

JUB1-amiRNA

В



JUB1-amiRNA

WT

#### Supplemental Figure 1. Early Leaf Senescence in *JUB1-amiRNA* Lines.

(A) *JUB1* expression level is reduced in two *JUB1-amiRNA* lines (lines #66 and #24). Data are the means  $\pm$  SD; WT, n = 3; #66, n = 6; #24, n = 1. (B) *JUB1-amiRNA* lines exhibit earlier leaf senescence and bolt earlier (~2 d), as compared to wild-type (WT) plants. The picture was taken ~40 days after sowing.



. 10 μm

Supplemental Figure 2. Localization of JUB1-GFP Fusion Protein in Guard Cells of Transgenic *Arabidopsis*.

(A) GFP fluorescence. (B) Chlorophyll autofluorescence. (C) Transmitted light. (D) Merged. Arrows indicate green fluorescence due to the presence of JUB1-GFP fusion protein in nuclei.





В









# Supplemental Figure 3. Phenotypic and Physiological Analyses of Transgenic Plants Overexpressing *JUB1* under Control of Stress-inducible Promoter *RD29A*.

(A) *JUB1* expression in individual *RD29A:JUB1* transformants and the wild type (WT), determined by qRT-PCR (single measurements). Plants were grown in longday condition (16 h / 8 h, light / dark) and the five biggest rosette leaves of 35-dayold plants were harvested for expression analysis. Note the correlation of *JUB1* expression level and the strength of the observed phenotype (delayed bolting). (B) Phenotypes of 43-day-old 35S:*JUB1*, *RD29A:JUB1* (#4) and WT plants. (C) Leaves 1 to 11 of 50-day-old WT and *RD29A:JUB1* (#4) plants; leaf no. 1 is the first leaf emerging after the cotyledons. Delayed leaf senescence is observed in the overexpression line. (D) Chlorophyll content of leaves 8, 9 and 10 of *RD29A:JUB1* (#4) and WT plants at 50 DAS (from leaves equivalent to those shown in panel C). Values are means  $\pm$  SD; n = 3.



#### Supplemental Figure 4. Confirmation of T-DNA Insertion in *jub1-1 Mutant*.

(A) Schematic presentation of JUB1 (transcribed region) with the T-DNA insertion point labelled. Positions of primers used for PCR are shown by horizontal arrows. Numbers indicate nucleotide positions. (B) PCR-mediated amplification of genomic DNA using JUB1-specific primer GP (5'-ACTGTGTTGGTCTCAAGAAATC-3') and T-DNA-specific primer LBb1 (5'-GCGTGGACCGCTTGCTGCAACT-3'). The DNA band visible in the jub1-1 lane, indicated by a star (\*), was isolated from the gel and sequenced to confirm the T-DNA insertion site. No such band was generated from Arabidopsis Col-0 DNA, as expected. (C) Amplification of genomic DNA using JUB1-(5'-AGGAATAGCGTTCGACCAAAC-3') specific primers RP and LP (5'-TGGAATCTACTGTACGGTGGC-3'). DNA is only amplified from the Col-0 accession, but not from the homozygous jub1-1 mutant (results from two PCRs shown). Genomic input DNA was omitted in lane  $H_2O'$ . Fragment sizes are indicated.



#### Supplemental Figure 5. Dark-induced Senescence is Affected in Detached Leaves of *JUB1* Overexpressors.

(A) Rosette leaves of 39-day-old 35S:JUB1 overexpression, jub1-1 and EV control plants were detached and placed on moist filter paper in Petri dishes. Petri dishes were kept in continuous darkness for 6 days. Note the retarded senescence in 35S:JUB1 leaves. Similar results were obtained in two additional independent experiments. (B) Chlorophyll content in leaves incubated for 6 days. Data are the means of at least three replicates  $\pm$  SD obtained from plants at 39 DAS. For control experiments, plants were kept at a 16 h / 8 h light / dark cycle.

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## Supplemental Figure 6. Gene Expression and Hormone Levels in *Arabidopsis* Plants Subjected to Different Treatments.

(A) Induction of JUB1 expression upon pharmacological inhibition of the H<sub>2</sub>O<sub>2</sub>scavenging enzyme catalase by 3-amino-1,2,4-triazole (3-AT) in Arabidopsis seedlings. Two-week-old seedlings were transferred to medium containing 1 mM 3-AT and incubated for 5 h and 7 h, respectively. Values represent the means  $\pm$  SD from three independent biological experiments. Numbers on the Y axis indicate log2 fold-change expression ratio compared to untreated samples. (B) Analysis of JUB1 expression under salt stress. Arabidopsis Col-0 plants were grown in a hydroponic culture system and were subjected to short- or long-term (6 h and 4 d, respectively) salinity stress (150 mM NaCl). Salt stress was applied to plants at developmental stage 1, according to Balazadeh et al. (2010a). Values represent the means ± SD from three independent biological experiments. (C) Determination of dihydrozeatin (DHZ) and dihydrozeatin riboside (DHZR) in 43-day-old 35S:JUB1, jub1-1 and WT plants grown at long-day condition (16 h light / 8 h dark). Values represent the means ± SD from five independent biological sets of samples. (D) Induction of JUB1, DREB2A and HsfA3 expression after 5 h of H<sub>2</sub>O<sub>2</sub> treatment. (E) Induction of *MBF1c* expression after 1 h and 5 h of H<sub>2</sub>O<sub>2</sub> treatment. In (D) and (E), two-week-old seedlings were transferred to medium containing 10 mM H<sub>2</sub>O<sub>2</sub> and incubated for the indicated times. Numbers on the Y axis indicate log2 fold-change expression ratio compared to untreated control. Means from two independent experiments are shown.



Supplemental Figure 7.  $H_2O_2$  Content and *JUB1* Expression Level in Individual Leaves of 35-day-old Wild-type Plants.

Leaves were numbered consecutively. Leaf no. 2 was the second leaf emerging after the cotyledons. Younger leaves emerging after leaf number 14 were pooled in groups A (> 25 mm leaf length), B (15-25 mm) and C (below 15 mm), respectively. (A) *JUB1* expression was determined by qRT-PCR. (B)  $H_2O_2$  levels determined by Amplex Red assay. Data are the means of at least three technical replicates  $\pm$  SD from a representative experiment that included 35 plants.

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Supplemental Figure 8. Effect of NaCl, Cellulase and Methyl Viologen on *JUB1* Expression.

(A) GUS activity of  $Pro_{JUB1}$ : GUS seedlings measured by MUG assay 24 h after treatment with 150 mM or 200 mM NaCl, respectively. The asterisk (\*) indicates significant difference (p < 0.05) from the control treatment. (B) Twelve-day-old  $Pro_{JUB1}$ : GUS were treated with 50 µM methyl viologen or 0.5% (w/v) cellulase for 3 h. Elevated GUS activity was observed in both treatments. (C) JUB1 transcript abundance was determined by qRT-PCR in whole seedlings of wild-type Arabidopsis plants treated with 0.1% (w/v) cellulase or 10 µM methyl viologen after 5 h. Data are the means of three replicates  $\pm$  SD.

Α



- H<sub>2</sub>O<sub>2</sub>

В



10 mM H<sub>2</sub>O<sub>2</sub>

## Supplemental Figure 9. Effect of $H_2O_2$ on Detached Leaves of the *jub1-1* Mutant.

(A, B) Detached leaves of the 35-day-old *jub1-1* mutant and empty vector (EV) plants were incubated for 5 days in the absence or presence of 10 mM  $H_2O_2$ . Leaves of *jub1-1* plants retained less chlorophyll than those of the EV control. Data in (B) were obtained as three technical replicates from combined leaves of the experiment shown in (A). Means  $\pm$  SD are given.



#### Supplemental Figure 10. The *jub1-1* Mutant Exhibits Decreased Heat Stress Tolerance Compared to the Wild type.

Two-week-old *Arabidopsis* seedlings of *jub1-1* and wild-type (WT) plants were incubated at  $45^{\circ}$ C for 5 h and then returned to the growth chamber at 22°C for 5 d. Note the reduced survival of *jub1-1* seedlings after heat stress.



#### Supplemental Figure 11. Enhanced Heat Stress Tolerance of *JUB1* Overexpressor.

Seven-day-old *jub1-1*, wild-type (WT) and 35S:JUB1-GFP seedlings grown at 23°C in a phytotron were transferred to 45°C for 45 min (by floating the media plates on water of a pre-heated water bath) and then returned to growth temperature. Photographs were taken 8 days later. Seedlings surviving the heat stress treatment were counted. The graph shows the results obtained from three independent biological experiments. Means  $\pm$  SD.



Supplemental Figure 12. Expression of Secondary Metaboliteassociated Genes in *35S:JUB1*, *jub1-1* and Wild-type (WT) Plants, Determined by qRT-PCR.

(A) Anthocyanin biosynthetic genes. (B) Phenylpropanoid biosynthetic genes. (C) Flavonol-specific gene. Abbreviations: F3<sup>'</sup>H (TT7), flavonoid 3<sup>'</sup>hydroxylase; DFR (TT3),dihydroflavonol reductase; ANS (TT18),(UGT75C1), anthocyanidin synthase; AGT anthocyanin 5-0glucosyltransferase; AGT (UGT79B1), anthocyanin 3-O-glucoside 2"-Oxylosyltransferas; GST (TT19), glutathione-S-transferase; bHLH (TT8), transcription factor; WRKY (TTG2), transcription factor; PAP1, AtMYB75, transcription factor; PAP2, AtMYB90, transcription factor; FAH, CYP84A1, ferulate 5-hydroxylase; ALDH, ALDH2C4, aldehyde dehydrogenase; SMT, SNG1, malate sinapoyltransferase; FLS, AtFLS1, flavonol synthase. Data represent means  $\pm$  SD from three independent experiments. Asterisks (\*) indicate significant differences compared to WT (p < 0.05; Student's *t*-test).

AGI code	Gene	Line	Line Source	
At1g01720	ANAC002	SALK_067648	SALK	
		SALK_057618	SALK	
		SALK_090242	SALK	
At1g02220	ANAC003	SAIL_260_B02 (pCSA110)	Syngenta	
At1g34180	ANAC016	SALK_001597*	SALK	
		SALK_126338	SALK	
At1g52880	ANAC018	SALK_131128	SALK	
		SALK_056767	SALK	
At1g52890	ANAC019	SALK_096295	SALK	
		SALK_096310	SALK	
At1g69490	ANAC029/AtNAP	SALK_005010	SALK	
At1g77450	ANAC032	SALK_087702*	SALK	
At2g33480	ANAC041	SALK_066378	SALK	
		SALK_010291	SALK	
At2g43000	ANAC042/JUB1	SALK_036474*	SALK	
At3g04060	ANAC046	SALK_107861	SALK	
At3g04070	ANAC047	GABI_343H11-016164	GABI-KAT	
		SALK_066615	SALK	
At3g10500	ANAC053	SALK_009578	SALK	
		SALK_022946*	SALK	
At3g15500	ANAC055	SALK_014331	SALK	
		SALK_011069	SALK	
At3g15510	ANAC056	SALK_137131*	SALK	
At3g29035	ANAC059/ORS1	GK-778C04 (pAC161)	GABI-KAT	
At4g27410	ANAC072	SALK_063576	SALK	
		SALK_072286	SALK	
		SALK_083756	SALK	
At4g28530	ANAC074	SALK_094441	SALK	
		SALK_149691	SALK	
		SALK_104622*	SALK	
At5g13180	ANAC083/VNI2	SALK_143793	SALK	
At5g18270 ANAC087		SALK_011502*	SALK	
		SALK_079821	SALK	
At5g22290	ANAC089	SALK_099786	SALK	
At5g39610 ANAC092/ORE1		SALK_090154	SALK	
		SAIL_694_C04 (pDAP101)	Syngenta	
At5g63790	ANAC102	SALK_030702*	SALK	
		SALK_094437*	SALK	
At5g64530	ANAC104	SALK_023898*	SALK	
		SALK_046891*	SALK	
		SALK_022552	SALK	
At4g35580	NTL9	SALK_065051	SALK	
		SALK_102041*	SALK	

## Supplemental Table 1. NAC Transcription Factor T-DNA Insertion Lines Included in the Screen for Extended Longevity.

Mutants labelled with an asterisk (\*) were used in their homozygous state (with respect to the T-DNA insertion). CaMV 35S overexpressors of the following transcription factors were included in the longevity screen: At3g04070, At5g39610/ORE1, At3g29035/ORS1, At2g43000/JUB1, and At5g64530. Only *JUB1* overexpressors showed extended longevity.

PAL   At2g37040   APAL1   phenylalanine ammonia-lyase     PAL   At2g4230   APAL2   phenylalanine ammonia-lyase     PAL   At2g4230   APAL3   phenylalanine ammonia-lyase     C4H   At2g30490   CYP73A5   cinnamate-4-hydroxylase     C4H   At2g14240   At4CL1   4-coumarate CoA ligase     4CL   At3g1240   At4CL2   4-coumarate CoA ligase     4CL   At3g1240   At4CL3   4-coumarate CoA ligase     4CL   At3g1250   TT5   chalcone isomerase     CHI   At3g05270   CHI   chalcone isomerase     CHI   At5g05270   CHI   chalcone isomerase     F3H   At5g0540   FLS   flavonol 3-0-glucosyltransferase     F4SGICT   At5g0500   UGT78D1   flavonol 3-0-channosyltransferase     F3RhaT   At1g30530   UGT78D1   flavonol 3-0-channosyltransferase     F3RhaT   At1g30500   UGT89C1   flavonol 3-0-channosyltransferase     C3H   At2g40890   CYP98A3   coumarate 3-hydroxylase     CCA   At12g40890   CYP98A3   coumarate 3-hydroxylase     CCA   At14g30520   FAH1/CYP84A1   ferulate 5-hydroxylase     CAD   At3g19450   AtCAD4   cinnamoyl-cOA reductae <	Abbreviation	AGI code		Enzyme		
PALAt3g53260AtPAL2phenylalanine ammonia-lyasePALAt3g04230AtPAL3phenylalanine ammonia-lyaseC4HAt2g1040CYP73A5cimamate-Ahydroxylase4CLAt1g51680At4CL14-coumarate CoA ligase4CLAt3g21240At4CL34-coumarate CoA ligase4CLAt3g25060At4CL34-coumarate CoA ligaseCHIAt3g55120TT5chalcone isomeraseCHIAt3g5570CHIchalcone isomeraseF3HAt5g07900TT7flavonol 3'-bydroxylaseF3AAt5g07500UGT78D2flavonol 3'-o-glucosyltransferaseF3RhaTAt1g05000UGT78D1flavonol 3'-O-glucosyltransferaseF3RhaTAt1g05000UGT78D1flavonol 7-O-thannosyltransferaseF7RhaTAt1g06000UGT78D1flavonol 7-O-thannosyltransferaseC3HAt2g40890CYP98A3coumarate 3-hydroxylaseCCoAOMTAt4g34250AtCCR1cimanoyl-lacohol dehydrogenaseCADAt4g34200AtCR1cimanoyl-lacohol dehydrogenaseCADAt4g34203AtCCR1cimanoyl-aclohol dehydrogenaseCADAt4g34203ALCD4cimanoyl-aclohol dehydrogenaseCADAt4g24080CTYP8A1ferulate 5-hydroxylaseCADAt4g24030ALCD4cimanoyl-aclohol dehydrogenaseCADAt4g34200AtCCR1cimanoyl-aclohol dehydrogenaseCADAt4g24093ALDH2C4/ALDH1Aadehyde dehydrogenaseCADAt3g24503ALDH2C4/ALDH1A <td< td=""><td>PAL</td><td>At2g37040</td><td>AtPAL1</td><td>phenylalanine ammonia-lyase</td></td<>	PAL	At2g37040	AtPAL1	phenylalanine ammonia-lyase		
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CHIAt5g05270CHIchalcone isomeraseF37HAt5g07900TT7flavonoid 3'-hydroxylaseFLSAt5g08640FLS1flavonoid 3'-o-glucosyltransferaseF3GlcTAt5g17050UGT78D1flavonoid 3-O-glucosyltransferaseF3RhaTAt1g30530UGT78D1flavonoid 3-O-rhannosyltransferaseF7RhaTAt1g06000UGT89C1flavonoid 3-O-rhannosyltransferaseF7RhaTAt1g06000UGT89C1flavonoid 3-O-rhannosyltransferaseC3HAt2g40890CYP98A3coumarate 3-hydroxylaseCCoAOMTAt4g3050CCoAOMT1caffeoyl/CoA 3-O-metheltransferaseCCRAt1g15950AtCCR1cinnamoyl-CoA reductaseFAHAt4g36220FAH1/CYP84A1ferulate 5-hydroxylaseCADAt3g19450AtCAD4cinnamoyl-alcohol dehydrogenaseCADAt3g19450AtCAD5cinnamoyl-alcohol dehydrogenaseCADAt4g34230AtCAD4cinnamoyl-alcohol dehydrogenaseCADAt4g34230AtCAD5cinnamoyl-alcohol dehydrogenaseCMTAt5g54160AtCMT1caffeic acid/5-hydroxyferulic acid O- methyltransferaseflavonol 3'-O-methyltransferaseSGTAt3g24503ALDH2C4/ALDH1Aaldehyde dehydrogenaseSGTAt3g24500UGT75C1anthocyanin 5-O-glucosyltransferaseSMTAt2g22800TT3dihydroflavonol reductaseAGTAt4g24800TG3anthocyanin 5-O-glucoside 2"-O- xylosyltransferaseGSTAt5g42400UGT75C1anthocyanin 3-O-glucoside 6"-O- 	CHI	At3g55120	TT5	chalcone isomerase		
F3'HAt5g07990TT7flavonoid 3'-hydroxylaseFLSAt5g08640FLS1flavonol 3-O-glucosyltransferaseFd3GlcTAt5g17050UGT78D1flavonol 3-O-rhamosyltransferaseF7RhaTAt1g06000UGT8D1flavonol 3-O-rhamosyltransferaseF7RhaTAt1g06000UGT8D1flavonol 7-O-rhamnosyltransferaseF7RhaTAt1g10500UGT98D1flavonol 7-O-rhamnosyltransferaseC3HAt2g40890CYP98A3coumarte 3-hydroxylaseCCoAOMTAt4g34050CCoAOMT1caffeoyl/CoA 3-O-metheltransferaseCCRAt1g15950AtCCR1cinnamoyl-CoA reductaseFAHAt4g3620FAH1/CYP84A1ferulate 5-hydroxylaseCADAt4g319450AtCAD4cinnamoyl-alcohol dehydrogenaseCADAt4g34230AtCAD5cinnamoyl-alcohol dehydrogenaseCADAt4g34230AtCAD5cinnamoyl-alcohol dehydrogenaseALDHAt3g24503ALDH2C4/ALDH1Aaldehyde dehydrogenaseSGTAt3g21560UGT84A2sinapic acid 1-O-UDP-glucosyltransferaseSMTAt2g22990SNG1malate sinapoyltransferase.ANSAt4g22800TT3dihydroflavonol reductaseAGTAt3g24501UGT75C1anthocyanin 3-O-glucoside 2"-O- xylosyltransferaseAATAt3g29590ASG6":MaTanthocyanin 3-O-glucoside 6"-O- malonyltransferaseAATAt3g24502TTG1WD-40 repeat proteinAATAt1g03940A3G6"p-CouTcoumaroyltransferaseGSTAt5g45200 <t< td=""><td>CHI</td><td>At5g05270</td><td>СНІ</td><td>chalcone isomerase</td></t<>	CHI	At5g05270	СНІ	chalcone isomerase		
FLSAt5g08640FLS1flavonol synthaseFd3GlcTAt5g17050UGT78D2flavonol 3-O-glucosyltransferaseF3RhaTAt1g0500UGT78D1flavonol 3-O-rhannosyltransferaseF7RhaTAt1g06000UGT89C1flavonol 7-O-rhannosyltransferaseHCTAt5g48930HCThydroxycinnamoyltransferaseCOAOMTAt2g40890CYP98A3coumarte 3-hydroxylaseCCcAOMTAt4g34050CCoAOMT1caffcoyl/CA3-O-metheltransferaseCCAAt1g15950AtCCR1cinnamoyl-CoA reductaseFAHAt4g36220FAH1/CYP84A1ferulate 5-hydroxylaseCADAt3g19450AtCAD4cinnamoyl-alcohol dehydrogenaseCADAt3g19450AtCAD5cinnamoyl-alcohol dehydrogenaseCADAt3g19450AtCAD5cinnamoyl-alcohol dehydrogenaseOMTAt5g54160AtCMT1caffeic acid/5-hydroxyferulic acid O-methyltransferase/flavonol 3-O-methyltransferaseSGTAt3g21560UGT84A2sinapic acid 1-O-UDP-glucosyltransferaseSMTAt2g22900SNG1malate sinapoyltransferase.ANSAt4g28800TT3dihydroflavonol reductaseAGTAt4g34000UGT75C1anthocyanin 3-O-glucoside 2"-O-xylosyltransferaseAGTAt3g2950ASG6":'MaTanthocyanin 3-O-glucoside 6"-O-malonyltransferaseAATAt3g2950ASG6":'MaTanthocyanin 3-O-glucoside 6"-O-malonyltransferaseAATAt3g24500TTG1WD-40 repeat proteinAATAt3g24500TTG1WD-40 repeat protein <td>F3'H</td> <td>At5g07990</td> <td>TT7</td> <td>flavonoid 3'-hydroxylase</td>	F3'H	At5g07990	TT7	flavonoid 3'-hydroxylase		
Fd3GlcTAt5g17050UGT78D2flavonoid 3-O-glucosyltransferaseF3RhaTAt1g30530UGT78D1flavonoid 3-O-rhamnosyltransferaseF7RhaTAt1g06000UGT8D1flavonol 3-O-rhamnosyltransferaseHCTAt5g48930HCThydroxycinnamoyl-Coenzyme A shikimate/quinatehydroxycinnamoyl-Coenzyme A shikimate/quinatehydroxycinnamoyl-Coenzyme A shikimate/quinateC3HAt2g40890CYP98A3coumarate 3-hydroxylaseCCoAOMTAt4g34050CCoAOMT1caffeoyl/CoA 3-O-metheltransferaseCCRAt1g15950AtCCR1cinnamoyl-CoA reductaseFAHAt4g36220FAH1/CYP84A1ferulate 5-hydroxylaseCADAt3g19450AtCAD4cinnamoyl-alcohol dehydrogenaseCADAt4g34230AtCAD5cinnamoyl-alcohol dehydrogenaseOMTAt5g54160AtOMT1methyltransferase[flavonol 3'-O-methyltransferase]ALDHAt3g24503ALDH2C4/ALDH1Aaldehyde dehydrogenaseSGTAt3g21560UGT84A2sinapic acid 1-O-UDP-glucoyltransferaseSMTAt2g2280TT3dihydroflavonol reductaseAGTAt4g14090UGT75C1anthocyanin 5-O-glucosyltransferaseAGTAt3g25500ASG6'''MaTanthocyanin 5-O-glucoside 6''-O-malonyltransferaseAATAt3g2590ASG6'''MaTanthocyanin 5-O-glucoside 6''-O-malonyltransferaseGSTAt5g24520TTG1WD-40 repeat proteinHRAt4g09820TT8basic helix-loop-helix dimerisation regionWD40At5g24520TTG1	FLS	At5g08640	FLS1	flavonol synthase		
F3RhaTAt1g30530UGT78D1flavon013-O-rhamnosyltransferaseF7RhaTAt1g06000UGT89C1flavon013-O-rhamnosyltransferaseHCTAt5g48930HCThydroxycinnamoyl-Coenzyme A shikimate/quinateC3HAt2g40890CYP98A3coumarate 3-hydroxylaseCCoAOMTAt4g34050CCoAOMT1caffeoyl/CoA 3-O-metheltransferaseCCRAt1g15950AtCCR1cinnamoyl-CoA reductaseFAHAt4g36220FAH1/CYP84A1ferulate 5-hydroxylaseCADAt3g19450AtCAD4cinnamoyl-alcohol dehydrogenaseCADAt3g19450AtCAD5cinnamoyl-alcohol dehydrogenaseOMTAt5g54160AtOMT1caffeic acid/5-hydroxyferulic acid O- methyltransferase(flavon033-O-methyltransferase)SGTAt3g21560UGT84A2sinapic acid 1-O-UDP-glucosyltransferaseSMTAt2g22990SNG1malate sinapoyltransferase.ANSAt4g22880TT18LDOXanthocyanin 3-O-glucosyltransferaseDFRAt5g42800TT3dihydroflavon01 reductaseAGTAt1g03940A3G°p-CouTanthocyanin 3-O-glucoside 6''-O- malonyltransferaseAATAt1g03940A3G°p-CouTanthocyanin 5-O-glucoside 6''-O- malonyltransferaseAATAt1g03940TTG1WD-40 repeat proteinHHHAt1g06390TTG1WD-40 repeat proteinHHHAt1g60300PAP2/AtMYB90R2R3 MYB proteinMYBAt1g66300PAP2/AtMYB90R2R3 MYB proteinMYBAt1g66301AtMYB11R2R3 MYB protein <td>Fd3GlcT</td> <td>At5g17050</td> <td>UGT78D2</td> <td>flavonoid 3-O-glucosyltransferase</td>	Fd3GlcT	At5g17050	UGT78D2	flavonoid 3-O-glucosyltransferase		
F7RhaTAt1g06000UGT89C1flavonol 7-O-rhamnosyltransferaseHCTAt5g48930HCThydroxycinnamoyl-Coenzyme A shikimate/quinate hydroxycinnamoyltransferaseC3HAt2g40890CYP98A3coumarta 3-hydroxylaseCCoAOMTAt4g34050CCoAOMT1caffeoyl/CoA 3-O-metheltransferaseCCRAt1g15950AtCCR1cinnamoyl-CoA reductaseFAHAt4g34220FAH1/CYP84A1ferulate 5-hydroxylaseCADAt3g19450AtCAD4cinnamoyl-alcohol dehydrogenaseCADAt4g34230AtCAD5cinnamoyl-alcohol dehydrogenaseCADAt4g34230AtCAD5cinnamoyl-alcohol dehydrogenaseCADAt3g19450AtCAD4sinapic acid 1-O-UDP-glucosyltransferaseALDHAt3g2503ALDH2C4/ALDH1Aaldehyde dehydrogenaseSGTAt3g21560UGT84A2sinapic acid 1-O-UDP-glucosyltransferaseSMTAt2g22990SNG1malate sinapoyltransferase.ANSAt4g22880TT18 LDOXanthocyanin 5-O-glucosyltransferaseAGTAt5g4060UGT75C1anthocyanin 5-O-glucoside 6''-O- malonyltransferaseAATAt3g29590A5G'''MaTanthocyanin 5-O-glucoside 6''-O- malonyltransferaseAATAt3g2420TTG1WD-40 repeat proteinHHLHAt4g0820TT8basic helix-loop-helix dimerisation regionWD40At5g2420TTG1WD-40 repeat proteinHRAt3g29500A5G'''MaTmalbocyanin 3-O-glucoside 6''-O- malonyltransferaseAATAt1g03940A3G'	F3RhaT	At1g30530	UGT78D1	flavonol 3- <i>O</i> -rhamnosyltransferase		
HCTAt5g48930HCThydroxycinnamoyl-Coenzyme A shikimate/quinate hydroxycinnamoyltransferaseC3HAt2g40890CYP98A3coumarate 3-hydroxylaseCCoAOMTAt4g34050CCoAOMT1caffeoyl/CoA 3-O-metheltransferaseCCRAt1g15950AtCCR1cinnamoyl-CoA reductaseFAHAt4g34230AtCAD4cinnamoyl-alcohol dehydrogenaseCADAt3g19450AtCAD5cinnamoyl-alcohol dehydrogenaseCADAt4g34230AtCAD5cinnamoyl-alcohol dehydrogenaseOMTAt5g54160AtOMT1caffeic acid/5-hydroxyferulic acid O- methyltransferase[flavonol 3'-O-methyltransferase]ALDHAt3g24503ALDH2C4/ALDH1Aaldehyde dehydrogenaseSGTAt3g21560UGT84A2sinapic acid 1-0-UDP-glucosyltransferaseSMTAt2g22990SNG1malate sinapoyltransferase.ANSAt4g22880TT18 LDOXanthocyanin 5-0-glucosyltransferaseAGTAt4g14090UGT75C1anthocyanin 5-0-glucoside 2"-O- xylosyltransferaseAATAt3g2950A5G6'''MaTanthocyanin 5-0-glucoside 6"-O- malonyltransferaseAATAt3g2950TTG1WD-40 repeat proteinAATAt2g1720TTG1WD-40 repeat proteinMVBAt1g6630PAP/AtMYB75R2R3 MYB proteinMYBAt1g6630PAP/AtMYB75R2R3 MYB protein	F7RhaT	At1g06000	UGT89C1	flavonol 7- <i>O</i> -rhamnosyltransferase		
HCTAt5g48930HCThydroxycinnamoyltransferaseC3HAt2g40890CYP98A3coumarate 3-hydroxylaseCCoAOMTAt4g34050CCoAOMT1caffeoyl/CoA 3-O-metheltransferaseCCRAt1g15950AtCCR1cinnamoyl-CoA reductaseFAHAt4g36220FAH1/CYP84A1ferulate 5-hydroxylaseCADAt4g34230AtCAD4cinnamoyl-alcohol dehydrogenaseCADAt4g34230AtCAD5cinnamoyl-alcohol dehydrogenaseOMTAt5g54160AtOMT1caffeic acid/5-hydroxyferulic acid O- methyltransferase/flavonol 3'-O-methyltransferaseALDHAt3g24503ALDH2C4/ALDH1Aaldehyde dehydrogenaseSGTAt3g21500UGT84A2sinapic acid 1-O-UDP-glucosyltransferaseSMTAt2g2290SNG1malate sinapoyltransferase.ANSAt4g22880TT18 LDOXanthocyanin 5-O-glucosyltransferaseAGTAt4g14090UGT75C1anthocyanin 5-O-glucosyltransferaseAGTAt3g29590A5G6'''MaTanthocyanin 5-O-glucoside 2"-O- xylosyltransferaseAATAt3g29590A5G6'''MaTanthocyanin 5-O-glucoside 6"-O- malonyltransferaseAATAt1g03940A3G6'P-CouTcoumaroyltransferaseAATAt1g03940A3G6'P-CouTcoumaroyltransferaseGSTAt5g17220TTG1WD-40 repeat proteinbHLHAt4g09820TT8basic helix-loop-helix dimerisation regionWP40At5g24520TTG2DNA-binding WRKYMYBAt1g66300PAP1/AtMYB75R2R3 MYB protein </td <td></td> <td>400.00</td> <td rowspan="2">нст</td> <td>hydroxycinnamoyl-Coenzyme A shikimate/quinate</td>		400.00	нст	hydroxycinnamoyl-Coenzyme A shikimate/quinate		
C3HAt2g40890CYP98A3coumarate 3-hydroxylaseCCoAOMTAt4g34050CCoAOMT1caffcoyl/CoA 3-O-metheltransferaseCCRAt1g15950AtCCR1cinnamoyl-CoA reductaseFAHAt4g36220FAH1/CYP84A1ferulate 5-hydroxylaseCADAt3g19450AtCAD4cinnamoyl-alcohol dehydrogenaseCADAt4g34230AtCAD5cinnamoyl-alcohol dehydrogenaseCADAt4g34230AtCAD5cinnamoyl-alcohol dehydrogenaseOMTAt5g54160AtOMT1caffeic acid/5-hydroxyferulic acid O- methyltransferase flavonol 3'-O-methyltransferaseALDHAt3g21560UGT84A2sinapic acid 1-O-UDP-glucosyltransferaseSMTAt2g22990SNG1malate sinapoyltransferase.ANSAt4g22880TT18 LDOXanthocyanin 5-O-glucosyltransferaseAGTAt4g14090UGT75C1anthocyanin 5-O-glucosyltransferaseAGTAt3g29590A5G6'''MaTanthocyanin 5-O-glucoside 2"-O- malonyltransferaseAATAt3g29590A5G6''MaTanthocyanin 3-O-glucoside 6"-O- malonyltransferaseAATAt3g29500TTG1WD-40 repeat proteinAATAt3g24502TTG1WD-40 repeat proteinMYBAt1g66390PAP1/AtMYB75R2R3 MYB proteinMYBAt1g66310PAP1/AtMYB12R2R3 MYB protein	HCT	At5g48930		hydroxycinnamoyltransferase		
CCoAOMTAt4g34050CCoAOMT1caffeoyl/CoA 3-O-metheltransferaseCCRAt1g15950AtCCR1cinnamoyl-CoA reductaseFAHAt4g36220FAH1/CYP84A1ferulate 5-hydroxylaseCADAt3g19450AtCAD4cinnamoyl-alcohol dehydrogenaseCADAt4g34230AtCAD5cinnamoyl-alcohol dehydrogenaseOMTAt5g54160AtOMT1caffeic acid/5-hydroxyferulic acid O- methyltransferase/flavonol 3'-O-methyltransferaseALDHAt3g24503ALDH2C4/ALDH1Aaldehyde dehydrogenaseSGTAt3g21560UGT84A2sinapic acid 1-O-UDP-glucosyltransferaseSMTAt2g22990SNG1malate sinapoyltransferase.ANSAt4g28800TT18 LDOXanthocyanin fs-O-glucosyltransferaseDFRAt5g42800TT3dihydroflavonol reductaseAGTAt4g14090UGT75C1anthocyanin 5-O-glucoside 2"-O- xylosyltransferaseAATAt3g29590A5G6'''MaTanthocyanin 5-O-glucoside 6"-O- malonyltransferaseAATAt1g03940A3G6''p-CouTanthocyanin 3-O-glucoside 6"-O-p- coumaroyltransferaseGSTAt5g17220TT19/AtGSTF12glutathione-S-transferaseTranscription factorsTT62DNA-binding WRKYWD40At5g24520TTG2DNA-binding WRKYMYBAt1g66300PAP2/AtMYB90R2R3 MYB proteinMYBAt1g66300PAP2/AtMYB90R2R3 MYB proteinMYBAt1g66301AtMYB11R2R3 MYB protein	СЗН	At2g40890	CYP98A3	coumarate 3-hydroxylase		
CCRAt1g15950AtCCR1cinnamoyl-CoA reductaseFAHAt4g3620FAH1/CYP84A1ferulate 5-hydroxylaseCADAt3g19450AtCAD4cinnamoyl-alcohol dehydrogenaseCADAt4g34230AtCAD5cinnamoyl-alcohol dehydrogenaseOMTAt5g54160AtOMT1caffeic acid/5-hydroxyferulic acid O- methyltransferase[flavonol 3'-O-methyltransferaseALDHAt3g24503ALDH2C4/ALDH1Aaldehyde dehydrogenaseSGTAt3g21560UGT84A2sinapic acid 1-O-UDP-glucosyltransferaseSMTAt2g22990SNG1malate sinapoyl-ransferase.ANSAt4g2880TT3dihydroflavonol reductaseAGTAt4g14090UGT75C1anthocyanin 5-O-glucosyltransferaseAGTAt4g29590ASG6'''MaTanthocyanin 3-O-glucoside 2"-O- xylosyltransferaseAATAt3g29590ASG6'''MaTanthocyanin 3-O-glucoside 6"-O- malonyltransferaseAATAt1g03940A3G6''p-CouTanthocyanin 3-O-glucoside 6"-O-p- coumaroyltransferaseGSTAt5g17220TTG1WD-40 repeat proteinbHLHAt4g09820TT8basic helix-loop-helix dimerisation regionWB40At5g24520TTG1WD-40 repeat proteinbHLHAt1g6390PAP2/AtMYB90R2R3 MYB proteinMYBAt1g66390PAP2/AtMYB90R2R3 MYB proteinMYBAt2g47460AtMYB11R2R3 MYB protein	CCoAOMT	At4g34050	CCoAOMT1	caffeoyl/CoA 3-O-metheltransferase		
FAHAt4g36220FAH1/CYP84A1ferulate 5-hydroxylaseCADAt3g19450AtCAD4cinnamoyl-alcohol dehydrogenaseCADAt4g34230AtCAD5cinnamoyl-alcohol dehydrogenaseCADAt4g34230AtCAD5cinnamoyl-alcohol dehydrogenaseOMTAt5g54160AtOMT1caffeic acid/5-hydroxyferulic acid 0- methyltransferase[flavonol 3'-0-methyltransferaseALDHAt3g24503ALDH2C4/ALDH1Aaldehyde dehydrogenaseSGTAt3g21560UGT84A2sinapic acid 1-0-UDP-glucosyltransferaseSMTAt2g22900SNG1malate sinapoyltransferase.ANSAt4g22880TT18 LDOXanthocyanidin synthaseDFRAt5g42800TT3dihydroflavonol reductaseAGTAt4g14090UGT75C1anthocyanin 5-0-glucosyltransferaseAGTAt3g29590ASG6'''MaTanthocyanin 5-0-glucoside 2"-O- xylosyltransferaseAATAt3g29590ASG6'''MaTanthocyanin 3-0-glucoside 6"-O- malonyltransferaseAATAt3g1720TT19/AtGSTF12glutathione-S-transferaseAATAt1g03940A3G6''p-CouTanthocyanin 3-O-glucoside 6"-O-p- coumaroyltransferaseMD40At5g1720TTG1WD-40 repeat proteinbHLHAt4g09820TT8basic helix-loop-helix dimerisation regionWRKYAt2g37260TTG2DNA-binding WRKYMYBAt1g66300PAP1/AtMYB75R2R3 MYB proteinMYBAt2g610AtMYB11R2R3 MYB protein	CCR	At1g15950	AtCCR1	cinnamoyl-CoA reductase		
CADAt3g19450AtCAD4cinnamoyl-alcohol dehydrogenaseCADAt4g34230AtCAD5cinnamoyl-alcohol dehydrogenaseOMTAt5g54160AtOMT1caffeic acid/5-hydroxyferulic acid O- methyltransferase flavonol 3'-O-methyltransferaseALDHAt3g24503ALDH2C4/ALDH1Aaldehyde dehydrogenaseSGTAt3g21560UGT84A2sinapic acid 1-O-UDP-glucosyltransferaseSMTAt2g22990SNG1malate sinapoyltransferase.ANSAt4g22880TT18 LDOXanthocyanidin synthaseDFRAt5g42800TT3dihydroflavonol reductaseAGTAt4g14090UGT75C1anthocyanin 5-O-glucosyltransferaseAATAt5g54060UGT79B1anthocyanin 3-O-glucoside 2"-O- xylosyltransferaseAATAt1g03940A5G6'''MaTanthocyanin 3-O-glucoside 6"-O- malonyltransferaseAATAt1g22820TTG1WD-40 repeat proteinMD40At5g24520TTG1WD-40 repeat proteinbHLHAt4g09820TT8basic helix-loop-helix dimerisation regionWRKYAt2g37260TTG2DNA-binding WRKYMYBAt1g66300PAP2/AtMYB90R2R3 MYB proteinMYBAt2g47460AtMYB11R2R3 MYB protein	FAH	At4g36220	FAH1/CYP84A1	ferulate 5-hydroxylase		
CADAt4g34230AtCAD5cinnamoyl-alcohol dehydrogenaseOMTAt5g54160AtOMT1caffeic acid/5-hydroxyferulic acid <i>O</i> -methyltransferase flavonol 3'- <i>O</i> -methyltransferaseALDHAt3g24503ALDH2C4/ALDH1Aaldehyde dehydrogenaseSGTAt3g21560UGT84A2sinapic acid 1- <i>O</i> -UDP-glucosyltransferaseSMTAt2g22990SNG1malate sinapoyltransferase.ANSAt4g22880TT18 LDOXanthocyanidin synthaseDFRAt5g42800TT3dihydroflavonol reductaseAGTAt4g14090UGT75C1anthocyanin 5- <i>O</i> -glucosyltransferaseAGTAt5g54060UGT79B1xylosyltransferaseAATAt3g29590ASG6'''MaTanthocyanin 5- <i>O</i> -glucoside 6'''- <i>O</i> -malonyltransferaseAATAt1g03940A3G6'p-CouTanthocyanin 3- <i>O</i> -glucoside 6'''- <i>O</i> -malonyltransferaseGSTAt5g17220TT19/AtGSTF12glutathione-S-transferaseTranscription factorsTT61WD-40 repeat proteinWD40At5g24520TTG2DNA-binding WRKYMYBAt1g66300PAP1/AtMYB75R2R3 MYB proteinMYBAt2g67160AtMYB11R2R3 MYB proteinMYBAt2g67200AtMYB11R2R3 MYB protein	CAD	At3g19450	AtCAD4	cinnamoyl-alcohol dehydrogenase		
OMTAt5g54160At0MT1caffeic acid/5-hydroxyferulic acid <i>O</i> -methyltransferaseALDHAt3g24503ALDH2C4/ALDH1Aaldehyde dehydrogenaseSGTAt3g21560UGT84A2sinapic acid 1-O-UDP-glucosyltransferaseSMTAt2g22990SNG1malate sinapoyltransferase.ANSAt4g22880TT18 LDOXanthocyanidin synthaseDFRAt5g42800TT3dihydroflavonol reductaseAGTAt4g14090UGT75C1anthocyanin 5-O-glucosyltransferaseAGTAt5g54060UGT79B1anthocyanin 5-O-glucoside 2"-O-xylosyltransferaseAATAt3g29590ASG6'''MaTanthocyanin 5-O-glucoside 6"-O-malonyltransferaseAATAt3g29590ASG6''P-CouTanthocyanin 3-O-glucoside 6"-O-p-coumarolytransferaseGSTAt5g17220TT19/AtGSTF12glutathione-S-transferaseTranscription factorsTT61WD-40 repeat proteinWD40At5g24520TTG2DNA-binding WRKYMYBAt1g66300PAP1/AtMYB75R2R3 MYB proteinMYBAt2g6210AtMYB11R2R3 MYB proteinMYBAt3g66201AtMYB11R2R3 MYB protein	CAD	At4g34230	AtCAD5	cinnamoyl-alcohol dehydrogenase		
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	MYB	At3962610	AtMYB11	R2R3 MYB protein		
IMYR At5o4933()   AtMYR111   R2R3 MYR protein	MYB	At5049330	AtMYB111	R2R3 MYB protein		

#### Supplemental Table 2: Abbreviations of Enzyme Names.