Plastid control of abaxial-adaxial patterning

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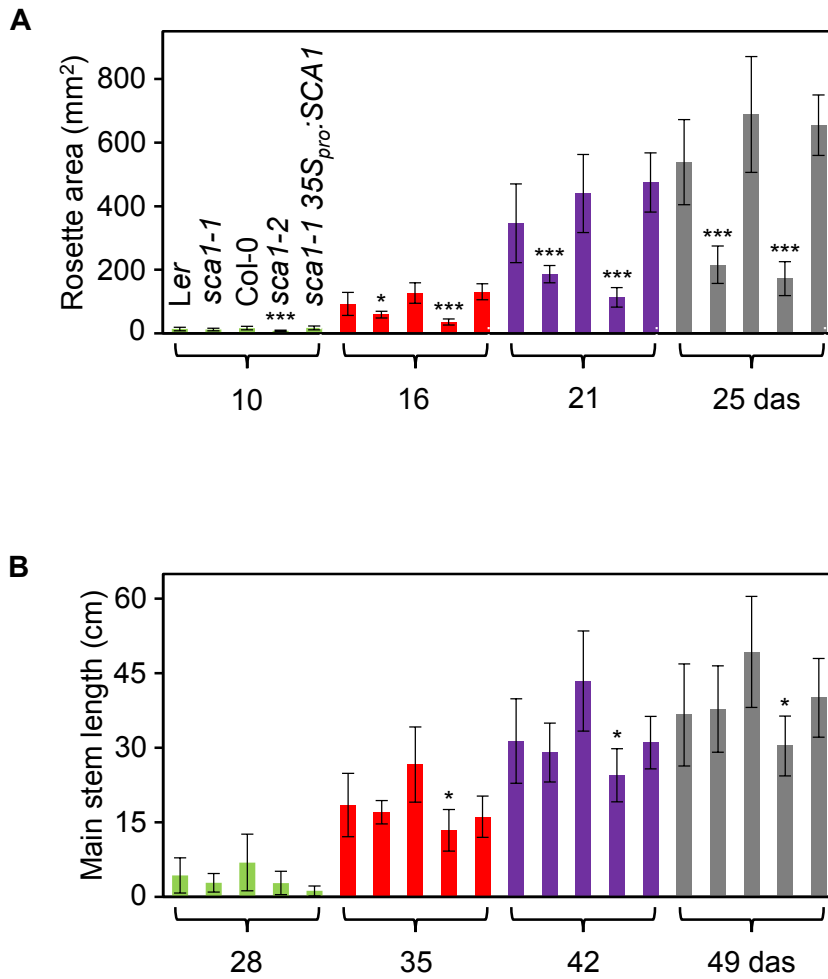
SUPPLEMENTARY DATA

Supplementary Table S1. Mutations found in the *sca1-1* candidate interval.

| Mutation	Region affected	Predicted effect
G→A	At2g32990, 3rd exon	Glu265→Glu (Synonymous)
G→A	At2g33060, 3'UTR	-
C→T	At2g33170, 2nd exon	Ile1011→Ile (Synonymous)
C→T	At2g33800, 2nd exon	Leu233→Phe
G→A	At2g34670, 5'UTR	-

Supplementary Table S2. Primer sets used in this work.

| Purpose	Oligonucleotide names	Oligonucleotide sequence (5' → 3')	
		Forward primer (F)	Reverse primer (R)
Linkage analysis	cer458065_F/R	CTGATCTTTTCAACATACATTATAG	GTTATTATTTCCATACTTTTTGGC
	cer450190_F/R	GGAGGGTTAGTTTATAATTG	GGTCGTTATTGTTAAATTATTG
	cer460386_F/R	TGGGTGCCACATAAAAAGGT	TCCATCAACGTTATTTTTCTCAAA
	cer449091_F/R	CCTCTTTCGTATAATTTGTG	CATTACACTACATATTCTGAATAG
	cer459006_F/R	TGGTATGCTCATGTATCGCTTA	AGAGCTGATGAACAAAGACTGA
	cer459780_F/R	CCAAAACAACAAAGGATTAGTGGA	CCTTGCCTGAAAGAAAAGTGAA
SCA1 sequencing	At2g33800_F/R	TGTTGCTTCCAAGCTGTTTCC	AAGTATTCTACTTTCCCTCACAG
	At2g33800_R2		CACAATCAATTAGAAGAATCGGTT
Gateway cloning	SCA1cds_F/R	GGGGACAAGTTTGTACAAAAAAGCAGGCT	GGGGACCACTTTGTACAAGAAAGCTGG
		ATGGCGACAGCATCAGCTCT	GTATCATCCAAGTAGTAGTATGAGC
Genotyping	Salk_095863_LP/RP	AGCAGATTTCTGAACAGCAGC	AATTAACGTTGCTCGTTGGTG
	LbB1.3_R		ATTTTGCCGATTTCGGAAC
	pst_11131_LP/RP	GGATGTGATGATTTGCTTGG	GGCACAAGTCTTCGCATGTA
	Ds5-1a_R		ACGGGATCCCGGTGAAACGGT
qRT-PCR	18SrRNA_qPCR_F/R	AGGATCCATTGGAGGGCAAGT	CGACGTTTTTAACTGCAACAACT
	qSCA1_F/R	TCAGGTATTGGTGGGAAGCC	CCCTCTGATCTGTGAGGGAAAG
	qACTIN2_F/R	GCACCCTGTTCTTCTTACCG	AACCCTCGTAGATTGGCACA
	rbcL_F/R	GTGTTGGGTTCAAAGCTGGT	CATCGGTCCACACAGTTGTC
	psbA_F/R	GAGCAGCAATGAATGCGATA	CCTATGGGGTCGCTTCTGTA
	rrn16_F/R	CGGTATCTGGGGAATAAGCA	GATTTGACGGCGGACTTAAA
	rrn23_F/R	GGGCGACTGTTTACCAAAAA	TTACCCGACAAGGAATTTCG
	atpB_F/R	GAGCTCGTATGAGAGTTGGT	ACCCAATAAGGCGGATACCT
	qKAN1_F/R	GATCCAGCATTCAAAATCAGG	TTTCTCGTGCCAATCTGGTCT
	qKAN2_F/R	TTTGCATGGGAAGTTAATCG	TTGTTCCCGAGATGCTTGAT
	qARF3_F/R	GGAAAGCCTGATATCCCTGTC	ACCATCCGAACAAGTGTTGA
	qREV_F/R	ATATTCGATGAATCGGGTCGTA	ATAACTCACATGTCTTCCCATCG

This list of oligonucleotides does not include those used for low-resolution mapping, which are described in Ponce *et al.*[15].

A

B

Supplementary Figure S1. Characterization of the growth of the *sca1* mutants. (A) Rosette area progression. (B) Main stem length progression. Asterisks indicate a significant difference with the corresponding wild type in a (A) Student's *t* test (n=16) or (B) Mann-Whitney test (n=8) (*p<0.05,***p<0.001).
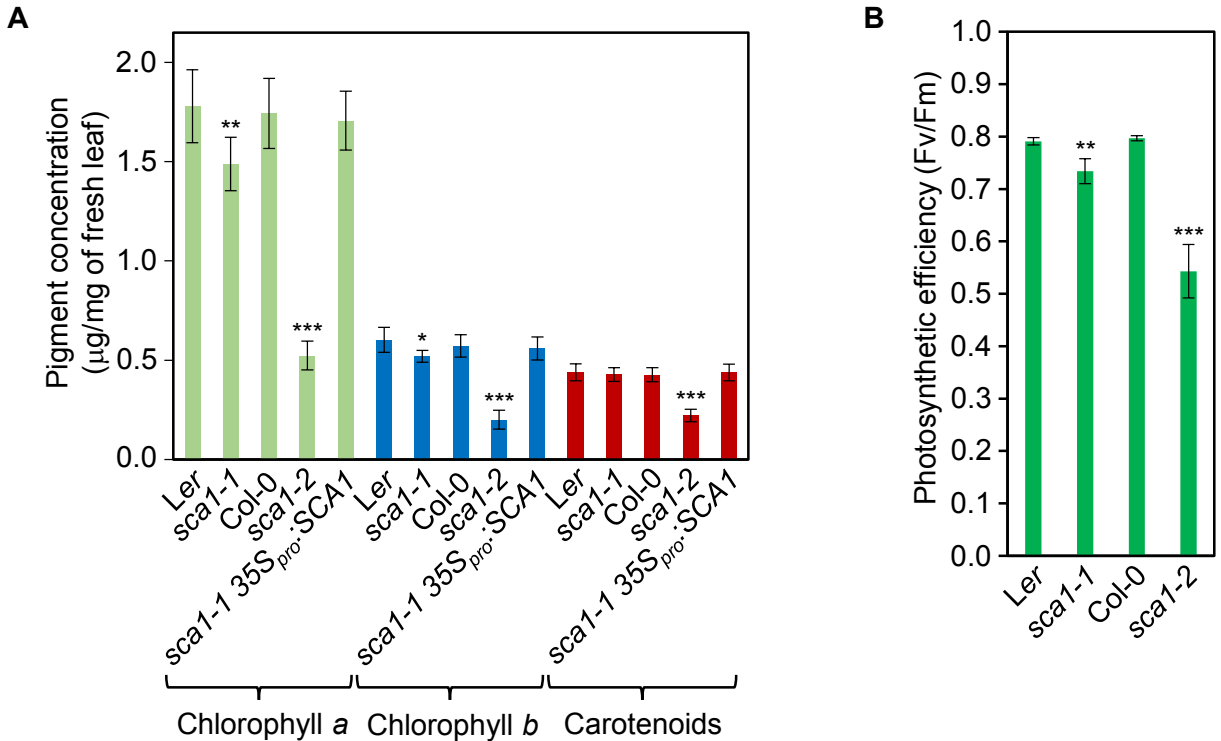
Supplementary Figure S2. Chlorophyll and carotenoid content and photosyntetic efficiency in the *sca1* mutants. (A) Chlorophyll and carotenoid concentration in plant leaves collected 14 das. (B) Maximum efficiencies of PSII measured as *Fv/Fm* in plant leaves at 20 das. Asterisks indicate a significant difference with the corresponding wild type in a Mann-Whitney test (n=8) (*p<0.05,**p<0.01,***p<0.001).

A

B
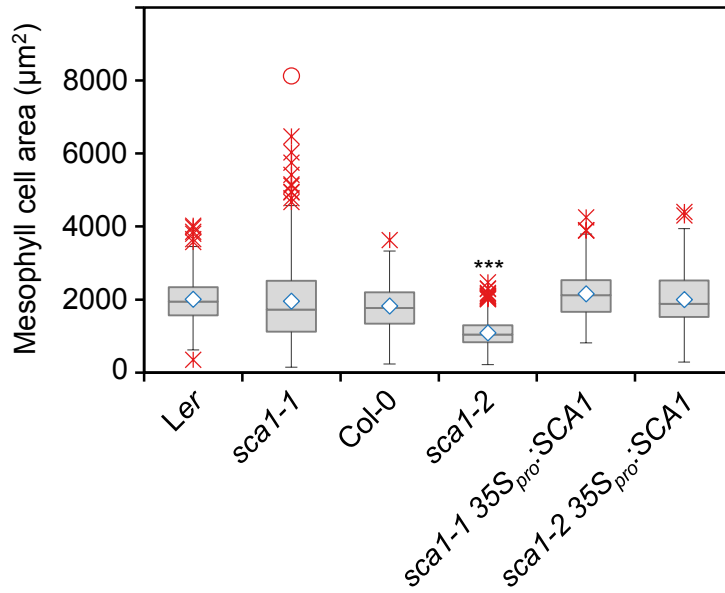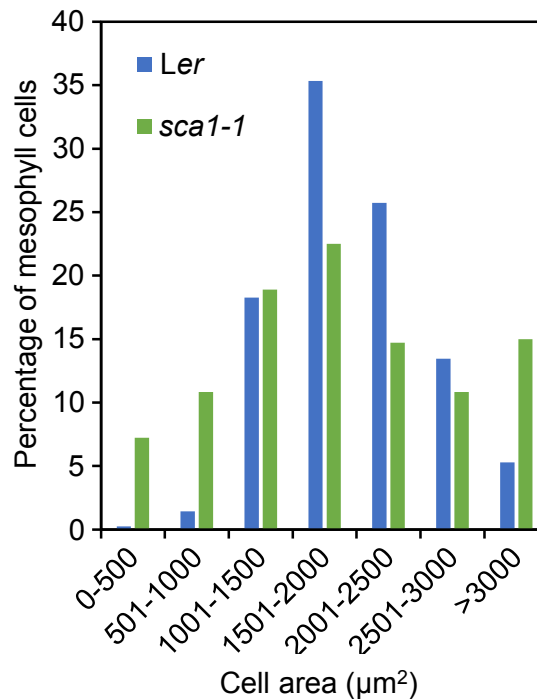
Supplementary Figure S3. Morphometric analysis of the palisade mesophyll cells of the *sca1* mutants. (A) Boxplot distribution of the palisade mesophyll cell area in first-node leaves from L*er*, *sca1-1*, Col-0, *sca1-2*, *sca1-1 35S$_{pro}$:SCA1* and *sca1-2 35S$_{pro}$:SCA1*. Boxes are delimited by the first (Q1, lower hinge) and third (Q3, upper hinge) quartiles. Whiskers represent Q1 - 1.5 IQ (lower) and Q3 + 1.5 IQ (upper), where IQ = Q3 - Q1. ◇: Mean. —: Median. ○: Extreme maximum outlier (> [Q3 + 3·IQ]). ✶: Maximum or minimum outlier. (B) Distribution of palisade mesophyll cell area in first-node leaves from L*er* and *sca1-1*. More than 350 cells were analyzed from at least 10 different samples. Asterisks indicate a significant difference with the corresponding wild type in a Student's *t* test (***p<0.001).