

Transcriptomic analysis reveals transcription factors related to leaf anthocyanin biosynthesis in *Paeonia qiui*

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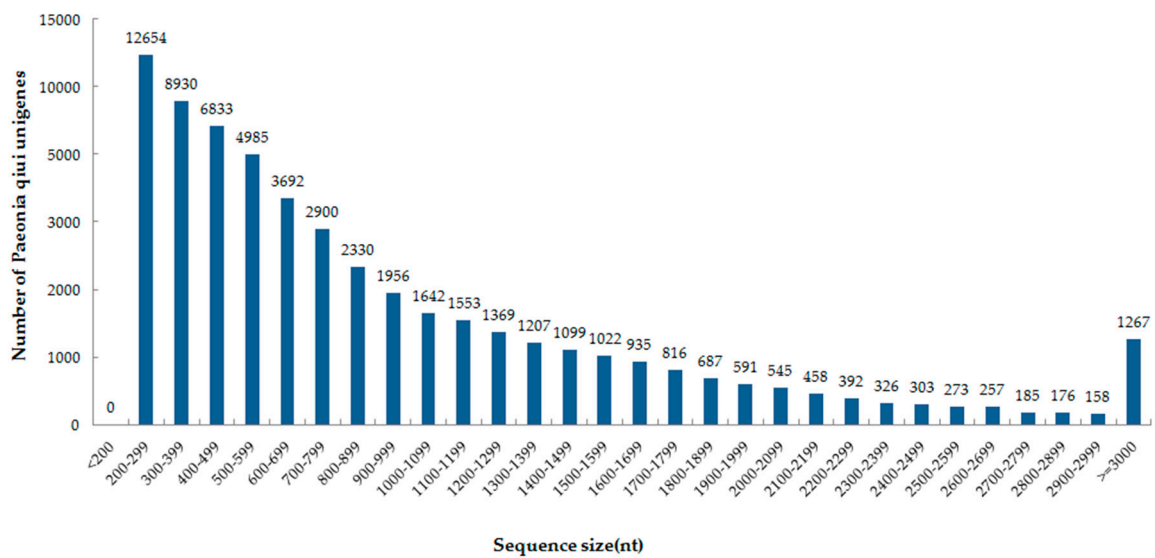


Figure S1: Size distribution of unigenes

Table S1. Primers used for q-PCR analysis

| Gene ID | Forward primer (5'–3') | Reverse primer (5'–3') |
|----------------|------------------------|------------------------|
| Unigene0006146 | TCCTCACTTCGCAAATCCTCC | TCAACCACACCCCTCTCCACA |
| Unigene0005081 | GCTTCAATCCTTACCGATACA | TCAATCAAACATCCCGCTCT |
| Unigene0024459 | GCTGTAGATTGAGGTGGTTGA | TCTTCTTGTGTAGGTGTGTGT |
| Unigene0050761 | TTGACCCTAATAACCATCGCC | TCAAGATTCAAGTCAAGCGAG |
| Unigene0054556 | CATAATCTCGCTATCTCATCC | GCATAATTCTCCTTCTCCTCC |
| Unigene0052849 | TCCACAACCTGAATTGGCACT | CAGCCCAGTTACCTTCTTTCC |
| Unigene0017118 | CTGCTATCATCATTGGTTCCG | GTCGCTTGTAGTTTTTCGGGT |
| Unigene0016797 | CTATTCTTTTCACACAGACACC | TGCTTCCCTATGATCGACTCC |
| Unigene0030889 | TTCATCGGTTTCATGGCTTGTC | CTCTCCGCACAGTTTTAGCC |
| Unigene0012475 | ACCAGCATCACCAACATCTTC | GCATATTTCTCCTTCTCTTCC |
| Unigene0014577 | TTGCTTCTTGGCCCTACTTTG | GTCCTCGGTTATGGTTTGTCT |
| Unigene0041187 | GATGTTGATAGCGAGGGTGG | AGGAAGGGGAGATTTGGGAG |
| Unigene0040486 | ATGGCTGGTCCTTCACTTACT | CGAAATGGATATGGAACCTGA |

Table S2. KEGG pathway enrichment of differentially expressed genes

| No. | Pathway | DEGs genes with pathway annotation (2333) | | All genes with pathway annotation (6335) | | <i>p</i> -value | Pathway ID |
|-----|---|--|----------|---|---------|-----------------------|------------|
| 1 | Ribosome | 248 | (10.63%) | 521 | (8.22%) | 9.81×10^{-8} | ko03010 |
| 2 | Phenylpropanoid biosynthesis | 81 | (3.47%) | 143 | (2.26%) | 8.74×10^{-7} | ko00940 |
| 3 | Plant hormone signal transduction | 113 | (4.84%) | 227 | (3.58%) | 3.36×10^{-5} | ko04075 |
| 4 | Starch and sucrose metabolism | 129 | (5.53%) | 266 | (4.20%) | 4.64×10^{-5} | ko00500 |
| 5 | Linoleic acid metabolism | 19 | (0.81%) | 25 | (0.39%) | 7.50×10^{-5} | ko00591 |
| 6 | DNA replication | 48 | (2.06%) | 84 | (1.33%) | 0.000109739 | ko03030 |
| 7 | Nitrogen metabolism | 29 | (1.24%) | 45 | (0.71%) | 0.00014794 | ko00910 |
| 8 | Pentose and glucuronate interconversions | 57 | (2.44%) | 108 | (1.70%) | 0.000472719 | ko00040 |
| 9 | Stilbenoid, diarylheptanoid and gingerol biosynthesis | 17 | (0.73%) | 24 | (0.38%) | 0.000731129 | ko00945 |
| 10 | Terpenoid backbone biosynthesis | 41 | (1.76%) | 74 | (1.17%) | 0.000814305 | ko00900 |
| 11 | Glycine, serine and threonine metabolism | 48 | (2.06%) | 90 | (1.42%) | 0.000955863 | ko00260 |
| 12 | Plant-pathogen interaction | 110 | (4.71%) | 238 | (3.76%) | 0.001548023 | ko04626 |
| 13 | Fatty acid elongation | 25 | (1.07%) | 42 | (0.66%) | 0.002246963 | ko00062 |
| 14 | Cyanoamino acid metabolism | 39 | (1.67%) | 73 | (1.15%) | 0.002667798 | ko00460 |
| 15 | Galactose metabolism | 42 | (1.80%) | 80 | (1.26%) | 0.002878465 | ko00052 |
| 16 | Monoterpenoid biosynthesis | 9 | (0.39%) | 11 | (0.17%) | 0.003047899 | ko00902 |
| 17 | Flavonoid biosynthesis | 25 | (1.07%) | 43 | (0.68%) | 0.003510991 | ko00941 |
| 18 | Sesquiterpenoid and triterpenoid biosynthesis | 15 | (0.64%) | 23 | (0.36%) | 0.005251659 | ko00909 |
| 19 | alpha-Linolenic acid metabolism | 32 | (1.37%) | 60 | (0.95%) | 0.00643939 | ko00592 |
| 20 | Glutathione metabolism | 51 | (2.19%) | 110 | (1.74%) | 0.02429231 | ko00480 |
| 21 | Biotin metabolism | 13 | (0.56%) | 22 | (0.35%) | 0.02770014 | ko00780 |
| 22 | Carotenoid biosynthesis | 21 | (0.90%) | 40 | (0.63%) | 0.03062768 | ko00906 |
| 23 | Fatty acid metabolism | 45 | (1.93%) | 99 | (1.56%) | 0.04693405 | ko01212 |
| 24 | Flavone and flavonol biosynthesis | 3 | (0.13%) | 3 | (0.05%) | 0.04990584 | ko00944 |

| No. | Pathway | DEGs genes with pathway | | All genes with pathway | | <i>p</i> -value | Pathway ID |
|-----|--|-------------------------|---------|------------------------|---------|-----------------|------------|
| | | annotation (2333) | (%) | annotation (6335) | (%) | | |
| 25 | Synthesis and degradation of ketone bodies | 6 | (0.26%) | 9 | (0.14%) | 0.06793747 | ko00072 |
| 26 | Phenylalanine metabolism | 24 | (1.03%) | 50 | (0.79%) | 0.06874378 | ko00360 |
| 27 | Zeatin biosynthesis | 10 | (0.43%) | 18 | (0.28%) | 0.08202637 | ko00908 |
| 28 | Alanine, aspartate and glutamate metabolism | 30 | (1.29%) | 66 | (1.04%) | 0.09248293 | ko00250 |
| 29 | Tropane, piperidine and pyridine alkaloid biosynthesis | 17 | (0.73%) | 35 | (0.55%) | 0.1034937 | ko00960 |
| 30 | Taurine and hypotaurine metabolism | 7 | (0.30%) | 12 | (0.19%) | 0.1079198 | ko00430 |
| 31 | Fatty acid biosynthesis | 23 | (0.99%) | 50 | (0.79%) | 0.1153628 | ko00061 |
| 32 | Diterpenoid biosynthesis | 14 | (0.60%) | 29 | (0.46%) | 0.1387011 | ko00904 |
| 33 | Isoquinoline alkaloid biosynthesis | 14 | (0.60%) | 29 | (0.46%) | 0.1387011 | ko00950 |
| 34 | Degradation of aromatic compounds | 8 | (0.34%) | 15 | (0.24%) | 0.1451353 | ko01220 |
| 35 | Tyrosine metabolism | 26 | (1.11%) | 59 | (0.93%) | 0.1532415 | ko00350 |
| 36 | Phenylalanine, tyrosine and tryptophan biosynthesis | 26 | (1.11%) | 59 | (0.93%) | 0.1532415 | ko00400 |
| 37 | Inositol phosphate metabolism | 33 | (1.41%) | 77 | (1.22%) | 0.1622349 | ko00562 |
| 38 | Glyoxylate and dicarboxylate metabolism | 51 | (2.19%) | 123 | (1.94%) | 0.1629265 | ko00630 |
| 39 | Pentose phosphate pathway | 36 | (1.54%) | 85 | (1.34%) | 0.1707624 | ko00030 |
| 40 | Phosphatidylinositol signaling system | 32 | (1.37%) | 75 | (1.18%) | 0.1747285 | ko04070 |
| 41 | Base excision repair | 31 | (1.33%) | 73 | (1.15%) | 0.188132 | ko03410 |
| 42 | Cysteine and methionine metabolism | 57 | (2.44%) | 140 | (2.21%) | 0.1901492 | ko00270 |
| 43 | Homologous recombination | 35 | (1.50%) | 84 | (1.33%) | 0.2075322 | ko03440 |
| 44 | Limonene and pinene degradation | 4 | (0.17%) | 7 | (0.11%) | 0.2309155 | ko00903 |
| 45 | Mismatch repair | 29 | (1.24%) | 70 | (1.10%) | 0.2471647 | ko03430 |
| 46 | Endocytosis | 98 | (4.20%) | 251 | (3.96%) | 0.2485607 | ko04144 |
| 47 | Biosynthesis of unsaturated fatty acids | 21 | (0.90%) | 50 | (0.79%) | 0.2671184 | ko01040 |
| 48 | Fatty acid degradation | 22 | (0.94%) | 53 | (0.84%) | 0.2827942 | ko00071 |
| 49 | Tryptophan metabolism | 12 | (0.51%) | 28 | (0.44%) | 0.3159318 | ko00380 |
| 50 | Ascorbate and aldarate metabolism | 22 | (0.94%) | 54 | (0.85%) | 0.3204958 | ko00053 |

| No. | Pathway | DEGs genes with pathway | | All genes with pathway | | <i>p</i> -value | Pathway ID |
|-----|---|-------------------------|---------|------------------------|---------|-----------------|------------|
| | | annotation (2333) | (%) | annotation (6335) | (%) | | |
| 51 | Ether lipid metabolism | 18 | (0.77%) | 44 | (0.69%) | 0.3382354 | ko00565 |
| 52 | Carbon fixation in photosynthetic organisms | 56 | (2.40%) | 145 | (2.29%) | 0.3549311 | ko00710 |
| 53 | Brassinosteroid biosynthesis | 7 | (0.30%) | 16 | (0.25%) | 0.3689303 | ko00905 |
| 54 | Steroid biosynthesis | 15 | (0.64%) | 37 | (0.58%) | 0.3776071 | ko00100 |
| 55 | Circadian rhythm - plant | 17 | (0.73%) | 43 | (0.68%) | 0.4115331 | ko04712 |
| 56 | Monobactam biosynthesis | 4 | (0.17%) | 9 | (0.14%) | 0.437184 | ko00261 |
| 57 | Photosynthesis | 42 | (1.80%) | 112 | (1.77%) | 0.4766864 | ko00195 |
| 58 | Carbon metabolism | 153 | (6.56%) | 414 | (6.54%) | 0.4968967 | ko01200 |
| 59 | Pyrimidine metabolism | 67 | (2.87%) | 181 | (2.86%) | 0.5072089 | ko00240 |
| 60 | Thiamine metabolism | 8 | (0.34%) | 21 | (0.33%) | 0.5340385 | ko00730 |
| 61 | Butanoate metabolism | 8 | (0.34%) | 21 | (0.33%) | 0.5340385 | ko00650 |
| 62 | Nucleotide excision repair | 35 | (1.50%) | 95 | (1.50%) | 0.5378195 | ko03420 |
| 63 | Glycolysis / Gluconeogenesis | 59 | (2.53%) | 161 | (2.54%) | 0.549408 | ko00010 |
| 64 | Nicotinate and nicotinamide metabolism | 9 | (0.39%) | 24 | (0.38%) | 0.5495391 | ko00760 |
| 65 | Glycosphingolipid biosynthesis - globo series | 5 | (0.21%) | 13 | (0.21%) | 0.5552117 | ko00603 |
| 66 | Arachidonic acid metabolism | 6 | (0.26%) | 16 | (0.25%) | 0.5714135 | ko00590 |
| 67 | Cutin, suberine and wax biosynthesis | 11 | (0.47%) | 30 | (0.47%) | 0.5758488 | ko00073 |
| 68 | Peroxisome | 41 | (1.76%) | 113 | (1.78%) | 0.5836469 | ko04146 |
| 69 | Sulfur metabolism | 13 | (0.56%) | 36 | (0.57%) | 0.5978298 | ko00920 |
| 70 | Other types of O-glycan biosynthesis | 3 | (0.13%) | 8 | (0.13%) | 0.6150762 | ko00514 |
| 71 | Anthocyanin biosynthesis | 3 | (0.13%) | 8 | (0.13%) | 0.6150762 | ko00942 |
| 72 | Amino sugar and nucleotide sugar metabolism | 56 | (2.40%) | 157 | (2.48%) | 0.6488985 | ko00520 |
| 73 | Non-homologous end-joining | 5 | (0.21%) | 15 | (0.24%) | 0.7016185 | ko03450 |
| 74 | Isoflavonoid biosynthesis | 3 | (0.13%) | 9 | (0.14%) | 0.7040224 | ko00943 |
| 75 | Lipoic acid metabolism | 2 | (0.09%) | 6 | (0.09%) | 0.7142406 | ko00785 |
| 76 | Arginine biosynthesis | 19 | (0.81%) | 56 | (0.88%) | 0.7198241 | ko00220 |

| No. | Pathway | DEGs genes with pathway | | All genes with pathway | | <i>p</i> -value | Pathway ID |
|-----|--|-------------------------|---------|------------------------|---------|-----------------|------------|
| | | annotation (2333) | (%) | annotation (6335) | (%) | | |
| 77 | Glycerophospholipid metabolism | 43 | (1.84%) | 124 | (1.96%) | 0.7223482 | ko00564 |
| 78 | Protein export | 20 | (0.86%) | 60 | (0.95%) | 0.7554342 | ko03060 |
| 79 | Photosynthesis - antenna proteins | 10 | (0.43%) | 31 | (0.49%) | 0.7599607 | ko00196 |
| 80 | Vitamin B6 metabolism | 5 | (0.21%) | 16 | (0.25%) | 0.7608027 | ko00750 |
| 81 | Fructose and mannose metabolism | 31 | (1.33%) | 92 | (1.45%) | 0.7677863 | ko00051 |
| 82 | Glycosaminoglycan degradation | 7 | (0.30%) | 23 | (0.36%) | 0.8014944 | ko00531 |
| 83 | Propanoate metabolism | 17 | (0.73%) | 53 | (0.84%) | 0.8050195 | ko00640 |
| 84 | Histidine metabolism | 5 | (0.21%) | 17 | (0.27%) | 0.8106426 | ko00340 |
| 85 | Lysine degradation | 13 | (0.56%) | 42 | (0.66%) | 0.8292116 | ko00310 |
| 86 | Sphingolipid metabolism | 12 | (0.51%) | 39 | (0.62%) | 0.8294074 | ko00600 |
| 87 | Spliceosome | 105 | (4.50%) | 306 | (4.83%) | 0.8401597 | ko03040 |
| 88 | Selenocompound metabolism | 6 | (0.26%) | 21 | (0.33%) | 0.8444504 | ko00450 |
| 89 | Pyruvate metabolism | 37 | (1.59%) | 114 | (1.80%) | 0.8590132 | ko00620 |
| 90 | Glycerolipid metabolism | 24 | (1.03%) | 77 | (1.22%) | 0.8767001 | ko00561 |
| 91 | Lysine biosynthesis | 5 | (0.21%) | 19 | (0.30%) | 0.8852201 | ko00300 |
| 92 | One carbon pool by folate | 8 | (0.34%) | 29 | (0.46%) | 0.8922036 | ko00670 |
| 93 | Riboflavin metabolism | 4 | (0.17%) | 16 | (0.25%) | 0.8960274 | ko00740 |
| 94 | Valine, leucine and isoleucine degradation | 20 | (0.86%) | 67 | (1.06%) | 0.9078143 | ko00280 |
| 95 | Arginine and proline metabolism | 18 | (0.77%) | 61 | (0.96%) | 0.9090556 | ko00330 |
| 96 | SNARE interactions in vesicular transport | 17 | (0.73%) | 58 | (0.92%) | 0.9099296 | ko04130 |
| 97 | Porphyrin and chlorophyll metabolism | 16 | (0.69%) | 55 | (0.87%) | 0.9110034 | ko00860 |
| 98 | mRNA surveillance pathway | 57 | (2.44%) | 178 | (2.81%) | 0.924301 | ko03015 |
| 99 | Other glycan degradation | 9 | (0.39%) | 34 | (0.54%) | 0.9272641 | ko00511 |
| 100 | Biosynthesis of amino acids | 105 | (4.50%) | 317 | (5.00%) | 0.9290205 | ko01230 |
| 101 | Ribosome biogenesis in eukaryotes | 50 | (2.14%) | 163 | (2.57%) | 0.959786 | ko03008 |
| 102 | Purine metabolism | 70 | (3.00%) | 222 | (3.50%) | 0.9598967 | ko00230 |

| No. | Pathway | DEGs genes with pathway | | All genes with pathway | | <i>p</i> -value | Pathway ID |
|-----|---|-------------------------|---------|------------------------|---------|-----------------|------------|
| | | annotation (2333) | (%) | annotation (6335) | (%) | | |
| 103 | Glycosphingolipid biosynthesis - ganglio series | 1 | (0.04%) | 8 | (0.13%) | 0.9746998 | ko00604 |
| 104 | Regulation of autophagy | 12 | (0.51%) | 49 | (0.77%) | 0.9770373 | ko04140 |
| 105 | Folate biosynthesis | 4 | (0.17%) | 21 | (0.33%) | 0.9776331 | ko00790 |
| 106 | Pantothenate and CoA biosynthesis | 7 | (0.30%) | 32 | (0.51%) | 0.9777182 | ko00770 |
| 107 | Protein processing in endoplasmic reticulum | 107 | (4.59%) | 336 | (5.30%) | 0.9782724 | ko04141 |
| 108 | beta-Alanine metabolism | 12 | (0.51%) | 50 | (0.79%) | 0.9817576 | ko00410 |
| 109 | Proteasome | 18 | (0.77%) | 71 | (1.12%) | 0.9857748 | ko03050 |
| 110 | Valine, leucine and isoleucine biosynthesis | 4 | (0.17%) | 23 | (0.36%) | 0.9884576 | ko00290 |
| 111 | C5-Branched dibasic acid metabolism | 1 | (0.04%) | 10 | (0.16%) | 0.989919 | ko00660 |
| 112 | Sulfur relay system | 2 | (0.09%) | 15 | (0.24%) | 0.9901401 | ko04122 |
| 113 | ABC transporters | 25 | (1.07%) | 97 | (1.53%) | 0.9925878 | ko02010 |
| 114 | Phagosome | 27 | (1.16%) | 104 | (1.64%) | 0.993332 | ko04145 |
| 115 | RNA degradation | 59 | (2.53%) | 204 | (3.22%) | 0.9936218 | ko03018 |
| 116 | 2-Oxocarboxylic acid metabolism | 17 | (0.73%) | 72 | (1.14%) | 0.9943988 | ko01210 |
| 117 | Glycosylphosphatidylinositol(GPI)-anchor biosynthesis | 8 | (0.34%) | 41 | (0.65%) | 0.9951002 | ko00563 |
| 118 | Ubiquitin mediated proteolysis | 60 | (2.57%) | 211 | (3.33%) | 0.9963919 | ko04120 |
| 119 | RNA polymerase | 15 | (0.64%) | 73 | (1.15%) | 0.9991898 | ko03020 |
| 120 | N-Glycan biosynthesis | 8 | (0.34%) | 49 | (0.77%) | 0.9995688 | ko00510 |
| 121 | Ubiquinone and other terpenoid-quinone biosynthesis | 13 | (0.56%) | 70 | (1.10%) | 0.9997493 | ko00130 |
| 122 | Oxidative phosphorylation | 50 | (2.14%) | 197 | (3.11%) | 0.9998066 | ko00190 |
| 123 | Basal transcription factors | 13 | (0.56%) | 74 | (1.17%) | 0.9999212 | ko03022 |
| 124 | Citrate cycle (TCA cycle) | 13 | (0.56%) | 75 | (1.18%) | 0.9999413 | ko00020 |
| 125 | RNA transport | 74 | (3.17%) | 291 | (4.59%) | 0.9999914 | ko03013 |
| 126 | Aminoacyl-tRNA biosynthesis | 8 | (0.34%) | 72 | (1.14%) | 0.9999998 | ko00970 |

Table S3. MYBs identified from differentially expressed genes

| GeneID | log2 Ratio(S3/S1)* | Annotation |
|----------------|--------------------|---|
| Unigene0029523 | -12.57036964 | Myb domain protein 106 (<i>Theobroma cacao</i>) |
| Unigene0057113 | -11.49290468 | transcription factor MYB108 (<i>Vitis vinifera</i>) |
| Unigene0029522 | -9.970046156 | Myb domain protein 106 (<i>Theobroma cacao</i>) |
| Unigene0016989 | -8.829383836 | transcription factor MYB108-like (<i>Populus euphratica</i>) |
| Unigene0032117 | -7.900304871 | myb-related protein Myb4-like (<i>Populus euphratica</i>) |
| Unigene0032319 | -6.93164243 | myb-related protein Myb4-like (<i>Juglans regia</i>) |
| Unigene0011406 | -6.137168382 | transcription repressor MYB6 isoform X1 (<i>Theobroma cacao</i>) |
| Unigene0025135 | -6.111096685 | transcription factor MYB48 (<i>Vitis vinifera</i>) |
| Unigene0016220 | -5.263146719 | transcription factor MYB44-like (<i>Ziziphus jujuba</i>) |
| Unigene0032116 | -4.832477733 | myb-related protein Myb4-like (<i>Populus euphratica</i>) |
| Unigene0030529 | -3.676597687 | myb-related protein 3R-1 isoform X1 (<i>Vitis vinifera</i>) |
| Unigene0047398 | -3.396310077 | transcription factor MYB3-like (<i>Jatropha curcas</i>) |
| Unigene0024459 | -3.356215515 | MYB transcription factor 113 (<i>Liquidambar formosana</i>) |
| Unigene0057357 | -3.23926588 | myb-related protein 308-like (<i>Vitis vinifera</i>) |
| Unigene0006047 | -3.163869449 | myb-related protein 3R-1 isoform X1 (<i>Vitis vinifera</i>) |
| Unigene0004419 | -2.655599465 | transcription repressor MYB6-like (<i>Juglans regia</i>) |
| Unigene0021641 | -2.603584268 | myb-related protein Myb4-like (<i>Ziziphus jujuba</i>) |
| Unigene0020583 | -2.448745375 | R2R3 Myb protein, partial (<i>Zea mays</i>) |
| Unigene0018062 | -2.350682055 | MYB1 protein (<i>Paeonia suffruticosa</i>) |
| Unigene0019972 | -2.028269696 | myb-related protein 3R-1-like (<i>Ziziphus jujuba</i>) |
| Unigene0039186 | -1.857530006 | L10-interacting MYB domain-containing (<i>Nicotiana attenuata</i>) |
| Unigene0025689 | -1.517664466 | myb-related protein B-like (<i>Juglans regia</i>) |
| Unigene0022939 | -1.509975137 | transcription factor MYB86-like (<i>Gossypium hirsutum</i>) |
| Unigene0033907 | -1.005823383 | myb-like protein B (<i>Vitis vinifera</i>) |
| Unigene0042748 | -1.003142265 | L10-interacting MYB domain-containing (<i>Malus domestica</i>) |
| Unigene0020998 | -1.000574525 | R2R3-MYB transcription factor MYB2 (<i>Epimedium sagittatum</i>) |
| Unigene0025517 | 1.022010118 | L10-interacting MYB domain-containing (<i>Vitis vinifera</i>) |
| Unigene0021289 | 1.112487772 | myb-related protein 308-like (<i>Populus euphratica</i>) |
| Unigene0050761 | 1.144656074 | transcription repressor MYB6 (<i>Ricinus communis</i>) |
| Unigene0025266 | 1.242155836 | MYB transcription factor R2R3-like (<i>Populus tremuloides</i>) |
| Unigene0027334 | 2.45635767 | MYB61 protein (<i>Betula platyphylla</i>) |
| Unigene0050423 | 2.477964054 | transcription factor MYB46-like (<i>Populus euphratica</i>) |
| Unigene0015505 | 2.615240635 | Myb DNA-binding domain-containing (<i>Cephalotus follicularis</i>) |
| Unigene0050035 | 3.121526809 | myb-related protein Hv33 (<i>Ipomoea nil</i>) |
| Unigene0009193 | 3.582518158 | MYB-like 102 (<i>Theobroma cacao</i>) |
| Unigene0015506 | 3.63032412 | myb-related protein 306-like (<i>Gossypium raimondii</i>) |
| Unigene0058209 | 3.7291144 | transcription factor MYB82 (<i>Vitis vinifera</i>) |
| Unigene0057664 | 5.385523072 | Myb_DNA-binding domain-containing (<i>Cephalotus follicularis</i>) |
| Unigene0057665 | 10.45703881 | Myb_DNA-binding domain-containing (<i>Cephalotus follicularis</i>) |
| Unigene0009481 | 10.88310146 | MYB transcriptional factor (<i>Populus tremula</i> × <i>P. tremuloides</i>) |

* Data were the mean value of three biological replicates.

Table S4. bHLHs identified from differentially expressed genes

| GeneID | log2 Ratio(S3/S1) | Annotation |
|----------------|-------------------|--|
| Unigene0000604 | -1.542977885 | transcription factor bHLH140 (<i>Citrus sinensis</i>) |
| Unigene0000838 | -1.184189305 | transcription factor bHLH69 isoform X2 (<i>Vitis vinifera</i>) |
| Unigene0004951 | -2.253690822 | transcription factor bHLH68-like (<i>Juglans regia</i>) |
| Unigene0005046 | -5.824634604 | transcription factor bHLH94-like (<i>Juglans regia</i>) |
| Unigene0009283 | -1.356731517 | bHLH transcription factor (<i>Paeonia suffruticosa</i>) |
| Unigene0009299 | 3.01694928 | transcription factor bHLH63 (<i>Vitis vinifera</i>) |
| Unigene0009765 | -11.03103489 | transcription factor bHLH93-like (<i>Juglans regia</i>) |
| Unigene0010263 | 1.190472009 | transcription factor bHLH14 (<i>Theobroma cacao</i>) |
| Unigene0011997 | -1.239357047 | transcription factor bHLH104 isoform X1 (<i>Citrus sinensis</i>) |
| Unigene0021524 | -10.39934147 | transcription factor MYC4 (<i>Vitis vinifera</i>) |
| Unigene0021927 | 2.310369042 | transcription factor bHLH36 (<i>Theobroma cacao</i>) |
| Unigene0022043 | -2.507522348 | transcription factor bHLH68 (<i>Ricinus communis</i>) |
| Unigene0022455 | -4.607713173 | transcription factor bHLH35-like (<i>Pyrus × bretschneideri</i>) |
| Unigene0023097 | -3.228124521 | transcription factor bHLH87 (<i>Theobroma cacao</i>) |
| Unigene0023465 | -1.040981906 | transcription factor bHLH113 isoform X1 (<i>Prunus mume</i>) |
| Unigene0024528 | -1.817136179 | basic helix-loop-helix 144-like protein transcript variant 1 (<i>Morus alba</i>) |
| Unigene0024541 | -1.430788575 | transcription factor bHLH74 isoform X2 (<i>Prunus mume</i>) |
| Unigene0025130 | 2.04495838 | transcription factor bHLH117 (<i>Vitis vinifera</i>) |
| Unigene0027604 | -9.020557667 | transcription factor bHLH92 (<i>Juglans regia</i>) |
| Unigene0028208 | -1.588286752 | transcription factor bHLH51 (<i>Vitis vinifera</i>) |
| Unigene0028225 | -1.066042545 | transcription factor bHLH147 isoform X1 (<i>Vitis vinifera</i>) |
| Unigene0028502 | -1.456043273 | transcription factor bHLH79-like isoform X2 (<i>Nelumbo nucifera</i>) |
| Unigene0029775 | -5.265879952 | HLH domain-containing protein (<i>Cephalotus follicularis</i>) |
| Unigene0029789 | -4.584853904 | Serine/threonine-protein kinase WNK-related (<i>Theobroma cacao</i>) |
| Unigene0030684 | -1.549969453 | transcription factor bHLH128-like isoform X1 (<i>Juglans regia</i>) |
| Unigene0031383 | 2.345274781 | BHLH transcription factor (<i>Medicago truncatula</i>) |
| Unigene0034290 | -5.735383852 | transcription factor bHLH70 isoform X2 (<i>Vitis vinifera</i>) |
| Unigene0034305 | -2.982852155 | transcription factor bHLH113 isoform X3 (<i>Vitis vinifera</i>) |
| Unigene0036614 | -1.576885394 | transcription factor bHLH140 (<i>Prunus mume</i>) |
| Unigene0036639 | -1.163393004 | transcription factor bHLH91 (<i>Ricinus communis</i>) |
| Unigene0037066 | 4.11563007 | transcription factor bHLH18-like (<i>Solanum tuberosum</i>) |
| Unigene0037598 | -7.711518195 | transcription factor bHLH36 (<i>Ziziphus jujuba</i>) |
| Unigene0037850 | -1.050886838 | immunoglobulin A1 protease autotransporter isoform X1 (<i>Arachis ipaensis</i>) |
| Unigene0037852 | -1.818022021 | transcription factor bHLH25-like (<i>Vitis vinifera</i>) |
| Unigene0045448 | -2.464557332 | transcription factor bHLH110 (<i>Theobroma cacao</i>) |
| Unigene0050646 | -7.156893165 | transcription factor bHLH36 (<i>Theobroma cacao</i>) |
| Unigene0053195 | -3.402985048 | Serine/threonine-protein kinase WNK-related isoform 1 (<i>Theobroma cacao</i>) |
| Unigene0056531 | -2.396829315 | transcription factor bHLH106-like isoform X2 (<i>Juglans regia</i>) |
| Unigene0005081 | -1.373426581 | myc anthocyanin regulatory protein isoform X1 (<i>Vitis vinifera</i>) |
| Unigene0027634 | -2.372379263 | transcription factor MYC2 (<i>Vitis vinifera</i>) |

* Data were the mean value of three biological replicates.

Table S5. WD40 identified from differentially expressed genes

| GeneID | log2 Ratio(S3/S1)* | Annotation |
|----------------|--------------------|---|
| Unigene0021880 | -3.526584548 | WD repeat-containing protein 76 isoform X2 (<i>Jatropha curcas</i>) |
| Unigene0038216 | -3.493187425 | WD repeat-containing protein 76 isoform X2 (<i>Jatropha curcas</i>) |
| Unigene0021324 | -1.948580414 | WD repeat-containing protein 43 isoform X2 (<i>Vitis vinifera</i>) |
| Unigene0042402 | -1.626752223 | WD repeat-containing protein 89 homolog (<i>Vitis vinifera</i>) |
| Unigene0014003 | -1.611681795 | mitogen-activated protein kinase-binding protein 1 isoform X3 (<i>Vitis vinifera</i>) |
| Unigene0035053 | -1.551363637 | WD repeat-containing protein 44 isoform X1 (<i>Cucumis melo</i>) |
| Unigene0032589 | -1.532298896 | WD40 domain-containing protein (<i>Cephalotus follicularis</i>) |
| Unigene0005462 | -1.430489052 | WD repeat-containing protein 43 isoform X1 (<i>Vitis vinifera</i>) |
| Unigene0006146 | -1.347867295 | WD40 protein (<i>Paeonia suffruticosa</i>) |
| Unigene0032023 | -1.224403755 | diphthine methyltransferase homolog isoform X1 (<i>Prunus mume</i>) |
| Unigene0038786 | -1.223522782 | WD repeat-containing protein 75 (<i>Juglans regia</i>) |
| Unigene0023327 | -1.205421898 | WD repeat-containing protein 3 (<i>Vitis vinifera</i>) |
| Unigene0037037 | -1.185212251 | WD repeat-containing protein 44 (<i>Nelumbo nucifera</i>) |
| Unigene0058895 | -1.129144023 | WD40 repeat (<i>Macleaya cordata</i>) |
| Unigene0008400 | 1.925910111 | WD repeat-containing protein 25 (<i>Jatropha curcas</i>) |

* Data were the mean value of three biological replicates.