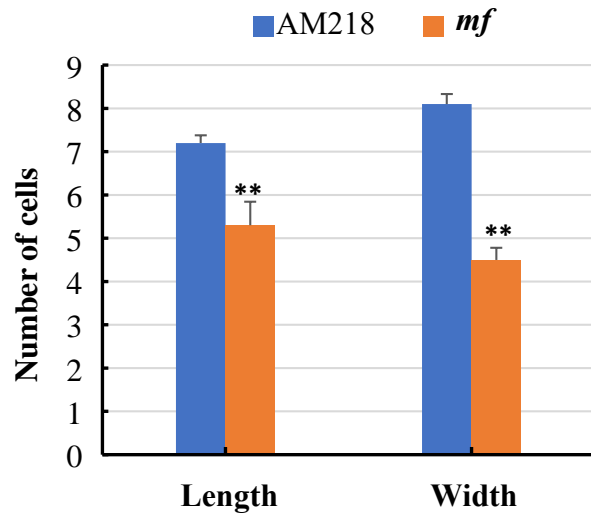
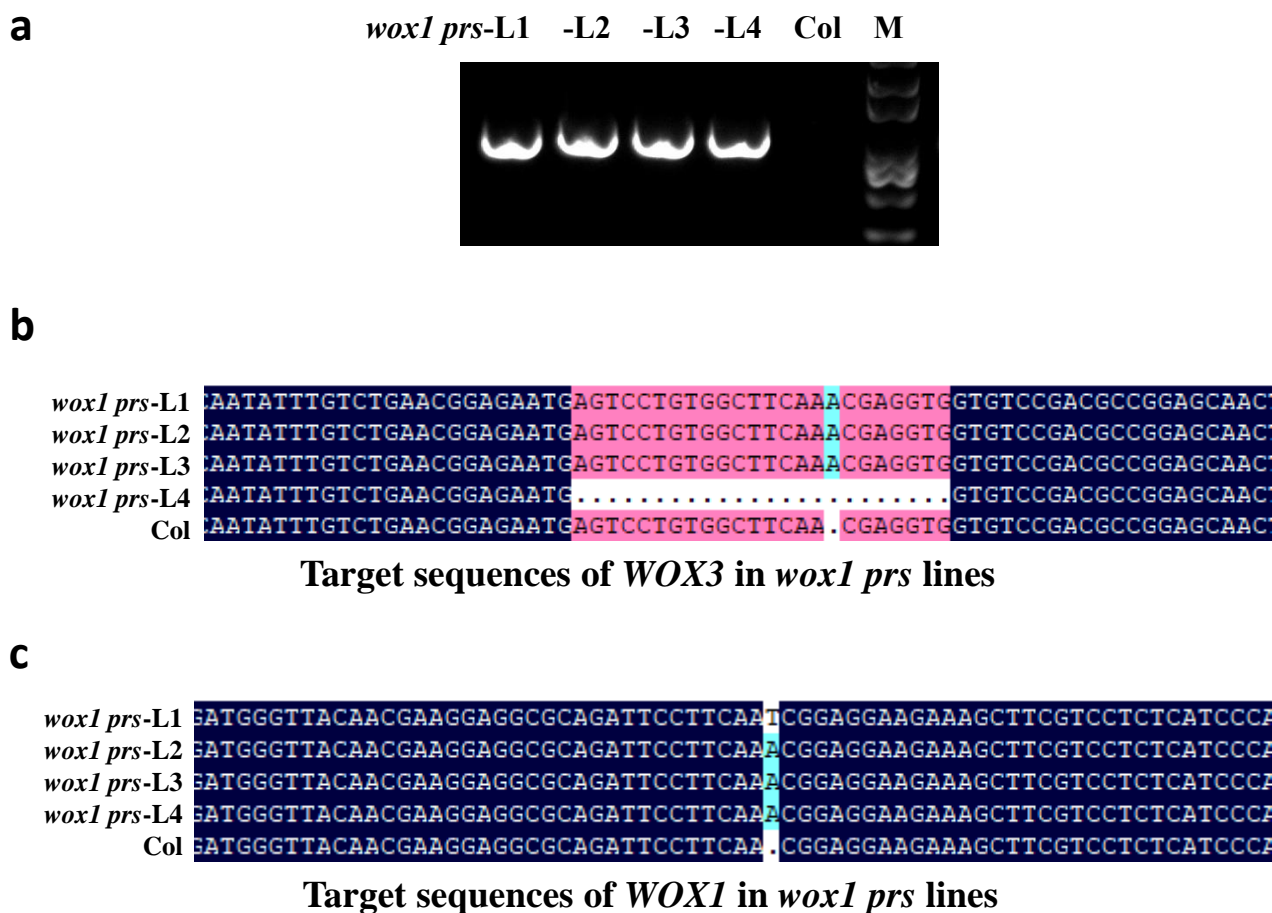


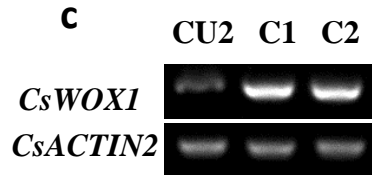
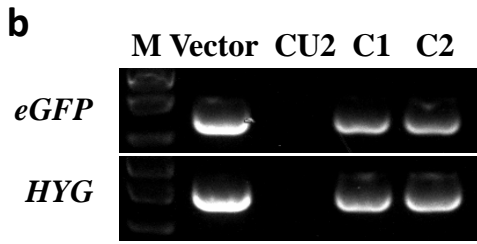
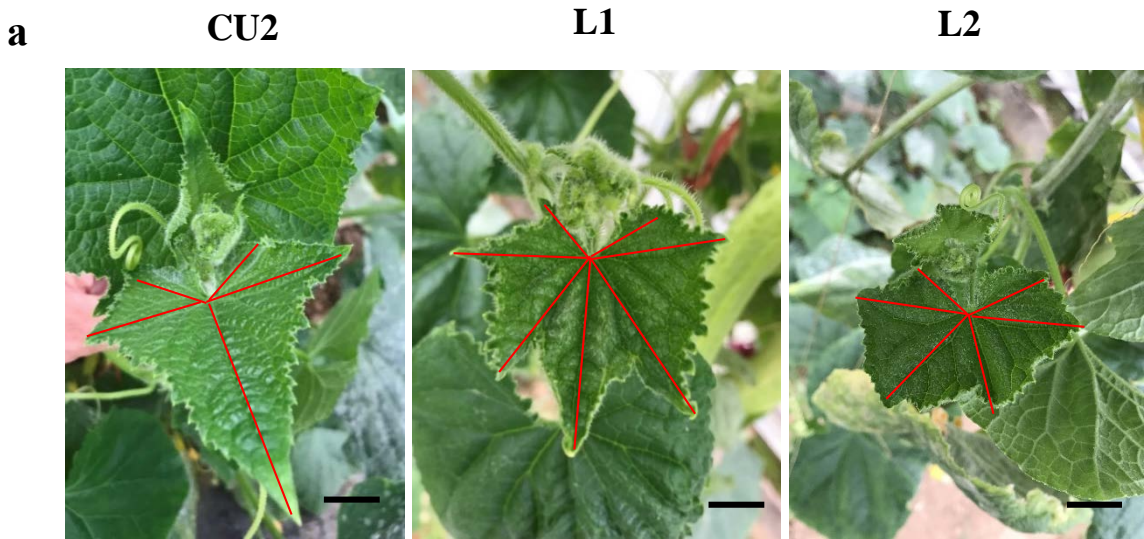
**Supplemental Figure S1** The relative average width of the distal region in mf and AM218 leaves. Leaf distal region is the blade tissue from midpoint of midvein to leaf tip. Significance tests are performed using the Student's t-test method at 0.05 and 0.01 levels (\*, p-value < 0.05; \*\*, p-value < 0.01).



**Supplemental Figure S2.** Measurements of cell number per 200  $\mu\text{m} \times 200 \mu\text{m}$  leaf area in the AM218 wild-type and *mf* mutant. Values represent the mean and SE of 10 measurements from a SEM assay, and asterisks indicate a significant difference (*t* test,  $P < 0.01$ ).



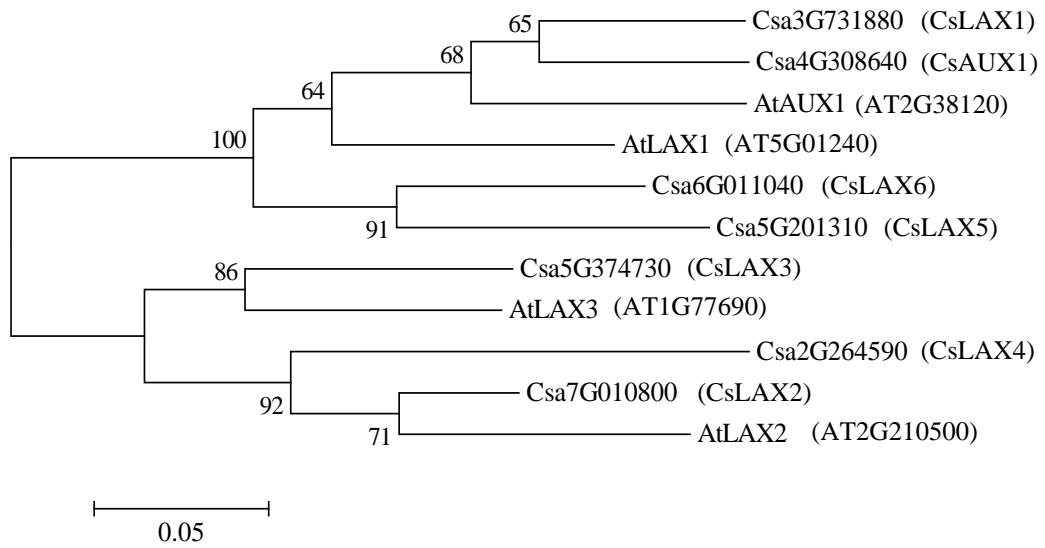
**Supplemental Figure S3.** Identification of *wox1 prs* double mutants in Arabidopsis. Four positive knockout lines (L1 to L4) were obtained from a CRISPR-Cas9 assay. a, PCR assay of the positive transgenic lines. M: DNA marker. b, Alignment of the target sequences of *WOX3* in the *wox1 prs* lines. c, Alignment of the target sequences of *WOX1* in the *wox1 prs* lines.



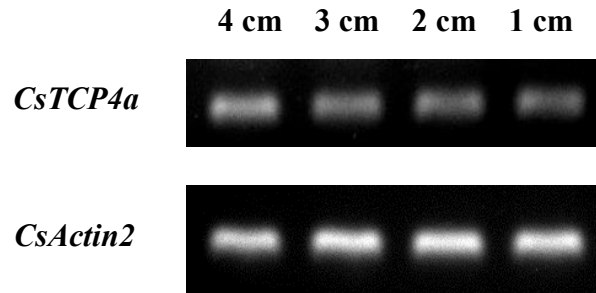
**Supplemental Figure S4** The vein pattern variation of *CsWOX1*-OE leaves. a, Leaves in two lines of *CsWOX1*-OE and CU2. b, PCR assay in leaves of *CsWOX1*-OE lines and CU2. PCR targeted the CDS of the *eGFP* and *HYP* genes in the plasmid. M: DNA marker; L1: Line 1; L2: Line 2. c, Semi-quantitative PCR assay of the OE and CU2 leaves. The red lines represents the primary veins. Bar = 1 cm

Csa3G731880	MLPQKQAEAAIVPNV.NETEHEG.KE.....EDKESQ.....SIFSVKNIIWHGGSAWDAWFCASCNQVAVLL	62
Csa4G308640	MLGQKQAEAAIVPTTANEVHEGG.GK.....EEGEEADGGGQPCNSVFMKMLIWHGGSAWDAWFCASCNQVAVLL	71
Csa6G011040	MATSKQGGEGMNNQS.MNESIER.DE.....EEKNG.....SPLSKSLIWHGGSVWDAWFCASCNQVAVLL	62
Csa5G201310	MTFARRSTEEMVSS.FNQTIQC.ED.....YREEEGRGEKDE..SMGGFKSFIWHGGSVWDAWFCASCNQVAVLL	68
Csa5G374730	.....MAS.EKVEVVIAGNYVEMEREEDSSK.....TKGKLSLFWHGGSVWDAWFCASCNQVAVLL	59
Csa7G010800	.....MATTAD.KVVETVIAGNYVEM..EADGNAPN.....VTKLSKSLFWHGGSVWDAWFCASCNQVAVLL	61
Csa2G264590	..MEMAEEAAETTTT.MTTTTVIWKNNSHNHNEFT...N.....AKTKLSKSLFWHGGSGWDAWFCASCNQVAVLL	66
AUX1	..MSEGVGAIVAND.NGTIQVN.GNRTKG..DNEEDHGS.....TGSNLSNFIWHGGSVWDAWFCASCNQVAVLL	65
LAX1	MSGEKQAEESIVVSG.EDEVAGR.KV..ED..SRAEEDIDGGNGG...FSMKSFIWHGGSAWDAWFCASCNQVAVLL	70
LAX2	.....MENGE.KAAETVVVGNVEM..EKDGKALD.....IKSKLSDMFWHGGSAWDAWFCASCNQVAVLL	59
LAX3	.....MAA.EKIEIVVAGNYLEMEREENISGNKRS...TKTKLSNFIWHGGSVWDAWFCASCNQVAVLL	63
Consensus	e v g l s lwhggsvydawfscasnqvaqvl	
Csa3G731880	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.S.FBNHVICWFVFLGLLGPYWKALGLFNC	140
Csa4G308640	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.N.FBNHVICWFVFLGLLGPYWKALGLFNC	149
Csa6G011040	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.S.FBNHVICWFVFLGLLGPYWKALGLFNC	140
Csa5G201310	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.S.FBNHVICWFVFLGLLGPYWKALGLFNC	146
Csa5G374730	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.D.FBNHVICWFVFLGLLGPYWKALGLFNC	137
Csa7G010800	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.D.FBNHVICWFVFLGLLGPYWKALGLFNC	139
Csa2G264590	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKTKRQY.FBNHVICWFVFLGLLGRFRNNGVLFNC	145
AUX1	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKTKRQY.FBNHVICWFVFLGLLGRFRNNGVLFNC	143
LAX1	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKTKRQY.FBNHVICWFVFLGLLGRFRNNGVLFNC	149
LAX2	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.N.FBNHVICWFVFLGLLGRFRNNGVLFNC	137
LAX3	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKERF.D.FBNHVICWFVFLGLLGRFRNNGVLFNC	141
Consensus	tlpysfqqlgmisglifq fygl gswtaylisvlyeyr rke v fknhvicwfvldgllg wka glafnc	
Csa3G731880	TFLLFQSVIQLIACASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	220
Csa4G308640	TFLLFQSVIQLIACASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	229
Csa6G011040	TFLLFQSVIQLIACASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	220
Csa5G201310	TFLLFQSVIQLIACASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	226
Csa5G374730	TFLLFQSVIQLIACASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	217
Csa7G010800	TFLLFQSVIQLIACASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	219
Csa2G264590	TFLLFQSVIQLIACASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	225
AUX1	TFLLFQSVIQLIACASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	223
LAX1	TFLLFQSVIQLIACASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	229
LAX2	TFLLFQSVIQLIACASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	217
LAX3	TFLLFQSVIQLIACASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	221
Consensus	tflfqsqqliacasniyyind ldkrtwtiyfgaccattvfpsfnryrwsfqlgmettytawwmtiapsalhgqvge	
Csa3G731880	VHSGSPKRWLVLYFTGATNILYTFGGHAVTVEIMAMWKKFKFKIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	300
Csa4G308640	VHSGSPKRWLVLYFTGATNILYTFGGHAVTVEIMAMWKKFKFKIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	309
Csa6G011040	VHSGSPKRWLVLYFTGATNILYTFGGHAVTVEIMAMWKKFKFKIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	300
Csa5G201310	VHSGSPKRWLVLYFTGATNILYTFGGHAVTVEIMAMWKKFKFKIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	306
Csa5G374730	VHSGSPKRWLVLYFTGATNILYTFGGHAVTVEIMAMWKKFKFKIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	297
Csa7G010800	VHSGSPKRWLVLYFTGATNILYTFGGHAVTVEIMAMWKKFKFKIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	299
Csa2G264590	VHSGSPKRWLVLYFTGATNILYTFGGHAVTVEIMAMWKKFKFKIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	305
AUX1	VHSGSPKRWLVLYFTGATNILYTFGGHAVTVEIMAMWKKFKFKIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	303
LAX1	VHSGSPKRWLVLYFTGATNILYTFGGHAVTVEIMAMWKKFKFKIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	309
LAX2	VHSGSPKRWLVLYFTGATNILYTFGGHAVTVEIMAMWKKFKFKIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	297
LAX3	VHSGSPKRWLVLYFTGATNILYTFGGHAVTVEIMAMWKKFKFKIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	301
Consensus	vhsqspkrlwlvlyftgatnilytfghavtveimamwkkfkfkiylmatlyvftltpsasavyvwafgdlilhnsnfs	
Csa3G731880	LPFKSRRLDAWMLLIHQFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	380
Csa4G308640	LPFKNRRLDAWMLLIHQFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	389
Csa6G011040	LPFTNGRRTTAWMLLIHQFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	380
Csa5G201310	LPFKSRRLDAWMLLIHQFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	386
Csa5G374730	LPFKNRRLDAWMLLIHQFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	377
Csa7G010800	LPFKSRRLDAWMLLIHQFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	379
Csa2G264590	LPFKSRRLDAWMLLIHQFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	385
AUX1	LPFKNRRLDAWMLLIHQFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	383
LAX1	LPFKTRRLDAWMLLIHQFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	389
LAX2	LPFKNRRLDAWMLLIHQFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	377
LAX3	LPFKTRRLDAWMLLIHQFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	381
Consensus	llpk frd avilmlhqqfitfgfactplyfvwek igmhetskclr arlpvvpipwflaifpffgpinsavgal	
Csa3G731880	LVSFTVYIIIPALAHMLTYRKASARCNAPREREFEP.SWVGMVAINFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	459
Csa4G308640	LVSFTVYIIIPALAHMLTYRKASARCNAPREREFEP.LSWTAMVYVNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	468
Csa6G011040	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.SWAMVYVNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	459
Csa5G201310	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.VIVARSNTVMYVNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	466
Csa5G374730	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.SWGLYVNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	456
Csa7G010800	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.RWVGAYVNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	458
Csa2G264590	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.KWVGTYNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	464
AUX1	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.SWTAMVYVNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	462
LAX1	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.SWAGVYVNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	468
LAX2	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.RWGTAFYNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	456
LAX3	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.GWVGTYNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	460
Consensus	lvsftvyiipalahlmtyrksasar navekpp f sw g yvin fvvvvlvvgfgfggwsmtnfvrqidtfglfa	
Csa3G731880	KCYQCKGP.....PLPAMAFIAHH.....	478
Csa4G308640	KCYQCKFS.....HPPAPPETHH.....	487
Csa6G011040	KCYQCP.....PQGPAIFHH.....	474
Csa5G201310	KCYQCP.....SKTPEVPTAAHR...	485
Csa5G374730	KCYQCPPEHKH.....	466
Csa7G010800	KCYQCPQCTFALPQGSFNATAAPFQCHHLHPGSH.	493
Csa2G264590	KCYQCP...PPLPSQHNFTMAPFPLHHHHNH.	494
AUX1	KCYQCKFA.....AAAHAFFVSALHHRL...	485
LAX1	KCYQCKFP.....PAPIAAGAHHR.....	488
LAX2	KCYQCPFVMVS.....PEEISHPFNHTHG	482
LAX3	KCYQCPPEHKP.....	470
Consensus	kcyqcpp pp h	

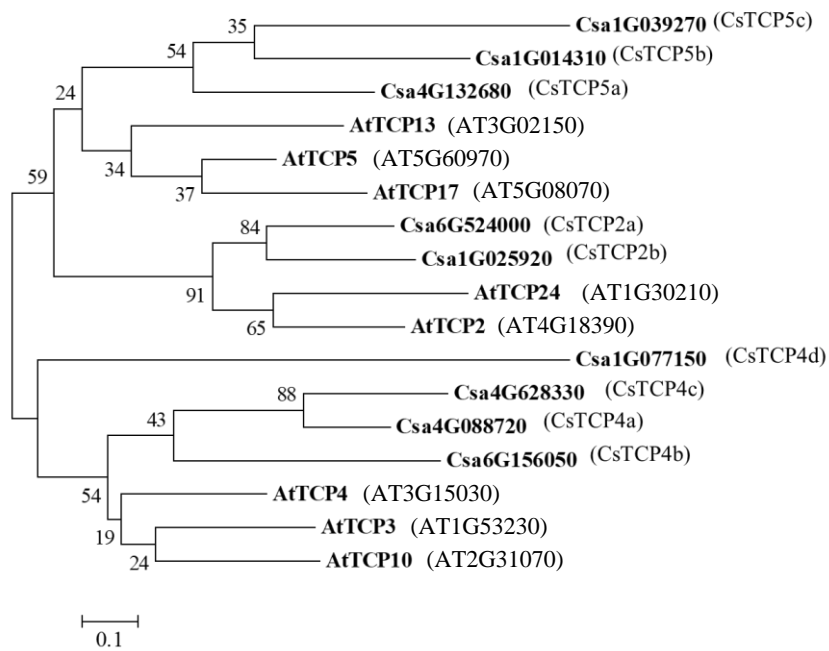
**Supplemental Figure S5.** Alignment of the amino acid sequences of seven AUX/LAX proteins in cucumber and four studied homologues in Arabidopsis. The gene names are listed in Supplemental Fig. S6 and Supplemental Table S3.



**Supplemental Figure S6.** Phylogram of the AUX/LAX family proteins based on the amino acid sequences of the four AtAUX/LAXs and seven CsAUX/LAXs shown in Supplemental Fig. S5.

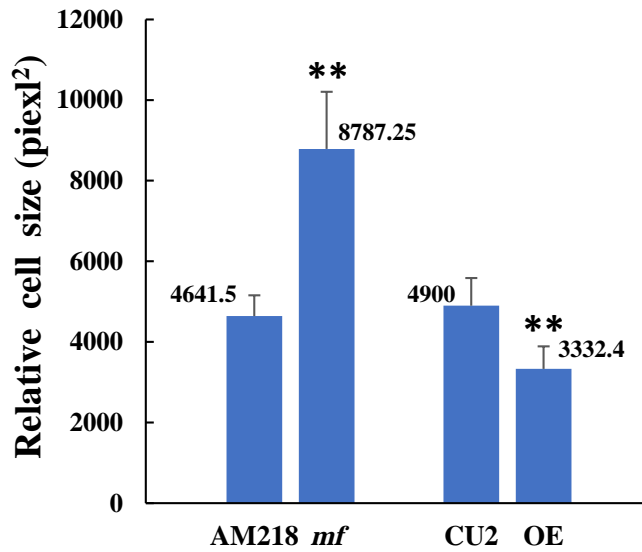


**Supplemental Figure S7.** The expression of *CsTCP4a* in cucumber leaf margin from different period. Leaf length is from 1 cm to 4 cm and the leaf margin is collected to extract RNA.



**Supplemental Figure S8.** Phylogram of the TCP family proteins based on the amino acid sequences from eight AtTCPs and nine CsTCPs. The gene names are listed in Supplemental Table S3.





**Supplemental Figure S9.** Relative sizes of leaf sub-epidermal cells in different plants. Values represent the mean and SE of 10 measurements, and asterisks indicate a significant difference (*t* test,  $P < 0.01$ ).