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Transcriptomic analysis of a near-isogenic line of melon with high fruit flesh firmness during ripening

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Runnig Title: Transcriptomics of melon during ripening

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Transcriptomic analysis of a near-isogenic line of melon with high fruit flesh firmness during ripening

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BACKGROUND: A near-isogenic line (NIL) of melon (SC10-2) with introgression in linkage group X was studied from harvest (at firm-ripe stage of maturity) until day 18 of postharvest storage at 20.5°C together with its parental control (´Piel de Sapo´, PS).

RESULTS: SC10-2 showed higher flesh firmness and whole fruit hardness but lower juiciness than its parental. SC10-2 showed a decrease in respiration rate accompanied by a decrease in ethylene production during ripening, both of which fell to a greater extent than in PS. The introgression affected eleven VOCs, the levels of which during ripening were generally higher in SC10-2 than in PS. Transcriptomic analysis from RNA-seq revealed differentially expressed genes (DEGs) associated with the effects studied. For example, 909 DEGs were exclusive to the introgression, and only 23 DEGs were exclusive to postharvest ripening time. Major functions of the DEGs associated with introgression or ripening time were identified by cluster analysis. About thirty-seven genes directly and/or indirectly affected the delay in ripening of SC10-2 compared with PS in general and, more particularly, the physiological and quality traits measured and, probably, the differential non-climacteric response. Of the former genes, we studied in more detail at least five that mapped in the introgression in linkage group (LG) X, and thirty-two outside it.

CONCLUSION: There is an apparent control of textural changes, VOCs and fruit ripening by an eQTL located in LG X together with a direct control on them due to genes presented in the introgression (*Cm*TrpD , *Cm*NADH1, *Cm*TCP15, *Cm*GDSL esterase/lipase and *Cm*NAC18).

Keywords: *Cucumis melo* L., fruit quality traits, fruit senescence, postharvest quality, RNA-seq, texture.

INTRODUCTION

Fruit ripening in melon (*Cucumis melo* L.) is characterized by a series of physiological, biochemical and organoleptic changes, as a consequence of a genetic program involving a coordinated cascade of responses that start in the placental tissue of the fruit and end in the rest of the mesocarp, with noticeable differences between climacteric and non-climacteric types.[1,2,3] Non-climacteric melon fruit ripening is still poorly understood, hindering the application of postharvest techniques to delay ethylene-independent processes such as flesh softening or the production of certain aromas.[4,5]

New genetic and genomic tools are available in melon for studying fruit ripening including collections of near-isogenic lines, tilling platforms, saturated genetic maps, the genome sequence, and many Quantitative Trait Loci (QTLs) and eQTLs positioned on the genetic map, gene expression atlas, etc.[6,7,8] However, this species still presents a challenge because of the size of its fruit and the difficulties in establishing the exact degree of maturity for harvesting.

Several collections of near-isogenic lines have recently been developed in this species. One of them was obtained by crossing the *Charentais* type *Védrantais* (*C. melo* L. subsp. *melo*, Cantalupensis Group) with the Japanese Ginsen makuwa cultivar (*C. melo* L. subsp. *agrestis*, Makuwa group),[9] several QTLs related to quality traits were reported in introgressions in linkage group (LG) X. Another involved crossing ´Piel de Sapo´ (*C. melo* L. subsp. *melo*, Ibericus Group; based on a recent classification[10] with dudaim (*C. melo* sp. *agrestis*, Dudaim group).[11] Recently, Pereira *et al.*[12] obtained two QTLs more in LG X. However, the most widely studied collection for flesh firmness (at least at harvest) was developed using exotic non-climacteric accession PI161375 (ssp. *agrestis*) as donor and the non-climacteric Spanish cultivar PS as recurrent parental.[13,14]

RNA-Seq technology has also been applied for transcriptomic analysis during melon fruit ripening and to determine QTLs, expression QTLs (eQTLs) and candidate genes related to fruit quality.[15,16,17] These authors concluded that the upregulation and downregulation of multiple set of genes act coordinately during fruit ripening, although environmental and seasonal effects need to be taken into account.[4,18] Also, genes of β-D-xylosidase, glyoxysomal malate synthase, chloroplastic anthranilate phosphoribosyltransferase (MELO3C011963), and histidine kinase (MELO3C020055) have been associated with flesh firmness.[19]

The aroma profile together with textural traits are efficient traits for discriminating climacteric NILs from non-climacteric ones at harvest or during postharvest,[20,21,22] but little information is available about aroma formation in non-climacteric melons, particularly during postharvest ripening[23] and in non-climacteric NILs during ripening.

One near-isogenic line (NIL) developed by Eduardo *et al.*[13] (SC10-2) contains QTLs that affect flesh properties: for example PI161375 allele (vs. PS) increases flesh firmness and flesh proportion vs. placental tissue at harvest[14,24] and reduces flesh juiciness, extractable juice, juice density and titratable acidity but increases pH, dry matter and the flesh lightness colour parameter.[25] SC10-2 also shows differential volatile organic compounds (VOCs) at harvest, lacking some compounds that are present in the PS parental, a pattern which is associated with delayed ripening at harvest.[24] Finally, SC10-2 in fresh-cut cubes also showed reduced juice leakage compared with PS during postharvest cold storage,[26] but a certain risk of cracking during preharvest.[27]

The aim of this study was to analyze and compare the transcriptomes of the NIL SC10-2 and its PS parental during ripening to reveal the genes associated with the introgression during melon postharvest ripening (particularly those associated with textural traits and VOCs), and also to provide further insights for identifying key potential pathways and regulators.

MATERIAL AND METHODS

Plant material, crop management experimental design and sampling

Fruits obtained from plants of the inbred parental *C. melo* ´Piel de sapo´ (PS), *inodorus* type, and the NIL SC10-2 from the collection developed by Eduardo *et al.*[13] were analysed. SC10-2 contains an introgression in homozygosis that covers the entire LG X from the Korean accession ´Shongwan Charmi´ (PI 161375) in a PS genetic background (Eduardo et al., 2005).[13]

Soil preparation, fertigation, plant protection, and other growing practices were those commonly used for melon cultivation in the Mediterranean conditions in Torre Pacheco (Murcia, Spain).[20, 22] To reduce fruit cracking, the measures reported by Fernández-Trujillo *et al.*[27] were followed. The experiment was conducted in the “Centro Experimental de Formación y Experiencias Agrarias” (CIFEA) located in Torre Pacheco (Murcia, Spain). The field was divided into rows 2 m apart, in which each replicate consisted of six plants 1.5 m apart, in parallel rows. Twelve replicates of PS and seven of SC10-2 were planted. The plantation was surrounded by a border of the cultivar ´Nicolás´ (Syngenta Seeds).

The fruit harvest and maturity indexes were slightly modified versions of those reported for non-climacteric melons.[4] Minimum harvest indexes were the presence of a well formed and defect-free fruit, firm, well healed and dry epidermis with lignified netting, high density, absence of trichomes, dark-green skin color, withering of the stem and leaf close to the fruit peduncle, peduncle suberization, and light yellowing of the ground spot. The most common harvest indices for both SC10-2 and PS were the rind netting and, in some fruit, an annular ring or yellow color around a partly suberized peduncle,[27] light yellowing of the ground spot (particularly in PS), and a slight suberized crack around the peduncle, and dark blue-green skin color (in SC10-2).

The harvest season lasted about 2 weeks in both lines, but all the fruit for this experiment (three different biological replicates per line and/or storage time for transcriptomic analysis; more fruit for the study of physiological traits) were collected on the same day. PS was harvested about one month later than SC10-2 (7 July for PS; 9 August for SC10-2), due to the later ripening of this NIL[24] and to the rain that fell during flowering, which provoked flower and fruit abscission in May. Fruits were harvested by an expert over a period of two weeks during morning hours (05.45 h to 10.00 h, at a usual temperature of 21-26 °C. Total soluble solids and flesh firmness were used to assess the differences in maturity at harvest.[25, 28] Fruit in the firm-ripe stage of maturity were used in this experiment after storing fruit for 18 days at 20.5 ± 0.6 °C and a relative humidity of 88.2 ± 5.4 % (means ± SD, n=3 biological replicates).

Fruits were immediately analysed after their arrival in the laboratory or during the postharvest storage. Flesh sampling was carried out following the methodology previously reported.[25] After storage, samples lyophilised according to Dos-Santos *et al.*[29]

Respiration rate, ethylene production

Both physiological measurements were made in another lot of individual fruit (n=6 of different biological replicates in firm-ripe stage of maturity) during postharvest ripening of 18 d at 20.5

°C and 88% relative humidity. The static method[30] was followed for gas sampling and analysis by gas chromatography of carbon dioxide and ethylene.

Textural traits

Whole fruit hardness (WFH) was determined at the equator (lateral hardness) as previously reported for measuring the compression force (in N) to achieve 2 mm deformation.[24] Flesh firmness (FF), flesh juiciness (FJ) and juice density (JD) were measured according to the methodology previously reported.[25,28] The results were expressed in N, grams of juice per kg fresh weight or kg juice per m^3 juice, respectively.

Volatile organic compounds (VOCs)

To analyze volatile organic compounds, the juice extracted from melons was filtered through a four-layer cheesecloth. After 3 min at 23 °C, the mixture containing 28.6% *v*/*v* of saturated $CaCl_2$ solution and the rest of the juice was poured into sterile polypropylene vials, which were stored at −80 °C until solid-phase microextraction and analysis by gas chromatography mass spectrometry.[4,31]

RNA extraction

The RNA extraction was performed using the TRI Reagent RNA isolation protocol (1 mL per 20–30 mg of lyophilized tissue per extraction) and treated with DNAse.

mRNA library preparation and sequencing

The library from DNA free total RNA was constructed following the TruSeq™ Stranded mRNA Sample Preparation kit protocol (Illumina Inc., Redwood. CA, USA).

The libraries were sequenced using TruSeq SBS Kit v3-HS, in paired end mode with a read length ranging from 35 to 76 bp by the National Centre of Genomics Analysis (CNAG) in Barcelona (Spain). A fraction of a sequencing lane on the Illumina HiSeq2000 sequencing system (Illumina, Inc.) was used to generate 6-12 million Paired End reads Passing Filter for each sample.

A quality read assessment was performed with FastQC package.[32] These reads were mapped against the *C. melo* genome CM3.5.1 (http://melonomics.cragenomica.es/) using the Hisat2 mapper,[33] counting the number of reads mapped to transcripts with StringTie.[34] This counting was guided using the genome annotation, and a unified set of transcripts was created for the samples analyzed. Then, a Fragments Per Kilobase of transcript per Million (FPKM) table with gene expression for each sample was generated and used to assess the expression profiles of each sample by principal components analysis (PCA). Expression profiles showed high differences between samples due to ribosomal genes expression, so this were removed from further analysis steps. Differential expression analyses of both lines over time were run using the Bioconductor package Ballgown,[35] using FPKMs as measurement of gene expression. Tables of DEGs, considering the effect of the introgression or the postharvest ripening time, were obtained separately. Mev (RNA-Seq analysis in MeV[36,37] was used to run PCA analyses on DEGs and separate those genes into expression profile clusters. These clusters were calculated by k-means algorithm with Pearson correlation as metric and FPKMs as measurement. GO terms enrichment analyses were run for each one with the Blast2GO package.[38]

Assessment of introgression effects on textural traits and VOCs

The experiment was analyzed by a two-way ANOVA using introgression (I= SC10-2 or PS) and postharvest ripening time (RT= 0, 4, 8, 12, 18 d) as factors followed by an LSD test at p=0.05 for the main effects or I x RT interaction. For the DEGs, the significant effects of the introgression (effect I alone) or the combined effect of postharvest ripening time and the interaction I x RT were calculated. The main introgression effects of SC10-2 were grouped into effects above or below the PS.

Association between quality traits and DEGs

A two-way hierarchical clustering (HC), using Euclidean distance as the similarity measure and Ward's linkage, was performed for analysing similarities between thirty-seven DEGs (Table 1) and the quality traits measured (textural traits and VOCs) over postharvest ripening time. Scaled and log-transformed data were presented in a heatmap (where columns are samples and rows are variables) including two dendrograms, for the samples and variables, to visualize the results of the clustering. The similarities between samples were explained by similarities with respect to the values of variables.

RESULTS

Physiological behaviour and textural traits

The depletion in respiration rate and ethylene production were most pronounced during the first four days of postharvest ripening and the rates of SC10-2, particularly of ethylene production, were generally below those of PS (Fig. 1). Early or late harvested fruits showed, respectively, higher or lower respiration and ethylene production rates irrespective of the line (data not shown). SC10-2 could be stored for more than 40 d and PS for around 30 d. The main problem of extending fruit storage further, particularly at high relative humidity levels, is flesh sugar loss and fungal decay (*Fusarium* sp.), particularly at the peduncle (data not shown).

Flesh firmness and whole fruit hardness were always higher in SC10-2 than in PS (fig. 2). The firm-ripe fruit of the NIL SC10-2 was slower to ripen postharvest than PS, as revealed by its slower softening (higher whole fruit hardness and flesh firmness during ripening and reduced juiciness (introgression and postharvest ripening time significant at $P<0.05$; Fig. 2). Juice density (overall 1017 ± 4 kg·m^{-3}) did not change significantly in either line.

Volatile organic compounds

During postharvest storage (Fig. 3) two significant introgression x ripening time interactions ($P<0.05$) were observed for some groups of VOCs. After 4 d, the relative levels of acetate esters were higher in PS than in SC10-2. The same was true for non-acetate esters but after 8 d, while the concentration of other VOCs abruptly also increased after 12 d of storage in SC10-2 compared with PS levels. The relative levels of aldehydes, alcohols, acids and terpenes showed generally higher levels in SC10-2 than in PS (introgression significant, $P<0.05$; Fig. 3). Aldehydes, alcohols and terpenes followed a similar pattern during ripening, with a maximum after 4-8 days and decreasing thereafter (time significant, $P<0.05$; Fig. 3).

A total of thirteen individual VOCs showed significant effects for the factors studied during storage (Fig. 4), all of them belonging to four compound classes (aldehydes, ketones, alcohols and sulphur-derived compounds). Two compounds (1-phenylethanone and dodecanal) showed significant introgression x ripening time effects ($P<0.05$), because of the differences in their respective patterns of ripening in both lines (convex for SC10-2; concave for PS). A total of eleven individual VOCs of different classes showed a significant introgression effect according to the two-way ANOVA (Fig. 4), most of them alcohols or aldehydes with lower levels in PS than in SC10-2 during ripening (methanethiol, S-methyl ethanethioate, hexanal, octanal, (Z)-non-6-enal, nonanal, decanal, 4-isopropylcyclohexanol (isomer 1), 2-ethylhexan-1-ol, nonan-1-ol, (E)-4-phenylbut-3-en-2-one). Decanal and hexanal also showed a significant time effect together with nonanal but decreased with the ripening time ($P<0.05$).

Effect of LG X introgression on textural traits and VOCs during ripening

Negative effects on the mean respiration rate and ethylene production rates and flesh juiciness were found in PS, while flesh firmness and whole fruit hardness showed an opposite trend**.** As regards the VOCs and considering the effects reported in the previous section, the introgression affected aldehydes (hexanal, octanal, (Z)-non-6-enal, nonanal, decanal); alcohols (4-isopropylcyclohexanol (isomer 1); 2-ethylhexan-1-ol; nonan-1-ol), ketones ((E)-4-phenylbut-3-en-2-one) and sulphur-derived compounds (methanethiol, and S-methyl ethanethioate). Two time-dependent effects were observed for 1-phenylethanone and dodecanal.

Differential expression analysis

PCA analysis showed expression differences between groups and low variability within groups, so further steps in the analysis could be done without any concern about samples' expression profiles. As expected, the PCA based on a comparison between lines with time separated SC10-2 from PS better than the other PCA involving ripening time (Supplementary Figs. 1 and 2, respectively).

A total of 2954 DEGs were found by comparing both lines (i.e. considering the introgression factor or the interaction introgression x ripening time; Supplementary Table 1). A total of 2068 DEGs changed during postharvest ripening in both lines (Supplementary Tables 2 and 3), while 2045 of the formers were also DEGs, as seen from the comparison between lines over time. Therefore, 23 DEGs were exclusive to the postharvest ripening time effect and with no introgression or introgression x ripening time effects (Supplementary Table 3). Only 909 of the 2954 DEGs found for introgression showed a significant effect for introgression but did not appear in the DEGs when the factor ripening time was analyzed (Supplementary Table 4), making them the most interesting ones for this study.

During postharvest ripening, most of the identified DEGs were downregulated to a greater degree in SC10-2 than in PS but accounted for a smaller proportion of the total DEGs than in PS (Fig. 5). Comparing lines during ripening time (introgression effect), most of the upregulated DEGs in almost all of the functional categories were more abundant in SC10-2 than in PS (Fig. 6), but, in contrast to the first factor studied (ripening time effect), some DEGs were upregulated in some biological processes (such as the negative regulation of cell growth, the biosynthesis of indole-containing compound, mRNA 3'-end processing, jasmonic acid mediated signaling and the initiation of DNA replication (Fig. 6).

Overall, the functions of the most abundant DEGs associated with the postharvest ripening time factor or I x RT interaction (Fig. 5) were mRNA metabolic process; lipid A biosynthetic process; mitotic S phase; glycolytic process and gluconeogenesis (Supplementary Fig. 3).

On the other hand, the most abundant functions of the DEGs associated with the introgression were as follows: DNA strand elongation involved in DNA replication; zinc ion binding; RNA binding; chloroplast stroma; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen; hydrolase activity, acting on glycosylic bonds; monooxygenase activity; positive regulation of growth rate; transcription from RNA polymerase II promoter (Fig. 6).

Cluster analysis. Seven clusters were found when the introgression effect was studied in a comparison of lines over time (Fig. 7; Supplementary Table 1). However, considering the expression patterns during postharvest ripening time, we classified the DEGs into six main clusters (Fig. 8; Supplementary Table 2).

As regards the study of clusters involving introgression differences over time (Fig. 7), the most noticeable differences were the presence of 30% of total DEGs with upregulation of SC10-2 vs PS (clusters 1.1, 1.3 and 1.6) and 34.3% with minor differences but the same trend except at harvest and after 12 days of ripening (cluster 1.2). These clusters were associated with the mRNA metabolic process, the response to abscisic acid, kinase activity, carbohydrate derivative biosynthetic processes, etc. (Supplementary Fig. 4). By contrast, only 7.3% of DEGs (cluster 1.7) were clearly upregulated in PS compared with SC10-2, which was associated with the nucleolus, small molecule metabolic processes and lyase activity. However, 28.5% of DEGs (clusters 1.4 and 1.5) showed the same trend but only from harvest up to 4 or 8 d, probably due to different responses between lines to oxidative stress, the polysaccharide metabolic process or zinc ion binding, etc. (Supplementary Fig. 4). Clusters 1.2, 1.4 and 1.5 showed a noticeable introgression x ripening time interaction (Fig. 7).

Generally, the genes expressed in the clusters were more abundant in PS than in SC10-2 considering both factors (Supplementary. Figs. 3 and 4). In general, the study of clusters referring to postharvest ripening time revealed that most of the DEGs related with this factor were upregulated from harvest levels, peaking after 4, 8 or 12 d of postharvest ripening (clusters 2.2, 2.3, and 2.4; 47.1% DEGs; Fig. 8). Also, clusters 2.5 and 2.6 represent genes highly expressed after 4 d of ripening and peaking after 18 d (17.6% DEGs; Fig. 8). In all the clusters except cluster 2.1 (35.3% of total DEGs, downregulated since harvest), slight introgression x ripening time interactions were evident (the lines during ripening tending to cross). Cluster 2.1 reflects downregulation of the mRNA metabolic process, the RNA biosynthetic process or cellular macromolecule biosynthetic process, among others (Supplementary Table 2). By contrast, the rest of the clusters mostly represent upregulated genes associated with processes such as transferase of hexosyl groups, binding (ATP, metal ion, RNA, zinc ion, coenzyme), mRNA metabolic process, glycolytic process, cell wall, gluconeogenesis, etc. (Supplementary Fig. 3).

Selected DEGs study. Overall, we selected and studied a total of thirty-seven differentially expressed genes (DEGs) as a result of the introgression and/or postharvest ripening time factors (nineteen of the selected ones) that were involved in different pathways and functions (Table 1; Supplementary Tables 4 and 5). Among them, two selected DEGs involved in primary metabolism, ATP-citrate synthase alpha chain protein (*Cm*ACLA-1), which is involved in ligase and catalytic activity, Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial (*Cm*SCOA) involved in pyruvate metabolism and Citric Acid (TCA) cycle, were generally upregulated in SC10-2 compared with PS (Fig. 9). However, some slight differences in expression between NIL SC10-2 and PS, particularly as regards postharvest ripening time, were found in four DEGs (*Cm*NADP, *Cm*ACLB-2, *Cm*SDHA).

An additional DEGs were selected considering the traits studied and postharvest fruit ripening: *Cm*LOX18, *Cm*AOS, *Cm*OPR2, *Cm*SWEET7, *Cm*DFR4, *Cm*PAL, *Cm*WRKY33, *Cm*GATA5, *Cm*TCP15, *Cm*GDSL esterase/lipase, *Cm*ERF027, *Cm*GDE4 and *Cm*ATC, and *Cm*TrpD were generally upregulated in SC10-2 compared with PS (Fig. 10) with some exceptions in the expression of *Cm*GDE4 and *Cm*ATC. In contrast, the genes of *Cm*ACO2, *Cm*ADH1, *Cm*CAD1, *Cm*NADH1 and *Cm*NAC18 were downregulated (Fig. 10). Only *Cm*NADH1, *Cm*TCP15 and *Cm*GDSL esterase/lipase were located in LG (Table 1), while for the other differentially expressed genes, some eQTLs could be found within LG X). Two genes involved in aminoacid metabolism *(Cm*IIL1 and *Cm*FAH were downregulated in SC10-2 vs. PS, while *Cm*IPMI3 was upregulated (Fig. 10). Another two selected DEGs (*Cm*L-GalDH and *Cm*GME) involved in ascorbic acid metabolism were generally upregulated in SC10-2 vs. PS (Fig. 10).

Fourteen selected DEGs were significant for the introgression: *Cm*MADS-box, *Cm*NAC18, *Cm*CAD1, *Cm*NADP, *Cm*ACLB-2, *Cm*IIL1 and *Cm*ACO2, which were generally downregulated in SC10-2 vs. PS (Fig. 11) with some exceptions in *Cm*NADP, *Cm*ACLB-2 and *Cm*IIL1 and some introgression x ripening time interactions (levels of SC10-2 increased over time and remained constant in PS) such as in *Cm*NAC18 (Fig. 11). As regards *Cm*WRKY33, *Cm*ACLA-1, *Cm*FAH, *Cm*SDHA, *Cm*IPMI3, *Cm*SCOA, *Cm*L-GalDH and *Cm*LOX18, they were generally upregulated in SC10-2 vs. PS (Fig. 11) with some exceptions in *Cm*ACLA-1, *Cm*SDHA, *Cm*IPMI3, *Cm*SCOA and *Cm*L-GalDH was downregulated after 12 d (Fig. 11).

Some evident introgression x ripening time interactions were identified in some DEGs using ANOVA: *Cm*IIL1, *Cm*ADH1, *Cm*CAD1, *Cm*AOS, *Cm*SWEET7, *Cm*DFR4, *Cm*WRK33, *Cm*GDSL esterase/lipase, *Cm*ERF027, *Cm*GDPDL4, *Cm*NAC18, *Cm*ACT, *Cm*LGalDH and *Cm*ACLB-2 (Figs. 9, 10 and 11).

About 23 DEGs changed as time progressed and followed the typical trend to decrease from high harvest levels, or the contrary after 4-8 d of ripening (Table 1; Supplementary Tables 1 and 4; Fig. 12).

Association between selected DEGs and quality traits (textural traits, VOCs).

The analysis of the heatmap of the hierarchical clustering reveals a clear separation between SC10-2 and PS, and also from harvest to postharvest ripening time particularly in PS), and DEGs and quality traits could be grouped into eight clusters (Cx, x=1-8) according to their values in the NIL and PS (Fig. 13; Supplementary Table 6). In general, in most of the clusters and cluster subgroups (Gx, x=1-8) studied with the values above 0 represents PS samples while the values below 0 represented the NIL SC10-2, with some exceptions for example in C3-G1 and C4-G2. Some associations were apparently unexpected according with the DEG function of Table 1. Certain association among the selected DEGs and textural traits were found within two of the eight clusters (C4, subgroup G2; C8, subgroup G8). In C4, the subgroup G2 associated *Cm*WRKY33 (DNA binding transcription factor), textural traits (whole fruit hardness and flesh firmness) and eight VOCs. In C8, two acetate esters were associated with *Cm*HK4-like gene and two textural traits (density and juiciness) (G8). In the former cases, PS levels were above SC10-2.

Of particular interest for postharvest ripening is the association detected in clusters C7 and C8 between some genes associated with aroma production or ripening with ester compounds (acetate, non-acetate or thioesters). For example, in C8 C8, two subgroups associated acetate and a sulfur-derived compound with *Cm*L-GalLDH (G6) or several thioester compounds, two ketones and isopropyl propionate with *Cm*NAC18 (G7). The main differences in both lines at harvest (caused mostly by the introgression) were due to nine DEGs (*Cm*ACLB-2, *Cm*FAH, *Cm*IIL1, *Cm*ALT-2, *Cm*NADP, *Cm*ACLA-1, *Cm*SCOA, *Cm*SDHA, *Cm*IPMI3), and eight VOCs (2-methylbutyl acetate, ethyl 2-methylpropanoate, methyl acetate, ethyl 2-methylbutanoate, (E)-pent-2-enal, unidentified (24.64), acetone, and 1-methyl-4-prop-1-en-2-ylcyclohexene) present in C7. Most of the previous DEGs at harvest (with the exception of *Cm*ALT-2; Fig. 4) were involved in the Kreb´s cycle (i.e., a clear association with differences in respiration rate between lines; Fig. 1). The main differences in both lines at postharvest ripening times 8, 12 and 18 were due to the four ester VOCs (2-methylbutyl acetate, ethyl 2-methylpropanoate, methyl acetate and ethyl 2-methylbutanoate and the DEG *Cm*ACLB-2.

The subgroup G4 of C7 was associating several volatiles and two important genes of secondary metabolism (ethylene biosynthesis such as *Cm*ACO2) and a transcription factor (*Cm*MADS-box) with higher levels in PS than in SC10-2. In C1, VOCs from 2-(2,2,3-trimethylcyclopent-3-en-1-yl) acetaldehyde up to tetradecanal showed differences due to the introgression but postharvest-ripening time dependent particularly with certain downregulation in time 12 in SC10-2 vs PS. In C2, the same situation that in C1 was true with other time-dependent trends depending on the introgression effect with volatile overproduction in SC10-2 particularly during the first days of ripening. In C3 the subgroup G1 was detected with certain association between *Cm*LOX18 (lipoxygenase activity) and methanethiol. In C7, the subgroup G5 associated two volatiles (1-tridecanol, isobutyl-benzoate with a cinnamyl-alcohol dehydrogenase (*Cm*ACLB-2).

DISCUSSION

Quality and physiological traits vs. gene expression

Primary metabolic changes vs gene expression. As is known, fruit ripening is classified as climacteric and non-climacteric, depending on tlhe presence or absence of a transient rise in the respiration rate and the production of autocatalytic ethylene.[5,21,39] Because the respiration rate was lower in SC10-2 than in PS (Fig. 1), it was thought to be of interest to check some genes of mitochondrial enzymatic activities, transporters that are involved in metabolic changes during fruit development,[40] and genes of the tricarboxylic acid (TCA) cycle.[41] In fact, these differences between the NIL and PS in DEG of the TCA cycle were confirmed by using a heatmap (Fig. 13; Supplementary Table 6). In particular, NADH:quinone oxidoreductase *Cm*NADH1 (MELO3C012476) expression, the largest complex of the respiratory chain[42], was higher in PS than in SC10-2 throughout the experimental time (Fig. 10), which would partly explain the higher respiration rate of PS (Fig. 1). This difference could also be attributed to several genes that codify for proteins that act as enzymes of the aerobic respiratory chains.[43,44] For example, isocitrate dehydrogenase (*Cm*NADP; MELO3C021563) expression was generally higher in PS than in NIL SC10-2 throughout the postharvest ripening time (Fig. 9). However, the mitochondrial succinate dehydrogenase (*Cm*SDHA) first decreased before increasing during the last few days of ripening, but differences between lines were negligible when both factors (introgression and ripening time) were considered (Fig. 11).

For ATP-citrate synthase, two genes were differentially expressed in our experiment: ATP-citrate synthase alpha chain protein (*Cm*ACLA-1; MELO3C010675) and ATP-citrate synthase beta chain protein 2-like (*Cm*ACLB-2; MELO3C011482) (Fig. 9). After decreasing from harvest to 4 d *Cm*ACLA-1 was higher in the NIL SC10-2 than in PS. By contrast, *Cm*ACLB-2 expression was higher in PS (Fig. 11), probably because of the contribution of ACL, which is necessary for the generation of the cytosolic pool of acetyl-CoA.[45,46] In fact, *Cm*ACLB-2 could be associated with formation of two acetate esters and perhaps two non-acetate esters (Fig. 13; Supplementary Table 6).

The expression of succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial gene (*Cm*SCOA; MELO3C002167) associated with GTP binding, ATP binding, succinate-CoA ligase (GDP-forming) activity, succinate-CoA ligase (ADP-forming) activity and ATP citrate synthase activity,[47] was not significantly different between PS and SC10-2 but the respiration rate followed a similar pattern (Figs. 1 and 9).

Postharvest ripening delay and textural traits vs gene expression. This paper confirms the effect of the long introgression covering the entire LG X[13] that contained the previously reported QTL *ff10.2* of flesh firmness and textural traits at harvest.[14,24,25] The introgression also delayed fruit ripening in general, as seen from by physiological traits (respiration rate, ethylene production, volatile production; Figs.1-4). Perpiñá *et al.*[9] reported QTLs affecting fruit ripening in a climacteric melon genetic background, including *ff.10* for flesh firmness at harvest, *al.10* for the suppression of the formation of abscission layer, *ar.10* that produced less aroma at harvest, or QTLs affecting soluble solids and sugar content. Due to the length of these introgressions in LG X, the effects on the aroma volatiles and textural traits could be due to independent genes, or to pleiotropic effects due to a unique gene.[24] In fact, the heatmap detected association between *Cm*WRKY33, textural traits and two VOCs (Fig. 13; Supplementary Table 6).

The candidate genes for *ff10.2* were *CmXTH5* and *CmEXP3*[14], but during postharvest ripening these genes did not show differential expression. Other authors[19] map candidate genes on LG X at harvest such anthranilate phosphoribosyltransferase: (*Cm*TrpD; MELO3C011963) o histidine kinase 4-like (*Cm*HK4-like; MELO3C020055). The gene *Cm*TrpD, with higher levels in SC10-2 than in PS, could be a putative candidate gene during postharvest and explained the differences due to the introgression in textural traits (Fig. 2). *Cm*TrpD plays a role in cell wall metabolism but in the presence of ethylene.[19] In tomato, QTLs affecting texture at harvest are distinguished from those affected softening and other ripening-associated textural traits during postharvest.[48]

The histidine kinase 4-like (*Cm*HK4-like) gene, due to the association with juice density and flesh juiciness affected by the introgression in LG X (Fig.13; Suppl. Table 4) and other traits important from fruit ripening point of view, would require further attention. Histidine Kinase 4 (HK4) and other plant hormones play essential and crucial roles in various aspects of Arabidopsis and generally plant growth and development [49] which maybe the case for *Cm*HK4-like in melon. HK4 positively regulates the cytokinin-signaling pathway as a direct receptor molecule, knowing that cytokinins are a class of phytohormones that promote cytokinesis in cell division in plant roots and shoots, and also in cell growth and differentiation.[49] Cytokinins also affect apical dominance, axillary bud growth, and leaf senescence.[50]

Several potential candidate genes have been proposed as being associated with melon textural traits during ripening (mostly firmness, *ffr10.2*, whole fruit hardness *wfhr10.2,* or flesh juiciness *fjr10.2*). This is common, as observed by the negative correlation between flesh firmness and juiciness, [25], because firmer fruit are usually less juicy.[25] Moreno *et al.*[14] reported *ff10.2* at harvest and the unpublished results of these experiments[25] would also confirm *wfh10.2*. However, juice density was not affected during ripening in contrast with the results of Obando et al.[25] who also reported the effect of the QTL of flesh firmness *fj10.2* but only at harvest time.

The expression of GDSL esterase/lipase (MELO3C011939) located in LG X was higher in SC10-2 than in PS (Fig. 10), and SC10-2 also showed lower ethylene production (Fig. 1). The expression of this gene could be associated with a delay or partial inhibition of some ethylene-dependent flesh or whole fruit softening in SC10-2 compared with PS, because GDSL expression in apple correlated negatively with ethylene production[51] and in tomato it was expressed in the epidermis of developing fruit.[52]

Of the potential candidate genes responsible for the increase in textural traits in SC10-2 compared with PS (Fig. 2), the glycerophosphoryl diester phosphodiesterase (*Cm*GDE1; MELO3C013101) gene has been found to play a role in plant cell wall remodelling.[53,54]

DEGs exclusive to postharvest ripening time. Of the 23 genes that changed over time (Table 1; Supplementary Tables 1 and 4; Fig. 12), we found typical ones in melon ripening changes such as polygalacturonase (*Cm*DHL92; MELO3C009970) (Table 1; Supplementary Tables 1 and 4; Fig. 12) associated with cell-wall disassembly[55] or other ongoing processes typical of maintaining homeostasis or hydrolase activity and hydrolyzing O-glycosyl compounds. For example, processes such as providing feed for diminished mitochondrial respiration during postharvest ripening (*Cm*MPC1; MELO3C007517) (Table 1; Supplementary Tables 1 and 4; Fig. 12), or increased protein detoxification (*Cm*DTX; MELO3C017343) (Table 1; Supplementary Tables 1 and 4; Fig. 12). Some of these genes, such as the one that is responsible for the increase of ABA receptors such as abscisic acid-insensitive 5-like protein 4 isoform X1 (*Cm*ABREX; MELO3C014384) (Table 1; Supplementary Tables 1 and 4; Fig. 12), or the gene that decreases in auxin-responsive protein (*Cm*IAA71; MELO3C000885) (Table 1; Supplementary Tables 1 and 4; Fig. 12), would deserve further investigation due to the possible similarity of non-climacteric ripening with the antagonist interaction of auxin and abscisic acid with ethylene during ripening in other non-climacteric and climacteric fruits.[56,57]

Physiological traits and gene expression. The expression of *Cm*ACO2 (MELO3C019735) increased during ripening, a trend that was more pronounced in PS than in SC10-2 (Fig. 10) (Fig. 11), which agrees with the faster ripening of PS (including higher level of respiration, ethylene production, and the synthesis of some ethylene-dependent VOCs, such as acetate esters and non-acetate esters; Figs. 1 and 4) in PS. *Cm*ACO2 and *Cm*MADS-box expression generally downregulated in SC10-2 vs PS (Figs. 10 and 11) also clustered with the level of four compounds unexpected that were generally more abundant in PS than in SC10-2 (C7, subgroup G4 of Fig. 13; Supplementary Table 6). The melon 1-aminocyclopropane-1-carboxylic acid oxidase gene (*Cm*ACO) is an ethylene-responsive gene that catalyses the conversion of ACC to ethylene during fruit ripening and is of greater importance in climacteric fruit.[2,58] However, *Cm*ACO2 has been mapped in LG VIII,[14] and consequently some eQTLs upstream of *Cm*ACO2 but affecting its expression should be mapping in LG X. On the other hand, other genes with no differential expression in our non-climacteric experiment such as *CmACO1* have been associated with ethylene biosynthesis, together with *CmACS1* and *CmACS5* in climacteric melon fruit ripening.[3]

More than four transcription factors were identified in our experiment; *Cm*WRKY33 (MELO3C009127), *Cm*TCP15 (MELO3C01208), *Cm*GATA5 (MELO3C023350) and *Cm*ERF027 (MELO3C005630) (Table 1). Almost all of them increased in SC10-2 more than in PS during the ripening time and therefore could be partially responsible for the delay of ripening in the NIL SC10-2 compared with PS.

The expression of *Cm*WRKY33 (ethylene-responsive gene during climacteric ripening,[59] *Cm*GATA5 (transcriptional regulators involved in metabolism regulation),[60] and *Cm*ERF027 (ethylene-inducible genes during fruit ripening)[61,62,63] decreased from their highest level of expression before 4 d of ripening but remained higher in SC10-2 than in PS throughout the postharvest ripening time (Figs. 10 and 11). The behaviour of these genes was apparently opposite to that of ethylene production, particularly during the first 4 days of non-climacteric melon ripening of both lines (Fig. 1), and so they could be associated with the ripening differences between climacteric and non-climacteric melon fruit.[21] Particularly *Cm*WRKY33 was found in the heatmap with association with textural traits (Fig. 13, Supplementary Table 6). *Cm*GATA5 could interact with cis-acting elements involved in the light regulation of nuclear genes encoding chloroplast glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and therefore glycolysis[64] or other processes such as ribosome biogenesis, mRNA metabolism or lipid A biosynthesis.[65,66]

Glycerophosphodiester phosphodiesterases (*Cm*GDPDL4; MELO3C013101) showed similar gene expression to GATA5 in our experiment, with higher levels after 8 d of ripening in SC10-2 than in PS (Fig. 10). This gene could be involved in fatty acid metabolism to further provide glycerol phosphate and alcohol resulting from the hydrolysis of deacylated glycerophospholipids.[67]

*Cm*NAC18 (MELO3C016540) expression was stable in SC10-2 but was present at higher levels than in PS, where it increased after harvest to reach levels similar to that of SC10-2 (Fig. 10). This *CmNAC-NOR* domain transcription factor was expressed in the flesh of both climacteric and non-climacteric melon types, but is probably transcriptionally regulated in non-climacteric types because it has been considered a candidate gene for the QTL *ETHQV6.3* of climacteric fruit ripening.[3] NAC transcription factor is a positive regulator of fruit ripening, affecting ethylene synthesis and carotenoid accumulation,[3,68] but NAC also interacts with other genes in the complex regulatory network of fruit ripening in tomato.[68] All the above information suggests a potential association of higher NAC levels with the delayed fruit ripening of the NIL SC10-2 compared with PS.

In our experiment, a MADS-box transcription factor was identified among the DEGs with higher relative expression in PS than in SC10-2 and decreasing with ripening time (Fig. 11). Some MADS-box genes are involved in the development and ripening of non-climacteric fruits such as bilberry[69] and strawberry.[56,70]

Postharvest VOCs vs gene expression. In previous investigations, noticeable differences were found between the aroma profile of NIL SC10-2 and the control PS at harvest.[24,71] Some VOCs were lacking from the NIL SC10-2 compared with PS [some ketones and alcohols, and one acid (e.g. 2-phenylpropanoic acid)], but also the concentration of aldehydes (e.g. 2,4-dimethylbenzaldehyde, 2-methylpropanal and 2-methylbutanal) were higher in the NIL.[24] In our experiment, too, the levels of many aldehydes (C6-up to C12) remained high during ripening (Fig. 4), in agreement with the above results at harvest, but ketone levels were similar, and acids were hardly present (data not shown). The NIL SC10-2 was characterized by a lower ketone content than PS.[24] In our experiment, aldehydes, alcohols, acids and terpenes were higher in SC10-2 than in PS during postharvest ripening, while the opposite trend was seen for acetate and non-acetate esters (Fig. 3). As regards other VOCs, they increased in SC10-2 and were higher than in PS at the end of the experiment (Fig. 3), which could be due to senescence processes.[22] Interestingly, the association among selected DEGs linked to DNA-binding, ATP-binding, or metal-ion binding (and in general the end of non-climacteric ripening) were more frequent with ester VOCs (see C7 and C8; Fig. 13; Supplementary Table 6).

As regards other metabolic pathways associated with the differences between PS and SC10-2 QTLs and volatiles, these were related in part to the free L-amino acid metabolism, in which phenylalanine, valine, isoleucine and leucine[24] are considered aroma precursors.[23] The higher aldehyde content was typical of the NIL SC10-2 and associated with its high flesh firmness at harvest compared with PS,[24] in agreement with our results (Figs. 2 and 3). Aldehydes are key-flavor compounds synthesized from α-keto acids particularly in melon fruit.[23]

The expression of GDPDL4 (MELO3C013101) in our experiment also was higher in SC10-2 than in PS from harvest to 8 d of postharvest ripening (Fig. 10), which might explain the abundance of alcohols in this NIL (Fig. 3), as explained above for *Cm*GDPDL4 gene. In this case, glycerophosphodiester phosphodiesterase (GDPD) hydrolyzes the glycerophosphodiesters into sn-glycerol-3-phosphate (G-3-P) and the corresponding alcohols,[72] particularly in fruit tissue.[73] GDPD have also been seen to be involved in the generation of phosphatidic acid, a precursor of diacylglycerol and inorganic phosphate by phosphatidate phosphatase,[74,75] or in the degradation of phospholipids into diacylglycerol and inorganic phosphate.[76]

*Cm*LOX18 (MELO3C024348) was highly expressed in the NIL SC10-2 compared with PS, which had higher levels of aldehydes, terpenes, alcohols and other VOCs than PS (Figs. 3; 10 and 11). Certain association between *Cm*LOX18 and methanethiol production was found (Fig. 13; Supplementary Table 6), perhaps because of its aminoacid precursor degradation such as methionine or phenylalanine (see aminoacid metabolism below). *Cm*LOX genes are involved in generating fruit aroma in melon.[77,78] Our results support that this is the LOX family gene responsible for producing LOX enzyme during ripening to form C6 VOCs such as hexanal, (Z)-3-hexenal, and (Z)-3-hexenol in fruit, and is also possibly involved in the formation of straight-chain ester.[78]

The enzymatic reaction of LOX causes polyunsaturated fatty acids, such as linoleic acid and linolenic acid, to generate hydroperoxide (HPO).[79,80] HPO is catalyzed by hydroperoxide lyase (HPL) to produce aldehydes, which are catalyzed by alcohol dehydrogenases (ADH) to produce alcohols.[77,81] The final step in ester biosynthesis is catalyzed by alcohol acyl-transferase (AAT).[82,83] Apparently, the higher expression of *Cm*ADH1 (MELO3C019548) in PS than in SC10-2 would explain the differences in aroma production between lines because in PS the former volatile metabolism would be more advanced and produce alcohols as precursors of the esters (Fig. 3). In fact, Chen *et al.*[85] observed the upregulation of *Cm*ADH1 after the addition of aldehydes, which indicated its potential function in aroma volatile or ester synthesis. Also, in climacteric tomato fruit, Moummou *et al.*[85] suggested a function of ADH1 of supplying C5 and C6 volatiles from the lipoxygenase pathway. Alcohol acetyl transferases (*Cm*AAT1 and *Cm*AAT2) showed similar relative expression in both lines in our experiment (data not shown), and it is known that the expression of AAT in PS is very low.[23] Therefore, we conclude that *Cm*ADH1 is a key enzyme, particularly in PS aroma formation.

12-oxophytodienoate reductase 2 (*Cm*OPR2; MELO3C008075) expression was also higher in SC10-2 than in PS (Fig. 10). Therefore, *Cm*OPR2 may increase the activity of the β-oxidation pathway because the oxophytodienoate reductase family (OPR) is expressed throughout the plant and co-localises with enzymes involved in the β-oxidation of very long fatty acids in peroxisomes.[86] In fact, the levels of most of the aldehydes in SC10-2 were higher than in PS (Fig. 3), and, consequently, alcohol dehydrogenase 1 (*Cm*ADH1; MELO3C019548) and cinnamyl alcohol dehydrogenase 1 (*Cm*CAD1; MELO3C018492) genes showed lower expression in SC10-2 than in PS. *Cm*CAD1 expression was also lower in SC10-2 than in PS (Fig. 11), which might have some influence in the conversion of cinnamyl aldehydes into alcohols, using NADPH (quinone oxidoreductase) as a cofactor.[87]

In our experiment, the expression of allene oxide synthase gene (*Cm*AOS; MELO3C010910) was higher in SC10-2 than in PS (Fig. 10). *Cm*AOS could be involved in the jasmonic acid metabolism from hydroperoxides because AOS and allene oxide cyclase mediated in the branch of α-linolenic acid metabolism for the formation of jasmonic acids.[2,88] Two AOS isozymes identified in oriental melon fruit catalysed 10-OPDA and 12-OPDA formation, and other AOS isozymes, identified in different ripening stages, are differently regulated by genetic and environmental factors.[2] Concomitant with jasmonic acid biosynthesis and ethylene production, AOS was downregulated during fruit development but increased again in the last stage of peach fruit development.[89] However, in SC10-2 the hypothetical stimulation of ethylene production by *Cm*AOS during the first 8 d of ripening was not evident (Figs. 1 and 10).

Aminoacid metabolism. The 3-isopropylmalate dehydratase small subunit 3-like (*Cm*IPMI3; MELO3C005518) was generally higher in the NIL SC10-2 than in PS, except at 12 d (Fig. 10 and 11), in contrast to the behaviour of 3-isopropylmalate dehydratase large subunit (*Cm*IIL1; MELO3C003344) at harvest and in senescence (Figs. 9 and 11). Generally, 3-isopropylmalate dehydratase catalyses the stereo-specific isomerisation of 2-isopropylmalate and 3-isopropylmalate, via the formation of 2-isopropylmaleate, which is the second step in the biosynthesis of the aminoacid leucine,[90] a potential precursor of some VOCs of interest here, such as 2-ethylhexan-1-ol, nonanol, or 4-Isopropylhexanol (isomer 1) (Fig. 4; Table 1).

By contrast, fumarylacetoacetase (*Cm*FAH; MELO3C007433) expression and alanine aminotransferase (CmALT-2; MELO3C010686) expression were always higher in PS than in NIL SC10-2 (Figs. 10 and 11). FAH is involved in the metabolism of amino acids (phenylalanine and tyrosine) and the catabolism of its derivatives,[90] Phe being of interest as a potential precursor of some VOCs of interest here such as methanetiol or S-methyl ethanethioate (Fig. 4; Table 1). ALT is active during melon ripening and it has positive correlation with chlorophyllase and carotenoid accumulation.[92]

Gene expression and other postharvest changes. Dihydroflavonol 4-reductase (*Cm*DFR4; MELO3C020508), the first committed enzyme of the flavonoid biosynthetic pathway including VOC regulation,[93] showed higher expression in SC10-2 compared with PS particularly after 4 days of postharvest ripening (Fig. 10).

Apparently in SC10-2, *Cm*PAL (MELO3C017811) gene expression is a response to late fruit ripening, which contrast with the lack of changes during ripening in PS (Fig. 10). Melon fruit phenylalanine ammonia-lyase (PAL), the first enzyme of phenylpropanoid biosynthesis, is transcriptionally induced in response to fruit ripening and *Cm*PAL gene expression follows the expression kinetics of the ethylene biosynthetic genes during fruit development.[94]

*Cm*ACT (MELO3C005591) regulatory domain expression showed higher levels in SC10-2 than PS during the first 8 days of postharvest ripening (Fig. 10), and the ACT was generally found in enzymes involved in amino acid and purine metabolism,[95,96] some of them probably associated with the formation of volatile precursors.

*Cm*TCP15 (MELO3C012086) expression was always higher in SC10-2 than in PS (Fig. 10). TCP proteins are involved in biological processes of potential interest for future studies in others aspects of factors affecting melon fruit ripening, such as hormone pathways,[97] mitochondrial biogenesis,[98] and regulation of the circadian clock.[99]

The higher expression of the bidirectional sugar transporter *Cm*SWEET7 (MELO3C016259) in SC10-2 compared with PS after 4 days of ripening (Fig. 10) could be related with fruit senescence, environmental adaptation, the sugar accumulation pattern, or other essential fruit biological processes.[100,101,102] Some QTLs in LG X associated with the soluble solids content and individual sugars (sucrose, fructose) in other genetic backgrounds have also been mapped[9]. Although sugars are not discussed here, SC10-2 is less sweet than PS at harvest. In fact, several QTLs that negatively affect sensory traits have been mapped at harvest in LG X (sweetness, taste and global sensorial quality appreciation) compared with PS, due to lower sucrose, total sugars and sucrose equivalents.[103] One hypothesis for the mechanism of *Cm*SWEET7 gene would be to delay ripening in order to supply additional sugar resources to the fruit metabolism in SC10-2. This hypothesis would agree with results in tomato, where SWEET transporter was also upregulated in the lines with a high fructose-to-glucose ratio.[102]

GalLDH catalyses the oxidation of the last precursor, L-galactono-γ-lactone, to ascorbic acid.[104] In our experiment, evidence of differences in ascorbate metabolism would include lower L-galactono-1, 4-lactone dehydrogenase (*Cm*L-GalLDH; MELO3C018576) relative expression with higher expression in PS than in SC10-2 until 8 d (Fig. 9 and 11). Other evidence is the report on one QTL that reduced levels of ascorbic at harvest in LG X.[103]

As regards GDP-mannose-3',5'-epimerase (*Cm*GME; MELO3C004377), in our experiment it showed higher expression in NIL SC10-2 than in PS but it decreased after 12 d

(Fig. 9). The GME, which converts GDP-d-mannose to GDP-l-galactose, is generally considered to be a central enzyme of the major ascorbate biosynthesis pathway in higher plants.[105] The formation of GDP-d-mannose is the initial step in the pathway of ascorbate biosynthesis, and GDP-d-mannose is also a known precursor for the synthesis of d-mannose, l-fucose and l-galactose, and therefore for hemicelluloses such as (galacto)glucomannans and for the pectin rhamnogalacturonan II.[106] This biosynthesis could be of importance for maintaining melon flesh firmness during ripening (Fig. 2).

General processes deduced from transcriptome analysis

As regards the comparison between lines, many of the genes downregulated in cluster 1.1 (Supplementary Table 1) were related with regulation of the cellular macromolecule biosynthetic process, the RNA biosynthetic process and other genes depending to the photosynthesis processes. The genes related to photosynthesis during fruit ripening are also downregulated in non-climacteric grape.[107]

As regards the postharvest ripening time effect (Supplementary Table 2), clusters 2.2 and 2.4 were the most closely associated with this effect (Fig. 8), a sharp rise in the expression of DEGs being evident in the two non-climacteric genotypes. The same is true for clusters 1.4, 1.5 and 1.6, considering the comparison between lines (Fig. 8; Supplementary Table 1). Most genes of both group of clusters were related to biosynthetic processes (Supplementary Tables 1 and 2), for example those related to ethylene-regulated and ripening-related genes,[108] including those involved in ethylene synthesis, fruit texture, and aroma volatile production.[5]

Considering the postharvest ripening time effect, most DEGs of clusters 2.3, 2.5 and 2.6 showed higher expression in PS than in SC10-2 and a trend to increase (Fig. 8). The same is true for clusters 1.5 and 1.6, but considering the comparison between lines over time (Fig. 7). The DEGs of the above-mentioned clusters were generally related to molecular function and cellular components (Supplementary Tables 1 and 2), and these genes affected in one way or another to flesh firmness and whole fruit hardness because they showed the opposite trend and led to fruit softening. As regards other non-climacteric NILs (i.e. SC7-2) with firm flesh and other climacteric melons and fruits in general, it has been reported that flesh textural changes are accompanied by loss of neutral sugars, solubilisation and depolymerisation of the polysaccharides of the cell wall, and rearrangements of their associations, as the result of the combined action of several cell wall-modifying enzymes such as polygalacturonase and others (see above), acting in both pectic and hemicellulosic fractions.[28,55] Consequently, it is these changes that probably make the PS fruit texture less resistant and juicier than SC10-2.

Implications for the future

The genetic changes described not only explain new aspects of the non-climacteric fruit ripening - such as the control of non-climacteric ripening, respiration and ethylene biosynthesis and action, texture, or aroma production - but also provide a few new ideas about the changes in different metabolic pathways. These could help growers and researchers to develop new melon varieties with good quality traits with a long shelf life, for example by manipulating genes such as *CmNAC18* or *CmSWEET7*.

To better understand the effect of introgressions in LG X and the transcriptional regulation of metabolic genes during fruit ripening, other specific development and textural transcriptome analyses are necessary, probably using NILs with shorter introgressions such as SC10-1, SC10-3 or SC10-4, or the development of NILs with shorter introgressions that are more useful for melon breeding.[109,110] Recently, Perpiñá *et al.*[111] developed a breeding line with a short introgression (between markers CMPSNP172 and CMPSNP65) in LG X from the cultivar Ginsen Makuwa (closely related to SC),[112] that also extended fruit shelf-life and maintained flesh firmness but in the *Charentais* genetic background (a climacteric type). This would confirm the presence of genes involved in fruit ripening in LG X from different germplasm sources which effects are stable in different genetic backgrounds and, therefore, with a potential for breeding. Unfortunately, the DEGs studied here with more detail that mapped in LG X (MELO3C012476, MELO3C012086 or MELO3C011939) were not within the LG X region flanked by the above-mentioned SNPs).

CONCLUSIONS

The introgressions in LG X delayed non-climacteric fruit ripening as demonstrated by physiological and textural traits: reduced ethylene production and respiration rates, and, consequently delayed softening and loss of whole fruit hardness and an increase in flesh juiciness. The ripening delay consequently delayed senescence processes, which impacted on volatile production in the NIL SC10-2 compared with PS, as evidenced by ester levels (acetate non-acetate thioester) in this experiment. The clusters of the DEGs associated with the factor postharvest ripening time show that most genes are upregulated over time, while the comparison between lines showed noticeable gene upregulation in SC10-2 compared with PS at harvest or after 8 d of ripening) and downregulation in 29% of the DEGs.

The transcriptome of the melon NIL SC10-2 and its parental PS suggest that the genes involved in the ripening pathways are regulated dynamically to activate the expression of some genes during ripening time (e.g. *Cm*LOX18, *Cm*AOS, *Cm*DFR4, *Cm*OPR2, *Cm*GATA5, *Cm*TCP15 and *Cm*GDSL esterase/lipase process genes) and to delay the expression of others (genes related to cellular component such as *Cm*NAC18, *Cm*NADH1, *Cm*CAD1, *Cm*ACO2 and *Cm*ADH1) during fruit ripening. Certain association of several DEGs with textural traits and volatiles were detected by heatmap and hierarchical clustering.

The identified genes differentially expressed during the ripening time and located in different linkage group (other than LG X in the case of *Cm*NADH1, *Cm*TCP15 and *Cm*GDSL esterase/lipase) might be controlled by an expression QTL (eQTL) located in LG X that would contribute to, or be involved in, crosstalk with other QTLs associated with differential textural traits and aroma volatile production in NIL SC10-2 and PS during postharvest ripening. Generally, all the genes identified in this experiment (whether or not located in the LG X) were affected by the introgression in LG X.

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Captions for Figures

Fig. 1 - Respiration rate and ethylene production of individual fruit, the near-isogenic line SC10-2 and its parental line 'Piel de Sapo' (PS), harvested in firm-ripe stage of maturity during 18 d of postharvest ripening at 20.5 ^{o}C and 88% relative humidity (mean ± SE, n=6).

Fig. 2 - Textural traits of melon fruit, the near-isogenic line SC10-2 and its parental line 'Piel de Sapo' (PS) harvested in firm-ripe stage of maturity during 18 d of ripening at 20.5 ^{o}C and 88% relative humidity (mean ± SE, n = 3). A. Flesh firmness B. Whole fruit hardness C. Flesh juiciness.

Fig. 3 - Main compound classes identified by static headspace solid-phase micro-extraction and gas chromatography–mass spectrometry (HS-SPME/GC-MS) in melon fruit of the near-isogenic line (NIL) SC10-2 and its parental line 'Piel de Sapo' (PS) harvested in firm-ripe stage of maturity and subjected to storage at 20.5 ^{o}C and 88% relative humidity for 18 d. Data are expressed as percentage of each compound class with match quality above 50 with respect to the sum of areas of the identified compounds without considering exogenous ones (mean ±SE, n=3). LSD were calculated after a two-way ANOVA with introgression and ripening time as factors.

Fig. 4 - Main compound classes identified by the static headspace solid-phase micro-extraction and gas chromatography–mass spectrometry (HS-SPME/GC-MS) technique in melon fruits of the near-isogenic line (NIL) SC10-2 and its parental line 'Piel de Sapo' (PS) (n= 3) subjected to storage at 20.5 ^{o}C and 88% relative humidity for18 d. The mean concentration was expressed in ng·g^{-1} equivalent of the internal standard (1-phenylethanol) on a fresh weight basis.

(transformed into log2). Means were statistically significant according to two-way ANOVA with introgression and ripening time as factors.

Fig. 5 - Gene Ontology (GO) of differentially expressed genes only considering the ripening time factor in melon fruit of the near-isogenic line NIL SC10-2 and its parental ´Piel de Sapo´ (PS) harvested in firm-ripe stage of maturity and stored at 20.5 ^{o}C and 88% relative humidity for 18 d.

Fig. 6 - Gene Ontology (GO) of differentially expressed genes only considering the introgression factor in melon fruit of the near-isogenic line NIL SC10-2 and its parental ´Piel de Sapo´ (PS) harvested in firm-ripe stage of maturity and stored at 20.5 ^{o}C and 88% relative humidity for 18 d.

Fig. 7 - Cluster analysis of the differentially expressed genes only considering the ripening time in fruit of the melon near-isogenic line SC10-2 and its parental control "´Piel de Sapo´ (PS). Differentially expressed genes were categorized into six clusters depending on their expression during fruit ripening (0, 4, 8, 12 and 18 d at 20.5 ^{o}C and 88% relative humidity).

Fig. 8 - Cluster analysis of the differentially expressed genes significant in the comparison between lines over time in fruit of the melon near-isogenic line SC10-2 and its parental control ´Piel de Sapo´ (PS). Differentially expressed genes were categorized into seven clusters depending on their expression during fruit ripening (0, 4, 8, 12 and 18 d at 20.5 ^{o}C and 88% relative humidity).

Fig. 9 - Relative expression of selective genes only considering the ripening time with differential expression involved in primary metabolism or ascorbic acid metabolism in fruit of the melon near-isogenic line SC10-2 and its parental control PS harvested in firm-ripe stage of maturity and stored during 18 d of ripening at 20.5 °C and 88% relative humidity. *Cm*SDHA: Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial/ *Cm*NADP: isocitrate dehydrogenase [NADP]/ *Cm*L-GalDH: L-galactose dehydrogenase/ *Cm*GME: GDP-mannose-3',5'-epimerase/ *Cm*ACLA-1: ATP-citrate synthase alpha chain protein/ *Cm*ACLB-2: ATP-citrate synthase beta chain protein 2-like/ *Cm*SCOA: Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial/ *Cm*IIL1: 3-isopropylmalate dehydratase large subunit/ *Cm*NADH1: NADPH:quinone oxidoreductase-like.

Fig. 10 - Relative expression of selective genes only considering the ripening time involved in quality and physiological process in fruit of the melon near-isogenic line SC10-2 and its parental control PS harvested in firm-ripe stage of maturity and stored during 18 d of ripening at 20.5°C and 88% relative humidity. *Cm*LOX18: Fruit ripening/ *Cm*ACO2: Ethylene biosynthesis/ *Cm*ADH1 and *Cm*CAD1: Phenylpropanoid biosynthesis/ CmAOS and CmOPR2: Oxylipin biosynthesis/ *Cm*SWEET7: Sugar transporter activity/ *Cm*DFR4: Flavonoid biosynthesis/ *Cm*NADH1: Oxidoreductase activity/ *Cm*PAL: Phenylpropanoid metabolism/ *Cm*WRKY33, *Cm*GATA5, *Cm*TCP15, *Cm*NAC18: Transcription factor activity/ *Cm*ERF027: Ethylene transcription factor activity/ *Cm*GDSL: Esterase and lipase activity/ *Cm*GDE4: Glycerol metabolism/ *Cm*TAC: Amino acid activity/ *Cm*IPMI3: 3-isopropylmalate dehydratase small subunit 3-like/ *Cm*ALT-2: alanine aminotransferase.

Fig. 11 - Relative expression of selective genes only mainly considering the comparison between lines over time and involved in different process in fruit of the melon near-isogenic

line SC10-2 and its parental control PS harvested in firm-ripe stage of maturity and stored during 18 d of ripening at 20.5oC and 88% relative humidity. *Cm*NAC18: Transcription factor activity/ *Cm*WRKY33: Transcription factor activity/ *Cm*CAD1: Phenylpropanoid biosynthesis/ *Cm*MADS-box: MADS-box transcription factor/ *Cm*ACLA-1: ATP-citrate synthase alpha chain protein/ *Cm*IIL1: 3-isopropylmalate dehydratase large subunit/ *Cm*FAH: fumarylacetoacetase/ *Cm*ACO2: Ethylene biosynthesis/ *Cm*SDHA: Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial/ *Cm*IPMI3: 3-isopropylmalate dehydratase small subunit 3-like/ C*m*SCOA: Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial/ *Cm*L-GalDH: L-galactose dehydrogenase/ C*m*LOX18: Fruit ripening/ *Cm*NADP: isocitrate dehydrogenase [NADP]/ *Cm*ACLB-2: ATP-citrate synthase beta chain protein 2-like. *Cm*TrpD: tryptophan biosynthetic process, transferase activity, transferring glycosyl groups/ *Cm*HK4-like: cytokinin receptor activity, two-component response regulator activity, two-component sensor activity.

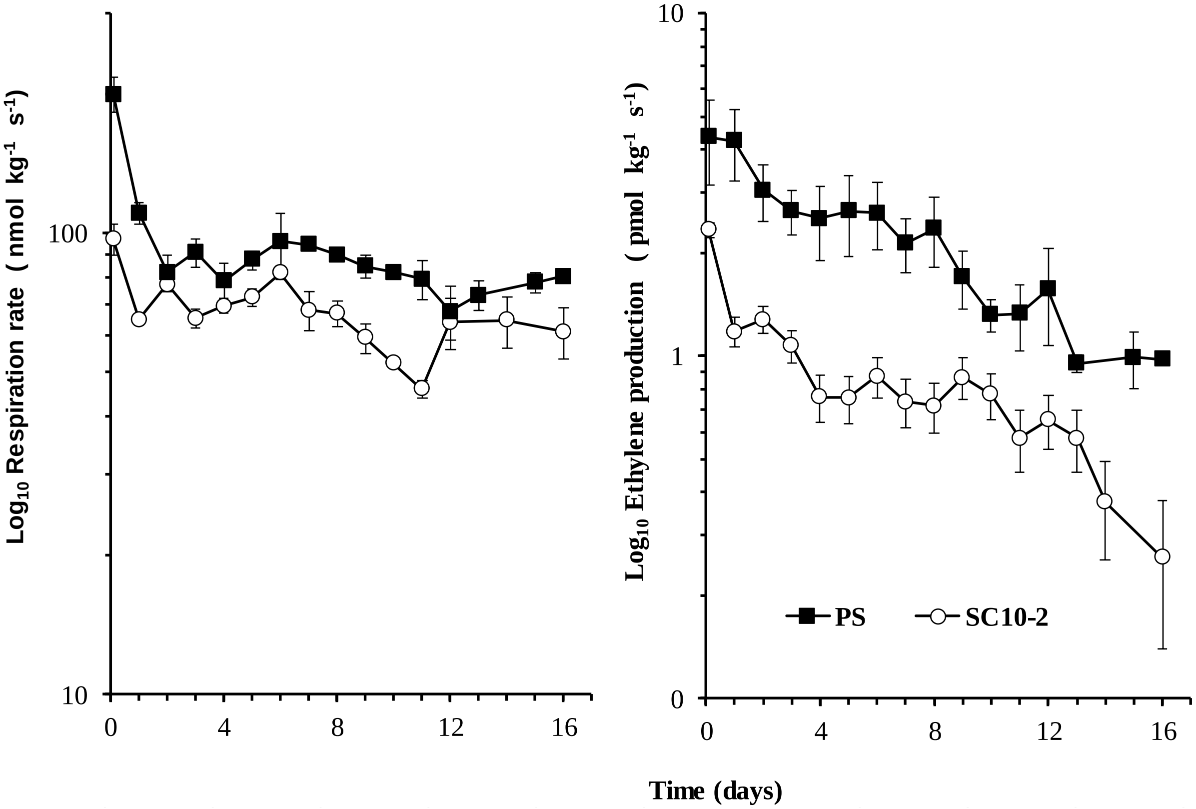
Fig. 12 - Relative expression of selective genes only considering the postharvest ripening time factor and involved in different process in fruit of the melon near-isogenic line SC10-2 and its parental control PS harvested in firm-ripe stage of maturity and stored during 18 d of ripening at 20.5°C and 88% relative humidity. *Cm*DHL92: Polygalacturonase At1g48100/ *Cm*MPC1: Mitochondrial pyruvate carrier/ *Cm*DTX: Protein detoxificatoin/ *Cm*ABREX1: Abscisic acid-insensitive 5-like protein 4 isoform X1/ *Cm*IAA71: auxin-responsive protein SAUR71-like.

Fig. 13. Heatmap and hierarchical clustering (using Euclidean distance as the similarity measure and Ward's linkage) applied to thirty-seven differentially expressed genes (Table 1) and the quality traits measured (textural traits and VOCs) over postharvest ripening time (columns represent the samples, and rows the variables). Original data were scaled and log2-

transformed. The eight clusters (C) found were numbered from one to eight, and the subcluster group´s (G) outlined were numbered also from one to eight.

Table 1. Differentially expressed genes (thirty-seven) transcripts from RNA-seq of the near-isogenic line (NIL) SC10-2 fruit (n = 3) of melon and its parental control ´Piel de Sapo´ (PS) during 18 d postharvest ripening at 20.5 ºC and 88% relative humidity. Effect of postharvest ripening time (RT) or the introgression (I) alone or combined with RT. All the information comes from Melonomics version 4.0 www.melonomics.net, including the chromosome (LG) location except when unavailable (LG 0).

Gene	Transcript name	LG	Locus start	Locus end	Gene description	Code	Factor
MELO3C024348	MELO3C024348.2.1	1	36244644	36249009	Lipoxygenase	*Cm*LOX18	RT/ I
MELO3C019735	MELO3C019735.2.1	11	23244951	23246562	1-aminocyclopropane-1-carboxylate oxidase	*Cm*ACO2	RT/ I
MELO3C019548	MELO3C019548.2.1	6	12928441	12930407	Cinnamyl alcohol dehydrogenase	*Cm*ADH1	RT
MELO3C018492	MELO3C018492.2.1	1	614743	617080	Cinnamyl alcohol dehydrogenase	*Cm*CAD1	RT/ I
MELO3C010910	MELO3C010910.2.1	3	30073454	30075374	Allene oxide synthase	*Cm*AOS	RT
MELO3C016259	MELO3C016259.2.1	7	22840158	22843162	Bidirectional sugar transporter SWEET	*Cm*SWEET7	RT
MELO3C008075	MELO3C008075.2.1	3	159591	162626	12-oxophytodienoate reductase-like protein	*Cm*OPR2	RT
MELO3C020508	MELO3C020508.2.1	12	399308	402564	Cinnamoyl-CoA reductase 1/ Bifunctional dihydroflavonol 4-reductase	*Cm*DFR4	RT
MELO3C012476	MELO3C012476.2.1	10	214914	216424	NADPH:quinone oxidoreductase-like	*Cm*NADH1	RT
MELO3C017811	MELO3C017811.2.1	7	27322473	27324829	Phenylalanine ammonia-lyase-like	*Cm*PAL	RT
MELO3C009127	MELO3C009127.2.1	4	34052833	34055772	WRKY family transcription factor family protein	*Cm*WRKY33	RT/ I
MELO3C023350	MELO3C023350.2.1	11	1856000	1857792	GATA transcription factor	*Cm*GATA5	RT
MELO3C005630	MELO3C005630.2.1	9	23110939	23111708	Ethylene-responsive transcription factor ERF027	*Cm*ERF027	RT
MELO3C012086	MELO3C012086.2.1	10	2703625	2705396	Transcription factor TCP15	*Cm*TCP15	RT
MELO3C011939	MELO3C011939.2.1	10	3788375	792148	GDSL esterase/lipase At3g26430	*Cm*GDSL esterase/ lipase	RT
MELO3C013101	MELO3C013101.2.1	1	12324577	12332243	Glycerophosphodiester phosphodiesterase GDPDL4-like	*Cm*GDPDL4	RT
MELO3C016540	MELO3C016540.2.1	6	27663292	27665351	NAC domain protein	*Cm*NAC18	RT/ I
MELO3C005591	MELO3C005591.2.1	9	22744057	22747399	ACT domain-containing family protein	*Cm*ACT	RT
MELO3C017560	MELO3C017560.2.1	7	25124825	25133417	Succinate dehydrogenase flavoprotein subunit, mitochondrial	*Cm*SDHA	RT/ I
MELO3C021563	MELO3C021563.2.1	9	3808841	3816628	isocitrate dehydrogenase [NADP]	*Cm*NADP	RT/ I
MELO3C018576	MELO3C018576.2.1	1	1201943	1207142	L-galactose dehydrogenase	*Cm*L-GalDH	RT/ I
MELO3C004377	MELO3C004377.2.1	5	26991180	26994294	GDP-mannose-3',5'-epimerase	*Cm*GME	RT
MELO3C010675	MELO3C010675.2.1	3	31551192	31555805	ATP-citrate synthase alpha chain protein	*Cm*ACLA-1	RT/ I
MELO3C011482	MELO3C011482.2.1	3	25714081	25722118	ATP-citrate synthase beta chain protein 2-like	*Cm*ACLB-2	RT/ I
MELO3C002167	MELO3C002167.2.1	12	25867931	25872728	Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial	*Cm*SCOA	RT/ I
MELO3C005518	MELO3C005518.2.1	9	22123330	22124520	3-isopropylmalate dehydratase small subunit 3-like	*Cm*IPMI3	RT/ I
MELO3C003344	MELO3C003344.2.1	4	456132	464549	3-isopropylmalate dehydratase large subunit	*Cm*IIL1	RT/ I
MELO3C007433	MELO3C007433.2.1	8	2763982	2767562	Fumarylacetoacetase	*Cm*FAH	I
MELO3C009970	MELO3C009970.2.1	4	27614894	27618780	Polygalacturonase At1g48100	*Cm*DHL92	RT
MELO3C007517	MELO3C007517.2.1	8	3320368	3322511	Mitochondrial pyruvate carrier	*Cm*MPC1	RT
MELO3C017343	MELO3C017343.2.1	2	24148159	24152142	Protein DETOXIFICATION	*Cm*DTX	RT
MELO3C014384	MELO3C014384.2.1	5	2954394	2961074	ABSCISIC ACID-INSENSITIVE 5-like protein 4 isoform X1	*Cm*ABREX	RT
MELO3C000885	MELO3C000885.2.1	0	20311284	20311754	auxin-responsive protein SAUR71-like	*Cm*IAA71	RT
MELO3C024001	MELO3C024001.2.1	4	23817884	23822674	MADS-box transcription factor	*Cm*MADS-box	I
MELO3C010686	MELO3C010686.2.1	3	31468671	31472617	Alanine aminotransferase 2	*Cm*ALT-2	I
MELO3C011963	MELO3C011963.2.1	10	3557598	3564518	Anthranilate phosphoribosyltransferase	*Cm*TrpD	RT
MELO3C020055	MELO3C020055.2.1	10	10840410	10848396	Histidine kinase 4-like	CmHK4-like	RT/I


Log10 Respiration rate (nmol kg-1 s-1)
100
10
0
4
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12
16
Log10 Ethylene production (pmol kg-1 s-1)
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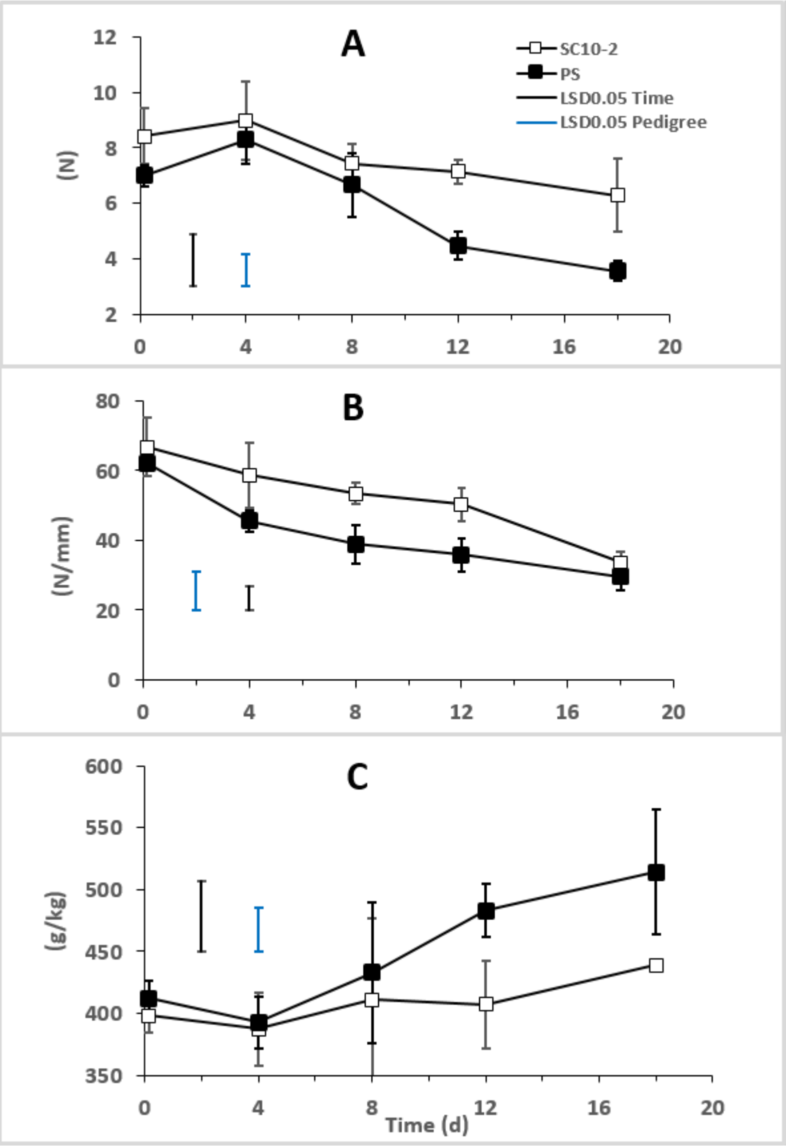
PS
SC10-2
Time (days)

Fig. 1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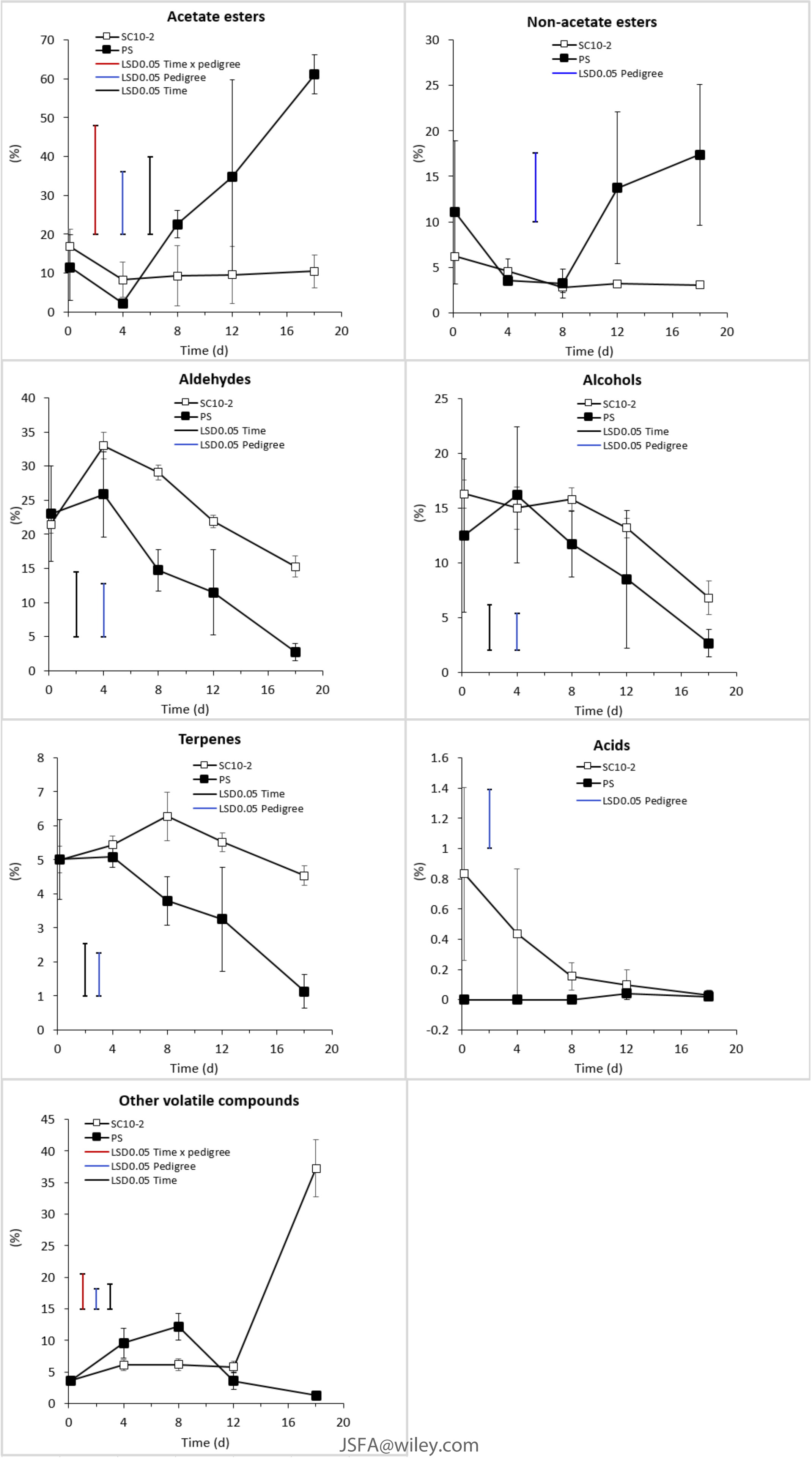
Time (d)

Figure 2


Acetate esters
SC10-2
PS
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Non-acetate esters
SC10-2
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LSD0.05 Pedigree
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Aldehydes
SC10-2
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Alcohols
SC10-2
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Terpenes
SC10-2
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(%)
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Acids
SC10-2
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Other volatile compounds
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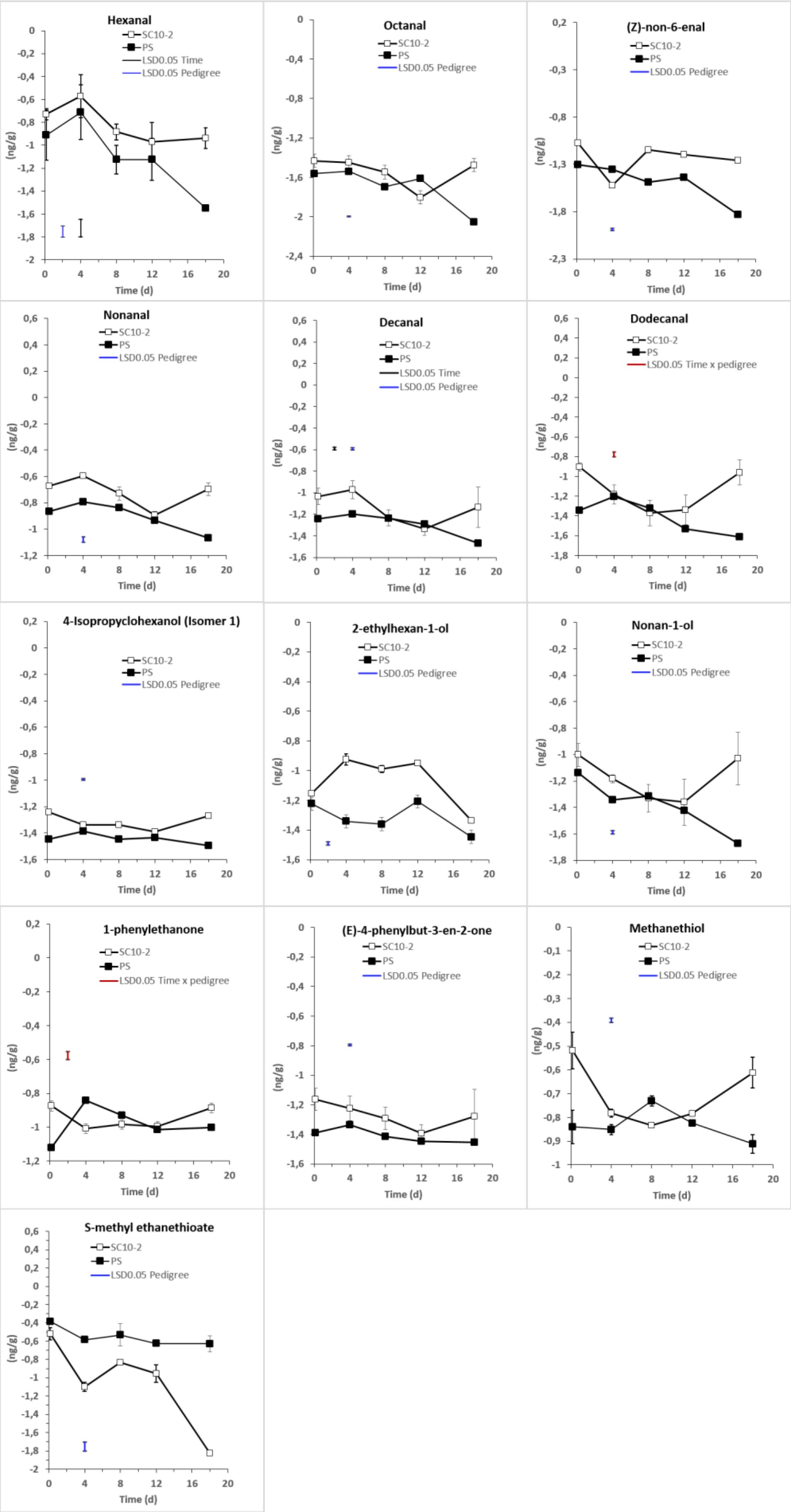
(%)
Time (d)

Fig. 3


Hexanal
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Octanal
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(ng/g)
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4-Isopropyclohexanol (Isomer 1)
SC10-2
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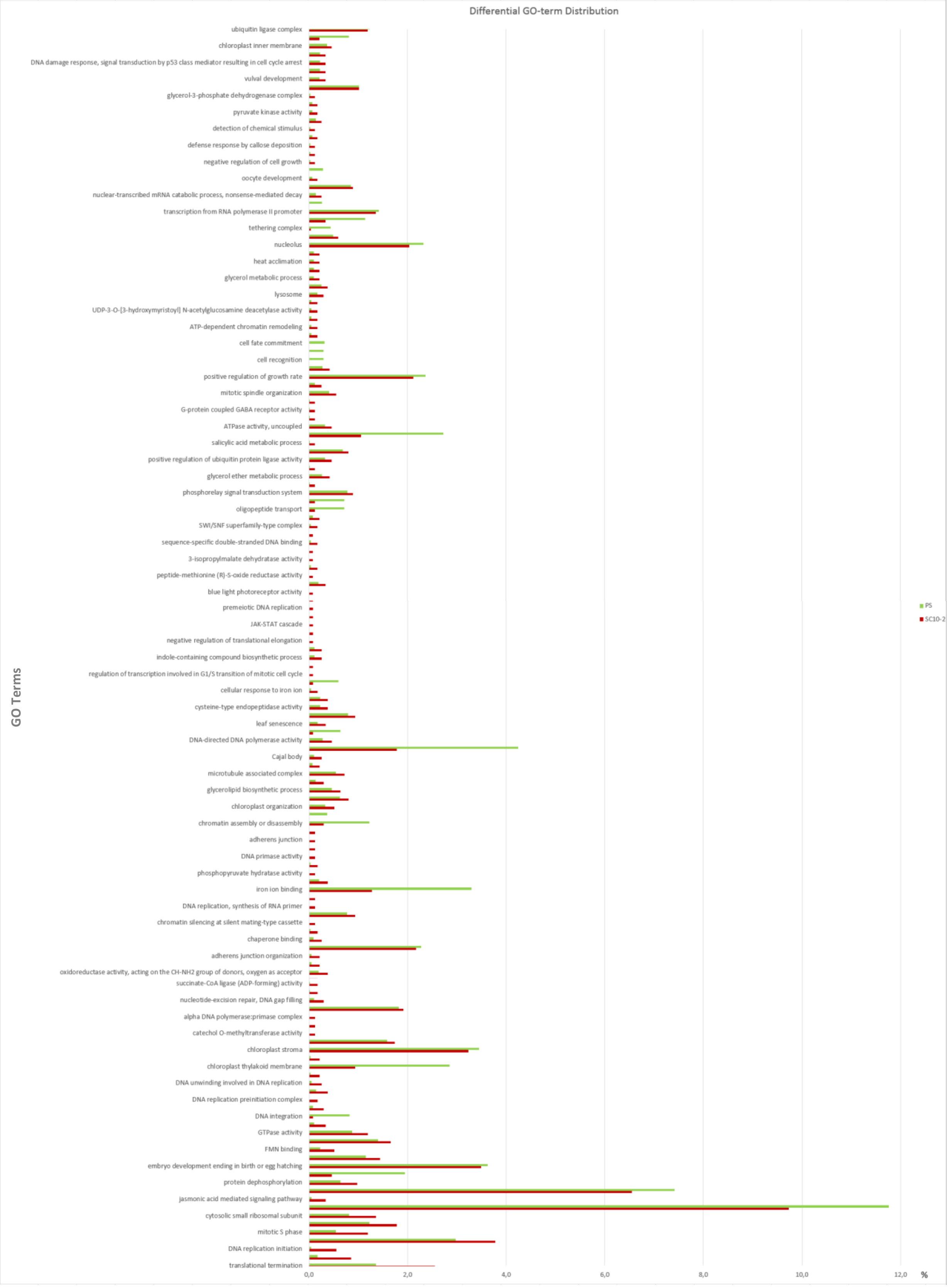
(ng/g)
Time (d)
2-ethylhexan-1-ol
SC10-2
PS
LSD0.05 Pedigree
0
-0,2
-0,4
-0,6
-0,8
-1
-1,2
-1,4
-1,6
(ng/g)
Time (d)
Nonan-1-ol
SC10-2
PS
LSD0.05 Pedigree
0
-0,2
-0,4
-0,6
-0,8
-1
-1,2
-1,4
-1,6
-1,8
(ng/g)
Time (d)
1-phenylethanone
SC10-2
PS
LSD0.05 Time x pedigree
0,2
0
-0,2
-0,4
-0,6
-0,8
-1
-1,2
(ng/g)
Time (d)
(E)-4-phenylbut-3-en-2-one
SC10-2
PS
LSD0.05 Pedigree
0
-0,2
-0,4
-0,6
-0,8
-1
-1,2
-1,4
-1,6
(ng/g)
Time (d)
Methanethiol
SC10-2
PS
LSD0.05 Pedigree
0
-0,1
-0,2
-0,3
-0,4
-0,5
-0,6
-0,7
-0,8
-0,9
-1
(ng/g)
Time (d)
S-methyl ethanethioate
SC10-2
PS
LSD0.05 Pedigree
0,6
0,4
0,2
0
-0,2
-0,4
-0,6
-0,8
-1
-1,2
-1,4
-1,6
-1,8
-2
(ng/g)
0
4
8
12
16
20
Time (d)

- Fig. 4


Differential GO-term Distribution
GO Terms
supramolecular fiber
organelle outer membrane
protein tyrosine phosphatase activity
ubiquitin-protein transferase activity
protein serine/threonine phosphatase activity
copper ion transmembrane transporter activity
protein kinase regulator activity
phosphorelay response regulator activity
aerobic respiration
phagocytosis
body morphogenesis
heat acclimation
glycerol metabolic process
Golgi organization
regulation of proteolysis involved in cellular protein catabolic process
microtubule-based movement
gravitropism
vulval development
unsaturated fatty acid biosynthetic process
positive regulation of flower development
floral whorl development
oxidoreductase activity, acting on a sulfur group of donors
cis-Golgi network
transcription factor TFIID complex
mitochondrial inner membrane
S-(hydroxymethyl)glutathione dehydrogenase activity
anthranilate N-benzoyltransferase activity
7S RNA binding
regulation of mitotic cell cycle
protein ubiquitination
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
ion channel activity
jasmonic acid mediated signaling pathway
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
endosome
ATP-dependent DNA helicase activity
sister chromatid segregation
microtubule cytoskeleton
protein serine/threonine phosphatase complex
cell surface
nuclear replisome
endoplasmic reticulum lumen
lateral plasma membrane
pyridoxamine-phosphate oxidase activity
2-hydroxy-1,4-benzoquinone reductase activity
triose-phosphate isomerase activity
NAD(P)H dehydrogenase (quinone) activity
asparagine-tRNA ligase activity
glucose-6-phosphate 1-epimerase activity
ARF guanyl-nucleotide exchange factor activity
maleylacetoacetate isomerase activity
ubiquitin-like protein-specific protease activity
mevalonate kinase activity
ubiquitin protein ligase binding
glucose-6-phosphate dehydrogenase activity
catechol O-methyltransferase activity
1-phosphatidylinositol 4-kinase activity
palmitoyltransferase activity
response to freezing
regulation of ARF protein signal transduction
regulation of meiotic nuclear division
asparaginyl-tRNA aminoacylation
transcription from plastid promoter
RNA polyadenylation
collagen and cuticulin-based cuticle development
RNA-dependent ATPase activity
O-acyltransferase activity
GTPase activator activity
cysteine-type endopeptidase activity
hermaphrodite genitalia development
chaperone mediated protein folding independent of cofactor
triglyceride biosynthetic process
termination of RNA polymerase II transcription
receptor-mediated endocytosis
circadian rhythm
regulation of ion transport
endocrine pancreas development
chloroplast organization
SRP-dependent cotranslational protein targeting to membrane
mRNA export from nucleus
viral transcription
locomotion
magnesium ion binding
oocyte development
glucose metabolic process
3-isopropylmalate dehydratase activity
threonine-type endopeptidase activity
glycerol kinase activity
glycerol-3-phosphate dehydrogenase activity
succinate-CoA ligase (GDP-forming) activity
chromatin silencing by small RNA
mRNA branch site recognition
chloroplast thylakoid membrane
ATP citrate synthase activity
alanine-tRNA ligase activity
protein tyrosine/serine/threonine phosphatase activity
salicylic acid metabolic process
alanyl-tRNA aminoacylation
monooxygenase activity
positive regulation of growth rate
anchored component of plasma membrane
carbon-carbon lyase activity
structural constituent of ribosome
melanosome
glycerol-3-phosphate metabolic process
glycerol ether metabolic process
production of siRNA involved in RNA interference
chromatin assembly or disassembly
chloroplast stroma
determination of adult lifespan
nucleosome binding
FMN binding
catalytic step 2 spliceosome
GTP binding
precatalytic spliceosome
cell-cell junction assembly
plant-type vacuole membrane
succinate-CoA ligase (ADP-forming) activity
embryo development ending in birth or egg hatching
response to salt stress
GTPase activity
serine-type peptidase activity
DNA integration
mRNA 3'-end processing
iron ion binding
cytosolic large ribosomal subunit
zinc ion binding
response to cadmium ion
protein dephosphorylation
translational termination
0.0
2.0
4.0
6.0
8.0
10.0
12.0
%
PS
SC10-2


Differential GO-term Distribution
GO Terms
ubiquitin ligase complex
chloroplast inner membrane
DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest
vulval development
glycerol-3-phosphate dehydrogenase complex
pyruvate kinase activity
detection of chemical stimulus
defense response by callose deposition
negative regulation of cell growth
oocyte development
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
transcription from RNA polymerase II promoter
tethering complex
nucleolus
heat acclimation
glycerol metabolic process
lysosome
UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase activity
ATP-dependent chromatin remodeling
cell fate commitment
cell recognition
positive regulation of growth rate
mitotic spindle organization
G-protein coupled GABA receptor activity
ATPase activity, uncoupled
salicylic acid metabolic process
positive regulation of ubiquitin protein ligase activity
glycerol ether metabolic process
phosphorelay signal transduction system
oligopeptide transport
SWI/SNF superfamily-type complex
sequence-specific double-stranded DNA binding
3-isopropylmalate dehydratase activity
peptide-methionine (R)-S-oxide reductase activity
blue light photoreceptor activity
premeiotic DNA replication
JAK-STAT cascade
negative regulation of translational elongation
indole-containing compound biosynthetic process
regulation of transcription involved in G1/S transition of mitotic cell cycle
cellular response to iron ion
cysteine-type endopeptidase activity
leaf senescence
DNA-directed DNA polymerase activity
Cajal body
microtubule associated complex
glycerolipid biosynthetic process
chloroplast organization
chromatin assembly or disassembly
adherens junction
DNA primase activity
phosphopyruvate hydratase activity
iron ion binding
DNA replication, synthesis of RNA primer
chromatin silencing at silent mating-type cassette
chaperone binding
adherens junction organization
oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor
succinate-CoA ligase (ADP-forming) activity
nucleotide-excision repair, DNA gap filling
alpha DNA polymerase:primase complex
catechol O-methyltransferase activity
chloroplast stroma
chloroplast thylakoid membrane
DNA unwinding involved in DNA replication
DNA replication preinitiation complex
DNA integration
GTPase activity
FMN binding
embryo development ending in birth or egg hatching
protein dephosphorylation
jasmonic acid mediated signaling pathway
cytosolic small ribosomal subunit
mitotic S phase
DNA replication initiation
translational termination
0,0
2,0
4,0
6,0
8,0
10,0
12,0
%
🟩 PS
🟥 SC10-2

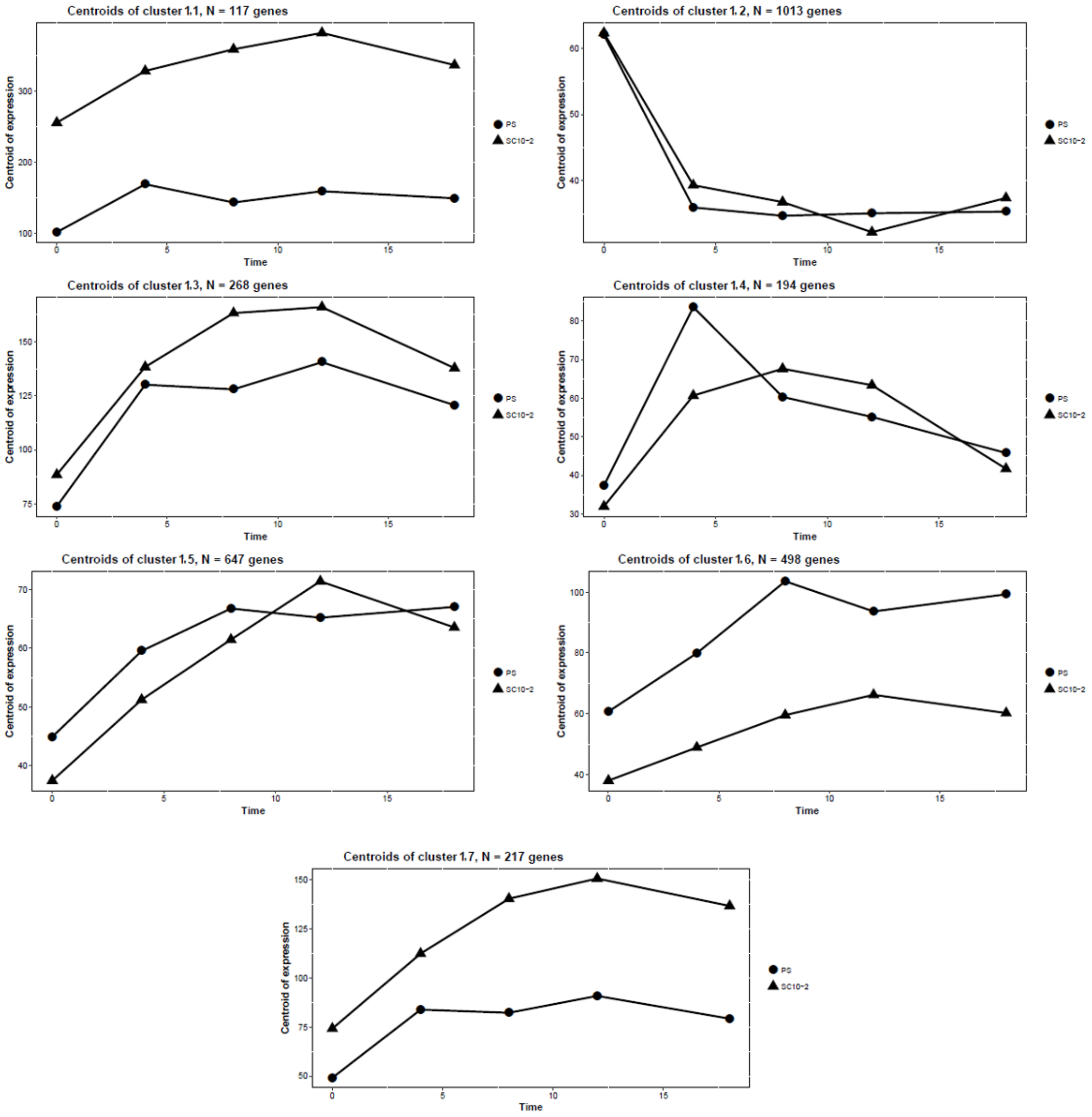

Centroids of cluster 1.1, N = 117 genes
Centroids of cluster 1.2, N = 1013 genes
Centroids of cluster 1.3, N = 268 genes
Centroids of cluster 1.4, N = 194 genes
Centroids of cluster 1.5, N = 647 genes
Centroids of cluster 1.6, N = 498 genes
Centroids of cluster 1.7, N = 217 genes
Centroid of expression
Time
0
5
10
15
● PS
▲ SC10-2

Fig. 7

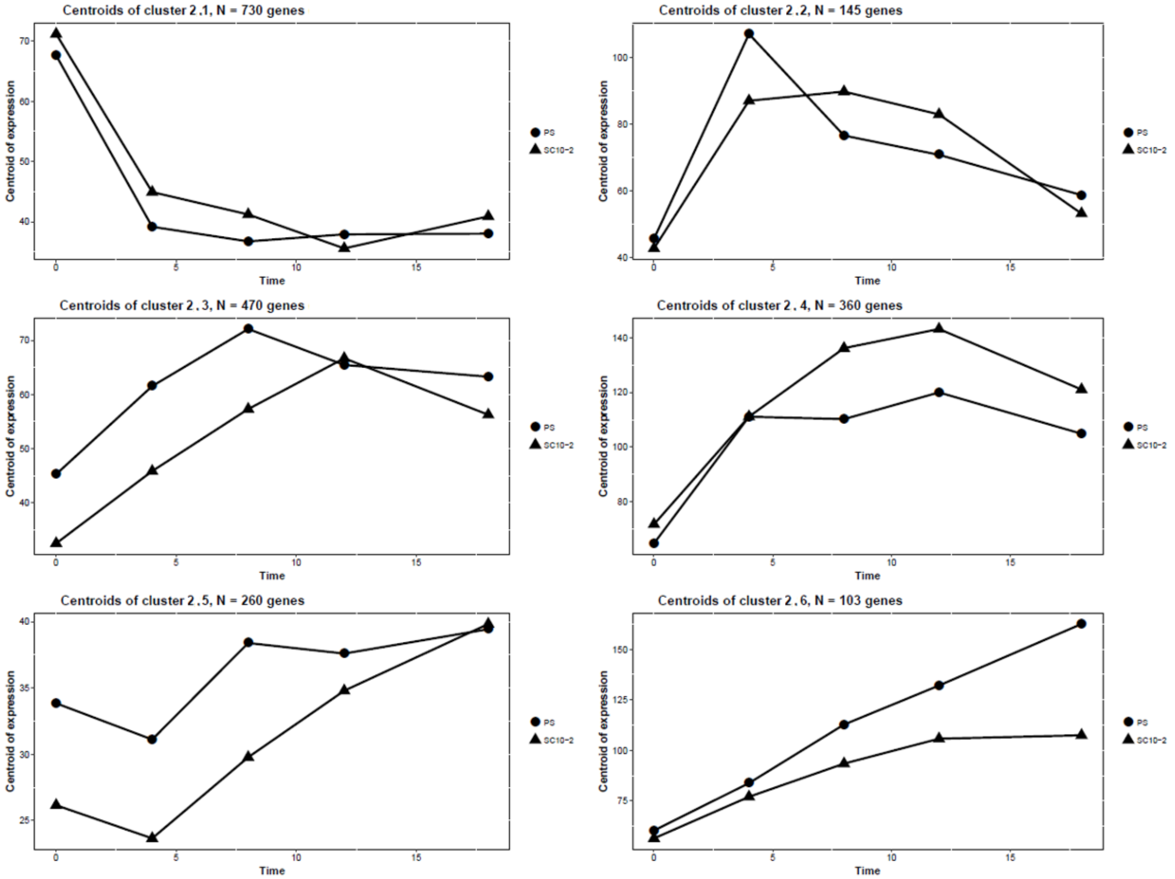

Centroids of cluster 2.1, N = 730 genes
Centroids of cluster 2.2, N = 145 genes
Centroids of cluster 2.3, N = 470 genes
Centroids of cluster 2.4, N = 360 genes
Centroids of cluster 2.5, N = 260 genes
Centroids of cluster 2.6, N = 103 genes
Centroid of expression
Time
0
5
10
15
PS
SC10−2

Figure 8

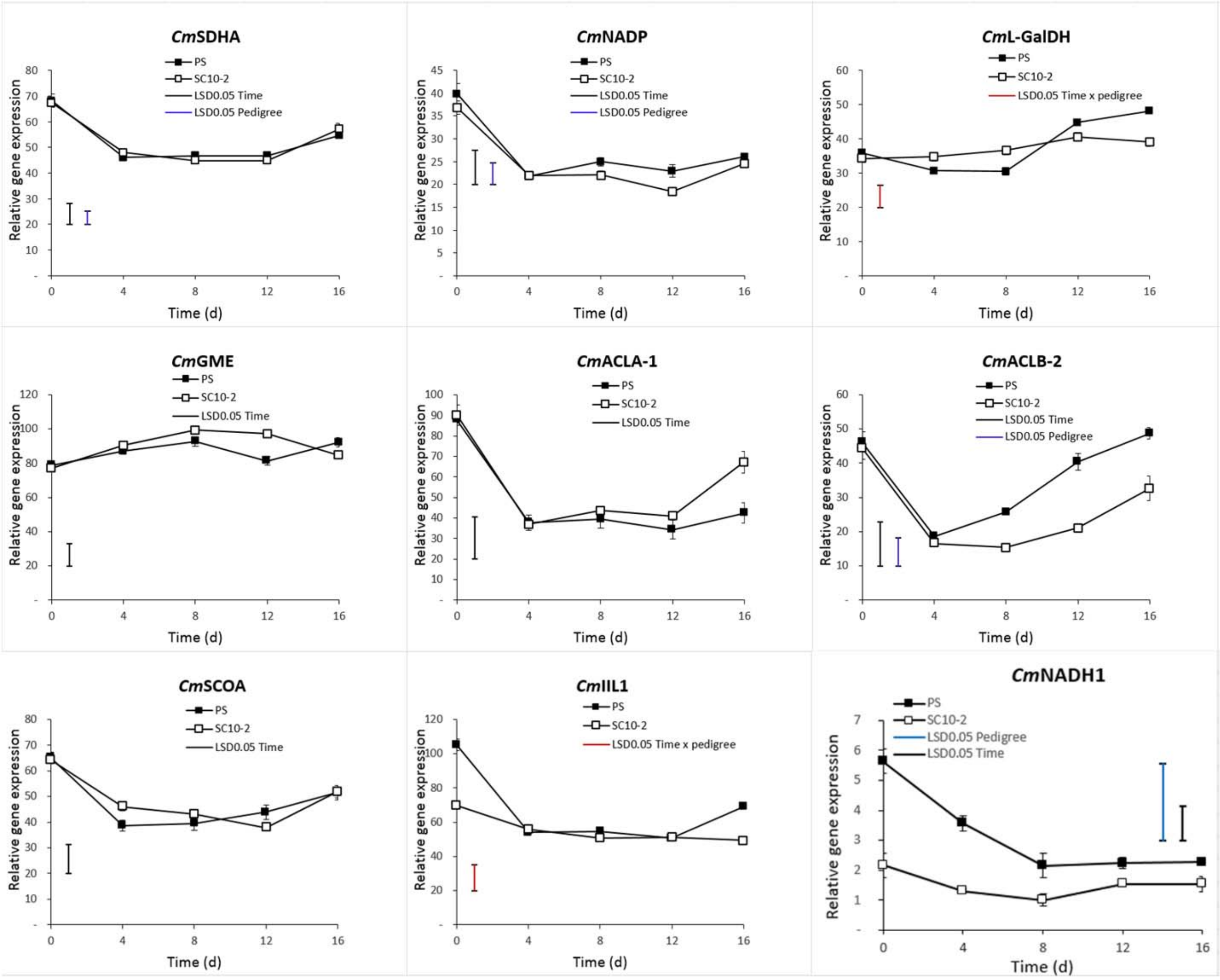

*Cm*SDHA
PS
SC10-2
LSD0.05 Time
LSD0.05 Pedigree
*Cm*NADP
PS
SC10-2
LSD0.05 Time
LSD0.05 Pedigree
*Cm*L-GalDH
PS
SC10-2
LSD0.05 Time x pedigree
*Cm*GME
PS
SC10-2
LSD0.05 Time
*Cm*ACLA-1
PS
SC10-2
LSD0.05 Time
*Cm*ACLB-2
PS
SC10-2
LSD0.05 Time
LSD0.05 Pedigree
*Cm*SCOA
PS
SC10-2
LSD0.05 Time
*Cm*IIL1
PS
SC10-2
LSD0.05 Time x pedigree
*Cm*NADH1
PS
SC10-2
LSD0.05 Pedigree
LSD0.05 Time
Relative gene expression
Time (d)
0
4
8
12
16

Fig. 9

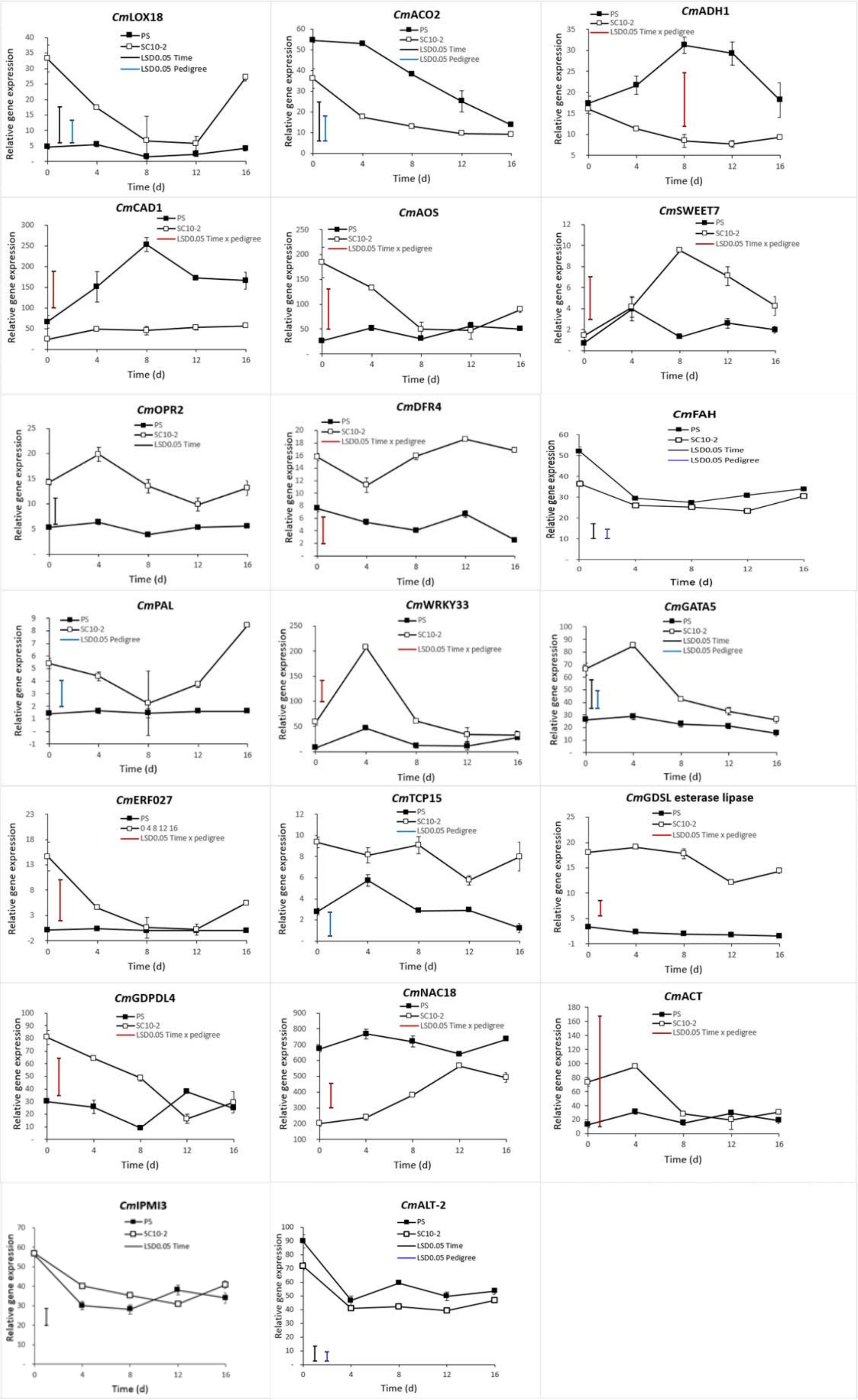

CmLOX18
CmACO2
CmADH1
CmCAD1
CmAOS
CmSWEET7
CmOPR2
CmDFR4
CmFAH
CmPAL
CmWRKY33
CmGATA5
CmERF027
CmTCP15
CmGDSL esterase lipase
CmGDPDL4
CmNAC18
CmACT
CmIPMI3
CmALT-2
PS
SC10-2
0 4 8 12 16
LSD0.05 Time
LSD0.05 Pedigree
LSD0.05 Time x pedigree
Relative gene expression
Time (d)

Fig. 10

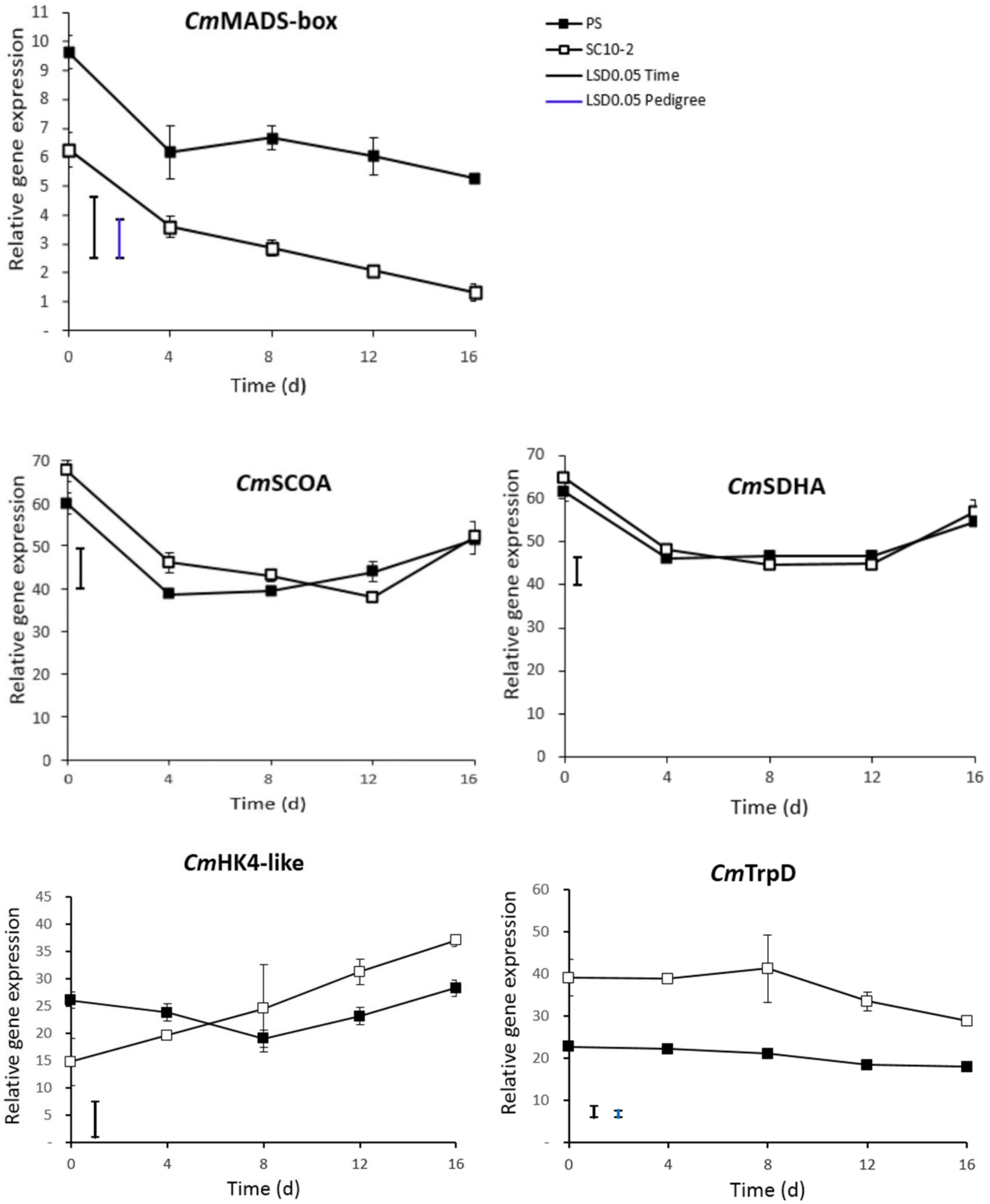

*Cm*MADS-box
PS
SC10-2
LSD0.05 Time
LSD0.05 Pedigree
Relative gene expression
11
10
9
8
7
6
5
4
3
2
1
-
0
4
8
12
16
Time (d)
*Cm*SCOA
Relative gene expression
70
60
50
40
30
20
10
0
Time (d)
*Cm*SDHA
Relative gene expression
Time (d)
*Cm*HK4-like
Relative gene expression
45
40
35
30
25
20
15
10
5
-
Time (d)
*Cm*TrpD
Relative gene expression
60
50
40
30
20
10
-
Time (d)

Fig. 11

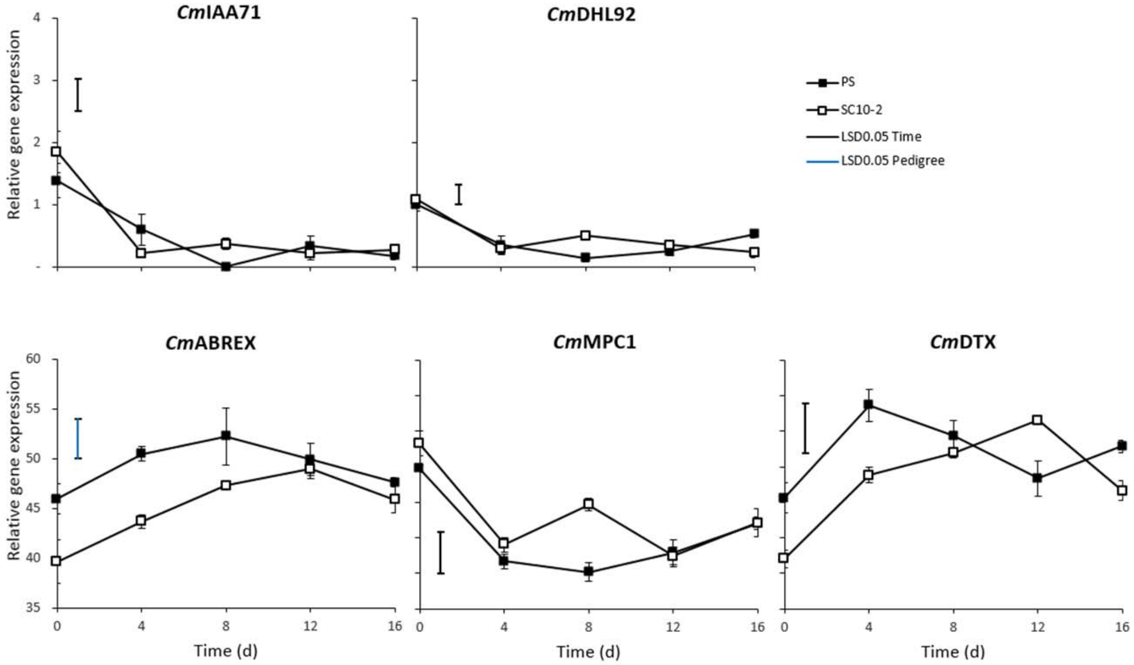

*Cm*IAA71
*Cm*DHL92
*Cm*ABREX
*Cm*MPC1
*Cm*DTX
PS
SC10-2
LSD0.05 Time
LSD0.05 Pedigree
Relative gene expression
4
3
2
1
-
60
55
50
45
40
35
0
4
8
12
16
Time (d)

Fig. 12

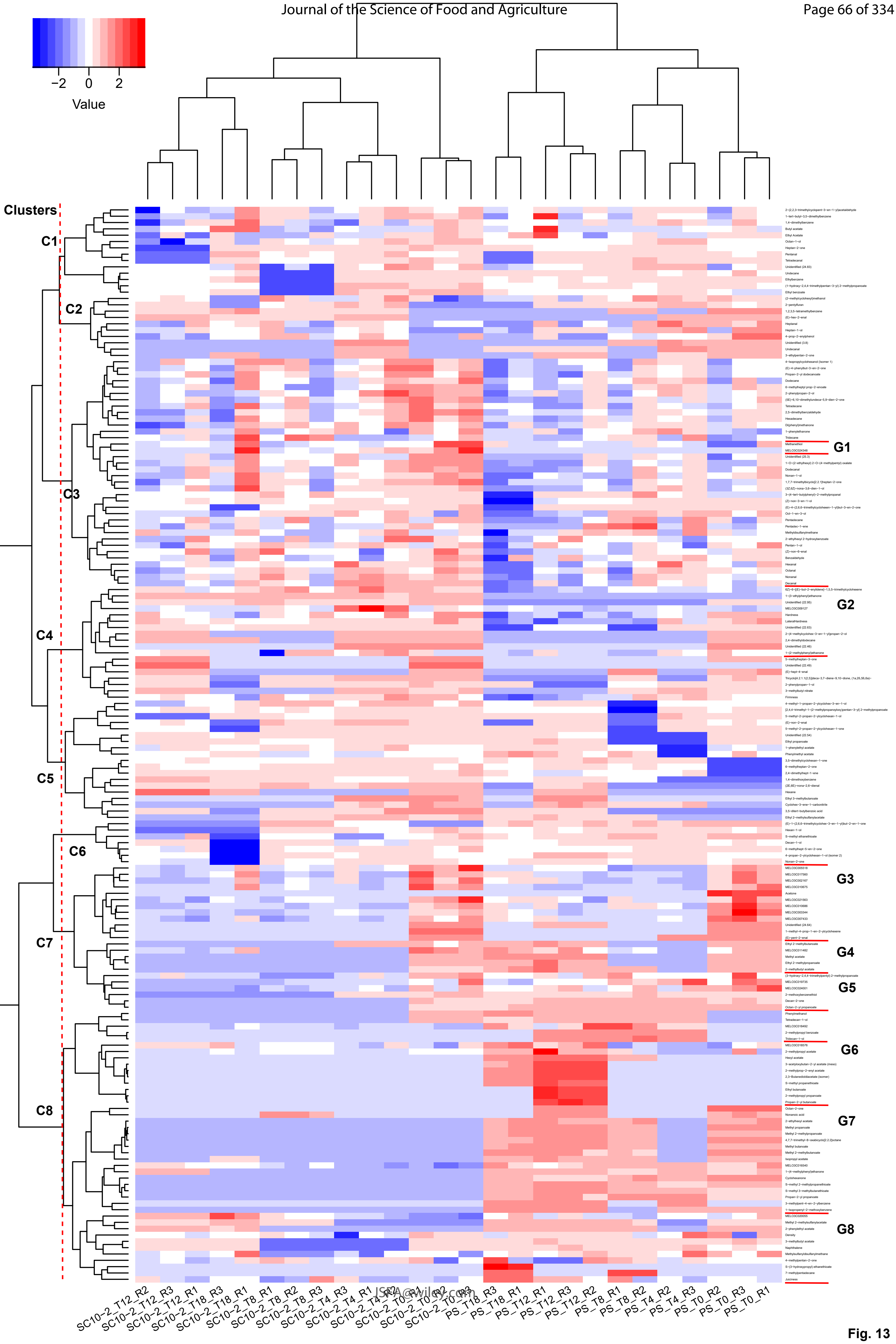
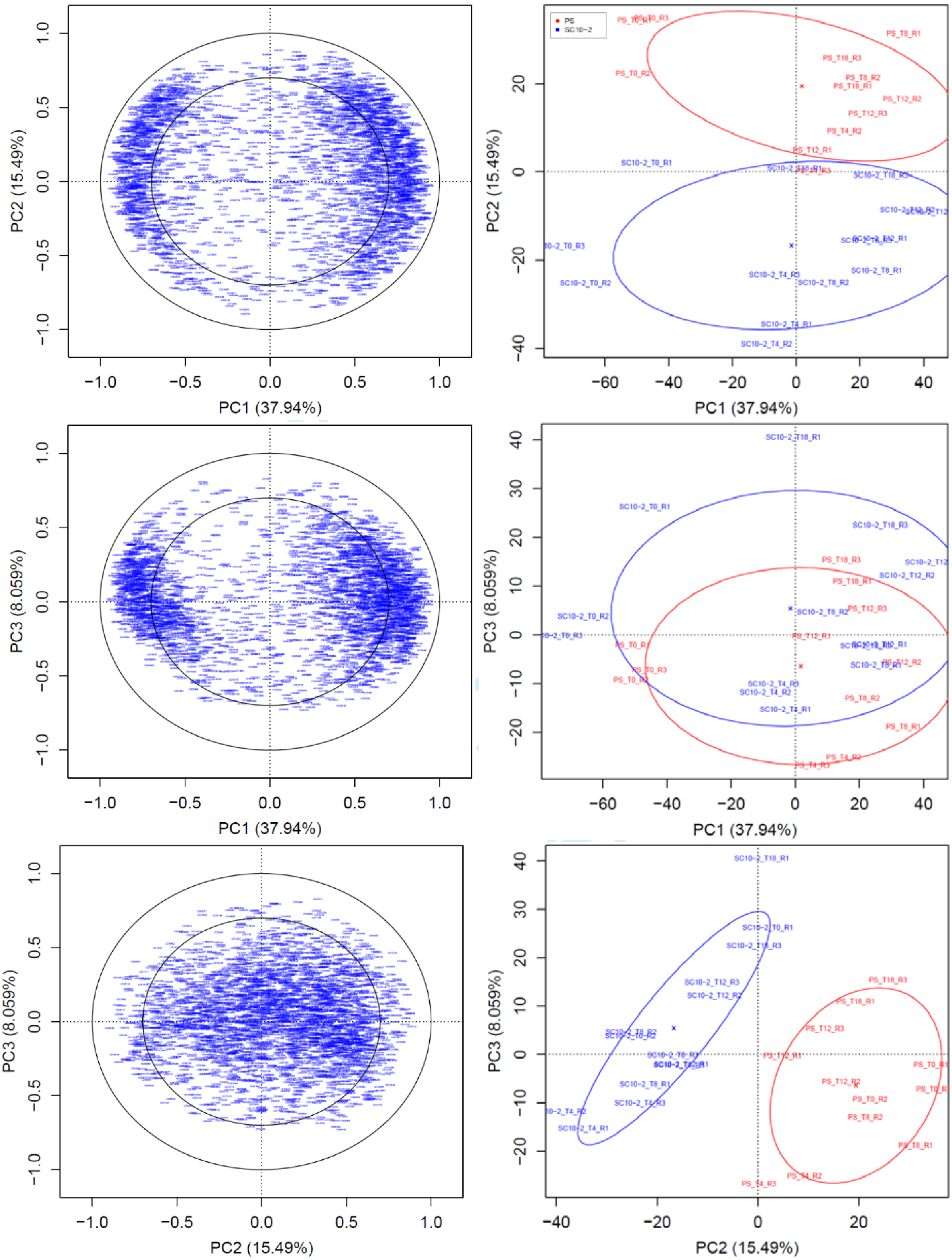
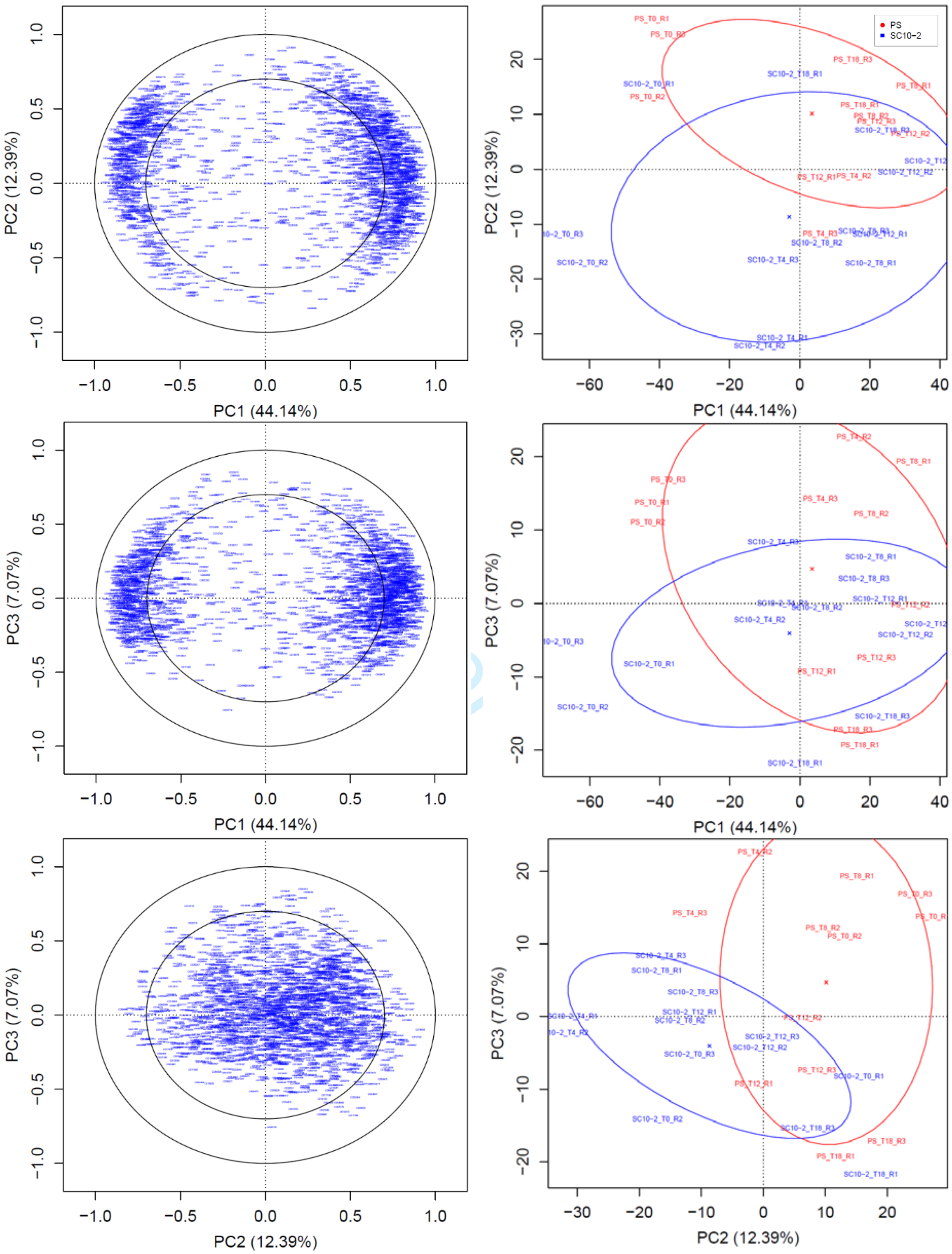

−2
0
2
Value
Clusters
C1
C2
C3
C4
C5
C6
C7
C8
2−(2,2,3−trimethylcyclopent−3−en−1−yl)acetaldehyde
1−tert−butyl−3,5−dimethylbenzene
1,4−dimethylbenzene
Butyl acetate
Ethyl Acetate
Octan−1−ol
Heptan−2−one
Pentanal
Tetradecanal
Unidentified (24.83)
Undecane
Ethylbenzene
(1−hydroxy−2,4,4−trimethylpentan−3−yl) 2−methylpropanoate
Ethyl benzoate
(2−methylcyclohexyl)methanol
2−pentylfuran
1,2,3,5−tetramethylbenzene
(E)−hex−2−enal
Heptanal
Heptan−1−ol
4−prop−2−enylphenol
Unidentified (3.8)
Undecanal
3−ethylpentan−2−one
4−Isopropylcyclohexanol (Isomer 1)
(E)−4−phenylbut−3−en−2−one
Propan−2−yl dodecanoate
Dodecane
6−methylheptyl prop−2−enoate
2−phenylpropan−2−ol
(5E)−6,10−dimethylundeca−5,9−dien−2−one
Tetradecane
2,5−dimethylbenzaldehyde
Hexadecane
Di(phenyl)methanone
1−phenylethanone
Tridecane
Methanethiol
MELO3C024348
G1
Unidentified (25.3)
1−O−(2−ethylhexyl) 2−O−(4−methylpentyl) oxalate
Dodecanal
Nonan−1−ol
1,7,7−trimethylbicyclo[2.2.1]heptan−2−one
(3Z,6Z)−nona−3,6−dien−1−ol
3−(4−tert−butylphenyl)−2−methylpropanal
(Z)−non−3−en−1−ol
(E)−4−(2,6,6−trimethylcyclohexen−1−yl)but−3−en−2−one
Oct−1−en−3−ol
Pentadecane
Pentadec−1−ene
Methyldisulfanylmethane
2−ethylhexyl 2−hydroxybenzoate
Pentan−1−ol
(Z)−non−6−enal
Benzaldehyde
Hexanal
Octanal
Nonanal
Decanal
6Z)−6−[(E)−but−2−enylidene]−1,5,5−trimethylcyclohexene
1−(3−ethylphenyl)ethanone
Unidentified (22.95)
MELO3C009127
G2
Hardness
LateralHardness
Unidentified (22.63)
2−(4−methylcyclohex−3−en−1−yl)propan−2−ol
2,4−dimethyldodecane
Unidentified (22.46)
1−(2−methylphenyl)ethanone
5−methylheptan−3−one
Unidentified (22.49)
(E)−hept−4−enal
Tricyclo[4.2.1.1(2,5)]deca−3,7−diene−9,10−dione, (1a,2ß,5ß,6a)−
2−phenylpropan−1−ol
3−methylbutyl nitrate
Firmness
4−methyl−1−propan−2−ylcyclohex−3−en−1−ol
[2,4,4−trimethyl−1−(2−methylpropanoyloxy)pentan−3−yl] 2−methylpropanoate
5−methyl−2−propan−2−ylcyclohexan−1−ol
(E)−non−2−enal
5−methyl−2−propan−2−ylcyclohexan−1−one
Unidentified (22.54)
Ethyl propanoate
1−phenylethyl acetate
Phenylmethyl acetate
3,5−dimethylcyclohexan−1−one
6−methylheptan−2−one
2,4−dimethylhept−1−ene
1,4−dimethoxybenzene
(2E,6E)−nona−2,6−dienal
Hexane
Ethyl 3−methylbutanoate
Cyclohex−3−ene−1−carbonitrile
3,5−ditert−butylbenzoic acid
Ethyl 2−methylsulfanylacetate
(E)−1−(2,6,6−trimethylcyclohex−3−en−1−yl)but−2−en−1−one
Hexan−1−ol
S−methyl ethanethioate
Decan−1−ol
6−methylhept−5−en−2−one
4−propan−2−ylcyclohexan−1−ol (isomer 2)
Nonan−2−one
MELO3C005518
MELO3C017560
MELO3C002167
G3
MELO3C010675
Acetone
MELO3C021563
MELO3C010686
MELO3C003344
MELO3C007433
Unidentified (24.64)
1−methyl−4−prop−1−en−2−ylcyclohexene
(E)−pent−2−enal
Ethyl 2−methylbutanoate
MELO3C011482
G4
Methyl acetate
Ethyl 2−methylpropanoate
2−methylbutyl acetate
(3−hydroxy−2,4,4−trimethylpentyl) 2−methylpropanoate
MELO3C019735
G5
MELO3C024001
2−methoxybenzenethiol
Decan−2−one
Octan−2−yl propanoate
Phenylmethanol
Tetradecan−1−ol
MELO3C018492
2−methylpropyl benzoate
Tridecan−1−ol
MELO3C018576
G6
2−methylpropyl acetate
Hexyl acetate
3−acetyloxybutan−2−yl acetate (meso)
2−methylprop−2−enyl acetate
2,3−Butanedioldiacetate (isomer)
S−methyl propanethioate
Ethyl butanoate
2−methylpropyl propanoate
Propan−2−yl butanoate
Octan−2−one
Nonanoic acid
G7
2−ethylhexyl acetate
Methyl propanoate
Methyl 2−methylpropanoate
4,7,7−trimethyl−8−oxabicyclo[2.2.2]octane
Methyl butanoate
Methyl 2−methylbutanoate
Isopropyl acetate
MELO3C016540
1−(4−methylphenyl)ethanone
Cyclohexanone
S−methyl 2−methylpropanethioate
S−methyl 3−methylbutanethioate
Propan−2−yl propanoate
3−methylpent−4−en−2−ylbenzene
1−Isopropenyl−2−methoxybenzene
MELO3C020055
Methyl 2−methylsulfanylacetate
G8
2−phenylethyl acetate
Density
3−methylbutyl acetate
Naphthalene
Methylsulfanyldisulfanylmethane
4−methylpentan−2−one
S−(3−hydroxypropyl) ethanethioate
7−methylpentadecane
Juiciness
SC10−2_T12_R2
SC10−2_T12_R3
SC10−2_T12_R1
SC10−2_T18_R3
SC10−2_T18_R1
SC10−2_T8_R1
SC10−2_T8_R2
SC10−2_T8_R3
SC10−2_T4_R3
SC10−2_T4_R1
SC10−2_T4_R2
SC10−2_T0_R1
SC10−2_T0_R2
SC10−2_T0_R3
PS_T18_R3
PS_T18_R1
PS_T12_R1
PS_T12_R3
PS_T12_R2
PS_T8_R1
PS_T8_R2
PS_T4_R2
PS_T4_R3
PS_T0_R2
PS_T0_R3
PS_T0_R1

Fig. 13

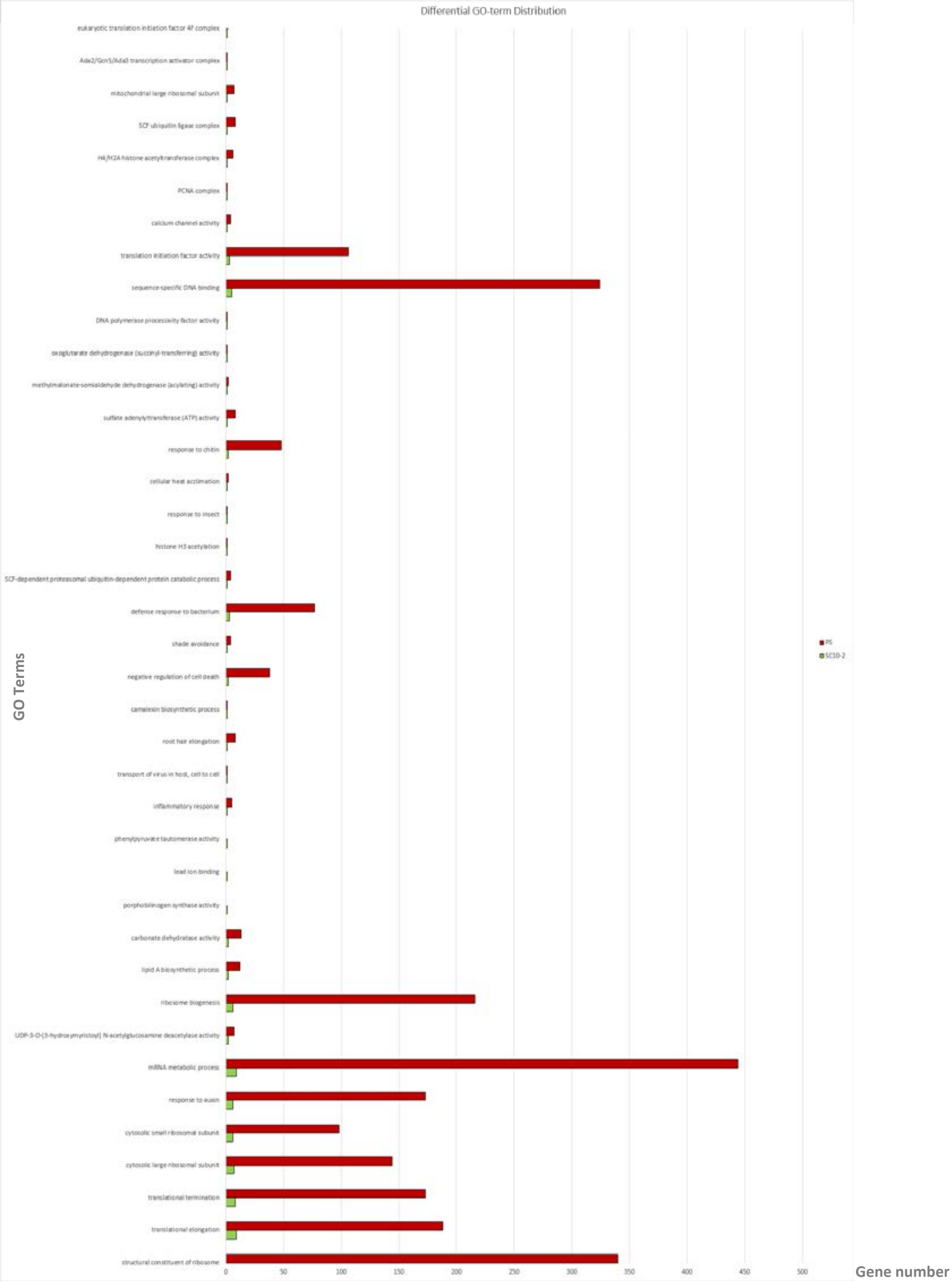


Supplementary Figure 1. Plot of the centroids of scores and loading plots of the Principal Component Analysis (PCA) of the expressed genes significant in introgression and identified in the near-isogenic line (NIL) SC10-2 and the parental control ´Piel de Sapo´ (PS)). Datasets and the corresponding centroids for the different lines and 65% confidence ellipses. Tx (x = 0, 4, 8, 12, 18) indicates the postharvest ripening time in days and Rn (n = 1-3) the corresponding replicate

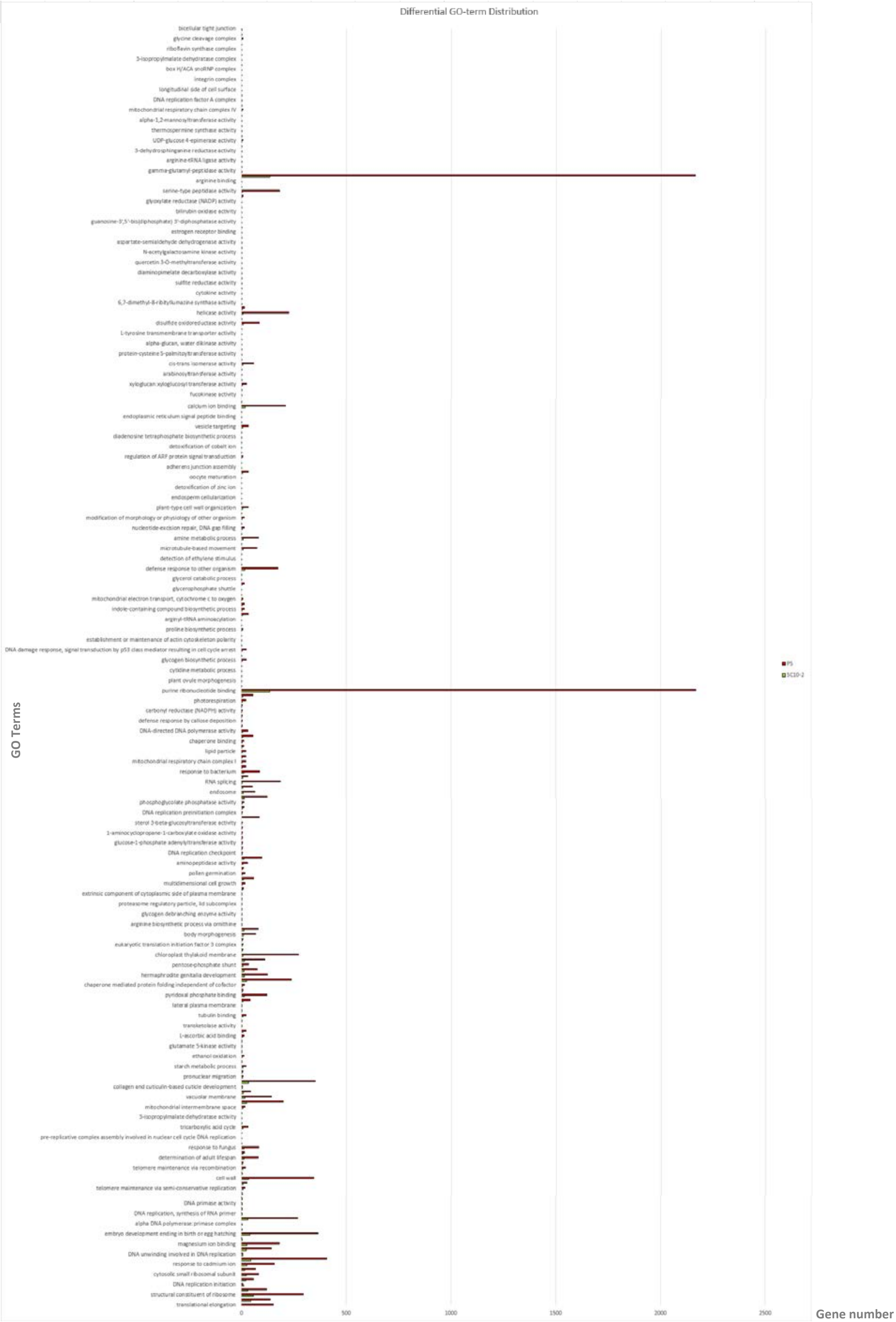


Supplementary Figure 2. Plot of the centroids of scores and loading plots of the Principal Component Analysis (PCA) of the expressed genes significant in ripening time identified in the near-isogenic line (NIL) SC10-2 and the parental control ´Piel de Sapo´ (PS). Datasets and the corresponding centroids for the different lines and 65% confidence ellipses. Tx (x = 0, 4, 8, 12, 18) indicates the postharvest ripening time in days and Rn (n = 1-3) the corresponding replicate.

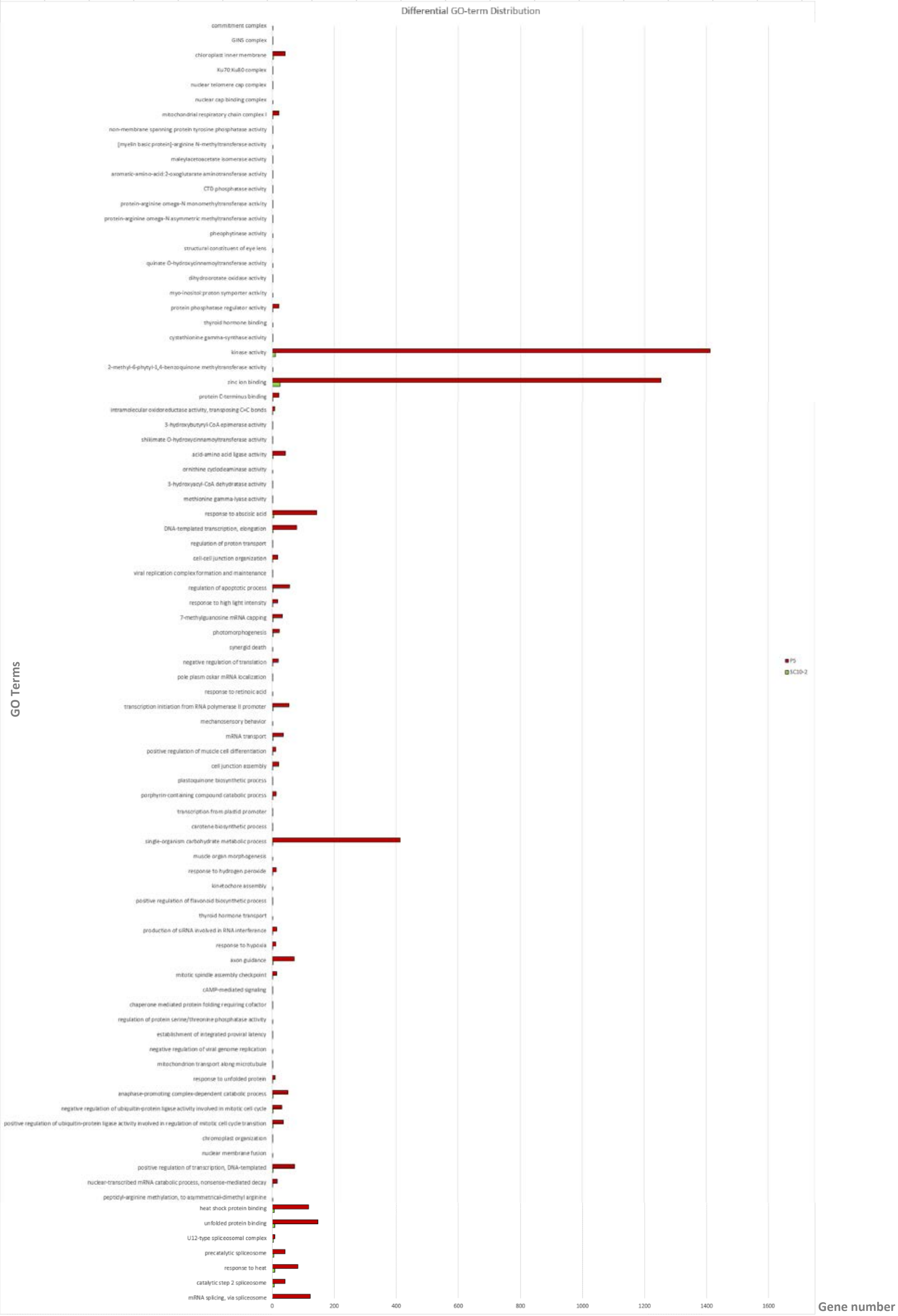
Supplementary Figure 3. Gene Ontology (GO) of the different clusters obtained using differentially expressed genes, only considering the postharvest ripening factor in melon fruit of the near-isogenic line NIL SC10-2 and its parental ´Piel de Sapo´ (PS) harvested in firm-ripe stage of maturity and stored at 20.5 ºC and 88% relative humidity for 18 d.


Differential GO-term Distribution
eukaryotic translation initiation factor 4F complex
Ada2/Gcn5/Ada3 transcription activator complex
mitochondrial large ribosomal subunit
SCF ubiquitin ligase complex
H4/H2A histone acetyltransferase complex
PCNA complex
calcium channel activity
translation initiation factor activity
sequence-specific DNA binding
DNA polymerase processivity factor activity
oxoglutarate dehydrogenase (succinyl-transferring) activity
methylmalonate-semialdehyde dehydrogenase (acylating) activity
sulfate adenylyltransferase (ATP) activity
response to chitin
cellular heat acclimation
response to insect
histone H3 acetylation
SCF-dependent proteasomal ubiquitin-dependent protein catabolic process
defense response to bacterium
shade avoidance
negative regulation of cell death
camalexin biosynthetic process
root hair elongation
transport of virus in host, cell to cell
inflammatory response
phenylpyruvate tautomerase activity
lead ion binding
porphobilinogen synthase activity
carbonate dehydratase activity
lipid A biosynthetic process
ribosome biogenesis
UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase activity
mRNA metabolic process
response to auxin
cytosolic small ribosomal subunit
cytosolic large ribosomal subunit
translational termination
translational elongation
structural constituent of ribosome
GO Terms
0
50
100
150
200
250
300
350
400
450
500
Gene number
🟥 PS
🟩 SC10-2

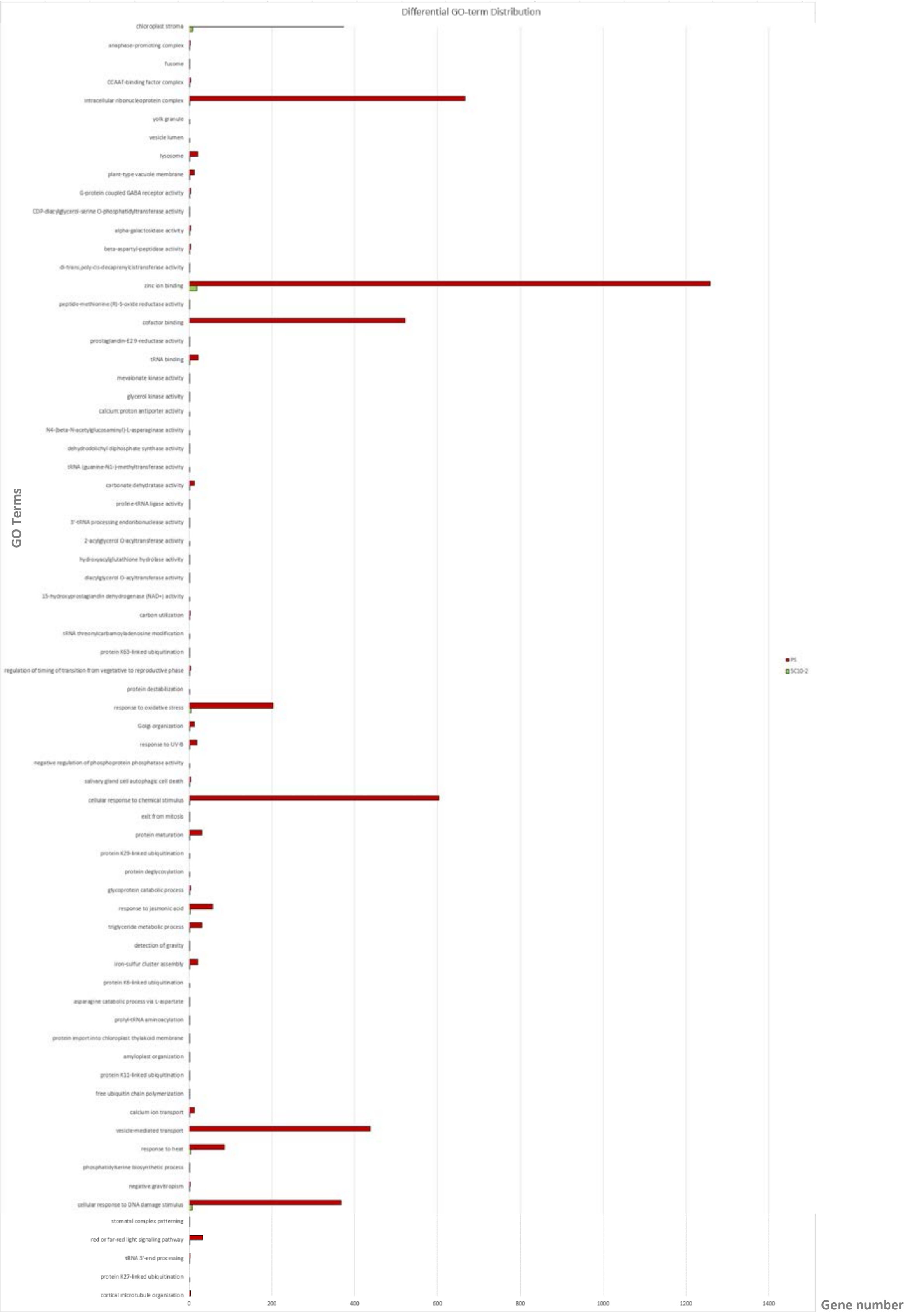
GO. Cluster 1


Differential GO-term Distribution
GO Terms
bicellular tight junction
glycine cleavage complex
riboflavin synthase complex
3-isopropylmalate dehydratase complex
box H/ACA snoRNP complex
integrin complex
longitudinal side of cell surface
DNA replication factor A complex
mitochondrial respiratory chain complex IV
alpha-1,2-mannosyltransferase activity
thermospermine synthase activity
UDP-glucose 4-epimerase activity
3-dehydrosphinganine reductase activity
arginine-tRNA ligase activity
gamma-glutamyl-peptidase activity
arginine binding
serine-type peptidase activity
glyoxylate reductase (NADP) activity
bilirubin oxidase activity
guanosine-3',5'-bis(diphosphate) 3'-diphosphatase activity
estrogen receptor binding
aspartate-semialdehyde dehydrogenase activity
N-acetylgalactosamine kinase activity
quercetin 3-O-methyltransferase activity
diaminopimelate decarboxylase activity
sulfite reductase activity
cytokine activity
6,7-dimethyl-8-ribityllumazine synthase activity
helicase activity
disulfide oxidoreductase activity
L-tyrosine transmembrane transporter activity
alpha-glucan, water dikinase activity
protein-cysteine S-palmitoyltransferase activity
cis-trans isomerase activity
arabinosyltransferase activity
xyloglucan xyloglucosyl transferase activity
fucokinase activity
calcium ion binding
endoplasmic reticulum signal peptide binding
vesicle targeting
diadenosine tetraphosphate biosynthetic process
detoxification of cobalt ion
regulation of ARF protein signal transduction
adherens junction assembly
oocyte maturation
detoxification of zinc ion
endosperm cellularization
plant-type cell wall organization
modification of morphology or physiology of other organism
nucleotide-excision repair, DNA gap filling
amine metabolic process
microtubule-based movement
detection of ethylene stimulus
defense response to other organism
glycerol catabolic process
glycerophosphate shuttle
mitochondrial electron transport, cytochrome c to oxygen
indole-containing compound biosynthetic process
arginyl-tRNA aminoacylation
proline biosynthetic process
establishment or maintenance of actin cytoskeleton polarity
DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest
glycogen biosynthetic process
cytidine metabolic process
plant ovule morphogenesis
purine ribonucleotide binding
photorespiration
carbonyl reductase (NADPH) activity
defense response by callose deposition
DNA-directed DNA polymerase activity
chaperone binding
lipid particle
mitochondrial respiratory chain complex I
response to bacterium
RNA splicing
endosome
phosphoglycolate phosphatase activity
DNA replication preinitiation complex
sterol 3-beta-glucosyltransferase activity
1-aminocyclopropane-1-carboxylate oxidase activity
glucose-1-phosphate adenylyltransferase activity
DNA replication checkpoint
aminopeptidase activity
pollen germination
multidimensional cell growth
extrinsic component of cytoplasmic side of plasma membrane
proteasome regulatory particle, lid subcomplex
glycogen debranching enzyme activity
arginine biosynthetic process via ornithine
body morphogenesis
eukaryotic translation initiation factor 3 complex
chloroplast thylakoid membrane
pentose-phosphate shunt
hermaphrodite genitalia development
chaperone mediated protein folding independent of cofactor
pyridoxal phosphate binding
lateral plasma membrane
tubulin binding
transketolase activity
L-ascorbic acid binding
glutamate 5-kinase activity
ethanol oxidation
starch metabolic process
pronuclear migration
collagen and cuticulin-based cuticle development
vacuolar membrane
mitochondrial intermembrane space
3-isopropylmalate dehydratase activity
tricarboxylic acid cycle
pre-replicative complex assembly involved in nuclear cell cycle DNA replication
response to fungus
determination of adult lifespan
telomere maintenance via recombination
cell wall
telomere maintenance via semi-conservative replication
DNA primase activity
DNA replication, synthesis of RNA primer
alpha DNA polymerase:primase complex
embryo development ending in birth or egg hatching
magnesium ion binding
DNA unwinding involved in DNA replication
response to cadmium ion
cytosolic small ribosomal subunit
DNA replication initiation
structural constituent of ribosome
translational elongation
0
500
1000
1500
2000
2500
Gene number
■ P5
■ SC10-2

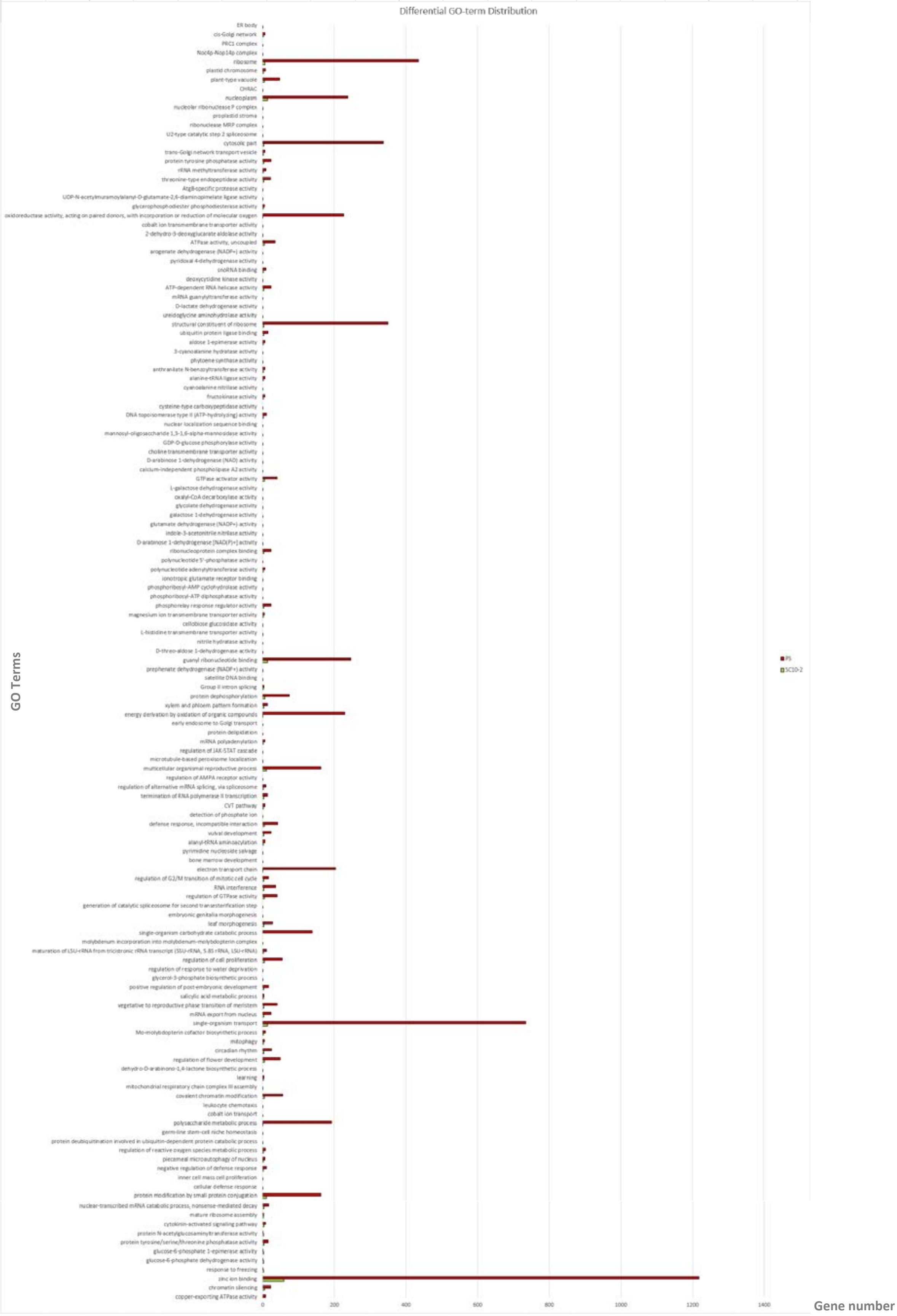
GO. Cluster 2


Differential GO-term Distribution
GO Terms
commitment complex
GINS complex
chloroplast inner membrane
Ku70:Ku80 complex
nuclear telomere cap complex
nuclear cap binding complex
mitochondrial respiratory chain complex I
non-membrane spanning protein tyrosine phosphatase activity
[myelin basic protein]-arginine N-methyltransferase activity
maleylacetoacetate isomerase activity
aromatic-amino-acid:2-oxoglutarate aminotransferase activity
CTD phosphatase activity
protein-arginine omega-N monomethyltransferase activity
protein-arginine omega-N asymmetric methyltransferase activity
pheophytinase activity
structural constituent of eye lens
quinate O-hydroxycinnamoyltransferase activity
dihydroorotate oxidase activity
myo-inositol:proton symporter activity
protein phosphatase regulator activity
thyroid hormone binding
cystathionine gamma-synthase activity
kinase activity
2-methyl-6-phytyl-1,4-benzoquinone methyltransferase activity
zinc ion binding
protein C-terminus binding
intramolecular oxidoreductase activity, transposing C=C bonds
3-hydroxybutyryl-CoA epimerase activity
shikimate O-hydroxycinnamoyltransferase activity
acid-amino acid ligase activity
ornithine cyclodeaminase activity
3-hydroxyacyl-CoA dehydratase activity
methionine gamma-lyase activity
response to abscisic acid
DNA-templated transcription, elongation
regulation of proton transport
cell-cell junction organization
viral replication complex formation and maintenance
regulation of apoptotic process
response to high light intensity
7-methylguanosine mRNA capping
photomorphogenesis
synergid death
negative regulation of translation
pole plasm oskar mRNA localization
response to retinoic acid
transcription initiation from RNA polymerase II promoter
mechanosensory behavior
mRNA transport
positive regulation of muscle cell differentiation
cell junction assembly
plastoquinone biosynthetic process
porphyrin-containing compound catabolic process
transcription from plastid promoter
carotene biosynthetic process
single-organism carbohydrate metabolic process
muscle organ morphogenesis
response to hydrogen peroxide
kinetochore assembly
positive regulation of flavonoid biosynthetic process
thyroid hormone transport
production of siRNA involved in RNA interference
response to hypoxia
axon guidance
mitotic spindle assembly checkpoint
cAMP-mediated signaling
chaperone mediated protein folding requiring cofactor
regulation of protein serine/threonine phosphatase activity
establishment of integrated proviral latency
negative regulation of viral genome replication
mitochondrion transport along microtubule
response to unfolded protein
anaphase-promoting complex-dependent catabolic process
negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition
chromoplast organization
nuclear membrane fusion
positive regulation of transcription, DNA-templated
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
peptidyl-arginine methylation, to asymmetrical-dimethyl arginine
heat shock protein binding
unfolded protein binding
U12-type spliceosomal complex
precatalytic spliceosome
response to heat
catalytic step 2 spliceosome
mRNA splicing, via spliceosome
0
200
400
600
800
1000
1200
1400
1600
Gene number
🟥 P5
🟩 SC10-2

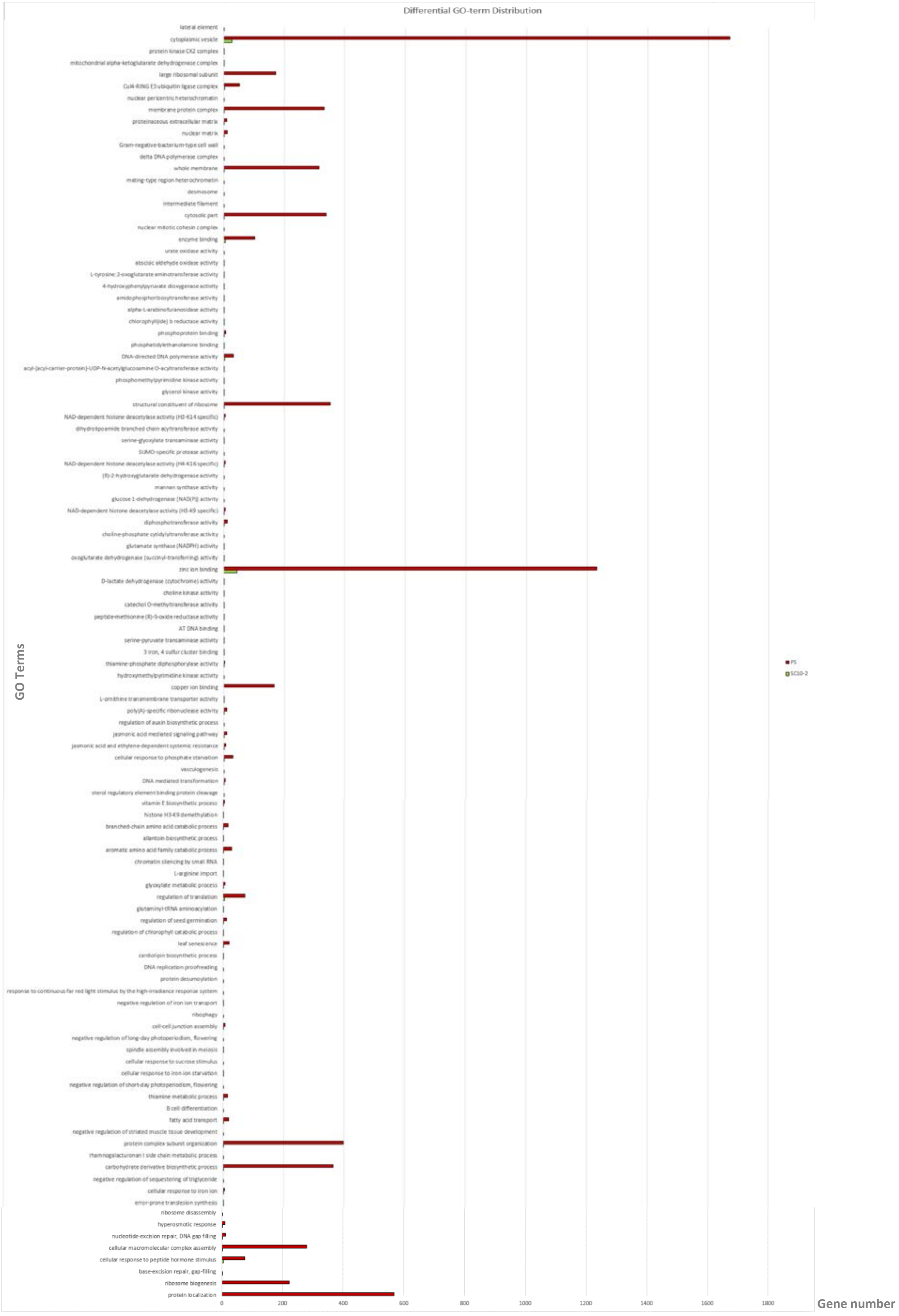
GO. Cluster 3


Differential GO-term Distribution
GO Terms
chloroplast stroma
anaphase-promoting complex
fusome
CCAAT-binding factor complex
intracellular ribonucleoprotein complex
yolk granule
vesicle lumen
lysosome
plant-type vacuole membrane
G-protein coupled GABA receptor activity
CDP-diacylglycerol-serine O-phosphatidyltransferase activity
alpha-galactosidase activity
beta-aspartyl-peptidase activity
di-trans,poly-cis-decaprenylcistransferase activity
zinc ion binding
peptide-methionine (R)-S-oxide reductase activity
cofactor binding
prostaglandin-E2 9-reductase activity
tRNA binding
mevalonate kinase activity
glycerol kinase activity
calcium:proton antiporter activity
N4-(beta-N-acetylglucosaminyl)-L-asparaginase activity
dehydrodolichyl diphosphate synthase activity
tRNA (guanine-N1-)-methyltransferase activity
carbonate dehydratase activity
proline-tRNA ligase activity
3'-tRNA processing endoribonuclease activity
2-acylglycerol O-acyltransferase activity
hydroxyacylglutathione hydrolase activity
diacylglycerol O-acyltransferase activity
15-hydroxyprostaglandin dehydrogenase (NAD+) activity
carbon utilization
tRNA threonylcarbamoyladenosine modification
protein K63-linked ubiquitination
regulation of timing of transition from vegetative to reproductive phase
protein destabilization
response to oxidative stress
Golgi organization
response to UV-B
negative regulation of phosphoprotein phosphatase activity
salivary gland cell autophagic cell death
cellular response to chemical stimulus
exit from mitosis
protein maturation
protein K29-linked ubiquitination
protein deglycosylation
glycoprotein catabolic process
response to jasmonic acid
triglyceride metabolic process
detection of gravity
iron-sulfur cluster assembly
protein K6-linked ubiquitination
asparagine catabolic process via L-aspartate
prolyl-tRNA aminoacylation
protein import into chloroplast thylakoid membrane
amyloplast organization
protein K11-linked ubiquitination
free ubiquitin chain polymerization
calcium ion transport
vesicle-mediated transport
response to heat
phosphatidylserine biosynthetic process
negative gravitropism
cellular response to DNA damage stimulus
stomatal complex patterning
red or far-red light signaling pathway
tRNA 3'-end processing
protein K27-linked ubiquitination
cortical microtubule organization
0
200
400
600
800
1000
1200
1400
Gene number
PS
SC10-2

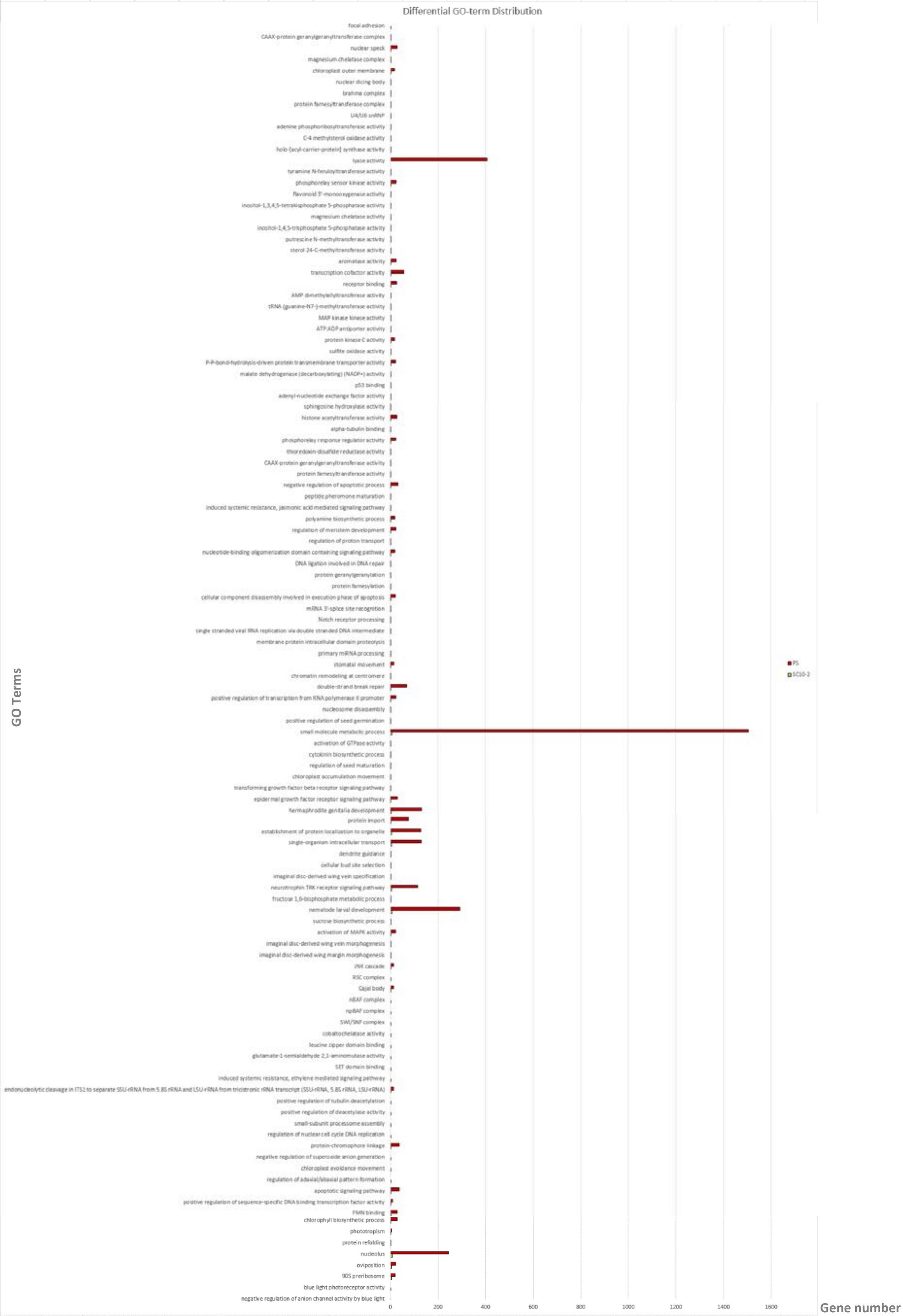
GO. Cluster 4


Differential GO-term Distribution
GO Terms
ER body
cis-Golgi network
PRC1 complex
Noc4p-Nop14p complex
ribosome
plastid chromosome
plant-type vacuole
CHRAC
nucleoplasm
nucleolar ribonuclease P complex
proplastid stroma
ribonuclease MRP complex
U2-type catalytic step 2 spliceosome
cytosolic part
trans-Golgi network transport vesicle
protein tyrosine phosphatase activity
rRNA methyltransferase activity
threonine-type endopeptidase activity
Atg8-specific protease activity
UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase activity
glycerophosphodiester phosphodiesterase activity
oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
cobalt ion transmembrane transporter activity
2-dehydro-3-deoxyglucarate aldolase activity
ATPase activity, uncoupled
arogenate dehydrogenase (NADP+) activity
pyridoxal 4-dehydrogenase activity
snoRNA binding
deoxycytidine kinase activity
ATP-dependent RNA helicase activity
mRNA guanylyltransferase activity
D-lactate dehydrogenase activity
ureidoglycine aminohydrolase activity
structural constituent of ribosome
ubiquitin protein ligase binding
aldose 1-epimerase activity
3-cyanoalanine hydratase activity
phytoene synthase activity
anthranilate N-benzoyltransferase activity
alanine-tRNA ligase activity
cyanoalanine nitrilase activity
fructokinase activity
cysteine-type carboxypeptidase activity
DNA topoisomerase type II (ATP-hydrolyzing) activity
nuclear localization sequence binding
mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase activity
GDP-D-glucose phosphorylase activity
choline transmembrane transporter activity
D-arabinose 1-dehydrogenase (NAD) activity
calcium-independent phospholipase A2 activity
GTPase activator activity
L-galactose dehydrogenase activity
oxalyl-CoA decarboxylase activity
glycolate dehydrogenase activity
galactose 1-dehydrogenase activity
glutamate dehydrogenase (NADP+) activity
indole-3-acetonitrile nitrilase activity
D-arabinose 1-dehydrogenase [NAD(P)+] activity
ribonucleoprotein complex binding
polynucleotide 5'-phosphatase activity
polynucleotide adenylyltransferase activity
ionotropic glutamate receptor binding
phosphoribosyl-AMP cyclohydrolase activity
phosphoribosyl-ATP diphosphatase activity
phosphorelay response regulator activity
magnesium ion transmembrane transporter activity
cellobiose glucosidase activity
L-histidine transmembrane transporter activity
nitrile hydratase activity
D-threo-aldose 1-dehydrogenase activity
guanyl ribonucleotide binding
prephenate dehydrogenase (NADP+) activity
satellite DNA binding
Group II intron splicing
protein dephosphorylation
xylem and phloem pattern formation
energy derivation by oxidation of organic compounds
early endosome to Golgi transport
protein delipidation
mRNA polyadenylation
regulation of JAK-STAT cascade
microtubule-based peroxisome localization
multicellular organismal reproductive process
regulation of AMPA receptor activity
regulation of alternative mRNA splicing, via spliceosome
termination of RNA polymerase II transcription
CVT pathway
detection of phosphate ion
defense response, incompatible interaction
vulval development
alanyl-tRNA aminoacylation
pyrimidine nucleoside salvage
bone marrow development
electron transport chain
regulation of G2/M transition of mitotic cell cycle
RNA interference
regulation of GTPase activity
generation of catalytic spliceosome for second transesterification step
embryonic genitalia morphogenesis
leaf morphogenesis
single-organism carbohydrate catabolic process
molybdenum incorporation into molybdenum-molybdopterin complex
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
regulation of cell proliferation
regulation of response to water deprivation
glycerol-3-phosphate biosynthetic process
positive regulation of post-embryonic development
salicylic acid metabolic process
vegetative to reproductive phase transition of meristem
mRNA export from nucleus
single-organism transport
Mo-molybdopterin cofactor biosynthetic process
mitophagy
circadian rhythm
regulation of flower development
dehydro-D-arabinono-1,4-lactone biosynthetic process
learning
mitochondrial respiratory chain complex III assembly
covalent chromatin modification
leukocyte chemotaxis
cobalt ion transport
polysaccharide metabolic process
germ-line stem-cell niche homeostasis
protein deubiquitination involved in ubiquitin-dependent protein catabolic process
regulation of reactive oxygen species metabolic process
piecemeal microautophagy of nucleus
negative regulation of defense response
inner cell mass cell proliferation
cellular defense response
protein modification by small protein conjugation
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
mature ribosome assembly
cytokinin-activated signaling pathway
protein N-acetylglucosaminyltransferase activity
protein tyrosine/serine/threonine phosphatase activity
glucose-6-phosphate 1-epimerase activity
glucose-6-phosphate dehydrogenase activity
response to freezing
zinc ion binding
chromatin silencing
copper-exporting ATPase activity
0
200
400
600
800
1000
1200
1400
Gene number
🟥 P5
🟩 SC10-2

GO. Cluster 5

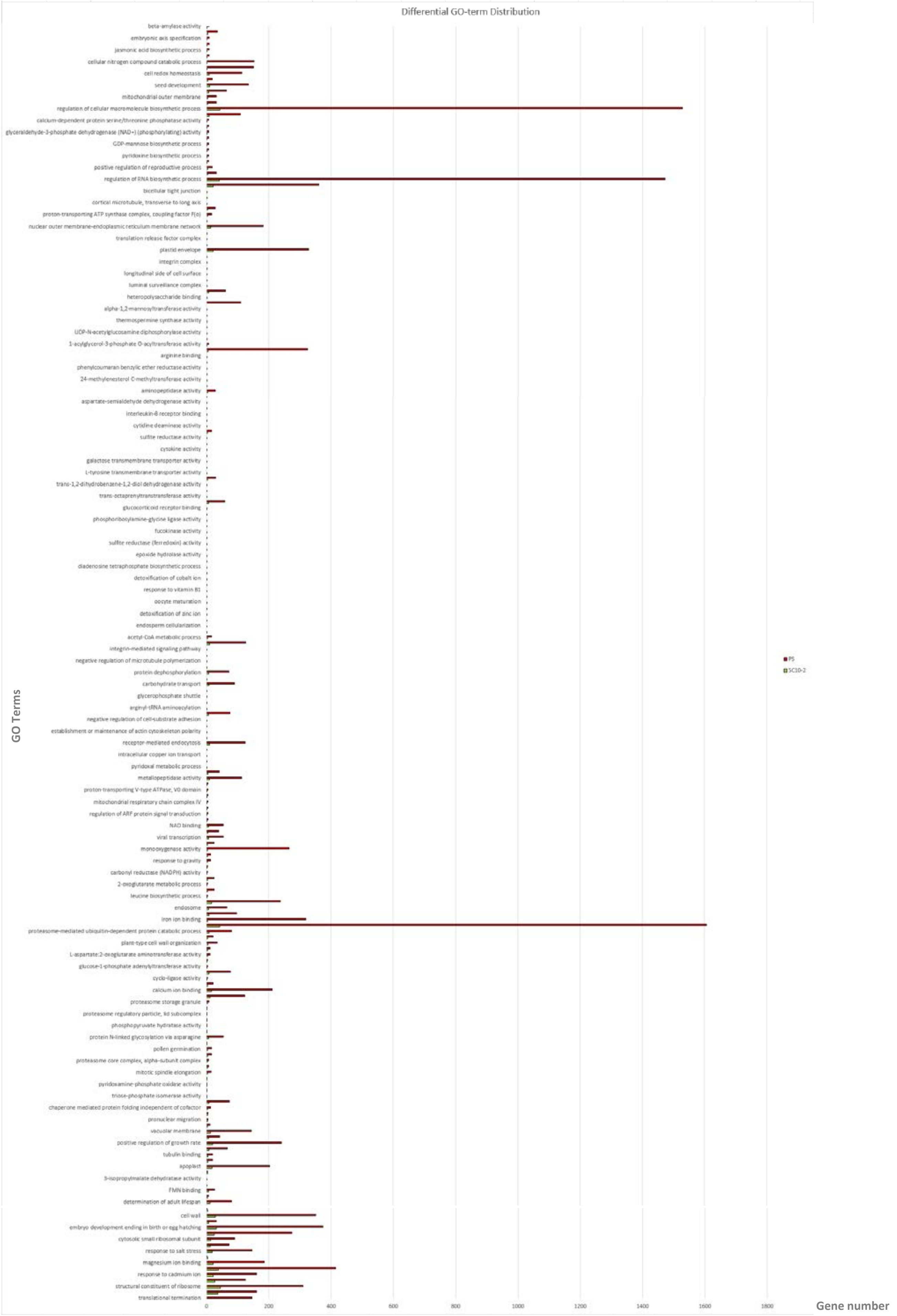

Differential GO-term Distribution
GO Terms
lateral element
cytoplasmic vesicle
protein kinase CK2 complex
mitochondrial alpha-ketoglutarate dehydrogenase complex
large ribosomal subunit
Cul4-RING E3 ubiquitin ligase complex
nuclear pericentric heterochromatin
membrane protein complex
proteinaceous extracellular matrix
nuclear matrix
Gram-negative-bacterium-type cell wall
delta DNA polymerase complex
whole membrane
mating-type region heterochromatin
desmosome
intermediate filament
cytosolic part
nuclear mitotic cohesin complex
enzyme binding
urate oxidase activity
abscisic aldehyde oxidase activity
L-tyrosine:2-oxoglutarate aminotransferase activity
4-hydroxyphenylpyruvate dioxygenase activity
amidophosphoribosyltransferase activity
alpha-L-arabinofuranosidase activity
chlorophyll(ide) b reductase activity
phosphoprotein binding
phosphatidylethanolamine binding
DNA-directed DNA polymerase activity
acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase activity
phosphomethylpyrimidine kinase activity
glycerol kinase activity
structural constituent of ribosome
NAD-dependent histone deacetylase activity (H3-K14 specific)
dihydrolipoamide branched chain acyltransferase activity
serine-glyoxylate transaminase activity
SUMO-specific protease activity
NAD-dependent histone deacetylase activity (H4-K16 specific)
(R)-2-hydroxyglutarate dehydrogenase activity
mannan synthase activity
glucose 1-dehydrogenase [NAD(P)] activity
NAD-dependent histone deacetylase activity (H3-K9 specific)
diphosphotransferase activity
choline-phosphate cytidylyltransferase activity
glutamate synthase (NADPH) activity
oxoglutarate dehydrogenase (succinyl-transferring) activity
zinc ion binding
D-lactate dehydrogenase (cytochrome) activity
choline kinase activity
catechol O-methyltransferase activity
peptide-methionine (R)-S-oxide reductase activity
AT DNA binding
serine-pyruvate transaminase activity
3 iron, 4 sulfur cluster binding
thiamine-phosphate diphosphorylase activity
hydroxymethylpyrimidine kinase activity
copper ion binding
L-ornithine transmembrane transporter activity
poly(A)-specific ribonuclease activity
regulation of auxin biosynthetic process
jasmonic acid mediated signaling pathway
jasmonic acid and ethylene-dependent systemic resistance
cellular response to phosphate starvation
vasculogenesis
DNA mediated transformation
sterol regulatory element binding protein cleavage
vitamin E biosynthetic process
histone H3-K9 demethylation
branched-chain amino acid catabolic process
allantoin biosynthetic process
aromatic amino acid family catabolic process
chromatin silencing by small RNA
L-arginine import
glyoxylate metabolic process
regulation of translation
glutaminyl-tRNA aminoacylation
regulation of seed germination
regulation of chlorophyll catabolic process
leaf senescence
cardiolipin biosynthetic process
DNA replication proofreading
protein desumoylation
response to continuous far red light stimulus by the high-irradiance response system
negative regulation of iron ion transport
ribophagy
cell-cell junction assembly
negative regulation of long-day photoperiodism, flowering
spindle assembly involved in meiosis
cellular response to sucrose stimulus
cellular response to iron ion starvation
negative regulation of short-day photoperiodism, flowering
thiamine metabolic process
B cell differentiation
fatty acid transport
negative regulation of striated muscle tissue development
protein complex subunit organization
rhamnogalacturonan I side chain metabolic process
carbohydrate derivative biosynthetic process
negative regulation of sequestering of triglyceride
cellular response to iron ion
error-prone translesion synthesis
ribosome disassembly
hyperosmotic response
nucleotide-excision repair, DNA gap filling
cellular macromolecular complex assembly
cellular response to peptide hormone stimulus
base-excision repair, gap-filling
ribosome biogenesis
protein localization
0
200
400
600
800
1000
1200
1400
1600
1800
Gene number
🟥 PS
🟩 SC10-2

GO. Cluster 6

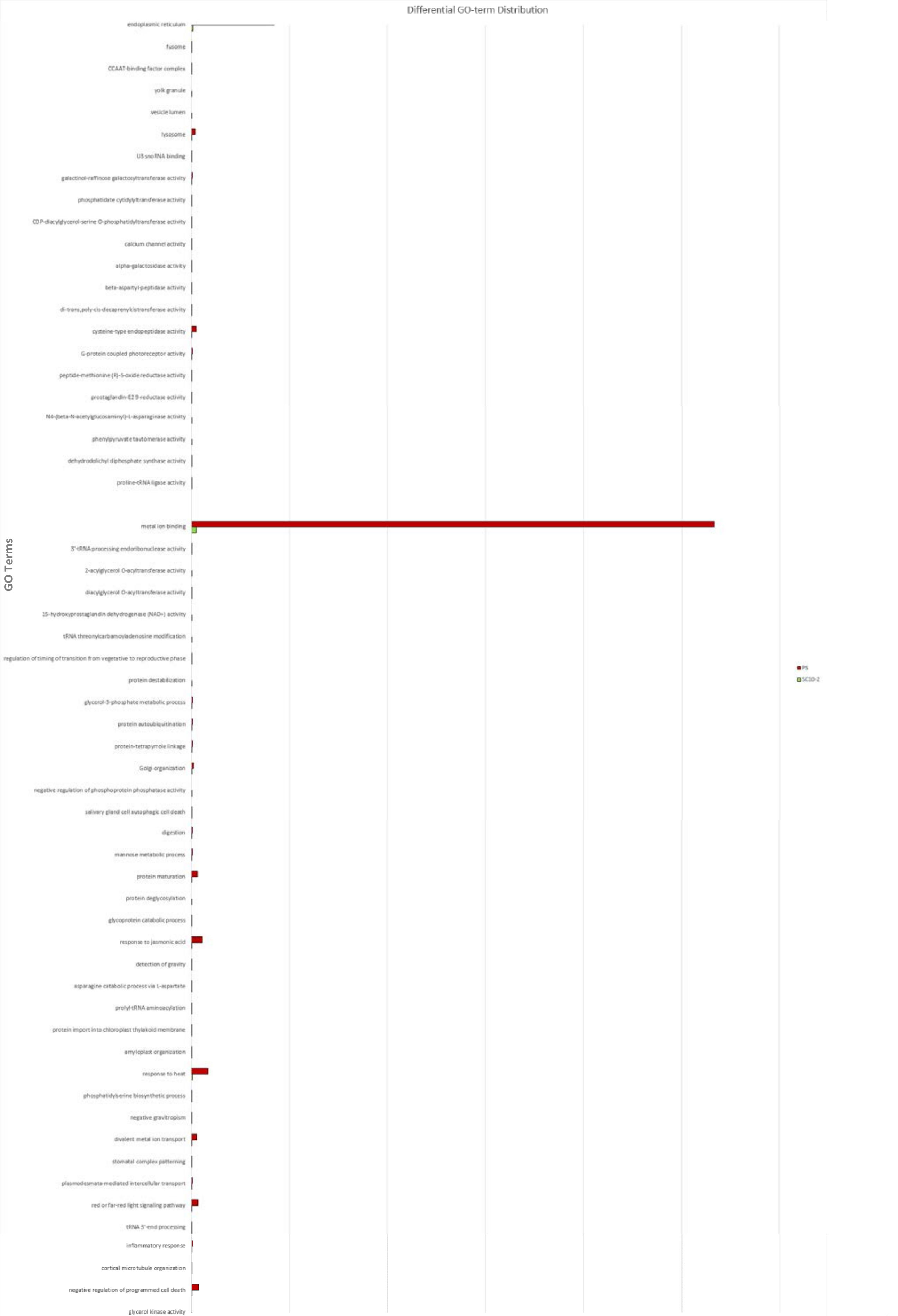

Differential GO-term Distribution
GO Terms
focal adhesion
CAAX-protein geranylgeranyltransferase complex
nuclear speck
magnesium chelatase complex
chloroplast outer membrane
nuclear dicing body
brahma complex
protein farnesyltransferase complex
U4/U6 snRNP
adenine phosphoribosyltransferase activity
C-4 methylsterol oxidase activity
holo-[acyl-carrier-protein] synthase activity
lyase activity
tyramine N-feruloyltransferase activity
phosphorelay sensor kinase activity
flavonoid 3'-monooxygenase activity
inositol-1,3,4,5-tetrakisphosphate 5-phosphatase activity
magnesium chelatase activity
inositol-1,4,5-trisphosphate 5-phosphatase activity
putrescine N-methyltransferase activity
sterol 24-C-methyltransferase activity
aromatase activity
transcription cofactor activity
receptor binding
AMP dimethylallyltransferase activity
tRNA (guanine-N7-)-methyltransferase activity
MAP kinase kinase activity
ATP:ADP antiporter activity
protein kinase C activity
sulfite oxidase activity
P-P-bond-hydrolysis-driven protein transmembrane transporter activity
malate dehydrogenase (decarboxylating) (NADP+) activity
p53 binding
adenyl-nucleotide exchange factor activity
sphingosine hydroxylase activity
histone acetyltransferase activity
alpha-tubulin binding
phosphorelay response regulator activity
thioredoxin-disulfide reductase activity
CAAX-protein geranylgeranyltransferase activity
protein farnesyltransferase activity
negative regulation of apoptotic process
peptide pheromone maturation
induced systemic resistance, jasmonic acid mediated signaling pathway
polyamine biosynthetic process
regulation of meristem development
regulation of proton transport
nucleotide-binding oligomerization domain containing signaling pathway
DNA ligation involved in DNA repair
protein geranylgeranylation
protein farnesylation
cellular component disassembly involved in execution phase of apoptosis
mRNA 3'-splice site recognition
Notch receptor processing
single stranded viral RNA replication via double stranded DNA intermediate
membrane protein intracellular domain proteolysis
primary miRNA processing
stomatal movement
chromatin remodeling at centromere
double-strand break repair
positive regulation of transcription from RNA polymerase II promoter
nucleosome disassembly
positive regulation of seed germination
small molecule metabolic process
activation of GTPase activity
cytokinin biosynthetic process
regulation of seed maturation
chloroplast accumulation movement
transforming growth factor beta receptor signaling pathway
epidermal growth factor receptor signaling pathway
hermaphrodite genitalia development
protein import
establishment of protein localization to organelle
single-organism intracellular transport
dendrite guidance
cellular bud site selection
imaginal disc-derived wing vein specification
neurotrophin TRK receptor signaling pathway
fructose 1,6-bisphosphate metabolic process
nematode larval development
sucrose biosynthetic process
activation of MAPK activity
imaginal disc-derived wing vein morphogenesis
imaginal disc-derived wing margin morphogenesis
JNK cascade
RSC complex
Cajal body
nBAF complex
npBAF complex
SWI/SNF complex
cobaltochelatase activity
leucine zipper domain binding
glutamate-1-semialdehyde 2,1-aminomutase activity
SET domain binding
induced systemic resistance, ethylene mediated signaling pathway
endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
positive regulation of tubulin deacetylation
positive regulation of deacetylase activity
small-subunit processome assembly
regulation of nuclear cell cycle DNA replication
protein-chromophore linkage
negative regulation of superoxide anion generation
chloroplast avoidance movement
regulation of adaxial/abaxial pattern formation
apoptotic signaling pathway
positive regulation of sequence-specific DNA binding transcription factor activity
FMN binding
chlorophyll biosynthetic process
phototropism
protein refolding
nucleolus
oviposition
90S preribosome
blue light photoreceptor activity
negative regulation of anion channel activity by blue light
0
200
400
600
800
1000
1200
1400
1600
Gene number
■ FS
□ SC10-2

GO. Cluster 7

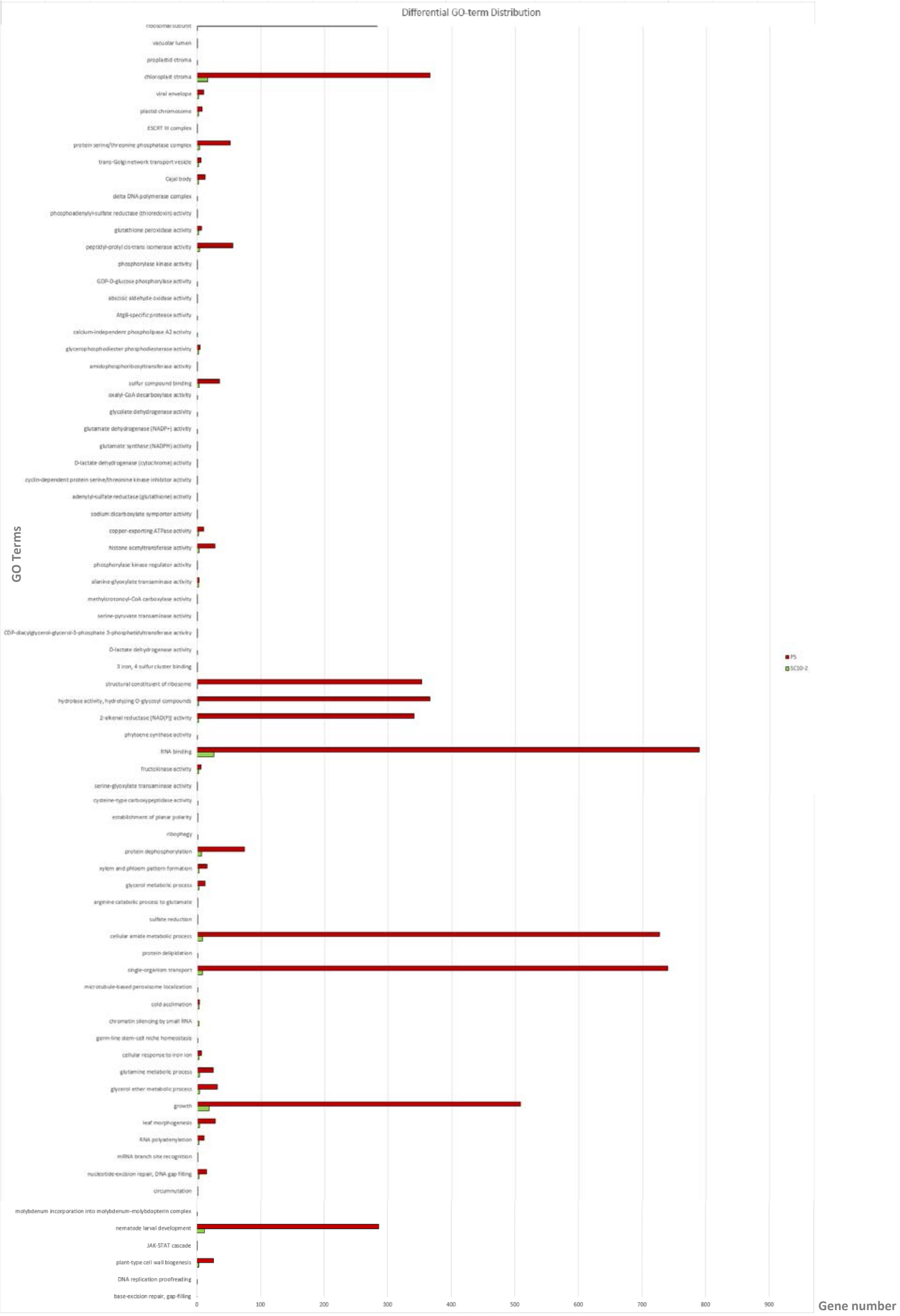
Supplementary Figure 4. Gene Ontology (GO) of the different clusters obtained using differentially expressed genes, only considering the introgression differences over time in melon fruit of the near-isogenic line NIL SC10-2 and its parental ´Piel de Sapo´ (PS) harvested in firm-ripe stage of maturity and stored at 20.5 ºC and 88% relative humidity for18 d.


Differential GO-term Distribution
beta-amylase activity
embryonic axis specification
jasmonic acid biosynthetic process
cellular nitrogen compound catabolic process
cell redox homeostasis
seed development
mitochondrial outer membrane
regulation of cellular macromolecule biosynthetic process
calcium-dependent protein serine/threonine phosphatase activity
glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity
GDP-mannose biosynthetic process
pyridoxine biosynthetic process
positive regulation of reproductive process
regulation of RNA biosynthetic process
bicellular tight junction
cortical microtubule, transverse to long axis
proton-transporting ATP synthase complex, coupling factor F(o)
nuclear outer membrane-endoplasmic reticulum membrane network
translation release factor complex
plastid envelope
integrin complex
longitudinal side of cell surface
luminal surveillance complex
heteropolysaccharide binding
alpha-1,2-mannosyltransferase activity
thermospermine synthase activity
UDP-N-acetylglucosamine diphosphorylase activity
1-acylglycerol-3-phosphate O-acyltransferase activity
arginine binding
phenylcoumaran benzylic ether reductase activity
24-methylenesterol C-methyltransferase activity
aminopeptidase activity
aspartate-semialdehyde dehydrogenase activity
interleukin-8 receptor binding
cytidine deaminase activity
sulfite reductase activity
cytokine activity
galactose transmembrane transporter activity
L-tyrosine transmembrane transporter activity
trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity
trans-octaprenyltranstransferase activity
glucocorticoid receptor binding
phosphoribosylamine-glycine ligase activity
fucokinase activity
sulfite reductase (ferredoxin) activity
epoxide hydrolase activity
diadenosine tetraphosphate biosynthetic process
detoxification of cobalt ion
response to vitamin B1
oocyte maturation
detoxification of zinc ion
endosperm cellularization
acetyl-CoA metabolic process
integrin-mediated signaling pathway
negative regulation of microtubule polymerization
protein dephosphorylation
carbohydrate transport
glycerophosphate shuttle
arginyl-tRNA aminoacylation
negative regulation of cell-substrate adhesion
establishment or maintenance of actin cytoskeleton polarity
receptor-mediated endocytosis
intracellular copper ion transport
pyridoxal metabolic process
metallopeptidase activity
proton-transporting V-type ATPase, V0 domain
mitochondrial respiratory chain complex IV
regulation of ARF protein signal transduction
NAD binding
viral transcription
monooxygenase activity
response to gravity
carbonyl reductase (NADPH) activity
2-oxoglutarate metabolic process
leucine biosynthetic process
endosome
iron ion binding
proteasome-mediated ubiquitin-dependent protein catabolic process
plant-type cell wall organization
L-aspartate:2-oxoglutarate aminotransferase activity
glucose-1-phosphate adenylyltransferase activity
cyclo-ligase activity
calcium ion binding
proteasome storage granule
proteasome regulatory particle, lid subcomplex
phosphopyruvate hydratase activity
protein N-linked glycosylation via asparagine
pollen germination
proteasome core complex, alpha-subunit complex
mitotic spindle elongation
pyridoxamine-phosphate oxidase activity
triose-phosphate isomerase activity
chaperone mediated protein folding independent of cofactor
pronuclear migration
vacuolar membrane
positive regulation of growth rate
tubulin binding
apoplast
3-isopropylmalate dehydratase activity
FMN binding
determination of adult lifespan
cell wall
embryo development ending in birth or egg hatching
cytosolic small ribosomal subunit
response to salt stress
magnesium ion binding
response to cadmium ion
structural constituent of ribosome
translational termination
GO Terms
0
200
400
600
800
1000
1200
1400
1600
1800
Gene number
PS
SC10-2

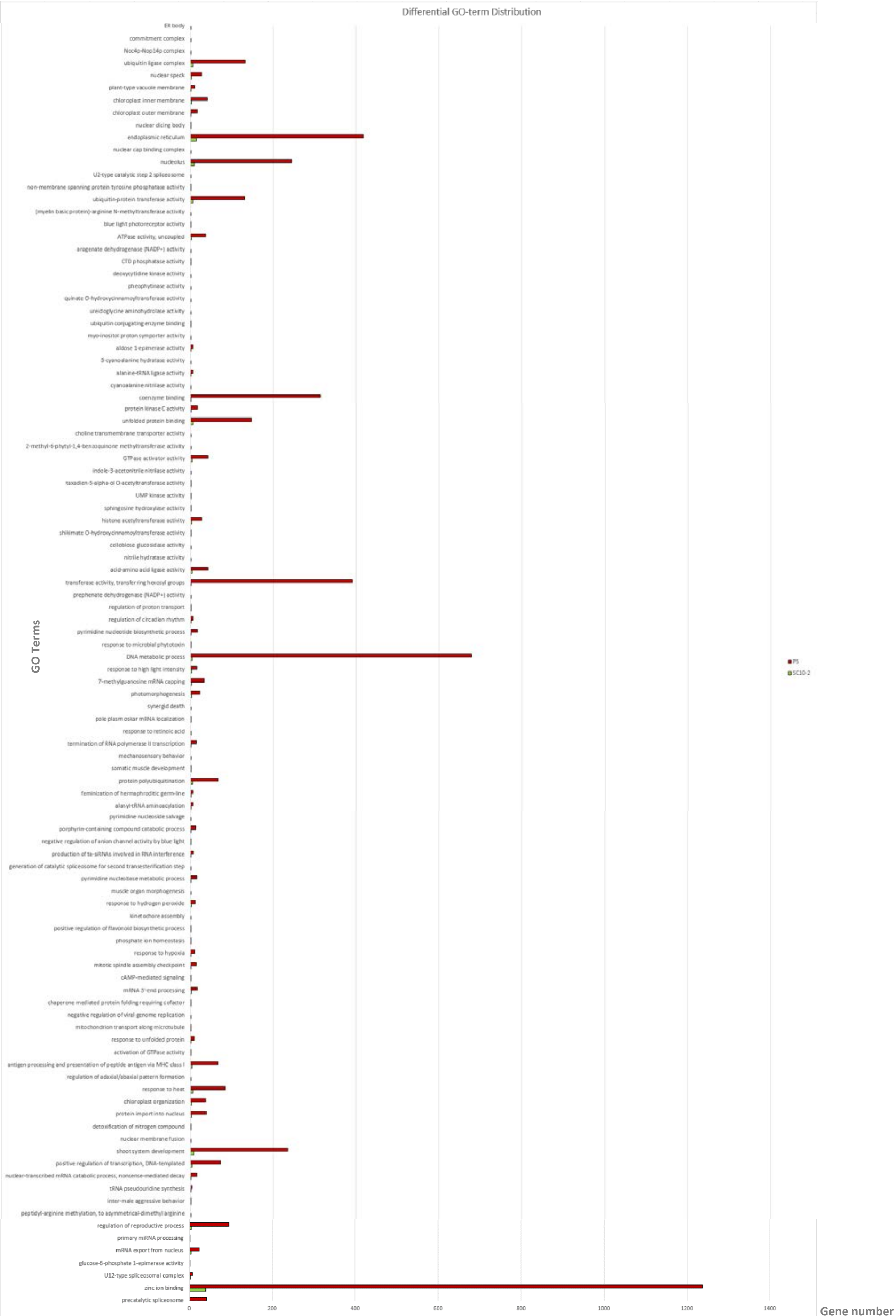
GO. Cluster 1


Differential GO-term Distribution
GO Terms
endoplasmic reticulum
fusome
CCAAT-binding factor complex
yolk granule
vesicle lumen
lysosome
U3 snoRNA binding
galactinol-raffinose galactosyltransferase activity
phosphatidate cytidylyltransferase activity
CDP-diacylglycerol-serine O-phosphatidyltransferase activity
calcium channel activity
alpha-galactosidase activity
beta-aspartyl-peptidase activity
di-trans,poly-cis-decaprenylcistransferase activity
cysteine-type endopeptidase activity
G-protein coupled photoreceptor activity
peptide-methionine (R)-S-oxide reductase activity
prostaglandin-E2 9-reductase activity
N4-(beta-N-acetylglucosaminyl)-L-asparaginase activity
phenylpyruvate tautomerase activity
dehydrodolichyl diphosphate synthase activity
proline-tRNA ligase activity
metal ion binding
3'-tRNA processing endoribonuclease activity
2-acylglycerol O-acyltransferase activity
diacylglycerol O-acyltransferase activity
15-hydroxyprostaglandin dehydrogenase (NAD+) activity
tRNA threonylcarbamoyladenosine modification
regulation of timing of transition from vegetative to reproductive phase
protein destabilization
glycerol-3-phosphate metabolic process
protein autoubiquitination
protein-tetrapyrrole linkage
Golgi organization
negative regulation of phosphoprotein phosphatase activity
salivary gland cell autophagic cell death
digestion
mannose metabolic process
protein maturation
protein deglycosylation
glycoprotein catabolic process
response to jasmonic acid
detection of gravity
asparagine catabolic process via L-aspartate
prolyl-tRNA aminoacylation
protein import into chloroplast thylakoid membrane
amyloplast organization
response to heat
phosphatidylserine biosynthetic process
negative gravitropism
divalent metal ion transport
stomatal complex patterning
plasmodesmata-mediated intercellular transport
red or far-red light signaling pathway
tRNA 5'-end processing
inflammatory response
cortical microtubule organization
negative regulation of programmed cell death
glycerol kinase activity
0
500
1000
1500
2000
2500
3000
Gene number
🟥 PS
🟩 SC10-2

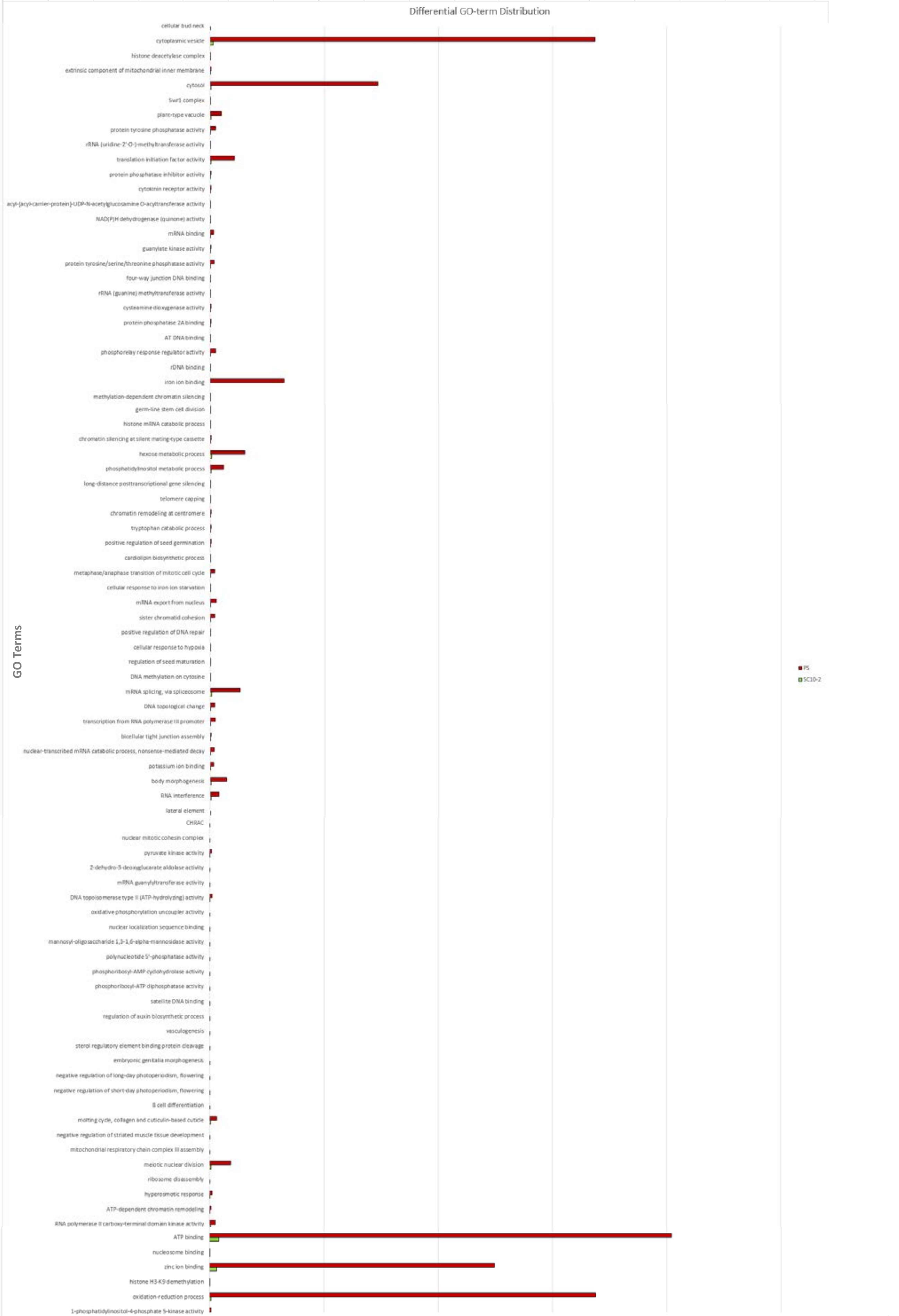
GO. Cluster 2


Differential GO-term Distribution
GO Terms
ribosomal subunit
vacuolar lumen
proplastid stroma
chloroplast stroma
viral envelope
plastid chromosome
ESCRT III complex
protein serine/threonine phosphatase complex
trans-Golgi network transport vesicle
Cajal body
delta DNA polymerase complex
phosphoadenylyl-sulfate reductase (thioredoxin) activity
glutathione peroxidase activity
peptidyl-prolyl cis-trans isomerase activity
phosphorylase kinase activity
GDP-D-glucose phosphorylase activity
abscisic aldehyde oxidase activity
Atg8-specific protease activity
calcium-independent phospholipase A2 activity
glycerophosphodiester phosphodiesterase activity
amidophosphoribosyltransferase activity
sulfur compound binding
oxalyl-CoA decarboxylase activity
glycolate dehydrogenase activity
glutamate dehydrogenase (NADP+) activity
glutamate synthase (NADPH) activity
D-lactate dehydrogenase (cytochrome) activity
cyclin-dependent protein serine/threonine kinase inhibitor activity
adenylyl-sulfate reductase (glutathione) activity
sodium:dicarboxylate symporter activity
copper-exporting ATPase activity
histone acetyltransferase activity
phosphorylase kinase regulator activity
alanine-glyoxylate transaminase activity
methylcrotonoyl-CoA carboxylase activity
serine-pyruvate transaminase activity
CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase activity
D-lactate dehydrogenase activity
3 iron, 4 sulfur cluster binding
structural constituent of ribosome
hydrolase activity, hydrolyzing O-glycosyl compounds
2-alkenal reductase [NAD(P)] activity
phytoene synthase activity
RNA binding
fructokinase activity
serine-glyoxylate transaminase activity
cysteine-type carboxypeptidase activity
establishment of planar polarity
ribophagy
protein dephosphorylation
xylem and phloem pattern formation
glycerol metabolic process
arginine catabolic process to glutamate
sulfate reduction
cellular amide metabolic process
protein delipidation
single-organism transport
microtubule-based peroxisome localization
cold acclimation
chromatin silencing by small RNA
germ-line stem-cell niche homeostasis
cellular response to iron ion
glutamine metabolic process
glycerol ether metabolic process
growth
leaf morphogenesis
RNA polyadenylation
mRNA branch site recognition
nucleotide-excision repair, DNA gap filling
circumnutation
molybdenum incorporation into molybdenum-molybdopterin complex
nematode larval development
JAK-STAT cascade
plant-type cell wall biogenesis
DNA replication proofreading
base-excision repair, gap-filling
0
100
200
300
400
500
600
700
800
900
Gene number
P5
SC10-2

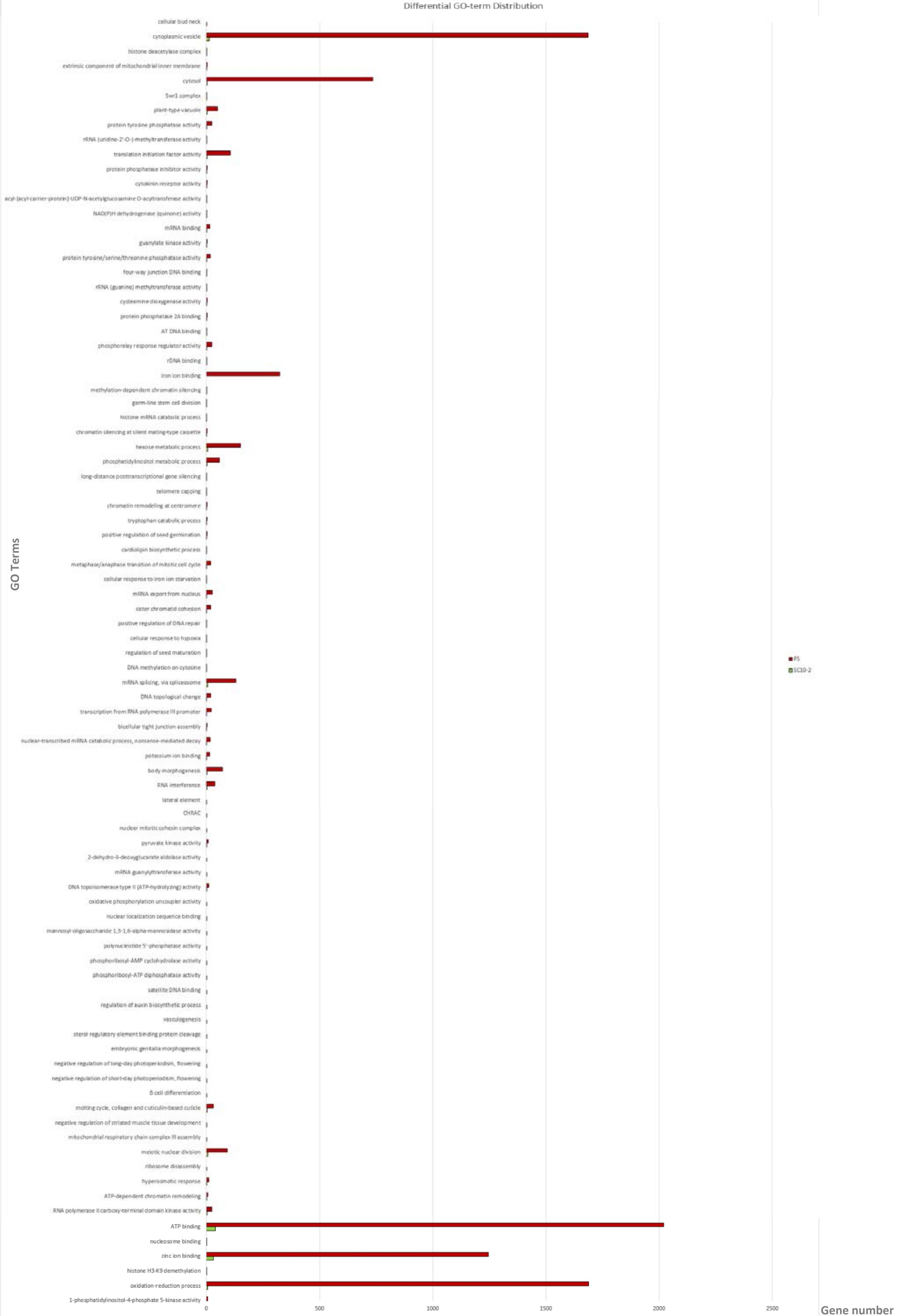
GO. Cluster 3


Differential GO-term Distribution
GO Terms
ER body
commitment complex
Noc4p-Nop14p complex
ubiquitin ligase complex
nuclear speck
plant-type vacuole membrane
chloroplast inner membrane
chloroplast outer membrane
nuclear dicing body
endoplasmic reticulum
nuclear cap binding complex
nucleolus
U2-type catalytic step 2 spliceosome
non-membrane spanning protein tyrosine phosphatase activity
ubiquitin-protein transferase activity
[myelin basic protein]-arginine N-methyltransferase activity
blue light photoreceptor activity
ATPase activity, uncoupled
arogenate dehydrogenase (NADP+) activity
CTD phosphatase activity
deoxycytidine kinase activity
pheophytinase activity
quinate O-hydroxycinnamoyltransferase activity
ureidoglycine aminohydrolase activity
ubiquitin conjugating enzyme binding
myo-inositol proton symporter activity
aldose 1-epimerase activity
3-cyanoalanine hydratase activity
alanine-tRNA ligase activity
cyanoalanine nitrilase activity
coenzyme binding
protein kinase C activity
unfolded protein binding
choline transmembrane transporter activity
2-methyl-6-phytyl-1,4-benzoquinone methyltransferase activity
GTPase activator activity
indole-3-acetonitrile nitrilase activity
taxadien-5-alpha-ol O-acetyltransferase activity
UMP kinase activity
sphingosine hydroxylase activity
histone acetyltransferase activity
shikimate O-hydroxycinnamoyltransferase activity
cellobiose glucosidase activity
nitrile hydratase activity
acid-amino acid ligase activity
transferase activity, transferring hexosyl groups
prephenate dehydrogenase (NADP+) activity
regulation of proton transport
regulation of circadian rhythm
pyrimidine nucleotide biosynthetic process
response to microbial phytotoxin
DNA metabolic process
response to high light intensity
7-methylguanosine mRNA capping
photomorphogenesis
synergid death
pole plasm oskar mRNA localization
response to retinoic acid
termination of RNA polymerase II transcription
mechanosensory behavior
somatic muscle development
protein polyubiquitination
feminization of hermaphroditic germ-line
alanyl-tRNA aminoacylation
pyrimidine nucleoside salvage
porphyrin-containing compound catabolic process
negative regulation of anion channel activity by blue light
production of ta-siRNAs involved in RNA interference
generation of catalytic spliceosome for second transesterification step
pyrimidine nucleobase metabolic process
muscle organ morphogenesis
response to hydrogen peroxide
kinetochore assembly
positive regulation of flavonoid biosynthetic process
phosphate ion homeostasis
response to hypoxia
mitotic spindle assembly checkpoint
cAMP-mediated signaling
mRNA 3'-end processing
chaperone mediated protein folding requiring cofactor
negative regulation of viral genome replication
mitochondrion transport along microtubule
response to unfolded protein
activation of GTPase activity
antigen processing and presentation of peptide antigen via MHC class I
regulation of adaxial/abaxial pattern formation
response to heat
chloroplast organization
protein import into nucleus
detoxification of nitrogen compound
nuclear membrane fusion
shoot system development
positive regulation of transcription, DNA-templated
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
tRNA pseudouridine synthesis
inter-male aggressive behavior
peptidyl-arginine methylation, to asymmetrical-dimethyl arginine
regulation of reproductive process
primary miRNA processing
mRNA export from nucleus
glucose-6-phosphate 1-epimerase activity
U12-type spliceosomal complex
zinc ion binding
precatalytic spliceosome
0
200
400
600
800
1000
1200
1400
Gene number
P5
SC10-2

GO. Cluster 4


Differential GO-term Distribution
GO Terms
cellular bud neck
cytoplasmic vesicle
histone deacetylase complex
extrinsic component of mitochondrial inner membrane
cytosol
Swr1 complex
plant-type vacuole
protein tyrosine phosphatase activity
rRNA (uridine-2'-O-)-methyltransferase activity
translation initiation factor activity
protein phosphatase inhibitor activity
cytokinin receptor activity
acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase activity
NAD(P)H dehydrogenase (quinone) activity
mRNA binding
guanylate kinase activity
protein tyrosine/serine/threonine phosphatase activity
four-way junction DNA binding
rRNA (guanine) methyltransferase activity
cysteamine dioxygenase activity
protein phosphatase 2A binding
AT DNA binding
phosphorelay response regulator activity
rDNA binding
iron ion binding
methylation-dependent chromatin silencing
germ-line stem cell division
histone mRNA catabolic process
chromatin silencing at silent mating-type cassette
hexose metabolic process
phosphatidylinositol metabolic process
long-distance posttranscriptional gene silencing
telomere capping
chromatin remodeling at centromere
tryptophan catabolic process
positive regulation of seed germination
cardiolipin biosynthetic process
metaphase/anaphase transition of mitotic cell cycle
cellular response to iron ion starvation
mRNA export from nucleus
sister chromatid cohesion
positive regulation of DNA repair
cellular response to hypoxia
regulation of seed maturation
DNA methylation on cytosine
mRNA splicing, via spliceosome
DNA topological change
transcription from RNA polymerase III promoter
bicellular tight junction assembly
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
potassium ion binding
body morphogenesis
RNA interference
lateral element
CHRAC
nuclear mitotic cohesin complex
pyruvate kinase activity
2-dehydro-3-deoxyglucarate aldolase activity
mRNA guanylyltransferase activity
DNA topoisomerase type II (ATP-hydrolyzing) activity
oxidative phosphorylation uncoupler activity
nuclear localization sequence binding
mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase activity
polynucleotide 5'-phosphatase activity
phosphoribosyl-AMP cyclohydrolase activity
phosphoribosyl-ATP diphosphatase activity
satellite DNA binding
regulation of auxin biosynthetic process
vasculogenesis
sterol regulatory element binding protein cleavage
embryonic genitalia morphogenesis
negative regulation of long-day photoperiodism, flowering
negative regulation of short-day photoperiodism, flowering
B cell differentiation
molting cycle, collagen and cuticulin-based cuticle
negative regulation of striated muscle tissue development
mitochondrial respiratory chain complex III assembly
meiotic nuclear division
ribosome disassembly
hyperosmotic response
ATP-dependent chromatin remodeling
RNA polymerase II carboxy-terminal domain kinase activity
ATP binding
nucleosome binding
zinc ion binding
histone H3-K9 demethylation
oxidation-reduction process
1-phosphatidylinositol-4-phosphate 5-kinase activity
0
500
1000
1500
2000
2500
Gene number
PS
SC10-2

GO. Cluster 5


Differential GO-term Distribution
GO Terms
cellular bud neck
cytoplasmic vesicle
histone deacetylase complex
extrinsic component of mitochondrial inner membrane
cytosol
Swr1 complex
plant-type vacuole
protein tyrosine phosphatase activity
rRNA (uridine-2'-O-)-methyltransferase activity
translation initiation factor activity
protein phosphatase inhibitor activity
cytokinin receptor activity
acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase activity
NAD(P)H dehydrogenase (quinone) activity
mRNA binding
guanylate kinase activity
protein tyrosine/serine/threonine phosphatase activity
four-way junction DNA binding
rRNA (guanine) methyltransferase activity
cysteamine dioxygenase activity
protein phosphatase 2A binding
AT DNA binding
phosphorelay response regulator activity
rDNA binding
iron ion binding
methylation-dependent chromatin silencing
germ-line stem cell division
histone mRNA catabolic process
chromatin silencing at silent mating-type cassette
hexose metabolic process
phosphatidylinositol metabolic process
long-distance posttranscriptional gene silencing
telomere capping
chromatin remodeling at centromere
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mRNA export from nucleus
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positive regulation of DNA repair
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regulation of seed maturation
DNA methylation on cytosine
mRNA splicing, via spliceosome
DNA topological change
transcription from RNA polymerase III promoter
bicellular tight junction assembly
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
potassium ion binding
body morphogenesis
RNA interference
lateral element
CHRAC
nuclear mitotic cohesin complex
pyruvate kinase activity
2-dehydro-3-deoxyglucarate aldolase activity
mRNA guanylyltransferase activity
DNA topoisomerase type II (ATP-hydrolyzing) activity
oxidative phosphorylation uncoupler activity
nuclear localization sequence binding
mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase activity
polynucleotide 5'-phosphatase activity
phosphoribosyl-AMP cyclohydrolase activity
phosphoribosyl-ATP diphosphatase activity
satellite DNA binding
regulation of auxin biosynthetic process
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sterol regulatory element binding protein cleavage
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negative regulation of long-day photoperiodism, flowering
negative regulation of short-day photoperiodism, flowering
B cell differentiation
molting cycle, collagen and cuticulin-based cuticle
negative regulation of striated muscle tissue development
mitochondrial respiratory chain complex III assembly
meiotic nuclear division
ribosome disassembly
hyperosmotic response
ATP-dependent chromatin remodeling
RNA polymerase II carboxy-terminal domain kinase activity
ATP binding
nucleosome binding
zinc ion binding
histone H3-K9 demethylation
oxidation-reduction process
1-phosphatidylinositol-4-phosphate 5-kinase activity
0
500
1000
1500
2000
2500
Gene number
🟥 PS
🟩 SC10-2

GO. Cluster 6

Supplementary Table 1. List of total Differentially Expressed Genes (2954 DEGs) only considering the comparison between lines over time fruit during postharvest storage at 20.5 ^{o}C and 88% relative humidity for 18 d of the near-isogenic line SC10-2 and its parental control ´Piel de Sapo´ (PS). 1 Presence 0 Absence in the list of DEGs during postharvest ripening time. Gene Ontology terms (GO terms) of the seven different clusters (named 1.x) obtained according to the differentially expressed gene pattern.

Gene ID	pval	qval	Description	
MELO3C010748	2.12940776123105e-12	4.2053673876552e-08	Heat shock transcription factor	1
MELO3C023889	1.64774860422767e-11	1.62706935924462e-07	Ultraviolet-B receptor UVR8	1
MELO3C005540	7.05828728797542e-11	4.64647052167422e-07	14 kDa proline-rich protein dc2.15	1
MELO3C026975	4.80710693473441e-10	1.99977760837466e-06	40S ribosomal protein S15a	1
MELO3C012728	5.06298447611186e-10	1.99977760837466e-06	Vacuolar sorting-associated protein 2-like protein	1
MELO3C003298	1.04465369688e-09	3.43847764328054e-06	high mobility group B protein 1	1
MELO3C013974	1.49749790345766e-09	4.22486944219789e-06	Hsp70-Hsp90 organizing protein 3	1
MELO3C026279	2.1098163216493e-09	5.20834531703152e-06	cell division cycle protein 48 homolog	1
MELO3C018265	2.94331214956145e-09	5.28431560378992e-06	ADP-ribosylation factor GTPase-activating protein	1
MELO3C020533	2.81429302084746e-09	5.28431560378992e-06	Ran-binding protein 1	1
MELO3C026613	2.4889622585178e-09	5.28431560378992e-06	Tubulin alpha chain	1
MELO3C015733	4.18112777733626e-09	6.88109103955115e-06	Pre-mRNA-splicing factor ATP-dependent RNA helicase	1
MELO3C016101	4.9076187558228e-09	6.92289734348174e-06	UBP1-associated protein 2C	1
MELO3C022036	4.56549242855431e-09	6.92289734348174e-06	protein LONGIFOLIA 2	1
MELO3C019941	6.56920629005242e-09	8.62635084597496e-06	T-complex protein 11	1
MELO3C018099	6.98878999116914e-09	8.62635084597496e-06	No data found	0
MELO3C023417	1.0827110208389e-08	1.25779176179691e-05	DUF4050 family protein	1
MELO3C002468	1.31388873114702e-08	1.44155491952347e-05	Tobamovirus multiplication protein 1	1
MELO3C003282	1.38912555902593e-08	1.44388635080016e-05	cleft lip and palate transmembrane protein 1 homolog	1
MELO3C024028	1.65297714405099e-08	1.63223228089315e-05	DEAD-box ATP-dependent RNA helicase	1
MELO3C014090	1.74401538766134e-08	1.6401218995678e-05	No data found	1
MELO3C008669	2.53079915912835e-08	2.11626693401623e-05	RING-type E3 ubiquitin transferase	1
MELO3C018038	2.64090955770513e-08	2.11626693401623e-05	proline iminopeptidase	1
MELO3C001317	2.67895454708622e-08	2.11626693401623e-05	Coiled-coil protein (DUF572)	1
MELO3C003752	2.55143854932527e-08	2.11626693401623e-05	gibberellin-regulated protein 11-like	1
MELO3C010731	2.89443125023325e-08	2.19854318310987e-05	cyclin-dependent kinase G-2 isoform X1	1
MELO3C008209	3.06606515732e-08	2.24265632562639e-05	Ankyrin	1
MELO3C013868	3.65972404603454e-08	2.41181691777337e-05	Cytochrome P450 family ent-kaurenoic acid oxidase	1
MELO3C019616	3.66370487281387e-08	2.41181691777337e-05	E3 ubiquitin-protein ligase RGLG2	1
MELO3C003444	3.45134805179725e-08	2.41181691777337e-05	transcription factor IWS1	1
MELO3C004023	4.57532089992441e-08	2.82368788914397e-05	NADPH--cytochrome P450 reductase	1
MELO3C019369	4.44710406277693e-08	2.82368788914397e-05	50S ribosomal protein L9	1
MELO3C015789	4.94272753837066e-08	2.84560916498596e-05	sucrose-binding protein-like	1
MELO3C024775	4.86891227335917e-08	2.84560916498596e-05	Bud13	1
MELO3C022533	5.04310703197675e-08	2.84560916498596e-05	shaggy-related protein kinase theta	1
MELO3C018195	6.19554454406313e-08	3.30691376218115e-05	Arf GTPase activating protein	1
MELO3C026898	6.14242697816181e-08	3.30691376218115e-05	Cathepsin B-like cysteine protease	1
MELO3C004204	6.59174723693923e-08	3.42580042585034e-05	Importin subunit alpha	1
MELO3C002485	7.36338064966091e-08	3.63548511125383e-05	Transmembrane protein, putative	1
MELO3C003812	7.18805542865297e-08	3.63548511125383e-05	Glucose-1-phosphate adenylyltransferase	1
MELO3C021514	8.24147254885332e-08	3.77341577131167e-05	No data found	0
MELO3C023342	8.40702283344541e-08	3.77341577131167e-05	kinesin-related protein 11-like	1
MELO3C002104	8.08121399797912e-08	3.77341577131167e-05	Receptor-like kinase	1
MELO3C015197	8.2265061651654e-08	3.77341577131167e-05	Translocation protein Sec62	1
MELO3C000452	9.44282844139721e-08	4.14414264198119e-05	Coiled-coil protein (DUF572)	1
MELO3C016073	9.75029128547078e-08	4.18605440427744e-05	Tudor/PWWP/MBT superfamily protein	1
MELO3C006028	1.07972809137991e-07	4.53692554822591e-05	cyclic nucleotide-gated ion channel 1	1
MELO3C007022	1.11002842029251e-07	4.56707318174099e-05	UDP-N-acetylglucosamine diphosphorylase 2-like	1
MELO3C003570	1.13579167182465e-07	4.57770402589081e-05	Protein ROOT PRIMORDIUM DEFECTIVE 1	1
MELO3C007499	1.18439269947146e-07	4.58638655330624e-05	protein DA1-related 1-like	1
MELO3C017271	1.17156354062509e-07	4.58638655330624e-05	Acetyl-coenzyme A synthetase	1
MELO3C014089	1.3594595926758e-07	5.16307067226047e-05	caffeic acid 3-O-methyltransferase 1-like	1
MELO3C012331	1.44328094586754e-07	5.37799158489398e-05	dnaJ protein homolog	0
MELO3C002508	1.4915760315759e-07	5.45502500881343e-05	thioredoxin-like protein CXXS1	1
MELO3C003905	1.80851489561817e-07	6.39831774649798e-05	glycine--tRNA ligase, mitochondrial 1	1
MELO3C021108	1.84669660008296e-07	6.39831774649798e-05	Peptidylprolyl isomerase	1
MELO3C005293	1.82100714729572e-07	6.39831774649798e-05	Phosphoglucomutase, putative	1
MELO3C017963	1.99110337106845e-07	6.77970697848806e-05	Lycopene beta-cyclase	1
MELO3C016475	2.08360193654222e-07	6.97441604148684e-05	Chloride channel protein	1
MELO3C019973	2.2593505843993e-07	7.4366524485503e-05	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	1

MELO3C013123	2.50657820832778e-07	7.98426016713957e-05	Syntaxin-51	1
MELO3C017095	2.50064974283148e-07	7.98426016713957e-05	CASP-like protein	1
MELO3C007204	2.70307014549331e-07	8.47348131799166e-05	60S ribosomal protein L11-like	0
MELO3C022213	2.95504305247718e-07	8.82741693322043e-05	Myb family transcription factor family protein	1
MELO3C025783	2.88477511212193e-07	8.82741693322043e-05	receptor-like serine/threonine-protein kinase NCRK	1
MELO3C003875	2.90642418132592e-07	8.82741693322043e-05	Protein phosphatase 2c, putative	1
MELO3C012788	2.99476902387852e-07	8.82741693322043e-05	Transcription initiation factor IIF alpha subunit family protein	1
MELO3C002464	3.08444173202638e-07	8.82820866170854e-05	polyadenylate-binding protein RBP45-like	1
MELO3C003563	3.07599423821081e-07	8.82820866170854e-05	No data found	1
MELO3C002736	3.17503783264783e-07	8.957688879566e-05	Calcyclin-binding protein	1
MELO3C026304	3.34660603895642e-07	9.30874967089442e-05	nuclear cap-binding protein subunit 2	1
MELO3C023110	3.42064934821806e-07	9.37785766616996e-05	Alkaline alpha galactosidase	1
MELO3C020989	3.46642163973065e-07	9.37785766616996e-05	phosphatidylinositol 4-kinase alpha 1	1
MELO3C017380	3.55206742130854e-07	9.4796999328949e-05	zinc finger CCHC domain-containing protein 7 isoform X3	1
MELO3C014061	3.64245731243606e-07	9.59131859510665e-05	WPP domain interacting protein, putative	1
MELO3C012356	3.74511264888966e-07	9.73187232933183e-05	Aspartyl aminopeptidase	1
MELO3C023146	4.04118919106189e-07	0.000102319801710617	villin-2-like	1
MELO3C023449	4.03846042607015e-07	0.000102319801710617	UPF0481 plant-like protein	1
MELO3C024278	4.11229531316337e-07	0.000102802177391979	Mitochondrial carrier protein	1
MELO3C015720	4.28536336860574e-07	0.000105789551458244	Smr (Small MutS-related) domain protein	1
MELO3C004433	4.57582358448505e-07	0.000111565357987648	calcium uptake protein 1, mitochondrial-like isoform X1	1
MELO3C010244	5.04511900589755e-07	0.000121507384448135	Temperature-induced lipocalin	1
MELO3C024910	5.28152974021978e-07	0.000125668591373013	FRIGIDA-like protein	1
MELO3C023537	5.4337361676815e-07	0.00012691733086263	zinc finger A20 and AN1 domain-containing stress-associated protein 8-like	0
MELO3C015590	5.46254145694647e-07	0.00012691733086263	protochlorophyllide-dependent translocon component 52, chloroplastic-like	1
MELO3C012930	5.68072576645484e-07	0.000130451922281066	Zinc knuckle family protein	1
MELO3C011379	5.84145015025683e-07	0.00013260091841083	Chaperone protein dnaJ	1
MELO3C017213	5.98506860738368e-07	0.000134317181735478	UDP-glucose 6-dehydrogenase	1
MELO3C014359	6.34542943744876e-07	0.000140804366247388	Calcium-binding EF-hand family protein	1
MELO3C011117	6.51958590447421e-07	0.00014284228791607	receptor-like protein kinase HSL1	1
MELO3C003581	6.58192728764107e-07	0.00014284228791607	signal peptide peptidase	1
MELO3C006120	7.02155050880116e-07	0.000148453468702257	MYB-related transcription factor	1
MELO3C011085	6.97631587276426e-07	0.000148453468702257	Argininosuccinate lyase	1
MELO3C003506	7.06599121880203e-07	0.000148453468702257	Rhamnogalacturonate lyase family protein	1
MELO3C012146	7.17645318282223e-07	0.000149187130429007	14-3-3 protein, putative	0
MELO3C023559	7.44244884831602e-07	0.000153105127401451	40S ribosomal protein S27	1
MELO3C011089	7.54406601521929e-07	0.000153595628592336	O-fucosyltransferase family protein	1
MELO3C016717	7.90376939896476e-07	0.00015927708353077	COP1-interacting protein, putative	1
MELO3C007177	8.23092384139024e-07	0.000164194459539006	Transcription factor GTE12	1
MELO3C011324	8.36300357853759e-07	0.000165160957672539	No data found	1
MELO3C004799	8.70907565730938e-07	0.000170292609065548	splicing factor U2af small subunit B-like	1
MELO3C006297	9.06615200468863e-07	0.000172160996096727	RNA recognition motif (RRM) containing protein	1
MELO3C007072	9.03693317066967e-07	0.000172160996096727	Caffeoylshikimate esterase	1
MELO3C025061	9.00795385505582e-07	0.000172160996096727	V-type proton ATPase subunit C	1
MELO3C005262	9.43659170360434e-07	0.000177488809099507	PLATZ transcription factor family protein, putative	1
MELO3C004194	9.58587341726158e-07	0.000178595673695754	calreticulin	1
MELO3C022416	9.74627697658548e-07	0.000179887125243539	Ubiquitin family protein	1
MELO3C021903	1.01411382180672e-06	0.000183740677677623	Alpha/beta hydrolase-3	1
MELO3C015327	1.01389569406862e-06	0.000183740677677623	isoaspartyl peptidase/L-asparaginase	1
MELO3C013136	1.03190995592861e-06	0.000185265361087583	GDP-L-galactose phosphorylase 1	1
MELO3C003448	1.2097755952567e-06	0.000215241966042564	Methyltransferase-related family protein	1
MELO3C024862	1.29411787552769e-06	0.000228192267176753	Plant peroxidase	1
MELO3C019120	1.32913722605821e-06	0.00023229319537543	R3H domain-containing protein 1-like isoform X1	1
MELO3C021462	1.37274241240881e-06	0.000237809560549663	DDT domain-containing protein PTM	1
MELO3C017749	1.39039915902917e-06	0.000238773852101452	BAG family molecular chaperone regulator 6-like	1
MELO3C015067	1.43038817013164e-06	0.000243523585964911	transcription factor LHW	1
MELO3C016754	1.51495070621621e-06	0.000253548826246305	Cold regulated gene 27, putative isoform 3	1
MELO3C005731	1.50559889966484e-06	0.000253548826246305	Intracellular protein transport protein USO1-like protein	1
MELO3C017884	1.52819748255872e-06	0.000253616572126489	DUF4050 family protein	1
MELO3C013622	1.60432891793683e-06	0.000264032431669453	mannan endo-1,4-beta-mannosidase 2	1
MELO3C022408	1.62486392341066e-06	0.000265201963830059	UV-stimulated scaffold protein A homolog	1
MELO3C024626	1.7288799445403e-06	0.000279865983809232	Protein LIKE COV 1	1
MELO3C009967	1.75992938844516e-06	0.000282575979613036	cyclin-dependent kinase C-2-like	1
MELO3C020570	1.778215225956e-06	0.000283209455624235	Maternal effect embryo arrest protein	1
MELO3C022066	1.8187769972311e-06	0.000287352215346536	Zinc finger CCHC domain-containing protein 8	1
MELO3C013988	1.86327363427274e-06	0.000292045960343273	Myelodysplasia-myeloid leukemia factor 1-interacting protein	1
MELO3C027330	1.90953358347734e-06	0.000294620146406984	Caffeic acid O-methyltransferase	1
MELO3C001987	1.90165617108828e-06	0.000294620146406984	cyclic dof factor 3	1

MELO3C006997	1.975027581258e-06	0.000302362943428406	galactan beta-1,4-galactosyltransferase GALS3-like	1
MELO3C018525	2.01982641567788e-06	0.000306842706794019	Myosin heavy chain-like protein	1
MELO3C021940	2.06217394693731e-06	0.00031088452884019	Cold acclimation protein	1
MELO3C025488	2.10223959085098e-06	0.000312158869772302	transcription initiation factor TFIID subunit 1-like	1
MELO3C020880	2.09783662086238e-06	0.000312158869772302	Pathogenesis-related protein 1	0
MELO3C009091	2.15805440451078e-06	0.000318055346527488	50S ribosomal protein L17	1
MELO3C007139	2.23241586572165e-06	0.000324832030554499	la-related protein 6A	1
MELO3C012149	2.23693129552949e-06	0.000324832030554499	PLASMODESMATA CALLOSE-BINDING PROTEIN 3	1
MELO3C007547	2.28760654796822e-06	0.000327376389245105	AT3g50560/T20E23_160	1
MELO3C007735	2.28658548895311e-06	0.000327376389245105	E3 ubiquitin-protein ligase RING1	1
MELO3C002689	2.36888940319258e-06	0.000336569761321224	serine/threonine-protein kinase STY8-like	1
MELO3C010985	2.3905490020848e-06	0.00033722108744409	B-box zinc finger protein 20-like	1
MELO3C009579	2.41978410275845e-06	0.000338924228690614	Myosin-binding protein 7	1
MELO3C003975	2.4639976213825e-06	0.000342686542427345	protein CHLOROPLAST IMPORT APPARATUS 2 isoform X2	1
MELO3C003331	2.48646479494852e-06	0.000343392959688379	BAX inhibitor-1	1
MELO3C021782	2.59632473731397e-06	0.000356075119702872	alpha-glucosidase	1
MELO3C014555	2.65481477645935e-06	0.000359109157673258	splicing factor 3B subunit 6-like protein	1
MELO3C022488	2.65025887680181e-06	0.000359109157673258	tubulin-folding cofactor D	1
MELO3C026045	2.71888340064308e-06	0.000365273661763947	alanine--glyoxylate aminotransferase 2 homolog 2, mitochondrial-like	0
MELO3C006929	2.74598986926833e-06	0.000366422661676893	BAHD acyltransferase DCR	1
MELO3C024188	2.78370137918316e-06	0.000368961869379115	ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-	1
MELO3C023188	2.84005641981722e-06	0.000373921828233135	Beta-galactosidase	1
MELO3C013183	2.90970862626416e-06	0.000379146148603654	elongation factor-like GTPase 1	1
MELO3C026090	2.91813330233204e-06	0.000379146148603654	Sec14p-like phosphatidylinositol transfer family protein	1
MELO3C012737	2.98116016383965e-06	0.00037983827145593	F21O3.15 protein	1
MELO3C021100	2.94284546042967e-06	0.00037983827145593	Heat shock 70 kDa protein	1
MELO3C018644	2.96391440057775e-06	0.00037983827145593	serine/arginine-rich splicing factor SC35	1
MELO3C022819	3.01520986245585e-06	0.000381713971625901	Myosin heavy chain-like protein, putative	1
MELO3C006921	3.11710684453015e-06	0.000389618627041936	No data found	1
MELO3C018149	3.10182773133327e-06	0.000389618627041936	Beta-glucosidase, putative	1
MELO3C008069	3.14379035937229e-06	0.000390482489353732	Phosphoinositide phosphatase family protein	1
MELO3C013712	3.18040612723447e-06	0.00039256150379221	Fact complex subunit spt16	1
MELO3C022511	3.22910355765593e-06	0.000396096684224516	synaptotagmin-5	1
MELO3C026068	3.27213557271833e-06	0.000398338562635824	Transcriptional adapter ADA2b-like protein	1
MELO3C010675	3.28772017366141e-06	0.000398338562635824	ATP-citrate synthase alpha chain protein	1
MELO3C009296	3.38391772602975e-06	0.000405601118255557	Energy-coupling factor transporter ATP-binding EcfA 1	1
MELO3C010235	3.38873788607863e-06	0.000405601118255557	No data found	1
MELO3C002056	3.41335219067318e-06	0.000406086098877136	O-fucosyltransferase family protein	1
MELO3C007008	3.47097234532079e-06	0.000408989535555527	cytochrome c6, chloroplastic	1
MELO3C022204	3.47917575438395e-06	0.000408989535555527	SART-1 family protein DOT2 isoform X2	1
MELO3C019002	3.51510799601051e-06	0.000410768448598885	Annexin	1
MELO3C002674	3.53997063085032e-06	0.000411240470521547	BnaA04g24650D protein	1
MELO3C008598	3.67564570480372e-06	0.000424504836398647	Lecithin:cholesterol acyltransferase family protein	1
MELO3C012074	3.70429519958027e-06	0.000425326313351806	Ubiquitin-conjugating enzyme, E2	0
MELO3C012400	3.73601575998084e-06	0.000426488874241974	pentatricopeptide repeat-containing protein At2g22070	1
MELO3C012597	3.76446955963061e-06	0.000427267295018074	Defective in cullin neddylation protein	1
MELO3C017897	3.79392199290063e-06	0.000428149516787397	Plant/protein	1
MELO3C005069	4.07248831202356e-06	0.000456974839057689	GEM-like protein 4	1
MELO3C013128	4.09613167873246e-06	0.000457031099001624	Golgin family A protein	1
MELO3C004439	4.20919038268686e-06	0.000467007308245409	Protein phosphatase 2c, putative	1
MELO3C007827	4.27775306732769e-06	0.00047169877077526	pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2-like	0
MELO3C026614	4.29924445488616e-06	0.00047169877077526	WD repeat-containing protein 55	1
MELO3C013870	4.40428128078985e-06	0.000477912917661092	Chloroplast 40 kDa outer membrane envelope protein	1
MELO3C015804	4.40195694373369e-06	0.000477912917661092	heat stress transcription factor A-6b-like isoform X1	1
MELO3C010295	4.43891109647154e-06	0.000478586239136045	Armadillo-like helical	1
MELO3C013000	4.45895326350865e-06	0.000478586239136045	Malic enzyme	0
MELO3C006926	4.53250933496463e-06	0.000480700689972296	Divalent ion symporter	1
MELO3C016805	4.5614759661694e-06	0.000480700689972296	No data found	0
MELO3C017908	4.58576324779969e-06	0.000480700689972296	No data found	1
MELO3C015891	4.59599066471306e-06	0.000480700689972296	U1 small nuclear ribonucleoprotein C	1
MELO3C004732	4.62469649575858e-06	0.000480700689972296	Alpha/beta-Hydrolases superfamily protein	1
MELO3C001976	4.62163323611264e-06	0.000480700689972296	Pentatricopeptide repeat-containing family protein	1
MELO3C015764	4.69261976665525e-06	0.000482679936310805	F-box/LRR-repeat protein 17	1
MELO3C000673	4.68826114552456e-06	0.000482679936310805	ATP-dependent zinc metalloprotease FtsH	0
MELO3C014178	4.90082299253736e-06	0.00049501531360691	Trigger factor	1
MELO3C016366	4.84117746490931e-06	0.00049501531360691	Phosphatidylcholine transfer protein	1
MELO3C022210	4.87671299553849e-06	0.00049501531360691	regulator of nonsense transcripts UPF3-like	1
MELO3C011196	4.91280578596154e-06	0.00049501531360691	ABC1 family protein, expressed	1

MELO3C002469	4.96222207591046e-06	0.000497456465873887	BnaC01g13120D protein	1
MELO3C025257	5.17156136781161e-06	0.000515824067943997	KH domain-containing family protein	1
MELO3C021534	5.25036197840389e-06	0.000517501450917762	homeobox-leucine zipper protein HAT5-like	1
MELO3C023408	5.26699031011546e-06	0.000517501450917762	Lactoylglutathione lyase	1
MELO3C025798	5.24348350627868e-06	0.000517501450917762	cytochrome P450 71A1-like	1
MELO3C015929	5.35053621086856e-06	0.000523107621922986	GTP-binding protein SAR1A	1
MELO3C017521	5.38464579769027e-06	0.000523849112603868	No data found	1
MELO3C006836	5.46398631773304e-06	0.000526381784336145	Activating transcription factor 7-interacting 2	1
MELO3C002148	5.44726792994776e-06	0.000526381784336145	NF-X1-type zinc finger protein NFXL1	1
MELO3C023857	5.61354392358826e-06	0.000538164460907498	GATA zinc finger domain-containing protein 10-like isoform X2	1
MELO3C024270	5.74599306712997e-06	0.000548201048708936	Terpene cyclase/mutase family member	1
MELO3C017104	5.97652550948791e-06	0.000567453857148446	Trehalose-6-phosphate synthase, putative	1
MELO3C005382	6.01113701315104e-06	0.0005680093056111	luc7-like protein 3	1
MELO3C023409	6.14485843719592e-06	0.000576681512004752	BEL1-like homeodomain protein 7	1
MELO3C020612	6.16131444797219e-06	0.000576681512004752	Unknown protein	1
MELO3C024316	6.22303370301225e-06	0.000579710814154665	Late embryogenesis abundant protein, LEA-14	1
MELO3C018948	6.26667399727943e-06	0.000581035421466063	Alpha-1,4 glucan phosphorylase	1
MELO3C009879	6.36776455420485e-06	0.000587649449443886	Cullin family protein	1
MELO3C026738	6.6257926438773e-06	0.000608617576390385	Acyl-CoA N-acyltransferase (NAT) superfamily protein	0
MELO3C007207	6.76358441276115e-06	0.000615548518744792	Kinase family protein	1
MELO3C024545	6.75704541253097e-06	0.000615548518744792	Transmembrane 9 superfamily member	1
MELO3C016298	7.03896222753464e-06	0.000634760114299459	Ribosome maturation factor	1
MELO3C010136	7.03790217027045e-06	0.000634760114299459	Glycogenin-1	1
MELO3C016877	7.08417712036447e-06	0.000635933699773081	Beta-fructofuranosidase, insoluble isoenzyme CWINV1	1
MELO3C013630	7.27915942988488e-06	0.000650480179098627	switch 2 isoform X1	1
MELO3C009482	7.35514913974278e-06	0.000651375965743409	Rho GTPase-activating protein	1
MELO3C004305	7.32999088659536e-06	0.000651375965743409	Pre-mRNA-splicing factor SLU7	1
MELO3C002767	7.40044993308153e-06	0.00065246198985905	Nuclear-interacting partner of ALK	1
MELO3C011284	7.49379739761746e-06	0.000657755576913543	Aspartate aminotransferase	1
MELO3C004591	7.82543966471039e-06	0.0006773432768121	Phosphotransferase	1
MELO3C003146	7.76221228304674e-06	0.0006773432768121	L-type lectin-domain containing receptor kinase IV.1-like	1
MELO3C022065	7.89187488892118e-06	0.0006773432768121	Nuclear matrix constituent protein 1	0
MELO3C023513	7.92274530070358e-06	0.0006773432768121	Metal tolerance protein C2	1
MELO3C011963	7.81226541701763e-06	0.0006773432768121	anthranilate phosphoribosyltransferase	0
MELO3C017093	7.90303656583724e-06	0.0006773432768121	Kinesin light chain	1
MELO3C025813	8.03564289664216e-06	0.000684034101576664	Polyadenylate-binding protein-interacting protein 3	1
MELO3C006383	8.19423848996692e-06	0.000685711931942189	acid phosphatase 1-like	1
MELO3C005211	8.1839472017009e-06	0.000685711931942189	Zinc finger, CCCH-type	1
MELO3C011984	8.09410918967135e-06	0.000685711931942189	pyrrolidone-carboxylate peptidase	1
MELO3C020001	8.17250552875848e-06	0.000685711931942189	Mini-chromosome maintenance complex-binding protein	1
MELO3C026410	8.27649747914272e-06	0.000689673201331601	transcription factor PIF4-like	0
MELO3C026629	8.48234927142144e-06	0.000703856788913034	potassium channel AKT1	1
MELO3C005952	8.62960587788564e-06	0.000713079859758843	60S acidic ribosomal protein P1-like	1
MELO3C026239	8.8767811139423e-06	0.000730448125913527	Protein tipD, putative	1
MELO3C020244	9.03752558945037e-06	0.000737638866316949	UTP--glucose-1-phosphate uridylyltransferase	1
MELO3C014083	9.07089525736815e-06	0.000737638866316949	Transmembrane protein, putative	1
MELO3C002302	9.07621877133113e-06	0.000737638866316949	Kinase family protein	1
MELO3C017657	9.15025518799517e-06	0.000738148417531329	branchpoint-bridging protein	1
MELO3C025502	9.15724149552766e-06	0.000738148417531329	Pentatricopeptide repeat-containing protein	1
MELO3C009423	9.29697871865365e-06	0.000746365986645085	Uridylate kinase	1
MELO3C005252	9.39636883812156e-06	0.000751291045279606	Ankyrin repeat-containing protein, putative	1
MELO3C020444	9.46083891961713e-06	0.000753301154100758	Purple acid phosphatase	1
MELO3C005301	9.59131909827882e-06	0.000753301154100758	At1g70780	1
MELO3C027060	9.50844332436862e-06	0.000753301154100758	Pectinesterase	1
MELO3C015322	9.61222800310857e-06	0.000753301154100758	cyclin-L1-1	1
MELO3C017346	9.60276551809081e-06	0.000753301154100758	alpha-dioxygenase 2	1
MELO3C014575	9.6661640416329e-06	0.000754533887977107	Saccharopine dehydrogenase	1
MELO3C013703	1.01872779812995e-05	0.000788974717069347	diacylglycerol O-acyltransferase 2-like	1
MELO3C026689	1.01759043160676e-05	0.000788974717069347	LRR receptor-like kinase, putative	0
MELO3C009339	1.05713260298845e-05	0.000815519991266366	Glycosyl transferase, family 31	1
MELO3C017385	1.078928932019e-05	0.000829096010834364	pollen receptor-like kinase 1	1
MELO3C008596	1.10425164834282e-05	0.000845266116400095	S-adenosyl-L-methionine-dependent methyltransferase	1
MELO3C024844	1.11280763014365e-05	0.000848526559370927	At5g24610	1
MELO3C013792	1.13111690041023e-05	0.000859170294853912	Ribosomal protein L28	1
MELO3C012136	1.13801551119286e-05	0.000861098403469263	Nodulin-related protein 1	1
MELO3C009461	1.15575520555078e-05	0.00086458369524327	Protein LITTLE ZIPPER 4	1
MELO3C007614	1.15006113516891e-05	0.00086458369524327	Leucine-rich repeat family protein	0
MELO3C010714	1.15230725494797e-05	0.00086458369524327	two-component response regulator ARR11	1

MELO3C014019	1.16203737828835e-05	0.000866002874861004	Rhomboid-like protein	1
MELO3C026749	1.20811670227816e-05	0.000896958524559827	DNA helicase	0
MELO3C021119	1.21310338159208e-05	0.00089728759112592	Cytochrome b561 and domon domain-containing protein	1
MELO3C011747	1.22550755131678e-05	0.000903080172796835	Protein FAR1-RELATED SEQUENCE 5	1
MELO3C009315	1.23509541338773e-05	0.00090491340308527	Ribosomal protein S12	0
MELO3C014678	1.2388353868964e-05	0.00090491340308527	Kelch repeat-containing F-box family protein	1
MELO3C016855	1.24174151722167e-05	0.00090491340308527	CRG16	0
MELO3C002700	1.24733027745405e-05	0.000905644325347061	Serine/threonine-protein kinase PLK4	1
MELO3C014174	1.25786625135849e-05	0.000909948739856364	(S)-ureidoglycine aminohydrolase	1
MELO3C003916	1.26667633769673e-05	0.000910771796448124	Cellulose synthase	1
MELO3C023590	1.2682274749265e-05	0.000910771796448124	Pheophytinase, chloroplastic	1
MELO3C017364	1.27819750068703e-05	0.000914605885545946	Ribosomal protein L19	1
MELO3C007033	1.28479493655131e-05	0.000916007769023535	protein SUPPRESSOR OF FRI 4 isoform X2	1
MELO3C014749	1.29109006289374e-05	0.000917184807629082	Acetyl-coenzyme A synthetase	1
MELO3C006107	1.32783063222508e-05	0.000939904199133086	RNA polymerase I-specific transcription initiation factor RRN3	1
MELO3C008910	1.34152483453054e-05	0.000942838930859203	transcription termination factor MTEF18, mitochondrial-like	1
MELO3C023986	1.33894728500117e-05	0.000942838930859203	DNA topoisomerase 2	1
MELO3C007432	1.35509775082143e-05	0.000949000903580584	Phosphatidate cytidylyltransferase	1
MELO3C003915	1.36025675472329e-05	0.000949247726114142	Pentatricopeptide repeat-containing protein	1
MELO3C022707	1.38477429754147e-05	0.000962954493033326	Ubiquitin-conjugating enzyme family protein	1
MELO3C009222	1.39431327602635e-05	0.000963333195559096	Protein RETICULATA, chloroplastic	1
MELO3C025451	1.39726341720214e-05	0.000963333195559096	Actin-depolymerizing factor family protein	1
MELO3C016016	1.39995254000436e-05	0.000963333195559096	xyloglucan 6-xylosyltransferase 1	1
MELO3C025977	1.4120841748122e-05	0.000968307304457158	OBERON-like protein	1
MELO3C020875	1.4385688624774e-05	0.000983055241005747	CLK4-associating serine/arginine-rich protein	1
MELO3C009276	1.46222781025607e-05	0.000995777138784382	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-	1
MELO3C022342	1.4755856923232e-05	0.00100142068170759	NAC domain-containing protein 83	1
MELO3C006313	1.50251507858856e-05	0.00101325938561605	Myb family transcription factor APL	1
MELO3C024262	1.5032913058155e-05	0.00101325938561605	activating signal cointegrator 1 complex subunit 1	1
MELO3C014825	1.52073123453889e-05	0.00102152793030301	Steroid nuclear receptor, ligand-binding	1
MELO3C004636	1.56355188315471e-05	0.00103625657153415	T-complex protein 1 subunit beta	1
MELO3C016380	1.55814578131075e-05	0.00103625657153415	Laccase	1
MELO3C024447	1.56364604950721e-05	0.00103625657153415	Protein SEC13 like	1
MELO3C011160	1.54835320682611e-05	0.00103625657153415	2-on-2 hemoglobin	1
MELO3C017720	1.5829999835848e-05	0.00104557413631492	protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	0
MELO3C006959	1.59256922638296e-05	0.0010483883217279	Reticulon-like protein	1
MELO3C009591	1.61324199619006e-05	0.0010508747649051	IQ domain-containing protein IQM6	1
MELO3C004553	1.60189519178289e-05	0.0010508747649051	multiprotein-bridging factor 1c	1
MELO3C025526	1.62295206489471e-05	0.0010508747649051	Pollen Ole e 1 allergen/extensin	1
MELO3C003813	1.61832411422758e-05	0.0010508747649051	Mannan endo-1,4-beta-mannosidase-like protein	1
MELO3C013093	1.62023783316645e-05	0.0010508747649051	glyoxylate/succinic semialdehyde reductase 2, chloroplastic-like	0
MELO3C013925	1.63110244950637e-05	0.00105270072795102	Myb transcription factor	1
MELO3C011731	1.65099639795052e-05	0.00106206931150244	Ubiquitin carboxyl-terminal hydrolase	1
MELO3C006948	1.66519377275964e-05	0.00106409276491677	Protein SGT1 homolog	1
MELO3C025282	1.67030612752139e-05	0.00106409276491677	SCARECROW	1
MELO3C025799	1.66160070578236e-05	0.00106409276491677	Alpha-ketoglutarate-dependent dioxygenase AlkB	1
MELO3C001954	1.67788745651931e-05	0.00106548551057234	Glycosyltransferase	1
MELO3C021588	1.71895920806353e-05	0.00108113775159384	CRS1/YhbY (CRM) domain protein	1
MELO3C021279	1.70987463855576e-05	0.00108113775159384	GTP-binding protein SAR1A-like	1
MELO3C008321	1.71502866039841e-05	0.00108113775159384	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	1
MELO3C012083	1.73075270275547e-05	0.00108509952783231	Actin-binding LIM protein 1, putative	1
MELO3C024407	1.74182752812335e-05	0.00108858708395279	Charged multivesicular body 1	1
MELO3C015627	1.76483058498267e-05	0.00109948388715529	serrate RNA effector molecule	1
MELO3C018053	1.80475750266584e-05	0.00112082251321219	Costars family protein At4g33640	1
MELO3C006602	1.86668661633638e-05	0.00115252448748568	serine/threonine-protein kinase RUNKEL	1
MELO3C017677	1.86747600382509e-05	0.00115252448748568	chitinase-like protein 1	1
MELO3C019451	1.89781614502449e-05	0.00116760034417722	Unknown protein	1
MELO3C008933	1.9062906662648e-05	0.00116917187478458	Zinc finger family protein	1
MELO3C021107	1.93475282579403e-05	0.00118295459927574	Peptidylprolyl isomerase	0
MELO3C023442	1.95211350888513e-05	0.00118988548416582	glycerol kinase	1
MELO3C004593	1.95826094848695e-05	0.00118995986066673	OXS3	1
MELO3C020394	1.97117608555786e-05	0.00119048185057132	Phospholipid-transporting ATPase	1
MELO3C012088	1.97023626935522e-05	0.00119048185057132	sphinganine C4-monooxygenase 2	1
MELO3C014649	2.00030745243218e-05	0.00120138093791952	Metal tolerance protein C2	1
MELO3C007069	2.00138907577863e-05	0.00120138093791952	Protein phosphatase 2c, putative	1
MELO3C012243	2.02363198715805e-05	0.00121105176104195	tetraketide alpha-pyrone reductase 2-like	0
MELO3C025855	2.11718078086953e-05	0.00125940371209013	Alkyl transferase	1
MELO3C020589	2.11652532021711e-05	0.00125940371209013	17.5 kDa class I heat shock protein	1

MELO3C011138	2.13686692861481e-05	0.00126729684604246	Ultraviolet-B receptor UVR8	1
MELO3C019527	2.14406552635493e-05	0.00126775898443065	CBS domain-containing protein CBSX1, chloroplastic	1
MELO3C015263	2.16246135184006e-05	0.00127481938022356	Werner syndrome-like exonuclease	1
MELO3C017683	2.17107562363594e-05	0.00127608846699959	Clathrin interactor EPSIN 2	1
MELO3C011825	2.18256773739656e-05	0.00127903650581141	nifU-like protein 2, chloroplastic	1
MELO3C008690	2.20750108673728e-05	0.00128982067934836	splicing factor 3B subunit 2	1
MELO3C022786	2.23215132971744e-05	0.00130037630119733	Phd finger protein, putative	1
MELO3C007075	2.28317060992911e-05	0.001326186363985	ADP-ribosylation factor GTPase-activating protein AGD12	1
MELO3C009187	2.32460548075242e-05	0.00134235770875379	Transferase family protein	1
MELO3C010761	2.32330067020392e-05	0.00134235770875379	far upstream element-binding protein 1	1
MELO3C024385	2.38134500429865e-05	0.00137028743648528	protein indeterminate-domain 7	1
MELO3C012378	2.39378786565103e-05	0.00137028743648528	phosphoglucan phosphatase DSP4, amyloplastic	1
MELO3C019633	2.39288368943935e-05	0.00137028743648528	Glyceraldehyde-3-phosphate dehydrogenase	1
MELO3C014114	2.42431211936456e-05	0.00137976196096054	RPM1-interacting protein 4	1
MELO3C011271	2.4241787024426e-05	0.00137976196096054	14 kDa proline-rich protein DC2.15	1
MELO3C025111	2.43574415158543e-05	0.00138228480602473	CoA ligase	1
MELO3C007673	2.49104628767816e-05	0.00140884079117347	tubulin alpha chain-like	1
MELO3C005467	2.49680630366456e-05	0.00140884079117347	At5g07590	1
MELO3C008520	2.63403040063892e-05	0.00144498517728383	Cysteine protease	1
MELO3C013369	2.6235044301437e-05	0.00144498517728383	Methyltransferase-like protein	1
MELO3C007265	2.60273344152573e-05	0.00144498517728383	Protein DEHYDRATION-INDUCED 19	1
MELO3C019056	2.61549670041994e-05	0.00144498517728383	two-component response regulator ARR8-like	1
MELO3C023560	2.58082812095717e-05	0.00144498517728383	PsaB RNA-binding protein	1
MELO3C012196	2.62297140761758e-05	0.00144498517728383	Phospholipid-transporting ATPase	1
MELO3C025859	2.62944593677483e-05	0.00144498517728383	zinc finger CCCH domain-containing protein 25	1
MELO3C021670	2.5745984559733e-05	0.00144498517728383	Nuclear inhibitor of protein phosphatase 1	1
MELO3C010119	2.58387265157367e-05	0.00144498517728383	U11/U12 small nuclear ribonucleoprotein 48 kDa protein	1
MELO3C009886	2.60319997607006e-05	0.00144498517728383	plant cysteine oxidase 2	1
MELO3C006493	2.65023384483642e-05	0.00144950576797161	ATP sulfurylase	1
MELO3C016552	2.6816575519617e-05	0.00144950576797161	Fiber expressed protein	1
MELO3C017856	2.66462100604326e-05	0.00144950576797161	extensin-like	1
MELO3C025079	2.6770532013165e-05	0.00144950576797161	universal stress protein A-like protein	1
MELO3C022436	2.67748264992651e-05	0.00144950576797161	Amaranthin-like lectin	1
MELO3C010042	2.68630872994891e-05	0.00144950576797161	endoribonuclease Dicer homolog 2 isoform X2	1
MELO3C024214	2.70940042867984e-05	0.0014579822633787	Cytochrome b561 and domon domain-containing protein	1
MELO3C004278	2.78234834507618e-05	0.00147094913094369	mevalonate kinase-like	1
MELO3C006705	2.79177989914725e-05	0.00147094913094369	Binding protein	1
MELO3C005490	2.77615447602519e-05	0.00147094913094369	U-box domain-containing protein 35-like isoform X2	1
MELO3C020109	2.78415158727618e-05	0.00147094913094369	Nop53 protein	1
MELO3C026470	2.79308280978219e-05	0.00147094913094369	Potassium transporter	1
MELO3C000817	2.77390788183673e-05	0.00147094913094369	Magnesium transporter MRS2-like protein	1
MELO3C002677	2.7819366417603e-05	0.00147094913094369	NAD(P)-binding Rossmann-fold superfamily protein	1
MELO3C002044	2.78036725491759e-05	0.00147094913094369	DNA polymerase alpha subunit B	1
MELO3C021398	2.8164374234807e-05	0.00147930379458299	serine incorporator 3	1
MELO3C014530	2.84013662230631e-05	0.00148385868132083	Nuclear transcription factor Y subunit C8	1
MELO3C012748	2.83333883075443e-05	0.00148385868132083	Lysine-specific demethylase	0
MELO3C014507	2.84858782809705e-05	0.00148434725638756	F-box family protein	1
MELO3C006260	2.87159989742491e-05	0.0014878051459065	Dynamin, putative	1
MELO3C025345	2.88485624249102e-05	0.0014878051459065	Polyol transporter 5-like protein	1
MELO3C010686	2.88107005061988e-05	0.0014878051459065	Alanine aminotransferase 2	1
MELO3C013022	2.88535809854773e-05	0.0014878051459065	Serine/threonine-protein kinase ATM	1
MELO3C016541	2.93398141502088e-05	0.00150893747305332	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein	1
MELO3C017836	2.96642891901566e-05	0.00152166246030235	UPF0326 protein	1
MELO3C003313	2.99724595917983e-05	0.00153348731730162	Membrane steroid-binding protein	1
MELO3C020701	3.0080522178122e-05	0.00153503936045408	Myb transcription factor	1
MELO3C016074	3.02469208611766e-05	0.00153552012010767	No data found	1
MELO3C024292	3.02042248422341e-05	0.00153552012010767	O-fucosyltransferase family protein	0
MELO3C008367	3.03231984830621e-05	0.00153552012010767	serine/threonine-protein kinase STY8-like	1
MELO3C013104	3.07867267796968e-05	0.00155028543425578	Upstream activation factor subunit spp27	1
MELO3C007083	3.07940069153023e-05	0.00155028543425578	187-kDa microtubule-associated protein AIR9	1
MELO3C022499	3.08502797945476e-05	0.00155028543425578	Myeloid leukemia factor	1
MELO3C012967	3.09977807957384e-05	0.00155374409374375	At5g57230	1
MELO3C009171	3.14944790682503e-05	0.00157464422055412	Mitochondrial carrier protein	1
MELO3C023731	3.17116579537924e-05	0.00157825662440481	phosphatidylcholine transfer protein-like isoform X1	1
MELO3C017474	3.17265623519525e-05	0.00157825662440481	Zinc finger protein	1
MELO3C007767	3.23184251792563e-05	0.00160365974589229	Lipoxygenase y domain-containing protein 1	1
MELO3C026235	3.25468898165759e-05	0.00161094868919188	haloacid dehalogenase-like hydrolase domain-containing protein At3g48420	1
MELO3C013383	3.32537247063058e-05	0.00163772521003699	Calcium-binding EF hand family protein	1

MELO3C005849	3.3214611836252e-05	0.00163772521003699	p-loop containing nucleoside triphosphate hydrolases superfamily protein	1
MELO3C023526	3.33581295046681e-05	0.00163878034723306	chaperone protein dnaJ GFA2, mitochondrial	1
MELO3C009996	3.39940585575293e-05	0.00166587757432419	dnaJ protein homolog	1
MELO3C016253	3.42100392104472e-05	0.00167231204051268	Zinc finger protein, putative	1
MELO3C013470	3.44618684419151e-05	0.00168046281446761	Ankyrin repeat domain-containing 2-like protein	0
MELO3C022144	3.4767194971419e-05	0.0016911756982526	TMV resistance protein N-like	1
MELO3C015277	3.55894665726719e-05	0.00172691984113931	GATA transcription factor 16-like	1
MELO3C020830	3.59045646862732e-05	0.00173793933330689	BZIP transcription factor, putative (DUF630 and DUF632)	1
MELO3C004542	3.60642823011847e-05	0.00174140222778997	tRNA (guanine(37)-N1)-methyltransferase	1
MELO3C004366	3.62660963766359e-05	0.00174687594473703	Prenylyltransferase superfamily protein	1
MELO3C009495	3.67311633746592e-05	0.00175067140545441	CASP-like protein	1
MELO3C013248	3.66059451775147e-05	0.00175067140545441	nucleolar complex protein 4 homolog	1
MELO3C014150	3.65614978239392e-05	0.00175067140545441	Fimbrin, putative	1
MELO3C024450	3.69654147589493e-05	0.00175067140545441	nuclear pore complex protein NUP35	1
MELO3C023306	3.68811505284672e-05	0.00175067140545441	adoMet-dependent rRNA methyltransferase spb1 isoform X1	1
MELO3C013664	3.66656130084131e-05	0.00175067140545441	Transcriptional elongation regulator MINIYO	1
MELO3C022386	3.69238571342745e-05	0.00175067140545441	50S ribosomal protein L14	1
MELO3C025256	3.74632503545858e-05	0.00176764322254611	protein RETICULATA-RELATED 3, chloroplastic-like	1
MELO3C005565	3.75027854699894e-05	0.00176764322254611	Elongation factor G, chloroplastic	1
MELO3C003911	3.78070399631447e-05	0.00177774102912415	protein BONZAI 3	1
MELO3C007825	3.79500651352949e-05	0.0017802276398027	random slug protein 5-like	1
MELO3C004492	3.83150140621513e-05	0.00179308818178537	methyl-CpG-binding domain-containing protein 11-like	1
MELO3C024005	3.84547735918783e-05	0.00179537428762649	Acyl-CoA--sterol O-acyltransferase 1	1
MELO3C017898	3.89913539624587e-05	0.00180760621925962	F-box family protein	1
MELO3C024586	3.89204117599018e-05	0.00180760621925962	Ribosomal protein S8e/ribosomal biogenesis NSA2	0
MELO3C002154	3.88440754720554e-05	0.00180760621925962	Monoglyceride lipase	1
MELO3C021113	3.92616078019881e-05	0.00180901640460669	asparagine--tRNA ligase, cytoplasmic 2	1
MELO3C001175	3.92192487606025e-05	0.00180901640460669	Glutathione s-transferase	1
MELO3C018502	3.92965738810203e-05	0.00180901640460669	MAR-binding filament-like protein	1
MELO3C013891	4.00972913509046e-05	0.00184140770420847	AT5g47090/K14A3_4	1
MELO3C020824	4.01866788451999e-05	0.00184140770420847	Pre-mRNA-splicing factor syf2	1
MELO3C024596	4.07119270215972e-05	0.00186115705266093	DNA polymerase	1
MELO3C002115	4.08557565708678e-05	0.0018634187910348	Poly(A) polymerase	1
MELO3C014175	4.15915338907169e-05	0.00189178845108025	Phospho-2-dehydro-3-deoxyheptonate aldolase	1
MELO3C014009	4.16693491427367e-05	0.00189178845108025	PGR5-like protein 1A, chloroplastic	1
MELO3C013366	4.18519287170849e-05	0.00189571958769199	Protein nuclear fusion defective 4	1
MELO3C024435	4.20256696651577e-05	0.00189923329569153	Poly(A) polymerase	1
MELO3C006736	4.24021129614705e-05	0.00191187061387233	Beta-1,3-galactosyltransferase-like protein	1
MELO3C015860	4.25403537831492e-05	0.00191373450310573	Calcium permeable stress-gated cation channel 1	1
MELO3C020132	4.28311459950148e-05	0.00192243705058079	Potassium transporter	1
MELO3C002226	4.29674849788952e-05	0.00192418335793243	polynucleotide 5'-hydroxyl-kinase NOL9	1
MELO3C010275	4.36787795317084e-05	0.00195161135061473	Serine-rich protein-like protein	1
MELO3C017620	4.38789811226803e-05	0.00195172522115273	BnaA10g17500D protein	1
MELO3C020780	4.38459148834891e-05	0.00195172522115273	Triosephosphate isomerase	1
MELO3C008330	4.42680489831648e-05	0.00196460606599668	S-acyltransferase	1
MELO3C004641	4.4476178534758e-05	0.00196941715220389	Protein BREVIS RADIX	1
MELO3C009595	4.45835594083954e-05	0.00196975551399642	serine/arginine-rich SC35-like splicing factor SCL33	1
MELO3C013455	4.49710978889239e-05	0.00197627470685878	Calcium ion-binding protein	1
MELO3C010297	4.49064579863823e-05	0.00197627470685878	Purple acid phosphatase	1
MELO3C003471	4.50313240207834e-05	0.00197627470685878	protein SAWADEE HOMEODOMAIN HOMOLOG 1-like isoform X2	1
MELO3C010997	4.52420342280657e-05	0.00198111958751678	Protein IQ-DOMAIN 32	1
MELO3C018394	4.6087660756533e-05	0.00201368409796631	Abscisic acid receptor	0
MELO3C004669	4.6537154970494e-05	0.00202648542403205	Pentatricopeptide repeat-containing protein	1
MELO3C026502	4.65858718168288e-05	0.00202648542403205	Phytochrome	1
MELO3C015043	4.71004272699638e-05	0.00204436557836157	DnaJ-like protein	0
MELO3C025034	4.73219853005524e-05	0.00204582515146751	peroxiredoxin Q, chloroplastic	1
MELO3C022721	4.73412372383741e-05	0.00204582515146751	Ninja-family protein AFP3	1
MELO3C005245	4.79549976355464e-05	0.00206782368625416	Xyloglucan endotransglucosylase/hydrolase	1
MELO3C024885	4.83734309704165e-05	0.00207353939040731	ATP-dependent DNA helicase	1
MELO3C025391	4.83084956899305e-05	0.00207353939040731	No data found	0
MELO3C025056	4.8402534760128e-05	0.00207353939040731	zinc finger CCCH domain-containing protein 53-like	0
MELO3C023753	4.85878972154019e-05	0.00207697485304539	BnaC06g27400D protein	1
MELO3C025784	4.88195283186998e-05	0.0020823690383715	Zinc finger (C3HC4-type RING finger) family protein	1
MELO3C024376	4.90235715564502e-05	0.00208656576437141	Eukaryotic initiation factor 4A (ATP-dependent RNA helicase eIF4A)	0
MELO3C024863	4.93566951739188e-05	0.00209622660858005	No data found	1
MELO3C021587	5.05070902130367e-05	0.00214048181248339	NAC domain-containing protein 8 isoform X1	1
MELO3C011705	5.07150635979947e-05	0.00214469334260556	Pyruvate dehydrogenase E1 component subunit alpha	1
MELO3C021999	5.12860701999962e-05	0.00215959189846423	Expansin protein	1

MELO3C025308	5.12768922132922e-05	0.00215959189846423	auxin-responsive protein IAA16-like	1
MELO3C025887	5.14003217724213e-05	0.00215979777592244	No data found	1
MELO3C023727	5.20365869023376e-05	0.00218189077438273	CDT1-like protein a, chloroplastic	1
MELO3C022647	5.23411990736022e-05	0.0021900134332724	UDP-glycosyltransferase 89A2-like	1
MELO3C023808	5.24853113137436e-05	0.00219140045060279	SAC3/GANP/Nin1/mts3/eIF-3 p25 family isoform 1	1
MELO3C024514	5.27174142808118e-05	0.00219644771019357	enolase	1
MELO3C026107	5.30162818748181e-05	0.00220424958051744	No data found	1
MELO3C006189	5.33192345207878e-05	0.00220818488486918	Glutathione S-transferase	1
MELO3C007609	5.33345582096612e-05	0.00220818488486918	Subtilisin-like protease	1
MELO3C009292	5.42517615724769e-05	0.00222633555573646	ABC transporter G family member 20	0
MELO3C023475	5.42682466746491e-05	0.00222633555573646	pre-mRNA-splicing factor ISY1 homolog	1
MELO3C011843	5.43007606186308e-05	0.00222633555573646	No data found	1
MELO3C020783	5.43366113658905e-05	0.00222633555573646	protein XAP5 CIRCADIAN TIMEKEEPER	1
MELO3C011285	5.41233647706196e-05	0.00222633555573646	60S ribosomal protein L39	1
MELO3C016696	5.44683324148476e-05	0.00222711200178225	PROTON PUMP INTERACTOR 1 family protein	1
MELO3C007010	5.52589988974672e-05	0.00225477266369025	phosphatidate cytidylyltransferase, mitochondrial isoform X1	1
MELO3C011003	5.59736594196725e-05	0.00227922432964765	transcription factor E2FC isoform X3	1
MELO3C022693	5.60978884305285e-05	0.00227958271319858	GDSL esterase/lipase 5	0
MELO3C016002	5.719334841503e-05	0.00231457261854186	Arginine/serine-rich splicing factor, putative	1
MELO3C020957	5.70871739773438e-05	0.00231457261854186	GDSL esterase/lipase 5-like	1
MELO3C007653	5.75656860861695e-05	0.00232040749860482	Protein PHLOEM PROTEIN 2-LIKE A10	1
MELO3C026835	5.75725188270981e-05	0.00232040749860482	Pentatricopeptide repeat-containing protein At2g30100, chloroplastic	1
MELO3C019411	5.82043706141011e-05	0.00234109595775536	Kinase superfamily protein	1
MELO3C007562	5.83480571787476e-05	0.00234210524638839	Lipase	1
MELO3C006145	5.87198712955761e-05	0.00235224896189925	F-box protein PP2-A13	1
MELO3C009338	5.94246730396542e-05	0.00235658206397616	60S ribosomal protein L12	1
MELO3C006854	5.93200212051226e-05	0.00235658206397616	transcription factor bHLH118-like	1
MELO3C019522	5.92040129191451e-05	0.00235658206397616	Exocyst complex component	1
MELO3C016186	5.91282394308834e-05	0.00235658206397616	No data found	1
MELO3C002384	5.94135676414975e-05	0.00235658206397616	Coiled-coil domain-containing protein SCD2	1
MELO3C018749	5.95836233487912e-05	0.00235815025554164	Phosphatase 2C family protein	1
MELO3C004273	6.01342544248595e-05	0.0023751827812731	Mitochondrial Rho GTPase	1
MELO3C021332	6.05753663890374e-05	0.00238547596635887	40S ribosomal protein S21	0
MELO3C015339	6.06364340023369e-05	0.00238547596635887	UDP-N-acetylglucosamine transferase subunit ALG13 homolog	1
MELO3C014260	6.11461584065776e-05	0.00240074648582803	Interactor of constitutive active ROPs-like protein	1
MELO3C003278	6.17486979386239e-05	0.0024195933245831	PHD finger protein At1g33420	1
MELO3C013736	6.21357963599412e-05	0.00242994028180689	basic endochitinase C	1
MELO3C021207	6.30709811876295e-05	0.00246163795943576	Signal peptide peptidase-like protein	1
MELO3C005992	6.3408310252755e-05	0.00246211971008436	homeobox-leucine zipper protein ATHB-7	0
MELO3C015734	6.34573361908419e-05	0.00246211971008436	No data found	1
MELO3C015439	6.32324988869559e-05	0.00246211971008436	Protein PLASTID MOVEMENT IMPAIRED 1-RELATED 1	1
MELO3C022162	6.40116656055456e-05	0.00247390681808986	mannan endo-1,4-beta-mannosidase 1-like	1
MELO3C011408	6.39667592298165e-05	0.00247390681808986	nucleolar protein 14 isoform X2	1
MELO3C013738	6.49744440790467e-05	0.00249335090143193	Ganglioside-induced differentiation-associated protein 2	1
MELO3C010439	6.49361610987054e-05	0.00249335090143193	structure-specific endonuclease subunit SLX4-like isoform X2	1
MELO3C027375	6.50197840010858e-05	0.00249335090143193	Pectinesterase	1
MELO3C011144	6.49593068970944e-05	0.00249335090143193	Translation initiation factor IF-2	1
MELO3C017813	6.58591244822038e-05	0.00251576760038499	ADP-ribosylation factor GTPase-activating protein AGD3	1
MELO3C025582	6.5766423634761e-05	0.00251576760038499	Ribosomal protein S5/S7	1
MELO3C011422	6.60698899755952e-05	0.0025189464423321	Pentatricopeptide repeat-containing protein	1
MELO3C020255	6.65873213148149e-05	0.00253378229026258	3-phosphoinositide-dependent protein kinase-1	0
MELO3C016660	6.74206308142189e-05	0.00255074719913795	Flavin-binding kelch domain F box protein	1
MELO3C008046	6.73044786470012e-05	0.00255074719913795	zinc finger CCCH domain-containing protein 38 isoform X1	1
MELO3C012391	6.73894846392464e-05	0.00255074719913795	NAC domain-containing protein 16	1
MELO3C008513	6.82229065330775e-05	0.00257616478225956	FAST kinase domain-containing 3	1
MELO3C022074	6.86128717086731e-05	0.00258102019690397	Tryptophan synthase-related	1
MELO3C016019	6.84870669735993e-05	0.00258102019690397	heat shock factor-binding protein 1	1
MELO3C013946	6.88829284867243e-05	0.00258625276555954	Small heat shock protein, chloroplastic	1
MELO3C021771	6.96161904623072e-05	0.00260882380538919	exocyst complex component EXO84C	1
MELO3C005703	6.97949721109037e-05	0.00261056989435272	Beta-carotene 3-hydroxylase	1
MELO3C011011	7.00407553777538e-05	0.00261481073337478	Transducin/WD40 repeat-like superfamily protein	1
MELO3C019135	7.0205236232912e-05	0.00261600605729015	4-alpha-glucanotransferase DPE2	1
MELO3C024138	7.04960768541651e-05	0.00262189646288683	Auxin response factor	1
MELO3C020860	7.10014079137178e-05	0.00263572707685717	DNA polymerase	1
MELO3C016468	7.31467793237961e-05	0.00271027344252467	No data found	1
MELO3C014658	7.36569729663517e-05	0.00271924112679749	Peroxidase	1
MELO3C005581	7.39243833014491e-05	0.00271924112679749	Ankyrin repeat/KH domain protein (DUF1442)	1
MELO3C017384	7.39395658053699e-05	0.00271924112679749	tRNA pseudouridine synthase	1

MELO3C025026	7.38424094659518e-05	0.00271924112679749	abscisic stress-ripening protein 2-like	0
MELO3C014419	7.56717115111272e-05	0.0027671089367998	Unknown protein	1
MELO3C014309	7.59720866843061e-05	0.0027671089367998	Magnesium transporter MRS2-like protein	1
MELO3C004308	7.65458843351441e-05	0.0027671089367998	Photosystem II reaction center PsbP family protein	1
MELO3C014027	7.6019752883516e-05	0.0027671089367998	Cytochrome P450 family protein	1
MELO3C021979	7.63281862419252e-05	0.0027671089367998	Glutaredoxin family protein, putative	1
MELO3C012242	7.65118129815168e-05	0.0027671089367998	ethylene-responsive transcription factor ERF118	1
MELO3C015202	7.64393255101581e-05	0.0027671089367998	zinc finger A20 and AN1 domain-containing stress-associated protein 4-like	1
MELO3C020003	7.64967470061606e-05	0.0027671089367998	40S ribosomal protein S26	1
MELO3C013084	7.63203350274688e-05	0.0027671089367998	Aminopeptidase	0
MELO3C009827	7.66422901630204e-05	0.0027671089367998	No data found	1
MELO3C004186	7.71375798698237e-05	0.00277519988206223	Unknown protein	1
MELO3C016917	7.71474370981906e-05	0.00277519988206223	Damaged dna-binding 2, putative isoform 1	1
MELO3C002821	7.79612487069592e-05	0.00279937581947952	Unknown protein	1
MELO3C015603	7.8575539132153e-05	0.00281631274468401	E3 ubiquitin-protein ligase RING1-like	1
MELO3C011173	7.89147137463253e-05	0.00282334543800032	Gamma-glutamylcyclotransferase	1
MELO3C006158	7.91940140983938e-05	0.00282821443838911	lysophospholipid acyltransferase LPEAT2 isoform X1	1
MELO3C010737	7.96416118012955e-05	0.00283906532755196	RING-type E3 ubiquitin transferase	1
MELO3C025265	8.02798553996009e-05	0.00284737098364442	Unknown protein	1
MELO3C015594	8.04513144398999e-05	0.00284737098364442	No data found	1
MELO3C008076	8.00977753115939e-05	0.00284737098364442	No data found	1
MELO3C003393	8.0430383471497e-05	0.00284737098364442	Plant intracellular ras group-related LRR protein	1
MELO3C019730	8.11006363776734e-05	0.00286521729485272	zinc finger CCCH domain-containing protein 3-like	1
MELO3C009560	8.21626649760709e-05	0.00289444859730923	Polyketide cyclase/dehydrase/lipid transport superfamily protein	1
MELO3C023161	8.22211586961608e-05	0.00289444859730923	nuclear transcription factor Y subunit A-7-like	1
MELO3C023018	8.26704742665774e-05	0.00290468115089194	splicing factor U2af large subunit B isoform X1	1
MELO3C021786	8.280598956667e-05	0.00290468115089194	Cyclin-T1-like protein	1
MELO3C015704	8.32907324128662e-05	0.00291193049597952	Protein trigalactosyldiacylglycerol 2, chloroplastic	1
MELO3C025307	8.33075462164379e-05	0.00291193049597952	Transmembrane 19	1
MELO3C016262	8.34670928354653e-05	0.00291235267916538	26S proteasome non-ATPase regulatory subunit 8	1
MELO3C025654	8.41080056708243e-05	0.00292498547025566	Transmembrane protein	0
MELO3C010913	8.4125360631182e-05	0.00292498547025566	Protein DA1-related 1	1
MELO3C023419	8.4525555592907e-05	0.00293373496907613	methyl-CpG-binding domain-containing protein 11	1
MELO3C022998	8.50718977087883e-05	0.00294235535525545	Malate dehydrogenase	1
MELO3C003977	8.50368989402384e-05	0.00294235535525545	Microtubule-associated family protein	1
MELO3C008197	8.52787411298461e-05	0.00294435289960373	Chloride channel protein	1
MELO3C016126	8.64520687487991e-05	0.00296335514244293	Pathogen-related protein	1
MELO3C005754	8.61995591473486e-05	0.00296335514244293	PHD finger family protein	1
MELO3C005828	8.65793669142523e-05	0.00296335514244293	SKP1-like protein 21	0
MELO3C025956	8.6286284875392e-05	0.00296335514244293	No data found	1
MELO3C021232	8.63064375860034e-05	0.00296335514244293	Novel plant snare, putative	1
MELO3C007483	8.75097762822463e-05	0.0029900182903081	ABC transporter family protein	1
MELO3C008879	8.77609174688709e-05	0.00299342030931387	Triosephosphate isomerase	1
MELO3C025073	8.93035963320798e-05	0.00303555374175946	GRIP and coiled-coil domain-containing protein 1	1
MELO3C005872	8.92453339496058e-05	0.00303555374175946	Polypyrimidine tract binding protein, putative	0
MELO3C019225	8.99096474886729e-05	0.00304860401862575	Formin-like protein	1
MELO3C003659	8.9996260208558e-05	0.00304860401862575	Glucan endo-1,3-beta-glucosidase, putative	1
MELO3C014565	9.04686218434758e-05	0.00304891606277612	Homeobox domain-containing protein	1
MELO3C022494	9.03951638639988e-05	0.00304891606277612	No data found	1
MELO3C010877	9.02100101682901e-05	0.00304891606277612	Phosphatidate phosphatase PAH2	1
MELO3C004610	9.15000192608373e-05	0.003067019032385	zinc finger CCCH domain-containing protein 20-like	1
MELO3C022068	9.14387798359728e-05	0.003067019032385	proline-rich receptor-like protein kinase PERK8	1
MELO3C021228	9.16269800550484e-05	0.003067019032385	tRNA pseudouridine synthase	1
MELO3C003638	9.1278293153696e-05	0.003067019032385	replication protein A 32 kDa subunit A-like	1
MELO3C006670	9.20264952706251e-05	0.00307398449987238	Translationally-controlled tumor protein homolog	0
MELO3C026234	9.21463782431742e-05	0.00307398449987238	elongator complex protein 3	1
MELO3C025779	9.2346093012563e-05	0.00307545192395465	Nucleotide/sugar transporter family protein	1
MELO3C007571	9.30114872104149e-05	0.00309239707225334	OTU domain-containing protein	1
MELO3C024850	9.32171318644981e-05	0.00309402544065878	60S ribosomal protein L9-like	1
MELO3C012943	9.46720039655125e-05	0.00313704262804514	ADP,ATP carrier protein	0
MELO3C013810	9.56120904125335e-05	0.00316288638786788	At3g49990	1
MELO3C021436	9.61451448351358e-05	0.00317520144707207	60S acidic ribosomal protein P2B-like	1
MELO3C010021	9.6358700537813e-05	0.00317694153075337	ER membrane protein complex subunit 10	0
MELO3C022901	9.65210274401773e-05	0.00317698961819344	Alpha/beta-Hydrolases superfamily protein, putative	1
MELO3C021923	9.72721588077263e-05	0.00319638579749382	CCG-binding protein 1	1
MELO3C017755	9.79998273007432e-05	0.00321494782286109	zinc finger protein CONSTANS-LIKE 15-like	1
MELO3C009312	9.82774985767154e-05	0.00321871031408218	Pentatricopeptide repeat-containing protein At3g09650, chloroplastic	1
MELO3C017946	9.85155856012554e-05	0.00322116605966754	bifunctional epoxide hydrolase 2-like	1

MELO3C016303	9.87452484355611e-05	0.00322333869645272	ATP-dependent zinc metalloprotease FtsH	1
MELO3C002041	9.90924691245398e-05	0.00322933526854874	RHOMBOID-like protein 12, mitochondrial	1
MELO3C009572	0.00010010530796678	0.00324566590511127	ABC transporter family protein	1
MELO3C006316	9.98384531540886e-05	0.00324566590511127	cytochrome b5	1
MELO3C020557	0.000100154739182123	0.00324566590511127	Tetratricopeptide repeat (TPR)-like superfamily protein	1
MELO3C023996	0.000100250959649495	0.00324566590511127	RNA polymerase sigma factor sigD, chloroplastic	1
MELO3C024366	0.000100516259118888	0.00324892897109479	Mitochondrial carrier protein	1
MELO3C017255	0.000101150217111434	0.00326407783943417	BSD domain-containing protein	1
MELO3C017754	0.000102643919310808	0.00328012097486915	NAC domain-containing protein	1
MELO3C025278	0.00010184182706352	0.00328012097486915	Emp24/gp25L/p24 family/GOLD family protein	1
MELO3C005405	0.000102359121522122	0.00328012097486915	CDGSH iron-sulfur domain-containing protein NEET	1
MELO3C021901	0.000102486479856445	0.00328012097486915	Alpha/beta hydrolase-3	0
MELO3C025903	0.000102095232691002	0.00328012097486915	At5g59460	1
MELO3C012956	0.00010262148165241	0.00328012097486915	Protein MARD1	1
MELO3C003145	0.000103066071958313	0.00328829055751975	Cyclin d, putative	1
MELO3C006853	0.000103656565781596	0.00329094438804991	receptor-like serine/threonine-protein kinase isoform X2	1
MELO3C013261	0.000104022481609345	0.00329094438804991	No data found	0
MELO3C013440	0.000103896359409772	0.00329094438804991	PHD domain-containing protein/BAH domain-containing protein	1
MELO3C021116	0.000104315721652704	0.00329094438804991	No data found	1
MELO3C015563	0.000103478026248882	0.00329094438804991	TATA-box-binding protein	1
MELO3C008332	0.000104296975344309	0.00329094438804991	5-formyltetrahydrofolate cyclo-ligase-like protein COG021	1
MELO3C025812	0.000103525632135115	0.00329094438804991	ATP-dependent zinc metalloprotease FtsH	1
MELO3C024396	0.000104622452385073	0.00329535695718149	Cytochrome p450	1
MELO3C003906	0.000107750928353134	0.00338431427849777	Ethylene receptor	0
MELO3C021258	0.00010778944155021	0.00338431427849777	flowering time control protein FCA isoform X2	1
MELO3C015373	0.000108200386231605	0.0033918244883936	40S ribosomal protein S25	1
MELO3C009776	0.000108425898432851	0.00339350723954101	DNA-directed RNA polymerase II, putative	1
MELO3C013031	0.000108816587797156	0.00340034619051587	Glutamate dehydrogenase, putative	1
MELO3C005869	0.000108994104927262	0.00340051276178279	Bidirectional sugar transporter SWEET	1
MELO3C009354	0.000109747032851715	0.00340558652863798	Glutathione gamma-glutamylcysteinyltransferase 1	1
MELO3C016198	0.000109404821318382	0.00340558652863798	No data found	1
MELO3C009076	0.000109755888868523	0.00340558652863798	Nucleolar protein gar2-like protein	1
MELO3C022658	0.000109846504569466	0.00340558652863798	Ubiquitin-specific protease family C19 protein	1
MELO3C007433	0.000111052139491363	0.00342197323004645	fumarylacetoacetase	1
MELO3C007572	0.000110860800119461	0.00342197323004645	AP2-like ethylene-responsive transcription factor TOE3	1
MELO3C005299	0.000110942650853096	0.00342197323004645	C2 domain-containing protein	1
MELO3C011955	0.000111068147271243	0.00342197323004645	Tetratricopeptide-like helical	1
MELO3C008752	0.00011157295959352	0.0034321719299259	TATA box-binding protein-associated factor RNA polymerase I subunit B	1
MELO3C014730	0.000111888076964051	0.00343651264690986	N utilization substance B	1
MELO3C025853	0.000112716329796925	0.00345657577198675	protein DAMAGED DNA-BINDING 2	1
MELO3C002085	0.000113224239913556	0.00346676823884159	ethylene-responsive transcription factor ERF071	0
MELO3C020294	0.000113888702424569	0.00348171514579384	DNA-directed RNA polymerase subunit beta	1
MELO3C023310	0.000114261528182169	0.00348771394137505	Glucose-1-phosphate adenylyltransferase	1
MELO3C022773	0.00011559372525527	0.00352293283960852	Transmembrane protein, putative	1
MELO3C012529	0.000116333438386462	0.00352495494601283	Ras-related Rab7	1
MELO3C002885	0.000116374025256993	0.00352495494601283	transcription factor GTE1	1
MELO3C024324	0.000116198570528248	0.00352495494601283	Chaperone protein DnaJ	0
MELO3C019844	0.000116328959425371	0.00352495494601283	ras-related protein RABC2a-like	1
MELO3C022837	0.000116753774780598	0.00352564265770953	Cysteine-rich repeat secretory protein 60	0
MELO3C010776	0.000116715602386908	0.00352564265770953	Branched-chain-amino-acid aminotransferase	0
MELO3C010102	0.000117010176775678	0.00352799081090514	O-linked n-acetylglucosamine transferase, ogt, putative	1
MELO3C019470	0.000118662693332494	0.00355835651190511	glutelin type-A 2-like	1
MELO3C005094	0.000118738009081243	0.00355835651190511	histidine biosynthesis bifunctional protein hisIE, chloroplastic	1
MELO3C012180	0.000118248526876918	0.00355835651190511	ruBisCO large subunit-binding protein subunit beta, chloroplastic-like	1
MELO3C003658	0.000118704100653622	0.00355835651190511	Protein MARD1	1
MELO3C025049	0.000119458467457201	0.00357452314213979	transcription factor TCP21-like	1
MELO3C005331	0.000120522869021755	0.00359934712416343	Acyl-[acyl-carrier-protein] hydrolase	1
MELO3C001323	0.000120652579684855	0.00359934712416343	transmembrane protein 184C	1
MELO3C015024	0.000121409478646695	0.00361646424403254	RING-type E3 ubiquitin transferase	1
MELO3C014719	0.00012160994411281	0.00361698009982514	Aldehyde oxidase, putative	1
MELO3C012622	0.000122331082063387	0.00363295720251103	peptidyl-prolyl cis-trans isomerase CYP59	1
MELO3C019012	0.000123020613497338	0.00364794909303142	peptidyl-prolyl cis-trans isomerase CYP59	1
MELO3C011773	0.00012378596496454	0.00366514096264573	Oxidoreductase/transition metal ion-binding protein (DUF3531)	1
MELO3C011099	0.000124519937175549	0.00368135365161664	Universal stress protein A-like protein	1
MELO3C001165	0.000124820210286147	0.00368471499692246	eukaryotic translation initiation factor 3 subunit M	0
MELO3C005945	0.000125956652920811	0.00369128273352684	Dihydroorotate dehydrogenase (DUF3598)	1
MELO3C014016	0.000125606445577908	0.00369128273352684	Phospholipase D	1
MELO3C016924	0.000125729655771067	0.00369128273352684	pentatricopeptide repeat-containing protein At4g33170-like	0

MELO3C011550	0.000125977242513398	0.00369128273352684	transcription factor HBP-1b(C38) isoform X2	1
MELO3C003326	0.000125964577002202	0.00369128273352684	Ataxin-10	1
MELO3C005679	0.000126310862371914	0.00369557514219695	Tyrosine--tRNA ligase	1
MELO3C003768	0.000126536742464767	0.00369670728836787	Auxin response factor	1
MELO3C023989	0.000126739273406784	0.00369715496382656	Methyltransferase	0
MELO3C018203	0.000127875492985874	0.00372479809878764	Lysine-specific histone demethylase 1-like protein	1
MELO3C024226	0.000128758289654418	0.00374498889894713	Sulfate transporter 3.1	1
MELO3C022501	0.00012898932198635	0.00374619135280652	SNARE-interacting protein KEULE	1
MELO3C013591	0.000130542508120834	0.0037857327355042	Sugar transporter, putative	1
MELO3C007450	0.000130883346322275	0.0037900516224613	No data found	1
MELO3C016245	0.00013277895743391	0.00382810456987195	Glycosyl transferase family 1 family protein	1
MELO3C005812	0.000132585965774146	0.00382810456987195	ARM repeat superfamily protein	1
MELO3C010286	0.000132474750104805	0.00382810456987195	pyrophosphate-energized vacuolar membrane proton pump	1
MELO3C005656	0.000133662942434221	0.00383121836013559	Protein LURP-one-related 11	1
MELO3C011868	0.000133236508693457	0.00383121836013559	Rubber elongation factor protein (REF)	1
MELO3C024004	0.000133474638887243	0.00383121836013559	No data found	1
MELO3C009836	0.000133335849776817	0.00383121836013559	Saccharopine dehydrogenase-like protein	1
MELO3C026097	0.000133883793933309	0.00383198702375207	Hexosyltransferase	1
MELO3C009272	0.000136632869338404	0.00384148920539927	UNC93-like protein 3	1
MELO3C004354	0.000136084094665589	0.00384148920539927	Cc-nbs-lrr resistance protein	1
MELO3C004448	0.000135177309396939	0.00384148920539927	DNA helicase	1
MELO3C006344	0.000136358697194305	0.00384148920539927	GDT1-like protein	1
MELO3C016879	0.000135264956713455	0.00384148920539927	Cytochrome P450, putative	1
MELO3C010548	0.000135760565941778	0.00384148920539927	Receptor-like protein kinase	1
MELO3C007153	0.000136188957985395	0.00384148920539927	No data found	1
MELO3C007246	0.000136437561226055	0.00384148920539927	28 kDa heat/acid-stable phosphoprotein-like protein	0
MELO3C023322	0.000135847690136526	0.00384148920539927	BnaC07g46810D protein	0
MELO3C017248	0.000136096223293025	0.00384148920539927	ATP-dependent helicase hrq1 isoform X6	1
MELO3C018521	0.000136744488905549	0.00384148920539927	DNA polymerase kappa	1
MELO3C010798	0.000136566235940494	0.00384148920539927	NADH dehydrogenase (Ubiquinone) iron-sulfur protein 4, mitochondrial	1
MELO3C009895	0.000134705562194748	0.00384148920539927	Actin cross-linking protein	1
MELO3C003344	0.000137728859039843	0.00386364664371855	3-isopropylmalate dehydratase large subunit	1
MELO3C020622	0.000138697018806866	0.00388528712683233	Rab5-interacting family protein	1
MELO3C021529	0.000139532513883989	0.00390315526444036	NHL domain-containing protein, putative	1
MELO3C013254	0.000140084319380063	0.0039130484065585	Kinase family protein	1
MELO3C015431	0.000140582970614034	0.00392084191800449	40S ribosomal protein S30	1
MELO3C011444	0.000140928428675302	0.00392084191800449	Mitogen-activated protein kinase	1
MELO3C011256	0.00014095892256738	0.00392084191800449	DEAD-box ATP-dependent RNA helicase-like protein	1
MELO3C023033	0.000141418977736452	0.00392810603560785	heterogeneous nuclear ribonucleoprotein 1-like	0
MELO3C002381	0.000142522202502882	0.00395318957476041	Bidirectional sugar transporter SWEET	1
MELO3C014860	0.000143769670123084	0.00395998216912243	Transcription factor GTE8	1
MELO3C017753	0.000143619980119469	0.00395998216912243	Glycerophosphodiester phosphodiesterase, putative	1
MELO3C027408	0.000143675590806192	0.00395998216912243	polygalacturonase-like	1
MELO3C011905	0.000143275905241325	0.00395998216912243	RING finger protein	1
MELO3C021273	0.000143610156909224	0.00395998216912243	Seed maturation protein PM36	1
MELO3C021552	0.000144105408032114	0.00396370153652676	universal stress protein A-like protein	1
MELO3C012410	0.000144501796441432	0.00396907646442537	thioredoxin-like 3-2, chloroplastic isoform X8	1
MELO3C009350	0.000144748238125936	0.00397032354826265	TSL-kinase interacting protein 1	1
MELO3C019087	0.000146130882510365	0.00398610331311767	UDP-glycosyltransferase 76E2-like	0
MELO3C013563	0.000146093610227327	0.00398610331311767	Metacaspase-5	0
MELO3C020626	0.000145762787050252	0.00398610331311767	Expansin	1
MELO3C003332	0.000145611556127134	0.00398610331311767	BAX inhibitor-1	1
MELO3C005692	0.000146809861828023	0.00399910063619536	E3 ubiquitin-protein ligase At3g02290-like	0
MELO3C023195	0.000147031826110533	0.00399963021192413	NAC domain-containing protein 2	1
MELO3C015186	0.000147641124904396	0.00400517112051775	Sulfite reductase	1
MELO3C026248	0.000147597711079306	0.00400517112051775	E3 ubiquitin-protein ligase RGLG2	1
MELO3C005182	0.000148326223665451	0.00401823675057476	Short-chain dehydrogenase/reductase family protein	1
MELO3C022443	0.000148550255063884	0.00401879313322828	flowering time control protein FPA	1
MELO3C003561	0.000149095804355959	0.00402803425475489	VQ motif-containing protein 9	1
MELO3C016354	0.000150065092783924	0.00404868240080563	Short-chain dehydrogenase TIC 32, chloroplastic	1
MELO3C024861	0.000151226502948631	0.00407445048667466	Caffeic acid O-methyltransferase	0
MELO3C014129	0.000151454412625762	0.00407503160074411	THO complex subunit 3	1
MELO3C017700	0.000151785072965982	0.00407691511311494	disease resistance protein RGA2-like	1
MELO3C000065	0.000151961111964471	0.00407691511311494	V-type proton ATPase proteolipid subunit	1
MELO3C018160	0.000152143725675513	0.00407691511311494	factor of DNA methylation 1-like	0
MELO3C010420	0.000153349701356276	0.00409707057209984	DUF581 family protein, putative (DUF581)	1
MELO3C016246	0.000153294831223838	0.00409707057209984	Kinase family protein	1
MELO3C015930	0.000153518265398445	0.00409707057209984	Translation initiation factor IF-2	1

MELO3C011402	0.000153953444997246	0.00410313979116141	D-aminoacyl-tRNA deacylase	1
MELO3C017560	0.000155454272554256	0.00413387924224256	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	1
MELO3C008974	0.000155525458351624	0.00413387924224256	60S ribosomal protein L35a	0
MELO3C023979	0.000156378911793542	0.00415097732393906	Cellulose synthase	1
MELO3C021064	0.000157428826421557	0.00417323744026756	malonyl-CoA:anthocyanidin 5-O-glucoside-6"-O-malonyltransferase	1
MELO3C006645	0.000158263172499673	0.00417852860119792	No data found	1
MELO3C003147	0.000158254093796217	0.00417852860119792	LOW QUALITY PROTEIN: L-type lectin-domain containing receptor kinase	1
MELO3C001121	0.00015812671487514	0.00417852860119792	Aspartate aminotransferase	1
MELO3C010760	0.000158563073288098	0.00418085732225187	Pollen specific protein sf21	1
MELO3C024871	0.000160253718284764	0.00421980090987441	serine/threonine-protein phosphatase 4 regulatory subunit 2 isoform X1	1
MELO3C017653	0.000160928051555986	0.00422261443857199	Isoaspartyl peptidase/L-asparaginase	1
MELO3C008785	0.000160986249053918	0.00422261443857199	BTB/POZ domain protein	1
MELO3C024222	0.000161002008822964	0.00422261443857199	aldo-keto reductase family 4 member C9-like	1
MELO3C025594	0.000161236287363531	0.00422315044979094	C2 domain-containing protein	1
MELO3C019722	0.000162089692921086	0.00423791057130512	Protein disulfide-isomerase like 2-2	1
MELO3C015230	0.000162228993463298	0.00423791057130512	Pectin acetylesterase	1
MELO3C018510	0.000162585414409389	0.00424161076508721	somatic embryogenesis receptor kinase 1-like	1
MELO3C013260	0.000162887802810818	0.00424389342705917	protein LAZ1 isoform X1	1
MELO3C009203	0.000165437336013374	0.00426283287985112	tubulin beta chain-like	1
MELO3C023685	0.000165296367253043	0.00426283287985112	alcohol dehydrogenase-like	1
MELO3C006088	0.000165137396803905	0.00426283287985112	50S ribosomal protein L5, chloroplastic	1
MELO3C006974	0.000165557386138326	0.00426283287985112	Plastid division protein PDV1	1
MELO3C023255	0.000164791051848967	0.00426283287985112	DNA-directed RNA polymerase subunit beta-beta protein, putative (DUF506)	1
MELO3C002817	0.000164407991422699	0.00426283287985112	No data found	1
MELO3C002163	0.000164730021437798	0.00426283287985112	E3 ubiquitin-protein ligase RING1-like	0
MELO3C010165	0.000165256170291617	0.00426283287985112	Cyclic nucleotide-gated ion channel-like protein	1
MELO3C026141	0.000165134912869958	0.00426283287985112	ADP-ribosylation factor-like	1
MELO3C014128	0.000165992853658037	0.00426848029543303	Calcium-dependent protein kinase	1
MELO3C012572	0.000166407907161714	0.00427358876272652	CTP synthase	1
MELO3C003973	0.000167132576897933	0.00427592256812336	SNW/SKI-interacting protein-like	1
MELO3C017838	0.000166939205969663	0.00427592256812336	Ubiquitin system component Cue	1
MELO3C014217	0.000167148322577915	0.00427592256812336	Telomere repeat-binding protein 4	0
MELO3C009063	0.000169160970210358	0.00432181112637045	serine/threonine-protein kinase Nek6 isoform X1	1
MELO3C018306	0.000169535131114396	0.00432577429506227	Mitogen-activated protein kinase	1
MELO3C005001	0.000170562545132369	0.00434637381137955	dof zinc finger protein DOF5.3-like	0
MELO3C005882	0.000171637761367083	0.00436813679025582	Eukaryotic translation initiation factor 3 subunit 10	1
MELO3C015374	0.000172882858217371	0.00439416160480678	Superoxide dismutase [Cu-Zn]	1
MELO3C012201	0.000173729943490741	0.0044017019494474	Isoprenylcysteine alpha-carbonyl methylesterase ICME proteir	1
MELO3C020583	0.000173737441671706	0.0044017019494474	Neutral ceramidase	0
MELO3C002566	0.000173848170569091	0.0044017019494474	Katanin p80 WD40 repeat-containing subunit B1 homolog	1
MELO3C014799	0.000175285251514445	0.00442673712552274	TRANSPORT INHIBITOR RESPONSE 1 protein, putative	0
MELO3C015185	0.000175088311723859	0.00442673712552274	MP domain-containing protein	1
MELO3C022562	0.00017556921672901	0.00442824579972059	protein CHROMATIN REMODELING 19 isoform X1	0
MELO3C010421	0.000176144776798615	0.00443709591453551	Random slug protein 5	1
MELO3C014379	0.000177515142250728	0.00446023733372727	Protein RETICULATA-RELATED 1, chloroplastic	1
MELO3C001948	0.000177457027202066	0.00446023733372727	Short-chain dehydrogenase, putative	1
MELO3C003508	0.000178471292703875	0.00447856360814335	UDP-glycosyltransferase 91C1	1
MELO3C005673	0.000183514922535988	0.00459928452431881	tubulin beta chain-like	1
MELO3C009561	0.000183781133722527	0.00460011864370873	iron-sulfur cluster co-chaperone protein HscB, mitochondrial	1
MELO3C006651	0.000184318937710204	0.00460191491888599	No data found	1
MELO3C017358	0.000184207700662187	0.00460191491888599	C2 domain-containing protein	1
MELO3C013346	0.000185552097884845	0.0046268540165755	Phospholipase-like protein (PEARLI 4) family protein	1
MELO3C015111	0.000188240908695514	0.00468798197456205	rho GTPase-activating protein 7	1
MELO3C010245	0.000189301601007941	0.00470846009862194	Two-component response regulator	1
MELO3C012076	0.00019072837700751	0.00473798077675636	UDP-galactose/UDP-glucose transporter family protein	1
MELO3C025468	0.000191221524523888	0.00474349870973502	ABC transporter B family protein	1
MELO3C004833	0.000191430881141263	0.00474349870973502	crooked neck-like protein 1	1
MELO3C015350	0.000191817108435632	0.0047471128753074	Sugar transporter ERD6-like protein	1
MELO3C006239	0.000194745937404539	0.0048075468972528	Receptor protein kinase, putative	0
MELO3C022684	0.000194616340531306	0.0048075468972528	peroxisomal (S)-2-hydroxy-acid oxidase GLO4-like	0
MELO3C011588	0.000195838236416002	0.00482847606863872	Phosphatidylinositol-4-phosphate 5-kinase 1-like protein	1
MELO3C003733	0.000196244446180049	0.00483245831372793	ribonuclease P protein subunit p25-like protein isoform X1	1
MELO3C000826	0.000197316742958864	0.00484075572260199	Transcription factor	1
MELO3C021280	0.000197073655135882	0.00484075572260199	Calmodulin-binding transcription activator	1
MELO3C018455	0.000197093459462172	0.00484075572260199	thioredoxin M3, chloroplastic	1
MELO3C024902	0.000197626941677576	0.00484235046053404	ABC subfamily C transporter	0
MELO3C005808	0.000198080417585844	0.00484539295425683	No data found	1
MELO3C024344	0.000198241810068334	0.00484539295425683	DUF1677 family protein (DUF1677)	1

MELO3C025606	0.000198581595278524	0.00484769830056313	Unknown protein	1
MELO3C016360	0.00019959105733458	0.00486632566827238	Transferring glycosyl group transferase	1
MELO3C019026	0.000200262784349703	0.00487668277203734	Phosphate transporter	1
MELO3C019564	0.000201417398875803	0.00489273334612328	High chlorophyll fluorescence phenotype 173	1
MELO3C000994	0.000201282242801692	0.00489273334612328	wall-associated receptor kinase 2-like	1
MELO3C013841	0.000206757258935486	0.00501012160333364	nucleolar protein 12	1
MELO3C003817	0.00020674784003627	0.00501012160333364	DNA polymerase epsilon catalytic subunit A	1
MELO3C004551	0.000207150930850553	0.00501350947716613	ARF guanine-nucleotide exchange factor GNL2	1
MELO3C005035	0.000208333784670112	0.00503596562233786	E3 SUMO-protein ligase SIZ1	1
MELO3C011395	0.000212015636750662	0.00511870025695455	Hydroxyproline O-arabinosyltransferase 1	1
MELO3C009566	0.000212899672441647	0.0051337675592797	Protein WVD2-like 4	1
MELO3C007624	0.00021680183247641	0.00519433149706969	Acyl-CoA N-acyltransferases (NAT) superfamily proteir	1
MELO3C005520	0.000216989391112588	0.00519433149706969	Ribosomal protein L15	1
MELO3C023503	0.000216126270384365	0.00519433149706969	Unknown protein	1
MELO3C022540	0.000216005163480082	0.00519433149706969	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	0
MELO3C013615	0.00021629852461702	0.00519433149706969	E3 ubiquitin-protein ligase RMA1H1	1
MELO3C003842	0.000216935765092741	0.00519433149706969	Dead box ATP-dependent RNA helicase, putative	1
MELO3C026764	0.000217488779697295	0.00519998294218144	Magnesium transporter MRS2-like protein	1
MELO3C020601	0.000218758247361506	0.00522354898241223	Protein phosphatase 2C	1
MELO3C017432	0.000219003420802943	0.00522354898241223	At1g16840/F17F16.27	1
MELO3C019629	0.000220238525441285	0.00524667145831115	ALA-interacting subunit 3-like	0
MELO3C004999	0.000222439350828108	0.00529271655361963	nicotinamide adenine dinucleotide transporter 1, chloroplastic-like	1
MELO3C010189	0.00022317153203999	0.00529927201732925	lactation elevated protein 1	1
MELO3C017165	0.000223376505001038	0.00529927201732925	HVA22-like protein	1
MELO3C009914	0.000223519853685517	0.00529927201732925	Alpha-mannosidase	1
MELO3C021308	0.00022430380657712	0.00530926236936354	Multiple organellar RNA editing factor 8, chloroplastic/mitochondrial	1
MELO3C019921	0.000224478914295334	0.00530926236936354	Phospholipid-transporting ATPase	0
MELO3C019139	0.000225618022833496	0.00532485097703111	Nascent polypeptide-associated complex subunit alpha-like protein	1
MELO3C026027	0.000225677263039903	0.00532485097703111	Macrophage migration inhibitory factor family protein	1
MELO3C012869	0.000228239696927757	0.00537888517258504	Adaptin ear-binding coat-associated protein, putative	1
MELO3C013214	0.000232109115587242	0.00546355533221984	DNA damage-inducible protein 1	1
MELO3C017043	0.000233289549711801	0.00547828218461161	Glutamate receptor	1
MELO3C011682	0.00023316957210473	0.00547828218461161	Fructose-1,6-bisphosphatase	0
MELO3C009429	0.000234027845987472	0.00548351994895583	peroxiredoxin-2E-2, chloroplastic	1
MELO3C005111	0.00023446163867713	0.00548351994895583	Coiled-coil protein	0
MELO3C005745	0.000234311765738404	0.00548351994895583	Abhydrolase_5 domain-containing protein	1
MELO3C023464	0.000234798570744266	0.00548351994895583	sister chromatid cohesion protein PDS5 homolog B-B-like	1
MELO3C021339	0.000234900900137558	0.00548351994895583	60S ribosomal protein L13a, putative	1
MELO3C014614	0.000235860026803869	0.00549292413838397	Leucine-rich repeat receptor-like protein kinase family	0
MELO3C010705	0.000235766264270243	0.00549292413838397	T-complex protein 1 subunit epsilon	1
MELO3C019435	0.000236976943461809	0.00550595018403207	MLO-like protein 4	1
MELO3C015852	0.000236938477880977	0.00550595018403207	adenylate isopentenyltransferase 3, chloroplastic	1
MELO3C002886	0.000237461224858571	0.00551071883634772	Alpha-taxilin	1
MELO3C017008	0.000239417539566356	0.00552722123260604	Ubiquitin family protein	0
MELO3C026804	0.000239213874166588	0.00552722123260604	histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH1-like	1
MELO3C000201	0.000239277857855269	0.00552722123260604	dof zinc finger protein DOF1.5-like	1
MELO3C021461	0.000239571693509077	0.00552722123260604	No data found	1
MELO3C021742	0.000238546835302778	0.00552722123260604	Glycine cleavage system H, mitochondrial	1
MELO3C024688	0.000240582824529545	0.00554407258066976	TATA-binding protein-associated factor 2N	0
MELO3C009127	0.000241609568591317	0.00556124402110712	WRKY family transcription factor family protein	0
MELO3C004441	0.000242392300670469	0.00557276547839475	RING-H2 finger protein ATL16	1
MELO3C016707	0.000243440104488402	0.00557737659343555	Choline transporter-like protein 2	1
MELO3C012173	0.00024337823626408	0.00557737659343555	DNA-directed RNA polymerase	1
MELO3C011044	0.000243145665177247	0.00557737659343555	cytochrome c oxidase subunit 6b-1-like	1
MELO3C003120	0.000244375341807102	0.00559231590422763	SLT1	1
MELO3C012004	0.000244992421164048	0.00559765608210468	Xyloglucan endotransglucosylase/hydrolase	1
MELO3C018437	0.000245175579068335	0.00559765608210468	Pentatricopeptide repeat-containing protein At5g39710	1
MELO3C002075	0.00024584132238592	0.00559990804590489	No data found	1
MELO3C011507	0.000245627075923016	0.00559990804590489	Vesicle transport protein GOT1	1
MELO3C024192	0.000247316007776055	0.0056205337601488	Fasciclin-like arabinogalactan protein	1
MELO3C007425	0.000247283160818346	0.0056205337601488	1-aminocyclopropane-1-carboxylate oxidase 1	0
MELO3C015496	0.000251336419125447	0.00570533671414766	Plant/F27B13-30 protein	1
MELO3C021292	0.000251956426508548	0.00571284439393493	Protein DEHYDRATION-INDUCED 19	1
MELO3C011986	0.000252668788317534	0.00572242649137956	Polygalacturonase	1
MELO3C013600	0.000256143100017092	0.00574837509345177	O-methyltransferase, putative	1
MELO3C005797	0.000255289098429867	0.00574837509345177	Unknown protein	1
MELO3C012033	0.000255521627540833	0.00574837509345177	Neurofilament heavy protein	1
MELO3C022354	0.000254944927874368	0.00574837509345177	Light-regulated protein, putative	1

MELO3C017242	0.00025602726417806	0.00574837509345177	protein COBRA-like	1
MELO3C026522	0.000255690699527245	0.00574837509345177	monosaccharide-sensing protein 2-like	1
MELO3C011105	0.000255669095747146	0.00574837509345177	Chaperone protein dnaJ	1
MELO3C009782	0.000254722393082774	0.00574837509345177	5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase	1
MELO3C026803	0.000258450915686992	0.00578701489104581	S-acyltransferase	1
MELO3C022442	0.000258437787819199	0.00578701489104581	At1g08760	1
MELO3C002351	0.000259527766881318	0.00580454571703188	Receptor protein kinase-like protein	0
MELO3C008058	0.000261626098192913	0.00581198404185809	mitogen-activated protein kinase kinase kinase YODA isoform X1	1
MELO3C022196	0.000261549622935453	0.00581198404185809	Kinase family protein	1
MELO3C010214	0.000261610083673203	0.00581198404185809	Nucleoid-associated protein At2g24020, chloroplastic	1
MELO3C026201	0.000260842116481808	0.00581198404185809	non-specific phospholipase C6	1
MELO3C011601	0.000260986200993574	0.00581198404185809	No data found	1
MELO3C011107	0.000261609531341023	0.00581198404185809	Serine hydroxymethyltransferase	1
MELO3C005967	0.000264984834755788	0.005879983709654	At3g15351	1
MELO3C022114	0.000265447627879833	0.00588364220314122	RmlC-like cupins superfamily protein	1
MELO3C003186	0.000266588800294176	0.00588910762529048	Proteasome inhibitor-related	1
MELO3C011622	0.000266085187327958	0.00588910762529048	Receptor-like kinase	1
MELO3C010958	0.000266339972744611	0.00588910762529048	Gamma carbonic anhydrase 1, mitochondrial	1
MELO3C011482	0.000266994123112263	0.00589147143837328	ATP-citrate synthase beta chain protein 2-like	1
MELO3C016601	0.000268047574068397	0.00590561416358361	No data found	1
MELO3C002470	0.000268233120904071	0.00590561416358361	Patatin	1
MELO3C003294	0.000268967860220348	0.00591519629342055	vacuolar cation/proton exchanger 3	1
MELO3C017993	0.000271532165540656	0.00596494853978021	40S ribosomal protein S29	1
MELO3C025255	0.000273271096768335	0.00599647876675316	Zinc transporter	1
MELO3C006594	0.000275652840892704	0.00602044287082797	Inosine-uridine preferring nucleoside hydrolase	1
MELO3C022014	0.000274733521762549	0.00602044287082797	WRKY transcription factor, putative	1
MELO3C005588	0.000275761756498127	0.00602044287082797	No data found	1
MELO3C002223	0.000275887427115262	0.00602044287082797	hydroxyproline O-galactosyltransferase GALT6	1
MELO3C024975	0.000275516874583381	0.00602044287082797	DUF3511 domain protein	1
MELO3C013766	0.000277047881957371	0.00602295331887094	Translocase of chloroplast	0
MELO3C017544	0.000276862046831305	0.00602295331887094	DNA-directed RNA polymerase III subunit RPC5	1
MELO3C018441	0.00027722236907457	0.00602295331887094	presequence protease 1, chloroplastic/mitochondrial-like	1
MELO3C022679	0.000277183104936407	0.00602295331887094	oligouridylate-binding protein 1B-like	0
MELO3C013188	0.000277872280472269	0.00602381961256513	Pentatricopeptide repeat-containing protein	1
MELO3C002118	0.000277836043142798	0.00602381961256513	Elongation factor 1 alpha	1
MELO3C013046	0.000278180830887376	0.0060238960846434	Kinase family protein	1
MELO3C005002	0.000281040859585691	0.00607916312810274	Interactor of constitutive active ROPs-like protein	0
MELO3C012349	0.000282115086382206	0.00609572302074638	replication protein A 14 kDa subunit B-like	0
MELO3C008097	0.000282891183413736	0.00610581200135287	Polyprotein	0
MELO3C022353	0.000283476774613156	0.0061117716395581	tRNA dimethylallyltransferase	0
MELO3C008236	0.000283857813457633	0.00611331293127022	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein isoform 1	1
MELO3C007082	0.000285601472570951	0.00613952992528879	No data found	1
MELO3C012218	0.000285696896113241	0.00613952992528879	Two-component response regulator	1
MELO3C009779	0.000287063425019052	0.00616219084858832	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	1
MELO3C020850	0.000287415273795277	0.00616304477978603	Filament-like plant protein 7	0
MELO3C009539	0.000288935313469407	0.00616328919688229	NC domain-containing protein	1
MELO3C008986	0.000288021661580151	0.00616328919688229	No data found	1
MELO3C023484	0.000288852383731109	0.00616328919688229	AP2-like ethylene-responsive transcription factor At1g16060	1
MELO3C010053	0.000289607650206358	0.00616328919688229	Isopentenyl diphosphate isomerase	1
MELO3C017226	0.000289611239794763	0.00616328919688229	glycine-rich RNA-binding protein 2, mitochondrial-like	1
MELO3C010630	0.000289461750767162	0.00616328919688229	40S ribosomal protein S8	1
MELO3C003771	0.000289095891857327	0.00616328919688229	Mitochondrial 39S ribosomal protein L53	0
MELO3C007084	0.000290601122250878	0.00617769813060558	BTB/POZ domain-containing protein	0
MELO3C008295	0.000291253199451558	0.0061849026193213	ABC1-like protein	1
MELO3C023251	0.000292832830838363	0.00621176753622646	callose synthase 5	1
MELO3C025232	0.000294396155300802	0.00623822926076775	Ubiquitin-conjugating enzyme, E2	1
MELO3C016288	0.000296833075818848	0.00628245353684985	F-box/LRR-repeat protein 14	1
MELO3C003487	0.0002971194290049	0.00628245353684985	receptor-like protein kinase HAIKU2	1
MELO3C006785	0.00030098724067229	0.00634386020921778	U11/U12 small nuclear ribonucleoprotein 35 kDa protein	1
MELO3C016573	0.000300781649135162	0.00634386020921778	Serine/threonine-protein kinase	1
MELO3C012335	0.00030093175099899	0.00634386020921778	Uricase	0
MELO3C002298	0.00030226452811033	0.00635973082156247	Methylthioribose-1-phosphate isomerase	0
MELO3C008469	0.00030238428484719	0.00635973082156247	Kinase family protein	1
MELO3C015385	0.000304250502092929	0.00638538062256456	Pentatricopeptide repeat-containing protein	1
MELO3C019777	0.000304243646278235	0.00638538062256456	U4/U6 small nuclear ribonucleoprotein PRP4-like protein	1
MELO3C025091	0.000304781112087205	0.0063897263085034	protein REVEILLE 1-like isoform X1	1

MELO3C017939	0.000306345373478512	0.00641571026598847	Ribosomal protein L19	1
MELO3C007011	0.000307586424169948	0.00642904807225306	No data found	1
MELO3C007611	0.000307633319574618	0.00642904807225306	Prolyl 4-hydroxylase alpha-like protein	1
MELO3C013883	0.000308162688031799	0.00643330330437632	BOI-related E3 ubiquitin-protein ligase 1	1
MELO3C022514	0.000309803504096484	0.00645779523213418	UTP:RNA uridylyltransferase 1	1
MELO3C002328	0.000310299011578308	0.00645779523213418	zinc finger CCCH domain-containing protein 43	1
MELO3C011090	0.000310316860362314	0.00645779523213418	Unknown protein	1
MELO3C008440	0.000311127156138014	0.00646784232270487	wall-associated receptor kinase 2-like	1
MELO3C004818	0.000313659812932854	0.00651363579980119	S-adenosyl-L-methionine-dependent methyltransferase superfamily protein	0
MELO3C014557	0.000316734499387072	0.00655680254548773	Peptidyl-prolyl cis-trans isomerase	1
MELO3C010478	0.000316303353062986	0.00655680254548773	Protein-methionine-s-oxide reductase	1
MELO3C013527	0.000316579852200904	0.00655680254548773	1D-myo-inositol 2-amino-2-deoxy-alpha-D-glucopyranoside ligase	1
MELO3C001849	0.000317464593990291	0.00656503483425577	No data found	1
MELO3C025628	0.000319630051430653	0.00660290155408364	Aspartyl/glutamyl-tRNA (Asn/Gln) amidotransferase subunit B	0
MELO3C017799	0.000320760795404995	0.00661242687729984	F2P16.20 protein, putative isoform 1	1
MELO3C011882	0.000320479602688328	0.00661242687729984	RING-type E3 ubiquitin transferase	1
MELO3C019053	0.000321423875051297	0.00661859054599197	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3	1
MELO3C021608	0.00032173005844105	0.00661859054599197	zinc finger protein CONSTANS-LIKE 6	1
MELO3C022345	0.000322137578457116	0.00662007808215357	somatic embryogenesis receptor kinase 2-like	1
MELO3C011110	0.000324177713222018	0.00665507864700794	transcription factor bHLH93-like	1
MELO3C008732	0.000326177477364187	0.00668529463580516	No data found	1
MELO3C016284	0.000326326600279314	0.00668529463580516	BnaC06g13730D protein	0
MELO3C013949	0.000326936864283978	0.00669085609610806	Ribosomal protein L20	1
MELO3C025848	0.000329847364902602	0.00674343230793115	Peptidyl-prolyl cis-trans isomerase	1
MELO3C016213	0.00033459521642587	0.00683342391850518	Beta-amylase	1
MELO3C018956	0.000335707153891862	0.00683492843526844	Ubiquitin carboxyl-terminal hydrolase, putative	1
MELO3C007152	0.000335088922765014	0.00683492843526844	Leucine-rich receptor-like protein kinase family protein	1
MELO3C010769	0.000335478511820808	0.00683492843526844	Protein EARLY FLOWERING 3	1
MELO3C015450	0.000340086584732724	0.00691696185570192	Pollen-specific protein SF21	1
MELO3C006413	0.000342652819556477	0.00696198614549472	Clathrin interactor EPSIN 2	1
MELO3C017698	0.00034384648671526	0.00697905885523091	Vesicle transport protein GOT1	0
MELO3C018478	0.000344872724779233	0.00698552968375904	kynurenine formamidase	1
MELO3C011104	0.00034473878406005	0.00698552968375904	Glucose-6-phosphate isomerase	1
MELO3C021510	0.000345680560706607	0.00699471864077334	Ferredoxin-thioredoxin reductase catalytic chain	0
MELO3C011212	0.000351043049657718	0.00709595617982627	Photosystem II reaction center PsbP family protein	1
MELO3C006983	0.000353401205477111	0.00713631943452705	Protein phosphatase 2C	1
MELO3C014307	0.000354028631387227	0.00714168686544059	PRA1 family protein	1
MELO3C026030	0.000355478001607956	0.00716360719770972	Protein phosphatase-2c, putative	1
MELO3C019462	0.000356006879700388	0.00716695195433533	Membralin, putative	1
MELO3C010774	0.000360111028847587	0.00724219216773014	Zinc finger CCCH domain-containing protein	1
MELO3C010329	0.000361489058516851	0.0072625100881478	methyl-CpG-binding domain-containing protein 11-like	1
MELO3C007086	0.000362295746433317	0.00727131981332476	ABC transporter C family member 12-like	1
MELO3C014306	0.000362983932115979	0.00727773571102382	signal recognition particle 9 kDa protein	1
MELO3C007119	0.000364741286312031	0.00730555341113216	E3 ubiquitin-protein ligase arkadia-A, putative	0
MELO3C022212	0.000369332025183966	0.00739000827290592	Deoxycytidine kinase	1
MELO3C002722	0.000370088987242112	0.00739765932089521	3-oxoacyl-[acyl-carrier-protein] synthase	1
MELO3C002607	0.000370819442000903	0.00740476558147202	Sulfate/thiosulfate import ATP-binding protein cysA, putative	1
MELO3C014272	0.000376517115107222	0.00750665144381306	Pyruvate kinase	1
MELO3C017784	0.000376681937354739	0.00750665144381306	Pentatricopeptide repeat-containing family protein	1
MELO3C026155	0.000378623549355916	0.00753773838329637	(+)-neomenthol dehydrogenase	1
MELO3C006598	0.000380672496428369	0.00757089741386089	serine/arginine-rich SC35-like splicing factor SCL28	1
MELO3C008040	0.000381908918189233	0.00758784630313799	RING-type E3 ubiquitin transferase	1
MELO3C012525	0.000384064071674795	0.00762299633317137	Receptor-like kinase	1
MELO3C026919	0.000385875008708902	0.00765125054918887	RuBisCO large subunit-binding protein subunit alpha, chloroplastic	0
MELO3C003242	0.000388061894538216	0.0076868950403563	Clathrin light chain	1
MELO3C006096	0.000388869747816378	0.00769517900764094	DNA replication complex GINS protein SLD5	0
MELO3C008925	0.000389715645112587	0.00770419847380229	GTPase LSG1-2-like	1
MELO3C007691	0.000390499220882301	0.00771196911320456	Auxin-responsive protein	1
MELO3C018720	0.000391460927158693	0.00772323861184519	F-box protein MAX2	1
MELO3C006726	0.000393613047360519	0.00775021343202681	Galactokinase	0
MELO3C023350	0.000393498277305726	0.00775021343202681	GATA transcription factor	0
MELO3C017960	0.00039484077823515	0.00775296869722632	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5-B	1
MELO3C007833	0.000394930705828633	0.00775296869722632	ATPase family AAA domain-containing protein 3	1
MELO3C005861	0.000394326202309614	0.00775296869722632	Hexosyltransferase	0
MELO3C019503	0.000397224747742952	0.00776020694699844	zinc-binding alcohol dehydrogenase domain-containing protein 2	1
MELO3C027373	0.000398384892281056	0.00776020694699844	ADP-ribosylation factor GTPase-activating protein AGD12-like	1
MELO3C022007	0.000397071538311811	0.00776020694699844	transmembrane emp24 domain-containing protein p24delta9	1

MELO3C024444	0.000395871151194438	0.00776020694699844	Avr9/Cf-9 rapidly elicited protein	1
MELO3C012447	0.00039769110672716	0.00776020694699844	Scarecrow-like 3	1
MELO3C020610	0.000397760016506599	0.00776020694699844	protein TOC75-3, chloroplastic	0
MELO3C002609	0.000398442951251021	0.00776020694699844	serine/threonine-protein kinase HT1-like	1
MELO3C024644	0.000397462342182631	0.00776020694699844	50S ribosomal protein L18	1
MELO3C019816	0.000399693237937981	0.00777688842959329	Amino acid transporter family protein	1
MELO3C009758	0.000402735654175146	0.00780045318224247	Amino acid transporter family protein	1
MELO3C009408	0.000402832046479062	0.00780045318224247	Tetratricopeptide repeat (TPR)-like superfamily protein	1
MELO3C016817	0.000402351344261254	0.00780045318224247	Calcium-transporting ATPase	1
MELO3C026025	0.000402879246842236	0.00780045318224247	Dehydration responsive element binding transcription factor	1
MELO3C017480	0.000401515371484806	0.00780045318224247	Xyloglucan endotransglucosylase/hydrolase	1
MELO3C024544	0.000404108671178793	0.00781659367983349	Cell division FtsZ-1, chloroplastic-like protein	1
MELO3C005517	0.0004077385948561	0.00787908953993455	Tryptophan RNA-binding attenuator protein-like	1
MELO3C007043	0.000408454688791027	0.00788521177803909	UDP-glucose 4-epimerase, putative	1
MELO3C013773	0.000410427524175638	0.00790881113427016	Mediator of RNA polymerase II transcription subunit	1
MELO3C003426	0.000410478070415055	0.00790881113427016	Inositol-tetrakisphosphate 1-kinase	1
MELO3C014619	0.000416573957624733	0.00798238170586701	IRK-interacting protein-like	1
MELO3C021139	0.000416728063664884	0.00798238170586701	No data found	0
MELO3C005875	0.000415414077330256	0.00798238170586701	Curved DNA-binding protein	0
MELO3C012171	0.000417125825128095	0.00798238170586701	phosphatidylinositol 4-kinase gamma 5	0
MELO3C025940	0.000416422648866988	0.00798238170586701	CONSTANS-like zinc finger protein	1
MELO3C002382	0.000417101743036552	0.00798238170586701	Kinase family protein	1
MELO3C017207	0.000416952793157011	0.00798238170586701	LYR motif-containing protein 4	1
MELO3C002312	0.000421192848875096	0.00805240810497025	cytochrome P450 71A1-like	1
MELO3C026966	0.00042238849588494	0.00806745687159737	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	1
MELO3C017319	0.000423412418095515	0.00807919985021093	BnaA06g03540D protein	1
MELO3C023667	0.000425142227014508	0.00809656108130136	Tetratricopeptide repeat-containing protein	1
MELO3C008086	0.00042505111070712	0.00809656108130136	Delta-aminolevulinic acid dehydratase	0
MELO3C010565	0.000429306516313455	0.00815720266161301	No data found	1
MELO3C007254	0.000428996821239314	0.00815720266161301	guanylate-binding protein 2	1
MELO3C026249	0.000429565586514635	0.00815720266161301	E3 ubiquitin-protein ligase RGLG2	1
MELO3C022021	0.00043037785930633	0.00816477650666735	Lysine--trna ligase	1
MELO3C016868	0.00043226379708261	0.00819268496025381	serine/threonine-protein kinase EDR1	1
MELO3C020924	0.000436769436912066	0.00827014344158809	zinc finger protein 830 isoform X1	1
MELO3C022005	0.000438006177052808	0.00828561684924894	Phosphate transporter PHO1-like protein	1
MELO3C025753	0.000438646630847916	0.0082897916867134	elongation factor 1-alpha	0
MELO3C022975	0.000440378076259629	0.00830959014615144	At1g04330	0
MELO3C018718	0.000440535768039929	0.00830959014615144	At2g42760	1
MELO3C005757	0.000442811253232867	0.00834454145047317	Luminal binding heat shock protein 70	1
MELO3C006289	0.000446332049387155	0.00840287096601232	Unknown protein	0
MELO3C020049	0.000448014525992635	0.00842651321317005	Ribosomal protein S5/S7	1
MELO3C007494	0.000451721422672913	0.00848815069112022	Hexosyltransferase	1
MELO3C023370	0.000452977173029057	0.00850365607428787	No data found	1
MELO3C000425	0.000455936542064439	0.00855108335159602	alanine--tRNA ligase-like	1
MELO3C023876	0.000456434521640348	0.00855230110804101	glycerol-3-phosphate acyltransferase 5-like	0
MELO3C016308	0.000457945081585698	0.00857247148458383	myosin-11-like	1
MELO3C009542	0.00046017704841339	0.00859657502875971	BEL1-like homeodomain protein 1	0
MELO3C016542	0.000460538578177516	0.00859657502875971	peptidyl-prolyl cis-trans isomerase CYP37, chloroplastic	1
MELO3C011208	0.000460347156840069	0.00859657502875971	acetylglutamate kinase, chloroplastic	1
MELO3C006160	0.000462267098868541	0.00861871471817833	Histone deacetylase complex subunit SAP18	1
MELO3C020721	0.000462597478417592	0.00861871471817833	triacylglycerol lipase SDP1	1
MELO3C007106	0.000465408661012523	0.00864826228616565	Remorin family protein	1
MELO3C015502	0.000465497129484738	0.00864826228616565	Integral membrane protein	1
MELO3C025336	0.000465391273717142	0.00864826228616565	BnaC03g47530D protein	0
MELO3C009550	0.000471294734155636	0.0087265283090437	33 kDa ribonucleoprotein, chloroplastic	1
MELO3C005109	0.000470509180352852	0.0087265283090437	alpha-mannosidase	1
MELO3C022406	0.000471916705171882	0.0087265283090437	phosphatidylinositol 4-kinase gamma 4	1
MELO3C019873	0.000471726154005148	0.0087265283090437	3-oxoacyl-[acyl-carrier-protein] synthase-like protein	1
MELO3C003825	0.00047191919763323	0.0087265283090437	Cysteine/Histidine-rich C1 domain family protein, putative	1
MELO3C000237	0.000472801986159843	0.00873467392392025	Major facilitator superfamily domain-containing protein 12	1
MELO3C007821	0.000476474174394781	0.00879428828983414	U1 small nuclear ribonucleoprotein 70 kDa	1
MELO3C009490	0.000477551177120339	0.00880593669182967	Ribosomal protein S11	0
MELO3C026433	0.000478847432524576	0.00882160256056703	U4/U6 small nuclear ribonucleoprotein PRP4-like protein	0
MELO3C026780	0.000482363906618488	0.00886692143153668	Ribosomal protein S19	0
MELO3C010512	0.000482211167430746	0.00886692143153668	Plastid transcriptionally active 6	1
MELO3C015867	0.00048265433889827	0.00886692143153668	E3 ubiquitin ligase-like protein	1
MELO3C007421	0.000484638644706603	0.00888684177744727	pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta	1
MELO3C019813	0.000484275792564381	0.00888684177744727	Lysine-specific demethylase REF6	1

MELO3C018368	0.000485361148193419	0.00889183424459354	omega-hydroxypalmitate O-feruloyl transferase	1
MELO3C021408	0.000486240439558361	0.00889968715554965	Protein trichome birefringence-like 10	1
MELO3C007181	0.00048750090623062	0.00891449573810048	MADS box transcription factor AGAMOUS	1
MELO3C013476	0.000489273029856685	0.00893862448347796	phototropin-2	1
MELO3C006813	0.000492228148743612	0.00894906064744133	monocopper oxidase-like protein SKS1	1
MELO3C023222	0.000492403978258671	0.00894906064744133	ABC transporter-like protein	1
MELO3C019735	0.000492040262321525	0.00894906064744133	1-aminocyclopropane-1-carboxylate oxidase	0
MELO3C021759	0.000492563113259847	0.00894906064744133	lecithin-cholesterol acyltransferase-like 4	1
MELO3C011484	0.000491054220355669	0.00894906064744133	Spermidine synthase	1
MELO3C026705	0.000490305274858382	0.00894906064744133	Vesicle-associated membrane protein, putative	0
MELO3C012651	0.00049485375550895	0.00898241435436238	FRIGIDA-like protein	1
MELO3C021368	0.000495830343627213	0.00899187645206044	DnaJ subfamily B member 14	1
MELO3C009670	0.000496738100771443	0.00900007408452774	PHD-finger protein	1
MELO3C020386	0.000500316681290025	0.00902351976145818	E3 ubiquitin-protein ligase LAP	1
MELO3C013938	0.000499419243035093	0.00902351976145818	Protein transport protein Sec16B	0
MELO3C009005	0.000499727849437859	0.00902351976145818	Unknown protein	1
MELO3C005238	0.000499204461091307	0.00902351976145818	GAGA-binding transcriptional activator	1
MELO3C011070	0.000500007962388027	0.00902351976145818	Rhamnogalacturonate lyase	0
MELO3C006420	0.000501794482363316	0.00903935208658677	Cotton fiber protein	1
MELO3C013436	0.000502109941717843	0.00903935208658677	DNA helicase	0
MELO3C012073	0.000503847273066516	0.00906236775572916	SNF1-related kinase regulatory subunit gamma 1	0
MELO3C006280	0.000504505272682865	0.00906236922916473	60S ribosomal protein L37a	1
MELO3C008245	0.000504765109731187	0.00906236922916473	Delta-1-pyrroline-5-carboxylate synthetase	0
MELO3C014007	0.000506074895368025	0.00907763225124716	Superoxide dismutase 1	1
MELO3C026398	0.000506910045428688	0.00908436160360359	APO protein 1, chloroplastic	1
MELO3C023998	0.000507430810900544	0.00908544975927003	Protein RETICULATA-RELATED 4, chloroplastic	0
MELO3C009506	0.000508124357512574	0.00908962675409042	secoisolariciresinol dehydrogenase-like	1
MELO3C003541	0.000510134406861762	0.00911732524987596	NAD(P)H-hydrate epimerase	1
MELO3C019404	0.000510767191047368	0.00912038088245431	phytosulfokine receptor 2	1
MELO3C021846	0.00051267436100022	0.00913791151208787	cytochrome P450 89A2-like	1
MELO3C019688	0.000512648137834137	0.00913791151208787	Peroxisomal and mitochondrial division factor 2	1
MELO3C006430	0.000517174720864766	0.00920981385244208	ethylene-responsive transcription factor 1B	0
MELO3C008866	0.000517893399529346	0.00921430337595049	Plasma-membrane choline transporter family protein	0
MELO3C020562	0.000520045834638383	0.00924427109655574	No data found	1
MELO3C009261	0.000521943976709904	0.0092563001622102	Peptide transporter family protein	1
MELO3C004505	0.000521802144234362	0.0092563001622102	Ribosomal protein L31	1
MELO3C025989	0.000522128633384078	0.0092563001622102	Kinase superfamily protein	1
MELO3C023163	0.000524847951735463	0.00928783351149074	Kinase superfamily protein	1
MELO3C026263	0.000524589257258512	0.00928783351149074	DEAD-box ATP-dependent RNA helicase-like protein	1
MELO3C014273	0.000526136935624533	0.00929398778322799	Pentatricopeptide repeat-containing protein family	1
MELO3C003695	0.00052583296602382	0.00929398778322799	ethylene-responsive transcription factor SHINE 2-like	1
MELO3C022609	0.000527154911452721	0.00930364820936531	No data found	1
MELO3C000279	0.000528395036966334	0.00930889704286184	Late cornified envelope protein 1E	1
MELO3C023830	0.000528124502867655	0.00930889704286184	protein-tyrosine-phosphatase MKP1 isoform X1	1
MELO3C007909	0.000529760023340375	0.00932462629318099	Armadillo repeat only protein	1
MELO3C005720	0.000530338114349549	0.0093264892433564	Late embryogenesis abundant protein	0
MELO3C008491	0.000531797074916351	0.00934382600758276	Zinc finger protein CONSTANS	0
MELO3C016775	0.000532384973778277	0.00934584075301973	Leucine-rich repeat receptor-like protein kinase family	1
MELO3C003292	0.000535229738756193	0.00938743526704801	protein N-methyltransferase NNT1 isoform X1	1
MELO3C015375	0.000536261199456822	0.00939718050405748	Sodium/hydrogen exchanger	1
MELO3C009346	0.000538853443754816	0.00942651619399203	translin	0
MELO3C009994	0.000538889907489848	0.00942651619399203	MD-2-related lipid recognition domain-containing protein / ML domain-	1
MELO3C007391	0.000540671539647652	0.00944931171371813	Glycosyl transferase, family 31	0
MELO3C002332	0.000541447285320018	0.00945450259751108	Telomere length regulation TEL2	1
MELO3C024016	0.000542761100591038	0.00946907153319118	Metal-dependent phosphohydrolase	1
MELO3C017902	0.000543462838672237	0.00947294580841837	monothiol glutaredoxin-S15, mitochondrial	1
MELO3C006175	0.000544486571854463	0.00947406635026766	ankyrin repeat and zinc finger domain-containing protein 1	1
MELO3C025062	0.000544142102876677	0.00947406635026766	transcription initiation factor TFIID subunit 11-like	0
MELO3C003567	0.000545821213981501	0.00948892883355692	Glycosyltransferase	0
MELO3C011576	0.000546754914670933	0.00949680106406003	zinc finger protein CONSTANS-LIKE 6	1
MELO3C012178	0.000548063155305423	0.00951115927427662	protein PHYLLO, chloroplastic isoform X1	0
MELO3C016015	0.000549275667963922	0.00952383245532879	AAA-type ATPase family protein	1
MELO3C022260	0.000550317736865757	0.00952517527200863	CDPK-related kinase 3 isoform X1	0
MELO3C026636	0.000550273723547212	0.00952517527200863	Protein arginine N-methyltransferase	1
MELO3C008806	0.000551102874571718	0.00953041214528622	Echinoderm microtubule-associated protein-like 6	0
MELO3C023776	0.000553621720863151	0.00955723371094962	Laminin subunit gamma-1	1
MELO3C026221	0.000553304287941092	0.00955723371094962	protein PLASTID TRANSCRIPTIONALLY ACTIVE 10-like	1
MELO3C023047	0.000555357376203602	0.00957882342589078	glutamyl-tRNA(Gln) amidotransferase subunit B, chloroplastic/mitochondrial	1

MELO3C021456	0.000557011378721106	0.00959059958008991	histone deacetylase HDT1-like	1
MELO3C002180	0.000556955335141218	0.00959059958008991	mRNA splicing factor, Cwf18	1
MELO3C015290	0.000557828007353156	0.00959629383032881	peptidyl-prolyl cis-trans isomerase G	1
MELO3C019497	0.000558942859338996	0.00960710402879532	Tubby-like F-box protein	1
MELO3C023291	0.000560242444828107	0.00962106786340025	glycine-rich RNA-binding protein 1-like	1
MELO3C017572	0.00056405672942228	0.00967815495165995	transcription factor TGA1 isoform X1	1
MELO3C006950	0.000566029637463883	0.0097035757901686	Pentatricopeptide repeat-containing protein At4g21190	1
MELO3C014394	0.000567251287668546	0.00971608471827071	Ribosomal N-lysine methyltransferase 5	1
MELO3C005706	0.000567796577401691	0.00971699705988388	40S ribosomal protein S10-1	0
MELO3C027308	0.000574051466060821	0.00981006784135699	alanine--tRNA ligase-like	1
MELO3C021404	0.000574228488764428	0.00981006784135699	Heavy metal-associated isoprenylated plant protein 21	1
MELO3C012284	0.000578777758954763	0.00987924110769024	Zinc finger, B-box	1
MELO3C002714	0.000579702326297893	0.00988647775652598	60S ribosomal protein L18a-like protein	0
MELO3C022359	0.000581911996475948	0.00991559967075366	F3H9.20 protein	1
MELO3C024951	0.000582445935391473	0.00991614205003984	cellulose synthase-like protein E6	1
MELO3C014321	0.000584951558469826	0.00993311120225331	2-methyl-6-phytyl-1,4-hydroquinone methyltransferase, chloroplastic	1
MELO3C017623	0.000584098236359187	0.00993311120225331	Metacaspase-1	1
MELO3C023413	0.000584468800800653	0.00993311120225331	Signal peptidase I	1
MELO3C004105	0.000588504749103658	0.00995066805654806	Cytochrome c oxidase subunit	1
MELO3C013315	0.000587711132197466	0.00995066805654806	O-methyltransferase, putative	1
MELO3C016140	0.000588364468219194	0.00995066805654806	Solanesyl diphosphate synthase, putative	1
MELO3C003017	0.000587375958133851	0.00995066805654806	Alpha/beta-Hydrolases superfamily protein	1
MELO3C025102	0.000587683965674879	0.00995066805654806	Phytoene synthase	1
MELO3C008018	0.000589155695845944	0.0099531529831151	Like-COV protein	1
MELO3C013760	0.000589668535514898	0.0099533024853707	26S proteasome non-ATPase regulatory subunit 4 homolog	1
MELO3C004944	0.000591070098526769	0.00996844011597367	polyadenylation and cleavage factor homolog 4 isoform X2	1
MELO3C024760	0.000592163910059229	0.00997836609194515	RNA polymerase sigma factor sigA	0
MELO3C011805	0.000592819805662836	0.00998090225237456	No data found	0
MELO3C014315	0.000595152627668183	0.00998400707837636	Bifunctional DNA-directed RNA polymerase subunit beta-beta	1
MELO3C013921	0.000595531942798488	0.00998400707837636	Protein-tyrosine phosphatase mitochondrial 1-like protein	1
MELO3C010524	0.000594398368218396	0.00998400707837636	arabinosyltransferase XEG113	1
MELO3C002757	0.000594856562811885	0.00998400707837636	signal recognition particle 14 kDa protein	1
MELO3C018461	0.00059493992894244	0.00998400707837636	E3 ubiquitin-protein ligase MARCH6	1
MELO3C020276	0.000599313743151031	0.0100354207566094	Tobamovirus multiplication 1	1
MELO3C012960	0.000599614992799591	0.0100354207566094	BZIP protein, putative	1
MELO3C011787	0.000601120982774539	0.0100436026132101	No data found	1
MELO3C018462	0.000600683577282934	0.0100436026132101	Polyadenylate-binding protein	0
MELO3C016314	0.00060235623438154	0.0100557339584117	Aldose 1-epimerase, putative	1
MELO3C006412	0.00060289070656494	0.0100561558817154	60S ribosomal protein L14, putative	1
MELO3C007492	0.000606809347387105	0.0101086526857278	elongation of fatty acids protein 3-like	1
MELO3C005899	0.000607220982714818	0.0101086526857278	Protein yippee-like	0
MELO3C025346	0.00060757358539465	0.0101086526857278	Sugar/inositol transporter	1
MELO3C010928	0.000609112966384107	0.0101257339841075	PPPDE putative thiol peptidase family protein	1
MELO3C025449	0.000611945427998251	0.0101642643040685	Zinc finger C3H1 domain-containing protein, putative	1
MELO3C024474	0.000615373567698807	0.0102126156205746	zinc finger protein 593	1
MELO3C005518	0.000616382245133273	0.0102207665483938	3-isopropylmalate dehydratase small subunit 3-like	1
MELO3C010055	0.000619950377860445	0.0102713087352063	4-hydroxy-4-methyl-2-oxoglutarate aldolase	1
MELO3C006418	0.000621568353065705	0.0102808654980692	Ankyrin repeat-containing protein	1
MELO3C011873	0.000621061425400415	0.0102808654980692	60S ribosomal protein L17	0
MELO3C024108	0.000623760788199368	0.0103084952352714	OBERON-like protein	1
MELO3C004100	0.000624466041786231	0.010311521621435	WD-repeat protein, putative	1
MELO3C006875	0.000627322932097107	0.0103500422606397	BAG family molecular chaperone regulator 1-like	1
MELO3C006051	0.000629690258800331	0.0103733540615013	BTB/POZ domain-containing protein POB1	1
MELO3C014161	0.000629786395247356	0.0103733540615013	aspartic proteinase A1-like	1
MELO3C017030	0.000630415357957714	0.0103750607535891	Bromodomain-containing protein	0
MELO3C012411	0.000630978450257835	0.0103756814439151	pumilio homolog 4	1
MELO3C015514	0.000632477107366913	0.0103916725402572	12-oxophytodienoate reductase 3	1
MELO3C017300	0.000634855988458249	0.0104220872120216	AT-rich interactive domain-containing protein 5A, putative	1
MELO3C018406	0.000637480217704711	0.0104564757636631	Cytochrome c biogenesis protein	1
MELO3C006154	0.000639515485286957	0.0104811546215204	Cyclin-D-binding Myb-like transcription factor 1	1
MELO3C013710	0.000641723438790986	0.0104878954442637	Auxin efflux carrier	1
MELO3C015270	0.000642051019905554	0.0104878954442637	single-stranded DNA-binding protein, mitochondrial	0
MELO3C003726	0.000640546691929922	0.0104878954442637	Methyltransferase	1
MELO3C009966	0.000641231456532054	0.0104878954442637	ADP-ribosylation factor-like	1
MELO3C011640	0.00064292610395178	0.0104935104354907	Zinc finger, C6HC-type	1
MELO3C018027	0.000645454282273139	0.0105173899510002	Pyruvate kinase	0
MELO3C007441	0.000645005876675375	0.0105173899510002	RING-type E3 ubiquitin transferase	1
MELO3C013429	0.000649935677337288	0.0105752863095764	kinesin-related protein 11	1

MELO3C002144	0.00065007836243991	0.0105752863095764	Receptor-like kinase 1	1
MELO3C006005	0.000651967117786256	0.0105972828058936	Bifunctional fucokinase/fucose pyrophosphorylase	1
MELO3C011675	0.000653292394574789	0.0106100916944552	Cmp-sialic acid transporter, putative	1
MELO3C015151	0.000654376429938264	0.0106189647615865	Alanine:glyoxylate aminotransferase	1
MELO3C024457	0.000656618608750104	0.010646601727591	ATP-dependent zinc metalloprotease FtsH	1
MELO3C021845	0.000659542009912029	0.0106852298226027	Cytochrome P450	1
MELO3C019630	0.000661812702282605	0.0107132287355567	ribosomal RNA large subunit methyltransferase I	1
MELO3C009148	0.000666792796674809	0.0107850048661186	Methionine aminopeptidase,related	1
MELO3C014722	0.000668654842860272	0.0107902195406569	ethylene-responsive transcription factor RAP2-11	1
MELO3C012452	0.000667682946013937	0.0107902195406569	CSC1-like protein isoform X1	0
MELO3C001971	0.000668754302383112	0.0107902195406569	HVA22-like protein	0
MELO3C007934	0.000669504598248771	0.010793507192502	methyltransferase-like protein 23 isoform X3	1
MELO3C019163	0.000671672363601994	0.0108196227640912	ABC transporter F family-like protein	1
MELO3C009771	0.000672773809379912	0.0108285329759119	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3	1
MELO3C004434	0.000674552868131673	0.0108483262155801	Serine-rich protein-like protein	1
MELO3C007012	0.000677563644158052	0.0108878799092574	DNA polymerase eta	0
MELO3C019820	0.000678838654992631	0.0108994996727231	Glycerol-3-phosphate dehydrogenase	1
MELO3C014297	0.000679949464106544	0.0109084662604713	type I inositol polyphosphate 5-phosphatase 4	1
MELO3C002872	0.000681526249681097	0.0109232372222944	Short-chain dehydrogenase/reductase family protein	1
MELO3C008099	0.00068197637830214	0.0109232372222944	eukaryotic translation initiation factor 2D	1
MELO3C012283	0.000684239705449396	0.0109506077333226	Small ubiquitin-related modifier	1
MELO3C017651	0.000689957443399614	0.0110331737244526	Receptor-like kinase	1
MELO3C017711	0.000692222789745456	0.0110604432643066	Proline--tRNA ligase	1
MELO3C009624	0.000694814321152259	0.0110660387326097	Actin family protein	1
MELO3C008494	0.000693792651051739	0.0110660387326097	E3 ubiquitin-protein ligase	1
MELO3C005367	0.000694218350740128	0.0110660387326097	dehydration-responsive element-binding protein 1D-like	1
MELO3C023990	0.000694276492963164	0.0110660387326097	Methyltransferase	1
MELO3C000881	0.000697534212565021	0.0111004054504002	Unknown protein	0
MELO3C020587	0.000701975152042733	0.0111620831543413	No data found	1
MELO3C007103	0.000705517478176043	0.0111962038589772	Protein plastid transcriptionally active 12	1
MELO3C022868	0.000706077302177532	0.0111962038589772	No data found	1
MELO3C005147	0.000706388678327285	0.0111962038589772	NADPH:QUINONE OXIDOREDUCTASE family protein	1
MELO3C013007	0.000705481661930962	0.0111962038589772	profilin-like	0
MELO3C008775	0.000711395060906339	0.0112574848219866	Elongation factor 4	0
MELO3C018120	0.000710958527238903	0.0112574848219866	Purple acid phosphatase	1
MELO3C025349	0.000711969357716224	0.0112575523182848	subtilisin-like protease SBT6.1	1
MELO3C005942	0.000713428603669519	0.0112716011950955	Kinase family protein	1
MELO3C013779	0.000715958032653785	0.0112844813941577	2-keto-3-deoxy-L-rhamnonate aldolase	1
MELO3C008959	0.000715790240196523	0.0112844813941577	1-acyl-sn-glycerol-3-phosphate acyltransferase	1
MELO3C003078	0.000715397659275085	0.0112844813941577	Protein MODIFIER OF SNC1 11	1
MELO3C017880	0.0007166424359909	0.0112862611390624	Glucan endo-1,3-beta-glucosidase	1
MELO3C007667	0.000719402723322826	0.0113207046875717	Epidermal patterning factor-like protein	0
MELO3C013343	0.000720118690283433	0.0113229490560569	FAD-dependent urate hydroxylase-like	1
MELO3C009128	0.000720765197783857	0.0113240985608858	F-box/LRR-repeat protein 15	0
MELO3C019871	0.00072164473946712	0.0113289045784866	Phytol kinase	1
MELO3C014358	0.000722535218217302	0.0113338745230925	transcription initiation factor TFIID subunit 6-like	1
MELO3C003394	0.000724782540440172	0.011360103485042	Protein LSD1	1
MELO3C012722	0.000725794860899187	0.0113669490149866	Pentatricopeptide repeat-containing family protein	1
MELO3C018052	0.000727486395143639	0.0113844126923072	dynamin-related protein 3A-like	1
MELO3C007899	0.000728120600503868	0.0113853157081163	WD repeat-containing protein 82	1
MELO3C010223	0.000729141268915101	0.0113922554745287	WRKY transcription factor	1
MELO3C019498	0.000730368821527216	0.0113934074694637	Tubby-like F-box protein	0
MELO3C007248	0.000730214662693074	0.0113934074694637	Transcription factor VOZ1	1
MELO3C003418	0.000731189926678533	0.0113972137821423	PLATZ transcription factor family protein	1
MELO3C018487	0.000731828295116532	0.0113981679812748	Lipase	1
MELO3C009133	0.0007353585541372	0.0114437336587229	Receptor-like kinase	1
MELO3C001997	0.000735912792879545	0.0114437336587229	Galactoside 2-alpha-L-fucosyltransferase	1
MELO3C014062	0.000737302663945227	0.0114563259718759	Tir-nbs resistance protein	0
MELO3C004589	0.000738241873302403	0.0114619015376173	Mitochondrial import inner membrane translocase subunit Tim17-like protein	0
MELO3C014459	0.000741853945029902	0.0114728845422048	Serine/threonine phosphatase	1
MELO3C013245	0.000740135031843447	0.0114728845422048	40S ribosomal protein S11-like	1
MELO3C017561	0.000741241733906883	0.0114728845422048	Gras family transcription factor	0
MELO3C015750	0.000739717212356328	0.0114728845422048	No data found	1
MELO3C001996	0.000741526118682501	0.0114728845422048	No data found	1
MELO3C017968	0.000742732357898568	0.0114774814836767	LOW QUALITY PROTEIN: translocase of chloroplast 159, chloroplastic-like	1
MELO3C003678	0.000746920851982136	0.0115331820999181	DNA-directed RNA polymerase subunit beta	0
MELO3C009747	0.000752031580646517	0.0116030247548344	Zinc finger (C3HC4-type RING finger) family protein, putative	1
MELO3C003086	0.000755050317633899	0.0116405064191662	protein GPR107	0

MELO3C002741	0.000764731490141668	0.0117805633376036	Protein TIFY 5A	1
MELO3C021326	0.000766461351612402	0.0117888202749169	Peroxisomal fatty acid beta-oxidation multifunctional protein	0
MELO3C015233	0.000766447720925711	0.0117888202749169	ABC1-like kinase	0
MELO3C015304	0.00076794260535884	0.0118024112943438	60S ribosomal protein L22-2	1
MELO3C014991	0.000770621360316692	0.0118343711080049	MLP-like protein 28	1
MELO3C025645	0.000773924241273871	0.0118566152606867	gamma-glutamyl hydrolase 2-like	0
MELO3C015686	0.000774471299118229	0.0118566152606867	Lectin receptor kinase	0
MELO3C024241	0.00077368783366849	0.0118566152606867	Kinesin-like protein	1
MELO3C013645	0.000774280158386098	0.0118566152606867	Alanine--tRNA ligase	1
MELO3C011793	0.000775832531782594	0.0118682545857277	transcription termination factor MTERF9, chloroplastic-like	1
MELO3C019253	0.000776921270584152	0.0118757106600359	thioredoxin domain-containing protein 9 homolog	1
MELO3C023481	0.000777841519056355	0.011880038253785	nudix hydrolase 3-like	1
MELO3C020808	0.000778407489006927	0.011880038253785	Choline transporter-related family protein	1
MELO3C009250	0.000782324663164635	0.0119187750503673	Laccase	1
MELO3C005971	0.000782531579639922	0.0119187750503673	E3 ubiquitin-protein ligase BRE1-like 1	1
MELO3C002662	0.00078275615172041	0.0119187750503673	Receptor kinase, putative	0
MELO3C023644	0.000784187854190543	0.0119225443154391	subtilisin-like protease SBT3.17	0
MELO3C007281	0.00078421110262572	0.0119225443154391	Transmembrane protein, putative	0
MELO3C016152	0.000786489841811733	0.0119479906814922	Gibberellin 2-oxidase	1
MELO3C016884	0.000792002683039694	0.0120040375958181	Methyltransferase	1
MELO3C007328	0.000791713477300116	0.0120040375958181	Wound-responsive family protein	1
MELO3C025585	0.000791107901455534	0.0120040375958181	bifunctional nitrilase/nitrile hydratase NIT4A	1
MELO3C023114	0.000793652645098342	0.0120106539547994	Cellulose synthase	1
MELO3C021548	0.000793655547673966	0.0120106539547994	BnaC05g50840D protein	0
MELO3C021170	0.00079612896994774	0.0120388598985436	BTB/POZ domain-containing protein POB1	0
MELO3C015844	0.000797345327828602	0.012048028216746	DNA repair helicase	0
MELO3C025549	0.000799268560659261	0.0120678553550915	vesicle-fusing ATPase	1
MELO3C011847	0.000801855921626515	0.0120792163205203	60S ribosomal protein L5	1
MELO3C024982	0.000801587460503073	0.0120792163205203	Farnesyl diphosphate synthase	1
MELO3C013076	0.000801616547371209	0.0120792163205203	casein kinase I	1
MELO3C013761	0.000803412442861307	0.0120892909496463	MLO-like protein	0
MELO3C007931	0.000803749000804377	0.0120892909496463	Protein preY, mitochondrial, putative	1
MELO3C021620	0.000804655961069711	0.0120937218989085	transcription initiation factor TFIID subunit 7	1
MELO3C012670	0.000806556187156526	0.0120946682916889	Ribosomal protein S5/S7	1
MELO3C026224	0.000806198958957616	0.0120946682916889	Aspartyl aminopeptidase family protein	0
MELO3C009797	0.000806319229198271	0.0120946682916889	HSP20-like chaperones superfamily protein	1
MELO3C023412	0.000810590269652245	0.0121374241605471	O-fucosyltransferase family protein	1
MELO3C019815	0.000810636612879723	0.0121374241605471	Receptor-like protein kinase	1
MELO3C011018	0.000812005118265402	0.0121487038489571	Thaumatin-like protein 1	0
MELO3C012730	0.00081283392472975	0.0121518979405661	Structural maintenance of chromosomes protein	1
MELO3C016522	0.000815966088231534	0.0121714739300738	Unknown protein	0
MELO3C005332	0.000815992277250377	0.0121714739300738	CDP-diacylglycerol--serine O-phosphatidyltransferase 1	1
MELO3C002819	0.000815110446897416	0.0121714739300738	eukaryotic translation initiation factor 3 subunit A-like	1
MELO3C006925	0.000817431595872442	0.0121837408202905	mitogen-activated protein kinase kinase kinase YODA-like	1
MELO3C017131	0.000818103995706476	0.0121845669767777	General negative regulator of transcription subunit 4	1
MELO3C007143	0.000819606583127408	0.0121977471063928	NAD(P)-binding domain-containing protein	0
MELO3C024558	0.000823867542946388	0.0122519277903978	sorting nexin 1	1
MELO3C005650	0.000828101492612809	0.0123056255662983	Dead box ATP-dependent RNA helicase, putative	1
MELO3C019948	0.000830095547025289	0.0123259826753402	Oxidoreductase family protein	1
MELO3C007495	0.000833697338175732	0.0123668718316225	protein LYK5-like	1
MELO3C005360	0.000834453426250992	0.0123668718316225	mediator of RNA polymerase II transcription subunit 36a-like	1
MELO3C013541	0.000834727841994676	0.0123668718316225	No data found	1
MELO3C018010	0.0008354022801359	0.012367585929838	At3g19650	0
MELO3C009687	0.000836070000848177	0.012368199585581	No data found	1
MELO3C003222	0.000839084099028331	0.012403496909963	mRNA-capping enzyme	1
MELO3C001947	0.000841859856859473	0.0124352208774254	eukaryotic translation initiation factor 3 subunit G-like	0
MELO3C025499	0.00084299621236239	0.0124426996995103	Gb|AAD43168.1	0
MELO3C006241	0.000846579502224443	0.0124676350405895	protein NRT1/ PTR FAMILY 7.3-like	1
MELO3C013173	0.000846446048688998	0.0124676350405895	NAC domain-containing protein 17-like	1
MELO3C017320	0.000846271674169286	0.0124676350405895	Zinc finger protein, putative	1
MELO3C003945	0.00085012626266634	0.0124919222927065	Protein trichome birefringence	1
MELO3C022639	0.000849764070270709	0.0124919222927065	No data found	1
MELO3C016408	0.000849878202600962	0.0124919222927065	D-2-hydroxyglutarate dehydrogenase, mitochondrial-like	0
MELO3C015796	0.000854500203095521	0.0125375367837544	Acetyl-CoA carboxylase, putative	1
MELO3C018591	0.00085408519847574	0.0125375367837544	Transcription factor, putative	1
MELO3C013338	0.000857578253785185	0.0125439869644173	RNA-binding protein 39 isoform X1	1
MELO3C024287	0.000858057790619982	0.0125439869644173	GATA transcription factor 24-like	0
MELO3C022319	0.000857819419544437	0.0125439869644173	DNA primase large subunit	0

MELO3C020710	0.000855996771340739	0.0125439869644173	THO complex subunit 4A	0
MELO3C011139	0.000858115671118931	0.0125439869644173	Nuclear pore complex protein NUP85	1
MELO3C013139	0.000862543291056284	0.0125993842123303	prohibitin-1, mitochondrial	1
MELO3C003439	0.000864308651512991	0.0126158400286253	NAD(P)-binding rossmann-fold protein	0
MELO3C013707	0.000869260816383277	0.0126787532221221	Thioredoxin reductase	0
MELO3C026026	0.000872361768709862	0.0127145923027683	PRA1 family protein	1
MELO3C014888	0.000874915018815425	0.012742401701022	yrdC domain-containing protein, mitochondrial isoform X2	1
MELO3C026198	0.000877911808357279	0.0127766251313544	Gamma carbonic anhydrase-like 1, mitochondrial	1
MELO3C002816	0.000879193317881222	0.0127858533393492	obg-like ATPase 1	1
MELO3C011944	0.000880749748052967	0.0127990631157454	Beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase	1
MELO3C016558	0.000881863372467206	0.0128058233403345	Cyclic nucleotide-gated ion channel, putative	1
MELO3C006320	0.000883864838401527	0.0128254567917647	Type 1 membrane protein, putative isoform 1	1
MELO3C015098	0.000890296667866552	0.012909301684065	Tubulin beta chain	1
MELO3C018689	0.000892082156492835	0.0129257010334387	nuclear transcription factor Y subunit C-2	0
MELO3C010693	0.000893079815306175	0.0129306695546053	Lysine ketoglutarate reductase trans-splicing protein (DUF707)	1
MELO3C010903	0.00089679269942633	0.0129749150336781	thylakoidal processing peptidase 1, chloroplastic-like	0
MELO3C012634	0.000897600518375397	0.0129755749429774	Receptor-like protein kinase	1
MELO3C020806	0.000898152359463777	0.0129755749429774	Peptidyl-prolyl cis-trans isomerase	1
MELO3C013437	0.000905985501302276	0.0129920969393496	V-type proton ATPase subunit a	1
MELO3C007398	0.000902959644092149	0.0129920969393496	5'-adenylylsulfate reductase	1
MELO3C007472	0.000905497264532817	0.0129920969393496	LRR receptor-like serine/threonine-protein kinase GSO1 isoform X1	1
MELO3C003057	0.00090625881451678	0.0129920969393496	Phosphatidylinositol-4-phosphate 5-kinase, putative	1
MELO3C016033	0.000904166343776214	0.0129920969393496	glutathione S-transferase-like	1
MELO3C024333	0.000905840775861422	0.0129920969393496	DNA-binding protein, putative	1
MELO3C025720	0.00090037014311295	0.0129920969393496	phototropin-1	0
MELO3C015198	0.000903708398408365	0.0129920969393496	Pentatricopeptide repeat-containing protein	1
MELO3C010183	0.000904336723108301	0.0129920969393496	glycine-rich cell wall structural protein 2-like	0
MELO3C017091	0.000906532461513176	0.0129920969393496	Pleckstrin homology domain-containing family M member 3	1
MELO3C003312	0.000901569386704937	0.0129920969393496	Protein kinase superfamily protein	1
MELO3C013403	0.000911652577039623	0.0130465411188083	auxin-responsive protein SAUR36-like	1
MELO3C026102	0.000911617325186298	0.0130465411188083	Rhodanese-like domain-containing protein 6	1
MELO3C003139	0.000913198703413887	0.013059204340131	ATP-dependent zinc metalloprotease FtsH	0
MELO3C014849	0.000914437911399668	0.0130674633228886	Alpha/beta hydrolase-3	1
MELO3C020172	0.000915802238327545	0.0130774970388508	Hydroxyacylglutathione hydrolase	0
MELO3C014258	0.000917959386003142	0.0130968989268235	IQ-domain 1	1
MELO3C004142	0.000918487265869183	0.0130968989268235	Unknown protein	1
MELO3C007144	0.000921378557700914	0.0131286472842968	DNA helicase	0
MELO3C019858	0.000923438376700947	0.0131485108157657	No data found	1
MELO3C018046	0.000926412561525591	0.0131718658585809	Zinc transport ZntB	0
MELO3C021858	0.000925765305583526	0.0131718658585809	WEB family protein At3g02930, chloroplastic	1
MELO3C025347	0.000928175455473412	0.0131874367411111	Short-chain dehydrogenase/reductase	0
MELO3C009770	0.000931788216151919	0.0132197453166553	two-component response regulator ORR9-like	0
MELO3C005244	0.000931247853704242	0.0132197453166553	ABC transporter F family member 3	1
MELO3C002159	0.000933740659770033	0.013237935599281	Nascent polypeptide-associated complex subunit beta	1
MELO3C015926	0.000935266432297022	0.0132500550727646	DNA helicase	0
MELO3C008149	0.000936996534496304	0.0132650498636326	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE	1
MELO3C017347	0.000938758613047153	0.0132804755365818	Actin-interacting protein 1-2	1
MELO3C007917	0.000939995495577994	0.013286163190543	thiosulfate sulfurtransferase 18 isoform X1	0
MELO3C025885	0.000940506159318399	0.013286163190543	ras-related protein Rab11C	1
MELO3C004539	0.000946307413841607	0.0133322132934015	serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' iota	0
MELO3C006569	0.000945446689776475	0.0133322132934015	Cytochrome P450 family protein	1
MELO3C013757	0.000947021349863686	0.0133322132934015	Proteasome subunit alpha type	1
MELO3C017581	0.000945962882874185	0.0133322132934015	inositol-3-phosphate synthase	1
MELO3C005046	0.000947141386938188	0.0133322132934015	protein indeterminate-domain 2	0
MELO3C024673	0.000950133026605071	0.0133647985344897	Trihelix transcription factor	1
MELO3C001994	0.000950855162021425	0.0133654367222499	thioredoxin-like 1-2, chloroplastic	1
MELO3C016464	0.00095330453726683	0.0133903352108696	No data found	1
MELO3C007646	0.000954499819987076	0.0133975955543175	heptahelical transmembrane protein 4-like	0
MELO3C020749	0.000958357604638915	0.0134231236411446	amidophosphoribosyltransferase, chloroplastic-like	1
MELO3C002897	0.000957057417631413	0.0134231236411446	Nuclear receptor corepressor 1	1
MELO3C012906	0.000957862608659155	0.0134231236411446	CDT1-like protein a, chloroplastic	1
MELO3C004480	0.000959813634533235	0.0134339897012026	No data found	1
MELO3C011759	0.000962693217067989	0.0134501480567726	transcription factor DIVARICATA	1
MELO3C026443	0.000961972935031419	0.0134501480567726	No data found	1
MELO3C002092	0.000963011258913182	0.0134501480567726	Receptor-like kinase	1
MELO3C020835	0.000965408283639557	0.0134740976633199	Unknown protein	1
MELO3C005939	0.000969123816900619	0.0135164027259677	nucleoside diphosphate kinase	1
MELO3C027064	0.000971938273088613	0.0135460895943733	Pentatricopeptide repeat-containing protein	1

MELO3C008088	0.000973514744218917	0.0135584927246681	phospholipase SGR2	1
MELO3C003880	0.000975348030759493	0.0135744526141432	Histone deacetylase complex subunit	1
MELO3C012016	0.00097897348711995	0.0136153150684027	MLP-like protein 423	0
MELO3C016915	0.000983430844025079	0.0136484720580824	copper-transporting ATPase PAA2, chloroplastic isoform X1	1
MELO3C007613	0.000983096242711756	0.0136484720580824	acyl-CoA-binding domain-containing protein 3	1
MELO3C017416	0.000982464041033859	0.0136484720580824	Cyclin-dependent protein kinase inhibitor SMR15	1
MELO3C005915	0.000986201687010468	0.0136581326204556	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein	0
MELO3C025944	0.000985917354598187	0.0136581326204556	ABC1 family protein	0
MELO3C010599	0.000985933718972154	0.0136581326204556	Gamma-glutamylcyclotransferase	1
MELO3C016811	0.000987087449194402	0.0136608199258166	Ubiquitin system component Cue	0
MELO3C012695	0.000991906014960131	0.0137178934800053	la-related protein 6B isoform X1	1
MELO3C005439	0.000993351291647127	0.0137282677807831	NO-associated protein 1, chloroplastic/mitochondrial	1
MELO3C009735	0.000998956915092108	0.0137301972062592	NF-kappa-B-activating protein	1
MELO3C009562	0.00100183372192109	0.0137301972062592	Pentatricopeptide repeat-containing protein	1
MELO3C013175	0.00100051618365293	0.0137301972062592	Pentatricopeptide repeat-containing family protein	1
MELO3C014176	0.000996507629712262	0.0137301972062592	30S ribosomal protein S6	1
MELO3C016139	0.00099980979828429	0.0137301972062592	Mitogen-activated protein kinase	1
MELO3C017878	0.00100181581724934	0.0137301972062592	Protein LURP-one-related 17	1
MELO3C018042	0.000996419011577765	0.0137301972062592	Phosphoglycerate mutase-like protein 1	1
MELO3C015770	0.000999619597627954	0.0137301972062592	phospholipase A1-Igamma1, chloroplastic-like isoform X1	0
MELO3C017467	0.000996740137645613	0.0137301972062592	Syntaxin/T-SNARE family protein	1
MELO3C010964	0.000998038684778546	0.0137301972062592	Cyclin-T1-like protein	1
MELO3C012873	0.000995473042618045	0.0137301972062592	NAC domain protein	1
MELO3C009961	0.000997510371846033	0.0137301972062592	At1g23710	1
MELO3C003951	0.00100473081766883	0.0137603529252023	No data found	0
MELO3C007467	0.00100905049094524	0.0138099363448909	No data found	0
MELO3C015523	0.00101538983608185	0.0138870733191	Cysteine protease	1
MELO3C007316	0.00101829843398527	0.0139089177661161	Transmembrane protein, putative	0
MELO3C010601	0.00101839561951511	0.0139089177661161	LysM domain-containing GPI-anchored protein 1	1
MELO3C025590	0.00102358772268074	0.0139605206734958	NF-kappa-B inhibitor-like protein 2 isoform 2	1
MELO3C010273	0.0010234211073139	0.0139605206734958	Transmembrane protein	1
MELO3C015727	0.00102505641861605	0.0139628570857366	Maternal effect embryo arrest 60	1
MELO3C001962	0.00102517306062677	0.0139628570857366	protein REVEILLE 2-like	1
MELO3C013125	0.00103621741953086	0.0140667073781726	Lipid-binding serum glycoprotein family protein, putative	1
MELO3C007127	0.00103536298460694	0.0140667073781726	9-cis-epoxycarotenoid dioxygenase	1
MELO3C005201	0.00103600206925747	0.0140667073781726	multicopper oxidase LPR1-like	1
MELO3C001943	0.00103568118847042	0.0140667073781726	17. class I heat shock protein	0
MELO3C010755	0.00103635927060819	0.0140667073781726	At5g11810	1
MELO3C009038	0.00103983524063711	0.0140953069960971	adenylosuccinate synthetase, chloroplastic	1
MELO3C024239	0.0010406075041931	0.0140953069960971	Mitochondrial carrier protein	0
MELO3C018758	0.00104031520097592	0.0140953069960971	Secretory carrier-associated membrane protein	1
MELO3C010959	0.00104181627537914	0.01410200796604 7	Adenosine kinase, putative	0
MELO3C002016	0.00104357250065368	0.0141161050105544	zinc finger protein ZAT4-like	1
MELO3C004597	0.0010513769558067	0.0142119394252064	DUF1005 family protein (DUF1005)	1
MELO3C014116	0.0010524633137019	0.0142168932847461	poly(A)-specific ribonuclease PARN	0
MELO3C007647	0.0010600013683566	0.0142852160059244	xyloglucan 6-xylosyltransferase 1	1
MELO3C021598	0.0010608705730426	0.0142852160059244	pre-rRNA-processing protein ESF2	0
MELO3C005286	0.00106186121305873	0.0142852160059244	Mediator of RNA polymerase II transcription subunit 23	1
MELO3C021366	0.00106142095838846	0.0142852160059244	Acyl carrier protein	1
MELO3C010052	0.00106101733938158	0.0142852160059244	Basic leucine zipper/W2 domain protein	1
MELO3C011488	0.00106087293661083	0.0142852160059244	ylmG homolog protein 2, chloroplastic	1
MELO3C010821	0.00106381826751312	0.0143018018823121	Glutamyl-tRNA (Gln) amidotransferase subunit A	0
MELO3C013824	0.00106573213139216	0.0143080515723071	inactive poly [ADP-ribose] polymerase RCD1-like	0
MELO3C005300	0.0010652510900182	0.0143080515723071	BnaC07g20870D protein	0
MELO3C000254	0.00107265318236205	0.014391187295155	Auxin response factor	0
MELO3C013964	0.00107467152470697	0.0144084778964277	Flavin-containing monooxygenase	0
MELO3C019125	0.00107877740647	0.0144537143828874	WAT1-related protein At5g07050-like	0
MELO3C013406	0.00108795323877697	0.0145667718729535	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]	1
MELO3C017833	0.00109169981020196	0.0145872662731249	Golgi SNAP receptor complex member 1-1	1
MELO3C002134	0.00109141215498465	0.0145872662731249	protection of telomeres protein 1a-like isoform X1	0
MELO3C018732	0.00109122951858942	0.0145872662731249	Histone-lysine N-methyltransferase, H3 lysine-36 specific	1
MELO3C002171	0.00109283685930461	0.0145925862977734	LOW QUALITY PROTEIN: probable metal-nicotianamine transporter YSL5	1
MELO3C008124	0.0010950939938712	0.0146128454628124	SNARE associated Golgi protein family	0
MELO3C020616	0.00110160610411703	0.0146898169819089	Haloacid dehalogenase-like hydrolase	0
MELO3C009334	0.00111024230362466	0.0147850136576423	Methyltransferase type 11	1
MELO3C016951	0.00110990724649795	0.0147850136576423	Glutathione peroxidase	1

MELO3C019907	0.00111354912043438	0.0148190576680987	40S ribosomal protein S17	1
MELO3C013702	0.00111548535806738	0.0148269770804629	kinesin-like calmodulin-binding protein	1
MELO3C021370	0.00111564575125667	0.0148269770804629	PAX-interacting protein 1	1
MELO3C004713	0.00111704118586142	0.0148355389237238	Ribosomal protein	0
MELO3C020825	0.00111940322596316	0.0148569182187812	Phospholipase-like protein	1
MELO3C012628	0.00112110321793302	0.0148595083563484	BOI-related E3 ubiquitin-protein ligase 1-like	1
MELO3C019140	0.00112109638180102	0.0148595083563484	Nascent polypeptide-associated complex subunit alpha-like protein	0
MELO3C009380	0.00112906693300263	0.0149353473849775	ras-related protein RABC2a	1
MELO3C013859	0.00112932514486075	0.0149353473849775	CAAX amino terminal protease	1
MELO3C006995	0.00112951941137085	0.0149353473849775	DNA helicase	0
MELO3C007743	0.00112985006801136	0.0149353473849775	Polyadenylate-binding 2	1
MELO3C008318	0.00113812614307651	0.0150346844144602	Dehydration-responsive element-binding protein 2C	1
MELO3C008052	0.00114026869495676	0.0150529187544793	No data found	1
MELO3C023492	0.00114758708393703	0.0151394103678506	Receptor kinase	1
MELO3C020963	0.00114885976832013	0.0151460824863513	WRKY family transcription factor	1
MELO3C008233	0.00115122999267281	0.0151672055538995	Thylakoid lumenal 15 kDa protein 1, chloroplastic	1
MELO3C024505	0.00115519001740017	0.0152092317690906	SRSF protein kinase 1-like	1
MELO3C022000	0.00115848232083415	0.0152424166250191	KH domain-containing protein	1
MELO3C025511	0.00116227454348072	0.0152506151645319	elongation factor 1-alpha-like	0
MELO3C005511	0.00116090537302926	0.0152506151645319	palmitoyl-protein thioesterase 1-like	1
MELO3C023317	0.00116296655211834	0.0152506151645319	phosphatidylinositol/phosphatidylcholine transfer protein SFH8-like	1
MELO3C003305	0.00116254711149832	0.0152506151645319	Protein CDI	1
MELO3C003420	0.0011601994899415	0.0152506151645319	Ring finger protein, putative	0
MELO3C018616	0.0011655704891641	0.0152746195026555	Alkyl transferase	1
MELO3C010482	0.00117143822600851	0.0153396734280064	F-box protein 7	1
MELO3C017259	0.0011720880653634	0.0153396734280064	Protoheme IX farnesyltransferase, mitochondrial	1
MELO3C024554	0.00117317342071144	0.0153437098580332	Chaperone dnaJ-like protein	0
MELO3C004437	0.0011762151255299	0.0153529891038268	Methyltransferase-related family protein	1
MELO3C018981	0.00117475910333109	0.0153529891038268	UNC93-like protein	0
MELO3C026230	0.00117574360508321	0.0153529891038268	Ribonuclease J	0
MELO3C023200	0.00117863846732424	0.015374459109106	Receptor-like protein kinase	1
MELO3C017757	0.00118580073769048	0.0154474793988452	Inositol transporter 1	1
MELO3C010651	0.00118541624822299	0.0154474793988452	No data found	1
MELO3C016562	0.00118807502290619	0.0154669041709784	At4g33560	1
MELO3C006802	0.00118904758520466	0.0154693680897278	Protein DEHYDRATION-INDUCED 19	1
MELO3C025917	0.00119861897500195	0.0155836248435244	CAX-interacting protein 4	1
MELO3C009101	0.00120197975122283	0.0156170382282234	B3 domain-containing transcription repressor VAL2	1
MELO3C018950	0.00120877376552109	0.015694985598472	Chaperone protein DNAj, putative	1
MELO3C011752	0.00121308127110931	0.0157405663752547	E3 ubiquitin ligase BIG BROTHER-related	1
MELO3C026886	0.00121509032211076	0.0157562828439694	Chaperone DnaJ	0
MELO3C002651	0.00121668506400485	0.0157666097959526	protein SCAR3	1
MELO3C022930	0.0012198997375259	0.0157772101613615	mitotic spindle checkpoint protein MAD1	1
MELO3C002363	0.00121933620530013	0.0157772101613615	TITAN-like protein	1
MELO3C017254	0.00121947301870651	0.0157772101613615	Sterile alpha motif domain-containing family protein	1
MELO3C014732	0.00122174468221292	0.0157907301891512	Pyruvate kinase	1
MELO3C006268	0.00122376359873888	0.015796148569604	10 kDa chaperonin isoform X1	1
MELO3C007914	0.00122356487409925	0.015796148569604	calmodulin-lysine N-methyltransferase isoform X1	0
MELO3C017945	0.00122821280365626	0.015832881631467	bifunctional epoxide hydrolase 2-like	1
MELO3C018617	0.00122760195676008	0.015832881631467	Pentatricopeptide repeat-containing protein	1
MELO3C023725	0.00123619916806539	0.0158993585323115	Protein ROOT PRIMORDIUM DEFECTIVE 1	1
MELO3C007724	0.00123610608361802	0.0158993585323115	Pesticidal crystal cry8Ba protein	0
MELO3C007986	0.00123446337349731	0.0158993585323115	Histidine phosphatase family (Branch 1) protein	1
MELO3C010353	0.00123739501059106	0.0158993585323115	protein NRT1/ PTR FAMILY 6.2-like	1
MELO3C003675	0.00123674154707298	0.0158993585323115	Protein TIFY 8	0
MELO3C003249	0.00124444883017238	0.0159795968446518	target of Myb protein 1 isoform X1	1
MELO3C024088	0.00124664245485939	0.0159973631195699	F-box family protein, putative	1
MELO3C014877	0.00124810334608227	0.0160057097284278	DNA/RNA-binding protein KIN17	1
MELO3C013822	0.0012520996871519	0.0160361327636594	Unknown protein	1
MELO3C025637	0.00125177019058254	0.0160361327636594	Mannosyltransferase	1
MELO3C022009	0.00125751310639199	0.0160950267907553	Vesicle transport v-SNARE family protein	0
MELO3C010375	0.00126258066098428	0.0161389679441932	DNA ligase	0
MELO3C026013	0.00126215947958241	0.0161389679441932	Plectin-like protein	0
MELO3C012713	0.00126675355311634	0.016174344703256	Zinc finger, CCCH-type	1
MELO3C008252	0.00126698624011023	0.016174344703256	Protease inhibitor/seed storage/lipid transfer family protein	0
MELO3C014398	0.00127170983656311	0.0162085217333131	Myosin-binding protein 1	0
MELO3C019504	0.00127161606417181	0.0162085217333131	Meiosis arrest female protein 1-like protein	1
MELO3C002271	0.00127212561074663	0.0162085217333131	F-box protein SKIP16	1
MELO3C008801	0.00127339795929893	0.0162142722747869	H/ACA ribonucleoprotein complex subunit	1

MELO3C002687	0.00127622712446374	0.0162398256965427	dynamin-related protein 4C-like	1
MELO3C012470	0.00127972386650055	0.0162738355695553	two-component response regulator ORR9-like	1
MELO3C007690	0.00128234955404771	0.0162967318808805	No data found	1
MELO3C015518	0.00128401665288447	0.0163074243587237	Acyl-CoA N-acyltransferase (NAT) superfamily protein	1
MELO3C016882	0.00128643995485178	0.0163277009436811	Magnesium transporter NIPA	0
MELO3C023961	0.00128738672658923	0.0163292231621135	ras-related protein RABA4c isoform X1	0
MELO3C011040	0.00129103487176252	0.0163649856755058	40S ribosomal protein S6-like	0
MELO3C023304	0.00129224801413341	0.0163698563381147	Isoflavone reductase like	1
MELO3C006507	0.00129529568976838	0.0163979452418178	40S ribosomal protein S3a	0
MELO3C015862	0.00129679606732103	0.0164064225070615	Unknown protein	1
MELO3C011193	0.00130134505932378	0.0164534337878267	COP9 signalosome complex subunit 5b	1
MELO3C014190	0.00130600334466013	0.0165017658692853	DUF4408 domain protein	0
MELO3C016890	0.00131018435614794	0.0165440094946072	aminopeptidase M1	1
MELO3C017808	0.00131120432915433	0.0165463094546126	Protein NEOXANTHIN-DEFICIENT 1	1
MELO3C018360	0.00131240394258225	0.0165508719425651	No data found	1
MELO3C016300	0.00132248461135576	0.0166461877352294	UDP-glucose 4-epimerase family protein	0
MELO3C012715	0.00132243173147539	0.0166461877352294	mediator of RNA polymerase II transcription subunit 19a-like	0
MELO3C005294	0.00132249068593726	0.0166461877352294	Myosin-binding protein 2	0
MELO3C021556	0.00132370263701453	0.0166508301773249	ADP-ribosylation factor-like	0
MELO3C006249	0.00132556843054021	0.0166636861456007	No data found	1
MELO3C009467	0.001327686515185	0.0166786633326799	Alpha/beta-Hydrolases superfamily protein	1
MELO3C016114	0.00132956872636503	0.0166786633326799	Protein ROOT INITIATION DEFECTIVE 3	1
MELO3C012296	0.00133013796895898	0.0166786633326799	Unknown protein	0
MELO3C026175	0.00132851382917032	0.0166786633326799	Long chain base biosynthesis protein	1
MELO3C002646	0.00133518613930561	0.0167313395083417	Transcription initiation factor IIB	1
MELO3C011088	0.00133656832394879	0.0167380392071431	mechanosensitive ion channel protein 3, chloroplastic-like	1
MELO3C004475	0.00133894602167994	0.016746576936135	arogenate dehydrogenase 1, chloroplastic-like	1
MELO3C012100	0.00133814393390308	0.016746576936135	ribonuclease 3-like	1
MELO3C015409	0.00134065781250059	0.0167467749140254	ABC transporter B family protein	0
MELO3C018106	0.0013404763400835	0.0167467749140254	ABC transporter B family protein	1
MELO3C014018	0.00134463174948718	0.0167857979902796	Pentatricopeptide repeat-containing protein family	1
MELO3C003846	0.00135074087660314	0.0168514097106983	Glucan endo-1,3-beta-glucosidase, putative	0
MELO3C020978	0.00135752330090511	0.0169253331247317	Adenylyl cyclase-associated protein	1
MELO3C011952	0.00136365991062004	0.0169911164510001	UDP-galactose:fucoside alpha-3-galactosyltransferase	1
MELO3C009873	0.00136459747634987	0.0169920779069569	zinc-finger homeodomain protein 9-like	0
MELO3C004461	0.00136807981374421	0.017024705886348	protein TOPLESS	1
MELO3C015398	0.00136911537600959	0.017026863703283	cysteine synthase-like	0
MELO3C018573	0.00137461012268614	0.017084440096242	Inorganic pyrophosphatase	1
MELO3C009172	0.00137678127435881	0.0171006625077434	RING finger protein	1
MELO3C016608	0.00137878915949885	0.0171148379075693	Transmembrane protein, putative	1
MELO3C003926	0.00138073092069713	0.0171179590713092	No data found	0
MELO3C005199	0.00138077415568361	0.0171179590713092	charged multivesicular body protein 7 isoform X1	1
MELO3C008375	0.00138251768956899	0.0171288217385809	Unknown protein	0
MELO3C008114	0.00138405655359919	0.017137136600019	TSA: Wollemia nobilis Ref_Wollemi_Transcript_28887_1569 transcribed RNA sequence	1
MELO3C017272	0.00138518236716068	0.0171403299304863	Ethylene-responsive transcription factor	0
MELO3C019561	0.00138619118409045	0.0171420724449607	At1g78995	1
MELO3C006587	0.0013871485080218	0.0171431763985747	Endonuclease/exonuclease/phosphatase family protein	0
MELO3C006136	0.00139306498415936	0.0171625953662903	Signal recognition particle 54 kDa protein	1
MELO3C019011	0.00139215182628716	0.0171625953662903	copper-transporting ATPase PAA1, chloroplastic isoform X1	1
MELO3C005696	0.00139171797478665	0.0171625953662903	E3 ubiquitin-protein ligase RHA1B	1
MELO3C021247	0.0013904593458578	0.0171625953662903	Dihydrolipoyl dehydrogenase	1
MELO3C018688	0.00139270363874489	0.0171625953662903	dynamin-like protein ARC5	1
MELO3C006754	0.0013989936942238	0.0171921631272379	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin	1
MELO3C027346	0.00139863809916196	0.0171921631272379	Indole-3-acetic acid-amido synthetase GH3.3	0
MELO3C015791	0.0013969561102013	0.0171921631272379	Pentatricopeptide repeat-containing protein	1
MELO3C022388	0.00139981762664432	0.0171921631272379	Pre-mRNA-processing factor 39	1
MELO3C026711	0.00139804378035702	0.0171921631272379	Protein FAM32A-like	1
MELO3C016623	0.00140078931774978	0.0171934047459543	NAD(P)H dehydrogenase (Quinone)	1
MELO3C016965	0.00140646424613533	0.0172416278069067	Formin-like protein	0
MELO3C015422	0.00140579592416201	0.0172416278069067	Arginine--tRNA ligase	1
MELO3C021047	0.00140828800908288	0.0172532753668597	nucleolin-like	1
MELO3C009663	0.00141290977451258	0.0172561584703465	1-acyl-sn-glycerol-3-phosphate acyltransferase-like protein	1
MELO3C004467	0.00141258546588374	0.0172561584703465	Exostosin family protein	1
MELO3C013359	0.00141108727208694	0.0172561584703465	Ubiquitin-conjugating enzyme, E2	1

MELO3C005079	0.00141241328020525	0.0172561584703465	protein ASPARTIC PROTEASE IN GUARD CELL 2	1
MELO3C021384	0.00141376598334197	0.0172561584703465	Cox19-like CHCH family protein	1
MELO3C026760	0.00141223060883444	0.0172561584703465	Arabinogalactan protein	1
MELO3C017133	0.00141800169024686	0.0172971682400774	No data found	0
MELO3C020927	0.00141984372965775	0.0173089468006241	Molybdenum cofactor sulfurase	1
MELO3C014895	0.00142136942562132	0.0173168567468202	squamosa promoter-binding-like protein 13A	1
MELO3C017703	0.00142356391852405	0.0173305233976508	disease resistance protein RGA2-like	1
MELO3C008096	0.00142424626433679	0.0173305233976508	Galactose-binding domain-like protein	0
MELO3C016382	0.00142850587618693	0.0173645781687618	small nuclear ribonucleoprotein Sm D2-like	1
MELO3C022448	0.00142880345963026	0.0173645781687618	Metal tolerance protein	1
MELO3C019524	0.0014304129339574	0.017373447129597	40S ribosomal protein S16	0
MELO3C023309	0.00143156903792496	0.0173768020466995	SNF1-related protein kinase regulatory subunit gamma-1-like	1
MELO3C011834	0.00143661881258605	0.0174273863204926	Protein EI24 like	0
MELO3C025593	0.00144052700680608	0.0174509693332693	Pentatricopeptide repeat-containing family protein	1
MELO3C013587	0.00144121378209339	0.0174509693332693	No data found	1
MELO3C003416	0.00144044124356046	0.0174509693332693	Unknown protein	1
MELO3C016383	0.00144678432164969	0.0175025482951149	RING-type E3 ubiquitin transferase	1
MELO3C017844	0.00144724600566726	0.0175025482951149	calcineurin subunit B	1
MELO3C014454	0.00145093122867479	0.0175329893825102	Receptor-like protein kinase	1
MELO3C007047	0.0014515386926125	0.0175329893825102	Protein kinase	1
MELO3C023367	0.00145318824654184	0.0175421850128085	DNA repair protein XRCC1	1
MELO3C004576	0.00145859722393693	0.0175954172565851	sugar transport protein 14-like	1
MELO3C022932	0.00145937989094569	0.0175954172565851	Auxin response factor	0
MELO3C021360	0.00146048979136648	0.0175980554543604	Pentatricopeptide repeat-containing family protein	1
MELO3C015477	0.00146228225489542	0.0176089099097132	No data found	0
MELO3C003375	0.00146380420207692	0.0176164955434596	Two-component response regulator-like protein APRR2	1
MELO3C014281	0.0014702360035872	0.0176508758874429	Aldo/keto reductase, putative	0
MELO3C005421	0.00146899146702206	0.0176508758874429	GTF2H2	1
MELO3C021914	0.00146823354847903	0.0176508758874429	peroxidase 10-like	0
MELO3C018768	0.00146951190071176	0.0176508758874429	Wound-responsive family protein	1
MELO3C023985	0.00147349210060765	0.0176792196202312	RNA/RNP complex-1-interacting phosphatase, putative	1
MELO3C007497	0.0014780779626572	0.0177234740039569	Transcription termination factor family protein	0
MELO3C002227	0.00147953668231926	0.0177302002057786	Unknown protein	1
MELO3C014008	0.00148146067848454	0.0177424905636089	Adenosine monophosphate-protein transferase and cysteine protease ibpA	1
MELO3C020591	0.00148245648757772	0.0177436564685893	Glycosyltransferase	1
MELO3C002416	0.00148622342396076	0.017777968746094	Ankyrin repeat family protein	0
MELO3C004577	0.00148880872396417	0.0177981134924749	CRS2-associated factor 1, chloroplastic	1
MELO3C018494	0.00150424303608299	0.0179717457468862	Protein TIC 21, chloroplastic	1
MELO3C000075	0.0015064080353504	0.0179867305260793	Myosin heavy chain-like protein, putative	1
MELO3C027219	0.00150762899745338	0.0179904320668923	Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase	1
MELO3C020942	0.00150894782427158	0.0179952962448909	PQ-loop repeat family protein / transmembrane family protein	1
MELO3C022059	0.00151061562675903	0.0180043138279203	Pentatricopeptide repeat-containing protein	1
MELO3C005651	0.00151252537705282	0.0180162024556189	30S ribosomal S1	1
MELO3C009588	0.00151414543658712	0.0180196286456078	Downstream neighbor of Son	1
MELO3C022783	0.00151463788301731	0.0180196286456078	transmembrane protein 50A	1
MELO3C021536	0.00151639341105281	0.0180296529048055	Quinone oxidoreductase-like protein	0
MELO3C015130	0.00152015005154871	0.0180417327932905	polygalacturonase-like	1
MELO3C025354	0.00151869336680555	0.0180417327932905	Late embryogenesis abundant protein	1
MELO3C008285	0.00151933283763561	0.0180417327932905	eukaryotic translation initiation factor 3 subunit F	1
MELO3C003457	0.00152415156525021	0.018078359917193	protein EMBRYONIC FLOWER 1-like isoform X3	0
MELO3C003826	0.00152506826935495	0.0180783753010149	No data found	1
MELO3C014604	0.0015283132911843	0.0181059743176957	F16F4.11 protein	1
MELO3C016826	0.00153179476841669	0.0181146196894978	At4g33800	1
MELO3C021148	0.00153136859350866	0.0181146196894978	Autophagy-related protein	0
MELO3C025035	0.00153071881752509	0.0181146196894978	lecithin-cholesterol acyltransferase-like 1	0
MELO3C020427	0.00153376154089113	0.018127023740909	DEAD-box ATP-dependent RNA helicase 42-like	0
MELO3C021563	0.00153757354735573	0.0181612081260337	isocitrate dehydrogenase [NADP]	1
MELO3C022392	0.00153951311588807	0.018173248371592	Cytochrome oxidase complex assembly protein	0
MELO3C011439	0.00154415748059011	0.0182171840407253	6,7-dimethyl-8-ribityllumazine synthase	0
MELO3C006294	0.00154543307012311	0.0182213478817083	Dna repair helicase xpb1	1
MELO3C013965	0.00154666283116955	0.0182249667379281	Flavin-containing monooxygenase	1
MELO3C014230	0.00155245603648058	0.0182793157660068	Ethylene insensitive 2	1
MELO3C017115	0.00155312632818672	0.0182793157660068	succinate dehydrogenase subunit 7B, mitochondrial-like	1
MELO3C004279	0.00156216413039512	0.0183747346105856	RING zinc finger family protein	1
MELO3C010197	0.00157227802397697	0.0184785490735071	Tetratricopeptide repeat (TPR)-like superfamily protein	0

MELO3C026288	0.00157286146096336	0.0184785490735071	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B	1
MELO3C010403	0.00157447526897514	0.0184865113477943	LOW QUALITY PROTEIN: LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.4	0
MELO3C016483	0.00158023620980208	0.0185349689647406	phosphoribosylamine--glycine ligase	1
MELO3C008947	0.00158137311774076	0.0185349689647406	CBS domain-containing protein	1
MELO3C024313	0.00158260126212806	0.0185349689647406	AT-rich interactive domain-containing protein 4-like	0
MELO3C002034	0.00158329498422793	0.0185349689647406	ninja-family protein 6-like isoform X2	1
MELO3C010600	0.00158218164950008	0.0185349689647406	DNA ligase 1 isoform X3	1
MELO3C013750	0.00158688511649507	0.0185356656353381	SKP1-like protein 1B	1
MELO3C015747	0.00158659415425944	0.0185356656353381	At3g60850	1
MELO3C005214	0.00158559844227557	0.0185356656353381	Defensin	1
MELO3C020906	0.00158710874420764	0.0185356656353381	60S ribosomal protein L26-1-like	1
MELO3C014944	0.00158975633025693	0.0185423015211278	homeobox-leucine zipper protein HAT22-like	0
MELO3C016193	0.00158896575333467	0.0185423015211278	Lysine-specific histone demethylase 1	0
MELO3C022042	0.00159143253219463	0.0185423015211278	DUF2039 family protein	0
MELO3C021348	0.00159087168485317	0.0185423015211278	E3 ubiquitin-protein ligase Topors	1
MELO3C010688	0.00159627418691699	0.0185877470031979	F-box protein At1g70590	1
MELO3C018476	0.0016042694552616	0.0186698394059878	cyclin-D3-3	1
MELO3C019491	0.00160887864625414	0.0186904378734547	Nucleolar complex protein 2 homolog	0
MELO3C007099	0.00160852551941759	0.0186904378734547	Nucleoporin protein Ndc1-Nup	0
MELO3C020159	0.00160703147890584	0.0186904378734547	transmembrane protein 87A	0
MELO3C023469	0.00161398184714412	0.0187386992940912	Protein LOW PSII ACCUMULATION 3, chloroplastic	1
MELO3C012604	0.00161829168735006	0.018777698315791	Phosphoglycerate kinase	1
MELO3C008773	0.00161989152750242	0.0187788394496662	Succinate dehydrogenase assembly factor 2, mitochondrial	1
MELO3C013829	0.00162029178298806	0.0187788394496662	Calmodulin family protein	1
MELO3C003734	0.00162208649782969	0.0187886136338056	T4O12.20	0
MELO3C009234	0.00162371681969942	0.0187964733131558	SUPERMAN-like zinc finger protein	1
MELO3C020789	0.00162576706990036	0.0188054398657658	Nucleoporin NUP188 like	1
MELO3C010960	0.0016263958322309	0.0188054398657658	Proteasome subunit alpha type	1
MELO3C023338	0.00163648326242916	0.018911005236813	cysteine proteinase RD19a-like	1
MELO3C010456	0.00163788891852379	0.0189161802642844	Phosphatidylinositol-4-phosphate 5-kinase, putative	1
MELO3C023852	0.00164327417852994	0.0189672833148964	Actin family protein	0
MELO3C014850	0.00164799342509903	0.0189971298758232	No data found	1
MELO3C015748	0.00164874579002283	0.0189971298758232	transcription factor EMB1444	1
MELO3C005404	0.00164747201365656	0.0189971298758232	LOW QUALITY PROTEIN: xyloglucan galactosyltransferase XLT2	1
MELO3C005918	0.00164998656602089	0.0190003409284819	NPL4 family protein	1
MELO3C008092	0.00165607824610392	0.01905937603864	50S ribosomal protein L14, putative	1
MELO3C014611	0.00166499764807648	0.0191508669492501	Pre-mRNA-splicing factor CWC22	1
MELO3C009455	0.00166599357714137	0.0191511683090599	BZIP transcription factor family protein	1
MELO3C015946	0.00166733441386024	0.0191554318437033	GATA transcription factor-like protein	1
MELO3C004391	0.00167241694262599	0.0192026524418143	PRA1 family protein	1
MELO3C013753	0.00168358970314475	0.0193016055803562	Vacuolar protein sorting-associated protein 35	0
MELO3C002314	0.00168227509520191	0.0193016055803562	cytochrome P450 71A1-like	1
MELO3C002117	0.00168396710795249	0.0193016055803562	T-complex protein 1 subunit delta	1
MELO3C008313	0.0016862201830351	0.0193162194865199	UTP--glucose-1-phosphate uridylyltransferase 3, chloroplastic	1
MELO3C024001	0.00169134873987065	0.0193637369644669	MADS-box transcription factor	0
MELO3C011109	0.00169484210432513	0.0193924894080632	Octicosapeptide/Phox/Bem1p	1
MELO3C018434	0.00169761795586676	0.019401769103248	Armadillo repeat-containing protein, putative	1
MELO3C003770	0.0016973381454457	0.019401769103248	TLD-domain nucleolar protein	0
MELO3C026046	0.00170144999900546	0.0194343181205082	alpha-ketoglutarate-dependent dioxygenase AlkB-like	1
MELO3C014346	0.00170775748623742	0.0194843255499909	protein PALE CRESS, chloroplastic	1
MELO3C020369	0.00170878788052986	0.0194843255499909	60S ribosomal protein L37a	1
MELO3C005759	0.00170806862709461	0.0194843255499909	30S ribosomal protein S6 alpha, chloroplastic	1
MELO3C026518	0.00171160126017267	0.0195051432701385	Photosystem II reaction center PsbP family protein	1
MELO3C005711	0.00171342810463715	0.0195147010602532	heavy metal-associated isoprenylated plant protein 3-like	1
MELO3C019488	0.00171945922624073	0.0195665520250788	Pentatricopeptide repeat-containing protein	1
MELO3C007617	0.00171996224191284	0.0195665520250788	At5g67390	1
MELO3C003852	0.00172185560495652	0.0195768142442639	DNA ligase-like protein	1
MELO3C004139	0.0017260170705593	0.0196128372419308	Ubiquitin carboxyl-terminal hydrolase, putative	1
MELO3C009090	0.00173121000396637	0.0196392051611116	Kinase family protein	0
MELO3C004645	0.00173460385515178	0.0196392051611116	40S ribosomal S3-like protein	1
MELO3C006409	0.0017350513931752	0.0196392051611116	Glycolipid transfer protein domain-containing protein	1
MELO3C019490	0.00173728752931601	0.0196392051611116	40S ribosomal protein S16	0
MELO3C008815	0.00173564949107596	0.0196392051611116	nucleolar MIF4G domain-containing protein 1	1
MELO3C005455	0.00173406833228484	0.0196392051611116	origin of replication complex subunit 3	0
MELO3C017223	0.00173331296437929	0.0196392051611116	Mitochondrial carrier protein, putative	1
MELO3C008195	0.00173319093407187	0.0196392051611116	Katanin p60 atpase-containing subunit a1	0

MELO3C018180	0.00173648133509596	0.0196392051611116	tRNA (guanine(37)-N1)-methyltransferase	1
MELO3C007601	0.00174263062211799	0.0196883364738033	Lysine-rich arabinogalactan protein 18	1
MELO3C016494	0.00174848962342988	0.019709430121642	Polygalacturonase	0
MELO3C007269	0.00174774945217715	0.019709430121642	Auxin repressed protein	1
MELO3C023451	0.00174626345788564	0.019709430121642	BRCA1-associated protein	1
MELO3C017294	0.00174730515676302	0.019709430121642	Carbon catabolite repressor protein 4 like 3	0
MELO3C003671	0.0017542994104538	0.0197636389372801	SPOC domain/transcription elongation factor S-II, putative	1
MELO3C015470	0.00175565135908395	0.0197675933241442	beta-galactosidase	0
MELO3C013769	0.0017643629105647	0.0198543607525597	Seven transmembrane receptor	1
MELO3C005913	0.00176561299034728	0.0198571132951984	Auxin-responsive family protein	1
MELO3C002390	0.001768224463224	0.0198751650109338	At5g44650	1
MELO3C015695	0.00176927873858901	0.0198757029626816	Expansin	1
MELO3C021264	0.00177097699103468	0.0198834704922933	Ubiquitin-conjugating enzyme, E2	0
MELO3C017440	0.00177258734143249	0.0198902428442899	U3 small nucleolar RNA-associated protein 25-like	1
MELO3C008115	0.0017806901857147	0.01996981855632	5'-3' exonuclease	1
MELO3C011496	0.00178431101807353	0.0199990682723803	BRCT domain DNA repair protein	1
MELO3C021452	0.00179794402675915	0.0201216026456491	No data found	1
MELO3C015692	0.00179684828190319	0.0201216026456491	Brefeldin A-inhibited guanine nucleotide-exchange protein	1
MELO3C018459	0.00179830009973014	0.0201216026456491	40S ribosomal protein S16	0
MELO3C026143	0.00179937326870028	0.0201222099000916	Unknown protein	1
MELO3C009032	0.00180618680062949	0.020186974038275	fructokinase-like 2, chloroplastic	1
MELO3C025142	0.00180918499272109	0.0202090466183534	Proliferating cell nuclear antigen	0
MELO3C017149	0.00181586970268244	0.0202722502873236	Pentatricopeptide repeat-containing protein	1
MELO3C007800	0.00181959699758183	0.0203023848052223	Receptor protein kinase, putative	1
MELO3C013929	0.0018284576743629	0.0203897293116844	Unknown protein	1
MELO3C002604	0.00183522225955302	0.0204536142234269	DUF2921 family protein	0
MELO3C019168	0.00184600708229754	0.0205622074835274	Metacaspase-9	1
MELO3C008786	0.00185244710486099	0.0206223099627394	Rhomboid protein, putative	0
MELO3C016694	0.00186271795353732	0.0207238791076526	VQ motif-containing protein	1
MELO3C007935	0.0018647188806673	0.0207238791076526	Peroxidase	1
MELO3C005389	0.00186395168082631	0.0207238791076526	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	1
MELO3C026593	0.00186878067212692	0.0207573394228541	Surfeit locus protein 2 (SURF2)	0
MELO3C012493	0.00187295993871484	0.0207687174787643	Choline/ethanolamine kinase	0
MELO3C012420	0.00187233804376197	0.0207687174787643	No data found	0
MELO3C003456	0.00187113290658125	0.0207687174787643	Alpha/beta-Hydrolases superfamily protein	1
MELO3C016923	0.00187914670450451	0.0208203232473985	No data found	1
MELO3C026058	0.00188077657974373	0.0208203232473985	Non-specific serine/threonine protein kinase	1
MELO3C012852	0.00188039613797097	0.0208203232473985	Protein BREAST CANCER SUSCEPTIBILITY 1-like protein	0
MELO3C015177	0.00188263980533365	0.0208292736781705	60S ribosomal protein L13a, putative	0
MELO3C008032	0.00188467890401967	0.020840158832858	Actin	0
MELO3C019226	0.00188936224392533	0.0208569116575077	transcription factor ILR3-like	1
MELO3C018413	0.00188895876601003	0.0208569116575077	Allene oxide synthase	0
MELO3C015664	0.00188866569845136	0.0208569116575077	RING-type E3 ubiquitin transferase	1
MELO3C020988	0.00189735927898682	0.020933490726654	Unknown protein	1
MELO3C014447	0.00190474460798895	0.0210027680620675	Nuclear ribonuclease Z	1
MELO3C023862	0.0019068491527422	0.0210027680620675	Factor of DNA methylation 1	0
MELO3C025744	0.00190635644741377	0.0210027680620675	Zinc finger family protein, putative	0
MELO3C002219	0.00190789234408573	0.0210027680620675	HIPL1 protein-like isoform X1	1
MELO3C025651	0.00193151944245629	0.0212510180886179	Intracellular protein transport protein USO1, putative	1
MELO3C026194	0.00193480153015102	0.0212752758457419	No data found	1
MELO3C004459	0.0019419027908818	0.0213410737977304	actin-related protein 6	1
MELO3C014099	0.00194294651315607	0.0213410737977304	BnaC03g71690D protein	1
MELO3C017167	0.00194967540488111	0.0214030792501374	Transmembrane protein	1
MELO3C009583	0.00195706642749194	0.0214493569525252	E3 ubiquitin-protein ligase BAH1-like protein, putative	1
MELO3C023799	0.00195756025201366	0.0214493569525252	12-oxophytodienoate reductase 3	1
MELO3C014091	0.00195604462548404	0.0214493569525252	caffeic acid 3-O-methyltransferase-like	1
MELO3C022124	0.00195823538333095	0.0214493569525252	Glycerophosphodiester phosphodiesterase GDPD4	1
MELO3C024926	0.00196315683099746	0.0214806908923386	two-pore potassium channel 1 isoform X1	1
MELO3C020588	0.00196327140921926	0.0214806908923386	17.5 kDa class I heat shock protein	0
MELO3C008516	0.00196685604928237	0.0214960930366782	Guanosine nucleotide diphosphate dissociation inhibitor	0
MELO3C024337	0.00196598778055268	0.0214960930366782	transmembrane protein 87B isoform X2	1
MELO3C017730	0.0019724064548432	0.0215448313477314	Pentatricopeptide repeat-containing family protein	1
MELO3C025272	0.00197489363397907	0.021549925840151	AT3g54190/F24B22_150	1
MELO3C008116	0.00197505523169139	0.021549925840151	Magnesium transporter NIPA	1
MELO3C014488	0.00198659047530292	0.0216518627465548	Cyclin T1 family protein	1
MELO3C022477	0.00198647332954294	0.0216518627465548	Protein nuclear fusion defective 4	1
MELO3C016469	0.00198908132816278	0.0216670530335834	zinc finger CCCH domain-containing protein 5	1
MELO3C023622	0.00199024853339758	0.0216678160342165	Short-chain dehydrogenase/reductase	1

MELO3C005260	0.00200197408497349	0.0217834634733562	Vacuolar iron transporter 1	1
MELO3C021345	0.00200657619838918	0.0218215161574823	cullin-1	1
MELO3C006870	0.0020155939407539	0.0218719472185081	ethylene-responsive transcription factor ERF027	1
MELO3C020834	0.00201564352309913	0.0218719472185081	Unknown protein	1
MELO3C002717	0.00201365744032933	0.0218719472185081	prefoldin subunit 6	1
MELO3C019814	0.00201274196770884	0.0218719472185081	ABC transporter G family member	0
MELO3C008766	0.00202108742744311	0.021892587246618	sister chromatid cohesion 1 protein 4 isoform X1	1
MELO3C006934	0.00202201822291359	0.021892587246618	protein REVEILLE 6-like isoform X2	0
MELO3C018999	0.00202098577629739	0.021892587246618	Transmembrane protein, putative	1
MELO3C007228	0.00202308834498344	0.021892587246618	GDSL esterase/lipase	0
MELO3C022845	0.00201915646106055	0.021892587246618	RING-type E3 ubiquitin transferase	1
MELO3C021622	0.00202499337392292	0.021901201610955	Elicitor-responsive protein 1	1
MELO3C013411	0.0020279124270397	0.0219207676637149	NADP dependent sorbitol 6-phosphate dehydrogenase family protein	1
MELO3C014706	0.00203201183773705	0.0219530644329699	Argonaute	1
MELO3C026657	0.00203570078237614	0.0219808937950499	Glycine-rich protein	1
MELO3C027092	0.00204005247370298	0.0220158449744045	DExH-box ATP-dependent RNA helicase DExH12-like	1
MELO3C014417	0.00204144586045041	0.0220188499716194	sugar transporter ERD6-like 7	0
MELO3C023473	0.00204448889464182	0.0220396349237343	Phosphatase 2C family protein	1
MELO3C019899	0.00204636292220117	0.0220478021552378	AMMECR1 family	1
MELO3C009149	0.00205119616259886	0.0220878260715184	Copper chaperone SCO1/SenC	1
MELO3C011654	0.00205279144184656	0.0220929581389797	RING zinc finger protein-like	1
MELO3C018781	0.0020542658700694	0.0220967846775603	Leucine-rich repeat family protein	0
MELO3C012131	0.00207255568294284	0.0222813838772119	eukaryotic translation initiation factor 5A-like	1
MELO3C003423	0.00207648623644074	0.0223114943870883	Zinc finger CCCH domain protein	1
MELO3C016550	0.00207952457836447	0.0223176578137305	Unknown protein	1
MELO3C011972	0.00208045004987989	0.0223176578137305	Alpha-glucan water dikinase, chloroplastic	0
MELO3C015616	0.00208012082145714	0.0223176578137305	BnaA04g07840D protein	1
MELO3C009119	0.00208260743603428	0.0223286722335727	Protein LURP-one-related 15	1
MELO3C006314	0.00208855728757984	0.0223803135498721	60S ribosomal protein L13a, putative	1
MELO3C019818	0.00209071289150375	0.0223912629578675	DVL8	1
MELO3C009600	0.00209252401614957	0.022398513167988	60S ribosomal protein L21	0
MELO3C013539	0.00209583349110565	0.0224217852740224	vesicle-associated protein 4-2-like	0
MELO3C010198	0.00210011636188545	0.0224554401899706	DNA-directed RNA polymerase subunit beta	0
MELO3C002372	0.00211176063197727	0.022567727662835	heavy metal-associated isoprenylated plant protein 3-like	1
MELO3C002268	0.00211346018252012	0.0225736750376365	Iron-sulfur cluster assembly protein	0
MELO3C026887	0.00212116551042296	0.022643728467753	Tryptophan synthase, alpha chain	0
MELO3C004015	0.00212540410728268	0.0226746301857241	Pentatricopeptide repeat-containing family protein	1
MELO3C011763	0.0021263565296451	0.0226746301857241	LRR receptor-like kinase	0
MELO3C021153	0.00213199409674547	0.0227224778287244	Arginine--tRNA ligase	0
MELO3C005926	0.00213685711803191	0.0227347077752584	protein BONZAI 1	1
MELO3C006092	0.00213681237477381	0.0227347077752584	Glycoside hydrolase family 28 protein/polygalacturonase family protein	1
MELO3C012052	0.00213774633341712	0.0227347077752584	dnaJ homolog subfamily B member 1	1
MELO3C009872	0.0021356274309372	0.0227347077752584	Gibberellin-regulated family protein	1
MELO3C025491	0.00215106029913348	0.0228516889981641	transcription initiation factor TFIID subunit 1-like	0
MELO3C023221	0.00215059543241081	0.0228516889981641	DNA cross-link repair family protein	1
MELO3C001656	0.00215343807777302	0.0228646497838383	Unknown protein	1
MELO3C015457	0.00216212621458034	0.0229445623921263	K(+) efflux antiporter	0
MELO3C020836	0.00216873957663433	0.0229900364460286	transportin-1	1
MELO3C025710	0.00216856106267871	0.0229900364460286	Nuclear factor related to kappa-B-binding protein	1
MELO3C002598	0.00217096035433062	0.0230012317798688	E3 ubiquitin-protein ligase RMA1H1-like	0
MELO3C005704	0.00217420806065527	0.0230232895388101	Beta-carotene hydroxylase	1
MELO3C004533	0.00218101748222876	0.0230830194300835	GDP-mannose transporter, putative	1
MELO3C005821	0.0021861903058622	0.0231253735139114	mRNA, clone: RTFL01-46-D12	1
MELO3C009489	0.0021885277242305	0.0231377055812785	Ribosomal protein S11	0
MELO3C024916	0.00219277810808238	0.0231525705960907	Agenet domain-containing protein / bromo-adjacent domain-containing protein, putative	1
MELO3C010727	0.00219323526137982	0.0231525705960907	3-oxoacyl-[acyl-carrier-protein] reductase 4	1
MELO3C003496	0.00219345078663657	0.0231525705960907	Phosphoglycerate mutase-like protein 1	0
MELO3C021777	0.00219600458758573	0.0231671445514052	Vesicle-associated membrane protein, putative	1
MELO3C011042	0.00220196138837392	0.0232175843347552	VQ motif-containing protein 9	0
MELO3C019361	0.00220806422194508	0.0232695092418321	fasciclin-like arabinogalactan protein 7	0
MELO3C016149	0.00220997904778486	0.0232772673145084	Cationic amino acid transporter, putative	1
MELO3C009308	0.00221549861231163	0.023322964869159	LRR receptor-like kinase	1
MELO3C006759	0.00221808743540164	0.023337777710041	Ca2+-activated RelA/SpoT-like protein	1
MELO3C007340	0.00222103371849125	0.023356333816019	NAD(P)H dehydrogenase (Quinone) FQR1-like	1
MELO3C006212	0.00222542135216774	0.0233900193102506	tRNA (Guanine-N(7)-)-methyltransferase	0
MELO3C009757	0.00222821468022771	0.0234069211275623	Amino acid transporter family protein	0

MELO3C008970	0.00223264451449334	0.023440986983907	vacuolar protein sorting-associated protein 20 homolog 2-like	0
MELO3C015292	0.00225207974747366	0.0236199272081026	Epoxide hydrolase 2	0
MELO3C020002	0.00225192014674969	0.0236199272081026	Protein IDA	1
MELO3C005976	0.00225640094494073	0.0236526869753898	Protein AATF	0
MELO3C007466	0.00225882808818756	0.0236530201026597	RNA cytidine acetyltransferase	0
MELO3C003532	0.00225770592718466	0.0236530201026597	Pesticidal crystal cry8Ba protein	1
MELO3C007270	0.00226366852216031	0.023678596209822	Ring finger protein, putative	0
MELO3C026053	0.00226283308011266	0.023678596209822	WEB family protein At2g38370	1
MELO3C010806	0.0022690529645768	0.0237223541542759	DNA excision repair protein ERCC-8	1
MELO3C013780	0.00227310793406177	0.0237475211628624	Early nodulin-like protein 1	1
MELO3C025943	0.00227386513337247	0.0237475211628624	RPM1-interacting protein 4	1
MELO3C014588	0.00227553039129758	0.0237523518486976	Calcium-dependent protein kinase	1
MELO3C018569	0.00229013798537503	0.0238909923541539	peptide methionine sulfoxide reductase B5-like	1
MELO3C026897	0.00229123193674452	0.0238909923541539	thioredoxin-like 1-1, chloroplastic	1
MELO3C011885	0.00229709778793552	0.0239287608363609	Lipoxygenase	1
MELO3C008100	0.00229727735813157	0.0239287608363609	gibberellin receptor GID1B	0
MELO3C006202	0.00230065370872889	0.0239386776046823	Peptidase_M22 domain-containing protein	1
MELO3C024312	0.00229967510877782	0.0239386776046823	At1g53885	0
MELO3C019333	0.00230343015017287	0.0239549457797599	DUF679 domain membrane protein	1
MELO3C008037	0.00230496063997476	0.0239582461467693	Ubiquinol-cytochrome C chaperone family protein	1
MELO3C013489	0.00230717829032479	0.0239686817757097	monosaccharide-sensing protein 2	1
MELO3C022165	0.00231035379912992	0.0239890521445934	Actin-binding LIM protein 1, putative	0
MELO3C018492	0.00231232472788601	0.0239969001844565	Cinnamyl alcohol dehydrogenase	0
MELO3C016031	0.0023175934401175	0.0240389458239919	glutathione S-transferase-like	1
MELO3C006106	0.00232061450614851	0.0240576461322451	U-box domain-containing protein kinase family protein, putative	0
MELO3C011216	0.00232275821897354	0.0240672361314315	Photosynthetic NDH subcomplex B 3	1
MELO3C012445	0.0023251385175671	0.0240792661685541	ATP synthase subunit d, mitochondrial	1
MELO3C018264	0.00232641112745924	0.0240798183208556	No data found	1
MELO3C009318	0.00234066344919559	0.0241830573770045	Ribonuclease P protein subunit p29	1
MELO3C016952	0.00234128339180883	0.0241830573770045	eukaryotic translation initiation factor-like	0
MELO3C023445	0.00234094296969889	0.0241830573770045	F-box/LRR-repeat protein 14	1
MELO3C015103	0.00233825502701834	0.0241830573770045	Histone deacetylase	1
MELO3C021217	0.00234540104667236	0.0242129248670844	MACPF domain-containing CAD1-like protein	1
MELO3C007793	0.00235058569176971	0.0242537705468966	cytochrome P450 CYP736A12-like	1
MELO3C010517	0.00235527000820146	0.0242640727135997	WAT1-related protein	1
MELO3C023224	0.00235334258523257	0.0242640727135997	Glutathione-S-transferase	1
MELO3C026247	0.00235451557099309	0.0242640727135997	Raffinose synthase	1
MELO3C019947	0.00236105137720877	0.0243109508073493	Oxidoreductase family protein	1
MELO3C011167	0.00236258553874436	0.0243140707684535	basic leucine zipper 9	1
MELO3C005136	0.00236472222389739	0.0243233849998695	Protein EARLY RESPONSIVE TO DEHYDRATION 15	1
MELO3C017817	0.0023669444389276	0.0243335688310157	transaldolase	0
MELO3C003722	0.00237262336257049	0.0243792605553614	serine/threonine-protein kinase STY46-like isoform X1	0
MELO3C020532	0.0023744538022763	0.0243853812486504	Potassium transporter	1
MELO3C009984	0.00237666292726679	0.0243953826146527	Zinc finger CCCH domain-containing protein 41	1
MELO3C017462	0.00238451283574159	0.0244603094659689	(DL)-glycerol-3-phosphatase 2	1
MELO3C013034	0.00238546539224549	0.0244603094659689	Charged multivesicular body 1	0
MELO3C004281	0.00239189379534643	0.0245134979576008	mevalonate kinase-like	1
MELO3C019725	0.00239709679529321	0.0245540791546917	ethylene-responsive transcription factor 3-like	0
MELO3C023404	0.00240231684114978	0.0245947927920513	DNA replication complex GINS protein PSF1	0
MELO3C004084	0.00240477987021892	0.0246043393730093	No data found	1
MELO3C021521	0.00240698686863405	0.0246043393730093	WAT1-related protein	0
MELO3C003593	0.00240673840906169	0.0246043393730093	Bromo-adjacent-like (BAH) domain protein	1
MELO3C016970	0.00240841038837392	0.0246061545576805	Chaperone protein	1
MELO3C026286	0.00240990356136972	0.0246086791279682	Protein MICRORCHIDIA 6	0
MELO3C008847	0.00241118052862543	0.0246089944495213	M50 family peptidase	1
MELO3C019724	0.00241443701091759	0.0246295023391588	Triacylglycerol lipase 2, putative	1
MELO3C023540	0.00242100412623403	0.024683743153844	Unknown protein	1
MELO3C027184	0.00242276758035198	0.0246889767514816	DNA primase	0
MELO3C021295	0.00243412618990746	0.0247919330193308	Transducin family protein/WD-40 repeat protein	1
MELO3C004761	0.00243983236026302	0.0248134188898108	CBS domain-containing protein CBSX1, chloroplastic	0
MELO3C021783	0.00244000503742026	0.0248134188898108	Peroxisome biogenesis protein 1	1
MELO3C018797	0.00243837045809947	0.0248134188898108	Cysteine-rich receptor-kinase-like protein	0
MELO3C022094	0.00244379917129034	0.024839212472369	T-complex protein 1 subunit zeta 1	1
MELO3C009908	0.00245124923270912	0.0249021199057471	Type I inositol polyphosphate 5-phosphatase, putative	0
MELO3C009019	0.00245329237328473	0.0249100622519281	Rhodanese-like domain-containing family protein	1
MELO3C015210	0.00245634052673682	0.0249280206155854	ETHYLENE INSENSITIVE 3-like 3 protein	1
MELO3C011264	0.00245758550501518	0.0249280206155854	Histone acetyltransferase	0
MELO3C009639	0.00246576674180576	0.0249496524561083	Squamosa promoter binding protein	0

MELO3C013353	0.00246544497319956	0.0249496524561083	heavy metal-associated isoprenylated plant protein 26-like	1
MELO3C010493	0.00246180150676134	0.0249496524561083	Aldehyde dehydrogenase	0
MELO3C012545	0.0024685614916824	0.0249496524561083	phosphatidylinositol 4-kinase alpha 1-like	1
MELO3C021185	0.00246257535260708	0.0249496524561083	Peptidase M48	1
MELO3C019827	0.00246720498745034	0.0249496524561083	MEF2BNB-like protein	0
MELO3C010794	0.00246827361479818	0.0249496524561083	No data found	1
MELO3C017333	0.00247027858353721	0.0249542361873536	BnaC05g35140D protein	0
MELO3C002785	0.00247438794712673	0.0249829691041952	epimerase family protein SDR39U1 homolog, chloroplastic-like	1
MELO3C012428	0.0024886778630655	0.0251144093600821	mRNA-decapping enzyme subunit 2-like	1
MELO3C019500	0.00249021021586082	0.0251170385868414	Protein-protein interaction regulator family protein	0
MELO3C018683	0.00249307436724266	0.0251330912091247	Actin	0
MELO3C011084	0.00250020007177665	0.0251920669477128	Ribosomal RNA small subunit methyltransferase A	0
MELO3C009268	0.00250588454406664	0.0252175084867174	SLT1	1
MELO3C013149	0.00250643639339809	0.0252175084867174	UPF0505 protein C16orf62 homolog isoform X1	1
MELO3C006957	0.0025065557324131	0.0252175084867174	DUF21 domain-containing protein	1
MELO3C009290	0.00251076561525454	0.0252470010874042	Phosphatidate phosphatase PAH1	1
MELO3C004381	0.00251245552795387	0.025251137008428	Auxin-responsive protein	0
MELO3C016067	0.00252103326446729	0.0253107646948902	Mitochondrial processing peptidase beta subunit	1
MELO3C023844	0.00252223327356038	0.0253107646948902	2-oxoglutarate dehydrogenase E1 component family protein	0
MELO3C019704	0.00252200355091303	0.0253107646948902	Serine/threonine protein phosphatase 7 long form	0
MELO3C013745	0.00252732137778466	0.0253372598900947	Phosphatase 2C family protein	1
MELO3C022231	0.00252743946445322	0.0253372598900947	Corepressor	1
MELO3C004564	0.00253284738789272	0.0253659355931144	protein NUCLEAR FUSION DEFECTIVE 6, chloroplastic/mitochondrial-like	1
MELO3C018460	0.00253286875232273	0.0253659355931144	O-acyltransferase WSD1-like	0
MELO3C005779	0.00253841918105957	0.025395765150327	Metal-dependent protein hydrolase	1
MELO3C025725	0.00253729953931148	0.025395765150327	RNA binding (RRM/RBD/RNP motifs) family protein	1
MELO3C004423	0.00253995268287976	0.0253982407768063	protease 2	1
MELO3C018716	0.00254246520730694	0.025410498673636	ras-related protein Rab11D	1
MELO3C019673	0.00254436052110441	0.0254165786197728	BOI-related E3 ubiquitin-protein ligase 1-like	1
MELO3C004321	0.00255025674306286	0.0254625987961317	Vat protein	1
MELO3C016014	0.0025571448957098	0.0255184712205016	thiamine pyrophosphokinase 1	0
MELO3C003874	0.00255880335336345	0.0255221249624115	cytochrome P450 734A1-like	1
MELO3C010640	0.00256492543970355	0.0255702738559845	zinc finger CCCH domain-containing protein 1	1
MELO3C015459	0.0025681230640956	0.0255892343051584	Cytidine deaminase	1
MELO3C010716	0.00256975248916946	0.0255925576947089	Protein HHL1, chloroplastic	1
MELO3C002167	0.0025805609976346	0.0256872475515553	Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial	1
MELO3C002589	0.00258385469115019	0.0257070762194081	At2g47960/T9J23.10	1
MELO3C024357	0.0025853839593345	0.0257093392814184	transcription initiation factor TFIID subunit 12b	1
MELO3C002277	0.0025908406468802	0.0257506350957408	Glutathione transport system permease protein gsiD	0
MELO3C022399	0.00259592798474784	0.0257882202066323	alcohol dehydrogenase-like	1
MELO3C016434	0.00260306171692859	0.0258067871092464	protein STICHEL	1
MELO3C015825	0.00260506410889971	0.0258067871092464	F-box protein, putative	1
MELO3C026572	0.00260563742446895	0.0258067871092464	Proline transporter	0
MELO3C008389	0.0026054713783954	0.0258067871092464	RNA-binding protein 2	1
MELO3C019810	0.00260464821668416	0.0258067871092464	Adenosine kinase	1
MELO3C003818	0.00260420294403418	0.0258067871092464	Tubby-like F-box protein	0
MELO3C007660	0.00260875272791905	0.0258116902544923	DUF21 domain-containing-like protein	1
MELO3C019661	0.00260850482660091	0.0258116902544923	No data found	1
MELO3C023969	0.00261005344261589	0.0258116902544923	Unknown protein	1
MELO3C024244	0.00261508509481012	0.0258485062749775	Ribosomal protein L37	0
MELO3C009587	0.00261788420547349	0.0258632292015487	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	1
MELO3C000251	0.00262134113062928	0.0258844329943989	Protein LAZ1	1
MELO3C018344	0.00262491390901554	0.0258938185759979	No data found	1
MELO3C017158	0.00262413446791454	0.0258938185759979	Serine/threonine-protein kinase atr	0
MELO3C007785	0.00263134950686683	0.0259431666044565	RING-H2 zinc finger protein RHA2a	0
MELO3C011498	0.00263254371742017	0.0259431666044565	Splicing factor u2af large subunit, putative	1
MELO3C009532	0.0026377958393965	0.025943562933669	NDR1/HIN1-like protein 12	0
MELO3C021618	0.00263523784937714	0.025943562933669	ribosomal RNA large subunit methyltransferase E-like	0
MELO3C027119	0.00263408267344634	0.025943562933669	1-aminocyclopropane-1-carboxylate oxidase 2	0
MELO3C026901	0.00263783859288103	0.025943562933669	HNH endonuclease	0
MELO3C026222	0.00264225576370025	0.0259740712181763	Transcription factor GTE10	1
MELO3C004385	0.00265207979831772	0.0260253671353869	pathogenesis-related protein PR-4-like	0
MELO3C006055	0.00265102172481946	0.0260253671353869	Aldose 1-epimerase	1
MELO3C010522	0.00264977766937746	0.0260253671353869	Zinc knuckle family protein	1
MELO3C018365	0.00265274515385761	0.0260253671353869	GDP-Man:Man(3)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase	1
MELO3C021604	0.00265591567654666	0.0260435346058193	glycerol-3-phosphate dehydrogenase [NAD(+)]	1
MELO3C024086	0.00266368909276027	0.0261052559442443	70 kDa heat shock protein	1
MELO3C017481	0.00266485371328151	0.0261052559442443	Xyloglucan endotransglucosylase/hydrolase	1

MELO3C004519	0.00267496625574049	0.0261783491499598	NADH-cytochrome b5 reductase-like protein	0
MELO3C007081	0.00267470348746146	0.0261783491499598	SIT4 phosphatase-associated family protein	1
MELO3C014687	0.00269195405579215	0.0263315505932833	Structural maintenance of chromosomes protein	1
MELO3C023385	0.00270256906142263	0.0264222952445721	molybdate transporter 2	1
MELO3C023358	0.00270407856419341	0.0264239720753368	Ubiquitin fusion degradation 1 protein	1
MELO3C006439	0.00270856493483707	0.0264476999835899	1-aminocyclopropane-1-carboxylate oxidase homolog 1-like	0
MELO3C022497	0.00270918512667995	0.0264476999835899	40S ribosomal protein S13	0
MELO3C015093	0.00271896315900721	0.0265169399640659	Fasciclin-like arabinogalactan protein 16	1
MELO3C026723	0.00271827361883736	0.0265169399640659	Plastidal glycolate/glycerate translocator 1, chloroplastic	0
MELO3C010744	0.00272509819331868	0.0265636546001237	CTD small phosphatase-like protein 2	1
MELO3C014925	0.00272905227228559	0.026570628428043	Glycerophosphodiester phosphodiesterase, putative	0
MELO3C007405	0.00272984986989211	0.026570628428043	peroxisomal membrane protein PMP22	1
MELO3C023569	0.00272901561183836	0.026570628428043	Alpha-N-acetylglucosaminidase	1
MELO3C005103	0.00273416426217743	0.0265885133692798	Cytochrome b-c1 complex subunit Rieske, mitochondrial	1
MELO3C023599	0.00273464015593183	0.0265885133692798	Glutamine synthetase	0
MELO3C011717	0.00273572632368102	0.0265885133692798	Protein kinase-like protein	1
MELO3C013603	0.0027441539772568	0.0266573029497514	Plant/protein (DUF789)	0
MELO3C006153	0.00275443894018501	0.0267440583233598	UDP-galactose/UDP-glucose transporter 2-like	0
MELO3C011263	0.00276183244145933	0.0267500877324082	EEIG1/EHBP1 protein amino-terminal domain protein	1
MELO3C019501	0.00275780114814639	0.0267500877324082	Transmembrane 53	1
MELO3C013331	0.0027606036489658	0.0267500877324082	hippocampus abundant transcript-like protein 1	1
MELO3C015131	0.00276010714569663	0.0267500877324082	Pentatricopeptide repeat-containing family protein	1
MELO3C003861	0.00275803858939361	0.0267500877324082	H/ACA ribonucleoprotein complex non-core subunit NAF1-like isoform X1	1
MELO3C008214	0.00276361792622737	0.0267542600122864	Emb|CAB62340.1	1
MELO3C017228	0.00276531793823609	0.0267576011573859	Replication protein A 70 kDa DNA-binding subunit	0
MELO3C007857	0.00277499196625031	0.0268074015965016	LOW QUALITY PROTEIN: protein HYPER-SENSITIVITY-RELATED 4-	0
MELO3C022228	0.00277292080975666	0.0268074015965016	Dienelactone hydrolase	1
MELO3C015861	0.00277506452761478	0.0268074015965016	isoamylase 2, chloroplastic	1
MELO3C012418	0.00277589428653835	0.0268074015965016	Tyramine N-feruloyltransferase 4/11	0
MELO3C025494	0.00278404522379472	0.0268729761117898	leukotriene A-4 hydrolase homolog	0
MELO3C013665	0.00278843488334646	0.0269021985887685	mechanosensitive ion channel protein 6-like	0
MELO3C018985	0.00280648064981326	0.0270630792740049	60S acidic ribosomal protein P1	1
MELO3C006949	0.0028143816981141	0.0271260244783091	NADH-ubiquinone oxidoreductase-related	1
MELO3C020733	0.00282827819139519	0.0272333817659014	Hexosyltransferase	1
MELO3C024984	0.00282776638965032	0.0272333817659014	12-oxophytodienoate reductase 3	1
MELO3C006681	0.00283034097739443	0.0272399629447186	bifunctional epoxide hydrolase 2-like	1
MELO3C015682	0.00283388627394909	0.0272607988427767	Zinc finger BED domain-containing protein DAYSLEEPER	0
MELO3C014199	0.00283809781829736	0.0272822307215747	E3 ubiquitin-protein ligase RING1-like	1
MELO3C010350	0.00283887711442787	0.0272822307215747	heme oxygenase 1, chloroplastic	1
MELO3C019326	0.00284198844840122	0.0272988472118073	Glutaredoxin	1
MELO3C011716	0.00285347093160948	0.0273958179039162	TBC1 domain family member 8B	1
MELO3C012175	0.00285815822128543	0.0274274862546968	Thioredoxin-like protein aaed1, chloroplastic	0
MELO3C025490	0.00286245136842622	0.0274553434070177	Protein TONNEAU 1b	1
MELO3C009188	0.00286979849156177	0.0274591329505104	transcription factor DIVARICATA-like	1
MELO3C006858	0.00286606413668511	0.0274591329505104	At5g51840	0
MELO3C016931	0.00286763125209966	0.0274591329505104	Hydroxyproline-rich glycoprotein	1
MELO3C020157	0.00286972839969413	0.0274591329505104	Glycerol-3-phosphate dehydrogenase [NAD(+)]	0
MELO3C018408	0.00286762071520663	0.0274591329505104	methyltransferase-like protein 13	0
MELO3C006576	0.00287199260083404	0.0274668193093808	ARM repeat superfamily protein	0
MELO3C008248	0.00287463929746568	0.0274788245332283	GRF1-interacting factor 3	1
MELO3C013852	0.00287625232888011	0.0274809420624351	Plant/protein	1
MELO3C007689	0.00289790596181549	0.0276681646798411	protein RMD5 homolog A	1
MELO3C008074	0.00289864968973574	0.0276681646798411	No data found	1
MELO3C012268	0.00290928855179373	0.0277428969625178	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.2 isoform X4	0
MELO3C011953	0.00290852105031103	0.0277428969625178	Unknown protein	1
MELO3C022246	0.00291399362481704	0.0277743533284323	cytochrome P450 78A9-like	0
MELO3C002232	0.00292148187912489	0.0278188744603845	serine/threonine-protein kinase fray2	0
MELO3C009949	0.00292063003617526	0.0278188744603845	Pentatricopeptide repeat-containing protein	1
MELO3C026782	0.0029315704215952	0.027901486388474	Protein WVD2-like 3	1
MELO3C025699	0.00293717560620022	0.0279413685196763	Mitochondrial carrier protein	1
MELO3C015807	0.00294721274408638	0.0279586801462572	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein	0
MELO3C023406	0.00294286704306013	0.0279586801462572	Polygalacturonase	0
MELO3C025872	0.00294290350336335	0.0279586801462572	protein NRT1/ PTR FAMILY 8.1-like	1
MELO3C025854	0.00294734785833395	0.0279586801462572	No data found	1
MELO3C022411	0.00294748959767621	0.0279586801462572	No data found	1
MELO3C008481	0.00294454167237668	0.0279586801462572	Glutamate synthase 1 [nadh], chloroplastic	1

MELO3C017624	0.0029620275572394	0.0280830927642443	Superoxide dismutase	0
MELO3C021565	0.00296685498420146	0.0281103720538155	DExH-box ATP-dependent RNA helicase DExH17-like	1
MELO3C022694	0.00296775156879869	0.0281103720538155	Ethylene-responsive transcription factor	0
MELO3C012527	0.00297250118494685	0.0281418628482816	Guanine nucleotide-binding protein beta subunit-like protein	0
MELO3C019044	0.00298063279371774	0.0282044227419728	Tubulin folding cofactor B	1
MELO3C002058	0.00298196540003237	0.0282044227419728	PHD and RING finger domain-containing protein 1	1
MELO3C021929	0.00299072573288184	0.0282602117218581	B3 domain-containing transcription factor VRN1-like	1
MELO3C026077	0.0029907075838328	0.0282602117218581	leucine-rich repeat extensin-like protein 3	0
MELO3C009278	0.00299360468042398	0.0282738875340474	Pectin acetylesterase	1
MELO3C019004	0.00299954481518294	0.0282948581551635	ENTH/ANTH/VHS superfamily protein, putative	0
MELO3C022500	0.00300012319494214	0.0282948581551635	Vacuolar protein sorting 26	1
MELO3C018495	0.00299853266939398	0.0282948581551635	Carbohydrate esterase, putative (DUF303)	1
MELO3C016801	0.00300623854141413	0.028338999978228	aspartic proteinase-like protein 2	1
MELO3C007413	0.00301537223321668	0.0283981409417135	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein	1
MELO3C026638	0.0030153881996442	0.0283981409417135	acyl-protein thioesterase 2	0
MELO3C006943	0.00303125387801784	0.0285138619671975	Keratin-associated protein, putative (DUF819)	1
MELO3C017687	0.00303163409125018	0.0285138619671975	solute carrier family 35 member F1	0
MELO3C002719	0.00303345100982744	0.0285138619671975	60S ribosomal protein L18a	1
MELO3C010135	0.00303274871299286	0.0285138619671975	Kelch repeat-containing protein family	1
MELO3C007950	0.00304051349157075	0.0285394966468777	Thiol-disulfide oxidoreductase LTO1	1
MELO3C022482	0.00303891540561274	0.0285394966468777	SWI/SNF complex component SNF12 homolog	0
MELO3C011123	0.00303966505635012	0.0285394966468777	oleosin 1-like	0
MELO3C006635	0.00304572063851438	0.0285701369470703	transcription termination factor MTEF1, chloroplastic-like	0
MELO3C017786	0.00304667114337587	0.0285701369470703	GPI-anchored protein	1
MELO3C007580	0.003050768630666	0.028581418257601	phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and protein-tyrosine-	1
MELO3C012211	0.00304978606683126	0.028581418257601	Coiled-coil domain-containing protein 130	0
MELO3C007841	0.00305590903747888	0.0286160016980419	Bacteriophage N4 adsorption B	1
MELO3C009328	0.00306327293243192	0.0286713635746909	Lectin receptor kinase-like protein	1
MELO3C013275	0.00307285130009638	0.0287238455479359	Eukaryotic translation initiation factor 3 subunit A, putative	0
MELO3C004134	0.00307469793348203	0.0287238455479359	leucine aminopeptidase 1-like	1
MELO3C025897	0.00307432554173359	0.0287238455479359	pumilio homolog 1-like	1
MELO3C026715	0.00307034640401294	0.0287238455479359	Tetratricopeptide repeat (TPR)-like superfamily protein	1
MELO3C019546	0.00308152563759556	0.0287740188259455	PRKR-interacting protein 1	0
MELO3C006945	0.00308380034190114	0.0287816507335566	mediator of RNA polymerase II transcription subunit 36a-like	0
MELO3C026015	0.00309308236949102	0.0288546451181285	cyclin-dependent kinase 11B-like	1
MELO3C015954	0.0030947715945715	0.0288567725312524	No data found	1
MELO3C023201	0.0030977794094238	0.0288575686588257	No data found	1
MELO3C025916	0.00309672394330129	0.0288575686588257	Triosephosphate isomerase, putative	0
MELO3C013879	0.00310242322052934	0.0288872023490023	Regulator of nonsense transcripts 1-like protein	1
MELO3C006833	0.00310508976483725	0.0288905872097688	AT-hook motif nuclear-localized protein 1	0
MELO3C019779	0.00310717541311201	0.0288905872097688	U4/U6 small nuclear ribonucleoprotein PRP4-like protein	1
MELO3C003821	0.00310708875855792	0.0288905872097688	agglutinin-like	1
MELO3C006596	0.00312259521677238	0.0290066476651166	squamosa promoter-binding-like protein 7	0
MELO3C016899	0.00312150091819829	0.0290066476651166	Mitochondrial carrier protein	1
MELO3C016315	0.00312509809007677	0.0290162492623066	Unknown protein	1
MELO3C024172	0.00313617279548883	0.0290917221879328	Histone deacetylase	1
MELO3C012716	0.00313511425606883	0.0290917221879328	ribonuclease 2-like	1
MELO3C006546	0.00313962609965124	0.0291100825549354	BRI1 kinase inhibitor 1-like	1
MELO3C007711	0.0031447472936853	0.0291438828263684	U-box domain-containing protein kinase family protein, putative	1
MELO3C011172	0.00314734549239759	0.0291542805484803	Proteasome subunit beta type	1
MELO3C020628	0.00314969349944749	0.0291623520490335	Protein kinase	0
MELO3C003368	0.0031518431083446	0.0291685799187898	Intron maturase, type II family protein	1
MELO3C018128	0.00315436270314007	0.0291782243673598	Pentatricopeptide repeat-containing protein	0
MELO3C026935	0.00315856654564306	0.0292034319802925	Homeobox-leucine zipper HOX24	0
MELO3C011323	0.0031636598807594	0.0292240016708344	No data found	1
MELO3C003790	0.00316375085180232	0.0292240016708344	subtilisin-like protease SBT3.17 isoform X1	0
MELO3C010057	0.00317500236112433	0.0293142223608436	WRKY transcription factor SUSIBA2-like isoform X2	1
MELO3C016435	0.00318004727588184	0.0293470811455095	PHD finger alfin-like protein	0
MELO3C026949	0.00318437434441865	0.0293732876823559	DNA ligase	0
MELO3C004179	0.0031931976062749	0.0294409241486102	RNA polymerase II-associated protein 3	1
MELO3C017665	0.00319763962111685	0.0294681217346882	Ubiquitin-protein ligase, putative	0
MELO3C020958	0.0032001673855715	0.0294776612395762	Shikimate kinase	0
MELO3C026019	0.00321334455151734	0.0295852408148792	Abscisic acid receptor	0
MELO3C027349	0.00321673340123285	0.0296026411653996	MACPF domain NSL1-like protein	1
MELO3C009275	0.00322209073351121	0.0296342880451715	No data found	1
MELO3C025912	0.00322317336174127	0.0296342880451715	Protein kinase	1
MELO3C013566	0.00323029250749773	0.0296859221640636	Indole-3-acetic acid-amido synthetase GH3.3	0
MELO3C006900	0.00323377434712158	0.0297040974796763	No data found	0

MELO3C008985	0.00323792539730006	0.0297284001261175	Glucose-6-phosphate 1-dehydrogenase	1
MELO3C011141	0.00324029178816565	0.0297363022883287	Transcriptional regulatory plant protein, putative	0
MELO3C020113	0.00324422109289979	0.029758533378392	ADP,ATP carrier protein	1
MELO3C023885	0.00324576723815473	0.0297588937726638	Tropinone reductase family protein	1
MELO3C010695	0.00325920601822216	0.0298682411386865	No data found	1
MELO3C011641	0.00326082986585996	0.0298692620690484	gamma-secretase subunit APH1-like	0
MELO3C015999	0.00327258479556591	0.0299630399293608	60S ribosomal protein L22-2	1
MELO3C002240	0.00327636508104368	0.0299837506883835	RING-type E3 ubiquitin transferase	1
MELO3C014270	0.00328035162177276	0.0300063289385781	No data found	1
MELO3C017682	0.00329068344277839	0.0300590690617162	extensin-2	0
MELO3C011626	0.00329055575005754	0.0300590690617162	Ribosomal protein S8	0
MELO3C010882	0.00328785247888019	0.0300590690617162	Origin recognition complex subunit 2 family protein	0
MELO3C015845	0.00329570830198256	0.030079897053516	basic 7S globulin 2	0
MELO3C006367	0.00329600978397937	0.030079897053516	histone-lysine N-methyltransferase family member SUVH9	1
MELO3C016702	0.00330136386296176	0.0301062021308803	translation initiation factor IF-1, chloroplastic	1
MELO3C018564	0.00330194105096393	0.0301062021308803	Protein trichome birefringence-like 12	1
MELO3C017142	0.00330403547657232	0.0301113966898139	tRNA (Ile)-lysidine synthase	1
MELO3C014696	0.00330563892729141	0.0301121140106449	Glycosyltransferase	0
MELO3C026387	0.00331292201755107	0.0301645444557935	Pentatricopeptide repeat-containing protein At3g59040	1
MELO3C024476	0.00332258243518369	0.0302260283252226	alpha carbonic anhydrase 7-like	0
MELO3C011977	0.00332273570783626	0.0302260283252226	polygalacturonase At1g48100	1
MELO3C006104	0.00332623952523958	0.0302439707108455	Atg8-interacting protein 1	1
MELO3C011450	0.00333358893825408	0.0302968467287528	Kelch repeat-containing F-box family protein	0
MELO3C016379	0.00333695453228211	0.0303134843873226	Ultraviolet-B receptor UVR8	1
MELO3C013981	0.00335602505490162	0.030418811552392	40S ribosomal protein S13	0
MELO3C024538	0.00335382112544536	0.030418811552392	zinc finger A20 and AN1 domain-containing stress-associated protein 4	1
MELO3C005084	0.00335625046193033	0.030418811552392	E3 ubiquitin-protein ligase	1
MELO3C021429	0.00335193882671869	0.030418811552392	Ribosomal protein	0
MELO3C004988	0.00335093209097537	0.030418811552392	Protein SIEL	1
MELO3C001354	0.00335814086479347	0.030421983458168	Kinase family protein	1
MELO3C012642	0.00336533823483554	0.0304732071525754	Glucan endo-1,3-beta-glucosidase-like protein 1	1
MELO3C004803	0.00336930114440837	0.0304951092121544	BnaC01g17260D protein	0
MELO3C014283	0.00337200910851509	0.0305056380595807	BIG SEEDS 1	1
MELO3C007612	0.00337643607475258	0.0305317014836486	molybdate-anion transporter	1
MELO3C022717	0.00338495688318097	0.0305947430141606	FHA domain-containing protein FHA2	0
MELO3C012390	0.00339255872463551	0.030635410266496	NAC domain-containing protein 53-like	0
MELO3C003646	0.00339160336545463	0.030635410266496	guanine nucleotide-binding protein subunit gamma 2-like	0
MELO3C007740	0.00339467117104308	0.0306404757572806	40S ribosomal protein S6-like	0
MELO3C012160	0.00339732236416479	0.0306437874748141	Protein BIG GRAIN 1-like E	1
MELO3C015670	0.00339843699782583	0.0306437874748141	Phosphatidylinositol N-acetylglucosaminyltransferase subunit A	0
MELO3C009826	0.0033996930658422	0.0306437874748141	Carboxypeptidase	0
MELO3C020709	0.00340145935932612	0.0306457212077242	K-stimulated pyrophosphate-energized sodium pump protein	0
MELO3C003618	0.00340400756003645	0.0306546946206839	Unknown protein	0
MELO3C003537	0.00340619799978614	0.0306604395158507	WD-40 repeat-containing protein MSI1	0
MELO3C005597	0.00341005728531718	0.0306784743320635	1-aminocyclopropane-1-carboxylate synthase	0
MELO3C012457	0.00341130840210702	0.0306784743320635	Annexin	1
MELO3C005446	0.00342424757612758	0.0307808217482675	60S ribosomal protein L13	1
MELO3C024964	0.00343821174470194	0.03089228559878	E3 ubiquitin-protein ligase	1
MELO3C012627	0.00344637204195242	0.0309515240820911	KRR1 small subunit processome component homolog	0
MELO3C008749	0.00344966036879268	0.0309669739196758	CBS domain-containing protein CBSX6	0
MELO3C025053	0.00345273664238088	0.0309805070197092	lysine-specific demethylase JMJ25	1
MELO3C017141	0.00345887223368579	0.03102146582337	Dynein light chain	0
MELO3C005776	0.00346706651856055	0.0310808427939411	Plant UBX domain-containing protein 10	1
MELO3C011443	0.00346914766687134	0.0310853889623603	Glycosyltransferase	0
MELO3C009159	0.00347745214263795	0.0311456700067832	ALC-interacting protein 1	1
MELO3C019807	0.00348962571938949	0.0312405341487865	Zinc finger (C3HC4-type RING finger) family protein	0
MELO3C004651	0.00349339114977409	0.0312600733198408	DENN (AEX-3) domain-containing protein	1
MELO3C016321	0.00351307924928468	0.0313935756082005	multiple RNA-binding domain-containing protein 1	0
MELO3C021455	0.00351239881555254	0.0313935756082005	BnaC04g30420D protein	0
MELO3C002644	0.00351114986297452	0.0313935756082005	Transcription factor	1
MELO3C013068	0.00352314090533479	0.0314579681657778	No data found	0
MELO3C007737	0.00352347083815385	0.0314579681657778	No data found	1
MELO3C003545	0.00352514241961388	0.0314586704224828	28 kDa ribonucleoprotein	1
MELO3C008002	0.0035312711957558	0.0314849096365604	serine/threonine-protein kinase D6PKL2	0
MELO3C013051	0.00353085892452476	0.0314849096365604	Dead box ATP-dependent RNA helicase, putative	1
MELO3C009284	0.00353465922443519	0.0314952662272863	Protein SLOW GREEN 1, chloroplastic	1
MELO3C006293	0.00354341023305915	0.0314952662272863	Werner Syndrome-like exonuclease	0
MELO3C006679	0.00354132679588104	0.0314952662272863	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase	0

MELO3C016574	0.00353635905852601	0.0314952662272863	Serine/threonine-protein kinase	1
MELO3C017979	0.00354359621029066	0.0314952662272863	Bifunctional protein FolD	1
MELO3C018634	0.00353843304329915	0.0314952662272863	7-deoxyloganetin glucosyltransferase-like	0
MELO3C012787	0.00354012354896582	0.0314952662272863	Sterol 3-beta-glucosyltransferase	1
MELO3C002187	0.00354604168811656	0.0315028237960477	Plant/protein (DUF789)	0
MELO3C013699	0.00354782004554266	0.0315044505752797	Pectinesterase	1
MELO3C002921	0.00354961794420117	0.0315062493393388	Cysteine proteinase inhibitor	0
MELO3C011266	0.00355690370295292	0.0315425645395677	Histone acetyltransferase	0
MELO3C010886	0.00355680004882486	0.0315425645395677	Succinate dehydrogenase subunit 5, mitochondrial	1
MELO3C009118	0.00356566194604402	0.0316060402928291	TOM1-like protein 2	0
MELO3C003452	0.00357083843738115	0.0316377246746704	Synaptonemal complex protein 1	0
MELO3C027277	0.00357454085905751	0.031648946287679	Polygalacturonase	0
MELO3C006224	0.00357531010014744	0.031648946287679	HOPM interactor 7	1
MELO3C006942	0.00357863116017443	0.0316511025151031	Receptor-like protein kinase, putative	1
MELO3C012303	0.00357875902153149	0.0316511025151031	Trichome birefringence-like protein	0
MELO3C006470	0.00359422249341379	0.0317736347459395	p-loop nucleoside triphosphate hydrolase superfamily protein	0
MELO3C013634	0.00359595157280856	0.0317746969178507	DNA-directed RNA polymerase subunit beta	0
MELO3C016056	0.00360431063231181	0.0318343160454052	monothiol glutaredoxin-S11	1
MELO3C008871	0.00360628755649928	0.0318375381999572	Chaperone protein dnaJ, putative	1
MELO3C020139	0.00361941064351767	0.0319105985709065	No data found	1
MELO3C018700	0.00361828856415125	0.0319105985709065	UDP-glycosyltransferase 74F2-like	0
MELO3C009973	0.00361824768775709	0.0319105985709065	Dead box ATP-dependent RNA helicase, putative	0
MELO3C019010	0.00362104834108679	0.0319107914717193	No data found	0
MELO3C010566	0.00362510291757867	0.0319266674182015	Topoisomerase II-associated protein PAT1	0
MELO3C011769	0.00362608309377821	0.0319266674182015	Pyruvate kinase	1
MELO3C016706	0.00362792550019198	0.031928654502358	E3 ubiquitin-protein ligase RMA3	1
MELO3C012844	0.00363671067198779	0.0319917145038248	Glutathione S-transferase family protein	1
MELO3C017291	0.00364457998267875	0.0320466652172407	40S ribosomal protein S28	1
MELO3C020055	0.00365494902297803	0.0321235372740512	histidine kinase 4-like	1
MELO3C026594	0.00365773426356975	0.0321337161793767	E3 ubiquitin-protein ligase RGLG2	0
MELO3C004333	0.00366799011256524	0.0321861378545134	DCD (Development and Cell Death) domain protein	1
MELO3C003135	0.0036685906279057	0.0321861378545134	Ribonuclease II, chloroplastic/mitochondrial	1
MELO3C026250	0.00366806256004015	0.0321861378545134	Rhodanese-like domain-containing protein 11, chloroplastic	1
MELO3C014100	0.00367353119137726	0.0321994102008483	Heavy metal-associated isoprenylated plant protein 21	1
MELO3C019954	0.00367499471328736	0.0321994102008483	NAC domain-containing protein 17-like	0
MELO3C018086	0.00367393222298185	0.0321994102008483	No data found	0
MELO3C002364	0.00368322380190222	0.0322572003830452	glucuronoxylan 4-O-methyltransferase 1	0
MELO3C007651	0.00368605120965426	0.0322676530760027	BSD domain-containing protein	0
MELO3C017041	0.00369325977155832	0.032289034232494	Protein canopy 1-like	0
MELO3C005067	0.00369064033854793	0.032289034232494	dihydroorotate dehydrogenase (Quinone), mitochondrial-like	1
MELO3C011580	0.00369339856859607	0.032289034232494	Selenoprotein K	0
MELO3C011306	0.00370901783915945	0.0324112359759115	U2 snRNP-associated SURP motif-containing protein	0
MELO3C013737	0.00371380927877951	0.032438752519512	Eukaryotic translation initiation factor 3 subunit A, putative	1
MELO3C009047	0.00371812788353043	0.0324621165215926	Endonuclease/exonuclease/phosphatase family protein	1
MELO3C009362	0.00372330748990279	0.032484415475003	4-coumarate--CoA ligase-like 7	0
MELO3C021694	0.003723971676308	0.032484415475003	equilibrative nucleotide transporter 3-like	0
MELO3C018849	0.0037317716935662	0.0325380835215183	Glycosyltransferase	1
MELO3C004466	0.00373428926178776	0.0325456657683347	Alpha-galactosidase	1
MELO3C012147	0.00373986616904487	0.0325742299591907	Chromatin modification-related protein EAF7	0
MELO3C022715	0.00374086553989794	0.0325742299591907	E3 ubiquitin-protein ligase RNF4-like isoform X1	1
MELO3C018156	0.00374297430987069	0.0325782281382267	HEAT repeat-containing 8	1
MELO3C020756	0.00374575962541046	0.032588108741071	auxin-responsive protein SAUR24-like	0
MELO3C009313	0.00374905481299304	0.0326024145758694	MCM domain-containing protein	0
MELO3C021441	0.00375323054063759	0.0326243617724699	Low molecular weight protein-tyrosine-phosphatase, putative	1
MELO3C019256	0.00375711455194661	0.0326437550754041	Glutamate receptor	0
MELO3C017659	0.00376166987941229	0.03265460151583	Ribosomal protein L15	1
MELO3C023561	0.00376053621892014	0.03265460151583	Zinc finger, PHD-type	0
MELO3C025595	0.00377304170472659	0.0326903479823329	Hydroxyacylglutathione hydrolase 3, mitochondrial-like protein	0
MELO3C024527	0.00377219600226342	0.0326903479823329	Monodehydroascorbate reductase family protein	0
MELO3C021072	0.00376902665796097	0.0326903479823329	p-loop containing nucleoside triphosphate hydrolases superfamily protein,	0
MELO3C022135	0.00377269415701442	0.0326903479823329	Dynamin homolog	0
MELO3C003511	0.00377406417538706	0.0326903479823329	No data found	1
MELO3C009659	0.00378297423157448	0.0327359654708158	WD-repeat protein, putative	0
MELO3C012087	0.00378286641513303	0.0327359654708158	At1g69680/T6C23_12	0
MELO3C025844	0.00378430346700454	0.0327359654708158	zinc finger CCCH domain-containing protein 66	0
MELO3C005590	0.00378620329661872	0.0327380599408595	AT-hook motif nuclear-localized protein 1	0
MELO3C017128	0.00379795715646769	0.0328253198613043	two-component response regulator ARR5-like	1
MELO3C023131	0.00380245973358373	0.0328498588270101	Magnesium chelatase subunit	0

MELO3C022307	0.00380791780284617	0.0328826273233096	Pentatricopeptide repeat-containing family protein	1
MELO3C015877	0.00381685302485724	0.0329453804142944	Autophagy-related protein 18g	0
MELO3C018872	0.00382096715178948	0.0329664833030539	eukaryotic translation initiation factor 1A-like	0
MELO3C007206	0.00382538871009896	0.0329902190549102	Receptor-like kinase	0
MELO3C007781	0.0038398486676372	0.0331004676286194	C2 domain-containing family protein	0
MELO3C007981	0.00384716409883801	0.0331397649451927	Plant intracellular ras group-related LRR protein	1
MELO3C026665	0.0038477634826739	0.0331397649451927	BTB/POZ domain-containing protein At5g48800	0
MELO3C011206	0.00384958612008623	0.0331410097147267	dentin sialophosphoprotein-like	1
MELO3C016629	0.00385657378659299	0.0331759691273178	integrator complex subunit 9 homolog isoform X1	0
MELO3C004813	0.00385700668977274	0.0331759691273178	No data found	0
MELO3C002951	0.00386183647055627	0.0331771225999734	Peptidyl-prolyl cis-trans isomerase	0
MELO3C024701	0.00386218060951637	0.0331771225999734	Elongation factor Ts, mitochondrial	1
MELO3C022756	0.00385939753056552	0.0331771225999734	No data found	0
MELO3C006362	0.00387559388006831	0.0332591859056182	Beta-amylase	1
MELO3C016972	0.00388047519379775	0.0332591859056182	stromal cell-derived factor 2-like protein	0
MELO3C026799	0.00387701403635354	0.0332591859056182	Kinase family protein	1
MELO3C005658	0.00387972951477389	0.0332591859056182	O-glucosyltransferase rumi homolog	0
MELO3C002698	0.00388183824560484	0.0332591859056182	Eukaryotic translation initiation factor 4E	0
MELO3C017496	0.00387421851442116	0.0332591859056182	pathogenesis-related protein PR-1	0
MELO3C007029	0.00388454470007149	0.0332679415792332	glycine-rich RNA-binding protein 4, mitochondrial	0
MELO3C026403	0.00388878465702924	0.033289817161539	60S ribosomal protein L27	1
MELO3C012831	0.0038908092763863	0.0332927176773627	WD repeat-containing protein 26	0
MELO3C014561	0.00389493667687124	0.0333068362123798	Hydroxyproline O-arabinosyltransferase 1	1
MELO3C017322	0.00389583227761392	0.0333068362123798	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE	0
MELO3C004334	0.00390896641762595	0.0333732318117167	ERAD-associated E3 ubiquitin-protein ligase HRD1B-like	1
MELO3C006528	0.00391035791241645	0.0333732318117167	At1g05410/T25N20_5	1
MELO3C000756	0.00390717971422494	0.0333732318117167	Alanine--tRNA ligase	1
MELO3C026504	0.00390827463156984	0.0333732318117167	centromere protein V isoform X1	0
MELO3C013878	0.00391222575567463	0.0333747500858826	haloacid dehalogenase-like hydrolase domain-containing protein Sgpp	1
MELO3C025139	0.00392025166600019	0.0334275900689354	No data found	1
MELO3C002556	0.0039218049617562	0.0334275900689354	heterogeneous nuclear ribonucleoprotein U-like protein 1	1
MELO3C008158	0.00393031276265376	0.0334712146397797	Protein PLASTID MOVEMENT IMPAIRED 2	0
MELO3C019983	0.00392989468547922	0.0334712146397797	Wound-responsive family protein	0
MELO3C016939	0.00394970593609312	0.0335715480937751	Protein phosphatase 2c, putative	0
MELO3C008944	0.00394846519055947	0.0335715480937751	ultraviolet-B receptor UVR8 isoform X2	0
MELO3C011989	0.00395059384120378	0.0335715480937751	Unknown protein	1
MELO3C026495	0.00394489756670136	0.0335715480937751	cytochrome P450 CYP82D47-like	0
MELO3C013044	0.00394792703568192	0.0335715480937751	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B	0
MELO3C004163	0.00395312441178808	0.0335786038745818	trafficking protein particle complex subunit 4	1
MELO3C007919	0.00395536602137492	0.0335819377854541	alpha-mannosidase	0
MELO3C022017	0.00395691777946994	0.0335819377854541	Ribosomal protein L18/L5	0
MELO3C011127	0.00395892010502719	0.0335844987775695	receptor-like protein kinase HSL1	0
MELO3C002789	0.00396747730644487	0.0336426403284584	BnaCnng71930D protein	1
MELO3C013221	0.00397472788079656	0.0336507765001755	KH domain-containing protein	1
MELO3C007232	0.00397436879822932	0.0336507765001755	spermidine coumaroyl-CoA acyltransferase	1
MELO3C021281	0.00397525249759023	0.0336507765001755	Beta-D-xylosidase family protein	0
MELO3C018648	0.00397329808233615	0.0336507765001755	Annexin	0
MELO3C009755	0.00399223218178957	0.0336852876960037	Sigma factor binding protein 1, chloroplastic	1
MELO3C006187	0.00398992103329143	0.0336852876960037	Proteasome subunit beta type	1
MELO3C006954	0.00399297475803051	0.0336852876960037	Ornithine cyclodeaminase/mu-crystallin	0
MELO3C026373	0.0039887085281346	0.0336852876960037	Glycosyltransferase	0
MELO3C007648	0.00398694127513544	0.0336852876960037	RuvB-like helicase	0
MELO3C019798	0.00398754437598248	0.0336852876960037	Acyl-CoA N-acyltransferase domain protein	0
MELO3C011236	0.00398898589143037	0.0336852876960037	Peptidyl-prolyl cis-trans isomerase	1
MELO3C018126	0.00399118870471526	0.0336852876960037	Autophagy-related protein 18f	1
MELO3C006817	0.003994972976333	0.0336877546155424	pectinesterase-like	1
MELO3C009105	0.0040092906562702	0.0337845085349958	Receptor-like kinase plant-like protein	0
MELO3C022425	0.00400986824679883	0.0337845085349958	15 kDa selenoprotein	1
MELO3C026103	0.00401371508088511	0.0338024985639232	DUF538 family protein	0
MELO3C016780	0.00401640311312934	0.0338107182784277	ethylene-responsive transcription factor ERF011-like	0
MELO3C006678	0.00402069563885754	0.0338324321141021	DUF581 family protein, putative (DUF581)	0
MELO3C011227	0.00402447276814755	0.0338353821618331	zeaxanthin epoxidase, chloroplastic-like	0
MELO3C023474	0.00402423910770855	0.0338353821618331	Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase	0
MELO3C015941	0.00403168091934258	0.0338815602025943	Long cell-linked locus protein, putative, expressed	1
MELO3C011726	0.00404263312343378	0.0339457259093174	Nuclear transcription factor Y subunit B	0
MELO3C017221	0.00404275392874143	0.0339457259093174	Histone deacetylase	1
MELO3C026210	0.00404664750198225	0.0339639785451115	SNF1-related protein kinase regulatory subunit gamma-1	0
MELO3C006574	0.00405142086150934	0.0339895966839201	guanylate kinase 3, chloroplastic-like	1

MELO3C006891	0.00405529113468006	0.0340076197956673	heat stress transcription factor B-2b-like	0
MELO3C002258	0.00406375095139522	0.0340640991252564	No data found	0
MELO3C007940	0.00406921847048769	0.0340954584529747	Protein phosphatase 2c, putative	1
MELO3C009601	0.00408256489346259	0.034175454074849	Dirigent protein	0
MELO3C006406	0.00409087920567841	0.034175454074849	Transducin/WD40 domain-like protein, putative	0
MELO3C008489	0.00408119611396818	0.034175454074849	Serine/threonine-protein kinase stt7, chloroplastic	1
MELO3C018935	0.00409080955661678	0.034175454074849	Unknown protein	1
MELO3C024610	0.004090155111938	0.034175454074849	Iron-sulfur binding oxidoreductase	0
MELO3C011869	0.00408858935710987	0.034175454074849	cytochrome P450 78A5-like	0
MELO3C019649	0.00408633114963042	0.034175454074849	auxin-responsive protein SAUR71	0
MELO3C016540	0.00409820484929724	0.0341932604853279	NAC domain protein	0
MELO3C024466	0.00409776864969524	0.0341932604853279	heavy metal-associated isoprenylated plant protein 3-like isoform X2	0
MELO3C015915	0.00409647381032929	0.0341932604853279	Heme binding	0
MELO3C013444	0.00410871929360257	0.0342665106965191	No data found	0
MELO3C011320	0.00411998198635644	0.0343459367870634	NAD(P)-binding rossmann-fold protein	0
MELO3C009370	0.00412796035380381	0.0343689245477535	ACT domain-containing protein	0
MELO3C024404	0.00412659958826311	0.0343689245477535	Tudor/PWWP/MBT superfamily protein	0
MELO3C015314	0.00412612017060354	0.0343689245477535	protein SRC2-like	0
MELO3C022568	0.00413550035043642	0.0344099668734598	protein indeterminate-domain 5, chloroplastic	0
MELO3C018374	0.00413637456871707	0.0344099668734598	DUF248-1	0
MELO3C024936	0.00413994951308028	0.03442520544582	Cleavage and polyadenylation specificity factor subunit	0
MELO3C005710	0.00414841548622957	0.0344810847801127	heavy metal-associated isoprenylated plant protein 3	0
MELO3C005504	0.00415565745621238	0.0345267476242063	Disease resistance family protein	0
MELO3C021144	0.00415874744190292	0.0345378903406816	squamosa promoter-binding-like protein 8	0
MELO3C014591	0.00417094646782634	0.0346116311413704	cyclin-dependent protein kinase inhibitor SMR3-like	0
MELO3C022382	0.00417453238090104	0.0346116311413704	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial	0
MELO3C010664	0.00417184497662493	0.0346116311413704	F28C11.19	0
MELO3C003323	0.00417463696282061	0.0346116311413704	Myosin heavy chain-like protein	0
MELO3C021407	0.00418955137017907	0.0347207091941529	Stem-specific protein TSJT1	0
MELO3C004316	0.00419185506808106	0.0347252289175893	Prefoldin chaperone subunit family protein, putative	0
MELO3C017094	0.00419379751734894	0.0347267535304504	No data found	0
MELO3C011908	0.00419762735150164	0.0347438988117376	Heat shock protein HSP26	0
MELO3C002084	0.00420015070006774	0.0347502204338659	Protein NEGATIVE REGULATOR OF RESISTANCE	0
MELO3C017520	0.00420329844082712	0.0347617005476946	L-allo-threonine aldolase	0
MELO3C027370	0.00420544322376737	0.0347648799607291	O-methyltransferase, putative	0
MELO3C011799	0.00420786589404742	0.0347703529462521	Cytochrome P450	0
MELO3C021944	0.00421779613002127	0.0348378317740652	Flavoprotein wrbA	0
MELO3C013419	0.00423115977641308	0.0349094003953484	30S ribosomal protein S31, mitochondrial	0
MELO3C012361	0.00422999190468754	0.0349094003953484	cell division control protein 2 homolog A	0
MELO3C027137	0.00423176386381408	0.0349094003953484	Gibberellin receptor GID1A	0
MELO3C004239	0.00424349429512305	0.0349623566267773	Zinc finger protein VAR3, chloroplastic	0
MELO3C016852	0.00424135737752129	0.0349623566267773	zinc finger CCCH domain-containing protein 20-like	1
MELO3C007071	0.00424254602009433	0.0349623566267773	WPP domain associated protein	1
MELO3C006348	0.00425488104939142	0.0350415537299546	PHD finger protein ING	1
MELO3C009713	0.00425803339606046	0.0350528976818666	translation factor GUF1 homolog, chloroplastic	1
MELO3C019295	0.00426894623574081	0.0351280913373522	Cellulose synthase family protein	0
MELO3C013835	0.00427577875347029	0.0351696603924552	Heat shock transcription factor family protein	0
MELO3C017571	0.00428197580447165	0.0352059700926356	alanine--glyoxylate aminotransferase 2 homolog 1, mitochondrial	1
MELO3C017989	0.00430088886261248	0.0353173613919892	PXMP2/4 family protein 4	0
MELO3C021636	0.00429798729381359	0.0353173613919892	No data found	1
MELO3C025550	0.00429966579888252	0.0353173613919892	No data found	1
MELO3C004637	0.00431383370119853	0.0354089367269201	pre-mRNA cleavage factor Im 25 kDa subunit 1	1
MELO3C009787	0.00431780204327548	0.0354267854394048	Protein SRC1	0
MELO3C002515	0.00433020588612543	0.0355138023443069	Eukaryotic translation initiation factor-like protein	1
MELO3C024896	0.00433539021546703	0.035541561380348	Calcium-dependent lipid-binding (CaLB domain) family protein	1
MELO3C004382	0.00433957988353706	0.035551505038091	Auxin-responsive protein	0
MELO3C005089	0.00434194979060565	0.035551505038091	40S ribosomal protein S27	1
MELO3C003793	0.0043420036534445	0.035551505038091	GTP-binding protein hflx, putative	1
MELO3C015857	0.00434471017132754	0.0355589229894519	No data found	1
MELO3C017187	0.00435977689092781	0.0356231832101503	Pectinesterase inhibitor	1
MELO3C007635	0.00435740828139641	0.0356231832101503	F-box protein, putative	1
MELO3C008977	0.00435899313719323	0.0356231832101503	Kinesin-like protein	1
MELO3C022236	0.00435478022543923	0.0356231832101503	Cation/H(+) antiporter 11	0
MELO3C019833	0.00436921025270542	0.0356854976346896	Glycine-rich RNA-binding family protein	0
MELO3C025454	0.00438074020671109	0.0357648773635127	2-oxoglutarate dehydrogenase E1 component family protein	0
MELO3C013892	0.00438636358545552	0.0357959894418021	Calcineurin B-like protein	1
MELO3C007055	0.00439030907538485	0.0358133886533562	reticuline oxidase-like protein	1
MELO3C017245	0.004395158508533	0.0358381442547557	squamosa promoter-binding-like protein 6	0

MELO3C020908	0.00439808294774702	0.0358471894903243	Glycosyl hydrolase family 43 protein	1
MELO3C017365	0.004401984544528	0.0358543790682549	DEAD-box ATP-dependent RNA helicase 42	1
MELO3C011106	0.00440441154588012	0.0358543790682549	Pentatricopeptide repeat-containing protein	1
MELO3C012982	0.00440400022067899	0.0358543790682549	Bet1-like SNARE 1-1	0
MELO3C006555	0.00441530169934157	0.0358838655392167	NEDD8-activating enzyme E1 catalytic subunit	1
MELO3C017756	0.0044125107954931	0.0358838655392167	calcium-dependent protein kinase 24	0
MELO3C022535	0.00441084542698378	0.0358838655392167	Methionine adenosyltransferase 2 subunit beta	0
MELO3C011419	0.00441372812875063	0.0358838655392167	Purple acid phosphatase	0
MELO3C011719	0.00441889278353991	0.0358951901894086	Adenylate kinase	0
MELO3C027061	0.00442033027194499	0.0358951901894086	PLATZ transcription factor family protein	1
MELO3C025492	0.00442331481104608	0.0359046626400941	transcription initiation factor TFIID subunit 1-like	0
MELO3C014781	0.00443181098567713	0.0359466902553953	AT5g13970/MAC12_6	1
MELO3C013364	0.00443433490235257	0.0359466902553953	MYB-related transcription factor	1
MELO3C007317	0.00443550104810231	0.0359466902553953	Transmembrane protein, putative	0
MELO3C027082	0.0044357731607878	0.0359466902553953	transcription factor bHLH149-like	1
MELO3C006341	0.00444064861850657	0.0359683622052152	Holliday junction resolvase	0
MELO3C026519	0.00444300260802799	0.0359683622052152	AT-hook motif nuclear-localized protein 10	0
MELO3C013004	0.00444391127554433	0.0359683622052152	protein IQ-DOMAIN 14-like	0
MELO3C007001	0.00444609229565951	0.035971272735346	Peptidylprolyl isomerase	1
MELO3C012080	0.00444939745034345	0.03598327200935	binding partner of ACD11 1	0
MELO3C016733	0.00445369614312496	0.0360032931357245	Estradiol 17-beta-dehydrogenase 1	0
MELO3C017857	0.00447660665509919	0.0361736926479353	Unknown protein	0
MELO3C025196	0.00448195650987304	0.0362021100668641	CTD small phosphatase-like protein	1
MELO3C006795	0.00448602272104126	0.0362201401135911	F-box protein SKIP16	1
MELO3C002811	0.00448958909934571	0.0362341214233668	SWIM zinc finger family protein	0
MELO3C009686	0.00449453289572133	0.0362592034957518	Pleiotropic drug resistance ABC transporter	1
MELO3C018333	0.00451435304406078	0.0364042295905089	Six-bladed beta-propeller, TolB-like protein	0
MELO3C009569	0.00452389862146674	0.0364365717273029	Gb|AAF02136.1	1
MELO3C017023	0.00452304563686967	0.0364365717273029	Catalase	0
MELO3C023402	0.00452320197757028	0.0364365717273029	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	1
MELO3C018884	0.00453160110978612	0.0364688632099291	No data found	0
MELO3C024747	0.00453016901239933	0.0364688632099291	30S ribosomal protein S5, putative	0
MELO3C002054	0.00454481945338836	0.0365603419083367	Movement protein binding protein 2C	1
MELO3C002292	0.00454712501382337	0.0365639950724747	transcription factor MYB86-like	1
MELO3C014381	0.00455362792746339	0.0366013829627491	Arginine/glutamate-rich 1 protein	0
MELO3C017274	0.00455931809361776	0.0366322103461583	G patch domain-containing protein TGH	1
MELO3C005627	0.00457680273778194	0.0367577378074239	UDP-galactose/UDP-glucose transporter 2	1
MELO3C011270	0.0045788351918522	0.0367591122780037	Adenine phosphoribosyltransferase, putative	0
MELO3C021242	0.00458194269778134	0.0367691126934107	YTH domain family protein 2	1
MELO3C022180	0.00458428047942672	0.0367729306207141	Protein DETOXIFICATION	1
MELO3C007661	0.00458836570581656	0.036790756932266	Transmembrane protein, putative	1
MELO3C009581	0.00459335511739778	0.036793997135694	D-lactate dehydrogenase, putative	1
MELO3C021302	0.00459515873505412	0.036793997135694	Phosphatase 2C (PP2C)-like protein	0
MELO3C002611	0.00459421197278376	0.036793997135694	VQ motif-containing protein	0
MELO3C022766	0.00459622213447552	0.036793997135694	50S ribosomal protein L35	0
MELO3C013309	0.00461226279515592	0.0368639930026092	Coiled-coil protein	0
MELO3C007896	0.00461243236161057	0.0368639930026092	DNA ligase 3	0
MELO3C022208	0.00461235112080338	0.0368639930026092	Transmembrane protein, putative	0
MELO3C002241	0.00460760544686867	0.0368639930026092	Protein ROS1	0
MELO3C022174	0.00461874366324821	0.0368845809160894	molybdopterin synthase sulfur carrier subunit	1
MELO3C021458	0.00461777456584467	0.0368845809160894	glucomannan 4-beta-mannosyltransferase 9-like	0
MELO3C014961	0.00462684788511114	0.0369343649486903	No data found	0
MELO3C007108	0.00462896316894279	0.0369363206559399	Auxilin-related protein 2	0
MELO3C024729	0.0046335805594675	0.0369582320149126	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	1
MELO3C025893	0.00464191527612789	0.0370097637417238	chaperone protein DnaJ	1
MELO3C010631	0.00465069359190351	0.0370647892439477	replication factor C subunit 5	1
MELO3C018500	0.00466513527941126	0.0371648877100012	TIP41-like family protein	1
MELO3C007936	0.00466850680925801	0.0371767503935631	aspartyl protease family protein 1-like	1
MELO3C014298	0.00468816507599967	0.0372301209290144	CST complex subunit STN1	1
MELO3C006119	0.00467883824833293	0.0372301209290144	Remorin	1
MELO3C025122	0.00469406507564141	0.0372301209290144	Transmembrane protein, putative	0
MELO3C024352	0.00469137170648004	0.0372301209290144	Transcription initiation factor TFIID subunit 9	1
MELO3C012231	0.00468490302386826	0.0372301209290144	Homologous-pairing protein 2-like protein	1
MELO3C011942	0.0046793778862565	0.0372301209290144	E3 ubiquitin-protein ligase	1
MELO3C002254	0.00469046994419164	0.0372301209290144	No data found	0
MELO3C010334	0.00469594567999265	0.0372301209290144	Non-specific serine/threonine protein kinase	1

MELO3C018609	0.00468423052131772	0.0372301209290144	nicotinamidase 1-like	0
MELO3C018637	0.00469303610003224	0.0372301209290144	outer envelope protein 64, mitochondrial	1
MELO3C010982	0.00469150142351815	0.0372301209290144	cysteine proteinase RD19a-like	0
MELO3C010869	0.00470255932622954	0.0372675939541361	Calcium-binding EF-hand	0
MELO3C008126	0.00471205326936386	0.0373278539978607	receptor homology region, transmembrane domain- and RING domain-	0
MELO3C024467	0.0047202723733617	0.037348183901565	No data found	0
MELO3C005850	0.00472341949742638	0.037348183901565	S-type anion channel SLAH2	1
MELO3C011045	0.00471896157234275	0.037348183901565	Histone H3	1
MELO3C003619	0.00472073883878732	0.037348183901565	serine/arginine-rich splicing factor RSZ22A	1
MELO3C018767	0.00472407531450247	0.037348183901565	Wound-responsive family protein	1
MELO3C006522	0.00474301631824137	0.0374679317075795	Acyl-CoA N-acyltransferases (NAT) superfamily protein, putative	1
MELO3C020620	0.00474164902427332	0.0374679317075795	telomere repeat-binding protein 5-like	0
MELO3C003924	0.00475797865690586	0.0375710997581903	Nuclear speckle splicing regulatory-like protein (DUF2040)	1
MELO3C007388	0.00476193222621446	0.0375724900381318	calcium-dependent protein kinase-like	0
MELO3C022903	0.00476195972279325	0.0375724900381318	No data found	1
MELO3C017526	0.00476558186294107	0.0375860528000093	No data found	0
MELO3C010860	0.00476961101908036	0.0376028135791688	thioredoxin-like 4, chloroplastic	0
MELO3C015779	0.00477524685384889	0.0376322227121555	peptidyl-prolyl cis-trans isomerase CYP63	1
MELO3C006867	0.00478082614067543	0.0376461465120411	ATP-dependent Clp protease ATP-binding subunit clpX	1
MELO3C024282	0.00477892180585116	0.0376461465120411	DUF3820 family protein	1
MELO3C021352	0.00478487268238359	0.0376629934652824	No data found	1
MELO3C025264	0.00480324345966632	0.0377390862236877	Auxin efflux carrier	0
MELO3C026332	0.00480409452460129	0.0377390862236877	DNA helicase INO80-like protein	1
MELO3C024359	0.00479821584987294	0.0377390862236877	40S ribosomal S3-like protein	0
MELO3C021766	0.00480031640730605	0.0377390862236877	Cysteine proteinase inhibitor	0
MELO3C010205	0.00480220260665098	0.0377390862236877	Myosin-binding protein 7	0
MELO3C026379	0.00481892308236753	0.0378405216515612	choline-phosphate cytidylyltransferase 2-like	0
MELO3C004128	0.00482450500558018	0.0378692962461061	hepatoma-derived growth factor-related protein 2-like isoform X1	0
MELO3C006557	0.00482848374613742	0.0378854690117076	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	0
MELO3C014503	0.00484227068846665	0.0379785559279301	Nuclear transcription factor Y subunit B	0
MELO3C004504	0.004853594233164	0.0380522558597681	SPX domain-containing protein 1	0
MELO3C009653	0.00486423822417426	0.0381054504915579	transcription factor bHLH48	1
MELO3C019979	0.00486300975469733	0.0381054504915579	40S ribosomal protein S18	0
MELO3C006846	0.00486680411514517	0.038110433969073	Mitochondrial metalloendopeptidase OMA1	1
MELO3C023373	0.00488233112164127	0.0381563740883631	Aspartate aminotransferase	1
MELO3C020848	0.00488021440735875	0.0381563740883631	AP2-like ethylene-responsive transcription factor TOE3 isoform X1	1
MELO3C021380	0.00487514380395182	0.0381563740883631	Prolyl 4-hydroxylase alpha subunit, putative	0
MELO3C011261	0.0048818429137143	0.0381563740883631	Peroxidase	1
MELO3C009865	0.00488061309291565	0.0381563740883631	No data found	0
MELO3C017766	0.0048895206154731	0.0381974456625705	Ras family	1
MELO3C024047	0.00489669867223619	0.0382383954440461	Kelch repeat-containing F-box family protein	1
MELO3C023098	0.00490672223331468	0.0383015246583919	No data found	1
MELO3C014607	0.00491102235340035	0.038307474285644	Zinc transporter ZTP29	1
MELO3C011936	0.00491136386101831	0.038307474285644	protein-tyrosine-phosphatase MKP1-like	0
MELO3C014848	0.00492368631958517	0.0383581385110405	Zinc finger, RING-type	0
MELO3C004616	0.00492100162867981	0.0383581385110405	No data found	0
MELO3C013809	0.00492199748758904	0.0383581385110405	calcium permeable stress-gated cation channel 1-like	0
MELO3C023525	0.00493771673994492	0.0384457842027261	60S ribosomal protein L6	0
MELO3C024980	0.00493883004315743	0.0384457842027261	No data found	1
MELO3C005683	0.0049435184544383	0.0384671181862498	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase	0
MELO3C026427	0.00494570982192477	0.0384690127109855	B-cell receptor-associated 31-like protein	1
MELO3C014560	0.00496315380380685	0.0385743110867302	Phospholipase A2	1
MELO3C024468	0.00496279709271841	0.0385743110867302	Thioredoxin, putative	1
MELO3C014666	0.00496701622528295	0.0385853581760918	Dirigent protein	0
MELO3C022914	0.00496848275061024	0.0385853581760918	50S ribosomal protein L15	0
MELO3C002200	0.00497295451208024	0.0386049051332833	ABC transporter A family protein	0
MELO3C005243	0.00498172170978672	0.0386577689770444	purple acid phosphatase 4-like	0
MELO3C004555	0.00498570584906988	0.0386734897145644	At3g13227	1
MELO3C019021	0.00499094402569167	0.0386837337375921	Endoplasmic reticulum-Golgi intermediate compartment 3	1
MELO3C026734	0.00499084688857632	0.0386837337375921	lamin-like protein	0
MELO3C024947	0.00499678096282596	0.0386903771333979	Inner centromere protein, ARK-binding region protein	1
MELO3C016831	0.00499389552060658	0.0386903771333979	RING-type E3 ubiquitin transferase	0
MELO3C024452	0.00499963757377242	0.0386903771333979	No data found	0
MELO3C018867	0.00499926959078445	0.0386903771333979	E6-like protein	0
MELO3C017478	0.00500308520310322	0.0387018917650159	Xyloglucan endotransglucosylase/hydrolase	1
MELO3C020617	0.00500844294115677	0.0387281674412314	Haloacid dehalogenase-like hydrolase	0
MELO3C002030	0.00501632420632747	0.0387739282781844	Glycine-rich RNA-binding protein	0
MELO3C009465	0.00502843552261645	0.0388523369077278	Terminal flower 1	0

MELO3C018257	0.00503800739884341	0.038911070832913	No data found	0
MELO3C002891	0.00504688773087425	0.0389644197799201	Pseudouridine synthase, RsuA/RluB/C/D/E/F	0
MELO3C006299	0.00505397492352333	0.0389713767143541	RNA-directed DNA polymerase (Reverse transcriptase)-related family protein	0
MELO3C022027	0.0050556821683212	0.0389713767143541	40S ribosomal protein S19	0
MELO3C021713	0.00505438158441507	0.0389713767143541	Ubiquinol oxidase	0
MELO3C012854	0.00505464637579456	0.0389713767143541	Long-chain-alcohol oxidase	0
MELO3C010569	0.00506299294919321	0.0390125040006308	Obg-like ATPase 1	1
MELO3C008932	0.00506938195028461	0.0390464992730775	thioredoxin-like 3-1, chloroplastic	1
MELO3C009748	0.00507356902590583	0.0390635145000446	Pentatricopeptide repeat-containing protein At1g80270, mitochondrial	1
MELO3C020574	0.00507969128465335	0.0390954104367183	No data found	1
MELO3C017092	0.00509335428043201	0.0391808196243162	diphthine methyltransferase	0
MELO3C018572	0.00509558321440995	0.0391808196243162	glutamate-1-semialdehyde 2,1-aminomutase 2, chloroplastic-like	0
MELO3C010865	0.00509674037241725	0.0391808196243162	Calcium-binding EF-hand family protein, putative	1
MELO3C002653	0.00510434896997825	0.0392240419486772	No data found	1
MELO3C002679	0.00510933008744363	0.0392470478012152	heat stress transcription factor A-4c	0
MELO3C017563	0.00512088786410558	0.0393052524011742	Protein AE7	1
MELO3C013472	0.0051198180085511	0.0393052524011742	Histone deacetylase	0
MELO3C019542	0.00513228821363398	0.0393774514106673	D-3-phosphoglycerate dehydrogenase	0
MELO3C016667	0.00514137660805702	0.0393847987498828	Random slug protein 5	0
MELO3C012583	0.00513599158009104	0.0393847987498828	nuclear-pore anchor-like	0
MELO3C021691	0.00514153474524282	0.0393847987498828	F-box protein family	0
MELO3C015299	0.00514189399425591	0.0393847987498828	serine/arginine-rich splicing factor SR30	0
MELO3C018610	0.0051432171743353	0.0393847987498828	Fructose-1,6-bisphosphatase	0
MELO3C014936	0.0051599163782603	0.0394820567819693	BRO1 domain-containing protein	0
MELO3C016335	0.00515823944960314	0.0394820567819693	F22C12.19	0
MELO3C022426	0.0051671505635198	0.0395220977842573	Something about silencing protein	0
MELO3C015455	0.00517018623505283	0.0395300069516293	Acyl--UDP-N-acetylglucosamine O-acyltransferase	1
MELO3C012084	0.00517341272002758	0.0395393683466814	40S ribosomal protein S9, putative	0
MELO3C007190	0.00518428034658769	0.0396070996382051	Splicing factor 3B, subunit 5	0
MELO3C024869	0.0051870663759751	0.0396130602703528	No data found	1
MELO3C005803	0.00519167594605396	0.0396329370926246	WAT1-related protein	0
MELO3C014288	0.00520148075471183	0.0396924433635255	VAN3-binding protein	0
MELO3C016221	0.00520810517208448	0.0397171785628582	ABC transporter G family member 14	0
MELO3C010745	0.00520874436567942	0.0397171785628582	mitochondrial import receptor subunit TOM20-like	1
MELO3C020579	0.00521804986638397	0.0397727776191497	Enolase	1
MELO3C013820	0.00522492446332201	0.0397791184372191	bZIP transcription factor 16	1
MELO3C022417	0.00522320791153241	0.0397791184372191	RNA-binding protein 24-B	1
MELO3C004917	0.00522269622442229	0.0397791184372191	sulfite oxidase-like	0
MELO3C006182	0.00523154057570219	0.0398141405894191	Pentatricopeptide repeat-containing protein At1g01970	0
MELO3C012683	0.00524867626788583	0.0399196237807747	Pentatricopeptide repeat-containing protein, mitochondrial	1
MELO3C022310	0.00524944366594116	0.0399196237807747	Histidine kinase	0
MELO3C005215	0.0052570899040556	0.0399623820304827	defensin Ec-AMP-D2-like	0
MELO3C019137	0.00526112589863548	0.0399776742486156	Plant/MNJ7-17 protein, putative	0
MELO3C017906	0.00526885628831797	0.0400210164761506	acyl-protein thioesterase 2	1
MELO3C007409	0.00527492254906536	0.0400516898967673	WRKY family transcription factor	0
MELO3C006221	0.00527834117750325	0.0400544508958836	Glutathione s-transferase, putative	0
MELO3C006760	0.00527934253288698	0.0400544508958836	Chromatin structure-remodeling complex protein BSH	0
MELO3C007195	0.00528427713697965	0.040066299931388	ER lumen protein-retaining receptor	1
MELO3C010941	0.00528496183711913	0.040066299931388	3-ketoacyl-CoA synthase	0
MELO3C008118	0.0052918874227319	0.0400863298080399	Inner membrane protein oxaA	0
MELO3C025023	0.00529572304770753	0.0400863298080399	thioredoxin-like protein slr0233	1
MELO3C003627	0.00529445457556355	0.0400863298080399	Transcriptional adapter 1	0
MELO3C003690	0.00529425199930755	0.0400863298080399	adenine nucleotide transporter BT1, chloroplastic/mitochondrial-like	0
MELO3C011062	0.00531329000863789	0.0402038943986934	Serine hydrolase FSH	1
MELO3C007688	0.00531587170426806	0.0402080238558368	tRNA-dihydrouridine synthase	0
MELO3C011704	0.00532175202668261	0.0402370906489108	RAS-related protein RABC1	1
MELO3C020748	0.00533361546979561	0.0402651268780556	Receptor-like protein kinase	0
MELO3C001920	0.00533117758364088	0.0402651268780556	No data found	0
MELO3C015481	0.00533354470146574	0.0402651268780556	Chloroplastic group IIA intron splicing facilitator CRS1	0
MELO3C011279	0.00532757903706893	0.0402651268780556	Hydroxyproline O-arabinosyltransferase 1	1
MELO3C005634	0.00533638245875689	0.0402706217722545	phosphatidylinositol glycan anchor biosynthesis class U protein-like	0
MELO3C012881	0.00533881960791294	0.0402736243073616	rho-N domain-containing protein 1, chloroplastic isoform X3	1
MELO3C023004	0.00534674243286837	0.040294608949124	casein kinase I-like isoform X1	0
MELO3C004825	0.00534772241914294	0.040294608949124	Ser/thr-rich protein T10 in DGCR region-like protein	1
MELO3C026640	0.00534644158281883	0.040294608949124	Mitogen-activated protein kinase kinase kinase 1 isoform 1	1
MELO3C007000	0.0053577184510808	0.0403545315371452	Katanin p80 WD40 repeat-containing subunit B1 homolog	1
MELO3C012295	0.00536354190955324	0.0403829924406279	Tetratricopeptide repeat-like superfamily protein	0
MELO3C012912	0.00536579815994709	0.0403845837884127	Chlorophyll a-b binding protein, chloroplastic	0

MELO3C002072	0.00536839161606895	0.0403887108669507	Adenine nucleotide alpha hydrolases-like superfamily protein	0
MELO3C014951	0.00538851756489089	0.0405092628051124	tRNA/rRNA methyltransferase family protein	0
MELO3C020489	0.00538680953554949	0.0405092628051124	WRKY transcription factor 1	0
MELO3C005380	0.00539842275126157	0.0405682842141038	protein phosphatase inhibitor 2	0
MELO3C009151	0.00540405465087668	0.0405797244487314	phosphoinositide phosphatase SAC8	0
MELO3C023173	0.00540260609983467	0.0405797244487314	sister chromatid cohesion 1 protein 3	1
MELO3C016700	0.00541295604689029	0.0406186957918544	Inner membrane protein oxaA	0
MELO3C024248	0.00541360366330046	0.0406186957918544	Dynein light chain family protein	0
MELO3C002313	0.00541541475618779	0.0406186957918544	Serine/threonine-protein kinase AFC2	1
MELO3C015113	0.00542243994015512	0.0406559477517553	Protein SMG7	0
MELO3C007235	0.00543615744316983	0.0407433295427556	Protein IQ-DOMAIN 1	0
MELO3C017551	0.00544379027512432	0.0407695920149526	Pentatricopeptide repeat-containing protein	0
MELO3C017169	0.0054419971112214	0.0407695920149526	60S ribosomal protein L34	0
MELO3C002293	0.00544667677743771	0.0407757466556548	Armadillo/beta-catenin repeat family protein	0
MELO3C009170	0.00545100219701766	0.0407926647930662	vacuolar cation/proton exchanger 3-like	0
MELO3C016881	0.00546445639647308	0.0408778596113435	Cytokinin riboside 5'-monophosphate phosphoribohydrolase	0
MELO3C010023	0.00548021836409496	0.0409802470550971	Ycf20-like protein	1
MELO3C022605	0.00548519315338203	0.0410019226291225	thiamine biosynthetic bifunctional enzyme TH1, chloroplastic-like	0
MELO3C006643	0.00548775039087324	0.0410039815297562	E3 ubiquitin-protein ligase	1
MELO3C019156	0.00549336446814186	0.0410039815297562	protein GrpE	0
MELO3C022885	0.00549564783216616	0.0410039815297562	methyl-CpG-binding domain protein 4-like protein	1
MELO3C015423	0.00549259467745444	0.0410039815297562	Damaged dna-binding 2, putative isoform 1	0
MELO3C026577	0.00549584987134866	0.0410039815297562	mitogen-activated protein kinase kinase 3	0
MELO3C022961	0.00549927721920196	0.0410140580823336	4-hydroxyphenylpyruvate dioxygenase	0
MELO3C009329	0.00550540936501021	0.0410288036036176	Peroxidase	0
MELO3C024348	0.00550384303802409	0.0410288036036176	Lipoxygenase	0
MELO3C005298	0.00551011550099556	0.0410336646483313	DELLA protein GAI	0
MELO3C003554	0.00551021715769784	0.0410336646483313	homeobox-leucine zipper protein ATHB-6-like	0
MELO3C009549	0.00551926640667522	0.0410855605975985	No data found	0
MELO3C017925	0.00552454836960814	0.0410939004713338	Myb transcription factor	1
MELO3C022530	0.00552368037194162	0.0410939004713338	Armadillo/beta-catenin repeat family protein	1
MELO3C011897	0.00553231331154147	0.0411361655081448	F-box protein SKIP14	1
MELO3C003453	0.00554160058650854	0.041189713956702	eukaryotic translation initiation factor 3 subunit L-like	1
MELO3C023308	0.0055442020245402	0.0411935461936209	F-box protein At2g16365	1
MELO3C006093	0.00554875124716214	0.0412118421888699	UDP-glycosyltransferase 91A1-like	0
MELO3C006553	0.00555487297960233	0.0412417994263784	3-dehydrosphinganine reductase TSC10A isoform X1	0
MELO3C022742	0.00556230935646029	0.0412814909735943	ATP-dependent DNA helicase, RecQ family protein, expressed	1
MELO3C009753	0.00556782329136662	0.0412913789640253	Transcription factor PERIANTHIA	0
MELO3C005559	0.00556759058409906	0.0412913789640253	transaldolase	0
MELO3C021715	0.00558441460505543	0.0413988753886035	E3 ubiquitin-protein ligase COP1-like	0
MELO3C026293	0.00561249329691038	0.041591418431776	DUF1645 family protein	1
MELO3C021818	0.00561839821362631	0.0416195597602798	Protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 10	1
MELO3C013030	0.00562152618538336	0.0416271168485699	Tudor/PWWP/MBT superfamily protein	0
MELO3C017430	0.0056314445582144	0.0416849320015653	Fiber protein Fb15	1
MELO3C007563	0.00564058020111158	0.0416900517933206	Lipase	0
MELO3C026567	0.00563811290088667	0.0416900517933206	Pentatricopeptide repeat-containing protein At4g18975, chloroplastic	1
MELO3C013581	0.00563795363412223	0.0416900517933206	shaggy-related protein kinase eta	0
MELO3C008152	0.00563998177954761	0.0416900517933206	Class I glutamine amidotransferase-like superfamily protein	0
MELO3C022309	0.00564333704074471	0.0416948235008108	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3	1
MELO3C019429	0.00564600559118555	0.0416989395737934	Basic-leucine zipper (BZIP) transcription factor family protein	1
MELO3C014876	0.00565538385941067	0.041752589098879	Kelch repeat-containing F-box family protein	0
MELO3C016778	0.00565933442381517	0.0417661418295686	SPla/RYanodine receptor (SPRY) domain protein	0
MELO3C004117	0.00566929710292929	0.0418240375367018	Carboxypeptidase	0
MELO3C007636	0.00567263519002581	0.0418330367318221	Calcium-transporting ATPase	0
MELO3C020997	0.00568704454460378	0.0419199713723186	Sterol 3-beta-glucosyltransferase	0
MELO3C026499	0.00568866895933029	0.0419199713723186	Zinc finger HIT domain-containing protein 3	0
MELO3C013692	0.00569296709952316	0.0419359967357266	Transmembrane protein, putative	0
MELO3C002261	0.00570743449773126	0.0420268918328466	serine/threonine-protein kinase HT1-like	0
MELO3C009193	0.005714154321319 5	0.0420606909026235	Transmembrane protein	0
MELO3C019997	0.0057189492179438	0.0420803010824039	Histone H4	0
MELO3C014390	0.00572324775500266	0.0420962457778575	mavicyanin-like	0
MELO3C026392	0.0057372614827349	0.042183610209431	RING/U-box superfamily protein	1
MELO3C006151	0.0057406825704176	0.0421920901889014	protein-ribulosamine 3-kinase, chloroplastic	0
MELO3C013951	0.00574760326577217	0.0421920901889014	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8,	1
MELO3C016676	0.00574342477656464	0.0421920901889014	Peptide methionine sulfoxide reductase	0
MELO3C003123	0.00574566882149075	0.0421920901889014	E3 ubiquitin-protein ligase XB3-like	0
MELO3C022650	0.00574909690102454	0.0421920901889014	At1g16840/F17F16.27	0
MELO3C025152	0.00576102443116722	0.0422639195732249	Coronatine-insensitive 1	0

MELO3C009325	0.00577467309870794	0.0423191774837995	POLAR LOCALIZATION DURING ASYMMETRIC DIVISION AND	0
MELO3C014035	0.00577498523058584	0.0423191774837995	No data found	1
MELO3C016723	0.00577229566189108	0.0423191774837995	serpin-ZX-like	0
MELO3C012351	0.00577787071656299	0.0423246175005202	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase like	0
MELO3C013215	0.00578362349766959	0.0423510494829354	Chaperone DnaJ domain protein	1
MELO3C016017	0.00578589705892163	0.0423519944464949	translocator protein homolog	0
MELO3C002023	0.00580928505066813	0.0425074362599648	DExH-box ATP-dependent RNA helicase DExH14	0
MELO3C007814	0.00582928347011036	0.0426221840989298	protein indeterminate-domain 2-like	0
MELO3C021695	0.0058292778713428	0.0426221840989298	Phosphatidate cytidylyltransferase	0
MELO3C022301	0.00583286609252087	0.0426325952854162	serine/threonine-protein kinase ATG1a isoform X4	1
MELO3C014353	0.00584390830887993	0.0426975009959562	Transmembrane protein, putative	0
MELO3C018739	0.00584621381637895	0.0426985490605281	GPI-anchored protein LORELEI	1
MELO3C011890	0.00585525734603176	0.0427329923602296	DNA-binding storekeeper protein-related	0
MELO3C025877	0.00585523358807216	0.0427329923602296	Glucose-6-phosphate isomerase	0
MELO3C007133	0.00586456153890169	0.0427776942902953	Transmembrane protein	0
MELO3C020666	0.0058657145241845	0.0427776942902953	ATP-dependent clp protease	1
MELO3C004534	0.00587048715416727	0.0427809706934379	Glycine-rich RNA-binding protein, putative	1
MELO3C024909	0.005876180212674	0.0427809706934379	Mitochondrial transcription termination factor family protein	0
MELO3C006765	0.00587699496132954	0.0427809706934379	DEAD-box ATP-dependent RNA helicase 50	0
MELO3C015718	0.00587510034530903	0.0427809706934379	ATP binding protein	1
MELO3C018802	0.00587443787186281	0.0427809706934379	Peroxisome biogenesis protein 22	0
MELO3C012708	0.00588417269765351	0.042817437953559	Pentatricopeptide repeat-containing protein	0
MELO3C004011	0.00590548212715403	0.0429352413293379	No data found	0
MELO3C006191	0.00590581813556534	0.0429352413293379	Katanin p80 WD40 repeat-containing subunit B1 homolog	0
MELO3C010772	0.00590688392788552	0.0429352413293379	clathrin interactor EPSIN 1	1
MELO3C009201	0.00591891723251758	0.0429423338585641	Immediate early response 3-interacting protein 1	0
MELO3C006188	0.00592525493769747	0.0429423338585641	ATP-dependent DNA helicase 2 subunit KU80	0
MELO3C013243	0.00591825048021155	0.0429423338585641	TOM1-like protein 2	1
MELO3C016108	0.0059234494023328	0.0429423338585641	Receptor-like protein kinase	0
MELO3C008056	0.0059159671652691	0.0429423338585641	NAC domain-containing protein 82	1
MELO3C019145	0.00591396721573012	0.0429423338585641	ER membrane protein complex subunit 8/9 homolog	0
MELO3C002690	0.00591329059347701	0.0429423338585641	Myosin heavy chain kinase B	0
MELO3C003396	0.00592368884294037	0.0429423338585641	Phospholipid hydroperoxide glutathione peroxidase	0
MELO3C010378	0.00592824461531416	0.0429482402449888	No data found	1
MELO3C024777	0.00593479565849098	0.0429799337952102	ABC transporter B family protein	0
MELO3C009446	0.00593804692995192	0.0429877158429694	Serine/threonine-protein phosphatase PP1	0
MELO3C026748	0.0059455675826553	0.043026388490238	Enolase	0
MELO3C014562	0.00599556157265702	0.0433154505707741	E3 ubiquitin-protein ligase ICP0	1
MELO3C003917	0.00599045408550714	0.0433154505707741	Heat shock 70 kDa protein	1
MELO3C016296	0.00599404152910388	0.0433154505707741	Chlororespiratory reduction31	1
MELO3C002981	0.00599647789055124	0.0433154505707741	transmembrane emp24 domain-containing protein p24delta9-like	1
MELO3C012239	0.00599508591673292	0.0433154505707741	Bowman-Birk type bran trypsin inhibitor	0
MELO3C018576	0.006001066828351	0.0433327491016833	L-galactose dehydrogenase	1
MELO3C007947	0.00601022964576781	0.0433812098520652	Ankyrin repeat domain-containing protein, chloroplastic	1
MELO3C000960	0.00601217131829979	0.0433812098520652	Peptidase_M22 domain-containing protein	0
MELO3C012636	0.00604022024987105	0.0435676806846981	Unknown protein	0
MELO3C007305	0.00604570718491382	0.0435754274433807	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-like protein	0
MELO3C002619	0.00604427870695745	0.0435754274433807	Mitochondrial carrier protein, expressed	1
MELO3C017434	0.00605024264847209	0.0435922079768973	Oxysterol-binding protein-related protein 4C	0
MELO3C024960	0.00605807790577961	0.0436165607897204	pentatricopeptide repeat-containing protein At5g66520-like	1
MELO3C011968	0.00606024825596196	0.0436165607897204	Lipase	0
MELO3C020484	0.0060595841623905	0.0436165607897204	B3 domain-containing transcription repressor VAL2-like isoform X1	0
MELO3C019453	0.00606717259072709	0.0436504887046518	Unknown protein	0
MELO3C004524	0.00608588071467309	0.0437596014526496	zinc finger CCCH domain-containing protein 39-like	1
MELO3C012929	0.00608677022585591	0.0437596014526496	Transmembrane protein, putative	0
MELO3C021977	0.00610215935596248	0.0438073774112173	Translation factor GUF1 homolog, mitochondrial	0
MELO3C005419	0.00610228848337935	0.0438073774112173	AT-hook motif nuclear-localized protein 6-like	0
MELO3C008275	0.00609738000015136	0.0438073774112173	Translation initiation factor 2 subunit gamma	0
MELO3C018119	0.00610157934889466	0.0438073774112173	CRS2-associated factor 2, mitochondrial	0
MELO3C012855	0.00610856561304385	0.043836505193315	Thioredoxin family protein	0
MELO3C018729	0.00611147585383698	0.0438414590037873	F21O3.6 protein	0
MELO3C004028	0.0061196128433687	0.0438679615403588	Syntaxin/T-SNARE family protein	0
MELO3C024761	0.00611839938520808	0.0438679615403588	GDSL esterase/lipase At2g30310-like	1

MELO3C024178	0.00612424666004419	0.0438852493792499	Histidine--tRNA ligase	0
MELO3C023608	0.00613091710727787	0.0439171135116542	Zinc finger family protein	0
MELO3C025210	0.00613790062530528	0.0439352662012157	gibberellin 2-beta-dioxygenase 2-like	1
MELO3C021934	0.00613720039845989	0.0439352662012157	Unknown protein	0
MELO3C006919	0.00614558306381441	0.0439743188142285	cleavage and polyadenylation specificity factor subunit 2	0
MELO3C018549	0.0061508796175187	0.0439962772786588	DUF21 domain-containing protein	1
MELO3C002746	0.00616727372711723	0.0440975701798835	Pyruvate dehydrogenase E1 component subunit beta	0
MELO3C011357	0.00619072089896822	0.0442492026904536	serine/arginine-rich splicing factor SC35-like	1
MELO3C024739	0.00619905310426472	0.0442927278423024	growth-regulating factor 4-like	1
MELO3C014540	0.00620616913018546	0.0443275349555272	blue copper protein-like	1
MELO3C002036	0.00622651950250241	0.0444568089858714	DUF1118-domain-containing protein	0
MELO3C016913	0.0062308640362656	0.0444628643048621	No data found	1
MELO3C007762	0.00623705673597619	0.0444628643048621	Mediator of RNA polymerase II transcription subunit 26, putative	0
MELO3C021058	0.00623574434668006	0.0444628643048621	cell division control protein 45 homolog	0
MELO3C015155	0.00623862458801827	0.0444628643048621	Scarecrow-like 3	0
MELO3C010763	0.00623461804273584	0.0444628643048621	vacuolar-processing enzyme-like	1
MELO3C027004	0.00624716628925381	0.0445033742420186	poly(A)-specific ribonuclease PARN-like	0
MELO3C026199	0.0062499307886954	0.0445033742420186	Transmembrane protein, putative	1
MELO3C018765	0.00625106892234339	0.0445033742420186	AT4g28240/F26K10_120	0
MELO3C003173	0.00627159763267748	0.0446281016666281	Proteasome subunit alpha type	1
MELO3C011375	0.00627310801694059	0.0446281016666281	BPS1-like protein	1
MELO3C022302	0.00627652237112752	0.044636312678213	protein LHY-like isoform X1	0
MELO3C020793	0.00628178082278441	0.0446576275986931	Amidase, putative	0
MELO3C008503	0.00629332806158112	0.0447075308950235	Protein ABIL2	1
MELO3C012054	0.00629326949914211	0.0447075308950235	Glycine-rich protein	0
MELO3C013884	0.00630182195868945	0.0447517734132175	E3 ubiquitin-protein ligase LAP	0
MELO3C024563	0.00631506277400962	0.0448296817842976	O-linked N-acetylglucosamine transferase, putative	0
MELO3C014872	0.00632247490555671	0.0448500563612929	Lipase	0
MELO3C007513	0.00632190735505112	0.0448500563612929	No data found	0
MELO3C005964	0.00632905007685847	0.044880578085414	Late cornified envelope protein 1E	1
MELO3C013087	0.00633709589246012	0.0449215027926041	5'/3'-nucleotidase SurE	0
MELO3C012701	0.00636922311907195	0.0451003657442134	Cysteine proteinase inhibitor	0
MELO3C018356	0.00636756099341584	0.0451003657442134	Protein WVD2-like 7	0
MELO3C021329	0.00636951373363392	0.0451003657442134	ATP-binding cassette sub-family C member 11	0
MELO3C021253	0.00637146288046764	0.0451003657442134	Beta-glucosidase	1
MELO3C026388	0.00637537403507316	0.0451026197189537	N-acetyl-D-glucosamine kinase-like	0
MELO3C010153	0.00637634889135241	0.0451026197189537	CTP-dependent diacylglycerol kinase 1	0
MELO3C007784	0.00638303272564489	0.0451337319365417	Unknown protein	1
MELO3C009381	0.00639888795602483	0.0452296486197332	splicing factor 3A subunit 2	0
MELO3C016674	0.00642353608518753	0.0453713927562119	cyclin-SDS-like isoform X1	0
MELO3C018174	0.00642233138082371	0.0453713927562119	zinc finger protein CONSTANS-LIKE 4	0
MELO3C004357	0.00642826459136869	0.0453852268631873	No data found	0
MELO3C016498	0.00643136952453571	0.0453852268631873	MACPF domain-containing protein At4g24290	1
MELO3C018412	0.00643238898121734	0.0453852268631873	allene oxide synthase 3-like	0
MELO3C016846	0.00644461626837156	0.0454066095911773	Phosphoribosyl-AMP cyclohydrolase	1
MELO3C025627	0.00644076471782506	0.0454066095911773	Sodium/calcium exchanger family protein	0
MELO3C025613	0.00644431749613228	0.0454066095911773	Tyrosine aminotransferase	0
MELO3C022004	0.00644429970006122	0.0454066095911773	SPX domain protein	1
MELO3C006050	0.00644986291475913	0.0454115548155478	Phosphatidylinositol-4-phosphate 5-kinase family protein	1
MELO3C006253	0.00646031208615239	0.0454115548155478	protein ECERIFERUM 1-like	0
MELO3C010427	0.00645475405348239	0.0454115548155478	aspartate-semialdehyde dehydrogenase	1
MELO3C010381	0.00645743435607238	0.0454115548155478	2-hydroxyacyl-CoA lyase	1
MELO3C016083	0.00645283144289732	0.0454115548155478	Ubiquitin	1
MELO3C002209	0.00645126342186264	0.0454115548155478	Homeobox leucine zipper family protein	1
MELO3C003341	0.00646141419979185	0.0454115548155478	Casein kinase II subunit beta	0
MELO3C009195	0.00646569829267873	0.0454150041623959	OTU domain-containing protein	0
MELO3C014214	0.00646880382342496	0.0454150041623959	ABC transporter G family-like protein	0
MELO3C010810	0.00646732888793111	0.0454150041623959	Sigma factor sigb regulation protein rsbq	0
MELO3C013814	0.00648131394496065	0.0454866627928315	26S proteasome non-ATPase regulatory subunit 13	0
MELO3C002275	0.00649370496098678	0.0455574349110223	anthranilate phosphoribosyltransferase, chloroplastic	0
MELO3C022225	0.00649818775899091	0.0455726953310765	protein NRT1/ PTR FAMILY 5.10-like	1
MELO3C004648	0.00650643547640417	0.045614339447464	Stress-response A/B barrel domain-containing protein UP3	0
MELO3C014127	0.00651810160220068	0.0456522271398093	Actin-related protein 8	0
MELO3C013774	0.00651526241483036	0.0456522271398093	Cystathionine gamma-synthase	0
MELO3C010338	0.00651877464855244	0.0456522271398093	Outward-rectifying potassium channel 4-like protein	1
MELO3C017394	0.00652352679417967	0.0456578253063655	No data found	0
MELO3C011399	0.00652419783353908	0.0456578253063655	LOW QUALITY PROTEIN: transcription factor BIM2	0
MELO3C009480	0.00653901503596366	0.0457291104621977	ABC transporter family protein	1

MELO3C009226	0.00653689188363704	0.0457291104621977	serine/threonine-protein kinase ATG1c	0
MELO3C006727	0.00654713755056613	0.0457697060127895	Neutral/alkaline invertase	0
MELO3C014592	0.00655080438696443	0.0457791351161219	heterogeneous nuclear ribonucleoprotein F	0
MELO3C025386	0.00655608608069769	0.04579983870099	Polyadenylate-binding protein-interacting protein 4	0
MELO3C002931	0.00656237554505812	0.0458275652897287	Paired amphipathic helix SIN3-like protein	1
MELO3C003629	0.00657160924631839	0.0458729395477752	Plasma membrane ATPase	0
MELO3C025085	0.00657351860449662	0.0458729395477752	Class I heat shock protein	0
MELO3C017111	0.00658733845633164	0.0459531427672531	39S ribosomal protein L47, mitochondrial	0
MELO3C000210	0.00659371367780071	0.0459813740900022	Unknown protein	0
MELO3C002863	0.00659694398511679	0.0459876621115677	patellin-4	0
MELO3C010710	0.00660311013512804	0.046014404396134	Short-chain dehydrogenase/reductase	0
MELO3C006770	0.00661343968116468	0.0460196052035173	At1g08580	0
MELO3C014101	0.00661437329406644	0.0460196052035173	Unknown protein	0
MELO3C005578	0.00660977458179657	0.0460196052035173	Amine oxidase	1
MELO3C020940	0.00661550757875262	0.0460196052035173	Pentatricopeptide repeat-containing family protein	0
MELO3C011317	0.00660728708017455	0.0460196052035173	zinc finger protein CONSTANS-LIKE 4	0
MELO3C003039	0.00663998790077891	0.0461736341734094	No data found	1
MELO3C023313	0.00665769860589904	0.0462804962224218	Transmembrane protein, putative	0
MELO3C002412	0.00666469864478825	0.0463128548683755	Ankyrin repeat family protein	0
MELO3C021730	0.00666911679857307	0.0463272555944494	calcium permeable stress-gated cation channel 1-like	0
MELO3C007344	0.0066785985161617	0.0463768080505195	No data found	1
MELO3C019691	0.00668174178677394	0.0463823263785584	Hexosyltransferase	1
MELO3C023315	0.00668561297068715	0.0463928919740339	diaminopimelate decarboxylase 2, chloroplastic-like	0
MELO3C010430	0.00670618584904936	0.0465193060529947	At1g78110	0
MELO3C010243	0.00671615745963616	0.046572118564029	VAMP-like protein YKT61	1
MELO3C016714	0.00672515339221591	0.0466181306924788	protochlorophyllide reductase, chloroplastic	0
MELO3C024515	0.00672876682696899	0.0466268126546704	splicing factor U2af small subunit B-like	0
MELO3C002102	0.00673479236241348	0.046652197251948	Receptor-like kinase	0
MELO3C006703	0.00674630940843268	0.0467155906406511	CoA ligase	0
MELO3C005600	0.0067735201512592	0.046871202383288	Phosphate translocator-related family protein	0
MELO3C022928	0.00677352836102607	0.046871202383288	No data found	0
MELO3C015597	0.00677974577639429	0.0468813723172307	Calcium ion binding	0
MELO3C018604	0.00677908066685062	0.0468813723172307	Ubiquitin-like-specific protease 2	0
MELO3C026067	0.00678676319927907	0.0469134709214429	tRNA (Guanine(9)-N1)-methyltransferase-like	0
MELO3C007325	0.00679902181931435	0.046981764139132	Sugar transporter, putative	0
MELO3C023845	0.00680785721675858	0.0470263631247867	serine/arginine-rich SC35-like splicing factor SCL30	0
MELO3C018418	0.00681891427759185	0.0470862720518047	No data found	0
MELO3C010532	0.00684685289919851	0.0472626696631497	Structural constituent of ribosome, putative	0
MELO3C026628	0.00686069658808242	0.0473416830601117	Zinc finger protein	0
MELO3C022323	0.00686333010384244	0.0473433133848356	proton pump-interactor 1-like	0
MELO3C007871	0.00687289009524761	0.0473761628240995	rRNA adenine N(6)-methyltransferase	0
MELO3C002405	0.00687058154327702	0.0473761628240995	50S ribosomal protein L7/L12	1
MELO3C022636	0.00688113418024483	0.0474164406579397	No data found	0
MELO3C003447	0.00688547634453296	0.04742981246187	Major facilitator superfamily transporter	1
MELO3C015424	0.00690715562065036	0.0475625580028675	Glucan endo-1,3-beta-glucosidase, putative	0
MELO3C016795	0.00692639658527194	0.04767842668614	Clavata3/ESR (CLE) gene family member MtCLE20	1
MELO3C026546	0.00693441822564089	0.0476860043919131	DNA-directed RNA polymerase subunit beta	0
MELO3C014262	0.00696264092237953	0.0476860043919131	60S ribosomal protein L4-like	0
MELO3C020440	0.00696854568206295	0.0476860043919131	UBX domain-containing protein 1	0
MELO3C004152	0.00696272408374665	0.0476860043919131	40S ribosomal protein S23-1	1
MELO3C006100	0.00695734585909258	0.0476860043919131	Ubiquitin-conjugating enzyme, E2	0
MELO3C014870	0.00695033903996145	0.0476860043919131	DSR6	0
MELO3C010475	0.00694843697490344	0.0476860043919131	UDP-glucuronosyltransferase 2B17	0
MELO3C018008	0.0069448281081157	0.0476860043919131	Glycyl-tRNA synthetase beta subunit	1
MELO3C007024	0.00695655689989738	0.0476860043919131	Phenylalanine--tRNA ligase	0
MELO3C025262	0.00696807649833175	0.0476860043919131	AAA+ ATPase domain-containing protein	0
MELO3C003085	0.00696185243230085	0.0476860043919131	Flagellin N-methylase	0
MELO3C022024	0.00693627676482245	0.0476860043919131	Hexosyltransferase	0
MELO3C020840	0.00696181741775093	0.0476860043919131	Formin-like protein	0
MELO3C025883	0.00696229192516018	0.0476860043919131	Gb|AAC95187.1	0
MELO3C025870	0.0069539047423004	0.0476860043919131	Transcription factor	0
MELO3C002552	0.00693441431194941	0.0476860043919131	Wound-responsive family protein	0
MELO3C008234	0.00696379313695883	0.0476860043919131	Transferring glycosyl group transferase	0
MELO3C005532	0.00697466168591299	0.0477113244319694	Pectinesterase	1
MELO3C021323	0.00699292881807612	0.0478197199543578	condensin-2 complex subunit D3	0
MELO3C011016	0.00701159249660366	0.0479307511995243	tubulin beta chain	1
MELO3C011386	0.00701788286723926	0.0479571518149163	DNA gyrase subunit A	1
MELO3C010709	0.0070296723169897	0.048021099477077	telomere-associated protein RIF1-like isoform X2	1

MELO3C026341	0.00704211024903056	0.0480894312960251	ubiquitin-conjugating enzyme E2 22	0
MELO3C006306	0.00704624370381213	0.048101025546694	beta-mannosyltransferase 1	0
MELO3C024211	0.00708416893756425	0.0483432109011598	BTB/POZ domain-containing protein At5g48130	1
MELO3C021434	0.00709534752098828	0.0484027696690838	DNA polymerase epsilon catalytic subunit A	0
MELO3C022219	0.00711140982249026	0.0484955913620028	SPla/RYanodine receptor (SPRY) domain-containing protein	1
MELO3C007597	0.00712542430296725	0.0485743888710046	Indole-3-acetic acid-amido synthetase GH3.3	0
MELO3C017791	0.00713147184175345	0.048598839683502	No data found	0
MELO3C008811	0.007139438811121	0.0486363494587198	importin-5	1
MELO3C024179	0.00715903843773669	0.0487239522278649	zinc finger protein CONSTANS-LIKE 9-like	0
MELO3C018056	0.00715686435559881	0.0487239522278649	Carbonic anhydrase	0
MELO3C011234	0.00715969969949182	0.0487239522278649	GTP-binding nuclear protein	1
MELO3C024853	0.00717709886898354	0.0488182782776459	GTP-binding protein, chloroplastic	0
MELO3C018841	0.00717850423405153	0.0488182782776459	Beta-adaptin-like protein	1
MELO3C022802	0.00718337005107827	0.0488345525434578	Sulfate transporter, putative	0
MELO3C009638	0.00720397515405002	0.0488443099327942	UBP1-associated protein 2C-like	0
MELO3C014057	0.00719121069185757	0.0488443099327942	Plant UBX domain-containing protein 8	0
MELO3C017745	0.00720673118743775	0.0488443099327942	F12F1.11	0
MELO3C014215	0.00719953826615072	0.0488443099327942	No data found	1
MELO3C003108	0.00720218464493627	0.0488443099327942	Histone H2A	0
MELO3C025150	0.00720791735611159	0.0488443099327942	No data found	0
MELO3C021391	0.00719687947412662	0.0488443099327942	Protein ABCI12, chloroplastic	0
MELO3C021274	0.00720832830460949	0.0488443099327942	Outer envelope pore protein 16-2, chloroplastic	0
MELO3C018769	0.00720953787301104	0.0488443099327942	Wound-responsive family protein	1
MELO3C012904	0.00719324434856972	0.0488443099327942	Autophagy-related protein 9	0
MELO3C019780	0.00721681585490708	0.0488768505893552	protein kinase 2B, chloroplastic-like	1
MELO3C010939	0.00722100799204228	0.0488884768031687	FK506-binding protein 4-like	0
MELO3C026824	0.00723804249067217	0.048987012045334	cytochrome P450 714A1-like	0
MELO3C021328	0.00724702951271161	0.0490182548751763	ubiquitin-like-specific protease ESD4	0
MELO3C022348	0.00724762287890601	0.0490182548751763	Protein TIFY 9	1
MELO3C004223	0.00725452501643375	0.0490313533708249	ATP-dependent Clp protease proteolytic subunit	0
MELO3C017562	0.00725386990279486	0.0490313533708249	Random slug protein 5	0
MELO3C008420	0.0072686274147804	0.0491098606960309	Transcriptional corepressor SEUSS	0
MELO3C009316	0.0072779413909807	0.0491559728216409	Interactor of constitutive active ROPs-like protein	0
MELO3C013370	0.00728490803364623	0.0491862047030699	translocase of chloroplast 120, chloroplastic-like	1
MELO3C021385	0.00728849085706462	0.0491935768749724	Phosphatase 2C family protein	1
MELO3C009552	0.00729901228807617	0.0491973357260124	Mads box protein, putative	1
MELO3C020458	0.00729730268308693	0.0491973357260124	cyclin-dependent kinase inhibitor 5-like	1
MELO3C016448	0.00729807390629156	0.0491973357260124	methionine S-methyltransferase	0
MELO3C019257	0.00729310653565496	0.0491973357260124	CDT1-like protein a, chloroplastic	0
MELO3C005288	0.00730395227585312	0.0492138360613522	F-box family protein	0
MELO3C018966	0.00730701020630065	0.0492176482142672	ATP-dependent 6-phosphofructokinase	1
MELO3C006035	0.00731675729151005	0.0492664983805087	Rhodanese-like domain-containing protein 4, chloroplastic	0
MELO3C004603	0.00732905066766798	0.0492894286514099	Protein-tyrosine phosphatase mitochondrial 1	1
MELO3C012007	0.00732642441238118	0.0492894286514099	spermidine synthase	0
MELO3C025324	0.00732887618986666	0.0492894286514099	Leucine-rich repeat extensin-like protein 4	1
MELO3C010766	0.00733014592886683	0.0492894286514099	UPF0587 protein C1orf123 homolog	0
MELO3C019260	0.00733326272891488	0.0492936030065827	Glutamate receptor	0
MELO3C017705	0.00734710733815036	0.0493698614566626	Transducin/WD40 repeat-like superfamily protein	0
MELO3C012421	0.0073514013120205	0.0493819130990112	Cytochrome c oxidase assembly protein COX16	0
MELO3C010584	0.00736507254652774	0.0494569254407944	ribosome maturation protein SBDS	0
MELO3C002071	0.00737535584584981	0.0495091443234833	single-stranded DNA-binding protein, mitochondrial	1
MELO3C005980	0.00738295761679109	0.0495433333245012	Protein ARABIDILLO 1	0
MELO3C020839	0.00739116720083399	0.0495801838855691	glutamine--tRNA ligase-like	0
MELO3C026554	0.00739347012 7247	0.0495801838855691	alcohol dehydrogenase-like 7	1
MELO3C008219	0.0074119726130466	0.0496873887084377	glyceraldehyde-3-phosphate dehydrogenase	1
MELO3C004992	0.00742737438247398	0.049773741662531	Protein nuclear fusion defective 4	1
MELO3C008610	0.00743112678605029	0.0497819955555316	No data found	0
MELO3C012753	0.00743754746958103	0.0497952801713388	Unknown protein	1
MELO3C021306	0.00743815264091596	0.0497952801713388	ethylene-responsive transcription factor RAP2-3-like	0
MELO3C017009	0.00744176012404185	0.0498025485224339	4-coumarate--CoA ligase family protein	0
MELO3C007097	0.00744929403958527	0.0498360799416564	F-box protein SKIP19	1
MELO3C022759	0.00746050443032131	0.0498941760902186	MOB kinase activator-like 1A	0
MELO3C016549	0.00746559537964697	0.0499113213109844	U3 small nucleolar RNA-associated protein 14 B isoform 3	0

Supplementary Table 1.B Gene Ontology terms (GO terms) of the cluster 1.1 obtained considering the comparison between lines over time fruit during storage at 20.5°C and 88% relative humidity for 18 d the near-isogenic line SC10-2 and its parental ''Piel de Sapo'' obtained according to the differentially expressed gene pattern (Supl. Table 1.A)

Tags	GO ID	GO Name	GO Category	FDR	P-Value	Nr Test	Nr Reference	Non Annot Test	Non Annot Reference	TestSet Sequences	RefSet Sequences
[OVER]	GO:0003735	structural constituent of ribosome	MOLECULAR_FUNCTION	4.094870144646738E-5	1.1921365876400271E-8	14	340	83	16691	MELO3C020906; MELO3C011873; MELO3C017939; MELO3C009315; MELO3C008974; MELO3C021332; MELO3C006507; MELO3C017111; MELO3C015177; MELO3C019524; MELO3C026780; MELO3C017169; MELO3C012967; MELO3C018459	MELO3C011310; MELO3C020704; MELO3C006088; MELO3C002164; MELO3C012084; MELO3C014262; MELO3C024506; MELO3C020945; MELO3C006400; MELO3C003258; MELO3C006766; MELO3C024747; MELO3C020141; MELO3C022441; MELO3C003811; MELO3C001514; MELO3C025276; MELO3C016201; MELO3C025030; MELO3C018985; MELO3C016688; MELO3C014824; MELO3C017659; MELO3C020836; MELO3C007740; MELO3C013981; MELO3C009489;
[OVER]	GO:0006414	translational elongation	BIOLOGICAL_PROCESS	0.0012733706759199884	1.7520976700846581E-6	9	188	88	16843	MELO3C020906; MELO3C011873; MELO3C006507; MELO3C025511; MELO3C017939; MELO3C026780; MELO3C017169; MELO3C012967; MELO3C008974	MELO3C008660; MELO3C015999; MELO3C011276; MELO3C010222; MELO3C006088; MELO3C014262; MELO3C024506; MELO3C006245; MELO3C003258; MELO3C005952; MELO3C022601; MELO3C026403; MELO3C020141; MELO3C022441; MELO3C020023; MELO3C023012; MELO3C010867; MELO3C016201; MELO3C025030; MELO3C018985; MELO3C011956; MELO3C016963; MELO3C014306; MELO3C017659; MELO3C010630; MELO3C007740; MELO3C013981;

[OVER]	GO:0006415	translational termination	BIOLOGICAL_PROCESS	0.004535439996171705	8.640762058752189E-6	8	173	89	16858	MELO3C020906; MELO3C011873; MELO3C006507; MELO3C017939; MELO3C026780; MELO3C017169; MELO3C012967; MELO3C008974	MELO3C015999; MELO3C011276; MELO3C010222; MELO3C006088; MELO3C014262; MELO3C024506; MELO3C006245; MELO3C003258; MELO3C005952; MELO3C022601; MELO3C026403; MELO3C020141; MELO3C022441; MELO3C023012; MELO3C010867; MELO3C016201; MELO3C016049; MELO3C025030; MELO3C011956; MELO3C016963; MELO3C017659; MELO3C013984; MELO3C010630; MELO3C007740; MELO3C013981; MELO3C002294; MELO3C012131;
[OVER]	GO:0022625	cytosolic large ribosomal subunit	CELLULAR_COMPONENT	0.010233764854266155	2.3829681074709507E-5	7	144	90	16887	MELO3C020906; MELO3C011873; MELO3C017939; MELO3C015177; MELO3C017169; MELO3C012967; MELO3C008974	MELO3C015999; MELO3C006088; MELO3C014262; MELO3C024506; MELO3C006245; MELO3C006922; MELO3C005952; MELO3C022601; MELO3C026403; MELO3C022441; MELO3C001514; MELO3C023012; MELO3C016201; MELO3C025030; MELO3C011956; MELO3C017659; MELO3C011285; MELO3C012254; MELO3C002294; MELO3C006412; MELO3C006411; MELO3C005844; MELO3C004995; MELO3C023820; MELO3C005446; MELO3C006657; MELO3C020556;
[OVER]	GO:0022627	cytosolic small ribosomal subunit	CELLULAR_COMPONENT	0.011249454162474009	2.7385419743533255E-5	6	98	91	16933	MELO3C019524; MELO3C026780; MELO3C021332; MELO3C009315; MELO3C006507; MELO3C018459	MELO3C011310; MELO3C003890; MELO3C012084; MELO3C005830; MELO3C020141; MELO3C010867; MELO3C010630; MELO3C013981; MELO3C009489; MELO3C025609; MELO3C023703; MELO3C024359; MELO3C022177; MELO3C024994; MELO3C022691; MELO3C018512; MELO3C024071; MELO3C009490; MELO3C007277; MELO3C005411; MELO3C003352; MELO3C020003; MELO3C023117; MELO3C022027; MELO3C000036; MELO3C000032; MELO3C024684;

[]	GO:0009733	response to auxin	BIOLOGICAL_PROCESS	0.14555473962843424	5.39205745871634E-4	6	173	91	16858	MELO3C008032; MELO3C013566; MELO3C020756; MELO3C027346; MELO3C019649; MELO3C022932	MELO3C015515; MELO3C012125; MELO3C007691; MELO3C014028; MELO3C006760; MELO3C006761; MELO3C021119; MELO3C022688; MELO3C021990; MELO3C003539; MELO3C003538; MELO3C000254; MELO3C026762; MELO3C017134; MELO3C024464; MELO3C016166; MELO3C003938; MELO3C027177; MELO3C016168; MELO3C015871; MELO3C016169; MELO3C015599; MELO3C018988; MELO3C017414; MELO3C017813; MELO3C006371; MELO3C014799;
[]	GO:0016071	mRNA metabolic process	BIOLOGICAL_PROCESS	0.258287212351632	0.0010684114237850173	9	444	88	16587	MELO3C020906; MELO3C011873; MELO3C006507; MELO3C017939; MELO3C026780; MELO3C012967; MELO3C008974; MELO3C016952; MELO3C007190	MELO3C020705; MELO3C004580; MELO3C014262; MELO3C013051; MELO3C002045; MELO3C020824; MELO3C003258; MELO3C007978; MELO3C006767; MELO3C026246; MELO3C017771; MELO3C016201; MELO3C015113; MELO3C025030; MELO3C017775; MELO3C019837; MELO3C017659; MELO3C020836; MELO3C007740; MELO3C002294; MELO3C002173; MELO3C020718; MELO3C006412; MELO3C006411; MELO3C006416; MELO3C005446; MELO3C008956;
[]	GO:0008759	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase activity	MOLECULAR_FUNCTION	0.258287212351632	0.0011135469572003578	2	7	95	17024	MELO3C019524; MELO3C018459	MELO3C012357; MELO3C006726; MELO3C003890; MELO3C005830; MELO3C019490; MELO3C016655; MELO3C016656

[]	GO:0042254	ribosome biogenesis	BIOLOGICAL_PROCESS	0.3609519560299322	0.001642774567028692	6	216	91	16815	MELO3C017169; MELO3C005360; MELO3C021332; MELO3C012967; MELO3C008974; MELO3C017939	MELO3C010584; MELO3C010582; MELO3C013051; MELO3C003135; MELO3C006766; MELO3C020141; MELO3C022441; MELO3C018062; MELO3C023654; MELO3C019034; MELO3C017650; MELO3C016321; MELO3C010355; MELO3C013185; MELO3C025609; MELO3C013183; MELO3C023545; MELO3C023306; MELO3C006657; MELO3C021484; MELO3C009808; MELO3C003946; MELO3C025168; MELO3C015489; MELO3C005096; MELO3C003474; MELO3C008920;
[]	GO:0009245	lipid A biosynthetic process	BIOLOGICAL_PROCESS	0.5020759494333862	0.0027633307970508134	2	12	95	17019	MELO3C019524; MELO3C018459	MELO3C019719; MELO3C012357; MELO3C006726; MELO3C025412; MELO3C017583; MELO3C013155; MELO3C003890; MELO3C007369; MELO3C005830; MELO3C019490; MELO3C016655; MELO3C016656
[]	GO:0004089	carbonate dehydratase activity	MOLECULAR_FUNCTION	0.5558096099709452	0.003176727237344522	2	13	95	17018	MELO3C016817; MELO3C024476	MELO3C009476; MELO3C011095; MELO3C009958; MELO3C007636; MELO3C004920; MELO3C009809; MELO3C004922; MELO3C004925; MELO3C018056; MELO3C025057; MELO3C004915; MELO3C026330; MELO3C011997
[]	GO:0004655	porphobilinogen synthase activity	MOLECULAR_FUNCTION	0.8493064359928953	0.005663241476243904	1	0	96	17031	MELO3C008086	
[]	GO:0032791	lead ion binding	MOLECULAR_FUNCTION	0.8493064359928953	0.005663241476243904	1	0	96	17031	MELO3C008086	
[]	GO:0050178	phenylpyruvate tautomerase activity	MOLECULAR_FUNCTION	0.8493064359928953	0.005663241476243904	1	0	96	17031	MELO3C026027	
[]	GO:0006954	inflammatory response	BIOLOGICAL_PROCESS	1.0	0.03350680336738886	1	5	96	17026	MELO3C026027	MELO3C026028; MELO3C015103; MELO3C017426; MELO3C018756; MELO3C022821
[]	GO:0046740	transport of virus in host, cell to cell	BIOLOGICAL_PROCESS	1.0	0.011294739437078653	1	1	96	17030	MELO3C016952	MELO3C010207
[]	GO:0048767	root hair elongation	BIOLOGICAL_PROCESS	1.0	0.04984107676659685	1	8	96	17023	MELO3C008032	MELO3C006684; MELO3C023264; MELO3C002781; MELO3C026629; MELO3C021704; MELO3C015501; MELO3C019823; MELO3C018182
[]	GO:0010120	camalexin biosynthetic process	BIOLOGICAL_PROCESS	1.0	0.011294739437078653	1	1	96	17030	MELO3C009127	MELO3C020718

[]	GO:0060548	negative regulation of cell death	BIOLOGICAL_PROCESS	1.0	0.021532204623148688	2	38	95	16993	MELO3C003911; MELO3C017623	MELO3C002481; MELO3C011470; MELO3C006121; MELO3C003331; MELO3C007237; MELO3C003332; MELO3C005976; MELO3C004622; MELO3C025417; MELO3C022346; MELO3C005757; MELO3C025413; MELO3C016083; MELO3C005912; MELO3C025752; MELO3C021057; MELO3C023972; MELO3C009939; MELO3C004827; MELO3C024340; MELO3C025355; MELO3C005718; MELO3C011710; MELO3C013522; MELO3C011983; MELO3C012376; MELO3C011021;
[]	GO:0009641	shade avoidance	BIOLOGICAL_PROCESS	1.0	0.028000528254957892	1	4	96	17027	MELO3C025152	MELO3C015549; MELO3C019731; MELO3C016115; MELO3C013923
[]	GO:0042742	defense response to bacterium	BIOLOGICAL_PROCESS	1.0	0.010560261351637559	3	77	94	16954	MELO3C025152; MELO3C006035; MELO3C009127	MELO3C021918; MELO3C006046; MELO3C014386; MELO3C004385; MELO3C002120; MELO3C004387; MELO3C004386; MELO3C005674; MELO3C009633; MELO3C009952; MELO3C003137; MELO3C023217; MELO3C026722; MELO3C003536; MELO3C004867; MELO3C023453; MELO3C021553; MELO3C025076; MELO3C014706; MELO3C011997; MELO3C016008; MELO3C013811; MELO3C013621; MELO3C016939; MELO3C014230; MELO3C020235; MELO3C014391;
[]	GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	BIOLOGICAL_PROCESS	1.0	0.028000528254957892	1	4	96	17027	MELO3C025152	MELO3C015764; MELO3C016791; MELO3C002401; MELO3C010832
[]	GO:0043966	histone H3 acetylation	BIOLOGICAL_PROCESS	1.0	0.011294739437078653	1	1	96	17030	MELO3C014503	MELO3C015732
[]	GO:0009625	response to insect	BIOLOGICAL_PROCESS	1.0	0.011294739437078653	1	1	96	17030	MELO3C025152	MELO3C003906
[]	GO:0070370	cellular heat acclimation	BIOLOGICAL_PROCESS	1.0	0.01689466996843291	1	2	96	17029	MELO3C009127	MELO3C025686; MELO3C016019

[]	GO:0010200	response to chitin	BIOLOGICAL_PROCESS	1.0	0.032608717776354594	2	48	95	16983	MELO3C006891; MELO3C009127	MELO3C013454; MELO3C007030; MELO3C004286; MELO3C009376; MELO3C021416; MELO3C006300; MELO3C024989; MELO3C002644; MELO3C005639; MELO3C019231; MELO3C004627; MELO3C026740; MELO3C016285; MELO3C010748; MELO3C013679; MELO3C004093; MELO3C006431; MELO3C013287; MELO3C008014; MELO3C016819; MELO3C020718; MELO3C005466; MELO3C022715; MELO3C005465; MELO3C007444; MELO3C025904; MELO3C020971;
[]	GO:0004781	sulfate adenylyltransferase (ATP) activity	MOLECULAR_FUNCTION	1.0	0.04984107676659685	1	8	96	17023	MELO3C025511	MELO3C006493; MELO3C002118; MELO3C025510; MELO3C002878; MELO3C026259; MELO3C003637; MELO3C003762; MELO3C014280
[]	GO:0004491	methylmalonate-semialdehyde dehydrogenase (acylating) activity	MOLECULAR_FUNCTION	1.0	0.01689466996843291	1	2	96	17029	MELO3C014951	MELO3C018583; MELO3C007705
[]	GO:0004591	oxoglutarate dehydrogenase (succinyl-transferring) activity	MOLECULAR_FUNCTION	1.0	0.011294739437078653	1	1	96	17030	MELO3C023844	MELO3C025454
[]	GO:0030337	DNA polymerase processivity factor activity	MOLECULAR_FUNCTION	1.0	0.011294739437078653	1	1	96	17030	MELO3C025142	MELO3C025879
[]	GO:0043565	sequence-specific DNA binding	MOLECULAR_FUNCTION	1.0	0.03907799114803682	5	324	92	16707	MELO3C009127; MELO3C023350; MELO3C020489; MELO3C006891; MELO3C014503	MELO3C011432; MELO3C010223; MELO3C011550; MELO3C005791; MELO3C014384; MELO3C024507; MELO3C008942; MELO3C013173; MELO3C022209; MELO3C001991; MELO3C025714; MELO3C007736; MELO3C006887; MELO3C022205; MELO3C002723; MELO3C025951; MELO3C020145; MELO3C018187; MELO3C017415; MELO3C019715; MELO3C007181; MELO3C023092; MELO3C011797; MELO3C015239; MELO3C017429; MELO3C003140; MELO3C002050;

[]	GO:0003743	translation initiation factor activity	MOLECULAR_FUNCTION	1.0	0.024004543271709398	3	106	94	16925	MELO3C016952; MELO3C010197; MELO3C001947	MELO3C010981; MELO3C010222; MELO3C020828; MELO3C004345; MELO3C004344; MELO3C020786; MELO3C023779; MELO3C020380; MELO3C000253; MELO3C019434; MELO3C014706; MELO3C016963; MELO3C012127; MELO3C017707; MELO3C011321; MELO3C006494; MELO3C014155; MELO3C012131; MELO3C002698; MELO3C023701; MELO3C015360; MELO3C018872; MELO3C018874; MELO3C014439; MELO3C011371; MELO3C006107; MELO3C002822;
[]	GO:0005262	calcium channel activity	MOLECULAR_FUNCTION	1.0	0.028000528254957892	1	4	96	17027	MELO3C016817	MELO3C017043; MELO3C022020; MELO3C018734; MELO3C007977
[]	GO:0043626	PCNA complex	CELLULAR_COMPONENT	1.0	0.011294739437078653	1	1	96	17030	MELO3C025142	MELO3C025879
[]	GO:0043189	H4/H2A histone acetyltransferase complex	CELLULAR_COMPONENT	1.0	0.038982205775400985	1	6	96	17025	MELO3C012147	MELO3C007015; MELO3C007903; MELO3C007894; MELO3C015904; MELO3C007648; MELO3C015732
[]	GO:0019005	SCF ubiquitin ligase complex	CELLULAR_COMPONENT	1.0	0.04984107676659685	1	8	96	17023	MELO3C025152	MELO3C025964; MELO3C016791; MELO3C015782; MELO3C006795; MELO3C012407; MELO3C015764; MELO3C015898; MELO3C010832
[]	GO:0005762	mitochondrial large ribosomal subunit	CELLULAR_COMPONENT	1.0	0.04442690678904297	1	7	96	17024	MELO3C017111	MELO3C022485; MELO3C017759; MELO3C013984; MELO3C023395; MELO3C012254; MELO3C014694; MELO3C006088
[]	GO:0005671	Ada2/Gcn5/Ada3 transcription activator complex	CELLULAR_COMPONENT	1.0	0.011294739437078653	1	1	96	17030	MELO3C014503	MELO3C007015
[]	GO:0016281	eukaryotic translation initiation factor 4F complex	CELLULAR_COMPONENT	1.0	0.01689466996843291	1	2	96	17029	MELO3C016952	MELO3C026612; MELO3C010207

Supplementary Table 1.C Gene Ontology terms (GO terms) of the cluster 1.2 obtained considering the comparison between lines over time fruit during storage at 20.5°C and 88% relative humidity for 18 d the near-isogenic line SC10-2 and its parental ''Piel de Sapo'' obtained according to the differentially expressed gene pattern (Supl. Table 1.A)

Tags	GO ID	GO Name	GO Category	FDR	P-Value	Nr Test	Nr Reference	Non Annot Test	Non Annot Reference	TestSet Sequences	RefSet Sequences
[OVER]	GO:0006414	translational elongation	BIOLOGICAL_PROCESS	1.3708907166724634E-15	6.524615516124876E-19	46	151	809	16122	MELO3C015999; MELO3C014262; MELO3C020049; MELO3C021339; MELO3C009338; MELO3C020003; MELO3C005952; MELO3C004645; MELO3C007635; MELO3C021436; MELO3C026403; MELO3C016083; MELO3C025753; MELO3C024244; MELO3C017993; MELO3C015431; MELO3C018985; MELO3C019979; MELO3C017659; MELO3C019907; MELO3C010630; MELO3C013245; MELO3C013981; MELO3C005089; MELO3C012670; MELO3C012131; MELO3C006412;	MELO3C008660; MELO3C011276; MELO3C010222; MELO3C017939; MELO3C006088; MELO3C024506; MELO3C006245; MELO3C003258; MELO3C022601; MELO3C020141; MELO3C022441; MELO3C020023; MELO3C023012; MELO3C010867; MELO3C016201; MELO3C025030; MELO3C011956; MELO3C016963; MELO3C014306; MELO3C007740; MELO3C002294; MELO3C005565; MELO3C023703; MELO3C006411; MELO3C005844; MELO3C023820; MELO3C020556;
[OVER]	GO:0006415	translational termination	BIOLOGICAL_PROCESS	1.3708907166724634E-15	7.254925469265789E-19	44	137	811	16136	MELO3C015999; MELO3C014262; MELO3C020049; MELO3C021339; MELO3C009338; MELO3C020003; MELO3C005952; MELO3C004645; MELO3C007635; MELO3C021436; MELO3C026403; MELO3C016083; MELO3C024244; MELO3C017993; MELO3C015431; MELO3C019979; MELO3C017659; MELO3C019907; MELO3C010630; MELO3C013245; MELO3C013981; MELO3C005089; MELO3C012670; MELO3C012131; MELO3C006412; MELO3C006314; MELO3C011040;	MELO3C011276; MELO3C010222; MELO3C017939; MELO3C006088; MELO3C024506; MELO3C006245; MELO3C003258; MELO3C022601; MELO3C020141; MELO3C022441; MELO3C023012; MELO3C010867; MELO3C016201; MELO3C016049; MELO3C025030; MELO3C011956; MELO3C016963; MELO3C013984; MELO3C007740; MELO3C002294; MELO3C023703; MELO3C006411; MELO3C014391; MELO3C005844; MELO3C023820; MELO3C020556; MELO3C022177;

[OVER]	GO:0003735	structural constituent of ribosome	MOLECULAR_FUNCTION	6.244379144367021E-13	8.464621208697664E-16	58	296	797	15977	MELO3C015999; MELO3C012084; MELO3C014262; MELO3C005952; MELO3C022766; MELO3C021436; MELO3C026403; MELO3C004505; MELO3C002405; MELO3C005759; MELO3C015431; MELO3C018985; MELO3C017659; MELO3C010630; MELO3C013981; MELO3C009489; MELO3C011285; MELO3C005089; MELO3C006412; MELO3C011040; MELO3C005520; MELO3C009600; MELO3C019490; MELO3C005446; MELO3C022497; MELO3C004713; MELO3C011847;	MELO3C011310; MELO3C020704; MELO3C006088; MELO3C002164; MELO3C024506; MELO3C020945; MELO3C006400; MELO3C003258; MELO3C006766; MELO3C024747; MELO3C020141; MELO3C022441; MELO3C003811; MELO3C001514; MELO3C025276; MELO3C016201; MELO3C025030; MELO3C016688; MELO3C014824; MELO3C020836; MELO3C007740; MELO3C002294; MELO3C025609; MELO3C006411; MELO3C007869; MELO3C023788; MELO3C025845;
[OVER]	GO:0022625	cytosolic large ribosomal subunit	CELLULAR_COMPONENT	5.6876240344621164E-9	1.324383242571619E-11	31	120	824	16153	MELO3C015999; MELO3C014262; MELO3C021339; MELO3C009338; MELO3C005952; MELO3C007635; MELO3C020369; MELO3C021436; MELO3C026403; MELO3C022386; MELO3C016083; MELO3C024244; MELO3C017659; MELO3C011285; MELO3C006412; MELO3C006314; MELO3C005520; MELO3C009600; MELO3C021429; MELO3C005446; MELO3C023525; MELO3C023201; MELO3C024850; MELO3C004713; MELO3C004616; MELO3C016198; MELO3C002719;	MELO3C017939; MELO3C006088; MELO3C024506; MELO3C006245; MELO3C006922; MELO3C022601; MELO3C022441; MELO3C001514; MELO3C023012; MELO3C016201; MELO3C025030; MELO3C011956; MELO3C012254; MELO3C002294; MELO3C006411; MELO3C005844; MELO3C004995; MELO3C023820; MELO3C006657; MELO3C020556; MELO3C025168; MELO3C000241; MELO3C023260; MELO3C011448; MELO3C016459; MELO3C011720; MELO3C002668;
[OVER]	GO:0006270	DNA replication initiation	BIOLOGICAL_PROCESS	1.5554343735842954E-8	4.230010148584021E-11	11	6	844	16267	MELO3C010882; MELO3C020860; MELO3C021058; MELO3C015926; MELO3C007144; MELO3C006995; MELO3C022319; MELO3C027184; MELO3C026749; MELO3C004448; MELO3C013436	MELO3C006096; MELO3C012616; MELO3C016227; MELO3C021204; MELO3C001937; MELO3C023404

[OVER]	GO:0000084	mitotic S phase	BIOLOGICAL_PROCESS	1.8207606004169125E-7	7.323126885673442E-10	20	57	835	16216	MELO3C010960; MELO3C010882; MELO3C015926; MELO3C009313; MELO3C012361; MELO3C007144; MELO3C006995; MELO3C022319; MELO3C026749; MELO3C004448; MELO3C016083; MELO3C003638; MELO3C020860; MELO3C021058; MELO3C016262; MELO3C020001; MELO3C017228; MELO3C027184; MELO3C010631; MELO3C013436	MELO3C002481; MELO3C014021; MELO3C014020; MELO3C008864; MELO3C004864; MELO3C025879; MELO3C025755; MELO3C026800; MELO3C005912; MELO3C023372; MELO3C010507; MELO3C010828; MELO3C018501; MELO3C012407; MELO3C013814; MELO3C017458; MELO3C006096; MELO3C007066; MELO3C012492; MELO3C002892; MELO3C025923; MELO3C025646; MELO3C021204; MELO3C019642; MELO3C024596; MELO3C013349; MELO3C002182;
[OVER]	GO:0022627	cytosolic small ribosomal subunit	CELLULAR_COMPONENT	1.3873219008327823E-6	6.901368473660115E-9	22	82	833	16191	MELO3C019907; MELO3C010630; MELO3C013245; MELO3C013981; MELO3C009489; MELO3C005089; MELO3C012670; MELO3C012084; MELO3C020049; MELO3C020003; MELO3C019490; MELO3C017291; MELO3C004645; MELO3C005706; MELO3C022497; MELO3C015373; MELO3C017993; MELO3C025582; MELO3C015431; MELO3C011626; MELO3C019979; MELO3C009490	MELO3C011310; MELO3C004020; MELO3C002481; MELO3C009036; MELO3C003890; MELO3C005830; MELO3C009315; MELO3C009716; MELO3C001556; MELO3C020141; MELO3C022363; MELO3C010867; MELO3C017338; MELO3C019879; MELO3C002091; MELO3C003061; MELO3C020759; MELO3C025609; MELO3C023703; MELO3C001168; MELO3C024359; MELO3C006733; MELO3C003986; MELO3C026975; MELO3C022177; MELO3C024994; MELO3C022691;
[OVER]	GO:0006096	glycolytic process	BIOLOGICAL_PROCESS	4.005000097036141E-4	3.3911939856360213E-6	16	68	839	16205	MELO3C014732; MELO3C007421; MELO3C007986; MELO3C025916; MELO3C020579; MELO3C026748; MELO3C024514; MELO3C022998; MELO3C008219; MELO3C008879; MELO3C020780; MELO3C004539; MELO3C012604; MELO3C011769; MELO3C018966; MELO3C011104	MELO3C005271; MELO3C009351; MELO3C007772; MELO3C013010; MELO3C008221; MELO3C009438; MELO3C024509; MELO3C024508; MELO3C024866; MELO3C006964; MELO3C009439; MELO3C019872; MELO3C017175; MELO3C025275; MELO3C018027; MELO3C019634; MELO3C011367; MELO3C020837; MELO3C003381; MELO3C004591; MELO3C014272; MELO3C025969; MELO3C024519; MELO3C021720; MELO3C016050; MELO3C016095; MELO3C017063;

[OVER]	GO:0046686	response to cadmium ion	BIOLOGICAL_PROCESS	4.817428058505066E-4	4.181087010980265E-6	25	157	830	16116	MELO3C005293; MELO3C011256; MELO3C013214; MELO3C017817; MELO3C013411; MELO3C009038; MELO3C003173; MELO3C006241; MELO3C025916; MELO3C005757; MELO3C022382; MELO3C026224; MELO3C004194; MELO3C009203; MELO3C011284; MELO3C003344; MELO3C024514; MELO3C021247; MELO3C008879; MELO3C002117; MELO3C018573; MELO3C002816; MELO3C015385; MELO3C010599; MELO3C011107	MELO3C013974; MELO3C006086; MELO3C021919; MELO3C020429; MELO3C003491; MELO3C003370; MELO3C008541; MELO3C005395; MELO3C004980; MELO3C009910; MELO3C007698; MELO3C005674; MELO3C009633; MELO3C009915; MELO3C002444; MELO3C019040; MELO3C003536; MELO3C026800; MELO3C021113; MELO3C024461; MELO3C017134; MELO3C018623; MELO3C026360; MELO3C011712; MELO3C019318; MELO3C006493; MELO3C006095;
[OVER]	GO:0016071	mRNA metabolic process	BIOLOGICAL_PROCESS	5.366657722896626E-4	4.941778385817173E-6	46	407	809	15866	MELO3C015999; MELO3C011256; MELO3C010960; MELO3C014262; MELO3C020049; MELO3C021339; MELO3C009338; MELO3C020003; MELO3C005952; MELO3C004645; MELO3C007635; MELO3C021436; MELO3C026403; MELO3C016083; MELO3C016382; MELO3C016262; MELO3C024244; MELO3C017993; MELO3C017659; MELO3C019907; MELO3C010630; MELO3C013245; MELO3C013981; MELO3C005089; MELO3C008332; MELO3C012670; MELO3C006412;	MELO3C020705; MELO3C004580; MELO3C013051; MELO3C002045; MELO3C020824; MELO3C003258; MELO3C007978; MELO3C006767; MELO3C026246; MELO3C017771; MELO3C016201; MELO3C015113; MELO3C025030; MELO3C017775; MELO3C019837; MELO3C020836; MELO3C007740; MELO3C002294; MELO3C002173; MELO3C020718; MELO3C006411; MELO3C006416; MELO3C008956; MELO3C008955; MELO3C019964; MELO3C016459; MELO3C014122;
[OVER]	GO:0006268	DNA unwinding involved in DNA replication	BIOLOGICAL_PROCESS	5.812401463168 43E-4	5.659832076751646E-6	6	5	849	16268	MELO3C006995; MELO3C015926; MELO3C026749; MELO3C004448; MELO3C007144; MELO3C013436	MELO3C014153; MELO3C009682; MELO3C003609; MELO3C006788; MELO3C003608

[OVER]	GO:0009651	response to salt stress	BIOLOGICAL_PROCESS	6.888800376818608E-4	7.072540607021645E-6	23	141	832	16132	MELO3C012136; MELO3C012445; MELO3C004194; MELO3C009203; MELO3C011044; MELO3C025916; MELO3C005147; MELO3C011172; MELO3C026629; MELO3C004105; MELO3C024514; MELO3C008879; MELO3C027349; MELO3C017242; MELO3C018573; MELO3C004519; MELO3C003906; MELO3C015098; MELO3C016033; MELO3C015186; MELO3C025595; MELO3C015374; MELO3C016017	MELO3C021918; MELO3C006086; MELO3C017935; MELO3C013454; MELO3C004580; MELO3C012085; MELO3C022725; MELO3C008666; MELO3C006648; MELO3C002203; MELO3C026009; MELO3C024345; MELO3C007739; MELO3C026245; MELO3C017134; MELO3C024222; MELO3C019039; MELO3C010625; MELO3C012925; MELO3C026482; MELO3C016738; MELO3C002170; MELO3C012099; MELO3C012097; MELO3C007067; MELO3C009123; MELO3C005444;
[OVER]	GO:0000287	magnesium ion binding	MOLECULAR_FUNCTION	0.004724750385781459	6.301000726169176E-5	25	182	830	16091	MELO3C005293; MELO3C010286; MELO3C011972; MELO3C007153; MELO3C009038; MELO3C026748; MELO3C024982; MELO3C020244; MELO3C005939; MELO3C014732; MELO3C012178; MELO3C010794; MELO3C012196; MELO3C020579; MELO3C024514; MELO3C006736; MELO3C004439; MELO3C021385; MELO3C021563; MELO3C018573; MELO3C022494; MELO3C020394; MELO3C011704; MELO3C011769; MELO3C013745	MELO3C005271; MELO3C020829; MELO3C013336; MELO3C018628; MELO3C018507; MELO3C005396; MELO3C008426; MELO3C024509; MELO3C022605; MELO3C024508; MELO3C001595; MELO3C004226; MELO3C003379; MELO3C026007; MELO3C002448; MELO3C026005; MELO3C026006; MELO3C025552; MELO3C026004; MELO3C002727; MELO3C015076; MELO3C000372; MELO3C000130; MELO3C011713; MELO3C019677; MELO3C013218; MELO3C014943;
[OVER]	GO:0004775	succinate-CoA ligase (ADP-forming) activity	MOLECULAR_FUNCTION	0.005883572491923695	8.531429206112895E-5	4	2	851	16271	MELO3C002167; MELO3C022382; MELO3C010675; MELO3C011482	MELO3C021268; MELO3C015245

[OVER]	GO:0009792	embryo development ending in birth or egg hatching	BIOLOGICAL_PROCESS	0.007257974306578477	1.067801046374268E-4	39	366	816	15907	MELO3C010243; MELO3C011256; MELO3C013753; MELO3C008285; MELO3C010960; MELO3C002180; MELO3C010882; MELO3C012361; MELO3C011193; MELO3C009338; MELO3C007433; MELO3C005679; MELO3C020369; MELO3C022540; MELO3C006949; MELO3C019253; MELO3C022488; MELO3C020860; MELO3C021058; MELO3C019997; MELO3C017993; MELO3C011285; MELO3C022319; MELO3C009600; MELO3C005421; MELO3C004278; MELO3C025549;	MELO3C010584; MELO3C011795; MELO3C012522; MELO3C009592; MELO3C006760; MELO3C002166; MELO3C002045; MELO3C004344; MELO3C019031; MELO3C022562; MELO3C018062; MELO3C026800; MELO3C026245; MELO3C018187; MELO3C019034; MELO3C025275; MELO3C014708; MELO3C015235; MELO3C015599; MELO3C019956; MELO3C006096; MELO3C008151; MELO3C020836; MELO3C008157; MELO3C002173; MELO3C004473; MELO3C014153;
[OVER]	GO:0004807	triose-phosphate isomerase activity	MOLECULAR_FUNCTION	0.008134044001450522	1.2397357495860236E-4	3	0	852	16273	MELO3C020780; MELO3C025916; MELO3C008879	
[OVER]	GO:0005658	alpha DNA polymerase:primase complex	CELLULAR_COMPONENT	0.008134044001450522	1.2397357495860236E-4	3	0	852	16273	MELO3C027184; MELO3C022319; MELO3C020860	
[OVER]	GO:0002119	nematode larval development	BIOLOGICAL_PROCESS	0.015229400702566667	2.4178769108647335E-4	30	268	825	16005	MELO3C010243; MELO3C011256; MELO3C008285; MELO3C010960; MELO3C010882; MELO3C016707; MELO3C011193; MELO3C009338; MELO3C007433; MELO3C020369; MELO3C022540; MELO3C006949; MELO3C022488; MELO3C016262; MELO3C019997; MELO3C017993; MELO3C011285; MELO3C009600; MELO3C005421; MELO3C004278; MELO3C025549; MELO3C004459; MELO3C023201; MELO3C002118; MELO3C002717; MELO3C003905; MELO3C022094;	MELO3C011795; MELO3C012522; MELO3C006760; MELO3C002166; MELO3C002045; MELO3C004344; MELO3C019031; MELO3C026800; MELO3C019034; MELO3C025275; MELO3C016321; MELO3C014708; MELO3C015235; MELO3C019956; MELO3C020836; MELO3C008157; MELO3C002173; MELO3C004473; MELO3C014153; MELO3C013185; MELO3C023545; MELO3C008835; MELO3C023306; MELO3C023427; MELO3C006657; MELO3C024757; MELO3C003703;
[OVER]	GO:0006269	DNA replication, synthesis of RNA primer	BIOLOGICAL_PROCESS	0.026531682698092328	4.773905650588162E-4	3	1	852	16272	MELO3C027184; MELO3C022319; MELO3C020860	MELO3C006956
[OVER]	GO:0004634	phosphopyruvate hydratase activity	MOLECULAR_FUNCTION	0.026531682698092328	4.773905650588162E-4	3	1	852	16272	MELO3C020579; MELO3C026748; MELO3C024514	MELO3C017268
[OVER]	GO:0003896	DNA primase activity	MOLECULAR_FUNCTION	0.026531682698092328	4.773905650588162E-4	3	1	852	16272	MELO3C027184; MELO3C022319; MELO3C020860	MELO3C006956
[OVER]	GO:0000015	phosphopyruvate hydratase complex	CELLULAR_COMPONENT	0.026531682698092328	4.773905650588162E-4	3	1	852	16272	MELO3C020579; MELO3C026748; MELO3C024514	MELO3C017268

[OVER]	GO:0032201	telomere maintenance via semi-conservative replication	BIOLOGICAL_PROCESS	0.030742106527155904	5.694187809327141E-4	6	16	849	16257	MELO3C003638; MELO3C022319; MELO3C020860; MELO3C017228; MELO3C027184; MELO3C010631	MELO3C005384; MELO3C014021; MELO3C014020; MELO3C008864; MELO3C002892; MELO3C026949; MELO3C025879; MELO3C025646; MELO3C010507; MELO3C024596; MELO3C001937; MELO3C025142; MELO3C014529; MELO3C015225; MELO3C014528; MELO3C017458
[OVER]	GO:0010181	FMN binding	MOLECULAR_FUNCTION	0.04325987025490484	8.470656220530689E-4	7	25	848	16248	MELO3C007340; MELO3C022684; MELO3C011062; MELO3C003541; MELO3C023799; MELO3C016623; MELO3C015514	MELO3C008482; MELO3C013476; MELO3C008481; MELO3C004023; MELO3C009759; MELO3C022683; MELO3C008805; MELO3C022681; MELO3C024281; MELO3C018625; MELO3C018626; MELO3C010940; MELO3C017636; MELO3C008075; MELO3C007124; MELO3C006296; MELO3C006011; MELO3C009702; MELO3C021944; MELO3C005229; MELO3C003644; MELO3C025720; MELO3C017461; MELO3C025861; MELO3C007808
[OVER]	GO:0005618	cell wall	CELLULAR_COMPONENT	0.05275184314947438	0.0010999272968296415	34	345	821	15928	MELO3C012004; MELO3C013699; MELO3C011256; MELO3C009133; MELO3C012100; MELO3C025916; MELO3C020049; MELO3C005757; MELO3C020840; MELO3C016067; MELO3C017478; MELO3C019979; MELO3C010686; MELO3C009203; MELO3C005089; MELO3C012670; MELO3C021404; MELO3C023406; MELO3C005201; MELO3C004597; MELO3C009429; MELO3C008879; MELO3C017480; MELO3C007609; MELO3C021782; MELO3C025645; MELO3C025324;	MELO3C015914; MELO3C020704; MELO3C007057; MELO3C013055; MELO3C026806; MELO3C005316; MELO3C002047; MELO3C008946; MELO3C003810; MELO3C021595; MELO3C021471; MELO3C019039; MELO3C018862; MELO3C018743; MELO3C008032; MELO3C009120; MELO3C005561; MELO3C012099; MELO3C009488; MELO3C009367; MELO3C012097; MELO3C005560; MELO3C012096; MELO3C004477; MELO3C008159; MELO3C009924; MELO3C010919;
[OVER]	GO:0003878	ATP citrate synthase activity	MOLECULAR_FUNCTION	0.05455418635648744	0.0011490562113612404	3	2	852	16271	MELO3C010675; MELO3C011482; MELO3C002167	MELO3C021268; MELO3C015245

[OVER]	GO:0000722	telomere maintenance via recombination	BIOLOGICAL_ PROCESS	0.05561106082724685	0.001188974839871281	6	19	849	16254	MELO3C003638; MELO3C022319; MELO3C020860; MELO3C017228; MELO3C027184; MELO3C010631	MELO3C013324; MELO3C006292; MELO3C005384; MELO3C014021; MELO3C014020; MELO3C008864; MELO3C002892; MELO3C026949; MELO3C025879; MELO3C025646; MELO3C019510; MELO3C010507; MELO3C024596; MELO3C001937; MELO3C025142; MELO3C014529; MELO3C015225; MELO3C014528; MELO3C017458
[OVER]	GO:0031018	endocrine pancreas development	BIOLOGICAL_ PROCESS	0.06903724351414402	0.0015344857258647593	4	7	851	16266	MELO3C023201; MELO3C017993; MELO3C009338; MELO3C017291	MELO3C014237; MELO3C017184; MELO3C006662; MELO3C017169; MELO3C018512; MELO3C023127; MELO3C017290
[OVER]	GO:0008340	determination of adult lifespan	BIOLOGICAL_ PROCESS	0.08214339829049341	0.0018518780520612932	12	79	843	16194	MELO3C014007; MELO3C011256; MELO3C023201; MELO3C022540; MELO3C006949; MELO3C008285; MELO3C010960; MELO3C020860; MELO3C016262; MELO3C022094; MELO3C004278; MELO3C011104	MELO3C016329; MELO3C010584; MELO3C012522; MELO3C014221; MELO3C006121; MELO3C005753; MELO3C007214; MELO3C024822; MELO3C008306; MELO3C004945; MELO3C025755; MELO3C025796; MELO3C020783; MELO3C004827; MELO3C025275; MELO3C015199; MELO3C019712; MELO3C022280; MELO3C027174; MELO3C013814; MELO3C011830; MELO3C017627; MELO3C010795; MELO3C009840; MELO3C015928; MELO3C014153; MELO3C022219;
[OVER]	GO:0000022	mitotic spindle elongation	BIOLOGICAL_ PROCESS	0.08711145299844858	0.0019824002986259916	5	14	850	16259	MELO3C009338; MELO3C009600; MELO3C011285; MELO3C006280; MELO3C020369	MELO3C014237; MELO3C007036; MELO3C003342; MELO3C025755; MELO3C004807; MELO3C023594; MELO3C024782; MELO3C016981; MELO3C024150; MELO3C024020; MELO3C026580; MELO3C015269; MELO3C017744; MELO3C012667

[OVER]	GO:0009620	response to fungus	BIOLOGICAL_PROCESS	0.09634197158665671	0.0022331595869472714	12	81	843	16192	MELO3C011972; MELO3C006870; MELO3C020628; MELO3C019983; MELO3C002470; MELO3C006187; MELO3C005214; MELO3C016972; MELO3C012527; MELO3C005215; MELO3C019735; MELO3C015514	MELO3C005550; MELO3C007375; MELO3C004385; MELO3C005312; MELO3C002120; MELO3C003133; MELO3C004387; MELO3C006765; MELO3C004386; MELO3C025914; MELO3C005674; MELO3C005630; MELO3C025912; MELO3C009838; MELO3C005633; MELO3C024989; MELO3C019595; MELO3C002608; MELO3C025152; MELO3C018623; MELO3C009441; MELO3C013621; MELO3C014230; MELO3C005642; MELO3C005643; MELO3C024319; MELO3C020956;
[OVER]	GO:0000083	regulation of transcription involved in G1/S transition of mitotic cell cycle	BIOLOGICAL_PROCESS	0.09880955899413238	0.002489063827328906	2	0	853	16273	MELO3C020860; MELO3C021058	
[OVER]	GO:0006267	pre-replicative complex assembly involved in nuclear cell cycle DNA replication	BIOLOGICAL_PROCESS	0.09880955899413238	0.002489063827328906	2	0	853	16273	MELO3C010882; MELO3C021058	
[OVER]	GO:0006279	premeiotic DNA replication	BIOLOGICAL_PROCESS	0.09880955899413238	0.002489063827328906	2	0	853	16273	MELO3C020860; MELO3C021058	
[OVER]	GO:0006099	tricarboxylic acid cycle	BIOLOGICAL_PROCESS	0.09880955899413238	0.002448335174535359	7	31	848	16242	MELO3C021563; MELO3C022382; MELO3C017560; MELO3C011482; MELO3C002167; MELO3C021247; MELO3C022998	MELO3C012389; MELO3C017938; MELO3C007674; MELO3C014221; MELO3C013153; MELO3C003577; MELO3C025636; MELO3C022343; MELO3C005539; MELO3C017175; MELO3C019711; MELO3C025076; MELO3C018724; MELO3C014824; MELO3C019879; MELO3C002350; MELO3C023506; MELO3C007968; MELO3C021268; MELO3C021545; MELO3C006734; MELO3C005348; MELO3C016050; MELO3C016095; MELO3C005968; MELO3C019300; MELO3C019243;
[OVER]	GO:0004776	succinate-CoA ligase (GDP-forming) activity	MOLECULAR_FUNCTION	0.09880955899413238	0.002489063827328906	2	0	853	16273	MELO3C022382; MELO3C002167	
[OVER]	GO:0003861	3-isopropylmalate dehydratase activity	MOLECULAR_FUNCTION	0.09880955899413238	0.002489063827328906	2	0	853	16273	MELO3C005518; MELO3C003344	
[OVER]	GO:0005656	nuclear pre-replicative complex	CELLULAR_COMPONENT	0.09880955899413238	0.002489063827328906	2	0	853	16273	MELO3C010882; MELO3C021058	

[]	GO:0005758	mitochondrial intermembrane space	CELLULAR_COMPONENT	0.1002429025175407	0.0025357804510681868	5	15	850	16258	MELO3C014007; MELO3C022540; MELO3C004519; MELO3C007281; MELO3C016067	MELO3C006281; MELO3C009258; MELO3C011470; MELO3C020586; MELO3C020686; MELO3C007829; MELO3C020331; MELO3C005802; MELO3C016297; MELO3C024266; MELO3C017991; MELO3C019413; MELO3C026182; MELO3C016512; MELO3C010721
[]	GO:0048046	apoplast	CELLULAR_COMPONENT	0.10044664832028213	0.002551566003055431	22	199	833	16074	MELO3C012004; MELO3C009038; MELO3C011284; MELO3C025916; MELO3C024514; MELO3C021247; MELO3C021434; MELO3C024527; MELO3C008879; MELO3C017480; MELO3C007609; MELO3C020780; MELO3C021782; MELO3C017481; MELO3C023188; MELO3C015186; MELO3C012604; MELO3C017478; MELO3C009250; MELO3C011107; MELO3C010686; MELO3C016723	MELO3C011430; MELO3C007058; MELO3C013055; MELO3C007059; MELO3C003137; MELO3C026800; MELO3C001998; MELO3C015470; MELO3C015472; MELO3C010901; MELO3C007061; MELO3C007064; MELO3C007065; MELO3C008274; MELO3C007062; MELO3C007063; MELO3C005561; MELO3C007068; MELO3C009247; MELO3C009367; MELO3C005565; MELO3C010919; MELO3C025840; MELO3C026259; MELO3C019168; MELO3C011329; MELO3C010114;
[]	GO:0005774	vacuolar membrane	CELLULAR_COMPONENT	0.10866829748299485	0.0027949191668467134	17	142	838	16131	MELO3C010286; MELO3C013489; MELO3C011279; MELO3C006320; MELO3C008749; MELO3C026614; MELO3C022448; MELO3C006926; MELO3C026522; MELO3C025035; MELO3C026224; MELO3C000065; MELO3C016067; MELO3C012604; MELO3C019979; MELO3C025061; MELO3C024192	MELO3C014821; MELO3C015914; MELO3C007695; MELO3C011151; MELO3C002042; MELO3C005831; MELO3C026800; MELO3C021595; MELO3C024346; MELO3C025310; MELO3C025157; MELO3C016044; MELO3C012405; MELO3C010992; MELO3C013467; MELO3C010991; MELO3C013102; MELO3C014796; MELO3C005561; MELO3C004075; MELO3C005441; MELO3C007980; MELO3C007100; MELO3C004477; MELO3C009887; MELO3C003783; MELO3C004874;

[]	GO:0006094	gluconeogenesis	BIOLOGICAL_PROCESS	0.11878871598209911	0.0031055051701501355	8	42	847	16231	MELO3C020780; MELO3C011284; MELO3C025916; MELO3C012604; MELO3C021604; MELO3C011104; MELO3C022998; MELO3C008879	MELO3C012444; MELO3C012389; MELO3C009351; MELO3C007674; MELO3C007772; MELO3C003491; MELO3C004980; MELO3C005333; MELO3C003577; MELO3C003214; MELO3C003215; MELO3C023354; MELO3C005539; MELO3C017175; MELO3C019634; MELO3C014724; MELO3C011710; MELO3C011367; MELO3C013203; MELO3C012375; MELO3C009147; MELO3C011682; MELO3C003265; MELO3C007687; MELO3C004433; MELO3C003266; MELO3C021863;
[]	GO:0040002	collagen and cuticulin-based cuticle development	BIOLOGICAL_PROCESS	0.1392557691939414	0.0037290124477209114	3	4	852	16269	MELO3C016707; MELO3C019253; MELO3C012361	MELO3C016321; MELO3C023052; MELO3C008151; MELO3C015126
[]	GO:0009570	chloroplast stroma	CELLULAR_COMPONENT	0.15319073575706385	0.004150807404086404	32	351	823	15922	MELO3C005293; MELO3C018948; MELO3C011972; MELO3C017817; MELO3C010860; MELO3C009038; MELO3C025916; MELO3C013093; MELO3C026887; MELO3C020780; MELO3C020562; MELO3C003439; MELO3C010727; MELO3C010427; MELO3C015233; MELO3C014749; MELO3C011439; MELO3C010686; MELO3C012378; MELO3C012410; MELO3C011284; MELO3C005147; MELO3C002275; MELO3C003344; MELO3C009429; MELO3C008879; MELO3C018573;	MELO3C013732; MELO3C021919; MELO3C012764; MELO3C002161; MELO3C008146; MELO3C006088; MELO3C009475; MELO3C013172; MELO3C004223; MELO3C005674; MELO3C003137; MELO3C001992; MELO3C008946; MELO3C003811; MELO3C001998; MELO3C003814; MELO3C021355; MELO3C016680; MELO3C016681; MELO3C017890; MELO3C024189; MELO3C015231; MELO3C025397; MELO3C019036; MELO3C017774; MELO3C014943; MELO3C015923;
[]	GO:0035046	pronuclear migration	BIOLOGICAL_PROCESS	0.20032826652597704	0.005746079617753998	3	5	852	16268	MELO3C019253; MELO3C012361; MELO3C020860	MELO3C022016; MELO3C005064; MELO3C019956; MELO3C006723; MELO3C004458
[]	GO:0051903	S-(hydroxymethyl)glutathione dehydrogenase activity	MOLECULAR_FUNCTION	0.20032826652597704	0.005746079617753998	3	5	852	16268	MELO3C023685; MELO3C026554; MELO3C022399	MELO3C002189; MELO3C005792; MELO3C026553; MELO3C027151; MELO3C026552

[]	GO:0005982	starch metabolic process	BIOLOGICAL_PROCESS	0.23043047449313317	0.007068005702295764	5	20	850	16253	MELO3C005293; MELO3C003812; MELO3C011972; MELO3C011104; MELO3C019135	MELO3C009960; MELO3C014105; MELO3C005396; MELO3C006585; MELO3C006552; MELO3C011682; MELO3C020949; MELO3C007155; MELO3C012071; MELO3C005795; MELO3C002455; MELO3C023105; MELO3C021412; MELO3C025149; MELO3C026536; MELO3C024754; MELO3C024175; MELO3C022275; MELO3C017942; MELO3C017735
[]	GO:0006277	DNA amplification	BIOLOGICAL_PROCESS	0.23043047449313317	0.007219244332130336	2	1	853	16272	MELO3C010882; MELO3C021058	MELO3C019031
[]	GO:0006069	ethanol oxidation	BIOLOGICAL_PROCESS	0.23043047449313317	0.006931616846499603	4	12	851	16261	MELO3C023685; MELO3C022399; MELO3C014749; MELO3C026554	MELO3C023687; MELO3C005792; MELO3C004383; MELO3C026553; MELO3C017100; MELO3C017125; MELO3C004430; MELO3C019622; MELO3C002189; MELO3C027151; MELO3C005081; MELO3C025328
[]	GO:0003688	DNA replication origin binding	MOLECULAR_FUNCTION	0.23043047449313317	0.007219244332130336	2	1	853	16272	MELO3C010882; MELO3C021058	MELO3C021204
[]	GO:0004349	glutamate 5-kinase activity	MOLECULAR_FUNCTION	0.23043047449313317	0.007219244332130336	2	1	853	16272	MELO3C008245; MELO3C011208	MELO3C009229
[]	GO:0050486	intramolecular transferase activity, transferring hydroxy groups	MOLECULAR_FUNCTION	0.23043047449313317	0.007219244332130336	2	1	853	16272	MELO3C012178; MELO3C003344	MELO3C017156
[]	GO:0031418	L-ascorbic acid binding	MOLECULAR_FUNCTION	0.23043047449313317	0.006931616846499603	4	12	851	16261	MELO3C007425; MELO3C007611; MELO3C021380; MELO3C019735	MELO3C006592; MELO3C010508; MELO3C021480; MELO3C005334; MELO3C017675; MELO3C020028; MELO3C005478; MELO3C006861; MELO3C006307; MELO3C007943; MELO3C014437; MELO3C004414
[]	GO:0004298	threonine-type endopeptidase activity	MOLECULAR_FUNCTION	0.23043047449313317	0.007068005702295764	5	20	850	16253	MELO3C010960; MELO3C011172; MELO3C003173; MELO3C013757; MELO3C006187	MELO3C011880; MELO3C006131; MELO3C007920; MELO3C021745; MELO3C021746; MELO3C000704; MELO3C025735; MELO3C023267; MELO3C025755; MELO3C026800; MELO3C000762; MELO3C006517; MELO3C019011; MELO3C019010; MELO3C019012; MELO3C027069; MELO3C024343; MELO3C010635; MELO3C026360; MELO3C011449
[]	GO:0004802	transketolase activity	MOLECULAR_FUNCTION	0.23043047449313317	0.007219244332130336	2	1	853	16272	MELO3C002746; MELO3C022494	MELO3C006200

[]	GO:0050625	2-hydroxy-1,4-benzoquinone reductase activity	MOLECULAR_FUNCTION	0.23043047449313317	0.007219244332130336	2	1	853	16272	MELO3C007340; MELO3C016623	MELO3C025861
[]	GO:0015631	tubulin binding	MOLECULAR_FUNCTION	0.23043047449313317	0.007068005702295764	5	20	850	16253	MELO3C022488; MELO3C013702; MELO3C002717; MELO3C017221; MELO3C006602	MELO3C004390; MELO3C010584; MELO3C006171; MELO3C018707; MELO3C007036; MELO3C007584; MELO3C022016; MELO3C001970; MELO3C022478; MELO3C006723; MELO3C022166; MELO3C022751; MELO3C024792; MELO3C016297; MELO3C024150; MELO3C017720; MELO3C018910; MELO3C011800; MELO3C019823; MELO3C011830
[]	GO:0004733	pyridoxamine-phosphate oxidase activity	MOLECULAR_FUNCTION	0.23043047449313317	0.007219244332130336	2	1	853	16272	MELO3C011062; MELO3C003541	MELO3C006011
[]	GO:0016328	lateral plasma membrane	CELLULAR_COMPONENT	0.23043047449313317	0.007219244332130336	2	1	853	16272	MELO3C017242; MELO3C022488	MELO3C007829
[]	GO:0005351	sugar:proton symporter activity	MOLECULAR_FUNCTION	0.23242722577311475	0.00735560335585958	7	39	848	16234	MELO3C013489; MELO3C011675; MELO3C025345; MELO3C026522; MELO3C004576; MELO3C016017; MELO3C014417	MELO3C008582; MELO3C008581; MELO3C014485; MELO3C020608; MELO3C000836; MELO3C003830; MELO3C024689; MELO3C000832; MELO3C007756; MELO3C018040; MELO3C019030; MELO3C007815; MELO3C021377; MELO3C017055; MELO3C015350; MELO3C009081; MELO3C010946; MELO3C017699; MELO3C017655; MELO3C000070; MELO3C017656; MELO3C013415; MELO3C011676; MELO3C012554; MELO3C006595; MELO3C013485; MELO3C007980;

[]	GO:0030170	pyridoxal phosphate binding	MOLECULAR_FUNCTION	0.25209707137125503	0.008111506106780433	14	120	841	16153	MELO3C018948; MELO3C020927; MELO3C011284; MELO3C001121; MELO3C020444; MELO3C001323; MELO3C023373; MELO3C000251; MELO3C026045; MELO3C026175; MELO3C015398; MELO3C011107; MELO3C010686; MELO3C016448	MELO3C005392; MELO3C013732; MELO3C010464; MELO3C020429; MELO3C010461; MELO3C004980; MELO3C002561; MELO3C023659; MELO3C007698; MELO3C009117; MELO3C017490; MELO3C026404; MELO3C022321; MELO3C024500; MELO3C011959; MELO3C016200; MELO3C011960; MELO3C013583; MELO3C004355; MELO3C022699; MELO3C018082; MELO3C026534; MELO3C019443; MELO3C017386; MELO3C019203; MELO3C010754; MELO3C016549;
[]	GO:0004723	calcium-dependent protein serine/threonine phosphatase activity	MOLECULAR_FUNCTION	0.25219961796018175	0.0083016597359882	3	6	852	16267	MELO3C017844; MELO3C013892; MELO3C022260	MELO3C023443; MELO3C019099; MELO3C018436; MELO3C014069; MELO3C026598; MELO3C007998
[]	GO:0051086	chaperone mediated protein folding independent of cofactor	BIOLOGICAL_PROCESS	0.2556145819474702	0.008711673940208024	4	13	851	16260	MELO3C002117; MELO3C009624; MELO3C022094; MELO3C010705	MELO3C014127; MELO3C015615; MELO3C008567; MELO3C021633; MELO3C003128; MELO3C004458; MELO3C023558; MELO3C004636; MELO3C026888; MELO3C017295; MELO3C023852; MELO3C018683; MELO3C023264
[]	GO:0040010	positive regulation of growth rate	BIOLOGICAL_PROCESS	0.26082029143776764	0.008944302966324801	23	238	832	16035	MELO3C010243; MELO3C011256; MELO3C008285; MELO3C010882; MELO3C011285; MELO3C009338; MELO3C007433; MELO3C005421; MELO3C026614; MELO3C017291; MELO3C020369; MELO3C023201; MELO3C022540; MELO3C006949; MELO3C002118; MELO3C024352; MELO3C002717; MELO3C003905; MELO3C019997; MELO3C017993; MELO3C025061; MELO3C006280; MELO3C013822	MELO3C012522; MELO3C009592; MELO3C006760; MELO3C002045; MELO3C004344; MELO3C018187; MELO3C019034; MELO3C025275; MELO3C016321; MELO3C014708; MELO3C026482; MELO3C019956; MELO3C021808; MELO3C020836; MELO3C004473; MELO3C014153; MELO3C013185; MELO3C004353; MELO3C023545; MELO3C023306; MELO3C006657; MELO3C002738; MELO3C025044; MELO3C017661; MELO3C018512; MELO3C016456; MELO3C015246;

[]	GO:0040035	hermaphrodite genitalia development	BIOLOGICAL_PROCESS	0.27042584344354126	0.009445441187168566	14	123	841	16150	MELO3C011256; MELO3C008285; MELO3C010882; MELO3C016707; MELO3C012361; MELO3C011193; MELO3C022319; MELO3C026614; MELO3C022540; MELO3C019253; MELO3C022488; MELO3C002717; MELO3C019997; MELO3C022094	MELO3C009592; MELO3C006760; MELO3C006121; MELO3C004344; MELO3C019031; MELO3C022166; MELO3C024586; MELO3C026888; MELO3C016321; MELO3C014708; MELO3C015235; MELO3C019956; MELO3C021808; MELO3C015647; MELO3C008151; MELO3C008157; MELO3C002173; MELO3C000924; MELO3C006498; MELO3C004873; MELO3C007466; MELO3C008835; MELO3C023823; MELO3C023427; MELO3C006657; MELO3C024757; MELO3C007903;
[]	GO:0019843	rRNA binding	MOLECULAR_FUNCTION	0.2735106144041594	0.009640033297691055	10	75	845	16198	MELO3C024850; MELO3C010630; MELO3C005759; MELO3C013245; MELO3C024244; MELO3C012084; MELO3C011847; MELO3C009091; MELO3C019979; MELO3C008801	MELO3C010584; MELO3C011276; MELO3C011310; MELO3C004020; MELO3C003890; MELO3C009795; MELO3C006682; MELO3C006088; MELO3C012480; MELO3C006245; MELO3C020945; MELO3C021312; MELO3C022601; MELO3C001556; MELO3C022485; MELO3C003811; MELO3C019631; MELO3C025474; MELO3C012967; MELO3C019879; MELO3C003061; MELO3C025609; MELO3C005844; MELO3C005800; MELO3C004995; MELO3C003986; MELO3C025845;
[]	GO:0006098	pentose-phosphate shunt	BIOLOGICAL_PROCESS	0.29874280924091884	0.010687454437280966	6	32	849	16241	MELO3C025916; MELO3C017817; MELO3C013093; MELO3C022494; MELO3C011104; MELO3C008879	MELO3C012301; MELO3C011230; MELO3C006200; MELO3C021811; MELO3C005310; MELO3C008985; MELO3C005910; MELO3C005559; MELO3C026309; MELO3C013091; MELO3C021375; MELO3C022343; MELO3C001998; MELO3C022063; MELO3C026301; MELO3C019475; MELO3C017499; MELO3C014967; MELO3C014965; MELO3C017506; MELO3C012159; MELO3C004370; MELO3C004590; MELO3C003280; MELO3C004075; MELO3C002813; MELO3C002814;

[]	GO:0008237	metallopeptidase activity	MOLECULAR_FUNCTION	0.29889066843941614	0.010724379403150092	13	111	842	16162	MELO3C012356; MELO3C008052; MELO3C009148; MELO3C011193; MELO3C004134; MELO3C006846; MELO3C008847; MELO3C003139; MELO3C018441; MELO3C026224; MELO3C016890; MELO3C016067; MELO3C025494	MELO3C006089; MELO3C014386; MELO3C022843; MELO3C019273; MELO3C017011; MELO3C026003; MELO3C010623; MELO3C016738; MELO3C000768; MELO3C005965; MELO3C026539; MELO3C023149; MELO3C005688; MELO3C015483; MELO3C004918; MELO3C023023; MELO3C004919; MELO3C013276; MELO3C014882; MELO3C003474; MELO3C006466; MELO3C025899; MELO3C026225; MELO3C000673; MELO3C004605; MELO3C025493; MELO3C019536;
[]	GO:0009535	chloroplast thylakoid membrane	CELLULAR_COMPONENT	0.30746432289120923	0.011227264119122268	5	271	850	16002	MELO3C007153; MELO3C011955; MELO3C005759; MELO3C022494; MELO3C003139	MELO3C009475; MELO3C005432; MELO3C001992; MELO3C026802; MELO3C019395; MELO3C025953; MELO3C001998; MELO3C025277; MELO3C002727; MELO3C022680; MELO3C017774; MELO3C018748; MELO3C010469; MELO3C009241; MELO3C005562; MELO3C014156; MELO3C009245; MELO3C006532; MELO3C022335; MELO3C021127; MELO3C009809; MELO3C027107; MELO3C005329; MELO3C006539; MELO3C027106; MELO3C007507; MELO3C026259;
[]	GO:0009695	jasmonic acid biosynthetic process	BIOLOGICAL_PROCESS	0.3092629935311	0.011423876454525179	3	7	852	16266	MELO3C009362; MELO3C002470; MELO3C015514	MELO3C004955; MELO3C012388; MELO3C010910; MELO3C004565; MELO3C008062; MELO3C018734; MELO3C002346
[]	GO:0005852	eukaryotic translation initiation factor 3 complex	CELLULAR_COMPONENT	0.3092629935311	0.011423876454525179	3	7	852	16266	MELO3C011193; MELO3C008285; MELO3C003453	MELO3C026327; MELO3C017707; MELO3C009841; MELO3C019434; MELO3C015553; MELO3C022038; MELO3C007050
[]	GO:0019773	proteasome core complex, alpha-subunit complex	CELLULAR_COMPONENT	0.3092629935311	0.011423876454525179	3	7	852	16266	MELO3C003173; MELO3C010960; MELO3C013757	MELO3C026800; MELO3C024343; MELO3C007920; MELO3C021745; MELO3C021746; MELO3C026360; MELO3C025735

[]	GO:0010171	body morphogenesis	BIOLOGICAL_PROCESS	0.32341077995372997	0.012117635066005548	9	66	846	16207	MELO3C011256; MELO3C008285; MELO3C022488; MELO3C010882; MELO3C002717; MELO3C019997; MELO3C017993; MELO3C005421; MELO3C004459	MELO3C009592; MELO3C014221; MELO3C002120; MELO3C004344; MELO3C004622; MELO3C007816; MELO3C025310; MELO3C019034; MELO3C018102; MELO3C025275; MELO3C014708; MELO3C019996; MELO3C013814; MELO3C017216; MELO3C012449; MELO3C019956; MELO3C020836; MELO3C014153; MELO3C000924; MELO3C003222; MELO3C022016; MELO3C023865; MELO3C008835; MELO3C007829; MELO3C007903; MELO3C023741; MELO3C026971;
[]	GO:1901617	organic hydroxy compound biosynthetic process	BIOLOGICAL_PROCESS	0.324046881660428	0.012175766616157064	10	78	845	16195	MELO3C024861; MELO3C024982; MELO3C003726; MELO3C017581; MELO3C004519; MELO3C014175; MELO3C011062; MELO3C017963; MELO3C003541; MELO3C004278	MELO3C017815; MELO3C013732; MELO3C011037; MELO3C010781; MELO3C012288; MELO3C012088; MELO3C008543; MELO3C009431; MELO3C008942; MELO3C011150; MELO3C007774; MELO3C005515; MELO3C006525; MELO3C020384; MELO3C022961; MELO3C019790; MELO3C017176; MELO3C017495; MELO3C017057; MELO3C027255; MELO3C024061; MELO3C016008; MELO3C016845; MELO3C007140; MELO3C017829; MELO3C009168; MELO3C006011;
[]	GO:0042450	arginine biosynthetic process via ornithine	BIOLOGICAL_PROCESS	0.3443980543808898	0.013961098097785857	2	2	853	16271	MELO3C011085; MELO3C011208	MELO3C023629; MELO3C003523
[]	GO:0006272	leading strand elongation	BIOLOGICAL_PROCESS	0.3443980543808898	0.013961098097785857	2	2	853	16271	MELO3C010631; MELO3C020860	MELO3C014021; MELO3C010507
[]	GO:0004133	glycogen debranching enzyme activity	MOLECULAR_FUNCTION	0.3443980543808898	0.013961098097785857	2	2	853	16271	MELO3C015861; MELO3C019135	MELO3C017391; MELO3C020949
[]	GO:0005664	nuclear origin of replication recognition complex	CELLULAR_COMPONENT	0.3443980543808898	0.013961098097785857	2	2	853	16271	MELO3C005455; MELO3C010882	MELO3C008530; MELO3C021204
[]	GO:0008541	proteasome regulatory particle, lid subcomplex	CELLULAR_COMPONENT	0.3443980543808898	0.013961098097785857	2	2	853	16271	MELO3C016262; MELO3C011193	MELO3C025923; MELO3C013814
[]	GO:0031307	integral component of mitochondrial outer membrane	CELLULAR_COMPONENT	0.3443980543808898	0.013961098097785857	2	2	853	16271	MELO3C004519; MELO3C019820	MELO3C019821; MELO3C013700

[]	GO:0031234	extrinsic component of cytoplasmic side of plasma membrane	CELLULAR_COMPONENT	0.3443980543808898	0.013961098097785857	2	2	853	16271	MELO3C012527; MELO3C026614	MELO3C006233; MELO3C016919
[]	GO:0010193	response to ozone	BIOLOGICAL_PROCESS	0.36472167372867004	0.015132397978581567	3	8	852	16265	MELO3C024348; MELO3C015374; MELO3C015514	MELO3C014004; MELO3C014587; MELO3C004372; MELO3C006046; MELO3C006545; MELO3C012945; MELO3C005674; MELO3C011885
[]	GO:0009825	multidimensional cell growth	BIOLOGICAL_PROCESS	0.3777018246393318	0.01575090166256316	4	16	851	16257	MELO3C012004; MELO3C007325; MELO3C017242; MELO3C007207	MELO3C012114; MELO3C002081; MELO3C005631; MELO3C007324; MELO3C021737; MELO3C001364; MELO3C002553; MELO3C024898; MELO3C020643; MELO3C023374; MELO3C015782; MELO3C011913; MELO3C015783; MELO3C015784; MELO3C015785; MELO3C011732
[]	GO:0005875	microtubule associated complex	CELLULAR_COMPONENT	0.3961474708972599	0.016562050275658092	8	58	847	16215	MELO3C011256; MELO3C024248; MELO3C023342; MELO3C022094; MELO3C013429; MELO3C017228; MELO3C005757; MELO3C010631	MELO3C005594; MELO3C006121; MELO3C009957; MELO3C024627; MELO3C021317; MELO3C004268; MELO3C008589; MELO3C003774; MELO3C026888; MELO3C026800; MELO3C018185; MELO3C025310; MELO3C010507; MELO3C015199; MELO3C017338; MELO3C012723; MELO3C009841; MELO3C005122; MELO3C014153; MELO3C005289; MELO3C025923; MELO3C022897; MELO3C022898; MELO3C007668; MELO3C017141; MELO3C004518; MELO3C007903;
[]	GO:0009846	pollen germination	BIOLOGICAL_PROCESS	0.44048666859038	0.018705669648721404	4	17	851	16256	MELO3C008285; MELO3C004551; MELO3C019522; MELO3C013702	MELO3C015989; MELO3C014698; MELO3C005099; MELO3C003581; MELO3C021702; MELO3C009734; MELO3C000736; MELO3C022308; MELO3C004336; MELO3C006326; MELO3C024874; MELO3C020044; MELO3C012924; MELO3C019825; MELO3C015654; MELO3C015689; MELO3C024093
[]	GO:0034515	proteasome storage granule	CELLULAR_COMPONENT	0.4523735681431247	0.019439423017157984	3	9	852	16264	MELO3C016262; MELO3C011193; MELO3C010960	MELO3C025755; MELO3C026800; MELO3C020453; MELO3C018764; MELO3C021746; MELO3C010635; MELO3C011449; MELO3C013814; MELO3C025923

[]	GO:0004177	aminopeptidase activity	MOLECULAR_FUNCTION	0.46461706997455804	0.020113080188356714	5	27	850	16246	MELO3C012356; MELO3C004134; MELO3C009148; MELO3C026224; MELO3C016890	MELO3C005470; MELO3C023479; MELO3C006206; MELO3C026225; MELO3C023478; MELO3C026003; MELO3C015673; MELO3C012427; MELO3C004172; MELO3C001380; MELO3C002074; MELO3C006077; MELO3C004255; MELO3C013085; MELO3C004135; MELO3C000768; MELO3C020895; MELO3C020334; MELO3C005688; MELO3C007807; MELO3C016891; MELO3C023023; MELO3C018038; MELO3C016894; MELO3C016895; MELO3C023481; MELO3C015446
[]	GO:0003924	GTPase activity	MOLECULAR_FUNCTION	0.4796011916051134	0.02101554755763304	11	95	844	16178	MELO3C011234; MELO3C002118; MELO3C025753; MELO3C022411; MELO3C024544; MELO3C025885; MELO3C009203; MELO3C007673; MELO3C015098; MELO3C005673; MELO3C002687	MELO3C011312; MELO3C008580; MELO3C003370; MELO3C015839; MELO3C007254; MELO3C008987; MELO3C021514; MELO3C009713; MELO3C023931; MELO3C014180; MELO3C004547; MELO3C026889; MELO3C003218; MELO3C025510; MELO3C025511; MELO3C018025; MELO3C018587; MELO3C015755; MELO3C015756; MELO3C018716; MELO3C010552; MELO3C004273; MELO3C003261; MELO3C004074; MELO3C014156; MELO3C007220; MELO3C002130;
[]	GO:0000076	DNA replication checkpoint	BIOLOGICAL_PROCESS	0.49442613026338766	0.022502459357880686	2	3	853	16270	MELO3C020860; MELO3C021058	MELO3C016039; MELO3C013324; MELO3C007925
[]	GO:0016882	cyclo-ligase activity	MOLECULAR_FUNCTION	0.49442613026338766	0.022502459357880686	2	3	853	16270	MELO3C016483; MELO3C008332	MELO3C005781; MELO3C017138; MELO3C017137
[]	GO:0008878	glucose-1-phosphate adenylyltransferase activity	MOLECULAR_FUNCTION	0.49442613026338766	0.022502459357880686	2	3	853	16270	MELO3C003812; MELO3C023310	MELO3C006552; MELO3C024175; MELO3C021412
[]	GO:0008963	phospho-N-acetylmuramoyl-pentapeptide-transferase activity	MOLECULAR_FUNCTION	0.49442613026338766	0.022502459357880686	2	3	853	16270	MELO3C009489; MELO3C009490	MELO3C002715; MELO3C002716; MELO3C014202
[]	GO:0009815	1-aminocyclopropane-1-carboxylate oxidase activity	MOLECULAR_FUNCTION	0.49442613026338766	0.022502459357880686	2	3	853	16270	MELO3C007425; MELO3C019735	MELO3C010508; MELO3C006437; MELO3C014437
[]	GO:0019781	NEDD8 activating enzyme activity	MOLECULAR_FUNCTION	0.49442613026338766	0.022502459357880686	2	3	853	16270	MELO3C011193; MELO3C006555	MELO3C008213; MELO3C014386; MELO3C013230

[]	GO:0016906	sterol 3-beta-glucosyltransferase activity	MOLECULAR_FUNCTION	0.49442613026338766	0.022502459357880686	2	3	853	16270	MELO3C020997; MELO3C012787	MELO3C010080; MELO3C010079; MELO3C008339
[]	GO:0016709	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen	MOLECULAR_FUNCTION	0.49442613026338766	0.022296311975877454	0	84	855	16189		MELO3C016329; MELO3C017815; MELO3C011158; MELO3C010781; MELO3C014027; MELO3C012088; MELO3C008543; MELO3C014463; MELO3C002043; MELO3C000537; MELO3C026802; MELO3C022404; MELO3C002007; MELO3C025798; MELO3C003933; MELO3C003932; MELO3C025797; MELO3C003934; MELO3C022246; MELO3C015551; MELO3C010823; MELO3C026561; MELO3C017219; MELO3C016845; MELO3C016219; MELO3C013589; MELO3C010272;
[]	GO:0031261	DNA replication preinitiation complex	CELLULAR_COMPONENT	0.49442613026338766	0.022502459357880686	2	3	853	16270	MELO3C010882; MELO3C021058	MELO3C006096; MELO3C024840; MELO3C023404
[]	GO:0006553	lysine metabolic process	BIOLOGICAL_PROCESS	0.5276703455771554	0.024350579029597773	3	10	852	16263	MELO3C010427; MELO3C023315; MELO3C021247	MELO3C024345; MELO3C009153; MELO3C008136; MELO3C003100; MELO3C018037; MELO3C006179; MELO3C013171; MELO3C015556; MELO3C006876; MELO3C006734
[]	GO:0008967	phosphoglycolate phosphatase activity	MOLECULAR_FUNCTION	0.5276703455771554	0.024350579029597773	3	10	852	16263	MELO3C017462; MELO3C013878; MELO3C007011	MELO3C018727; MELO3C002558; MELO3C025302; MELO3C006364; MELO3C016693; MELO3C022462; MELO3C008753; MELO3C008533; MELO3C009765; MELO3C019407
[]	GO:0006898	receptor-mediated endocytosis	BIOLOGICAL_PROCESS	0.5453900055429007	0.02539919585508852	13	122	842	16151	MELO3C010243; MELO3C013753; MELO3C008285; MELO3C009338; MELO3C022319; MELO3C025549; MELO3C026614; MELO3C002118; MELO3C002717; MELO3C003905; MELO3C019997; MELO3C013822; MELO3C018758	MELO3C011795; MELO3C016968; MELO3C006760; MELO3C011151; MELO3C006121; MELO3C002045; MELO3C008306; MELO3C022166; MELO3C026888; MELO3C025310; MELO3C015235; MELO3C015512; MELO3C021808; MELO3C017707; MELO3C013982; MELO3C008151; MELO3C020836; MELO3C004074; MELO3C014153; MELO3C023545; MELO3C005963; MELO3C023306; MELO3C023427; MELO3C006657; MELO3C017020; MELO3C007903; MELO3C016297;

[]	GO:0005768	endosome	CELLULAR_COMPONENT	0.5658057208745785	0.02664940154415616	8	64	847	16209	MELO3C010243; MELO3C006926; MELO3C013753; MELO3C004391; MELO3C010772; MELO3C025783; MELO3C026614; MELO3C018758	MELO3C014821; MELO3C011795; MELO3C009473; MELO3C014542; MELO3C005199; MELO3C007457; MELO3C012481; MELO3C014180; MELO3C004945; MELO3C025310; MELO3C004827; MELO3C026440; MELO3C013816; MELO3C012728; MELO3C015433; MELO3C006171; MELO3C010795; MELO3C023828; MELO3C024558; MELO3C005328; MELO3C004874; MELO3C018195; MELO3C016491; MELO3C026971; MELO3C025682; MELO3C026096; MELO3C022490;
[]	GO:0005543	phospholipid binding	MOLECULAR_FUNCTION	0.5678709126777027	0.0269269865452594	7	52	848	16221	MELO3C015704; MELO3C019002; MELO3C014288; MELO3C015111; MELO3C017091; MELO3C012457; MELO3C012545	MELO3C014301; MELO3C024309; MELO3C020987; MELO3C002682; MELO3C026608; MELO3C020069; MELO3C003655; MELO3C003976; MELO3C018420; MELO3C010305; MELO3C015554; MELO3C008391; MELO3C017813; MELO3C012455; MELO3C013864; MELO3C014435; MELO3C012456; MELO3C014433; MELO3C020518; MELO3C023429; MELO3C005525; MELO3C024558; MELO3C003700; MELO3C026612; MELO3C003708; MELO3C019004; MELO3C020154;
[]	GO:0008380	RNA splicing	BIOLOGICAL_PROCESS	0.5703306946368167	0.027116409352641695	3	185	852	16088	MELO3C011256; MELO3C008332; MELO3C016382	MELO3C010981; MELO3C005030; MELO3C012489; MELO3C013333; MELO3C004580; MELO3C008146; MELO3C008023; MELO3C021758; MELO3C002045; MELO3C020824; MELO3C006125; MELO3C023531; MELO3C018062; MELO3C000014; MELO3C020022; MELO3C017775; MELO3C017657; MELO3C011313; MELO3C013741; MELO3C014555; MELO3C007183; MELO3C010355; MELO3C008151; MELO3C008157; MELO3C002173; MELO3C009922; MELO3C023428;

[]	GO:0000323	lytic vacuole	CELLULAR_COMPONENT	0.5960089379346575	0.028702801308241866	5	30	850	16243	MELO3C010243; MELO3C006926; MELO3C025645; MELO3C025061; MELO3C023569	MELO3C015218; MELO3C014920; MELO3C014821; MELO3C013676; MELO3C003291; MELO3C025752; MELO3C025972; MELO3C020442; MELO3C004827; MELO3C025355; MELO3C018764; MELO3C017653; MELO3C026440; MELO3C017414; MELO3C014458; MELO3C006034; MELO3C005243; MELO3C004353; MELO3C008897; MELO3C004477; MELO3C004874; MELO3C026977; MELO3C026898; MELO3C026415; MELO3C026971; MELO3C022495; MELO3C014818;
[]	GO:0009617	response to bacterium	BIOLOGICAL_PROCESS	0.6033053896150709	0.029676057561601084	10	87	845	16186	MELO3C012136; MELO3C018573; MELO3C003906; MELO3C016033; MELO3C015374; MELO3C005147; MELO3C016972; MELO3C013757; MELO3C024348; MELO3C009429	MELO3C021918; MELO3C006046; MELO3C014386; MELO3C004385; MELO3C002120; MELO3C004387; MELO3C004386; MELO3C005674; MELO3C009633; MELO3C009952; MELO3C003137; MELO3C023217; MELO3C026722; MELO3C003536; MELO3C004867; MELO3C023453; MELO3C021553; MELO3C025152; MELO3C025076; MELO3C014706; MELO3C011997; MELO3C016008; MELO3C013811; MELO3C013621; MELO3C014633; MELO3C016937; MELO3C014631;
[]	GO:0009225	nucleotide-sugar metabolic process	BIOLOGICAL_PROCESS	0.6033053896150709	0.029524383754019796	4	20	851	16253	MELO3C003812; MELO3C023310; MELO3C007043; MELO3C020244	MELO3C009473; MELO3C011431; MELO3C006552; MELO3C021813; MELO3C011180; MELO3C004113; MELO3C002112; MELO3C008467; MELO3C002113; MELO3C021412; MELO3C005458; MELO3C003703; MELO3C024175; MELO3C020220; MELO3C017213; MELO3C016068; MELO3C017126; MELO3C026482; MELO3C015301; MELO3C011346

[]	GO:0005747	mitochondrial respiratory chain complex I	CELLULAR_COMPONENT	0.6033053896150709	0.029524383754019796	4	20	851	16253	MELO3C022540; MELO3C005389; MELO3C013951; MELO3C006949	MELO3C012522; MELO3C014894; MELO3C009702; MELO3C000924; MELO3C024729; MELO3C006999; MELO3C025525; MELO3C026758; MELO3C023322; MELO3C020331; MELO3C023357; MELO3C025258; MELO3C017010; MELO3C022394; MELO3C025540; MELO3C019212; MELO3C016861; MELO3C010701; MELO3C023063; MELO3C017843
[]	GO:0005615	extracellular space	CELLULAR_COMPONENT	0.6033053896150709	0.029524383754019796	4	20	851	16253	MELO3C025645; MELO3C005679; MELO3C012100; MELO3C011104	MELO3C013885; MELO3C012099; MELO3C012251; MELO3C005357; MELO3C007874; MELO3C007613; MELO3C000533; MELO3C005859; MELO3C005858; MELO3C018077; MELO3C025355; MELO3C018487; MELO3C001915; MELO3C011737; MELO3C013439; MELO3C009580; MELO3C010972; MELO3C011368; MELO3C014735; MELO3C010655
[]	GO:0005811	lipid particle	CELLULAR_COMPONENT	0.6033053896150709	0.029524383754019796	4	20	851	16253	MELO3C009338; MELO3C022094; MELO3C009600; MELO3C005757	MELO3C014237; MELO3C010795; MELO3C011123; MELO3C011021; MELO3C002077; MELO3C005464; MELO3C021946; MELO3C002289; MELO3C021576; MELO3C002027; MELO3C009988; MELO3C017282; MELO3C021891; MELO3C022793; MELO3C024575; MELO3C002813; MELO3C019485; MELO3C017752; MELO3C017642; MELO3C027174
[]	GO:0004069	L-aspartate:2-oxoglutarate aminotransferase activity	MOLECULAR_FUNCTION	0.604221642679414	0.029865739535487545	3	11	852	16262	MELO3C023373; MELO3C001121; MELO3C011284	MELO3C015944; MELO3C010464; MELO3C008136; MELO3C010461; MELO3C018037; MELO3C004980; MELO3C006840; MELO3C005597; MELO3C003577; MELO3C017998; MELO3C026051
[]	GO:0051087	chaperone binding	MOLECULAR_FUNCTION	0.604221642679414	0.029865739535487545	3	11	852	16262	MELO3C005757; MELO3C002717; MELO3C022488	MELO3C004390; MELO3C006948; MELO3C009561; MELO3C010013; MELO3C014179; MELO3C011373; MELO3C019156; MELO3C022725; MELO3C009611; MELO3C022478; MELO3C011830

[]	GO:0051287	NAD binding	MOLECULAR_FUNCTION	0.622789509948272	0.031640449277642944	7	54	848	16219	MELO3C021563; MELO3C019542; MELO3C010727; MELO3C010427; MELO3C021604; MELO3C019633; MELO3C008219	MELO3C006085; MELO3C021919; MELO3C011431; MELO3C006164; MELO3C014221; MELO3C009956; MELO3C024942; MELO3C005116; MELO3C023217; MELO3C017213; MELO3C025076; MELO3C025791; MELO3C027054; MELO3C017853; MELO3C015407; MELO3C014752; MELO3C022537; MELO3C022538; MELO3C020158; MELO3C020157; MELO3C026337; MELO3C024039; MELO3C002813; MELO3C027223; MELO3C013505; MELO3C011129; MELO3C019405;
[]	GO:0003887	DNA-directed DNA polymerase activity	MOLECULAR_FUNCTION	0.62498135374969	0.032009283040244606	5	31	850	16242	MELO3C002044; MELO3C022319; MELO3C020860; MELO3C010631; MELO3C021434	MELO3C011257; MELO3C016705; MELO3C007194; MELO3C005496; MELO3C007012; MELO3C014021; MELO3C014020; MELO3C009536; MELO3C021435; MELO3C005956; MELO3C005957; MELO3C001935; MELO3C010507; MELO3C001936; MELO3C025396; MELO3C001937; MELO3C018521; MELO3C025395; MELO3C014529; MELO3C011159; MELO3C014503; MELO3C002892; MELO3C004237; MELO3C004239; MELO3C004238; MELO3C024597; MELO3C018652;
[]	GO:0009098	leucine biosynthetic process	BIOLOGICAL_PROCESS	0.6282109890968163	0.03264728997105597	2	4	853	16269	MELO3C005518; MELO3C003344	MELO3C017853; MELO3C024817; MELO3C014221; MELO3C020296
[]	GO:0052542	defense response by callose deposition	BIOLOGICAL_PROCESS	0.6282109890968163	0.03264728997105597	2	4	853	16269	MELO3C027349; MELO3C003906	MELO3C014230; MELO3C013621; MELO3C005674; MELO3C005718
[]	GO:0006103	2-oxoglutarate metabolic process	BIOLOGICAL_PROCESS	0.6282109890968163	0.03264728997105597	2	4	853	16269	MELO3C021563; MELO3C011284	MELO3C025076; MELO3C004980; MELO3C003577; MELO3C019166
[]	GO:0004090	carbonyl reductase (NADPH) activity	MOLECULAR_FUNCTION	0.6282109890968163	0.03264728997105597	2	4	853	16269	MELO3C002872; MELO3C001948	MELO3C019918; MELO3C014897; MELO3C021704; MELO3C020605
[]	GO:0009331	glycerol-3-phosphate dehydrogenase complex	CELLULAR_COMPONENT	0.6282109890968163	0.03264728997105597	2	4	853	16269	MELO3C021604; MELO3C019820	MELO3C026337; MELO3C020158; MELO3C020157; MELO3C005116

[]	GO:0009853	photorespiration	BIOLOGICAL_PROCESS	0.6451703098531466	0.033801789095820024	4	21	851	16252	MELO3C022540; MELO3C006949; MELO3C017960; MELO3C026045	MELO3C022919; MELO3C007674; MELO3C007124; MELO3C002086; MELO3C012384; MELO3C012252; MELO3C016909; MELO3C013350; MELO3C009759; MELO3C023322; MELO3C020331; MELO3C023357; MELO3C015151; MELO3C017571; MELO3C000130; MELO3C025540; MELO3C019212; MELO3C013927; MELO3C017388; MELO3C023063; MELO3C023371
[]	GO:0018279	protein N-linked glycosylation via asparagine	BIOLOGICAL_PROCESS	0.6462655173874357	0.03419195373089502	7	55	848	16218	MELO3C003812; MELO3C023310; MELO3C011944; MELO3C025637; MELO3C021279; MELO3C024447; MELO3C013822	MELO3C009473; MELO3C007374; MELO3C002165; MELO3C002166; MELO3C007137; MELO3C021632; MELO3C009914; MELO3C009912; MELO3C026524; MELO3C023850; MELO3C026763; MELO3C020220; MELO3C018343; MELO3C010625; MELO3C017413; MELO3C026482; MELO3C017019; MELO3C004196; MELO3C015929; MELO3C024710; MELO3C017661; MELO3C024194; MELO3C010319; MELO3C015246; MELO3C016018; MELO3C013830; MELO3C014202;
[]	GO:0032555	purine ribonucleotide binding	MOLECULAR_FUNCTION	0.6558991675750125	0.034919271940117624	136	2169	719	14104	MELO3C010189; MELO3C012361; MELO3C006005; MELO3C005673; MELO3C002167; MELO3C001354; MELO3C005679; MELO3C007857; MELO3C003139; MELO3C002687; MELO3C003812; MELO3C011719; MELO3C025550; MELO3C002609; MELO3C015233; MELO3C012525; MELO3C015926; MELO3C021247; MELO3C001920; MELO3C005849; MELO3C020394; MELO3C011208; MELO3C027184; MELO3C010631; MELO3C011256; MELO3C013951; MELO3C007673;	MELO3C014269; MELO3C003133; MELO3C004463; MELO3C007972; MELO3C006648; MELO3C007978; MELO3C008825; MELO3C008829; MELO3C026243; MELO3C019951; MELO3C000093; MELO3C025392; MELO3C015599; MELO3C018624; MELO3C004471; MELO3C020958; MELO3C020959; MELO3C008832; MELO3C008831; MELO3C014272; MELO3C003146; MELO3C021803; MELO3C002299; MELO3C008835; MELO3C005329; MELO3C008838; MELO3C026259;
[]	GO:0042817	pyridoxal metabolic process	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C003541	
[]	GO:0048482	plant ovule morphogenesis	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C010913	
[]	GO:0015680	intracellular copper ion transport	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C014007	

[]	GO:0046087	cytidine metabolic process	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C015459	
[]	GO:0071398	cellular response to fatty acid	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C019735	
[]	GO:0005978	glycogen biosynthetic process	BIOLOGICAL_PROCESS	0.6586979665414314	0.03842062202444051	4	22	851	16251	MELO3C005293; MELO3C003812; MELO3C023310; MELO3C020244	MELO3C011991; MELO3C013146; MELO3C004270; MELO3C005396; MELO3C009445; MELO3C006552; MELO3C009861; MELO3C007155; MELO3C008045; MELO3C005795; MELO3C002455; MELO3C021412; MELO3C008407; MELO3C008614; MELO3C021249; MELO3C026536; MELO3C025521; MELO3C024175; MELO3C012925; MELO3C018534; MELO3C010862; MELO3C011346
[]	GO:0006616	SRP-dependent cotranslational protein targeting to membrane, translocation	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C005757	
[]	GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	BIOLOGICAL_PROCESS	0.6586979665414314	0.04868599878337037	4	24	851	16249	MELO3C016083; MELO3C010960; MELO3C016262; MELO3C012361	MELO3C011983; MELO3C002481; MELO3C011470; MELO3C021746; MELO3C014086; MELO3C000704; MELO3C004136; MELO3C021715; MELO3C025923; MELO3C025417; MELO3C005738; MELO3C023476; MELO3C026239; MELO3C003316; MELO3C025755; MELO3C026800; MELO3C005912; MELO3C020453; MELO3C018099; MELO3C019642; MELO3C019587; MELO3C019731; MELO3C013814; MELO3C016699
[]	GO:0031938	regulation of chromatin silencing at telomere	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C021058	
[]	GO:0030950	establishment or maintenance of actin cytoskeleton polarity	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C026614	
[]	GO:0046292	formaldehyde metabolic process	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C022399	
[]	GO:0006561	proline biosynthetic process	BIOLOGICAL_PROCESS	0.6586979665414314	0.044214600976853265	2	5	853	16268	MELO3C008245; MELO3C011208	MELO3C019039; MELO3C009229; MELO3C005129; MELO3C024239; MELO3C002752
[]	GO:0010812	negative regulation of cell-substrate adhesion	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C022488	
[]	GO:0006420	arginyl-tRNA aminoacylation	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C015422	

[]	GO:0040018	positive regulation of multicellular organism growth	BIOLOGICAL_PROCESS	0.6586979665414314	0.03931024287564423	5	33	850	16240	MELO3C013753; MELO3C002118; MELO3C010882; MELO3C011285; MELO3C025061	MELO3C012740; MELO3C002182; MELO3C022308; MELO3C004344; MELO3C009413; MELO3C020586; MELO3C022588; MELO3C022888; MELO3C004945; MELO3C026228; MELO3C025972; MELO3C026663; MELO3C018102; MELO3C004807; MELO3C023594; MELO3C016981; MELO3C014708; MELO3C024020; MELO3C017676; MELO3C010721; MELO3C027090; MELO3C009702; MELO3C000924; MELO3C008835; MELO3C021342; MELO3C026578; MELO3C017365;
[]	GO:0042435	indole-containing compound biosynthetic process	BIOLOGICAL_PROCESS	0.6586979665414314	0.04268318608102429	3	13	852	16260	MELO3C026887; MELO3C002275; MELO3C013757	MELO3C008294; MELO3C014311; MELO3C020718; MELO3C007920; MELO3C009018; MELO3C005674; MELO3C009127; MELO3C002476; MELO3C018082; MELO3C026789; MELO3C022074; MELO3C024189; MELO3C011963
[]	GO:1901264	carbohydrate derivative transport	BIOLOGICAL_PROCESS	0.6586979665414314	0.04268318608102429	3	13	852	16260	MELO3C006409; MELO3C011675; MELO3C004533	MELO3C010474; MELO3C012236; MELO3C013485; MELO3C013186; MELO3C008403; MELO3C020559; MELO3C007756; MELO3C006217; MELO3C021055; MELO3C017661; MELO3C011559; MELO3C011623; MELO3C011676
[]	GO:0006123	mitochondrial electron transport, cytochrome c to oxygen	BIOLOGICAL_PROCESS	0.6586979665414314	0.044214600976853265	2	5	853	16268	MELO3C004105; MELO3C011044	MELO3C015922; MELO3C003366; MELO3C016120; MELO3C018157; MELO3C006242
[]	GO:0006121	mitochondrial electron transport, succinate to ubiquinone	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C017560	
[]	GO:0006127	glycerophosphate shuttle	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C019820	
[]	GO:0009629	response to gravity	BIOLOGICAL_PROCESS	0.6586979665414314	0.04268318608102429	3	13	852	16260	MELO3C005293; MELO3C008847; MELO3C025282	MELO3C008088; MELO3C005396; MELO3C002781; MELO3C002354; MELO3C000009; MELO3C021982; MELO3C025310; MELO3C017043; MELO3C004827; MELO3C024155; MELO3C026110; MELO3C013815; MELO3C017414
[]	GO:0019563	glycerol catabolic process	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C019820	

[]	GO:0009401	phosphoenolpyruvate-dependent sugar phosphotransferase system	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C016017	
[]	GO:0098542	defense response to other organism	BIOLOGICAL_PROCESS	0.6586979665414314	0.040943794239169086	16	173	839	16100	MELO3C006870; MELO3C020628; MELO3C010042; MELO3C006187; MELO3C005147; MELO3C005214; MELO3C009429; MELO3C005215; MELO3C018573; MELO3C003906; MELO3C016033; MELO3C015374; MELO3C018841; MELO3C016972; MELO3C012527; MELO3C013757	MELO3C021918; MELO3C005550; MELO3C014386; MELO3C005312; MELO3C003133; MELO3C006765; MELO3C005035; MELO3C005674; MELO3C009633; MELO3C007214; MELO3C003137; MELO3C024989; MELO3C003536; MELO3C004867; MELO3C022283; MELO3C019155; MELO3C002608; MELO3C019315; MELO3C025152; MELO3C015872; MELO3C014706; MELO3C010623; MELO3C013621; MELO3C007583; MELO3C002054; MELO3C020956; MELO3C020157;
[]	GO:0007310	oocyte dorsal/ventral axis specification	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C011193	
[]	GO:0009727	detection of ethylene stimulus	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C003906	
[]	GO:0000738	DNA catabolic process, exonucleolytic	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C006293	
[]	GO:0007018	microtubule-based movement	BIOLOGICAL_PROCESS	0.6586979665414314	0.03646946081068046	9	74	846	16199	MELO3C009203; MELO3C024241; MELO3C007673; MELO3C023342; MELO3C015098; MELO3C005673; MELO3C013429; MELO3C013702; MELO3C008977	MELO3C017936; MELO3C017937; MELO3C005594; MELO3C015839; MELO3C014142; MELO3C004267; MELO3C020741; MELO3C020742; MELO3C005479; MELO3C007217; MELO3C009715; MELO3C005678; MELO3C021238; MELO3C003218; MELO3C023013; MELO3C015272; MELO3C002528; MELO3C010629; MELO3C015273; MELO3C018025; MELO3C017377; MELO3C010988; MELO3C016369; MELO3C010147; MELO3C010787; MELO3C009760; MELO3C004273;
[]	GO:0008347	glial cell migration	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C011193	

[]	GO:0009308	amine metabolic process	BIOLOGICAL_PROCESS	0.6586979665414314	0.04701433570500883	9	82	846	16191	MELO3C026887; MELO3C010960; MELO3C016262; MELO3C011484; MELO3C003906; MELO3C016881; MELO3C002275; MELO3C023315; MELO3C005578	MELO3C016208; MELO3C012201; MELO3C004185; MELO3C004184; MELO3C004187; MELO3C010461; MELO3C005153; MELO3C005877; MELO3C007417; MELO3C004624; MELO3C004626; MELO3C025755; MELO3C026800; MELO3C023775; MELO3C017173; MELO3C026323; MELO3C024189; MELO3C015199; MELO3C013814; MELO3C015478; MELO3C012007; MELO3C014479; MELO3C014478; MELO3C014311; MELO3C008477; MELO3C002293; MELO3C014035;
[]	GO:0031115	negative regulation of microtubule polymerization	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C022488	
[]	GO:0006297	nucleotide-excision repair, DNA gap filling	BIOLOGICAL_PROCESS	0.6586979665414314	0.04268318608102429	3	13	852	16260	MELO3C017228; MELO3C010631; MELO3C003638	MELO3C014021; MELO3C014020; MELO3C008864; MELO3C026949; MELO3C025879; MELO3C010507; MELO3C024596; MELO3C001937; MELO3C018521; MELO3C025142; MELO3C014529; MELO3C014528; MELO3C017458
[]	GO:0042149	cellular response to glucose starvation	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C005757	
[]	GO:0035821	modification of morphology or physiology of other organism	BIOLOGICAL_PROCESS	0.6586979665414314	0.04268318608102429	3	13	852	16260	MELO3C005214; MELO3C016972; MELO3C005215	MELO3C012664; MELO3C011257; MELO3C010750; MELO3C015938; MELO3C007375; MELO3C005642; MELO3C005643; MELO3C005641; MELO3C021126; MELO3C023207; MELO3C023203; MELO3C005929; MELO3C001957
[]	GO:0007229	integrin-mediated signaling pathway	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C007690	

[]	GO:0009664	plant-type cell wall organization	BIOLOGICAL_PROCESS	0.6586979665414314	0.043310123129766544	5	34	850	16239	MELO3C012004; MELO3C021999; MELO3C020626; MELO3C017242; MELO3C010524	MELO3C010062; MELO3C021619; MELO3C011350; MELO3C020005; MELO3C003134; MELO3C005613; MELO3C001993; MELO3C017181; MELO3C024488; MELO3C025996; MELO3C024487; MELO3C016062; MELO3C026188; MELO3C020143; MELO3C003916; MELO3C015695; MELO3C025095; MELO3C012108; MELO3C011732; MELO3C016517; MELO3C016916; MELO3C014013; MELO3C025907; MELO3C008552; MELO3C020810; MELO3C005962; MELO3C006318;
[]	GO:0046827	positive regulation of protein export from nucleus	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C007207	
[]	GO:0010342	endosperm cellularization	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C006602	
[]	GO:0060904	regulation of protein folding in endoplasmic reticulum	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C005757	
[]	GO:0010312	detoxification of zinc ion	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C022448	
[]	GO:0048759	xylem vessel member cell differentiation	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C011484	
[]	GO:0001556	oocyte maturation	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C012361	
[]	GO:0046474	glycerophospholipid biosynthetic process	BIOLOGICAL_PROCESS	0.6586979665414314	0.03931024287564423	5	33	850	16240	MELO3C007931; MELO3C008959; MELO3C025637; MELO3C015670; MELO3C012545	MELO3C013830; MELO3C007010; MELO3C012286; MELO3C020821; MELO3C020987; MELO3C005332; MELO3C022308; MELO3C020989; MELO3C005634; MELO3C021052; MELO3C026440; MELO3C017214; MELO3C013319; MELO3C017019; MELO3C010621; MELO3C011215; MELO3C015647; MELO3C011047; MELO3C013842; MELO3C009088; MELO3C009186; MELO3C013982; MELO3C014212; MELO3C008992; MELO3C005285; MELO3C006258; MELO3C014054;
[]	GO:0034333	adherens junction assembly	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C022488	
[]	GO:0010266	response to vitamin B1	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C020562	
[]	GO:0032012	regulation of ARF protein signal transduction	BIOLOGICAL_PROCESS	0.6586979665414314	0.044214600976853265	2	5	853	16268	MELO3C004551; MELO3C006224	MELO3C023883; MELO3C012923; MELO3C012924; MELO3C006181; MELO3C015692

[]	GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C005757	
[]	GO:0010299	detoxification of cobalt ion	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C022448	
[]	GO:0048730	epidermis morphogenesis	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C006929	
[]	GO:0015966	diadenosine tetraphosphate biosynthetic process	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C003905	
[]	GO:0034484	raffinose catabolic process	BIOLOGICAL_PROCESS	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C023110	
[]	GO:0006903	vesicle targeting	BIOLOGICAL_PROCESS	0.6586979665414314	0.03931024287564423	5	33	850	16240	MELO3C010243; MELO3C004551; MELO3C021279; MELO3C024447; MELO3C009966	MELO3C013434; MELO3C006782; MELO3C023339; MELO3C021556; MELO3C009912; MELO3C023630; MELO3C020980; MELO3C025796; MELO3C024225; MELO3C026763; MELO3C018343; MELO3C012923; MELO3C012528; MELO3C019856; MELO3C010666; MELO3C007042; MELO3C009240; MELO3C004196; MELO3C007300; MELO3C009269; MELO3C012991; MELO3C007583; MELO3C015929; MELO3C005422; MELO3C005423; MELO3C009969; MELO3C023883;
[]	GO:0004301	epoxide hydrolase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C017946	
[]	GO:0030942	endoplasmic reticulum signal peptide binding	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C002757	
[]	GO:0050311	sulfite reductase (ferredoxin) activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C015186	

[]	GO:0005509	calcium ion binding	MOLECULAR_FUNCTION	0.6586979665414314	0.04599840092609351	18	209	837	16064	MELO3C014016; MELO3C004194; MELO3C014588; MELO3C010794; MELO3C013892; MELO3C006158; MELO3C014150; MELO3C005757; MELO3C026749; MELO3C006759; MELO3C019002; MELO3C022494; MELO3C022260; MELO3C019820; MELO3C017844; MELO3C013702; MELO3C014658; MELO3C012457	MELO3C003372; MELO3C004465; MELO3C008705; MELO3C024866; MELO3C025712; MELO3C023415; MELO3C005319; MELO3C002967; MELO3C019035; MELO3C019036; MELO3C020263; MELO3C015597; MELO3C016569; MELO3C010348; MELO3C020719; MELO3C014279; MELO3C013982; MELO3C023542; MELO3C007507; MELO3C020277; MELO3C016330; MELO3C016333; MELO3C018876; MELO3C018877; MELO3C013504; MELO3C018517; MELO3C018879;
[]	GO:0016532	superoxide dismutase copper chaperone activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C014007	
[]	GO:0050201	fucokinase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C006005	
[]	GO:0008908	isochorismatase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C011747	
[]	GO:0016762	xyloglucan:xyloglucosyl transferase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04868599878337037	4	24	851	16249	MELO3C012004; MELO3C017480; MELO3C017481; MELO3C017478	MELO3C014469; MELO3C014468; MELO3C014467; MELO3C014466; MELO3C014465; MELO3C002480; MELO3C009367; MELO3C004087; MELO3C003441; MELO3C024704; MELO3C005245; MELO3C021686; MELO3C004941; MELO3C018292; MELO3C026945; MELO3C001951; MELO3C026755; MELO3C017482; MELO3C021685; MELO3C018033; MELO3C011706; MELO3C017476; MELO3C018785; MELO3C017479
[]	GO:0004637	phosphoribosylamine-glycine ligase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C016483	
[]	GO:0052636	arabinosyltransferase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C010524	
[]	GO:0035259	glucocorticoid receptor binding	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C012231	

[]	GO:0016859	cis-trans isomerase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.042652839615580286	7	58	848	16215	MELO3C014557; MELO3C023224; MELO3C007001; MELO3C020806; MELO3C021108; MELO3C025848; MELO3C002951	MELO3C011036; MELO3C012489; MELO3C013896; MELO3C017816; MELO3C010261; MELO3C013375; MELO3C015916; MELO3C006285; MELO3C008222; MELO3C021912; MELO3C009952; MELO3C002126; MELO3C007778; MELO3C026524; MELO3C003338; MELO3C019631; MELO3C024662; MELO3C017776; MELO3C025192; MELO3C016887; MELO3C011236; MELO3C008553; MELO3C006176; MELO3C004752; MELO3C022335; MELO3C023984; MELO3C016495;
[]	GO:0050347	trans-octaprenyltranstransferase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C016140	
[]	GO:0019706	protein-cysteine S-palmitoyltransferase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C010243	
[]	GO:0047115	trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C019948	
[]	GO:0050521	alpha-glucan, water dikinase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C011972	
[]	GO:0030732	methionine S-methyltransferase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C016448	
[]	GO:0005302	L-tyrosine transmembrane transporter activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C006926	
[]	GO:0004334	fumarylacetoacetase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C007433	
[]	GO:0015036	disulfide oxidoreductase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04886177695251247	9	83	846	16190	MELO3C017902; MELO3C012410; MELO3C010860; MELO3C016056; MELO3C019722; MELO3C019326; MELO3C018455; MELO3C022425; MELO3C024527	MELO3C009478; MELO3C011352; MELO3C008421; MELO3C005790; MELO3C007253; MELO3C022405; MELO3C021955; MELO3C006322; MELO3C009556; MELO3C003731; MELO3C021554; MELO3C001994; MELO3C023932; MELO3C026569; MELO3C021276; MELO3C024468; MELO3C025752; MELO3C014909; MELO3C021350; MELO3C021351; MELO3C017411; MELO3C012969; MELO3C017410; MELO3C019913; MELO3C008750; MELO3C012053; MELO3C009882;

[]	GO:0005354	galactose transmembrane transporter activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C004576	
[]	GO:0004386	helicase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04642639838006491	5	224	850	16049	MELO3C011256; MELO3C006754; MELO3C008195; MELO3C010042; MELO3C007144	MELO3C014025; MELO3C004343; MELO3C006765; MELO3C013051; MELO3C005432; MELO3C004226; MELO3C008825; MELO3C019281; MELO3C021352; MELO3C022562; MELO3C008829; MELO3C021353; MELO3C003935; MELO3C004905; MELO3C003937; MELO3C003936; MELO3C015231; MELO3C008833; MELO3C008832; MELO3C008831; MELO3C005443; MELO3C008835; MELO3C018998; MELO3C019967; MELO3C006188; MELO3C005650; MELO3C003111;
[]	GO:0004022	alcohol dehydrogenase (NAD) activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04268318608102429	3	13	852	16260	MELO3C023685; MELO3C026554; MELO3C022399	MELO3C014897; MELO3C005792; MELO3C011043; MELO3C005482; MELO3C003251; MELO3C005521; MELO3C008767; MELO3C007314; MELO3C002189; MELO3C005129; MELO3C004714; MELO3C026553; MELO3C027151
[]	GO:0000906	6,7-dimethyl-8-ribityllumazine synthase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C011439	
[]	GO:0052591	sn-glycerol-3-phosphate:ubiquinone-8 oxidoreductase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C019820	
[]	GO:0005125	cytokine activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C011104	
[]	GO:0051499	D-aminoacyl-tRNA deacylase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C011402	
[]	GO:0016002	sulfite reductase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C015186	
[]	GO:0004126	cytidine deaminase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C015459	
[]	GO:0008836	diaminopimelate decarboxylase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C023315	
[]	GO:0004369	glycerol-3-phosphate oxidase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C019820	
[]	GO:0030755	quercetin 3-O-methyltransferase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C024861	
[]	GO:0005153	interleukin-8 receptor binding	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C005679	

[]	GO:0033858	N-acetylgalactosamine kinase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C006726	
[]	GO:0015088	copper uptake transmembrane transporter activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C018494	
[]	GO:0004073	aspartate-semialdehyde dehydrogenase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C010427	
[]	GO:0033961	cis-stilbene-oxide hydrolase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C015292	
[]	GO:0030331	estrogen receptor binding	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C012231	
[]	GO:0004048	anthranilate phosphoribosyltransferase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C002275	
[]	GO:0008893	guanosine-3',5'-bis(diphosphate) 3'-diphosphatase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C006759	
[]	GO:0030797	24-methylenesterol C-methyltransferase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C003726	
[]	GO:0047705	bilirubin oxidase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C005201	
[]	GO:0032442	phenylcoumaran benzylic ether reductase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C023304	
[]	GO:0030267	glyoxylate reductase (NADP) activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C013093	
[]	GO:0005086	ARF guanyl-nucleotide exchange factor activity	MOLECULAR_FUNCTION	0.6586979665414314	0.044214600976853265	2	5	853	16268	MELO3C004551; MELO3C006224	MELO3C023883; MELO3C012923; MELO3C012924; MELO3C006181; MELO3C015692
[]	GO:0008236	serine-type peptidase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.03826395328303021	3	181	852	16092	MELO3C007609; MELO3C004551; MELO3C004117	MELO3C014268; MELO3C014267; MELO3C016729; MELO3C011396; MELO3C007179; MELO3C002041; MELO3C006885; MELO3C004189; MELO3C001076; MELO3C011392; MELO3C004223; MELO3C008786; MELO3C023414; MELO3C004228; MELO3C003810; MELO3C005832; MELO3C023899; MELO3C021473; MELO3C021474; MELO3C021475; MELO3C024346; MELO3C022444; MELO3C017011; MELO3C021472; MELO3C019830; MELO3C026085; MELO3C026240;

[]	GO:0047837	D-xylose 1-dehydrogenase (NADP+) activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C019948	
[]	GO:0034618	arginine binding	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C011208	
[]	GO:0032550	purine ribonucleoside binding	MOLECULAR_FUNCTION	0.6586979665414314	0.03943443736037198	135	2163	720	14110	MELO3C010189; MELO3C012361; MELO3C006005; MELO3C005673; MELO3C002167; MELO3C001354; MELO3C005679; MELO3C007857; MELO3C003139; MELO3C002687; MELO3C003812; MELO3C011719; MELO3C025550; MELO3C002609; MELO3C015233; MELO3C012525; MELO3C015926; MELO3C021247; MELO3C001920; MELO3C005849; MELO3C020394; MELO3C011208; MELO3C027184; MELO3C010631; MELO3C011256; MELO3C013951; MELO3C007673;	MELO3C014269; MELO3C003133; MELO3C004463; MELO3C007972; MELO3C006648; MELO3C007978; MELO3C008825; MELO3C008829; MELO3C026243; MELO3C019951; MELO3C000093; MELO3C025392; MELO3C015599; MELO3C018624; MELO3C004471; MELO3C020958; MELO3C020959; MELO3C008832; MELO3C008831; MELO3C014272; MELO3C003146; MELO3C021803; MELO3C002299; MELO3C008835; MELO3C005329; MELO3C008838; MELO3C026259;
[]	GO:0034722	gamma-glutamyl-peptidase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C025645	
[]	GO:0033799	myricetin 3'-O-methyltransferase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C024861	
[]	GO:0004814	arginine-tRNA ligase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C015422	
[]	GO:0070205	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C012178	
[]	GO:0047560	3-dehydrosphinganine reductase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C006553	
[]	GO:0003977	UDP-N-acetylglucosamine diphosphorylase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C007022	
[]	GO:0003978	UDP-glucose 4-epimerase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.044214600976853265	2	5	853	16268	MELO3C007043; MELO3C016300	MELO3C019557; MELO3C005769; MELO3C026841; MELO3C021813; MELO3C005640
[]	GO:0080007	S-nitrosoglutathione reductase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C022399	
[]	GO:0010487	thermospermine synthase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C011484	
[]	GO:0034020	neoxanthin synthase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C017963	
[]	GO:0000026	alpha-1,2-mannosyltransferase activity	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C025637	

[]	GO:0010297	heteropolysaccharide binding	MOLECULAR_FUNCTION	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C019135	
[]	GO:0005751	mitochondrial respiratory chain complex IV	CELLULAR_COMPONENT	0.6586979665414314	0.044214600976853265	2	5	853	16268	MELO3C004105; MELO3C011044	MELO3C015922; MELO3C003366; MELO3C016926; MELO3C014946; MELO3C016120
[]	GO:0034099	luminal surveillance complex	CELLULAR_COMPONENT	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C005757	
[]	GO:0005662	DNA replication factor A complex	CELLULAR_COMPONENT	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C017228	
[]	GO:0009842	cyanelle	CELLULAR_COMPONENT	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C016140	
[]	GO:0009930	longitudinal side of cell surface	CELLULAR_COMPONENT	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C017242	
[]	GO:0042555	MCM complex	CELLULAR_COMPONENT	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C020001	
[]	GO:0008305	integrin complex	CELLULAR_COMPONENT	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C007690	
[]	GO:0031672	A band	CELLULAR_COMPONENT	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C011193	
[]	GO:0031429	box H/ACA snoRNP complex	CELLULAR_COMPONENT	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C008801	
[]	GO:0018444	translation release factor complex	CELLULAR_COMPONENT	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C002118	
[]	GO:0009316	3-isopropylmalate dehydratase complex	CELLULAR_COMPONENT	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C005518	
[]	GO:0034663	endoplasmic reticulum chaperone complex	CELLULAR_COMPONENT	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C005757	
[]	GO:0009349	riboflavin synthase complex	CELLULAR_COMPONENT	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C011439	
[]	GO:0010005	cortical microtubule, transverse to long axis	CELLULAR_COMPONENT	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C012361	
[]	GO:0005960	glycine cleavage complex	CELLULAR_COMPONENT	0.6586979665414314	0.044214600976853265	2	5	853	16268	MELO3C021742; MELO3C021247	MELO3C003386; MELO3C003734; MELO3C002444; MELO3C006734; MELO3C010754
[]	GO:0033162	melanosome membrane	CELLULAR_COMPONENT	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C006926	
[]	GO:0005923	bicellular tight junction	CELLULAR_COMPONENT	0.6586979665414314	0.04991826249403735	1	0	854	16273	MELO3C022488	

Supplementary Table 1.D Gene Ontology terms (GO terms) of the cluster 1.3 obtained considering the comparison between lines over time fruit during storage at 20.5°C and 88% relative humidity for 18 d the near-isogenic line SC10-2 and its parental ''Piel de Sapo'' obtained according to the differentially expressed gene pattern (Supl. Table 1.A)

Tags	GO ID	GO Name	GO Category	FDR	P-Value	Nr Test	Nr Reference	Non Annot Test	Non Annot Reference	TestSet Sequences	RefSet Sequences
[OVER]	GO:0000398	mRNA splicing, via spliceosome	BIOLOGICAL_PROCESS	7.023016141773119E-4	1.997384714123258E-7	12	123	211	16782	MELO3C026304;MELO3C008076;MELO3C024028;MELO3C014555;MELO3C008690;MELO3C024775;MELO3C015043;MELO3C015299;MELO3C020824;MELO3C009776;MELO3C003973;MELO3C012788	MELO3C010981;MELO3C012489;MELO3C013333;MELO3C004580;MELO3C008023;MELO3C021758;MELO3C002045;MELO3C006125;MELO3C023531;MELO3C018062;MELO3C000014;MELO3C020022;MELO3C017775;MELO3C011313;MELO3C013741;MELO3C010355;MELO3C008151;MELO3C008157;MELO3C002173;MELO3C023428;MELO3C008798;MELO3C006416;MELO3C023545;MELO3C023823;MELO3C023427;MELO3C024757;MELO3C004637;MELO3C024993;MELO3C017020;MELO3C026776;MELO3C003707;MELO3C012778;MELO3C007190;MELO3C011
[OVER]	GO:0071013	catalytic step 2 spliceosome	CELLULAR_COMPONENT	0.003643956269614251	2.6997982522544195E-6	7	41	216	16864	MELO3C026304;MELO3C008076;MELO3C024028;MELO3C014555;MELO3C008690;MELO3C024775;MELO3C020824	MELO3C011851;MELO3C008488;MELO3C008344;MELO3C014122;MELO3C004440;MELO3C008023;MELO3C004123;MELO3C002120;MELO3C007631;MELO3C009413;MELO3C024822;MELO3C023475;MELO3C021157;MELO3C017338;MELO3C009580;MELO3C011414;MELO3C012449;MELO3C009381;MELO3C015733;MELO3C012622;MELO3C012214;MELO3C013443;MELO3C008151;MELO3C008332;MELO3C015907;MELO3C004752;MELO3C023545;MELO3C023823;MELO3C023427;MELO3C002633;MELO3C024757;MELO3C021320;MELO3C017020;MELO3C003
[OVER]	GO:0009408	response to heat	BIOLOGICAL_PROCESS	0.02665513427358699	2.2569969749015234E-5	8	82	215	16823	MELO3C006188;MELO3C018950;MELO3C010748;MELO3C004553;MELO3C013946;MELO3C009996;MELO3C023526;MELO3C020589	MELO3C013974;MELO3C008263;MELO3C005873;MELO3C005035;MELO3C008589;MELO3C014183;MELO3C005674;MELO3C018780;MELO3C026886;MELO3C018023;MELO3C018660;MELO3C001916;MELO3C019039;MELO3C012925;MELO3C015312;MELO3C016449;MELO3C012455;MELO3C012136;MELO3C012456;MELO3C015608;MELO3C012331;MELO3C009840;MELO3C014230;MELO3C005884;MELO3C008677;MELO3C009127;MELO3C020872;MELO3C005129;MELO3C003785;MELO3C006536;MELO3C005923;MELO3C025686;MELO3C003906;MELO3C016
[OVER]	GO:0071011	precatalytic spliceosome	CELLULAR_COMPONENT	0.032866255319277844	3.1307821536145275E-5	6	41	217	16864	MELO3C026304;MELO3C008076;MELO3C024028;MELO3C014555;MELO3C008690;MELO3C020824	MELO3C012489;MELO3C011851;MELO3C002181;MELO3C013333;MELO3C008488;MELO3C008344;MELO3C014122;MELO3C004440;MELO3C022928;MELO3C008023;MELO3C004123;MELO3C002120;MELO3C006787;MELO3C024822;MELO3C024685;MELO3C023475;MELO3C017338;MELO3C009580;MELO3C011414;MELO3C012449;MELO3C009381;MELO3C012622;MELO3C012214;MELO3C013443;MELO3C008151;MELO3C008332;MELO3C015907;MELO3C023823;MELO3C023427;MELO3C002633;MELO3C002556;MELO3C024757;MELO3C021320;MELO3C017
[]	GO:0005689	U12-type spliceosomal complex	CELLULAR_COMPONENT	0.1964010444402452	3.326012606947421E-4	3	8	220	16897	MELO3C014555;MELO3C008690;MELO3C006785	MELO3C019829;MELO3C017020;MELO3C001824;MELO3C015907;MELO3C006787;MELO3C024822;MELO3C016998;MELO3C023823

[]	GO:0051082	unfolded protein binding	MOLECULAR_FUNCTION	0.4249246706176366	9.739001164321701E-4	8	147	215	16758	MELO3C024554;MELO3C013792;MELO3C008871;MELO3C015043;MELO3C018950;MELO3C009996;MELO3C009408;MELO3C023526	MELO3C013215;MELO3C013333;MELO3C014661;MELO3C020425;MELO3C007610;MELO3C008428;MELO3C003534;MELO3C026888;MELO3C004506;MELO3C026886;MELO3C024104;MELO3C019433;MELO3C001916;MELO3C017379;MELO3C018866;MELO3C004194;MELO3C014551;MELO3C009245;MELO3C010230;MELO3C020799;MELO3C005449;MELO3C002214;MELO3C023267;MELO3C004636;MELO3C006935;MELO3C007908;MELO3C016178;MELO3C015366;MELO3C010357;MELO3C010356;MELO3C014249;MELO3C015615;MELO3C016946;MELO3C013
[]	GO:0031072	heat shock protein binding	MOLECULAR_FUNCTION	0.49441100596981835	0.00125591280093942	7	118	216	16787	MELO3C024554;MELO3C008871;MELO3C015043;MELO3C018950;MELO3C009996;MELO3C009408;MELO3C023526	MELO3C013215;MELO3C013333;MELO3C014661;MELO3C020425;MELO3C022725;MELO3C007610;MELO3C008941;MELO3C008428;MELO3C003534;MELO3C004506;MELO3C026886;MELO3C024104;MELO3C025310;MELO3C019433;MELO3C003815;MELO3C010989;MELO3C001916;MELO3C017379;MELO3C018866;MELO3C009245;MELO3C020799;MELO3C005449;MELO3C002214;MELO3C007108;MELO3C023267;MELO3C007908;MELO3C016178;MELO3C015366;MELO3C010357;MELO3C010356;MELO3C014249;MELO3C016946;MELO3C004040;MELO3C004
[]	GO:0019919	peptidyl-arginine methylation, to asymmetrical-dimethyl arginine	BIOLOGICAL_PROCESS	1.0	0.01301961700147596	1	0	222	16905	MELO3C026636	
[]	GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	BIOLOGICAL_PROCESS	1.0	0.024946795985492702	2	17	221	16888	MELO3C026304;MELO3C024028	MELO3C015714;MELO3C011145;MELO3C013051;MELO3C008956;MELO3C006767;MELO3C021931;MELO3C008955;MELO3C026612;MELO3C026327;MELO3C007816;MELO3C025497;MELO3C003804;MELO3C025498;MELO3C026263;MELO3C015113;MELO3C013879;MELO3C026290
[]	GO:0045893	positive regulation of transcription, DNA-templated	BIOLOGICAL_PROCESS	1.0	0.018069972302826434	4	73	219	16832	MELO3C010748;MELO3C007103;MELO3C004553;MELO3C012788	MELO3C013015;MELO3C006760;MELO3C005791;MELO3C008304;MELO3C006520;MELO3C007015;MELO3C004622;MELO3C003216;MELO3C022562;MELO3C017295;MELO3C019433;MELO3C019554;MELO3C017650;MELO3C024460;MELO3C015512;MELO3C017429;MELO3C015209;MELO3C006131;MELO3C020474;MELO3C003429;MELO3C015360;MELO3C024352;MELO3C016099;MELO3C011649;MELO3C015367;MELO3C015885;MELO3C018910;MELO3C015447;MELO3C014514;MELO3C010512;MELO3C010435;MELO3C009890;MELO3C016827;MELO3C005
[]	GO:0000740	nuclear membrane fusion	BIOLOGICAL_PROCESS	1.0	0.01301961700147596	1	0	222	16905	MELO3C023526	
[]	GO:0009661	chromoplast organization	BIOLOGICAL_PROCESS	1.0	0.025870473860622564	1	1	222	16904	MELO3C024554	MELO3C005449

[]	GO:0051437	positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	BIOLOGICAL_PROCESS	1.0	0.014098846254561674	3	36	220	16869	MELO3C025232;MELO3C013814;MELO3C013359	MELO3C010960;MELO3C013750;MELO3C014684;MELO3C002481;MELO3C012361;MELO3C014086;MELO3C025417;MELO3C005733;MELO3C025413;MELO3C023476;MELO3C016083;MELO3C025755;MELO3C024685;MELO3C026800;MELO3C005615;MELO3C005912;MELO3C016262;MELO3C016464;MELO3C026580;MELO3C012407;MELO3C011345;MELO3C011983;MELO3C014573;MELO3C021746;MELO3C000704;MELO3C004136;MELO3C006972;MELO3C005866;MELO3C025923;MELO3C020453;MELO3C018099;MELO3C019642;MELO3C019587;MELO3C015
[]	GO:0051436	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	BIOLOGICAL_PROCESS	1.0	0.010487172374009144	3	32	220	16873	MELO3C025232;MELO3C013814;MELO3C013359	MELO3C010960;MELO3C014684;MELO3C002481;MELO3C025417;MELO3C005733;MELO3C025413;MELO3C023476;MELO3C016083;MELO3C025755;MELO3C024685;MELO3C026800;MELO3C005615;MELO3C005912;MELO3C016262;MELO3C016147;MELO3C026580;MELO3C011983;MELO3C014573;MELO3C021349;MELO3C021746;MELO3C000704;MELO3C004136;MELO3C006972;MELO3C002234;MELO3C005866;MELO3C025923;MELO3C008916;MELO3C020453;MELO3C018099;MELO3C019642;MELO3C019587;MELO3C012437
[]	GO:0031145	anaphase-promoting complex-dependent catabolic process	BIOLOGICAL_PROCESS	1.0	0.03481435066814285	3	52	220	16853	MELO3C025232;MELO3C013814;MELO3C013359	MELO3C002481;MELO3C012361;MELO3C016083;MELO3C025755;MELO3C026800;MELO3C005912;MELO3C023372;MELO3C010828;MELO3C018501;MELO3C012407;MELO3C006173;MELO3C006972;MELO3C025923;MELO3C008916;MELO3C019642;MELO3C013349;MELO3C010960;MELO3C011895;MELO3C013750;MELO3C014684;MELO3C003672;MELO3C014086;MELO3C003476;MELO3C003673;MELO3C025417;MELO3C005733;MELO3C025413;MELO3C023476;MELO3C024685;MELO3C005615;MELO3C016262;MELO3C026341;MELO3C016147;MELO3C026
[]	GO:0006986	response to unfolded protein	BIOLOGICAL_PROCESS	1.0	0.010220396281260216	2	10	221	16895	MELO3C022707;MELO3C010748	MELO3C021891;MELO3C007383;MELO3C010795;MELO3C012198;MELO3C018660;MELO3C009730;MELO3C006478;MELO3C012527;MELO3C017118;MELO3C005757
[]	GO:0047497	mitochondrion transport along microtubule	BIOLOGICAL_PROCESS	1.0	0.025870473860622564	1	1	222	16904	MELO3C004273	MELO3C015839
[]	GO:0045071	negative regulation of viral genome replication	BIOLOGICAL_PROCESS	1.0	0.01301961700147596	1	0	222	16905	MELO3C026304	
[]	GO:0075713	establishment of integrated proviral latency	BIOLOGICAL_PROCESS	1.0	0.03855474831574392	1	2	222	16903	MELO3C006188	MELO3C018624;MELO3C017678
[]	GO:0080163	regulation of protein serine/threonine phosphatase activity	BIOLOGICAL_PROCESS	1.0	0.01301961700147596	1	0	222	16905	MELO3C005380	
[]	GO:0051085	chaperone mediated protein folding requiring cofactor	BIOLOGICAL_PROCESS	1.0	0.025870473860622564	1	1	222	16904	MELO3C023526	MELO3C007116
[]	GO:0019933	cAMP-mediated signaling	BIOLOGICAL_PROCESS	1.0	0.025870473860622564	1	1	222	16904	MELO3C006948	MELO3C026602
[]	GO:0007094	mitotic spindle assembly checkpoint	BIOLOGICAL_PROCESS	1.0	0.020180825328422795	2	15	221	16890	MELO3C025232;MELO3C013359	MELO3C011895;MELO3C014684;MELO3C014573;MELO3C003047;MELO3C006972;MELO3C022930;MELO3C004622;MELO3C005866;MELO3C005733;MELO3C024685;MELO3C017066;MELO3C017087;MELO3C026580;MELO3C017995;MELO3C012437

[]	GO:0007411	axon guidance	BIOLOGICAL_PROCESS	1.0	0.01730293846073584	4	72	219	16833	MELO3C026613;MELO3C008367;MELO3C018683;MELO3C003722	MELO3C006283;MELO3C003092;MELO3C011354;MELO3C014785;MELO3C012361;MELO3C014383;MELO3C022407;MELO3C002124;MELO3C022842;MELO3C021633;MELO3C008306;MELO3C023852;MELO3C024269;MELO3C018025;MELO3C019315;MELO3C025790;MELO3C002609;MELO3C013739;MELO3C012526;MELO3C004594;MELO3C003341;MELO3C022219;MELO3C005123;MELO3C020439;MELO3C004635;MELO3C024993;MELO3C026577;MELO3C023264;MELO3C017224;MELO3C018159;MELO3C024150;MELO3C025481;MELO3C016777;MELO3C017
[]	GO:0001666	response to hypoxia	BIOLOGICAL_PROCESS	1.0	0.013852993988198267	2	12	221	16893	MELO3C024028;MELO3C010748	MELO3C025534;MELO3C025535;MELO3C008938;MELO3C011021;MELO3C017087;MELO3C009145;MELO3C004189;MELO3C007039;MELO3C026482;MELO3C015302;MELO3C013879;MELO3C021953
[]	GO:0030422	production of siRNA involved in RNA interference	BIOLOGICAL_PROCESS	1.0	0.020180825328422795	2	15	221	16890	MELO3C026304;MELO3C014129	MELO3C010254;MELO3C011257;MELO3C015627;MELO3C014035;MELO3C005153;MELO3C014440;MELO3C010042;MELO3C022813;MELO3C023207;MELO3C023332;MELO3C015492;MELO3C005929;MELO3C014706;MELO3C017106;MELO3C012127
[]	GO:0070327	thyroid hormone transport	BIOLOGICAL_PROCESS	1.0	0.01301961700147596	1	0	222	16905	MELO3C006954	
[]	GO:0009963	positive regulation of flavonoid biosynthetic process	BIOLOGICAL_PROCESS	1.0	0.025870473860622564	1	1	222	16904	MELO3C027219	MELO3C016879
[]	GO:0051382	kinetochore assembly	BIOLOGICAL_PROCESS	1.0	0.01301961700147596	1	0	222	16905	MELO3C006948	
[]	GO:0042542	response to hydrogen peroxide	BIOLOGICAL_PROCESS	1.0	0.01795882780640618	2	14	221	16891	MELO3C010748;MELO3C020589	MELO3C013974;MELO3C013522;MELO3C016937;MELO3C002020;MELO3C007439;MELO3C006536;MELO3C002338;MELO3C005923;MELO3C018023;MELO3C012939;MELO3C012925;MELO3C017883;MELO3C021171;MELO3C017636
[]	GO:0048644	muscle organ morphogenesis	BIOLOGICAL_PROCESS	1.0	0.01301961700147596	1	0	222	16905	MELO3C008076	
[]	GO:0044723	single-organism carbohydrate metabolic process	BIOLOGICAL_PROCESS	1.0	0.04723164295509872	1	413	222	16492	MELO3C017104	MELO3C019719;MELO3C021918;MELO3C018628;MELO3C003491;MELO3C020949;MELO3C002287;MELO3C004465;MELO3C005795;MELO3C002047;MELO3C005559;MELO3C009914;MELO3C009913;MELO3C025275;MELO3C027332;MELO3C019711;MELO3C026482;MELO3C020837;MELO3C003381;MELO3C004591;MELO3C012097;MELO3C007986;MELO3C003265;MELO3C012096;MELO3C014272;MELO3C003266;MELO3C025044;MELO3C024194;MELO3C018994;MELO3C016697;MELO3C015367;MELO3C013155;MELO3C006984;MELO3C003597;MELO3C003
[]	GO:0016120	carotene biosynthetic process	BIOLOGICAL_PROCESS	1.0	0.03855474831574392	1	2	222	16903	MELO3C024554	MELO3C017709;MELO3C005449
[]	GO:0042793	transcription from plastid promoter	BIOLOGICAL_PROCESS	1.0	0.03855474831574392	1	2	222	16903	MELO3C007103	MELO3C002988;MELO3C010512
[]	GO:0006787	porphyrin-containing compound catabolic process	BIOLOGICAL_PROCESS	1.0	0.01795882780640618	2	14	221	16891	MELO3C010350;MELO3C023590	MELO3C016736;MELO3C019918;MELO3C014286;MELO3C006434;MELO3C008435;MELO3C024905;MELO3C020912;MELO3C007554;MELO3C025347;MELO3C004867;MELO3C022310;MELO3C005616;MELO3C018440;MELO3C025982
[]	GO:0010236	plastoquinone biosynthetic process	BIOLOGICAL_PROCESS	1.0	0.03855474831574392	1	2	222	16903	MELO3C014321	MELO3C022961;MELO3C009589

[]	GO:0034329	cell junction assembly	BIOLOGICAL_PROCESS	1.0	0.03568002057009693	2	21	221	16884	MELO3C018683;MELO3C026613	MELO3C014127;MELO3C006574;MELO3C007673;MELO3C009624;MELO3C006575;MELO3C004655;MELO3C021633;MELO3C003128;MELO3C023558;MELO3C007829;MELO3C023674;MELO3C023852;MELO3C022488;MELO3C002407;MELO3C026840;MELO3C018025;MELO3C023264;MELO3C018159;MELO3C018532;MELO3C015103;MELO3C014723
[]	GO:0051149	positive regulation of muscle cell differentiation	BIOLOGICAL_PROCESS	1.0	0.013852993988198267	2	12	221	16893	MELO3C008367;MELO3C003722	MELO3C005705;MELO3C021187;MELO3C013322;MELO3C003518;MELO3C020718;MELO3C002609;MELO3C016399;MELO3C013739;MELO3C010966;MELO3C007280;MELO3C026848;MELO3C011446
[]	GO:0051028	mRNA transport	BIOLOGICAL_PROCESS	1.0	0.015098464837553907	3	37	220	16868	MELO3C026304;MELO3C024028;MELO3C014129	MELO3C011256;MELO3C020407;MELO3C005694;MELO3C006121;MELO3C012087;MELO3C003078;MELO3C004622;MELO3C021931;MELO3C016280;MELO3C022166;MELO3C015492;MELO3C025497;MELO3C025498;MELO3C019034;MELO3C026441;MELO3C015113;MELO3C011139;MELO3C013879;MELO3C011459;MELO3C015733;MELO3C011875;MELO3C014532;MELO3C013443;MELO3C005265;MELO3C011385;MELO3C020899;MELO3C004111;MELO3C021328;MELO3C022237;MELO3C021887;MELO3C009808;MELO3C005946;MELO3C019464;MELO3C011
[]	GO:0007638	mechanosensory behavior	BIOLOGICAL_PROCESS	1.0	0.01301961700147596	1	0	222	16905	MELO3C008076	
[]	GO:0006367	transcription initiation from RNA polymerase II promoter	BIOLOGICAL_PROCESS	1.0	0.03981384359494245	3	55	220	16850	MELO3C015563;MELO3C009776;MELO3C012788	MELO3C010981;MELO3C016968;MELO3C009592;MELO3C008106;MELO3C021758;MELO3C008589;MELO3C008105;MELO3C002888;MELO3C022087;MELO3C020022;MELO3C007819;MELO3C017775;MELO3C017579;MELO3C015712;MELO3C014358;MELO3C013741;MELO3C008157;MELO3C002173;MELO3C014155;MELO3C002891;MELO3C020235;MELO3C020474;MELO3C024357;MELO3C026776;MELO3C023983;MELO3C024352;MELO3C001923;MELO3C017342;MELO3C003707;MELO3C015844;MELO3C003391;MELO3C009890;MELO3C010201;MELO3C015
[]	GO:0032526	response to retinoic acid	BIOLOGICAL_PROCESS	1.0	0.01301961700147596	1	0	222	16905	MELO3C026102	
[]	GO:0045451	pole plasm oskar mRNA localization	BIOLOGICAL_PROCESS	1.0	0.025870473860622564	1	1	222	16904	MELO3C024028	MELO3C005946
[]	GO:0017148	negative regulation of translation	BIOLOGICAL_PROCESS	1.0	0.03285405520246976	2	20	221	16885	MELO3C026304;MELO3C024028	MELO3C008571;MELO3C015627;MELO3C015608;MELO3C007375;MELO3C006121;MELO3C005354;MELO3C004347;MELO3C005963;MELO3C026327;MELO3C002757;MELO3C005929;MELO3C001957;MELO3C022495;MELO3C026154;MELO3C023063;MELO3C015158;MELO3C017338;MELO3C012206;MELO3C014306;MELO3C012127
[]	GO:0010198	synergid death	BIOLOGICAL_PROCESS	1.0	0.01301961700147596	1	0	222	16905	MELO3C023526	

[]	GO:0009640	photomorphogenesis	BIOLOGICAL_PROCESS	1.0	0.0045386406249040695	3	23	220	16882	MELO3C023560;MELO3C013440;MELO3C020783	MELO3C027290;MELO3C009584;MELO3C007283;MELO3C006046;MELO3C014684;MELO3C003141;MELO3C005593;MELO3C008232;MELO3C020865;MELO3C000307;MELO3C005179;MELO3C000009;MELO3C004148;MELO3C000029;MELO3C026327;MELO3C021982;MELO3C002738;MELO3C024155;MELO3C019731;MELO3C010759;MELO3C016115;MELO3C011159;MELO3C017834
[]	GO:0006370	7-methylguanosine mRNA capping	BIOLOGICAL_PROCESS	1.0	0.012216092898517552	3	34	220	16871	MELO3C026304;MELO3C009776;MELO3C012788	MELO3C010981;MELO3C010201;MELO3C005694;MELO3C021758;MELO3C008589;MELO3C002888;MELO3C022087;MELO3C020022;MELO3C017775;MELO3C015158;MELO3C019837;MELO3C017579;MELO3C027194;MELO3C015712;MELO3C007284;MELO3C013741;MELO3C008774;MELO3C008157;MELO3C002173;MELO3C006473;MELO3C008414;MELO3C005421;MELO3C003222;MELO3C007526;MELO3C020474;MELO3C026776;MELO3C023983;MELO3C018155;MELO3C023562;MELO3C017342;MELO3C003707;MELO3C019700;MELO3C015844;MELO3C007
[]	GO:0009644	response to high light intensity	BIOLOGICAL_PROCESS	1.0	0.02748448831335454	2	18	221	16887	MELO3C010748;MELO3C020589	MELO3C013974;MELO3C009241;MELO3C006079;MELO3C005482;MELO3C006384;MELO3C002020;MELO3C011150;MELO3C024348;MELO3C006536;MELO3C005923;MELO3C018023;MELO3C026365;MELO3C010229;MELO3C012925;MELO3C017883;MELO3C021171;MELO3C017876;MELO3C011885
[]	GO:0042981	regulation of apoptotic process	BIOLOGICAL_PROCESS	1.0	0.04155688228530235	3	56	220	16849	MELO3C026898;MELO3C003332;MELO3C013814	MELO3C002481;MELO3C011470;MELO3C006121;MELO3C003331;MELO3C004622;MELO3C005757;MELO3C019031;MELO3C016083;MELO3C025755;MELO3C026800;MELO3C005912;MELO3C025752;MELO3C023972;MELO3C004827;MELO3C024340;MELO3C025355;MELO3C013816;MELO3C017338;MELO3C011710;MELO3C012376;MELO3C004950;MELO3C025923;MELO3C007109;MELO3C008835;MELO3C021442;MELO3C019642;MELO3C024034;MELO3C018910;MELO3C013822;MELO3C010960;MELO3C007237;MELO3C014086;MELO3C005976;MELO3C025
[]	GO:0046786	viral replication complex formation and maintenance	BIOLOGICAL_PROCESS	1.0	0.03855474831574392	1	2	222	16903	MELO3C002468	MELO3C003378;MELO3C003376
[]	GO:0045216	cell-cell junction organization	BIOLOGICAL_PROCESS	1.0	0.02748448831335454	2	18	221	16887	MELO3C018683;MELO3C026613	MELO3C014127;MELO3C014025;MELO3C006574;MELO3C007673;MELO3C009624;MELO3C006575;MELO3C021633;MELO3C003128;MELO3C023558;MELO3C007829;MELO3C023852;MELO3C022488;MELO3C018025;MELO3C016297;MELO3C023264;MELO3C018532;MELO3C015103;MELO3C014723
[]	GO:0010155	regulation of proton transport	BIOLOGICAL_PROCESS	1.0	0.025870473860622564	1	1	222	16904	MELO3C016696	MELO3C025720

[]	GO:0006354	DNA-templated transcription, elongation	BIOLOGICAL_PROCESS	1.0	0.023114760978852972	4	79	219	16826	MELO3C026304;MELO3C009776;MELO3C003444;MELO3C012788	MELO3C010981;MELO3C011355;MELO3C016968;MELO3C006760;MELO3C008106;MELO3C006520;MELO3C021758;MELO3C007015;MELO3C008589;MELO3C008105;MELO3C003216;MELO3C002888;MELO3C021430;MELO3C022087;MELO3C020022;MELO3C019712;MELO3C017775;MELO3C015158;MELO3C019837;MELO3C015512;MELO3C017579;MELO3C015712;MELO3C017658;MELO3C014358;MELO3C013741;MELO3C008157;MELO3C002173;MELO3C014155;MELO3C007348;MELO3C014153;MELO3C005963;MELO3C026899;MELO3C020474;MELO3C026
[]	GO:0009737	response to abscisic acid	BIOLOGICAL_PROCESS	1.0	0.04549514960642969	5	144	218	16761	MELO3C006160;MELO3C013925;MELO3C004553;MELO3C003563;MELO3C003973	MELO3C021918;MELO3C014700;MELO3C006086;MELO3C007299;MELO3C004580;MELO3C012481;MELO3C012085;MELO3C022725;MELO3C005035;MELO3C022726;MELO3C006521;MELO3C024345;MELO3C018062;MELO3C022047;MELO3C026245;MELO3C017134;MELO3C005718;MELO3C021190;MELO3C013854;MELO3C017309;MELO3C012136;MELO3C017949;MELO3C006095;MELO3C015408;MELO3C006497;MELO3C011682;MELO3C003263;MELO3C010197;MELO3C020718;MELO3C005840;MELO3C009889;MELO3C024514;MELO3C021643;MELO3C006
[]	GO:0018826	methionine gamma-lyase activity	MOLECULAR_FUNCTION	1.0	0.025870473860622564	1	1	222	16904	MELO3C013774	MELO3C005786
[]	GO:0018812	3-hydroxyacyl-CoA dehydratase activity	MOLECULAR_FUNCTION	1.0	0.03855474831574392	1	2	222	16903	MELO3C021326	MELO3C004565;MELO3C021318
[]	GO:0008473	ornithine cyclodeaminase activity	MOLECULAR_FUNCTION	1.0	0.01301961700147596	1	0	222	16905	MELO3C006954	
[]	GO:0016881	acid-amino acid ligase activity	MOLECULAR_FUNCTION	1.0	0.021920573141519677	3	43	220	16862	MELO3C022707;MELO3C025232;MELO3C013359	MELO3C016407;MELO3C011378;MELO3C006100;MELO3C011153;MELO3C006046;MELO3C014684;MELO3C020827;MELO3C005691;MELO3C009310;MELO3C011072;MELO3C005277;MELO3C005674;MELO3C026704;MELO3C007439;MELO3C005733;MELO3C009417;MELO3C021530;MELO3C021252;MELO3C024782;MELO3C026341;MELO3C015867;MELO3C014115;MELO3C009120;MELO3C007283;MELO3C020814;MELO3C005683;MELO3C006555;MELO3C006710;MELO3C014350;MELO3C007489;MELO3C009821;MELO3C011060;MELO3C020654;MELO3C009
[]	GO:0047172	shikimate O-hydroxycinnamoyltransferase activity	MOLECULAR_FUNCTION	1.0	0.025870473860622564	1	1	222	16904	MELO3C027219	MELO3C023474
[]	GO:0008692	3-hydroxybutyryl-CoA epimerase activity	MOLECULAR_FUNCTION	1.0	0.03855474831574392	1	2	222	16903	MELO3C021326	MELO3C004565;MELO3C021318
[]	GO:0016863	intramolecular oxidoreductase activity, transposing C=C bonds	MOLECULAR_FUNCTION	1.0	0.008590199613574084	2	9	221	16896	MELO3C010053;MELO3C021326	MELO3C023478;MELO3C008717;MELO3C017829;MELO3C004565;MELO3C021318;MELO3C023481;MELO3C023479;MELO3C025448;MELO3C006525
[]	GO:0008022	protein C-terminus binding	MOLECULAR_FUNCTION	1.0	0.03568002057009693	2	21	221	16884	MELO3C006188;MELO3C012788	MELO3C014028;MELO3C009412;MELO3C005694;MELO3C008694;MELO3C016909;MELO3C011193;MELO3C005328;MELO3C022188;MELO3C003338;MELO3C021463;MELO3C021783;MELO3C022521;MELO3C018187;MELO3C025022;MELO3C022351;MELO3C016047;MELO3C012868;MELO3C010769;MELO3C018624;MELO3C017678;MELO3C018910

[]	GO:0008270	zinc ion binding	MOLECULAR_FUNCTION	1.0	0.039097915237540186	25	1252	198	15653	MELO3C007075;MELO3C007033;MELO3C009996;MELO3C006802;MELO3C004305;MELO3C025977;MELO3C020440;MELO3C015891;MELO3C026640;MELO3C003619;MELO3C010985;MELO3C019616;MELO3C013587;MELO3C013440;MELO3C014199;MELO3C007265;MELO3C002075;MELO3C023526;MELO3C004139;MELO3C001987;MELO3C018950;MELO3C013925;MELO3C015202;MELO3C016435;MELO3C011942	MELO3C004460;MELO3C005792;MELO3C014022;MELO3C007732;MELO3C005559;MELO3C009914;MELO3C007735;MELO3C003139;MELO3C009913;MELO3C026249;MELO3C010904;MELO3C015110;MELO3C019951;MELO3C018864;MELO3C017536;MELO3C018624;MELO3C017777;MELO3C017537;MELO3C021804;MELO3C021806;MELO3C004472;MELO3C012095;MELO3C004232;MELO3C002297;MELO3C002055;MELO3C004237;MELO3C004239;MELO3C004238;MELO3C007503;MELO3C003149;MELO3C009923;MELO3C006418;MELO3C015360;MELO3C017
[]	GO:0051741	2-methyl-6-phytyl-1,4-benzoquinone methyltransferase activity	MOLECULAR_FUNCTION	1.0	0.01301961700147596	1	0	222	16905	MELO3C014321	
[]	GO:0016301	kinase activity	MOLECULAR_FUNCTION	1.0	0.03698824387283609	10	1411	213	15494	MELO3C008076;MELO3C008367;MELO3C007047;MELO3C007711;MELO3C009967;MELO3C003487;MELO3C017756;MELO3C016139;MELO3C023889;MELO3C003722	MELO3C014269;MELO3C002280;MELO3C013178;MELO3C013176;MELO3C003133;MELO3C002286;MELO3C004463;MELO3C009910;MELO3C002287;MELO3C013172;MELO3C007972;MELO3C003379;MELO3C006648;MELO3C007978;MELO3C010907;MELO3C007739;MELO3C009916;MELO3C010909;MELO3C026243;MELO3C027331;MELO3C018865;MELO3C000093;MELO3C025392;MELO3C024063;MELO3C015359;MELO3C020958;MELO3C006890;MELO3C020718;MELO3C003146;MELO3C003147;MELO3C006415;MELO3C008838;MELO3C026256;MELO3C010
[]	GO:0003962	cystathionine gamma-synthase activity	MOLECULAR_FUNCTION	1.0	0.03855474831574392	1	2	222	16903	MELO3C013774	MELO3C009845;MELO3C005786
[]	GO:0070324	thyroid hormone binding	MOLECULAR_FUNCTION	1.0	0.01301961700147596	1	0	222	16905	MELO3C006954	
[]	GO:0019888	protein phosphatase regulator activity	MOLECULAR_FUNCTION	1.0	0.03568002057009693	2	21	221	16884	MELO3C005380;MELO3C026288	MELO3C009297;MELO3C008041;MELO3C004581;MELO3C020837;MELO3C013044;MELO3C008221;MELO3C022749;MELO3C008705;MELO3C023006;MELO3C006623;MELO3C022178;MELO3C004539;MELO3C024478;MELO3C024401;MELO3C002748;MELO3C021670;MELO3C011702;MELO3C010720;MELO3C012229;MELO3C011214;MELO3C013337
[]	GO:0005366	myo-inositol:proton symporter activity	MOLECULAR_FUNCTION	1.0	0.01301961700147596	1	0	222	16905	MELO3C017757	
[]	GO:0004158	dihydroorotate oxidase activity	MOLECULAR_FUNCTION	1.0	0.03855474831574392	1	2	222	16903	MELO3C005067	MELO3C015352;MELO3C002149
[]	GO:0047205	quinate O-hydroxycinnamoyltransferase activity	MOLECULAR_FUNCTION	1.0	0.01301961700147596	1	0	222	16905	MELO3C027219	
[]	GO:0005212	structural constituent of eye lens	MOLECULAR_FUNCTION	1.0	0.01301961700147596	1	0	222	16905	MELO3C006954	
[]	GO:0080124	pheophytinase activity	MOLECULAR_FUNCTION	1.0	0.01301961700147596	1	0	222	16905	MELO3C023590	
[]	GO:0035242	protein-arginine omega-N asymmetric methyltransferase activity	MOLECULAR_FUNCTION	1.0	0.03855474831574392	1	2	222	16903	MELO3C026636	MELO3C005078;MELO3C015447
[]	GO:0035241	protein-arginine omega-N monomethyltransferase activity	MOLECULAR_FUNCTION	1.0	0.03855474831574392	1	2	222	16903	MELO3C026636	MELO3C005078;MELO3C015447
[]	GO:0008420	CTD phosphatase activity	MOLECULAR_FUNCTION	1.0	0.025870473860622564	1	1	222	16904	MELO3C010744	MELO3C007164
[]	GO:0008793	aromatic-amino-acid:2-oxoglutarate aminotransferase activity	MOLECULAR_FUNCTION	1.0	0.025870473860622564	1	1	222	16904	MELO3C005597	MELO3C006840
[]	GO:0016034	maleylacetoacetate isomerase activity	MOLECULAR_FUNCTION	1.0	0.03855474831574392	1	2	222	16903	MELO3C006189	MELO3C023224;MELO3C023220
[]	GO:0016277	[myelin basic protein]-arginine N-methyltransferase activity	MOLECULAR_FUNCTION	1.0	0.01301961700147596	1	0	222	16905	MELO3C026636	
[]	GO:0004726	non-membrane spanning protein tyrosine phosphatase activity	MOLECULAR_FUNCTION	1.0	0.025870473860622564	1	1	222	16904	MELO3C021441	MELO3C009840

[]	GO:0005747	mitochondrial respiratory chain complex I	CELLULAR_COMPONENT	1.0	0.038596267237901986	2	22	221	16883	MELO3C023322;MELO3C024729	MELO3C013951;MELO3C012522;MELO3C014894;MELO3C005389;MELO3C009702;MELO3C000924;MELO3C006999;MELO3C025525;MELO3C026758;MELO3C022540;MELO3C006949;MELO3C020331;MELO3C023357;MELO3C025258;MELO3C017010;MELO3C022394;MELO3C025540;MELO3C019212;MELO3C016861;MELO3C010701;MELO3C023063;MELO3C017843
[]	GO:0005846	nuclear cap binding complex	CELLULAR_COMPONENT	1.0	0.01301961700147596	1	0	222	16905	MELO3C026304	
[]	GO:0000783	nuclear telomere cap complex	CELLULAR_COMPONENT	1.0	0.03855474831574392	1	2	222	16903	MELO3C006188	MELO3C017678;MELO3C023972
[]	GO:0043564	Ku70:Ku80 complex	CELLULAR_COMPONENT	1.0	0.025870473860622564	1	1	222	16904	MELO3C006188	MELO3C017678
[]	GO:0009706	chloroplast inner membrane	CELLULAR_COMPONENT	1.0	0.019488870688019518	3	41	220	16864	MELO3C016354;MELO3C014321;MELO3C014379	MELO3C011311;MELO3C011950;MELO3C014389;MELO3C006105;MELO3C011150;MELO3C006344;MELO3C005999;MELO3C020500;MELO3C026802;MELO3C023998;MELO3C020560;MELO3C004867;MELO3C005838;MELO3C026723;MELO3C023994;MELO3C023131;MELO3C021073;MELO3C021074;MELO3C010989;MELO3C017774;MELO3C010229;MELO3C014578;MELO3C015704;MELO3C016817;MELO3C010074;MELO3C014596;MELO3C023747;MELO3C002210;MELO3C005827;MELO3C018494;MELO3C021464;MELO3C024754;MELO3C026314;MELO3C016
[]	GO:0000811	GINS complex	CELLULAR_COMPONENT	1.0	0.03855474831574392	1	2	222	16903	MELO3C006096	MELO3C024840;MELO3C023404
[]	GO:0000243	commitment complex	CELLULAR_COMPONENT	1.0	0.01301961700147596	1	0	222	16905	MELO3C026304	

Supplementary Table 1.E Gene Ontology terms (GO terms) of the cluster 1.4 obtained considering the comparison between lines over time fruit during storage at 20.5°C and 88% relative humidity for 18 d the near-isogenic line SC10-2 and its parental ''Piel de Sapo'' obtained according to the differentially expressed gene pattern (Supl. Table 1.A)

Tags	GO ID	GO Name	GO Category	FDR	P-Value	Nr Test	Nr Reference	Non Annot Test	Non Annot Reference	TestSet Sequences	RefSet Sequences
[]	GO:0043622	cortical microtubule organization	BIOLOGICAL_PROCESS	1.0	0.0452853672488166	1	4	157	16966	MELO3C002054	MELO3C007829; MELO3C014496; MELO3C002717; MELO3C023374
[]	GO:0044314	protein K27-linked ubiquitination	BIOLOGICAL_PROCESS	1.0	0.009224661372776416	1	0	157	16970	MELO3C026341	
[]	GO:0042780	tRNA 3'-end processing	BIOLOGICAL_PROCESS	1.0	0.03639435510742036	1	3	157	16967	MELO3C014447	MELO3C020738; MELO3C010582; MELO3C024265
[]	GO:0010017	red or far-red light signaling pathway	BIOLOGICAL_PROCESS	1.0	0.043416625286064055	2	34	156	16936	MELO3C026502; MELO3C014459	MELO3C009692; MELO3C006046; MELO3C014684; MELO3C012221; MELO3C006142; MELO3C014386; MELO3C011250; MELO3C003075; MELO3C006225; MELO3C021715; MELO3C003574; MELO3C024805; MELO3C026506; MELO3C004148; MELO3C002742; MELO3C005738; MELO3C002705; MELO3C005939; MELO3C019731; MELO3C010769; MELO3C025191; MELO3C014699; MELO3C008213; MELO3C009202; MELO3C005120; MELO3C002793; MELO3C006717;
[]	GO:0010375	stomatal complex patterning	BIOLOGICAL_PROCESS	1.0	0.027421072152703972	1	2	157	16968	MELO3C002054	MELO3C021111; MELO3C020718
[]	GO:0006974	cellular response to DNA damage stimulus	BIOLOGICAL_PROCESS	1.0	0.023182426598434357	8	367	150	16603	MELO3C025853; MELO3C009561; MELO3C013630; MELO3C002271; MELO3C018500; MELO3C006136; MELO3C022742; MELO3C010378	MELO3C006760; MELO3C020706; MELO3C014386; MELO3C014021; MELO3C014020; MELO3C004226; MELO3C023535; MELO3C008825; MELO3C004227; MELO3C019281; MELO3C008829; MELO3C026800; MELO3C027337; MELO3C017096; MELO3C018187; MELO3C020022; MELO3C017775; MELO3C010901; MELO3C018624; MELO3C014703; MELO3C011434; MELO3C006096; MELO3C018518; MELO3C013741; MELO3C013740; MELO3C008157; MELO3C002173;
[]	GO:0009959	negative gravitropism	BIOLOGICAL_PROCESS	1.0	0.03639435510742036	1	3	157	16967	MELO3C008088	MELO3C025310; MELO3C008847; MELO3C024155
[]	GO:0006659	phosphatidylserine biosynthetic process	BIOLOGICAL_PROCESS	1.0	0.01836476200573981	1	1	157	16969	MELO3C005332	MELO3C012286

[]	GO:0009408	response to heat	BIOLOGICAL_PROCESS	1.0	0.009642058645419857	4	86	154	16884	MELO3C016970; MELO3C025139; MELO3C025085; MELO3C003917	MELO3C013974; MELO3C008263; MELO3C005873; MELO3C005035; MELO3C008589; MELO3C014183; MELO3C005674; MELO3C009996; MELO3C020589; MELO3C018780; MELO3C026886; MELO3C018023; MELO3C018660; MELO3C001916; MELO3C019039; MELO3C012925; MELO3C010748; MELO3C015312; MELO3C016449; MELO3C012455; MELO3C012136; MELO3C012456; MELO3C015608; MELO3C012331; MELO3C009840; MELO3C014230; MELO3C005884;
[]	GO:0016192	vesicle-mediated transport	BIOLOGICAL_PROCESS	1.0	0.03685791634803103	0	438	158	16532		MELO3C006760; MELO3C002045; MELO3C004465; MELO3C006648; MELO3C009912; MELO3C010900; MELO3C015235; MELO3C010901; MELO3C017779; MELO3C021808; MELO3C018518; MELO3C020836; MELO3C003263; MELO3C014154; MELO3C014153; MELO3C006413; MELO3C005328; MELO3C006657; MELO3C025044; MELO3C015246; MELO3C015126; MELO3C018758; MELO3C015218; MELO3C019819; MELO3C014122; MELO3C002027; MELO3C004205;
[]	GO:0006816	calcium ion transport	BIOLOGICAL_PROCESS	1.0	0.007154720384386039	2	12	156	16958	MELO3C007636; MELO3C009170	MELO3C009809; MELO3C020683; MELO3C010795; MELO3C010794; MELO3C016817; MELO3C025057; MELO3C015780; MELO3C004374; MELO3C018734; MELO3C017953; MELO3C003950; MELO3C024291
[]	GO:0010994	free ubiquitin chain polymerization	BIOLOGICAL_PROCESS	1.0	0.01836476200573981	1	1	157	16969	MELO3C026341	MELO3C016132
[]	GO:0070979	protein K11-linked ubiquitination	BIOLOGICAL_PROCESS	1.0	0.027421072152703972	1	2	157	16968	MELO3C026341	MELO3C024685; MELO3C026580
[]	GO:0009660	amyloplast organization	BIOLOGICAL_PROCESS	1.0	0.01836476200573981	1	1	157	16969	MELO3C008088	MELO3C025310
[]	GO:0045038	protein import into chloroplast thylakoid membrane	BIOLOGICAL_PROCESS	1.0	0.027421072152703972	1	2	157	16968	MELO3C006136	MELO3C020652; MELO3C018772
[]	GO:0006433	prolyl-tRNA aminoacylation	BIOLOGICAL_PROCESS	1.0	0.027421072152703972	1	2	157	16968	MELO3C017711	MELO3C019492; MELO3C005193
[]	GO:0033345	asparagine catabolic process via L-aspartate	BIOLOGICAL_PROCESS	1.0	0.01836476200573981	1	1	157	16969	MELO3C017653	MELO3C006131

[]	GO:0085020	protein K6-linked ubiquitination	BIOLOGICAL_PROCESS	1.0	0.009224661372776416	1	0	157	16970	MELO3C026341	
[]	GO:0016226	iron-sulfur cluster assembly	BIOLOGICAL_PROCESS	1.0	0.018842646131421188	2	21	156	16949	MELO3C009561; MELO3C002268	MELO3C013522; MELO3C014533; MELO3C015905; MELO3C012350; MELO3C009520; MELO3C004002; MELO3C007469; MELO3C024903; MELO3C002463; MELO3C020686; MELO3C003389; MELO3C007668; MELO3C025534; MELO3C025535; MELO3C002307; MELO3C019892; MELO3C022175; MELO3C011825; MELO3C017456; MELO3C010697; MELO3C013205
[]	GO:0009590	detection of gravity	BIOLOGICAL_PROCESS	1.0	0.027421072152703972	1	2	157	16968	MELO3C008088	MELO3C005293; MELO3C005396
[]	GO:0006641	triglyceride metabolic process	BIOLOGICAL_PROCESS	1.0	0.037042295682690206	2	31	156	16939	MELO3C002154; MELO3C004084	MELO3C021918; MELO3C011132; MELO3C006545; MELO3C004221; MELO3C008249; MELO3C002421; MELO3C024667; MELO3C003017; MELO3C023893; MELO3C006429; MELO3C006803; MELO3C024187; MELO3C017954; MELO3C013265; MELO3C009147; MELO3C003087; MELO3C011482; MELO3C002571; MELO3C003088; MELO3C021604; MELO3C021268; MELO3C004632; MELO3C022793; MELO3C019485; MELO3C022099; MELO3C012939; MELO3C025383;
[]	GO:0009753	response to jasmonic acid	BIOLOGICAL_PROCESS	1.0	0.0179600613801609	3	57	155	16913	MELO3C010774; MELO3C006120; MELO3C011885	MELO3C006086; MELO3C006046; MELO3C014386; MELO3C006765; MELO3C020701; MELO3C005674; MELO3C024348; MELO3C008625; MELO3C017292; MELO3C001913; MELO3C017134; MELO3C025152; MELO3C012527; MELO3C011439; MELO3C015436; MELO3C010353; MELO3C004231; MELO3C005840; MELO3C020637; MELO3C021643; MELO3C006934; MELO3C021645; MELO3C004513; MELO3C026577; MELO3C024357; MELO3C010910; MELO3C016852;
[]	GO:0006516	glycoprotein catabolic process	BIOLOGICAL_PROCESS	1.0	0.0452853672488166	1	4	157	16966	MELO3C017653	MELO3C001609; MELO3C026905; MELO3C016787; MELO3C015327
[]	GO:0006517	protein deglycosylation	BIOLOGICAL_PROCESS	1.0	0.009224661372776416	1	0	157	16970	MELO3C017653	

[]	GO:0035519	protein K29-linked ubiquitination	BIOLOGICAL_PROCESS	1.0	0.009224661372776416	1	0	157	16970	MELO3C026341	
[]	GO:0051604	protein maturation	BIOLOGICAL_PROCESS	1.0	0.037042295682690206	2	31	156	16939	MELO3C017653; MELO3C016970	MELO3C005470; MELO3C009174; MELO3C006089; MELO3C012220; MELO3C008520; MELO3C004285; MELO3C022725; MELO3C020322; MELO3C020686; MELO3C003576; MELO3C023413; MELO3C006206; MELO3C022525; MELO3C025156; MELO3C017891; MELO3C004827; MELO3C025353; MELO3C014926; MELO3C015335; MELO3C011874; MELO3C011641; MELO3C013522; MELO3C013881; MELO3C006131; MELO3C009684; MELO3C025349; MELO3C025589;
[]	GO:0010458	exit from mitosis	BIOLOGICAL_PROCESS	1.0	0.01836476200573981	1	1	157	16969	MELO3C026341	MELO3C002182
[]	GO:0070887	cellular response to chemical stimulus	BIOLOGICAL_PROCESS	1.0	0.04729310123083138	1	603	157	16367	MELO3C010774	MELO3C021918; MELO3C014027; MELO3C006760; MELO3C005792; MELO3C006765; MELO3C008942; MELO3C013050; MELO3C004465; MELO3C025152; MELO3C026482; MELO3C015599; MELO3C017414; MELO3C016219; MELO3C007740; MELO3C002050; MELO3C020837; MELO3C014035; MELO3C004594; MELO3C020718; MELO3C003385; MELO3C007984; MELO3C020956; MELO3C014392; MELO3C003387; MELO3C009804; MELO3C016330; MELO3C024193;
[]	GO:0035071	salivary gland cell autophagic cell death	BIOLOGICAL_PROCESS	1.0	0.0452853672488166	1	4	157	16966	MELO3C015523	MELO3C026898; MELO3C022308; MELO3C007891; MELO3C025809
[]	GO:0032515	negative regulation of phosphoprotein phosphatase activity	BIOLOGICAL_PROCESS	1.0	0.009224661372776416	1	0	157	16970	MELO3C018500	
[]	GO:0010224	response to UV-B	BIOLOGICAL_PROCESS	1.0	0.015829085893849265	2	19	156	16951	MELO3C025853; MELO3C008944	MELO3C014587; MELO3C001390; MELO3C006046; MELO3C002152; MELO3C007012; MELO3C007457; MELO3C007677; MELO3C020812; MELO3C003442; MELO3C019670; MELO3C003316; MELO3C019231; MELO3C009939; MELO3C025022; MELO3C004719; MELO3C025183; MELO3C014739; MELO3C015730; MELO3C018801

[]	GO:0007030	Golgi organization	BIOLOGICAL_PROCESS	1.0	0.007154720384386039	2	12	156	16958	MELO3C008088; MELO3C004825	MELO3C021320; MELO3C005918; MELO3C008037; MELO3C025044; MELO3C008782; MELO3C024284; MELO3C021946; MELO3C022038; MELO3C006811; MELO3C015756; MELO3C016416; MELO3C022305
[]	GO:0006979	response to oxidative stress	BIOLOGICAL_PROCESS	1.0	0.04377311773428759	5	203	153	16767	MELO3C015857; MELO3C019503; MELO3C025085; MELO3C024505; MELO3C011885	MELO3C013974; MELO3C012522; MELO3C010344; MELO3C021914; MELO3C004220; MELO3C009112; MELO3C002164; MELO3C003377; MELO3C005674; MELO3C007618; MELO3C017096; MELO3C016564; MELO3C011313; MELO3C020719; MELO3C010351; MELO3C020718; MELO3C020711; MELO3C007984; MELO3C007868; MELO3C008835; MELO3C009924; MELO3C006536; MELO3C025724; MELO3C002978; MELO3C018077; MELO3C011328; MELO3C018756;
[]	GO:0031648	protein destabilization	BIOLOGICAL_PROCESS	1.0	0.009224661372776416	1	0	157	16970	MELO3C015523	
[]	GO:0048510	regulation of timing of transition from vegetative to reproductive phase	BIOLOGICAL_PROCESS	1.0	0.0452853672488166	1	4	157	16966	MELO3C022388	MELO3C027290; MELO3C019330; MELO3C013793; MELO3C009465
[]	GO:0070534	protein K63-linked ubiquitination	BIOLOGICAL_PROCESS	1.0	0.027421072152703972	1	2	157	16968	MELO3C026341	MELO3C022725; MELO3C020654
[]	GO:0002949	tRNA threonylcarbamoyladenosine modification	BIOLOGICAL_PROCESS	1.0	0.009224661372776416	1	0	157	16970	MELO3C006202	
[]	GO:0015976	carbon utilization	BIOLOGICAL_PROCESS	1.0	0.03639435510742036	1	3	157	16967	MELO3C018056	MELO3C011997; MELO3C011095; MELO3C009958
[]	GO:0016404	15-hydroxyprostaglandin dehydrogenase (NAD+) activity	MOLECULAR_FUNCTION	1.0	0.009224661372776416	1	0	157	16970	MELO3C019503	
[]	GO:0004144	diacylglycerol O-acyltransferase activity	MOLECULAR_FUNCTION	1.0	0.027421072152703972	1	2	157	16968	MELO3C013703	MELO3C004632; MELO3C018460
[]	GO:0004416	hydroxyacylglutathione hydrolase activity	MOLECULAR_FUNCTION	1.0	0.027421072152703972	1	2	157	16968	MELO3C020172	MELO3C017798; MELO3C025595
[]	GO:0003846	2-acylglycerol O-acyltransferase activity	MOLECULAR_FUNCTION	1.0	0.009224661372776416	1	0	157	16970	MELO3C013703	
[]	GO:0042781	3'-tRNA processing endoribonuclease activity	MOLECULAR_FUNCTION	1.0	0.027421072152703972	1	2	157	16968	MELO3C014447	MELO3C020738; MELO3C024265
[]	GO:0004827	proline-tRNA ligase activity	MOLECULAR_FUNCTION	1.0	0.027421072152703972	1	2	157	16968	MELO3C017711	MELO3C019492; MELO3C005193

[]	GO:0004089	carbonate dehydratase activity	MOLECULAR_FUNCTION	1.0	0.008205750996366041	2	13	156	16957	MELO3C018056; MELO3C007636	MELO3C016817; MELO3C009476; MELO3C011095; MELO3C009958; MELO3C004920; MELO3C009809; MELO3C004922; MELO3C024476; MELO3C004925; MELO3C025057; MELO3C004915; MELO3C026330; MELO3C011997
[]	GO:0009019	tRNA (guanine-N1-)-methyltransferase activity	MOLECULAR_FUNCTION	1.0	0.009224661372776416	1	0	157	16970	MELO3C026067	
[]	GO:0045547	dehydrodolichyl diphosphate synthase activity	MOLECULAR_FUNCTION	1.0	0.027421072152703972	1	2	157	16968	MELO3C025855	MELO3C021891; MELO3C018615
[]	GO:0003948	N4-(beta-N-acetylglucosaminyl)-L-asparaginase activity	MOLECULAR_FUNCTION	1.0	0.009224661372776416	1	0	157	16970	MELO3C017653	
[]	GO:0015369	calcium:proton antiporter activity	MOLECULAR_FUNCTION	1.0	0.009224661372776416	1	0	157	16970	MELO3C009170	
[]	GO:0004370	glycerol kinase activity	MOLECULAR_FUNCTION	1.0	0.01836476200573981	1	1	157	16969	MELO3C004084	MELO3C023442
[]	GO:0004496	mevalonate kinase activity	MOLECULAR_FUNCTION	1.0	0.027421072152703972	1	2	157	16968	MELO3C004281	MELO3C004282; MELO3C004278
[]	GO:0000049	tRNA binding	MOLECULAR_FUNCTION	1.0	0.02207675931852026	2	23	156	16947	MELO3C007024; MELO3C013645	MELO3C011157; MELO3C013873; MELO3C006088; MELO3C011163; MELO3C007996; MELO3C009668; MELO3C004347; MELO3C005679; MELO3C003269; MELO3C023997; MELO3C024899; MELO3C020358; MELO3C003479; MELO3C023582; MELO3C019532; MELO3C017266; MELO3C020154; MELO3C017760; MELO3C024350; MELO3C011328; MELO3C024031; MELO3C013207; MELO3C011005
[]	GO:0050221	prostaglandin-E2 9-reductase activity	MOLECULAR_FUNCTION	1.0	0.027421072152703972	1	2	157	16968	MELO3C026155	MELO3C015622; MELO3C011853
[]	GO:0048037	cofactor binding	MOLECULAR_FUNCTION	1.0	0.016502026782680274	0	522	158	16448		MELO3C016208; MELO3C016329; MELO3C021919; MELO3C013057; MELO3C007612; MELO3C013171; MELO3C006405; MELO3C008946; MELO3C007613; MELO3C026007; MELO3C026005; MELO3C026006; MELO3C026004; MELO3C027332; MELO3C016200; MELO3C018625; MELO3C015478; MELO3C016448; MELO3C018626; MELO3C004590; MELO3C002293; MELO3C014035; MELO3C004231; MELO3C004475; MELO3C003386; MELO3C007984; MELO3C004113;

[]	GO:0033743	peptide-methionine (R)-S-oxide reductase activity	MOLECULAR_FUNCTION	1.0	0.01836476200573981	1	1	157	16969	MELO3C018569	MELO3C016676
[]	GO:0008270	zinc ion binding	MOLECULAR_FUNCTION	1.0	0.04557358511781277	19	1258	139	15712	MELO3C009583; MELO3C012284; MELO3C025917; MELO3C004334; MELO3C022715; MELO3C003420; MELO3C006202; MELO3C026628; MELO3C007636; MELO3C026249; MELO3C025853; MELO3C006418; MELO3C005109; MELO3C020172; MELO3C025940; MELO3C018056; MELO3C019503; MELO3C016468; MELO3C010774	MELO3C004460; MELO3C005792; MELO3C014022; MELO3C007732; MELO3C005559; MELO3C009914; MELO3C007735; MELO3C003139; MELO3C009913; MELO3C010904; MELO3C015110; MELO3C019951; MELO3C018864; MELO3C017536; MELO3C018624; MELO3C017777; MELO3C017537; MELO3C021804; MELO3C021806; MELO3C004472; MELO3C012095; MELO3C004232; MELO3C002297; MELO3C002055; MELO3C004237; MELO3C004239; MELO3C004238;
[]	GO:0008834	di-trans,poly-cis-decaprenylcistransferase activity	MOLECULAR_FUNCTION	1.0	0.027421072152703972	1	2	157	16968	MELO3C025855	MELO3C021891; MELO3C018615
[]	GO:0008798	beta-aspartyl-peptidase activity	MOLECULAR_FUNCTION	1.0	0.0452853672488166	1	4	157	16966	MELO3C017653	MELO3C001609; MELO3C016787; MELO3C006131; MELO3C015327
[]	GO:0004557	alpha-galactosidase activity	MOLECULAR_FUNCTION	1.0	0.0452853672488166	1	4	157	16966	MELO3C020139	MELO3C020138; MELO3C011771; MELO3C010698; MELO3C011770
[]	GO:0003882	CDP-diacylglycerol-serine O-phosphatidyltransferase activity	MOLECULAR_FUNCTION	1.0	0.01836476200573981	1	1	157	16969	MELO3C005332	MELO3C012286
[]	GO:0004965	G-protein coupled GABA receptor activity	MOLECULAR_FUNCTION	1.0	0.0452853672488166	1	4	157	16966	MELO3C019256	MELO3C019258; MELO3C017043; MELO3C007977; MELO3C019260
[]	GO:0009705	plant-type vacuole membrane	CELLULAR_COMPONENT	1.0	0.007154720384386039	2	12	156	16958	MELO3C008088; MELO3C009170	MELO3C011146; MELO3C025972; MELO3C026522; MELO3C026971; MELO3C007980; MELO3C016475; MELO3C003783; MELO3C012405; MELO3C010334; MELO3C008406; MELO3C017757; MELO3C022448
[]	GO:0005764	lysosome	CELLULAR_COMPONENT	1.0	0.018842646131421188	2	21	156	16949	MELO3C017653; MELO3C015523	MELO3C014821; MELO3C003291; MELO3C006034; MELO3C005243; MELO3C004353; MELO3C008897; MELO3C004477; MELO3C026977; MELO3C023569; MELO3C006926; MELO3C026898; MELO3C026415; MELO3C025645; MELO3C025752; MELO3C025972; MELO3C020442; MELO3C026971; MELO3C025355; MELO3C018764; MELO3C014818; MELO3C026110

[]	GO:0031983	vesicle lumen	CELLULAR_COMPONENT	1.0	0.009224661372776416	1	0	157	16970	MELO3C015523	
[]	GO:0042718	yolk granule	CELLULAR_COMPONENT	1.0	0.009224661372776416	1	0	157	16970	MELO3C015523	
[]	GO:0030529	intracellular ribonucleoprotein complex	CELLULAR_COMPONENT	1.0	0.0225449296878492	1	666	157	16304	MELO3C024747	MELO3C013179; MELO3C020704; MELO3C020705; MELO3C021915; MELO3C004580; MELO3C013175; MELO3C002164; MELO3C012084; MELO3C014262; MELO3C007973; MELO3C020945; MELO3C020824; MELO3C006400; MELO3C014381; MELO3C003258; MELO3C006766; MELO3C026246; MELO3C017650; MELO3C025276; MELO3C016321; MELO3C016201; MELO3C026360; MELO3C025030; MELO3C018985; MELO3C016688; MELO3C017659; MELO3C020836;
[]	GO:0016602	CCAAT-binding factor complex	CELLULAR_COMPONENT	1.0	0.0452853672488166	1	4	157	16966	MELO3C023161	MELO3C009551; MELO3C015320; MELO3C023554; MELO3C007077
[]	GO:0045169	fusome	CELLULAR_COMPONENT	1.0	0.027421072152703972	1	2	157	16968	MELO3C015523	MELO3C006951; MELO3C024150
[]	GO:0005680	anaphase-promoting complex	CELLULAR_COMPONENT	1.0	0.03639435510742036	1	3	157	16967	MELO3C026341	MELO3C002234; MELO3C024685; MELO3C026580
[]	GO:0009570	chloroplast stroma	CELLULAR_COMPONENT	1.0	0.009235598713916146	9	374	149	16596	MELO3C007024; MELO3C014178; MELO3C016970; MELO3C008932; MELO3C024086; MELO3C004223; MELO3C024701; MELO3C018569; MELO3C013645	MELO3C013732; MELO3C021919; MELO3C012764; MELO3C002161; MELO3C008146; MELO3C006088; MELO3C009475; MELO3C013172; MELO3C005674; MELO3C003137; MELO3C001992; MELO3C008946; MELO3C003811; MELO3C001998; MELO3C003814; MELO3C021355; MELO3C016680; MELO3C016681; MELO3C017890; MELO3C024189; MELO3C015231; MELO3C025397; MELO3C019036; MELO3C017774; MELO3C015233; MELO3C011439; MELO3C014943;

Supplementary Table 1.F Gene Ontology terms (GO terms) of the cluster 1.5 obtained considering the comparison between lines over time fruit during storage at 20.5°C and 88% relative humidity for 18 d the near-isogenic line SC10-2 and its parental ''Piel de Sapo'' obtained according to the differentially expressed gene pattern (Supl. Table 1.A)

Tags	GO ID	GO Name	GO Category	FDR	P-Value	Nr Test	Nr Reference	Non Annot Test	Non Annot Reference	TestSet Sequences	RefSet Sequences
[]	GO:0004008	copper-exporting ATPase activity	MOLECULAR_FUNCTION	0.3674898023835551	3.473735973621571E-4	4	8	518	16598	MELO3C019011; MELO3C016915; MELO3C019010; MELO3C019012	MELO3C000189; MELO3C018643; MELO3C005665; MELO3C007027; MELO3C008846; MELO3C020853; MELO3C008845; MELO3C003996
[]	GO:0006342	chromatin silencing	BIOLOGICAL_PROCESS	0.7382510466190081	0.0011943650135181208	5	22	517	16584	MELO3C022443; MELO3C013879; MELO3C023986; MELO3C014035; MELO3C007648	MELO3C011256; MELO3C015649; MELO3C010882; MELO3C007894; MELO3C008048; MELO3C009773; MELO3C014440; MELO3C014153; MELO3C003583; MELO3C024942; MELO3C023217; MELO3C004615; MELO3C022562; MELO3C021585; MELO3C021442; MELO3C023752; MELO3C021058; MELO3C015560; MELO3C027223; MELO3C012615; MELO3C014706; MELO3C017558
[]	GO:0008270	zinc ion binding	MOLECULAR_FUNCTION	0.7382510466190081	0.0012502134574411653	59	1218	463	15388	MELO3C009276; MELO3C010584; MELO3C005035; MELO3C026803; MELO3C009914; MELO3C026804; MELO3C005754; MELO3C022568; MELO3C004944; MELO3C002767; MELO3C019470; MELO3C018461; MELO3C024385; MELO3C018265; MELO3C018264; MELO3C017131; MELO3C017571; MELO3C015277; MELO3C011317; MELO3C027373; MELO3C015477; MELO3C017657; MELO3C017813; MELO3C011640; MELO3C002690; MELO3C004279; MELO3C004239;	MELO3C004460; MELO3C005792; MELO3C014022; MELO3C007732; MELO3C005559; MELO3C007735; MELO3C003139; MELO3C009913; MELO3C026249; MELO3C010904; MELO3C015110; MELO3C019951; MELO3C018864; MELO3C017536; MELO3C018624; MELO3C017777; MELO3C017537; MELO3C021804; MELO3C021806; MELO3C004472; MELO3C012095; MELO3C004232; MELO3C002297; MELO3C002055; MELO3C004237; MELO3C004238; MELO3C007503;
[]	GO:0050826	response to freezing	BIOLOGICAL_PROCESS	0.827121087427183	0.002724961000167915	2	1	520	16605	MELO3C021253; MELO3C005035	MELO3C022358
[]	GO:0004345	glucose-6-phosphate dehydrogenase activity	MOLECULAR_FUNCTION	0.827121087427183	0.002724961000167915	2	1	520	16605	MELO3C008986; MELO3C008985	MELO3C003280
[]	GO:0047938	glucose-6-phosphate 1-epimerase activity	MOLECULAR_FUNCTION	0.827121087427183	0.002724961000167915	2	1	520	16605	MELO3C016314; MELO3C006055	MELO3C004001

[]	GO:0008138	protein tyrosine/serine/threonine phosphatase activity	MOLECULAR_FUNCTION	0.827121087427183	0.0022958457581069703	4	15	518	16591	MELO3C004603; MELO3C023830; MELO3C003222; MELO3C013921	MELO3C012378; MELO3C009960; MELO3C014446; MELO3C007580; MELO3C009840; MELO3C021405; MELO3C004587; MELO3C020114; MELO3C002645; MELO3C026602; MELO3C019894; MELO3C018474; MELO3C026166; MELO3C011936; MELO3C026163
[]	GO:0016262	protein N-acetylglucosaminyltransferase activity	MOLECULAR_FUNCTION	0.827121087427183	0.002724961000167915	2	1	520	16605	MELO3C010102; MELO3C024563	MELO3C013249
[]	GO:0009736	cytokinin-activated signaling pathway	BIOLOGICAL_PROCESS	0.9522274503872248	0.0038681071564413854	3	8	519	16598	MELO3C014230; MELO3C024563; MELO3C024357	MELO3C004183; MELO3C016937; MELO3C003198; MELO3C025617; MELO3C016973; MELO3C010714; MELO3C017877; MELO3C024439
[]	GO:0042256	mature ribosome assembly	BIOLOGICAL_PROCESS	1.0	0.005339884106746404	2	2	520	16604	MELO3C010584; MELO3C013183	MELO3C023215; MELO3C015319
[]	GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	BIOLOGICAL_PROCESS	1.0	0.018962465976286615	3	16	519	16590	MELO3C026263; MELO3C013879; MELO3C013051	MELO3C015714; MELO3C011145; MELO3C008956; MELO3C006767; MELO3C021931; MELO3C008955; MELO3C026304; MELO3C026612; MELO3C026327; MELO3C007816; MELO3C024028; MELO3C025497; MELO3C003804; MELO3C025498; MELO3C015113; MELO3C026290
[]	GO:0032446	protein modification by small protein conjugation	BIOLOGICAL_PROCESS	1.0	0.04405438912341239	10	163	512	16443	MELO3C008494; MELO3C018461; MELO3C011882; MELO3C005490; MELO3C018720; MELO3C016464; MELO3C005035; MELO3C005971; MELO3C013879; MELO3C009879	MELO3C003490; MELO3C011153; MELO3C013694; MELO3C020827; MELO3C012361; MELO3C003650; MELO3C020149; MELO3C022725; MELO3C006520; MELO3C022726; MELO3C007214; MELO3C026528; MELO3C007339; MELO3C021512; MELO3C008669; MELO3C026527; MELO3C019281; MELO3C005717; MELO3C026800; MELO3C023372; MELO3C022280; MELO3C012406; MELO3C018501; MELO3C012407; MELO3C014436; MELO3C009880; MELO3C008310;
[]	GO:0006968	cellular defense response	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C006765	
[]	GO:0001833	inner cell mass cell proliferation	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C010584	

[]	GO:0031348	negative regulation of defense response	BIOLOGICAL_PROCESS	1.0	0.04999061953532355	2	10	520	16596	MELO3C014230; MELO3C005035	MELO3C012752; MELO3C008938; MELO3C021057; MELO3C023037; MELO3C006046; MELO3C025152; MELO3C002630; MELO3C022346; MELO3C010631; MELO3C023217
[]	GO:0034727	piecemeal microautophagy of nucleus	BIOLOGICAL_PROCESS	1.0	0.028955822976624575	2	7	520	16599	MELO3C024558; MELO3C008520	MELO3C019565; MELO3C004827; MELO3C025809; MELO3C022280; MELO3C022308; MELO3C023607; MELO3C007214
[]	GO:2000377	regulation of reactive oxygen species metabolic process	BIOLOGICAL_PROCESS	1.0	0.035475308030445664	2	8	520	16598	MELO3C024563; MELO3C002148	MELO3C021918; MELO3C009709; MELO3C008938; MELO3C006046; MELO3C007039; MELO3C015872; MELO3C023805; MELO3C005976
[]	GO:0071947	protein deubiquitination involved in ubiquitin-dependent protein catabolic process	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C018956	
[]	GO:0060250	germ-line stem-cell niche homeostasis	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C022219	
[]	GO:0005976	polysaccharide metabolic process	BIOLOGICAL_PROCESS	1.0	0.032991136145829165	1	192	521	16414	MELO3C024951	MELO3C012004; MELO3C008022; MELO3C005272; MELO3C017935; MELO3C014147; MELO3C005396; MELO3C017818; MELO3C006362; MELO3C020949; MELO3C025718; MELO3C004465; MELO3C005795; MELO3C002047; MELO3C005716; MELO3C003812; MELO3C002603; MELO3C023251; MELO3C020263; MELO3C012925; MELO3C023250; MELO3C010862; MELO3C013621; MELO3C006491; MELO3C022739; MELO3C009367; MELO3C011682; MELO3C024917;
[]	GO:0006824	cobalt ion transport	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C021391	
[]	GO:0030595	leukocyte chemotaxis	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C010584	

[]	GO:0016569	covalent chromatin modification	BIOLOGICAL_PROCESS	1.0	0.037983413892163344	5	56	517	16550	MELO3C024172; MELO3C018203; MELO3C005971; MELO3C014035; MELO3C007648	MELO3C016968; MELO3C007894; MELO3C006520; MELO3C007015; MELO3C026448; MELO3C002327; MELO3C016482; MELO3C019997; MELO3C014706; MELO3C019996; MELO3C017536; MELO3C015556; MELO3C015512; MELO3C017537; MELO3C014503; MELO3C013424; MELO3C008473; MELO3C015649; MELO3C008475; MELO3C014670; MELO3C004752; MELO3C024438; MELO3C021442; MELO3C007903; MELO3C004836; MELO3C024352; MELO3C023584;
[]	GO:0034551	mitochondrial respiratory chain complex III assembly	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C008037	
[]	GO:0007612	learning	BIOLOGICAL_PROCESS	1.0	0.008720572673184374	2	3	520	16603	MELO3C010584; MELO3C026234	MELO3C009672; MELO3C015782; MELO3C026582
[]	GO:0070485	dehydro-D-arabinono-1,4-lactone biosynthetic process	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C018576	
[]	GO:0009909	regulation of flower development	BIOLOGICAL_PROCESS	1.0	0.023954859652834663	5	49	517	16557	MELO3C021929; MELO3C004944; MELO3C022443; MELO3C005035; MELO3C010769	MELO3C006243; MELO3C011550; MELO3C007457; MELO3C020900; MELO3C006520; MELO3C009633; MELO3C004347; MELO3C026243; MELO3C020263; MELO3C025152; MELO3C015512; MELO3C026161; MELO3C017812; MELO3C025191; MELO3C005161; MELO3C005162; MELO3C002050; MELO3C008475; MELO3C004398; MELO3C004752; MELO3C008956; MELO3C008955; MELO3C003743; MELO3C024438; MELO3C002019; MELO3C016413; MELO3C012931;

[]	GO:0007623	circadian rhythm	BIOLOGICAL_PROCESS	1.0	0.011067071885078236	4	25	518	16581	MELO3C013369; MELO3C025049; MELO3C010769; MELO3C001962	MELO3C011079; MELO3C003075; MELO3C011130; MELO3C008920; MELO3C024448; MELO3C002588; MELO3C020783; MELO3C001999; MELO3C025357; MELO3C023076; MELO3C023350; MELO3C016660; MELO3C002949; MELO3C025091; MELO3C025191; MELO3C011754; MELO3C015209; MELO3C012992; MELO3C007882; MELO3C005120; MELO3C006336; MELO3C022995; MELO3C003466; MELO3C004018; MELO3C015782
[]	GO:0000422	mitophagy	BIOLOGICAL_PROCESS	1.0	0.017585801731193642	2	5	520	16601	MELO3C024558; MELO3C008520	MELO3C022280; MELO3C023607; MELO3C007214; MELO3C019565; MELO3C025809
[]	GO:0006777	Mo-molybdopterin cofactor biosynthetic process	BIOLOGICAL_PROCESS	1.0	0.035475308030445664	2	8	520	16598	MELO3C022174; MELO3C019661	MELO3C014007; MELO3C014535; MELO3C009365; MELO3C014186; MELO3C023505; MELO3C015599; MELO3C024139; MELO3C007668
[]	GO:0044765	single-organism transport	BIOLOGICAL_PROCESS	1.0	0.029403874525730116	13	735	509	15871	MELO3C016308; MELO3C020836; MELO3C014230; MELO3C022501; MELO3C004999; MELO3C021783; MELO3C003629; MELO3C015350; MELO3C018720; MELO3C011139; MELO3C016149; MELO3C009480; MELO3C013437	MELO3C014028; MELO3C005550; MELO3C012087; MELO3C004222; MELO3C006883; MELO3C007731; MELO3C005311; MELO3C004465; MELO3C007613; MELO3C008709; MELO3C006409; MELO3C017891; MELO3C025277; MELO3C010900; MELO3C019951; MELO3C017655; MELO3C010901; MELO3C017414; MELO3C016326; MELO3C017656; MELO3C016689; MELO3C019956; MELO3C004591; MELO3C007980; MELO3C014397; MELO3C002052; MELO3C013186;

[]	GO:0006406	mRNA export from nucleus	BIOLOGICAL_PROCESS	1.0	0.009771068479987946	4	24	518	16582	MELO3C003078; MELO3C013879; MELO3C012713; MELO3C015733	MELO3C011256; MELO3C014532; MELO3C013443; MELO3C020407; MELO3C005265; MELO3C005694; MELO3C004622; MELO3C021931; MELO3C021887; MELO3C026304; MELO3C016280; MELO3C022166; MELO3C009808; MELO3C005946; MELO3C015492; MELO3C025497; MELO3C025498; MELO3C019034; MELO3C026441; MELO3C011924; MELO3C015113; MELO3C015447; MELO3C016756; MELO3C014129
[]	GO:0010228	vegetative to reproductive phase transition of meristem	BIOLOGICAL_PROCESS	1.0	0.0443686145552901	4	40	518	16566	MELO3C013369; MELO3C022443; MELO3C005971; MELO3C010769	MELO3C012301; MELO3C014401; MELO3C009890; MELO3C005593; MELO3C005310; MELO3C006520; MELO3C026009; MELO3C002588; MELO3C022205; MELO3C006888; MELO3C019330; MELO3C002327; MELO3C017295; MELO3C015173; MELO3C025211; MELO3C019731; MELO3C015158; MELO3C021171; MELO3C019813; MELO3C012645; MELO3C025191; MELO3C013458; MELO3C007681; MELO3C012312; MELO3C007085; MELO3C008232; MELO3C020854;
[]	GO:0009696	salicylic acid metabolic process	BIOLOGICAL_PROCESS	1.0	0.008720572673184374	2	3	520	16603	MELO3C005035; MELO3C002148	MELO3C027349; MELO3C002099; MELO3C016008
[]	GO:0048582	positive regulation of post-embryonic development	BIOLOGICAL_PROCESS	1.0	0.0218144141696528	3	17	519	16589	MELO3C004944; MELO3C022443; MELO3C009101	MELO3C011221; MELO3C011771; MELO3C011299; MELO3C002050; MELO3C004398; MELO3C007457; MELO3C006520; MELO3C022995; MELO3C004632; MELO3C023325; MELO3C009627; MELO3C020484; MELO3C016660; MELO3C024265; MELO3C025183; MELO3C026161; MELO3C011104
[]	GO:0046167	glycerol-3-phosphate biosynthetic process	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C020157	
[]	GO:2000070	regulation of response to water deprivation	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C005035	

[]	GO:0042127	regulation of cell proliferation	BIOLOGICAL_PROCESS	1.0	0.03572930418181029	5	55	517	16551	MELO3C023475; MELO3C010640; MELO3C007648; MELO3C015733; MELO3C026068	MELO3C006085; MELO3C004380; MELO3C006760; MELO3C012361; MELO3C024822; MELO3C020422; MELO3C018062; MELO3C021157; MELO3C027255; MELO3C024782; MELO3C013816; MELO3C017216; MELO3C026161; MELO3C007383; MELO3C008151; MELO3C004198; MELO3C004752; MELO3C023545; MELO3C023823; MELO3C003468; MELO3C024757; MELO3C023741; MELO3C010759; MELO3C018910; MELO3C014514; MELO3C014877; MELO3C008488;
[]	GO:0000463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	BIOLOGICAL_PROCESS	1.0	0.04999061953532355	2	10	520	16596	MELO3C013183; MELO3C023306	MELO3C018272; MELO3C024586; MELO3C022134; MELO3C008994; MELO3C003340; MELO3C015907; MELO3C004873; MELO3C023052; MELO3C027392; MELO3C017744
[]	GO:0018315	molybdenum incorporation into molybdenum-molybdopterin complex	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C022174	
[]	GO:0044724	single-organism carbohydrate catabolic process	BIOLOGICAL_PROCESS	1.0	0.023430499533914177	0	138	522	16468		MELO3C005271; MELO3C005272; MELO3C009351; MELO3C005396; MELO3C010186; MELO3C020949; MELO3C024509; MELO3C020428; MELO3C004465; MELO3C024508; MELO3C024866; MELO3C020780; MELO3C025275; MELO3C027332; MELO3C020263; MELO3C012925; MELO3C013979; MELO3C010862; MELO3C006491; MELO3C020837; MELO3C003381; MELO3C004591; MELO3C007986; MELO3C014272; MELO3C025969; MELO3C024519; MELO3C024514;

[]	GO:0009965	leaf morphogenesis	BIOLOGICAL_PROCESS	1.0	0.013979137532245188	4	27	518	16579	MELO3C005971; MELO3C022204; MELO3C017813; MELO3C021534	MELO3C006085; MELO3C007098; MELO3C011771; MELO3C007870; MELO3C004347; MELO3C024446; MELO3C020860; MELO3C015173; MELO3C001957; MELO3C025450; MELO3C017559; MELO3C013621; MELO3C016916; MELO3C011142; MELO3C013287; MELO3C007121; MELO3C020854; MELO3C014670; MELO3C002670; MELO3C007500; MELO3C004752; MELO3C024898; MELO3C018380; MELO3C007207; MELO3C003009; MELO3C023064; MELO3C018952
[]	GO:0030538	embryonic genitalia morphogenesis	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C013879	
[]	GO:0000350	generation of catalytic spliceosome for second transesterification step	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C015733	
[]	GO:0043087	regulation of GTPase activity	BIOLOGICAL_PROCESS	1.0	0.011547741936802408	5	40	517	16566	MELO3C011716; MELO3C027373; MELO3C018265; MELO3C018264; MELO3C017813	MELO3C007075; MELO3C012464; MELO3C013850; MELO3C002160; MELO3C013431; MELO3C004462; MELO3C014242; MELO3C025639; MELO3C004547; MELO3C003413; MELO3C003977; MELO3C021110; MELO3C006408; MELO3C017792; MELO3C020360; MELO3C025077; MELO3C019359; MELO3C002808; MELO3C018603; MELO3C017338; MELO3C017779; MELO3C013721; MELO3C005121; MELO3C009269; MELO3C003662; MELO3C025406; MELO3C002478;

[]	GO:0016246	RNA interference	BIOLOGICAL_PROCESS	1.0	0.03281131996060644	4	36	518	16570	MELO3C020836; MELO3C013879; MELO3C014035; MELO3C007648	MELO3C011257; MELO3C007894; MELO3C014221; MELO3C005153; MELO3C014440; MELO3C010042; MELO3C005757; MELO3C021974; MELO3C026304; MELO3C003636; MELO3C023332; MELO3C007816; MELO3C015492; MELO3C016262; MELO3C019378; MELO3C001957; MELO3C019712; MELO3C025450; MELO3C014706; MELO3C012127; MELO3C014129; MELO3C010254; MELO3C015627; MELO3C008151; MELO3C015907; MELO3C013185; MELO3C022813;
[]	GO:0010389	regulation of G2/M transition of mitotic cell cycle	BIOLOGICAL_PROCESS	1.0	0.018962465976286615	3	16	519	16590	MELO3C023986; MELO3C007648; MELO3C005971	MELO3C014699; MELO3C013324; MELO3C008213; MELO3C014386; MELO3C009014; MELO3C006121; MELO3C013230; MELO3C011193; MELO3C008414; MELO3C005963; MELO3C003338; MELO3C023189; MELO3C021058; MELO3C002738; MELO3C024782; MELO3C017228
[]	GO:0022900	electron transport chain	BIOLOGICAL_PROCESS	1.0	0.023004593432375684	1	204	521	16402	MELO3C025023	MELO3C012522; MELO3C009472; MELO3C013050; MELO3C004105; MELO3C025712; MELO3C001994; MELO3C010229; MELO3C014824; MELO3C015922; MELO3C019607; MELO3C012410; MELO3C006533; MELO3C014390; MELO3C023424; MELO3C023548; MELO3C021127; MELO3C005329; MELO3C027106; MELO3C016333; MELO3C008482; MELO3C008481; MELO3C014124; MELO3C009453; MELO3C024729; MELO3C009458; MELO3C022303; MELO3C002027;
[]	GO:0048539	bone marrow development	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C010584	
[]	GO:0043097	pyrimidine nucleoside salvage	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C022212	
[]	GO:0006419	alanyl-tRNA aminoacylation	BIOLOGICAL_PROCESS	1.0	0.028955822976624575	2	7	520	16599	MELO3C000756; MELO3C000425	MELO3C012870; MELO3C010097; MELO3C024031; MELO3C018624; MELO3C027271; MELO3C027308; MELO3C013645

[]	GO:0040025	vulval development	BIOLOGICAL_PROCESS	1.0	0.008577774856974713	4	23	518	16583	MELO3C013369; MELO3C026234; MELO3C011206; MELO3C018956	MELO3C004390; MELO3C006171; MELO3C013015; MELO3C010882; MELO3C007894; MELO3C015904; MELO3C004473; MELO3C006500; MELO3C002045; MELO3C022308; MELO3C023325; MELO3C023545; MELO3C004459; MELO3C019031; MELO3C017020; MELO3C007903; MELO3C003703; MELO3C016262; MELO3C024552; MELO3C024265; MELO3C010839; MELO3C024782; MELO3C016321
[]	GO:0009814	defense response, incompatible interaction	BIOLOGICAL_PROCESS	1.0	0.01380017548419755	5	42	517	16564	MELO3C014230; MELO3C006765; MELO3C005035; MELO3C005971; MELO3C020157	MELO3C005550; MELO3C006046; MELO3C006187; MELO3C013472; MELO3C007039; MELO3C005674; MELO3C009838; MELO3C005633; MELO3C008527; MELO3C021055; MELO3C004867; MELO3C021057; MELO3C019595; MELO3C022340; MELO3C012527; MELO3C014706; MELO3C013757; MELO3C016008; MELO3C010623; MELO3C005061; MELO3C007920; MELO3C002099; MELO3C024319; MELO3C020956; MELO3C020912; MELO3C005547; MELO3C007429;
[]	GO:0010247	detection of phosphate ion	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C005035	
[]	GO:0032258	CVT pathway	BIOLOGICAL_PROCESS	1.0	0.028955822976624575	2	7	520	16599	MELO3C024558; MELO3C008520	MELO3C019565; MELO3C025809; MELO3C022280; MELO3C022308; MELO3C023607; MELO3C007214; MELO3C008406
[]	GO:0006369	termination of RNA polymerase II transcription	BIOLOGICAL_PROCESS	1.0	0.013918545482621425	3	14	519	16592	MELO3C024435; MELO3C002115; MELO3C015733	MELO3C008873; MELO3C003340; MELO3C002045; MELO3C008589; MELO3C006125; MELO3C021974; MELO3C026304; MELO3C004637; MELO3C017020; MELO3C005946; MELO3C001923; MELO3C016377; MELO3C016378; MELO3C011126
[]	GO:0000381	regulation of alternative mRNA splicing, via spliceosome	BIOLOGICAL_PROCESS	1.0	0.04249913044589533	2	9	520	16597	MELO3C017365; MELO3C015733	MELO3C011256; MELO3C008151; MELO3C005694; MELO3C022928; MELO3C004123; MELO3C026110; MELO3C026275; MELO3C023545; MELO3C019636

[]	GO:2000311	regulation of AMPA receptor activity	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C018956	
[]	GO:0048609	multicellular organismal reproductive process	BIOLOGICAL_PROCESS	1.0	0.04405438912341239	10	163	512	16443	MELO3C023475; MELO3C021783; MELO3C010640; MELO3C026234; MELO3C009101; MELO3C015322; MELO3C005971; MELO3C008815; MELO3C011139; MELO3C015733	MELO3C009592; MELO3C006760; MELO3C014386; MELO3C012361; MELO3C006121; MELO3C005791; MELO3C022725; MELO3C002045; MELO3C023535; MELO3C005831; MELO3C008306; MELO3C019031; MELO3C026885; MELO3C019674; MELO3C025310; MELO3C024340; MELO3C025275; MELO3C018500; MELO3C016048; MELO3C022282; MELO3C019956; MELO3C012376; MELO3C008151; MELO3C013860; MELO3C005441; MELO3C004198; MELO3C004473;
[]	GO:0060152	microtubule-based peroxisome localization	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C021783	
[]	GO:0046425	regulation of JAK-STAT cascade	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C005634	
[]	GO:0006378	mRNA polyadenylation	BIOLOGICAL_PROCESS	1.0	0.028955822976624575	2	7	520	16599	MELO3C004944; MELO3C022443	MELO3C005162; MELO3C008873; MELO3C021828; MELO3C008722; MELO3C002045; MELO3C027241; MELO3C021974
[]	GO:0051697	protein delipidation	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C008520	
[]	GO:0034498	early endosome to Golgi transport	BIOLOGICAL_PROCESS	1.0	0.030476412893692188	1	0	521	16606	MELO3C024558	
[]	GO:0015980	energy derivation by oxidation of organic compounds	BIOLOGICAL_PROCESS	1.0	0.011188405010692742	1	230	521	16376	MELO3C009581	MELO3C014700; MELO3C012522; MELO3C009472; MELO3C002167; MELO3C004465; MELO3C005795; MELO3C004105; MELO3C005559; MELO3C023413; MELO3C003812; MELO3C017891; MELO3C020263; MELO3C019711; MELO3C014824; MELO3C015922; MELO3C020837; MELO3C021247; MELO3C023548; MELO3C021249; MELO3C005329; MELO3C025960; MELO3C024193; MELO3C013505; MELO3C017759; MELO3C006068; MELO3C014123; MELO3C013153;

[]	GO:0010051	xylem and phloem pattern formation	BIOLOGICAL_PROCESS	1.0	0.013918545482621425	3	14	519	16592	MELO3C007450; MELO3C022204; MELO3C017813	MELO3C012125; MELO3C009584; MELO3C002670; MELO3C005236; MELO3C004752; MELO3C006307; MELO3C024898; MELO3C003768; MELO3C003009; MELO3C025774; MELO3C019573; MELO3C016850; MELO3C016301; MELO3C018952
[]	GO:0006470	protein dephosphorylation	BIOLOGICAL_PROCESS	1.0	0.03518145507167628	6	74	516	16532	MELO3C004603; MELO3C023830; MELO3C007940; MELO3C003222; MELO3C013921; MELO3C023473	MELO3C020829; MELO3C013336; MELO3C018507; MELO3C008426; MELO3C004587; MELO3C003574; MELO3C024667; MELO3C002645; MELO3C026602; MELO3C023893; MELO3C026166; MELO3C018500; MELO3C011713; MELO3C026163; MELO3C010744; MELO3C012378; MELO3C009960; MELO3C007580; MELO3C015408; MELO3C013860; MELO3C016939; MELO3C009840; MELO3C006852; MELO3C021405; MELO3C023626; MELO3C020114; MELO3C008478;
[]	GO:0000373	Group II intron splicing	BIOLOGICAL_PROCESS	1.0	0.012818100287924994	2	4	520	16602	MELO3C004577; MELO3C026398	MELO3C011982; MELO3C009922; MELO3C026699; MELO3C008146
[]	GO:0003696	satellite DNA binding	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C023986	
[]	GO:0004665	prephenate dehydrogenase (NADP+) activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C004475	
[]	GO:0032561	guanyl ribonucleotide binding	MOLECULAR_FUNCTION	1.0	0.04234916628340181	14	247	508	16359	MELO3C018716; MELO3C017968; MELO3C010165; MELO3C003793; MELO3C009713; MELO3C013183; MELO3C003222; MELO3C008925; MELO3C020721; MELO3C018052; MELO3C012529; MELO3C019844; MELO3C026141; MELO3C011016	MELO3C011312; MELO3C003370; MELO3C012760; MELO3C005673; MELO3C002167; MELO3C021114; MELO3C011684; MELO3C004471; MELO3C003261; MELO3C014156; MELO3C020959; MELO3C015929; MELO3C005565; MELO3C006896; MELO3C013185; MELO3C007742; MELO3C021803; MELO3C018080; MELO3C013180; MELO3C000761; MELO3C026259; MELO3C016695; MELO3C006063; MELO3C019819; MELO3C018848; MELO3C013158; MELO3C003590;
[]	GO:0047834	D-threo-aldose 1-dehydrogenase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C018576	
[]	GO:0018822	nitrile hydratase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C025585	
[]	GO:0005290	L-histidine transmembrane transporter activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C002619	

[]	GO:0080079	cellobiose glucosidase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C021253	
[]	GO:0015095	magnesium ion transmembrane transporter activity	MOLECULAR_FUNCTION	1.0	0.017585801731193642	2	5	520	16601	MELO3C026764; MELO3C000817	MELO3C026733; MELO3C000103; MELO3C011418; MELO3C019432; MELO3C004841
[]	GO:0000156	phosphorelay response regulator activity	MOLECULAR_FUNCTION	1.0	0.0478966847581391	3	24	519	16582	MELO3C017128; MELO3C010245; MELO3C020055	MELO3C005250; MELO3C009770; MELO3C004183; MELO3C016937; MELO3C012031; MELO3C006451; MELO3C006693; MELO3C003075; MELO3C012470; MELO3C005156; MELO3C005336; MELO3C000311; MELO3C022310; MELO3C001999; MELO3C017472; MELO3C025982; MELO3C019056; MELO3C005927; MELO3C003906; MELO3C010624; MELO3C021290; MELO3C010714; MELO3C013758; MELO3C016975
[]	GO:0004636	phosphoribosyl-ATP diphosphatase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C005094	
[]	GO:0004635	phosphoribosyl-AMP cyclohydrolase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C005094	
[]	GO:0035255	ionotropic glutamate receptor binding	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C018956	
[]	GO:0004652	polynucleotide adenylyltransferase activity	MOLECULAR_FUNCTION	1.0	0.022979181029695876	2	6	520	16600	MELO3C024435; MELO3C002115	MELO3C017806; MELO3C013730; MELO3C009952; MELO3C023722; MELO3C026172; MELO3C011126
[]	GO:0004651	polynucleotide 5'-phosphatase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C003222	
[]	GO:0043021	ribonucleoprotein complex binding	MOLECULAR_FUNCTION	1.0	0.0478966847581391	3	24	519	16582	MELO3C010584; MELO3C013183; MELO3C014306	MELO3C012489; MELO3C008571; MELO3C015319; MELO3C011298; MELO3C011981; MELO3C010222; MELO3C004130; MELO3C006662; MELO3C012131; MELO3C011380; MELO3C021977; MELO3C009668; MELO3C023215; MELO3C000865; MELO3C022402; MELO3C007816; MELO3C002704; MELO3C017760; MELO3C015553; MELO3C016963; MELO3C015126; MELO3C011898; MELO3C014746; MELO3C012667
[]	GO:0045290	D-arabinose 1-dehydrogenase [NAD(P)+] activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C018576	
[]	GO:0080061	indole-3-acetonitrile nitrilase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C025585	
[]	GO:0004354	glutamate dehydrogenase (NADP+) activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C013031	

[]	GO:0019151	galactose 1-dehydrogenase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C018576	
[]	GO:0019154	glycolate dehydrogenase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C009581	
[]	GO:0008949	oxalyl-CoA decarboxylase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C010381	
[]	GO:0010349	L-galactose dehydrogenase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C018576	
[]	GO:0005096	GTPase activator activity	MOLECULAR_FUNCTION	1.0	0.01264004813944158	5	41	517	16565	MELO3C011716; MELO3C027373; MELO3C018265; MELO3C018264; MELO3C017813	MELO3C007075; MELO3C012464; MELO3C013850; MELO3C002160; MELO3C013431; MELO3C004462; MELO3C014242; MELO3C004980; MELO3C025639; MELO3C006548; MELO3C004547; MELO3C003413; MELO3C003977; MELO3C021110; MELO3C006408; MELO3C022488; MELO3C017792; MELO3C020360; MELO3C025077; MELO3C019359; MELO3C015111; MELO3C002808; MELO3C017654; MELO3C017779; MELO3C013721; MELO3C005121; MELO3C009269;
[]	GO:0047499	calcium-independent phospholipase A2 activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C020721	
[]	GO:0047816	D-arabinose 1-dehydrogenase (NAD) activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C018576	
[]	GO:0015220	choline transmembrane transporter activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C020808	
[]	GO:0080048	GDP-D-glucose phosphorylase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C013136	
[]	GO:0004572	mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C009914	
[]	GO:0008139	nuclear localization sequence binding	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C020836	
[]	GO:0003918	DNA topoisomerase type II (ATP-hydrolyzing) activity	MOLECULAR_FUNCTION	1.0	0.04999061953532355	2	10	520	16596	MELO3C023986; MELO3C011386	MELO3C019163; MELO3C022420; MELO3C003071; MELO3C019089; MELO3C014153; MELO3C024924; MELO3C014639; MELO3C019090; MELO3C024756; MELO3C024755
[]	GO:0016807	cysteine-type carboxypeptidase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C008520	
[]	GO:0008865	fructokinase activity	MOLECULAR_FUNCTION	1.0	0.022979181029695876	2	6	520	16600	MELO3C015750; MELO3C009032	MELO3C022452; MELO3C015749; MELO3C020278; MELO3C003755; MELO3C005395; MELO3C009200
[]	GO:0047427	cyanoalanine nitrilase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C025585	

[]	GO:0004813	alanine-tRNA ligase activity	MOLECULAR_FUNCTION	1.0	0.028955822976624575	2	7	520	16599	MELO3C000756; MELO3C000425	MELO3C012870; MELO3C010097; MELO3C024031; MELO3C018624; MELO3C027271; MELO3C027308; MELO3C013645
[]	GO:0047672	anthranilate N-benzoyltransferase activity	MOLECULAR_FUNCTION	1.0	0.022979181029695876	2	6	520	16600	MELO3C009187; MELO3C023474	MELO3C016974; MELO3C008281; MELO3C026188; MELO3C003230; MELO3C006929; MELO3C027219
[]	GO:0046905	phytoene synthase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C025102	
[]	GO:0047558	3-cyanoalanine hydratase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C025585	
[]	GO:0004034	aldose 1-epimerase activity	MOLECULAR_FUNCTION	1.0	0.022979181029695876	2	6	520	16600	MELO3C016314; MELO3C006055	MELO3C017161; MELO3C004001; MELO3C017162; MELO3C017363; MELO3C017448; MELO3C009884
[]	GO:0031625	ubiquitin protein ligase binding	MOLECULAR_FUNCTION	1.0	0.016330894362943167	3	15	519	16591	MELO3C005581; MELO3C006645; MELO3C009879	MELO3C011795; MELO3C009880; MELO3C022725; MELO3C006647; MELO3C002960; MELO3C021345; MELO3C014291; MELO3C005757; MELO3C020654; MELO3C026612; MELO3C002958; MELO3C002738; MELO3C026177; MELO3C002959; MELO3C016559
[]	GO:0003735	structural constituent of ribosome	MOLECULAR_FUNCTION	1.0	0.02802070656731054	4	350	518	16256	MELO3C020836; MELO3C017364; MELO3C014176; MELO3C008092	MELO3C011310; MELO3C020704; MELO3C006088; MELO3C002164; MELO3C012084; MELO3C014262; MELO3C024506; MELO3C020945; MELO3C006400; MELO3C003258; MELO3C006766; MELO3C024747; MELO3C020141; MELO3C022441; MELO3C003811; MELO3C001514; MELO3C025276; MELO3C016201; MELO3C025030; MELO3C018985; MELO3C016688; MELO3C014824; MELO3C017659; MELO3C007740; MELO3C013981; MELO3C009489; MELO3C002294;
[]	GO:0071522	ureidoglycine aminohydrolase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C014174	
[]	GO:0008720	D-lactate dehydrogenase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C009581	
[]	GO:0004484	mRNA guanylyltransferase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C003222	

[]	GO:0004004	ATP-dependent RNA helicase activity	MOLECULAR_FUNCTION	1.0	0.0478966847581391	3	24	519	16582	MELO3C013879; MELO3C006765; MELO3C003842	MELO3C011256; MELO3C017528; MELO3C009324; MELO3C006121; MELO3C015907; MELO3C007111; MELO3C004343; MELO3C009668; MELO3C004663; MELO3C021158; MELO3C007659; MELO3C026716; MELO3C021203; MELO3C006514; MELO3C020573; MELO3C024028; MELO3C023741; MELO3C025387; MELO3C003937; MELO3C018389; MELO3C010734; MELO3C023052; MELO3C019636; MELO3C010733
[]	GO:0004137	deoxycytidine kinase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C022212	
[]	GO:0030515	snoRNA binding	MOLECULAR_FUNCTION	1.0	0.04249913044589533	2	9	520	16597	MELO3C017440; MELO3C011408	MELO3C001556; MELO3C026228; MELO3C002060; MELO3C002835; MELO3C024126; MELO3C017650; MELO3C013185; MELO3C015885; MELO3C008801
[]	GO:0050235	pyridoxal 4-dehydrogenase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C018576	
[]	GO:0033730	arogenate dehydrogenase (NADP+) activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C004475	
[]	GO:0042624	ATPase activity, uncoupled	MOLECULAR_FUNCTION	1.0	0.007038772705743546	5	35	517	16571	MELO3C021783; MELO3C003629; MELO3C017365; MELO3C015733; MELO3C003842	MELO3C015615; MELO3C005694; MELO3C004004; MELO3C002023; MELO3C011192; MELO3C021972; MELO3C004027; MELO3C007659; MELO3C017150; MELO3C022562; MELO3C023476; MELO3C026888; MELO3C024028; MELO3C021157; MELO3C017450; MELO3C024243; MELO3C016189; MELO3C023052; MELO3C024284; MELO3C017528; MELO3C009324; MELO3C017908; MELO3C015907; MELO3C010251; MELO3C026913; MELO3C025549; MELO3C002213;
[]	GO:0008672	2-dehydro-3-deoxyglucarate aldolase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C013779	
[]	GO:0015087	cobalt ion transmembrane transporter activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C021391	

[]	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	MOLECULAR_FUNCTION	1.0	0.016972575131300436	1	226	521	16380	MELO3C026824	MELO3C016329; MELO3C007174; MELO3C007175; MELO3C014027; MELO3C012088; MELO3C002043; MELO3C020028; MELO3C006644; MELO3C007611; MELO3C004584; MELO3C000537; MELO3C007856; MELO3C000655; MELO3C026802; MELO3C003933; MELO3C003932; MELO3C003934; MELO3C017772; MELO3C010229; MELO3C011799; MELO3C014945; MELO3C016219; MELO3C010350; MELO3C020832; MELO3C005686; MELO3C020833; MELO3C002735;
[]	GO:0008889	glycerophosphodiester phosphodiesterase activity	MOLECULAR_FUNCTION	1.0	0.017585801731193642	2	5	520	16601	MELO3C022124; MELO3C017753	MELO3C007806; MELO3C002033; MELO3C014925; MELO3C013101; MELO3C011029
[]	GO:0008765	UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C005683	
[]	GO:0019786	Atg8-specific protease activity	MOLECULAR_FUNCTION	1.0	0.030476412893692188	1	0	521	16606	MELO3C008520	
[]	GO:0004298	threonine-type endopeptidase activity	MOLECULAR_FUNCTION	1.0	0.039368996150302954	3	22	519	16584	MELO3C019012; MELO3C019011; MELO3C019010	MELO3C010960; MELO3C003173; MELO3C011880; MELO3C006131; MELO3C006187; MELO3C007920; MELO3C021745; MELO3C021746; MELO3C011172; MELO3C000704; MELO3C025735; MELO3C023267; MELO3C025755; MELO3C026800; MELO3C000762; MELO3C006517; MELO3C027069; MELO3C024343; MELO3C010635; MELO3C026360; MELO3C011449; MELO3C013757
[]	GO:0008649	rRNA methyltransferase activity	MOLECULAR_FUNCTION	1.0	0.04249913044589533	2	9	520	16597	MELO3C013369; MELO3C023306	MELO3C002238; MELO3C003647; MELO3C010971; MELO3C010154; MELO3C006150; MELO3C007871; MELO3C015412; MELO3C003643; MELO3C009184

[]	GO:0004725	protein tyrosine phosphatase activity	MOLECULAR_FUNCTION	1.0	0.008577774856974713	4	23	518	16583	MELO3C004603; MELO3C023830; MELO3C003222; MELO3C013921	MELO3C018606; MELO3C014446; MELO3C007580; MELO3C011186; MELO3C013860; MELO3C009840; MELO3C021405; MELO3C010061; MELO3C020114; MELO3C002645; MELO3C023674; MELO3C026602; MELO3C021441; MELO3C018474; MELO3C026166; MELO3C019876; MELO3C018159; MELO3C019734; MELO3C011936; MELO3C019875; MELO3C026163; MELO3C024481; MELO3C014438
[]	GO:0030140	trans-Golgi network transport vesicle	CELLULAR_COMPONENT	1.0	0.022979181029695876	2	6	520	16600	MELO3C003242; MELO3C017813	MELO3C025730; MELO3C013605; MELO3C024167; MELO3C007298; MELO3C005579; MELO3C008306
[]	GO:0044445	cytosolic part	CELLULAR_COMPONENT	1.0	0.037633646104854285	4	337	518	16269	MELO3C015796; MELO3C017364; MELO3C014176; MELO3C008092	MELO3C011310; MELO3C006088; MELO3C013175; MELO3C012084; MELO3C014262; MELO3C024506; MELO3C020141; MELO3C022441; MELO3C026800; MELO3C001514; MELO3C016201; MELO3C026360; MELO3C025030; MELO3C018985; MELO3C017659; MELO3C013981; MELO3C009489; MELO3C002294; MELO3C006412; MELO3C025609; MELO3C006411; MELO3C024514; MELO3C023666; MELO3C005446; MELO3C006657; MELO3C024994; MELO3C025168;
[]	GO:0071007	U2-type catalytic step 2 spliceosome	CELLULAR_COMPONENT	1.0	0.030476412893692188	1	0	521	16606	MELO3C015733	
[]	GO:0000172	ribonuclease MRP complex	CELLULAR_COMPONENT	1.0	0.030476412893692188	1	0	521	16606	MELO3C009318	
[]	GO:0009571	proplastid stroma	CELLULAR_COMPONENT	1.0	0.030476412893692188	1	0	521	16606	MELO3C023469	
[]	GO:0005655	nucleolar ribonuclease P complex	CELLULAR_COMPONENT	1.0	0.030476412893692188	1	0	521	16606	MELO3C009318	

[]	GO:0005654	nucleoplasm	CELLULAR_COMPONENT	1.0	0.026283398317527608	14	238	508	16368	MELO3C021929; MELO3C005382; MELO3C014035; MELO3C005035; MELO3C003222; MELO3C008815; MELO3C007648; MELO3C006107; MELO3C024357; MELO3C026234; MELO3C017365; MELO3C017544; MELO3C015733; MELO3C019779	MELO3C009592; MELO3C006760; MELO3C014263; MELO3C014021; MELO3C002044; MELO3C014020; MELO3C006520; MELO3C002045; MELO3C004347; MELO3C023531; MELO3C018187; MELO3C019034; MELO3C016321; MELO3C019712; MELO3C014706; MELO3C012407; MELO3C013857; MELO3C018624; MELO3C014823; MELO3C017658; MELO3C006096; MELO3C013741; MELO3C008151; MELO3C008157; MELO3C002173; MELO3C003141; MELO3C014153;
[]	GO:0008623	CHRAC	CELLULAR_COMPONENT	1.0	0.030476412893692188	1	0	521	16606	MELO3C023986	
[]	GO:0000325	plant-type vacuole	CELLULAR_COMPONENT	1.0	0.022276131344187322	5	48	517	16558	MELO3C016475; MELO3C011601; MELO3C025627; MELO3C010334; MELO3C013437	MELO3C011894; MELO3C008088; MELO3C010286; MELO3C012542; MELO3C009852; MELO3C002042; MELO3C022009; MELO3C024902; MELO3C003992; MELO3C020983; MELO3C020984; MELO3C008406; MELO3C022448; MELO3C000631; MELO3C025972; MELO3C026522; MELO3C025057; MELO3C024284; MELO3C015314; MELO3C012405; MELO3C010983; MELO3C011599; MELO3C017757; MELO3C014458; MELO3C011146; MELO3C007086; MELO3C007087;
[]	GO:0009508	plastid chromosome	CELLULAR_COMPONENT	1.0	0.035475308030445664	2	8	520	16598	MELO3C026221; MELO3C010512	MELO3C019372; MELO3C006321; MELO3C017774; MELO3C002396; MELO3C007103; MELO3C022303; MELO3C003216; MELO3C025888

[]	GO:0005840	ribosome	CELLULAR_COMPONENT	1.0	0.034208601081400294	6	435	516	16171	MELO3C014381; MELO3C015796; MELO3C020836; MELO3C017364; MELO3C014176; MELO3C008092	MELO3C020704; MELO3C020705; MELO3C013175; MELO3C002164; MELO3C012084; MELO3C014262; MELO3C020945; MELO3C006400; MELO3C003258; MELO3C006766; MELO3C025276; MELO3C016201; MELO3C026360; MELO3C025030; MELO3C018985; MELO3C016688; MELO3C017659; MELO3C007740; MELO3C002294; MELO3C006412; MELO3C006411; MELO3C007869; MELO3C005446; MELO3C006657; MELO3C025168; MELO3C018512; MELO3C015489;
[]	GO:0030692	Noc4p-Nop14p complex	CELLULAR_COMPONENT	1.0	0.030476412893692188	1	0	521	16606	MELO3C011408	
[]	GO:0035102	PRC1 complex	CELLULAR_COMPONENT	1.0	0.030476412893692188	1	0	521	16606	MELO3C007648	
[]	GO:0005801	cis-Golgi network	CELLULAR_COMPONENT	1.0	0.022979181029695876	2	6	520	16600	MELO3C017833; MELO3C007195	MELO3C004163; MELO3C004336; MELO3C005845; MELO3C003263; MELO3C022890; MELO3C022888
[]	GO:0010168	ER body	CELLULAR_COMPONENT	1.0	0.030476412893692188	1	0	521	16606	MELO3C012716	

Supplementary Table 1.G Gene Ontology terms (GO terms) of the cluster 1.6 obtained considering the comparison between lines over time fruit during storage at 20.5°C and 88% relative humidity for 18 d the near-isogenic line SC10-2 and its parental ''Piel de Sapo'' obtained according to the differentially expressed gene pattern (Supl. Table 1.A)

Tags	GO ID	GO Name	GO Category	FDR	P-Value	Nr Test	Nr Reference	Non Annot Test	Non Annot Reference	TestSet Sequences	RefSet Sequences
[]	GO:0008104	protein localization	BIOLOGICAL_PROCESS	1.0	0.0340259580381457	6	568	391	16163	MELO3C017705; MELO3C007010; MELO3C021328; MELO3C015113; MELO3C003249; MELO3C021274	MELO3C014028; MELO3C004581; MELO3C014143; MELO3C012087; MELO3C014382; MELO3C004347; MELO3C004589; MELO3C009912; MELO3C017891; MELO3C026482; MELO3C018988; MELO3C016326; MELO3C018518; MELO3C020836; MELO3C004471; MELO3C020837; MELO3C003263; MELO3C003141; MELO3C004111; MELO3C005445; MELO3C007742; MELO3C006532; MELO3C021803; MELO3C005328; MELO3C013180; MELO3C009808; MELO3C025044;
[]	GO:0042254	ribosome biogenesis	BIOLOGICAL_PROCESS	1.0	0.011069894197904951	0	222	397	16509		MELO3C010584; MELO3C010582; MELO3C013051; MELO3C003135; MELO3C006766; MELO3C020141; MELO3C022441; MELO3C018062; MELO3C023654; MELO3C019034; MELO3C017650; MELO3C016321; MELO3C010355; MELO3C013185; MELO3C025609; MELO3C013183; MELO3C023545; MELO3C023306; MELO3C006657; MELO3C021484; MELO3C009808; MELO3C003946; MELO3C025168; MELO3C015489; MELO3C005096; MELO3C003474; MELO3C008920;
[]	GO:0006287	base-excision repair, gap-filling	BIOLOGICAL_PROCESS	1.0	0.023178421297923826	1	0	396	16731	MELO3C024596	
[]	GO:0071375	cellular response to peptide hormone stimulus	BIOLOGICAL_PROCESS	1.0	0.03991598719037741	5	76	392	16655	MELO3C017705; MELO3C012073; MELO3C007740; MELO3C026210; MELO3C009659	MELO3C014700; MELO3C013334; MELO3C012361; MELO3C002124; MELO3C002766; MELO3C025555; MELO3C018463; MELO3C020380; MELO3C025790; MELO3C013815; MELO3C010983; MELO3C010992; MELO3C012376; MELO3C011365; MELO3C010151; MELO3C009840; MELO3C004594; MELO3C010790; MELO3C011040; MELO3C023626; MELO3C006454; MELO3C009887; MELO3C021246; MELO3C004635; MELO3C026614; MELO3C004439; MELO3C024039;

[]	GO:0034622	cellular macromolecular complex assembly	BIOLOGICAL_PROCESS	1.0	0.02447360019157677	1	280	396	16451	MELO3C018406	MELO3C010584; MELO3C012522; MELO3C020706; MELO3C014386; MELO3C005673; MELO3C026801; MELO3C004227; MELO3C021472; MELO3C016321; MELO3C012648; MELO3C014823; MELO3C019956; MELO3C008151; MELO3C008037; MELO3C014156; MELO3C004473; MELO3C010592; MELO3C013185; MELO3C013183; MELO3C024877; MELO3C022335; MELO3C005328; MELO3C003700; MELO3C023427; MELO3C006657; MELO3C024757; MELO3C015363;
[]	GO:0006297	nucleotide-excision repair, DNA gap filling	BIOLOGICAL_PROCESS	1.0	0.0055288419775967506	3	13	394	16718	MELO3C018521; MELO3C024596; MELO3C026949	MELO3C014021; MELO3C014020; MELO3C008864; MELO3C025879; MELO3C003638; MELO3C010507; MELO3C001937; MELO3C025142; MELO3C014529; MELO3C017228; MELO3C014528; MELO3C017458; MELO3C010631
[]	GO:0006972	hyperosmotic response	BIOLOGICAL_PROCESS	1.0	0.03530894445099476	2	11	395	16720	MELO3C024239; MELO3C025349	MELO3C004428; MELO3C009971; MELO3C010211; MELO3C006142; MELO3C006721; MELO3C012085; MELO3C008666; MELO3C004127; MELO3C008815; MELO3C002752; MELO3C013249
[]	GO:0032790	ribosome disassembly	BIOLOGICAL_PROCESS	1.0	0.023178421297923826	1	0	396	16731	MELO3C005565	
[]	GO:0042276	error-prone translesion synthesis	BIOLOGICAL_PROCESS	1.0	0.04582092534215229	1	1	396	16730	MELO3C007012	MELO3C005496
[]	GO:0071281	cellular response to iron ion	BIOLOGICAL_PROCESS	1.0	0.013679577378288468	2	6	395	16725	MELO3C015210; MELO3C014099	MELO3C014230; MELO3C019550; MELO3C015531; MELO3C026952; MELO3C016340; MELO3C003906
[]	GO:0010891	negative regulation of sequestering of triglyceride	BIOLOGICAL_PROCESS	1.0	0.023178421297923826	1	0	396	16731	MELO3C003537	

[]	GO:1901137	carbohydrate derivative biosynthetic process	BIOLOGICAL_PROCESS	1.0	0.02009307069662561	2	364	395	16367	MELO3C018521; MELO3C018365	MELO3C019719; MELO3C011311; MELO3C012884; MELO3C009473; MELO3C010102; MELO3C011431; MELO3C002165; MELO3C002166; MELO3C005674; MELO3C003379; MELO3C006648; MELO3C009914; MELO3C005799; MELO3C009912; MELO3C003812; MELO3C025277; MELO3C015352; MELO3C019951; MELO3C017413; MELO3C011438; MELO3C026482; MELO3C016445; MELO3C010469; MELO3C009120; MELO3C009489; MELO3C005683; MELO3C005680;
[]	GO:0010400	rhamnogalacturonan I side chain metabolic process	BIOLOGICAL_PROCESS	1.0	0.023178421297923826	1	0	396	16731	MELO3C003916	
[]	GO:0071822	protein complex subunit organization	BIOLOGICAL_PROCESS	1.0	0.028103588265637146	3	397	394	16334	MELO3C022562; MELO3C007740; MELO3C018406	MELO3C014028; MELO3C014386; MELO3C014262; MELO3C005673; MELO3C003258; MELO3C009912; MELO3C016201; MELO3C025030; MELO3C017659; MELO3C019956; MELO3C014156; MELO3C002294; MELO3C004473; MELO3C006412; MELO3C006411; MELO3C014391; MELO3C005328; MELO3C005446; MELO3C006657; MELO3C009808; MELO3C025168; MELO3C018512; MELO3C015246; MELO3C016459; MELO3C004440; MELO3C005411; MELO3C005895;
[]	GO:0045843	negative regulation of striated muscle tissue development	BIOLOGICAL_PROCESS	1.0	0.023178421297923826	1	0	396	16731	MELO3C015103	
[]	GO:0015908	fatty acid transport	BIOLOGICAL_PROCESS	1.0	0.01372248418261736	3	19	394	16712	MELO3C012073; MELO3C026210; MELO3C007613	MELO3C014700; MELO3C016628; MELO3C010151; MELO3C007110; MELO3C004761; MELO3C026917; MELO3C021347; MELO3C008009; MELO3C002766; MELO3C022793; MELO3C025522; MELO3C018463; MELO3C025960; MELO3C022495; MELO3C024193; MELO3C011108; MELO3C017863; MELO3C015601; MELO3C019527
[]	GO:0030183	B cell differentiation	BIOLOGICAL_PROCESS	1.0	0.023178421297923826	1	0	396	16731	MELO3C015103	

[]	GO:0006772	thiamine metabolic process	BIOLOGICAL_PROCESS	1.0	0.009087864176985786	3	16	394	16715	MELO3C016014; MELO3C022609; MELO3C022605	MELO3C014401; MELO3C014400; MELO3C011230; MELO3C022607; MELO3C006346; MELO3C025408; MELO3C021005; MELO3C021375; MELO3C020562; MELO3C018097; MELO3C017499; MELO3C016136; MELO3C024240; MELO3C014967; MELO3C014965; MELO3C024092
[]	GO:0048577	negative regulation of short-day photoperiodism, flowering	BIOLOGICAL_PROCESS	1.0	0.023178421297923826	1	0	396	16731	MELO3C019813	
[]	GO:0010106	cellular response to iron ion starvation	BIOLOGICAL_PROCESS	1.0	0.04582092534215229	1	1	396	16730	MELO3C017320	MELO3C017166
[]	GO:0071329	cellular response to sucrose stimulus	BIOLOGICAL_PROCESS	1.0	0.023178421297923826	1	0	396	16731	MELO3C022310	
[]	GO:0090306	spindle assembly involved in meiosis	BIOLOGICAL_PROCESS	1.0	0.04582092534215229	1	1	396	16730	MELO3C015113	MELO3C008594
[]	GO:0048579	negative regulation of long-day photoperiodism, flowering	BIOLOGICAL_PROCESS	1.0	0.023178421297923826	1	0	396	16731	MELO3C019813	
[]	GO:0007043	cell-cell junction assembly	BIOLOGICAL_PROCESS	1.0	0.021322474207042183	2	8	395	16723	MELO3C006574; MELO3C015103	MELO3C007829; MELO3C026613; MELO3C022488; MELO3C007673; MELO3C018025; MELO3C018532; MELO3C006575; MELO3C014723
[]	GO:0034517	ribophagy	BIOLOGICAL_PROCESS	1.0	0.023178421297923826	1	0	396	16731	MELO3C011731	
[]	GO:0034757	negative regulation of iron ion transport	BIOLOGICAL_PROCESS	1.0	0.04582092534215229	1	1	396	16730	MELO3C022310	MELO3C025982
[]	GO:0010201	response to continuous far red light stimulus by the high-irradiance response system	BIOLOGICAL_PROCESS	1.0	0.023178421297923826	1	0	396	16731	MELO3C009542	
[]	GO:0016926	protein desumoylation	BIOLOGICAL_PROCESS	1.0	0.023178421297923826	1	0	396	16731	MELO3C021328	
[]	GO:0045004	DNA replication proofreading	BIOLOGICAL_PROCESS	1.0	0.023178421297923826	1	0	396	16731	MELO3C024596	
[]	GO:0032049	cardiolipin biosynthetic process	BIOLOGICAL_PROCESS	1.0	0.04582092534215229	1	1	396	16730	MELO3C007010	MELO3C013700

[]	GO:0010150	leaf senescence	BIOLOGICAL_PROCESS	1.0	0.01743216186630687	3	21	394	16710	MELO3C022310; MELO3C004610; MELO3C016852	MELO3C012114; MELO3C012862; MELO3C013621; MELO3C014230; MELO3C002233; MELO3C007214; MELO3C007439; MELO3C022932; MELO3C020468; MELO3C004856; MELO3C006803; MELO3C008938; MELO3C019565; MELO3C022341; MELO3C016101; MELO3C016035; MELO3C019513; MELO3C017346; MELO3C026161; MELO3C010774; MELO3C015436
[]	GO:0010271	regulation of chlorophyll catabolic process	BIOLOGICAL_PROCESS	1.0	0.04582092534215229	1	1	396	16730	MELO3C022310	MELO3C025982
[]	GO:0010029	regulation of seed germination	BIOLOGICAL_PROCESS	1.0	0.04057388019809542	2	12	395	16719	MELO3C022310; MELO3C023484	MELO3C020484; MELO3C004460; MELO3C007222; MELO3C025982; MELO3C009256; MELO3C024155; MELO3C009101; MELO3C009889; MELO3C004632; MELO3C009627; MELO3C006547; MELO3C010435
[]	GO:0006425	glutaminyl-tRNA aminoacylation	BIOLOGICAL_PROCESS	1.0	0.04582092534215229	1	1	396	16730	MELO3C020839	MELO3C023301
[]	GO:0006417	regulation of translation	BIOLOGICAL_PROCESS	1.0	0.03475601968548277	5	73	392	16658	MELO3C012411; MELO3C021977; MELO3C002023; MELO3C014706; MELO3C002698	MELO3C008660; MELO3C010584; MELO3C010222; MELO3C020705; MELO3C009158; MELO3C008146; MELO3C007375; MELO3C006121; MELO3C005354; MELO3C004345; MELO3C004587; MELO3C004344; MELO3C004347; MELO3C004622; MELO3C024305; MELO3C004027; MELO3C006206; MELO3C026327; MELO3C024028; MELO3C019510; MELO3C001957; MELO3C015553; MELO3C015158; MELO3C017338; MELO3C016963; MELO3C012206; MELO3C014306;
[]	GO:0046487	glyoxylate metabolic process	BIOLOGICAL_PROCESS	1.0	0.021322474207042183	2	8	395	16723	MELO3C015151; MELO3C006703	MELO3C018816; MELO3C007674; MELO3C019243; MELO3C002350; MELO3C007942; MELO3C019711; MELO3C016751; MELO3C025076
[]	GO:0043091	L-arginine import	BIOLOGICAL_PROCESS	1.0	0.04582092534215229	1	1	396	16730	MELO3C024239	MELO3C002398
[]	GO:0031048	chromatin silencing by small RNA	BIOLOGICAL_PROCESS	1.0	0.04582092534215229	1	1	396	16730	MELO3C014706	MELO3C022443

[]	GO:0009074	aromatic amino acid family catabolic process	BIOLOGICAL_PROCESS	1.0	0.040365369900272056	3	30	394	16701	MELO3C022961; MELO3C025613; MELO3C012201	MELO3C014227; MELO3C014226; MELO3C014225; MELO3C014224; MELO3C014223; MELO3C006189; MELO3C014222; MELO3C010461; MELO3C007433; MELO3C023775; MELO3C023373; MELO3C016089; MELO3C019811; MELO3C017998; MELO3C017811; MELO3C017810; MELO3C014229; MELO3C014228; MELO3C015944; MELO3C008136; MELO3C019809; MELO3C013583; MELO3C017809; MELO3C025786; MELO3C023224; MELO3C024595; MELO3C023220;
[]	GO:0019428	allantoin biosynthetic process	BIOLOGICAL_PROCESS	1.0	0.04582092534215229	1	1	396	16730	MELO3C012335	MELO3C006233
[]	GO:0009083	branched-chain amino acid catabolic process	BIOLOGICAL_PROCESS	1.0	0.012054887373608313	3	18	394	16713	MELO3C011705; MELO3C010776; MELO3C006679	MELO3C008063; MELO3C004297; MELO3C006792; MELO3C006434; MELO3C007664; MELO3C004545; MELO3C021247; MELO3C006734; MELO3C025757; MELO3C007705; MELO3C002813; MELO3C018583; MELO3C018456; MELO3C026065; MELO3C015564; MELO3C015796; MELO3C013913; MELO3C024190
[]	GO:0033169	histone H3-K9 demethylation	BIOLOGICAL_PROCESS	1.0	0.003117472032681783	2	2	395	16729	MELO3C025053; MELO3C019813	MELO3C002327; MELO3C004836
[]	GO:0010189	vitamin E biosynthetic process	BIOLOGICAL_PROCESS	1.0	0.013679577378288468	2	6	395	16725	MELO3C022961; MELO3C025613	MELO3C011150; MELO3C017176; MELO3C004006; MELO3C014321; MELO3C024736; MELO3C014712
[]	GO:0035103	sterol regulatory element binding protein cleavage	BIOLOGICAL_PROCESS	1.0	0.023178421297923826	1	0	396	16731	MELO3C025349	
[]	GO:0009294	DNA mediated transformation	BIOLOGICAL_PROCESS	1.0	0.013679577378288468	2	6	395	16725	MELO3C013472; MELO3C015103	MELO3C023256; MELO3C020854; MELO3C019754; MELO3C026234; MELO3C004806; MELO3C017558
[]	GO:0001570	vasculogenesis	BIOLOGICAL_PROCESS	1.0	0.023178421297923826	1	0	396	16731	MELO3C015103	

[]	GO:0016036	cellular response to phosphate starvation	BIOLOGICAL_PROCESS	1.0	0.04353512472774495	3	31	394	16700	MELO3C004504; MELO3C022310; MELO3C010877	MELO3C011056; MELO3C012200; MELO3C011057; MELO3C014189; MELO3C005035; MELO3C002545; MELO3C022244; MELO3C012848; MELO3C013218; MELO3C019856; MELO3C015898; MELO3C014710; MELO3C013048; MELO3C007283; MELO3C006133; MELO3C005122; MELO3C006156; MELO3C012199; MELO3C004211; MELO3C004474; MELO3C003165; MELO3C004336; MELO3C020373; MELO3C020374; MELO3C026532; MELO3C011808; MELO3C010978;
[]	GO:0009861	jasmonic acid and ethylene-dependent systemic resistance	BIOLOGICAL_PROCESS	1.0	0.017320713109288028	2	7	395	16724	MELO3C013472; MELO3C022693	MELO3C022690; MELO3C006046; MELO3C014230; MELO3C024319; MELO3C020956; MELO3C005633; MELO3C024318
[]	GO:0009867	jasmonic acid mediated signaling pathway	BIOLOGICAL_PROCESS	1.0	0.03530894445099476	2	11	395	16720	MELO3C004610; MELO3C016852	MELO3C026577; MELO3C024357; MELO3C006046; MELO3C012221; MELO3C005466; MELO3C025152; MELO3C012527; MELO3C011439; MELO3C010774; MELO3C015436; MELO3C017559
[]	GO:0010600	regulation of auxin biosynthetic process	BIOLOGICAL_PROCESS	1.0	0.023178421297923826	1	0	396	16731	MELO3C025091	
[]	GO:0004535	poly(A)-specific ribonuclease activity	MOLECULAR_FUNCTION	1.0	0.030334190563045385	2	10	395	16721	MELO3C014116; MELO3C017294	MELO3C015714; MELO3C014512; MELO3C015061; MELO3C009599; MELO3C011292; MELO3C017303; MELO3C010539; MELO3C008896; MELO3C011291; MELO3C025580
[]	GO:0000064	L-ornithine transmembrane transporter activity	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C024239	MELO3C002619
[]	GO:0005507	copper ion binding	MOLECULAR_FUNCTION	1.0	0.03555266938167073	0	167	397	16564		MELO3C016208; MELO3C021919; MELO3C014540; MELO3C009355; MELO3C005153; MELO3C004980; MELO3C004342; MELO3C008424; MELO3C002167; MELO3C003137; MELO3C000533; MELO3C002447; MELO3C025433; MELO3C001915; MELO3C015873; MELO3C013977; MELO3C016569; MELO3C013743; MELO3C008274; MELO3C005561; MELO3C009247; MELO3C002293; MELO3C014035; MELO3C007468; MELO3C005201; MELO3C024519; MELO3C020432;

[]	GO:0008902	hydroxymethylpyrimidine kinase activity	MOLECULAR_FUNCTION	1.0	0.023178421297923826	1	0	396	16731	MELO3C022605	
[]	GO:0004789	thiamine-phosphate diphosphorylase activity	MOLECULAR_FUNCTION	1.0	0.007556976946859572	2	4	395	16727	MELO3C022609; MELO3C022605	MELO3C006346; MELO3C014401; MELO3C014400; MELO3C022607
[]	GO:0051538	3 iron, 4 sulfur cluster binding	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C008481	MELO3C009759
[]	GO:0004760	serine-pyruvate transaminase activity	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C015151	MELO3C014568
[]	GO:0003680	AT DNA binding	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C012730	MELO3C022471
[]	GO:0033743	peptide-methionine (R)-S-oxide reductase activity	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C016676	MELO3C018569
[]	GO:0016206	catechol O-methyltransferase activity	MOLECULAR_FUNCTION	1.0	0.0015830306037039165	2	1	395	16730	MELO3C027330; MELO3C014089	MELO3C024861
[]	GO:0004103	choline kinase activity	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C012493	MELO3C024063
[]	GO:0004458	D-lactate dehydrogenase (cytochrome) activity	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C016408	MELO3C009581
[]	GO:0008270	zinc ion binding	MOLECULAR_FUNCTION	1.0	0.00483257327157594	45	1232	352	15499	MELO3C009670; MELO3C014562; MELO3C009234; MELO3C021536; MELO3C003278; MELO3C006367; MELO3C021715; MELO3C005559; MELO3C024964; MELO3C004524; MELO3C024108; MELO3C002646; MELO3C002328; MELO3C026886; MELO3C025454; MELO3C023451; MELO3C003916; MELO3C012628; MELO3C025053; MELO3C010522; MELO3C012622; MELO3C019813; MELO3C019807; MELO3C007689; MELO3C013084; MELO3C007785; MELO3C003423;	MELO3C004460; MELO3C005792; MELO3C014022; MELO3C007732; MELO3C009914; MELO3C007735; MELO3C003139; MELO3C009913; MELO3C026249; MELO3C010904; MELO3C015110; MELO3C019951; MELO3C018864; MELO3C017536; MELO3C018624; MELO3C017777; MELO3C017537; MELO3C021804; MELO3C021806; MELO3C004472; MELO3C012095; MELO3C004232; MELO3C002297; MELO3C002055; MELO3C004237; MELO3C004239; MELO3C004238;
[]	GO:0004591	oxoglutarate dehydrogenase (succinyl-transferring) activity	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C025454	MELO3C023844
[]	GO:0004355	glutamate synthase (NADPH) activity	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C008481	MELO3C009759
[]	GO:0004105	choline-phosphate cytidylyltransferase activity	MOLECULAR_FUNCTION	1.0	0.023178421297923826	1	0	396	16731	MELO3C026379	

[]	GO:0016778	diphosphotransferase activity	MOLECULAR_FUNCTION	1.0	0.04057388019809542	2	12	395	16719	MELO3C024869; MELO3C016014	MELO3C006759; MELO3C018097; MELO3C011909; MELO3C013871; MELO3C014474; MELO3C020077; MELO3C024870; MELO3C017941; MELO3C003379; MELO3C025318; MELO3C011962; MELO3C024092
[]	GO:0046969	NAD-dependent histone deacetylase activity (H3-K9 specific)	MOLECULAR_FUNCTION	1.0	0.010418338915837976	2	5	395	16726	MELO3C013472; MELO3C015103	MELO3C021442; MELO3C008064; MELO3C026267; MELO3C025575; MELO3C016865
[]	GO:0047936	glucose 1-dehydrogenase [NAD(P)] activity	MOLECULAR_FUNCTION	1.0	0.023178421297923826	1	0	396	16731	MELO3C025347	
[]	GO:0051753	mannan synthase activity	MOLECULAR_FUNCTION	1.0	0.023178421297923826	1	0	396	16731	MELO3C021458	
[]	GO:0051990	(R)-2-hydroxyglutarate dehydrogenase activity	MOLECULAR_FUNCTION	1.0	0.023178421297923826	1	0	396	16731	MELO3C016408	
[]	GO:0046970	NAD-dependent histone deacetylase activity (H4-K16 specific)	MOLECULAR_FUNCTION	1.0	0.010418338915837976	2	5	395	16726	MELO3C013472; MELO3C015103	MELO3C021442; MELO3C008064; MELO3C026267; MELO3C025575; MELO3C016865
[]	GO:0016929	SUMO-specific protease activity	MOLECULAR_FUNCTION	1.0	0.023178421297923826	1	0	396	16731	MELO3C021328	
[]	GO:0050281	serine-glyoxylate transaminase activity	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C015151	MELO3C014568
[]	GO:0004147	dihydrolipoamide branched chain acyltransferase activity	MOLECULAR_FUNCTION	1.0	0.023178421297923826	1	0	396	16731	MELO3C006679	
[]	GO:0032041	NAD-dependent histone deacetylase activity (H3-K14 specific)	MOLECULAR_FUNCTION	1.0	0.010418338915837976	2	5	395	16726	MELO3C013472; MELO3C015103	MELO3C021442; MELO3C008064; MELO3C026267; MELO3C025575; MELO3C016865
[]	GO:0003735	structural constituent of ribosome	MOLECULAR_FUNCTION	1.0	0.019217811351406117	2	352	395	16379	MELO3C007740; MELO3C022017	MELO3C011310; MELO3C020704; MELO3C006088; MELO3C002164; MELO3C012084; MELO3C014262; MELO3C024506; MELO3C020945; MELO3C006400; MELO3C003258; MELO3C006766; MELO3C024747; MELO3C020141; MELO3C022441; MELO3C003811; MELO3C001514; MELO3C025276; MELO3C016201; MELO3C025030; MELO3C018985; MELO3C016688; MELO3C014824; MELO3C017659; MELO3C020836; MELO3C013981; MELO3C009489; MELO3C002294;
[]	GO:0004370	glycerol kinase activity	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C023442	MELO3C004084

[]	GO:0008972	phosphomethylpyrimidine kinase activity	MOLECULAR_FUNCTION	1.0	0.0015830306037039165	2	1	395	16730	MELO3C022609; MELO3C022605	MELO3C022607
[]	GO:0008780	acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase activity	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C015455	MELO3C007369
[]	GO:0003887	DNA-directed DNA polymerase activity	MOLECULAR_FUNCTION	1.0	0.009324061419061221	4	32	393	16699	MELO3C018521; MELO3C016434; MELO3C024596; MELO3C007012	MELO3C011257; MELO3C016705; MELO3C007194; MELO3C005496; MELO3C014021; MELO3C002044; MELO3C014020; MELO3C009536; MELO3C021434; MELO3C021435; MELO3C005956; MELO3C020860; MELO3C005957; MELO3C001935; MELO3C010507; MELO3C001936; MELO3C025396; MELO3C001937; MELO3C025395; MELO3C014529; MELO3C011159; MELO3C014503; MELO3C002892; MELO3C022319; MELO3C004237; MELO3C004239; MELO3C004238;
[]	GO:0008429	phosphatidylethanolamine binding	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C009465	MELO3C009141
[]	GO:0051219	phosphoprotein binding	MOLECULAR_FUNCTION	1.0	0.017320713109288028	2	7	395	16724	MELO3C009316; MELO3C005002	MELO3C008473; MELO3C025740; MELO3C015782; MELO3C009317; MELO3C016377; MELO3C016378; MELO3C014260
[]	GO:0034256	chlorophyll(ide) b reductase activity	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C025347	MELO3C019918
[]	GO:0046556	alpha-L-arabinofuranosidase activity	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C021281	MELO3C009722
[]	GO:0004044	amidophosphoribosyltransferase activity	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C020749	MELO3C025646
[]	GO:0003868	4-hydroxyphenylpyruvate dioxygenase activity	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C022961	MELO3C013690
[]	GO:0004838	L-tyrosine:2-oxoglutarate aminotransferase activity	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C025613	MELO3C013583
[]	GO:0010293	abscisic aldehyde oxidase activity	MOLECULAR_FUNCTION	1.0	0.04582092534215229	1	1	396	16730	MELO3C014719	MELO3C014717
[]	GO:0004846	urate oxidase activity	MOLECULAR_FUNCTION	1.0	0.023178421297923826	1	0	396	16731	MELO3C012335	

[]	GO:0019899	enzyme binding	MOLECULAR_FUNCTION	1.0	0.04129893308657816	6	103	391	16628	MELO3C022310; MELO3C015113; MELO3C014488; MELO3C021345; MELO3C010964; MELO3C011138	MELO3C021918; MELO3C011795; MELO3C007970; MELO3C020705; MELO3C012361; MELO3C012087; MELO3C004189; MELO3C022725; MELO3C006647; MELO3C002960; MELO3C006645; MELO3C009879; MELO3C018461; MELO3C023372; MELO3C022280; MELO3C018501; MELO3C017812; MELO3C009880; MELO3C023546; MELO3C022335; MELO3C003942; MELO3C002974; MELO3C022178; MELO3C017020; MELO3C017022; MELO3C002738; MELO3C024350;
[]	GO:0034990	nuclear mitotic cohesin complex	CELLULAR_COMPONENT	1.0	0.023178421297923826	1	0	396	16731	MELO3C012730	
[]	GO:0044445	cytosolic part	CELLULAR_COMPONENT	1.0	0.027077262658931633	2	339	395	16392	MELO3C013175; MELO3C017023	MELO3C011310; MELO3C006088; MELO3C012084; MELO3C014262; MELO3C024506; MELO3C020141; MELO3C022441; MELO3C026800; MELO3C001514; MELO3C016201; MELO3C026360; MELO3C025030; MELO3C018985; MELO3C017659; MELO3C013981; MELO3C009489; MELO3C002294; MELO3C006412; MELO3C025609; MELO3C006411; MELO3C024514; MELO3C023666; MELO3C005446; MELO3C006657; MELO3C024994; MELO3C025168; MELO3C022691;
[]	GO:0005882	intermediate filament	CELLULAR_COMPONENT	1.0	0.023178421297923826	1	0	396	16731	MELO3C019500	
[]	GO:0030057	desmosome	CELLULAR_COMPONENT	1.0	0.023178421297923826	1	0	396	16731	MELO3C019500	
[]	GO:0031934	mating-type region heterochromatin	CELLULAR_COMPONENT	1.0	0.023178421297923826	1	0	396	16731	MELO3C022562	

[]	GO:0098805	whole membrane	CELLULAR_COMPONENT	1.0	0.007859635296469604	1	316	396	16415	MELO3C004591	MELO3C014821; MELO3C011795; MELO3C014028; MELO3C009473; MELO3C015914; MELO3C002042; MELO3C007298; MELO3C020821; MELO3C022448; MELO3C026800; MELO3C021595; MELO3C009917; MELO3C025035; MELO3C025157; MELO3C019034; MELO3C012528; MELO3C012405; MELO3C005561; MELO3C004471; MELO3C005441; MELO3C007980; MELO3C007188; MELO3C004474; MELO3C004477; MELO3C007508; MELO3C015246; MELO3C017788;
[]	GO:0043625	delta DNA polymerase complex	CELLULAR_COMPONENT	1.0	0.023178421297923826	1	0	396	16731	MELO3C024596	
[]	GO:0009276	Gram-negative-bacterium-type cell wall	CELLULAR_COMPONENT	1.0	0.023178421297923826	1	0	396	16731	MELO3C011834	
[]	GO:0016363	nuclear matrix	CELLULAR_COMPONENT	1.0	0.04057388019809542	2	12	395	16719	MELO3C022562; MELO3C014877	MELO3C004615; MELO3C020860; MELO3C012993; MELO3C016792; MELO3C024350; MELO3C010637; MELO3C024228; MELO3C010830; MELO3C007648; MELO3C005127; MELO3C021953; MELO3C011710
[]	GO:0005578	proteinaceous extracellular matrix	CELLULAR_COMPONENT	1.0	0.030334190563045385	2	10	395	16721	MELO3C014128; MELO3C021281	MELO3C005073; MELO3C011366; MELO3C019374; MELO3C021496; MELO3C007904; MELO3C005528; MELO3C007695; MELO3C006312; MELO3C004465; MELO3C005965
[]	GO:0098796	membrane protein complex	CELLULAR_COMPONENT	1.0	0.02676098437841954	2	332	395	16399	MELO3C019163; MELO3C026518	MELO3C012522; MELO3C009472; MELO3C002042; MELO3C007298; MELO3C009358; MELO3C004105; MELO3C001992; MELO3C025156; MELO3C025277; MELO3C002727; MELO3C019951; MELO3C012648; MELO3C012527; MELO3C012528; MELO3C014946; MELO3C018748; MELO3C010469; MELO3C015922; MELO3C009240; MELO3C024877; MELO3C024756; MELO3C024755; MELO3C003700; MELO3C023548; MELO3C023542; MELO3C027107; MELO3C005329;
[]	GO:0031618	nuclear pericentric heterochromatin	CELLULAR_COMPONENT	1.0	0.023178421297923826	1	0	396	16731	MELO3C021323	

[]	GO:0080008	Cul4-RING E3 ubiquitin ligase complex	CELLULAR_COMPONENT	1.0	0.04293399340984404	4	53	393	16678	MELO3C003537; MELO3C017705; MELO3C009659; MELO3C007899	MELO3C001390; MELO3C008023; MELO3C003650; MELO3C002045; MELO3C023339; MELO3C007855; MELO3C022166; MELO3C012527; MELO3C010423; MELO3C018869; MELO3C017903; MELO3C005162; MELO3C011365; MELO3C025729; MELO3C004353; MELO3C025728; MELO3C026614; MELO3C021320; MELO3C026578; MELO3C023340; MELO3C002738; MELO3C022131; MELO3C004719; MELO3C013434; MELO3C011851; MELO3C011774; MELO3C006381;
[]	GO:0015934	large ribosomal subunit	CELLULAR_COMPONENT	1.0	0.03639119816595434	0	172	397	16559		MELO3C015999; MELO3C017939; MELO3C006088; MELO3C014262; MELO3C024506; MELO3C006245; MELO3C020549; MELO3C006922; MELO3C005952; MELO3C022601; MELO3C026403; MELO3C022441; MELO3C001514; MELO3C023012; MELO3C016201; MELO3C025030; MELO3C011956; MELO3C017659; MELO3C013984; MELO3C011285; MELO3C012254; MELO3C002294; MELO3C006412; MELO3C006411; MELO3C005844; MELO3C004995; MELO3C023820;
[]	GO:0005947	mitochondrial alpha-ketoglutarate dehydrogenase complex	CELLULAR_COMPONENT	1.0	0.04582092534215229	1	1	396	16730	MELO3C006679	MELO3C015564
[]	GO:0005956	protein kinase CK2 complex	CELLULAR_COMPONENT	1.0	0.04582092534215229	1	1	396	16730	MELO3C003341	MELO3C020365

[]	GO:0031410	cytoplasmic vesicle	CELLULAR_COMPONENT	1.0	0.033590926224202275	27	1672	370	15059	MELO3C014027; MELO3C012201; MELO3C016608; MELO3C002381; MELO3C005252; MELO3C005511; MELO3C022208; MELO3C007613; MELO3C026689; MELO3C026723; MELO3C003659; MELO3C025255; MELO3C014925; MELO3C011731; MELO3C014215; MELO3C013125; MELO3C016939; MELO3C014353; MELO3C006594; MELO3C013261; MELO3C013260; MELO3C005245; MELO3C004732; MELO3C023644; MELO3C007206; MELO3C026594; MELO3C011227	MELO3C015119; MELO3C002280; MELO3C012088; MELO3C002286; MELO3C012085; MELO3C026249; MELO3C026243; MELO3C017775; MELO3C015599; MELO3C025391; MELO3C003142; MELO3C003144; MELO3C003146; MELO3C004477; MELO3C014270; MELO3C005328; MELO3C020951; MELO3C008838; MELO3C017300; MELO3C019962; MELO3C019939; MELO3C020928; MELO3C014249; MELO3C012068; MELO3C014246; MELO3C003595; MELO3C012061;
[]	GO:0000800	lateral element	CELLULAR_COMPONENT	1.0	0.023178421297923826	1	0	396	16731	MELO3C014687	

Supplementary Table 1.H Gene Ontology terms (GO terms) of the cluster 1.7 obtained considering the comparison between lines over time fruit during storage at 20.5°C and 88% relative humidity for 18 d the near-isogenic line SC10-2 and its parental ''Piel de Sapo'' obtained according to the differentially expressed gene pattern (Supl. Table 1.A)

Tags	GO ID	GO Name	GO Category	FDR	P-Value	Nr Test	Nr Reference	Non Annot Test	Non Annot Reference	TestSet Sequences	RefSet Sequences
[OVER]	GO:0010362	negative regulation of anion channel activity by blue light	BIOLOGICAL_PROCESS	0.07717817672404814	1.0619351158050656E-4	2	0	175	16951	MELO3C025720; MELO3C013476	
[OVER]	GO:0009882	blue light photoreceptor activity	MOLECULAR_FUNCTION	0.07717817672404814	1.0619351158050656E-4	2	0	175	16951	MELO3C025720; MELO3C013476	
[OVER]	GO:0030686	90S preribosome	CELLULAR_COMPONENT	0.07717817672404814	9.965070318380818E-5	4	20	173	16931	MELO3C016321; MELO3C007466; MELO3C012627; MELO3C005976	MELO3C015548; MELO3C008994; MELO3C009324; MELO3C020849; MELO3C015907; MELO3C013185; MELO3C004873; MELO3C024305; MELO3C020422; MELO3C022402; MELO3C001556; MELO3C026228; MELO3C015060; MELO3C024322; MELO3C022134; MELO3C002835; MELO3C024126; MELO3C011408; MELO3C015960; MELO3C019636
[OVER]	GO:0018991	oviposition	BIOLOGICAL_PROCESS	0.09310180733627443	1.3795780087932281E-4	4	22	173	16929	MELO3C012627; MELO3C017720; MELO3C006760; MELO3C009381	MELO3C014699; MELO3C004473; MELO3C022725; MELO3C021737; MELO3C007109; MELO3C021984; MELO3C014291; MELO3C023325; MELO3C008835; MELO3C022305; MELO3C015060; MELO3C019066; MELO3C019253; MELO3C003703; MELO3C019883; MELO3C025275; MELO3C024782; MELO3C018500; MELO3C012616; MELO3C017338; MELO3C011139; MELO3C006082
[]	GO:0005730	nucleolus	CELLULAR_COMPONENT	0.1933394037383517	3.2741643308780983E-4	10	245	167	16706	MELO3C015627; MELO3C006760; MELO3C020255; MELO3C024474; MELO3C016321; MELO3C007466; MELO3C012627; MELO3C021598; MELO3C004204; MELO3C005976	MELO3C011795; MELO3C021919; MELO3C003491; MELO3C002168; MELO3C022204; MELO3C024989; MELO3C004227; MELO3C018062; MELO3C019034; MELO3C017650; MELO3C014706; MELO3C024180; MELO3C008032; MELO3C010355; MELO3C008157; MELO3C002173; MELO3C014153; MELO3C013185; MELO3C002299; MELO3C023545; MELO3C008835; MELO3C023306; MELO3C006657; MELO3C026259; MELO3C015363; MELO3C018994; MELO3C015126;

[]	GO:0042026	protein refolding	BIOLOGICAL_ PROCESS	0.319871748 92373604	0.001040397 5368459023	2	3	175	16948	MELO3C012180; MELO3C026919	MELO3C023058; MELO3C021741; MELO3C024388
[]	GO:0009638	phototropism	BIOLOGICAL_ PROCESS	0.532788278 1604056	0.002155253 2981376532	2	5	175	16946	MELO3C025720; MELO3C013476	MELO3C024837; MELO3C018590; MELO3C009692; MELO3C022995; MELO3C016232
[]	GO:0015995	chlorophyll biosynthetic process	BIOLOGICAL_ PROCESS	0.846589907 8972182	0.003942628 69892862	3	28	174	16923	MELO3C016714; MELO3C023131; MELO3C018572	MELO3C008086; MELO3C007233; MELO3C013592; MELO3C026802; MELO3C006606; MELO3C017176; MELO3C019337; MELO3C018565; MELO3C026000; MELO3C026160; MELO3C011657; MELO3C010892; MELO3C016717; MELO3C010053; MELO3C014571; MELO3C006512; MELO3C020115; MELO3C005189; MELO3C023105; MELO3C008717; MELO3C016131; MELO3C024010; MELO3C024155; MELO3C010614; MELO3C016115; MELO3C016339; MELO3C014712
[]	GO:0010181	FMN binding	MOLECULAR _FUNCTION	0.849954170 1733855	0.004317778 572168493	3	29	174	16922	MELO3C021944; MELO3C025720; MELO3C013476	MELO3C008481; MELO3C004023; MELO3C023799; MELO3C009759; MELO3C022683; MELO3C022684; MELO3C008805; MELO3C022681; MELO3C024281; MELO3C018625; MELO3C016623; MELO3C018626; MELO3C010940; MELO3C015514; MELO3C017636; MELO3C007340; MELO3C008075; MELO3C007124; MELO3C006296; MELO3C006011; MELO3C009702; MELO3C011062; MELO3C003541; MELO3C005229; MELO3C003644; MELO3C017461; MELO3C025861;
[]	GO:0051091	positive regulation of sequence-specific DNA binding transcription factor activity	BIOLOGICAL_ PROCESS	0.923487244 6965384	0.006547341 533695067	2	10	175	16941	MELO3C006760; MELO3C018099	MELO3C016083; MELO3C011983; MELO3C005912; MELO3C019642; MELO3C002481; MELO3C019932; MELO3C025417; MELO3C023325; MELO3C005424; MELO3C025767

[]	GO:0097190	apoptotic signaling pathway	BIOLOGICAL_PROCESS	0.9234872446965384	0.008097951336000693	3	37	174	16914	MELO3C011641; MELO3C005976; MELO3C018099	MELO3C013754; MELO3C011354; MELO3C012146; MELO3C002481; MELO3C003572; MELO3C020322; MELO3C025417; MELO3C025413; MELO3C016083; MELO3C003536; MELO3C005912; MELO3C015493; MELO3C016340; MELO3C019157; MELO3C019315; MELO3C025010; MELO3C018726; MELO3C011421; MELO3C013522; MELO3C011983; MELO3C020816; MELO3C011041; MELO3C015928; MELO3C007243; MELO3C003562; MELO3C002032; MELO3C025009;
[]	GO:2000011	regulation of adaxial/abaxial pattern formation	BIOLOGICAL_PROCESS	0.9234872446965384	0.010333956095153881	1	0	176	16951	MELO3C015627	
[]	GO:0009903	chloroplast avoidance movement	BIOLOGICAL_PROCESS	0.9234872446965384	0.010333956095153881	1	0	176	16951	MELO3C025720	
[]	GO:0032929	negative regulation of superoxide anion generation	BIOLOGICAL_PROCESS	0.9234872446965384	0.010333956095153881	1	0	176	16951	MELO3C005976	
[]	GO:0018298	protein-chromophore linkage	BIOLOGICAL_PROCESS	0.9234872446965384	0.008671871761091517	3	38	174	16913	MELO3C012912; MELO3C025720; MELO3C013476	MELO3C012066; MELO3C007154; MELO3C001595; MELO3C001992; MELO3C026506; MELO3C024206; MELO3C003238; MELO3C017180; MELO3C026502; MELO3C000131; MELO3C002727; MELO3C002705; MELO3C015076; MELO3C016660; MELO3C010807; MELO3C000173; MELO3C019677; MELO3C015536; MELO3C015998; MELO3C008358; MELO3C020213; MELO3C004214; MELO3C022995; MELO3C001664; MELO3C004018; MELO3C003644; MELO3C000500;
[]	GO:0033262	regulation of nuclear cell cycle DNA replication	BIOLOGICAL_PROCESS	0.9234872446965384	0.010333956095153881	1	0	176	16951	MELO3C006760	
[]	GO:0034462	small-subunit processome assembly	BIOLOGICAL_PROCESS	0.9234872446965384	0.010333956095153881	1	0	176	16951	MELO3C016321	
[]	GO:0090045	positive regulation of deacetylase activity	BIOLOGICAL_PROCESS	0.9234872446965384	0.010333956095153881	1	0	176	16951	MELO3C017720	
[]	GO:0090044	positive regulation of tubulin deacetylation	BIOLOGICAL_PROCESS	0.9234872446965384	0.010333956095153881	1	0	176	16951	MELO3C017720	

[]	GO:0000447	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	BIOLOGICAL_PROCESS	0.9234872446965384	0.010206693282011533	2	13	175	16938	MELO3C016321; MELO3C012627	MELO3C008994; MELO3C006662; MELO3C020849; MELO3C024305; MELO3C020422; MELO3C015060; MELO3C002835; MELO3C024126; MELO3C017650; MELO3C011408; MELO3C015663; MELO3C019636; MELO3C015997
[]	GO:0009866	induced systemic resistance, ethylene mediated signaling pathway	BIOLOGICAL_PROCESS	0.9234872446965384	0.010333956095153881	1	0	176	16951	MELO3C026577	
[]	GO:0070984	SET domain binding	MOLECULAR_FUNCTION	0.9234872446965384	0.010333956095153881	1	0	176	16951	MELO3C006760	
[]	GO:0042286	glutamate-1-semialdehyde 2,1-aminomutase activity	MOLECULAR_FUNCTION	0.9234872446965384	0.010333956095153881	1	0	176	16951	MELO3C018572	
[]	GO:0043522	leucine zipper domain binding	MOLECULAR_FUNCTION	0.9234872446965384	0.010333956095153881	1	0	176	16951	MELO3C005976	
[]	GO:0051116	cobaltochelatase activity	MOLECULAR_FUNCTION	0.9234872446965384	0.010333956095153881	1	0	176	16951	MELO3C023131	
[]	GO:0016514	SWI/SNF complex	CELLULAR_COMPONENT	0.9234872446965384	0.010333956095153881	1	0	176	16951	MELO3C006760	
[]	GO:0071564	npBAF complex	CELLULAR_COMPONENT	0.9234872446965384	0.010333956095153881	1	0	176	16951	MELO3C006760	
[]	GO:0071565	nBAF complex	CELLULAR_COMPONENT	0.9234872446965384	0.010333956095153881	1	0	176	16951	MELO3C006760	
[]	GO:0015030	Cajal body	CELLULAR_COMPONENT	0.9234872446965384	0.010206693282011533	2	13	175	16938	MELO3C026433; MELO3C022928	MELO3C012871; MELO3C004440; MELO3C023809; MELO3C017908; MELO3C006422; MELO3C005127; MELO3C004018; MELO3C008801; MELO3C019034; MELO3C017365; MELO3C017696; MELO3C014706; MELO3C022370
[]	GO:0016586	RSC complex	CELLULAR_COMPONENT	0.9234872446965384	0.010333956095153881	1	0	176	16951	MELO3C006760	
[]	GO:0007254	JNK cascade	BIOLOGICAL_PROCESS	0.9687274905171933	0.011586177649073121	2	14	175	16937	MELO3C018099; MELO3C026577	MELO3C011983; MELO3C002150; MELO3C002481; MELO3C004594; MELO3C025417; MELO3C005328; MELO3C004635; MELO3C016083; MELO3C026602; MELO3C005912; MELO3C021442; MELO3C019642; MELO3C025790; MELO3C015497
[]	GO:0008587	imaginal disc-derived wing margin morphogenesis	BIOLOGICAL_PROCESS	1.0	0.020561718679675958	1	1	176	16950	MELO3C006760	MELO3C006520
[]	GO:0008586	imaginal disc-derived wing vein morphogenesis	BIOLOGICAL_PROCESS	1.0	0.020561718679675958	1	1	176	16950	MELO3C006760	MELO3C006520

[]	GO:0000187	activation of MAPK activity	BIOLOGICAL_PROCESS	1.0	0.023301891810173274	2	21	175	16930	MELO3C018099; MELO3C026577	MELO3C011983; MELO3C002150; MELO3C002481; MELO3C004594; MELO3C012361; MELO3C020718; MELO3C002124; MELO3C025417; MELO3C003004; MELO3C026848; MELO3C004635; MELO3C005705; MELO3C021187; MELO3C016083; MELO3C005912; MELO3C019642; MELO3C025790; MELO3C015497; MELO3C016399; MELO3C010966; MELO3C011446
[]	GO:0005986	sucrose biosynthetic process	BIOLOGICAL_PROCESS	1.0	0.040702992789935	1	3	176	16948	MELO3C011682	MELO3C025149; MELO3C012320; MELO3C009570
[]	GO:0002119	nematode larval development	BIOLOGICAL_PROCESS	1.0	0.03547934538526353	7	291	170	16660	MELO3C006760; MELO3C024474; MELO3C016321; MELO3C007466; MELO3C012627; MELO3C017720; MELO3C009381	MELO3C012522; MELO3C002166; MELO3C002045; MELO3C004344; MELO3C019031; MELO3C026800; MELO3C019034; MELO3C025275; MELO3C014708; MELO3C015235; MELO3C019956; MELO3C020836; MELO3C008157; MELO3C002173; MELO3C004473; MELO3C014153; MELO3C013185; MELO3C023545; MELO3C008835; MELO3C023306; MELO3C023427; MELO3C006657; MELO3C024757; MELO3C003703; MELO3C025044; MELO3C011207; MELO3C011449;
[]	GO:0030388	fructose 1,6-bisphosphate metabolic process	BIOLOGICAL_PROCESS	1.0	0.020561718679675958	1	1	176	16950	MELO3C011682	MELO3C003214
[]	GO:0048011	neurotrophin TRK receptor signaling pathway	BIOLOGICAL_PROCESS	1.0	0.035020126629563865	4	115	173	16836	MELO3C011641; MELO3C026577; MELO3C005976; MELO3C018099	MELO3C005393; MELO3C012361; MELO3C008942; MELO3C022209; MELO3C004465; MELO3C001991; MELO3C022205; MELO3C008306; MELO3C003536; MELO3C003778; MELO3C020263; MELO3C019157; MELO3C019315; MELO3C025790; MELO3C007181; MELO3C011444; MELO3C007580; MELO3C012376; MELO3C006491; MELO3C002050; MELO3C020837; MELO3C004594; MELO3C011041; MELO3C020718; MELO3C002691; MELO3C004635; MELO3C024478;
[]	GO:0007474	imaginal disc-derived wing vein specification	BIOLOGICAL_PROCESS	1.0	0.020561718679675958	1	1	176	16950	MELO3C006760	MELO3C015173
[]	GO:0000282	cellular bud site selection	BIOLOGICAL_PROCESS	1.0	0.030684372877273734	1	2	176	16949	MELO3C024474	MELO3C013504; MELO3C015367
[]	GO:0070983	dendrite guidance	BIOLOGICAL_PROCESS	1.0	0.020561718679675958	1	1	176	16950	MELO3C006760	MELO3C017295

[]	GO:1902582	single-organism intracellular transport	BIOLOGICAL_ PROCESS	1.0	0.049266416 36975816	4	129	173	16822	MELO3C004761; MELO3C019156; MELO3C004204; MELO3C020533	MELO3C014028; MELO3C006001; MELO3C011153; MELO3C007211; MELO3C012087; MELO3C008306; MELO3C016280; MELO3C022166; MELO3C018463; MELO3C016047; MELO3C010745; MELO3C013982; MELO3C020836; MELO3C004074; MELO3C010592; MELO3C006136; MELO3C006015; MELO3C000249; MELO3C002456; MELO3C023548; MELO3C009808; MELO3C005329; MELO3C025960; MELO3C002738; MELO3C024193; MELO3C024350; MELO3C010637;
[]	GO:0072594	establishment of protein localization to organelle	BIOLOGICAL_ PROCESS	1.0	0.048157211 38180463	4	128	173	16823	MELO3C019156; MELO3C004204; MELO3C020533; MELO3C013766	MELO3C011153; MELO3C007211; MELO3C012087; MELO3C007214; MELO3C016280; MELO3C022166; MELO3C025310; MELO3C016047; MELO3C010745; MELO3C022280; MELO3C023371; MELO3C026482; MELO3C014306; MELO3C018518; MELO3C013982; MELO3C020836; MELO3C004471; MELO3C004074; MELO3C010592; MELO3C006136; MELO3C006015; MELO3C004874; MELO3C000249; MELO3C009808; MELO3C019565; MELO3C002738; MELO3C010637;
[]	GO:0017038	protein import	BIOLOGICAL_ PROCESS	1.0	0.048496417 87186457	3	76	174	16875	MELO3C019156; MELO3C004204; MELO3C020533	MELO3C013775; MELO3C007010; MELO3C011153; MELO3C007211; MELO3C012087; MELO3C020586; MELO3C020500; MELO3C016280; MELO3C022166; MELO3C000453; MELO3C022521; MELO3C026441; MELO3C022242; MELO3C024782; MELO3C016047; MELO3C010745; MELO3C016326; MELO3C017339; MELO3C013940; MELO3C013982; MELO3C020836; MELO3C009840; MELO3C010592; MELO3C006136; MELO3C006015; MELO3C020637; MELO3C000249;

[]	GO:0040035	hermaphrodite genitalia development	BIOLOGICAL_ PROCESS	1.0	0.013933141 239127323	5	132	172	16819	MELO3C016321; MELO3C007466; MELO3C017720; MELO3C006760; MELO3C009381	MELO3C012361; MELO3C006121; MELO3C004344; MELO3C019031; MELO3C022166; MELO3C024586; MELO3C026888; MELO3C014708; MELO3C015235; MELO3C019956; MELO3C021808; MELO3C015647; MELO3C008151; MELO3C008157; MELO3C002173; MELO3C000924; MELO3C006498; MELO3C004873; MELO3C008835; MELO3C023823; MELO3C023427; MELO3C006657; MELO3C024757; MELO3C007903; MELO3C002738; MELO3C025044; MELO3C016297;
[]	GO:0007173	epidermal growth factor receptor signaling pathway	BIOLOGICAL_ PROCESS	1.0	0.045482947 61164327	2	31	175	16920	MELO3C018099; MELO3C026577	MELO3C002481; MELO3C012361; MELO3C013251; MELO3C002124; MELO3C025417; MELO3C020644; MELO3C003754; MELO3C008306; MELO3C023674; MELO3C016083; MELO3C005912; MELO3C023851; MELO3C022241; MELO3C018841; MELO3C025790; MELO3C015497; MELO3C010966; MELO3C011983; MELO3C002150; MELO3C004594; MELO3C006413; MELO3C003004; MELO3C022237; MELO3C004635; MELO3C021463; MELO3C005946; MELO3C019642;
[]	GO:0007179	transforming growth factor beta receptor signaling pathway	BIOLOGICAL_ PROCESS	1.0	0.040702992 789935	1	3	176	16948	MELO3C017720	MELO3C015782; MELO3C016377; MELO3C016378
[]	GO:0009904	chloroplast accumulation movement	BIOLOGICAL_ PROCESS	1.0	0.020561718 679675958	1	1	176	16950	MELO3C025720	MELO3C003878
[]	GO:2000034	regulation of seed maturation	BIOLOGICAL_ PROCESS	1.0	0.030684372 877273734	1	2	176	16949	MELO3C020484	MELO3C005929; MELO3C009101
[]	GO:0009691	cytokinin biosynthetic process	BIOLOGICAL_ PROCESS	1.0	0.040702992 789935	1	3	176	16948	MELO3C015852	MELO3C009521; MELO3C007417; MELO3C016881
[]	GO:0090630	activation of GTPase activity	BIOLOGICAL_ PROCESS	1.0	0.020561718 679675958	1	1	176	16950	MELO3C018195	MELO3C013721

[]	GO:0044281	small molecule metabolic process	BIOLOGICAL_ PROCESS	1.0	0.016383216 252722998	7	1506	170	15445	MELO3C023599; MELO3C012088; MELO3C011682; MELO3C013000; MELO3C011270; MELO3C018027; MELO3C004761	MELO3C003131; MELO3C020949; MELO3C005310; MELO3C002287; MELO3C013171; MELO3C004465; MELO3C004226; MELO3C005558; MELO3C006405; MELO3C003379; MELO3C006648; MELO3C005559; MELO3C009914; MELO3C005556; MELO3C009913; MELO3C015352; MELO3C027332; MELO3C016200; MELO3C019711; MELO3C019951; MELO3C018622; MELO3C019710; MELO3C026482; MELO3C018625; MELO3C015599; MELO3C018624; MELO3C019716;
[]	GO:0010030	positive regulation of seed germination	BIOLOGICAL_ PROCESS	1.0	0.040702992 789935	1	3	176	16948	MELO3C020484	MELO3C004632; MELO3C009627; MELO3C009101
[]	GO:0006337	nucleosome disassembly	BIOLOGICAL_ PROCESS	1.0	0.020561718 679675958	1	1	176	16950	MELO3C006760	MELO3C007085
[]	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	BIOLOGICAL_ PROCESS	1.0	0.029336667 88391751	2	24	175	16927	MELO3C006760; MELO3C005976	MELO3C019508; MELO3C013015; MELO3C009890; MELO3C007085; MELO3C012231; MELO3C005694; MELO3C009730; MELO3C002074; MELO3C008414; MELO3C007015; MELO3C007526; MELO3C003216; MELO3C025349; MELO3C020474; MELO3C023752; MELO3C024352; MELO3C016065; MELO3C011649; MELO3C019932; MELO3C014817; MELO3C015367; MELO3C017678; MELO3C018910; MELO3C015447
[]	GO:0006302	double-strand break repair	BIOLOGICAL_ PROCESS	1.0	0.038512363 9460339	3	69	174	16882	MELO3C003108; MELO3C006760; MELO3C016674	MELO3C020706; MELO3C006201; MELO3C023535; MELO3C004027; MELO3C004227; MELO3C003655; MELO3C002448; MELO3C003338; MELO3C020860; MELO3C018187; MELO3C019510; MELO3C019511; MELO3C017258; MELO3C015555; MELO3C015434; MELO3C018624; MELO3C017458; MELO3C010422; MELO3C006096; MELO3C012730; MELO3C016858; MELO3C009682; MELO3C006292; MELO3C006496; MELO3C021605; MELO3C002299; MELO3C022216;
[]	GO:0031055	chromatin remodeling at centromere	BIOLOGICAL_ PROCESS	1.0	0.040702992 789935	1	3	176	16948	MELO3C006760	MELO3C005059; MELO3C017558; MELO3C023986

[]	GO:0010118	stomatal movement	BIOLOGICAL_PROCESS	1.0	0.013042579502851575	2	15	175	16936	MELO3C025720; MELO3C013476	MELO3C021918; MELO3C016937; MELO3C014004; MELO3C006046; MELO3C016919; MELO3C014230; MELO3C007027; MELO3C022995; MELO3C007427; MELO3C005718; MELO3C016330; MELO3C003906; MELO3C025152; MELO3C019731; MELO3C018734
[]	GO:0031053	primary miRNA processing	BIOLOGICAL_PROCESS	1.0	0.040702992789935	1	3	176	16948	MELO3C015627	MELO3C026304; MELO3C005929; MELO3C015158
[]	GO:0031293	membrane protein intracellular domain proteolysis	BIOLOGICAL_PROCESS	1.0	0.040702992789935	1	3	176	16948	MELO3C011641	MELO3C002032; MELO3C020322; MELO3C019157
[]	GO:0039692	single stranded viral RNA replication via double stranded DNA intermediate	BIOLOGICAL_PROCESS	1.0	0.020561718679675958	1	1	176	16950	MELO3C006760	MELO3C008414
[]	GO:0007220	Notch receptor processing	BIOLOGICAL_PROCESS	1.0	0.040702992789935	1	3	176	16948	MELO3C011641	MELO3C002032; MELO3C020322; MELO3C019157
[]	GO:0000389	mRNA 3'-splice site recognition	BIOLOGICAL_PROCESS	1.0	0.040702992789935	1	3	176	16948	MELO3C009381	MELO3C008488; MELO3C023427; MELO3C008151
[]	GO:0006921	cellular component disassembly involved in execution phase of apoptosis	BIOLOGICAL_PROCESS	1.0	0.02726218007250078	2	23	175	16928	MELO3C026577; MELO3C017720	MELO3C006260; MELO3C011145; MELO3C009676; MELO3C002150; MELO3C004594; MELO3C005895; MELO3C005255; MELO3C005893; MELO3C025857; MELO3C004635; MELO3C025602; MELO3C018052; MELO3C023146; MELO3C022411; MELO3C025790; MELO3C018587; MELO3C015497; MELO3C016301; MELO3C023063; MELO3C024030; MELO3C015225; MELO3C011414; MELO3C017447
[]	GO:0018343	protein farnesylation	BIOLOGICAL_PROCESS	1.0	0.020561718679675958	1	1	176	16950	MELO3C017720	MELO3C009957
[]	GO:0018344	protein geranylgeranylation	BIOLOGICAL_PROCESS	1.0	0.030684372877273734	1	2	176	16949	MELO3C017720	MELO3C013721; MELO3C021654
[]	GO:0051103	DNA ligation involved in DNA repair	BIOLOGICAL_PROCESS	1.0	0.040702992789935	1	3	176	16948	MELO3C010375	MELO3C018624; MELO3C015121; MELO3C026949
[]	GO:0070423	nucleotide-binding oligomerization domain containing signaling pathway	BIOLOGICAL_PROCESS	1.0	0.019603395228084016	2	19	175	16932	MELO3C018099; MELO3C026577	MELO3C011983; MELO3C002150; MELO3C002481; MELO3C004594; MELO3C020718; MELO3C025417; MELO3C026848; MELO3C004635; MELO3C005705; MELO3C021187; MELO3C016083; MELO3C005912; MELO3C019642; MELO3C016132; MELO3C025790; MELO3C015497; MELO3C016399; MELO3C010966; MELO3C011446
[]	GO:0010155	regulation of proton transport	BIOLOGICAL_PROCESS	1.0	0.020561718679675958	1	1	176	16950	MELO3C025720	MELO3C016696

[]	GO:0048509	regulation of meristem development	BIOLOGICAL_PROCESS	1.0	0.02933666788391751	2	24	175	16927	MELO3C015627; MELO3C017720	MELO3C016879; MELO3C027290; MELO3C009584; MELO3C011021; MELO3C013793; MELO3C009465; MELO3C020975; MELO3C009957; MELO3C008612; MELO3C004752; MELO3C025617; MELO3C007417; MELO3C022995; MELO3C026749; MELO3C003743; MELO3C019330; MELO3C022310; MELO3C024446; MELO3C022388; MELO3C025982; MELO3C018720; MELO3C018455; MELO3C016413; MELO3C017812
[]	GO:0006596	polyamine biosynthetic process	BIOLOGICAL_PROCESS	1.0	0.019603395228084016	2	19	175	16932	MELO3C012418; MELO3C012007	MELO3C006580; MELO3C011484; MELO3C004110; MELO3C002252; MELO3C004683; MELO3C005877; MELO3C023359; MELO3C023315; MELO3C006538; MELO3C023787; MELO3C004624; MELO3C021386; MELO3C023786; MELO3C017264; MELO3C022492; MELO3C027387; MELO3C012419; MELO3C012417; MELO3C011335
[]	GO:0009864	induced systemic resistance, jasmonic acid mediated signaling pathway	BIOLOGICAL_PROCESS	1.0	0.030684372877273734	1	2	176	16949	MELO3C026577	MELO3C005466; MELO3C006046
[]	GO:0007323	peptide pheromone maturation	BIOLOGICAL_PROCESS	1.0	0.020561718679675958	1	1	176	16950	MELO3C017720	MELO3C022525
[]	GO:0043066	negative regulation of apoptotic process	BIOLOGICAL_PROCESS	1.0	0.048004930886737456	2	32	175	16919	MELO3C005976; MELO3C018099	MELO3C011470; MELO3C006121; MELO3C003331; MELO3C007237; MELO3C003332; MELO3C004622; MELO3C025417; MELO3C005757; MELO3C025413; MELO3C016083; MELO3C005912; MELO3C025752; MELO3C023972; MELO3C009939; MELO3C004827; MELO3C024340; MELO3C025355; MELO3C011710; MELO3C013522; MELO3C011983; MELO3C012376; MELO3C011021; MELO3C004950; MELO3C007109; MELO3C022237; MELO3C021442; MELO3C017087;
[]	GO:0004660	protein farnesyltransferase activity	MOLECULAR_FUNCTION	1.0	0.020561718679675958	1	1	176	16950	MELO3C017720	MELO3C009957
[]	GO:0004662	CAAX-protein geranylgeranyltransferase activity	MOLECULAR_FUNCTION	1.0	0.020561718679675958	1	1	176	16950	MELO3C017720	MELO3C021654
[]	GO:0004791	thioredoxin-disulfide reductase activity	MOLECULAR_FUNCTION	1.0	0.030684372877273734	1	2	176	16949	MELO3C013707	MELO3C023105; MELO3C007984

[]	GO:0000156	phosphorelay response regulator activity	MOLECULAR_FUNCTION	1.0	0.03147205845062728	2	25	175	16926	MELO3C009770; MELO3C019056	MELO3C005250; MELO3C004183; MELO3C010245; MELO3C003075; MELO3C005156; MELO3C005336; MELO3C000311; MELO3C001999; MELO3C017472; MELO3C010624; MELO3C021290; MELO3C013758; MELO3C016937; MELO3C012031; MELO3C006451; MELO3C006693; MELO3C012470; MELO3C022310; MELO3C025982; MELO3C005927; MELO3C003906; MELO3C020055; MELO3C010714; MELO3C017128; MELO3C016975
[]	GO:0043014	alpha-tubulin binding	MOLECULAR_FUNCTION	1.0	0.030684372877273734	1	2	176	16949	MELO3C017720	MELO3C006171; MELO3C011830
[]	GO:0004402	histone acetyltransferase activity	MOLECULAR_FUNCTION	1.0	0.04059369943336301	2	29	175	16922	MELO3C026433; MELO3C017030	MELO3C013698; MELO3C011851; MELO3C011774; MELO3C013356; MELO3C009471; MELO3C006243; MELO3C007211; MELO3C014860; MELO3C013253; MELO3C004100; MELO3C009635; MELO3C007015; MELO3C009633; MELO3C002885; MELO3C022788; MELO3C026222; MELO3C010806; MELO3C015474; MELO3C012527; MELO3C005161; MELO3C005162; MELO3C010476; MELO3C007627; MELO3C004615; MELO3C001964; MELO3C002318; MELO3C026234;
[]	GO:0000170	sphingosine hydroxylase activity	MOLECULAR_FUNCTION	1.0	0.020561718679675958	1	1	176	16950	MELO3C012088	MELO3C008543
[]	GO:0000774	adenyl-nucleotide exchange factor activity	MOLECULAR_FUNCTION	1.0	0.030684372877273734	1	2	176	16949	MELO3C019156	MELO3C014179; MELO3C011373
[]	GO:0002039	p53 binding	MOLECULAR_FUNCTION	1.0	0.040702992789935	1	3	176	16948	MELO3C006760	MELO3C024469; MELO3C011731; MELO3C015367
[]	GO:0004473	malate dehydrogenase (decarboxylating) (NADP+) activity	MOLECULAR_FUNCTION	1.0	0.040702992789935	1	3	176	16948	MELO3C013000	MELO3C011129; MELO3C015407; MELO3C024441

[]	GO:0015450	P-P-bond-hydrolysis-driven protein transmembrane transporter activity	MOLECULAR_FUNCTION	1.0	0.025250083755878006	2	22	175	16929	MELO3C020610; MELO3C013766	MELO3C014403; MELO3C012288; MELO3C009258; MELO3C010164; MELO3C014143; MELO3C014891; MELO3C009667; MELO3C006532; MELO3C020586; MELO3C002366; MELO3C025649; MELO3C000347; MELO3C006547; MELO3C005915; MELO3C005802; MELO3C019213; MELO3C024375; MELO3C016112; MELO3C016113; MELO3C010745; MELO3C017676; MELO3C013337
[]	GO:0008482	sulfite oxidase activity	MOLECULAR_FUNCTION	1.0	0.020561718679675958	1	1	176	16950	MELO3C004917	MELO3C008194
[]	GO:0004697	protein kinase C activity	MOLECULAR_FUNCTION	1.0	0.017856240060880827	2	18	175	16933	MELO3C025720; MELO3C013476	MELO3C012376; MELO3C012751; MELO3C007047; MELO3C002781; MELO3C004520; MELO3C006602; MELO3C005408; MELO3C023003; MELO3C001920; MELO3C024168; MELO3C001921; MELO3C005407; MELO3C015495; MELO3C017135; MELO3C001919; MELO3C010857; MELO3C016889; MELO3C021090
[]	GO:0005471	ATP:ADP antiporter activity	MOLECULAR_FUNCTION	1.0	0.030684372877273734	1	2	176	16949	MELO3C012943	MELO3C018705; MELO3C002052
[]	GO:0004708	MAP kinase kinase activity	MOLECULAR_FUNCTION	1.0	0.040702992789935	1	3	176	16948	MELO3C026577	MELO3C015497; MELO3C004594; MELO3C004635
[]	GO:0008176	tRNA (guanine-N7-)-methyltransferase activity	MOLECULAR_FUNCTION	1.0	0.030684372877273734	1	2	176	16949	MELO3C006212	MELO3C009351; MELO3C011163
[]	GO:0009824	AMP dimethylallyltransferase activity	MOLECULAR_FUNCTION	1.0	0.030684372877273734	1	2	176	16949	MELO3C015852	MELO3C012255; MELO3C011541
[]	GO:0005102	receptor binding	MOLECULAR_FUNCTION	1.0	0.033666886820020205	2	26	175	16925	MELO3C026499; MELO3C017526	MELO3C004380; MELO3C005357; MELO3C007654; MELO3C022726; MELO3C005679; MELO3C005579; MELO3C023992; MELO3C017991; MELO3C012406; MELO3C017338; MELO3C017812; MELO3C012752; MELO3C013885; MELO3C014699; MELO3C011021; MELO3C012231; MELO3C010073; MELO3C012251; MELO3C005328; MELO3C022237; MELO3C003743; MELO3C003429; MELO3C015581; MELO3C011104; MELO3C018956; MELO3C013788

[]	GO:0003712	transcription cofactor activity	MOLECULAR_FUNCTION	1.0	0.024152859110298835	3	57	174	16894	MELO3C005286; MELO3C021598; MELO3C024474	MELO3C013698; MELO3C013015; MELO3C004380; MELO3C013773; MELO3C009592; MELO3C008420; MELO3C011193; MELO3C009635; MELO3C007015; MELO3C009633; MELO3C002326; MELO3C002448; MELO3C000135; MELO3C021430; MELO3C025950; MELO3C021751; MELO3C008473; MELO3C008876; MELO3C004873; MELO3C002299; MELO3C004553; MELO3C007627; MELO3C023189; MELO3C001964; MELO3C021320; MELO3C003429; MELO3C021442;
[]	GO:0070330	aromatase activity	MOLECULAR_FUNCTION	1.0	0.03147205845062728	2	25	175	16926	MELO3C021845; MELO3C021846	MELO3C006168; MELO3C007379; MELO3C013194; MELO3C009458; MELO3C021851; MELO3C004742; MELO3C009738; MELO3C009737; MELO3C020561; MELO3C021850; MELO3C023592; MELO3C011799; MELO3C014945; MELO3C016879; MELO3C006172; MELO3C008532; MELO3C021844; MELO3C005686; MELO3C021842; MELO3C021205; MELO3C024015; MELO3C026212; MELO3C024495; MELO3C016233; MELO3C014879
[]	GO:0003838	sterol 24-C-methyltransferase activity	MOLECULAR_FUNCTION	1.0	0.020561718679675958	1	1	176	16950	MELO3C023989	MELO3C023990
[]	GO:0030750	putrescine N-methyltransferase activity	MOLECULAR_FUNCTION	1.0	0.040702992789935	1	3	176	16948	MELO3C012007	MELO3C008477; MELO3C002252; MELO3C005877
[]	GO:0052658	inositol-1,4,5-trisphosphate 5-phosphatase activity	MOLECULAR_FUNCTION	1.0	0.040702992789935	1	3	176	16948	MELO3C009908	MELO3C005242; MELO3C013872; MELO3C014293
[]	GO:0016851	magnesium chelatase activity	MOLECULAR_FUNCTION	1.0	0.030684372877273734	1	2	176	16949	MELO3C023131	MELO3C007233; MELO3C014571
[]	GO:0052659	inositol-1,3,4,5-tetrakisphosphate 5-phosphatase activity	MOLECULAR_FUNCTION	1.0	0.040702992789935	1	3	176	16948	MELO3C009908	MELO3C005242; MELO3C013872; MELO3C014293
[]	GO:0016711	flavonoid 3'-monooxygenase activity	MOLECULAR_FUNCTION	1.0	0.040702992789935	1	3	176	16948	MELO3C022246	MELO3C005572; MELO3C009741; MELO3C017219

[]	GO:0000155	phosphorelay sensor kinase activity	MOLECULAR_FUNCTION	1.0	0.03147205845062728	2	25	175	16926	MELO3C025720; MELO3C013476	MELO3C005250; MELO3C004183; MELO3C012066; MELO3C026506; MELO3C021931; MELO3C026502; MELO3C024168; MELO3C006749; MELO3C002705; MELO3C016660; MELO3C013758; MELO3C016937; MELO3C005265; MELO3C006451; MELO3C005266; MELO3C003205; MELO3C006717; MELO3C022310; MELO3C025982; MELO3C003906; MELO3C020055; MELO3C024196; MELO3C015961; MELO3C024195; MELO3C011940
[]	GO:0050366	tyramine N-feruloyltransferase activity	MOLECULAR_FUNCTION	1.0	0.020561718679675958	1	1	176	16950	MELO3C012418	MELO3C012417
[]	GO:0016829	lyase activity	MOLECULAR_FUNCTION	1.0	0.02372951707526035	0	406	177	16545		MELO3C013057; MELO3C003491; MELO3C006520; MELO3C002288; MELO3C003259; MELO3C026007; MELO3C026005; MELO3C026006; MELO3C026004; MELO3C024189; MELO3C018622; MELO3C014039; MELO3C004110; MELO3C007744; MELO3C014392; MELO3C004355; MELO3C009809; MELO3C019840; MELO3C025168; MELO3C016693; MELO3C018994; MELO3C010910; MELO3C015368; MELO3C016339; MELO3C013152; MELO3C011095; MELO3C012184;
[]	GO:0008897	holo-[acyl-carrier-protein] synthase activity	MOLECULAR_FUNCTION	1.0	0.020561718679675958	1	1	176	16950	MELO3C012351	MELO3C011647
[]	GO:0000254	C-4 methylsterol oxidase activity	MOLECULAR_FUNCTION	1.0	0.040702992789935	1	3	176	16948	MELO3C012088	MELO3C008543; MELO3C013991; MELO3C020602
[]	GO:0003999	adenine phosphoribosyltransferase activity	MOLECULAR_FUNCTION	1.0	0.040702992789935	1	3	176	16948	MELO3C011270	MELO3C010812; MELO3C013962; MELO3C005556
[]	GO:0071001	U4/U6 snRNP	CELLULAR_COMPONENT	1.0	0.020561718679675958	1	1	176	16950	MELO3C026433	MELO3C012489
[]	GO:0005965	protein farnesyltransferase complex	CELLULAR_COMPONENT	1.0	0.020561718679675958	1	1	176	16950	MELO3C017720	MELO3C009957
[]	GO:0035060	brahma complex	CELLULAR_COMPONENT	1.0	0.020561718679675958	1	1	176	16950	MELO3C006760	MELO3C017295
[]	GO:0010445	nuclear dicing body	CELLULAR_COMPONENT	1.0	0.020561718679675958	1	1	176	16950	MELO3C015627	MELO3C005929

[]	GO:0009707	chloroplast outer membrane	CELLULAR_COMPONENT	1.0	0.017856240060880827	2	18	175	16933	MELO3C020610; MELO3C013766	MELO3C015416; MELO3C017968; MELO3C006133; MELO3C004471; MELO3C016719; MELO3C004591; MELO3C004474; MELO3C006974; MELO3C002387; MELO3C024587; MELO3C021253; MELO3C017360; MELO3C018772; MELO3C019874; MELO3C014409; MELO3C014605; MELO3C011502; MELO3C011415
[]	GO:0010007	magnesium chelatase complex	CELLULAR_COMPONENT	1.0	0.020561718679675958	1	1	176	16950	MELO3C023131	MELO3C014571
[]	GO:0016607	nuclear speck	CELLULAR_COMPONENT	1.0	0.038229114226002024	2	28	175	16923	MELO3C015627; MELO3C022928	MELO3C012489; MELO3C008488; MELO3C004440; MELO3C014086; MELO3C005035; MELO3C024822; MELO3C002326; MELO3C024028; MELO3C016008; MELO3C014823; MELO3C005382; MELO3C015826; MELO3C013781; MELO3C023809; MELO3C017908; MELO3C023427; MELO3C024757; MELO3C021320; MELO3C017365; MELO3C026275; MELO3C019500; MELO3C016115; MELO3C012616; MELO3C010637; MELO3C019702; MELO3C014459; MELO3C012579
[]	GO:0005953	CAAX-protein geranylgeranyltransferase complex	CELLULAR_COMPONENT	1.0	0.020561718679675958	1	1	176	16950	MELO3C017720	MELO3C021654
[]	GO:0005925	focal adhesion	CELLULAR_COMPONENT	1.0	0.030684372877273734	1	2	176	16949	MELO3C005976	MELO3C005382; MELO3C007007

Supplementary Table 2.A List of the Differentially Expressed Genes (2068 DEGs) only considering the postharvest ripening time in melon fruit during postharvest storage at 20.5 °C and 88% relative humidity for 18 d of the near-isogenic line SC10-2 and its parental control ´Piel de Sapo´ (PS). Gene Ontology terms (GO terms) of the six different clusters (named 2.x) obtained according to the differentially expressed gene.

Gene ID	pval	qval	Description
MELO3C010748	5,90E-12	1,16E-07	Heat shock transcription factor
MELO3C005540	1,88E-11	1,86E-07	14 kDa proline-rich protein dc2.15
MELO3C023889	7,79E-11	5,13E-07	Ultraviolet-B receptor UVR8
MELO3C003298	6,24E-10	2,94E-06	high mobility group B protein 1
MELO3C018265	7,45E-10	2,94E-06	ADP-ribosylation factor GTPase-activating protein
MELO3C015733	1,56E-09	5,14E-06	Pre-mRNA-splicing factor ATP-dependent RNA helicase
MELO3C003282	3,84E-09	1,08E-05	cleft lip and palate transmembrane protein 1 homolog
MELO3C008669	1,05E-08	2,60E-05	RING-type E3 ubiquitin transferase
MELO3C026279	1,50E-08	3,29E-05	cell division cycle protein 48 homolog
MELO3C018038	2,96E-08	4,66E-05	proline iminopeptidase
MELO3C007022	3,77E-08	4,66E-05	UDP-N-acetylglucosamine diphosphorylase 2-like
MELO3C022036	3,28E-08	4,66E-05	protein LONGIFOLIA 2
MELO3C015789	2,62E-08	4,66E-05	sucrose-binding protein-like
MELO3C023342	2,79E-08	4,66E-05	kinesin-related protein 11-like
MELO3C002468	3,61E-08	4,66E-05	Tobamovirus multiplication protein 1
MELO3C003752	3,53E-08	4,66E-05	gibberellin-regulated protein 11-like
MELO3C003570	4,19E-08	4,87E-05	Protein ROOT PRIMORDIUM DEFECTIVE 1
MELO3C006028	5,64E-08	5,45E-05	cyclic nucleotide-gated ion channel 1
MELO3C021108	5,62E-08	5,45E-05	Peptidylprolyl isomerase
MELO3C002508	5,38E-08	5,45E-05	thioredoxin-like protein CXXS1
MELO3C024028	5,80E-08	5,45E-05	DEAD-box ATP-dependent RNA helicase
MELO3C004023	7,06E-08	6,18E-05	NADPH--cytochrome P450 reductase
MELO3C019973	7,20E-08	6,18E-05	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase
MELO3C016073	8,21E-08	6,49E-05	Tudor/PWWP/MBT superfamily protein
MELO3C001317	8,13E-08	6,49E-05	Coiled-coil protein (DUF572)
MELO3C003905	9,86E-08	7,31E-05	glycine--tRNA ligase, mitochondrial 1
MELO3C003444	9,99E-08	7,31E-05	transcription factor IWS1
MELO3C022213	1,09E-07	7,43E-05	Myb family transcription factor family protein
MELO3C022533	1,07E-07	7,43E-05	shaggy-related protein kinase theta
MELO3C023449	1,40E-07	9,21E-05	UPF0481 plant-like protein
MELO3C016475	1,70E-07	0,000104363	Chloride channel protein
MELO3C024278	1,74E-07	0,000104363	Mitochondrial carrier protein
MELO3C012356	1,74E-07	0,000104363	Aspartyl aminopeptidase
MELO3C023146	2,03E-07	0,000104556	villin-2-like
MELO3C025783	1,81E-07	0,000104556	receptor-like serine/threonine-protein kinase NCRK
MELO3C010244	2,06E-07	0,000104556	Temperature-induced lipocalin
MELO3C017271	2,05E-07	0,000104556	Acetyl-coenzyme A synthetase
MELO3C017213	1,95E-07	0,000104556	UDP-glucose 6-dehydrogenase
MELO3C003563	1,86E-07	0,000104556	No data found
MELO3C014061	2,13E-07	0,000105194	WPP domain interacting protein, putative
MELO3C004433	2,20E-07	0,000106054	calcium uptake protein 1, mitochondrial-like isoform X1
MELO3C013868	2,32E-07	0,000107032	Cytochrome P450 family ent-kaurenoic acid oxidase
MELO3C019616	2,33E-07	0,000107032	E3 ubiquitin-protein ligase RGLG2
MELO3C006120	2,88E-07	0,000129143	MYB-related transcription factor
MELO3C004799	3,03E-07	0,000132974	splicing factor U2af small subunit B-like
MELO3C017380	3,28E-07	0,000141013	zinc finger CCHC domain-containing protein 7 isoform X3
MELO3C006297	3,64E-07	0,000148781	RNA recognition motif (RRM) containing protein
MELO3C012728	3,67E-07	0,000148781	Vacuolar sorting-associated protein 2-like protein
MELO3C023559	3,89E-07	0,000148781	40S ribosomal protein S27
MELO3C003812	3,77E-07	0,000148781	Glucose-1-phosphate adenylyltransferase
MELO3C012788	3,82E-07	0,000148781	Transcription initiation factor IIF alpha subunit family protein
MELO3C012930	3,92E-07	0,000148781	Zinc knuckle family protein
MELO3C013136	4,05E-07	0,000150962	GDP-L-galactose phosphorylase 1
MELO3C015720	4,16E-07	0,000152121	Smr (Small MutS-related) domain protein
MELO3C022416	4,70E-07	0,000168621	Ubiquitin family protein
MELO3C003875	5,08E-07	0,000179224	Protein phosphatase 2c, putative
MELO3C016754	6,18E-07	0,000214273	Cold regulated gene 27, putative isoform 3
MELO3C004194	6,44E-07	0,000215458	calreticulin
MELO3C022408	6,40E-07	0,000215458	UV-stimulated scaffold protein A homolog
MELO3C013622	6,73E-07	0,000217727	mannan endo-1,4-beta-mannosidase 2
MELO3C011379	6,66E-07	0,000217727	Chaperone protein dnaJ
MELO3C024626	7,24E-07	0,000230696	Protein LIKE COV 1
MELO3C000452	8,00E-07	0,000243073	Coiled-coil protein (DUF572)
MELO3C021903	7,87E-07	0,000243073	Alpha/beta hydrolase-3
MELO3C002485	7,94E-07	0,000243073	Transmembrane protein, putative
MELO3C022066	8,16E-07	0,000244276	Zinc finger CCHC domain-containing protein 8
MELO3C003448	8,87E-07	0,000261442	Methyltransferase-related family protein
MELO3C003331	9,74E-07	0,0002828	BAX inhibitor-1
MELO3C012149	1,01E-06	0,000288475	PLASMODESMATA CALLOSE-BINDING PROTEIN 3
MELO3C013183	1,07E-06	0,00029567	elongation factor-like GTPase 1
MELO3C006997	1,05E-06	0,00029567	galactan beta-1,4-galactosyltransferase GALS3-like
MELO3C021100	1,08E-06	0,00029567	Heat shock 70 kDa protein
MELO3C024188	1,12E-06	0,000299785	ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase, chloroplastic
MELO3C009091	1,15E-06	0,000299785	50S ribosomal protein L17

MELO3C014359	1,17E-06	0,000299785	Calcium-binding EF-hand family protein
MELO3C007735	1,15E-06	0,000299785	E3 ubiquitin-protein ligase RING1
MELO3C022511	1,15E-06	0,000299785	synaptotagmin-5
MELO3C013988	1,23E-06	0,000311097	Myelodysplasia-myeloid leukemia factor 1-interacting protein
MELO3C013712	1,34E-06	0,000334119	Fact complex subunit spt16
MELO3C006921	1,37E-06	0,000338067	No data found
MELO3C014555	1,47E-06	0,000358476	splicing factor 3B subunit 6-like protein
MELO3C018149	1,51E-06	0,000364822	Beta-glucosidase, putative
MELO3C002104	1,54E-06	0,000366033	Receptor-like kinase
MELO3C018525	1,56E-06	0,00036677	Myosin heavy chain-like protein
MELO3C005069	1,60E-06	0,00037138	GEM-like protein 4
MELO3C026068	1,65E-06	0,000379411	Transcriptional adapter ADA2b-like protein
MELO3C017897	1,77E-06	0,000398202	Plant/protein
MELO3C015804	1,77E-06	0,000398202	heat stress transcription factor A-6b-like isoform X1
MELO3C022210	1,96E-06	0,000434452	regulator of nonsense transcripts UPF3-like
MELO3C007072	2,12E-06	0,000465214	Caffeoylshikimate esterase
MELO3C008069	2,15E-06	0,000466976	Phosphoinositide phosphatase family protein
MELO3C005382	2,26E-06	0,000478687	luc7-like protein 3
MELO3C024270	2,28E-06	0,000478687	Terpene cyclase/mutase family member
MELO3C020612	2,30E-06	0,000478687	Unknown protein
MELO3C018644	2,26E-06	0,000478687	serine/arginine-rich splicing factor SC35
MELO3C001976	2,35E-06	0,000483125	Pentatricopeptide repeat-containing family protein
MELO3C023857	2,40E-06	0,000488711	GATA zinc finger domain-containing protein 10-like isoform X2
MELO3C002674	2,57E-06	0,000518413	BnaA04g24650D protein
MELO3C015067	2,65E-06	0,000527841	transcription factor LHW
MELO3C021462	2,70E-06	0,000532957	DDT domain-containing protein PTM
MELO3C024775	2,85E-06	0,000552422	Bud13
MELO3C002056	2,83E-06	0,000552422	O-fucosyltransferase family protein
MELO3C005952	3,12E-06	0,000597548	60S acidic ribosomal protein P1-like
MELO3C026898	3,24E-06	0,000614621	Cathepsin B-like cysteine protease
MELO3C022204	3,44E-06	0,000647494	SART-1 family protein DOT2 isoform X2
MELO3C009579	3,54E-06	0,000647539	Myosin-binding protein 7
MELO3C025257	3,54E-06	0,000647539	KH domain-containing family protein
MELO3C005301	3,52E-06	0,000647539	At1g70780
MELO3C014083	3,77E-06	0,000680058	Transmembrane protein, putative
MELO3C025488	3,79E-06	0,000680058	transcription initiation factor TFIID subunit 1-like
MELO3C025502	3,82E-06	0,000680058	Pentatricopeptide repeat-containing protein
MELO3C015322	3,94E-06	0,000689115	cyclin-L1-1
MELO3C011284	3,94E-06	0,000689115	Aspartate aminotransferase
MELO3C017093	4,18E-06	0,000723327	Kinesin light chain
MELO3C009482	4,24E-06	0,000725607	Rho GTPase-activating protein
MELO3C023408	4,26E-06	0,000725607	Lactoylglutathione lyase
MELO3C009461	4,48E-06	0,000737581	Protein LITTLE ZIPPER 4
MELO3C020244	4,48E-06	0,000737581	UTP--glucose-1-phosphate uridylyltransferase
MELO3C002302	4,42E-06	0,000737581	Kinase family protein
MELO3C019941	4,38E-06	0,000737581	T-complex protein 11
MELO3C007207	4,57E-06	0,000746373	Kinase family protein
MELO3C013630	4,62E-06	0,000748551	switch 2 isoform X1
MELO3C006383	5,10E-06	0,000812025	acid phosphatase 1-like
MELO3C006836	5,09E-06	0,000812025	Activating transcription factor 7-interacting 2
MELO3C016101	5,14E-06	0,000812025	UBP1-associated protein 2C
MELO3C017908	5,32E-06	0,000827253	No data found
MELO3C020989	5,28E-06	0,000827253	phosphatidylinositol 4-kinase alpha 1
MELO3C010295	5,46E-06	0,000841847	Armadillo-like helical
MELO3C017364	5,64E-06	0,000856673	Ribosomal protein L19
MELO3C023986	5,61E-06	0,000856673	DNA topoisomerase 2
MELO3C002700	5,84E-06	0,000880994	Serine/threonine-protein kinase PLK4
MELO3C016366	5,94E-06	0,000888531	Phosphatidylcholine transfer protein
MELO3C018948	5,99E-06	0,000889151	Alpha-1,4 glucan phosphorylase
MELO3C024262	6,09E-06	0,000897106	activating signal cointegrator 1 complex subunit 1
MELO3C014178	6,21E-06	0,000905978	Trigger factor
MELO3C007432	6,24E-06	0,000905978	Phosphatidate cytidylyltransferase
MELO3C007139	6,36E-06	0,000909299	la-related protein 6A
MELO3C007499	6,35E-06	0,000909299	protein DA1-related 1-like
MELO3C021534	6,54E-06	0,000909299	homeobox-leucine zipper protein HAT5-like
MELO3C024447	6,54E-06	0,000909299	Protein SEC13 like
MELO3C012136	6,51E-06	0,000909299	Nodulin-related protein 1
MELO3C020875	6,61E-06	0,000909299	CLK4-associating serine/arginine-rich protein
MELO3C022342	6,63E-06	0,000909299	NAC domain-containing protein 83
MELO3C002148	6,45E-06	0,000909299	NF-X1-type zinc finger protein NFXL1
MELO3C006107	6,91E-06	0,000940831	RNA polymerase I-specific transcription initiation factor RRN3
MELO3C009423	7,01E-06	0,000948429	Uridylate kinase
MELO3C003915	7,08E-06	0,000950539	Pentatricopeptide repeat-containing protein
MELO3C013703	7,12E-06	0,000950539	diacylglycerol O-acyltransferase 2-like
MELO3C009276	7,30E-06	0,00096137	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain-containing protein
MELO3C005731	7,29E-06	0,00096137	Intracellular protein transport protein USO1-like protein
MELO3C017657	7,42E-06	0,000970741	branchpoint-bridging protein
MELO3C008933	7,84E-06	0,001018808	Zinc finger family protein
MELO3C004591	8,11E-06	0,001046869	Phosphotransferase
MELO3C008910	8,25E-06	0,001058188	transcription termination factor MTEF18, mitochondrial-like

MELO3C009591	8,33E-06	0,001061017	IQ domain-containing protein IQM6
MELO3C006959	8,45E-06	0,001062493	Reticulon-like protein
MELO3C014174	8,41E-06	0,001062493	(S)-ureidoglycine aminohydrolase
MELO3C006602	8,54E-06	0,001066875	serine/threonine-protein kinase RUNKEL
MELO3C017677	8,66E-06	0,001075323	chitinase-like protein 1
MELO3C025526	8,87E-06	0,001089274	Pollen Ole e 1 allergen/extensin
MELO3C011117	8,88E-06	0,001089274	receptor-like protein kinase HSL1
MELO3C024862	9,68E-06	0,001180217	Plant peroxidase
MELO3C014649	9,79E-06	0,001181894	Metal tolerance protein C2
MELO3C023188	9,81E-06	0,001181894	Beta-galactosidase
MELO3C009187	1,01E-05	0,001194634	Transferase family protein
MELO3C005211	1,00E-05	0,001194634	Zinc finger, CCCH-type
MELO3C011825	1,02E-05	0,001194634	nifU-like protein 2, chloroplastic
MELO3C011747	1,01E-05	0,001194634	Protein FAR1-RELATED SEQUENCE 5
MELO3C005262	1,04E-05	0,001220292	PLATZ transcription factor family protein, putative
MELO3C007075	1,06E-05	0,001234544	ADP-ribosylation factor GTPase-activating protein AGD12
MELO3C013128	1,09E-05	0,001251957	Golgin family A protein
MELO3C022707	1,09E-05	0,001251957	Ubiquitin-conjugating enzyme family protein
MELO3C008520	1,13E-05	0,001262069	Cysteine protease
MELO3C017856	1,13E-05	0,001262069	extensin-like
MELO3C007069	1,12E-05	0,001262069	Protein phosphatase 2c, putative
MELO3C025855	1,12E-05	0,001262069	Alkyl transferase
MELO3C017521	1,13E-05	0,001262069	No data found
MELO3C010119	1,15E-05	0,00127045	U11/U12 small nuclear ribonucleoprotein 48 kDa protein
MELO3C012196	1,15E-05	0,001273125	Phospholipid-transporting ATPase
MELO3C011271	1,18E-05	0,001298592	14 kDa proline-rich protein DC2.15
MELO3C013925	1,20E-05	0,001311679	Myb transcription factor
MELO3C018053	1,21E-05	0,001311679	Costars family protein At4g33640
MELO3C016877	1,22E-05	0,001313028	Beta-fructofuranosidase, insoluble isoenzyme CWINV1
MELO3C013369	1,24E-05	0,001313028	Methyltransferase-like protein
MELO3C025451	1,23E-05	0,001313028	Actin-depolymerizing factor family protein
MELO3C013022	1,24E-05	0,001313028	Serine/threonine-protein kinase ATM
MELO3C004278	1,25E-05	0,00131307	mevalonate kinase-like
MELO3C020701	1,24E-05	0,00131307	Myb transcription factor
MELO3C013123	1,27E-05	0,001314742	Syntaxin-51
MELO3C025079	1,27E-05	0,001314742	universal stress protein A-like protein
MELO3C026613	1,26E-05	0,001314742	Tubulin alpha chain
MELO3C025061	1,31E-05	0,001334848	V-type proton ATPase subunit C
MELO3C023417	1,31E-05	0,001334848	DUF4050 family protein
MELO3C000817	1,30E-05	0,001334848	Magnesium transporter MRS2-like protein
MELO3C006260	1,32E-05	0,001336381	Dynamin, putative
MELO3C009296	1,35E-05	0,00135638	Energy-coupling factor transporter ATP-binding EcfA 1
MELO3C023513	1,35E-05	0,00135638	Metal tolerance protein C2
MELO3C006926	1,39E-05	0,001386896	Divalent ion symporter
MELO3C025977	1,44E-05	0,001425409	OBERON-like protein
MELO3C007177	1,45E-05	0,001426946	Transcription factor GTE12
MELO3C017474	1,47E-05	0,001441788	Zinc finger protein
MELO3C021398	1,49E-05	0,00145805	serine incorporator 3
MELO3C016541	1,55E-05	0,001475351	Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein
MELO3C024844	1,52E-05	0,001475351	At5g24610
MELO3C025256	1,54E-05	0,001475351	protein RETICULATA-RELATED 3, chloroplastic-like
MELO3C019633	1,54E-05	0,001475351	Glyceraldehyde-3-phosphate dehydrogenase
MELO3C026235	1,54E-05	0,001475351	haloacid dehalogenase-like hydrolase domain-containing protein At3g48420
MELO3C014575	1,61E-05	0,001502947	Saccharopine dehydrogenase
MELO3C007083	1,61E-05	0,001502947	187-kDa microtubule-associated protein AIR9
MELO3C025282	1,61E-05	0,001502947	SCARECROW
MELO3C022499	1,59E-05	0,001502947	Myeloid leukemia factor
MELO3C011324	1,61E-05	0,001502947	No data found
MELO3C002677	1,63E-05	0,001510878	NAD(P)-binding Rossmann-fold superfamily protein
MELO3C014530	1,68E-05	0,001520089	Nuclear transcription factor Y subunit C8
MELO3C004492	1,69E-05	0,001520089	methyl-CpG-binding domain-containing protein 11-like
MELO3C020109	1,68E-05	0,001520089	Nop53 protein
MELO3C015263	1,67E-05	0,001520089	Werner syndrome-like exonuclease
MELO3C015197	1,68E-05	0,001520089	Translocation protein Sec62
MELO3C025345	1,68E-05	0,001520089	Polyol transporter 5-like protein
MELO3C026090	1,71E-05	0,001534494	Sec14p-like phosphatidylinositol transfer family protein
MELO3C008330	1,75E-05	0,001565386	S-acyltransferase
MELO3C014749	1,81E-05	0,001606901	Acetyl-coenzyme A synthetase
MELO3C007033	1,81E-05	0,001606901	protein SUPPRESSOR OF FRI 4 isoform X2
MELO3C013248	1,85E-05	0,00160794	nucleolar complex protein 4 homolog
MELO3C023526	1,82E-05	0,00160794	chaperone protein dnaJ GFA2, mitochondrial
MELO3C001987	1,84E-05	0,00160794	cyclic dof factor 3
MELO3C026629	1,84E-05	0,00160794	potassium channel AKT1
MELO3C002226	1,86E-05	0,00161177	polynucleotide 5'-hydroxyl-kinase NOL9
MELO3C015277	1,88E-05	0,001621496	GATA transcription factor 16-like
MELO3C016380	1,90E-05	0,001633533	Laccase
MELO3C003506	1,91E-05	0,001636029	Rhamnogalacturonate lyase family protein
MELO3C013366	1,94E-05	0,001654622	Protein nuclear fusion defective 4
MELO3C010997	1,97E-05	0,001670415	Protein IQ-DOMAIN 32
MELO3C020444	2,03E-05	0,00171292	Purple acid phosphatase

MELO3C017620	2,06E-05	0,001732538	BnaA10g17500D protein
MELO3C024407	2,10E-05	0,001750958	Charged multivesicular body 1
MELO3C020780	2,10E-05	0,001750958	Triosephosphate isomerase
MELO3C014678	2,13E-05	0,001751257	Kelch repeat-containing F-box family protein
MELO3C006313	2,12E-05	0,001751257	Myb family transcription factor APL
MELO3C021113	2,11E-05	0,001751257	asparagine--tRNA ligase, cytoplasmic 2
MELO3C025859	2,14E-05	0,001755197	zinc finger CCCH domain-containing protein 25
MELO3C007825	2,17E-05	0,001755992	random slug protein 5-like
MELO3C025784	2,16E-05	0,001755992	Zinc finger (C3HC4-type RING finger) family protein
MELO3C021782	2,16E-05	0,001755992	alpha-glucosidase
MELO3C004305	2,19E-05	0,001765171	Pre-mRNA-splicing factor SLU7
MELO3C011160	2,21E-05	0,001773889	2-on-2 hemoglobin
MELO3C016552	2,23E-05	0,001775985	Fiber expressed protein
MELO3C011089	2,22E-05	0,001775985	O-fucosyltransferase family protein
MELO3C016074	2,29E-05	0,001811186	No data found
MELO3C025887	2,29E-05	0,001811186	No data found
MELO3C009595	2,32E-05	0,001817184	serine/arginine-rich SC35-like splicing factor SCL33
MELO3C022721	2,32E-05	0,001817184	Ninja-family protein AFP3
MELO3C017346	2,34E-05	0,001823593	alpha-dioxygenase 2
MELO3C007673	2,35E-05	0,001827806	tubulin alpha chain-like
MELO3C013383	2,37E-05	0,001839283	Calcium-binding EF hand family protein
MELO3C024514	2,42E-05	0,0018583	enolase
MELO3C021587	2,42E-05	0,0018583	NAC domain-containing protein 8 isoform X1
MELO3C014507	2,49E-05	0,001907765	F-box family protein
MELO3C004641	2,56E-05	0,001939773	Protein BREVIS RADIX
MELO3C013104	2,57E-05	0,001939773	Upstream activation factor subunit spp27
MELO3C017749	2,58E-05	0,001939773	BAG family molecular chaperone regulator 6-like
MELO3C007609	2,56E-05	0,001939773	Subtilisin-like protease
MELO3C001175	2,58E-05	0,001939773	Glutathione s-transferase
MELO3C017813	2,62E-05	0,00195107	ADP-ribosylation factor GTPase-activating protein AGD3
MELO3C015327	2,61E-05	0,00195107	isoaspartyl peptidase/L-asparaginase
MELO3C002384	2,71E-05	0,00201456	Coiled-coil domain-containing protein SCD2
MELO3C002115	2,75E-05	0,002026023	Poly(A) polymerase
MELO3C011422	2,75E-05	0,002026023	Pentatricopeptide repeat-containing protein
MELO3C015734	2,76E-05	0,002026925	No data found
MELO3C022647	2,77E-05	0,002028876	UDP-glycosyltransferase 89A2-like
MELO3C013870	2,80E-05	0,002034696	Chloroplast 40 kDa outer membrane envelope protein
MELO3C007265	2,80E-05	0,002034696	Protein DEHYDRATION-INDUCED 19
MELO3C006929	2,82E-05	0,002036511	BAHD acyltransferase DCR
MELO3C026502	2,83E-05	0,002036891	Phytochrome
MELO3C015439	2,90E-05	0,002077194	Protein PLASTID MOVEMENT IMPAIRED 1-RELATED 1
MELO3C011285	2,89E-05	0,002077194	60S ribosomal protein L39
MELO3C006736	2,95E-05	0,002099278	Beta-1,3-galactosyltransferase-like protein
MELO3C011144	2,96E-05	0,002099278	Translation initiation factor IF-2
MELO3C020570	3,03E-05	0,002147341	Maternal effect embryo arrest protein
MELO3C014009	3,07E-05	0,002148255	PGR5-like protein 1A, chloroplastic
MELO3C025111	3,05E-05	0,002148255	CoA ligase
MELO3C004669	3,06E-05	0,002148255	Pentatricopeptide repeat-containing protein
MELO3C006493	3,10E-05	0,002161953	ATP sulfurylase
MELO3C004553	3,16E-05	0,002169827	multiprotein-bridging factor 1c
MELO3C008046	3,18E-05	0,002169827	zinc finger CCCH domain-containing protein 38 isoform X1
MELO3C016002	3,17E-05	0,002169827	Arginine/serine-rich splicing factor, putative
MELO3C013664	3,17E-05	0,002169827	Transcriptional elongation regulator MINIYO
MELO3C022436	3,14E-05	0,002169827	Amaranthin-like lectin
MELO3C026107	3,14E-05	0,002169827	No data found
MELO3C008690	3,24E-05	0,002208703	splicing factor 3B subunit 2
MELO3C011843	3,28E-05	0,002219494	No data found
MELO3C010136	3,28E-05	0,002219494	Glycogenin-1
MELO3C014019	3,42E-05	0,002291067	Rhomboid-like protein
MELO3C005581	3,42E-05	0,002291067	Ankyrin repeat/KH domain protein (DUF1442)
MELO3C021786	3,41E-05	0,002291067	Cyclin-T1-like protein
MELO3C025956	3,48E-05	0,00232373	No data found
MELO3C017095	3,49E-05	0,002323867	CASP-like protein
MELO3C009339	3,54E-05	0,00234295	Glycosyl transferase, family 31
MELO3C008596	3,57E-05	0,002359948	S-adenosyl-L-methionine-dependent methyltransferase
MELO3C021119	3,61E-05	0,00237836	Cytochrome b561 and domon domain-containing protein
MELO3C011003	3,62E-05	0,00237836	transcription factor E2FC isoform X3
MELO3C019730	3,74E-05	0,002443832	zinc finger CCCH domain-containing protein 3-like
MELO3C009827	3,85E-05	0,002508953	No data found
MELO3C019522	3,87E-05	0,002510923	Exocyst complex component
MELO3C026239	3,88E-05	0,002510923	Protein tipD, putative
MELO3C012737	3,94E-05	0,002539535	F21O3.15 protein
MELO3C020783	3,95E-05	0,002539535	protein XAP5 CIRCADIAN TIMEKEEPER
MELO3C009967	3,99E-05	0,002557116	cyclin-dependent kinase C-2-like
MELO3C006705	4,03E-05	0,00257263	Binding protein
MELO3C021207	4,04E-05	0,00257263	Signal peptide peptidase-like protein
MELO3C024863	4,14E-05	0,002631109	No data found
MELO3C009222	4,25E-05	0,002692175	Protein RETICULATA, chloroplastic
MELO3C015594	4,32E-05	0,002725898	No data found
MELO3C015603	4,37E-05	0,002745529	E3 ubiquitin-protein ligase RING1-like

MELO3C016303	4,47E-05	0,002801259	ATP-dependent zinc metalloprotease FtsH
MELO3C011196	4,53E-05	0,002833395	ABC1 family protein, expressed
MELO3C002041	4,55E-05	0,002835312	RHOMBOID-like protein 12, mitochondrial
MELO3C016262	4,65E-05	0,002880684	26S proteasome non-ATPase regulatory subunit 8
MELO3C010761	4,65E-05	0,002880684	far upstream element-binding protein 1
MELO3C013810	4,76E-05	0,002891896	At3g49990
MELO3C017946	4,74E-05	0,002891896	bifunctional epoxide hydrolase 2-like
MELO3C022162	4,69E-05	0,002891896	mannan endo-1,4-beta-mannosidase 1-like
MELO3C021771	4,76E-05	0,002891896	exocyst complex component EXO84C
MELO3C026234	4,74E-05	0,002891896	elongator complex protein 3
MELO3C010675	4,74E-05	0,002891896	ATP-citrate synthase alpha chain protein
MELO3C017754	4,84E-05	0,002913268	NAC domain-containing protein
MELO3C024316	4,83E-05	0,002913268	Late embryogenesis abundant protein, LEA-14
MELO3C019225	4,84E-05	0,002913268	Formin-like protein
MELO3C023419	4,93E-05	0,002938396	methyl-CpG-binding domain-containing protein 11
MELO3C020132	4,94E-05	0,002938396	Potassium transporter
MELO3C021228	4,91E-05	0,002938396	tRNA pseudouridine synthase
MELO3C018502	4,91E-05	0,002938396	MAR-binding filament-like protein
MELO3C025812	5,00E-05	0,002963418	ATP-dependent zinc metalloprotease FtsH
MELO3C010297	5,05E-05	0,002983067	Purple acid phosphatase
MELO3C024005	5,08E-05	0,00299654	Acyl-CoA--sterol O-acyltransferase 1
MELO3C007562	5,21E-05	0,003030419	Lipase
MELO3C024545	5,20E-05	0,003030419	Transmembrane 9 superfamily member
MELO3C021979	5,20E-05	0,003030419	Glutaredoxin family protein, putative
MELO3C022786	5,23E-05	0,003030419	Phd finger protein, putative
MELO3C016019	5,23E-05	0,003030419	heat shock factor-binding protein 1
MELO3C013031	5,23E-05	0,003030419	Glutamate dehydrogenase, putative
MELO3C009776	5,30E-05	0,003063321	DNA-directed RNA polymerase II, putative
MELO3C011731	5,41E-05	0,003103925	Ubiquitin carboxyl-terminal hydrolase
MELO3C022901	5,40E-05	0,003103925	Alpha/beta-Hydrolases superfamily protein, putative
MELO3C014309	5,53E-05	0,003104434	Magnesium transporter MRS2-like protein
MELO3C016660	5,43E-05	0,003104434	Flavin-binding kelch domain F box protein
MELO3C012529	5,49E-05	0,003104434	Ras-related Rab7
MELO3C007450	5,49E-05	0,003104434	No data found
MELO3C025278	5,51E-05	0,003104434	Emp24/gp25L/p24 family/GOLD family protein
MELO3C015764	5,52E-05	0,003104434	F-box/LRR-repeat protein 17
MELO3C020957	5,52E-05	0,003104434	GDSL esterase/lipase 5-like
MELO3C010102	5,50E-05	0,003104434	O-linked n-acetylglucosamine transferase, ogt, putative
MELO3C025265	5,59E-05	0,003125624	Unknown protein
MELO3C016917	5,63E-05	0,003130049	Damaged dna-binding 2, putative isoform 1
MELO3C024435	5,62E-05	0,003130049	Poly(A) polymerase
MELO3C022773	5,68E-05	0,003148872	Transmembrane protein, putative
MELO3C017683	5,78E-05	0,00319616	Clathrin interactor EPSIN 2
MELO3C009495	5,81E-05	0,003205231	CASP-like protein
MELO3C024214	5,88E-05	0,003207012	Cytochrome b561 and domon domain-containing protein
MELO3C012242	5,88E-05	0,003207012	ethylene-responsive transcription factor ERF118
MELO3C021273	5,86E-05	0,003207012	Seed maturation protein PM36
MELO3C002469	5,86E-05	0,003207012	BnaC01g13120D protein
MELO3C025779	5,92E-05	0,003220471	Nucleotide/sugar transporter family protein
MELO3C009272	5,94E-05	0,003223467	UNC93-like protein 3
MELO3C005094	6,04E-05	0,003257855	histidine biosynthesis bifunctional protein hisIE, chloroplastic
MELO3C005565	6,03E-05	0,003257855	Elongation factor G, chloroplastic
MELO3C021232	6,15E-05	0,003309755	Novel plant snare, putative
MELO3C010548	6,17E-05	0,003313352	Receptor-like protein kinase
MELO3C023731	6,23E-05	0,003315726	phosphatidylcholine transfer protein-like isoform X1
MELO3C020001	6,20E-05	0,003315726	Mini-chromosome maintenance complex-binding protein
MELO3C019844	6,22E-05	0,003315726	ras-related protein RABC2a-like
MELO3C002885	6,28E-05	0,003331834	transcription factor GTE1
MELO3C024385	6,38E-05	0,003375474	protein indeterminate-domain 7
MELO3C025853	6,51E-05	0,003437938	protein DAMAGED DNA-BINDING 2
MELO3C020626	6,59E-05	0,003471635	Expansin
MELO3C022998	6,69E-05	0,003506	Malate dehydrogenase
MELO3C018749	6,69E-05	0,003506	Phosphatase 2C family protein
MELO3C008321	6,73E-05	0,003517413	Biotin carboxyl carrier protein of acetyl-CoA carboxylase
MELO3C014016	6,77E-05	0,003517802	Phospholipase D
MELO3C017700	6,77E-05	0,003517802	disease resistance protein RGA2-like
MELO3C023018	6,87E-05	0,00352199	splicing factor U2af large subunit B isoform X1
MELO3C004354	6,85E-05	0,00352199	Cc-nbs-lrr resistance protein
MELO3C005945	6,86E-05	0,00352199	Dihydroorotate dehydrogenase (DUF3598)
MELO3C005293	6,82E-05	0,00352199	Phosphoglucomutase, putative
MELO3C003561	6,86E-05	0,00352199	VQ motif-containing protein 9
MELO3C008367	6,97E-05	0,003567809	serine/threonine-protein kinase STY8-like
MELO3C014129	7,03E-05	0,003567921	THO complex subunit 3
MELO3C023560	7,00E-05	0,003567921	PsaB RNA-binding protein
MELO3C021923	7,03E-05	0,003567921	CCG-binding protein 1
MELO3C009879	7,24E-05	0,003665313	Cullin family protein
MELO3C005405	7,26E-05	0,003665515	CDGSH iron-sulfur domain-containing protein NEET
MELO3C016468	7,29E-05	0,003671413	No data found
MELO3C016354	7,36E-05	0,003696337	Short-chain dehydrogenase TIC 32, chloroplastic
MELO3C026097	7,37E-05	0,003696337	Hexosyltransferase

MELO3C008752	7,44E-05	0,003709205	TATA box-binding protein-associated factor RNA polymerase I subunit B
MELO3C005656	7,42E-05	0,003709205	Protein LURP-one-related 11
MELO3C003147	7,53E-05	0,003744722	LOW QUALITY PROTEIN: L-type lectin-domain containing receptor kinase S.4-like
MELO3C026470	7,55E-05	0,003744722	Potassium transporter
MELO3C022501	7,65E-05	0,003777968	SNARE-interacting protein KEULE
MELO3C026141	7,65E-05	0,003777968	ADP-ribosylation factor-like
MELO3C009203	7,74E-05	0,003814164	tubulin beta chain-like
MELO3C014114	7,85E-05	0,003854576	RPM1-interacting protein 4
MELO3C026614	7,87E-05	0,00385474	WD repeat-containing protein 55
MELO3C017384	7,90E-05	0,003863001	tRNA pseudouridine synthase
MELO3C005812	8,05E-05	0,003913918	ARM repeat superfamily protein
MELO3C011099	8,05E-05	0,003913918	Universal stress protein A-like protein
MELO3C025903	8,07E-05	0,003917532	At5g59460
MELO3C004610	8,12E-05	0,003927962	zinc finger CCCH domain-containing protein 20-like
MELO3C007571	8,15E-05	0,003927962	OTU domain-containing protein
MELO3C021116	8,14E-05	0,003927962	No data found
MELO3C019012	8,19E-05	0,00393172	No data found
MELO3C021529	8,20E-05	0,00393172	NHL domain-containing protein, putative
MELO3C019120	8,32E-05	0,003965589	R3H domain-containing protein 1-like isoform X1
MELO3C021999	8,29E-05	0,003965589	Expansin protein
MELO3C012410	8,35E-05	0,003965589	thioredoxin-like 3-2, chloroplastic isoform X8
MELO3C015590	8,37E-05	0,003965589	protochlorophyllide-dependent translocon component 52, chloroplastic-like
MELO3C010165	8,36E-05	0,003965589	Cyclic nucleotide-gated ion channel-like protein
MELO3C009350	8,41E-05	0,003972539	TSL-kinase interacting protein 1
MELO3C023590	8,49E-05	0,004002215	Pheophytinase, chloroplastic
MELO3C015374	8,52E-05	0,004004007	Superoxide dismutase [Cu-Zn]
MELO3C020589	8,72E-05	0,004091828	17.5 kDa class I heat shock protein
MELO3C013736	8,76E-05	0,004101537	basic endochitinase C
MELO3C007483	8,91E-05	0,004151361	ABC transporter family protein
MELO3C021258	8,91E-05	0,004151361	flowering time control protein FCA isoform X2
MELO3C016360	8,94E-05	0,004153313	Transferring glycosyl group transferase
MELO3C023979	8,96E-05	0,004155775	Cellulose synthase
MELO3C004308	9,02E-05	0,004171791	Photosystem II reaction center PsbP family protein
MELO3C011085	9,09E-05	0,004195778	Argininosuccinate lyase
MELO3C005490	9,19E-05	0,004222227	U-box domain-containing protein 35-like isoform X2
MELO3C013455	9,18E-05	0,004222227	Calcium ion-binding protein
MELO3C025582	9,26E-05	0,004241924	Ribosomal protein S5/S7
MELO3C012378	9,28E-05	0,004243844	phosphoglucan phosphatase DSP4, amyloplastic
MELO3C007153	9,32E-05	0,004249426	No data found
MELO3C015704	9,36E-05	0,004249426	Protein trigalactosyldiacylglycerol 2, chloroplastic
MELO3C024344	9,35E-05	0,004249426	DUF1677 family protein (DUF1677)
MELO3C014150	9,44E-05	0,004256592	Fimbrin, putative
MELO3C008197	9,44E-05	0,004256592	Chloride channel protein
MELO3C025034	9,44E-05	0,004256592	peroxiredoxin Q, chloroplastic
MELO3C009895	9,61E-05	0,004324758	Actin cross-linking protein
MELO3C009354	9,65E-05	0,004329302	Glutathione gamma-glutamylcysteinyltransferase 1
MELO3C017560	9,71E-05	0,004337109	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial
MELO3C025468	9,70E-05	0,004337109	ABC transporter B family protein
MELO3C023685	9,76E-05	0,00435218	alcohol dehydrogenase-like
MELO3C026975	9,80E-05	0,00436109	40S ribosomal protein S15a
MELO3C003471	9,87E-05	0,004378557	protein SAWADEE HOMEODOMAIN HOMOLOG 1-like isoform X2
MELO3C005467	0,000100246	0,004438907	At5g07590
MELO3C003508	0,000100674	0,004447917	UDP-glycosyltransferase 91C1
MELO3C013591	0,000102175	0,00450416	Sugar transporter, putative
MELO3C005035	0,000102449	0,004506164	E3 SUMO-protein ligase SIZ1
MELO3C010760	0,000102713	0,004507639	Pollen specific protein sf21
MELO3C010705	0,000102939	0,004507639	T-complex protein 1 subunit epsilon
MELO3C027060	0,000103272	0,004512221	Pectinesterase
MELO3C019722	0,000103716	0,004515705	Protein disulfide-isomerase like 2-2
MELO3C003733	0,000103809	0,004515705	ribonuclease P protein subunit p25-like protein isoform X1
MELO3C014175	0,000105084	0,004551125	Phospho-2-dehydro-3-deoxyheptonate aldolase
MELO3C023808	0,000105023	0,004551125	SAC3/GANP/Nin1/mts3/eIF-3 p25 family isoform 1
MELO3C015339	0,000107667	0,004652752	UDP-N-acetylglucosamine transferase subunit ALG13 homolog
MELO3C026764	0,000108528	0,004659375	Magnesium transporter MRS2-like protein
MELO3C013214	0,00010835	0,004659375	DNA damage-inducible protein 1
MELO3C000826	0,000108179	0,004659375	Transcription factor
MELO3C009076	0,000109346	0,004669937	Nucleolar protein gar2-like protein
MELO3C021461	0,00010932	0,004669937	No data found
MELO3C010245	0,000109483	0,004669937	Two-component response regulator
MELO3C026804	0,000109889	0,00467717	histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH1-like
MELO3C023161	0,000110585	0,004696648	nuclear transcription factor Y subunit A-7-like
MELO3C024366	0,000111579	0,004728701	Mitochondrial carrier protein
MELO3C010189	0,000113033	0,004780062	lactation elevated protein 1
MELO3C006645	0,000115046	0,004851885	No data found
MELO3C013254	0,000115548	0,004851885	Kinase family protein
MELO3C016245	0,000115714	0,004851885	Glycosyl transferase family 1 family protein
MELO3C024450	0,000115488	0,004851885	nuclear pore complex protein NUP35
MELO3C004999	0,000117465	0,004914861	nicotinamide adenine dinucleotide transporter 1, chloroplastic-like
MELO3C009561	0,000118756	0,004916778	iron-sulfur cluster co-chaperone protein HscB, mitochondrial
MELO3C004593	0,000118147	0,004916778	OXS3

MELO3C006651	0,000118406	0,004916778	No data found
MELO3C020294	0,00011852	0,004916778	DNA-directed RNA polymerase subunit beta
MELO3C017104	0,000118047	0,004916778	Trehalose-6-phosphate synthase, putative
MELO3C025594	0,000119502	0,004937323	C2 domain-containing protein
MELO3C017653	0,000120136	0,004942865	Isoaspartyl peptidase/L-asparaginase
MELO3C015496	0,000120135	0,004942865	Plant/F27B13-30 protein
MELO3C003911	0,000121139	0,004973739	protein BONZAI 3
MELO3C003294	0,000123184	0,005040585	vacuolar cation/proton exchanger 3
MELO3C015230	0,000123277	0,005040585	Pectin acetylesterase
MELO3C002075	0,000125653	0,005127117	No data found
MELO3C000994	0,000126324	0,005143843	wall-associated receptor kinase 2-like
MELO3C012076	0,000126973	0,005159631	UDP-galactose/UDP-glucose transporter family protein
MELO3C005797	0,000127327	0,005163393	Unknown protein
MELO3C011601	0,000128223	0,005189103	No data found
MELO3C013346	0,000129469	0,005200251	Phospholipase-like protein (PEARLI 4) family protein
MELO3C008986	0,000129552	0,005200251	No data found
MELO3C015186	0,000128867	0,005200251	Sulfite reductase
MELO3C026522	0,000129123	0,005200251	monosaccharide-sensing protein 2-like
MELO3C003146	0,000130195	0,00520807	L-type lectin-domain containing receptor kinase IV.1-like
MELO3C018455	0,000130274	0,00520807	thioredoxin M3, chloroplastic
MELO3C023484	0,000131214	0,00522447	AP2-like ethylene-responsive transcription factor At1g16060
MELO3C021940	0,000131077	0,00522447	Cold acclimation protein
MELO3C011044	0,000133374	0,005299798	cytochrome c oxidase subunit 6b-1-like
MELO3C016601	0,000133904	0,005310178	No data found
MELO3C011868	0,000134717	0,005331706	Rubber elongation factor protein (REF)
MELO3C016298	0,00013613	0,005366137	Ribosome maturation factor
MELO3C024396	0,000135867	0,005366137	Cytochrome p450
MELO3C019451	0,000136453	0,005368136	Unknown protein
MELO3C006854	0,000137541	0,005397731	transcription factor bHLH118-like
MELO3C003186	0,000138025	0,005397731	Proteasome inhibitor-related
MELO3C022443	0,000137848	0,005397731	flowering time control protein FPA
MELO3C025606	0,000138545	0,005407372	Unknown protein
MELO3C007082	0,000138903	0,005410626	No data found
MELO3C012173	0,000141571	0,005501034	DNA-directed RNA polymerase
MELO3C013046	0,000141781	0,005501034	Kinase family protein
MELO3C009338	0,000142572	0,005520885	60S ribosomal protein L12
MELO3C024885	0,000144879	0,005555765	ATP-dependent DNA helicase
MELO3C019139	0,000144203	0,005555765	Nascent polypeptide-associated complex subunit alpha-like protein
MELO3C015930	0,00014451	0,005555765	Translation initiation factor IF-2
MELO3C003332	0,000143831	0,005555765	BAX inhibitor-1
MELO3C024004	0,000144864	0,005555765	No data found
MELO3C001948	0,000145692	0,0055761	Short-chain dehydrogenase, putative
MELO3C008469	0,000146222	0,00558555	Kinase family protein
MELO3C013883	0,000147575	0,005615542	BOI-related E3 ubiquitin-protein ligase 1
MELO3C025307	0,000147486	0,005615542	Transmembrane 19
MELO3C010053	0,000148287	0,005631773	Isopentenyl diphosphate isomerase
MELO3C006853	0,000149737	0,005640063	receptor-like serine/threonine-protein kinase isoform X2
MELO3C016126	0,000149702	0,005640063	Pathogen-related protein
MELO3C007653	0,000149933	0,005640063	Protein PHLOEM PROTEIN 2-LIKE A10
MELO3C010913	0,000149696	0,005640063	Protein DA1-related 1
MELO3C009782	0,000149106	0,005640063	5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase
MELO3C019435	0,000151452	0,005664813	MLO-like protein 4
MELO3C017248	0,000150882	0,005664813	ATP-dependent helicase hrq1 isoform X6
MELO3C010769	0,000151363	0,005664813	Protein EARLY FLOWERING 3
MELO3C026201	0,000152382	0,005688818	non-specific phospholipase C6
MELO3C003975	0,000152984	0,00568979	protein CHLOROPLAST IMPORT APPARATUS 2 isoform X2
MELO3C006594	0,000152844	0,00568979	Inosine-uridine preferring nucleoside hydrolase
MELO3C026248	0,000153686	0,005705154	E3 ubiquitin-protein ligase RGLG2
MELO3C017226	0,00015485	0,005737567	glycine-rich RNA-binding protein 2, mitochondrial-like
MELO3C019470	0,000156016	0,005754372	glutelin type-A 2-like
MELO3C018956	0,000156177	0,005754372	Ubiquitin carboxyl-terminal hydrolase, putative
MELO3C011444	0,000156102	0,005754372	Mitogen-activated protein kinase
MELO3C022658	0,000156684	0,005762284	Ubiquitin-specific protease family C19 protein
MELO3C015111	0,000157133	0,005768053	rho GTPase-activating protein 7
MELO3C006344	0,000157815	0,00578234	GDT1-like protein
MELO3C004542	0,000158277	0,005788536	tRNA (guanine(37)-N1)-methyltransferase
MELO3C005967	0,000160086	0,005843894	At3g15351
MELO3C009171	0,000160419	0,005845212	Mitochondrial carrier protein
MELO3C017884	0,000161451	0,005871985	DUF4050 family protein
MELO3C011588	0,000161995	0,005880967	Phosphatidylinositol-4-phosphate 5-kinase 1-like protein
MELO3C010214	0,00016233	0,005882308	Nucleoid-associated protein At2g24020, chloroplastic
MELO3C023475	0,000163152	0,005890462	pre-mRNA-splicing factor ISY1 homolog
MELO3C018441	0,000163123	0,005890462	presequence protease 1, chloroplastic/mitochondrial-like
MELO3C024138	0,000164805	0,005931329	Auxin response factor
MELO3C011408	0,000164884	0,005931329	nucleolar protein 14 isoform X2
MELO3C009063	0,000165244	0,005933466	serine/threonine-protein kinase Nek6 isoform X1
MELO3C021279	0,000165964	0,005933924	GTP-binding protein SAR1A-like
MELO3C022345	0,000165703	0,005933924	somatic embryogenesis receptor kinase 2-like
MELO3C020557	0,000166158	0,005933924	Tetratricopeptide repeat (TPR)-like superfamily protein
MELO3C013527	0,000166518	0,005936027	1D-myo-inositol 2-amino-2-deoxy-alpha-D-glucopyranoside ligase

MELO3C022196	0,000167781	0,005970265	Kinase family protein
MELO3C013841	0,000168271	0,005970729	nucleolar protein 12
MELO3C007611	0,000168612	0,005970729	Prolyl 4-hydroxylase alpha-like protein
MELO3C022514	0,000168701	0,005970729	UTP:RNA uridylyltransferase 1
MELO3C014719	0,000171133	0,006045972	Aldehyde oxidase, putative
MELO3C014557	0,000171945	0,006048	Peptidyl-prolyl cis-trans isomerase
MELO3C014128	0,000172955	0,006048	Calcium-dependent protein kinase
MELO3C021064	0,000173027	0,006048	malonyl-CoA:anthocyanidin 5-O-glucoside-6''-O-malonyltransferase
MELO3C001849	0,000172465	0,006048	No data found
MELO3C003393	0,000171685	0,006048	Plant intracellular ras group-related LRR protein
MELO3C003842	0,000172433	0,006048	Dead box ATP-dependent RNA helicase, putative
MELO3C018437	0,000173525	0,006054682	Pentatricopeptide repeat-containing protein At5g39710
MELO3C017242	0,000174787	0,006087962	protein COBRA-like
MELO3C018195	0,000175905	0,006116118	Arf GTPase activating protein
MELO3C027373	0,000176765	0,00613522	ADP-ribosylation factor GTPase-activating protein AGD12-like
MELO3C027375	0,000177846	0,006151116	Pectinesterase
MELO3C002689	0,000177821	0,006151116	serine/threonine-protein kinase STY8-like
MELO3C009539	0,000181792	0,006274078	NC domain-containing protein
MELO3C024910	0,000182037	0,006274078	FRIGIDA-like protein
MELO3C008879	0,000182842	0,006279914	Triosephosphate isomerase
MELO3C023255	0,000182737	0,006279914	DNA-directed RNA polymerase subunit beta-beta protein, putative (DUF506)
MELO3C015373	0,000184106	0,006312352	40S ribosomal protein S25
MELO3C011622	0,000184591	0,006318019	Receptor-like kinase
MELO3C003977	0,000188808	0,006428914	Microtubule-associated family protein
MELO3C016696	0,000188295	0,006428914	PROTON PUMP INTERACTOR 1 family protein
MELO3C008440	0,000188691	0,006428914	wall-associated receptor kinase 2-like
MELO3C010877	0,000191246	0,006500733	Phosphatidate phosphatase PAH2
MELO3C004551	0,00019215	0,00651951	ARF guanine-nucleotide exchange factor GNL2
MELO3C009996	0,000192459	0,00651951	dnaJ protein homolog
MELO3C009429	0,000194464	0,006544185	peroxiredoxin-2E-2, chloroplastic
MELO3C012572	0,000194952	0,006544185	CTP synthase
MELO3C003145	0,000194632	0,006544185	Cyclin d, putative
MELO3C005245	0,000195037	0,006544185	Xyloglucan endotransglucosylase/hydrolase
MELO3C025848	0,000195176	0,006544185	Peptidyl-prolyl cis-trans isomerase
MELO3C010275	0,000194973	0,006544185	Serine-rich protein-like protein
MELO3C015450	0,000195936	0,006558527	Pollen-specific protein SF21
MELO3C007624	0,00019699	0,006582664	Acyl-CoA N-acyltransferases (NAT) superfamily protein
MELO3C017898	0,000199382	0,006651329	F-box family protein
MELO3C005252	0,000199914	0,006657858	Ankyrin repeat-containing protein, putative
MELO3C020394	0,000201726	0,006662025	Phospholipid-transporting ATPase
MELO3C019462	0,000200747	0,006662025	Membralin, putative
MELO3C010565	0,000201305	0,006662025	No data found
MELO3C012201	0,000200408	0,006662025	Isoprenylcysteine alpha-carbonyl methylesterase ICME protein
MELO3C004732	0,000201502	0,006662025	Alpha/beta-Hydrolases superfamily protein
MELO3C025049	0,000202498	0,006676334	transcription factor TCP21-like
MELO3C002382	0,000203267	0,006679412	Kinase family protein
MELO3C010235	0,000203253	0,006679412	No data found
MELO3C007086	0,000204456	0,006707317	ABC transporter C family member 12-like
MELO3C006974	0,000205083	0,006716729	Plastid division protein PDV1
MELO3C014007	0,000205522	0,00671996	Superoxide dismutase 1
MELO3C012525	0,000206484	0,00674026	Receptor-like kinase
MELO3C024444	0,000208262	0,006778458	Avr9/Cf-9 rapidly elicited protein
MELO3C002154	0,000208341	0,006778458	Monoglyceride lipase
MELO3C008332	0,000209733	0,006812512	5-formyltetrahydrofolate cyclo-ligase-like protein COG0212
MELO3C010439	0,000212163	0,006880133	structure-specific endonuclease subunit SLX4-like isoform X2
MELO3C024850	0,000213884	0,00692458	60S ribosomal protein L9-like
MELO3C024975	0,000215317	0,006948193	DUF3511 domain protein
MELO3C010798	0,000215009	0,006948193	NADH dehydrogenase (Ubiquinone) iron-sulfur protein 4, mitochondrial
MELO3C011507	0,000215859	0,006954317	Vesicle transport protein GOT1
MELO3C020824	0,000216965	0,006978582	Pre-mRNA-splicing factor syf2
MELO3C011905	0,00021792	0,006997901	RING finger protein
MELO3C005517	0,000218944	0,007019354	Tryptophan RNA-binding attenuator protein-like
MELO3C025798	0,00022376	0,007162141	cytochrome P450 71A1-like
MELO3C024644	0,000224718	0,007181155	50S ribosomal protein L18
MELO3C000425	0,000225399	0,007191293	alanine--tRNA ligase-like
MELO3C016288	0,000228158	0,007267571	F-box/LRR-repeat protein 14
MELO3C011107	0,000229497	0,007298438	Serine hydroxymethyltransferase
MELO3C019777	0,000230207	0,007309266	U4/U6 small nuclear ribonucleoprotein PRP4-like protein
MELO3C018478	0,000231655	0,007343421	kynurenine formamidase
MELO3C002566	0,000232154	0,007347439	Katanin p80 WD40 repeat-containing subunit B1 homolog
MELO3C015502	0,000232658	0,007351626	Integral membrane protein
MELO3C020924	0,00023482	0,007408081	zinc finger protein 830 isoform X1
MELO3C018720	0,00023523	0,007409188	F-box protein MAX2
MELO3C016213	0,000235725	0,007412948	Beta-amylase
MELO3C010512	0,000236489	0,007425151	Plastid transcriptionally active 6
MELO3C005808	0,000237926	0,007446607	No data found
MELO3C000237	0,000237808	0,007446607	Major facilitator superfamily domain-containing protein 12
MELO3C022212	0,000238624	0,007456609	Deoxycytidine kinase
MELO3C010478	0,000239375	0,007468269	Protein-methionine-s-oxide reductase
MELO3C008925	0,000239951	0,007474446	GTPase LSG1-2-like

MELO3C020386	0,000241205	0,007489865	E3 ubiquitin-protein ligase LAP
MELO3C021292	0,000240838	0,007489865	Protein DEHYDRATION-INDUCED 19
MELO3C017799	0,000243307	0,007543272	F2P16.20 protein, putative isoform 1
MELO3C005882	0,000246426	0,007628007	Eukaryotic translation initiation factor 3 subunit 10
MELO3C021339	0,000248214	0,007671325	60S ribosomal protein L13a, putative
MELO3C012651	0,00024916	0,007676646	FRIGIDA-like protein
MELO3C011395	0,000249164	0,007676646	Hydroxyproline O-arabinosyltransferase 1
MELO3C003541	0,00025058	0,007708259	NAD(P)H-hydrate epimerase
MELO3C007691	0,000252707	0,007749561	Auxin-responsive protein
MELO3C003242	0,000252682	0,007749561	Clathrin light chain
MELO3C008236	0,000253956	0,00777579	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein isoform 1
MELO3C010329	0,00025456	0,007782212	methyl-CpG-binding domain-containing protein 11-like
MELO3C007821	0,00025592	0,007787613	U1 small nuclear ribonucleoprotein 70 kDa
MELO3C009994	0,0002553	0,007787613	MD-2-related lipid recognition domain-containing protein / ML domain-containing protein
MELO3C018718	0,000255613	0,007787613	At2g42760
MELO3C015431	0,000257438	0,007821755	40S ribosomal protein S30
MELO3C022114	0,000259465	0,00786941	RmlC-like cupins superfamily protein
MELO3C015929	0,000260097	0,00786941	GTP-binding protein SAR1A
MELO3C025940	0,000260202	0,00786941	CONSTANS-like zinc finger protein
MELO3C019503	0,000260858	0,00787719	zinc-binding alcohol dehydrogenase domain-containing protein 2
MELO3C018203	0,000262	0,007899594	Lysine-specific histone demethylase 1-like protein
MELO3C008295	0,000262691	0,00790837	ABC1-like protein
MELO3C007421	0,000263489	0,00792031	pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta
MELO3C023830	0,000263933	0,007921598	protein-tyrosine-phosphatase MKP1 isoform X1
MELO3C017572	0,000267737	0,008023584	transcription factor TGA1 isoform X1
MELO3C006175	0,000268353	0,008029865	ankyrin repeat and zinc finger domain-containing protein 1
MELO3C016707	0,000269787	0,008060539	Choline transporter-like protein 2
MELO3C002609	0,000270664	0,008074539	serine/threonine-protein kinase HT1-like
MELO3C016016	0,000273434	0,008136071	xyloglucan 6-xylosyltransferase 1
MELO3C023291	0,000273551	0,008136071	glycine-rich RNA-binding protein 1-like
MELO3C026966	0,000275157	0,008158176	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
MELO3C020049	0,000275744	0,008158176	Ribosomal protein S5/S7
MELO3C002223	0,000275412	0,008158176	hydroxyproline O-galactosyltransferase GALT6
MELO3C003658	0,000275946	0,008158176	Protein MARD1
MELO3C023667	0,000277469	0,008190939	Tetratricopeptide repeat-containing protein
MELO3C005673	0,000278018	0,0081949	tubulin beta chain-like
MELO3C004105	0,000280336	0,008214178	Cytochrome c oxidase subunit
MELO3C022406	0,000280149	0,008214178	phosphatidylinositol 4-kinase gamma 4
MELO3C002332	0,000279544	0,008214178	Telomere length regulation TEL2
MELO3C015185	0,000280098	0,008214178	MP domain-containing protein
MELO3C026398	0,00028134	0,008231374	APO protein 1, chloroplastic
MELO3C016868	0,000285092	0,008267658	serine/threonine-protein kinase EDR1
MELO3C026803	0,00028349	0,008267658	S-acyltransferase
MELO3C023464	0,000284025	0,008267658	sister chromatid cohesion protein PDS5 homolog B-B-like
MELO3C026155	0,000284337	0,008267658	(+)-neomenthol dehydrogenase
MELO3C003695	0,000284827	0,008267658	ethylene-responsive transcription factor SHINE 2-like
MELO3C003768	0,000285069	0,008267658	Auxin response factor
MELO3C010928	0,000285792	0,00827581	PPPDE putative thiol peptidase family protein
MELO3C017784	0,000287022	0,008283948	Pentatricopeptide repeat-containing family protein
MELO3C005754	0,000287719	0,008283948	PHD finger family protein
MELO3C023306	0,000286822	0,008283948	adoMet-dependent rRNA methyltransferase spb1 isoform X1
MELO3C002328	0,000287751	0,008283948	zinc finger CCCH domain-containing protein 43
MELO3C024596	0,000288618	0,008294506	DNA polymerase
MELO3C011402	0,000288957	0,008294506	D-aminoacyl-tRNA deacylase
MELO3C024192	0,00029184	0,00834476	Fasciclin-like arabinogalactan protein
MELO3C006413	0,000291842	0,00834476	Clathrin interactor EPSIN 2
MELO3C026221	0,00029224	0,00834476	protein PLASTID TRANSCRIPTIONALLY ACTIVE 10-like
MELO3C011090	0,000292398	0,00834476	Unknown protein
MELO3C025449	0,000294384	0,008389297	Zinc finger C3H1 domain-containing protein, putative
MELO3C024544	0,000294894	0,00839174	Cell division FtsZ-1, chloroplastic-like protein
MELO3C013188	0,000296733	0,008410413	Pentatricopeptide repeat-containing protein
MELO3C018461	0,000296828	0,008410413	E3 ubiquitin-protein ligase MARCH6
MELO3C003817	0,000296781	0,008410413	DNA polymerase epsilon catalytic subunit A
MELO3C010524	0,000297643	0,008421422	arabinosyltransferase XEG113
MELO3C016542	0,000298955	0,008446441	peptidyl-prolyl cis-trans isomerase CYP37, chloroplastic
MELO3C016140	0,000300483	0,008465387	Solanesyl diphosphate synthase, putative
MELO3C026030	0,000300216	0,008465387	Protein phosphatase-2c, putative
MELO3C005238	0,000301079	0,008470097	GAGA-binding transcriptional activator
MELO3C016717	0,000303125	0,008515536	COP1-interacting protein, putative
MELO3C011640	0,0003039	0,008525163	Zinc finger, C6HC-type
MELO3C009566	0,000305243	0,008550704	Protein WVD2-like 4
MELO3C014089	0,00030836	0,008607261	caffeic acid 3-O-methyltransferase 1-like
MELO3C026025	0,00030857	0,008607261	Dehydration responsive element binding transcription factor
MELO3C021759	0,000308348	0,008607261	lecithin-cholesterol acyltransferase-like 4
MELO3C003825	0,000312163	0,008695208	Cysteine/Histidine-rich C1 domain family protein, putative
MELO3C001954	0,000313336	0,008715584	Glycosyltransferase
MELO3C009550	0,000314264	0,00871686	33 kDa ribonucleoprotein, chloroplastic
MELO3C015514	0,000314106	0,00871686	12-oxophytodienoate reductase 3
MELO3C011256	0,00031477	0,008718633	DEAD-box ATP-dependent RNA helicase-like protein
MELO3C011173	0,000316606	0,008757205	Gamma-glutamylcyclotransferase

MELO3C014658	0,000321415	0,008832526	Peroxidase
MELO3C014394	0,000321565	0,008832526	Ribosomal N-lysine methyltransferase 5
MELO3C007492	0,000321389	0,008832526	elongation of fatty acids protein 3-like
MELO3C008785	0,000320693	0,008832526	BTB/POZ domain protein
MELO3C009886	0,000320267	0,008832526	plant cysteine oxidase 2
MELO3C004434	0,000323167	0,00886421	Serine-rich protein-like protein
MELO3C016314	0,000324657	0,00888041	Aldose 1-epimerase, putative
MELO3C023996	0,000324312	0,00888041	RNA polymerase sigma factor sigD, chloroplastic
MELO3C020587	0,000326013	0,008892853	No data found
MELO3C017165	0,000325784	0,008892853	HVA22-like protein
MELO3C006813	0,000326594	0,008896413	monocopper oxidase-like protein SKS1
MELO3C009670	0,000328256	0,008917104	PHD-finger protein
MELO3C016015	0,000327885	0,008917104	AAA-type ATPase family protein
MELO3C005588	0,000329536	0,008939583	No data found
MELO3C009624	0,000330877	0,008963643	Actin family protein
MELO3C006418	0,000334017	0,009036314	Ankyrin repeat-containing protein
MELO3C015563	0,000337528	0,009118805	TATA-box-binding protein
MELO3C014619	0,000339532	0,009141554	IRK-interacting protein-like
MELO3C022488	0,000339917	0,009141554	tubulin-folding cofactor D
MELO3C020622	0,000339005	0,009141554	Rab5-interacting family protein
MELO3C010714	0,000340222	0,009141554	two-component response regulator ARR11
MELO3C015375	0,000341602	0,00916616	Sodium/hydrogen exchanger
MELO3C000065	0,000343344	0,009198122	V-type proton ATPase proteolipid subunit
MELO3C019816	0,000343724	0,009198122	Amino acid transporter family protein
MELO3C008494	0,000344946	0,009218319	E3 ubiquitin-protein ligase
MELO3C016573	0,000346012	0,009221845	Serine/threonine-protein kinase
MELO3C001121	0,000345871	0,009221845	Aspartate aminotransferase
MELO3C013921	0,000347074	0,009237694	Protein-tyrosine phosphatase mitochondrial 1-like protein
MELO3C019404	0,000348394	0,009241571	phytosulfokine receptor 2
MELO3C008018	0,000347799	0,009241571	Like-COV protein
MELO3C021608	0,000348624	0,009241571	zinc finger protein CONSTANS-LIKE 6
MELO3C001996	0,000350501	0,009278878	NAC domain-containing protein 100-like
MELO3C000201	0,000355846	0,009407762	dof zinc finger protein DOF1.5-like
MELO3C023990	0,00035901	0,009478731	Methyltransferase
MELO3C002872	0,000359765	0,009485971	Short-chain dehydrogenase/reductase family protein
MELO3C022068	0,000360452	0,009491434	proline-rich receptor-like protein kinase PERK8
MELO3C017755	0,000361737	0,009512585	zinc finger protein CONSTANS-LIKE 15-like
MELO3C024871	0,000362308	0,009514927	serine/threonine-protein phosphatase 4 regulatory subunit 2 isoform X1
MELO3C009836	0,000363929	0,009544809	Saccharopine dehydrogenase-like protein
MELO3C022005	0,000367548	0,00962694	Phosphate transporter PHO1-like protein
MELO3C002767	0,000371429	0,009715694	Nuclear-interacting partner of ALK
MELO3C022359	0,00037247	0,009730034	F3H9.20 protein
MELO3C012956	0,000374173	0,009761609	Protein MARD1
MELO3C007909	0,000376025	0,00979698	Armadillo repeat only protein
MELO3C026835	0,000376753	0,009803012	Pentatricopeptide repeat-containing protein At2g30100, chloroplastic
MELO3C025349	0,000377451	0,00980825	subtilisin-like protease SBT6.1
MELO3C019688	0,000378015	0,009810011	Peroxisomal and mitochondrial division factor 2
MELO3C002886	0,000379322	0,009822965	Alpha-taxilin
MELO3C017480	0,000379509	0,009822965	Xyloglucan endotransglucosylase/hydrolase
MELO3C024457	0,00038239	0,009884581	ATP-dependent zinc metalloprotease FtsH
MELO3C015290	0,000386293	0,009972425	peptidyl-prolyl cis-trans isomerase G
MELO3C026263	0,000387563	0,00997912	DEAD-box ATP-dependent RNA helicase-like protein
MELO3C011208	0,000387115	0,00997912	acetylglutamate kinase, chloroplastic
MELO3C004100	0,000389113	0,010005992	WD-repeat protein, putative
MELO3C014565	0,000391002	0,01003445	Homeobox domain-containing protein
MELO3C006950	0,000391236	0,01003445	Pentatricopeptide repeat-containing protein At4g21190
MELO3C021280	0,000394794	0,010112568	Calmodulin-binding transcription activator
MELO3C012670	0,000397299	0,010150395	Ribosomal protein S5/S7
MELO3C012411	0,000397107	0,010150395	pumilio homolog 4
MELO3C011773	0,000399887	0,010203324	Oxidoreductase/transition metal ion-binding protein (DUF3531)
MELO3C025346	0,000403884	0,010291994	Sugar/inositol transporter
MELO3C003659	0,000407065	0,010359693	Glucan endo-1,3-beta-glucosidase, putative
MELO3C005971	0,00040998	0,010393714	E3 ubiquitin-protein ligase BRE1-like 1
MELO3C022868	0,000409725	0,010393714	No data found
MELO3C012283	0,000409036	0,010393714	Small ubiquitin-related modifier
MELO3C003078	0,000410585	0,010395704	Protein MODIFIER OF SNC1 11
MELO3C018487	0,000411533	0,01040636	Lipase
MELO3C010774	0,000415371	0,010489987	Zinc finger CCCH domain-containing protein
MELO3C023409	0,000416908	0,010515345	BEL1-like homeodomain protein 7
MELO3C024982	0,000417648	0,01052057	Farnesyl diphosphate synthase
MELO3C007441	0,000419687	0,010527378	RING-type E3 ubiquitin transferase
MELO3C025102	0,000419977	0,010527378	Phytoene synthase
MELO3C015627	0,00042005	0,010527378	serrate RNA effector molecule
MELO3C011110	0,000418692	0,010527378	transcription factor bHLH93-like
MELO3C008732	0,000421822	0,010558394	No data found
MELO3C019813	0,000425661	0,010640976	Lysine-specific demethylase REF6
MELO3C017753	0,000427866	0,010642221	Glycerophosphodiester phosphodiesterase, putative
MELO3C007398	0,000427556	0,010642221	5'-adenylylsulfate reductase
MELO3C023163	0,000427278	0,010642221	Polygalacturonase inhibitor
MELO3C020808	0,000427603	0,010642221	Choline transporter-related family protein

MELO3C013429	0,000430502	0,010654347	kinesin-related protein 11
MELO3C005147	0,00043159	0,010654347	NADPH:QUINONE OXIDOREDUCTASE family protein
MELO3C012447	0,000430274	0,010654347	Scarecrow-like 3
MELO3C011986	0,000431246	0,010654347	Polygalacturonase
MELO3C008209	0,000430571	0,010654347	Ankyrin
MELO3C011212	0,000430422	0,010654347	Photosystem II reaction center PsbP family protein
MELO3C019630	0,000435381	0,010734505	ribosomal RNA large subunit methyltransferase I
MELO3C011139	0,000437758	0,010779657	Nuclear pore complex protein NUP85
MELO3C017711	0,000441544	0,010859341	Proline--tRNA ligase
MELO3C021670	0,000443308	0,01088614	Nuclear inhibitor of protein phosphatase 1
MELO3C003312	0,000443736	0,01088614	Protein kinase superfamily protein
MELO3C013779	0,000446718	0,010945695	2-keto-3-deoxy-L-rhamnonate aldolase
MELO3C013139	0,000447584	0,010947544	prohibitin-1, mitochondrial
MELO3C013615	0,000447902	0,010947544	E3 ubiquitin-protein ligase RMA1H1
MELO3C008959	0,000451143	0,011013129	1-acyl-sn-glycerol-3-phosphate acyltransferase
MELO3C027064	0,000453055	0,011037513	Pentatricopeptide repeat-containing protein
MELO3C015385	0,00045326	0,011037513	Pentatricopeptide repeat-containing protein
MELO3C006051	0,000453925	0,011040104	BTB/POZ domain-containing protein POB1
MELO3C006241	0,000457096	0,011089916	protein NRT1/ PTR FAMILY 7.3-like
MELO3C025549	0,000456881	0,011089916	vesicle-fusing ATPase
MELO3C007767	0,000462486	0,011197199	Lipoxygenase y domain-containing protein 1
MELO3C007931	0,000462652	0,011197199	Protein preY, mitochondrial, putative
MELO3C021742	0,000463278	0,011198624	Glycine cleavage system H, mitochondrial
MELO3C014297	0,000466624	0,011265711	type I inositol polyphosphate 5-phosphatase 4
MELO3C003017	0,000469162	0,01130037	Alpha/beta-Hydrolases superfamily protein
MELO3C019820	0,000469204	0,01130037	Glycerol-3-phosphate dehydrogenase
MELO3C020830	0,000469883	0,011302944	BZIP transcription factor, putative (DUF630 and DUF632)
MELO3C020835	0,000472388	0,011349391	Unknown protein
MELO3C017432	0,000475584	0,011405846	At1g16840/F17F16.27
MELO3C018510	0,000475893	0,011405846	somatic embryogenesis receptor kinase 1-like
MELO3C007248	0,000478865	0,011433429	Transcription factor VOZ1
MELO3C020721	0,000478166	0,011433429	triacylglycerol lipase SDP1
MELO3C003313	0,000478841	0,011433429	Membrane steroid-binding protein
MELO3C012873	0,00047936	0,011433429	NAC domain protein
MELO3C024951	0,000481456	0,011455744	cellulose synthase-like protein E6
MELO3C005757	0,000481084	0,011455744	Luminal binding heat shock protein 70
MELO3C013974	0,000483505	0,011463072	Hsp70-Hsp90 organizing protein 3
MELO3C018052	0,000482496	0,011463072	dynamin-related protein 3A-like
MELO3C011576	0,000483087	0,011463072	zinc finger protein CONSTANS-LIKE 6
MELO3C024558	0,00048545	0,01149538	sorting nexin 1
MELO3C009133	0,00048648	0,011505988	Receptor-like kinase
MELO3C005703	0,000487478	0,011506551	Beta-carotene 3-hydroxylase
MELO3C012960	0,000487669	0,011506551	BZIP protein, putative
MELO3C011675	0,000489723	0,011541219	Cmp-sialic acid transporter, putative
MELO3C009250	0,000492684	0,011564161	Laccase
MELO3C004186	0,000492599	0,011564161	Unknown protein
MELO3C006280	0,000492176	0,011564161	60S ribosomal protein L37a
MELO3C015098	0,000493039	0,011564161	Tubulin beta chain
MELO3C014358	0,000494212	0,01157792	transcription initiation factor TFIID subunit 6-like
MELO3C010630	0,00049758	0,011643018	40S ribosomal protein S8
MELO3C011793	0,000502871	0,011742725	transcription termination factor MTERF9, chloroplastic-like
MELO3C001962	0,00050303	0,011742725	protein REVEILLE 2-like
MELO3C007833	0,000504272	0,011751999	ATPase family AAA domain-containing protein 3
MELO3C009797	0,000504618	0,011751999	HSP20-like chaperones superfamily protein
MELO3C008099	0,000506949	0,011792393	eukaryotic translation initiation factor 2D
MELO3C005518	0,000507675	0,011795371	3-isopropylmalate dehydratase small subunit 3-like
MELO3C005679	0,000509158	0,011815931	Tyrosine--tRNA ligase
MELO3C013315	0,000512098	0,011863977	O-methyltransferase, putative
MELO3C026026	0,00051243	0,011863977	PRA1 family protein
MELO3C007495	0,000515516	0,011921451	protein LYK5-like
MELO3C000254	0,00051635	0,011926777	Auxin response factor
MELO3C016915	0,000518351	0,011959004	copper-transporting ATPase PAA2, chloroplastic isoform X1
MELO3C026443	0,000520272	0,011989319	No data found
MELO3C025885	0,000521179	0,011996228	ras-related protein Rab11C
MELO3C003880	0,000522313	0,012008341	Histone deacetylase complex subunit
MELO3C009562	0,000524514	0,012044923	Pentatricopeptide repeat-containing protein
MELO3C009408	0,000526576	0,01204955	Tetratricopeptide repeat (TPR)-like superfamily protein
MELO3C017544	0,000525788	0,01204955	DNA-directed RNA polymerase III subunit RPC5
MELO3C023481	0,000527659	0,01204955	nudix hydrolase 3-like
MELO3C023412	0,000526748	0,01204955	O-fucosyltransferase family protein
MELO3C013645	0,000527767	0,01204955	Alanine--tRNA ligase
MELO3C015350	0,000528832	0,012059945	Sugar transporter ERD6-like protein
MELO3C013600	0,000530899	0,012093112	O-methyltransferase, putative
MELO3C013757	0,000533573	0,012140022	Proteasome subunit alpha type
MELO3C012622	0,000536651	0,012169726	peptidyl-prolyl cis-trans isomerase CYP59
MELO3C015860	0,000536727	0,012169726	Calcium permeable stress-gated cation channel 1
MELO3C021858	0,000536048	0,012169726	WEB family protein At3g02930, chloroplastic
MELO3C025585	0,000538898	0,012204926	bifunctional nitrilase/nitrile hydratase NIT4A
MELO3C009758	0,000540825	0,012230611	Amino acid transporter family protein
MELO3C017878	0,000541271	0,012230611	Protein LURP-one-related 17

MELO3C014176	0,00054293	0,0122525	30S ribosomal protein S6
MELO3C005869	0,000544101	0,0122525	Bidirectional sugar transporter SWEET
MELO3C017320	0,000543557	0,0122525	Zinc finger protein, putative
MELO3C006320	0,000545691	0,01227432	Type 1 membrane protein, putative isoform 1
MELO3C010964	0,000547068	0,012291283	Cyclin-T1-like protein
MELO3C005520	0,000548142	0,012301423	Ribosomal protein L15
MELO3C013437	0,000550127	0,012331966	V-type proton ATPase subunit a
MELO3C025989	0,00055226	0,012354603	Kinase superfamily protein
MELO3C010052	0,000552388	0,012354603	Basic leucine zipper/W2 domain protein
MELO3C013946	0,000560347	0,012494896	Small heat shock protein, chloroplastic
MELO3C015198	0,000560559	0,012494896	Pentatricopeptide repeat-containing protein
MELO3C025813	0,000559301	0,012494896	Polyadenylate-binding protein-interacting protein 3
MELO3C004597	0,000562498	0,012509883	DUF1005 family protein (DUF1005)
MELO3C002817	0,000562464	0,012509883	No data found
MELO3C005300	0,000565577	0,012564217	BnaC07g20870D protein
MELO3C009966	0,000573553	0,012727086	ADP-ribosylation factor-like
MELO3C002816	0,000574467	0,012733052	obg-like ATPase 1
MELO3C021588	0,000578257	0,01280268	CRS1/YhbY (CRM) domain protein
MELO3C009038	0,000579828	0,01280876	adenylosuccinate synthetase, chloroplastic
MELO3C011138	0,000579399	0,01280876	Ultraviolet-B receptor UVR8
MELO3C004437	0,000581551	0,012832462	Methyltransferase-related family protein
MELO3C003057	0,000585005	0,012894272	Phosphatidylinositol-4-phosphate 5-kinase, putative
MELO3C012628	0,000585702	0,012895245	BOI-related E3 ubiquitin-protein ligase 1-like
MELO3C021552	0,000587182	0,012899069	universal stress protein A-like protein
MELO3C019948	0,000586876	0,012899069	Oxidoreductase family protein
MELO3C003916	0,000590103	0,012905799	Cellulose synthase
MELO3C019527	0,000589502	0,012905799	CBS domain-containing protein CBSX1, chloroplastic
MELO3C019163	0,00058932	0,012905799	ABC transporter F family-like protein
MELO3C017347	0,000589846	0,012905799	Actin-interacting protein 1-2
MELO3C006802	0,000591331	0,012918363	Protein DEHYDRATION-INDUCED 19
MELO3C004505	0,000592869	0,012937653	Ribosomal protein L31
MELO3C014849	0,000597937	0,013033838	Alpha/beta hydrolase-3
MELO3C003120	0,000600664	0,013048329	SLT1
MELO3C011752	0,00060038	0,013048329	E3 ubiquitin ligase BIG BROTHER-related
MELO3C022609	0,000601905	0,013048329	No data found
MELO3C021408	0,000599518	0,013048329	Protein trichome birefringence-like 10
MELO3C002159	0,000601837	0,013048329	Nascent polypeptide-associated complex subunit beta
MELO3C005439	0,000603103	0,013059956	NO-associated protein 1, chloroplastic/mitochondrial
MELO3C011193	0,00060643	0,013117619	COP9 signalosome complex subunit 5b
MELO3C017300	0,000607829	0,013119132	AT-rich interactive domain-containing protein 5A, putative
MELO3C017091	0,000607555	0,013119132	Pleckstrin homology domain-containing family M member 3
MELO3C013710	0,000611069	0,013174678	Auxin efflux carrier
MELO3C023725	0,000616646	0,013210354	Protein ROOT PRIMORDIUM DEFECTIVE 1
MELO3C014306	0,000615127	0,013210354	signal recognition particle 9 kDa protein
MELO3C003945	0,000616214	0,013210354	Protein trichome birefringence
MELO3C023492	0,000614151	0,013210354	Receptor kinase
MELO3C012100	0,000616737	0,013210354	ribonuclease 3-like
MELO3C003726	0,000614743	0,013210354	Methyltransferase
MELO3C003326	0,000619344	0,013251824	Ataxin-10
MELO3C002819	0,000620421	0,013260494	eukaryotic translation initiation factor 3 subunit A-like
MELO3C009101	0,000623036	0,013301987	B3 domain-containing transcription repressor VAL2
MELO3C008052	0,000624482	0,013318459	No data found
MELO3C022930	0,000627924	0,013377414	mitotic spindle checkpoint protein MAD1
MELO3C025637	0,000630045	0,013382351	Mannosyltransferase
MELO3C017968	0,000629519	0,013382351	LOW QUALITY PROTEIN: translocase of chloroplast 159, chloroplastic-like
MELO3C010651	0,000630188	0,013382351	No data found
MELO3C006948	0,000634012	0,013449086	Protein SGT1 homolog
MELO3C010273	0,000635076	0,013457201	Transmembrane protein
MELO3C009380	0,000638714	0,013501767	ras-related protein RABC2a
MELO3C015796	0,000639351	0,013501767	Acetyl-CoA carboxylase, putative
MELO3C023200	0,000639914	0,013501767	Receptor-like protein kinase
MELO3C008088	0,000639383	0,013501767	phospholipase SGR2
MELO3C002470	0,00064277	0,013547571	Patatin
MELO3C008775	0,000644342	0,013566207	Elongation factor 4
MELO3C009735	0,000646709	0,013588861	NF-kappa-B-activating protein
MELO3C023114	0,000646794	0,013588861	Cellulose synthase
MELO3C013343	0,000648394	0,013608008	FAD-dependent urate hydroxylase-like
MELO3C014732	0,000652227	0,013620321	Pyruvate kinase
MELO3C016464	0,000649795	0,013620321	No data found
MELO3C013440	0,000651079	0,013620321	PHD domain-containing protein/BAH domain-containing protein
MELO3C005745	0,000652429	0,013620321	Abhydrolase_5 domain-containing protein
MELO3C009779	0,000650797	0,013620321	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
MELO3C017467	0,00065854	0,01373337	Syntaxin/T-SNARE family protein
MELO3C010693	0,000663173	0,013815404	Lysine ketoglutarate reductase trans-splicing protein (DUF707)
MELO3C006268	0,000670702	0,013942832	10 kDa chaperonin isoform X1
MELO3C003638	0,000670016	0,013942832	replication protein A 32 kDa subunit A-like
MELO3C017902	0,000676531	0,014049225	monothiol glutaredoxin-S15, mitochondrial
MELO3C014090	0,000679738	0,014100991	No data found
MELO3C024333	0,000689727	0,014293207	DNA-binding protein, putative
MELO3C023776	0,000692692	0,014335035	Laminin subunit gamma-1

MELO3C017757	0,000693923	0,014335035	Inositol transporter 1
MELO3C016033	0,000693729	0,014335035	glutathione S-transferase-like
MELO3C011944	0,00069511	0,01434455	Beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase
MELO3C023442	0,000695857	0,014344959	glycerol kinase
MELO3C008149	0,000702007	0,014454388	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.4 isoform X1
MELO3C011488	0,000702629	0,014454388	ylmG homolog protein 2, chloroplastic
MELO3C021436	0,000709823	0,014587203	60S acidic ribosomal protein P2B-like
MELO3C019873	0,000712436	0,01462568	3-oxoacyl-[acyl-carrier-protein] synthase-like protein
MELO3C017254	0,0007278	0,014925576	Sterile alpha motif domain-containing family protein
MELO3C015750	0,000730788	0,014971299	No data found
MELO3C007472	0,000737797	0,015099226	LRR receptor-like serine/threonine-protein kinase GSO1 isoform X1
MELO3C014454	0,000743376	0,015119403	Receptor-like protein kinase
MELO3C007690	0,000741216	0,015119403	No data found
MELO3C002180	0,000743002	0,015119403	mRNA splicing factor, Cwf18
MELO3C018494	0,000741174	0,015119403	Protein TIC 21, chloroplastic
MELO3C017385	0,000742664	0,015119403	pollen receptor-like kinase 1
MELO3C018120	0,000740158	0,015119403	Purple acid phosphatase
MELO3C014722	0,000746062	0,015120083	ethylene-responsive transcription factor RAP2-11
MELO3C019369	0,000746633	0,015120083	50S ribosomal protein L9
MELO3C016139	0,000748004	0,015120083	Mitogen-activated protein kinase
MELO3C009005	0,000746916	0,015120083	Unknown protein
MELO3C022074	0,000747376	0,015120083	Tryptophan synthase-related
MELO3C018732	0,000744619	0,015120083	Histone-lysine N-methyltransferase, H3 lysine-36 specific
MELO3C016152	0,000750497	0,015154969	Gibberellin 2-oxidase
MELO3C013338	0,00075512	0,015201698	RNA-binding protein 39 isoform X1
MELO3C007743	0,000754472	0,015201698	Polyadenylate-binding 2
MELO3C023304	0,000754129	0,015201698	Isoflavone reductase like
MELO3C011482	0,000757284	0,01522973	ATP-citrate synthase beta chain protein 2-like
MELO3C007152	0,000760376	0,015276373	Leucine-rich receptor-like protein kinase family protein
MELO3C017131	0,000764993	0,015353508	General negative regulator of transcription subunit 4
MELO3C008233	0,000766033	0,015358769	Thylakoid lumenal 15 kDa protein 1, chloroplastic
MELO3C021404	0,000767416	0,015370886	Heavy metal-associated isoprenylated plant protein 21
MELO3C023047	0,000770707	0,015405551	glutamyl-tRNA(Gln) amidotransferase subunit B, chloroplastic/mitochondrial
MELO3C027308	0,000770119	0,015405551	alanine--tRNA ligase-like
MELO3C011759	0,000772506	0,015410315	transcription factor DIVARICATA
MELO3C026198	0,000771969	0,015410315	Gamma carbonic anhydrase-like 1, mitochondrial
MELO3C013173	0,000780326	0,01553626	NAC domain-containing protein 17-like
MELO3C007494	0,000780392	0,01553626	Hexosyltransferase
MELO3C017115	0,000781959	0,015551777	succinate dehydrogenase subunit 7B, mitochondrial-like
MELO3C020978	0,000785857	0,015597885	Adenylyl cyclase-associated protein
MELO3C002034	0,000785617	0,015597885	ninja-family protein 6-like isoform X2
MELO3C005942	0,000788048	0,015605062	Kinase family protein
MELO3C016383	0,00078938	0,015605062	RING-type E3 ubiquitin transferase
MELO3C012713	0,000788594	0,015605062	Zinc finger, CCCH-type
MELO3C001997	0,000788804	0,015605062	Galactoside 2-alpha-L-fucosyltransferase
MELO3C016562	0,000790211	0,015605875	At4g33560
MELO3C024241	0,000794484	0,015658951	Kinesin-like protein
MELO3C026760	0,000794199	0,015658951	Arabinogalactan protein
MELO3C021368	0,00080597	0,015869496	DnaJ subfamily B member 14
MELO3C008285	0,000806924	0,015872456	eukaryotic translation initiation factor 3 subunit F
MELO3C026027	0,000808771	0,015892961	Macrophage migration inhibitory factor family protein
MELO3C001994	0,000811478	0,015930293	thioredoxin-like 1-2, chloroplastic
MELO3C009588	0,000814919	0,015934492	Downstream neighbor of Son
MELO3C005199	0,000814794	0,015934492	charged multivesicular body protein 7 isoform X1
MELO3C015422	0,000812644	0,015934492	Arginine--tRNA ligase
MELO3C025799	0,000814018	0,015934492	Alpha-ketoglutarate-dependent dioxygenase AlkB
MELO3C002271	0,000822787	0,016072425	F-box protein SKIP16
MELO3C009961	0,000827069	0,01614011	At1g23710
MELO3C021384	0,000828633	0,016154657	Cox19-like CHCH family protein
MELO3C009148	0,00083221	0,016208388	Methionine aminopeptidase,related
MELO3C011847	0,000834449	0,016235996	60S ribosomal protein L5
MELO3C017833	0,000835285	0,01623626	Golgi SNAP receptor complex member 1-1
MELO3C018360	0,000837062	0,016254804	No data found
MELO3C014230	0,000837903	0,016255158	Ethylene insensitive 2
MELO3C004480	0,000841204	0,016303183	No data found
MELO3C010421	0,000847224	0,016397526	Random slug protein 5
MELO3C022059	0,000847733	0,016397526	Pentatricopeptide repeat-containing protein
MELO3C020963	0,000849397	0,016413642	WRKY family transcription factor
MELO3C012715	0,00085277	0,016462712	mediator of RNA polymerase II transcription subunit 19a-like
MELO3C009771	0,000855185	0,01648973	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3
MELO3C006154	0,000856674	0,01648973	Cyclin-D-binding Myb-like transcription factor 1
MELO3C023367	0,000856226	0,01648973	DNA repair protein XRCC1
MELO3C013587	0,000858523	0,016493166	No data found
MELO3C017416	0,000858187	0,016493166	Cyclin-dependent protein kinase inhibitor SMR15
MELO3C002651	0,000861593	0,016536046	protein SCAR3
MELO3C013541	0,000864234	0,016570635	No data found
MELO3C002314	0,000873986	0,016741364	cytochrome P450 71A1-like
MELO3C017945	0,000876911	0,016781123	bifunctional epoxide hydrolase 2-like
MELO3C007181	0,000880809	0,016839406	MADS box transcription factor AGAMOUS
MELO3C019564	0,000883614	0,01687668	High chlorophyll fluorescence phenotype 173

MELO3C012722	0,000891105	0,016964184	Pentatricopeptide repeat-containing family protein
MELO3C007800	0,00089249	0,016964184	Receptor protein kinase, putative
MELO3C007986	0,000892438	0,016964184	Histidine phosphatase family (Branch 1) protein
MELO3C022783	0,000891729	0,016964184	transmembrane protein 50A
MELO3C003344	0,000890474	0,016964184	3-isopropylmalate dehydratase large subunit
MELO3C004366	0,000900021	0,017090883	Prenylyltransferase superfamily protein
MELO3C004577	0,000902227	0,017099894	CRS2-associated factor 1, chloroplastic
MELO3C010042	0,000901754	0,017099894	endoribonuclease Dicer homolog 2 isoform X2
MELO3C010456	0,000904831	0,017125726	Phosphatidylinositol-4-phosphate 5-kinase, putative
MELO3C020789	0,000905325	0,017125726	Nucleoporin NUP188 like
MELO3C017960	0,000907356	0,017147725	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5-B
MELO3C003222	0,0009085	0,017152936	mRNA-capping enzyme
MELO3C006412	0,000910434	0,01717303	60S ribosomal protein L14, putative
MELO3C025255	0,00091322	0,017209147	Zinc transporter
MELO3C014273	0,000917455	0,017236905	Pentatricopeptide repeat-containing protein family
MELO3C013965	0,000916457	0,017236905	Flavin-containing monooxygenase
MELO3C022639	0,000915894	0,017236905	No data found
MELO3C009914	0,000918184	0,017236905	Alpha-mannosidase
MELO3C020591	0,000923743	0,01732478	Glycosyltransferase
MELO3C015748	0,00092849	0,017397286	transcription factor EMB1444
MELO3C019253	0,000930162	0,017412104	thioredoxin domain-containing protein 9 homolog
MELO3C019858	0,000933305	0,017454393	No data found
MELO3C014611	0,0009373	0,017512516	Pre-mRNA-splicing factor CWC22
MELO3C009455	0,000940284	0,017551679	BZIP transcription factor family protein
MELO3C002363	0,00094684	0,017650564	TITAN-like protein
MELO3C003671	0,000947369	0,017650564	SPOC domain/transcription elongation factor S-II, putative
MELO3C004204	0,00095	0,017666245	Importin subunit alpha
MELO3C008058	0,000949138	0,017666245	mitogen-activated protein kinase kinase kinase YODA isoform X1
MELO3C018476	0,000953839	0,01772094	cyclin-D3-3
MELO3C013769	0,000956211	0,017748314	Seven transmembrane receptor
MELO3C004279	0,00096026	0,017756725	RING zinc finger family protein
MELO3C014018	0,000957996	0,017756725	Pentatricopeptide repeat-containing protein family
MELO3C007047	0,000959447	0,017756725	Protein kinase
MELO3C026518	0,000958725	0,017756725	Photosystem II reaction center PsbP family protein
MELO3C010055	0,000964219	0,01781324	4-hydroxy-4-methyl-2-oxoglutarate aldolase
MELO3C016246	0,000969134	0,017870612	Kinase family protein
MELO3C025917	0,000968892	0,017870612	CAX-interacting protein 4
MELO3C016469	0,000970779	0,01788425	zinc finger CCCH domain-containing protein 5
MELO3C002741	0,000973931	0,017925603	Protein TIFY 5A
MELO3C003375	0,000975079	0,01793001	Two-component response regulator-like protein APRR2
MELO3C013406	0,000976852	0,017945908	tRNA-dihydrouridine(47) synthase [NAD(P)(+)]
MELO3C019504	0,000978735	0,017952113	Meiosis arrest female protein 1-like protein
MELO3C010686	0,000979008	0,017952113	Alanine aminotransferase 2
MELO3C003973	0,000982277	0,017995345	SNW/SKI-interacting protein-like
MELO3C009172	0,000986526	0,018006515	RING finger protein
MELO3C017703	0,000986533	0,018006515	disease resistance protein RGA2-like
MELO3C007010	0,000985587	0,018006515	phosphatidate cytidylyltransferase, mitochondrial isoform X1
MELO3C010353	0,000986326	0,018006515	protein NRT1/ PTR FAMILY 6.2-like
MELO3C022144	0,000992835	0,018104803	TMV resistance protein N-like
MELO3C014850	0,000995059	0,018128608	No data found
MELO3C009334	0,000999425	0,01819137	Methyltransferase type 11
MELO3C021622	0,001003418	0,01823046	Elicitor-responsive protein 1
MELO3C002464	0,001003114	0,01823046	polyadenylate-binding protein RBP45-like
MELO3C014604	0,001005214	0,01824629	F16F4.11 protein
MELO3C009663	0,001009648	0,018276383	1-acyl-sn-glycerol-3-phosphate acyltransferase-like protein
MELO3C014161	0,001009339	0,018276383	aspartic proteinase A1-like
MELO3C010286	0,001008161	0,018276383	pyrophosphate-energized vacuolar membrane proton pump
MELO3C027408	0,001010878	0,018281896	polygalacturonase-like
MELO3C014346	0,001017641	0,018370564	protein PALE CRESS, chloroplastic
MELO3C018950	0,001016798	0,018370564	Chaperone protein DNAj, putative
MELO3C016923	0,001022046	0,018401207	No data found
MELO3C015867	0,001022134	0,018401207	E3 ubiquitin ligase-like protein
MELO3C008092	0,001020377	0,018401207	50S ribosomal protein L14, putative
MELO3C010601	0,001025788	0,018433383	LysM domain-containing GPI-anchored protein 1
MELO3C010958	0,001025271	0,018433383	Gamma carbonic anhydrase 1, mitochondrial
MELO3C015747	0,001032087	0,018529709	At3g60850
MELO3C015692	0,001037635	0,018612402	Brefeldin A-inhibited guanine nucleotide-exchange protein
MELO3C013076	0,001042091	0,018675371	casein kinase I
MELO3C006189	0,001045776	0,018713312	Glutathione S-transferase
MELO3C020825	0,001046103	0,018713312	Phospholipase-like protein
MELO3C015518	0,001051409	0,018791208	Acyl-CoA N-acyltransferase (NAT) superfamily protein
MELO3C008773	0,001052661	0,01879657	Succinate dehydrogenase assembly factor 2, mitochondrial
MELO3C008766	0,001057254	0,018861521	sister chromatid cohesion 1 protein 4 isoform X1
MELO3C014895	0,001064445	0,018972668	squamosa promoter-binding-like protein 13A
MELO3C022014	0,001066831	0,018998061	WRKY transcription factor, putative
MELO3C000075	0,00107158	0,01906543	Myosin heavy chain-like protein, putative
MELO3C015304	0,001074501	0,019094858	60S ribosomal protein L22-2
MELO3C018768	0,001075167	0,019094858	Wound-responsive family protein
MELO3C013175	0,00108687	0,019285347	Pentatricopeptide repeat-containing family protein
MELO3C017440	0,001088108	0,019289993	U3 small nucleolar RNA-associated protein 25-like

MELO3C024226	0,00109041	0,019313455	Sulfate transporter 3.1
MELO3C009261	0,001093328	0,019347793	Peptide transporter family protein
MELO3C014027	0,001103763	0,019442977	Cytochrome P450 family protein
MELO3C025232	0,001102913	0,019442977	Ubiquitin-conjugating enzyme, E2
MELO3C015946	0,001106583	0,019442977	GATA transcription factor-like protein
MELO3C023413	0,001105341	0,019442977	Signal peptidase I
MELO3C002757	0,001104571	0,019442977	signal recognition particle 14 kDa protein
MELO3C017149	0,001102634	0,019442977	Pentatricopeptide repeat-containing protein
MELO3C018617	0,001106334	0,019442977	Pentatricopeptide repeat-containing protein
MELO3C011484	0,001104414	0,019442977	Spermidine synthase
MELO3C011088	0,001108133	0,019452898	mechanosensitive ion channel protein 3, chloroplastic-like
MELO3C006088	0,001117354	0,019562608	50S ribosomal protein L5, chloroplastic
MELO3C012391	0,001117266	0,019562608	NAC domain-containing protein 16
MELO3C020942	0,001115702	0,019562608	PQ-loop repeat family protein / transmembrane family protein
MELO3C006409	0,001125418	0,019651524	Glycolipid transfer protein domain-containing protein
MELO3C016775	0,001123501	0,019651524	Leucine-rich repeat receptor-like protein kinase family
MELO3C010517	0,001125381	0,019651524	WAT1-related protein
MELO3C007103	0,001130481	0,019689543	Protein plastid transcriptionally active 12
MELO3C005918	0,001128976	0,019689543	NPL4 family protein
MELO3C020806	0,001131583	0,019689543	Peptidyl-prolyl cis-trans isomerase
MELO3C017223	0,001130983	0,019689543	Mitochondrial carrier protein, putative
MELO3C021345	0,001136978	0,019761011	cullin-1
MELO3C010985	0,001137691	0,019761011	B-box zinc finger protein 20-like
MELO3C020834	0,00113984	0,019780936	Unknown protein
MELO3C004448	0,001143358	0,019824557	DNA helicase
MELO3C013773	0,001144942	0,019834607	Mediator of RNA polymerase II transcription subunit
MELO3C022477	0,001146898	0,019851081	Protein nuclear fusion defective 4
MELO3C002144	0,001148916	0,019868609	Receptor-like kinase 1
MELO3C006294	0,001154872	0,019954119	Dna repair helicase xpb1
MELO3C004015	0,001156853	0,019970875	Pentatricopeptide repeat-containing family protein
MELO3C007433	0,001159232	0,019994482	fumarylacetoacetase
MELO3C008815	0,001162718	0,02001964	nucleolar MIF4G domain-containing protein 1
MELO3C008313	0,00116263	0,02001964	UTP--glucose-1-phosphate uridylyltransferase 3, chloroplastic
MELO3C014315	0,001169638	0,020034938	Bifunctional DNA-directed RNA polymerase subunit beta-beta
MELO3C027330	0,001170708	0,020034938	Caffeic acid O-methyltransferase
MELO3C008801	0,001169091	0,020034938	H/ACA ribonucleoprotein complex subunit
MELO3C005079	0,001166811	0,020034938	protein ASPARTIC PROTEASE IN GUARD CELL 2
MELO3C005332	0,001165013	0,020034938	CDP-diacylglycerol--serine O-phosphatidyltransferase 1
MELO3C021456	0,001170444	0,020034938	histone deacetylase HDT1-like
MELO3C003305	0,001167299	0,020034938	Protein CDI
MELO3C004439	0,001173596	0,02006408	Protein phosphatase 2c, putative
MELO3C005367	0,001174443	0,02006408	dehydration-responsive element-binding protein 1D-like
MELO3C014091	0,001178037	0,020108075	caffeic acid 3-O-methyltransferase-like
MELO3C017255	0,001182788	0,020171749	BSD domain-containing protein
MELO3C021620	0,001185964	0,02020329	transcription initiation factor TFIID subunit 7
MELO3C005651	0,001186684	0,02020329	30S ribosomal S1
MELO3C004142	0,001189887	0,020211881	Unknown protein
MELO3C016826	0,001188294	0,020211881	At4g33800
MELO3C002219	0,001190259	0,020211881	HIPL1 protein-like isoform X1
MELO3C006314	0,001193205	0,020244514	60S ribosomal protein L13a, putative
MELO3C024505	0,001194936	0,02025648	SRSF protein kinase 1-like
MELO3C006160	0,001197871	0,020288819	Histone deacetylase complex subunit SAP18
MELO3C018758	0,001202	0,020341295	Secretory carrier-associated membrane protein
MELO3C005704	0,001205731	0,020386969	Beta-carotene hydroxylase
MELO3C015202	0,001210885	0,02045661	zinc finger A20 and AN1 domain-containing stress-associated protein 4-like
MELO3C026288	0,001212665	0,020469162	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B
MELO3C017581	0,001216996	0,02052472	inositol-3-phosphate synthase
MELO3C009583	0,001222917	0,020606981	E3 ubiquitin-protein ligase BAH1-like protein, putative
MELO3C017358	0,001226322	0,020646745	C2 domain-containing protein
MELO3C024222	0,00122875	0,020670004	aldo-keto reductase family 4 member C9-like
MELO3C023338	0,001234763	0,020744986	cysteine proteinase RD19a-like
MELO3C022494	0,001235308	0,020744986	No data found
MELO3C009234	0,001237827	0,020744988	SUPERMAN-like zinc finger protein
MELO3C008598	0,001240561	0,020744988	Lecithin:cholesterol acyltransferase family protein
MELO3C017939	0,00123777	0,020744988	Ribosomal protein L19
MELO3C022819	0,001239145	0,020744988	Myosin heavy chain-like protein, putative
MELO3C012004	0,001240427	0,020744988	Xyloglucan endotransglucosylase/hydrolase
MELO3C013829	0,001245009	0,020801755	Calmodulin family protein
MELO3C005849	0,001247648	0,020828226	p-loop containing nucleoside triphosphate hydrolases superfamily protein
MELO3C008947	0,001248718	0,020828498	CBS domain-containing protein
MELO3C016623	0,001251995	0,020865521	NAD(P)H dehydrogenase (Quinone)
MELO3C006145	0,001255715	0,02090987	F-box protein PP2-A13
MELO3C026304	0,001256932	0,020912504	nuclear cap-binding protein subunit 2
MELO3C013750	0,001262209	0,020982623	SKP1-like protein 1B
MELO3C003826	0,001266017	0,021028241	No data found
MELO3C018434	0,001269051	0,021060915	Armadillo repeat-containing protein, putative
MELO3C013489	0,001281695	0,021236976	monosaccharide-sensing protein 2
MELO3C010223	0,00128181	0,021236976	WRKY transcription factor
MELO3C014447	0,001297412	0,021444979	Nuclear ribonuclease Z
MELO3C022094	0,001296764	0,021444979	T-complex protein 1 subunit zeta 1

MELO3C005201	0,001297623	0,021444979	multicopper oxidase LPR1-like
MELO3C006420	0,001299336	0,021455341	Cotton fiber protein
MELO3C007127	0,001302118	0,021483309	9-cis-epoxycarotenoid dioxygenase
MELO3C014307	0,001311889	0,021626452	PRA1 family protein
MELO3C008076	0,001313603	0,021636651	No data found
MELO3C014258	0,00131955	0,021716499	IQ-domain 1
MELO3C005913	0,001328415	0,021844183	Auxin-responsive family protein
MELO3C017730	0,001329905	0,021850495	Pentatricopeptide repeat-containing family protein
MELO3C016550	0,001332312	0,021871848	Unknown protein
MELO3C002227	0,001334843	0,021895188	Unknown protein
MELO3C009467	0,001336203	0,021899309	Alpha/beta-Hydrolases superfamily protein
MELO3C023985	0,001340004	0,021943403	RNA/RNP complex-1-interacting phosphatase, putative
MELO3C012131	0,001342593	0,021962024	eukaryotic translation initiation factor 5A-like
MELO3C018180	0,001343365	0,021962024	tRNA (guanine(37)-N1)-methyltransferase
MELO3C005779	0,001350039	0,022052878	Metal-dependent protein hydrolase
MELO3C004645	0,001354559	0,022099308	40S ribosomal S3-like protein
MELO3C013149	0,001355635	0,022099308	UPF0505 protein C16orf62 homolog isoform X1
MELO3C007899	0,001357906	0,022099308	WD repeat-containing protein 82
MELO3C026058	0,001357441	0,022099308	Non-specific serine/threonine protein kinase
MELO3C005214	0,001360416	0,022099308	Defensin
MELO3C026194	0,001361813	0,022099308	No data found
MELO3C018688	0,001360022	0,022099308	dynamin-like protein ARC5
MELO3C010731	0,001361834	0,022099308	cyclin-dependent kinase G-2 isoform X1
MELO3C010640	0,00136367	0,022110937	zinc finger CCCH domain-containing protein 1
MELO3C005711	0,001366829	0,022131961	heavy metal-associated isoprenylated plant protein 3-like
MELO3C021185	0,001367208	0,022131961	Peptidase M48
MELO3C016149	0,001369639	0,022153147	Cationic amino acid transporter, putative
MELO3C015695	0,001377374	0,022260026	Expansin
MELO3C019011	0,001378575	0,022261231	copper-transporting ATPase PAA1, chloroplastic isoform X1
MELO3C006759	0,001385022	0,022347062	Ca2+-activated RelA/SpoT-like protein
MELO3C013780	0,001388796	0,022389659	Early nodulin-like protein 1
MELO3C001656	0,001392959	0,022438453	Unknown protein
MELO3C005389	0,001395363	0,022458857	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12
MELO3C018264	0,001399616	0,022508972	No data found
MELO3C003423	0,001400854	0,022510545	Zinc finger CCCH domain protein
MELO3C007413	0,001405347	0,02255593	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein
MELO3C021308	0,001405962	0,02255593	Multiple organellar RNA editing factor 8, chloroplastic/mitochondrial
MELO3C013745	0,001413439	0,02265747	Phosphatase 2C family protein
MELO3C013760	0,001414678	0,022658937	26S proteasome non-ATPase regulatory subunit 4 homolog
MELO3C014687	0,001418108	0,022695105	Structural maintenance of chromosomes protein
MELO3C021360	0,001419955	0,022695105	Pentatricopeptide repeat-containing family protein
MELO3C002687	0,001420383	0,022695105	dynamin-related protein 4C-like
MELO3C004084	0,001428955	0,022709919	No data found
MELO3C006202	0,00143051	0,022709919	Peptidase_M22 domain-containing protein
MELO3C019501	0,001430486	0,022709919	Transmembrane 53
MELO3C017880	0,001423996	0,022709919	Glucan endo-1,3-beta-glucosidase
MELO3C025272	0,001429508	0,022709919	AT3g54190/F24B22_150
MELO3C004833	0,001425696	0,022709919	crooked neck-like protein 1
MELO3C008116	0,001429946	0,022709919	Magnesium transporter NIPA
MELO3C011498	0,001426771	0,022709919	Splicing factor u2af large subunit, putative
MELO3C021563	0,001441577	0,022867225	isocitrate dehydrogenase [NADP]
MELO3C010599	0,001442786	0,022868044	Gamma-glutamylcyclotransferase
MELO3C002717	0,001445458	0,022892023	prefoldin subunit 6
MELO3C005939	0,001448732	0,022925487	nucleoside diphosphate kinase
MELO3C022399	0,00145033	0,022932398	alcohol dehydrogenase-like
MELO3C004475	0,001453822	0,022939204	arogenate dehydrogenase 1, chloroplastic-like
MELO3C000251	0,001453758	0,022939204	Protein LAZ1
MELO3C002821	0,001454245	0,022939204	Unknown protein
MELO3C004467	0,001460846	0,02302494	Exostosin family protein
MELO3C005926	0,001468715	0,023093668	protein BONZAI 1
MELO3C005821	0,001467018	0,023093668	mRNA, clone: RTFL01-46-D12
MELO3C022448	0,001467626	0,023093668	Metal tolerance protein
MELO3C013702	0,001471309	0,023116053	kinesin-like calmodulin-binding protein
MELO3C016558	0,001475647	0,023129006	Cyclic nucleotide-gated ion channel, putative
MELO3C007269	0,001475218	0,023129006	Auxin repressed protein
MELO3C020749	0,001473578	0,023129006	amidophosphoribosyltransferase, chloroplastic-like
MELO3C018985	0,001478932	0,023162115	60S acidic ribosomal protein P1
MELO3C019053	0,001482362	0,023197442	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3
MELO3C015954	0,001488106	0,023261476	No data found
MELO3C021295	0,001489848	0,023261476	Transducin family protein/WD-40 repeat protein
MELO3C003394	0,001489988	0,023261476	Protein LSD1
MELO3C012730	0,001497104	0,023335688	Structural maintenance of chromosomes protein
MELO3C002092	0,001496421	0,023335688	Receptor-like kinase
MELO3C017167	0,001501045	0,023378654	Transmembrane protein
MELO3C023251	0,001504394	0,023393301	callose synthase 5
MELO3C020927	0,001505539	0,023393301	Molybdenum cofactor sulfurase
MELO3C019661	0,00150409	0,023393301	No data found
MELO3C022124	0,001507441	0,023404444	Glycerophosphodiester phosphodiesterase GDPD4
MELO3C016608	0,001511362	0,023428483	Transmembrane protein, putative
MELO3C005331	0,001510473	0,023428483	Acyl-[acyl-carrier-protein] hydrolase

MELO3C009587	0,001521811	0,023553483	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
MELO3C005136	0,001521725	0,023553483	Protein EARLY RESPONSIVE TO DEHYDRATION 15
MELO3C025590	0,001526407	0,023587651	NF-kappa-B inhibitor-like protein 2 isoform 2
MELO3C009872	0,001525706	0,023587651	Gibberellin-regulated family protein
MELO3C003416	0,001529192	0,023612208	Unknown protein
MELO3C004564	0,001534372	0,023673689	protein NUCLEAR FUSION DEFECTIVE 6, chloroplastic/mitochondrial-like isoform X2
MELO3C016884	0,001539685	0,023737111	Methyltransferase
MELO3C004273	0,001542611	0,023745402	Mitochondrial Rho GTPase
MELO3C010727	0,001542628	0,023745402	3-oxoacyl-[acyl-carrier-protein] reductase 4
MELO3C023503	0,001549719	0,023827649	Unknown protein
MELO3C018573	0,001550384	0,023827649	Inorganic pyrophosphatase
MELO3C019724	0,001557475	0,023918018	Triacylglycerol lipase 2, putative
MELO3C014888	0,001567833	0,024026857	yrdC domain-containing protein, mitochondrial isoform X2
MELO3C012545	0,001569051	0,024026857	phosphatidylinositol 4-kinase alpha 1-like
MELO3C003249	0,001569429	0,024026857	target of Myb protein 1 isoform X1
MELO3C004944	0,001569178	0,024026857	polyadenylation and cleavage factor homolog 4 isoform X2
MELO3C021217	0,001571244	0,024036012	MACPF domain-containing CAD1-like protein
MELO3C009149	0,001572553	0,024037418	Copper chaperone SCO1/SenC
MELO3C024337	0,001576201	0,024074551	transmembrane protein 87B isoform X2
MELO3C003487	0,00157823	0,024086905	receptor-like protein kinase HAIKU2
MELO3C019026	0,001585064	0,024172538	Phosphate transporter
MELO3C004134	0,001588934	0,024178861	leucine aminopeptidase 1-like
MELO3C023358	0,001586845	0,024178861	Ubiquitin fusion degradation 1 protein
MELO3C011654	0,001589152	0,024178861	RING zinc finger protein-like
MELO3C007617	0,001591437	0,024194985	At5g67390
MELO3C006316	0,001593731	0,024211227	cytochrome b5
MELO3C020369	0,001597715	0,024215862	60S ribosomal protein L37a
MELO3C006870	0,001595901	0,024215862	ethylene-responsive transcription factor ERF027
MELO3C018106	0,001596976	0,024215862	ABC transporter B family protein
MELO3C004281	0,001605072	0,024290084	mevalonate kinase-like
MELO3C024916	0,001604299	0,024290084	Agenet domain-containing protein / bromo-adjacent domain-containing protein, putative
MELO3C019333	0,001606757	0,02429697	DUF679 domain membrane protein
MELO3C011011	0,001610571	0,024336007	Transducin/WD40 repeat-like superfamily protein
MELO3C007254	0,001613304	0,024340055	guanylate-binding protein 2
MELO3C005103	0,00161323	0,024340055	Cytochrome b-c1 complex subunit Rieske, mitochondrial
MELO3C016315	0,001620821	0,024434804	Unknown protein
MELO3C020836	0,001625795	0,024472427	transportin-1
MELO3C026715	0,001625262	0,024472427	Tetratricopeptide repeat (TPR)-like superfamily protein
MELO3C005511	0,001628068	0,024487975	palmitoyl-protein thioesterase 1-like
MELO3C007328	0,001631145	0,024515588	Wound-responsive family protein
MELO3C004321	0,001634236	0,024534462	Vat protein
MELO3C007405	0,001634885	0,024534462	peroxisomal membrane protein PMP22
MELO3C025308	0,001637045	0,024548219	auxin-responsive protein IAA16-like
MELO3C008847	0,001648475	0,024700867	M50 family peptidase
MELO3C002167	0,001652239	0,024723069	Succinate--CoA ligase [ADP-forming] subunit alpha, mitochondrial
MELO3C017207	0,001652461	0,024723069	LYR motif-containing protein 4
MELO3C005109	0,00165439	0,024733189	alpha-mannosidase
MELO3C010057	0,001655678	0,024733726	WRKY transcription factor SUSIBA2-like isoform X2
MELO3C012445	0,001657268	0,024738761	ATP synthase subunit d, mitochondrial
MELO3C002118	0,001660133	0,024762816	Elongation factor 1 alpha
MELO3C002390	0,00166271	0,024763845	At5g44650
MELO3C022228	0,001662029	0,024763845	Dienelactone hydrolase
MELO3C020733	0,001666156	0,024777792	Hexosyltransferase
MELO3C018306	0,001665461	0,024777792	Mitogen-activated protein kinase
MELO3C009506	0,00166957	0,024782586	secoisolariciresinol dehydrogenase-like
MELO3C025490	0,001670243	0,024782586	Protein TONNEAU 1b
MELO3C025725	0,001669696	0,024782586	RNA binding (RRM/RBD/RNP motifs) family protein
MELO3C025872	0,001673066	0,024805848	protein NRT1/ PTR FAMILY 8.1-like
MELO3C009188	0,001675463	0,02482275	transcription factor DIVARICATA-like
MELO3C013738	0,00167882	0,02483522	Ganglioside-induced differentiation-associated protein 2
MELO3C002312	0,00167825	0,02483522	cytochrome P450 71A1-like
MELO3C002646	0,001687107	0,024939126	Transcription initiation factor IIB
MELO3C021845	0,001689148	0,02495062	Cytochrome P450
MELO3C026143	0,001694488	0,025010794	Unknown protein
MELO3C023540	0,001697192	0,025022503	Unknown protein
MELO3C011172	0,001697815	0,025022503	Proteasome subunit beta type
MELO3C006949	0,001709312	0,025138388	NADH-ubiquinone oxidoreductase-related
MELO3C012597	0,00171077	0,025138388	Defective in cullin neddylation protein
MELO3C002016	0,00170755	0,025138388	zinc finger protein ZAT4-like
MELO3C026657	0,001709578	0,025138388	Glycine-rich protein
MELO3C006136	0,00171365	0,025161981	Signal recognition particle 54 kDa protein
MELO3C009119	0,001718851	0,025219605	Protein LURP-one-related 15
MELO3C009318	0,001727588	0,02528348	Ribonuclease P protein subunit p29
MELO3C023310	0,001728325	0,02528348	Glucose-1-phosphate adenylyltransferase
MELO3C018521	0,001726606	0,02528348	DNA polymerase kappa
MELO3C019818	0,001724792	0,02528348	DVL8
MELO3C009278	0,0017382	0,025405911	Pectin acetylesterase
MELO3C009019	0,001741661	0,025405911	Rhodanese-like domain-containing family protein
MELO3C023309	0,001739777	0,025405911	SNF1-related protein kinase regulatory subunit gamma-1-like
MELO3C009949	0,00174184	0,025405911	Pentatricopeptide repeat-containing protein

MELO3C009275	0,001749203	0,02541754	No data found
MELO3C006005	0,001751647	0,02541754	Bifunctional fucokinase/fucose pyrophosphorylase
MELO3C006569	0,001747599	0,02541754	Cytochrome P450 family protein
MELO3C016483	0,001744253	0,02541754	phosphoribosylamine--glycine ligase
MELO3C016879	0,001748919	0,02541754	Cytochrome P450, putative
MELO3C005299	0,001746783	0,02541754	C2 domain-containing protein
MELO3C012967	0,00175148	0,02541754	At5g57230
MELO3C017043	0,001755354	0,025433964	Glutamate receptor
MELO3C022231	0,001755155	0,025433964	Corepressor
MELO3C021047	0,001762342	0,025479124	nucleolin-like
MELO3C021370	0,001762177	0,025479124	PAX-interacting protein 1
MELO3C003456	0,001761414	0,025479124	Alpha/beta-Hydrolases superfamily protein
MELO3C004139	0,00176555	0,025506839	Ubiquitin carboxyl-terminal hydrolase, putative
MELO3C018495	0,001768672	0,025533265	Carbohydrate esterase, putative (DUF303)
MELO3C017838	0,001777557	0,025642781	Ubiquitin system component Cue
MELO3C005286	0,001783225	0,025687028	Mediator of RNA polymerase II transcription subunit 23
MELO3C019947	0,001782242	0,025687028	Oxidoreductase family protein
MELO3C020860	0,001789058	0,025752271	DNA polymerase
MELO3C002240	0,001807554	0,025999557	RING-type E3 ubiquitin transferase
MELO3C009032	0,001813381	0,026064389	fructokinase-like 2, chloroplastic
MELO3C013353	0,001817417	0,026103398	heavy metal-associated isoprenylated plant protein 26-like
MELO3C007081	0,001821971	0,026149788	SIT4 phosphatase-associated family protein
MELO3C014099	0,001824298	0,026164165	BnaC03g71690D protein
MELO3C022021	0,001827571	0,026192087	Lysine--trna ligase
MELO3C025593	0,001834197	0,026267986	Pentatricopeptide repeat-containing family protein
MELO3C016931	0,001837696	0,026276854	Hydroxyproline-rich glycoprotein
MELO3C017462	0,001838808	0,026276854	(DL)-glycerol-3-phosphatase 2
MELO3C008248	0,001836651	0,026276854	GRF1-interacting factor 3
MELO3C006943	0,001845063	0,026347185	Keratin-associated protein, putative (DUF819)
MELO3C005446	0,001846912	0,026354528	60S ribosomal protein L13
MELO3C016951	0,001854951	0,02639962	Glutathione peroxidase
MELO3C011952	0,001855104	0,02639962	UDP-galactose:fucoside alpha-3-galactosyltransferase
MELO3C008389	0,001855419	0,02639962	RNA-binding protein 2
MELO3C003593	0,001853717	0,02639962	Bromo-adjacent-like (BAH) domain protein
MELO3C002589	0,001869205	0,026576627	At2g47960/T9J23.10
MELO3C010716	0,001872575	0,026605377	Protein HHL1, chloroplastic
MELO3C006367	0,001875238	0,026624071	histone-lysine N-methyltransferase family member SUVH9
MELO3C023469	0,001878526	0,026651592	Protein LOW PSII ACCUMULATION 3, chloroplastic
MELO3C008040	0,001881556	0,026675408	RING-type E3 ubiquitin transferase
MELO3C017808	0,001885382	0,026702269	Protein NEOXANTHIN-DEFICIENT 1
MELO3C026053	0,001887507	0,026702269	WEB family protein At2g38370
MELO3C010350	0,001886706	0,026702269	heme oxygenase 1, chloroplastic
MELO3C023473	0,001895232	0,02679237	Phosphatase 2C family protein
MELO3C007011	0,001898043	0,026793748	No data found
MELO3C013051	0,001897813	0,026793748	Dead box ATP-dependent RNA helicase, putative
MELO3C006598	0,001903585	0,026833623	serine/arginine-rich SC35-like splicing factor SCL28
MELO3C016379	0,00190291	0,026833623	Ultraviolet-B receptor UVR8
MELO3C011705	0,001905403	0,026840092	Pyruvate dehydrogenase E1 component subunit alpha
MELO3C022411	0,001916373	0,026975379	No data found
MELO3C013859	0,001926227	0,027063223	CAAX amino terminal protease
MELO3C013331	0,001924304	0,027063223	hippocampus abundant transcript-like protein 1
MELO3C017481	0,001926725	0,027063223	Xyloglucan endotransglucosylase/hydrolase
MELO3C007612	0,001929109	0,027077453	molybdate-anion transporter
MELO3C018999	0,001934757	0,02710801	Transmembrane protein, putative
MELO3C026015	0,001938149	0,02710801	cyclin-dependent kinase 11B-like
MELO3C015999	0,001937128	0,02710801	60S ribosomal protein L22-2
MELO3C011885	0,001937355	0,02710801	Lipoxygenase
MELO3C027092	0,0019373	0,02710801	DExH-box ATP-dependent RNA helicase DExH12-like
MELO3C023885	0,001943686	0,027166205	Tropinone reductase family protein
MELO3C025699	0,001945414	0,027171132	Mitochondrial carrier protein
MELO3C014825	0,001948929	0,027200989	Steroid nuclear receptor, ligand-binding
MELO3C011716	0,001953014	0,027238758	TBC1 domain family member 8B
MELO3C017836	0,001960071	0,027306672	UPF0326 protein
MELO3C011206	0,001960649	0,027306672	dentin sialophosphoprotein-like
MELO3C019899	0,001972807	0,027456636	AMMECR1 family
MELO3C004391	0,001978193	0,027512209	PRA1 family protein
MELO3C011977	0,001982034	0,027546231	polygalacturonase At1g48100
MELO3C006681	0,001986267	0,027579088	bifunctional epoxide hydrolase 2-like
MELO3C007737	0,001987191	0,027579088	No data found
MELO3C019326	0,001990879	0,027610857	Glutaredoxin
MELO3C002372	0,002008671	0,027838061	heavy metal-associated isoprenylated plant protein 3-like
MELO3C026247	0,002012254	0,027868159	Raffinose synthase
MELO3C002897	0,002014896	0,027885197	Nuclear receptor corepressor 1
MELO3C011109	0,002016465	0,027887376	Octicosapeptide/Phox/Bem1p
MELO3C017786	0,002018683	0,027898511	GPI-anchored protein
MELO3C010755	0,002023602	0,027946928	At5g11810
MELO3C009159	0,002035301	0,028051229	ALC-interacting protein 1
MELO3C014488	0,002035415	0,028051229	Cyclin T1 family protein
MELO3C021929	0,002034457	0,028051229	B3 domain-containing transcription factor VRN1-like
MELO3C026782	0,002039701	0,028090688	Protein WVD2-like 3

MELO3C011984	0,002046965	0,028171092	pyrrolidone-carboxylate peptidase
MELO3C003852	0,00205307	0,028226406	DNA ligase-like protein
MELO3C003861	0,002053843	0,028226406	H/ACA ribonucleoprotein complex non-core subunit NAF1-like isoform X1
MELO3C019561	0,002059087	0,028228772	At1g78995
MELO3C017979	0,002059733	0,028228772	Bifunctional protein FolD
MELO3C012218	0,00205906	0,028228772	Two-component response regulator
MELO3C018406	0,002057861	0,028228772	Cytochrome c biogenesis protein
MELO3C006528	0,002063123	0,028235108	At1g05410/T25N20_5
MELO3C002785	0,002062723	0,028235108	epimerase family protein SDR39U1 homolog, chloroplastic-like
MELO3C024673	0,002067343	0,028235108	Trihelix transcription factor
MELO3C019810	0,002067002	0,028235108	Adenosine kinase
MELO3C003511	0,002064632	0,028235108	No data found
MELO3C012160	0,002082866	0,028427444	Protein BIG GRAIN 1-like E
MELO3C010420	0,002085005	0,028436991	DUF581 family protein, putative (DUF581)
MELO3C001323	0,002089158	0,02844162	transmembrane protein 184C
MELO3C017259	0,002087757	0,02844162	Protoheme IX farnesyltransferase, mitochondrial
MELO3C003545	0,002089665	0,02844162	28 kDa ribonucleoprotein
MELO3C022500	0,002094619	0,02848941	Vacuolar protein sorting 26
MELO3C003292	0,002110998	0,028692428	protein N-methyltransferase NNT1 isoform X1
MELO3C020906	0,002112654	0,028695185	60S ribosomal protein L26-1-like
MELO3C021441	0,002119311	0,028765823	Low molecular weight protein-tyrosine-phosphatase, putative
MELO3C009687	0,002121381	0,028767693	No data found
MELO3C023402	0,002122362	0,028767693	Biotin carboxyl carrier protein of acetyl-CoA carboxylase
MELO3C026403	0,002124813	0,028781161	60S ribosomal protein L27
MELO3C014272	0,002126328	0,028781935	Pyruvate kinase
MELO3C009328	0,00213544	0,028885477	Lectin receptor kinase-like protein
MELO3C010600	0,002138232	0,028903446	DNA ligase 1 isoform X3
MELO3C013822	0,002143379	0,028953215	Unknown protein
MELO3C017142	0,002151301	0,029040357	tRNA (Ile)-lysidine synthase
MELO3C025073	0,002156608	0,029092111	GRIP and coiled-coil domain-containing protein 1
MELO3C023201	0,002162151	0,029146973	No data found
MELO3C018368	0,002174462	0,029292935	omega-hydroxypalmitate O-feruloyl transferase
MELO3C008318	0,002183195	0,029390538	Dehydration-responsive element-binding protein 2C
MELO3C022425	0,002187971	0,029434771	15 kDa selenoprotein
MELO3C023799	0,002193667	0,029491311	12-oxophytodienoate reductase 3
MELO3C023753	0,002198867	0,029541101	BnaC06g27400D protein
MELO3C008985	0,002200413	0,029541772	Glucose-6-phosphate 1-dehydrogenase
MELO3C015941	0,002203298	0,029560419	Long cell-linked locus protein, putative, expressed
MELO3C016253	0,002213095	0,029671694	Zinc finger protein, putative
MELO3C018365	0,002215524	0,029684113	GDP-Man:Man(3)GlcNAc(2)-PP-Dol alpha-1,2-mannosyltransferase
MELO3C021777	0,002218623	0,029705479	Vesicle-associated membrane protein, putative
MELO3C015151	0,002226652	0,02977262	Alanine:glyoxylate aminotransferase
MELO3C010737	0,002225506	0,02977262	RING-type E3 ubiquitin transferase
MELO3C014860	0,002232141	0,029805646	Transcription factor GTE8
MELO3C018042	0,002230883	0,029805646	Phosphoglycerate mutase-like protein 1
MELO3C012695	0,002239626	0,029885381	la-related protein 6B isoform X1
MELO3C007232	0,00224746	0,029969679	spermidine coumaroyl-CoA acyltransferase
MELO3C010695	0,002255474	0,030056245	No data found
MELO3C026636	0,002257047	0,030056923	Protein arginine N-methyltransferase
MELO3C006754	0,0022639	0,030107586	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A-like protein 1
MELO3C000756	0,00226318	0,030107586	Alanine--tRNA ligase
MELO3C025854	0,002276317	0,030252349	No data found
MELO3C023370	0,002278528	0,030261358	No data found
MELO3C011263	0,002281069	0,03027475	EEIG1/EHBP1 protein amino-terminal domain protein
MELO3C004533	0,00230233	0,030536406	GDP-mannose transporter, putative
MELO3C009284	0,002314987	0,030667975	Protein SLOW GREEN 1, chloroplastic
MELO3C005759	0,002315355	0,030667975	30S ribosomal protein S6 alpha, chloroplastic
MELO3C002058	0,002320837	0,030709077	PHD and RING finger domain-containing protein 1
MELO3C018569	0,002321785	0,030709077	peptide methionine sulfoxide reductase B5-like
MELO3C018591	0,002323123	0,030709077	Transcription factor, putative
MELO3C012457	0,002324859	0,030711465	Annexin
MELO3C014588	0,002329523	0,030720166	Calcium-dependent protein kinase
MELO3C004461	0,002328875	0,030720166	protein TOPLESS
MELO3C007580	0,002330184	0,030720166	phosphatidylinositol 3,4,5-trisphosphate 3-phosphatase and protein-tyrosine-phosphatase PTEN2A-like
MELO3C012642	0,002340501	0,030835587	Glucan endo-1,3-beta-glucosidase-like protein 1
MELO3C007613	0,0023421	0,030836086	acyl-CoA-binding domain-containing protein 3
MELO3C008074	0,002345054	0,030854414	No data found
MELO3C026711	0,002357921	0,031003045	Protein FAM32A-like
MELO3C026250	0,002366285	0,031092325	Rhodanese-like domain-containing protein 11, chloroplastic
MELO3C016308	0,00236964	0,031115699	myosin-11-like
MELO3C011105	0,002372222	0,031128911	Chaperone protein dnaJ
MELO3C022382	0,002378877	0,031195509	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial
MELO3C003426	0,002381324	0,031206873	Inositol-tetrakisphosphate 1-kinase
MELO3C024108	0,002390668	0,031302545	OBERON-like protein
MELO3C017571	0,002393379	0,031302545	alanine--glyoxylate aminotransferase 2 homolog 1, mitochondrial
MELO3C012634	0,002392484	0,031302545	Receptor-like protein kinase
MELO3C011989	0,002396412	0,031321469	Unknown protein
MELO3C019411	0,002402097	0,031367529	Kinase superfamily protein
MELO3C016970	0,002408407	0,031367529	Chaperone protein
MELO3C026046	0,002406738	0,031367529	alpha-ketoglutarate-dependent dioxygenase AlkB-like

MELO3C003278	0,002403885	0,031367529	PHD finger protein At1g33420
MELO3C022568	0,002409466	0,031367529	protein indeterminate-domain 5, chloroplastic
MELO3C017274	0,002405103	0,031367529	G patch domain-containing protein TGH
MELO3C019815	0,002415556	0,031426095	Receptor-like protein kinase
MELO3C012361	0,002418655	0,0314457	cell division control protein 2 homolog A
MELO3C023445	0,00242176	0,031465348	F-box/LRR-repeat protein 14
MELO3C008977	0,00242354	0,031467785	Kinesin-like protein
MELO3C009290	0,002430501	0,031537432	Phosphatidate phosphatase PAH1
MELO3C020988	0,002436848	0,031599023	Unknown protein
MELO3C015664	0,00244087	0,031630406	RING-type E3 ubiquitin transferase
MELO3C004459	0,002445923	0,031675097	actin-related protein 6
MELO3C014877	0,002454349	0,031763391	DNA/RNA-binding protein KIN17
MELO3C006546	0,00245917	0,031784128	BRI1 kinase inhibitor 1-like
MELO3C010794	0,002457811	0,031784128	No data found
MELO3C019871	0,002461341	0,031791379	Phytol kinase
MELO3C006362	0,002466494	0,031837123	Beta-amylase
MELO3C006224	0,002471833	0,031843597	HOPM interactor 7
MELO3C016382	0,002470672	0,031843597	small nuclear ribonucleoprotein Sm D2-like
MELO3C025893	0,002470417	0,031843597	chaperone protein DnaJ
MELO3C002644	0,002480634	0,03193614	Transcription factor
MELO3C009581	0,002484269	0,03196211	D-lactate dehydrogenase, putative
MELO3C018344	0,00248821	0,031991964	No data found
MELO3C008115	0,002491333	0,032011282	5'-3' exonuclease
MELO3C006942	0,002496694	0,032054016	Receptor-like protein kinase, putative
MELO3C017094	0,002497905	0,032054016	No data found
MELO3C024357	0,002500774	0,032069996	transcription initiation factor TFIID subunit 12b
MELO3C011216	0,002506002	0,032116174	Photosynthetic NDH subcomplex B 3
MELO3C009748	0,002525227	0,032323842	Pentatricopeptide repeat-containing protein At1g80270, mitochondrial
MELO3C016056	0,002528753	0,032323842	monothiol glutaredoxin-S11
MELO3C026427	0,002527159	0,032323842	B-cell receptor-associated 31-like protein
MELO3C025897	0,002525532	0,032323842	pumilio homolog 1-like
MELO3C012604	0,002533219	0,032358543	Phosphoglycerate kinase
MELO3C010664	0,002534744	0,032358543	F28C11.19
MELO3C016031	0,002536861	0,032364646	glutathione S-transferase-like
MELO3C016574	0,00253857	0,032365535	Serine/threonine-protein kinase
MELO3C007940	0,002540917	0,032374558	Protein phosphatase 2c, putative
MELO3C014321	0,002547808	0,032420527	2-methyl-6-phytyl-1,4-hydroquinone methyltransferase, chloroplastic
MELO3C011104	0,002547373	0,032420527	Glucose-6-phosphate isomerase
MELO3C006158	0,002565104	0,032556707	lysophospholipid acyltransferase LPEAT2 isoform X1
MELO3C011769	0,002564335	0,032556707	Pyruvate kinase
MELO3C025550	0,002564713	0,032556707	No data found
MELO3C020003	0,002561197	0,032556707	40S ribosomal protein S26
MELO3C016706	0,002573575	0,032622291	E3 ubiquitin-protein ligase RMA3
MELO3C020533	0,002573546	0,032622291	Ran-binding protein 1
MELO3C015210	0,002582759	0,032717708	ETHYLENE INSENSITIVE 3-like 3 protein
MELO3C006348	0,002586612	0,032745518	PHD finger protein ING
MELO3C006055	0,002590276	0,032749907	Aldose 1-epimerase
MELO3C001354	0,002590061	0,032749907	Kinase family protein
MELO3C014730	0,002592731	0,032759975	N utilization substance B
MELO3C006104	0,002599318	0,03278029	Atg8-interacting protein 1
MELO3C023317	0,002598954	0,03278029	phosphatidylinositol/phosphatidylcholine transfer protein SFH8-like
MELO3C011045	0,002596188	0,03278029	Histone H3
MELO3C022715	0,002602778	0,032802982	E3 ubiquitin-protein ligase RNF4-like isoform X1
MELO3C006785	0,002604786	0,032807344	U11/U12 small nuclear ribonucleoprotein 35 kDa protein
MELO3C005776	0,002606831	0,03281218	Plant UBX domain-containing protein 10
MELO3C021348	0,002612184	0,032840187	E3 ubiquitin-protein ligase Topors
MELO3C011550	0,002612382	0,032840187	transcription factor HBP-1b(C38) isoform X2
MELO3C006555	0,00261696	0,032861199	NEDD8-activating enzyme E1 catalytic subunit
MELO3C006817	0,002620451	0,032861199	pectinesterase-like
MELO3C018616	0,002618082	0,032861199	Alkyl transferase
MELO3C003793	0,002620709	0,032861199	GTP-binding protein hflx, putative
MELO3C015779	0,002624553	0,032888516	peptidyl-prolyl cis-trans isomerase CYP63
MELO3C003924	0,00263039	0,032919884	Nuclear speckle splicing regulatory-like protein (DUF2040)
MELO3C015791	0,002629404	0,032919884	Pentatricopeptide repeat-containing protein
MELO3C004163	0,002635886	0,032948877	trafficking protein particle complex subunit 4
MELO3C011320	0,002636044	0,032948877	NAD(P)-binding rossmann-fold protein
MELO3C003135	0,002638042	0,032952998	Ribonuclease II, chloroplastic/mitochondrial
MELO3C026799	0,002650628	0,033089282	Kinase family protein
MELO3C022000	0,002660118	0,033186779	KH domain-containing protein
MELO3C007601	0,00266637	0,033223806	Lysine-rich arabinogalactan protein 18
MELO3C011236	0,002666451	0,033223806	Peptidyl-prolyl cis-trans isomerase
MELO3C012844	0,002668541	0,033228888	Glutathione S-transferase family protein
MELO3C009572	0,00267166	0,033246763	ABC transporter family protein
MELO3C016114	0,002679947	0,033286969	Protein ROOT INITIATION DEFECTIVE 3
MELO3C017128	0,002678091	0,033286969	two-component response regulator ARR5-like
MELO3C003532	0,0026795	0,033286969	Pesticidal crystal cry8Ba protein
MELO3C004441	0,002681757	0,033288505	RING-H2 finger protein ATL16
MELO3C014706	0,002688709	0,033291105	Argonaute
MELO3C022174	0,002686306	0,033291105	molybdopterin synthase sulfur carrier subunit
MELO3C023622	0,002688572	0,033291105	Short-chain dehydrogenase/reductase

MELO3C023451	0,002686991	0,033291105	BRCA1-associated protein
MELO3C026897	0,002693668	0,03333161	thioredoxin-like 1-1, chloroplastic
MELO3C013125	0,002696375	0,033344218	Lipid-binding serum glycoprotein family protein, putative
MELO3C013852	0,002701952	0,033392271	Plant/protein
MELO3C024701	0,002722685	0,033627463	Elongation factor Ts, mitochondrial
MELO3C024086	0,002730488	0,033681705	70 kDa heat shock protein
MELO3C022386	0,002729666	0,033681705	50S ribosomal protein L14
MELO3C014100	0,002733928	0,033703091	Heavy metal-associated isoprenylated plant protein 21
MELO3C013699	0,002735738	0,033704361	Pectinesterase
MELO3C017906	0,002748047	0,033834902	acyl-protein thioesterase 2
MELO3C009047	0,002752363	0,033866931	Endonuclease/exonuclease/phosphatase family protein
MELO3C017993	0,002756806	0,033900477	40S ribosomal protein S29
MELO3C025710	0,002766025	0,033992675	Nuclear factor related to kappa-B-binding protein
MELO3C005084	0,002768466	0,034001512	E3 ubiquitin-protein ligase
MELO3C016434	0,002785114	0,034043854	protein STICHEL
MELO3C027219	0,002778258	0,034043854	Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase
MELO3C008932	0,002780255	0,034043854	thioredoxin-like 3-1, chloroplastic
MELO3C021604	0,00278398	0,034043854	glycerol-3-phosphate dehydrogenase [NAD(+)]
MELO3C002736	0,002774689	0,034043854	Calcyclin-binding protein
MELO3C017478	0,002785704	0,034043854	Xyloglucan endotransglucosylase/hydrolase
MELO3C010631	0,002785354	0,034043854	replication factor C subunit 5
MELO3C018156	0,002778243	0,034043854	HEAT repeat-containing 8
MELO3C018637	0,002795115	0,03413774	outer envelope protein 64, mitochondrial
MELO3C014008	0,002799344	0,034147159	Adenosine monophosphate-protein transferase and cysteine protease ibpA
MELO3C007572	0,002797667	0,034147159	AP2-like ethylene-responsive transcription factor TOE3
MELO3C018716	0,002801119	0,034147712	ras-related protein Rab11D
MELO3C014199	0,002811106	0,034248325	E3 ubiquitin-protein ligase RING1-like
MELO3C013444	0,002818216	0,034313781	No data found
MELO3C016186	0,002820951	0,03431424	No data found
MELO3C016198	0,002821729	0,03431424	No data found
MELO3C009755	0,002830707	0,034386002	Sigma factor binding protein 1, chloroplastic
MELO3C010334	0,002831112	0,034386002	Non-specific serine/threonine protein kinase
MELO3C020848	0,002843447	0,034514594	AP2-like ethylene-responsive transcription factor TOE3 isoform X1
MELO3C014298	0,002848395	0,034553407	CST complex subunit STN1
MELO3C011496	0,002862369	0,034701612	BRCT domain DNA repair protein
MELO3C019673	0,002864285	0,034703532	BOI-related E3 ubiquitin-protein ligase 1-like
MELO3C005244	0,00287285	0,034764654	ABC transporter F family member 3
MELO3C027082	0,002872432	0,034764654	transcription factor bHLH149-like
MELO3C014560	0,002886753	0,034890143	Phospholipase A2
MELO3C011106	0,002886027	0,034890143	Pentatricopeptide repeat-containing protein
MELO3C023727	0,002889946	0,034907366	CDT1-like protein a, chloroplastic
MELO3C017963	0,00289547	0,034952714	Lycopene beta-cyclase
MELO3C027349	0,002897783	0,034959267	MACPF domain NSL1-like protein
MELO3C006867	0,002901755	0,034967061	ATP-dependent Clp protease ATP-binding subunit clpX
MELO3C024404	0,00290197	0,034967061	Tudor/PWWP/MBT superfamily protein
MELO3C006795	0,002905902	0,034993084	F-box protein SKIP16
MELO3C007935	0,002914473	0,035049105	Peroxidase
MELO3C011717	0,002914359	0,035049105	Protein kinase-like protein
MELO3C021242	0,002915878	0,035049105	YTH domain family protein 2
MELO3C019488	0,002921813	0,035099083	Pentatricopeptide repeat-containing protein
MELO3C021247	0,002929612	0,035171372	Dihydrolipoyl dehydrogenase
MELO3C007934	0,002950461	0,035383526	methyltransferase-like protein 23 isoform X3
MELO3C023224	0,002950867	0,035383526	Glutathione-S-transferase
MELO3C013878	0,002957395	0,035401287	haloacid dehalogenase-like hydrolase domain-containing protein Sgpp
MELO3C010569	0,002957726	0,035401287	Obg-like ATPase 1
MELO3C005260	0,002957489	0,035401287	Vacuolar iron transporter 1
MELO3C013221	0,002962542	0,035416003	KH domain-containing protein
MELO3C020139	0,00296188	0,035416003	No data found
MELO3C022885	0,002964338	0,035416035	methyl-CpG-binding domain protein 4-like protein
MELO3C008871	0,002966193	0,035416771	Chaperone protein dnaJ, putative
MELO3C021452	0,002968697	0,03542525	No data found
MELO3C017319	0,002971065	0,0354321	BnaA06g03540D protein
MELO3C013260	0,002980565	0,035473547	protein LAZ1 isoform X1
MELO3C013879	0,002977994	0,035473547	Regulator of nonsense transcripts 1-like protein
MELO3C007001	0,002983521	0,035473547	Peptidylprolyl isomerase
MELO3C020574	0,002982642	0,035473547	No data found
MELO3C024984	0,002982609	0,035473547	12-oxophytodienoate reductase 3
MELO3C006957	0,002986868	0,035491975	DUF21 domain-containing protein
MELO3C019021	0,002990581	0,035514727	Endoplasmic reticulum-Golgi intermediate compartment 3
MELO3C024729	0,002999388	0,035597902	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial
MELO3C016890	0,003010612	0,035709654	aminopeptidase M1
MELO3C010886	0,003017045	0,035764474	Succinate dehydrogenase subunit 5, mitochondrial
MELO3C027370	0,003021861	0,035778621	O-methyltransferase, putative
MELO3C025196	0,003020505	0,035778621	CTD small phosphatase-like protein
MELO3C022180	0,003023713	0,035779094	Protein DETOXIFICATION
MELO3C019044	0,003030012	0,035832154	Tubulin folding cofactor B
MELO3C024869	0,003033633	0,035853509	No data found
MELO3C014561	0,003046338	0,035942705	Hydroxyproline O-arabinosyltransferase 1
MELO3C012284	0,003044031	0,035942705	Zinc finger, B-box
MELO3C018849	0,00304664	0,035942705	Glycosyltransferase

MELO3C014781	0,003053533	0,03600252	AT5g13970/MAC12_6
MELO3C008481	0,003067925	0,036149299	Glutamate synthase 1 [nadh], chloroplastic
MELO3C011261	0,003069643	0,036149299	Peroxidase
MELO3C007950	0,003073946	0,03617543	Thiol-disulfide oxidoreductase LTO1
MELO3C023110	0,003077357	0,03617543	Alkaline alpha galactosidase
MELO3C023308	0,003076209	0,03617543	F-box protein At2g16365
MELO3C007661	0,003080611	0,036192143	Transmembrane protein, putative
MELO3C025139	0,003083892	0,036209142	No data found
MELO3C015862	0,003094223	0,036308865	Unknown protein
MELO3C012787	0,003098021	0,036331842	Sterol 3-beta-glucosyltransferase
MELO3C006983	0,003103923	0,036379454	Protein phosphatase 2C
MELO3C003418	0,00312099	0,036557785	PLATZ transcription factor family protein
MELO3C025651	0,00312838	0,036611552	Intracellular protein transport protein USO1, putative
MELO3C002117	0,003129288	0,036611552	T-complex protein 1 subunit delta
MELO3C017551	0,003135065	0,036657431	Pentatricopeptide repeat-containing protein
MELO3C011955	0,003151726	0,036830441	Tetratricopeptide-like helical
MELO3C007043	0,003158388	0,036886457	UDP-glucose 4-epimerase, putative
MELO3C024047	0,003169067	0,036989311	Kelch repeat-containing F-box family protein
MELO3C003323	0,003174141	0,037026649	Myosin heavy chain-like protein
MELO3C004576	0,003176483	0,037030643	sugar transport protein 14-like
MELO3C013476	0,003178234	0,037030643	phototropin-2
MELO3C011323	0,003180577	0,037036095	No data found
MELO3C014607	0,003194901	0,037110629	Zinc transporter ZTP29
MELO3C013949	0,003200132	0,037110629	Ribosomal protein L20
MELO3C013891	0,003198512	0,037110629	AT5g47090/K14A3_4
MELO3C024474	0,003199865	0,037110629	zinc finger protein 593
MELO3C005504	0,0031908	0,037110629	Disease resistance family protein
MELO3C022307	0,003194397	0,037110629	Pentatricopeptide repeat-containing family protein
MELO3C002719	0,003197284	0,037110629	60S ribosomal protein L18a
MELO3C016702	0,003207778	0,037177474	translation initiation factor IF-1, chloroplastic
MELO3C012906	0,003217846	0,037272286	CDT1-like protein a, chloroplastic
MELO3C017430	0,003244779	0,037562214	Fiber protein Fb15
MELO3C016083	0,003254038	0,037647333	Ubiquitin
MELO3C020055	0,003260646	0,037701701	histidine kinase 4-like
MELO3C013359	0,003263656	0,037714419	Ubiquitin-conjugating enzyme, E2
MELO3C012180	0,00326865	0,037750045	ruBisCO large subunit-binding protein subunit beta, chloroplastic-like
MELO3C016846	0,003282629	0,037889324	Phosphoribosyl-AMP cyclohydrolase
MELO3C003619	0,003300998	0,038079098	serine/arginine-rich splicing factor RSZ22A
MELO3C007340	0,003313583	0,038201954	NAD(P)H dehydrogenase (Quinone) FQR1-like
MELO3C023222	0,003316953	0,038218502	ABC transporter-like protein
MELO3C022442	0,003319357	0,0382239	At1g08760
MELO3C024172	0,003325012	0,038233085	Histone deacetylase
MELO3C022903	0,003325963	0,038233085	No data found
MELO3C003874	0,003325589	0,038233085	cytochrome P450 734A1-like
MELO3C004825	0,00333147	0,038274119	Ser/thr-rich protein T10 in DGCR region-like protein
MELO3C009653	0,003335391	0,03829688	transcription factor bHLH48
MELO3C009569	0,003341995	0,038336453	Gb|AAF02136.1
MELO3C013245	0,003345101	0,038336453	40S ribosomal protein S11-like
MELO3C007947	0,003346602	0,038336453	Ankyrin repeat domain-containing protein, chloroplastic
MELO3C026640	0,003346185	0,038336453	Mitogen-activated protein kinase kinase kinase 1 isoform 1
MELO3C006187	0,003373939	0,038382447	Proteasome subunit beta type
MELO3C013411	0,003359761	0,038382447	NADP dependent sorbitol 6-phosphate dehydrogenase family protein
MELO3C017651	0,003365623	0,038382447	Receptor-like kinase
MELO3C011897	0,003364709	0,038382447	F-box protein SKIP14
MELO3C002607	0,003368718	0,038382447	Sulfate/thiosulfate import ATP-binding protein cysA, putative
MELO3C002313	0,003361391	0,038382447	Serine/threonine-protein kinase AFC2
MELO3C017221	0,003372724	0,038382447	Histone deacetylase
MELO3C020002	0,003354814	0,038382447	Protein IDA
MELO3C011279	0,003373493	0,038382447	Hydroxyproline O-arabinosyltransferase 1
MELO3C010865	0,003371209	0,038382447	Calcium-binding EF-hand family protein, putative
MELO3C010744	0,003353091	0,038382447	CTD small phosphatase-like protein 2
MELO3C003368	0,003371584	0,038382447	Intron maturase, type II family protein
MELO3C004651	0,003388972	0,038411752	DENN (AEX-3) domain-containing protein
MELO3C013243	0,003386839	0,038411752	TOM1-like protein 2
MELO3C013737	0,00339013	0,038411752	Eukaryotic translation initiation factor 3 subunit A, putative
MELO3C026387	0,003383352	0,038411752	Pentatricopeptide repeat-containing protein At3g59040
MELO3C015852	0,003381614	0,038411752	adenylate isopentenyltransferase 3, chloroplastic
MELO3C021352	0,003385027	0,038411752	No data found
MELO3C012869	0,003384461	0,038411752	Adaptin ear-binding coat-associated protein, putative
MELO3C011787	0,003395586	0,038451502	No data found
MELO3C019429	0,00339882	0,038466072	Basic-leucine zipper (BZIP) transcription factor family protein
MELO3C006925	0,003401941	0,038479344	mitogen-activated protein kinase kinase kinase YODA-like
MELO3C006522	0,003406663	0,038510695	Acyl-CoA N-acyltransferases (NAT) superfamily protein, putative
MELO3C014459	0,003412741	0,038513275	Serine/threonine phosphatase
MELO3C002381	0,003410916	0,038513275	Bidirectional sugar transporter SWEET
MELO3C015616	0,003409437	0,038513275	BnaA04g07840D protein
MELO3C006846	0,003415532	0,038514691	Mitochondrial metalloendopeptidase OMA1
MELO3C011704	0,003416767	0,038514691	RAS-related protein RABC1
MELO3C008489	0,003421744	0,03854879	Serine/threonine-protein kinase stt7, chloroplastic
MELO3C026175	0,003426007	0,03857481	Long chain base biosynthesis protein

MELO3C011882	0,003434884	0,038652717	RING-type E3 ubiquitin transferase
MELO3C021636	0,003446073	0,038756546	No data found
MELO3C012052	0,003452074	0,038801943	dnaJ homolog subfamily B member 1
MELO3C018126	0,003462355	0,038895368	Autophagy-related protein 18f
MELO3C020666	0,003464992	0,038902854	ATP-dependent clp protease
MELO3C013892	0,003475055	0,038971525	Calcineurin B-like protein
MELO3C002722	0,003474179	0,038971525	3-oxoacyl-[acyl-carrier-protein] synthase
MELO3C025912	0,003482485	0,03901055	Protein kinase
MELO3C018739	0,003480823	0,03901055	GPI-anchored protein LORELEI
MELO3C019827	0,00348579	0,039025439	MEF2BNB-like protein
MELO3C007008	0,003505922	0,039206378	cytochrome c6, chloroplastic
MELO3C007106	0,003505337	0,039206378	Remorin family protein
MELO3C009713	0,00351416	0,039276258	translation factor GUF1 homolog, chloroplastic
MELO3C009747	0,003531004	0,039397631	Zinc finger (C3HC4-type RING finger) family protein, putative
MELO3C025091	0,003530344	0,039397631	protein REVEILLE 1-like isoform X1
MELO3C005532	0,003527148	0,039397631	Pectinesterase
MELO3C015131	0,003533209	0,039399968	Pentatricopeptide repeat-containing family protein
MELO3C027061	0,003535623	0,039404641	PLATZ transcription factor family protein
MELO3C011942	0,003539061	0,03942071	E3 ubiquitin-protein ligase
MELO3C016296	0,003541354	0,039424015	Chlororespiratory reduction31
MELO3C014270	0,003548068	0,039432076	No data found
MELO3C004534	0,003544491	0,039432076	Glycine-rich RNA-binding protein, putative
MELO3C007344	0,003547741	0,039432076	No data found
MELO3C014260	0,00356425	0,039481967	Interactor of constitutive active ROPs-like protein
MELO3C006765	0,003561252	0,039481967	DEAD-box ATP-dependent RNA helicase 50
MELO3C008503	0,003567236	0,039481967	Protein ABIL2
MELO3C016694	0,00356367	0,039481967	VQ motif-containing protein
MELO3C012088	0,003568551	0,039481967	sphinganine C4-monooxygenase 2
MELO3C022354	0,00356635	0,039481967	Light-regulated protein, putative
MELO3C015093	0,003557723	0,039481967	Fasciclin-like arabinogalactan protein 16
MELO3C010763	0,003555075	0,039481967	vacuolar-processing enzyme-like
MELO3C008037	0,003570997	0,039486906	Ubiquinol-cytochrome C chaperone family protein
MELO3C002653	0,003573311	0,039490386	No data found
MELO3C007055	0,003581872	0,039540431	reticuline oxidase-like protein
MELO3C015718	0,003581143	0,039540431	ATP binding protein
MELO3C002891	0,003585267	0,039540431	Pseudouridine synthase, RsuA/RluB/C/D/E/F
MELO3C002981	0,003585848	0,039540431	transmembrane emp24 domain-containing protein p24delta9-like
MELO3C012083	0,003592586	0,039584422	Actin-binding LIM protein 1, putative
MELO3C010745	0,003593846	0,039584422	mitochondrial import receptor subunit TOM20-like
MELO3C017766	0,003610937	0,039717805	Ras family
MELO3C020908	0,003610566	0,039717805	Glycosyl hydrolase family 43 protein
MELO3C022417	0,003611989	0,039717805	RNA-binding protein 24-B
MELO3C012428	0,003616813	0,03974872	mRNA-decapping enzyme subunit 2-like
MELO3C022004	0,003620939	0,039771924	SPX domain protein
MELO3C004466	0,003624832	0,039792552	Alpha-galactosidase
MELO3C024980	0,003638813	0,039923839	No data found
MELO3C020601	0,00364269	0,039944192	Protein phosphatase 2C
MELO3C013403	0,003646581	0,039964669	auxin-responsive protein SAUR36-like
MELO3C007784	0,003649542	0,039974931	Unknown protein
MELO3C026293	0,003656398	0,040027832	DUF1645 family protein
MELO3C026249	0,003662455	0,040071928	E3 ubiquitin-protein ligase RGLG2
MELO3C026102	0,003665971	0,040088183	Rhodanese-like domain-containing protein 6
MELO3C024088	0,003673788	0,040151428	F-box family protein, putative
MELO3C015825	0,00367858	0,04018157	F-box protein, putative
MELO3C007635	0,003691045	0,040295438	F-box protein, putative
MELO3C017844	0,003701289	0,040360967	calcineurin subunit B
MELO3C023195	0,003703179	0,040360967	NAC domain-containing protein 2
MELO3C025023	0,003700209	0,040360967	thioredoxin-like protein slr0233
MELO3C016913	0,003713995	0,040418482	No data found
MELO3C010482	0,003712349	0,040418482	F-box protein 7
MELO3C024352	0,003714595	0,040418482	Transcription initiation factor TFIID subunit 9
MELO3C005089	0,0037201	0,040456085	40S ribosomal protein S27
MELO3C019497	0,003727132	0,040510255	Tubby-like F-box protein
MELO3C023221	0,003736333	0,040587924	DNA cross-link repair family protein
MELO3C025053	0,003746829	0,040657217	lysine-specific demethylase JMJ25
MELO3C011399	0,003746213	0,040657217	LOW QUALITY PROTEIN: transcription factor BIM2
MELO3C004637	0,003756844	0,040671892	pre-mRNA cleavage factor Im 25 kDa subunit 1
MELO3C016852	0,003760096	0,040671892	zinc finger CCCH domain-containing protein 20-like
MELO3C021385	0,003760539	0,040671892	Phosphatase 2C family protein
MELO3C020532	0,003759449	0,040671892	Potassium transporter
MELO3C015523	0,003757061	0,040671892	Cysteine protease
MELO3C018576	0,003753217	0,040671892	L-galactose dehydrogenase
MELO3C010023	0,003766895	0,040718344	Ycf20-like protein
MELO3C007547	0,003777406	0,040809619	AT3g50560/T20E23_160
MELO3C003813	0,003780437	0,040820042	Mannan endo-1,4-beta-mannosidase-like protein
MELO3C015455	0,003791053	0,040912299	Acyl--UDP-N-acetylglucosamine O-acyltransferase
MELO3C009308	0,003803179	0,040971692	LRR receptor-like kinase
MELO3C024282	0,003804855	0,040971692	DUF3820 family protein
MELO3C021366	0,00380155	0,040971692	Acyl carrier protein
MELO3C012881	0,003803284	0,040971692	rho-N domain-containing protein 1, chloroplastic isoform X3

MELO3C024947	0,003815395	0,041062803	Inner centromere protein, ARK-binding region protein
MELO3C004524	0,003821849	0,041109857	zinc finger CCCH domain-containing protein 39-like
MELO3C005600	0,003831717	0,041193563	Phosphate translocator-related family protein
MELO3C024761	0,003834984	0,041206251	GDSL esterase/lipase At2g30310-like
MELO3C019691	0,003841997	0,041242606	Hexosyltransferase
MELO3C010338	0,003842544	0,041242606	Outward-rectifying potassium channel 4-like protein
MELO3C010688	0,003849725	0,041297244	F-box protein At1g70590
MELO3C024739	0,003857873	0,041362184	growth-regulating factor 4-like
MELO3C009560	0,003869597	0,041400198	Polyketide cyclase/dehydrase/lipid transport superfamily protein
MELO3C004555	0,003869804	0,041400198	At3g13227
MELO3C024926	0,003865295	0,041400198	two-pore potassium channel 1 isoform X1
MELO3C002209	0,003866952	0,041400198	Homeobox leucine zipper family protein
MELO3C004423	0,00387519	0,041435366	protease 2
MELO3C016067	0,003886455	0,041533337	Mitochondrial processing peptidase beta subunit
MELO3C022388	0,003895212	0,041584413	Pre-mRNA-processing factor 39
MELO3C021783	0,003899657	0,041584413	Peroxisome biogenesis protein 1
MELO3C026222	0,003897988	0,041584413	Transcription factor GTE10
MELO3C023969	0,003899371	0,041584413	Unknown protein
MELO3C021407	0,0039026	0,041593331	Stem-specific protein TSJT1
MELO3C021846	0,00390593	0,041606376	cytochrome P450 89A2-like
MELO3C007841	0,003917636	0,041708569	Bacteriophage N4 adsorption B
MELO3C010378	0,003926868	0,041741601	No data found
MELO3C005360	0,00392708	0,041741601	mediator of RNA polymerase II transcription subunit 36a-like
MELO3C005850	0,003925023	0,041741601	S-type anion channel SLAH2
MELO3C002789	0,003938719	0,041842795	BnaCnng71930D protein
MELO3C024960	0,003956688	0,041913419	pentatricopeptide repeat-containing protein At5g66520-like
MELO3C026392	0,003958903	0,041913419	RING/U-box superfamily protein
MELO3C008056	0,003957199	0,041913419	NAC domain-containing protein 82
MELO3C019135	0,003951906	0,041913419	4-alpha-glucanotransferase DPE2
MELO3C021253	0,003960223	0,041913419	Beta-glucosidase
MELO3C011386	0,003948698	0,041913419	DNA gyrase subunit A
MELO3C022742	0,003952049	0,041913419	ATP-dependent DNA helicase, RecQ family protein, expressed
MELO3C022225	0,003974648	0,04204356	protein NRT1/ PTR FAMILY 5.10-like
MELO3C015024	0,003977944	0,042055892	RING-type E3 ubiquitin transferase
MELO3C002556	0,003983689	0,0420941	heterogeneous nuclear ribonucleoprotein U-like protein 1
MELO3C003039	0,003992429	0,042163897	No data found
MELO3C013929	0,004016596	0,042396446	Unknown protein
MELO3C019002	0,00402459	0,042458132	Annexin
MELO3C012683	0,004034378	0,042538673	Pentatricopeptide repeat-containing protein, mitochondrial
MELO3C024468	0,004043191	0,042608845	Thioredoxin, putative
MELO3C007936	0,004053995	0,042677153	aspartyl protease family protein 1-like
MELO3C005650	0,004052481	0,042677153	Dead box ATP-dependent RNA helicase, putative
MELO3C010427	0,004077216	0,042853085	aspartate-semialdehyde dehydrogenase
MELO3C007195	0,004077084	0,042853085	ER lumen protein-retaining receptor
MELO3C002292	0,004074355	0,042853085	transcription factor MYB86-like
MELO3C004334	0,004082556	0,042886386	ERAD-associated E3 ubiquitin-protein ligase HRD1B-like
MELO3C012231	0,004086041	0,042900167	Homologous-pairing protein 2-like protein
MELO3C026332	0,004092545	0,042945629	DNA helicase INO80-like protein
MELO3C003917	0,004095247	0,042951162	Heat shock 70 kDa protein
MELO3C013792	0,004109432	0,043077059	Ribosomal protein L28
MELO3C006643	0,004132745	0,043229655	E3 ubiquitin-protein ligase
MELO3C010381	0,00413255	0,043229655	2-hydroxyacyl-CoA lyase
MELO3C024538	0,004127031	0,043229655	zinc finger A20 and AN1 domain-containing stress-associated protein 4
MELO3C011908	0,004132723	0,043229655	Heat shock protein HSP26
MELO3C012400	0,004137771	0,043259309	pentatricopeptide repeat-containing protein At2g22070
MELO3C017187	0,004145526	0,043294547	Pectinesterase inhibitor
MELO3C023569	0,004145485	0,043294547	Alpha-N-acetylglucosaminidase
MELO3C009178	0,004153711	0,043339304	No data found
MELO3C012716	0,0041542	0,043339304	ribonuclease 2-like
MELO3C009268	0,004161762	0,043387488	SLT1
MELO3C021818	0,004163213	0,043387488	Protein LIGHT-DEPENDENT SHORT HYPOCOTYLS 10
MELO3C020579	0,004171474	0,043450658	Enolase
MELO3C007517	0,004177658	0,043492126	Mitochondrial pyruvate carrier
MELO3C014384	0,004183069	0,043525516	ABSCISIC ACID-INSENSITIVE 5-like protein 4 isoform X1
MELO3C026567	0,004192935	0,043582254	Pentatricopeptide repeat-containing protein At4g18975, chloroplastic
MELO3C022309	0,004191627	0,043582254	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3
MELO3C022301	0,004197551	0,043607279	serine/threonine-protein kinase ATG1a isoform X4
MELO3C003173	0,004207307	0,043685655	Proteasome subunit alpha type
MELO3C017343	0,004218144	0,043775159	Protein DETOXIFICATION
MELO3C017925	0,004233382	0,043910224	Myb transcription factor
MELO3C015891	0,004238724	0,043942551	U1 small nuclear ribonucleoprotein C
MELO3C023098	0,004242721	0,04396091	No data found
MELO3C009370	0,004260693	0,043990453	ACT domain-containing protein
MELO3C006875	0,004249928	0,043990453	BAG family molecular chaperone regulator 1-like
MELO3C014035	0,00425177	0,043990453	No data found
MELO3C017623	0,004256934	0,043990453	Metacaspase-1
MELO3C005067	0,004263392	0,043990453	dihydroorotate dehydrogenase (Quinone), mitochondrial-like
MELO3C024371	0,004262261	0,043990453	Hydroxyproline-rich glycoprotein family protein
MELO3C011742	0,004252653	0,043990453	No data found
MELO3C018549	0,004260993	0,043990453	DUF21 domain-containing protein

MELO3C009480	0,004270564	0,044018463	ABC transporter family protein
MELO3C013951	0,004268865	0,044018463	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial
MELO3C007097	0,004276916	0,044042639	F-box protein SKIP19
MELO3C018374	0,004278249	0,044042639	DUF248-1
MELO3C010135	0,0042796	0,044042639	Kelch repeat-containing protein family
MELO3C019168	0,004293298	0,04416059	Metacaspase-9
MELO3C017365	0,004301125	0,044218068	DEAD-box ATP-dependent RNA helicase 42
MELO3C011234	0,004308579	0,044271653	GTP-binding nuclear protein
MELO3C007000	0,004317741	0,044319683	Katanin p80 WD40 repeat-containing subunit B1 homolog
MELO3C019226	0,004317006	0,044319683	transcription factor ILR3-like
MELO3C023373	0,004327562	0,044397416	Aspartate aminotransferase
MELO3C019907	0,004348841	0,044592553	40S ribosomal protein S17
MELO3C010243	0,004352503	0,044606949	VAMP-like protein YKT61
MELO3C022007	0,00436531	0,044714989	transmembrane emp24 domain-containing protein p24delta9
MELO3C022530	0,004370793	0,044747951	Armadillo/beta-catenin repeat family protein
MELO3C022219	0,00437392	0,044756755	SPla/RYanodine receptor (SPRY) domain-containing protein
MELO3C020562	0,004381523	0,044811338	No data found
MELO3C014562	0,004383797	0,044811393	E3 ubiquitin-protein ligase ICP0
MELO3C003447	0,004388805	0,044839378	Major facilitator superfamily transporter
MELO3C015857	0,004393219	0,044861266	No data found
MELO3C002619	0,004397541	0,044882192	Mitochondrial carrier protein, expressed
MELO3C014283	0,004405154	0,044891527	BIG SEEDS 1
MELO3C007793	0,004410314	0,044891527	cytochrome P450 CYP736A12-like
MELO3C023173	0,004408955	0,044891527	sister chromatid cohesion 1 protein 3
MELO3C005182	0,004412094	0,044891527	Short-chain dehydrogenase/reductase family protein
MELO3C005421	0,004410409	0,044891527	GTF2H2
MELO3C025324	0,00440425	0,044891527	Leucine-rich repeat extensin-like protein 4
MELO3C020541	0,004415679	0,044904867	Omega-3 fatty acid desaturase
MELO3C024896	0,004425602	0,044973267	Calcium-dependent lipid-binding (CaLB domain) family protein
MELO3C007660	0,00442696	0,044973267	DUF21 domain-containing-like protein
MELO3C002171	0,004433773	0,04501932	LOW QUALITY PROTEIN: probable metal-nicotianamine transporter YSL5
MELO3C006119	0,004436391	0,045022754	Remorin
MELO3C010522	0,004443462	0,045071359	Zinc knuckle family protein
MELO3C016498	0,004450952	0,045078873	MACPF domain-containing protein At4g24290
MELO3C007981	0,004451051	0,045078873	Plant intracellular ras group-related LRR protein
MELO3C024434	0,004448586	0,045078873	protein IQ-DOMAIN 14-like
MELO3C007689	0,004468911	0,045229993	protein RMD5 homolog A
MELO3C008214	0,004470553	0,045229993	Emb|CAB62340.1
MELO3C018008	0,004484931	0,045352224	Glycyl-tRNA synthetase beta subunit
MELO3C012753	0,004495256	0,045433371	Unknown protein
MELO3C011357	0,004510552	0,045564646	serine/arginine-rich splicing factor SC35-like
MELO3C020113	0,004517785	0,045614382	ADP,ATP carrier protein
MELO3C002044	0,004521056	0,045624084	DNA polymerase alpha subunit B
MELO3C015727	0,004533629	0,045727594	Maternal effect embryo arrest 60
MELO3C013370	0,004542785	0,045796557	translocase of chloroplast 120, chloroplastic-like
MELO3C004636	0,004562754	0,045956283	T-complex protein 1 subunit beta
MELO3C018966	0,004563283	0,045956283	ATP-dependent 6-phosphofructokinase
MELO3C026199	0,0045674	0,045974302	Transmembrane protein, putative
MELO3C019056	0,004577074	0,046048208	two-component response regulator ARR8-like
MELO3C011953	0,004581695	0,046071233	Unknown protein
MELO3C014991	0,004592244	0,046153801	MLP-like protein 28
MELO3C016801	0,004595981	0,046167865	aspartic proteinase-like protein 2
MELO3C016795	0,004616259	0,046347994	Clavata3/ESR (CLE) gene family member MtCLE20
MELO3C009312	0,004637357	0,046443786	Pentatricopeptide repeat-containing protein At3g09650, chloroplastic
MELO3C020458	0,004640894	0,046443786	cyclin-dependent kinase inhibitor 5-like
MELO3C013215	0,004637275	0,046443786	Chaperone DnaJ domain protein
MELO3C007647	0,004642262	0,046443786	xyloglucan 6-xylosyltransferase 1
MELO3C000279	0,004642023	0,046443786	Late cornified envelope protein 1E
MELO3C008114	0,004641918	0,046443786	TSA: Wollemia nobilis Ref_Wollemi_Transcript_28887_1569 transcribed RNA sequence
MELO3C018767	0,004631049	0,046443786	Wound-responsive family protein
MELO3C004603	0,004650444	0,046502086	Protein-tyrosine phosphatase mitochondrial 1
MELO3C005627	0,004658441	0,046558473	UDP-galactose/UDP-glucose transporter 2
MELO3C005404	0,004661356	0,046564044	LOW QUALITY PROTEIN: xyloglucan galactosyltransferase XLT2
MELO3C018500	0,004666952	0,04659638	TIP41-like family protein
MELO3C025210	0,004670139	0,046604633	gibberellin 2-beta-dioxygenase 2-like
MELO3C026171	0,004684672	0,046726052	Phosphate carrier, mitochondrial
MELO3C008513	0,004697722	0,046832565	FAST kinase domain-containing 3
MELO3C013820	0,004711581	0,046872055	bZIP transcription factor 16
MELO3C011375	0,00471355	0,046872055	BPS1-like protein
MELO3C010991	0,004708747	0,046872055	No data found
MELO3C003453	0,004711087	0,046872055	eukaryotic translation initiation factor 3 subunit L-like
MELO3C003821	0,004712946	0,046872055	agglutinin-like
MELO3C004992	0,004716173	0,046874535	Protein nuclear fusion defective 4
MELO3C017563	0,004720256	0,046891514	Protein AE7
MELO3C015861	0,00473689	0,047033107	isoamylase 2, chloroplastic
MELO3C018841	0,00474106	0,047050848	Beta-adaptin-like protein
MELO3C012033	0,004754153	0,047146974	Neurofilament heavy protein
MELO3C002083	0,00475552	0,047146974	Bowman-Birk type bran trypsin inhibitor
MELO3C023385	0,004763871	0,047206067	molybdate transporter 2
MELO3C004333	0,00477455	0,047288161	DCD (Development and Cell Death) domain protein

MELO3C003581	0,004779227	0,047310758	signal peptide peptidase
MELO3C005964	0,004786932	0,047363283	Late cornified envelope protein 1E
MELO3C010772	0,004792676	0,047396378	clathrin interactor EPSIN 1
MELO3C013364	0,004797805	0,047423351	MYB-related transcription factor
MELO3C011490	0,004807445	0,047494858	Myosin
MELO3C011715	0,004821563	0,047586732	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase 2
MELO3C025943	0,004819407	0,047586732	RPM1-interacting protein 4
MELO3C024211	0,004835288	0,047626989	BTB/POZ domain-containing protein At5g48130
MELO3C018935	0,004829019	0,047626989	Unknown protein
MELO3C005513	0,004833075	0,047626989	E3 ubiquitin-protein ligase HOS1
MELO3C025354	0,004832401	0,047626989	Late embryogenesis abundant protein
MELO3C010709	0,004851085	0,047758765	telomere-associated protein RIF1-like isoform X2
MELO3C007871	0,00485956	0,047818358	rRNA adenine N(6)-methyltransferase
MELO3C004179	0,004867492	0,047872556	RNA polymerase II-associated protein 3
MELO3C007325	0,00487634	0,047934223	Sugar transporter, putative
MELO3C015459	0,004878616	0,047934223	Cytidine deaminase
MELO3C021353	0,004882791	0,047951391	Chromatin remodeling factor, putative
MELO3C021565	0,004892331	0,048017693	DExH-box ATP-dependent RNA helicase DExH17-like
MELO3C011062	0,004894406	0,048017693	Serine hydrolase FSH
MELO3C015103	0,004900855	0,04805709	Histone deacetylase
MELO3C014540	0,004906707	0,048066291	blue copper protein-like
MELO3C006050	0,004905261	0,048066291	Phosphatidylinositol-4-phosphate 5-kinase family protein
MELO3C009984	0,004909095	0,048066291	Zinc finger CCCH domain-containing protein 41
MELO3C009686	0,004920878	0,048110111	Pleiotropic drug resistance ABC transporter
MELO3C022845	0,004920763	0,048110111	RING-type E3 ubiquitin transferase
MELO3C002054	0,00491912	0,048110111	Movement protein binding protein 2C
MELO3C016817	0,004932507	0,048184439	Calcium-transporting ATPase
MELO3C010960	0,00493336	0,048184439	Proteasome subunit alpha type
MELO3C005578	0,004939104	0,048216689	Amine oxidase
MELO3C020276	0,004949485	0,048270311	Tobamovirus multiplication 1
MELO3C018564	0,004948426	0,048270311	Protein trichome birefringence-like 12
MELO3C011383	0,004955995	0,04830994	DNA-directed RNA polymerase subunit beta
MELO3C004152	0,004959362	0,04831891	40S ribosomal protein S23-1
MELO3C022348	0,004994168	0,048634032	Protein TIFY 9
MELO3C006574	0,005016799	0,048830338	guanylate kinase 3, chloroplastic-like
MELO3C007071	0,005035167	0,048946423	WPP domain associated protein
MELO3C004988	0,00503616	0,048946423	Protein SIEL
MELO3C011016	0,005035252	0,048946423	tubulin beta chain
MELO3C005710	0,005041507	0,048948249	heavy metal-associated isoprenylated plant protein 3
MELO3C017291	0,005040338	0,048948249	40S ribosomal protein S28
MELO3C008219	0,005046262	0,048948249	glyceraldehyde-3-phosphate dehydrogenase
MELO3C019779	0,005045138	0,048948249	U4/U6 small nuclear ribonucleoprotein PRP4-like protein
MELO3C002071	0,005049346	0,048954117	single-stranded DNA-binding protein, mitochondrial
MELO3C024964	0,005065109	0,049058772	E3 ubiquitin-protein ligase
MELO3C010806	0,005063283	0,049058772	DNA excision repair protein ERCC-8
MELO3C026554	0,005078	0,049159522	alcohol dehydrogenase-like 7
MELO3C002931	0,00508282	0,049182075	Paired amphipathic helix SIN3-like protein
MELO3C014724	0,00509845	0,049274668	Mitochondrial carrier family
MELO3C014519	0,005095436	0,049274668	BEL1-like homeodomain protein 1
MELO3C012470	0,00510131	0,049274668	two-component response regulator ORR9-like
MELO3C002405	0,00510237	0,049274668	50S ribosomal protein L7/L12
MELO3C006249	0,005116632	0,049340898	No data found
MELO3C007711	0,005112354	0,049340898	U-box domain-containing protein kinase family protein, putative
MELO3C002385	0,005116723	0,049340898	Transcription factor Inducer of CBF expression 1
MELO3C011167	0,00512558	0,049402188	basic leucine zipper 9
MELO3C013378	0,005138683	0,049422864	Unknown protein
MELO3C013419	0,005140238	0,049422864	30S ribosomal protein S31, mitochondrial
MELO3C014215	0,005140167	0,049422864	No data found
MELO3C002515	0,005137092	0,049422864	Eukaryotic translation initiation factor-like protein
MELO3C024016	0,005132207	0,049422864	Metal-dependent phosphohydrolase
MELO3C005696	0,005146382	0,049457856	E3 ubiquitin-protein ligase RHA1B
MELO3C015130	0,005149257	0,04946142	polygalacturonase-like
MELO3C014379	0,005165809	0,049596282	Protein RETICULATA-RELATED 1, chloroplastic
MELO3C016899	0,005169158	0,049604328	Mitochondrial carrier protein
MELO3C006092	0,005178299	0,04966489	Glycoside hydrolase family 28 protein/polygalacturonase family protein
MELO3C003072	0,005180499	0,04966489	Thioredoxin-like protein AAED1, chloroplastic
MELO3C009552	0,005195047	0,049780192	Mads box protein, putative
MELO3C000885	0,005198453	0,049788673	auxin-responsive protein SAUR71-like
MELO3C008811	0,005201536	0,049794056	importin-5
MELO3C009970	0,005205874	0,04981144	polygalacturonase At1g48100
MELO3C014419	0,005215486	0,049855095	Unknown protein
MELO3C017659	0,005213556	0,049855095	Ribosomal protein L15
MELO3C018769	0,005218299	0,049857856	Wound-responsive family protein
MELO3C019780	0,005232823	0,049972446	protein kinase 2B, chloroplastic-like

Supplementary Table 2.B Gene Ontology terms (GO terms) of the cluster 2.1 obtained considering the comparison between lines the postharvest ripening time fruit during storage at 20.5°C and 88% relative humidity for 18 d the near-isogenic line SC10-2 and its parental ''Piel de Sapo'' obtained according to the differentially expressed gene pattern (Supl. Table 2.A)

GO ID	GO Name	GO Category	FDR	P-Value	SC10-2	PS	Non Annot Test	Non Annot Reference	TestSet Sequences	RefSet Sequences
GO:0006415	translational termination	BIOLOGICAL_PROCESS	7,88E-13	4,17E-16	35	146	592	16355	MELO3C020906; MELO3C015999; MELO3C017939; MELO3C020049; MELO3C021339; MELO3C009338; MELO3C020003; MELO3C005952; MELO3C004645; MELO3C021436; MELO3C007635; MELO3C026403; MELO3C016083; MELO3C017993; MELO3C015431; MELO3C012967; MELO3C017659; MELO3C019907; MELO3C010630; MELO3C013245; MELO3C005089; MELO3C012131; MELO3C012670; MELO3C006412; MELO3C006314; MELO3C005446; MELO3C017291;	MELO3C011276; MELO3C010222; MELO3C006088; MELO3C014262; MELO3C024506; MELO3C006245; MELO3C003258; MELO3C022601; MELO3C020141; MELO3C022441; MELO3C023012; MELO3C010867; MELO3C016201; MELO3C016049; MELO3C025030; MELO3C011956; MELO3C016963; MELO3C013984; MELO3C007740; MELO3C013981; MELO3C002294; MELO3C011040; MELO3C023703; MELO3C006411; MELO3C014391; MELO3C005844; MELO3C023820;
GO:0006414	translational elongation	BIOLOGICAL_PROCESS	1,61E-12	1,02E-15	36	161	591	16340	MELO3C020906; MELO3C015999; MELO3C017939; MELO3C020049; MELO3C021339; MELO3C009338; MELO3C020003; MELO3C005952; MELO3C004645; MELO3C021436; MELO3C007635; MELO3C026403; MELO3C016083; MELO3C017993; MELO3C015431; MELO3C012967; MELO3C018985; MELO3C017659; MELO3C019907; MELO3C010630; MELO3C013245; MELO3C005089; MELO3C012131; MELO3C012670; MELO3C006412; MELO3C006314; MELO3C005446;	MELO3C008660; MELO3C011276; MELO3C010222; MELO3C006088; MELO3C014262; MELO3C024506; MELO3C006245; MELO3C003258; MELO3C022601; MELO3C020141; MELO3C022441; MELO3C020023; MELO3C023012; MELO3C010867; MELO3C016201; MELO3C025030; MELO3C011956; MELO3C016963; MELO3C014306; MELO3C007740; MELO3C013981; MELO3C002294; MELO3C005565; MELO3C011040; MELO3C023703; MELO3C006411; MELO3C005844;
GO:0003735	structural constituent of ribosome	MOLECULAR_FUNCTION	7,01E-10	1,19E-12	44	310	583	16191	MELO3C020906; MELO3C015999; MELO3C017939; MELO3C020049; MELO3C021339; MELO3C009338; MELO3C020003; MELO3C005952; MELO3C004645; MELO3C020369; MELO3C021436; MELO3C007635; MELO3C026403; MELO3C004505; MELO3C022386; MELO3C002405; MELO3C024644; MELO3C005759; MELO3C015373; MELO3C017993; MELO3C015431; MELO3C012967; MELO3C018985; MELO3C017659; MELO3C019907; MELO3C010630; MELO3C013245;	MELO3C011310; MELO3C020704; MELO3C006088; MELO3C002164; MELO3C012084; MELO3C014262; MELO3C024506; MELO3C020945; MELO3C006400; MELO3C003258; MELO3C006766; MELO3C024747; MELO3C020141; MELO3C022441; MELO3C003811; MELO3C001514; MELO3C025276; MELO3C016201; MELO3C025030; MELO3C016688; MELO3C014824; MELO3C020836; MELO3C007740; MELO3C013981; MELO3C009489; MELO3C002294; MELO3C025609;
GO:0022625	cytosolic large ribosomal subunit	CELLULAR_COMPONENT	3,67E-09	7,00E-12	27	124	600	16377	MELO3C020906; MELO3C015999; MELO3C017939; MELO3C021339; MELO3C009338; MELO3C005952; MELO3C020369; MELO3C021436; MELO3C007635; MELO3C026403; MELO3C022386; MELO3C016083; MELO3C012967; MELO3C017659; MELO3C011285; MELO3C006412; MELO3C006314; MELO3C005520; MELO3C005446; MELO3C023201; MELO3C024850; MELO3C016198; MELO3C002719; MELO3C011847; MELO3C009091; MELO3C006280; MELO3C015304	MELO3C006088; MELO3C014262; MELO3C024506; MELO3C006245; MELO3C006922; MELO3C022601; MELO3C022441; MELO3C001514; MELO3C023012; MELO3C016201; MELO3C025030; MELO3C011956; MELO3C012254; MELO3C002294; MELO3C006411; MELO3C005844; MELO3C004995; MELO3C023820; MELO3C006657; MELO3C020556; MELO3C025168; MELO3C000241; MELO3C023260; MELO3C011448; MELO3C016459; MELO3C011720; MELO3C002668;

GO:0046686	response to cadmium ion	BIOLOGICAL_PROCESS	1,84E-04	8,95E-07	22	160	605	16341	MELO3C011256; MELO3C005293; MELO3C013214; MELO3C013411; MELO3C004194; MELO3C009038; MELO3C009203; MELO3C003173; MELO3C006241; MELO3C011284; MELO3C003344; MELO3C024514; MELO3C005757; MELO3C021247; MELO3C008879; MELO3C002117; MELO3C022382; MELO3C018573; MELO3C002816; MELO3C015385; MELO3C010599; MELO3C011107	MELO3C013974; MELO3C006086; MELO3C021919; MELO3C017817; MELO3C020429; MELO3C003491; MELO3C003370; MELO3C008541; MELO3C005395; MELO3C004980; MELO3C009910; MELO3C007698; MELO3C005674; MELO3C009633; MELO3C009915; MELO3C002444; MELO3C019040; MELO3C003536; MELO3C026800; MELO3C021113; MELO3C024461; MELO3C017134; MELO3C018623; MELO3C026360; MELO3C011712; MELO3C019318; MELO3C006493;
GO:0016071	mRNA metabolic process	BIOLOGICAL_PROCESS	4,59E-04	2,52E-06	38	415	589	16086	MELO3C020906; MELO3C015999; MELO3C011256; MELO3C010960; MELO3C017939; MELO3C020049; MELO3C021339; MELO3C009338; MELO3C020003; MELO3C005952; MELO3C004645; MELO3C021436; MELO3C007635; MELO3C026403; MELO3C016083; MELO3C016382; MELO3C016262; MELO3C017993; MELO3C012967; MELO3C017659; MELO3C019907; MELO3C010630; MELO3C013245; MELO3C005089; MELO3C008332; MELO3C012670; MELO3C006412;	MELO3C020705; MELO3C004580; MELO3C014262; MELO3C013051; MELO3C002045; MELO3C020824; MELO3C003258; MELO3C007978; MELO3C006767; MELO3C026246; MELO3C017771; MELO3C016201; MELO3C015113; MELO3C025030; MELO3C017775; MELO3C019837; MELO3C020836; MELO3C007740; MELO3C002294; MELO3C002173; MELO3C020718; MELO3C006411; MELO3C006416; MELO3C008956; MELO3C008955; MELO3C019964; MELO3C016459;
GO:0000287	magnesium ion binding	MOLECULAR_FUNCTION	0,002863815	2,48E-05	21	186	606	16315	MELO3C005293; MELO3C010286; MELO3C014732; MELO3C007153; MELO3C010794; MELO3C009038; MELO3C012196; MELO3C020579; MELO3C024514; MELO3C006736; MELO3C004439; MELO3C021385; MELO3C024982; MELO3C021563; MELO3C020244; MELO3C018573; MELO3C022494; MELO3C005939; MELO3C020394; MELO3C011704; MELO3C013745	MELO3C005271; MELO3C020829; MELO3C013336; MELO3C018628; MELO3C018507; MELO3C005396; MELO3C008426; MELO3C024509; MELO3C022605; MELO3C024508; MELO3C001595; MELO3C004226; MELO3C003379; MELO3C026007; MELO3C002448; MELO3C026005; MELO3C026006; MELO3C025552; MELO3C026004; MELO3C002727; MELO3C015076; MELO3C000372; MELO3C000130; MELO3C011713; MELO3C019677; MELO3C013218; MELO3C014943;
GO:0004775	succinate-CoA ligase (ADP-forming) activity	MOLECULAR_FUNCTION	0,002863815	2,52E-05	4	2	623	16499	MELO3C002167; MELO3C022382; MELO3C010675; MELO3C011482	MELO3C021268; MELO3C015245
GO:0009651	response to salt stress	BIOLOGICAL_PROCESS	0,00360577	3,28E-05	18	146	609	16355	MELO3C012136; MELO3C012445; MELO3C004194; MELO3C009203; MELO3C011044; MELO3C005147; MELO3C011172; MELO3C026629; MELO3C004105; MELO3C024514; MELO3C008879; MELO3C027349; MELO3C017242; MELO3C018573; MELO3C015098; MELO3C016033; MELO3C015186; MELO3C015374	MELO3C021918; MELO3C006086; MELO3C017935; MELO3C013454; MELO3C004580; MELO3C012085; MELO3C022725; MELO3C008666; MELO3C006648; MELO3C002203; MELO3C026009; MELO3C024345; MELO3C007739; MELO3C026245; MELO3C017134; MELO3C024222; MELO3C019039; MELO3C010625; MELO3C012925; MELO3C026482; MELO3C016738; MELO3C002170; MELO3C012099; MELO3C012097; MELO3C007067; MELO3C009123; MELO3C005444;

GO:0006096	glycolytic process	BIOLOGICAL_PROCESS	0,005205084	5,29E-05	12	72	615	16429	MELO3C020780; MELO3C014732; MELO3C007421; MELO3C007986; MELO3C020579; MELO3C012604; MELO3C018966; MELO3C024514; MELO3C011104; MELO3C022998; MELO3C008219; MELO3C008879	MELO3C005271; MELO3C009351; MELO3C007772; MELO3C013010; MELO3C008221; MELO3C025916; MELO3C009438; MELO3C024509; MELO3C024508; MELO3C024866; MELO3C006964; MELO3C009439; MELO3C019872; MELO3C017175; MELO3C025275; MELO3C018027; MELO3C019634; MELO3C011367; MELO3C020837; MELO3C003381; MELO3C004591; MELO3C014272; MELO3C025969; MELO3C024519; MELO3C021720; MELO3C016050; MELO3C016095;
GO:0022627	cytosolic small ribosomal subunit	CELLULAR_COMPONENT	0,009406002	1,08E-04	13	91	614	16410	MELO3C019907; MELO3C010630; MELO3C013245; MELO3C005089; MELO3C012670; MELO3C020049; MELO3C020003; MELO3C017291; MELO3C004645; MELO3C015373; MELO3C017993; MELO3C015431; MELO3C025582	MELO3C011310; MELO3C004020; MELO3C002481; MELO3C009036; MELO3C003890; MELO3C012084; MELO3C005830; MELO3C009315; MELO3C009716; MELO3C001556; MELO3C020141; MELO3C022363; MELO3C010867; MELO3C017338; MELO3C019879; MELO3C002091; MELO3C003061; MELO3C020759; MELO3C013981; MELO3C009489; MELO3C025609; MELO3C023703; MELO3C019490; MELO3C001168; MELO3C024359; MELO3C006733; MELO3C003986;
GO:0002119	nematode larval development	BIOLOGICAL_PROCESS	0,010270399	1,20E-04	25	273	602	16228	MELO3C011256; MELO3C010243; MELO3C008285; MELO3C010960; MELO3C016707; MELO3C011193; MELO3C009338; MELO3C007433; MELO3C020369; MELO3C006949; MELO3C022488; MELO3C016262; MELO3C017993; MELO3C011285; MELO3C005421; MELO3C004278; MELO3C025549; MELO3C023201; MELO3C002118; MELO3C002717; MELO3C003905; MELO3C022094; MELO3C006280; MELO3C025061; MELO3C013822	MELO3C011795; MELO3C012522; MELO3C006760; MELO3C002166; MELO3C002045; MELO3C004344; MELO3C019031; MELO3C026800; MELO3C019034; MELO3C025275; MELO3C016321; MELO3C014708; MELO3C015235; MELO3C019956; MELO3C020836; MELO3C008157; MELO3C002173; MELO3C004473; MELO3C014153; MELO3C013185; MELO3C023545; MELO3C008835; MELO3C023306; MELO3C023427; MELO3C006657; MELO3C024757; MELO3C003703;
GO:0009792	embryo development ending in birth or egg hatching	BIOLOGICAL_PROCESS	0,010669712	1,25E-04	31	374	596	16127	MELO3C011256; MELO3C010243; MELO3C008285; MELO3C010960; MELO3C002180; MELO3C012361; MELO3C011193; MELO3C009338; MELO3C007433; MELO3C005679; MELO3C020369; MELO3C006949; MELO3C019253; MELO3C022488; MELO3C020860; MELO3C017993; MELO3C011285; MELO3C005421; MELO3C004278; MELO3C025549; MELO3C023201; MELO3C002118; MELO3C024352; MELO3C002717; MELO3C003905; MELO3C022094; MELO3C006280;	MELO3C010584; MELO3C011795; MELO3C012522; MELO3C009592; MELO3C006760; MELO3C002166; MELO3C002045; MELO3C004344; MELO3C019031; MELO3C022562; MELO3C018062; MELO3C026800; MELO3C026245; MELO3C018187; MELO3C019034; MELO3C025275; MELO3C014708; MELO3C015235; MELO3C015599; MELO3C019956; MELO3C006096; MELO3C008151; MELO3C020836; MELO3C008157; MELO3C002173; MELO3C004473; MELO3C014153;

GO:0006099	tricarboxylic acid cycle	BIOLOGICAL_PROCESS	0,029273395	4,00E-04	7	31	620	16470	MELO3C021563; MELO3C022382; MELO3C017560; MELO3C011482; MELO3C002167; MELO3C021247; MELO3C022998	MELO3C012389; MELO3C017938; MELO3C007674; MELO3C014221; MELO3C013153; MELO3C003577; MELO3C025636; MELO3C022343; MELO3C005539; MELO3C017175; MELO3C019711; MELO3C025076; MELO3C018724; MELO3C014824; MELO3C019879; MELO3C002350; MELO3C023506; MELO3C007968; MELO3C021268; MELO3C021545; MELO3C006734; MELO3C005348; MELO3C016050; MELO3C016095; MELO3C005968; MELO3C019300; MELO3C019243;
GO:0005618	cell wall	CELLULAR_COMPONENT	0,030634705	4,34E-04	28	351	599	16150	MELO3C013699; MELO3C012004; MELO3C011256; MELO3C009133; MELO3C012100; MELO3C020049; MELO3C005757; MELO3C016067; MELO3C017478; MELO3C010686; MELO3C009203; MELO3C005089; MELO3C012670; MELO3C021404; MELO3C005201; MELO3C004597; MELO3C009429; MELO3C008879; MELO3C007609; MELO3C017480; MELO3C021782; MELO3C025324; MELO3C017481; MELO3C017242; MELO3C017560; MELO3C023188; MELO3C025582;	MELO3C015914; MELO3C020704; MELO3C007057; MELO3C013055; MELO3C026806; MELO3C005316; MELO3C002047; MELO3C008946; MELO3C003810; MELO3C021595; MELO3C021471; MELO3C019039; MELO3C018862; MELO3C018743; MELO3C008032; MELO3C009120; MELO3C005561; MELO3C012099; MELO3C009488; MELO3C009367; MELO3C012097; MELO3C005560; MELO3C012096; MELO3C004477; MELO3C008159; MELO3C009924; MELO3C010919;
GO:0003878	ATP citrate synthase activity	MOLECULAR_FUNCTION	0,031860458	4,62E-04	3	2	624	16499	MELO3C010675; MELO3C011482; MELO3C002167	MELO3C021268; MELO3C015245
GO:0008340	determination of adult lifespan	BIOLOGICAL_PROCESS	0,032223247	4,81E-04	11	80	616	16421	MELO3C014007; MELO3C011256; MELO3C023201; MELO3C006949; MELO3C008285; MELO3C010960; MELO3C020860; MELO3C016262; MELO3C022094; MELO3C004278; MELO3C011104	MELO3C016329; MELO3C010584; MELO3C012522; MELO3C014221; MELO3C006121; MELO3C005753; MELO3C007214; MELO3C024822; MELO3C008306; MELO3C004945; MELO3C025755; MELO3C025796; MELO3C020783; MELO3C004827; MELO3C025275; MELO3C015199; MELO3C019712; MELO3C022280; MELO3C027174; MELO3C013814; MELO3C011830; MELO3C017627; MELO3C010795; MELO3C009840; MELO3C015928; MELO3C014153; MELO3C022219;
GO:0031018	endocrine pancreas development	BIOLOGICAL_PROCESS	0,032223247	4,78E-04	4	7	623	16494	MELO3C023201; MELO3C017993; MELO3C009338; MELO3C017291	MELO3C014237; MELO3C017184; MELO3C006662; MELO3C017169; MELO3C018512; MELO3C023127; MELO3C017290
GO:0010181	FMN binding	MOLECULAR_FUNCTION	0,057904252	9,44E-04	6	26	621	16475	MELO3C007340; MELO3C011062; MELO3C003541; MELO3C023799; MELO3C016623; MELO3C015514	MELO3C008482; MELO3C013476; MELO3C008481; MELO3C004023; MELO3C009759; MELO3C022683; MELO3C022684; MELO3C008805; MELO3C022681; MELO3C024281; MELO3C018625; MELO3C018626; MELO3C010940; MELO3C017636; MELO3C008075; MELO3C007124; MELO3C006296; MELO3C006011; MELO3C009702; MELO3C021944; MELO3C005229; MELO3C003644; MELO3C025720; MELO3C017461; MELO3C025861; MELO3C007808

GO:0004776	succinate-CoA ligase (GDP-forming) activity	MOLECULAR_FUNCTION	0,076614304	0,001337993	2	0	625	16501	MELO3C022382; MELO3C002167	
GO:0003861	3-isopropylmalate dehydratase activity	MOLECULAR_FUNCTION	0,076614304	0,001337993	2	0	625	16501	MELO3C005518; MELO3C003344	
GO:0040002	collagen and cuticulin-based cuticle development	BIOLOGICAL_PROCESS	0,086570236	0,001530189	3	4	624	16497	MELO3C016707; MELO3C019253; MELO3C012361	MELO3C016321; MELO3C023052; MELO3C008151; MELO3C015126
GO:0048046	apoplast	CELLULAR_COMPONENT	0,08752412	0,001574841	18	203	609	16298	MELO3C012004; MELO3C009038; MELO3C011284; MELO3C024514; MELO3C021247; MELO3C008879; MELO3C007609; MELO3C020780; MELO3C017480; MELO3C021782; MELO3C017481; MELO3C023188; MELO3C015186; MELO3C012604; MELO3C017478; MELO3C009250; MELO3C011107; MELO3C010686	MELO3C011430; MELO3C007058; MELO3C013055; MELO3C007059; MELO3C003137; MELO3C026800; MELO3C001998; MELO3C015470; MELO3C015472; MELO3C010901; MELO3C007061; MELO3C007064; MELO3C007065; MELO3C008274; MELO3C007062; MELO3C007063; MELO3C005561; MELO3C007068; MELO3C009247; MELO3C009367; MELO3C005565; MELO3C010919; MELO3C025840; MELO3C026259; MELO3C019168; MELO3C011329; MELO3C010114;
GO:0004298	threonine-type endopeptidase activity	MOLECULAR_FUNCTION	0,099790014	0,001869478	5	20	622	16481	MELO3C010960; MELO3C011172; MELO3C003173; MELO3C013757; MELO3C006187	MELO3C011880; MELO3C006131; MELO3C007920; MELO3C021745; MELO3C021746; MELO3C000704; MELO3C025735; MELO3C023267; MELO3C025755; MELO3C026800; MELO3C000762; MELO3C006517; MELO3C019011; MELO3C019010; MELO3C019012; MELO3C027069; MELO3C024343; MELO3C010635; MELO3C026360; MELO3C011449
GO:0015631	tubulin binding	MOLECULAR_FUNCTION	0,099790014	0,001869478	5	20	622	16481	MELO3C022488; MELO3C013702; MELO3C002717; MELO3C017221; MELO3C006602	MELO3C004390; MELO3C010584; MELO3C006171; MELO3C018707; MELO3C007036; MELO3C007584; MELO3C022016; MELO3C001970; MELO3C022478; MELO3C006723; MELO3C022166; MELO3C022751; MELO3C024792; MELO3C016297; MELO3C024150; MELO3C017720; MELO3C018910; MELO3C011800; MELO3C019823; MELO3C011830
GO:0000084	mitotic S phase	BIOLOGICAL_PROCESS	0,102607716	0,001954846	9	68	618	16433	MELO3C016083; MELO3C010960; MELO3C003638; MELO3C020860; MELO3C016262; MELO3C020001; MELO3C012361; MELO3C010631; MELO3C004448	MELO3C009313; MELO3C002481; MELO3C014021; MELO3C014020; MELO3C008864; MELO3C004864; MELO3C025879; MELO3C025755; MELO3C026800; MELO3C005912; MELO3C023372; MELO3C010507; MELO3C010828; MELO3C018501; MELO3C012407; MELO3C013814; MELO3C017458; MELO3C006096; MELO3C015926; MELO3C007066; MELO3C007144; MELO3C012492; MELO3C002892; MELO3C025923; MELO3C025646; MELO3C021204; MELO3C019642;

GO:0040010	positive regulation of growth rate	BIOLOGICAL_PROCESS	0,110013724	0,002155258	20	241	607	16260	MELO3C011256; MELO3C010243; MELO3C008285; MELO3C011285; MELO3C009338; MELO3C005421; MELO3C007433; MELO3C026614; MELO3C017291; MELO3C020369; MELO3C023201; MELO3C006949; MELO3C002118; MELO3C024352; MELO3C002717; MELO3C003905; MELO3C017993; MELO3C006280; MELO3C025061; MELO3C013822	MELO3C012522; MELO3C009592; MELO3C006760; MELO3C002045; MELO3C004344; MELO3C018187; MELO3C019034; MELO3C025275; MELO3C016321; MELO3C014708; MELO3C026482; MELO3C019956; MELO3C021808; MELO3C020836; MELO3C004473; MELO3C014153; MELO3C013185; MELO3C004353; MELO3C023545; MELO3C023306; MELO3C006657; MELO3C002738; MELO3C025044; MELO3C017661; MELO3C018512; MELO3C016456; MELO3C015246;
GO:0006094	gluconeogenesis	BIOLOGICAL_PROCESS	0,110013724	0,002165808	7	43	620	16458	MELO3C020780; MELO3C011284; MELO3C012604; MELO3C021604; MELO3C011104; MELO3C022998; MELO3C008879	MELO3C012444; MELO3C012389; MELO3C009351; MELO3C007674; MELO3C007772; MELO3C003491; MELO3C025916; MELO3C004980; MELO3C005333; MELO3C003577; MELO3C003214; MELO3C003215; MELO3C023354; MELO3C005539; MELO3C017175; MELO3C019634; MELO3C014724; MELO3C011710; MELO3C011367; MELO3C013203; MELO3C012375; MELO3C009147; MELO3C011682; MELO3C003265; MELO3C007687; MELO3C004433; MELO3C003266;
GO:0005774	vacuolar membrane	CELLULAR_COMPONENT	0,110013724	0,002147824	14	145	613	16356	MELO3C013489; MELO3C011279; MELO3C010286; MELO3C010991; MELO3C006320; MELO3C026614; MELO3C022448; MELO3C006926; MELO3C026522; MELO3C000065; MELO3C016067; MELO3C012604; MELO3C025061; MELO3C024192	MELO3C014821; MELO3C015914; MELO3C007695; MELO3C011151; MELO3C002042; MELO3C005831; MELO3C026800; MELO3C021595; MELO3C024346; MELO3C025035; MELO3C025310; MELO3C025157; MELO3C016044; MELO3C012405; MELO3C010992; MELO3C013467; MELO3C013102; MELO3C014796; MELO3C005561; MELO3C004075; MELO3C005441; MELO3C007980; MELO3C007100; MELO3C004477; MELO3C009887; MELO3C003783; MELO3C004874;
GO:0006069	ethanol oxidation	BIOLOGICAL_PROCESS	0,115059486	0,00227732	4	12	623	16489	MELO3C023685; MELO3C022399; MELO3C014749; MELO3C026554	MELO3C023687; MELO3C005792; MELO3C004383; MELO3C026553; MELO3C017100; MELO3C017125; MELO3C004430; MELO3C019622; MELO3C002189; MELO3C027151; MELO3C005081; MELO3C025328
GO:0035046	pronuclear migration	BIOLOGICAL_PROCESS	0,117208756	0,002381888	3	5	624	16496	MELO3C019253; MELO3C012361; MELO3C020860	MELO3C022016; MELO3C005064; MELO3C019956; MELO3C006723; MELO3C004458
GO:0051903	S-(hydroxymethyl)glutathione dehydrogenase activity	MOLECULAR_FUNCTION	0,117208756	0,002381888	3	5	624	16496	MELO3C023685; MELO3C026554; MELO3C022399	MELO3C002189; MELO3C005792; MELO3C026553; MELO3C027151; MELO3C026552

GO:0051086	chaperone mediated protein folding independent of cofactor	BIOLOGICAL_PROCESS	0,132668929	0,002892654	4	13	623	16488	MELO3C002117; MELO3C009624; MELO3C022094; MELO3C010705	MELO3C014127; MELO3C015615; MELO3C008567; MELO3C021633; MELO3C003128; MELO3C004458; MELO3C023558; MELO3C004636; MELO3C026888; MELO3C017295; MELO3C023852; MELO3C018683; MELO3C023264
GO:0007018	microtubule-based movement	BIOLOGICAL_PROCESS	0,14661594	0,00328355	9	74	618	16427	MELO3C009203; MELO3C024241; MELO3C007673; MELO3C023342; MELO3C015098; MELO3C005673; MELO3C013429; MELO3C013702; MELO3C008977	MELO3C017936; MELO3C017937; MELO3C005594; MELO3C015839; MELO3C014142; MELO3C004267; MELO3C020741; MELO3C020742; MELO3C005479; MELO3C007217; MELO3C009715; MELO3C005678; MELO3C021238; MELO3C003218; MELO3C023013; MELO3C015272; MELO3C002528; MELO3C010629; MELO3C015273; MELO3C018025; MELO3C017377; MELO3C010988; MELO3C016369; MELO3C010147; MELO3C010787; MELO3C009760; MELO3C004273;
GO:0004807	triose-phosphate isomerase activity	MOLECULAR_FUNCTION	0,16359848	0,003916322	2	1	625	16500	MELO3C020780; MELO3C008879	MELO3C025916
GO:0050625	2-hydroxy-1,4-benzoquinone reductase activity	MOLECULAR_FUNCTION	0,16359848	0,003916322	2	1	625	16500	MELO3C007340; MELO3C016623	MELO3C025861
GO:0004733	pyridoxamine-phosphate oxidase activity	MOLECULAR_FUNCTION	0,16359848	0,003916322	2	1	625	16500	MELO3C011062; MELO3C003541	MELO3C006011
GO:0016328	lateral plasma membrane	CELLULAR_COMPONENT	0,16359848	0,003916322	2	1	625	16500	MELO3C017242; MELO3C022488	MELO3C007829
GO:0000022	mitotic spindle elongation	BIOLOGICAL_PROCESS	0,179478323	0,004445166	4	15	623	16486	MELO3C009338; MELO3C011285; MELO3C006280; MELO3C020369	MELO3C014237; MELO3C007036; MELO3C003342; MELO3C009600; MELO3C025755; MELO3C004807; MELO3C023594; MELO3C024782; MELO3C016981; MELO3C024150; MELO3C024020; MELO3C026580; MELO3C015269; MELO3C017744; MELO3C012667
GO:0005852	eukaryotic translation initiation factor 3 complex	CELLULAR_COMPONENT	0,19261379	0,004831654	3	7	624	16494	MELO3C011193; MELO3C008285; MELO3C003453	MELO3C026327; MELO3C017707; MELO3C009841; MELO3C019434; MELO3C015553; MELO3C022038; MELO3C007050
GO:0019773	proteasome core complex, alpha-subunit complex	CELLULAR_COMPONENT	0,19261379	0,004831654	3	7	624	16494	MELO3C003173; MELO3C010960; MELO3C013757	MELO3C026800; MELO3C024343; MELO3C007920; MELO3C021745; MELO3C021746; MELO3C026360; MELO3C025735
GO:0009825	multidimensional cell growth	BIOLOGICAL_PROCESS	0,21338209	0,00539779	4	16	623	16485	MELO3C012004; MELO3C007325; MELO3C017242; MELO3C007207	MELO3C012114; MELO3C002081; MELO3C005631; MELO3C007324; MELO3C021737; MELO3C001364; MELO3C002553; MELO3C024898; MELO3C020643; MELO3C023374; MELO3C015782; MELO3C011913; MELO3C015783; MELO3C015784; MELO3C015785; MELO3C011732
GO:0009846	pollen germination	BIOLOGICAL_PROCESS	0,246779923	0,006477712	4	17	623	16484	MELO3C008285; MELO3C004551; MELO3C019522; MELO3C013702	MELO3C015989; MELO3C014698; MELO3C005099; MELO3C003581; MELO3C021702; MELO3C009734; MELO3C000736; MELO3C022308; MELO3C004336; MELO3C006326; MELO3C024874; MELO3C020044; MELO3C012924; MELO3C019825; MELO3C015654; MELO3C015689; MELO3C024093

GO:0042450	arginine biosynthetic process via ornithine	BIOLOGICAL_PROCESS	0,267436664	0,007642665	2	2	625	16499	MELO3C011085; MELO3C011208	MELO3C023629; MELO3C003523
GO:0018279	protein N-linked glycosylation via asparagine	BIOLOGICAL_PROCESS	0,267436664	0,007321952	7	55	620	16446	MELO3C003812; MELO3C023310; MELO3C011944; MELO3C025637; MELO3C021279; MELO3C024447; MELO3C013822	MELO3C009473; MELO3C007374; MELO3C002165; MELO3C002166; MELO3C007137; MELO3C021632; MELO3C009914; MELO3C009912; MELO3C026524; MELO3C023850; MELO3C026763; MELO3C020220; MELO3C018343; MELO3C010625; MELO3C017413; MELO3C026482; MELO3C017019; MELO3C004196; MELO3C015929; MELO3C024710; MELO3C017661; MELO3C024194; MELO3C010319; MELO3C015246; MELO3C016018; MELO3C013830; MELO3C014202;
GO:0006272	leading strand elongation	BIOLOGICAL_PROCESS	0,267436664	0,007642665	2	2	625	16499	MELO3C010631; MELO3C020860	MELO3C014021; MELO3C010507
GO:0004634	phosphopyruvate hydratase activity	MOLECULAR_FUNCTION	0,267436664	0,007642665	2	2	625	16499	MELO3C020579; MELO3C024514	MELO3C017268; MELO3C026748
GO:0004133	glycogen debranching enzyme activity	MOLECULAR_FUNCTION	0,267436664	0,007642665	2	2	625	16499	MELO3C015861; MELO3C019135	MELO3C017391; MELO3C020949
GO:0008541	proteasome regulatory particle, lid subcomplex	CELLULAR_COMPONENT	0,267436664	0,007642665	2	2	625	16499	MELO3C016262; MELO3C011193	MELO3C025923; MELO3C013814
GO:0000015	phosphopyruvate hydratase complex	CELLULAR_COMPONENT	0,267436664	0,007642665	2	2	625	16499	MELO3C020579; MELO3C024514	MELO3C017268; MELO3C026748
GO:0034515	proteasome storage granule	CELLULAR_COMPONENT	0,285040264	0,008387087	3	9	624	16492	MELO3C016262; MELO3C011193; MELO3C010960	MELO3C025755; MELO3C026800; MELO3C020453; MELO3C018764; MELO3C021746; MELO3C010635; MELO3C011449; MELO3C013814; MELO3C025923
GO:0030170	pyridoxal phosphate binding	MOLECULAR_FUNCTION	0,330546323	0,010250854	11	123	616	16378	MELO3C018948; MELO3C023373; MELO3C000251; MELO3C020927; MELO3C011284; MELO3C026175; MELO3C001121; MELO3C011107; MELO3C010686; MELO3C020444; MELO3C001323	MELO3C005392; MELO3C013732; MELO3C010464; MELO3C020429; MELO3C010461; MELO3C004980; MELO3C002561; MELO3C023659; MELO3C007698; MELO3C009117; MELO3C017490; MELO3C026404; MELO3C022321; MELO3C024500; MELO3C011959; MELO3C016200; MELO3C016448; MELO3C011960; MELO3C013583; MELO3C004355; MELO3C022699; MELO3C018082; MELO3C026534; MELO3C019443; MELO3C017386; MELO3C019203; MELO3C010754;
GO:0005509	calcium ion binding	MOLECULAR_FUNCTION	0,358334546	0,011491889	16	211	611	16290	MELO3C014016; MELO3C014588; MELO3C004194; MELO3C010794; MELO3C013892; MELO3C014150; MELO3C006158; MELO3C005757; MELO3C006759; MELO3C019002; MELO3C022494; MELO3C019820; MELO3C017844; MELO3C013702; MELO3C014658; MELO3C012457	MELO3C003372; MELO3C004465; MELO3C008705; MELO3C024866; MELO3C025712; MELO3C023415; MELO3C005319; MELO3C002967; MELO3C019035; MELO3C019036; MELO3C020263; MELO3C015597; MELO3C016569; MELO3C010348; MELO3C020719; MELO3C014279; MELO3C013982; MELO3C023542; MELO3C007507; MELO3C020277; MELO3C016330; MELO3C016333; MELO3C018876; MELO3C018877; MELO3C013504; MELO3C018517; MELO3C018879;

GO:0005982	starch metabolic process	BIOLOGICAL_PROCESS	0,376688631	0,012200119	4	21	623	16480	MELO3C003812; MELO3C005293; MELO3C011104; MELO3C019135	MELO3C009960; MELO3C014105; MELO3C011972; MELO3C005396; MELO3C006585; MELO3C006552; MELO3C011682; MELO3C020949; MELO3C007155; MELO3C012071; MELO3C005795; MELO3C002455; MELO3C023105; MELO3C021412; MELO3C025149; MELO3C026536; MELO3C024754; MELO3C024175; MELO3C022275; MELO3C017942; MELO3C017735
GO:0016882	cyclo-ligase activity	MOLECULAR_FUNCTION	0,37679878	0,012429782	2	3	625	16498	MELO3C016483; MELO3C008332	MELO3C005781; MELO3C017138; MELO3C017137
GO:0019843	rRNA binding	MOLECULAR_FUNCTION	0,37679878	0,012522737	8	77	619	16424	MELO3C024850; MELO3C010630; MELO3C005759; MELO3C013245; MELO3C011847; MELO3C009091; MELO3C012967; MELO3C008801	MELO3C010584; MELO3C011276; MELO3C011310; MELO3C004020; MELO3C003890; MELO3C009795; MELO3C006682; MELO3C006088; MELO3C012480; MELO3C012084; MELO3C006245; MELO3C020945; MELO3C021312; MELO3C022601; MELO3C001556; MELO3C022485; MELO3C003811; MELO3C019631; MELO3C025474; MELO3C019879; MELO3C003061; MELO3C025609; MELO3C005844; MELO3C005800; MELO3C004995; MELO3C003986; MELO3C025845;
GO:0008878	glucose-1-phosphate adenylyltransferase activity	MOLECULAR_FUNCTION	0,37679878	0,012429782	2	3	625	16498	MELO3C003812; MELO3C023310	MELO3C006552; MELO3C024175; MELO3C021412
GO:0019781	NEDD8 activating enzyme activity	MOLECULAR_FUNCTION	0,37679878	0,012429782	2	3	625	16498	MELO3C011193; MELO3C006555	MELO3C008213; MELO3C014386; MELO3C013230
GO:0004069	L-aspartate:2-oxoglutarate aminotransferase activity	MOLECULAR_FUNCTION	0,384072065	0,013141879	3	11	624	16490	MELO3C023373; MELO3C001121; MELO3C011284	MELO3C015944; MELO3C010464; MELO3C008136; MELO3C010461; MELO3C018037; MELO3C004980; MELO3C006840; MELO3C005597; MELO3C003577; MELO3C017998; MELO3C026051
GO:0051087	chaperone binding	MOLECULAR_FUNCTION	0,384072065	0,013141879	3	11	624	16490	MELO3C005757; MELO3C002717; MELO3C022488	MELO3C004390; MELO3C006948; MELO3C009561; MELO3C010013; MELO3C014179; MELO3C011373; MELO3C019156; MELO3C022725; MELO3C009611; MELO3C022478; MELO3C011830
GO:0009664	plant-type cell wall organization	BIOLOGICAL_PROCESS	0,387087609	0,013315355	5	34	622	16467	MELO3C012004; MELO3C021999; MELO3C020626; MELO3C017242; MELO3C010524	MELO3C010062; MELO3C021619; MELO3C011350; MELO3C020005; MELO3C003134; MELO3C005613; MELO3C001993; MELO3C017181; MELO3C024488; MELO3C025996; MELO3C024487; MELO3C016062; MELO3C026188; MELO3C020143; MELO3C003916; MELO3C015695; MELO3C025095; MELO3C012108; MELO3C011732; MELO3C016517; MELO3C016916; MELO3C014013; MELO3C025907; MELO3C008552; MELO3C020810; MELO3C005962; MELO3C006318;

GO:0005978	glycogen biosynthetic process	BIOLOGICAL_PROCESS	0,403293101	0,014009997	4	22	623	16479	MELO3C003812; MELO3C005293; MELO3C023310; MELO3C020244	MELO3C011991; MELO3C013146; MELO3C004270; MELO3C005396; MELO3C009445; MELO3C006552; MELO3C009861; MELO3C007155; MELO3C008045; MELO3C005795; MELO3C002455; MELO3C021412; MELO3C008407; MELO3C008614; MELO3C021249; MELO3C026536; MELO3C025521; MELO3C024175; MELO3C012925; MELO3C018534; MELO3C010862; MELO3C011346
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	BIOLOGICAL_PROCESS	0,425423227	0,015219417	8	80	619	16421	MELO3C016083; MELO3C010960; MELO3C005918; MELO3C016262; MELO3C012361; MELO3C011193; MELO3C015764; MELO3C005757	MELO3C014542; MELO3C002481; MELO3C022725; MELO3C007137; MELO3C002401; MELO3C025755; MELO3C026800; MELO3C005912; MELO3C023372; MELO3C025232; MELO3C010828; MELO3C025152; MELO3C018501; MELO3C012407; MELO3C013814; MELO3C017338; MELO3C011710; MELO3C006173; MELO3C007383; MELO3C003464; MELO3C006972; MELO3C025923; MELO3C008916; MELO3C019642; MELO3C026177; MELO3C010635; MELO3C011449;
GO:0006351	transcription, DNA-templated	BIOLOGICAL_PROCESS	0,432026982	0,015592845	43	1606	584	14895	MELO3C011256; MELO3C014722; MELO3C007691; MELO3C012242; MELO3C011110; MELO3C009653; MELO3C020848; MELO3C011193; MELO3C020701; MELO3C011172; MELO3C008847; MELO3C002644; MELO3C016083; MELO3C023412; MELO3C020860; MELO3C016660; MELO3C011759; MELO3C023195; MELO3C007181; MELO3C016623; MELO3C009188; MELO3C011003; MELO3C007340; MELO3C011167; MELO3C010057; MELO3C002292; MELO3C006870;	MELO3C007971; MELO3C014266; MELO3C005791; MELO3C014263; MELO3C007974; MELO3C014261; MELO3C006648; MELO3C012081; MELO3C000099; MELO3C016444; MELO3C017775; MELO3C017308; MELO3C021809; MELO3C021804; MELO3C003140; MELO3C007500; MELO3C002299; MELO3C012094; MELO3C005327; MELO3C012091; MELO3C007989; MELO3C007988; MELO3C027103; MELO3C027102; MELO3C017782; MELO3C027101; MELO3C017303;
GO:0005506	iron ion binding	MOLECULAR_FUNCTION	0,432026982	0,015575442	4	320	623	16181	MELO3C005103; MELO3C007611; MELO3C013868; MELO3C006943	MELO3C007174; MELO3C012522; MELO3C007175; MELO3C021914; MELO3C012088; MELO3C007058; MELO3C020028; MELO3C006644; MELO3C004221; MELO3C004584; MELO3C007059; MELO3C025712; MELO3C026802; MELO3C020385; MELO3C023893; MELO3C023530; MELO3C000772; MELO3C015591; MELO3C026487; MELO3C000770; MELO3C015592; MELO3C015593; MELO3C015595; MELO3C015596; MELO3C026484; MELO3C016686; MELO3C016687;

GO:0003924	GTPase activity	MOLECULAR_FUNCTION	0,434527948	0,015729102	9	97	618	16404	MELO3C011234; MELO3C002118; MELO3C024544; MELO3C025885; MELO3C009203; MELO3C007673; MELO3C015098; MELO3C005673; MELO3C002687	MELO3C011312; MELO3C003370; MELO3C021514; MELO3C023931; MELO3C026889; MELO3C018587; MELO3C015755; MELO3C015756; MELO3C003261; MELO3C004074; MELO3C014156; MELO3C007220; MELO3C005565; MELO3C013185; MELO3C013183; MELO3C003786; MELO3C013180; MELO3C000761; MELO3C026259; MELO3C016695; MELO3C006063; MELO3C019819; MELO3C018848; MELO3C013158; MELO3C014400; MELO3C004440; MELO3C021977;
GO:0005768	endosome	CELLULAR_COMPONENT	0,437568879	0,016070745	7	65	620	16436	MELO3C006926; MELO3C010243; MELO3C010772; MELO3C004391; MELO3C025783; MELO3C026614; MELO3C018758	MELO3C014821; MELO3C011795; MELO3C009473; MELO3C014542; MELO3C005199; MELO3C007457; MELO3C012481; MELO3C014180; MELO3C004945; MELO3C025310; MELO3C004827; MELO3C026440; MELO3C013816; MELO3C012728; MELO3C015433; MELO3C006171; MELO3C010795; MELO3C023828; MELO3C024558; MELO3C005328; MELO3C004874; MELO3C018195; MELO3C016491; MELO3C026971; MELO3C025682; MELO3C026096; MELO3C022490;
GO:0005525	GTP binding	MOLECULAR_FUNCTION	0,448993888	0,016680446	17	237	610	16264	MELO3C011234; MELO3C009038; MELO3C009203; MELO3C007673; MELO3C005673; MELO3C002167; MELO3C021279; MELO3C002687; MELO3C009966; MELO3C002118; MELO3C024544; MELO3C025885; MELO3C022382; MELO3C002816; MELO3C015098; MELO3C011704; MELO3C010569	MELO3C011312; MELO3C003370; MELO3C012760; MELO3C021114; MELO3C012529; MELO3C011684; MELO3C004471; MELO3C003261; MELO3C014156; MELO3C020959; MELO3C015929; MELO3C005565; MELO3C006896; MELO3C013185; MELO3C007742; MELO3C013183; MELO3C021803; MELO3C018080; MELO3C013180; MELO3C000761; MELO3C026259; MELO3C016695; MELO3C019844; MELO3C006063; MELO3C019819; MELO3C018848; MELO3C013158;
GO:0009098	leucine biosynthetic process	BIOLOGICAL_PROCESS	0,463366121	0,018195262	2	4	625	16497	MELO3C005518; MELO3C003344	MELO3C017853; MELO3C024817; MELO3C014221; MELO3C020296
GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	BIOLOGICAL_PROCESS	0,463366121	0,018118465	4	24	623	16477	MELO3C016083; MELO3C010960; MELO3C016262; MELO3C012361	MELO3C011983; MELO3C002481; MELO3C011470; MELO3C021746; MELO3C014086; MELO3C000704; MELO3C004136; MELO3C021715; MELO3C025923; MELO3C025417; MELO3C005738; MELO3C023476; MELO3C026239; MELO3C003316; MELO3C025755; MELO3C026800; MELO3C005912; MELO3C020453; MELO3C018099; MELO3C019642; MELO3C019587; MELO3C019731; MELO3C013814; MELO3C016699
GO:0006103	2-oxoglutarate metabolic process	BIOLOGICAL_PROCESS	0,463366121	0,018195262	2	4	625	16497	MELO3C021563; MELO3C011284	MELO3C025076; MELO3C004980; MELO3C003577; MELO3C019166

GO:0016762	xyloglucan:xyloglucosyl transferase activity	MOLECULAR_FUNCTION	0,463366121	0,018118465	4	24	623	16477	MELO3C012004; MELO3C017480; MELO3C017481; MELO3C017478	MELO3C014469; MELO3C014468; MELO3C014467; MELO3C014466; MELO3C014465; MELO3C002480; MELO3C009367; MELO3C004087; MELO3C003441; MELO3C024704; MELO3C005245; MELO3C021686; MELO3C004941; MELO3C018292; MELO3C026945; MELO3C001951; MELO3C026755; MELO3C017482; MELO3C021685; MELO3C018033; MELO3C011706; MELO3C017476; MELO3C018785; MELO3C017479
GO:0004090	carbonyl reductase (NADPH) activity	MOLECULAR_FUNCTION	0,463366121	0,018195262	2	4	625	16497	MELO3C002872; MELO3C001948	MELO3C019918; MELO3C014897; MELO3C021704; MELO3C020605
GO:0009331	glycerol-3-phosphate dehydrogenase complex	CELLULAR_COMPONENT	0,463366121	0,018195262	2	4	625	16497	MELO3C021604; MELO3C019820	MELO3C026337; MELO3C020158; MELO3C020157; MELO3C005116
GO:0009629	response to gravity	BIOLOGICAL_PROCESS	0,483810141	0,019151672	3	13	624	16488	MELO3C005293; MELO3C008847; MELO3C025282	MELO3C008088; MELO3C005396; MELO3C002781; MELO3C002354; MELO3C000009; MELO3C021982; MELO3C025310; MELO3C017043; MELO3C004827; MELO3C024155; MELO3C026110; MELO3C013815; MELO3C017414
GO:0004022	alcohol dehydrogenase (NAD) activity	MOLECULAR_FUNCTION	0,483810141	0,019151672	3	13	624	16488	MELO3C023685; MELO3C026554; MELO3C022399	MELO3C014897; MELO3C005792; MELO3C011043; MELO3C005482; MELO3C003251; MELO3C005521; MELO3C008767; MELO3C007314; MELO3C002189; MELO3C005129; MELO3C004714; MELO3C026553; MELO3C027151
GO:0004497	monooxygenase activity	MOLECULAR_FUNCTION	0,49629696	0,020391656	3	265	624	16236	MELO3C016879; MELO3C024396; MELO3C015590	MELO3C016329; MELO3C018628; MELO3C014027; MELO3C012088; MELO3C002043; MELO3C021118; MELO3C013050; MELO3C000537; MELO3C007856; MELO3C000655; MELO3C002720; MELO3C026802; MELO3C003933; MELO3C003932; MELO3C023530; MELO3C023533; MELO3C003934; MELO3C015591; MELO3C026487; MELO3C015592; MELO3C015593; MELO3C015595; MELO3C015596; MELO3C026484; MELO3C016685; MELO3C018623; MELO3C011799;
GO:0046658	anchored component of plasma membrane	CELLULAR_COMPONENT	0,49629696	0,020424758	4	25	623	16476	MELO3C021119; MELO3C017242; MELO3C024192; MELO3C010601	MELO3C002461; MELO3C005751; MELO3C020643; MELO3C022861; MELO3C003659; MELO3C018862; MELO3C014428; MELO3C018888; MELO3C010006; MELO3C013347; MELO3C011860; MELO3C005561; MELO3C013101; MELO3C005361; MELO3C013264; MELO3C012392; MELO3C020855; MELO3C024938; MELO3C006813; MELO3C004636; MELO3C025700; MELO3C002219; MELO3C018774; MELO3C012714; MELO3C016635

GO:0019083	viral transcription	BIOLOGICAL_PROCESS	0,526860835	0,022082651	6	54	621	16447	MELO3C023201; MELO3C017993; MELO3C009338; MELO3C005421; MELO3C024352; MELO3C017291	MELO3C010981; MELO3C016968; MELO3C008106; MELO3C021758; MELO3C008589; MELO3C008105; MELO3C002888; MELO3C022087; MELO3C020022; MELO3C017775; MELO3C017579; MELO3C015712; MELO3C014237; MELO3C014358; MELO3C008157; MELO3C002173; MELO3C014155; MELO3C003222; MELO3C020474; MELO3C017184; MELO3C026776; MELO3C003707; MELO3C018512; MELO3C009890; MELO3C015937; MELO3C006662; MELO3C005694;
GO:1903050	regulation of proteolysis involved in cellular protein catabolic process	BIOLOGICAL_PROCESS	0,554297243	0,023649485	5	40	622	16461	MELO3C011193; MELO3C016083; MELO3C010960; MELO3C016262; MELO3C012361	MELO3C013750; MELO3C014684; MELO3C002481; MELO3C004484; MELO3C014086; MELO3C022725; MELO3C025417; MELO3C005733; MELO3C025413; MELO3C023476; MELO3C025755; MELO3C024685; MELO3C026800; MELO3C005615; MELO3C005912; MELO3C024402; MELO3C025232; MELO3C016464; MELO3C026580; MELO3C012407; MELO3C013814; MELO3C017338; MELO3C013359; MELO3C011345; MELO3C011983; MELO3C014573; MELO3C021746;
GO:0051287	NAD binding	MOLECULAR_FUNCTION	0,554297243	0,023760625	6	55	621	16446	MELO3C010427; MELO3C021563; MELO3C021604; MELO3C019633; MELO3C010727; MELO3C008219	MELO3C006085; MELO3C021919; MELO3C011431; MELO3C006164; MELO3C014221; MELO3C009956; MELO3C024942; MELO3C005116; MELO3C023217; MELO3C017213; MELO3C025076; MELO3C025791; MELO3C027054; MELO3C017853; MELO3C015407; MELO3C014752; MELO3C022537; MELO3C022538; MELO3C020158; MELO3C020157; MELO3C026337; MELO3C024039; MELO3C002813; MELO3C027223; MELO3C013505; MELO3C011129; MELO3C019405;
GO:0006123	mitochondrial electron transport, cytochrome c to oxygen	BIOLOGICAL_PROCESS	0,561936534	0,02486129	2	5	625	16496	MELO3C004105; MELO3C011044	MELO3C015922; MELO3C003366; MELO3C016120; MELO3C018157; MELO3C006242
GO:0032012	regulation of ARF protein signal transduction	BIOLOGICAL_PROCESS	0,561936534	0,02486129	2	5	625	16496	MELO3C004551; MELO3C006224	MELO3C023883; MELO3C012923; MELO3C012924; MELO3C006181; MELO3C015692
GO:0005086	ARF guanyl-nucleotide exchange factor activity	MOLECULAR_FUNCTION	0,561936534	0,02486129	2	5	625	16496	MELO3C004551; MELO3C006224	MELO3C023883; MELO3C012923; MELO3C012924; MELO3C006181; MELO3C015692
GO:0005751	mitochondrial respiratory chain complex IV	CELLULAR_COMPONENT	0,561936534	0,02486129	2	5	625	16496	MELO3C004105; MELO3C011044	MELO3C015922; MELO3C003366; MELO3C016926; MELO3C014946; MELO3C016120
GO:0043601	nuclear replisome	CELLULAR_COMPONENT	0,561936534	0,02486129	2	5	625	16496	MELO3C020001; MELO3C020860	MELO3C022319; MELO3C017228; MELO3C027184; MELO3C024596; MELO3C001937
GO:0033179	proton-transporting V-type ATPase, V0 domain	CELLULAR_COMPONENT	0,561936534	0,02486129	2	5	625	16496	MELO3C000065; MELO3C010991	MELO3C010992; MELO3C009887; MELO3C013122; MELO3C011225; MELO3C003677

GO:0005960	glycine cleavage complex	CELLULAR_COMPONENT	0,561936534	0,02486129	2	5	625	16496	MELO3C021247; MELO3C021742	MELO3C003386; MELO3C003734; MELO3C002444; MELO3C006734; MELO3C010754
GO:0008237	metallopeptidase activity	MOLECULAR_FUNCTION	0,569490972	0,025353183	10	114	617	16387	MELO3C012356; MELO3C008052; MELO3C009148; MELO3C018441; MELO3C016890; MELO3C016067; MELO3C011193; MELO3C004134; MELO3C006846; MELO3C008847	MELO3C006089; MELO3C014386; MELO3C003139; MELO3C022843; MELO3C019273; MELO3C017011; MELO3C026003; MELO3C010623; MELO3C016738; MELO3C000768; MELO3C005965; MELO3C026539; MELO3C023149; MELO3C005688; MELO3C015483; MELO3C004918; MELO3C023023; MELO3C004919; MELO3C013276; MELO3C014882; MELO3C003474; MELO3C006466; MELO3C025899; MELO3C026225; MELO3C000673; MELO3C004605; MELO3C026224;
GO:0005351	sugar:proton symporter activity	MOLECULAR_FUNCTION	0,571343664	0,025761262	5	41	622	16460	MELO3C013489; MELO3C011675; MELO3C025345; MELO3C026522; MELO3C004576	MELO3C008582; MELO3C008581; MELO3C014485; MELO3C020608; MELO3C000836; MELO3C003830; MELO3C024689; MELO3C000832; MELO3C007756; MELO3C018040; MELO3C019030; MELO3C007815; MELO3C021377; MELO3C017055; MELO3C015350; MELO3C009081; MELO3C010946; MELO3C017699; MELO3C017655; MELO3C000070; MELO3C017656; MELO3C013415; MELO3C011676; MELO3C012554; MELO3C006595; MELO3C013485; MELO3C007980;
GO:0042817	pyridoxal metabolic process	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C003541	
GO:0048482	plant ovule morphogenesis	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C010913	
GO:0015680	intracellular copper ion transport	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C014007	
GO:0046087	cytidine metabolic process	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C015459	
GO:0006898	receptor-mediated endocytosis	BIOLOGICAL_PROCESS	0,583238357	0,03304935	10	125	617	16376	MELO3C010243; MELO3C002118; MELO3C008285; MELO3C002717; MELO3C003905; MELO3C009338; MELO3C025549; MELO3C026614; MELO3C013822; MELO3C018758	MELO3C011795; MELO3C016968; MELO3C006760; MELO3C011151; MELO3C006121; MELO3C002045; MELO3C008306; MELO3C022166; MELO3C026888; MELO3C025310; MELO3C015235; MELO3C015512; MELO3C021808; MELO3C017707; MELO3C013982; MELO3C008151; MELO3C020836; MELO3C004074; MELO3C014153; MELO3C023545; MELO3C005963; MELO3C023306; MELO3C023427; MELO3C006657; MELO3C017020; MELO3C007903; MELO3C016297;
GO:0006616	SRP-dependent cotranslational protein targeting to membrane, translocation	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C005757	
GO:0030950	establishment or maintenance of actin cytoskeleton polarity	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C026614	
GO:0046292	formaldehyde metabolic process	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C022399	
GO:0010812	negative regulation of cell-substrate adhesion	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C022488	

GO:0007409	axonogenesis	BIOLOGICAL_PROCESS	0,583238357	0,030460745	7	75	620	16426	MELO3C007673; MELO3C012361; MELO3C018841; MELO3C011193; MELO3C002609; MELO3C009624; MELO3C020978	MELO3C006283; MELO3C003092; MELO3C011354; MELO3C014785; MELO3C014383; MELO3C007015; MELO3C022407; MELO3C002124; MELO3C022842; MELO3C021633; MELO3C008306; MELO3C023852; MELO3C024269; MELO3C018025; MELO3C019315; MELO3C025790; MELO3C013739; MELO3C017734; MELO3C012526; MELO3C004594; MELO3C003341; MELO3C022219; MELO3C005123; MELO3C020439; MELO3C004635; MELO3C021683; MELO3C026613;
GO:0006420	arginyl-tRNA aminoacylation	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C015422	
GO:0006121	mitochondrial electron transport, succinate to ubiquinone	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C017560	
GO:0006127	glycerophosphate shuttle	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C019820	
GO:0019563	glycerol catabolic process	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C019820	
GO:0008643	carbohydrate transport	BIOLOGICAL_PROCESS	0,583238357	0,027238541	8	90	619	16411	MELO3C013489; MELO3C025345; MELO3C026522; MELO3C012076; MELO3C013591; MELO3C007325; MELO3C004576; MELO3C004533	MELO3C008582; MELO3C008581; MELO3C004222; MELO3C005631; MELO3C021558; MELO3C011150; MELO3C007818; MELO3C016280; MELO3C022166; MELO3C019030; MELO3C002966; MELO3C007815; MELO3C015350; MELO3C026441; MELO3C027013; MELO3C010946; MELO3C017655; MELO3C010269; MELO3C017656; MELO3C011115; MELO3C011875; MELO3C008674; MELO3C004591; MELO3C007980; MELO3C013186; MELO3C009724; MELO3C004111;
GO:0007310	oocyte dorsal/ventral axis specification	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C011193	
GO:0006470	protein dephosphorylation	BIOLOGICAL_PROCESS	0,583238357	0,027068299	7	73	620	16428	MELO3C004439; MELO3C012378; MELO3C021385; MELO3C007580; MELO3C011704; MELO3C006736; MELO3C013745	MELO3C020829; MELO3C013336; MELO3C018507; MELO3C008426; MELO3C004587; MELO3C003574; MELO3C024667; MELO3C002645; MELO3C026602; MELO3C023893; MELO3C026166; MELO3C018500; MELO3C011713; MELO3C026163; MELO3C010744; MELO3C009960; MELO3C015408; MELO3C013860; MELO3C016939; MELO3C009840; MELO3C006852; MELO3C021405; MELO3C023626; MELO3C007940; MELO3C020114; MELO3C003222; MELO3C008478;
GO:0008347	glial cell migration	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C011193	
GO:0031115	negative regulation of microtubule polymerization	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C022488	
GO:0042149	cellular response to glucose starvation	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C005757	
GO:0007229	integrin-mediated signaling pathway	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C007690	

GO:0040035	hermaphrodite genitalia development	BIOLOGICAL_PROCESS	0,583238357	0,035053154	10	127	617	16374	MELO3C011256; MELO3C008285; MELO3C019253; MELO3C022488; MELO3C016707; MELO3C012361; MELO3C002717; MELO3C011193; MELO3C022094; MELO3C026614	MELO3C009592; MELO3C006760; MELO3C006121; MELO3C004344; MELO3C019031; MELO3C022166; MELO3C024586; MELO3C026888; MELO3C016321; MELO3C014708; MELO3C015235; MELO3C019956; MELO3C021808; MELO3C015647; MELO3C008151; MELO3C008157; MELO3C002173; MELO3C000924; MELO3C006498; MELO3C004873; MELO3C007466; MELO3C008835; MELO3C023823; MELO3C023427; MELO3C006657; MELO3C024757; MELO3C007903;
GO:0006084	acetyl-CoA metabolic process	BIOLOGICAL_PROCESS	0,583238357	0,030564468	3	16	624	16485	MELO3C021247; MELO3C011482; MELO3C004278	MELO3C013864; MELO3C012235; MELO3C014017; MELO3C006661; MELO3C003131; MELO3C025919; MELO3C014031; MELO3C007940; MELO3C003445; MELO3C021268; MELO3C013081; MELO3C006734; MELO3C022343; MELO3C006529; MELO3C019872; MELO3C015245
GO:0046827	positive regulation of protein export from nucleus	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C007207	
GO:0010342	endosperm cellularization	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C006602	
GO:0060904	regulation of protein folding in endoplasmic reticulum	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C005757	
GO:0010312	detoxification of zinc ion	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C022448	
GO:0048759	xylem vessel member cell differentiation	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C011484	
GO:0001556	oocyte maturation	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C012361	
GO:0034333	adherens junction assembly	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C022488	
GO:0010266	response to vitamin B1	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C020562	
GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C005757	
GO:0010299	detoxification of cobalt ion	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C022448	
GO:0048730	epidermis morphogenesis	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C006929	
GO:0015966	diadenosine tetraphosphate biosynthetic process	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C003905	
GO:0034484	raffinose catabolic process	BIOLOGICAL_PROCESS	0,583238357	0,036606726	1	0	626	16501	MELO3C023110	
GO:0004301	epoxide hydrolase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C017946	
GO:0030942	endoplasmic reticulum signal peptide binding	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C002757	
GO:0050311	sulfite reductase (ferredoxin) activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C015186	
GO:0016532	superoxide dismutase copper chaperone activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C014007	
GO:0050201	fucokinase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C006005	
GO:0008908	isochorismatase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C011747	
GO:0004637	phosphoribosylamine-glycine ligase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C016483	
GO:0052636	arabinosyltransferase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C010524	
GO:0035259	glucocorticoid receptor binding	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C012231	
GO:0016859	cis-trans isomerase activity	MOLECULAR_FUNCTION	0,583238357	0,03131995	6	59	621	16442	MELO3C014557; MELO3C021108; MELO3C025848; MELO3C023224; MELO3C020806; MELO3C007001	MELO3C011036; MELO3C012489; MELO3C013896; MELO3C017816; MELO3C010261; MELO3C013375; MELO3C015916; MELO3C006285; MELO3C008222; MELO3C021912; MELO3C009952; MELO3C002126; MELO3C007778; MELO3C026524; MELO3C003338; MELO3C019631; MELO3C024662; MELO3C017776; MELO3C025192; MELO3C016887; MELO3C011236; MELO3C008553; MELO3C006176; MELO3C004752; MELO3C022335; MELO3C023984; MELO3C016495;
GO:0050347	trans-octaprenyltranstransferase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C016140	
GO:0019706	protein-cysteine S-palmitoyltransferase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C010243	
GO:0047115	trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C019948	

GO:0005319	lipid transporter activity	MOLECULAR_FUNCTION	0,583238357	0,031398208	4	29	623	16472	MELO3C006409; MELO3C015704; MELO3C012196; MELO3C020394	MELO3C016505; MELO3C012044; MELO3C011330; MELO3C002064; MELO3C014000; MELO3C020821; MELO3C002065; MELO3C008403; MELO3C002188; MELO3C021055; MELO3C023696; MELO3C025675; MELO3C000372; MELO3C011559; MELO3C012726; MELO3C012236; MELO3C000868; MELO3C022654; MELO3C024378; MELO3C025304; MELO3C025224; MELO3C017660; MELO3C018077; MELO3C017661; MELO3C019921; MELO3C018710; MELO3C017027;
GO:0005302	L-tyrosine transmembrane transporter activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C006926	
GO:0004334	fumarylacetoacetase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C007433	
GO:0005354	galactose transmembrane transporter activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C004576	
GO:0052591	sn-glycerol-3-phosphate:ubiquinone-8 oxidoreductase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C019820	
GO:0005125	cytokine activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C011104	
GO:0051499	D-aminoacyl-tRNA deacylase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C011402	
GO:0016002	sulfite reductase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C015186	
GO:0004364	glutathione transferase activity	MOLECULAR_FUNCTION	0,583238357	0,030564468	3	16	624	16485	MELO3C016031; MELO3C016033; MELO3C023224	MELO3C011334; MELO3C009300; MELO3C009299; MELO3C020204; MELO3C022821; MELO3C017341; MELO3C001978; MELO3C016032; MELO3C016166; MELO3C016034; MELO3C023220; MELO3C016167; MELO3C016168; MELO3C016169; MELO3C011714; MELO3C016349
GO:0004126	cytidine deaminase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C015459	
GO:0004369	glycerol-3-phosphate oxidase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C019820	
GO:0005153	interleukin-8 receptor binding	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C005679	
GO:0015088	copper uptake transmembrane transporter activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C018494	
GO:0004073	aspartate-semialdehyde dehydrogenase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C010427	
GO:0030331	estrogen receptor binding	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C012231	
GO:0004177	aminopeptidase activity	MOLECULAR_FUNCTION	0,583238357	0,028388178	4	28	623	16473	MELO3C012356; MELO3C004134; MELO3C009148; MELO3C016890	MELO3C005470; MELO3C023479; MELO3C006206; MELO3C026225; MELO3C023478; MELO3C026003; MELO3C026224; MELO3C015673; MELO3C012427; MELO3C004172; MELO3C001380; MELO3C002074; MELO3C006077; MELO3C004255; MELO3C013085; MELO3C004135; MELO3C000768; MELO3C020895; MELO3C020334; MELO3C005688; MELO3C007807; MELO3C016891; MELO3C023023; MELO3C018038; MELO3C016894; MELO3C016895; MELO3C023481;
GO:0008893	guanosine-3',5'-bis(diphosphate) 3'-diphosphatase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C006759	
GO:0030797	24-methylenesterol C-methyltransferase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C003726	
GO:0047705	bilirubin oxidase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C005201	
GO:0032442	phenylcoumaran benzylic ether reductase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C023304	
GO:0047837	D-xylose 1-dehydrogenase (NADP+) activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C019948	
GO:0034618	arginine binding	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C011208	

GO:0043565	sequence-specific DNA binding	MOLECULAR_FUNCTION	0,583238357	0,036287843	5	324	622	16177	MELO3C025282; MELO3C011167; MELO3C010057; MELO3C007181; MELO3C024192	MELO3C011432; MELO3C010223; MELO3C011550; MELO3C005791; MELO3C014384; MELO3C024507; MELO3C008942; MELO3C013173; MELO3C022209; MELO3C001991; MELO3C025714; MELO3C007736; MELO3C006887; MELO3C022205; MELO3C002723; MELO3C025951; MELO3C020145; MELO3C018187; MELO3C017415; MELO3C019715; MELO3C023092; MELO3C011797; MELO3C015239; MELO3C017429; MELO3C003140; MELO3C002050; MELO3C006891;
GO:0003841	1-acylglycerol-3-phosphate O-acyltransferase activity	MOLECULAR_FUNCTION	0,583238357	0,032354424	2	6	625	16495	MELO3C009663; MELO3C008959	MELO3C014054; MELO3C025383; MELO3C010918; MELO3C014475; MELO3C009182; MELO3C012571
GO:0004814	arginine-tRNA ligase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C015422	
GO:0003977	UDP-N-acetylglucosamine diphosphorylase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C007022	
GO:0080007	S-nitrosoglutathione reductase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C022399	
GO:0010487	thermospermine synthase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C011484	
GO:0034020	neoxanthin synthase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C017963	
GO:0000026	alpha-1,2-mannosyltransferase activity	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C025637	
GO:0016830	carbon-carbon lyase activity	MOLECULAR_FUNCTION	0,583238357	0,035904578	0	110	627	16391		MELO3C018628; MELO3C013057; MELO3C003491; MELO3C003259; MELO3C026007; MELO3C022321; MELO3C018340; MELO3C026005; MELO3C002329; MELO3C026006; MELO3C026004; MELO3C024189; MELO3C000130; MELO3C015998; MELO3C014547; MELO3C004110; MELO3C012252; MELO3C007227; MELO3C024519; MELO3C023787; MELO3C019050; MELO3C025446; MELO3C023786; MELO3C000483; MELO3C018994; MELO3C006580; MELO3C010162;
GO:0010297	heteropolysaccharide binding	MOLECULAR_FUNCTION	0,583238357	0,036606726	1	0	626	16501	MELO3C019135	
GO:0005875	microtubule associated complex	CELLULAR_COMPONENT	0,583238357	0,033428346	6	60	621	16441	MELO3C011256; MELO3C022094; MELO3C013429; MELO3C005757; MELO3C010631; MELO3C023342	MELO3C005594; MELO3C006121; MELO3C009957; MELO3C024627; MELO3C021317; MELO3C004268; MELO3C008589; MELO3C003774; MELO3C026888; MELO3C026800; MELO3C018185; MELO3C025310; MELO3C010507; MELO3C015199; MELO3C017338; MELO3C012723; MELO3C009841; MELO3C005122; MELO3C014153; MELO3C005289; MELO3C025923; MELO3C022897; MELO3C022898; MELO3C007668; MELO3C017141; MELO3C004518; MELO3C007903;
GO:0034099	luminal surveillance complex	CELLULAR_COMPONENT	0,583238357	0,036606726	1	0	626	16501	MELO3C005757	
GO:0009842	cyanelle	CELLULAR_COMPONENT	0,583238357	0,036606726	1	0	626	16501	MELO3C016140	
GO:0009930	longitudinal side of cell surface	CELLULAR_COMPONENT	0,583238357	0,036606726	1	0	626	16501	MELO3C017242	
GO:0042555	MCM complex	CELLULAR_COMPONENT	0,583238357	0,036606726	1	0	626	16501	MELO3C020001	
GO:0008305	integrin complex	CELLULAR_COMPONENT	0,583238357	0,036606726	1	0	626	16501	MELO3C007690	
GO:0031672	A band	CELLULAR_COMPONENT	0,583238357	0,036606726	1	0	626	16501	MELO3C011193	

GO:0009526	plastid envelope	CELLULAR_COMPONENT	0,583238357	0,028872683	21	328	606	16173	MELO3C005293; MELO3C015704; MELO3C008052; MELO3C011284; MELO3C006344; MELO3C002785; MELO3C006943; MELO3C020780; MELO3C023222; MELO3C018494; MELO3C015590; MELO3C008959; MELO3C018573; MELO3C020001; MELO3C010727; MELO3C019026; MELO3C015186; MELO3C015594; MELO3C019871; MELO3C009171; MELO3C011104	MELO3C011311; MELO3C009474; MELO3C014389; MELO3C003373; MELO3C006088; MELO3C007298; MELO3C006523; MELO3C004223; MELO3C005432; MELO3C001992; MELO3C026802; MELO3C003811; MELO3C001998; MELO3C015591; MELO3C015592; MELO3C025036; MELO3C022680; MELO3C015593; MELO3C017772; MELO3C015595; MELO3C017774; MELO3C010229; MELO3C015596; MELO3C026000; MELO3C009480; MELO3C006094; MELO3C004471;
GO:0031429	box H/ACA snoRNP complex	CELLULAR_COMPONENT	0,583238357	0,036606726	1	0	626	16501	MELO3C008801	
GO:0018444	translation release factor complex	CELLULAR_COMPONENT	0,583238357	0,036606726	1	0	626	16501	MELO3C002118	
GO:0009316	3-isopropylmalate dehydratase complex	CELLULAR_COMPONENT	0,583238357	0,036606726	1	0	626	16501	MELO3C005518	
GO:0042175	nuclear outer membrane-endoplasmic reticulum membrane network	CELLULAR_COMPONENT	0,583238357	0,03313727	13	182	614	16319	MELO3C010960; MELO3C016706; MELO3C010794; MELO3C009663; MELO3C007931; MELO3C021108; MELO3C025637; MELO3C005757; MELO3C005405; MELO3C006926; MELO3C020541; MELO3C005918; MELO3C013822	MELO3C017815; MELO3C009197; MELO3C006089; MELO3C009630; MELO3C020821; MELO3C002165; MELO3C002166; MELO3C006007; MELO3C021634; MELO3C026524; MELO3C022166; MELO3C026800; MELO3C022321; MELO3C018461; MELO3C025156; MELO3C018066; MELO3C019034; MELO3C017413; MELO3C015597; MELO3C012527; MELO3C017019; MELO3C025390; MELO3C010621; MELO3C008270; MELO3C014306; MELO3C015756; MELO3C016219;
GO:0034663	endoplasmic reticulum chaperone complex	CELLULAR_COMPONENT	0,583238357	0,036606726	1	0	626	16501	MELO3C005757	
GO:0045263	proton-transporting ATP synthase complex, coupling factor F(o)	CELLULAR_COMPONENT	0,583238357	0,035005647	3	17	624	16484	MELO3C012445; MELO3C000065; MELO3C010991	MELO3C010992; MELO3C000827; MELO3C007468; MELO3C022944; MELO3C001387; MELO3C000965; MELO3C001566; MELO3C000995; MELO3C002745; MELO3C003769; MELO3C004618; MELO3C015443; MELO3C027395; MELO3C027032; MELO3C027031; MELO3C011269; MELO3C013404
GO:0045271	respiratory chain complex I	CELLULAR_COMPONENT	0,583238357	0,028388178	4	28	623	16473	MELO3C005389; MELO3C006949; MELO3C013951; MELO3C017960	MELO3C012488; MELO3C012522; MELO3C012486; MELO3C002086; MELO3C024729; MELO3C026725; MELO3C022540; MELO3C023357; MELO3C025258; MELO3C017010; MELO3C019212; MELO3C016861; MELO3C010701; MELO3C022919; MELO3C014894; MELO3C009702; MELO3C000924; MELO3C009644; MELO3C006999; MELO3C025525; MELO3C026758; MELO3C023322; MELO3C020331; MELO3C022394; MELO3C025540; MELO3C017388; MELO3C023063;
GO:0010005	cortical microtubule, transverse to long axis	CELLULAR_COMPONENT	0,583238357	0,036606726	1	0	626	16501	MELO3C012361	
GO:0033162	melanosome membrane	CELLULAR_COMPONENT	0,583238357	0,036606726	1	0	626	16501	MELO3C006926	
GO:0005923	bicellular tight junction	CELLULAR_COMPONENT	0,583238357	0,036606726	1	0	626	16501	MELO3C022488	

GO:0009570	chloroplast stroma	CELLULAR_COMPONENT	0,595676803	0,037450468	22	361	605	16140	MELO3C018948; MELO3C012378; MELO3C005293; MELO3C012410; MELO3C009038; MELO3C011284; MELO3C005147; MELO3C003344; MELO3C009429; MELO3C008879; MELO3C020780; MELO3C020562; MELO3C018573; MELO3C010727; MELO3C016033; MELO3C015186; MELO3C010427; MELO3C018455; MELO3C014749; MELO3C011208; MELO3C010686; MELO3C011104	MELO3C013732; MELO3C021919; MELO3C012764; MELO3C002161; MELO3C008146; MELO3C006088; MELO3C009475; MELO3C013172; MELO3C004223; MELO3C005674; MELO3C003137; MELO3C001992; MELO3C008946; MELO3C003811; MELO3C001998; MELO3C003814; MELO3C021355; MELO3C016680; MELO3C016681; MELO3C017890; MELO3C024189; MELO3C015231; MELO3C025397; MELO3C019036; MELO3C017774; MELO3C015233; MELO3C011439;
GO:2001141	regulation of RNA biosynthetic process	BIOLOGICAL_PROCESS	0,596654655	0,037575097	41	1472	586	15029	MELO3C011256; MELO3C014722; MELO3C007691; MELO3C012242; MELO3C011110; MELO3C009653; MELO3C020848; MELO3C020701; MELO3C011172; MELO3C008847; MELO3C002644; MELO3C016083; MELO3C023412; MELO3C020860; MELO3C016660; MELO3C011759; MELO3C023195; MELO3C007181; MELO3C016623; MELO3C009188; MELO3C011003; MELO3C007340; MELO3C011167; MELO3C010057; MELO3C002292; MELO3C006870; MELO3C012231;	MELO3C014029; MELO3C007971; MELO3C005791; MELO3C003372; MELO3C014263; MELO3C007974; MELO3C013173; MELO3C014261; MELO3C007736; MELO3C012081; MELO3C006887; MELO3C002049; MELO3C026008; MELO3C000099; MELO3C010904; MELO3C010906; MELO3C010905; MELO3C019712; MELO3C016202; MELO3C016444; MELO3C015355; MELO3C025151; MELO3C017775; MELO3C019715; MELO3C017308; MELO3C021809; MELO3C003140;
GO:0000323	lytic vacuole	CELLULAR_COMPONENT	0,60175772	0,037960161	4	31	623	16470	MELO3C006926; MELO3C010243; MELO3C025061; MELO3C023569	MELO3C015218; MELO3C014920; MELO3C014821; MELO3C013676; MELO3C003291; MELO3C025752; MELO3C025972; MELO3C020442; MELO3C004827; MELO3C025355; MELO3C018764; MELO3C017653; MELO3C026440; MELO3C017414; MELO3C014458; MELO3C006034; MELO3C005243; MELO3C004353; MELO3C008897; MELO3C004477; MELO3C004874; MELO3C026977; MELO3C026898; MELO3C026415; MELO3C025645; MELO3C026971; MELO3C022495;
GO:2000243	positive regulation of reproductive process	BIOLOGICAL_PROCESS	0,611865368	0,039760302	3	18	624	16483	MELO3C016660; MELO3C012361; MELO3C011104	MELO3C011221; MELO3C011771; MELO3C011299; MELO3C002050; MELO3C006121; MELO3C014473; MELO3C004398; MELO3C007457; MELO3C006520; MELO3C022995; MELO3C019031; MELO3C004944; MELO3C024578; MELO3C022443; MELO3C018187; MELO3C025183; MELO3C026161; MELO3C014514
GO:0015780	nucleotide-sugar transport	BIOLOGICAL_PROCESS	0,611865368	0,040605375	2	7	625	16494	MELO3C011675; MELO3C004533	MELO3C010474; MELO3C013485; MELO3C013186; MELO3C020559; MELO3C011623; MELO3C011676; MELO3C007756
GO:0008615	pyridoxine biosynthetic process	BIOLOGICAL_PROCESS	0,611865368	0,040605375	2	7	625	16494	MELO3C011062; MELO3C003541	MELO3C020384; MELO3C013732; MELO3C025766; MELO3C009168; MELO3C006011; MELO3C024240; MELO3C025846

GO:0007023	post-chaperonin tubulin folding pathway	BIOLOGICAL_PROCESS	0,611865368	0,040605375	2	7	625	16494	MELO3C007673; MELO3C022488	MELO3C026613; MELO3C017607; MELO3C018025; MELO3C018532; MELO3C022478; MELO3C011830; MELO3C014723
GO:0009298	GDP-mannose biosynthetic process	BIOLOGICAL_PROCESS	0,611865368	0,040605375	2	7	625	16494	MELO3C003812; MELO3C023310	MELO3C006552; MELO3C024175; MELO3C020220; MELO3C017126; MELO3C026482; MELO3C021412; MELO3C005458
GO:0005544	calcium-dependent phospholipid binding	MOLECULAR_FUNCTION	0,611865368	0,040605375	2	7	625	16494	MELO3C019002; MELO3C012457	MELO3C012455; MELO3C012456; MELO3C018326; MELO3C015135; MELO3C026608; MELO3C018327; MELO3C018648
GO:0004365	glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity	MOLECULAR_FUNCTION	0,611865368	0,040605375	2	7	625	16494	MELO3C008219; MELO3C019633	MELO3C012598; MELO3C012599; MELO3C014752; MELO3C017044; MELO3C002342; MELO3C002343; MELO3C024866
GO:0005199	structural constituent of cell wall	MOLECULAR_FUNCTION	0,611865368	0,040605375	2	7	625	16494	MELO3C022068; MELO3C025324	MELO3C027328; MELO3C006506; MELO3C021194; MELO3C004550; MELO3C007279; MELO3C021192; MELO3C018704
GO:0004723	calcium-dependent protein serine/threonine phosphatase activity	MOLECULAR_FUNCTION	0,611865368	0,040605375	2	7	625	16494	MELO3C017844; MELO3C013892	MELO3C023443; MELO3C019099; MELO3C014069; MELO3C026598; MELO3C018436; MELO3C022260; MELO3C007998
GO:0000139	Golgi membrane	CELLULAR_COMPONENT	0,611865368	0,040465342	9	108	618	16393	MELO3C010243; MELO3C011675; MELO3C001997; MELO3C010135; MELO3C019691; MELO3C019026; MELO3C006736; MELO3C004533; MELO3C026614	MELO3C017935; MELO3C009473; MELO3C017818; MELO3C004583; MELO3C011272; MELO3C008782; MELO3C020821; MELO3C007456; MELO3C020428; MELO3C021517; MELO3C024503; MELO3C024227; MELO3C009914; MELO3C005799; MELO3C021595; MELO3C019674; MELO3C021590; MELO3C018066; MELO3C021591; MELO3C027332; MELO3C013979; MELO3C008270; MELO3C011676; MELO3C015756; MELO3C018919; MELO3C007101; MELO3C004074;
GO:2000112	regulation of cellular macromolecule biosynthetic process	BIOLOGICAL_PROCESS	0,613024982	0,040747215	43	1527	584	14974	MELO3C011256; MELO3C014722; MELO3C007691; MELO3C012242; MELO3C011110; MELO3C009653; MELO3C020848; MELO3C020701; MELO3C011172; MELO3C008847; MELO3C002644; MELO3C016083; MELO3C023412; MELO3C020860; MELO3C016660; MELO3C011759; MELO3C023195; MELO3C007181; MELO3C016623; MELO3C009188; MELO3C011003; MELO3C007340; MELO3C011167; MELO3C010057; MELO3C002292; MELO3C006870; MELO3C012231;	MELO3C014029; MELO3C007971; MELO3C020705; MELO3C005791; MELO3C003372; MELO3C014263; MELO3C007974; MELO3C013173; MELO3C014261; MELO3C007736; MELO3C012081; MELO3C006887; MELO3C002049; MELO3C026008; MELO3C000099; MELO3C010904; MELO3C010906; MELO3C010905; MELO3C019712; MELO3C016202; MELO3C016444; MELO3C015355; MELO3C025151; MELO3C019715; MELO3C017308; MELO3C021809; MELO3C003140;

GO:0048199	vesicle targeting, to, from or within Golgi	BIOLOGICAL_PROCESS	0,619619031	0,041513426	4	32	623	16469	MELO3C004551; MELO3C021279; MELO3C024447; MELO3C009966	MELO3C013434; MELO3C006782; MELO3C023339; MELO3C021556; MELO3C009912; MELO3C023630; MELO3C020980; MELO3C025796; MELO3C024225; MELO3C026763; MELO3C018343; MELO3C012923; MELO3C012528; MELO3C019856; MELO3C010666; MELO3C007042; MELO3C009240; MELO3C004196; MELO3C007300; MELO3C009269; MELO3C012991; MELO3C007583; MELO3C015929; MELO3C005422; MELO3C005423; MELO3C009969; MELO3C023883;
GO:0005741	mitochondrial outer membrane	CELLULAR_COMPONENT	0,619619031	0,041513426	4	32	623	16469	MELO3C010745; MELO3C019820; MELO3C005405; MELO3C016067	MELO3C020808; MELO3C013775; MELO3C014885; MELO3C024929; MELO3C015839; MELO3C020905; MELO3C004681; MELO3C009893; MELO3C020821; MELO3C025739; MELO3C000215; MELO3C017471; MELO3C019213; MELO3C019776; MELO3C017676; MELO3C017019; MELO3C017439; MELO3C007542; MELO3C004273; MELO3C014531; MELO3C016818; MELO3C021943; MELO3C006378; MELO3C003464; MELO3C002035; MELO3C020973; MELO3C018052;
GO:0015035	protein disulfide oxidoreductase activity	MOLECULAR_FUNCTION	0,63535636	0,042769543	6	64	621	16437	MELO3C019722; MELO3C019326; MELO3C017902; MELO3C018455; MELO3C012410; MELO3C016056	MELO3C010860; MELO3C009478; MELO3C011352; MELO3C008421; MELO3C005790; MELO3C007253; MELO3C022405; MELO3C009556; MELO3C001994; MELO3C026569; MELO3C024468; MELO3C025752; MELO3C014909; MELO3C021350; MELO3C021351; MELO3C017411; MELO3C012969; MELO3C017410; MELO3C019913; MELO3C008750; MELO3C012053; MELO3C009882; MELO3C005763; MELO3C022339; MELO3C007026; MELO3C005206; MELO3C026855;
GO:0048316	seed development	BIOLOGICAL_PROCESS	0,646422686	0,043582901	10	134	617	16367	MELO3C007609; MELO3C003768; MELO3C022399; MELO3C008959; MELO3C022488; MELO3C020848; MELO3C012361; MELO3C010913; MELO3C015764; MELO3C016019	MELO3C006243; MELO3C021518; MELO3C007451; MELO3C003650; MELO3C006402; MELO3C008942; MELO3C022204; MELO3C005714; MELO3C006925; MELO3C005957; MELO3C025310; MELO3C021196; MELO3C011830; MELO3C012653; MELO3C005162; MELO3C015649; MELO3C006530; MELO3C002052; MELO3C014670; MELO3C003389; MELO3C004632; MELO3C006811; MELO3C026934; MELO3C024874; MELO3C002738; MELO3C017662; MELO3C019205;

GO:0032201	telomere maintenance via semi-conservative replication	BIOLOGICAL_PROCESS	0,660678447	0,04482376	3	19	624	16482	MELO3C010631; MELO3C003638; MELO3C020860	MELO3C005384; MELO3C014021; MELO3C014020; MELO3C008864; MELO3C002892; MELO3C022319; MELO3C026949; MELO3C025879; MELO3C025646; MELO3C010507; MELO3C024596; MELO3C001937; MELO3C025142; MELO3C014529; MELO3C017228; MELO3C015225; MELO3C027184; MELO3C014528; MELO3C017458
GO:0045454	cell redox homeostasis	BIOLOGICAL_PROCESS	0,665413214	0,045616041	9	113	618	16388	MELO3C017902; MELO3C019253; MELO3C012410; MELO3C016056; MELO3C019722; MELO3C019326; MELO3C018455; MELO3C021247; MELO3C009429	MELO3C010860; MELO3C009478; MELO3C008421; MELO3C005790; MELO3C011030; MELO3C011393; MELO3C009872; MELO3C009519; MELO3C001994; MELO3C024103; MELO3C024468; MELO3C021350; MELO3C025034; MELO3C021351; MELO3C017411; MELO3C010625; MELO3C017410; MELO3C009882; MELO3C002450; MELO3C022339; MELO3C005206; MELO3C000126; MELO3C026897; MELO3C016053; MELO3C016055; MELO3C010633; MELO3C012465;
GO:0046700	heterocycle catabolic process	BIOLOGICAL_PROCESS	0,681717933	0,047117042	1	151	626	16350	MELO3C002118	MELO3C016969; MELO3C020705; MELO3C010461; MELO3C006121; MELO3C013051; MELO3C002562; MELO3C024905; MELO3C002203; MELO3C006767; MELO3C018062; MELO3C004867; MELO3C000014; MELO3C023775; MELO3C023136; MELO3C020380; MELO3C017771; MELO3C015199; MELO3C015113; MELO3C017811; MELO3C017810; MELO3C016736; MELO3C012257; MELO3C008154; MELO3C014554; MELO3C010350; MELO3C021769; MELO3C008435;
GO:0044270	cellular nitrogen compound catabolic process	BIOLOGICAL_PROCESS	0,684298913	0,047440282	1	152	626	16349	MELO3C002118	MELO3C016969; MELO3C020705; MELO3C010461; MELO3C006121; MELO3C013051; MELO3C002562; MELO3C024905; MELO3C006767; MELO3C018062; MELO3C004867; MELO3C000014; MELO3C023775; MELO3C023136; MELO3C020380; MELO3C017771; MELO3C015199; MELO3C015113; MELO3C017811; MELO3C017810; MELO3C016736; MELO3C012257; MELO3C008154; MELO3C014554; MELO3C010350; MELO3C021769; MELO3C008435; MELO3C023545;
GO:0042023	DNA endoreduplication	BIOLOGICAL_PROCESS	0,699756525	0,049548806	2	8	625	16493	MELO3C011003; MELO3C012361	MELO3C019031; MELO3C012214; MELO3C008916; MELO3C018187; MELO3C012492; MELO3C026580; MELO3C014639; MELO3C002168

GO:0009695	jasmonic acid biosynthetic process	BIOLOGICAL_PROCESS	0,699756525	0,049548806	2	8	625	16493	MELO3C002470; MELO3C015514	MELO3C004955; MELO3C009362; MELO3C012388; MELO3C010910; MELO3C004565; MELO3C008062; MELO3C018734; MELO3C002346
GO:0007043	cell-cell junction assembly	BIOLOGICAL_PROCESS	0,699756525	0,049548806	2	8	625	16493	MELO3C007673; MELO3C022488	MELO3C007829; MELO3C026613; MELO3C006574; MELO3C018025; MELO3C018532; MELO3C006575; MELO3C015103; MELO3C014723
GO:0000578	embryonic axis specification	BIOLOGICAL_PROCESS	0,699756525	0,049548806	2	8	625	16493	MELO3C003768; MELO3C011193	MELO3C025389; MELO3C024028; MELO3C005946; MELO3C024874; MELO3C005099; MELO3C007036; MELO3C024782; MELO3C019956
GO:0046474	glycerophospholipid biosynthetic process	BIOLOGICAL_PROCESS	0,699756525	0,049164821	4	34	623	16467	MELO3C007931; MELO3C008959; MELO3C025637; MELO3C012545	MELO3C013830; MELO3C007010; MELO3C012286; MELO3C020821; MELO3C020987; MELO3C005332; MELO3C022308; MELO3C020989; MELO3C005634; MELO3C021052; MELO3C015670; MELO3C026440; MELO3C017214; MELO3C013319; MELO3C017019; MELO3C010621; MELO3C011215; MELO3C015647; MELO3C011047; MELO3C013842; MELO3C009088; MELO3C009186; MELO3C013982; MELO3C014212; MELO3C008992; MELO3C005285; MELO3C006258;
GO:0016161	beta-amylase activity	MOLECULAR_FUNCTION	0,699756525	0,049548806	2	8	625	16493	MELO3C006362; MELO3C016213	MELO3C014105; MELO3C022740; MELO3C022739; MELO3C023067; MELO3C018794; MELO3C021362; MELO3C021214; MELO3C013887

Supplementary Table 2.C Gene Ontology terms (GO terms) of the cluster 2.2 obtained considering the comparison between lines the postharvest ripening time fruit during storage at 20.5°C and 88% relative humidity for 18 d the near-isogenic line SC10-2 and its parental ''Piel de Sapo'' obtained according to the differentially expressed gene pattern (Supl. Table 2.A)

GO ID	GO Name	GO Category	FDR	P-Value	SC10-2	PS	Non Annot Test	Non Annot Reference	TestSet Sequences	RefSet Sequences
GO:0004370	glycerol kinase activity	MOLECULAR_FUNCTION	0,459917717	4,87E-05	2	0	118	17008	MELO3C023442; MELO3C004084	
GO:0043069	negative regulation of programmed cell death	BIOLOGICAL_PROCESS	1	0,030471862	2	37	118	16971	MELO3C003331; MELO3C017623	MELO3C002481; MELO3C011470; MELO3C006121; MELO3C007237; MELO3C003332; MELO3C005976; MELO3C004622; MELO3C025417; MELO3C022346; MELO3C005757; MELO3C025413; MELO3C016083; MELO3C005912; MELO3C025752; MELO3C021057; MELO3C023972; MELO3C009939; MELO3C004827; MELO3C024340; MELO3C025355; MELO3C005718; MELO3C011710; MELO3C013522; MELO3C011983; MELO3C012376; MELO3C011021; MELO3C004950;
GO:0043622	cortical microtubule organization	BIOLOGICAL_PROCESS	1	0,034546914	1	4	119	17004	MELO3C002054	MELO3C007829; MELO3C014496; MELO3C002717; MELO3C023374
GO:0006954	inflammatory response	BIOLOGICAL_PROCESS	1	0,041312923	1	5	119	17003	MELO3C026027	MELO3C026028; MELO3C015103; MELO3C017426; MELO3C018756; MELO3C022821
GO:0042780	tRNA 3'-end processing	BIOLOGICAL_PROCESS	1	0,027733554	1	3	119	17005	MELO3C014447	MELO3C020738; MELO3C010582; MELO3C024265
GO:0010017	red or far-red light signaling pathway	BIOLOGICAL_PROCESS	1	0,026260641	2	34	118	16974	MELO3C026502; MELO3C014459	MELO3C009692; MELO3C006046; MELO3C014684; MELO3C012221; MELO3C006142; MELO3C014386; MELO3C011250; MELO3C003075; MELO3C006225; MELO3C021715; MELO3C003574; MELO3C024805; MELO3C026506; MELO3C004148; MELO3C002742; MELO3C005738; MELO3C002705; MELO3C005939; MELO3C019731; MELO3C010769; MELO3C025191; MELO3C014699; MELO3C008213; MELO3C009202; MELO3C005120; MELO3C002793; MELO3C006717;
GO:0010497	plasmodesmata-mediated intercellular transport	BIOLOGICAL_PROCESS	1	0,041312923	1	5	119	17003	MELO3C002054	MELO3C018455; MELO3C002933; MELO3C014025; MELO3C010974; MELO3C012843
GO:0010375	stomatal complex patterning	BIOLOGICAL_PROCESS	1	0,020872515	1	2	119	17006	MELO3C002054	MELO3C021111; MELO3C020718
GO:0070838	divalent metal ion transport	BIOLOGICAL_PROCESS	1	0,019826524	2	29	118	16979	MELO3C016817; MELO3C014607	MELO3C007271; MELO3C003950; MELO3C008308; MELO3C024920; MELO3C007636; MELO3C020600; MELO3C022448; MELO3C024289; MELO3C020683; MELO3C009917; MELO3C025057; MELO3C025255; MELO3C019215; MELO3C017953; MELO3C010795; MELO3C010794; MELO3C012595; MELO3C004374; MELO3C006259; MELO3C006257; MELO3C026832; MELO3C009809; MELO3C026378; MELO3C015780; MELO3C021780; MELO3C010753; MELO3C018734;
GO:0009959	negative gravitropism	BIOLOGICAL_PROCESS	1	0,027733554	1	3	119	17005	MELO3C008088	MELO3C025310; MELO3C008847; MELO3C024155
GO:0006659	phosphatidylserine biosynthetic process	BIOLOGICAL_PROCESS	1	0,013963465	1	1	119	17007	MELO3C005332	MELO3C012286

GO:0009408	response to heat	BIOLOGICAL_PROCESS	1	4,24E-04	5	85	115	16923	MELO3C016970; MELO3C025139; MELO3C013946; MELO3C009996; MELO3C003917	MELO3C013974; MELO3C008263; MELO3C005873; MELO3C005035; MELO3C008589; MELO3C014183; MELO3C005674; MELO3C020589; MELO3C018780; MELO3C026886; MELO3C018023; MELO3C018660; MELO3C001916; MELO3C019039; MELO3C012925; MELO3C010748; MELO3C015312; MELO3C016449; MELO3C012455; MELO3C012136; MELO3C012456; MELO3C015608; MELO3C012331; MELO3C009840; MELO3C014230; MELO3C005884; MELO3C008677;
GO:0009660	amyloplast organization	BIOLOGICAL_PROCESS	1	0,013963465	1	1	119	17007	MELO3C008088	MELO3C025310
GO:0045038	protein import into chloroplast thylakoid membrane	BIOLOGICAL_PROCESS	1	0,020872515	1	2	119	17006	MELO3C006136	MELO3C020652; MELO3C018772
GO:0006433	prolyl-tRNA aminoacylation	BIOLOGICAL_PROCESS	1	0,020872515	1	2	119	17006	MELO3C017711	MELO3C019492; MELO3C005193
GO:0033345	asparagine catabolic process via L-aspartate	BIOLOGICAL_PROCESS	1	0,013963465	1	1	119	17007	MELO3C017653	MELO3C006131
GO:0009590	detection of gravity	BIOLOGICAL_PROCESS	1	0,020872515	1	2	119	17006	MELO3C008088	MELO3C005293; MELO3C005396
GO:0009753	response to jasmonic acid	BIOLOGICAL_PROCESS	1	0,00858548	3	57	117	16951	MELO3C010774; MELO3C006120; MELO3C011885	MELO3C006086; MELO3C006046; MELO3C014386; MELO3C006765; MELO3C020701; MELO3C005674; MELO3C024348; MELO3C008625; MELO3C017292; MELO3C001913; MELO3C017134; MELO3C025152; MELO3C012527; MELO3C011439; MELO3C015436; MELO3C010353; MELO3C004231; MELO3C005840; MELO3C020637; MELO3C021643; MELO3C006934; MELO3C021645; MELO3C004513; MELO3C026577; MELO3C024357; MELO3C010910; MELO3C016852;
GO:0006516	glycoprotein catabolic process	BIOLOGICAL_PROCESS	1	0,034546914	1	4	119	17004	MELO3C017653	MELO3C001609; MELO3C026905; MELO3C016787; MELO3C015327
GO:0006517	protein deglycosylation	BIOLOGICAL_PROCESS	1	0,007006072	1	0	119	17008	MELO3C017653	
GO:0051604	protein maturation	BIOLOGICAL_PROCESS	1	0,022309646	2	31	118	16977	MELO3C017653; MELO3C016970	MELO3C005470; MELO3C009174; MELO3C006089; MELO3C012220; MELO3C008520; MELO3C004285; MELO3C022725; MELO3C020322; MELO3C020686; MELO3C003576; MELO3C023413; MELO3C006206; MELO3C022525; MELO3C025156; MELO3C017891; MELO3C004827; MELO3C025353; MELO3C014926; MELO3C015335; MELO3C011874; MELO3C011641; MELO3C013522; MELO3C013881; MELO3C006131; MELO3C009684; MELO3C025349; MELO3C025589;
GO:0006013	mannose metabolic process	BIOLOGICAL_PROCESS	1	0,041312923	1	5	119	17003	MELO3C005109	MELO3C016048; MELO3C026482; MELO3C009914; MELO3C007919; MELO3C009913
GO:0007586	digestion	BIOLOGICAL_PROCESS	1	0,048031907	1	6	119	17002	MELO3C015523	MELO3C012302; MELO3C012071; MELO3C005751; MELO3C017002; MELO3C019036; MELO3C022495
GO:0035071	salivary gland cell autophagic cell death	BIOLOGICAL_PROCESS	1	0,034546914	1	4	119	17004	MELO3C015523	MELO3C026898; MELO3C022308; MELO3C007891; MELO3C025809
GO:0032515	negative regulation of phosphoprotein phosphatase activity	BIOLOGICAL_PROCESS	1	0,007006072	1	0	119	17008	MELO3C018500	
GO:0007030	Golgi organization	BIOLOGICAL_PROCESS	1	0,00419236	2	12	118	16996	MELO3C008088; MELO3C004825	MELO3C021320; MELO3C005918; MELO3C008037; MELO3C025044; MELO3C008782; MELO3C024284; MELO3C021946; MELO3C022038; MELO3C006811; MELO3C015756; MELO3C016416; MELO3C022305

GO:0017006	protein-tetrapyrrole linkage	BIOLOGICAL_PROCESS	1	0,048031907	1	6	119	17002	MELO3C026502	MELO3C006717; MELO3C024196; MELO3C024195; MELO3C026506; MELO3C002705; MELO3C015204
GO:0051865	protein autoubiquitination	BIOLOGICAL_PROCESS	1	0,041312923	1	5	119	17003	MELO3C025853	MELO3C011752; MELO3C022725; MELO3C010168; MELO3C011153; MELO3C023546
GO:0006072	glycerol-3-phosphate metabolic process	BIOLOGICAL_PROCESS	1	0,00132592	2	6	118	17002	MELO3C023442; MELO3C004084	MELO3C026337; MELO3C021604; MELO3C020158; MELO3C019820; MELO3C020157; MELO3C005116
GO:0031648	protein destabilization	BIOLOGICAL_PROCESS	1	0,007006072	1	0	119	17008	MELO3C015523	
GO:0048510	regulation of timing of transition from vegetative to reproductive phase	BIOLOGICAL_PROCESS	1	0,034546914	1	4	119	17004	MELO3C022388	MELO3C027290; MELO3C019330; MELO3C013793; MELO3C009465
GO:0002949	tRNA threonylcarbamoyladenosine modification	BIOLOGICAL_PROCESS	1	0,007006072	1	0	119	17008	MELO3C006202	
GO:0016404	15-hydroxyprostaglandin dehydrogenase (NAD+) activity	MOLECULAR_FUNCTION	1	0,007006072	1	0	119	17008	MELO3C019503	
GO:0004144	diacylglycerol O-acyltransferase activity	MOLECULAR_FUNCTION	1	0,020872515	1	2	119	17006	MELO3C013703	MELO3C004632; MELO3C018460
GO:0003846	2-acylglycerol O-acyltransferase activity	MOLECULAR_FUNCTION	1	0,007006072	1	0	119	17008	MELO3C013703	
GO:0042781	3'-tRNA processing endoribonuclease activity	MOLECULAR_FUNCTION	1	0,020872515	1	2	119	17006	MELO3C014447	MELO3C020738; MELO3C024265
GO:0046872	metal ion binding	MOLECULAR_FUNCTION	1	0,031268561	28	2666	92	14342	MELO3C008088; MELO3C014447; MELO3C012284; MELO3C004441; MELO3C025917; MELO3C006202; MELO3C009996; MELO3C025855; MELO3C005711; MELO3C026249; MELO3C025853; MELO3C011216; MELO3C018569; MELO3C009380; MELO3C009583; MELO3C009561; MELO3C016817; MELO3C013383; MELO3C022715; MELO3C004139; MELO3C006418; MELO3C005109; MELO3C025940; MELO3C019503; MELO3C010774; MELO3C011885; MELO3C014459;	MELO3C018628; MELO3C004460; MELO3C005792; MELO3C012088; MELO3C006644; MELO3C020945; MELO3C004465; MELO3C005316; MELO3C003137; MELO3C003139; MELO3C005315; MELO3C005319; MELO3C015590; MELO3C015591; MELO3C015592; MELO3C015593; MELO3C015594; MELO3C015110; MELO3C015595; MELO3C015596; MELO3C019951; MELO3C015597; MELO3C015599; MELO3C018624; MELO3C017777; MELO3C017309; MELO3C014279;
GO:0004827	proline-tRNA ligase activity	MOLECULAR_FUNCTION	1	0,020872515	1	2	119	17006	MELO3C017711	MELO3C019492; MELO3C005193
GO:0045547	dehydrodolichyl diphosphate synthase activity	MOLECULAR_FUNCTION	1	0,020872515	1	2	119	17006	MELO3C025855	MELO3C021891; MELO3C018615
GO:0050178	phenylpyruvate tautomerase activity	MOLECULAR_FUNCTION	1	0,007006072	1	0	119	17008	MELO3C026027	
GO:0003948	N4-(beta-N-acetylglucosaminyl)-L-asparaginase activity	MOLECULAR_FUNCTION	1	0,007006072	1	0	119	17008	MELO3C017653	
GO:0050221	prostaglandin-E2 9-reductase activity	MOLECULAR_FUNCTION	1	0,020872515	1	2	119	17006	MELO3C026155	MELO3C015622; MELO3C011853
GO:0033743	peptide-methionine (R)-S-oxide reductase activity	MOLECULAR_FUNCTION	1	0,013963465	1	1	119	17007	MELO3C018569	MELO3C016676
GO:0008020	G-protein coupled photoreceptor activity	MOLECULAR_FUNCTION	1	0,041312923	1	5	119	17003	MELO3C026502	MELO3C006717; MELO3C024196; MELO3C024195; MELO3C026506; MELO3C002705
GO:0004197	cysteine-type endopeptidase activity	MOLECULAR_FUNCTION	1	0,017468633	2	27	118	16981	MELO3C015523; MELO3C017623	MELO3C010982; MELO3C008520; MELO3C007578; MELO3C023338; MELO3C021359; MELO3C017053; MELO3C024402; MELO3C024666; MELO3C025355; MELO3C016781; MELO3C010702; MELO3C015576; MELO3C015577; MELO3C015578; MELO3C013438; MELO3C010763; MELO3C015634; MELO3C012403; MELO3C013563; MELO3C006275; MELO3C005564; MELO3C026898; MELO3C018473; MELO3C019168; MELO3C010976; MELO3C018636; MELO3C015701
GO:0008834	di-trans,poly-cis-decaprenylcistransferase activity	MOLECULAR_FUNCTION	1	0,020872515	1	2	119	17006	MELO3C025855	MELO3C021891; MELO3C018615
GO:0008798	beta-aspartyl-peptidase activity	MOLECULAR_FUNCTION	1	0,034546914	1	4	119	17004	MELO3C017653	MELO3C001609; MELO3C016787; MELO3C006131; MELO3C015327
GO:0004557	alpha-galactosidase activity	MOLECULAR_FUNCTION	1	0,034546914	1	4	119	17004	MELO3C020139	MELO3C020138; MELO3C011771; MELO3C010698; MELO3C011770
GO:0005262	calcium channel activity	MOLECULAR_FUNCTION	1	0,034546914	1	4	119	17004	MELO3C016817	MELO3C017043; MELO3C022020; MELO3C018734; MELO3C007977
GO:0003882	CDP-diacylglycerol-serine O-phosphatidyltransferase activity	MOLECULAR_FUNCTION	1	0,013963465	1	1	119	17007	MELO3C005332	MELO3C012286
GO:0004605	phosphatidate cytidylyltransferase activity	MOLECULAR_FUNCTION	1	0,027733554	1	3	119	17005	MELO3C007432	MELO3C020525; MELO3C021695; MELO3C021145

GO:0047268	galactinol-raffinose galactosyltransferase activity	MOLECULAR_FUNCTION	1	0,048031907	1	6	119	17002	MELO3C026247	MELO3C015912; MELO3C009979; MELO3C002287; MELO3C025599; MELO3C023110; MELO3C010314
GO:0034511	U3 snoRNA binding	MOLECULAR_FUNCTION	1	0,013963465	1	1	119	17007	MELO3C017440	MELO3C013185
GO:0005764	lysosome	CELLULAR_COMPONENT	1	0,011186588	2	21	118	16987	MELO3C017653; MELO3C015523	MELO3C014821; MELO3C003291; MELO3C006034; MELO3C005243; MELO3C004353; MELO3C008897; MELO3C004477; MELO3C026977; MELO3C023569; MELO3C006926; MELO3C026898; MELO3C026415; MELO3C025645; MELO3C025752; MELO3C025972; MELO3C020442; MELO3C026971; MELO3C025355; MELO3C018764; MELO3C014818; MELO3C026110
GO:0031983	vesicle lumen	CELLULAR_COMPONENT	1	0,007006072	1	0	119	17008	MELO3C015523	
GO:0042718	yolk granule	CELLULAR_COMPONENT	1	0,007006072	1	0	119	17008	MELO3C015523	
GO:0016602	CCAAT-binding factor complex	CELLULAR_COMPONENT	1	0,034546914	1	4	119	17004	MELO3C023161	MELO3C009551; MELO3C015320; MELO3C023554; MELO3C007077
GO:0045169	fusome	CELLULAR_COMPONENT	1	0,020872515	1	2	119	17006	MELO3C015523	MELO3C006951; MELO3C024150
GO:0005783	endoplasmic reticulum	CELLULAR_COMPONENT	1	0,011232603	8	425	112	16583	MELO3C008088; MELO3C016817; MELO3C019333; MELO3C017653; MELO3C014607; MELO3C013703; MELO3C015523; MELO3C014459	MELO3C019959; MELO3C012088; MELO3C003372; MELO3C020821; MELO3C002165; MELO3C002166; MELO3C006405; MELO3C009914; MELO3C006525; MELO3C025156; MELO3C017891; MELO3C024187; MELO3C018740; MELO3C017652; MELO3C017413; MELO3C025390; MELO3C016449; MELO3C016219; MELO3C018518; MELO3C002052; MELO3C003263; MELO3C003383; MELO3C017661; MELO3C019722; MELO3C017542; MELO3C016696; MELO3C015246;

Supplementary Table 2.D Gene Ontology terms (GO terms) of the cluster 2.3 obtained considering the comparison between lines the postharvest ripening time fruit during storage at 20.5°C and 88% relative humidity for 18 d the near-isogenic line SC10-2 and its parental ''Piel de Sapo'' obtained according to the differentially expressed gene pattern (Supl. Table 2.A)

GO ID	GO Name	GO Category	FDR	P-Value	SC10-2	PS	Non Annot Test	Non Annot Reference	TestSet Sequences	RefSet Sequences
GO:0006287	base-excision repair, gap-filling	BIOLOGICAL_PROCESS	1	0,021251752	1	0	363	16764	MELO3C024596	
GO:0045004	DNA replication proofreading	BIOLOGICAL_PROCESS	1	0,021251752	1	0	363	16764	MELO3C024596	
GO:0009832	plant-type cell wall biogenesis	BIOLOGICAL_PROCESS	1	0,023114647	3	26	361	16738	MELO3C007450; MELO3C008069; MELO3C018365	MELO3C005051; MELO3C017818; MELO3C010062; MELO3C007036; MELO3C005791; MELO3C023836; MELO3C026947; MELO3C026188; MELO3C023551; MELO3C023374; MELO3C003916; MELO3C022385; MELO3C016301; MELO3C013319; MELO3C010524; MELO3C012573; MELO3C009322; MELO3C009189; MELO3C002672; MELO3C003783; MELO3C003488; MELO3C003569; MELO3C020651; MELO3C017242; MELO3C026156; MELO3C016777
GO:0007259	JAK-STAT cascade	BIOLOGICAL_PROCESS	1	0,042053081	1	1	363	16763	MELO3C022219	MELO3C005634
GO:0002119	nematode larval development	BIOLOGICAL_PROCESS	1	0,037981651	12	286	352	16478	MELO3C003924; MELO3C010640; MELO3C026234; MELO3C024596; MELO3C017365; MELO3C011383; MELO3C015322; MELO3C011139; MELO3C011206; MELO3C012622; MELO3C002556; MELO3C003842	MELO3C011795; MELO3C012522; MELO3C006760; MELO3C002166; MELO3C002045; MELO3C004344; MELO3C019031; MELO3C026800; MELO3C019034; MELO3C025275; MELO3C016321; MELO3C014708; MELO3C015235; MELO3C019956; MELO3C020836; MELO3C008157; MELO3C002173; MELO3C004473; MELO3C014153; MELO3C013185; MELO3C023545; MELO3C008835; MELO3C023306; MELO3C023427; MELO3C006657; MELO3C024757; MELO3C003703;
GO:0018315	molybdenum incorporation into molybdenum-molybdopterin complex	BIOLOGICAL_PROCESS	1	0,021251752	1	0	363	16764	MELO3C022174	
GO:0010031	circumnutation	BIOLOGICAL_PROCESS	1	0,042053081	1	1	363	16763	MELO3C010769	MELO3C001999
GO:0006297	nucleotide-excision repair, DNA gap filling	BIOLOGICAL_PROCESS	1	0,044412945	2	14	362	16750	MELO3C018521; MELO3C024596	MELO3C014021; MELO3C014020; MELO3C008864; MELO3C026949; MELO3C025879; MELO3C003638; MELO3C010507; MELO3C001937; MELO3C025142; MELO3C014529; MELO3C017228; MELO3C014528; MELO3C017458; MELO3C010631
GO:0000348	mRNA branch site recognition	BIOLOGICAL_PROCESS	1	0,042053081	1	1	363	16763	MELO3C017365	MELO3C011256
GO:0043631	RNA polyadenylation	BIOLOGICAL_PROCESS	1	0,025823813	2	10	362	16754	MELO3C022443; MELO3C024435	MELO3C005162; MELO3C004944; MELO3C008873; MELO3C021828; MELO3C008722; MELO3C002045; MELO3C027241; MELO3C021974; MELO3C002115; MELO3C011126
GO:0009965	leaf morphogenesis	BIOLOGICAL_PROCESS	1	0,027567914	3	28	361	16736	MELO3C021534; MELO3C017813; MELO3C005971	MELO3C006085; MELO3C007098; MELO3C011771; MELO3C007870; MELO3C004347; MELO3C022204; MELO3C024446; MELO3C020860; MELO3C015173; MELO3C001957; MELO3C025450; MELO3C017559; MELO3C013621; MELO3C016916; MELO3C011142; MELO3C013287; MELO3C007121; MELO3C020854; MELO3C014670; MELO3C002670; MELO3C007500; MELO3C004752; MELO3C024898; MELO3C018380; MELO3C007207; MELO3C003009; MELO3C023064;
GO:0040007	growth	BIOLOGICAL_PROCESS	1	0,044484447	18	508	346	16256	MELO3C014358; MELO3C008481; MELO3C010640; MELO3C008069; MELO3C011383; MELO3C005971; MELO3C002556; MELO3C003842; MELO3C003924; MELO3C026234; MELO3C022174; MELO3C017365; MELO3C019225; MELO3C015322; MELO3C010769; MELO3C011139; MELO3C011206; MELO3C012622	MELO3C021918; MELO3C006760; MELO3C002166; MELO3C002045; MELO3C004344; MELO3C006648; MELO3C025275; MELO3C019953; MELO3C016321; MELO3C026482; MELO3C019956; MELO3C021808; MELO3C020836; MELO3C005561; MELO3C002173; MELO3C004473; MELO3C014153; MELO3C013185; MELO3C004353; MELO3C008835; MELO3C006657; MELO3C006415; MELO3C025044; MELO3C017661; MELO3C010913; MELO3C018512; MELO3C016456;

GO:0006662	glycerol ether metabolic process	BIOLOGICAL_PROCESS	1	0,035039541	3	31	361	16733	MELO3C008932; MELO3C026897; MELO3C025023	MELO3C010860; MELO3C007211; MELO3C008421; MELO3C003791; MELO3C015939; MELO3C009894; MELO3C008127; MELO3C007873; MELO3C006026; MELO3C004822; MELO3C001994; MELO3C022106; MELO3C008988; MELO3C026569; MELO3C024468; MELO3C025752; MELO3C021431; MELO3C002508; MELO3C010009; MELO3C012969; MELO3C016516; MELO3C012410; MELO3C011340; MELO3C004371; MELO3C012053; MELO3C007026; MELO3C010490;
GO:0006541	glutamine metabolic process	BIOLOGICAL_PROCESS	1	0,021047312	3	25	361	16739	MELO3C012572; MELO3C020749; MELO3C008481	MELO3C022828; MELO3C013152; MELO3C026828; MELO3C018290; MELO3C007757; MELO3C009759; MELO3C018382; MELO3C023599; MELO3C024486; MELO3C024189; MELO3C024485; MELO3C013218; MELO3C012434; MELO3C012156; MELO3C011485; MELO3C008152; MELO3C005680; MELO3C006577; MELO3C006993; MELO3C025766; MELO3C025645; MELO3C011808; MELO3C020230; MELO3C019622; MELO3C012435
GO:0071281	cellular response to iron ion	BIOLOGICAL_PROCESS	1	0,011586716	2	6	362	16758	MELO3C014230; MELO3C014099	MELO3C015210; MELO3C019550; MELO3C015531; MELO3C026952; MELO3C016340; MELO3C003906
GO:0060250	germ-line stem-cell niche homeostasis	BIOLOGICAL_PROCESS	1	0,021251752	1	0	363	16764	MELO3C022219	
GO:0031048	chromatin silencing by small RNA	BIOLOGICAL_PROCESS	1	4,50E-04	2	0	362	16764	MELO3C022443; MELO3C014706	
GO:0009631	cold acclimation	BIOLOGICAL_PROCESS	1	0,004316803	2	3	362	16761	MELO3C021940; MELO3C026068	MELO3C011972; MELO3C018668; MELO3C015546
GO:0060152	microtubule-based peroxisome localization	BIOLOGICAL_PROCESS	1	0,021251752	1	0	363	16764	MELO3C021783	
GO:0044765	single-organism transport	BIOLOGICAL_PROCESS	1	0,037521218	8	740	356	16024	MELO3C004999; MELO3C021783; MELO3C017343; MELO3C018720; MELO3C014230; MELO3C016149; MELO3C011139; MELO3C007613	MELO3C014028; MELO3C005550; MELO3C012087; MELO3C004222; MELO3C006883; MELO3C007731; MELO3C005311; MELO3C004465; MELO3C008709; MELO3C006409; MELO3C017891; MELO3C025277; MELO3C015350; MELO3C010900; MELO3C019951; MELO3C017655; MELO3C010901; MELO3C017414; MELO3C016326; MELO3C017656; MELO3C016689; MELO3C019956; MELO3C020836; MELO3C004591; MELO3C007980; MELO3C014397; MELO3C002052;
GO:0051697	protein delipidation	BIOLOGICAL_PROCESS	1	0,021251752	1	0	363	16764	MELO3C008520	
GO:0043603	cellular amide metabolic process	BIOLOGICAL_PROCESS	1	0,048516947	8	727	356	16037	MELO3C023047; MELO3C008099; MELO3C014611; MELO3C021113; MELO3C026234; MELO3C017364; MELO3C014706; MELO3C000756	MELO3C020704; MELO3C020705; MELO3C002164; MELO3C012084; MELO3C014262; MELO3C004345; MELO3C004587; MELO3C020945; MELO3C006400; MELO3C004344; MELO3C005674; MELO3C004226; MELO3C004347; MELO3C005679; MELO3C003258; MELO3C006648; MELO3C006766; MELO3C025279; MELO3C025156; MELO3C017891; MELO3C025276; MELO3C016200; MELO3C017653; MELO3C016201; MELO3C024061; MELO3C015598; MELO3C025030;
GO:0019419	sulfate reduction	BIOLOGICAL_PROCESS	1	0,042053081	1	1	363	16763	MELO3C007398	MELO3C002450
GO:0019544	arginine catabolic process to glutamate	BIOLOGICAL_PROCESS	1	0,042053081	1	1	363	16763	MELO3C017571	MELO3C002752
GO:0006071	glycerol metabolic process	BIOLOGICAL_PROCESS	1	0,034627522	2	12	362	16752	MELO3C022124; MELO3C017753	MELO3C007806; MELO3C013101; MELO3C001925; MELO3C024364; MELO3C001926; MELO3C002033; MELO3C019820; MELO3C014925; MELO3C013703; MELO3C011029; MELO3C021466; MELO3C004632
GO:0010051	xylem and phloem pattern formation	BIOLOGICAL_PROCESS	1	0,049643023	2	15	362	16749	MELO3C007450; MELO3C017813	MELO3C012125; MELO3C009584; MELO3C002670; MELO3C005236; MELO3C004752; MELO3C006307; MELO3C024898; MELO3C022204; MELO3C003768; MELO3C003009; MELO3C025774; MELO3C019573; MELO3C016850; MELO3C016301; MELO3C018952

GO:0006470	protein dephosphorylation	BIOLOGICAL_PROCESS	1	0,007099285	6	74	358	16690	MELO3C020601; MELO3C004603; MELO3C007940; MELO3C006983; MELO3C013921; MELO3C023473	MELO3C020829; MELO3C013336; MELO3C018507; MELO3C008426; MELO3C004587; MELO3C003574; MELO3C024667; MELO3C002645; MELO3C026602; MELO3C023893; MELO3C026166; MELO3C018500; MELO3C011713; MELO3C026163; MELO3C010744; MELO3C012378; MELO3C009960; MELO3C007580; MELO3C015408; MELO3C013860; MELO3C016939; MELO3C009840; MELO3C006852; MELO3C021405; MELO3C023626; MELO3C020114; MELO3C003222;
GO:0034517	ribophagy	BIOLOGICAL_PROCESS	1	0,021251752	1	0	363	16764	MELO3C011731	
GO:0001736	establishment of planar polarity	BIOLOGICAL_PROCESS	1	0,042053081	1	1	363	16763	MELO3C014230	MELO3C005892
GO:0016807	cysteine-type carboxypeptidase activity	MOLECULAR_FUNCTION	1	0,021251752	1	0	363	16764	MELO3C008520	
GO:0050281	serine-glyoxylate transaminase activity	MOLECULAR_FUNCTION	1	0,042053081	1	1	363	16763	MELO3C015151	MELO3C014568
GO:0008865	fructokinase activity	MOLECULAR_FUNCTION	1	0,011586716	2	6	362	16758	MELO3C015750; MELO3C009032	MELO3C022452; MELO3C015749; MELO3C020278; MELO3C003755; MELO3C005395; MELO3C009200
GO:0003723	RNA binding	MOLECULAR_FUNCTION	1	0,044838422	26	789	338	15975	MELO3C011498; MELO3C009550; MELO3C005650; MELO3C009713; MELO3C013051; MELO3C005651; MELO3C025897; MELO3C022443; MELO3C019630; MELO3C026221; MELO3C015750; MELO3C014706; MELO3C012428; MELO3C019858; MELO3C016468; MELO3C016469; MELO3C012622; MELO3C008099; MELO3C014358; MELO3C005382; MELO3C007821; MELO3C013183; MELO3C003842; MELO3C024435; MELO3C017365; MELO3C026398	MELO3C014025; MELO3C020705; MELO3C014263; MELO3C012084; MELO3C003135; MELO3C002045; MELO3C020945; MELO3C026246; MELO3C015110; MELO3C019953; MELO3C019951; MELO3C019957; MELO3C017309; MELO3C012099; MELO3C005565; MELO3C013185; MELO3C009922; MELO3C007743; MELO3C007741; MELO3C006657; MELO3C026259; MELO3C015360; MELO3C018872; MELO3C019964; MELO3C018874; MELO3C017303; MELO3C015126;
GO:0046905	phytoene synthase activity	MOLECULAR_FUNCTION	1	0,021251752	1	0	363	16764	MELO3C025102	
GO:0032440	2-alkenal reductase [NAD(P)] activity	MOLECULAR_FUNCTION	1	0,037244384	2	341	362	16423	MELO3C017385; MELO3C023492	MELO3C002280; MELO3C014387; MELO3C007179; MELO3C008942; MELO3C022209; MELO3C004465; MELO3C001991; MELO3C024986; MELO3C004228; MELO3C022205; MELO3C021359; MELO3C019030; MELO3C015350; MELO3C020263; MELO3C018865; MELO3C017655; MELO3C014948; MELO3C017656; MELO3C015359; MELO3C010352; MELO3C013982; MELO3C002050; MELO3C011440; MELO3C011682; MELO3C007980; MELO3C006890; MELO3C010351;
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	MOLECULAR_FUNCTION	1	0,026860295	2	366	362	16398	MELO3C022162; MELO3C011977	MELO3C014148; MELO3C011430; MELO3C014147; MELO3C013055; MELO3C025718; MELO3C005431; MELO3C005438; MELO3C009914; MELO3C009913; MELO3C007734; MELO3C003813; MELO3C015470; MELO3C019035; MELO3C015471; MELO3C015472; MELO3C019036; MELO3C006092; MELO3C026480; MELO3C013622; MELO3C009488; MELO3C009367; MELO3C005560; MELO3C006777; MELO3C009924; MELO3C027109; MELO3C026811; MELO3C025840;
GO:0003735	structural constituent of ribosome	MOLECULAR_FUNCTION	1	0,007957351	1	353	363	16411	MELO3C017364	MELO3C011310; MELO3C020704; MELO3C006088; MELO3C002164; MELO3C012084; MELO3C014262; MELO3C024506; MELO3C020945; MELO3C006400; MELO3C003258; MELO3C006766; MELO3C024747; MELO3C020141; MELO3C022441; MELO3C003811; MELO3C001514; MELO3C025276; MELO3C016201; MELO3C025030; MELO3C018985; MELO3C016688; MELO3C014824; MELO3C017659; MELO3C020836; MELO3C007740; MELO3C013981; MELO3C009489;
GO:0051538	3 iron, 4 sulfur cluster binding	MOLECULAR_FUNCTION	1	0,042053081	1	1	363	16763	MELO3C008481	MELO3C009759
GO:0008720	D-lactate dehydrogenase activity	MOLECULAR_FUNCTION	1	0,021251752	1	0	363	16764	MELO3C009581	
GO:0008444	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase activity	MOLECULAR_FUNCTION	1	0,042053081	1	1	363	16763	MELO3C011715	MELO3C007382
GO:0004760	serine-pyruvate transaminase activity	MOLECULAR_FUNCTION	1	0,042053081	1	1	363	16763	MELO3C015151	MELO3C014568

GO:0004485	methylcrotonoyl-CoA carboxylase activity	MOLECULAR_FUNCTION	1	0,042053081	1	1	363	16763	MELO3C015796	MELO3C018456
GO:0008453	alanine-glyoxylate transaminase activity	MOLECULAR_FUNCTION	1	0,004316803	2	3	362	16761	MELO3C015151; MELO3C017571	MELO3C014568; MELO3C026045; MELO3C009117
GO:0008607	phosphorylase kinase regulator activity	MOLECULAR_FUNCTION	1	0,042053081	1	1	363	16763	MELO3C026234	MELO3C025450
GO:0004402	histone acetyltransferase activity	MOLECULAR_FUNCTION	1	0,027567914	3	28	361	16736	MELO3C026234; MELO3C002885; MELO3C026222	MELO3C007593; MELO3C013698; MELO3C011851; MELO3C011774; MELO3C013356; MELO3C009471; MELO3C006243; MELO3C007211; MELO3C014860; MELO3C013253; MELO3C004100; MELO3C009635; MELO3C007015; MELO3C009633; MELO3C022788; MELO3C017030; MELO3C010806; MELO3C015474; MELO3C012527; MELO3C005161; MELO3C005162; MELO3C010476; MELO3C007627; MELO3C004615; MELO3C001964; MELO3C002318; MELO3C026433;
GO:0004008	copper-exporting ATPase activity	MOLECULAR_FUNCTION	1	0,025823813	2	10	362	16754	MELO3C019011; MELO3C016915	MELO3C000189; MELO3C019010; MELO3C019012; MELO3C018643; MELO3C005665; MELO3C007027; MELO3C008846; MELO3C020853; MELO3C008845; MELO3C003996
GO:0017153	sodium:dicarboxylate symporter activity	MOLECULAR_FUNCTION	1	0,042053081	1	1	363	16763	MELO3C017343	MELO3C023446
GO:0033741	adenylyl-sulfate reductase (glutathione) activity	MOLECULAR_FUNCTION	1	0,042053081	1	1	363	16763	MELO3C007398	MELO3C002450
GO:0004861	cyclin-dependent protein serine/threonine kinase inhibitor activity	MOLECULAR_FUNCTION	1	0,042053081	1	1	363	16763	MELO3C020458	MELO3C026998
GO:0004458	D-lactate dehydrogenase (cytochrome) activity	MOLECULAR_FUNCTION	1	0,042053081	1	1	363	16763	MELO3C009581	MELO3C016408
GO:0004355	glutamate synthase (NADPH) activity	MOLECULAR_FUNCTION	1	0,042053081	1	1	363	16763	MELO3C008481	MELO3C009759
GO:0004354	glutamate dehydrogenase (NADP+) activity	MOLECULAR_FUNCTION	1	0,021251752	1	0	363	16764	MELO3C013031	
GO:0019154	glycolate dehydrogenase activity	MOLECULAR_FUNCTION	1	0,021251752	1	0	363	16764	MELO3C009581	
GO:0008949	oxalyl-CoA decarboxylase activity	MOLECULAR_FUNCTION	1	0,021251752	1	0	363	16764	MELO3C010381	
GO:1901681	sulfur compound binding	MOLECULAR_FUNCTION	1	0,046452118	3	35	361	16729	MELO3C010381; MELO3C015796; MELO3C007613	MELO3C024609; MELO3C013153; MELO3C007612; MELO3C005894; MELO3C000358; MELO3C008625; MELO3C000599; MELO3C026205; MELO3C026007; MELO3C026005; MELO3C026006; MELO3C026004; MELO3C001913; MELO3C025454; MELO3C016066; MELO3C019218; MELO3C012235; MELO3C012993; MELO3C004231; MELO3C009145; MELO3C003386; MELO3C003265; MELO3C007227; MELO3C003266; MELO3C020531; MELO3C021742; MELO3C013081;
GO:0004044	amidophosphoribosyltransferase activity	MOLECULAR_FUNCTION	1	0,042053081	1	1	363	16763	MELO3C020749	MELO3C025646
GO:0008889	glycerophosphodiester phosphodiesterase activity	MOLECULAR_FUNCTION	1	0,008813139	2	5	362	16759	MELO3C022124; MELO3C017753	MELO3C007806; MELO3C002033; MELO3C014925; MELO3C013101; MELO3C011029
GO:0047499	calcium-independent phospholipase A2 activity	MOLECULAR_FUNCTION	1	0,021251752	1	0	363	16764	MELO3C020721	
GO:0019786	Atg8-specific protease activity	MOLECULAR_FUNCTION	1	0,021251752	1	0	363	16764	MELO3C008520	
GO:0010293	abscisic aldehyde oxidase activity	MOLECULAR_FUNCTION	1	0,042053081	1	1	363	16763	MELO3C014719	MELO3C014717
GO:0080048	GDP-D-glucose phosphorylase activity	MOLECULAR_FUNCTION	1	0,021251752	1	0	363	16764	MELO3C013136	
GO:0004689	phosphorylase kinase activity	MOLECULAR_FUNCTION	1	0,042053081	1	1	363	16763	MELO3C008469	MELO3C023218
GO:0003755	peptidyl-prolyl cis-trans isomerase activity	MOLECULAR_FUNCTION	1	0,038575996	4	56	360	16708	MELO3C015779; MELO3C016542; MELO3C014178; MELO3C012622	MELO3C011036; MELO3C012489; MELO3C013896; MELO3C017816; MELO3C010261; MELO3C013375; MELO3C015916; MELO3C006285; MELO3C008222; MELO3C021912; MELO3C009952; MELO3C002126; MELO3C007778; MELO3C026524; MELO3C003338; MELO3C019631; MELO3C024662; MELO3C017776; MELO3C025192; MELO3C016887; MELO3C011236; MELO3C014557; MELO3C008553; MELO3C006176; MELO3C004752; MELO3C025848; MELO3C022335;
GO:0004602	glutathione peroxidase activity	MOLECULAR_FUNCTION	1	0,014689493	2	7	362	16757	MELO3C015857; MELO3C016951	MELO3C014348; MELO3C017729; MELO3C015858; MELO3C015859; MELO3C005666; MELO3C022821; MELO3C005667
GO:0004604	phosphoadenylyl-sulfate reductase (thioredoxin) activity	MOLECULAR_FUNCTION	1	0,042053081	1	1	363	16763	MELO3C007398	MELO3C002450
GO:0043625	delta DNA polymerase complex	CELLULAR_COMPONENT	1	0,021251752	1	0	363	16764	MELO3C024596	
GO:0015030	Cajal body	CELLULAR_COMPONENT	1	0,039403779	2	13	362	16751	MELO3C017365; MELO3C014706	MELO3C012871; MELO3C004440; MELO3C023809; MELO3C022928; MELO3C017908; MELO3C006422; MELO3C005127; MELO3C004018; MELO3C008801; MELO3C026433; MELO3C019034; MELO3C017696; MELO3C022370
GO:0030140	trans-Golgi network transport vesicle	CELLULAR_COMPONENT	1	0,011586716	2	6	362	16758	MELO3C003242; MELO3C017813	MELO3C025730; MELO3C013605; MELO3C024167; MELO3C007298; MELO3C005579; MELO3C008306

GO:0008287	protein serine/threonine phosphatase complex	CELLULAR_COMPONENT	1	0,03101136	4	52	360	16712	MELO3C020601; MELO3C007940; MELO3C006983; MELO3C023473	MELO3C020829; MELO3C013336; MELO3C018507; MELO3C008221; MELO3C008426; MELO3C024667; MELO3C023893; MELO3C026288; MELO3C011713; MELO3C013337; MELO3C015408; MELO3C020837; MELO3C016939; MELO3C006852; MELO3C023626; MELO3C008478; MELO3C024635; MELO3C021246; MELO3C006736; MELO3C004439; MELO3C024478; MELO3C013745; MELO3C009093; MELO3C011765; MELO3C006581; MELO3C014325; MELO3C009297;
GO:0000815	ESCRT III complex	CELLULAR_COMPONENT	1	0,042053081	1	1	363	16763	MELO3C005199	MELO3C004945
GO:0009508	plastid chromosome	CELLULAR_COMPONENT	1	0,018106304	2	8	362	16756	MELO3C026221; MELO3C010512	MELO3C019372; MELO3C006321; MELO3C017774; MELO3C002396; MELO3C007103; MELO3C022303; MELO3C003216; MELO3C025888
GO:0019031	viral envelope	CELLULAR_COMPONENT	1	0,025823813	2	10	362	16754	MELO3C017968; MELO3C013370	MELO3C013688; MELO3C013687; MELO3C013686; MELO3C014389; MELO3C014321; MELO3C019997; MELO3C005059; MELO3C019996; MELO3C020500; MELO3C013766
GO:0009570	chloroplast stroma	CELLULAR_COMPONENT	1	0,005873914	17	366	347	16398	MELO3C009550; MELO3C009032; MELO3C008481; MELO3C007398; MELO3C014178; MELO3C011196; MELO3C008932; MELO3C009713; MELO3C023469; MELO3C022228; MELO3C023047; MELO3C019011; MELO3C026897; MELO3C015151; MELO3C025023; MELO3C011825; MELO3C016951	MELO3C013732; MELO3C021919; MELO3C012764; MELO3C002161; MELO3C008146; MELO3C006088; MELO3C009475; MELO3C013172; MELO3C004223; MELO3C005674; MELO3C003137; MELO3C001992; MELO3C008946; MELO3C003811; MELO3C001998; MELO3C003814; MELO3C021355; MELO3C016680; MELO3C016681; MELO3C017890; MELO3C024189; MELO3C015231; MELO3C025397; MELO3C019036; MELO3C017774; MELO3C015233; MELO3C011439;
GO:0009571	proplastid stroma	CELLULAR_COMPONENT	1	0,021251752	1	0	363	16764	MELO3C023469	
GO:0005775	vacuolar lumen	CELLULAR_COMPONENT	1	0,042053081	1	1	363	16763	MELO3C008520	MELO3C025752
GO:0044391	ribosomal subunit	CELLULAR_COMPONENT	1	0,034251243	1	283	363	16481	MELO3C017364	MELO3C011310; MELO3C006088; MELO3C012084; MELO3C014262; MELO3C024506; MELO3C020141; MELO3C022441; MELO3C001514; MELO3C016201; MELO3C025030; MELO3C017659; MELO3C013984; MELO3C013981; MELO3C009489; MELO3C002294; MELO3C006412; MELO3C025609; MELO3C006411; MELO3C005446; MELO3C006657; MELO3C024994; MELO3C025168; MELO3C022691; MELO3C018512; MELO3C011448; MELO3C016459; MELO3C024071;

Supplementary Table 2.E Gene Ontology terms (GO terms) of the cluster 2.4 obtained considering the comparison between lines the postharvest ripening time fruit during storage at 20.5°C and 88% relative humidity for 18 d the near-isogenic line SC10-2 and its parental ''Piel de Sapo'' obtained according to the differentially expressed gene pattern (Supl. Table 2.A)

GO ID	GO Name	GO Category	FDR	P-Value	SC10-2	PS	Non Annot Test	Non Annot Reference	TestSet Sequences	RefSet Sequences
GO:0071011	precatalytic spliceosome	CELLULAR_COMPONENT	0,191781685	1,83E-04	6	41	301	16780	MELO3C026304; MELO3C008076; MELO3C024028; MELO3C014555; MELO3C008690; MELO3C020824	MELO3C012489; MELO3C011851; MELO3C002181; MELO3C013333; MELO3C008488; MELO3C008344; MELO3C014122; MELO3C004440; MELO3C022928; MELO3C008023; MELO3C004123; MELO3C002120; MELO3C006787; MELO3C024822; MELO3C024685; MELO3C023475; MELO3C017338; MELO3C009580; MELO3C011414; MELO3C012449; MELO3C009381; MELO3C012622; MELO3C012214; MELO3C013443; MELO3C008151; MELO3C008332; MELO3C015907;
GO:0008270	zinc ion binding	MOLECULAR_FUNCTION	0,502199987	5,85E-04	40	1237	267	15584	MELO3C007075; MELO3C007033; MELO3C025859; MELO3C026803; MELO3C022786; MELO3C006802; MELO3C002148; MELO3C004305; MELO3C025977; MELO3C004944; MELO3C002767; MELO3C018461; MELO3C018265; MELO3C024385; MELO3C017131; MELO3C015891; MELO3C026640; MELO3C003619; MELO3C017657; MELO3C010985; MELO3C019616; MELO3C008330; MELO3C015867; MELO3C013587; MELO3C015627; MELO3C013440; MELO3C014199;	MELO3C004460; MELO3C005792; MELO3C014022; MELO3C007732; MELO3C005559; MELO3C009914; MELO3C007735; MELO3C003139; MELO3C009913; MELO3C026249; MELO3C010904; MELO3C015110; MELO3C019951; MELO3C018864; MELO3C017536; MELO3C018624; MELO3C017777; MELO3C017537; MELO3C021804; MELO3C021806; MELO3C004472; MELO3C012095; MELO3C004232; MELO3C002297; MELO3C002055; MELO3C004237; MELO3C004239;
GO:0005689	U12-type spliceosomal complex	CELLULAR_COMPONENT	0,614567138	8,46E-04	3	8	304	16813	MELO3C014555; MELO3C008690; MELO3C006785	MELO3C019829; MELO3C017020; MELO3C001824; MELO3C015907; MELO3C006787; MELO3C024822; MELO3C016998; MELO3C023823
GO:0047938	glucose-6-phosphate 1-epimerase activity	MOLECULAR_FUNCTION	0,64064555	9,49E-04	2	1	305	16820	MELO3C016314; MELO3C006055	MELO3C004001
GO:0006406	mRNA export from nucleus	BIOLOGICAL_PROCESS	0,826988708	0,001475555	4	24	303	16797	MELO3C026304; MELO3C003078; MELO3C015733; MELO3C014129	MELO3C011256; MELO3C014532; MELO3C013443; MELO3C020407; MELO3C005265; MELO3C005694; MELO3C004622; MELO3C021931; MELO3C021887; MELO3C016280; MELO3C022166; MELO3C009808; MELO3C005946; MELO3C015492; MELO3C025497; MELO3C025498; MELO3C019034; MELO3C026441; MELO3C011924; MELO3C015113; MELO3C013879; MELO3C012713; MELO3C015447; MELO3C016756
GO:0031053	primary miRNA processing	BIOLOGICAL_PROCESS	0,826988708	0,001876102	2	2	305	16819	MELO3C026304; MELO3C015627	MELO3C005929; MELO3C015158

GO:2000241	regulation of reproductive process	BIOLOGICAL_ PROCESS	1	0,03397942	5	95	302	16726	MELO3C026304; MELO3C004944; MELO3C011550; MELO3C007033; MELO3C015733	MELO3C006243; MELO3C012361; MELO3C006121; MELO3C007457; MELO3C020900; MELO3C006520; MELO3C005035; MELO3C009633; MELO3C004347; MELO3C024822; MELO3C019031; MELO3C018062; MELO3C022443; MELO3C021157; MELO3C018187; MELO3C026243; MELO3C020263; MELO3C025152; MELO3C017216; MELO3C015512; MELO3C026161; MELO3C017812; MELO3C025191; MELO3C005161; MELO3C021929; MELO3C005162; MELO3C008151;
GO:0019919	peptidyl-arginine methylation, to asymmetrical-dimethyl arginine	BIOLOGICAL_ PROCESS	1	0,017923867	1	0	306	16821	MELO3C026636	
GO:0002121	inter-male aggressive behavior	BIOLOGICAL_ PROCESS	1	0,035527497	1	1	306	16820	MELO3C015733	MELO3C026612
GO:0031119	tRNA pseudouridine synthesis	BIOLOGICAL_ PROCESS	1	0,004579945	2	4	305	16817	MELO3C021228; MELO3C017384	MELO3C004192; MELO3C019957; MELO3C021593; MELO3C011820
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	BIOLOGICAL_ PROCESS	1	0,044805879	2	17	305	16804	MELO3C026304; MELO3C024028	MELO3C015714; MELO3C011145; MELO3C013051; MELO3C008956; MELO3C006767; MELO3C021931; MELO3C008955; MELO3C026612; MELO3C026327; MELO3C007816; MELO3C025497; MELO3C003804; MELO3C025498; MELO3C026263; MELO3C015113; MELO3C013879; MELO3C026290
GO:0045893	positive regulation of transcription, DNA-templated	BIOLOGICAL_ PROCESS	1	0,049494568	4	73	303	16748	MELO3C010748; MELO3C007103; MELO3C004553; MELO3C012788	MELO3C013015; MELO3C006760; MELO3C005791; MELO3C008304; MELO3C006520; MELO3C007015; MELO3C004622; MELO3C003216; MELO3C022562; MELO3C017295; MELO3C019433; MELO3C019554; MELO3C017650; MELO3C024460; MELO3C015512; MELO3C017429; MELO3C015209; MELO3C006131; MELO3C020474; MELO3C003429; MELO3C015360; MELO3C024352; MELO3C016099; MELO3C011649; MELO3C015367; MELO3C015885; MELO3C018910;
GO:0048367	shoot system development	BIOLOGICAL_ PROCESS	1	0,043991757	9	235	298	16586	MELO3C018195; MELO3C004944; MELO3C015627; MELO3C011550; MELO3C007033; MELO3C010350; MELO3C016101; MELO3C008248; MELO3C022204	MELO3C006085; MELO3C021918; MELO3C006880; MELO3C008942; MELO3C006520; MELO3C022209; MELO3C005674; MELO3C004347; MELO3C007615; MELO3C006888; MELO3C022443; MELO3C003937; MELO3C026243; MELO3C020263; MELO3C025152; MELO3C013857; MELO3C021929; MELO3C013621; MELO3C002050; MELO3C006890; MELO3C002052; MELO3C020718; MELO3C007500; MELO3C023546; MELO3C007746; MELO3C008956; MELO3C008955;
GO:0000740	nuclear membrane fusion	BIOLOGICAL_ PROCESS	1	0,017923867	1	0	306	16821	MELO3C023526	
GO:0051410	detoxification of nitrogen compound	BIOLOGICAL_ PROCESS	1	0,035527497	1	1	306	16820	MELO3C025585	MELO3C021201

GO:0006606	protein import into nucleus	BIOLOGICAL_ PROCESS	1	0,039165002	3	39	304	16782	MELO3C004204; MELO3C016308; MELO3C020533	MELO3C012585; MELO3C008488; MELO3C012584; MELO3C012087; MELO3C004123; MELO3C021613; MELO3C005895; MELO3C014681; MELO3C005893; MELO3C016280; MELO3C022166; MELO3C000796; MELO3C000453; MELO3C026441; MELO3C024782; MELO3C013982; MELO3C014532; MELO3C020836; MELO3C004174; MELO3C004173; MELO3C009840; MELO3C011020; MELO3C010592; MELO3C012192; MELO3C006015; MELO3C000249; MELO3C005424;
GO:0009658	chloroplast organization	BIOLOGICAL_ PROCESS	1	0,036841102	3	38	304	16783	MELO3C023560; MELO3C006974; MELO3C013476	MELO3C013793; MELO3C008920; MELO3C020966; MELO3C003135; MELO3C007638; MELO3C008847; MELO3C002785; MELO3C020500; MELO3C020985; MELO3C003878; MELO3C005838; MELO3C015693; MELO3C025397; MELO3C010707; MELO3C019337; MELO3C010989; MELO3C014926; MELO3C024185; MELO3C011812; MELO3C014943; MELO3C019509; MELO3C009680; MELO3C014156; MELO3C005683; MELO3C003560; MELO3C026919; MELO3C005565;
GO:0009408	response to heat	BIOLOGICAL_ PROCESS	1	0,005582333	6	84	301	16737	MELO3C013974; MELO3C018950; MELO3C010748; MELO3C004553; MELO3C023526; MELO3C020589	MELO3C008263; MELO3C005873; MELO3C005035; MELO3C008589; MELO3C014183; MELO3C005674; MELO3C009996; MELO3C018780; MELO3C026886; MELO3C018023; MELO3C018660; MELO3C001916; MELO3C019039; MELO3C012925; MELO3C015312; MELO3C016449; MELO3C012455; MELO3C012136; MELO3C012456; MELO3C015608; MELO3C012331; MELO3C009840; MELO3C014230; MELO3C005884; MELO3C008677; MELO3C009127; MELO3C020872;
GO:2000011	regulation of adaxial/abaxial pattern formation	BIOLOGICAL_ PROCESS	1	0,017923867	1	0	306	16821	MELO3C015627	
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	BIOLOGICAL_ PROCESS	1	0,038566615	4	67	303	16754	MELO3C022707; MELO3C025232; MELO3C013359; MELO3C009879	MELO3C012564; MELO3C020827; MELO3C021718; MELO3C002481; MELO3C002361; MELO3C009310; MELO3C003650; MELO3C022725; MELO3C006565; MELO3C007214; MELO3C021950; MELO3C005757; MELO3C016083; MELO3C005912; MELO3C010625; MELO3C012407; MELO3C014436; MELO3C014876; MELO3C009880; MELO3C014395; MELO3C003660; MELO3C006972; MELO3C006615; MELO3C025768; MELO3C019642; MELO3C022053; MELO3C016132;
GO:0090630	activation of GTPase activity	BIOLOGICAL_ PROCESS	1	0,035527497	1	1	306	16820	MELO3C018195	MELO3C013721

GO:0006986	response to unfolded protein	BIOLOGICAL_ PROCESS	1	0,018771079	2	10	305	16811	MELO3C022707; MELO3C010748	MELO3C021891; MELO3C007383; MELO3C010795; MELO3C012198; MELO3C018660; MELO3C009730; MELO3C006478; MELO3C012527; MELO3C017118; MELO3C005757
GO:0047497	mitochondrion transport along microtubule	BIOLOGICAL_ PROCESS	1	0,035527497	1	1	306	16820	MELO3C004273	MELO3C015839
GO:0045071	negative regulation of viral genome replication	BIOLOGICAL_ PROCESS	1	0,017923867	1	0	306	16821	MELO3C026304	
GO:0051085	chaperone mediated protein folding requiring cofactor	BIOLOGICAL_ PROCESS	1	0,035527497	1	1	306	16820	MELO3C023526	MELO3C007116
GO:0031124	mRNA 3'-end processing	BIOLOGICAL_ PROCESS	1	0,005969919	3	18	304	16803	MELO3C026304; MELO3C004944; MELO3C015733	MELO3C005161; MELO3C011256; MELO3C005162; MELO3C008873; MELO3C009412; MELO3C005265; MELO3C021828; MELO3C008722; MELO3C002045; MELO3C006125; MELO3C021974; MELO3C002115; MELO3C004637; MELO3C024435; MELO3C022443; MELO3C005946; MELO3C027241; MELO3C011126
GO:0019933	cAMP-mediated signaling	BIOLOGICAL_ PROCESS	1	0,035527497	1	1	306	16820	MELO3C006948	MELO3C026602
GO:0007094	mitotic spindle assembly checkpoint	BIOLOGICAL_ PROCESS	1	0,036476381	2	15	305	16806	MELO3C025232; MELO3C013359	MELO3C011895; MELO3C014684; MELO3C014573; MELO3C003047; MELO3C006972; MELO3C022930; MELO3C004622; MELO3C005866; MELO3C005733; MELO3C024685; MELO3C017066; MELO3C017087; MELO3C026580; MELO3C017995; MELO3C012437
GO:0001666	response to hypoxia	BIOLOGICAL_ PROCESS	1	0,025279833	2	12	305	16809	MELO3C024028; MELO3C010748	MELO3C025534; MELO3C025535; MELO3C008938; MELO3C011021; MELO3C017087; MELO3C009145; MELO3C004189; MELO3C007039; MELO3C026482; MELO3C015302; MELO3C013879; MELO3C021953
GO:0055062	phosphate ion homeostasis	BIOLOGICAL_ PROCESS	1	0,035527497	1	1	306	16820	MELO3C010297	MELO3C007283
GO:0009963	positive regulation of flavonoid biosynthetic process	BIOLOGICAL_ PROCESS	1	0,035527497	1	1	306	16820	MELO3C027219	MELO3C016879
GO:0051382	kinetochore assembly	BIOLOGICAL_ PROCESS	1	0,017923867	1	0	306	16821	MELO3C006948	
GO:0042542	response to hydrogen peroxide	BIOLOGICAL_ PROCESS	1	0,002685504	3	13	304	16808	MELO3C013974; MELO3C010748; MELO3C020589	MELO3C013522; MELO3C016937; MELO3C002020; MELO3C007439; MELO3C006536; MELO3C002338; MELO3C005923; MELO3C018023; MELO3C012939; MELO3C012925; MELO3C017883; MELO3C021171; MELO3C017636
GO:0048644	muscle organ morphogenesis	BIOLOGICAL_ PROCESS	1	0,017923867	1	0	306	16821	MELO3C008076	
GO:0006206	pyrimidine nucleobase metabolic process	BIOLOGICAL_ PROCESS	1	0,04055957	2	16	305	16805	MELO3C005067; MELO3C022212	MELO3C018607; MELO3C014554; MELO3C012330; MELO3C005122; MELO3C014189; MELO3C002362; MELO3C003165; MELO3C009854; MELO3C023314; MELO3C002149; MELO3C003814; MELO3C011808; MELO3C015352; MELO3C015199; MELO3C010935; MELO3C013218
GO:0000350	generation of catalytic spliceosome for second transesterification step	BIOLOGICAL_ PROCESS	1	0,017923867	1	0	306	16821	MELO3C015733	
GO:0010267	production of ta-siRNAs involved in RNA interference	BIOLOGICAL_ PROCESS	1	0,013103927	2	8	305	16813	MELO3C015627; MELO3C014129	MELO3C010254; MELO3C011257; MELO3C015492; MELO3C005929; MELO3C010042; MELO3C022813; MELO3C023207; MELO3C012127
GO:0010362	negative regulation of anion channel activity by blue light	BIOLOGICAL_ PROCESS	1	0,035527497	1	1	306	16820	MELO3C013476	MELO3C025720

GO:0006787	porphyrin-containing compound catabolic process	BIOLOGICAL_PROCESS	1	0,032563635	2	14	305	16807	MELO3C010350; MELO3C023590	MELO3C016736; MELO3C019918; MELO3C014286; MELO3C006434; MELO3C008435; MELO3C024905; MELO3C020912; MELO3C007554; MELO3C025347; MELO3C004867; MELO3C022310; MELO3C005616; MELO3C018440; MELO3C025982
GO:0043097	pyrimidine nucleoside salvage	BIOLOGICAL_PROCESS	1	0,017923867	1	0	306	16821	MELO3C022212	
GO:0006419	alanyl-tRNA aminoacylation	BIOLOGICAL_PROCESS	1	0,010607789	2	7	305	16814	MELO3C000425; MELO3C027308	MELO3C012870; MELO3C010097; MELO3C024031; MELO3C000756; MELO3C018624; MELO3C027271; MELO3C013645
GO:0040022	feminization of hermaphroditic germ-line	BIOLOGICAL_PROCESS	1	0,008348753	2	6	305	16815	MELO3C026304; MELO3C015733	MELO3C006787; MELO3C005946; MELO3C021157; MELO3C009413; MELO3C017216; MELO3C015907
GO:0000209	protein polyubiquitination	BIOLOGICAL_PROCESS	1	0,009420097	5	67	302	16754	MELO3C018461; MELO3C022707; MELO3C025232; MELO3C013359; MELO3C009879	MELO3C012564; MELO3C011153; MELO3C020827; MELO3C021718; MELO3C002481; MELO3C002361; MELO3C009310; MELO3C003650; MELO3C022725; MELO3C006565; MELO3C007214; MELO3C021950; MELO3C016083; MELO3C005912; MELO3C012407; MELO3C014436; MELO3C014876; MELO3C009880; MELO3C014395; MELO3C003660; MELO3C006972; MELO3C006615; MELO3C025768; MELO3C026578; MELO3C019642; MELO3C022053; MELO3C002738;
GO:0007525	somatic muscle development	BIOLOGICAL_PROCESS	1	0,035527497	1	1	306	16820	MELO3C018265	MELO3C025387
GO:0007638	mechanosensory behavior	BIOLOGICAL_PROCESS	1	0,017923867	1	0	306	16821	MELO3C008076	
GO:0006369	termination of RNA polymerase II transcription	BIOLOGICAL_PROCESS	1	0,036476381	2	15	305	16806	MELO3C026304; MELO3C015733	MELO3C008873; MELO3C003340; MELO3C002045; MELO3C008589; MELO3C006125; MELO3C021974; MELO3C002115; MELO3C004637; MELO3C017020; MELO3C024435; MELO3C005946; MELO3C001923; MELO3C016377; MELO3C016378; MELO3C011126
GO:0032526	response to retinoic acid	BIOLOGICAL_PROCESS	1	0,017923867	1	0	306	16821	MELO3C026102	
GO:0045451	pole plasm oskar mRNA localization	BIOLOGICAL_PROCESS	1	0,035527497	1	1	306	16820	MELO3C024028	MELO3C005946
GO:0010198	synergid death	BIOLOGICAL_PROCESS	1	0,017923867	1	0	306	16821	MELO3C023526	
GO:0009640	photomorphogenesis	BIOLOGICAL_PROCESS	1	0,010927009	3	23	304	16798	MELO3C023560; MELO3C013440; MELO3C020783	MELO3C027290; MELO3C009584; MELO3C007283; MELO3C006046; MELO3C014684; MELO3C003141; MELO3C005593; MELO3C008232; MELO3C020865; MELO3C000307; MELO3C005179; MELO3C000009; MELO3C004148; MELO3C000029; MELO3C026327; MELO3C021982; MELO3C002738; MELO3C024155; MELO3C019731; MELO3C010759; MELO3C016115; MELO3C011159; MELO3C017834

GO:0006370	7-methylguanosine mRNA capping	BIOLOGICAL_PROCESS	1	0,028283234	3	34	304	16787	MELO3C026304; MELO3C009776; MELO3C012788	MELO3C010981; MELO3C010201; MELO3C005694; MELO3C021758; MELO3C008589; MELO3C002888; MELO3C022087; MELO3C020022; MELO3C017775; MELO3C015158; MELO3C019837; MELO3C017579; MELO3C027194; MELO3C015712; MELO3C007284; MELO3C013741; MELO3C008774; MELO3C008157; MELO3C002173; MELO3C006473; MELO3C008414; MELO3C005421; MELO3C003222; MELO3C007526; MELO3C020474; MELO3C026776; MELO3C023983;
GO:0009644	response to high light intensity	BIOLOGICAL_PROCESS	1	0,005185079	3	17	304	16804	MELO3C013974; MELO3C010748; MELO3C020589	MELO3C009241; MELO3C006079; MELO3C005482; MELO3C006384; MELO3C002020; MELO3C011150; MELO3C024348; MELO3C006536; MELO3C005923; MELO3C018023; MELO3C026365; MELO3C010229; MELO3C012925; MELO3C017883; MELO3C021171; MELO3C017876; MELO3C011885
GO:0006259	DNA metabolic process	BIOLOGICAL_PROCESS	1	0,011324473	4	678	303	16143	MELO3C009776; MELO3C026141; MELO3C010378; MELO3C010806	MELO3C006760; MELO3C020706; MELO3C014263; MELO3C013053; MELO3C014021; MELO3C002044; MELO3C014020; MELO3C006520; MELO3C004226; MELO3C002168; MELO3C003016; MELO3C008825; MELO3C008704; MELO3C004227; MELO3C008829; MELO3C003019; MELO3C027337; MELO3C026127; MELO3C027214; MELO3C025396; MELO3C025395; MELO3C017775; MELO3C010901; MELO3C018624; MELO3C014035; MELO3C002173; MELO3C008833;
GO:0010188	response to microbial phytotoxin	BIOLOGICAL_PROCESS	1	0,035527497	1	1	306	16820	MELO3C002148	MELO3C004372
GO:0006221	pyrimidine nucleotide biosynthetic process	BIOLOGICAL_PROCESS	1	0,04920819	2	18	305	16803	MELO3C009423; MELO3C005067	MELO3C008043; MELO3C012572; MELO3C005122; MELO3C014189; MELO3C006256; MELO3C006993; MELO3C009854; MELO3C023314; MELO3C002149; MELO3C002338; MELO3C024340; MELO3C016297; MELO3C015352; MELO3C005939; MELO3C017855; MELO3C015940; MELO3C011305; MELO3C013218
GO:0042752	regulation of circadian rhythm	BIOLOGICAL_PROCESS	1	0,008348753	2	6	305	16815	MELO3C025049; MELO3C020783	MELO3C015209; MELO3C025357; MELO3C005120; MELO3C004018; MELO3C025191; MELO3C011754
GO:0010155	regulation of proton transport	BIOLOGICAL_PROCESS	1	0,035527497	1	1	306	16820	MELO3C016696	MELO3C025720
GO:0004665	prephenate dehydrogenase (NADP+) activity	MOLECULAR_FUNCTION	1	0,017923867	1	0	306	16821	MELO3C004475	

GO:0016758	transferase activity, transferring hexosyl groups	MOLECULAR _FUNCTION	1	0,011308174	1	391	306	16430	MELO3C017104	MELO3C018629; MELO3C019719; MELO3C020949; MELO3C002165; MELO3C002287; MELO3C002166; MELO3C005795; MELO3C002047; MELO3C005799; MELO3C026247; MELO3C026369; MELO3C016445; MELO3C018627; MELO3C021805; MELO3C012097; MELO3C004474; MELO3C012096; MELO3C007749; MELO3C018630; MELO3C018632; MELO3C026373; MELO3C024194; MELO3C018631; MELO3C018634; MELO3C016697; MELO3C025283; MELO3C018635;
GO:0016881	acid-amino acid ligase activity	MOLECULAR _FUNCTION	1	0,009142966	4	42	303	16779	MELO3C015867; MELO3C022707; MELO3C025232; MELO3C013359	MELO3C016407; MELO3C011378; MELO3C006100; MELO3C011153; MELO3C006046; MELO3C014684; MELO3C020827; MELO3C005691; MELO3C009310; MELO3C011072; MELO3C005277; MELO3C005674; MELO3C026704; MELO3C007439; MELO3C005733; MELO3C009417; MELO3C021530; MELO3C021252; MELO3C024782; MELO3C026341; MELO3C014115; MELO3C009120; MELO3C007283; MELO3C020814; MELO3C005683; MELO3C006555; MELO3C006710;
GO:0018822	nitrile hydratase activity	MOLECULAR _FUNCTION	1	0,017923867	1	0	306	16821	MELO3C025585	
GO:0080079	cellobiose glucosidase activity	MOLECULAR _FUNCTION	1	0,017923867	1	0	306	16821	MELO3C021253	
GO:0047172	shikimate O-hydroxycinnamoyltransferase activity	MOLECULAR _FUNCTION	1	0,035527497	1	1	306	16820	MELO3C027219	MELO3C023474
GO:0004402	histone acetyltransferase activity	MOLECULAR _FUNCTION	1	0,017693064	3	28	304	16793	MELO3C014860; MELO3C004100; MELO3C010806	MELO3C007593; MELO3C013698; MELO3C011851; MELO3C011774; MELO3C013356; MELO3C009471; MELO3C006243; MELO3C007211; MELO3C013253; MELO3C009635; MELO3C007015; MELO3C009633; MELO3C002885; MELO3C022788; MELO3C017030; MELO3C026222; MELO3C015474; MELO3C012527; MELO3C005161; MELO3C005162; MELO3C010476; MELO3C007627; MELO3C004615; MELO3C001964; MELO3C002318; MELO3C026234; MELO3C026433;
GO:0000170	sphingosine hydroxylase activity	MOLECULAR _FUNCTION	1	0,035527497	1	1	306	16820	MELO3C012088	MELO3C008543
GO:0033862	UMP kinase activity	MOLECULAR _FUNCTION	1	0,035527497	1	1	306	16820	MELO3C009423	MELO3C008043
GO:0050638	taxadien-5-alpha-ol O-acetyltransferase activity	MOLECULAR _FUNCTION	1	0,035527497	1	1	306	16820	MELO3C018368	MELO3C025311
GO:0080061	indole-3-acetonitrile nitrilase activity	MOLECULAR _FUNCTION	1	0,017923867	1	0	306	16821	MELO3C025585	

GO:0005096	GTPase activator activity	MOLECULAR_FUNCTION	1	0,009142966	4	42	303	16779	MELO3C018195; MELO3C007075; MELO3C011716; MELO3C018265	MELO3C012464; MELO3C013850; MELO3C002160; MELO3C013431; MELO3C004462; MELO3C014242; MELO3C004980; MELO3C025639; MELO3C006548; MELO3C004547; MELO3C003413; MELO3C003977; MELO3C021110; MELO3C006408; MELO3C022488; MELO3C017792; MELO3C018264; MELO3C020360; MELO3C025077; MELO3C019359; MELO3C015111; MELO3C002808; MELO3C027373; MELO3C017654; MELO3C017813; MELO3C017779; MELO3C013721;
GO:0051741	2-methyl-6-phytyl-1,4-benzoquinone methyltransferase activity	MOLECULAR_FUNCTION	1	0,017923867	1	0	306	16821	MELO3C014321	
GO:0015220	choline transmembrane transporter activity	MOLECULAR_FUNCTION	1	0,017923867	1	0	306	16821	MELO3C020808	
GO:0051082	unfolded protein binding	MOLECULAR_FUNCTION	1	0,021826864	7	148	300	16673	MELO3C004636; MELO3C013792; MELO3C008871; MELO3C018950; MELO3C009408; MELO3C023526; MELO3C011379	MELO3C013215; MELO3C013333; MELO3C014661; MELO3C020425; MELO3C007610; MELO3C009996; MELO3C008428; MELO3C003534; MELO3C026888; MELO3C004506; MELO3C026886; MELO3C024104; MELO3C019433; MELO3C001916; MELO3C017379; MELO3C018866; MELO3C004194; MELO3C014551; MELO3C009245; MELO3C010230; MELO3C020799; MELO3C005449; MELO3C002214; MELO3C023267; MELO3C006935; MELO3C007908; MELO3C016178;
GO:0004697	protein kinase C activity	MOLECULAR_FUNCTION	1	0,04920819	2	18	305	16803	MELO3C007047; MELO3C013476	MELO3C012376; MELO3C012751; MELO3C002781; MELO3C004520; MELO3C006602; MELO3C005408; MELO3C023003; MELO3C001920; MELO3C024168; MELO3C001921; MELO3C005407; MELO3C025720; MELO3C015495; MELO3C017135; MELO3C001919; MELO3C010857; MELO3C016889; MELO3C021090
GO:0050662	coenzyme binding	MOLECULAR_FUNCTION	1	0,048984136	1	314	306	16507	MELO3C008985	MELO3C006085; MELO3C016329; MELO3C007053; MELO3C021919; MELO3C007054; MELO3C007051; MELO3C011431; MELO3C013057; MELO3C007057; MELO3C007055; MELO3C007056; MELO3C007612; MELO3C013171; MELO3C006405; MELO3C008946; MELO3C025712; MELO3C007613; MELO3C002842; MELO3C026007; MELO3C002843; MELO3C020385; MELO3C002844; MELO3C026005; MELO3C026006; MELO3C026004; MELO3C027332; MELO3C013979;
GO:0047427	cyanoalanine nitrilase activity	MOLECULAR_FUNCTION	1	0,017923867	1	0	306	16821	MELO3C025585	
GO:0004813	alanine-tRNA ligase activity	MOLECULAR_FUNCTION	1	0,010607789	2	7	305	16814	MELO3C000425; MELO3C027308	MELO3C012870; MELO3C010097; MELO3C024031; MELO3C000756; MELO3C018624; MELO3C027271; MELO3C013645
GO:0047558	3-cyanoalanine hydratase activity	MOLECULAR_FUNCTION	1	0,017923867	1	0	306	16821	MELO3C025585	

GO:0004034	aldose 1-epimerase activity	MOLECULAR_FUNCTION	1	0,008348753	2	6	305	16815	MELO3C016314; MELO3C006055	MELO3C017161; MELO3C004001; MELO3C017162; MELO3C017363; MELO3C017448; MELO3C009884
GO:0005366	myo-inositol:proton symporter activity	MOLECULAR_FUNCTION	1	0,017923867	1	0	306	16821	MELO3C017757	
GO:0031624	ubiquitin conjugating enzyme binding	MOLECULAR_FUNCTION	1	0,035527497	1	1	306	16820	MELO3C018461	MELO3C023546
GO:0071522	ureidoglycine aminohydrolase activity	MOLECULAR_FUNCTION	1	0,017923867	1	0	306	16821	MELO3C014174	
GO:0047205	quinate O-hydroxycinnamoyltransferase activity	MOLECULAR_FUNCTION	1	0,017923867	1	0	306	16821	MELO3C027219	
GO:0080124	pheophytinase activity	MOLECULAR_FUNCTION	1	0,017923867	1	0	306	16821	MELO3C023590	
GO:0004137	deoxycytidine kinase activity	MOLECULAR_FUNCTION	1	0,017923867	1	0	306	16821	MELO3C022212	
GO:0008420	CTD phosphatase activity	MOLECULAR_FUNCTION	1	0,035527497	1	1	306	16820	MELO3C010744	MELO3C007164
GO:0033730	arogenate dehydrogenase (NADP+) activity	MOLECULAR_FUNCTION	1	0,017923867	1	0	306	16821	MELO3C004475	
GO:0042624	ATPase activity, uncoupled	MOLECULAR_FUNCTION	1	0,034590522	3	37	304	16784	MELO3C024028; MELO3C015733; MELO3C017908	MELO3C015615; MELO3C005694; MELO3C004004; MELO3C002023; MELO3C011192; MELO3C021972; MELO3C004027; MELO3C007659; MELO3C017150; MELO3C022562; MELO3C023476; MELO3C026888; MELO3C021157; MELO3C017450; MELO3C024243; MELO3C016189; MELO3C023052; MELO3C024284; MELO3C017528; MELO3C009324; MELO3C015907; MELO3C010251; MELO3C026913; MELO3C025549; MELO3C002213; MELO3C022910; MELO3C002633;
GO:0009882	blue light photoreceptor activity	MOLECULAR_FUNCTION	1	0,035527497	1	1	306	16820	MELO3C013476	MELO3C025720
GO:0016277	[myelin basic protein]-arginine N-methyltransferase activity	MOLECULAR_FUNCTION	1	0,017923867	1	0	306	16821	MELO3C026636	
GO:0004842	ubiquitin-protein transferase activity	MOLECULAR_FUNCTION	1	0,01225715	7	131	300	16690	MELO3C018461; MELO3C011882; MELO3C005490; MELO3C022707; MELO3C025232; MELO3C007711; MELO3C003563	MELO3C003490; MELO3C012003; MELO3C004460; MELO3C011153; MELO3C013694; MELO3C020827; MELO3C014022; MELO3C020149; MELO3C012481; MELO3C022725; MELO3C005277; MELO3C022726; MELO3C026528; MELO3C024469; MELO3C022842; MELO3C007339; MELO3C021512; MELO3C026527; MELO3C004903; MELO3C018740; MELO3C012406; MELO3C012407; MELO3C014427; MELO3C008310; MELO3C020316; MELO3C014270; MELO3C023546;
GO:0004726	non-membrane spanning protein tyrosine phosphatase activity	MOLECULAR_FUNCTION	1	0,035527497	1	1	306	16820	MELO3C021441	MELO3C009840
GO:0071007	U2-type catalytic step 2 spliceosome	CELLULAR_COMPONENT	1	0,017923867	1	0	306	16821	MELO3C015733	

GO:0005730	nucleolus	CELLULAR_COMPONENT	1	0,026607121	10	245	297	16576	MELO3C006160; MELO3C024028; MELO3C015627; MELO3C006154; MELO3C024474; MELO3C016101; MELO3C011408; MELO3C004553; MELO3C004204; MELO3C022204	MELO3C010584; MELO3C011795; MELO3C021919; MELO3C006760; MELO3C003491; MELO3C002168; MELO3C021598; MELO3C024989; MELO3C004227; MELO3C018062; MELO3C019034; MELO3C017650; MELO3C016321; MELO3C014706; MELO3C024180; MELO3C008032; MELO3C010355; MELO3C008157; MELO3C002173; MELO3C014153; MELO3C013185; MELO3C002299; MELO3C023545; MELO3C008835; MELO3C023306; MELO3C006657; MELO3C026259;
GO:0005846	nuclear cap binding complex	CELLULAR_COMPONENT	1	0,017923867	1	0	306	16821	MELO3C026304	
GO:0005783	endoplasmic reticulum	CELLULAR_COMPONENT	1	0,014998725	15	418	292	16403	MELO3C012088; MELO3C022707; MELO3C003282; MELO3C015929; MELO3C003581; MELO3C004023; MELO3C004366; MELO3C003313; MELO3C006316; MELO3C006959; MELO3C022783; MELO3C018461; MELO3C024474; MELO3C012716; MELO3C016696	MELO3C019959; MELO3C003372; MELO3C020821; MELO3C002165; MELO3C002166; MELO3C006405; MELO3C009914; MELO3C006525; MELO3C025156; MELO3C017891; MELO3C024187; MELO3C018740; MELO3C017653; MELO3C017652; MELO3C017413; MELO3C025390; MELO3C016449; MELO3C016219; MELO3C018518; MELO3C002052; MELO3C003263; MELO3C003383; MELO3C017661; MELO3C019722; MELO3C017542; MELO3C015246; MELO3C015126;
GO:0010445	nuclear dicing body	CELLULAR_COMPONENT	1	0,035527497	1	1	306	16820	MELO3C015627	MELO3C005929
GO:0009707	chloroplast outer membrane	CELLULAR_COMPONENT	1	0,04920819	2	18	305	16803	MELO3C021253; MELO3C006974	MELO3C015416; MELO3C017968; MELO3C006133; MELO3C004471; MELO3C016719; MELO3C004591; MELO3C004474; MELO3C002387; MELO3C020610; MELO3C024587; MELO3C017360; MELO3C018772; MELO3C019874; MELO3C014409; MELO3C014605; MELO3C011502; MELO3C011415; MELO3C013766
GO:0009706	chloroplast inner membrane	CELLULAR_COMPONENT	1	0,044030549	3	41	304	16780	MELO3C016354; MELO3C014321; MELO3C014379	MELO3C011311; MELO3C011950; MELO3C014389; MELO3C006105; MELO3C011150; MELO3C006344; MELO3C005999; MELO3C020500; MELO3C026802; MELO3C023998; MELO3C020560; MELO3C004867; MELO3C005838; MELO3C026723; MELO3C023994; MELO3C023131; MELO3C021073; MELO3C021074; MELO3C010989; MELO3C017774; MELO3C010229; MELO3C014578; MELO3C015704; MELO3C016817; MELO3C010074; MELO3C014596; MELO3C023747;
GO:0009705	plant-type vacuole membrane	CELLULAR_COMPONENT	1	0,025279833	2	12	305	16809	MELO3C016475; MELO3C017757	MELO3C011146; MELO3C008088; MELO3C025972; MELO3C026522; MELO3C026971; MELO3C007980; MELO3C003783; MELO3C012405; MELO3C010334; MELO3C008406; MELO3C009170; MELO3C022448

GO:0016607	nuclear speck	CELLULAR_COMPONENT	1	0,016191216	3	27	304	16794	MELO3C024028; MELO3C015627; MELO3C017908	MELO3C011256; MELO3C012489; MELO3C008488; MELO3C004440; MELO3C022928; MELO3C014086; MELO3C005035; MELO3C024822; MELO3C002326; MELO3C016008; MELO3C014823; MELO3C005382; MELO3C015826; MELO3C013781; MELO3C023809; MELO3C023427; MELO3C024757; MELO3C021320; MELO3C017365; MELO3C026275; MELO3C019500; MELO3C016115; MELO3C012616; MELO3C010637; MELO3C019702; MELO3C014459; MELO3C012579
GO:0000151	ubiquitin ligase complex	CELLULAR_COMPONENT	1	0,038140521	6	132	301	16689	MELO3C006948; MELO3C007711; MELO3C011882; MELO3C005490; MELO3C014129; MELO3C009879	MELO3C012003; MELO3C013212; MELO3C013694; MELO3C008023; MELO3C003650; MELO3C020149; MELO3C022725; MELO3C002045; MELO3C022726; MELO3C006647; MELO3C002960; MELO3C026528; MELO3C006645; MELO3C007339; MELO3C021512; MELO3C007855; MELO3C026527; MELO3C019281; MELO3C003537; MELO3C022166; MELO3C025152; MELO3C022280; MELO3C012406; MELO3C012527; MELO3C012407; MELO3C018869; MELO3C017705;
GO:0030692	Noc4p-Nop14p complex	CELLULAR_COMPONENT	1	0,017923867	1	0	306	16821	MELO3C011408	
GO:0000243	commitment complex	CELLULAR_COMPONENT	1	0,017923867	1	0	306	16821	MELO3C026304	
GO:0010168	ER body	CELLULAR_COMPONENT	1	0,017923867	1	0	306	16821	MELO3C012716	

Supplementary Table 2.F Gene Ontology terms (GO terms) of the cluster 2.5 obtained considering the comparison between lines the postharvest ripening time fruit during storage at 20.5°C and 88% relative humidity for 18 d the near-isogenic line SC10-2 and its parental ''Piel de Sapo'' obtained according to the differentially expressed gene pattern (Supl. Table 2.A)

GO ID	GO Name	GO Category	FDR	P-Value	SC10-2	PS	Non Annot Test	Non Annot Reference	TestSet Sequences	RefSet Sequences
GO:0016308	1-phosphatidylinositol-4-phosphate 5-kinase activity	MOLECULAR_FUNCTION	0,304197153	2,25E-04	3	7	214	16904	MELO3C010456; MELO3C006050; MELO3C003057	MELO3C019075; MELO3C000333; MELO3C012475; MELO3C014374; MELO3C005148; MELO3C009382; MELO3C010116
GO:0055114	oxidation-reduction process	BIOLOGICAL_PROCESS	0,340910349	3,28E-04	7	1688	210	15223	MELO3C024222; MELO3C013829; MELO3C019404; MELO3C009886; MELO3C023986; MELO3C011601; MELO3C001994	MELO3C018628; MELO3C002280; MELO3C005792; MELO3C012088; MELO3C006644; MELO3C004465; MELO3C005795; MELO3C012080; MELO3C015590; MELO3C015591; MELO3C015592; MELO3C015593; MELO3C017772; MELO3C015595; MELO3C015596; MELO3C024061; MELO3C018623; MELO3C018625; MELO3C018626; MELO3C002293; MELO3C007980; MELO3C004475; MELO3C007984; MELO3C008836; MELO3C020952; MELO3C003149; MELO3C005329;
GO:0033169	histone H3-K9 demethylation	BIOLOGICAL_PROCESS	0,404853209	9,43E-04	2	2	215	16909	MELO3C025053; MELO3C019813	MELO3C002327; MELO3C004836
GO:0008270	zinc ion binding	MOLECULAR_FUNCTION	0,404853209	5,80E-04	31	1246	186	15665	MELO3C009670; MELO3C009234; MELO3C014562; MELO3C006367; MELO3C009914; MELO3C022568; MELO3C005513; MELO3C004524; MELO3C002646; MELO3C018264; MELO3C022066; MELO3C012628; MELO3C025053; MELO3C010522; MELO3C013879; MELO3C017755; MELO3C019813; MELO3C009984; MELO3C013883; MELO3C009101; MELO3C025725; MELO3C003423; MELO3C021348; MELO3C021462; MELO3C017380; MELO3C021047; MELO3C017320;	MELO3C004460; MELO3C005792; MELO3C014022; MELO3C007732; MELO3C005559; MELO3C007735; MELO3C003139; MELO3C009913; MELO3C026249; MELO3C010904; MELO3C015110; MELO3C019951; MELO3C018864; MELO3C017536; MELO3C018624; MELO3C017777; MELO3C017537; MELO3C021804; MELO3C021806; MELO3C004472; MELO3C012095; MELO3C004232; MELO3C002297; MELO3C002055; MELO3C004237; MELO3C004239; MELO3C004238;
GO:0031491	nucleosome binding	MOLECULAR_FUNCTION	0,404853209	9,43E-04	2	2	215	16909	MELO3C021353; MELO3C004459	MELO3C021352; MELO3C009890
GO:0005524	ATP binding	MOLECULAR_FUNCTION	0,705878947	0,00310521	41	2020	176	14891	MELO3C016868; MELO3C014687; MELO3C005094; MELO3C013254; MELO3C002382; MELO3C008489; MELO3C003057; MELO3C020666; MELO3C021353; MELO3C006925; MELO3C023098; MELO3C026025; MELO3C019411; MELO3C018344; MELO3C026263; MELO3C018106; MELO3C013879; MELO3C009480; MELO3C012730; MELO3C027092; MELO3C004591; MELO3C005565; MELO3C009328; MELO3C014272; MELO3C003146; MELO3C003222; MELO3C023986;	MELO3C014269; MELO3C003133; MELO3C004463; MELO3C007972; MELO3C006648; MELO3C007978; MELO3C008825; MELO3C003139; MELO3C008829; MELO3C026243; MELO3C019951; MELO3C000093; MELO3C025392; MELO3C015599; MELO3C018624; MELO3C020958; MELO3C008832; MELO3C008831; MELO3C002299; MELO3C008835; MELO3C005329; MELO3C008838; MELO3C026256; MELO3C024079; MELO3C019967; MELO3C019939; MELO3C019938;

GO:0008353	RNA polymerase II carboxy-terminal domain kinase activity	MOLECULAR_FUNCTION	0,780094579	0,00520173	3	25	214	16886	MELO3C022196; MELO3C019411; MELO3C002382	MELO3C007454; MELO3C002140; MELO3C012361; MELO3C009014; MELO3C002003; MELO3C004567; MELO3C007615; MELO3C001212; MELO3C004349; MELO3C001378; MELO3C006605; MELO3C020186; MELO3C022286; MELO3C017059; MELO3C015376; MELO3C025274; MELO3C014702; MELO3C013799; MELO3C008774; MELO3C009967; MELO3C007623; MELO3C024972; MELO3C017342; MELO3C026178; MELO3C011886
GO:0043044	ATP-dependent chromatin remodeling	BIOLOGICAL_PROCESS	0,788464754	0,00542445	2	7	215	16904	MELO3C021353; MELO3C004459	MELO3C021352; MELO3C021430; MELO3C007903; MELO3C007894; MELO3C006760; MELO3C005059; MELO3C007648
GO:0006972	hyperosmotic response	BIOLOGICAL_PROCESS	0,819860774	0,01136775	2	11	215	16900	MELO3C008815; MELO3C025349	MELO3C004428; MELO3C009971; MELO3C010211; MELO3C006142; MELO3C006721; MELO3C012085; MELO3C008666; MELO3C004127; MELO3C024239; MELO3C002752; MELO3C013249
GO:0032790	ribosome disassembly	BIOLOGICAL_PROCESS	0,819860774	0,01266931	1	0	216	16911	MELO3C005565	
GO:0007126	meiotic nuclear division	BIOLOGICAL_PROCESS	0,819860774	0,00816862	5	93	212	16818	MELO3C023475; MELO3C014687; MELO3C023986; MELO3C004459; MELO3C014877	MELO3C012361; MELO3C003892; MELO3C006201; MELO3C024822; MELO3C004027; MELO3C016280; MELO3C018062; MELO3C003338; MELO3C026602; MELO3C005714; MELO3C026127; MELO3C021157; MELO3C019674; MELO3C018187; MELO3C019510; MELO3C021272; MELO3C024265; MELO3C024782; MELO3C015113; MELO3C017258; MELO3C015235; MELO3C017338; MELO3C015434; MELO3C017216; MELO3C012446; MELO3C010743; MELO3C008594;
GO:0034551	mitochondrial respiratory chain complex III assembly	BIOLOGICAL_PROCESS	0,819860774	0,01266931	1	0	216	16911	MELO3C008037	
GO:0045843	negative regulation of striated muscle tissue development	BIOLOGICAL_PROCESS	0,819860774	0,01266931	1	0	216	16911	MELO3C015103	
GO:0018996	molting cycle, collagen and cuticulin-based cuticle	BIOLOGICAL_PROCESS	0,819860774	0,0089881	3	31	214	16880	MELO3C008815; MELO3C023475; MELO3C003222	MELO3C015218; MELO3C014920; MELO3C010960; MELO3C008488; MELO3C006662; MELO3C004440; MELO3C007374; MELO3C004123; MELO3C009413; MELO3C004945; MELO3C026800; MELO3C025972; MELO3C025310; MELO3C023594; MELO3C016321; MELO3C024020; MELO3C017216; MELO3C013218; MELO3C010795; MELO3C008690; MELO3C007085; MELO3C014153; MELO3C023127; MELO3C017291; MELO3C005963; MELO3C023427; MELO3C017290;
GO:0030183	B cell differentiation	BIOLOGICAL_PROCESS	0,819860774	0,01266931	1	0	216	16911	MELO3C015103	
GO:0048577	negative regulation of short-day photoperiodism, flowering	BIOLOGICAL_PROCESS	0,819860774	0,01266931	1	0	216	16911	MELO3C019813	
GO:0048579	negative regulation of long-day photoperiodism, flowering	BIOLOGICAL_PROCESS	0,819860774	0,01266931	1	0	216	16911	MELO3C019813	
GO:0030538	embryonic genitalia morphogenesis	BIOLOGICAL_PROCESS	0,819860774	0,01266931	1	0	216	16911	MELO3C013879	
GO:0035103	sterol regulatory element binding protein cleavage	BIOLOGICAL_PROCESS	0,819860774	0,01266931	1	0	216	16911	MELO3C025349	
GO:0001570	vasculogenesis	BIOLOGICAL_PROCESS	0,819860774	0,01266931	1	0	216	16911	MELO3C015103	
GO:0010600	regulation of auxin biosynthetic process	BIOLOGICAL_PROCESS	0,819860774	0,01266931	1	0	216	16911	MELO3C025091	
GO:0003696	satellite DNA binding	MOLECULAR_FUNCTION	0,819860774	0,01266931	1	0	216	16911	MELO3C023986	
GO:0004636	phosphoribosyl-ATP diphosphatase activity	MOLECULAR_FUNCTION	0,819860774	0,01266931	1	0	216	16911	MELO3C005094	
GO:0004635	phosphoribosyl-AMP cyclohydrolase activity	MOLECULAR_FUNCTION	0,819860774	0,01266931	1	0	216	16911	MELO3C005094	
GO:0004651	polynucleotide 5'-phosphatase activity	MOLECULAR_FUNCTION	0,819860774	0,01266931	1	0	216	16911	MELO3C003222	
GO:0004572	mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase activity	MOLECULAR_FUNCTION	0,819860774	0,01266931	1	0	216	16911	MELO3C009914	
GO:0008139	nuclear localization sequence binding	MOLECULAR_FUNCTION	0,819860774	0,01266931	1	0	216	16911	MELO3C020836	
GO:0017077	oxidative phosphorylation uncoupler activity	MOLECULAR_FUNCTION	0,819860774	0,01266931	1	0	216	16911	MELO3C014724	

GO:0003918	DNA topoisomerase type II (ATP-hydrolyzing) activity	MOLECULAR_FUNCTION	0,819860774	0,00969922	2	10	215	16901	MELO3C019163; MELO3C023986	MELO3C022420; MELO3C011386; MELO3C003071; MELO3C019089; MELO3C014153; MELO3C024924; MELO3C014639; MELO3C019090; MELO3C024756; MELO3C024755
GO:0004484	mRNA guanylyltransferase activity	MOLECULAR_FUNCTION	0,819860774	0,01266931	1	0	216	16911	MELO3C003222	
GO:0008672	2-dehydro-3-deoxyglucarate aldolase activity	MOLECULAR_FUNCTION	0,819860774	0,01266931	1	0	216	16911	MELO3C013779	
GO:0004743	pyruvate kinase activity	MOLECULAR_FUNCTION	0,819860774	0,00672422	2	8	215	16903	MELO3C014272; MELO3C011769	MELO3C005271; MELO3C014732; MELO3C003381; MELO3C018027; MELO3C019624; MELO3C024509; MELO3C024508; MELO3C006964
GO:0034990	nuclear mitotic cohesin complex	CELLULAR_COMPONENT	0,819860774	0,01266931	1	0	216	16911	MELO3C012730	
GO:0008623	CHRAC	CELLULAR_COMPONENT	0,819860774	0,01266931	1	0	216	16911	MELO3C023986	
GO:0000800	lateral element	CELLULAR_COMPONENT	0,819860774	0,01266931	1	0	216	16911	MELO3C014687	
GO:0016246	RNA interference	BIOLOGICAL_PROCESS	0,861424734	0,014041	3	37	214	16874	MELO3C020836; MELO3C013879; MELO3C014035	MELO3C011257; MELO3C007894; MELO3C014221; MELO3C005153; MELO3C014440; MELO3C010042; MELO3C005757; MELO3C021974; MELO3C026304; MELO3C003636; MELO3C023332; MELO3C007816; MELO3C015492; MELO3C016262; MELO3C019378; MELO3C001957; MELO3C019712; MELO3C025450; MELO3C014706; MELO3C012127; MELO3C014129; MELO3C010254; MELO3C015627; MELO3C008151; MELO3C015907; MELO3C013185; MELO3C022813;
GO:0010171	body morphogenesis	BIOLOGICAL_PROCESS	0,898501477	0,01512608	4	71	213	16840	MELO3C003222; MELO3C020836; MELO3C004459; MELO3C014877	MELO3C009592; MELO3C014221; MELO3C002120; MELO3C004344; MELO3C004622; MELO3C007816; MELO3C022488; MELO3C025310; MELO3C019034; MELO3C018102; MELO3C025275; MELO3C019997; MELO3C014708; MELO3C019996; MELO3C013814; MELO3C017216; MELO3C012449; MELO3C019956; MELO3C014153; MELO3C000924; MELO3C022016; MELO3C023865; MELO3C008835; MELO3C007829; MELO3C007903; MELO3C023741; MELO3C026971;
GO:0030955	potassium ion binding	MOLECULAR_FUNCTION	0,959488919	0,0170587	2	14	215	16897	MELO3C014272; MELO3C011769	MELO3C005271; MELO3C020719; MELO3C014732; MELO3C003381; MELO3C004198; MELO3C012593; MELO3C024509; MELO3C024508; MELO3C023606; MELO3C006964; MELO3C018027; MELO3C019624; MELO3C024471; MELO3C012911
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	BIOLOGICAL_PROCESS	1	0,02371263	2	17	215	16894	MELO3C026263; MELO3C013879	MELO3C015714; MELO3C011145; MELO3C013051; MELO3C008956; MELO3C006767; MELO3C021931; MELO3C008955; MELO3C026304; MELO3C026612; MELO3C026327; MELO3C007816; MELO3C024028; MELO3C025497; MELO3C003804; MELO3C025498; MELO3C015113; MELO3C026290
GO:0070830	bicellular tight junction assembly	BIOLOGICAL_PROCESS	1	0,04972657	1	3	216	16908	MELO3C006574	MELO3C007829; MELO3C006575; MELO3C022488

GO:0006383	transcription from RNA polymerase III promoter	BIOLOGICAL_PROCESS	1	0,03672829	2	22	215	16889	MELO3C002646; MELO3C017544	MELO3C021804; MELO3C014058; MELO3C012297; MELO3C008157; MELO3C002173; MELO3C009662; MELO3C007348; MELO3C012480; MELO3C021758; MELO3C013095; MELO3C009776; MELO3C023634; MELO3C026899; MELO3C015360; MELO3C003707; MELO3C017782; MELO3C019700; MELO3C017775; MELO3C016456; MELO3C017579; MELO3C015712; MELO3C017658
GO:0006265	DNA topological change	BIOLOGICAL_PROCESS	1	0,02864406	2	19	215	16892	MELO3C019163; MELO3C023986	MELO3C014689; MELO3C009682; MELO3C011386; MELO3C003071; MELO3C005694; MELO3C009586; MELO3C014153; MELO3C019090; MELO3C024756; MELO3C024755; MELO3C006788; MELO3C022750; MELO3C022420; MELO3C019089; MELO3C003609; MELO3C003608; MELO3C014639; MELO3C016965; MELO3C012446
GO:0000398	mRNA splicing, via spliceosome	BIOLOGICAL_PROCESS	1	0,02876654	5	130	212	16781	MELO3C012730; MELO3C023475; MELO3C019779; MELO3C022000; MELO3C014877	MELO3C010981; MELO3C012489; MELO3C013333; MELO3C004580; MELO3C008023; MELO3C021758; MELO3C002045; MELO3C020824; MELO3C006125; MELO3C023531; MELO3C018062; MELO3C000014; MELO3C020022; MELO3C017775; MELO3C011313; MELO3C013741; MELO3C014555; MELO3C010355; MELO3C008151; MELO3C008157; MELO3C002173; MELO3C023428; MELO3C008798; MELO3C006416; MELO3C023545; MELO3C023823; MELO3C023427;
GO:0032776	DNA methylation on cytosine	BIOLOGICAL_PROCESS	1	0,0375306	1	2	216	16909	MELO3C025053	MELO3C022551; MELO3C015649
GO:2000034	regulation of seed maturation	BIOLOGICAL_PROCESS	1	0,0375306	1	2	216	16909	MELO3C009101	MELO3C005929; MELO3C020484
GO:0071456	cellular response to hypoxia	BIOLOGICAL_PROCESS	1	0,02517885	1	1	216	16910	MELO3C013879	MELO3C026482
GO:0045739	positive regulation of DNA repair	BIOLOGICAL_PROCESS	1	0,0375306	1	2	216	16909	MELO3C026332	MELO3C002326; MELO3C016858
GO:0007062	sister chromatid cohesion	BIOLOGICAL_PROCESS	1	0,03124992	2	20	215	16891	MELO3C012730; MELO3C014687	MELO3C006251; MELO3C009682; MELO3C013696; MELO3C008766; MELO3C009536; MELO3C006327; MELO3C005824; MELO3C016064; MELO3C016065; MELO3C018187; MELO3C020001; MELO3C010507; MELO3C023581; MELO3C024243; MELO3C017664; MELO3C017663; MELO3C017258; MELO3C015235; MELO3C011228; MELO3C010631
GO:0006406	mRNA export from nucleus	BIOLOGICAL_PROCESS	1	0,04867873	2	26	215	16885	MELO3C013879; MELO3C012713	MELO3C011256; MELO3C020407; MELO3C005694; MELO3C003078; MELO3C004622; MELO3C021931; MELO3C026304; MELO3C016280; MELO3C022166; MELO3C015492; MELO3C025497; MELO3C025498; MELO3C019034; MELO3C026441; MELO3C015113; MELO3C015733; MELO3C014129; MELO3C014532; MELO3C013443; MELO3C005265; MELO3C021887; MELO3C009808; MELO3C005946; MELO3C011924; MELO3C015447; MELO3C016756
GO:0010106	cellular response to iron ion starvation	BIOLOGICAL_PROCESS	1	0,02517885	1	1	216	16910	MELO3C017320	MELO3C017166

GO:0007091	metaphase/anaphase transition of mitotic cell cycle	BIOLOGICAL_PROCESS	1	0,02864406	2	19	215	16892	MELO3C012730; MELO3C022930	MELO3C011895; MELO3C014684; MELO3C014573; MELO3C003047; MELO3C006972; MELO3C002234; MELO3C004622; MELO3C005866; MELO3C005733; MELO3C024685; MELO3C017066; MELO3C017087; MELO3C025232; MELO3C026580; MELO3C017995; MELO3C015235; MELO3C012437; MELO3C010920; MELO3C013359
GO:0032049	cardiolipin biosynthetic process	BIOLOGICAL_PROCESS	1	0,02517885	1	1	216	16910	MELO3C007010	MELO3C013700
GO:0010030	positive regulation of seed germination	BIOLOGICAL_PROCESS	1	0,04972657	1	3	216	16908	MELO3C009101	MELO3C020484; MELO3C004632; MELO3C009627
GO:0006569	tryptophan catabolic process	BIOLOGICAL_PROCESS	1	0,04972657	1	3	216	16908	MELO3C012201	MELO3C023775; MELO3C010461; MELO3C024595
GO:0031055	chromatin remodeling at centromere	BIOLOGICAL_PROCESS	1	0,04972657	1	3	216	16908	MELO3C023986	MELO3C006760; MELO3C005059; MELO3C017558
GO:0016233	telomere capping	BIOLOGICAL_PROCESS	1	0,0375306	1	2	216	16909	MELO3C014298	MELO3C018187; MELO3C006292
GO:0010495	long-distance posttranscriptional gene silencing	BIOLOGICAL_PROCESS	1	0,02517885	1	1	216	16910	MELO3C014035	MELO3C017106
GO:0046488	phosphatidylinositol metabolic process	BIOLOGICAL_PROCESS	1	0,0422135	3	58	214	16853	MELO3C010456; MELO3C006050; MELO3C003057	MELO3C013178; MELO3C007931; MELO3C020821; MELO3C024309; MELO3C020987; MELO3C020989; MELO3C025637; MELO3C005634; MELO3C019075; MELO3C000333; MELO3C022481; MELO3C015670; MELO3C026365; MELO3C026440; MELO3C017214; MELO3C019875; MELO3C022480; MELO3C017019; MELO3C010621; MELO3C010667; MELO3C015647; MELO3C011047; MELO3C016737; MELO3C013982; MELO3C009840; MELO3C008992; MELO3C005285;
GO:0019318	hexose metabolic process	BIOLOGICAL_PROCESS	1	0,04860452	5	151	212	16760	MELO3C014272; MELO3C011769; MELO3C009914; MELO3C014724; MELO3C013829	MELO3C005272; MELO3C009351; MELO3C005396; MELO3C003491; MELO3C010186; MELO3C020949; MELO3C004980; MELO3C002287; MELO3C024509; MELO3C020428; MELO3C004465; MELO3C024508; MELO3C009913; MELO3C020780; MELO3C025275; MELO3C027332; MELO3C020263; MELO3C019557; MELO3C012925; MELO3C016048; MELO3C026482; MELO3C013979; MELO3C010862; MELO3C011710; MELO3C006491; MELO3C020837; MELO3C003381;
GO:0030466	chromatin silencing at silent mating-type cassette	BIOLOGICAL_PROCESS	1	0,04972657	1	3	216	16908	MELO3C013879	MELO3C022562; MELO3C009773; MELO3C010882
GO:0071044	histone mRNA catabolic process	BIOLOGICAL_PROCESS	1	0,0375306	1	2	216	16909	MELO3C013879	MELO3C011748; MELO3C017087
GO:0042078	germ-line stem cell division	BIOLOGICAL_PROCESS	1	0,02517885	1	1	216	16910	MELO3C008815	MELO3C008594
GO:0006346	methylation-dependent chromatin silencing	BIOLOGICAL_PROCESS	1	0,02517885	1	1	216	16910	MELO3C014035	MELO3C017558
GO:0005506	iron ion binding	MOLECULAR_FUNCTION	1	0,03808894	0	324	217	16587		MELO3C007174; MELO3C012522; MELO3C007175; MELO3C021914; MELO3C012088; MELO3C007058; MELO3C020028; MELO3C006644; MELO3C004221; MELO3C007611; MELO3C004584; MELO3C007059; MELO3C025712; MELO3C026802; MELO3C020385; MELO3C023893; MELO3C023530; MELO3C000772; MELO3C015591; MELO3C026487; MELO3C000770; MELO3C015592; MELO3C015593; MELO3C015595; MELO3C015596; MELO3C026484; MELO3C016686;
GO:0000182	rDNA binding	MOLECULAR_FUNCTION	1	0,0375306	1	2	216	16909	MELO3C023986	MELO3C012480; MELO3C020235

GO:0000156	phosphorelay response regulator activity	MOLECULAR_FUNCTION	1	0,04557323	2	25	215	16886	MELO3C017128; MELO3C020055	MELO3C005250; MELO3C009770; MELO3C004183; MELO3C010245; MELO3C003075; MELO3C005156; MELO3C005336; MELO3C000311; MELO3C001999; MELO3C017472; MELO3C019056; MELO3C010624; MELO3C021290; MELO3C013758; MELO3C016937; MELO3C012031; MELO3C006451; MELO3C006693; MELO3C012470; MELO3C022310; MELO3C025982; MELO3C005927; MELO3C003906; MELO3C010714; MELO3C016975
GO:0003680	AT DNA binding	MOLECULAR_FUNCTION	1	0,02517885	1	1	216	16910	MELO3C012730	MELO3C022471
GO:0051721	protein phosphatase 2A binding	MOLECULAR_FUNCTION	1	0,04972657	1	3	216	16908	MELO3C013879	MELO3C002748; MELO3C022178; MELO3C015113
GO:0047800	cysteamine dioxygenase activity	MOLECULAR_FUNCTION	1	0,04972657	1	3	216	16908	MELO3C009886	MELO3C017267; MELO3C008836; MELO3C013579
GO:0016435	rRNA (guanine) methyltransferase activity	MOLECULAR_FUNCTION	1	0,0375306	1	2	216	16909	MELO3C023306	MELO3C002238; MELO3C015412
GO:0000400	four-way junction DNA binding	MOLECULAR_FUNCTION	1	0,02517885	1	1	216	16910	MELO3C023986	MELO3C015928
GO:0008138	protein tyrosine/serine/threonine phosphatase activity	MOLECULAR_FUNCTION	1	0,02371263	2	17	215	16894	MELO3C023830; MELO3C003222	MELO3C012378; MELO3C009960; MELO3C014446; MELO3C007580; MELO3C009840; MELO3C021405; MELO3C004587; MELO3C020114; MELO3C002645; MELO3C004603; MELO3C026602; MELO3C019894; MELO3C018474; MELO3C026166; MELO3C011936; MELO3C026163; MELO3C013921
GO:0004385	guanylate kinase activity	MOLECULAR_FUNCTION	1	0,04972657	1	3	216	16908	MELO3C006574	MELO3C018452; MELO3C006575; MELO3C023150
GO:0003729	mRNA binding	MOLECULAR_FUNCTION	1	0,01917371	2	15	215	16896	MELO3C012411; MELO3C023986	MELO3C011157; MELO3C005382; MELO3C015714; MELO3C020705; MELO3C011385; MELO3C005482; MELO3C023836; MELO3C008722; MELO3C024822; MELO3C008956; MELO3C008955; MELO3C017020; MELO3C021296; MELO3C019953; MELO3C017841
GO:0003955	NAD(P)H dehydrogenase (quinone) activity	MOLECULAR_FUNCTION	1	0,0375306	1	2	216	16909	MELO3C007950	MELO3C005147; MELO3C012476
GO:0008780	acyl-[acyl-carrier-protein]-UDP-N-acetylglucosamine O-acyltransferase activity	MOLECULAR_FUNCTION	1	0,02517885	1	1	216	16910	MELO3C015455	MELO3C007369
GO:0009884	cytokinin receptor activity	MOLECULAR_FUNCTION	1	0,04972657	1	3	216	16908	MELO3C020055	MELO3C005250; MELO3C022310; MELO3C025982
GO:0004864	protein phosphatase inhibitor activity	MOLECULAR_FUNCTION	1	0,04972657	1	3	216	16908	MELO3C021670	MELO3C002748; MELO3C022178; MELO3C005380
GO:0003743	translation initiation factor activity	MOLECULAR_FUNCTION	1	0,04989364	4	105	213	16806	MELO3C002646; MELO3C002819; MELO3C002817; MELO3C006107	MELO3C010981; MELO3C010222; MELO3C020828; MELO3C004345; MELO3C004344; MELO3C020786; MELO3C023779; MELO3C020380; MELO3C000253; MELO3C019434; MELO3C014706; MELO3C016963; MELO3C012127; MELO3C017707; MELO3C011321; MELO3C006494; MELO3C014155; MELO3C010197; MELO3C012131; MELO3C002698; MELO3C023701; MELO3C015360; MELO3C018872; MELO3C018874; MELO3C014439; MELO3C011371; MELO3C002822;
GO:0008650	rRNA (uridine-2'-O-)-methyltransferase activity	MOLECULAR_FUNCTION	1	0,02517885	1	1	216	16910	MELO3C023306	MELO3C009184

GO:0004725	protein tyrosine phosphatase activity	MOLECULAR_FUNCTION	1	0,04557323	2	25	215	16886	MELO3C023830; MELO3C003222	MELO3C018606; MELO3C014446; MELO3C010061; MELO3C002645; MELO3C023674; MELO3C004603; MELO3C026602; MELO3C026166; MELO3C019876; MELO3C019734; MELO3C011936; MELO3C019875; MELO3C026163; MELO3C024481; MELO3C007580; MELO3C011186; MELO3C013860; MELO3C009840; MELO3C021405; MELO3C020114; MELO3C021441; MELO3C018474; MELO3C018159; MELO3C014438; MELO3C013921
GO:0000325	plant-type vacuole	CELLULAR_COMPONENT	1	0,02955212	3	50	214	16861	MELO3C011601; MELO3C013437; MELO3C013829	MELO3C002042; MELO3C022009; MELO3C024902; MELO3C020983; MELO3C020984; MELO3C022448; MELO3C026522; MELO3C015314; MELO3C012405; MELO3C010983; MELO3C011599; MELO3C007980; MELO3C003783; MELO3C001488; MELO3C009809; MELO3C026971; MELO3C016010; MELO3C016011; MELO3C024398; MELO3C026330; MELO3C009170; MELO3C011600; MELO3C011894; MELO3C008088; MELO3C010286; MELO3C012542; MELO3C009852;
GO:0000812	Swr1 complex	CELLULAR_COMPONENT	1	0,0375306	1	2	216	16909	MELO3C004459	MELO3C007894; MELO3C007648
GO:0005829	cytosol	CELLULAR_COMPONENT	1	0,02743781	3	734	214	16177	MELO3C020836; MELO3C013175; MELO3C007800	MELO3C021918; MELO3C014028; MELO3C004343; MELO3C014021; MELO3C012084; MELO3C014262; MELO3C004344; MELO3C004347; MELO3C005679; MELO3C005559; MELO3C008944; MELO3C007739; MELO3C026245; MELO3C025275; MELO3C016201; MELO3C026360; MELO3C026482; MELO3C025030; MELO3C018985; MELO3C010901; MELO3C018624; MELO3C017659; MELO3C016569; MELO3C019956; MELO3C018518; MELO3C002294; MELO3C003263;
GO:0031314	extrinsic component of mitochondrial inner membrane	CELLULAR_COMPONENT	1	0,04972657	1	3	216	16908	MELO3C007010	MELO3C013534; MELO3C018763; MELO3C022197
GO:0000118	histone deacetylase complex	CELLULAR_COMPONENT	1	0,0375306	1	2	216	16909	MELO3C015103	MELO3C016865; MELO3C021442
GO:0031410	cytoplasmic vesicle	CELLULAR_COMPONENT	1	0,02912388	12	1687	205	15224	MELO3C003659; MELO3C012201; MELO3C008037; MELO3C025255; MELO3C025594; MELO3C013780; MELO3C009328; MELO3C003146; MELO3C008815; MELO3C013769; MELO3C005513; MELO3C007800	MELO3C015119; MELO3C002280; MELO3C012088; MELO3C002286; MELO3C012085; MELO3C026249; MELO3C026243; MELO3C017775; MELO3C015599; MELO3C025391; MELO3C003142; MELO3C003144; MELO3C004477; MELO3C014270; MELO3C005328; MELO3C020951; MELO3C008838; MELO3C017300; MELO3C019962; MELO3C019939; MELO3C020928; MELO3C014249; MELO3C012068; MELO3C014246; MELO3C003595; MELO3C012061; MELO3C004445;
GO:0005935	cellular bud neck	CELLULAR_COMPONENT	1	0,0375306	1	2	216	16909	MELO3C020836	MELO3C013504; MELO3C013982

Supplementary Table 2.G Gene Ontology terms (GO terms) of the cluster 2.6 obtained considering the comparison between lines the postharvest ripening time fruit during storage at 20.5°C and 88% relative humidity for 18 d the near-isogenic line SC10-2 and its parental ''Piel de Sapo'' obtained according to the differentially expressed gene pattern (Supl. Table 2.A)

GO ID	GO Name	GO Category	FDR	P-Value	SC10-2	PS	Non Annot Test	Non Annot Reference	TestSet Sequences	RefSet Sequences
GO:0016206	catechol O-methyltransferase activity	MOLECULAR_FUNCTION	0,281888732	5,97E-05	2	1	75	17050	MELO3C027330; MELO3C014089	MELO3C024861
GO:0042446	hormone biosynthetic process	BIOLOGICAL_PROCESS	0,510918541	1,62E-04	4	57	73	16994	MELO3C027330; MELO3C027370; MELO3C014089; MELO3C013315	MELO3C011158; MELO3C012321; MELO3C013411; MELO3C013410; MELO3C007417; MELO3C022404; MELO3C024861; MELO3C025355; MELO3C024222; MELO3C016881; MELO3C009362; MELO3C002170; MELO3C009521; MELO3C009124; MELO3C000525; MELO3C021600; MELO3C002775; MELO3C002776; MELO3C004955; MELO3C000487; MELO3C019323; MELO3C012817; MELO3C014719; MELO3C019324; MELO3C014716; MELO3C017668; MELO3C016416;
GO:0015095	magnesium ion transmembrane transporter activity	MOLECULAR_FUNCTION	0,659113425	4,13E-04	2	5	75	17046	MELO3C026764; MELO3C000817	MELO3C026733; MELO3C000103; MELO3C011418; MELO3C019432; MELO3C004841
GO:0006968	cellular defense response	BIOLOGICAL_PROCESS	0,94386839	0,004495563	1	0	76	17051	MELO3C006765	
GO:0071395	cellular response to jasmonic acid stimulus	BIOLOGICAL_PROCESS	0,94386839	0,002016649	2	13	75	17038	MELO3C006765; MELO3C024357	MELO3C006046; MELO3C012221; MELO3C005466; MELO3C004610; MELO3C020450; MELO3C026577; MELO3C025152; MELO3C012527; MELO3C016852; MELO3C011439; MELO3C010774; MELO3C015436; MELO3C017559
GO:0071947	protein deubiquitination involved in ubiquitin-dependent protein catabolic process	BIOLOGICAL_PROCESS	0,94386839	0,004495563	1	0	76	17051	MELO3C018956	
GO:0010247	detection of phosphate ion	BIOLOGICAL_PROCESS	0,94386839	0,004495563	1	0	76	17051	MELO3C005035	
GO:0010400	rhamnogalacturonan I side chain metabolic process	BIOLOGICAL_PROCESS	0,94386839	0,004495563	1	0	76	17051	MELO3C003916	
GO:0070485	dehydro-D-arabinono-1,4-lactone biosynthetic process	BIOLOGICAL_PROCESS	0,94386839	0,004495563	1	0	76	17051	MELO3C018576	
GO:2000311	regulation of AMPA receptor activity	BIOLOGICAL_PROCESS	0,94386839	0,004495563	1	0	76	17051	MELO3C018956	
GO:0034498	early endosome to Golgi transport	BIOLOGICAL_PROCESS	0,94386839	0,004495563	1	0	76	17051	MELO3C024558	
GO:2000070	regulation of response to water deprivation	BIOLOGICAL_PROCESS	0,94386839	0,004495563	1	0	76	17051	MELO3C005035	
GO:0047834	D-threo-aldose 1-dehydrogenase activity	MOLECULAR_FUNCTION	0,94386839	0,004495563	1	0	76	17051	MELO3C018576	
GO:0005290	L-histidine transmembrane transporter activity	MOLECULAR_FUNCTION	0,94386839	0,004495563	1	0	76	17051	MELO3C002619	
GO:0035255	ionotropic glutamate receptor binding	MOLECULAR_FUNCTION	0,94386839	0,004495563	1	0	76	17051	MELO3C018956	
GO:0050235	pyridoxal 4-dehydrogenase activity	MOLECULAR_FUNCTION	0,94386839	0,004495563	1	0	76	17051	MELO3C018576	
GO:0045290	D-arabinose 1-dehydrogenase [NAD(P)+] activity	MOLECULAR_FUNCTION	0,94386839	0,004495563	1	0	76	17051	MELO3C018576	
GO:0019151	galactose 1-dehydrogenase activity	MOLECULAR_FUNCTION	0,94386839	0,004495563	1	0	76	17051	MELO3C018576	
GO:0010349	L-galactose dehydrogenase activity	MOLECULAR_FUNCTION	0,94386839	0,004495563	1	0	76	17051	MELO3C018576	
GO:0047816	D-arabinose 1-dehydrogenase (NAD) activity	MOLECULAR_FUNCTION	0,94386839	0,004495563	1	0	76	17051	MELO3C018576	
GO:0000172	ribonuclease MRP complex	CELLULAR_COMPONENT	0,94386839	0,004495563	1	0	76	17051	MELO3C009318	
GO:0005655	nucleolar ribonuclease P complex	CELLULAR_COMPONENT	0,94386839	0,004495563	1	0	76	17051	MELO3C009318	
GO:0007098	centrosome cycle	BIOLOGICAL_PROCESS	1	0,026675887	1	5	76	17046	MELO3C013369	MELO3C015782; MELO3C024150; MELO3C022094; MELO3C019034; MELO3C010920
GO:0016925	protein sumoylation	BIOLOGICAL_PROCESS	1	0,026675887	1	5	76	17046	MELO3C005035	MELO3C005717; MELO3C025617; MELO3C014183; MELO3C023325; MELO3C024782
GO:0046854	phosphatidylinositol phosphorylation	BIOLOGICAL_PROCESS	1	0,0397492	1	8	76	17043	MELO3C020989	MELO3C012544; MELO3C008054; MELO3C013045; MELO3C020987; MELO3C026141; MELO3C012545; MELO3C010667; MELO3C021931
GO:0030259	lipid glycosylation	BIOLOGICAL_PROCESS	1	0,044068338	1	9	76	17042	MELO3C015339	MELO3C011311; MELO3C010079; MELO3C020997; MELO3C004474; MELO3C010080; MELO3C002112; MELO3C002113; MELO3C012787; MELO3C008339

GO:0034727	piecemeal microautophagy of nucleus	BIOLOGICAL_PROCESS	1	0,0397492	1	8	76	17043	MELO3C024558	MELO3C019565; MELO3C004827; MELO3C008520; MELO3C025809; MELO3C022280; MELO3C022308; MELO3C023607; MELO3C007214
GO:0030001	metal ion transport	BIOLOGICAL_PROCESS	1	0,016770116	4	214	73	16837	MELO3C026764; MELO3C014309; MELO3C000817; MELO3C002372	MELO3C010221; MELO3C007854; MELO3C008943; MELO3C007853; MELO3C020822; MELO3C009910; MELO3C022329; MELO3C005316; MELO3C004225; MELO3C005315; MELO3C026802; MELO3C022448; MELO3C009917; MELO3C016324; MELO3C008392; MELO3C005687; MELO3C001880; MELO3C009809; MELO3C021364; MELO3C027105; MELO3C009927; MELO3C026378; MELO3C014007; MELO3C015218; MELO3C014920; MELO3C007271; MELO3C014000;
GO:0010113	negative regulation of systemic acquired resistance	BIOLOGICAL_PROCESS	1	0,008971177	1	1	76	17050	MELO3C005035	MELO3C002630
GO:0040025	vulval development	BIOLOGICAL_PROCESS	1	0,006510321	2	25	75	17026	MELO3C013369; MELO3C018956	MELO3C013015; MELO3C010882; MELO3C007894; MELO3C006500; MELO3C002045; MELO3C022308; MELO3C019031; MELO3C016262; MELO3C024265; MELO3C024782; MELO3C016321; MELO3C004390; MELO3C006171; MELO3C015904; MELO3C004473; MELO3C023325; MELO3C023545; MELO3C004459; MELO3C017020; MELO3C007903; MELO3C003703; MELO3C026234; MELO3C024552; MELO3C010839; MELO3C011206
GO:0000050	urea cycle	BIOLOGICAL_PROCESS	1	0,035410803	1	7	76	17044	MELO3C002619	MELO3C003814; MELO3C011085; MELO3C002352; MELO3C002353; MELO3C013218; MELO3C026229; MELO3C003523
GO:0019853	L-ascorbic acid biosynthetic process	BIOLOGICAL_PROCESS	1	0,013426929	1	2	76	17049	MELO3C018576	MELO3C026482; MELO3C004377
GO:0032258	CVT pathway	BIOLOGICAL_PROCESS	1	0,0397492	1	8	76	17043	MELO3C024558	MELO3C019565; MELO3C008520; MELO3C025809; MELO3C022280; MELO3C022308; MELO3C023607; MELO3C007214; MELO3C008406
GO:0010187	negative regulation of seed germination	BIOLOGICAL_PROCESS	1	0,026675887	1	5	76	17046	MELO3C023484	MELO3C009889; MELO3C007222; MELO3C024155; MELO3C006547; MELO3C010435
GO:0045053	protein retention in Golgi apparatus	BIOLOGICAL_PROCESS	1	0,017862908	1	3	76	17048	MELO3C018052	MELO3C013753; MELO3C015420; MELO3C006811
GO:0010337	regulation of salicylic acid metabolic process	BIOLOGICAL_PROCESS	1	0,017862908	1	3	76	17048	MELO3C005035	MELO3C027349; MELO3C002099; MELO3C016008
GO:0016559	peroxisome fission	BIOLOGICAL_PROCESS	1	0,035410803	1	7	76	17044	MELO3C018052	MELO3C022531; MELO3C019045; MELO3C010926; MELO3C011193; MELO3C006147; MELO3C015136; MELO3C006810
GO:0000422	mitophagy	BIOLOGICAL_PROCESS	1	0,03105306	1	6	76	17045	MELO3C024558	MELO3C022280; MELO3C023607; MELO3C007214; MELO3C019565; MELO3C008520; MELO3C025809

GO:0006379	mRNA cleavage	BIOLOGICAL_PROCESS	1	0,0397492	1	8	76	17043	MELO3C009318	MELO3C005162; MELO3C008873; MELO3C005929; MELO3C021828; MELO3C008722; MELO3C002045; MELO3C027241; MELO3C021974
GO:0071446	cellular response to salicylic acid stimulus	BIOLOGICAL_PROCESS	1	0,0397492	1	8	76	17043	MELO3C006765	MELO3C020450; MELO3C013621; MELO3C008938; MELO3C005061; MELO3C022341; MELO3C007039; MELO3C018037; MELO3C012836
GO:0010104	regulation of ethylene-activated signaling pathway	BIOLOGICAL_PROCESS	1	0,026675887	1	5	76	17046	MELO3C024357	MELO3C007039; MELO3C016937; MELO3C015961; MELO3C003906; MELO3C016866
GO:0006065	UDP-glucuronate biosynthetic process	BIOLOGICAL_PROCESS	1	0,026675887	1	5	76	17046	MELO3C017213	MELO3C016068; MELO3C003703; MELO3C011431; MELO3C020244; MELO3C011346
GO:0060625	regulation of protein deneddylation	BIOLOGICAL_PROCESS	1	0,008971177	1	1	76	17050	MELO3C016464	MELO3C014386
GO:0009736	cytokinin-activated signaling pathway	BIOLOGICAL_PROCESS	1	0,048368299	1	10	76	17041	MELO3C024357	MELO3C004183; MELO3C016937; MELO3C024563; MELO3C014230; MELO3C003198; MELO3C025617; MELO3C016973; MELO3C010714; MELO3C017877; MELO3C024439
GO:0045900	negative regulation of translational elongation	BIOLOGICAL_PROCESS	1	0,008971177	1	1	76	17050	MELO3C014306	MELO3C002757
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	BIOLOGICAL_PROCESS	1	0,048368299	1	10	76	17041	MELO3C014306	MELO3C002757; MELO3C004130; MELO3C024550; MELO3C006951; MELO3C023371; MELO3C006136; MELO3C017841; MELO3C011898; MELO3C006747; MELO3C005757
GO:0050826	response to freezing	BIOLOGICAL_PROCESS	1	0,013426929	1	2	76	17049	MELO3C005035	MELO3C021253; MELO3C022358
GO:0008988	rRNA (adenine-N6-)-methyltransferase activity	MOLECULAR_FUNCTION	1	0,017862908	1	3	76	17048	MELO3C013369	MELO3C010154; MELO3C007871; MELO3C006150
GO:0000064	L-ornithine transmembrane transporter activity	MOLECULAR_FUNCTION	1	0,008971177	1	1	76	17050	MELO3C002619	MELO3C024239
GO:0008234	cysteine-type peptidase activity	MOLECULAR_FUNCTION	1	0,034577805	2	63	75	16988	MELO3C019168; MELO3C018956	MELO3C007571; MELO3C010982; MELO3C017814; MELO3C009196; MELO3C012000; MELO3C005793; MELO3C004340; MELO3C011193; MELO3C009559; MELO3C007578; MELO3C002321; MELO3C023338; MELO3C021359; MELO3C017053; MELO3C024666; MELO3C026400; MELO3C025355; MELO3C016165; MELO3C010702; MELO3C019434; MELO3C015634; MELO3C012403; MELO3C014753; MELO3C004472; MELO3C021328; MELO3C005564; MELO3C002334;
GO:0004430	1-phosphatidylinositol 4-kinase activity	MOLECULAR_FUNCTION	1	0,013426929	1	2	76	17049	MELO3C020989	MELO3C008054; MELO3C012545
GO:0008239	dipeptidyl-peptidase activity	MOLECULAR_FUNCTION	1	0,017862908	1	3	76	17048	MELO3C023481	MELO3C015446; MELO3C023479; MELO3C023478
GO:0003979	UDP-glucose 6-dehydrogenase activity	MOLECULAR_FUNCTION	1	0,013426929	1	2	76	17049	MELO3C017213	MELO3C016068; MELO3C011431
GO:0032266	phosphatidylinositol-3-phosphate binding	MOLECULAR_FUNCTION	1	0,017862908	1	3	76	17048	MELO3C024558	MELO3C026612; MELO3C020154; MELO3C003655
GO:0016633	galactonolactone dehydrogenase activity	MOLECULAR_FUNCTION	1	0,013426929	1	2	76	17049	MELO3C018576	MELO3C020737; MELO3C020736
GO:0004652	polynucleotide adenylyltransferase activity	MOLECULAR_FUNCTION	1	0,035410803	1	7	76	17044	MELO3C002115	MELO3C017806; MELO3C024435; MELO3C013730; MELO3C009952; MELO3C023722; MELO3C026172; MELO3C011126

GO:0004526	ribonuclease P activity	MOLECULAR_FUNCTION	1	0,022279198	1	4	76	17047	MELO3C009318	MELO3C016319; MELO3C023673; MELO3C025708; MELO3C010071
GO:0008312	7S RNA binding	MOLECULAR_FUNCTION	1	0,035410803	1	7	76	17044	MELO3C014306	MELO3C018272; MELO3C002757; MELO3C024550; MELO3C006136; MELO3C017841; MELO3C011898; MELO3C006747
GO:0005047	signal recognition particle binding	MOLECULAR_FUNCTION	1	0,022279198	1	4	76	17047	MELO3C014306	MELO3C011981; MELO3C004130; MELO3C015126; MELO3C011898
GO:0047763	caffeate O-methyltransferase activity	MOLECULAR_FUNCTION	1	0,013426929	1	2	76	17049	MELO3C014089	MELO3C024861; MELO3C009403
GO:0033843	xyloglucan 6-xylosyltransferase activity	MOLECULAR_FUNCTION	1	0,022279198	1	4	76	17047	MELO3C007647	MELO3C006664; MELO3C017190; MELO3C017191; MELO3C000841
GO:0004564	beta-fructofuranosidase activity	MOLECULAR_FUNCTION	1	0,048368299	1	10	76	17041	MELO3C016877	MELO3C004170; MELO3C013379; MELO3C006727; MELO3C005363; MELO3C024384; MELO3C009488; MELO3C005560; MELO3C012360; MELO3C024083; MELO3C024383
GO:0005524	ATP binding	MOLECULAR_FUNCTION	1	0,021994726	3	2058	74	14993	MELO3C006765; MELO3C013076; MELO3C016434	MELO3C014269; MELO3C003133; MELO3C004463; MELO3C007972; MELO3C006648; MELO3C007978; MELO3C008825; MELO3C003139; MELO3C008829; MELO3C026243; MELO3C019951; MELO3C000093; MELO3C025392; MELO3C015599; MELO3C018624; MELO3C020958; MELO3C008832; MELO3C008831; MELO3C014272; MELO3C003146; MELO3C002299; MELO3C008835; MELO3C005329; MELO3C008838; MELO3C026256; MELO3C024079; MELO3C019967;
GO:0019789	SUMO transferase activity	MOLECULAR_FUNCTION	1	0,013426929	1	2	76	17049	MELO3C005035	MELO3C025617; MELO3C024782
GO:0015189	L-lysine transmembrane transporter activity	MOLECULAR_FUNCTION	1	0,008971177	1	1	76	17050	MELO3C002619	MELO3C002398
GO:0004452	isopentenyl-diphosphate delta-isomerase activity	MOLECULAR_FUNCTION	1	0,022279198	1	4	76	17047	MELO3C023481	MELO3C023478; MELO3C008717; MELO3C023479; MELO3C010053
GO:0015181	arginine transmembrane transporter activity	MOLECULAR_FUNCTION	1	0,008971177	1	1	76	17050	MELO3C002619	MELO3C002398
GO:0004577	N-acetylglucosaminyldiphosphodolichol N-acetylglucosaminyltransferase activity	MOLECULAR_FUNCTION	1	0,008971177	1	1	76	17050	MELO3C015339	MELO3C013839
GO:0044297	cell body	CELLULAR_COMPONENT	1	0,035410803	1	7	76	17044	MELO3C018956	MELO3C008571; MELO3C009840; MELO3C016990; MELO3C009668; MELO3C005662; MELO3C018534; MELO3C017338
GO:0043541	UDP-N-acetylglucosamine transferase complex	CELLULAR_COMPONENT	1	0,008971177	1	1	76	17050	MELO3C015339	MELO3C013839
GO:0009507	chloroplast	CELLULAR_COMPONENT	1	0,046022234	2	1593	75	15458	MELO3C006765; MELO3C003916	MELO3C018628; MELO3C020948; MELO3C020949; MELO3C002287; MELO3C003135; MELO3C005795; MELO3C003137; MELO3C003139; MELO3C015590; MELO3C015591; MELO3C015592; MELO3C026246; MELO3C015593; MELO3C017772; MELO3C015594; MELO3C025397; MELO3C015595; MELO3C017774; MELO3C015596; MELO3C017776; MELO3C018622; MELO3C017309; MELO3C002291; MELO3C014278; MELO3C004471; MELO3C007986; MELO3C004475;

GO:0005669	transcription factor TFIID complex	CELLULAR_COMPONENT	1	0,035410803	1	7	76	17044	MELO3C024357	MELO3C016968; MELO3C003391; MELO3C024352; MELO3C021620; MELO3C010016; MELO3C000238; MELO3C024537
GO:0009360	DNA polymerase III complex	CELLULAR_COMPONENT	1	0,013426929	1	2	76	17049	MELO3C016434	MELO3C007194; MELO3C014529
GO:0005768	endosome	CELLULAR_COMPONENT	1	0,041648667	2	70	75	16981	MELO3C024558; MELO3C018956	MELO3C014821; MELO3C011795; MELO3C009473; MELO3C014542; MELO3C005199; MELO3C007457; MELO3C012481; MELO3C014180; MELO3C004945; MELO3C006926; MELO3C025310; MELO3C004827; MELO3C026440; MELO3C013816; MELO3C012728; MELO3C015433; MELO3C006171; MELO3C010795; MELO3C004391; MELO3C023828; MELO3C005328; MELO3C004874; MELO3C026614; MELO3C018195; MELO3C016491; MELO3C026971; MELO3C025682;
GO:0042406	extrinsic component of endoplasmic reticulum membrane	CELLULAR_COMPONENT	1	0,013426929	1	2	76	17049	MELO3C015339	MELO3C011649; MELO3C018518
GO:0000407	pre-autophagosomal structure	CELLULAR_COMPONENT	1	0,03105306	1	6	76	17045	MELO3C024558	MELO3C007534; MELO3C022308; MELO3C023607; MELO3C007214; MELO3C019565; MELO3C025809
GO:0005785	signal recognition particle receptor complex	CELLULAR_COMPONENT	1	0,008971177	1	1	76	17050	MELO3C014306	MELO3C004130
GO:0005786	signal recognition particle, endoplasmic reticulum targeting	CELLULAR_COMPONENT	1	0,035410803	1	7	76	17044	MELO3C014306	MELO3C002757; MELO3C024550; MELO3C017841; MELO3C015126; MELO3C011898; MELO3C006747; MELO3C013306

Supplementary Table 3. List of the Differentially Expressed Genes (909 DEGs) exclusive of considering the comparison between lines over time in melon fruit of the near-isogenic line SC10-2 and its parental "Piel de sapo" during storage at 20.5^{o}C and 88% relative humidity for 18 d.

Gene ID	pval	qval	Description
MELO3C018099	6.98878999116914e-09	8.62635084597496e-06	No data found
MELO3C021514	8.24147254885332e-08	3.77341577131167e-05	No data found
MELO3C012331	1.44328094586754e-07	5.37799158489398e-05	dnaJ protein homolog
MELO3C007204	2.70307014549331e-07	8.47348131799166e-05	60S ribosomal protein L11-like
MELO3C023537	5.4337361676815e-07	0.00012691733086263	zinc finger A20 and AN1 domain-containing stress-associated protein 8-like
MELO3C012146	7.17645318282223e-07	0.000149187130429007	14-3-3 protein, putative
MELO3C020880	2.09783662086238e-06	0.000312158869772302	Pathogenesis-related protein 1
MELO3C026045	2.71888340064308e-06	0.000365273661763947	alanine--glyoxylate aminotransferase 2 homolog 2, mitochondrial-like
MELO3C012074	3.70429519958027e-06	0.000425326313351806	Ubiquitin-conjugating enzyme, E2
MELO3C007827	4.27775306732769e-06	0.00047169877077526	pyridine nucleotide-disulfide oxidoreductase domain-containing protein 2-like
MELO3C013000	4.45895326350865e-06	0.000478586239136045	Malic enzyme
MELO3C016805	4.5614759661694e-06	0.000480700689972296	No data found
MELO3C000673	4.68826114552456e-06	0.000482679936310805	ATP-dependent zinc metalloprotease FtsH
MELO3C026738	6.6257926438773e-06	0.000608617576390385	Acyl-CoA N-acyltransferase (NAT) superfamily protein
MELO3C022065	7.89187488892118e-06	0.0006773432768121	Nuclear matrix constituent protein 1
MELO3C011963	7.81226541701763e-06	0.0006773432768121	anthranilate phosphoribosyltransferase
MELO3C026410	8.27649747914272e-06	0.000689673201331601	transcription factor PIF4-like
MELO3C026689	1.01759043160676e-05	0.000788974717069347	LRR receptor-like kinase, putative
MELO3C007614	1.15006113516891e-05	0.00086458369524327	Leucine-rich repeat family protein
MELO3C026749	1.20811670227816e-05	0.000896958524559827	DNA helicase
MELO3C009315	1.23509541338773e-05	0.00090491340308527	Ribosomal protein S12
MELO3C016855	1.24174151722167e-05	0.00090491340308527	CRG16
MELO3C017720	1.5829999835848e-05	0.00104557413631492	protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha
MELO3C013093	1.62023783316645e-05	0.0010508747649051	glyoxylate/succinic semialdehyde reductase 2, chloroplastic-like
MELO3C021107	1.93475282579403e-05	0.00118295459927574	Peptidylprolyl isomerase
MELO3C012243	2.02363198715805e-05	0.00121105176104195	tetraketide alpha-pyrone reductase 2-like
MELO3C012748	2.83333883075443e-05	0.00148385868132083	Lysine-specific demethylase
MELO3C024292	3.02042248422341e-05	0.00153552012010767	O-fucosyltransferase family protein
MELO3C013470	3.44618684419151e-05	0.00168046281446761	Ankyrin repeat domain-containing 2-like protein
MELO3C024586	3.89204117599018e-05	0.00180760621925962	Ribosomal protein S8e/ribosomal biogenesis NSA2
MELO3C018394	4.6087660756533e-05	0.00201368409796631	Abscisic acid receptor
MELO3C015043	4.71004272699638e-05	0.00204436557836157	DnaJ-like protein
MELO3C025391	4.83084956899305e-05	0.00207353939040731	No data found
MELO3C025056	4.8402534760128e-05	0.00207353939040731	zinc finger CCCH domain-containing protein 53-like
MELO3C024376	4.90235715564502e-05	0.00208656576437141	Eukaryotic initiation factor 4A (ATP-dependent RNA helicase eIF4A)
MELO3C009292	5.42517615724769e-05	0.00222633555573646	ABC transporter G family member 20
MELO3C022693	5.60978884305285e-05	0.00227958271319858	GDSL esterase/lipase 5
MELO3C021332	6.05753663890374e-05	0.00238547596635887	40S ribosomal protein S21
MELO3C005992	6.3408310252755e-05	0.00246211971008436	homeobox-leucine zipper protein ATHB-7
MELO3C020255	6.65873213148149e-05	0.00253378229026258	3-phosphoinositide-dependent protein kinase-1
MELO3C025026	7.38424094659518e-05	0.00271924112679749	abscisic stress-ripening protein 2-like
MELO3C013084	7.63203350274688e-05	0.0027671089367998	Aminopeptidase
MELO3C025654	8.41080056708243e-05	0.00292498547025566	Transmembrane protein
MELO3C005828	8.65793669142523e-05	0.00296335514244293	SKP1-like protein 21
MELO3C005872	8.92453339496058e-05	0.00303555374175946	Polypyrimidine tract binding protein, putative
MELO3C006670	9.20264952706251e-05	0.00307398449987238	Translationally-controlled tumor protein homolog
MELO3C012943	9.46720039655125e-05	0.00313704262804514	ADP,ATP carrier protein
MELO3C010021	9.6358700537813e-05	0.00317694153075337	ER membrane protein complex subunit 10
MELO3C021901	0.000102486479856445	0.00328012097486915	Alpha/beta hydrolase-3
MELO3C013261	0.000104022481609345	0.00329094438804991	No data found
MELO3C003906	0.000107750928353134	0.00338431427849777	Ethylene receptor
MELO3C002085	0.000113224239913556	0.00346676823884159	ethylene-responsive transcription factor ERF071
MELO3C024324	0.000116198570528248	0.00352495494601283	Chaperone protein DnaJ
MELO3C022837	0.000116753774780598	0.00352564265770953	Cysteine-rich repeat secretory protein 60
MELO3C010776	0.000116715602386908	0.00352564265770953	Branched-chain-amino-acid aminotransferase
MELO3C001165	0.000124820210286147	0.00368471499692246	eukaryotic translation initiation factor 3 subunit M
MELO3C016924	0.000125729655771067	0.00369128273352684	pentatricopeptide repeat-containing protein At4g33170-like
MELO3C023989	0.000126739273406784	0.00369715496382656	Methyltransferase
MELO3C007246	0.000136437561226055	0.00384148920539927	28 kDa heat/acid-stable phosphoprotein-like protein
MELO3C023033	0.000141418977736452	0.00392810603560785	heterogeneous nuclear ribonucleoprotein 1-like
MELO3C019087	0.000146130882510365	0.00398610331311767	UDP-glycosyltransferase 76E2-like
MELO3C013563	0.000146093610227327	0.00398610331311767	Metacaspase-5
MELO3C005692	0.000146809861828023	0.00399910063619536	E3 ubiquitin-protein ligase At3g02290-like
MELO3C024861	0.000151226502948631	0.00407445048667466	Caffeic acid O-methyltransferase
MELO3C018160	0.000152143725675513	0.00407691511311494	factor of DNA methylation 1-like
MELO3C008974	0.000155525458351624	0.00413387924224256	60S ribosomal protein L35a
MELO3C002163	0.000164730021437798	0.00426283287985112	E3 ubiquitin-protein ligase RING1-like
MELO3C014217	0.000167148322577915	0.00427592256812336	Telomere repeat-binding protein 4
MELO3C005001	0.000170562545132369	0.00434637381137955	dof zinc finger protein DOF5.3-like
MELO3C020583	0.000173737441671706	0.0044017019494474	Neutral ceramidase
MELO3C014799	0.000175285251514445	0.00442673712552274	TRANSPORT INHIBITOR RESPONSE 1 protein, putative
MELO3C022562	0.00017556921672901	0.00442824579972059	protein CHROMATIN REMODELING 19 isoform X1
MELO3C006239	0.000194745937404539	0.0048075468972528	Receptor protein kinase, putative
MELO3C022684	0.000194616340531306	0.0048075468972528	peroxisomal (S)-2-hydroxy-acid oxidase GLO4-like
MELO3C024902	0.000197626941677576	0.00484235046053404	ABC subfamily C transporter
MELO3C022540	0.000216005163480082	0.00519433149706969	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7
MELO3C019629	0.000220238525441285	0.00524667145831115	ALA-interacting subunit 3-like
MELO3C019921	0.000224478914295334	0.00530926236936354	Phospholipid-transporting ATPase
MELO3C011682	0.00023316957210473	0.00547828218461161	Fructose-1,6-bisphosphatase
MELO3C005111	0.00023446163867713	0.00548351994895583	Coiled-coil protein
MELO3C014614	0.000235860026803869	0.00549292413838397	Leucine-rich repeat receptor-like protein kinase family
MELO3C017008	0.000239417539566356	0.00552722123260604	Ubiquitin family protein
MELO3C024688	0.000240582824529545	0.00554407258066976	TATA-binding protein-associated factor 2N
MELO3C009127	0.000241609568591317	0.00556124402110712	WRKY family transcription factor family protein
MELO3C007425	0.000247283160818346	0.0056205337601488	1-aminocyclopropane-1-carboxylate oxidase 1
MELO3C002351	0.000259527766881318	0.00580454571703188	Receptor protein kinase-like protein

MELO3C013766	0.000277047881957371	0.00602295331887094	Translocase of chloroplast
MELO3C022679	0.000277183104936407	0.00602295331887094	oligouridylate-binding protein 1B-like
MELO3C005002	0.000281040859585691	0.00607916312810274	Interactor of constitutive active ROPs-like protein
MELO3C012349	0.000282115086382206	0.00609572302074638	replication protein A 14 kDa subunit B-like
MELO3C008097	0.000282891183413736	0.00610581200135287	Polyprotein
MELO3C022353	0.000283476774613156	0.0061117716395581	tRNA dimethylallyltransferase
MELO3C020850	0.000287415273795277	0.00616304477978603	Filament-like plant protein 7
MELO3C003771	0.000289095891857327	0.00616328919688229	Mitochondrial 39S ribosomal protein L53
MELO3C007084	0.000290601122250878	0.00617769813060558	BTB/POZ domain-containing protein
MELO3C012335	0.00030093175099899	0.00634386020921778	Uricase
MELO3C002298	0.00030226452811033	0.00635973082156247	Methylthioribose-1-phosphate isomerase
MELO3C004818	0.000313659812932854	0.00651363579980119	S-adenosyl-L-methionine-dependent methyltransferase superfamily protein
MELO3C025628	0.000319630051430653	0.00660290155408364	Aspartyl/glutamyl-tRNA (Asn/Gln) amidotransferase subunit B
MELO3C017698	0.00034384648671526	0.00697905885523091	Vesicle transport protein GOT1
MELO3C021510	0.000345680560706607	0.00699471864077334	Ferredoxin-thioredoxin reductase catalytic chain
MELO3C007119	0.000364741286312031	0.00730555341113216	E3 ubiquitin-protein ligase arkadia-A, putative
MELO3C026919	0.000385875008708902	0.00765125054918887	RuBisCO large subunit-binding protein subunit alpha, chloroplastic
MELO3C006096	0.000388869747816378	0.00769517900764094	DNA replication complex GINS protein SLD5
MELO3C006726	0.000393613047360519	0.00775021343202681	Galactokinase
MELO3C023350	0.000393498277305726	0.00775021343202681	GATA transcription factor
MELO3C005861	0.000394326202309614	0.00775296869722632	Hexosyltransferase
MELO3C020610	0.000397760016506599	0.00776020694699844	protein TOC75-3, chloroplastic
MELO3C021139	0.000416728063664884	0.00798238170586701	No data found
MELO3C005875	0.000415414077330256	0.00798238170586701	Curved DNA-binding protein
MELO3C012171	0.000417125825128095	0.00798238170586701	phosphatidylinositol 4-kinase gamma 5
MELO3C008086	0.00042505111070712	0.00809656108130136	Delta-aminolevulinic acid dehydratase
MELO3C025753	0.000438646630847916	0.0082897916867134	elongation factor 1-alpha
MELO3C006289	0.000446332049387155	0.00840287096601232	Unknown protein
MELO3C023876	0.000456434521640348	0.00855230110804101	glycerol-3-phosphate acyltransferase 5-like
MELO3C009542	0.00046017704841339	0.00859657502875971	BEL1-like homeodomain protein 1
MELO3C009490	0.000477551177120339	0.00880593669182967	Ribosomal protein S11
MELO3C026433	0.000478847432524576	0.00882160256056703	U4/U6 small nuclear ribonucleoprotein PRP4-like protein
MELO3C026780	0.000482363906618488	0.00886692143153668	Ribosomal protein S19
MELO3C019735	0.000492040262321525	0.00894906064744133	1-aminocyclopropane-1-carboxylate oxidase
MELO3C026705	0.000490305274858382	0.00894906064744133	Vesicle-associated membrane protein, putative
MELO3C013938	0.000499419243035093	0.00902351976145818	Protein transport protein Sec16B
MELO3C011070	0.000500007962388027	0.00902351976145818	Rhamnogalacturonate lyase
MELO3C013436	0.000502109941717843	0.00903935208658677	DNA helicase
MELO3C012073	0.000503847273066516	0.00906236775572916	SNF1-related kinase regulatory subunit gamma 1
MELO3C008245	0.000504765109731187	0.00906236922916473	Delta-1-pyrroline-5-carboxylate synthetase
MELO3C023998	0.000507430810900544	0.00908544975927003	Protein RETICULATA-RELATED 4, chloroplastic
MELO3C006430	0.000517174720864766	0.00920981385244208	ethylene-responsive transcription factor 1B
MELO3C008866	0.000517893399529346	0.00921430337595049	Plasma-membrane choline transporter family protein
MELO3C005720	0.000530338114349549	0.0093264892433564	Late embryogenesis abundant protein
MELO3C008491	0.000531797074916351	0.00934382600758276	Zinc finger protein CONSTANS
MELO3C009346	0.000538853443754816	0.00942651619399203	translin
MELO3C007391	0.000540671539647652	0.00944931171371813	Glycosyl transferase, family 31
MELO3C025062	0.000544142102876677	0.00947406635026766	transcription initiation factor TFIID subunit 11-like
MELO3C003567	0.000545821213981501	0.00948892883355692	Glycosyltransferase
MELO3C012178	0.000548063155305423	0.00951115927427662	protein PHYLLO, chloroplastic isoform X1
MELO3C022260	0.000550317736865757	0.00952517527200863	CDPK-related kinase 3 isoform X1
MELO3C008806	0.000551102874571718	0.00953041214528622	Echinoderm microtubule-associated protein-like 6
MELO3C005706	0.000567796577401691	0.00971699705988388	40S ribosomal protein S10-1
MELO3C002714	0.000579702326297893	0.00988647775652598	60S ribosomal protein L18a-like protein
MELO3C024760	0.000592163910059229	0.00997836609194515	RNA polymerase sigma factor sigA
MELO3C011805	0.000592819805662836	0.00998090225237456	No data found
MELO3C018462	0.000600683577282934	0.0100436026132101	Polyadenylate-binding protein
MELO3C005899	0.000607220982714818	0.0101086526857278	Protein yippee-like
MELO3C011873	0.000621061425400415	0.0102808654980692	60S ribosomal protein L17
MELO3C017030	0.000630415357957714	0.0103750607535891	Bromodomain-containing protein
MELO3C015270	0.000642051019905554	0.0104878954442637	single-stranded DNA-binding protein, mitochondrial
MELO3C018027	0.000645454282273139	0.0105173899510002	Pyruvate kinase
MELO3C012452	0.000667682946013937	0.0107902195406569	CSC1-like protein isoform X1
MELO3C001971	0.000668754302383112	0.0107902195406569	HVA22-like protein
MELO3C007012	0.000677563644158052	0.0108878799092574	DNA polymerase eta
MELO3C000881	0.000697534212565021	0.0111004054504002	Unknown protein
MELO3C013007	0.000705481661930962	0.0111962038589772	profilin-like
MELO3C008775	0.000711395060906339	0.0112574848219866	Elongation factor 4
MELO3C007667	0.000719402723322826	0.0113207046875717	Epidermal patterning factor-like protein
MELO3C009128	0.000720765197783857	0.0113240985608858	F-box/LRR-repeat protein 15
MELO3C019498	0.000730368821527216	0.0113934074694637	Tubby-like F-box protein
MELO3C014062	0.000737302663945227	0.0114563259718759	Tir-nbs resistance protein
MELO3C004589	0.000738241873302403	0.0114619015376173	Mitochondrial import inner membrane translocase subunit Tim17-like protein
MELO3C017561	0.000741241733906883	0.0114728845422048	Gras family transcription factor
MELO3C003678	0.000746920851982136	0.0115331820999181	DNA-directed RNA polymerase subunit beta
MELO3C003086	0.000755050317633899	0.0116405064191662	protein GPR107
MELO3C021326	0.000766461351612402	0.0117888202749169	Peroxisomal fatty acid beta-oxidation multifunctional protein
MELO3C015233	0.000766447720925711	0.0117888202749169	ABC1-like kinase
MELO3C025645	0.000773924241273871	0.0118566152606867	gamma-glutamyl hydrolase 2-like
MELO3C015686	0.000774471299118229	0.0118566152606867	Lectin receptor kinase
MELO3C002662	0.00078275615172041	0.0119187750503673	Receptor kinase, putative
MELO3C023644	0.000784187854190543	0.0119225443154391	subtilisin-like protease SBT3.17
MELO3C007281	0.00078421110262572	0.0119225443154391	Transmembrane protein, putative
MELO3C021170	0.00079612896994774	0.0120388598985436	BTB/POZ domain-containing protein POB1
MELO3C015844	0.000797345327828602	0.012048028216746	DNA repair helicase
MELO3C013761	0.000803412442861307	0.0120892909496463	MLO-like protein
MELO3C026224	0.000806198958957616	0.0120946682916889	Aspartyl aminopeptidase family protein
MELO3C011018	0.000812005118265402	0.0121487038489571	Thaumatin-like protein 1
MELO3C016522	0.000815966088231534	0.0121714739300738	Unknown protein
MELO3C007143	0.000819606583127408	0.0121977471063928	NAD(P)-binding domain-containing protein
MELO3C001947	0.000841859856859473	0.0124352208774254	eukaryotic translation initiation factor 3 subunit G-like

MELO3C016408	0.000849878202600962	0.0124919222927065	D-2-hydroxyglutarate dehydrogenase, mitochondrial-like
MELO3C024287	0.000858057790619982	0.0125439869644173	GATA transcription factor 24-like
MELO3C022319	0.000857819419544437	0.0125439869644173	DNA primase large subunit
MELO3C020710	0.000855996771340739	0.0125439869644173	THO complex subunit 4A
MELO3C003439	0.000864308651512991	0.0126158400286253	NAD(P)-binding rossmann-fold protein
MELO3C013707	0.000869260816383277	0.0126787532221221	Thioredoxin reductase
MELO3C018689	0.000892082156492835	0.0129257010334387	nuclear transcription factor Y subunit C-2
MELO3C010903	0.00089679269942633	0.0129749150336781	thylakoidal processing peptidase 1, chloroplastic-like
MELO3C025720	0.00090037014311295	0.0129920969393496	phototropin-1
MELO3C010183	0.000904336723108301	0.0129920969393496	glycine-rich cell wall structural protein 2-like
MELO3C003139	0.000913198703413887	0.013059204340131	ATP-dependent zinc metalloprotease FtsH
MELO3C020172	0.000915802238327545	0.0130774970388508	Hydroxyacylglutathione hydrolase
MELO3C007144	0.000921378557700914	0.0131286472842968	DNA helicase
MELO3C018046	0.000926412561525591	0.0131718658585809	Zinc transport ZntB
MELO3C025347	0.000928175455473412	0.0131874367411111	Short-chain dehydrogenase/reductase
MELO3C009770	0.000931788216151919	0.0132197453166553	two-component response regulator ORR9-like
MELO3C015926	0.000935266432297022	0.0132500550727646	DNA helicase
MELO3C007917	0.000939995495577994	0.013286163190543	thiosulfate sulfurtransferase 18 isoform X1
MELO3C004539	0.000946307413841607	0.0133322132934015	serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' iota isoform-like
MELO3C005046	0.000947141386938188	0.0133322132934015	protein indeterminate-domain 2
MELO3C007646	0.000954499819987076	0.0133975955543175	heptahelical transmembrane protein 4-like
MELO3C012016	0.00097897348711995	0.0136153150684027	MLP-like protein 423
MELO3C005915	0.000986201687010468	0.0136581326204556	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein
MELO3C025944	0.000985917354598187	0.0136581326204556	ABC1 family protein
MELO3C016811	0.000987087449194402	0.0136608199258166	Ubiquitin system component Cue
MELO3C015770	0.000999619597627954	0.0137301972062592	phospholipase A1-Igamma1, chloroplastic-like isoform X1
MELO3C007467	0.00100905049094524	0.0138099363448909	No data found
MELO3C007316	0.00101829843398527	0.0139089177661161	Transmembrane protein, putative
MELO3C001943	0.00103568118847042	0.0140667073781726	17. class I heat shock protein
MELO3C024239	0.0010406075041931	0.0140953069960971	Mitochondrial carrier protein
MELO3C010959	0.00104181627537914	0.014102007966047	Adenosine kinase, putative
MELO3C014116	0.0010524633137019	0.0142168932847461	poly(A)-specific ribonuclease PARN
MELO3C021598	0.0010608705730426	0.0142852160059244	pre-rRNA-processing protein ESF2
MELO3C010821	0.00106381826751312	0.0143018018823121	Glutamyl-tRNA (Gln) amidotransferase subunit A
MELO3C013824	0.00106573213139216	0.0143080515723071	inactive poly [ADP-ribose] polymerase RCD1-like
MELO3C000254	0.00107265318236205	0.014391187295155	Auxin response factor
MELO3C013964	0.00107467152470697	0.0144084778964277	Flavin-containing monooxygenase
MELO3C019125	0.00107877740647	0.0144537143828874	WAT1-related protein At5g07050-like
MELO3C002134	0.00109141215498465	0.0145872662731249	protection of telomeres protein 1a-like isoform X1
MELO3C008124	0.0010950939938712	0.0146128454628124	SNARE associated Golgi protein family
MELO3C020616	0.00110160610411703	0.0146898169819089	Haloacid dehalogenase-like hydrolase
MELO3C004713	0.00111704118586142	0.0148355389237238	Ribosomal protein
MELO3C019140	0.00112109638180102	0.0148595083563484	Nascent polypeptide-associated complex subunit alpha-like protein
MELO3C006995	0.00112951941137085	0.0149353473849775	DNA helicase
MELO3C025511	0.00116227454348072	0.0152506151645319	elongation factor 1-alpha-like
MELO3C003420	0.0011601994899415	0.0152506151645319	Ring finger protein, putative
MELO3C024554	0.00117317342071144	0.0153437098580332	Chaperone dnaJ-like protein
MELO3C018981	0.00117475910333109	0.0153529891038268	UNC93-like protein
MELO3C026230	0.00117574360508321	0.0153529891038268	Ribonuclease J
MELO3C026886	0.00121509032211076	0.0157562828439694	Chaperone DnaJ
MELO3C007914	0.00122356487409925	0.015796148569604	calmodulin-lysine N-methyltransferase isoform X1
MELO3C007724	0.00123610608361802	0.0158993585323115	Pesticidal crystal cry8Ba protein
MELO3C003675	0.00123674154707298	0.0158993585323115	Protein TIFY 8
MELO3C022009	0.00125751310639199	0.0160950267907553	Vesicle transport v-SNARE family protein
MELO3C010375	0.00126258066098428	0.0161389679441932	DNA ligase
MELO3C026013	0.00126215947958241	0.0161389679441932	Plectin-like protein
MELO3C008252	0.00126698624011023	0.016174344703256	Protease inhibitor/seed storage/lipid transfer family protein
MELO3C014398	0.00127170983656311	0.0162085217333131	Myosin-binding protein 1
MELO3C016882	0.00128643995485178	0.0163277009436811	Magnesium transporter NIPA
MELO3C023961	0.00128738672658923	0.0163292231621135	ras-related protein RABA4c isoform X1
MELO3C011040	0.00129103487176252	0.0163649856755058	40S ribosomal protein S6-like
MELO3C006507	0.00129529568976838	0.0163979452418178	40S ribosomal protein S3a
MELO3C014190	0.00130600334466013	0.0165017658692853	DUF4408 domain protein
MELO3C016300	0.00132248461135576	0.0166461877352294	UDP-glucose 4-epimerase family protein
MELO3C012715	0.00132243173147539	0.0166461877352294	mediator of RNA polymerase II transcription subunit 19a-like
MELO3C005294	0.00132249068593726	0.0166461877352294	Myosin-binding protein 2
MELO3C021556	0.00132370263701453	0.0166508301773249	ADP-ribosylation factor-like
MELO3C012296	0.00133013796895898	0.0166786633326799	Unknown protein
MELO3C015409	0.00134065781250059	0.0167467749140254	ABC transporter B family protein
MELO3C003846	0.00135074087660314	0.0168514097106983	Glucan endo-1,3-beta-glucosidase, putative
MELO3C009873	0.00136459747634987	0.0169920779069569	zinc-finger homeodomain protein 9-like
MELO3C015398	0.00136911537600959	0.017026863703283	cysteine synthase-like
MELO3C008375	0.00138251768956899	0.0171288217385809	Unknown protein
MELO3C017272	0.00138518236716068	0.0171403299304863	Ethylene-responsive transcription factor
MELO3C006587	0.0013871485080218	0.0171431763985747	Endonuclease/exonuclease/phosphatase family protein
MELO3C027346	0.00139863809916196	0.0171921631272379	Indole-3-acetic acid-amido synthetase GH3.3
MELO3C016965	0.00140646424613533	0.0172416278069067	Formin-like protein
MELO3C017133	0.00141800169024686	0.0172971682400774	No data found
MELO3C008096	0.00142424626433679	0.0173305233976508	Galactose-binding domain-like protein
MELO3C019524	0.0014304129339574	0.017373447129597	40S ribosomal protein S16
MELO3C011834	0.00143661881258605	0.0174273863204926	Protein EI24 like
MELO3C022932	0.00145937989094569	0.0175954172565851	Auxin response factor
MELO3C015477	0.00146228225489542	0.0176089099097132	No data found
MELO3C014281	0.0014702360035872	0.0176508758874429	Aldo/keto reductase, putative
MELO3C021914	0.00146823354847903	0.0176508758874429	peroxidase 10-like
MELO3C007497	0.0014780779626572	0.0177234740039569	Transcription termination factor family protein
MELO3C002416	0.00148622342396076	0.017777968746094	Ankyrin repeat family protein
MELO3C021536	0.00151639341105281	0.0180296529048055	Quinone oxidoreductase-like protein
MELO3C003457	0.00152415156525021	0.018078359917193	protein EMBRYONIC FLOWER 1-like isoform X3
MELO3C021148	0.00153136859350866	0.0181146196894978	Autophagy-related protein
MELO3C025035	0.00153071881752509	0.0181146196894978	lecithin-cholesterol acyltransferase-like 1

MELO3C020427	0.00153376154089113	0.018127023740909	DEAD-box ATP-dependent RNA helicase 42-like
MELO3C022392	0.00153951311588807	0.018173248371592	Cytochrome oxidase complex assembly protein
MELO3C011439	0.00154415748059011	0.0182171840407253	6,7-dimethyl-8-ribityllumazine synthase
MELO3C010197	0.00157227802397697	0.0184785490735071	Tetratricopeptide repeat (TPR)-like superfamily protein
MELO3C010403	0.00157447526897514	0.0184865113477943	LOW QUALITY PROTEIN: LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.4
MELO3C024313	0.00158260126212806	0.0185349689647406	AT-rich interactive domain-containing protein 4-like
MELO3C014944	0.00158975633025693	0.0185423015211278	homeobox-leucine zipper protein HAT22-like
MELO3C016193	0.00158896575333467	0.0185423015211278	Lysine-specific histone demethylase 1
MELO3C022042	0.00159143253219463	0.0185423015211278	DUF2039 family protein
MELO3C019491	0.00160887864625414	0.0186904378734547	Nucleolar complex protein 2 homolog
MELO3C007099	0.00160852551941759	0.0186904378734547	Nucleoporin protein Ndc1-Nup
MELO3C020159	0.00160703147890584	0.0186904378734547	transmembrane protein 87A
MELO3C023852	0.00164327417852994	0.0189672833148964	Actin family protein
MELO3C013753	0.00168358970314475	0.0193016055803562	Vacuolar protein sorting-associated protein 35
MELO3C024001	0.00169134873987065	0.0193637369644669	MADS-box transcription factor
MELO3C003770	0.0016973381454457	0.019401769103248	TLD-domain nucleolar protein
MELO3C009090	0.00173121000396637	0.0196392051611116	Kinase family protein
MELO3C019490	0.00173728752931601	0.0196392051611116	40S ribosomal protein S16
MELO3C005455	0.00173406833228484	0.0196392051611116	origin of replication complex subunit 3
MELO3C008195	0.00173319093407187	0.0196392051611116	Katanin p60 atpase-containing subunit a1
MELO3C016494	0.00174848962342988	0.019709430121642	Polygalacturonase
MELO3C017294	0.00174730515676302	0.019709430121642	Carbon catabolite repressor protein 4 like 3
MELO3C015470	0.00175565135908395	0.0197675933241442	beta-galactosidase
MELO3C021264	0.00177097699103468	0.0198834704922933	Ubiquitin-conjugating enzyme, E2
MELO3C018459	0.00179830009973014	0.0201216026456491	40S ribosomal protein S16
MELO3C025142	0.00180918499272109	0.0202090466183534	Proliferating cell nuclear antigen
MELO3C002604	0.00183522225955302	0.0204536142234269	DUF2921 family protein
MELO3C008786	0.00185244710486099	0.0206223099627394	Rhomboid protein, putative
MELO3C026593	0.00186878067212692	0.0207573394228541	Surfeit locus protein 2 (SURF2)
MELO3C012493	0.00187295993871484	0.0207687174787643	Choline/ethanolamine kinase
MELO3C012420	0.00187233804376197	0.0207687174787643	No data found
MELO3C012852	0.00188039613797097	0.0208203232473985	Protein BREAST CANCER SUSCEPTIBILITY 1-like protein
MELO3C015177	0.00188263980533365	0.0208292736781705	60S ribosomal protein L13a, putative
MELO3C008032	0.00188467890401967	0.020840158832858	Actin
MELO3C018413	0.00188895876601003	0.0208569116575077	Allene oxide synthase
MELO3C023862	0.0019068491527422	0.0210027680620675	Factor of DNA methylation 1
MELO3C025744	0.00190635644741377	0.0210027680620675	Zinc finger family protein, putative
MELO3C020588	0.00196327140921926	0.0214806908923386	17.5 kDa class I heat shock protein
MELO3C008516	0.00196685604928237	0.0214960930366782	Guanosine nucleotide diphosphate dissociation inhibitor
MELO3C019814	0.00201274196770884	0.0218719472185081	ABC transporter G family member
MELO3C006934	0.00202201822291359	0.021892587246618	protein REVEILLE 6-like isoform X2
MELO3C007228	0.00202308834498344	0.021892587246618	GDSL esterase/lipase
MELO3C014417	0.00204144586045041	0.0220188499716194	sugar transporter ERD6-like 7
MELO3C018781	0.0020542658700694	0.0220967846775603	Leucine-rich repeat family protein
MELO3C011972	0.00208045004987989	0.0223176578137305	Alpha-glucan water dikinase, chloroplastic
MELO3C009600	0.00209252401614957	0.022398513167988	60S ribosomal protein L21
MELO3C013539	0.00209583349110565	0.0224217852740224	vesicle-associated protein 4-2-like
MELO3C010198	0.00210011636188545	0.0224554401899706	DNA-directed RNA polymerase subunit beta
MELO3C002268	0.00211346018252012	0.0225736750376365	Iron-sulfur cluster assembly protein
MELO3C026887	0.00212116551042296	0.022643728467753	Tryptophan synthase, alpha chain
MELO3C011763	0.0021263565296451	0.0226746301857241	LRR receptor-like kinase
MELO3C021153	0.00213199409674547	0.0227224778287244	Arginine--tRNA ligase
MELO3C025491	0.00215106029913348	0.0228516889981641	transcription initiation factor TFIID subunit 1-like
MELO3C015457	0.00216212621458034	0.0229445623921263	K(+) efflux antiporter
MELO3C002598	0.00217096035433062	0.0230012317798688	E3 ubiquitin-protein ligase RMA1H1-like
MELO3C009489	0.0021885277242305	0.0231377055812785	Ribosomal protein S11
MELO3C003496	0.00219345078663657	0.0231525705960907	Phosphoglycerate mutase-like protein 1
MELO3C011042	0.00220196138837392	0.0232175843347552	VQ motif-containing protein 9
MELO3C019361	0.00220806422194508	0.0232695092418321	fasciclin-like arabinogalactan protein 7
MELO3C006212	0.00222542135216774	0.0233900193102506	tRNA (Guanine-N(7)-)-methyltransferase
MELO3C009757	0.00222821468022771	0.0234069211275623	Amino acid transporter family protein
MELO3C008970	0.00223264451449334	0.023440986983907	vacuolar protein sorting-associated protein 20 homolog 2-like
MELO3C015292	0.00225207974747366	0.0236199272081026	Epoxide hydrolase 2
MELO3C005976	0.00225640094494073	0.0236526869753898	Protein AATF
MELO3C007466	0.00225882808818756	0.0236530201026597	RNA cytidine acetyltransferase
MELO3C007270	0.00226366852216031	0.023678596209822	Ring finger protein, putative
MELO3C008100	0.00229727735813157	0.0239287608363609	gibberellin receptor GID1B
MELO3C022165	0.00231035379912992	0.0239890521445934	Actin-binding LIM protein 1, putative
MELO3C018492	0.00231232472788601	0.0239969001844565	Cinnamyl alcohol dehydrogenase
MELO3C006106	0.00232061450614851	0.0240576461322451	U-box domain-containing protein kinase family protein, putative
MELO3C016952	0.00234128339180883	0.0241830573770045	eukaryotic translation initiation factor-like
MELO3C017817	0.0023669444389276	0.0243335688310157	transaldolase
MELO3C003722	0.00237262336257049	0.0243792605553614	serine/threonine-protein kinase STY46-like isoform X1
MELO3C013034	0.00238546539224549	0.0244603094659689	Charged multivesicular body 1
MELO3C019725	0.00239709679529321	0.0245540791546917	ethylene-responsive transcription factor 3-like
MELO3C023404	0.00240231684114978	0.0245947927920513	DNA replication complex GINS protein PSF1
MELO3C021521	0.00240698686863405	0.0246043393730093	WAT1-related protein
MELO3C026286	0.00240990356136972	0.0246086791279682	Protein MICRORCHIDIA 6
MELO3C027184	0.00242276758035198	0.0246889767514816	DNA primase
MELO3C004761	0.00243983236026302	0.0248134188898108	CBS domain-containing protein CBSX1, chloroplastic
MELO3C018797	0.00243837045809947	0.0248134188898108	Cysteine-rich receptor-kinase-like protein
MELO3C009908	0.00245124923270912	0.0249021199057471	Type I inositol polyphosphate 5-phosphatase, putative
MELO3C011264	0.00245758550501518	0.0249280206155854	Histone acetyltransferase
MELO3C009639	0.00246576674180576	0.0249496524561083	Squamosa promoter binding protein
MELO3C010493	0.00246180150676134	0.0249496524561083	Aldehyde dehydrogenase
MELO3C019827	0.00246720498745034	0.0249496524561083	MEF2BNB-like protein
MELO3C019500	0.00249021021586082	0.0251170385868414	Protein-protein interaction regulator family protein
MELO3C018683	0.00249307436724266	0.0251330912091247	Actin
MELO3C011084	0.00250020007177665	0.0251920669477128	Ribosomal RNA small subunit methyltransferase A
MELO3C004381	0.00251245552795387	0.025251137008428	Auxin-responsive protein
MELO3C023844	0.00252223327356038	0.0253107646948902	2-oxoglutarate dehydrogenase E1 component family protein

MELO3C019704	0.00252200355091303	0.0253107646948902	Serine/threonine protein phosphatase 7 long form
MELO3C018460	0.00253286875232273	0.0253659355931144	O-acyltransferase WSD1-like
MELO3C016014	0.0025571448957098	0.0255184712205016	thiamine pyrophosphokinase 1
MELO3C002277	0.0025908406468802	0.0257506350957408	Glutathione transport system permease protein gsiD
MELO3C026572	0.00260563742446895	0.0258067871092464	Proline transporter
MELO3C003818	0.00260420294403418	0.0258067871092464	Tubby-like F-box protein
MELO3C024244	0.00261508509481012	0.0258485062749775	Ribosomal protein L37
MELO3C017158	0.00262413446791454	0.0258938185759979	Serine/threonine-protein kinase atr
MELO3C007785	0.00263134950686683	0.0259431666044565	RING-H2 zinc finger protein RHA2a
MELO3C009532	0.0026377958393965	0.025943562933669	NDR1/HIN1-like protein 12
MELO3C021618	0.00263523784937714	0.025943562933669	ribosomal RNA large subunit methyltransferase E-like
MELO3C027119	0.00263408267344634	0.025943562933669	1-aminocyclopropane-1-carboxylate oxidase 2
MELO3C026901	0.00263783859288103	0.025943562933669	HNH endonuclease
MELO3C004385	0.00265207979831772	0.0260253671353869	pathogenesis-related protein PR-4-like
MELO3C004519	0.00267496625574049	0.0261783491499598	NADH-cytochrome b5 reductase-like protein
MELO3C006439	0.00270856493483707	0.0264476999835899	1-aminocyclopropane-1-carboxylate oxidase homolog 1-like
MELO3C022497	0.00270918512667995	0.0264476999835899	40S ribosomal protein S13
MELO3C014925	0.00272905227228559	0.026570628428043	Glycerophosphodiester phosphodiesterase, putative
MELO3C023599	0.00273464015593183	0.0265885133692798	Glutamine synthetase
MELO3C013603	0.0027441539772568	0.0266573029497514	Plant/protein (DUF789)
MELO3C006153	0.00275443894018501	0.0267440583233598	UDP-galactose/UDP-glucose transporter 2-like
MELO3C017228	0.00276531793823609	0.0267576011573859	Replication protein A 70 kDa DNA-binding subunit
MELO3C007857	0.00277499196625031	0.0268074015965016	LOW QUALITY PROTEIN: protein HYPER-SENSITIVITY-RELATED 4-like
MELO3C012418	0.00277589428653835	0.0268074015965016	Tyramine N-feruloyltransferase 4/11
MELO3C025494	0.00278404522379472	0.0268729761117898	leukotriene A-4 hydrolase homolog
MELO3C013665	0.00278843488334646	0.0269021985887685	mechanosensitive ion channel protein 6-like
MELO3C015682	0.00283388627394909	0.0272607988427767	Zinc finger BED domain-containing protein DAYSLEEPER
MELO3C012175	0.00285815822128543	0.0274274862546968	Thioredoxin-like protein aaed1, chloroplastic
MELO3C020157	0.00286972839969413	0.0274591329505104	Glycerol-3-phosphate dehydrogenase [NAD(+)]
MELO3C018408	0.00286762071520663	0.0274591329505104	methyltransferase-like protein 13
MELO3C006576	0.00287199260083404	0.0274668193093808	ARM repeat superfamily protein
MELO3C012268	0.00290928855179373	0.0277428969625178	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.2 isoform X4
MELO3C022246	0.00291399362481704	0.0277743533284323	cytochrome P450 78A9-like
MELO3C002232	0.00292148187912489	0.0278188744603845	serine/threonine-protein kinase fray2
MELO3C015807	0.00294721274408638	0.0279586801462572	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
MELO3C023406	0.00294286704306013	0.0279586801462572	Polygalacturonase
MELO3C017624	0.0029620275572394	0.0280830927642443	Superoxide dismutase
MELO3C022694	0.00296775156879869	0.0281103720538155	Ethylene-responsive transcription factor
MELO3C012527	0.00297250118494685	0.0281418628482816	Guanine nucleotide-binding protein beta subunit-like protein
MELO3C026077	0.0029907075838328	0.0282602117218581	leucine-rich repeat extensin-like protein 3
MELO3C019004	0.00299954481518294	0.0282948581551635	ENTH/ANTH/VHS superfamily protein, putative
MELO3C026638	0.0030153881996442	0.0283981409417135	acyl-protein thioesterase 2
MELO3C017687	0.00303163409125018	0.0285138619671975	solute carrier family 35 member F1
MELO3C022482	0.00303891540561274	0.0285394966468777	SWI/SNF complex component SNF12 homolog
MELO3C011123	0.00303966505635012	0.0285394966468777	oleosin 1-like
MELO3C006635	0.00304572063851438	0.0285701369470703	transcription termination factor MTEF1, chloroplastic-like
MELO3C012211	0.00304978606683126	0.028581418257601	Coiled-coil domain-containing protein 130
MELO3C013275	0.00307285130009638	0.0287238455479359	Eukaryotic translation initiation factor 3 subunit A, putative
MELO3C019546	0.00308152563759556	0.0287740188259455	PRKR-interacting protein 1
MELO3C006945	0.00308380034190114	0.0287816507335566	mediator of RNA polymerase II transcription subunit 36a-like
MELO3C025916	0.00309672394330129	0.0288575686588257	Triosephosphate isomerase, putative
MELO3C006833	0.00310508976483725	0.0288905872097688	AT-hook motif nuclear-localized protein 1
MELO3C006596	0.00312259521677238	0.0290066476651166	squamosa promoter-binding-like protein 7
MELO3C020628	0.00314969349944749	0.0291623520490335	Protein kinase
MELO3C026935	0.00315856654564306	0.0292034319802925	Homeobox-leucine zipper HOX24
MELO3C003790	0.00316375085180232	0.0292240016708344	subtilisin-like protease SBT3.17 isoform X1
MELO3C016435	0.00318004727588184	0.0293470811455095	PHD finger alfin-like protein
MELO3C026949	0.00318437434441865	0.0293732876823559	DNA ligase
MELO3C017665	0.00319763962111685	0.0294681217346882	Ubiquitin-protein ligase, putative
MELO3C020958	0.0032001673855715	0.0294776612395762	Shikimate kinase
MELO3C026019	0.00321334455151734	0.0295852408148792	Abscisic acid receptor
MELO3C013566	0.00323029250749773	0.0296859221640636	Indole-3-acetic acid-amido synthetase GH3.3
MELO3C006900	0.00323377434712158	0.0297040974796763	No data found
MELO3C011141	0.00324029178816565	0.0297363022883287	Transcriptional regulatory plant protein, putative
MELO3C011641	0.00326082986585996	0.0298692620690484	gamma-secretase subunit APH1-like
MELO3C017682	0.00329068344277839	0.0300590690617162	extensin-2
MELO3C011626	0.00329055575005754	0.0300590690617162	Ribosomal protein S8
MELO3C010882	0.00328785247888019	0.0300590690617162	Origin recognition complex subunit 2 family protein
MELO3C015845	0.00329570830198256	0.030079897053516	basic 7S globulin 2
MELO3C014696	0.00330563892729141	0.0301121140106449	Glycosyltransferase
MELO3C024476	0.00332258243518369	0.0302260283252226	alpha carbonic anhydrase 7-like
MELO3C011450	0.00333358893825408	0.0302968467287528	Kelch repeat-containing F-box family protein
MELO3C013981	0.00335602505490162	0.030418811552392	40S ribosomal protein S13
MELO3C021429	0.00335193882671869	0.030418811552392	Ribosomal protein
MELO3C022717	0.00338495688318097	0.0305947430141606	FHA domain-containing protein FHA2
MELO3C012390	0.00339255872463551	0.030635410266496	NAC domain-containing protein 53-like
MELO3C003646	0.00339160336545463	0.030635410266496	guanine nucleotide-binding protein subunit gamma 2-like
MELO3C007740	0.00339467117104308	0.0306404757572806	40S ribosomal protein S6-like
MELO3C015670	0.00339843699782583	0.0306437874748141	Phosphatidylinositol N-acetylglucosaminyltransferase subunit A
MELO3C009826	0.0033996930658422	0.0306437874748141	Carboxypeptidase
MELO3C020709	0.00340145935932612	0.0306457212077242	K-stimulated pyrophosphate-energized sodium pump protein
MELO3C003618	0.00340400756003645	0.0306546946206839	Unknown protein
MELO3C003537	0.00340619799978614	0.0306604395158507	WD-40 repeat-containing protein MSI1
MELO3C005597	0.00341005728531718	0.0306784743320635	1-aminocyclopropane-1-carboxylate synthase
MELO3C012627	0.00344637204195242	0.0309515240820911	KRR1 small subunit processome component homolog
MELO3C008749	0.00344966036879268	0.0309669739196758	CBS domain-containing protein CBSX6
MELO3C017141	0.00345887223368579	0.03102146582337	Dynein light chain
MELO3C011443	0.00346914766687134	0.0310853889623603	Glycosyltransferase
MELO3C019807	0.00348962571938949	0.0312405341487865	Zinc finger (C3HC4-type RING finger) family protein
MELO3C016321	0.00351307924928468	0.0313935756082005	multiple RNA-binding domain-containing protein 1
MELO3C013068	0.00352314090533479	0.0314579681657778	No data found

MELO3C008002	0.0035312711957558	0.0314849096365604	serine/threonine-protein kinase D6PKL2
MELO3C006293	0.00354341023305915	0.0314952662272863	Werner Syndrome-like exonuclease
MELO3C006679	0.00354132679588104	0.0314952662272863	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex
MELO3C018634	0.00353843304329915	0.0314952662272863	7-deoxyloganetin glucosyltransferase-like
MELO3C002187	0.00354604168811656	0.0315028237960477	Plant/protein (DUF789)
MELO3C002921	0.00354961794420117	0.0315062493393388	Cysteine proteinase inhibitor
MELO3C011266	0.00355690370295292	0.0315425645395677	Histone acetyltransferase
MELO3C009118	0.00356566194604402	0.0316060402928291	TOM1-like protein 2
MELO3C003452	0.00357083843738115	0.0316377246746704	Synaptonemal complex protein 1
MELO3C027277	0.00357454085905751	0.031648946287679	Polygalacturonase
MELO3C012303	0.00357875902153149	0.0316511025151031	Trichome birefringence-like protein
MELO3C006470	0.00359422249341379	0.0317736347459395	p-loop nucleoside triphosphate hydrolase superfamily protein
MELO3C013634	0.00359595157280856	0.0317746969178507	DNA-directed RNA polymerase subunit beta
MELO3C018700	0.00361828856415125	0.0319105985709065	UDP-glycosyltransferase 74F2-like
MELO3C009973	0.00361824768775709	0.0319105985709065	Dead box ATP-dependent RNA helicase, putative
MELO3C019010	0.00362104834108679	0.0319107914717193	No data found
MELO3C010566	0.00362510291757867	0.0319266674182015	Topoisomerase II-associated protein PAT1
MELO3C026594	0.00365773426356975	0.0321337161793767	E3 ubiquitin-protein ligase RGLG2
MELO3C019954	0.00367499471328736	0.0321994102008483	NAC domain-containing protein 17-like
MELO3C018086	0.00367393222298185	0.0321994102008483	No data found
MELO3C002364	0.00368322380190222	0.0322572003830452	glucuronoxylan 4-O-methyltransferase 1
MELO3C007651	0.00368605120965426	0.0322676530760027	BSD domain-containing protein
MELO3C017041	0.00369325977155832	0.032289034232494	Protein canopy 1-like
MELO3C011580	0.00369339856859607	0.032289034232494	Selenoprotein K
MELO3C011306	0.00370901783915945	0.0324112359759115	U2 snRNP-associated SURP motif-containing protein
MELO3C009362	0.00372330748990279	0.032484415475003	4-coumarate--CoA ligase-like 7
MELO3C021694	0.003723971676308	0.032484415475003	equilibrative nucleotide transporter 3-like
MELO3C012147	0.00373986616904487	0.0325742299591907	Chromatin modification-related protein EAF7
MELO3C020756	0.00374575962541046	0.032588108741071	auxin-responsive protein SAUR24-like
MELO3C009313	0.00374905481299304	0.0326024145758694	MCM domain-containing protein
MELO3C019256	0.00375711455194661	0.0326437550754041	Glutamate receptor
MELO3C023561	0.00376053621892014	0.03265460151583	Zinc finger, PHD-type
MELO3C025595	0.00377304170472659	0.0326903479823329	Hydroxyacylglutathione hydrolase 3, mitochondrial-like protein
MELO3C024527	0.00377219600226342	0.0326903479823329	Monodehydroascorbate reductase family protein
MELO3C021072	0.00376902665796097	0.0326903479823329	p-loop containing nucleoside triphosphate hydrolases superfamily protein, putative
MELO3C022135	0.00377269415701442	0.0326903479823329	Dynamin homolog
MELO3C009659	0.00378297423157448	0.0327359654708158	WD-repeat protein, putative
MELO3C025844	0.00378430346700454	0.0327359654708158	zinc finger CCCH domain-containing protein 66
MELO3C005590	0.00378620329661872	0.0327380599408595	AT-hook motif nuclear-localized protein 1
MELO3C023131	0.00380245973358373	0.0328498588270101	Magnesium chelatase subunit
MELO3C015877	0.00381685302485724	0.0329453804142944	Autophagy-related protein 18g
MELO3C018872	0.00382096715178948	0.0329664833030539	eukaryotic translation initiation factor 1A-like
MELO3C007206	0.00382538871009896	0.0329902190549102	Receptor-like kinase
MELO3C007781	0.0038398486676372	0.0331004676286194	C2 domain-containing family protein
MELO3C026665	0.0038477634826739	0.0331397649451927	BTB/POZ domain-containing protein At5g48800
MELO3C016629	0.00385657378659299	0.0331759691273178	integrator complex subunit 9 homolog isoform X1
MELO3C004813	0.00385700668977274	0.0331759691273178	No data found
MELO3C002951	0.00386183647055627	0.0331771225999734	Peptidyl-prolyl cis-trans isomerase
MELO3C022756	0.00385939753056552	0.0331771225999734	No data found
MELO3C016972	0.00388047519379775	0.0332591859056182	stromal cell-derived factor 2-like protein
MELO3C005658	0.00387972951477389	0.0332591859056182	O-glucosyltransferase rumi homolog
MELO3C002698	0.00388183824560484	0.0332591859056182	Eukaryotic translation initiation factor 4E
MELO3C017496	0.00387421851442116	0.0332591859056182	pathogenesis-related protein PR-1
MELO3C007029	0.00388454470007149	0.0332679415792332	glycine-rich RNA-binding protein 4, mitochondrial
MELO3C012831	0.0038908092763863	0.0332927176773627	WD repeat-containing protein 26
MELO3C017322	0.00389583227761392	0.0333068362123798	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.2 isoform X2
MELO3C026504	0.00390827463156984	0.0333732318117167	centromere protein V isoform X1
MELO3C008158	0.00393031276265376	0.0334712146397797	Protein PLASTID MOVEMENT IMPAIRED 2
MELO3C019983	0.00392989468547922	0.0334712146397797	Wound-responsive family protein
MELO3C016939	0.00394970593609312	0.0335715480937751	Protein phosphatase 2c, putative
MELO3C008944	0.00394846519055947	0.0335715480937751	ultraviolet-B receptor UVR8 isoform X2
MELO3C026495	0.00394489756670136	0.0335715480937751	cytochrome P450 CYP82D47-like
MELO3C013044	0.00394792703568192	0.0335715480937751	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B
MELO3C007919	0.00395536602137492	0.0335819377854541	alpha-mannosidase
MELO3C022017	0.00395691777946994	0.0335819377854541	Ribosomal protein L18/L5
MELO3C011127	0.00395892010502719	0.0335844987775695	receptor-like protein kinase HSL1
MELO3C021281	0.00397525249759023	0.0336507765001755	Beta-D-xylosidase family protein
MELO3C018648	0.00397329808233615	0.0336507765001755	Annexin
MELO3C006954	0.00399297475803051	0.0336852876960037	Ornithine cyclodeaminase/mu-crystallin
MELO3C026373	0.0039887085281346	0.0336852876960037	Glycosyltransferase
MELO3C007648	0.00398694127513544	0.0336852876960037	RuvB-like helicase
MELO3C019798	0.00398754437598248	0.0336852876960037	Acyl-CoA N-acyltransferase domain protein
MELO3C009105	0.0040092906562702	0.0337845085349958	Receptor-like kinase plant-like protein
MELO3C026103	0.00401371508088511	0.0338024985639232	DUF538 family protein
MELO3C016780	0.00401640311312934	0.0338107182784277	ethylene-responsive transcription factor ERF011-like
MELO3C006678	0.00402069563885754	0.0338324321141021	DUF581 family protein, putative (DUF581)
MELO3C011227	0.00402447276814755	0.0338353821618331	zeaxanthin epoxidase, chloroplastic-like
MELO3C023474	0.00402423910770855	0.0338353821618331	Hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase
MELO3C011726	0.00404263312343378	0.0339457259093174	Nuclear transcription factor Y subunit B
MELO3C026210	0.00404664750198225	0.0339639785451115	SNF1-related protein kinase regulatory subunit gamma-1
MELO3C006891	0.00405529113468006	0.0340076197956673	heat stress transcription factor B-2b-like
MELO3C002258	0.00406375095139522	0.0340640991252564	No data found
MELO3C009601	0.00408256489346259	0.034175454074849	Dirigent protein
MELO3C006406	0.00409087920567841	0.034175454074849	Transducin/WD40 domain-like protein, putative
MELO3C024610	0.004090155111938	0.034175454074849	Iron-sulfur binding oxidoreductase
MELO3C011869	0.00408858935710987	0.034175454074849	cytochrome P450 78A5-like
MELO3C019649	0.00408633114963042	0.034175454074849	auxin-responsive protein SAUR71
MELO3C016540	0.00409820484929724	0.0341932604853279	NAC domain protein
MELO3C024466	0.00409776864969524	0.0341932604853279	heavy metal-associated isoprenylated plant protein 3-like isoform X2
MELO3C015915	0.00409647381032929	0.0341932604853279	Heme binding
MELO3C013444	0.00410871929360257	0.0342665106965191	No data found

MELO3C011320	0.00411998198635644	0.0343459367870634	NAD(P)-binding rossmann-fold protein
MELO3C009370	0.00412796035380381	0.0343689245477535	ACT domain-containing protein
MELO3C024404	0.00412659958826311	0.0343689245477535	Tudor/PWWP/MBT superfamily protein
MELO3C015314	0.00412612017060354	0.0343689245477535	protein SRC2-like
MELO3C022568	0.00413550035043642	0.0344099668734598	protein indeterminate-domain 5, chloroplastic
MELO3C018374	0.00413637456871707	0.0344099668734598	DUF248-1
MELO3C024936	0.00413994951308028	0.03442520544582	Cleavage and polyadenylation specificity factor subunit
MELO3C005710	0.00414841548622957	0.0344810847801127	heavy metal-associated isoprenylated plant protein 3
MELO3C005504	0.00415565745621238	0.0345267476242063	Disease resistance family protein
MELO3C021144	0.00415874744190292	0.0345378903406816	squamosa promoter-binding-like protein 8
MELO3C014591	0.00417094646782634	0.0346116311413704	cyclin-dependent protein kinase inhibitor SMR3-like
MELO3C022382	0.00417453238090104	0.0346116311413704	Succinate--CoA ligase [ADP-forming] subunit beta, mitochondrial
MELO3C003323	0.00417463696282061	0.0346116311413704	Myosin heavy chain-like protein
MELO3C021407	0.00418955137017907	0.0347207091941529	Stem-specific protein TSJT1
MELO3C004316	0.00419185506808106	0.0347252289175893	Prefoldin chaperone subunit family protein, putative
MELO3C017094	0.00419379751734894	0.0347267535304504	No data found
MELO3C011908	0.00419762735150164	0.0347438988117376	Heat shock protein HSP26
MELO3C002084	0.00420015070006774	0.0347502204338659	Protein NEGATIVE REGULATOR OF RESISTANCE
MELO3C017520	0.00420329844082712	0.0347617005476946	L-allo-threonine aldolase
MELO3C027370	0.00420544322376737	0.0347648799607291	O-methyltransferase, putative
MELO3C011799	0.00420786589404742	0.0347703529462521	Cytochrome P450
MELO3C021944	0.00421779613002127	0.0348378317740652	Flavoprotein wrbA
MELO3C013419	0.00423115977641308	0.0349094003953484	30S ribosomal protein S31, mitochondrial
MELO3C012361	0.00422999190468754	0.0349094003953484	cell division control protein 2 homolog A
MELO3C027137	0.00423176386381408	0.0349094003953484	Gibberellin receptor GID1A
MELO3C004239	0.00424349429512305	0.0349623566267773	Zinc finger protein VAR3, chloroplastic
MELO3C019295	0.00426894623574081	0.0351280913373522	Cellulose synthase family protein
MELO3C013835	0.00427577875347029	0.0351696603924552	Heat shock transcription factor family protein
MELO3C017989	0.00430088886261248	0.0353173613919892	PXMP2/4 family protein 4
MELO3C009787	0.00431780204327548	0.0354267854394048	Protein SRC1
MELO3C004382	0.00433957988353706	0.035551505038091	Auxin-responsive protein
MELO3C022236	0.00435478022543923	0.0356231832101503	Cation/H(+) antiporter 11
MELO3C019833	0.00436921025270542	0.0356854976346896	Glycine-rich RNA-binding family protein
MELO3C025454	0.00438074020671109	0.0357648773635127	2-oxoglutarate dehydrogenase E1 component family protein
MELO3C017245	0.00439515850853 3	0.0358381442547557	squamosa promoter-binding-like protein 6
MELO3C012982	0.00440400022067899	0.0358543790682549	Bet1-like SNARE 1-1
MELO3C017756	0.0044125107954931	0.0358838655392167	calcium-dependent protein kinase 24
MELO3C022535	0.00441084542698378	0.0358838655392167	Methionine adenosyltransferase 2 subunit beta
MELO3C011419	0.00441372812875063	0.0358838655392167	Purple acid phosphatase
MELO3C011719	0.00441889278353991	0.0358951901894086	Adenylate kinase
MELO3C025492	0.00442331481104608	0.0359046626400941	transcription initiation factor TFIID subunit 1-like
MELO3C007317	0.00443550104810231	0.0359466902553953	Transmembrane protein, putative
MELO3C006341	0.00444064861850657	0.0359683622052152	Holliday junction resolvase
MELO3C026519	0.00444300260802799	0.0359683622052152	AT-hook motif nuclear-localized protein 10
MELO3C013004	0.00444391127554433	0.0359683622052152	protein IQ-DOMAIN 14-like
MELO3C012080	0.00444939745034345	0.03598327200935	binding partner of ACD11 1
MELO3C016733	0.00445369614312496	0.0360032931357245	Estradiol 17-beta-dehydrogenase 1
MELO3C017857	0.00447660665509919	0.0361736926479353	Unknown protein
MELO3C002811	0.00448958909934571	0.0362341214233668	SWIM zinc finger family protein
MELO3C018333	0.00451435304406078	0.0364042295905089	Six-bladed beta-propeller, TolB-like protein
MELO3C017023	0.00452304563686967	0.0364365717273029	Catalase
MELO3C018884	0.00453160110978612	0.0364688632099291	No data found
MELO3C024747	0.00453016901239933	0.0364688632099291	30S ribosomal protein S5, putative
MELO3C014381	0.00455362792746339	0.0366013829627491	Arginine/glutamate-rich 1 protein
MELO3C011270	0.0045788351918522	0.0367591122780037	Adenine phosphoribosyltransferase, putative
MELO3C021302	0.00459515873505412	0.036793997135694	Phosphatase 2C (PP2C)-like protein
MELO3C002611	0.00459421197278376	0.036793997135694	VQ motif-containing protein
MELO3C022766	0.00459622213447552	0.036793997135694	50S ribosomal protein L35
MELO3C013309	0.00461226279515592	0.0368639930026092	Coiled-coil protein
MELO3C007896	0.00461243236161057	0.0368639930026092	DNA ligase 3
MELO3C022208	0.00461235112080338	0.0368639930026092	Transmembrane protein, putative
MELO3C002241	0.00460760544686867	0.0368639930026092	Protein ROS1
MELO3C021458	0.00461777456584467	0.0368845809160894	glucomannan 4-beta-mannosyltransferase 9-like
MELO3C014961	0.00462684788511114	0.0369343649486903	No data found
MELO3C007108	0.00462896316894279	0.0369363206559399	Auxilin-related protein 2
MELO3C025122	0.00469406507564141	0.0372301209290144	Transmembrane protein, putative
MELO3C002254	0.00469046994419164	0.0372301209290144	No data found
MELO3C018609	0.00468423052131772	0.0372301209290144	nicotinamidase 1-like
MELO3C010982	0.00469150142351815	0.0372301209290144	cysteine proteinase RD19a-like
MELO3C010869	0.00470255932622954	0.0372675939541361	Calcium-binding EF-hand
MELO3C008126	0.00471205326936386	0.0373278539978607	receptor homology region, transmembrane domain- and RING domain-containing protein 2-like isoform X2
MELO3C024467	0.0047202723733617	0.037348183901565	No data found
MELO3C020620	0.00474164902427332	0.0374679317075795	telomere repeat-binding protein 5-like
MELO3C007388	0.00476193222621446	0.0375724900381318	calcium-dependent protein kinase-like
MELO3C017526	0.00476558186294107	0.0375860528000093	No data found
MELO3C010860	0.00476961101908036	0.0376028135791688	thioredoxin-like 4, chloroplastic
MELO3C025264	0.00480324345966632	0.0377390862236877	Auxin efflux carrier
MELO3C024359	0.00479821584987294	0.0377390862236877	40S ribosomal S3-like protein
MELO3C021766	0.00480031640730605	0.0377390862236877	Cysteine proteinase inhibitor
MELO3C010205	0.00480220260665098	0.0377390862236877	Myosin-binding protein 7
MELO3C026379	0.00481892308236753	0.0378405216515612	choline-phosphate cytidylyltransferase 2-like
MELO3C004128	0.00482450500558018	0.0378692962461061	hepatoma-derived growth factor-related protein 2-like isoform X1
MELO3C006557	0.00482848374613742	0.0378854690117076	ATP-dependent (S)-NAD(P)H-hydrate dehydratase
MELO3C014503	0.00484227068846665	0.0379785559279301	Nuclear transcription factor Y subunit B
MELO3C004504	0.004853594233164	0.0380522558597681	SPX domain-containing protein 1
MELO3C019979	0.00486300975469733	0.0381054504915579	40S ribosomal protein S18
MELO3C021380	0.00487514380395182	0.0381563740883631	Prolyl 4-hydroxylase alpha subunit, putative
MELO3C009865	0.00488061309291565	0.0381563740883631	No data found
MELO3C011936	0.00491136386101831	0.038307474285644	protein-tyrosine-phosphatase MKP1-like
MELO3C014848	0.00492368631958517	0.0383581385110405	Zinc finger, RING-type
MELO3C004616	0.00492100162867981	0.0383581385110405	No data found

MELO3C013809	0.00492199748758904	0.0383581385110405	calcium permeable stress-gated cation channel 1-like
MELO3C023525	0.00493771673994492	0.0384457842027261	60S ribosomal protein L6
MELO3C005683	0.0049435184544383	0.0384671181862498	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase
MELO3C014666	0.00496701622528295	0.0385853581760918	Dirigent protein
MELO3C022914	0.00496848275061024	0.0385853581760918	50S ribosomal protein L15
MELO3C002200	0.00497295451208024	0.0386049051332833	ABC transporter A family protein
MELO3C005243	0.00498172170978672	0.0386577689770444	purple acid phosphatase 4-like
MELO3C026734	0.00499084688857632	0.0386837337375921	lamin-like protein
MELO3C016831	0.00499389552060658	0.0386903771333979	RING-type E3 ubiquitin transferase
MELO3C024452	0.00499963757377242	0.0386903771333979	No data found
MELO3C018867	0.00499926959078445	0.0386903771333979	E6-like protein
MELO3C020617	0.00500844294115677	0.0387281674412314	Haloacid dehalogenase-like hydrolase
MELO3C002030	0.00501632420632747	0.0387739282781844	Glycine-rich RNA-binding protein
MELO3C009465	0.00502843552261645	0.0388523369077278	Terminal flower 1
MELO3C018257	0.00503800739884341	0.038911070832913	No data found
MELO3C002891	0.00504688773087425	0.0389644197799201	Pseudouridine synthase, RsuA/RluB/C/D/E/F
MELO3C006299	0.00505397492352333	0.0389713767143541	RNA-directed DNA polymerase (Reverse transcriptase)-related family protein
MELO3C022027	0.0050556821683212	0.0389713767143541	40S ribosomal protein S19
MELO3C021713	0.00505438158441507	0.0389713767143541	Ubiquinol oxidase
MELO3C012854	0.00505464637579456	0.0389713767143541	Long-chain-alcohol oxidase
MELO3C017092	0.00509335428043201	0.0391808196243162	diphthine methyltransferase
MELO3C018572	0.00509558321440995	0.0391808196243162	glutamate-1-semialdehyde 2,1-aminomutase 2, chloroplastic-like
MELO3C002679	0.00510933008744363	0.0392470478012152	heat stress transcription factor A-4c
MELO3C013472	0.0051198180085511	0.0393052524011742	Histone deacetylase
MELO3C019542	0.00513228821363398	0.0393774514106673	D-3-phosphoglycerate dehydrogenase
MELO3C016667	0.00514137660805702	0.0393847987498828	Random slug protein 5
MELO3C012583	0.00513599158009104	0.0393847987498828	nuclear-pore anchor-like
MELO3C021691	0.00514153474524282	0.0393847987498828	F-box protein family
MELO3C015299	0.00514189399425591	0.0393847987498828	serine/arginine-rich splicing factor SR30
MELO3C018610	0.0051432171743353	0.0393847987498828	Fructose-1,6-bisphosphatase
MELO3C014936	0.0051599163782603	0.0394820567819693	BRO1 domain-containing protein
MELO3C022426	0.0051671505635198	0.0395220977842573	Something about silencing protein
MELO3C012084	0.00517341272002758	0.0395393683466814	40S ribosomal protein S9, putative
MELO3C007190	0.00518428034658769	0.0396070996382051	Splicing factor 3B, subunit 5
MELO3C005803	0.00519167594605396	0.0396329370926246	WAT1-related protein
MELO3C014288	0.00520148075471183	0.0396924433635255	VAN3-binding protein
MELO3C016221	0.00520810517208448	0.0397171785628582	ABC transporter G family member 14
MELO3C004917	0.00522269622442229	0.0397791184372191	sulfite oxidase-like
MELO3C006182	0.00523154057570219	0.0398141405894191	Pentatricopeptide repeat-containing protein At1g01970
MELO3C022310	0.00524944366594116	0.0399196237807747	Histidine kinase
MELO3C005215	0.0052570899040556	0.0399623820304827	defensin Ec-AMP-D2-like
MELO3C019137	0.00526112589863548	0.0399776742486156	Plant/MNJ7-17 protein, putative
MELO3C007409	0.00527492254906536	0.0400516898967673	WRKY family transcription factor
MELO3C006221	0.00527834117750325	0.0400544508958836	Glutathione s-transferase, putative
MELO3C006760	0.00527934253288698	0.0400544508958836	Chromatin structure-remodeling complex protein BSH
MELO3C010941	0.00528496183711913	0.040066299931388	3-ketoacyl-CoA synthase
MELO3C008118	0.0052918874227319	0.0400863298080399	Inner membrane protein oxaA
MELO3C003627	0.00529445457556355	0.0400863298080399	Transcriptional adapter 1
MELO3C003690	0.00529425199930755	0.0400863298080399	adenine nucleotide transporter BT1, chloroplastic/mitochondrial-like
MELO3C007688	0.00531587170426806	0.0402080238558368	tRNA-dihydrouridine synthase
MELO3C020748	0.00533361546979561	0.0402651268780556	Receptor-like protein kinase
MELO3C001920	0.00533117758364088	0.0402651268780556	No data found
MELO3C015481	0.00533354470146574	0.0402651268780556	Chloroplastic group IIA intron splicing facilitator CRS1
MELO3C005634	0.00533638245875689	0.0402706217722545	phosphatidylinositol glycan anchor biosynthesis class U protein-like
MELO3C023004	0.00534674243286837	0.040294608949124	casein kinase I-like isoform X1
MELO3C012295	0.00536354190955324	0.0403829924406279	Tetratricopeptide repeat-like superfamily protein
MELO3C012912	0.00536579815994709	0.0403845837884127	Chlorophyll a-b binding protein, chloroplastic
MELO3C002072	0.00536839161606895	0.0403887108669507	Adenine nucleotide alpha hydrolases-like superfamily protein
MELO3C014951	0.00538851756489089	0.0405092628051124	tRNA/rRNA methyltransferase family protein
MELO3C020489	0.00538680953554949	0.0405092628051124	WRKY transcription factor 1
MELO3C005380	0.00539842275126157	0.0405682842141038	protein phosphatase inhibitor 2
MELO3C009151	0.00540405465087668	0.0405797244487314	phosphoinositide phosphatase SAC8
MELO3C016700	0.00541295604689029	0.0406186957918544	Inner membrane protein oxaA
MELO3C024248	0.00541360366330046	0.0406186957918544	Dynein light chain family protein
MELO3C015113	0.00542243994015512	0.0406559477517553	Protein SMG7
MELO3C007235	0.00543615744316983	0.0407433295427556	Protein IQ-DOMAIN 1
MELO3C017551	0.00544379027512432	0.0407695920149526	Pentatricopeptide repeat-containing protein
MELO3C017169	0.0054419971112214	0.0407695920149526	60S ribosomal protein L34
MELO3C002293	0.00544667677743771	0.0407757466556548	Armadillo/beta-catenin repeat family protein
MELO3C009170	0.00545100219701766	0.0407926647930662	vacuolar cation/proton exchanger 3-like
MELO3C016881	0.00546445639647308	0.0408778596113435	Cytokinin riboside 5'-monophosphate phosphoribohydrolase
MELO3C022605	0.00548519315338203	0.0410019226291225	thiamine biosynthetic bifunctional enzyme TH1, chloroplastic-like
MELO3C019156	0.00549336446814186	0.0410039815297562	protein GrpE
MELO3C015423	0.00549259467745444	0.0410039815297562	Damaged dna-binding 2, putative isoform 1
MELO3C026577	0.00549584987134866	0.0410039815297562	mitogen-activated protein kinase kinase 3
MELO3C022961	0.00549927721920196	0.0410140580823336	4-hydroxyphenylpyruvate dioxygenase
MELO3C009329	0.00550540936501021	0.0410288036036176	Peroxidase
MELO3C024348	0.00550384303802409	0.0410288036036176	Lipoxygenase
MELO3C005298	0.00551011550099556	0.0410336646483313	DELLA protein GAI
MELO3C003554	0.00551021715769784	0.0410336646483313	homeobox-leucine zipper protein ATHB-6-like
MELO3C009549	0.00551926640667522	0.0410855605975985	No data found
MELO3C006093	0.00554875124716214	0.0412118421888699	UDP-glycosyltransferase 91A1-like
MELO3C006553	0.00555487297960233	0.0412417994263784	3-dehydrosphinganine reductase TSC10A isoform X1
MELO3C009753	0.00556782329136662	0.0412913789640253	Transcription factor PERIANTHIA
MELO3C005559	0.00556759058409906	0.0412913789640253	transaldolase
MELO3C021715	0.00558441460505543	0.0413988753886035	E3 ubiquitin-protein ligase COP1-like
MELO3C007563	0.00564058020111158	0.0416900517933206	Lipase
MELO3C013581	0.00563795363412223	0.0416900517933206	shaggy-related protein kinase eta
MELO3C008152	0.00563998177954761	0.0416900517933206	Class I glutamine amidotransferase-like superfamily protein
MELO3C014876	0.00565538385941067	0.041752589098879	Kelch repeat-containing F-box family protein
MELO3C016778	0.00565933442381517	0.0417661418295686	SPla/RYanodine receptor (SPRY) domain protein

MELO3C004117	0.00566929710292929	0.0418240375367018	Carboxypeptidase
MELO3C007636	0.00567263519002581	0.0418330367318221	Calcium-transporting ATPase
MELO3C020997	0.00568704454460378	0.0419199713723186	Sterol 3-beta-glucosyltransferase
MELO3C026499	0.00568866895933029	0.0419199713723186	Zinc finger HIT domain-containing protein 3
MELO3C013692	0.00569296709952316	0.0419359967357266	Transmembrane protein, putative
MELO3C002261	0.00570743449773126	0.0420268918328466	serine/threonine-protein kinase HT1-like
MELO3C009193	0.0057141543213195	0.0420606909026235	Transmembrane protein
MELO3C019997	0.0057189492179438	0.0420803010824039	Histone H4
MELO3C014390	0.00572324775500266	0.0420962457778575	mavicyanin-like
MELO3C006151	0.0057406825704176	0.0421920901889014	protein-ribulosamine 3-kinase, chloroplastic
MELO3C016676	0.00574342477656464	0.0421920901889014	Peptide methionine sulfoxide reductase
MELO3C003123	0.00574566882149075	0.0421920901889014	E3 ubiquitin-protein ligase XB3-like
MELO3C025152	0.00576102443116722	0.0422639195732249	Coronatine-insensitive 1
MELO3C009325	0.00577467309870794	0.0423191774837995	POLAR LOCALIZATION DURING ASYMMETRIC DIVISION AND protein
MELO3C016723	0.00577229566189108	0.0423191774837995	serpin-ZX-like
MELO3C012351	0.00577787071656299	0.0423246175005202	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase-like
MELO3C016017	0.00578589705892163	0.0423519944464949	translocator protein homolog
MELO3C002023	0.00580928505066813	0.0425074362599648	DExH-box ATP-dependent RNA helicase DExH14
MELO3C007814	0.00582928347011036	0.0426221840989298	protein indeterminate-domain 2-like
MELO3C021695	0.0058292778713428	0.0426221840989298	Phosphatidate cytidylyltransferase
MELO3C014353	0.00584390830887993	0.0426975009959562	Transmembrane protein, putative
MELO3C011890	0.00585525734603176	0.0427329923602296	DNA-binding storekeeper protein-related
MELO3C025877	0.00585523358807216	0.0427329923602296	Glucose-6-phosphate isomerase
MELO3C007133	0.00586456153890169	0.0427776942902953	Transmembrane protein
MELO3C024909	0.005876180212674	0.0427809706934379	Mitochondrial transcription termination factor family protein
MELO3C006765	0.00587699496132954	0.0427809706934379	DEAD-box ATP-dependent RNA helicase 50
MELO3C018802	0.00587443787186281	0.0427809706934379	Peroxisome biogenesis protein 22
MELO3C012708	0.00588417269765351	0.042817437953559	Pentatricopeptide repeat-containing protein
MELO3C004011	0.00590548212715403	0.0429352413293379	No data found
MELO3C006191	0.00590581813556534	0.0429352413293379	Katanin p80 WD40 repeat-containing subunit B1 homolog
MELO3C009201	0.00591891723251758	0.0429423338585641	Immediate early response 3-interacting protein 1
MELO3C006188	0.00592525493769747	0.0429423338585641	ATP-dependent DNA helicase 2 subunit KU80
MELO3C016108	0.0059234494023328	0.0429423338585641	Receptor-like protein kinase
MELO3C019145	0.00591396721573012	0.0429423338585641	ER membrane protein complex subunit 8/9 homolog
MELO3C002690	0.00591329059347701	0.0429423338585641	Myosin heavy chain kinase B
MELO3C003396	0.00592368884294037	0.0429423338585641	Phospholipid hydroperoxide glutathione peroxidase
MELO3C024777	0.00593479565849098	0.0429799337952102	ABC transporter B family protein
MELO3C009446	0.00593804692995192	0.0429877158429694	Serine/threonine-protein phosphatase PP1
MELO3C026748	0.0059455675826553	0.043026388490238	Enolase
MELO3C012239	0.00599508591673292	0.0433154505707741	Bowman-Birk type bran trypsin inhibitor
MELO3C000960	0.00601217131829979	0.0433812098520652	Peptidase_M22 domain-containing protein
MELO3C012636	0.00604022024987105	0.0435676806846981	Unknown protein
MELO3C007305	0.00604570718491382	0.0435754274433807	SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-like protein
MELO3C017434	0.00605024264847209	0.0435922079768973	Oxysterol-binding protein-related protein 4C
MELO3C011968	0.00606024825596196	0.0436165607897204	Lipase
MELO3C020484	0.0060595841623905	0.0436165607897204	B3 domain-containing transcription repressor VAL2-like isoform X1
MELO3C019453	0.00606717259072709	0.0436504887046518	Unknown protein
MELO3C012929	0.00608677022585591	0.0437596014526496	Transmembrane protein, putative
MELO3C021977	0.00610215935596248	0.0438073774112173	Translation factor GUF1 homolog, mitochondrial
MELO3C005419	0.00610228848337935	0.0438073774112173	AT-hook motif nuclear-localized protein 6-like
MELO3C008275	0.00609738000015136	0.0438073774112173	Translation initiation factor 2 subunit gamma
MELO3C018119	0.00610157934889466	0.0438073774112173	CRS2-associated factor 2, mitochondrial
MELO3C012855	0.00610856561304385	0.043836505193315	Thioredoxin family protein
MELO3C004028	0.0061196128433687	0.0438679615403588	Syntaxin/T-SNARE family protein
MELO3C024178	0.00612424666004419	0.0438852493792499	Histidine--tRNA ligase
MELO3C023608	0.00613091710727787	0.0439171135116542	Zinc finger family protein
MELO3C021934	0.00613720039845989	0.0439352662012157	Unknown protein
MELO3C006919	0.00614558306381441	0.0439743188142285	cleavage and polyadenylation specificity factor subunit 2
MELO3C002746	0.00616727372711723	0.0440975701798835	Pyruvate dehydrogenase E1 component subunit beta
MELO3C002036	0.00622651950250241	0.0444568089858714	DUF1118-domain-containing protein
MELO3C007762	0.00623705673597619	0.0444628643048621	Mediator of RNA polymerase II transcription subunit 26, putative
MELO3C021058	0.00623574434668006	0.0444628643048621	cell division control protein 45 homolog
MELO3C015155	0.00623862458801827	0.0444628643048621	Scarecrow-like 3
MELO3C027004	0.00624716628925381	0.0445033742420186	poly(A)-specific ribonuclease PARN-like
MELO3C022302	0.00627652237112752	0.044636312678213	protein LHY-like isoform X1
MELO3C020793	0.00628178082278441	0.0446576275986931	Amidase, putative
MELO3C012054	0.00629326949914211	0.0447075308950235	Glycine-rich protein
MELO3C013884	0.00630182195868945	0.0447517734132175	E3 ubiquitin-protein ligase LAP
MELO3C024563	0.00631506277400962	0.0448296817842976	O-linked N-acetylglucosamine transferase, putative
MELO3C014872	0.00632247490555671	0.0448500563612929	Lipase
MELO3C007513	0.00632190735505112	0.0448500563612929	No data found
MELO3C013087	0.00633709589246012	0.0449215027926041	5'/3'-nucleotidase SurE
MELO3C012701	0.00636922311907195	0.0451003657442134	Cysteine proteinase inhibitor
MELO3C018356	0.00636756099341584	0.0451003657442134	Protein WVD2-like 7
MELO3C021329	0.00636951373363392	0.0451003657442134	ATP-binding cassette sub-family C member 11
MELO3C026388	0.00637537403507316	0.0451026197189537	N-acetyl-D-glucosamine kinase-like
MELO3C010153	0.00637634889135241	0.0451026197189537	CTP-dependent diacylglycerol kinase 1
MELO3C009381	0.00639888795602483	0.0452296486197332	splicing factor 3A subunit 2
MELO3C016674	0.00642353608518753	0.0453713927562119	cyclin-SDS-like isoform X1
MELO3C018174	0.00642233138082371	0.0453713927562119	zinc finger protein CONSTANS-LIKE 4
MELO3C004357	0.00642826459136869	0.0453852268631873	No data found
MELO3C018412	0.00643238898121734	0.0453852268631873	allene oxide synthase 3-like
MELO3C025627	0.00644076471782506	0.0454066095911773	Sodium/calcium exchanger family protein
MELO3C025613	0.00644431749613228	0.0454066095911773	Tyrosine aminotransferase
MELO3C006253	0.00646031208615239	0.0454115548155478	protein ECERIFERUM 1-like
MELO3C003341	0.00646141419979185	0.0454115548155478	Casein kinase II subunit beta
MELO3C009195	0.00646569829267873	0.0454150041623959	OTU domain-containing protein
MELO3C014214	0.00646880382342496	0.0454150041623959	ABC transporter G family-like protein
MELO3C010810	0.00646732888793111	0.0454150041623959	Sigma factor sigb regulation protein rsbq
MELO3C013814	0.00648131394496065	0.0454866627928315	26S proteasome non-ATPase regulatory subunit 13
MELO3C002275	0.00649370496098678	0.0455574349110223	anthranilate phosphoribosyltransferase, chloroplastic

MELO3C004648	0.00650643547640417	0.045614339447464	Stress-response A/B barrel domain-containing protein UP3
MELO3C014127	0.00651810160220068	0.0456522271398093	Actin-related protein 8
MELO3C013774	0.00651526241483036	0.0456522271398093	Cystathionine gamma-synthase
MELO3C017394	0.00652352679417967	0.0456578253063655	No data found
MELO3C011399	0.00652419783353908	0.0456578253063655	LOW QUALITY PROTEIN: transcription factor BIM2
MELO3C009226	0.00653689188363704	0.0457291104621977	serine/threonine-protein kinase ATG1c
MELO3C006727	0.00654713755056613	0.0457697060127895	Neutral/alkaline invertase
MELO3C014592	0.00655080438696443	0.0457791351161219	heterogeneous nuclear ribonucleoprotein F
MELO3C025386	0.00655608608069769	0.04579983870099	Polyadenylate-binding protein-interacting protein 4
MELO3C003629	0.00657160924631839	0.0458729395477752	Plasma membrane ATPase
MELO3C025085	0.00657351860449662	0.0458729395477752	Class I heat shock protein
MELO3C017111	0.00658733845633164	0.0459531427672531	39S ribosomal protein L47, mitochondrial
MELO3C000210	0.00659371367780071	0.0459813740900022	Unknown protein
MELO3C002863	0.00659694398511679	0.0459876621115677	patellin-4
MELO3C010710	0.00660311013512804	0.046014404396134	Short-chain dehydrogenase/reductase
MELO3C014101	0.00661437329406644	0.0460196052035173	Unknown protein
MELO3C020940	0.00661550757875262	0.0460196052035173	Pentatricopeptide repeat-containing family protein
MELO3C011317	0.00660728708017455	0.0460196052035173	zinc finger protein CONSTANS-LIKE 4
MELO3C023313	0.00665769860589904	0.0462804962224218	Transmembrane protein, putative
MELO3C002412	0.00666469864478825	0.0463128548683755	Ankyrin repeat family protein
MELO3C021730	0.00666911679857307	0.0463272555944494	calcium permeable stress-gated cation channel 1-like
MELO3C023315	0.00668561297068715	0.0463928919740339	diaminopimelate decarboxylase 2, chloroplastic-like
MELO3C016714	0.00672515339221591	0.0466181306924788	protochlorophyllide reductase, chloroplastic
MELO3C024515	0.00672876682696899	0.0466268126546704	splicing factor U2af small subunit B-like
MELO3C002102	0.00673479236241348	0.046652197251948	Receptor-like kinase
MELO3C006703	0.00674630940843268	0.0467155906406511	CoA ligase
MELO3C005600	0.0067735201512592	0.046871202383288	Phosphate translocator-related family protein
MELO3C022928	0.00677352836102607	0.046871202383288	No data found
MELO3C015597	0.00677974577639429	0.0468813723172307	Calcium ion binding
MELO3C018604	0.00677908066685062	0.0468813723172307	Ubiquitin-like-specific protease 2
MELO3C026067	0.00678676319927907	0.0469134709214429	tRNA (Guanine(9)-N1)-methyltransferase-like
MELO3C007325	0.00679902181931435	0.046981764139132	Sugar transporter, putative
MELO3C023845	0.00680785721675858	0.0470263631247867	serine/arginine-rich SC35-like splicing factor SCL30
MELO3C018418	0.00681891427759185	0.0470862720518047	No data found
MELO3C010532	0.00684685289919851	0.0472626696631497	Structural constituent of ribosome, putative
MELO3C026628	0.00686069658808242	0.0473416830601117	Zinc finger protein
MELO3C022323	0.00686333010384244	0.0473433133848356	proton pump-interactor 1-like
MELO3C007871	0.00687289009524761	0.0473761628240995	rRNA adenine N(6)-methyltransferase
MELO3C022636	0.00688113418024483	0.0474164406579397	No data found
MELO3C015424	0.00690715562065036	0.0475625580028675	Glucan endo-1,3-beta-glucosidase, putative
MELO3C026546	0.00693441822564089	0.0476860043919131	DNA-directed RNA polymerase subunit beta
MELO3C014262	0.00696264092237953	0.0476860043919131	60S ribosomal protein L4-like
MELO3C020440	0.00696854568206295	0.0476860043919131	UBX domain-containing protein 1
MELO3C006100	0.00695734585909258	0.0476860043919131	Ubiquitin-conjugating enzyme, E2
MELO3C014870	0.00695033903996145	0.0476860043919131	DSR6
MELO3C010475	0.00694843697490344	0.0476860043919131	UDP-glucuronosyltransferase 2B17
MELO3C007024	0.00695655689989738	0.0476860043919131	Phenylalanine--tRNA ligase
MELO3C025262	0.00696807649833175	0.0476860043919131	AAA+ ATPase domain-containing protein
MELO3C003085	0.00696185243230085	0.0476860043919131	Flagellin N-methylase
MELO3C022024	0.00693627676482245	0.0476860043919131	Hexosyltransferase
MELO3C020840	0.00696181741775093	0.0476860043919131	Formin-like protein
MELO3C025870	0.0069539047423004	0.0476860043919131	Transcription factor
MELO3C002552	0.00693441431194941	0.0476860043919131	Wound-responsive family protein
MELO3C008234	0.00696379313695883	0.0476860043919131	Transferring glycosyl group transferase
MELO3C021323	0.00699292881807612	0.0478197199543578	condensin-2 complex subunit D3
MELO3C026341	0.00704211024903056	0.0480894312960251	ubiquitin-conjugating enzyme E2 22
MELO3C006306	0.00704624370381213	0.048101025546694	beta-mannosyltransferase 1
MELO3C021434	0.00709534752098828	0.0484027696690838	DNA polymerase epsilon catalytic subunit A
MELO3C007597	0.00712542430296725	0.0485743888710046	Indole-3-acetic acid-amido synthetase GH3.3
MELO3C017791	0.00713147184175345	0.048598839683502	No data found
MELO3C024179	0.00715903843773669	0.0487239522278649	zinc finger protein CONSTANS-LIKE 9-like
MELO3C018056	0.00715686435559881	0.0487239522278649	Carbonic anhydrase
MELO3C024853	0.00717709886898354	0.0488182782776459	GTP-binding protein, chloroplastic
MELO3C022802	0.00718337005107827	0.0488345525434578	Sulfate transporter, putative
MELO3C009638	0.00720397515405002	0.0488443099327942	UBP1-associated protein 2C-like
MELO3C014057	0.00719121069185757	0.0488443099327942	Plant UBX domain-containing protein 8
MELO3C003108	0.00720218464493627	0.0488443099327942	Histone H2A
MELO3C025150	0.00720791735611159	0.0488443099327942	No data found
MELO3C021391	0.00719687947412662	0.0488443099327942	Protein ABCI12, chloroplastic
MELO3C021274	0.00720832830460949	0.0488443099327942	Outer envelope pore protein 16-2, chloroplastic
MELO3C012904	0.00719324434856972	0.0488443099327942	Autophagy-related protein 9
MELO3C010939	0.00722100799204228	0.0488884768031687	FK506-binding protein 4-like
MELO3C026824	0.00723804249067217	0.048987012045334	cytochrome P450 714A1-like
MELO3C021328	0.00724702951271161	0.0490182548751763	ubiquitin-like-specific protease ESD4
MELO3C004223	0.00725452501643375	0.0490313533708249	ATP-dependent Clp protease proteolytic subunit
MELO3C017562	0.00725386990279486	0.0490313533708249	Random slug protein 5
MELO3C008420	0.0072686274147804	0.0491098606960309	Transcriptional corepressor SEUSS
MELO3C009316	0.0072779413909807	0.0491559728216409	Interactor of constitutive active ROPs-like protein
MELO3C016448	0.00729807390629156	0.0491973357260124	methionine S-methyltransferase
MELO3C019257	0.00729310653565496	0.0491973357260124	CDT1-like protein a, chloroplastic
MELO3C005288	0.00730395227585312	0.0492138360613522	F-box family protein
MELO3C006035	0.00731675729151005	0.0492664983805087	Rhodanese-like domain-containing protein 4, chloroplastic
MELO3C012007	0.00732642441238118	0.0492894286514099	spermidine synthase
MELO3C010766	0.00733014592886683	0.0492894286514099	UPF0587 protein C1orf123 homolog
MELO3C019260	0.00733326272891488	0.0492936030065827	Glutamate receptor
MELO3C017705	0.00734710733815036	0.0493698614566626	Transducin/WD40 repeat-like superfamily protein
MELO3C012421	0.0073514013120205	0.0493819130990112	Cytochrome c oxidase assembly protein COX16
MELO3C010584	0.00736507254652774	0.0494569254407944	ribosome maturation protein SBDS
MELO3C005980	0.00738295761679109	0.0495433333245012	Protein ARABIDILLO 1
MELO3C020839	0.00739116720083399	0.0495801838855691	glutamine--tRNA ligase-like
MELO3C008610	0.00743112678605029	0.0497819955555316	No data found

MELO3C021306	0.00743815264091596	0.0497952801713388	ethylene-responsive transcription factor RAP2-3-like
MELO3C017009	0.00744176012404185	0.0498025485224339	4-coumarate--CoA ligase family protein
MELO3C022759	0.00746050443032131	0.0498941760902186	MOB kinase activator-like 1A
MELO3C016549	0.00746559537964697	0.0499113213109844	U3 small nucleolar RNA-associated protein 14 B isoform 3

Supplementary Table 4. Functionality of differentially expressed genes transcripts from RNA-seq (23 DEGs) that were exclusive to the effect of introgression over time in the near-isogenic line (NIL) SC10-2 fruit (n = 3) of melon and its parental control ´Piel de Sapo´ (PS) during postharvest ripening at 20.5 ºC and 88% relative humidity for 18 d.

Gene ID	Functionality*
MELO3C009178	kinase activity, Similar to Probable LRR receptor-like serine/threonine-protein kinase At3g47570 (*Arabidopsis* thaliana) (uniprot_sprot:sp|C0LGP4|Y3475_ARATH)
MELO3C007517	Similar to Brain protein 44-like protein (Homo sapiens) (uniprot_sprot:sp|Q9Y5U8|BR44L_HUMAN)
MELO3C014384	protein dimerization activity, sequence-specific DNA binding, sequence-specific DNA binding transcription factor activity.
MELO3C017343	sodium:dicarboxylate symporter activity, antiporter activity, drug transmembrane transporter activity.
MELO3C024371	Similar to Putative uncharacterized protein (Glycine max) (uniref90:UniRef90_C6THY2)
MELO3C011742	Similar to Putative uncharacterized protein (Vitis vinifera) (uniref90:UniRef90_A5AT31)
MELO3C020541	delta12-fatty acid dehydrogenase activity.
MELO3C024434	Similar to Putative uncharacterized protein (Ricinus communis) (uniref90:UniRef90_B9RQD6)
MELO3C026171	integral to membrane, mitochondrial inner membrane.
MELO3C010991	proton-transporting ATPase activity, rotational mechanism, hydrogen ion transporting ATP synthase activity, rotational mechanism.
MELO3C002083	Similar to Putative uncharacterized protein (Glycine max) (uniref90:UniRef90_C6SZD6)
MELO3C011490	ATP binding, actin binding, motor activity.
MELO3C011715	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase activity.
MELO3C005513	metal ion binding, zinc ion binding, protein binding, ubiquitin-protein ligase activity.
MELO3C021353	regulation of transcription, DNA-dependent, ATP-dependent chromatin remodeling.
MELO3C011383	ribonucleoside binding, DNA-directed RNA polymerase activity, DNA binding.
MELO3C014724	gluconeogenesis, glucose metabolic process, carbohydrate metabolic process.
MELO3C014519	sequence-specific DNA binding, sequence-specific DNA binding transcription factor activity.
MELO3C002385	regulation of transcription, DNA-dependent.
MELO3C013378	No data found
MELO3C003072	oxidoreductase activity, antioxidant activity.
MELO3C000885	auxin mediated signaling pathway.
MELO3C009970	cellular cell wall organization, carbohydrate metabolic process.

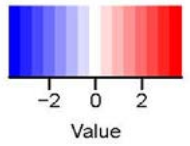
(*According to www.melonomics.net, New Melonomics (v3.5))

Supplementary Table 5. Expression levels of differentially expressed genes in melon fruit of the near-isogenic line SC10-2 and its parental control ´Piel de Sapo´ (PS) during postharvest storage at 20.5^{o}C and 88% relative humidity for 18 d. *, **; ***, ****: significance at P ≤ 0.05, 0.01, 0.001 or 0.0001, respectively. Gene code according with Melonomics 4.0

		Expression levels of the lines over time (mean ±SE, n=3)												
		PS					SC10-2					ANOVA significance		
Gene ID	Gene abbreviation	0	4	8	12	16	0	4	8	12	16	Ripening time (RT)	Introgression (I)	RT x I
MELO3C024348	*Cm* LOX18	5,1 ±0,7	5,6 ±0,2	1,6 ±0,2	2,4 ±0,1	4,2 ±0,1	33 ±4,5	17,2 ±2,3	6,7 ±1,1	5,8 ±0,5	27,1 ±8,0	**	****	NS
MELO3C019735	*Cm* ACO2	45,7 ±5,0	53,0 ±5,1	38,0 ±0,5	25,1 ±0,8	13,6 ±0,5	32,7 ±5,4	17,5 ±0,3	12,8 ±1,1	9,5 ±0,4	9,1 ±0,8	***	****	NS
MELO3C019548	*Cm* ADH1	4,2 ±0,17	4,4 ±0,11	5,0 ±0,13	5,0 ±0,14	3,4 ±0,5	4,1 ±0,1	3,8 ±0,1	3,2 ±0,1	3,3 ±0,1	3,1 ±0,3	*	**	*
MELO3C018492	*Cm* CAD1	55,8 ±4,1	151,0 ±0,4	252,9 ±20,5	172,0 ±36,4	166,2 ±17,2	19,4 ±4,5	48,0 ±5,7	44,8 ±1,6	52,3 ±3,5	56,2 ±10,4	**	****	*
MELO3C010910	*Cm* AOS	4,7 ±0,0	5,7 ±0,1	5,1 ±0,1	6,0 ±0,1	5,6 ±0,3	7,8 ±0,2	7,2 ±0,3	5,7 ±0,2	5,8 ±0,1	6,5 ±0,2	*	****	**
MELO3C016259	*Cm* SWEET7	0,5 ±0,3	1,6 ±0,2	0,5 ±0,2	0,5 ±0,6	0,9 ±0,9	0,2 ±0,1	2,0 ±0,4	3,4 ±0,2	3,0 ±0,2	2,3 ±0,1	*	**	*
MELO3C008075	*Cm* OPR2	2,3 ±0,2	2,8 ±0,1	2,5 ±0,1	2,7 ±0,0	2,2 ±0,2	4,0 ±0,1	4,6 ±0,1	3,9 ±0,2	3,1 ±0,2	3,8 ±0,1	****	NS	NS
MELO3C020508	*Cm* DFR4	3.1 ±0,1	2,6 ±0,1	2,6 ±0,1	3,0 ±0,1	1,2 ±0.3	4,2 ±0,1	3,77 ±0,0	4,2 ±0,1	4,5 ±0,1	4,3 ±0,5	**	****	*
MELO3C012476	*Cm* NADH1	2,5 ±0,1	2,4 ±0,0	1,7 ±0,1	1,6 ±0,1	0,7 ±0,1	0,3 ±0,0	0,8 ±0,0	0,7 ±0,1	1,0 ±0,1	0,7 ±0,1	*	**	NS
MELO3C017811	*Cm* PAL	0,6 ±0,7	0,5 ±0,1	0,5 ±0,2	0,4 ±0,2	0,1 ±0,0	2,0 ±0,2	2,1 ±0,1	1,3 ±0,1	1,8 ±0,1	2,5 ±0,2	NS	****	NS
MELO3C009127	*Cm* WRKY33	7,3 ±1,3	46,7 ±7,8	12,4 ±0,1	10,8 ±1,5	28,2 ±4,8	56,3 ±5,5	207,4 ±13,7	60,4 ±7,1	34,1 ±2,8	33,4 ±1,0	**	****	*
MELO3C023350	*Cm* GATA5	5,1 ±0,1	5,0 ±0,1	4,6 ±0,1	4,7 ±0,1	4,3 ±0,1	6,2 ±0,3	6,8 ±0,1	5,6 ±0,1	5,3 ±0,1	5,0 ±0,0	***	****	NS
MELO3C005630	*Cm* ERF027	0,0 ±0,0	0,0 ±0,0	0,0 ±0,0	0,0 ±0,0	0,0 ±0,0	3,4 ±0,6	2,0 ±0,4	0,2 ±0,1	0,7 ±0,2	1,8 ±0,7	*	**	*
MELO3C012086	*Cm* TCP15	1,7 ±0,0	2,1 ±0,1	2,0 ±0,1	1,4 ±0,3	0,0 ±0,0	3,3 ±0,2	3,3 ±0.1	3,2 ±0,1	2,7 ±0,1	3,1 ±0,1	*	****	NS
MELO3C011939	*Cm* GDSL esterase/lipase	1,6 ±0,0	1,0 ±0,1	1,0 ±0,1	0,9 ±0,1	0,1 ±0,0	4,2 ±0,1	4,5 ±0,0	4,3 ±0,0	3,9 ±0,0	4,1 ±0,1	***	****	*
MELO3C013101	*Cm* GDPDL4	30,2 ±1,4	27,1 ±1,2	11,3 ±0,8	46,6 ±1,8	28,6 ±1,4	81,2 ±2,3	67,1 ±1,5	58,2 ±2,1	20,1 ±0,8	34,1 ±1,2	*	****	****
MELO3C016540	*Cm* NAC18	677,9 ±31,6	766,9 ±6,8	719,8 ±3,0	639,3 ±32,2	733,9 ±34,3	177,0 ±32,8	240,4 ±11,3	380,4 ±30,4	564,7 ±20,6	491,8 ±3,0	*	****	**
MELO3C005591	*Cm* ACT	17,1 ±0,5	37,2 ±0,9	20,1 ±2,1	38,2 ±2,1	32,1 ±1,6	78,8 ±2,4	100,2 ±0,8	32,2 ±1,8	24,6 ±2,1	40,2 ±2,1	*	***	**
MELO3C017560	*Cm* SDHA	68,2 ±2,4	46,1 ±0,5	46,8 ±0,3	46,8 ±1,1	54,6 ±0,3	67,3 ±1,2	48,1 ±1,2	44,7 ±0,9	44,9 ±0,62	56,9 ±2,4	****	NS	NS
MELO3C021563	*Cm* NADP	39,9 ±2,2	21,8 ±0,2	25,0 ±0,9	23,0 ±1,4	26,0 ±0,4	36,9 ±1,5	22,0 ±0,3	22,1 ±0,9	18,5 ±0,7	24,6 ±0,3	****	NS	NS
MELO3C018576	*Cm* L-GalDH	36,0 ±0,8	30,7 ±0,2	30,5 ±1,2	44,9 ±1,0	48,1 ±0,6	34,3 ±1,2	34,8 ±1,0	36,6 ±0,1	40,6 ±0,1	39,1 ±1,2	***	NS	NS
MELO3C004377	*Cm* GME	78,6 ±2,1	87,1 ±0,3	92,4 ±0,9	81,3 ±5,7	92,2 ±4,7	77,1 ±1,7	90,4 ±2,0	99,2 ±1,6	97,2 ±2,6	84,7 ±0,4	*	NS	NS
MELO3C010675	*Cm* ACLA-1	88,0 ±2,7	37,5 ±1,0	39,5 ±0,7	34,3 ±1,4	42,4 ±1,3	90,1 ±6,8	36,9 ±1,7	43,6 ±1,1	41,0 ±1,0	67,2 ±7,2	****	NS	NS
MELO3C011482	*Cm* ACLB-2	46,1 ±3,0	18,7 ±0,3	25,9 ±0,9	40,3 ±2,4	48,8 ±1,8	44,3 ±3,2	16,6 ±0,1	15,3 ±0,4	21,0 ±1,0	32,6 ±3,7	***	*	NS
MELO3C002167	*Cm* SCOA	65,1 ±3,1	38,7 ±0,3	39,4 ±1,0	43,9 ±2.0	51,5 ±0,4	64,2 ±2,0	46,0 ±2,1	43,0 ±1,2	38,0 ±0,2	52,0 ±3,6	****	NS	NS
MELO3C005518	*Cm* IPMI3	56,3 ±2,5	30,1 ±0,4	28,2 ±0,9	38,0 ±0,3	34,0 ±0,7	57,0 ±1,4	40,2 ±0,8	35,2 ±0,7	30,8 ±0,8	40,8 ±2,9	****	NS	NS
MELO3C003344	*Cm* IIL1	105,2 ±3,6	54,0 ±0,1	54,4 ±0,7	50,6 ±1,3	68,8 ±1,2	69,9 ±1,3	55,8 ±0,6	50,8 ±0,1	51,1 ±0,8	49,2 ±2,3	****	**	***
MELO3C007433	*Cm* FAH	52,0 ±2,1	29,6 ±0,2	27,6 ±0,2	30,9 ±1,1	34,0 ±0,6	36,6 ±1,4	26,0 ±0,3	25,2 ±0,9	23,5 ±0,8	30,5 ±1,0	****	**	NS
MELO3C009970	*Cm* DHL92	1,0 ±0,1	0,3 ±0,1	0,1 ±0,1	0,2 ±0,1	0,5 ±0,1	1,1 ±0,0	0,3 ±0,1	0,5 ±0,1	0,3 ±0,0	0,2 ±0,1	***	NS	NS
MELO3C007517	*Cm* MPC1	44,8 ±0,5	31,7 ±1,0	30,2 ±1,3	32,8 ±1,9	37,0 ±0,9	48,3 ±1,8	34,1 ±1,0	39,7 ±0,9	32,4 ±1,2	37,1 ±2,0	***	NS	NS
MELO3C017343	*Cm* DTX	25,7 ±2,1	38,7 ±2,3	34,4 ±2,1	28,4 ±2,5	33,0 ±0,8	17,8 ±1,2	28,9 ±1,1	32,0 ±0,6	36,7 ±0,7	26,7 ±1,4	*	NS	NS
MELO3C014384	*Cm* ABREX1	46,0 ±1,5	50,5 ±0,7	52,2 ±2,9	50 ±1,6	47,7 ±0,5	39,7 ±2,1	43,7 ±0,7	47,3 ±0,3	49,0 ±1,0	45,9 ±1,3	NS	*	NS
MELO3C000885	*Cm* IAA71	1,4 ±0,3	0,6 ±0,2	0,0 ±0,0	0,3 ±0,2	0,2 ±0,1	1,9 ±0,3	0,2 ±0,1	0,4 ±0,1	0,2 ±0,1	0,3 ±0,1	**	NS	NS
MELO3C024001	*Cm* MADS-box	9,6 ±0,6	6,1 ±1,0	6,7 ±0,4	6,1 ±0,6	5,2 ±0,1	6,2 ±0,6	3,6 ±0,4	2,9 ±0,3	2,1 ±0,1	1,3 ±0,1	**	***	NS
MELO3C010686	*Cm* ALT-2	89,9 ±4,7	46,6 ±3,1	59,5 ±0,2	49,9 ±3,0	53,6 ±2,1	71,8 ±2,7	41,1 ±1,3	42,3 ±1,2	39,2 ±0,8	47,0 ±0,3	****	**	NS

Supplementary Table 6. Clustes obtained the heatmap and hierarchical clustering (using Euclidean distance as the similarity measure and Ward's linkage) applied to thirty-seven differentially expressed genes (Table 1) and the quality traits measured

(textural traits and VOCs) over postharvest ripening time (columns represent samples and rows variables). Original data were scaled and log-transformed. Predominant trend in the heatmap was represented in red or blue color and the main melon line (NIL SC10-2 or the parental PS).



Cluster groups	**Cluster subgroup**	**Gene**	**Gene code**	**VOCs (IUPAC name)**	Texture	**Functions**	PREDOMINANT TREND (HEATMAP)
C3	G1	MELO3C024348	*Cm* LOX18	Methanethiol		lipoxygenase activity, iron ion binding.	🟥 SC10-2 🟦 PS
C4	G2	MELO3C009127	*Cm* WRKY33	(6E)-6-[(E)-but-2-enylidene]-1,5,5-trimethylcyclohexene 1-(3-Ethylphenyl)ethanone Unidentified (22.95) Unidentified (22.63) 2−(4−methylcyclohex−3−en−1−yl)propan−2−ol 2,4−dimethyldodecane Unidentified (22.46) 1−(2−methylphenyl)ethanone	LateralHardness Hardness Firmness	sequence-specific DNA binding, protein binding, sequence-specific DNA binding transcription factor activity.	🟥 SC10-2 🟦 PS
C7	G3	MELO3C005518	*Cm* IPMI3	Propan-2-one		3-isopropylmalate dehydratase activity.	🟦 SC10-2 🟥 PS
		MELO3C017560	*Cm* SDHA	1-methyl-4-prop-1-en-2-ylcyclohexene		succinate dehydrogenase (ubiquinone) activity.	
		MELO3C002167	*Cm* SCOA	(2E)-2-Pentenal		copper ion binding, succinate-CoA ligase (GDP forming) activity, succinate-CoA ligase (ADP-forming) activity, ATP citrate synthase activity.	
		MELO3C010675	*Cm* ACLA-1			ligase activity, catalytic activity, ATP binding, succinate-CoA ligase (ADP-forming) activity.	
		MELO3C021563	*Cm* NADP			NAD binding, isocitrate dehydrogenase (NADP+) activity, isocitrate dehydrogenase (NAD+) activity, magnesium ion binding.	
		MELO3C010686	*Cm* ALT-2			pyridoxal phosphate binding, 1-aminocyclopropane-1-carboxylate synthase activity, transaminase activity.	
		MELO3C003344	*Cm* IIL1			intramolecular transferase activity, transferring hydroxy groups, metal ion binding, hydro-lyase activity, 4 iron, 4 sulfur cluster binding, 3-isopropylmalate dehydratase activity.	
		MELO3C007433	*Cm* FAH			metal ion binding, fumarylacetoacetase activity.	

Suppl. Table 6 (continuation)

Cluster groups	**Cluster subgroup**	**Gene**	**Gene code**	**VOCs (IUPAC name)**	Texture	**Functions**	PREDOMINANT TREND (HEATMAP)	
C7	G3 (cont)	MELO3C011482	*Cm* ACLB-2	Ethyl 2-methylbutanoate Methyl acetate Ethyl-2-methylpropanoate 2-Methylbutyl-acetate		Lyase activity, acyltransferase activity, binding, succinate-CoA ligase (ADP-forming) activity, ATP citrate synthase activity. Necessary for the generation of the cytosolic pool of acetyl-CoA		
C7	G4	MELO3C019735	*Cm* ACO2	3-Hydroxy-2,4,4-trimethylpentyl-2-methylpropanoate		metal ion binding, L-ascorbic acid binding, 1 aminocyclopropane-1-carboxylate oxidase activity.	SC10-2	PS
		MELO3C024001	*Cm* MADS-box	2-Methoxybenzenethiol 2-Decanone 2-Octanylpropionate		sequence-specific DNA binding, protein binding, sequence-specific DNA binding transcription factor activity.		
C7	G5	MELO3C018492	*Cm* ACLB-2	Isobutyl-benzoate 1-Tridecanol		cinnamyl-alcohol dehydrogenase activity, zinc ion binding.	SC10-2	PS
C8	G6	MELO3C018576	*Cm* L-GalLDH	2-methylpropyl acetate Hexyl acetate 2,3-Butanediyl diacetate 2-Methyl-2-propen-1-yl acetate 2,3-Butanediyl diacetate–r (isomer) S-Methyl propanethioate		D-arabinose 1-dehydrogenase (NAD) activity, D arabinose 1-dehydrogenase [NAD(P)+] activity, oxidoreductase activity, protein binding, pyridoxal 4-dehydrogenase activity, L-galactose dehydrogenase activity.	SC10-2	PS
C8	G7	MELO3C016540	*Cm* NAC18	1-(4-Methylphenyl)ethanone Cyclohexanone S-Methyl 2-methylpropanethioate S-Methyl 3-methylbutanethioate Isopropyl propionate		DNA binding.	SC10-2	PS
C8	G8	MELO3C020055	*Cm* HK4-like	Methyl (methylsulfanyl)acetate 2-Phenylethyl acetate	Density Juiciness	ATP binding, protein binding, receptor activity, two-component response regulator activity, two-component sensor activity.	SC10-2	PS