Inhibiting ethylene perception with 1–methylcyclopropene triggers molecular responses aimed to cope with cell toxicity and increased respiration in citrus fruits

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ABSTRACT

The ethylene perception inhibitor 1-methylcyclopropene (1-MCP) has been critical in understanding the hormone's mode of action. However, 1-MCP may trigger other processes that could vary the interpretation of results related until now to ethylene, which we aim to understand by using transcriptomic analysis. Transcriptomic changes in ethylene- and 1-MCP-treated 'Navelate' (*Citrus sinensis* L. Osbeck) oranges were studied in parallel with changes in ethylene production, respiration and peel damage. The effects of compounds modifying the levels of the ethylene co-product cyanide and nitric oxide (NO) on fruit physiology were also studied. Results suggested that: 1) The ethylene treatment caused sub-lethal stress since it induced stress-related responses and reduced peel damage; 2) 1-MCP induced ethylene-dependent and ethylene-independent responsive networks; 3) 1-MCP triggered ethylene overproduction, stress-related responses and metabolic shifts aimed to cope with cell toxicity, which mostly affected to the inner part of the peel (albedo); 4) 1-MCP increased respiration and drove metabolism reconfiguration for favoring energy conservation but up-regulated genes related to lipid and protein degradation and triggered the over-expression of genes associated with the plasma membrane cellular component; 5) Xenobiotics and/or reactive oxygen species (ROS) might act as signals for defense responses in the ethylene-treated fruit, while their uncontrolled generation would induce processes mimicking cell death and damage in 1-MCP-treated fruit; 6) ROS, the ethylene co-product cyanide and NO may converge in the toxic effects of 1-MCP.

KEYWORDS

Ethylene, 1-methylcyclopropene (1-MCP), non-climacteric fruits, oxidative stress, respiration, xenobiotics.

1. INTRODUCTION

The hormone ethylene plays important roles in development, fruit ripening, abscission, senescence and stress (Abeles et al., 1992). The ethylene signalling pathway and the responses related to the hormone in stressed plants and climacteric fruits have been widely investigated. Less information exists concerning non–climacteric fruits (Wang et al., 2010). The discovery of 1–methylcyclopropene (1–MCP) as a specific inhibitor of ethylene, counteracting ethylene at the receptor level, was a critical breakthrough in understanding the diverse roles of the hormone in plants and also in fruits (Watkins, 2006). As a gas, 1–MCP offers the possibility of facile and uniform delivery, even to bulky plant organs. Therefore, 1–MCP has been especially relevant in research done in fruits from woody plants, where artificially generated mutants are uncommon. Nevertheless, there is a general consensus within the scientific community regarding the fact that 1–MCP may induce additional mechanisms to those regulated by ethylene that may be relevant for the interpretation of results derived from 1–MCP application when studying the diverse roles of ethylene. These mechanisms are still unknown in site of the nearly 20 years that have passed since 1–MCP was discovered and the huge number of studies performed using 1–MCP. None of these studies considered additional effects of 1–MCP.

Different reports suggest that the production of new ethylene receptors may be responsible for the loss of efficacy of 1–MCP blocking the perception of ethylene (Prange et al., 2005); that 1–MCP may be metabolized in plants (Huber et al., 2010); and that ethylene and 1–MCP may bind with different affinities to different ethylene receptors (Cools et al., 2011). The situation is not simple because the effects of 1–MCP, like those of ethylene, differ among species and depend on the physiological stage. Moreover, 1–MCP may have contrary effects, either reducing or enhancing physiological disorders. Two examples are the 1–MCP–induced reduction of postharvest superficial scalding in apples, which produce high ethylene levels (Watkins, 2006), and the 1–MCP–induced increase in postharvest peel damage disorders in citrus fruits, which produce very low hormone levels (Lafuente and Sala, 2002; Lafuente et al., 2001). These differences might be related to the effect of ethylene on the mechanisms operating in the development of such disorders, but we cannot exclude the different

effect of 1-MCP on the biosynthesis of ethylene and its co-products as well as on its associated responses in such fruits.

Mature non-climacteric citrus fruit evolves very low amounts of ethylene, but ethylene sharply increases in response to stress and following inhibition of its perception because this fruit displays autoinhibitory ethylene production (Lafuente et al., 2001; Marcos et al., 2005; McCollum and Maul, 2007). Responses to ethylene include induction of ripening-related changes, accelerated respiration and activation of stress-defense responses (Gonzalez-Candelas et al., 2010; John-Karuppiah and Burns, 2010; McCollum and Maul, 2007). Previous investigations suggest a link between carbon starvation stress and the 1-MCP-induced rises in respiration and peel damage in detached mature citrus fruit (Cajuste et al., 2011), and show that conditioning citrus fruits with ethylene reduces this disorder known as non-chilling peel pitting (NCPP) (Supplementary Fig. S1A) (Lafuente and Sala, 2002). The symptoms of NCPP are collapsed areas of part of the albedo (inner part of the peel) and the flavedo (outer colored part), which may become brown with time if the severity of the disorder is very high. 1-MCP should block protective mechanisms induced by the hormone or modify its interaction with other molecules and pathways in the complex network of regulatory defense responses. These reasons, in addition to the fact that 1-MCP increases endogenous ethylene in citrus fruit, make mature citrus fruit a good experimental system for studying whether 1-MCP has additional effects to those regulated by the hormone.

Genomic tools have been quickly adopted to address major challenges of citrus fruit. Yet only one comprehensive transcriptomic study has been performed to determine the effect of ethylene in the flavedo of still green fruits (Fujii et al., 2007). This study used very high ethylene levels (100 $\mu L\ L^{-1}$) and focused on the mechanisms occurring during the conversion of chloroplast to chromoplast during degreening. Physiological responses to ethylene, however, are influenced by the maturity stage in citrus fruit (John-Karuppiah and Burns, 2010). Transcriptomic studies have been also performed to study the role of ethylene in the regulation of citrus peel genes induced by fungal infection (Gonzalez-Candelas et al., 2010). However, no large-gene expression analysis has been conducted yet comparing the responses of the albedo and the flavedo to ethylene and 1-MCP and their effects in detached mature fruits.

Our working hypothesis was that 1-MCP, besides inhibiting ethylene action, may regulate complex mechanisms related to ethylene co-products and/or to increased

respiration and that such mechanisms might favor, in part, stress that may end in peel collapse in harvested mature citrus fruit. To test this hypothesis, and to compare such mechanisms with those induced by ethylene concentrations that reduce peel collapse, we have investigated the effects of ethylene and 1-MCP at the transcriptomic level. Transcriptome analysis of the flavedo and the albedo was performed because both tissues are highly affected by NCPP (Cajuste et al., 2011) and their morphology and ability to provide energy is different (Matas et al., 2011). Moreover, previous research from our group showed that structural and histochemical changes induced by ethylene were more marked in the albedo (Cajuste et al., 2011). Considering results from the transcriptomic analysis, we further examined whether cyanide, stoichiometrically co-produced during ethylene biosynthesis (Peiser et al., 1984), and nitric oxide (NO) may mimic the postharvest NCPP syndrome, and whether inhibiting or scavenging cyanide or NO may reduce the deleterious effect of 1-MCP.

2. MATERIALS AND METHODS

2.1. Plant material and treatments

'Navelate' sweet oranges (*Citrus sinensis* L. Osbeck) were harvested 3 months after color change from adult trees in Castellón, Spain. The oranges were immediately divided into three groups containing an equal number of fruits and exposed to the following treatments: continuous flow of air after being conditioned with 10 μL L^{-1} ethylene for 4 days (EC, group 1); continuous flow of air (AC, group 2); continuous flow of air after being treated with 1 μL L^{-1} 1-MCP for 14 h (group 3) (Fig. 1). All the treatments were performed in sealed containers, which were kept in controlled temperature and humidity storage rooms, and in the presence of $Ca(OH)_2$ to prevent the accumulation of respiratory CO_2. Fruits were always kept at 20 ºC and 90–95% relative humidity (RH) to avoid environmental stress. 1-MCP, donated by Rohm and Haas Spain, S.A., was prepared and fumigated following the manufacturer's instructions. Fruits from each group were ventilated after fumigation and randomly divided into 3 replicates of 10 fruits to estimate ethylene production, respiratory rate and NCPP index. Additional replicate samples of 5 fruits per treatment and storage period and of freshly harvested fruits were used for transcriptomic analysis. Transcriptomic data were

gathered from freshly harvested fruits and from air control (AC), EC and 1-MCP-treated oranges held for 4 and 14 days at 20 ºC. The experimental design, outlined in Fig. 1, was established to focus on short- (4 days) and long-term (14 days) responses induced after 1-MCP application and also to compare these responses with those induced by ethylene at day 4 since the 4 days of EC treatment showed a high efficacy in reducing NCPP. Although transient changes in gene expression might be induced by ethylene at 20 ºC in a few hours, it is important to note previous results from our group showing that the high efficacy of the EC treatment is reduced when the treatment is shortened (Lafuente and Sala, 2002). These initial transient responses would be also induced by the shorter treatments in spite of their lower efficacy. Therefore, the effectiveness of the EC treatment was not limited to transient responses induced during the ethylene treatment. Taking into account this, our experimental design focused on initial responses induced by ethylene that persisted for at least 4 days and on other secondary responses occurring by day 4. These responses should be especially relevant for the persistence of the efficacy of the EC treatment. Moreover, the incidence of peel collapse sharply increased after 4 days in the 1-MCP-treated fruits. At this time point differences in NCPP between the control CA fruits and the 1-MCP-treated fruits started to be apparent. The 14 days period was selected to further know the long-term 1-MCP-induced responses. This approach also allowed focusing on mechanisms occurring in fruits exposed for prolonged periods to the high ethylene levels produced by the 1-MCP-treated fruits, or related to putative co-products generated during hormone biosynthesis or to the increased respiration. Harvested fruits treated for 4 days with the hormone were transferred to air for 10 additional days to compare long-term responses induced by day 14 in 1-MCP-treated and the EC-treated fruits, respect to their control sample held for 14 days in air (control fruit, AC). Similarly, changes induced at day 4 by ethylene were compared with those occurring in AC and 1-MCP-treated fruits (Fig. 1). The flavedo and the external layer of the albedo were collected periodically from the total fruit surface, immediately frozen and grounded in liquid nitrogen and stored at -80 ºC. Three biological replicates originate from different sample sets coming from three independent experiments performed in different citrus seasons were collected at each sampling period and used for each analysis.

2.2.Feeding experiments

For each treatment, 3 replicates of 10 fruits were used. Fruits were dipped for 2 min in different solutions (1 μM, 10 μM, 100 μM and 1 mM) of sodium nitroprusside (SNP), 300 μM hydroxocobalamin (HB), 300 μM 2-[4-carboxyphenyl],4,4,5,5-tetramethylimidazoline-1-oxy-3-oxide (cPTIO) or de-ionized water. Fruits treated with HB and cPTIO were treated with 1-MCP following the same procedure described above. All the fruits were then stored in the dark at 20 ºC and 90-95% RH. All chemicals were from Sigma-Aldrich (St. Louis, MO, USA).

2.3. Ethylene production and respiratory rate determination

Ethylene production from whole fruits was measured periodically by incubating 3 replicate samples of 10 fruits in 3 L sealed glass jars at 20 ºC for 3 h. Ethylene samples were withdrawn from each jar and injected into a gas chromatograph, equipped with an activated alumina column and a flame ionization detector (Lafuente et al., 2001). The respiratory rate was determined by measuring CO_2 production. CO_2 evolution was determined following the same procedure but using a Chromosorb 102 column and a thermal conductivity detector (Cajuste et al., 2011).

2.4. Estimation of nonchilling peel pitting damage

A visual rating scale was used to estimate the extent of NCPP development (Supplementary Fig. S1). This scale was established on the basis of surface damage and ranged from 0 (no damage) to 4 (severe damage). The average NCPP index was calculated according to Lafuente and Sala (2002), and the results are the means of the three replicate samples ± SE.

2.5. RNA isolation and preparation of labelled cDNA probes

Total RNA was isolated from flavedo and albedo tissues, its concentration was measured spectrophotometrically, and its integrity verified by agarose gel electrophoresis and ethidium-bromide staining (Ballester et al., 2011). Processing of RNA samples for microarray hybridizations, reverse transcription, cDNA purification, dye coupling, and fluorescent cDNA purification were performed according to Ballester

et al. (2011). Three biological replicates were used for RNA isolation and the subsequent microarray hybridization and validation by RT–qPCR.

2.6. Microarray hybridization, data acquisition and data analysis

A 12k citrus cDNA microarray developed by the Spanish Citrus Functional Genomic Project (CFGP, http://bioinfo.ibmcp.upv.es/genomics/cfgpDB/) (Martinez–Godoy et al., 2008) was used. The microarray contains 24,288 probes corresponding to 11,241 putative unigenes from citrus, which constitutes a high representation of the citrus genome. Of these genes, 77.1% have an *A. thaliana* homolog (Ballester et al., 2011). Microarray hybridization and scanning were performed as described by Ballester et al. (2011). Samples were hybridized against a reference sample containing a mix of equal amounts of RNA of all the experimental samples. The use of this reference sample has been widely used in *Citrus* transcriptomic research since represent a powerful tool for reducing the number of hybridizations to make all the possible pairwise comparisons between samples (Ballester et al., 2011; Romero et al., 2012). SAM (Significant Analysis of Microarrays), included in the TM4 Microarray Software Suite, was used to identify differentially expressed genes using a False Discovery Rate threshold p–value<0.01 as previously described (Ballester et al., 2011; Romero et al., 2012). FatiGO+ (Babelomics, http://babelomics.bioinfo.cipf.es) was used to identify processes that were significantly over– or under–represented in a particular set of differentially expressed genes relative to a reference group composed of all genes in the microarray with an *Arabidopsis thaliana* homolog (Ballester et al., 2011; Romero et al., 2012). Gene ontology analysis for induced and repressed genes was independently performed applying a Fisher two–tailed test (p–value<0.05). Transcriptomic data were also loaded into MapMan (http://www.gabipd.de/projects/MapMan/) to visualize the gene expression data on a metabolic map (Thimm et al., 2004).

2.7. RT-qPCR expression analysis

Reverse transcription of flavedo and albedo RNA samples followed by quantitative polymerase chain reaction analysis (RT–qPCR) was performed to validate microarray results as previously described by Romero et al. (2012). The LightCycler SW 1.5 software was used and a two–step RT–qPCR assay designed. Forward (F) and

reverse (R) sequences for selected primers and reference genes used for data normalization, whose constitutive expression was confirmed by using the geNorm program, are summarized in Supplementary Table S1. Statistical analysis (Pair Wise Fixed Reallocation Randomisation Test) was performed by the ΔΔCt method using the Relative Expression Software Tool (REST, http://rest.gene-quantification.info/). Each biological replicate sample was analyzed in duplicate.

2.8. Statistics

A mean comparison using Tukey's test and Statgraphics.5.1 Software was performed to determine significant differences ($p \leq 0.05$) in NCPP, ethylene production and the respiratory rate.

3. RESULTS

3.1. 1-MCP triggers a maintained ethylene overproduction and enhances respiration and peel collapse in citrus fruit

The 1-MCP treatment had a more marked effect on increasing ethylene levels than the ethylene applied during the EC treatment (Fig. 2A). During the first day of hormone treatment the endogenous ethylene level of the fruits was barely modified, but it increased 3-fold by day 2 and remained high until the fruits were transferred to air (Fig. 2A, insert panel). 1-MCP led to a sharp increase in hormone levels, reaching a maximum by day 7 (Fig. 2A). At this time point, a ca. 200-fold ethylene increase was observed. Ethylene production decreased thereafter, but it was still much higher than in control fruits. The 1-MCP-induced rise in CO_2 was much lower (ca. 3-fold increase) (Fig. 2B). Detachment and continuous holding of oranges in air under non-stressful environmental conditions (AC fruits) induced the development of NCPP symptoms after 3 days (Fig. 2C). The incidence of the disorder was lower in the EC fruits and enhanced by the 1-MCP treatment. This trend, as well as that of ethylene production, was confirmed in fruits harvested in a second citrus season.

3.2. 1-MCP and ethylene elicit common but also different transcriptional profiles

Global gene expression was analyzed in EC, AC and 1-MCP-treated fruits and compared to that of freshly harvested fruits according to the experimental design described above and outlined in Fig. 1. The number of differentially expressed genes is summarized in Fig. 3. SAM analysis revealed major changes in fruits treated for 4 days with ethylene and at long-term (14 days) in the 1-MCP-treated fruits. The largest differences were observed by day 14 in the albedo of the 1-MCP-treated fruits. The number of ethylene-induced genes (4 days) decreased considerably after transferring the fruits to air. In contrast, the number of up-regulated genes increased more than 10-fold between 4 and 14 days in the 1-MCP-treated fruits. The sensitivity and consistency of the microarray analysis was confirmed by determining the expression of selected genes (Supplementary Table S1) using RT-qPCR. Results showed a high correlation (r^2 = 0.807, $p \leq 0.05$) between the microarray and the RT-qPCR results (Supplementary Fig. S2).

Differentially expressed genes were classified into biological processes that were clustered according to their over-/infra-representation either in the albedo or the flavedo of fruits treated with ethylene or 1-MCP (Table 1). As explained above, both tissues are highly affected by NCPP and they show different ability to provide energy, and also different structural and histochemical changes in response to ethylene. Therefore, results from both tissues are complementary. No biological process was over- or infra-represented after short-term (4 days) in the 1-MCP-treated fruits (Table 1). Pattern 1 in Table 1 includes processes induced only at long-term in the 1-MCP-treated fruits and pattern 2 processes that might be counteracted by 1-MCP. Processes related to the defense response to pathogens prevailed within pattern 1, although other processes involving abiotic stresses and response to toxins were also over-represented. Processes related to fatty acid biosynthesis prevailed in pattern 2. Other processes were over-represented at long-term in the 1-MCP-treated fruits and induced at day 4 by ethylene (pattern 3); while processes within pattern 6 were counteracted by ethylene and 1-MCP. Ethylene specifically repressed photosynthesis-related processes and induced processes related to lignin biosynthesis in the albedo and flavedo (pattern 4). Other processes like **'response to hypoxia' were only over-represented in the albedo. The 'oxylipin metabolic process'**, which included abundant genes encoding lipoxygenases (LOX), was the only

over-represented process that persisted at long-term after fruit transference to air. By day 14, expression levels of these *LOX* genes were in general lower in the 1-MCP-treated fruit (Supplementary Table S2). Processes within pattern 5 might be counteracted by ethylene and belonged to general GO levels, except the 'response to jasmonic acid stimulus'. Gene ontology analysis also revealed that, at long-term, 1-MCP induced molecular functions related to serine/threonine and tyrosine kinase activity and to ATP binding (Table 2). Molecular functions over-represented specifically in the EC fruits showed oxidoreductase, UDP-glycosyltransferase and nucleotide kinase activities. Moreover, the 'kinase activity' and the 'heme and iron ion binding' functions were induced by both ethylene and 1-MCP. Both treatments infra-represented the 'thylakoid membrane' cellular component in the albedo, although this effect was reversed after transferring EC fruit to air (Table 2). Moreover, the over-expression of genes associated with the 'plasma membrane' component only occurred at long-term in this tissue in response to 1-MCP. The study of protein domains (InterPro Table 2) further indicated the relevance of protein phosphorylation at long-term in the 1-MCP-treated fruits and of proteins containing LOX domains in EC fruits by day 14.

3.3. 1-MCP-induced metabolism alteration in the peel of citrus fruit

To better visualize the gene expression data on a metabolic map, transcriptomic data were analyzed with MapMan. Little changes were found by day 4 in the albedo and the flavedo of the 1-MCP-treated fruits respect to control fruits (data not shown). Changes in the transcript levels in the albedo of the 1-MCP-treated fruits (14 days) have been highlighted in this paper (Fig. 4) since major changes were observed in this sample. 1-MCP favored the repression of genes involved in starch synthesis and degradation and increased the expression levels of sucrose synthase genes involved in sucrolysis via the sucrose pathway and of genes encoding cell wall hydrolases. The ethylene antagonist also favored the up-regulation of glycolytic genes and of genes within the fermentative anaerobic pathway, which fits with the induction of other genes within the biological process 'response to hypoxia' (Supplementary Table S2). The most important change within this process corresponded to the gene encoding hemoglobin II, whose expression increased 8-fold. Moreover, 1-MCP up-regulated genes encoding lipases and esterases and participating in lipid β-oxidation and in amino acid and protein catabolism (Fig. 4). 1-MCP also raised the expression of genes

involved in mitochondrial electron transport and of cytochrome P450 and ATP synthase-encoding genes. In contrast, 1-MCP barely affected the alternative respiration pathway and slightly repressed the mitochondrial uncoupling protein (UCP) pathway (Fig. 4).

Among genes within the TCA-cycle, the most relevant inductions corresponded to those coding for aconitase and isocitrate dehydrogenase. These genes participate not only in cell energetics but also in the generation of intermediates leading to nitrogen assimilation via amino acid biosynthesis by the concerted action of glutamine synthase (GS) and glutamate 2-oxoglutarate amminotransferase (GOGAT) in the GS/GOGAT cycle, which was activated by 1-MCP. In concordance with this result, 1-MCP had, at long-term, an important effect on activating the chorismate and the subsequent phenylpropanoid pathways (Fig. 4), and this effect was more marked than in EC fruit (4 days, data not shown). Transcriptomic data further showed that 1-MCP down-regulated genes associated with light reaction centers and the Calvin cycle and up-regulated oxidative stress-related genes (Fig. 4).

3.4. 1-MCP up-regulates at long-term genes involved in ethylene biosynthesis and perception and in cyanide and reactive oxygen species (ROS) detoxification

Changes in fruit endogenous ethylene levels and the examination of genes within the process 'response to toxin' (Supplementary Table S2) suggested that overproduction of ethylene and/or cyanide, which is stoichiometrically co-produced during ethylene biosynthesis from 1-aminocyclopropane-1-carboxylic acid (ACC), may contribute to higher NCPP in the 1-MCP-treated fruits. To verify this, and to further investigate whether some of the 1-MCP-induced transcriptional profiles found in the albedo and the flavedo may be related to ethylene overproduction, changes in the expression of genes printed in the microarray related to ethylene biosynthesis, perception and signalling, and also to cyanide detoxification, were examined in the peel (Table 3). Major changes were found in ACC oxidase (ACO)-encoding genes and ACC oxidase oxidizes ACC to ethylene and cyanide. Some of them are still annotated as ethylene-forming enzymes in the *Arabidopsis* database. These changes were, in general, higher in the albedo of the 1-MCP-treated fruits. Furthermore, ethylene and 1-MCP treatments modulated genes involved in ethylene perception and signal transduction. From a total of 4 genes encoding ethylene receptors printed in the microarray, 2 were induced at long-term in

the 1-MCP-treated fruits. Likewise, ethylene (4 days) and 1-MCP (14 days) modulated ethylene-responsive factors. Only 1-MCP was able to induce the 'response to ethylene stimulus' (Supplementary Table S2). Although transient responses induced initially by either ethylene or 1-MCP were not determined, these results suggest that some responses induced by 1-MCP at long-term are indeed regulated by ethylene.

Expression levels of the genes involved in cyanide detoxification were clearly higher in the 1-MCP-treated fruits by day 14 (Table 3). Major expression levels were observed in a β-cyanoalanine synthase (CAS)-encoding gene, whereas this gene was down-regulated in the 1-MCP-treated fruits by day 4. Its expression was lower in the 1-MCP-treated fruits (14 days) than in the EC fruits (4 days). Therefore, the ability of 1-MCP-treated fruits to detoxify cyanide should be lower. Two of these cyanide detoxifying genes belonged to the 'response to toxin' process, which is relevant for xenobiotic and ROS detoxification and mostly groups genes encoding glutathione transferases (GSTs) (Supplementary Table S2). MapMan visualization of transcriptomic data also suggested that 1-MCP favor oxidative stress. Considering that an excess of ethylene and/or cyanide may favor ROS in plants (Munné-Bosch et al., 2004; Oracz et al., 2009), we further focused on transcriptomic data related to generation and detoxification of ROS. Ethylene modulated genes involved in oxidative stress, but major changes were observed by day 14 in the 1-MCP-treated fruits. Besides the high representation of *GSTs*, we observed the induction of the blue copper oxidases, annotated as dicyanins, and of genes in the ascorbate-glutathione cycle (Supplementary Table S3). Genes leading to the detoxification of ROS within the thioredoxin-dependent pathway or favoring H_2O_2 formation, such as those encoding glycolate and amine oxidases, were also mostly induced at long-term by 1-MCP (Supplementary Table S3). Furthermore, 1-MCP activated protein serine/threonine kinase cascades (Table 2) and up-regulated oxidative genes like CPR2 or nectarin, whose expression increased more than 16- and 32-fold in the albedo, respectively. Likewise, data summarized in Table 4 showed that 1-MCP induced a high representation of genes involved in detoxification or in response to toxin in the albedo (Riechers et al., 2010). Many of these genes have been related to safeners (Riechers et al., 2010) or to nitric oxide (NO) (Arasimowicz and Floryszak-Wieczorek, 2007), which can partly mediate some of the effects of cyanide (Bethke et al., 2006).

3.5. 1-MCP-induced damage is reduced by inhibiting cyanide or scavenging nitric oxide

To further test whether cyanide can participate in the detrimental effect of 1–MCP, fruits were treated with SNP, which releases cyanide and NO. Therefore, SNP offers the possibility of testing the involvement of both molecules in 1–MCP–mediated toxicity. The effect of HB, which binds cyanide to form harmless cyanocobalamin, and of the NO scavenger cPTIO on the incidence of damage in 1–MCP–treated fruit was also examined. SNP mimicked the NCPP syndrome (Supplementary Fig. S1) in a dose–dependent manner (Fig. 5A). Moreover, both HB and cPTIO reduced NCPP in the 1–MCP–treated fruits (Fig. 5B) and had little effect on control fruits (data not shown). These results, together with the fact that HB and cPTIO did not modify endogenous ethylene levels (Supplementary Fig. S3), indicate that the 1–MCP–induced ethylene co–product cyanide and NO may modulate additional responses to those regulated by the hormone and that these molecules may be involved in the peel damage associated with the 1–MCP treatment.

4. DISCUSSION

Results revealed that 1–MCP triggers, after 4 days, a maintained ethylene overproduction and a marked but lower increase in respiration in citrus fruit, and that changes in gene expression triggered by day 4 by 1–MCP were less relevant than those triggered at long–term. Moreover, results revealed that the long–term responses involve metabolic shifts aimed to cope with cell toxicity and extra energy demand in the peel of detached non–photosynthetic sink mature citrus fruits. These results indicate that 1–MCP regulates complex secondary stress–related responses associated with overproduction of ethylene and its co–products and/or with increased respiration that may end in peel damage.

The fact that 1–MCP up–regulated at long–term genes involved in β–oxidation and lipolysis (Fig. 4) is remarkable. This metabolic reconfiguration could be caused by the combination of fruit detachment and extra energy demand associated with the 1–MCP–induced respiratory rise. This energy stress would be complicated by the fact that 1–MCP inhibited the photosynthetic machinery (Fig. 4) that coordinates energy metabolism and balances cell redox status. Extra energy can be obtained from lipid

445 catabolism, and it is known that a respiratory burst is accompanied by a switch in substrate from carbohydrates to lipids (Theologis and Laties, 1981). Moreover, 1-MCP favored protein degradation (Fig. 4), which suggests protein utilization as an additional energy resource. Therefore, lipid and protein degradation might lead to membrane deterioration, as it has been observed in 1-MCP-treated oranges (Cajuste et al., 2011), 450 and ultimately to damage. Interestingly, plasma membrane was the only cellular component over-represented at long-term in the albedo of the 1-MCP-treated fruit (Table 2). Likewise, results suggesting that 1-MCP might favor the sucrose synthase pathway fit with the carbon economy and imbalance between carbohydrate import and demand in plants lacking carbohydrate supply. The importance of the interplay between 455 energy status sensing and oxygen availability in the optimization of plant metabolism should be also kept in mind. In this regard, 1-MCP up-regulated genes involved in fermentation, which may be induced by a drop in plant energy status (Zabalza et al., 2009), and up-regulated low oxygen sensors, including hypoxia-responsive genes and genes involved in trehalose-6-phosphate metabolism (Fig. 4) (Bailey-Serres et al., 460 2012). Major hypoxia-related responses occurred in the albedo, in agreement with its lower capacity to provide energy with respect to the flavedo (Matas et al., 2011) and with the lower environmental oxygen availability in the inner part of the peel. Therefore, extra energy demand induced by 1-MCP might contribute to the increased damage in the peel of citrus fruits. Nevertheless, results from this study suggest a higher 465 influence of ethylene overproduction and the associated toxic molecules than the higher energy requirements of 1-MCP-treated fruits on damage development. This might be related in part to the fact that the 1-MCP-induced rise in ethylene was much higher than the rise in respiration.

Physiological data revealed that endogenous ethylene levels increased during fruit 470 exposure to exogenous ethylene, that ethylene production of the EC fruits was lower than that of the control AC fruits after fruit transference to air, and that the hormone increase induced by exogenous ethylene was much lower than that induced by 1-MCP. Ethylene production increases in response to stresses in non-climacteric citrus fruit. Since the EC treatment reduced postharvest NCPP, and ethylene negatively regulates its 475 own biosynthesis in citrus fruit, the observed increase in hormone biosynthesis during the EC treatment indicates that the exogenous ethylene levels used were high enough to produce non-lethal stress. In fact, ethylene induced stress-related responses that might be involved in cross-protective mechanisms participating in NCPP reduction. The

hormone thus induced responses related to lignin biosynthesis and to the 'oxilypin metabolic' process, which participates in the containment of lesion propagation in stressed tissues. Furthermore, shortening the ethylene treatment results in a lower NCPP reduction (Lafuente and Sala, 2002).

In line with the idea that EC produces sub-lethal stress, 1-MCP induced after 4 days a maintained high non-physiological ethylene overproduction and favored NCPP. As ethylene is perceived at long-term by the fruit because of the synthesis of new ethylene receptors, this huge ethylene production could lead to damage. The long-term 1-MCP-induced responses within pattern 3 (Table 1) should be mediated by ethylene, although these responses were not sufficient to avoid damage. Initial responses induced immediately after 1-MCP application were not determined, and no biological process was specifically induced by day 4, but the nature of other responses expressed only in the 1-MCP-treated fruits by day 14 indicates that 1-MCP produces severe stress and that this stress might be caused by the excess of ethylene and/or its co-product cyanide. Changes in the expression of cyanide detoxifying genes (Table 3) suggested that the ability of 1-MCP-treated fruits to detoxify cyanide should be lower. This, together with results showing that the expression of ACO-encoding genes and ethylene production were much higher in this sample, further suggests that an excess of cyanide may contribute to the harmful effect of 1-MCP.

Ethylene causes the disruption of chloroplast integrity in green citrus peel (Purvis, 1980). The chloroplast is a major site of ROS production, and severe stress-induced changes in its redox state may trigger programmed cell death (PCD). The effect of the hormone on mature fruits, where chloroplast has been transformed to chromoplast, is lesser-known. Results show that ethylene treatment led to an infra-representation of the 'thylakoid membrane' component (Table 2) and down-regulated the 'photosynthesis' process (Table 1). These changes did not persist after transferring EC fruit to air. Results further showed that 1-MCP has at long-term an important effect on the thylakoid membrane, photosynthesis and light reaction-related genes of the PSII and PSI centers (Fig. 4 and Supplementary Table S2). These changes resemble photorespiration energy-sensing responses. Balanced excitation of both PSs is required for avoidance of oxidative stress and subsequent PCD (Asada, 2006). Therefore, ethylene overproduction for prolonged periods might cause damage in plastids and favor ROS. This is in concordance with changes in the expression of oxidative stress-related genes (Supplementary Table S3). These changes, together with the reported

H_2O_2–induced responses in plants (Van Breusegem and Dat, 2006), further suggest that H_2O_2 may lead to PCD induction in citrus fruits that over–produce ethylene. The hydroxyl and $^1O_2$ radicals could also contribute to the harmful effect of 1–MCP. These radicals are triggered by PSII inhibition or by dicyanins in the presence of cyanide (Asada, 2006; Van Breusegem and Dat, 2006), and dicyanins were highly induced at long–term by 1–MCP (Supplementary Table S3). Furthermore, 1–MCP at long–term up–regulated a high number of *GSTs* (Table 4). Although the primary function of *GSTs* is xenobiotic detoxification, they may also act as peroxidases or regenerating ascorbate (Dixon et al., 2009). Increases in expression of *GSTs* in response to exogenous ethylene were less relevant and declined after transferring the fruits to air (Supplementary Table S3). This indicates that the stress caused by ethylene may be reversible. *GSTs* may thus participate in the cross–protection responses induced by the hormone and may also be induced in the 1–MCP–treated fruits to cope with the persistence of ROS or xenobiotics caused by an excess of ethylene and/or its co–products. In this regard, previous data showed the involvement of ROS in ethylene–induced damage in plants (Hodges and Forney, 2000). The fact that 1–MCP barely affected the alternative respiration and the UCP pathways (Fig. 4) is remarkable since it indicates that they would not contribute to ROS prevention in 1–MCP–treated fruits. Likewise, changes in the ethylene–treated oranges agree with the idea that the ethylene–induced acclimation of plants to stress involves oxidative stress–related responses (Munné–Bosch et al., 2004). An excess of ethylene may favor ROS and senescence (Hodges and Forney, 2000) and some of the 1–MCP–induced responses showed similarities to the responses related to the postharvest senescence process in citrus fruit (Ding et al., 2015). However, besides NCPP incidence, there were no relevant differences in external appearance among AC, EC and 1–MCP–treated fruits. Therefore, senescence appears not to be a limiting factor for NCPP development.

The activation of *GSTs* and other stress–related responses further suggests that an excess of cyanide and NO may contribute to the 1–MCP–induced damage. It was surprising to find the over–representation of processes related to defense response to pathogens since these processes were not up–regulated by ethylene in the present work or in infected citrus fruit (Gonzalez–Candelas et al., 2010). Cyanide and NO stimulate responses associated with the plant immune system (García et al., 2013; Scheler et al., 2013). Therefore, these compounds might modulate additional responses to those regulated by the hormone in the 1–MCP–treated fruits. It is worth noticing that both

cyanide and 1-MCP trigger similar oxidative stress-related responses, such as the induction of genes encoding amine oxidases or involved in signalling within the MAPK and Ser/ThrPK cascade, as well as the repression of *CAT* and *Cu/Zn SODs* (Oracz et al., 2009). Considering these results, and that cyanide increases the expression of hypoxic responsive genes, as 1-MCP does, the participation of cyanide in the development of peel damage was confirmed by showing that SNP mimicked the NCPP syndrome and that HB reduced it in the 1-MCP-treated fruit. What we may learn from these results is that some of the 1-MCP-related responses may be associated with cyanide. This finding might help to understand the different effects of 1-MCP on damage in different fruits. Cyanide release might explain in part why 1-MCP favors stress-induced disorders in citrus fruits but reduces them in apple fruit. Contrary to what happens in citrus fruit, apples shows high and autocatalytic ethylene production, 1-MCP reduces ethylene biosynthesis in apples, and hence cyanide levels must be lower in MCP-treated apples. Another example of the relevance of this finding is the suggestion that cyanide might influence the response of antisense ACO plants and fruits to stresses, since ethylene, but also cyanide formation, should be curtailed in these plants.

The link between ethylene/cyanide and NO release remains unknown, although it has been reported that some effects of cyanide can be mediated through NO (Bethke et al., 2006). Results from the present study showed that 1-MCP induced the response to salicylic acid stimulus in citrus fruit and has the thylakoid membrane and the Calvin cycle as target sites (Table 2 and Fig. 4), which resembles cyanide- and NO-related changes in plants (García et al., 2013; Scheler et al., 2013). 1-MCP induced other NO stress-related responses (Parani et al., 2004) and specifically over-expressed the PCD, **the 'defense response, immune interaction' and the 'jasmonic acid mediated signalling pathway' biological processes in mature oranges (Table 1)**. In the context of the present work, it is noticing that NO and ROS signalling pathways are connected and related to cell death (Van Breusegem and Dat, 2006; Wodala, 2006) and to plant defense mechanisms involving plant biotic interactions (Scheler et al., 2013). Likewise, the ethylene and the 1-MCP-induced changes in abundant LOX-encoding genes (Supplementary Table S2) within the oxylipin metabolic process found in the present work resembled results showing that prolonged NO stress inhibit LOX isoforms in spite of LOX activity increases at the beginning of NO stress (Arasimowicz and Floryszak-Wieczorek, 2007). Considering these findings, the participation of NO in the harmful effect of 1-MCP was further confirmed by applying SNP as well as cPTIO. The facts

that HB and cPTIO were very effective in reducing 1-MCP-enhanced damage further indicated a higher influence of an excess of ethylene and/or its co-products than the higher energy requirements of the detached 1-MCP-treated citrus fruits on NCPP development.

In conclusion, 1-MCP mimics, at long-term, stress-related responses and triggers the overproduction of ethylene and metabolic shifts aimed to cope with cell toxicity and increased respiration and extra energy demand in detached non-climacteric citrus fruit. Although the external manifestation of NCCP affects the flavedo, global data indicate that the albedo is the most affected tissue in this disorder. Cyanide and NO may converge in the toxic effects of 1-MCP. ROS and/or xenobiotic downstream mechanisms might act as signals for defense responses in the EC fruit, while a higher uncontrolled generation of ethylene/cyanide in the 1-MCP-treated fruits would lead to damage. Another lesson to be learned from this work is that further attention should be paid to understanding the effects of ethylene co-products on the physiological effects attributed until now only to the hormone. Such effects may vary the interpretation of results derived from 1-MCP application when studying the role of ethylene, associated with sharp increases/decreases in endogenous ethylene levels, or derived from transgenic fruit and plants with altered ethylene biosynthesis.

SUPPLEMENTARY MATERIAL

Supplemental Fig. S1. NCPP syndrome in fruit held in air (A), and in fruits pretreated with 1-MCP (B) and SNP (C).

Supplemental Fig. S2. Correlation in the expression of selected genes (Table S1) quantified using either the citrus microarray or RT-qPCR. The expression of these genes was quantified in the flavedo and albedo of AC, EC and 1-MCP fruits stored for 4 and 14 days at 20 ºC ($r^2 = 0.807$, $p \leq 0.05$).

Supplemental Fig. S3. Effect of HB (■) and cPTIO (▲) on the ethylene production of fruits treated with 1-MCP (●) and stored at 20 ºC. No significant differences were found among mean values of these samples for the same storage period ($p \leq 0.05$), and the values always differed significantly from the means of fruits treated only with water (○).

Supplemental Table S1. Selected genes and primers used for comparison between the *Citrus* 12 k microarray and RT-qPCR gene expression data. Reference genes *CsACT*, ***CsEF1α***, and *CsTUB* were used for data normalization.

Supplemental Table S2. Expression levels of citrus genes in the flavedo (F) and albedo (A) of AC, EC and 1-MCP-treated fruit stored for 4 and 14 days at 20 ºC grouped according to the biological processes they belong to. Numbers in bold indicate statistically significant differences (SAM, FDR < 0.01).

Supplemental Table S3. Fold changes (log_2) in expression of oxidative stress-related genes in the flavedo (F) and albedo (A) of AC, EC and 1-MCP-treated fruits stored for 4 and 14 days at 20 ºC as compared to freshly harvested (FH) fruit. The symbol + indicates no expression in FH fruits, and the symbol – indicates expression in FH fruits but not in the compared treatment. Numbers in bold indicate differential expression in the compared condition according to SAM (FDR < 0.01).

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6. CONTRIBUTIONS

LGC, BE and MTL designed the research. BE and MTL performed the treatments and BE the microarray experiments. LGC, AB and PR contributed to the bioinformatics analyses. AB and PR designed primers used for the transcription studies and performed the expression assays. MTL performed experiments related to fruit physiology and LGC and MTL wrote the paper. All the authors contributed to improve the paper and approved the final manuscript.

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Figure Legends

Figure 1. Schematic diagram of the experimental design.

Figure 2. Ethylene (A), CO_2 production (B) and non-chilling peel pitting (NCPP) index (C) of 'Navelate' fruits stored at 20 ºC. Fruits were held in i) air (○, AC control); ii) air after being conditioned for 4 days with 10 µL L^{-1} ethylene (□, EC); and iii) air after being treated for 14 h with 1 µL L^{-1} 1-MCP (■, 1-MCP). Insert panel in Fig. 2A shows values corresponding to the ethylene production of the control AC fruits and of the EC fruits on a smaller scale to better illustrate differences found in these samples. Significant differences ($p \leq 0.05$) within the same storage period in CO_2 production between AC and EC or 1-MCP-treated fruits are labelled with one or two asterisks, respectively. Significant differences in ethylene production and in NCPP index between 1-MCP-treated samples and AC samples were found from day 4. NCPP index in EC fruits was lower than in AC and 1-MCP-treated fruits from day 3. Significant differences in ethylene production between AC and EC samples are labelled with an asterisk in the insert panel. Error bars represent SE.

Figure 3. Venn diagrams showing the number of differentially expressed genes (SAM, FDR<0.01) in the flavedo (A, B) and albedo (C,D) of AC (control), EC and 1-MCP-treated 'Navelate' fruits stored for 4 (A,C) and 14 days (B,D) at 20 ºC. Expression levels of up-regulated (bold) and down-regulated (italics) genes in these samples were compared with the levels of freshly harvested fruits. Numbers in brackets are the sum of all induced and repressed genes under each particular condition. The sizes of the circles are shown relative to the total number of differentially expressed genes for each condition.

Figure 4. Metabolic overview using MapMan (Thimm et al., 2004) comparing transcript accumulation in the albedo of 1-MCP-treated (A) and of control air (AC) (B) fruits held for 14 days at 20 ºC. Red and blue squares represent transcripts with decreasing and increasing levels, respectively, with respect to freshly harvested fruit. Color scale is indicated in the figure.

Figure 5. Effect of increasing concentrations of SNP (A) and of 300 µM HB (■) and 300 µM cPTIO (▲) on NCPP index of fruits treated with 1 µL L^{-1} 1-MCP (●) and stored at 20 ºC in air (B). Results are represented as means of the three replicate samples. Significant differences ($P \leq 0.05$) in NCPP index between fruits treated with different SNP concentrations (A) are indicated by different letters. Means

within Fig. 5B labelled with the same letter for the same storage period did not differ significantly ($p \leq 0.05$). Significant differences in peel damage index were not found between air and HB+1-MCP–treated fruits within the same storage period.

Table 1. Gene ontology (GO) analysis (FatiGO+, $P<0.05$) of biological processes over– (↑) or infra–represented (↓) in the flavedo (F) or albedo (A) of air (AC control fruits), EC (ethylene) and 1-MCP–treated fruits (1-MCP), with respect to freshly harvested fruit. Black bars refer to the treatments in which the processes included in a specific pattern were differentially expressed. Lower GO levels represent general biological processes, whereas higher levels denote more precise information.

GO Level	GO Code	Description	Pattern of expression											
			4 days						14 days					
			Air		Ethylene		1-MCP		Air		Ethylene		1-MCP	
			F	A	F	A	F	A	F	A	F	A	F	A
Pattern 1		Differentially expressed only by 1-MCP												
3	0007154	Cell communication											↑	
3	0008037	Cell recognition												↑
3	0006955	Immune response												↑
4	0006793	Phosphorus metabolic process											↑	↑
4	0006970	Response to osmotic stress											↑	
4	0009636	Response to toxin											↑	
4	0006952	Defense response												↑
5	0006796	Phosphate metabolic process											↑	↑
5	0010038	Response to metal ion											↑	↑
5	0009651	Response to salt stress											↑	
5	0007165	Signal transduction											↑	
5	0045087	Innate immune response												↑
5	0012501	Programmed cell death												↑
5	0009620	Response to fungus												↑
5	0009751	Response to salicylic acid stimulus												↑
6	0016310	Phosphorylation											↑	↑
6	0009723	Response to ethylene stimulus											↑	
6	0006464	Cellular protein modification process												↑
6	0009814	Defense response, incompatible interaction												↑
7	0043687	Post–translational protein modification											↑	↑
7	0006468	Protein amino acid phosphorylation											↑	↑
8	0009867	Jasmonic acid mediated signaling pathway												↑
Pattern 2		Differentially expressed by Air and/or Ethylene but not by 1-MCP												
4	0006629	Lipid metabolic process	↑		↑									
4	0015977	Carbon fixation	↓	↓	↓									
5	0008610	Lipid biosynthetic process	↑		↑	↑								
8	0006631	Fatty acid metabolic process			↑				↑					
9	0006633	Fatty acid biosynthetic process			↑				↑					
Pattern 3		Differentially expressed by Ethylene and 1-MCP												
3	0042221	Response to chemical stimulus			↑	↑							↑	↑
3	0006950	Response to stress			↑	↑							↑	↑
5	0009743	Response to carbohydrate stimulus				↑								↑
6	0046686	Response to cadmium ion			↑								↑	↑
6	0010200	Response to chitin				↑								↑
7	0009813	Flavonoid biosynthetic process			↑	↑							↑	
9	0042398	Amino acid derivative biosynthetic process			↑	↑							↑	
Pattern 4		Differentially expressed by Ethylene but not by Air or 1-MCP												
3	0009628	Response to abiotic stimulus			↓	↓								
3	0019748	Secondary metabolic process			↑	↑								
3	0009605	Response to external stimulus			↑									
4	0015979	Photosynthesis			↓	↓								
4	0006790	Sulfur metabolic process			↑	↑								
4	0009314	Response to radiation			↓									
4	0008104	Protein localization				↑								
5	0009698	Phenylpropanoid metabolic process			↑	↑								
5	0009416	Response to light stimulus			↓									
5	0019684	Photosynthesis, light reaction				↓								
5	0001666	Response to hipoxia				↑								
5	0009409	Response to cold				↓								
6	0009808	Lignin metabolic process			↑	↑								
6	0009699	Phenylpropanoid biosynthetic process			↑	↑								
6	0015031	Protein transport				↑								
7	0009809	Lignin biosynthetic process			↑	↑								
9	0031407	Oxylipin metabolic process			↑						↑			
Pattern 5		Differentially expressed by Air or 1-MCP but not by Ethylene												
3	0009607	Response to biotic stimulus	↑	↓										↑
4	0010033	Response to organic substance	↑											↑
4	0051707	Response to other organism		↓										↑
6	0009753	Response to jasmonic acid stimulus	↑											↑
Pattern 6		Differentially expressed by Air but not by 1-MCP or Ethylene												
5	0016051	Carbohydrate biosynthetic process							↓					
6	0009966	Regulation of signal transduction	↑											
7	0009968	Negative regulation of signal transduction	↑											
8	0009072	Aromatic amino acid family metabolic process	↑											
9	0009073	Aromatic amino acid family biosynthetic process	↑											

Table 2. Gene ontology (GO) analysis (FatiGO+, $P<0.05$) of molecular function, cellular component and interpro domain over–(↑) or infra–represented (↓) in the flavedo (F) or albedo (A) tissues of 'Navelate' oranges held in air (AC, control), conditioned for 4 days with ethylene and transferred to air (EC), or treated with 1–MCP and held in air (MCP), with respect to freshly harvested fruit.

GO Level	GO Code	Description	Pattern of expression											
			4 days						14 days					
		Molecular function	AC		EC		MCP		AC		EC		MCP	
			F	A	F	A	F	A	F	A	F	A	F	A
5	0016773	phosphotransferase activity, alcohol group as											↑	↑
5	0046982	protein heterodimerization activity											↑	
6	0004672	protein kinase activity											↑	↑
6	0046914	transition metal ion binding												↑
7	0004674	protein serine/threonine kinase activity											↑	↑
7	0004713	protein tyrosine kinase activity											↑	↑
8	0017076	purine nucleotide binding												↑
9	0005524	ATP binding												↑
5	0016301	kinase activity				↑							↑	↑
8	0020037	heme binding			↑	↑							↑	
9	0005506	iron ion binding			↑	↑					↑		↑	
5	0008194	UDP–glycosyltransferase activity			↑	↑								
5	0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen			↑									
5	0016616	oxidoreductase activity, acting on the CH–OH group of donors, NAD or NADP as acceptor			↑									
5	0016757	transferase activity, transferring glycosyl groups				↑								
5	0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of									↑			
6	0019205	nucleobase, nucleoside, nucleotide kinase activity				↑								
6	0016776	phosphotransferase activity, phosphate group as acceptor				↑								
7	0019201	nucleotide kinase activity				↑								
5	0004497	monooxygenase activity	↑											
		Cellular Component												
5	0005886	plasma membrane												↑
6	0009579	thylakoid				↓								↓
9	0042651	thylakoid membrane				↓								↓
5	0009523	photosystem II				↓								
9	0009521	photosystem				↓								
		InterPro												
	IPR017442	Serine/threonine protein kinase–related											↑	↑
	IPR008271	Serine/threonine protein kinase, active site											↑	↑
	IPR017441	Protein kinase, ATP binding site											↑	↑
	IPR001246	Lipoxygenase, plant							↑		↑			
	IPR013819	Lipoxygenase, C–terminal							↑		↑			
	IPR016040	NAD(P)–binding domain			↑									
	IPR008976	Lipase/lipooxygenase, PLAT/LH2									↑			
	IPR001024	Lipoxygenase, LH2									↑			
	IPR013747	3–Oxoacyl–[acyl–carrier–protein (ACP)] synthase III							↑					
	IPR012328	Chalcone/stilbene synthase, C–terminal							↑					
	IPR013601	FAE1/Type III polyketide synthase–like protein							↑					
	IPR016039	Thiolase–like							↑					
	IPR012392	Very–long–chain 3–ketoacyl–CoA synthase							↑					

Table 3. Relative expression level of genes involved in ethylene biosynthesis, perception and signalling, and in cyanide detoxification, printed in the microarray and differentially expressed in the albedo (A) and/or flavedo (F) of AC (air, control), EC and 1-MCP-treated 'Navelate' fruits. The symbol + indicates no expression in freshly harvested fruits, and the symbol – indicates expression in freshly harvested fruits but not in the compared treatment. Numbers in bold indicate differential expression in the compared condition according to SAM (P<0.01)

Citrus unigene	Description	4 days						14 days					
		AC		EC		1-MCP		AC		EC		1-MCP	
		F	A	F	A	F	A	F	A	F	A	F	A
		Fold Change (log_2)											
Ethylene biosynthesis													
aCL414Contig2	S-adenosyl-L-methionine synthetase 1	0.08	0.16	0.36	0.68	–0.16	0.06	–0.14	–0.05	–0.35	0.00	0.87	0.55
aC08030G11SK_c	S-adenosylmethionine synthetase	0.28	+	0.60		–	+	–0.11	+	0.03	+	–0.02	+
aC31207B09EF_c	S-adenosylmethionine synthetase	0.34	0.15	0.50	0.52	–0.18	–0.04	0.08	–0.19	–0.15	–0.12	0.44	0.27
aCL33Contig2	S-adenosylmethionine synthetase 2	0.24	0.19	0.52	0.12	–0.13	–0.06	0.05	–	0.03	–	–	–0.02
aCL55Contig2	S-adenosylmethionine synthetase 2	0.45	0.27	0.82	0.81	–0.80	–0.77	–0.23	–0.81	–0.37	–0.34	1.26	0.59
aCL7172Contig1	ACC synthase	–0.18	0.21	0.42	1.07	0.33	0.95	–0.36	0.40	–0.22	0.23	–	2.01
aCL4017Contig1	ACC synthase	–0.13	–0.06	0.03	–0.02	–0.05	0.14	–0.11	0.01	–0.17	–0.13	–0.20	0.60
aC31605B08EF_c	ACC oxidase	–0.22	0.24	0.48	1.73	1.25	2.08	–0.91	–0.25	–1.84	–0.22	1.27	3.96
aCL4439Contig1	ACC oxidase 1	1.43	0.23	2.04	1.21	2.64	2.07	0.70	0.45	–0.32	0.19	2.45	2.89
aCL3488Contig1	ACC oxidase ACCO2	–0.40	–0.10	–0.12	0.36	0.53	0.00	–0.10	–0.05	0.18	0.36	0.35	1.40
aCL7299Contig1	Ethylene-forming-enzyme-like dioxygenase	0.07	0.33	0.48	0.66	2.73	0.58	0.13	0.36	0.03	0.26	0.06	0.89
aC08019A01SK_c	Ethylene-forming-enzyme-like dioxygenase	–0.17	0.33	0.37	0.49	0.45	0.61	–0.30	0.11	–0.44	–0.03	–0.03	0.68
aC31703B04EF_c	Putative ethylene-forming enzyme	–0.10	0.74	0.03	0.70	–0.52	0.03	–0.09	0.43	–0.19	0.24	–0.09	0.04
Ethylene perception/signaling													
aCL3291Contig1	Ethylene receptor	0.29	0.33	0.05	0.13	–0.19	–0.54	–0.23	–0.46	–0.32	–0.51	0.27	–0.10
aCL7399Contig1	Ethylene receptor homolog	–0.09	0.75	–0.29	0.01	–0.09	–0.34	–0.07	0.01	–0.27	0.21	1.09	0.56
aCL7700Contig1	Putative ethylene receptor	0.73	1.62	0.40	0.99	0.85	0.45	0.55	0.31	0.51	0.59	1.49	1.72
aCL5522Contig1	Anther ethylene-upregulated protein ER1	0.36	0.08	0.05	0.02	0.37	0.09	0.38	–0.06	0.51	0.08	0.62	0.46
aCL5870Contig1	Auxin and ethylene responsive GH3-like prot	0.98	1.24	0.93	1.78	0.09	–0.33	0.23	–0.04	–0.08	0.03	0.66	0.05
aCL7060Contig1	AP2/EREBP transcription factor ERF-2	0.17	0.72	–0.27	0.14	0.09	0.34	0.27	0.64	0.33	0.72	0.48	0.27
aCL1363Contig1	AP2/EREBP transcription factor ERF-2	0.23	0.60	0.04	–0.01	0.36	0.15	0.41	0.34	0.38	0.56	0.69	0.26
aCL1567Contig2	Putative ethylene response factor ERF3a	0.36	0.29	–0.14	0.48	0.24	0.47	0.03	0.88	–0.19	0.88	0.56	0.86
aCL337Contig1	Putative ethylene response factor 5	0.24	–0.04	0.31	0.77	1.04	1.02	–0.16	0.85	0.01	0.63	0.60	0.55
aCL5870Contig1	Auxin and ethylene responsive GH3-like prot	0.98	1.24	0.93	1.78	0.09	–0.33	0.23	–0.04	–0.08	0.03	0.66	0.05
aCL9142Contig1	Ethylene-responsive element binding factor	–0.10	0.03	–0.33	0.08	0.64	0.02	0.63	0.46	0.01	0.14	–0.09	–0.59
aCL152Contig1	Ethylene-responsive factor-like protein 1	0.31	0.18	0.85	0.86	0.57	0.30	0.57	1.06	0.80	1.28	1.04	1.21
aCL2320Contig1	Ethylene-responsive transcription factor 13	–0.68	–0.56	–0.99	–0.92	–0.78	–0.79	–0.36	–0.73	–0.31	–0.73	–1.06	–1.19
aCL1087Contig1	Ethylene responsive element binding prot	–0.02	0.37	–0.07	0.33	1.03	1.08	0.49	0.84	–0.20	0.42	0.69	0.94
aCL5023Contig1	EIN3-like protein	0.32	0.67	–0.16	0.40	0.39	0.20	0.44	0.36	0.32	0.66	0.99	0.36
Cyanide detoxification													
aC06021C12SK_c	Beta-cyanoalanine synthase	0.17	0.22	–0.05	0.40	–0.04	–0.04	–0.13	–0.02	–0.03	–0.09	–0.05	–0.01
aCL5505Contig1	Beta-cyanoalanine synthase	1.66	4.23	2.18	4.51	–1.91	–1.49	–0.95	0.89	–1.96	0.66	2.18	2.92
aC31502A08EF_c	Nitrilase 4	0.68	1.12	0.45	1.17	0.29	0.38	0.42	0.73	0.38	0.79	1.17	1.21
aCL6373Contig1	Putative alpha-hydroxynitrile lyase	0.10	–0.05	–0.31	–0.41	0.33	0.10	0.25	–0.03	0.33	0.01	–0.45	–0.17
aCL4704Contig1	Putative alpha-hydroxynitrile lyase	0.31	0.43	0.51	0.92	0.44	0.13	–0.08	0.03	0.17	0.12	1.08	1.31

Table 4. Classification of xenobiotic/cyanide–related genes up– (U) and down– (D) **regulated in the flavedo and/or albedo of 'Navelate'** fruits held in air (AC, control), treated for 4 days with ethylene and then transferred to air (EC) or treated with 1–MCP before holding in air (MCP), with respect to freshly harvested fruit. Blanks indicate that no gene was either up– or down–regulated in the compared treatment

		Flavedo						Albedo					
		4 days			14 days			4 days			14 days		
Description	Probes[a]	AC	EC	MCP	AC	EC	MCP	AC	EC	MCP	AC	EC	MCP
		U/D	U/D	U/D	U/D	U/D	U/D	U/D	U/D	U/D	U/D	U/D	U/D
Glutathione S-transferase	27	1/0	7/0				10/0	3/0	7/1	3/0	2/0	2/0	17/1
Cytochrome P450	50	1/1	4/3		0/1	1/0	5/1	6/2	13/2	1/0	3/1	3/1	21/3
Gycosyl/glucosytransferase	62	1/1	11/0		2/0	1/2	3/3	1/2	11/1	0/2	0/2	0/2	14/4
O-methyltransferase	29		5/1		0/1		4/1	1/1	4/1		0/1	0/1	13/3
Peptidases	66		1/0		0/2	0/1	1/0	4/0	5/0	3/0	3/0	7/0	18/2
Calcium/calmodulin-binding	20	0/1	2/2		2/2		2/2	1/2	5/3	2/1	1/3	1/2	11/6
ABC transporters	32	1/1	3/2	0/2	4/2	3/1	3/1	2/0	5/1	2/1	3/0		11/2

[a]Total number of probes in the microarray

***Contribution**

CONTRIBUTIONS: LGC, BE and MTL designed the research. BE and MTL performed the treatments and BE the microarray experiments. LGC, AB and PR contributed to the bioinformatics analyses. AB and PR designed primers used for the transcription studies and performed the expression assays. MTL performed experiments related to fruit physiology and LGC and MTL wrote the paper. All the authors contributed to improve the paper and approved the final manuscript.

Figure 1

Revised Fig. 1

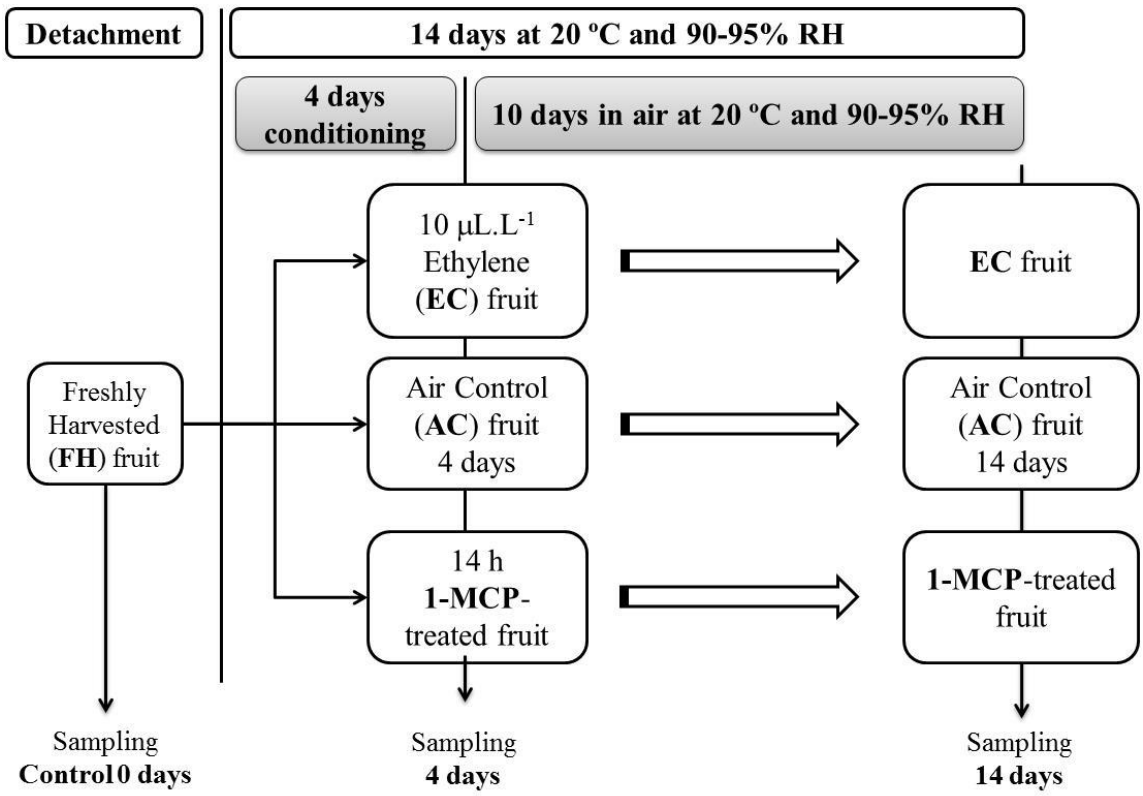


Figure 2

Fig. 2

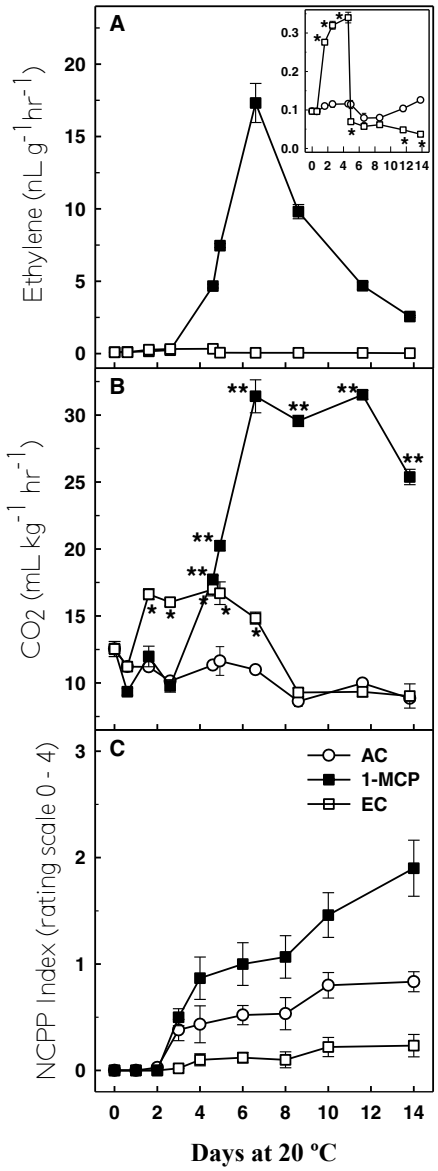


Figure 3

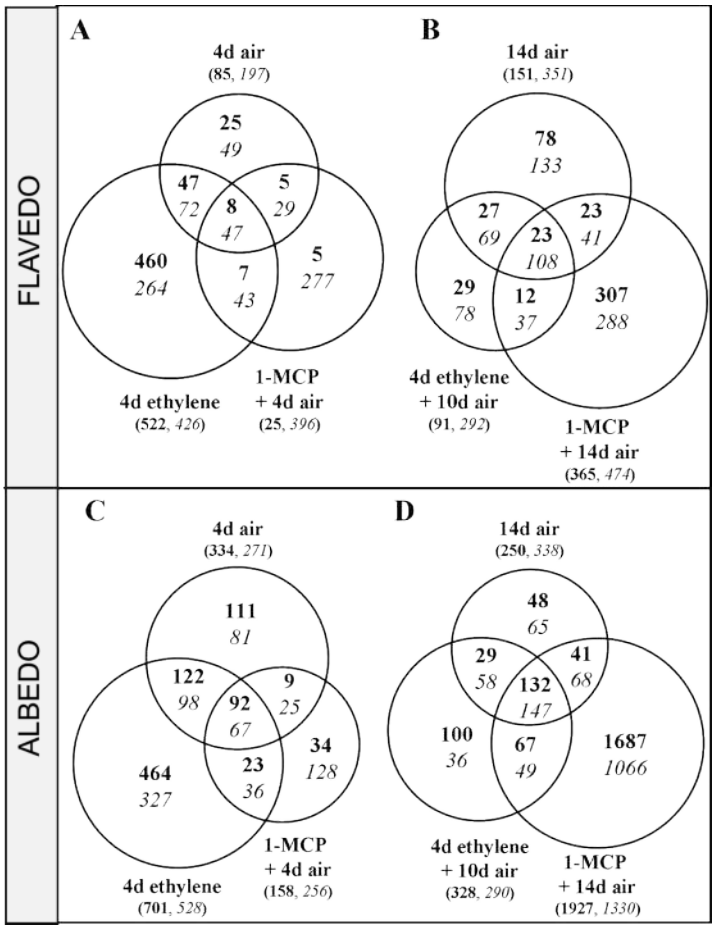


Figure 3

Figure 4

Fig. 4

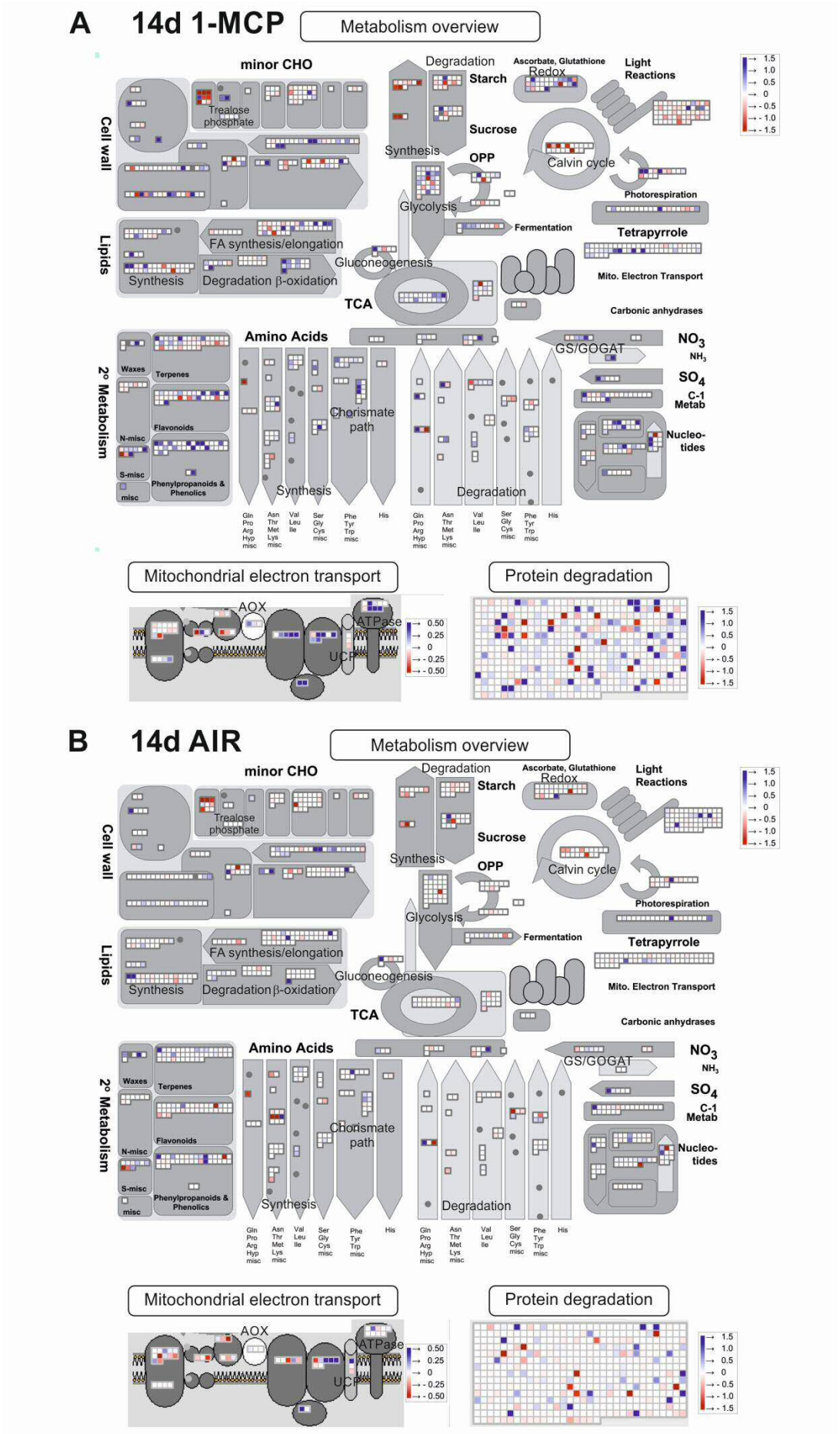


Figure 5

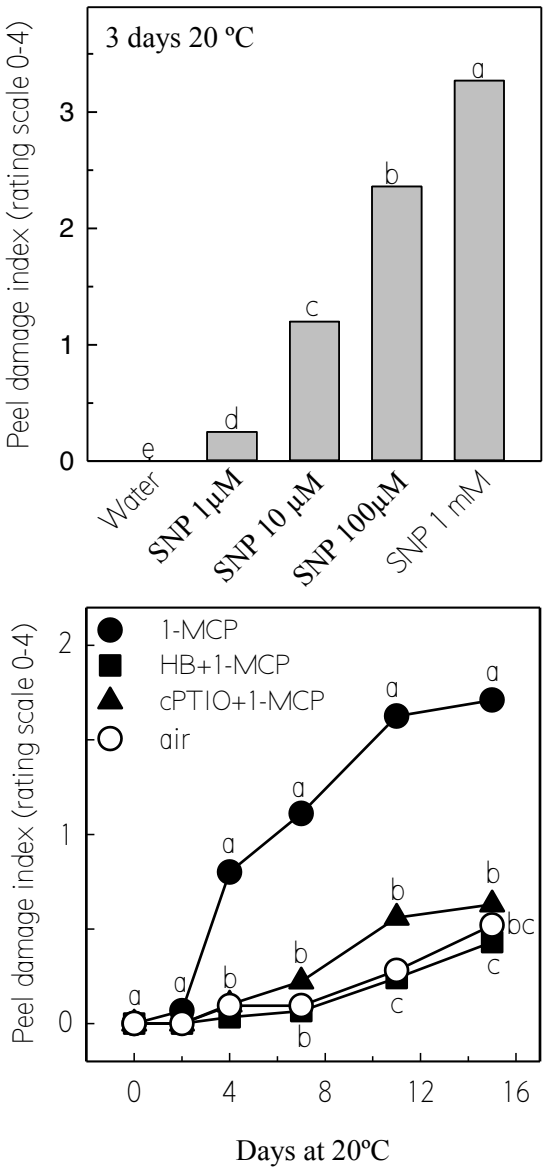
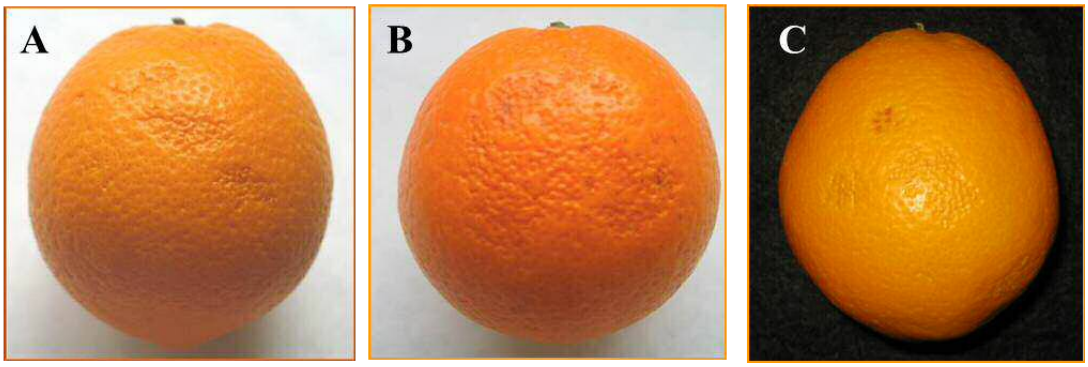


Figure 5.



Supplemental Fig. S1. Nonchilling peel pitting (NCPP) syndrome in fruit held in air (A), and in fruits pretreated with 1-MCP (B) and SNP (C).

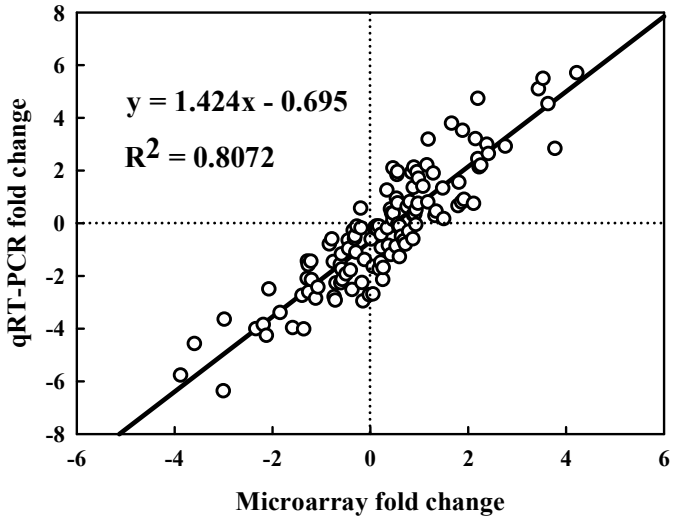


Fig. S2. Correlation in the expression of selected genes (Table S1) quantified using either the 12k citrus microarray or RT-qPCR. The expression of these genes was quantified in the flavedo and albedo of AC, EC and 1-MCP-treated fruits stored for 4 and 14 days at 20 ºC ($r^2 = 0.807$, $p \leq 0.05$).

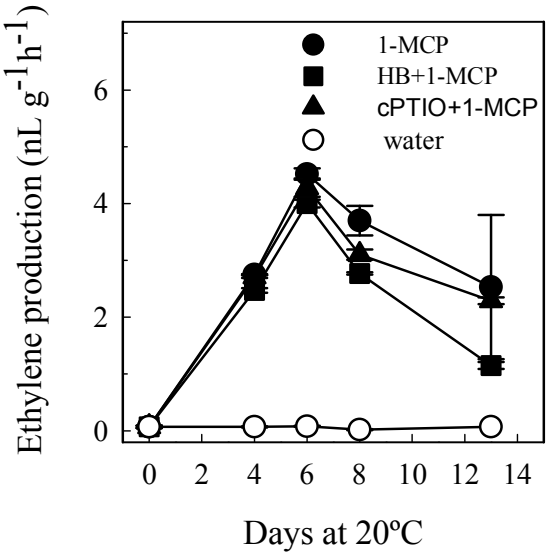


Fig. S3. Effect of HB (■) and cPTIO (▲) on the ethylene production of fruits treated with 1-MCP (●) and stored at 20 ºC. No significant differences were found among mean values of these samples for the same storage period ($p \leq 0.05$) according to Tukey's test, and the values always differed significantly from the means of fruits treated only with water (○).

Table S1. Selected genes and primers used for comparison between the Citrus 12 k microarray and RT-qPCR gene expression data. Reference genes *CsACT, CsEF1α*, and *CsTUB* were used for data normalization.

Gene	Citrus code	Most similar protein	Homolog in *A. thaliana*	Forward / Reverse	Sequence 5' → 3'	Amplicon size (pb)
CsiACO1	*orange1.1g020953m*	ACC oxidase 1	At1g05010	F	GCGGCTATCTTGGAGAAGATCAACGAGG	**148**
				R	GCCCTGCTTGCAACAAGCTC	
CsiCSC1	*orange1.1g021775m*	Cysteine Synthase C1 (β-Cyanoalanine Synthase)	At3g61440	F	GCAGCGAACCCATGTTGATGAG	**256**
				R	GGCCACTGCTGGTCTGTCC	
CsiERL1	*orange1.1g004636m*	Ethylene Receptor-Like 1	At2g40940	F	CCGGAGCACTCAAATGATTC	**141**
				R	CCGTCATTACATCACATCCCAGG	
CsiGDP	*orange1.1g001531m*	Glycine Dehydrogenase Protein (Victorin Binding Protein)	At4g33010	F	GCCTGGTTAATGAGTCCAAGC	**229**
				R	GCCTCAACAGAAATGCCTCG	
CsiGST1	*orange1.1g027524m*	Glutathione S Transferase	At2g29420	F	GGGAGCTGCTGTTTGG	**244**
				R	CACGCGTGCAAGCCTGG	
CsiSPS	*orange1.1g001705m*	Sucrose-Phosphate Synthase	At4g10120	F	GCATGCATGGATTGGTGCGTGG	**147**
				R	GCTAGAATCTACTTCCGGTGAGGC	
CsiACT	*orange1.1g017088m*	Actin7. Structural constituent	AT5G09810	F	TTAACCCCAAGGCCAACAGA	**176**
				R	TCCCTCATAGATTGGTACAGTATGAGA	
CsiEF1 α	*orange1.1g010310m*	Translation elongation factor EF1A	AT1G18070	F	ATTGACAAGCGTGTGATTGAGC	**171**
				R	TCCACAAGGCAATATCAATGGTA	
CsiTUB	*orange1.1g013335m*	Tubulin1. Structural constituent	AT1G75780	F	GCATCTTGAACCCGGTAC	**158**
				R	ATCAATTCGGCGCCTTCAG	

Table S2. Expression levels of citrus genes in the flavedo (F) and albedo (A) tissues of AC, EC and 1-MCP-treated fruit stored for 4 and 14 days at 20 ºC grouped according to the biological processes they belong to. Numbers in bold indicate statistically significant differences (SAM, FDR <0.05)

Biological Process	GO Level	Comparison *vs* Fresly Harvested (FH)											
RESPONSE TO HIPOXIA	5	4 days						14 days					
Gene Description	Homolog in *A. thaliana*	Log2 (AC/FH)		Log2 (EC/FH)		Log_2 (MCP/FH)		Log2 (AC/FH)		Log2 (EC/FH)		Log_2 (MCP/FH)	
		Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo
Non-symbiotic hemoglobin 1	AT2G16060	-0.387	+	1.076	+	0.116	+	-1.302	+	-	+	0.705	+
Hemoglobin II	AT2G16060	-0.096	**0.874**	**1.262**	**1.800**	0.735	1.407	-0.246	**1.364**	-0.288	1.380	**0.818**	**2.818**
Phytoalexin-deficient 4-2 protein	AT3G52430	**0.606**	**0.640**	**0.940**	**0.833**	-0.075	-0.125	-0.086	0.378	0.187	0.237	**0.592**	**1.546**
Pyruvate decarboxylase isozyme 1	AT5G54960	-0.119	0.081	0.279	**0.523**	0.445	0.332	0.208	0.249	0.272	0.273	0.490	**0.702**
2-on-2 hemoglobin	AT4G32690	0.458	0.314	0.777	**0.654**	0.508	0.435	0.451	0.453	0.509	0.363	0.665	**0.683**
F18C1.18 protein	AT3G05550	0.092	0.458	**0.613**	**0.945**	-0.015	-0.083	-0.138	0.293	-0.112	0.352	0.020	**0.339**

Biological Process	GO Level	Comparison vs FH											
Response to toxin	4	4 days						14 days					
Gene Description	Homolog in A. thaliana	Log2 (AC/FH)		Log2 (EC/FH)		Log_2 (MCP/FH)		Log2 (AC/FH)		Log2 (EC/FH)		Log_2 (MCP/FH)	
		Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo
Glutathione S-transferase	At1g10360		0.225	+	-		-		-		-	+	-
Glutathione S-transferase	At2g29420	0.859	-0.105	**1.416**	0.533	1.024	1.107	0.248	0.081	0.460	0.253	**1.051**	**3.802**
Glutathione S-transferase	At2g29420	0.767	0.185	**1.664**	0.697	1.317	1.508	0.342	0.484	0.584	0.236	**1.178**	**3.667**
Beta-cyanoalanine synthase	At3g61440	1.656	**4.227**	**2.181**	**4.510**	-1.911	-1.491	-0.952	0.890	**-1.958**	0.662	**2.182**	**2.917**
Putative glutathione S-transferase T3	At2g29420	0.252	0.173	**0.552**	**0.540**	1.068	**1.158**	0.111	0.381	0.202	0.654	**1.383**	**2.896**
Glutathione S-transferase GST 22	At2g30860	0.523	**1.369**	0.429	**1.424**	1.345	**1.891**	0.537	**1.195**	0.445	**1.143**	**1.398**	**2.618**
Glutathione S-transferase GST 22	At2g30860	0.532	**1.036**	0.288	**1.063**	1.166	1.423	0.549	0.768	0.467	0.920	**1.274**	**2.270**
Glutathione S-transferase GST 22	At2g30870	0.384	**1.034**	0.263	**1.068**	0.887	1.501	0.129	**0.866**	0.031	**0.858**	**1.142**	**2.214**
Hydroquinone glucosyltransferase	At4g01070	0.433	-0.476	**1.064**	0.125	0.325	0.217	**1.030**	0.549	1.193	0.628	**1.033**	**1.764**
Hydroquinone glucosyltransferase	At4g01070	0.285	-0.300	**0.708**	0.208	0.421	0.543	**1.192**	0.661	**1.210**	0.737	**1.156**	**1.695**
Glutathione S-transferase GST 14	At2g29420	0.709	0.608	**0.560**	**0.619**	0.955	0.905	0.529	0.355	0.459	0.326	**0.913**	**1.429**
Glutathione S-transferase	At2g29420	**0.802**	0.322	**0.908**	0.430	0.869	0.748	0.329	0.277	0.517	0.355	**0.916**	**1.393**
Nitrilase 4	At5g22300	0.677	**1.124**	0.454	**1.166**	0.289	0.378	0.416	0.729	0.377	0.790	**1.166**	**1.207**

Biological Process	GO Level	Comparison *vs* Fresly Harvested (FH)											
RESPONSE TO ETHYLELE STIMULUS	6	4 days						14 days					
Gene Description	Homolog in *A. thaliana*	Log2 (AC/FH)		Log2 (EC/FH)		Log_2 (MCP/FH)		Log2 (AC/FH)		Log2 (EC/FH)		Log_2 (MCP/FH)	
		Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo
WRKY transcription factor 6	At1g62300	0.596	1.199	1.230	**1.832**	-0.106	0.596	-0.555	1.085	-0.375	0.906	**0.610**	**2.170**
MYB6	At4g37260	1.312	0.795	1.279	1.433	1.384	0.934	0.746	0.709	0.938	0.982	**1.677**	1.767
Putative ethylene receptor	At2g40940	0.734	1.620	**0.399**	**0.991**	0.852	0.450	0.547	0.312	0.509	0.585	**1.488**	**1.719**
expressed protein	At2g26070	**0.588**	**1.253**	0.239	**0.239**	0.375	0.088	0.120	0.163	-0.082	0.114	**0.994**	**1.256**
Ethylene-responsive factor-like protein 1	At3g16770	0.305	0.180	0.853	**0.860**	0.573	0.300	0.567	**1.063**	0.798	**1.282**	**1.041**	**1.206**
G protein beta subunit	At4g34460	0.248	0.206	**-0.184**	**0.216**	0.299	-0.617	0.469	0.174	0.336	0.326	**0.740**	**0.936**
Transcription factor Myb1	At3g23250	0.551	0.300	**0.529**	**0.339**	0.539	0.201	0.700	0.367	0.423	0.263	**1.195**	**0.626**
Pathogenesis-related genes transcriptio	At4g11140	0.242	0.437	-0.035	-0.096	0.599	0.657	0.390	0.232	0.438	0.340	**0.456**	**0.517**
EIN3-like protein	At2g27050	0.321	0.670	-0.158	0.401	0.392	0.199	0.438	0.358	0.318	0.664	**0.991**	**0.365**
AP2/EREBP transcription factor ERF-2	At3g16770	0.227	0.598	0.037	-0.009	0.362	0.151	0.410	0.337	0.381	0.560	**0.686**	**0.255**
Anthranilate synthase beta subunit	At1g25220	0.647	**0.529**	1.147	**0.883**	-0.119	-0.232	0.152	0.146	**0.112**	-0.056	**1.126**	**0.059**

Biological Process	GO Level	Comparison *vs* Fresly Harvested (FH)											
OXYLIPIN METABOLIC PROCESS	9	4 days						14 days					
Gene Description	Homolog in *A. thaliana*	Log2 (AC/FH)		Log2 (EC/FH)		Log_2 (MCP/FH)		Log2 (AC/FH)		Log2 (EC/FH)		Log_2 (MCP/FH)	
		Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo
Lipoxygenase LOX1	AT3G45140	1.212	+	**1.353**	+	1.875	+	**2.104**	+	**2.382**	+	0.184	+
4-coumarate-CoA ligase-like protein	AT4G05160	0.011	-0.346	**1.120**	**0.696**	-0.403	-0.032	-0.713	-0.333	-0.516	**-0.558**	-0.146	**1.444**
12-oxophytodienoate reductase	AT2G06050	**0.602**	0.260	**0.775**	**0.617**	-0.189	-0.396	0.435	-0.049	0.171	0.151	0.468	**0.907**
Caffeine synthase	AT1G19640	0.240	0.111	**1.120**	0.403	1.295	0.863	-0.268	0.242	-0.386	0.217	0.011	**0.772**
Allene oxide synthase	AT5G42650	0.457	**0.923**	**0.878**	**1.193**	-0.134	0.191	0.416	0.473	0.427	0.965	0.739	**0.729**
SAMT	AT1G19640	0.163	-0.145	**0.818**	0.014	0.640	0.182	-0.247	-0.032	-0.269	0.150	-0.127	0.281
Mangrin	AT1G13280	0.451	0.496	**0.762**	0.356	0.084	-0.123	0.432	0.348	0.281	0.245	0.464	0.248
Lipoxygenase LOX1	AT1G72520	1.427	-0.247	**1.228**	-0.216	1.434	1.308	2.520	0.410	**2.411**	**1.682**	-0.014	0.190
Lipoxygenase	AT1G17420	0.097	0.096	**0.530**	0.392	0.023	-0.090	0.018	0.072	0.022	0.181	0.311	0.176
Lipoxygenase	AT1G72520	0.094	0.055	**0.354**	0.108	0.105	0.039	0.366	0.242	0.343	0.256	0.269	0.170
Lipoxygenase	AT3G45140	**1.564**	-0.105	**1.300**	0.080	1.653	1.595	2.248	0.606	**2.503**	1.728	0.019	0.135
Lipoxygenase	AT1G72520	1.361	-0.546	**1.077**	-0.228	1.353	0.574	**2.253**	0.147	**2.373**	1.016	0.231	0.128
Lipoxygenase LOX1	AT1G17420	**1.607**	-0.202	**1.434**	0.021	1.608	-0.743	**2.606**	0.638	**2.665**	1.395	0.053	0.117
Lipoxygenase	AT3G45140	**1.442**	-0.170	**1.393**	0.270	1.621	1.729	**2.022**	0.743	**2.397**	**1.836**	-0.233	0.070
Allene oxide cyclase precursor	AT3G25780	0.635	-0.042	**0.799**	0.179	0.357	-0.113	1.380	0.377	**1.059**	0.440	0.046	-0.168
Mangrin	AT1G13280	0.224	0.257	**0.596**	0.225	-0.147	-0.342	0.217	-0.157	0.131	-0.273	0.150	-0.295

Biological Process

FATTY ACID BIOSYNTHETIC PROCESS

Gene Description	Homolog in *A. thaliana*	Comparison *vs* Fresly Harvested (FH)											
		4 days						14 days					
		Log2 (AC/FH)		Log2 (EC/FH)		Log_2 (MCP/FH)		Log2 (AC/FH)		Log2 (EC/FH)		Log_2 (MCP/FH)	
		Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo
Lipoxygenase LOX1	AT3G45140	1.212	+	**1.353**	+	1.875	+	**2.104**	+	**2.382**	+	0.184	+
Fiddlehead-like protein	AT2G26250	0.580	2.181	-0.439	0.465	0.928	1.076	**1.692**	2.392	0.641	2.036	**0.999**	1.639
4-coumarate-CoA ligase-like protein	AT4G05160	0.011	-0.346	**1.120**	**0.696**	-0.403	-0.032	-0.713	-0.333	-0.516	**-0.558**	-0.146	**1.444**
Homogentisate geranylgeranyl transfera	AT2G18950	0.638	-0.152	**0.821**	0.066	0.410	0.409	-0.093	-0.056	0.197	-0.108	0.728	**0.940**
12-oxophytodienoate reductase	AT2G06050	**0.602**	0.260	**0.775**	**0.617**	-0.189	-0.396	0.435	-0.049	0.171	0.151	0.468	**0.907**
no_annotation_available	AT2G18950	0.824	-0.465	**1.353**	-0.132	0.504	0.109	-0.878	-0.232	0.110	-0.234	1.240	**0.780**
Caffeine synthase	AT1G19640	0.240	0.111	**1.120**	0.403	1.295	0.863	-0.268	0.242	-0.386	0.217	0.011	**0.772**
Homogentisate geranylgeranyl transfera	AT2G18950	0.949	-0.365	**0.927**	-0.466	0.618	0.459	0.016	-0.045	0.546	0.425	1.055	**0.758**
Allene oxide synthase	AT5G42650	0.457	**0.923**	**0.878**	**1.193**	-0.134	0.191	0.416	0.473	0.427	0.965	0.739	**0.729**
Homogentisate geranylgeranyl transfera	AT2G18950	0.861	-0.357	**1.152**	0.140	0.451	0.377	-0.716	-0.179	0.243	-0.071	1.109	0.596
F18O14.21	AT1G19440	0.240	0.094	**0.442**	0.343	0.229	0.426	0.297	0.305	0.397	0.321	0.424	**0.553**
SAMT	AT1G19640	0.163	-0.145	**0.818**	0.014	0.640	0.182	-0.247	-0.032	-0.269	0.150	-0.127	0.281
Mangrin	AT1G13280	0.451	0.496	**0.762**	0.356	0.084	-0.123	0.432	0.348	0.281	0.245	0.464	0.248
Putative fatty acid elongase	AT2G28630	1.404	-0.481	-0.148	-0.609	0.736	0.420	**2.092**	0.030	0.639	0.167	**1.834**	0.209
Lipoxygenase LOX1	AT1G72520	1.427	-0.247	**1.228**	-0.216	1.434	1.308	2.520	0.410	**2.411**	**1.682**	-0.014	0.190
Chloroplast fatty acid desaturase 6	AT4G30950	0.335	-0.281	**0.631**	-0.197	0.202	-0.501	0.496	-0.095	0.349	0.168	-0.078	0.189
Putative fatty acid elongase	AT5G04530	0.836	-0.128	-0.365	-0.259	1.068	0.297	**1.828**	0.253	0.920	0.477	0.598	0.176
Lipoxygenase	AT1G17420	0.097	0.096	**0.530**	0.392	0.023	-0.090	0.018	0.072	0.022	0.181	0.311	0.176
Lipoxygenase	AT1G72520	0.094	0.055	**0.354**	0.108	0.105	0.039	0.366	0.242	0.343	0.256	0.269	0.170
Lipoxygenase	AT3G45140	**1.564**	-0.105	**1.300**	0.080	1.653	1.595	2.248	0.606	**2.503**	1.728	0.019	0.135
Lipoxygenase	AT1G72520	1.361	-0.546	**1.077**	-0.228	1.353	0.574	**2.253**	0.147	**2.373**	1.016	0.231	0.128
Lipoxygenase LOX1	AT1G17420	**1.607**	-0.202	**1.434**	0.021	1.608	-0.743	**2.606**	0.638	**2.665**	1.395	0.053	0.117
Lipoxygenase	AT3G45140	**1.442**	-0.170	**1.393**	0.270	1.621	1.729	**2.022**	0.743	**2.397**	**1.836**	-0.233	0.070
Omega-3 fatty acid desaturase	AT5G05580	0.564	0.177	**0.814**	**0.564**	-0.181	-0.627	0.655	0.023	0.354	-0.463	-0.098	-0.028
Allene oxide cyclase precursor	AT3G25780	0.635	-0.042	**0.799**	0.179	0.357	-0.113	1.380	0.377	**1.059**	0.440	0.046	-0.168
Protein At1g02190	AT1G02190	0.463	0.420	**1.001**	-0.486	-0.483	-0.184	0.153	**0.773**	0.082	0.682	-0.170	-0.212
Acyl carrier protein 1, chloroplast precu	AT4G25050	0.371	0.135	**0.730**	-0.044	-0.404	-0.281	0.547	-0.054	0.152	0.037	0.216	-0.238
T25K16.11	AT1G01120	1.266	-0.531	**1.189**	-0.412	0.445	-0.142	**1.075**	-0.517	0.506	0.173	**1.117**	-0.291
Mangrin	AT1G13280	0.224	0.257	**0.596**	0.225	-0.147	-0.342	0.217	-0.157	0.131	-0.273	0.150	-0.295
Enoyl-ACP reductase precursor	AT2G05990	0.173	0.226	**0.652**	0.189	-0.427	-0.175	0.260	-0.094	-0.079	-0.228	0.081	**-0.510**
Cuticle protein	AT5G57800	0.674	0.060	0.276	-0.777	-0.147	-0.192	**0.959**	**0.680**	**0.920**	0.723	**0.536**	**-0.586**

Biological Process	GO Level	Comparison *vs* Fresly Harvested (FH)											
PHOTOSYNTHESIS	4	4 days						14 days					
Gene Description	Homolog in *A. thaliana*	Log2 (AC/FH)		Log2 (EC/FH)		Log_2 (MCP/FH)		Log2 (AC/FH)		Log2 (EC/FH)		Log_2 (MCP/FH)	
		Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo
Chlorophyll a-b binding protein 8, chlorc	AT1G61520	-	-0.117	0.084	-	-	-0.036	0.059	0.048	0.362	0.005	-0.164	-0.255
Photosystem I reaction center subunit V	AT1G52230	-0.388	-0.047	**-0.693**	-0.393	-0.036	0.160	0.137	0.223	-0.017	0.321	-0.422	-0.271
Ultraviolet-B-repressible protein	AT2G06520	-0.357	-0.361	-0.381	**-0.490**	-0.075	-0.095	-0.157	-0.224	0.188	-0.123	-0.758	-0.271
expressed protein	AT4G11960	-0.525	-0.432	-0.419	**-0.681**	-0.203	-0.720	0.306	-0.069	0.737	0.354	-0.371	-0.360
no_annotation_available	ATCG00510	0.033	-0.282	-0.296	**-0.626**	0.626	0.146	0.660	0.308	0.363	0.103	-0.012	-0.408
Serine/threonine-protein kinase SNT7, c	AT1G68830	-0.113	-0.173	-0.198	**-0.597**	0.045	-0.116	0.707	0.288	0.702	0.517	-0.061	**-0.465**
Chlorophyll a-b binding protein CP29.3,	AT2G40100	-0.425	-0.126	-0.647	**-0.820**	0.442	-0.029	0.428	0.181	0.346	0.085	-0.286	**-0.466**
Photosystem II 5 kDa protein, chloroplas	AT3G21055	-1.324	-0.778	-0.976	-	-0.090	-1.403	-0.200	-0.203	-0.222	-0.125	-0.870	-0.494
Oxygen evolving enhancer protein 1 pre	AT3G50820	-0.858	-0.459	**-1.622**	**-1.348**	0.095	**0.526**	0.143	0.434	0.076	**0.788**	**-1.479**	-0.509
Photosystem I reaction center subunit V	AT1G55670	-0.285	-0.749	-0.571	**-0.630**	-0.143	-0.123	-0.130	-0.430	0.293	0.197	-0.805	-0.529
Ribulose bisphosphate carboxylase smal	AT5G38410	**-1.475**	**-0.936**	**-1.262**	**-0.763**	**-0.885**	-0.556	**-1.350**	**-0.773**	**-1.319**	-0.665	**-1.685**	**-0.719**
Chloroplast photosystem II 10 kDa prote	AT1G79040	0.013	-0.318	-0.523	**-0.645**	0.207	-0.104	0.510	0.117	0.427	0.264	-0.523	**-0.761**
Photosystem I subunit XI	AT4G12800	0.202	0.706	**-0.684**	-0.260	0.160	0.431	0.949	1.188	0.495	**1.283**	-1.096	-0.797
ATP synthase delta chain, chloroplast pr	AT4G09650	-0.412	**-0.389**	-0.188	**-0.480**	-0.506	-0.413	0.025	0.079	0.307	-0.137	-0.375	**-0.801**
Cytochrome b6-f complex iron-sulfur sul	AT4G03280	-0.906	-0.479	**-1.190**	**-0.943**	-0.763	-0.489	0.028	-0.269	-0.048	0.089	-1.166	**-0.829**
Phosphoenolpyruvate carboxylase 2	AT1G53310	**-1.383**	**-0.864**	**-0.860**	-0.260	-1.360	**-0.825**	**-1.892**	**-1.424**	**-2.035**	**-1.359**	**-1.312**	**-0.890**
Chlorophyll a/b-binding protein	AT1G29910	**-1.425**	**-1.093**	**-1.225**	**-1.073**	-1.130	-0.877	**-0.950**	-0.828	-0.218	-0.186	**-1.970**	**-0.902**
Cell division protein ftsH homolog 1, chl	AT1G50250	-0.463	-0.308	**-0.432**	**-0.455**	-0.544	-0.430	-0.273	**-0.389**	-0.370	-0.426	**-0.866**	**-0.976**
NADH-plastoquinone oxidoreductase su	ATCG00440	-0.598	-0.462	**-1.023**	-0.613	-0.167	-0.146	0.076	-0.217	-0.393	-0.230	-0.939	**-1.041**
Photosystem II reaction center W protei	AT2G30570	-0.847	**-1.023**	**-0.902**	**-1.345**	-0.290	-0.218	0.343	0.077	0.290	0.313	**-1.122**	**-1.093**
Glyceraldehyde-3-phosphate dehydroge	AT1G42970	**-0.994**	**-1.223**	**-0.756**	**-1.115**	-0.251	-0.443	-0.108	**-0.802**	-0.085	-0.338	**-1.327**	**-1.228**
Chloroplast protease precursor	AT2G30950	-0.797	-0.294	**-0.976**	**-0.751**	-1.036	**-1.047**	-0.750	-0.818	-0.922	-0.499	**-1.163**	**-1.627**
CP12 precursor	AT3G62410	**-1.455**	**-1.937**	**-1.530**	**-2.167**	**-0.958**	-1.089	**-0.860**	**-0.799**	**-0.710**	-0.379	**-2.686**	**-2.334**
Phosphoribulokinase, chloroplast precur	AT1G32060	**-1.133**	**-1.173**	**-1.389**	**-1.882**	-1.057	**-1.403**	-0.239	**-1.202**	-0.034	**-1.275**	**-1.652**	**-2.636**

Cellular component	GO Level	Comparison *vs* Fresly Harvested											
PLASMA MEMBRANE	5	4 days						14 days					
Gene Description	Homolog in *A. thaliana*	Log2 (AC/FH)		Log2 (EC/FH)		Log_2 (MCP/FH)		Log2 (AC/FH)		Log2 (EC/FH)		Log_2 (MCP/FH)	
		Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo	Flavedo	Albedo
LRR receptor-like protein kinase	AT1G66150	-0.158	+	-0.035	+	-0.469	+	0.007	+	-0.230	+	-0.222	+
Seven transmembrane protein Mlo4	AT1G11000	-0.333	+	0.138		-	+	1.035	+	1.865	+	-	+
Non-symbiotic hemoglobin 1	AT2G16060	-0.387	+	1.076	+	0.116	+	-1.302	+	-	+	0.705	+
no_annotation_available	AT2G26570	-0.229	+	-0.394	+	-0.398	+	-	+	-	+	-0.363	+
UPI00004DA1E9; LOC395048 protein	AT3G54960	0.122	+	0.280	+	0.324	+	0.320	+	0.257	+	0.721	+
Putative mitochondrial processing pepti	AT3G16480	-0.169	+	-0.261	+	-0.102	+	0.118	+	-0.168	+	-0.207	+
no_annotation_available	AT4G21380	0.538	+	0.236	+	0.327	+	**1.058**	+	1.165	+	0.480	+
Cellulose synthase	AT4G32410	0.169	+	-0.034	+	0.271	+	0.243	+	0.496	+	0.033	+
Phosphatidylinositol transfer-like protei	AT4G39170	-0.069	+	-0.056	+	0.032	+	0.088	+	0.154	+	0.215	+
RIB40 genomic DNA, SC003	AT4G31700	-0.029	+	-0.244	+	-	+	-	+	-1.348	+	0.020	+
Secreted glycoprotein 3	AT4G21380	0.082	+	-0.288	+	-0.281	+	-0.123	+	-0.136	+	0.663	+
ENSANGP00000000953	AT5G10940	0.497	+	0.215	+	0.326	+	0.643	+	0.346	+	0.746	+
Elongation factor 1-alpha	AT5G60390	+					+						+
40S ribosome protein S5	AT2G37270	0.334	2.254	**1.459**	**3.860**	-0.514	2.054	0.072	2.577	0.663	2.530	1.775	**4.196**
Receptor-like protein kinase	AT2G31880	-0.324	1.617	-0.091	2.653	0.120	2.692	-2.775	2.564	0.093	2.501	0.578	**3.845**
Eugenol O-methyltransferase	AT5G54160	0.036	-0.256	**1.532**	1.282	0.095	0.488	-0.773	-0.281	-0.199	-0.019	**3.692**	**3.837**
Multidrug resistance-associated protein	AT3G13080	0.300	-0.113	**0.726**	**0.836**	0.843	1.689	-0.464	-0.062	0.160	0.166	**1.083**	**3.227**
Dicyanin	AT5G20230	0.480	0.023	**2.493**	**1.564**	-0.098	1.176	-0.353	0.199	0.671	0.432	**2.052**	**2.960**
Catechol O-methyltransferase	AT5G54160	0.929	0.345	**1.735**	**1.542**	0.635	0.886	0.378	-0.060	0.560	-0.025	**3.019**	**2.932**
Caffeic acid 3-O-methyltransferase	AT5G54160	0.541	**1.076**	**1.153**	**0.978**	0.698	1.448	-0.797	0.116	-0.306	-0.205	**1.882**	**2.880**
Hemoglobin II	AT2G16060	-0.096	**0.874**	**1.262**	**1.800**	0.735	1.407	-0.246	**1.364**	-0.288	1.380	**0.818**	**2.818**
no_annotation_available	AT3G02600	-0.402	-0.057	**0.429**	**0.943**	0.234	1.135	-0.563	0.669	-0.409	0.621	0.431	**2.684**
CYP81E8	AT4G37370	**0.927**	**1.973**	**0.624**	**1.670**	**1.925**	**2.001**	**1.007**	0.866	**0.906**	**1.031**	**2.236**	**2.638**
Glutathione S-transferase GST 22	AT2G30860	0.523	**1.369**	0.429	**1.424**	1.345	**1.891**	0.537	**1.195**	0.445	**1.143**	**1.398**	**2.618**
AT4g08850/T32A17_160	AT4G08850	0.191	0.072	**0.665**	**0.679**	0.358	0.566	0.023	0.438	0.398	0.573	**1.073**	**2.538**
Receptor-like protein kinase	AT2G31880	0.278	0.134	0.349	**1.018**	0.616	1.078	0.466	**1.194**	0.207	**1.261**	**1.214**	**2.475**
Receptor-like protein kinase	AT2G31880	-0.074	-0.289	0.007	0.251	0.347	1.051	-0.361	0.705	-0.105	0.891	**0.854**	**2.471**
Serine/threonine-protein phosphatase E	AT2G27210	1.986	0.672	2.854	**2.064**	0.654	0.236	1.728	0.555	2.049	0.626	2.919	**2.433**
Sulfate adenylyltransferase	AT3G22890	**1.118**	**1.253**	**1.445**	**1.828**	1.106	0.948	**1.552**	**1.338**	**1.045**	**1.577**	**2.433**	**2.421**
Ascorbate peroxidase	AT1G07890	0.521	0.000	0.597	0.056	0.610	0.738	0.670	0.325	0.802	0.890	**1.500**	**2.382**
Genomic DNA, chromosome 5, TAC clon	AT5G52450	0.426	0.271	**0.733**	**0.884**	0.736	0.760	0.522	-0.034	-0.101	-0.052	**1.850**	**2.362**
OSJNBa0010D21.1 protein	AT3G24240	-0.315	-0.439	0.111	-0.208	0.429	0.310	-0.155	-0.204	0.292	-0.043	**1.179**	**2.308**
Glutathione S-transferase GST 22	AT2G30860	0.532	**1.036**	0.288	**1.063**	1.166	1.423	0.549	0.768	0.467	0.920	**1.274**	**2.270**
Glutathione S-transferase GST 22	AT2G30860	0.384	**1.034**	0.263	**1.068**	0.887	1.501	0.129	**0.866**	0.031	**0.858**	**1.142**	**2.214**
Putative quinone oxidoreductase	AT4G27270	-0.245	0.103	0.252	0.319	-0.291	0.084	-0.628	-0.163	-0.548	-0.363	**1.054**	**2.188**

P-glycoprotein-like proetin	AT3G62150	0.091	0.987	**0.631**	1.542	0.195	1.596	0.278	1.570	0.313	1.275	0.731	**2.165**
Cinnamyl alcohol dehydrogenase	AT5G19440	**1.029**	**1.296**	**1.599**	**1.946**	0.527	0.403	0.895	0.564	0.819	0.970	**1.934**	**2.102**
Putative exostoses	AT5G04500	0.210	**1.046**	0.403	**1.390**	0.782	**1.185**	0.457	**1.655**	0.173	**1.305**	**1.388**	**2.040**
Chitinase precursor	AT3G12500	-0.085	0.101	0.381	0.375	0.063	0.327	-0.192	0.405	-0.236	0.191	0.058	**2.033**
F10B6.27	AT1G14870	-0.111	0.319	0.428	0.342	0.252	0.547	-0.367	0.580	-0.539	0.436	0.963	**1.960**
40S ribosomal protein S18	AT4G09800	0.342	0.189	**1.012**	**1.415**	-0.426	0.165	-0.216	0.427	0.345	0.507	0.974	**1.924**
Putative exostoses	AT5G04500	0.265	**0.836**	**0.341**	**1.167**	0.625	0.990	0.573	**1.225**	0.459	1.271	**1.370**	**1.923**
Adenine phosphoribosyltransferase-like	AT1G27450	1.007	**1.335**	**1.174**	**1.796**	0.134	**0.598**	0.621	0.917	0.198	0.729	**1.595**	**1.882**
Sugar transport protein 14	AT1G77210	0.046	-0.675	0.203	-0.527	0.188	-0.048	-0.132	-0.487	0.095	-0.558	**1.127**	**1.842**
Putative xyloglucan endotransglycosylas	AT4G30270	-0.042	-0.769	0.506	**0.763**	-0.079	0.224	**-1.988**	0.335	-1.389	0.139	**1.155**	**1.828**
Pyridoxine biosynthesis protein	AT5G01410	0.262	**0.966**	0.147	**1.035**	0.277	0.797	0.215	0.735	-0.040	**1.089**	**0.984**	**1.824**
T1N24.22 protein	AT5G25930	0.291	0.911	**0.824**	**1.233**	0.228	1.306	0.309	1.075	0.209	0.982	**0.876**	**1.789**
Receptor-like protein kinase	AT2G31880	0.103	-0.196	0.187	**0.619**	0.509	0.805	-0.040	0.624	0.254	0.698	**0.812**	**1.766**
OSJNBa0021F22.13 protein	AT3G47570	-0.017	-0.269	-0.094	-0.270	1.005	0.638	0.390	0.420	0.501	0.487	**1.198**	**1.701**
Inorganic phosphate transporter 1-4 (At	AT2G38940	0.498	0.175	**0.575**	**0.834**	0.389	1.139	0.482	0.173	0.272	0.340	0.028	**1.635**
no_annotation_available	AT1G34320	0.826	0.289	**1.493**	**1.607**	0.074	0.057	0.710	0.388	1.242	0.438	1.211	**1.622**
Receptor kinase Lecrk	AT2G37710	0.245	**0.699**	0.209	**0.817**	0.617	0.912	0.386	**0.711**	0.341	0.737	**1.100**	**1.573**
Adenosine kinase 2	AT5G03300	0.313	0.318	**1.081**	**1.279**	-0.414	-0.031	-0.399	-0.391	-0.425	-0.377	1.252	**1.559**
Caffeic acid 3-O-methyltransferase 1	AT5G54160	0.149	0.536	**0.403**	0.567	0.320	0.750	-0.473	0.084	-0.535	-0.033	**0.539**	**1.539**
Glutamine synthetase	AT5G37600	0.638	**1.033**	**0.941**	**1.279**	0.226	0.586	0.395	0.518	0.209	0.501	1.026	**1.509**
no_annotation_available	AT2G46330	-0.107	0.437	0.574	**1.525**	0.245	1.097	**-1.438**	1.301	-1.189	1.055	0.188	**1.470**
NADP-dependent isocitrate dehydrogen	AT1G65930	0.474	0.646	0.532	0.402	0.632	0.663	**1.191**	0.749	**1.288**	**1.581**	0.980	**1.413**
Putative bacterial blight resistance prote	AT3G49670	0.145	-0.483	-0.065	-0.122	0.972	1.164	0.544	0.132	0.096	0.244	**0.758**	**1.398**
Putative ABC transporter; 66585-65723	AT1G67940	-0.093	**1.070**	-0.372	**1.267**	0.314	0.307	0.124	0.996	0.083	0.827	1.540	**1.393**
no_annotation_available	AT4G35470	0.225	0.141	-0.063	**0.536**	0.730	1.215	0.822	0.632	0.489	0.596	0.847	**1.372**
Multidrug resistance-associated protein	AT3G21250	-0.057	-0.057	0.438	0.409	-0.218	0.190	-0.348	-0.152	-0.074	-0.016	**0.976**	**1.350**
Putative serine/threonine-specific prote	AT2G33580	0.267	0.231	0.393	**0.505**	0.595	0.631	0.164	0.474	0.283	0.431	**0.908**	**1.305**
Integral membrane protein, putative	AT3G21690	0.202	**0.705**	**0.708**	**1.359**	0.286	0.602	-0.515	0.212	-0.327	0.366	**1.132**	**1.298**
Receptor-like protein kinase	AT5G48380	0.182	0.105	0.038	0.339	0.509	1.010	0.031	0.285	-0.011	0.615	**0.505**	**1.294**
VDAC2.1	AT5G67500	0.231	**0.494**	0.340	**0.565**	0.322	0.653	0.197	0.260	0.129	0.177	0.643	**1.254**
Adenine phosphoribosyltransferase-like	AT1G27450	0.804	**0.828**	**0.797**	**1.094**	0.237	0.231	0.637	0.511	0.354	0.561	**1.423**	**1.221**
SNAP25 homologous protein SNAP33	AT5G61210	0.013	0.209	0.215	**0.605**	0.109	0.545	-0.094	0.355	-0.307	0.260	0.169	**1.216**
Putative peptide transport protein	AT3G54140	0.077	0.239	0.178	0.350	0.142	0.385	0.345	-0.006	0.433	0.432	**0.736**	**1.214**
5-methyltetrahydropteroyltriglutamate-	AT5G17920	0.335	0.514	0.295	0.554	0.172	0.380	-0.068	-0.592	-0.366	-0.291	0.815	**1.209**
Nitrilase 4	AT5G22300	0.677	**1.124**	0.454	**1.166**	0.289	0.378	0.416	0.729	0.377	0.790	**1.166**	**1.207**
Protein kinase domain, putative	AT4G21380	0.184	0.129	0.242	0.338	0.318	0.328	0.398	0.127	0.547	0.332	**0.799**	**1.205**
Allyl alcohol dehydrogenase	AT5G16990	-0.010	-0.232	0.210	0.101	0.331	0.495	0.502	0.147	0.459	0.256	0.084	**1.204**
Adenylate kinase, putative	AT5G50370	0.605	**0.876**	**0.667**	**1.628**	0.248	0.716	0.056	0.563	-0.192	0.631	**0.521**	**1.202**
F9L1.11 protein	AT1G71140	-0.046	0.106	-0.035	0.240	0.095	0.583	-0.299	-0.120	-0.272	-0.044	0.091	**1.200**
RING/C3HC4/PHD zinc finger-like protei	AT3G05200	0.188	0.183	0.404	**0.804**	0.253	0.476	-0.516	0.797	-0.490	0.933	0.364	**1.199**
40S ribosomal protein S5	AT3G11940	0.300	0.124	0.747	**1.221**	-0.325	-0.849	0.394	0.338	0.317	0.254	0.498	**1.198**
Glutamate dehydrogenase 2	AT5G07440	-0.293	0.012	-0.009	0.216	0.146	0.183	-0.156	-0.212	-0.208	-0.311	0.514	**1.187**

Cysteine protease	AT4G35350	-0.106	-0.271	-0.051	0.082	-0.082	-0.214	-0.223	-0.071	0.050	-0.162	0.503	**1.186**
ADP,ATP carrier protein 1, mitochondria	AT3G08580	0.303	0.440	0.152	**0.602**	0.381	0.603	0.720	0.182	0.124	0.462	0.453	**1.164**
Secreted glycoprotein 3	AT4G21380	-0.094	-0.100	0.190	**0.497**	0.026	0.309	-0.045	0.341	0.097	0.293	0.313	**1.146**
Sucrose synthase	AT3G43190	0.312	0.291	0.232	0.364	0.349	0.226	0.636	0.265	0.288	0.331	0.660	**1.104**
5-methyltetrahydropteroyltriglutamate-	AT5G17920	0.169	0.443	0.218	0.337	0.436	0.511	-0.105	-0.052	0.107	-0.046	**0.631**	**1.097**
Hexose transporter	AT1G11260	0.184	-0.065	0.230	0.109	0.353	0.693	0.241	0.036	0.182	0.040	0.305	**1.091**
Putative receptor protein kinase PERK1	AT2G33580	0.222	0.434	0.366	0.311	0.433	0.452	0.360	0.660	0.476	0.848	**0.907**	**1.082**
Receptor-protein kinase-like protein	AT3G51550	0.264	0.498	0.327	0.469	0.450	0.380	**0.576**	0.646	**0.631**	**0.790**	0.915	**1.066**
Nodulin26-like major intrinsic protein	AT4G18910	1.676	0.338	1.381	0.188	2.238	0.581	1.097	0.177	1.671	0.255	1.247	**1.054**
Receptor-like protein kinase	AT5G48380	0.217	0.023	0.072	0.235	0.571	0.693	-0.052	0.080	-0.057	0.192	0.583	**1.052**
S glycoprotein	AT4G21380	0.132	-0.112	0.170	0.275	0.281	0.143	0.403	0.395	0.306	0.313	**0.664**	**1.044**
Receptor-protein kinase-like protein	AT3G51550	-0.082	-0.344	0.155	-0.014	0.439	0.776	-0.184	-0.005	-0.272	-0.049	0.187	**1.042**
PDR6 ABC transporter	AT2G36380	0.394	0.271	0.252	0.383	0.761	1.140	**0.472**	**1.008**	0.160	0.689	0.345	**1.034**
Wall-associated kinase, putative	AT1G25390	0.194	-0.328	0.019	0.205	0.255	-0.120	0.020	-0.089	0.068	0.191	0.461	**1.030**
T17B22.4 protein	AT3G03270	-0.391	-0.198	-0.020	0.024	-1.100	-0.377	**-1.341**	**-0.556**	-1.081	-0.630	-0.417	**1.029**
expressed protein	AT5G12010	-0.360	-0.513	0.373	0.274	0.025	0.270	0.154	0.388	0.124	0.198	0.172	**1.018**
LEM3-like	AT1G79450	0.284	0.369	0.168	**0.548**	0.356	0.539	0.130	0.443	-0.017	0.422	0.480	**1.011**
Putative wall-associated kinase 2	AT1G21240	0.003	-0.089	0.126	0.173	0.264	0.428	0.311	0.386	0.297	0.289	0.385	**0.989**
Gb|AAD56319.1	AT5G41330	0.004	0.091	**0.532**	**0.998**	0.518	0.816	-0.285	1.001	0.111	0.634	0.221	**0.985**
F15H18.11	AT1G18390	0.105	-0.033	0.150	0.353	0.133	0.107	0.179	0.290	0.282	0.263	0.306	**0.970**
Armadillo repeat-containing protein	AT1G76390	0.380	0.556	0.368	**0.559**	0.322	0.387	0.093	0.447	0.200	0.539	0.740	**0.969**
Glucose-6-phosphate/phosphate-translc	AT1G61800	0.464	0.248	0.575	**0.776**	0.110	0.109	0.313	-0.010	0.190	-0.012	0.757	**0.962**
Glyceraldehyde-3-phosphate dehydroge	AT3G04120	-0.153	0.117	-0.080	0.174	0.010	0.401	0.027	0.292	0.068	0.326	0.248	**0.960**
Putative ABC transporter	AT1G17840	0.858	-0.153	**1.090**	0.417	0.196	-0.567	**1.475**	-0.882	**1.629**	-0.230	0.789	**0.958**
Pto kinase interactor 1	AT1G48210	-0.355	-0.207	0.182	0.043	0.196	0.611	-0.177	-0.070	-0.190	-0.044	0.282	**0.945**
AT4g26970/F10M23_310	AT2G05710	0.268	0.186	0.193	**0.508**	0.298	0.537	0.607	0.205	0.161	0.560	**0.773**	**0.936**
G protein beta subunit	AT4G34460	0.248	0.206	-0.184	0.216	0.299	-0.617	0.469	0.174	0.336	0.326	**0.740**	**0.936**
Cytochrome b5 isoform Cb5-A	AT5G53560	0.365	0.045	0.151	0.160	0.162	0.109	0.044	-0.200	0.116	-0.149	0.373	**0.936**
MAP kinase phosphatase 1	AT3G06110	0.115	0.007	0.022	0.051	0.545	0.738	0.256	0.375	0.120	0.409	0.251	**0.935**
At2g25260	AT5G25265	0.257	0.437	0.339	**0.598**	-0.013	-0.062	-0.198	-0.031	-0.073	-0.091	0.479	**0.929**
Synaptobrevin-like protein	AT2G33120	-0.033	0.274	-0.063	0.274	0.427	0.636	0.177	**0.679**	0.088	**0.712**	0.353	**0.927**
Putative leucine-rich repeat receptor kir	AT2G16250	-0.414	-0.224	-0.127	-0.076	0.034	0.126	-0.498	-0.240	-0.689	-0.137	-0.306	**0.919**
Thiolase, putative	AT2G33150	0.159	0.050	0.268	0.352	0.249	0.213	0.258	0.003	0.055	0.094	**0.496**	**0.915**
Ammonium transporter	AT4G13510	0.152	0.351	0.740	0.348	0.135	0.414	0.451	0.123	0.040	0.187	0.588	**0.912**
At2g31880/F20M17.8	AT2G31880	0.099	0.251	-0.086	0.101	0.056	0.036	-0.267	0.156	-0.152	0.576	0.365	**0.907**
Putative acyl-CoA synthetase	AT4G23850	-0.148	0.084	0.090	0.169	0.020	0.065	-0.005	-0.095	-0.057	0.078	0.476	**0.905**
Adenylate kinase B	AT5G50370	0.155	0.140	0.068	0.065	0.103	0.145	0.209	0.134	0.096	0.394	0.299	**0.905**
Seed maturation protein PM37	AT3G44110	0.379	0.743	-0.023	0.188	0.626	0.723	**1.150**	**1.094**	**1.166**	**1.738**	0.896	**0.898**
no_annotation_available	AT4G35310	0.128	0.039	0.237	**0.726**	0.690	0.809	-0.078	0.113	-0.365	-0.149	0.634	**0.885**
Cytochrome P450 monooxygenase CYP8	AT4G31500	-0.001	-0.391	0.034	0.092	0.167	0.499	1.782	1.969	1.647	1.501	0.183	**0.882**
NOI protein, nitrate-induced	AT5G55850	-0.249	0.265	-0.045	0.355	-0.185	0.116	-0.492	0.015	-0.560	0.230	0.175	**0.877**
Putative UDP-glucuronate decarboxylase	AT2G28760	-0.074	**0.893**	0.077	**0.570**	-0.049	0.098	-0.042	-0.071	-0.252	-0.383	0.506	**0.873**

Calmodulin-like protein	AT3G10190	-0.131	-0.038	-0.354	0.128	0.636	1.003	**-0.836**	**-0.642**	-0.511	-0.201	0.165	**0.867**
Phloem calmodulin-like-domain protein	AT2G17290	0.298	0.186	0.197	**0.527**	0.411	0.426	0.270	0.027	0.143	0.087	0.595	**0.859**
Secretory carrier membrane protein	AT1G61250	0.157	0.005	-0.014	0.022	0.188	0.429	-0.015	-0.019	0.033	0.180	0.306	**0.851**
Cytochrome P450 monooxygenase CYP9	AT2G40890	0.225	0.505	0.417	**1.251**	-0.526	-0.305	-0.393	-0.457	0.128	0.110	1.239	**0.850**
Glyceraldehyde-3-phosphate dehydroge	AT3G04120	0.035	0.333	-0.426	0.097	0.036	0.097	0.431	0.221	0.336	0.707	0.834	**0.842**
At1g30270/F12P21_6	AT1G30270	0.673	0.774	**0.692**	**1.017**	0.098	-0.014	0.753	0.497	0.652	0.545	**1.544**	**0.836**
Zinc transporter, putative	AT1G55910	0.725	0.229	**0.781**	**0.625**	0.568	0.290	0.022	0.201	0.403	0.246	**1.115**	**0.833**
Hypersensitive-induced response protei	AT5G62740	-0.355	-0.320	0.118	0.293	0.246	1.123	-0.392	0.074	-0.187	0.091	0.034	**0.831**
Cystinosin homolog	AT5G40670	0.388	**1.192**	0.647	**1.104**	0.145	-0.368	0.076	0.086	-0.105	0.576	1.132	**0.827**
Fructose-bisphosphate aldolase	AT2G36460	-0.243	-0.023	-0.116	0.099	-0.250	-0.040	-0.207	-0.075	-0.239	0.226	-0.053	**0.820**
Putative clathrin assembly protein At5g3	AT5G35200	0.120	0.403	-0.078	0.185	0.507	0.593	0.216	**0.665**	0.216	**0.634**	0.338	**0.817**
Receptor-like protein kinase 4	AT4G23180	0.510	0.136	0.006	-0.022	0.729	-0.365	**0.554**	0.249	0.414	0.353	0.543	**0.815**
Nuclear transport factor 2	AT1G27970	0.734	0.668	0.362	0.301	1.006	0.708	1.080	**1.180**	0.995	**1.330**	1.140	**0.815**
1,4-benzoquinone reductase-like; Trp re	AT4G27270	-0.283	0.134	0.209	0.240	-0.281	-0.171	**-0.663**	-0.337	-0.696	-0.412	0.106	**0.812**
Aconitase-iron regulated protein 1	AT2G05710	0.147	0.394	0.194	0.442	0.173	0.340	0.382	0.147	0.128	0.341	0.531	**0.810**
AR781	AT2G26530	0.202	0.315	0.473	**0.695**	0.341	0.505	-0.055	0.667	-0.088	0.661	0.503	**0.802**
DnaJ homolog subfamily B member 11 p	AT3G62600	-0.229	-0.065	-0.029	0.090	0.169	0.650	-0.097	0.289	0.014	0.359	-0.088	**0.801**
Putative receptor protein kinase PERK1	AT2G33580	0.384	0.165	**0.485**	0.308	0.300	0.209	0.240	0.531	0.396	0.675	**0.677**	**0.801**
Heat shock cognate 70 kDa protein 3	AT5G02500	0.018	0.247	-0.125	0.154	-0.139	0.281	0.490	0.105	0.505	0.259	0.744	**0.794**
Caffeic acid 3-O-methyltransferase	AT5G54160	-0.121	-0.365	0.204	-0.111	-0.198	-0.116	0.443	0.255	0.296	0.105	0.735	**0.789**
Adenosine kinase isoform 1T-like protei	AT5G03300	0.057	0.149	0.475	**0.581**	-0.068	0.012	0.150	-0.217	0.068	0.032	0.775	**0.787**
COBRA-like protein 7 precursor	AT4G16120	0.369	0.306	**0.771**	**0.744**	0.436	0.263	0.189	0.304	0.213	0.254	**1.051**	**0.786**
Ubiquitin-conjugating enzyme E2-17 kDa	AT1G64230	0.533	**0.968**	-0.164	0.146	0.497	0.506	1.030	1.158	0.866	**1.523**	0.732	**0.785**
Reversibly glycosylated polypeptide	AT3G02230	-0.084	-0.044	-0.159	0.283	0.117	0.500	0.451	0.542	0.128	0.242	-0.012	**0.775**
OSJNBa0058K23.17 protein	AT1G30400	0.206	-2.013	0.459	**0.640**	-0.072	0.279	-0.277	0.037	-0.134	0.022	0.633	**0.766**
UPI0000162F22; F26G16.2 protein	AT1G30440	0.557	-0.125	0.042	0.042	0.403	0.386	0.084	-0.103	0.196	0.090	0.627	**0.763**
Putative heat-shock protein 90	AT4G24190	-0.034	-0.095	-0.255	-0.263	0.046	0.210	0.146	0.026	0.200	0.184	0.144	**0.762**
Monodehydroascorbate reductase	AT3G52880	0.196	0.075	0.162	0.111	0.187	0.000	0.383	-0.217	0.313	-0.023	0.357	**0.750**
Aconitate hydratase, cytoplasmic	AT4G35830	-0.010	0.218	0.416	**0.621**	0.307	0.087	0.203	0.222	0.327	0.361	0.321	**0.749**
no_annotation_available	AT1G27190	0.469	0.267	0.235	0.291	0.403	0.443	0.558	0.434	0.391	0.434	0.612	**0.748**
27k vesicle-associated membrane protei	AT4G21450	0.098	0.141	0.157	**0.370**	0.103	0.208	0.038	0.287	0.011	0.288	0.291	**0.743**
Aconitase-iron regulated protein 1	AT2G05710	-0.074	0.294	0.222	**0.479**	0.022	0.280	-0.073	0.184	-0.063	0.050	0.488	**0.742**
Polyubiquitin	AT4G05320	-0.018	0.233	-0.003	0.232	-0.027	-0.011	0.348	0.134	0.438	0.422	0.379	**0.739**
Reticuline oxidase-like protein	AT4G20840	-0.429	0.179	0.160	**0.859**	-0.935	-0.592	-0.220	0.240	-0.421	0.278	-0.349	**0.738**
Mitochondrial phosphate transporter	AT5G14040	0.259	0.227	-0.007	0.344	-0.140	0.197	0.049	-0.190	-0.335	-0.135	0.075	**0.733**
Wall-associated kinase 4	AT1G21210	1.736	0.210	1.496	-0.009	1.844	0.187	1.589	0.135	1.630	0.266	1.962	**0.726**
Plastidic glucose 6-phoaphate/phosphat	AT1G61800	0.534	0.036	**0.464**	**0.530**	0.302	0.277	-0.059	0.047	-0.192	0.051	0.287	**0.723**
Adenylate kinase B	AT5G50370	0.206	0.107	0.151	0.040	0.184	0.085	0.344	0.207	0.330	0.217	**0.403**	**0.723**
Glucose-6-phosphate/phosphate-translo	AT1G61800	0.246	0.269	**0.605**	**0.543**	-0.132	0.050	-0.203	-0.088	-0.296	-0.236	0.362	**0.719**
Metal transport protein	AT1G05300	0.140	-0.641	0.651	0.128	0.852	0.650	0.129	-0.325	0.130	-0.185	0.604	**0.714**
Gb|AAF07369.1	AT1G63830	-0.057	0.153	0.007	0.196	0.137	0.431	-0.024	-0.014	-0.071	0.154	0.239	**0.713**
Polyubiquitin	AT5G03240	-0.141	0.155	-0.182	0.122	-0.210	0.113	-0.057	-0.109	-0.177	0.112	0.054	**0.710**

Multidrug resistance-associated protein	AT2G34660	0.321	-0.061	0.372	-0.066	0.455	0.453	0.113	0.000	0.077	0.006	0.304	**0.700**
G protein beta subunit	AT4G34460	0.278	0.195	-0.040	0.137	0.428	0.025	0.438	0.114	0.369	0.328	0.556	**0.697**
40S ribosomal protein S8	AT5G20290	0.254	0.208	0.009	0.004	0.268	0.390	0.599	0.596	0.543	0.786	0.261	**0.694**
Steroid membrane binding protein, puta	AT3G48890	0.152	0.296	0.278	0.202	0.181	0.362	0.447	0.313	0.517	0.590	0.497	**0.687**
Luminal-binding protein 1 precursor	AT5G42020	-0.173	-0.140	-0.312	-0.245	0.001	-0.238	0.712	-0.336	0.555	0.129	0.562	**0.687**
Patellin 1	AT1G72160	0.135	0.534	0.165	0.390	0.223	0.138	-0.008	0.683	0.432	0.940	**1.235**	**0.685**
60S ribosomal protein L40	AT3G52590	-0.156	0.230	-0.146	0.284	-0.152	0.055	0.236	0.062	0.232	0.163	0.518	**0.685**
SNAP25 homologous protein SNAP33	AT5G61210	0.070	-0.065	0.313	0.231	0.094	0.327	-0.087	0.020	-0.055	0.038	0.184	**0.683**
Ubiquitin and ribosomal protein S27a,	AT2G47110	-0.149	0.281	-0.010	0.231	-0.133	0.028	0.267	0.031	0.300	0.317	0.598	**0.682**
Serine/threonine/tyrosine kinase	AT2G24360	0.188	0.060	0.089	0.109	0.226	0.137	0.248	-0.148	0.166	0.049	0.421	**0.681**
TOM (Target of myb1)-like protein	AT5G16880	-0.141	0.119	-0.039	0.237	0.094	0.261	0.285	0.206	-0.032	0.226	0.175	**0.679**
Alcohol dehydrogenase	AT1G77120	0.199	0.162	0.237	0.189	0.427	0.008	0.776	0.470	**1.014**	0.888	0.387	**0.678**
At1g66480	AT1G66480	0.386	0.164	-0.022	0.104	0.129	0.222	0.321	0.252	0.372	0.409	0.435	**0.677**
F22C12.16	AT1G64080	-0.051	-0.220	-0.081	-0.062	-0.194	0.135	-0.329	-0.056	-0.177	0.512	-0.227	**0.677**
Putative phytosulfokine receptor precur	AT2G02220	1.718	0.323	1.939	-0.195	2.056	0.217	2.203	0.233	2.047	0.049	2.264	**0.672**
Cinnamyl alcohol dehydrogenase	AT5G19440	0.258	**0.398**	0.459	**0.700**	0.195	0.290	0.370	0.389	0.524	0.547	**0.611**	**0.666**
F15H18.11	AT1G18390	0.538	0.685	**0.424**	**0.728**	0.337	0.403	**0.811**	0.522	**0.848**	0.726	**1.038**	**0.664**
T23K8.15 protein	AT1G65240	0.364	0.350	0.181	0.263	0.309	0.298	0.563	0.382	0.462	0.836	0.383	**0.661**
Polyubiquitin	AT5G20620	-0.174	-0.017	-0.123	0.042	-0.209	0.029	0.093	-0.072	-0.106	0.090	0.249	**0.660**
Enolase 1	AT2G36530	-0.115	0.220	0.075	0.379	0.110	0.301	0.306	0.213	0.197	0.462	0.246	**0.656**
Heat shock cognate 70 kDa protein 3	AT3G12580	0.031	0.352	-0.195	0.153	-0.061	0.084	0.555	0.151	0.552	0.321	0.454	**0.656**
P58IPK	AT5G03160	-0.112	0.245	0.361	0.144	-0.167	0.093	-0.020	0.072	0.004	0.305	0.431	**0.652**
At1g65020	AT1G65020	-0.244	0.239	-0.328	0.157	0.046	0.484	0.180	0.430	0.202	0.507	0.170	**0.651**
Ras-related GTP-binding protein	AT5G45130	-0.108	0.126	-0.038	0.112	-0.038	0.040	-0.302	-0.156	-0.406	-0.096	0.355	**0.651**
Caffeic acid O-methyltransferase	AT5G54160	0.308	0.219	0.435	0.243	0.091	-0.034	-0.365	-0.157	-1.059	-0.079	0.957	**0.650**
Mitochondrial carrier-like protein	AT4G01100	0.605	0.548	0.305	**0.648**	0.535	0.425	0.546	0.251	0.419	0.462	0.864	**0.646**
SDL12A	AT5G42080	0.082	0.628	0.010	0.393	0.026	0.264	0.314	0.404	0.066	0.551	0.338	**0.642**
Syntaxin 121	AT3G11820	-0.102	0.076	0.393	**0.711**	-0.113	0.220	-0.913	0.117	**-0.746**	0.160	0.320	**0.640**
T13M11.15 protein	AT1G61790	0.062	0.211	-0.022	0.086	0.052	0.499	-0.093	0.109	-0.179	0.102	0.013	**0.633**
Receptor-like protein kinase	AT2G31880	0.023	0.402	0.098	**0.530**	-0.092	0.171	-0.178	0.214	-0.176	0.336	0.026	**0.629**
prolyl 4-hydroxylase, beta polypeptide	AT5G60640	0.088	0.044	0.398	0.298	-0.031	-0.014	-0.341	-0.023	-0.142	0.063	0.237	**0.628**
DnaJ-like protein MsJ1	AT3G44110	0.202	0.153	-0.331	0.169	0.544	0.479	0.532	0.173	0.492	0.584	0.545	**0.627**
UPI000009CD7E; P0401G10.6	AT4G24290	0.209	0.301	0.028	0.231	-0.025	0.335	0.447	0.278	0.255	0.533	0.399	**0.620**
Synaptobrevin-like protein	AT1G04760	0.183	0.315	0.084	0.090	0.276	0.646	0.299	**0.659**	0.197	**0.604**	0.220	**0.619**
F9F8.20 protein	AT3G10980	0.071	0.107	0.348	0.317	-0.053	-0.174	-0.050	0.296	-0.161	0.226	-0.031	**0.617**
SDL12A	AT5G42080	0.356	0.453	-0.113	0.349	-	0.187	0.077	0.371	-	0.665	0.338	**0.606**
Eugenol O-methyltransferase	AT5G54160	0.789	-0.236	0.455	-0.407	0.751	-0.260	0.151	-0.420	0.584	-0.126	0.955	**0.606**
At2g18730/MSF3.11	AT2G18730	0.346	0.107	0.446	0.022	0.504	0.562	0.983	0.576	0.797	0.885	0.770	**0.604**
Amt2-like protein	AT2G38290	0.089	0.212	-0.094	0.074	0.170	0.304	-0.218	-0.012	-0.259	0.074	0.175	**0.595**
Hexose transporter	AT5G26340	0.030	0.290	-0.095	0.257	-0.197	0.169	-0.521	**-0.431**	-0.549	-0.223	0.135	**0.592**
Receptor-like serine/threonine kinase	AT1G70530	0.380	0.344	-0.171	0.218	0.299	0.410	0.312	0.462	0.286	0.469	0.101	**0.584**
AT3g28670/MZN14_13	AT3G28670	0.110	0.069	0.134	0.083	0.248	-0.764	0.206	-0.074	-0.088	-0.015	0.240	**0.582**

Cytosolic ascorbate peroxidase	AT1G07890	0.082	0.143	-0.179	-0.219	-0.002	0.079	0.268	0.549	0.182	0.498	0.361	**0.581**
Polyubiquitin	AT5G20620	-0.033	0.249	0.110	0.178	-0.111	-0.078	0.286	0.044	0.365	0.356	0.510	**0.581**
Putative membrane transporter	AT2G26510	0.349	0.357	0.122	0.211	0.170	0.169	0.327	0.057	0.183	0.364	**0.727**	**0.580**
Erwinia induced protein 1	AT2G17120	0.040	0.078	0.184	-0.102	0.447	0.319	0.561	0.272	0.178	0.300	0.539	**0.579**
F8L10.9 protein	AT1G53050	-0.178	-0.018	0.128	0.311	-0.004	0.172	-0.481	-0.138	-0.333	-0.104	0.400	**0.579**
Sucrose synthase	AT3G43190	0.129	0.061	0.077	-0.094	0.207	0.324	0.298	0.087	0.185	0.213	0.418	**0.573**
14-3-3 protein	AT5G16050	-0.016	0.262	-0.131	0.141	-0.169	-0.128	0.038	-0.145	-0.049	0.041	0.385	**0.573**
14-3-3-like protein D	AT2G42590	-0.011	0.271	0.165	0.244	0.104	-0.029	0.221	0.128	0.163	0.193	0.645	**0.572**
40S ribosomal protein S7	AT1G48830	0.053	0.081	0.073	0.256	0.006	0.263	-0.026	0.174	-0.120	0.119	0.071	**0.570**
AT4g34700/T4L20_280	AT4G34700	0.276	0.219	0.119	0.248	0.042	0.122	0.283	0.298	0.160	0.173	0.211	**0.568**
Heat shock 70 kDa protein	AT3G12580	0.236	0.022	0.055	0.036	0.124	0.356	0.569	0.316	0.700	0.273	0.485	**0.568**
Aluminum-induced protein	AT5G19140	0.544	**0.646**	0.516	**0.790**	0.717	0.415	0.712	0.805	**0.828**	**1.044**	**0.942**	**0.567**
UBC protein	AT4G05320	-0.182	0.032	-0.100	-0.015	-0.243	-0.008	0.003	-0.028	0.021	-0.145	0.295	**0.567**
T24D18.14 protein	AT1G16030	-0.147	0.168	-0.301	0.048	-0.070	0.077	0.544	0.160	0.356	0.352	0.439	**0.565**
Disulfide-isomerase-like protein	AT2G47470	0.194	-0.235	0.061	-0.013	-0.255	-0.616	0.315	-0.533	0.335	-0.264	0.466	**0.561**
Cytosolic phosphoglycerate kinase 1	AT1G79550	0.169	0.108	0.069	0.191	0.172	0.068	0.369	-0.034	0.267	0.209	0.258	**0.549**
S-adenosyl-L-methionine synthetase 1	AT3G17390	0.080	0.157	0.363	**0.675**	-0.162	0.059	-0.143	-0.047	-0.350	0.003	0.867	**0.545**
AtPK2324	AT2G48010	0.320	0.270	0.225	0.377	0.106	-0.003	0.207	0.073	0.154	0.216	**0.742**	**0.544**
Glutamine synthetase	AT5G37600	0.124	0.362	**0.740**	**0.854**	-0.154	0.183	**-0.408**	-0.021	-0.415	-0.188	0.051	**0.540**
ATP synthase delta chain, mitochondrial	AT5G13450	-0.067	0.083	0.141	0.124	-0.066	-0.008	0.114	-0.099	-0.023	-0.149	0.221	**0.540**
Putative aluminum-induced protein	AT3G22850	-0.212	0.026	-0.031	-0.080	-0.300	-0.181	-0.364	-0.352	-0.525	-0.501	-0.015	**0.537**
AT5g36940/MLF18_60	AT1G58030	-0.002	0.168	-0.098	0.150	0.370	-0.162	0.403	-0.029	-0.012	0.342	0.448	**0.536**
Ribosomal protein L10, putative	AT1G66580	0.112	0.075	0.052	0.302	0.150	0.354	-0.198	0.037	-0.076	0.060	0.007	**0.531**
F3O9.32 protein	AT1G16520	0.121	0.318	0.145	0.326	0.117	0.132	0.432	0.323	0.269	0.395	0.604	**0.523**
no_annotation_available	AT5G40450	0.376	0.462	0.485	**1.375**	0.041	-0.190	-0.120	0.140	-0.122	0.280	**1.173**	**0.521**
Pectinesterase-like protein	AT5G48450	0.056	0.490	-0.155	0.256	0.285	0.496	0.219	0.687	-0.667	0.587	0.410	**0.519**
Putative ripening regulated protein	AT5G52450	0.214	0.491	0.363	**0.670**	-0.210	0.134	-0.177	0.291	-0.012	0.082	0.302	**0.517**
UDP-glucose:sterol 3-O-glucosyltransfer	AT3G07020	0.118	-0.374	0.575	0.006	0.115	0.436	0.643	0.440	0.651	0.429	0.132	**0.503**
Leucine-rich repeat protein, putative	AT4G35470	-0.270	0.317	-0.187	0.416	0.402	0.358	0.258	0.554	0.010	0.499	0.243	**0.498**
Putative elongation factor 1 gamma	AT1G57720	0.390	0.352	-0.095	0.104	0.329	0.281	0.482	0.209	0.308	0.606	0.447	**0.497**
Putative peroxisomal membrane carrier	AT2G39970	0.028	0.124	0.163	0.372	-0.260	-0.058	-0.237	-0.127	-0.330	-0.329	-0.052	**0.494**
Allyl alcohol dehydrogenase	AT5G16990	0.062	-0.282	0.136	-0.072	0.167	0.302	0.552	0.109	0.596	0.166	-0.004	**0.490**
Actin-11	AT5G09810	0.079	0.463	0.156	0.364	-0.105	0.048	0.228	0.260	0.020	0.428	0.495	**0.489**
Zinc finger, C3HC4 type, putative	AT5G22000	0.181	0.053	0.019	0.012	0.624	0.391	0.329	0.053	0.252	0.149	0.287	**0.489**
Polyubiquitin	AT4G05320	-0.273	-0.046	-0.047	0.023	-0.261	-0.025	-0.162	-0.114	-0.131	-0.150	0.147	**0.486**
14-3-3-like protein	AT1G78300	0.384	0.185	0.074	-0.022	0.297	0.082	0.394	0.189	0.303	0.703	0.464	**0.483**
RE10554p	AT3G52590	-0.135	0.130	-0.253	0.034	-0.206	0.078	-0.132	-0.092	-0.231	-0.008	-0.046	**0.482**
F10O3.10 protein	AT1G03080	0.035	**0.601**	0.019	0.406	-0.049	0.015	0.076	0.326	-0.108	0.157	0.304	**0.482**
Protein At1g23170	AT1G70770	0.007	0.169	-0.176	0.287	-0.026	0.135	0.048	0.185	0.022	0.255	0.084	**0.482**
SF16 protein-like	AT2G33990	0.093	0.012	0.074	0.101	0.019	0.124	-0.207	-0.122	-0.298	0.061	0.384	**0.475**
YUP8H12.24 protein	AT1G05150	-0.097	-0.184	0.048	0.010	-0.786	0.158	-0.763	0.165	-0.861	0.311	-1.029	**0.471**
OSJNBb0022F16.9 protein	AT1G78830	0.102	-0.145	0.148	-0.006	0.344	0.156	0.474	0.014	0.353	0.021	0.582	**0.469**

Ribosomal protein L40	AT3G52590	0.328	0.280	0.364	0.390	0.036	0.221	0.119	0.240	0.224	0.375	0.318	**0.466**
Polyubiquitin	AT4G02890	-0.102	0.236	0.056	0.101	0.008	0.157	0.271	0.205	0.324	0.255	0.562	**0.465**
Putative iron inhibited ABC transporter 2	AT5G60790	0.343	**0.826**	-0.036	0.504	0.081	0.249	0.104	0.269	0.152	0.310	0.442	**0.464**
Patellin-3	AT1G72160	0.012	**0.393**	0.042	0.322	0.169	0.292	-0.317	0.257	-0.077	0.296	0.174	**0.463**
Protein kinase APK1A, chloroplast precu	AT1G07570	0.094	-0.088	0.284	0.154	0.387	0.510	0.321	0.385	0.305	0.345	0.384	**0.461**
Putative receptor-like protein kinase	AT1G34300	0.027	0.227	0.101	0.280	0.197	0.154	-0.046	0.199	0.136	0.247	0.323	**0.458**
T14P8.16	AT4G02350	0.069	0.147	-0.017	0.420	0.084	0.028	0.210	0.364	0.185	0.211	0.303	**0.457**
Ubiquitin	AT2G47110	-0.215	0.125	-0.242	-0.004	-0.301	-0.065	-0.211	-0.198	-0.246	0.098	0.193	**0.456**
UTP:alpha-D-glucose-1-phosphate uridy	AT5G17310	0.039	0.122	0.161	0.179	-0.042	0.250	0.401	0.397	-0.037	0.071	0.191	**0.456**
Sterol delta-7 reductase	AT1G50430	0.263	0.122	0.408	0.279	0.110	0.065	0.136	-0.157	0.079	-0.035	0.605	**0.453**
Triosephosphate isomerase	AT3G55440	0.035	0.072	-0.013	0.062	-0.207	-0.024	-0.016	-0.171	-0.188	-0.055	0.030	**0.451**
Emb|CAB83315.1	AT5G03540	0.125	0.211	-0.010	0.126	0.100	0.011	0.079	0.024	0.082	-0.028	0.154	**0.448**
Protein kinase APK1B, chloroplast precu	AT2G28930	0.254	0.143	0.124	0.244	0.200	0.308	0.135	0.339	0.084	0.285	0.348	**0.446**
Putative phragmoplastin	AT3G60190	0.415	-0.289	-0.044	-0.083	0.161	0.258	0.341	0.385	0.388	0.341	0.157	**0.446**
Receptor-protein kinase-like protein	AT3G51550	0.386	-0.293	0.407	0.001	0.466	0.332	**0.852**	0.249	0.934	0.248	-0.141	**0.444**
Translationally-controlled tumor protein	AT3G16640	0.189	0.409	0.084	0.149	0.416	0.435	0.490	**0.844**	0.418	**1.219**	0.249	**0.442**
NADH:cytochrome b5 reductase	AT5G17770	0.123	-0.007	0.231	0.190	0.037	0.036	0.178	-0.078	0.240	0.137	0.398	**0.442**
Whitefly-induced gp91-phox	AT5G47910	-0.191	-0.141	0.182	-0.060	-0.185	-0.107	0.299	0.341	0.075	0.129	-0.005	**0.442**
Copine III-like	AT5G14420	0.002	0.261	0.223	**0.596**	-0.293	-0.012	**-0.707**	-0.178	**-0.723**	-0.339	0.342	**0.436**
UPI000009DA03; putative GTP-binding p	AT4G17530	-0.072	0.103	0.266	**0.415**	-0.293	-0.305	-0.285	-0.278	-0.271	-0.120	0.433	**0.433**
Putative UDP-N-acetylglucosamine trans	AT4G32270	0.132	0.062	-0.013	0.140	0.017	0.123	-0.143	0.084	-0.122	0.090	0.193	**0.428**
40S ribosomal protein S24	AT3G04920	0.211	0.158	0.359	0.111	-0.038	0.281	0.250	0.421	0.099	0.146	0.220	**0.427**
Polyubiquitin	AT1G31340	-0.249	0.058	0.011	-0.001	-0.254	-0.075	-0.010	-0.067	-0.004	0.118	0.366	**0.424**
Proton pump interactor	AT4G27500	0.484	0.226	0.183	0.116	0.143	0.124	0.505	0.328	0.536	0.357	**0.538**	**0.419**
Calcineurin B-like	AT4G33000	-0.111	0.110	-0.166	0.218	0.243	**0.568**	0.099	**0.380**	0.027	**0.400**	**0.507**	**0.418**
40S ribosomal protein S4	AT5G07090	0.101	0.180	-0.175	0.069	0.082	0.289	0.148	0.001	-0.077	0.226	0.077	**0.418**
Small GTP-binding protein	AT1G02130	-0.031	0.138	0.122	0.302	-0.205	-0.426	-0.139	0.002	-0.234	-0.111	0.278	**0.417**
Syntaxin 132	AT5G08080	0.154	0.175	0.124	0.261	0.234	0.343	-0.168	0.098	-0.080	0.050	0.003	**0.416**
F6N23.9 protein	AT4G00710	0.148	**0.488**	0.248	**0.621**	0.429	0.464	0.374	0.753	0.390	**0.839**	0.623	**0.415**
Ankyrin-like protein	AT2G31820	0.289	**0.543**	0.299	**0.442**	-0.217	-0.049	-0.332	-0.016	-0.307	0.055	0.381	**0.413**
Putative dolichyl-di-phosphooligosaccha	AT5G66680	0.047	0.102	-0.281	-0.073	-0.033	0.049	0.031	-0.292	-0.093	-0.030	-0.006	**0.412**
Nucleoside diphosphate kinase 1	AT4G09320	0.189	-0.108	0.386	0.072	-0.065	0.249	0.254	0.275	0.200	0.339	0.244	**0.411**
PDR6 ABC transporter	AT2G36380	0.174	0.497	0.107	0.461	0.362	0.686	0.043	0.636	-0.214	0.645	-0.127	**0.410**
F6F9.12 protein	AT1G19835	0.530	-0.302	0.281	-0.176	0.598	0.388	0.752	0.435	0.907	0.789	0.703	**0.409**
Putative Clathrin coat assembly protein	AT5G46630	0.050	0.083	-0.001	0.108	0.074	0.073	0.507	0.247	0.417	0.062	0.546	**0.405**
Cyclic nucleotide-gated ion channel 1	AT5G53130	0.116	-0.030	-0.070	-0.116	0.498	0.367	0.388	0.128	0.302	0.146	0.389	**0.402**
Ankyrin-like protein; 93648-91299	AT3G12360	0.027	0.400	-0.081	0.157	0.195	0.213	0.352	0.113	0.200	0.283	0.483	**0.396**
LysM receptor-like kinase	AT3G21630	-0.063	0.081	-0.068	0.158	-0.180	0.040	-0.227	0.116	-0.213	0.058	0.153	**0.396**
VDAC1.3	AT3G01280	-0.152	-0.118	0.223	0.072	-0.199	-0.199	-0.028	-0.295	-0.114	-0.218	0.085	**0.393**
Proteasome subunit beta type 1	AT3G60820	-0.190	-0.057	-0.029	0.032	-0.347	-0.274	-0.210	-0.423	-0.465	-0.529	0.047	**0.391**
Histidine amino acid transporter	AT5G40780	0.106	-0.218	0.007	0.057	0.156	0.051	0.256	-0.252	-0.440	-0.368	-0.093	**0.381**
UPI0000196B24; ATP binding / kinase/ p	AT5G01950	0.270	0.038	-0.108	-0.082	0.432	0.081	0.293	0.048	0.152	-0.124	0.558	**0.381**

Acetyl-CoA acyltransferase	AT2G33150	0.053	-0.053	-0.128	-0.066	-0.192	0.008	-0.280	-0.229	-0.400	-0.334	-0.056	**0.379**
Putative carbonyl reductase	AT3G61220	-0.082	-0.074	-0.165	0.243	-0.067	-0.303	0.592	0.021	0.586	0.273	0.625	**0.379**
KUP-related potassium transporter	AT2G30070	0.197	0.500	-0.107	0.131	0.127	0.448	0.388	**0.937**	0.403	**0.848**	0.177	**0.376**
Vesicle-associated membrane protein 7	AT4G15780	-0.089	0.091	0.231	0.027	0.301	0.334	0.103	0.427	0.256	0.397	0.319	**0.370**
Protein kinase-like protein	AT2G24360	0.304	0.024	0.048	-0.070	0.046	-0.067	0.466	-0.066	0.318	0.082	0.419	**0.369**
Mitochondrial-processing peptidase alpl	AT3G16480	0.171	0.098	0.256	0.199	0.050	0.089	0.187	-0.033	0.200	0.066	0.248	**0.368**
Plasma membrane H+ ATPase	AT2G24520	0.225	0.189	**0.748**	0.302	-0.160	-0.091	-0.100	-0.254	0.074	-0.037	0.080	**0.367**
Expressed protein	AT2G41705	0.002	0.077	0.083	-0.137	0.203	0.130	0.314	0.050	0.149	0.019	0.231	**0.367**
F21H2.4 protein	AT1G34750	0.037	0.169	0.103	0.351	0.207	0.256	-0.022	0.037	-0.137	-0.019	0.114	**0.361**
Arabidopsis thaliana genomic DNA, chro	AT4G27450	-0.177	-0.047	-0.331	0.059	0.074	0.107	0.078	0.392	0.246	0.655	0.178	**0.361**
F23M19.3	AT1G34320	-0.017	-0.019	-0.087	0.077	0.048	-0.018	0.179	0.075	0.181	0.482	0.202	**0.357**
Syntaxin 132	AT5G08080	-0.005	0.094	0.177	0.201	0.105	0.236	0.130	0.240	0.002	0.091	-0.028	**0.351**
Serine hydroxymethyltransferase, mitoc	AT4G37930	-0.023	0.109	0.185	0.345	-0.159	-0.097	-0.065	0.014	0.125	0.185	0.512	**0.350**
Gb|AAF01580.1	AT5G08440	-0.396	0.136	-0.361	0.434	-0.068	-1.152	-0.258	0.037	-0.231	-0.035	-0.016	**0.349**
Similarity to kinesin protein	AT3G16630	0.114	0.360	0.283	0.185	0.093	0.297	0.304	0.404	0.293	0.305	0.468	**0.342**
Cysteine synthase (EC 2.5.1.47) (Beta-py	AT4G14880	-0.145	-0.098	-0.096	0.142	0.049	0.097	-0.269	-0.165	-0.129	-0.171	-0.005	**0.342**
T14P4.10 protein	AT4G02075	0.193	-0.027	0.211	0.284	0.046	0.076	-	0.143	0.120	0.138	0.182	**0.341**
Zinc finger, C3HC4 type, putative	AT5G22000	-0.016	0.080	0.014	0.129	0.018	0.129	-0.174	0.095	-0.115	0.177	0.348	**0.341**
Probable 26S proteasome non-ATPase r	AT4G24820	-0.059	0.062	0.038	0.060	0.024	-0.020	-0.132	-0.220	-0.100	-0.223	0.149	**0.339**
F8K4.10 protein	AT1G61900	0.001	-0.174	0.150	-0.124	0.115	0.204	0.238	0.077	0.114	0.190	0.299	**0.331**
F2D10.25	AT1G20760	0.050	0.097	0.093	0.036	0.240	0.224	0.425	0.115	0.452	0.416	0.471	**0.330**
Protein kinase CDG1-like	AT5G56890	0.034	0.041	0.273	0.122	0.030	0.025	-0.036	-0.008	0.073	-0.109	0.318	**0.329**
Ser-thr protein kinase	AT2G40270	0.137	-0.062	0.099	0.152	-0.023	-0.020	-0.130	-0.117	0.106	-0.078	0.507	**0.326**
ADP,ATP carrier protein 1, mitochondria	AT5G13490	0.259	0.029	0.118	0.211	0.186	0.309	0.190	0.002	0.020	-0.043	0.103	**0.322**
60S ribosomal protein L5	AT3G25520	0.030	0.219	-0.217	0.176	0.117	0.234	0.469	0.207	0.074	0.187	0.290	**0.320**
Receptor protein kinase-like	AT3G46290	0.225	0.289	0.097	0.144	0.311	0.035	**0.626**	0.547	0.589	**0.649**	**0.672**	**0.317**
Calcium-dependent protein kinase 8	AT5G19450	-0.134	-0.242	0.016	0.201	-0.361	-0.066	-0.067	0.014	0.009	-0.158	0.094	**0.314**
Putative receptor-like protein kinase	AT2G01210	0.334	0.317	0.364	0.189	0.411	0.283	0.472	0.565	0.403	0.559	0.393	**0.312**
Squamosa promoter-binding-like protei	AT1G76580	0.019	0.071	0.073	0.203	0.271	0.401	0.336	0.173	0.287	0.191	0.325	**0.307**
OSJNBa0091D06.14 protein	AT1G62740	0.322	0.271	0.102	0.273	0.059	0.102	0.071	0.143	0.095	0.322	0.172	**0.297**
Transthyretin-like protein	AT5G58220	0.112	0.170	0.051	0.083	0.088	-0.077	0.156	0.066	0.128	0.226	0.185	**0.293**
Proteasome subunit beta type 3-A	AT1G21720	0.246	0.020	0.354	0.142	-0.132	-0.069	0.028	-0.090	-0.135	-0.231	0.070	**0.289**
Steroid 5-alpha reductase	AT3G55360	0.233	0.102	0.009	-0.026	0.137	-0.197	0.295	0.036	0.069	0.259	0.244	**0.287**
Putative mitogen-activated protein kina	AT4G29810	0.098	-0.003	0.103	0.046	0.261	0.201	0.132	-0.079	0.118	0.084	0.275	**0.286**
Putative S-phase specific ribosomal prot	AT4G34670	-0.022	0.233	-0.456	0.185	-2.098	0.130	0.115	0.226	0.187	0.319	0.030	**0.286**
Putative NTS2 protein	AT1G34470	0.002	-0.156	-0.088	-0.070	-0.228	-0.303	-0.019	-0.327	0.035	-0.202	0.376	**0.277**
F25I16.1 protein	AT1G18650	0.183	0.383	0.352	0.311	-0.168	-0.121	0.067	0.049	0.130	0.309	0.163	**0.275**
AP2/EREBP transcription factor ERF-2	AT3G16770	0.167	**0.720**	-0.265	0.137	0.095	0.337	0.265	**0.639**	0.329	**0.716**	0.482	**0.265**
Peroxisomal 2,4-dienoyl-CoA reductase	AT3G12800	-0.448	-0.254	-0.117	0.165	-0.698	-0.562	-0.535	**-0.697**	-0.664	-0.539	-0.296	**0.265**
Formate--tetrahydrofolate ligase	AT1G50480	-0.389	-0.033	-0.247	0.029	-0.501	-0.247	-0.547	-0.173	-0.572	-0.204	0.379	**0.261**
Arabidopsis thaliana genomic DNA, chro	AT3G26090	0.009	0.141	0.219	0.023	0.062	0.043	-0.012	0.019	0.176	0.032	0.358	**0.260**
Putative carbonyl reductase	AT3G61220	-0.046	-0.193	-0.253	0.160	0.025	-0.244	0.592	-0.024	0.658	0.119	0.679	**0.251**

40S ribosomal protein S33, putative	AT5G03850	0.468	0.016	0.349	0.117	-0.128	-0.014	-0.085	-0.093	-0.108	-0.016	0.070	**0.250**
Pectinesterase-3 precursor	AT1G53840	-0.325	-0.107	-0.108	-0.088	-0.137	-0.052	-0.027	0.011	-0.065	0.017	0.039	**0.246**
Armadillo repeat-containing protein-like	AT1G20780	-0.019	-0.051	0.123	0.028	0.196	0.254	-0.003	0.062	0.192	0.078	0.077	**0.224**
Latex-abundant protein	AT1G79340	0.027	0.187	0.025	0.188	0.130	-0.061	0.427	0.142	0.346	0.310	0.157	**0.201**
Glutamate dehydrogenase 2	AT5G07440	-0.242	0.109	0.045	0.292	-0.099	0.333	-0.105	0.361	-0.047	0.276	-0.207	**0.160**

Table S3. Fold changes (log2) in expression of oxidative stress-related genes in the flavedo (F) and albedo (A) tissues of AC, EC and 1-MCP-treated fruits stored for 4 and 14 days at 20 ºC as compared to freshly harvested (FH) fruit. The symbol + indicates no expression in FH fruits, and the symbol -, indicates expression in FH fruits but not in the compared treatment. Numbers in bold indicate differential expression in the compared condition according to SAM (*p* -value<0.01).

Citrus unigen	Description	4 days						14 days					
		AC		EC		1-MCP		AC		EC		1-MCP	
		F	A	F	A	F	A	F	A	F	A	F	A
Glutathione S-transferase/Glutathione peroxidase													
aC18011D05Rv_c	Glutathione S-transferase	0.246	0.459	0.254	0.464	0.199	0.008	0.118	-0.141	-0.048	-0.138	1.069	**4.646**
aC31502H06EF_c	Glutathione S-transferase	0.290	0.074	0.127	0.223	0.577	1.342	0.249	-0.100	0.425	0.366	**1.051**	**3.802**
aCL184Contig2	Glutathione S-transferase	0.351	0.617	0.357	0.556	0.327	0.064	0.289	-0.154	0.053	-0.140	**1.178**	**3.667**
aCL184Contig1	Glutathione S-transferase	0.364	0.425	0.414	0.483	0.504	-0.071	0.221	-0.363	0.337	-0.223	**1.383**	**2.896**
aCL3761Contig1	Glutathione S-transferase	0.767	0.185	**1.664**	0.697	1.317	1.508	0.342	0.484	0.584	0.236	**1.398**	**2.618**
aC31704E06EF_c	Glutathione S-transferase	**0.802**	0.322	**0.908**	0.430	0.869	0.748	0.329	0.277	0.517	0.355	**1.274**	**2.270**
aC34105C06EF_c	Glutathione S-transferase	0.859	-0.105	**1.416**	0.533	1.024	1.107	0.248	0.081	0.460	0.253	**1.142**	**2.214**
aCL110Contig2	Glutathione S-transferase		0.225	**+**	**-**		**-**		**-**		**-**	0.684	**2.058**
aC05811E06SK_c	Glutathione S-transferase 12	0.500	0.601	-0.620	**-0.837**	0.143	-0.420	0.395	0.781	0.511	0.645	0.904	**1.569**
aCL1507Contig2	Glutathione S-transferase GST 14	0.164	0.141	0.096	0.039	0.274	0.265	0.120	-0.002	0.121	0.055	**0.913**	**1.429**
aCL1249Contig1	Glutathione S-transferase GST 14	0.341	0.518	0.442	**0.603**	0.714	**1.034**	0.352	0.485	0.306	0.347	**0.916**	**1.393**
aCL4064Contig1	Glutathione S-transferase GST 14	0.709	0.608	**0.560**	**0.619**	0.955	0.905	0.529	0.355	0.459	0.326	0.588	**1.325**
aC31303F07EF_c	Glutathione S-transferase GST 22	0.384	**1.034**	0.263	**1.068**	0.887	1.501	0.129	**0.866**	0.031	**0.858**	0.433	**1.057**
aC16016H02SK_c	Glutathione S-transferase	0.029	0.077	0.021	0.113	0.095	0.065	-0.160	-0.082	0.010	0.033	0.267	**0.839**
aC08034B04SK_c	Glutathione S-transferase GST 22	0.523	**1.369**	0.429	**1.424**	1.345	**1.891**	0.537	**1.195**	0.445	**1.143**	0.265	**0.653**
aCL7288Contig1	Glutathione S-transferase GST 22	0.532	**1.036**	0.288	**1.063**	1.166	1.423	0.549	0.768	0.467	0.920	0.817	0.467
aC06017H12SK_c	Glutathione S-transferase zeta class	0.120	-0.051	0.189	0.084	0.132	0.152	0.242	0.102	0.299	-0.013	0.282	**0.338**
aCL3279Contig1	Glutathione S-transferase zeta class	0.291	0.104	0.231	0.174	0.314	0.053	0.055	-0.108	0.176	0.053	0.174	**0.240**
aCL4101Contig1	Glutathione S-transferase, C-terminal-like	0.384	0.675	**0.583**	**0.856**	-0.222	-0.213	0.224	0.007	0.254	0.016	**0.834**	0.223
aC31304H09EF_c	Putative glutathione S-transferase T3	0.252	0.173	**0.552**	**0.540**	1.068	**1.158**	0.111	0.381	0.202	0.654	-0.282	-0.175
aCL1099Contig1	Similarity to glutathione-S-transferase/glutaredoxin	0.032	-0.094	0.060	-0.036	-0.100	-0.048	-0.080	-0.078	-0.049	-0.080	-0.407	**-0.951**
aC20007C12SK_c	Glutathione S-transferase	0.061	-0.071	0.041	0.020	0.109	-1.288	0.266	0.215	0.132	0.159	**+**	**-**
Blue copper oxidases													
aCL3449Contig1	Dicyanin	0.480	0.023	**2.493**	**1.564**	-0.098	1.176	-0.353	0.199	0.671	0.432	**2.052**	**2.960**
aCL12Contig4	Dicyanin	-0.070	0.114	**0.830**	**1.270**	0.222	1.483	-1.174	0.147	-0.909	0.407	0.553	**2.835**
aCL5752Contig1	Dicyanin	0.115	0.111	**0.791**	-0.008	0.359	0.294	0.499	0.308	-1.174	0.458	0.696	**0.740**

Citrus unigen	Description	4 days						14 days					
		AC		EC		1-MCP		AC		EC		1-MCP	
		F	A	F	A	F	A	F	A	F	A	F	A
Ascorbate-gluthatione cycle and related													
aCL622Contig2	Cationic peroxidase isozyme 40K precursor	-0.278	+	0.160	+	-	+	-0.054	+	0.062	+	0.326	+
aCL47Contig2	Ascorbate peroxidase	0.521	0.000	0.597	0.056	0.610	0.738	0.670	0.325	0.802	0.890	**1.500**	**2.382**
aC31401A05EF_c	Phospholipid hydroperoxide glutathione peroxidase	0.146	0.226	0.470	**0.528**	0.133	0.170	-0.208	0.074	-0.087	0.108	0.477	**1.366**
aCL2220Contig3	Class III peroxidase	0.089	0.766	0.356	0.284	-0.050	1.415	0.109	0.848	0.805	1.065	-0.071	0.926
aCL14Contig2	Fe-superoxide dismutase 1	0.285	0.012	0.078	-0.119	0.447	0.348	0.559	0.180	0.605	0.504	0.381	**0.867**
aCL8011Contig1	Fe-superoxide dismutase 1	0.435	-0.031	0.255	0.035	0.586	0.347	0.392	0.166	0.588	0.389	0.516	**0.827**
aCL1534Contig1	Peroxidase	0.307	-0.345	0.557	-0.141	0.144	-0.364	0.002	-0.132	0.717	0.122	**1.132**	0.776
aC31302C03EF_c	Monodehydroascorbate reductase	0.196	0.075	0.162	0.111	0.187	0.000	0.383	-0.217	0.313	-0.023	0.357	**0.750**
aCL1413Contig1	Glutathione reductase, cytosolic	-0.389	0.006	0.011	**0.402**	-0.573	-0.269	-0.650	**-0.427**	-0.612	-0.397	-0.244	**0.587**
aCL5500Contig1	Cytosolic ascorbate peroxidase	0.082	0.143	-0.179	-0.219	-0.002	0.079	0.268	0.549	0.182	0.498	0.361	**0.581**
aCL277Contig1	Chloroplast thylakoid-bound ascorbate peroxidase	0.047	0.035	-0.004	0.028	-0.116	-0.141	0.070	-0.110	-0.203	0.073	0.435	**0.576**
aCL2981Contig2	Lactoylglutathione lyase	0.110	-0.098	-0.131	-0.165	0.386	0.385	0.509	-0.012	0.333	-0.018	0.467	**0.570**
aC31101F04EF_c	Peroxidase 21 precursor	0.762	0.907	0.864	0.370	0.995	0.381	1.128	0.773	0.886	**0.662**	1.266	**0.518**
aCL8529Contig1	Peroxidase precursor	0.135	-0.284	**0.902**	0.174	0.099	0.038	0.083	0.032	0.477	-0.030	1.015	**0.461**
aCL7572Contig1	Cu-Zn superoxide dismutase	-0.155	0.079	**-0.684**	-0.499	-0.272	0.082	-0.045	-0.049	0.133	-0.131	0.251	0.125
aC31003C03EF_c	Catalase	-0.264	-0.427	-0.610	**-0.847**	-0.188	-0.370	-0.049	-0.376	-0.183	0.011	-0.115	-0.207
aCL3047Contig2	Cu/Zn superoxide dismutase	0.029	0.310	0.111	0.192	0.750	0.292	-0.101	0.644	0.037	0.333	0.088	**-0.307**
aCL74Contig2	Phospholipid hydroperoxide glutathione peroxidase	-0.318	-0.566	-0.391	**-0.927**	-0.370	-0.396	0.179	-0.252	0.120	-0.117	-0.767	-0.318
aCL63Contig3	Catalase	-0.295	-0.517	-0.423	**-0.894**	-0.121	-0.303	-0.222	-0.368	-0.238	-0.152	-0.340	-0.385
aCL3047Contig1	Cu/Zn superoxide dismutase	-0.432	0.532	0.040	0.185	0.015	0.039	-0.672	0.781	-0.477	0.417	-0.286	**-0.408**
aCL2220Contig2	Class III peroxidase	0.194	-0.313	0.478	-0.138	-0.156	-0.396	0.378	-0.131	0.354	-0.321	-0.065	**-0.482**
aCL8723Contig1	Putative sodium-dependent bile acid symporter	-0.032	-0.121	**-0.845**	-0.529	0.278	-0.468	0.595	-0.213	0.494	0.032	0.093	**-0.531**
aCL193Contig1	Dehydroascorbate reductase	-0.118	-0.291	-0.340	-0.262	-0.007	0.157	-0.350	-0.226	-0.253	-0.122	-0.506	**-0.561**
aCL1389Contig1	Glutathione reductase	0.095	-0.011	**0.756**	0.245	-0.854	-0.875	-0.397	-0.703	-0.688	-0.524	0.323	-0.694
aCL3818Contig1	Monodehydroascorbate reductase	-0.301	-0.024	**-0.818**	**-0.693**	-0.047	0.084	-0.282	-0.518	-0.731	**-0.894**	-0.506	**-0.781**
aC31305D02EF_c	Cu/Zn superoxide dismutase	-0.949	**1.009**	-0.487	0.641	-0.129	0.240	-0.980	1.256	-0.831	**1.060**	-0.434	**-1.286**
aCL36Contig2	Peroxidase precursor	-0.414	-0.009	**-1.509**	**-0.912**	0.755	0.146	0.372	0.180	-1.232	**-0.748**	**-2.354**	**-2.275**
aC08032B11SK_c	Peroxidase precursor	0.085	-	0.206	-	-	-	-	-	0.597	0.316	-	-

Citrus unigen	Description	4 days						14 days					
		AC		EC		1-MCP		AC		EC		1-MCP	
		F	A	F	A	F	A	F	A	F	A	F	A
Thioredoxin-dependent pathway_redoxin													
aC08015E04SK_c	Thioredoxin	-0.143	+	0.316	+	-0.048	+	-0.089	+	-0.153	+	0.179	+
aCL8673Contig1	Thioredoxin M-type 3, chloroplast precursor	-0.019	+	**0.653**	+	-0.046	+	-2.240	+	0.199	+	0.282	+
aCL709Contig1	Thioredoxin reductase 1	0.265	-0.167	**0.632**	0.537	-0.028	-0.390	0.209	0.288	0.090	0.338	0.524	**1.091**
aC07002C08SK_c	UPI000034F380; Glutaredoxin-like protein	-0.150	-0.307	0.104	0.008	0.122	0.392	-0.164	-0.135	-0.081	-0.013	**0.935**	**1.076**
aCL5456Contig1	Glutaredoxin-related-like protein	0.052	0.407	-0.110	0.157	-0.114	0.230	-0.024	-0.060	-0.011	0.240	0.322	**0.813**
aCL5576Contig1	Glutaredoxin-related-like protein	0.285	0.493	0.042	0.331	0.254	0.162	-0.030	0.019	-0.051	0.219	0.304	**0.782**
aC08008G07SK_c	Thioredoxin H	-0.348	-0.464	0.204	0.241	-0.400	-0.141	**-1.100**	-0.535	-0.978	**-0.548**	**-0.894**	**0.710**
aC08011E03SK_c	Thioredoxin X, chloroplast precursor	-0.224	0.235	0.133	0.234	-0.089	0.146	0.186	0.227	0.325	0.199	**0.479**	**0.394**
aCL18Contig3	Thioredoxin H	-0.202	0.017	0.120	0.267	-0.440	-0.129	**-0.588**	-0.333	-0.665	-0.248	-0.223	**0.292**
aCL4011Contig1	Thioredoxin X, chloroplast precursor	-0.242	**-0.934**	**-1.172**	**-1.057**	0.367	0.116	0.609	-0.393	0.523	-0.209	-0.519	-0.160
aCL130Contig3	Glutaredoxin	-0.374	-0.336	-0.350	-0.430	-0.391	-0.381	**-0.983**	-0.587	-0.756	**-0.609**	-0.682	-0.251
aCL4509Contig1	Chloroplast thioredoxin M-type	0.048	-0.134	-0.079	-0.017	-0.050	-0.021	-0.222	-0.088	-0.097	-0.193	-0.352	-0.258
aCL2621Contig1	Glutaredoxin precursor	-0.097	-0.158	-0.179	0.037	-0.261	-0.066	-0.179	-0.143	-0.266	-0.242	**-0.534**	-0.288
aCL6997Contig1	Putative glutaredoxin	-0.200	-0.150	-0.228	-0.258	-0.286	-1.160	-0.465	-0.159	-0.434	-0.258	-0.537	**-0.432**
aCL1978Contig1	Thioredoxin F-type, chloroplast precursor	-1.039	**-0.887**	**-1.472**	**-0.959**	-1.265	-0.774	-0.824	-0.577	-0.922	-0.704	-0.941	-0.541
aCL1232Contig1	Putative thioredoxin m2	-0.125	0.075	-0.129	-0.138	-0.040	-0.010	0.206	-0.159	0.060	-0.021	-0.179	**-0.576**
aC08001H10SK_c	Thioredoxin family Trp26-like protein	0.103	0.495	-0.695	**-0.757**	-0.078	-0.142	0.382	**0.769**	0.585	0.662	-0.447	**-0.689**
aCL3764Contig1	Ferredoxin-thioredoxin-reductase catalytic subunit B precursor	-0.303	-0.183	-0.457	-0.353	-0.706	-0.519	-0.442	-0.290	**-0.666**	-0.526	**-0.894**	**-0.742**
aCL149Contig1	Thioredoxin H-type	-0.289	-0.356	-0.301	-0.621	-0.616	-0.881	-0.459	-0.853	-0.678	-0.701	-0.519	**-1.265**
aC07008A11SK_c	Thioredoxin-like 5, chloroplast precursor	-0.612	**-0.861**	**-0.728**	**-1.047**	-0.160	-0.679	-0.607	-0.556	-0.602	-0.526	**-1.283**	**-1.442**
Miscellaneous													
aC08027E03SK_c	Nectarin 5	0.180	2.112	**1.167**	**3.157**	0.828	3.400	-2.829	1.816	-0.975	1.572	**1.017**	**5.469**
aCL1084Contig1	CPRD2 protein	0.741	0.534	**1.607**	**1.330**	0.585	0.992	-0.335	0.168	0.284	0.350	**1.906**	**3.696**
aCL494Contig3	Glycolate oxidase	0.082	0.000	0.021	0.242	0.247	0.438	-0.008	-0.109	-0.184	0.113	0.951	**1.711**
aCL5192Contig1	Putative short-chain acyl-CoA oxidase	0.030	-0.269	-0.156	0.144	0.161	-0.138	0.031	-0.218	0.071	-0.242	0.603	**1.245**
aC08018H06SK_c	Urate oxidase	0.489	**0.946**	**0.881**	**1.171**	0.568	0.090	0.979	**1.246**	**1.498**	**1.463**	**1.473**	**1.184**
aC01017A05SK_c	Amine oxidase	0.188	0.898	-0.296	0.550	0.704	0.404	0.823	0.852	0.744	**1.156**	**1.125**	**1.060**
aC31105C08EF_c	Acyl-coenzyme A oxidase 4, peroxisomal	-0.016	-0.155	0.031	0.025	0.120	-0.099	-0.045	-0.126	-0.017	-0.214	0.550	**0.938**
aCL784Contig1	Reticuline oxidase-like protein (berberine)	-0.429	0.179	0.160	**0.859**	-0.935	-0.592	-0.220	0.240	-0.421	0.278	-0.349	**0.738**
aCL4451Contig1	Zeta-carotene desaturase	0.119	0.230	0.093	**0.337**	-0.045	0.084	0.313	0.370	0.288	0.206	0.144	**-0.437**
aCL35Contig1	Beta carotene hydoxylase	0.579	**1.008**	0.337	0.639	-0.354	-0.327	0.188	-0.047	-0.146	0.317	0.252	-0.565
aCL3421Contig1	Zeaxanthin epoxidase	0.121	0.507	0.095	0.360	-0.445	-0.751	0.135	-0.315	0.126	-0.128	-0.434	**-0.841**
aC07010E12SK_c	Copper amine oxidase, putative	-0.555	-0.311	**-0.537**	-0.591	-0.537	-0.720	**-0.661**	**-0.741**	-0.598	-0.635	**-0.735**	**-1.057**
aCL1551Contig1	Zeaxanthin epoxidase	-0.005	**0.671**	-0.052	0.425	-0.755	**-0.841**	-0.254	-0.456	-0.285	-0.329	**-0.684**	**-1.160**
aC31706A07EF_c	Zeaxanthin epoxidase	-0.249	0.486	-0.262	0.341	-0.935	**-1.244**	-0.217	-0.538	-0.300	-0.353	-0.485	**-1.331**