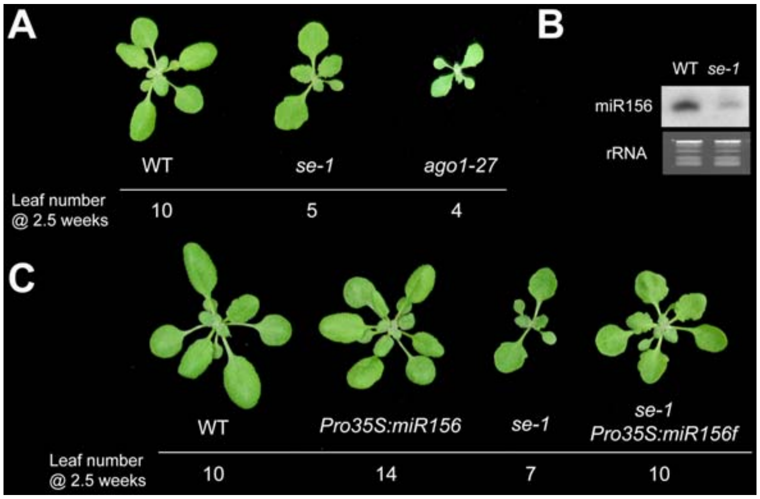
Supplemental Data. Wang et al. (2008). Dual effects of miR156-targeted *SPL* genes and *CYP78A5/KLUH* on plastochron length and organ size in *Arabidopsis thaliana*.

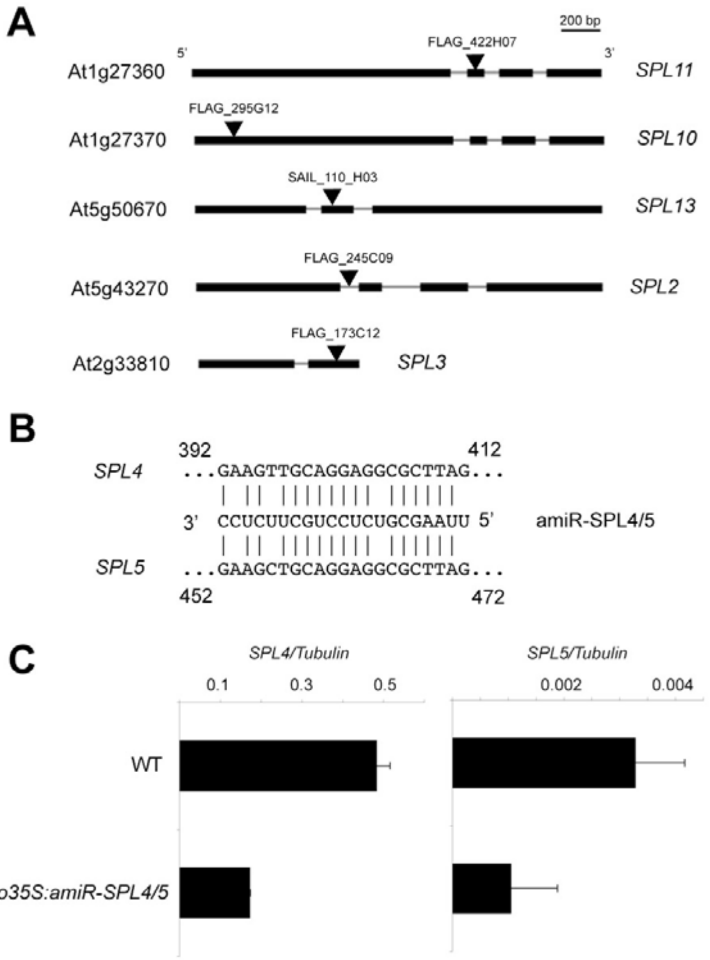


Supplemental Figure 1. MiRNA-dependence of plastochron length, assessed in long days.

(A) Plastochron phenotype of wild type, *se-1* and *ago1-27* mutants.

(B) Small RNA blot showing expression of miR156 in wild type and *se-1* plants. Total RNA was extracted from 10-day-old seedlings. rRNA is shown as loading control below.

(C) Rescue of the *se*-1 plastochron phenotype by miR156 overexpression.



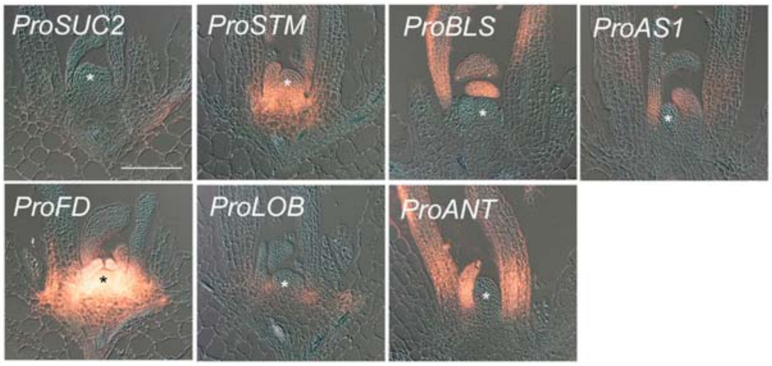
Supplemental Figure 2. T-DNA insertion mutants and amiRNA targeting *SPL4/5.*

(A) Diagram of *SPL* transcribed regions, with thin lines indicating introns. Arrowheads mark T-DNA insertion sites.

(B) Sequence of amiRNA against *SPL4* and *SPL5*.

(C) Expression of *SPL4* and *SPL5* mRNA in amiRNA plants. Ten 10-day-old T1 seedlings were pooled and subjected to qRT-PCR analysis.

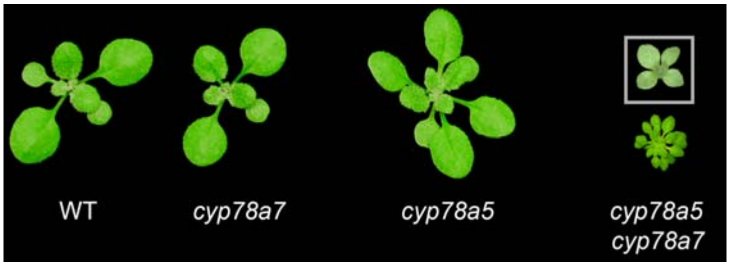
Bars indicate standard deviation.



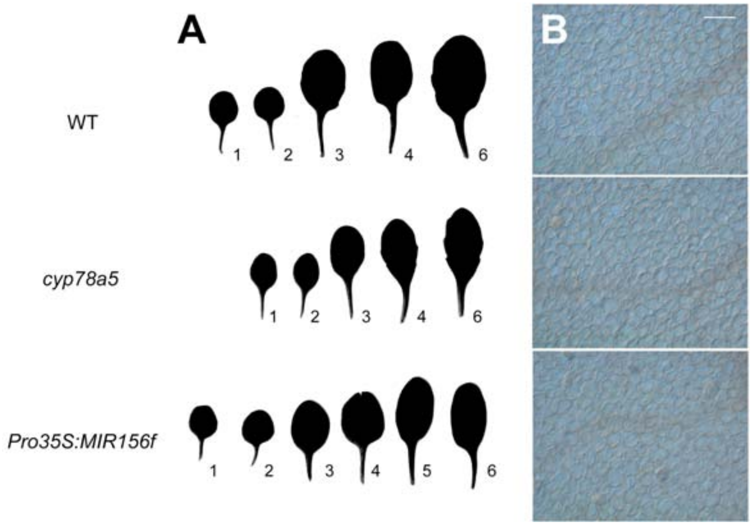
Supplemental Figure 3. Activity of promoter fusions.

Ten-day-old transgenic seedlings were stained for GUS activity, sectioned and photographed under dark field illumination. At least ten T_1 seedlings were examined for each construct, with all showing similar staining patterns. Asterisks indicated meristems proper.

Scale bars indicate 50 µm.



Supplemental Figure 4. Phenotype of *cyp78a5 cyp78a7* double mutants grown in long days. Wild type and the two single mutant plants are 15 days old. The double mutant plant, which germinated later and grew only slowly the first 10 days, is 25 days old. The inset shows a magnified seedling with four cotyledons.



Supplemental Figure 5. Leaf and cell size in wild-type, mutant and transgenic plants.

(A) Outlines of leaves of 20-day-old plants grown in long days. *Pro35S:MIR156f* and *cyp78a5* leaves are smaller than those of the wild type. Numbers indicate order of leaves.

(B) Subepidermal palisade cells from the largest leaves of each genotype, viewed under differential interference contrast. Note similar cell size in all genotypes.

Scale bar indicates 200 µm.

SUPPLEMENTAL TABLES

Supplemental Table 1. Leaf initiation rates of different genotypes.

Genotype	Leaves/day	Range	*n*
Wild type	0.67 ± 0.033	0.60 - 0.70	11
Pro35S:MIR156f	1.07 ± 0.081	0.93 - 1.17	10
spl9 spl15	0.82 ± 0.017	0.80 - 0.83	11
ProANT:MIR156f	1.05 ± 0.032	1.00 - 1.06	10
ProAS1:MIR156f	1.00 ± 0.065	0.93 - 1.13	10
ProBLS:MIR156f	0.89 ± 0.077	0.76 - 1.00	10
ProLOB:MIR156f	0.68 ± 0.028	0.63 - 0.70	10
ProFD:MIR156f	0.69 ± 0.049	0.60 - 0.77	11
ProSTM:MIR156f	0.68 ± 0.018	0.67 - 0.70	10
ProSUC2:MIR156f	0.89 ± 0.065	0.77 - 0.97	12
Pro35S:rSPL3	0.58 ± 0.029	0.50 - 0.67	10
ProSPL9:rSPL9	0.22 ± 0.014	0.20 - 0.23	10
ProSPL9:rSPL9 Pro35S:MIR156f	0.22 ± 0.016	0.20 - 0.23	10
ProANT:rSPL9	0.30 ± 0.012	0.27 - 0.33	10
ProAS1:rSPL9	0.34 ± 0.016	0.30 - 0.37	10
ProFD:rSPL9	0.30 ± 0.010	0.23 - 0.35	10
ProSUC2:rSPL9	0.39 ± 0.016	0.37 - 0.43	10
Pro35S:rSPL10	0.35 ± 0.023	0.33 - 0.40	10
ProANT:rSPL10	0.37 ± 0.044	0.30 - 0.43	12
cyp78a5	0.99 ± 0.022	0.97 - 1.03	12
ProSPL9:rSPL9 cyp78a5	0.48 ± 0.023	0.43 - 0.50	10
Pro35S:MIR156f cyp78a5	1.23 ± 0.034	1.17 - 1.30	12

Total rosette leaf number was counted on 30-day-old plants in short days, except for the earlyflowering *ProFD:SPL3* and *Pro35S:rSPL3* genotypes, for which 20-day old plants were used. Standard deviation is given.

Supplemental Table 2. Flowering time of *cyp78a5* mutants.

Genotype	**Rosette leaf number**	**Days to flowering**
Wild type	10.8 ± 0.63 (10 - 12)	18.6 ± 0.7(18 - 20)
cyp78a5	14.6 ± 0.70 (14 - 16)	15.0 ± 0.47 (14 - 16)

Standard deviation and range (in parentheses) for 10 long-day grown plants are given. Rosette leaf number is significantly different between the two genotypes (Student's t-test, $P < 0.005$).

Supplemental Table 3. Petal and petal cell size (with standard deviation) of different genotypes.

Genotype	**Length (mm)**	**Width (mm)**	**Cell size (μm^2)**
Wild type	3.19 ± 0.05	0.97 ± 0.05	731.3 ± 55.2
Pro35S:MIR156f	2.12 ± 0.05**	0.78 ± 0.05**	740.0 ± 33.1
cyp78a5	2.23 ± 0.08**	0.68 ± 0.04**	749.7 ± 25.1

Student’s t-test with Bonferroni correction.

*significantly different from wild type at $P < 0.02$.

**significantly different from wild type at $P < 0.01$.

Supplemental Table 4. Oligonucleotide primer sequences.

ID	Gene	Sequence (5’-3’)	Purpose
G-7683	*SPL4/5*	GAT TAA GCG TCT CCT GCA ACT CCT CTC TCT TTT GTA TTC C	amiRNA
G-7684	*SPL4/5*	GAG GAG TTG CAG GAG ACG CTT AAT CAA AGA GAA TCA ATG A	amiRNA
G-7685	*SPL4/5*	GAG GCG TTG CAG GAG TCG CTT ATT CAC AGG TCG TGA TAT G	amiRNA
G-7686	*SPL4/5*	GAA TAA GCG ACT CCT GCA ACG CCT CTA CAT ATA TAT TCC T	amiRNA
N-1461	*SPL4*	TCC CAT GGC ATG GAG GGT AAG AGA TCA CAA G	qRT
N-1462	*SPL4*	TCA GAA TTC CTA TCT AAT CTG TGG TCG CTT G	qRT
N-1463	*SPL5*	TCC CAT GGC ATG GAG GGT CAG AGA ACA CAA C	qRT
N-1464	*SPL5*	TCA GAA TTC TTA TCT GAT CTG TGG TCG CTT G	qRT
G-8936	*ANT*	AAA CTG CAG TTG TTT TGG ACT TTT TGG TCT TCG	promoter
G-8937	*ANT*	AAA TCT AGA CAT GGT TTC TTT TTT TGG TTT CTG	promoter
G-7944	*AS1*	AAA TCT AGA ACG GAG GGT GTG AGT GAG TAG TGG TA	promoter
G-7945	*AS1*	AAA GGA TCC CTC CTA CTC CTC CTG ACA TCA CTT CT	promoter
G-9947	*BLS*	AAA CTG CAG GAT ATA ATT CGT CGG TGG TGT ACT A	promoter
G-9948	*BLS*	AAA GGA TCC GAG TCT GGT TTT AGA GAG AAA TGT ACG	promoter
G-7812	*CYP78A5*	AAA CTG CAG ATG TCT CCG GAA GCT TAC GTT CTG TTC	T-DNA, genomic fragment
G-7813	*CYP78A5*	AAA CTG CAG ACA AGG ACC ACG CAG GCT TCT AA	T-DNA, genomic fragment

G-16238	*CYP78A5*	TGT CGG CGG AAT AAT TGA GAA ACA C	qRT
G-16239	*CYP78A5*	CAC CCA TTC CAC TAG AAT CGC AAC T	qRT
G-8452	*CYP78A7*	TCG GTT TAA CGA ACC TCA TTG	T-DNA
G-8453	*CYP78A7*	GAG GCG ACA TCA GAA TCT CAC	T-DNA
G-9194	*FD*	AAA CTG CAG GTA GTT ATC CAA GGC CCT CTC TAC TTG	promoter
G-9195	*FD*	AAA GGA TCC TGG AAA AGA GAA CAG AAG TGA ACC AAC	promoter
G-4815	*Histone H4*	CAC ATC TTT CTC ACC CAA ATC	probe
G-4816	*Histone H4*	CGA TTT ATA TTT CAA CCG AAA CTG	probe
G-8957	*miR156f*	AAA GGA TCC CAG CCA ATG AGC CAA AGA TAA AGA	genomic fragmen
G-8958	*miR156f*	AAA GAG CTC AGG CTC ATG TTG GAA TTC GAA TC	genomic fragmen
G-8946	*LOB*	ACG ACG CCA TTT GTT TTT CTT	promoter
G-8945	*LOB*	AAA CTG CAG TTG CTT GGT CAT CGT GTC TT	promoter
G-8515	*SPL15*	TGT TGG TGT CTG AAG TTG CTG	T-DNA
G-8516	*SPL15*	TCC ACC GAG TCT TCT TCA CTC	T-DNA
G-8517	*SPL9*	TGG TTC CTC CAC TGA GTC ATC	T-DNA
G-8518	*SPL9*	GCT CAT TAT GAC CAG CGA GTC	T-DNA
G-7981	*SPL9*	AAA CCC GGG ATG GAG ATG GGT TCC AAC TCG GGT	genomic fragmen
G-7982	*SPL9*	AAA GAG CTC TCA GAG AGA CCA GTT GGT ATG GTG A	genomic fragmen
G-9908	*SPL9*	AAA CTG CAG GAA TGA CAA ATT GAC CTG AGG CTT G	promoter

G-7985	*SPL9*	AAA CCC GGG GTT GGT TTC CTC TTA CTC AGA CAG AAA	promoter
G-1761	*SPL9*	CGC CTT AAG CTT GTT AAG CAA TCC ACA TCA ACC ACA T	rSPL9
G-1762	*SPL9*	GCT TAA CAA GCT TAA GGC GCA GTT TGA GTC GCC AAT TC	rSPL9
G-7933	*STM*	AAA AAG CTT AGA AAT GGC AGT GAA GGC AGT GGC T	promoter
G-7934	*STM*	AAA GGA TCC ACT AGT ATT ATT ATT CAC TTT GGC T	promoter
G-1588	T-DNA	GCC TTT TCA GAA ATG GAT AAA TAG CCT TGC TTC C	SAIL line
G-7536	T-DNA	GCG TGG ACC GCT TGC TGC AAC T	SALK line
G-8533	T-DNA	TAC GAA TAA GAG CGT CCA TTT TAG AGT GA	SM line
N-0078	β-TUBLIN-2	GAG CCT TAC AAC GCT ACT CTG TCT GTC	qRT
N-0079	β-TUBLIN-2	ACA CCA GAC ATA GTA GCA GAA ATC AAG	qRT