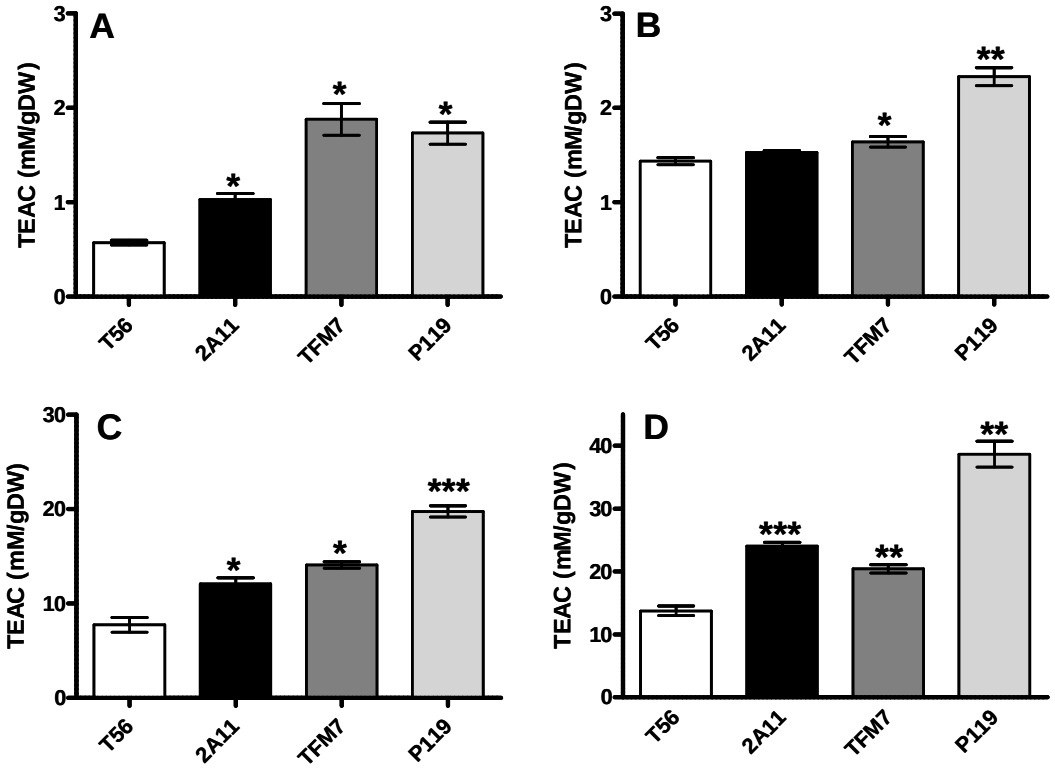
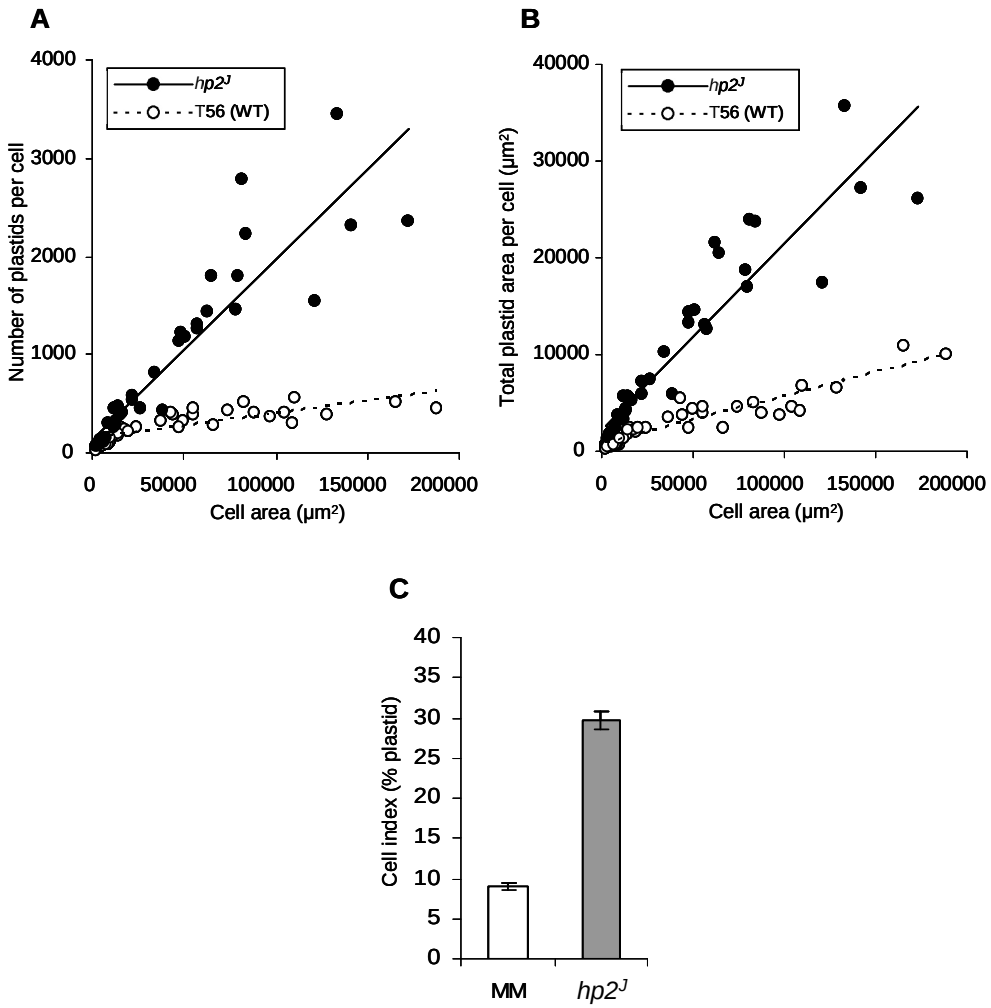
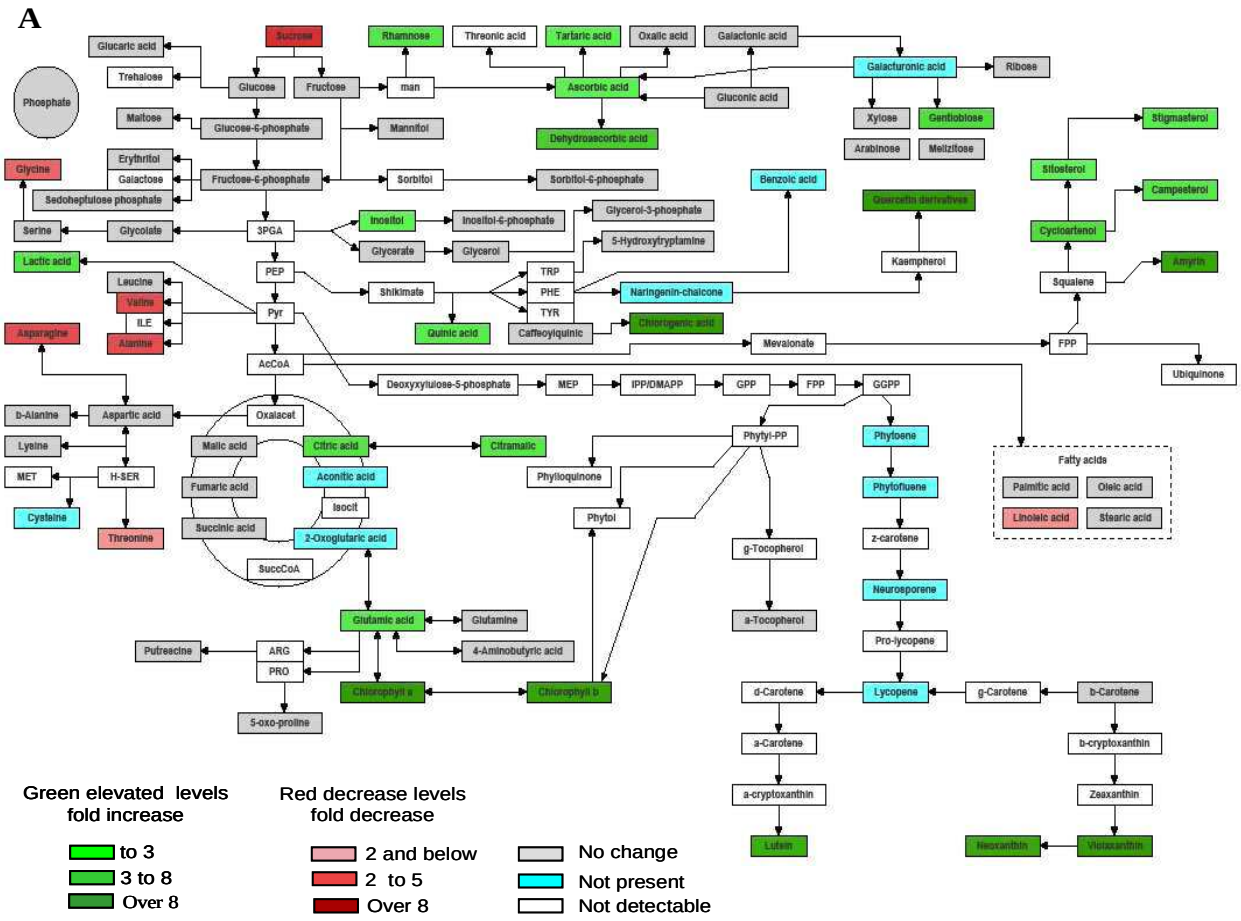


Supplemental Figure 1. Determination of both lipophilic (A and B) and hydrophilic (C and D) antioxidant activity in both mature green (A and C) and ripe fruit (B and D). TEAC assays were performed as described in the methods section with data represented as mean +/- SD. Measurements were made on three biological and three technical replicates. The biological replicates were three plants (three fruit being pooled per plant). Aqueous methanol (80% v/v) and chloroform extracts were used for the determination of hydrophilic and lipophilic antioxidants respectively. Student *t*-tests were used to determine significant differences, between pairwise comparison between the wild type and the transgenic varieties. $P<0.05$, $P<0.01$, $P<0.001$ are indicated by *, **, *** respectively.



Supplemental Figure 2. Altered plastid parameters resulting from the *hp2^J* mutant allele.

The cellular plastid compartment in the *hp2^J* mutant has been compared to its Moneymaker (MM) background. Individual cells were examined microscopically and their plan area, number of chloroplasts and size of a chloroplast sample (20 per cell) quantified. (**A**) shows the number of plastids represented as a function of the cells plan area (the plan area being the area of the cells projection onto one plan). Twenty cells were used in the measurements. (**B**) represents the total area of plastid per cell. These data were obtained from twenty individual cells, counting the total number of plastids per cell and the average area of twenty plastids in one randomly selected region, these values were then plotted as a function of the cells plan area (the plan area being the area of the cells projection onto one plan). (**C**) shows the average cell index (ratio of total plastid area to cell plan area, expressed as a percentage), again the cell plan area is the area of the cells projection onto one plan. The data in (C) is represented as the mean +/- SD.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Rhamnose
Threonic acid
Tartaric acid
Oxalic acid
Galactonic acid
Trehalose
Glucose
Fructose
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Ascorbic acid
Galacturonic acid
Ribose
Phosphate
Gluconic acid
Maltose
Glucose-6-phosphate
Mannitol
Dehydroascorbic acid
Xylose
Gentiobiose
Stigmasterol
Arabinose
Melizitose
Glycine
Erythritol
Galactose
Fructose-6-phosphate
Sorbitol
Sorbitol-6-phosphate
Benzoic acid
Sitosterol
Campesterol
Sedoheptulose phosphate
Quercetin derivatives
Serine
Glycolate
3PGA
Inositol
Inositol-6-phosphate
Glycerol-3-phosphate
Cycloartenol
Glycerate
Glycerol
5-Hydroxytryptamine
Lactic acid
Kaempherol
Amyrin
PEP
TRP
Leucine
Shikimate
PHE
Naringenin-chalcone
Squalene
Valine
TYR
Pyr
ILE
Quinic acid
Caffeoylquinic
Chlorogenic acid
Asparagine
Alanine
Mevalonate
FPP
AcCoA
Ubiquinone
Deoxyxylulose-5-phosphate
MEP
IPP/DMAPP
GPP
FPP
GGPP
b-Alanine
Aspartic acid
Oxalacet
Phytyl-PP
Phytoene
Lysine
Malic acid
Citric acid
Citramalic
Fatty acids
MET
H-SER
Fumaric acid
Aconitic acid
Phylloquinone
Palmitic acid
Oleic acid
Isocit
Phytol
Phytofluene
Cysteine
Succinic acid
2-Oxoglutaric acid
Linoleic acid
Stearic acid
Threonine
z-carotene
g-Tocopherol
SuccCoA
Neurosporene
a-Tocopherol
Glutamic acid
Glutamine
Pro-lycopene
Putrescine
ARG
4-Aminobutyric acid
PRO
d-Carotene
Lycopene
g-Carotene
b-Carotene
Chlorophyll a
Chlorophyll b
5-oxo-proline
a-Carotene
b-cryptoxanthin
a-cryptoxanthin
Zeaxanthin
Lutein
Neoxanthin
Violaxanthin
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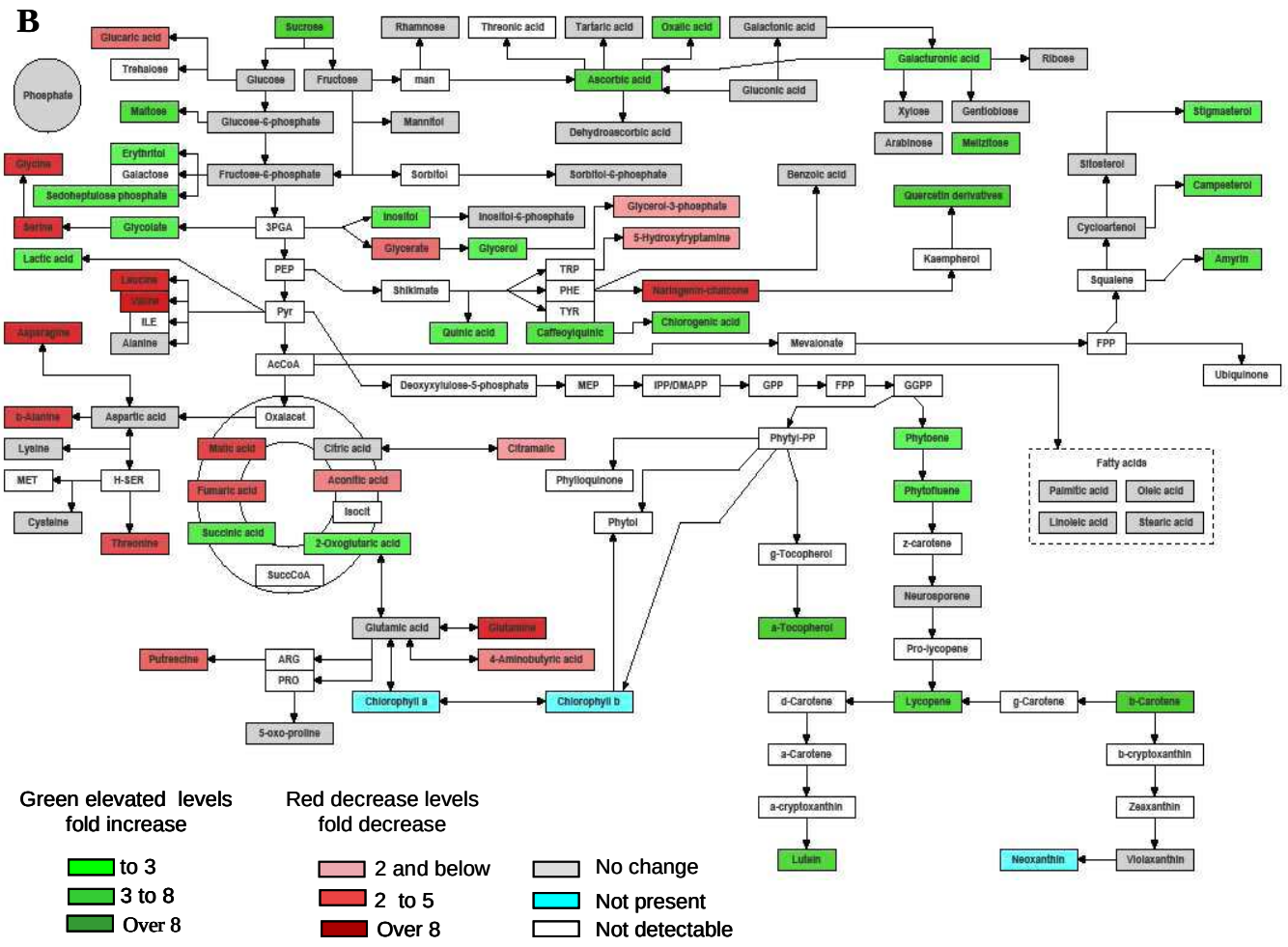
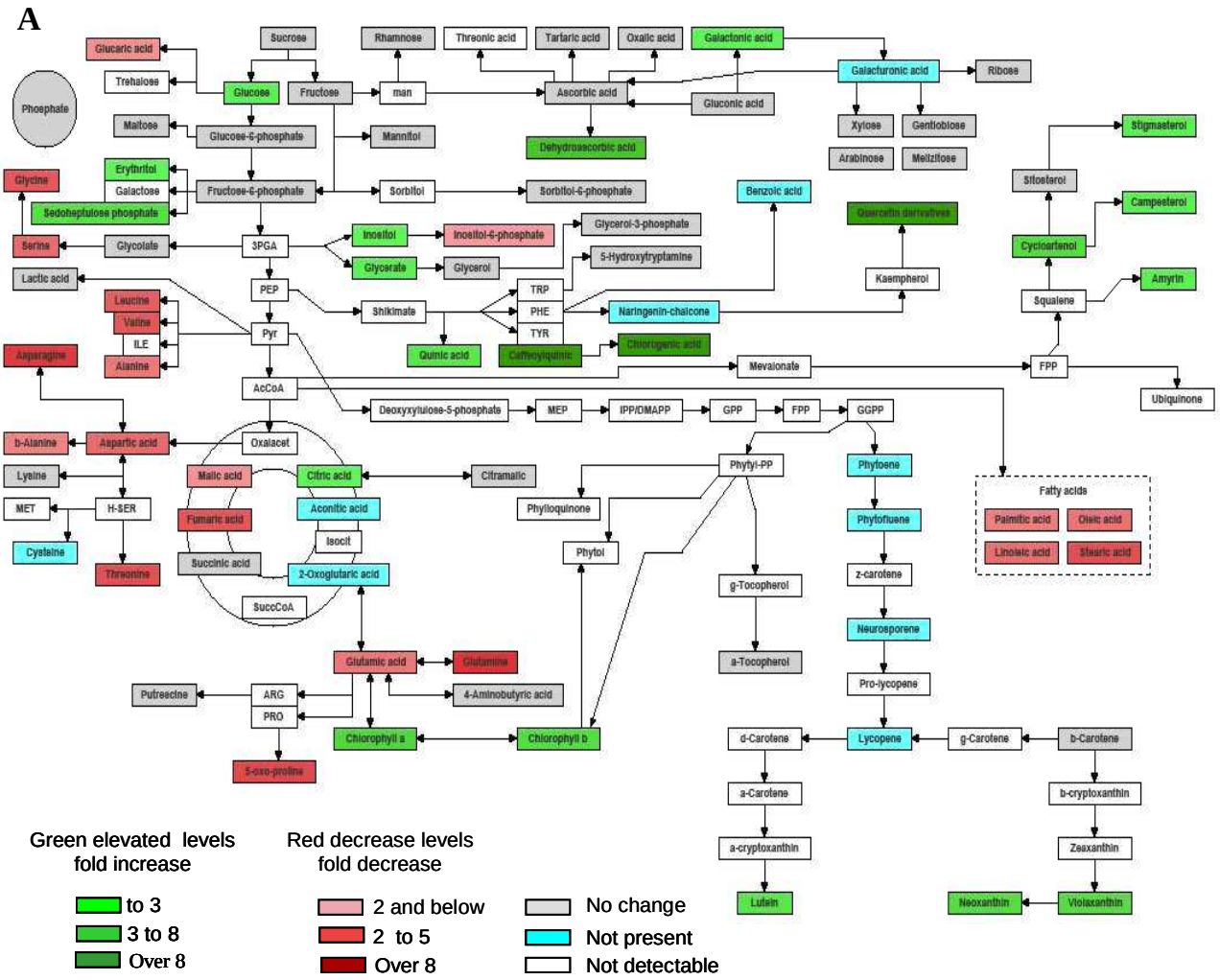
fold increase
to 3
3 to 8
Over 8
Red decrease levels
fold decrease
2 and below
2 to 5
Over 8
No change
Not present
Not detectable



Supplemental Figure 3 A and B. Changes in metabolites occurring in mature green (A) and ripe (B) fruit as a result of *DET1* down-regulation under the control of the TFM7 promoter.

The metabolomic data has been displayed quantitatively over schematic representations of biochemical pathways produced with BioSynLab software (www.biosynlab.com). A false colour scale has been used to display the quantity of each metabolite. Green indicates an increase in the metabolite has occurred compared to the control (T56). Pale Green indicates a significant three-fold increase; a three-fold to eight-fold increase is green, and more than eight-fold is dark green. Grey indicates no significant change, while blue indicates that the metabolite was not detected in the samples. White indicates that the compound cannot be detected using the analytical platforms available. Red coloration has been used to represent decreased metabolite levels; dark red is below eight-fold, red is below two-fold to five-fold, and pale red is below twofold. Abbreviations are as follows; Aco, aconitic acid; L-Asc, ascorbic acid; citramal, citramalic acid; Cit, citric acid; dehydroasc, dehydroascorbic acid; Fum, fumaric acid; Mal, malic acid; 2-oxoglut, 2-oxoglutaric acid; Succ, succinic acid; Thre, threonic acid; 5HT, 5-hydroytryptamine; 5-OxoPRO, 5-oxo-proline; Arab, arabinose; DXP, 1-deoxy-D-xylulose-5-phosphate; F6P, fructose-6-phosphate; G6P, glucose-6-phosphate; 3-CaQuinic, 3-caffeoylquinic acid; CGA, chlorogenic acid; FPP, farnesyl diphosphate; GPP, geranyl diphosphate.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Rhamnose
Threonic acid
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Oxalic acid
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Trehalose
Glucose
Fructose
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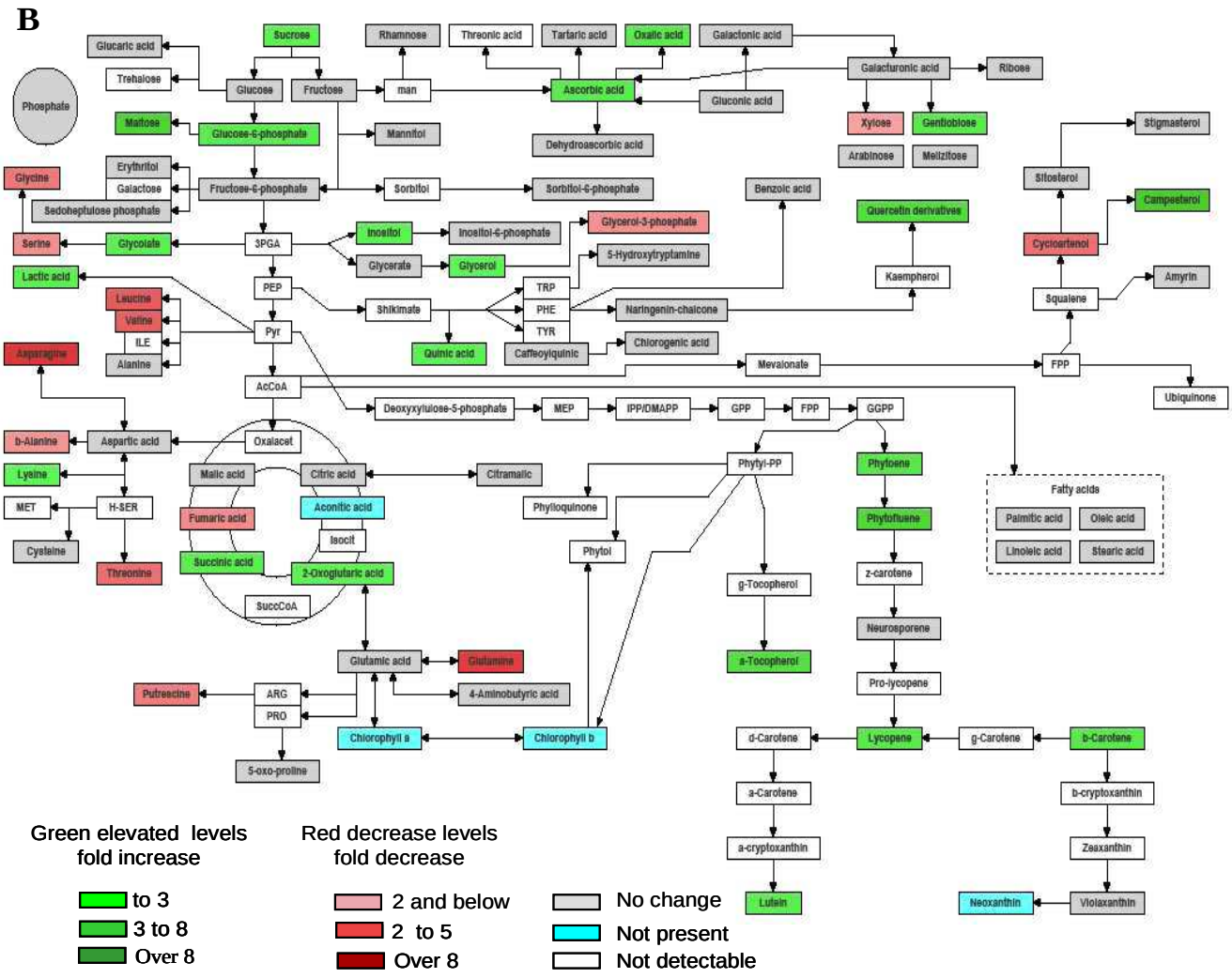
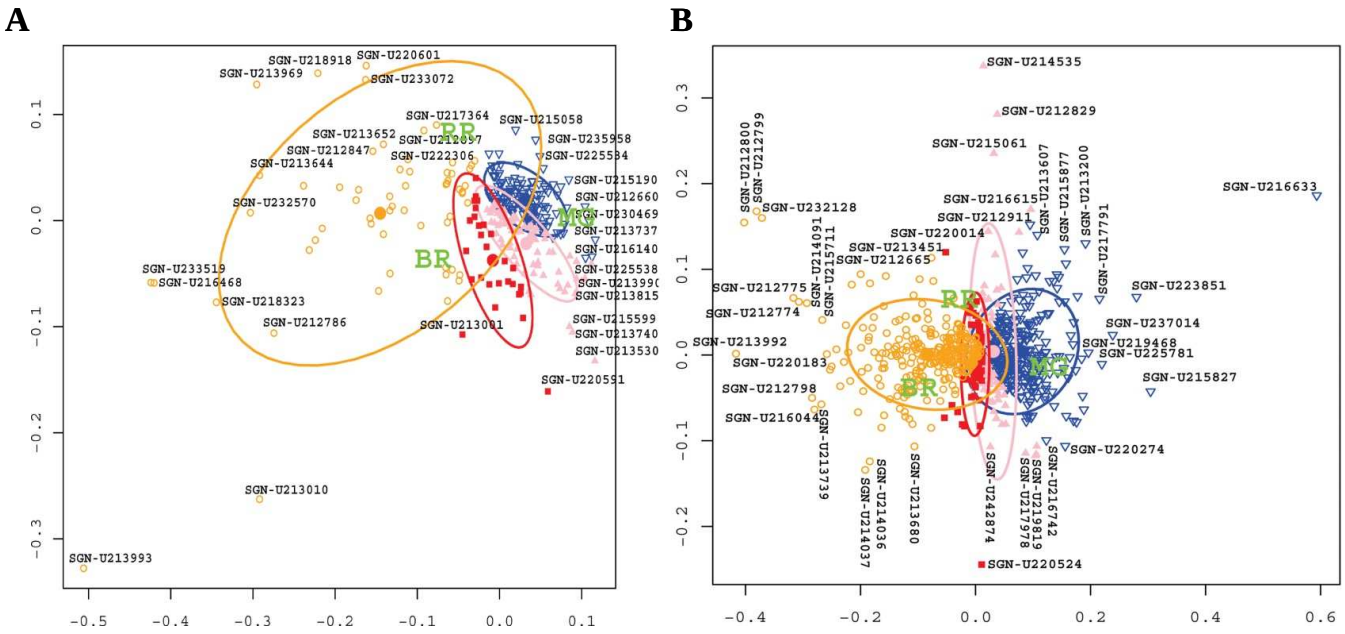
Ascorbic acid
Galacturonic acid
Ribose
Phosphate
Maltose
Glucose-6-phosphate
Mannitol
Gluconic acid
Xylose
Gentiobiose
Dehydroascorbic acid
Arabinose
Melizitose
Stigmasterol
Glycine
Erythritol
Galactose
Fructose-6-phosphate
Sorbitol
Sorbitol-6-phosphate
Benzoic acid
Sitosterol
Sedoheptulose phosphate
Quercetin derivatives
Campesterol
Serine
Glycolate
3PGA
Inositol
Inositol-6-phosphate
Glycerol-3-phosphate
Cycloartenol
Glycerate
Glycerol
5-Hydroxytryptamine
Lactic acid
Kaempherol
Amyrin
PEP
TRP
Leucine
Shikimate
PHE
Naringenin-chalcone
Squalene
Valine
Pyr
TYR
ILE
Quinic acid
Caffeoylquinic
Chlorogenic acid
Asparagine
Alanine
Mevalonate
FPP
AcCoA
Ubiquinone
Deoxyxylulose-5-phosphate
MEP
IPP/DMAPP
GPP
FPP
GGPP
b-Alanine
Aspartic acid
Oxalacet
Phytyl-PP
Phytoene
Lysine
Malic acid
Citric acid
Citramalic
Fatty acids
MET
H-SER
Aconitic acid
Phylloquinone
Phytofluene
Palmitic acid
Oleic acid
Fumaric acid
Isocit
Linoleic acid
Stearic acid
Cysteine
Phytol
Succinic acid
2-Oxoglutaric acid
g-Tocopherol
z-carotene
Threonine
SuccCoA
Neurosporene
a-Tocopherol
Glutamic acid
Glutamine
Pro-lycopene
Putrescine
ARG
4-Aminobutyric acid
PRO
d-Carotene
Lycopene
g-Carotene
b-Carotene
Chlorophyll a
Chlorophyll b
5-oxo-proline
a-Carotene
b-cryptoxanthin
a-cryptoxanthin
Zeaxanthin
Lutein
Neoxanthin
Violaxanthin
Green elevated levels
fold increase
to 3
3 to 8
Over 8
Red decrease levels
fold decrease
2 and below
2 to 5
Over 8
No change
Not present
Not detectable

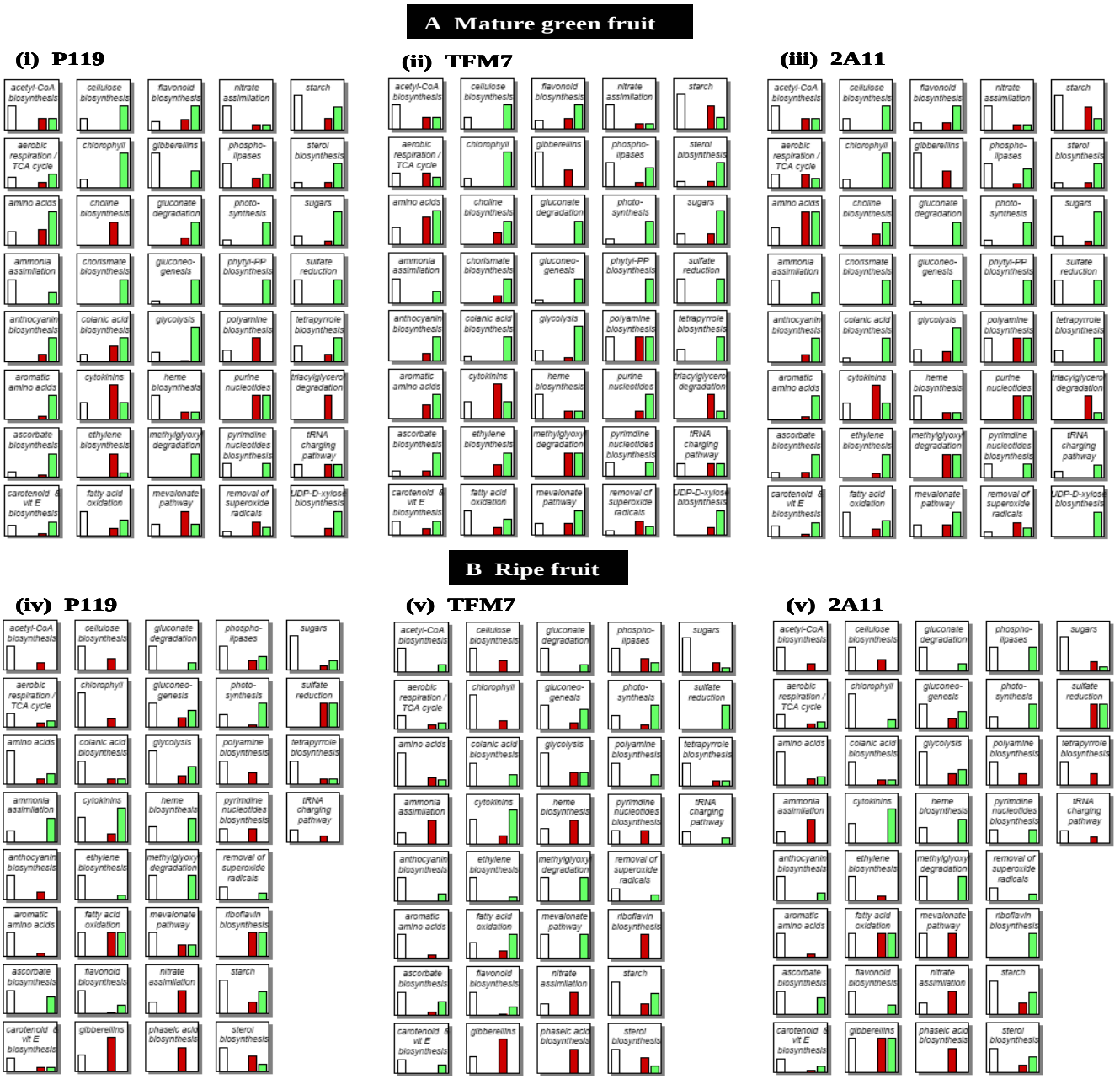


Supplemental Figure 4 A and B. Changes in metabolites occurring in mature green (A) and ripe (B) fruit as a result of *DET1* down-regulation under the control of the 2A11 promoter.

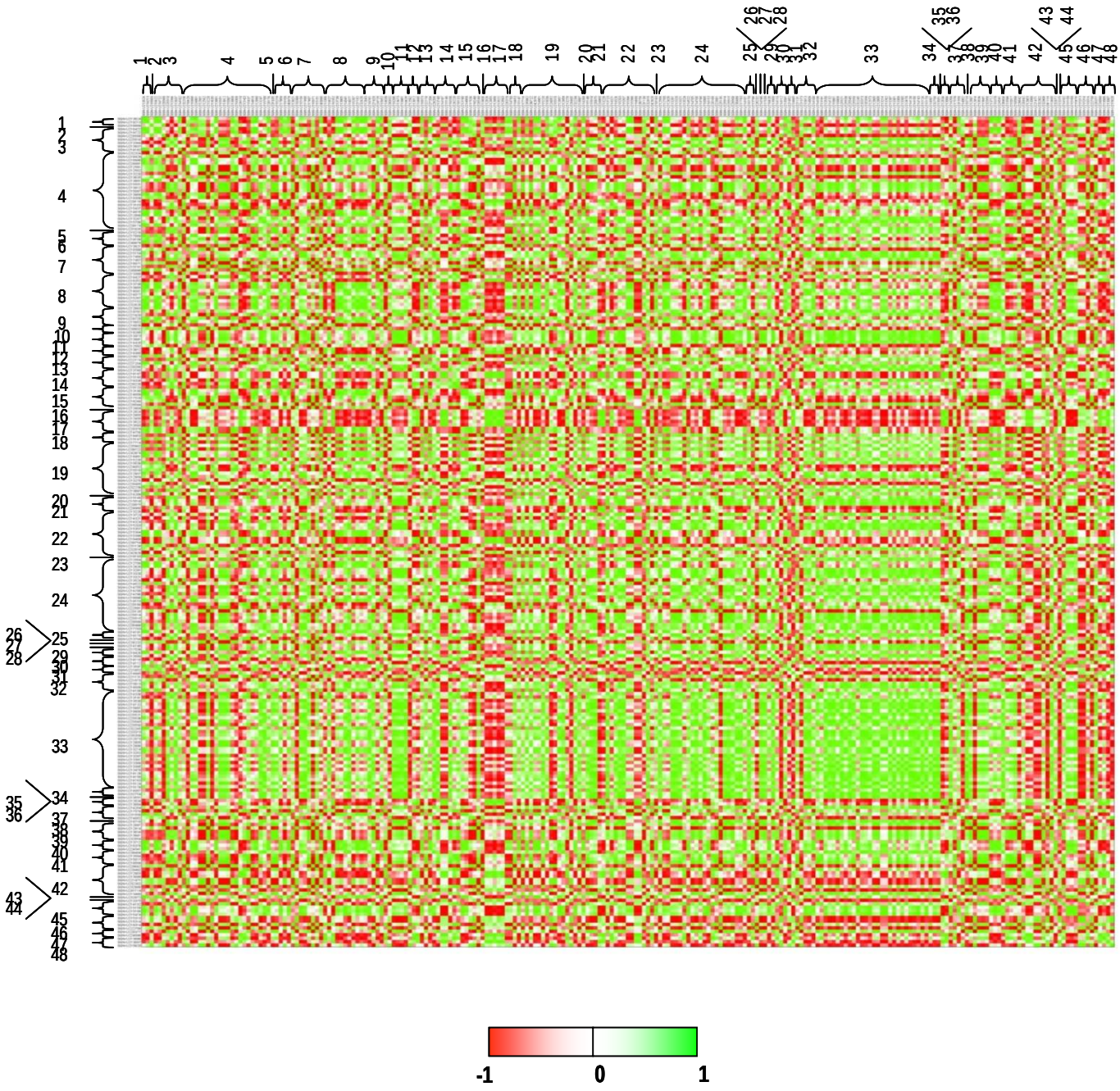
The metabolomic data has been displayed quantitatively over schematic representations of biochemical pathways produced with BioSynLab software (www.biosynlab.com). A false colour scale has been used to display the quantity of each metabolite. Green indicates an increase in the metabolite has occurred compared to the control (T56). Pale Green indicates a significant three-fold increase in pale green, a three-fold to eight-fold increase is green, and more than eight-fold is dark green. Grey indicates no significant change, while blue indicates that the metabolite was not detected in the samples. White indicates that the compound cannot be detected using the analytical platforms available. Red coloration has been used to represent decreased metabolite levels; dark red is below eight-fold, red is below two-fold to five-fold, and pale red is below two-fold. Abbreviations are as follows; Aco, aconitic acid; L-Asc, ascorbic acid; citramal, citramalic acid; Cit, citric acid; dehydroasc, dehydroascorbic acid; Fum, fumaric acid; Mal, malic acid; 2-oxoglut, 2-oxoglutaric acid; Succ, succinic acid; Thre, threonic acid; 5HT, 5-hydroytryptamine; 5-OxoPRO, 5-oxo-proline; Arab, arabinose; DXP, 1-deoxy-D-xylulose-5-phosphate; F6P, fructose-6-phosphate; G6P, glucose-6-phosphate; 3-CaQuinic, 3-caffeoylquinic acid; CGA, chlorogenic acid; FPP, farnesyl diphosphate; GPP, geranyl diphosphate.



Supplemental Figure 5. Correspondence Analysis (CA) for P119 (A) and TFM7 (B).
The biplot shows genes plotted as per their correspondence Axis1 (x-axis) and Axis2 (y-axis) values from the origin and separates genes and hybridizations (developmental stages) according to their similarity. Genes are coloured as per the classes in SOM (Figure 7C and D) and a concentration ellipse is drawn to enclose more than 80 percent of data in each group. A differentially expressed gene in a particular developmental stage contributes more towards the total inertia and its distance from the plot centre will be based on deviation from expected value, larger the deviation larger the distance. A gene will lie in the same direction of a hybridisation (MG-mature green, BR-breaker or RR-red ripe) if it is positively associated (up-regulated) with it or on the opposite direction of the plot if it is specifically down-regulated in this condition. Transcripts having the greatest deviation (not within 80% of the data) among each group are labeled with their unigene number.



Supplemental Figure 6. Overview of relative changes in gene expression occurring at (A) the mature green and (B) ripe stages of fruit development and ripening, in the P119 (i) and (iv), TFM7 (ii) and (v) and 2A11 (iii) and (vi), varieties respectively.
Transcripts have been classified on the basis of function. Changes in gene expression are relative to levels determined in control (T56) samples. For each given functional classification those bars coloured green represent the proportion of transcripts that are up-regulated, the red coloured bars indicate down-regulation and the white coloured bar indicates no change. For accurate comparison those transcripts present in all varieties have been used. The parameters used to functionally classify the transcripts and statistical methods used to determine significance are detailed in the methods section. Supplemental Dataset 1 details individual genes classified within each functional category, their changes in expression levels and significance.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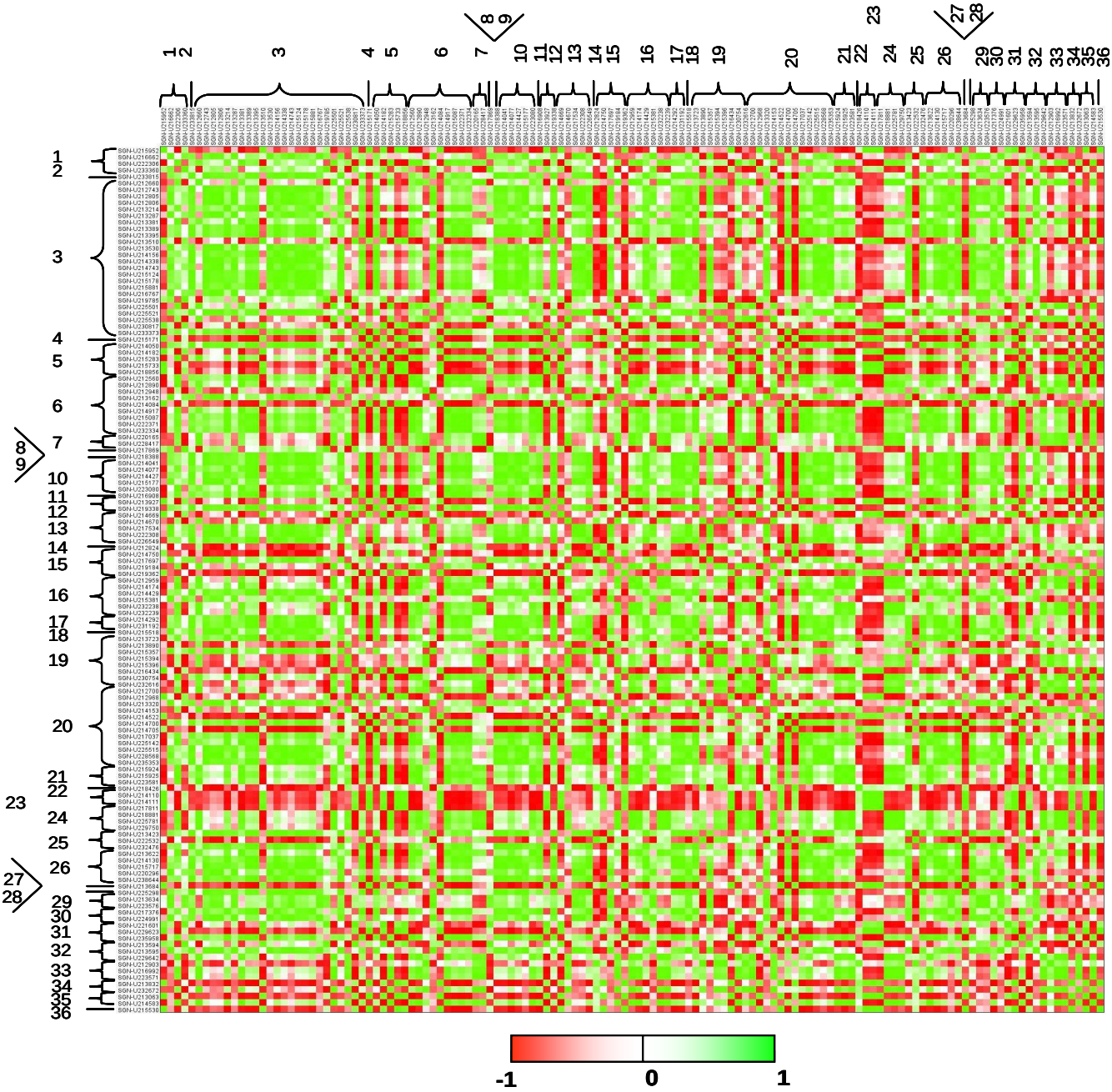
Supplemental Figure 7. . Heatmap illustrating the changes occurring in gene to gene correlations resulting from *DET1* down-regulation at the mature green stage of fruit development.

Data was generated from microarray experiments performed on all three *DET1* varieties compared to their respective wild type controls. Only gene transcripts present in all varieties were used in these analyses (~ 250 genes). Pearson correlation coefficients (*r*) were calculated using datasets for all the *DET1* genotypes, with triplicate biological replication per genotype, calculations were carried out using BioSynLab software (www.Biosynlab.com). The degree of correlation is provided in a false colour scale. Each cell has an *r*-value as indicated in the scale insert provided. A significance of $P < 0.05$ was used for *r* value. Positive correlations are represented by green and negative red coloration. The transcripts have been categorised functionally into pathways and processes and labeled numerically along the axes as follows;1: acetyl-CoA biosynthesis, 2: acyl-ACP thioesterase pathway, 3: aerobic respiration/TCA cycle, 4: amino acids, 5: ammonia assimilation cycle, 6: anothocyanin biosynthesis, 7: aromatic amino acids, 8: ascorbate biosynthesis, 9: carotenoid biosynthesis, 10: cellulose biosynthesis, 11: chlorophyll, 12: choline biosynthesis, 13: chorismate biosynthesis, 14: colanic acid biosynthesis, 15: cytokinins, 16: epicuticular wax biosynthesis, 17: ethylene biosynthesis, 18: fatty acid oxidation, 19: phenylpropanoid biosynthesis, 20: gibberellins, 21: gluconate degradation, 22: gluconeogenesis, 23: glutathione biosynthesis, 24: glycolysis, 25: heme biosynthesis, 26: homogalacturonan degradation, 27: IAA biosynthesis, 28: methylerythritol phosphate pathway, 29: methylglyoxal degradation, 30: mevalonate pathway, 31: nitrate assimilation pathway, 32: phospholipases, 33: photosynthesis, 34: phytl-PP biosynthesis, 35: plastoquinone biosynthesis, 36: polyamine biosynthesis, 37: purine nucleotides, 38: pyrimidine deoxyribonucleotides, 39: removal of superoxide radicals, 40: starch, 41: sterol biosynthesis, 42: sugars, 43: sulphate reduction, 44: tetrahydrofolate biosynthesis, 45: tetrapyrrole biosynthesis, 46: triacylglycerol degradation, 47: tRNA charging pathway, 48: UDP-D-xylose biosynthesis.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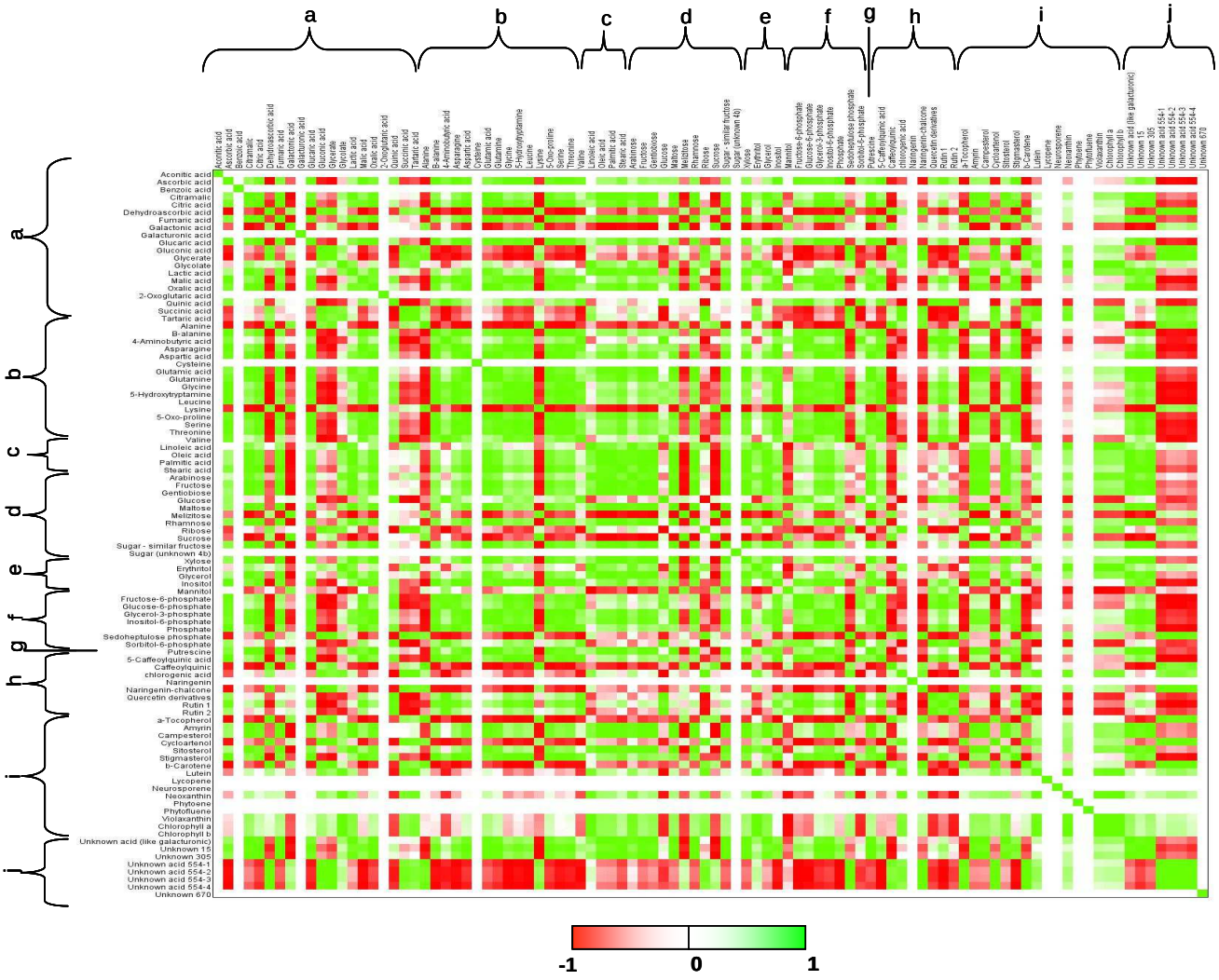
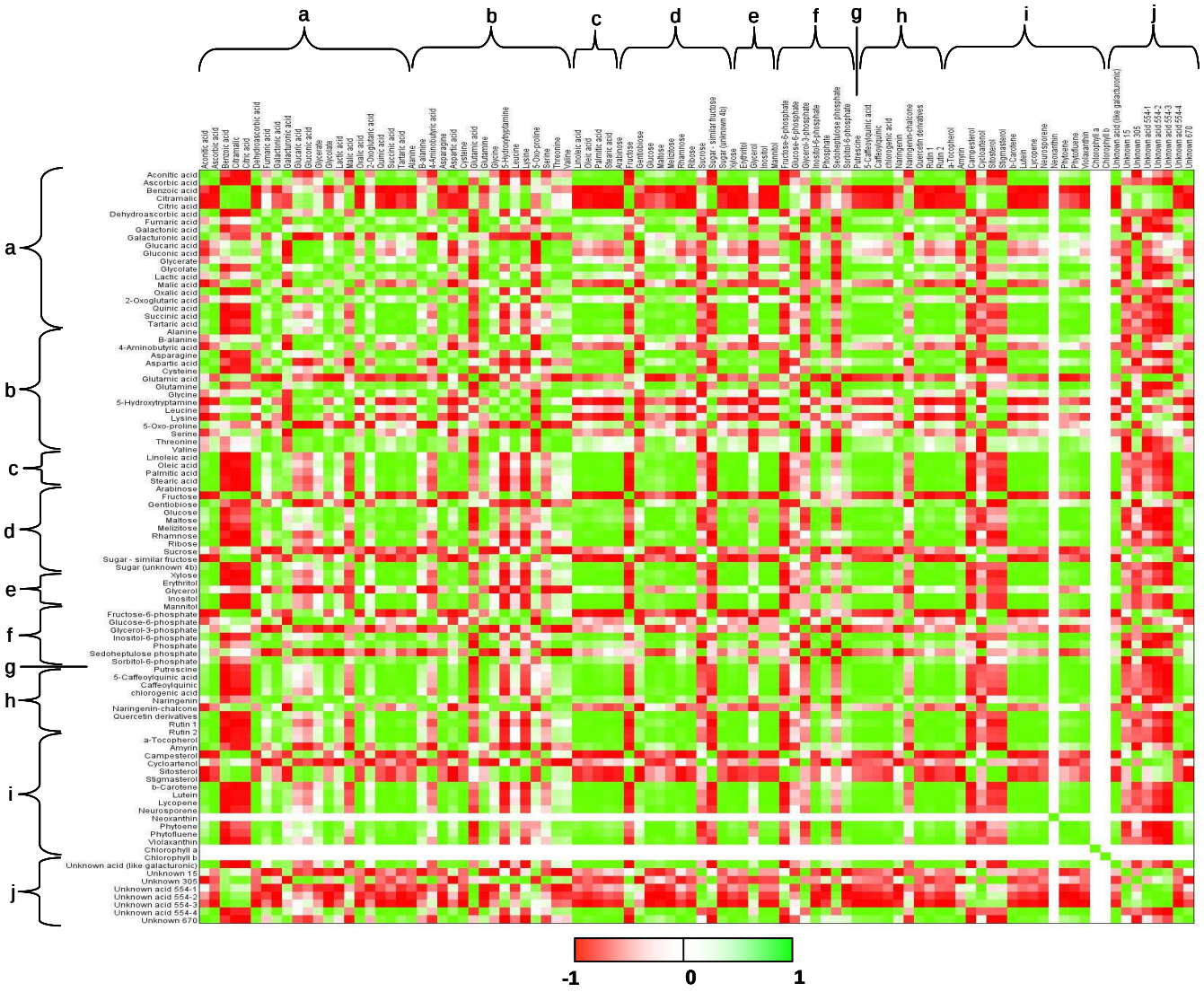
Supplemental Figure 8. Heatmap illustrating the changes occurring in gene to gene correlations resulting from *DET*-1 down-regulation at the stage of ripe fruit.
The data processing performed is detailed in the Methods section. Only gene transcripts present in all varieties were used in these analyses (~ 150 genes). Pearson correlation coefficients (*r*) were calculated using datasets for all the *DET1* genotypes, with triplicate biological replication per genotype, calculations were carried out using BioSynLab software (www.Biosynlab.com). The degree of correlation is provided in a false colour scale. Each cell has an *r*-value as indicated in the scale insert provided. A significance of $P < 0.05$ was used for *r* value. Positive correlations are represented by green and negative by red coloration. The transcripts have been categorised functionally into pathways and processes and labeled numerically along the axes as follows; 1: carotenoid/Vitamin E biosynthesis, 2: Chlorophyll, 3: photosynthesis, 4: acetyl-CoA biosynthesis, 5: aerobic respiration/TCA cycle, 6: amino acids, 7: ammonia assimilation cycle, 8: anthocyanin biosynthesis, 9: aromatic amino acids, 10: ascorbate biosynthesis, 11: cellulose biosynthesis, 12: colanic acid biosynthesis, 13: cytokinins, 14: ethylene biosynthesis, 15: fatty acid oxidation, 16: phenylpropanoid biosynthesis, 17: gibberellins, 18: gluconate degradation, 19: gluconeogenesis, 20: glycolysis, 21: heme biosynthesis, 22: methylglyoxal degradation, 23: mevalonate pathway, 24: nitrate assimilation pathway, 25: phaseic acid biosynthesis, 26: phospholipases, 27: polyamine biosynthesis, 28: pyrimidine deoxyribonucleotides, 29: removal of superoxide radicals, 30: riboflavin biosynthesis, 31: starch, 32: sterol biosynthesis, 33: sugars, 34: sulphate reduction, 35: tetrapyrrole biosynthesis, 36: tRNA charging pathway.



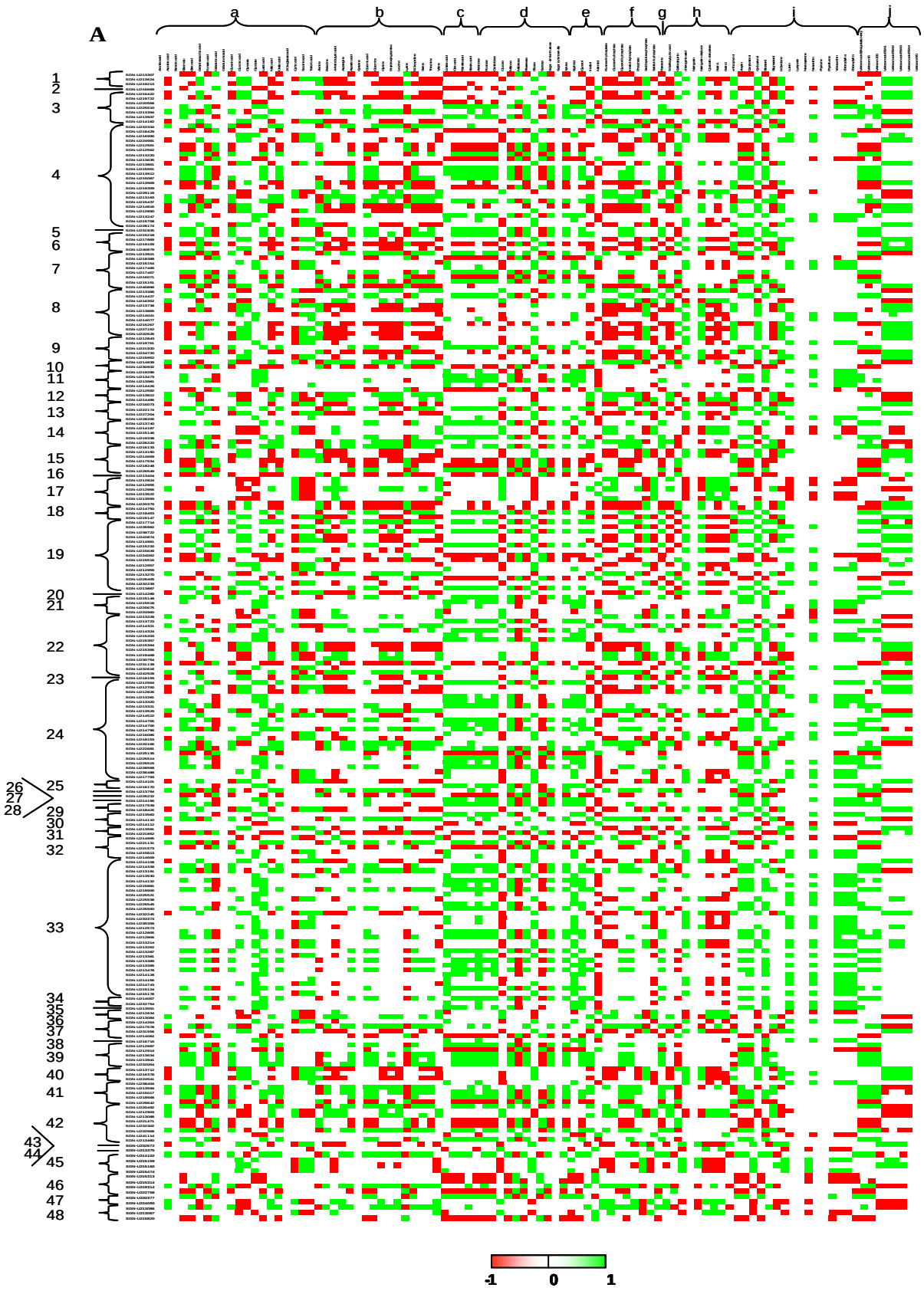
Supplemental Figure 9. Heatmap showing the changes occurring in metabolite to metabolite correlations resulting from *DET1* down-regulation at the mature green stage of fruit development.

Data was generated using various metabolite profiling platforms as detailed in the Methods section. Analyses were performed on all three *DET*-1 varieties compared to their respective wild type controls. The data processing performed is detailed in the Methods section. Only metabolites present in all varieties were used in these analyses (~ 100 metabolites know and unknown). Pearson correlation coefficients (*r*) were calculated using datasets for all the *DET1* genotypes, with triplicate biological replication per genotype, calculations were carried out using BioSynLab software (www.Biosynlab.com). The degree of correlation is provided in a false colour scale. Each cell has an *r*-value as indicated in the scale insert provided. A significance of $P < 0.05$ was used for *r* value. Positive correlations are represented by green and negative by red coloration. The metabolites have been grouped into chemical classes and labeled accordingly along the axes as follows; a: organic acids, b: amino acids, c: fatty acids, d: sugars, e: polyols, f: phosphates, g: N-containing compounds, h: phenylpropanoids/flavonoids, i: terpenoids and j: known and unknowns.



Supplemental Figure 10. Heatmap showing the changes occurring in metabolite to metabolite correlations resulting from *DET1* down-regulation at ripe stage of fruit development.

Data was generated from various metabolite profiling platforms as detailed in the Methods section. Analyses were performed on all three *DET*-1 varieties compared to their respective wild type controls. The data processing performed is detailed in the Methods section. Only metabolites present in all varieties were used in these analyses (~ 100 metabolites know and unknown). Pearson correlation coefficients (*r*) were calculated using datasets for all the *DET1* genotypes, with triplicate biological replication per genotype, calculations were carried out using BioSynLab software (www.Biosynlab.com). The degree of correlation is provided in a false colour scale. Each cell has an *r*-value as indicated in the scale insert provided. A significance of $P < 0.05$ was used for *r* value. Positive correlations are represented by green and negative by red coloration. The metabolites have been grouped into chemical classes and labeled accordingly along the axes as follows; a: organic acids, b: amino acids, c: fatty acids, d: sugars, e: polyols, f: phosphates, g: N-containing compounds, h: phenylpropanoids/flavonoids, i: terpenoids and j: known and unknowns.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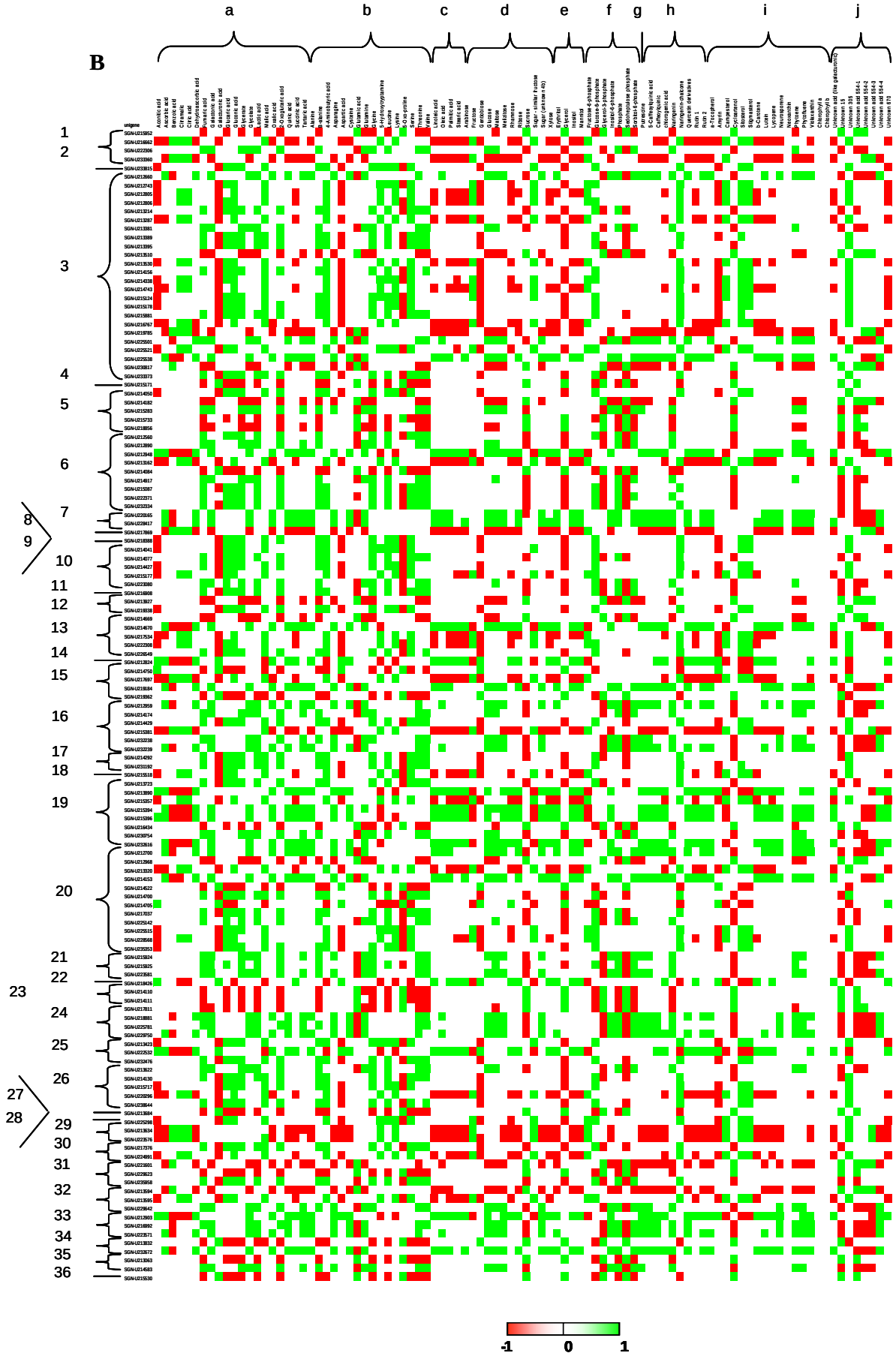
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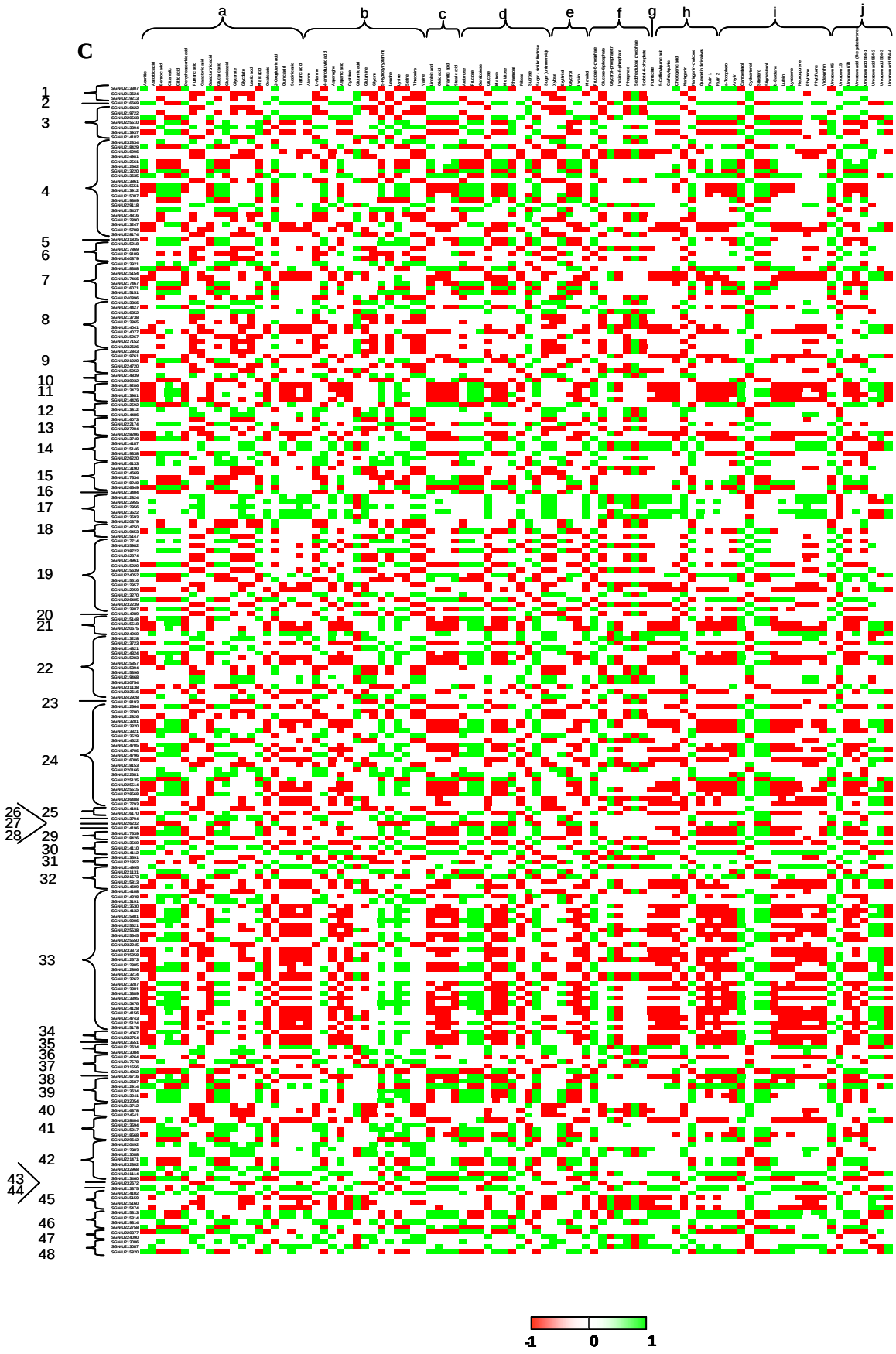
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Supplemental Figure 11. Heatmap displaying gene transcript and metabolite correlations associated with the relative changes resulting from *DET1* down-regulation compared to the wild type (T56) control at the mature green fruit developmental stage (A), ripe fruit (B) and mature green transcripts to ripe metabolites (C).

Data was generated from microarray and metabolomic analysis of all three varieties (P119, TFM7 and 2A11). In Panel **(A)**, transcripts have been grouped by function and numbered using the following key; 1: acetyl-CoA biosynthesis, 2: acyl-ACP thioesterase pathway, 3: aerobic respiration/TCA cycle, 4: amino acids, 5: ammonia assimilation cycle, 6: anthocyanin biosynthesis, 7: aromatic amino acids, 8: ascorbate biosynthesis, 9: carotenoid biosynthesis, 10: cellulose biosynthesis, 11: chlorophyll, 12: choline biosynthesis, 13: chorismate biosynthesis, 14: colanic acid biosynthesis, 15: cytokinins, 16: epicuticular wax biosynthesis, 17: ethylene biosynthesis, 18: fatty acid oxidation, 19: phenylpropanoid biosynthesis, 20: gibberellins, 21: gluconate degradation, 22: gluconeogenesis, 23: glutathione biosynthesis, 24: glycolysis, 25: heme biosynthesis, 26: homogalacturonan degradation, 27: IAA biosynthesis, 28: methylerythritol phosphate pathway, 29: methylglyoxal degradation, 30: mevalonate pathway, 31: nitrate assimilation pathway, 32: phospholipases, 33: photosynthesis, 34: phytl-PP biosynthesis, 35: plastoquinone biosynthesis, 36: polyamine biosynthesis, 37: purine nucleotides, 38: pyrimidine deoxyribonucleotides, 39: removal of superoxide radicals, 40: starch, 41: sterol biosynthesis, 42: sugars, 43: sulphate reduction, 44: tetrahydrofolate biosynthesis, 45: tetrapyrrole biosynthesis, 46: triacylglycerol degradation, 47: tRNA charging pathway, 48: UDP-D-xylose biosynthesis. Metabolites have been grouped by compound class using the following designation a: organic acids, b: amino acids, c: fatty acids, d: sugars, e: polyols, f: phosphates, g: N-containing compounds, h: phenylpropanoids/flavonoids, i: terpenoids and j: known and unknowns. In Panel **(B),** transcripts have been grouped by function and numbered using the following key; 1: carotenoid/Vitamin E biosynthesis, 2: Chlorophyll, 3: photosynthesis, 4: acetyl-CoA biosynthesis, 5: aerobic respiration/TCA cycle, 6: amino acids, 7: ammonia assimilation cycle, 8: anthocyanin biosynthesis, 9: aromatic amino acids, 10: ascorbate biosynthesis, 11: cellulose biosynthesis, 12: colanic acid biosynthesis, 13: cytokinins, 14: ethylene biosynthesis, 15: fatty acid oxidation, 16: phenylpropanoid biosynthesis, 17: gibberellins, 18: gluconate degradation, 19: gluconeogenesis, 20: glycolysis, 21: heme biosynthesis, 22: methylglyoxal degradation, 23: mevalonate pathway, 24: nitrate assimilation pathway, 25: phaseic acid biosynthesis, 26: phospholipases, 27: polyamine biosynthesis, 28: pyrimidine deoxyribonucleotides, 29: removal of superoxide radicals, 30: riboflavin biosynthesis, 31: starch, 32: sterol biosynthesis, 33: sugars, 34: sulphate reduction, 35: tetrapyrrole biosynthesis, 36: tRNA charging pathway. Metabolites have been grouped by compound class using the following designation, a: organic acids, b: amino acids, c: fatty acids, d: sugars, e: polyols, f: phosphates, g: N-containing compounds, h: phenylpropanoids/flavonoids, i: terpenoids, j: known and unknowns. In panel **(C)** Transcripts have been grouped by function and numbered using the following key; 1: acetyl-CoA biosynthesis, 2: acyl-ACP thioesterase pathway, 3: aerobic respiration/TCA cycle, 4: amino acids, 5: ammonia assimilation cycle, 6: anthocyanin biosynthesis, 7: aromatic amino acids, 8: ascorbate biosynthesis, 9: carotenoid biosynthesis, 10: cellulose biosynthesis, 11: chlorophyll, 12: choline biosynthesis, 13: chorismate biosynthesis, 14: colanic acid biosynthesis, 15: cytokinins, 16: epicuticular wax biosynthesis, 17: ethylene biosynthesis, 18: fatty acid oxidation, 19: phenylpropanoid biosynthesis, 20: gibberellins, 21: gluconate degradation, 22: gluconeogenesis, 23: glutathione biosynthesis, 24: glycolysis, 25: heme biosynthesis, 26: homogalacturonan degradation, 27: IAA biosynthesis, 28: methylerythritol phosphate pathway, 29: methylglyoxal degradation, 30: mevalonate pathway, 31: nitrate assimilation pathway, 32: phospholipases, 33: photosynthesis, 34: phytl-PP biosynthesis, 35: plastoquinone biosynthesis, 36: polyamine biosynthesis, 37: purine nucleotides, 38: pyrimidine deoxyribonucleotides, 39: removal of superoxide radicals, 40: starch, 41: sterol biosynthesis, 42: sugars, 43: sulphate reduction, 44: tetrahydrofolate biosynthesis, 45: tetrapyrrole biosynthesis, 46: triacylglycerol degradation, 47: tRNA charging pathway, 48: UDP-D-xylose biosynthesis. Metabolites have been grouped by compound class using the following designation a: organic acids, b: amino acids, c: fatty acids, d: sugars, e: polyols, f: phosphates, g: N-containing compounds, h: phenylpropanoids/flavonoids, i: terpenoids and j: known and unknowns. Transcripts for genes of unknown function have not been included into the data matrix; in contrast metabolites classified as "known unknowns were incorporated. Pearson correlation coefficients (*r*) were calculated using datasets for all the *DET1* genotypes, with triplicate biological replication per genotype, calculations were carried out using BioSynLab software (www.Biosynlab.com). The degree of correlation was selected as 0.8 and -0.8 for positive and negative correlations respectively. These values are represented by a false colour scale where a red coloration indicates a negative correlation and green indicates a positive correlation.

Supplemental Table 1. The stability of the increased carotenoid phenotype in *DET1* lines over the T_3 to T_5 generations.

The T56 is the background used. 2A11, TFM7 and P119 lines are the different transgenic genotypes developed. Data displayed is represented in fold change relative to the T56 control. The total carotenoid contents of T56 ranged from 321.7 +/- 8.7 to 708 +/- 14.0 mg/g DW. Therefore data are represented as relative increases compared to the respective control (T56) grown simultaneously with each group. A minimum of three representative fruit from each of the six plants generated per genotype were harvested and pooled. Three technical replicate measurements were carried out on each of the biological replications. The data are presented as mean +/- SD. Student *t*-tests were used to determine significant differences, between pairwise comparison between the wild type and the transgenic varieties. $P<0.001$ is indicated by *** respectively.

	Carotenoid content (-fold increase)		
	2A11	TFM7	P119
T3 Generation	2.3 ***	3.0 ***	6.0 ***
T4 Generation	2.4 ***	7.3 ***	8.8 ***
T5 Generation	2.3 ***	3.0 ***	5.9 ***

Supplemental Table 2. Metabolite levels of *DET1* varieties relative to their respective controls at the mature green (A) and ripe fruit (B) stages.

Data has been compiled from multiple analytical platforms as outlined in the methods section. Data have been normalized to sample weight and expressed relative to their wild type either at the mature green (40 days after anthesis or ripe stage 7 days after breaking. Values are represented as means +/- SD. P values are shown as <0.001, 0.01 and 0.05 by ***, ** and * respectively. ~10.0 is an arbitrary unit representing an increase in a metabolite in one line while being absent in another. –indicates not determined, bold indicates a statistically significant increase. ND-not detected in one of the pairwise ratios. Abbreviations for the site of synthesis are MT-mitochondria, CY-cytosol, Pl-plastid and PE-peroxisomes.

A

Metabolite	Main site of synthesis	2A11	TFM7	P119
Organic Acids				
Aconitic acid	MT	n/d	n/d	n/d
Ascorbic acid	CY	1.47 ±0.35	**1.69 ±0.09***	0.95 ±0.32
Benzoic acid	CY	n/d	n/d	n/d
Citramalic	CY	1.24 ±0.62	**2.33 ±0.33****	1.34 ±0.35
Citric acid	MT	**1.36 ±0.31***	**2.71 ±0.09****	0.87 ±0.23
Dehydroascorbic acid	CY	**4.86 ±1.88****	**4.36 ±0.29*****	**6.06 ±1.43*****
Fumaric acid	MT	**0.41 ±0.16****	0.70 ±0.10	**0.38 ±0.06****
Galactonic acid	CY	**1.42 ±0.23****	1.10 ±0.04	**1.38 ±0.15*****
Galacturonic acid	CY	n/d	n/d	n/d
Glucaric acid	CY	**0.68 ±0.29***	1.08 ±0.09	**0.39 ±0.12*****
Gluconic acid	CY	1.00 ±0.10	1.02 ±0.12	**1.17 ±0.11****
Glycerate	CY	**1.67 ±0.41****	1.51 ±0.58	**2.83 ±0.43*****
Glycolate	PL	0.88 ±0.32	1.34 ±0.30	**1.33 ±0.17****
Lactic acid	CY	1.57 ±0.66	**2.40 ±0.42****	**1.81 ±0.53****
Malic acid	MT/CY	**0.70 ±0.10*****	0.80 ±0.15	**0.47 ±0.05*****
Oxalic acid	CY	1.25 ±1.11	2.24 ±2.21	1.00 ±0.28
2-Oxoglutaric acid	MT	n/d	n/d	n/d
Quinic acid	CY	**2.28 ±0.43*****	**2.10 ±0.45***	**1.79 ±0.25****
Succinic acid	MT	1.16 ±0.20	**2.02 ±0.58***	**3.47 ±0.97*****
Tartaric acid	CY	1.26 ±0.36	**1.71 ±0.07*****	**2.13 ±0.32*****
Amino Acids				
Alanine	PL	**0.58 ±0.07****	**0.38 ±0.24***	0.76 ±0.19
B-alanine	CY	**0.63 ±0.16****	0.86 ±0.27	**0.25 ±0.04*****
4-Aminobutyric acid	CY/PL	0.84 ±0.13	0.72 ±0.37	**0.48 ±0.05*****
Asparagine	CY	**0.29 ±0.15*****	**0.38 ±0.16****	**0.11 ±0.04*****
Aspartic acid	CY	**0.51 ±0.12*****	1.16 ±0.47	**0.15 ±0.04*****
Cysteine	PL	n/d	n/d	n/d
Glutamic acid	PL/CY	**0.56 ±0.15***	**2.21 ±0.12*****	**0.44 ±0.12****
Glutamine	PL/CY	**0.25 ±0.11****	0.78 ±0.046	**0.04 ±0.02*****
Glycine	CY(PE)	**0.42 ±0.06*****	**0.49 ±0.02*****	**0.13 ±0.01*****
5-Hydroxytryptamine	PL	0.70 ±0.09	0.90 ±0.05	**0.37 ±0.07*****
Leucine	PL	**0.45 ±0.25*****	0.57 ±0.21	**0.06 ±0.01*****
Lysine	PL	1.77 ±0.42	1.74 ±1.1	**1.78 ±0.14***
5-Oxo-proline	CY	**0.35 ±0.10*****	0.81 ±0.19	**0.15 ±0.01*****
Serine	MT	**0.52 ±0.10*****	0.78 ±0.46	**0.18 ±0.03*****
Threonine	PL	**0.39 ±*****	**0.71 ±0.06****	**0.09 ±0.01*****
Valine	PL	**0.42 ±0.11*****	**0.37 ±0.13****	**0.13 ±0.02*****
Fatty Acids				

Linoleic acid	CY	**0.53 ±0.16****	**0.70 ±0.07***	**0.66 ±0.18***
Oleic acid	CY	**0.55 ±0.27***	1.60 ±1.03	0.79 ±0.22
Palmitic acid	PL	**0.61 ±0.27****	1.28 ±0.09	**0.74 ±0.12****
Stearic acid	CY	**0.39 ±0.39****	1.52 ±0.71	**0.21 ±0.03*****
Sugars				
Arabinose	CY	1.00 ±0.32	1.80 ±0.88	**1.39 ±0.24****
Fructose	CY	0.78 ±0.24	0.95 ±0.16	**0.78 ±0.14***
Gentiobiose	CY	0.82 ±0.17	**3.28 ±0.16*****	1.27 ±0.27
Glucose	CY/PL	**1.50 ±0.28****	1.38 ±0.45	1.28 ±0.37
Maltose	PL	0.79 ±0.46	2.05 ±0.56	0.96 ±0.12
Melizitose	CY	1.40 ±0.56	0.36 ±0.16	1.10 ±1.06
Rhamnose	CY	0.001 ±0.0004	**2.42 ±0.05***	0.001 ±0.0004
Ribose	CY	0.84 ±0.23	1.18 ±0.12	**1.68 ±0.67***
Sucrose	CY	1.07 ±0.73	**0.23 ±0.05*****	0.93 ±0.31
Sugar - similar fructose		0.73 ±0.28	0.89 ±0.16	**0.73 ±0.15***
Sugar (unknown 4b)		n/d	n/d	n/d
Xylose	CY/PL	1.09 ±0.14	1.51 ±0.63	1.10 ±0.16
Polyols				
Erythritol	PL	**1.23 ±0.09****	1.50 ±0.27	**1.48 ±0.11*****
Glycerol	CY/PL	1.07 ±0.27	4.27 ±2.84	**1.92 ±0.25*****
Inositol	CY	**1.37 ±0.25***	**1.57 ±0.17***	**1.14 ±0.12***
Mannitol	CY	2.30 ±0.46	0.88 ±0.61	1.17 ±0.40
Phosphates				
Fructose-6-phosphate	PL/CY	1.00 ±0.14	1.03 ±0.07	**0.50 ±0.15*****
Glucose-6-phosphate	PL/CY	1.01 ±0.34	0.97 ±0.15	**0.58 ±0.14****
Glycerol-3-phosphate	CY	0.84 ±0.20	1.37 ±0.20	**0.54 ±0.06*****
Inositol-6-phosphate	CY	**0.74 ±0.13***	1.06 ±0.24	**0.63 ±0.16****
Phosphate		0.90 ±0.10	0.91 ±0.04	**0.84 ±0.09***
Sedoheptulose phosphate	PL	**2.82 ±0.31*****	3.58 ±2.29	**9.86 ±3.31*****
Sorbitol-6-phosphate	PL	0.95 ±0.05	**0.64 ±0.01***	**0.37 ±0.07****
N-Containing Compounds				
Putrescine	CY	1.05 ±0.48	1.25 ±0.33	1.01 ±0.62
Known Unknowns				
Unknown acid (like galacturonic)		1.08 ±0.15	**1.32 ±0.07***	1.11 ±0.13
Unknown 15		**0.34 ±0.18*****	0.80 ±0.12	**0.20 ±0.06*****
Unknown 305		0.00	1.70 ±0.51	n/d
Unknown acid 554-1		1.26 ±0.29	0.77 ±0.11	**2.92 ±0.55*****
Unknown acid 554-2		**2.05 ±0.66***	**1.80 ±0.08****	**8.25 ±4.64****
Unknown acid 554-3		**1.85 ±0.62***	**1.49 ±0.07****	**7.29 ±3.65****
Unknown acid 554-4		**1.62 ±0.45****	**1.43 ±0.04*****	**2.24 ±0.59****
Unknown 670		n/d	n/d	n/d
Isoprenoids				
β-Carotene	PL	**2.41 ±0.71***	**7.33 ±1.63****	**8.83 ±1.10****
Lutein	PL	**2.44 ±0.16*****	**6.82 ±0.25*****	**8.51 ±0.10*****
Lycopene	PL	n/d	n/d	n/d
Neurosporene	PL	n/d	n/d	n/d
Neoxanthin	PL	**3.06 ±0.35****	**7.26 ±0.33*****	**7.82 ±0.55*****
Phytoene	PL	n/d	n/d	n/d
Phytofluene	PL	n/d	n/d	n/d
Violaxanthin	PL	**3.10 ±0.15*****	**9.83 ±0.20*****	**9.07 ±0.54*****
Chlorophyll a	PL	**3.50 ±0.50****	**11.04 ±0.98****	**10.57 ±0.20*****
Chlorophyll b	PL	**3.03 ±0.11*****	**7.55 ±0.12*****	**7.38 ±0.27*****
α-Tocopherol	PL	1.73 ±0.94	2.13 ±1.49	**3.27 ±1.18****
Amyrin	CY	**1.74 ±0.34****	**2.86 ±0.28*****	**2.53 ±0.16*****
Campesterol	CY	**1.77 ±0.49****	**2.46 ±0.24*****	**1.89 ±0.29*****
Cycloartenol	CY	**3.05 ±1.88***	**3.25 ±1.20****	**5.67 ±0.72*****
Sitosterol	CY	**1.24 ±0.27**	**1.37 ±0.13****	**1.28 ±0.11***
Stigmasterol	CY	**1.75 ±0.69***	**2.08 ±0.43*****	1.20 ±0.2

Phenylpropanoids				
5-Caffeoylquinic acid	CY	**10.30 ±0.3**	**10.40 ±0.003**	**9.79 ±0.01**
Caffeoylquinic	CY	**8.24 ±0.02**	**3.64 ±0.36**	**10.50 ±0.01**
chlorogenic acid	CY	**10.30 ±0.0001**	**10.40 ±0.03**	**10.50 ±0.0002**
Naringenin	CY	n/d	n/d	n/d
Naringenin-chalcone	CY	n/d	n/d	10.50 ±0.01
Quercetin derivative 1	CY	**11.63 ±5.89****	**11.14 ±2.23*****	**5.32 ±0.40*****
Quercetin derivative 2	CY	**30.52 ±15.53****	**17.72 ±2.39*****	**9.38 ±0.55*****

B

Metabolite	**Main site of synthesis**	**2A11**	**TFM7**	**P119**
Organic Acids				
Aconitic acid	MT	n/d	**0.64 ±0.08*****	0.85 ±.29
Ascorbic acid	CY	**2.08 ±0.75****	**2.93 ±1.73***	**6.25 ±2.59****
Benzoic acid	CY	1.08 ±0.17	1.08 ±0.12	1.05 ±0.09
Citramalic	CY	1.03 ±0.21	**0.75 ±0.07***	**0.45 ±0.08*****
Citric acid	MT	1.02 ±0.09	0.92 ±0.22	0.82 ±0.10
Dehydroascorbic acid	CY	1.29 ±0.70	1.98 ±0.40	**7.13 ±1.84*****
Fumaric acid	MT	**0.67 ±0.18****	**0.42 ±0.65*****	**0.65 ±0.16*****
Galactonic acid	CY	1.05 ±0.25	0.87 ±0.21	1.35 ±0.36
Galacturonic acid	CY	0.89 ±0.34	**1.30 ±0.12***	1.21 ±0.32
Glucaric acid	CY	0.83 ±0.16	**0.55 ±0.14***	0.68 ±0.09
Gluconic acid	CY	1.11 ±0.13	0.82 ±0.19	0.90 ±0.14
Glycerate	CY	0.89 ±0.10	**0.54 ±0.08****	0.81 ±0.09
Glycolate	PL	**1.80 ±0.56****	**1.58 ±0.36***	**2.34 ±0.27*****
Lactic acid	CY	**1.72 ±0.58***	**1.37 ±0.25***	**1.75 ±0.57***
Malic acid	MT/CY	0.67 ±0.08	**0.34 ±0.01****	**0.35 ±0.11****
Oxalic acid	CY	**2.13 ±0.99***	**2.50 ±1.37***	**4.67 ±2.61****
2-Oxoglutaric acid	MT	**1.54 ±0.34****	**1.44 ±0.30***	**1.52 ±0.28****
Quinic acid	CY	**1.57 ±0.11*****	**1.67 ±0.21*****	**3.64 ±0.71*****
Succinic acid	MT	**1.86 ±0.27****	**2.11 ±0.24*****	**2.68 ±0.86****
Tartaric acid	CY	1.01 ±0.12	0.81 ±0.10	**1.76 ±0.24*****
Amino Acids				
Alanine	PL	1.38 ±0.36	1.61 ±0.62	**5.35 ±1.63*****
B-alanine	CY	**0.72 ±0.05*****	**0.32 ±0.04*****	**0.64 ±0.10*****
4-Aminobutyric acid	CY/PL	0.94 ±0.12	**0.65 ±0.11****	**0.72 ±0.07****
Asparagine	CY	**0.27 ±0.20*****	**0.22 ±0.15*****	0.64 ±0.50
Aspartic acid	CY	**0.67 ±0.15***	1.02 ±0.48	1.06 ±0.23
Cysteine	PL	0.77 ±0.42	0.80 ±0.44	**1.52 ±0.30****
Glutamic acid	PL/CY	0.62 ±0.32	1.67 ±0.45	n/d
Glutamine	PL/CY	**0.30 ±0.24****	**0.21 ±0.16****	**0.41 ±0.37***
Glycine	CY(PE)	**0.58 ±0.12*****	**0.26 ±0.02*****	**0.51 ±0.18*****
5-Hydroxytryptamine	PL	0.89 ±0.18	**0.75 ±0.04*****	**0.67 ±0.11*****
Leucine	PL	**0.45 ±0.26****	**0.22 ±0.04*****	**0.36 ±0.08*****
Lysine	PL	**1.37 ±0.21****	1.14 ±0.33	1.04 ±0.27
5-Oxo-proline	CY	**0.70 ±0.26***	0.94 ±0.44	0.83 ±0.29
Serine	MT	**0.68 ±0.21****	**0.26 ±0.05*****	**0.41 ±0.13*****
Threonine	PL	**0.54 ±0.33****	**0.39 ±0.09*****	**0.55 ±0.16*****
Valine	PL	**0.47 ±0.21*****	**0.14 ±0.02*****	**0.45 ±0.07*****
Fatty Acids				
Linoleic acid	CY	1.12 ±0.75	1.52 ±0.48	**2.35 ±0.84***
Oleic acid	CY	1.24 ±1.00	1.41 ±0.54	**2.77 ±0.61****
Palmitic acid	PL	1.05 ±0.17	1.42 ±0.39	**2.22 ±0.37*****

Stearic acid	CY	0.97 ±0.37	1.33 ±0.69	**1.69 ±0.38***
Sugars				
Arabinose	CY	0.71 ±0.20	0.80 ±0.26	0.93 ±0.17
Fructose	CY	1.18 ±0.24	0.84 ±0.24	**0.61 ±0.09****
Gentiobiose	CY	**2.25 ±0.99***	**2.57 ±1.53***	**2.56 ±0.22*****
Glucose	CY/PL	1.06 ±0.24	0.99 ±0.15	1.28 ±0.63
Maltose	PL	**3.87 ±2.06****	**2.99 ±1.83***	**5.08 ±1.29*****
Melizitose	CY	2.79 ±1.54	**2.75 ±0.21****	**3.06 ±0.66****
Rhamnose	CY	0.01 ±0.001	0.01 ±0.005	0.02 ±0.003
Ribose	CY	0.64 ±0.48	0.75 ±0.58	1.06 ±0.84
Sucrose	CY	**1.70 ±0.67***	**3.74 ±0.10*****	1.27 ±0.62
Sugar - similar fructose		1.17 ±0.34	0.77 ±0.24	**0.52 ±0.09*****
Sugar (unknown 4b)		0.96 ±0.15	0.94 ±0.14	**1.35 ±0.24***
Xylose	CY/PL	**0.77 ±0.14****	1.04 ±0.22	**1.46 ±0.17*****
Polyols				
Erythritol	PL	1.15 ±0.18	**1.35 ±0.10*****	**2.01 ±0.26*****
Glycerol	CY/PL	**1.29 ±0.20***	**1.50 ±0.12*****	**1.37 ±0.17****
Inositol	CY	**1.63 ±0.34****	**1.92 ±0.39*****	**2.65 ±0.37*****
Mannitol	CY	0.53 ±0.09	1.16 ±0.55	**2.70 ±0.4*****
Phosphates				
Fructose-6-phosphate	PL/CY	1.29 ±0.40	1.11 ±0.28	0.97 ±0.18
Glucose-6-phosphate	PL/CY	**2.11 ±0.33****	1.48 ±0.67	**1.80 ±0.42****
Glycerol-3-phosphate	CY	**0.69 ±0.03*****	**0.75 ±0.15****	**0.68 ±0.13*****
Inositol-6-phosphate	CY	1.16 ±0.21	1.07 ±0.22	**1.93 ±0.74***
Phosphate		1.03 ±0.12	0.93 ±0.03	1.07 ±0.12
Sedoheptulose phosphate	PL	1.06 ±0.30	**1.98 ±0.85***	1.04 ±0.55
Sorbitol-6-phosphate	PL	1.47 ±0.62	0.88 ±0.29	1.82 ±0.39**
N-Containing Compounds				
Putrescine	CY	**0.61 ±0.08*****	**0.50 ±0.08*****	**1.37 ±0.19****
Known Unknowns				
Unknown acid (like galacturonic)		0.95 ±0.13	1.16 ±0.10	**1.48 ±0.33***
Unknown 15		**0.48 ±0.09***	0.86 ±0.19	**0.41 ±0.03***
Unknown 305		**15.52 ±5.10***	0.23 ±0.02	0.12 ±0.02
Unknown acid 554-1		1.03 ±0.09	1.28 ±0.26	0.94 ±0.03
Unknown acid 554-2		1.15 ±0.19	1.33 ±0.42	0.86 ±0.38
Unknown acid 554-3		1.18 ±0.23	1.21 ±0.48	0.76 ±0.37
Unknown acid 554-4		1.31 ±0.29	1.29 ±0.41	**2.39 ±0.55*****
Unknown 670		**0.34 ±0.10*****	1.16 ±0.36	**1.60 ±0.39***
Isoprenoids				
β-Carotene	PL	**2.25 ±0.15****	**4.30 ±0.29****	**7.35 ±0.34*****
Lutein	PL	**1.83 ±0.08****	**3.43 ±0.10*****	**9.77 ±0.03*****
Lycopene	PL	**2.25 ±0.07*****	**2.97 ±0.09*****	**4.90 ±0.07*****
Neurosporene	PL	n/d	n/d	14.26 ±12.70
Neoxanthin	PL	n/d	n/d	n/d
Phytoene	PL	**2.44 ±0.06*****	**1.06 ±0.02***	**4.51 ±0.01*****
Phytofluene	PL	**3.54 ±0.28****	**1.68 ±0.08*****	**8.96 ±0.13*****
Violaxanthin	PL	1.19 ±1.0	2.05 ±1.79	**12.11 ±0.48*****
Chlorophyll a	PL	n/d	n/d	n/d
Chlorophyll b	PL	n/d	n/d	n/d
α-Tocopherol	PL	**2.47 ±0.85****	**3.07 ±1.34****	**11.41 ±4.04*****
Amyrin	CY	**3.21 ±0.69*****	**2.40 ±0.39*****	1.23 ±0.20
Campesterol	CY	1.69 ±0.03	**2.23 ±0.40*****	0.80 ±0.09
Cycloartenol	CY	1.16 ±0.20	0.96 ±0.19	0.49 ±0.09
Sitosterol	CY	1.42 ±0.21	1.20 ±0.20	**0.40 ±0.06*****
Stigmasterol	CY	1.45 ±0.12	**1.47 ±0.43***	**0.40 ±0.05*****
Phenylpropanoids				
5-Caffeoylquinic acid	CY	0.94 ±0.60	1.40 ±0.51	**3.51 ±0.71*****
Caffeoylquinic	CY			

chlorogenic acid	CY	**3.97 ±2.23***	**6.18 ±4.19***	**16.05 ±6.11*****
Naringenin	CY			
Naringenin-chalcone	CY	0.54 ±0.51	**0.26 ±0.13*****	**0.61 ±0.58***
Quercetin derivative 1	CY	**4.42 ±2.65***	**3.96 ±1.65****	**7.05 ±1.38*****
Quercetin derivative 2	CY	**6.31 ±5.80***	**3.78 ±2.76***	**17.23 ±5.03*****

Supplemental Table 3. Changes in relative metabolite levels found in *DET1* varieties during fruit development and ripening.

The data has been calculated from the relative change in a metabolite from mature green to ripe for all *DET1* varieties compared to their respective wild type (T56). Values are represented as means +/- SD. *P* values are shown as <0.001, 0.01 and 0.05 by ***, ** and * respectively. ~10.0 is an arbitrary unit representing an increase in a metabolite in one line while being absent in another. –indicates not determined, bold indicates a statistically significant increase. ND-not detected in one of the pairwise ratios. Abbreviations for the site of synthesis are MT-mitochondria, CY-cytosol, Pl-plastid and PE-peroxisomes.

Metabolite	Main site of synthesis	T56	2A11	TFM7	P119
Organic acids					
Ascorbic acid	CY	12.30 ±4.31	17.41 ±6.30	21.37 ±12.66	**80.54 ±33.43****
Citramalic	CY	10.94 ±2.63	9.05 ±1.85	**3.50 ±0.36*****	**3.65 ±0.65*****
Citric acid	MT	4.06 ±1.52	3.05 ±0.28	**1.38 ±0.33****	3.82 ±0.50
Dehydroascorbic acid	CY	3.46 ±2.64	0.92 ±0.50	1.57 ±.032	4.07 ±1.05
Fumaric acid	MT	0.46 ±0.05	**0.74 ±0.21***	**0.27 ±0.04*****	**0.79 ±0.20****
Galactonic acid	CY	1.51 ±0.24	**1.11 ±0.27***	1.20 ±0.29	1.48 ±0.40
Glucaric acid	CY	1.83 ±0.55	2.23 ±0.43	**0.93 ±0.24***	**3.21 ±0.44****
Gluconic acid	CY	0.78 ±0.12	0.87 ±0.11	0.62 ±0.15	**0.60 ±0.10***
Glycerate	CY	0.65 ±0.15	**0.35 ±0.04****	**0.23 ±0.04*****	**0.18 ±0.02*****
Glycolate	PL	0.31 ±0.12	**0.63 ±0.20****	0.37 ±0.08	**0.55 ±0.06****
Lactic acid	CY	0.50 ±0.12	0.55 ±0.19	**0.29 ±0.05****	0.49 ±0.16
Malic acid	MT/CY	0.80 ±0.28	0.77 ±0.10	**0.34 ±0.02****	0.60 ±0.20
Oxalic acid	CY	0.66 ±0.27	1.13 ±0.52	0.74 ±0.41	**3.09 ±1.73***
Quinic acid	CY	1.31 ±0.27	**0.90 ±0.06****	1.04 ±0.13	**2.66 ±0.52*****
Succinic acid	MT	0.78 ±0.37	**1.24 ±0.18***	0.81 ±0.09	0.60 ±0.19
Tartaric acid	CY	3.31 ±0.76	2.66 ±0.33	**1.58 ±0.20****	2.72 ±0.37
Amino acids					
Alanine	PL	0.82 ±0.18	**1.95 ±0.52****	**3.42 ±1.34****	**5.78 ±1.77*****
B-alanine	CY	0.94 ±0.07	**1.07 ±0.08***	**0.36 ±0.05*****	**2.38 ±0.38*****
4-Aminobutyric acid	CY/PL	1.24 ±0.22	1.40 ±0.19	1.13 ±0.20	**1.89 ±0.20*****
Asparagine	CY	5.46 ±1.44	5.06 ±3.90	3.17 ±2.21	**33.03 ±25.77***
Aspartic acid	CY	3.25 ±1.06	4.32 ±1.02	2.88 ±1.37	**22.81 ±5.01*****
Cysteine	PL	2.92 ±0.74	**27.03 ±14.72****	**0.68 ±0.38*****	**8.50 ±1.68*****
Glutamic acid	PL/CY	40.17 ±22.55	44.27 ±23.25	30.36 ±8.28	62.54 ±31.03
Glutamine	PL/CY	3.76 ±1.69	4.56 ±3.76	**1.02 ±0.78****	**43.29 ±31.03***
Glycine	CY(PE)	0.92 ±0.08	**1.27 ±0.28***	**0.48 ±0.05*****	**3.59 ±1.26****
Leucine	PL	1.09 ±0.11	1.07 ±0.64	**0.41 ±0.09*****	**6.34 ±1.52*****
Lysine	PL	1.45 ±0.17	**1.12 ±0.18***	**0.95 ±0.28***	**0.85 ±0.23****
5-Oxo-proline	CY	2.30 ±0.45	**4.59 ±1.71***	2.69 ±1.28	**12.68 ±4.56****
Serine	MT	0.89 ±0.09	1.17 ±0.38	**0.29 ±0.07*****	**2.00 ±0.68****
Threonine	PL	1.49 ±0.16	2.06 ±1.29	**0.81 ±0.19*****	**9.22 ±2.71*****
Valine	PL	0.70 ±0.07	0.79 ±0.36	**0.26 ±0.04*****	**2.49 ±0.43*****
Fatty acids					
Linoleic acid	CY	0.20 ±0.06	0.42 ±0.28	**0.43 ±0.14****	**0.71 ±0.26***
Oleic acid	CY	0.33 ±0.27	0.73 ±0.60	0.29 ±0.11	**1.15 ±0.26*****
Palmitic acid	PL	0.38 ±0.13	**0.66 ±0.11****	0.43 ±0.12	**1.15 ±0.19*****
Stearic acid	CY	0.12 ±0.05	**0.31 ±0.12****	0.11 ±0.06	**0.97 ±0.22*****
Sugars					

Arabinose	CY	3.29 ±1.84	2.33 ±0.68	1.46 ±0.49	2.21 ±0.41
Fructose	CY	0.61 ±0.12	**0.93 ±0.19****	0.54 ±0.15	**0.47 ±0.08***
Gentiobiose	CY	2.43 ±0.35	**6.67 ±2.96***	1.90 ±1.14	**4.88 ±0.42*****
Glucose	CY/PL	1.02 ±0.18	**0.73 ±0.17***	**0.73 ±0.12***	1.02 ±0.50
Maltose	PL	1.25 ±0.83	**6.12 ±3.27****	1.83 ±1.12	**6.66 ±1.69*****
Melizitose	CY	0.83 ±0.60	1.65 ±0.91	**1.64 ±0.13***	**2.30 ±0.50****
Rhamnose	CY	0.30 ±0.73	**1.74 ±0.44****	0.001 ±0.0007	**3.55 ±0.90*****
Ribose	CY	6.72 ±3.09	5.14 ±3.88	4.27 ±3.35	4.22 ±3.36
Sucrose	CY	0.22 ±0.03	0.35 ±0.14	**3.57 ±0.10*****	0.30 ±0.15
Sugar - similar fructose		0.60 ±0.13	**0.96 ±0.28***	0.52 ±0.16	**0.43 ±0.08***
Xylose	CY/PL	4.19 ±0.35	**2.97 ±0.55****	**2.87 ±0.62****	**5.57 ±0.68****
Polyols					
Erythritol	PL	1.20 ±0.19	1.12 ±0.18	1.08 ±0.08	**1.63 ±0.21****
Glycerol	CY/PL	1.41 ±0.28	1.70 ±0.27	**0.49 ±0.04*****	**1.01 ±0.13****
Inositol	CY	0.63 ±0.15	0.75 ±0.16	0.78 ±0.16	**1.47 ±0.21*****
Mannitol	CY	0.89 ±0.58	0.32 ±0.06	1.17 ±0.56	**2.07 ±0.32****
Phosphates					
Fructose-6-phosphate	PL/CY	0.97 ±0.34	1.25 ±0.40	1.05 ±0.27	**1.87 ±0.35****
Glucose-6-phosphate	PL/CY	1.39 ±0.28	**2.89 ±0.45****	2.12 ±0.97	**4.28 ±1.00****
Glycerol-3-phosphate	CY	0.87 ±0.11	**0.71 ±0.04****	**0.47 ±0.10*****	**1.09 ±0.21***
Inositol-6-phosphate	CY	1.16 ±0.29	**1.82 ±0.34****	1.18 ±0.25	**3.56 ±1.38****
Phosphate		1.13 ±0.11	1.30 ±0.16	1.15 ±0.05	**1.44 ±0.17****
Sedoheptulose phosphate	PL	40.88 ±13.72	**15.31 ±4.41****	**22.57 ±9.81***	**4.29 ±2.31****
Sorbitol-6-phosphate	PL	0.50 ±0.16	0.78 ±0.33	0.69 ±0.23	**2.48 ±0.54*****
N-containing compounds					
Putrescine	CY	14.33 ±1.38	**8.29 ±1.20*****	**5.74 ±0.94*****	**19.35 ±2.71****
Known unknowns					
Unknown acid (like galacturonic)		1.23 ±0.20	1.09 ±0.16	1.09 ±0.10	1.65 ±0.37
Unknown 15		0.10 ±0.04	0.13 ±0.03	0.11 ±0.02	**0.20 ±0.02****
Unknown 305		0.01 ±0.02	**55.88 ±18.39***	0.001 ±0.0001	**0.39 ±0.07*****
Unknown acid 554-1		7.52 ±1.81	6.14 ±0.57	**12.44 ±2.55****	**2.43 ±0.10****
Unknown acid 554-2		14.27 ±2.92	**8.01 ±1.36****	10.54 ±3.33	**1.48 ±0.66*****
Unknown acid 554-3		11.47 ±2.57	**7.53 ±1.49***	9.59 ±3.82	**1.23 ±0.60*****
Unknown acid 554-4		1.20 ±0.34	0.97 ±0.22	1.08 ±0.35	1.28 ±0.30
Isoprenoids					
β-Carotene	PL	49.77 ±1.32	46.45 ±3.20	**29.17 ±2.03*****	**41.44 ±1.95****
Lutein	PL	1.76 ±0.01	**1.33 ±0.06****	**0.89 ±0.02*****	**2.02 ±0.01*****
Violaxanthin	PL	1.02 ±0.06	0.59 ±0.13	**0.34 ±0.02*****	**1.37 ±0.05****
α-Tocopherol	PL	7.65 ±0.68	9.91 ±3.43	10.98 ±4.79	**26.75 ±9.46****
Amyrin	CY	1.26 ±0.53	**2.34 ±0.50****	1.06 ±0.17	**0.61 ±0.10***
Campesterol	CY	2.12 ±0.55	2.01 ±0.66	1.91 ±0.34	**0.89 ±0.11****
Cycloartenol	CY	1.01 ±0.07	**0.68 ±0.12*****	**0.53 ±0.10*****	**0.16 ±0.02*****
Sitosterol	CY	0.85 ±0.16	0.98 ±0.14	0.74 ±0.21	**0.27 ±0.04*****
Stigmasterol	CY	2.58 ±0.22	**2.13 ±0.19****	**1.83 ±0.54****	**0.88 ±0.11*****
Phenylpropanoids					
Caffeoylquinic	CY	0.17 ±0.004	**0.04 ±0.02*****	**0.05 ±0.02*****	0.19 ±0.05
Quercetin derivative 1	CY	1.51 ±0.55	**0.57 ±0.34****	**0.54 ±0.22****	1.99 ±0.39
Quercetin derivative 2	CY	0.88 ±0.50	**0.14 ±0.13****	**0.17 ±0.13****	**1.63 ±0.47***

Supplemental Table 4. Overview of global changes in the transcript levels in the P119 and TFM7 varieties during ripening.

Only IDs corresponding to a unique transcript and giving a significant signal relative to background (pVal 0.05) were included in the analysis. Total numbers of transcripts statistically qualifying for analysis are indicated (genes). Misregulated genes correspond to a minimum of 2-fold change ratio (up- or down) as compared to wild-type T56.

P119	**Mature Green**	**Breaker**	**Red Ripe**
Transcipts	2586	1275	1166
Up-regulated	(22.1%)	(30.4%)	(11.7%)
Down-regulated	(3.8%)	(0%)	(2.1%)
Total misregulated	(26.0%)	(30.4%)	(13.8%)
TFM7	**Mature Green**	**Breaker**	**Red Ripe**
Transcripts	2731	3013	2756
Up-regulated	(13.9%)	(10.8 %)	(5.3 %)
Down-regulated	(5.2%)	(9.6 %)	(4.6 %)
Total misregulated	(19.2%)	(20.5 %)	(9.9 %)

Supplemental Table 5. Hierarchy of pathways significantly affected in P119 (A) and TFM7 (B) *DET1* varieties.

The 10 most affected pathways at the mature green, breaker and red ripe developmental stages are listed and ranked as sorted using Plant MetGenMap web-based analysis (www. http://bioinfo.bti.cornell.edu/cgi-bin/MetGenMAP/home.cgi). For each transcriptome analysis, the plate IDs available for the entire set of transcripts data with pVal<0.05 has been utilized. The software uses hyper geometric test to check the significance of pathway changes, performed on a set of pathways simultaneously using pValues that correspond to raw p values corrected by False Discovery Rate (FDR). ns, not significantly affected or not determined.

A

P119	Mature Green		Breaker		Red Ripe	
Rank	**Pathway**	**pVal**	**Pathway**	**pVal**	**Pathway**	**pVal**
1	**Calvin cycle**	5.1E-12	**Calvin cycle**	1.1E-10	**gluconeogenesis**	1.4E-03
2	**photorespiration**	1.2E-08	**photorespiration**	2.6E-10	**glycolysis I and IV (plant cytosol)**	1.4E-03
3	**gluconeogenesis**	5.9E-05	**gluconeogenesis**	1.3E-06	**superpathway of glycolysis and TCA variant VIII**	1.4E-03
4	**xylulose-monophosphate cycle**	3.3E-04	**fructose degradation to pyruvate and lactate**	1.4E-06	**superpathway of glycolysis, pyruvate dehydrogenase, TCA, and glyoxylate bypass**	1.4E-03
5	**superpathway of glycolysis+Entner-Doudoroff**	2.5E-03	**superpathway of glycolysis+Entner-Doudoroff**	9.4E-06	**Calvin cycle**	1.4E-03
6	**xanthophyll cycle**	7.0E-03	**carotenoid biosynthesis**	1.8E-05	**fructose degradation to pyruvate and lactate**	1.6E-03
7	**glycolysis I**	8.3E-03	**sucrose degradation to ethanol and lactate**	3.1E-05	**superpathway of glycolysis+Entner-Doudoroff**	1.6E-03
8	**fructose degradation to pyruvate and lactate**	8.3E-03	**glycolysis I and IV (plant cytosol)**	5.8E-05	**photorespiration**	1.6E-03
9	**carotenoid biosynthesis**	8.3E-03	**glucose heterofermentation to lactate I**	2.5E-04	**phenylpropanoid biosynthesis, initial reactions**	1.9E-03
10	**chlorophyllide a biosynthesis**	9.3E-03	**xylulose-monophosphate cycle**	3.8E-04	**salicylic acid biosynthesis**	1.9E-03

B

TFM7	Mature Green		Breaker		Red Ripe	
Rank	**Pathway**	**pVal**	**Pathway**	**pVal**	**Pathway**	**pVal**
1	**chlorophyllide a biosynthesis**	6.6E-04	**Calvin cycle**	3.4E-04	**sucrose degradation I**	2.5E-04
2	**tRNA charging pathway**	6.6E-04	**tRNA charging pathway**	3.4E-04	**GDP-mannose metabolism**	2.4E-03
3	**lipoxygenase pathway**	3.7E-02	**photorespiration**	2.2E-03	**colanic acid building blocks biosynthesis**	4.8E-03
4	**jasmonic acid biosynthesis**	3.7E-02	**gluconeogenesis**	5.4E-03	**lipoxygenase pathway**	7.1E-03
5			**xylulose-monophosphate cycle**	5.4E-03	**jasmonic acid biosynthesis**	9.4E-03
6			**chlorophyllide a biosynthesis**	1.3E-02	**ascorbate biosynthesis**	3.3E-02
7			**fructose degradation to pyruvate and lactate**	2.2E-02	**mannose degradation**	3.3E-02
8			**sucrose degradation to ethanol and lactate**	2.8E-02	**superpathway of polyamine biosynthesis II**	3.3E-02
9			**glycosylglyceride biosynthesis**	2.8E-02	**spermidine biosynthesis**	3.3E-02
10					**triacylglycerol degradation**	3.3E-02

Supplemental Table 6. Sequences of primers used in real-time RT-PCR and PCR. *PAL*-phenylalanine ammonia lyase, *CHS*-chalcone synthase, *CHI*-chalcone isomerise, *F3H*-flavanone-3-hydroxylase, *F3'H*-flavonoid-3'-hydroxylase, *F3'5'H*-flavonoid-3'5'-hydroxylase, *FLS*-flavonol synthase, *DFR*-dihydroflavonol reductase, *ANS*-anthocyanidin synthase, 3-*GT*-flavonol-3-glucosyltransferase, *RT*-flavonol-3-glucoside. *DXS*-1-deoxy-D-xylulose-5-pyrophosphate synthase, 2. *GGPPS*-1-geranylgeranyl pyrophosphate synthase-1, 3. *GGPPS*-2- geranylgeranyl pyrophosphate synthase-2, 4. *PSY*-1- phytoene synthase-1, 5. *PSY*-2-phytoene synthase-2, 6. *PDS*-phytoene desaturase, 7. *ZDS*-ζ–carotene desaturase, 8. *CRTISO*-carotene isomerase, 9. *CYC-B*-β-lycopene cyclase, 10. *LCY-B*-β-lycopene cyclase, 11. *LCY-E*-ε-lycopene cyclase, 12. *GGPPR*-geranylgeranyl pyrophosphate reductase, 13. *GMTT-g*-methyl tocopherol transferase, *rbcL*-large subunit of rubisco.

Gene ID	Accession numbers or Reference	Primer sequences	
		Forward	Reverse
PAL	M83314	ATTGGGAAATGGCTGCTGATT	TCAACATTTGCAATGGATGCA
CHS	X55194	TGGTCACCGTGGAGGAGTATC	GATCGTAGCTGGACCCTCTGC
CHI	TC198728	GTTTTTCACAAACCAACAGTTCTGAT	GAAGCAGTGCTCGATTCCATAAT
F3H	TC171483	CACACCGATCCAGGAACCAAT	GCCCACCAACTTGGTCTTGTA
F3'H	TC175149	GCACCACGAATGCACTTGC	CGTTAGTACCGTCGGCGAAT
F3'5'H	Luo et al., 2008	GGCAATTGGACGAGATCCTG	AAGGAACCTCTCGGGAGTGAA
FLS	TC172800	GAGCATGAAGTTGGGCCAAT	TGGTGGGTTGGCCTCATTAA
DFR	Luo et al., 2008	TCCGAAGACGACAACGGTTT	TGACAAGCCAAGAGCCGATAA
ANS	Luo et al., 2008	GAACTAGCACTTGGCGTCGAA	TTGCAAGCCAGGCACCATA
3-*GT*	TC1766549	CGAACGACGAAACACTGTTGA	TGCAGCATAGATGGCATTGG
RT	TC1952951	CTGGCAATGCAAACAGAGTGA	TCGACTTGCGGAAGAGTGAGA
rbcL	AF479571	CTGCAGGTACATGCGAAGAA	TTGCTAATACCCGGAAGTGG
DXS	AF143812	GCGGAGCTATTTCACATGGT	CTGCTGAGCATCCCAAT
GGPP-1	DQ267902	GACAGCATCTGAGTCCGTCA	CTTGGCCAGGACAGAGTAGC
GGPP-2	SGN-U223568	GGGATTGGAAAAGGCTAAGG	AGCAATCAATGGAGCAGCTT
PSY-1	Y00521	TGGCCCAAACGCATCATATA	CACCATCGAGCATGTCAAATG
PSY-2	L23424	GTTGATGGCCCTAATGCATCA	TCAAGCATATCAAATGGCCG
PDS	X59948	GTGCATTTTGATCATCGCATTGAAC	GCAAAGTCTCTCAGGATTACC
PDSG	X78271	CTAGGTTCTTGCTGCCTTGC	CCAACTTTTTGGCAATGCTT
ZDS	AF195507	TTGGAGCGTTCGAGGCAA T	AGAAATCTGCATCTGGCGTATAGA
CRTISO	AF416727	TTTTGGCGGAATCAACTACC	GAAAGCTTCACTCCCACAGC
LCY-B	AF254793	TCGTTGGAATCGGTGGTACAG	AGCTAGTGT CCTTGCCACCAT
CYC-B	Y18297	TGTTATTGAGGAAGAGAAATGTGTGAT	TCCCACCAATAGCCATAACATTTT
LCY-E	Y14387	AACACTTGCATTTGGTGCTG	AGTACAGAGGCGCATTTTGG
Actin	BT013524	AGGTATTGTGTTGGACTCTGGTGAT	ACGGAGAATGGCATGTGGAA
GGPPR	SGN-U564570	AGACTGAGAGCCCATTCCAA	CATCCCCAACTAATGCGACT
GMTT	SGN-U584511	GCAATTCGACTTGGTTTGGT	AAGGATGATTGTGCGTCC