

Genetic regulation of anthocyanin biosynthesis in *Cornus* species: The roles of R2R3-MYB transcription factors

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ABSTRACT

Flowering dogwood (*Cornus florida* L.) and Asian dogwood (*C. kousa* F. Buerger ex Hance) are popular deciduous ornamental trees native to a wide range of the eastern and southeastern United States and East Asia, respectively. Anthocyanin pigments enhance desirable pink or dark red colored bracts in dogwoods. Although anthocyanin biosynthesis is one of the best-studied biological processes in nature, genomic and genetic resources to understand the molecular regulation of its synthesis in dogwoods are still lacking. Two classes of genes control anthocyanin production; both structural genes and MYB transcription factors may function as positive or negative regulators of anthocyanin biosynthesis. To reveal the molecular mechanisms that govern color production in ornamental dogwoods, mature bracts of three cultivars of *C. florida* (white bracts: 'Cloud Nine'; red bracts: 'Cherokee Brave' and 'Cherokee Chief') and two cultivars of *C. kousa* (light green bracts: 'Greensleeves' and mid-tone pink bracts 'Rosy Teacups') were sampled when color was maximally visible. Differential gene expression analysis of the RNAseq data identified 1,156 differentially expressed genes in *C. florida* and 1,396 in *C. kousa*. Phylogenetic analysis with functional orthologues in other plants grouped the candidate R2R3-MYB identified in this study into two distinct subgroups. *CfMYB2*, *CfMYB3*, and *CkMYB2* belonged to subgroup 4, whereas *CfMYB1 80* and *CkMYB1* clustered in subgroup 5. The former repress anthocyanin and proanthocyanidin synthesis in flowering and Asian dogwoods, whereas the latter increase it. Our study contributes to understanding processes behind anthocyanin production and lays foundation to future development of molecular markers for faster development of desirable red-bracted dogwoods.

22 **Keywords:** Differential gene expression; Dogwoods; Functional genomics; Molecular breeding;
23 Ornamental plants; Phenylpropanoid pathway; Phylogenetic analysis; Plant pigmentation;
24 RNAseq analysis

INTRODUCTION

Flowering dogwood (*Cornus florida* L.) and Asian dogwood (*C. kousa* F. Buerger ex Hance) are popular understory and deciduous ornamental trees of the *Cornus* genus, which includes about 60 species of trees and shrubs mostly found throughout the temperate regions of North America, Europe, and Asia (Eyde 1987, Cappiello and Shadow 2005, Wadl, Windham et al. 2014). Native to a wide range of states in the eastern and southeastern United States (US), flowering dogwoods owe their exceptional appeal to showy snow-white, pink, or red bracts, red fall foliage, and drupes (Witte, Windham et al. 2000, Cappiello and Shadow 2005). Asian dogwoods also are valued for their spring display of white, pink, or red bracts, brilliant-red fall foliage, colorful fruits, and exfoliating bark, and were introduced from Eastern Asia to the US because of their generally high resistance to insects and pathogens and overall better stress tolerance compared to flowering dogwood (Ranney, Grand and Knighten 1995, Li, Mmbaga et al. 2009, Wadl, Windham et al. 2014).

The majority of plant pigments are flavonoids, which are ubiquitous across the plant kingdom, and typically show functions in insect pollination and seed dispersal, hormone signaling, and abiotic and biotic defense (Liu, Osbourn and Ma 2015, Cao, Li et al. 2020, Wu, Wen et al. 2022). The desirable pink or dark red colors in bracts of flowering and Asian dogwoods are enhanced by biosynthesis of anthocyanin pigments (Kabir, Bautista et al. 2022). Two classes of genes control biosynthesis of anthocyanins and other phenylpropanoid-derived compounds: (1) structural genes encoding enzymes participating in formation of anthocyanins and (2) regulatory genes networks consisting of three types of transcription factors (TFs): v-myb avian myeloblastosis viral oncogene homolog proteins (MYBs), basic helix-loop-helix proteins

(bHLHs), and WD repeat proteins (WDRs) (Allan, Hellens and Laing 2008, Dubos, Stracke et al. 2010, Zhang, Butelli and Martin 2014).

Anthocyanin profiles in both dogwood species are similar, with major fruit anthocyanins as cyanidin 3-O-galactoside in *C. florida* and cyanidin 3-O-glucoside in *C. kousa*, respectively (Du, Wang and Francis 1974, Eyde 1987, Vareed, Reddy et al. 2006, Lev-Yadun and Gould 2009). Anthocyanins are specialized flavonoid metabolites found in plants and play an important role in conferring defense against plant pathogens and abiotic stresses such as UV radiation, drought, or cold (Jin, Cominelli et al. 2000, Lev-Yadun and Gould 2009, Zhang, Wang et al. 2019, Gong, Li et al. 2020, Wajahat 2023). Moreover, their impact on plant crop quality contributes to the horticultural, industrial, and nutritional value of various plant products, such as apple (*Malus domestica* Borkh.) (Lin-Wang, Bolitho et al. 2010, Meng, Zhang et al. 2016), chrysanthemum (*Chrysanthemum morifolium* (Ramat.) Hemst.) (Liu, Xiang et al. 2015), eggplant (*Solanum melongena* L.) (Zhang, Hu et al. 2014), grape (*Vitis vinifera* L.) (Czemmel, Heppel and Bogs 2012), morning glory (*Ipomea purpurea* L.) (Park, Ishikawa et al. 2007), petunia (*Petunia hybrida* D. Don ex W. H. Baxter) (Park, Ishikawa et al. 2007, Albert, Lewis et al. 2009, Albert, Lewis et al. 2011), royal lily (*Lilium regale* E. H. Wilson) (Yamagishi 2011), snapdragon (*Antirrhinum majus* L.) (Naing, Ai et al. 2018), or strawberry (*Fragaria vesca* L.) (Aharoni, De Vos et al. 2001), among many others. Their antioxidant activity has recently evoked tractable attention in protection against cancer, strokes, and other chronic human disorders (Zhang, Butelli and Martin 2014, Kodama, Brinch-Pedersen et al. 2018). Anthocyanins produced in the leaves of *C. kousa* were found to have anti-obesity effects (Khan, Shin et al. 2018).

Although flavonoid pigment biosynthesis is one of the best-studied biological processes in nature and R2R3-MYBs are widely distributed in the plant kingdom (Pei, Huang et al. 2024), key players involved in phenylpropanoid pathway and anthocyanin regulation in flowering and Asian dogwoods have not yet been identified. This means that the regulatory mechanisms of anthocyanin biosynthesis in *Cornus* species remain poorly understood. That knowledge gap delays the development of functional markers or the application of marker-assisted selection in dogwood breeding. We hypothesize that *Cornus* species have evolved divergent MYB regulatory networks to achieve convergent red bract phenotypes, thus providing a model for studying evolutionary plasticity in flavonoid pathways. Therefore, this work aimed to investigate the global transcription profiles of MYB TFs and structural genes using the RNA sequencing (RNAseq) approach within various cultivars to identify candidate R2R3-MYB transcription factors that are either positive or negative regulators of the anthocyanin pathway and other flavonoid compounds.

MATERIAL AND METHODS

Plant Materials

Four- week -old bracts were collected and immediately frozen in liquid nitrogen. Bracts from three cultivars of *C. florida* (white bracts: 'Cloud Nine'; red bracts: 'Cherokee Brave' and 'Cherokee Chief') and two cultivars of *C. kousa* (light green bracts: 'Greensleeves,' and light to medium pink 'Rosy Teacups') were harvested when color was maximally visible (April and May 2017) (Figure 1A). Trees were grown at the University of Tennessee Knoxville, USA greenhouse and were about 5 years old and disease-free.

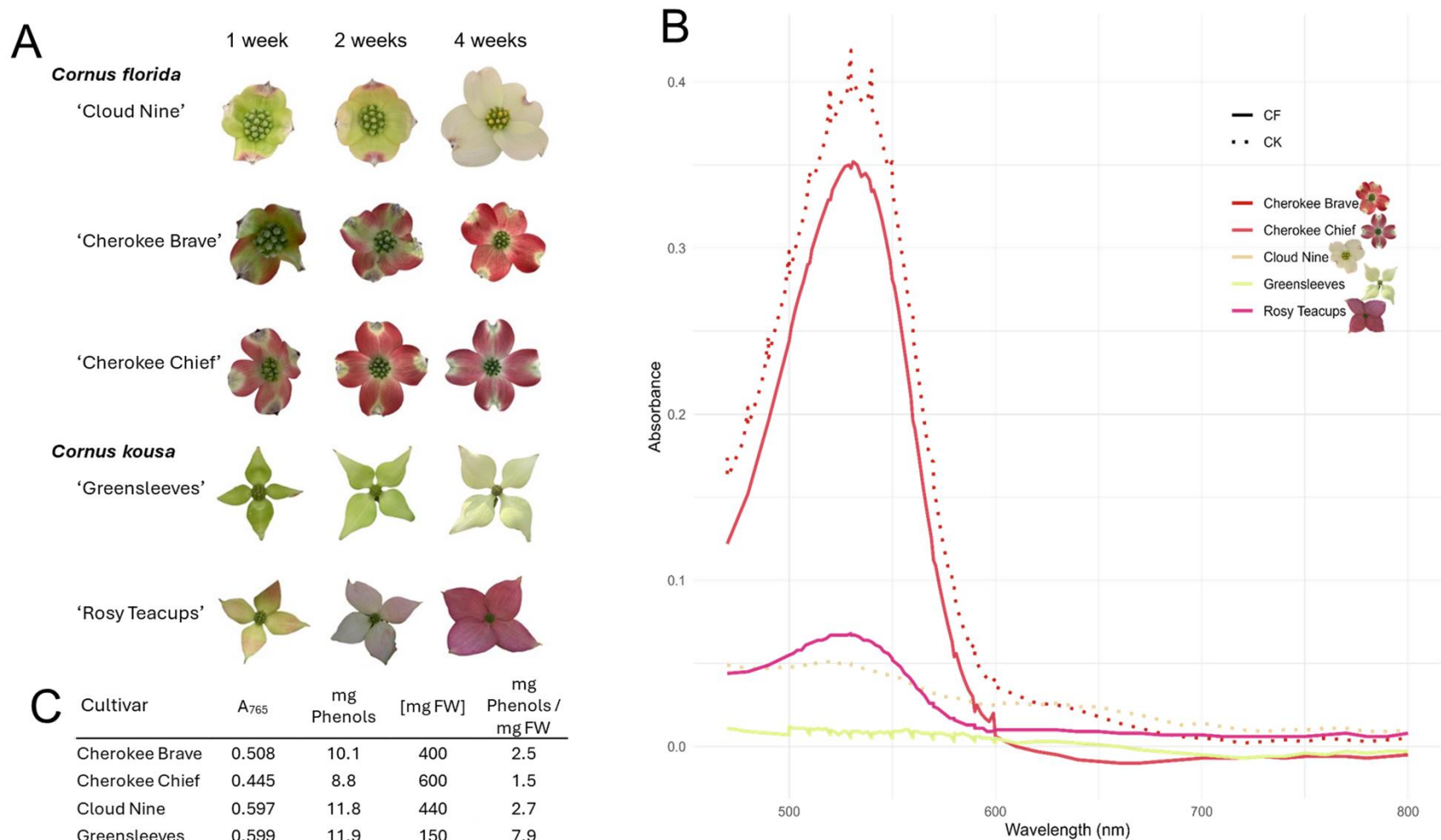


Figure 1. Phenotypes of *Cornus florida* and *C. kousa* bracts. (A) Representative bract phenotypes at 1, 2, and 4 weeks post-emergence for five cultivars: *C. florida* 'Cloud Nine', 'Cherokee Brave', 'Cherokee Chief'; *C. kousa* 'Greensleeves', and 'Rosy Teacups'. **(B)** Absorbance spectra (400–to–800 nm) of anthocyanin extracts from 4-week-old bracts. **(C)** Total phenolic content measured by Folin-Ciocalteu assay at 765 nm. Values are expressed as mg gallic acid equivalents (GAE) per mg fresh weight (FW).

Anthocyanin isolation and spectral analyses

About 2 g of frozen samples per cultivar were homogenized in liquid nitrogen, and acetone extraction was performed as follows. Frozen tissue was ground to a fine powder. Two sequential extractions with ice-cold acetone (1:1 w:v) were performed, followed by centrifugation ($21,000 \times g$, 4°C). Supernatants were pooled and re-extracted with 70% acetone containing 0.01% HCl (v/v). Combined acetone extracts were mixed with chloroform (1:1 v/v), vortexed, and centrifuged ($21,000 \times g$, 4°C). The aqueous phase was collected and concentrated using a rotary evaporator (35°C , 5 min under vacuum with 4°C cooling). Final extracts were stored at -80°C . Absorbance spectra (400 to 800 nm) were collected using Shimadzu UV-VIS Spectrophotometer UB-1900i (Shimadzu Scientific Instruments Inc., Coulmbia, MD). Total phenolic content was quantified using the Folin-Ciocalteu method (Folin and Ciocalteu 1927). Gallic acid (50–500 mg/L in H_2O) served as the reference. Reactions included 20 μL sample or standard and 100 μL Folin-Ciocalteu reagent with 300 μL 7.5% Na_2CO_3 (w/v). Absorbance was measured at 755 nm and 765 nm (validation step; primary quantification at 765 nm). Phenolic content was expressed as gallic acid equivalents (GAE) using the standard curve ($R^2 = 0.9792$ at 765 nm).

RNA Extraction and Sequencing

RNA was extracted using 500 mg of frozen tissue per sample with the GeneAll® Ribospin™ Plant Total RNA Kit (GeneAll Biotechnology, Seoul, Korea), following the manufacturer's instructions. Bract samples were homogenized using zirconia beads at 6 m/s for 30 sec in a Bead mill 24 (Fisher Scientific, Waltham, MA). Subsequently, total RNA integrity was assessed with Agilent 2100 Bioanalyzer system using the RNA 6000 Nano LabChip® kit

(Agilent Technologies, Palo Alto, CA). Four of the 20 isolated RNA samples were below the required quality threshold (RIN ≥ 6.0). The 16 RNA samples from three cultivars of flowering dogwood and two of Asian dogwood were submitted to GeneWiz (South Plainfield, NJ) for library preparation and sequencing using Illumina HiSeq 2500, which generated 150 bp paired end reads. All analyzed cultivars had at least two biological replicates.

Quality Control

RNAseq yielded between 20 and 37 million reads per library, which were subjected to error correction using Rcorrector (RNAseq error CORRECTOR) (Song and Florea 2015). Read quality control was performed using FastQC v0.11.4 (Andrews, Krueger et al. 2010). Adaptors, short (<30 bases), and low-quality reads were trimmed using SKEWER v0.2.2 (Jiang, Lei et al. 2014). Subsequently, read quality control was reassessed using FastQC v0.11.4 (Andrews, Krueger et al. 2010) (Supplementary Table T1).

Read Alignment and Gene Quantification

Reference genomes for flowering and Asian dogwood were not available at this study's onset. Therefore, trimmed reads were mapped to the *C. florida* or *C. kousa* transcriptomes (Yu, Xiang et al. 2017) using Genomic short-read Nucleotide Alignment Program (GSNAP version 2018-01-31) (Wu, Reeder et al. 2016). Aligned reads were used to generate a gene-specific count matrix across samples using a standalone script provided by HTSeq (Anders, Pyl and Huber 2015), which counts the number of reads mapped to each gene.

Differential Expression Analysis and Functional Enrichment

To identify R2R3-MYB TFs and structural genes involved in anthocyanin biosynthesis, gene counts were analyzed for gene-level differential expression using DESeq2 (Love, Huber and Anders 2014). This package provides an option to test differential expression by shrinking estimators of the negative binomial distribution. Count results from HTSeq were imported with an underlying experimental design that modeled the bract color as the effect of treatment while adjusting for cultivar or species as factors. Genes with less than one count across samples were removed. Regularized log transformation function was used to calculate sample distances using t-SNE plot functionality in the R package *tsne* (Donaldson and Donaldson 2010). The Wald test (Ghosh 1992) was employed to identify differentially expressed genes (DEGs) between two sample classes, red-bracted and non-pigmented for either species. Significant DEGs were identified with adjusted p-value < 0.05 after multiple testing using the Benjamini-Hochberg method (Benjamini and Hochberg 1995). Heatmaps with the expression profiles of DEGs after mapping to each of the two *Cornus* species transcriptomes were generated using the R package *pheatmap* with correlation distances (Pearson 1895). TransDecoder v3.0.0 was used to predict encoded peptides based on *C. florida* and *C. kousa* transcriptomes. TransDecoder identified all open reading frames (ORFs) that were at least 50 amino acids long in the transcripts. These ORFs were then scanned for homology to known proteins using blastp (Altschul, Gish et al. 1990) against the UniProtKB/TrEMBL database (Boutet, Lieberherr et al. 2007) for plants and searched against Pfam (Finn, Coghill et al. 2016) for conserved protein domains with HMMER v3.1b2 (Potter, Luciani et al. 2018). TransDecoder was rerun with the outputs generated from blastp and HMMER to improve the prediction of coding regions. All predicted peptides were used on InterProScan 5.21-60.0 software for ortholog assignment and annotation of GO terms.

Additionally, DEG transcripts were uploaded to the KAAS server for KEGG (Kyoto Encyclopedia of Genes and Genomes) (Kanehisa and Goto 2000). Finally, a custom database for the GAPDH housekeeping gene in eudicots was used to devise putative sequences in *C. florida* and *C. kousa* transcriptomes (see below).

Gene Ontology enrichment analysis

To gain insights into the functions of the DEGs, genes were annotated and analyzed through gene ontology (GO) by AgriGO v2.0 (Tian, Liu et al. 2017) and the plugin BiNGO v3.0.3 (Maere, Heymans and Kuiper 2005) for Cytoscape v3.3.0 using the *C. florida* or *C. kousa* transcriptomes (Yu, Xiang et al. 2017) GO annotations as background reference. BiNGO was used to calculate overrepresented GO terms in lists of up- and down-regulated DEGs using a hypergeometric test and the Benjamini and Hochberg method to adjust *p*-values, considering significantly enriched GO terms with FDR < 0.05. Additionally, AgriGO was used to perform Singular Enrichment Analysis of GO terms in the lists of DEGs using the hypergeometric statistical test method and the Yekutieli multi-test adjustment method for FDR correction under dependency (Benjamini and Yekutieli 2001) under the significance level of 0.05. Complete GO was selected as the Gene Ontology type. REVIGO (Supek, Bošnjak et al. 2011) was used to summarize and visualize the results of AgriGO.

Phylogenetic analysis and the conserved motif discovery

Phylogenetic relationships of selected R2R3-MYB protein sequences associated with phenylpropanoid pathways from various plant species downloaded from NCBI were inferred using the Neighbor-Joining method (Saitou and Nei 1987) implemented into MEGA11 (Stecher,

Tamura and Kumar 2020, Tamura, Stecher and Kumar 2021). The evolutionary distances were computed using the p-distance method (Nei and Kumar 2000) and are expressed in the units of the number of amino acid substitutions per site. This analysis involved 105 amino acid sequences and had 768 informative positions in the final dataset. All ambiguous positions were removed for each sequence pair (pairwise deletion option). Bootstrap values are shown as percentages of 1,000 replicates whenever greater than 50%. The subgroups labels S1 through S28 are designated as per previous studies (Stracke, Werber and Weisshaar 2001, Dubos, Stracke et al. 2010, Shelton, Stranne et al. 2012, Liu, Osbourn and Ma 2015). The species and accession numbers of labeled MYB proteins are provided in Supplementary Table T2. Multiple expectation maximization for Motif Elicitation (MEME), an online bioinformatic tool (<http://memesuite.org/>), has been used to search for characterized distinctive motifs in MYB repressors, such as EAR with conserved sequence LxLxL and SID interacting motif containing GY/FDFLGL conserved sequence. The species and accession numbers of R2R3-MYB repressor proteins are given in Supplementary Table T3.

Reverse Transcription Quantitative PCR (RT-qPCR)

Bracts were collected from three cultivars of *C. florida* and two cultivars of *C. kousa* one week after emergence, followed by bract collections at two and four weeks after emergence. Samples were collected during the flowering period for three consecutive years (April 2019 – May 2021). Three biological replicates were used for each time point collection. From the total RNA extracted from all samples as described above (Ribospin), cDNA was prepared using qScript™ cDNA SuperMix (Quantabio, Beverly, MA, USA) according to the manufacturer's instructions. Primers for the six and four consistently up-or down-regulated candidate regulatory

and structural genes were designed based on *C. florida* and *C. kousa* sequences, respectively (Supplementary Table T4). Primers were designed using Primer-BLAST NCBI Genbank with amplification lengths between 70 and 200 bp (Supplementary Table T4). Gene expression was analyzed using PerfeCTa SYBR Green Fast Mix (Quantabio, Beverly, MA, USA). A reaction volume of 20 μ L contained 1 μ L of previously diluted cDNA (1:10), 2 μ L of gene-specific primers (1 μ M each), and 12 μ L of SYBR Green Fast Mix. RT-qPCR experiments were performed on QuantStudio™ 6 Flex (Applied Biosystems, Waltham, MA, USA), and the program was run for 40 cycles, each consisting of 15 s at 95 °C and 1 min at 60 °C. All samples were run in three technical replicates, and no-template controls were included in all plates. The expression of each gene, respectively, was normalized to GAPDH expression for each plant at 1 week post emergence using the $2^{-\Delta\Delta CT}$ method (Livak and Schmittgen 2001). Data analysis was performed using R v4.2.0 with the following packages: ggplot2 v3.5.1, dplyr v1.1.4, tidyr v1.3.1, multcomp v1.4-26, emmeans v1.10.5, stringr v1.5.1, and broom v1.0.6. RT-qPCR data for each gene was analyzed using a two-way ANOVA (Kaufmann and Schering 2007) to examine the effects of time after bracts emergence and cultivar on that gene's expression. Post-hoc analyses were performed using Tukey's HSD test with Sidak adjustment for main effects and Tukey adjustment for interactions at $\alpha = 0.05$. Compact letter displays were generated to visualize significant differences between groups. Mean expression values were calculated for each Cultivar and Stage.

RNA-seq Data Processing and Pathway-Centric Analysis

RNA sequencing data from 13 SRA libraries representing the five *Cornus* cultivars were processed through a reproducible computational pipeline. Raw reads were quality-controlled

using FastQC and trimmed with Trimmomatic to remove adapters and low-quality bases. *De novo* transcriptome assemblies for *C. florida* and *C. kousa* were generated using Trinity v2.15.1, followed by protein-coding sequence prediction via TransDecoder. Pathway-specific gene identification focused on 14 anthocyanin biosynthesis steps (e.g., PAL, CHS, ANS), as advised by KEGG (Kanehisa and Goto 2000). Putative paralogs were annotated by querying assembled transcripts against reference protein sequences (UniProt/SwissProt) using BLASTP (e-value $\leq 1e-20$, query coverage $\geq 80\%$). Reciprocal BLAST validation ensured orthology, and isoforms were resolved using Salmon-based transcript quantification.

Expression values from multiple SRA replicates per cultivar were aggregated using a two-tiered approach: paralogs within each pathway step were averaged, and biological replicates were combined via median expression values. Zero counts, representing undetected expression, were treated as missing data and excluded from calculations, consistent with recommendations for handling sparse expression values in RNAseq studies (Biesecker 2013). Metadata integration linked SRA accessions to cultivar phenotypes through structured column headers (e.g., "Cherokee Brave_SRR21411472"), which enabled cross-referencing of molecular data with bract coloration traits. Normalized expression values were analyzed using a hierarchical statistical approach: (1) Cultivar-level comparisons: One-way ANOVA identified significant expression differences ($\alpha = 0.05$) across cultivars, with Tukey's HSD post-hoc testing (critical Q = 3.74–4.58, gene-specific degrees of freedom) assigning letter groupings (A/B/C) to distinguish non-significant pairs. (2) Phenotype-species interactions: Two-way ANOVA evaluated the main effects of species (*C. florida* vs. *C. kousa*) and phenotype (red/pink vs. white/green), with Benjamini-Hochberg correction controlling false discovery rates. This integrative methodology enabled robust identification of regulatory nodes (e.g., *05_CHI* in *C. florida*, *12_ANS* in *C.*

256 *kousa*) underlying species-specific anthocyanin accumulation patterns, while maintaining
257 transparency across 148 paralogs and 14 enzymatic steps.

RESULTS

Color Variation in Dogwood Bracts

The variation in anthocyanins content and color intensity in flowering and Asian dogwood cultivars depended on the season, climate, and stage of plant development. Among *C. florida* red-bracted cultivars used in this study, 'Cherokee Chief' mature bracts exhibited the deepest rose-red blooms with beige to pale green edges and highlights in the center (Figure 1A). 'Cherokee Brave' displayed reddish-pink bracts with a pale green center, which was prevalent in the early stages of development (Figure 1A). 'Cloud Nine' was the only pure white-bracted cultivar, which occasionally had dark purple notches (Figure 1A). Asian dogwood cultivar 'Rosy Teacups' (Figure 1A) manifested light to medium pink bracts, whereas 'Greensleeves' (Figure 1A) produced white bracts with green to creamy highlights.

Absorbance maxima of anthocyanins isolated from 4-week-old bracts was between 520 and 540 nm (Figure 1B). This is in agreement with known spectra of two major anthocyanin species detected in the fruits *C. florida* and *C. kousa*, cyanidin-3-O-glucoside and cyanidin-3-O-galactoside, respectively. These spectra confirm production of similar anthocyanins in fruits and in bracts of both species. A minor peak in the same range detected for 'Cloud Nine' could originate from the colored bracts edges or anthocyanins that are not visual to the bare-eye (Figure 1A). Lack of such a peak in 'Greensleeves' was not due to diminished phenolics metabolism; indeed, this cultivar had the highest phenolics levels of all analyzed samples (7.9 mg phenols per mg fresh weight; Figure 1C). Similarly, the white-bracted 'Cloud Nine' had the highest levels of phenolics among the three analyzed cultivars of *C. florida*.

RNA sequencing and alignment

RNAseq was performed with individual libraries for each set of bracts collected from each tree, yielding between ~28 million to ~ 39.2 million raw paired end reads per library. After the adaptor and low-quality sequences trimming, more than 71% and 74% of total clean reads were successfully mapped to flowering and Asian dogwood transcriptomes, respectively, because their reference genomes and annotations were not publicly available at this study's completion (Supplementary Table T1).

Phylogenetic analysis

Phylogenetic analysis of R2R3-MYB TFs involved in regulating phenylpropanoid-derived compounds, such as monolignols, anthocyanins, proanthocyanidins, flavonols, and isoflavonoids, was conducted to assess the candidate roles of identified *C. florida* and *C. kousa* R2R3-MYB genes (Supplementary Figure F1). CfMYB1 80 and CkMYB1 protein sequences were clustered to subgroup 5, to which activators of anthocyanin and proanthocyanidin synthesis are classified. All of these activators harbor R3 repeat [D/E]Lx2[R/K]x3Lx6Lx3R, which is an interacting bHLH motif (Grotewold, Sainz et al. 2000, Zimmermann, Heim et al. 2004). Correspondingly, Pfam database (Finn, Coggill et al. 2016) was used for protein and domain sequence classification. MYB-like DNA binding domains were detected in CfMYB2, CfMYB3, CfMYB5 78, CfMYB6 30, CkMYB1, and CkMYB2 protein sequences. All six sequences belonged to Pfam clan CLO123, which contains a diverse range of DNA-binding domains with a bHLH motif. Notably, MYB-like DNA binding domains were not detected in CfMYB1 80 protein sequence, which could be due to sequence fragmentation. CfMYB2, CfMYB3, and CkMYB2 protein sequences were clustered to subgroup 4. Majority of known MYB protein

repressors negatively regulate phenylpropanoid metabolism and belong to this subgroup 4. In contrast, C-terminal sequence of these proteins contains either C1 GDIP or C2 EAR conserved motifs (Jin, Cominelli et al. 2000). CfMYB5 78 and CfMYB6 30 did not cluster with any designated subgroups; that could be due to lineage- or species-specific "orphan" genes or the phylogenetic analysis methodology used here (Supplementary Figure F1). MEME, an online tool, was used to search for GDIP and EAR motives (Figure 2A). CfMYB2, CfMYB3 in *C. florida*, and CkMYB2 in *C. kousa* contained EAR pdLNLD/ELxiG/S motif located at C-terminal behind MYB R repeat (Figure 2B).

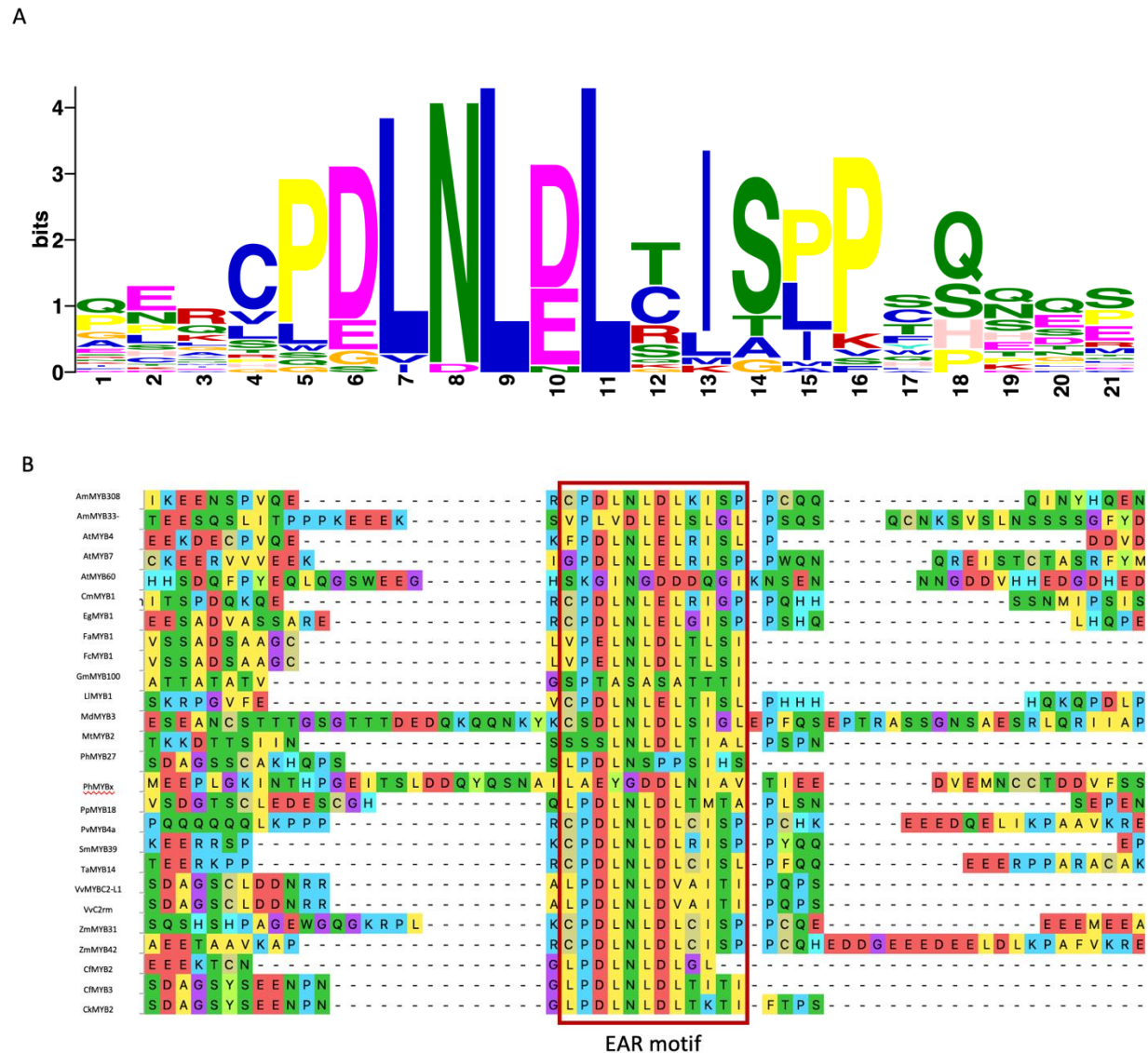


Figure 2. Positional enrichment of Ethylene-responsive element binding factor-associated Amphiphilic Repression (EAR) motif in R2R3-MYB transcription factors of *Cornus florida* and *C. kousa*. (A) Distribution of the Ethylene-responsive element binding factor-associated Amphiphilic Repression (EAR) motif in 26 R2R3-MYB protein sequences from *C. florida* and *C. kousa*. (B) Multiple sequence alignment showing EAR motif localization at the C-terminal region of CfMYB2, CfMYB3, and CkMYB2, downstream of the MYB R repeat.

DEGs Involved in Anthocyanin Biosynthesis Pathway

Differential gene expression analysis identified 1,156 significant DEGs in *C. florida*, of which 615 were upregulated and 541 were downregulated, based on the thresholds for log2 fold change $|\log_2FC| \geq 1$ and false discovery rate (FDR) ≤ 0.05 (Supplementary Table T5). In *C. kousa*, 1,396 were identified as DEGs, of which 753 were upregulated and 643 were downregulated (Supplementary Table T6). Sample distances were represented using t-SNE plots and heatmaps to evaluate the overall transcriptomes of three flowering dogwood cultivars (Figure 3A-B) and two Asian dogwood cultivars (Figure 3C-D). The 13 transcriptome profiles were separated into five clusters that correlated with bract color and cultivar when reads were mapped to either *C. florida* or *C. kousa* transcriptome. GO enrichment analysis was applied to identify the functions and biological pathways involved in the DEGs (Supplementary Table T7-8). Moreover, DEGs for both species were employed for the KEGG pathway enrichment using AgriGO v2.0 analysis (Tian, Liu et al. 2017) and yielded significant GO terms (FDR < 0.05) involved in pathways such as plant hormone signal transduction, metabolic pathways, and membrane transporters belonging to MATE (Multidrug and Toxic Compound Extrusion) which are involved in the transport of anthocyanins to the vacuole (Supplementary Figure F2A-B). This study's goal was to better understand phenylpropanoid metabolism regulation, mainly anthocyanin regulation; hence, MYB TFs as key regulators were studied further. The seven candidates *R2R3-MYB* genes were identified as differentially expressed using the RNAseq data at an adjusted *p*-value or FDR < 0.05 when comparing *C. florida* red and white-bracted cultivars and *C. kousa* pink and light green-bracted cultivars, respectively. Candidate genes designated as *CfMYB1* 80, *CfMYB2*, *CfMYB3*, *CfMYB5* 78, *CfMYB6* 30, *CkMYB1*, and *CkMYB2* were identified as downregulated in non-red bracted *C. florida* and *C. kousa* cultivars. Additionally,

343 three structural genes involved in anthocyanin biosynthesis – *CHI*, *CHS*, and *F3H* – were
344 downregulated in non-red bracted *C. florida* and *C. kousa* cultivars.

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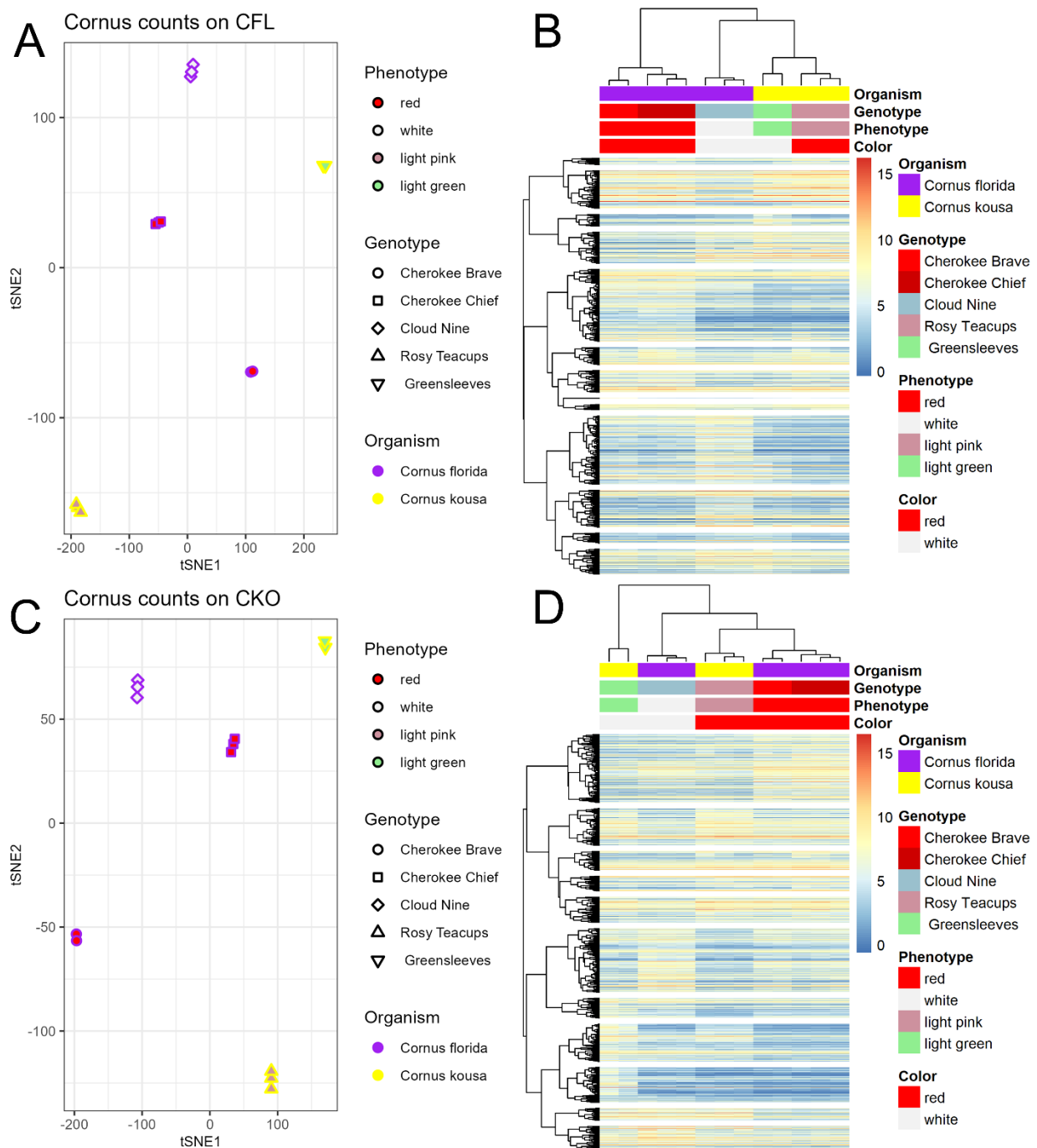


Figure 3. Transcriptomic clustering and expression heatmaps of *Cornus* bract samples. (A, C) Hierarchical clustering of 13 RNA-seq samples mapped to the *C. florida* (A) and *C. kousa* (C) transcriptomes, grouped by cultivar and bract color. (B, D) Heatmaps of normalized

350 expression values for bract color-associated DEGs, showing clustering by species (**B**) and by
351 color (**D**).

Expression Dynamics of R2R3-MYB Transcription Factors Across Dogwood Cultivars and Developmental Stages

The qRT-PCR analysis revealed distinct, statistically robust patterns of gene expression for both regulatory (R2R3-MYBs; Figure 4) and structural genes (Supplementary Figure 3) involved in the anthocyanin biosynthesis pathway in *Cornus florida* and *C. kousa*. Expression data were evaluated across multiple cultivars, species, and three developmental stages, with biological replicates that provided high statistical power. Two-way and three-way ANOVA, followed by Tukey HSD post-hoc tests, demonstrated that cultivar, developmental stage, and their interaction frequently had significant effects on the transcriptional regulation of key genes.

CfMYB1_80 (Figure 4A): For the gene *CfMYB1_80*, cultivar had a significant effect ($F=30.81$, $p=0.000002$), and the cultivar $\times$ stage interaction was also significant ($F=9.56$, $p=0.00025$). Post-hoc groupings indicated that only the ‘Cherokee Chief’ at stages II and III were significantly different from all other combinations, consistent with the role of subgroup 5 MYBs as positive regulators of anthocyanin and proanthocyanidin biosynthesis, particularly in red-bracted cultivars during late development.

CfMYB2 (Figure 4B): A significant main effect of both cultivar ($F=10.04$, $p=0.0012$) and stage ($F=5.21$, $p=0.0164$), as well as a highly significant cultivar $\times$ stage interaction ($F=8.79$, $p=0.0004$), was observed for *CfMYB2* expression. Post-hoc analysis revealed that the ‘Cloud Nine’ sampled at stage II was uniquely elevated compared to all other cultivar-stage combinations ($p<0.05$), which suggested a distinct role for this gene in suppressing anthocyanin accumulation at this specific developmental window. This fine-tuned, temporally restricted expression is consistent with the function of subgroup 4 MYBs as negative regulators of flavonoid biosynthesis.

CfMYB3 (Figure 4C): This gene displayed significant main effects for both cultivar (F=5.79, p=0.0089) and stage (F=6.41, p=0.0059), with significant interaction between both factors (F=8.54, p=0.0005). Post-hoc HSD revealed that ‘Cherokee Brave’ at stages II and II, as well as ‘Cherokee Chief’ at stages II and III were significantly different from ‘Cloud Nine’ sampled at various stages, which indicated that *CfMYB3* is differentially regulated across genetic backgrounds and developmental phases. This pattern supports the hypothesis that *CfMYB3* contributes to the suppression of anthocyanin synthesis in specific cultivars and stages, in line with its phylogenetic placement among known repressors.

CkMYB1 (Figure 4D): In *C. kousa*, *CkMYB1* expression was significantly affected by cultivar (F=6.75, p=0.019) and the cultivar × stage interaction (F=5.49, p=0.020). ‘Rosy Teacups’ sampled at stage III showed significantly higher expression of *CkMYB1* than all other combinations, suggesting a cultivar-specific, developmentally regulated activation of anthocyanin synthesis in this pink-bracted variety.

CkMYB2 (Figure 4E): *CkMYB2* was significantly regulated by stage (F=23.60, p=0.00002), with no significant cultivar or interaction effects. Tukey HSD revealed that stage II had the highest expression, followed by stage i, and the lowest levels were seen at the latest stage III. This developmental regulation is consistent with the role of subgroup 4 MYBs in temporally restricting anthocyanin accumulation.

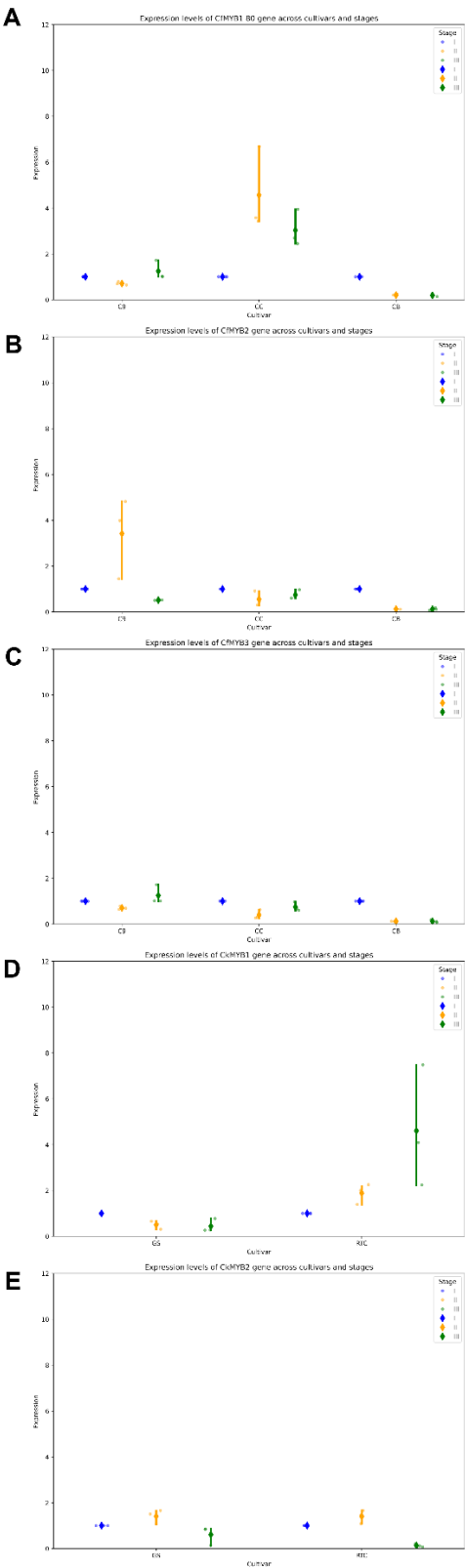


Figure 4. qRT-PCR validation of candidate R2R3-MYB gene expression in *Cornus* bracts. Expression levels of (A) CfMYB1_80, (B) CfMYB2, (C) CfMYB3, (D) CkMYB1, and (E) CkMYB2 across three developmental stages (1, 2, and 4 weeks post-emergence) in five cultivars.

398 Expression normalized to GAPDH and analyzed using the $2^{-\Delta\Delta CT}$ method. Error bars represent
399 standard deviation of three biological replicates.

Expression Dynamics of Biosynthesis Genes Across Dogwood Cultivars and Developmental Stages

CHI (Supplementary Figure F3A): The chalcone isomerase (CHI) expression was strongly affected by cultivar ($F=11.28$, $p=0.0002$), stage ($F=12.50$, $p=0.0001$), and species $\times$ cultivar ($F=8.74$, $p=0.0010$), with a significant three-way interaction ($F=2.98$, $p=0.035$). The highest expression was observed in the *C. florida* ‘Cloud Nine’ stage II, which was significantly different from all other combinations. This suggests that CHI is a major regulatory checkpoint for anthocyanin accumulation in dogwood bracts, with strong genetic and developmental control. The consistent upregulation in ‘Cloud Nine’ as compared with RNA-seq data solidifies CHI’s role as a key flux control point. Phenotype-specific discrepancies in white cultivars suggest post-transcriptional modulation, necessitating protein-level validation.

CHS (Supplementary Figure F3B): The chalcone synthase (CHS) was significantly regulated by stage ($F=10.85$, $p=0.0003$), species $\times$ cultivar ($F=14.75$, $p=0.00004$), and species $\times$ cultivar $\times$ stage ($F=6.18$, $p=0.00094$). The *C. florida* ‘Cloud Nine’ at stage II again showed the highest expression, consistent with this gene’s role as the first committed step in flavonoid biosynthesis. The disconnect between transcript abundance and statistical significance in RNA-seq, alongside qRT-PCR’s stage-specific spikes, implies post-transcriptional regulation (e.g., translational control or protein stability). This decoupling underscores the limitation of relying solely on mRNA data for pathway flux interpretation.

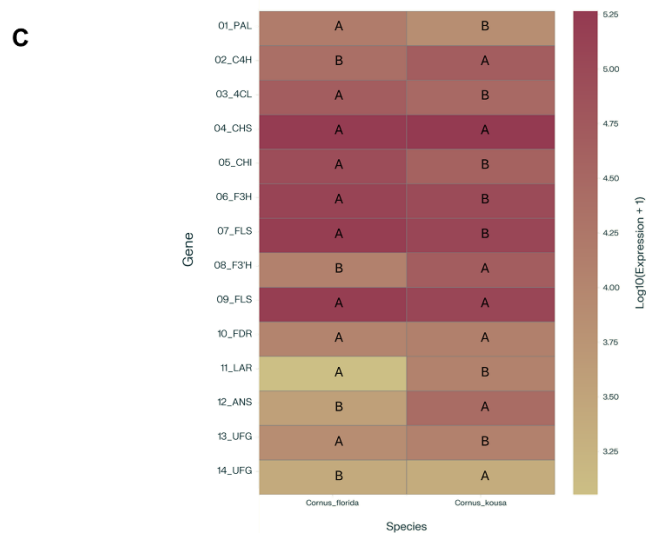
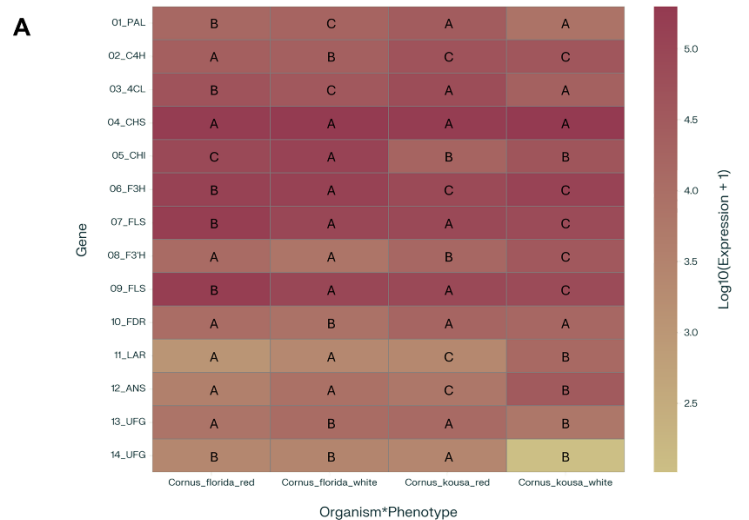
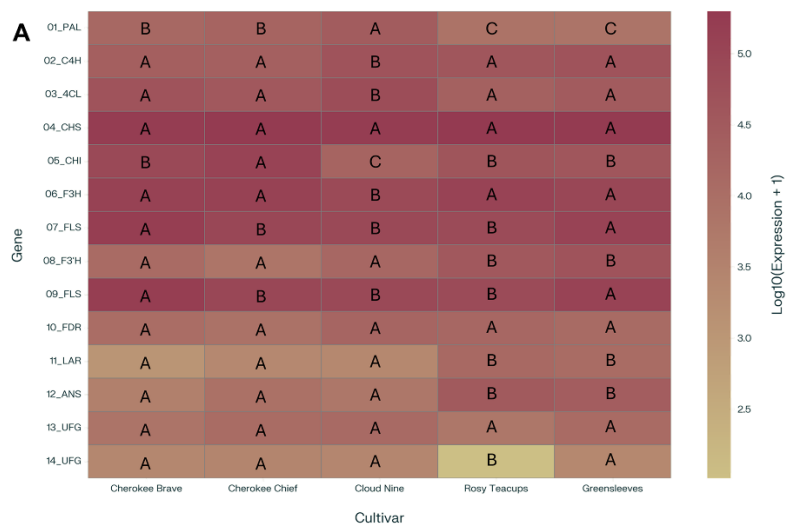
F3H (Supplementary Figure F3C): The flavanone 3-hydroxylase (F3H) expression was significantly influenced by developmental stage ($F=5.93$, $p=0.0081$), but not by cultivar or interaction of the factors. Tukey HSD post-hoc tests indicated that the latest-sampled stage III was significantly lower than stages I and II ($p<0.05$), which suggested a developmentally

regulated downregulation of this early biosynthetic gene as bracts mature. Whereas RNA-seq identified genetic background-driven regulation of this gene (see above), qRT-PCR highlighted temporal specificity, particularly in *C. kousa*. This suggests stage-specific sampling bias in RNA-seq's whole-bract approach, which may average temporal fluctuations.

Collectively, these results demonstrate that the regulation of anthocyanin biosynthesis in dogwood bracts is highly complex and involves multiple layers of control by R2R3-MYB transcription factors and structural genes, with strong effects of genetic background, developmental stage, and interactions. The fine-scale, temporally restricted expression of MYB repressors and activators suggests that dogwoods have evolved distinct, cultivar-specific regulatory circuits to modulate brightly colored bracts, a trait of high horticultural and ecological significance (ALBORNOZ, ROSAS and LÓPEZ 2023).

Expression Patterns in the Anthocyanin Biosynthesis Pathway

RNA-seq analysis across the 14 enzymatic steps of the anthocyanin biosynthesis pathway revealed distinct, multi-tiered regulation associated with species identity, cultivar, and bract coloration (Figure 5; Supplementary Table T9). Our three-tiered statistical approach (cultivar vs. species vs. species $\times$ phenotype) uncovered regulatory patterns obscured in single-level analyses, which resolved contradictions between transcript abundance and phenotypic outcomes. Three complementary analyses-per-cultivar (Figure 5A), species $\times$ phenotype Figure 5B), (and per-species (Figure 5C) demonstrated that 13/14 genes exhibited significant expression differences (ANOVA Type III, $p < 0.05$), with only chalcone synthase (04_CHS) showing conserved expression across all tiers ($p > 0.05$). This comprehensive approach uncovered evolutionarily divergent regulatory strategies underlying similar floral phenotypes.



447 **Figure 5: Heatmap of phenylpropanoid pathway gene expression across *Cornus* cultivars.**
 448 Log10-transformed weighted mean expression values for 14 pathway genes across five cultivars.
 449 (A) Cultivar-level expression; (B) phenotype and species-level; (C) species-level. Color
 450 gradient: low (whitish #CCBF85) to high (crimson #943A51). Letters indicate statistically
 451 homogeneous groups (Tukey HSD, $\alpha = 0.05$).

The white-bracted *C. florida* cultivar ‘Cloud Nine’ emerged as a metabolic outlier and exhibited statistically distinct expression patterns (Tukey HSD, $p < 0.001$) for key upstream enzymes. 01_PAL was 2.2-fold higher than ‘Cherokee Brave’ (28,648 vs. 14,502 TPM); 02_C4H was 1.9-fold elevated vs. ‘Rosy Teacups’ (47,740 vs. 40,262 TPM); and 03_4CL showed 3.8-fold increase vs. *C. kousa* ‘Greensleeves’ (67,521 vs. 17,718 TPM). These findings position ‘Cloud Nine’ as a model for upstream flux control, with prioritized phenylpropanoid precursor synthesis. In contrast, *C. kousa* cultivars specialized in late-pathway modification. The 11_LAR (leucoanthocyanidin reductase) expression was 7.0-fold higher in ‘Rosy Teacups’, red-bracted *C. kousa* cultivar, than ‘Cherokee Brave’ (17,987 vs. 2,574 TPM; $p < 0.001$), which suggested species-specific diversion into proanthocyanidins. Despite extreme 04_CHS expression in ‘Rosy Teacups’ (198,697 TPM), statistical analysis revealed no significant differences across cultivars, species, or phenotypes ($p = 0.312\text{--}0.406$). This unexpected conservation at the pathway’s first committed step implies regulatory constraint, with flux controlled downstream through species-specific mechanisms.

Chalcone isomerase 05_CHI emerged as a nexus of evolutionary divergence and exemplified complex regulatory plasticity with tier-specific groupings. Under per-cultivar aggregation ‘Cloud Nine’ was distinct from either *C. kousa* cultivar or from *C. florida* red-bracted cultivars ($p < 0.001$). The same pattern emerged when aggregated at species $\times$ phenotype tier, with ‘Cloud Nine’ being distinct from *C. florida* red or *C. kousa* white/red ($p < 0.001$). The 4.8-fold difference between *C. florida* red (86,898 TPM) and *C. kousa* ‘Greensleeves’ (4,013 TPM) highlights the 05_CHI’s role as a key phenotypic checkpoint, with species employing distinct mechanisms to modulate flavanone production.

The interplay between species and phenotype uncovered divergent molecular strategies for red bract development. In *C. florida* red cultivars, 05_CHI expression reached exceptional levels (86,898 TPM; $p < 0.001$), which underscored this enzyme's role in directing flux toward flavanone synthesis. By contrast, *C. kousa* 'Rosy Teacups' prioritized late-step modification, with 12_ANS (anthocyanidin synthase) expression peaking at 36,125 TPM ($p = 0.004$), a critical enzyme for generating colored anthocyanidins. A paradox emerged in white-bracted cultivars, where 12_ANS expression was 2.1-fold higher in *C. kousa* white (36,125 TPM) than in its red counterparts (17,987 TPM; $p = 0.004$). This counterintuitive pattern suggests non-canonical roles for 12_ANS in pigment stabilization or UV protection and disentangled the transcript abundance from visible pigmentation and hinted at post-transcriptional regulatory mechanisms (Ray, Mishra et al. 2023).

The statistical grouping patterns across analytical tiers provide a compelling insight into convergent evolution. Both dogwood species achieve vivid red bracts, but *C. florida* relies on upstream commitment through elevated 01_PAL and 05_CHI expression, whereas *C. kousa* employs downstream diversification via 08_F3'H and 12_ANS activation. White phenotypes, despite their visual similarity, achieve convergent downregulation through distinct pathways: *C. florida* white-bracted 'Cloud Nine' reduces flux at the pathway's entry point (01_PAL, 18,375 TPM), whereas *C. kousa* 'Greensleeves' suppresses terminal steps (11_LAR, 11,737 TPM).

Floral color evolution in *Cornus* spp. thus emerges as a model for regulatory plasticity, where species traverse unique molecular trajectories to converge on similar phenotypes. The conserved expression of 04_CHS alongside species-specific late-step regulation illustrates how metabolic pathways balance evolutionary constraint with innovation—a paradigm for probing the molecular underpinnings of biodiversity (Treder, Klamkowski et al. 2023). This duality of

497 conservation and divergence underscores the anthocyanin pathway's remarkable adaptability, to
498 offer new avenues for exploring the genetic basis of floral diversification.

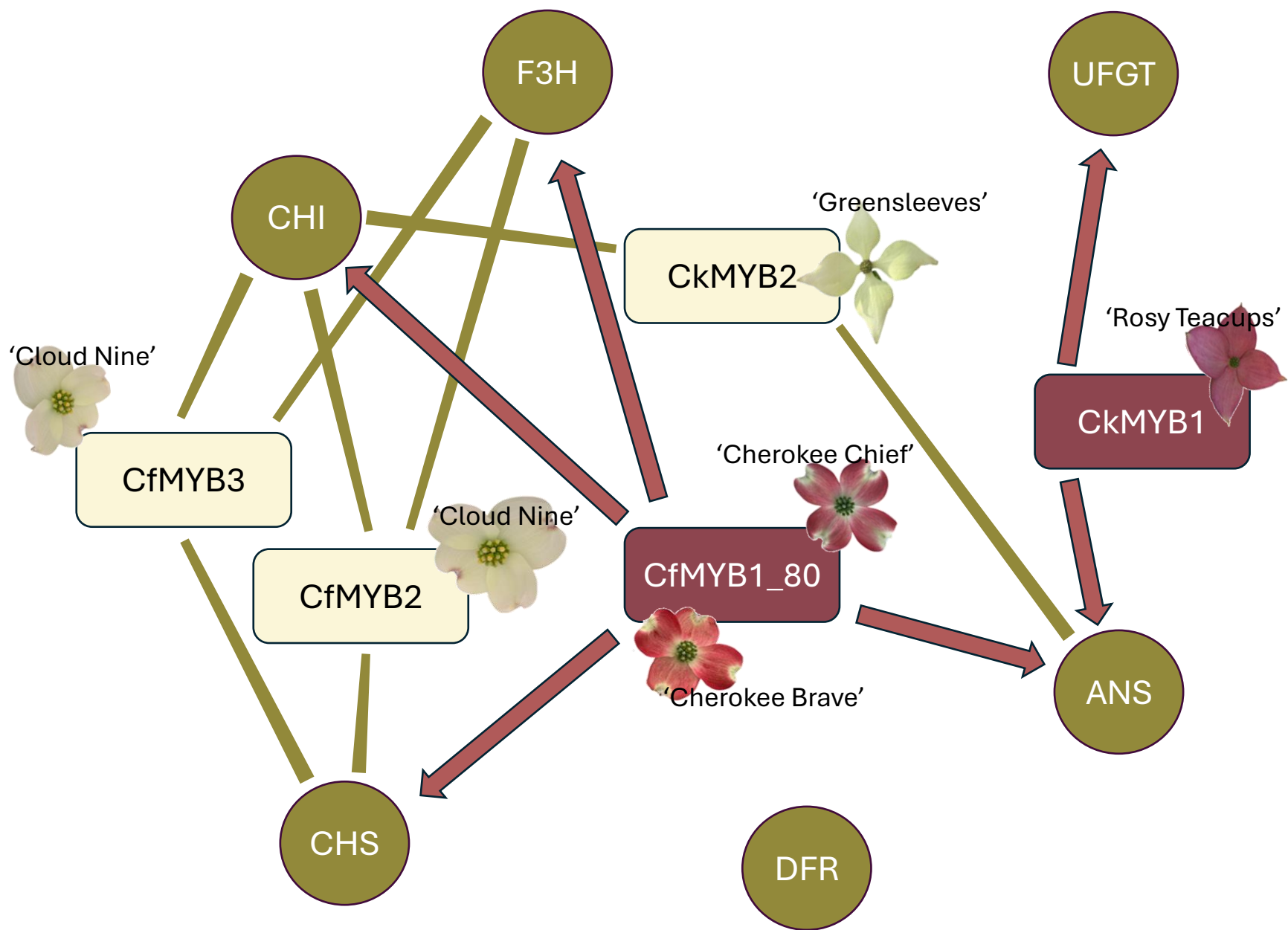
DISCUSSION

Importance of Anthocyanin Regulation in Ornamental Dogwoods

Ornamental plants constitute an economically vital component of agriculture and horticulture. Aesthetically important traits such as leaf morphology, flower color, size, and scent, bark color, and plant habitat improve the living ambiance and enhance cultivating sentiment (Linde, Yan and Debener 2007, Wadl, Saxton et al. 2011, Zheng, Li et al. 2021). The whole-genome sequences and draft genome sequences of 69 ornamental plants were published between 2012 and the end of 2020 (Zheng, Li et al. 2021). Yet, less than 20 of these are ornamental trees, and among them only a few produced red, pink, or violet blooms, such as *Prunus mume* SIEB. et ZUCC. (Zhang, Chen et al. 2012), *P. serrulate* L. (Yi, Yu et al. 2020), and *P. yedoensis* Matsumura (Baek, Choi et al. 2018), *Cercis canadensis* L. (Stai, Yadav et al. 2019), *Osmanthus fragrans* Lour. (Yang, Yue et al. 2018), *Handroanthus impetiginosus* Mart. Ex DC (Silva-Junior, Grattapaglia et al. 2018) and *Bombax ceiba* L. (Gao, Wang et al. 2018). Moreover, candidate genes controlling anthocyanin synthesis, an essential pigment for flower and leaf color, have not been identified in many ornamental woody plants. Recently, the anthocyanin profile has been determined in *C. canadensis* but not the gene machinery orchestrating its production (Veazie, Ma and Werner 2017).

To carry that momentum further, here we aimed to uncover the molecular mechanisms behind bracts color in flowering and Asian dogwoods, important woody ornamentals. Integration of the biochemical spectral analyses of bract extracts with RNAseq and its confirmation using qRT-PCR, as well as the phylogenetic analyses, identified genes involved in anthocyanin production in ornamental dogwoods. To synthesize these multilayered findings, we constructed a

521 regulatory network model (Figure 6) that illustrates the possible interactions between R2R3-
 522 MYB transcription factors and structural genes across the anthocyanin biosynthesis pathway.
 523 This schematic highlights the cultivar-specific expression patterns and regulatory divergence
 524 between *C. florida* and *C. kousa*, thereby providing a visual framework for understanding the
 525 molecular basis of bract pigmentation. Our findings generate a great springboard for future
 526 functional studies and molecular breeding efforts.



528 **Figure 6. Regulatory network of R2R3-MYB transcription factors and anthocyanin biosynthetic genes.**
529 Nodes represent MYB TFs (red = activators, green = repressors) and structural genes (green). Edges indicate
530 regulatory interactions: arrows = activation, rectangles = repression. Gene expression patterns are cultivar-specific,
531 based on RNA-seq and RT-qPCR data. Cultivars are labeled.

Challenges in Dogwood Breeding and the Role of Molecular Tools

In addition to providing nourishment for wildlife due to the high level of fat, protein, and available calcium in fruit (Thomas 1969), flowering and Asian dogwoods are important ornamental crops essential for the economy of Tennessee, Oregon, North Carolina, and Ohio, among other states, and in 2019, total dogwood sales exceeded USD31 million annually (USDA-NASS 2021). Although more than 150 cultivars are commercially available for both species, consumer demands for specific traits of interest, such as dark red bract or foliage display, resistance to pathogens, variegated foliage, and dwarf or weeping habit, have not been satisfied (Witte, Windham et al. 2000, Cappiello and Shadow 2005, Wadl, Windham et al. 2014, Nowicki, Houston et al. 2020). For instance, white bracted cultivars Kay's Appalachian Mist, Jean's Appalachian Snow, and Karen's Appalachian Blush are resistant to dogwood powdery mildew pathogen (*Erysiphe pulchra* [Cooke & Peck]; (Windham, Witte and Trigiano 2003)). But they lack desirable dark red or pink bracts of cultivars belonging to the Cherokee series, such as 'Cherokee Brave', 'Cherokee Chief', 'Cherokee Sunset', 'Cherokee Daybreak', and 'Appalachian Sunrise' (personal comm. R. N. Trigiano) which are generally considered either moderately or susceptible to *E. pulchra* (Thurn, Lamb and Eshenaur 2019).

In contrast, Asian dogwoods typically lack variation in bracts colors and do not display a range of bract colors from white to dark red as flowering dogwoods do (Cappiello and Shadow 2005, Molnar, Muehlbauer et al. 2017). 'Rosy Teacups', 'Miss Satomi', and 'Rutpink' are among the few cultivars exhibiting dark to bright red or pink bracts (Trigiano, Ament et al. 2004, Molnar, Muehlbauer et al. 2017). Moreover, a hybrid breeding program between *C. florida* and *C. kousa* was initiated almost a half-century ago, aiming to enhance ornamental traits and develop attractive landscape trees that do not require extensive maintenance (Molnar,

Muehlbauer et al. 2017). Notably, time-demanding development of dogwood cultivars typically depends on repeated selection for desirable traits. To achieve development of new cultivars with desirable traits, several challenges need to be overcome, such as a long juvenile period (3 to 5 years), self-incompatibility, inbreeding depression, and high susceptibility of flowering dogwood to two fungal foliar pathogens causing dogwood anthracnose (*Discula destructiva*) or powdery mildew (*E. pulchra*) (Gunatilleke and Gunatilleke 1984, Ament, Windham and Trigiano 2000, Reed 2004, Wang, Wadl et al. 2009, Hadziabdic, Fitzpatrick et al. 2010, Hagan, Akridge et al. 2011, Wadl, Saxton et al. 2011, Mantooth, Hadziabdic et al. 2017, Nowicki, Redington et al. 2025). These challenges highlight the need for molecular approaches to accelerate breeding programs and develop cultivars with desired traits. Red and pink bracted blossoms with their variations foster the attractive ornamental appeal, and in flowering and Asian dogwoods, anthocyanin pigments provide the basis for bract and foliage coloration (Vareed, Reddy et al. 2006, Wadl, Wang et al. 2010, Wadl, Saxton et al. 2011). However, to our knowledge, structural and regulatory genes to control the biosynthesis of anthocyanins and other phenylpropanoid-derived compounds in flowering and Asian dogwoods have not been reported yet. Moreover, genetic resources, quality reference genome, and annotation for *Cornus* sp. are still under active development, though certain genomic information is available (Bewick and Leebens-Mack 2020).

R2R3-MYB Transcription Factors as Key Regulators of Anthocyanin Biosynthesis

Among the genes controlling anthocyanin production, R2R3-MYB TFs fine-tune flavonoid production and their biological functions, such as involvement in developmental and cell differentiation processes, response to environmental stress, and metabolite biosynthesis, and they have been functionally characterized in cereals, vegetables, fruit, and ornamental crops (Du,

Zhang et al. 2009, Dubos, Stracke et al. 2010, Liu, Osbourn and Ma 2015, Wang, Ma et al. 2019, Zhang, Wang et al. 2019, Ding, Patterson et al. 2020, Gong, Li et al. 2020, Yan, Chen et al. 2020, Yan, Li et al. 2020). Concomitantly, to date, a whooping 61 R2R3-MYB TFs have been identified in herbaceous ornamental plants such as *Petunia* sp. (Quattrocchio, Wing et al. 1999, Albert, Lewis et al. 2009, Albert, Lewis et al. 2011), *Rosa* sp. (Lin-Wang, Bolitho et al. 2010), *Lilium* sp. (Nakatsuka, Haruta et al. 2008, Yamagishi, Shimoyamada et al. 2010, Yamagishi 2011, Yamagishi, Yoshida and Nakayama 2012, Yamagishi 2016), *Antirrhinum* sp. (Martin, Prescott et al. 1991, Moyano, Martínez-Garcia and Martin 1996, Schwinn, Venail et al. 2006, Shang, Venail et al. 2011), *Gerbera* sp. (Elomaa, Uimari et al. 2003) but only one in a woody plant, *P. meme* (Zhang, Hao et al. 2017).

The MYB TF family is one of the largest in plants and regulates a broad range of metabolic pathways, including responses to abiotic stimuli, regulation of benzenoid, glucosinolate, phenylpropanoid, and terpenoid biosynthesis, and control of developmental and cell differentiation process, e.g., organ formation, cuticle development, and trichome initiation and branching (Shin, Choi et al. 2002, Liu, Osbourn and Ma 2015, Zhao, Cheng et al. 2018, Tan, Man et al. 2019, Fichman, Zandalinas et al. 2020, Gong, Li et al. 2020). MYB TFs are characterized by a highly conserved N-terminal DNA-binding domain repeat (R) and a variable C-terminal regulatory region (C). Each MYB repeat contains approximately 50 amino acids, including unique DNA motifs and MYB binding sites. Based on the sequence similarities, MYB domain repeats are named R1, R2, and R3 depending on the number of repeats, ranging from 1 to 4 repeats. Accordingly, the MYB gene superfamily is divided into the following four families: 1R-MYB, 2R-MYB (R2R3), 3R-MYB, and 4R-MYB. (Lipsick 1996, Rosinski and Atchley 1998, Kranz, Scholz and Weisshaar 2000, Dubos, Stracke et al. 2010, Jiang and Rao 2020).

Comparative Expression and Phylogenetic Insights into MYB Regulators

The first plant R2R3-MYB gene, COLOREDI, was identified in *Zea mays* and is crucial for enhancing anthocyanin biosynthesis in the aleurone tissue (Klempnauer, Gonda and Bishop 1982). Since the identification of COLOREDI, the scientific interest in R2R3-MYB family has yielded insights and breeding progress in many economically important crops. The constant development of fast and cost-effective next-generation sequencing technologies has enabled the identification of more than 600 R2R3-MYB genes across 130 plant species (Morozova and Marra 2008, Wu, Wen et al. 2022, Yin, Guo et al. 2022). Although the consensus regarding the classification schemes and nomenclature uniformity of R2R3-MYB TFs is still lacking, mainly because of lineage-specific gene loss or expansion, differences in sample coverage, and the type of phylogenetic analysis applied, R2R3-MYB TFs have been classified into 23 to 90 subgroups (Du, Liang et al. 2015, Jiang and Rao 2020, Li, Wen et al. 2020). Accordingly, each R2R3-MYB subgroup regulates a specific metabolic pathway (Wu, Wen et al. 2022).

Anthocyanin and proanthocyanidins activators of subgroup 5 required specific bHLH TFs to encode transcription of structural genes (Chen, Hu et al. 2019, Ma and Constabel 2019, Wu, Wen et al. 2022). In contrast, MYB repressors, which act to reduce anthocyanin biosynthesis, belong exclusively to subgroup 4 and contain the N-terminal regions with a DNA-binding domain as well. The N-terminal region of MYBs is highly conserved, and its function usually depends on the C-terminal region's distinct motifs. The C1 LlsrGIDPxT/SHRxI/L region and C2 region pdLNLD/ELxiG/S are referred to as GIDP and EAR motif (Ethylene-responsive element-binding factor associated Amphiphilic Repression motif), respectively. EAR is the most common transcriptional repression motif found in plants. The C3 and C4 motifs are also present in a small segment of the R2R3-MYB structural domain (Ohta, Matsui et al. 2001, Kagale and

Rozwadowski 2011, Chen, Hu et al. 2019, Ma and Constabel 2019). Majority of the identified and functionally characterized MYBs involved in anthocyanin biosynthesis, such as MdMYB1, MdMYBA, and MdMYB3 in apples, ROSEA1 and ROSEA2 in snapdragon, AN2, DPL, and PHZ in petunia positively regulate the transcriptional expression of structural genes involved in this pathway (Moyano, Martínez-Garcia and Martin 1996, Schwinn, Venail et al. 2006, Albert, Lewis et al. 2011, Albert, Davies et al. 2014). Upstream genes (early biosynthetic genes) such as CHI (chalcone isomerase), CHS (chalcone synthase), and F3H (flavanone 3-hydroxylase), are the key enzymes to mediate and regulate anthocyanin biosynthesis, which is branched from the phenylpropanoid pathway. In comparison, DFR (dihydroflavonol 4-reductase), ANS (anthocyanidin synthase), and UFGT (flavonoid 3-O-glucosyltransferase) are downstream genes (late biosynthetic genes) (Pelletier, Burbulis and Winkel-Shirley 1999, Takos, Jaffé et al. 2006, Cominelli, Gusmaroli et al. 2008, Vimolmangkang, Han et al. 2013).

Structural Gene Expression and Developmental Timing

Our transcriptome study aimed to identify important genes involved in phenylpropanoid metabolite biosynthesis, particularly anthocyanin and proanthocyanidins production, using RNAseq and RT-qPCR for validation. Five R2R3-MYB TFs were detected as downregulated in *C. florida* and only two in *C. kousa*, which are lower numbers compared to other plant species such as 126 genes in *A. thaliana* (Stracke, Werber and Weisshaar 2001), 192 in *Populus* (Wilkins, Nahal et al. 2009), 244 in soybean (Du, Yang et al. 2012), or 406 in *Gossypium hirsutum* L. (Wang, Ma et al. 2019). Genome unavailability and mapping of the RNAseq reads to *C. florida* and *C. kousa* leaf transcriptomes likely affected our ability to mine more R2R3-MYB TFs. In contrast, downregulation of the R2R3-MYB TFs and of the upstream structural genes *CHS*, *CHI*, and *F3H* might result from RNAseq of physiologically fully developed bracts at four

weeks after emergence – a possible artifact of sampling at the stage where the transcripts are past their peak levels. Moreover, expression levels of *CHS* and *F3H*, key enzymes involved in flavonoid and anthocyanin synthesis, were increased in emerging two weeks old bracts of 'Cloud Nine', 'Cherokee Chief', and 'Rosy Teacups'. As we focused on detailed analyses of DEGs, late biosynthetic genes were not detected as significantly up- or downregulated, which could possibly limit our detection of other MYB TFs or upstream structural genes in dogwoods. In apples, MdMYB10 orchestrates the synthesis of anthocyanins in the peel, flesh, and color of foliage at the early stage (Espley, Hellens et al. 2007); whereas MdMYB10b regulates the color of the fruit cortex at the later phases (Chagné, Lin-Wang et al. 2013). Collectively, this confirms previous findings that the anthocyanins content varies greatly depending on the species' genetic background, environmental conditions, and stage of plant development (Wadl, Saxton et al. 2011, Jaakola 2013, Mattioli, Francioso et al. 2020). Contrastingly, others (Salvatierra, Pimentel et al. 2013) showed that expression levels of early biosynthetic genes are not crucial in the flavonoid pathway for pigment manifestation. Finally, phenylpropanoid biosynthesis is a complex metabolic grid with many branches and alternative metabolic routes (Yan, Chen et al. 2020, Yan, Li et al. 2020, Chen, Nowicki et al. 2023).

Functions and characteristics of R2R3-MYB proteins have been studied extensively, and their comparative phylogenetic analysis brought to light both the diversity and the conservation in this gene family (Stracke, Werber and Weisshaar 2001, Wilkins, Nahal et al. 2009, Du, Yang et al. 2012, Wang, Tang et al. 2019, Wang, Ma et al. 2019). Also, studies in soybean and petunia indicated that anthocyanin activators and repressors could be identified by phylogenetic analysis (Elomaa, Uimari et al. 2003, Albert, Lewis et al. 2011). Accordingly, phylogenetic analysis grouped the candidate R2R3-MYB proteins identified in this study in two major subgroups, 4

and 5. R2R3-MYB TFs CfMYB2, CfMYB3, and CkMYB2 clustered in subgroup 4, which genes negatively regulate phenylpropanoid metabolism. Consistently, repressors of this group were identified in various plant species, including strawberry FaMYB1 (*Fragaria x ananassa* Duchesne) (Aharoni, De Vos et al. 2001) and FcMYB1 (*Fragaria chiloensis*) (Salvatierra, Pimentel et al. 2013), petunia PhMYB27 (Albert, Davies et al. 2014), grapevine VvMYBC2-L1/ and VvMYB4-like (Cavallini, Matus et al. 2015, Pérez-Díaz, Pérez-Díaz et al. 2016), poplar PtrMYB182 and PtrMYB57 (Yoshida, Ma and Constabel 2015, Wan, Li et al. 2017), crabapple MdMYB3 (Tian, Zhang et al. 2017), peach PpMYB17-20 (Zhou, Peng et al. 2016), and Chinese narcissus NtMYB2 (Anwar, Wang et al. 2018).

PhMYB27 is part of the R2R3-MYB, bHLH, and WDR complex and functions as an anthocyanin repressor in petunia petals (Albert, Davies et al. 2014). *NtMYB2* suppresses red pigmentation in the petals and corona of Chinese narcissus by repressing the transcript levels of structural genes involved in the anthocyanin biosynthetic pathway (Anwar, Wang et al. 2018). Likewise, expression levels of *CfMYB2* significantly increased in 'Cloud Nine' white bracts at two weeks after emergence, whereas *CfMYB3* levels slightly increased in the same cultivar when four weeks old. CfMYB2 showed protein sequence similarity with AtMYB4. *AtMYB4* is known to negatively regulate the sinapate ester biosynthesis induced by UV-B in *Arabidopsis*; therefore, it is a regulator of the phenylpropanoid pathway through the expression of the cinnamate-4-hydroxylase (*C4H*) gene (Jin, Cominelli et al. 2000). Moreover, phylogenetic analysis indicated strong sequence similarity of CfMYB2 with FaMYB1 from strawberry and PhMYB27 from petunia (Aharoni, De Vos et al. 2001, Albert, Lewis et al. 2011), which appear to be R2R3-MYB suppressors of structural genes involved in the anthocyanin pathway. CfMYB3 and CkMYB2 protein sequences were most similar to AtMYB3, which affects sinapoyl malate and negatively

regulates anthocyanin biosynthesis in *Arabidopsis*. Its activity is regulated by corepressors NIGHT LIGHT-INDUCIBLE (LNK1) and CLOCK-REGULATED (LNK2), which mediate the binding of AtMYB3 to the *C4H* (Zhou, Zhang et al. 2017). Phylogenetic analyses of CfMYB3 and CkMYB2 placed them closest to grapes repressors VVMYBC2-L1 and VVC2rm, which are involved in suppressing anthocyanin and proanthocyanidins production (Cavallini, Matus et al. 2015). Surprisingly, *CkMYB2* transcript levels increased in both *C. kousa* cultivars used in this study, which may explain the color variation pink intensity of 'Rosy Teacup' bracts. Finally, in grapes and petunia, R2R3-MYB repressors affect both anthocyanins and proanthocyanidins, thereby suggesting that their role is less specific compared to R2R3-MYB activators (Cavallini, Matus et al. 2015, Ma and Constabel 2019). CfMYB1 80 and CkMYB1 were clustered to subgroup 5 with other anthocyanin and proanthocyanidin R2R3-MYB activators. In 'Cherokee Chief', which bracts displayed the darkest shade of red, expression levels of *CfMYB1 80* were significantly increased when bracts were two and four weeks old. Also, the expression levels of *CkMYB1* were comparably greater in the pink bracted cultivar 'Rosy Teacup' over 'Greensleeves'. Anthocyanin-encoding genes belonging to subgroup 5 were reported in maize *aleurone 1* (C1) (Carey, Strahle et al. 2004) and *purple leaf* (PL) (Cone, Cocciolone et al. 1993) and in orchid *OgMYB1* (Chiou and Yeh 2008). *OgMYB1* undergoes active expression during floral development in red sepal and petal tissues, to regulate the color patterns in *Oncidium* spp. Gower Ramsey (Chiou and Yeh 2008).

Another R2R3 MYB TFs of subgroup 5 encompass the proanthocyanidins or condensed tannins activators. They are colorless flavonoid polymers in many plants' leaves and seeds. They confer defense against pathogens and herbivore feeding (Dixon, Xie and Sharma 2005). Proanthocyanidins have not been reported in *C. florida* and *C. kousa*. In this study, CfMYB1 80

716 and CkMYB1 showed the highest sequence similarity with AtMYB123 protein. *AtMYB123*
717 regulates the production of proanthocyanidins in Arabidopsis, regulating
718 *DIHYDROFLAVONOL-4-REDUCTASE (DFR)* gene synthesis (Nesi, Jond et al. 2001). R2R3-
719 MYB TFs regulating proanthocyanidins activation were identified in strawberry FaMYB11
720 (Schaart, Dubos et al. 2013), lotus LjTT2a, LjTT2b, and LjTT2c (Yoshida, Iwasaka et al. 2008),
721 kiwi fruit DkMYB2 and DkMYB4 (Akagi, Ikegami et al. 2009) among other plant species.

CONCLUSIONS

Our results provided an essential foundation for further analysis of R2R3-MYB TFs that may be responsible for anthocyanin and proanthocyanidins regulation in bracts of *C. florida* and *C. kousa*. Based on our data, future efforts could be directed toward elucidating how these and other candidate genes regulate complex phenylpropanoid metabolism in these species. Moreover, functional characterization of these genes through CRISPR-Cas9, ectopic plant leaf expressions, or genetic engineering will enable heterologous production of anthocyanins. The envisioned development of functional markers or the application of marker-assisted selection in complicated dogwood breeding will allow early selection of red-bracted dogwood cultivars for gainful commercial release.

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Ethics and Data Availability Statement

No protected species were used in this study.

All relevant data are within the paper and its Supporting Information files. Raw RNAseq data are available at NCBI under the short reads accession numbers SRR21411460 through SRR21411472. Sequences of MYBs identified in this research are available in GenBank: OP382880 through OP382884.

Competing interests

The authors have declared that no competing interests exist.

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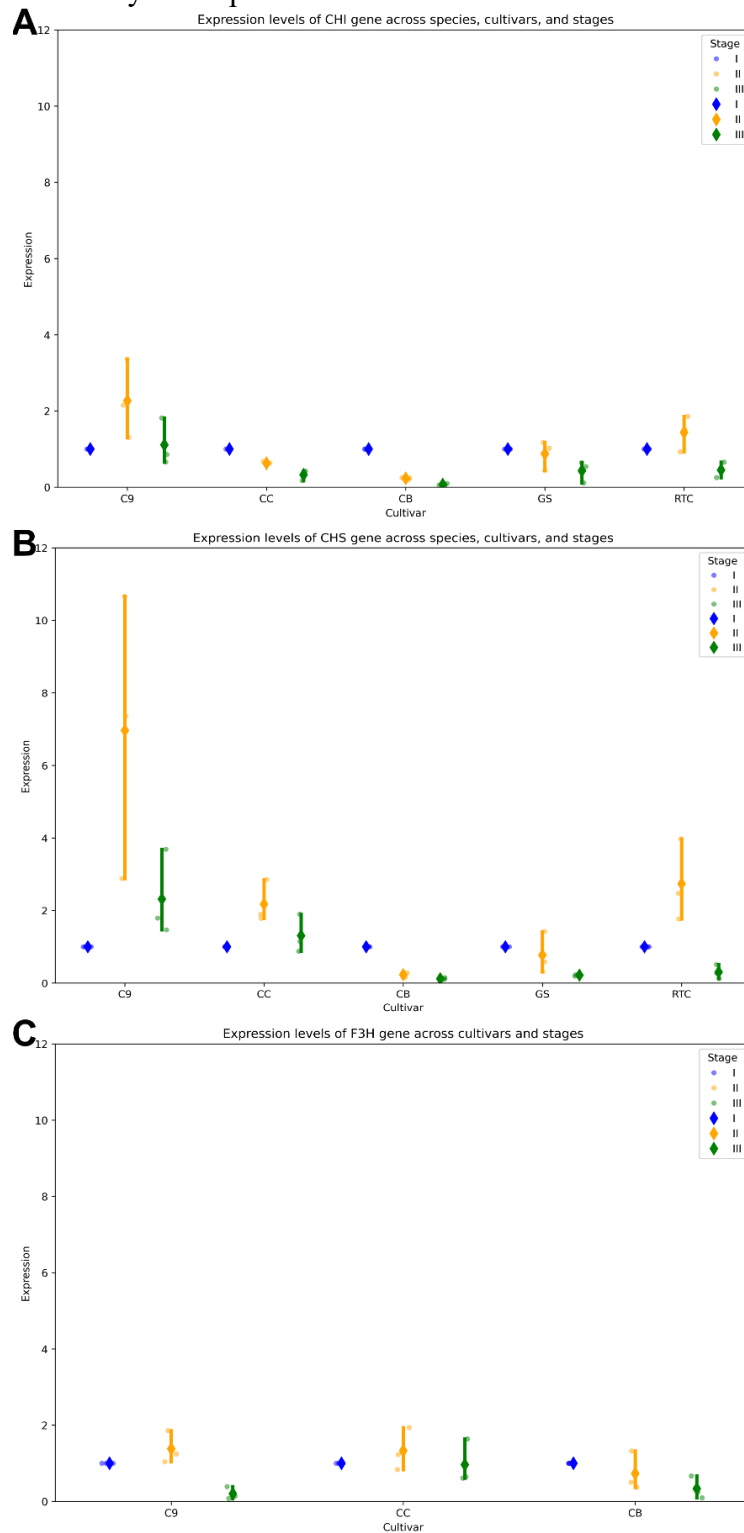
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7 **Supplementary Figure 3. RT-qPCR validation of structural gene expression.** Expression of
8 (A) CHI, (B) CHS, and (C) F3H in five cultivars across three developmental stages. Cultivars
9 abbreviated: C9 = 'Cloud Nine', CB = 'Cherokee Brave', CC = 'Cherokee Chief', GS =
10 'Greensleeves', RTC = 'Rosy Teacups'.



Supplementary Tables

Supplementary Table T1. Metadata for RNA-seq samples used in this study, including species, phenotype, cultivar, SRA accession numbers, total reads, and mapping statistics to *C. florida* and *C. kousa* transcriptomes.

Sample name	Organism	Phenotype	Genotype	SRA accession	Numbers of reads	Numbers of uniquely mapped to <i>Cornus florida</i> transcriptome (CFT)	Percentage of uniquely mapped reads to CFT	Numbers of uniquely mapped to <i>Cornus kousa</i> transcriptome (CKT)	Percentage of uniquely mapped reads to CKT
1*1	<i>Cornus florida</i>	red	Cherokee Brave	SRR21411472	34140879	24818316.5	72.69%	27686788.5	81.10%
1*2	<i>Cornus florida</i>	red	Cherokee Brave	SRR21411471	35366608	20950536	59.24%	24000797.5	67.86%
1*3	<i>Cornus florida</i>	red	Cherokee Chief	SRR21411467	31649684	23509163	74.28%	24587183.5	77.69%
1*6	<i>Cornus florida</i>	white	Cloud Nine	SRR21411466	28399202	21460142.5	75.57%	21425521	75.44%
1*10	<i>Cornus kousa</i>	light pink	Rosy Teacups	SRR21411465	29668132	22965778.5	77.41%	23004720.5	77.54%
1*13	<i>Cornus kousa</i>	light green	Greensleeves	SRR21411464	33082227	26184769	79.15%	25745124.5	77.82%
2*1	<i>Cornus florida</i>	red	Cherokee Chief	SRR21411463	35782681	24181390	67.58%	24398398.5	68.18%
2*2	<i>Cornus florida</i>	red	Cherokee Chief	SRR21411462	34453910	26047989.5	75.60%	25499764.5	74.01%
2*3	<i>Cornus florida</i>	white	Cloud Nine	SRR21411461	28919895	23053520.5	79.72%	22646851.5	78.31%

2*4	<i>Cornus florida</i>	white	Cloud Nine	SRR21411460	37510289	26976299	71.92%	26287991	70.08%
2*5	<i>Cornus kousa</i>	light pink	Rosy Teacups	SRR21411470	38487414	25455388.5	66.14%	28869402.5	75.01%
2*5	<i>Cornus kousa</i>	light pink	Rosy Teacups	SRR21411469	39321965	23799064.5	60.52%	27216224.5	69.21%
2*8	<i>Cornus kousa</i>	light green	Greensleeves	SRR21411468	30532090	18797761	61.57%	21492150.5	70.39%

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18 **Supplementary Table T2.** Species names and GenBank accession numbers of MYB transcription factors used for phylogenetic
 19 analysis of R2R3-MYB proteins.

Species	Labeled MYB
Apple (<i>Malus domestica</i> Borkh.)	MdMYB1 (ADQ27443), MdMYB3 (AEX08668), MdMYB6 (AAZ20429), MdMYB10, MdMYB10, (ACQ45201), MdMYB110a (AFC88038), MdMYBA (BAF80582) AtMYB4 (NP_195574), AtMYB11 (NP_191820), AtMYB12 (NP_182268), AtMYB14 (NP_180676), AtMYB15 (NP_188966), AtMYB46 (NP_196791), AtMYB58 (NP_173098), AtMYB60 (NP_172358), AtMYB61 (NP_172425), AtMYB63 (NP_178039), AtMYB75 (NP_176057), AtMYB83 (NP_187463), AtMYB85 (NP_567664), AtMYB90 (NP_176813), AtMYB111 (NP_199744), AtMYB113 (NP_176811), AtMYB114
Arabidopsis thaliana L.	(NP_176812), AtMYB123 (NP_198405)
Asian dogwood (<i>Cornus kousa</i> F. Buerger ex Hance)	CkMYB1 (OP382883), CkMYB2 (OP382884)
Cauliflower (<i>Brassica oleracea</i> L.)	PR (ADP76651)
Chinese bayberry (<i>Myrica rubra</i> Sieb. et Zucc.)	MrMYB1 (ADG21957)
Cider gum (<i>Eucalyptus gunnii</i> Hook)	EgMYB1 (CAE09058), EgMYB2 (CAE09057)
Flowering dogwood (<i>C. florida</i> L.)	CfMYB1 (OP382880), CfMYB2 (OP382881), CfMYB3 (OP382882)
Garden chrysanthemum (<i>Chrysanthemum morifolium</i> (Ramat.) Hemst.)	CmMYB1 (AEO27497)
Gerbera (<i>Gerbera hybrida</i> L.)	GMYB10 (CAD87010) VIMYBA1-1 (BAC07537), VIMYBA1-2 (BAC07539), VIMYBA1-3 (BAG55463), VIMYBA2 (BAC07540), VvMYBC2-L1 (AFX64995), VvMYBPA1 (CAJ90831), VvMYBPA2 (ACK56131), VvMYBA2 (BAD18978), VvMYBF1 (ACV81697), VvMYB5a (AAS68190), VvMYB5b (AAX51291), VvC2rm (NP_001268133)
Grapevine (<i>Vitis</i> spp.)	
Herba epimedii (<i>Epimedium sagittatum</i> Sieb. Et Zucc.)	EsMYBA1 (AGT39059)

Japanese gentian (<i>Gentiana triflora</i> Pall.)	GtMYBP3 (BAM71801)
Japanese morning glory (<i>Ipomoea nil</i> Roth)	InMYB1 (BAE94388)
Kale (<i>Brassica oleracea</i> L.)	BoPAP1 (ADP76649)
Kiwifruit (<i>Actinidia</i> spp.)	DkMYB2 (BAI49719), DkMYB4 (BAI49721)
Kousa dogwood (<i>C. kousa</i> F. Buerger ex Hance F)	CkMYB1 (OP382883), CkMYB2 (OP382884)
Legume (<i>Medicago truncatula</i> Gaertn.)	LAP1 (ACN79541)
Leucaena (<i>Leucaena leucocephala</i> (Lam.) de Wit)	LIMYB1 (ADY38393)
Lily (<i>Lilium</i> spp.)	LhMYB6 (BAJ05399), LhMYB12 (BAJ05398), LhMYB12-Lat (BAO04194)
Lotus (<i>Lotus japonicus</i> L.)	LjTT2a (BAG12893), LjTT2b (BAG12894), LjTT2c (BAG12895)
Maize (<i>Zea mays</i> L.)	PL (AAA19820), PL-BH (AAA33492), P1 (ABM21535), ZmMYB31, (NP_001105949), ZmMYB42 (ADX60106), ZmMYB-IF35 (AAO48737)
Mangosteen (<i>Garcinia mangostana</i> L.)	GmMYB10 (ACM62751)
Nectarine (<i>Prunus persica</i> (L.) Batsch)	PpMYB10 (ABX79945)
Orange (<i>Citrus sinensis</i> L.)	CsRUBY (AFB73913)
Orchid (<i>Oncidium</i> spp.)	OgMYB1 (ABS58501)
Pear (<i>Pyrus</i> spp.)	PcMYB10 (ABX71487)
Petunia (<i>Petunia hybrida</i> D. Don ex W. H. Baxter)	AN2 (AAF66727), DPL (ADW94950), PHZ (ADW94951), PhMYB27 (AHX24372)
Pine (<i>Pinus taeda</i> L.)	PtMYB1 (AAQ62541), PtMYB4 (AAQ62540),)
Poplar (<i>Populus tremula</i> L.)	PtMYB3 (AGT02395), PttMYB21a (CAD98761), PtMYB134
Potato (<i>Solanum tuberosum</i> L.)	StAN1 (AGC31676), StAN2 (AAX53089),
Rabbit-foot clover (<i>Trifolium arvense</i> L.)	TaMYB14 (AEG64799)

Red sage (<i>Salvia miltiorrhiza</i> Bunge)	SmMYB39 (AGS55356)
Snapdragon (<i>Antirrhinum majus</i> L.)	AmMYB308 (P81393), AmMYB330 (P81395), ROSEA1 (ABB83826), ROSEA2, (ABB83827), VENOSA (ABB83828)
Sorghum (<i>Sorghum bicolor</i> Moench)	Y1 (AAX44239)
Soybean (<i>Glycine max</i> Merr.)	GmMYB12B2 (AEC13303), GmMYB-G20-1 (BAK24100)
Strawberry (<i>Fragaria x ananassa</i> Duchesne)	FaMYB1 (AAK84064), FaMYB9 (AFL02460), FaMYB10 (ABX79947), FaMYB11
Switchgrass (<i>Panicum virgatum</i> L.)	PvMYB4a (AEM17348)
Tobacco (<i>Nicotiana tabacum</i> L.)	NtAN2 (ACO52470)
Tomato (<i>Lycopersicum</i> <i>esculentum</i> L.)	LeANT1 (AAQ55181)

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22 **Supplementary Table T3.** R2R3-MYB repressor proteins used for EAR motif analysis, including species, gene function, accession
23 numbers, and references.

Name	Species	Function	Accessions	References
AmMYB308	<i>Antirrhinum majus</i> L.	monolignol	P81393	Tamagnane et al. 1998
AmMYB330	<i>A. majus</i>	monolignol	P81395	
AtMYB4	<i>Arabidopsis thaliana</i> L.	phenylpropanoid	AT4G38620	Jin et al. 2000
AtMYB7	<i>A. thaliana</i>	flavanol	AT2G16720	Fornale et al. 2014
AtMYB60	<i>A. thaliana</i>	anthocyanin	AT1G08810	Park et al. 2008
CmMYB1	<i>Chrysanthemum x morifolium</i> (Ramat.) Hemst.	monolignol	AEO27497	Zhu et. Al. 2013
CfMYB2	<i>Cornus florida</i> L.	proanthocyanidin	OP382881	Pavlovic et al. (under preparation)
CfMYB3	<i>C. florida</i>	proanthocyanidin	OP382882	Pavlovic et al. (under preparation)
CkMYB2	<i>C. kousa</i> F. Buerger ex Hance F	anthocyanin, proanthocyanidin	OP382884	Pavlovic et al. (under preparation)
EgMYB1	<i>Eucalyptus gunni</i> Hook	monolignol	CAE09058	Paux et al. 2004
FaMYB1	<i>Fragaria x ananassa</i> Duchesne	anthocyanin, flavonol	AF401220	Aharoni et al. 2001
FcMYB1	<i>F. chiloensis</i> Mill.	anthocyanin	ADK56163.1	Salvatierra et al. 2013
GmMYB100	<i>Glycine max</i> Merr.	isoflavanol, flavanol	ABH02893.1	Yan et al. 2015
LlMYB1	<i>Leucaena leucocephala</i> (Lam.) de Wit	moloignol	ADY3839	Omer et al. 2013
MdMYB3	<i>Malus domestica</i> Borkh.	anthocyanin, flavanol	AEX08668	Tian et al. 2017
MtMYB2	<i>Medicago truncatula</i> Gaertn.	anthocyanin	XM_003616340	Jun et al. 2015
PhMYB27	<i>Petunia hybrida</i>	anthocyanin	KF985023	Albert et al. 2014
PhMYBx	D. Don ex W. H. Baxter	anthocyanin	AHX24371.1	
PpMYB18	<i>P. hybrida</i>	anthocyanin	ALO81021.1	Zhou and Han 2017

PvMYB4a	<i>Prunus persica</i> (L.) Batsch	monolignol	AEM17348	Shen et al. 2012
SmMYB39	<i>Panicum vulgare</i> L.	phenolic acid	AGS55356	Wang et al. 2013
TaMYB14	<i>Salvia miltiorrhiza</i> Bunge	proanthocyanidin	AEG64799	Ma et al. 2011
VvMYBC2-L1	<i>Triticum aestivum</i> L.	proanthocyanidin	AFX64995	Huang et al. 2014
VvC2rm	<i>Vitis vinifera</i> L.	proanthocyanidin	NP_001268133	Da Silva et al. 2013
ZmMYB31	<i>V. vinifera</i>	monolignol	NP_001105949	Carey et al. 2004
ZmMYB42	<i>Zea mays</i> L.	monolignol	ADX60106	

25 **Supplementary Table T4.** Primer sequences used for RT-qPCR validation of candidate MYB and structural genes. Includes target
 26 gene, forward and reverse primer sequences, expected amplicon size, and transcriptome contig IDs.

Target transcript	Forward Primer sequence (5' to 3')	Reverse Primer sequence (5' to 3')
CfCHI	CGGAAGCATTGTTGGAGTCG	CCGACCACCTGATCATCACA
CfCHS	AGCATCCAATGAGCGTTCCA	TTGATCAGAGCACGTACCCG
CfF3H	GGGAGGTTCAAGAATGCCGA	GACCTTCAGTGGGTACACCG
CfMYB1 80	GTGGGAAGAGTTGTCGCCTT	TCCCAAGAGGTTGTGAAGCC
CfMYB2	CGAACCGACAACGAGGTGAA	CGCGGTTGCACATGATTTGT
CfMYB3	TGGCAATCGGTGGTCACTTA	TTTTGAGGCCGAGGACGATT
CkCHI	AAAGGGGTGCCCACCTAAAC	CCACTGGCCGAGGATTTGTA
CkCHS	CGTCTTGAGCGAGTATGGCA	TGGTCTTGAGCCCTTCCTCT
CkMYB1	GAGTCCGGAGAAGTCCGAAT	ATCGAATTCGTGTGTGGGGG
CkMYB2	GCAAGCCGTTAGGGTTTTCC	CCATGCATGTCAACCCGAGA
GAPDH	GACCACTGTTCACTCCAT	CAGCCTTGGCAGCTCCAG

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28 **Supplementary Table T5.** Differentially expressed genes (DEGs) identified between white- and red-bracted cultivars of *C. florida*.

29 Includes transcript ID, log2 fold change, adjusted p-value, KEGG ortholog, and functional annotation.

Transcript name	log2FC	adjusted p-value	Kegg Ortholog	KO description
C381440	-6.718	1.96E-21		
scaffold11743	-6.100	1.76E-10		
C327051	-5.781	3.21E-19		
C290075	-5.338	3.33E-07	K03065	PSMC3, RPT5; 26S proteasome regulatory subunit T5
C321950	-5.164	2.71E-03		
C139755	-4.893	3.73E-02		
C360216	-4.842	6.46E-03	K00799	GST, gst; glutathione S-transferase [EC:2.5.1.18]
C206860	-4.837	8.29E-04		
scaffold12114	-4.834	3.74E-04		
C65252	-4.797	2.94E-06		
C192483	-4.665	2.87E-02		
C82020	-4.631	7.12E-06		
C306236	-4.612	2.57E-04		
scaffold18000	-4.611	4.97E-03	K09264	K09264; MADS-box transcription factor, plant
C328059	-4.478	4.59E-02		
C79282	-4.447	4.29E-02		
C60364	-4.340	1.26E-02		
C87204	-4.285	1.10E-02		
C106614	-4.234	2.12E-02		
C328147	-4.189	2.51E-03		
C259063	-4.172	1.90E-02	K09422	mybP; transcription factor myb, plant
C292929	-4.113	2.18E-05		
C121914	-4.109	1.20E-03		
C254457	-4.103	1.56E-02		

C370256	-4.052	4.27E-03	K06185	ABCF2; ATP-binding cassette, subfamily F, member 2
C331323	-4.052	1.96E-02		
scaffold12115	-4.020	1.95E-02		
C50380	-4.008	1.42E-03		
C85302	-4.005	2.20E-02		
scaffold10878	-3.996	4.78E-02		
C313225	-3.981	2.32E-03		
C284179	-3.952	2.84E-02		
C44938	-3.924	4.40E-02		
C229862	-3.900	1.72E-03		
C270493	-3.876	2.85E-03		
C75844	-3.853	6.34E-03		
C41121	-3.771	1.09E-02		
scaffold6526	-3.731	1.61E-03		
C302024	-3.721	5.08E-05		
C353651	-3.715	9.23E-05		
C259863	-3.679	2.15E-02		
C259861	-3.671	8.13E-03		
C381804	-3.633	4.74E-02		
C342993	-3.622	1.54E-02		
C361090	-3.583	4.38E-02	K02736	PSMB4; 20S proteasome subunit beta 7 [EC:3.4.25.1]
C117980	-3.522	7.29E-03		
C320744	-3.494	9.78E-03		
C292829	-3.454	1.49E-04		
C256451	-3.416	2.84E-02		
C283001	-3.415	3.61E-03		
C292273	-3.390	3.18E-02		
C330505	-3.355	1.78E-02		
C98604	-3.333	1.26E-02		

C394096	-3.262	4.62E-04		
C314199	-3.262	9.78E-03		
C280949	-3.249	4.94E-02		
C74822	-3.235	7.74E-03		
C142717	-3.194	4.62E-02	K08360	CYB561; cytochrome b-561 [EC:1.16.5.1]
C375580	-3.191	7.40E-04	K09422	mybP; transcription factor myb, plant
C98220	-3.179	2.85E-02	K15103	UCP2_3, SLC25A8_9; solute carrier family 25 (mitochondrial uncoupling protein), member 8/9
C200556	-3.170	3.82E-02	K14709	SLC39A1_2_3, ZIP1_2_3; solute carrier family 39 (zinc transporter), member 1/2/3
scaffold8961	-3.150	2.34E-03		
C225712	-3.137	1.34E-03		
C181895	-3.132	2.30E-02		
C110816	-3.109	5.42E-04		
C252129	-3.107	2.32E-03		
C264557	-3.061	2.84E-02		
C338581	-3.001	1.48E-06		
C330743	-2.981	4.72E-02		
C321634	-2.977	1.67E-03		
C290845	-2.922	2.43E-02		
C315353	-2.918	1.70E-02		
C132606	-2.909	3.11E-02	K19882	NOTUM; O-palmitoleoyl-L-serine hydrolase [EC:3.1.1.98]
C56932	-2.884	3.03E-03		
C272367	-2.880	4.36E-03		
C62096	-2.861	1.26E-03		
C136411	-2.847	1.57E-02		
C245023	-2.844	1.95E-02	K01652	E2.2.1.6L, ilvB, ilvG, ilvI; acetolactate synthase I/II/III large subunit [EC:2.2.1.6]
C324579	-2.840	3.73E-02		
scaffold15988	-2.814	1.16E-02		

C337633	-2.808	5.25E-04		
C315151	-2.806	2.62E-02		
C98222	-2.792	1.94E-03		
C44340	-2.777	1.89E-03		
C182705	-2.775	2.01E-03		
scaffold5054	-2.761	3.95E-02		
C113580	-2.747	4.70E-03		
scaffold10843	-2.730	9.27E-05		
C62196	-2.717	4.59E-02		
C329203	-2.706	2.17E-02		
C256887	-2.697	4.90E-02		
scaffold11516	-2.696	4.91E-02		
scaffold11614	-2.683	1.39E-02		
scaffold795	-2.681	2.58E-02	K00454	LOX2S; lipoxygenase [EC:1.13.11.12]
C50382	-2.673	1.43E-03		
C327519	-2.665	1.88E-03	K16732	PRC1; protein regulator of cytokinesis 1
C120670	-2.663	4.48E-04	K09874	NIP; aquaporin NIP
C312865	-2.646	4.62E-04		
C325583	-2.644	2.70E-02		
C233857	-2.639	2.58E-02		
scaffold6752	-2.628	1.57E-03		
scaffold8556	-2.627	3.80E-03		
C270433	-2.623	3.73E-02		
C321722	-2.608	1.04E-02		
C324907	-2.597	4.17E-03		
C197227	-2.577	2.01E-02		
scaffold14165	-2.558	2.22E-02		
C251927	-2.539	3.74E-04		

C249333	-2.538	3.31E-02	K14709	SLC39A1_2_3, ZIP1_2_3; solute carrier family 39 (zinc transporter), member 1/2/3
scaffold14811	-2.537	4.53E-05	K01859	E5.5.1.6; chalcone isomerase [EC:5.5.1.6]
C77642	-2.531	1.51E-02		
C252457	-2.526	4.89E-02	K05350	bglB; beta-glucosidase [EC:3.2.1.21]
C237142	-2.510	2.05E-03		
C368700	-2.505	2.17E-03		
C268283	-2.487	3.02E-03		
scaffold14631	-2.451	1.08E-02		
C299698	-2.443	8.16E-03		
C261531	-2.428	7.88E-03	K10999	CESA; cellulose synthase A [EC:2.4.1.12]
C318092	-2.418	8.13E-03		
C350597	-2.404	2.80E-02		
C385124	-2.404	7.87E-04		
C263205	-2.394	1.57E-02		
C309703	-2.362	1.62E-03		
C391648	-2.335	3.40E-02	K05350	bglB; beta-glucosidase [EC:3.2.1.21]
C216424	-2.322	2.63E-02		
scaffold5289	-2.281	2.36E-02		
C386938	-2.277	2.87E-02	K06892	F6H1; feruloyl-CoA ortho-hydroxylase [EC:1.14.11.-]
C173859	-2.270	1.78E-03		
C265137	-2.269	2.18E-02		
C321992	-2.263	4.79E-02		
C347397	-2.255	4.63E-03		
C40403	-2.228	4.83E-02		
C403366	-2.224	2.87E-02		
C291789	-2.214	4.88E-03		
C357659	-2.207	2.17E-04		
C62520	-2.198	2.00E-04		

C229178	-2.197	2.60E-02		
C402974	-2.196	3.56E-03		
C285177	-2.190	1.85E-02		
scaffold16574	-2.160	1.95E-02	K14505	CYCD3; cyclin D3, plant
C267701	-2.151	3.78E-02		
C167545	-2.151	3.10E-02	K01728	pel; pectate lyase [EC:4.2.2.2]
C62522	-2.145	4.82E-02		
C292309	-2.141	2.98E-02		
scaffold16487	-2.141	7.46E-03		
C332743	-2.119	9.39E-03	K15403	ACE, HTH; fatty acid omega-hydroxy dehydrogenase [EC:1.1.-.-]
C70726	-2.117	2.87E-02		
scaffold1210	-2.112	2.45E-02		
C313917	-2.102	2.35E-03		
scaffold1216	-2.098	6.81E-03		
C299250	-2.095	2.72E-03	K00485	FMO; dimethylaniline monooxygenase (N-oxide forming) [EC:1.14.13.8]
scaffold12818	-2.089	3.87E-02	K04733	IRAK4; interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]
C363824	-2.076	3.80E-02		
scaffold2606	-2.064	1.26E-03		
C321270	-2.058	2.50E-02		
C329945	-2.051	5.96E-03	K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family
scaffold18382	-2.051	1.51E-02		
C375950	-2.050	2.73E-02		
C128534	-2.047	2.78E-02		
C220968	-2.043	2.31E-02		
scaffold14989	-2.024	1.03E-04	K00588	E2.1.1.104; caffeoyl-CoA O-methyltransferase [EC:2.1.1.104]
scaffold10572	-2.013	2.30E-02		
C352817	-2.010	7.05E-03		
C57342	-2.010	2.30E-02		

C326709	-1.986	2.45E-02	K05929	E2.1.1.103, NMT; phosphoethanolamine N-methyltransferase [EC:2.1.1.103]
C308563	-1.983	3.54E-02	K03549	kup; KUP system potassium uptake protein
scaffold18370	-1.978	1.41E-02		
C285255	-1.977	3.10E-03		
scaffold18649	-1.967	4.33E-03		
C309749	-1.959	4.63E-02		
C265575	-1.935	3.56E-02		
C292251	-1.930	5.83E-03		
scaffold11615	-1.930	4.11E-02		
C317964	-1.927	1.26E-02		
C238127	-1.907	6.63E-03		
scaffold1217	-1.905	3.23E-02		
C234454	-1.898	8.28E-03		
C229840	-1.896	4.82E-02	K01870	IARS, ileS; isoleucyl-tRNA synthetase [EC:6.1.1.5]
scaffold1590	-1.887	3.23E-02		
C364582	-1.886	6.28E-03	K08902	psb27; photosystem II Psb27 protein
scaffold3888	-1.884	1.07E-03	K16297	SCPL-II; serine carboxypeptidase-like clade II [EC:3.4.16.-]
C394164	-1.881	1.02E-03	K08057	CALR; calreticulin
C314823	-1.880	3.13E-02		
C334813	-1.855	4.97E-02		
scaffold4481	-1.845	2.82E-06		
C285139	-1.844	2.55E-04		
C366486	-1.834	1.26E-02		
scaffold11878	-1.832	8.69E-03	K09264	K09264; MADS-box transcription factor, plant
C141723	-1.816	2.27E-02		
scaffold12451	-1.802	3.83E-03	K08341	GABARAP, ATG8, LC3; GABA(A) receptor-associated protein
C348671	-1.801	2.99E-02		
C318614	-1.793	3.72E-03	K14484	IAA; auxin-responsive protein IAA

C316688	-1.791	1.87E-02	K09422	mybP; transcription factor myb, plant
C215610	-1.787	1.78E-02		
C257085	-1.785	3.59E-02		
C238863	-1.783	2.50E-02		
C307827	-1.773	7.61E-03		
C178739	-1.771	4.94E-02		
C269257	-1.765	8.94E-04		
C363430	-1.764	7.26E-03		
C225872	-1.752	2.71E-02	K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family
C373090	-1.747	4.53E-05		
scaffold14164	-1.743	1.26E-02		
C299610	-1.736	5.75E-03	K10355	ACTF; actin, other eukaryote
scaffold9827	-1.733	5.25E-04		
C284351	-1.726	4.67E-03		
C266909	-1.724	6.96E-03		
C205556	-1.723	1.63E-02		
C235120	-1.723	3.20E-02		
C300966	-1.722	2.15E-02		
C400620	-1.709	4.04E-02		
scaffold793	-1.707	3.97E-02	K00454	LOX2S; lipoxygenase [EC:1.13.11.12]
scaffold4034	-1.706	1.04E-02		
C335513	-1.701	4.75E-02		
C338641	-1.691	6.61E-04		
C104276	-1.687	3.35E-02		
scaffold3470	-1.670	1.65E-03		
C327397	-1.667	3.00E-02	K10999	CESA; cellulose synthase A [EC:2.4.1.12]
scaffold19369	-1.650	1.29E-03		
C272431	-1.649	8.03E-03		

C388574	-1.637	1.54E-02		
C401286	-1.623	1.73E-02		
scaffold10942	-1.621	4.72E-02		
scaffold10278	-1.617	1.41E-02	K00799	GST, gst; glutathione S-transferase [EC:2.5.1.18]
C362650	-1.613	2.17E-04		
C268227	-1.608	1.91E-02		
C396154	-1.608	2.49E-02		
C395584	-1.607	4.38E-02		
C387896	-1.598	1.41E-02		
scaffold794	-1.586	1.43E-02	K00454	LOX2S; lipoxygenase [EC:1.13.11.12]
scaffold14330	-1.583	4.53E-04		
C313501	-1.572	1.86E-02		
				DLAT, aceF, pdhC; pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]
C263715	-1.568	1.56E-03	K00627	
C312931	-1.567	5.87E-03		
C299958	-1.565	9.39E-03		
C287303	-1.557	4.70E-02		
C378798	-1.555	2.87E-02	K04730	IRAK1; interleukin-1 receptor-associated kinase 1 [EC:2.7.11.1]
C204270	-1.547	1.91E-02		
C340221	-1.546	4.82E-02		
scaffold4704	-1.540	3.56E-02	K01188	E3.2.1.21; beta-glucosidase [EC:3.2.1.21]
scaffold15622	-1.539	6.17E-03		
C344917	-1.538	7.84E-03		
scaffold4360	-1.530	4.72E-02		
C396894	-1.517	2.50E-03	K00475	E1.14.11.9; naringenin 3-dioxygenase [EC:1.14.11.9]
C344281	-1.512	6.11E-04		
scaffold17308	-1.509	4.70E-02		
C297253	-1.505	2.38E-02		
scaffold372	-1.502	2.70E-02	K00454	LOX2S; lipoxygenase [EC:1.13.11.12]

C335989	-1.499	7.46E-03		
C290491	-1.494	4.72E-02		
scaffold6523	-1.493	2.80E-02		
C46792	-1.492	2.77E-02		
C210254	-1.488	7.39E-03	K07375	TUBB; tubulin beta
C292811	-1.488	1.29E-02		
C296057	-1.483	1.41E-02	K00604	MTFMT, fmt; methionyl-tRNA formyltransferase [EC:2.1.2.9]
C155003	-1.477	4.65E-02		
C102902	-1.458	1.27E-02	K01183	E3.2.1.14; chitinase [EC:3.2.1.14]
C300536	-1.457	4.69E-02		
C317036	-1.451	7.46E-03		
				SLC32A, VGAT; solute carrier family 32 (vesicular inhibitory amino acid transporter)
C334211	-1.447	2.54E-03	K15015	
C220150	-1.445	3.32E-02	K20456	OSBP; oxysterol-binding protein 1
scaffold1021	-1.430	4.23E-03		
C291571	-1.428	4.67E-02		
scaffold17490	-1.427	1.26E-02	K00134	GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]
C390444	-1.423	2.73E-02	K01191	MAN2C1; alpha-mannosidase [EC:3.2.1.24]
C250913	-1.421	4.05E-02		
C385702	-1.417	4.13E-02	K06085	SSX2IP, ADIP; synovial sarcoma, X breakpoint 2 interacting protein
scaffold11078	-1.411	1.57E-02		
C279535	-1.409	4.90E-02	K17681	ATAD3A_B; ATPase family AAA domain-containing protein 3A/B
C346915	-1.405	3.28E-02	K14442	DHX36, RHAU; ATP-dependent RNA helicase DHX36 [EC:3.6.4.13]
C309641	-1.405	4.84E-02	K09338	HD-ZIP; homeobox-leucine zipper protein
C300080	-1.401	1.63E-05		
C381344	-1.400	3.69E-02		
scaffold7014	-1.388	1.66E-05	K08900	BCS1; mitochondrial chaperone BCS1
C376372	-1.387	1.89E-04		
C336587	-1.380	3.55E-03		

C273565	-1.378	2.61E-02	K12462	ARHGD1, RHOGDI; Rho GDP-dissociation inhibitor
C391406	-1.371	3.04E-03	K19042	BOI; E3 ubiquitin-protein ligase BOI and related proteins [EC:2.3.2.27]
C367448	-1.364	3.69E-02		
C391712	-1.359	5.94E-03	K14489	AHK2_3_4; arabidopsis histidine kinase 2/3/4 (cytokinin receptor) [EC:2.7.13.3]
C220316	-1.358	3.57E-02		
C279053	-1.356	1.36E-02		
scaffold10420	-1.352	1.54E-02		
C162259	-1.349	8.13E-03		
C89652	-1.344	1.42E-02		
C350135	-1.342	2.36E-02	K04733	IRAK4; interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]
C344443	-1.342	4.79E-03		
C315543	-1.339	9.05E-03	K13449	PR1; pathogenesis-related protein 1
C283317	-1.332	4.21E-02		
C93898	-1.332	8.03E-03		
scaffold17826	-1.328	1.51E-02	K01465	URA4, pyrC; dihydroorotase [EC:3.5.2.3]
C386334	-1.324	2.59E-03	K01051	E3.1.1.11; pectinesterase [EC:3.1.1.11]
C363278	-1.318	9.92E-03		
C343243	-1.316	4.05E-02		
C356815	-1.311	4.15E-02		
C385298	-1.299	1.05E-02		
scaffold2722	-1.298	2.79E-02		
scaffold6716	-1.296	6.61E-03		
C335827	-1.286	2.27E-02		
scaffold10017	-1.286	2.60E-04	K14190	VTC2_5; GDP-L-galactose phosphorylase [EC:2.7.7.69]
scaffold8964	-1.282	4.29E-02	K15403	ACE, HTH; fatty acid omega-hydroxy dehydrogenase [EC:1.1.-.-]
C363634	-1.273	9.43E-03		
C60500	-1.267	4.55E-02		
C387744	-1.260	3.23E-02		

scaffold113	-1.259	4.83E-02		
scaffold12991	-1.259	1.03E-02		
C351971	-1.255	1.26E-02	K14763	NAF1; H/ACA ribonucleoprotein complex non-core subunit NAF1
scaffold15220	-1.254	8.77E-04	K04730	IRAK1; interleukin-1 receptor-associated kinase 1 [EC:2.7.11.1]
C342351	-1.253	4.11E-02		
C343067	-1.243	4.19E-02		
scaffold6071	-1.230	4.57E-02		
scaffold17814	-1.224	4.41E-03	K14794	RRP12; ribosomal RNA-processing protein 12
C230849	-1.223	2.82E-02		
C382262	-1.217	3.48E-02		
scaffold18152	-1.216	1.42E-03		
C397340	-1.215	4.83E-02	K14489	AHK2_3_4; arabidopsis histidine kinase 2/3/4 (cytokinin receptor) [EC:2.7.13.3]
scaffold14255	-1.213	4.11E-02	K00058	serA, PHGDH; D-3-phosphoglycerate dehydrogenase / 2-oxoglutarate reductase [EC:1.1.1.95 1.1.1.399]
scaffold7351	-1.209	6.28E-03		
C275477	-1.206	3.23E-02	K03320	amt, AMT, MEP; ammonium transporter, Amt family
scaffold10096	-1.204	9.23E-03		
C387276	-1.204	3.83E-02	K03768	PPIB, ppiB; peptidyl-prolyl cis-trans isomerase B (cyclophilin B) [EC:5.2.1.8]
C398086	-1.202	2.74E-03		
C287207	-1.195	1.26E-02		
C385462	-1.192	5.12E-03		
C311777	-1.191	1.95E-02		
C343757	-1.186	4.20E-03		
C323853	-1.180	2.39E-02	K02983	RP-S30e, RPS30; small subunit ribosomal protein S30e
C392538	-1.179	3.28E-02	K00660	CHS; chalcone synthase [EC:2.3.1.74]
C390880	-1.174	3.77E-02	K08054	CANX; calnexin
scaffold17640	-1.173	1.20E-02	K09490	HSPA5, BIP; heat shock 70kDa protein 5
scaffold16202	-1.168	4.64E-02		

scaffold16566	-1.168	2.38E-02	K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family
scaffold9876	-1.163	9.32E-04	K01537	E3.6.3.8; Ca ²⁺ -transporting ATPase [EC:3.6.3.8]
C332209	-1.155	7.42E-03		
C395164	-1.151	2.16E-02		
C230613	-1.150	8.08E-03		
scaffold18738	-1.144	1.04E-02		
scaffold8879	-1.143	2.02E-03		
C88302	-1.142	2.84E-03		
C383874	-1.136	2.12E-02	K08911	LHCA5; light-harvesting complex I chlorophyll a/b binding protein 5
C201784	-1.133	1.96E-02		
C269763	-1.132	8.92E-03		
scaffold8351	-1.131	4.23E-03		
C375714	-1.122	2.79E-02		
scaffold12596	-1.117	2.87E-02		
C393372	-1.115	4.50E-02	K18787	ACL5; thermospermine synthase [EC:2.5.1.79]
C292721	-1.114	2.36E-02		
C391484	-1.107	1.75E-02		
C283515	-1.102	3.83E-02		
scaffold11200	-1.094	2.99E-02		
C320170	-1.088	1.35E-02	K13347	PXMP2, PMP22; peroxisomal membrane protein 2
scaffold8963	-1.083	2.14E-02	K15403	ACE, HTH; fatty acid omega-hydroxy dehydrogenase [EC:1.1.-.-]
C313737	-1.082	1.91E-02		
C371440	-1.081	2.30E-03	K12462	ARHGD1, RHOGDI; Rho GDP-dissociation inhibitor
scaffold13985	-1.079	6.54E-03	K02699	psaL; photosystem I subunit XI
C351407	-1.077	4.57E-02		
C329131	-1.073	2.85E-03		
scaffold9826	-1.072	6.16E-03		
C391520	-1.069	4.12E-02	K15275	SLC35B1; solute carrier family 35 (UDP-galactose transporter), member B1

C402200	-1.069	2.30E-03		
C311615	-1.069	2.12E-02		
scaffold12692	-1.068	2.54E-02	K14753	RACK1; guanine nucleotide-binding protein subunit beta-2-like 1 protein
C254653	-1.067	1.63E-02		
scaffold645	-1.067	9.39E-03		
C321742	-1.065	4.39E-02		
C382922	-1.063	1.23E-02	K02864	RP-L10, MRPL10, rplJ; large subunit ribosomal protein L10
C391684	-1.061	7.28E-03		
scaffold18534	-1.061	1.96E-02		
scaffold13375	-1.057	5.56E-03		
C242015	-1.056	3.57E-02		
C322658	-1.056	1.51E-02	K08193	SLC17A; MFS transporter, ACS family, solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), other
scaffold18844	-1.053	1.16E-02		
scaffold9067	-1.050	2.66E-02		
C320544	-1.050	1.41E-02		
C388982	-1.049	1.95E-02	K02906	RP-L3, MRPL3, rplC; large subunit ribosomal protein L3
scaffold19326	-1.049	1.19E-02		
C369236	-1.043	1.70E-02	K09569	FKBP2; FK506-binding protein 2 [EC:5.2.1.8]
C358415	-1.040	1.01E-02	K20843	GALT2S; hydroxyproline O-galactosyltransferase 2/3/4/5/6 [EC:2.4.1.-]
scaffold12064	-1.037	3.02E-03		
scaffold3172	-1.037	4.34E-02	K09761	rsmE; 16S rRNA (uracil1498-N3)-methyltransferase [EC:2.1.1.193]
scaffold15035	-1.036	2.27E-02		
C386972	-1.035	4.78E-02		
C342049	-1.033	9.73E-03		
C374558	-1.029	8.16E-03		
C314713	-1.028	4.31E-02		
C381590	-1.026	3.22E-02	K12619	XRN2, RAT1; 5'-3' exoribonuclease 2 [EC:3.1.13.-]
scaffold15195	-1.024	4.70E-02		

C387354	-1.023	7.72E-03	K00384	trxB, TRR; thioredoxin reductase (NADPH) [EC:1.8.1.9]
scaffold16303	-1.022	2.36E-02	K01807	rpiA; ribose 5-phosphate isomerase A [EC:5.3.1.6]
C334553	-1.017	4.74E-03		
scaffold17888	-1.015	4.48E-04	K09753	CCR; cinnamoyl-CoA reductase [EC:1.2.1.44]
C386576	-1.012	2.61E-02	K03027	RPC40, POLR1C; DNA-directed RNA polymerases I and III subunit RPAC1
scaffold11356	-1.010	2.28E-02		
scaffold3679	-1.009	1.91E-02	K01177	E3.2.1.2; beta-amylase [EC:3.2.1.2]
C338783	-1.008	4.29E-03		
C361766	-1.006	4.83E-02	K13508	GPAT; glycerol-3-phosphate acyltransferase [EC:2.3.1.15 2.3.1.198]
C361798	-1.005	6.34E-03		
scaffold1099	-1.004	2.70E-02	K05928	E2.1.1.95; tocopherol O-methyltransferase [EC:2.1.1.95]
C282271	-1.001	2.17E-02		
scaffold5634	-0.992	2.78E-02		
scaffold14168	-0.992	3.00E-02		
scaffold18868	-0.989	5.10E-03		
C309835	-0.989	4.82E-02		
C281543	-0.989	3.91E-02	K03549	kup; KUP system potassium uptake protein
C360932	-0.988	2.04E-02		
C393954	-0.987	9.43E-03	K15104	SLC25A11, OGC; solute carrier family 25 (mitochondrial oxoglutarate transporter), member 11
C285959	-0.982	3.83E-02		
C351965	-0.974	2.98E-02		
C382636	-0.974	2.87E-02	K02372	fabZ; 3-hydroxyacyl-[acyl-carrier-protein] dehydratase [EC:4.2.1.59]
scaffold13334	-0.973	4.59E-03		
C244395	-0.970	1.41E-02		
scaffold14111	-0.965	4.77E-02	K02716	psbO; photosystem II oxygen-evolving enhancer protein 1
C374722	-0.963	1.50E-03		
C339919	-0.962	4.05E-02	K03377	CASD1; N-acetylneuraminate 9-O-acetyltransferase [EC:2.3.1.45]
C364552	-0.959	1.26E-02	K07766	E3.6.1.52; diphosphoinositol-polyphosphate diphosphatase [EC:3.6.1.52]

C396852	-0.953	2.95E-02	K05359	ADT, PDT; arogenate/prephenate dehydratase [EC:4.2.1.91 4.2.1.51]
scaffold16063	-0.950	2.96E-02		
C327383	-0.942	4.56E-02	K00059	fabG; 3-oxoacyl-[acyl-carrier protein] reductase [EC:1.1.1.100]
C362864	-0.942	2.21E-02		
C386546	-0.941	3.76E-02		
C347329	-0.940	7.17E-03		
scaffold4886	-0.932	1.16E-02		
C362120	-0.931	4.54E-02	K13806	DAGL; sn1-specific diacylglycerol lipase [EC:3.1.1.-]
C301544	-0.930	3.42E-02	K03006	RPB1, POLR2A; DNA-directed RNA polymerase II subunit RPB1 [EC:2.7.7.6]
scaffold10837	-0.926	1.86E-02	K15032	MTERFD; mTERF domain-containing protein, mitochondrial
scaffold4004	-0.923	1.92E-02		
scaffold10496	-0.922	3.46E-03	K19355	MAN; mannan endo-1,4-beta-mannosidase [EC:3.2.1.78]
				IRX7, FRA8, F8H; probable glucuronoxylan glucuronosyltransferase IRX7 [EC2.4.1.-]
C400742	-0.921	1.20E-02	K20889	
C399534	-0.917	3.80E-03	K01531	mgtA, mgtB; Mg2+-importing ATPase [EC:3.6.3.2]
scaffold3867	-0.908	4.83E-02	K09422	mybP; transcription factor myb, plant
C392452	-0.900	4.23E-03		
scaffold16012	-0.897	3.05E-02		
C380976	-0.893	4.06E-02	K02939	RP-L9, MRPL9, rplI; large subunit ribosomal protein L9
scaffold18719	-0.893	3.00E-02		
C94712	-0.891	2.93E-02		
C347073	-0.888	1.22E-02	K16675	ZDHHC9_14_18; palmitoyltransferase ZDHHC9/14/18 [EC:2.3.1.225]
scaffold13361	-0.886	3.82E-02	K01507	ppa; inorganic pyrophosphatase [EC:3.6.1.1]
scaffold4769	-0.881	7.76E-03		
C337771	-0.881	2.02E-02		
scaffold8228	-0.880	2.88E-02		
scaffold11490	-0.874	1.19E-02		
C366902	-0.872	1.43E-02		
C380584	-0.871	3.67E-02		

scaffold13721	-0.871	4.11E-02		
scaffold3757	-0.863	2.71E-02		
C316249	-0.855	4.90E-02		
scaffold18085	-0.849	8.80E-03	K01227	E3.2.1.96; mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase [EC:3.2.1.96]
C393838	-0.849	3.56E-03		
C366354	-0.843	2.40E-02	K02437	gcvH, GCSH; glycine cleavage system H protein
scaffold17541	-0.833	5.96E-03		
scaffold4970	-0.832	4.94E-02	K08770	UBC; ubiquitin C
C394830	-0.830	4.66E-03	K15285	SLC35E3; solute carrier family 35, member E3
scaffold14135	-0.828	1.31E-02	K15446	TRM13, CCDC76; tRNA:m4X modification enzyme [EC:2.1.1.225]
C394312	-0.822	2.02E-02	K12501	HST; homogentisate solanesyltransferase [EC:2.5.1.117]
C381012	-0.816	4.11E-02		
C395286	-0.810	3.88E-02	K09517	DNAJB11; DnaJ homolog subfamily B member 11
scaffold12953	-0.805	3.85E-02		
C303016	-0.803	1.35E-02		
scaffold4959	-0.797	3.44E-02		
scaffold13421	-0.793	2.45E-02		
C365178	-0.790	4.82E-02		
C335835	-0.787	3.42E-02	K13993	HSP20; HSP20 family protein
C387372	-0.785	6.61E-03	K12607	CNOT10; CCR4-NOT transcription complex subunit 10
scaffold18309	-0.784	2.12E-02		
C366410	-0.779	3.22E-02		
C355703	-0.769	3.20E-02	K05658	ABCB1, CD243; ATP-binding cassette, subfamily B (MDR/TAP), member 1 [EC:3.6.3.44]
C388732	-0.765	2.23E-02	K00254	DHODH, pyrD; dihydroorotate dehydrogenase [EC:1.3.5.2]
C395620	-0.760	3.73E-02	K00930	argB; acetylglutamate kinase [EC:2.7.2.8]
scaffold7981	-0.759	1.63E-02	K08057	CALR; calreticulin
scaffold10322	-0.746	4.74E-02	K00326	E1.6.2.2; cytochrome-b5 reductase [EC:1.6.2.2]

scaffold4329	-0.745	9.62E-03		
C354435	-0.743	9.39E-03		
C396100	-0.742	6.46E-03	K01247	alkA; DNA-3-methyladenine glycosylase II [EC:3.2.2.21]
C362494	-0.742	4.69E-02	K14833	NOC2; nucleolar complex protein 2
scaffold8370	-0.741	4.17E-02		
scaffold6064	-0.738	1.70E-02	K00895	pfp, PFP; diphosphate-dependent phosphofructokinase [EC:2.7.1.90]
scaffold13261	-0.735	1.73E-02	K13519	LPT1, ALE1; lysophospholipid acyltransferase [EC:2.3.1.51 2.3.1.23 2.3.1.-]
C384408	-0.735	3.57E-03		
scaffold6509	-0.728	1.33E-02	K10782	FATA; fatty acyl-ACP thioesterase A [EC:3.1.2.14]
C292255	-0.724	2.27E-02		
C354999	-0.720	1.09E-02	K16253	NRPD7, NRPE7; DNA-directed RNA polymerase IV and V subunit 7
scaffold6242	-0.719	4.22E-02	K12394	AP1S1_2; AP-1 complex subunit sigma 1/2
scaffold11638	-0.718	9.78E-03		
C58856	-0.718	4.84E-02		
scaffold18050	-0.717	4.05E-02	K07976	RAB; Rab family, other
scaffold6948	-0.713	2.62E-02		
scaffold14125	-0.713	1.17E-02	K00889	PIP5K; 1-phosphatidylinositol-4-phosphate 5-kinase [EC:2.7.1.68]
C379286	-0.710	4.04E-02	K02931	RP-L5, MRPL5, rplE; large subunit ribosomal protein L5
scaffold11277	-0.708	3.44E-02		
scaffold5702	-0.699	3.45E-02		
scaffold16414	-0.695	2.87E-02		
C376288	-0.689	1.41E-02		
C399090	-0.686	2.83E-02		
C400316	-0.684	6.54E-03	K00627	DLAT, aceF, pdhC; pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]
C357433	-0.683	4.85E-02		
C397910	-0.683	4.82E-02	K14546	UTP5, WDR43; U3 small nucleolar RNA-associated protein 5
C368168	-0.677	4.34E-02	K21594	GUF1; translation factor GUF1, mitochondrial [EC:3.6.5.-]
C377658	-0.675	3.40E-02		

scaffold6142	-0.670	6.28E-03	K07937	ARF1; ADP-ribosylation factor 1
C399140	-0.668	8.02E-04	K00384	trxB, TRR; thioredoxin reductase (NADPH) [EC:1.8.1.9]
scaffold19308	-0.666	4.72E-02	K15283	SLC35E1; solute carrier family 35, member E1
C376426	-0.665	3.83E-02		
C322304	-0.663	4.05E-02	K03109	SRP9; signal recognition particle subunit SRP9
scaffold12994	-0.663	2.71E-03	K03921	FAB2, SSI2, desA1; acyl-[acyl-carrier-protein] desaturase [EC:1.14.19.2 1.14.19.11 1.14.19.26]
scaffold15562	-0.662	6.49E-03		
C386614	-0.660	2.38E-02	K11876	PSMG2, PAC2; proteasome assembly chaperone 2
C372902	-0.659	4.32E-02		
scaffold1461	-0.659	8.65E-03		
C329503	-0.648	4.04E-02		
C397504	-0.642	1.77E-02	K00811	ASP5; aspartate aminotransferase, chloroplastic [EC:2.6.1.1]
C340731	-0.634	3.78E-02		
scaffold18855	-0.633	2.51E-03		
C398966	-0.625	1.43E-02		
C388296	-0.605	2.21E-02		
C381128	-0.600	4.90E-02	K14396	PABPN1, PABP2; polyadenylate-binding protein 2
C376998	-0.594	4.19E-02		
scaffold546	-0.591	4.74E-02		
C394064	-0.588	8.03E-03	K14442	DHX36, RHAU; ATP-dependent RNA helicase DHX36 [EC:3.6.4.13]
C359765	-0.582	4.13E-02		
C400740	-0.574	4.65E-02	K20165	TBC1D2; TBC1 domain family member 2A
C378918	-0.573	4.74E-02	K03676	grxC, GLRX, GLRX2; glutaredoxin 3
C381236	-0.572	1.69E-02	K14401	CPSF1, CFT1; cleavage and polyadenylation specificity factor subunit 1
scaffold17925	-0.564	7.72E-03		
scaffold7779	-0.563	2.91E-02	K02876	RP-L15, MRPL15, rpL10; large subunit ribosomal protein L15
scaffold11589	-0.562	1.78E-02	K00993	EPT1; ethanolaminephosphotransferase [EC:2.7.8.1]
C402828	-0.560	3.45E-02		

scaffold18839	-0.533	8.33E-03	K17085	TM9SF1; transmembrane 9 superfamily member 1
C335225	-0.519	4.99E-02		
scaffold5833	-0.511	1.10E-02	K11498	CENPE; centromeric protein E
scaffold19478	-0.505	3.27E-02		
C389008	-0.495	2.14E-02	K16277	DRIP; E3 ubiquitin-protein ligase DRIP [EC:2.3.2.27]
C398568	-0.494	1.67E-02	K00111	glpA, glpD; glycerol-3-phosphate dehydrogenase [EC:1.1.5.3]
scaffold18876	-0.494	6.46E-03	K01528	DNM; dynamin GTPase [EC:3.6.5.5]
scaffold15199	-0.486	2.55E-02	K03320	amt, AMT, MEP; ammonium transporter, Amt family
scaffold4913	-0.478	2.95E-02	K07893	RAB6A; Ras-related protein Rab-6A
C403358	-0.475	3.76E-02		
C396162	-0.457	3.45E-02		
scaffold18411	-0.444	1.91E-02		
C399336	-0.434	2.73E-02	K09510	DNAJB4; DnaJ homolog subfamily B member 4
C398470	-0.369	4.38E-02		
scaffold19221	-0.367	4.74E-02		
scaffold18693	0.424	2.51E-03		
C395300	0.488	2.95E-02	K03843	ALG2; alpha-1,3/alpha-1,6-mannosyltransferase [EC:2.4.1.132 2.4.1.257]
scaffold988	0.549	1.03E-02	K11137	TELO2, TEL2; telomere length regulation protein
C392572	0.567	2.23E-02		
scaffold19575	0.600	1.36E-02		
scaffold17320	0.611	2.21E-02		
C403486	0.626	4.67E-02		
scaffold959	0.639	4.74E-02	K07877	RAB2A; Ras-related protein Rab-2A
C389254	0.644	3.23E-02		
C399200	0.645	1.34E-02		
scaffold6864	0.652	4.67E-02		
C402064	0.657	3.64E-02		
C393648	0.657	1.63E-02		
scaffold10935	0.658	3.39E-03		

C318064	0.659	2.85E-02		
C351769	0.683	2.46E-02		
scaffold19740	0.691	1.23E-02		
scaffold3584	0.702	4.20E-02		
scaffold17892	0.712	8.72E-03	K15639	CYP734A1, BAS1; PHYB activation tagged suppressor 1 [EC:1.14.-.-]
C388890	0.713	2.87E-02		
scaffold15983	0.716	3.00E-02		
C387532	0.721	7.88E-03	K00878	thiM; hydroxyethylthiazole kinase [EC:2.7.1.50]
scaffold11234	0.723	4.14E-02		
C403460	0.730	4.72E-02		
C293673	0.733	4.72E-02		
scaffold7860	0.749	3.73E-02		
scaffold7194	0.756	2.07E-03		
scaffold19197	0.758	3.83E-02		
scaffold6994	0.765	3.55E-02	K02980	RP-S29e, RPS29; small subunit ribosomal protein S29e
scaffold5489	0.773	3.79E-02		
C378280	0.781	2.71E-02		
C390156	0.781	4.38E-02		
C400038	0.782	4.05E-02		
C388208	0.787	3.87E-02	K10886	XRCC4; DNA-repair protein XRCC4
scaffold9302	0.795	3.27E-02		
scaffold19483	0.798	7.46E-03		
scaffold6035	0.809	3.78E-02	K10872	DMC1; meiotic recombination protein DMC1
C402220	0.810	4.33E-02		
scaffold2594	0.815	4.32E-02	K14431	TGA; transcription factor TGA
C387616	0.825	4.84E-02	K12185	VPS37; ESCRT-I complex subunit VPS37
scaffold6485	0.839	1.29E-02		
C399416	0.848	1.78E-03	K03797	E3.4.21.102, prc, ctpA; carboxyl-terminal processing protease [EC:3.4.21.102]

scaffold10058	0.853	4.54E-02	K00029	E1.1.1.40, maeB; malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+) [EC:1.1.1.40]
scaffold12640	0.855	3.00E-02	K17991	PXG; peroxygenase [EC:1.11.2.3]
C392948	0.856	4.07E-02		
C401998	0.857	2.60E-02		
scaffold6808	0.860	1.25E-02		
C377386	0.861	8.96E-04		
C336953	0.865	2.85E-02		
scaffold2861	0.880	4.80E-02		
scaffold5549	0.883	6.61E-03	K01897	ACSL, fadD; long-chain acyl-CoA synthetase [EC:6.2.1.3]
scaffold13287	0.909	2.60E-02	K19038	ATL41; E3 ubiquitin-protein ligase ATL41 [EC:2.3.2.27]
C269273	0.913	2.87E-02		
scaffold14524	0.915	4.34E-02		
scaffold14151	0.924	3.83E-02	K00366	nirA; ferredoxin-nitrite reductase [EC:1.7.7.1]
scaffold18184	0.926	8.84E-03		
scaffold12926	0.927	2.01E-02		
scaffold461	0.938	4.05E-02		
C394198	0.941	1.17E-02	K01176	AMY, amyA, malS; alpha-amylase [EC:3.2.1.1]
C395020	0.953	6.28E-03		
C336403	0.954	1.57E-02		
scaffold2436	0.965	4.43E-02		
C105588	0.966	2.38E-02		
scaffold12537	0.969	1.96E-02		
scaffold5947	0.974	3.20E-02		
C355345	0.975	4.43E-03		
C372862	0.977	2.87E-02		
scaffold18927	0.980	1.78E-03		
C331067	0.981	3.56E-02		
C394592	0.984	4.41E-03	K18270	RAB3GAP1; Rab3 GTPase-activating protein catalytic subunit

C403216	0.986	4.27E-03		
scaffold13683	0.986	4.11E-02	K17586	PHRF1; PHD and RING finger domain-containing protein 1
scaffold355	0.987	1.04E-02		
scaffold12853	0.991	1.84E-02		
C368058	0.993	3.95E-02		
C354359	0.995	1.73E-02		
scaffold18466	0.996	3.41E-02		
scaffold731	1.000	3.91E-02		
scaffold9080	1.001	3.31E-02		
C359107	1.003	1.31E-02		
C393844	1.003	2.61E-02		
scaffold13572	1.004	1.88E-02		
scaffold835	1.004	1.78E-02		
scaffold4059	1.005	2.80E-02	K14664	ILR1; IAA-amino acid hydrolase [EC:3.5.1.-]
scaffold5751	1.007	2.25E-02		
C334961	1.008	4.90E-02	K13946	AUX1, LAX; auxin influx carrier (AUX1 LAX family)
scaffold10675	1.011	4.74E-02	K13457	RPM1, RPS3; disease resistance protein RPM1
C240809	1.014	3.93E-02		
C302612	1.014	1.27E-02		
scaffold6434	1.016	3.35E-02	K18857	ADH1; alcohol dehydrogenase class-P [EC:1.1.1.1]
scaffold17228	1.022	3.18E-02		
scaffold16797	1.024	4.99E-02		
scaffold4311	1.035	4.94E-02		
C360622	1.037	1.57E-02		
C383110	1.051	1.14E-02		
scaffold8214	1.060	6.93E-05		
scaffold19286	1.060	9.78E-03		
scaffold14433	1.060	4.04E-02		
scaffold9782	1.061	3.64E-02		

C401290	1.063	4.27E-03	K00764	purF, PPAT; amidophosphoribosyltransferase [EC:2.4.2.14]
scaffold19402	1.067	1.12E-02	K08900	BCS1; mitochondrial chaperone BCS1
C257241	1.068	2.49E-02	K06966	K06966; uncharacterized protein
C106800	1.071	4.30E-02	K07410	CYP1B1; cytochrome P450 family 1 subfamily B polypeptide 1 [EC:1.14.14.1]
scaffold19289	1.077	7.46E-03		
C320856	1.084	2.59E-02		
C394862	1.090	3.11E-02	K00128	ALDH; aldehyde dehydrogenase (NAD+) [EC:1.2.1.3]
C220522	1.090	3.24E-02		
C378102	1.095	3.10E-02		
C330471	1.096	1.11E-02	K18270	RAB3GAP1; Rab3 GTPase-activating protein catalytic subunit
C401550	1.099	4.99E-02		
scaffold2411	1.108	2.37E-02		
C346491	1.112	4.69E-02		
C362822	1.112	1.91E-02		
scaffold14207	1.114	2.79E-02	K07408	CYP1A1; cytochrome P450 family 1 subfamily A polypeptide 1 [EC:1.14.14.1]
scaffold15472	1.123	2.12E-02		
scaffold11660	1.146	3.59E-04	K19042	BOI; E3 ubiquitin-protein ligase BOI and related proteins [EC:2.3.2.27]
scaffold2930	1.148	8.94E-04		
C76734	1.157	2.01E-02	K22419	VEP1; Delta4-3-oxosteroid 5beta-reductase [EC:1.3.1.3]
scaffold15391	1.167	4.64E-02	K10144	RCHY1, PIRH2; RING finger and CHY zinc finger domain-containing protein 1 [EC:2.3.2.27]
C332223	1.172	3.21E-02		
scaffold8430	1.182	1.34E-02		
C387520	1.184	3.73E-03		
C250031	1.186	2.23E-03		
scaffold5668	1.190	3.87E-02		
C359445	1.200	4.29E-03		
scaffold5403	1.200	4.08E-02	K08235	E2.4.1.207; xyloglucan:xyloglucosyl transferase [EC:2.4.1.207]

scaffold13187	1.203	3.21E-02		
scaffold12708	1.208	1.35E-02		
scaffold8540	1.213	2.07E-02		
scaffold14360	1.219	5.04E-03		
scaffold12034	1.220	1.10E-02		
C400186	1.221	2.83E-02		
C318774	1.225	3.23E-02	K13457	RPM1, RPS3; disease resistance protein RPM1
scaffold11593	1.227	4.11E-02		
scaffold8923	1.231	1.35E-02		
C310021	1.234	4.92E-03		
scaffold6354	1.239	4.72E-02		
C279881	1.239	4.68E-02		
scaffold9542	1.242	2.98E-02		
C287893	1.244	6.58E-04		
scaffold10925	1.251	7.66E-03		
C374092	1.252	3.29E-02		
C312429	1.252	1.23E-03		
C328933	1.253	3.74E-03		
scaffold4150	1.253	3.31E-02		
C382744	1.264	4.93E-02		
scaffold19138	1.267	1.57E-02		
C369814	1.278	9.27E-05		
C359081	1.279	2.86E-02		
C366046	1.282	4.75E-02		
C384376	1.287	6.80E-03		
scaffold17609	1.295	6.78E-03		
scaffold5855	1.295	1.25E-02		
scaffold9189	1.295	4.77E-02		
C240549	1.296	4.74E-02		

scaffold16447	1.296	6.01E-03		
scaffold12193	1.305	3.54E-03		
C235028	1.306	4.72E-02		
C261497	1.307	2.95E-02		
scaffold5344	1.307	2.58E-02	K01953	asnB, ASNS; asparagine synthase (glutamine-hydrolysing) [EC:6.3.5.4]
scaffold17544	1.309	3.74E-04		
C205350	1.314	4.90E-02		
scaffold19051	1.315	1.43E-02		
scaffold1428	1.319	4.22E-02		
C335531	1.320	6.36E-03		
C315847	1.321	2.45E-02		
C317184	1.321	3.67E-02	K10144	RCHY1, PIRH2; RING finger and CHY zinc finger domain-containing protein 1 [EC:2.3.2.27]
C342767	1.323	3.42E-02		
scaffold8069	1.323	2.87E-02		
C41617	1.327	3.77E-02		
C381148	1.328	1.20E-02	K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family
scaffold15986	1.333	3.31E-02	K03879	ND2; NADH-ubiquinone oxidoreductase chain 2 [EC:1.6.5.3]
C374370	1.343	1.34E-02	K13420	FLS2; LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]
scaffold3080	1.348	1.55E-02		
scaffold9419	1.352	1.53E-02		
scaffold14332	1.352	1.57E-02		
C322302	1.359	1.48E-02		
C399854	1.360	3.47E-02		
scaffold5091	1.362	4.70E-02		
scaffold6794	1.364	7.17E-03		
C312903	1.365	8.85E-04		
C368344	1.368	9.78E-03	K10144	RCHY1, PIRH2; RING finger and CHY zinc finger domain-containing protein 1 [EC:2.3.2.27]

scaffold6110	1.369	2.64E-02		
scaffold14461	1.369	4.31E-02		
C386930	1.381	6.34E-03	K03511	POLK; DNA polymerase kappa [EC:2.7.7.7]
scaffold19205	1.383	1.81E-02		
C376700	1.384	4.56E-02		
C389688	1.388	1.10E-02		
scaffold11659	1.392	7.03E-04	K19042	BOI; E3 ubiquitin-protein ligase BOI and related proteins [EC:2.3.2.27]
C340421	1.395	5.48E-03		
C276101	1.397	1.18E-02		
scaffold18203	1.398	7.00E-03	K16903	TAA1; L-tryptophan---pyruvate aminotransferase [EC:2.6.1.99]
scaffold16108	1.399	7.14E-03		
C386180	1.399	1.19E-02	K10755	RFC2_4; replication factor C subunit 2/4
scaffold17555	1.409	1.89E-04	K11816	YUCCA; indole-3-pyruvate monooxygenase [EC:1.14.13.168]
C261133	1.415	4.66E-02	K22285	OSBPL8, ORP8; oxysterol-binding protein-related protein 8
C364662	1.416	3.96E-02		
C394332	1.420	2.95E-02		
C302582	1.422	1.54E-04		
scaffold13234	1.428	2.49E-02	K22374	DMAS1; 3''-deamino-3''-oxonicotianamine reductase [EC:1.1.1.285]
C282963	1.432	4.81E-02		
scaffold19234	1.436	4.08E-02	K13783	SLC37A1_2; MFS transporter, OPA family, solute carrier family 37 (glycerol-3-phosphate transporter), member 1/2
scaffold14856	1.437	3.15E-03		
scaffold11669	1.437	2.12E-05		
scaffold1086	1.438	8.30E-03		
C400546	1.438	1.54E-02		
scaffold3474	1.445	1.97E-02	K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family
scaffold3977	1.446	2.88E-04		
scaffold4140	1.449	2.01E-02	K20667	CYP716A; beta-amyrin 28-monooxygenase [EC:1.14.13.201]

C389854	1.451	5.68E-05		
scaffold9404	1.452	1.67E-02		
scaffold3154	1.453	1.32E-02		
C399062	1.470	9.51E-03		
C394082	1.471	2.61E-02		
scaffold6311	1.477	4.43E-03		
scaffold12121	1.478	2.98E-02	K00815	TAT; tyrosine aminotransferase [EC:2.6.1.5]
C340905	1.480	3.74E-04		
scaffold13453	1.485	3.18E-02	K19613	SHOC2, SUR8; leucine-rich repeat protein SHOC2
scaffold10410	1.488	6.18E-04		
scaffold823	1.489	3.64E-02		
C401680	1.490	2.01E-02		
scaffold8626	1.491	6.01E-03		
scaffold15467	1.491	3.65E-02	K03353	APC6, CDC16; anaphase-promoting complex subunit 6
C389560	1.501	1.81E-02		
C350779	1.510	2.27E-02		
C298918	1.511	6.98E-03		
C199864	1.513	8.72E-03		
C389030	1.513	1.39E-03		
scaffold13083	1.523	2.02E-03		
C399988	1.523	8.54E-03		
C256333	1.528	2.38E-02		
C350695	1.530	9.49E-03		
C399180	1.531	2.60E-04	K21371	UGT75L6, UGTcs2; crocetin glucosyltransferase [EC:2.4.1.271]
C382928	1.531	2.95E-02		
scaffold6626	1.543	2.56E-02	K14638	SLC15A3_4, PHT; solute carrier family 15 (peptide/histidine transporter), member 3/4
scaffold3542	1.554	4.34E-02		
C402264	1.556	4.09E-02		

scaffold15680	1.562	4.53E-04		
C317168	1.563	2.70E-02		
C267297	1.567	2.25E-02		
C284973	1.581	4.91E-02		
C384388	1.581	1.14E-04		
C252813	1.581	1.64E-03		
C172215	1.587	3.67E-02		
C207546	1.589	9.39E-03		
C338281	1.589	3.85E-02		
C347727	1.596	7.46E-03		
C289599	1.598	4.94E-02	K14638	SLC15A3_4, PHT; solute carrier family 15 (peptide/histidine transporter), member 3/4
scaffold16140	1.600	1.38E-04		
C297353	1.606	2.75E-03		
C362800	1.608	4.72E-02	K01537	E3.6.3.8; Ca ²⁺ -transporting ATPase [EC:3.6.3.8]
C379596	1.620	1.09E-02		
C354071	1.630	1.19E-02	K22285	OSBPL8, ORP8; oxysterol-binding protein-related protein 8
scaffold1654	1.636	1.37E-02		
C348729	1.638	1.35E-02		
scaffold3264	1.642	1.57E-03	K20659	LUS; lupeol synthase [EC:5.4.99.41]
scaffold17358	1.643	4.72E-02	K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family
scaffold17783	1.658	2.45E-02	K21480	HO, pbsA1, hmuO; heme oxygenase (biliverdin-producing, ferredoxin) [EC:1.14.15.20]
scaffold12122	1.662	5.11E-04	K00815	TAT; tyrosine aminotransferase [EC:2.6.1.5]
C292107	1.662	1.96E-02		
C394022	1.668	3.28E-02	K08235	E2.4.1.207; xyloglucan:xyloglucosyl transferase [EC:2.4.1.207]
C340659	1.668	1.77E-02		
C293283	1.670	3.03E-02		
C337853	1.680	9.78E-03		

C338961	1.681	2.91E-02	K08241	E2.1.1.141; jasmonate O-methyltransferase [EC:2.1.1.141]
scaffold778	1.683	6.28E-03		
scaffold6463	1.684	2.68E-02		
C38565	1.686	2.54E-02		
scaffold391	1.691	3.89E-02		
scaffold28	1.692	1.05E-02		
C374730	1.699	2.50E-02	K05387	GRIP; glutamate receptor, ionotropic, plant
C322028	1.701	4.53E-04		
scaffold365	1.703	4.72E-02		
C362752	1.703	2.95E-02		
C296111	1.704	4.18E-02		
scaffold19107	1.705	7.31E-03	K09286	EREBP; EREBP-like factor
scaffold6290	1.708	1.75E-04		
C335031	1.712	2.85E-02		
C83582	1.713	4.99E-02	K15397	KCS; 3-ketoacyl-CoA synthase [EC:2.3.1.199]
				TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE
scaffold13835	1.732	4.34E-02	K03327	family
C360316	1.735	2.87E-02		
scaffold15963	1.744	3.71E-02		
C387596	1.758	7.17E-03		
C90292	1.764	1.80E-02		
				SLC15A3_4, PHT; solute carrier family 15 (peptide/histidine transporter),
scaffold6625	1.766	4.51E-02	K14638	member 3/4
scaffold613	1.775	5.00E-02		
C384894	1.776	2.98E-02		
scaffold17625	1.777	1.14E-02		
scaffold18516	1.780	8.93E-03	K04733	IRAK4; interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]
C227106	1.783	1.78E-02		
C185411	1.783	4.05E-02		

C84452	1.785	3.83E-02	K20667	CYP716A; beta-amyrin 28-monooxygenase [EC:1.14.13.201]
C388386	1.789	3.77E-02	K18980	EO, FaQR; 2-methylene-furan-3-one reductase [EC:1.3.1.105]
C394770	1.790	3.25E-02	K05387	GRIP; glutamate receptor, ionotropic, plant
scaffold17394	1.795	2.60E-02		
C290329	1.808	1.73E-02		
C336693	1.808	2.73E-02		
C316460	1.809	2.85E-02	K14638	SLC15A3_4, PHT; solute carrier family 15 (peptide/histidine transporter), member 3/4
C247567	1.811	4.29E-03		
scaffold7794	1.823	6.52E-03		
C322856	1.828	3.71E-02		
C269201	1.833	4.62E-02	K14638	SLC15A3_4, PHT; solute carrier family 15 (peptide/histidine transporter), member 3/4
C298756	1.844	1.20E-02		
C224004	1.851	2.71E-02	K01057	PGLS, pgl, devB; 6-phosphogluconolactonase [EC:3.1.1.31]
C245003	1.853	1.81E-02	K17991	PXG; peroxygenase [EC:1.11.2.3]
C265805	1.853	3.36E-02		
C320990	1.877	1.59E-02		
scaffold15723	1.880	2.49E-02		
C378662	1.891	2.99E-02		
scaffold16189	1.892	1.90E-02	K10418	DYNLL; dynein light chain LC8-type
C302960	1.897	4.89E-02		
scaffold8348	1.897	2.07E-02		
scaffold10503	1.899	2.36E-02		
C303186	1.900	1.18E-02		
scaffold12445	1.903	9.99E-03		
scaffold10143	1.908	4.99E-02		
C255159	1.913	1.55E-02		
C358967	1.918	4.28E-02		

scaffold13944	1.922	2.79E-02	K17506	PPM1L, PP2CE; protein phosphatase 1L [EC:3.1.3.16]
C254863	1.928	3.42E-02		
C402336	1.930	4.23E-02		
C378380	1.934	4.23E-03		
C346451	1.938	2.58E-02		
C376796	1.939	7.60E-03		
scaffold6233	1.939	3.81E-02	K02328	POLD2; DNA polymerase delta subunit 2
C363708	1.950	4.23E-03		
scaffold18108	1.953	2.60E-02		
C38937	1.958	4.13E-02		
C256245	1.958	2.79E-02		
C363942	1.966	4.67E-02		
scaffold6458	1.977	9.39E-03		
scaffold3262	1.978	1.84E-04	K20659	LUS; lupeol synthase [EC:5.4.99.41]
C381356	1.979	2.72E-03	K00799	GST, gst; glutathione S-transferase [EC:2.5.1.18]
C392932	1.980	4.43E-03	K19041	RNF38_44; E3 ubiquitin-protein ligase RNF38/44 [EC:2.3.2.27]
C86512	1.982	3.21E-02		
scaffold10409	1.984	5.03E-05		
scaffold12240	1.990	1.43E-03	K21373	UGT8, UGT709C2; 7-deoxyloganetic acid glucosyltransferase [EC:2.4.1.323]
C292055	1.992	1.95E-02		
scaffold13768	1.998	2.98E-02	K17302	COPB2, SEC27; coatomer subunit beta'
C345111	1.999	4.90E-02		
C311911	1.999	2.02E-02	K07456	mutS2; DNA mismatch repair protein MutS2
C371922	2.003	4.17E-02	K19042	BOI; E3 ubiquitin-protein ligase BOI and related proteins [EC:2.3.2.27]
scaffold8647	2.012	1.36E-02	K04733	IRAK4; interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]
scaffold18859	2.022	8.08E-03	K22374	DMAS1; 3''-deamino-3''-oxonicotianamine reductase [EC:1.1.1.285]
C226104	2.029	3.12E-02		
C323232	2.032	4.75E-02		

C384478	2.032	2.90E-04		
C179661	2.033	7.14E-03		
C239887	2.033	5.96E-03		
C125124	2.035	1.27E-02		
C402378	2.045	2.36E-02	K09422	mybP; transcription factor myb, plant
C350893	2.046	4.04E-02		
C364420	2.048	2.02E-02		
C226900	2.050	3.21E-02		
C390106	2.051	1.07E-02		
C78214	2.051	4.34E-02	K05933	E1.14.17.4; aminocyclopropanecarboxylate oxidase [EC:1.14.17.4]
C101570	2.054	3.23E-02		
C179703	2.057	3.31E-02		
C135835	2.060	2.55E-03		
scaffold14411	2.062	6.36E-03	K07198	PRKAA, AMPK; 5'-AMP-activated protein kinase, catalytic alpha subunit [EC:2.7.11.11]
C268619	2.065	2.51E-04		
scaffold17409	2.072	3.09E-04		
scaffold9573	2.073	1.94E-03		
C215568	2.075	4.64E-02		
scaffold13517	2.077	3.56E-03		
scaffold12080	2.078	1.62E-03	K07408	CYP1A1; cytochrome P450 family 1 subfamily A polypeptide 1 [EC:1.14.14.1]
C392158	2.090	1.63E-05		
scaffold5952	2.094	1.16E-02		
C332715	2.101	9.50E-03		
scaffold9839	2.101	3.38E-02		
C385868	2.101	2.72E-03	K08235	E2.4.1.207; xyloglucan:xyloglucosyl transferase [EC:2.4.1.207]
C388278	2.102	3.14E-04		
C276671	2.104	4.74E-03		

C333381	2.114	1.44E-06		
C358913	2.115	4.52E-04	K03676	grxC, GLRX, GLRX2; glutaredoxin 3
C359271	2.120	3.28E-02		
scaffold13080	2.123	3.45E-02		
C386382	2.128	4.59E-02	K07088	K07088; uncharacterized protein
C273699	2.131	3.25E-02		
C325287	2.141	3.74E-04		
C306138	2.141	3.56E-03		
C235144	2.148	2.03E-03		
C375438	2.149	4.23E-03		
scaffold8777	2.149	3.68E-02	K13448	CML; calcium-binding protein CML
C283393	2.151	7.64E-04		
C244165	2.160	7.84E-03		
C95752	2.162	4.82E-02		
C332499	2.166	1.35E-02	K16298	SCPL-IV; serine carboxypeptidase-like clade IV [EC:3.4.16.-]
scaffold1284	2.169	5.72E-05		
C191197	2.171	9.78E-03		
C274689	2.180	3.74E-03		
scaffold13542	2.181	2.30E-02		
C300388	2.183	3.93E-02		
C383092	2.185	4.37E-03	K14504	TCH4; xyloglucan:xyloglucosyl transferase TCH4 [EC:2.4.1.207]
C273275	2.185	2.20E-02		
C376716	2.203	8.69E-03		
scaffold1080	2.204	1.26E-02		
scaffold13691	2.211	5.08E-05	K21371	UGT75L6, UGTCS2; crocetin glucosyltransferase [EC:2.4.1.271]
C375036	2.211	4.41E-02		
C398456	2.213	2.37E-02	K07198	PRKAA, AMPK; 5'-AMP-activated protein kinase, catalytic alpha subunit [EC:2.7.11.11]

scaffold5632	2.224	2.03E-03	K08145	SLC2A8, GLUT8; MFS transporter, SP family, solute carrier family 2 (facilitated glucose transporter), member 8
scaffold18670	2.228	2.24E-03		
C350045	2.232	2.87E-02		
scaffold16286	2.236	3.31E-05		
scaffold14987	2.238	1.78E-02		
C269155	2.246	2.47E-02		
scaffold12607	2.248	1.75E-02		
C227896	2.250	1.85E-02		
scaffold11310	2.253	2.31E-02		
C95896	2.254	3.67E-02		
C378518	2.267	1.48E-03		
scaffold10654	2.268	9.86E-04		
C57652	2.273	1.99E-02		
scaffold7383	2.288	1.48E-06		
scaffold18908	2.316	1.65E-02		
C404388	2.323	1.41E-04		
scaffold12909	2.333	1.55E-02		
C322910	2.333	2.85E-02		
C293259	2.343	1.96E-02		
C354505	2.344	4.42E-02		
C176913	2.347	2.12E-02		
C283881	2.349	2.61E-02		
C265891	2.356	2.66E-02		
C86048	2.358	3.47E-02		
C306496	2.358	5.40E-04		
C357195	2.367	3.38E-02		
C294849	2.370	2.05E-02		
C341987	2.372	2.94E-05		

C154861	2.392	3.91E-02		
C297883	2.393	1.55E-02		
scaffold16951	2.398	6.97E-04		
C360020	2.404	5.74E-04		
C245531	2.415	1.56E-03		
scaffold10118	2.418	4.56E-02		
C347921	2.419	9.67E-04	K01850	E5.4.99.5; chorismate mutase [EC:5.4.99.5]
scaffold7806	2.421	1.36E-02		
C224584	2.422	4.12E-03		
C327871	2.427	2.46E-03		
C253275	2.430	3.21E-02		
scaffold5631	2.431	4.76E-03	K08145	SLC2A8, GLUT8; MFS transporter, SP family, solute carrier family 2 (facilitated glucose transporter), member 8
C390852	2.434	7.40E-06		
scaffold4238	2.434	3.82E-06		
C358609	2.444	2.04E-02		
C297687	2.447	3.51E-02		
C383950	2.458	8.94E-04		
scaffold19555	2.459	9.89E-03	K20667	CYP716A; beta-amyrin 28-monooxygenase [EC:1.14.13.201]
C282849	2.464	1.51E-02		
C330973	2.470	3.83E-02		
scaffold7382	2.472	2.22E-06		
C334731	2.477	2.30E-02	K22312	ST2A, SOT15; hydroxyjasmonate sulfotransferase [EC:2.8.2.39]
C372548	2.480	2.54E-02		
C90654	2.485	3.00E-02		
scaffold15386	2.487	1.03E-08	K20617	CYP71A; cytochrome P450 family 71 subfamily A
scaffold9378	2.495	6.63E-03		
C247389	2.502	1.86E-02		
C127760	2.503	6.46E-03		

scaffold9308	2.506	1.44E-06		
scaffold2826	2.511	6.34E-03		
scaffold7432	2.513	1.90E-02		
scaffold811	2.518	3.77E-02		
scaffold8056	2.519	3.68E-03		
C371744	2.519	1.56E-03		
C404052	2.525	3.84E-14		
C244959	2.526	4.65E-02		
C373778	2.529	4.92E-03	K03021	RPC2, POLR3B; DNA-directed RNA polymerase III subunit RPC2 [EC:2.7.7.6]
scaffold18673	2.532	1.94E-03		
scaffold2413	2.536	7.53E-03		
scaffold6889	2.537	2.22E-03		
scaffold1857	2.543	3.18E-02		
C219526	2.546	4.33E-03		
C41463	2.561	2.63E-03	K00789	metK; S-adenosylmethionine synthetase [EC:2.5.1.6]
C278493	2.561	2.28E-02		
scaffold9100	2.563	1.03E-03		
C367286	2.566	3.11E-02		
C296105	2.574	6.34E-03		
scaffold4634	2.576	2.71E-02	K02206	CDK2; cyclin-dependent kinase 2 [EC:2.7.11.22]
C184053	2.590	2.58E-02		
C342983	2.596	1.07E-03		
scaffold6850	2.638	3.83E-02		
C80348	2.646	4.29E-02		
scaffold253	2.663	4.29E-03		
C269577	2.672	3.20E-02		
C318052	2.676	3.18E-02		
C393342	2.677	3.12E-22		

C325183	2.682	2.54E-03		
scaffold16406	2.683	1.26E-02		
C334829	2.685	1.44E-02		
scaffold3664	2.690	1.80E-03		
scaffold2412	2.691	7.88E-03		
C104046	2.707	1.95E-02	K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family
C280115	2.725	8.48E-04		
C177729	2.731	1.26E-02		
C86346	2.751	4.84E-02		
C330499	2.753	1.41E-02		
C356571	2.757	1.02E-02		
C242079	2.758	7.88E-03		
C288005	2.758	1.83E-03	K03671	trxA; thioredoxin 1
C303134	2.760	1.51E-02		
C371730	2.772	1.21E-02	K09422	mybP; transcription factor myb, plant
scaffold9929	2.776	2.76E-02		
C399052	2.777	4.77E-05	K01051	E3.1.1.11; pectinesterase [EC:3.1.1.11]
C254399	2.798	1.07E-03	K00279	CKX; cytokinin dehydrogenase [EC:1.5.99.12]
scaffold5550	2.800	1.39E-02		
C305198	2.806	8.44E-08	K13260	CYP81E1_7; isoflavone/4'-methoxyisoflavone 2'-hydroxylase [EC:1.14.13.89 1.14.13.53]
scaffold11606	2.818	3.40E-02		
C306800	2.826	2.84E-02		
C131846	2.829	1.15E-02	K05663	ABC.ATM; mitochondrial ABC transporter ATM
C217788	2.834	4.57E-02		
C292961	2.850	1.69E-02	K04123	KAO; ent-kaurenoic acid hydroxylase [EC:1.14.13.79]
scaffold16053	2.850	1.07E-03		
C231307	2.858	7.14E-03		

C120590	2.862	3.67E-02		
C279615	2.872	9.39E-03		
C130734	2.873	4.92E-03		
C364096	2.879	4.72E-02		
C291849	2.905	3.71E-02		
C380410	2.922	2.82E-06	K13260	CYP81E1_7; isoflavone/4'-methoxyisoflavone 2'-hydroxylase [EC:1.14.13.89 1.14.13.53]
C334665	2.923	1.54E-04		
C328617	2.923	8.47E-03		
C334853	2.933	2.79E-06		
C277069	2.934	2.37E-02		
C274955	2.938	1.63E-02		
C318506	2.939	1.58E-02		
C370518	2.941	6.18E-03		
C66318	2.947	1.59E-03	K20617	CYP71A; cytochrome P450 family 71 subfamily A
C270653	2.961	2.54E-02		
C381020	2.967	2.87E-02	K11886	ECM29; proteasome component ECM29
scaffold18463	2.999	3.68E-02	K09338	HD-ZIP; homeobox-leucine zipper protein
C257641	3.014	3.61E-03		
C301508	3.016	2.02E-02		
C286921	3.024	1.55E-02		
scaffold10251	3.037	1.12E-03		
C335133	3.045	3.80E-03		
C350407	3.060	1.28E-07		
C306050	3.065	7.40E-04		
C330063	3.103	2.59E-02		
C358419	3.112	2.04E-02		
C394142	3.116	1.18E-02		
scaffold12214	3.124	2.54E-03		

C365390	3.137	3.38E-04	K00279	CKX; cytokinin dehydrogenase [EC:1.5.99.12]
scaffold18799	3.151	2.58E-02	K07889	RAB5C; Ras-related protein Rab-5C
C266583	3.151	4.83E-02		
C129892	3.152	2.95E-02		
scaffold225	3.164	9.78E-03		
C352279	3.169	2.05E-14	K17422	MRPL41; large subunit ribosomal protein L41
C196073	3.184	1.94E-02		
C323182	3.205	5.81E-03		
C380088	3.210	2.65E-03		
C193877	3.225	1.94E-02		
C248291	3.272	8.03E-03		
C81812	3.274	7.31E-03		
C342287	3.276	8.13E-05	K03671	trxA; thioredoxin 1
scaffold8982	3.290	4.92E-03		
C380996	3.291	1.26E-02	K10355	ACTF; actin, other eukaryote
C57840	3.297	4.76E-03		
C262435	3.305	4.73E-04	K00512	CYP17A; steroid 17alpha-monooxygenase / 17alpha-hydroxyprogesterone deacetylase [EC:1.14.14.19 1.14.14.32]
C350159	3.306	2.06E-07		
C401898	3.341	1.01E-02		
C215790	3.350	7.14E-04		
C217130	3.358	3.57E-03	K00512	CYP17A; steroid 17alpha-monooxygenase / 17alpha-hydroxyprogesterone deacetylase [EC:1.14.14.19 1.14.14.32]
C254015	3.381	2.30E-03	K09841	ABA2; xanthoxin dehydrogenase [EC:1.1.1.288]
C267779	3.391	8.32E-05		
C201094	3.391	2.17E-04		
C50778	3.409	1.03E-02		
C368562	3.415	1.86E-02		
scaffold16243	3.438	2.98E-02		

C310453	3.458	1.02E-03		
C255095	3.542	2.07E-03		
C233935	3.595	7.76E-04		
C213388	3.601	1.41E-02		
scaffold8956	3.735	1.08E-05	K13459	RPS2; disease resistance protein RPS2
C208238	3.765	6.28E-03		
C319948	3.808	7.32E-04		
scaffold3586	3.818	1.40E-02		
scaffold15460	3.846	1.38E-04		
C229026	3.869	4.97E-03		
C336619	3.869	3.60E-03		
C267067	3.881	2.29E-08		
scaffold10602	3.900	2.45E-02		
C80574	3.901	5.43E-03		
C289157	3.926	4.86E-02		
C39919	3.933	1.12E-03		
C90652	3.942	1.26E-03		
C246257	3.978	9.91E-03		
C104860	4.066	1.25E-07		
scaffold13377	4.093	3.37E-02	K02900	RP-L27Ae, RPL27A; large subunit ribosomal protein L27Ae
C91260	4.119	1.94E-03		
C360374	4.126	3.59E-04		
C125620	4.220	3.31E-02		
C370660	4.254	9.92E-08	K01051	E3.1.1.11; pectinesterase [EC:3.1.1.11]
scaffold4691	4.321	7.17E-03	K00574	cfa; cyclopropane-fatty-acyl-phospholipid synthase [EC:2.1.1.79]
scaffold9679	4.353	8.77E-06		
C327389	4.377	1.42E-03		
C258059	4.398	3.23E-02		
C330741	4.500	4.66E-03		

scaffold8721	4.534	2.70E-02	K14638	SLC15A3_4, PHT; solute carrier family 15 (peptide/histidine transporter), member 3/4
scaffold10595	4.615	2.58E-02	K10355	ACTF; actin, other eukaryote
C74980	4.624	3.10E-04		
scaffold885	4.744	6.98E-03	K14826	FPR3_4; FK506-binding nuclear protein [EC:5.2.1.8]
C270645	4.772	5.43E-05		
scaffold14813	4.810	2.51E-04	K03252	EIF3C; translation initiation factor 3 subunit C
scaffold9319	4.814	3.41E-02		
scaffold19380	4.815	7.53E-03	K03517	nadA; quinolinate synthase [EC:2.5.1.72]
scaffold1318	4.819	2.46E-03		
C247391	4.851	2.36E-05		
C246665	4.888	7.39E-04		
C341817	5.032	3.85E-05		
C95510	5.320	6.18E-04		
C37807	5.338	7.40E-06		
C278711	5.545	2.98E-06		
scaffold5104	5.640	3.10E-04		
C106174	5.678	1.95E-03		
C382590	6.506	1.38E-04		
scaffold12078	6.703	8.13E-05		
scaffold11050	7.611	8.99E-07		

- 31 **Supplementary Table T6.** Differentially expressed genes (DEGs) identified between light green- and pink-bracted cultivars of C.
- 32 kousa. Includes transcript ID, log2 fold change, adjusted p-value, KEGG ortholog, and functional annotation.

Transcript name	log2FC	adjusted p-value	Kegg Ortholog	KO description
C443453	3.855	7.51E-36		
scaffold25379	2.943	1.79E-23		
scaffold10279	3.640	7.89E-20		
C484525	2.780	3.85E-15		
C270113	4.875	5.09E-15		
scaffold32662	4.078	2.20E-12	K21374	UGT85A; 7-deoxyloganetin glucosyltransferase [EC:2.4.1.324]
C180903	3.600	6.18E-12		
C453903	4.931	4.08E-11		
scaffold11880	3.256	1.49E-10		
scaffold28451	2.561	3.46E-10	K13459	RPS2; disease resistance protein RPS2
scaffold20310	2.174	1.94E-09		
scaffold23476	-4.093	2.41E-09	K22312	ST2A, SOT15; hydroxyjasmonate sulfotransferase [EC:2.8.2.39]
C497564	1.413	8.10E-09		
C521740	2.915	5.15E-08		
C481975	-4.318	5.69E-08		
scaffold27004	2.302	5.69E-08	K04730	IRAK1; interleukin-1 receptor-associated kinase 1 [EC:2.7.11.1]
scaffold11042	2.723	7.43E-08		
C249735	4.879	1.11E-07		
C534679	3.745	2.41E-07		
C385357	-3.260	2.70E-07		
scaffold24832	2.127	2.70E-07		
scaffold26008	3.538	6.32E-07		
scaffold23617	3.246	1.11E-06	K01051	E3.1.1.11; pectinesterase [EC:3.1.1.11]
scaffold25834	-5.539	1.17E-06	K01728	pel; pectate lyase [EC:4.2.2.2]

scaffold8368	2.600	1.17E-06		
C520076	3.008	1.30E-06		
scaffold21461	4.900	1.90E-06		
scaffold8041	3.024	2.18E-06	K13459	RPS2; disease resistance protein RPS2
scaffold31191	2.429	2.28E-06		
C549533	-2.565	2.44E-06		
C486101	3.576	3.11E-06	K01051	E3.1.1.11; pectinesterase [EC:3.1.1.11]
scaffold3826	-2.003	4.30E-06		
scaffold1122	-1.731	5.33E-06	K01191	MAN2C1; alpha-mannosidase [EC:3.2.1.24]
C496107	2.347	7.59E-06		
scaffold15458	7.494	7.59E-06		
C530830	4.750	9.90E-06		
C487197	2.447	1.10E-05		
C516512	2.135	1.11E-05		
C521508	-1.178	1.11E-05		
C493350	4.505	1.75E-05		
C527738	4.785	1.75E-05		
scaffold10278	2.534	1.75E-05		
C552077	-2.323	1.92E-05		
C495176	2.329	2.16E-05		
scaffold31254	-1.442	2.17E-05	K08900	BCS1; mitochondrial chaperone BCS1
scaffold27241	2.828	2.81E-05		
scaffold22303	-3.212	3.08E-05		
C124798	-4.170	3.19E-05		
scaffold31104	2.073	3.21E-05	K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family
C359588	2.929	3.21E-05	K13459	RPS2; disease resistance protein RPS2
C459181	3.372	3.34E-05		
scaffold14896	1.333	3.34E-05		

C319351	-2.996	3.53E-05		
scaffold25189	5.183	3.95E-05		
C94452	5.261	4.70E-05	K07203	MTOR, FRAP, TOR; serine/threonine-protein kinase mTOR [EC:2.7.11.1]
scaffold25789	-2.220	4.70E-05	K02132	ATPeF1A, ATP5A1, ATP1; F-type H ⁺ -transporting ATPase subunit alpha
scaffold25905	1.919	4.70E-05	K01858	INO1, ISYNA1; myo-inositol-1-phosphate synthase [EC:5.5.1.4]
C440684	3.018	5.07E-05		
C534949	8.394	5.07E-05	K15382	SLC50A, SWEET; solute carrier family 50 (sugar transporter)
C504763	2.527	5.08E-05		
C422161	3.445	5.23E-05		
C479392	-1.386	5.23E-05		
scaffold4308	1.125	5.23E-05		
C473266	2.122	5.64E-05		
scaffold11117	2.034	5.92E-05	K08332	VAC8; vacuolar protein 8
C142138	3.100	6.05E-05		
C511336	3.326	6.29E-05		
scaffold1121	-1.988	7.23E-05	K01191	MAN2C1; alpha-mannosidase [EC:3.2.1.24]
scaffold6451	5.087	7.23E-05		
C354193	-3.144	7.30E-05		
C288227	3.435	7.66E-05		
scaffold24254	3.939	7.66E-05	K03671	trxA; thioredoxin 1
scaffold31613	-2.448	8.78E-05	K01859	E5.5.1.6; chalcone isomerase [EC:5.5.1.6]
C460717	2.460	9.15E-05	K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family
C516402	2.165	9.33E-05	K03676	grxC, GLRX, GLRX2; glutaredoxin 3
C549761	4.932	9.33E-05		
scaffold2649	2.884	9.33E-05	K13457	RPM1, RPS3; disease resistance protein RPM1
scaffold8668	3.739	9.68E-05		
C368630	3.039	9.88E-05		

C412352	3.258	9.88E-05		
C531410	2.384	9.88E-05		
C503769	2.842	1.00E-04	K13457	RPM1, RPS3; disease resistance protein RPM1
scaffold1071	-1.717	1.03E-04	K02183	CALM; calmodulin
scaffold31892	2.069	1.09E-04		
C183346	3.131	1.19E-04		
C539465	3.324	1.19E-04		
scaffold13407	2.245	1.24E-04		
scaffold8569	1.707	1.24E-04		
scaffold20563	4.525	1.41E-04	K02961	RP-S17, MRPS17, rpsQ; small subunit ribosomal protein S17
scaffold658	1.908	1.41E-04		
C103099	3.622	1.52E-04		
C181857	-2.918	1.52E-04		
scaffold15100	3.978	1.52E-04		
scaffold21420	-1.587	1.56E-04		
scaffold3071	1.472	1.56E-04		
scaffold19308	-3.124	1.63E-04	K09422	MYBP; transcription factor MYB, plant
scaffold27702	1.752	1.63E-04		
scaffold18267	1.365	1.97E-04		
C527836	4.401	1.97E-04		
C533907	-1.148	2.17E-04		
C538039	2.700	2.17E-04	K01051	E3.1.1.11; pectinesterase [EC:3.1.1.11]
C478804	-2.220	2.21E-04		
scaffold18382	5.203	2.25E-04		
scaffold10631	2.660	2.29E-04		
C510366	3.211	2.38E-04	K03671	trxA; thioredoxin 1
scaffold24823	2.694	2.44E-04		
scaffold2426	1.967	2.79E-04	K13459	RPS2; disease resistance protein RPS2
scaffold15099	3.230	2.82E-04		

C466066	-1.490	2.83E-04		
scaffold22862	2.077	2.83E-04	K20659	LUS; lupeol synthase [EC:5.4.99.41]
C425145	-1.995	2.85E-04	K09874	NIP; aquaporin NIP
scaffold20602	1.923	3.29E-04		
scaffold30834	-1.550	3.40E-04		
scaffold31511	-1.035	3.44E-04	K09753	CCR; cinnamoyl-CoA reductase [EC:1.2.1.44]
scaffold18457	3.527	3.46E-04		
scaffold21684	-1.681	3.46E-04	K00895	pfp, PFP; diphosphate-dependent phosphofructokinase [EC:2.7.1.90]
scaffold27087	2.571	3.72E-04		
scaffold6462	2.507	3.97E-04		
C324631	3.055	4.09E-04		
C449653	-1.535	4.09E-04		
scaffold17309	1.393	4.09E-04	K11816	YUCCA; indole-3-pyruvate monooxygenase [EC:1.14.13.168]
scaffold31791	1.305	4.28E-04		
scaffold23616	4.067	4.40E-04	K01051	E3.1.1.11; pectinesterase [EC:3.1.1.11]
C170819	2.795	4.52E-04		
C353027	-4.729	4.52E-04	K11254	H4; histone H4
C509786	4.047	4.52E-04		
C540369	3.048	4.58E-04		
scaffold13622	1.292	4.65E-04	K19042	BOI; E3 ubiquitin-protein ligase BOI and related proteins [EC:2.3.2.27]
C398645	-4.388	4.66E-04		
C281751	-1.575	4.71E-04	K01051	E3.1.1.11; pectinesterase [EC:3.1.1.11]
scaffold27630	2.316	4.90E-04	K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family
scaffold14506	-2.822	5.12E-04		
C482017	-2.790	5.15E-04		
scaffold4777	-3.286	5.15E-04		
C506219	-2.342	5.32E-04		
scaffold11914	2.414	5.32E-04		

scaffold20030	2.151	5.36E-04		
C433996	2.577	5.38E-04		
C412176	2.755	5.45E-04		
C521516	-1.504	5.46E-04		
C536067	2.917	5.46E-04	K15639	CYP734A1, BAS1; PHYB activation tagged suppressor 1 [EC:1.14.-.-]
C464312	3.506	5.63E-04	K16292	CEP, CYSEP; KDEL-tailed cysteine endopeptidase [EC:3.4.22.-]
C415131	-2.418	5.71E-04	K15925	XYL1; alpha-D-xyloside xylohydrolase [EC:3.2.1.177]
C459905	-1.378	5.72E-04		
C372236	-3.000	5.93E-04		
C532946	1.806	5.96E-04		
scaffold18582	1.702	5.96E-04	K08235	E2.4.1.207; xyloglucan:xyloglucosyl transferase [EC:2.4.1.207]
C129027	2.783	6.16E-04		
C290059	-2.354	6.16E-04		
C502625	3.289	6.16E-04		
scaffold2425	2.406	6.16E-04	K13459	RPS2; disease resistance protein RPS2
scaffold24443	3.962	6.16E-04	K01568	PDC, pdc; pyruvate decarboxylase [EC:4.1.1.1]
scaffold31596	2.346	6.20E-04		
scaffold6402	2.709	6.20E-04		
C527754	-2.172	6.28E-04		
C543305	-1.482	6.28E-04	K01051	E3.1.1.11; pectinesterase [EC:3.1.1.11]
scaffold14192	1.478	6.28E-04		
scaffold22460	-1.549	6.28E-04		
scaffold3710	-1.485	6.28E-04		
scaffold6929	3.363	6.47E-04		
C486095	2.515	6.60E-04		
scaffold12492	1.138	6.60E-04	K13525	VCP, CDC48; transitional endoplasmic reticulum ATPase
scaffold28227	-4.479	6.60E-04	K09264	K09264; MADS-box transcription factor, plant
C503557	1.723	6.75E-04		
C434474	-4.757	6.97E-04	K04733	IRAK4; interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]

scaffold10503	4.050	7.07E-04		
scaffold3611	-1.138	7.07E-04		
scaffold23474	2.919	7.62E-04	K00512	CYP17A; steroid 17alpha-monooxygenase / 17alpha-hydroxyprogesterone deacetylase [EC:1.14.14.19 1.14.14.32]
C500853	2.992	7.80E-04		
scaffold18149	-2.028	8.12E-04	K00588	E2.1.1.104; caffeoyl-CoA O-methyltransferase [EC:2.1.1.104]
scaffold24271	2.481	8.16E-04	K02146	ATPeV0D, ATP6D; V-type H ⁺ transporting ATPase subunit d
scaffold11041	1.932	8.35E-04		
scaffold23254	1.580	8.70E-04	K13420	FLS2; LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]
C416041	1.671	8.73E-04		
C513926	-1.649	9.03E-04		
C129291	-4.696	9.06E-04		
scaffold18406	1.750	9.06E-04		
C536603	-1.431	9.25E-04	K19042	BOI; E3 ubiquitin-protein ligase BOI and related proteins [EC:2.3.2.27]
C549603	1.490	9.33E-04	K21371	UGT75L6, UGTCS2; crocetin glucosyltransferase [EC:2.4.1.271]
C486201	-2.236	9.47E-04		
scaffold14797	-0.994	9.96E-04		
scaffold29318	-2.308	0.001018257		
C407494	-1.693	0.001042814	K01061	E3.1.1.45; carboxymethylenebutenolidase [EC:3.1.1.45]
C524048	-2.116	0.001042814		
C550937	-0.995	0.001042814		
scaffold20449	1.322	0.001042814	K05643	ABCA3; ATP-binding cassette, subfamily A (ABC1), member 3
C428111	-4.942	0.001067917	K01728	pel; pectate lyase [EC:4.2.2.2]
C492633	-1.237	0.001087085		
scaffold18681	3.898	0.001087085	K07428	CYP4X; cytochrome P450 family 4 subfamily X [EC:1.14.14.1]
scaffold27959	-1.500	0.001098048	K15015	SLC32A, VGAT; solute carrier family 32 (vesicular inhibitory amino acid transporter)
C532026	-1.448	0.001127092		
scaffold32349	-1.872	0.001147337	K08057	CALR; calreticulin

C538767	1.415	0.001148965	K10755	RFC2_4; replication factor C subunit 2/4
C486655	2.324	0.00120279		
C529272	-0.985	0.00120279		
scaffold13405	-1.364	0.00120279	K04712	DEGS; sphingolipid 4-desaturase/C4-monooxygenase [EC:1.14.19.17 1.14.18.5]
scaffold14594	-0.521	0.001204093		
C502279	-1.757	0.001228825		
C521406	3.692	0.001239543		
scaffold21835	2.612	0.001239543		
scaffold23318	3.264	0.001239543		
scaffold32122	-1.108	0.001239543		
C452833	-1.557	0.0012564		
scaffold24899	-0.692	0.001266777	K00384	trxB, TRR; thioredoxin reductase (NADPH) [EC:1.8.1.9]
C548593	-0.972	0.001276913		
C489093	3.089	0.001335573		
scaffold22818	-1.400	0.001343309	K21373	UGT8, UGT709C2; 7-deoxyloganetic acid glucosyltransferase [EC:2.4.1.323]
C247504	3.314	0.001357979		
C394739	4.891	0.001357979		
scaffold26290	2.470	0.001378173		
scaffold29159	-1.244	0.001382677		
C352989	-1.520	0.001389213		
scaffold9186	-1.100	0.001389213	K00831	serC, PSAT1; phosphoserine aminotransferase [EC:2.6.1.52]
scaffold1224	2.634	0.001399484		
C328267	3.518	0.001435164	K16292	CEP, CYSEP; KDEL-tailed cysteine endopeptidase [EC:3.4.22.-]
C494848	-1.015	0.00147349	K07466	RFA1, RPA1, rpa; replication factor A1
C393027	3.163	0.001475407		
C448426	5.825	0.001475407		
scaffold10850	1.995	0.001475407	K08145	SLC2A8, GLUT8; MFS transporter, SP family, solute carrier family 2 (facilitated glucose transporter), member 8

C535591	-2.448	0.001492383		
C170817	2.659	0.00150735		
C437286	-2.832	0.00150824	K22312	ST2A, SOT15; hydroxyjasmonate sulfotransferase [EC:2.8.2.39]
C533223	-1.684	0.00150824		
C151900	-1.852	0.001552413		
scaffold18682	3.917	0.001552413	K07428	CYP4X; cytochrome P450 family 4 subfamily X [EC:1.14.14.1]
C268545	-4.061	0.001567001		
C543049	-2.740	0.001589053	K12930	BZ1; anthocyanidin 3-O-glucosyltransferase [EC:2.4.1.115]
scaffold18975	1.335	0.001599714		
C521506	-2.004	0.001643567		
scaffold23022	-0.851	0.001643567	K15285	SLC35E3; solute carrier family 35, member E3
scaffold7498	2.842	0.001661809		
scaffold179	-0.608	0.00168359	K14617	LMBRD1; LMBR1 domain-containing protein 1
C150658	6.278	0.001710074		
C527834	0.806	0.001720264		
scaffold21558	1.523	0.001726714		
C108071	2.861	0.001785313		
C395335	2.945	0.001785805	K14638	SLC15A3_4, PHT; solute carrier family 15 (peptide/histidine transporter), member 3/4
scaffold7397	-0.645	0.001785805		
scaffold27553	1.256	0.001804338		
scaffold4122	2.473	0.001805468		
C451563	2.716	0.001811659	K00279	CKX; cytokinin dehydrogenase [EC:1.5.99.12]
scaffold27360	-0.766	0.001890449	K01247	alkA; DNA-3-methyladenine glycosylase II [EC:3.2.2.21]
scaffold8246	1.953	0.00190383		
C286925	2.634	0.001929369		
C527952	-1.362	0.001977715		
scaffold26687	2.459	0.001991348		
scaffold1255	1.433	0.002025326		

C526924	3.077	0.002039721		
scaffold13238	-1.967	0.002039721	K00588	E2.1.1.104; caffeoyl-CoA O-methyltransferase [EC:2.1.1.104]
scaffold21083	1.762	0.002039721		
scaffold32391	-1.258	0.002039721	K14794	RRP12; ribosomal RNA-processing protein 12
scaffold21577	3.825	0.002043996		
scaffold10909	2.211	0.002117727	K07408	CYP1A1; cytochrome P450 family 1 subfamily A polypeptide 1 [EC:1.14.14.1]
scaffold15928	3.477	0.002122434		
C472930	2.130	0.002161411		
C441311	-1.226	0.002197794		
C172343	3.480	0.002239647		
scaffold32316	2.718	0.002259161		
C442951	3.633	0.00226443		
C449267	2.306	0.00226443		
scaffold19414	2.113	0.00226443		
scaffold431	2.053	0.00226443	K21398	SLC11A2, DMT1, NRAMP2; natural resistance-associated macrophage protein 2
scaffold73	4.272	0.00226443		
C542643	2.178	0.002291063	K18857	ADH1; alcohol dehydrogenase class-P [EC:1.1.1.1]
scaffold13093	2.715	0.002345839		
C196012	2.910	0.002387025		
C511026	-2.208	0.002387025		
scaffold23483	-1.564	0.002387025		
scaffold30049	1.953	0.002387025		
C425837	-1.884	0.002404535		
C547759	-0.682	0.00243222	K03921	FAB2, SSI2, desA1; acyl-[acyl-carrier-protein] desaturase [EC:1.14.19.2 1.14.19.11 1.14.19.26]
C494994	2.502	0.002468334		
scaffold31956	2.207	0.002468334		
scaffold31668	2.394	0.002510482		

scaffold21711	-1.265	0.002544037		
C531728	-3.681	0.002607453		
C542223	-1.541	0.00268686	K00475	E1.14.11.9; naringenin 3-dioxygenase [EC:1.14.11.9]
C386057	-2.024	0.002708349	K10352	MYH; myosin heavy chain
C491839	1.909	0.002708349		
C525586	1.431	0.002708349		
scaffold11852	-2.979	0.002708349		
scaffold23368	2.355	0.002708349		
C447788	3.118	0.002807791		
C511564	-2.184	0.002813043		
scaffold29070	-0.950	0.00283257		
C286295	-2.247	0.002852841	K15403	ACE, HTH; fatty acid omega-hydroxy dehydrogenase [EC:1.1.-.-]
C415343	-2.264	0.002938281		
C496934	2.301	0.002975112	K15639	CYP734A1, BAS1; PHYB activation tagged suppressor 1 [EC:1.14.-.-]
scaffold1452	3.034	0.002975112		
scaffold22015	2.215	0.002975112	K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family
C541893	-1.291	0.003000415		
C121546	-2.058	0.003057605		
C172345	2.649	0.003057605		
C427941	4.716	0.003057605		
C546471	2.186	0.003057605		
scaffold15484	3.382	0.003057605		
scaffold19115	1.681	0.003057605	K22374	DMAS1; 3''-deamino-3''-oxonicotianamine reductase [EC:1.1.1.285]
scaffold30559	-0.777	0.003057605		
scaffold30920	-1.185	0.003093502		
C536085	-1.967	0.003112443	K15925	XYL1; alpha-D-xyloside xylohydrolase [EC:3.2.1.177]
scaffold23924	1.714	0.003112443		
scaffold19118	1.774	0.003136323	K22374	DMAS1; 3''-deamino-3''-oxonicotianamine reductase [EC:1.1.1.285]

scaffold7335	2.889	0.003177411		
scaffold399	-1.379	0.003186184	K14492	ARR-A; two-component response regulator ARR-A family
C527238	-0.991	0.003237292		
scaffold24521	0.900	0.003237292	K12179	COPS6, CSN6; COP9 signalosome complex subunit 6
C532432	-1.106	0.003246952		
scaffold14068	-2.567	0.003246952		
C395381	1.806	0.003252011		
scaffold32499	-1.026	0.003252113	K12462	ARHGDI, RHOGDI; Rho GDP-dissociation inhibitor
C547671	-0.834	0.003412867		
scaffold6334	4.113	0.003455116		
C550181	0.824	0.003586638	K03797	E3.4.21.102, prc, ctpA; carboxyl-terminal processing protease [EC:3.4.21.102]
scaffold27305	-2.372	0.003586638		
C379814	2.977	0.003657197		
C394111	-4.212	0.003657197		
C450279	1.817	0.003657197		
C538501	-1.044	0.003657197	K20843	GALT2S; hydroxyproline O-galactosyltransferase 2/3/4/5/6 [EC:2.4.1.-]
scaffold20914	-1.044	0.003657197		
C487149	1.667	0.003659758		
scaffold31558	1.468	0.003666795		
scaffold11290	3.207	0.003829868		
scaffold25398	-2.645	0.003829868		
C536083	-1.452	0.003835053		
C447150	-2.950	0.003866482		
C469222	2.678	0.003984242		
scaffold9185	-0.923	0.003984242	K00831	serC, PSAT1; phosphoserine aminotransferase [EC:2.6.1.52]
scaffold12614	-1.044	0.004000894		
C172573	-3.936	0.004008187		

scaffold10775	1.958	0.004017068	K07408	CYP1A1; cytochrome P450 family 1 subfamily A polypeptide 1 [EC:1.14.14.1]
scaffold27029	1.970	0.004017068		
scaffold3692	-0.916	0.004017068		
C519056	-0.690	0.004042736		
C552953	-1.301	0.0040943	K09487	HSP90B, TRA1; heat shock protein 90kDa beta
scaffold17647	1.930	0.004110142		
C346012	2.603	0.004119727		
C547733	-0.678	0.004142758	K00627	DLAT, aceF, pdhC; pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]
C544071	-1.250	0.004235689		
scaffold27679	-1.892	0.004235689	K00134	GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]
scaffold2436	1.191	0.004294926		
scaffold25123	1.038	0.004294926	K02083	allC; allantoate deiminase [EC:3.5.3.9]
scaffold13211	2.769	0.004299726		
C400881	3.685	0.004326801		
C86806	-2.301	0.004389516	K00454	LOX2S; lipoxygenase [EC:1.13.11.12]
scaffold7361	-1.284	0.004389516		
C540933	2.093	0.004403271	K04706	PIAS1; E3 SUMO-protein ligase PIAS1
scaffold6637	1.816	0.004403271		
C378970	-2.671	0.004454647	K15403	ACE, HTH; fatty acid omega-hydroxy dehydrogenase [EC:1.1.-.-]
scaffold29338	2.857	0.004454647	K20556	CYP76C; cytochrome P450 family 76 subfamily C
C170141	-4.146	0.00454292		
C180123	-1.932	0.00454292		
C462496	3.344	0.00454292		
C547009	-1.303	0.00454292		
scaffold15276	2.693	0.00454292		
scaffold25400	-0.705	0.00454292		
scaffold10145	-4.861	0.004712008	K00799	GST, gst; glutathione S-transferase [EC:2.5.1.18]

scaffold19600	-1.795	0.004721759		
C492217	3.615	0.004740173		
C497532	3.238	0.004740173		
C318655	3.840	0.004774749		
C541419	2.109	0.004790243		
scaffold797	0.966	0.004798808		
scaffold12200	3.235	0.004811204	K07305	msrB; peptide-methionine (R)-S-oxide reductase [EC:1.8.4.12]
C516946	3.654	0.004817824		
scaffold27237	1.296	0.004835261		
C490631	2.857	0.004909656		
scaffold23239	1.939	0.004909656		
C459663	2.551	0.004956295		
scaffold8699	2.835	0.004956295		
C496768	-2.719	0.005080423		
scaffold17263	-1.053	0.005088598		
C133960	2.823	0.005144856		
C521622	3.922	0.005144856		
C461753	2.106	0.005177235		
scaffold32518	-0.586	0.005177235	K14442	DHX36, RHAU; ATP-dependent RNA helicase DHX36 [EC:3.6.4.13]
C338033	-0.978	0.005182702		
scaffold19457	0.784	0.005207815		
scaffold30154	1.785	0.005229076		
scaffold25383	3.547	0.005243805		
C552193	-1.189	0.005271765		
C505541	1.252	0.005305133	K12486	SMAP; stromal membrane-associated protein AHK2_3_4; arabidopsis histidine kinase 2/3/4 (cytokinin receptor) [EC:2.7.13.3]
C546339	-1.367	0.005342628	K14489	
scaffold20737	1.508	0.005342628	K05663	ABC.ATM; mitochondrial ABC transporter ATM

scaffold21135	-1.008	0.005342628	K15104	SLC25A11, OGC; solute carrier family 25 (mitochondrial oxoglutarate transporter), member 11
C393969	-0.903	0.00534768	K19355	MAN; mannan endo-1,4-beta-mannosidase [EC:3.2.1.78]
C489133	-2.058	0.005367179		
C535277	2.076	0.005367179	K08235	E2.4.1.207; xyloglucan:xyloglucosyl transferase [EC:2.4.1.207]
C551375	-2.199	0.005367179		
C304686	-2.391	0.005418026	K00454	LOX2S; lipoxygenase [EC:1.13.11.12]
C527314	3.957	0.005418026		
scaffold13326	-4.972	0.005418026		
C295012	2.443	0.005451635	K16298	SCPL-IV; serine carboxypeptidase-like clade IV [EC:3.4.16.-]
C330193	-3.717	0.005451635		
C379812	2.609	0.005451635	K00278	nadB; L-aspartate oxidase [EC:1.4.3.16]
C504209	2.573	0.005451635		
C520698	3.846	0.005451635		
C528996	2.512	0.005451635		
C533211	-1.412	0.005451635		
scaffold24475	-1.467	0.005451635	K01465	URA4, pyrC; dihydroorotase [EC:3.5.2.3]
scaffold2977	3.725	0.005451635		
C92254	4.115	0.005504825		
C127037	-2.847	0.005594262		
C409838	2.235	0.005713813		
scaffold32864	2.732	0.005718674		
C397395	2.829	0.005794256		
C489537	-1.527	0.005794256		
C548939	-1.019	0.00583619	K22390	ACP7; acid phosphatase type 7
scaffold10502	1.849	0.00583619	K13459	RPS2; disease resistance protein RPS2
C397373	-3.896	0.005858769		
C547695	1.515	0.005858769		
C553097	1.352	0.005858769	K10534	NR; nitrate reductase (NAD(P)H) [EC:1.7.1.1 1.7.1.2 1.7.1.3]

C533605	2.173	0.005899434	K14504	TCH4; xyloglucan:xyloglucosyl transferase TCH4 [EC:2.4.1.207]
scaffold23614	1.201	0.005938542	K00764	purF, PPAT; amidophosphoribosyltransferase [EC:2.4.2.14]
scaffold2059	3.722	0.006087879		
scaffold3217	1.506	0.006108711		
scaffold10427	3.189	0.006153486		
C509320	1.770	0.006192697		
scaffold17841	3.787	0.006216979		
scaffold20898	2.005	0.00623968		
scaffold27911	-1.939	0.006270825	K08902	psb27; photosystem II Psb27 protein
C415841	-1.862	0.006279213		
scaffold27285	1.749	0.006279213		
C455813	-1.513	0.006300429		
scaffold30672	-1.666	0.006319352	K14484	IAA; auxin-responsive protein IAA
scaffold10788	-1.724	0.006347024		
scaffold13923	1.603	0.006347024		
scaffold21355	-1.090	0.006347024	K02699	psaL; photosystem I subunit XI
scaffold30688	-1.252	0.006354635		
C530656	2.554	0.006357849		
C514160	3.408	0.00644262		
C551339	0.647	0.00644745	K00878	thiM; hydroxyethylthiazole kinase [EC:2.7.1.50]
C467558	1.682	0.006486335		
scaffold4788	-1.179	0.006486335	K17292	TBCA; tubulin-specific chaperone A
C370262	2.278	0.006492373		
C528030	1.197	0.006492373		
C538887	-1.064	0.006492373		
scaffold10860	-0.964	0.006492373	K01507	ppa; inorganic pyrophosphatase [EC:3.6.1.1]
C453091	-2.939	0.006502401		
scaffold12230	2.962	0.006507805	K01673	cynT, can; carbonic anhydrase [EC:4.2.1.1]
scaffold11835	-0.802	0.006561684		

C342446	-2.590	0.006585369		
scaffold29210	-0.720	0.006585369	K15283	SLC35E1; solute carrier family 35, member E1
C541985	1.280	0.006613732		
scaffold10080	1.779	0.006613732	K21371	UGT75L6, UGTcs2; crocetin glucosyltransferase [EC:2.4.1.271]
scaffold20152	2.357	0.006613732	K00799	GST, gst; glutathione S-transferase [EC:2.5.1.18]
scaffold28978	-0.919	0.006613732		
scaffold30641	-1.142	0.006613732	K14753	RACK1; guanine nucleotide-binding protein subunit beta-2-like 1 protein
scaffold9780	1.140	0.006734059		
scaffold24963	5.229	0.006807819		
scaffold8185	-2.442	0.007000872		
C468990	-1.399	0.007003143	K02938	RP-L8e, RPL8; large subunit ribosomal protein L8e
scaffold31464	3.286	0.007004897		
C265747	1.847	0.007164822		
C510354	1.004	0.007164822		
C530016	4.850	0.007164822	K13457	RPM1, RPS3; disease resistance protein RPM1
scaffold22725	1.705	0.007164822		
C459011	-3.232	0.007359795	K11251	H2A; histone H2A
scaffold18491	-1.587	0.007359795		
scaffold8663	-2.281	0.007359795		
C449511	2.820	0.00744109		
scaffold23680	-0.734	0.007476748	K03262	EIF5; translation initiation factor 5
scaffold27162	-1.295	0.00750408		
C546561	-0.835	0.007604908		
scaffold10989	4.234	0.00763442		
C533715	-1.146	0.007634658		
scaffold32281	-1.655	0.007634658		
C337407	-3.126	0.007708824		
C445680	-3.293	0.007708824		

scaffold6974	2.008	0.007708824		
scaffold17700	1.955	0.007719946		
scaffold25324	1.946	0.007721512		
scaffold29316	-1.906	0.007721512	K15403	ACE, HTH; fatty acid omega-hydroxy dehydrogenase [EC:1.1.-.-]
scaffold3025	2.221	0.007721512		
scaffold19697	1.840	0.007735759		
C242528	-1.952	0.00777529		
C390007	-2.249	0.00777529		
C529284	-1.166	0.00777529	K16675	ZDHHC9_14_18; palmitoyltransferase ZDHHC9/14/18 [EC:2.3.1.225]
C441082	2.750	0.007780365		
C290667	-2.996	0.007944514		
C547545	-0.978	0.007950965		
scaffold29044	1.664	0.008051092		
scaffold12197	1.301	0.008063198		
scaffold24118	1.458	0.008107396	K09250	CNBP; cellular nucleic acid-binding protein
scaffold20514	-0.878	0.0081735		
scaffold972	-1.865	0.008219116		
scaffold18287	4.617	0.008307259		
C546855	1.143	0.008334254		
scaffold26694	-1.495	0.008385617		
scaffold11927	-1.052	0.008399092	K09569	FKBP2; FK506-binding protein 2 [EC:5.2.1.8]
scaffold32409	-1.194	0.008496512	K12619	XRN2, RAT1; 5'-3' exoribonuclease 2 [EC:3.1.13.-]
C513462	1.614	0.008513362		
scaffold27283	1.236	0.008530431		
scaffold1457	1.224	0.008581383	K22389	LCAT3; phospholipase A1 [EC:3.1.1.32]
scaffold27868	1.188	0.008608242		
C496627	-1.608	0.008639616		
C346018	2.454	0.008714747		
C533629	1.672	0.008714747		

C492173	2.408	0.008737904		
scaffold7655	1.672	0.008769186		
C547391	-0.940	0.008808423		
C462008	-2.138	0.008960777		
scaffold20687	1.277	0.008960777		
C465342	1.166	0.009014794		
scaffold15781	-2.683	0.009014794		
scaffold2126	1.698	0.009014794		
C539445	-1.441	0.009042441		
C508610	1.745	0.009062214		
scaffold23744	-3.078	0.009062214		
scaffold11274	0.893	0.009117402		
C536625	1.397	0.009142357		
scaffold23029	0.814	0.009238711	K15639	CYP734A1, BAS1; PHYB activation tagged suppressor 1 [EC:1.14.-.-]
C545089	1.334	0.009240762	K03511	POLK; DNA polymerase kappa [EC:2.7.7.7]
scaffold20401	-1.306	0.009240762		
scaffold26130	1.691	0.009240762		
C420135	-2.120	0.009398306		
scaffold25857	-1.076	0.009406108	K02864	RP-L10, MRPL10, rplJ; large subunit ribosomal protein L10
scaffold10946	-1.084	0.009465473		
C431128	2.355	0.009468716		
scaffold24697	1.506	0.009468716		
scaffold26784	-0.786	0.009468716		
scaffold7511	1.171	0.009468716		
scaffold9647	1.653	0.009468716		
C552493	0.967	0.009551619		
C538351	4.702	0.009579708	K03517	nadA; quinolinate synthase [EC:2.5.1.72]
scaffold32949	-0.517	0.009614758	K11498	CENPE; centromeric protein E
C532380	-0.769	0.009618674		

C475680	2.299	0.00964149	K16298	SCPL-IV; serine carboxypeptidase-like clade IV [EC:3.4.16.-]
C127061	-2.993	0.009690968	K09422	MYBP; transcription factor MYB, plant
C388893	-2.361	0.009699333		
C489347	2.333	0.009699333		
C497846	-1.579	0.009699333	K13993	HSP20; HSP20 family protein
C89656	1.634	0.009699333		
scaffold12812	-2.260	0.009699333	K14085	ALDH7A1; aldehyde dehydrogenase family 7 member A1 [EC:1.2.1.31 1.2.1.8 1.2.1.3]
scaffold16208	-1.238	0.009699333		
scaffold12226	2.728	0.009755991		
scaffold7399	-3.329	0.009755991		
scaffold19528	-1.627	0.00975951		
scaffold30569	-3.031	0.009840019		
scaffold32813	-0.920	0.009871432	K20889	IRX7, FRA8, F8H; probable glucuronoxylan glucuronosyltransferase IRX7 [EC2.4.1.-]
C437138	-0.613	0.009883783		
scaffold20166	1.671	0.009883783	K14297	NUP98, ADAR2, NUP116; nuclear pore complex protein Nup98-Nup96
scaffold6768	-1.155	0.009883783		
C530740	4.409	0.009935293		
scaffold29253	-2.506	0.009943653	K00521	E1.16.1.7; ferric-chelate reductase [EC:1.16.1.7]
scaffold13359	-1.033	0.009948098		
C549795	2.509	0.010029414	K20667	CYP716A; beta-amyrin 28-monooxygenase [EC:1.14.13.201]
scaffold19162	1.395	0.010136993		
scaffold22129	2.468	0.010154776		
C545711	-0.727	0.010175215	K10782	FATA; fatty acyl-ACP thioesterase A [EC:3.1.2.14]
C533667	-1.678	0.010229915	K15404	K15404, CER1; aldehyde decarbonylase [EC:4.1.99.5]
C528024	-1.388	0.010250952		
scaffold29116	4.293	0.010250952		
C540287	4.012	0.010285565		

C367136	3.699	0.010311621		
scaffold19119	1.656	0.010346261	K22374	DMAS1; 3''-deamino-3''-oxonicotianamine reductase [EC:1.1.1.285]
C405968	2.371	0.010412889		
C398001	1.837	0.010428062		
scaffold16996	1.895	0.010453511		
scaffold16117	1.356	0.010538396		
scaffold14375	1.315	0.010568439		
C537975	-0.873	0.010706326		
scaffold29138	-1.495	0.010723917		
C103257	-5.058	0.010770879		
scaffold18148	-1.651	0.010887143	K00588	E2.1.1.104; caffeoyl-CoA O-methyltransferase [EC:2.1.1.104]
C331923	3.137	0.010977057		
C529312	2.053	0.01098377		
scaffold27703	-0.770	0.011080026	K00895	pfp, PFP; diphosphate-dependent phosphofructokinase [EC:2.7.1.90]
C458008	-1.761	0.011087432	K00588	E2.1.1.104; caffeoyl-CoA O-methyltransferase [EC:2.1.1.104]
C496241	3.204	0.011101355		
scaffold10553	-2.833	0.011101355		
C274313	-1.760	0.011136533		
scaffold30141	-1.015	0.011218628		
scaffold28812	-1.607	0.01122897		
C402931	-3.656	0.011366507	K12930	BZ1; anthocyanidin 3-O-glucosyltransferase [EC:2.4.1.115]
scaffold4897	-0.851	0.011366507		
C359578	2.454	0.011433743	K09338	HD-ZIP; homeobox-leucine zipper protein
C440032	-3.141	0.011733048	K04733	IRAK4; interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]
C365165	3.531	0.011756964		
C140934	2.006	0.01179026		
scaffold22733	-1.543	0.01179026		
scaffold12675	-1.883	0.011811561		
C533157	-1.879	0.011872417	K14505	CYCD3; cyclin D3, plant

scaffold23783	1.803	0.011955693	K01057	PGLS, pgl, devB; 6-phosphogluconolactonase [EC:3.1.1.31]
C508656	-0.878	0.012042382		
C218366	-1.771	0.012163235		
C260369	2.526	0.012214657		
scaffold29934	0.928	0.012214657	K01897	ACSL, fadD; long-chain acyl-CoA synthetase [EC:6.2.1.3]
C394037	4.009	0.012295156		
C525808	-1.517	0.012295156	K21842	EFR3; protein EFR3
C91508	3.183	0.012295156		
scaffold27273	1.497	0.012295156		
scaffold28754	1.994	0.012295156	K22374	DMAS1; 3''-deamino-3''-oxonicotianamine reductase [EC:1.1.1.285]
scaffold20508	1.065	0.012296794		
C383974	0.879	0.012346553		
scaffold2243	1.950	0.012346553		
scaffold21502	3.958	0.012394405	K01267	DNPEP; aspartyl aminopeptidase [EC:3.4.11.21]
scaffold24896	-0.775	0.012453954		
C526962	-1.013	0.012500717	K14484	IAA; auxin-responsive protein IAA
C497732	-1.659	0.012506771		
scaffold32181	-1.320	0.012506771		
C485483	2.351	0.012509973		
scaffold16213	-0.945	0.012509973	K13566	NIT2, yafV; omega-amidase [EC:3.5.1.3]
C534347	3.291	0.012526113		
scaffold22769	-2.148	0.012857357		
C546951	-0.713	0.012943761	K13519	LPT1, ALE1; lysophospholipid acyltransferase [EC:2.3.1.51 2.3.1.23 2.3.1.-]
C543753	1.011	0.012957388		
scaffold18455	-3.447	0.012973238		
C433286	3.224	0.013044266		
scaffold15359	2.185	0.013115731	K16298	SCPL-IV; serine carboxypeptidase-like clade IV [EC:3.4.16.-]
scaffold26722	-0.925	0.013115731		

scaffold3179	-4.437	0.013115731	K07374	TUBA; tubulin alpha
C160060	-2.228	0.013350959		
scaffold24838	-0.895	0.013350959	K13993	HSP20; HSP20 family protein
scaffold29881	-0.807	0.013350959		
C540625	-0.676	0.013418374	K11876	PSMG2, PAC2; proteasome assembly chaperone 2
scaffold3469	3.065	0.013452563		
C302056	2.792	0.013462503		
scaffold1948	1.442	0.013462503		
				E3.2.1.96; mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase [EC:3.2.1.96]
scaffold27088	-0.846	0.013462503	K01227	
scaffold16622	-2.046	0.013516256		
C319859	3.078	0.013549984		
C535767	-0.994	0.013549984		
scaffold23433	2.996	0.013549984	K09338	HD-ZIP; homeobox-leucine zipper protein
C392473	2.469	0.013588512		
scaffold24837	-0.794	0.013598105	K13993	HSP20; HSP20 family protein
scaffold26	2.511	0.013669117		
scaffold29461	3.097	0.013669117		
C518208	-3.007	0.013868592		
C530098	-0.791	0.013868592	K14546	UTP5, WDR43; U3 small nucleolar RNA-associated protein 5
scaffold22261	1.732	0.013868592	K14490	AHP; histidine-containing phosphotransfer peotein
C327876	-2.029	0.013920417		
C510564	2.196	0.013920417		
scaffold15131	-1.304	0.013920417	K08911	LHCA5; light-harvesting complex I chlorophyll a/b binding protein 5
scaffold8311	1.755	0.013920417		
scaffold3513	2.183	0.014003192	K13448	CML; calcium-binding protein CML
scaffold9448	-1.767	0.014003192		
scaffold22972	-1.459	0.014016164	K04730	IRAK1; interleukin-1 receptor-associated kinase 1 [EC:2.7.11.1]
scaffold32430	-1.187	0.014016164	K09490	HSPA5, BIP; heat shock 70kDa protein 5

C482925	-1.132	0.014077534	K06041	kdsD, kpsF; arabinose-5-phosphate isomerase [EC:5.3.1.13]
C112531	-2.593	0.014153688		
scaffold31334	1.367	0.014167816		
scaffold4310	1.317	0.014188		
C553037	-0.555	0.014199813		
C481631	-1.497	0.014267455		
scaffold30272	0.898	0.014267455		
scaffold17734	2.359	0.014314194		
scaffold8783	-0.711	0.014449022		
C419607	1.341	0.014467113		
scaffold6020	1.097	0.014517931		
C542227	-1.001	0.01457159	K00384	trxB, TRR; thioredoxin reductase (NADPH) [EC:1.8.1.9]
C339553	2.672	0.01465066		
C361736	2.452	0.014718984	K14638	SLC15A3_4, PHT; solute carrier family 15 (peptide/histidine transporter), member 3/4
scaffold19094	2.725	0.014718984	K02266	COX6A; cytochrome c oxidase subunit 6a
scaffold28157	4.091	0.014720069		
C452759	-2.533	0.014961806		
C534303	3.495	0.015048171		
C473102	1.696	0.015051166		
scaffold25511	-0.742	0.015051166	K08057	CALR; calreticulin
scaffold27145	-1.130	0.015051166		
scaffold968	0.948	0.015051166	K01176	AMY, amyA, malS; alpha-amylase [EC:3.2.1.1]
C428225	-2.067	0.015120261		
C412036	-1.222	0.015167727		
scaffold31728	0.835	0.015202175		
scaffold15006	-2.119	0.015316127	K14840	NOP53, GLTSCR2; nucleolar protein 53
scaffold21427	-0.819	0.015402941	K04712	DEGS; sphingolipid 4-desaturase/C4-monooxygenase [EC:1.14.19.17 1.14.18.5]

C314309	-3.547	0.015428449		
scaffold16652	3.275	0.015441082		
C402321	4.898	0.015499184		
C359986	2.753	0.015537494		
C363092	1.834	0.015537494		
C546291	0.852	0.015537494		
scaffold22042	1.572	0.015554552	K00276	AOC3, AOC2, tynA; primary-amine oxidase [EC:1.4.3.21]
scaffold18993	1.961	0.015678368		
scaffold11315	1.470	0.015681751		
C498072	2.696	0.015798872		
C548961	-1.241	0.015807359		
scaffold11228	-0.965	0.015807359	K10956	SEC61A; protein transport protein SEC61 subunit alpha
scaffold12045	-2.282	0.015917765		
scaffold2609	2.266	0.015930171		
C125809	-1.956	0.016026581	K00454	LOX2S; lipoxygenase [EC:1.13.11.12]
scaffold24272	1.281	0.016046067	K02146	ATPeV0D, ATP6D; V-type H ⁺ -transporting ATPase subunit d
C547025	1.431	0.016094777		
C429358	3.972	0.016163909		
scaffold30494	0.410	0.016163909		
C480773	1.883	0.016330083		
scaffold12712	-2.512	0.016330083		
scaffold24283	-0.504	0.016330083	K16277	DRIP; E3 ubiquitin-protein ligase DRIP [EC:2.3.2.27]
C527122	-0.785	0.016356049		
C538737	1.093	0.016356049		
C330297	2.285	0.016358247		
C513460	-2.350	0.016358247	K14505	CYCD3; cyclin D3, plant
C270115	1.936	0.016436905		
C523202	-2.203	0.01651311		

scaffold31520	1.351	0.01651311	K10144	RCHY1, PIRH2; RING finger and CHY zinc finger domain-containing protein 1 [EC:2.3.2.27]
C453187	3.230	0.016515774		
scaffold565	-0.591	0.016515774		
scaffold12106	-1.803	0.016624606		
scaffold5369	1.333	0.016624606	K13459	RPS2; disease resistance protein RPS2
C548787	1.431	0.016750787		
scaffold27748	2.341	0.016750787		
scaffold7281	-0.811	0.016750787		
scaffold31826	-1.065	0.0167535		
C443115	2.588	0.016768633		
C501689	2.272	0.016875208		
C95806	1.363	0.016875208		
scaffold21590	-0.633	0.016875208		
C543755	-0.780	0.016967243	K00930	argB; acetylglutamate kinase [EC:2.7.2.8]
C536203	-0.588	0.016997849	K02876	RP-L15, MRPL15, rplO; large subunit ribosomal protein L15
C326918	1.134	0.017009615		
C495010	-2.313	0.017033181		
scaffold23380	-2.991	0.017033181	K00326	E1.6.2.2; cytochrome-b5 reductase [EC:1.6.2.2]
scaffold28240	-0.875	0.017033181	K02437	gcvH, GCSH; glycine cleavage system H protein
scaffold9437	-1.244	0.017077974		
scaffold24641	1.052	0.017095967		
scaffold11745	3.766	0.017198331		
C404767	-3.052	0.017258683		
C512038	-1.618	0.017315537	K03798	ftsH, hflB; cell division protease FtsH [EC:3.4.24.-]
scaffold11928	-0.856	0.017345353	K09569	FKBP2; FK506-binding protein 2 [EC:5.2.1.8]
C146012	1.857	0.017347209		
C440476	-1.499	0.017347209		
C486421	-2.991	0.017347209		

scaffold22945	-2.135	0.017347209	K19001	HELLS, DDM1; ATP-dependent DNA helicase
C426787	-1.948	0.017354363		
C483861	1.604	0.017354363		
scaffold7719	-1.180	0.01736196	K03768	PPiB, ppiB; peptidyl-prolyl cis-trans isomerase B (cyclophilin B) [EC:5.2.1.8]
scaffold15083	-1.754	0.017397157		
C459447	-1.088	0.017448608		
C273183	1.957	0.017546893		
C540889	-0.800	0.017574594	K09761	rsmE; 16S rRNA (uracil1498-N3)-methyltransferase [EC:2.1.1.193]
scaffold18153	-1.873	0.017657786		
C538745	-1.057	0.017692665	K02906	RP-L3, MRPL3, rplC; large subunit ribosomal protein L3
scaffold16664	-0.708	0.017772242		
scaffold22917	-0.887	0.017820903		
C519922	1.805	0.017830072		
C434762	-2.501	0.017907004		
C543519	-0.841	0.01813403	K12501	HST; homogentisate solanesyltransferase [EC:2.5.1.117]
C376090	0.896	0.018163766		
C541301	-1.027	0.018163766		
scaffold17155	-1.557	0.018163766		
scaffold23621	1.845	0.018163766		
C424163	1.151	0.018238851		
C541759	1.595	0.018238851	K22285	OSBPL8, ORP8; oxysterol-binding protein-related protein 8
C547711	-0.644	0.018259315	K00811	ASP5; aspartate aminotransferase, chloroplastic [EC:2.6.1.1]
C114290	-2.631	0.018312675		
scaffold22038	2.319	0.018566937		
C502285	0.950	0.018682631		
C400985	2.216	0.01873127		
C363158	1.952	0.018838638		
scaffold30344	-1.069	0.018838638		

C394713	2.356	0.018888449		
scaffold1728	1.776	0.018888449		
scaffold32733	-1.311	0.018888449	K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family
C174627	1.591	0.018946371		
C397191	-2.199	0.018966931		
scaffold1480	-1.301	0.019069988	K09754	CYP98A, C3'H; coumaroylquininate(coumaroylshikimate) 3'-monooxygenase [EC:1.14.13.36]
C389145	-2.619	0.019140042		
C489165	-1.463	0.019140042	K00083	E1.1.1.195; cinnamyl-alcohol dehydrogenase [EC:1.1.1.195]
C494984	2.806	0.019140042		
C501907	1.609	0.019140042		
C512582	2.004	0.019140042		
scaffold10010	2.003	0.019140042		
scaffold23818	1.955	0.019140042		
scaffold6791	1.459	0.019140042	K05666	ABCC2; ATP-binding cassette, subfamily C (CFTR/MRP), member 2
scaffold8861	-0.817	0.019140042	K11086	SNRNPB, SMB; small nuclear ribonucleoprotein B and B'
scaffold14366	1.151	0.019158972		
C94622	2.789	0.019189724	K12158	NEDD8; ubiquitin-like protein Nedd8
scaffold26552	2.369	0.019189724		
scaffold17766	-0.510	0.019198849	K14842	NSA2; ribosome biogenesis protein NSA2
C447224	-1.150	0.019241936		
C536355	1.541	0.019241936		
C538647	-1.040	0.019241936	K01807	rpiA; ribose 5-phosphate isomerase A [EC:5.3.1.6]
scaffold18613	1.147	0.019241936		
scaffold32795	-0.523	0.019241936		
scaffold26860	-2.179	0.019266297	K01426	E3.5.1.4, amiE; amidase [EC:3.5.1.4]
C472322	-1.205	0.019325798	K02983	RP-S30e, RPS30; small subunit ribosomal protein S30e
C499452	-1.321	0.019325798	K04733	IRAK4; interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]

scaffold16529	1.582	0.019325798		
scaffold21372	1.106	0.019325798		
scaffold22014	2.989	0.019325798		
C191614	-2.550	0.019335595		
C450781	1.837	0.019335595		
C525798	1.330	0.019335595	K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family
C529610	-1.817	0.019397806	K15404	K15404, CER1; aldehyde decarbonylase [EC:4.1.99.5]
C429966	3.331	0.019415104		
C400479	-1.346	0.019438307	K20720	RTN4; reticulon-4
scaffold14183	-0.815	0.019438307	K00847	E2.7.1.4, scrK; fructokinase [EC:2.7.1.4]
C350162	3.206	0.019575917		
scaffold11736	1.658	0.01967337		
scaffold21503	0.847	0.01970465		
C433322	-1.855	0.01979119		
scaffold10858	-1.015	0.019831123		
scaffold29259	4.514	0.019874924		
C529948	-0.998	0.020002103		
C474716	-1.747	0.020038464		
C313445	1.248	0.020108557		
C507141	1.332	0.020114404		
scaffold9124	-2.925	0.020134474		
C340954	-1.587	0.020194094		
scaffold18814	0.938	0.020194094		
C478466	2.519	0.020276111		
scaffold15713	0.874	0.020495226		
scaffold10978	1.043	0.020498227		
scaffold23170	1.633	0.020526525		
scaffold31732	-0.674	0.020608405	K12607	CNOT10; CCR4-NOT transcription complex subunit 10

scaffold24266	-1.975	0.020641536		
C443017	-1.114	0.020823904	K19748	GORAB, SCYL1BP1; RAB6-interacting golgin
C356640	2.259	0.020825288	K13459	RPS2; disease resistance protein RPS2
C189364	3.268	0.020838241	K20180	VPS16; vacuolar protein sorting-associated protein 16
scaffold4066	-1.710	0.021050274	K00799	GST, gst; glutathione S-transferase [EC:2.5.1.18]
scaffold9224	2.285	0.021341752		
scaffold2872	1.197	0.021362659	K03676	grxC, GLRX, GLRX2; glutaredoxin 3
C135076	1.095	0.021365588		
C384332	2.985	0.021365588		
scaffold10925	3.723	0.021365588		
scaffold8638	1.037	0.021365588		
scaffold9591	1.753	0.021365588		
C361352	-2.208	0.021427622		
C518578	1.037	0.021446469		
C474532	2.090	0.021447287		
C451575	-0.953	0.021486189		
scaffold1828	1.497	0.021490454		
C265503	5.114	0.021498165		
C347016	-1.008	0.021498165	K03549	kup; KUP system potassium uptake protein
scaffold28029	1.513	0.021535732		
scaffold5373	2.929	0.021554507	K04123	KAO; ent-kaurenoic acid hydroxylase [EC:1.14.13.79]
C504741	-1.736	0.021585333		
scaffold5815	-2.858	0.021586011		
scaffold4724	0.860	0.02161105		
C399121	-2.376	0.021748747		
scaffold5146	-1.017	0.021748747		
C539267	1.205	0.021819103		
C188314	1.988	0.021863672		
C407880	2.619	0.021999742		

C527170	1.478	0.022110224		
C413410	-1.581	0.02214544	K09527	DNAJC7; DnaJ homolog subfamily C member 7
C503945	2.125	0.02214544	K21437	ANKRD13; ankyrin repeat domain-containing protein 13
C455103	0.864	0.02227825	K00279	CKX; cytokinin dehydrogenase [EC:1.5.99.12]
scaffold6141	-1.404	0.022301154		
C544779	-1.192	0.02237124		
C213420	-2.752	0.02241354	K14505	CYCD3; cyclin D3, plant
C276299	2.713	0.02241354		
C430988	2.069	0.02241354	K20562	CYP736A; biphenyl-4-hydroxylase
C464150	2.433	0.02241354		
scaffold22238	1.885	0.02241354	K10418	DYNLL; dynein light chain LC8-type
scaffold26145	2.339	0.022426902		
scaffold3896	2.279	0.022449499		
C531682	-1.251	0.022463533	K01531	mgtA, mgtB; Mg ²⁺ -importing ATPase [EC:3.6.3.2]
C537329	-1.995	0.022585034	K12657	ALDH18A1, P5CS; delta-1-pyrroline-5-carboxylate synthetase [EC:2.7.2.11 1.2.1.41]
scaffold29765	-0.804	0.022585034		
scaffold6713	2.139	0.022585034	K00512	CYP17A; steroid 17alpha-monooxygenase / 17alpha-hydroxyprogesterone deacetylase [EC:1.14.14.19 1.14.14.32]
C490763	1.511	0.022688427		
C330421	-2.074	0.022758598		
scaffold4362	-0.727	0.022758598		
C339441	1.144	0.02277164		
C138138	3.697	0.022839643		
scaffold14329	-1.042	0.022979307	K03251	EIF3D; translation initiation factor 3 subunit D
scaffold8009	-0.691	0.02305215		
scaffold8276	5.049	0.02307291		
scaffold23360	1.151	0.023192158	K21989	TMEM63; calcium permeable stress-gated cation channel
C504579	-1.004	0.023281603	K15111	SLC25A26; solute carrier family 25 (mitochondrial S-adenosylmethionine transporter), member 26

scaffold11939	3.887	0.02335493		
C277457	-1.258	0.023378954		
C417679	-1.774	0.023378954		
scaffold29840	-2.673	0.023378954		
scaffold32765	0.581	0.023378954		
C370228	-2.335	0.023385116		
scaffold4401	1.597	0.023385116		
C292841	-2.475	0.023447241		
scaffold13823	-1.007	0.023447241		
scaffold9582	1.711	0.023447241		
C517820	1.444	0.023564124	K11982	RNF115_126; E3 ubiquitin-protein ligase RNF115/126 [EC:2.3.2.27]
scaffold28354	-0.330	0.023564124	K17087	TM9SF3; transmembrane 9 superfamily member 3
scaffold6090	-0.895	0.02364099		
C525510	-1.500	0.023770808		
C480541	-2.188	0.023868494		
C514936	-1.982	0.023868494		
scaffold10387	1.732	0.023868494		
scaffold28620	2.073	0.023962045		
C188956	3.162	0.024231092		
scaffold417	-0.701	0.024231092		
C287031	-2.534	0.024276667		
C499440	2.674	0.024284163		
C372588	-1.523	0.024368802	K01956	carA, CPA1; carbamoyl-phosphate synthase small subunit [EC:6.3.5.5]
C543919	2.174	0.024391762		
C408736	1.373	0.024562064		
C545351	-0.973	0.024562064	K05359	ADT, PDT; arogenate/prephenate dehydratase [EC:4.2.1.91 4.2.1.51]
scaffold12208	2.490	0.024562064		
scaffold1875	-1.658	0.024562064	K00454	LOX2S; lipxygenase [EC:1.13.11.12]
scaffold27348	0.934	0.024562064	K19038	ATL41; E3 ubiquitin-protein ligase ATL41 [EC:2.3.2.27]

scaffold17393	1.814	0.024587132		
scaffold19602	-1.646	0.024654807	K00454	LOX2S; lipoxygenase [EC:1.13.11.12]
scaffold4262	1.806	0.024654807		
scaffold6439	2.577	0.024654807		
scaffold28814	-1.634	0.024676922		
C544893	2.625	0.024695955		
scaffold26258	1.678	0.024739211	K08241	E2.1.1.141; jasmonate O-methyltransferase [EC:2.1.1.141]
C540973	2.050	0.024833221		
scaffold12687	-1.129	0.0249625	K00700	GBE1, glgB; 1,4-alpha-glucan branching enzyme [EC:2.4.1.18]
C441787	-1.410	0.024964552		
scaffold10777	2.156	0.025002515	K07408	CYP1A1; cytochrome P450 family 1 subfamily A polypeptide 1 [EC:1.14.14.1]
scaffold13252	2.605	0.025388874		
C518580	-1.358	0.025395462		
scaffold16071	0.614	0.02543369		
scaffold16762	-1.509	0.02543369	K19045	BB; E3 ubiquitin-protein ligase BIG BROTHER and related proteins [EC:2.3.2.27]
C541205	0.563	0.025459935		
C124070	2.124	0.025484283		
C125006	2.711	0.025558801		
C136096	-3.110	0.025558801		
C519600	1.243	0.025632342		
C259667	-2.144	0.025660807		
scaffold22478	-0.506	0.025660807		
scaffold7776	1.369	0.025712463		
C506923	1.259	0.025738071		
scaffold16647	-1.206	0.025743647		
C457177	1.431	0.025753664		
C441535	1.500	0.02584774		

C458198	1.825	0.02584774		
C537765	-0.786	0.02584774		
scaffold28135	1.522	0.02584774		
scaffold24370	-0.948	0.025920328		
C497936	1.855	0.026018043	K17991	PXG; peroxygenase [EC:1.11.2.3]
C431920	-1.583	0.026107909	K17279	REEP5_6; receptor expression-enhancing protein 5/6
scaffold10844	2.336	0.026169882		
scaffold11087	0.823	0.026169882		
scaffold25415	2.663	0.026169882		
scaffold9787	1.346	0.026169882		
scaffold10541	2.467	0.026177357		
C473144	-0.964	0.026187573	K07943	ARL2; ADP-ribosylation factor-like protein 2
C524740	-0.886	0.0261908		
scaffold23977	-1.629	0.0261908	K13832	aroDE, DHQ-SDH; 3-dehydroquinate dehydratase / shikimate dehydrogenase [EC:4.2.1.10 1.1.1.25]
scaffold19421	2.365	0.026217614		
scaffold18290	-1.454	0.026286259	K16732	PRC1; protein regulator of cytokinesis 1
C529832	-2.049	0.026295135		
scaffold26400	0.949	0.026367327		
C526520	-0.737	0.026452414		
scaffold7253	-0.779	0.026452414		
C206742	-4.314	0.026506982		
C467720	1.775	0.026506982	K05658	ABCB1, CD243; ATP-binding cassette, subfamily B (MDR/TAP), member 1 [EC:3.6.3.44]
C545245	0.838	0.026517939		
scaffold19207	-0.616	0.026517939		
C478964	1.910	0.026699439		
scaffold2541	2.378	0.02671111		
scaffold18141	-0.681	0.026833051		

C469458	1.439	0.026917922	K04733	IRAK4; interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]
scaffold16013	1.630	0.027082861	K13525	VCP, CDC48; transitional endoplasmic reticulum ATPase
scaffold8719	2.477	0.027082861		
scaffold7718	-1.292	0.027143674	K03768	PPIB, ppiB; peptidyl-prolyl cis-trans isomerase B (cyclophilin B) [EC:5.2.1.8]
C497842	-1.899	0.027242982		
C132113	-3.256	0.027429029		
C477060	2.213	0.027463794	K16298	SCPL-IV; serine carboxypeptidase-like clade IV [EC:3.4.16.-]
scaffold25774	-1.237	0.027463794	K14442	DHX36, RHAU; ATP-dependent RNA helicase DHX36 [EC:3.6.4.13]
scaffold28246	1.747	0.027463794	K13457	RPM1, RPS3; disease resistance protein RPM1
scaffold14302	0.898	0.027552786	K16241	HY5; transcription factor HY5
C415589	2.347	0.027672891		
C422745	-2.906	0.027806864		
scaffold14529	1.064	0.027806864	K00914	PIK3C3, VPS34; phosphatidylinositol 3-kinase [EC:2.7.1.137]
scaffold15946	-0.561	0.027823678	K00600	glyA, SHMT; glycine hydroxymethyltransferase [EC:2.1.2.1]
C121600	5.479	0.027901535		
scaffold26610	0.844	0.027901535		
C361698	-2.236	0.027925038		
C284597	-2.240	0.028132439	K21374	UGT85A; 7-deoxyloganetin glucosyltransferase [EC:2.4.1.324]
C510002	1.779	0.028150038		
C541039	1.447	0.028186039		
scaffold19111	1.374	0.028186039		
scaffold19137	1.366	0.028186039		
C472992	-1.565	0.028402158		
C548167	-2.545	0.028402158		
C550891	-0.470	0.028402158		
scaffold17366	-1.196	0.028413239		
C493502	1.483	0.028421689		
scaffold26212	-0.940	0.028421689		

C446126	1.078	0.028440354		
C462822	2.354	0.028440354		
C464720	-1.237	0.028440354		
scaffold13406	1.496	0.028440354		
scaffold22288	0.962	0.028440354		
scaffold26776	1.251	0.028440354	K13066	E2.1.1.68, COMT; caffeic acid 3-O-methyltransferase [EC:2.1.1.68]
C469018	2.026	0.02845142		
C126845	-2.683	0.028541947		
C504837	1.136	0.028541947		
scaffold19255	-2.002	0.028588029		
C510832	1.705	0.028615192		
scaffold3338	-0.825	0.028615192		
C502825	-3.053	0.02866275	K07374	TUBA; tubulin alpha
C530572	-1.455	0.028675648	K10999	CESA; cellulose synthase A [EC:2.4.1.12]
scaffold1223	1.935	0.028675648		
scaffold29469	-1.840	0.028697173		
scaffold21731	3.947	0.028758657	K03946	NDUFA2; NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 2
scaffold16783	1.256	0.029184297		
C315835	3.631	0.029214001		
C468808	-1.111	0.029214001		
scaffold17350	-0.735	0.029214001		
scaffold28099	-1.292	0.029256785		
scaffold27433	1.608	0.029310591		
C408934	4.277	0.029465998		
C86808	-1.847	0.029465998		
C484601	2.186	0.029510025		
C428079	1.343	0.029513945		
C523686	2.117	0.029887594		

C485401	2.039	0.030245031		
C369798	1.695	0.03055987		
C369906	-2.133	0.03055987		
C466220	1.561	0.03055987		
C495965	1.425	0.03055987		
C506041	2.767	0.03055987		
C506603	2.225	0.03055987		
C517694	-0.611	0.03055987		
C543237	-0.840	0.03055987		
scaffold31580	-1.176	0.03055987	K10999	CESA; cellulose synthase A [EC:2.4.1.12]
scaffold3964	1.985	0.03055987		
C369540	2.594	0.030617581		
C449611	2.114	0.030617733		
C532344	-1.127	0.030617733	K10999	CESA; cellulose synthase A [EC:2.4.1.12]
C507675	3.015	0.030624698		
C540725	-0.831	0.030624698		
C544741	-2.384	0.030624698	K05350	bglB; beta-glucosidase [EC:3.2.1.21]
scaffold29014	-1.651	0.030624698		
C322451	-2.847	0.030811491		
C398927	-2.796	0.030823596		
scaffold10102	1.477	0.030823596	K20667	CYP716A; beta-amyrin 28-monooxygenase [EC:1.14.13.201]
scaffold1095	0.883	0.030823596	K09571	FKBP4_5; FK506-binding protein 4/5 [EC:5.2.1.8]
C454441	2.109	0.03096636		
C237744	2.714	0.030982881		
C394205	-1.732	0.031079422		
C422489	1.507	0.031106277		
scaffold19599	-1.626	0.031106277		
C551681	-0.597	0.031181019		
scaffold16877	-2.272	0.031181019		

scaffold2329	2.392	0.031204991		
scaffold2641	-0.769	0.031205507	K15109	SLC25A20_29, CACT, CACL, CRC1; solute carrier family 25 (mitochondrial carnitine/acylcarnitine transporter), member 20/29
C442284	1.046	0.03122381		
C530096	-1.043	0.031421328		
C503009	-1.364	0.031451595		
C538417	-1.618	0.031451595		
C549597	2.203	0.031451595	K07198	PRKAA, AMPK; 5'-AMP-activated protein kinase, catalytic alpha subunit [EC:2.7.11.11]
scaffold18192	-1.841	0.031451595		
scaffold1863	0.639	0.031451595		
scaffold20523	1.205	0.031451595		
scaffold23538	-1.227	0.031451595	K00627	DLAT, aceF, pdhC; pyruvate dehydrogenase E2 component (dihydrolipoamide acetyltransferase) [EC:2.3.1.12]
scaffold30733	-0.494	0.031451595	K07893	RAB6A; Ras-related protein Rab-6A
scaffold5774	1.267	0.031451595		
C518132	-2.634	0.031504026		
scaffold29567	-3.359	0.031504026		
C125398	-1.487	0.031557395		
C333681	1.550	0.031557395		
C401273	-3.018	0.031557395		
C485595	-1.293	0.031557395		
scaffold18865	1.185	0.031557395		
C450383	1.286	0.031632609		
C548329	1.377	0.031632609	K00815	TAT; tyrosine aminotransferase [EC:2.6.1.5]
scaffold2637	1.522	0.031632609		
C136098	-2.665	0.031806185		
scaffold3509	1.987	0.031806185	K13448	CML; calcium-binding protein CML
C415527	-2.329	0.031923561		
scaffold29994	1.141	0.031923561		

C500557	-1.474	0.031986432		
C545455	1.342	0.031986432		
scaffold31945	-1.655	0.031986432	K10757	E2.4.1.91; flavonol 3-O-glucosyltransferase [EC:2.4.1.91]
C265749	1.696	0.032052328		
C546581	-0.669	0.032052328	K00889	PIP5K; 1-phosphatidylinositol-4-phosphate 5-kinase [EC:2.7.1.68]
C489297	-2.969	0.032131898		
C337313	1.722	0.03254472		
scaffold138	-0.880	0.032723369	K01530	E3.6.3.1; phospholipid-translocating ATPase [EC:3.6.3.1]
C293577	1.350	0.032780335		
C326264	3.283	0.032780335		
C506825	-1.248	0.032780335		
scaffold13408	1.359	0.032780335		
scaffold13618	1.355	0.032780335		
C476648	-1.162	0.032917996	K14763	NAF1; H/ACA ribonucleoprotein complex non-core subunit NAF1 SLC17A; MFS transporter, ACS family, solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), other
C534121	-0.979	0.032917996	K08193	
C552661	-1.990	0.032939106		
scaffold5768	2.245	0.032980665		
scaffold6243	-1.381	0.032980665		
C460353	-2.109	0.033065971		
scaffold25190	1.634	0.033124423		
scaffold13651	-0.588	0.033185003	K01409	KAE1, tsaD, QRI7; N6-L-threonylcarbamoyladenine synthase [EC:2.3.1.234]
scaffold16421	-2.380	0.033185003		
C527324	-1.881	0.03322605	K13680	CSLA; beta-mannan synthase [EC:2.4.1.32]
C127249	3.230	0.033390402		
C550055	-1.243	0.033390402	K00058	serA, PHGDH; D-3-phosphoglycerate dehydrogenase / 2-oxoglutarate reductase [EC:1.1.1.95 1.1.1.399]
C449529	2.120	0.033413579		
scaffold29845	1.377	0.033413579	K05387	GRIP; glutamate receptor, ionotropic, plant

scaffold22663	0.454	0.033536937		
C524182	2.308	0.033542379		
C542587	-1.132	0.033576388	K01626	E2.5.1.54, aroF, aroG, aroH; 3-deoxy-7-phosphoheptulonate synthase [EC:2.5.1.54]
C382772	2.976	0.03357645		
C502683	-1.002	0.03357645		
C511046	2.380	0.033831245		
C475682	-1.441	0.033831615		
scaffold11889	-0.685	0.033831615	K02377	TSTA3, fcl; GDP-L-fucose synthase [EC:1.1.1.271]
scaffold11772	3.013	0.033949594	K21889	TMBIM6, BI1, TEGT; Bax inhibitor 1
C502057	1.569	0.034093763		
C189272	-1.819	0.034174126		
C484619	3.848	0.034174126	K01757	STR1; strictosidine synthase [EC:4.3.3.2]
C503115	1.068	0.034174126		
scaffold15029	1.146	0.034174126		
scaffold26197	-0.758	0.034174126	K14396	PABPN1, PABP2; polyadenylate-binding protein 2
scaffold449	2.533	0.034174126		
C175913	1.800	0.034291161		
C375750	1.907	0.034341371		
scaffold32454	-0.718	0.034391656	K03027	RPC40, POLR1C; DNA-directed RNA polymerases I and III subunit RPAC1
scaffold22400	-1.392	0.034436394		
C467812	-1.436	0.034508138	K12761	SNF1; carbon catabolite-derepressing protein kinase [EC:2.7.11.1]
C547707	-0.824	0.034508138	K00789	metK; S-adenosylmethionine synthetase [EC:2.5.1.6]
scaffold19856	-0.583	0.034508138	K21594	GUF1; translation factor GUF1, mitochondrial [EC:3.6.5.-]
scaffold6205	1.881	0.034529801		
C456463	2.692	0.03459241	K08145	SLC2A8, GLUT8; MFS transporter, SP family, solute carrier family 2 (facilitated glucose transporter), member 8
C533939	-0.908	0.03459241	K02939	RP-L9, MRPL9, rplI; large subunit ribosomal protein L9
scaffold10087	1.893	0.034622093		

C546509	-1.190	0.034692946	K00660	CHS; chalcone synthase [EC:2.3.1.74] HO, pbsA1, hmuO; heme oxygenase (biliverdin-producing, ferredoxin) [EC:1.14.15.20]
scaffold30206	1.662	0.034753088	K21480	
scaffold17286	2.525	0.034758335		
scaffold20125	-1.212	0.035005785	K11971	RNF14, ARA54; E3 ubiquitin-protein ligase RNF14 [EC:2.3.2.31]
scaffold2326	2.976	0.035005785		
scaffold31457	1.970	0.035005785	K05894	OPR; 12-oxophytodienoic acid reductase [EC:1.3.1.42]
scaffold597	3.086	0.035064047		
C389975	-1.444	0.035221154		
C371198	-1.950	0.035272684		
C162932	3.097	0.03540455	K04733	IRAK4; interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]
scaffold5270	-0.881	0.03540455	K05359	ADT, PDT; arogenate/prephenate dehydratase [EC:4.2.1.91 4.2.1.51]
scaffold24784	-2.147	0.035450499		
C374648	1.464	0.03549897		
C413799	-0.960	0.035579407		
scaffold19849	0.616	0.035579407		
scaffold25043	-0.419	0.035596124		
scaffold13595	-1.224	0.035703942		
scaffold7653	1.236	0.035705213		
scaffold28419	1.361	0.035728968		
C183600	2.915	0.035862039		
scaffold10079	2.430	0.035921174	K21371	UGT75L6, UGTCS2; crocetin glucosyltransferase [EC:2.4.1.271]
scaffold30302	-0.507	0.035921174	K17086	TM9SF2_4; transmembrane 9 superfamily member 2/4
C332021	-2.085	0.03593727		
scaffold4648	1.816	0.035999964	K04733	IRAK4; interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]
scaffold23289	2.350	0.036268508		
scaffold11502	-1.259	0.036293766		
scaffold11252	1.281	0.036313841		
scaffold12607	-0.974	0.036370661		

scaffold29622	-0.808	0.036404332	K02977	RP-S27Ae, RPS27A; small subunit ribosomal protein S27Ae
C499470	-2.368	0.036406833		
C407054	1.308	0.03649201		
scaffold17576	1.929	0.03649201	K05387	GRIP; glutamate receptor, ionotropic, plant
scaffold30957	-1.085	0.036597593	K09338	HD-ZIP; homeobox-leucine zipper protein
C452547	2.729	0.036907626		
C189366	4.266	0.037051737	K20556	CYP76C; cytochrome P450 family 76 subfamily C
C516350	4.757	0.037051737		
C524460	-0.913	0.037051737		
C539163	-0.901	0.037051737		
scaffold32347	-2.226	0.037051737	K04730	IRAK1; interleukin-1 receptor-associated kinase 1 [EC:2.7.11.1]
C373914	0.988	0.037061185	K08245	E3.4.23.40; phytepsin [EC:3.4.23.40]
C475744	1.636	0.037061185		
C445444	-1.181	0.037147519	K20456	OSBP; oxysterol-binding protein 1
scaffold32986	-0.387	0.037154215		
C548277	-0.878	0.037170678	K01102	PDP; pyruvate dehydrogenase phosphatase [EC:3.1.3.43]
C433728	1.420	0.037269647		
C411794	1.223	0.037437235		
C513306	2.093	0.037437235		
scaffold26862	1.185	0.037437235		
scaffold25285	-0.715	0.037567802		
C484131	-0.992	0.037623935		
C503951	-1.144	0.037680904		
scaffold26179	-0.595	0.037680904	K20165	TBC1D2; TBC1 domain family member 2A
C539597	1.494	0.037683073		
C540261	-1.159	0.037709571	K08054	CANX; calnexin
C542493	-0.795	0.037753315		
C100098	-1.069	0.037779244		
scaffold12311	1.757	0.037779244		

scaffold21489	1.032	0.037779244		
scaffold23926	2.582	0.037779244		
C542437	-1.004	0.037782283		
C101596	1.937	0.037816619		
scaffold29458	-0.847	0.037818191		
C526174	-1.560	0.037831987		
C98690	2.220	0.037862047		
C495833	-0.979	0.037921151		
scaffold8261	-1.020	0.038066806	K05928	E2.1.1.95; tocopherol O-methyltransferase [EC:2.1.1.95]
scaffold8330	2.769	0.038067767	K18674	GALK2; N-acetylgalactosamine kinase [EC:2.7.1.157]
scaffold15105	-1.607	0.038204157		
scaffold24820	-1.900	0.038204157		
C536985	1.169	0.03828238		
C551595	0.838	0.038331988		
scaffold15780	-1.580	0.038331988		
scaffold25720	1.077	0.038331988		
scaffold29062	-0.533	0.038331988	K14684	SLC25A23S; solute carrier family 25 (mitochondrial phosphate transporter), member 23/24/25/41
C183212	-2.882	0.03836236		
C190156	-2.097	0.03836236		
C238234	-2.338	0.03836236		
C436612	3.593	0.03836236		
scaffold23083	1.975	0.03836236		
scaffold27309	-1.855	0.03836236		
scaffold31725	1.144	0.03836236	K09587	CYP90B1, DWF4; steroid 22-alpha-hydroxylase [EC:1.14.13.-]
scaffold9068	-1.093	0.03836236		
scaffold13327	-3.858	0.038409465		
scaffold14074	-0.997	0.038409465	K17757	CARKD; ATP-dependent NAD(P)H-hydrate dehydratase [EC:4.2.1.93]
C521642	-0.808	0.038653054		

C464494	2.374	0.038834358		
C535891	-0.853	0.038834358	K14299	SEH1; nucleoporin SEH1
scaffold5244	1.007	0.038834358	K22419	VEP1; Delta4-3-oxosteroid 5beta-reductase [EC:1.3.1.3]
C235926	-1.343	0.038861325		
C198060	2.110	0.038976205		
C401993	-1.308	0.038976205		
C530942	-0.907	0.038976205		
scaffold25173	2.414	0.038976205		
scaffold1730	2.395	0.03902195		
scaffold34	-1.078	0.039096447		
C521994	-1.200	0.039171822		
C527332	-1.143	0.039171822	K08876	SCYL1; SCY1-like protein 1
C544965	-0.783	0.039171822	K20899	GBP1_3_4_7; guanylate-binding protein 1/3/4/7
scaffold31014	1.547	0.039242457		
C496713	3.039	0.039473355		
C519272	-2.006	0.039473355		
C552981	-0.761	0.039486928	K11593	ELF2C, AGO; eukaryotic translation initiation factor 2C
scaffold10354	1.809	0.039492312		
scaffold32150	-0.921	0.039492312	K01177	E3.2.1.2; beta-amylase [EC:3.2.1.2]
C509654	1.173	0.039522437		
C479815	-1.766	0.039649116		
C547519	-1.005	0.039649116		
scaffold32588	-2.278	0.039649116		
scaffold7735	1.203	0.039864789		
C517978	1.464	0.039941281		
scaffold4710	-0.693	0.039959371		
scaffold26238	1.326	0.040076742		
scaffold12408	2.260	0.04012219	K13420	FLS2; LRR receptor-like serine/threonine-protein kinase FLS2 [EC:2.7.11.1]

scaffold2006	-0.828	0.04012219		
scaffold30337	3.761	0.040132865		
C529252	1.155	0.040137449		
C544311	0.492	0.040137449	K03843	ALG2; alpha-1,3/alpha-1,6-mannosyltransferase [EC:2.4.1.132 2.4.1.257]
C548401	-1.141	0.040137449	K13832	aroDE, DHQ-SDH; 3-dehydroquinate dehydratase / shikimate dehydrogenase [EC:4.2.1.10 1.1.1.25]
scaffold14647	1.796	0.040137449		
C513696	-0.932	0.040292663	K00783	rlmH; 23S rRNA (pseudouridine1915-N3)-methyltransferase [EC:2.1.1.177]
scaffold26468	-0.735	0.040292663		
scaffold2631	3.699	0.040328153		
scaffold8176	-1.549	0.04035951		
C292843	2.506	0.040366292		
C466848	2.300	0.040366292	K03021	RPC2, POLR3B; DNA-directed RNA polymerase III subunit RPC2 [EC:2.7.7.6]
C510706	1.436	0.040407387		
C417025	-1.672	0.040420657		
scaffold27363	-0.750	0.040663592	K19042	BOI; E3 ubiquitin-protein ligase BOI and related proteins [EC:2.3.2.27]
scaffold4578	-0.632	0.040737914		
C452997	1.031	0.040858668		
scaffold2163	0.849	0.040947244		
scaffold29654	-0.821	0.040947244		
C471080	-1.807	0.040984514		
scaffold8146	1.761	0.041009975	K03327	TC.MATE, SLC47A, norM, mdtK, dinF; multidrug resistance protein, MATE family
C540555	2.318	0.041255127		
C532290	-1.540	0.041395287		
C526186	-1.040	0.041588617		
C501573	2.328	0.041620982	K15639	CYP734A1, BAS1; PHYB activation tagged suppressor 1 [EC:1.14.-.-]

C402933	-1.474	0.041626212		E3.6.1.52; diphosphoinositol-polyphosphate diphosphatase [EC:3.6.1.52]
C482923	-0.836	0.041668784	K07766	DYNLL; dynein light chain LC8-type
scaffold9671	2.871	0.04170237	K10418	RPS2; disease resistance protein RPS2
C321305	1.715	0.041718484	K13459	
C394493	2.313	0.041718484		
C505643	-1.313	0.041718484		
C506049	2.207	0.041718484	K21373	UGT8, UGT709C2; 7-deoxyloganetic acid glucosyltransferase [EC:2.4.1.323]
C520328	-2.390	0.041718484		
C551445	-1.751	0.041718484		
scaffold15196	-1.865	0.041718484		
scaffold15678	0.832	0.041718484		
scaffold16012	1.937	0.041718484		
scaffold1967	-0.955	0.041718484	K14855	RSA4, NLE1; ribosome assembly protein 4
scaffold21582	-0.667	0.041718484		
scaffold25984	-0.662	0.041718484		
scaffold28198	1.190	0.041718484		
scaffold30605	-1.294	0.041718484		
scaffold6242	2.016	0.041718484		
C510928	-0.753	0.041771152	K02942	RP-LP1, RPLP1; large subunit ribosomal protein LP1
C497906	2.042	0.041852808		
scaffold20658	2.949	0.041852808	K04123	KA0; ent-kaurenoic acid hydroxylase [EC:1.14.13.79]
C448919	-3.871	0.041873437	K04733	IRAK4; interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]
scaffold29440	-1.076	0.042287476	K07976	RAB; Rab family, other
C522498	-2.689	0.042769628		
scaffold6804	-1.753	0.042769628		
scaffold27475	-1.577	0.04281207		
C549149	-0.913	0.042869935	K10389	TUBG; tubulin gamma

C496906	1.484	0.04288969		
scaffold31420	1.218	0.043004813		
scaffold30843	1.913	0.043077733		
C489487	-1.688	0.043108021		
C534621	0.704	0.043111129		
C491649	1.284	0.043161349		
C114292	-1.576	0.043345414	K00454	LOX2S; lipoxygenase [EC:1.13.11.12]
scaffold32284	0.753	0.043539451		
C461381	2.001	0.044160948		
C539323	-0.799	0.044215141	K01081	E3.1.3.5; 5'-nucleotidase [EC:3.1.3.5]
C454631	-1.210	0.04435758		
C405970	1.914	0.044403128		
C463542	3.298	0.044403128	K15638	CYP72C1, SOB7; cytochrome P450 family 72 subfamily C polypeptide 1
C528634	1.280	0.044403128		
C397561	-2.289	0.044449549		
C318649	2.662	0.044595365		
C496375	-1.162	0.044595365		
C537101	-0.750	0.04495933	K02987	RP-S4e, RPS4; small subunit ribosomal protein S4e
C346642	-2.630	0.045066938		
scaffold1453	1.679	0.045066938		
scaffold26691	1.358	0.045066938		
C404397	-0.696	0.045290743		
C343410	2.516	0.045394016		
C451617	1.186	0.045506092		
scaffold7111	0.737	0.045506092		
C492814	-2.815	0.045523335	K11253	H3; histone H3
C299294	1.632	0.045667735		
C535659	0.856	0.045667735		
C548595	-0.526	0.045667735	K11437	PRMT6; type I protein arginine methyltransferase [EC:2.1.1.319]

scaffold18917	-0.597	0.045731295		
scaffold25520	-0.810	0.045800969		
C537845	-0.765	0.045809274	K00326	E1.6.2.2; cytochrome-b5 reductase [EC:1.6.2.2]
C539159	-0.749	0.045843462	K00599	METTL6; methyltransferase-like protein 6 [EC:2.1.1.-]
C370706	1.469	0.045927081		
scaffold1873	-1.726	0.04605943	K00454	LOX2S; lipoxygenase [EC:1.13.11.12]
scaffold27188	1.743	0.04605943	K17609	NXN; nucleoredoxin [EC:1.8.1.8]
C438036	-0.568	0.046125154		
scaffold4073	1.337	0.046125154		
C527328	-0.836	0.046184288		
scaffold13789	2.406	0.046190066	K22063	ISCA1; iron-sulfur cluster assembly 1
scaffold27365	1.648	0.046399694	K08235	E2.4.1.207; xyloglucan:xyloglucosyl transferase [EC:2.4.1.207]
scaffold16977	-1.913	0.046417334		
scaffold23095	-1.488	0.046430278		
C505495	-1.342	0.046431902		
scaffold2706	2.218	0.046431902	K01388	MMP1; matrix metalloproteinase-1 (interstitial collagenase) [EC:3.4.24.7]
scaffold10311	3.622	0.046455523		
scaffold15587	1.472	0.046455523		
scaffold20420	-1.026	0.046455523	K12180	COPS7, CSN7; COP9 signalosome complex subunit 7
scaffold25856	1.290	0.046455523		
scaffold23793	-1.536	0.046584396		
C417183	-1.104	0.046604755		
C544303	-0.626	0.046620402		
scaffold26818	-0.684	0.046620402		
C519286	2.157	0.046675077		
C452575	-1.734	0.046678431		
C294173	2.612	0.046724274		
C447708	4.358	0.046724274		

scaffold12785	-1.658	0.046724274	K16732	PRC1; protein regulator of cytokinesis 1
scaffold21625	-0.575	0.046724274	K17261	CAP1_2, SRV2; adenylyl cyclase-associated protein
C513036	-1.858	0.046756354		
C202446	-5.830	0.046829408		
scaffold26344	2.900	0.046903024		
scaffold1349	1.079	0.046911208	K05658	ABCB1, CD243; ATP-binding cassette, subfamily B (MDR/TAP), member 1 [EC:3.6.3.44]
C429626	2.468	0.046983882		
C456329	-1.596	0.046983882		
C485703	-0.831	0.046983882		
C487103	1.799	0.046983882		
scaffold2752	-2.162	0.046983882	K00799	GST, gst; glutathione S-transferase [EC:2.5.1.18]
scaffold6423	-0.925	0.046983882	K09422	MYBP; transcription factor MYB, plant
scaffold25817	-1.170	0.047024484		
scaffold14967	-1.235	0.04709235	K12161	URM1; ubiquitin related modifier 1
C508556	-1.754	0.04723449		
scaffold20475	-0.814	0.047254618	K09517	DNAJB11; DnaJ homolog subfamily B member 11
scaffold806	1.906	0.047297651		
scaffold24609	0.765	0.047322649		
scaffold11915	2.147	0.047693255		
scaffold420	-0.836	0.04781515		
C437824	1.565	0.047842332		
C420353	2.268	0.047846509		
scaffold26171	1.512	0.047846509		
scaffold30042	-0.555	0.047846509		
scaffold32650	-2.611	0.047888694	K06892	F6H1; feruloyl-CoA ortho-hydroxylase [EC:1.14.11.-]
scaffold12463	-1.822	0.047975973		
C490521	-1.053	0.048136823		
C542075	1.931	0.048136823	K01054	MGLL; acylglycerol lipase [EC:3.1.1.23]

scaffold16074	-1.610	0.048159082	K00382	DLD, lpd, pdhD; dihydrolipoamide dehydrogenase [EC:1.8.1.4]
C536983	-0.947	0.048202995		
scaffold27998	-1.492	0.048416604	K04733	IRAK4; interleukin-1 receptor-associated kinase 4 [EC:2.7.11.1]
scaffold25865	0.888	0.048515204	K00366	nirA; ferredoxin-nitrite reductase [EC:1.7.7.1]
C355822	1.426	0.04852945		
scaffold19923	3.762	0.04852945		
C538073	-1.213	0.048667633		
scaffold8994	1.048	0.04879263	K20718	ER; LRR receptor-like serine/threonine-protein kinase ERECTA [EC:2.7.11.1]
scaffold24925	1.174	0.048860821		
C380174	-1.265	0.048873575		
C432340	-2.042	0.048873575	K11971	RNF14, ARA54; E3 ubiquitin-protein ligase RNF14 [EC:2.3.2.31]
scaffold2653	0.830	0.048873575	K01595	ppc; phosphoenolpyruvate carboxylase [EC:4.1.1.31]
scaffold32431	1.501	0.048873575	K15014	SLC29A1_2_3, ENT1_2_3; solute carrier family 29 (equilibrative nucleoside transporter), member 1/2/3
C482083	-1.017	0.048883288		
C190154	-2.345	0.049156075		
C544193	0.814	0.049156075		
C536257	0.983	0.049232143		
C417753	2.126	0.049292849		
scaffold28661	-0.878	0.049301841	K03978	engB; GTP-binding protein
C552543	0.861	0.049319344		
scaffold2456	-1.060	0.049364424		
C175503	-1.371	0.049390483	K00454	LOX2S; lipoxygenase [EC:1.13.11.12]
C483793	-0.958	0.049390483	K03377	CASD1; N-acetylneuraminate 9-O-acetyltransferase [EC:2.3.1.45]
C416033	-2.060	0.049401387		
C427533	1.751	0.049401387		
C516936	1.994	0.049401387		
scaffold19493	3.146	0.049437757		

scaffold29556	1.433	0.049437757		
scaffold29673	2.394	0.049437757		
C529546	1.908	0.049650866		
scaffold22722	-0.810	0.049650866	K02915	RP-L34e, RPL34; large subunit ribosomal protein L34e
C542269	1.757	0.049702443	K18980	EO, FaQR; 2-methylene-furan-3-one reductase [EC:1.3.1.105]
C523042	1.629	0.049754857		
C551733	-0.785	0.049754857		
scaffold5814	-1.865	0.049816675		
C542955	-0.739	0.049972577	K00645	fabD; [acyl-carrier-protein] S-malonyltransferase [EC:2.3.1.39]
scaffold23068	1.201	0.049972577	K08235	E2.4.1.207; xyloglucan:xyloglucosyl transferase [EC:2.4.1.207]

- 34 **Supplementary Table T7.** Gene Ontology (GO) terms significantly enriched among DEGs upregulated in *C. florida*, identified using
- 35 BiNGO plugin in Cytoscape.

Ontology	GO-ID	Description
<u>Upregulated genes</u>		
<i>Biological process</i>		
	10411	xyloglucan metabolic process
	10383	cell wall polysaccharide metabolic process
	10410	hemicellulose metabolic process
	44042	glucan metabolic process
	6073	cellular glucan metabolic process
	44264	cellular polysaccharide metabolic process
	15893	drug transport
	6855	drug transmembrane transport
	42493	response to drug
	5976	polysaccharide metabolic process
	71554	cell wall organization or biogenesis
	42546	cell wall biogenesis
	10817	regulation of hormone levels
	34754	cellular hormone metabolic process
	42445	hormone metabolic process
	9690	cytokinin metabolic process
	44036	cell wall macromolecule metabolic process
	30244	cellulose biosynthetic process
	44262	cellular carbohydrate metabolic process
	6468	protein phosphorylation
	30243	cellulose metabolic process
<i>Molecular function</i>		

oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular
 16705 oxygen
 16762 xyloglucan:xyloglucosyl transferase activity
 5506 iron ion binding
 90484 drug transporter activity
 15238 drug transmembrane transporter activity
 16758 transferase activity, transferring hexosyl groups
 20037 heme binding
 46906 tetrapyrrole binding
 16757 transferase activity, transferring glycosyl groups
 16740 transferase activity
 30247 polysaccharide binding
 1871 pattern binding
 19139 cytokinin dehydrogenase activity
 15297 antiporter activity
 16759 cellulose synthase activity
 16760 cellulose synthase (UDP-forming) activity
 30246 carbohydrate binding
 4672 protein kinase activity
 15291 secondary active transmembrane transporter activity
 30234 enzyme regulator activity
 4553 hydrolase activity, hydrolyzing O-glycosyl compounds
 4857 enzyme inhibitor activity
 4842 ubiquitin-protein transferase activity
 19787 ubiquitin-like protein transferase activity
 16798 hydrolase activity, acting on glycosyl bonds
 16773 phosphotransferase activity, alcohol group as acceptor
 98772 molecular function regulator
 16301 kinase activity

<i>Cellular component</i>	30599	pectinesterase activity
	48046	apoplast
	30312	external encapsulating structure
	5618	cell wall
	5576	extracellular region
	16020	membrane
	71944	cell periphery
<i>Slim ontology</i>	30312	external encapsulating structure
	5618	cell wall
	16740	transferase activity
	5576	extracellular region
	30246	carbohydrate binding
	30234	enzyme regulator activity
	6464	cellular protein modification process
	16301	kinase activity
	5215	transporter activity

Downregulated genes

<i>Molecular function</i>	4553	hydrolase activity, hydrolyzing O-glycosyl compounds
	16740	transferase activity
	16301	kinase activity
	4672	protein kinase activity
	16773	phosphotransferase activity, alcohol group as acceptor
	16798	hydrolase activity, acting on glycosyl bonds
	16772	transferase activity, transferring phosphorus-containing groups
<i>Slim ontology</i>	16740	transferase activity

16301 kinase activity
6464 cellular protein modification process
15979 photosynthesis
5576 extracellular region

37 **Supplementary Table T8.** Gene Ontology (GO) terms significantly enriched among DEGs upregulated in *C. kousa*, identified using
 38 BiNGO plugin in Cytoscape.

Ontology	GO-ID	Description
	<u>Upregulated genes</u>	
<i>Biological process</i>		
	GO-ID	Description
	10411	xyloglucan metabolic process
	10383	cell wall polysaccharide metabolic process
	10410	hemicellulose metabolic process
	71554	cell wall organization or biogenesis
	55114	oxidation-reduction process
	42546	cell wall biogenesis
	44042	glucan metabolic process
	6073	cellular glucan metabolic process
	44264	cellular polysaccharide metabolic process
	44036	cell wall macromolecule metabolic process
	5976	polysaccharide metabolic process
	42545	cell wall modification
	44262	cellular carbohydrate metabolic process
	44710	single-organism metabolic process
	44699	single-organism process
	45229	external encapsulating structure organization
	71555	cell wall organization
	10817	regulation of hormone levels
	34754	cellular hormone metabolic process
	42445	hormone metabolic process
	9690	cytokinin metabolic process
	44092	negative regulation of molecular function

<i>Molecular function</i>	43086	negative regulation of catalytic activity
		oxidoreductase activity, acting on paired donors, with incorporation or reduction of
	16705	molecular oxygen
	20037	heme binding
	46906	tetrapyrrole binding
	5506	iron ion binding
	16491	oxidoreductase activity
	16762	xyloglucan:xyloglucosyl transferase activity
	16758	transferase activity, transferring hexosyl groups
	46914	transition metal ion binding
	16757	transferase activity, transferring glycosyl groups
	3824	catalytic activity
	30599	pectinesterase activity
	52689	carboxylic ester hydrolase activity
	19139	cytokinin dehydrogenase activity
	4857	enzyme inhibitor activity
	16843	amine-lyase activity
	16844	strictosidine synthase activity
<i>Cellular component</i>	30312	external encapsulating structure
	5618	cell wall
	48046	apoplast
	71944	cell periphery
	5576	extracellular region
<i>Slim ontology</i>	30312	external encapsulating structure
	5618	cell wall
	3824	catalytic activity

	5576	extracellular region
		<u>Downregulated genes</u>
<i>Biological process</i>		
	6457	protein folding
	46394	carboxylic acid biosynthetic process
	6564	L-serine biosynthetic process
	8652	cellular amino acid biosynthetic process
	16053	organic acid biosynthetic process
	9069	serine family amino acid metabolic process
	6563	L-serine metabolic process
	6520	cellular amino acid metabolic process
<i>Molecular function</i>		
	4648	O-phospho-L-serine:2-oxoglutarate aminotransferase activity
	16740	transferase activity
	3824	catalytic activity
	4791	thioredoxin-disulfide reductase activity
	8171	O-methyltransferase activity
<i>Slim ontology</i>		
	16740	transferase activity
	3824	catalytic activity

40 **Supplementary Table T9.** Normalized expression matrix of 14 phenylpropanoid pathway genes across 13 RNA-seq samples from
 41 five *Cornus* cultivars. Includes gene IDs and expression values used for heatmap visualization (Figure 5).

Organism	Cornus florida	Cornus florida	Cornus florida	Cornus florida	Cornus florida	Cornus florida	Cornus florida	Cornus florida	Cornus kousa	Cornus kousa	Cornus kousa	Cornus kousa	Cornus kousa
Phenotype	red Cherokee Brave	red Cherokee Brave	red Cherokee Chief	red Cherokee Chief	red Cherokee Chief	white Cloud Nine	white Cloud Nine	white Cloud Nine	red Rosy Teacups	red Rosy Teacups	red Rosy Teacups	white Greensleeves	white Greensleeves
Genotype													
Name	SRR21411472	SRR21411471	SRR21411467	SRR21411463	SRR21411462	SRR21411466	SRR21411461	SRR21411460	SRR21411470	SRR21411469	SRR21411465	SRR21411464	SRR21411468
01_PAL TRINITY_DN1512_c0_g1_i15	1682	1993	1191	867	4251	1331	2700	3119	347	568	291	136	243
01_PAL TRINITY_DN1512_c0_g1_i27	17574	18488	17445	22144	28424	29324	38382	40575	3293	2950	2703	2307	3025
01_PAL TRINITY_DN1512_c0_g1_i8	13767	14643	10122	12055	22020	17185	24479	27594	9847	6676	5819	9111	7011
01_PAL TRINITY_DN8939_c0_g2_i1	1926	1936	1637	3592	4881	1836	4721	5956	4140	4747	10881	4817	6933
01_PAL TRINITY_DN8939_c0_g2_i2		16	17				40	11	7338	4085	4524	8490	5173
01_PAL TRINITY_DN8939_c0_g3_i1	745	1049	671	348	728	793	859	657	9285	12823	6299	8632	9445
02_C4H TRINITY_DN1033_c0_g1_i1	2388	2729	4482	2741	5067	13170	13859	8585	61370	40441	59413	70003	56883
02_C4H TRINITY_DN1033_c0_g1_i2	75	150	154	64	218	128	248	368	13242	17693	22465	24116	21817
02_C4H TRINITY_DN1033_c0_g1_i4	268	221	154	243	346	389	546	553	7881	20438	17562	7757	19578
02_C4H TRINITY_DN1937_c0_g1_i2	26378	30952	24720	18698	34618	60971	75254	53662	149	79	257	566	266
02_C4H TRINITY_DN1937_c0_g1_i4	22869	22284	26386	23103	26948	31856	31231	28086	1305	1765	1988	269	1260
02_C4H TRINITY_DN1937_c0_g1_i6	1736	660	1196	7154	4027	2385	1560	1620		254			91
03_4CL TRINITY_DN1672_c0_g1_i1	274	945	357	727	1132	910	1069	1762	288	418	115	203	114
03_4CL TRINITY_DN1672_c0_g1_i3	76	101	6	255	435	39		411	8	21	19		28
03_4CL TRINITY_DN1672_c0_g1_i4	100	168	119	109	417	491	351	649	67	85	75	117	87
03_4CL TRINITY_DN1672_c0_g1_i5	39463	60265	34048	34926	49654	66472	73497	77774	2803	2648	3004	148	1862
03_4CL TRINITY_DN3755_c0_g1_i1	32	131	24	22	26	64	145	113	23934	27028	21843	34823	25798
03_4CL TRINITY_DN4362_c0_g1_i1	6128	3510	4219	5199	1401	1358	8359	2833	902		69		568
04_CHS TRINITY_DN1124_c0_g1_i1	8775	18519	8684	8493	9614	31329	23919	22740	20273	12616	25625	18781	34414
04_CHS TRINITY_DN14545_c0_g1_i1	2603	4697	2236	2087	1571	6751	7448	4553		189	212		900
04_CHS TRINITY_DN14545_c0_g1_i2	165	348			826	1467		1154	2760	1780	1845	1273	4612

04_CHS TRINITY_DN1578_c1_g1_i3	12056	11496	18266	14103	10613	12290	7294	7882	191608	293190	227343	240242	229449
04_CHS TRINITY_DN4188_c0_g1_i1	112036	108423	136706	134844	98347	174768	147553	115909	117652	162272	188342	104639	152561
04_CHS TRINITY_DN54657_c0_g1_i1	237520	195083	241000	213780	256991	191571	182081	228322	2293	13142	4321	1960	5165
05_CHI TRINITY_DN13710_c0_g1_i1	146	210	127	96	113	301	199	212	41817	52379	39908	20353	50189
05_CHI TRINITY_DN607_c0_g1_i2	82478	91563	121008	128643	94953	21410	14655	18667	435	775	751	1266	917
05_CHI TRINITY_DN607_c0_g1_i4	368		449	1134	514	75	187	534	963	829	789		652
06_F3H TRINITY_DN1651_c0_g1_i1	10773	13370	11598	13709	23248	4556	8913	13981	46	7	51	187	51
06_F3H TRINITY_DN28_c5_g1_i1	154150	117331	151974	150227	125501	96335	83521	87078	5378	6244	6927	3164	4761
06_F3H TRINITY_DN5669_c0_g1_i4	8		10	12	24		9		1911	105	592	1142	424
06_F3H TRINITY_DN6034_c0_g1_i2	2109	6231	3049	3639	7579	3326	1872	3457	14		7	10	10
06_F3H TRINITY_DN6766_c7_g1_i1	247	376	443	313	437	851	559	678	111234	143641	120159	79313	129922
06_F3H TRINITY_DN8903_c2_g2_i2	13	15	21	13	33	36	101	30	10883	1113	7932	17432	5492
07_FLS TRINITY_DN12984_c0_g1_i1	174790	163504	94840	111130	101170	80860	105330	95581	94626	3395	16618	131502	11101
07_FLS TRINITY_DN2707_c0_g1_i6	1463	3609	2664	3265	2211	3330	3891	4001	6		18	20	14
07_FLS TRINITY_DN2707_c0_g1_i8	2247	2478	1491	705	1587	2411	2729	1669	6	11	5	25	
07_FLS TRINITY_DN2824_c0_g1_i8	5024	6076	2397	1753	2021	11401	11391	6503	47	19	41	103	117
07_FLS TRINITY_DN52108_c0_g1_i1	654	905	555	365	417	637	650	696	3413	1175	1569	4578	3615
07_FLS TRINITY_DN68864_c0_g1_i1				13	5	40		42	134	32	71	532	305
08_F3'H TRINITY_DN1460_c0_g1_i1	2571	4570	4789	9343	3933	9857	9539	10379	189	25	94	183	86
08_F3'H TRINITY_DN17047_c0_g1_i1	443	286	2391	2826	161	1247	592	1090	57	4758	428	24	2668
08_F3'H TRINITY_DN1836_c1_g1_i1	243	415	283	174	219	473	503	477	56373	47028	43940	70312	52508
08_F3'H TRINITY_DN33534_c0_g1_i1	17	35	40	15	36	78	68	62	16496	1678	13743	21308	5908
08_F3'H TRINITY_DN496_c1_g2_i2	11579	17141	8827	7568	9300	17103	19297	19206	16218	11441	12759	3712	5877
08_F3'H TRINITY_DN9158_c2_g1_i1	34	53	2829	873	3715	75	73	133	1772	2039	3617	9771	7155
09_FLS TRINITY_DN12984_c0_g1_i1	174790	163504	94840	111130	101170	80860	105330	95581	94626	3395	16618	131502	11101
09_FLS TRINITY_DN2707_c0_g1_i6	1463	3609	2664	3265	2211	3330	3891	4001	6		18	20	14
09_FLS TRINITY_DN2707_c0_g1_i8	2247	2478	1491	705	1587	2411	2729	1669	6	11	5	25	
09_FLS TRINITY_DN2824_c0_g1_i8	5024	6076	2397	1753	2021	11401	11391	6503	47	19	41	103	117
09_FLS TRINITY_DN52108_c0_g1_i1	654	905	555	365	417	637	650	696	3413	1175	1569	4578	3615

09_FLS TRINITY_DN68864_c0_g1_i1				13	5	40		42	134	32	71	532	305
10_FDR TRINITY_DN4923_c0_g1_i3					12				672	969	1140	1518	2422
10_FDR TRINITY_DN4923_c0_g1_i5									191	138	177	46	280
10_FDR TRINITY_DN4923_c0_g1_i6	64	222	107	14	92	268	279	174	2483	1904	3648	1225	4108
10_FDR TRINITY_DN4923_c1_g1_i3	146	263	96	252	253	170	247	423	4940	3063	5315	1323	5854
10_FDR TRINITY_DN57678_c0_g1_i1	8416	11560	7910	7977	10363	8398	8551	10907	29696	9821	23637	8988	20340
10_FDR TRINITY_DN683_c0_g2_i1	8880	16162	8370	8104	12421	20290	25357	24472	10931	8420	8546	9019	18196
10_FDR TRINITY_DN683_c1_g1_i1	848	1353	911	602	696	1253	1159	1114	1765	1093	2191	550	1864
10_FDR TRINITY_DN683_c1_g3_i1	3990	11068	2708	1712	4698	15408	12153	11551	253	192	505	470	408
11_LAR TRINITY_DN11466_c0_g1_i2	480	622	490	661	930	1497	851	2250	3677	20665	12380	326	14611
11_LAR TRINITY_DN13855_c0_g1_i1	81	134	75	47	78	112	115	279	16115	644	7374	17199	2719
11_LAR TRINITY_DN15612_c0_g1_i3	60	207	67	91	212	290	101	251	215	148	79	575	303
11_LAR TRINITY_DN15612_c0_g1_i4	1370	2023	3242	3753	2453	2246	2260	4441	4392	579	3245	1059	1445
11_LAR TRINITY_DN3004_c1_g1_i1	250	375	396	527	176	70	141	40	17987	2420	11938	3427	5386
11_LAR TRINITY_DN3181_c0_g1_i4	263	523	461	288	401	209	283	625	811	25	140	715	93
12_ANS TRINITY_DN2824_c0_g1_i1	2316	6032	1303	464	1091	6472	9640	7645					
12_ANS TRINITY_DN2922_c0_g1_i1	452	1430	3524	302	1406	4478	831	2918	25636	865	2341	12430	4178
12_ANS TRINITY_DN9186_c4_g1_i1	1144	865	7688	13988	1352	5651	2490	5597	15635	43656	33852	1315	36125
13_UFGT TRINITY_DN1648_c0_g1_i1	9123	10575	10775	14991	17062	18133	16228	18049	854	58	13	415	87
13_UFGT TRINITY_DN2030_c0_g1_i4	1940	3487	2427	1633	3486	3787	3782	3986	9608	1229	7169	12283	7271
13_UFGT TRINITY_DN67516_c0_g1_i1	1477	3121	1341	1186	2072	6357	4906	4783	319	323	148	36	226
13_UFGT TRINITY_DN7708_c0_g1_i1								59		767	658	18431	3124
13_UFGT TRINITY_DN7708_c0_g1_i5		19	574	352	106		84	25	5837	152	137	94	557
13_UFGT TRINITY_DN7708_c0_g1_i6	5	40	75	53	22	71			5122	195	197	2522	869
14_UFGaIT TRINITY_DN1648_c0_g1_i3	706	2944	3837	1631	884	3560	866	1049	55	71	138	2704	476

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44 **Supplementary Table T10.** Summary of gene expression patterns and regulatory roles of candidate MYB transcription factors and
 45 structural genes used in the regulatory network diagram (Figure 6).

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RNAseq							qRT-PCR				
	Cultivar	Cherokee Brave	Cherokee Chief	Cloud Nine	Greensleeves	Rosy Teacups	Cherokee Brave	Cherokee Chief	Cloud Nine	Greensleeves	Rosy Teacups
Biosynthetic genes	CHS	59,310	72,385	68,649	74,439	72,181	0.122347	1.30718	2.316051	0.220051	0.301854
	CHI	34,953	38,560	6,249	15,405	14,675	0.070134	0.325537	1.110746	0.431329	0.451316
	F3H	27,693	27,324	19,082	24,485	20,159	0.334709	0.965182	0.200766		
	CkMYB1				250,000	313,333				0.439753	4.603546
	CkMYB2				430,000	283,333				0.607235	0.130656
	CfMYB1 80	180,000	540,000	46,667			0.188234	3.028993	1.248436		
MYB TFs	CfMYB2	65,000	36,667	53,333			0.121665	0.746938	0.513667		
	CfMYB3	490,000	266,667	620,000			0.121665	0.746938	1.248436		