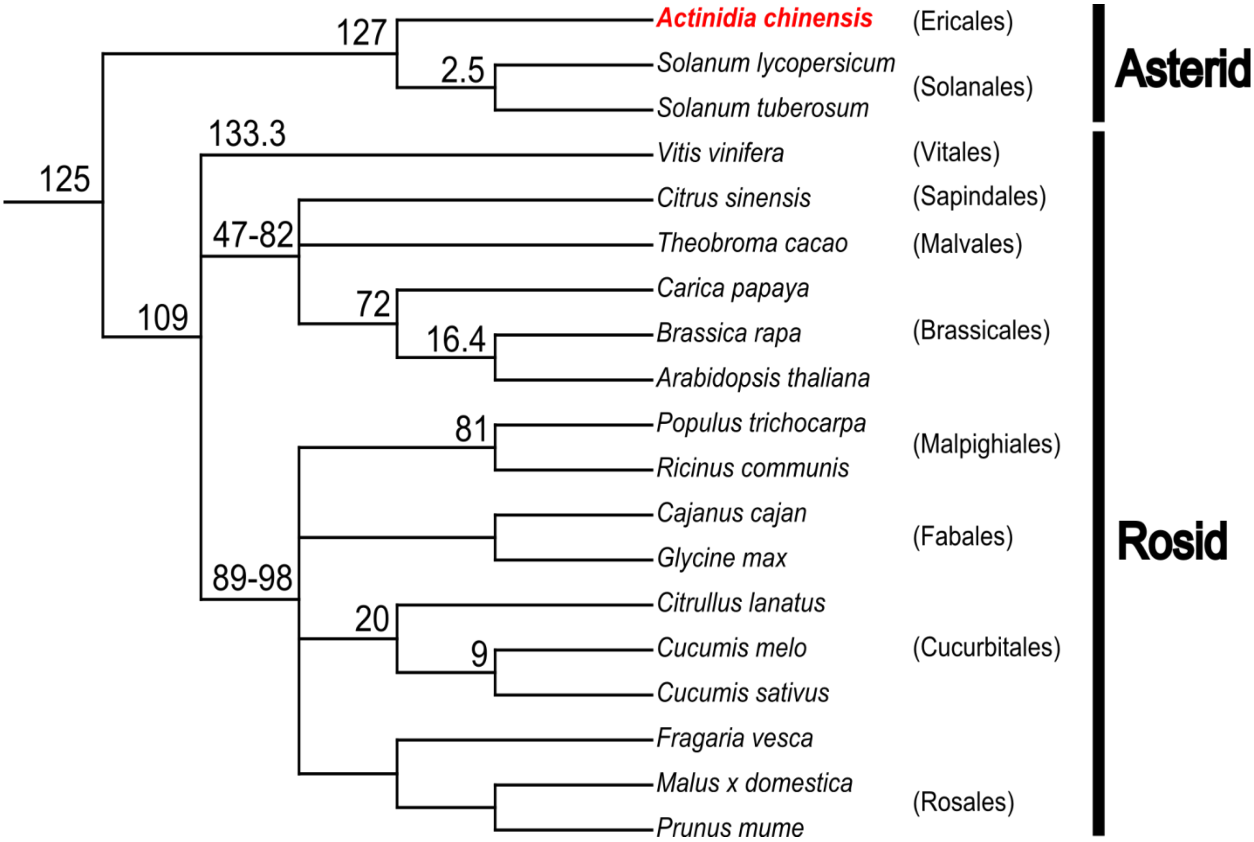
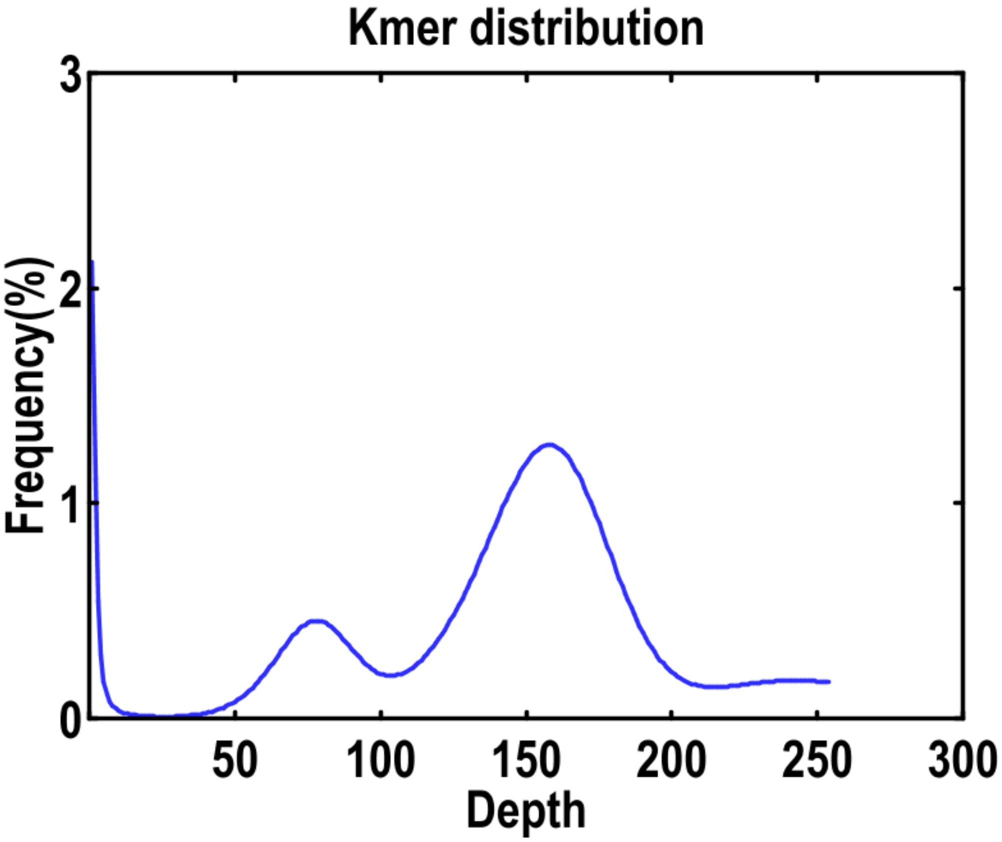
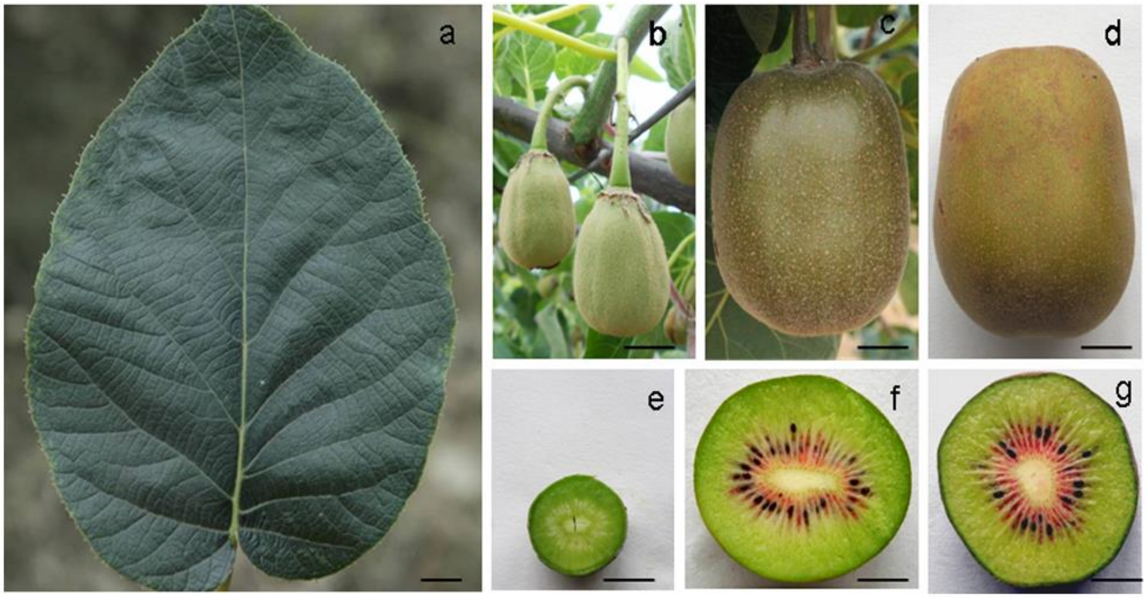


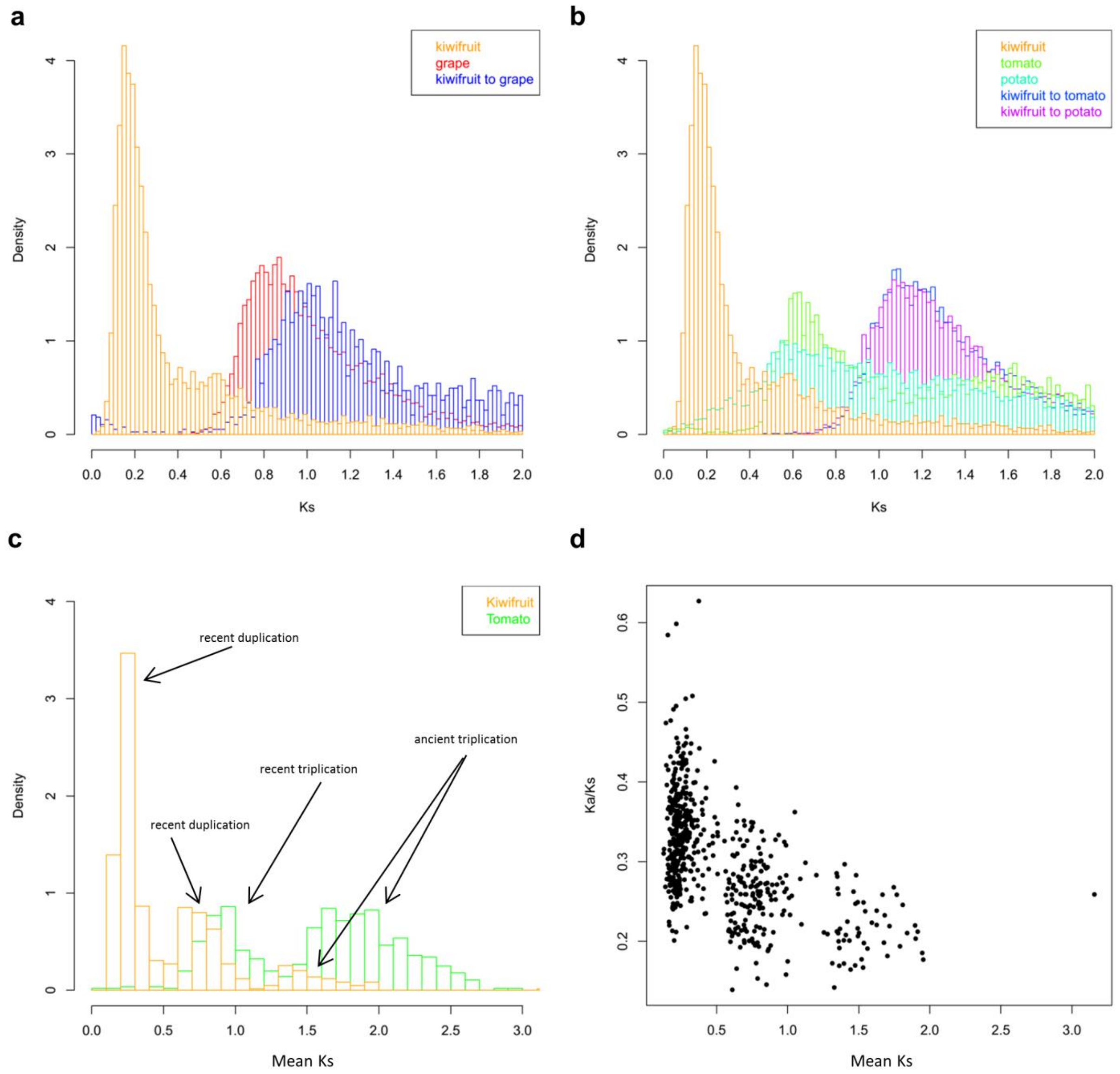
**Supplementary Figure S1.** Taxonomic tree of major sequenced eudicots. The tree was constructed using Interactive Tree Of Life (iTOL) (http://itol.embl.de/) based on the NCBI taxonomy database (http://www.ncbi.nlm.nih.gov/taxonomy). The number on the branches indicates the time of divergence (million years ago) among different organisms, which was obtained from the TimeTree website (http://www.timetree.org/).



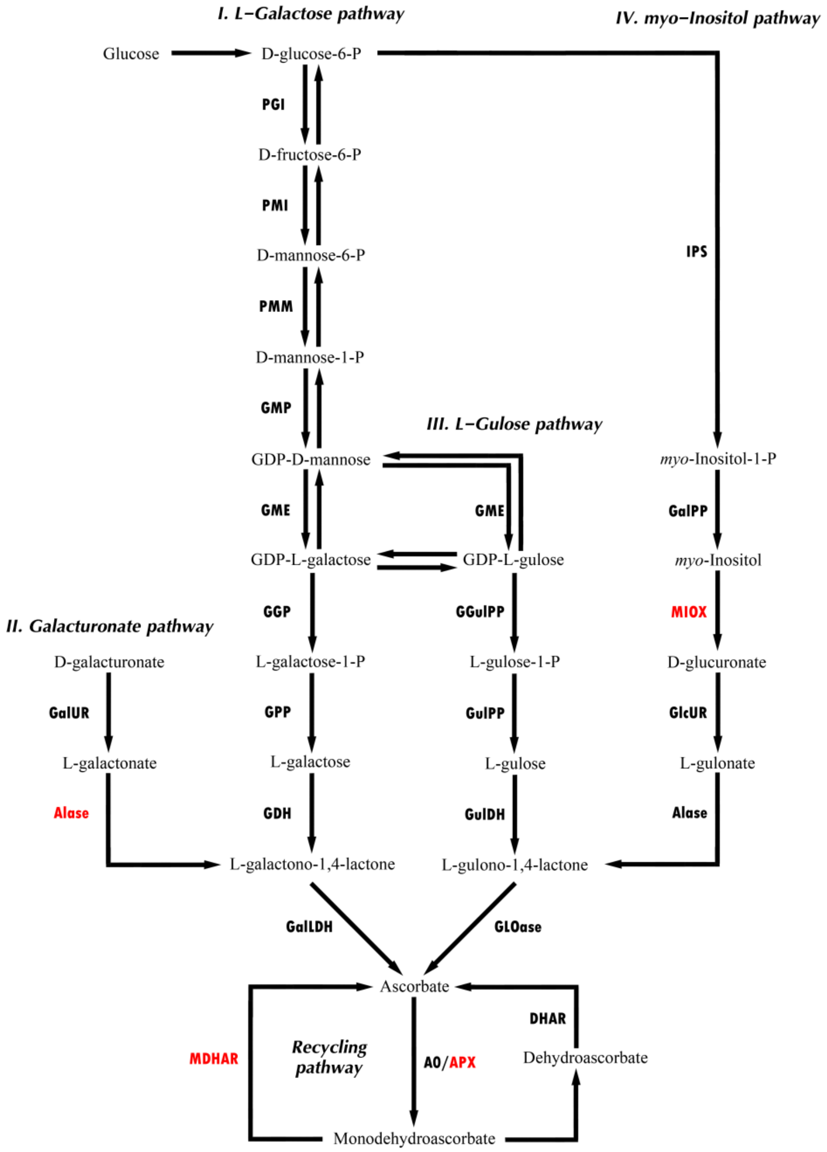
**Supplementary Figure S2.** 17-mer depth distribution of the kiwifruit genome sequencing reads. The frequency of each 17-mer was calculated based on the filtered paired-end reads from libraries with short inserts (≤ 500bp). Two peaks were observed (at 78x and 157x, respectively) indicating heterozygosity in "Hongyang".



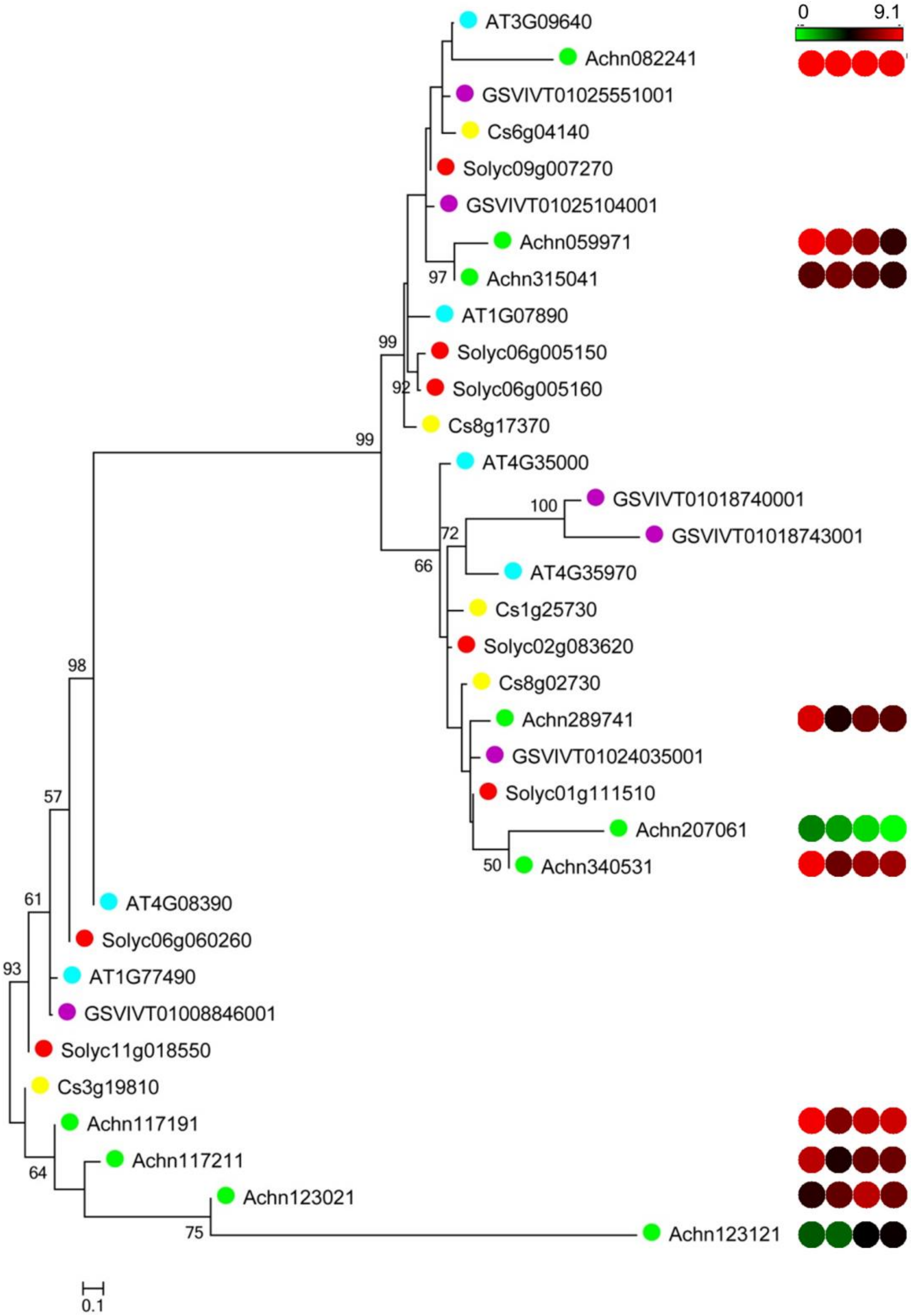
**Supplementary Figure S3.** Kiwifruit tissues used for RNA-seq analysis. Mature leaves (**a**), immature fruits [20 days after pollination (DAP)] (**b**), mature green fruits (120 DAP) (**c**) and ripe fruits (127 DAP) (**d**) were collected from a five-year-old **"**Hongyang**"** tree. Cross-sections of immature fruits (**e**), mature green fruits (**f**), and ripe fruits (**g**) are also shown. Scale bar = 1 cm



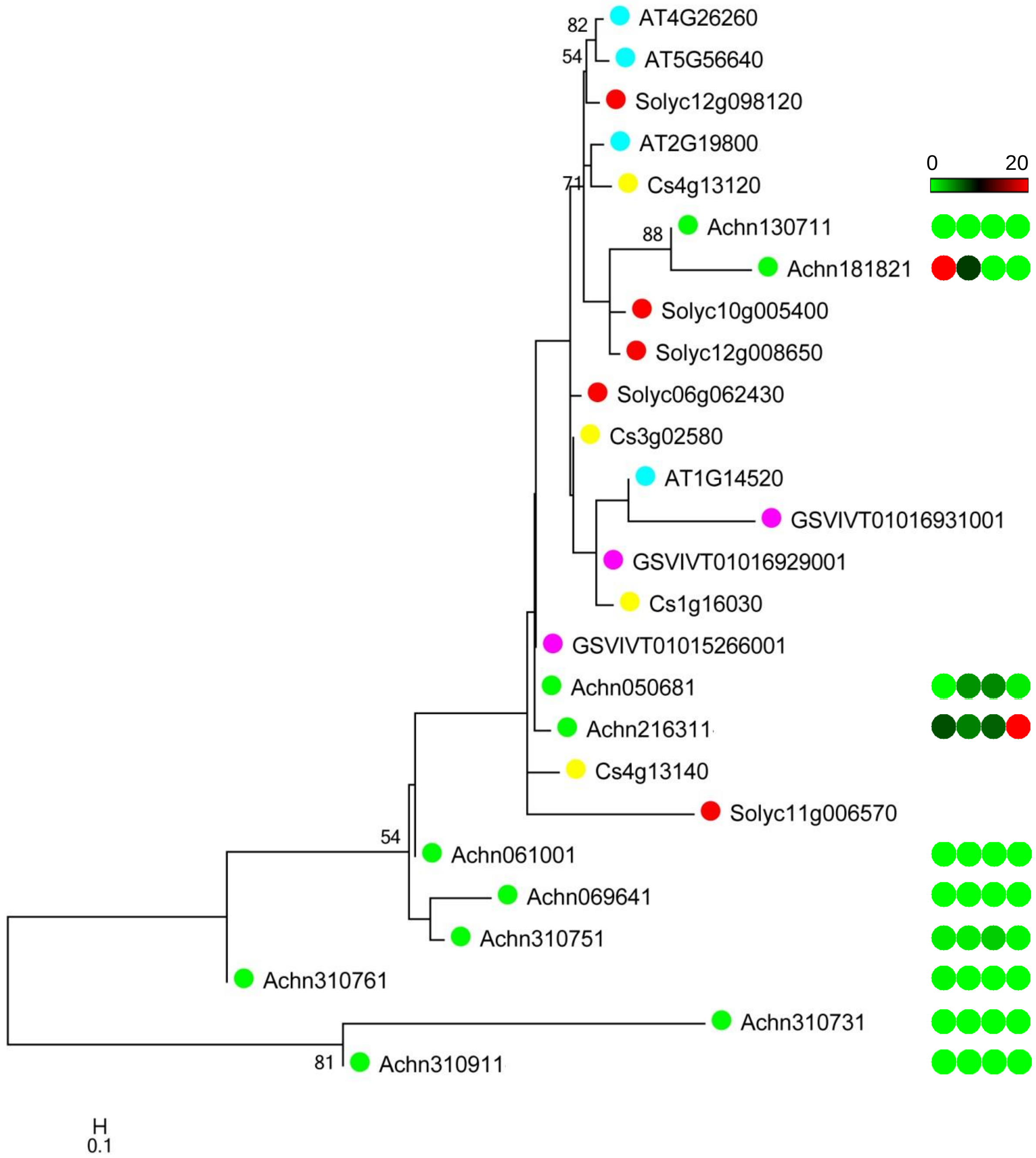
**Supplementary Figure S4.** Distribution of synonymous nucleotide substitution (Ks) rates. (**a**) Ks distribution between syntenic gene pairs within kiwifruit (orange), grape (red) and between kiwifruit and grape (blue). (**b**) Ks distribution between syntenic gene pairs within kiwifruit (orange), tomato (green) , potato (cyan), and between kiwifruit and tomato (blue) and kiwifruit and potato (pink). (**c**) Distribution of the mean Ks value of each syntenic block in kiwifruit (orange) and tomato (green). (**d**) Kiwifruit synteny blocks can be grouped into three different age classes by their mean Ks values.



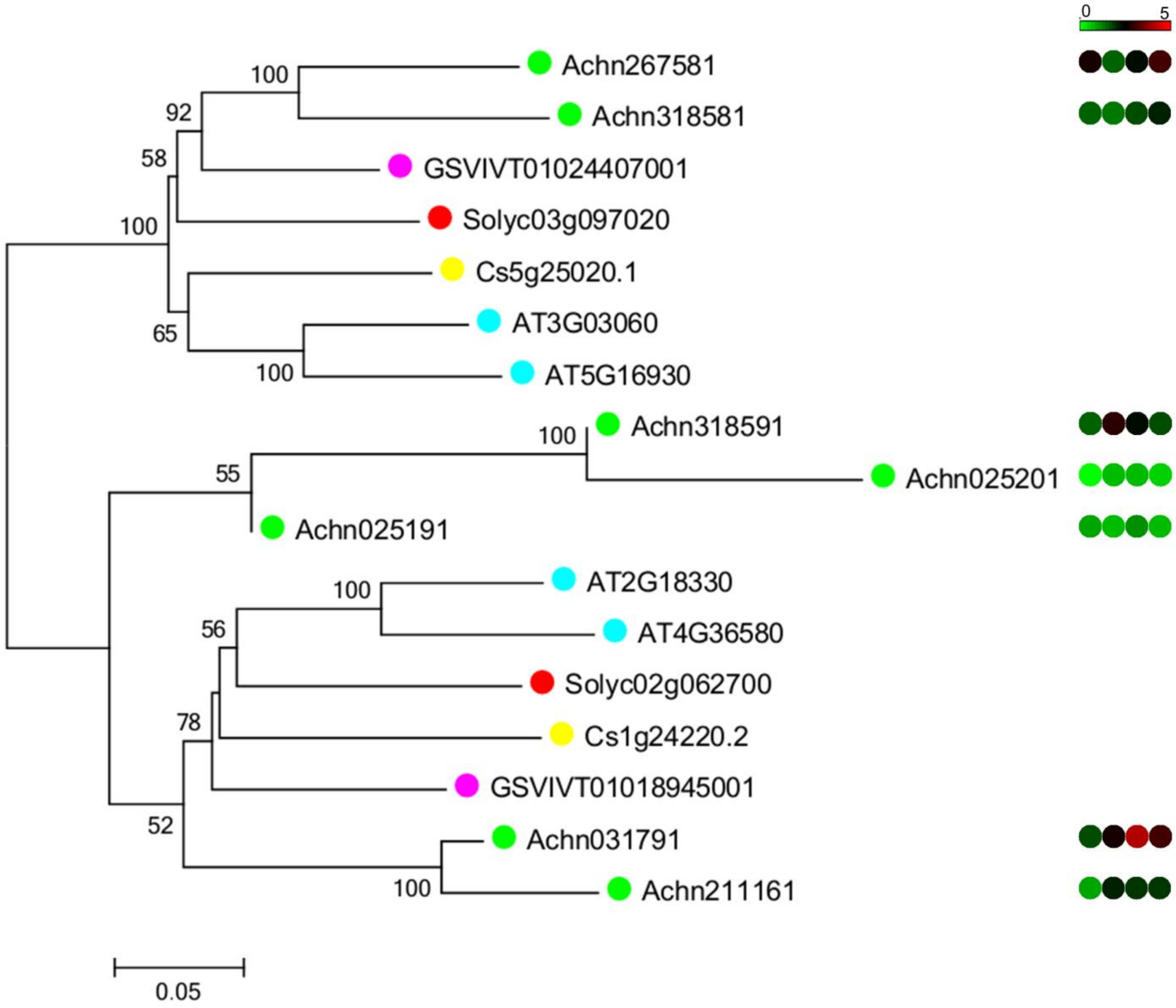
**Supplementary Figure S5.** Ascorbic acid (vitamin C) biosynthesis and recycling pathway in kiwifruit. Gene families with expanded members in kiwifruit are shown in red. Alase, aldonolactonase; AO, L-ascorbate oxidase; APX, L-ascorbate peroxidase; DHAR, dehydroascorbate reductase; GalLDH, L-galactono-1,4-lactone dehydrogenase; GalUR, D-galacturonic acid reductase; GDH, L-galactose dehydrogenase; GGP, GDP-L-galactose phosphorylase; GLOase, L-galactono-1,4-lactone dehydrogenase; GME, GDP-D-mannose-3,5-epimerase; GMP, GDP-D-mannose pyrophosphorylase; GPP, L-galactose-1-phosphate phosphatase; IPS, inositol-3-phosphate synthase; MDHAR, monodehydroascorbate reductase; MIOX, myo-inositol oxygenase; PG, polygalacturonase; PGI, glucose-6-phosphate isomerase; PME, pectinesterase; PMI, mannose-6-phosphate isomerase; PMM, phosphomannomutase.



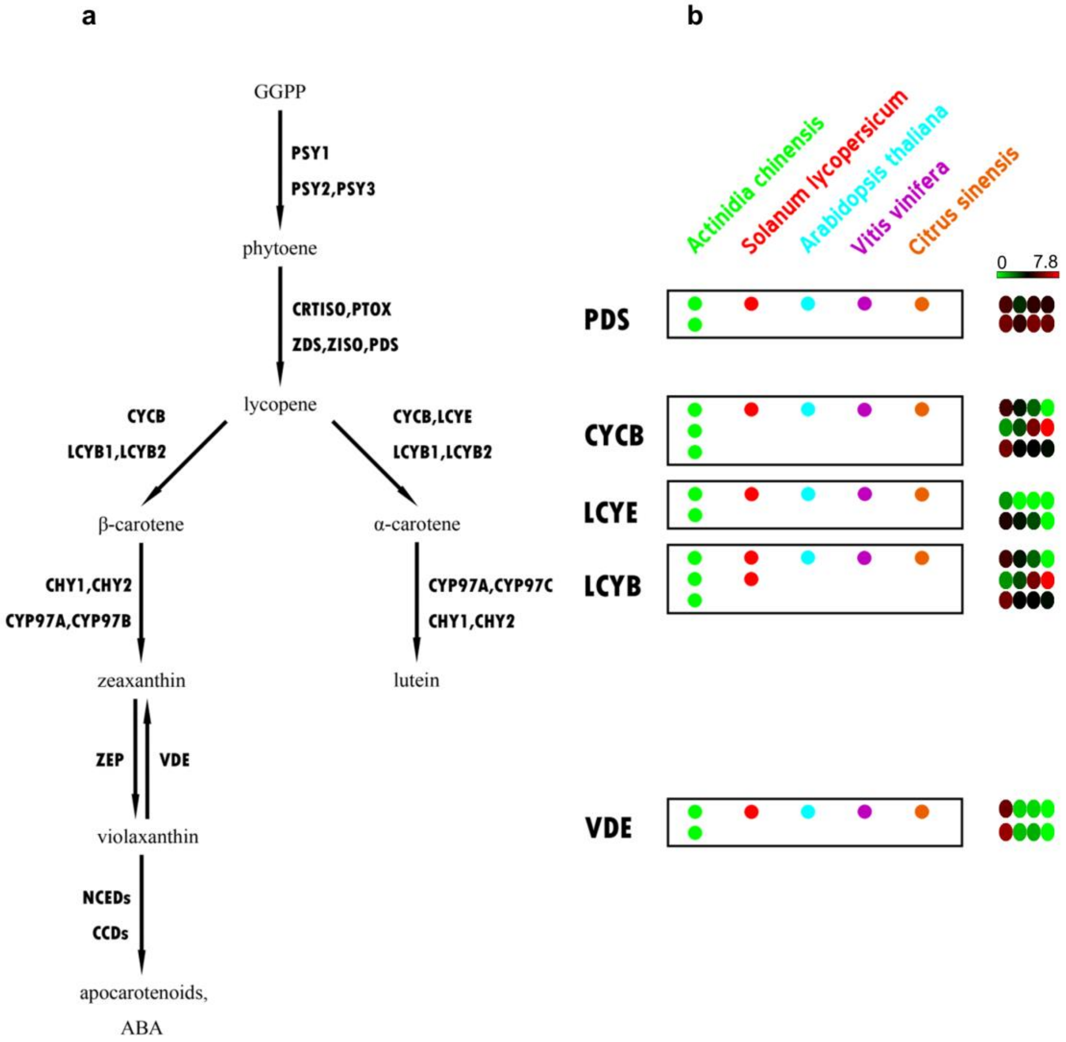
**Supplementary Figure S6.** Phylogenetic analysis of APX (L-ascorbate peroxidase) genes in kiwifruit (green), Arabidopsis (cyan), tomato (red), grape (purple), and sweet orange (yellow). Heatmaps representing expression levels of kiwifruit APX genes in leaf, immature fruit, mature green fruit and ripe fruit (from left to right) are shown on the right of the tree. Log2-transformed gene expression values were used to generate heatmaps.



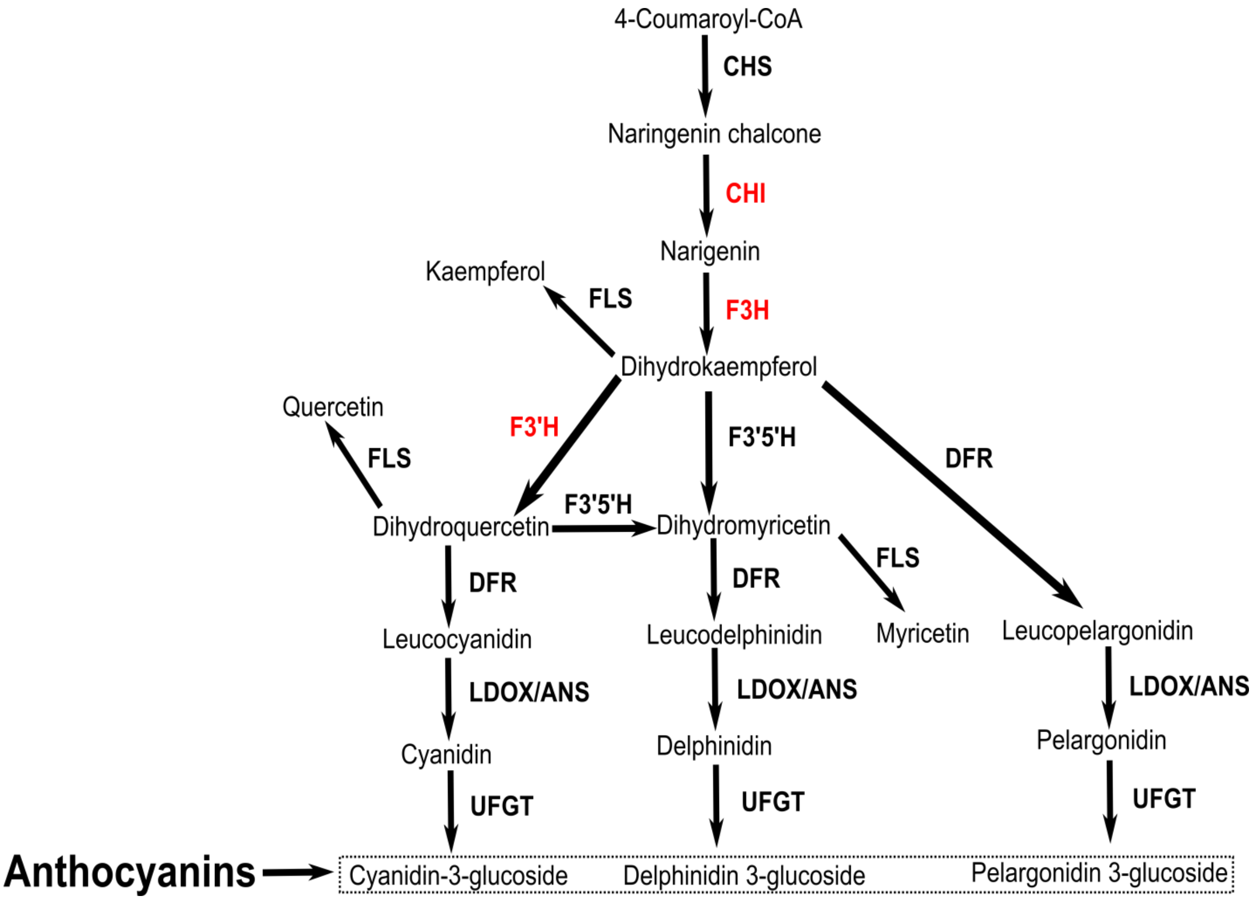
**Supplementary Figure S7.** Phylegenetic analysis of MIOX (myo-inositol oxygenase) genes in kiwifruit (green), Arabidopsis (cyan), tomato (red), grape (purple), and sweet orange (yellow). Heatmaps representing expression levels of kiwifruit MIOX genes in leaf, immature fruit, mature green fruit and ripe fruit (from left to right) are shown on the right of the tree. Normalized gene expression values were used to generate heatmaps.



**Supplementary Figure S8.** Phylegenetic analysis of Alase (aldonolactonase) genes in kiwifruit (green), Arabidopsis (cyan), tomato (red), grape (pink), and sweet orange (yellow). Heatmaps representing expression levels of kiwifruit Alase genes in leaf, immature fruit, mature green fruit and ripe fruit (from left to right) are shown on the right of the tree. Normalized gene expression values were used to generate heatmaps.



**Supplementary Figure S9.** Carotenoid biosynthesis pathway in kiwifruit. (**a**) Simplified carotenoid biosynthesis pathway in kiwifruit. CCD, carotenoid cleavage dioxygenases; CHY, non-heme hydroxylases; CrtISO, 7,9,7',9'-tetra-cis-lycopene isomerase; CYCB, lycopene beta-cyclase; CYP, P450 hydroxylase; LCYB, lycopene beta-cyclase; LCYE, lycopene epsilon-cyclase; NCED, 9-cis-epoxycarotenoid dioxygenase; PDS, phytoene desaturase; PSY, phytoene synthase; PTOX, alternative oxidase; VDE, violaxanthin deepoxidase; ZDS, zeta-carotene desaturase; ZEP, zeaxanthin epoxidase; ZISO, 9, 15, 9’-tri-cis-zeta-carotene isomerase. (**b**) Kiwifruit gene families in which expansions occurred are shown with the comparison of gene members in Arabidopsis (cyan), tomato (red), grape (purple), sweet orange (dark orange) and kiwifruit (green). Heatmaps representing expression levels of kiwifruit genes in leaf, immature fruit, mature green fruit and ripe fruit (from left to right) are shown on the right. Log2-transformed gene expression values were used to generate heatmaps.



**Supplementary Figure S10.** Biosynthesis pathway of anthocyanins. Compared to Arabidopsis, tomato, grape, and sweet orange, gene families with expanded members in kiwifruit are shown in red. CHS, Chalcone synthase; CHI, Chalcone isomerase; F3H, Flavanone 3-hydroxylase; F3’H, Flavonoid 3’-hydroxylase; F3’5’H, Flavonoid 3’5’-hydroxylase; DFR, Dihydroflavonol 4-reductase; LDOX, Leucoanthocyanidin dioxygenase; ANS, Anthocyanidin synthase; UFGT, UDP-glucose flavonoid 3-O-glucosyltransferase; FLS, Flavonol synthase.

**Supplementary Table S1. Physical or physiological parameters of tissues/organs of kiwifruit cv. Hongyang**

| | fruit (20 DAP) | fruit (120 DAP) | fruit (127 DAP) | leaf |
|---|---|---|---|---|
| Weight per fruit or leaf (g) | 2.83±0.33 | 78.14±8.29 | 76.30±8.19 | 3.28±0.41 |
| Tranverse diameter (cm) | 1.39±0.20 | 4.66±0.30 | 4.62±0.22 | 10.86±0.56 |
| Longitudinal diameter (cm) | 1.85±0.20 | 5.65±0.32 | 5.77±0.23 | 11.69±1.10 |
| Brix | 6.97+0.05 | 7.47±0.46 | 9.57±0.68 | 10.6+0.14 |
| Starch (mg/g FW) | 0.63±0.09 | 14.95±0.76 | 10.55±0.25 | 0.03±0.003 |
| Ascorbic acid (Vitamin C) (mg/100g FW) | 100.54±1.87 | 76.84±1.04 | 75.21±2.75 | 57.87±2.24 |
| Total carotenoids (mg/100g FW) | 1.40±0.02 | 0.89±0.02 | 0.91±0.03 | 30.04±0.71 |
| Total anthocyanins (mg/100g FW) | 1.91±0.10 | 2.44±0.08 | 2.65±0.01 | 5.97±0.06 |
| Total flavonoids (mg/g FW) | 0.90±0.09 | 0.13±0.001 | 0.19±0.003 | 1.34±0.01 |
| Chlorophyll a (mg/100g FW) | 4.82±0.27 | 2.51±0.05 | 1.95±0.12 | 187.95±10.99 |
| Chlorophyll b (mg/100g FW) | 2.27±0.15 | 1.54±0.04 | 1.03±0.03 | 71.02±4.81 |
| Total Chlorophyll (mg/100g FW) | 7.08±0.41 | 4.05±0.07 | 2.98±0.15 | 258.91±15.78 |
| Reducing Sugar (mg/g FW) | 6.44±0.37 | 6.59±0.32 | 18.18±1.40 | 12.64±0.81 |
| Total sugar (mg/g FW) | 22.47±1.35 | 113.12±5.94 | 114.71±6.23 | 16.30±0.78 |

[a] Data is shown as the mean ± standard error of triplicated samples

**Supplementary Table S2. Summary of kiwifruit genome DNA sequencing data**

| Sequence data | Library insert size | Library number | Base numbers | Read length(bp) | Base number after filtering | Coverage |
|---|---|---|---|---|---|---|
| Illumina reads | 180 bp | 1 | 29,993,534,760 | 105 | 28,604,783,130 | 37.74 |
| | 330 bp | 1 | 22,101,901,104 | 101 | 21,131,288,680 | 27.88 |
| | 500 bp | 1 | 36,446,507,712 | 101 | 33,895,628,482 | 44.72 |
| | 500 bp* | 1 | 37,992,919,318 | 101 | 35,452,582,872 | 46.77 |
| | 2 kb | 1 | 13,687,594,740 | 101 | 12,552,927,006 | 16.56 |
| | 5 kb | 1 | 5,348,257,848 | 101 | 4,785,837,732 | 6.31 |
| | 8 kb | 1 | 2,440,967,798 | 101 | 2,230,080,606 | 2.94 |
| | 20 kb | 1 | 4,078,442,822 | 101 | 2,646,350,490 | 3.49 |
| Total | | 7 | 114,097,206,784 | | 105,846,896,126 | 139.64 |

* This library was only used for the quality evaluation of the genome assembly and not used for assembly and counting total bases and coverage.

**Supplementary Table S3. Potential structure variations (misassemblies) identified in the kiwifruit genome assembly**

| Scaffold | Scaffold size | Left anchor start | Left anchor end | Right anchor start | Right anchor end | SV type | No. supporting read pairs |
|---|---|---|---|---|---|---|---|
| scaffold_166 | 826808 | 302666 | 302919 | 303706 | 303980 | DELETION | 13 |
| scaffold_291 | 5122 | 54 | 294 | 1279 | 1425 | DELETION | 13 |
| scaffold_254 | 9562 | 3990 | 4165 | 7462 | 7778 | DELETION | 14 |
| scaffold_28 | 1512218 | 1189099 | 1189518 | 1192907 | 1193321 | DELETION | 15 |
| scaffold_706 | 1224238 | 722882 | 723195 | 731258 | 731624 | DELETION | 18 |
| scaffold_200 | 715646 | 155902 | 156173 | 157057 | 157491 | DELETION | 20 |
| scaffold_101 | 123009 | 11514 | 11789 | 13618 | 13905 | INVERSIO | 20 |
| scaffold_158 | 360270 | 273363 | 273771 | 274867 | 275270 | DELETION | 22 |
| scaffold_911 | 169783 | 113471 | 113912 | 123637 | 124004 | DELETION | 23 |
| scaffold_350 | 17337 | 51 | 520 | 10401 | 10857 | DELETION | 23 |
| scaffold_257 | 591908 | 13253 | 13619 | 14440 | 14868 | DELETION | 24 |
| scaffold_619 | 3646 | 5 | 405 | 2696 | 3123 | DELETION | 27 |
| scaffold_353 | 471192 | 187221 | 187790 | 190102 | 190620 | DELETION | 30 |
| scaffold_186 | 775636 | 699350 | 699766 | 702540 | 702914 | DELETION | 31 |
| scaffold_379 | 667387 | 250182 | 250602 | 260684 | 261090 | DELETION | 32 |
| scaffold_291 | 575355 | 200956 | 201362 | 202109 | 202488 | DELETION | 37 |
| scaffold_865 | 174759 | 140760 | 141214 | 151291 | 151734 | DELETION | 37 |
| scaffold_134 | 894100 | 480533 | 481116 | 491083 | 491683 | DELETION | 41 |
| scaffold_18 | 1619216 | 1525534 | 1526024 | 1530671 | 1531286 | DELETION | 44 |
| scaffold_933 | 766304 | 408844 | 409247 | 410359 | 410740 | DELETION | 46 |
| scaffold_899 | 180565 | 133877 | 134454 | 135468 | 136050 | DELETION | 47 |
| scaffold_342 | 508507 | 281063 | 281536 | 282572 | 282979 | DELETION | 51 |
| scaffold_114 | 892888 | 284044 | 284535 | 288096 | 288603 | DELETION | 54 |
| scaffold_894 | 156532 | 62271 | 62837 | 63245 | 63757 | DELETION | 63 |

**Supplementary Table S4. Summary of statistics of EST mapping to the kiwifruit genome assembly**

| Dataset | Number | Total length (bp) | Base pair covered | | >90% of sequence covered by one scaffold by one scaffold | | >50% of sequence coverred by one scaffold by one scaffold | |
|---|---|---|---|---|---|---|---|---|
| | | | Length | Percent | Number | Percent | Number | Percent |
| EST from *A. chinese* | | | | | | | | |
| >=100 | 47,357 | 26,302,430 | 25,842,324 | 98.25 | 46,024 | 97.19 | 47,012 | 99.27 |
| >=500 | 34,596 | 21,323,296 | 20,928,981 | 98.15 | 33,679 | 97.35 | 34,374 | 99.36 |
| >=1000 | 3 | 3,563 | 3,560 | 99.92 | 3 | 100.00 | 3 | 100.00 |
| EST from *A. deliciosa* | | | | | | | | |
| >=100 | 56,509 | 26,004,153 | 24,539,929 | 94.37 | 51,298 | 90.78 | 54,324 | 96.13 |
| >=500 | 27,412 | 16,259,283 | 15,288,368 | 94.03 | 24,977 | 91.12 | 26,253 | 95.77 |
| >=1000 | 3 | 4,848 | 4,836 | 99.75 | 3 | 100.00 | 3 | 100.00 |
| EST from *A. eriantha* | | | | | | | | |
| >=100 | 12,336 | 6,117,919 | 5,868,986 | 95.93 | 11,577 | 93.85 | 12,030 | 97.52 |
| >=500 | 7,236 | 4,403,289 | 4,230,956 | 96.09 | 6,888 | 95.19 | 7,088 | 97.95 |
| >=1000 | 2 | 3,218 | 3,070 | 95.40 | 2 | 100.00 | 2 | 100.00 |

**Supplementary Table S5. Repetitive sequences in the kiwifruit genome**

| | Element Type | Number (copies) | Lengths (bp) |
|---|---|---|---|
| Class I | LTR/Copia | 75,720 | 33,834,772 |
| | LTR/Gypsy | 76,771 | 40,764,135 |
| | LTR/BEL | 1,582 | 241,885 |
| | LTR/ERV1 | 16,034 | 3,674,207 |
| | LTR/ERV2 | 4,992 | 930,049 |
| | LTR/ERV3 | 4,014 | 966,031 |
| | Caulimoviridae | 2,002 | 1,203,627 |
| | Endogenous | 3,830 | 669,198 |
| | LTR/other | 504 | 280,071 |
| | SINE/5S_rRNA | 32 | 87,467 |
| | SINE/45S_rRNA | 641 | 129,219 |
| | SINE/other | 5,102 | 1,945,511 |
| | LINE/CR1 | 7,976 | 2,459,485 |
| | LINE/L1 | 6,735 | 1,445,426 |
| | LINE/L2 | 517 | 490,532 |
| | LINE/LINE | 3,634 | 817,017 |
| | LINE/R1 | 7 | 1,750 |
| | LINE/Penelope | 1,731 | 277,573 |
| Class II | DNA/MuDR | 18,664 | 4,239,939 |
| | DNA/PIF_Harbinger | 2,219 | 319,171 |
| | DNA/hAT | 20,786 | 6,348,660 |
| | DNA/Helitron | 16,518 | 3,256,637 |
| | DNA/P | 290 | 201,446 |
| | DNA/EnSpm | 31,928 | 7,716,352 |
| | DNA/Kolobok | 3,234 | 947,798 |
| | DNA/Mariner/Tc1 | 4,413 | 1,086,953 |
| | DNA/Chapaev | 3,076 | 582,307 |
| | DNA/other | 18,641 | 4,549,450 |
| | Satellite/Satellite | 346 | 287,823 |
| Other repeat | — | 128,956 | 35,487,734 |
| Unclassified | — | 242,989 | 69,439,758 |
| Total | | 698,275 | ~222M |

**Supplementary Table S6. Enriched GO terms in gene clusters specific to flesh fruits (kiwifruit, tomato and grape)**

| Gene Ontology term | Enrichment FDR |
|---|---|
| RNA-dependent DNA replication | 7.94E-07 |
| response to gibberellin stimulus | 1.56E-05 |
| response to UV-B | 4.10E-05 |
| flavonoid biosynthetic process | 0.00012 |
| response to cyclopentenone | 0.00016 |
| regulation of gibberellic acid mediated signaling pathway | 0.00021 |
| flavonoid metabolic process | 0.0003 |
| regulation of chlorophyll biosynthetic process | 0.00063 |
| regulation of cellular biosynthetic process | 0.00074 |
| phenylpropanoid metabolic process | 0.00108 |
| regulation of biosynthetic process | 0.00114 |
| regulation of nitrogen compound metabolic process | 0.00125 |
| response to toxin | 0.00149 |
| regulation of chlorophyll metabolic process | 0.00161 |
| phenylpropanoid biosynthetic process | 0.00204 |
| nucleic acid metabolic process | 0.00228 |
| raffinose family oligosaccharide biosynthetic process | 0.00234 |
| response to stress | 0.00259 |
| response to osmotic stress | 0.00268 |
| regulation of cellular metabolic process | 0.00275 |
| anthocyanin-containing compound biosynthetic process | 0.00299 |
| response to auxin stimulus | 0.00303 |
| response to light stimulus | 0.00318 |
| negative regulation of heterochromatin assembly | 0.00376 |
| negative regulation of chromatin assembly or disassembly | 0.00376 |
| toxin catabolic process | 0.00495 |
| anthocyanin-containing compound metabolic process | 0.00575 |
| response to salt stress | 0.00603 |
| primary metabolic process | 0.0061 |
| toxin metabolic process | 0.00628 |
| regulation of cofactor metabolic process | 0.00697 |
| regulation of secondary metabolic process | 0.00714 |
| defense response | 0.00717 |
| response to radiation | 0.00783 |
| oligosaccharide biosynthetic process | 0.00856 |
| response to organic cyclic compound | 0.00976 |

**Supplementary Table S7. Enriched GO terms in gene clusters specific to kiwifruit**

| Gene Ontology term | Enrichment FDR |
|---|---|
| RNA-dependent DNA replication | 9.88E-15 |
| DNA integration | 7.40E-12 |
| pollen tube reception | 2.02E-06 |
| intraspecies interaction between organisms | 1.72E-05 |
| steroid hormone mediated signaling pathway | 0.00025 |
| response to brassinosteroid stimulus | 0.00026 |
| positive regulation of protein export from nucleus | 0.00041 |
| brassinosteroid mediated signaling pathway | 0.00065 |
| cellular response to brassinosteroid stimulus | 0.00065 |
| positive regulation of cell fate commitment | 0.00371 |
| specification of floral organ identity | 0.00405 |
| formation of organ boundary | 0.00635 |
| formation of anatomical boundary | 0.00635 |
| regulation of cell fate commitment | 0.0066 |
| cellular response to steroid hormone stimulus | 0.00784 |

**Supplementary Table S8. Comparative analysis of gene families in the vitamin C biosynthesis and recycling pathway**

| Gene | Description | Number of genes | | | | |
|---|---|---|---|---|---|---|
| | | Arabidopsis | Kiwifruit | Tomato | Grape | Sweet orange |
| Alase | aldonolactonase | 4 | 7 | 2 | 2 | 2 |
| AO | L-ascorbate oxidase | 3 | 7 | 4 | 7 | 2 |
| APX | L-ascorbate peroxidase | 6 | 10 | 7 | 6 | 5 |
| DHAR | dehydroascorbate reductase | 4 | 2 | 2 | 3 | 2 |
| GalLDH | L-galactono-1,4-lactone dehydrogenase | 1 | 1 | 1 | 1 | 2 |
| GalUR | D-galacturonic acid reductase | 8 | 17 | 11 | 21 | 18 |
| GDH | L-galactose dehydrogenase | 1 | 1 | 1 | 1 | 1 |
| GGP | GDP-L-galactose phosphorylase | 2 | 2 | 2 | 2 | 3 |
| GLOase | L-galactono-1,4-lactone dehydrogenase | 1 | 1 | 1 | 1 | 2 |
| GME | GDP-D-mannose-3,5-epimerase | 1 | 2 | 2 | 2 | 3 |
| GMP | GDP-D-mannose pyrophosphorylase | 3 | 3 | 3 | 1 | 2 |
| GPP | L-galactose-1-phosphate phosphatase | 1 | 2 | 3 | 1 | 1 |
| IPS | inositol-3-phosphate synthase | 3 | 4 | 5 | 1 | 1 |
| MDHAR | monodehydroascorbate reductase | 5 | 7 | 3 | 3 | 3 |
| MIOX | myo-inositol oxygenase | 4 | 10 | 5 | 3 | 4 |
| PGI | glucose-6-phosphate isomerase | 2 | 4 | 2 | 4 | 2 |
| PMI | mannose-6-phosphate isomerase | 2 | 3 | 3 | 2 | 2 |
| PMM | phosphomannomutase | 1 | 1 | 3 | 1 | 1 |

**Supplementary table S9. Expression of kiwifruit genes in the vitamin C biosynthesis and recycling pathway**

| Gene | Description | Gene ID | Normalized expression (FPKM) | | | |
|---|---|---|---|---|---|---|
| | | | Leaf | Immature fruit | Mature green fruit | Ripe fruit |
| Alase | aldonolactonase | Achn025191 | 0.85 | 0.83 | 1.15 | 0.71 |
| | | Achn025201 | 0 | 0.81 | 0.8 | 0.45 |
| | | Achn031791 | 1.8 | 2.85 | 4.37 | 3.22 |
| | | Achn211161 | 0.9 | 2.14 | 2.01 | 1.9 |
| | | Achn267581 | 2.81 | 1.64 | 2.47 | 3.14 |
| | | Achn318581 | 1.56 | 1.29 | 1.84 | 2.13 |
| | | Achn318591 | 1.6 | 3.04 | 2.48 | 1.83 |
| AO | L-ascorbate oxidase | Achn228031 | 22.93 | 66.36 | 2.45 | 0.12 |
| | | Achn228041 | 20.23 | 29.11 | 3.56 | 0.02 |
| | | Achn230551 | 0.24 | 0.69 | 1.42 | 4.97 |
| | | Achn230561 | 8.26 | 4.71 | 16.47 | 22.67 |
| | | Achn230681 | 0.26 | 0.53 | 1.26 | 2.04 |
| | | Achn267251 | 0.5 | 2.26 | 0 | 0 |
| | | Achn335061 | 20.39 | 11.25 | 0.18 | 0.17 |
| APX | L-ascorbate peroxidase | Achn059971 | 152.8 | 98.32 | 57.35 | 20.95 |
| | | Achn082241 | 255.37 | 535.25 | 280.44 | 154.05 |
| | | Achn117191 | 158.46 | 45.16 | 95.66 | 99.05 |
| | | Achn117211 | 81.21 | 17.28 | 36.71 | 38.26 |
| | | Achn123021 | 18.51 | 35.99 | 88.84 | 37.82 |
| | | Achn123121 | 5.11 | 4.67 | 13.49 | 14.31 |
| | | Achn207061 | 3.42 | 2.52 | 1.46 | 0.93 |
| | | Achn289741 | 118.17 | 17.57 | 39.54 | 32.98 |
| | | Achn315041 | 30.75 | 40.56 | 31.97 | 20.9 |
| | | Achn340531 | 147.6 | 37.61 | 66.48 | 65.88 |
| DHAR | dehydroascorbate reductase | Achn224431 | 13.66 | 2.1 | 3.38 | 3.47 |
| | | Achn278191 | 121.01 | 15.99 | 22.96 | 20.11 |
| GalLDH | L-galactono-1,4-lactone dehydrogenase | Achn136491 | 16.45 | 22.87 | 21.02 | 7.47 |
| GalUR | D-galacturonic acid reductase | Achn018821 | 13.78 | 13.9 | 51.56 | 23.56 |
| | | Achn022001 | 2.15 | 0.79 | 0.8 | 0.77 |
| | | Achn022021 | 0.56 | 2.44 | 1.53 | 3.2 |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | Achn040261 | 1.25 | 0.5 | 1.55 | 0.3 |
| | | Achn073761 | 0.85 | 5.3 | 27.31 | 14.6 |
| | | Achn101501 | 124.62 | 87.48 | 70.89 | 31.53 |
| | | Achn105301 | 85.52 | 8.56 | 104.24 | 34.32 |
| | | Achn110361 | 56.55 | 4.04 | 3.52 | 21.41 |
| | | Achn110371 | 55.16 | 4.57 | 3.31 | 11.69 |
| | | Achn110381 | 19.61 | 8.58 | 1.22 | 4.64 |
| | | Achn144491 | 10.58 | 1.85 | 1.73 | 1.13 |
| | | Achn162311 | 27.22 | 33.64 | 8.41 | 0.35 |
| | | Achn162861 | 50.61 | 56.71 | 309.83 | 189.25 |
| | | Achn297831 | 0 | 0 | 0 | 0 |
| | | Achn319141 | 0 | 0.04 | 0 | 0.02 |
| | | Achn354661 | 0.39 | 0.1 | 0.12 | 0 |
| | | Achn375871 | 13.74 | 12.99 | 24.93 | 52.28 |
| GDH | L-galactose dehydrogenase | Achn334011 | 24.81 | 55.85 | 20.52 | 3.78 |
| GGP | GDP-L-galactose phosphorylase | Achn155031 | 521.02 | 664.35 | 73.23 | 64.35 |
| | | Achn339231 | 45.93 | 13.48 | 8.53 | 15.26 |
| GLOase | L-galactono-1,4-lactone dehydrogenase | Achn136491 | 16.45 | 22.87 | 21.02 | 7.47 |
| GME | GDP-D-mannose-3,5-epimerase | Achn030021 | 420.44 | 722.72 | 119.08 | 51.85 |
| | | Achn054171 | 870.11 | 293.4 | 99.38 | 47.61 |
| GMP | GDP-D-mannose pyrophosphorylase | Achn055281 | 85.02 | 313.61 | 100.13 | 62.47 |
| | | Achn212141 | 14.5 | 64.94 | 28.65 | 29.08 |
| | | Achn258021 | 344.27 | 58.94 | 63.24 | 63.03 |
| GPP | L-galactose-1-phosphate phosphatase | Achn262331 | 72.99 | 33.9 | 27.11 | 49.89 |
| | | Achn341581 | 39.8 | 25.01 | 7.19 | 13.71 |
| IPS | inositol-3-phosphate synthase | Achn093931 | 4690.43 | 53.74 | 9.23 | 10.56 |
| | | Achn093941 | 1485.98 | 112.97 | 7.98 | 12.92 |
| | | Achn171511 | 1643.32 | 1598.71 | 34.83 | 69.24 |
| | | Achn332511 | 1643.22 | 1598.59 | 34.79 | 68.77 |
| MDHAR | monodehydroascorbate reductase | Achn005611 | 14.31 | 16.97 | 19.01 | 10.83 |
| | | Achn044901 | 0.19 | 0 | 0 | 0 |
| | | Achn075231 | 68.15 | 60.95 | 72.44 | 66.37 |
| | | Achn091771 | 94.21 | 33.69 | 57.72 | 75.33 |
| | | Achn132811 | 23.4 | 5.74 | 8.75 | 11.85 |
| | | Achn297231 | 52.19 | 8.78 | 39.63 | 21.92 |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | Achn389481 | 0.27 | 0.89 | 0.61 | 0.01 |
| MIOX | myo-inositol oxygenase | Achn050681 | 0.08 | 4.63 | 5.55 | 2.64 |
| | | Achn061001 | 0.08 | 0 | 0.1 | 0 |
| | | Achn069641 | 0 | 0 | 0 | 0 |
| | | Achn130711 | 0 | 0 | 0 | 0 |
| | | Achn181821 | 89.3 | 6.52 | 0.2 | 0.06 |
| | | Achn216311 | 5.91 | 4.61 | 4.79 | 15.53 |
| | | Achn310731 | 0.1 | 0.13 | 0.16 | 0.35 |
| | | Achn310751 | 0.79 | 0.53 | 2.45 | 0.65 |
| | | Achn310761 | 0.32 | 0 | 0.52 | 0 |
| | | Achn310911 | 0.29 | 0 | 0 | 0 |
| PGI | glucose-6-phosphate isomerase | Achn014461 | 31.91 | 60.61 | 64.92 | 37.22 |
| | | Achn087691 | 24.1 | 12.29 | 18.47 | 23.88 |
| | | Achn197361 | 22.8 | 33.39 | 49.25 | 37.06 |
| | | Achn221981 | 13.14 | 23.64 | 32.24 | 31.57 |
| PMI | mannose-6-phosphate isomerase | Achn292661 | 5.69 | 5.54 | 1.47 | 3.21 |
| | | Achn330131 | 25.44 | 32.57 | 27.33 | 23.56 |
| | | Achn339561 | 8.6 | 11.18 | 4.84 | 6.51 |
| PMM | phosphomannomutase | Achn302501 | 30.45 | 58.86 | 27.32 | 26.86 |

**Supplementary Table S10. Comparative analysis of gene families in the carotenoid biosynthesis pathway**

| Gene | Description | Number of genes | | | | |
|---|---|---|---|---|---|---|
| | | Arabidopsis | Kiwifruit | Tomato | Grape | Sweet orange |
| CCD | carotenoid cleavage enzymes | 4 | 8 | 6 | 6 | 9 |
| CHY | non-heme hydroxylases | 2 | 2 | 2 | 2 | 2 |
| CrtISO | 7,9,7',9'-tetra-cis-lycopene isomerase | 1 | 1 | 1 | 1 | 1 |
| CYCB | lycopene beta-cyclases | 1 | 3 | 1 | 1 | 1 |
| CYP | P450 hydroxylases | 3 | 2 | 3 | 3 | 3 |
| LCYB | lycopene beta-cyclases | 1 | 3 | 2 | 1 | 1 |
| LCYE | lycopene epsilon-cyclase | 1 | 2 | 1 | 1 | 1 |
| NCED | carotenoid cleavage enzymes | 5 | 5 | 3 | 3 | 3 |
| PDS | phytoene desaturase | 1 | 2 | 1 | 1 | 1 |
| PSY | phytoene synthases | 1 | 3 | 3 | 3 | 3 |
| PTOX | alternative oxidase | 1 | 1 | 1 | 1 | 1 |
| VDE | violaxanthin deepoxidase | 1 | 2 | 1 | 1 | 1 |
| ZDS | zeta-carotene desaturase | 1 | 1 | 1 | 1 | 8 |
| ZEP | zeaxanthin epoxidase | 1 | 1 | 1 | 2 | 2 |
| ZISO | 9,15,9'-tri-cis-zeta-carotene isomerase | 1 | 1 | 1 | 1 | 1 |

**Supplementary Table S11. Comparative analysis of gene families in the flavonoid and anthocyanin biosynthesis pathway**

| Gene | Description | Number of genes | | | | |
|---|---|---|---|---|---|---|
| | | Arabidopsis | Kiwifruit | Tomato | Grape | Sweet orange |
| CHS | Chalcone synthase | 1 | 6 | 6 | 24 | 14 |
| CHI | Chalcone isomerase | 4 | 6 | 4 | 2 | 2 |
| F3H | Flavanone 3-hydroxylase | 1 | 4 | 1 | 3 | 2 |
| F3’H | Flavonoid 3’-hydroxylase | 1 | 17 | 2 | 3 | 12 |
| DFR | Dihydroflavonol 4-reductase | 1 | 7 | 4 | 10 | 5 |
| LDOX / ANS | Leucoanthocyanidin dioxygenase / Anthocyanidin synthase | 2 | 5 | 2 | 6 | 7 |
| UFGT | UDP-glucose flavonoid 3-O-glucosyltransferase | 15 | 8 | 7 | 13 | 5 |
| FLS | Flavonol synthase | 6 | 4 | 1 | 3 | 4 |

**Supplementary Table S12. Comparative analysis of gene families in Chlorophyll biosynthesis and degradation pathway**

| Gene | Description | Number of genes | | | |
|---|---|---|---|---|---|
| | | Arabidopsis | Kiwifruit | Tomato | Grape |
| CAO | chlorophyll a oxygenase | 1 | 1 | 3 | 1 |
| GluTR | glutamyl-tRNA reductase | 3 | 4 | 3 | 2 |
| LHCB | light harvesting complex photosystem II | 3 | 4 | 4 | 2 |
| RBCS | Rubisco small subunit | 4 | 2 | 4 | 2 |
| CBR | chlorophyll b reductase | 3 | 2 | 2 | 2 |
| CLH | chlorophyllase | 2 | 2 | 2 | 3 |
| CLS | chlorophyll synthase | 1 | 2 | 1 | 1 |
| PAO | pheophorbide a oxygenase | 3 | 6 | 4 | 6 |
| PPH | pheophytin pheophorbide hydrolase | 7 | 3 | 2 | 5 |
| SGR | chloroplast stay-green protein | 4 | 4 | 3 | 4 |

## Supplementary Table S13. Expression of kiwifruit genes in the carotenoid biosynthesis pathway

| Gene | Description | Gene ID | Normalized expression (FPKM) | | | |
|---|---|---|---|---|---|---|
| | | | Leaf | Immature fruit | Mature green fruit | Ripe fruit |
| CCD | carotenoid cleavage enzymes | Achn007091 | 0.03 | 0 | 0.06 | 0.04 |
| | | Achn029551 | 1.07 | 2.66 | 6.39 | 4.64 |
| | | Achn219871 | 0.03 | 0 | 0 | 0 |
| | | Achn228731 | 44.55 | 0.13 | 0.1 | 0.08 |
| | | Achn238521 | 0 | 0 | 0.04 | 0.04 |
| | | Achn260561 | 99.7 | 8.37 | 3.55 | 1.44 |
| | | Achn276731 | 0.06 | 0.67 | 0.03 | 0 |
| | | Achn378731 | 104.63 | 32.73 | 50.88 | 38.4 |
| CHY | non-heme hydroxylases | Achn011691 | 95.12 | 0.46 | 0.1 | 1.15 |
| | | Achn188121 | 38.98 | 2.68 | 2.17 | 12.81 |
| CrtISO | 7,9,7',9'-tetra-cis-lycopene isomerase | Achn058301 | 11.42 | 6.07 | 13.83 | 17.54 |
| CYCB | lycopene beta-cyclases | Achn198281 | 29.77 | 19.28 | 8.04 | 3.09 |
| | | Achn347121 | 3.26 | 8.36 | 66.25 | 267.75 |
| | | Achn358971 | 49.26 | 16.68 | 15.47 | 13.77 |
| CYP | P450 hydroxylases | Achn106371 | 65.13 | 11.77 | 8.62 | 4.5 |
| | | Achn318041 | 18.33 | 4.85 | 3.92 | 2.2 |
| LCYB | lycopene beta-cyclases | Achn198281 | 29.77 | 19.28 | 8.04 | 3.09 |
| | | Achn347121 | 3.26 | 8.36 | 66.25 | 267.75 |
| | | Achn358971 | 49.26 | 16.68 | 15.47 | 13.77 |
| LCYE | lycopene epsilon-cyclase | Achn061261 | 3.08 | 2.21 | 1.72 | 0.48 |
| | | Achn326611 | 21.69 | 12.42 | 6.6 | 0.82 |
| NCED | carotenoid cleavage enzymes | Achn061851 | 0.33 | 0.71 | 0 | 1.73 |
| | | Achn140141 | 2.33 | 1.85 | 0.21 | 0.31 |
| | | Achn176351 | 0.34 | 0.58 | 0.15 | 0.48 |
| | | Achn209971 | 6.11 | 4.37 | 0.85 | 6.07 |
| | | Achn275221 | 0.65 | 0.47 | 0 | 0.05 |
| PDS | phytoene desaturase | Achn199641 | 32 | 13.27 | 32.14 | 27.43 |
| | | Achn226031 | 49.38 | 26.88 | 57.51 | 49.17 |
| PSY | phytoene synthases | Achn148841 | 0.14 | 0 | 0.07 | 0.07 |
| | | Achn335751 | 168.8 | 22.91 | 7.21 | 22.35 |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | Achn388591 | 156.27 | 13.53 | 10.16 | 15.14 |
| PTOX | alternative oxidase | Achn150731 | 157.6 | 7.56 | 30.53 | 100.24 |
| VDE | violaxanthin deepoxidase | Achn368031 | 48.42 | 1.31 | 1.41 | 0.37 |
| | | Achn368041 | 75.13 | 1.68 | 1.67 | 0.63 |
| ZDS | zeta-carotene desaturase | Achn274521 | 28.34 | 8.37 | 11.82 | 11.7 |
| ZEP | zeaxanthin epoxidase | Achn013171 | 97.32 | 3.99 | 6.15 | 4.82 |
| ZISO | 9,15,9'-tri-cis-zeta-carotene isomerase | Achn248961 | 17.29 | 12.72 | 16.41 | 9.81 |

**Supplementary Table S14. Expression of genes involved in flavonoid and anthocyanin biosynthetic pathway in kiwifruit**

| Gene | Description | Gene ID | Gene expression value (FPKM) | | | |
|---|---|---|---|---|---|---|
| | | | leaf | immature fruit | mature green fruit | ripe fruit |
| CHS | Chalcone synthase | Achn109041 | 2406.03 | 296.96 | 28.61 | 70.19 |
| | | Achn168721 | 1260.27 | 200.31 | 67.73 | 23.1 |
| | | Achn214721 | 2303.44 | 289.48 | 28.66 | 67.39 |
| | | Achn238171 | 338.13 | 89.65 | 0.56 | 10.23 |
| | | Achn246931 | 0.08 | 0.03 | 0 | 0.46 |
| | | Achn369761 | 1277.77 | 157.04 | 0.85 | 8.79 |
| CHI | Chalcone isomerase | Achn076261 | 0 | 0 | 0 | 0.05 |
| | | Achn159571 | 14.88 | 3.57 | 0.03 | 0 |
| | | Achn200891 | 4.03 | 2.09 | 0.08 | 0 |
| | | Achn203601 | 55.24 | 9.71 | 5.81 | 4.4 |
| | | Achn203611 | 0 | 0 | 0 | 0 |
| | | Achn328591 | 137.83 | 3.78 | 0.33 | 0.39 |
| F3H | Flavanone 3-hydroxylase | Achn075731 | 121.29 | 23.94 | 1.39 | 1.1 |
| | | Achn141511 | 0.36 | 0 | 0 | 0 |
| | | Achn201551 | 0.75 | 0 | 0 | 0 |
| | | Achn201561 | 1.16 | 0 | 0.05 | 0.02 |
| F3’H | Flavonoid 3’-hydroxylase | Achn001761 | 0.26 | 0.04 | 0 | 0 |
| | | Achn028801 | 5.88 | 0.53 | 0.34 | 1.24 |
| | | Achn085041 | 0.26 | 0 | 0.02 | 6.32 |
| | | Achn090851 | 6.67 | 1.66 | 3.09 | 137.66 |
| | | Achn093081 | 1.73 | 0.31 | 0.29 | 0.13 |
| | | Achn118151 | 9.51 | 7.28 | 12.8 | 4.85 |
| | | Achn135091 | 0 | 0 | 0.17 | 26.52 |
| | | Achn173761 | 46.52 | 7.79 | 0.4 | 0.4 |
| | | Achn194551 | 553.22 | 489.07 | 244.61 | 17.22 |
| | | Achn280521 | 1.88 | 6.47 | 40.29 | 50.49 |
| | | Achn305921 | 3.95 | 0.59 | 0.22 | 2.75 |
| | | Achn332801 | 9.3 | 0.15 | 0.35 | 11.23 |
| | | Achn332811 | 0.6 | 0.29 | 0 | 11.45 |
| | | Achn336691 | 0 | 0 | 0 | 0 |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | Achn361641 | 1.97 | 0.92 | 1.57 | 1.93 |
| | | Achn364321 | 0.2 | 0 | 0.16 | 38.68 |
| | | Achn382121 | 7.25 | 2.01 | 1.1 | 0.2 |
| DFR | Dihydroflavonol 4-reductase | Achn014341 | 2.75 | 1.96 | 4.89 | 13.52 |
| | | Achn014351 | 1.1 | 0.68 | 2.26 | 2.9 |
| | | Achn030761 | 920.59 | 170.7 | 5.01 | 3.75 |
| | | Achn111861 | 543.11 | 126.76 | 33.01 | 14.03 |
| | | Achn135311 | 820.58 | 219.77 | 74.64 | 24.7 |
| | | Achn201151 | 458.43 | 83.7 | 6.41 | 1.43 |
| | | Achn314951 | 36.77 | 13.42 | 16.04 | 18.92 |
| LDOX / ANS | Leucoanthocyanidin dioxygenase / Anthocyanidin synthase | Achn002561 | 546.14 | 318.24 | 3.22 | 1.07 |
| | | Achn117061 | 1295.45 | 138.78 | 35.36 | 17.02 |
| | | Achn243221 | 1.15 | 3.79 | 1.73 | 0.87 |
| | | Achn308611 | 0.14 | 1.08 | 0.94 | 0.01 |
| | | Achn361621 | 646.28 | 466.15 | 40.28 | 2.81 |
| UFGT | UDP-glucose flavonoid 3-O-glucosyltransferase | Achn017071 | 104.34 | 4.08 | 0.72 | 0.15 |
| | | Achn034091 | 0.04 | 0 | 0 | 0.06 |
| | | Achn133151 | 0 | 0.03 | 0 | 0 |
| | | Achn209671 | 18.06 | 0.42 | 0.74 | 0.14 |
| | | Achn209701 | 5.09 | 0.35 | 0 | 0.2 |
| | | Achn321621 | 8.32 | 2.57 | 0.15 | 0.01 |
| | | Achn335201 | 19.99 | 66.05 | 16.76 | 0.45 |
| | | Achn385311 | 36.26 | 9.51 | 1.34 | 0.26 |

**Supplementary Table S15. Expression of kiwifruit genes in Chlorophyll biosynthesis and degradation pathway**

| Gene | Description | Gene ID | Normalized expression (FPKM) | | | |
|---|---|---|---|---|---|---|
| | | | Leaf | Immature fruit | Mature green fruit | Ripe fruit |
| CAO | chlorophyll a oxygenase | Achn353001 | 74.75 | 14.05 | 14.8 | 50.1 |
| GluTR | glutamyl-tRNA reductase | Achn041311 | 29.84 | 7 | 11.65 | 7.28 |
| | | Achn086941 | 24.53 | 4.94 | 3.52 | 0.9 |
| | | Achn126121 | 63.87 | 9.75 | 10.93 | 22.16 |
| | | Achn222561 | 52.49 | 12.81 | 16.08 | 21.85 |
| LHCB | light harvesting complex photosystem II | Achn036661 | 727.81 | 200.11 | 331.66 | 27.17 |
| | | Achn152591 | 0 | 0 | 0 | 0 |
| | | Achn154321 | 720.19 | 123.76 | 177.14 | 51.68 |
| | | Achn385091 | 3297.33 | 419.05 | 762.2 | 43.5 |
| RBCS | Rubisco small subunit | Achn185051 | 9.83 | 142.42 | 629.16 | 1329.51 |
| | | Achn311511 | 5.33 | 13.29 | 10.05 | 12.16 |
| CBR | chlorophyll b reductase | Achn069361 | 20.8 | 5.6 | 25.73 | 16.11 |
| | | Achn146001 | 32.27 | 3.76 | 10.49 | 19.59 |
| CLH | chlorophyllase | Achn378091 | 57.13 | 25.28 | 24.81 | 13.45 |
| | | Achn378101 | 33.75 | 12.59 | 5.99 | 4.93 |
| CLS | chlorophyll synthase | Achn001951 | 3.17 | 7.98 | 11.06 | 5.01 |
| | | Achn152481 | 58.47 | 25.81 | 28.59 | 18.93 |
| PAO | pheophorbide a oxygenase | Achn013811 | 38.51 | 10.07 | 31.53 | 17.25 |
| | | Achn052661 | 5.47 | 2.67 | 19.2 | 22.11 |
| | | Achn068721 | 48.09 | 10.99 | 40.64 | 22.88 |
| | | Achn212711 | 22.7 | 12.75 | 79.94 | 67.82 |
| | | Achn279481 | 85 | 20.91 | 12.63 | 4.59 |
| | | Achn282201 | 10.7 | 0.65 | 2.66 | 3.24 |
| PPH | pheophytin pheophorbide hydrolase | Achn193491 | 16.83 | 2.07 | 9.8 | 8.38 |
| | | Achn193501 | 6.15 | 3.39 | 5.72 | 6.93 |
| | | Achn334341 | 32.26 | 2.32 | 12.89 | 51.32 |
| SGR | chloroplast stay-green protein | Achn121171 | 22.03 | 2.94 | 0 | 0 |
| | | Achn284841 | 41.44 | 7.27 | 0 | 0 |
| | | Achn317301 | 16.65 | 0.57 | 0.69 | 1.56 |
| | | Achn361611 | 25.18 | 1.51 | 23.53 | 70.55 |