SUPPLEMENTARY INFORMATION

MicroRNA858 is a potential regulator of phenylpropanoid pathway and plant development in *Arabidopsis*

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Short title: Flavanoid pathway regulation by miR858

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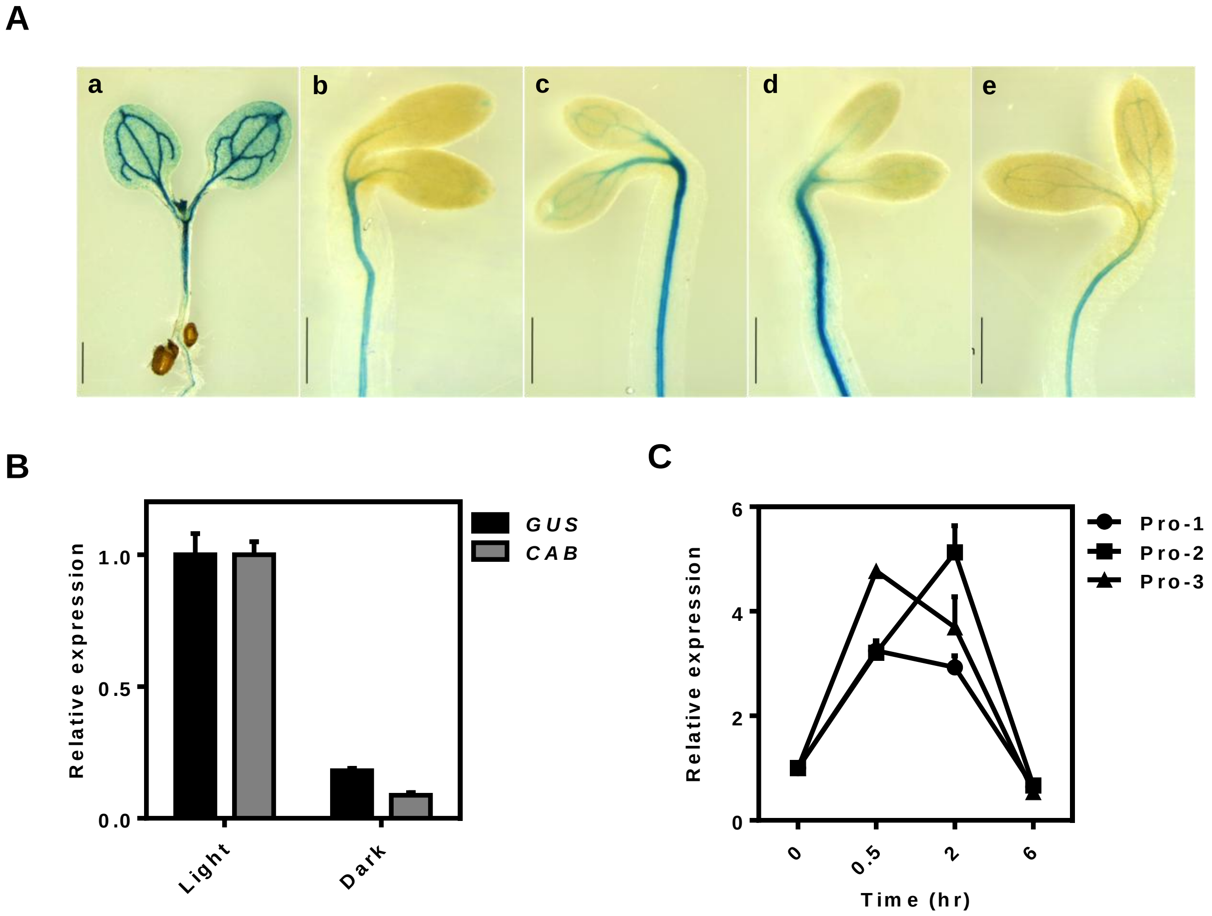
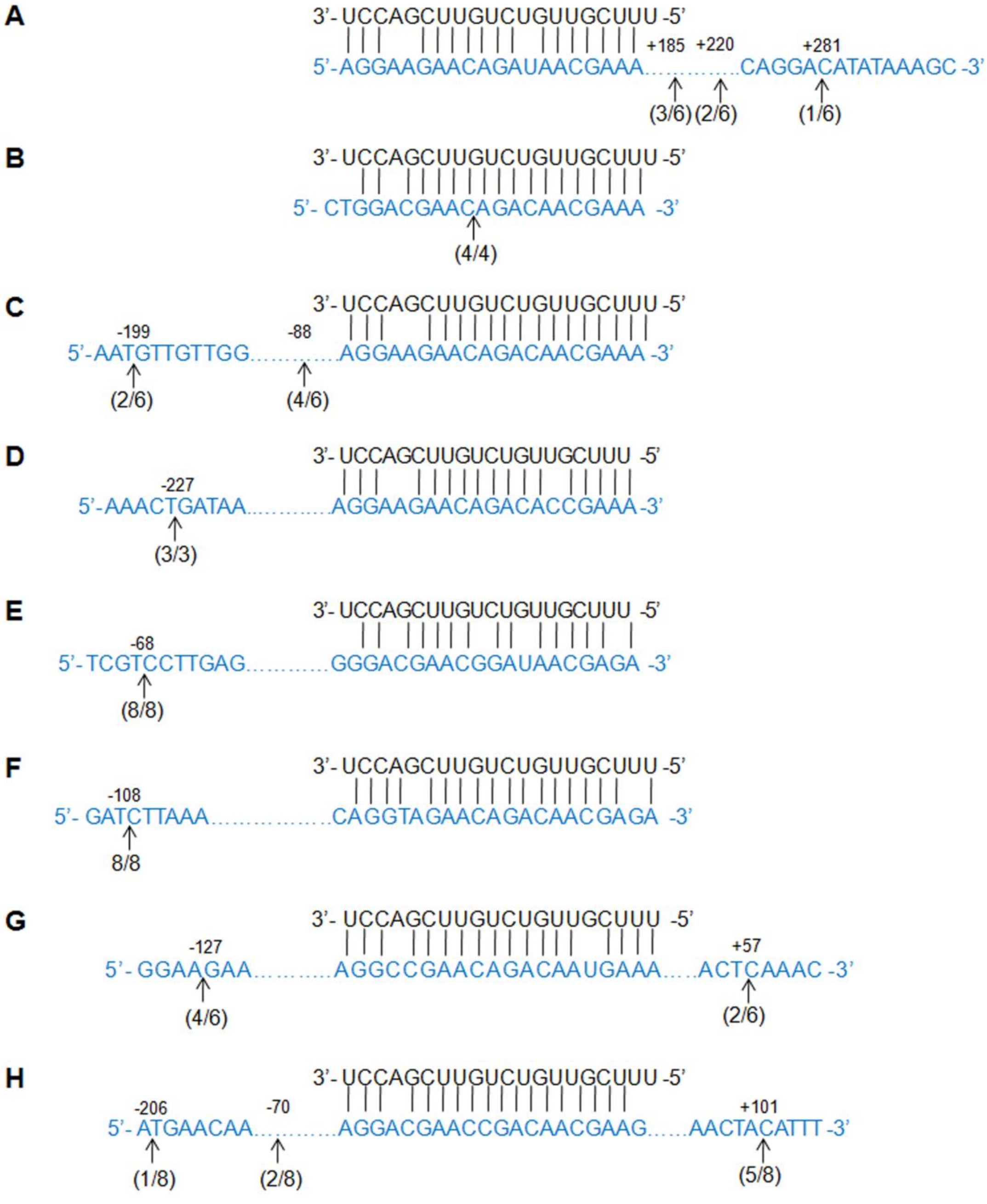
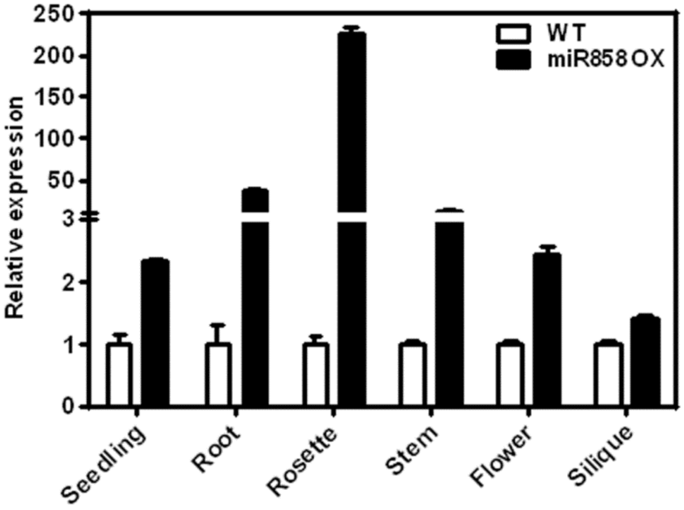


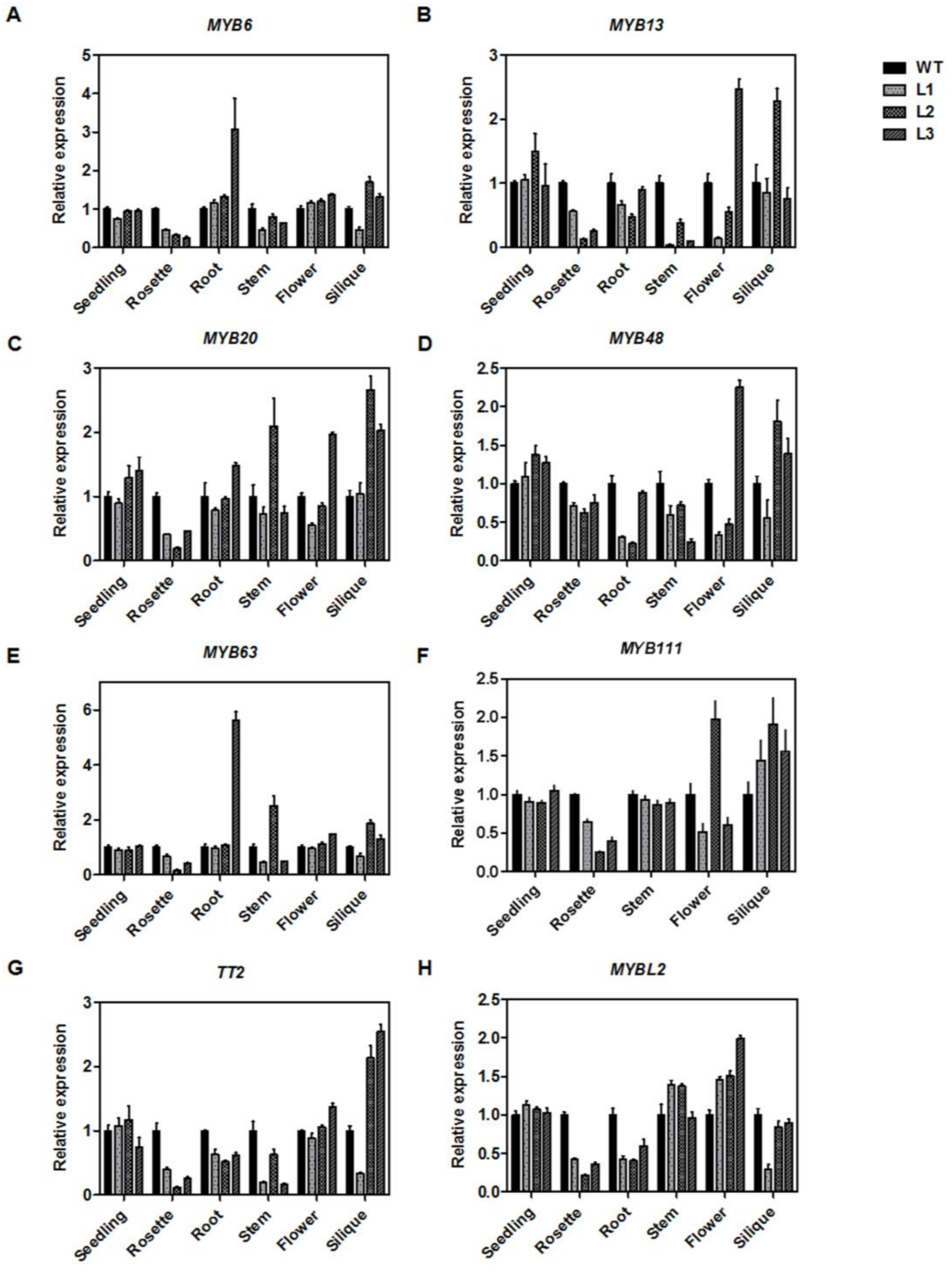
Supplementary Figure S1. Expression of the miR858a is regulated by light. (**A**) GUS activity in *ProMIR858:GUS* transgenic driven by light. (**a**) GUS activity driven by a 1.8 kbp upstream promoter sequence of pre-miR858a in the *ProMIR858:GUS* expressing seedlings after 5 days of germination in light. Bar = 1 mm (**b**) GUS activity in *ProMIR858:GUS* expressing seedlings grown in complete dark condition for 5 days. (**c**) GUS activity in dark grown seedlings exposed to light for 0.5 hr. (**d**) GUS activity in dark grown seedlings exposed to light for 2 hr. (**e**) GUS activity in dark grown seedlings exposed to light for 6 hr. For b to e, Bar = 0.5 mm. (**B**) Relative expression of *GUS* and Chlorophyll A/B Binding (*CAB*) genes in *ProMIR858:GUS* expressing seedling grown under light and dark conditions for 5 days. *CAB* is taken as positive control. Transcript abundance of each gene was normalized by the level of *TUBULIN* gene. (**C**) Relative expression of *GUS* gene in *ProMIR858:GUS* transgenic lines (Pro-1, Pro-2 and Pro-3) at different times of exposure to light after 5 days of growth in dark. Error bars indicate ±SE (n=3) from three biological replicates (each with three technical replicates).



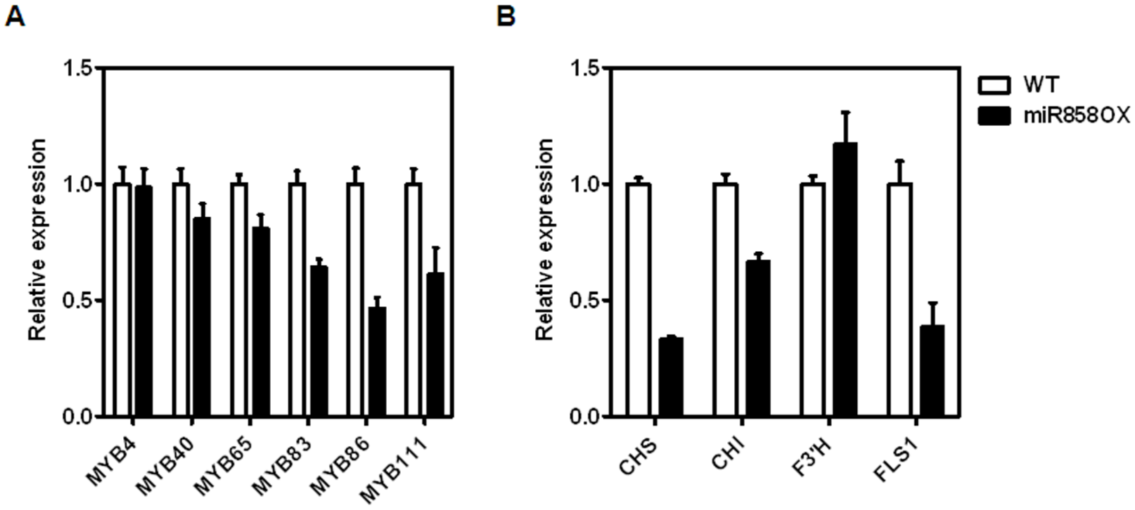
Supplementary Figure S2. miR858a-mediated cleavage of MYB genes. Cleavage analysis was performed using RLM-RACE. Amplified products were sequenced for (**A**) *MYB6*, (**B**) *MYB13*, (**C**) *MYB20*, (**D**) *MYB42*, (**E**) *MYB48*, (**F**) *MYB83*, (**G**) *TT2* and (**H**) *MYBL2*. miR858a mature sequence is written in 3' to 5' direction while target gene sequence in 5' to 3'. The identified cleavage sites are indicated by black arrows with the frequency of cleavage showing on bottom of the arrows and position of cleavage showing on the top of target sequence.



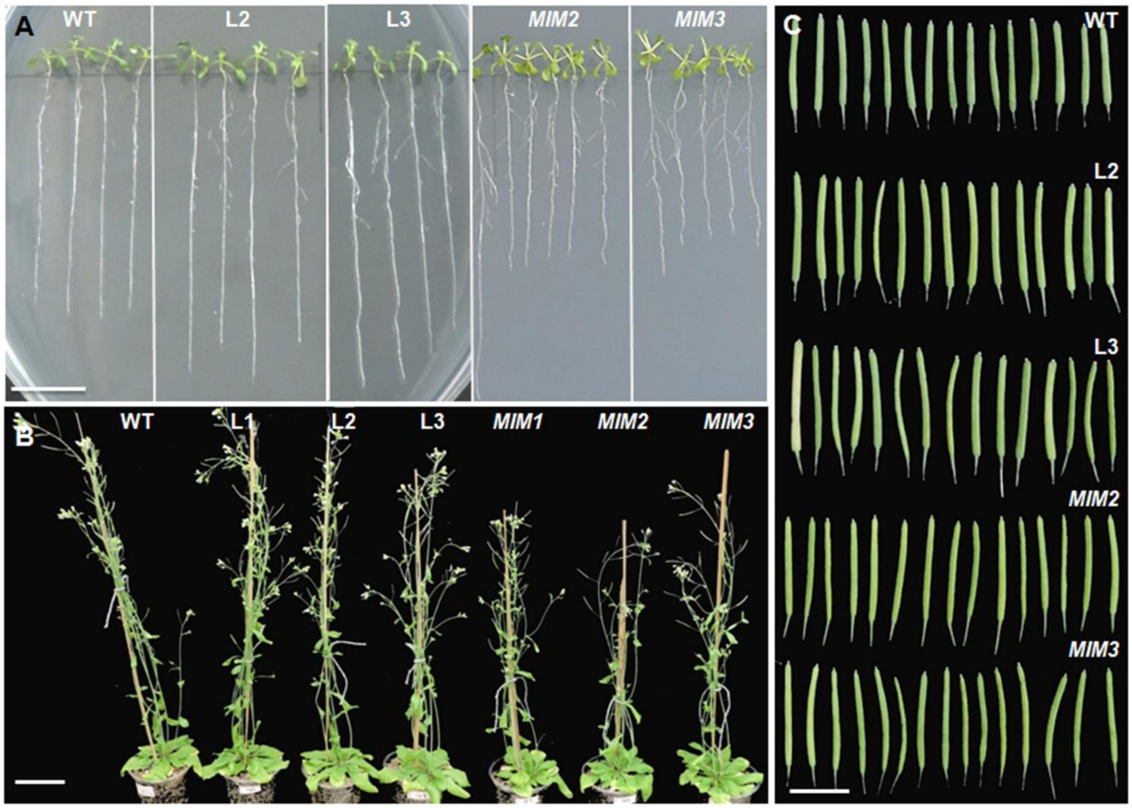
Supplementary Figure S3. Expression analysis of miR858a in *Arabidopsis.* Expressions of mature miR858a gene in different tissues of WT and miR858OX transgenic lines. *TUBULIN* was taken as internal control for normalization. Error bars represents ±SE (n=3).



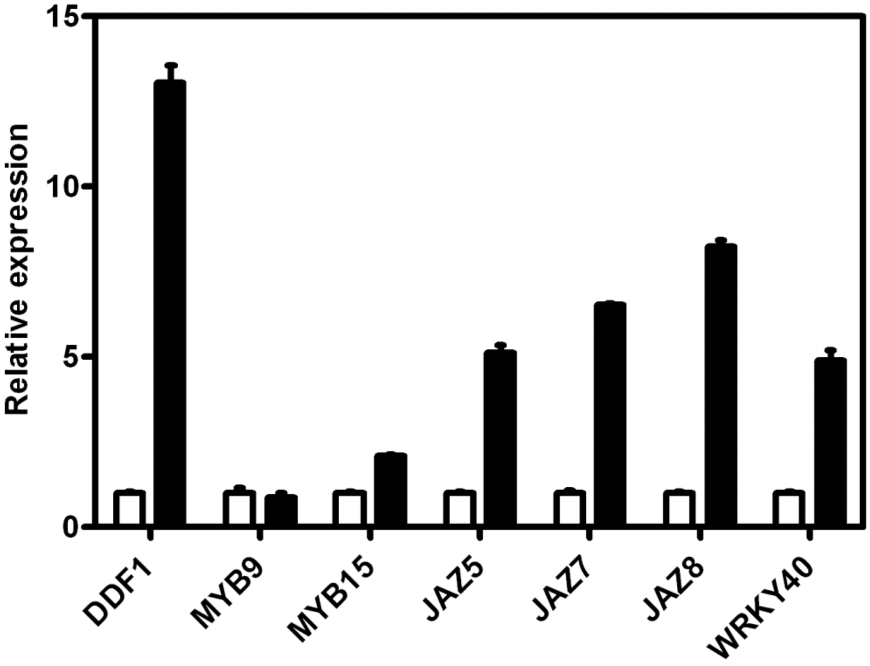
Supplementary Figure S4. Relative expression of MYB transcription factors in miR858OX transgenic lines. **A** to **H**, Expression of *MYB6*, *MYB13*, *MYB20*, *MYB48*, *MYB63*, *MYB111*, *TT2*, *MYBL2* in seedling, rosette, root, stem, flower and silique tissue of miR858OX lines. For *MYB111* (**F**) no expression was obtained in root. *TUBULIN* was taken as internal control for normalization. Error bars represents ±SE (n=3).



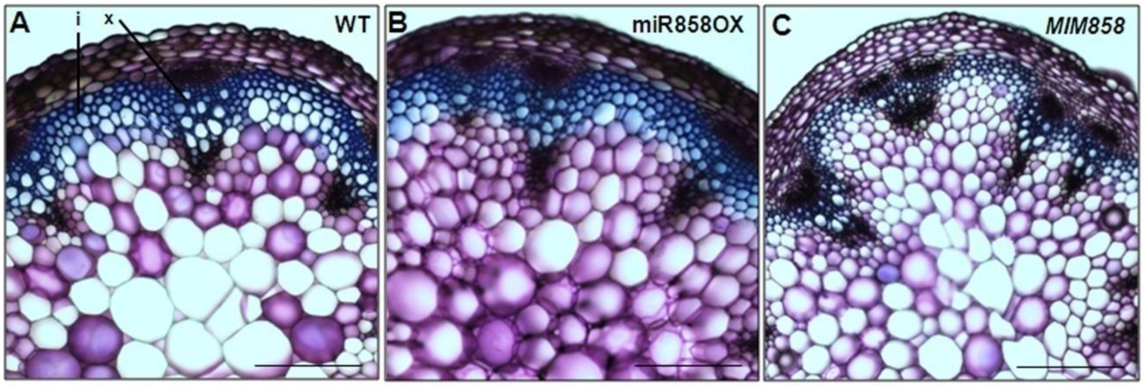
Supplementary Figure S5. Modulation of gene expression in miR858OX transgenic line. (**A**) Relative expression of MYB genes identified through microarray analysis. (**B**) Relative expression of structural genes of flavonoid pathway. *TUBULIN* was taken as endogenous control. Data given are fold expression $\log_2$ (transgenic/wild-type). Error bars represents ±SE (n=3).



Supplementary Figure S6. Phenotypic variations in miR858OX transgenic lines. (**A**) Seedling phenotype of wild-type, miR858OX (L2 and L3) and *MIM858* (*MIM2* and *MIM3*) transgenic lines. Phenotypic changes in wild-type, miR858OX and *MIM858* transgenic lines grown on ½ MS media for 10 days are shown. Bars = 1 cm. (**B**) Growth phenotypes of 5-week-old wild-type, miR858OX and *MIM858* transgenic plants. Bar = 1 cm. (**C**) Phenotype of transgenic lines producing longer silique than wild-type. Photograph of 6 week grown plants was taken.



Supplementary Figure S7. Expression analysis of significantly up-regulated genes in miR858OX transgenic lines. Relative expression of significantly up-regulated genes in miR858OX line. *TUBULIN* was taken as endogenous control. Data given are fold expression $\log_2$ (transgenic/wild-type). Error bars represents ±SE (n=3).



Supplementary Figure S8. miR858a affects lignin depositions in *Arabidopsis* stem. Histochemical staining of stem sections of mature *Arabidopsis* stem sections with toluidine blue O (TBO) for detection of lignin. i, interfascicular fiber; x, xylem. Bars = 500 µm. (**A**) TBO staining (blue colour) of a wild-type stem section showing the normal lignin deposition in the walls of interfascicular fibers and xylem cells. (**B**) TBO stained miR858OX stem section showing ectopic lignin deposition in the walls of interfascicular fibers and xylem cells. (**C**) TBO stained *MIM858* stem section showing lesser lignin deposition in the walls of interfascicular fibers and xylem cells.

Supplementary Table S1. Alignment of miR858a mature sequence among different plant species

miRNA ID	Sequence (5' to 3')	Strand	Nucleotides
ath-miR858a	**UUUCGUUGUCUGUUCGACCUU**	-	21
ath-miR858b	**UUCGUUGUCUGUUCGACCUU**	+	20
aly-miR858-5p	**UUUCGUUGUCUGUUCGACCUU**	+	21
aly-miR858-3p	**UUCGUUGUCUGCUCGACC**	-	18
cme-miR858	**UCUCGUUGUCUGUUCGACCUU**	+	21
mdm-miR858	**UUCGUUGUCUGUUCGACCU**	+	19
ppe-miR858	**UCGUUGUCUGUUCGACCUU**	+	20
gh-miR858	**UUCAUUGUCUGUUCGACCUGA**	+	21
sly-miR858	**UUUCGUUGUCUGUUCGACCUU**	+	21

A. thaliana (ath), *A. lyrata* (aly), *C. melo* (cme), *P. Persica* (ppe), *G. hirsutum* (gh) and *S. lycopersicum* (sly).

Supplementary Table S2. Putative *cis*-acting elements in miR858a promoter

Site Name	Sequence	Position	Function
3-AF1	AAGAGATATTT	-1366	Light responsive element
ACE	ACGTGGA	+346	
	CTAACGTAT	+591	
Box 4	ATTAAT	+437	
		+612	
		+465	
Box I	TTTCAAA	-849	
CATT motif	GCATTC	+596	
G box	CACGTA	+1167	
	CACGTG	+1224	
GAG motif	GGAGATG	+144	
		+1441	
GT1 motif	AATCCACA	-1300	
L box	CTCACCTACCAA	-375	
Sp1	CC(G/A)CCC	-1054	
TCT motif	TCTTAC	+1332	
ARE	TGGTTT	-315	Anaerobic induction
		-1193	
LTR	CCGAAA	-969	Low-temperature responsive
ABRE	TACGTG	-1167	ABA responsive element
	CACGTG	+1224	
P box	CCTTTTG	-795	GA-responsive element
TCA element	TCAGAAGAGG	+1432	SA-responsive
TGACG motif	TGACG	+344	MeJA-responsive
CGTCA motif	CGTCA	-344	
GCN4 motif	TGAGTCA	+1184	Endosperm expression
Skn 1 motif	GTCAT	-343	
		-890	
O2 site	GATGACATGG	+342	Zein metabolism regulation
circadian	CAAAGATATC	+1363	Involved in circadian control

Supplementary Table S3. Putative targets of *Arabidopsis* miR858a

Target accession	**Target description**	**Functions**
AT1G22640	MYB3	Phenylpropanoid pathway
AT5G26660	MYB4/86	Negative regulation, flavonol biosynthesis
AT4G09460	MYB6	-
AT3G62610	MYB11	Phenylpropanoid pathway / flavonol biosynthesis
AT2G47460	MYB12	Phenylpropanoid pathway / flavonol biosynthesis
AT1G06180	MYB13	Abiotic stress response / drought, light and wounding
AT2G31180	MYB14	Regulates seed mucilage biosynthesis and trichome branching
AT3G61250	MYB17	Flower development, response to JA and SA stimulus
AT5G52260	MYB19	-
AT1G66230	MYB20	Secondary cell wall biosynthesis
AT3G27810	MYB21	Stamen development, GA- and JA-mediated
AT4G34990	MYB32	Phenylpropanoid pathway
AT5G60890	MYB34	Glucosinolate biosynthesis / indolic pool
AT5G23000	MYB37	Axillary meristem regulation / lateral organ formation
AT4G17785	MYB39	Sequence-specific DNA binding transcription factor
AT5G14340	MYB40	-
AT4G12350	MYB42	Secondary cell wall biosynthesis
AT3G46130	MYB48	Response to salicylic acid stimulus
AT5G54230	MYB49	-
AT1G09540	MYB61	Mucilage deposition and extrusion
AT1G79180	MYB63	Phenylpropanoid pathway / lignin biosynthesis
AT3G11440	MYB65	Stamen development / anther development (tapetum)
AT4G05100	MYB74	-
AT4G13480	MYB79	-
AT5G56110	MYB80	Stamen development / anther (tapetum) and pollen (exine)
AT2G26960	MYB81	-

AT5G52600	MYB82	Regulation of trichome development
AT3G08500	MYB83	Secondary cell wall biosynthesis
AT3G49690	MYB84	Axillary meristem regulation / lateral organ formation
AT4G22680	MYB85	Lignin deposition / cell wall thickening (fiber cells)
AT4G37780	MYB87	Cell wall organization
AT5G10280	MYB92	Branching, GA-mediated
AT1G34670	MYB93	-
AT4G26930	MYB97	Participate in pollen tube reception
AT5G62320	MYB99	Stamen development / anther development (tapetum)
AT2G26950	MYB104	-
AT3G02940	MYB107	DNA-dependent, response to SA stimulus
AT5G49330	MYB111	Phenylpropanoid pathway / flavonol biosynthesis
AT1G25340	MYB116	Stamen development / anther development (tapetum)
AT5G55020	MYB120	Participate in pollen tube reception
AT3G30210	MYB121	-
AT5G35550	MYB123/TT2	Phenylpropanoid pathway / proanthocyanindins biosynthesis
AT3G24310	MYB71/305	-
AT1G71030	MYBL2	Proanthocyanidin biosynthetic process
AT1G17760	ATCSTF77	Involve in mRNA polyadenylation

Supplementary Table S4. Differentially expressed MYB transcription factors and flavonoid structural genes

AGI accession	Gene symbol	Fold Change
MYB transcription factors		
AT5G62320	MYB99	-1.58
AT5G49330	MYB111	-1.55
AT1G09540	MYB61	-1.52
AT5G11510	MYB3R-4	-1.47
AT4G32730	PC-MYB1	-1.45
AT5G58850	MYB119	-1.42
AT3G18100	MYB4R1	-1.39
AT1G22640	MYB3	-1.38
AT1G74080	MYB122	-1.34
AT5G59780	MYB59	-1.31
AT2G16720	MYB7	-1.3
AT2G23290	MYB70	-1.29
AT3G50060	MYB77	-1.28
AT5G14340	MYB40	-1.28
AT3G08500	MYB83	-1.26
AT4G22680	MYB85	-1.25
AT2G32460	MYB101	-1.23
AT1G66390	MYB90	-1.22
AT5G26660	MYB86	-1.22
AT1G66370	MYB113	-1.2
AT4G01680	MYB55	-1.2
Pathway genes		
AT5G13930	CHS/TT4	-1.72
AT3G55120	CHI/TT5	-1.43
AT3G51240	F3H/TT6	-1.43
AT5G07990	F3’H/TT7	-1.35
AT5G46330	FLS2	-1.5
AT5G63590	FLS3	-1.38
AT5G63600	FLS5	-1.31
AT4G34135	UGT73B2	-1.33
AT1G30530	UGT78D1	-1.25
AT5G17050	UGT78D2	-1.24

Down-regulated genes with at least a 1.2 fold change in expression levels are shown. Total RNA (250 ng) from 3-week-old rosette leaves of Col-0 and miR858OX plants was used for hybridization. Raw data from CEL files were initially analyzed by Affymetrix Expression

Console.The $\log_2$ transformed data were analysed using Affymetrix Transcriptome Analysis Console (TAC) 2.0 software.

Supplementary Table S5. Comparisons of seedling root length, fresh weight and rosette diameter in wild-type and miR858a transgenic lines

Genotype	**Root length (cm)**	**Seedling fresh weight (mg)**	**Rosette diameter (cm)**
WT	3.41 ± 0.054	2.84 ± 0.05	7.32 ± 0.37
L1	-	-	7.72 ± 0.16
L2	4.09 ± 0.08*	3.46 ± 0.07**	7.56 ± 0.23
L2	4.31 ± 0.06**	3.45 ± 0.08**	7.8 ± 0.1
MIM1	-	-	5.88 ± 0.08**
MIM2	2.42 ± 0.08**	2.11 ± 0.04**	5.84 ± 0.18**
MIM3	2.35 ± 0.04**	2.18 ± 0.06**	5.72 ± 0.1**

10-days-old seedlings grown on ½MS media under SD growth conditions were analysed. Mean value and standard error of triplicate analyses are presented. One-way ANOVA followed by post hoc Newman–Keuls was used for multiple comparison test of significance. L1 and *MIM1* data were shown in the main text.

Supplementary Table S6. Comparisons of plant height, rosette fresh weight and rosette diameter in mature wild-type and miR858a transgenic lines

Genotype	**Plant height (inches)**	**Rosette fresh weight (mg)**	**Rosette diameter (cm)**
WT	19.35 ± 0.35	916.6 ± 47.4	9.2 ± 0.1
L1	19.66 ± 0.23	833.22 ± 100	10.2 ± 0.37
L2	20.22 ± 0.36*	939.3 ± 49.3	8.52 ± 1.76
L3	20 ± 0.33*	683.92 ± 52.5	10.56 ± 0.16
MIM1	15 ± 0.43***	466.52 ± 8.8***	8.5 ± 0.12
MIM2	14.85 ± 0.26***	533.35 ± 31.1***	9.32 ± 0.07
MIM3	16 ± 0.37***	676.02 ± 32.1***	9.5 ± 0.12

40-days-old plants were analysed. Mean value and standard error of triplicate analyses are presented. One-way ANOVA followed by post hoc Newman–Keuls was used for multiple comparison test of significance.

Supplementary Table S7. Comparisons of flower size in wild-type and miR858a transgenic lines

Genotype	Flower size	
	Length (mm)	**Width (mm)**
WT	4.72 ± 0.4	2.02 ± 0.2
L2	4.6 ± 0.2	1.65 ± 0.2
L3	4.75 ± 0.2	1.75 ± 0.2
MIM2	2.57 ± 0.2***	1.12 ± 0.2***
MIM3	2.9 ± 0.2***	1.22 ± 0.2***

40-days-old plants were analysed. Mean value and standard error of triplicate analyses are presented. One-way ANOVA was used for multiple comparison test of significance.

Supplementary Table S8. Comparisons of silique, seed number and morphology in wild-type and miR858a transgenic lines

Genotype	Siliques per plant	Silique length (cm)	Seeds per silique	Seeds per 5 mg
WT	192.2 ± 10.2	10.7 ± 0.18	35.2 ± 0.8	193.5 ± 5
L2	235.2 ± 4.3**	13.6 ± 0.18**	26.7 ± 0.7**	156.25 ± 2.3**
L3	229.2 ± 3.4**	13.8 ± 0.25**	34.5 ± 1.5**	165.75 ± 2.7**
MIM2	168.4 ± 10.2**	13 ± 0.21**	61.5 ± 1.3**	369.25 ± 4.1***
MIM3	143.8 ± 4.9**	14.4 ± 0.13**	67.5 ± 1.6**	370.25 ± 6.2***

40-days-old plants were analysed. Mean value and standard error of triplicate analyses are presented. One-way ANOVA was used for multiple comparison test of significance.

Supplementary Table S9. Metabolite content in stem tissues of wild-type, miR858OX and *MIM858* transgenic lines

MOLECULE	**ESI**	**Precursor Ion**	**Daughter Ion**	**WT**	**miR858OX**	***MIM858***
Naringenin	Positive (M+H)	273	153	4.92 ± 0.06	9.53 ± 0.1*	8.72 ± 0.1*
Naringin	Positive (M+H)	581	419, 273	23.53 ± 0.3	20.56 ± 0.2	21.39 ± 0.3
Kaempferol	Positive (M+H)	287	153, 121	2453.23 ± 33.5	3830.88 ± 63.9**	3506.09 ± 47.9**
Quercetin	Positive (M+H)	303	229, 153	553.81 ± 6.9	847.87 ± 11.5**	795.79 ± 13.2**
Q-3-*O*-G	Positive (M+H)	465	303	19.21 ± 0.3	24.66 ± 0.4*	40.06 ± 0.6**
Rutin hydrate	Positive (M+H)	611	303	3178.47 ± 53.0	5221.99 ± 71.3**	4544.61 ± 75.9*
Gallocatechin	Negative (M-H)	305	125	35.65 ± 0.5	14.32 ± 0.2*	79.3 ± 1.6**
p-Coumaric acid	Positive (M+H)	165	119, 91	647.83 ± 8.8	3230.87 ± 44.1***	1229.26 ± 23.9***
Caffeic acid	Positive (M+H)	181	145, 117	526.42 ± 7.1	725.76 ± 9.9**	688.89 ± 9.4**
Ferulic acid	Positive (M+H)	195	145, 117	182.63 ± 2.4	334.96 ± 5.5**	99.98 ± 1.3**
Sinapic Acid	Positive (M+H)	225	175	495.39 ± 8.2	715.72 ± 9.7**	525.22 ± 7.1*
Syringic acid	Negative (M-H)	197	182	644.1 ± 10.7	1167.39 ± 20.5***	1564.99 ± 26.1***

Stem tissue samples from plants were taken and metabolite contents analyzed by LC/MS/MS. Values presented are means ±SE (n=6) (µg 100 g^{-1} dry weight) of measurements from at least five biological replicates per genotype. Statistically significant values from the wild-type is based on One-way ANOVA (*P < 0.01, **P < 0.001 and ***P < 0.0001). The ESI, precursor and daughter ions for the single metabolites are listed.

Supplementary Table S10. Information of primers used

Primer name	Primer Sequence (5’ to 3’)
For cloning and construct preparation	
miR858_F	ACGGTGGACATCAGAAGATGGAGATG
miR858_R	TATATACGAACGTAAAGACTTAAGC
mi858BamHI_F	GATTGGATCCGATGCTAGGCTTG
mi858SacI_R	GACTTGAGCTCATATATACCTAC
ProMIR858_F	CTAAAAGCTTTTCAAATTCAGTGGTCTTAC
ProMIR858_R	AACACATAGGATCCTCACTTTGTCAAGCCTAG
MIM858_F	ATCTACCAGGAAGAACAGACAACGAAATAAAAACAGGAAGAACAGACAACGAAATAAAAACAGGAAGAACACATGACAACGAAAATC
MIM858_R	TTTTTATTTCGTTGTCATGTGTTCTTCCTGTTTTTATTTCGTTGTCTGTTCTTCCTGGTAGATTTTCGTTGTCATG
MIM858V_F	AGGGAAATCTAGAATGCAGGCCTCTGCAG
MIM858V_R	GAATTCGAGCTCGGTACCTCGCGAATGCACCTA
M13_F	GTAAAACGACGGCCAGT
M13_R	CAGGAAACAGCTATGAC
CaMV 35S	GTAAGGGATGACGCACAATCC
Nos T	GGACTCTAATCATAAAAACCC
For qRT-PCR	
Aly-miR858	UUUCGUUGUCUGUUCGACCUU
SnoR41Y	GTTTTATTGTCATCTGATTCTCATGATGAATATATACCTCCTACTCATTCTGAGTG
TUB_RTF	GAGCCTTACAACGCTACTCTGTCTGTC
TUB_RTR	ACACCAGACATAGTAGCAGAAATCAAG
mi858_RTF	CGATCTCTCCTCAAAACCCTA
mi858_RTR	CGATCGTCTATCTACCCCAATC
CAB_RTF	ATTCTTCGTTCAAGCCATCG
CAB_RTR	CAAGCGTTGTTGTGGACTGG
CHS_RTF	GGAGAAGTTCAAGCGCATGTG
CHS_RTR	ATGTGACGTTTCCGAATTGTCG
CHI_RTF	CTCTCTTACGGTTGCGTTTTCG
CHI_RTR	CACCGTTCTTCCCGATGATAGA
F3’H_RTF	TTCCTTACCTTCAGGCGGTTATC
F3’H_RTR	CGAGAGTGGTGTTGGTGGATG
FLS1_RTF	CCACCGTCATGCGTCAATTACAG
FLS1_RTR	TCTCCGCCGAGACCTTCTTTCAA
DFR_RTF	AGCCGCCAAGGGACGTTATATTTG
DFR_RTR	CCGGGAGAAAACCCTTTTGACGA
MYB4_RTF	CGCTTATTGCCGGGAGATTAC
MYB4_RTR	TTTCTTCGTATATGCGTGTTCCA
MYB6_RTF	TCAAACTCCATAGCTTACTCGGT
MYB6_RTR	GTTTGTGGATCAATACCGTGACT
MYB11_RTF	CCGGGAAGAACAGACAACGA
MYB11_RTR	TTCTCGACGGTATTGGCGAC
MYB12_RTF	ACCAGGGAGAACAGACAACG
MYB12_RTR	TCGTCATGATTACGGCGGAG
MYB13_RTF	CTGCAAAATTGCCTGGACGA
MYB13_RTR	GATCTTGACTGTGGTGGAGTCT
MYB20_RTF	TACCAGGAAGAACAGACAACGA
MYB20_RTR	AGGATCAATCCCCATTTTCCTC

MYB40_RTF	TTGCCTCGCATTTCTCTGGT
MYB40_RTR	CCGGATCCAACCCAAGATGT
MYB63_RTF	TCGCTTCTCAACTTCCAGGTA
MYB63_RTR	GAGCTCTGAGCCAGTCTTTTCT
MYB65_RTF	GGCTGAACATTTACCTGGTCG
MYB65_RTR	TGCTCGTTGTCTCCTCTTGA
MYB83_RTF	TAGCTACTCGGCTTCCAGGT
MYB83_RTR	AAGCCGCTTCTTCAATGTCG
MYB86_RTF	ATGGTCTCAAATCGCAACGC
MYB86_RTR	TGTGTTGTTGGGTCAATGCCT
MYB93_RTF	CGCATTTGCAAGGTCGTACA
MYB93_RTR	GGCTGATGAGTCACAGGATCG
MYB111_RTF	AAAGAGGAAATATTACTTCCGACGAA
MYB111_RTR	TTGTCTGTTCTTCCTGGTAGATGTG
TT2_RTF	GATGGTCGTTGATAGCTGGGA
TT2_RTR	TTTTGCGGAGGTTTGAGTTCC
MYBL2_RTF	GGGAAGATTGCCAGGACGAA
MYBL2_RTR	GGTGTGATGGTGGAGACGAT
CESA4_F	GATCCGCTCAAGGAACCTC
CESA4_R	TCAACGGCTAAGATCGAAAGA
HCT_F	GCTCTTAAGGCGAAATCCAAG
HCT_R	CTTTCCCACTGATCTCCACAC
CCOAOMT1_F	CTCACAAGATCGACTTCAGGG
CCOAOMT1_R	ACGCTTGTGGTAGTTGATGTAG
CCR1_F	ACCAAGTGCAAGGACGAGAA
CCR1_R	GTCGTAGAGGCTTTGCTTGG
SND1_F	AAGCTTGAGCCTTGGGATATT
SND1_R	TCCCGGTTGGATACTTCTTG
CAD6_F	TTGGGACGAAAATCGATAGC
CAD6_R	TGCTTTTATGCCATGCTCTG
MYB58_F	CATCATCAAACTTCACCAGAGC
MYB58_R	GCCACACATTCTTGATCTCATT
DDF1_F	CGGAGATGAGGCCTAAGAAG
DDF1_R	TGCCTCTGTAAACTGGGTGA
JAZ5_F	TCTTTGCTAAACGGAAAGACAGA
JAZ5_R	TGTCCTGCCTCTAGTGGTTGA
JAZ7_F	TGTGTTTTTCTTCAGATGTTACCC
JAZ7_R	TCTCTGCTTGCGATCGATATT
JAZ8_F	GATGTTACCCATCTTCAGGCAA
JAZ8_R	CGACCCGTTTGAGGATGACT
AtMYB15_F	GCCTGATATTAAACGTGGCAAT
AtMYB15_R	GCTGCAATCGCTGACCAT
WRKY40_F	TTGAAGAAGATCCACCGACA
WRKY40_R	CGAGAGCTTCTTGTTCTCAGC
ATMYB9_F	TTCTCCAAATGGGGATTGAT
ATMYB9_R	GCGGGAGAGCTGCTAAAAC
For RLM-RACE	
RACE OUTER	GCTGATGGCGATGAATGAACACTG
RACE INNER	CGCGGATCCGAACACTGCGTTTGCTGGCTTTGATG
AtMyb6_R	TTACAACAGTGACAAACGCGCCT

AtMyb11_R	ACAAAGCTCCATCGTCGCCATT
AtMyb12_R	TCGTCATGATTACGGCGGAG
AtMyb13_R	CTTATCGTTTCTATCTAGTGAGCC
AtMyb20_R	AAGAATGCGAAGATGTGGACGTG
AtMyb42_R	CTTCCTCGGCAGCAGTGTTGTTC
AtMyb48_R	CTGATCATTTGCAAAGTAAGACG
AtMyb83_R	CACCTTCTACTGATACTCTCTTGC
AtTT2_R	CAAGTGAAGTCTCGGAGCCAATC
AtMybL2_R	TCATCGGAATAGAAGAAGCGTTT