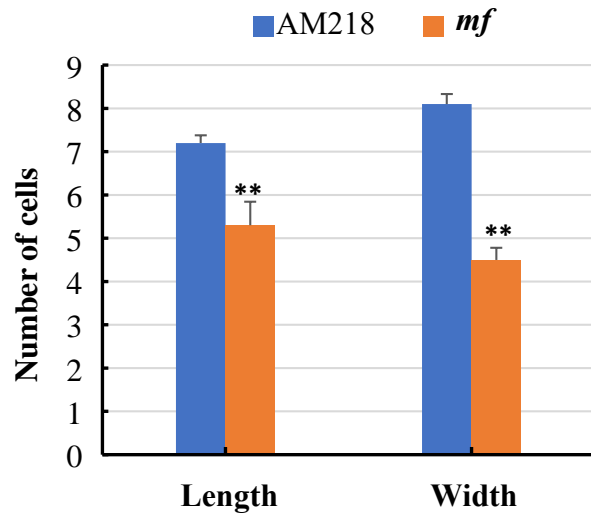
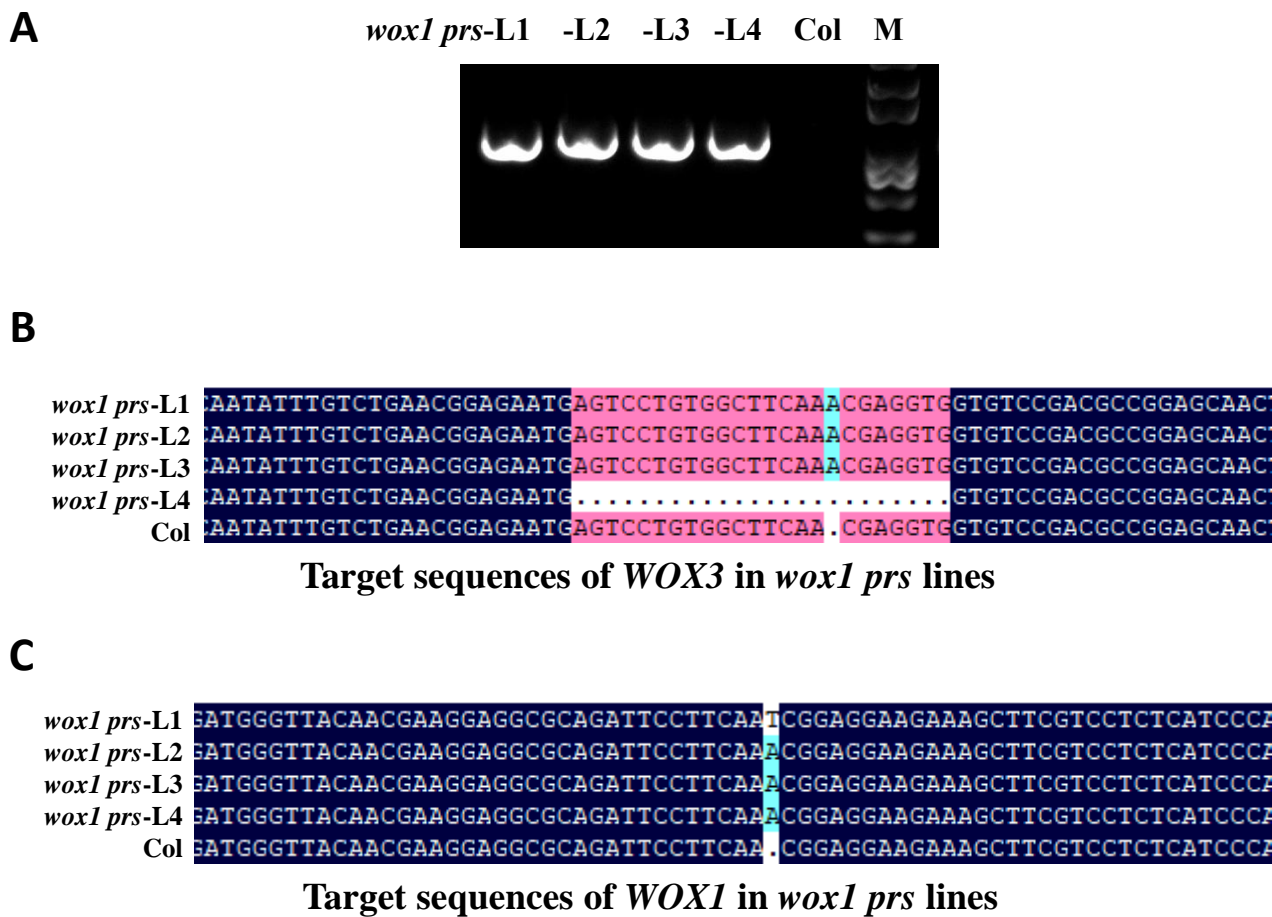


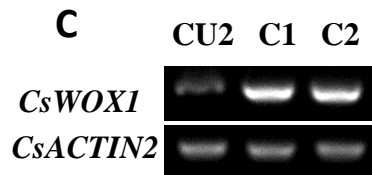
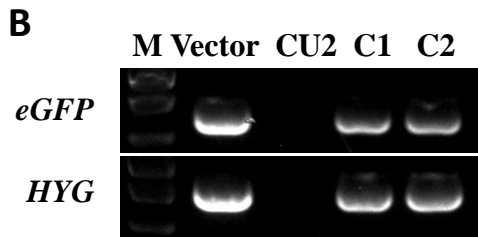
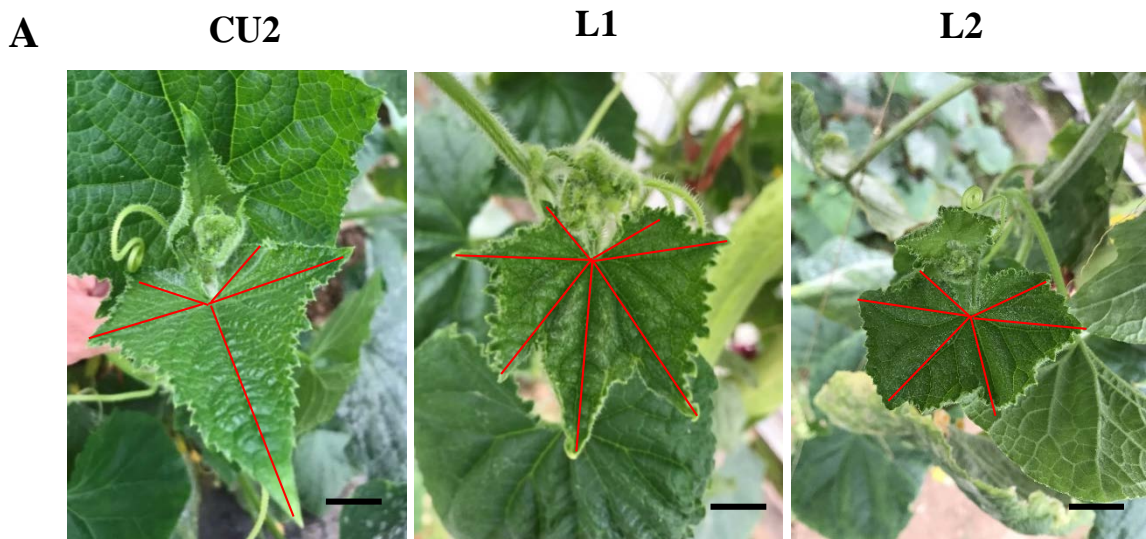
**Supplemental Figure S1** The relative average width of the distal region in mf and AM218 leaves. Leaf distal region is the blade tissue from midpoint of midvein to leaf tip. Significance tests are performed using the Student's t-test method at 0.05 and 0.01 levels (\*, p-value < 0.05; \*\*, p-value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



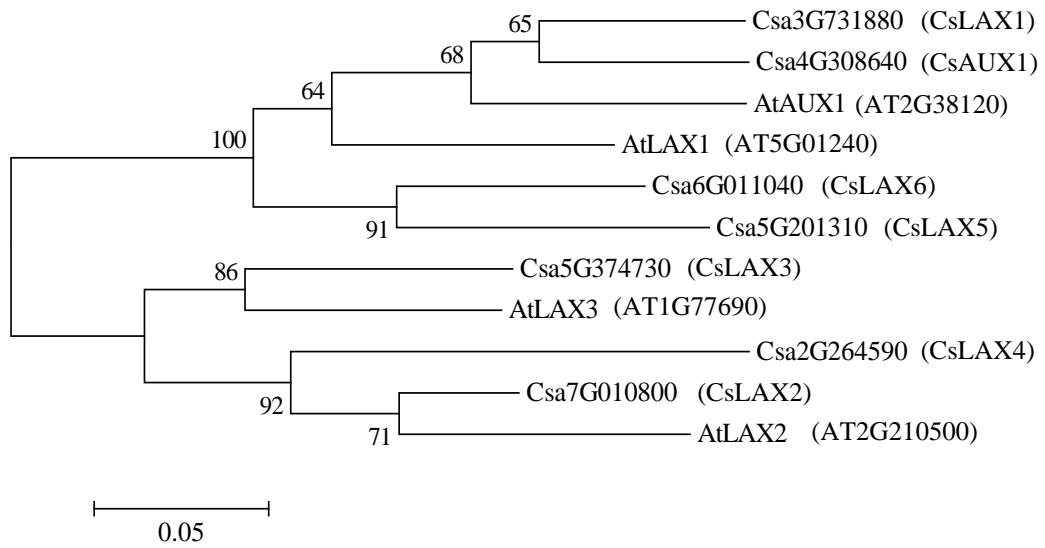
**Supplemental Figure S3.** Identification of *wox1 prs* double mutants in Arabidopsis. Four positive knockout lines (L1 to L4) were obtained from a CRISPR-Cas9 assay. A, PCR assay of the positive transgenic lines. M: DNA marker. B, Alignment of the target sequences of *WOX3* in the *wox1 prs* lines.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



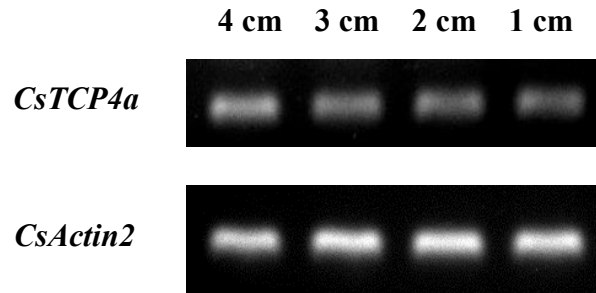
**Supplemental Figure S4** The vein pattern variation of *CsWOX1*-OE leaves. A, Leaves in two lines of *CsWOX1*-OE and CU2. B, PCR assay in leaves of *CsWOX1*-OE lines and CU2. PCR targeted the CDS of the *eGFP* and *HYP* genes in the plasmid. M: DNA marker; L1: Line 1; L2: Line 2. C, Semi-quantitative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

Csa3G731880	MLPQKQAEAAIVPNV.NETEHEG.KE.....EDKESQ.....SIFSVKNIIWHGGSSAWDAWFCASCNQVAQVLL	62
Csa4G308640	MLGQKQAEAAIVPTTANVEVHGG.GK.....EEGEEADGGGCPQNSVFMKMLIWHGGSSAWDAWFCASCNQVAQVLL	71
Csa6G011040	MATSKQGGEGMNNQS.MNESIER.DE.....EEKNG.....SPLSKSLIWHGGSSAWDAWFCASCNQVAQVLL	62
Csa5G201310	MTFARRSTEEMAVSS.FNQTIQC.ED.....YREEEGRGEKDE..SMGGFKSFIWHGGSSAWDAWFCASCNQVAQVLL	68
Csa5G374730	.....MAS.EKVEIVIAGNYVEMEREEDSSK.....TKGKLSLFWHGGSSAWDAWFCASCNQVAQVLL	59
Csa7G010800	.....MATTAD.KVVETVIAGNYVEM..EADGNAPN.....VTKLSKSLFWHGGSSAWDAWFCASCNQVAQVLL	61
Csa2G264590	..MEMAEEAAETTTT.MTTTTVIWKNNSHNNHNEPT...N.....AKTKLSKSLFWHGGSSAWDAWFCASCNQVAQVLL	66
AUX1	..MSEGVSAIVAND.NGTIQVN.GNRTGK..DNEEDHGS.....TGSNLSNFIWHGGSSAWDAWFCASCNQVAQVLL	65
LAX1	MSGEKQAEESIVVSG.EDEVAGR.KV..ED..SRAEEDIDGGNGG.....FSMKSFIWHGGSSAWDAWFCASCNQVAQVLL	70
LAX2	.....MENGE.KAAETVVVGNVEM..EKDGKALD.....IKSKLSDMFWHGGSSAWDAWFCASCNQVAQVLL	59
LAX3	.....MAA.EKIEIVVAGNYLEMEREENISGNKSS....TKTKLSNFIWHGGSSAWDAWFCASCNQVAQVLL	63
Consensus	e v g l s lwhggsvydawfscasnqvaqvl	
Csa3G731880	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.S.FBNHVICWFVFLGLLGPYWKAGLGFNC	140
Csa4G308640	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.N.FBNHVICWFVFLGLLGPYWKAGLGFNC	149
Csa6G011040	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.S.FBNHVICWFVFLGLLGPYWKAGLGFNC	140
Csa5G201310	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.S.FBNHVICWFVFLGLLGPYWKAGLGFNC	146
Csa5G374730	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.D.FBNHVICWFVFLGLLGPYWKAGLGFNC	137
Csa7G010800	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.D.FBNHVICWFVFLGLLGPYWKAGLGFNC	139
Csa2G264590	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.QYFBNHVICWFVFLGLLGPYWKAGLGFNC	145
AUX1	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.S.FBNHVICWFVFLGLLGPYWKAGLGFNC	143
LAX1	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.S.FBNHVICWFVFLGLLGPYWKAGLGFNC	149
LAX2	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.N.FBNHVICWFVFLGLLGPYWKAGLGFNC	137
LAX3	TLPYSFSCIGMISGLIFCLFYGLGWSWTAYLISVLYEYRSRREKENV.D.FBNHVICWFVFLGLLGPYWKAGLGFNC	141
Consensus	tlpysfscigmlsglilfclyglgswtaylorislyveyr rke v fknhvicwfvldgllg wka glafnc	
Csa3G731880	TFLLFQSVIQLIPCASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	220
Csa4G308640	TFLLFQSVIQLIPCASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	229
Csa6G011040	TFLLFQSVIQLIPCASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	220
Csa5G201310	TFLLFQSVIQLIPCASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	226
Csa5G374730	TFLLFQSVIQLIPCASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	217
Csa7G010800	TFLLFQSVIQLIPCASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	219
Csa2G264590	TFLLFQSVIQLIPCASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	225
AUX1	TFLLFQSVIQLIPCASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	223
LAX1	TFLLFQSVIQLIPCASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	229
LAX2	TFLLFQSVIQLIPCASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	217
LAX3	TFLLFQSVIQLIPCASNIYYINDLIDKRTWTYIFGACCATTVPSPFNRYRWSFGLGEMTTYTAWWMTIAPALHGQVGE	221
Consensus	tflfqsqliplcasniyyindlkdrtwtiyfgaccattvfpsfnryrwsfllgmltmttyawwmtiapsalhqqvge	
Csa3G731880	VHSGSPKRWLYFTGATNILYTFGGHAVTVEIMAMWKEKFKFIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	300
Csa4G308640	VHSGSPKRWLYFTGATNILYTFGGHAVTVEIMAMWKEKFKFIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	309
Csa6G011040	VHSGSPKRWLYFTGATNILYTFGGHAVTVEIMAMWKEKFKFIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	300
Csa5G201310	VHSGSPKRWLYFTGATNILYTFGGHAVTVEIMAMWKEKFKFIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	306
Csa5G374730	VHSGSPKRWLYFTGATNILYTFGGHAVTVEIMAMWKEKFKFIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	297
Csa7G010800	VHSGSPKRWLYFTGATNILYTFGGHAVTVEIMAMWKEKFKFIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	299
Csa2G264590	VHSGSPKRWLYFTGATNILYTFGGHAVTVEIMAMWKEKFKFIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	305
AUX1	VHSGSPKRWLYFTGATNILYTFGGHAVTVEIMAMWKEKFKFIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	303
LAX1	VHSGSPKRWLYFTGATNILYTFGGHAVTVEIMAMWKEKFKFIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	309
LAX2	VHSGSPKRWLYFTGATNILYTFGGHAVTVEIMAMWKEKFKFIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	297
LAX3	VHSGSPKRWLYFTGATNILYTFGGHAVTVEIMAMWKEKFKFIYLMATLYVFTLTPSASAVYVWAFGDLILHNSNFS	301
Consensus	vhsqspkrlwlyftgatnilytfghavtveimamwkefkfkiylmatlyvftltpsasavyvwafgdlilhnsnfs	
Csa3G731880	LPFKSRRLDAWMLLIHQIFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	380
Csa4G308640	LPFKNRRLDAWMLLIHQIFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	389
Csa6G011040	LPFTNGRRTTAWMLLIHQIFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	380
Csa5G201310	LPFKSRRLDAWMLLIHQIFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	386
Csa5G374730	LPFKNRRLDAWMLLIHQIFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	377
Csa7G010800	LPFKSRRLDAWMLLIHQIFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	379
Csa2G264590	LPFKSRRLDAWMLLIHQIFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	385
AUX1	LPFKNRRLDAWMLLIHQIFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	383
LAX1	LPFKTRRLDAWMLLIHQIFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	389
LAX2	LPFKNRRLDAWMLLIHQIFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	377
LAX3	LPFKTRRLDAWMLLIHQIFITFGFACTPLYFVWEKIGMHEKSLCLRALRLPVVPIWFLAIFPFFGPINSAVGL	381
Consensus	llpk frd avilmlhlihqifitfgfactplyfvwek igmhetskclora arlpvvpipwflaifpffgpinsavgal	
Csa3G731880	LVSFTVYIIIPALAHMLTYRKASARCNAPREREFEP.SWVGMVAINFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	459
Csa4G308640	LVSFTVYIIIPALAHMLTYRKASARCNAPREREFEP.LSWTAMVYVNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	468
Csa6G011040	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.SWAMVYVNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	459
Csa5G201310	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.VIVARSNTVMYVNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	466
Csa5G374730	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.SWVGMVAINFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	456
Csa7G010800	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.RWVGAYVNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	458
Csa2G264590	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.KWVGTYNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	464
AUX1	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.SWTAMVYVNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	462
LAX1	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.SWAGVYVNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	468
LAX2	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.RWVGTYNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	456
LAX3	LVSFTVYIIIPALAHMLTYRSASARCNAPREREFEP.GWVGTYNFVWVVLVVGFGFGGWSMNFVRCIDTFGLFA	460
Consensus	lvsftvyiipalahlmlyrksasar navekpp f sw g yvin fvvvvlvvgfvggwsmtnfvrqidtfglfa	
Csa3G731880	KCYQCKGP.....PLPAMAFIAHH.....	478
Csa4G308640	KCYQCKFS.....HPPAPPETHH.....	487
Csa6G011040	KCYQCP.....PQGPAIFHH.....	474
Csa5G201310	KCYQCP.....SKTPEVPTAAHR...	485
Csa5G374730	KCYQCPFHK.....	466
Csa7G010800	KCYQCPCTFALPQGSFNATAAPFQHLLHHPGSH.	493
Csa2G264590	KCYQCP...PPLPSQHNFTMAFPFLHHHHNH.	494
AUX1	KCYQCKFA.....AAAHAFFVSALHHR...	485
LAX1	KCYQCKFP.....PAPIAAGAHHR.....	488
LAX2	KCYQCPFVMVS.....PEEISHPFNHTHG	482
LAX3	KCYQCPFHKE.....	470
Consensus	kcyqcpp pp h	

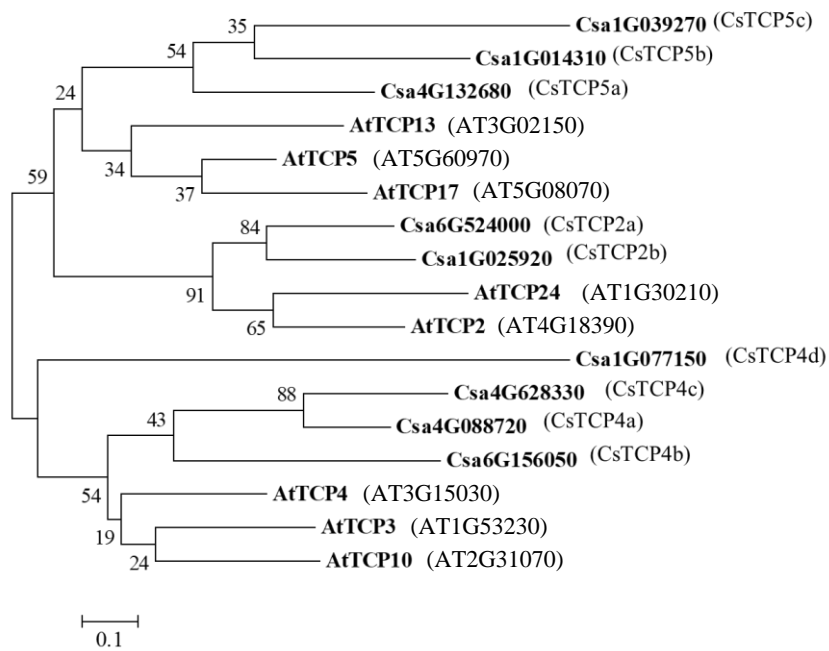
**Supplemental Figure S5.** Alignment of the amino acid sequences of seven AUX/LAX proteins in cucumber and four studied homologues in Arabidopsis. The gene names are listed in Supplemental Fig. S6 and Supplemental Table S3.



**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.

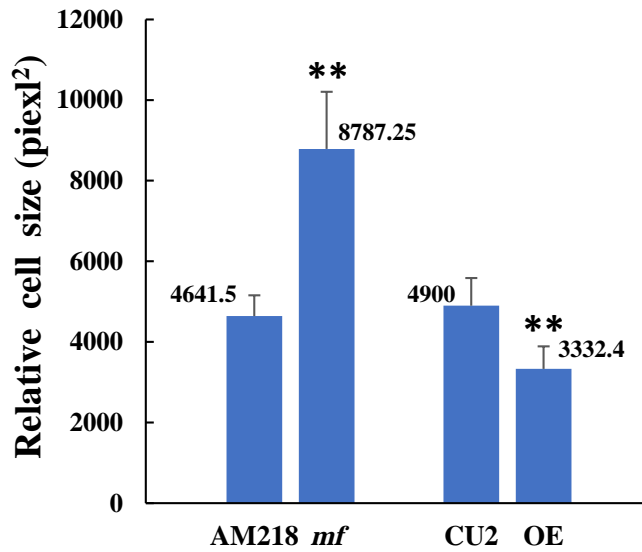


**Supplemental Figure S7.** The expression of *CsTCP4a* in cucumber leaf margin from different period. Leaf length is from 1 cm to 4 cm and the leaf margin is collected to extract RNA.



**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,  $P < 0.01$ ).