 5 mRNA, complete cds [NM_125343]
-3,83	0.00000000	AT1G08570	ACHT4	ref|Arabidopsis thaliana atypical CYS HIS rich thioredoxin 4 mRNA, complete cds [NM_001123776]
-3,83	0.00000000	AT4G34138	UGT73B1	ref|Arabidopsis thaliana UDP-glucosyl transferase 73B1 mRNA, complete cds [NM_119576]
-3,84	0.00000000	AT1G03220	AT1G03220	ref|Arabidopsis thaliana aspartyl protease-like protein mRNA, complete cds [NM_100204]
-3,85	0.00000000	AT5G59310	LTP4	ref|Arabidopsis thaliana non-specific lipid-transfer protein 4 mRNA, complete cds [NM_125322]
-3,85	0.00000000	AT4G24160	AT4G24160	ref|Arabidopsis thaliana lysophosphatidic acid acyltransferase mRNA, complete cds [NM_202876]
-3,85	0.00000001	AT5G64190	AT5G64190	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125815]
-3,87	0.00000040	AT2G34430	LHB1B1	ref|Arabidopsis thaliana light-harvesting chlorophyll protein complex II subunit B1 mRNA, complete cds [NM_128995]
-3,89	0.00000000	AT4G33150	AT4G33150	ref|Arabidopsis thaliana lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme mRNA, complete cds [NM_001160811]
-3,89	0.00000000	AT1G77450	NAC032	ref|Arabidopsis thaliana NAC domain containing protein 32 mRNA, complete cds [NM_106394]
-3,9	0.00000001	AT2G18193	AT2G18193	ref|Arabidopsis thaliana P-loop containing nucleoside triphosphate hydrolases superfamily protein mRNA, complete cds [NM_179641]
-3,91	0.00000000	AT5G02160	AT5G02160	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_120294]
-3,92	0.00000011	AT2G02930	GSTF3	ref|Arabidopsis thaliana glutathione S-transferase F3 mRNA, complete cds [NM_126346]
-3,93	0.00000001	AT2G40340	DREB2C	ref|Arabidopsis thaliana dehydration-responsive element-binding protein 2C mRNA, complete cds [NM_129594]
-3,96	0.00000001	AK221828	AK221828	gb|Arabidopsis thaliana mRNA for hypothetical protein, complete cds, clone: RAFL21-96-E04 [AK221828]
-3,99	0.00000000	AT1G56220	AT1G56220	ref|Arabidopsis thaliana dormancy/auxin associated protein mRNA, complete cds [NM_104501]
-4,01	0.00000000	AT5G65207	AT5G65207	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_148161]
-4,02	0.00000010	AT4G15690	AT4G15690	ref|Arabidopsis thaliana monothiol glutaredoxin-S5 mRNA, complete cds [NM_117660]
-4,04	0.00000000	AT1G18020	AT1G18020	ref|Arabidopsis thaliana putative 12-oxophytodienoate reductase-like protein 2B mRNA, complete cds [NM_179352]
-4,06	0.00000000	AT4G03320	tic20-IV	ref|Arabidopsis thaliana translocon at the inner envelope membrane of chloroplasts 20-IV mRNA, complete cds [NM_116570]
-4,06	0.00000001	AT2G41730	AT2G41730	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_129737]
-4,08	0.00000000	AT4G15550	IAGLU	ref|Arabidopsis thaliana UDP-glucose:indole-3-acetate beta-D-glucosyltransferase mRNA, complete cds [NM_117646]
-4,09	0.00000000	AT2G47180	GolS1	ref|Arabidopsis thaliana galactinol synthase 1 mRNA, complete cds [NM_130286]
-4,09	0.00000026	AT5G47860	AT5G47860	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_124160]
-4,1	0.00000000	AT1G55920	SERAT2;1	ref|Arabidopsis thaliana serine acetyltransferase 1 mRNA, complete cds [NM_104470]
-4,1	0.00000000	AT5G63190	AT5G63190	ref|Arabidopsis thaliana MA3 domain-containing protein mRNA, complete cds [NM_125714]
-4,11	0.00000000	AT4G25390	AT4G25390	ref|Arabidopsis thaliana receptor-like serine/threonine-protein kinase mRNA, complete cds [NM_118671]
-4,11	0.00000000	AT3G45730	AT3G45730	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_114442]
-4,12	0.00000001	AT2G25080	GPX1	ref|Arabidopsis thaliana phospholipid hydroperoxide glutathione peroxidase 1 mRNA, complete cds [NM_128065]
-4,13	0.00000109	AT5G14110	AT5G14110	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_121415]
-4,16	0.00000000	AT3G48990	AT3G48990	ref|Arabidopsis thaliana 4-coumarate--CoA ligase-like 10 mRNA, complete cds [NM_114758]
-4,17	0.00000000	AT5G53970	AT5G53970	ref|Arabidopsis thaliana tyrosine aminotransferase mRNA, complete cds [NM_124776]
-4,21	0.00000000	AT2G26980	CIPK3	ref|Arabidopsis thaliana CBL-interacting serine/threonine-protein kinase 3 mRNA, complete cds [NM_001036350]
-4,21	0.00000000	AT2G23030	SNRK2.9	ref|Arabidopsis thaliana serine/threonine-protein kinase SNRK2.9 mRNA, complete cds [NM_127867]
-4,22	0.00000000	AT1G21550	AT1G21550	ref|Arabidopsis thaliana putative calcium-binding protein CML44 mRNA, complete cds [NM_102004]
-4,23	0.00000000	AT1G19660	AT1G19660	ref|Arabidopsis thaliana putative wound-responsive protein mRNA, complete cds [NM_001035991]
-4,24	0.00000000	AT5G20230	BCB	ref|Arabidopsis thaliana blue-copper-binding protein mRNA, complete cds [NM_122030]

-4,25	0.00000000	AT3G06500	AT3G06500	ref|Arabidopsis thaliana protein alkaline/neutral invertase C mRNA, complete cds [NM_111526]
-4,25	0.00000000	AT5G07440	GDH2	ref|Arabidopsis thaliana glutamate dehydrogenase 2 mRNA, complete cds [NM_001125712]
-4,25	0.00000000	AT5G07100	WRKY26	ref|Arabidopsis thaliana WRKY DNA-binding protein 26 mRNA, complete cds [NM_203017]
-4,26	0.00000000	AT1G71000	AT1G71000	ref|Arabidopsis thaliana chaperone DnaJ-domain containing protein mRNA, complete cds [NM_105769]
-4,26	0.00000000	AT2G28120	AT2G28120	ref|Arabidopsis thaliana major facilitator protein mRNA, complete cds [NM_128372]
-4,27	0.00000000	AT2G17880	AT2G17880	ref|Arabidopsis thaliana DNAJ heat shock N-terminal domain-containing protein mRNA, complete cds [NM_127342]
-4,28	0.00000000	AT2G47730	GSTF8	ref|Arabidopsis thaliana glutathione S-transferase phi 8 mRNA, complete cds [NM_180148]
-4,32	0.00000000	AT1G53280	AT1G53280	ref|Arabidopsis thaliana DJ1-like protein B mRNA, complete cds [NM_104206]
-4,35	0.00000000	AT5G14780	FDH	ref|Arabidopsis thaliana formate dehydrogenase mRNA, complete cds [NM_121482]
-4,38	0.00000004	AT1G66570	SUC7	ref|Arabidopsis thaliana putative sucrose transport protein SUC7 mRNA, complete cds [NM_001036165]
-4,38	0.00000004	AT4G25580	AT4G25580	ref|Arabidopsis thaliana CAP160 protein mRNA, complete cds [NM_118690]
-4,4	0.00000000	AT5G49740	FRO7	ref|Arabidopsis thaliana ferric reduction oxidase 7 mRNA, complete cds [NM_124352]
-4,4	0.00000000	AT3G62260	AT3G62260	ref|Arabidopsis thaliana putative protein phosphatase 2C 49 mRNA, complete cds [NM_116091]
-4,41	0.00000000	BU917423	BU917423	Unknown
-4,44	0.00000000	AT4G26530	AT4G26530	ref|Arabidopsis thaliana fructose-bisphosphate aldolase 5 mRNA, complete cds [NM_001036644]
-4,44	0.00000000	AT1G33110	AT1G33110	ref|Arabidopsis thaliana MATE efflux family protein mRNA, complete cds [NM_103045]
-4,45	0.00000000	AT3G22460	OASA2	ref|Arabidopsis thaliana O-acetylserine (thiol) lyase (OAS-TL) isoform A2 mRNA, complete cds [NM_113145]
-4,45	0.00000000	AT2G15960	AT2G15960	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_127155]
-4,45	0.00000000	AT3G20395	AT3G20395	ref|Arabidopsis thaliana RING-finger domain-containing protein mRNA, complete cds [NM_001084725]
-4,46	0.00000000	AT5G49730	FRO6	ref|Arabidopsis thaliana ferric reduction oxidase 6 mRNA, complete cds [NM_124351]
-4,46	0.00000000	AT1G79700	AT1G79700	ref|Arabidopsis thaliana AP2-like ethylene-responsive transcription factor WRI4 mRNA, complete cds [NM_001084380]
-4,46	0.00000000	AT5G51070	ERD1	ref|Arabidopsis thaliana chaperone protein ClpD mRNA, complete cds [NM_124486]
-4,46	0.00000000	AT3G15630	AT3G15630	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_112433]
-4,48	0.00000000	AT5G24490	AT5G24490	ref|Arabidopsis thaliana putative 30S ribosomal protein mRNA, complete cds [NM_122357]
-4,48	0.00000000	AT1G73750	AT1G73750	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_106034]
-4,49	0.00000000	AT5G56100	AT5G56100	ref|Arabidopsis thaliana glycine-rich protein / oleosin mRNA, complete cds [NM_124992]
-4,49	0.00000000	AT4G38470	AT4G38470	ref|Arabidopsis thaliana ACT-like protein tyrosine kinase family protein mRNA, complete cds [NM_120008]
-4,5	0.00000000	AT2G25900	ATCTH	ref|Arabidopsis thaliana putative Cys3His zinc finger protein ATCTH mRNA, complete cds [NM_128150]
-4,51	0.00000000	AT1G01240	AT1G01240	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_202007]
-4,54	0.00000000	AT5G16970	AER	ref|Arabidopsis thaliana 2-alkenal reductase mRNA, complete cds [NM_121703]
-4,56	0.00000000	AT5G57655	AT5G57655	ref|Arabidopsis thaliana xylose isomerase mRNA, complete cds [NM_180872]
-4,56	0.00000000	AT3G46080	AT3G46080	ref|Arabidopsis thaliana zinc finger protein ZAT8 mRNA, complete cds [NM_114477]
-4,57	0.00000000	AT5G16980	AT5G16980	ref|Arabidopsis thaliana zinc-binding dehydrogenase family protein mRNA, complete cds [NM_121704]
-4,57	0.00000000	AT1G15415	AT1G15415	ref|Arabidopsis thaliana phosphatase 2A B'gamma subunit mRNA, complete cds [NM_101411]
-4,58	0.00000000	AT3G15770	AT3G15770	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001035628]
-4,6	0.00000018	AT1G05340	AT1G05340	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_100413]
-4,62	0.00000000	AT2G24550	AT2G24550	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_128016]
-4,62	0.00000000	CF652575	TA32560_3702	tc|Rep: Beta-glucosidase - Arabidopsis thaliana (Mouse-ear cress), partial (29%) [TC395229]
-4,63	0.00000000	AT3G61060	PP2-A13	ref|Arabidopsis thaliana phloem protein 2-A13 mRNA, complete cds [NM_202741]
-4,66	0.00000044	AT5G44973	AT5G44973	ref|Arabidopsis thaliana defensin-like protein 285 mRNA, complete cds [NM_001036935]
-4,66	0.00000000	AT5G64260	EXL2	ref|Arabidopsis thaliana protein EXORDIUM like 2 mRNA, complete cds [NM_125822]
-4,67	0.00000000	AT1G63180	UGE3	ref|Arabidopsis thaliana UDP-glucose 4-epimerase mRNA, complete cds [NM_104996]
-4,69	0.00000000	AT4G13250	NYC1	ref|Arabidopsis thaliana probable chlorophyll(ide) b reductase NYC1 mRNA, complete cds [NM_117396]
-4,72	0.00000000	AT3G49620	DIN11	ref|Arabidopsis thaliana 2-oxoacid-dependent dioxygenase-like protein DIN11 mRNA, complete cds [NM_114822]
-4,72	0.00000000	NP229859	NP229859	tc|GB|AL391141.1|CAC01711.1 quinone oxidoreductase-like protein [NP229859]
-4,73	0.00000010	AT5G13330	Rap2.6L	ref|Arabidopsis thaliana ethylene-responsive transcription factor ERF113 mRNA, complete cds [NM_121336]
-4,74	0.00000001	AT3G14660	CYP72A13	ref|Arabidopsis thaliana cytochrome P450, family 72, subfamily A, polypeptide 13 mRNA, complete cds [NM_112327]
-4,74	0.00000000	AT3G16770	EBP	ref|Arabidopsis thaliana ethylene-responsive transcription factor RAP2-3 mRNA, complete cds [NM_112550]
-4,74	0.00000000	AT5G14120	AT5G14120	ref|Arabidopsis thaliana major facilitator protein mRNA, complete cds [NM_121416]
-4,75	0.00000000	AT3G10740	ASD1	ref|Arabidopsis thaliana bifunctional alpha-l-arabinofuranosidase/beta-d-xylosidase mRNA, complete cds [NM_111911]
-4,75	0.00000000	AT5G49480	CP1	ref|Arabidopsis thaliana Ca2+-binding protein 1 mRNA, complete cds [NM_124325]

-4,77	0.00000000	AT4G12735	AT4G12735	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_202810]
-4,82	0.00000000	AT2G45170	ATG8E	ref|Arabidopsis thaliana autophagy-related protein 8e mRNA, complete cds [NM_180100]
-4,82	0.00000000	AT2G22990	SNG1	ref|Arabidopsis thaliana sinapoylglucose:malate sinapoyltransferase mRNA, complete cds [NM_127864]
-4,85	0.00000000	AT2G39400	AT2G39400	ref|Arabidopsis thaliana alpha/beta-Hydrolases superfamily protein mRNA, complete cds [NM_129497]
-4,85	0.00000000	AT5G48180	NSP5	ref|Arabidopsis thaliana nitrile specifier protein 5 mRNA, complete cds [NM_124193]
-4,85	0.00000000	AT5G15850	COL1	ref|Arabidopsis thaliana zinc finger protein CONSTANS-LIKE 1 mRNA, complete cds [NM_121590]
-4,86	0.00000000	AT3G14630	CYP72A9	ref|Arabidopsis thaliana cytochrome P450, family 72, subfamily A, polypeptide 9 mRNA, complete cds [NM_112324]
-4,87	0.00000000	AT1G37130	NIA2	ref|Arabidopsis thaliana nitrate reductase [NADH] 2 mRNA, complete cds [NM_103364]
-4,87	0.00000000	AT3G46660	UGT76E12	ref|Arabidopsis thaliana UDP-glucosyl transferase 76E12 mRNA, complete cds [NM_114533]
-4,92	0.00000000	AT1G23390	AT1G23390	ref|Arabidopsis thaliana F-box/kelch-repeat protein mRNA, complete cds [NM_102188]
-4,95	0.00000001	AT1G72900	AT1G72900	ref|Arabidopsis thaliana Toll-Interleukin-Resistance domain-containing protein mRNA, complete cds [NM_105948]
-4,95	0.00000001	TC309308	TC396119	tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vinifera (Grape), partial (29%) [TC396119]
-4,98	0.00000000	AT1G07890	APX1	ref|Arabidopsis thaliana L-ascorbate peroxidase 1 mRNA, complete cds [NM_001123772]
-5	0.00000000	AT5G22920	AT5G22920	ref|Arabidopsis thaliana ring finger and CHY zinc finger domain-containing protein 1 mRNA, complete cds [NM_122198]
-5,04	0.00000000	AT5G52640	HSP90.1	ref|Arabidopsis thaliana heat shock protein 90.1 mRNA, complete cds [NM_124642]
-5,05	0.00000000	AT3G28210	PMZ	ref|Arabidopsis thaliana zinc finger (AN1-like) family protein mRNA, complete cds [NM_113740]
-5,09	0.00000000	AT5G54080	HGO	ref|Arabidopsis thaliana homogentisate 1,2-dioxygenase mRNA, complete cds [NM_180856]
-5,1	0.00000000	AT2G20670	AT2G20670	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_127631]
-5,14	0.00000000	AT1G70290	TPS8	ref|Arabidopsis thaliana putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 8 mRNA, complete cds [NM_105697]
-5,14	0.00000000	AT1G72680	CAD1	ref|Arabidopsis thaliana cinnamyl-alcohol dehydrogenase mRNA, complete cds [NM_105927]
-5,14	0.00000000	AT2G23150	NRAMP3	ref|Arabidopsis thaliana metal transporter Nramp3 mRNA, complete cds [NM_127879]
-5,18	0.00000000	AT1G22890	AT1G22890	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_102136]
-5,2	0.00000000	AT5G39050	AT5G39050	ref|Arabidopsis thaliana phenolic glucoside malonyltransferase 1 mRNA, complete cds [NM_123267]
-5,29	0.00000002	AT2G31945	AT2G31945	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_128753]
-5,31	0.00000000	AT1G60140	TPS10	ref|Arabidopsis thaliana putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 10 mRNA, complete cds [NM_104705]
-5,33	0.00000000	AT4G36040	AT4G36040	ref|Arabidopsis thaliana chaperone protein dnaJ 11 mRNA, complete cds [NM_119771]
-5,33	0.00000000	AT1G68190	AT1G68190	ref|Arabidopsis thaliana putative zinc finger protein mRNA, complete cds [NM_105490]
-5,33	0.00000000	AT4G16680	AT4G16680	ref|Arabidopsis thaliana putative RNA helicase mRNA, complete cds [NM_117769]
-5,34	0.00000000	AT5G21170	AKINBETA1	ref|Arabidopsis thaliana SNF1-related protein kinase regulatory subunit beta-1 mRNA, complete cds [NM_001036841]
-5,34	0.00000000	AT2G41380	AT2G41380	ref|Arabidopsis thaliana S-adenosyl-L-methionine-dependent methyltransferase-like protein mRNA, complete cds [NM_129701]
-5,35	0.00000000	AT5G24800	BZIP9	ref|Arabidopsis thaliana basic leucine zipper 9 mRNA, complete cds [NM_122389]
-5,35	0.00000000	AT1G69490	NAP	ref|Arabidopsis thaliana NAC transcription factor protein family mRNA, complete cds [NM_105616]
-5,37	0.00000000	AT4G37370	CYP81D8	ref|Arabidopsis thaliana cytochrome P450, family 81, subfamily D, polypeptide 8 mRNA, complete cds [NM_119900]
-5,39	0.00000000	AT4G36850	AT4G36850	ref|Arabidopsis thaliana PQ-loop repeat family protein / transmembrane family protein mRNA, complete cds [NM_119849]
-5,4	0.00000000	AT1G22400	UGT85A1	ref|Arabidopsis thaliana UDP-glycosyltransferase 85A1 mRNA, complete cds [NM_102089]
-5,41	0.00000000	AT5G26200	AT5G26200	ref|Arabidopsis thaliana mitochondrial substrate carrier family protein mRNA, complete cds [NM_122521]
-5,42	0.00000000	AT1G15040	AT1G15040	ref|Arabidopsis thaliana putative glutamine amidotransferase mRNA, complete cds [NM_101374]
-5,46	0.00000000	AT5G54165	AT5G54165	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001125962]
-5,48	0.00000000	BP660593	BP660593	Unknown
-5,49	0.00000000	AT1G10070	BCAT-2	ref|Arabidopsis thaliana branched-chain-amino-acid aminotransferase 2 mRNA, complete cds [NM_001035939]
-5,53	0.00000006	TA32559_3702	TA32559_3702	tc|Rep: AT3g60140/T2O9_120 - Arabidopsis thaliana (Mouse-ear cress), partial (9%) [TC397325]
-5,55	0.00000000	AT1G54100	ALDH7B4	ref|Arabidopsis thaliana aldehyde dehydrogenase 7B4 mRNA, complete cds [NM_104287]
-5,55	0.00000000	AT3G13750	BGAL1	ref|Arabidopsis thaliana beta galactosidase 1 mRNA, complete cds [NM_112225]
-5,61	0.00000000	AT3G12580	HSP70	ref|Arabidopsis thaliana heat shock protein 70-4 mRNA, complete cds [NM_112093]
-5,63	0.00000000	AT2G37130	AT2G37130	ref|Arabidopsis thaliana peroxidase mRNA, complete cds [NM_001124989]
-5,64	0.00000000	AT5G47560	TDT	ref|Arabidopsis thaliana tonoplast dicarboxylate transporter mRNA, complete cds [NM_124129]
-5,67	0.00000000	AT1G03090	MCCA	ref|Arabidopsis thaliana methylcrotonoyl-CoA carboxylase subunit alpha mRNA, complete cds [NM_179252]
-5,71	0.00000000	AT4G30270	XTH24	ref|Arabidopsis thaliana xyloglucan endotransglucosylase/hydrolase protein 24 mRNA, complete cds [NM_119173]
-5,75	0.00000000	AT2G37770	AT2G37770	ref|Arabidopsis thaliana aldo-keto reductase family 4 member C9 mRNA, complete cds [NM_001036428]
-5,81	0.00000000	AT2G26150	HSFA2	ref|Arabidopsis thaliana heat stress transcription factor A-2 mRNA, complete cds [NM_001124916]
-5,81	0.00000000	AT2G29420	GSTU7	ref|Arabidopsis thaliana glutathione S-transferase tau 7 mRNA, complete cds [NM_128496]

-5,82	0.00000000	AT4G17840	AT4G17840	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_117893]
-5,86	0.00000000	AT1G06570	PDS1	ref|Arabidopsis thaliana 4-hydroxyphenylpyruvate dioxygenase mRNA, complete cds [NM_100536]
-5,87	0.00000000	AT5G25130	CYP71B12	ref|Arabidopsis thaliana cytochrome P450 71B12 mRNA, complete cds [NM_122422]
-5,89	0.00000000	AT5G06860	PGIP1	ref|Arabidopsis thaliana polygalacturonase inhibitor 1 mRNA, complete cds [NM_120769]
-5,9	0.00000000	AT1G52690	AT1G52690	ref|Arabidopsis thaliana Late embryogenesis abundant protein (LEA) family protein mRNA, complete cds [NM_202280]
-5,91	0.00000000	AT5G17170	ENH1	ref|Arabidopsis thaliana protein ENHANCER OF SOS3-1 mRNA, complete cds [NM_001085129]
-5,99	0.00000000	AT3G29035	NAC3	ref|Arabidopsis thaliana NAC domain-containing protein 3 mRNA, complete cds [NM_113825]
-6,02	0.00000000	AT2G43820	UGT74F2	ref|Arabidopsis thaliana UDP-glucosyltransferase 74F2 mRNA, complete cds [NM_129944]
-6,05	0.00000000	AT2G47770	TSPO	ref|Arabidopsis thaliana tryptophan-rich sensory protein-like protein mRNA, complete cds [NM_130344]
-6,09	0.00000004	AT1G02610	AT1G02610	ref|Arabidopsis thaliana RING/FYVE/PHD zinc finger-containing protein mRNA, complete cds [NM_100141]
-6,12	0.00000000	AT3G07350	AT3G07350	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_111614]
-6,16	0.00000000	AT5G39610	NAC6	ref|Arabidopsis thaliana NAC-domain transcription factor mRNA, complete cds [NM_123323]
-6,18	0.00000000	AT4G24972	TPD1	ref|Arabidopsis thaliana protein TAPETUM DETERMINANT 1 mRNA, complete cds [NM_202883]
-6,22	0.00000000	AT1G13990	AT1G13990	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_001160863]
-6,23	0.00000000	AT1G75490	AT1G75490	ref|Arabidopsis thaliana dehydration-responsive element-binding protein 2D mRNA, complete cds [NM_106202]
-6,25	0.00000000	AT1G22500	AT1G22500	ref|Arabidopsis thaliana putative C3HC4-type RING zinc finger protein mRNA, complete cds [NM_102099]
-6,27	0.00000000	AT5G61820	AT5G61820	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125576]
-6,28	0.00000000	AT5G63160	BT1	ref|Arabidopsis thaliana BTB and TAZ domain protein 1 mRNA, complete cds [NM_125711]
-6,29	0.00000000	AT4G15610	AT4G15610	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_117652]
-6,31	0.00000000	AT5G14730	AT5G14730	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_121477]
-6,34	0.00000000	AT5G59400	AT5G59400	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125331]
-6,36	0.00000000	AT2G02710	PLPB	ref|Arabidopsis thaliana PAS/LOV protein B mRNA, complete cds [NM_201672]
-6,46	0.00000000	AT5G33355	AT5G33355	ref|Arabidopsis thaliana defensin-like protein mRNA, complete cds [NM_147989]
-6,49	0.00000000	AT2G29490	GSTU1	ref|Arabidopsis thaliana glutathione S-transferase tau 1 mRNA, complete cds [NM_128503]
-6,49	0.00000000	AT3G10020	AT3G10020	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_111837]
-6,51	0.00000000	AT3G48360	BT2	ref|Arabidopsis thaliana TAC1-mediated telomerase activation pathway protein BT2 mRNA, complete cds [NM_114697]
-6,52	0.00000000	AT5G64230	AT5G64230	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_125819]
-6,54	0.00000000	AT3G59930	AT3G59930	ref|Arabidopsis thaliana defensin-like protein 206 mRNA, complete cds [NM_115856]
-6,56	0.00000000	TC309871	TC396686	tc|Rep: Conglutin gamma-like protein - Arabidopsis thaliana (Mouse-ear cress), partial (35%) [TC396686]
-6,63	0.00000000	AT1G02820	AT1G02820	ref|Arabidopsis thaliana late embryogenesis abundant 3-like protein mRNA, complete cds [NM_100163]
-6,65	0.00000000	AT4G34131	UGT73B3	ref|Arabidopsis thaliana UDP-glucosyl transferase 73B3 mRNA, complete cds [NM_119574]
-6,7	0.00000000	AT4G34135	UGT73B2	ref|Arabidopsis thaliana UDP-glucosyltransferase 73B2 mRNA, complete cds [NM_179161]
-6,73	0.00000000	AT3G14990	AT3G14990	ref|Arabidopsis thaliana protein DJ-1-like A mRNA, complete cds [NM_001035621]
-6,74	0.00000002	BP667596	BP667596	tc|Rep: Uncharacterized protein At4g35770.3 - Arabidopsis thaliana (Mouse-ear cress), partial (53%) [TC406344]
-6,79	0.00000000	AT1G62510	AT1G62510	ref|Arabidopsis thaliana bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin-like protein mRNA, complete cds [NM_104930]
-6,88	0.00000000	AT1G10585	AT1G10585	ref|Arabidopsis thaliana basic helix-loop-helix domain-containing protein mRNA, complete cds [NM_100934]
-6,98	0.00000000	AT5G51720	AT5G51720	ref|Arabidopsis thaliana CDGSH iron-sulfur domain-containing protein NEET mRNA, complete cds [NM_124551]
-7,01	0.00000000	AT4G39675	AT4G39675	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_120128]
-7,03	0.00000000	AT5G05410	DREB2A	ref|Arabidopsis thaliana dehydration-responsive element-binding protein 2A mRNA, complete cds [NM_120623]
-7,04	0.00000000	AT4G37610	BT5	ref|Arabidopsis thaliana BTB and TAZ domain protein 5 mRNA, complete cds [NM_119924]
-7,1	0.00000000	AT5G49450	bZIP1	ref|Arabidopsis thaliana basic leucine-zipper 1 mRNA, complete cds [NM_124322]
-7,14	0.00000000	AT1G23870	TPS9	ref|Arabidopsis thaliana putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 9 mRNA, complete cds [NM_102235]
-7,17	0.00000000	AT1G71030	MYBL2	ref|Arabidopsis thaliana putative myb family transcription factor mRNA, complete cds [NM_105772]
-7,22	0.00000000	AT3G49790	AT3G49790	ref|Arabidopsis thaliana Carbohydrate-binding protein mRNA, complete cds [NM_114839]
-7,25	0.00000000	AT5G39520	AT5G39520	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_123314]
-7,29	0.00000005	AT1G19530	AT1G19530	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_101811]
-7,32	0.00000000	AT2G15490	UGT73B4	ref|Arabidopsis thaliana UDP-glycosyltransferase 73B4 mRNA, complete cds [NM_127109]
-7,46	0.00000000	AT1G28330	DYL1	ref|Arabidopsis thaliana dormancy-associated protein-like 1 mRNA, complete cds [NM_001160906]
-7,65	0.00000000	AT5G19120	AT5G19120	ref|Arabidopsis thaliana aspartyl protease family protein mRNA, complete cds [NM_121917]
-7,66	0.00000002	AT5G52570	BETA-OHASE 2	ref|Arabidopsis thaliana beta-carotene hydroxylase 2 mRNA, complete cds [NM_124636]
-7,85	0.00000000	AT1G72060	AT1G72060	ref|Arabidopsis thaliana serine-type endopeptidase inhibitor mRNA, complete cds [NM_105864]

-7,86	0.00000000	AT1G08630	THA1	ref|Arabidopsis thaliana threonine aldolase mRNA, complete cds [NM_100736]
-7,95	0.00000071	AT1G71520	AT1G71520	ref|Arabidopsis thaliana ERF/AP2 transcription factor family protein DREB A-5 mRNA, complete cds [NM_105820]
-7,98	0.00000015	AT2G36750	UGT73C1	ref|Arabidopsis thaliana UDP-glucosyl transferase 73C1 mRNA, complete cds [NM_129230]
-8,03	0.00000000	AT3G45300	IVD	ref|Arabidopsis thaliana isovaleryl-CoA-dehydrogenase mRNA, complete cds [NM_114399]
-8,48	0.00000000	AT1G66760	AT1G66760	ref|Arabidopsis thaliana MATE efflux family protein mRNA, complete cds [NM_179523]
-8,61	0.00000003	AT1G43160	RAP2.6	ref|Arabidopsis thaliana ethylene-responsive transcription factor RAP2-6 mRNA, complete cds [NM_103468]
-8,64	0.00000000	AT2G15480	UGT73B5	ref|Arabidopsis thaliana UDP-glucosyl transferase 73B5 mRNA, complete cds [NM_127108]
-8,71	0.00000000	AT1G15380	AT1G15380	ref|Arabidopsis thaliana Lactoylglutathione lyase / glyoxalase I family protein mRNA, complete cds [NM_101407]
-8,71	0.00000000	AT2G29480	GSTU2	ref|Arabidopsis thaliana glutathione S-transferase tau 2 mRNA, complete cds [NM_128502]
-8,75	0.00000000	AT1G05560	UGT75B1	ref|Arabidopsis thaliana UDP-glucosyltransferase 75B1 mRNA, complete cds [NM_100435]
-8,76	0.00000000	AT1G11260	STP1	ref|Arabidopsis thaliana sugar transporter 1 mRNA, complete cds [NM_100998]
-8,85	0.00000008	AT1G15010	AT1G15010	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_101370]
-9,32	0.00000000	AT1G77760	NIA1	ref|Arabidopsis thaliana nitrate reductase [NADH] 1 mRNA, complete cds [NM_106425]
-9,76	0.00000022	AT2G40000	HSPRO2	ref|Arabidopsis thaliana HS1 PRO-1 2-like protein mRNA, complete cds [NM_129558]
-9,94	0.00000000	AT2G36800	DOGT1	ref|Arabidopsis thaliana UDP-glycosyltransferase 73C5 mRNA, complete cds [NM_129235]
-10,1	0.00000000	AT1G76600	AT1G76600	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_106310]
-10,12	0.00000000	AT4G35090	CAT2	ref|Arabidopsis thaliana catalase 2 mRNA, complete cds [NM_119675]
-10,19	0.00000000	AT4G15760	MO1	ref|Arabidopsis thaliana monooxygenase 1 mRNA, complete cds [NM_001203809]
-10,72	0.00000000	AT5G20250	DIN10	ref|Arabidopsis thaliana putative galactinol--sucrose galactosyltransferase 6 mRNA, complete cds [NM_001036833]
-10,8	0.00000000	AT1G76680	OPR1	ref|Arabidopsis thaliana 12-oxophytodienoate reductase 1 mRNA, complete cds [NM_106318]
-11,01	0.00000000	AT5G51440	AT5G51440	ref|Arabidopsis thaliana heat shock protein 23.5 mRNA, complete cds [NM_124523]
-11,06	0.00000000	AT1G80440	AT1G80440	ref|Arabidopsis thaliana F-box/kelch-repeat protein mRNA, complete cds [NM_106692]
-11,13	0.00000000	AT1G65970	TPX2	ref|Arabidopsis thaliana thioredoxin-dependent peroxidase 2 mRNA, complete cds [NM_105269]
-11,18	0.00000000	AT4G16690	MES16	ref|Arabidopsis thaliana methyl esterase 16 mRNA, complete cds [NM_117770]
-11,56	0.00000000	AT4G33666	AT4G33666	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_119524]
-11,92	0.00000000	AT2G47270	AT2G47270	ref|Arabidopsis thaliana transcription factor UPBEAT1 mRNA, complete cds [NM_130295]
-12,02	0.00000000	AT5G54585	AT5G54585	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_148130]
-12,03	0.00000000	AT1G80920	J8	ref|Arabidopsis thaliana chaperone protein dnaJ 8 mRNA, complete cds [NM_106740]
-12,2	0.00000000	AT2G36780	AT2G36780	ref|Arabidopsis thaliana UDP-glucosyl transferase 73C3 mRNA, complete cds [NM_129233]
-12,35	0.00000000	AT5G22140	AT5G22140	ref|Arabidopsis thaliana FAD/NAD(P)-binding oxidoreductase family protein mRNA, complete cds [NM_147895]
-12,43	0.00000012	AT5G16960	AT5G16960	ref|Arabidopsis thaliana zinc-binding dehydrogenase family protein mRNA, complete cds [NM_121702]
-13,14	0.00000000	AT3G04000	AT3G04000	ref|Arabidopsis thaliana aldehyde reductase mRNA, complete cds [NM_111271]
-13,43	0.00000000	AT1G17170	GSTU24	ref|Arabidopsis thaliana glutathione S-transferase TAU 24 mRNA, complete cds [NM_101578]
-14,23	0.00000000	AT1G07400	AT1G07400	ref|Arabidopsis thaliana class I heat shock protein mRNA, complete cds [NM_100614]
-14,85	0.00000000	AT5G66400	RAB18	ref|Arabidopsis thaliana dehydrin Rab18 mRNA, complete cds [NM_126038]
-14,87	0.00000000	AT1G80160	AT1G80160	ref|Arabidopsis thaliana GLYOXYLASE I 7 mRNA, complete cds [NM_001084382]
-15,89	0.00000000	AT4G27450	AT4G27450	ref|Arabidopsis thaliana aluminum induced protein with YGL and LRDR motifs mRNA, complete cds [NM_118880]
-16,14	0.00000000	AT2G33830	AT2G33830	ref|Arabidopsis thaliana dormancy/auxin associated protein mRNA, complete cds [NM_179889]
-16,16	0.00000000	AT2G18700	TPS11	ref|Arabidopsis thaliana putative alpha,alpha-trehalose-phosphate synthase [UDP-forming] 11 mRNA, complete cds [NM_127426]
-16,54	0.00000000	TC304561	TC384346	tc|Rep: Xylosidase - Arabidopsis thaliana (Mouse-ear cress), complete [TC384346]
-16,74	0.00000000	AT1G09500	AT1G09500	ref|Arabidopsis thaliana alcohol dehydrogenase-like protein mRNA, complete cds [NM_001035935]
-17,51	0.00000000	AT5G14180	MPL1	ref|Arabidopsis thaliana Myzus persicae-induced lipase 1 mRNA, complete cds [NM_121422]
-17,67	0.00000000	AT5G02020	AT5G02020	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_180421]
-17,72	0.00000000	AT5G56870	BGAL4	ref|Arabidopsis thaliana beta-galactosidase 4 mRNA, complete cds [NM_125070]
-19,16	0.00000000	AT5G14470	AT5G14470	ref|Arabidopsis thaliana GHMP kinase family protein mRNA, complete cds [NM_121451]
-19,62	0.00000000	AT2G05540	AT2G05540	ref|Arabidopsis thaliana glycine-rich protein mRNA, complete cds [NM_126577]
-20,85	0.00000000	AT3G24420	AT3G24420	ref|Arabidopsis thaliana hydrolase, alpha/beta fold family protein mRNA, complete cds [NM_113349]
-22,75	0.00000000	AT4G08555	AT4G08555	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_179014]
-23	0.00000000	AT3G28740	CYP81D1	ref|Arabidopsis thaliana cytochrome P450 CYP81D11 mRNA, complete cds [NM_113795]
-24,7	0.00000000	AT3G60140	DIN2	ref|Arabidopsis thaliana beta-glucosidase 30 mRNA, complete cds [NM_115877]
-25,49	0.00000000	AT5G01600	FER1	ref|Arabidopsis thaliana ferretin 1 mRNA, complete cds [NM_120238]

-31,28	0.00000000	AT1G73120	AT1G73120	ref|Arabidopsis thaliana uncharacterized protein mRNA, complete cds [NM_105970]
-34,59	0.00000000	AT3G20340	AT3G20340	ref|Arabidopsis thaliana paraquat downregulated protein mRNA, complete cds [NM_112925]
-41,4	0.00000000	AT3G15450	AT3G15450	ref|Arabidopsis thaliana aluminum induced protein with YGL and LRDR motif mRNA, complete cds [NM_001035625]
-41,54	0.00000000	AT1G05680	UGT74E2	ref|Arabidopsis thaliana Uridine diphosphate glycosyltransferase 74E2 mRNA, complete cds [NM_100448]
-41,68	0.00000000	AT5G49360	BXL1	ref|Arabidopsis thaliana bifunctional {beta}-D-xylosidase/{alpha}-L-arabinofuranosidase mRNA, complete cds [NM_124313]
-41,95	0.00000000	AT4G01870	AT4G01870	ref|Arabidopsis thaliana tolB-related protein mRNA, complete cds [NM_116417]
-42,02	0.00000000	BE039144	BE039144	tc|Rep: Chromosome chr19 scaffold_4, whole genome shotgun sequence - Vitis vinifera (Grape), partial (59%) [TC393828]
-48,66	0.00000000	AT3G47340	ASN1	ref|Arabidopsis thaliana asparagine synthetase [glutamine-hydrolyzing] mRNA, complete cds [NM_180333]
-111,32	0.00000000	AT4G35770	SEN1	ref|Arabidopsis thaliana senescence-associated protein DIN1 mRNA, complete cds [NM_119743]

Table S4: List of genes whose expression is altered by high irradiance treatment (Athanasiou, Dyson, Webster, & Johnson, 2010).
Genes that are differentially regulated by A. alternata VCs (cf. Supplemental Table 3 in Sánchez-López, Baslam, et al. 2016) are highlighted in yellow color.

Representative Public ID	Gene Title	Fold change
At1g74670	gibberellin-responsive protein, putative	-22,4
At2g40610	expansin, putative (EXP8)	-16,2
At5g48490	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	-15,4
At3g15450	expressed protein	-12,1
At1g70290	trehalose-6-phosphate synthase, putative	-10,4
At1g23390	kelch repeat-containing F-box family protein	-10,2
At2g25900	zinc finger (CCCH-type) family protein	-9,8
At2g22980	serine carboxypeptidase S10 family protein	-9,6
At2g18700	glycosyl transferase family 20 protein / trehalose-phosphatase family protein	-9,5
At2g33830	dormancy/auxin associated family protein	-9,2
At5g59080	expressed protein	-9,2
At5g61590	AP2 domain-containing transcription factor family protein	-9
At5g02760	protein phosphatase 2C family protein / PP2C family protein	-8,8
At2g15890	expressed protein	-8,6
At1g80920	DNAJ heat shock N-terminal domain-containing protein	-8,5
At5g40890	chloride channel protein (CLC-a)	-8,3
At1g72150	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	-8
At5g24490	30S ribosomal protein, putative	-8
At5g22920	zinc finger (C3HC4-type RING finger) family protein	-8
At4g24800	MA3 domain-containing protein	-7,8
At1g18620	expressed protein	-7,7
At2g44740	cyclin family protein	-7,4
At4g30690	translation initiation factor 3 (IF-3) family protein	-7
At3g19850	phototropic-responsive NPH3 family protein	-6,9
At3g13750	beta-galactosidase, putative / lactase, putative	-6,7
At1g63800	ubiquitin-conjugating enzyme 5 (UBC5)	-6,6
At3g62550	universal stress protein (USP) family protein	-6,5
At5g35790	glucose-6-phosphate 1-dehydrogenase / G6PD (APG1)	-6,5
At1g19660	wound-responsive family protein /// wound-responsive protein-related	-6,4
At1g80440	kelch repeat-containing F-box family protein	-6,3
At1g52200	expressed protein	-6,3
At5g16030	expressed protein	-6,3

At1g25230	purple acid phosphatase family protein	-6,1
At4g33666	L-galactose dehydrogenase (L-GalDH) /// expressed protein	-6,1
At3g53800	armadillo/beta-catenin repeat family protein	-6,1
At4g20260	DREPP plasma membrane polypeptide family protein	-6,1
At1g08980	amidase family protein	-5,9
At1g11260	glucose transporter (STP1)	-5,8
At1g15740	leucine-rich repeat family protein	-5,8
At3g26510	octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	-5,6
At1g56220	dormancy/auxin associated family protein	-5,6
At5g03350	legume lectin family protein	-5,6
At5g63190	MA3 domain-containing protein	-5,4
At2g32100	ovate protein-related	-5,4
At1g68190	zinc finger (B-box type) family protein	-5,3
At5g18600	glutaredoxin family protein	-5,3
At4g27450	expressed protein	-5,3
At5g60680	expressed protein	-5,1
At1g13260	DNA-binding protein RAV1 (RAV1)	-5,1
At1g02300	cathepsin B-like cysteine protease, putative	-5,1
At4g39090	cysteine proteinase RD19a (RD19A) / thiol protease	-5
At5g14120	nodulin family protein	-5
At3g61060	F-box family protein / lectin-related	-4,9
At2g27050	ethylene-insensitive3-like1 (EIL1)	-4,8
At1g13650	expressed protein	-4,7
At3g47160	expressed protein	-4,6
At2g15960	expressed protein	-4,4
At4g04330	expressed protein	-4,4
At4g27440	protochlorophyllide reductase B, chloroplast / PCR B / NADPH-protochlorophyllide oxidoreductase B (PORB)	-4,4
At4g14270	expressed protein	-4,4
At3g51840	short-chain acyl-CoA oxidase	-4,4
At3g28860	multidrug resistance P-glycoprotein, putative	-4,4
At4g26530	fructose-bisphosphate aldolase, putative	-4,3
At5g49730	ferric reductase-like transmembrane component family protein /// ferric reductase-like transmembrane component family protein	-4,3
At1g12780	UDP-glucose 4-epimerase / UDP-galactose 4-epimerase / Galactowaldenase	-4,3
At4g01026	expressed protein	-4,2
At1g54820	protein kinase family protein	-4,2
At5g02160	expressed protein	-4,1
At2g39400	hydrolase, alpha/beta fold family protein	-4

At4g05070	expressed protein	-4
At4g32340	expressed protein	-4
At1g71030	myb family transcription factor	-4
At1g01240	expressed protein	-4
At5g02020	expressed protein	-4
At2g18300	basic helix-loop-helix (bHLH) family protein	-4
At1g29395	stress-responsive protein, putative	-4
At2g46220	expressed protein	-3,9
At1g17990	12-oxophytodienoate reductase, putative /// 12-oxophytodienoate reductase, putative	-3,9
At5g44680	methyladenine glycosylase family protein	-3,9
At5g44530	subtilase family protein	-3,9
At3g18080	glycosyl hydrolase family 1 protein	-3,9
At3g26170	cytochrome P450 71B20, putative (CYP71B2) /// cytochrome P450 71B19, putative (CYP71B19)	-3,9
At3g59940	autophagy 4b (APG4b) /// kelch repeat-containing F-box family protein	-3,8
At1g11530	thioredoxin family protein	-3,8
At1g09750	chloroplast nucleoid DNA-binding protein-related	-3,8
At2g30510	signal transducer of phototropic response (RPT2)	-3,8
At4g03510	zinc finger (C3HC4-type RING finger) family protein (RMA1)	-3,8
At5g06690	thioredoxin family protein	-3,7
At5g62360	invertase/pectin methylesterase inhibitor family protein	-3,7
At2g40750	WRKY family transcription factor	-3,7
At2g02710	PAC motif-containing protein	-3,6
At3g26740	light responsive protein-related	-3,6
At4g36040	DNAJ heat shock N-terminal domain-containing protein (J11)	-3,6
At1g49500	expressed protein	-3,6
At4g28240	wound-responsive protein-related /// NADH dehydrogenase-related	-3,6
At1g33240	trihelix DNA-binding protein, putative	-3,6
At5g05690	cytochrome P450 90A1 (CYP90A1) (CYP90) (CPD)	-3,6
At4g39510	cytochrome P450 family protein	-3,6
At2g34620	mitochondrial transcription termination factor-related / mTERF-related	-3,6
At2g22990	sinapoylglucose:malate sinapoyltransferase (SNG1)	-3,5
At2g29290	tropinone reductase, putative / tropine dehydrogenase, putative	-3,5
At1g32540	zinc finger protein, putative	-3,5
At5g63800	glycosyl hydrolase family 35 protein	-3,5
At2g27830	expressed protein	-3,5
At5g10860	CBS domain-containing protein	-3,5
At1g13210	haloacid dehalogenase-like hydrolase family protein	-3,5

At5g62630	expressed protein	-3,5
At1g27290	expressed protein	-3,4
At5g28020	cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative	-3,4
At2g46330	arabinogalactan-protein (AGP16)	-3,4
At5g24470	pseudo-response regulator 5 (APRR5)	-3,4
At1g21500	expressed protein	-3,4
At4g16520	autophagy 8f (APG8f)	-3,4
At4g39640	gamma-glutamyltranspeptidase family protein	-3,4
At1g25275	expressed protein	-3,4
At5g47040	Lon protease homolog 1, mitochondrial (LON)	-3,3
At1g19770	purine permease-related	-3,3
At1g80460	glycerol kinase, putative	-3,3
At3g52840	beta-galactosidase, putative / lactase, putative	-3,3
At5g25280	serine-rich protein-related	-3,3
At3g26280	cytochrome P450 family protein	-3,3
At3g56360	expressed protein	-3,3
At5g04490	phosphatidate cytidylyltransferase family protein	-3,3
At1g68520	zinc finger (B-box type) family protein	-3,3
At2g37490	expressed protein	-3,3
At1g54130	RelA/SpoT protein, putative (RSH3)	-3,3
At1g30250	expressed protein	-3,3
At5g16150	hexose transporter, putative	-3,3
At4g29190	zinc finger (CCCH-type) family protein	-3,3
At1g52190	proton-dependent oligopeptide transport (POT) family protein	-3,3
At4g34220	leucine-rich repeat transmembrane protein kinase, putative	-3,2
At1g73480	hydrolase, alpha/beta fold family protein	-3,2
At1g09350	galactinol synthase, putative	-3,2
At4g19860	lecithin:cholesterol acyltransferase family protein / LACT family protein	-3,2
At5g08520	myb family transcription factor	-3,2
At1g63690	protease-associated (PA) domain-containing protein	-3,2
At4g19170	9-cis-epoxycarotenoid dioxygenase, putative / neoxanthin cleavage enzyme, putative / carotenoid cleavage dioxygenase, putative	-3,1
At3g50270	transferase family protein	-3,1
At2g41870	remorin family protein	-3,1
At1g74840	myb family transcription factor	-3,1
At3g16520	UDP-glucoronosyl/UDP-glucosyl transferase family protein	-3,1
At2g30930	expressed protein	-3,1

At1g08930	early-responsive to dehydration stress protein (ERD6) / sugar transporter family protein	-3,1
At5g40450	expressed protein	-3
At1g75460	ATP-dependent protease La (LON) domain-containing protein	-3
At5g22270	expressed protein	-3
At2g43010	phytochrome-interacting factor 4 (PIF4) / basic helix-loop-helix protein 9 (bHLH9) / short under red-light 2 (SRL2)	-3
At3g27690	chlorophyll A-B binding protein (LHCB2:4)	-3
At5g65730	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	-3
At1g69850	nitrate transporter (NTL1)	-3
At4g23820	glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	-3
At3g14050	RelA/SpoT protein, putative (RSH2)	-3
At1g48300	expressed protein	-3
At5g19140	auxin/aluminum-responsive protein, putative	-3
At5g03230	expressed protein	-3
At3g50500	protein kinase, putative	-3
At1g72160	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	-3
At1g24070	glycosyl transferase family 2 protein	3
At4g25700	beta-carotene hydroxylase	3
At4g29510	protein arginine N-methyltransferase, putative	3
At4g32720	RNA recognition motif (RRM)-containing protein	3
At1g31860	histidine biosynthesis bifunctional protein (HISIE)	3
At3g03920	Gar1 RNA-binding region family protein	3
At1g09240	nicotianamine synthase, putative	3
At5g06110	DNAJ heat shock N-terminal domain-containing protein / cell division protein-related	3
At4g27570	glycosyltransferase family protein /// glycosyltransferase family protein	3
At2g23340	AP2 domain-containing transcription factor, putative	3
At3g23810	adenosylhomocysteinase, putative / S-adenosyl-L-homocysteine hydrolase, putative / AdoHcyase, putative	3,1
At3g44990	xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	3,1
At5g14050	transducin family protein / WD-40 repeat family protein	3,1
At2g18230	inorganic pyrophosphatase (soluble) (PPA) / pyrophosphate phospho-hydrolase / PPase	3,1
At1g61570	mitochondrial import inner membrane translocase (TIM13)	3,1
At4g39950	cytochrome P450 79B2, putative (CYP79B2)	3,1
At3g56070	peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative	3,1
At1g31970	DEAD/DEAH box helicase, putative	3,1
At5g14520	pescadillo-related	3,1
At3g51240	naringenin 3-dioxygenase / flavanone 3-hydroxylase (F3H)	3,2
At1g67360	rubber elongation factor (REF) family protein	3,2

At1g80750	60S ribosomal protein L7 (RPL7A)	3,2
At1g17100	SOUL heme-binding family protein	3,2
At3g58070	zinc finger (C2H2 type) family protein	3,2
At5g65860	ankyrin repeat family protein	3,2
At1g26770	expansin, putative (EXP10)	3,2
At5g55915	nucleolar protein, putative	3,2
At3g16810	pumilio/Puf RNA-binding domain-containing protein	3,3
At2g44860	60S ribosomal protein L24, putative	3,3
At2g28600	expressed protein	3,3
At3g03770	leucine-rich repeat transmembrane protein kinase, putative	3,3
At1g55900	NLI interacting factor (NIF) family protein	3,3
At2g37250	adenylate kinase family protein	3,3
At1g07890	L-ascorbate peroxidase 1, cytosolic (APX1)	3,3
At3g16780	60S ribosomal protein L19 (RPL19B)	3,4
At5g08180	ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	3,4
At3g13940	expressed protein	3,4
At1g55210	disease resistance response protein-related/ dirigent protein-related	3,5
At5g64680	expressed protein	3,5
At1g15100	zinc finger (C3HC4-type RING finger) family protein	3,5
At1g25260	acidic ribosomal protein P0-related	3,5
At1g63780	brix domain-containing protein	3,5
At3g23620	brix domain-containing protein	3,6
At3g57490	40S ribosomal protein S2 (RPS2D)	3,6
At3g23990	chaperonin (CPN60) (HSP60)	3,7
At3g17790	acid phosphatase type 5 (ACP5)	3,7
At3g21890	zinc finger (B-box type) family protein	3,7
At2g38210	stress-responsive protein, putative /// ethylene-responsive protein, putative	3,7
At1g15425	expressed protein	3,7
At5g09590	heat shock protein 70 / HSP70 (HSC70-5)	3,8
At3g57000	nucleolar essential protein-related	3,8
At1g63810	nucleolar RNA-associated family protein / Nrap family protein	3,8
At3g08590	2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative	3,8
At1g15440	transducin family protein / WD-40 repeat family protein	3,9
At1g31660	bystin family	3,9
At4g01560	brix domain-containing protein	3,9
At5g15550	transducin family protein / WD-40 repeat family protein	3,9
At3g22310	DEAD box RNA helicase, putative /// DEAD box RNA helicase, putative (RH9)	4

At4g37910	heat shock protein 70, mitochondrial, putative / HSP70, mitochondrial, putative	4
At2g36630	expressed protein	4
At3g57150	dyskerin, putative / nucleolar protein NAP57, putative	4,1
At3g05060	SAR DNA-binding protein, putative	4,1
At5g61770	brix domain-containing protein	4,1
At1g19640	S-adenosyl-L-methionine:jasmonic acid carboxyl methyltransferase (JMT)	4,2
At4g20170	expressed protein /// expressed protein	4,3
At4g34710	arginine decarboxylase 2 (SPE2)	4,3
At1g60850	DNA-directed RNA polymerase, putative	4,4
At3g56090	ferritin, putative	4,4
At1g29940	DNA-directed RNA polymerase family protein	4,4
At5g02050	mitochondrial glycoprotein family protein / MAM33 family protein	4,5
At2g40360	transducin family protein / WD-40 repeat family protein	4,6
At1g56110	nucleolar protein Nop56, putative	4,6
At5g01600	ferritin 1 (FER1)	4,6
At1g52930	brix domain-containing protein	4,6
At1g57590	pectinacetylesterase, putative	4,7
At4g15770	60S ribosome subunit biogenesis protein, putative	4,9
At2g03760	steroid sulfotransferase, putative	5
At1g80270	DNA-binding protein, putative	5,1
At3g14720	mitogen-activated protein kinase, putative / MAPK, putative (MPK19)	5,2
At4g33030	UDP-sulfoquinovose synthase / sulfite:UDP-glucose sulfotransferase / sulfolipid biosynthesis protein (SQD1)	5,4
At4g01080	expressed protein	5,5
At3g06530	BAP28-related	5,5
At1g02820	late embryogenesis abundant 3 family protein / LEA3 family protein	5,6
At3g13230	expressed protein	5,7
At2g47990	transducin family protein / WD-40 repeat family protein	5,9
At5g42760	O-methyltransferase N-terminus domain-containing protein	6
At3g44750	histone deacetylase, putative (HD2A)	6,1
At4g34590	bZIP transcription factor family protein	6,1
At1g56650	myb family transcription factor (MYB75)	6,2
At1g06000	UDP-glucoronosyl/UDP-glucosyl transferase family protein	6,4
At3g18600	DEAD/DEAH box helicase, putative	6,7
At2g27840	histone deacetylase-related / HD-related	6,8
At3g14395	expressed protein	6,8
At5g58770	dehydrodolichyl diphosphate synthase, putative / DEDOL-PP synthase, putative	6,9
At2g34260	transducin family protein / WD-40 repeat family protein	7,2

At3g10530	transducin family protein / WD-40 repeat family protein	7,2
At4g16590	glucosyltransferase-related	7,6
At1g32900	starch synthase, putative	8
At4g25630	fibrillarin 2 (FIB2)	9
At2g27420	cysteine proteinase, putative	9,2
At5g49480	sodium-inducible calcium-binding protein (ACP1) / sodium-responsive calcium-binding protein (ACP1)	9,7
At1g64780	ammonium transporter 1, member 2 (AMT1.2)	10
At4g15210	beta-amylase (BMY1) / 1,4-alpha-D-glucan maltohydrolase	13,7
At1g61800	glucose-6-phosphate/phosphate translocator, putative	34