**Supplemental Figure S1.** Leaf series of *shr* and *scn* mutants.

Area measurements of leaf series of wild-type, *scr-3* and *shr-6* plants grown on soil and harvested before bolting (c=cotyledons). Error bars represent SE (n≥5).
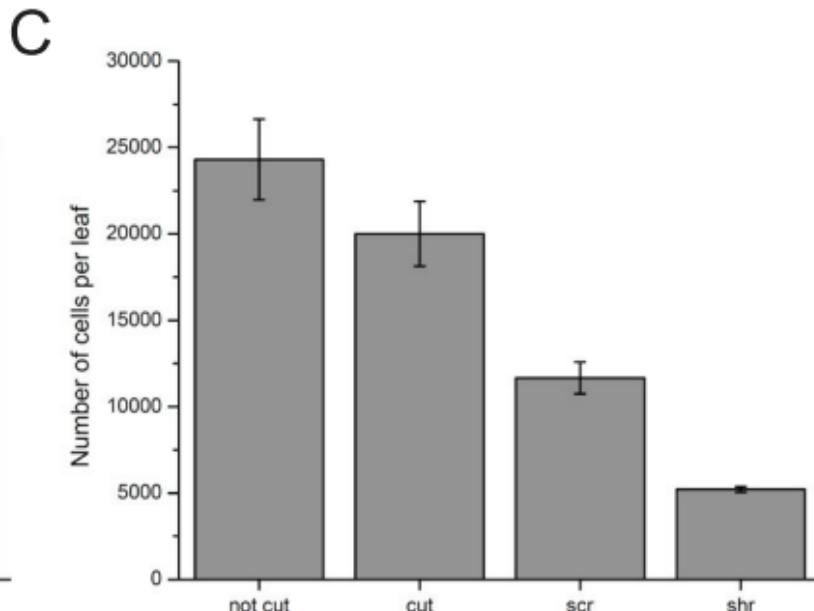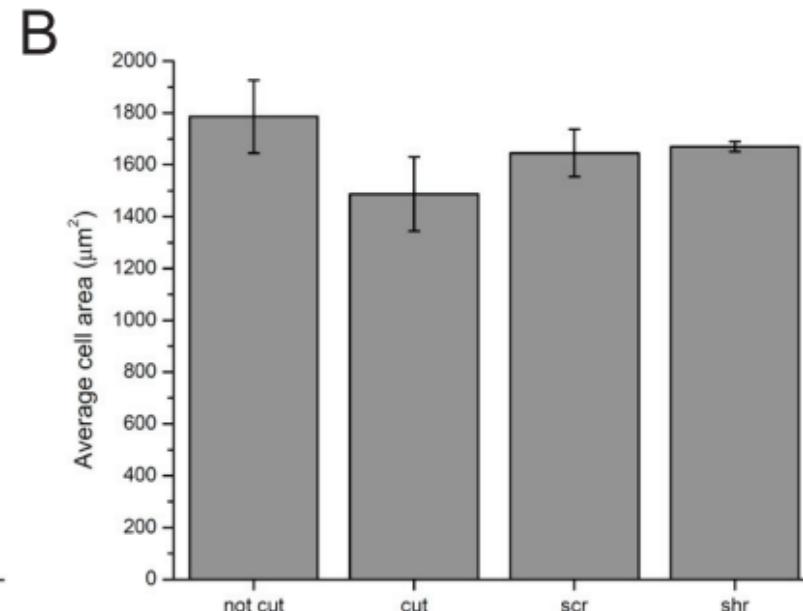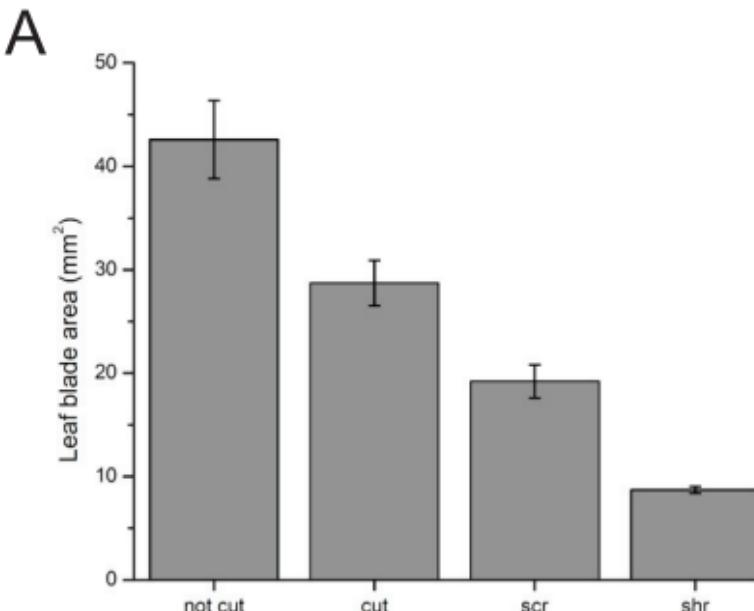
Supplemental Figure S2. The effect of cutting the root system in WT plants on leaf growth compared to *shr* and *scr* mutants.

Roots of WT plants were cut at 2 cm under the hypocotyl every three days after germination. At 24 days after sowing leaves 1 and 2 of normal-grown and de-rooted plants were harvested and compared to *scr-3* and *shr-6* leaves. **(A)** Leaf blade area. **(B)** Average cell size of the abaxial epidermis. **(C)** Number of epidermal cells per leaf. Error bars represent SE (n=5).
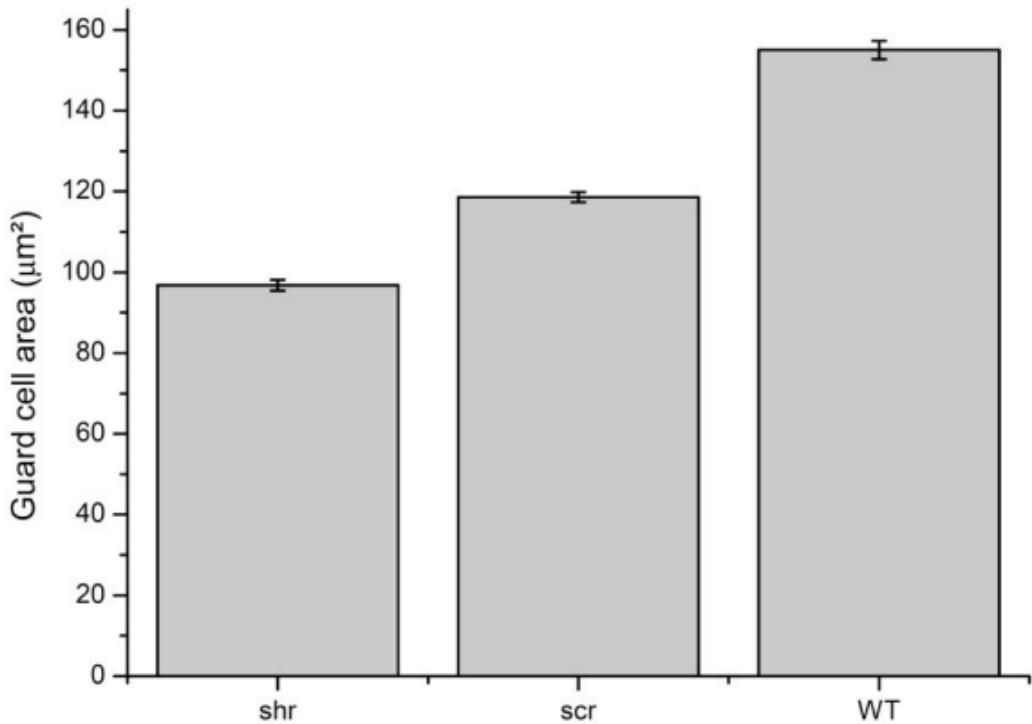
Supplemental Figure S3. Guard cell areas in *shr* and *scr* mutants.

Average guard cell size in the abaxial epidermis of *shr-6*, *scr-3* and wild-type leaves at 24 DAS. Error bars represent SE.

Supplemental Table 1. Top ten of most differentially expressed genes in *shr* and *scr* shoot transcriptomes.

	shr shoot			*scr* shoot		
nr.	AGI-code	FC		AGI-code	FC	
1	AT3G08860	20.18	*	AT5G48850	8.22	*
2	AT5G48850	19.26	*	AT3G49580	7.41	*
3	AT3G49580	19.22	*	AT4G36700	-6.41	*
4	AT5G59310	16.13	* S	AT3G08860	5.96	*
5	AT4G36700	-14.91	*	AT2G44460	5.70	* S
6	AT1G73010	14.20		AT5G03545	4.86	*
7	AT5G03545	13.11	*	AT5G26220	4.76	
8	AT2G44460	12.95	* S	AT1G17700	-4.25	
9	AT1G61800	12.06		AT3G05690	3.80	
10	AT2G39330	9.73		AT5G59310	3.72	* S

(FC) fold change; (*) recurrent in table; (S) expression peak during S-phase according to Menges et al. (2003).

Supplemental Table 2. Expression of A, B, and C-type subunits of the nuclear transcription factor Y family.

AGI-code	gene name	FC *scr*	FC *shr*	p-value
At5g12840	NF-YA1	-1,04	1,07	5,13E+00
At3g05690	NF-YA2	3,80	4,55	4,38E-09
At1g72830	NF-YA3	2,69	3,54	4,61E-07
At2g34720	NF-YA4	1,22	1,45	2,52E-01
At1g54160	NF-YA5	2,02	2,48	6,02E-04
At3g14020	NF-YA6	2,29	3,30	4,73E-03
At1g30500	NF-YA7	1,59	2,65	1,90E-03
At1g17590	NF-YA8	1,80	2,31	4,62E-05
At3g20910	NF-YA9	1,22	1,36	1,02E-01
At5g06510	NF-YA10	2,36	5,20	2,28E-07
At2g38880	NF-YB1	-1,08	1,10	1,46E-01
At5g47640	NF-YB2	*NA*	*NA*	*NA*
At4g14540	NF-YB3	-1,14	-1,12	3,50E+00
At1g09030	NF-YB4	1,04	-1,09	6,39E-01
At2g47810	NF-YB5	-1,05	-1,18	3,92E-03
At5g47670	NF-YB6	*NA*	*NA*	*NA*
At2g13570	NF-YB7	1,09	-1,16	7,76E-03
At2g37060	NF-YB8	-1,43	-1,24	7,45E-03
At1g21970	NF-YB9	-1,01	-1,16	2,73E-04
At3g53340	NF-YB10	-1,09	-1,08	4,72E-02
At2g27470	NF-YB11	1,12	1,12	1,68E+01
At5g08190	NF-YB12	-1,03	1,10	4,31E+00
At5g23090	NF-YB13	-1,00	1,12	6,82E-01
At3g48590	NF-YC1	*NA*	*NA*	*NA*
At1g56170	NF-YC2	1,15	1,51	1,13E-01
At1g54830	NF-YC3	-1,13	-1,03	1,86E-01
At5g63470	NF-YC4	*NA*	*NA*	*NA*
At5g50490	NF-YC5	*NA*	*NA*	*NA*
At5g50480	NF-YC6	-1,10	1,01	1,15E+00
At5g50470	NF-YC7	-1,08	-1,11	2,42E+00
At5g27910	NF-YC8	1,03	-1,13	2,21E+00
At1g08970	NF-YC9	-1,02	1,01	2,09E+00
At1g07980	NF-YC10	-1,02	1,08	1,20E-03
At3g12480	NF-YC11	-1,10	-1,15	1,77E-02
At5g38140	NF-YC12	-1,05	-1,10	6,81E+00
At5g43250	NF-YC13	*NA*	*NA*	*NA*

(FC) fold change; (*NA*) not on array.

Supplemental Table 3. Primer sequences used for Q-RT-PCR.

AGI-code	gene name / description	forward primer	reverse primer
AT3G48750	CDKA	ATTGCGTATTGCCACTCTCATAGG	TCCTGACAGGGATACCGAATGC
AT3G50000	CKA2	ACCACCATTAACGTGCGTCAAC	GATCTTGGCGAGAGAATCGGTATC
AT5G44200	CBP20	GAGCATCTACAACGGTTTACATTGG	TAGGCCGGTCATCGAGAATAGTC
AT4G37490	CYCB1;1	CCTGGTGGAGTGGTTGATTGATG	CGACATGAGAAGAGCACTGAGAC
AT4G37650	SHR	ACCACAACCATCACAACCACAAC	CGAAGGACGGAGGAGTTTGAGG
-	overlap between SHR cds and transposon in *shr-3* mutant	AGAGACAGCGAGGAAGTG	AATTAACTGACACTCCTTTGAC
-	over transposon in *shr-3* mutant	GTCGGATTCCACGGAGAG	ATCAGGACACTGTACCATCG
AT5G59970	H4	ACCAAATTGCGTGTTTCCATTG	ATGTCTGGTCGTGGAAAGGGAG
AT5G16250	-	GCTCTGTCTCTGTTCTCATCTTCAC	TCTTCATCGCAACGCCATCAC
AT1G70210	CYCD1;1	GCGAACGAGTTACCTTCTCTATCC	GCTCAATCCGTCACACCAAGTC
AT4G34160	CYCD3;1	CGTTCGTAGACCACATTATCAGGAG	CGGAGATTACAGAGAGGAGGAGAC
AT5G10440	CYCD4;2	CCTAGTGGAAAAGCTTGGACTG	TTAGCCTCAAACACGAACATGG
AT4G37630	CYCD5;1	TTGGTTCGATCTCTTGGTGGAC	TTTCCGGTGGAGGTGTCATATG
AT4G03270	CYCD6;1	GCGCTCTGTTACTCCTTTCTCC	CGCCTGCAATCACCGATGG
AT3G48160	DEL1	GCCGTTACTTCTCCTTCTTCC	CGTCTCTCCACTCCTAATTTCG
AT5G14960	DEL2	GCAGGCACTTCTGAGAGTAAC	ATGGTTGGTAAAGAGTAGAAAGGG
AT3G01330	DEL3	ACACAGAGCAGGAATCGAAACC	TCCGTGAAATGCCCAAGAAGAC
AT5G02470	DPA	GCAAGAACAGAAGCAAGAACAGAAC	CGGTCAGCGAGTATCAATGGATC.
AT5G03415	DPB	ATCACCGTTGTTACATCTACTAGCG	TTGAGAACCAGCATCATCACCTTG
AT2G36010	E2Fa	GCTTTCGCCTCAACAAAACCTC	CCCGATCTACAACACCACAACC
AT5G22220	E2Fb	CCGATGAAAGAGGAAAGCACCG	CGCCTACCTCTGATCGAAACC
AT1G47870	E2Fc	TCCCTCTTCTCCTTCTTCATCTTCC	CCATGTAACGGCGGTGTATCTC
AT3G12280	RBR	CTCATAAGTCGCCTGCTGCTAAG	TTGCTGTGCTCACTGGTGTTG
AT1G02970	WEE1	AAGTGGGGATGGCTTGTCAAG	ACCGTCCATTCTCTTCAACACC