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(54) Title: FRUIT WITH INCREASED FRUIT SIZE, ANTIOXIDANTS, AND RESISTANCE TO BLOSSOM END ROT

(57) Abstract: The present disclosure is directed to methods and compositions for increasing resistance to blossom end rot in fruit, increasing fruit size, and increasing antioxidant content in fruits. Embodiments of the disclosure also include plant cells, plants, and fruits including a modified ADP-glucose pyrophosphorylase (AGPase). Also included are nucleic acid constructs, and methods of breeding for enhanced blossom end rot resistance.



FRUIT WITH INCREASED FRUIT SIZE, ANTIOXIDANTS, AND RESISTANCE TO BLOSSOM END ROT

CROSS-REFERENCE TO RELATED APPLICATIONS

5 **[0001]** This application claims priority of US Provisional application number 63/504,949 filed May 30, 2023, the entire contents being incorporated herein by reference as though set forth in full.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

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[0002] This invention was made with government support under grant number IOS1339287 awarded by the National Science Foundation, and grant number 2019-67013-29240 awarded by the U.S. Department of Agriculture. The government has certain rights in the invention.

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INCORPORATION-BY-REFERENCE OF MATERIAL SUBMITTED IN ELECTRONIC FORM

[0003] The Contents of the electronic sequence listing (BTCO-102-PCT.xml; Size: 413,534 bytes; and Date of Creation: May 30, 2024) is herein incorporated by reference in its
20 entirety.

FIELD

[0004] The present disclosure is directed to methods and compositions for increasing resistance to blossom end rot in fruit, increasing fruit size, and increasing antioxidant content in
25 fruits.

BACKGROUND

[0005] The regulation of carbohydrate availability is crucial in plant growth and development under both favorable and challenging conditions. Appropriate carbon partitioning
30 between photosynthetically active source tissues, such as leaves, and sink tissues, such as fruits and roots, is required for optimal plant growth and reproductive development. Starch, the major

carbohydrate store in plants, plays a key role in maintaining sugar homeostasis in a fluctuating environment (MacNeill et al., “Starch as a Source, Starch as a Sink: The Bifunctional Role of Starch in Carbon Allocation,” *J Exp Bot* 68:4433–4453 (2017)). In source organs fixed carbon is exported to sink tissues, mainly in the form of sucrose, or transformed into transitory starch in the plastids, a carbon reservoir that accumulates during the day and is degraded at night to provide carbon and energy when photosynthesis is nonfunctional (Stitt and Zeeman, “Starch Turnover: Pathways, Regulation and Role in Growth,” *Curr Opin Plant Biol* 15:282–292 (2012)). The metabolic activity of photosynthetic leaves and phloem unloading has an effect on sugar accumulation in sink tissues, where carbohydrate metabolism and accumulation are also tightly regulated (Osorio et al., “An Update on Source-to-Sink Carbon Partitioning in Tomato,” *Front Plant Sci* 5:516 (2014)) to coordinate photoassimilate delivery and consumption. Sucrose allocated to sink tissues can be metabolized for starch biosynthesis, which acts as a more or less stable carbohydrate storage, depending on the nature of the sink tissue (MacNeill et al., “Starch as a Source, Starch as a Sink: The Bifunctional Role of Starch in Carbon Allocation,” *J Exp Bot* 68:4433–4453 (2017)). In dedicated storage sinks (*e.g.*, seeds and tubers), starch accumulates for long-term energy storage. However, in other heterotrophic organs, such as reproductive tissues, starch constitutes a temporary carbon storage that is rapidly remobilized during specific developmental stages (Hedhly et al., “Starch Turnover and Metabolism During Flower and Early Embryo Development,” *Plant Physiol* 172:2388–2402 (2016)). Although the pattern of accumulation can vary between fruit species, several fruit store starch early during fruit growth, and degrade it during ripening (Roch et al., “Fruit Salad in the Lab: Comparing Botanical Species to Help Deciphering Fruit Primary Metabolism,” *Front Plant Sci* 10:836 (2019)).

[0006] Tomato (*Solanum lycopersicum*) is an important fruit crop and a model system for fleshy fruit development. During tomato fruit development, the majority of photoassimilates are imported as sucrose from the leaves, therefore, sucrose import and metabolism are considered major factors contributing to fruit sink strength and metabolic composition (Fridman et al., “A Recombination Hotspot Delimits a Wild-Species Quantitative Trait Locus for Tomato Sugar Content to 484 bp Within an Invertase Gene,” *PNAS* 97:4718–4723 (2000); Zanol et al., “RNA Interference of LIN5 in Tomato Confirms its Role In Controlling Brix Content, Uncovers the Influence of Sugars on the Levels of Fruit Hormones, and Demonstrates the Importance of Sucrose Cleavage for Normal Fruit Development and Fertility,” *Plant Physiol* 150:1204–1218

(2009); Ruan et al., “Molecular Regulation of Seed and Fruit Set,” *Trends Plant Sci* 17:656–665 (2012); Beauvoit et al., “Model-Assisted Analysis of Sugar Metabolism Throughout Tomato Fruit Development Reveals Enzyme and Carrier Properties in Relation to Vacuole Expansion,” *Plant Cell* 26:3224–3242 (2014)). Tomato fruit store carbon as transitory starch, which peaks during fruit growth (Schaffer and Petreikov, “Sucrose-to-Starch Metabolism in Tomato Fruit Undergoing Transient Starch Accumulation,” *Plant Physiol* 113:739–746 (1997)) and is mobilized during ripening. It has been proposed that this transient starch accumulation contributes to maintaining sink strength during fruit development, and to fuel ripening associated metabolism (Osorio et al., “An Update on Source-to-Sink Carbon Partitioning in Tomato,” *Front Plant Sci* 5:516 (2014); Quinet et al., “Tomato Fruit Development and Metabolism,” *Front Plant Sci.* 10:1554 (2019)). A positive correlation has been found between the size of the starch pool and the final levels of fruit soluble sugars (Baxter et al., “Fruit Carbohydrate Metabolism in an Introgression Line of Tomato with Increased Fruit Soluble Solids,” *Plant Cell Physiol* 46:425–437 (2005); Petreikov et al., “Carbohydrate Balance and Accumulation During Development of Near-Isogenic Tomato Lines Differing in the AGPase-L1 Allele,” *J Amer Soc Hort Sci* 134:134–140 (2009); Powell et al., “Uniform Ripening Encodes a Golden 2-Like Transcription Factor Regulating Tomato Fruit Chloroplast Development,” *Science* 336:1711–1715 (2012); Sagar et al “SlARF4, An Auxin Response Factor Involved in the Control of Sugar Metabolism During Tomato Fruit Development,” *Plant Physiol* 161:1362–1374 (2013)), and between the activity levels of ADP-glucose pyrophosphorylase (AGPase), a limiting enzyme in starch synthesis (Geigenberger P., “Regulation of Starch Biosynthesis in Response to a Fluctuating Environment,” *Plant Physiol* 155:1566–1577 (2011)), and fruit sugar content at ripening (Centeno et al., “Malate Plays a Crucial Role in Starch Metabolism, Ripening, and Soluble Solid Content of Tomato Fruit and Affects Postharvest Softening,” *Plant Cell* 23:162–184 (2011); Hou et al., “Responses of Water Accumulation and Solute Metabolism in Tomato Fruit to Water Scarcity and Implications for Main Fruit Quality Variables,” *J Exp Bot* 71:1249–1264 (2020)). Thus, it has been suggested that degradation of the starch accumulated in the immature fruit contributes to an increase in sugar levels in the ripe fruit (Quinet et al., “Tomato Fruit Development and Metabolism,” *Front Plant Sci.* 10:1554 (2019)), which support the metabolic changes associated with ripening (Biais et al., “Remarkable Reproducibility of Enzyme Activity Profiles in Tomato Fruits Grown Under Contrasting Environments Provides a Roadmap for

Studies of Fruit Metabolism,” *Plant Physiol* 164:1204–1221 (2014)). An additional proposed role for starch is to act as a buffer for carbon supply fluctuations during fruit set and growth under abiotic stress conditions (Ruan et al., “Molecular Regulation of Seed and Fruit Set,” *Trends Plant Sci* 17:656–665 (2012); Roch et al., “Fruit Salad in the Lab: Comparing Botanical Species to Help Deciphering Fruit Primary Metabolism,” *Front Plant Sci* 10:836 (2019); Yu et al., “Starch and Sugars as Determinants of Postharvest Shelf Life and Quality: Some New and Surprising Roles,” *Curr Opin Biotechnol* 78:102844 (2022)). However, the physiological significance of starch accumulation and metabolism during fruit development is not fully understood.

[0007] Starch metabolism is also critical in plant tolerance to abiotic stress, serving as a carbon reserve that is remobilized to release energy, sugars, and derived metabolites needed for stress mitigation (Pommerrenig et al., “In Concert: Orchestrated Changes in Carbohydrate Homeostasis are Critical for Plant Abiotic Stress Tolerance,” *Plant Cell Physiol* 59:1290–1299 (2018); Dong and Beckles, “Dynamic Changes in the Starch-Sugar Interconversion Within Plant Source and Sink Tissues Promote a Better Abiotic Stress Response,” *J Plant Physiol* 234–235:80–93 (2019)). Starch accumulation can be induced in certain organs and developmental stages in response to various abiotic stresses (Dong and Beckles, “Dynamic Changes in the Starch-Sugar Interconversion Within Plant Source and Sink Tissues Promote a Better Abiotic Stress Response,” *J Plant Physiol* 234–235:80–93 (2019)), and enzymes involved in starch metabolism are tightly regulated during environmental stress (Thalmann and Santelia, “Starch as a Determinant of Plant Fitness Under Abiotic Stress,” *New Phytol* 214:943–951 (2017); Fàbregas and Fernie, “The Metabolic Response to Drought,” *J Exp Bot* 70:1077–1085 (2019)). An increase in sugar supply, caused by activation of starch mobilization, may play an important role in withstanding the effects of abiotic stress. As highly hydroxylated soluble molecules, sugars can function as ROS scavengers, osmoprotectants, and protein and membrane stabilizers. In addition, sugars can act as signaling molecules, thus participating in stress perception, signaling, and gene expression regulation during abiotic stress responses (Saddhe et al., “Plant Sugars: Homeostasis and Transport Under Abiotic Stress in Plants. *Physiol Plant* 171:739–755 (2021)). Accordingly, a tight control of sugar homeostasis, through starch or sucrose metabolism, is required during the stress response to maintain or even increase sugar levels under challenging environmental conditions (Pommerrenig et al., “In Concert:

Orchestrated Changes in Carbohydrate Homeostasis are Critical for Plant Abiotic Stress Tolerance,” *Plant Cell Physiol* 59:1290–1299 (2018); Saddhe et al., “Plant Sugars: Homeostasis and Transport Under Abiotic Stress in Plants. *Physiol Plant* 171:739–755 (2021)). Although starch-sugar interconversions have been suggested as a key determinant of plant fitness under abiotic stress (Thalmann and Santelia, “Starch as a Determinant of Plant Fitness Under Abiotic Stress,” *New Phytol* 214:943–951 (2017); Dong and Beckles, “Dynamic Changes in the Starch-Sugar Interconversion Within Plant Source and Sink Tissues Promote a Better Abiotic Stress Response,” *J Plant Physiol* 234–235:80–93 (2019)), most information about the contribution of starch turnover to the plant stress response has been obtained from *Arabidopsis* and cereal grains. Notably, the role of starch metabolism in the regulation of carbon use during fruit development under abiotic stress conditions, remains largely unexplored (Ma et al., “Molecular Genetic Analyses of Abiotic Stress Responses During Plant Reproductive Development,” *J Exp Bot* 71:2870–2885 (2020); Yu et al., “Starch and Sugars as Determinants of Postharvest Shelf Life and Quality: Some New and Surprising Roles,” *Curr Opin Biotechnol* 78:102844 (2022)).

[0008] Blossom end rot (BER) is a disease affecting tomato fruit as well as other fruits such as peppers, watermelons, and eggplants, resulting in significant yield losses worldwide. BER causes the presence of damaged and necrotic tissue at the distal end in fruit that typically first appears in the placenta, and later affects the pericarp. BER is induced by environmental stress, such as drought, although it is also thought that calcium deficiency plays a role in BER incidence (Topcu et al., “Blossom-End Rot: A Century-Old Problem in Tomato (*Solanum lycopersicum* L.) and Other Vegetables,” *Mol Hort* 2:1 (2022)). Due to these factors, BER is difficult to manage in diverse agricultural settings. Effective solutions to reduce or prevent the incidence of BER and impart BER resistance to fruit are needed.

[0009] This disclosure is directed to overcoming these and other deficiencies in the art.

SUMMARY

[0010] One aspect of the present disclosure relates to a method for imparting blossom end rot resistance to fruit from a plant. The method comprises modifying a plant or a plant cell to reduce or eliminate the expression, stability, and/or activity of ADP-glucose pyrophosphorylase (AGPase) protein, where the reduction or elimination of the expression, stability, and/or activity of AGPase protein is effective in reducing or eliminating starch synthesis and imparting blossom

end rot resistance to fruit from the plant or a plant produced from the plant cell, as compared to fruit from a plant without the modification.

[0011] Another aspect of the present disclosure relates to a method of increasing size of fruit from a plant. The method comprises modifying a plant or a plant cell to reduce or eliminate the expression, stability, and/or activity of ADP-glucose pyrophosphorylase (AGPase) protein, where the reduction or elimination of the expression, stability, and/or activity of AGPase protein is effective in reducing or eliminating starch synthesis and increasing fruit size in fruit from the plant or a plant produced from the plant cell, as compared to fruit from a plant without the modification.

[0012] A further aspect of the present disclosure relates to a method of increasing antioxidants in fruit from a plant. The method comprises modifying a plant or a plant cell to reduce or eliminate the expression, stability, and/or activity of ADP-glucose pyrophosphorylase (AGPase) protein, where the reduction or elimination of the expression, stability, and/or activity of AGPase protein is effective in reducing or eliminating starch synthesis and increasing antioxidant levels in a fruit from the plant or a plant produced from the plant cell, as compared to a fruit from a plant without the modification.

[0013] Another aspect of the present disclosure relates to a plant cell comprising a nucleic acid molecule comprising a modified ADP-glucose pyrophosphorylase (AGPase) gene encoding an AGPase protein or fragment thereof, where the expression, stability, and/or activity of the AGPase protein is reduced or eliminated in the plant cell as compared to a plant cell without the modification.

[0014] Yet another aspect of the present disclosure relates to a plant cell comprising an inhibitory polynucleotide targeting an AGPase gene encoding an AGPase protein, wherein the expression, stability, and/or activity of the AGPase protein is reduced or eliminated in the plant cell as compared to a plant cell without the inhibitory polynucleotide.

[0015] A further aspect of the present disclosure relates to a nucleic acid construct comprising a nucleotide sequence targeting an AGPase gene comprising: (i) a guide RNA, or (ii) an inhibitory polynucleotide, a 5' heterologous DNA promoter sequence, and a 3' terminator sequence.

[0016] Another aspect of the present disclosure relates to a method of breeding for enhanced blossom end rot resistance. The method comprises providing a candidate plant,

analyzing the candidate plant for the presence, in its genome, of a modified ADP-glucose pyrophosphorylase (AGPase) polynucleotide encoding an AGPase protein, wherein the expression, stability, and/or activity of said AGPase protein is reduced or eliminated as compared to a plant without the modification, identifying, based on said analyzing, a candidate plant suitable for breeding that includes in its genome, the modified ADP-glucose pyrophosphorylase (AGPase) polynucleotide, and breeding the identified plant with at least one other plant.

[0017] Yet another aspect of the present disclosure relates to a method for imparting blossom end rot resistance to fruit from a plant. The method comprises modifying a plant or a plant cell to reduce or eliminate the expression, stability, and/or activity of ADP-glucose pyrophosphorylase (AGPase) protein, where the reduction or elimination of the expression, stability, and/or activity of AGPase protein is effective in reducing or eliminating starch synthesis and imparting blossom end rot resistance to fruit from the plant or a plant produced from the plant cell, as compared to fruit from a plant without the modification, and selectively expressing a functional AGPase protein in non-fruit tissues.

[0018] As disclosed herein, the agravitropic tomato mutant *adpressa* (*adp*) was found to carry a mutation in the gene encoding the small subunit of ADP-glucose pyrophosphorylase (AGPase), which abolished starch synthesis. The effects of the lack of starch accumulation on the fruit were evaluated. Fruit development was largely unaffected, although *adp* fruit showed an increased size and a slight delay in ripening. It was surprisingly shown that the starch deficiency correlated with a remarkable resistance of the fruit to blossom-end-rot (BER), an environmental stress-induced physiological disorder. To assess the broader implications of the starch deficiency, changes in the *adp* fruit transcriptome and metabolome were analyzed and molecular pathways affected by the altered sugar metabolism were identified. These results suggested that disabling starch biosynthesis caused an important transcriptional reprogramming and triggered metabolic shifts affecting central carbon metabolic pathways and lipid metabolism. The data also indicated that the molecular and metabolic changes in *adp* were potentially mediated by epigenetic regulators and the activation of sugar signaling, leading to enhanced growth and stress response pathways. These results provided insights into the role of carbohydrate metabolism in regulating fruit development and stress responses, with broad relevance for the development of strategies to enhance fruit stress tolerance.

BRIEF DESCRIPTION OF THE DRAWINGS

[0019] FIGs. 1A-1D show the characterization of the tomato mutant *adpressa* (*adp*). FIG. 1A is a photograph of wild type (WT) and *adp* six-week-old plants grown in greenhouse conditions showing the decumbent stems of *adp*. Scale bar = 10 cm. FIG. 1B is a photograph of root agravitropism of seedlings grown in agar plates. Scale bar = 1 cm. FIG. 1C is an illustration of map-based cloning of *adp*. The *adp* mutation mapped to an 86 kb region of chromosome 7 that contained 11 gene models including *Solanum lycopersicum APS1* (SEQ ID NO:1) shown with the single base pair deletion in red (SEQ ID NO:130). A protein diagram shows the characteristic motifs and domains labeled, the frame shift (white X) and the premature stop codon (asterisk). FIG. 1D is a photograph of Lugol staining of starch in wild type and *adp* vegetative tissues. Starch is revealed by dark purple-blue color in root (left), stem (middle) and leaves (right). Arrows show the starch granules as aggregated spots at the root tip, and at the innermost layer of the cortex in stems. Scale bars: root = 150 μ m; stem = 1 mm; leaves = 10 mm.

[0020] FIGs. 2A-2B show starch content in wild type and *adp* throughout fruit development. FIG. 2A is a photograph of Lugol staining of fruit cross sections revealing starch as a dark blue color. FIG. 2B is a graph of starch quantification in pericarp and placenta dissected from WT, *adp* and *APS1pro::APS1* (CL) fruit at four developmental stages (dpa (days post anthesis), MG (mature green)). Statistically significant differences were determined using Student's *t*-test: *** = p -value < 0.0001, n = 12. Scale bar = 10 mm.

[0021] FIGs. 3A-3F show phenotypic characteristics of WT, *adp* and CL fruit. FIG. 3A is a representative photograph of fruit, FIG. 3B is a graph of fruit weight and FIG. 3C is a graph of fruit volume of WT, *adp* and CL (dpa (days post anthesis), MG (mature green)). Statistically significant differences were determined using Student's *t*-test: * = p -value < 0.05, ** = p -value < 0.001, n = 70. FIG. 3D is a graph of time to the breaker stage in WT, *adp* and CL fruit. Statistically significant differences were determined using Student's *t*-test: * = p -value < 0.05, n = 50. FIG. 3E is a photograph of representative pictures showing BER symptoms (white arrow) in fruit grown under water stress. FIG. 3F is a graph showing BER incidence in WT, *adp* and CL fruit under control and water stress conditions. BER incidence was calculated as (number of tagged fruit with BER symptoms / total number of tagged fruit per plant) $\times$ 100. Data are means ($\pm$ SD) of three independent experiments (n > 150). Each experiment was performed using 5

plants per genotype and at least 10 fruit per plant. None of the *adp* fruit were affected by BER. Scale bar = 1 cm.

[0022] FIGs. 4A-4F are graphs, diagrams, and heat maps of transcriptome analysis of *adp* fruit. FIG. 4A is a graph of the number of differentially expressed genes (“DEGs”) in placenta and pericarp and FIG. 4B is a Venn diagram showing DEGs shared between 6 dpa, 20 dpa, mature green (MG) and ripe fruit. UP, upregulated; DOWN, downregulated. FIG. 4C is a heatmap showing the expression profiles of five DEGs shared between different fruit stages in placenta and pericarp. Columns from left to right on each arrow: 6 dpa, 20 dpa, MG, and ripe. FIGs. 4D and 4E are graphs of selected gene ontology (“GO”) terms enriched in up- and downregulated genes at different developmental stages. Columns from left to right on each arrow: 6 dpa, 20 dpa, MG, and ripe. Point size represents the number of DEGs (Count) in each GO term. All GO terms significantly enriched (adjusted $p < 0.05$) in each tissue and developmental stage are listed in Table 4. FIG. 4F is a heatmap showing examples of gene expression changes related to TOR signaling, cell cycle related pathways, DNA repair, and epigenetic and stress responses, in the placenta of *adp* fruit at 6 dpa, 20 dpa and MG stage.

[0023] FIG. 5 shows box plots of changes in levels of sugars and amino acids in *adp*, WT and CL placenta throughout fruit development. Box plots show the distribution dynamics of a subset of the metabolites identified by GC/MS with significant changes ($FDR < 0.05$) in both, *adp* vs. WT and *adp* vs. CL, comparisons. MG, mature green. Statistically significant differences were determined using Student’s *t*-test (* = p -value < 0.05). Data can be found in Table 6.

[0024] FIG. 6 is a heatmap of metabolomic analysis of the placenta of *adp*, WT and CL fruit at 20 dpa. The heatmap shows metabolites identified by untargeted LC-MS/MS with significant changes ($FDR < 0.05$) in both *adp* vs. WT and *adp* vs. CL pairwise comparisons. Only metabolites with best match score $> 80\%$ to an in-house spectral library and/or mzcloud references are shown. Data can be found in Table 7. Individual columns represent biological replicates of WT, CL and *adp*. Fold changes are indicated in blue (decreased level) and red (increased level).

[0025] FIGs. 7A-7C show lipid related gene expression and metabolite changes in *adp* fruit. FIG. 7A is a heatmap showing expression profiles of lipid related DEGs in placenta and pericarp at different developmental stages. Columns from left to right on each arrow for each genotype: 6 dpa, 20 dpa, MG, and ripe. FIG. 7B is a lipidomic analysis of the placenta of *adp*,

WT and CL fruit at 20 dpa. The heatmap shows lipids with significant changes (FDR < 0.05) in both, *adp* vs. WT and *adp* vs. CL comparisons. Data can be found in Table 8. Sample replicates are labeled 1-4. FIG. 7C shows photographs of lipid droplet accumulation in the septum of 20 dpa *adp* fruit, visualized by staining with BODIPY (green). Top: fluorescence only (505 nm excitation; 515 nm emission). Bottom: merged bright light and fluorescence images. Scale bar = 260 μ m.

[0026] FIG. 8 is an illustration of an overview of metabolic changes in the placenta of growing *adp* fruit compared to WT and CL. Metabolites with reduced levels, or genes downregulated in *adp* are shown in blue. Metabolites with increased levels, or genes upregulated in *adp* are shown in red. Metabolites not measured or without significant changes are shown in black. Red arrows show the pathway to lipid biosynthesis predicted to be enhanced in *adp*. ADCS, Aminodeoxychorismate synthase; DGK, Diacylglycerol kinase; ELO, Elongation of fatty acids protein; GAPDH, Glyceraldehyde-3-phosphate dehydrogenase; GPAT, Glycerol-3-phosphate acyltransferase; HMG, 3-Hydroxy-3-methylglutaryl; IPCS1, Phosphatidylinositol:ceramide inositolphosphotransferase; LACS, Long-chain acyl-CoA synthetase; LCB2, LONG-CHAIN BASE2 subunit of serine palmitoyltransferase; LKR, Lysine-ketoglutarate reductase; PA, Phosphatidic acid; PI, Phosphatidyl inositol; PIP, phosphatidylinositol-4-phosphate.

[0027] FIGs. 9A-9B show photographs of Lugol staining of WT, *adp*, and CL transgenic lines complemented with the *SIAPSI* genomic clone: leaves (FIG. 9A) and fruit (FIG. 9B). Scale bar = 10 mm.

[0028] FIG. 10 shows photographs of the development of BER symptoms during fruit growth. For each genotype the top panel shows a distal end view of the fruit and the bottom panel shows a distal cross-section. Scale bar = 1 cm.

[0029] FIGs. 11A-11B shows the global gene expression differences between *adp*, WT and CL fruit tissues. Principal component (FIG. 11A) and hierarchical clustering (FIG. 11B) analyses of gene expression in placenta and pericarp from 6 dpa, 20 dpa, mature green (MG) and ripe fruit are shown. Sample replicates are shown as identically colored circles (FIG. 11A) or identical font color (FIG. 11B).

[0030] FIG. 12 shows graphs of the expression of cell wall and ethylene-related genes in the pericarp of *adp*, WT and CL fruit at the MG stage. Expression data (RPKM) are the mean ($\pm$

SD) of three biological replicates. Statistically significant differences were determined using Student's *t*-test: ** = *p*-value < 0.001, *n* = 3. *ACS2*: Aminocyclopropane-1-carboxylate synthase (*ACC*) 2; *ACS4*: *ACC* synthase 4; *ACO6*: 1-aminocyclopropane-1-carboxylate oxidase 6; *ETR4*: ethylene receptor 4; *EXP1*: Expansin 1; *PM3*: Pectin methylesterase 3; *XTH5*: Xyloglucan endotransglucosylase-hydrolase 5; *PG*: Polygalacturonase.

[0031] FIG. 13 shows graphs of changes in levels of soluble sugars throughout fruit development in *adp*, WT and CL fruit. MG: mature green. Data are means ($\pm$ SD) of three independent experiments, with four biological replicates per experiment. Statistically significant differences were determined using Student's *t*-test: * = *p*-value < 0.05, ** = *p*-value < 0.001, *n* = 12.

[0032] FIGs. 14A-14C show graphs of clustering of the metabolite profiles of placenta (PI) and pericarp (Pe) from *adp*, WT and CL fruit at different developmental stages. Principal component (FIGs. 14A and 14B), and hierarchical clustering (FIG. 14C) analysis of metabolites identified by GC/MS. Sample replicates are shown as identically colored circles in (FIG. 14A) and (FIG. 14B) and labeled 1 to 4 in (FIG. 14C). MG, mature green. RR, ripe.

[0033] FIGs. 15A-15D show graphs of principal component analysis of metabolites of *adp*, WT and CL placenta tissue from 20 dpa fruit. Metabolites were identified by untargeted LC-MS/MS using: C18-NEG (FIG. 15A), C18-POS (FIG. 15B), HILIC-NEG (FIG. 15C) and HILIC-POS (FIG. 15D). Negative mode (NEG) and positive mode (POS). Sample replicates are shown as identically colored circles.

[0034] FIGs. 16A-16F show graphs of clustering of the lipidomic profiles of placenta and pericarp from *adp*, WT and CL fruit at different developmental stages. Principal component analysis (FIGs. 16A-16D) and hierarchical clustering analysis (FIGs. 16E-16F) of compounds identified using an untargeted LC/MS analysis with both negative (NEG) and positive (POS) modes. Sample replicates are shown as identically colored circles (FIGs. 16A-16D) or numbered 1 to 4 (FIGs. 16E-16F). MG, mature green. RR, ripe.

[0035] FIGs. 17A-17B show photographs of lipid droplet accumulation in *adp* fruit placenta at 20 dpa visualized by staining with BODIPY (green). In both (FIG. 17A) and (FIG. 17B) the left panels show fluorescence only (505 nm excitation; 515 nm emission) and the right panels show merged bright light and fluorescence images. (FIG. 17B) shows a higher

magnification of the area enclosed by a black rectangle in (FIG. 17A). Scale bar = 670 μ m in (FIG. 17A), 260 μ m in (FIG. 17B).

[0036] FIGs. 18A-18D show the characterization of the tomato *aps1* CRISPR mutant *aps1*-CR13 and phenotypic comparison with *aps1*-adp. (FIG. 18A) *APS1* gene structure indicating the position of the *aps1*-adp and *aps1*-CR13 mutations. Red dashed lines indicate base pair deletions. Change in amino acids are also shown in red. WT, wild type. (FIG. 18B) *APS1* protein diagram showing the characteristic motifs and domains labeled, the frame shift (white X) and the premature stop codon (asterisk) in the two *aps1* mutants (*aps1*-adp and *aps1*-CR13). (FIG. 18C) 6-week-old wild-type (WT) plants and *aps1* mutants grown in greenhouse conditions showing the decumbent stems of *aps1*-adp (Ailsa Craig, AC, background) and *aps1*-CR13 (M82 background). (FIG. 18D) Lugol staining of starch in wild-type and *aps1* mutant leaf tissues. Starch accumulation is revealed by dark purple–blue color.

[0037] FIG. 19A-19E shows expression levels of promoter of tomato genes *STM3* (Soly01g092950) (FIG. 1A), *SIMBP24* (Soly01g105800)(FIG. 19B), and β CA1 (Soly02g086820) (FIG. 19D). Also shown are construct maps of promoters of tomato gene *SIMBP24* (Soly01g105800)(FIG. 19C) and tomato gene β CA1 (Soly02g086820)(FIG. 19E) assembled with *APS1* into a pGWB401 backbone.

[0038] FIG. 20A-20C shows the expression levels of melon promoters MELO3C022515 (FIG. 20A), MELO3C007716 (FIG. 20B), and MELO3C009958 (FIG. 20C) in different plant tissues.

DETAILED DESCRIPTION

[0039] Embodiments of the disclosure relate to methods of imparting blossom end rot resistance, increasing size, and increasing antioxidant content of fruit, and compositions useful in imparting blossom end rot resistance, increasing size, and increasing antioxidant content of fruit are also provided.

[0040] Unless otherwise indicated, the definitions and embodiments described in this, and other sections are intended to be applicable to all embodiments and aspects of the present application herein described for which they are suitable as would be understood by a person skilled in the art.

[0041] Singular forms “a”, “an”, and “the” include plural references unless the context clearly dictates otherwise. Thus, for example, a reference to “a method” includes one or more methods, and/or steps of the type described herein and/or which will become apparent to those persons skilled in the art upon reading this disclosure. In another example, reference to “a compound” includes both a single compound and a plurality of different compounds.

[0042] The term “about” includes being within a statistically meaningful range of a value. Such a range can be within an order of magnitude, such as within 10% or within 5% of a given value or range.

[0043] The term “and/or” as used herein means that the listed items are present, or used, individually or in combination. In effect, this term means that “at least one of” or “one or more” of the listed items is used or present.

[0044] In understanding the scope of the present disclosure, the term “comprising” and its derivatives, as used herein, are intended to be open ended terms that specify the presence of the stated features, elements, components, groups, integers, and/or steps, but do not exclude the presence of other unstated features, elements, components, groups, integers and/or steps. The foregoing also applies to words having similar meanings such as the terms, “including”, “involving”, “having”, and their derivatives. The term “consisting” and its derivatives, as used herein, are intended to be closed terms that specify the presence of the stated features, elements, components, groups, integers, and/or steps, but exclude the presence of other unstated features, elements, components, groups, integers and/or steps.

[0045] A “nucleic acid”, “nucleotide”, or “polynucleotide” is a polymeric compound comprised of covalently linked subunits called nucleotides. Nucleic acids include polyribonucleic acid (“RNA”) and polydeoxyribonucleic acid (“DNA”), both of which may be single-stranded or double-stranded. DNA includes, but is not limited to, cDNA, genomic DNA, plasmid DNA, synthetic DNA, and semi-synthetic DNA. DNA may be linear, circular, or supercoiled.

[0046] A “gene” refers to an assembly of nucleotides that encode a functional RNA or a polypeptide and includes cDNA and genomic DNA nucleic acids. “Gene” also refers to a nucleic acid fragment that expresses a specific protein or polypeptide, optionally including regulatory sequences preceding (5’ noncoding sequences) and following (3’ noncoding sequences) the coding sequence. “Endogenous gene” refers to a native gene in its natural

location in the genome of an organism. A “foreign” gene, “heterologous” gene, or “exogenous” gene refers to a gene not normally found in the host organism, but that is introduced into the host organism by gene transfer. Heterologous genes can comprise native genes inserted into a non-native organism, or chimeric genes, such as a native gene under control of a different promoter than its endogenous promoter. A “transgene” is a gene that has been introduced into the genome by a transformation or transfection procedure. A “foreign” gene or “exogenous” gene refers to a gene not normally found in the host organism, but that is introduced into the host organism by gene transfer. Foreign genes can comprise native genes inserted into a nonnative location, or organisms, as well as chimeric genes.

[0047] A “coding region” is a portion of a nucleic acid, which is transcribed and translated into a polypeptide or protein.

[0048] A “polypeptide” is a naturally occurring or synthetic peptide, oligopeptide, polypeptide, gene product, expression product, or protein comprising an amino acid sequence, where the amino acids are joined to each other by peptide bonds or modified peptide bonds.

[0049] The term “fragment” when referring to a polynucleotide or polypeptide will be understood to mean a nucleotide or polypeptide sequence of reduced length relative to the reference nucleic acid or polypeptide sequence (*e.g.*, a wild type) and comprising, over the common portion, a nucleotide or polypeptide sequence identical to the reference sequence. Such a fragment according to the present disclosure may be, where appropriate, included in a larger polynucleotide or polypeptide of which it is a constituent. Such fragments comprise, or alternatively consist of, oligonucleotides or polypeptides ranging in length from at least 8, 10, 12, 15, 18, 20 to 25, 30, 40, 50, 70, 80, 100, 200, 500, 1000, 1500, or any number or range therein, consecutive nucleotides of a nucleic acid or amino acids of a polypeptide described herein.

[0050] A “reference sequence” means a nucleic acid or amino acid sequence used as a comparator for another nucleic acid or amino acid sequence, respectively, when determining sequence identity. A reference sequence can be a wildtype sequence or a sequence that has not been modified as described herein.

[0051] “Sequence identity,” “percent identity,” or “% identical” refers to the exactness of a match between a reference sequence and a sequence being compared to it when optimally aligned. For example, sequence alignments and percent identity calculations may be determined using a variety of comparison methods designed to detect homologous sequences including, but

not limited to, the Multalin program (Corpet, "Multiple Sequence Alignment with Hierarchical Clustering," *Nucleic Acids Res.* 16:10881-90 (1988), which is hereby incorporated by reference in its entirety) or the Megalign[®] program of the LASERGENE[®] bioinformatics computing suite (DNASTAR[®] Inc., Madison, Wis.). Sequences may also be aligned using algorithms known in the art including, but not limited to, CLUSTAL V algorithm or the BLASTN or BLAST 2 sequence programs.

[0052] As used herein, the term "plant cell" includes cells, protoplasts, cell tissue cultures from which plants can be regenerated, calli, clumps, and cells that are intact in plants or parts of plants (plant parts) including, but not limited to seeds, leaves, stems, roots, vegetative buds, floral buds, meristems, embryos, hypocotyls, cotyledons, endosperm, sepals, petals, pistils, carpels, stamens, anthers, microspores, pollen, pollen tubes, ovules, nucellar tissue, ovaries, and other plant tissue or cells. In some embodiments, the plant cell is a protoplast.

[0053] Preferences and options for a given aspect, feature, embodiment, or parameter of the disclosure should, unless the context indicates otherwise, be regarded as having been disclosed in combination with any and all preferences and options for all other aspects, features, embodiments, and parameters of the disclosure.

ADP-Glucose Pyrophosphorylase Genes, Proteins, and Subunits

[0054] One aspect of the present disclosure relates to a method for imparting blossom end rot resistance to fruit from a plant. The method comprises modifying a plant or a plant cell to reduce or eliminate the expression, stability, and/or activity of an ADP-glucose pyrophosphorylase (AGPase) protein, where the reduction or elimination of the expression, stability, and/or activity of AGPase protein is effective in reducing or eliminating starch synthesis and imparting blossom end rot resistance to fruit from the plant or a plant produced from the plant cell, as compared to fruit from a plant without the modification.

[0055] This aspect of the present disclosure can be carried out with any of the embodiments disclosed herein.

[0056] In some embodiments, methods of the present disclosure comprise modifying a plant or a plant cell to reduce or eliminate the expression, stability, and/or activity of an ADP-glucose pyrophosphorylase ("AGPase") protein. AGPase is enzyme that catalyzes the first committed step in starch synthesis. AGPase synthesizes ADP-glucose from Glucose-1 phosphate and ATP. AGPase typically functions as a heterotetramer of two AGPase small subunits ("APS")

and two AGPase large subunits (“APL”). Accordingly, some embodiments of the disclosure involve modifying a plant or a plant cell to reduce or eliminate the expression, stability, and/or activity of one or more APS subunits and/or one or more APL subunits as described *infra* relative to an unmodified, or wild-type APS subunit and/or APL subunit.

5 **[0057]** Starch content in various tissues in a plant can be detected by any means known in the art. For example, starch can be detected by staining with Lugol’s solution as shown in FIGs. 1D, FIG. 2A, and FIGs. 9A-B. Starch can also be quantified as shown in FIG. 2B by digestion with α -amylase and amyloglucosidase as described in Vargas-Ortiz et al., “Grain Amaranths are Defoliation Tolerant Crop Species Capable of Utilizing Stem and Root

10 Carbohydrate Reserves to Sustain Vegetative and Reproductive Growth After Leaf Loss,” *PLoS One* 8:e67879 (2013), which is hereby incorporated by reference in its entirety.

[0058] In some embodiments of the disclosure, the AGPase polypeptide or protein (or fragment or variant thereof) is an ADP-glucose pyrophosphorylase small subunit (APS) protein and/or an ADP-glucose pyrophosphorylase large subunit (APL) protein. Accordingly, the

15 polynucleotide or gene (or fragment or variant thereof) in some embodiments of the disclosure is an ADP-glucose pyrophosphorylase small subunit (APS) gene and/or an ADP-glucose pyrophosphorylase large subunit (APL) gene. In some embodiments, the AGPase gene comprises an ADP-glucose pyrophosphorylase small subunit (APS) coding sequence or an ADP-glucose pyrophosphorylase large subunit (APL) coding sequence.

20 **[0059]** A plant may comprise one or more than one endogenous APS and/or APL subunit gene(s). The expression of these various subunit genes may vary by level, tissue type, developmental timing, as well as in response to various environmental factors, as non-limiting examples. For example, tomato (*Solanum lycopersicum*) includes three APS subunit genes. Tomato APS1 is expressed in all tissue types, while tomato APS2 is only expressed in the first

25 roots, and APS3 is only expressed in the stamen. In some embodiments, the ADP-glucose pyrophosphorylase protein whose expression, stability, and/or activity is reduced or eliminated is the expression product of an APS or APL gene that is expressed in the leaves and/or developing fruit of the plant.

[0060] Endogenous ADP-glucose pyrophosphorylase small subunit (APS) and large

30 subunit (APL) genes, coding sequences, and amino acid sequences from various plant species are disclosed herein as SEQ ID NOs:1-129 (see Tables 1 and 13, *infra*). These endogenous (which

may also be referred to as unmodified, wild-type, target, or reference) sequences are used in various embodiments of the disclosure to generate modified ADP-glucose pyrophosphorylase small subunits and/or large subunits that reduce or eliminate the expression, stability, and/or activity of AGPase.

5 **[0061]** In some embodiments, the *APS* gene is an *APS1* gene from *Solanum lycopersicum* (*i.e.*, Solgenomics.net Accession No. Solyc07g056140, which is hereby incorporated by reference in its entirety). The genomic sequence (SEQ ID NO:1), coding sequence (SEQ ID NO:2), and amino acid sequence (SEQ ID NO:3) of *Solanum lycopersicum APS1* are provided in Table 13 *infra*. In some embodiments, the *APS* gene is an *APS2* gene from *Solanum*
10 *lycopersicum* (*i.e.*, Solgenomics.net Accession No. Solyc08g015670, which is hereby incorporated by reference in its entirety). The genomic sequence (SEQ ID NO:4), coding sequence (SEQ ID NO:5), and amino acid sequence (SEQ ID NO:6) of *Solanum lycopersicum APS2* are provided in Table 13 *infra*. In some embodiments, the *APS* gene is an *APS3* gene from *Solanum lycopersicum* (*i.e.*, Solgenomics.net Accession No. Solyc12g011120, which is hereby
15 incorporated by reference in its entirety). The genomic sequence (SEQ ID NO:7), coding sequence (SEQ ID NO:8), and amino acid sequence (SEQ ID NO:9) of *Solanum lycopersicum APS3* are provided in Table 13 *infra*.

[0062] Additional exemplary endogenous *APS* sequences from *Solanum melogena*, *Capsicum annuum*, *Cucumis sativus*, *Cucurbita maxima*, *Cucurbita pepo*, *Cucumis melo*,
20 *Cucurbita moschata*, and *Citrullus lanatus* are described in Tables 1 and 13 *infra* and are intended to illustrate the various types of AGPase *APS* sequences that are useful in embodiments of the present disclosure.

[0063] Accordingly, in some embodiments, the *APS* gene encoding an AGPase protein of
embodiments of the present disclosure comprises the nucleotide sequence encoding the amino
25 acid sequence of any one of SEQ ID NOs:3, 6, 9, 21, 24, 36, 39, 42, 54, 66, 69, 81, 93, 105, 117, and 120, or having at least 90% sequence identity to the amino acid sequence of any one of SEQ ID NOs:3, 6, 9, 21, 24, 36, 39, 42, 54, 66, 69, 81, 93, 105, 117, and 120. Due to genetic variation that can occur between various species and/or varieties of the plants described herein, the *APS* gene encoding an AGPase protein may comprise at least 75%, 76%, 77%, 78%, 79%, 80%, 81%,
30 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%,

98%, or 99% sequence identity to the genomic, coding, or amino acid sequence of any one of SEQ ID NOs:1-9, 19-24, 34-42, 52-54, 64-69, 79-81, 91-93, 103-105, and 115-120.

[0064] In some embodiments, the *APL* gene is an *APL1* gene from *Solanum lycopersicum* (i.e., Solgenomics.net Accession No. Solyc01g079790, which is hereby

5 incorporated by reference in its entirety). The genomic sequence (SEQ ID NO:10), coding sequence (SEQ ID NO:11), and amino acid sequence (SEQ ID NO:12) of *Solanum lycopersicum APL1* are provided in Table 13 *infra*. In some embodiments, the *APL* gene is an *APL2* gene from *Solanum lycopersicum* (i.e., Solgenomics.net Accession No. Solyc07g019440, which is hereby incorporated by reference in its entirety). The genomic sequence (SEQ ID NO:13), coding
10 sequence (SEQ ID NO:14), and amino acid sequence (SEQ ID NO:15) of *Solanum lycopersicum APL2* are provided in Table 13 *infra*. In some embodiments, the *APL* gene is an *APL3* gene from *Solanum lycopersicum* (i.e., Solgenomics.net Accession No. Solyc01g109790, which is hereby incorporated by reference in its entirety). The genomic sequence (SEQ ID NO:16), coding
15 sequence (SEQ ID NO:17), and amino acid sequence (SEQ ID NO:18) of *Solanum lycopersicum APL3* are provided in Table 13 *infra*.

[0065] Additional exemplary endogenous *APL* sequences from *Solanum melogena*, *Capsicum annuum*, *Cucumis sativus*, *Cucurbita maxima*, *Cucurbita pepo*, *Cucumis melo*, *Cucurbita moschata*, and *Citrullus lanatus* are described in Tables 1 and 13 *infra* and are intended to illustrate the various types of AGPase *APL* sequences that are useful in the
20 embodiments of the present disclosure.

[0066] In some embodiments, the *APL* gene comprises the nucleotide sequence encoding the protein sequence of any one of SEQ ID NOs:12, 15, 18, 27, 30, 33, 45, 48, 51, 57, 60, 63, 72, 75, 78, 84, 87, 90, 96, 99, 102, 108, 111, 114, 123, 126, and 129 or having at least 90% sequence identity to the amino acid sequence of any one of SEQ ID NOs:12, 15, 18, 27, 30, 33, 45, 48, 51,
25 57, 60, 63, 72, 75, 78, 84, 87, 90, 96, 99, 102, 108, 111, 114, 123, 126, and 129. Due to genetic variation that can occur between various species and/or varieties of the plants described herein, the *APL* gene encoding an AGPase protein may comprise at least 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the genomic, coding, or amino acid sequence of
30 any one of SEQ ID Nos:10-18, 25-33, 43-51, 55-63, 70-78, 82-90, 94-102, 106-114, and 121-129.

Table 1. Exemplary Endogenous AGPase Sequences

Crop	AGPase Subunits	SEQ ID NOs:
Tomato (<i>Solanum lycopersicum</i>)	APS1, APS2, APS3	1-3, 4-6, 7-9
	APL1, APL2, APL3	10-12, 13-15, 16-18
Eggplant (<i>Solanum melongena</i>)	APS1, APS2	19-21, 22-24
	APL1, APL2, APL3	25-27, 28-30, 31-33
Pepper (<i>Capsicum annuum</i>)	APS1, APS2, APS3	34-36, 37-39, 40-42
	APL1, APL2, APL3	43-45, 46-48, 49-51
Cucumber (<i>Cucumis sativus</i>)	APS1	52-54
	APL1, APL2, APL3	55-57, 58-60, 61-63
Squash (<i>Cucurbita maxima</i>)	APS1, APS3	64-66, 67-69
	APL1, APL2, APL3	70-72, 73-75, 76-78
Zucchini (<i>Cucurbita pepo</i>)	APS1	79-81
	APL1, APL2, APL3	82-84, 85-87, 88-90
Melon (<i>Cucumis melo</i>)	APS1	91-93
	APL1, APL2, APL3	94-96, 97-99, 100-102
Watermelon (<i>Citrullus lanatus</i>)	APS1	103-105
	APL1, APL2, APL3	106-108, 109-111, 112-114
Pumpkin (<i>Cucurbita moschata</i>)	APS1, APS3	115-117, 118-120
	APL1, APL2, APL3	121-123, 124-126, 127-129

5 **Modifications of AGPase: Mutagenesis & Genome Editing**

[0067] In some embodiments of the disclosure, modifying a plant or plant cell to reduce or eliminate the expression, stability, and/or activity of an ADP-glucose pyrophosphorylase (AGPase) protein comprises: (i) introducing a mutation into a coding sequence and/or a regulatory sequence of an AGPase gene encoding the AGPase protein; or (ii) introducing into the plant or plant cell an inhibitory polynucleotide targeting the AGPase gene encoding the AGPase protein. As used herein, a “regulatory sequence” is a sequence that regulates the expression and/or activity of a gene or protein.

[0068] In some embodiments of the disclosure, the expression stability, and/or activity of an AGPase can be reduced or eliminated by mutating one or more *APS* and/or *APL* genes. In some embodiments, the one or more *APS* and/or *APL* genes in a plant or plant cell has a mutation that inhibits normal expression, stability, and/or activity of the gene or the protein encoded by the gene.

[0069] The terms “mutation” or “genome edit” mean a human-induced change in the genetic sequence compared to a wild type or reference sequence (*i.e.*, a sequence that exists in nature). In some embodiments, mutations are those that cause the gene coding sequence or a promoter to not be expressed or to have a reduced level of mRNA expression, or those that reduce the activity, expression, or stability of the encoded protein. In some embodiments, the methods of the present disclosure comprise introducing the mutation by mutagenesis or genome editing. The terms “modify”, “modifying,” and the like used herein encompass modifying by, *e.g.*, mutation or genome editing.

[0070] A mutation may be, without limitation, a “substitution mutation”, which is a change in the nucleic acid sequence that results in the substitution of an amino acid for another amino acid; a “nonsense mutation” or “stop codon mutation”, which is a change in the nucleic acid sequence that results in the introduction of a premature stop codon and thus the termination of translation (resulting in a truncated protein); an “insertion mutation” of one or more amino acids, due to one or more codons having been added in the coding sequence of the nucleic acid; a “deletion mutation” of one or more amino acids, due to one or more codons having been deleted in the coding sequence of the nucleic acid; and a “frameshift mutation”, resulting in the nucleic acid sequence being translated in a different frame downstream of the mutation, or any combination of mutation types. A frameshift mutation can have various causes, such as the insertion, deletion, substitution, and/or duplication of one or more nucleotides. Mutations that affect pre-mRNA splicing (splice junction mutations) can also result in frameshifts. A “splice junction mutation”, which alters or abolishes the correct splicing of the pre-mRNA sequence, resulting in a protein of different amino acid sequence than the wild type. For example, one or more exons may be skipped during RNA splicing, resulting in a protein lacking the amino acids encoded by the skipped exons. Alternatively, the reading frame may be altered through incorrect splicing, or one or more introns may be retained, or alternate splice donors or acceptors may be generated, or splicing may be initiated at an alternate position (*e.g.*, within an intron), or alternate

polyadenylation signals may be generated. Accordingly, in some embodiments, the mutation is an insertion, a deletion, a substitution mutation, or any combination thereof. In some embodiments, the mutation is a “knock-out” mutation.

[0071] As used herein, a “knock-out” mutation is a mutant allele having no functional AGPase expression, *i.e.*, the mutant allele produces no AGPase protein having the ability to synthesize ADP-glucose from Glucose-1 phosphate and ATP, in a plant cell *in vivo*. Knock-out mutant AGPase alleles include, for instance, insertion and/or deletion mutations that disrupt the coding region, delete a portion or the entire coding region, and frameshift or stop-codon mutations that lead to a substantial or entire deletion of the protein. For example, a knock-out *APS* allele may comprise a mutation that disrupts or deletes the regulatory sequence containing the allosteric activator, glycerate 3-phosphate, binding site (*e.g.*, *see* FIG. 1C). Any stop codon, frame shift, or splice site mutation that leads to a C-terminal truncation of the *APS* protein that includes the allosteric activator, glycerate 3-phosphate, binding site will result in a full knock-out *APS* allele.

[0072] An exemplary mutation in *Solanum lycopersicum APS1* causing a reduction or elimination of the expression, stability, and/or activity of AGPase protein, which is effective in reducing or eliminating starch synthesis and imparting blossom end rot resistance to fruit, comprises a deletion of the T residue at nucleotide position 1,321 of SEQ ID NO:2 resulting in a frameshift mutation (1321delT; FIG. 1C). The nucleotide sequence of the *Solanum lycopersicum APS1* mutation 1321delT is provided as SEQ ID NO:130, as follows:
GCAGATACTACGAGACTGAT (SEQ ID NO:130).

[0073] In some embodiments, the *APS* gene is an *APS1* gene comprising a deletion mutation corresponding to the deletion mutation of SEQ ID NO:130, resulting in a frameshift mutation.

[0074] Other exemplary knock-out mutations include substitution mutations, insertions, and/or deletions in the nucleotide sequence encoding the allosteric activator, glycerate 3-phosphate, binding site itself, *i.e.*, nucleotides 1512-1563 of SEQ ID NO:2 (corresponding to amino acid positions 504-521 of SEQ ID NO:3), and in similar allosteric binding site regions of other *APS* genes described herein (*see* Table 13). Other regulatory regions of *APS1* include the ATP binding site at nucleotides 558-582 of SEQ ID NO:2 (corresponding to amino acid positions 186-194 of SEQ ID NO:3), the catalytic site at nucleotides 638-666 of SEQ ID NO:2

(corresponding to amino acid positions 213-222 of SEQ ID NO:3), and the glucose-1 phosphate binding site starting at nucleotides 789-1062 of SEQ ID NO:2 (corresponding to amino acid positions 263-354 of SEQ ID NO:3), and similar sequences of regulatory regions in *APS* genes described herein (*see, e.g.*, Table 13). Exemplary knock-out mutations of *APLI* include

substitution mutations, insertions, or deletions in the nucleotide sequence encoding the allosteric activator, glycerate 3-phosphate, binding site itself, *i.e.*, nucleotides 1494-1545 of SEQ ID NO:11 (corresponding to amino acid positions 498-515 of SEQ ID NO:12), and in similar allosteric binding site regions of other *APL* genes described herein (*see, e.g.*, Table 13). Other regulatory regions of *APLI* include the ATP binding site at nucleotides 537-561 of SEQ ID NO:11 (corresponding to amino acid positions 179-187 of SEQ ID NO:12), the catalytic site at nucleotides 627-653 of SEQ ID NO:11 (corresponding to amino acid positions 209-218 of SEQ ID NO:12), and the glucose-1 phosphate binding site starting at nucleotides 777-801 of SEQ ID NO:11 (corresponding to amino acid positions 259-267 of SEQ ID NO:12), and in similar sequences of regulatory regions in *APL* genes described herein (*see, e.g.*, Table 13).

[0075] In some embodiments, a mutation may be introduced by mutagenesis such as by treatment with a mutagenic agent. Any suitable mutagenic agent can be used for embodiments of the present disclosure. For example, mutagens creating point mutations, deletions, insertions, rearrangements, transversions, transitions, or any combination thereof may be used. Suitable radiation mutagens include, without limitation, ultraviolet light, x-rays, gamma rays, and fast neutrons. Suitable chemical mutagens include, but are not limited to, ethyl methanesulfonate (EMS), methylmethane sulfonate (MMS), N-ethyl-N-nitrosourea (ENU), triethylmelamine (TEM), N-methyl-N-nitrosourea (MNU), procarbazine, chlorambucil, cyclophosphamide, diethyl sulfate, acrylamide monomer, melphalan, nitrogen mustard, vincristine, dimethylnitrosamine, N-methyl-N'-nitro-nitrosoguanidine 25 (MNNG), nitrosoguanidine, 2-aminopurine, 7, 12 dimethyl-benz(a)anthracene (DMBA), ethylene oxide, hexamethylphosphoramide, bisulfan, diepoxyalkanes (diepoxyoctane (DEO), diepoxybutane (DEB), 2-methoxy-6-chloro-9[3-(ethyl-2-chloro-ethyl) aminopropylamino] acridine dihydrochloride (ICR-170), sodium azide, formaldehyde, or combinations thereof.

[0076] In some embodiments, a mutation may be introduced by genome editing. Genome editing is a type of genetic engineering in which DNA is inserted, replaced, or removed, or any combination thereof, from a genome using artificially engineered nucleases or “molecular

scissors.” The nucleases typically create double-stranded breaks (“DSBs”) at desired locations in the genome and harness the cell’s endogenous mechanisms to repair the induced break by processes of homology dependent repair (“HDR”) or nonhomologous end-joining (“NHEJ”).

Four main families of engineered nucleases include: Zinc finger nucleases (“ZFNs”),

- 5 Transcription Activator-Like Effector Nucleases (“TALENs”), the Clustered Regularly Interspaced Short Palindromic Repeats (“CRISPR”) system, and engineered meganuclease with re-engineered homing endonucleases. Any method of genome editing may be used in the embodiments of the present application.

[0077] Use of systems for gene editing has been widely described. For example, the use
 10 of CRISPR guide RNA in conjunction with CRISPR/Cas technology to target RNA is described in Wiedenheft et al., “RNA-Guided Genetic Silencing Systems in Bacteria and Archaea,” *Nature* 482:331-338 (2012); Zhang et al., “Multiplex Genome Engineering Using CRISPR/Cas Systems,” *Science* 339:819-23 (2013); and Gaj et al., “ZFN, TALEN, and CRISPR/Cas-based Methods for Genome Engineering,” *Cell* 31:397-405 (2013), which are hereby incorporated by
 15 reference in their entirety.

[0078] CRISPR/Cas type RNA-guided endonucleases provide an efficient system for inducing genetic modifications in genomes of many organisms and can be used in the methods described herein to introduce one or more genetic modifications in a plant genome. Non-limiting examples of genome editing nucleases include Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas6,
 20 Cas7, Cas8, Cas9 (also known as Csn1 and Csx12), Cas10, Csy1, Csy2, Csy3, Cse1, Cse2, Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, Cpf1, CasX, CasY, Mad7, or homologs, modified versions, and endonuclease inactive versions thereof. An example of a fusion protein to Cas9 is a cytidine deaminase–Cas9 fusion protein
 25 used in cytidine base editing to mutate nucleotides in target genes without generating double-strand breaks as described in Komor et al., “Programmable Editing of a Target Base in Genomic DNA without Double-Stranded DNA Cleavage,” *Nature* 533:420-424 (2016), which is hereby incorporated by reference in its entirety.

[0079] There are two distinct components to a CRISPR/Cas system, a guide RNA and an
 30 endonuclease, such as Cas9. The guide RNA is a combination of the endogenous bacterial CRISPR RNA (“crRNA”) and trans-activating crRNA (“tracrRNA”) into a single chimeric guide

RNA (“gRNA”) transcript. The gRNA combines the targeting specificity of the crRNA with the scaffolding properties of the tracrRNA into a single transcript. When the gRNA and Cas9 are expressed in the cell, the genomic target sequence can be modified or permanently disrupted. The gRNA/Cas9 complex is recruited to the target sequence by the base-pairing between the gRNA sequence which has a region of the complementarity to the target sequence in the genomic DNA. For successful binding of Cas9, the genomic target sequence must also contain the correct Protospacer Adjacent Motif (“PAM”) sequence immediately following the target sequence. The binding of the gRNA/Cas9 complex localizes the Cas9 to the genomic target sequence so that the wild type Cas9 can cut both strands of DNA causing a DSB. Cas9 generates DSBs through the combined activity of two nuclease domains, RuvC and HNH. Cas9 will cut 3-4 nucleotides upstream of the PAM sequence. A DSB can be repaired through one of two general repair pathways: (1) NHEJ DNA repair pathway or (2) the HDR pathway. The NHEJ repair pathway often results in insertions/deletions (InDels) at the DSB site that can lead to frameshifts and/or premature stop codons, effectively disrupting the open reading frame (ORF) of the targeted gene. The HDR pathway requires the presence of a repair template, which is used to fix the DSB. HDR faithfully copies the sequence of the repair template to the cut target sequence. Specific nucleotide changes can be introduced into a targeted gene by the use of HDR with a repair template. CRISPR specificity can be controlled by level of homology and binding strength of the specific gRNA for a given gene target, or by modification of the Cas endonuclease itself. For example, a D10A mutant of the RuvC domain, retains only the HNH domain and generates a DNA nick rather than a DSB.

[0080] When the guide RNA and the gene editing endonuclease are expressed in the cell, the genomic target sequence can be modified and/or permanently disrupted. The guide RNA/gene editing endonuclease complex is recruited to the target sequence by the base-pairing between the guide RNA sequence and the complementary sequence of the target sequence in the genomic DNA.

[0081] In some embodiments, CRISPR gene editing is used to generate an AGPase gene mutation by causing nucleotide insertions or deletions (indels) at the DSB site. In some embodiments, a point mutation, insertions, deletions, or any combination thereof, can be generated in an AGPase gene. In yet other embodiments, one or more AGPase gene targets (such as one or more *APS* genes, one or more *APL* genes, or combinations of one or more *APS* and

APL genes) can be modified using CRISPR gene editing in a single experiment using single or multiple guide RNAs having specificity for the different gene targets. In some embodiments, two AGPase gene targets are mutated. In other embodiments, more than two AGPase genes are mutated. Thus, a wide range of genetic modifications using the described methods and CRISPR gene editing can be attained.

[0082] In some embodiments, one or more mutations reduce AGPase gene expression by 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% (*i.e.*, no expression product is produced by the cell), or any number or range therein, as compared to the amount of AGPase gene expression in a control. In some embodiments, one or more mutations reduce *APS* gene expression by 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% (*i.e.*, no expression product is produced by the cell), or any number or range therein, as compared to the amount of *APS* gene expression in a control. In further embodiments, one or more mutations reduce *APL* gene expression by 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% (*i.e.*, no expression product is produced by the cell), or any number or range therein, as compared to the amount of *APL* gene expression in a control.

[0083] In some embodiments, one or more mutations reduce the amount of functional AGPase protein by at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% (*i.e.*, no functional AGPase protein having the ability to synthesize ADP-glucose from Glucose-1 phosphate and ATP is produced by the cell), or any number or range therein, as compared to the amount of the functional AGPase protein produced by the cell not comprising the mutant AGPase allele. Also encompassed is (i) the production of a “non-functional” AGPase protein (*e.g.*, a truncated AGPase protein) having no detectable biological activity *in vivo*; (ii) the reduction in the absolute amount of the functional AGPase protein (*e.g.*, reduced amount of AGPase protein being made due to the mutation in the AGPase gene); or (iii) the production of an AGPase protein with significantly reduced detectable biological activity (such as an AGPase protein in which one or more regulatory amino acid residues that are crucial for the biological activity of the encoded AGPase protein, are substituted or deleted), each as compared to the activity of a functional wild type (or unmodified) AGPase protein. In some embodiments, one or more mutations reduce the

amount of functional APS protein by at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% (*i.e.*, no functional protein is produced by the cell) or any number or range therein, as compared to the amount of the functional APS protein produced by the cell not comprising the mutant APS allele.

- 5 In some embodiments, one or more mutations reduce the amount of functional APL protein by at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% (*i.e.*, no functional protein is produced by the cell) or any number or range therein as compared to the amount of the functional APL protein produced by the cell not comprising the mutant APL allele.

10 ***Inhibitory Polynucleotides***

- [0084] In some embodiments, the methods of the present disclosure further comprise introducing into the plant or plant cell an inhibitory polynucleotide targeting the AGPase gene encoding the AGPase protein. A plant or plant cell of this and other aspects of the present disclosure may comprise an inhibitory polynucleotide targeting one or more AGPase genes to
15 reduce their expression. Methods for reducing gene expression involving the expression of “inhibitory polynucleotide” sequences in plants are known in the art, and include, but are not limited to, cosuppression, antisense suppression, double-stranded RNA (dsRNA) interference, hairpin RNA (hpRNA) interference, intron-containing hairpin RNA (ihpRNA) interference, transcriptional gene silencing, and micro RNA (miRNA) interference, as non-limiting examples.

- 20 [0085] For example, an inhibitory polynucleotide may be an antisense polynucleotide or an RNA inhibitor (RNAi) polynucleotide capable of down-regulating gene expression of one or more *APS* and/or *APL* subunits of AGPase.

- [0086] RNA interference (RNAi) occurs when an organism recognizes double-stranded RNA molecules and hydrolyzes them. The resulting hydrolysis products are small RNA
25 fragments of 19-24 nucleotides in length, called small interfering RNAs (siRNAs) or microRNAs (miRNAs). The siRNAs then hybridize to mRNAs (or other RNAs) and cause hydrolysis of the RNA. Most plant miRNAs show extensive base pairing to, and guide cleavage of their target mRNAs.

- [0087] The RNAi pathway can be exploited in plants by using recombinant technology,
30 which entails transforming a plant with a vector comprising DNA that when expressed produces a dsRNA homologous or nearly homologous to a gene target. The gene target can be

homologous to an endogenous plant RNA. RNA interference in plants can also be referred to as post-transcriptional gene silencing or RNA silencing and can be triggered by expression of an antisense strand of a target sequence of interest. In general, a plant is transformed with DNA that is incorporated into the plant genome, and when expressed produces a dsRNA that is

5 complementary to a gene of interest, which can be an endogenous plant gene (*e.g.*, AGPase), leading to the reduction or elimination of expression of that gene.

[0088] In some embodiments, the inhibitory polynucleotide is an RNAi polynucleotide comprising a sense polynucleotide strand comprising at least 20 contiguous nucleotides from an AGPase gene sequence, and an antisense polynucleotide strand that hybridizes to the sense

10 polynucleotide strand, where the sense and the antisense polynucleotide strand form a duplex. In some embodiments, the RNAi polynucleotide comprises a sense polynucleotide strand comprising at least 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400 or more than 400 contiguous nucleotides from an AGPase sequence, and an antisense polynucleotide strand that hybridizes to the sense polynucleotide strand, wherein the sense and the antisense polynucleotide

15 strand form a duplex. In some embodiments, the RNAi polynucleotide comprises a sense polynucleotide strand 20-400 contiguous nucleotides from an AGPase sequence, and an antisense polynucleotide strand that hybridizes to the sense polynucleotide strand, wherein the sense and the antisense polynucleotide strand form a duplex.

[0089] RNAi constructs may also include a polynucleotide sequence that separates the

20 sense and antisense strands to facilitate duplex formation. In some embodiments, the RNAi polynucleotide further comprises a polynucleotide sequence heterologous to the sense and antisense polynucleotides. In some embodiments, the RNAi polynucleotide comprises an intron.

[0090] In some embodiments, the inhibitory polynucleotide comprises an antisense polynucleotide. In some embodiments, the inhibitory polynucleotide comprises an antisense

25 polynucleotide of an *AGPase* coding sequence of at least 20 base pairs (bp), 25 bp, 30 bp, 35bp, 40 bp, 45 bp, 50 bp, 55 bp, 60 bp, 65 bp, 70 bp, 75 bp, 80 bp, 85 bp, 90 bp, 95 bp, 100 bp, 125 bp, 150 bp, 175 bp, 200 bp, 300 bp, 400 bp, 500 bp, 600 bp, 700 bp, 800 bp, 900 bp, or greater than 1000 bp, or any number of base pairs or range of base pairs between 20 bp and 1000 bp.

[0091] In some embodiments, the inhibitory polynucleotide reduces AGPase gene

30 expression by 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% (*i.e.*, no expression product is produced

by the cell), or any amount or range therein, as compared to the amount of AGPase gene expression in a control. In some embodiments, the inhibitory polynucleotide reduces *APS* gene expression by 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 100% (*i.e.*, no expression product is produced by the cell), or any number or range therein, as compared to the amount of *APS* gene expression in a control. In further embodiments, the inhibitory polynucleotide reduces *APL* gene expression by 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% (*i.e.*, no expression is produced by the cell), or any number or range therein, as compared to the amount of *APL* gene expression in a control.

[0092] In some embodiments, the inhibitory polynucleotide reduces the amount of functional AGPase protein by at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% (*i.e.*, no functional protein is produced by the cell) as compared to the amount of the functional AGPase protein produced by the cell not comprising the inhibitory polynucleotide. In some embodiments, the inhibitory polynucleotide reduces the amount of functional APS protein by at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% (*i.e.*, no functional protein is produced by the cell), or any number or range therein, as compared to the amount of the functional APS protein produced by the cell not comprising the mutant *APS* allele. In some embodiments, the inhibitory polynucleotide reduces the amount of functional APL protein by at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% (*i.e.*, no functional protein is produced by the cell) or any number or range therein, as compared to the amount of the functional APL protein produced by the cell not comprising the mutant *APL* allele.

Plant Cells, Plants, & Fruits

[0093] In some embodiments, a plant comprises the plant cell of any of the embodiments of the present disclosure. Also provided is the fruit of a plant of any of the embodiments disclosed herein.

[0094] In some embodiments, the fruit, plant, or plant cell is from the Solanaceae family.

In some embodiments, the fruit, plant, or plant cell is tomato (*Solanum lycopersicum*).

[0095] As used herein, a “fruit” is the mature ovary of a flowering plant that is typically edible. In some embodiments, the fruit is a tomato fruit.

[0096] In some embodiments, the type of a tomato fruit is a cherry, bell, blocky, currant, deep round oval or roma, elongated, flattened globe, grape, hybrid, heirloom, long blocky, long pointed, oxheart, pear, beefsteak, round, small pear, small pointed, stuffer, tomatillo, processing, or plum shape.

[0097] In some embodiments, a tomato fruit has a skin colour dark, bi-color, deep pink, golden, green, orange, pink, red, white, or yellow color.

[0098] In some embodiments, the tomato plant is indeterminate, determinate, or dwarf. In some embodiments the tomato plant is an open-pollinated or hybrid plant.

[0099] In some embodiments, the tomato cultivar is, without limitation, Alicante, Amish Paste, Aunt Ruby's German Green, Azoychka, Beefsteak, Berkeley Tie-Dye Green, Better Boy, Big Beef, Big Mama, Big Rainbow, Blaby Special, Black Beauty, Black Cherry, Black Icicle, Black Krim, Brandywine, Breonice, Campari, Canario, Carbon, Celebrity, Cherokee Purple, Cherry Bambelo, Cherry Nebula, Chocolate Pear, Dad's Sunset, Dester, Dr. Wyche's Yellow, Early Girl, Ed's Millennium, Emerald Evergreen, Enchantment, Ferreira, Ferris Wheel, Flamenco, Fourth of July, Garden Peach, Gardener's Delight, German Johnson, German Lunchbox, German Pink, Giulietta F1, Granadero, Great White, Green Doctors, Green Giant, Green Zebra, Hanover tomato, Henderson's Pink Ponderosa, Heinz, Hillbilly, Hungarian Heart, Japanese Black Trifele, Jersey Boy, Jubilee, Juliet, Kellogg's Breakfast, Kentucky Beefsteak, Kumato, Lillian's Yellow, Malakhitovaya Shkatulka, Matt's Wild Cherry, McDreamy, Micro Tom, Millionaire, Moneymaker, Monterosa, Montserrat, Mortgage Lifter, Mr. Stripey, Mushroom Basket, M82, Napa Rose Blush, Orange Hat, Orange Icicle, Pantano Romanesco, Paul Robeson, Pink Boar, Plum tomato, Raf tomato, Raspberry Lyanna, Rebekah Allen, Rebellion, Red Currant, Roma, Rosa de Barbastro, Rosella, Rutgers, San Marzano, Santorini, Sasha Altai, Scorpio (Skorpion), Stupice, Super Sweet 100, Thorburn's Terra-cotta, Tigerella, Tiny Tim, Tomaccio, Tomkin, Traveller / Arkansas Traveler, True Black Brandywine, Violet Jasper (Tzi Bi U), Viva Italia, Wagner Blue Green, White Queen, Yellow Brandywine, Yellow Pear, or hybrid thereof. In some embodiments, the tomato cultivar is not Condine Red or Ailsa Craig.

[0100] In some embodiments, the fruit, plant, or plant cell is from the Solanaceae family. In some embodiments, the fruit, plant, or plant cell is from the Cucurbitaceae family. In some embodiments, the fruit, plant, or plant cell is from the Solanaceae or Cucurbitaceae family. In some embodiments, the fruit, plant, or plant cell is from the genus *Solanum*, *Capsicum*, *Cucurbita*, *Cucumis*, or *Citrullus*. In some embodiments, the fruit, plant, or plant cell is from the genus *Solanum*. In some embodiments, the fruit, plant, or plant cell is from the genus *Capsicum*, *Cucurbita*, *Cucumis*, or *Citrullus*. In some embodiments, the fruit or plant is, or the plant cell is from, a tomato, eggplant, pepper, squash, zucchini, cucumber, or melon. In some embodiments, the fruit or plant is (or plant cell is from) an eggplant, pepper, zucchini, cucumber, watermelon, pumpkin, squash, or melon. Exemplary melons include, without limitation, calabash, bitter melon, banana melon, crane melon, cantaloupe, Charentais melon, honeydew, winter melon, canary melon, and muskmelon. Exemplary squashes include, without limitation, butternut, crookneck, acorn, banana, butternut, carnival, delicata, and spaghetti.

Blossom End Rot, Fruit Size, & Antioxidants

[0101] Blossom end rot can occur in response to environmental stress such as drought, or due to other factors, such as nutritional stress. In some embodiments, the fruit of the modified plants of the present disclosure has reduced levels of blossom end rot as compared to fruit from a plant without the modification. A plant without the modification as described herein may be, *e.g.*, a wildtype plant. In some embodiments, blossom end rot is reduced in the fruit by 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% (i.e., no blossom end rot), or any number or range therein, as compared to the amount of blossom end rot in fruit from a plant without the modification. In some embodiments, the fruit has reduced or no blossom end rot under normal growth or water stress conditions as compared to fruit from a plant without the modification. As used herein, “water stress conditions” are conditions in which the plant is grown in a pot with a volumetric water content (“VWC”) of less than 40-50% VWC or in a field or garden with 10-95% less water than is typically provided to a crop. In some embodiments, the water stress conditions comprise irregular watering. In some embodiments, the water stress conditions comprise pot VWC of 35%, 30%, 25%, 20%, 15%, 10%, 5%, or any number or range of VWC therein. In some embodiments, water stress conditions occur during fruit development. In some embodiments, water stress conditions occur in the period from 0 dpa (days post anthesis) to 30 dpa.

[0102] In some embodiments, the plant of the present disclosure is grown indoors. In some embodiments, the plant is grown hydroponically or aeroponically. In some embodiments, the plant is grown outdoors (*e.g.*, in a field or a garden).

[0103] Another aspect of the present disclosure relates to a method of increasing size of fruit from a plant. The method comprises modifying a plant or a plant cell to reduce or eliminate the expression, stability, and/or activity of an ADP-glucose pyrophosphorylase (AGPase) protein, where the reduction or elimination of the expression, stability, and/or activity of AGPase protein is effective in reducing or eliminating starch synthesis and increasing fruit size in fruit from the plant or a plant produced from the plant cell, as compared to fruit from a plant without the modification.

[0104] This aspect of the present disclosure can be carried out with any of the embodiments disclosed herein.

[0105] In some embodiments, the fruit of the modified plants of the present disclosure has increased fruit size as compared to fruit from a plant without the modification. In some embodiments, increased fruit size comprises an increase in fruit weight. In some embodiments, the fruit of the modified plants has an increase in fruit weight of at least 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, or any number or range therein, as compared to fruit from a plant without the modification. In some embodiments, the increased fruit size comprises an increase in fruit weight by at least 10% compared to fruit from a plant without the modification.

In some embodiments, increased fruit size comprises an increase in fruit volume. In some embodiments, the fruit of the modified plants has an increase in fruit volume of at least 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, or any number or range therein, as compared to fruit from a plant without the modification. In some embodiments, the increased fruit size comprises an increase in fruit volume by at least 5% compared to fruit from a plant without the modification.

[0106] A further aspect of the present disclosure relates to a method of increasing antioxidants in fruit from a plant. The method comprises modifying a plant or a plant cell to reduce or eliminate the expression, stability, and/or activity of an ADP-glucose pyrophosphorylase (AGPase) protein, where the reduction or elimination of the expression, stability, and/or activity of AGPase protein is effective in reducing or eliminating starch

synthesis and increasing antioxidant levels in a fruit from the plant or a plant produced from the plant cell, as compared to a fruit from a plant without the modification.

[0107] This aspect of the present disclosure can be carried out with any of the embodiments disclosed herein.

5 [0108] Antioxidants are substances that can remove or inhibit potentially damaging oxidation. In some embodiments, the fruit of the modified plants of the present disclosure has increased antioxidants compared to fruit from a plant without the modification. In some embodiments, the increased antioxidants comprise raffinose, phenolics, and/or pyridoxal. In some embodiments, the antioxidants are increased by 1.1-fold to 3-fold, or any number or range
10 therein, as compared to fruit from a plant without the modification.

[0109] Another aspect of the present disclosure relates to a plant cell comprising a nucleic acid molecule comprising a modified ADP-glucose pyrophosphorylase (AGPase) gene encoding an AGPase protein or fragment thereof, wherein the expression, stability, and/or activity of the AGPase protein is reduced or eliminated in the plant cell as compared to a plant
15 cell without the modification.

[0110] Yet another aspect of the present disclosure relates to a plant cell comprising an inhibitory polynucleotide targeting an AGPase gene encoding an AGPase protein, wherein the expression, stability, and/or activity of the AGPase protein is reduced or eliminated in the plant cell as compared to a plant cell without the inhibitory polynucleotide.

20 [0111] These aspects of the present disclosure can be carried out with any of the embodiments disclosed herein.

Nucleic Acid Constructs

[0112] A further aspect of the present disclosure relates to a nucleic acid construct comprising a nucleotide sequence targeting an AGPase gene comprising: (i) a guide RNA, or (ii)
25 an inhibitory polynucleotide, a 5' heterologous DNA promoter sequence; and a 3' terminator sequence.

[0113] In some embodiments, the guide RNA targets one or more *AGPase* genes, *APS* genes, and/or *APL* genes. In some embodiments, the inhibitory polynucleotide targets one or more *AGPase* genes, *APS* genes, and/or *APL* genes.

30 [0114] A "nucleic acid construct" or "vector" is a nucleic acid, plasmid, or virus used to transfer coding information to a host cell. Typically, the vector contains sequences directing

transcription and translation of the relevant gene, a selectable marker, and sequences allowing autonomous replication or chromosomal integration. Suitable “expression vectors” comprise a region 5' of the gene which harbors transcriptional initiation controls and a region 3' of the DNA fragment which controls transcriptional termination.

5 **[0115]** The DNA sequence in the expression vector is operably linked to appropriate expression control sequences, including a promoter, to direct RNA synthesis and protein expression. “Operably linked” means an association between polynucleotide (*e.g.*, nucleic acid) sequences on a single nucleic acid molecule such that the function of one is affected by the other. For example, a promoter is operably linked to a coding sequence when the coding sequence is
10 under the transcriptional control of the promoter. Coding sequences can be operably linked to regulatory sequences in sense or antisense orientation. The expression vector can contain one or more selectable marker genes to provide a phenotypic trait for selection of a transformed host cell. Useful selectable markers include dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or tetracycline or ampicillin resistance in *E. coli*. The vector may be
15 introduced into the host cell(s) using any of a variety of techniques, including transformation, transfection, transduction, viral infection, gene guns, Ti-mediated gene transfer, calcium phosphate transfection, DEAE-Dextran-mediated transfection, lipofection, or electroporation. Examples of vectors include, but are not limited to, viral particles, baculovirus, phage, plasmids, phagemids, cosmids, fosmids, bacterial artificial chromosomes, viral DNA, such as vaccinia and
20 adenovirus, Ti vectors, P1-based artificial chromosomes, yeast plasmids, *Bacillus* vectors, and *Aspergillus* vectors. Examples of bacterial vectors include, but are not limited to, pQE vectors, pBluescript plasmids, pNH vectors, and lambda-ZAP vectors. Examples of eukaryotic vectors include pXT1, pSG5, pSVK3, pBPV, pMSG, and pSVLSV40 vectors.

[0116] U.S. Patent No. 4,237,224 to Cohen and Boyer, which is hereby incorporated by
25 reference in its entirety, describes the production of expression systems in the form of recombinant plasmids using restriction enzyme cleavage and ligation with DNA ligase. These recombinant plasmids are then introduced by means of transformation and replicated in unicellular cultures including prokaryotic organisms and eukaryotic cells grown in tissue culture.

[0117] Depending upon the targeted expression profile in a cell or tissue type, or
30 developmental timeframe, any one of a number of suitable promoters may be used. A “promoter” refers to a nucleic acid fragment capable of controlling transcription of another nucleic acid

fragment. A promoter is a non-coding genomic DNA sequence, usually upstream (5') to and operably linked to the relevant coding sequence, and its primary function is to act as a binding site for RNA polymerase to initiate transcription by the RNA polymerase. A promoter may also include distal enhancer or repressor elements, which can be located as much as several thousand
5 base pairs from the start site of transcription. The terms “capable of controlling expression” or “initiating transcription”, refer to the primary function of a promoter. Additionally, there is “expression” of RNA, including functional RNA, or the expression of polypeptide for operably linked encoding nucleotide sequences, as the transcribed RNA ultimately may be translated into the corresponding polypeptide. Promoters vary in their “strength” (*i.e.*, their ability to promote
10 transcription). The nucleotide sequence of the promoter determines the nature of the RNA polymerase binding and other related protein factors that attach to the RNA polymerase and/or promoter, and the rate of RNA synthesis.

[0118] A “constitutive” promoter is a promoter that is active under most environmental and developmental conditions. An “inducible” promoter is a promoter that is active under
15 environmental or developmental regulation. Suitable constitutive promoters that are functional in a plant cell include, but are not limited to, the cauliflower mosaic virus 35S (CaMV35S) promoter, a tandem 35S promoter, a cauliflower mosaic virus 19S promoter, a figwort mosaic virus 35S (FMV35S) promoter, a nopaline synthase gene promoter, an octopine synthase gene promoter, a potato or tomato protease inhibitor I or II gene promoter, and a ubiquitin promoter.
20 Suitable inducible promoters that are functional in a plant cell may include, but are not limited to, a phenylalanine ammonia-lyase gene promoter, a chalcone synthase gene promoter, a pathogenesis-related protein gene promoter, a copper-inducible regulatory element, tetracycline, and chlor-tetracycline-inducible regulatory elements.

[0119] A “tissue-specific” promoter is a promoter that primarily are functional in a
25 specific tissue type. For example, tissue specific promoters can be employed which regulate expression in only one or some tissues or organs, such as leaves, roots, fruit, seeds, anthers, ovaries, pollen, meristem, stems or flowers, or parts thereof. Methods for identifying and characterizing promoter regions in plant genomic DNA include, for example, those described in the following references: Jordano et al., Plant Cell, 1:855-866 (1989); Bustos et al., Plant Cell,
30 1:839-854 (1989); Green et al., EMBO J., 7:4035-4044 (1988); Meier et al., Plant Cell, 3:309-316 (1991); and Zhang et al., Plant Physiology, 110:1069-1079 (1996). Non-limiting examples

of tissue-specific promoters include, without limitation, B29 promoter, CD14 promoter, CD43 promoter, CD45 promoter, CD68 promoter, desmin promoter, elastase-1 promoter, endoglin promoter, fibronectin promoter, Fli-1 promoter, GFAP promoter, GPIIb promoter, ICAM-2 promoter, INF- γ promoter, Mb promoter, Nphs1 promoter, OG-2 promoter, SP-B promoter, SYN1 promoter, and WASP promoter.

[0120] The tissue-specific ES promoter from tomato is particularly useful for directing gene expression so that a desired gene product is located in fruits (see, e.g., Lincoln et al. "Diverse Mechanisms for the Regulation of Ethylene-Inducible Gene Expression," *Proc Natl Acad Sci USA* 84:2793-2797 (1988), which is hereby incorporated by reference in its entirety).

An example of a seed-specific promoter is the promoter from the gene encoding oleosin from *Arabidopsis* (Genbank Accession No. Z17657, which is hereby incorporated by reference in its entirety). Other exemplary promoters are described in Fernandez et al., "Flexible Tools for Gene Expression and Silencing in Tomato," *Plant Physiology* 151: 1729-1740 (2009) (which is hereby incorporated by reference in its entirety). In some embodiments, the 5' heterologous DNA promoter sequence is a tissue-specific promoter. In certain embodiments, the tissue-specific promoter is a promoter identified on the ePlant database (available on the world wide web at bar.utoronto.ca/eplant_tomato, incorporated herein by reference) or on the Melonet database (available on the world wide web at melonnet-db.dna.affrc.go.jp/ap/mvw, incorporated herein by reference).

[0121] In certain embodiments, the tissue-specific promoter is a promoter of the tomato gene STM3 (Solyc01g092950) which is mostly expressed in leaf and root tissues, but not in fruits. In certain embodiments, the tissue-specific promoter is a promoter of the tomato gene SIMBP24 (Solyc01g105800) which is mostly expressed in leaf and root tissues, but not in fruits. The Solyc01g105800 tissue specific promoter has been assembled with the APS1 into the pGWB401 backbone (See FIG. 19A). In certain embodiments, the tissue-specific promoter is a promoter of the tomato gene β CA1 (Solyc02g086820) which is mostly expressed in leaf tissues, but not in fruits. The Solyc02g086820 tissue specific promoter has been assembled with the APS1 into the pGWB401 backbone (See FIG. 19B).

[0122] In certain embodiments, the tissue-specific promoter is a promoter of melon gene MELO3C022515 which is primarily expressed in plant flowers (FIG 20A). In certain embodiments, the tissue-specific promoter is a promoter of melon gene MELO3C007716 which

is primarily expressed in plant leaves stems and roots (FIG 20B). In certain embodiments, the tissue-specific promoter is a promoter of melon gene MELO3C00958 which is primarily expressed in plant seeds and leaves (FIG 20C). Other exemplary tissue-specific promoter can be found in Table 14.

Table 14: Tissue Specific Promoters	
Promoter	Tissue of Expression
Phosphoenolpyruvate Carboxylase 2 (PPC2) promoter	Fruit
Tomato Proline Rich Protein (TPRP) Promoter	Fruit
Inhibitor of Meristem Activity (IMA) Promoter	Fruit (Accession number AC122544)
Arabidopsis CRABS CLAW (CRC) promoter	Fruit
Tomato Polyhglacturonase (PG) promoter	Fruit
P _{RSGA}	Seed
P _{2RSGA}	Seed
BiGSSP2	Green Tissues
BiGSSP3	Green Tissues
BiGSSP6	Green Tissues
BiGSSP7	Green Tissues
SynR2	Root
SynR1	Root
GSSP1	Green Tissues

GSSP3	Green Tissues
GSSP5	Green Tissues
GSSP6	Green Tissues
GSSP7	Green Tissues
P35S-PCHS-Ω	Flower
P35S-LCHS-Ω	Flower
EFCFS-HS-1	Vascular Tissues
EFCHFS-HS-1	Vascular Tissues
EFCFSHS-3	Vascular Tissues

[0123] Promoters may also be plant-specific promoters, or promoters that function in plants. A wide variety of plant promoters are known to those of ordinary skill in the art, as are other regulatory elements that may be used alone or in combination with promoters.

[0124] The protein-encoding nucleic acid, a promoter molecule of choice, a suitable 3' regulatory region and, if desired, polyadenylation signals and/or a reporter gene, are incorporated into a vector-expression system of choice to prepare a nucleic acid construct using standard cloning procedures known in the art, such as described by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Third Edition, Cold Spring Harbor: Cold Spring Harbor Laboratory Press, New York (2001), which is hereby incorporated by reference in its entirety.

[0125] Single or multiple nucleic acids may be ligated into an appropriate vector, under the control of one or more suitable promoters, to prepare a nucleic acid construct. In some embodiments, the expression vector comprising the nucleic acid construct. In some embodiments, the expression vector further comprises a genome editing nuclease.

[0126] Once the nucleic acid molecule has been inserted into an expression vector, it is ready to be incorporated into a host cell. Recombinant molecules can be introduced into cells via transformation, particularly transduction, conjugation, lipofection, protoplast fusion, mobilization, particle bombardment, or electroporation. "Transformation" or "transforming" refers to the introduction of a nucleic acid into a host organism. Host organisms containing a transformed nucleic acid construct or DNA fragment may be referred to as "transgenic" or "recombinant" organisms.

[0127] In some embodiments, a cell is transformed with the nucleic acid construct. In some embodiments, the cell is a bacterial cell or a plant cell. A transformed plant cell may be regenerated into a plant by any method known in the art. In some embodiments, a plant is transformed with the nucleic acid construct. Fruit from the plant or a plant grown from the plant cell of any of the embodiments of the present disclosure are also contemplated. In some embodiments, a plant seed produced from the plant of any of the embodiments of the present disclosure is contemplated.

Plant Breeding

[0128] Another aspect of the present disclosure relates to a method of breeding for enhanced blossom end rot resistance. The method comprises providing a candidate plant, analyzing the candidate plant for the presence, in its genome, of a modified ADP-glucose pyrophosphorylase (AGPase) polynucleotide encoding an AGPase protein, wherein the expression, stability, and/or activity of said AGPase protein is reduced or eliminated as compared to a plant without the modification, identifying, based on said analyzing, a candidate plant suitable for breeding that includes in its genome, the modified ADP-glucose pyrophosphorylase (AGPase) polynucleotide, and breeding the identified plant with at least one other plant.

[0129] This aspect of the present disclosure can be carried out with any of the embodiments disclosed herein.

[0130] In some embodiments, identifying the presence of a modified AGPase polynucleotide sequence is achieved based on sequencing the sequences set forth herein, by identifying a sequence based on homology to the sequences set forth herein. In some embodiments, a molecular marker is developed to identify a modified AGPase polynucleotide sequence. Sequencing can be accomplished, for example, using next generation sequencing, Sanger sequencing, TaqMan assays, UniTaq assays, real-time PCR assays, digital PCR, microarray, hybridization or other detection methods.

[0131] In some embodiments, analyzing the candidate plant for the presence, in its genome, of a modified ADP-glucose pyrophosphorylase (AGPase) polynucleotide encoding an AGPase protein, wherein the expression, stability, and/or activity of said AGPase protein is reduced or eliminated as compared to a plant without the modification involves isolating nucleic acids from the plant or plant part, analyzing nucleic acids from the plant, or plant parts for the

presence of the modified AGPase polynucleotide, and detecting the modified AGPase polynucleotide.

[0132] In some embodiments, identifying comprises sequencing the nucleic acids of one or more AGPases from the plant, or plant part. In some embodiments, identifying comprises detecting a mutation corresponding to 1321delT of SEQ ID NO:130. In some embodiments, identifying comprises detecting the nucleotide sequence of SEQ ID NO:130. In some embodiments, analyzing the candidate plant for a modified AGPase involves testing starch content. In some embodiments, testing starch content involves staining with iodine or Lugol's reagent. In some embodiments, said identifying comprises detecting a plant or fruit with no or low staining with iodine or Lugol's reagent, compared to a plant without a modified AGPase. In some embodiments, testing starch content involves quantifying starch enzymatically.

[0133] In some embodiments, the breeding involves crossing, making hybrids, backcrossing, self-crossing, double haploid breeding, and/or combinations thereof.

Selective Expression of AGPase

[0134] Yet another aspect of the present disclosure relates to a method for imparting blossom end rot resistance to fruit from a plant. The method comprises modifying a plant or a plant cell to reduce or eliminate the expression, stability, and/or activity of ADP-glucose pyrophosphorylase (AGPase) protein, where the reduction or elimination of the expression, stability, and/or activity of AGPase protein is effective in reducing or eliminating starch synthesis and imparting blossom end rot resistance to fruit from the plant or a plant produced from the plant cell, as compared to fruit from a plant without the modification, and selectively expressing a functional AGPase protein in non-fruit tissues.

[0135] This aspect of the present disclosure can be carried out with any of the embodiments disclosed herein.

[0136] In some embodiments, the methods of the present disclosure comprise selectively expressing a functional AGPase in the non-fruit tissue of the plant. "Selectively expressed" or "selectively expressing" means that expression of the functional AGPase is targeted to a particular non-fruit tissue or tissue types. Selective expression may be performed by introducing a nucleic acid construct comprising a functional AGPase gene operably linked to a non-fruit specific promoter into a plant or plant cell. For example, a functional AGPase (unmutated or

unmodified) could be expressed in non-fruit tissue (such as leaves) to restore starch synthesis in non-fruit tissues.

[0137] In some embodiments, a polynucleotide encoding a functional AGPase corresponding to the modified AGPase is operably linked to a non-fruit specific promoter (or a promoter that does not drive expression during fruit development) is introduced into the plant having a modified AGPase. For example, in an embodiment where a mutated *APSI* gene is present, a polynucleotide encoding the functional *APSI* gene operably linked to a non-fruit specific promoter (or a promoter that does not drive expression during fruit development) is introduced into the plant.

[0138] The following examples are provided to illustrate embodiments of the present disclosure but are by no means intended to limit its scope.

EXAMPLES

Example 1 – Materials and Methods used for Examples 2-6

[0139] *Plant growth conditions and sample collection.* Seed stocks for wild type (*Solanum lycopersicum*, LA2838A) and the *adp* mutant (*S. lycopersicum*, LA3763) were obtained from the Tomato Genetics Resource Center (TGRC) at the University of California, Davis. Tomato plants were grown in a greenhouse at Cornell University (Ithaca, NY, USA) with a light/dark photoperiod of 16/8 h. Soil moisture sensors (MAS-1, Decagon Devices, Pullman, USA) were used to monitor pot volumetric water content (VWC) and to regulate an irrigation system to maintain 40-50% VWC. Flowers were tagged and manually pollinated at anthesis, and fruits were harvested at 6 days post anthesis (dpa), 20 dpa, and at the mature green (MG, ~ 35 dpa) and ripe (breaker + 8 days) stages, from 10 randomly selected individual plants per genotype.

[0140] To assess BER incidence, water stress was applied by lowering pot VWC to 30% (Nicolas et al “Spatiotemporal Dynamics of The Tomato Fruit Transcriptome Under Prolonged Water Stress,” *Plant Physiology* 190:2557–2578 (2022), which is hereby incorporated by reference in its entirety) 5 to 7 days after flowers were tagged and pollinated. Five plants per genotype were used with at least 10 fruit per plant, and BER incidence was assessed in fruit at 30 dpa. The experiment was repeated three times.

[0141] *Map-based cloning.* To identify the gene responsible for the *adp* mutation, an F2 mapping population was generated by crossing *adp* to *Solanum pimpinellifolium* (LA1589), and

this population was phenotyped for agravitropism at the seedling stage on vertical petri dishes. Approximately 200 agravitropic seedlings were genotyped using PCR markers, across chromosome 7, designed based on indels and SNP positions according to the tomato Heinz 1706 reference genome (The Tomato Genome Consortium, “The Tomato Genome Sequence Provides Insights into Fleshy Fruit Evolution,” *Nature* 485:635–641 (2012), which is hereby incorporated by reference in its entirety).

[0142] *RNA isolation, sequencing and analysis.* Dissected pericarp and placenta were ground in liquid nitrogen and total RNA was isolated using an RNeasy Mini Kit (Qiagen). Strand-specific libraries were constructed according to Zhong et al., “High-Throughput Illumina Strand-Specific RNA Sequencing Library Preparation,” *Cold Spring Harb Protoc* 8:940-9 (2011), which is hereby incorporated by reference in its entirety, and sequenced on an Illumina NextSeq 500 from a single end for 75 cycles. After removing adapter and low-quality sequences using Trimmomatic (Bolger et al., Trimmomatic: A Flexible Trimmer for Illumina Sequence Data,” *Bioinformatics* 30:2114–2120 (2014), which is hereby incorporated by reference in its entirety), RNA-Seq reads were aligned to the ribosomal RNA database (Quast et al., “The SILVA ribosomal RNA gene database project: improved data processing and web-based tools,” *Nucleic Acids Res* 41:D590–D596 (2013), which is hereby incorporated by reference in its entirety) using Bowtie (Langmead et al., “Ultrafast and Memory-Efficient Alignment of Short DNA Sequences to the Human Genome,” *Genome Biol* 10:R25 (2009), which is hereby incorporated by reference in its entirety) and the mappable reads discarded. The resulting high-quality cleaned reads were aligned to the tomato Heinz 1706 reference genome (The Tomato Genome Consortium, “The Tomato Genome Sequence Provides Insights into Fleshy Fruit Evolution,” *Nature* 485:635–641 (2012), which is hereby incorporated by reference in its entirety) SL 3.0 with gene models iTAG3.2 using HISAT (Kim et al., “HISAT: A Fast Spliced Aligner with Low Memory Requirements,” *Nat Methods* 12:357–360 (2015), which is hereby incorporated by reference in its entirety) and raw counts for each tomato gene were derived and normalized to reads per kilobase of transcript per million mapped reads (RPKM). Genes were considered expressed if their averaged RPKM among replicates was ≥ 1 . Pairwise Pearson correlation coefficient values between biological replicates were calculated with log₂-transformed RPKM values (*i.e.*, log₂ [RPKM + 1]) using the cor function in the R program (www.r-project.org). Pairwise Pearson correlation coefficient values between biological

replicates ranged from 0.88 to 1.00. PCA was performed to compare the log₂-transformed RPKM values of the expressed gene profiles among genotypes, tissue-types and stages, using the `prcomp` function in R v3.5.1. The log₂-transformed (RPKM+1) values of all the genes were used for hierarchical clustering using `dist` (method = "Euclidean") function and `hclust` (method = "average") function in R. Raw read count data were imported to edgeR (Robinson et al., "edgeR: A Bioconductor Package for Differential Expression Analysis of Digital Gene Expression Data," *Bioinformatics* 26:139–140 (2010), which is hereby incorporated by reference in its entirety) to identify differentially expressed genes (DEGs) between each pair of adp and control samples with a cutoff of absolute fold change ≥ 1.5 and false discovery rate (FDR) < 0.05 . Gene annotations, iTAG3.2 gene ontology (GO) terms, were obtained from the PANTHER classification system version 10 (Mi et al., 2016). GO enrichment analysis was performed for GO Biological Process Complete using the Bioconductor R library `clusterProfiler` (Yu et al., "ClusterProfiler: An R Package for Comparing Biological Themes Among Gene Clusters," *OMICS* 16:284–287 (2012), which is hereby incorporated by reference in its entirety), applying a hypergeometric test with FDR correction (adjusted p value < 0.05).

[0143] *Metabolite analysis.* Soluble sugars and starch measurements were performed according to Vargas-Ortiz et al., "Grain Amaranths are Defoliation Tolerant Crop Species Capable of Utilizing Stem and Root Carbohydrate Reserves to Sustain Vegetative and Reproductive Growth After Leaf Loss," *PLoS One* 8:e67879 (2013), which is hereby incorporated by reference in its entirety. Briefly, 50 mg of frozen tissue were extracted in 50 mM Hepes KOH (pH 7.4), 5 mM MgCl₂, 80% ethanol (v/v), three times at 80°C. Soluble extracts were then combined and assayed enzymatically for glucose, fructose and sucrose in a microplate reader (Synergy 2, BioTeck Instruments). The insoluble starch pellets were dissolved in 0.25 ml 10 mM KOH at 95°C for 1h. Starch was hydrolyzed in 50 mM sodium acetate buffer (pH 5.5) at 37°C overnight by the addition of 10 units of α -amylase and 10 units of amyloglucosidase and solubilized sugars were enzymatically assayed for glucose, as mentioned above.

[0144] Metabolite extraction, derivatization, standard addition, and sample injection for GC-MS were performed according to Osorio et al., "Profiling Primary Metabolites of Tomato Fruit with Gas Chromatography/Mass Spectrometry," *Methods Mol Biol* 860:101–109 (2012), which is hereby incorporated by reference in its entirety. The mass spectra were cross-referenced with those in the Golm Metabolome Database (Kopka et al., "GMD@CSB.DB: The Golm

Metabolome Database,” *Bioinformatics* 21:1635–1638 (2005), which is hereby incorporated by reference in its entirety).

[0145] For untargeted LC-MS/MS analysis, frozen samples were extracted with 80% MeOH and homogenized in a Tissue Lyser for 3 min at 25/s. Methanolic extracts were centrifuged twice for 10 min at 12000 rpm and supernatants were stored at -80°C until analysis. LC-MS/MS analysis was performed using orthogonal UPLC separation strategies (reversed phase and HILIC), in both positive and negative ionization modes to maximize identification of metabolites. Chromatographic separation was performed on a Vanquish UHPLC system coupled to a Q Exactive™ Hybrid Quadrupole-Orbitrap High Resolution Mass Spectrometer (Thermo Fisher Scientific, San Jose, CA, USA). A SeQuant ZIC pHILIC column (5 µm, 2.1 x 150 mm) and a Thermo Accucore Vanquish C18+, 1.5 µm column (2.1 mm id x 100 mm) were used for the HILIC and Reversed phase methods, respectively. Acquired MS1 and DDMS2 files, in both positive and negative ion mode were processed separately in Compound Discoverer 2.1 using untargeted workflow (5 ppm mass tolerance and 0.1 min RT tolerance). Successful compound annotation was assessed using an in-house spectral library and references retrieved from the database mzCloud (www.mzcloud.org) with best match scores > 80%.

[0146] Glycerolipids were analyzed using LC-MS according to Lapidot-Cohen et al., (2020). Briefly, samples were extracted using methyltert-butyl ether (MTBE) and injected in an ultra-performance liquid chromatography (UPLC) system (Waters Acquity UPLC) with a lipophilic column (BEH C8 1.7 µm) coupled to a Q Exactive mass spectrometer in positive and negative ionization modes (UPLC-MS).

[0147] Metabolomic data analyses (statistical analysis, PCA, hierarchical clustering and heat-maps) were performed using MetaboAnalyst 4.0 (Chong et al., “Using MetaboAnalyst 4.0 for Comprehensive and Integrative Metabolomics Data Analysis,” *Curr Protoc Bioinformatics* 68:e86 (2019), which is hereby incorporated by reference in its entirety).

[0148] *Fluorescence Microscopy*. Equatorial sections of tomato fruit were incubated with 1µg/ml of the fluorophore BODIPY (4,4-difluoro-3a,4adiaza-s-indacene) 505/515 (ThermoFisher Scientific, USA) for 15 min, in the dark, and then rinsed three times with water. Samples were observed with a Leica M205 stereomicroscope using 505 nm and 515 nm as excitation and emission wavelengths, respectively.

[0149] *Data Availability.* Raw transcriptome sequencing reads have been deposited in the National Center for Biotechnology Information BioProject database under the accession no. PRJNA912612.

Example 2 – Characterization of *adpressa* as a Starch-Deficient Tomato Mutant

5 [0150] The *adpressa* (*adp*) mutant (*Solanum lycopersicum*, LA3763) was initially isolated in the tomato cultivar Condine Red as a radiation induced mutation and described as having directionless hypocotyl growth and a crawling growth habit (Stubbe, “Mutanten der Kulturtomate *Lycopersicon Esculentum* Miller III. Die Kulturpflanze 7: 82–112 (1959), which is hereby incorporated by reference in its entirety). The mutation was later introgressed into the
10 Ailsa Craig cultivar (*Solanum lycopersicum*, LA2838A) by five backcrosses, and the *adp* gene was putatively assigned to chromosome 7 (Smith and Ritchie, “A Collection of Near-Isogenic Lines of Tomato: Research Tool of the Future?,” *Plant Mol Biol Rep* 1:41–45 (1983), which is hereby incorporated by reference in its entirety). Morphological analysis under greenhouse growth conditions showed that *adp* plants were shorter and with decumbent stem growth (FIG.
15 1A). In addition, *adp* seedlings grown in agar plates displayed agravitropic root growth (FIG. 1B).

[0151] To identify the *adp* gene, a mapping strategy using a F2 population derived from a cross between *adp* and the wild tomato *Solanum pimpinellifolium* (LA1589) was employed. The *adp* mutation mapped to an 86 Kb region of chromosome 7 that contained 11 genes
20 including *Solyc07g056140* encoding the ADP-glucose pyrophosphorylase (AGPase) small subunit, APS1 (FIG. 1C). AGPase catalyzes the conversion of glucose 1-phosphate and ATP into ADP-glucose and inorganic pyrophosphate, a rate-limiting step in the starch biosynthesis pathway (Geigenberger P., “Regulation of Starch Biosynthesis in Response to a Fluctuating Environment,” *Plant Physiol* 155:1566–1577 (2011), which is hereby incorporated by reference
25 in its entirety). Given the role of starch in gravitropism (Morita and Tasaka, “Gravity Sensing and Signaling,” *Curr Opin Plant Biol* 7:712–718 (2004), which is hereby incorporated by reference in its entirety) this candidate gene was further investigated. Sanger sequencing of this genomic region identified a single base deletion close to the 3’ end of the AGPase coding sequence that resulted in a frame shift and premature stop codon, producing a protein missing 44
30 amino acids at the C-terminus (FIG. 1C), the region containing the allosteric activator, glycerate 3-phosphate, binding site (Geigenberger P., “Regulation of Starch Biosynthesis in Response to a

Fluctuating Environment,” *Plant Physiol* 155:1566–1577 (2011), which is hereby incorporated by reference in its entirety).

[0152] To further confirm that the mutation in *APSI* was responsible for the *adp* phenotype, the starch content was determined by Lugol staining in wild type (WT) and *adp* tissues. A blue stain after treatment with Lugol reagent indicates the presence of starch. WT plants showed starch accumulation in the root tip, stem cross sections, and leaves, while *adp* plants showed no Lugol staining (FIG. 1D). Transgenic complementation of *adp* with a construct comprising the *APSI* gene with 2.1 kb upstream and 0.5 kb downstream regions (*APSIpro::APSI*; CL), generated plants with restored levels of starch (FIGs. 9A-B).

Example 3 – Fruit Development in *adpressa*

[0153] The effect of the *adp* mutation on the starch content of the fruit at different stages of development by comparing *adp* to wild type (WT, Ailsa Craig) and CL. In WT and CL fruit, starch accumulated in the pericarp, septum and placenta at the early stages of fruit development, and its level decreased at the onset of ripening (FIGs. 2A-B). The starch content was greater in the internal tissues (e.g., placenta) than in the pericarp (FIG. 2B), where it only accumulated in the inner cell layers (FIG. 2A). Consistent with the starch deficiency observed in the vegetative tissues, no starch staining was observed in the *adp* fruit throughout development (FIGs. 2A-B). Transgenic complementation of *adp* also restored levels of starch in the fruit (FIG. 2B and FIGs. 9A-B). To investigate the phenotypic effects of the lack of starch accumulation in the fruit, fruit growth and the time to reach ripening was monitored (FIGs. 3A-D). The overall phenotype of *adp* fruit was similar to WT, except for a slightly larger size and weight and a minor delay in ripening (~1 day). However, it was observed that *adp* fruits were remarkably resistant to blossom end rot (BER), a common physiological disorder in tomato that is induced by environmental stress (Topcu et al., “Blossom-End Rot: A Century-Old Problem in Tomato (*Solanum lycopersicum* L.) and Other Vegetables,” *Mol Hort* 2:1 (2022), which is hereby incorporated by reference in its entirety), such as drought. To further test BER incidence in *adp*, WT and *adp* plants were subjected to water deficit conditions by lowering pot volumetric water content (VWC) to 30% VWC (Nicolas et al., 2022) 5 to 7 days after flowering (DAF), and BER occurrence was assessed. The presence of damaged and necrotic tissue, characteristic of BER, was observed appearing first in the placenta, and later affecting the pericarp, in fruit from the WT and complemented lines (FIG. 10) but not from *adp*. Evaluation of the BER incidence under

control and water stress conditions, showed that *adp* fruit were never affected by BER (FIGS. 3E-F).

Example 4 – Transcriptional Changes in *adpressa* Fruit

[0154] To evaluate the effect of the starch deficiency on the fruit transcriptome, an RNA-seq analysis of placenta and pericarp tissues collected from *adp*, WT and CL fruits at four developmental stages spanning growth and ripening was performed (Table 2).

Table 2. Total Mapped Reads per Sample

Samples	No. reads	% mapped	Samples	No. reads	% mapped
Pericarp_WT_6dpa_rep1	11,632,708	94.98	Pericarp_WT_MG_rep1	7,587,173	96.68
Pericarp_WT_6dpa_rep2	13,624,308	95.45	Pericarp_WT_MG_rep2	9,900,335	96.10
Pericarp_WT_6dpa_rep3	9,603,081	95.30	Pericarp_WT_MG_rep3	14,467,428	96.53
Placenta_WT_6dpa_rep1	9,564,970	95.40	Placenta_WT_MG_rep1	12,033,567	96.62
Placenta_WT_6dpa_rep2	8,718,742	94.83	Placenta_WT_MG_rep2	8,432,321	95.58
Placenta_WT_6dpa_rep3	6,997,935	94.89	Placenta_WT_MG_rep3	7,883,133	94.27
Pericarp_adp_6dpa_rep1	9,284,974	95.00	Pericarp_adp_MG_rep1	10,529,521	96.37
Pericarp_adp_6dpa_rep2	9,183,419	95.09	Pericarp_adp_MG_rep2	9,602,416	94.04
Pericarp_adp_6dpa_rep3	16,088,363	95.68	Pericarp_adp_MG_rep3	11,383,976	96.07
Placenta_adp_6dpa_rep1	11,922,934	96.62	Placenta_adp_MG_rep1	8,022,300	96.13
Placenta_adp_6dpa_rep2	9,294,131	94.44	Placenta_adp_MG_rep2	8,724,312	94.47
Placenta_adp_6dpa_rep3	10,255,737	96.03	Placenta_adp_MG_rep3	8,954,166	94.35
Pericarp_CL_6dpa_rep1	15,690,078	95.97	Pericarp_CL_MG_rep1	8,741,040	95.78
Pericarp_CL_6dpa_rep2	12,329,030	95.44	Pericarp_CL_MG_rep2	7,383,971	95.71
Pericarp_CL_6dpa_rep3	10,419,427	95.59	Pericarp_CL_MG_rep3	6,166,166	95.57
Placenta_CL_6dpa_rep1	7,750,380	94.06	Placenta_CL_MG_rep1	8,922,519	95.11
Placenta_CL_6dpa_rep2	8,609,206	94.67	Placenta_CL_MG_rep2	7,135,769	94.61
Placenta_CL_6dpa_rep3	9,893,362	94.60	Placenta_CL_MG_rep3	8,837,481	95.90
Pericarp_WT_20dpa_rep1	8,547,565	94.59	Pericarp_WT_Ripe_rep1	9,514,218	94.24
Pericarp_WT_20dpa_rep2	8,726,764	95.30	Pericarp_WT_Ripe_rep2	7,511,784	80.53
Pericarp_WT_20dpa_rep3	9,720,021	96.31	Pericarp_WT_Ripe_rep3	8,192,717	93.44
Placenta_WT_20dpa_rep1	10,095,622	94.88	Placenta_WT_Ripe_rep1	17,507,040	88.70
Placenta_WT_20dpa_rep2	9,844,591	95.71	Placenta_WT_Ripe_rep2	7,307,289	90.01
Placenta_WT_20dpa_rep3	10,979,194	94.65	Placenta_WT_Ripe_rep3	12,200,981	92.84
Pericarp_adp_20dpa_rep1	12,590,146	96.23	Pericarp_adp_Ripe_rep1	8,880,889	93.96
Pericarp_adp_20dpa_rep2	10,498,902	95.25	Pericarp_adp_Ripe_rep2	9,005,080	94.88
Pericarp_adp_20dpa_rep3	6,455,664	94.96	Pericarp_adp_Ripe_rep3	8,270,860	94.79
Placenta_adp_20dpa_rep1	6,246,065	94.50	Placenta_adp_Ripe_rep1	11,422,241	95.12
Placenta_adp_20dpa_rep2	7,320,577	95.06	Placenta_adp_Ripe_rep2	7,935,900	93.79
Placenta_adp_20dpa_rep3	10,614,049	94.72	Placenta_adp_Ripe_rep3	8,164,079	94.62

Pericarp_CL_20dpa_rep1	12,484,732	96.05	Pericarp_CL_Ripe_rep1	12,106,508	95.27
Pericarp_CL_20dpa_rep2	10,241,110	95.45	Pericarp_CL_Ripe_rep2	8,629,593	95.33
Pericarp_CL_20dpa_rep3	11,417,448	96.22	Pericarp_CL_Ripe_rep3	9,082,562	94.82
Placenta_CL_20dpa_rep1	9,505,782	96.04	Placenta_CL_Ripe_rep1	7,825,693	92.24
Placenta_CL_20dpa_rep2	6,496,419	95.05	Placenta_CL_Ripe_rep2	7,809,071	89.44
Placenta_CL_20dpa_rep3	12,753,917	95.93	Placenta_CL_Ripe_rep3	8,616,252	89.45
Mean No. Reads: 9,723,496; % Mapped: 95					

[0155] Principal component (PCA) and hierarchical clustering analysis revealed a separation of samples mostly by fruit developmental stage and tissue type (FIGs 11A-B). A distinct clustering between starch containing (CL and WT) and starchless (*adp*) fruit was also revealed for all tissues and developmental stages, suggesting major transcriptional changes in *adp* fruit (FIGs. 11A-B). To increase the confidence of identifying gene expression changes due solely to differences in fruit starch content, differentially expressed genes (DEGs) common to both comparisons: *adp* vs. CL and *adp* vs. WT were focused on. The number of DEGs was higher in placenta than in pericarp (FIG. 4A), which correlated with their relative starch content (FIG. 2B). Similarly, the number of DEGs was higher at 20 days post anthesis (dpa), when the placenta starch content peaks, than at 6 dpa at the beginning of the starch accumulation. A higher number of DEGs was identified at the mature green (MG) stage, which marks the end of the starch accumulation phase and is characterized by active starch hydrolysis (FIG. 4A). Overall, upregulated genes were prevalent over downregulated genes in most developmental stages and tissues (FIG. 4A). Except for a significant overlap between 20 dpa and MG developmental stages in placenta, DEGs showed high developmental stage-specificity (FIG. 4B). However, several DEGs were common to pericarp and placenta at different fruit stages (FIG. 4C, Table 3). These included a *MICRORCHIDIA* (*MORC*) gene, predicted to be involved in heterochromatin condensation and gene silencing (Koch et al., “MORC Proteins: Novel Players in Plant and Animal Health,” *Front Plant Sci* 8:1720 (2017), which is hereby incorporated by reference in its entirety), a transcription factor of the BSD (mammalian *BTF2-like* transcription factors, *Drosophila* synapse-associated proteins and yeast DOS2-like proteins) family (Fan et al., “A Novel BSD Domain-Containing Transcription Factor Controls Vegetative Growth, Leaf Senescence, and Fruit Quality in Tomato,” *J Exp Bot* 71:6945–6957 (2020), which is hereby incorporated by reference in its entirety), and a gene encoding a serine/threonine-protein phosphatase, all upregulated in *adp*. Genes downregulated in *adp*, at all stages and in all tissues,

included a transcription factor of the homeodomain-leucine zipper (HD-Zip) family and *APSI*. The fact that *APSI* transcript levels decreased in *adp* fruit, suggested that the presence of a non-functional APS1 protein had a negative effect on the expression of this gene (FIG. 4C).

[0156] To gain insight into biological processes altered in response to starch deficiency in the fruit, a gene ontology (GO) term enrichment analysis of DEGs downregulated or upregulated in *adp* fruit at different developmental stages was performed (FIGs. 4D-E, Table 4).

[0157] GO terms related to the Target Of Rapamycin (TOR) signaling pathway, regulation of cell growth, DNA repair and epigenetic pathways were predominantly enriched in DEGs upregulated in the placenta at the 20 dpa and MG stages, when starch accumulation peaks in WT fruit (FIG. 4D). Examples of genes in the TOR pathway, cell cycle, chromatin remodeling and gene silencing, that show an increase in expression in the placenta of *adp* fruit during the starch accumulation period, are shown in FIG. 4F and Table 5. In Table 5, the biological pathway column was manually curated based on the closest homologs in *Arabidopsis* (TAIR BLAST P best hit). Downregulated DEGs showed a significant enrichment with GO terms related to photosynthesis and glucose related pathways in the placenta at 20 dpa. GO terms related to ripening processes such as cell wall organization, pectin catabolism and ethylene biosynthesis were primarily associated with DEGs downregulated in the *adp* pericarp at MG (FIG. 4E). These categories comprised ripening-related genes encoding cell wall-modifying enzymes such as expansin, xyloglucan endotransglycosylase/glycosylase, pectin methylesterase, and polygalacturonase, and ethylene-related genes, which all showed reduced expression levels in *adp* pericarp at the MG stage (FIG. 12).

[0158] GO terms associated with stress responses, such as oxidative stress or heat stress response were enriched in DEGs from various developmental stages and tissues. For example, several genes encoding enzymes involved in oxidative stress (*e.g.*, glutathione S-transferases), heat shock proteins and abiotic stress related transcription factors belonging to the C-REPEAT BINDING FACTOR (CBF; Haake et al., “Transcription Factor CBF4 is a Regulator of Drought Adaptation in *Arabidopsis*,” *Plant Physiol* 130:639–648 (2002), which is hereby incorporated by reference in its entirety; Medina et al., 2011), HEAT SHOCK FACTOR (HSF; Pérez-Salamó et al., “The Heat Shock Factor A4A Confers Salt Tolerance and is Regulated by Oxidative Stress and the Mitogen-Activated Protein Kinases MPK3 and MPK6,” *Plant Physiol* 165:319–334 (2014), which is hereby incorporated by reference in its entirety), Ethylene Responsive Factor

(ERF; Bahieldin et al., “Ethylene Responsive Transcription Factor ERF109 Retards PCD and Improves Salt Tolerance in Plant,” *BMC Plant Biol* 16:216 (2016), which is hereby incorporated by reference in its entirety) and Nuclear Factor-Y (NF-Y; Sato et al “*Arabidopsis* DPB3-1, a DREB2A Interactor, specifically Enhances Heat Stress-Induced Gene Expression by Forming a Heat Stress-Specific Transcriptional Complex with NF-Y Subunits,” *Plant Cell* 26:4954–4973 (2014), which is hereby incorporated by reference in its entirety) families, were up-regulated in *adp* during fruit growth (FIG. 4F, Table 5).

[0159] Several GO terms associated with lipid metabolism such as glycerolipid metabolism, sphingolipid biosynthesis, sterol metabolism or fatty acid biosynthesis, were associated to DEG in *adp* placenta and pericarp (FIG. 4D-E). Analysis of lipid-related gene expression changes (FIG. 7A, Table 5) showed genes involved in sphingolipid metabolism and genes encoding acyltransferases, and lipases implicated in membrane lipid remodeling and in the generation of lipid derived signals, among the DEGs upregulated in the placenta of developing *adp* fruit, while at the ripe stage upregulated genes comprised those involved in lipid catabolism, sterol biosynthesis and genes encoding fatty acid desaturases. In the pericarp, genes associated with sterol biosynthesis, lipid signaling, and phospholipid metabolism increased in expression at the MG and ripe stage. In contrast, several genes encoding lipoxygenases involved in fatty acid oxidation and the oxylipin/jasmonic acid pathway, were downregulated in *adp* at the ripe stage (FIG. 7A, Table 4).

Example 5 – Metabolite Changes in *adpressa* Fruit

[0160] To determine the effects of starch deficiency on fruit metabolism, changes in metabolite composition in pericarp and placenta from *adp* fruit compared to WT and CL were analyzed. First, levels of the soluble sugars, glucose, fructose, and sucrose, which are sources of carbon for starch biosynthesis, were quantified using an enzymatic method (Vargas-Ortiz et al., 2013). Surprisingly, despite their close link with starch metabolism, the levels of glucose, fructose, and sucrose were only slightly affected, with an increase in glucose levels (~1.4 x) at 20 dpa and a decrease (~0.8 x) in ripe fruit being the major changes (FIG. 13).

[0161] To further investigate the metabolic changes in *adp*, GC/MS was used to profile primary metabolism compounds (Osorio et al., “Profiling Primary Metabolites of Tomato Fruit with Gas Chromatography/Mass Spectrometry,” *Methods Mol Biol* 860:101–109 (2012), which is hereby incorporated by reference in its entirety). This analysis showed distinct clusters for

each genotype, with replicates for WT and CL tissues showing a closer profile separated from *adp* (FIGs. 14A-C). Samples separated first according to developmental stages and then by tissue at 6 dpa and the ripe stage but were grouped first by tissue and then by stage at 20 dpa and MG (FIG. 14C). A total of 20 amino acids, 12 sugars, 4 organic acids were quantified, as well as putrescine and phosphoric acid. Significant changes ($FDR < 0.05$) in both, *adp* vs. WT and *adp* vs. CL, comparisons were found for 20 metabolites in the placenta, and 15 metabolites in the pericarp, in at least one developmental stage (FIG. 5, Table 6). Bold font indicates significantly lower content in *adp* vs. both WT and CL fruit ($FDR < 0.05$), and bold italics font indicates significantly higher content in *adp* vs. both WT and CL fruit ($FDR < 0.05$). These included changes in glucose content, consistent with the sugar enzymatic assay results. Additionally, a significant increase in glucose 6-phosphate (Glc-6-P), a metabolic hub connecting glycolysis and the pentose phosphate pathway, with a key role in energy metabolism, was observed in *adp* fruit at all developmental stages and tissue. In contrast, *adp* tissues showed an overall decrease in amino acid content, especially amino acids derived from the tricarboxylic acid (TCA) cycle, such as asparagine, aspartic acid, glutamic acid, glutamine, lysine, threonine, proline and ornithine. The citric acid content was also lower in *adp*, at the 20 dpa stage, while levels of quinic acid 3-caffeoyl, a phenolic organic acid, were higher at 6 dpa.

[0162] To maximize identification of metabolites with altered levels in *adp* fruit, an untargeted LC-MS/MS analysis using reversed phase and hydrophilic interaction liquid chromatography (HILIC) was also performed, in both positive and negative ionization modes. The placenta of 20 dpa fruit, the tissue that accumulates the highest level of starch in WT and CL lines was analyzed (FIG. 2B). Principal component analysis showed that sample replicates separated according to genotype, with WT and CL samples being closer together than to *adp* samples (FIGs. 15A-D). 243 metabolites were found showing significant changes ($FDR < 0.05$) in both, *adp* vs. WT and *adp* vs. CL comparisons, from which 75 were successfully annotated (Table 7). All listed metabolites showed significant changes in *adp* vs. both WT and CL ($FDR < 0.05$). This analysis confirmed GC/MS data and showed an increase in soluble sugars (*e.g.*, glucose, Glc-6-P and fructose) and a decrease in the content of several amino acids (*e.g.*, Asn, Asp, Ala, Gln, Glu, Orn, Phe and Pro), and amino acid derivatives (*e.g.*, spermidine and pyroglutamic acid), in *adp* (FIG. 6). Organic acids derived from the TCA cycle, such as citric acid, trans-aconitic acid and isocitric acid, were also lower in *adp*. Interestingly, there was also

an increase in nucleosides and nucleotides (*e.g.*, pseudouridine, adenine and adenosine) and their derivatives (*e.g.*, zeatin), as well as changes in the levels of stress-related metabolites. The latest included a decrease in pipecolic acid (Wang et al., “Pipecolic Acid Confers Systemic Immunity by Regulating Free Radicals,” *Sci Adv* 4:eaar4509 (2018), which is hereby incorporated by reference in its entirety) and increases in raffinose, an abiotic stress tolerance mediator (Van den Ende, “Multifunctional Fructans and Raffinose Family Oligosaccharides,” *Front Plant Sci* 4:247, which is hereby incorporated by reference in its entirety), and various compounds with reactive oxygen species quenching capacity, such as pyridoxal (Czégény et al., “Multiple Roles for Vitamin B6 in Plant Acclimation to UV-B,” *Sci Rep* 9:1259 (2019), which is hereby incorporated by reference in its entirety) and phenolics (FIG. 6).

[0163] Since the transcriptome data suggested that the *adp* mutation affected lipid metabolism, a lipidomic analysis comparing *adp* to the WT and CL fruit tissues was performed. Several classes of glycerolipids were identified and quantified using LC/MS and an in-house library (Lapidot-Cohen et al., “Liquid Chromatography-Mass Spectrometry (LC-MS)-Based Analysis for Lipophilic Compound Profiling in Plants,” *Curr Protoc Plant Biol* 5:e20109 (2020), which is hereby incorporated by reference in its entirety). PCA and hierarchical clustering analysis of the samples are shown in FIGs. 16A-F. Major differences in the glycerolipid profile of *adp* tissues were detected, which showed significant changes in 70 and 16 annotated compounds from placenta and pericarp, respectively, in both, *adp* vs. WT and *adp* vs. CL, comparisons (Table 8). *Italics* font indicates significantly higher content in *adp* vs. both WT and CL fruit (FDR<0.05), and regular font indicates significantly lower content in *adp* vs. both WT and CL fruit (FDR<0.05). Notably, an important decrease in the chloroplast membrane lipids, monogalactosyldiacylglycerols (MGDGs) and digalactosyldiacylglycerols (DGDGs), was observed in the placenta of *adp* fruit at the 20 dpa stage, the peak of starch accumulation in WT and CL lines (FIG. 7B). At the ripe stage, significant differences involved a general decrease in the degree of desaturation of MGDGs, DGDGs and sulfoquinovosyldiacylglycerols (SQDG), and changes in levels and desaturation of some phospholipids (FIG. 7B).

[0164] Mutants in starch biosynthesis have been shown to redirect carbon to lipid synthesis which accumulate as triacylglycerols (TAG) in lipid droplets (LDs) (Yu et al., “Starch Deficiency Enhances Lipid Biosynthesis and Turnover in Leaves,” *Plant Physiol* 178:118–129 (2018); Xu et al., “Upregulated Lipid Biosynthesis at the Expense of Starch Production in Potato

(*Solanum Tuberosum*) Vegetative Tissues Via Simultaneous Downregulation of ADP-Glucose Pyrophosphorylase and Sugar Dependent1 Expressions,” *Front Plant Sci.* 10:1444 (2019); each of which is hereby incorporated by reference in its entirety). Further indication of changes in lipid metabolism in *adp* was obtained by the visualization of lipid droplets in 20 dpa *adp* fruit.

5 Fruit sections stained with the fluorophore BODIPY 505/515, which primarily stains neutral storage LDs (Govender et al., “BODIPY Staining, an Alternative to the Nile Red Fluorescence Method for the Evaluation of Intracellular Lipids in Microalgae,” *Bioresour Technol* 114:507-511 (2012), which is hereby incorporated by reference in its entirety), revealed an accumulation of LDs in the *adp* septum (FIG. 7C), and to a lesser extent in the placenta (FIGs. 17A-B), while
10 they were not detected in WT and CL lines. This suggests a buildup of lipids stored as TAGs as a consequence of the starch deficiency in *adp*.

[0165] A summary of the metabolic changes in the placenta of growing *adp* fruit as a result of the starch deficiency is shown in FIG. 8.

Example 6 – Discussion of Examples 2-5

15 **[0166]** Tomato fruit development is accompanied by a transient accumulation of starch which is thought to act as a carbon reservoir to support sink strength, buffer fluctuations in energy supply, and contribute to sugar accumulation at ripening (Ruan et al., “Molecular Regulation of Seed and Fruit Set,” *Trends Plant Sci* 17:656–665 (2012); Colombié et al., “Respiration Climacteric in Tomato Fruits Elucidated by Constraint-Based Modelling,” *New*
20 *Phytol* 213:1726–1739 (2017); Roch et al., “Fruit Salad in the Lab: Comparing Botanical Species to Help Deciphering Fruit Primary Metabolism,” *Front Plant Sci* 10:836 (2019), each of which is hereby incorporated by reference in its entirety). However, despite these suggested key roles of starch, the impact that transitory starch accumulation has on transcriptional and metabolic pathways during fruit development is still unknown. Starch biosynthesis mutants in *Arabidopsis*
25 (Streb and Zeeman, “Starch Metabolism in Arabidopsis,” *The Arabidopsis Book* 10:e0160 (2012), which is hereby incorporated by reference in its entirety) and grain crop species (Baysal et al., “Inactivation of Rice Starch Branching Enzyme IIb Triggers Broad and Unexpected Changes in Metabolism by Transcriptional Reprogramming,” *PNAS* 117:26503–26512 (2020); Finegan et al., “Genetic Perturbation of the Starch Biosynthesis in Maize Endosperm Reveals
30 Sugar-Responsive Gene Networks,” *Front Plant Sci* 12:800326 (2022), each of which is hereby incorporated by reference in its entirety) have provided insight on the molecular and

physiological effects of perturbing starch metabolism, however, starch-deficient mutants have not been characterized in fleshy fruit species to date.

[0167] The identification of the *adp* mutation in tomato was investigated and found to be a consequence of a deletion in the AGPase small subunit, which renders *adp* plants unable to synthesize starch. The effect of starch deficiency on fruit growth and development was investigated, and the transcriptional and metabolic responses that are triggered in the fruit by the lack of starch accumulation were analyzed.

[0168] Surprisingly, the lack of starch biosynthesis did not cause major changes in fruit development except for an increase in size and weight (FIG. 3). One of the significant metabolic effects of the starch deficiency was the higher levels of soluble sugars, mainly glucose (FIG. 5 and FIG. 13) which can act as a signaling molecule and osmolyte to stimulate cell division and expansion, respectively (Wang and Ruan, "Regulation of Cell Division and Expansion by Sugar and Auxin Signaling," *Front Plant Sci* 4:163 (2013); Lastdrager et al., "Sugar Signals and the Control of Plant Growth and Development," *J Exp Bot* 65:799–807 (2014), each of which is hereby incorporated by reference in its entirety). Therefore, the higher soluble sugar content could be stimulating fruit growth in *adp* fruit.

[0169] Although there were only minor changes in fruit development, the lack of starch synthesis generated an important transcriptional remodeling in *adp* fruit. This was especially significant in the tissue (placenta) and developmental stages (20 dpa, MG) corresponding to higher levels of starch accumulation in WT fruit (FIGs. 2A-B and FIG. 4A). DEGs in *adp* were enriched with genes involved in small RNA biogenesis and chromatin remodeling, suggesting that changes in *adp* fruit may be the result of post-transcriptional and/or epigenetic regulation. A member of the MORC protein family, involved in chromatin remodeling (Koch et al., "MORC Proteins: Novel Players in Plant and Animal Health," *Front Plant Sci* 8:1720 (2017); Xue et al., "*Arabidopsis* MORC Proteins Function in the Efficient Establishment of RNA Directed DNA Methylation," *Nat Commun* 12:4292 (2021), each of which is hereby incorporated by reference in its entirety), was strongly upregulated in *adp* tissues at all developmental stages (FIG. 4C). *Arabidopsis* MORC mutants show modified photosynthesis efficiency accompanied by stunted growth and increased starch accumulation (van Tol et al., "An *Arabidopsis* Mutant with High Operating Efficiency of Photosystem II and Low Chlorophyll Fluorescence," *Sci Rep* 7:3314 (2017), which is hereby incorporated by reference in its entirety). This is consistent with the data

from this study showing that, in reverse, starch deficiency associates with greater *MORC* expression and fruit growth. The fact that starch content may be inversely correlated with *MORC* expression and cell growth suggests a link between sugar metabolism/signaling and *MORC*-mediated transcriptional gene silencing.

5 **[0170]** The transcriptional response to starch deficiency also involved a significant increase in expression of TOR signaling genes, including the TOR kinase and its associated proteins (FIG. 4F). The TOR pathway is involved in sugar sensing and is a key regulator integrating environmental and nutrient signals to control growth and development (Ryabova et al., “Target of Rapamycin Kinase: Central Regulatory Hub for Plant Growth and Metabolism,” *J Exp Bot* 70:2211–2216 (2019); McCready et al., “The Importance of TOR Kinase in Plant Development,” *Front Plant Sci* 11:16 (2020), each of which is hereby incorporated by reference in its entirety). Glucose upregulates the TOR pathway and glucose-TOR signaling dictates transcriptional reprogramming involving central and secondary metabolism, cell cycle, transcription, signaling, transport and protein folding (Xiong et al., “Glucose-TOR Signalling Reprograms the Transcriptome and Activates Meristems,” *Nature* 496:181–186 (2013), which is hereby incorporated by reference in its entirety). The repression of TOR expression in *Arabidopsis* caused an increase in starch content (Caldana et al., “Systemic Analysis of Inducible Target of Rapamycin Mutants Reveal a General Metabolic Switch Controlling Growth in *Arabidopsis thaliana*,” *Plant J* 73:897–909 (2013), which is hereby incorporated by reference in its entirety), and it has recently been shown that, in algae, starch deficiency upregulates TOR activity (Mallén-Ponce et al., “Photosynthetic Assimilation of CO₂ Regulates TOR Activity,” *PNAS* 119:e2115261119 (2022), which is hereby incorporated by reference in its entirety), suggesting a link between the TOR pathway and starch metabolism. These results indicate that part of the transcriptional changes in *adp* might be mediated by the glucose-TOR signaling pathway and triggered by the increase in glucose content during fruit growth (FIG. 5; FIG. 13; Table 6). Significant gene expression changes in *adp* also included upregulation of genes encoding cell cycle related proteins (e.g. cyclins, DNA repair proteins, myosins, formins, actin-cross-linking protein; FIG. 4, Table 4). The potential stimulation of cell cycle in *adp* is also supported by an increase in trans-zeatin (FIG. 6), the prevalent plant cytokinin, in the placenta of *adp* fruit. Consistent with this observation, higher levels of cytokinin have been found in AGPase-deficient pea embryos (Weigelt et al., “ADP-Glucose Pyrophosphorylase-Deficient Pea

Embryos Reveal Specific Transcriptional and Metabolic Changes of Carbon-Nitrogen Metabolism and Stress Responses,” *Plant Physiol* 149:395–411 (2009), which is hereby incorporated by reference in its entirety). These results suggest a positive regulation of the cell cycle, growth promotion, and stimulation of cytokinin-mediated cell proliferation, possibly through an activation of the TOR pathway in *adp*.

[0171] Ripening-related transcriptional changes in *adp* fruit which occurred mainly in the pericarp and included downregulation of genes involved in ethylene biosynthesis and of multiple cell wall modifying genes was also observed (FIG. 12) associated with ripening (Quinet et al., “Tomato Fruit Development and Metabolism,” *Front Plant Sci.* 10:1554 (2019), which is hereby incorporated by reference in its entirety). These changes, together with the slight delay of *adp* fruit to reach the ripening phase, further suggest that starch hydrolysis at the end of the growth period may influence the onset of ripening (Colombié et al., “Respiration Climacteric in Tomato Fruits Elucidated by Constraint-Based Modelling,” *New Phytol* 213:1726–1739 (2017), which is hereby incorporated by reference in its entirety). However, the absence of major changes in fruit ripening capability in *adp* indicates that starch hydrolysis is not required for the initiation and completion of the ripening process in tomato.

[0172] Changes in the metabolite composition of *adp* fruit indicate that the disruption of starch synthesis causes an important redirection of metabolic flux (FIG. 8, FIGs. 14A-C, and FIGs. 15A-D). During fruit growth, higher levels of soluble sugars in *adp* were observed together with an increase in glucose-6-P, and a decrease in amino acids and TCA cycle organic acids (FIG. 5 and FIG. 6). This could be caused by the redirection of the acetyl CoA pool towards fatty acid biosynthesis, and/or to an elevated metabolism of TCA cycle intermediates, and amino acids, to support the higher fruit growth in *adp*. The overall decrease in amino acids in *adp*, contrasts with the increase in amino acid levels observed in rice starch mutants (Baysal et al., “Inactivation of Rice Starch Branching Enzyme IIb Triggers Broad and Unexpected Changes in Metabolism by Transcriptional Reprogramming,” *PNAS* 117:26503–26512 (2020), which is hereby incorporated by reference in its entirety). In pea embryos, the reduction in AGPase expression caused a decrease in levels of certain amino acids, while an increase in others (Weigelt et al., “ADP-Glucose Pyrophosphorylase-Deficient Pea Embryos Reveal Specific Transcriptional and Metabolic Changes of Carbon-Nitrogen Metabolism and Stress Responses,” *Plant Physiol* 149:395–411 (2009), which is hereby incorporated by reference in its entirety).

Therefore, it is likely that different species, tissues, organs, and developmental stages differ in how carbon flux is redirected, and which metabolite pools are affected in absence of starch synthesis. These results also suggest that metabolic adjustments in *adp* involve channeling the excess of sugars into specific branches fueled by the glycolytic pathway. For example, the downregulation of transketolase and ribulose-phosphate 3-epimerase observed in *adp* could result in glucose-6-P and ribulose-5-P being directed towards nucleotide and nucleoside synthesis, causing an increase in the levels of these metabolites (FIG. 6 and FIG. 8).

[0173] Disruption of starch synthesis in *adp* also resulted in the remodeling of the lipid metabolism. Metabolomics data highlighted substantial changes in the profile of glycerolipids, the main structural components of cellular membranes (Yu et al., “Mechanisms and Functions of Membrane Lipid Remodeling in Plants,” *Plant J* 107:37–53 (2021), which is hereby incorporated by reference in its entirety) which in the growing fruit (20 dpa) was reflected in a strong decrease in MGDG and DGDG and, in ripe tissue, by a decrease in the level of membrane lipid unsaturation (FIG. 7B). The lower expression of a glycerol 3-phosphate acyltransferase and/or the potential redirection of glycerolipid biosynthesis towards phosphatidic acid (PA), due to increased expression of LPAAT and DGK encoding genes (FIG. 7A, FIG. 8), could contribute to the decrease in MGDG and DGDG. This transcriptome data also suggests upregulation of the biosynthesis of sphingolipids, long chain fatty acids, and sterols in *adp* (FIG. 7A). Whether this translates into elevated levels of these compounds will need to be validated using a targeted metabolite analysis approach. It was also observed an enhanced accumulation of LD in the septum of *adp* fruit (FIG. 7C, Supplemental FIG. S9), indicative of increased TGA levels. This underscores the redirection of carbon skeletons towards fatty acid and lipid biosynthesis due to a disruption in starch biosynthesis. Although both septum and placenta accumulate starch in WT fruit (FIG. 2A), LDs were present preferentially in the septum, suggesting tissue specificity in the capacity for TGA accumulation (Lu et al., “Spatial Analysis of Lipid Metabolites and Expressed Genes Reveals Tissue-Specific Heterogeneity of Lipid Metabolism in High- and Low-Oil Brassica Napus L. Seeds,” *Plant J* 94:915–932 (2018), which is hereby incorporated by reference in its entirety).

[0174] A striking phenotypic trait of *adp* fruit was their total lack of BER symptoms even when subjected to water stress, which is a common trigger of BER (FIG. 3E-F; FIG. 2A-B). In tomato, as well as other fruit crops (*e.g.*, peppers, squash, cucumber, and melon), environmental

stresses cause BER, characterized by water-soaked tissues and necrosis. Calcium deficiency (Ho and White, "A Cellular Hypothesis for the Induction of Blossom-End Rot in Tomato Fruit," *Ann Bot* 95:571–581 (2005); De Freitas et al., "Role of Pectin Methylesterases in Cellular Calcium Distribution and Blossom-End Rot Development in Tomato Fruit," *Plant J* 71:824–835 (2012), each of which is hereby incorporated by reference in its entirety), and increased ROS production (Saure, "Why Calcium Deficiency is not the Cause of Blossom-End Rot in Tomato and Pepper Fruit – A Reappraisal," *Sci Hortic* 174:151–154 (2014); De Freitas et al., "Role of Pectin Methylesterases in Cellular Calcium Distribution and Blossom-End Rot Development in Tomato Fruit," *Plant J* 71:824–835 (2012); Hagassou et al., "Blossom End-Rot in Tomato (*Solanum lycopersicum* L.): A Multi-Disciplinary Overview of Inducing Factors and Control Strategies," *Scientia Horticulturae* 249: 49–58 (2019), each of which is hereby incorporated by reference in its entirety) have been suggested as the origins of BER. However, the molecular mechanisms underlying this physiological disorder are not understood and still a matter of debate (Topcu et al., "Blossom-End Rot: A Century-Old Problem in Tomato (*Solanum lycopersicum* L.) and Other Vegetables," *Mol Hort* 2:1 (2022); Hagassou et al., "Blossom End-Rot in Tomato (*Solanum lycopersicum* L.): A Multi-Disciplinary Overview of Inducing Factors and Control Strategies," *Scientia Horticulturae* 249: 49–58 (2019), each of which is hereby incorporated by reference in its entirety). A link with carbohydrate metabolism has also been suggested after observations of higher levels of symplastic starch in pepper fruits affected by BER (Turhan et al., "Blossom-End Rot is Associated with Impairment of Sugar Metabolism and Growth of Pepper (*Capsicum Annuum* L.) Fruits," *J Hortic Sci Biotechnol* 81:921–927 (2006), which is hereby incorporated by reference in its entirety). The data disclosed herein suggest that sugar metabolism plays a central role in BER resistance. In *adp* this resistance could potentially be an indirect consequence of TOR-mediated activation of cell growth and survival (Gonzalez and Rallis, "The TOR Signaling Pathway in Spatial and Temporal Control of Cell Size and Growth," *Front Cell and Dev Biol* 5:61 (2017), which is hereby incorporated by reference in its entirety) (FIG. 4F, Table 5), together with the promotion of abiotic stress responses and stress adaptation (Fu et al., "Target of Rapamycin Signaling in Plant Stress Responses," *Plant Physiol* 182:1613–1623 (2020); Haq et al., "Roles of TOR Signaling in Nutrient Deprivation and Abiotic Stress," *J Plant Physiol* 274:153716 (2022), each of which is hereby incorporated by reference in its entirety). Changes in *adp* fruit included an upregulation of genes encoding

enzymes involved in suppressing oxidative damage, and transcription factors involved in the adaptive response to various abiotic stresses (FIG. 4F). Similarly, metabolites involved in tolerance to stress and ROS quenching, such as raffinose, phenolics or pyridoxal, showed increased levels in *adp* (FIG. 6, Table 6). In addition to an up-regulation of stress-related

pathways, the lipid composition changes observed in *adp* could also lead to a better protection of fruit tissues from stress, therefore contributing to the BER resistant phenotype. Lipid remodeling of cell membranes is a critical mechanism countering loss of membrane integrity and cell death during stress responses (Yu et al., “Mechanisms and Functions of Membrane Lipid Remodeling in Plants,” *Plant J* 107:37–53 (2021), which is hereby incorporated by reference in its entirety).

The lipid-related changes in *adp* mimic lipid-remodeling responses triggered by abiotic stresses, such as cold, heat or drought (FIG. 7B-C). These include a reduction in MGDG levels, increase in TGA accumulation and a decrease in the degree of membrane lipid unsaturation (de Vries. and Ischebeck, “Ties Between Stress and Lipid Droplets Pre-Date Seeds,” *Trends Plant Sci* 25:1203–1214 (2020); Yu et al., “Mechanisms and Functions of Membrane Lipid Remodeling in Plants,” *Plant J* 107:37–53 (2021), each of which is hereby incorporated by reference in its entirety).

Both TGA accumulation and a decrease in the degree of membrane lipid unsaturation have been associated with heat stress in tomato fruit (Almeida et al., “A Transcriptomic, Metabolomic and Cellular Approach to the Physiological Adaptation of Tomato Fruit to High Temperature,” *Plant, Cell & Environ* 44:2211–2229 (2021), which is hereby incorporated by reference in its entirety).

Furthermore, genes involved in PA formation and sphingolipid biosynthesis (FIG. 7A, Table 5), both with a role during abiotic stress responses (Yao and Xue, “Phosphatidic Acid Plays Key Roles Regulating Plant Development and Stress Responses,” *J Integr Plant Biol* 60:851–863 (2018); Huby et al., “Sphingolipids: Towards an Integrated View of Metabolism During the Plant Stress Response,” *New Phytol* 225:659–670 (2020); each of which is hereby incorporated by reference in its entirety), were expressed at higher levels in *adp* growing fruit.

[0175] In summary, these results indicate that the starch deficiency in *adp* causes major transcriptional and metabolic adjustments affecting core metabolic pathways (FIG. 8). The lack of carbon flux into starch generates a greater abundance of sugars, increased carbon reallocation towards lipid biosynthesis, and modification of gene expression that leads to enhanced growth and stress-protection responses. This study offers insights into the significance of starch metabolism for fruit growth and ripening and highlights the link between sugar metabolism and

resistance to cellular damage in fruit tissues, which can open new paths to improve fruit yield and quality under abiotic stress conditions.

[0176] *Accession Numbers.* The accession number of the genes mentioned in Examples 1-6 can be found in Tables 9-12. Sequence data can be found in the Solanaceae Genomics

- 5 Network (SGN) database (solgenomics.net/organism/Solanum_lycopersicum/genome; ITAG Release 3.2).

Table 3. List of DEGs Shared Between Pericarp and Placenta at Least in One Developmental Stage

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	UP/DOWN	Developmental stages
Solyc07g022920	Solyc07g022920.3.1	BSD domain-containing family protein (AHRD V3.3 *** B9IBP6_POPTR)	UP	6 dpa, 20 dpa, MG, Ripe
Solyc06g071580	Solyc06g071580.3.1	MORC family CW-type zinc finger protein 4 (AHRD V3.3 *** A0A0B0PTV2_GOSAR)	UP	6 dpa, 20 dpa, MG, Ripe
Solyc07g064380	Solyc07g064380.3.1	serine/threonine-protein phosphatase 7 long form-like protein (AHRD V3.3 *-* AT1G32120.1)	UP	6 dpa, 20 dpa, MG
Solyc07g056140	Solyc07g056140.3.1	ADP-glucose pyrophosphorylase small subunit	DOWN	6 dpa, 20 dpa, MG
Solyc06g035940	Solyc06g035940.3.1	Homeobox leucine zipper protein (AHRD V3.3 *** A0A072TNH2_MEDTR)	DOWN	6 dpa, 20 dpa
Solyc06g033850	Solyc06g033850.3.1	Dehydration responsive element-binding factor protein (AHRD V3.3 *-* A0A0K0K9Y3_ELECO)	UP	20 dpa, MG
Solyc08g016440	Solyc08g016440.3.1	Polynucleotidyl transferase, ribonuclease H-like superfamily protein (AHRD V3.3 --* AT2G13980.1)	UP	6 dpa
Solyc02g091990	Solyc02g091990.3.1	l-aminocyclopropane-1-carboxylate synthase 3	UP	6 dpa
Solyc03g058910	Solyc03g058910.3.1	Pectate lyase (AHRD V3.3 *** M1A3P9_SOLTU)	DOWN	6 dpa
Solyc12g087830	Solyc12g087830.2.1	MADS-box transcription factor (AHRD V3.3 *** F1T119_9ERIC)	DOWN	6 dpa
Solyc02g093600	Solyc02g093600.3.1	Class I heat shock protein (AHRD V3.3 *** F4YBC5_SOLNI)	UP	20 dpa
Solyc06g076560	Solyc06g076560.2.1	17.6 kD class I small heat shock protein	UP	20 dpa
Solyc03g082420	Solyc03g082420.3.1	Heat shock protein (AHRD V3.3 *** A9QVH3_9FABA)	UP	20 dpa
Solyc03g113930	Solyc03g113930.2.1	Heat-shock protein, putative (AHRD V3.3 *** B9S5K5_RICCO)	UP	20 dpa
Solyc07g056510	Solyc07g056510.3.1	Glutathione S-transferase (AHRD V1 ***** D3Y4H6_9ROSI)	UP	20 dpa
Solyc02g071820	Solyc02g071820.3.1	Receptor-like protein kinase (AHRD V3.3 *** B9IIR1_POPTR)	UP	20 dpa
Solyc11g020330	Solyc11g020330.1.1	leer-sHSP small heat shock protein	UP	20 dpa
Solyc06g009190	Solyc06g009190.3.1	Pectinesterase (AHRD V3.3 *** K4C3U9_SOLLC)	DOWN	20 dpa
Solyc04g064690	Solyc04g064690.3.1	Peroxidase (AHRD V3.3 *** K4BT60_SOLLC)	DOWN	20 dpa
Solyc02g084280	Solyc02g084280.3.1	Nuclear pore complex protein Nup98b (AHRD V3.3 *-* W6JLG1_NICBE)	UP	MG
Solyc10g076260	Solyc10g076260.2.1	Regulatory-associated protein of TOR protein (AHRD V3.3 *-* G7KW32_MEDTR)	UP	MG
Solyc07g032180	Solyc07g032180.3.1	Abhydrolase domain-containing protein 4 (AHRD V3.3 *** A0A0B2SN17_GLYSO)	UP	MG

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	UP/DOWN	Developmental stages
Solyc07g025490	Solyc07g025490.2.1	OSBP(oxysterol binding protein)-related protein 4B (AHRD V3.3 --* AT4G25850.3)	UP	MG
Solyc05g056040	Solyc05g056040.3.1	Auxin Response Factor 24	UP	MG
Solyc11g020960	Solyc11g020960.2.1	Proteinase inhibitor II (AHRD V3.3 *- B3F0C1_TOBAC)	UP	MG
Solyc06g011530	Solyc06g011530.3.1	Hydroxymethylglutaryl-CoA lyase (AHRD V3.3 *- W9QRW1_9ROSA)	UP	MG
Solyc09g066080	Solyc09g066080.2.1	Protein BREAST CANCER SUSCEPTIBILITY 1-like protein (AHRD V3.3 *- W9R323_9ROSA)	UP	MG
Solyc09g010320	Solyc09g010320.3.1	Mitochondrial fission protein ELM1 (AHRD V3.3 *** A0A199UV44_ANACO)	UP	MG
Solyc03g059150	Solyc03g059150.3.1	Ion channel DMI1 (AHRD V3.3 *** DMI1_MEDTR)	UP	MG
Solyc02g082770	Solyc02g082770.3.1	Phosphoinositide phosphatase family protein (AHRD V3.3 *- AT3G51460.1)	UP	MG
Solyc02g091030	Solyc02g091030.3.1	Nuclear transcription factor Y subunit C-2 (AHRD V3.3 *- W9SQ52_9ROSA)	UP	MG
Solyc11g008530	Solyc11g008530.2.1	Dicer-like 2d	UP	MG
Solyc02g088950	Solyc02g088950.2.1	Superoxide dismutase [Cu-Zn] (AHRD V3.3 --* A9NTC6_PICSI)	UP	MG
Solyc05g013300	Solyc05g013300.1.1	Pseudomonas syringae pv tomato resis.	UP	MG
Solyc03g078570	Solyc03g078570.3.1	Ras-related protein (AHRD V3.3 *** W9QNC0_9ROSA)	UP	MG
Solyc04g050760	Solyc04g050760.3.1	U11/U12 small nuclear ribonucleoprotein (AHRD V3.3 *** AT3G04160.3)	UP	MG
Solyc08g023570	Solyc08g023570.2.1	WD repeat-containing protein 48 (AHRD V3.3 *- A0A1D1X150_9ARAE)	UP	MG
Solyc07g053250	Solyc07g053250.3.1	F-box protein family (AHRD V3.3 --* A0A151SU61_CAJCA)	UP	MG
Solyc11g030550	Solyc11g030550.2.1	Cyclin family protein (AHRD V3.3 *- AT5G06150.2)	UP	MG
Solyc08g061880	Solyc08g061880.2.1	Peroxisome biogenesis factor 10 (AHRD V3.3 *- B9U2H6_TOBAC)	UP	MG
Solyc01g104160	Solyc01g104160.3.1	arginine/glutamate-rich 1 protein (AHRD V3.3 *** AT1G10890.2)	UP	MG
Solyc04g057990	Solyc04g057990.3.1	Zinc finger transcription factor 33	UP	MG
Solyc07g052720	Solyc07g052720.3.1	MADS-box transcription factor (AHRD V3.3 *** A0A072UYG7_MEDTR)	UP	MG
Solyc02g089010	Solyc02g089010.2.1	Receptor protein kinase, putative (AHRD V3.3 *- B9RXG1_RICCO)	UP	MG
Solyc09g074730	Solyc09g074730.2.1	Homeobox protein LUMINIDEPENDENS (AHRD V3.3 *** A0A0B2S9W0_GLYSO)	UP	MG
Solyc01g067570	Solyc01g067570.3.1	Adaptin family protein (AHRD V3.3 --* AT4G23460.1)	UP	MG
Solyc01g090860	Solyc01g090860.3.1	Nucleotidyltransferase family protein (AHRD V3.3 *** AT4G00060.4)	UP	MG
Solyc02g067270	Solyc02g067270.2.1	RING/U-box superfamily protein (AHRD V3.3 *- AT1G26800.1)	UP	MG

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	UP/DOWN	Developmental stages
Solyc10g076270	Solyc10g076270.2.1	Katanin p80 WD40 repeat-containing subunit B1 homolog (AHRD V3.3 *-*	UP	MG
Solyc12g027540	Solyc12g027540.2.1	IIHS93_BRAD1 Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 *-*	UP	MG
Solyc07g032170	Solyc07g032170.3.1	A0A151RV17_CAJCA alpha/beta-Hydrolases superfamily protein (AHRD V3.3 *-*	UP	MG
Solyc02g036290	Solyc02g036290.3.1	malonyl-CoA decarboxylase family protein (AHRD V3.3 *-*	UP	MG
Solyc02g091620	Solyc02g091620.2.1	Nuclear pore complex protein (AHRD V3.3 *-*	UP	MG
Solyc02g084285	Solyc02g084285.1.1	Nuclear pore complex protein (AHRD V3.3 *-*	UP	MG
Solyc05g047540	Solyc05g047540.3.1	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 ***	UP	MG
Solyc01g104410	Solyc01g104410.3.1	A0A061GY15_THECC Sterol glucosyltransferase-like protein (AHRD V3.3 ***	UP	MG
Solyc01g007980	Solyc01g007980.3.1	Protein kinase family protein (AHRD V3.3 ***	UP	MG
Solyc01g016460	Solyc01g016460.3.1	C6ZRU6_SOYBN Phototropic-responsive NPH3 family protein (AHRD V3.3 *-*	UP	MG
Solyc02g078490	Solyc02g078490.3.1	TSA: Wollemia nobilis Ref. Wollemi_Transcript_5456_2539 transcribed RNA sequence (AHRD V3.3 *-*	UP	MG
Solyc12g088920	Solyc12g088920.2.1	A0A0C9RPH5_9SPER Calcineurin-like metallo-phosphoesterase superfamily protein (AHRD V3.3 ***	UP	MG
Solyc04g016550	Solyc04g016550.3.1	AT4G11800.1 Folypolyglutamate synthase (AHRD V3.3 ***	UP	MG
Solyc00g005094	Solyc00g005094.1.1	FPGS2_ARATH Glucose-6-phosphate 1-dehydrogenase 3, chloroplastic (AHRD V3.3 *-*	UP	MG
Solyc01g087410	Solyc01g087410.3.1	G6PD3_ARATH RING/FYVE/PHD zinc finger protein, putative (AHRD V3.3 *-*	UP	MG
Solyc02g005510	Solyc02g005510.3.1	A0A072UJ97_MEDTR Transcriptional coactivator/pterin dehydratase (AHRD V3.3 ***	UP	MG
Solyc11g008540	Solyc11g008540.2.1	AT1G29810.1 Dicer-like 2b	UP	MG
Solyc02g085220	Solyc02g085220.3.1	Vacuolar sorting protein 39 (AHRD V3.3 ***	UP	MG
Solyc02g067285	Solyc02g067285.1.1	AT4G36630.1 Structural maintenance of chromosomes protein (AHRD V3.3 *-*	UP	MG
Solyc01g106947	Solyc01g106947.1.1	A0A068U3R5_COECA Exocyst complex component SEC3A (AHRD V3.3 *-*	UP	MG
Solyc01g108410	Solyc01g108410.2.1	A0A1D1XZ59_9ARAE Pentatricopeptide repeat-containing protein (AHRD V3.3 ***	UP	MG
Solyc01g103610	Solyc01g103610.3.1	A0A103XM66_CYNCS Disease resistance protein (AHRD V3.3 ***	UP	MG
Solyc03g059160	Solyc03g059160.2.1	A0A103XDQ0_CYNCS Ion channel CASTOR (AHRD V3.3 *-*	UP	MG
Solyc01g097500	Solyc01g097500.3.1	CASTO_LOTJA LSTK-1-like kinase	UP	MG

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	UP/DOWN	Developmental stages
Solyc10g006210	Solyc10g006210.2.1	Endoribonuclease Dicer (AHRD V3.3 *- * A0A0B0P4A5_GOSAR)	UP	MG
Solyc05g025905	Solyc05g025905.1.1	Starch synthase, chloroplastic/amyloplastic (AHRD V3.3 *- * K4BBV6_SOLLC)	UP	MG
Solyc07g053255	Solyc07g053255.1.1	F-box protein (AHRD V3.3 *- * G7KUJ4_MEDTR)	UP	MG
Solyc01g058260	Solyc01g058260.3.1	Poly(A) polymerase, putative (AHRD V3.3 *** B9RZU0_RICCO)	UP	MG
Solyc01g057477	Solyc01g057477.1.1	mediator of RNA polymerase II transcription subunit 15a-like protein (AHRD V3.3 *- * AT1G15780.3)	UP	MG
Solyc06g066460	Solyc06g066460.3.1	Poly(A) polymerase (AHRD V3.3 *- * A0A0B2Q923_GLYSO)	UP	MG
Solyc08g060970	Solyc08g060970.3.1	polygalacturonase AF118567	UP	MG
Solyc04g072010	Solyc04g072010.3.1	carboxypeptidase D (AHRD V3.3 *** AT1G71696.2)	UP	MG
Solyc02g089515	Solyc02g089515.1.1	NAD(P)H-quinone oxidoreductase subunit K, chloroplastic (AHRD V3.3 *- * NDHK_NUPAD)	UP	MG
Solyc09g014415	Solyc09g014415.1.1	BTB/POZ domain-containing protein (AHRD V3.3 *** AT3G09030.1)	UP	MG
Solyc04g016010	Solyc04g016010.3.1	Thioredoxin reductase (AHRD V3.3 *** M1C6N0_SOLTU)	UP	MG
Solyc01g106205	Solyc01g106205.1.1	myosin-M heavy protein (AHRD V3.3 *- * AT3G54060.2)	UP	MG
Solyc06g071620	Solyc06g071620.3.1	U5 small nuclear ribonucleoprotein helicase (AHRD V3.3 *** AT1G20960.2)	UP	MG
Solyc12g077460	Solyc12g077460.2.1	WD-40 repeat family protein / beige-like protein (AHRD V3.3 *- * AT2G45540.6)	UP	MG
Solyc03g058930	Solyc03g058930.3.1	Hypersensitive-induced response protein (AHRD V3.3 *** Q6UNT3_CUCSA)	UP	MG
Solyc05g016395	Solyc05g016395.1.1	Rhomboid family protein (AHRD V3.3 *** B9HXC8_POPTR)	UP	MG
Solyc02g082613	Solyc02g082613.1.1	Phototropic-responsive NPH3 family protein (AHRD V3.3 *- * AT1G03010.3)	UP	MG
Solyc02g090500	Solyc02g090500.3.1	Phenylalanine ammonia-lyase (AHRD V3.3 *- * D3K195_9ROSA)	UP	MG
Solyc05g005620	Solyc05g005620.3.1	RNA-binding 25 (AHRD V3.3 *** A0A0B0MSI7_GOSAR)	UP	MG
Solyc06g066473	Solyc06g066473.1.1	Poly(A) polymerase (AHRD V3.3 *- * W9RV28_9ROSA)	UP	MG
Solyc12g036800	Solyc12g036800.1.1	Receptor like protein (AHRD V3.3 *- * A2V882_TOBAC)	UP	MG
Solyc04g014400	Solyc04g014400.3.1	LRR receptor-like kinase (AHRD V3.3 *- * A0A072UI52_MEDTR)	UP	MG
Solyc02g089490	Solyc02g089490.3.1	Plant Tudor-like RNA-binding protein (AHRD V3.3 *- * AT4G32440.3)	UP	MG
Solyc06g011550	Solyc06g011550.3.1	Myosin-11 (AHRD V3.3 *- * MYO11_ARATH)	UP	MG
Solyc02g084315	Solyc02g084315.1.1	embryo defective 2410 (AHRD V3.3 *- * AT2G25660.4)	UP	MG
Solyc05g011970	Solyc05g011970.3.1	Cytochrome P450 (AHRD V3.3 *** A0A103XV52_CYNCS)	UP	MG
Solyc02g084300	Solyc02g084300.1.1	CTP synthase (AHRD V3.3 *- * M1B2B1_SOLTU)	UP	MG

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	UP/DOWN	Developmental stages
Solyc02g021060	Solyc02g021060.3.1	Uracil-DNA glycosylase (AHRD V3.3 *** K4B4V6_SOLLCC)	UP	MG
Solyc01g057340	Solyc01g057340.3.1	WD-40 repeat family protein-2 (AHRD V3.3 --* A0A172CCS3_POPTO)	UP	MG
Solyc03g120910	Solyc03g120910.3.1	Homeobox leucine-zipper protein (AHRD V3.3 *** Q76CL1_ZINVI)	UP	MG
Solyc02g088958	Solyc02g088958.1.1	telomeric repeat binding protein 1 (AHRD V3.3 --* AT5G59430.5)	UP	MG
Solyc11g012550	Solyc11g012550.2.1	F-box family protein, putative (AHRD V3.3 *** A0A061GHK4_THECC)	UP	MG
Solyc09g055570	Solyc09g055570.3.1	Leucine-rich repeat protein kinase family protein (AHRD V3.3 *** AT1G06840.1)	UP	MG
Solyc07g007840	Solyc07g007840.2.1	SPOC domain / Transcription elongation factor S-II protein (AHRD V3.3 --* AT2G25640.1)	UP	MG
Solyc03g033825	Solyc03g033825.1.1	Ubiquitin-related modifier 1 homolog (AHRD V3.3 --* URM1_ORYSJ)	UP	MG
Solyc10g006190	Solyc10g006190.3.1	Cell differentiation protein rcd1, putative (AHRD V3.3 *** B9STZ0_RICCO)	UP	MG
Solyc04g005540	Solyc04g005540.3.1	Disease resistance protein (NBS-LRR class) family (AHRD V3.3 --* AT5G38350.1)	UP	MG
Solyc02g082767	Solyc02g082767.1.1	ARM repeat superfamily protein (AHRD V3.3 --* AT3G60740.3)	UP	MG
Solyc02g067275	Solyc02g067275.1.1	Dehydration-responsive protein RD22 (AHRD V3.3 --* K7XKT0_SOLTU)	UP	MG
Solyc00g005040	Solyc00g005040.3.1	Potassium channel (AHRD V3.3 --* D0EM91_9ROSI)	UP	MG
Solyc02g084310	Solyc02g084310.2.1	CTP synthase (AHRD V3.3 --* M1BXT3_SOLTU)	UP	MG
Solyc07g055020	Solyc07g055020.3.1	F-box protein family (AHRD V3.3 *** A0A151SU61_CAJCA)	UP	MG
Solyc06g060140	Solyc06g060140.3.1	Kinesin-like protein (AHRD V3.3 *** A0A061FI31_THECC)	UP	MG
Solyc01g081320	Solyc01g081320.3.1	Pentatricopeptide repeat-containing protein, putative (AHRD V3.3 *** B9R1S7_RICCO)	UP	MG
Solyc03g115190	Solyc03g115190.3.1	Phosphoglycerate mutase family protein (AHRD V3.3 --* AT5G64460.5)	UP	MG
Solyc03g111410	Solyc03g111410.3.1	B3 domain-containing protein (AHRD V3.3 --* W9S5V1_9ROSA)	UP	MG
Solyc11g030475	Solyc11g030475.1.1	Mannosyltransferase (AHRD V3.3 --* K4AYT1_SOLLCC)	UP	MG
Solyc01g016455	Solyc01g016455.1.1	Ubiquitin carboxyl-terminal hydrolase-related protein (AHRD V3.3 --* AT3G47890.2)	UP	MG
Solyc02g021063	Solyc02g021063.1.1	Unknown protein (AHRD V3.3)	UP	MG
Solyc04g080390	Solyc04g080390.3.1	plasma membrane fusion protein (AHRD V3.3 *** AT5G42765.1)	UP	MG
Solyc02g092600	Solyc02g092600.3.1	Phototropic-responsive NPH3 family protein (AHRD V3.3 --* A0A061DGZ5_THECC)	UP	MG
Solyc02g082763	Solyc02g082763.1.1	Phosphoinositide phosphatase family protein (AHRD V3.3 --* AT5G66020.1)	UP	MG

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	UP/DOWN	Developmental stages
Solyc07g008475	Solyc07g008475.1.1	Subtilisin-like protease (AHRD V3.3 *-# A0A1D1Z5J1_9ARAE)	UP	MG
Solyc03g080010	Solyc03g080010.3.1	DNA mismatch repair protein MutS2-like (AHRD V3.3 *** Q9LVW1_ARATH)	UP	MG
Solyc05g021535	Solyc05g021535.1.1	calmodulin-binding transcription activator (AHRD V3.3 --# AT3G16940.3)	UP	MG
Solyc02g090505	Solyc02g090505.1.1	haloacid dehalogenase-like hydrolase family protein (AHRD V3.3 *-# AT1G56500.2)	UP	MG
Solyc05g021510	Solyc05g021510.2.1	Amino acid/polyamine transporter 1 (AHRD V3.3 --# A0A124SH48_CYNCS)	UP	MG
Solyc12g005090	Solyc12g005090.2.1	Vacuolar protein sorting-associated protein 35 (AHRD V3.3 *** V4V8H5_9ROSI)	UP	MG
Solyc05g014275	Solyc05g014275.1.1	HAT dimerisation domain-containing protein-like (AHRD V3.3 *-# C8TFH5_ORYSI)	UP	MG
Solyc01g080310	Solyc01g080310.3.1	Pentatricopeptide repeat-containing protein family (AHRD V3.3 *** A0A151TET9_CAJCA)	UP	MG
Solyc06g076253	Solyc06g076253.1.1	DCD (Development and cell death) domain protein (AHRD V3.3 *-# A0A072V4A1_MEDTR)	UP	MG
Solyc02g066940	Solyc02g066940.3.1	Protein RIK-like protein (AHRD V3.3 *** A0A0B0MTZ1_GOSAR)	UP	MG
Solyc02g081620	Solyc02g081620.3.1	Zinc finger family protein (AHRD V3.3 *** B9GY13_POPTR)	UP	MG
Solyc06g076230	Solyc06g076230.1.1	Zinc finger CCCH domain-containing protein 19 (AHRD V3.3 --# C3H19_ORYSJ)	UP	MG
Solyc02g088940	Solyc02g088940.3.1	CTP synthase family protein (AHRD V3.3 *-# AT1G30820.1)	UP	MG
Solyc07g062900	Solyc07g062900.3.1	Protein yippe-like (AHRD V3.3 *-# A0A0V0H2B2_SOLCH)	UP	MG
Solyc02g088952	Solyc02g088952.1.1	DNA mismatch repair protein mutL (AHRD V3.3 --# A0A0B2SBZ1_GLYSO)	UP	MG
Solyc01g087290	Solyc01g087290.3.1	tRNA-dihydrouridine synthase (AHRD V3.3 *** A0A0V018M3_SOLCH)	UP	MG
Solyc03g071533	Solyc03g071533.1.1	catalase 3 (AHRD V3.3 --# AT1G20620.6)	UP	MG
Solyc02g085315	Solyc02g085315.1.1	Sec14p-like phosphatidylinositol transfer family protein (AHRD V3.3 --# A0A061DH70_THECC)	UP	MG
Solyc01g006000	Solyc01g006000.3.1	GPI mannosyltransferase 2 (AHRD V3.3 *** W9S353_9ROSA)	UP	MG
Solyc01g108973	Solyc01g108973.1.1	Sorting nexin-16 (AHRD V3.3 *-# W9R163_9ROSA)	UP	MG
Solyc11g045110	Solyc11g045110.2.1	Sucrose-phosphate synthase family protein (AHRD V3.3 *** AT4G10120.3)	UP	MG
Solyc12g036793	Solyc12g036793.1.1	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *-# AT4G08850.1)	UP	MG
Solyc05g014100	Solyc05g014100.2.1	F-box family protein (AHRD V3.3 --# AT3G06240.1)	UP	MG
Solyc05g021530	Solyc05g021530.2.1	Alcohol dehydrogenase (AHRD V3.3 --# Q4LAW8_CAPCH)	UP	MG
Solyc02g089510	Solyc02g089510.3.1	UDP-Glycosyltransferase superfamily protein (AHRD V3.3 --# AT3G22250.1)	UP	MG

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	UP/DOWN	Developmental stages
Solyc02g088945	Solyc02g088945.1.1	DNA mismatch repair protein MLH3-like protein (AHRD V3.3 --* A0A0X7YCF6_SOLITU)	UP	MG
Solyc05g021555	Solyc05g021555.1.1	Alcohol dehydrogenase (AHRD V3.3 *** Q4LAW8_CAPCH)	UP	MG
Solyc02g089530	Solyc02g089530.3.1	AMP-dependent synthetase and ligase family protein (AHRD V3.3 --* AT5G35930.3)	UP	MG
Solyc06g011540	Solyc06g011540.3.1	Myosin (AHRD V3.3 *-* W5ZT55_MAIZE)	UP	MG
Solyc01g034150	Solyc01g034150.3.1	DNA polymerase eta (AHRD V3.3 *** A0A0B2R9V1_GLYSO)	UP	MG
Solyc05g021550	Solyc05g021550.2.1	Sister-chromatid cohesion protein 3 (AHRD V3.3 *-* D7M8Q0_ARALL)	UP	MG
Solyc03g117370	Solyc03g117370.3.1	TOPELESS-related 1 (AHRD V3.3 *-* AT1G80490.3)	UP	MG
Solyc06g018004	Solyc06g018004.1.1	tetraspanin10 (AHRD V3.3 --* AT1G63260.6)	UP	MG
Solyc03g059110	Solyc03g059110.1.1	LOW QUALITY:AP2/B3-like transcriptional factor family protein (AHRD V3.3 --* AT3G11580.3)	UP	MG
Solyc04g080285	Solyc04g080285.1.1	Pentatricopeptide repeat (PPR) superfamily protein (AHRD V3.3 --* AT3G54980.2)	UP	MG
Solyc03g006260	Solyc03g006260.3.1	Calcium-binding EF-hand (AHRD V3.3 *-* A0A103XMB0_CYNCS)	DOWN	MG
Solyc09g009590	Solyc09g009590.1.1	A20/AN1 zinc finger protein	DOWN	MG
Solyc02g036350	Solyc02g036350.3.1	l-aminocyclopropane-1-carboxylate oxidase EF501822	DOWN	MG
Solyc02g090120	Solyc02g090120.1.1	LOW QUALITY:Inositol 1,4,5-trisphosphate receptor-interacting protein-like 2 (AHRD V3.3 --* A0A1D1XL30_9ARAE)	DOWN	MG
Solyc00g060810	Solyc00g060810.3.1	Sn-1 protein (AHRD V3.3 *** Q42393_CAPAN)	DOWN	MG
Solyc06g060840	Solyc06g060840.1.1	Oleosin (AHRD V3.3 *** K4C6R4_SOLLIC)	DOWN	MG
Solyc03g111730	Solyc03g111730.3.1	KDEL-tailed cysteine endopeptidase	DOWN	MG
Solyc01g088400	Solyc01g088400.3.1	ECERIFERUM 1	DOWN	MG
Solyc06g009140	Solyc06g009140.3.1	Late embryogenesis abundant protein (AHRD V3.3 *** E3W6T3_SESPO)	DOWN	MG
Solyc01g111250	Solyc01g111250.3.1	l-phosphatidylinositol phosphodiesterase-related family protein (AHRD V3.3 *** B9H168_POPTR)	DOWN	MG
Solyc08g082160	Solyc08g082160.3.1	Subtilisin-like protease (AHRD V3.3 *-* W9RY25_9ROSA)	DOWN	MG
Solyc10g079690	Solyc10g079690.2.1	callose synthase 1 (AHRD V3.3 --* AT1G05570.4)	DOWN	MG
Solyc12g088220	Solyc12g088220.2.1	SIBCAT1	DOWN	MG
Solyc03g120570	Solyc03g120570.3.1	Major facilitator superfamily protein (AHRD V3.3 *** AT1G52190.1)	DOWN	MG
Solyc06g076320	Solyc06g076320.1.1	LOW QUALITY:Rundifolia-like protein (AHRD V3.3 *** G7JUW7_MEDTR)	DOWN	MG

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	UP/DOWN	Developmental stages
Solyc01g099040	Solyc01g099040.3.1	GDSL esterase/lipase (AHRD V3.3 *** A0A199UFA2_ANACO)	DOWN	MG
Solyc08g066250	Solyc08g066250.3.1	Histidine decarboxylase (AHRD V3.3 *** DCHS_SOLLIC)	DOWN	MG
Solyc05g013640	Solyc05g013640.1.1	DEAD-box ATP-dependent RNA helicase-like protein (AHRD V3.3 --* AT1G24575.1)	DOWN	MG
Solyc05g013620	Solyc05g013620.2.1	Retrovirus-related Pol polyprotein from transposon TNT 1-94 (AHRD V3.3 --* A0A151U3Z8_CAICA)	DOWN	MG
Solyc10g078440	Solyc10g078440.1.1	LOW QUALITY:VQ motif family protein (AHRD V3.3 *-* B6TQH0_MAIZE)	DOWN	MG
Solyc03g098100	Solyc03g098100.3.1	NAD(PH)-dependent oxidoreductase (AHRD V3.3 *** B6TLR8_MAIZE)	DOWN	MG
Solyc03g097700	Solyc03g097700.3.1	O-methyltransferase (AHRD V3.3 *** F6M2M1_VITPS)	DOWN	MG
Solyc03g111720	Solyc03g111720.3.1	Peptide methionine sulfoxide reductase (AHRD V3.3 *** MSRA_SOLLIC)	DOWN	MG
Solyc10g080900	Solyc10g080900.2.1	ripening related X72730	DOWN	MG
Solyc12g096570	Solyc12g096570.1.1	ARGOS (AHRD V3.3 *** C7SFP7_SOLLIC)	DOWN	MG
Solyc04g007000	Solyc04g007000.1.1	AP2/B3 transcription factor family protein (AHRD V3.3 *** AT1G25560.1)	DOWN	MG
Solyc07g006600	Solyc07g006600.1.1	glutamine dumper 3 (AHRD V3.3 *** AT5G57685.1)	DOWN	MG
Solyc09g005730	Solyc09g005730.3.1	Plant protein 1589 of unknown function (AHRD V3.3 *** AT3G55240.1)	DOWN	MG
Solyc08g066240	Solyc08g066240.3.1	Histidine decarboxylase (AHRD V3.3 *** DCHS_SOLLIC)	DOWN	MG
Solyc10g052490	Solyc10g052490.2.1	Isoflavone reductase homolog (AHRD V3.3 *** IFRH_SOLTU)	DOWN	MG
Solyc09g061700	Solyc09g061700.3.1	Tetrapeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT5G48850.1)	UP	Ripe
Solyc09g082860	Solyc09g082860.3.1	ATP-sulfurylase (AHRD V3.3 *** Q1W2K0_CAMSI)	UP	Ripe
Solyc10g017980	Solyc10g017980.1.1	Chitinase (AHRD V3.3 *-* B8QVJ5_ZEAMP)	UP	Ripe
Solyc07g062500	Solyc07g062500.3.1	Cytochrome P450 (AHRD V3.3 *** A0A124SAX2_CYNCS)	UP	Ripe
Solyc09g090900	Solyc09g090900.3.1	Aconitate hydratase (AHRD V3.3 *** A0A059LL79_9CHLO)	UP	Ripe
Solyc03g034375	Solyc03g034375.1.1	Lipid transfer protein (AHRD V3.3 *** S4TID2_GOSHI)	UP	Ripe
Solyc07g052250	Solyc07g052250.3.1	Unknown protein (AHRD V3.3)	UP	Ripe
Solyc04g072760	Solyc04g072760.3.1	Sulfate transporter (AHRD V3.3 *** S6A1Z9_NICAT)	UP	Ripe
Solyc09g098510	Solyc09g098510.3.1	Extensin (Class I) (AHRD V3.3 *-* Q01945_SOLLIC)	UP	Ripe
Solyc08g077330	Solyc08g077330.3.1	Expansin-like protein (AHRD V3.3 *** W9SU42_9ROSA)	UP	Ripe
Solyc08g006880	Solyc08g006880.3.1	Multidrug resistance protein ABC transporter family protein (AHRD V3.3 *** G7IP56_MEDTR)	UP	Ripe

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	UP/DOWN	Developmental stages
Solyc03g114960	Solyc03g114960.3.1	ABC transporter B family protein (AHRD V3.3 *** A0A072URQ8_MEDTR)	UP	Ripe
Solyc03g080100	Solyc03g080100.3.1	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *-*	UP	Ripe
Solyc02g092860	Solyc02g092860.3.1	Cytochrome P450, putative (AHRD V3.3 *** B9R747_RICCO)	UP	Ripe
Solyc07g006145	Solyc07g006145.1.1	Cytochrome P450 (AHRD V3.3 *** A9ZT56_COPJA)	UP	Ripe
Solyc12g088670	Solyc12g088670.2.1	cysteine protease CYP1	UP	Ripe
Solyc02g087770	Solyc02g087770.3.1	Aldose 1-epimerase (AHRD V3.3 *** K4BBT3_SOLLC)	UP	Ripe
Solyc04g010155	Solyc04g010155.1.1	Pax6 (AHRD V3.3 *-* A0A0B0PQB1_GOSAR)	UP	Ripe
Solyc11g069940	Solyc11g069940.1.1	Glutaredoxin (AHRD V3.3 *** A0A118JSL8_CYNCS)	UP	Ripe
Solyc02g079500	Solyc02g079500.4.1	Peroxisidase (AHRD V1 ***** Q50LG4_TOBAC)	UP	Ripe
Solyc01g099180	Solyc01g099180.3.1	Lipoxygenase (AHRD V3.3 *** Q43800_TOBAC)	DOWN	Ripe
Solyc07g054790	Solyc07g054790.1.1	Wound-responsive family protein (AHRD V3.3 *** A0A061E3U8_THECC)	DOWN	Ripe
Solyc07g064180	Solyc07g064180.3.1	pectin methylesterase 2	DOWN	Ripe
Solyc09g075420	Solyc09g075420.3.1	ethylene response factor E.1	DOWN	Ripe
Solyc06g062600	Solyc06g062600.3.1	Glucose-methanol-choline (GMC) oxidoreductase family protein (AHRD V3.3 *** AT1G72970.1)	DOWN	Ripe
Solyc07g026650	Solyc07g026650.3.1	l-aminocyclopropane-l-carboxylate oxidase 5	DOWN	Ripe
Solyc02g085910	Solyc02g085910.3.1	LOB domain-containing protein (AHRD V3.3 *** A0A0K9PUI8_ZOSMR)	DOWN	Ripe
Solyc07g054770	Solyc07g054770.1.1	Wound-responsive family protein (AHRD V3.3 *** A0A061E3U8_THECC)	DOWN	Ripe
Solyc06g066430	Solyc06g066430.3.1	SUN-like protein 18	DOWN	Ripe
Solyc01g100370	Solyc01g100370.3.1	Adenine nucleotide alpha hydrolases-like superfamily protein (AHRD V3.3 *** AT3G62550.1)	DOWN	Ripe
Solyc07g054750	Solyc07g054750.1.1	LOW QUALITY: Wound-responsive family protein (AHRD V3.3 *** A0A061E3U8_THECC)	DOWN	Ripe
Solyc10g050980	Solyc10g050980.1.1	PAB-dependent poly(A)-specific ribonuclease subunit PAN2 (AHRD V3.3 *-* A0A1D1XPR6_9ARAE)	DOWN	Ripe
Solyc06g050870	Solyc06g050870.3.1	Hypoxia-responsive family protein (AHRD V3.3 *** A0A061FY00_THECC)	DOWN	Ripe
Solyc04g054340	Solyc04g054340.1.1	LOW QUALITY: transmembrane protein (AHRD V3.3 *-* AT5G65440.9)	DOWN	Ripe
Solyc06g007580	Solyc06g007580.1.1	LOW QUALITY: DUF506 family protein (AHRD V3.3 *** G7LF52_MEDTR)	DOWN	Ripe
Solyc07g054810	Solyc07g054810.1.1	LOW QUALITY: glutamate-1-semialdehyde 2,1-aminomutase 2 (AHRD V3.3 *-* AT3G48730.1)	DOWN	Ripe

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	UP/DOWN	Developmental stages
Solyc12g006560	Solyc12g006560.2.1	Early nodulin-93 (AHRD V3.3 *** A0A061GV12_THECC)	DOWN	Ripe
Solyc02g090750	Solyc02g090750.3.1	Eukaryotic initiation factor 4A (ATP-dependent RNA helicase eIF4A) (AHRD V3.3 *-E[ZM95_CHLVA])	DOWN	Ripe
Solyc01g109100	Solyc01g109100.2.1	LOW QUALITY:phytochrome interacting factor 3-like 5 (AHRD V3.3 --* AT2G20180.6)	DOWN	Ripe
Solyc11g008680	Solyc11g008680.2.1	Acyl-[acyl-carrier-protein] desaturase (AHRD V3.3 *** A0A060IKL1_NICBE)	DOWN	Ripe
Solyc06g066770	Solyc06g066770.1.1	Kelch repeat-containing F-box family protein (AHRD V3.3 *** B9GEJ8_POPTR)	DOWN	Ripe
Solyc12g056510	Solyc12g056510.2.1	Trihelix transcription factor GT-2 (AHRD V3.3 *** A0A0B2SAG9_GLYSO)	DOWN	Ripe
Solyc02g081830	Solyc02g081830.3.1	Haloacid dehalogenase-like hydrolase domain-containing protein 3 (AHRD V3.3 *** W9RRW5_9ROSA).Pfam:PF00702	DOWN	Ripe
Solyc07g065970	Solyc07g065970.1.1	Chaperone protein DNAj, putative (AHRD V3.3 *** B9SXA3_RICCO)	DOWN	Ripe
Solyc10g050990	Solyc10g050990.1.1	Pyruvate kinase (AHRD V3.3 --* A9TZX1_PHYPA)	DOWN	Ripe

Table 4. Gene Ontology Enrichment Analysis of the DEG in *adp* Fruit

Cluster	ID	Description	Adjusted p	Gene ID	Count
Placenta_6dpa_UP	GO:0034599	cellular response to oxidative stress	2.29E-02	Solyc05g006860/Solyc05g006850	2
Placenta_6dpa_UP	GO:0006571	tyrosine biosynthetic process	4.27E-02	Solyc06g050630	1
Placenta_6dpa_UP	GO:0019346	transsulfuration	4.27E-02	Solyc08g083110	1
Placenta_6dpa_UP	GO:0007205	protein kinase C-activating G-protein coupled receptor signaling pathway	4.27E-02	Solyc03g115370	1
Placenta_6dpa_UP	GO:0009415	response to water	4.27E-02	Solyc01g109920	1
Placenta_6dpa_UP	GO:0009693	ethylene biosynthetic process	4.44E-02	Solyc02g091990	1
Placenta_6dpa_UP	GO:0046486	glycerolipid metabolic process	4.54E-02	Solyc02g094400	1
Placenta_6dpa_UP	GO:0006665	sphingolipid metabolic process	4.69E-02	Solyc10g086690	1
Placenta_6dpa_DOWN	GO:0045490	pectin catabolic process	4.98E-02	Solyc06g009190/Solyc03g058910	2
Placenta_6dpa_DOWN	GO:0006672	ceramide metabolic process	4.98E-02	Solyc08g082920	1
Placenta_6dpa_DOWN	GO:0006880	intracellular sequestering of iron ion	4.98E-02	Solyc01g104780	1
Placenta_6dpa_DOWN	GO:0019252	starch biosynthetic process	4.98E-02	Solyc07g056140	1
Placenta_6dpa_DOWN	GO:0034755	iron ion transmembrane transport	4.98E-02	Solyc01g104780	1
Placenta_6dpa_DOWN	GO:0090156	cellular sphingolipid homeostasis	4.98E-02	Solyc08g082920	1
Placenta_20dpa_UP	GO:0006629	lipid metabolic process	1.50E-02	Solyc07g032180/Solyc06g030590/Solyc07g032220/Solyc06g011530/ Solyc03g044910/Solyc07g032170/Solyc09g075790	7
Placenta_20dpa_UP	GO:0006281	DNA repair	3.68E-02	Solyc09g009080/Solyc04g051490/Solyc05g051680/Solyc12g042000/Solyc02g005310/Solyc09g066080	6
Placenta_20dpa_UP	GO:0045944	positive regulation of transcription by RNA polymerase II	1.93E-02	Solyc09g008520/Solyc01g087320/Solyc01g087400/Solyc11g062010/Solyc09g066080	5
Placenta_20dpa_UP	GO:0006457	protein folding	3.96E-03	Solyc11g020330/Solyc03g117630/Solyc02g093600/Solyc09g092690/Solyc03g113930	5
Placenta_20dpa_UP	GO:0009408	response to heat	1.86E-02	Solyc11g020330/Solyc02g072000/Solyc02g093600/Solyc03g113930	4
Placenta_20dpa_UP	GO:0019752	carboxylic acid metabolic process	5.57E-03	Solyc04g049360/Solyc03g112060/Solyc06g011530/Solyc03g044910	4
Placenta_20dpa_UP	GO:0030307	positive regulation of cell growth	1.04E-02	Solyc10g076270/Solyc10g076260/Solyc05g021580/Solyc01g106770	4
Placenta_20dpa_UP	GO:0031929	TOR signaling	1.63E-02	Solyc10g076270/Solyc10g076260/Solyc05g021580/Solyc01g106770	4
Placenta_20dpa_UP	GO:0009651	response to salt stress	2.60E-02	Solyc11g020330/Solyc02g093600/Solyc03g113930	3

Cluster	ID	Description	Adjusted p	Gene ID	Count
Placenta_20dpa_UP	GO:0000302	response to reactive oxygen species	1.67E-02	Solyc11g020330/Solyc02g093600/Solyc03g113930	3
Placenta_20dpa_UP	GO:0006633	fatty acid biosynthetic process	4.72E-03	Solyc03g044910/Solyc02g036290/Solyc09g075790	3
Placenta_20dpa_UP	GO:0009835	fruit ripening	3.68E-02	Solyc07g049530/Solyc10g080210	2
Placenta_20dpa_UP	GO:0031401	positive regulation of protein modification process	4.25E-02	Solyc10g076270/Solyc09g066080	2
Placenta_20dpa_UP	GO:0006665	sphingolipid metabolic process	2.50E-02	Solyc06g030590/Solyc03g044910	2
Placenta_20dpa_DOWN	GO:0015979	photosynthesis	4.22E-06	Solyc02g069450/Solyc06g083680/Solyc08g006930/Solyc03g034220/Solyc10g077040/Solyc03g005760/Solyc03g005780/Solyc01g105050/Solyc03g005770	9
Placenta_20dpa_DOWN	GO:0009416	response to light stimulus	1.76E-05	Solyc03g005760/Solyc03g005780/Solyc03g006880/Solyc01g105050/Solyc03g005770/Solyc02g070430	6
Placenta_20dpa_DOWN	GO:0009765	photosynthesis, light harvesting	1.76E-05	Solyc03g005760/Solyc02g071030/Solyc03g005780/Solyc01g105050/Solyc03g005770	5
Placenta_20dpa_DOWN	GO:0006091	generation of precursor metabolites and energy	8.43E-03	Solyc03g005770/Solyc01g105050/Solyc03g005760/Solyc10g018300/Solyc03g115820	5
Placenta_20dpa_DOWN	GO:0009768	photosynthesis, light harvesting in photosystem I	1.47E-04	Solyc03g005760/Solyc03g005780/Solyc01g105050/Solyc03g005770	4
Placenta_20dpa_DOWN	GO:0018298	protein-chromophore linkage	8.59E-04	Solyc03g005760/Solyc03g005780/Solyc01g105050/Solyc03g005770	4
Placenta_20dpa_DOWN	GO:0006979	response to oxidative stress	2.51E-02	Solyc06g005160/Solyc10g086680/Solyc10g083650	3
Placenta_20dpa_DOWN	GO:0031640	killing of cells of other organism	3.18E-02	Solyc07g007750/Solyc07g007760	2
Placenta_20dpa_DOWN	GO:0006006	glucose metabolic process	3.94E-02	Solyc04g009030/Solyc04g082630	2
Placenta_20dpa_DOWN	GO:0006098	pentose-phosphate shunt	2.15E-02	Solyc10g018300/Solyc03g115820	2
Placenta_MG_UP	GO:0006281	DNA repair	1.61E-05	Solyc01g109080/Solyc02g083900/Solyc02g091120/Solyc11g067140/Solyc11g018510/Solyc01g034150/Solyc09g066080/Solyc09g011930/Solyc03g111790/Solyc09g018690/Solyc12g041980/Solyc03g025890/Solyc09g009080/Solyc01g106770/Solyc05g051680/Solyc12g042000/Solyc01g111870/Solyc03g112950/Solyc01g107510/Solyc02g094590/Solyc02g005310/Solyc01g099220/Solyc02g021060	23
Placenta_MG_UP	GO:0006396	RNA processing	5.18E-07	Solyc06g048960/Solyc11g008530/Solyc10g080130/Solyc02g081960/Solyc10g006180/Solyc11g008540/Solyc01g103690/Solyc04g005690/Solyc09g064590/Solyc01g086890/Solyc10g006210/Solyc11g018770/Solyc10g006200/Solyc10g005130/Solyc03g053105/Solyc01g086900/Solyc10g006153/Solyc08g077850/Solyc04g007510/Solyc01g006710	20

Cluster	ID	Description	Adjusted p	Gene ID	Count
Placenta_MG_UP	GO:0034470	ncRNA processing	3.65E-04	Solyc04g072265/Solyc11g018810/Solyc04g072260/Solyc12g017860/Solyc08g062560/Solyc01g086900/Solyc05g051230/Solyc04g049226/Solyc06g049090/Solyc08g077850/Solyc11g018770/Solyc10g080130/Solyc03g093480/Solyc03g097550/Solyc12g015710/Solyc07g032180/Solyc05g08790/Solyc02g082763/Solyc11g010550/Solyc09g072710/Solyc04g007650/Solyc07g045420/Solyc01g104310/Solyc07g032220/Solyc01g006000/Solyc01g095930/Solyc06g011530/Solyc10g005840	15
Placenta_MG_UP	GO:0006629	lipid metabolic process	3.65E-03	Solyc06g048960/Solyc11g008530/Solyc10g006180/Solyc05g013210/Solyc11g008540/Solyc10g006210/Solyc10g006200/Solyc06g082890/Solyc10g005130	13
Placenta_MG_UP	GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	3.64E-02	Solyc02g091120/Solyc09g066080/Solyc12g041980/Solyc03g025890/Solyc12g042000/Solyc03g112950/Solyc01g107510/Solyc02g021060	9
Placenta_MG_UP	GO:0006974	cellular response to DNA damage stimulus	1.26E-03	Solyc01g108910/Solyc06g048460/Solyc02g086500/Solyc03g059420/Solyc01g090200/Solyc01g106950/Solyc01g106770/Solyc09g092100	8
Placenta_MG_UP	GO:0009793	embryo development ending in seed dormancy	4.22E-02	Solyc11g005650/Solyc11g005640/Solyc07g065630/Solyc10g084760/Solyc06g053210/Solyc04g076620/Solyc01g067273/Solyc01g067210	8
Placenta_MG_UP	GO:0016567	protein ubiquitination	1.11E-04	Solyc11g099460/Solyc07g049720/Solyc03g115530/Solyc11g0657140/Solyc12g098860/Solyc01g068260/Solyc11g020770/Solyc01g099450	8
Placenta_MG_UP	GO:0006260	DNA replication	1.35E-03	Solyc12g095890/Solyc01g058260/Solyc06g066470/Solyc08g066200/Solyc06g066477/Solyc06g066460/Solyc06g066473	7
Placenta_MG_UP	GO:0043631	RNA polyadenylation	5.18E-07	Solyc01g073750/Solyc01g006370/Solyc01g006350/Solyc03g111575/Solyc02g078230/Solyc07g056260/Solyc01g073755	7
Placenta_MG_UP	GO:0006075	(1->3)-beta-D-glucan biosynthetic process	1.25E-06	Solyc06g048960/Solyc11g008530/Solyc10g006180/Solyc11g008540/Solyc10g006210/Solyc10g006200/Solyc10g005130	7
Placenta_MG_UP	GO:0090501	RNA phosphodiester bond hydrolysis	2.75E-02	Solyc07g032180/Solyc02g082763/Solyc11g010550/Solyc04g007650/Solyc01g104310/Solyc01g006000/Solyc01g095930	7
Placenta_MG_UP	GO:0046486	glycerolipid metabolic process	4.59E-03	Solyc06g048960/Solyc11g008530/Solyc10g006180/Solyc10g006210/Solyc10g005130/Solyc01g096390	6
Placenta_MG_UP	GO:0030422	production of siRNA involved in RNA interference	5.94E-03	Solyc08g068010/Solyc01g099460/Solyc09g066080/Solyc09g018690/Solyc12g041980/Solyc05g051680	6
Placenta_MG_UP	GO:0000724	double-strand break repair via homologous recombination	2.75E-02	Solyc12g062480/Solyc10g006780/Solyc07g021120/Solyc01g111870/Solyc02g091120/Solyc03g112950	6
Placenta_MG_UP	GO:0000723	telomere maintenance	2.65E-03	Solyc09g090870/Solyc03g080010/Solyc03g025890/Solyc02g082660/Solyc10g018530	5
Placenta_MG_UP	GO:0006298	mismatch repair	9.02E-03	Solyc02g090130/Solyc12g099010/Solyc04g012170/Solyc08g077500/Solyc09g009370	5
Placenta_MG_UP	GO:0006623	protein targeting to vacuole	1.62E-02		

Cluster	ID	Description	Adjusted p	Gene ID	Count
Placenta_MG_UP	GO:0031929	TOR signaling	9.53E-03	Solyc10g076270/Solyc10g076260/Solyc01g107415/Solyc01g106770/Solyc05g021580	5
Placenta_MG_UP	GO:0051276	chromosome organization	3.40E-03	Solyc05g054200/Solyc06g048460/Solyc12g041980/Solyc09g066080/Solyc08g067190	5
Placenta_MG_UP	GO:0045053	protein retention in Golgi apparatus	3.86E-03	Solyc08g077500/Solyc11g045185/Solyc02g090130/Solyc11g045160/Solyc09g009370	5
Placenta_MG_UP	GO:0031123	RNA 3'-end processing	2.48E-03	Solyc12g095890/Solyc01g058260/Solyc06g066470/Solyc08g066200	4
Placenta_MG_UP	GO:0006378	mRNA polyadenylation	2.73E-02	Solyc12g095890/Solyc01g058260/Solyc06g066470/Solyc08g066200	4
Placenta_MG_UP	GO:0006221	pyrimidine nucleotide biosynthetic process	2.75E-02	Solyc01g098530/Solyc01g098527/Solyc02g084300/Solyc02g088940	4
Placenta_MG_UP	GO:0017148	negative regulation of translation	3.05E-02	Solyc10g006170/Solyc06g075590/Solyc10g006190/Solyc01g090780	4
Placenta_MG_UP	GO:0042147	retrograde transport, endosome to Golgi	3.05E-02	Solyc02g069650/Solyc12g005090/Solyc02g069660/Solyc03g078570	4
Placenta_MG_UP	GO:0006402	mRNA catabolic process	4.93E-02	Solyc10g006157/Solyc10g006170/Solyc10g006190/Solyc10g006153	4
Placenta_MG_UP	GO:0046488	phosphatidylinositol metabolic process	4.93E-02	Solyc12g049590/Solyc04g007650/Solyc04g017595/Solyc04g017620	4
Placenta_MG_UP	GO:0030488	tRNA methylation	3.21E-03	Solyc01g086900/Solyc06g049090/Solyc08g077850/Solyc01g068070	4
Placenta_MG_UP	GO:0000710	meiotic mismatch repair	2.75E-02	Solyc09g090870/Solyc03g025890/Solyc10g018530	3
Placenta_MG_UP	GO:0002943	tRNA dihydrouridine synthesis	2.75E-02	Solyc01g087380/Solyc01g087320/Solyc01g087290	3
Placenta_MG_UP	GO:0009396	folic acid-containing compound biosynthetic process	4.22E-02	Solyc04g016550/Solyc04g049360/Solyc08g048240	3
Placenta_MG_UP	GO:0042127	regulation of cell proliferation	4.93E-02	Solyc05g054200/Solyc09g066080/Solyc12g041980	3
Placenta_MG_UP	GO:0035066	positive regulation of histone acetylation	1.72E-03	Solyc05g054200/Solyc12g041980/Solyc09g066080	3
Placenta_MG_UP	GO:0034058	endosomal vesicle fusion	1.19E-03	Solyc02g085220/Solyc05g044610/Solyc05g044615	3
Placenta_MG_DOWN	GO:0006979	response to oxidative stress	3.30E-02	Solyc10g078890/Solyc01g080410/Solyc02g092580/Solyc02g083480/Solyc04g071890/Solyc01g079830/Solyc03g111720/Solyc04g064690	8
Placenta_MG_DOWN	GO:0030001	metal ion transport	3.30E-02	Solyc03g043640/Solyc03g025800/Solyc05g008300/Solyc03g025795/Solyc02g032100/Solyc03g007870	6
Placenta_MG_DOWN	GO:0051603	proteolysis involved in cellular protein catabolic process	4.56E-02	Solyc01g087970/Solyc02g069110/Solyc05g041540/Solyc03g111730/Solyc01g108490/Solyc05g013920	6
Placenta_MG_DOWN	GO:0009693	ethylene biosynthetic process	5.95E-06	Solyc02g036350/Solyc07g049530/Solyc12g0005940/Solyc09g089580/Solyc07g049550	5

Cluster	ID	Description	Adjusted p	Gene ID	Count
Placenta_MG_DOWN	GO:0009607	response to biotic stimulus	3.55E-02	Solyc02g082920/Solyc00g060810/Solyc00g174340/Solyc01g097240/Solyc08g080640	5
Placenta_MG_DOWN	GO:0006032	chitin catabolic process	2.08E-02	Solyc10g055810/Solyc02g082920/Solyc05g050130/Solyc10g055800	4
Placenta_MG_DOWN	GO:0050832	defense response to fungus	4.56E-02	Solyc07g007750/Solyc00g174340/Solyc01g097240/Solyc08g080640	4
Placenta_MG_DOWN	GO:0006720	isoprenoid metabolic process	4.20E-02	Solyc07g056670/Solyc03g032020/Solyc04g083160/Solyc11g072310	4
Placenta_MG_DOWN	GO:0009835	fruit ripening	8.07E-03	Solyc07g049530/Solyc09g089580/Solyc07g049550	3
Placenta_MG_DOWN	GO:0031640	killing of cells of other organism	2.08E-02	Solyc07g007750/Solyc00g174340/Solyc08g080640	3
Placenta_MG_DOWN	GO:0016998	cell wall macromolecule catabolic process	3.30E-02	Solyc10g055810/Solyc02g082920/Solyc10g055800	3
Placenta_MG_DOWN	GO:0009685	gibberellin metabolic process	3.90E-02	Solyc07g056670/Solyc04g083160/Solyc11g072310	3
Placenta_RR_UP	GO:0006629	lipid metabolic process	9.06E-03	Solyc01g109140/Solyc08g080170/Solyc12g100270/Solyc01g103650/Solyc09g061840/Solyc02g038740/Solyc03g019670/Solyc02g084930/ Solyc03g122340/Solyc07g007870/Solyc02g084740/Solyc07g045350/Solyc08g080130/Solyc04g079820/Solyc08g029000	15
Placenta_RR_UP	GO:0044550	secondary metabolite biosynthetic process	1.56E-03	Solyc02g065190/Solyc02g090350/Solyc04g078290/Solyc12g045020/Solyc07g052370/Solyc11g030730/Solyc12g042480/Solyc02g092860/Solyc08g079420/Solyc03g112030/Solyc04g083140	11
Placenta_RR_UP	GO:0007049	cell cycle	5.59E-04	Solyc06g073610/Solyc04g082430/Solyc04g071650/Solyc08g066050/Solyc05g006050/Solyc10g080950/Solyc03g032190/Solyc02g087880/Solyc06g076640/Solyc06g065680/Solyc04g082840	11
Placenta_RR_UP	GO:0007018	microtubule-based movement	1.19E-05	Solyc07g064030/Solyc03g119220/Solyc06g075580/Solyc09g010060/Solyc01g098985/Solyc07g065210/Solyc02g084390/Solyc12g098630/Solyc09g010810/Solyc11g071730	10
Placenta_RR_UP	GO:0009664	plant-type cell wall organization	2.38E-02	Solyc12g098757/Solyc09g098510/Solyc04g071080/Solyc12g098780/Solyc05g007830/Solyc02g088100/Solyc04g071085	7
Placenta_RR_UP	GO:0006559	L-phenylalanine catabolic process	2.93E-06	Solyc09g007900/Solyc09g007920/Solyc10g011920/Solyc00g282510/Solyc09g007890/Solyc09g007910	6
Placenta_RR_UP	GO:0016125	sterol metabolic process	4.15E-02	Solyc01g109140/Solyc12g100270/Solyc02g038740/Solyc02g084930/Solyc02g084740	5
Placenta_RR_UP	GO:0009800	cinnamic acid biosynthetic process	6.54E-05	Solyc09g007900/Solyc09g007920/Solyc09g007890/Solyc09g007910	4
Placenta_RR_UP	GO:0009698	phenylpropanoid metabolic process	2.23E-04	Solyc09g007900/Solyc09g007920/Solyc09g007890/Solyc09g007910	4
Placenta_RR_UP	GO:1902358	sulfate transmembrane transport	2.65E-03	Solyc05g054740/Solyc04g072760/Solyc12g056930/Solyc04g054730	4

Cluster	ID	Description	Adjusted p	Gene ID	Count
Placenta_RR_UP	GO:0008272	sulfate transport	3.86E-03	Solyc05g054740/Solyc04g072760/Solyc12g056930/Solyc04g054730	4
Placenta_RR_UP	GO:0009558	embryo sac cellularization	4.97E-02	Solyc03g096890/Solyc03g119220	2
Placenta_RR_UP	GO:0048443	stamen development	4.97E-02	Solyc02g084740/Solyc09g008240	2
Placenta_RR_DOWN	GO:0009835	fruit ripening	1.32E-02	Solyc07g064180/Solyc07g064170	2
Placenta_RR_DOWN	GO:0031408	oxylipin biosynthetic process	4.54E-02	Solyc01g099180/Solyc01g099190	2
Placenta_RR_DOWN	GO:1901605	alpha-amino acid metabolic process	2.88E-02	Solyc08g008000/Solyc03g083440	2
Pericarp_6dpa_UP	GO:0031408	oxylipin biosynthetic process	2.75E-02	Solyc01g099180/Solyc01g099190	2
Pericarp_6dpa_UP	GO:0000973	posttranscriptional tethering of RNA polymerase II gene DNA at nuclear periphery	3.55E-02	Solyc01g104434/Solyc02g084285	2
Pericarp_6dpa_UP	GO:0015996	chlorophyll catabolic process	4.11E-02	Solyc12g005300	1
Pericarp_6dpa_DOWN	GO:0045490	pectin catabolic process	3.02E-03	Solyc02g080220/Solyc02g080200/Solyc03g058910	3
Pericarp_6dpa_DOWN	GO:0042545	cell wall modification	2.93E-02	Solyc02g080220/Solyc02g080200	2
Pericarp_6dpa_DOWN	GO:0071555	cell wall organization	2.93E-02	Solyc02g080220/Solyc02g080200	2
Pericarp_6dpa_DOWN	GO:0009617	response to bacterium	2.93E-02	Solyc04g081560	1
Pericarp_6dpa_DOWN	GO:0009070	serine family amino acid biosynthetic process	2.93E-02	Solyc11g020060	1
Pericarp_6dpa_DOWN	GO:0006379	mRNA cleavage	2.93E-02	Solyc05g055890	1
Pericarp_6dpa_DOWN	GO:0019252	starch biosynthetic process	2.93E-02	Solyc07g056140	1
Pericarp_6dpa_DOWN	GO:0000911	cytokinesis by cell plate formation	3.07E-02	Solyc01g108670	1
Pericarp_6dpa_DOWN	GO:0009723	response to ethylene	3.18E-02	Solyc04g081560	1
Pericarp_6dpa_DOWN	GO:0010215	cellulose microfibril organization	4.51E-02	Solyc03g114890	1
Pericarp_6dpa_DOWN	GO:0045892	negative regulation of transcription, DNA-templated	4.51E-02	Solyc08g068170	1
Pericarp_6dpa_DOWN	GO:0006032	chitin catabolic process	4.92E-02	Solyc07g005100	1
Pericarp_20dpa_UP	GO:0051259	protein complex oligomerization	2.44E-02	Solyc11g020330/Solyc02g093600/Solyc03g113930	3
Pericarp_20dpa_UP	GO:0009651	response to salt stress	2.99E-02	Solyc11g020330/Solyc02g093600/Solyc03g113930	3
Pericarp_20dpa_UP	GO:0042542	response to hydrogen peroxide	2.14E-02	Solyc11g020330/Solyc02g093600/Solyc03g113930	3
Pericarp_20dpa_UP	GO:0009408	response to heat	3.01E-02	Solyc11g020330/Solyc02g093600/Solyc03g113930	3

Cluster	ID	Description	Adjusted p	Gene ID	Count
Pericarp_20dpa_DOWN	GO:0043086	negative regulation of catalytic activity	2.27E-03	Solyc09g090990/Solyc03g123620/Solyc06g009190	3
Pericarp_20dpa_DOWN	GO:0042545	cell wall modification	1.67E-02	Solyc03g123620/Solyc06g009190	2
Pericarp_20dpa_DOWN	GO:0045490	pectin catabolic process	1.67E-02	Solyc03g123620/Solyc06g009190	2
Pericarp_20dpa_DOWN	GO:0009058	biosynthetic process	2.59E-02	Solyc07g056140/Solyc02g082900	2
Pericarp_20dpa_DOWN	GO:0009693	ethylene biosynthetic process	2.89E-02	Solyc02g036350	1
Pericarp_20dpa_DOWN	GO:0019252	starch biosynthetic process	2.89E-02	Solyc07g056140	1
Pericarp_20dpa_DOWN	GO:0031408	oxylipin biosynthetic process	4.83E-02	Solyc03g122340	1
Pericarp_MG_UP	GO:0006952	defense response	1.85E-05	Solyc04g077270/Solyc03g120110/Solyc02g080040/Solyc01g113620/Solyc07g009230/Solyc09g014530/Solyc02g082920/Solyc07g063820/Solyc05g007170/Solyc02g080070/Solyc10g006710/Solyc04g005540/Solyc00g174340/Solyc02g077370/Solyc01g103610/Solyc02g079580/Solyc01g007980/Solyc01g097240/Solyc10g006720/Solyc02g082930/Solyc02g080080/Solyc02g080010/Solyc07g007760/Solyc06g050810	24
Pericarp_MG_UP	GO:0006629	lipid metabolic process	1.09E-02	Solyc07g032180/Solyc06g048570/Solyc02g082763/Solyc01g103650/Solyc02g086180/Solyc01g080900/Solyc06g035960/Solyc00g009110/Solyc04g072020/Solyc01g006000/Solyc06g011530/Solyc03g044790	12
Pericarp_MG_UP	GO:0007049	cell cycle	4.61E-02	Solyc12g000866/Solyc03g117530/Solyc08g066050/Solyc10g080950/Solyc11g030550/Solyc09g075550/Solyc02g087880/Solyc01g087500/Solyc08g007330/Solyc04g082840	10
Pericarp_MG_UP	GO:0006281	DNA repair	3.02E-02	Solyc08g074740/Solyc03g117530/Solyc02g021060/Solyc01g034150/Solyc05g006120/Solyc01g105520/Solyc08g007330/Solyc09g066080	8
Pericarp_MG_UP	GO:0009407	toxin catabolic process	1.76E-02	Solyc09g011600/Solyc07g056470/Solyc09g011590/Solyc09g011630/Solyc01g086680/Solyc09g011550	6
Pericarp_MG_UP	GO:0051276	chromosome organization	3.99E-02	Solyc03g117530/Solyc02g084285/Solyc02g091020/Solyc01g087500/Solyc03g120200	5
Pericarp_MG_UP	GO:0016998	cell wall macromolecule catabolic process	2.87E-02	Solyc02g082920/Solyc10g055800/Solyc11g066270/Solyc02g082930	4
Pericarp_MG_UP	GO:0043631	RNA polyadenylation	2.90E-02	Solyc01g058260/Solyc06g066460/Solyc06g066473	3
Pericarp_MG_DOWN	GO:0071555	cell wall organization	5.26E-06	Solyc03g093110/Solyc07g064180/Solyc07g064190/Solyc03g093120/Solyc03g093130/Solyc03g093080/Solyc07g064170/Solyc07g056000/Solyc10g080210/Solyc07g009380	10
Pericarp_MG_DOWN	GO:0006629	lipid metabolic process	1.84E-02	Solyc01g099190/Solyc04g078900/Solyc01g006540/Solyc03g031860/Solyc08g005610/Solyc02g070430/Solyc04g079730/Solyc01g088400/Solyc01g099180	9

Cluster	ID	Description	Adjusted p	Gene ID	Count
Pericarp_MG_DOWN	GO:0006073	cellular glucan metabolic process	6.29E-06	Solyc03g093110/Solyc03g093120/Solyc03g093130/Solyc03g093080/Solyc07g056000/Solyc07g009380	6
Pericarp_MG_DOWN	GO:0010411	xyloglucan metabolic process	6.29E-06	Solyc03g093110/Solyc03g093120/Solyc03g093130/Solyc03g093080/Solyc07g056000/Solyc07g009380	6
Pericarp_MG_DOWN	GO:0042546	cell wall biogenesis	7.13E-06	Solyc03g093110/Solyc03g093120/Solyc03g093130/Solyc03g093080/Solyc07g056000/Solyc07g009380	6
Pericarp_MG_DOWN	GO:0006950	response to stress	5.03E-04	Solyc07g064160/Solyc04g014600/Solyc06g009050/Solyc06g009140/Solyc02g084840/Solyc02g062390	6
Pericarp_MG_DOWN	GO:0006633	fatty acid biosynthetic process	1.44E-03	Solyc01g099180/Solyc01g065400/Solyc01g099190/Solyc04g079730/Solyc01g088400/Solyc02g085870	6
Pericarp_MG_DOWN	GO:0009058	biosynthetic process	4.57E-03	Solyc08g081550/Solyc07g056140/Solyc10g007110/Solyc01g095080/Solyc03g031860/Solyc05g050010	6
Pericarp_MG_DOWN	GO:0045490	pectin catabolic process	5.40E-03	Solyc07g064180/Solyc03g123620/Solyc07g064190/Solyc07g064170/Solyc03g055510	5
Pericarp_MG_DOWN	GO:0043086	negative regulation of catalytic activity	1.47E-02	Solyc07g064180/Solyc03g123620/Solyc07g064190/Solyc07g064170/Solyc01g088590	5
Pericarp_MG_DOWN	GO:0009835	fruit ripening	6.69E-06	Solyc07g064180/Solyc07g064170/Solyc01g095080/Solyc10g080210	4
Pericarp_MG_DOWN	GO:0031408	oxylipin biosynthetic process	2.91E-04	Solyc01g099180/Solyc01g065400/Solyc01g099190/Solyc04g079730	4
Pericarp_MG_DOWN	GO:0006869	lipid transport	9.71E-03	Solyc01g090350/Solyc02g086310/Solyc01g090360/Solyc05g015490	4
Pericarp_MG_DOWN	GO:0042545	cell wall modification	1.84E-02	Solyc07g064180/Solyc03g123620/Solyc07g064190/Solyc07g064170	4
Pericarp_MG_DOWN	GO:0009414	response to water deprivation	3.61E-02	Solyc08g082210/Solyc02g084840/Solyc02g062390	3
Pericarp_MG_DOWN	GO:0009415	response to water	1.08E-02	Solyc02g084840/Solyc02g062390	2
Pericarp_MG_DOWN	GO:0009693	ethylene biosynthetic process	1.47E-02	Solyc02g036350/Solyc01g095080	2
Pericarp_MG_DOWN	GO:0019953	sexual reproduction	1.84E-02	Solyc06g034040/Solyc06g060840	2
Pericarp_MG_DOWN	GO:0009631	cold acclimation	2.48E-02	Solyc02g084840/Solyc02g062390	2
Pericarp_MG_DOWN	GO:0019915	lipid storage	2.48E-02	Solyc06g034040/Solyc06g060840	2
Pericarp_RR_UP	GO:0044281	small molecule metabolic process	1.59E-03	Solyc11g007990/Solyc12g056830/Solyc04g082630/Solyc02g065280/Solyc04g009960/Solyc02g080540/Solyc02g089620/Solyc12g008430/Solyc12g006450/Solyc07g021750/Solyc04g009030/Solyc10g086730	13
Pericarp_RR_UP	GO:0006082	organic acid metabolic process	2.41E-02	Solyc11g007990/Solyc02g065280/Solyc04g009960/Solyc02g089620/Solyc12g008430/Solyc12g006450	6
Pericarp_RR_UP	GO:0006091	generation of precursor metabolites and energy	4.00E-02	Solyc11g007990/Solyc12g056830/Solyc07g047850/Solyc03g115900/Solyc08g075540	5

Cluster	ID	Description	Adjusted p	Gene ID	Count
Pericarp_RR_UP	GO:0019318	hexose metabolic process	4.43E-02	Solyc04g082630/Solyc04g09030/Solyc10g086730	3
Pericarp_RR_UP	GO:0006108	malate metabolic process	4.98E-02	Solyc11g007990/Solyc12g008430	2
Pericarp_RR_DOWN	GO:0006633	fatty acid biosynthetic process	1.31E-03	Solyc01g099180/Solyc06g053480/Solyc11g008680/Solyc01g099200/Solyc08g014000	5
Pericarp_RR_DOWN	GO:0006096	glycolytic process	1.31E-03	Solyc08g066100/Solyc04g011510/Solyc04g082880/Solyc09g009260	4
Pericarp_RR_DOWN	GO:0031408	oxylipin biosynthetic process	1.31E-03	Solyc01g099180/Solyc01g099200/Solyc08g014000	3
Pericarp_RR_DOWN	GO:0006631	fatty acid metabolic process	3.85E-03	Solyc06g053480/Solyc11g008680/Solyc08g014000	3
Pericarp_RR_DOWN	GO:0061615	glycolytic process through fructose-6-phosphate	1.08E-02	Solyc08g066100/Solyc04g082880	2
Pericarp_RR_DOWN	GO:0006950	response to stress	3.59E-02	Solyc07g064160/Solyc01g100370/Solyc09g075210	3
Pericarp_RR_DOWN	GO:0015743	malate transport	4.59E-02	Solyc11g010500	1

Table 5. Examples of DEGs in *adp* Placenta During Fruit Growth

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	FC <i>adp</i> /CL	FC <i>adp</i> /WT	UP/DOWN	Stage	Biological pathway
Solyc05g013490	Solyc05g013490.3.1	Cyclin-related family protein (AHRD V3.3 *** B9HLR1_POPTR)	2.31527719	1.87042735	UP	20DPA	Cell cycle
Solyc11g030550	Solyc11g030550.2.1	Cyclin B2	2.023072061	1.595264798	UP	20DPA	Cell cycle
Solyc09g065610	Solyc09g065610.2.1	Bax inhibitor (AHRD V3.3 *-.* A0A0K1ETI6_TECGR)	1.526055015	2.297522078	UP	6DPA	Cell death regulation
Solyc01g091590	Solyc01g091590.3.1	LOW QUALITY:BON1-associated protein 2 (AHRD V3.3 *** W9QRQ0_9ROSA)	1.658871422	1.516309081	UP	6DPA	Cell death regulation
Solyc04g076710	Solyc04g076710.3.1	COBRA-like protein 11 precursor (AHRD V3.3 -.* AT4G27110.1)	2.680906149	2.575870647	UP	20DPA	Cell wall
Solyc09g010860	Solyc09g010860.3.1	expansin precursor 4	3.176774194	3.448179272	UP	20DPA	Cell wall
Solyc03g025600	Solyc03g025600.3.1	Pectinacetyltransferase family protein (AHRD V3.3 *** AT5G23870.3)	1.821187077	1.578810248	UP	20DPA	Cell wall
Solyc11g005150	Solyc11g005150.2.1	entensin X55687	1.939546449	1.536767149	UP	20DPA	Cell wall
Solyc10g080210	Solyc10g080210.2.1	polygalacturonase	14.53389831	163.3333333	UP	20DPA	Cell wall
Solyc12g040860	Solyc12g040860.2.1	Glucan endo-1,3-beta-glucosidase, putative (AHRD V3.3 *** A0A061PDC8_THECC)	0.367623173	0.495258935	DOWN	6DPA	Cell wall
Solyc06g009190	Solyc06g009190.3.1	Pectinesterase (AHRD V3.3 *** K4C3U9_SOLLC)	0.5985557	0.473231	DOWN	6DPA	Cell wall
Solyc11g005820	Solyc11g005820.1.1	Pectinesterase inhibitor (AHRD V3.3 *** A0A103Y9H8_CYNCS)	0.657661515	0.653020448	DOWN	6DPA	Cell wall
Solyc03g058910	Solyc03g058910.3.1	Pectate lyase (AHRD V3.3 *** M1A3P9_SOLTU)	0.114709852	0.077554745	DOWN	6DPA	Cell wall
Solyc06g074630	Solyc06g074630.3.1	Cellulose synthase-like protein (AHRD V3.3 *** L0ATP8_POPTO)	0.644669181	0.598504137	DOWN	6DPA	Cell wall
Solyc09g005530	Solyc09g005530.3.1	UDP-glucuronic acid decarboxylase 1 (AHRD V3.3 *-.* AT3G53520.4)	0	0	DOWN	20DPA	Cell wall
Solyc12g055970	Solyc12g055970.2.1	Endoglucanase (AHRD V3.3 *** Q93WY9_TOBAC)	0.304654443	0.235294118	DOWN	20DPA	Cell wall
Solyc12g056960	Solyc12g056960.2.1	Glucan 1,3-beta-glucosidase (AHRD V3.3 *** A0A151TZN5_CAJCA)	0.30551817	0.320169252	DOWN	20DPA	Cell wall
Solyc05g005170	Solyc05g005170.3.1	Pectin lyase-like superfamily protein (AHRD V3.3 *** A0A061E6B2_THECC)	0.335311573	0.374792703	DOWN	20DPA	Cell wall
Solyc03g058910	Solyc03g058910.3.1	Pectate lyase (AHRD V3.3 *** M1A3P9_SOLTU)	0.10041841	0.157377049	DOWN	20DPA	Cell wall
Solyc04g008210	Solyc04g008210.2.1	ETAG-A3	0.559619238	0.545010978	DOWN	20DPA	Cell wall
Solyc04g008230	Solyc04g008230.3.1	Pectin lyase-like superfamily protein (AHRD V3.3 *** AT1G48100.1)	0.352300351	0.541891705	DOWN	20DPA	Cell wall

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	FC <i>adp</i> /CL	FC <i>adp</i> /WT	UP/DOWN	Stage	Biological pathway
Solyc09g092520	Solyc09g092520.3.1	xyloglucan endotransglycosylase	0.523869717	0.59311102	DOWN	20DPA	Cell wall
Solyc03g119080	Solyc03g119080.4.1	beta-mannosidase enzyme	0.644282941	0.657890055	DOWN	20DPA	Cell wall
Solyc06g009190	Solyc06g009190.3.1	Pectinesterase (AHRD V3.3 *** K4C3U9_SOLLC)	0.487106938	0.607263107	DOWN	20DPA	Cell wall
Solyc04g074830	Solyc04g074830.1.1	At4g40080-like protein	1.667910448	1.689581857	UP	6DPA	Cellular trafficking
Solyc01g106950	Solyc01g106950.3.1	myosin heavy chain-like protein (AHRD V3.3 *** AT2G14680.3)	1.912198181	1.754315305	UP	20DPA	Cellular trafficking
Solyc01g010430	Solyc01g010430.3.1	Actin cross-linking protein, putative (AHRD V3.3 *** A0A061E7B5_THECC)	1.987230799	1.567498497	UP	20DPA	Cellular trafficking
Solyc02g069660	Solyc02g069660.3.1	Vacuolar protein sorting-associated protein 54 (AHRD V3.3 *_* A0A118JS09_CYNCS)	1.937256599	1.571428571	UP	20DPA	Cellular trafficking
Solyc10g006540	Solyc10g006540.3.1	Formin-like protein (AHRD V3.3 *** K4CXI5_SOLLC)	1.963244613	1.603519669	UP	20DPA	Cellular trafficking
Solyc09g064200	Solyc09g064200.3.1	Myosin (AHRD V3.3 *** W5ZTD6_MAIZE)	2.149462778	1.504768301	UP	20DPA	Cellular trafficking
Solyc02g090260	Solyc02g090260.2.1	Golgin candidate 6 isoform 2 (AHRD V3.3 *** A0A061DMU6_THECC)	2.472154964	1.833034111	UP	20DPA	Cellular trafficking
Solyc12g010110	Solyc12g010110.2.1	Formin-like protein (AHRD V3.3 *** K4DC98_SOLLC)	2.378099174	1.70014771	UP	20DPA	Cellular trafficking
Solyc08g075650	Solyc08g075650.3.1	Formin-like protein (AHRD V3.3 *** K4CMT2_SOLLC)	1.953210011	1.598871734	UP	20DPA	Cellular trafficking
Solyc01g081540	Solyc01g081540.3.1	Myosin family protein, putative, expressed (AHRD V3.3 *** Q10CX1_ORYSJ)	1.857811586	1.573534878	UP	20DPA	Cellular trafficking
Solyc02g091730	Solyc02g091730.2.1	Chromatin SPT2 (AHRD V3.3 *** A0A118JSU1_CYNCS)	1.57419511	2.208149406	UP	6DPA	Chromatin remodeling
Solyc06g071580	Solyc06g071580.3.1	MORC family CW-type zinc finger protein 4 (AHRD V3.3 *** A0A0B0PTV2_GOSAR)	2.56932966	4.455414013	UP	6DPA	Chromatin remodeling
Solyc11g062010	Solyc11g062010.2.1	Chromodomain-helicase-DNA-binding protein 1	1.746601722	1.506791752	UP	20DPA	Chromatin remodeling
Solyc09g009080	Solyc09g009080.3.1	DNA demethylase 1	1.810532341	1.75527192	UP	20DPA	Chromatin remodeling
Solyc09g008520	Solyc09g008520.3.1	RING/FYVE/PHD zinc finger protein (AHRD V3.3 *** A0A072VVJ3_MEDTR)	1.60664523	1.587923729	UP	20DPA	Chromatin remodeling
Solyc06g071580	Solyc06g071580.3.1	MORC family CW-type zinc finger protein 4 (AHRD V3.3 *** A0A0B0PTV2_GOSAR)	3.7347876	11.91575092	UP	20DPA	Chromatin remodeling
Solyc01g006880	Solyc01g006880.3.1	Histone-lysine N-methyltransferase (AHRD V3.3 *_* A0A0K9PTQ5_ZOSMR)	1.998004988	1.597288676	UP	20DPA	Chromatin remodeling
Solyc08g065820	Solyc08g065820.2.1	Transcription factor jumoni (jmiC) domain-containing protein (AHRD V3.3 *_* AT3G07610.1)	2.200471698	1.729379055	UP	20DPA	Chromatin remodeling

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	FC <i>adp</i> /CL	FC <i>adp</i> /WT	UP/DOWN	Stage	Biological pathway
Solyc07g052020	Solyc07g052020.2.1	SNF2 domain-containing protein / helicase domain-containing protein (AHRD V3.3 *-* AT3G12810.2)	#DIV/0!	6.655172414	UP	20DPA	Chromatin remodeling
Solyc12g099910	Solyc12g099910.2.1	Chromatin remodeling 5 (AHRD V3.3 *** AT2G13370.3)	1.567672611	1.555580762	UP	20DPA	Chromatin remodeling
Solyc06g050320	Solyc06g050320.3.1	High mobility group (HMG) box domain-containing protein (AHRD V3.3 *** A0A103YDE8_CYNCS)	0.596166307	0.632251045	DOWN	6DPA	Chromatin remodeling
Solyc01g006680	Solyc01g006680.3.1	Transcription factor jumonji jmjC domain protein	0.6562732	0.591304348	DOWN	20DPA	Chromatin remodeling
Solyc01g087400	Solyc01g087400.3.1	Histone-lysine N-methyltransferase M1.1.4 (AHRD V3.3 *** A0A0B0PKG0_GOSAR)	1.739947656	1.600218818	UP	20DPA	Chromatin remodeling
Solyc04g051490	Solyc04g051490.3.1	essential meiotic endonuclease 1B (AHRD V3.3 *-* AT2G22140.1)	1.821969697	2.586021505	UP	20DPA	DNA repair
Solyc02g091620	Solyc02g091620.2.1	DNA mismatch repair protein-like	3.071135431	2.388297872	UP	20DPA	DNA repair
Solyc05g051680	Solyc05g051680.3.1	Structural maintenance of chromosomes family protein (AHRD V3.3 *** D7M0L2_ARALL)	1.767430025	1.796689084	UP	20DPA	DNA repair
Solyc12g042000	Solyc12g042000.2.1	Protein BREAST CANCER SUSCEPTIBILITY 1 like (AHRD V3.3 *-* A0A0B2PNV8_GLYSO)	3.879882093	2.119565217	UP	20DPA	DNA repair
Solyc09g066080	Solyc09g066080.2.1	Protein BREAST CANCER SUSCEPTIBILITY 1-like protein (AHRD V3.3 *-* W9R323_9ROSA)	2.148946595	1.570916905	UP	20DPA	DNA repair
Solyc07g052010	Solyc07g052010.2.1	SNF2 domain-containing protein (AHRD V3.3 *** D7KEB6_ARALL)	13.92857143	8.125	UP	20DPA	DNA repair
Solyc01g098520	Solyc01g098520.3.1	DNA mismatch repair protein mutL (AHRD V3.3 *-* A0A151THR9_CAJCA)	2.139931741	1.628571429	UP	20DPA	DNA repair
Solyc10g006200	Solyc10g006200.3.1	Ribonuclease 3-like protein 2 (AHRD V3.3 *** A0A061F5X1_THECC)	2.343592965	1.79375	UP	20DPA	Gene silencing/siRNA production
Solyc11g008530	Solyc11g008530.2.1	Dicer-like 2d	1.662682927	1.607024988	UP	20DPA	Gene silencing/siRNA production
Solyc04g082630	Solyc04g082630.3.1	Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** K4BVZ0_SOLLC)	0.50319231	0.667224858	DOWN	20DPA	Glycolysis
Solyc04g009030	Solyc04g009030.3.1	Glyceraldehyde-3-phosphate dehydrogenase (AHRD V3.3 *** K4BP59_SOLLC)	0.6181287	0.657776323	DOWN	20DPA	Glycolysis
Solyc09g059170	Solyc09g059170.2.1	Glycosyltransferase (AHRD V3.3 *** M1C989_SOLTU)	0.393763214	0.413028413	DOWN	20DPA	Glycosylation
Solyc12g098600	Solyc12g098600.1.1	Glycosyltransferase (AHRD V3.3 *** K4DHN3_SOLLC)	0.602474449	0.583789419	DOWN	20DPA	Glycosylation

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	FC <i>adp</i> /CL	FC <i>adp</i> /WT	UP/DOWN	Stage	Biological pathway
Solyc09g092500	Solyc09g092500.1.1	Glycosyltransferase (AHRD V3.3 *** K4CWS6_SOLLIC)	0.650985317	0.54067715	DOWN	20DPA	Glycosylation
Solyc07g043500	Solyc07g043500.1.1	Glycosyltransferase (AHRD V3.3 *** K4CEK8_SOLLIC)	0.476422404	0.374586597	DOWN	20DPA	Glycosylation
Solyc03g116530	Solyc03g116530.3.1	Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 *** AT1G80160.3)	0.619135518	0.458584938	DOWN	20DPA	Glyoxalase pathway
Solyc01g103590	Solyc01g103590.3.1	Lactoylglutathione lyase / glyoxalase I family protein (AHRD V3.3 *** A0A061DWL3_THECC)	0.282135524	0.313412409	DOWN	20DPA	Glyoxalase pathway
Solyc07g044750	Solyc07g044750.3.1	N-acetyl-D-glucosamine kinase (AHRD V3.3 *** A0A0B0P7N8_GOSAR)	1.946481665	1.921722114	UP	6DPA	Metabolism/Amino-sugar
Solyc02g093430	Solyc02g093430.3.1	Beta-1,4-N-acetylglucosaminyltransferase-like protein (AHRD V3.3 *** A0A072U8DI_MEDTR)	1.938682551	1.723676012	UP	6DPA	Metabolism/Amino-sugar
Solyc12g008900	Solyc12g008900.2.1	cytokinin oxidase6	5.77124183	7.483050847	UP	20DPA	Metabolism/Cytokinin
Solyc02g091990	Solyc02g091990.3.1	1-aminocyclopropane-1-carboxylate synthase 3	2.124171187	2.631814787	UP	6DPA	Metabolism/Ethylene
Solyc07g049530	Solyc07g049530.3.1	1-aminocyclopropane-1-carboxylate oxidase 1	1.808275198	3.122974657	UP	20DPA	Metabolism/Ethylene
Solyc04g049360	Solyc04g049360.3.1	aminodeoxychorismate synthase/glutamine amidotransferase	2.429983526	1.855345912	UP	20DPA	Metabolism/Folate
Solyc03g006880	Solyc03g006880.3.1	gibberellin 20-oxidase-1	0.609409856	0.513499658	DOWN	20DPA	Metabolism/Gibberellin
Solyc02g070430	Solyc02g070430.3.1	Gibberellin 2 oxidase (AHRD V3.3 *** Q53CC60_NEROL)	0.283244681	0.241770715	DOWN	20DPA	Metabolism/Gibberellin
Solyc08g083110	Solyc08g083110.3.1	Cystathionine gamma-synthase, putative (AHRD V3.3 *_* B9RYU1_RICCO)	2.235622817	1.624703892	UP	6DPA	Metabolism/Amino acids
Solyc06g050630	Solyc06g050630.3.1	arogenate dehydrogenase (AHRD V3.3 *_* AT5G34930.3)	2.589939024	4.732590529	UP	6DPA	Metabolism/Amino acids
Solyc06g011530	Solyc06g011530.3.1	Hydroxymethylglutaryl-CoA lyase (AHRD V3.3 *_* W9QRW1_9ROSA)	1.890455095	1.66749556	UP	20DPA	Metabolism/Amino acids
Solyc07g017670	Solyc07g017670.2.1	Lysine-ketoglutarate reductase/saccharopine dehydrogenase (AHRD V3.3 *_* A0A072V2T5_MEDTR)	4.587163233	3.828703704	UP	20DPA	Metabolism/Amino acids
Solyc08g068600	Solyc08g068600.3.1	Aromatic amino acid decarboxylase 1B (AHRD V3.3 *** Q1KSC5_SOLLIC)	1.755698333	1.538059501	UP	6DPA	Metabolism/lipid
Solyc02g094400	Solyc02g094400.3.1	Glycerophosphodiester phosphodiesterase, putative (AHRD V3.3 *** B9RH28_RICCO)	1.891148525	1.763837065	UP	6DPA	Metabolism/Lipid
Solyc03g115370	Solyc03g115370.3.1	Diacylglycerol kinase (AHRD V3.3 *** K4BL39_SOLLIC)	1.700235571	2.023125438	UP	6DPA	Metabolism/Lipid

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	FC <i>adp</i> /CL	FC <i>adp</i> /WT	UP/DOWN	Stage	Biological pathway
Solyc10g086690	Solyc10g086690.2.1	Phosphatidylinositol:ceramide inositolphosphotransferase (AHRD V3.3 *** IPCS_ORYSI)	1.860497238	2.748979592	UP	6DPA	Metabolism/Lipid
Solyc02g036290	Solyc02g036290.3.1	malonyl-CoA decarboxylase family protein (AHRD V3.3 * AT4G04320.2)	1.76147541	1.960766423	UP	20DPA	Metabolism/Lipid
Solyc03g044910	Solyc03g044910.1.1	GNS1/SUR4 membrane protein family (AHRD V3.3 *** AT4G36830.1)	1.678817056	1.543308746	UP	20DPA	Metabolism/Lipid
Solyc07g032180	Solyc07g032180.3.1	Abhydrolase domain-containing protein 4 (AHRD V3.3 *** A0A0B2SN17_GLYSO)	3.23032491	1.641232575	UP	20DPA	Metabolism/Lipid
Solyc09g075790	Solyc09g075790.3.1	Long-Chain Acyl-CoA Synthetase (AHRD V3.3 *** A0A0R5QM74_SAI.MI)	2.800166528	1.9782335294	UP	20DPA	Metabolism/Lipid
Solyc07g032170	Solyc07g032170.3.1	Abhydrolase domain-containing protein	3.223153693	2.155365723	UP	20DPA	Metabolism/Lipid
Solyc07g054830	Solyc07g054830.3.1	diacylglycerol kinase	1.643932684	1.500404204	UP	20DPA	Metabolism/Lipid
Solyc02g082770	Solyc02g082770.3.1	Phosphatidylinositol-4-phosphatase SAC1	2.655472363	1.753708551	UP	20DPA	Metabolism/Lipid
Solyc05g042070	Solyc05g042070.3.1	1-phosphatidylinositol-4-phosphate 5-kinase 3 (AHRD V3.3 ** AT2G26420.3)	2.133703825	2.020117611	UP	20DPA	Metabolism/Lipid
Solyc06g030590	Solyc06g030590.2.1	8-amino-7-oxononanoate synthase	14.24	6.592592593	UP	20DPA	Metabolism/Lipid
Solyc08g082920	Solyc08g082920.3.1	ORMDL family protein (AHRD V3.3 *** AT5G42000.1)	0.660786366	0.668582665	DOWN	6DPA	Metabolism/Lipid
Solyc07g014730	Solyc07g014730.3.1	Phospholipase A2 (AHRD V3.3 *** Q5CCT8_TOBAC)	0.459466139	0.486776643	DOWN	20DPA	Metabolism/Lipid
Solyc01g005930	Solyc01g005930.3.1	Lipase/lipoxygenase, PLAT/LH2 (AHRD V3.3 *** A0A118IU91_CYNCS)	0.573055028	0.516902011	DOWN	20DPA	Metabolism/Lipid
Solyc06g068010	Solyc06g068010.3.1	Biotin carboxyl carrier protein (AHRD V3.3 *** A0A0H5BV69_PEA)	0.548246885	0.510248112	DOWN	20DPA	Metabolism/Lipid
Solyc07g056320	Solyc07g056320.3.1	Glycerol-3-phosphate acyltransferase (AHRD V3.3 *** G7K3C7_MEDTR)	0.35976016	0.494505495	DOWN	20DPA	Metabolism/Lipid
Solyc06g069640	Solyc06g069640.3.1	dCTP pyrophosphatase 1 (AHRD V3.3 *** A0A151SL49_CAJCA)	0.513905831	0.498697917	DOWN	20DPA	Metabolism/Nucleoti de
Solyc06g074710	Solyc06g074710.1.1	hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase (AHRD V3.3 *** AT5G48930.1)	0.464136092	0.531781818	DOWN	20DPA	Metabolism/Phenylpr opanoide
Solyc04g054260	Solyc04g054260.3.1	Cytochrome P450 family protein (AHRD V3.3 *** B9HFw5_POPTR)	0.144254279	0.207017544	DOWN	20DPA	Metabolism/Phenylpr opanoide
Solyc06g068440	Solyc06g068440.3.1	cinnamoyl-CoA reductase	0.662819456	0.619017067	DOWN	20DPA	Metabolism/Phenylpr opanoide
Solyc01g081050	Solyc01g081050.4.1	D-alanine--poly(phosphoribitol) ligase subunit 1 (AHRD V1 *** DLTA_BACSU)%3B contains Interpro domain(s) IPR000873	2.796927188	1.628549203	UP	20DPA	Metabolism/RNA

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	FC <i>adp</i> /CL	FC <i>adp</i> /WT	UP/DOWN	Stage	Biological pathway
Solyc08g066650	Solyc08g066650.3.1	Carotenoid Cleavage Dioxygenase 8	0.400986031	0.315857605	DOWN	20DPA	Metabolism/Strigolactone
Solyc08g082440	Solyc08g082440.3.1	UDP-glucose 4-epimerase (AHRD V3.3 *** Q6XZA0_SOLTU)	0.639279438	0.581302437	DOWN	20DPA	Metabolism/Sugar
Solyc07g064160	Solyc07g064160.3.1	Thiamine thiazole synthase, chloroplastic (AHRD V3.3 *** K4CH99_SOLLIC)	0.591909213	0.396333686	DOWN	20DPA	Metabolism/Thiamine
Solyc10g018300	Solyc10g018300.2.1	Transketolase (AHRD V3.3 *** AT3G60750.1)	0.523392963	0.593076374	DOWN	20DPA	Pentose phosphate pathway
Solyc03g115820	Solyc03g115820.3.1	Ribulose-phosphate 3-epimerase (AHRD V3.3 *** A0A072V1G6_MEDTR)	0.637219731	0.591590341	DOWN	20DPA	Pentose phosphate pathway
Solyc06g054220	Solyc06g054220.2.1	Photosystem II reaction center PsbP family protein (AHRD V3.3 --* AT4G15510.1)	2.715497301	2.537463977	UP	20DPA	Photosynthesis
Solyc00g230080	Solyc00g230080.1.1	LOW QUALITY:Photosystem II D2 protein (AHRD V3.3 --* PSBD_PLETE)	54.63636364	6.326315789	UP	20DPA	Photosynthesis
Solyc02g069450	Solyc02g069450.3.1	Photosystem I reaction center subunit III (AHRD V3.3 *** I3SN70_MEDTR)	0.347567312	0.631696429	DOWN	20DPA	Photosynthesis
Solyc06g074200	Solyc06g074200.3.1	photosystem I subunit O (AHRD V3.3 *** AT1G08380.1)	0.407573526	0.606689696	DOWN	20DPA	Photosynthesis
Solyc06g083680	Solyc06g083680.3.1	Photosystem I reaction center subunit IV (AHRD V3.3 *** A0A0K9P6J8_ZOSMR)	0.438852215	0.669402247	DOWN	20DPA	Photosynthesis
Solyc10g006370	Solyc10g006370.3.1	Lhcb translocation defect-like protein (AHRD V3.3 *** A0A0B0PFC4_GOSAR)	0.53268945	0.65014357	DOWN	20DPA	Photosynthesis
Solyc08g006930	Solyc08g006930.3.1	Photosystem I reaction center subunit psaK (AHRD V3.3 *** W9SCM1_9ROSA)	0.565051353	0.641728273	DOWN	20DPA	Photosynthesis
Solyc07g065200	Solyc07g065200.3.1	Mitochondrial import inner membrane translocase subunit tim22 (AHRD V3.3 *** A0A0B0NT47_GOSAR)	0.606244685	0.656233561	DOWN	20DPA	Photosynthesis
Solyc03g034220	Solyc03g034220.3.1	Tomato RuBP carboxylase small subunit	0.605714146	0.57717745	DOWN	20DPA	Photosynthesis
Solyc10g077040	Solyc10g077040.2.1	putative magnesium-protoporphyrin monomethyl ester cyclase	0.563306206	0.65136675	DOWN	20DPA	Photosynthesis
Solyc03g005760	Solyc03g005760.1.1	chlorophyll a/b-binding protein	0.505873923	0.607866064	DOWN	20DPA	Photosynthesis
Solyc02g071030	Solyc02g071030.2.1	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** Q41422_SOLTU)	0.380725582	0.594533543	DOWN	20DPA	Photosynthesis
Solyc03g005780	Solyc03g005780.3.1	chlorophyll a/b-binding protein Cab-3C	0.290474466	0.453876627	DOWN	20DPA	Photosynthesis
Solyc01g105050	Solyc01g105050.3.1	Chlorophyll a-b binding protein, chloroplastic (AHRD V3.3 *** M1AY18_SOLTU)	0.432724108	0.552567237	DOWN	20DPA	Photosynthesis
Solyc03g005770	Solyc03g005770.3.1	chlorophyll a/b-binding protein	0.53302625	0.569032909	DOWN	20DPA	Photosynthesis
Solyc03g112340	Solyc03g112340.1.1	RING/U-box superfamily protein (AHRD V3.3 *** AT3G05200.1)	1.500472441	1.676284307	UP	6DPA	Protein degradation

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	FC <i>adp</i> /CL	FC <i>adp</i> /WT	UP/DOWN	Stage	Biological pathway
Solyc04g082420	Solyc04g082420.3.1	BTB/POZ domain-containing protein (AHRD V3.3 *** AT2G30600.6)	1.712795549	1.813696613	UP	6DPA	Protein degradation
Solyc04g005040	Solyc04g005040.1.1	Matrix metalloproteinase (AHRD V3.3 *** I7K140_SOLLIC)	1.508605127	1.669330137	UP	6DPA	Protein degradation
Solyc01g106820	Solyc01g106820.3.1	Peptidase M50 family	1.680029696	2.628339141	UP	6DPA	Protein degradation
Solyc07g043510	Solyc07g043510.3.1	OTU domain-containing (AHRD V3.3 *** A0A0B0PSP5_GOSAR)	1.751452282	1.676330421	UP	6DPA	Protein degradation
Solyc04g008100	Solyc04g008100.2.1	U-box domain-containing protein (AHRD V3.3 *** A0A0A0RAL4_9ROSI)	2.491947291	2.30936228	UP	6DPA	Protein degradation
Solyc11g068710	Solyc11g068710.2.1	F-box family protein (AHRD V3.3 *** B9MYU0_POPTIR)	1.594758621	1.529567403	UP	6DPA	Protein degradation
Solyc03g117860	Solyc03g117860.3.1	RING/U-box superfamily protein (AHRD V3.3 *-* AT3G14250.1)	2.351815824	2.889641434	UP	20DPA	Protein degradation
Solyc11g005650	Solyc11g005650.1.1	Ubiquitin family protein (AHRD V3.3 *-* AT4G02890.4)	2.378167641	2.513736264	UP	20DPA	Protein degradation
Solyc11g005640	Solyc11g005640.2.1	Polyubiquitin (AHRD V3.3 *-* UBI2P_PETCR)	1.839530333	2.30958231	UP	20DPA	Protein degradation
Solyc02g067260	Solyc02g067260.2.1	RING/U-box superfamily protein (AHRD V3.3 *-* AT1G26800.1)	2.705641864	3.250491159	UP	20DPA	Protein degradation
Solyc02g014170	Solyc02g014170.3.1	RING/U-box superfamily protein (AHRD V3.3 -_* AT2G38195.1)	1.832647462	1.652442795	UP	20DPA	Protein degradation
Solyc07g007170	Solyc07g007170.3.1	RING/U-box superfamily protein (AHRD V3.3 *** A0A061GN77_THECC)	1.654096339	1.96	UP	20DPA	Protein degradation
Solyc11g020960	Solyc11g020960.2.1	Proteinase inhibitor II (AHRD V3.3 *-* B3F0C1_TOBAC)	2.266082034	1.902516309	UP	20DPA	Protein degradation
Solyc07g008430	Solyc07g008430.2.1	RING/U-box superfamily protein (AHRD V3.3 -_* AT3G56580.3)	0.416714404	0.511664257	DOWN	20DPA	Protein degradation
Solyc11g066510	Solyc11g066510.2.1	RING/U-box superfamily protein (AHRD V3.3 *** AT2G27940.1)	0.487200161	0.575339205	DOWN	20DPA	Protein degradation
Solyc04g079780	Solyc04g079780.3.1	RING/U-box superfamily protein (AHRD V3.3 *** AT2G16090.1)	0.659682247	0.647750396	DOWN	20DPA	Protein degradation
Solyc07g049140	Solyc07g049140.3.1	Metalloproteinase inhibitor (AHRD V3.3 *** O24639_SOLITU)	0.663099208	0.544436272	DOWN	20DPA	Protein degradation
Solyc01g096450	Solyc01g096450.3.1	Aspartic proteinase nepenthesin-1-like protein (AHRD V3.3 *** T2DNA5_PHAVU)	0.485988387	0.633119553	DOWN	20DPA	Protein degradation
Solyc12g056410	Solyc12g056410.2.1	F-box protein PP2-A13 (AHRD V3.3 *** P2A13_ARATH)	0.651685393	0.635077519	DOWN	20DPA	Protein degradation
Solyc02g069110	Solyc02g069110.3.1	Cathepsin B-like cysteine protease (AHRD V3.3 *** B7FJ05_MEDTR)	0.566188198	0.479915025	DOWN	20DPA	Protein degradation
Solyc09g075080	Solyc09g075080.3.1	Phytochrome A-associated F-box protein, putative (AHRD V3.3 *** B9SAQ8_RICCO)	0.534989648	0.515974441	DOWN	20DPA	Protein degradation

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	FC <i>adp</i> /CL	FC <i>adp</i> /WT	UP/DOWN	Stage	Biological pathway
Solyc05g041860	Solyc05g041860.3.1	N-acetyltransferase (AHRD V3.3 *** B6TRH8_MAIZE)	2.106119926	1.804873742	UP	20DPA	Protein modification
Solyc12g062340	Solyc12g062340.2.1	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein (AHRD V3.3 --* AT3G44840.1)	9.468085106	6.267605634	UP	20DPA	Protein modification
Solyc04g072260	Solyc04g072260.2.1	Midasin (AHRD V3.3 *-* K4BTL3_SOLLIC)	2.013583138	1.854616048	UP	20DPA	Ribosome biogenesis
Solyc01g104470	Solyc01g104470.3.1	Acidic ribosomal protein P0 (AHRD V3.3 *** B9I0W5_POPTR)	0.66043877	0.6111390435	DOWN	20DPA	Ribosome biogenesis
Solyc04g081330	Solyc04g081330.3.1	30S ribosomal protein S16, chloroplastic (AHRD V3.3 --* RR16_MORIN)	0.665914221	0.664663913	DOWN	20DPA	Ribosome biogenesis
Solyc04g079790	Solyc04g079790.3.1	30S ribosomal protein S9 (AHRD V3.3 *** A9PB01_POPTR)	0.663109049	0.653929756	DOWN	20DPA	Ribosome biogenesis
Solyc03g081300	Solyc03g081300.3.1	Mitochondrial transcription termination factor-related family protein (AHRD V3.3 *** B9ID10_POPTR)	1.537971014	1.685514612	UP	6DPA	RNA processing
Solyc02g084330	Solyc02g084330.3.1	decapping 5-like protein (AHRD V3.3 --* AT5G45330.3)	2.805687204	2.524520256	UP	20DPA	RNA processing
Solyc05g009540	Solyc05g009540.3.1	Protein kinase-like protein (AHRD V3.3 *** Q8RWN3_ARATH)	1.675944334	1.581613508	UP	20DPA	RNA processing
Solyc06g076850	Solyc06g076850.3.1	Tetratricopeptide repeat (TPR)-like superfamily protein (AHRD V3.3 *** AT2G29670.2)	1.675384392	1.524694013	UP	20DPA	RNA processing
Solyc01g087320	Solyc01g087320.3.1	tRNA-dihydrouridine synthase A	1.88104724	1.833056018	UP	20DPA	RNA processing
Solyc11g008470	Solyc11g008470.2.1	U4/U6.U5 tri-snRNP-associated protein 1 (AHRD V3.3 *** A0A0B2S142_GLYSO)	1.55006105	1.611722387	UP	20DPA	RNA processing
Solyc11g022600	Solyc11g022600.2.1	Mitochondrial transcription termination factor-like (AHRD V3.3 *-* Q6Z8L0_ORYSJ)	1.745073109	1.654278827	UP	20DPA	RNA processing
Solyc01g090860	Solyc01g090860.3.1	Nucleotidyltransferase family protein (AHRD V3.3 *** AT4G00060.4)	2.043956044	1.564120533	UP	20DPA	RNA processing
Solyc11g039950	Solyc11g039950.2.1	Splicing factor 3B subunit 4	2.296890424	1.871129875	UP	20DPA	RNA processing
Solyc04g050760	Solyc04g050760.3.1	U11/U12 small nuclear ribonucleoprotein (AHRD V3.3 *** AT3G04160.3)	2.014789534	1.690692124	UP	20DPA	RNA processing
Solyc08g077310	Solyc08g077310.3.1	RNA-binding protein, putative (AHRD V3.3 *** A0A072U387_MEDTR)	1.51488	1.525620367	UP	20DPA	RNA processing
Solyc02g086600	Solyc02g086600.3.1	polynucleotide nucleotidyltransferase (AHRD V3.3 *** AT5G14580.1)	1.651977401	1.558635394	UP	20DPA	RNA processing
Solyc05g013400	Solyc05g013400.3.1	Pentatricopeptide repeat superfamily protein, putative (AHRD V3.3 *** A0A061GR61_THECC)	1.770477816	1.658673062	UP	20DPA	RNA processing

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	FC <i>adp</i> /CL	FC <i>adp</i> /WT	UP/DOWN	Stage	Biological pathway
Solyc03g063370	Solyc03g063370.3.1	Pentatricopeptide repeat-containing protein (AHRD V3.3 *_* A0A0B2RWF1_GLYSO)	6.605381166	3.024640657	UP	20DPA	RNA processing
Solyc04g057990	Solyc04g057990.3.1	mRNA 3'-terminal processing protein YTH1	2.365453248	2.221179625	UP	20DPA	RNA processing
Solyc07g041020	Solyc07g041020.3.1	RNA-binding protein (AHRD V3.3 *** B4FIJ2_MAIZE)	0.629372497	0.634967672	DOWN	6DPA	RNA processing
Solyc10g050450	Solyc10g050450.2.1	CSL zinc finger protein, putative (AHRD V3.3 *** G7JEX8_MEDTR)	0.337520481	0.340495868	DOWN	20DPA	RNA processing
Solyc01g028800	Solyc01g028800.2.1	RNA binding protein, putative (AHRD V3.3 *** B9SBN7_RICCO)	0.135483871	0.168	DOWN	20DPA	RNA processing
Solyc03g058190	Solyc03g058190.3.1	elongation factor family protein (AHRD V3.3 *** AT5G13650.2)	1.71155034	1.522457763	UP	20DPA	RNA processing
Solyc03g113490	Solyc03g113490.3.1	HPL1-like protein (AHRD V3.3 *** A0A0B0MLG6_GOSAR)	4.25	4.25	UP	6DPA	Signaling
Solyc01g096340	Solyc01g096340.3.1	Small auxin up-regulated RNA2	0.529204499	0.478612575	DOWN	20DPA	Signaling/auxin
Solyc11g071760	Solyc11g071760.3.1	Calmodulin-like protein	3.099150142	2.912673056	UP	6DPA	Signaling/calcium signaling
Solyc02g094000	Solyc02g094000.1.1	Calcium-binding protein (AHRD V3.3 *** A0A199V9T9_ANACO)	2.249836779	1.833433831	UP	6DPA	Signaling/calcium signaling
Solyc11g071740	Solyc11g071740.2.1	Calmodulin-like protein (AHRD V1 ***-Q0VJ70_DATME)	2.158940397	2.391015356	UP	6DPA	Signaling/calcium signaling
Solyc11g071750	Solyc11g071750.2.1	Calmodulin-like protein (AHRD V1 ***-Q0VJ70_DATME)	2.594620104	3.154331612	UP	6DPA	Signaling/calcium signaling
Solyc07g056560	Solyc07g056560.3.1	cytokinin response factor 2 (AHRD V3.3 *-* AT4G223750.2)	0.229086229	0.26969697	DOWN	20DPA	Signaling/Cytokinin
Solyc10g079700	Solyc10g079700.2.1	Two-component response regulator (AHRD V3.3 *** A0A059T9P7_ROSCN)	0.454265949	0.591295648	DOWN	6DPA	Signaling/Cytokinin
Solyc07g064380	Solyc07g064380.3.1	serine/threonine-protein phosphatase 7 long form-like protein (AHRD V3.3 *-* AT1G32120.1)	206.6666667	44.28571429	UP	20DPA	Signaling/Kinase
Solyc02g089010	Solyc02g089010.2.1	Receptor protein kinase, putative (AHRD V3.3 *_* B9RXG1_RICCO)	4.50174703	1.970030581	UP	20DPA	Signaling/kinase
Solyc05g013300	Solyc05g013300.1.1	Pseudomonas syringae pv tomato resis. B911R1_POPTTR	1.912342328	1.519923858	UP	20DPA	Signaling/kinase
Solyc02g071820	Solyc02g071820.3.1	Receptor-like protein kinase (AHRD V3.3 *** B911R1_POPTTR)	2.835045971	2.558321132	UP	20DPA	Signaling/kinase
Solyc12g006980	Solyc12g006980.1.1	Leucine-rich repeat receptor-like protein kinase family (AHRD V3.3 *-* A0A0K9PTR8_ZOSMR)	2.304904133	1.806471891	UP	20DPA	Signaling/Kinase
Solyc08g077630	Solyc08g077630.3.1	Kinase family protein (AHRD V3.3 *** B9MTV7_POPTTR)	2.173628174	1.739187418	UP	20DPA	Signaling/Kinase

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	FC <i>adp</i> /CL	FC <i>adp</i> /WT	UP/DOWN	Stage	Biological pathway
Solyc11g061720	Solyc11g061720.1.1	Kinase family protein (AHRD V3.3 *** D7KZX1_ARALL)	0.584471843	0.514067995	DOWN	20DPA	Signaling/kinase
Solyc05g005810	Solyc05g005810.3.1	Serine/threonine-protein kinase WNK-related (AHRD V3.3 *** A0A061E6Z5_THECC)	0.528430371	0.575240919	DOWN	20DPA	Signaling/kinase
Solyc02g084600	Solyc02g084600.3.1	Leucine-rich repeat receptor-like protein kinase family protein (AHRD V3.3 *** A0A061DFG6_THECC)	0.41943271	0.443098502	DOWN	20DPA	Signaling/kinase
Solyc01g080770	Solyc01g080770.3.1	Non-specific serine/threonine protein kinase (AHRD V3.3 *** K4XXX0_SOLLC)	0.44885971	0.614765736	DOWN	20DPA	Signaling/kinase
Solyc05g052520	Solyc05g052520.3.1	Protein phosphatase 2C family protein (AHRD V3.3 *** AT1G07160.1)	1.640196078	1.846170823	UP	6DPA	Signaling/Protein phosphatase
Solyc07g064380	Solyc07g064380.3.1	serine/threonine-protein phosphatase 7 long form-like protein (AHRD V3.3 *-* AT1G32120.1)	76.41666667	101.8888889	UP	6DPA	Signaling/Protein phosphatase
Solyc12g010450	Solyc12g010450.2.1	Protein phosphatase 2c, putative (AHRD V3.3 *** B9T2N5_RICCO)	0.541573868	0.613540791	DOWN	20DPA	Signaling/Protein phosphatase
Solyc01g007030	Solyc01g007030.3.1	U-box domain-containing family protein (AHRD V3.3 *** B9P691_POPTR)	2.445914397	2.641176471	UP	6DPA	Stress responses
Solyc02g087210	Solyc02g087210.3.1	Zinc finger AN1 domain-containing stress-associated protein 12 (AHRD V3.3 *** A0A151RAZ5_CAJCA)	1.769731632	2.136498832	UP	6DPA	Stress responses
Solyc01g109920	Solyc01g109920.2.1	Dehydrin protein	1.949245542	1.869736842	UP	6DPA	Stress responses
Solyc04g007580	Solyc04g007580.1.1	cDNA clone J100026116 full insert sequence	1.881307747	1.665565518	UP	6DPA	Stress responses
Solyc09g011030	Solyc09g011030.3.1	Hsp70-binding protein 1 (AHRD V3.3 *** W9RWP5_9ROSA)	1.540306701	1.661774173	UP	6DPA	Stress responses
Solyc05g006860	Solyc05g006860.3.1	Thioredoxin family protein (AHRD V3.3 *** B9IJS4_POPTR)	1.692465402	2.742524917	UP	6DPA	Stress responses
Solyc03g080150	Solyc03g080150.3.1	Peroxidase (AHRD V3.3 *** K4BHZ1_SOLLC)	2.697038724	1.887755102	UP	6DPA	Stress responses
Solyc05g006850	Solyc05g006850.3.1	Thioredoxin family protein (AHRD V3.3 *** B9IJS4_POPTR)	1.792703151	2.675742574	UP	6DPA	Stress responses
Solyc12g011310	Solyc12g011310.2.1	Glutathione S-transferase (AHRD V3.3 *** Q0PN10_9FABA)	6.224431818	6.488647581	UP	20DPA	Stress responses
Solyc03g113930	Solyc03g113930.2.1	Heat-shock protein, putative (AHRD V3.3 *** B9S5K5_RICCO)	4.816214359	16.7543021	UP	20DPA	Stress responses
Solyc06g076560	Solyc06g076560.2.1	17.6 kD class I small heat shock protein	1.792508835	3.91039318	UP	20DPA	Stress responses
Solyc03g117630	Solyc03g117630.1.1	heat shock protein 70 (AHRD V3.3 *** AT3G12580.1)	3.838081297	5.919763807	UP	20DPA	Stress responses
Solyc03g082420	Solyc03g082420.3.1	Heat shock protein (AHRD V3.3 *** A9QVH3_9FABA)	3.17882212	4.912686863	UP	20DPA	Stress responses

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	FC <i>adp</i> /CL	FC <i>adp</i> /WT	UP/DOWN	Stage	Biological pathway
Solyc02g093600	Solyc02g093600.3.1	Class I heat shock protein (AHRD V3.3 *** F4YBC5_SOLNI)	3.823698315	3.516725352	UP	20DPA	Stress responses
Solyc11g020330	Solyc11g020330.1.1	leer-sHSP small heat shock protein	5.78839032	6.662272006	UP	20DPA	Stress responses
Solyc07g056510	Solyc07g056510.3.1	Glutathione S-transferase (AHRD V1 **** D3Y4H6_9ROSI)	10.27952756	20.888	UP	20DPA	Stress responses
Solyc08g075540	Solyc08g075540.4.1	alternative oxidase 1au	2.849583066	2.64907573	UP	20DPA	Stress responses
Solyc01g100640	Solyc01g100640.3.1	Catalase (AHRD V3.3 *-1.0SQ20_TOBAC)	2.874439462	2.082521118	UP	20DPA	Stress responses
Solyc01g100630	Solyc01g100630.2.1	Catalase (AHRD V3.3 *-1.0CAT_SOLAP)	2.571348941	1.801249512	UP	20DPA	Stress responses
Solyc07g054790	Solyc07g054790.1.1	Wound-responsive family protein (AHRD V3.3 *** A0A061E3U8_THECC)	0.648975965	0.64007338	DOWN	6DPA	Stress responses
Solyc04g071890	Solyc04g071890.3.1	Peroxidase (AHRD V3.3 *** K4BTH6_SOLLIC)	0.338122605	0.277297722	DOWN	6DPA	Stress responses
Solyc07g007760	Solyc07g007760.3.1	defensin-like protein	0.623769001	0.600975001	DOWN	6DPA	Stress responses
Solyc07g065110	Solyc07g065110.1.1	Lipid transfer protein (AHRD V3.3 *** G7J041_MEDTR)	0.52919492	0.576541979	DOWN	20DPA	Stress responses
Solyc12g094380	Solyc12g094380.2.1	Thioredoxin superfamily protein (AHRD V3.3 *** A0A061FEH2_THECC)	0.615970842	0.587733165	DOWN	20DPA	Stress responses
Solyc01g100230	Solyc01g100230.3.1	DnaI-like protein (AHRD V3.3 *** D5FNB3_SOYBN)	0.471981695	0.654880478	DOWN	20DPA	Stress responses
Solyc03g095180	Solyc03g095180.3.1	Superoxide dismutase (AHRD V3.3 *** Q7YK44_SOLLIC)	0.541666667	0.664335664	DOWN	20DPA	Stress responses
Solyc06g005160	Solyc06g005160.3.1	Ascorbate peroxidase (AHRD V3.3 *** Q9SMD3_SOLLIC)	0.638551928	0.602310481	DOWN	20DPA	Stress responses
Solyc10g083650	Solyc10g083650.1.1	Peroxiredoxin, putative (AHRD V3.3 *** B9SRG0_RICCO)	0.587717723	0.597480832	DOWN	20DPA	Stress responses
Solyc04g064690	Solyc04g064690.3.1	Peroxidase (AHRD V3.3 *** K4BT60_SOLLIC)	0.388	0.507705728	DOWN	20DPA	Stress responses
Solyc09g011710	Solyc09g011710.3.1	Class I heat shock protein (AHRD V3.3 *** F4YBC5_SOLNI)	0.596822282	0.658960597	DOWN	20DPA	Stress responses
Solyc10g086680	Solyc10g086680.1.1	Class I heat shock protein (AHRD V3.3 *** F4YBC5_SOLNI)	0.615196318	0.557794744	DOWN	20DPA	Stress responses
Solyc01g109390	Solyc01g109390.3.1	Protease inhibitor/seed storage/lipid transfer protein family protein (AHRD V3.3 *** D7MM18_ARALL)	0.321157617	0.455507194	DOWN	20DPA	Stress responses
Solyc12g044420	Solyc12g044420.1.1	LOW QUALITY:Avr9/Cf-9 rapidly elicited protein (AHRD V3.3 *** G7LFFZ0_MEDTR)	0.464480037	0.488239085	DOWN	20DPA	Stress responses
Solyc08g005960	Solyc08g005960.2.1	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein (AHRD V3.3 *** AT2G45180.1)	0.569076869	0.578581115	DOWN	20DPA	Stress responses

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Solyc01g099180	Solyc01g099180.3.1	Lipoxygenase (AHRD V3.3 *** Q43800_TOBAC)	0.617602428	0.471428571	DOWN	20DPA	Stress responses
Solyc07g007750	Solyc07g007750.3.1	Defensin protein (AHRD V3.3 *** B1N678_SOLLC)	0.379452621	0.444513741	DOWN	20DPA	Stress responses
Solyc07g007760	Solyc07g007760.3.1	defensin-like protein	0.435407221	0.592067147	DOWN	20DPA	Stress responses
Solyc05g021580	Solyc05g021580.3.1	Serine/threonine-protein kinase TOR (AHRD V3.3 *_* TOR_ARATH)	2.922606925	3.28375286	UP	20DPA	TOR signaling
Solyc10g076260	Solyc10g076260.2.1	Regulatory-associated protein of TOR protein (AHRD V3.3 *_* G7KW32_MEDTR)	3.815831987	2.197209302	UP	20DPA	TOR signaling
Solyc10g076270	Solyc10g076270.2.1	WD repeat-containing protein mip1	3.570068747	1.851110502	UP	20DPA	TOR signaling
Solyc01g106770	Solyc01g106770.3.1	Serine/threonine-protein kinase (AHRD V3.3 *** A0A0K0XR78_TOBAC)	1.659192825	1.522633745	UP	20DPA	TOR signaling
Solyc10g050970	Solyc10g050970.1.1	Ethylene responsive transcription factor 2b	1.966744874	1.755600073	UP	6DPA	Transcription factor
Solyc02g077370	Solyc02g077370.1.1	Ethylene Response Factor C.5	2.189150264	1.981747066	UP	6DPA	Transcription factor
Solyc08g007820	Solyc08g007820.1.1	C-repeat binding factor (AHRD V3.3 *** A0A0BSKMN4_ACTCH)	1.871333843	1.769138035	UP	6DPA	Transcription factor
Solyc03g124110	Solyc03g124110.2.1	CRT binding factor 2	2.334019293	1.505975104	UP	6DPA	Transcription factor
Solyc06g035620	Solyc06g035620.3.1	GRAS family transcription factor (AHRD V3.3 *** D4QD66_DIACA)	1.593004769	1.906755471	UP	6DPA	transcription factor
Solyc10g011910	Solyc10g011910.3.1	WRKY transcription factor 25	1.744964029	2.636413043	UP	6DPA	Transcription factor
Solyc08g007830	Solyc08g007830.1.1	C-repeat binding factor (AHRD V3.3 *** E7D090_PRUPE)	2.02105615	2.027833669	UP	6DPA	Transcription factor
Solyc07g022920	Solyc07g022920.3.1	BSD domain-containing family protein (AHRD V3.3 *** B9IBP6_POPTK)	5.666666667	12.12403101	UP	6DPA	Transcription factor
Solyc05g056040	Solyc05g056040.3.1	Auxin Response Factor 24	1.585884048	1.70763862	UP	20DPA	Transcription factor
Solyc07g022920	Solyc07g022920.3.1	BSD domain-containing family protein (AHRD V3.3 *** B9IBP6_POPTK)	17.08268734	2.748856549	UP	20DPA	Transcription factor
Solyc12g010310	Solyc12g010310.2.1	Zinc finger CCH domain-containing protein 32 (AHRD V3.3 *_* C3H32_ORYSJ)	3.426413977	2.177865613	UP	20DPA	Transcription factor
Solyc02g091030	Solyc02g091030.3.1	Nuclear transcription factor Y subunit C-2 (AHRD V3.3 *_* W9SQ52_9ROSA)	2.217877095	2.422701383	UP	20DPA	Transcription factor
Solyc03g058160	Solyc03g058160.3.1	Zinc finger family protein (AHRD V3.3 *** B9HA00_POPTK)	3.284789644	2.362662942	UP	20DPA	Transcription factor
Solyc01g100660	Solyc01g100660.3.1	Basic helix-loop-helix transcription factor (AHRD V3.3 *** A0A0S3TVX2_CITUN)	2.083223808	2.258612144	UP	20DPA	Transcription factor
Solyc07g052720	Solyc07g052720.3.1	MADS-box transcription factor (AHRD V3.3 *** A0A072UYG7_MEDTR)	2.304771178	1.506300115	UP	20DPA	Transcription factor

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	FC <i>adp</i> /CL	FC <i>adp</i> /WT	UP/DOWN	Stage	Biological pathway
Solyc09g074730	Solyc09g074730.2.1	Homeobox protein LUMINIDEPENDENS (AHRD V3.3 *** A0A0B2S9W0_GLYSO)	1.914443422	1.682295877	UP	20DPA	Transcription factor
Solyc05g007880	Solyc05g007880.3.1	Dof zinc finger protein (AHRD V3.3 *** W9S8B0_9ROSA)	1.928070823	1.591171994	UP	20DPA	Transcription factor
Solyc08g021820	Solyc08g021820.3.1	auxin-regulated IAA29	2.03106394	1.946898263	UP	20DPA	Transcription factor
Solyc12g038450	Solyc12g038450.1.1	Ethylene-responsive transcription factor, putative (AHRD V3.3 *- B9RVV2_RICCO)	6.959086584	5.478651685	UP	20DPA	Transcription factor
Solyc06g033850	Solyc06g033850.3.1	Dehydration responsive element-binding factor protein (AHRD V3.3 -* A0A0K0K9Y3_ELECO)	3.880482456	2.323703217	UP	20DPA	Transcription factor
Solyc02g072000	Solyc02g072000.3.1	SolycHsfA4c	1.630136986	1.621253406	UP	20DPA	Transcription factor
Solyc08g083130	Solyc08g083130.3.1	Homeobox-leucine zipper protein (AHRD V3.3 *** K4MNF8_MEDSA)	4.826612903	2.164556962	UP	20DPA	Transcription factor
Solyc11g072500	Solyc11g072500.2.1	Dof domain, zinc finger family protein (AHRD V3.3 *** Q6L3K2_SOLDE)	0.580781524	0.492008036	DOWN	6DPA	Transcription factor
Solyc12g087830	Solyc12g087830.2.1	MADS-box transcription factor (AHRD V3.3 *** FIT119_9ERIC)	0.367420272	0.528082634	DOWN	6DPA	Transcription factor
Solyc06g035940	Solyc06g035940.3.1	Homeobox leucine zipper protein (AHRD V3.3 *** A0A072TNH2_MEDTR)	0.481864683	0.264957811	DOWN	6DPA	Transcription factor
Solyc06g066020	Solyc06g066020.3.1	auxin-regulated IAA36	0.535213591	0.593887262	DOWN	6DPA	Transcription factor
Solyc03g113270	Solyc03g113270.3.1	LEVAHOX1G L-esculentum homeobox	0.639419908	0.655848546	DOWN	6DPA	Transcription factor
Solyc02g061990	Solyc02g061990.3.1	Bzip transcription factor (AHRD V3.3 *** A0A087GK23_ARAAL)	0.550367314	0.606050532	DOWN	6DPA	Transcription factor
Solyc12g087810	Solyc12g087810.2.1	MADS-box transcription factor (AHRD V3.3 *** FIT119_9ERIC)	0.372759857	0.664047151	DOWN	6DPA	Transcription factor
Solyc03g095770	Solyc03g095770.3.1	WRKY transcription factor 80	0.359659781	0.590074494	DOWN	6DPA	Transcription factor
Solyc09g015770	Solyc09g015770.3.1	WRKY transcription factor 81	0.51974474	0.498273669	DOWN	6DPA	Transcription factor
Solyc03g093610	Solyc03g093610.1.1	ethylene response factor A.2	0.555830428	0.621448328	DOWN	20DPA	Transcription factor
Solyc08g077110	Solyc08g077110.3.1	NAC domain protein. (AHRD V3.3 *** A0A061GAH7_THECC)	0.322394678	0.446834665	DOWN	20DPA	Transcription factor
Solyc06g035940	Solyc06g035940.3.1	Homeobox leucine zipper protein (AHRD V3.3 *** A0A072TNH2_MEDTR)	0.443478261	0.245712886	DOWN	20DPA	Transcription factor
Solyc09g014250	Solyc09g014250.3.1	MYB transcription factor (AHRD V3.3 *** Q66RNI_HEVBR)	0.582278481	0.603410582	DOWN	20DPA	Transcription factor
Solyc11g012930	Solyc11g012930.2.1	WAT1-related protein (AHRD V3.3 *** K4D697_S01LC)	0.593751398	0.636636133	DOWN	20DPA	Transport

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	FC <i>adp</i> /CL	FC <i>adp</i> /WT	UP/DOWN	Stage	Biological pathway
Solyc04g080940	Solyc04g080940.3.1	WAT1-related protein (AHRD V3.3 *** MOZW99_SOLTU)	0.55545438	0.532069547	DOWN	20DPA	Transport
Solyc05g056470	Solyc05g056470.1.1	ABC transporter family protein (AHRD V3.3 *** B9H498_POPT)	0.413522013	0.322106552	DOWN	20DPA	Transport
Solyc04g006960	Solyc04g006960.3.1	ABC transporter family protein (AHRD V3.3 *** A0A097P9T3_HEVBR)	0.487366167	0.456661316	DOWN	20DPA	Transport
Solyc07g025490	Solyc07g025490.2.1	OSBP(oxysterol binding protein)-related protein 4B (AHRD V3.3 --* AT4G25850.3)	2.456157635	1.650993377	UP	20DPA	Transport/ammonium
Solyc03g006260	Solyc03g006260.3.1	Calcium-binding EF-hand (AHRD V3.3 *- A0A103XMB0_CYNCS)	0.39636273	0.596550431	DOWN	20DPA	Transport/Calcium
Solyc08g075430	Solyc08g075430.3.1	ABC transporter family protein (AHRD V3.3 *** U5GKR9_POPT)	0.475724501	0.599478302	DOWN	20DPA	Transport/Cytokinins
Solyc12g006360	Solyc12g006360.2.1	Multidrug resistance protein mdtK	1.579957356	1.684090909	UP	6DPA	Transport/Flavonoids
Solyc03g059150	Solyc03g059150.3.1	Ion channel DMI1 (AHRD V3.3 *** DMI1_MEDTR)	1.844827586	1.715166461	UP	20DPA	Transport/Ion
Solyc05g008780	Solyc05g008780.3.1	PROTON PUMP INTERACTOR 1 family protein (AHRD V3.3 *- U5GXF2_POPT)	1.875879718	1.542346134	UP	20DPA	Transport/ion
Solyc05g006640	Solyc05g006640.3.1	Phospholipid-transporting ATPase (AHRD V3.3 *** A0A0V0YV6_SOLCH)	1.910931174	1.593056895	UP	20DPA	Transport/Lipid
Solyc01g104780	Solyc01g104780.3.1	Vacuolar iron transporter family protein (AHRD V3.3 *** A0A061DXK2_THECC)	0.593037131	0.452713926	DOWN	6DPA	Transport/Metal ion
Solyc11g012690	Solyc11g012690.2.1	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *** I3STQ6_MEDTR)	0.179023508	0.22147651	DOWN	20DPA	Transport/Metal ion
Solyc11g007200	Solyc11g007200.2.1	Heavy metal transport/detoxification superfamily protein (AHRD V3.3 *- AT5G27690.1)	0.591736695	0.560344828	DOWN	20DPA	Transport/Metal ion
Solyc12g042240	Solyc12g042240.2.1	Peptide transporter (AHRD V3.3 *- W9SG60_9ROSA)	4.027504912	2.867132867	UP	20DPA	Transport/Peptide
Solyc09g011390	Solyc09g011390.3.1	Major facilitator superfamily protein (AHRD V3.3 *** AT3G53960.1)	0.448669202	0.465789474	DOWN	20DPA	Transport/Peptide
Solyc01g099370	Solyc01g099370.3.1	SRC2 homolog	1.51145372	1.615402594	UP	6DPA	Transport/protein
Solyc03g078570	Solyc03g078570.3.1	Ras-related protein (AHRD V3.3 *** W9QNC0_9ROSA)	1.988673699	1.537911206	UP	20DPA	Transport/protein
Solyc03g058470	Solyc03g058470.2.1	Ypt/Rab-GAP domain of gyp1p superfamily protein (AHRD V3.3 *** AT2G43490.8)	2.163239075	1.966121495	UP	20DPA	Transport/protein
Solyc08g061880	Solyc08g061880.2.1	Peroxisome biogenesis factor 10 (AHRD V3.3 *- * B9U2H6_TOBAC)	2.232269504	1.8885	UP	20DPA	Transport/protein
Solyc08g048290	Solyc08g048290.3.1	inositol transporter 2	1.656700761	1.573349938	UP	20DPA	Transport/Sugar
Solyc03g097590	Solyc03g097590.3.1	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BH6_SOLLC)	2.099173554	7.055555556	UP	20DPA	Transport/Sugar

Locus	Identifier (ITAG 3.2)	Annotation (ITAG 3.2)	FC <i>adp</i> /CL	FC <i>adp</i> /WT	UP/DOWN	Stage	Biological pathway
Solyc03g097870	Solyc03g097870.3.1	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BJK4_SOLLIC)	3.539928129	10.30901163	UP	20DPA	Transport/Sugar
Solyc04g064630	Solyc04g064630.3.1	Bidirectional sugar transporter SWEET (AHRD V3.3 *** K4BT54_SOLLIC)	0.501702259	0.439652834	DOWN	20DPA	Transport/Sugar
Solyc10g055630	Solyc10g055630.2.1	plasma membrane intrinsic protein 2.9	0.649546669	0.548698424	DOWN	20DPA	Transport/Water
Solyc08g066840	Solyc08g066840.3.1	tonoplast intrinsic protein 4.1	0.471994965	0.328371278	DOWN	20DPA	Transport/Water

Table 6. Changes in Primary Metabolites Identified by GC-MS in *adp* Fruit: Placenta 6dpa & 20dpa

PLACENTA													
6 dpa							20 dpa						
<i>adp</i> vs. WT							<i>adp</i> vs. CL						
FC	log2(FC)	p-adjusted	FC	log2(FC)	p-adjusted	FC	log2(FC)	p-adjusted	FC	log2(FC)	p-adjusted	log2(FC)	p-adjusted
Alanine	0.8736	-0.19496	0.055147	0.93446	-0.0978	0.21886	0.87959	-0.1851	0.32369	1.0039	0.005654	0.005654	0.96263
Asparagine	0.62015	-0.68931	0.000403	0.66936	-0.57914	0.003767	0.33021	-1.5985	0.004036	0.36134	-1.4686	-1.4686	0.010327
Aspartic acid	0.86032	-0.21705	0.055147	0.97474	-0.03691	0.87352	0.33478	-1.5787	0.000284	0.40989	-1.2867	-1.2867	0.002323
beta-alanine	0.99946	-0.00078	0.96763	0.95974	-0.05929	0.71228	0.82744	-0.27328	0.003041	0.82644	-0.27502	-0.27502	0.011707
GABA	1.0255	0.036346	0.20269	1.0318	0.045112	0.36247	0.82976	-0.26924	0.099436	0.87432	-0.19376	-0.19376	0.23459
Glutamic acid	0.69701	-0.52074	0.008796	0.69719	-0.52037	0.026099	0.20802	-2.2652	6.11E-05	0.20523	-2.2847	-2.2847	4.78E-05
Glutamine	0.58907	-0.76348	0.003178	0.59595	-0.74675	0.027644	0.15388	-2.7001	2.83E-06	0.18211	-2.4571	-2.4571	0.000193
Isoleucine	0.9306	-0.10376	0.60686	0.98826	-0.01704	0.89163	0.83846	-0.25418	0.034851	0.97734	-0.03306	-0.03306	0.92432
Leucine	0.9908	-0.01333	0.96763	0.98145	-0.02702	0.88468	0.79259	-0.33536	0.059331	0.93028	-0.10426	-0.10426	0.85702
Lysine	0.62856	-0.66987	0.000403	0.72045	-0.47303	0.003767	0.90257	-0.14789	0.42126	0.93054	-0.10386	-0.10386	0.60475
Methionine	0.76582	-0.38492	0.028868	0.76825	-0.38034	0.027644	0.60789	-0.71813	0.034851	0.68688	-0.54187	-0.54187	0.075446
O-acetyl-serine	0.9345	-0.09774	0.59178	0.97273	-0.03989	0.84967	0.94551	-0.08083	0.42102	0.94551	-0.08083	-0.08083	0.15884
Ornithine	0.66157	-0.59603	0.002906	0.6579	-0.60406	0.002583	0.27058	-1.8859	0.000811	0.33964	-1.5579	-1.5579	0.00479
Phenylalanine	0.85298	-0.22941	0.055124	0.86646	-0.20679	0.14701	0.69647	-0.52186	0.003203	0.70691	-0.5004	-0.5004	0.002892
Proline	0.44571	-1.1658	0.000403	0.46089	-1.1175	0.001465	0.32435	-1.6244	0.000509	0.34488	-1.5358	-1.5358	0.00227
Serine	0.86549	-0.20841	0.26673	0.98034	-0.02865	0.88468	0.7253	-0.46336	0.13603	0.7777	-0.36272	-0.36272	0.13326
Threonine	0.58286	-0.77879	0.000403	0.59523	-0.74849	0.00351	0.39082	-1.3554	0.000605	0.48717	-1.0375	-1.0375	0.005609
Tryptophan	1.0388	0.054886	0.88032	1.0426	0.060161	0.84967	0.90574	-0.14283	0.44005	0.89371	-0.16213	-0.16213	0.4735
Tyrosine	1.0226	0.032304	0.96763	0.98406	-0.02318	0.94113	0.9583	-0.06146	0.73534	1.0912	0.12586	0.12586	0.66965
Valine	0.93708	-0.09376	0.59178	1.0434	0.061326	0.64815	0.9327	-0.10051	0.44005	1.0369	0.052318	0.052318	0.7556
Citric acid	1.1511	0.20299	0.076996	1.0506	0.07128	0.67333	0.6628	-0.59335	0.005534	0.74378	-0.42705	-0.42705	0.025566
Malic acid	1.0574	0.080479	0.59178	1.0137	0.019623	0.88468	0.96304	-0.05433	0.70774	0.99564	-0.0063	-0.0063	0.96263

Amino acids

Organic acids

		PLACENTA											
		6 dpa						20 dpa					
		adp vs. WT			adp vs. CL			adp vs. WT			adp vs. CL		
		FC	log2(FC)	p.adjusted	FC	log2(FC)	p.adjusted	FC	log2(FC)	p.adjusted	FC	log2(FC)	p.adjusted
Main sugars	Quinic acid-3-caffeoyl	1.1358	0.18374	0.001001	1.1246	0.16947	0.004851	1.2352	0.30469	0.028625	1.052	0.0731	0.60475
	Galactonic acid-1,4-lactone	1.1581	0.211176	0.22566	1.0795	0.11039	0.36247	0.90989	-0.13623	0.28892	1.0552	0.077575	0.66965
	Glucose	1.0735	0.10237	0.028868	1.0755	0.10497	0.038585	1.3993	0.48474	0.000103	1.3911	0.47619	0.000468
	Fructose	1.0339	0.048098	0.67553	1.0346	0.049017	0.75482	1.2157	0.28181	0.002467	1.1844	0.24412	0.004188
	Sucrose	0.99308	-0.01003	0.88032	0.96585	-0.05013	0.027102	1.2062	0.27042	0.1252	1.1545	0.20724	0.26396
Main sugar phosphates	Glucose-6-phosphate	2.9448	1.5582	1.40E-05	2.7106	1.4386	4.06E-05	2.4488	1.2921	0.00078	2.7714	1.4706	0.000468
	Fructose-6-phosphate	1.1398	0.18879	0.028868	1.1278	0.17349	0.21886	1.1303	0.17666	0.6169	1.1257	0.17088	0.66965
Sugar alcohol	Galactinol	1.0438	0.061802	0.88032	1.0432	0.061004	0.84967	1.0338	0.047945	0.84468	0.91647	-0.12584	0.60475
	myo-Inositol	0.99683	-0.00458	0.96763	0.97955	-0.02981	0.71398	0.82298	-0.28106	0.016252	0.87221	-0.19725	0.113326
	myo-Inositol-1-phosphate	0.97411	-0.03784	0.88032	0.93937	-0.09023	0.82361	0.71429	-0.48543	0.002308	0.75873	-0.39835	0.005609
Cell wall-related sugars	Fucose	1.1486	0.19994	0.24661	1.0944	0.13017	0.42581	0.96306	-0.0543	0.84468	1.0196	0.027937	0.96263
	Galacturonic acid	0.82059	-0.28526	0.076996	0.80574	-0.31161	0.054807	0.83385	-0.26215	0.24616	0.86006	-0.21749	0.26572
	Rhamnose	1.146	0.19659	0.20728	1.0778	0.10807	0.62669	1.0044	0.0063	0.91443	1.0166	0.023768	0.85702
	Xylose	1.0008	0.001157	0.96763	1.0175	0.025081	0.61943	0.99677	-0.00467	0.90718	0.99277	-0.01048	0.9
Miscellaneous	Putrescine	0.975	-0.03653	0.88032	0.89116	-0.16624	0.62089	1.0093	0.013348	0.86517	0.96805	-0.04684	0.60855
	Phosphoric acid	1.0265	0.037772	0.88032	1.0483	0.068097	0.75482	0.54977	-0.86309	0.002053	0.55197	-0.85733	0.0025

Table 6 (cont). Changes in Primary Metabolites Identified by GC-MS in *adp* Fruit: Placenta MG & RR

	PLACENTA											
	MG						RR					
	adp vs. WT						adp vs. WT					
	FC	log2(FC)	p-adjusted	FC	log2(FC)	p-adjusted	FC	log2(FC)	p-adjusted	FC	log2(FC)	p-adjusted
	Alanine	0.90769	-0.13972	0.6048	1.0243	0.034646	0.8897	0.95903	-0.06036	0.75585	0.99734	-0.00385
	Asparagine	0.83628	-0.25794	0.16447	0.74118	-0.43211	0.08323 ₁	0.56276	-0.82942	0.03484	0.65274	-0.61541
	Aspartic acid	0.59673	-0.74486	0.00772	0.6148	-0.70181	0.00305₇	0.84371	-0.24518	0.086838	0.89092	-0.16663
	beta-alanine	1.058	0.081308	0.65408	0.96813	-0.04672	0.8122	1.1158	0.15806	0.18731	1.1292	0.17529
	GABA	0.87348	-0.19516	0.15424	0.91477	-0.12852	0.25425	0.71137	-0.49134	0.022054	0.74117	-0.43212
	Glutamic acid	0.33877	-1.5616	1.70E-05	0.33466	-1.5792	8.87E-06	0.86083	-0.2162	0.15312	0.86595	-0.20764
	Glutamine	0.85354	-0.22847	0.46437	0.93027	-0.10428	0.60157	0.84217	-0.24782	0.024061	1.0336	0.047682
	Isoleucine	1.03	0.042704	0.86819	1.1892	0.25003	0.37915	0.88891	-0.1699	0.52783	1.0003	0.000478
	Leucine	0.97765	-0.03261	0.86819	0.99742	-0.00373	0.97159	0.86689	-0.20609	0.363	1.0502	0.070695
	Lysine	0.88323	-0.17914	0.36583	0.99483	-0.00748	0.97159	1.0119	0.017061	0.93281	0.97272	-0.0399
	Methionine	0.98787	-0.01761	0.98055	1.0215	0.030697	0.85319	0.90012	-0.1518	0.38604	0.94003	-0.08923
	O-acetyl-serine	0.83372	-0.26236	0.028302	0.80543	-0.31217₉	0.00847₉	0.91228	-0.13245	0.15312	0.91228	-0.13245
	Ornithine	1.071	0.098942	0.46973	1.0547	0.076848	0.60157	1.0511	0.071893	0.75237	1.0141	0.020178
	Phenylalanine	0.72651	-0.46095	0.009977	0.75294	-0.4094₈	0.00587₈	1.0474	0.066815	0.46732	1.1123	0.15354
	Proline	0.80199	-0.31834	0.043857	0.69973	-0.51512₇	0.03000₇	0.23118	-2.1129	0.009657	0.28558	-1.808₃
	Serine	0.78484	-0.34953	0.095456	0.76775	-0.38129	0.02254 ₄	0.94271	-0.08512	0.46732	0.91424	-0.12936
	Threonine	1.028	0.039815	0.86819	0.85644	-0.22357	0.44307	0.7564	-0.40278	0.076268	0.86965	-0.2015
	Tryptophan	0.89415	-0.16141	0.43844	0.85676	-0.22303	0.1976	1.0419	0.05922	0.72649	1.0384	0.054327
	Tyrosine	1.1046	0.14357	0.46437	0.91235	-0.13234	0.37915	0.62933	-0.66811	0.022054	0.61667	-0.69742₄
	Valine	1.0292	0.041577	0.8367	1.0711	0.099048	0.41787	0.84003	-0.25149	0.15312	0.94696	-0.07863
	Citric acid	0.79274	-0.33508	0.36583	0.86599	-0.20757	0.46156	1.0311	0.044141	0.75237	0.97108	-0.04234
	Organic acids											

PLACENTA													
MG												RR	
adp vs. WT						adp vs. CL			adp vs. WT			adp vs. CL	
	FC	log2(FC)	p.adjusted	FC	log2(FC)	p.adjusted	FC	log2(FC)	p.adjusted	FC	log2(FC)	p.adjusted	
Malic acid	0.84482	-0.24329	0.46437	0.89099	-0.16653	0.44307	0.89703	-0.15677	0.39334	0.96478	-0.05173	0.93049	
Quinic acid-3-caffeoyl	1.0139	0.019916	0.86819	0.83277	-0.264	0.03219 ₂	1.3073	0.38663	0.022288	1.3349	0.41673	0.05952	
Galactonic acid-1-4-lactone	1.1409	0.19017	0.46973	1.1776	0.23584	0.37915	0.97918	-0.03035	0.86473	0.96581	-0.05019	0.92344	
Glucose	1.1396	0.18854	0.024235	1.1248	0.16964	0.03219₂	0.72727	-0.45944	0.001504	0.72831	-0.45737	0.00081₁	
Fructose	1.0944	0.13017	0.007019	1.0758	0.10545	0.00587₈	0.7932	-0.33424	0.022288	0.85829	-0.22046	0.23395	
Sucrose	1.0464	0.06543	0.49009	1.0315	0.044801	0.46156	0.841	-0.24982	0.18157	0.84174	-0.24856	0.36071	
Glucose-6-phosphate	2.571	1.3623	5.33E-05	2.8132	1.4922	0.00060₃	2.7687	1.4692	0.001504	2.9269	1.5494	0.00081₁	
Fructose-6-phosphate	1.0229	0.032605	0.86623	0.94046	-0.08857	0.65711	1.1059	0.14528	0.39563	0.93701	-0.09387	0.90958	
Galactinol	1.0791	0.10989	0.68028	0.85628	-0.22385	0.25425	1.1649	0.22023	0.39334	1.0251	0.035717	0.93049	
myo-Inositol	0.56728	-0.81788	0.002554	0.55285	-0.85504	0.00159₃	0.59573	-0.74727	0.036138	0.56551	-0.82238	0.05569	
myo-Inositol-1-phosphate	0.48246	-1.0515	0.009977	0.51643	-0.95335	0.01147₁	0.58161	-0.78187	0.015768	0.60429	-0.72669	0.11641	
Fucose	0.71175	-0.49055	0.054375	0.77913	-0.36007	0.15155	0.87935	-0.1855	0.15312	0.89027	-0.16769	0.3594	
Galacturonic acid	1.1339	0.1813	0.50802	0.9861	-0.0202	0.94654	0.75056	-0.41395	0.28017	0.94752	-0.07777	0.93049	
Rhamnose	1.0731	0.10181	0.52203	1.0796	0.11056	0.47543	1.1355	0.18336	0.15312	1.1199	0.16335	0.43318	
Xylose	1.0165	0.023593	0.52203	0.99838	-0.00234	0.97159	0.99317	-0.00989	0.84895	0.98643	-0.01972	0.92344	
Putrescine	0.94711	-0.0784	0.76173	0.91649	-0.12581	0.46156	0.94013	-0.08906	0.52783	0.92308	-0.11548	0.90958	
Phosphoric acid	1.0165	0.023649	0.86819	1.0361	0.051137	0.60157	0.93866	-0.09133	0.51247	1.0244	0.034719	0.93049	

Table 6 (cont). Changes in Primary Metabolites Identified by GC-MS in *adp* Fruit: Pericarp 6dpa & 20dpa

	PERICARP										
	6 dpa						20 dpa				
	<i>adp</i> vs. WT			<i>adp</i> vs. CL			<i>adp</i> vs. WT			<i>adp</i> vs. CL	
	FC	log2(FC)	p.adjusted	FC	log2(FC)	p.adjusted	FC	log2(FC)	p.adjusted	FC	log2(FC)
Alanine	0.66163	-0.5959	0.16081	0.70136	-0.51177	0.3675	1.3113	0.39095	0.046387	1.1419	0.1914
Asparagine	0.90816	-0.13898	0.014671	0.96644	-0.04925	0.77394	0.41732	-1.2608	0.000206	0.48752	-1.0365
Aspartic acid	0.90802	-0.1392	0.06179	1.0421	0.059429	0.43453	0.60906	-0.71534	5.05E-05	0.71871	-0.47653
beta-alanine	1.0466	0.065719	0.47029	1.0349	0.049449	0.64518	0.75159	-0.41198	0.000206	0.74283	-0.42889
GABA	0.961	-0.05739	0.47029	0.99245	-0.01093	0.83765	0.96178	-0.05621	0.16075	0.96775	-0.04729
Glutamic acid	0.70827	-0.49762	0.025061	0.77358	-0.37038	0.08501	0.63301	-0.65969	5.05E-05	0.67868	-0.55919
Glutamine	0.96214	-0.05569	0.65889	1.0121	0.017303	0.821	0.53656	-0.89818	0.000328	0.59577	-0.74718
Isoleucine	1.0825	0.11433	0.61125	1.1057	0.14497	0.64518	0.89594	-0.15853	0.11888	0.89993	-0.15212
Leucine	1.0442	0.062453	0.54703	1.0376	0.053232	0.66807	0.99921	-0.00114	0.9771	1.0493	0.069456
Lysine	1.0337	0.047837	0.72301	0.97561	-0.03562	0.821	0.90276	-0.14758	0.1598	0.96293	-0.0545
Methionine	1.0942	0.12987	0.21798	1.0905	0.12503	0.3675	0.93418	-0.09822	0.46315	0.95291	-0.06959
O-acetyl-serine	0.9557	-0.06538	0.51913	1.0134	0.019236	0.83765	1.0129	0.018437	0.68052	1.0227	0.032421
Ornithine	0.94602	-0.08006	0.47029	0.94792	-0.07717	0.64518	1.1233	0.16769	0.30599	1.1637	0.21878
Phenylalanine	1.3015	0.38015	0.002441	1.3057	0.3848	0.001909	0.9361	-0.09527	0.037266	0.94514	-0.0814
Proline	0.48488	-1.0443	0.010451	0.57879	-0.78889	0.073571	0.39099	-1.3548	0.000199	0.46253	-1.1124
Serine	1.0107	0.015285	0.79318	0.94151	-0.08695	0.43453	0.83647	-0.25762	0.037967	0.90131	-0.1499
Threonine	1.097	0.13355	0.45426	1.0614	0.085934	0.64518	0.89525	-0.15964	0.16075	0.96272	-0.05481
Tryptophan	1.0397	0.056137	0.70447	1.0814	0.11294	0.43453	0.92832	-0.1073	0.5719	0.92087	-0.11893
Tyrosine	1.0961	0.1324	0.55164	1.2017	0.26513	0.15013	1.0341	0.048324	0.71338	0.98854	-0.01663
Valine	0.95895	-0.06047	0.61125	0.93094	-0.10323	0.43453	0.92815	-0.10757	0.45483	0.94903	-0.07547
Citric acid	1.0274	0.038989	0.36184	1.0259	0.03683	0.3675	0.84438	-0.24404	0.000537	0.82293	-0.28115
Malic acid	0.99552	-0.00648	0.79318	1.017	0.024326	0.64518	0.9583	-0.06145	0.46315	1.019	0.027184

Amino acids

Organic acids

PERICARP													
6 dpa							20 dpa						
<i>adp</i> vs. WT							<i>adp</i> vs. CL						
FC	log2(FC)	p.adjusted	FC	log2(FC)	p.adjusted	FC	log2(FC)	p.adjusted	FC	log2(FC)	p.adjusted	FC	p.adjusted
Quinic acid-3-caffeoyl	-0.09864	0.36184	1.0289	0.04106	0.64518	3.0463	1.607	0.60675	3.5046	1.8093	0.54613		
Galactonic acid-1-4-lactone	-0.03066	0.72301	0.92815	-0.10757	0.38648	0.98208	-0.02609	0.89242	0.96701	-0.0484	0.64254		
Glucose	0.045696	0.60749	1.0314	0.04455	0.64518	1.0687	0.095829	0.039303	1.0994	0.13666	0.027772		
Fructose	0.16955	0.47029	0.99135	-0.01254	0.92884	1.013	0.018624	0.68052	1.0314	0.044642	0.40978		
Sucrose	0.082209	0.67051	1.022	0.031339	0.83765	1.0333	0.047299	0.62369	1.0001	3.01E-05	0.98044		
Glucose-6-phosphate	1.0244	3.21E-05	2.013	1.0093	2.68E-06	3.0537	1.6106	5.05E-05	3.0921	1.6286	0.000139		
Fructose-6-phosphate	0.03008	0.77469	1.0744	0.10357	0.38648	1.0518	0.072879	0.5719	0.86752	-0.20503	0.29692		
Galactinol	0.015676	0.79318	1.0168	0.024036	0.72041	0.86212	-0.21405	0.070139	0.71275	-0.48854	0.002097		
myo-Inositol	0.040133	0.47029	1.0813	0.11274	0.10708	0.84114	-0.24959	0.027867	0.92186	-0.11738	0.46597		
myo-Inositol-1-phosphate	0.26535	0.16081	1.2402	0.31053	0.11072	0.88901	-0.16972	0.3636	0.97445	-0.03734	0.89218		
Fucose	-0.78705	0.01023	0.63198	-0.66206	0.014527	0.76627	-0.38408	0.00924	0.73611	-0.442	0.003176		
Galacturonic acid	-0.26124	0.10597	0.97379	-0.03831	0.83765	0.93015	-0.10446	0.48484	1.1362	0.18422	0.40978		
Rhamnose	-0.01001	0.85551	1.0527	0.074067	0.59222	0.91929	-0.12141	0.5719	0.90889	-0.13783	0.46597		
Xylose	-0.01206	0.77469	1.0162	0.023251	0.64518	1.0033	0.004692	0.90921	1.0216	0.030772	0.48843		
Putrescine	0.094985	0.54703	1.0349	0.049506	0.72459	0.91569	-0.12707	0.38304	0.85705	-0.22255	0.13135		
Phosphoric acid	-0.00999	0.47029	1.0074	0.010589	0.72041	0.9498	-0.0743	0.3636	0.92565	-0.11146	0.16445		

Table 6 (Cont.). Changes in Primary Metabolites Identified by GC-MS in *adp* Fruit: Pericarp MG & RR

PERICARP														

PERICARP																																		
MG										Ripe																								
adp vs. WT										adp vs. CL																								
FC										log2(FC)					p.adjusted					FC					log2(FC)					p.adjusted				
Main sugars	Quinic acid-3-caffeoyl	0.95229	-0.07052	0.87583	0.34416	-1.5388	0.87106	0.94248	-0.08547	0.29246	0.94667	-0.07907	0.69155	0.69155																				
	Galactonic acid-1-4-lactone	0.96415	-0.05267	0.72668	1.0287	0.040851	0.8477	0.88863	-0.17035	0.12748	0.94985	-0.07424	0.69155	0.69155																				
	Glucose	1.0457	0.06449	0.55942	1.007	0.010085	0.96078	0.74501	-0.42467	0.000102	0.77084	-0.3755	0.001868	0.001868																				
	Fructose	1.0305	0.043374	0.40848	1.0137	0.019632	0.8477	0.95874	-0.06079	0.15233	0.97507	-0.03643	0.65782	0.65782																				
	Sucrose	1.0602	0.084334	0.46106	1.0015	0.002133	0.96078	0.76642	-0.38379	0.003505	0.78578	-0.34781	0.018466	0.018466																				
Main sugar phosphates	Glucose-6-phosphate	3.0182	1.5937	1.76E-05	2.9567	1.564	0.000137	2.4871	1.3145	0.00018	2.493	1.3179	0.000307	0.000307																				
	Fructose-6-phosphate	0.9784	-0.03151	0.85656	1.1007	0.13841	0.013609	0.95022	-0.07367	0.87789	0.91649	-0.1258	0.74874	0.74874																				
Sugar alcohol	Galactinol	1.0057	0.008193	0.96478	0.97461	-0.0371	0.8973	0.78878	-0.34231	0.29246	0.82883	-0.27085	0.1537	0.1537																				
	myo-Inositol	0.77929	-0.35976	0.27204	0.85084	-0.23304	0.59048	0.46019	-1.1197	0.000102	0.4132	-1.2751	0.000307	0.000307																				
	myo-Inositol-1-phosphate	0.98015	-0.02893	0.96478	0.9947	-0.00767	0.96078	1.001	0.001422	0.97145	0.92441	-0.1134	0.69155	0.69155																				
Cell wall-related sugars	Fucose	1.0824	0.1143	0.5161	0.96217	-0.05563	0.87106	0.94947	-0.07481	0.59693	0.76774	-0.38131	0.024229	0.024229																				
	Galacturonic acid	0.94977	-0.07434	0.81061	0.94835	-0.07652	0.8477	0.79294	-0.33471	0.30864	1.0046	0.006624	0.96717	0.96717																				
	Rhamnose	0.98555	-0.021	0.96478	0.92434	-0.11351	0.8477	0.9709	-0.04261	0.88444	0.83333	-0.26303	0.084248	0.084248																				
	Xylose	0.99719	-0.00406	0.96478	1.0085	0.012244	0.8973	0.98985	-0.01472	0.83575	0.98109	-0.02755	0.69155	0.69155																				
Miscellaneous	Putrescine	0.86627	-0.20712	0.27204	0.88285	-0.17976	0.35804	0.92751	-0.10856	0.20741	0.96591	-0.05004	0.74874	0.74874																				
	Phosphoric acid	0.96003	-0.05884	0.70739	0.99742	-0.00372	0.96078	0.97868	-0.03109	0.55511	0.96012	-0.05872	0.6022	0.6022																				

Table 7. Changes in Metabolites Identified in *adp* Fruit Using an Untargeted LC-MS/MS Analysis

Name	Mode	Formula	Molecular Weight	RT [min]	mzCloud Best Match (%)	In-house spectral library Best Match (%)	<i>adp</i> vs. CL			<i>adp</i> vs. WT		
							FC	log2(FC)	adjusted p	FC	log2(FC)	adjusted p
α -D-Mannose 1-phosphate	C18_NEG	C6 H13 O9 P	260.02907	0.999	92.2		3.8117	1.9304	0.02612	3.6385	1.8633	0.049427
N-Undecanoylglycine	HILIC_POS	C13 H25 N O3	243.18367	2.741			2.964	1.5675	0.017356	2.1417	1.0987	0.034121
L-2-aminodecanoate	C18_POS	C10 H21 N O2	187.1575	8.462			2.6918	1.4286	0.00591	7.1891	2.8458	0.00053
3-Hydroxy-3-methylglutaric acid	HILIC_NEG	C6 H10 O5	162.05312	9.182	82.6		2.5267	1.3372	0.005756	2.7669	1.4683	0.007556
(2R)-2-Hydroxy-3-(phosphonoxy)propyl heptadecanoate	HILIC_NEG	C20 H41 O7 P	424.25916	1.352			2.4494	1.2924	0.000367	3.1012	1.6328	0.000551
2'-hydroxy 3,6,7,4'-tetramethylquercetin 3'-O- β -D-glucoside	HILIC_POS	C25 H28 O14	552.14733	8.419			2.0895	1.0632	0.002747	2.2261	1.1545	0.001682
cyanidin 3,5-di-O- β -D-glucoside	HILIC_POS	C27 H31 O16	610.15361	8.345			2.0073	1.0053	0.016372	1.767	0.82132	0.040258
cyanidin 3,5-di-O- β -D-glucoside	C18_NEG	C27 H31 O16	610.15274	9.498			1.9448	0.95963	0.009704	1.9837	0.98818	0.02163
D-Raffinose	HILIC_POS	C18 H32 O16	526.15127	9.169	88.8		1.8962	0.92314	0.002822	1.6311	0.70587	0.001451
Adenosine	HILIC_POS	C10 H13 N5 O4	267.09688	4.922	94.9		1.8912	0.91927	0.028026	1.5854	0.6648	0.014428
Acetylcholine	HILIC_POS	C7 H15 N O2	145.11049	5.557	86.4		1.8591	0.8946	0.008922	1.9723	0.97988	0.004309
1-O-feruloyl- β -D-glucose	C18_NEG	C16 H20 O9	356.11006	9.407			1.8386	0.87857	0.019436	1.9845	0.98876	0.017945
D-(+)-Glucose	HILIC_POS	C6 H12 O6	197.08991	7.607	87.2		1.8034	0.85075	0.001791	1.651	0.72335	0.001057
3-(3,4-Dihydroxyphenyl)lactate	C18_POS	C9 H10 O5	198.05254	1.012			1.767	0.82133	0.004672	1.7864	0.83706	0.001007
4-Methoxychalcone	HILIC_POS	C16 H14 O2	238.09897	8.314	56.2		1.7518	0.80884	0.014009	2.4419	1.288	5.26E-05
5-hydroxy-coniferaldehyde	C18_POS	C10 H10 O4	194.05822	9.385			1.7503	0.8076	0.009457	1.4257	0.51169	0.009377
2-keto-L-xylose	C18_POS	C5 H8 O5	148.03707	1.024			1.7431	0.80161	0.032587	2.1571	1.1091	0.008134
D-(+)-Mannose	HILIC_NEG	C6 H12 O6	180.06369	8.204	91		1.7066	0.77112	0.003904	1.7599	0.81547	0.004162

Name	Mode	Formula	Molecular Weight	RT [min]	mzCloud Best Match (%)	In-house spectral library Best Match (%)	adp vs. CL			adp vs. WT		
							FC	log2(FC)	adjusted p	FC	log2(FC)	adjusted p
3,4-Dihydroxymandelaldehyde	C18_POS	C8 H8 O4	168.04212	1.01			1.6891	0.75628	0.011451	1.8823	0.9125	0.000588
Sinapinic acid	C18_POS	C11 H12 O5	224.0681	1.008	84.8		1.6668	0.73704	0.002219	2.7835	1.4769	0.000733
(4Z)-3-(Dihydroxymethylene)-7-methyl-2,6-dioxo-4-octenoic acid	C18_POS	C10 H12 O6	228.0631	1.004			1.6604	0.73149	0.002442	1.7106	0.77453	0.001905
D-Saccharic acid	C18_NEG	C6 H10 O8	210.03725	1.022	83.3	94.1	1.6452	0.71826	0.027487	1.493	0.57818	0.026458
pyridoxal	C18_POS	C8 H9 N O3	167.058	1.011			1.6447	0.71785	0.007387	1.5278	0.61148	0.003859
2-benzyl-3-hydroxybutanedioate	C18_POS	C11 H12 O5	222.05241	1.005			1.6391	0.71287	0.0004	2.1135	1.0797	0.000242
hypotauroine	HILIC_POS	C2 H7 N O2 S	109.01998	8.344			1.6218	0.69758	0.005349	2.3057	1.2052	0.000157
9(Z),11(E)-Conjugated linoleic acid	HILIC_NEG	C18 H32 O2	280.24019	1.403			1.5993	0.4847	0.033221	1.5669	0.55274	0.03217
D-Glucose 6-phosphate	HILIC_POS	C6 H13 O9 P	260.02996	9.925	85.6		1.589	0.66809	0.000661	1.5192	0.60333	0.001682
(2R)-2-[(9Z)-9-Hexadecenoyloxy]-3-[(9Z)-9-tetradecenoyloxy]propyl 2-(trimethylammonio)ethyl phosphate	HILIC_POS	C38 H72 N O8 P	701.50009	1.118			1.5879	0.66714	0.014976	1.662	0.7329	0.034361
benzyl-2-methyl-3-oxobutanoate	C18_POS	C12 H14 O3	206.09452	9.433			1.5855	0.66491	0.039554	1.509	0.5936	0.013102
1,3,6,8-Naphthalenetetrol	C18_POS	C10 H8 O4	192.04189	1.011			1.5654	0.64649	0.011886	1.6837	0.75161	0.004598
Chlorogenic acid	HILIC_POS	C16 H18 O9	752.16902	7.488	78.7		1.5653	0.64641	0.008434	2.0575	1.0409	7.00E-05
Pyridoxal	HILIC_POS	C8 H9 N O3	167.05849	5.689	84.1		1.5603	0.64182	0.001452	1.33	0.41144	0.006923
β-D-ribose/Inicotinate	HILIC_POS	C11 H14 N O6	255.07428	7.453			1.5479	0.63036	0.00125	1.3536	0.43681	0.007061

Name	Mode	Formula	Molecular Weight	RT [min]	mzCloud Best Match (%)	In-house spectral library Best Match (%)	adp vs. CL			adp vs. WT		
							FC	log2(FC)	adjusted p	FC	log2(FC)	adjusted p
Phenyl D-glucopyranosiduronic acid	C18_POS	C12 H14 O7	270.07341	1.007			1.5412	0.62408	0.001786	1.8789	0.90987	0.00056
2-Succinylbenzoate	C18_POS	C11 H10 O5	222.05225	1.009			1.539	0.62195	0.001555	1.7629	0.81796	9.66E-05
L-erythrulose	HILIC_NEG	C4 H8 O4	120.04254	8.183			1.5362	0.61941	0.002404	1.6179	0.69416	0.001959
Adenine	HILIC_NEG	C5 H5 N5	135.05477	4.894	51.3		1.5284	0.61202	0.000586	1.2185	0.28516	0.018246
2-Hydroxy-3,4,5-trimethoxybenzoic acid	C18_POS	C10 H12 O6	228.0631	1.01			1.5161	0.60036	0.038041	1.3828	0.46758	0.040874
1,5-Anhydro-1-(2,4,6-trihydroxyphenyl)hexitol	C18_POS	C12 H16 O8	288.084	1.016			1.5077	0.59231	0.007091	1.6217	0.69751	0.037876
3-Methylcrotonylglycine	HILIC_POS	C7 H11 N O3	157.0741	8.097	33.6		1.507	0.59171	0.003581	2.7849	1.4776	0.000273
(1R,6R)-6-Hydroxy-2-succinylcyclohexa-2,4-diene-1-carboxylate	C18_POS	C11 H12 O6	240.06298	1.012			1.5057	0.59041	0.011375	1.6785	0.74715	0.000428
2,3-Dihydro-2,3-dihydroxybenzoate	C18_POS	C7 H8 O4	156.04216	1.037			1.4988	0.5838	0.039355	1.3507	0.43375	0.017195
DL-Lactic Acid	HILIC_NEG	C3 H6 O3	90.03183	8.182	59.3		1.4948	0.57999	0.000463	1.5662	0.64722	0.001229
Taurine	HILIC_NEG	C2 H7 N O3 S	125.01489	8.207	87.9		1.4899	0.3236	0.010834	1.7855	0.83633	0.000112
Scopoletin	C18_POS	C10 H8 O4	192.04198	1.006			1.4896	0.57491	0.000526	2.1286	1.0899	0.000866
D-Glucosamine	C18_POS	C6 H13 N O5	179.07912	1.011	70.1		1.4765	0.56222	0.003453	1.6001	0.67814	0.001291
Phenylglyoxylic acid	C18_POS	C8 H6 O3	150.03147	1.012			1.4715	0.55732	0.028154	1.4081	0.49378	0.034378
Hypotaurine	HILIC_NEG	C2 H7 N O2 S	109.02005	8.22	85		1.4563	0.28838	0.01241	1.8349	0.87568	5.31E-05
Crotonic acid	HILIC_NEG	C4 H6 O2	86.03688	8.19	61.9		1.4285	0.51455	0.000398	1.5042	0.58902	0.00014
Lysylvaline	C18_POS	C11 H23 N3 O3	245.17367	0.934			1.4244	0.51037	0.006732	2.0971	1.0684	0.006152
Methylglyoxal	C18_POS	C3 H4 O2	72.02108	1.019			1.4219	0.50777	0.001555	1.4003	0.48575	0.000958

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							FC	log2(FC)	adjusted p	FC	log2(FC)	adjusted p
Pyruvic acid	HILIC_NEG	C3 H4 O3	88.01616	8.169	87.5		1.4189	0.50475	0.003217	1.416	0.50182	0.005034
(2R,3S)-2,3-Dimethylmalate	C18_POS	C6 H10 O5	162.05261	1.02			1.4149	0.50073	0.007619	1.4346	0.52065	0.002722
enolaldehyde	C18_POS	C3 H4 O2	72.02108	1.013			1.4148	0.50058	0.000686	1.5621	0.6435	0.000472
Fructose 1,6-diphosphate	HILIC_POS	C6 H14 O12 P2	339.99616	11.983			1.4138	0.44359	0.001835	1.5789	0.65891	0.000229
Pseudouridine	HILIC_NEG	C9 H12 N2 O6	244.06952	6.725	88.9	54.1	1.4096	0.4953	0.009004	1.1851	0.24499	0.039456
trans-4-hydroxy-L-proline betaine	HILIC_POS	C7 H14 N O3	159.08983	6.948			1.4096	0.49524	0.015447	1.6343	0.70871	0.000282
2',4',6'-trihydroxyacetophenone	C18_POS	C8 H8 O4	168.04195	1.005			1.4023	0.4878	0.008369	1.8094	0.85555	0.001137
4H-pyran	C18_POS	C5 H6 O	82.04182	1.026			1.3932	0.47841	0.005148	1.6875	0.75486	0.008907
N2-Methylguanosine	HILIC_POS	C11 H15 N5 O5	297.10747	5.662	91.5		1.3924	0.47757	0.01836	1.1954	0.25753	0.006945
D-(-)-Arabinose	HILIC_NEG	C5 H10 O5	150.05305	8.2	85.4		1.3829	0.46769	0.014238	1.3614	0.44514	0.008407
L-(-)-Serine	C18_NEG	C3 H7 N O3	105.04262	0.934			1.3811	0.46579	0.015288	1.3326	0.4143	0.003844
D-(+)-Maltose	HILIC_POS	C12 H22 O11	364.0984	9.54	94.5		1.3793	0.37913	0.003581	1.9505	0.96381	0.000501
Malondialdehyde	HILIC_NEG	C3 H4 O2	72.02141	7.939			1.3721	0.4564	0.021998	1.3574	0.44088	0.046394
(S)-Methylmalonatesemi aldehyde	C18_POS	C4 H6 O3	102.03165	1.031			1.3717	0.45594	0.039785	1.3312	0.41272	0.048284
Diaminopimelic acid	HILIC_POS	C7 H14 N2 O4	190.09559	8.106	66.9		1.3559	0.4392	0.007408	1.3738	0.45821	0.002862
Glycolic acid	HILIC_NEG	C2 H4 O3	76.01594	7.548	99.2		1.3381	0.30814	0.027255	1.3685	0.34309	0.025645
5-hydroxy-4-methoxy-5,6-dihydro-2H-pyran-2-one	C18_POS	C6 H8 O4	144.04212	1.02	61		1.3331	0.41483	0.001962	1.3171	0.39736	0.00254
Adenine	HILIC_POS	C5 H5 N5	135.05478	9.697	75.5		1.3249	0.40592	0.002822	1.1355	0.18336	0.039441
2-Oxobutyric acid	HILIC_NEG	C4 H6 O3	102.03195	7.486			1.3148	0.39485	0.000399	1.4693	0.55518	0.006556
Levulinic acid	HILIC_NEG	C5 H8 O3	116.04761	7.486			1.3143	0.39426	0.000152	1.3428	0.42524	1.32E-05

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							FC	log2(FC)	adjusted p	FC	log2(FC)	adjusted p
Ascorbyl glucoside	HILIC_NEG	C12 H18 O11	338.08498	8.924			1.3096	0.38917	0.011138	1.1958	0.25792	0.021363
D-Glucosamine	HILIC_POS	C6 H13 N O5	162.05293	8.562	70		1.3061	0.14549	0.02776	1.5547	0.63659	0.021802
N6,N6,N6-Trimethyl-L-lysine	HILIC_POS	C9 H20 N2 O2	188.15281	10.789	93.4	95.5	1.2973	0.37549	0.009825	1.2258	0.2937	0.013161
D-(-)-Fructose	HILIC_NEG	C6 H12 O6	180.06375	7.456	92.2		1.2806	0.23948	0.003083	1.307	0.38623	0.000897
2-Oxovaleric acid	C18_POS	C5 H8 O3	116.04725	1.026			1.2787	0.35469	0.047828	1.3332	0.41492	0.031689
1,2-benzoquinone	C18_POS	C6 H4 O2	108.02111	1.017			1.2769	0.35259	0.004356	1.5338	0.61713	0.000429
[Similar to: D-(+)-Galactose; ΔMass: -37.9732 Da]	C18_NEG	C7 H10 N2 O4 S	218.03663	0.991			1.2741	0.34943	0.02027	1.1266	0.17196	0.023302
trans-Zeaxanthin	HILIC_POS	C10 H13 N5 O	219.11084	6.44	43.6	91.7	1.271	0.17757	0.00184	1.3281	0.40941	0.008021
Bis-D-fructose2'-1,2'-dianhydride	C18_POS	C12 H20 O10	324.10493	1.015			1.2657	0.33994	0.015843	1.3876	0.47256	0.000589
Glutaric acid	HILIC_NEG	C5 H8 O4	132.04257	7.477			1.2638	0.33776	0.002641	1.4051	0.49068	0.021986
Glutaric acid	C18_NEG	C5 H8 O4	132.04219	0.999			1.2632	0.33703	0.03335	1.3925	0.47765	0.002326
1,2-Benzoquinone	C18_POS	C6 H4 O2	108.02106	1.023			1.2469	0.3184	0.011375	1.3447	0.42727	0.002194
D-(-)-Fructose	C18_NEG	C6 H12 O6	120.04213	0.997	85		1.2301	0.29874	0.035999	1.4416	0.52771	0.010484
DL-Lactic Acid	C18_NEG	C3 H6 O3	90.03156	0.997	67.5		1.2219	0.28918	0.043214	1.4409	0.52693	0.007205
His-glu	C18_POS	C11 H17 N5 O4	283.12695	0.984			1.2196	0.28647	0.016343	1.4568	0.54282	0.004828
4-hydroxy-5-methyl-3-furanone	C18_NEG	C5 H6 O3	114.03169	0.996			1.214	0.27981	0.033153	1.3309	0.41241	0.002751
(2R)-2,3-Dihydroxypropanoic acid	HILIC_NEG	C3 H6 O4	106.02686	7.866	70.5	94	1.2125	0.27793	0.021863	1.1961	0.25829	0.016298
[Similar to: α,α-Trehalose; ΔMass: -35.9760 Da]	C18_NEG	C12 H23 Cl O11	378.09224	1.042			1.2082	0.27289	0.044863	1.2735	0.34876	0.039251
D-(-)-Erythrose	HILIC_NEG	C4 H8 O4	120.04256	7.479			1.2032	0.26687	0.002052	1.3217	0.4024	0.001356
Glucosaminic Acid	HILIC_NEG	C7 H14 O8	226.06904	7.508			1.1567	0.21004	0.025905	1.2301	0.29872	0.006079

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							FC	log2(FC)	adjusted p	FC	log2(FC)	adjusted p
1-O-4-hydroxybenzoyl-β-D-glucose	HILIC_NEG	C13 H16 O8	300.08449	8.653			1.1035	0.14206	0.014905	1.5051	0.58982	0.00302
Threonine	HILIC_NEG	C4 H9 N O3	119.0586	8.036	85.1		0.95167	-0.07147	0.043555	0.67401	-0.56915	2.89E-05
Citric acid	HILIC_NEG	C6 H8 O7	192.02729	11.06	94.8		0.87375	-0.19471	0.032342	0.8134	-0.29796	0.00302
L-citrulline	HILIC_NEG	C6 H13 N3 O3	175.09585	8.747		67.4	0.85117	-0.23247	0.016699	0.32732	-1.6112	1.49E-05
L-Aspartic acid	C18_NEG	C4 H7 N O4	133.03746	0.951	85.7	91.5	0.84212	-0.2479	0.03446	0.85285	-0.22964	0.031889
Ornithine	HILIC_NEG	C5 H12 N2 O2	132.09016	12.11	87.1		0.83781	-0.2553	0.023258	0.32523	-1.6205	1.08E-05
L-alanyl-L-alanine	C18_POS	C6 H12 N2 O3	160.08459	1.033			0.83112	-0.26686	0.001243	0.73428	-0.4456	0.00053
4-Oxoproline	HILIC_NEG	C5 H7 N O3	129.04292	7.288	88.8		0.82416	-0.27901	0.014221	0.43901	-1.1877	6.26E-05
2-[(2-Amino-2-carboxyethyl)thio]butanedioic acid	HILIC_NEG	C7 H11 N O6 S	237.03077	10.625			0.81433	-0.29631	0.0397	0.81569	-0.29391	0.045862
Glycerol 3-phosphate	HILIC_NEG	C3 H9 O6 P	172.01393	9.33	71		0.81312	-0.29847	0.003221	0.91699	-0.12502	0.035111
4-Hydroxybenzaldehyde	C18_POS	C7 H6 O2	122.03697	2.54	98.2		0.81025	-0.30356	0.039472	0.63402	-0.65741	0.000507
sn-glycero-3-Phosphocholine	C18_POS	C8 H20 N O6 P	257.10286	0.98			0.8083	-0.30704	0.004286	0.77406	-0.36948	0.019742
L-(+)-Alanine	C18_NEG	C3 H7 N O2	89.04755	0.949			0.80505	-0.31285	0.043739	0.8211	-0.28437	0.04555
2-Amino-4-methylpyrimidine	HILIC_POS	C5 H7 N3	92.0377	8.234	84.5		0.80303	-0.28098	0.035145	0.53383	-0.90555	0.000155
Oxalic acid	HILIC_NEG	C2 H2 O4	89.99547	10.751			0.79107	-0.33812	0.001802	0.79922	-0.32333	0.001602
trans-Aconitic acid	HILIC_NEG	C6 H6 O6	174.01666	11.643	83.6	76.6	0.78541	-0.34849	0.013483	0.68721	-0.5265	0.002396
γ-Aminobutyric acid (GABA)	HILIC_NEG	C4 H9 N O2	103.06362	8.519	87.9		0.78506	-0.34913	0.002556	0.88078	-0.18315	0.027693
Histamine	C18_POS	C5 H9 N3	111.07976	0.852	99.3		0.77781	-0.36252	0.003384	0.44653	-1.1632	4.14E-05
N-6-Methyl-L-lysine	HILIC_POS	C7 H16 N2 O2	160.12145	11.319			0.77723	-0.36358	0.020598	0.4443	-1.1704	0.000202
1-deoxy-L-glycero-tetralose 4-phosphate	C18_POS	C4 H9 O6 P	181.998	1.325			0.77014	-0.3768	0.012401	0.8311	-0.26691	0.008107

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2-Hydroxy-2, 4-pentadienoate	C18_POS	C5 H6 O3	114.03168	9.564			0.76482	-0.38681	0.009344	0.84766	-0.23845	0.013235
N-Stenoyl-L-phenylalanine	C18_POS	C27 H45 N O3	431.3401	9.44			0.76353	-0.38925	0.02006	0.80527	-0.31246	0.020583
2-iminopropanoate	C18_POS	C3 H5 N O2	87.03193	1.019			0.76253	-0.39113	0.011902	0.75916	-0.39753	0.021272
4-hydroxycoumarin	C18_POS	C9 H6 O3	162.03198	7.976			0.761	-0.39404	0.02811	0.64421	-0.63439	0.010557
DL-Glutamine	C18_POS	C5 H10 N2 O3	146.06935	0.947	99.9		0.7608	-0.39442	0.003343	0.58399	-0.5835	0.001385
N5-(L-1-Carboxyethyl)-L-ornithine	C18_POS	C8 H16 N2 O4	204.11072	1.043			0.75745	-0.32653	0.044088	0.87887	-0.18628	0.027825
(4R)-5-Hydroxy-L-leucine	C18_POS	C6 H13 N O3	147.08961	1.069			0.75669	-0.40222	0.024785	0.69508	-0.52475	0.003751
Pipecolic acid	C18_POS	C6 H11 N O2	129.07916	1.069	54.7		0.75604	-0.40347	0.001991	0.78771	-0.34426	0.010557
N-Benzylformamide	C18_POS	C8 H9 N O	118.04211	2.541	69.9		0.75269	-0.40987	0.045091	0.65196	-0.61714	0.022646
DL-Arginine	HILIC_NEG	C6 H14 N4 O2	174.1119	12.11	85.4		0.74971	-0.4156	0.002308	0.31081	-1.6859	5.15E-06
L-cysteinyl-glycine	C18_POS	C5 H10 N2 O3 S	178.04143	1.683			0.74854	-0.41786	0.039346	0.71199	-0.49007	0.004175
L-Glutamic acid	HILIC_NEG	C5 H9 N O4	147.05348	8.931	85.1		0.74714	-0.42055	0.000137	0.66713	-0.58395	8.77E-05
D-Pipecolic acid	C18_POS	C6 H11 N O2	129.07921	0.868			0.74613	-0.35772	0.009718	0.4497	-1.153	5.24E-05
L-alanyl-L-alanine	HILIC_POS	C6 H12 N2 O3	160.08504	7.678			0.74613	-0.42251	0.022478	0.55654	-0.84545	0.000249
L-Lysine	HILIC_POS	C6 H14 N2 O2	146.10581	11.872	92.1		0.74207	-0.43038	0.016901	0.42279	-1.242	7.03E-05
D-(+)-Pipecolinic acid	HILIC_POS	C6 H11 N O2	129.07928	7.016	95.6		0.74053	-0.43336	0.000726	0.69803	-0.51864	4.38E-05
(S)-2-Acetolactate	C18_POS	C5 H8 O4	132.04232	9.559			0.74019	-0.43404	0.012648	0.84387	-0.24491	0.009238
L-Histidine	HILIC_POS	C6 H9 N3 O2	155.0698	8.231	96.4		0.73851	-0.4373	0.002822	0.5604	-0.83548	7.00E-05
pyridoxine	HILIC_POS	C8 H11 N O3	169.07409	8.596			0.73851	-0.43732	0.002948	0.67735	-0.56203	0.000219
N-Acetylmethionine	HILIC_POS	C7 H14 N2 O3	174.10069	7.782	79		0.73723	-0.43981	0.011151	0.46176	-1.1148	0.00013
DL-Lysine	C18_NEG	C6 H14 N2 O2	146.10535	0.916			0.73286	-0.4484	0.035488	0.40621	-1.2997	0.005602
L-Histidine	C18_POS	C6 H9 N3 O2	155.06969	0.935	84.4	59.9	0.72855	-0.45691	0.017015	0.58308	-0.77823	0.002217

Name	Mode	Formula	Molecular Weight	RT [min]	mzCloud Best Match (%)	In-house spectral library Best Match (%)	adp vs. CL			adp vs. WT		
							FC	log2(FC)	adjusted p	FC	log2(FC)	adjusted p
L-isoleucyl-glycine	C18_POS	C8 H16 N2 O3	188.11622	1.463			0.72597	-0.46202	0.032081	0.54972	-0.86324	0.018028
Valylvaline	C18_POS	C10 H20 N2 O3	216.14764	9.128			0.72319	-0.46755	0.011944	0.86098	-0.21596	0.023517
D-Glucosamine 6-phosphate	HILIC_NEG	C6 H14 N O8 P	259.04559	9.317			0.72256	-0.46882	0.002196	0.78114	-0.35635	0.012044
nicotinamide	C18_POS	C6 H6 N2 O	122.04778	1.695	96.9		0.72149	-0.47096	0.00842	0.6758	-0.56534	0.018456
N-2--[2-(Carboxymethyl)-2-hydroxy-3-methoxy-oxopropanoyl]arginine	HILIC_POS	C12 H20 N4 O8	348.12818	10.383			0.72118	-0.47158	0.020796	0.40823	-1.2925	0.000248
2-Amino-2-deoxy-6-O-phosphono-D-glucopyranose	HILIC_NEG	C6 H14 N O8 P	259.04559	9.299			0.71577	-0.48244	0.001564	0.78298	-0.35295	0.013568
Cysteinylglycine(Cys-Gly)	C18_POS	C5 H10 N2 O3 S	178.04144	1.686			0.71164	-0.49077	0.018392	0.66913	-0.57965	0.014432
4-methyl-3-oxoadipate	HILIC_NEG	C7 H10 O5	172.03741	7.914			0.71159	-0.49088	0.002803	0.77584	-0.36617	0.003815
pyrimidine	HILIC_POS	C4 H4 N2	80.03759	7.825			0.70835	-0.49747	0.002822	0.61349	-0.7049	0.000302
S-methyl-5'-thiadenosine	C18_POS	C11 H15 N5 O3 S	297.08978	8.452			0.70697	-0.50028	0.010361	0.8067	-0.3099	0.042765
asp-glu	C18_POS	C9 H15 N3 O6	261.0962	0.998			0.70647	-0.50131	0.026254	0.55451	-0.85073	0.008754
Methionine	HILIC_POS	C5 H11 N O2 S	132.02475	6.788	85.2	92.7	0.70623	-0.50179	0.020019	0.47838	-1.0638	0.000202
nicotinamide	HILIC_POS	C6 H6 N2 O	122.04817	9.039			0.70614	-0.50198	0.004909	0.6607	-0.59794	0.001359
4-Methylene-L-glutamic acid	HILIC_NEG	C6 H9 N O4	159.05339	5.758			0.70558	-0.50312	0.008486	0.67694	-0.5629	0.002359
glu-aspartate	HILIC_NEG	C9 H14 N2 O7	262.08004	9.169			0.70311	-0.50817	0.004223	0.72932	-0.45537	0.005176
N-Acetyl-L-phenylalanine	HILIC_NEG	C11 H13 N O3	207.08962	7.911	54.9		0.70271	-0.50899	0.000591	0.76064	-0.39472	0.003868
phosphoglycolohydroxamate	C18_POS	C2 H6 N O6 P	170.99358	0.926			0.70261	-0.50921	0.004091	0.70874	-0.49667	0.001007
L-Aspartic acid	HILIC_NEG	C4 H7 N O4	133.03781	9.045	83.2	93.7	0.69951	-0.51558	2.17E-05	0.5585	-0.84037	5.31E-05

Name	Mode	Formula	Molecular Weight	RT [min]	mzCloud Best Match (%)	In-house spectral library Best Match (%)	adp vs. CL			adp vs. WT		
							FC	log2(FC)	adjusted p	FC	log2(FC)	adjusted p
Methylmalonic acid	HILIC_NEG	C4 H6 O4	118.02692	9.617	86.6	90.2	0.69796	-0.51879	0.001046	0.6371	-0.65042	0.000738
asn-pro	HILIC_POS	C9 H15 N3 O4	229.10645	8.493			0.69788	-0.51896	0.003477	0.4967	-1.0096	7.03E-05
L-Glutamic acid	HILIC_POS	C5 H9 N O4	147.05341	9.069	96.1	95.8	0.69732	-0.52011	0.01415	0.69473	-0.52548	0.000856
(+/-)-Tartaric acid	HILIC_NEG	C4 H6 O6	150.01666	10.537			0.69697	-0.52083	0.026201	0.75628	-0.403	0.008487
4-Acetamidobutanoic acid	HILIC_POS	C6 H11 N O3	145.07413	8.584	42.7		0.69176	-0.53166	0.02169	0.58028	-0.78518	0.003214
L-Gluthathione (reduced)	HILIC_POS	C10 H17 N3 O6	307.08392	9.045	94.2	95.5	0.68777	-0.54	0.030047	0.7764	-0.36513	0.004022
L-Aspartic acid	HILIC_POS	C4 H7 N O4	133.03774	9.203	99.6		0.68666	-0.54233	0.006698	0.63204	-0.66191	0.000634
(2R,3S,4S,5R,6R)-2-((1(2R,3R,4R,5S)-3,4-dihydroxy-5-(hydroxymethyl)oxolan-2-yl)oxy)methyl)-6-((1(2E)-3,7-dimethylocta-2,6-dien-1-yl)oxy)oxane-3,4,5-triol	C18_POS	C21 H36 O10	465.25775	9.711	93.9		0.68423	-0.54744	0.006113	0.70153	-0.51142	0.009238
β-Alanine	HILIC_NEG	C3 H7 N O2	89.0478	9.045	93	81.6	0.68372	-0.54853	0.000137	0.56067	-0.83478	0.000139
L-gamma-Glutamyl-L-leucine	HILIC_POS	C11 H20 N2 O5	260.13742	7.704			0.68363	-0.54872	0.030047	0.46367	-1.1088	0.002377
benzaldehyde	C18_POS	C7 H6 O	106.042	2.554			0.6829	-0.55026	0.008413	0.55445	-0.85087	0.030514
L-Tyrosine	C18_POS	C9 H11 N O3	181.07425	2.546	99.8	90.4	0.6814	-0.55344	0.009413	0.65496	-0.61051	0.004136
gamma-Glu-Ala	C18_POS	C8 H14 N2 O5	218.09043	1.458			0.68137	-0.55349	0.006628	0.56495	-0.8238	0.008907
Cytidine	HILIC_NEG	C9 H13 N3 O5	243.08739	8.101	37.4		0.68089	-0.5545	0.003767	0.70921	-0.49571	0.006577
(R)-Lactaldehyde	C18_POS	C3 H6 O2	74.0367	1.042			0.68084	-0.55461	0.000452	0.54252	-0.88226	8.18E-05
N-acetyl-(L)-arginine	C18_POS	C8 H16 N4 O3	216.12245	1.504			0.67912	-0.55826	0.013264	0.62432	-0.67963	0.02867
L-Gluthathione (reduced)	HILIC_NEG	C10 H17 N3 O6	307.0839	8.913	85.7		0.67841	-0.55976	0.002556	0.70782	-0.49854	0.008188
Maleamic acid	HILIC_POS	C4 H5 N O3	115.02715	9.205			0.67832	-0.55995	0.001911	0.62008	-0.68948	0.000284

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							FC	log2(FC)	adjusted p	FC	log2(FC)	adjusted p
D-(+)-Proline	HILIC_POS	C5 H9 N O2	115.06351	7.17	96.8	86.4	0.67577	-0.56539	0.006497	0.48824	-1.0344	7.00E-05
Asparagine	HILIC_POS	C4 H8 N2 O3	132.05372	8.58	94.8	93.1	0.67412	-0.56892	0.007846	0.54493	-0.87587	0.001676
1-Pyrroline	C18_POS	C4 H7 N	69.05786	1.042			0.67239	-0.57262	0.001853	0.47958	-1.0602	9.66E-05
DL-β-hydroxyornithine	C18_POS	C5 H11 N O3	133.0738	1.037			0.67166	-0.5742	0.000449	0.57554	-0.79701	0.001222
3-Methylhistidine	HILIC_POS	C7 H11 N3 O2	169.08536	7.674	93.2		0.6679	-0.5823	0.006497	0.51412	-0.95983	0.000113
phenol	C18_POS	C6 H6 O	94.04213	2.54			0.66597	-0.58647	0.017107	0.63894	-0.64625	0.014124
2-iminopropanoate	HILIC_POS	C3 H5 N O2	87.03218	9.204			0.66122	-0.59679	0.001452	0.60252	-0.73092	9.07E-05
DL-Lysine	HILIC_NEG	C6 H14 N2 O2	146.1058	11.803			0.65872	-0.60226	0.008689	0.32428	-1.6247	0.000104
Asparagine	HILIC_NEG	C4 H8 N2 O3	132.05372	8.463	80.4		0.65743	-0.6051	0.002084	0.40452	-1.3057	4.87E-05
5'-S-Methyl-5'-thioadenosine	HILIC_POS	C11 H15 N5 O3 S	297.09371	9.232	46		0.65685	-0.60636	0.002532	0.35908	-1.4776	0.000351
D-proline	C18_POS	C5 H9 N O2	115.06332	1.036			0.65455	-0.61142	0.000255	0.51943	-0.80411	0.000343
D-Idarate	HILIC_NEG	C6 H10 O8	208.02208	10.226			0.65415	-0.6123	0.009237	0.63577	-0.65341	0.020223
Gluconic acid	HILIC_NEG	C6 H12 O7	196.05851	8.833	94.3	59.7	0.64985	-0.62182	0.000707	0.81307	-0.29856	0.037625
Mevalonic acid	HILIC_NEG	C6 H12 O4	148.07361	8.327	53.9		0.6464	-0.6295	0.000599	0.43972	-1.1853	2.89E-05
D-(+)-Glutamine	HILIC_NEG	C5 H10 N2 O3	146.06944	8.328	81.2		0.64549	-0.63154	0.000211	0.44817	-1.1579	5.15E-06
(9S,13S)-12-Oxophytodienoic acid	C18_POS	C18 H28 O3	292.20403	10.513			0.63616	-0.65254	0.00384	0.72919	-0.45564	0.009155
asp-gln	HILIC_NEG	C9 H15 N3 O6	261.096	9.405			0.63122	-0.66378	0.01241	0.43284	-1.2081	0.001045
Uridine monophosphate (UMP)	HILIC_NEG	C9 H13 N2 O9 P	324.03587	9.463	88		0.63052	-0.66539	0.010889	0.71438	-0.48523	0.016695
L-Pyroglutamic acid	HILIC_POS	C5 H7 N O3	129.04287	9.067	91.1	88.6	0.62646	-0.6747	0.001452	0.57011	-0.81068	0.002321
Tomatidine	C18_POS	C27 H45 N O2	415.34508	9.565	92.1		0.6213	-0.68664	0.001766	0.82411	-0.27909	0.012621
D-(+)-Pipicolinic acid	C18_POS	C6 H11 N O2	129.07915	1.443	94.8		0.617	-0.69665	0.015025	0.57934	-0.78751	0.008365

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glycyl-L-valine	C18_POS	C7 H14 N2 O3	174.10049	1.041			0.61651	-0.69779	0.021253	0.28561	-1.8079	0.038285
asp-gln	HILIC_POS	C9 H15 N3 O6	261.09626	9.541			0.61457	-0.70234	0.0154	0.39995	-1.3221	0.00096
N-(4-Amino-L-carboxybutyl)glutamic acid	HILIC_POS	C10 H18 N2 O6	262.11665	9.212			0.6137	-0.7044	0.00411	0.57592	-0.79607	0.001551
L-prolyl-trans-4-hydroxy-L-proline (3beta.5alpha.25S)-	C18_POS	C10 H16 N2 O4	228.11124	0.988			0.60459	-0.72596	0.014626	0.50951	-0.97282	0.014988
Spirosolan-3-yl beta-D-galactopyranoside	C18_POS	C33 H55 N O7	577.3981	9.565			0.60227	-0.73152	0.001567	0.82056	-0.28532	0.01063
4-Oxoproline	C18_NEG	C5 H7 N O3	129.04259	1.92	87.7		0.60047	-0.73583	0.009704	0.41846	-1.2568	0.02163
Phosphoric acid	HILIC_NEG	H3 O4 P	97.97708	9.638		91	0.60017	-0.73656	0.000178	0.66029	-0.59882	0.000124
4-Pyridoxic acid	HILIC_NEG	C8 H9 N O4	183.0533	2.462	94.5		0.59371	-0.75217	0.002354	0.63901	-0.64609	0.012017
L-Pyrroglutamic acid	C18_POS	C5 H7 N O3	129.04283	1.801	94.7		0.58856	-0.76475	0.048637	0.38805	-1.3657	0.005241
(E)-p-coumaric acid	C18_NEG	C9 H8 O3	164.04723	9.601			0.58305	-0.7783	0.028081	0.62934	-0.66809	0.023263
geranyl 6-O-β-D-xylopyranosyl-β-D-glucopyranoside	HILIC_NEG	C21 H36 O10	448.23091	2.725			0.5766	-0.79437	0.044009	0.5133	-0.96213	0.037665
Isocitric acid	C18_NEG	C6 H8 O7	192.02681	1.341	97.5	96.8	0.5672	-0.81808	0.015288	0.49602	-1.0115	0.045351
4-Pyridoxic acid	C18_POS	C8 H9 N O4	183.05345	4.948	97.9		0.55322	-0.85407	0.060742	0.61622	-0.69847	0.019742
Pyrophosphoric Acid	HILIC_NEG	H4 O7 P2	177.94348	9.651			0.5512	-0.85935	0.000143	0.57064	-0.80934	0.000108
L-Threonic acid	HILIC_NEG	C4 H8 O5	136.03747	10.244	79.5	90.3	0.54845	-0.86656	0.003994	0.5456	-0.87409	0.004315
O-Acetylsene	HILIC_NEG	C5 H9 N O4	147.05342	7.491	70.3		0.54679	-0.87095	0.00251	0.61207	-0.70824	0.004162
Cytidine; l-beta-delta-Ribofuranosyl-Cytosine	C18_POS	C9 H13 N3 O5	243.08513	1.043			0.5418	-0.88418	0.004672		-1.6248	0.000276
Itaconic acid	HILIC_NEG	C5 H6 O4	130.02693	11.127	98.5	90.3	0.54113	-0.88595	0.026267	0.4972	-1.0081	0.019264
gamma-Glu-gln	C18_NEG	C10 H17 N3 O6	275.11108	1.049			0.53817	-0.89387	0.04371	0.29893	-1.7421	0.003857
l-L-Glutamyl-L-glutamine	C18_POS	C10 H17 N3 O6	275.11113	1.04			0.53236	-0.90952	0.004672	0.31799	-1.653	0.000276

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trp-lys	HILIC_NEG	C17 H24 N4 O3	332.18348	2.634			0.52453	-0.9309	0.001445	0.68472	-0.54642	0.015836
gamma-Glu-gln	HILIC_NEG	C10 H17 N3 O6	275.1118	9.139			0.51103	-0.96852	0.00371	0.29213	-1.7753	0.000163
Methylmalonic acid	C18_NEG	C4 H6 O4	118.02666	2.268	44	70.5	0.50405	-0.98835	0.02027	0.59207	-0.75615	0.023263
β -L-arabinose 1-phosphate	HILIC_NEG	C5 H11 O8 P	228.00381	7.762			0.50395	-0.98865	0.028578	0.64164	-0.64015	0.026304
3-Phosphoglyceric acid	C18_NEG	C3 H7 O7 P	185.9927	1.853	37.8		0.5025	-0.99279	0.03335	0.68504	-0.54575	0.046445
dihydrocoumarin	HILIC_NEG	C9 H8 O2	148.05271	8.892			0.50119	-0.99657	0.000171	0.47542	-1.0727	8.16E-05
trans-Aconitic acid	C18_NEG	C6 H6 O6	174.01625	1.358	69.2	67.1	0.49875	-1.0036	0.00043	0.59224	-0.34103	0.00983
5,6-dihydrothymine	C18_POS	C5 H8 N2 O2	128.05858	0.938			0.49096	-1.0263	0.006324	0.43031	-1.2165	0.005316
Nicotinic acid	HILIC_POS	C6 H5 N O2	123.03225	5.74	47.4		0.48642	-1.0397	0.001452	0.67604	-0.56483	0.003262
L-(-)-Methionine	C18_POS	C5 H11 N O2 S	149.05133	1.507	99.6	94.6	0.48229	-1.052	0.031838	0.31043	-1.6877	0.005896
gamma-Glu-Thr	HILIC_POS	C9 H16 N2 O6	248.10091	9.061			0.47706	-1.0678	0.00327	0.27614	-1.8565	0.00013
L-Phenylalanine	HILIC_NEG	C9 H11 N O2	165.07921	8.895	92.6		0.47616	-1.0705	0.000131	0.48474	-1.0447	8.16E-05
Spermidine	C18_POS	C7 H19 N3	128.13157	0.821	91.2		0.47203	-1.0831	0.028622	0.50884	-0.97473	0.005862
L-glyceraldehyde 3-phosphate	C18_POS	C3 H7 O6 P	167.98255	1.851			0.47092	-1.0864	0.000865	0.75072	-0.41364	0.025598
gamma-Glutamyl-aminobutyrate	C18_POS	C9 H16 N2 O5	232.10614	1.701			0.47026	-1.0885	0.033938	0.5179	-0.94926	0.022646
glu-tyr	C18_POS	C14 H18 N2 O6	310.11656	7.132			0.46729	-1.0976	0.004239	0.27544	-1.8602	0.000276
L-gamma-Glutamyl-L-leucine	C18_POS	C11 H20 N2 O5	260.13737	8.185			0.46044	-1.1189	0.001282	0.30255	-1.7248	0.000343
Methionine	C18_POS	C5 H11 N O2 S	149.05132	1.518	91.3		0.45948	-1.1219	0.011607	0.35732	-1.4847	0.010557
L-gamma-Glutamyl-L-leucine	C18_NEG	C11 H20 N2 O5	260.13662	8.466			0.45831	-1.1256	0.023051	0.38832	-1.3647	0.017945
Dehydro-L-ascorbic acid	HILIC_NEG	C6 H6 O6	174.01659	6.025		60.1	0.4574	-1.1285	0.005115	0.63427	-0.65683	0.022663
DL-Phenylalanine	C18_NEG	C9 H11 N O2	165.07869	1.006			0.45503	-1.136	0.015288	0.5664	-0.82011	0.002751

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							FC	log2(FC)	adjusted p	FC	log2(FC)	adjusted p
(3R)-β-phenylalanine	C18_POS	C9 H11 N O2	165.07927	1.019			0.45407	-1.139	0.000158	0.69661	-0.52157	0.004648
fumarate	HILIC_NEG	C4 H4 O4	113.99548	6.003			0.44887	-1.1556	0.000564	0.51096	-0.96871	0.000333
asn-pro	HILIC_NEG	C9 H15 N3 O4	229.10624	8.33			0.44447	-1.1699	0.000419	0.2239	-2.159	5.15E-06
Methyl alpha-aspartylphenylalaninate	C18_NEG	C14 H18 N2 O5	294.121	9.194			0.43506	-1.2007	0.017907	0.27606	-1.857	0.005993
(R)-4-hydroxy-4-methyl-2-oxoglutarate	HILIC_NEG	C6 H8 O6	174.01659	6.006			0.40585	-1.301	0.000586	0.50469	-0.98652	0.000492
Oxalosuccinic acid	C18_NEG	C6 H6 O7	190.01117	1.744			0.40195	-1.3149	0.015288	0.63723	-0.65011	0.039667
gamma-L-glutamyl-L-tyrosine	C18_NEG	C14 H18 N2 O6	310.11594	7.139			0.40027	-1.321	0.019457	0.43184	-1.2114	0.023756
p-cymene	C18_POS	C10 H14	134.1097	9.603			0.39549	-1.3383	0.000526	0.46504	-1.1046	0.001754
L-Glutathione oxidized	C18_NEG	C20 H32 N6 O12 S2	612.15081	3.568	81.3	91.7	0.31245	-1.6783	0.015288	0.62572	-0.67641	0.04888
Citramalic acid	HILIC_NEG	C5 H8 O5	148.03748	8.668		68.3	0.28247	-1.8238	0.04879	0.36167	-1.4673	0.02781
2-Isopropylmalic acid	HILIC_NEG	C7 H12 O5	176.06864	8.333	92.4	86.9	0.23328	-2.0999	0.000398	0.25516	-1.9705	0.000319
7-O-Phosphonohept-2-ulose	HILIC_NEG	C7 H15 O10 P	290.04029	9.841			0.04405 ₅	-4.5046	2.29E-07	0.08883 ₆	-3.4927	2.68E-05

Table 8. Changes in Glycerolipids Identified Using LC-MS in *adp* Fruit

							adp vs. CL			adp vs. WT		
Tissue	Stage	Mode	Peak_ID	Lipid class	mz	RT (min)	FC	log2(FC)	adjusted p	FC	log2(FC)	adjusted p
Placenta	6 dpa	POS	MGDG 32:0	Monogalactosyl diacylglycerol	748.5934529	9.224245	0.64018	-0.64344	0.046779	0.53973	-0.88968	0.005602
Placenta	20 dpa	NEG	SQDG 32:3	Sulfoquinovosyl diacylglycerol	787.4997841	5.329678	1.7607	0.81612	0.000478	1.6463	0.71926	0.000874
Placenta	20 dpa	POS	TAG 50:6	Triacylglycerol	840.7072541	13.62613	1.3987	0.48414	0.000245	1.9031	0.92839	0.002516
Placenta	20 dpa	NEG	SQDG 32:2	Sulfoquinovosyl diacylglycerol	789.5159361	5.76877	1.3693	0.45348	0.004597	1.4253	0.51129	0.01695
Placenta	20 dpa	NEG	SQDG 36:6	Sulfoquinovosyl diacylglycerol	837.4821293	5.145032	1.3507	0.43372	0.026141	1.3669	0.45094	0.02174
Placenta	20 dpa	POS	MGDG 34:3	Monogalactosyl diacylglycerol	770.5762785	7.97749	0.60852	-0.71662	0.00234	0.62336	-0.68186	0.030585
Placenta	20 dpa	POS	DGDG 32:3	Digalactosyl diacylglycerol	904.5989096	6.497954	0.57709	-0.79312	0.006145	0.59228	-0.75565	0.049944
Placenta	20 dpa	POS	DGDG 32:1	Digalactosyl diacylglycerol	908.6308191	7.657834	0.56911	-0.81323	0.003031	0.5773	-0.7926	0.033397
Placenta	20 dpa	POS	DGDG 34:3	Digalactosyl diacylglycerol	932.6299042	7.225584	0.53834	-0.8934	0.000919	0.57957	-0.78694	0.030141
Placenta	20 dpa	POS	MGDG 34:2	Monogalactosyl diacylglycerol	772.5928779	8.659586	0.53724	-0.89636	0.000145	0.64787	-0.62621	0.013369
Placenta	20 dpa	POS	DGDG 34:2	Digalactosyl diacylglycerol	934.6456211	7.877595	0.49006	-1.029	0.000188	0.57491	-0.79859	0.037915
Placenta	20 dpa	POS	MGDG 36:3	Monogalactosyl diacylglycerol	798.6083615	8.856581	0.48787	-1.0354	0.00041	0.56124	-0.83332	0.012591
Placenta	20 dpa	POS	DGDG 38:5	Digalactosyl diacylglycerol	984.6600594	6.735676	0.45772	-1.1274	0.004363	0.59115	-0.75839	0.021535
Placenta	20 dpa	NEG	SQDG 32:0	Sulfoquinovosyl diacylglycerol	793.513623	6.800176	0.40607	-1.3002	0.002727	0.58386	-0.7763	0.007893
Placenta	20 dpa	POS	MGDG 36:4	Monogalactosyl diacylglycerol	796.5917938	8.09914	0.40591	-1.3008	0.000302	0.61051	-0.7119	0.037915
Placenta	20 dpa	POS	DGDG 38:4	Digalactosyl diacylglycerol	986.6758223	7.355799	0.40003	-1.3218	0.001222	0.50851	-0.97566	0.016275
Placenta	20 dpa	POS	DGDG 36:2	Digalactosyl diacylglycerol	962.677015	8.877216	0.39326	-1.3464	6.87E-05	0.64499	-0.63265	0.041043
Placenta	20 dpa	POS	DGDG 32:2	Digalactosyl diacylglycerol	906.6149351	7.103352	0.38756	-1.3675	0.005946	0.39273	-1.3484	0.001807
Placenta	20 dpa	POS	DGDG 36:5	Digalactosyl diacylglycerol	956.6290688	6.736353	0.38628	-1.3723	9.91E-05	0.56524	-0.82307	0.030585
Placenta	20 dpa	POS	MGDG 32:0	Monogalactosyl diacylglycerol	748.5934529	9.224245	0.35238	-1.5048	5.08E-05	0.44769	-1.1594	0.001807
Placenta	20 dpa	POS	DGDG 36:4	Digalactosyl diacylglycerol	958.6445553	7.356304	0.32606	-1.6168	6.57E-05	0.47219	-1.0825	0.01901
Placenta	20 dpa	POS	DGDG 34:0	Digalactosyl diacylglycerol	938.6777283	9.405775	0.24477	-2.0305	2.81E-05	0.34369	-1.5408	0.001807
Placenta	20 dpa	POS	DGDG 32:0	Digalactosyl diacylglycerol	910.6460983	8.390417	0.18524	-2.4325	5.08E-05	0.25081	-1.9953	0.001506
Placenta	MG	NEG	SQDG 36:6	Sulfoquinovosyl diacylglycerol	837.4821293	5.145032	1.4642	0.55015	0.043236	1.4528	0.53883	0.025428
Placenta	MG	POS	MGDG 36:3	Monogalactosyl diacylglycerol	798.6083615	8.856581	0.59024	-0.76064	0.002642	0.74615	-0.42246	0.035085

Tissue	Stage	Mode	Peak_ID	Lipid class	mz	RT (min)	adp vs. CL			adp vs. WT		
							FC	log2(FC)	adjusted p	FC	log2(FC)	adjusted p
Placenta	MG	POS	PC 32:1	Phosphatidylcholine	732.5542264	7.743365	0.54934	-0.86423	0.011553	0.59992	-0.73716	0.001976
Placenta	MG	NEG	SQDG 34:2	Sulfoquinovosyl diacylglycerol	817.5140252	6.399002	0.53798	-0.89437	0.006699	0.68744	-0.54069	0.035428
Placenta	MG	NEG	SQDG 32:0	Sulfoquinovosyl diacylglycerol	793.513623	6.800176	0.49447	-1.016	0.000897	0.56774	-0.81669	0.02066
Placenta	MG	NEG	PG 34:1	Phosphatidylglycerol	747.5179288	7.318514	0.40133	-1.3171	0.000725	0.70785	-0.49849	0.012553
Placenta	MG	POS	DGDG 32:1	Digalactosyl diacylglycerol	908.6308191	7.657834	0.39991	-1.3223	0.001744	0.45989	-1.1206	0.011126
Placenta	MG	POS	DGDG 34:3	Digalactosyl diacylglycerol	932.6299042	7.225584	0.39375	-1.3446	0.002183	0.55964	-0.83743	0.041386
Placenta	MG	POS	DGDG 34:2	Digalactosyl diacylglycerol	934.6456211	7.877595	0.36013	-1.4734	0.000641	0.56435	-0.82534	0.011346
Placenta	MG	POS	MGDG 32:0	Monogalactosyl diacylglycerol	748.5934529	9.224245	0.35872	-1.4791	0.000199	0.60115	-0.7342	0.025252
Placenta	MG	POS	DGDG 36:4	Digalactosyl diacylglycerol	958.6445553	7.356304	0.33803	-1.5648	0.001047	0.57039	-0.80999	0.031692
Placenta	MG	POS	DGDG 36:2	Digalactosyl diacylglycerol	962.677015	8.877216	0.31531	-1.6652	0.001047	0.66286	-0.59323	0.014164
Placenta	MG	POS	DGDG 34:0	Digalactosyl diacylglycerol	938.6777283	9.405775	0.16955	-2.5602	0.000199	0.40573	-1.3014	0.009902
Placenta	MG	POS	DGDG 32:0	Digalactosyl diacylglycerol	910.6460983	8.390417	0.14726	-2.7636	0.000165	0.28802	-1.7958	0.001325
Placenta	RR	POS	DGDG 36:1	Digalactosyl diacylglycerol	964.692874	9.638398	1.8726	0.90502	0.035209	2.4885	1.3153	0.001635
Placenta	RR	POS	MGDG 36:3	Monogalactosyl diacylglycerol	798.6083615	8.856581	1.6909	0.75775	0.015795	1.4582	0.54414	0.016375
Placenta	RR	POS	TAG 60:5	Triacylglycerol	982.8794078	15.60353	1.6757	0.74474	0.018794	1.6596	0.73082	0.005012
Placenta	RR	NEG	PS 40:2	Phosphatidylserine	842.5908886	8.164167	1.535	0.61826	0.004783	1.1732	0.23043	0.0103
Placenta	RR	POS	MGDG 36:4	Monogalactosyl diacylglycerol	796.5917938	8.09914	1.4874	0.57284	0.043767	1.3669	0.4509	0.018965
Placenta	RR	NEG	PG 34:0	Phosphatidylglycerol	749.533836	8.03903	1.4742	0.55989	0.002571	1.8053	0.85226	0.003919
Placenta	RR	POS	DGDG 36:4	Digalactosyl diacylglycerol	958.6445553	7.356304	1.4596	0.54559	0.020377	1.4804	0.56594	0.000243
Placenta	RR	NEG	PS 42:1	Phosphatidylserine	872.6393998	10.04242	1.4384	0.52446	0.002555	2.3176	1.2126	0.000357
Placenta	RR	POS	MGDG 34:0	Monogalactosyl diacylglycerol	776.6247732	10.24769	1.382	0.46681	0.019601	1.5028	0.58765	0.011005
Placenta	RR	POS	MGDG 36:2	Monogalactosyl diacylglycerol	800.6238267	9.680866	1.3335	0.41517	0.039364	1.8281	0.87036	0.001161
Placenta	RR	POS	MGDG 36:1	Monogalactosyl diacylglycerol	802.6413022	10.45046	1.308	0.38736	0.027689	1.7996	0.8477	0.000695
Placenta	RR	POS	PC 38:2	Phosphatidylcholine	814.6318604	10.04102	1.3067	0.3859	0.027071	2.3619	1.24	0.000402
Placenta	RR	NEG	SQDG 32:1	Sulfoquinovosyl diacylglycerol	791.5319008	6.259773	1.2798	0.3559	0.046685	1.3333	0.41498	0.009588

Tissue	Stage	Mode	Peak_ID	Lipid class	mz	RT (min)	adp vs. CL			adp vs. WT		
							FC	log2(FC)	adjusted p	FC	log2(FC)	adjusted p
Placenta	RR	NEG	PS 40:0	Phosphatidylserine	846.6234936	9.765872	1.2713	0.34626	0.035501	1.8786	0.90967	0.00173
Placenta	RR	NEG	PS 42:2	Phosphatidylserine	870.6226294	9.115818	1.217	0.28336	0.025644	3.5779	1.8391	0.000501
Placenta	RR	NEG	PS 40:1	Phosphatidylserine	844.6075846	8.976524	1.1884	0.24901	0.01896	2.056	1.0398	0.001039
Placenta	RR	POS	MGDG 36:6	Monogalactosyldiacylglycerol	792.5606238	6.815294	0.79513	-0.33074	0.03106	0.71332	-0.48739	0.008361
Placenta	RR	POS	TAG 54:9	Triacylglycerol	890.7224362	13.35717	0.75927	-0.39732	0.011927	0.45027	-1.1511	0.000695
Placenta	RR	NEG	PG 36:5	Phosphatidylglycerol	767.487021	5.773432	0.71264	-0.48875	0.020728	0.74267	-0.4292	0.01131
Placenta	RR	NEG	SQDG 36:5	Sulfoquinovosyl diacylglycerol	839.4974664	5.549654	0.69513	-0.52465	0.013285	0.6306	-0.6652	0.002299
Placenta	RR	POS	DGDG 36:6	Digalactosyldiacylglycerol	954.6136146	6.169967	0.69169	-0.5318	0.045779	0.6667	-0.58489	0.005078
Placenta	RR	NEG	PS 40:5	Phosphatidylserine	836.5445562	6.222667	0.68495	-0.54592	0.012085	0.52832	-0.9205	0.000821
Placenta	RR	POS	TAG 50:6	Triacylglycerol	840.7072541	13.62613	0.68213	-0.55188	0.023585	0.25922	-1.9477	3.55E-05
Placenta	RR	POS	MGDG 34:6	Monogalactosyldiacylglycerol	764.5291036	6.109162	0.6795	-0.55746	0.036011	0.51217	-0.96529	0.018498
Placenta	RR	NEG	PI 36:6	Phosphatidylinositol	853.486525	5.136754	0.67162	-0.57429	0.045268	0.54919	-0.86462	0.037662
Placenta	RR	POS	PC 36:6	Phosphatidyletholine	778.5370782	6.221897	0.67036	-0.57699	0.036905	0.53767	-0.8952	0.010129
Placenta	RR	POS	PE 34:3	Phosphatidylethanolamine	714.5051574	7.433308	0.65861	-0.60251	0.037689	0.52858	-0.91982	0.000538
Placenta	RR	NEG	SQDG 32:3	Sulfoquinovosyl diacylglycerol	787.4997841	5.329678	0.63177	-0.66253	0.002571	0.49222	-1.0226	0.000501
Placenta	RR	POS	PE 36:6	Phosphatidylethanolamine	736.490567	6.333115	0.59924	-0.7388	0.029383	0.49917	-1.0024	0.000609
Placenta	RR	POS	DGDG 34:3	Digalactosyldiacylglycerol	932.6299042	7.225584	0.59054	-0.7599	0.008398	0.41062	-1.2841	0.000325
Placenta	RR	NEG	SQDG 34:3	Sulfoquinovosyl diacylglycerol	815.4974281	5.901407	0.57761	-0.79184	0.00098	0.41742	-1.2604	0.000501
Placenta	RR	POS	DGDG 34:4	Digalactosyldiacylglycerol	930.6149915	6.528241	0.52571	-0.92767	0.033065	0.22776	-2.1344	0.000144
Placenta	RR	NEG	SQDG 36:6	Sulfoquinovosyl diacylglycerol	837.4821293	5.145032	0.49774	-1.0065	0.001265	0.43671	-1.1953	0.000501
Pericarp	20 dpa	NEG	PG 36:5	Phosphatidylglycerol	767.487021	5.773432	0.791	-0.33825	0.030182	0.68696	-0.5417	0.002244
Pericarp	20 dpa	NEG	PS 42:4	Phosphatidylserine	866.59383	7.629547	0.7502	-0.41465	0.018009	0.69238	-0.53037	0.004317
Pericarp	20 dpa	NEG	PS 40:5	Phosphatidylserine	836.5445562	6.222667	0.67697	-0.56283	0.037507	0.48637	-1.0399	0.002657
Pericarp	20 dpa	POS	TAG 52:6	Triacylglycerol	868.7384924	14.10849	0.66714	-0.58394	0.028419	0.59662	-0.74511	0.012242
Pericarp	20 dpa	POS	TAG 54:8	Triacylglycerol	892.7383921	13.78206	0.64086	-0.64191	0.038419	0.70259	-0.50924	0.021277

Tissue	Stage	Mode	Peak_ID	Lipid class	mz	RT (min)	adp vs. CL			adp vs. WT		
							FC	log2(FC)	adjusted p	FC	log2(FC)	adjusted p
Pericarp	20 dpa	POS	TAG 54:9	Triacylglycerol	890.7224362	13.35717	0.62559	-0.6767	0.023275	0.60231	-0.73142	0.020292
Pericarp	20 dpa	POS	PE 38:3	Phosphatidylethanolamine	770.5691763	7.776976	0.52149	-0.93929	0.033275	0.60492	-0.72518	0.033791
Pericarp	MG	NEG	SQDG 32:3	Sulfoquinovosyl diacylglycerol	787.4997841	5.329678	0.68605	-0.54361	0.089538	0.73008	-0.45386	0.058076
Pericarp	RR	NEG	SQDG 32:1	Sulfoquinovosyl diacylglycerol	791.5319008	6.259773	1.5718	0.65239	0.019293	1.6885	0.75578	0.01981
Pericarp	RR	POS	PC 36:6	Phosphatidylcholine	778.5370782	6.221897	0.69895	-0.51675	0.017319	0.53203	-0.91043	0.000755
Pericarp	RR	NEG	SQDG 34:3	Sulfoquinovosyl diacylglycerol	815.4974281	5.901407	0.69487	-0.52518	0.01054	0.53538	-0.90136	0.001056
Pericarp	RR	POS	TAG 54:8	Triacylglycerol	892.7383921	13.78206	0.68071	-0.55488	0.034655	0.41013	-1.2859	0.000271
Pericarp	RR	NEG	PI 36:6	Phosphatidylinositol	853.486525	5.136754	0.66842	-0.58117	0.015658	0.7525	-0.41024	0.02586
Pericarp	RR	NEG	SQDG 36:6	Sulfoquinovosyl diacylglycerol	837.4821293	5.145032	0.62719	-0.67302	0.038537	0.69063	-0.53401	0.007133
Pericarp	RR	NEG	PS 40:5	Phosphatidylserine	836.5445562	6.222667	0.62298	-0.68274	0.017002	0.47077	-1.0869	0.000694
Pericarp	RR	POS	DGDG 34:4	Digalactosyldiacylglycerol	930.6149915	6.528241	0.5254	-0.92851	0.016439	0.27487	-1.8632	0.000313

Table 9. Gene identifiers for FIG. 4

Genes included in FIG. 4		
Gene ID	Annotation	Function
Solyc06g071580	MORC family protein	Chromatin remodeling
Solyc12g042000	BREAST CANCER ASSOCIATED RING 1 like protein	DNA repair
Solyc12g099910	Chromodomain helicase DNA binding protein	Chromatin remodeling
Solyc01g087400	Histone-lysine N-methyltransferase	Chromatin remodeling
Solyc11g062010	Chromodomain helicase DNA binding protein	Chromatin remodeling
Solyc01g006880	Histone-lysine N-methyltransferase	Chromatin remodeling
Solyc10g006200	Endoribonuclease Dicer homolog 1	Gene silencing/siRNA production
Solyc02g091620	DNA mismatch repair protein-like	DNA repair
Solyc09g066080	BREAST CANCER ASSOCIATED RING 1 like protein	DNA repair
Solyc01g098520	DNA mismatch repair protein-like	DNA repair
Solyc11g008530	Dicer-like protein <i>SIDCL2d</i>	Gene silencing/siRNA production
Solyc01g106770	Serine/threonine-protein kinase TOR	TOR signaling
Solyc11g030550	Cyclin B2	Cell cycle
Solyc09g064200	Myosin XI-2	Cellular trafficking
Solyc02g090260	Golgin	Cellular trafficking
Solyc10g076260	Regulatory-associated protein of TOR RAPTOR1	TOR signaling
Solyc10g076270	Regulatory-associated protein of TOR RAPTOR2	TOR signaling
Solyc05g013490	Cyclin like protein	Cell cycle
Solyc08g075650	Formin-like protein	Cellular trafficking
Solyc01g106950	Myosin heavy chain-like protein	Cellular trafficking
Solyc02g069660	Vacuolar protein sorting-associated protein 54	Cellular trafficking
Solyc06g076560	Heat shock protein Hsp20	Stress responses
Solyc03g113930	Heat shock protein Hsp20	Stress responses

Genes included in FIG. 4		
Gene ID	Annotation	Function
Solyc03g117630	Heat shock protein 70	Stress responses
Solyc12g011310	Glutathione S-transferase	Stress responses
Solyc03g082420	Heat shock protein Hsp20	Stress responses
Solyc11g020330	Leer-sHSP small heat shock protein	Stress responses
Solyc07g056510	Glutathione S-transferase	Stress responses
Solyc02g093600	Heat shock protein Hsp20	Stress responses
Solyc02g072000	Heat Stress transcription factor SolycHsfA4c	Transcription factor
Solyc01g100640	Catalase	Stress responses
Solyc01g100630	Catalase	Stress responses
Solyc06g033850	DREB2D like transcription factor	Transcription factor
Solyc02g091030	NF-YC4 like transcription factor	Transcription factor
Solyc03g080150	Peroxidase	Stress responses
Solyc03g124110	CBF2 like transcription factor	Transcription factor
Solyc10g050970	Ethylene Response Factor SL-ERF.D4	Transcription factor
Solyc08g007820	CBF4/DDF2 like transcription factor	Transcription factor
Solyc08g007830	CBF/DDF1 like transcription factor	Transcription factor

Table 10. Gene identifiers for FIG. 7A

Genes included in FIG. 7A		
Placenta		
Gene ID	Annotation	Function
Solyc02g036290	Malonyl-CoA decarboxylase	Fatty acid metabolism
Solyc05g008790	Ceramide kinase	Sphingolipid metabolism
Solyc02g082770	Phosphatidylinositide phosphatase	Phosphatidylinositol dephosphorylation; Signaling
Solyc02g082763	Phosphatidylinositide phosphatase	Phosphatidylinositol dephosphorylation; Signaling
Solyc09g075790	Long-chain acyl-CoA synthetase (LACS)	Fatty acid elongation

Genes included in FIG. 7A		
Placenta		
Gene ID	Annotation	Function
Solyc07g032180	Lysophosphatidic acid acyltransferase (LPAAT)	Glycerolipid biosynthesis; Phosphatidic acid biosynthesis
Solyc05g042070	Phosphatidylinositol-4-phosphate 5-kinase	Synthesis of phosphatidylinositol (4,5)-bisphosphate; Lipid signaling
Solyc10g005840	Farnesyl diphosphate synthase	Sterol biosynthesis
Solyc07g032170	Lysophosphatidic acid acyltransferase	Glycerolipid biosynthesis, Phosphatidic acid biosynthesis
Solyc07g032220	Phospholipase A2	Phospholipid metabolism; Cleavage at the sn-2 produce lysophospholipid and free fatty acid
Solyc03g019670	Phospholipase C	Phospholipid catabolism
Solyc02g084930	Cytochrome P450 family protein	Sterol metabolism
Solyc08g080130	Phospholipase PLDb1	Phospholipid catabolism; Generates phosphatidic acid (PA) and a free head group
Solyc11g011610	Fatty acid-binding protein	Lipid biosynthesis
Solyc09g061840	3-Ketoacyl-CoA thiolase	Fatty acid β -oxidation
Solyc03g044910	ELO family protein	Fatty acid elongation; Very-long-chain fatty acid synthesis
Solyc07g056320	Glycerol-3-phosphate acyltransferase (GPAT)	Glycerolipid biosynthesis
Solyc06g030590	Subunit of serine palmitoyltransferase (LCB2)	Sphingolipid biosynthesis
Solyc10g086690	Phosphatidylinositol:ceramide inositolphosphotransferase (IPCS1)	Sphingolipid biosynthesis
Solyc12g100270	Fatty acid hydroxylase	Sterol/Wax biosynthesis
Solyc04g040130	Omega-6 fatty acid desaturase	Phospholipid desaturation in the ER; Synthesis of 18:2 fatty acids in the endoplasmic reticulum
Solyc12g100250	Omega-6 fatty acid desaturase	Phospholipid desaturation in the ER
Solyc02g038740	3-Hydroxy-3-methylglutaryl CoA reductase	Sterol biosynthesis
Solyc02g084740	Cytochrome P450 family protein	Sterol metabolism
Solyc01g109140	CYP74 cytochrome P450 family protein	Lipid oxidation/Oxylipin metabolism

Genes included in FIG. 7A		
Placenta		
Gene ID	Annotation	Function
Solyc04g079820	Phosphatidylinositol polyphosphate 5-phosphatase	Phosphatidylinositol dephosphorylation; Signaling
Solyc08g029000	Lipoxygenase	Lipid oxidation; Oxylipin biosynthesis
Solyc01g103650	Phospholipase ABHD3 isoform	Phospholipid catabolism
Solyc01g005930	Lipase/lipoxygenase, PLAT/LH2 family protein	Lipid oxidation; Oxylipin biosynthesis
Solyc01g095930	O-acyltransferase WSD1-like protein	Wax ester and TGA biosynthesis
Solyc01g099180	Lipoxygenase	Lipid oxidation; Oxylipin biosynthesis
Solyc01g099190	Lipoxygenase B	Lipid oxidation; Oxylipin biosynthesis
Solyc03g115370	Diacylglycerol kinase (DGK)	Phosphatidic acid production; Lipid signaling
Solyc07g054830	Diacylglycerol kinase (DGK)	Phosphatidic acid production; Lipid signaling
Pericarp		
Gene ID	Annotation	Function
Solyc05g050090	Fatty acid/sphingolipid desaturase	Sphingolipid metabolism
Solyc01g006000	GPI mannosyltransferase 2	Glycosylphosphatidylinositol-Anchor synthesis
Solyc07g032180	Lysophosphatidic acid acyltransferase(LPAAT)	Glycerolipid biosynthesis; Phosphatidic acid biosynthesis
Solyc01g080900	CYP88A3 Cytochrome P450 family protein/ ent-kaurenoic acid oxidase	Sterol biosynthesis
Solyc01g103650	Phospholipase ABHD3 isoform	Phospholipid catabolism
Solyc06g011530	Hydroxymethylglutaryl-CoA lyase	Branched-chain amino acid catabolism; Production of Acetyl-CoA
Solyc00g009110	Phosphatidylinositol polyphosphate 5-phosphatase	Phosphatidylinositol dephosphorylation; Signaling
Solyc01g099180	Lipoxygenase	Lipid oxidation; Oxylipin biosynthesis
Solyc01g099190	Lipoxygenase B	Lipid oxidation; Oxylipin biosynthesis
Solyc06g053480	Stearoyl-ACP desaturase	Omega-9 monounsaturated fatty acid biosynthesis
Solyc11g008680	Stearoyl-ACP desaturase	Omega-9 monounsaturated fatty acid biosynthesis
Solyc01g099200	Lipoxygenase	Lipid oxidation; Oxylipin biosynthesis

Genes included in FIG. 7A		
Placenta		
Gene ID	Annotation	Function
Solyc12g005380	Diacylglycerol kinase	Phosphatidic acid production; Lipid signaling
Solyc08g005630	Long-chain-alcohol oxidase	Wax biosynthesis
Solyc01g099170	Lipoxygenase	Lipid oxidation; Oxylipin biosynthesis

Table 11. Gene identifiers for FIG. 8

Genes included in FIG. 8			
Gene ID	Gene Name	Annotation	Function
Solyc04g049360	ADCS	Aminodeoxychorismate synthase	Folic acid-containing compound biosynthetic process
Solyc03g115370	DGK	Diacylglycerol kinase	Phosphatidic acid production; Lipid signaling
Solyc07g054830	DGK	Diacylglycerol kinase	Phosphatidic acid production; Lipid signaling
Solyc03g044910	ELO	Elongation of fatty acids protein	Fatty acid elongation; Very-long-chain fatty acid synthesis
Solyc04g009030	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	Glycolysis
Solyc07g056320	GPAT	Glycerol-3-phosphate acyltransferase	Glycerolipid biosynthesis
Solyc10g086690	IPCS1	Phosphatidylinositol:ceramide inositolphosphotransferase	Sphingolipid biosynthesis
Solyc09g075790	LACS	Long-chain acyl-CoA synthetase	Fatty acid elongation
Solyc06g030590	LCB2	LONG-CHAIN BASE2 subunit of serine palmitoyltransferase	Sphingolipid biosynthesis
Solyc07g017670	LKR	Lysine-ketoglutarate reductase	Amino acid metabolism
Solyc05g042070		PI kinase	Lipid signaling
Solyc02g082770		PI phosphatase	Lipid signaling
Solyc03g115820	RPE	Ribulose-phosphate 3-epimerase	Pentose phosphate pathway
Solyc10g018300		Transketolase	Pentose phosphate pathway

Table 12. Gene identifiers for FIG. 12

Genes included in FIG. 12			
Gene ID	Gene Name	Annotation	Function
Solyc01g095080	ACS2	1-aminocyclopropane-1-carboxylic acid synthase-2	Ethylene biosynthesis
Solyc05g050010	ACS4	1-aminocyclopropane-1-carboxylic acid synthase-4	Ethylene biosynthesis
Solyc02g036350	ACO6	1-aminocyclopropane-1-carboxylate oxidase	Ethylene biosynthesis
Solyc06g053710	ETR4	Ethylene receptor homolog	Ethylene signaling
Solyc06g051800	EXP1	Expansin 1	Cell wall modification
Solyc07g064190	PME3	Pectin methylesterase	Cell wall modification
Solyc08g005610	XTH5	Xyloglucan endotransglucosylase-hydrolase	Cell wall modification
Solyc10g080210	PG	Polygalacturonase	Cell wall modification

Example 7 – Characterization of asp1-CR13 KO Tomatos

[0177] To test if another mutation/KO of APS1 would lead to a similar phenotype in another tomato cultivar, we generated CRISPR mutants targeting the APS1 gene in the tomato cv. M82 (FIG. 18A). Several independent CRISPR mutant lines were obtained by causing mutations in the different motifs and domains of the APS1 protein (FIG. 18B). We identified one homozygous line for the edited site (line CR13, harboring a 5 bp deletion at the target site leading to a frameshift and a very early stop codon in the APS1 gene (FIG. 18A).

[0178] At 6 weeks old, the *aps1*-CR13 KO tomato showed an altered vegetative phenotype with decumbent stems caused by a lack of starch accumulation. Indeed the *aps1*-CR13 KO tomatoes showed a similar phenotype to *aps1*-adp (i.e. having an altered vegetative phenotype and no starch accumulation)(FIG 18C). In stark contrast to the wild type plant, the leaves of both the *aps1*-adp and *aps1*-CR13 lacked any starch accumulation.

[0179] In view of this data, we have identified another mutation of the APS1 protein that is capable of increasing blossom end rot resistance in, increasing the size of, and/or increasing the antioxidants in fruit of tomato plants.

Example 8 – ADP-Glucose Pyrophosphorylase Genes

[0180] Genomic sequences, coding sequences, and amino acid sequences for *AGPase* small subunits (*APS*) and large subunits (*APL*) from various Solanaceae and Cucurbitae species are provided in Table 13. Tomato (*Solanum lycopersicum* Heinz ITAG 4.1), eggplant (*Solanum melongena* V3), and pepper (*Capsicum annuum* cv CM334 v1.55) sequences are from solgenomics.net. Cucumber (*Cucumis sativus* L. var. *sativus* cv. 9930 v3), squash (*Cucurbita maxima* Rimu), zucchini (*Cucurbita pepo*), melon (*Cucumis melo* DHL92 v3.6.1), watermelon (*Citrullus lanatus* 97103 v1), and pumpkin (*Cucurbita moschata* Rifu) sequences are from cucurbitgenomics.org.

[0181] Exemplary eggplant sequences include *APSI* (Accession No. SMEL_007g292070), *APS2* (Accession No. SMEL_008g302690.1.01), *APL1* (Accession No. SMEL_001g137380.1), *APL2* (Accession No. SMEL_006g246970.1.01), *APL3* (Accession No. SMEL_001g117310.1.01), each of which is hereby incorporated by reference in its entirety).

[0182] Exemplary pepper sequences include *APSI* (Accession No. CA07g15620), *APS2* (Accession No. CA00g10930), *APS3* (Accession No. CA09g08040), *APL1* (Accession No. CA01g24580), *APL2* (Accession No. CA07g05920), *APL3* (Accession No. CA01g05120), each of which is hereby incorporated by reference in its entirety).

5 **[0183]** Exemplary cucumber sequences include *APSI* (Accession No. CsaV3_7G002310), *APL1* (Accession No. CsaV3_3G013570.1), *APL2* (Accession No. CsaV3_3G045370.1), *APL3* (Accession No. CsaV3_2G014910.1), each of which is hereby incorporated by reference in its entirety).

[0184] Exemplary squash sequences include *APSI* (Accession No. CmaCh19G008330),
10 *APS3* (Accession No. CmaCh11G013000.1), *APL1* (Accession No. CmaCh14G016860.1), *APL2* (Accession No. CmaCh09G001450), *APL3* (Accession No. CmaCh02G003870), each of which is hereby incorporated by reference in its entirety).

[0185] Exemplary zucchini sequences include *APSI* (Accession No. Cp4.1LG15g06700),
15 *APL1* (Accession No. Cp4.1LG03g10860.1), *APL2* (Accession No. Cp4.1LG06g01040.1), *APL3* (Accession No. Cp4.1LG16g02590.1), each of which is hereby incorporated by reference in its entirety).

[0186] Exemplary melon sequences include *APSI* (Accession No. MELO3C024175.2.1),
20 *APL1* (Accession No. MELO3C006552), *APL2* (Accession No. MELO3C003812), *APL3* (Accession No. MELO3C023310), each of which is hereby incorporated by reference in its entirety).

[0187] Exemplary watermelon sequences include *APSI* (Accession No. Cla015710),
APL1 APL1 (Accession No. Cla021651), *APL2* (Accession No. Cla020783), *APL3* (Accession No. Cla016574), each of which is hereby incorporated by reference in its entirety).

[0188] Exemplary pumpkin sequences include *APSI* (Accession No.
25 CmoCh19G008490), *APS3* (Accession No. CmoCh11G018220), *APL1* (Accession No. CmoCh14G017310), *APL2* (Accession No. CmoCh09G001430), *APL3* (Accession No. CmoCh02G003940), each of which is hereby incorporated by reference in its entirety).

30 **TABLE 14: Exemplary APS and APL Sequences are set forth in the Sequence Listing that is incorporated herein by reference.**

Organism, Gene Name, Sequence Type (Accession No.) (SEQ ID NO:)

<i>Solanum lycopersicum</i> APS1 Genomic Sequence (Soly07g056140) (SEQ ID NO:1) >Soly07g056140_SL4.0ch07 SL4.0ch07:63906315..63911061_APS1_tomato_genomic
<i>Solanum lycopersicum</i> APS1 Coding Sequence (Soly07g056140) (SEQ ID NO:2) >Soly07g056140.3.1_APS1 tomato_CDS
<i>Solanum lycopersicum</i> APS1 Amino Acid Sequence (Soly07g056140) (SEQ ID NO:3)
<i>Solanum lycopersicum</i> APS2 Genomic Sequence (Soly08g015670) (SEQ ID NO:4) > Soly08g015670_SL4.0ch08 SL4.0ch08:5145629..5149158_APS2_tomato_genomic
<i>Solanum lycopersicum</i> APS2 Coding Sequence (Soly08g015670) (SEQ ID NO:5) >Soly08g015670.4.1_APS2_tomato_CDS
<i>Solanum lycopersicum</i> APS2 Amino Acid Sequence (Soly08g015670) (SEQ ID NO:6)
<i>Solanum lycopersicum</i> APS3 Genomic Sequence (Soly12g011120) (SEQ ID NO:7) > Soly12g011120_SL4.0ch12:4007641..4012840_APS3_tomato_genomic
<i>Solanum lycopersicum</i> APS3 Coding Sequence (Soly12g011120) (SEQ ID NO:8) >Soly12g011120.4.1_APS3_tomato_CDS
<i>Solanum lycopersicum</i> APS3 Amino Acid Sequence (Soly12g011120) (SEQ ID NO:9)
<i>Solanum lycopersicum</i> APL1 Genomic Sequence (Soly01g079790) (SEQ ID NO:10) >Soly01g079790.2 SL2.50ch01:78922547..78926789 _APL1_tomato_genomic
<i>Solanum lycopersicum</i> APL1 Coding Sequence (Soly01g079790) (SEQ ID NO:11) >Soly01g079790.5.1_APL1 tomato_CDS
<i>Solanum lycopersicum</i> APL1 Amino Acid Sequence (Soly01g079790) (SEQ ID NO:12)
<i>Solanum lycopersicum</i> APL2 Genomic Sequence (Soly07g019440) (SEQ ID NO:13) > Soly07g019440.2 SL2.50ch07:11198353..11193230_APL2_tomato_genomic
<i>Solanum lycopersicum</i> APL2 Coding Sequence (Soly07g019440) (SEQ ID NO:14) >Soly07g019440.3.1_APL2 tomato_CDS
<i>Solanum lycopersicum</i> APL2 Amino Acid Sequence (Soly07g019440) (SEQ ID NO:15)
<i>Solanum lycopersicum</i> APL3 Genomic Sequence (Soly01g109790) (SEQ ID NO:16) >Soly01g109790.2_SL2.50ch01:96641133..96636500_APL3_tomato_genomic
<i>Solanum lycopersicum</i> APL3 Coding Sequence (Soly01g109790) (SEQ ID NO:17) >Soly01g109790.3.1_APL3 tomato_CDS
<i>Solanum lycopersicum</i> APL3 Amino Acid Sequence (Soly01g109790) (SEQ ID NO:18)
<i>Solanum melongena</i> APS1 Genomic Sequence (SMEL_007g292070) (SEQ ID NO:19) >SMEL_007g292070_SMEL3Ch07 SMEL3Ch07: 136735949..136741018_APS1_eggplant_genomic
<i>Solanum melongena</i> APS1 Coding Sequence (SMEL_007g292070) (SEQ ID NO:20) >SMEL_007g292070_SMEL_007g292070.1.01_APS1_eggplant_CDS
<i>Solanum melongena</i> APS1 Amino Acid Sequence (SMEL_007g292070) (SEQ ID NO:21)

<i>Solanum melongena</i> APS2 Genomic Sequence (SMEL_008g302690) (SEQ ID NO:22) > SMEL_008g302690_SMEL3Ch08:12017224..12020376_APS2_eggplant_genomic
<i>Solanum melongena</i> APS2 Coding Sequence (SMEL_008g302690) (SEQ ID NO:23) >SMEL_008g302690.1.01_APS2_eggplant_CDS
<i>Solanum melongena</i> APS2 Amino Acid Sequence (SMEL_008g302690) (SEQ ID NO:24)
<i>Solanum melongena</i> APL1 Genomic Sequence (SMEL_001g137380) (SEQ ID NO:25) >SMEL_001g137380.1_SMEL3Ch01 SMEL3Ch01:30484136..30490159 APL1_eggplant_genomic
<i>Solanum melongena</i> APL1 Coding Sequence (SMEL_001g137380) (SEQ ID NO:26) >SMEL_001g137380.1.01 SMEL_001g137380.1 _APL1_eggplant_CDS
<i>Solanum melongena</i> APL1 Amino Acid Sequence (SMEL_001g137380) (SEQ ID NO:27)
<i>Solanum melongena</i> APL2 Genomic Sequence (SMEL_006g246970) (SEQ ID NO:28) >SMEL_006g246970.1_ SMEL3Ch06:35481639..35487138_APL2_eggplant_genomic
<i>Solanum melongena</i> APL2 Coding Sequence (SMEL_006g246970) (SEQ ID NO:29) >SMEL_006g246970.1.01_SMEL_006g246970.1_APL2_eggplant_CDS
<i>Solanum melongena</i> APL2 Amino Acid Sequence (SMEL_006g246970) (SEQ ID NO:30)
<i>Solanum melongena</i> APL3 Genomic Sequence (SMEL_001g117310) (SEQ ID NO:31) > SMEL_001g117310.1 _ SMEL3Ch01:2170347..2175222_APL3_eggplant_genomic
<i>Solanum melongena</i> APL3 Coding Sequence (SMEL_001g117310) (SEQ ID NO:32) >SMEL_001g117310.1.01_SMEL_001g117310.1_APL3_eggplant_CDS
<i>Solanum melongena</i> APL3 Amino Acid Sequence (SMEL_001g117310) (SEQ ID NO:33)
<i>Capsicum annuum</i> APS1 Genomic Sequence (CA07g15620) (SEQ ID NO:34) >CA07g15620_Pepper1.55ch07:217965311..217970340_APS1_pepper_genomic
<i>Capsicum annuum</i> APS1 Coding Sequence (CA07g15620) (SEQ ID NO:35) >CA07g15620_APS1_pepper_CDS
<i>Capsicum annuum</i> APS1 Amino Acid Sequence (CA07g15620) (SEQ ID NO:36)
<i>Capsicum annuum</i> APS2 Genomic Sequence (CA00g10930) (SEQ ID NO:37) > CA00g10930_PGAv.1.5.contig154378:4700-6300_APS2_pepper_genomic
<i>Capsicum annuum</i> APS2 Coding Sequence (CA00g10930) (SEQ ID NO:38) >CA00g10930_APS2_pepper_CDS
<i>Capsicum annuum</i> APS2 Amino Acid Sequence (CA00g10930) (SEQ ID NO:39)
<i>Capsicum annuum</i> APS3 Genomic Sequence (CA09g08040) (SEQ ID NO:40) >CA09g08040_Pepper1.55ch09:72144554..72153286_APS3_pepper_genomic
<i>Capsicum annuum</i> APS3 Coding Sequence (CA09g08040) (SEQ ID NO:41) >CA09g08040_APS3_pepper_CDS
<i>Capsicum annuum</i> APS3 Amino Acid Sequence (CA09g08040) (SEQ ID NO:42)

<i>Capsicum annuum</i> APL1 Genomic Sequence (CA01g24580) (SEQ ID NO:43) >CA01g24580_Pepper1.55ch01:194778153..194782547_APL1_pepper_genomic
<i>Capsicum annuum</i> APL1 Coding Sequence (CA01g24580) (SEQ ID NO:44) >CA01g24580_APL1_pepper_CDS
<i>Capsicum annuum</i> APL1 Amino Acid Sequence (CA01g24580) (SEQ ID NO:45)
<i>Capsicum annuum</i> APL2 Genomic Sequence (CA07g05920) (SEQ ID NO:46) >CA07g05920_Pepper1.55ch07:58609942..58614480_APL2_pepper_genomic
<i>Capsicum annuum</i> APL2 Coding Sequence (CA07g05920) (SEQ ID NO:47) >CA07g05920_APL2_pepper_CDS
<i>Capsicum annuum</i> APL2 Amino Acid Sequence (CA07g05920) (SEQ ID NO:48)
<i>Capsicum annuum</i> APL3 Genomic Sequence (CA01g05120) (SEQ ID NO:49) >CA01g05120_Pepper1.55ch01:9269020..9272451_APL3_pepper_genomic
<i>Capsicum annuum</i> APL3 Coding Sequence (CA01g05120) (SEQ ID NO:50) >CA01g05120_APL3_pepper_CDS
<i>Capsicum annuum</i> APL3 Amino Acid Sequence (CA01g05120) (SEQ ID NO:51)
<i>Cucumis sativus</i> APS1 Genomic Sequence (CsaV3_7G002310) (SEQ ID NO:52) >CsaV3_7G002310_chr7:1820139..1826014_APS1_cucumber_genomic
<i>Cucumis sativus</i> APS1 Coding Sequence (CsaV3_7G002310) (SEQ ID NO:53) >CsaV3_7G002310_APS1_cucumber_CDS
<i>Cucumis sativus</i> APS1 Amino Acid Sequence (CsaV3_7G002310) (SEQ ID NO:54)
<i>Cucumis sativus</i> APL1 Genomic Sequence (CsaV3_3G013570) (SEQ ID NO:55) >CsaV3_3G013570_chr3:10239897..10244727_APL1_cucumber_genomic
<i>Cucumis sativus</i> APL1 Coding Sequence (CsaV3_3G013570) (SEQ ID NO:56) >CsaV3_3G013570.1_APL1_cucumber_CDS
<i>Cucumis sativus</i> APL1 Amino Acid Sequence (CsaV3_3G013570) (SEQ ID NO:57)
<i>Cucumis sativus</i> APL2 Genomic Sequence (CsaV3_3G045370) (SEQ ID NO:58) > CsaV3_3G045370_chr3:37045768..37050213_APL2_cucumber_genomic
<i>Cucumis sativus</i> APL2 Coding Sequence (CsaV3_3G045370) (SEQ ID NO:59) >CsaV3_3G045370.1_APL2_cucumber_CDS
<i>Cucumis sativus</i> APL2 Amino Acid Sequence (CsaV3_3G045370) (SEQ ID NO:60)
<i>Cucumis sativus</i> APL3 Genomic Sequence (CsaV3_2G014910) (SEQ ID NO:61) > CsaV3_2G014910_chr2:12410201..12415462_APL3_cucumber_genomic
<i>Cucumis sativus</i> APL3 Coding Sequence (CsaV3_2G014910) (SEQ ID NO:62) >CsaV3_2G014910.1_APL3_cucumber_CDS
<i>Cucumis sativus</i> APL3 Amino Acid Sequence (CsaV3_2G014910) (SEQ ID NO:63)
<i>Cucurbita maxima</i> APS1 Genomic Sequence (CmaCh19G008330) (SEQ ID NO:64)

>CmaCh19G008330_APS1_squash_genomic
<i>Cucurbita maxima</i> APS1 Coding Sequence (CmaCh19G008330) (SEQ ID NO:65) >CmaCh19G008330_APS1_squash_CDS
<i>Cucurbita maxima</i> APS1 Amino Acid Sequence (CmaCh19G008330) (SEQ ID NO:66)
<i>Cucurbita maxima</i> APS3 Genomic Sequence (CmaCh11G013000) (SEQ ID NO:67) >CmaCh11G013000_APS3_squash_genomic
<i>Cucurbita maxima</i> APS3 Coding Sequence (CmaCh11G013000) (SEQ ID NO:68) >CmaCh11G013000.1_APS3_squash_CDS
<i>Cucurbita maxima</i> APS3 Amino Acid Sequence (CmaCh11G013000) (SEQ ID NO:69)
<i>Cucurbita maxima</i> APL1 Genomic Sequence (CmaCh14G016860) (SEQ ID NO:70) > CmaCh14G016860_APL1_squash_genomic
<i>Cucurbita maxima</i> APL1 Coding Sequence (CmaCh14G016860) (SEQ ID NO:71) > CmaCh14G016860.1_APL1_squash_CDS
<i>Cucurbita maxima</i> APL1 Amino Acid Sequence (CmaCh14G016860) (SEQ ID NO:72)
<i>Cucurbita maxima</i> APL2 Genomic Sequence (CmaCh09G001450) (SEQ ID NO:73) >CmaCh09G001450_APL2_squash_genomic
<i>Cucurbita maxima</i> APL2 Coding Sequence (CmaCh09G001450) (SEQ ID NO:74) > CmaCh09G001450_APL2_squash_CDS
<i>Cucurbita maxima</i> APL2 Amino Acid Sequence (CmaCh09G001450) (SEQ ID NO:75)
<i>Cucurbita maxima</i> APL3 Genomic Sequence (CmaCh02G003870) (SEQ ID NO:76) > CmaCh02G003870_APL3_squash_genomic
<i>Cucurbita maxima</i> APL3 Coding Sequence (CmaCh02G003870) (SEQ ID NO:77) >CmaCh02G003870_APL3_squash_CDS
<i>Cucurbita maxima</i> APL3 Amino Acid Sequence (CmaCh02G003870) (SEQ ID NO:78)
<i>Cucurbita pepo</i> APS1 Genomic Sequence (Cp4.1LG15g06700) (SEQ ID NO:79) >Cp4.1LG15g06700_APS1_zucchini_genomic
<i>Cucurbita pepo</i> APS1 Coding Sequence (Cp4.1LG15g06700) (SEQ ID NO:80) >Cp4.1LG15g06700_APS1_zucchini_CDS
<i>Cucurbita pepo</i> APS1 Amino Acid Sequence (Cp4.1LG15g06700) (SEQ ID NO:81)
<i>Cucurbita pepo</i> APL1 Genomic Sequence (Cp4.1LG03g10860) (SEQ ID NO:82) >Cp4.1LG03g10860_Cp4.1LG03:11416566..11424647_APL1_zucchini_genomic
<i>Cucurbita pepo</i> APL1 Coding Sequence (Cp4.1LG03g10860) (SEQ ID NO:83) >Cp4.1LG03g10860.1_APL1_zucchini_CDS
<i>Cucurbita pepo</i> APL1 Amino Acid Sequence (Cp4.1LG03g10860) (SEQ ID NO:84)
<i>Cucurbita pepo</i> APL2 Genomic Sequence (Cp4.1LG06g01040) (SEQ ID NO:85) >Cp4.1LG06g01040_ Cp4.1LG06:497971..502927_APL2_zucchini_genomic

<i>Cucurbita pepo</i> APL2 Coding Sequence (Cp4.1LG06g01040) (SEQ ID NO:86) >Cp4.1LG06g01040.1_APL2_zucchini_CDS
<i>Cucurbita pepo</i> APL2 Amino Acid Sequence (Cp4.1LG15g06700) (SEQ ID NO:87)
<i>Cucurbita pepo</i> APL3 Genomic Sequence (Cp4.1LG16g02590) (SEQ ID NO:88) > Cp4.1LG16g02590_ Cp4.1LG16:4527849..4532781_APL3_zucchini_genomic
<i>Cucurbita pepo</i> APL3 Coding Sequence (Cp4.1LG16g02590) (SEQ ID NO:89) >Cp4.1LG16g02590.1_APL3_zucchini_CDS
<i>Cucurbita pepo</i> APL3 Amino Acid Sequence (Cp4.1LG16g02590) (SEQ ID NO:90)
<i>Cucumis melo</i> APS1 Genomic Sequence (MELO3C024175) (SEQ ID NO:91) >MELO3C024175.2.1_APS1_melon_genomic
<i>Cucumis melo</i> APS1 Coding Sequence (MELO3C024175) (SEQ ID NO:92) >MELO3C024175.2.1_APS1_melon_CDS
<i>Cucumis melo</i> APS1 Amino Acid Sequence (MELO3C024175) (SEQ ID NO:93)
<i>Cucumis melo</i> APL1 Genomic Sequence (MELO3C006552) (SEQ ID NO:94) > MELO3C006552_APL1_melon_genomic
<i>Cucumis melo</i> APL1 Coding Sequence (MELO3C006552) (SEQ ID NO:95) > MELO3C006552_APL1_melon_CDS
<i>Cucumis melo</i> APL1 Amino Acid Sequence (MELO3C006552) (SEQ ID NO:96)
<i>Cucumis melo</i> APL2 Genomic Sequence (MELO3C003812) (SEQ ID NO:97) >MELO3C003812_APL2_melon_genomic
<i>Cucumis melo</i> APL2 Coding Sequence (MELO3C003812) (SEQ ID NO:98) >MELO3C003812_APL2_melon_CDS
<i>Cucumis melo</i> APL2 Amino Acid Sequence (MELO3C003812) (SEQ ID NO:99)
<i>Cucumis melo</i> APL3 Genomic Sequence (MELO3C023310) (SEQ ID NO:100) > MELO3C023310_APL3_melon_genomic
<i>Cucumis melo</i> APL3 Coding Sequence (MELO3C023310) (SEQ ID NO:101) > MELO3C023310_APL3_melon_CDS
<i>Cucumis melo</i> APL3 Amino Acid Sequence (MELO3C023310) (SEQ ID NO:102)
<i>Citrullus lanatus</i> APS1 Genomic Sequence (Cla015710) (SEQ ID NO:103) >Cla015710_APS1_watermelon_genomic
<i>Citrullus lanatus</i> APS1 Coding Sequence (Cla015710) (SEQ ID NO:104) >Cla015710_APS1_watermelon_CDS
<i>Citrullus lanatus</i> APS1 Amino Acid Sequence (Cla015710) (SEQ ID NO:105)
<i>Citrullus lanatus</i> APL1 Genomic Sequence (Cla021651) (SEQ ID NO:106) >Cla021651_APL1_watermelon_genomic
<i>Citrullus lanatus</i> APL1 Coding Sequence (Cla021651) (SEQ ID NO:107)

> Cla021651_APL1_watermelon_CDS
<i>Citrullus lanatus</i> APS1 Amino Acid Sequence (Cla021651) (SEQ ID NO:108)
<i>Citrullus lanatus</i> APL2 Genomic Sequence (Cla020783) (SEQ ID NO:109)
> Cla020783_APL2_watermelon_genomic
<i>Citrullus lanatus</i> APL2 Coding Sequence (Cla020783) (SEQ ID NO:110)
>Cla020783_APL2_watermelon_CDS
<i>Citrullus lanatus</i> APL2 Amino Acid Sequence (Cla015710) (SEQ ID NO:111)
<i>Citrullus lanatus</i> APL3 Genomic Sequence (Cla020783) (SEQ ID NO:112)
>Cla016574_APL3_watermelon_genomic
<i>Citrullus lanatus</i> APL3 Coding Sequence (Cla020783) (SEQ ID NO:113)
>Cla016574_APL3_watermelon_CDS
<i>Citrullus lanatus</i> APL3 Amino Acid Sequence (Cla020783) (SEQ ID NO:114)
<i>Cucurbita moschata</i> APS1 Genomic Sequence (CmoCh19G008490) (SEQ ID NO:115)
>CmoCh19G008490__APS1_pumpkin_genomic
<i>Cucurbita moschata</i> APS1 Coding Sequence (CmoCh19G008490) (SEQ ID NO:116)
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<i>Cucurbita moschata</i> APS1 Amino Acid Sequence (CmoCh19G008490) (SEQ ID NO:117)
<i>Cucurbita moschata</i> APS3 Genomic Sequence (CmoCh11G018220) (SEQ ID NO:118)
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<i>Cucurbita moschata</i> APS3 Coding Sequence (CmoCh11G018220) (SEQ ID NO:119)
>CmoCh11G018220_APS3_pumpkin_CDS
<i>Cucurbita moschata</i> APS3 Genomic Sequence (CmoCh11G018220) (SEQ ID NO:120)
<i>Cucurbita moschata</i> APL1 Genomic Sequence (CmoCh14G017310) (SEQ ID NO:121)
> CmoCh14G017310__APL1_pumpkin_genomic
<i>Cucurbita moschata</i> APL1 Coding Sequence (CmoCh14G017310) (SEQ ID NO:122)
> CmoCh14G017310_APL1_pumpkin_CDS
<i>Cucurbita moschata</i> APL1 Amino Acid Sequence (CmoCh14G017310) (SEQ ID NO:123)
<i>Cucurbita moschata</i> APL2 Genomic Sequence (CmoCh09G001430) (SEQ ID NO:124)
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<i>Cucurbita moschata</i> APL2 Coding Sequence (CmoCh09G001430) (SEQ ID NO:125)
>CmoCh09G001430_APL2_pumpkin_CDS
<i>Cucurbita moschata</i> APL2 Amino Acid Sequence (CmoCh09G001430) (SEQ ID NO:126)
<i>Cucurbita moschata</i> APL3 Genomic Sequence (CmoCh02G003940) (SEQ ID NO:127)
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<i>Cucurbita moschata</i> APL3 Coding Sequence (CmoCh02G003940) (SEQ ID NO:128)
>CmoCh02G003940_APL3_pumpkin_CDS

<i>Cucurbita moschata</i> APL3 Amino Acid Sequence (CmoCh02G003940) (SEQ ID NO:129)

[0189] Although preferred embodiments have been depicted and described in detail herein, it will be apparent to those skilled in the relevant art that various modifications, additions, substitutions, and the like can be made without departing from the spirit of the invention and
5 these are therefore considered to be within the scope of the invention as defined in the claims which follow.

WHAT IS CLAIMED:

1. A plant cell comprising:
a heterologous nucleic acid molecule having
a) a modified ADP-glucose pyrophosphorylase (AGPase) sequence encoding an altered AGPase protein subunit or fragment thereof, or
b) an inhibitory polynucleotide sequence targeting an AGPase gene encoding an AGPase protein,
wherein the expression, stability, and/or activity of the AGPase protein is reduced or eliminated in the plant cell as compared to a plant cell without the modification.
2. The plant cell of claim 1, wherein the nucleic acid molecule comprises a modified ADP-glucose pyrophosphorylase (AGPase) sequence encoding an altered AGPase protein subunit or fragment thereof.
3. The plant cell according to claim 1 or 2, wherein said heterologous nucleic acid is a modified ADP-glucose pyrophosphorylase small subunit (APS) polynucleotide encoding an amino acid sequence that is at least 90% identical to any one of SEQ ID NOs: 3, 6, 9, 21, 24, 36, 39, 42, 54, 66, 69, 81, 93, 105, 117, and 120.
4. The plant cell according to claim 3, wherein the amino acid sequence is at least 90% identical to SEQ ID NO: 3, 6, or 9.
5. The plant cell according to claim 3, wherein the amino acid sequence is at least 90% identical to SEQ ID NO: 54.
6. The plant cell according to any one of claims 1-5, wherein the modified APS polynucleotide is SEQ ID NO: 130 comprising a deletion causing a frameshift mutation.
7. The plant cell according to claim 1 or 2, wherein said heterologous nucleic acid is a modified ADP-glucose pyrophosphorylase large subunit (APL) polynucleotide encoding

an amino acid sequence that is at least 90% identical to any one of SEQ ID NOs: 12, 15, 18, 27, 30, 33, 45, 48, 51, 57, 60, 63, 72, 75, 78, 84, 87, 90, 96, 99, 102, 108, 111, 114, 123, 126, and 129.

8. The plant cell according to claim 7, wherein the amino acid sequence is at least 90% identical to SEQ ID NO: 12, 15, or 18.

9. The plant cell according to claim 7, wherein the amino acid sequence is at least 90% identical to SEQ ID NO: 57, 60, or 63.

10. The plant cell according to any one of claims 1-9, further comprising a second nucleic acid molecule encoding a functional AGPase protein operably linked to a promoter which functions in a non-fruit tissue of the plant.

11. The plant cell of claim 10, wherein the tissue specific promoter is selected from the promoters listed in table 14.

12. A plant comprising the plant cell of any one of claims 1-11.

13. The plant or plant cell according to claim 12, which is a member of the Cucurbitaceae family.

14. The plant or plant cell according to claim 13, wherein the plant or plant cell is selected from the genus *Cucurbita*, *Cucumis*, or *Citrullus*.

15. The plant or plant cell according to claim 13, wherein the plant or plant cell is selected from a zucchini, cucumber, watermelon, pumpkin, squash, or melon.

16. The plant or plant cell according to claim 12, which is a member of the Solanaceae family.

17. The plant or plant cell according to claim 16, wherein the plant or plant cell is from the genus *Solanum* or *Capsicum*.

18. The plant or plant cell according to claim 17, wherein the plant or plant cell is an eggplant or pepper.

19. The plant or plant cell according to claim 17, wherein the plant or plant cell is selected from a tomato plant or tomato plant cell.

20. The tomato plant or plant cell according to claim 19, selected from Alicante, Amish Paste, Aunt Ruby's German Green, Azoychka, Beefsteak, Berkeley Tie-Dye Green, Better Boy, Big Beef, Big Mama, Big Rainbow, Blaby Special, Black Beauty, Black Cherry, Black Icicle, Black Krim, Brandywine, Breonice, Campari, Canario, Carbon, Celebrity, Cherokee Purple, Cherry Bambelo, Cherry Nebula, Chocolate Pear, Dad's Sunset, Dester, Dr. Wyche's Yellow, Early Girl, Ed's Millennium, Emerald Evergreen, Enchantment, Ferreira, Ferris Wheel, Flamenco, Fourth of July, Garden Peach, Gardener's Delight, German Johnson, German Lunchbox, German Pink, Giulietta F1, Granadero, Great White, Green Doctors, Green Giant, Green Zebra, Hanover tomato, Henderson's Pink Ponderosa, Heinz, Hillbilly, Hungarian Heart, Japanese Black Trifele, Jersey Boy, Jubilee, Juliet, Kellogg's Breakfast, Kentucky Beefsteak, Kumato, Lillian's Yellow, Malakhitovaya Shkatulka, Matt's Wild Cherry, McDreamy, Micro Tom, Millionaire, Moneymaker, Monterosa, Montserrat, Mortgage Lifter, Mr. Stripey, Mushroom Basket, M82, Napa Rose Blush, Orange Hat, Orange Icicle, Pantano Romanesco, Paul Robeson, Pink Boar, Plum tomato, Raf tomato, Raspberry Lyanna, Rebekah Allen, Rebellion, Red Currant, Roma, Rosa de Barbastro, Rosella, Rutgers, San Marzano, Santorini, Sasha Altai, Scorpio (Skorpion), Stupice, Super Sweet 100, Thorburn's Terra-cotta, Tigerella, Tiny Tim, Tomaccio, Tomkin, Traveller / Arkansas Traveler, True Black Brandywine, Violet Jasper (Tzi Bi U), Viva Italia, Wagner Blue Green, White Queen, Yellow Brandywine, Yellow Pear, or hybrids thereof.

21. A fruit of the plant according to any one of claims 12-20.
22. A method of enhancing at least one of blossom end rot resistance to, size of, or antioxidants in fruit from a plant comprising:
- a) introducing, into a plant cell, an exogenous nucleic acid molecule comprising
 - i) a modified ADP-glucose pyrophosphorylase (AGPase) sequence encoding an altered AGPase subunit protein or fragment thereof, or
 - ii) an inhibitory polynucleotide sequence targeting an AGPase gene encoding an AGPase protein, and
 - b) regenerating a transgenic plant from the plant cell.
23. The method of claim 22, wherein the nucleic acid molecule comprises a modified ADP-glucose pyrophosphorylase (AGPase) sequence encoding an altered AGPase subunit protein or fragment thereof.
24. The method of claim 22 or 23, wherein said reduction or elimination of the expression, stability, and/or activity of AGPase protein is effective in reducing or eliminating starch synthesis and
- a) imparting blossom end rot resistance to fruit from the plant or a plant produced from the plant cell, as compared to fruit from a plant without the modification, and/or
 - b) increasing fruit size in fruit from the plant or a plant produced from the plant cell, as compared to fruit from a plant without the modification, and/or
 - c) increasing antioxidant levels in a fruit from the plant or a plant produced from the plant cell, as compared to a fruit from a plant without the modification.
25. The method of claim 24, wherein the increased fruit size comprises an increase in fruit weight by at least 10%.

26. The method of claim 24, wherein the increased fruit size comprises an increase in fruit volume by at least 5%.

27. The method of claim 24, wherein the increased antioxidants comprise raffinose, phenolics, and/or pyridoxal.

28. The method according to claim 22 or 23, wherein said heterologous nucleic acid is a modified ADP-glucose pyrophosphorylase small subunit (APS) polynucleotide encoding an amino acid sequence that is at least 90% identical to any one of SEQ ID NOs: 3, 6, 9, 21, 24, 36, 39, 42, 54, 66, 69, 81, 93, 105, 117, and 120.

29. The method of claim 28, wherein the amino acid sequence is at least 90% identical to SEQ ID NO: 3, 6, or 9.

30. The method according to claim 28, wherein the amino acid sequence is at least 90% identical to SEQ ID NO: 54.

31. The method according to any one of claims 22-30, wherein the modified APS polynucleotide is SEQ ID NO: 130 and comprises a deletion mutation causing a frameshift mutation.

32. The method according to claim 22 or 23, wherein said heterologous nucleic acid is a modified ADP-glucose pyrophosphorylase large subunit (APL) polynucleotide encoding an amino acid sequence that is at least 90% identical to any one of SEQ ID NOs: 12, 15, 18, 27, 30, 33, 45, 48, 51, 57, 60, 63, 72, 75, 78, 84, 87, 90, 96, 99, 102, 108, 111, 114, 123, 126, and 129.

33. The method according to claim 32, wherein the amino acid sequence is at least 90% identical to SEQ ID NO: 12, 15, or 18.

34. The method according to claim 32, wherein the amino acid sequence is at

least 90% identical to SEQ ID NO: 57, 60, or 63.

35. The method according to anyone of claims 22-34, wherein the modified AGPase gene comprises a mutation in a coding sequence and/or regulatory sequence.

36. The method of claim 35, wherein the mutation is an insertion, a deletion, a substitution mutation, or any combination thereof.

37. The method according to claim 22, further comprising introducing a second nucleic acid molecule encoding a functional AGPase protein operably linked to a promoter which functions in a non-fruit tissue of the plant.

38. The method of claim 37, wherein the tissue specific promoter is selected from the promoters listed in table 14.

39. A plant or plant cell produced from the method of any one of claims 22-38.

40. A nucleic acid construct comprising:
a nucleotide sequence targeting an AGPase encoding nucleic acid comprising:
(i) a guide RNA; or
(ii) an inhibitory polynucleotide;
a 5' heterologous DNA promoter sequence; and
a 3' terminator sequence.

41. An expression vector comprising the nucleic acid construct according to claim 40.

42. The nucleic acid construct of claim 40 or the expression vector of claim 41, further comprising a genome editing nuclease.

43. The nucleic acid construct of claim 40 or the expression vector of claim 41, targeting a sequence present in a small subunit of said AGPase gene (*APS*) and inhibiting expression of a protein having an amino acid sequence selected from any one of SEQ ID NOs: 3, 6, 9, 21, 24, 36, 39, 42, 54, 66, 69, 81, 93, 105, 117, and 120, or having at least 90% sequence identity to any one of SEQ ID NOs: 3, 6, 9, 21, 24, 36, 39, 42, 54, 66, 69, 81, 93, 105, 117, and 120.

44. The nucleic acid construct or the expression vector of claim 43, for inhibition of an amino acid sequence at least 90% identical to SEQ ID NO: 3, 6, or 9.

45. The nucleic acid construct or the expression vector of claim 43, for inhibition of expression of an amino acid sequence at least 90% identical to SEQ ID NO: 54.

46. The nucleic acid construct or the expression vector of claim 43, wherein the modified *APS* polynucleotide is SEQ ID NO: 130 and comprises a deletion causing a frameshift mutation.

47. The nucleic acid construct of claim 40 or the expression vector of claim 41, targeting a sequence present in a small subunit of said AGPase gene (*APL*) and inhibiting expression of an amino acid sequence selected from any one of SEQ ID NOs: 12, 15, 18, 27, 30, 33, 45, 48, 51, 57, 60, 63, 72, 75, 78, 84, 87, 90, 96, 99, 102, 108, 111, 114, 123, 126, and 129 or having at least 90% sequence identity to any one of SEQ ID NOs: 12, 15, 18, 27, 30, 33, 45, 48, 51, 57, 60, 63, 72, 75, 78, 84, 87, 90, 96, 99, 102, 108, 111, 114, 123, 126, and 129.

48. The nucleic acid construct or the expression vector of claim 47, for inhibiting expression of an amino acid sequence at least 90% identical to SEQ ID NO: 12, 15, or 18.

49. The nucleic acid construct or the expression vector of claim 47, for inhibiting expression of an amino acid sequence at least 90% identical to SEQ ID NO: 57, 60, or 63.

50. The nucleic acid construct of claim 40 or the expression vector of claim 41, further comprising a second nucleic acid molecule encoding a functional AGPase protein operably linked to a promoter which functions in a non-fruit tissue of the plant.
51. A cell transformed with the nucleic acid construct according to any one of claims 40-50.
52. The cell according to claim 51, wherein the cell is a bacterial cell or a plant cell.
53. A plant transformed with the nucleic acid construct according to any one of claims 40-50.
54. The cell or plant according to claim 52 or 53, wherein the plant cell or plant is from the Solanaceae or Cucurbitaceae family.
55. The cell or plant according to any one of claims 51-54, selected from a tomato, eggplant, pepper, zucchini, cucumber, watermelon, pumpkin, squash, or melon.
56. The cell or plant according to any one of claims 51-55, selected from the genus *Solanum*, *Capsicum*, *Cucurbita*, *Cucumis*, or *Citrullus*.
57. The cell or plant according to any one of claims 51-55, which is a tomato plant or tomato plant cell.
58. A fruit from the plant, or plant grown from the plant cell, according to any one of claims 51-57.
59. A plant seed produced from the plant according to any one of claims 51-58.

60. A method for breeding plants having enhanced blossom end rot resistance, said method comprising:

providing a candidate plant or plant part;

analyzing the candidate plant or plant part for the presence, in its genome, of a modified ADP-glucose pyrophosphorylase (AGPase) polynucleotide encoding an AGPase subunit protein, wherein the expression, stability, and/or activity of said AGPase subunit protein is reduced or eliminated as compared to a plant without the modification;

identifying, based on said analyzing, a candidate plant suitable for breeding that includes in its genome, the modified AGPase polynucleotide; and

breeding the identified plant with at least one other plant.

61. The method according to claim 60, wherein said analyzing comprises:

isolating nucleic acids from the plant or plant part;

analyzing nucleic acids from the plant or plant part for the presence of the modified AGPase polynucleotide; and

detecting the modified AGPase polynucleotide.

62. The method according to claim 60, wherein said breeding comprises

crossing, making hybrids, backcrossing, self-crossing, double haploid breeding, and/or combinations thereof.

63. The method according to any one of claims 60-62, wherein said AGPase

comprises a modified ADP-glucose pyrophosphorylase small subunit (APS) polynucleotide encoding an amino acid sequence that is at least 90% identical to any one of SEQ ID NOs:3, 6, 9, 21, 24, 36, 39, 42, 54, 66, 69, 81, 93, 105, 117, and 120.

64. The method of claim 63, wherein the amino acid sequence is SEQ ID NO:

3, 6, or 9.

65. The method according to claim 63, wherein the amino acid sequence

is SEQ ID NO: 54.

66. The method according to claim 63, wherein the modified *APS* polynucleotide is an *APSI* polynucleotide comprising the deletion mutation of SEQ ID NO:130 resulting in a frameshift mutation.

67. The method according to any one of claims 60-62, said AGPase comprises a modified ADP-glucose pyrophosphorylase large subunit (*APL*) polynucleotide, a encoding the amino acid sequence that has at least 90% identity with SEQ ID NOs:12, 15, 18, 27, 30, 33, 45, 48, 51, 57, 60, 63, 72, 75, 78, 84, 87, 90, 96, 99, 102, 108, 111, 114, 123, 126, and 129.

68. The method according to claim 67, wherein the amino acid sequence is to SEQ ID NO: 12, 15, or 18.

69. The method according to claim 67, wherein the amino acid sequence is SEQ ID NO: 57, 60, or 63.

70. The method according to any one of claims 60-69, wherein the plant is from the Solanaceae or Cucurbitaceae family.

71. The method of claim 60-70, wherein the plant is selected from a a tomato, eggplant, pepper, zucchini, cucumber, watermelon, pumpkin, squash, or melon.

72. The method according to any one of claims 60-71, wherein the plant is from the genus *Solanum*, *Capsicum*, *Cucurbita*, *Cucumis*, or *Citrullus*.

73. The method according to any one of claims 60-72, wherein the plant or plant cell is a tomato plant or tomato plant cell.

74. A fruit from the plant, or plant grown from the plant cell, according to any one of claims 60-73.

75. A method of imparting blossom end rot resistance to fruit from a plant comprising:

modifying a plant or a plant cell to reduce or eliminate the expression, stability, and/or activity of an ADP-glucose pyrophosphorylase (AGPase) subunit protein,

wherein said reduction or elimination of the expression, stability, and/or activity of AGPase protein is effective in reducing or eliminating starch synthesis and imparting blossom end rot resistance to fruit from the plant or a plant produced from the plant cell, as compared to fruit from a plant without the modification; and

selectively expressing a functional AGPase protein in non-fruit tissues.

FIG. 1A



FIG. 1B

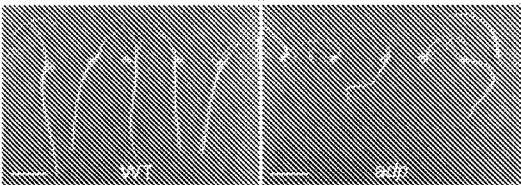


FIG. 1C

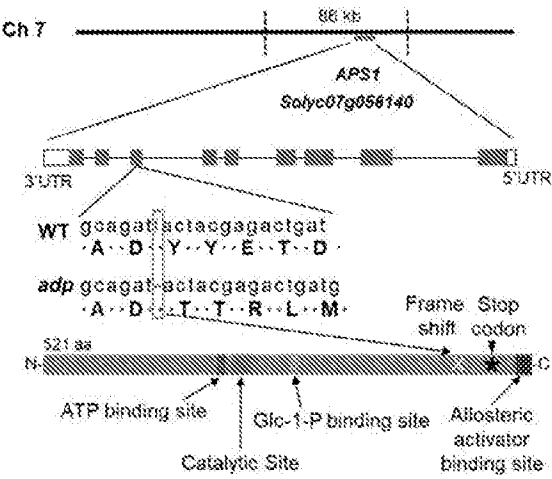


FIG. 1D

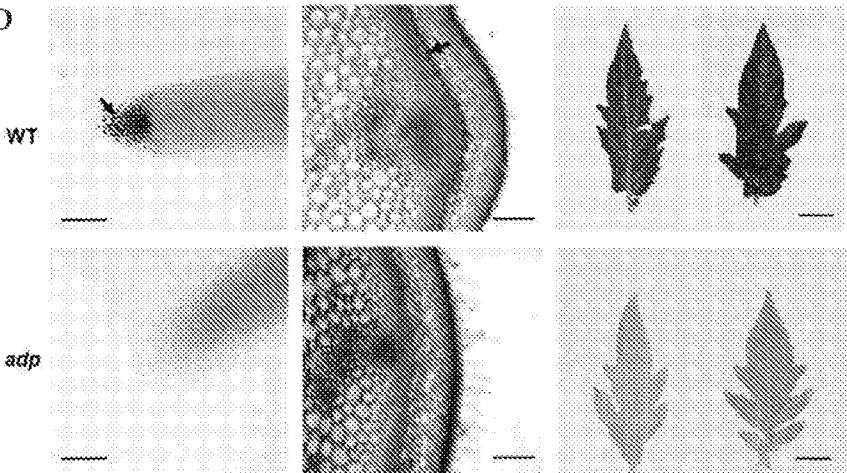


FIG. 2A

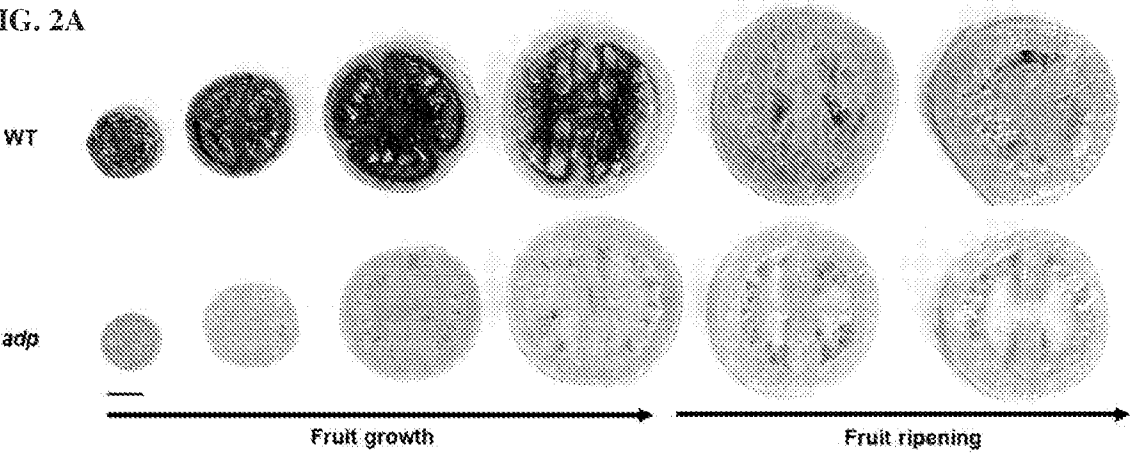


FIG. 2B

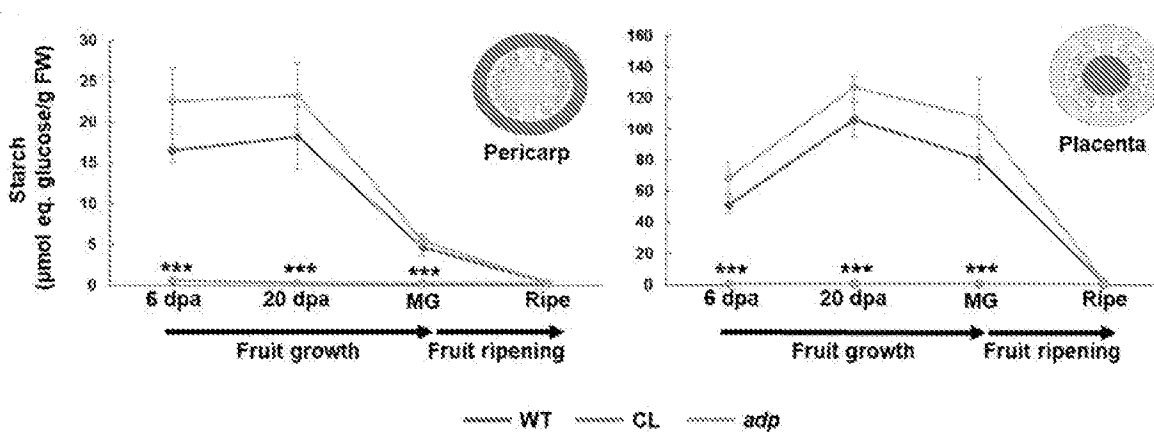


FIG. 3A

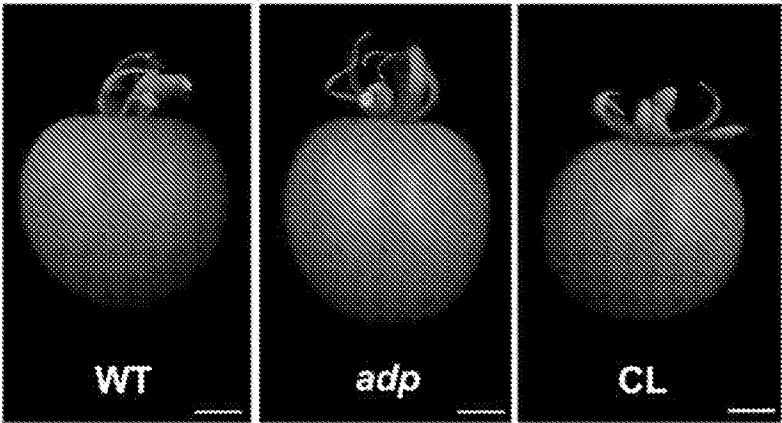


FIG. 3B

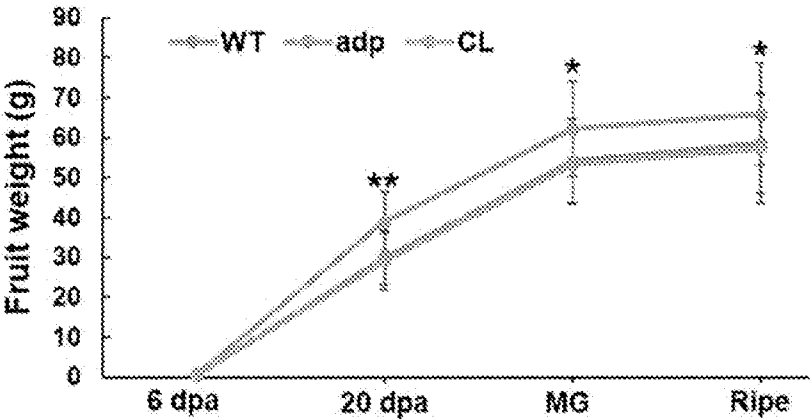


FIG. 3C

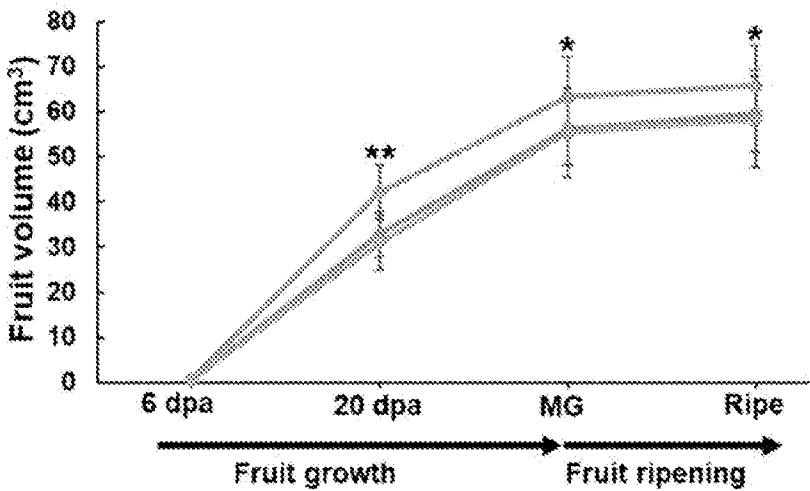


FIG. 3D

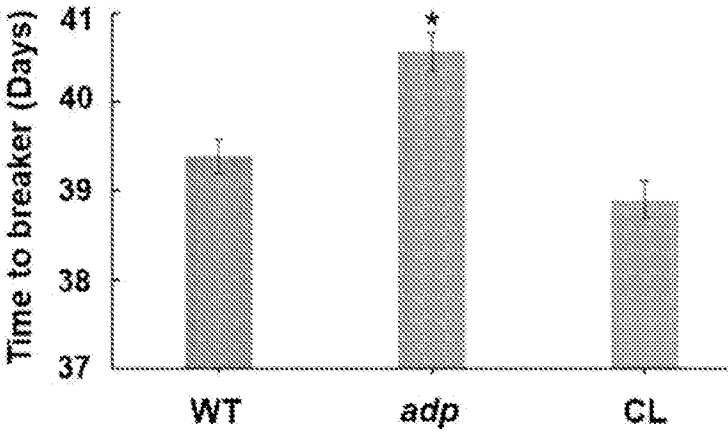


FIG. 3E

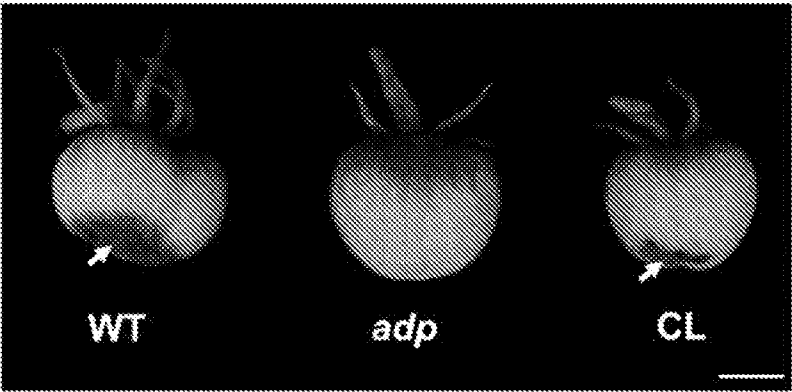


FIG. 3F

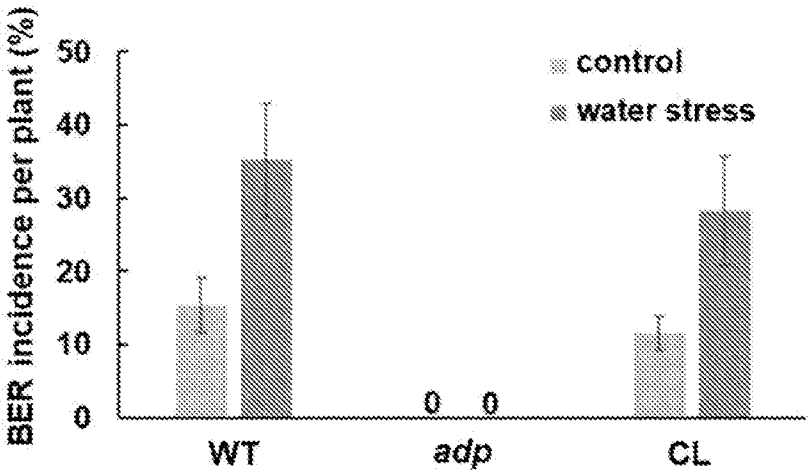


FIG. 4A

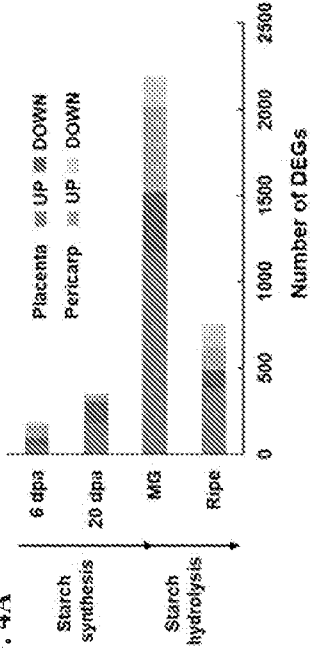


FIG. 4B

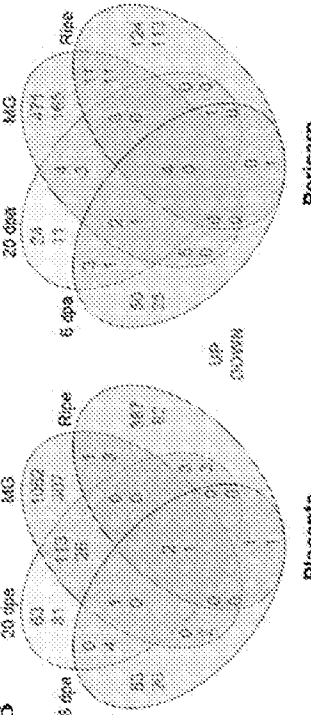


FIG. 4C

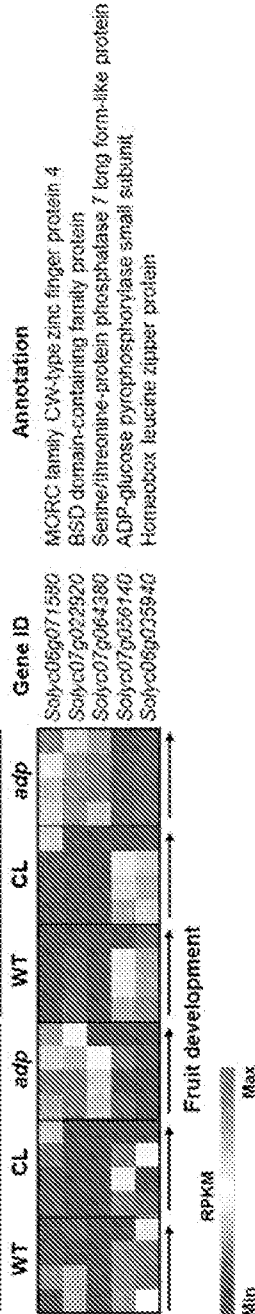


FIG. 4

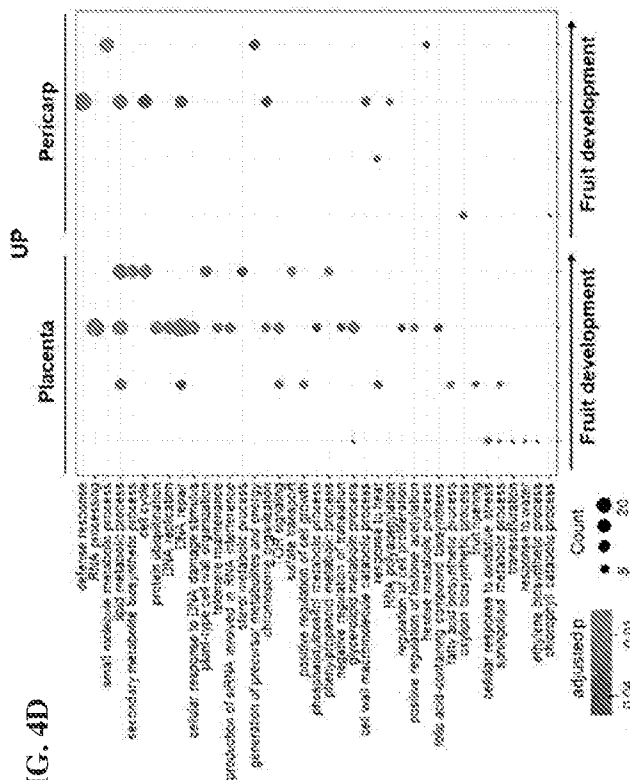


FIG. 4.

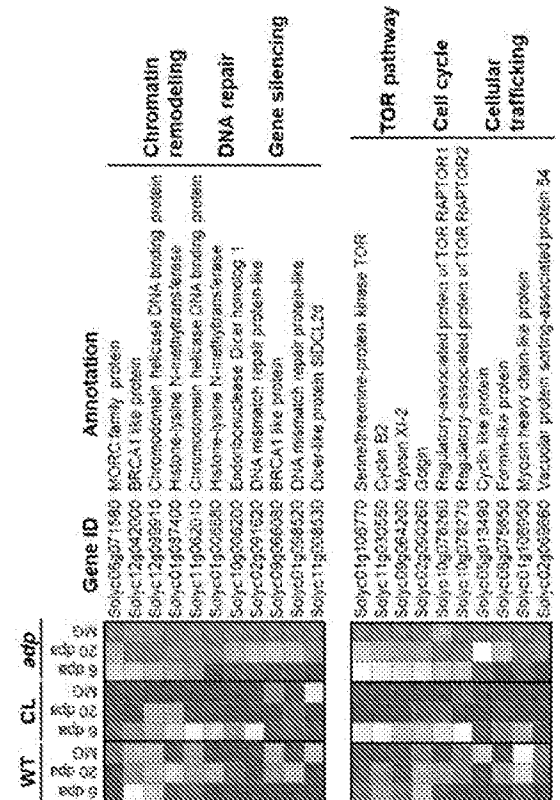
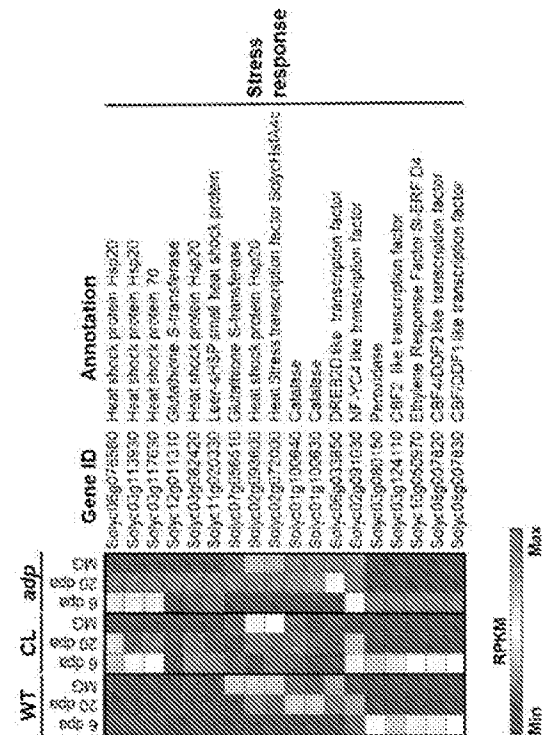
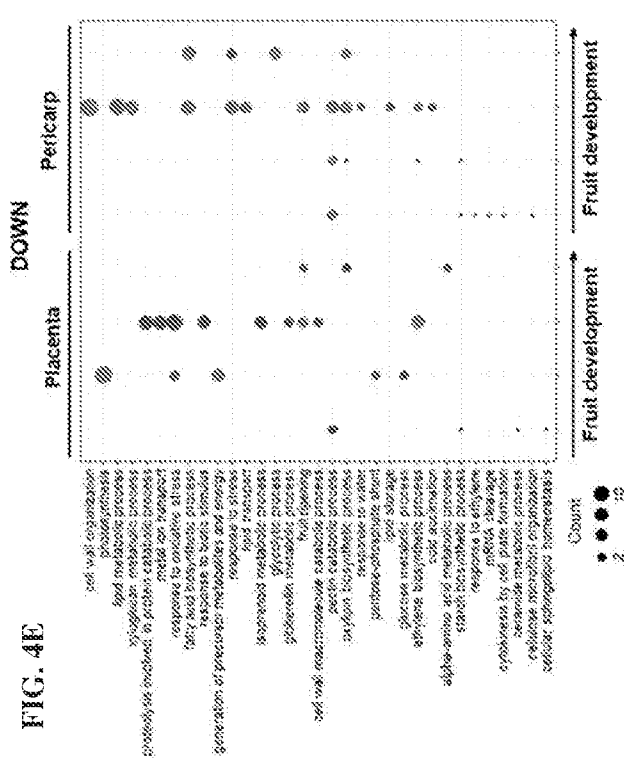


FIG. 4B



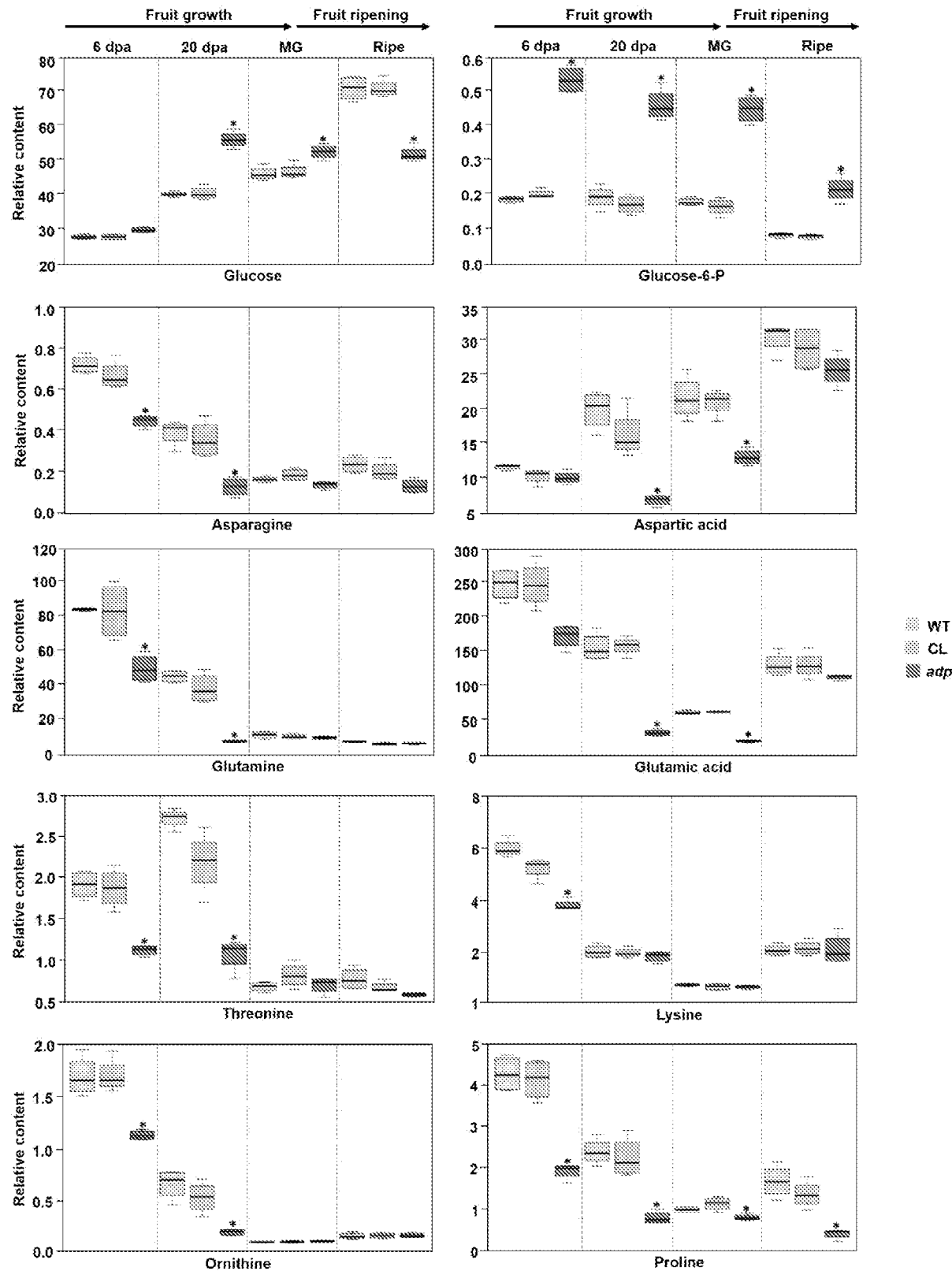


FIG. 5

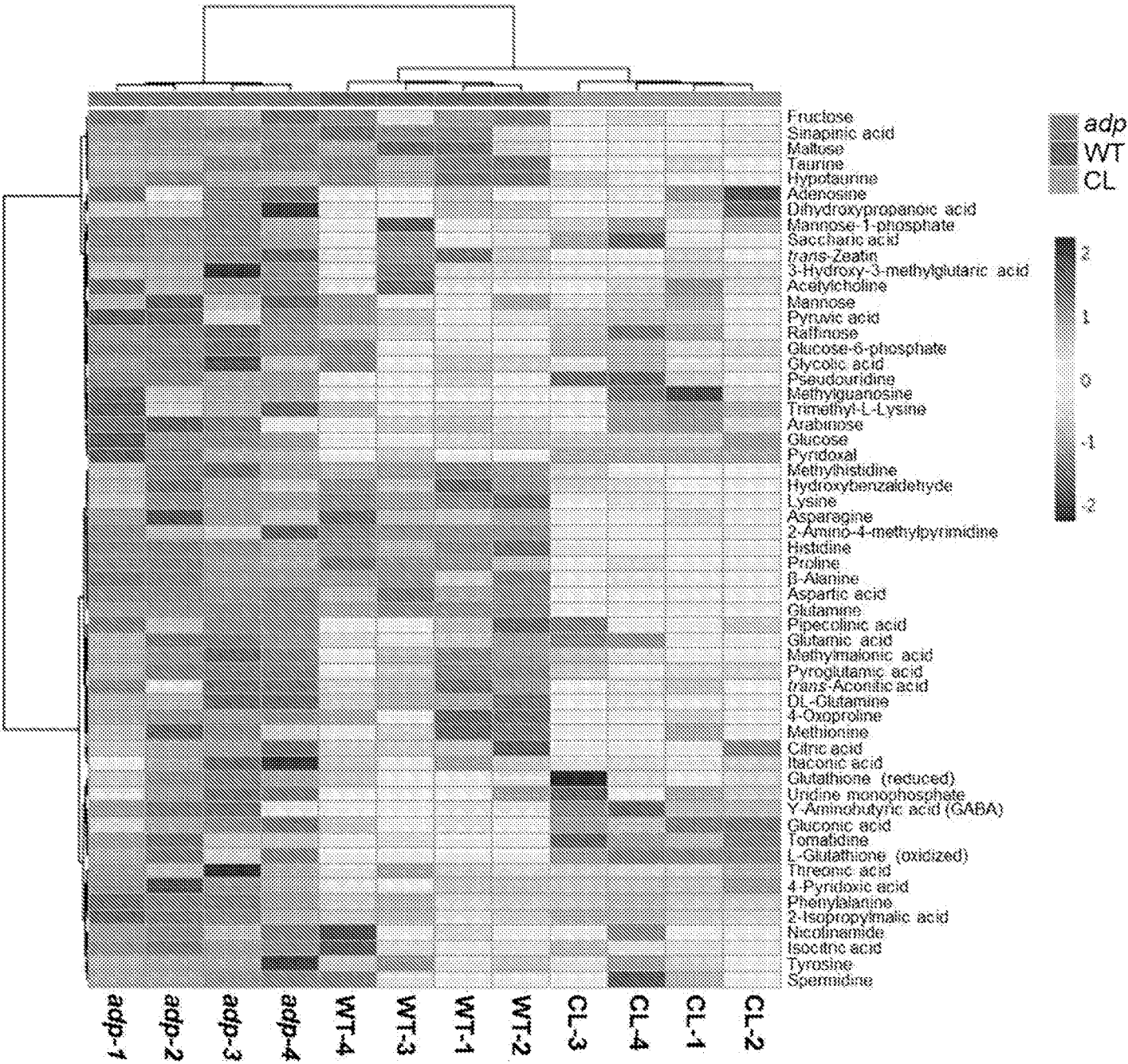


FIG. 6

FIG. 7A

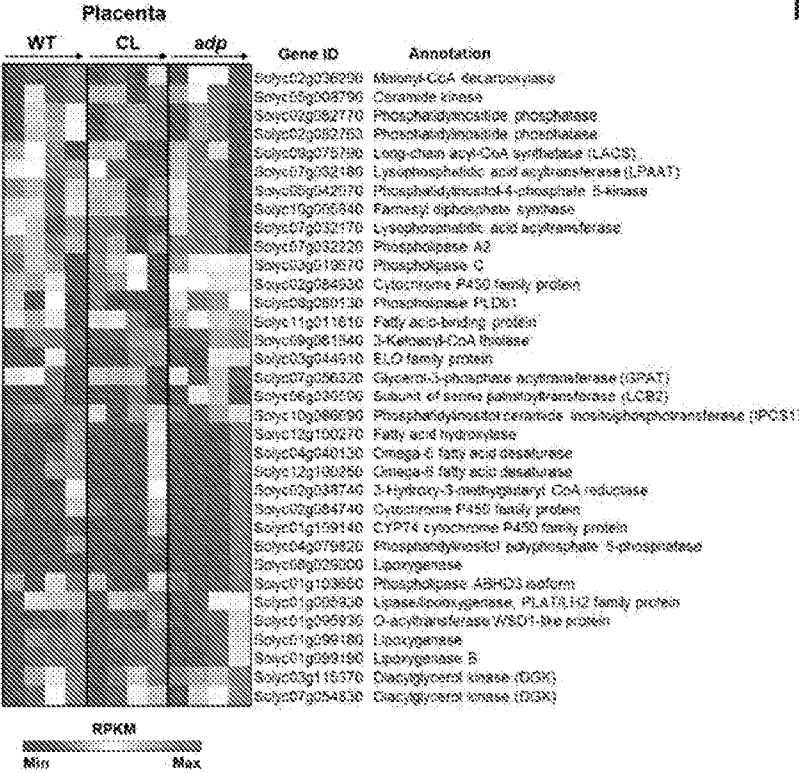


FIG. 7B

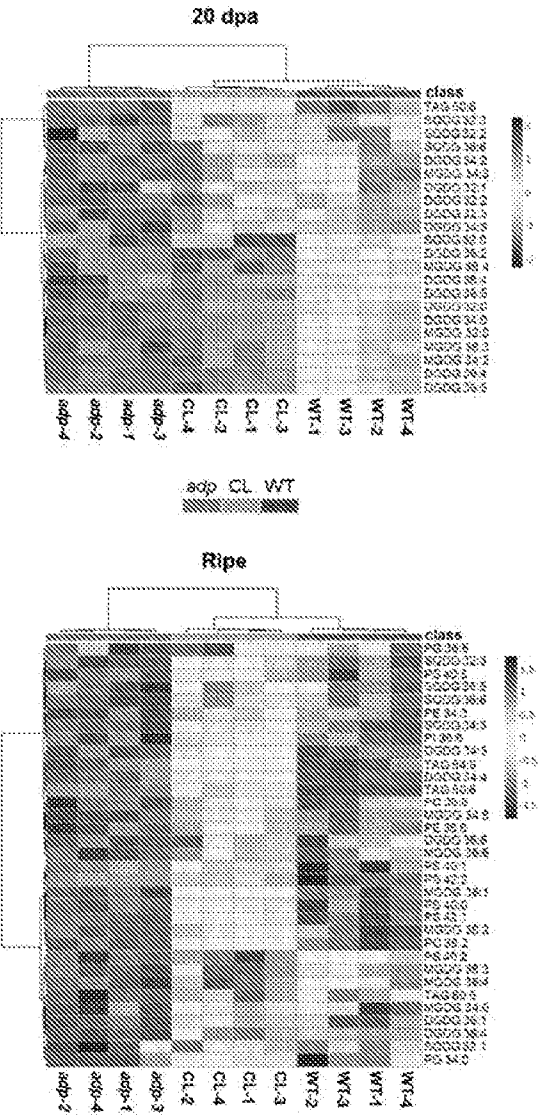
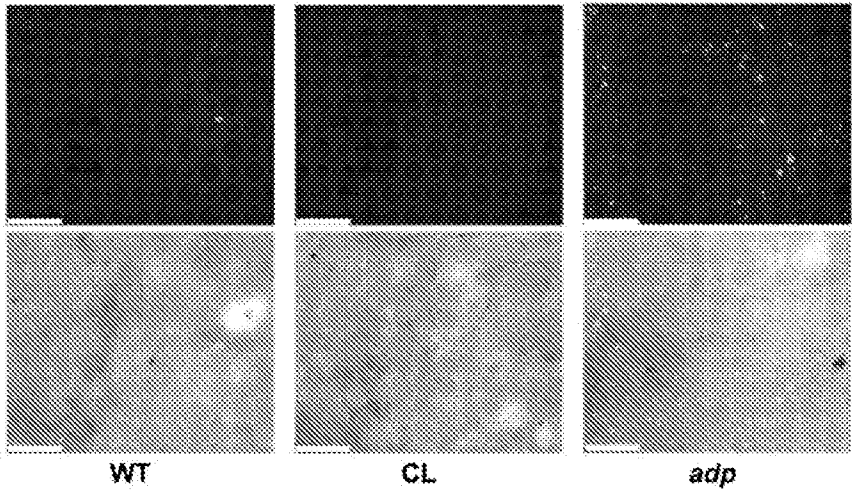


FIG. 7C



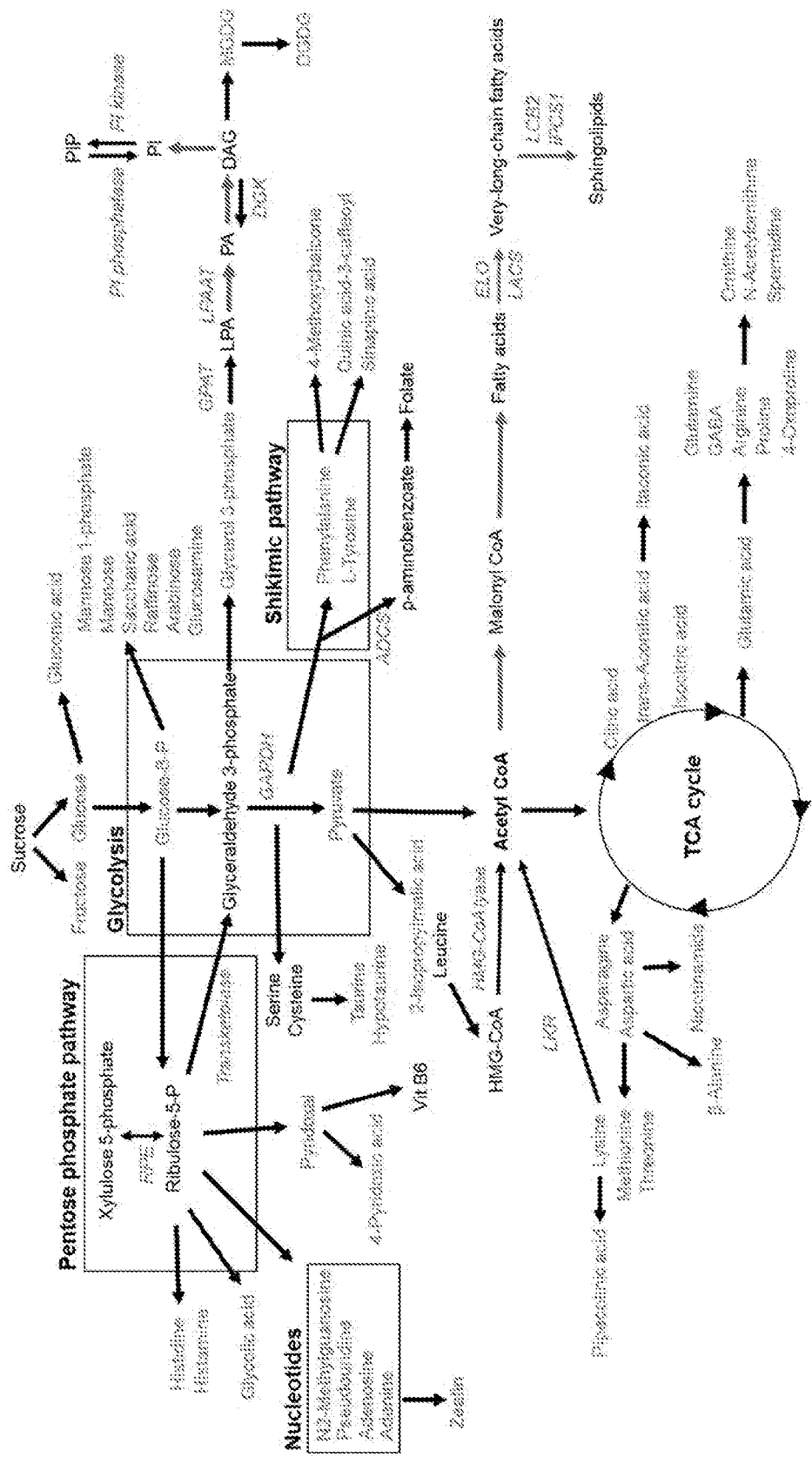


FIG 8

WT

adp

APS1pro::APS1 (CL)

FIG. 9A

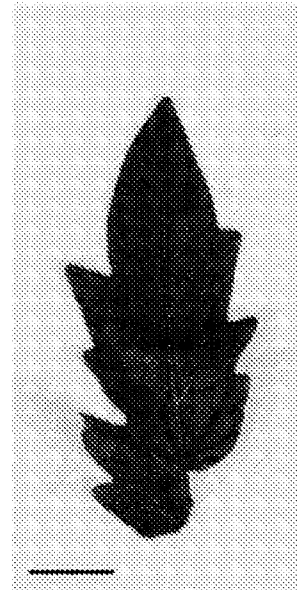
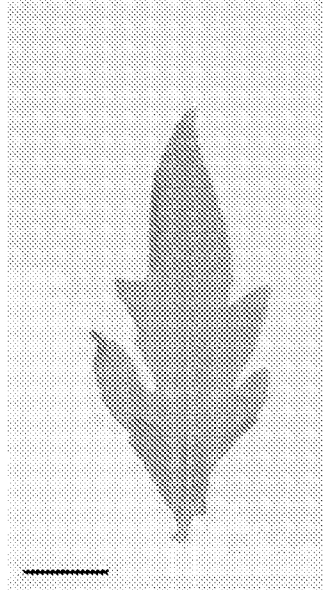
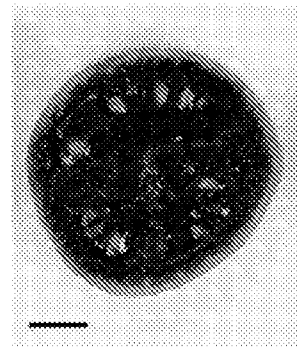
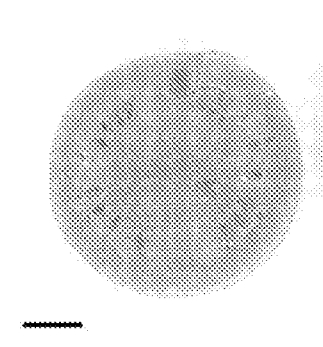
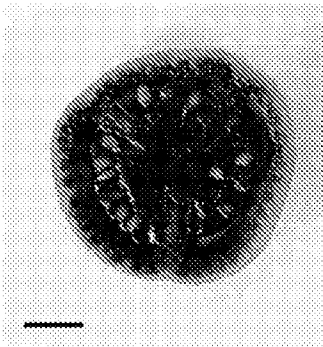


FIG. 9B



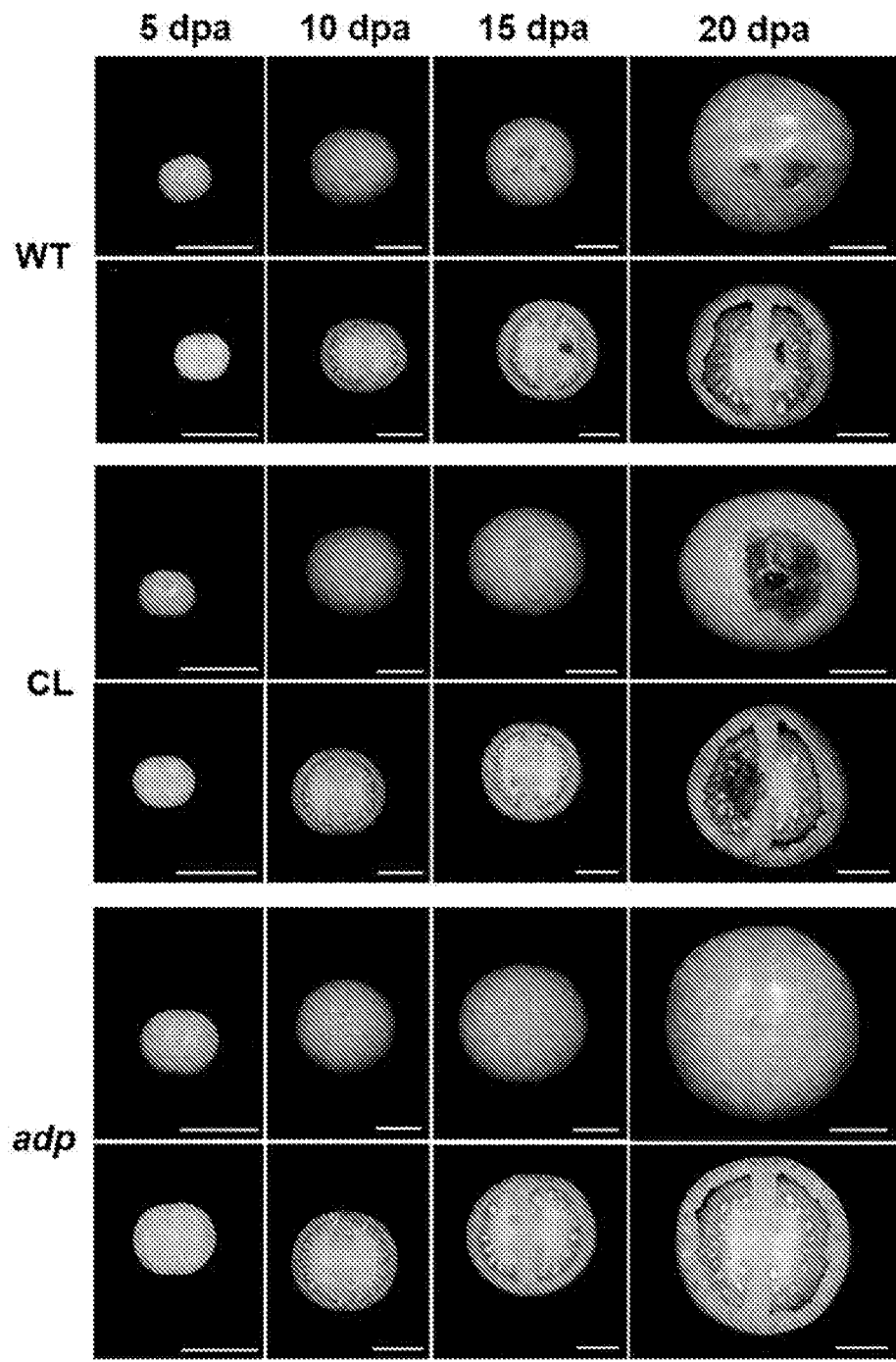


FIG. 10

FIG. 11A

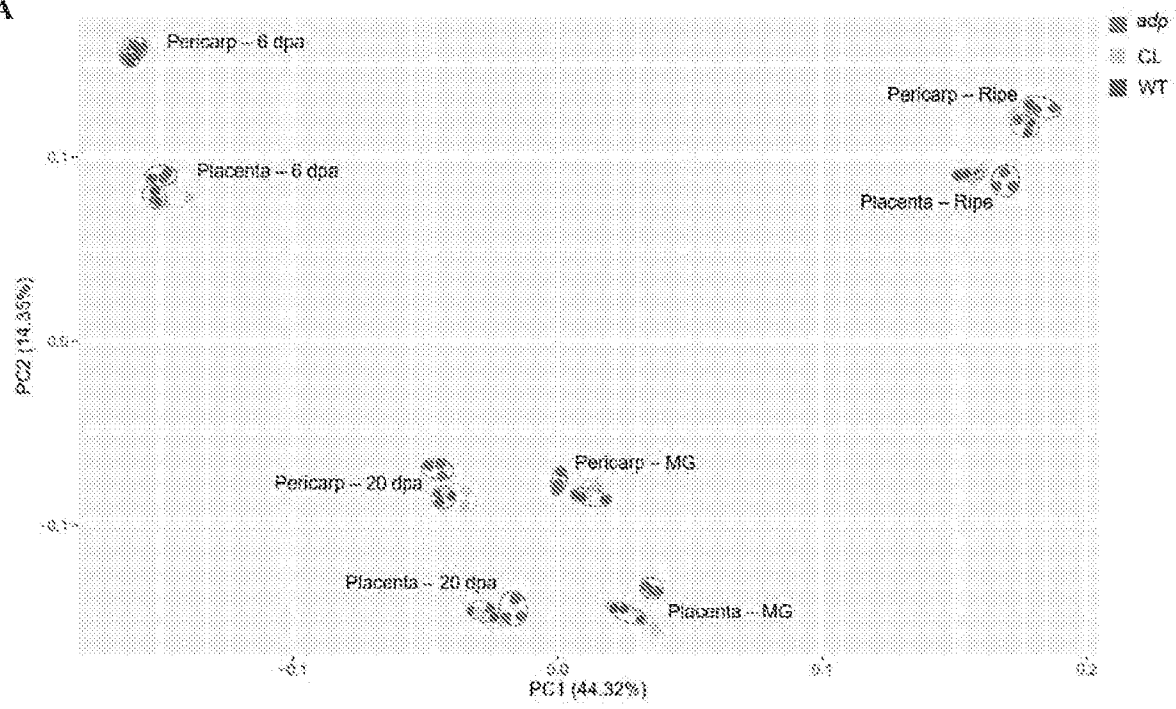
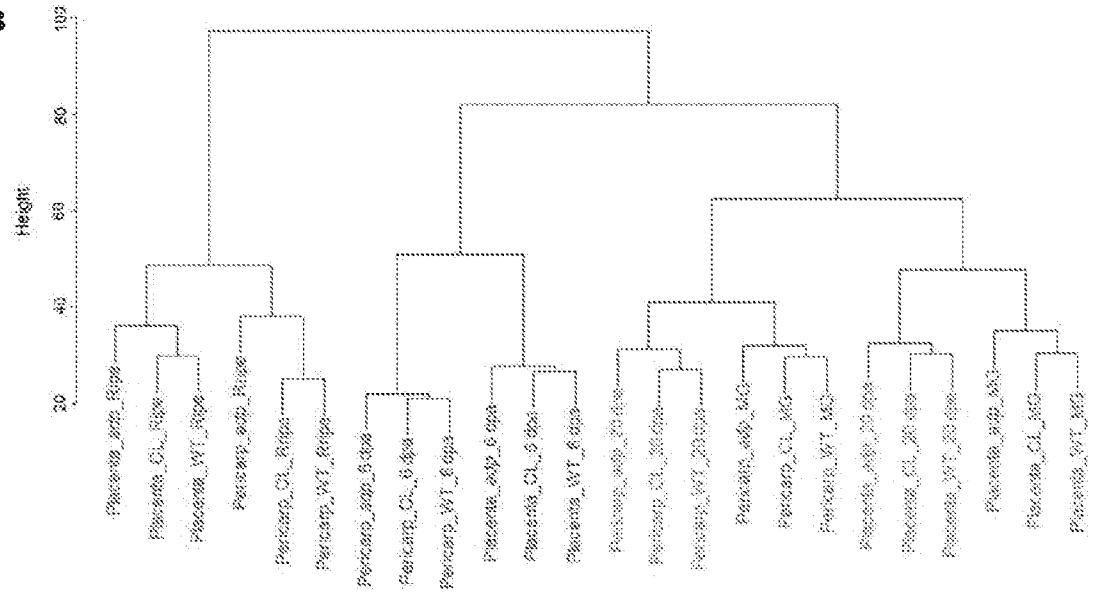


FIG. 11B



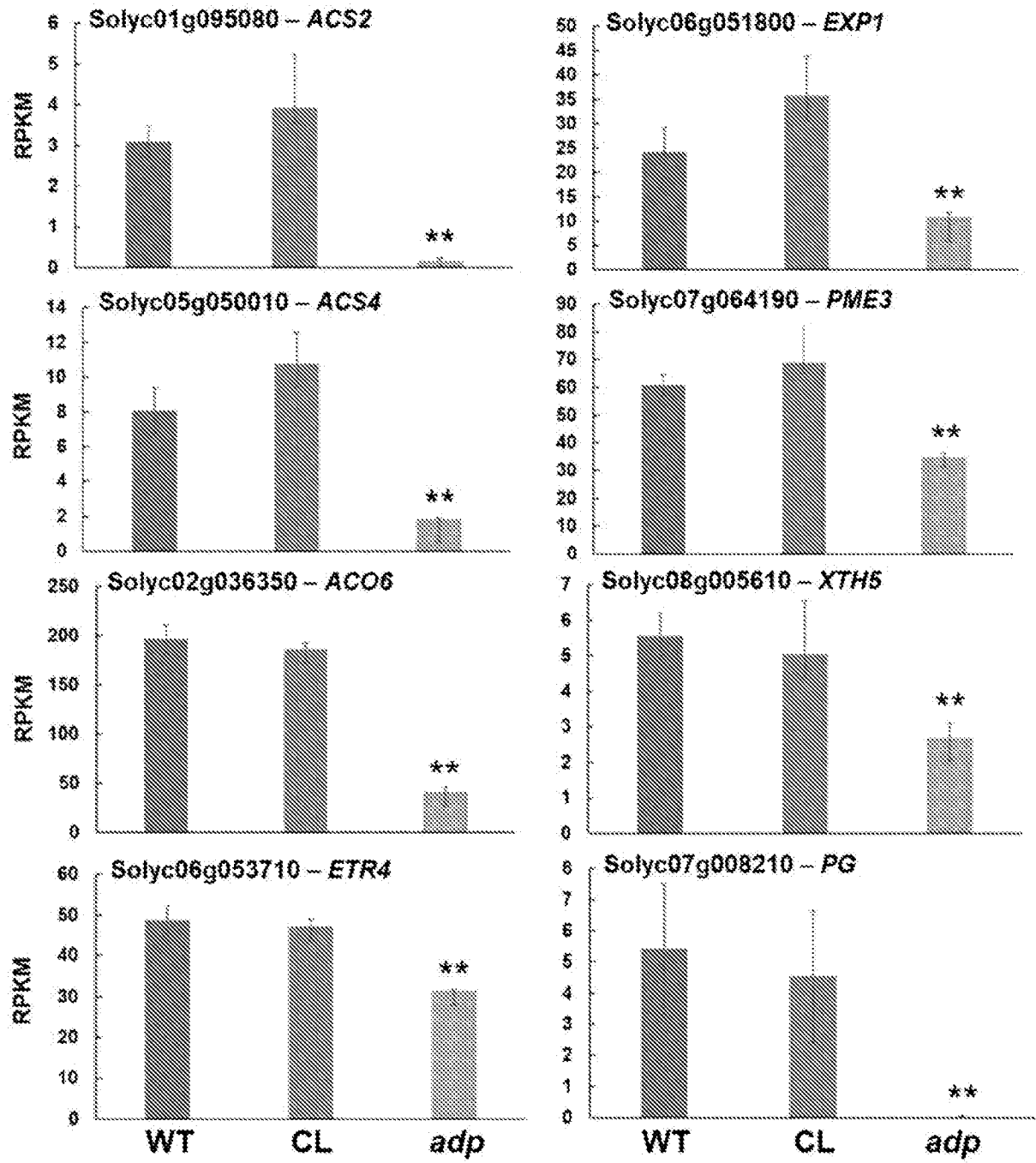


FIG. 12

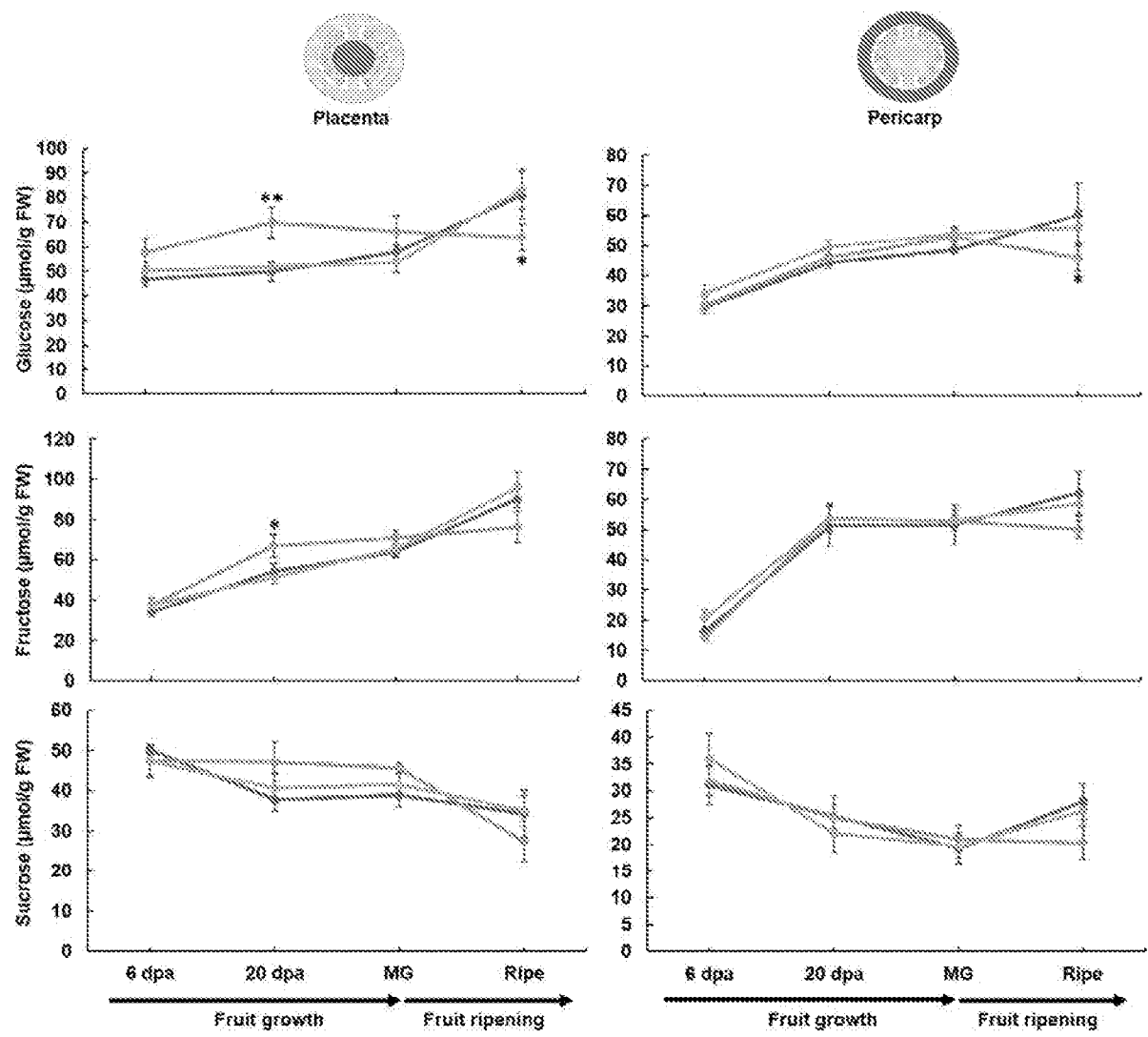


FIG. 13

FIG. 14A

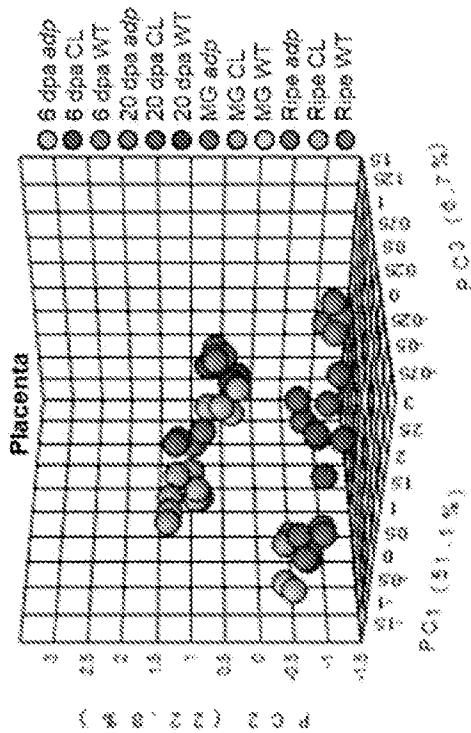
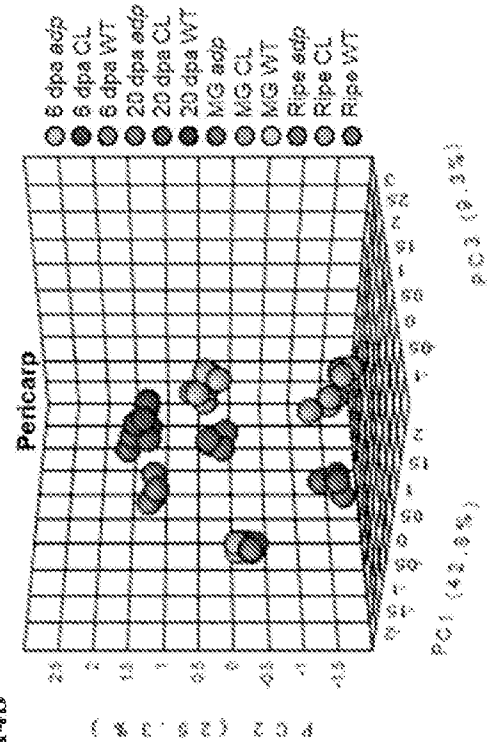


FIG. 14B



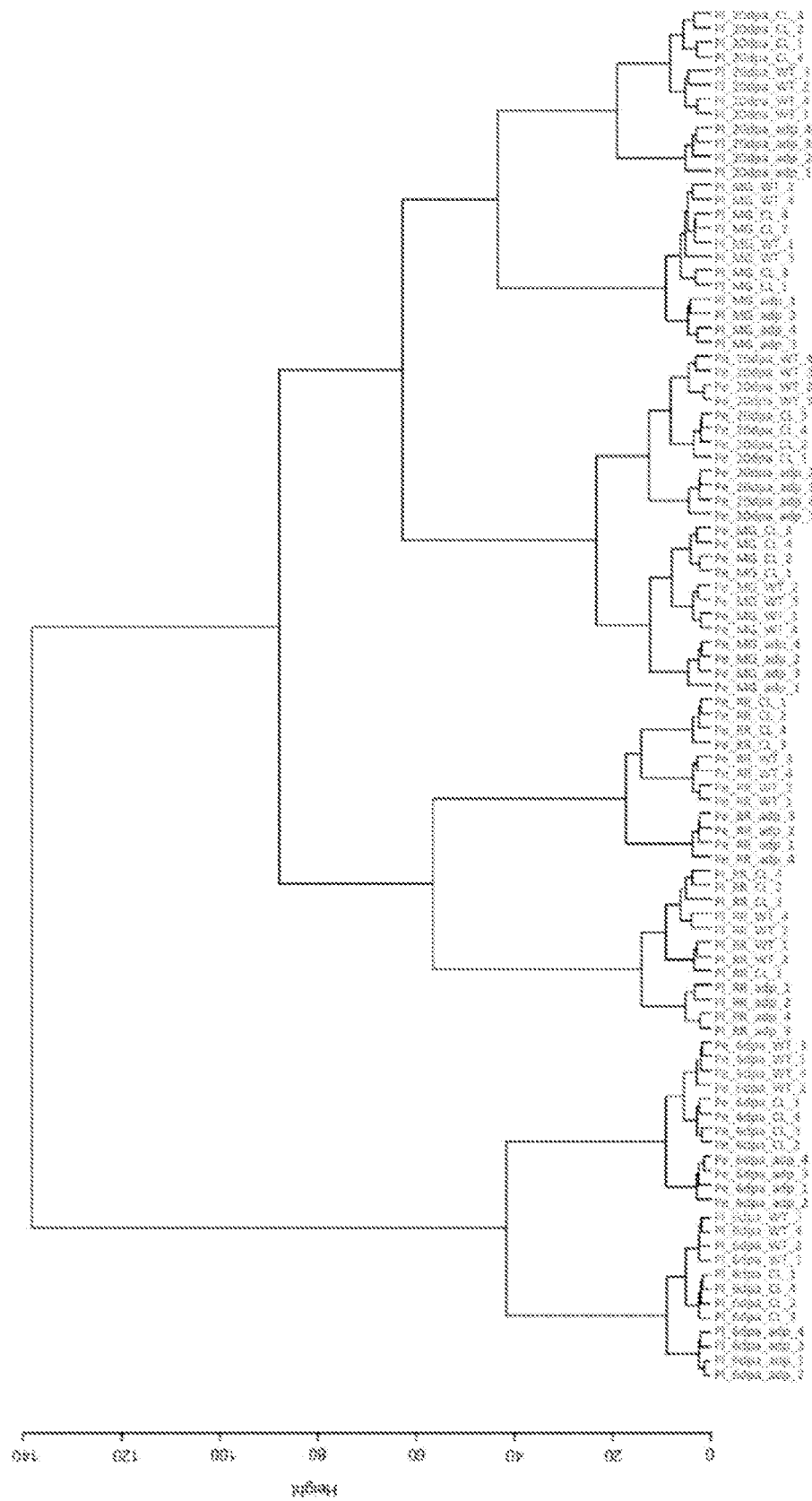


FIG. 14C

FIG. 15B

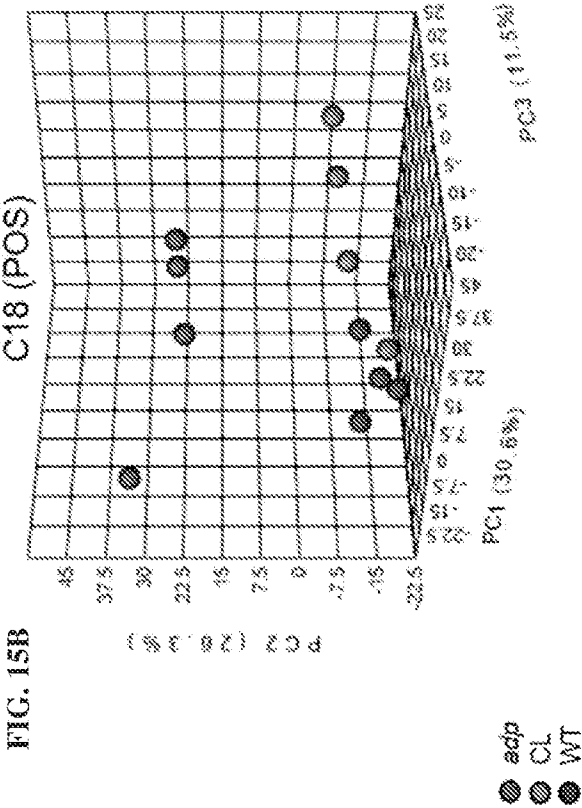


FIG. 16A

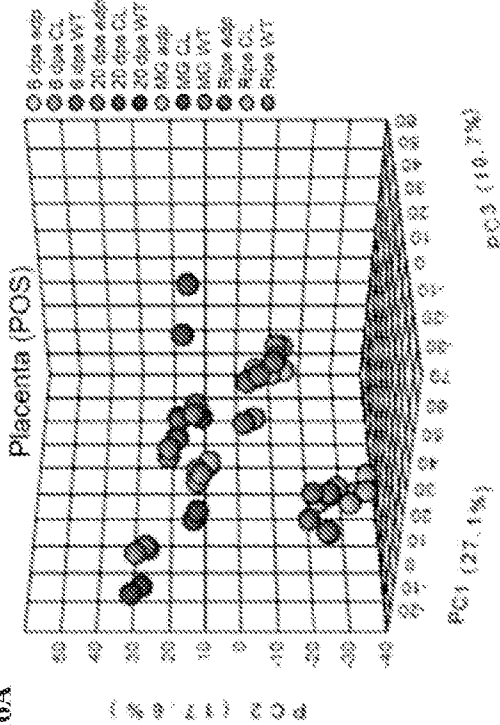


FIG. 16B

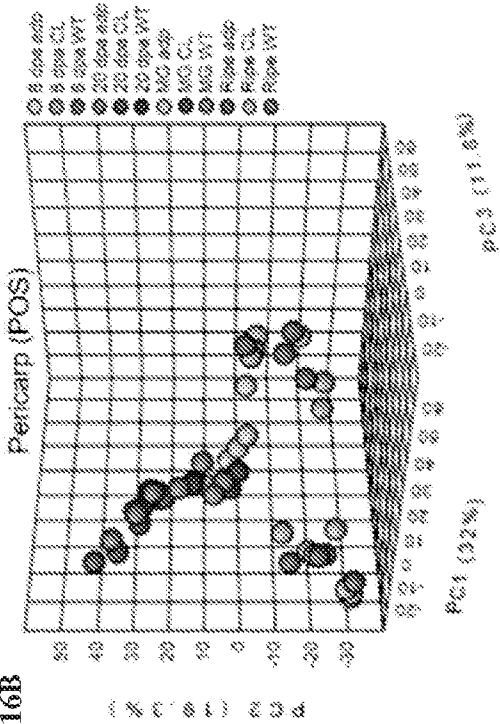


FIG. 16C

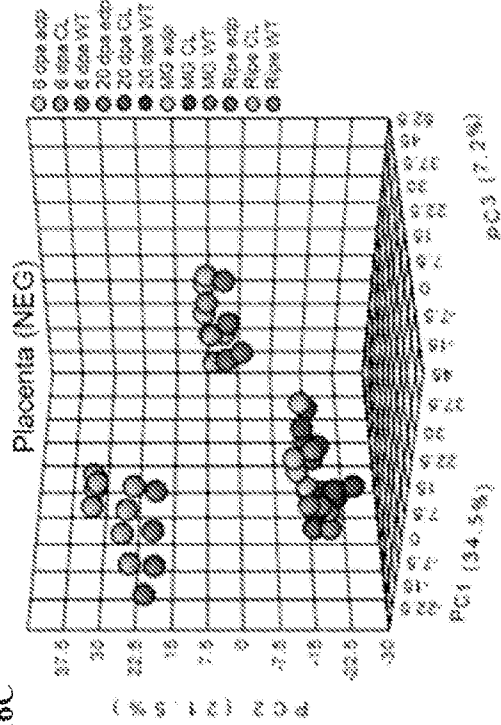


FIG. 16D

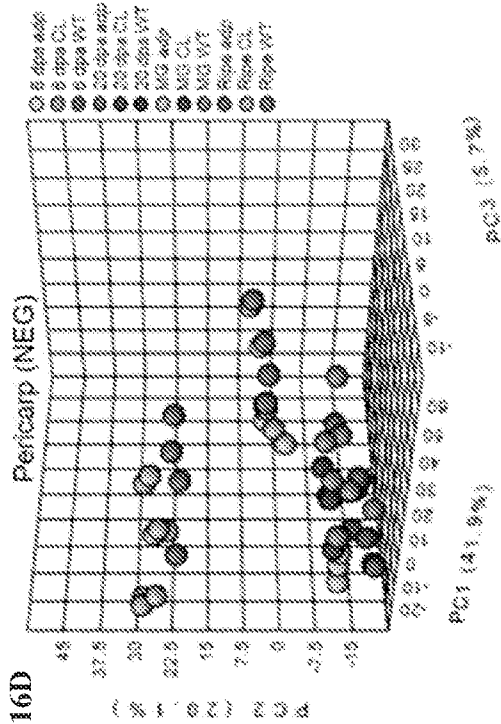


FIG. 16E

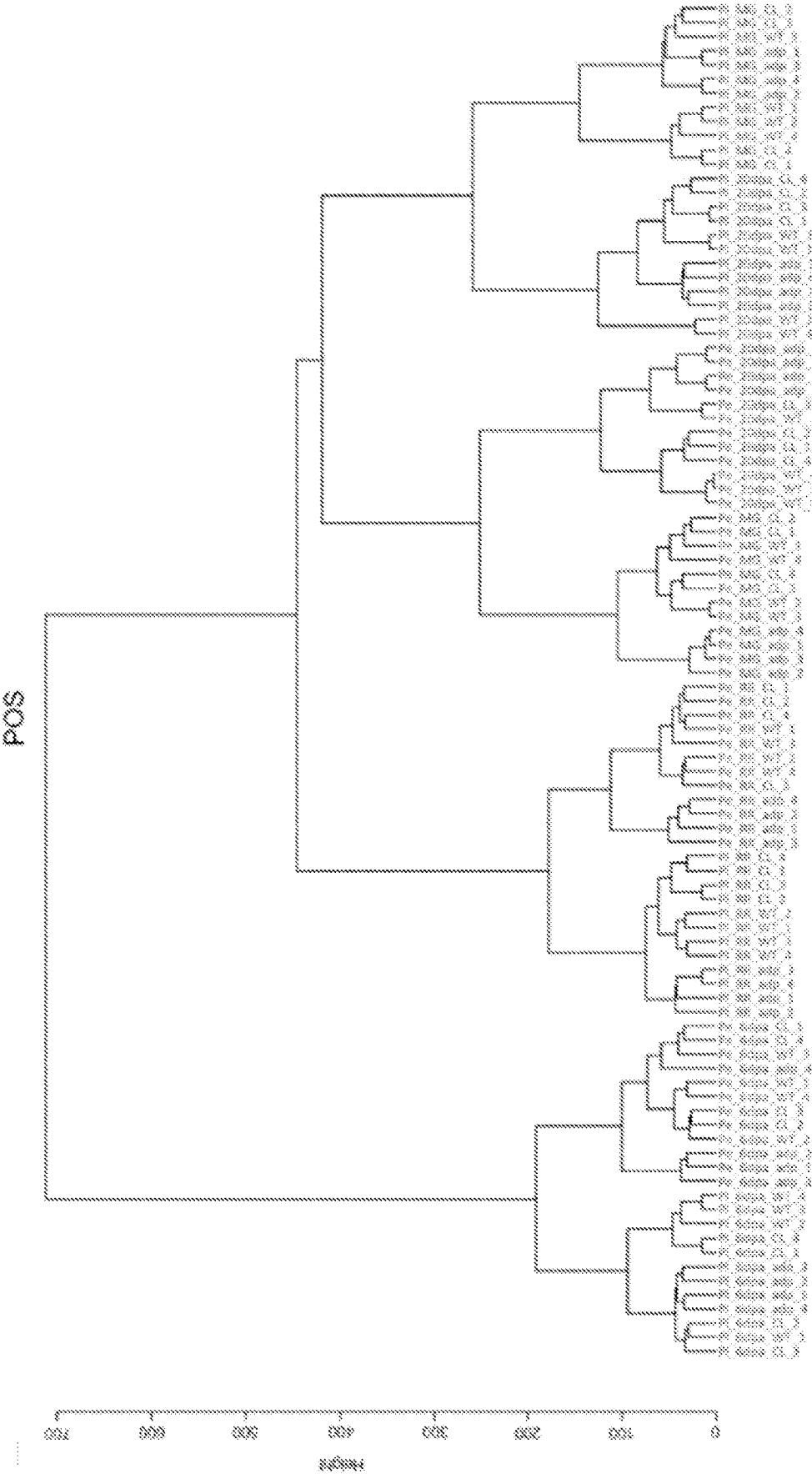


FIG. 16F

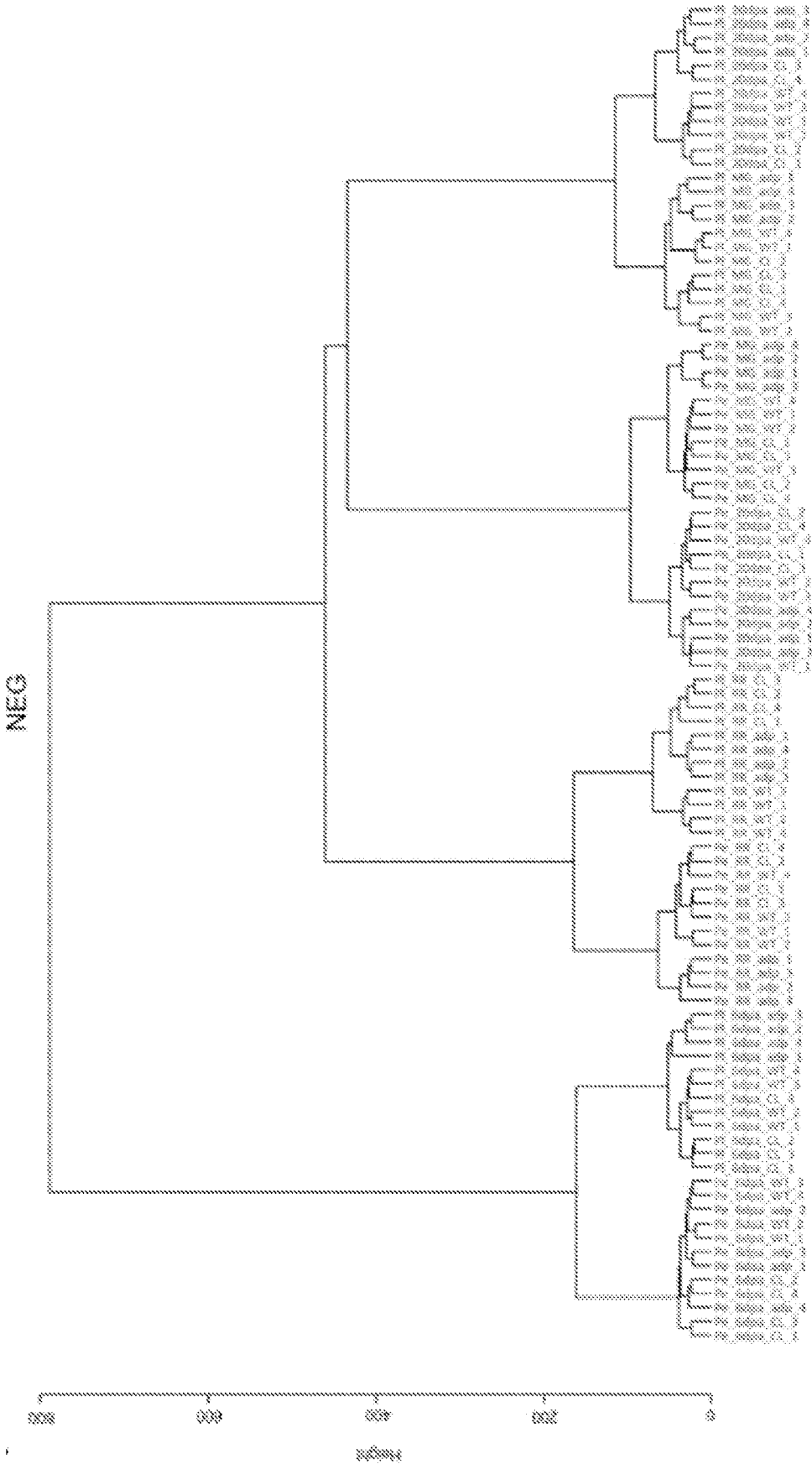
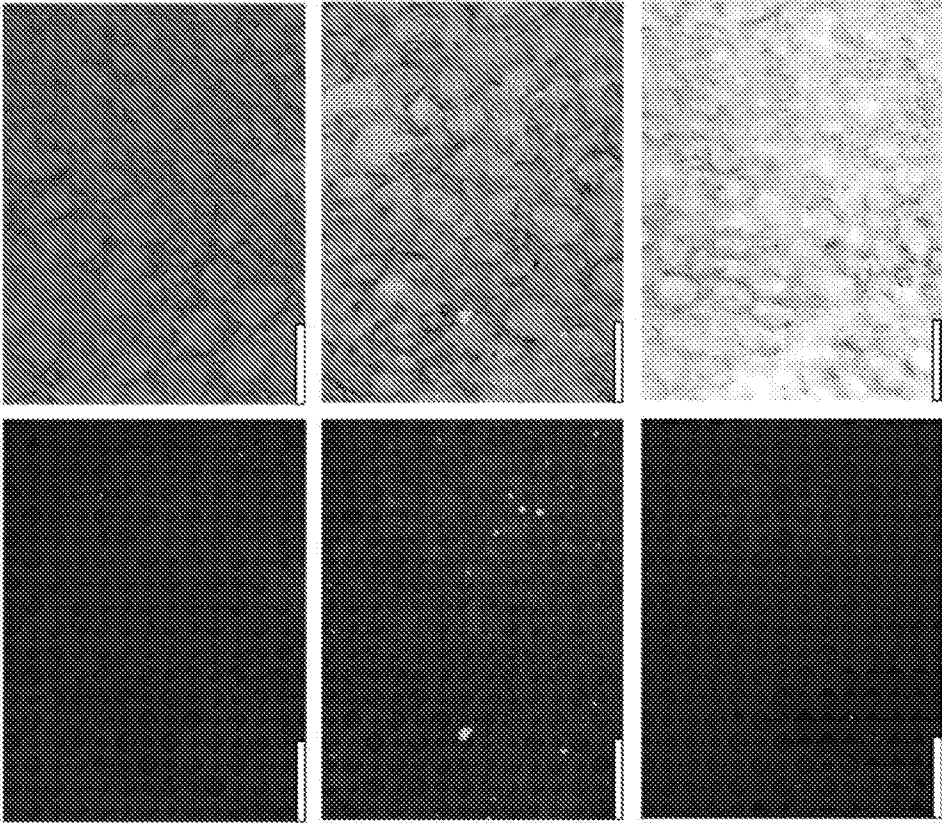


FIG. 17B

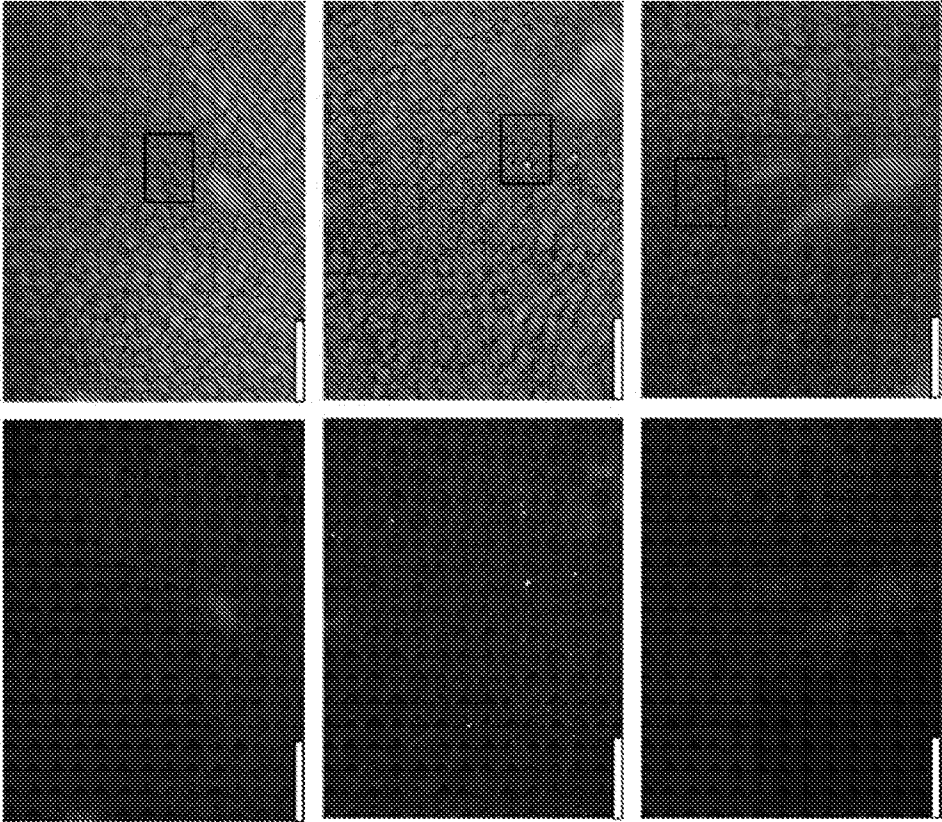


WT

adp

CL

FIG. 17A



WT

adp

CL

FIG. 18A

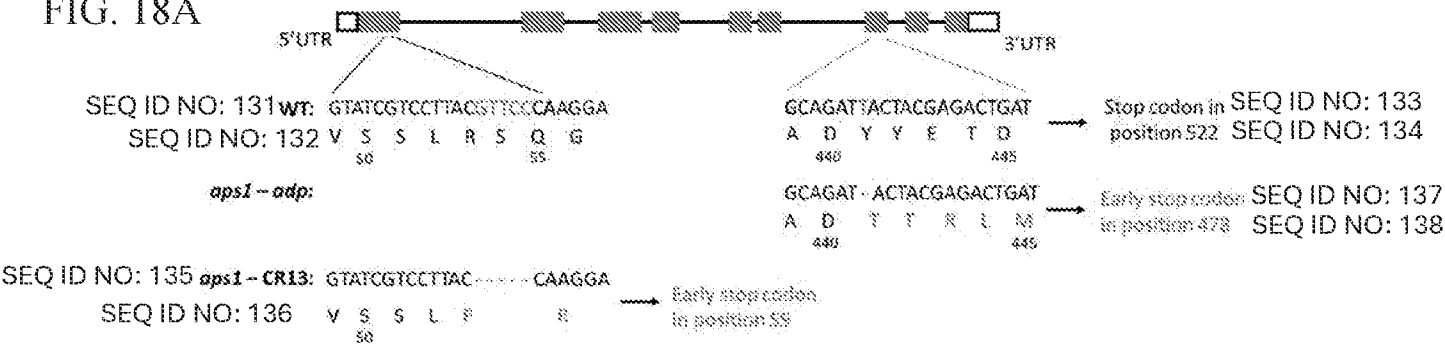


FIG. 18B

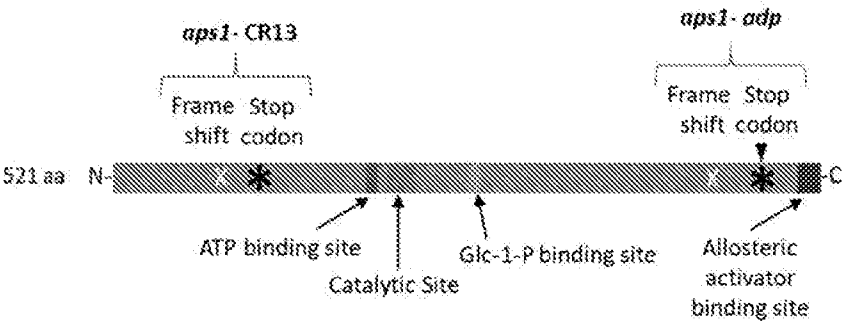


FIG. 18C

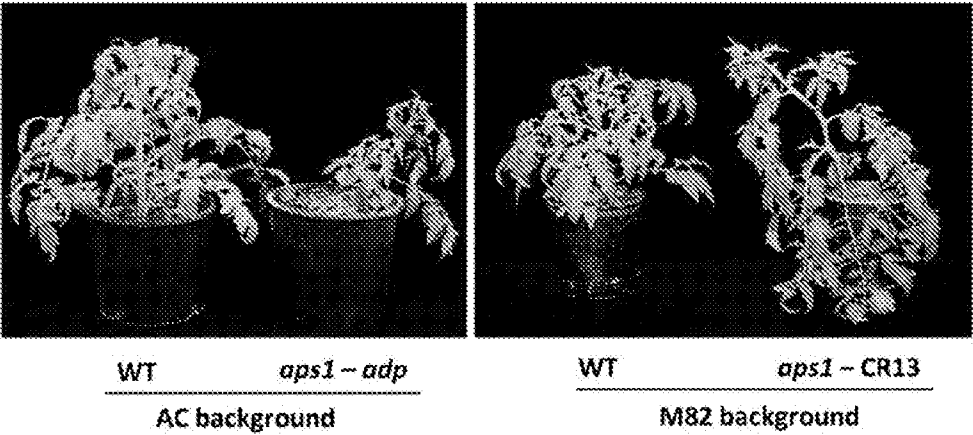


FIG. 18D

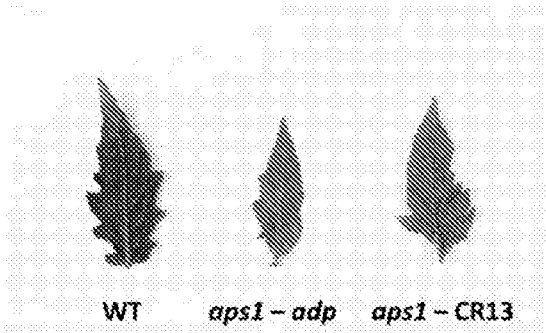


FIG. 19A

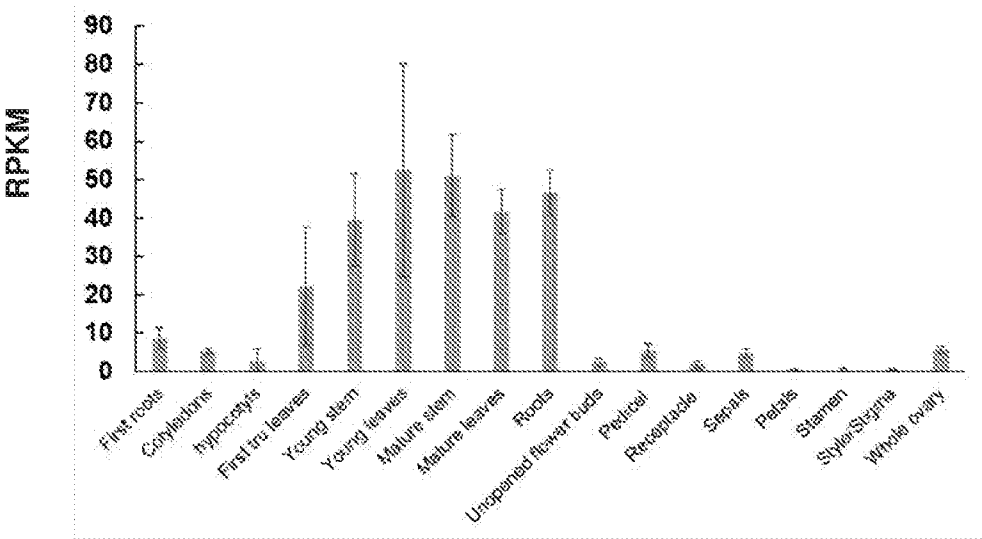
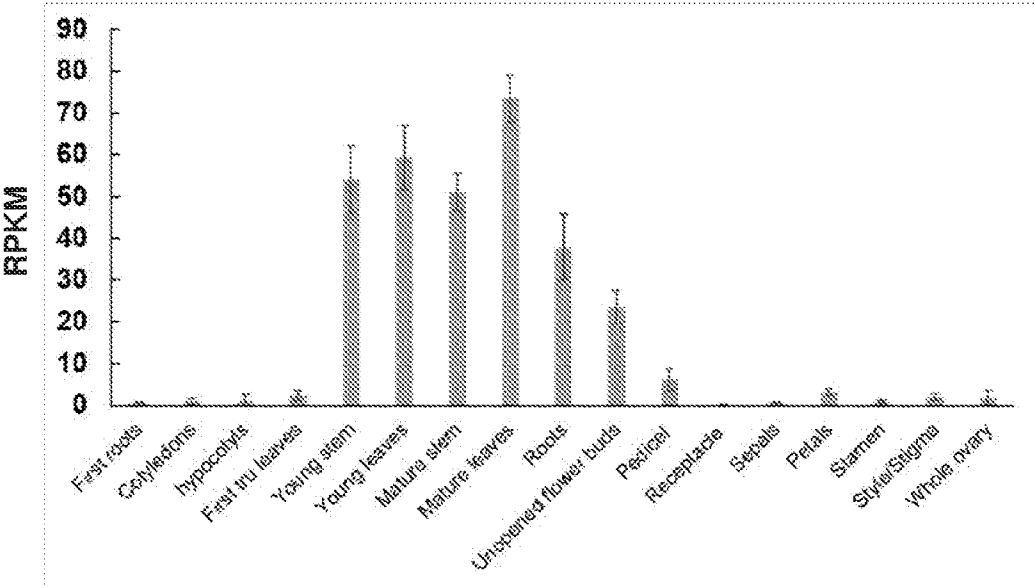


FIG. 19B



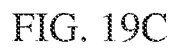
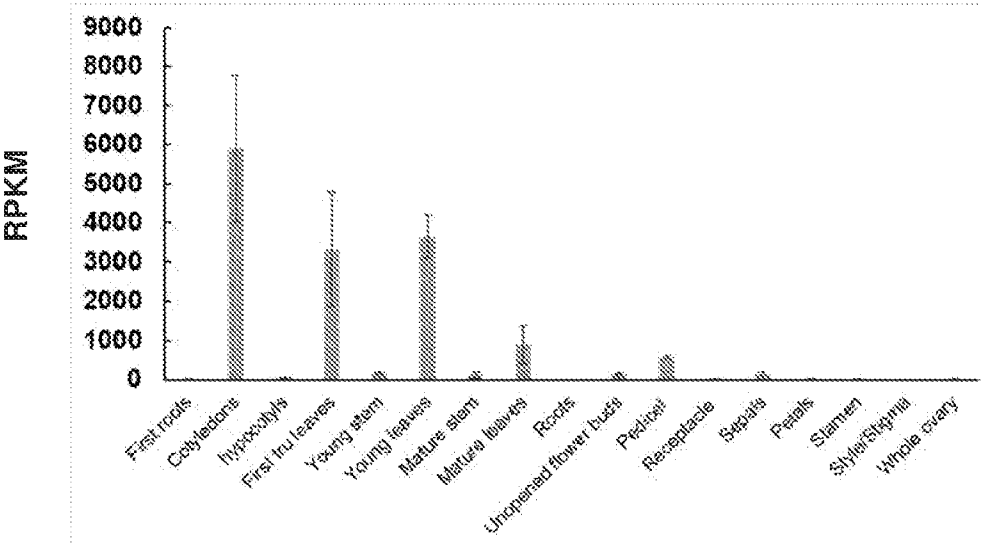


FIG. 19C

FIG. 19D



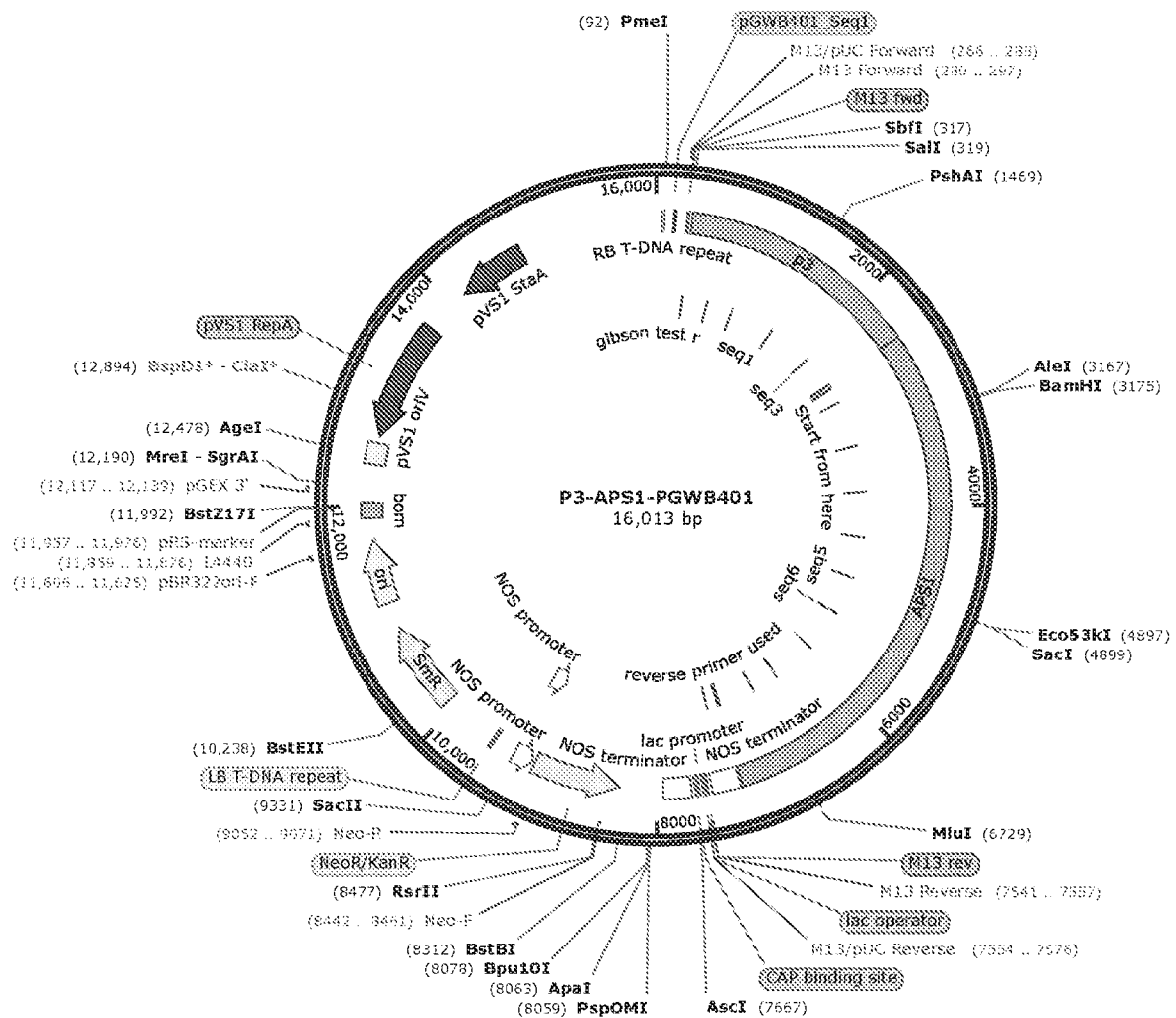


FIG. 19E

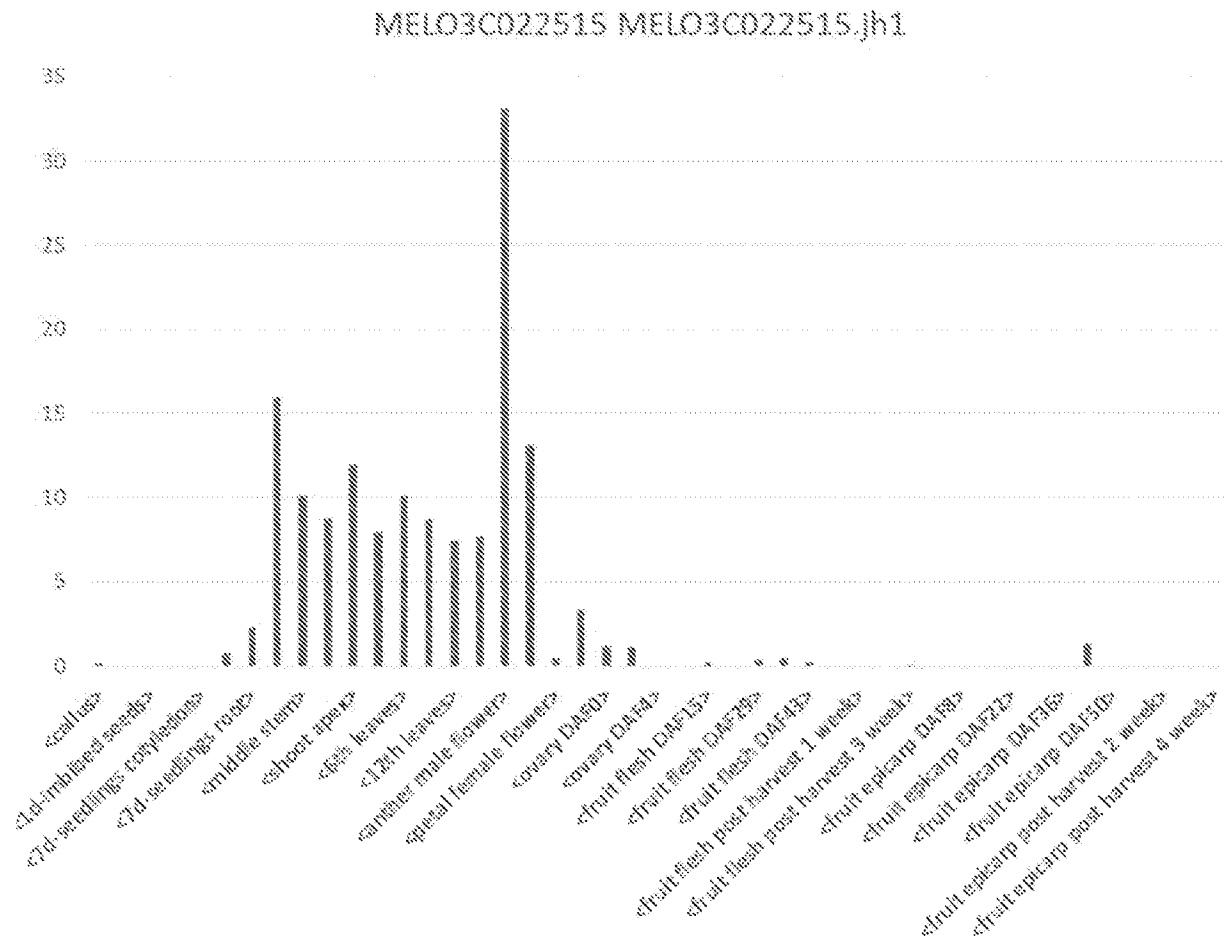


FIG. 20A

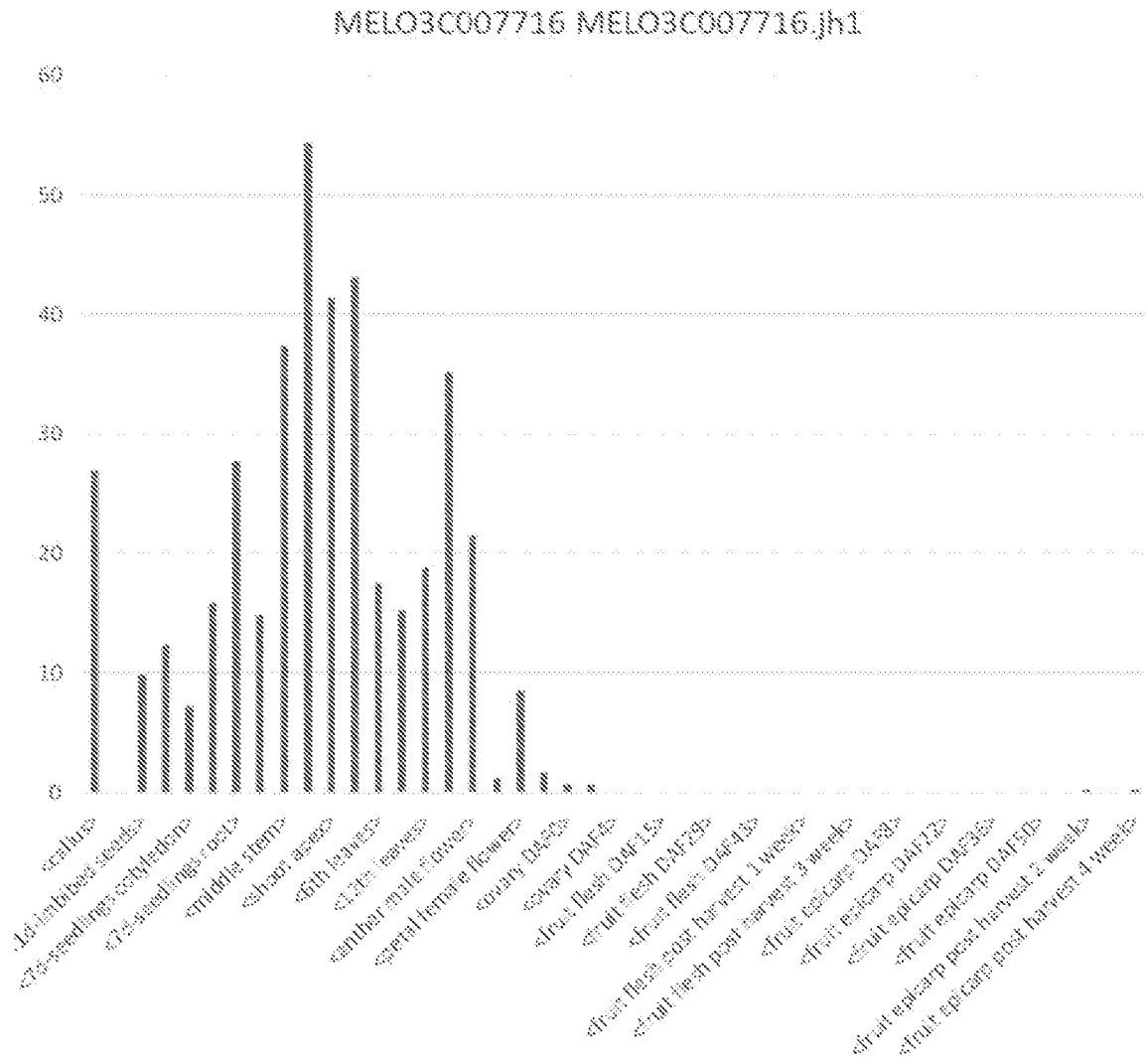


FIG. 20B

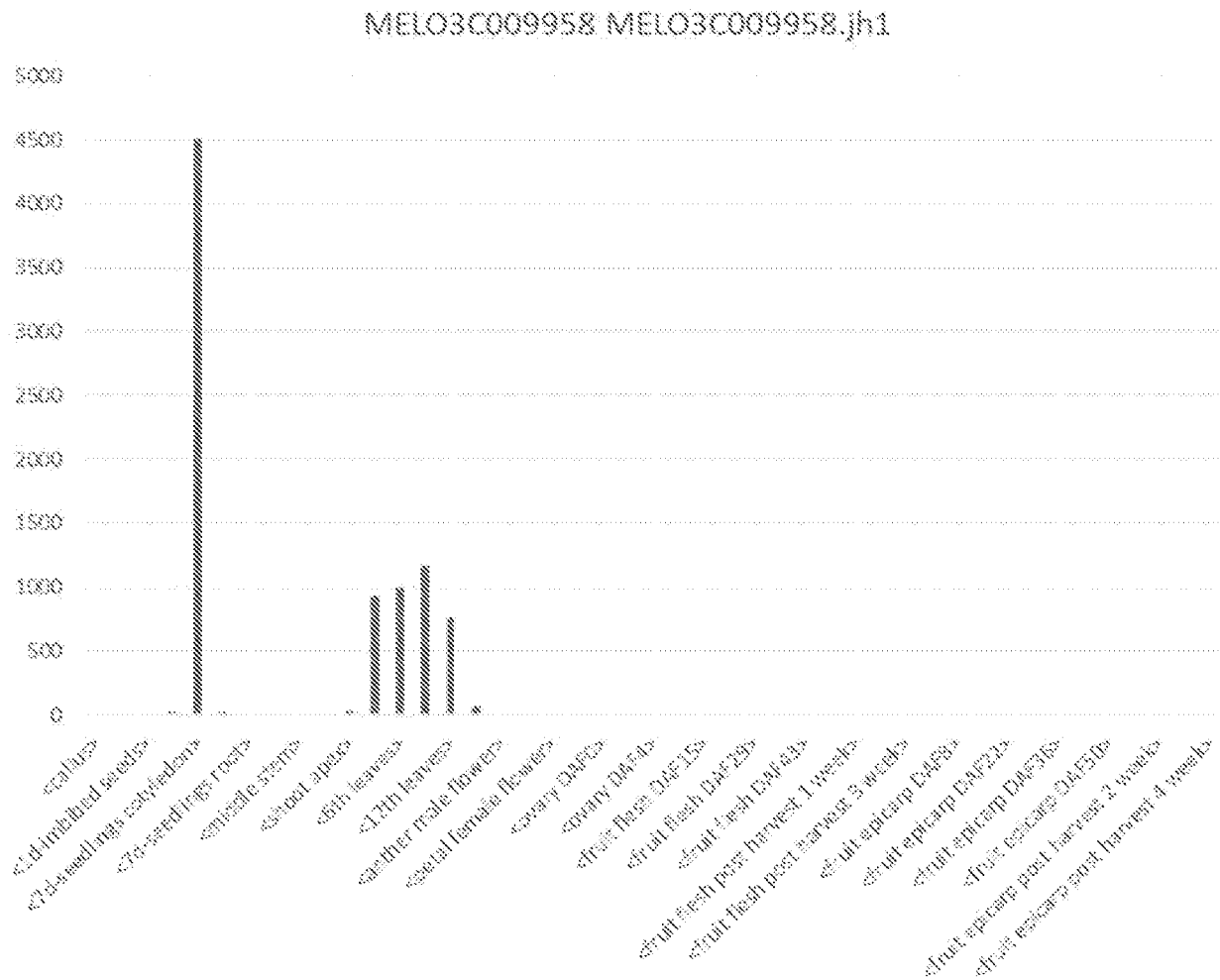


FIG. 20C