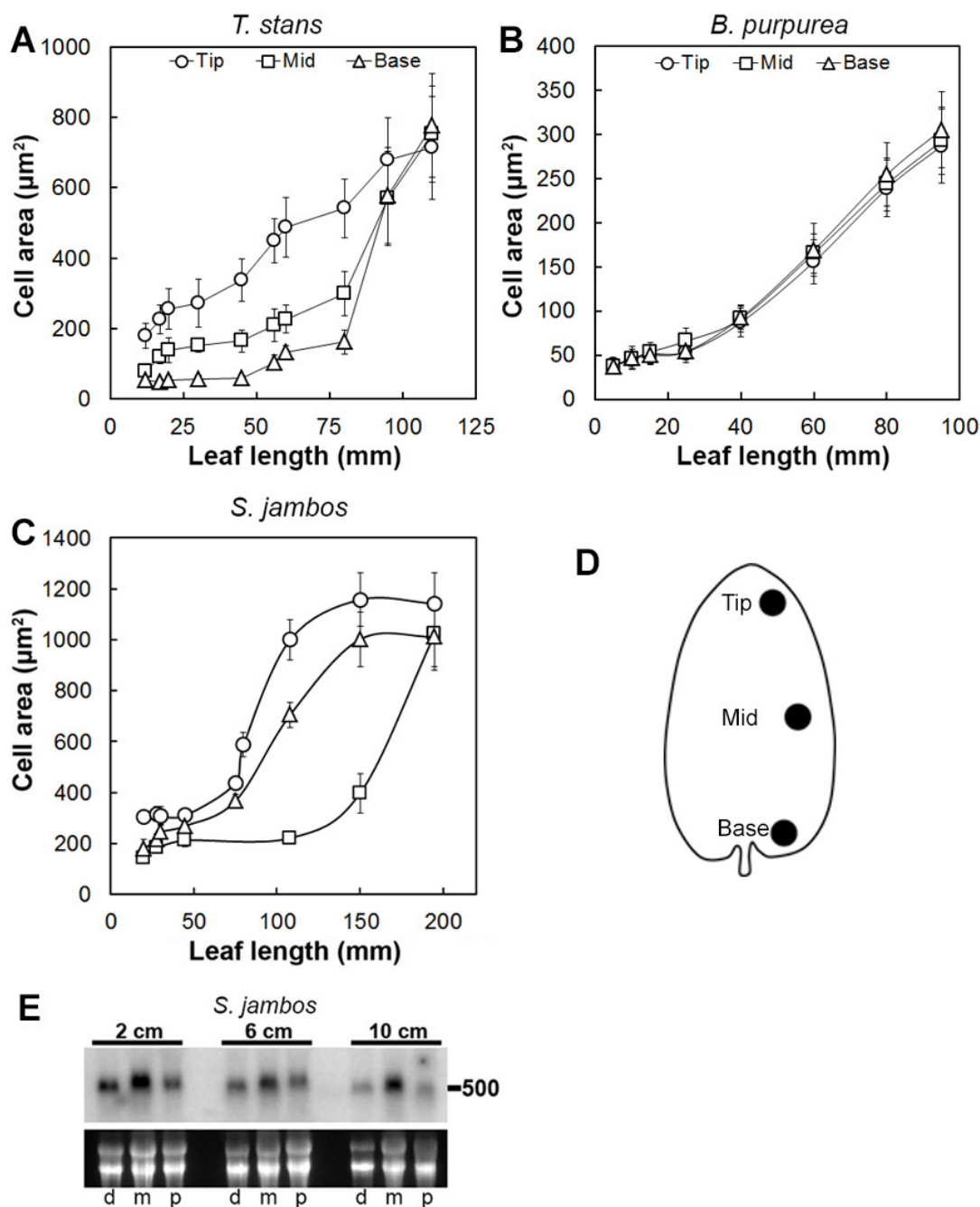
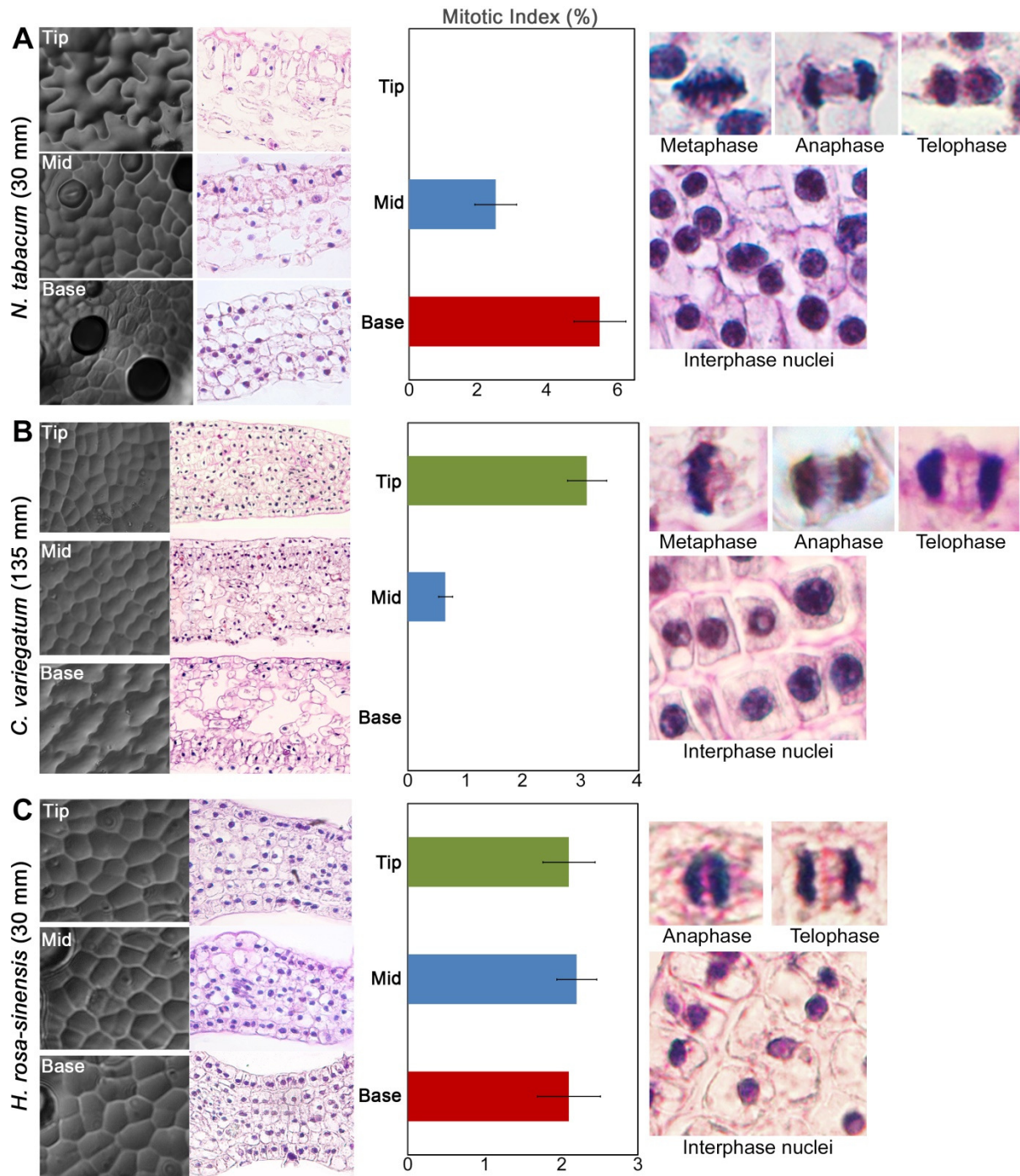


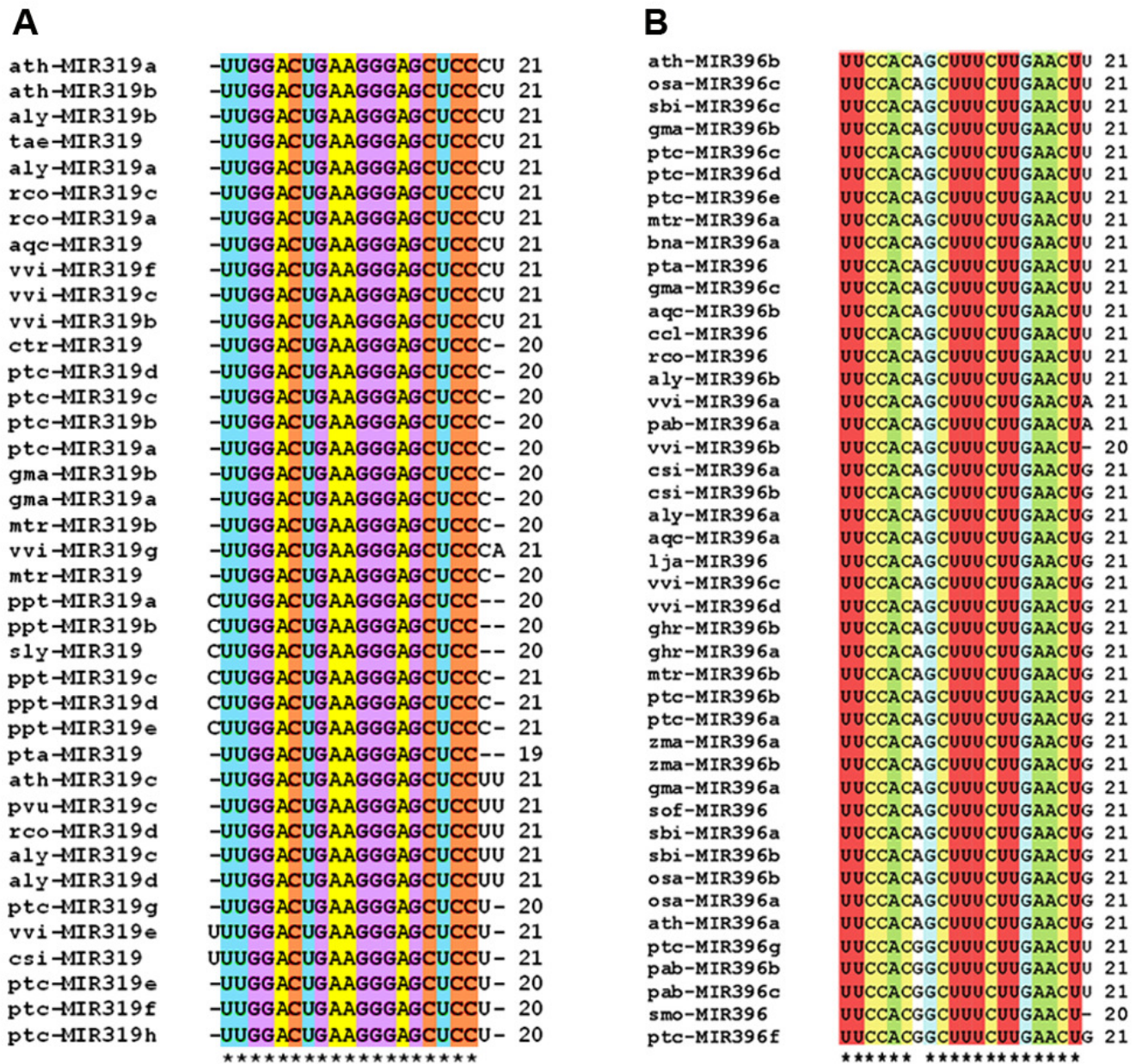
**Supplemental Figure 1. Ink-tracking studies on growing leaves reveal different forms of polar growth in leaves.** (A-D) Panels showing different growth stages of leaves that were marked with ink spots early in growth (picture on the left in each panel). Leaf lengths are indicated. (E-H) Comparative distribution of ink spots in young and mature leaves. Lengths of the young and the mature leaves have been normalized and a horizontal line has been drawn through the middle of the leaves. The numbers above and below the lines indicate the number of spots adjacent to the midrib of the leaf. Leaf lengths are indicated.



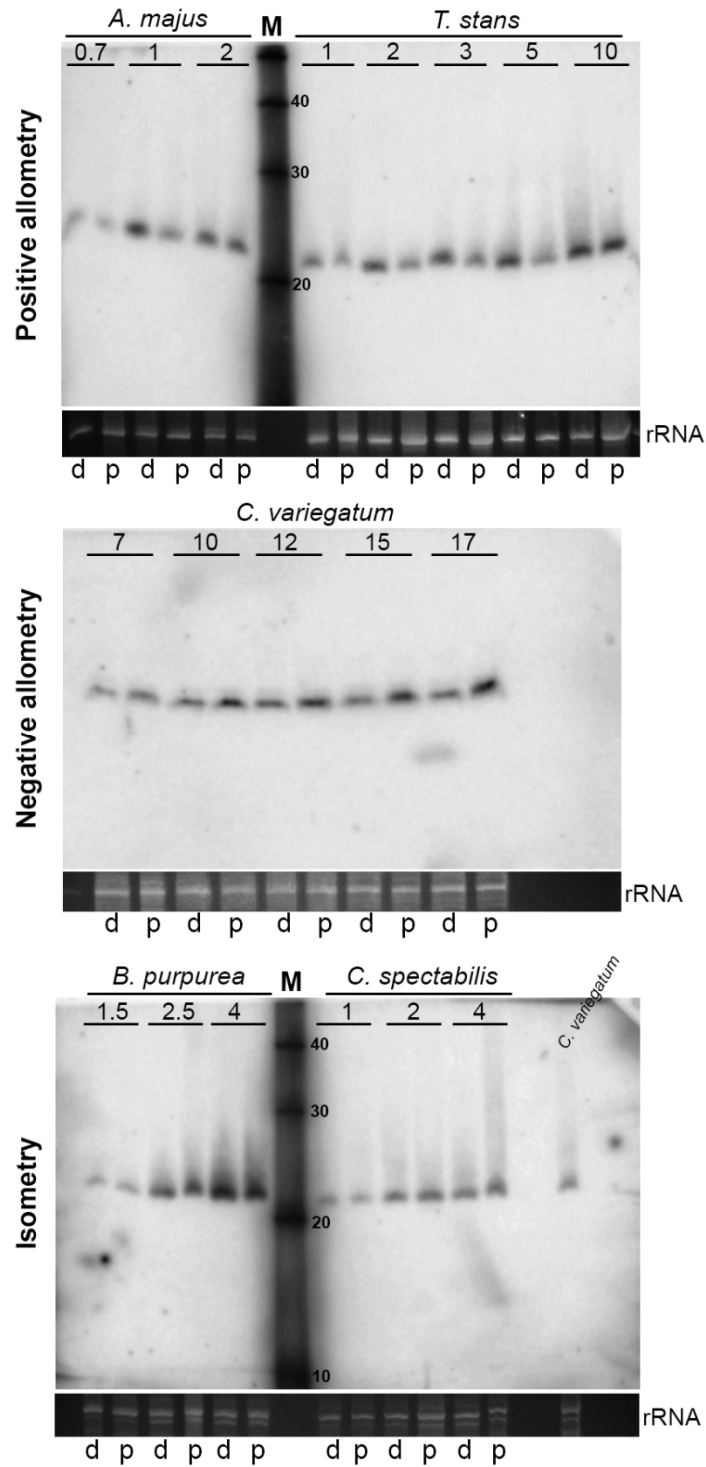
**Supplemental Figure 2. Epidermal cell-size in growing leaves of *T. stans*, *B. purpurea*, and *S. jambos*.** Epidermal cell size on the adaxial surface of leaves at different developmental stages. Cells were measured near tip (○), middle (□) and base (△) ( $n = 250-500$ ; average  $\pm$  SD). (D) Schematic representation showing the regions of the leaves used to measure the cell areas. (E) RNA gel blot showing the distribution of *HISTONE H4* at different developmental stages of *S. jambos* leaves. Leaf lengths (in cm) are indicated above the blots. Proximal, medial and distal parts of the leaves are represented by p, m and d, respectively. The migration of a 500 base single-stranded RNA marker is shown. Ethidium bromide-stained gel is shown below the blot to indicate RNA loading.



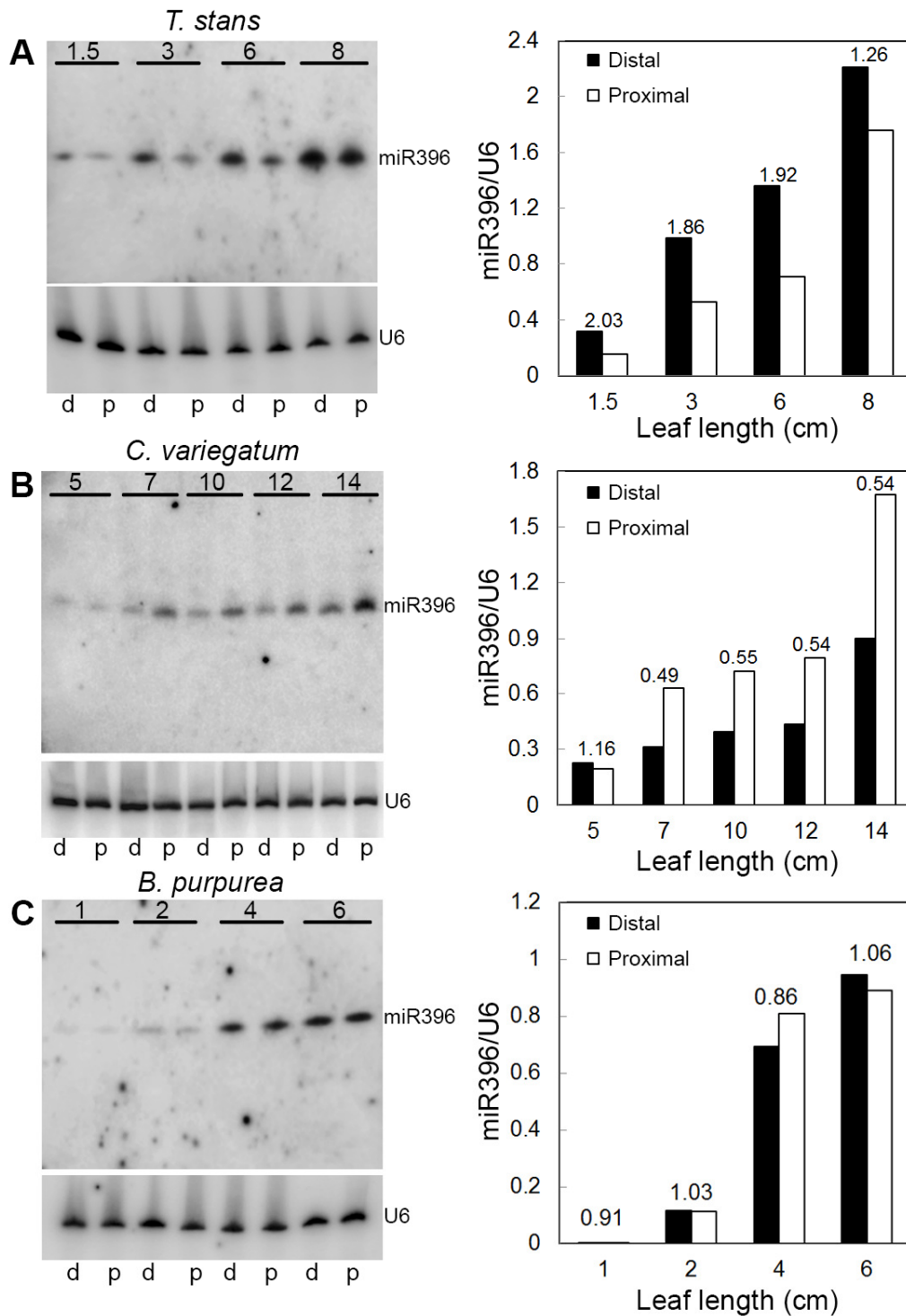
**Supplemental Figure 3. Correlation between epidermal cell morphology, tissue anatomy, and cell division.** Adaxial epidermal cell morphology (left panels) and the associated internal tissue anatomy from tip, middle, and basal regions of *N. tabacum* (A), *C. variegatum* (B) and *H. rosa-sinensis* (C) leaves of indicated lengths. Surface imprints (shown in the left panels) were taken before fixing the tissues for histochemical staining. Dark circles on the imprints in (A) are distortions caused by the trichomes. Mitotic indices from the leaf sections near the tip (green bars), middle (blue bars) and base (red bars) are shown as bar graphs ( $n=1000-1500$ ; average  $\pm$  SD). Representative mitotic nuclei used for calculation of mitotic indices are shown on the right for each species.



**Supplemental Figure 4. Sequence alignment of miR319 and miR396 from different species. (A)** miR319 (B) miR396. Sequences were retrieved from miRbase (<http://www.mirbase.org>) and aligned using ClustalW with default settings. ath - *Arabidopsis thaliana*; aly - *Arabidopsis lyrata*; ptc – *Populus trichocarpa*; osa – *Oriza sativa*; vvi – *Vitis vinifera*; sly – *Solanum lycopersicum*; mtr – *Medicago truncatula*; lja - *Lotus japonicus*; ppt - *Physcomitrella patens*; rco – *Ricinus communis*; ctr - ; gma - *Glycine max*; sbi - *Shorgum bicolor*; pta – *Pinus taeda*; Zma - *Zea maize*; csi - *Citrus sinensis*; bna- *Brassica napus*; aqc - *Aquilegia caerulea*; pab – *Picea abies*; sof – *Saccharum officinarum*; smo – *Selaginella moellendorffii*. Accession numbers for these sequences are given in Supplemental Table 3.



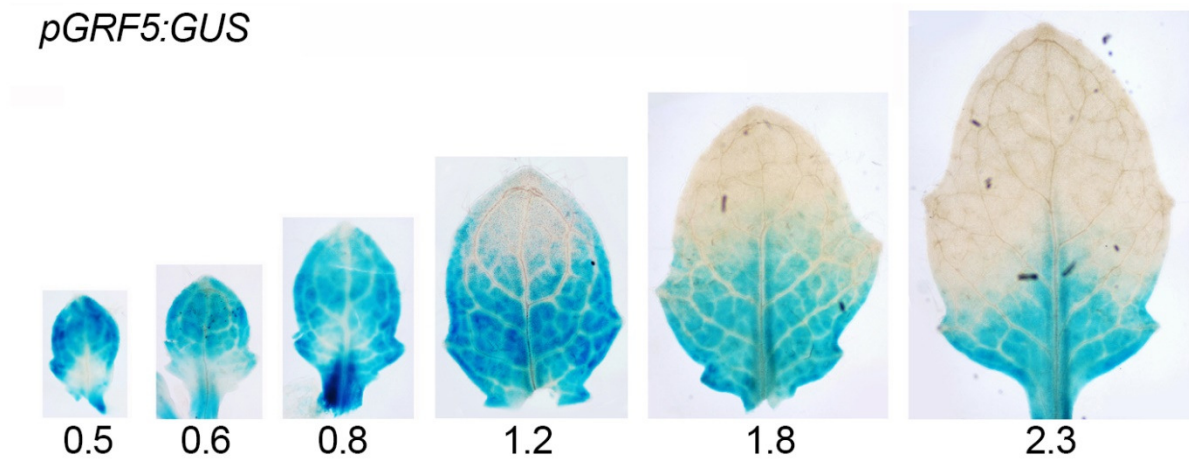
**Supplemental Figure 5. Expression patterns of miR396 in developing leaves.** Full length small RNA gel blots showing the expression of miR396 in the distal (d) and proximal (p) halves of developing leaves with positive allometry, negative allometry, and isometry. Molecular weights (M) of single-stranded RNA markers are indicated. All blots were repeated 3-5 times and similar results were obtained. The plant species are indicated above the blots. Numbers above the blots indicate leaf length in cm. Ethidium bromide-stained gels are shown below the blots as loading controls.



**Supplemental Figure 6. Quantification of relative distribution of miR396 in developing leaves.**

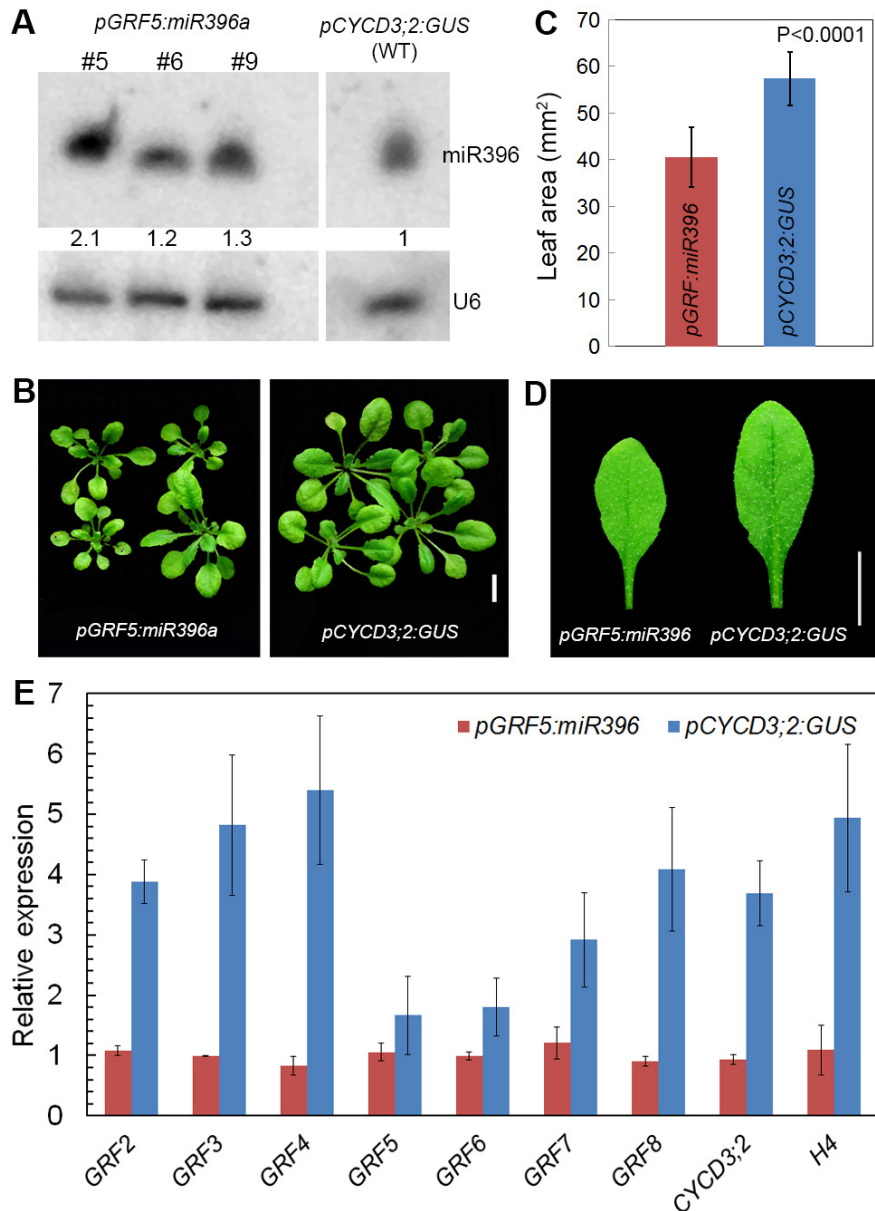
Left panels show the small RNA gel blots and the right panels show the quantification of band intensities. Levels of miR396 were normalized relative to *U6* RNA. The ratios of the expression levels in the distal (d) to the proximal (p) halves are indicated above the bars. All blots were repeated 3-5 times and similar results were obtained. The plant species are indicated above the blots. Numbers above the blots indicate leaf length in cm.



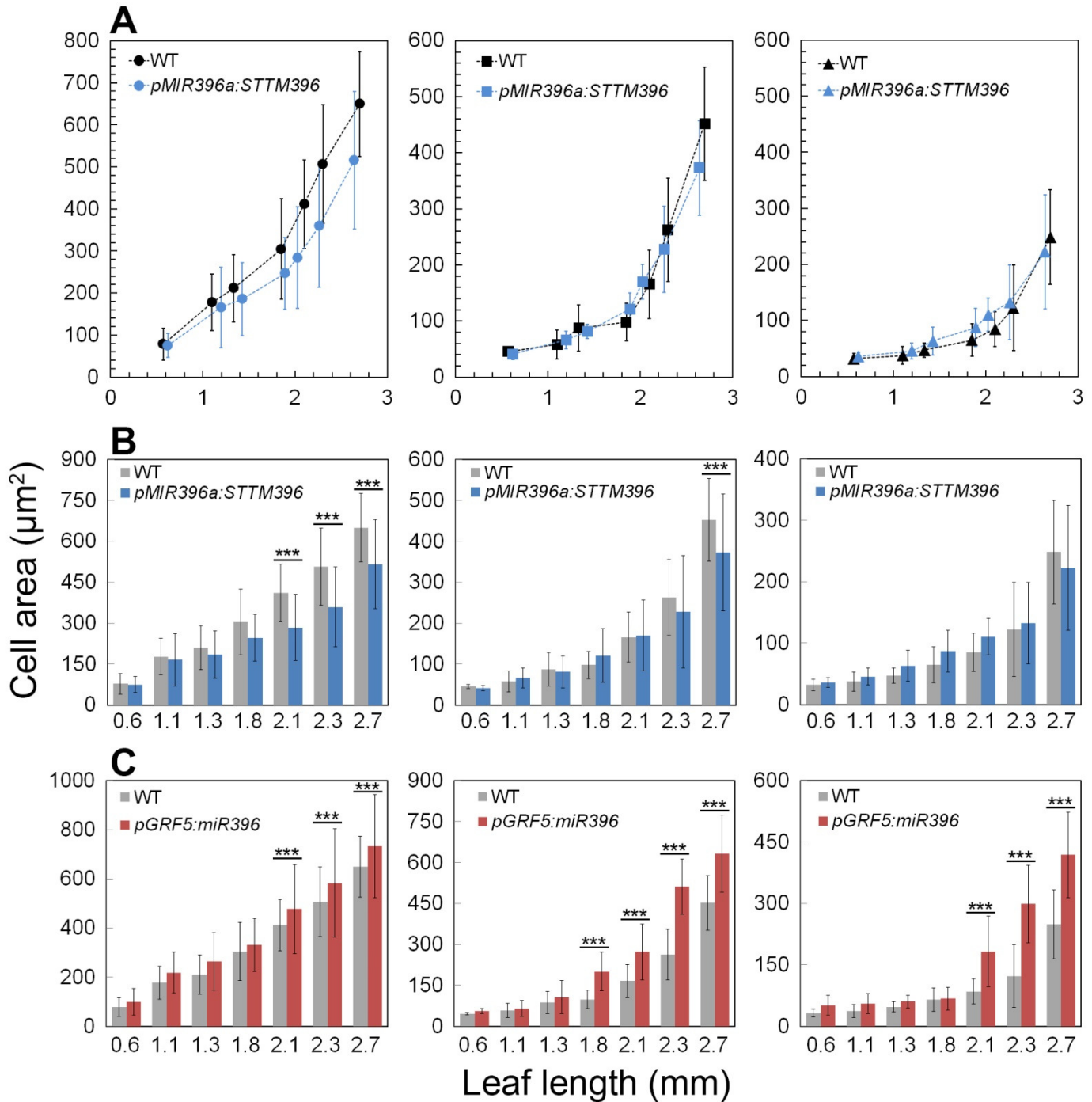


**Supplemental Figure 8. Promoter activity of *At-GRF5*.** (A) GUS histochemical staining of *pGRF5:GUS* leaves showing the promoter activity of *GRF5* in the 5<sup>th</sup> leaf of *Arabidopsis*.

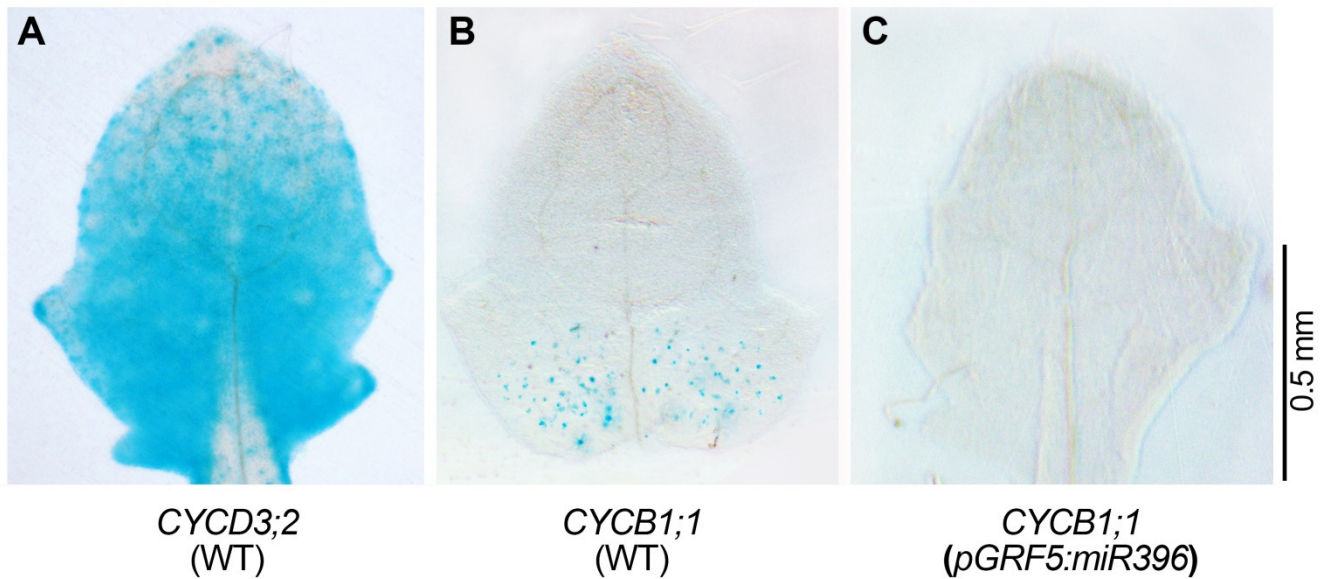




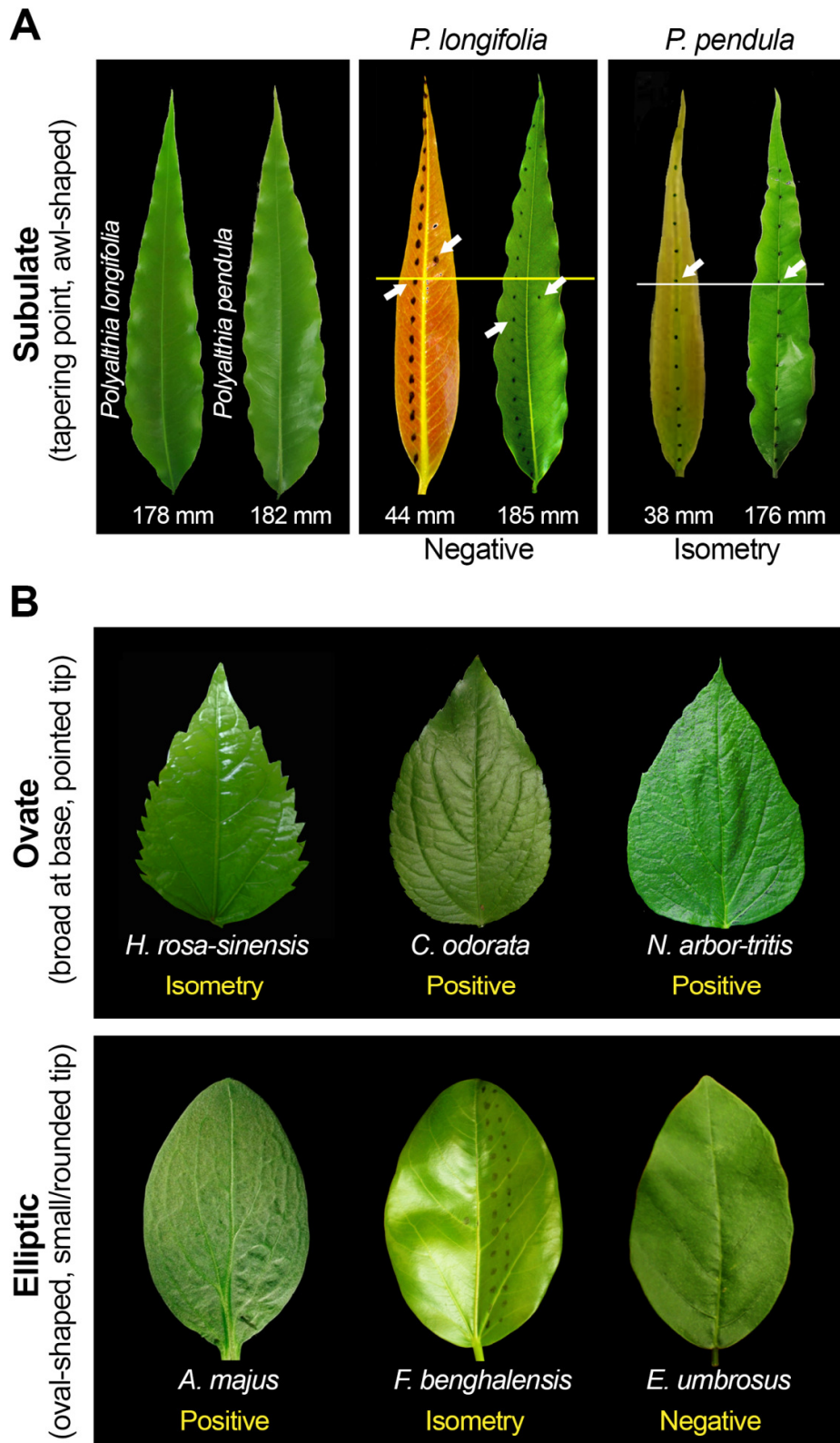
**Supplemental Figure 9. Expression of miR396 and phenotypes of transgenic *Arabidopsis* plants with altered miR396 expression.** (A) Small RNA gel blot showing the altered expression of miR396 in three independent *pGRF5:miR396a* transgenic lines (#5, #6 and #9) and WT with the indicated genotypes. Values for relative expression of miR396 normalized to *U6* are indicated below the blots. (B) Rosettes of 20-day-old *Arabidopsis* plants with the indicated genotypes. (C) Area of the 5<sup>th</sup> leaf in 20-day-old plants of indicated genotypes ( $n=25-30$ ; average  $\pm$  SD). Leaf areas for the transgenic lines were calculated from three independent lines for each genotype. The P value represents the results of two-tailed Mann-Whitney test on the two groups of data sets using GraphPad Prism (Version 5.01). (D) 5<sup>th</sup> leaf from 20-day-old plants of indicated genotypes. Scale bars in (B, D), 1 cm. (E) RT-qPCR analysis of expression levels of *GRFs*, *CYCD3;2* and *H4* in 10-day-old rosettes of WT and *pGRF5:miR396a* plants. The expression levels were normalized to *ACTIN-2* expression ( $n=3$ ; average  $\pm$  SD).



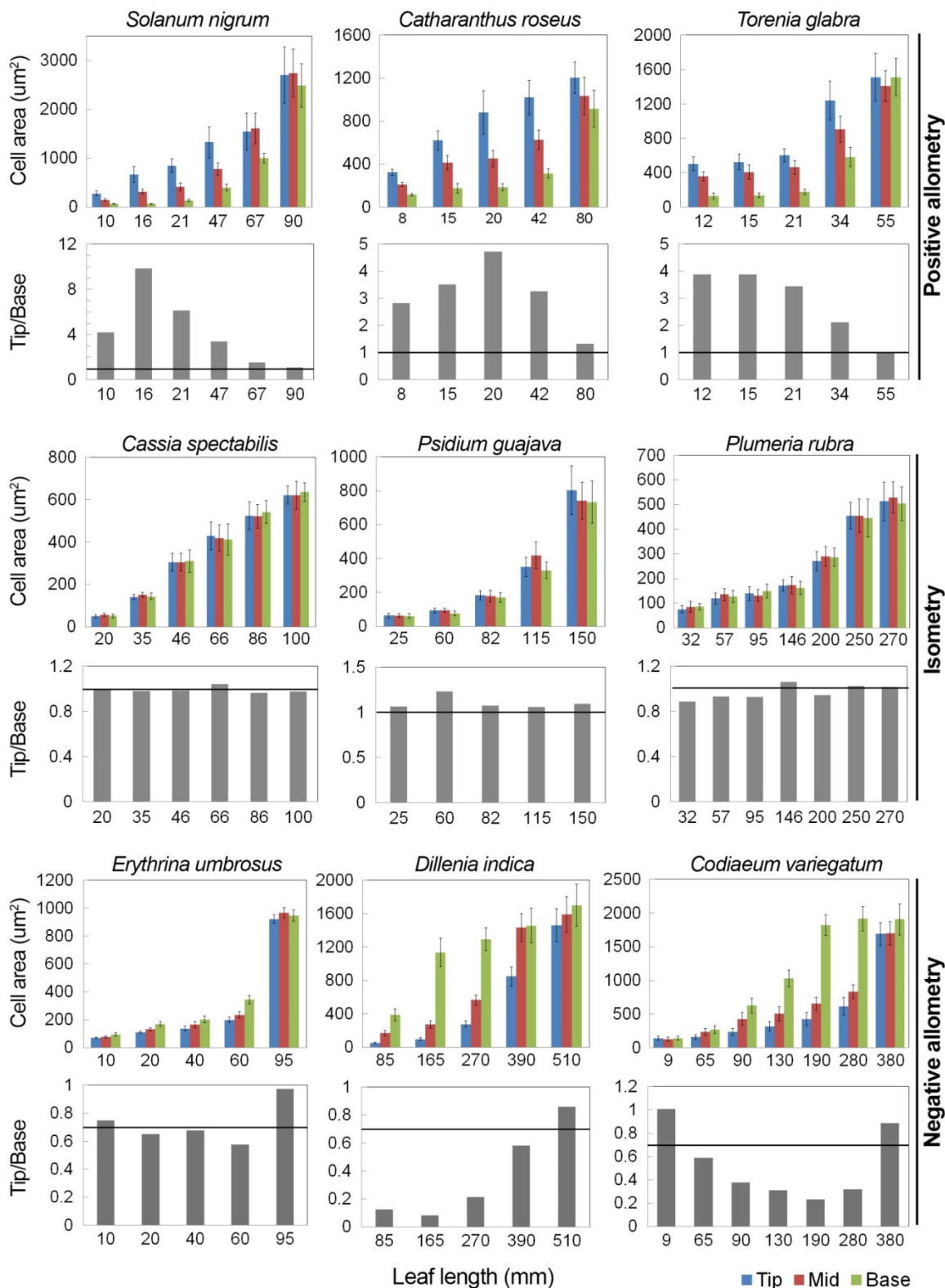
**Supplemental Figure 10. Effects of altered miR396 expression on cell expansion.** (A-B) Epidermal cell size of the 5<sup>th</sup> leaf in the *pMIR396a:STTM396* and WT plants ( $n=40-90$ ; average  $\pm$  SD). (C) Epidermal cell size of the 5<sup>th</sup> leaf in the *pMIR396a:STTM396* and WT plants ( $n=50-100$ ; average  $\pm$  SD). Cell sizes were measured near the tip, middle, and base of the leaves. Unpaired t-test was carried out using GraphPad Prism software to compare the datasets. \*,  $p \leq 0.05$ ; \*\*\*,  $p \leq 0.005$ . P-value summaries are shown only above the datasets that showed significant differences.



**Supplemental Figure 11. Effect of miR396 mis-expression on *CYCB1;1* expression.** GUS reporter assay showing the expression of *CYCD3;2* (A) and *CYCB1;1* (B, C) in young WT (A, B) and *pGRF5:miR396* (C) leaves. Note that the GUS activity is completely absent from the ~1 mm long *pGRF5:miR396* leaf while it is still present at the base of WT leaf of similar growth stage.



**Supplemental Figure 12. Different allometric growth patterns in leaves with similar final shapes.** (A) The leaves of *P. pendula* and *P. longifolia* have similar final shape and size but show isometry and negative allometry, respectively, during growth. Numbers indicate leaf length. (B) Leaves with similar final shapes that show different allometric growth patterns.



**Supplemental Figure 13. Determination of allometric growth patterns in leaves using cell size difference.** Under each allometry class, the upper panels show cell size measurements near the tip, mid, and base of growing leaves and the lower panels show the ratio of average epidermal cell area near the tip to that of the base. The species with cell size ratio 0.9-1.2 were classified under isometry and the species with the ratio <0.7 for at least three growth stages were assigned to negative allometry. The species with tip:base cell size ratios  $\geq 1.5$  for three or more growth stages were assigned to positive allometry. This classification is supported by the  $\alpha$  values shown in Figure 2.

**Supplemental Table 1.** List of species used in the study

	<b>Species</b>	<b>Order</b>	<b>Family</b>	<b>Allometry</b>
1	<i>Schefflera arboricola</i>	Apiales	Araliaceae	Isometry
2	<i>Chromolaena odorata</i>	Asterales	Asteraceae	Positive
3	<i>Dahlia x hybrid</i>	Asterales	Asteraceae	Positive
4	<i>Gaillardia aristata</i>	Asterales	Asteraceae	Positive
5	<i>Helianthus annuus</i>	Asterales	Asteraceae	Positive
6	<i>Lactuca sativa</i>	Asterales	Asteraceae	Positive
7	<i>Raphanus sativus</i>	Asterales	Asteraceae	Positive
8	<i>Sonchus oleraceus</i>	Asterales	Asteraceae	Positive
9	<i>Syndrella nodiflora</i>	Asterales	Asteraceae	Positive
10	<i>Arabidopsis thaliana</i>	Brassicales	Brassicaceae	Positive
11	<i>Brassica juncea</i>	Brassicales	Brassicaceae	Positive
12	<i>Cleome speciosa</i>	Brassicales	Capparidaceae	Positive
13	<i>Spinacia oleracea,</i>	Caryophyllales	Amaranthaceae	Positive
14	<i>Momordica pudica</i>	Cucurbitales	Cucurbitaceae	Positive
15	<i>Impatiens balsamina</i>	Ericales	Balsaminaceae	Positive
16	<i>Bauhinia purpurea</i>	Fabales	Fabaceae	Isometry
17	<i>Brownea coccinea</i>	Fabales	Fabaceae	Isometry
18	<i>Butea monosperma</i>	Fabales	Fabaceae	Isometry
19	<i>Cassia spectabilis</i>	Fabales	Fabaceae	Isometry
20	<i>Erythrina standleyana</i>	Fabales	Fabaceae	Isometry
21	<i>Erythrina umbrosus</i>	Fabales	Fabaceae	Negative
22	<i>Samanea saman</i>	Fabales	Fabaceae	Isometry
23	<i>Saraca asoca</i>	Fabales	Fabaceae	Isometry
24	<i>Alstonia scholaris</i>	Gentianales	Apocynaceae	Isometry
25	<i>Calotropis gigantea</i>	Gentianales	Apocynaceae	Positive
26	<i>Catharantus roseus</i>	Gentianales	Apocynaceae	Positive
27	<i>Coffea arabica</i>	Gentianales	Rubiaceae	Isometry
28	<i>Ixora coccinea</i>	Gentianales	Rubiaceae	Isometry
29	<i>Mussaenda glabra</i>	Gentianales	Rubiaceae	Positive
30	<i>Neolamarckia cadamba</i>	Gentianales	Rubiaceae	Isometry
31	<i>Plumeria rubra</i>	Gentianales	Apocynaceae	Isometry
32	<i>Tabernaemontana divaricata</i>	Gentianales	Apocynaceae	Isometry
33	<i>Antirrhinum majus</i>	Lamiales	Plantaginaceae	Positive
34	<i>Mentha arvensis</i>	Lamiales	Lamiaceae	Positive
35	<i>Salvia coccinea</i>	Lamiales	Lamiaceae	Positive
36	<i>Torenia glabra</i>	Lamiales	Scrophulariaceae	Positive
37	<i>Citharexylum fruticosum</i>	Lamiales	Verbenaceae	Positive
38	<i>Hemigraphis colorata</i>	Lamiales	Acanthaceae	Positive
39	<i>Lantana camara</i>	Lamiales	Verbenaceae	Positive
40	<i>Leucas stelligera</i>	Lamiales	Lamiaceae	Positive
41	<i>Nyctanthes arbor-tritis</i>	Lamiales	Oleaceae	Positive
42	<i>Ocimum tenuiflorum</i>	Lamiales	Lamiaceae	Positive
43	<i>Spathodea campanulata</i>	Lamiales	Bignoniaceae	Isometry
44	<i>Tecoma stans</i>	Lamiales	Bignoniaceae	Positive

<b>Species</b>	<b>Order</b>	<b>Family</b>	<b>Allometry</b>
45 <i>Cananga odorata</i>	Magnoliales	Annonaceae	Isometry
46 <i>Polyalthia longifolia</i>	Magnoliales	Annonaceae	Negative
47 <i>Polyalthia pendula</i>	Magnoliales	Annonaceae	Isometry
48 <i>Codiaeum variegatum</i>	Malpighiales	Euphorbiaceae	Negative
49 <i>Abutilon indicum</i>	Malvales	Malvaceae	Isometry
50 <i>Ceiba pentandra</i>	Malvales	Bombacaceae	Isometry
51 <i>Ceiba speciosa</i>	Malvales	Bombacaceae	Isometry
52 <i>Hibiscus rosa-sinensis</i>	Malvales	Malvaceae	Isometry
53 <i>Callistemon viminalis</i>	Myrtales	Myrtaceae	Isometry
54 <i>Psidium guajava</i>	Myrtales	Myrtaceae	Isometry
55 <i>Syzygium jambos</i>	Myrtales	Myrtaceae	Bidirectional
56 <i>Terminalia catappa</i>	Myrtales	Combretaceae	Negative
57 <i>Artocarpus heterophyllus</i>	Rosales	Moraceae	Isometry
58 <i>Broussonetia papyrifera</i>	Rosales	Moraceae	Isometry
59 <i>Ficus auriculata</i>	Rosales	Moraceae	Isometry
60 <i>Ficus benghalensis</i>	Rosales	Moraceae	Isometry
61 <i>Ficus religiosa</i>	Rosales	Moraceae	Isometry
62 <i>Aeglem armelos</i>	Sapindales	Rutaceae	Isometry
63 <i>Azadirachta indica</i>	Sapindales	Meliaceae	Positive
64 <i>Cedrela odorata</i>	Sapindales	Meliaceae	Isometry
65 <i>Citrus grandis</i>	Sapindales	Rutaceae	Isometry
66 <i>Mangifera indica</i>	Sapindales	Anacardiaceae	Isometry
67 <i>Capsicum annuum</i>	Solanales	Solanaceae	Positive
68 <i>Solanum lycopersicum</i>	Solanales	Solanaceae	Positive
69 <i>Nicotiana tabacum</i>	Solanales	Solanaceae	Positive
70 <i>Nycandra physaloides</i>	Solanales	Solanaceae	Positive
71 <i>Petunia x hybrid</i>	Solanales	Solanaceae	Positive
72 <i>Solanum nigrum</i>	Solanales	Solanaceae	Positive
73 <i>Datura metel</i>	Solanales	Solanaceae	Positive
74 <i>Heliotropium indicum</i>	unplaced	Boraginaceae	Positive
75 <i>Dillenia indica</i>	unplaced	Dilleniaceae	Negative

**Supplemental Table 2.** Methods used to classify the growth patterns.

	<b>Species</b>	<b>Allometry</b>	<b>Methods applied to classify pattern</b>		
			Distribution of spots	Growth ratio determination	Cell size distribution
1	<i>Schefflera arboricola</i>	Isometry	Blue	White	Green
2	<i>Chromolaena odorata</i>	Positive	Blue	Red	Green
3	<i>Dahlia x hybrid</i>	Positive	Blue	White	Green
4	<i>Gaillardia aristata</i>	Positive	White	Red	White
5	<i>Helianthus annuus</i>	Positive	Blue	Red	Green
6	<i>Lactuca sativa</i>	Positive	Blue	White	Green
7	<i>Raphanus sativus</i>	Positive	White	White	Green
8	<i>Sonchus oleraceus</i>	Positive	White	White	Green
9	<i>Syndrella nodiflora</i>	Positive	Blue	White	White
10	<i>Arabidopsis thaliana</i>	Positive	White	White	Green
11	<i>Brassica juncea</i>	Positive	White	White	Green
12	<i>Cleome speciosa</i>	Positive	White	White	Green
13	<i>Spinacia oleracea,</i>	Positive	White	White	Green
14	<i>Momordica pudica</i>	Positive	White	White	Green
15	<i>Impatiens balsamina</i>	Positive	Blue	Red	Green
16	<i>Bauhinia purpurea</i>	Isometry	Blue	Red	Green
17	<i>Brownea coccinea</i>	Isometry	White	White	Green
18	<i>Butea monosperma</i>	Isometry	White	White	Green
19	<i>Cassia spectabilis</i>	Isometry	Blue	Red	Green
20	<i>Erythrina standleyana</i>	Isometry	Blue	Red	Green
21	<i>Erythrina umbrosus</i>	Negative	Blue	Red	Green
22	<i>Samanea saman</i>	Isometry	White	White	Green
23	<i>Saraca asoca</i>	Isometry	Blue	Red	Green
24	<i>Alstonia scholaris</i>	Isometry	Blue	White	Green
25	<i>Calotropis gigantea</i>	Positive	Blue	Red	Green
26	<i>Catharantus roseus</i>	Positive	Blue	White	Green
27	<i>Coffea arabica</i>	Isometry	Blue	Red	Green
28	<i>Ixora coccinea</i>	Isometry	Blue	Red	Green
29	<i>Mussaenda glabra</i>	Positive	Blue	White	Green
30	<i>Neolamarckia cadamba</i>	Isometry	White	White	Green
31	<i>Plumeria rubra</i>	Isometry	Blue	White	Green
32	<i>Tabernaemontana divaricata</i>	Isometry	White	White	Green
33	<i>Antirrhinum majus</i>	Positive	Blue	Red	Green
34	<i>Mentha arvensis</i>	Positive	White	White	Green
35	<i>Salvia coccinea</i>	Positive	White	White	Green
36	<i>Torenia glabra</i>	Positive	Blue	Red	Green
37	<i>Citharexylum fruiticosum</i>	Positive	White	White	Green
38	<i>Hemigraphis colorata</i>	Positive	White	White	Green
39	<i>Lantana camara</i>	Positive	Blue	White	Green



	Species	Allometry	Methods applied to classify pattern		
			Distribution of spots	Growth ratio determination	Cell size distribution
40	<i>Leucas stelligera</i>	Positive			
41	<i>Nyctanthes arbor-tritis</i>	Positive			
42	<i>Ocimum tenuiflorum</i>	Positive			
43	<i>Spathodea campanulata</i>	Isometry			
44	<i>Tecoma stans</i>	Positive			
45	<i>Cananga odorata</i>	Isometry			
48	<i>Codiaeum variegatum</i>	Negative			
49	<i>Abutilon indicum</i>	Isometry			
50	<i>Ceiba pentandra</i>	Isometry			
51	<i>Ceiba speciosa</i>	Isometry			
52	<i>Hibiscus rosa-sinensis</i>	Isometry			
53	<i>Callistemon viminalis</i>	Isometry			
54	<i>Psidium guajava</i>	Isometry			
55	<i>Syzygium jambos</i>	Bidirectional			
56	<i>Terminalia catappa</i>	Negative			
57	<i>Artocarpus heterophyllus</i>	Isometry			
58	<i>Broussonetia papyrifera</i>	Isometry			
59	<i>Ficus auriculata</i>	Isometry			
60	<i>Ficus benghalensis</i>	Isometry			
61	<i>Ficus religiosa</i>	Isometry			
62	<i>Aegle marmelos</i>	Isometry			
63	<i>Azadirachta indica</i>	Positive			
64	<i>Cedrela odorata</i>	Isometry			
65	<i>Citrus grandis</i>	Isometry			
66	<i>Mangifera indica</i>	Isometry			
67	<i>Capsicum annuum</i>	Positive			
68	<i>Solanum lycopersicum</i>	Positive			
69	<i>Nicotiana tabacum</i>	Positive			
70	<i>Nycandra physaloides</i>	Positive			
71	<i>Petunia x hybrid</i>	Positive			
72	<i>Solanum nigrum</i>	Positive			
73	<i>Datura metel</i>	Positive			
74	<i>Heliotropium indicum</i>	Positive			
75	<i>Dillenia indica</i>	Negative			

Highlighted cells indicate the method/s applied to assign the growth patterns

**Supplemental Table 3.** Accession numbers of sequences used in the study

<b>Gene</b>	<b>Species</b>	<b>Accession</b>
Growth-regulating factor 2 ( <i>GRF2</i> )	<i>Arabidopsis thaliana</i>	NM_119936
GRF domain class transcription factor ( <i>GRF2</i> )	<i>Arabidopsis lyrata</i>	XM_002866887
Growth-regulating factor 2 ( <i>GRF2B2</i> )	<i>Brassica napus</i>	JN831663
Growth-regulating factor 2J ( <i>GRF2J</i> )	<i>Brassica rapa</i>	JN698987
GRF domain class transcription factor ( <i>GRF2</i> )	<i>Populus trichocarpa</i>	XM_002320632
GRF domain class transcription factor ( <i>GRF2</i> )	<i>Vitis vinifera</i>	XM_003635328
GRF domain class transcription factor ( <i>GRF2</i> )	<i>Malus x domestica</i>	HM122562
GRF domain class transcription factor ( <i>GRF2</i> )	<i>Glycine max</i>	XM_003549319
GRF domain class transcription factor ( <i>GRF2</i> )	<i>Ricinus communis</i>	XM_002510006
GRF domain class transcription factor ( <i>GRF2</i> )	<i>Capsicum annuum</i>	FJ997852
Growth-regulating factor 2 (Ts- <i>GRF2</i> )	<i>Tecoma stans</i>	KF188429
Growth-regulating factor 2 (Bh- <i>GRF2</i> )	<i>Bauhinia purpurea</i>	KF042295
Growth-regulating factor 2 (Cv- <i>GRF2</i> )	<i>Codiaeum variegatum</i>	KF042296
Histone H4 (Ts- <i>H4</i> )	<i>Tecoma stans</i>	KF042290
Histone H4 (Bp- <i>H4</i> )	<i>Bauhinia purpurea</i>	KF042292
Histone H4 (Cv- <i>H4</i> )	<i>Codiaeum variegatum</i>	KF042291
Actin 1 (Ts- <i>ACT1</i> )	<i>Tecoma stans</i>	KF188428
Actin 1 (Bp- <i>ACT1</i> )	<i>Bauhinia purpurea</i>	KF042293
Tubulin 1 (Cv- <i>TUB1</i> )	<i>Codiaeum variegatum</i>	KF042294
miR396b	<i>Arabidopsis thaliana</i>	MI0001014
miR396c	<i>Oryza sativa</i>	MI0001048
miR396c	<i>Sorghum bicolor</i>	MI0001540
miR396b	<i>Glycine max</i>	MI0001786
miR396c	<i>Populus trichocarpa</i>	MI0002327
miR396d	<i>Populus trichocarpa</i>	MI0002328
miR396e	<i>Populus trichocarpa</i>	MI0002329
miR396a	<i>Medicago truncatula</i>	MI0005621
miR396a	<i>Brassica napus</i>	MI0005773
miR396	<i>Pinus taeda</i>	MI0005788
miR396c	<i>Glycine max</i>	MI0010572
miR396b	<i>Aquilegia caerulea</i>	MI0012095
miR396	<i>Citrus clementine</i>	MI0013304
miR396	<i>Ricinus communis</i>	MI0013418
miR396b	<i>Arabidopsis lyrata</i>	MI0014582
miR396a	<i>Aquilegia caerulea</i>	MI0012094
miR396	<i>Lotus japonicus</i>	MI0010581
miR396c	<i>Vitis vinifera</i>	MI0007955
miR396d	<i>Vitis vinifera</i>	MI0006571
miR319a	<i>Arabidopsis thaliana</i>	MI0000544
miR319b	<i>Arabidopsis thaliana</i>	MI0000545
miR319b	<i>Arabidopsis lyrata</i>	MI0014519
miR319	<i>Triticum aestivum</i>	MI0016453
miR319a	<i>Arabidopsis lyrata</i>	MI0014518
miR319a	<i>Ricinus communis</i>	MIMAT0014180
miR319c	<i>Ricinus communis</i>	MIMAT0014181
miR319	<i>Aquilegia caerulea</i>	MI0012091
miR319c	<i>Vitis vinifera</i>	MIMAT0005704
miR319f	<i>Vitis vinifera</i>	MIMAT0005705
miR319	<i>Citrus trifoliata</i>	MI0013303
miR319c	<i>Populus trichocarpa</i>	MI0002298
miR319d	<i>Populus trichocarpa</i>	MI0002299
miR319b	<i>Populus trichocarpa</i>	MI0002297
miR319a	<i>Glycine max</i>	MI0001782
miR319b	<i>Glycine max</i>	MI0001783
miR319	<i>Medicago truncatula</i>	MI0001751
miR319a	<i>Physcomitrella patens</i>	MI0003496
miR319b	<i>Physcomitrella patens</i>	MI0003497
miR319	<i>Solanum lycopersicum</i>	MI0009978

<b>Gene</b>	<b>Species</b>	<b>Accession</b>
miR319	<i>Pinus taeda</i>	MI0005786
miR319	<i>Phaseolus vulgaris</i>	MIMAT0011176
miR319	<i>Citrus sinensis</i>	MIMAT0018459

**Supplemental Table 4.** Primers used in the study

Sl. No.	Primer Name	Sequence 5'-3'	Forward/Reverse	Purpose
1	P02047	GAGYTDGARCAHCARGCVTTGATC	FP	Degenerate primer for cloning <i>GRF</i>
2	P02048	CWCARTGGRYKGAGYTRGARCAHC	FP	Degenerate primer for cloning <i>GRF</i>
3	P02049	CTTYTG HARVACHCCHGTNGG RGA	RP	Degenerate primer for cloning <i>GRF</i>
4	P02050	TTYTG HARVACHCCHGTNGG RGA	RP	Degenerate primer for cloning <i>GRF</i>
5	P02233	ATGGAYCTNGARCCNGGNACNATGG	FP	Degenerate primer for cloning <i>TUBULIN</i>
6	P02234	GRGARGARTAYCCNGAYMGRATGATG	FP	Degenerate primer for cloning <i>TUBULIN</i>
7	P02235	CRTTCATRTRCTYTCNGCYTCNG	RP	Degenerate primer for cloning <i>TUBULIN</i>
8	P02236	CATNCCYTCNCCDGTTRTACCARTG	RP	Degenerate primer for cloning <i>TUBULIN</i>
9	P02237	GGDACNGGHATGGTBAARGCBGG	FP	Degenerate primer for cloning <i>ACTIN</i>
10	P02238	CCWCCDATCCAGACRCTRAYTTYC	RP	Degenerate primer for cloning <i>ACTIN</i>
11	P02124	GGNGAYGARGCNCARTCHAARMGDGG	FP	Degenerate primer for cloning <i>ACTIN</i>
12	P02125	CRTGDATDCCHGVDGCTTCCATHCC	RP	Degenerate primer for cloning <i>ACTIN</i>
13	P00658	ATGTCDGGNMGNNGVAARGGMGGNAARGG	FP	Degenerate primer for cloning <i>HISTONE4</i>
14	P00659	CCDCCRAANCCRTANAGDGTNCKNCC	RP	Degenerate primer for cloning <i>HISTONE4</i>
15	P02237	GTCATCCTTGCGCAGGGGCCATGC		Probe sequence for <i>A. thaliana</i> U6 snoRNA
16	P01524	AGAATTCGCCGTCGAGTGTGAGTTTAGTCC G	FP	Clone miR396a promoter from <i>A. thaliana</i> ( <i>Eco</i> RI)
17	P01525	AGGATCCAGAGAGGGTCATGTAGAGCAGA CG	RP	Clone miR396a promoter from <i>A. thaliana</i> ( <i>Bam</i> HI)
18	P01503	ATCTAGA CTATCGACCATCTTCCTTCTCAC	FP	Clone miR396a hairpin from <i>A. thaliana</i> ( <i>Xba</i> I)
19	P01504	TTTCTGCAGCATAAACACCGATTAACTCAT AGAC	RP	Clone miR396a hairpin from <i>A. thaliana</i> ( <i>Pst</i> I)
20	P01564	ACCCGGGCGTGGTCATCGCAAGGTAACC	FP	Clone <i>GRF5</i> promoter from <i>A. thaliana</i> ( <i>Sma</i> I)
21	P01529	AGGATCCGTTCTCCCGCTACTTCCACTTAG	RP	Clone <i>GRF5</i> promoter from <i>A. thaliana</i> ( <i>Bam</i> HI)
22	P02258	CGAGCGTGGGTACTCTTTCACC	FP	qRT-PCR for <i>BpACT1</i>
23	P02259	GAAGAGTACTTCAGGGCAGCGG	RP	qRT-PCR for <i>BpACT1</i>
24	P02260	CCTTGTCCTTCCCTCGGTTG	FP	qRT-PCR for <i>CvTUB1</i>
25	P02261	GCCGTGACGAGGATCAGCAGC	RP	qRT-PCR for <i>CvTUB1</i>
26	P02262	GATCTCTACGGCAACATTGTA CTAG	FP	qRT-PCR for <i>TsACT1</i>
27	P02263	GGGTGGTGCGACCACCTTAATC	RP	qRT-PCR for <i>TsACT1</i>
28	P02264	GTCCATCCCTGTGGCTCCCG	FP	qRT-PCR for <i>TsGRF2</i>
29	P02265	CGGTTCCGCAAGATCGTGACTC	RP	qRT-PCR for <i>TsGRF2</i>
30	P02266	CACCGATCCTGAGCCAGGGAG	FP	qRT-PCR for <i>BpGRF2</i>
31	P02267	GTGACGGCATGGCCTGATTGGC	RP	qRT-PCR for <i>BpGRF2</i>
32	P02268	GTGAACGCCATATGAACAGGGGC	FP	qRT-PCR for <i>CvGRF2</i>

Sl. No.	Primer Name	Sequence 5'-3'	Forward/Reverse	Purpose
33	P02269	GTGGTGATGCTGTGCAATGGCG	RP	qRT-PCR for <i>CvGRF2</i>
34	P02270	CAAGGAATCACCAAGCCGGCG	FP	qRT-PCR for <i>CvH4</i>
35	P02271	CTTCTCCGAAACCATATAGAGTACG	RP	qRT-PCR for <i>CvH4</i>
36	P02272	CATCCAGGGTATCACGAAGCCGG	FP	qRT-PCR for <i>TsH4</i>
37	P02273	GTCAGTGTCTTCCGGCGAGCG	RP	qRT-PCR for <i>TsH4</i>
38	P02274	GGGTATCACGAAGCCTGCAATTCG	FP	qRT-PCR for <i>BpH4</i>
39	P02275	CCGTCCGAGCATGCTCAGTGTAGG	RP	qRT-PCR for <i>BpH4</i>
40	P01840	GGTTAGGCAAAGGAGGAGCAAAG	FP	qRT-PCR for <i>AtH4</i>
41	P01841	CCATAGCAGTCACCGTCTTCCTC	RP	qRT-PCR for <i>AtH4</i>
42	P02052	TCCTCCCATGGCAACTATCTC	FP	qRT-PCR for <i>AtGRF2</i>
43	P02053	GCTTCGTTGCAAGCAATCCT	RP	qRT-PCR for <i>AtGRF2</i>
44	P01845	GCTCTTCGTAACCCAACCAACAAGA	FP	qRT-PCR for <i>AtGRF3</i>
45	P01847	GCTGCTGCTGGCTTCTCCATTG	RP	qRT-PCR for <i>AtGRF3</i>
46	P01848	TGGTCATGGACCAACAACAACCA	FP	qRT-PCR for <i>AtGRF4</i>
47	P01850	AGGACGTGTTGTTACCGGGCA	RP	qRT-PCR for <i>AtGRF4</i>
48	P01852	GGGCTTGGTGGAAGTAGTAGTAACA	FP	qRT-PCR for <i>AtGRF5</i>
49	P01853	ACGTTCTCTCCCAACTCCTCCA	RP	qRT-PCR for <i>AtGRF5</i>
50	P01855	CCATAGAACCTTCCGGGTCAATC	FP	qRT-PCR for <i>AtGRF6</i>
51	P01856	ACATCAATGGCCTCTCACGTGTC	RP	qRT-PCR for <i>AtGRF6</i>
52	P01857	TGCAGGAAATGGACTTTTGGGTTGT	FP	qRT-PCR for <i>AtGRF7</i>
53	P01857	TCCGGCATCTTCCCGGCTCT	RP	qRT-PCR for <i>AtGRF7</i>
54	P01860	CACACCCGCCGTTCTGGTT	FP	qRT-PCR for <i>AtGRF8</i>
55	P01862	GTGTGAGAAGCTCTGGAGGAACAG	RP	qRT-PCR for <i>AtGRF8</i>
56	P02042	GTCTAGACAGTTCAAGAACTAAGCTGTGGAA GTTGTTGTTGTTATGGTCTAATTTAAATATGG TCTAAAGAAGAAGAATCAGTTCAAGAACTGA GCTGTGGAACTGCAGAT	FP	STTM396 (XbaI and PstI)
57	P02043	ATCTGCAGTTCCACAGCTCAGTTCTTGA ACTGATTCTTCTTTAGACCATATTTAAATTAG ACCATAACAACAACA ACTTCCACAGCTTAGT TCTTGA ACTGTCTAGAC	RP	STTM396 (XbaI and PstI)

Degenerate (wobble) bases for degenerate primers:

M= AC	Y= CT	N= AGCT
R= AG	K= GT	V= AGC
W= AT	D= AGT	H= ACT
S= GC	B= GCT	

Enzyme sites are highlighted in yellow