## SI Materials

**Tomato fruit and treatment.** Tomato Ailsa Craig, FLA 8059, Pearson and *Nr* mutant were grown in a heated greenhouse on the University of Florida campus. In order to evaluate the effect of cold storage on fruit flavor quality, fruit of Ailsa Craig and FLA 8059 were harvested at full-red ripe stage from 12 plants, followed by storage at 5$^{o}$ with 92% relative humidity for 1, 3, 7 or 8 days followed by with or without recovery at ambient temperature. To test whether ethylene is associated with volatile production during tomato fruit ripening, Pearson and *Nr* mutant were harvested at 59 days after pollination (DAP) to 67 DAP with one or two day intervals.

## Reference cited

Fujisawa M, Nakano T, Shima Y. Ito Y (2013) A large-scale identification of direct targets of the tomato MADS box transcription factor RIPENING INHIBITOR reveals the regulation of fruit ripening. *Plant Cell* 25(2):371-386.

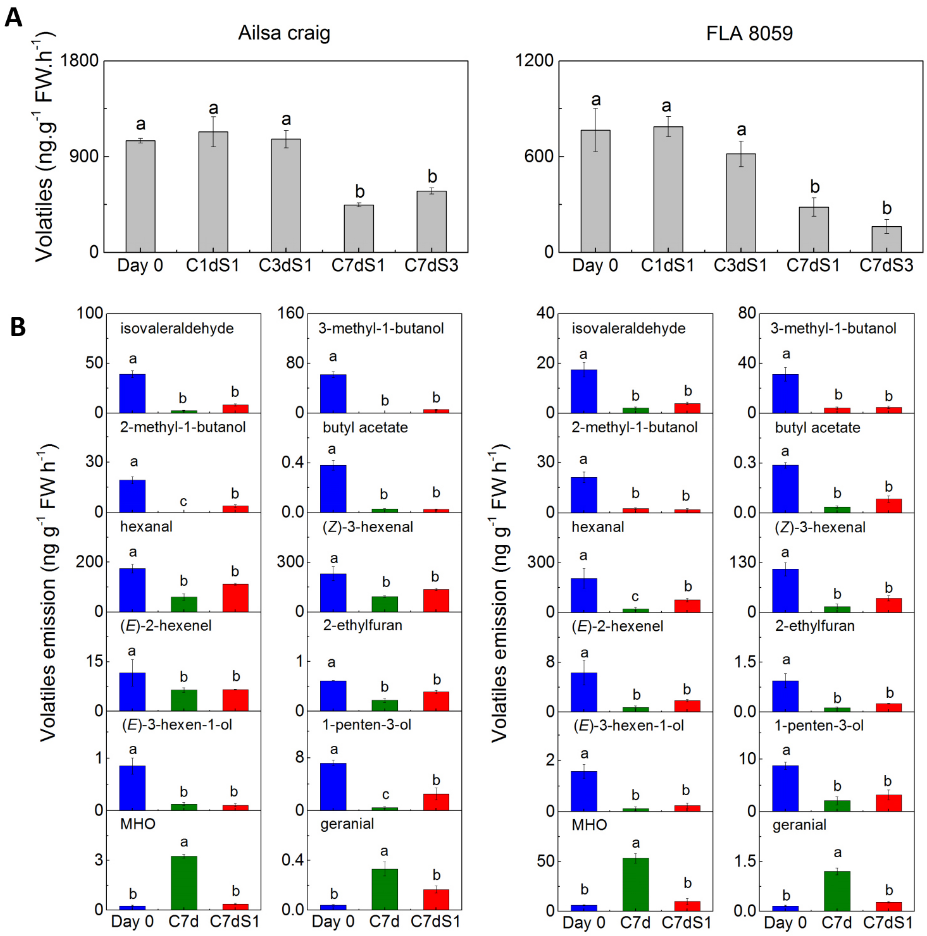

**Figure S1.** Tomato fruit (Ailsa Craig and FLA 8059) volatile content in response to cold storage and subsequent storage at 20$^{o}$. (A) Effect of cold storage time on volatile emissions. (B) Volatiles significantly influenced by cold storage. Blue bar (Day 0), red ripe fruit at harvest; Green bar (C8d), fruit following 8 days of cold storage; Red bar (C7dS1), fruit stored in the cold for 7 days followed by a one day recovery at 20$^{o}$. Significant differences ($P$ <0.05) are denoted by different letters. Error bars indicate means ± SE; three biological replicates.

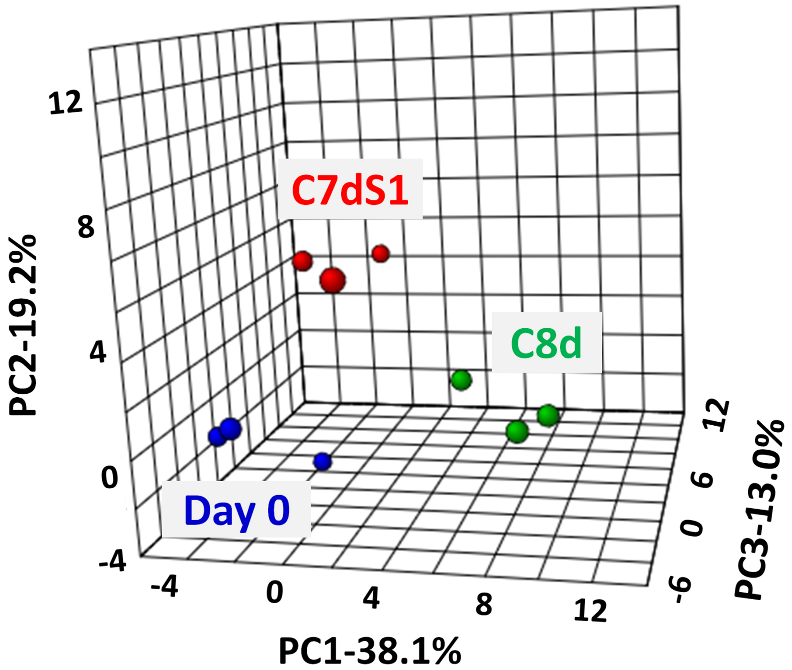

**Figure S2.** Principal component analysis of volatiles in response cold storage of Ailsa Craig tomato fruit. Volatiles produced by three biological replicates were used as variables. Blue dots represent Day 0, full red ripe tomato fruit at harvest; Green dots represent C8d, fruit following 8 days of cold storage; Red dots represent C7dS1, fruit stored in the cold for 7 days followed by a one day recovery at 20$^{o}$.

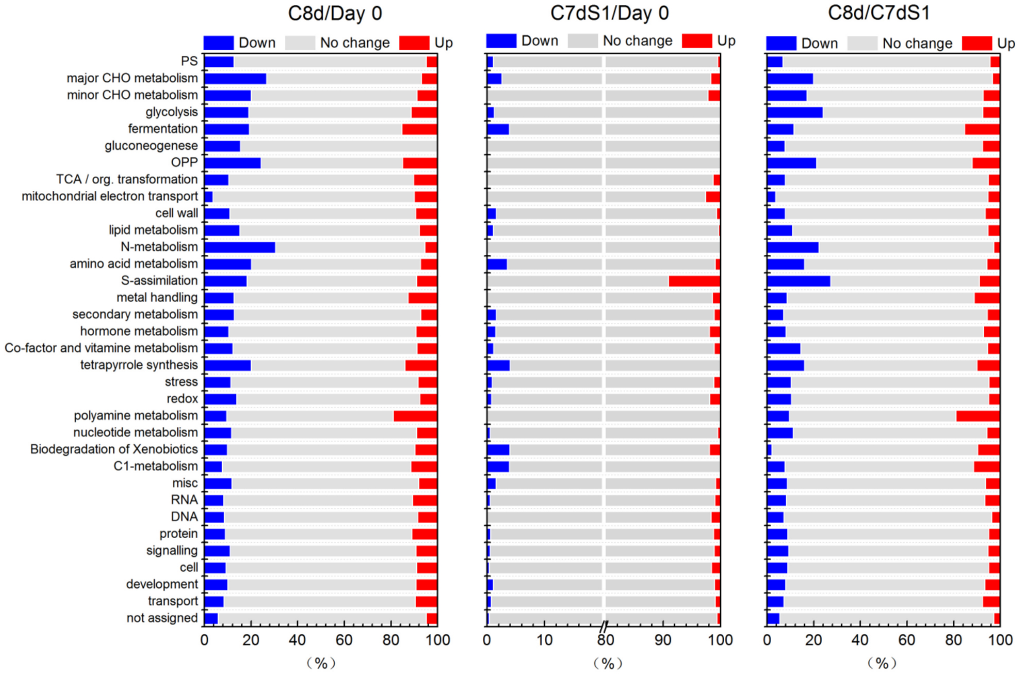

**Figure S3.** Quantitative patterns of differentially expressed genes (DEGs) belonging to specific functional categories defined by MapMan BINs. Day 0, red ripe fruit at harvest; C8d, fruit following 8 days of cold storage; C7dS1, fruit stored in the cold for 7 days followed by a one day recovery at 20°. Red BINs are significantly up-regulated, gray BINs are not significantly changed, blue BINs are down-regulated.

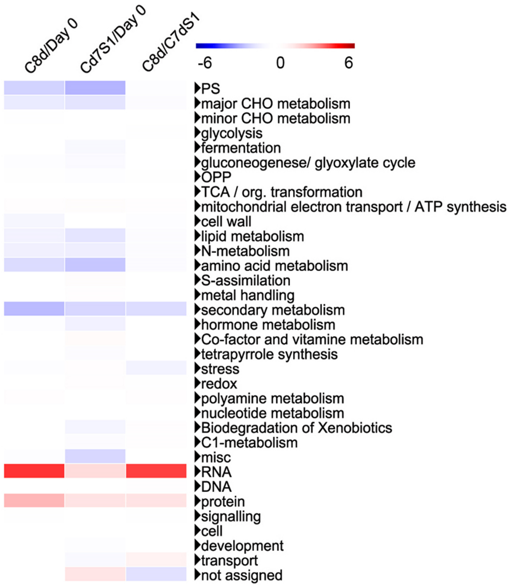

**Figure S4.** PageMan display of coordinated differentially expressed genes (DEGs) belonging to specific BINs. Red BINs are significantly up-regulated, whereas blue BINs are down-regulated. Day 0, full red ripe tomato fruit at harvest; C8d, fruit following 8 days of cold storage; C7dS1, fruit stored in the cold for 7 days followed by a one day recovery at 20$^{o}$.

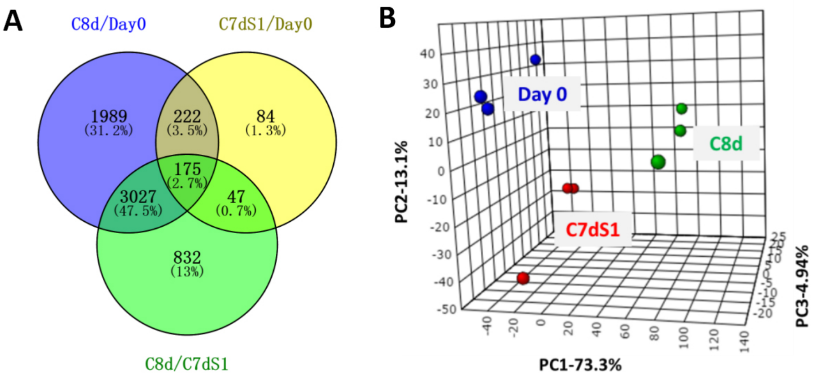

**Figure S5.** Transcriptional analysis of Ailsa Craig tomato fruit in response to cold storage. (A), Venn diagram representing differentially expressed genes (DEGs) by RNA-Seq analysis. Day 0, full red ripe tomato fruit at harvest; C8d, fruit following 8 days of cold storage; C7dS1, fruit stored in the cold for 7 days followed by a one day recovery at 20°. The number in brackets represents percentage of gene number in each pair compared to total detected transcripts. (B), Principal component analysis of DEGs using RPKM as variables. Principal component 1 (PC1), PC2 and PC3 accounted for 73.3%, 13.1% and 4.9% of the variation, respectively. Results were from three replicates.

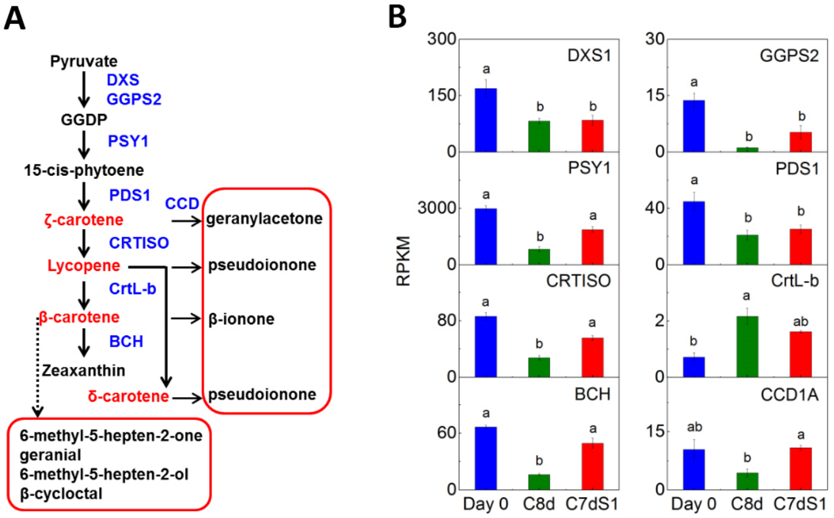

**Figure S6.** Effect of cold storage on transcripts of genes involved in carotenoid biosynthesis in Ailsa Craig tomato fruit. (A), Summary of the carotenoid biosynthesis pathway. (B), Transcript levels of carotenoid biosynthetic genes. Blue bar represents Day 0, full red ripe tomato fruit at harvest; Green bar represents C8d, fruit following 8 days of cold storage; Red bar represents C7dS1, fruit stored in the cold for 7 days followed by a one day recovery at 20°. Significant differences (FDR <0.05) are denoted by different letters. Error bars indicate means ± SE; three biological replicates.

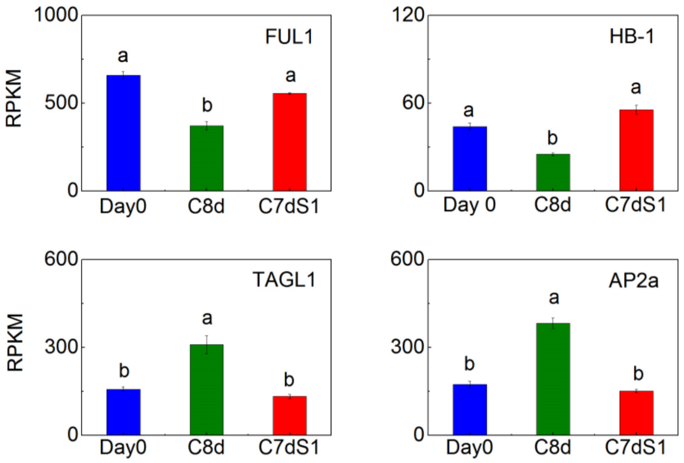

**Figure S7.** Expression of ripening related transcript factors FUL1, HB-1, TAGL1 and AP2a of Ailsa Craig tomato fruit in response to chilling. Blue bar represents Day 0, full red ripe tomato fruit at harvest; Green bar represents C8d, fruit following 8 days of cold storage; Red bar represents C7dS1, fruit stored in the cold for 7 days followed by a one day recovery at 20$^{o}$. Significant differences (FDR < 0.05) are denoted by different letters. Error bars indicate means ± SE; three biological replicates.

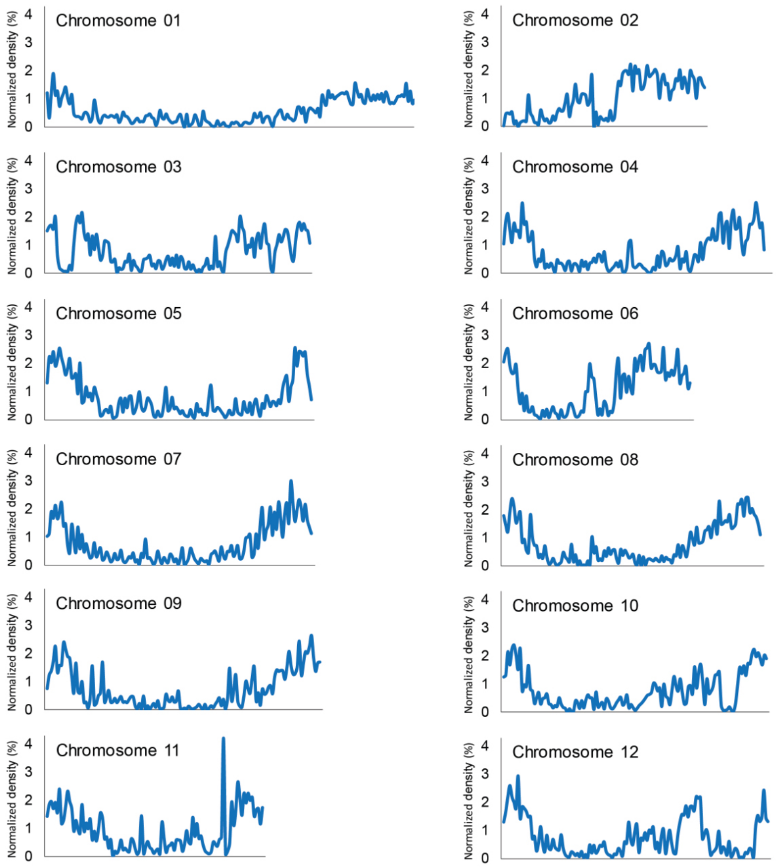

**Figure S8.** Distribution of differentially methylated regions (DMRs) in Ailsa Craig tomato fruit chromosomes in response to cold storage.

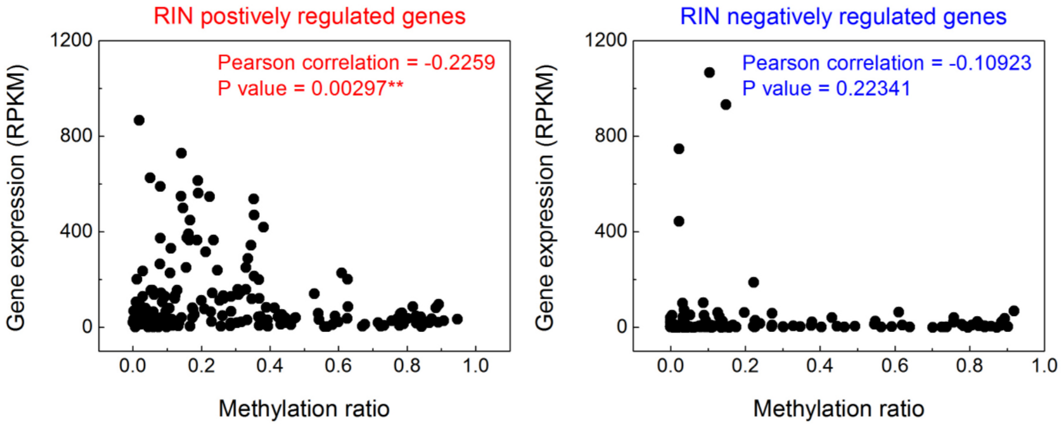

**Figure S9.** Correlation of RIN target genes methylation level with RPKM values of Ailsa Craig tomato fruit in response to cold storage. RIN positively and negatively regulated genes were based on (1).

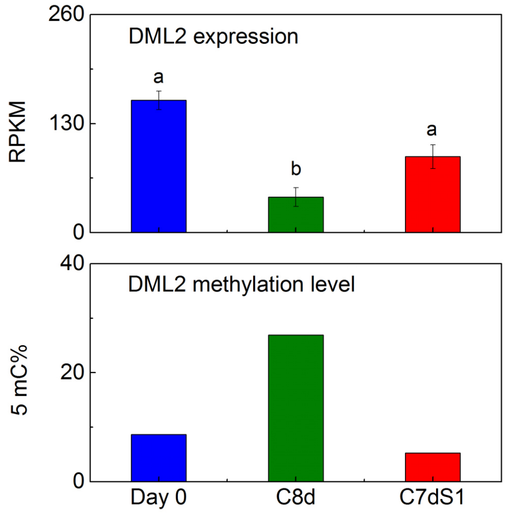

**Figure S10.** Expression and methylation level of *DML2* in response to chilling of Ailsa Craig tomato fruit. Blue bar represents Day 0, full red ripe tomato fruit at harvest; Green bar represents C8d, fruit following 8 days of cold storage; Red bar represents C7dS1, fruit stored in the cold for 7 days followed by a one day recovery at 20$^{o}$. Significant differences (FDR<0.05) are denoted by different letters. Error bars indicate means ± SE; three biological replicates.

**Table S1** Content of Alisa Craig tomato fruit volatiles in response to cold storage

| Volatiles (ng.g$^{-1}$ FW h$^{-1}$) | Day 0 | C8d | C7dS1 | Precursors |
|---|---|---|---|---|
| isovaleraldehyde | 16.56 ± 2.20a | 2.1 ± 0.44 b | 3.58 ± 0.53 b | leucine |
| 3-methyl-2-butenal | 0.01 ± 0.01 | 0.01 ± 0.01 | 0.01 ± 0.01 | leucine |
| isovaleric acid | 0.28 ± 0.14 | 0.23 ± 0.02 | 0.22 ± 0.18 | leucine |
| 2-isobutylthiazole | 2.36 ± 0.66 a | 2.53 ± 0.54 a | 0.47 ± 0.15 b | leucine |
| 2-methylbuteraldehyde | 4.01 ± 0.39 | 3.41 ± 1.87 | 3 ± 0.15 | isoleucine |
| isovaleronitrile | 17.81 ± 1.93 a | 10.99 ± 2.66 a | 5.10 ± 1.42 b | isoleucine |
| 3-methyl-1-butanol | 69.49 ± 3.66 a | 6.45 ± 4.18 b | 18.3 ± 5.24 b | isoleucine |
| 2-methyl-1-butanol | 25.42 ± 1.77 a | 2.89 ± 1.41 c | 13.52 ± 3.52 b | isoleucine |
| 2-methyl-2-butenal | 11.32 ± 1.32 a | 5.45 ± 0.73 b | 15.65 ± 2.97 a | isoleucine |
| 1-nitro-3-methylbutane | 15.78 ± 2.62 a | 10.82 ± 2.00 a | 2.60 ± 0.64 b | isoleucine |
| butyl acetate | 0.12 ± 0.02 a | 0.03 ± 0.01 b | 0.06 ± 0.02 b | valine |
| sec-butyl acetate | 0.02 ± 0.01 | 0.02 ± 0.01 | 0.02 ± 0.02 | valine |
| isobutyl acetate | 0.92 ± 0.14 | 0.28 ± 0.04 | 0.82 ± 0.30 | valine |
| 2-methylbutyl acetate | 0.70 ± 0.28 | 0.16 ± 0.05 | 0.59 ± 0.23 | valine |
| phenylacetaldehyde | 0.04 ± 0.03 b | 0.17 ± 0.02 a | 0.09 ± 0.04 b | phenylalanine |
| 2-phenyl ethanol | 0.02 ± 0.01 | 0.02 ± 0.01 | 0.02 ± 0.01 | phenylalanine |
| benzyl cyanide | 0.03 ± 0.01 | 0.05 ± 0.01 | 0.03 ± 0.01 | phenylalanine |
| 1-nitro-2-phenylethane | 0.02 ± 0.02 b | 0.04 ± 0.01 a | 0.02 ± 0.01 b | phenylpropanoid |
| guaiacol | 2.01 ± 0.49 | 2.24 ± 0.20 | 2.06 ± 0.47 | phenylpropanoid |
| benzaldehyde | 1.49 ± 0.52 | 1.77 ± 0.39 | 0.68 ± 0.10 | phenylpropanoid |
| benzyl alcohol | 0.25 ± 0.03 | 0.35 ± 0.14 | 0.07 ± 0.02 | phenylpropanoid |
| salicylaldehyde | 0.73 ± 0.14 b | 1.38 ± 0.11 a | 0.94 ± 0.24 b | phenylpropanoid |
| methylsalicylate | 0.08 ± 0.02 b | 0.35 ± 0.06 a | 0.18 ± 0.05 a | phenylpropanoid |
| benzothiazole | 0.13 ± 0.07 | 0.18 ± 0.04 | 0.10 ± 0.03 | phenylpropanoid |
| eugenol | 0.03 ± 0.01 b | 0.13 ± 0.03 a | 0.02 ± 0.01 b | phenylpropanoid |
| p-anisaldehyde | 0.01 ± 0.01 | 0.01 ± 0.01 | 0.01 ± 0.01 | phenylpropanoid |
| 1-penten-3-ol | 10.76 ± 0.30 a | 6.48 ± 0.85 b | 9.65 ± 0.79 a | lipid |
| ethyl vinyl ketone | 8.87 ± 1.53 | 10.33 ± 0.79 | 10.94 ± 0.64 | lipid |
| 3-pentanone | 16.89 ± 1.26 | 18.2 ± 1.71 | 20.16 ± 0.98 | lipid |
| (*E*)-2-pentenal | 5.86 ± 0.64 a | 4.29 ± 0.76 b | 6.45 ± 0.26 a | lipid |
| 1-pentanol | 8.01 ± 0.85 | 6.94 ± 1.46 | 9.94 ± 0.36 | lipid |
| (Z)-2-penten-1-ol | 1.99 ± 0.24 a | 0.68 ± 0.09 b | 1.72 ± 0.30 a | lipid |
| (Z)-3-hexenal | 91.96 ± 17.22 a | 24.37 ± 4.30 b | 30.89 ± 7.60 b | lipid |
| hexanal | 106.74 ± 17.05 a | 35.71 ± 0.35 b | 39.6 ± 4.40 b | lipid |
| (E)-3-hexen-1-ol | 0.38 ± 0.13 a | 0.05 ± 0.02 b | 0.15 ± 0.06 ab | lipid |
| (E)-2-hexenal | 12.85 ± 3.54 a | 4.22 ± 0.77 b | 5.91 ± 0.50 b | lipid |
| (Z)-3-hexen-1-ol | 80.36 ± 11.75 a | 37.46 ± 5.92 b | 71.53 ± 14.39a | lipid |
| hexyl alcohol | 15.05 ± 3.05 a | 5.72 ± 1.57 b | 11.87 ± 2.18 a | lipid |
| propyl acetate | 0.66 ± 0.06 | 0.34 ± 0.01 | 1.42 ± 0.22 | lipid |
| isopentyl acetate | 0.37 ± 0.25 | 0.01 ± 0.01 | 0.12 ± 0.10 | lipid |
| (Z)-3-hexenyl acetate | 1.87 ± 0.34 | 1.62 ± 0.23 | 1.89 ± 0.56 | lipid |

|  |  |  |  |  |
|---|---|---|---|---|
| hexyl acetate | 0.10 ± 0.04 | 0.16 ± 0.03 | 0.19 ± 0.07 | lipid |
| heptaldehyde | 2.76 ± 0.59 | 2.31 ± 0.74 | 1.3 ± 0.48 | lipid |
| (E)-2-heptenal | 1.25 ± 0.37 | 1.14 ± 0.47 | 1.22 ± 0.10 | lipid |
| 1-octen-3-one | 0.12 ± 0.04 | 0.09 ± 0.01 | 0.1 ± 0.02 | lipid |
| 3-methyl-1-pentanol | 0.09 ± 0.04 | 0.02 ± 0.01 | 0.02 ± 0.01 | lipid |
| nonyl aldehyde | 0.32 ± 0.14 | 0.19 ± 0.04 | 0.46 ± 0.14 | lipid |
| (E),(E)-2,4-decadienal | 0.07 ± 0.02 | 0.15 ± 0.06 | 0.10 ± 0.01 | lipid |
| n-decyl aldehyde | 0.07 ± 0.01 | 0.14 ± 0.03 | 0.16 ± 0.05 | lipid |
| (Z)-4-decenal | 1.46 ± 0.31 | 2.22 ± 0.43 | 1.64 ± 0.35 | lipid |
| 6-methyl-5-hepten-2-one | 2.51 ± 0.61 b | 5.93 ± 0.99 a | 2.32 ± 0.34 b | open chain carotenoid lycopene |
| 6-methyl-5-hepten-2-ol | 0.01 ± 0.01 | 0.01 ± 0.01 | 0.02 ± 0.01 | open chain carotenoid lycopene |
| neral | 0.25 ± 0.14 | 0.47 ± 0.17 | 0.22 ± 0.08 | open chain carotenoid lycopene |
| geranial | 0.14 ± 0.05 b | 0.33 ± 0.07 a | 0.15 ± 0.04 b | open chain carotenoid lycopene |
| geranylacetone | 0.97 ± 0.41 | 1.54 ± 0.47 | 0.74 ± 0.14 | open chain carotenoid lycopene |
| farnesyl acetone | 0.01 ± 0.01 | ud | 0.01 ± 0.01 | open chain carotenoid lycopene |
| pseudoionone 1 | 0.01 ± 0.01 | 0.02 ± 0.01 | 0.02 ± 0.01 | open chain carotenoid lycopene |
| pseudoionone 2 | 0.01 ± 0.01 | 0.01 ± 0.01 | 0.01 ± 0.01 | open chain carotenoid lycopene |
| β-cyclocitral | 0.15 ± 0.04 | 0.24 ± 0.05 | 0.16 ± 0.13 | cyclic carotenoid lycopene |
| β-damascenone | 0.01 ± 0.01 | 0.01 ± 0.01 | 0.01 ± 0.01 | cyclic carotenoid lycopene |
| β-ionone | 0.16 ± 0.05 | 0.12 ± 0.02 | 0.10 ± 0.01 | cyclic carotenoid lycopene |
| 2-ethylfuran | 0.31 ± 0.04 a | 0.18 ± 0.01 a | 0.15 ± 0.01 b | unknown |
| 2,5-dimethyl-4-hydroxy-3(2H)-furanone | 1.42 ± 0.36 | 2.21 ± 0.79 | 1.76 ± 0.23 | unknown |
| 4-carene | 0.02 ± 0.01 | 0.01 ± 0.01 | 0.01 ± 0.01 | unknown |
| prenyl acetate | 0.02 ± 0.01 | ud | 0.02 ± 0.01 | unknown |
| methional | 0.02 ± 0.01 | ud | 0.02 ± 0.01 | unknown |

Data are means of three biological replicates and standard errors. Ud, under detected limit. Significant differences (*P* <0.05) are denoted by different letters.

**Table S2** GO enrichment analysis of DEGs

| GO ID | Description | GO_term | P value |
|---|---|---|---|
| Group A | | | |
| GO:0008152 | metabolic process | biological_process | 1.42E-04 |
| GO:0000105 | histidine biosynthetic process | | 6.23E-03 |
| GO:0006006 | glucose metabolic process | | 7.93E-03 |
| GO:0005975 | carbohydrate metabolic process | | 2.07E-02 |
| GO:0006470 | protein dephosphorylation | | 2.11E-02 |
| GO:0009058 | biosynthetic process | | 2.41E-02 |
| GO:0006807 | nitrogen compound metabolic process | | 2.42E-02 |
| GO:0006631 | fatty acid metabolic process | | 2.73E-02 |
| GO:0006096 | glycolysis | | 2.75E-02 |
| GO:0006013 | mannose metabolic process | | 2.80E-02 |
| GO:0008610 | lipid biosynthetic process | | 3.02E-02 |
| GO:0016192 | vesicle-mediated transport | | 3.29E-02 |
| GO:0006633 | fatty acid biosynthetic process | | 3.84E-02 |
| GO:0055114 | oxidation-reduction process | | 3.85E-02 |
| GO:0006886 | intracellular protein transport | | 3.95E-02 |
| GO:0015937 | coenzyme A biosynthetic process | | 4.04E-02 |
| GO:0007165 | signal transduction | | 4.40E-02 |
| GO:0005945 | 6-phosphofructokinase complex | cellular_component | 1.04E-02 |
| GO:0031361 | integral to thylakoid membrane | | 1.74E-02 |
| GO:0005515 | protein binding | molecular_function | 1.78E-03 |
| GO:0000155 | two-component sensor activity | | 2.66E-03 |
| GO:0003824 | catalytic activity | | 7.37E-03 |
| GO:0003676 | nucleic acid binding | | 7.90E-03 |
| GO:0003910 | DNA ligase (ATP) activity | | 7.93E-03 |
| GO:0004345 | glucose-6-phosphate dehydrogenase activity | | 7.93E-03 |
| GO:0003872 | 6-phosphofructokinase activity | | 1.04E-02 |
| GO:0016638 | oxidoreductase activity, acting on the CH-NH2 group of donors | | 1.56E-02 |
| GO:0016773 | phosphotransferase activity, alcohol group as acceptor | | 1.58E-02 |
| GO:0004112 | cyclic-nucleotide phosphodiesterase activity | | 1.74E-02 |
| GO:0004096 | catalase activity | | 2.06E-02 |
| GO:0003968 | RNA-directed RNA polymerase activity | | 2.63E-02 |
| GO:0004484 | mRNA guanylyltransferase activity | | 2.80E-02 |
| GO:0004559 | alpha-mannosidase activity | | 2.80E-02 |
| GO:0008474 | palmitoyl-(protein) hydrolase activity | | 2.80E-02 |
| GO:0015923 | mannosidase activity | | 2.80E-02 |
| GO:0016491 | oxidoreductase activity | | 3.29E-02 |
| GO:0008168 | methyltransferase activity | | 3.35E-02 |
| GO:0004607 | phosphatidylcholine-sterol O-acyltransferase activity | | 4.01E-02 |

| | | | |
|---|---|---|---|
| GO:0008138 | protein tyrosine/serine/threonine phosphatase activity | | 4.25E-02 |
| GO:0008374 | O-acyltransferase activity | | 4.81E-02 |
| GO:0047800 | cysteamine dioxygenase activity | | 1.14E-02 |
| Group B | | | |
| GO:0042545 | cell wall modification | biological_process | 2.76E-03 |
| GO:0009607 | response to biotic stimulus | | 1.62E-02 |
| GO:0015936 | coenzyme A metabolic process | | 1.69E-02 |
| GO:0000160 | two-component signal transduction system (phosphorelay) | | 1.84E-02 |
| GO:0006508 | proteolysis | | 1.93E-02 |
| GO:0009081 | branched chain family amino acid metabolic process | | 2.36E-02 |
| GO:0005985 | sucrose metabolic process | | 3.36E-02 |
| GO:0006952 | defense response | | 3.41E-02 |
| GO:0006694 | steroid biosynthetic process | | 3.78E-02 |
| GO:0055114 | oxidation-reduction process | | 4.03E-02 |
| GO:0005618 | cell wall | cellular_component | 1.03E-02 |
| GO:0004857 | enzyme inhibitor activity | molecular_function | 2.61E-04 |
| GO:0004190 | aspartic-type endopeptidase activity | | 5.57E-04 |
| GO:0030599 | pectinesterase activity | | 1.04E-03 |
| GO:0016747 | transferase activity, transferring acyl groups other than amino-acyl groups | | 2.11E-03 |
| GO:0016702 | oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen | | 4.99E-03 |
| GO:0016616 | oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor | | 1.31E-02 |
| GO:0004420 | hydroxymethylglutaryl-CoA reductase (NADPH) activity | | 1.69E-02 |
| GO:0004084 | branched-chain-amino-acid transaminase activity | | 2.36E-02 |
| GO:0004315 | 3-oxoacyl-[acyl-carrier-protein] synthase activity | | 3.03E-02 |
| GO:0003854 | 3-beta-hydroxy-delta5-steroid dehydrogenase activity | | 3.41E-02 |
| GO:0016717 | oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water | | 4.02E-02 |
| Group C | | | |
| GO:0019752 | carboxylic acid metabolic process | biological_process | 7.78E-08 |
| GO:0006730 | one-carbon metabolic process | | 1.16E-04 |
| GO:0006633 | fatty acid biosynthetic process | | 7.81E-04 |
| GO:0005975 | carbohydrate metabolic process | | 5.60E-03 |
| GO:0055114 | oxidation-reduction process | | 1.18E-02 |
| GO:0009097 | isoleucine biosynthetic process | | 1.40E-02 |
| GO:0019318 | hexose metabolic process | | 2.51E-02 |

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|---|---|---|---|
| GO:0006306 | DNA methylation |  | 2.79E-02 |
| GO:0016831 | carboxy-lyase activity | molecular_function | 6.80E-08 |
| GO:0030170 | pyridoxal phosphate binding |  | 1.01E-07 |
| GO:0004013 | adenosylhomocysteinase activity |  | 1.16E-04 |
| GO:0004144 | diacylglycerol O-acyltransferase activity |  | 4.23E-04 |
| GO:0016884 | carbon-nitrogen ligase activity, with glutamine as amido-N-donor |  | 1.16E-03 |
| GO:0005506 | iron ion binding |  | 2.35E-03 |
| GO:0048037 | cofactor binding |  | 4.14E-03 |
| GO:0042626 | ATPase activity, coupled to transmembrane movement of substances |  | 9.13E-03 |
| GO:0004794 | L-threonine ammonia-lyase activity |  | 1.40E-02 |
| GO:0016887 | ATPase activity |  | 1.67E-02 |
| GO:0004315 | 3-oxoacyl-[acyl-carrier-protein] synthase activity |  | 2.51E-02 |
| GO:0004553 | hydrolase activity, hydrolyzing O-glycosyl compounds |  | 3.35E-02 |
| GO:0016851 | magnesium chelatase activity |  | 3.89E-02 |
| GO:0016705 | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen |  | 3.92E-02 |
| Group D |  |  |  |
| GO:0006355 | regulation of transcription, DNA-dependent | biological_process | 3.02E-04 |
| GO:0006073 | cellular glucan metabolic process |  | 5.20E-04 |
| GO:0008152 | metabolic process |  | 7.70E-04 |
| GO:0009765 | photosynthesis, light harvesting |  | 5.48E-03 |
| GO:0008295 | spermidine biosynthetic process |  | 7.18E-03 |
| GO:0006527 | arginine catabolic process |  | 1.01E-02 |
| GO:0000902 | cell morphogenesis |  | 1.70E-02 |
| GO:0006021 | inositol biosynthetic process |  | 3.24E-02 |
| GO:0006556 | S-adenosylmethionine biosynthetic process |  | 3.24E-02 |
| GO:0015969 | guanosine tetraphosphate metabolic process |  | 3.24E-02 |
| GO:0006820 | anion transport |  | 3.80E-02 |
| GO:0009103 | lipopolysaccharide biosynthetic process |  | 4.00E-02 |
| GO:0006479 | protein methylation |  | 4.38E-02 |
| GO:0048046 | apoplast | cellular_component | 5.20E-04 |
| GO:0016020 | membrane |  | 3.21E-02 |
| GO:0016762 | xyloglucan:xyloglucosyl transferase activity | molecular_function | 5.20E-04 |
| GO:0003700 | sequence-specific DNA binding transcription factor activity |  | 2.35E-03 |
| GO:0016758 | transferase activity, transferring hexosyl groups |  | 2.38E-03 |
| GO:0019904 | protein domain specific binding |  | 4.81E-03 |
| GO:0003913 | DNA photolyase activity |  | 7.18E-03 |
| GO:0008792 | arginine decarboxylase activity |  | 1.01E-02 |
| GO:0016891 | endoribonuclease activity, producing |  | 1.24E-02 |

| | | | |
|---|---|---|---|
| | 5'-phosphomonoesters | | |
| GO:0016757 | transferase activity, transferring glycosyl groups | | 2.85E-02 |
| GO:0004478 | methionine adenosyltransferase activity | | 3.24E-02 |
| GO:0004512 | inositol-3-phosphate synthase activity | | 3.24E-02 |
| GO:0008964 | phosphoenolpyruvate carboxylase activity | | 3.24E-02 |
| GO:0008276 | protein methyltransferase activity | | 4.38E-02 |
| GO:0020037 | heme binding | | 4.84E-02 |
| Group E | | | |
| GO:0006810 | transport | biological_process | 8.38E-03 |
| GO:0006825 | copper ion transport | | 9.33E-03 |
| GO:0042823 | pyridoxal phosphate biosynthetic process | | 9.33E-03 |
| GO:0009228 | thiamine biosynthetic process | | 2.47E-02 |
| GO:0006012 | galactose metabolic process | | 2.77E-02 |
| GO:0006694 | steroid biosynthetic process | | 3.21E-02 |
| GO:0006796 | phosphate-containing compound metabolic process | | 3.68E-02 |
| GO:0006614 | SRP-dependent cotranslational protein targeting to membrane | | 3.98E-02 |
| GO:0005758 | mitochondrial intermembrane space | cellular_component | 9.33E-03 |
| GO:0016272 | prefoldin complex | | 2.77E-02 |
| GO:0005801 | cis-Golgi network | | 3.38E-02 |
| GO:0048500 | signal recognition particle | | 3.38E-02 |
| GO:0005840 | ribosome | | 4.32E-02 |
| GO:0000139 | Golgi membrane | | 4.58E-02 |
| GO:0016531 | copper chaperone activity | molecular_function | 9.33E-03 |
| GO:0042626 | ATPase activity, coupled to transmembrane movement of substances | | 1.10E-02 |
| GO:0003978 | UDP-glucose 4-epimerase activity | | 2.47E-02 |
| GO:0003854 | 3-beta-hydroxy-delta5-steroid dehydrogenase activity | | 2.89E-02 |
| GO:0008312 | 7S RNA binding | | 3.38E-02 |
| GO:0016758 | transferase activity, transferring hexosyl groups | | 3.65E-02 |
| GO:0003700 | sequence-specific DNA binding transcription factor activity | | 4.57E-02 |
| GO:0004427 | inorganic diphosphatase activity | | 4.58E-02 |
| GO:0003735 | structural constituent of ribosome | | 4.84E-02 |
| Group F | | | |
| GO:0009415 | response to water | biological_process | 3.05E-04 |
| GO:0006541 | glutamine metabolic process | | 1.29E-03 |
| GO:0031120 | snRNA pseudouridine synthesis | | 1.00E-02 |
| GO:0006102 | isocitrate metabolic process | | 1.33E-02 |
| GO:0007585 | respiratory gaseous exchange | | 2.00E-02 |
| GO:0007050 | cell cycle arrest | | 2.32E-02 |
| GO:0006950 | response to stress | | 2.37E-02 |

| | | | |
|---|---|---|---|
| GO:0006626 | protein targeting to mitochondrion | | 2.65E-02 |
| GO:0045039 | protein import into mitochondrial inner membrane | | 2.65E-02 |
| GO:0006259 | DNA metabolic process | | 2.98E-02 |
| GO:0008283 | cell proliferation | | 3.63E-02 |
| GO:0030001 | metal ion transport | | 3.67E-02 |
| GO:0042254 | ribosome biogenesis | | 4.27E-02 |
| GO:0030259 | lipid glycosylation | | 4.60E-02 |
| GO:0055085 | transmembrane transport | | 4.96E-02 |
| GO:0031429 | box H/ACA snoRNP complex | cellular_component | 6.70E-03 |
| GO:0042719 | mitochondrial intermembrane space protein transporter complex | | 2.65E-02 |
| GO:0005740 | mitochondrial envelope | | 2.98E-02 |
| GO:0005739 | mitochondrion | | 3.95E-02 |
| GO:0005576 | extracellular region | | 4.27E-02 |
| GO:0016758 | transferase activity, transferring hexosyl groups | molecular_function | 1.15E-03 |
| GO:0022857 | transmembrane transporter activity | | 4.47E-03 |
| GO:0030515 | snoRNA binding | | 1.00E-02 |
| GO:0004450 | isocitrate dehydrogenase (NADP+) activity | | 1.33E-02 |
| GO:0004861 | cyclin-dependent protein kinase inhibitor activity | | 2.32E-02 |
| GO:0004869 | cysteine-type endopeptidase inhibitor activity | | 2.65E-02 |
| GO:0008083 | growth factor activity | | 2.98E-02 |
| GO:0018580 | nitronate monooxygenase activity | | 2.98E-02 |
| GO:0004497 | monooxygenase activity | | 3.63E-02 |
| GO:0030246 | carbohydrate binding | | 4.27E-02 |

**Table S3** Significantly altered expression of tomato homologues to AtCBF regulon genes

| Arabidopsis genes ID | Tomato gene ID | Annotation | C7dS1/Day 0 | | C8d/Day 0 | | C8d/C7dS1 | |
|---|---|---|---|---|---|---|---|---|
| | | | Fold change | FDR | Fold change | FDR | Fold change | FDR |
| Significantly altered expression of tomato homologues to up-regulated AtCBF regulon genes. | | | | | | | | |
| AT5G64260 | Solyc04g074470 | Os06g0220000 protein | 6.01 | 6.16E-02 | 27.66 | 1.26E-05 | 4.6 | 9.31E-03 |
| AT1G01470 | Solyc01g095140 | Late embryogenesis abundant protein | 9.18 | 1.17E-04 | 27.12 | 2.27E-76 | 2.95 | 2.83E-13 |
| AT5G57660 | Solyc07g006630 | CONSTANS-like protein CCT domain | 1.4 | 1.00E+00 | 16.28 | 3.48E-35 | 11.6 | 7.13E-31 |
| AT1G47710 | Solyc04g079460 | Serpin 3 | 8.67 | 1.23E-02 | 13.53 | 1.37E-05 | 1.56 | 2.36E-01 |
| AT2G16700 | Solyc01g111380 | Actin depolymerizing factor 5 | 1.81 | 2.32E-01 | 6.09 | 7.44E-17 | 3.37 | 3.89E-11 |
| AT2G28550 | Solyc11g072600 | AP2-like ethylene-responsive transcription factor | 2 | 9.86E-01 | 6.07 | 2.78E-03 | 3.04 | 5.72E-02 |
| AT5G27930 | Solyc01g100040 | Integrin-linked kinase-associated serine/threonine phosphatase 2C | 1.06 | 1.00E+00 | 4.94 | 1.27E-06 | 4.67 | 1.08E-06 |
| AT2G17840 | Solyc01g111440 | Senescence-associated protein 12 | 2.18 | 1.53E-04 | 4.6 | 1.83E-23 | 2.11 | 1.32E-07 |
| AT2G47890 | Solyc09g074560 | CONSTANS-like zinc finger protein | 1.58 | 2.23E-01 | 2.75 | 5.81E-10 | 1.74 | 2.27E-04 |
| AT5G13200 | Solyc08g078510 | GRAM-containing/ABA-responsive protein | 1.32 | 8.22E-01 | 2.45 | 2.88E-09 | 1.86 | 8.72E-06 |
| AT5G47650 | Solyc10g005950 | Nudix hydrolase 2 | 1.4 | 9.54E-01 | 2.33 | 1.29E-04 | 1.67 | 1.07E-02 |
| AT1G27200 | Solyc05g006560 | Ring zinc finger protein | 1.41 | 8.64E-01 | 2.3 | 5.92E-03 | 1.64 | 8.46E-02 |
| AT4G18270 | Solyc02g070560 | Phospho-N-acetylmuramoyl-pentapeptide-transferase | 1.09 | 1.00E+00 | 2.21 | 2.25E-04 | 2.03 | 4.89E-04 |
| AT1G77600 | Solyc06g060380 | Sister chromatid cohesion protein PDS5 homolog A | 1.28 | 1.00E+00 | 2.19 | 8.09E-04 | 1.71 | 8.46E-03 |
| AT2G39800 | Solyc08g043170 | Gamma-glutamyl phosphate reductase | 1.07 | 1.00E+00 | 0.45 | 1.69E-04 | 0.41 | 9.49E-04 |
| AT1G51700 | Solyc03g121400 | Dof zinc finger protein 4 | 1.25 | 1.00E+00 | 0.42 | 2.97E-04 | 0.34 | 4.22E-05 |
| AT1G78070 | Solyc04g072890 | WD-40 repeat family protein | 1.1 | 1.00E+00 | 0.39 | 7.24E-08 | 0.35 | 1.02E-06 |
| AT5G17210 | Solyc03g096860 | Fiber protein Fb34 | 1.13 | 1.00E+00 | 0.36 | 5.84E-09 | 0.32 | 3.76E-08 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| AT3G55760 | Solyc06g053920 | Os11g0586300 protein (Fragment) | 0.87 | 7.39E-01 | 0.31 | 9.46E-08 | 0.35 | 1.83E-04 |
| AT1G10760 | Solyc05g005020 | R1 protein alpha-glucan water dikinase | 0.67 | 1.39E-02 | 0.3 | 1.71E-12 | 0.45 | 6.19E-04 |
| AT1G21790 | Solyc01g079770 | TLC domain-containing protein 2 | 0.79 | 8.82E-01 | 0.28 | 6.14E-03 | 0.35 | 8.40E-02 |
| AT4G39730 | Solyc04g054980 | Lipoxygenase homology domain-containing protein 1 | 1.1 | 1.00E+00 | 0.16 | 1.27E-15 | 0.15 | 8.41E-13 |
| Significantly altered expression of tomato homologues to down-regulated AtCBF regulon genes. | | | | | | | | |
| | | | C7dS1/Day 0 | | C8d/Day 0 | | C8d/C7dS1 | |
| Arabidopsis genes ID | Tomato gene ID | Annotation | Fold change | FDR | Fold change | FDR | Fold change | FDR |
| AT3G58710 | Solyc02g072190 | WRKY transcription factor 5 | 1.75 | 6.59E-01 | 4.61 | 4.53E-09 | 2.63 | 3.50E-05 |
| AT4G12290 | Solyc08g079430 | Primary amine oxidase | 0.69 | 2.10E-01 | 0.46 | 1.67E-03 | 0.67 | 4.71E-01 |
| AT3G20810 | Solyc01g006680 | Transcription factor jumonji jmjC domain protein | 1.4 | 6.89E-01 | 0.46 | 5.07E-04 | 0.33 | 5.90E-06 |
| AT1G21920 | Solyc11g013010 | MORN repeat protein | 1.03 | 1.00E+00 | 0.33 | 7.79E-03 | 0.32 | 2.78E-02 |
| AT1G52190 | Solyc12g095810 | Solute carrier family 15 member 4 | 0.75 | 1.00E+00 | 0.14 | 4.21E-02 | 0.19 | 2.43E-01 |

**Table S4** Changes in volatile contents of *Nr* and Pearson during fruit ripening

| Volatiles (ng.g$^{-1}$ FW h$^{-1}$) | Fruit | Days after pollination | | | | | |
|---|---|---|---|---|---|---|---|
| | | 59 | 61 | 62 | 64 | 65 | 67 |
| isovaleraldehyde | *Nr* | 0.19 ± 0.05 | 0.20 ± 0.03 | 0.19 ± 0.04 | 0.15 ± 0.01 | 0.12 ± 0.01 | 0.20 ± 0.02 |
| | Pearson | 2.84 ± 1.11 | 3.77 ± 0.69 | 2.3 ± 0.96 | 3.92 ± 0.70 | 3.69 ± 0.89 | 4.02 ± 0.46 |
| 2-methylbuteraldehyde | *Nr* | 1.66 ± 0.32 | 3.38 ± 0.67 | 1.67 ± 0.60 | 3.07 ± 0.60 | 1.85 ± 0.24 | 1.98 ± 0.12 |
| | Pearson | 4.77 ± 0.91 | 3.99 ± 0.34 | 3.50 ± 0.65 | 3.68 ± 0.22 | 4.13 ± 0.45 | 3.45 ± 0.27 |
| isovaleronitrile | *Nr* | 0.01 ± 0.01 | ud | 0.01 ± 0.01 | ud | ud | ud |
| | Pearson | 2.01 ± 1.99 | 3.78 ± 0.90 | 1.72 ± 1.39 | 3.68 ± 1.33 | 3.42 ± 0.81 | 5.34 ± 1.17 |
| 3-methyl-1-butanol | *Nr* | 0.58 ± 0.22 | 0.75 ± 0.23 | 0.57 ± 0.05 | 0.59 ± 0.08 | 0.35 ± 0.05 | 0.67 ± 0.07 |
| | Pearson | 12.41 ± 4.16 | 19.37 ± 2.31 | 15.78 ± 7.81 | 19.31 ± 4.98 | 24.54 ± 4.70 | 23.65 ± 0.79 |
| 2-methyl-1-butanol | *Nr* | 0.13 ± 0.03 | 0.26 ± 0.13 | 0.16 ± 0.02 | 0.17 ± 0.04 | 0.13 ± 0.01 | 0.18 ± 0.02 |
| | Pearson | 8.21 ± 0.18 | 17.83 ± 4.57 | 19.41 ± 13.07 | 13.57 ± 2.19 | 22.89 ± 3.28 | 20.89 ± 3.93 |
| isobutyl acetate | *Nr* | 0.20 ± 0.04 | 0.27 ± 0.05 | 0.19 ± 0.04 | 0.26 ± 0.07 | 0.33 ± 0.04 | 0.26 ± 0.03 |
| | Pearson | 2.73 ± 1.44 | 2.36 ± 0.74 | 2.91 ± 0.72 | 2.20 ± 0.50 | 3.80 ± 1.07 | 1.76 ± 0.18 |
| ethyl vinyl ketone | *Nr* | 0.03 ± 0.01 | 0.09 ± 0.02 | 0.06 ± 0.01 | 0.06 ± 0.01 | 0.05 ± 0.01 | 0.10 ± 0.01 |
| | Pearson | 0.40 ± 0.12 | 0.56 ± 0.12 | 0.27 ± 0.14 | 0.45 ± 0.08 | 0.60 ± 0.~~15~~ | 1.05 ± 0.17 |
| (*Z*)-3-hexenal | *Nr* | 0.64 ± 0.20 | 4.45 ± 2.71 | 4.60 ± 1.89 | 4.44 ± 2.46 | 7.32 ± 2.45 | 6.65 ± 2.33 |
| | Pearson | 26.18 ± 4.92 | 61.72 ± 12.91 | 65.30 ± 31.58 | 50.63 ± 4.44 | 56.63 ± 11.03 | 78.49 ± 14.11 |
| hexanal | *Nr* | 0.89 ± 0.06 | 2.19 ± 0.53 | 1.74 ± 0.49 | 1.92 ± 0.51 | 2.48 ± 0.69 | 2.42 ± 0.61 |
| | Pearson | 19.44 ± 10.27 | 39.21 ± 5.99 | 35.41 ± 20.77 | 44.50 ± 9.43 | 50.4 ± 0.77 | 86.01 ± 14.35 |
| (*E*)-2-hexenal | *Nr* | 0.02 ± 0.01 | 0.06 ± 0.02 | 0.06 ± 0.02 | 0.07 ± 0.03 | 0.10 ± 0.02 | 0.08 ± 0.02 |
| | Pearson | 0.81 ± 0.36 | 0.79 ± 0.34 | 0.60 ± 0.23 | 0.94 ± 0.30 | 1.06 ± 0.04 | 1.12 ± 0.12 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| (*Z*)-3-hexen-1-ol | *Nr* | 4.04 ± 2.77 | 22.45 ± 8.81 | 17.54 ± 4.37 | 19.62 ± 7.29 | 32.81 ± 5.96 | 25.14 ± 4.94 |
| | Pearson | 60.92 ± 19.81 | 57.09 ± 9.95 | 71.2 ± 18.18 | 63.28 ± 15.19 | 77.66 ± 10.13 | 74.43 ± 7.33 |
| 6-methyl-5-hepten-2-one | *Nr* | 0.03 ± 0.01 | 0.08 ± 0.01 | 0.07 ± 0.01 | 0.08 ± 0.02 | 0.11 ± 0.03 | 0.09 ± 0.02 |
| | Pearson | 1.57 ± 1.10 | 1.81 ± 0.09 | 1.46 ± 0.85 | 2.21 ± 0.53 | 1.08 ± 0.10 | 4.45 ± 1.19 |
| guaiacol | *Nr* | 0.31 ± 0.05 | 1.11 ± 0.46 | 0.75 ± 0.14 | 0.79 ± 0.34 | 1.19 ± 0.24 | 1.12 ± 0.10 |
| | Pearson | 0.70 ± 0.17 | 0.52 ± 0.06 | 0.56 ± 0.39 | 0.73 ± 0.17 | 0.68 ± 0.11 | 1.29 ± 0.37 |
| geranylacetone | *Nr* | 0.06 ± 0.01 | 0.07 ± 0.03 | 0.09 ± 0.03 | 0.05 ± 0.01 | 0.05 ± 0.01 | 0.03 ± 0.01 |
| | Pearson | 0.32 ± 0.09 | 0.28 ± 0.17 | 0.23 ± 0.11 | 0.38 ± 0.09 | 0.18 ± 0.01 | 0.67 ± 0.15 |
| methylsalicylate | *Nr* | 0.17 ± 0.05 | 2.34 ± 1.72 | 2.01 ± 0.87 | 1.76 ± 1.52 | 2.49 ± 0.85 | 1.96 ± 0.42 |
| | Pearson | 0.02 ± 0.02 | 0.08 ± 0.04 | 0.34 ± 0.23 | 0.08 ± 0.04 | 0.23 ± 0.08 | 0.14 ± 0.06 |
| Total volatiles | *Nr* | 13.73 ± 3.60 | 49.41 ± 7.07 | 38.25 ± 8.38 | 37.53 ± 11.41 | 52.70 ± 10.06 | 42.79 ± 8.30 |
| | Pearson | 156.81 ± 12.38 | 217.24 ± 27.31 | 225.46 ± 88.17 | 215.96 ± 43.60 | 257.03 ± 5.88 | 312.19 ± 28.23 |

Data are means of three biological replicates and standard errors. Ud, under detected limit.

28 **Table S5** Expression of genes associated with ethylene biosynthesis and signaling in response to cold storage of tomato fruit

| Gene ID | Annotation | Day 0 | C8d | C7dS1 | C8d/Day 0 | | C7dS1/Day 0 | | C8d/C7dS1 | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | Fold change | FDR | Fold change | FDR | Fold change | FDR |
| Solyc08g081550 | ACS1A | 4.7 | 7.37 | 5.07 | 1.57 | 7.25E-02 | 1.08 | 1.00E+00 | 1.45 | 5.14E-02 |
| Solyc08g081540 | ACS1B | 1.34 | 2.02 | 1.47 | 1.51 | 3.51E-01 | 1.1 | 1.00E+00 | 1.37 | 3.84E-01 |
| Solyc01g095080 | ACS2 | 405.9 | 485.87 | 355.08 | 1.2 | 4.99E-01 | 0.87 | 8.53E-01 | 1.37 | 1.42E-01 |
| Solyc02g091990 | ACS3 | 0.23 | 6.02 | 0.99 | 26.17 | 2.67E-05 | 4.29 | 3.63E-01 | 6.1 | 4.73E-03 |
| Solyc05g050010 | ACS4 | 74.56 | 152.35 | 40.57 | 2.04 | 3.35E-03 | 0.54 | 7.03E-05 | 3.76 | 2.32E-06 |
| Solyc04g077410 | ACS5 | 0 | 0 | 0 | 1 | NA | 1 | NA | 1 | NA |
| Solyc08g008100 | ACS6 | 1.37 | 2.24 | 0.93 | 1.64 | 2.84E-01 | 0.68 | 1.00E+00 | 2.41 | 1.04E-01 |
| Solyc02g063540 | ACS7 | 0 | 0 | 0 | 1 | NA | 1 | NA | 1 | NA |
| Solyc03g043890 | ACS8 | 0.55 | 0.45 | 0.23 | 0.82 | 1.00E+00 | 0.41 | 8.78E-01 | 1.99 | 6.53E-01 |
| Solyc07g026900 | ACS9 | 0 | 0 | 0 | 1 | NA | 1 | NA | 1 | NA |
| Solyc12g008740 | ACS10 | 0 | 0 | 0.32 | 1 | NA | 31.67 | 8.73E-01 | 0.03 | 5.33E-01 |
| Solyc03g007070 | ACS11 | 13.33 | 8.07 | 18.07 | 0.61 | 5.66E-02 | 1.36 | 7.82E-01 | 0.45 | 4.01E-03 |
| Solyc08g079750 | ACS12 | 14.06 | 3.06 | 9.32 | 0.22 | 9.47E-12 | 0.66 | 5.44E-02 | 0.33 | 2.82E-04 |
| Solyc12g056180 | ACS13 | 0 | 0 | 0.03 | 1 | NA | 2.67 | 1.00E+00 | 0.38 | 1.00E+00 |
| Solyc07g049530 | ACO1 | 1441.38 | 2133.83 | 1315.53 | 1.48 | 9.33E-02 | 0.91 | 7.85E-01 | 1.62 | 3.50E-02 |
| Solyc12g005940 | ACO2 | 4.07 | 32.7 | 4.25 | 8.04 | 6.67E-07 | 1.05 | 1.00E+00 | 7.69 | 3.64E-07 |
| Solyc07g049550 | ACO3 | 574.76 | 889.02 | 550.89 | 1.55 | 7.27E-02 | 0.96 | 9.67E-01 | 1.61 | 4.78E-02 |
| Solyc02g081190 | ACO4 | 7.66 | 53.04 | 4.72 | 6.92 | 1.10E-05 | 0.62 | 3.38E-01 | 11.25 | 1.85E-07 |
| Solyc07g026650 | ACO5 | 193.15 | 9.03 | 103.87 | 0.05 | 6.97E-28 | 0.54 | 1.28E-02 | 0.09 | 5.12E-12 |
| Solyc02g036350 | ACO6 | 31.91 | 30.11 | 32.49 | 0.94 | 1.00E+00 | 1.02 | 1.00E+00 | 0.93 | 9.57E-01 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Solyc12g011330 | ETR1 | 14.86 | 15.75 | 16.12 | 1.06 | 7.58E-01 | 1.08 | 1.00E+00 | 0.98 | 7.98E-01 |
| Solyc07g056580 | ETR2 | 6.11 | 0.56 | 6 | 0.09 | 1.22E-16 | 0.98 | 1.00E+00 | 0.09 | 5.37E-13 |
| Solyc09g075440 | NR | 255.78 | 96.99 | 200.71 | 0.38 | 3.78E-09 | 0.78 | 1.63E-01 | 0.48 | 1.28E-03 |
| Solyc06g053710 | ETR4 | 216.98 | 168.18 | 158.75 | 0.78 | 2.83E-01 | 0.73 | 4.52E-02 | 1.06 | 3.93E-01 |
| Solyc11g006180 | ETR5 | 8.04 | 4.7 | 8.34 | 0.59 | 5.66E-02 | 1.04 | 1.00E+00 | 0.56 | 1.51E-01 |
| Solyc09g089610 | ETR6 | 23.83 | 5.56 | 26.26 | 0.23 | 4.48E-14 | 1.1 | 1.00E+00 | 0.21 | 1.39E-12 |
| Solyc05g055070 | ETR7 | 30.58 | 16.91 | 25.73 | 0.55 | 2.67E-03 | 0.84 | 4.54E-01 | 0.66 | 2.76E-01 |
| Solyc01g104340 | GR | 0.45 | 1.63 | 0.66 | 3.64 | 1.43E-01 | 1.47 | 1.00E+00 | 2.48 | 2.49E-01 |
| Solyc08g065320 | GRL1 | 16.16 | 3.63 | 17.42 | 0.22 | 3.55E-08 | 1.08 | 1.00E+00 | 0.21 | 3.87E-07 |
| Solyc02g062420 | GRL2 | 6.54 | 11.66 | 9.6 | 1.78 | 1.41E-02 | 1.47 | 8.01E-01 | 1.21 | 2.63E-01 |
| Solyc02g068490 | RAN1 | 29.61 | 20.74 | 28.54 | 0.7 | 1.39E-01 | 0.96 | 1.00E+00 | 0.73 | 5.26E-01 |
| Solyc07g006180 | TPR1 | 132.65 | 144.64 | 182.72 | 1.09 | 5.97E-01 | 1.38 | 5.70E-01 | 0.79 | 8.63E-01 |
| Solyc10g083610 | CTR1 | 19.7 | 21.81 | 17.73 | 1.11 | 6.06E-01 | 0.9 | 7.87E-01 | 1.23 | 1.32E-01 |
| Solyc01g097980 | CTR2 | 25.82 | 32.37 | 24.94 | 1.25 | 1.96E-01 | 0.97 | 9.28E-01 | 1.3 | 4.74E-02 |
| Solyc09g009090 | CTR3 | 13.91 | 12.86 | 13.37 | 0.92 | 1.00E+00 | 0.96 | 9.69E-01 | 0.96 | 8.14E-01 |
| Solyc10g085570 | CTR4 | 5.6 | 16.38 | 7.32 | 2.92 | 1.64E-08 | 1.31 | 1.00E+00 | 2.24 | 5.02E-06 |
| Solyc06g073720 | EIL1 | 101.19 | 133.92 | 96.95 | 1.32 | 7.28E-02 | 0.96 | 8.97E-01 | 1.38 | 1.18E-02 |
| Solyc01g009170 | EIL2 | 40.49 | 109.86 | 55.87 | 2.71 | 3.57E-11 | 1.38 | 5.70E-01 | 1.97 | 1.99E-06 |
| Solyc01g096810 | EIL3 | 140.3 | 149.78 | 125.64 | 1.07 | 6.71E-01 | 0.9 | 6.57E-01 | 1.19 | 1.17E-01 |
| Solyc06g073730 | EIL4 | 125.7 | 153.3 | 90.1 | 1.22 | 2.16E-01 | 0.72 | 4.44E-02 | 1.7 | 1.33E-04 |
| Solyc01g014480 | EIL5 | 13.65 | 11.04 | 14.71 | 0.81 | 6.24E-01 | 1.08 | 1.00E+00 | 0.75 | 7.45E-01 |
| Solyc01g006650 | EIL6 | 1.62 | 3.65 | 2.41 | 2.26 | 2.39E-01 | 1.49 | 9.24E-01 | 1.51 | 5.58E-01 |
| Solyc09g007870 | EIN2 | 41.3 | 26.95 | 31.07 | 0.65 | 3.48E-02 | 0.75 | 1.03E-01 | 0.87 | 1.00E+00 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| Solyc08g060810 | EBF1 | 62.5 | 54.85 | 52 | 0.88 | 7.97E-01 | 0.83 | 3.05E-01 | 1.05 | 4.06E-01 |
| Solyc12g009560 | EBF2 | 72.23 | 23.87 | 42.18 | 0.33 | 1.64E-10 | 0.58 | 3.26E-04 | 0.57 | 8.32E-02 |
| Solyc07g008250 | EBF3 | 102.64 | 74.72 | 67.11 | 0.73 | 1.79E-01 | 0.65 | 2.05E-02 | 1.11 | 2.15E-01 |
| Solyc06g049010 | EBF4 | 0 | 0 | 0 | 1 | NA | 1 | NA | 1 | NA |
| Solyc05g052050 | ERF.A3 | 34.04 | 123.44 | 44.65 | 3.63 | 8.60E-03 | 1.31 | 1.00E+00 | 2.76 | 3.25E-02 |
| Solyc05g052040 | ERF.B1 | 33.05 | 43.23 | 21.3 | 1.31 | 1.64E-01 | 0.64 | 3.53E-01 | 2.03 | 3.76E-05 |
| Solyc08g078190 | ERF.B13 | 5.92 | 5.28 | 6.73 | 0.89 | 1.00E+00 | 1.14 | 1.00E+00 | 0.79 | 1.00E+00 |
| Solyc03g093560 | ERF.B2 | 25.97 | 7.82 | 18.77 | 0.3 | 4.76E-04 | 0.72 | 3.02E-01 | 0.42 | 1.90E-02 |
| Solyc05g052030 | ERF.B3 | 42.53 | 29.69 | 25.99 | 0.7 | 4.98E-01 | 0.61 | 3.55E-02 | 1.14 | 8.30E-01 |
| Solyc05g051200 | ERF.C1 | 31.78 | 18.6 | 30.1 | 0.59 | 1.92E-01 | 0.95 | 1.00E+00 | 0.62 | 3.81E-01 |
| Solyc12g056590 | ERF.D2 | 170.84 | 711.58 | 271.49 | 4.17 | 1.19E-21 | 1.59 | 8.16E-01 | 2.62 | 3.01E-09 |
| Solyc09g075420 | ERF.E1 | 466.94 | 147.73 | 337.68 | 0.32 | 1.09E-12 | 0.72 | 4.98E-02 | 0.44 | 1.16E-04 |
| Solyc06g063070 | ERF.E2 | 433.15 | 827.86 | 350.87 | 1.91 | 1.46E-05 | 0.81 | 2.00E-01 | 2.36 | 1.84E-09 |
| Solyc01g065980 | ERF.E4 | 643.29 | 633.31 | 504.24 | 0.98 | 1.00E+00 | 0.78 | 1.17E-01 | 1.26 | 4.23E-02 |
| Solyc12g049560 | ERF.E5 | 32.09 | 24.34 | 37.58 | 0.76 | 3.86E-01 | 1.17 | 1.00E+00 | 0.65 | 2.94E-01 |
| Solyc10g006130 | ERF.F1 | 61.19 | 88.29 | 96.01 | 1.44 | 3.88E-02 | 1.57 | 2.35E-01 | 0.92 | 9.92E-01 |
| Solyc07g064890 | ERF.F2 | 262.41 | 231.24 | 268 | 0.88 | 8.31E-01 | 1.02 | 1.00E+00 | 0.86 | 1.00E+00 |
| Solyc07g049490 | ERF.F3 | 57.96 | 41.48 | 51.15 | 0.72 | 2.20E-01 | 0.88 | 7.17E-01 | 0.81 | 9.92E-01 |
| Solyc07g053740 | ERF.F4 | 44.88 | 119.53 | 91.58 | 2.66 | 3.58E-04 | 2.04 | 3.87E-03 | 1.31 | 1.99E-01 |
| Solyc10g009110 | ERF.F5 | 37.02 | 59.04 | 66.98 | 1.59 | 5.95E-02 | 1.81 | 4.81E-02 | 0.88 | 1.00E+00 |
| Solyc12g005960 | ERF.F6 | 17.35 | 10.85 | 19.53 | 0.63 | 1.94E-01 | 1.13 | 1.00E+00 | 0.56 | 2.23E-01 |
| Solyc04g054910 | ERF.H10 | 101.15 | 46.8 | 110.58 | 0.46 | 1.03E-04 | 1.09 | 1.00E+00 | 0.42 | 9.73E-05 |
| Solyc04g072900 | ERF.H12 | 78.78 | 73.13 | 74.2 | 0.93 | 1.00E+00 | 0.94 | 9.67E-01 | 0.99 | 7.89E-01 |

**Table S6** GO enrichment analysis of DEGs with DMRs

| GO_ID | GO_Description | GO_term | p value |
|---|---|---|---|
| Group A | | | |
| GO:0006013 | mannose metabolic process | biological_process | 3.22E-03 |
| GO:0008152 | metabolic process | | 4.87E-03 |
| GO:0009058 | biosynthetic process | | 5.65E-03 |
| GO:0006950 | response to stress | | 1.15E-02 |
| GO:0006096 | glycolysis | | 1.31E-02 |
| GO:0008610 | lipid biosynthetic process | | 1.40E-02 |
| GO:0043039 | tRNA aminoacylation | | 2.63E-02 |
| GO:0006633 | fatty acid biosynthetic process | | 3.12E-02 |
| GO:0000042 | protein targeting to Golgi | | 3.63E-02 |
| GO:0006817 | phosphate ion transport | | 3.63E-02 |
| GO:0032968 | positive regulation of transcription elongation from RNA polymerase II promoter | | 3.63E-02 |
| GO:0006464 | cellular protein modification process | | 4.13E-02 |
| GO:0006631 | fatty acid metabolic process | | 4.66E-02 |
| GO:0005945 | 6-phosphofructokinase complex | cellular_component | 2.35E-03 |
| GO:0005788 | endoplasmic reticulum lumen | | 3.63E-02 |
| GO:0003872 | 6-phosphofructokinase activity | molecular_function | 2.35E-03 |
| GO:0004559 | alpha-mannosidase activity | | 3.22E-03 |
| GO:0015923 | mannosidase activity | | 3.22E-03 |
| GO:0004719 | protein-L-isoaspartate (D-aspartate) O-methyltransferase activity | | 6.61E-03 |
| GO:0016876 | ligase activity, forming aminoacyl-tRNA and related compounds | | 1.36E-02 |
| GO:0050664 | oxidoreductase activity, acting on NADH or NADPH, oxygen as acceptor | | 1.36E-02 |
| GO:0003824 | catalytic activity | | 1.44E-02 |
| GO:0004607 | phosphatidylcholine-sterol O-acyltransferase activity | | 2.28E-02 |
| GO:0048037 | cofactor binding | | 2.58E-02 |
| GO:0008374 | O-acyltransferase activity | | 2.63E-02 |
| GO:0003676 | nucleic acid binding | | 2.70E-02 |
| GO:0001671 | ATPase activator activity | | 3.63E-02 |
| GO:0003711 | transcription elongation regulator activity | | 3.63E-02 |
| GO:0004358 | glutamate N-acetyltransferase activity | | 3.63E-02 |
| GO:0004872 | receptor activity | | 3.63E-02 |
| GO:0005315 | inorganic phosphate transmembrane transporter activity | | 3.63E-02 |
| GO:0008158 | hedgehog receptor activity | | 3.63E-02 |
| GO:0008531 | riboflavin kinase activity | | 3.63E-02 |
| Group B | | | |
| GO:0042545 | cell wall modification | biological_process | 4.46E-03 |

| | | | |
|---|---|---|---|
| GO:0006694 | steroid biosynthetic process | | 5.48E-03 |
| GO:0015684 | ferrous iron transport | | 2.93E-02 |
| GO:0008299 | isoprenoid biosynthetic process | | 3.17E-02 |
| GO:0009058 | biosynthetic process | | 4.35E-02 |
| GO:0005618 | cell wall | cellular_component | 1.13E-02 |
| GO:0016747 | transferase activity, transferring acyl groups other than amino-acyl groups | molecular_function | 9.32E-04 |
| GO:0003854 | 3-beta-hydroxy-delta5-steroid dehydrogenase activity | | 4.90E-03 |
| GO:0004857 | enzyme inhibitor activity | | 5.36E-03 |
| GO:0030599 | pectinesterase activity | | 1.10E-02 |
| GO:0004315 | 3-oxoacyl-[acyl-carrier-protein] synthase activity | | 1.11E-02 |
| GO:0016616 | oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor | | 1.33E-02 |
| GO:0016717 | oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water | | 1.48E-02 |
| GO:0051087 | chaperone binding | | 1.96E-02 |
| GO:0016614 | oxidoreductase activity, acting on CH-OH group of donors | | 2.33E-02 |
| GO:0015093 | ferrous iron transmembrane transporter activity | | 2.93E-02 |
| GO:0016301 | kinase activity | | 4.48E-02 |
| Group C | | | |
| GO:0019752 | carboxylic acid metabolic process | biological_process | 5.16E-04 |
| GO:0006633 | fatty acid biosynthetic process | | 1.58E-03 |
| GO:0006730 | one-carbon metabolic process | | 4.71E-03 |
| GO:0009097 | isoleucine biosynthetic process | | 4.71E-03 |
| GO:0008610 | lipid biosynthetic process | | 4.44E-02 |
| GO:0030170 | pyridoxal phosphate binding | molecular_function | 2.40E-04 |
| GO:0016831 | carboxy-lyase activity | | 4.88E-04 |
| GO:0004013 | adenosylhomocysteinase activity | | 4.71E-03 |
| GO:0004794 | L-threonine ammonia-lyase activity | | 4.71E-03 |
| GO:0004315 | 3-oxoacyl-[acyl-carrier-protein] synthase activity | | 8.46E-03 |
| GO:0016884 | carbon-nitrogen ligase activity, with glutamine as amido-N-donor | | 1.59E-02 |
| GO:0048037 | cofactor binding | | 3.07E-02 |
| GO:0005506 | iron ion binding | | 3.74E-02 |
| GO:0042626 | ATPase activity, coupled to transmembrane movement of substances | | 4.62E-02 |
| GO:0016491 | oxidoreductase activity | | 4.85E-02 |
| Group D | | | |
| GO:0006073 | cellular glucan metabolic process | biological_process | 4.03E-05 |

|  |  |  |  |
|---|---|---|---|
| GO:0016567 | protein ubiquitination |  | 3.47E-03 |
| GO:0006556 | S-adenosylmethionine biosynthetic process |  | 4.45E-03 |
| GO:0006099 | tricarboxylic acid cycle |  | 7.47E-03 |
| GO:0008152 | metabolic process |  | 2.03E-02 |
| GO:0005975 | carbohydrate metabolic process |  | 2.19E-02 |
| GO:0005992 | trehalose biosynthetic process |  | 3.88E-02 |
| GO:0015977 | carbon fixation |  | 4.22E-02 |
| GO:0031120 | snRNA pseudouridine synthesis |  | 4.42E-02 |
| GO:0009725 | response to hormone stimulus |  | 4.95E-02 |
| GO:0032313 | regulation of Rab GTPase activity |  | 4.95E-02 |
| GO:0048046 | apoplast | cellular_component | 4.03E-05 |
| GO:0000151 | ubiquitin ligase complex |  | 3.47E-03 |
| GO:0005618 | cell wall |  | 1.60E-02 |
| GO:0005665 | DNA-directed RNA polymerase II, core complex |  | 2.97E-02 |
| GO:0016762 | xyloglucan:xyloglucosyl transferase activity | molecular_function | 4.03E-05 |
| GO:0004553 | hydrolase activity, hydrolyzing O-glycosyl compounds |  | 1.79E-03 |
| GO:0004842 | ubiquitin-protein ligase activity |  | 3.94E-03 |
| GO:0004478 | methionine adenosyltransferase activity |  | 4.45E-03 |
| GO:0008964 | phosphoenolpyruvate carboxylase activity |  | 4.45E-03 |
| GO:0003913 | DNA photolyase activity |  | 7.47E-03 |
| GO:0020037 | heme binding |  | 1.59E-02 |
| GO:0016758 | transferase activity, transferring hexosyl groups |  | 2.76E-02 |
| GO:0003904 | deoxyribodipyrimidine photo-lyase activity |  | 2.97E-02 |
| GO:0008987 | quinolinate synthetase A activity |  | 2.97E-02 |
| GO:0005542 | folic acid binding |  | 4.42E-02 |
| GO:0015105 | arsenite transmembrane transporter activity |  | 4.42E-02 |
| GO:0030515 | snoRNA binding |  | 4.42E-02 |
| GO:0005097 | Rab GTPase activator activity |  | 4.95E-02 |
| Group E |  |  |  |
| GO:0006810 | transport | biological_process | 3.20E-03 |
| GO:0006825 | copper ion transport |  | 3.53E-03 |
| GO:0006012 | galactose metabolic process |  | 1.06E-02 |
| GO:0005992 | trehalose biosynthetic process |  | 2.33E-02 |
| GO:0045226 | extracellular polysaccharide biosynthetic process |  | 4.16E-02 |
| GO:0005758 | mitochondrial intermembrane space | cellular_component | 3.53E-03 |
| GO:0005643 | nuclear pore |  | 2.10E-02 |
| GO:0016531 | copper chaperone activity | molecular_function | 3.53E-03 |
| GO:0003978 | UDP-glucose 4-epimerase activity |  | 9.40E-03 |

| | | | |
|---|---|---|---|
| GO:0016706 | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors | | 1.84E-02 |
| GO:0004518 | nuclease activity | | 2.68E-02 |
| GO:0003700 | sequence-specific DNA binding transcription factor activity | | 3.59E-02 |
| GO:0008831 | dTDP-4-dehydrorhamnose reductase activity | | 4.16E-02 |
| Group F | | | |
| GO:0008283 | cell proliferation | biological_process | 1.10E-02 |
| GO:0006541 | glutamine metabolic process | | 1.49E-02 |
| GO:0005576 | extracellular region | cellular_component | 1.30E-02 |
| GO:0004869 | cysteine-type endopeptidase inhibitor activity | molecular_function | 7.99E-03 |
| GO:0008083 | growth factor activity | | 8.99E-03 |

**Table S7** GO enrichment analysis of genes with negative correlation between the level of methylation and expression

| GO_ID | GO_Description | GO_term | p value |
|---|---|---|---|
| GO:0008150 | biological_process | Biological process | 1.54E-58 |
| GO:0009987 | cellular process | | 4.58E-40 |
| GO:0008152 | metabolic process | | 6.33E-32 |
| GO:0044699 | single-organism process | | 6.92E-27 |
| GO:0071704 | organic substance metabolic process | | 1.02E-26 |
| GO:0044763 | single-organism cellular process | | 9.84E-25 |
| GO:0044237 | cellular metabolic process | | 7.55E-24 |
| GO:0044238 | primary metabolic process | | 1.58E-20 |
| GO:0044710 | single-organism metabolic process | | 4.81E-13 |
| GO:0065007 | biological regulation | | 1.01E-12 |
| GO:0044281 | small molecule metabolic process | | 5.94E-11 |
| GO:0006793 | phosphorus metabolic process | | 8.48E-11 |
| GO:0006796 | phosphate-containing compound metabolic process | | 1.44E-10 |
| GO:0043170 | macromolecule metabolic process | | 2.55E-10 |
| GO:0050896 | response to stimulus | | 3.39E-10 |
| GO:0044260 | cellular macromolecule metabolic process | | 4.58E-10 |
| GO:0009058 | biosynthetic process | | 1.69E-09 |
| GO:0043412 | macromolecule modification | | 5.42E-09 |
| GO:0006082 | organic acid metabolic process | | 5.57E-09 |
| GO:0044267 | cellular protein metabolic process | | 6.37E-09 |
| GO:0006464 | cellular protein modification process | | 9.79E-09 |
| GO:0036211 | protein modification process | | 9.79E-09 |
| GO:0050789 | regulation of biological process | | 1.69E-08 |
| GO:0016310 | phosphorylation | | 3.14E-08 |
| GO:0050794 | regulation of cellular process | | 6.11E-08 |
| GO:0043436 | oxoacid metabolic process | | 8.00E-08 |
| GO:0019752 | carboxylic acid metabolic process | | 1.08E-07 |
| GO:0019538 | protein metabolic process | | 1.99E-07 |
| GO:0044711 | single-organism biosynthetic process | | 2.95E-07 |
| GO:1901576 | organic substance biosynthetic process | | 6.67E-07 |
| GO:0051179 | localization | | 4.72E-06 |
| GO:0051716 | cellular response to stimulus | | 4.80E-06 |
| GO:0007154 | cell communication | | 4.81E-06 |
| GO:0006807 | nitrogen compound metabolic process | | 9.43E-06 |
| GO:0006810 | transport | | 9.76E-06 |
| GO:0006468 | protein phosphorylation | | 1.19E-05 |
| GO:0051234 | establishment of localization | | 1.36E-05 |
| GO:0042221 | response to chemical | | 4.16E-05 |
| GO:0044249 | cellular biosynthetic process | | 5.22E-05 |
| GO:1901360 | organic cyclic compound metabolic process | | 6.94E-05 |
| GO:0006725 | cellular aromatic compound metabolic process | | 4.06E-04 |
| GO:0032787 | monocarboxylic acid metabolic process | | 4.37E-04 |

| | | | |
|---|---|---|---|
| GO:0009889 | regulation of biosynthetic process | | 5.35E-04 |
| GO:0007165 | signal transduction | | 6.61E-04 |
| GO:0034641 | cellular nitrogen compound metabolic process | | 6.61E-04 |
| GO:0031326 | regulation of cellular biosynthetic process | | 6.72E-04 |
| GO:0044700 | single organism signaling | | 7.03E-04 |
| GO:0023052 | signaling | | 7.03E-04 |
| GO:0046483 | heterocycle metabolic process | | 9.48E-04 |
| GO:2000112 | regulation of cellular macromolecule biosynthetic process | | 1.30E-03 |
| GO:0010556 | regulation of macromolecule biosynthetic process | | 1.58E-03 |
| GO:1901575 | organic substance catabolic process | | 1.71E-03 |
| GO:0010468 | regulation of gene expression | | 2.80E-03 |
| GO:0009056 | catabolic process | | 3.09E-03 |
| GO:0051171 | regulation of nitrogen compound metabolic process | | 3.47E-03 |
| GO:0006355 | regulation of transcription, DNA-templated | | 3.61E-03 |
| GO:0044283 | small molecule biosynthetic process | | 3.64E-03 |
| GO:0046394 | carboxylic acid biosynthetic process | | 4.26E-03 |
| GO:2001141 | regulation of RNA biosynthetic process | | 4.37E-03 |
| GO:1903506 | regulation of nucleic acid-templated transcription | | 4.37E-03 |
| GO:0051252 | regulation of RNA metabolic process | | 6.16E-03 |
| GO:1901564 | organonitrogen compound metabolic process | | 6.75E-03 |
| GO:0055085 | transmembrane transport | | 7.45E-03 |
| GO:0019219 | regulation of nucleobase-containing compound metabolic process | | 7.52E-03 |
| GO:0006629 | lipid metabolic process | | 7.93E-03 |
| GO:0006139 | nucleobase-containing compound metabolic process | | 8.67E-03 |
| GO:0009605 | response to external stimulus | | 1.01E-02 |
| GO:0006950 | response to stress | | 1.19E-02 |
| GO:0016053 | organic acid biosynthetic process | | 1.65E-02 |
| GO:0055114 | oxidation-reduction process | | 1.81E-02 |
| GO:0006811 | ion transport | | 2.40E-02 |
| GO:1902578 | single-organism localization | | 3.00E-02 |
| GO:0019222 | regulation of metabolic process | | 3.14E-02 |
| GO:0044765 | single-organism transport | | 3.99E-02 |
| GO:0010033 | response to organic substance | | 4.13E-02 |
| GO:0060255 | regulation of macromolecule metabolic process | | 4.20E-02 |
| GO:0080090 | regulation of primary metabolic process | | 4.88E-02 |
| GO:0003674 | molecular_function | Molecular function | 8.04E-57 |
| GO:0003824 | catalytic activity | | 1.61E-31 |
| GO:0005488 | binding | | 2.96E-27 |
| GO:0016740 | transferase activity | | 8.15E-16 |
| GO:1901363 | heterocyclic compound binding | | 2.04E-12 |
| GO:0097159 | organic cyclic compound binding | | 2.19E-12 |
| GO:0000166 | nucleotide binding | | 2.02E-10 |

| | | | |
|---|---|---|---|
| GO:1901265 | nucleoside phosphate binding | | 2.02E-10 |
| GO:0036094 | small molecule binding | | 2.13E-10 |
| GO:0035639 | purine ribonucleoside triphosphate binding | | 6.79E-09 |
| GO:0016773 | phosphotransferase activity, alcohol group as acceptor | | 7.22E-09 |
| GO:0043167 | ion binding | | 8.06E-09 |
| GO:0016301 | kinase activity | | 1.03E-08 |
| GO:0032553 | ribonucleotide binding | | 1.28E-08 |
| GO:0017076 | purine nucleotide binding | | 1.40E-08 |
| GO:0001883 | purine nucleoside binding | | 1.64E-08 |
| GO:0032555 | purine ribonucleotide binding | | 1.64E-08 |
| GO:0032550 | purine ribonucleoside binding | | 1.64E-08 |
| GO:0097367 | carbohydrate derivative binding | | 2.60E-08 |
| GO:0032549 | ribonucleoside binding | | 3.34E-08 |
| GO:0001882 | nucleoside binding | | 3.49E-08 |
| GO:0016772 | transferase activity, transferring phosphorus-containing groups | | 7.79E-08 |
| GO:0046872 | metal ion binding | | 1.20E-07 |
| GO:0005524 | ATP binding | | 1.85E-07 |
| GO:0043169 | cation binding | | 1.86E-07 |
| GO:0030554 | adenyl nucleotide binding | | 3.69E-07 |
| GO:0032559 | adenyl ribonucleotide binding | | 4.29E-07 |
| GO:0004672 | protein kinase activity | | 7.40E-06 |
| GO:0004674 | protein serine/threonine kinase activity | | 1.31E-04 |
| GO:0046914 | transition metal ion binding | | 8.84E-04 |
| GO:0003700 | transcription factor activity, sequence-specific DNA binding | | 2.04E-03 |
| GO:0001071 | nucleic acid binding transcription factor activity | | 2.04E-03 |
| GO:0016491 | oxidoreductase activity | | 5.76E-03 |
| GO:0005506 | iron ion binding | | 1.41E-02 |
| GO:0022857 | transmembrane transporter activity | | 3.62E-02 |
| GO:0016746 | transferase activity, transferring acyl groups | | 4.67E-02 |
| GO:0042802 | identical protein binding | | 4.84E-02 |
| GO:0005575 | cellular_component | Cellular component | 2.71E-38 |
| GO:0044464 | cell part | | 5.95E-36 |
| GO:0005623 | cell | | 1.04E-35 |
| GO:0005622 | intracellular | | 1.35E-26 |
| GO:0044424 | intracellular part | | 9.92E-24 |
| GO:0005737 | cytoplasm | | 5.07E-20 |
| GO:0043226 | organelle | | 2.03E-19 |
| GO:0043227 | membrane-bounded organelle | | 2.41E-19 |
| GO:0043229 | intracellular organelle | | 2.82E-19 |
| GO:0043231 | intracellular membrane-bounded organelle | | 3.37E-19 |
| GO:0044444 | cytoplasmic part | | 2.47E-15 |
| GO:0016020 | membrane | | 2.15E-10 |
| GO:0071944 | cell periphery | | 1.78E-08 |
| GO:0005886 | plasma membrane | | 4.96E-07 |

|  |  |  |  |
|---|---|---|---|
| GO:0012505 | endomembrane system |  | 2.95E-05 |
| GO:0044422 | organelle part |  | 6.12E-05 |
| GO:0044446 | intracellular organelle part |  | 8.18E-05 |
| GO:0044425 | membrane part |  | 9.89E-05 |
| GO:0009536 | plastid |  | 4.70E-04 |
| GO:0031224 | intrinsic component of membrane |  | 9.77E-04 |
| GO:0098805 | whole membrane |  | 1.03E-03 |
| GO:0016021 | integral component of membrane |  | 1.13E-03 |
| GO:0005634 | nucleus |  | 1.27E-03 |
| GO:0009507 | chloroplast |  | 1.56E-03 |
| GO:0009506 | plasmodesma |  | 2.27E-03 |
| GO:0005911 | cell-cell junction |  | 2.27E-03 |
| GO:0055044 | symplast |  | 2.27E-03 |
| GO:0030054 | cell junction |  | 2.27E-03 |
| GO:0031090 | organelle membrane |  | 2.48E-03 |
| GO:0005829 | cytosol |  | 5.79E-03 |
| GO:0005773 | vacuole |  | 8.72E-03 |
| GO:0098588 | bounding membrane of organelle |  | 8.87E-03 |
| GO:0044435 | plastid part |  | 3.92E-02 |

**Table S8** DMRs found in promoter regions of RIN target genes

| Gene ID | Gene descriptions | DMR methylation level | | |
|---|---|---|---|---|
| | | Day0 | C8d | C7dS1 |
| Solyc01g006540 | Lipoxygenase | 36.62% | 13.27% | 33.30% |
| Solyc01g006720 | ABC transporter G family member 22 | 13.58% | 39.54% | 41.04% |
| Solyc01g007200 | Unknown Protein | 14.35% | 30.18% | 9.25% |
| Solyc01g008710 | Mannan endo-1 4-beta-mannosidase | 18.52% | 37.55% | 31.77% |
| Solyc01g008910 | Scarecrow transcription factor family protein | 11.51% | 28.39% | 10.77% |
| Solyc01g009860 | NAC domain transcription factor | 4.52% | 0.00% | 1.33% |
| Solyc01g010870 | Dehydration-responsive family protein | 28.61% | 52.91% | 43.52% |
| Solyc01g067670 | Unknown Protein | 31.61% | 56.70% | 36.88% |
| Solyc01g067670 | Unknown Protein | 59.91% | 84.21% | 77.83% |
| Solyc01g087820 | Subtilisin-like protease | 70.09% | 78.99% | 38.51% |
| Solyc01g087820 | Subtilisin-like protease | 50.39% | 70.84% | 50.07% |
| Solyc01g087820 | Subtilisin-like protease | 71.54% | 88.68% | 71.34% |
| Solyc01g087950 | Serine carboxypeptidase 1 | 57.83% | 34.06% | 42.22% |
| Solyc01g087950 | Serine carboxypeptidase 1 | 55.00% | 64.25% | 77.88% |
| Solyc01g087970 | Serine carboxypeptidase 1 | 7.42% | 9.82% | 4.42% |
| Solyc01g090700 | Enoyl-CoA-hydratase | 2.85% | 7.92% | 2.70% |
| Solyc01g095900 | Protein TIF31 homolog | 62.76% | 79.73% | 54.31% |
| Solyc01g095900 | Protein TIF31 homolog | 81.67% | 94.64% | 84.25% |
| Solyc01g098110 | Hydrolase alpha/beta fold family protein | 2.19% | 9.35% | 5.56% |
| Solyc01g098500 | Glucose transporter 8 | 31.43% | 51.45% | 24.32% |
| Solyc01g099040 | GDSL esterase/lipase At5g03980 | 11.14% | 7.78% | 0.89% |
| Solyc01g099040 | GDSL esterase/lipase At5g03980 | 48.44% | 74.48% | 41.00% |
| Solyc01g099200 | Lipoxygenase | 44.20% | 72.30% | 58.24% |
| Solyc01g100200 | GRAS family transcription factor | 2.97% | 16.81% | 13.10% |
| Solyc01g100460 | BZIP transcription factor | 3.37% | 10.52% | 2.61% |
| Solyc01g102310 | Unknown Protein | 12.60% | 27.11% | 19.68% |
| Solyc01g104850 | Serine carboxypeptidase F13S12.6 | 1.41% | 1.48% | 5.77% |
| Solyc01g107400 | Indole-3-acetic acid-amido synthetase GH3.8 | 82.67% | 88.41% | 78.60% |
| Solyc01g107400 | Indole-3-acetic acid-amido synthetase GH3.8 | 5.93% | 17.30% | 7.84% |
| Solyc01g107400 | Indole-3-acetic acid-amido synthetase GH3.8 | 28.50% | 41.29% | 22.91% |
| Solyc01g107830 | UDP-glucosyltransferase family 1 protein | 14.64% | 1.82% | 14.01% |
| Solyc01g107840 | Immediate-early salicylate-induced glucosyltransferase | 23.11% | 26.37% | 25.37% |
| Solyc01g107890 | Filament-like plant protein | 75.08% | 57.38% | 77.96% |
| Solyc01g108570 | Gibberellin receptor GID1L2 | 22.74% | 54.91% | 64.60% |
| Solyc01g111400 | Subtilisin-like protease | 80.58% | 75.78% | 61.95% |
| Solyc02g021680 | WRKY transcription factor 37 | 46.42% | 56.43% | 43.95% |
| Solyc02g037500 | Unknown Protein | 46.04% | 67.02% | 39.36% |
| Solyc02g037500 | Unknown Protein | 8.98% | 25.72% | 16.71% |
| Solyc02g037530 | Auxin response factor 8 | 1.73% | 19.92% | 6.15% |

| | | | | |
|---|---|---|---|---|
| Solyc02g063360 | C2 domain-containing protein | 8.09% | 28.36% | 9.37% |
| Solyc02g064690 | Acetyltransferase-like protein | 76.48% | 82.94% | 70.10% |
| Solyc02g065680 | Amino acid transporter | 5.79% | 13.36% | 18.20% |
| Solyc02g068340 | Kinesin-like calmodulin binding protein | 6.69% | 0.18% | 2.70% |
| Solyc02g071110 | Purine permease family protein | 76.33% | 56.17% | 84.47% |
| Solyc02g071110 | Purine permease family protein | 2.99% | 16.72% | 6.91% |
| Solyc02g071110 | Purine permease family protein | 41.51% | 58.58% | 49.49% |
| Solyc02g077920 | Squamosa promoter binding-like protein | 60.90% | 36.89% | 30.82% |
| Solyc02g077920 | Squamosa promoter binding-like protein | 10.90% | 26.49% | 6.22% |
| Solyc02g078030 | DNA-binding WRKY VQ | 35.33% | 33.59% | 15.70% |
| Solyc02g078150 | Plant-specific domain TIGR01615 family protein | 3.35% | 0.00% | 0.00% |
| Solyc02g078150 | Plant-specific domain TIGR01615 family protein | 22.60% | 37.77% | 43.14% |
| Solyc02g079010 | Cotton fiber expressed protein 1 | 81.89% | 92.25% | 77.04% |
| Solyc02g079590 | Serine/threonine kinase receptor | 13.42% | 30.38% | 2.27% |
| Solyc02g079590 | Serine/threonine kinase receptor | 71.57% | 86.52% | 67.63% |
| Solyc02g080510 | Arabidopsis thaliana genomic DNA chromosome 5 P1 clone MOK16 | 1.37% | 3.48% | 0.51% |
| Solyc02g085350 | Succinate dehydrogenase flavoprotein subunit | 16.70% | 11.02% | 34.47% |
| Solyc02g087970 | Zinc finger-homeodomain protein 1 | 88.56% | 91.83% | 82.09% |
| Solyc02g088390 | Blue copper-like protein | 38.40% | 74.32% | 67.50% |
| Solyc02g089350 | Gibberellin regulated protein | 54.44% | 80.85% | 78.03% |
| Solyc02g089630 | Proline dehydrogenase | 75.65% | 89.37% | 81.75% |
| Solyc02g090510 | Calcium-dependent protein kinase-like | 2.37% | 0.00% | 0.24% |
| Solyc02g090680 | Cyclin-dependent kinase inhibitor 7 | 22.49% | 15.69% | 11.22% |
| Solyc02g091500 | Calmodulin | 76.39% | 83.32% | 71.14% |
| Solyc02g093150 | AP2-like ethylene-responsive transcription factor At1g16060 | 4.01% | 14.08% | 3.63% |
| Solyc03g007430 | Mitochondrial carrier family | 5.19% | 17.52% | 5.51% |
| Solyc03g025970 | Methyl binding domain protein | 82.62% | 90.74% | 80.14% |
| Solyc03g025970 | Methyl binding domain protein | 59.02% | 75.52% | 77.22% |
| Solyc03g031860 | Phytoene synthase 1 | 11.44% | 37.74% | 24.98% |
| Solyc03g078360 | Receptor-like protein kinase | 82.59% | 90.82% | 81.99% |
| Solyc03g083910 | Acid beta-fructofuranosidase | 1.61% | 0.29% | 2.58% |
| Solyc03g083910 | Acid beta-fructofuranosidase | 79.71% | 91.40% | 87.96% |
| Solyc03g095900 | 1-aminocyclopropane-1-carboxylate oxidase-like protein | 13.96% | 15.28% | 0.60% |
| Solyc03g095900 | 1-aminocyclopropane-1-carboxylate oxidase-like protein | 59.70% | 77.68% | 54.83% |
| Solyc03g097440 | 11-beta-hydroxysteroid dehydrogenase-like | 16.90% | 19.68% | 7.35% |
| Solyc03g097440 | 11-beta-hydroxysteroid dehydrogenase-like | 2.29% | 13.35% | 5.05% |
| Solyc03g097700 | O-methyltransferase | 6.73% | 23.97% | 20.76% |
| Solyc03g098320 | MYB transcription factor | 3.08% | 0.95% | 0.00% |
| Solyc03g111690 | Pectate lyase | 49.93% | 68.97% | 58.15% |
| Solyc03g111970 | Cytochrome P450 | 77.34% | 89.18% | 71.06% |

| | | | | |
|---|---|---|---|---|
| Solyc03g112060 | Quinolinate synthase A | 73.60% | 82.45% | 63.98% |
| Solyc03g112060 | Quinolinate synthase A | 3.80% | 16.82% | 3.00% |
| Solyc03g113340 | Nodulin-like protein | 80.57% | 81.39% | 91.41% |
| Solyc03g113420 | Peptide transporter | 81.26% | 94.83% | 78.37% |
| Solyc03g114730 | Os03g0169000 protein | 84.01% | 87.26% | 72.51% |
| Solyc03g115870 | Thioredoxin 2 | 0.85% | 2.69% | 9.50% |
| Solyc03g120450 | Aminotransferase | 22.67% | 11.59% | 30.06% |
| Solyc03g120450 | Aminotransferase | 2.88% | 0.30% | 0.65% |
| Solyc03g120500 | Auxin responsive protein | 84.07% | 88.17% | 78.35% |
| Solyc03g120500 | Auxin responsive protein | 1.18% | 1.16% | 7.71% |
| Solyc03g120560 | Proton-dependent oligopeptide transport family protein | 25.04% | 47.97% | 31.39% |
| Solyc03g120560 | Proton-dependent oligopeptide transport family protein | 43.77% | 23.03% | 45.77% |
| Solyc03g120570 | Proton-dependent oligopeptide transport family protein | 50.77% | 74.59% | 61.85% |
| Solyc03g120570 | Proton-dependent oligopeptide transport family protein | 75.75% | 67.98% | 84.44% |
| Solyc04g005020 | WD-40 repeat family protein | 0.47% | 0.00% | 4.89% |
| Solyc04g005800 | Homeobox-leucine zipper protein | 10.95% | 13.56% | 2.02% |
| Solyc04g006970 | Phosphoenolpyruvate carboxylase | 60.72% | 77.03% | 67.53% |
| Solyc04g011520 | Serine/threonine kinase-like protein ABC1063 | 8.39% | 3.23% | 4.20% |
| Solyc04g011520 | Serine/threonine kinase-like protein ABC1063 | 47.42% | 62.48% | 44.23% |
| Solyc04g015340 | Serine carboxypeptidase K10B2.2 | 0.27% | 10.98% | 4.29% |
| Solyc04g015340 | Serine carboxypeptidase K10B2.2 | 14.17% | 16.47% | 1.09% |
| Solyc04g015560 | Beta-D-glucosidase | 76.32% | 85.02% | 86.78% |
| Solyc04g053120 | 4-alpha-glucanotransferase | 16.09% | 40.32% | 22.10% |
| Solyc04g072030 | Interferon-induced GTP-binding protein Mx | 2.63% | 1.63% | 0.36% |
| Solyc04g073950 | VQ motif family protein expressed | 4.46% | 1.16% | 0.97% |
| Solyc04g073950 | VQ motif family protein expressed | 83.95% | 62.64% | 78.03% |
| Solyc04g076860 | Inter-alpha-trypsin inhibitor heavy chain H2 | 3.69% | 20.55% | 9.44% |
| Solyc04g076880 | Phosphoenolpyruvate carboxykinase | 45.42% | 36.89% | 51.49% |
| Solyc04g076880 | Phosphoenolpyruvate carboxykinase | 81.82% | 87.26% | 60.70% |
| Solyc04g077980 | Zinc-finger protein | 19.98% | 31.03% | 11.64% |
| Solyc04g078550 | WRKY transcription factor 2 | 44.51% | 64.87% | 54.19% |
| Solyc04g079420 | Nbs-lrr%2C resistance protein | 74.49% | 84.00% | 85.66% |
| Solyc04g079420 | Nbs-lrr%2C resistance protein | 58.30% | 54.88% | 56.42% |
| Solyc04g081290 | Lysine decarboxylase-like protein | 5.07% | 22.55% | 3.44% |
| Solyc04g081870 | Expansin | 18.92% | 16.03% | 6.05% |
| Solyc04g081900 | Nucleoredoxin 1 | 2.83% | 18.74% | 5.27% |
| Solyc04g081900 | Nucleoredoxin 1 | 28.68% | 23.51% | 12.86% |
| Solyc04g081900 | Nucleoredoxin 1 | 9.31% | 16.46% | 5.66% |
| Solyc04g082480 | Nodule inception protein | 15.93% | 27.14% | 10.44% |
| Solyc05g009120 | Os03g0731050 protein | 6.76% | 0.93% | 0.22% |

| | | | | |
|---|---|---|---|---|
| Solyc05g009340 | Unknown Protein | 8.76% | 19.23% | 9.19% |
| Solyc05g009550 | IST1 homolog | 5.20% | 22.27% | 3.20% |
| Solyc05g009610 | Acetyl esterase | 82.36% | 84.59% | 70.16% |
| Solyc05g012020 | Ripening Inhibitor | 14.12% | 38.15% | 18.95% |
| Solyc05g013530 | Octicosapeptide/Phox/Bem1p domain-containing protein | 87.86% | 85.68% | 67.79% |
| Solyc05g013570 | AT1G67900-like protein | 90.20% | 73.73% | 85.75% |
| Solyc05g016310 | Aspartic proteinase nepenthesin I | 0.54% | 0.74% | 5.02% |
| Solyc05g050010 | 1-aminocyclopropane-1-carboxylate synthase | 17.62% | 31.75% | 14.17% |
| Solyc05g051660 | Gibberellin receptor GID1L2 | 77.82% | 61.01% | 82.49% |
| Solyc05g054560 | UPF0497 membrane protein 2 | 1.46% | 12.15% | 0.74% |
| Solyc05g054560 | UPF0497 membrane protein 2 | 46.48% | 46.77% | 64.18% |
| Solyc06g006100 | Anthranilate synthase component I family protein expressed | 15.24% | 33.49% | 24.96% |
| Solyc06g035720 | BCL-2 binding anthanogene-1 | 84.83% | 87.30% | 74.49% |
| Solyc06g053710 | Ethylene receptor | 81.43% | 90.62% | 78.59% |
| Solyc06g059740 | Alcohol dehydrogenase 2 | 2.89% | 15.71% | 5.41% |
| Solyc06g059740 | Alcohol dehydrogenase 2 | 16.12% | 41.66% | 24.73% |
| Solyc06g062670 | Zinc finger family protein | 32.75% | 54.54% | 37.56% |
| Solyc06g068460 | WRKY transcription factor 1 | 2.88% | 2.31% | 7.54% |
| Solyc06g068900 | Nudix hydrolase 4 | 89.26% | 87.17% | 78.51% |
| Solyc06g068990 | Mitogen-activated protein kinase | 80.86% | 76.46% | 64.28% |
| Solyc06g068990 | Mitogen-activated protein kinase | 82.97% | 82.81% | 93.74% |
| Solyc06g068990 | Mitogen-activated protein kinase | 64.03% | 79.27% | 70.84% |
| Solyc06g069430 | MADS box transcription factor | 26.31% | 44.74% | 19.41% |
| Solyc06g069430 | MADS box transcription factor | 0.00% | 3.27% | 0.20% |
| Solyc06g073740 | Beta-D-glucosidase | 12.21% | 22.68% | 8.51% |
| Solyc06g073850 | Unknown Protein | 84.61% | 87.45% | 74.07% |
| Solyc06g082080 | Integrin-linked kinase-associated serine/threonine phosphatase 2C | 0.67% | 12.86% | 3.88% |
| Solyc07g006280 | Senescence-associated protein | 0.40% | 0.40% | 4.53% |
| Solyc07g006890 | Cytochrome P450 | 3.63% | 2.25% | 8.76% |
| Solyc07g007420 | Leucine-rich repeat family protein | 28.28% | 45.84% | 28.55% |
| Solyc07g018340 | DNA mismatch repair protein mutS | 10.59% | 9.15% | 4.22% |
| Solyc07g042390 | Pectinesterase | 6.27% | 0.45% | 0.76% |
| Solyc07g049530 | 1-aminocyclopropane-1-carboxylate oxidase | 85.40% | 68.96% | 70.19% |
| Solyc07g051880 | Protein serine/threonine kinase | 19.79% | 48.58% | 40.00% |
| Solyc07g053550 | Glutaredoxin | 79.37% | 84.80% | 91.65% |
| Solyc07g054850 | Uncharacterized GPI-anchored protein At4g28100 | 6.84% | 9.19% | 0.87% |
| Solyc07g054850 | Uncharacterized GPI-anchored protein At4g28100 | 81.34% | 89.41% | 76.99% |
| Solyc07g054850 | Uncharacterized GPI-anchored protein At4g28100 | 1.66% | 9.43% | 0.59% |
| Solyc07g056570 | 9-cis-epoxycarotenoid dioxygenase | 10.10% | 29.99% | 8.01% |
| Solyc07g062550 | UDP-N-acetylglucosamine 1-carboxyvinyltransferase | 1.61% | 0.73% | 4.44% |

| | | | | |
|---|---|---|---|---|
| Solyc07g062670 | Unknown Protein | 7.53% | 17.57% | 13.32% |
| Solyc07g064410 | Ubiquitin-conjugating enzyme-like protein | 43.12% | 54.03% | 38.68% |
| Solyc08g005630 | Glucose-methanol-choline oxidoreductase | 30.77% | 52.66% | 27.35% |
| Solyc08g005630 | Glucose-methanol-choline oxidoreductase | 31.82% | 48.90% | 61.06% |
| Solyc08g005630 | Glucose-methanol-choline oxidoreductase | 33.31% | 44.21% | 24.38% |
| Solyc08g005770 | Alcohol acetyltransferase | 7.84% | 19.94% | 8.17% |
| Solyc08g008330 | Unknown Protein | 7.88% | 4.17% | 1.77% |
| Solyc08g008330 | Unknown Protein | 81.63% | 90.89% | 82.38% |
| Solyc08g048290 | Myo-inositol transporter 1 | 49.31% | 46.48% | 26.99% |
| Solyc08g048290 | Myo-inositol transporter 1 | 44.51% | 56.32% | 59.16% |
| Solyc08g048290 | Myo-inositol transporter 1 | 0.00% | 8.00% | 0.00% |
| Solyc08g061270 | Unknown Protein | 35.38% | 16.24% | 36.79% |
| Solyc08g062820 | Cytokinin riboside 5%26apos%3B-monophosphate phosphoribohydrolase LOG | 39.24% | 37.19% | 17.32% |
| Solyc08g066690 | Exostosin family protein | 22.42% | 38.96% | 21.21% |
| Solyc08g066700 | Polyribonucleotide nucleotidyltransferase | 32.94% | 47.18% | 30.56% |
| Solyc08g066700 | Polyribonucleotide nucleotidyltransferase | 15.52% | 44.53% | 32.96% |
| Solyc08g067410 | Fatty acid elongase 3-ketoacyl-CoA synthase | 16.72% | 34.68% | 23.94% |
| Solyc08g068600 | Decarboxylase family protein | 67.52% | 78.46% | 66.31% |
| Solyc08g068680 | Decarboxylase family protein | 7.79% | 28.02% | 13.65% |
| Solyc08g075880 | Metal ion binding protein | 7.09% | 7.01% | 0.34% |
| Solyc08g075880 | Metal ion binding protein | 57.14% | 48.41% | 36.04% |
| Solyc08g076220 | Phosphoribulokinase/uridine kinase | 33.26% | 40.20% | 51.51% |
| Solyc08g076480 | Plastid lipid-associated protein 3%2C chloroplastic | 8.93% | 9.34% | 0.42% |
| Solyc08g077430 | Glycine-rich protein | 88.62% | 94.89% | 83.90% |
| Solyc08g078460 | Inositol 2-dehydrogenase like protein | 1.87% | 9.31% | 0.23% |
| Solyc08g079750 | 1-aminocyclopropane-1-carboxylate synthase | 65.93% | 83.89% | 54.83% |
| Solyc08g079750 | 1-aminocyclopropane-1-carboxylate synthase | 35.02% | 65.28% | 45.94% |
| Solyc08g081010 | Glutamate-cysteine ligase | 8.01% | 19.08% | 5.05% |
| Solyc08g081890 | Multidrug resistance protein ABC transporter family | 0.87% | 5.98% | 0.75% |
| Solyc09g010210 | Endoglucanase 1 | 35.22% | 55.87% | 34.67% |
| Solyc09g010630 | heat shock protein | 10.38% | 2.30% | 14.78% |
| Solyc09g011060 | Receptor like protein kinase | 70.16% | 79.57% | 87.22% |
| Solyc09g013150 | Vesicular glutamate transporter 3 | 7.74% | 24.36% | 12.33% |
| Solyc09g065520 | Homocysteine s-methyltransferase | 5.70% | 0.21% | 3.14% |
| Solyc09g082460 | Homocysteine s-methyltransferase | 5.91% | 26.13% | 9.54% |
| Solyc09g091470 | 3-ketoacyl CoA thiolase 2 | 67.08% | 82.16% | 56.31% |
| Solyc10g006880 | NAC domain protein | 8.00% | 24.70% | 2.87% |
| Solyc10g055760 | NAC domain protein IPR003441 | 5.32% | 0.00% | 1.16% |
| Solyc10g076240 | Peroxidase 1 | 21.13% | 2.62% | 5.78% |
| Solyc10g079570 | Acyltransferase | 13.35% | 21.60% | 4.73% |
| Solyc10g079570 | Acyltransferase | 64.22% | 75.16% | 61.75% |

|  |  |  |  |  |
|---|---|---|---|---|
| Solyc10g079570 | Acyltransferase | 59.81% | 74.57% | 54.05% |
| Solyc10g079690 | Unknown Protein | 31.01% | 45.58% | 52.04% |
| Solyc10g080210 | Polygalacturonase A | 69.65% | 81.12% | 64.81% |
| Solyc10g080210 | Polygalacturonase A | 31.22% | 49.04% | 26.21% |
| Solyc10g081910 | Receptor like kinase%2C RLK | 75.26% | 88.91% | 63.92% |
| Solyc10g083580 | Phytosulfokines 5 | 11.34% | 16.16% | 2.64% |
| Solyc10g084600 | Plant-specific domain TIGR01589 family protein | 60.62% | 80.00% | 63.97% |
| Solyc10g085810 | Vacuolar protein-sorting-associated protein 37 homolog 1 | 19.24% | 25.73% | 12.10% |
| Solyc10g086180 | Phenylalanine ammonia-lyase | 5.20% | 0.51% | 3.02% |
| Solyc10g086580 | Ribulose-1 5-bisphosphate carboxylase/oxygenase activase 1 | 79.46% | 89.17% | 83.74% |
| Solyc11g008140 | Pectate lyase family protein | 2.94% | 17.48% | 3.43% |
| Solyc11g008440 | Amino acid transporter | 0.45% | 6.81% | 0.14% |
| Solyc11g011930 | Isocitrate dehydrogenase | 3.61% | 17.90% | 10.63% |
| Solyc11g022460 | Phosphoribosylanthranilate transferase like protein | 13.08% | 54.78% | 13.87% |
| Solyc11g065070 | Hydroxymethylglutaryl-CoA lyase | 89.13% | 73.22% | 78.96% |
| Solyc11g066360 | Unknown Protein | 82.46% | 93.86% | 82.19% |
| Solyc11g072890 | Unknown Protein | 0.92% | 11.30% | 0.91% |
| Solyc12g006230 | RING-H2 finger protein | 17.91% | 35.17% | 12.14% |
| Solyc12g008660 | Zinc finger CCCH domain-containing protein 20 | 4.26% | 13.18% | 1.84% |
| Solyc12g017240 | Xyloglucan endotransglucosylase/hydrolase 7 | 72.25% | 75.46% | 59.88% |
| Solyc12g017240 | Xyloglucan endotransglucosylase/hydrolase 7 | 20.75% | 43.06% | 31.17% |
| Solyc12g017240 | Xyloglucan endotransglucosylase/hydrolase 7 | 60.18% | 48.72% | 72.33% |
| Solyc12g055930 | UDP-glucose 4-epimerase | 79.31% | 80.11% | 67.54% |
| Solyc12g089240 | Zinc finger protein CONSTANS-LIKE 3 | 0.98% | 2.85% | 13.04% |
| Solyc12g096500 | CONSTANS-like protein | 1.04% | 3.34% | 0.32% |
| Solyc12g096570 | ARGOS | 12.32% | 42.33% | 20.93% |

**Table S9** Statistics of RNA-Seq reads

| Sample | Barcode | Raw reads | Clean reads* | | rRNA reads | | Final clean reads | Mapped | |
|---|---|---|---|---|---|---|---|---|---|
| | | | # | % | # | % | | # | % |
| Day 0-1 | ATCACG | 7318318 | 6,402,353 | 87.48 | 138,924 | 2.17 | 6,263,429 | 5,947,457 | 94.96 |
| Day 0-2 | CGATGT | 8829495 | 8,011,401 | 90.73 | 155,495 | 1.94 | 7,855,906 | 7,518,593 | 95.71 |
| Day 0-3 | TTAGGC | 7203613 | 6,305,760 | 87.54 | 148,748 | 2.36 | 6,157,012 | 5,885,973 | 95.60 |
| C7dS1-1 | CAGATC | 11376542 | 9,912,379 | 87.13 | 286,343 | 2.89 | 9,626,036 | 9,158,830 | 95.15 |
| C7dS1-2 | ACTTGA | 10840784 | 9,405,066 | 86.76 | 373,987 | 3.98 | 9,031,079 | 8,665,852 | 95.96 |
| C7dS1-3 | GATCAG | 9081290 | 7,625,402 | 83.97 | 482,406 | 6.33 | 7,142,996 | 6,835,232 | 95.69 |
| C8d-1 | TGACCA | 7568876 | 6,629,357 | 87.59 | 136,214 | 2.05 | 6,493,143 | 6,220,847 | 95.81 |
| C8d-2 | ACAGTG | 8801124 | 7,626,898 | 86.66 | 173,255 | 2.27 | 7,453,643 | 7,068,644 | 94.83 |
| C8d-3 | GCCAAT | 7884236 | 7,087,789 | 89.90 | 156,629 | 2.21 | 6,931,160 | 6,629,618 | 95.65 |

**Table S10** Correlation coefficients of transcriptome profiles among the RNA-Seq samples

| Sample | Day 0-1 | Day 0-2 | Day 0-3 | C7dS1-1 | C7dS1-2 | C7dS1-3 | C8d-1 | C8d-2 | C8d-3 |
|---|---|---|---|---|---|---|---|---|---|
| Day 0-1 | 1 | 0.96 | 0.98 | 0.97 | 0.92 | 0.96 | 0.84 | 0.83 | 0.83 |
| Day 0-2 | 0.96 | 1 | 0.98 | 0.94 | 0.84 | 0.94 | 0.89 | 0.91 | 0.85 |
| Day 0-3 | 0.98 | 0.98 | 1 | 0.94 | 0.88 | 0.96 | 0.86 | 0.87 | 0.84 |
| C7dS1-1 | 0.97 | 0.94 | 0.94 | 1 | 0.95 | 0.98 | 0.88 | 0.87 | 0.88 |
| C7dS1-2 | 0.92 | 0.84 | 0.88 | 0.95 | 1 | 0.95 | 0.81 | 0.77 | 0.82 |
| C7dS1-3 | 0.96 | 0.94 | 0.96 | 0.98 | 0.95 | 1 | 0.89 | 0.87 | 0.88 |
| C8d-1 | 0.84 | 0.89 | 0.86 | 0.88 | 0.81 | 0.89 | 1 | 0.98 | 0.98 |
| C8d-2 | 0.83 | 0.91 | 0.87 | 0.87 | 0.77 | 0.87 | 0.98 | 1 | 0.96 |
| C8d-3 | 0.83 | 0.85 | 0.84 | 0.88 | 0.82 | 0.88 | 0.98 | 0.96 | 1 |