

Supplemental Table S1. Frequency Distribution for the Ratios of Membrane-Associated CLC1 at the Both Sides of Roots.

Frequency Distribution for the Ratios of Membrane-Associated CLC1 (%)				
Ratio ^a	Vertically grown roots ^b		Gravistimulated roots ^b	
	PM	Intracellular	PM	Intracellular
< 0.8	0 (0/37) ^c	0 (0/37)	48.8 (21/43)	53.5 (23/43)
0.8-1.2	94.6 (35/37)	94.6 (35/37)	37.2 (16/43)	37.2 (16/43)
> 1.2	5.4 (2/37)	5.4 (2/37)	14 (6/43)	9.3 (4/43)

^aThe ratios of PM- and intracellular compartments-associated CLC1 signal intensities at the right/left or the bottom/top sides of the root epidermis were artificially classified into three types of the levels: (1) the ratios of < 0.8 indicate reduced signal intensity at the right or bottom side; (2) the ratios of 0.8-1.2 indicate similar signal distribution at the both sides; (3) the ratios of > 1.2 indicate increased signal intensity at the right or bottom side.

^bThe vertically grown seedlings were treated for 2 h with or without gravistimulation.

^cThe fractional number in the brackets denotes that the number of roots with one of three types of the ratios was divided by the total number of examined roots, whereas the number before the brackets is a percentage (%).

Supplemental Table S2. Summary of Effects of Loss of AP2 μ or AP2 σ on the PM Association of Other AP-2 Subunits.

<i>ap-2</i> mutants	Reduction (%) in PM-associated levels of the AP-2 subunits			
	AP2 α 1-GFP	AP1/2 β 1	AP2 μ -YFP /AP2 μ	AP2 σ -GFP /AP2 σ
<i>ap2μ</i>	56% (44.3 \pm 14.2 ^{***})	49% (51.0 \pm 23.9 ^{***})	ND	57% (42.5 \pm 19.5 ^{***}) /41% (59.4 \pm 31.7 ^{***})
<i>ap2σ</i>	37% (63.1 \pm 17.0 ^{***})	27% (73.4 \pm 34.8 ^{***})	32% (67.9 \pm 13.0 ^{***}) /37% (63.4 \pm 31.7 ^{***})	ND

Summary of quantitative data from Fig. 5 and Supplemental Fig. S12. Reduction levels were calculated as 100% - % of the wild type. Data (% of the wild type \pm SD) in brackets present the PM-associated levels of the AP-2 subunits in *ap2 μ* or *ap2 σ* . Student's *t* test (^{***}*P* < 0.0001). ND, not determined. Numbers of roots and cells examined are indicated in the figure legends.

Supplemental Table S3. PCR Primer Sequences for qRT-PCR and Genotyping.

Genes/mutants	Primers	Sequences
<i>AP2α1</i>	<i>qAP2α1-F</i>	ACGGATCCCAGCAACCTTAA
	<i>qAP2α1-R</i>	TGCCATTTCCGGAAGAGCTA
<i>AP1/2β1</i>	<i>qAP1/2β1-F</i>	CCGGTTGATAGTGCAGCTTC
	<i>qAP1/2β1-R</i>	CTTGAAGCTGGGACGACAAC
<i>AP2μ</i>	<i>qAP2μ-F</i>	AATCCAGTGCCAAAACAAACA
	<i>qAP2μ-R</i>	GCGCGACCAGTTGTCACTT
<i>AP2σ</i>	<i>qAP2σ-F</i>	TCCGAGAAACACAAAGTCGA
	<i>qAP2σ-R</i>	GTCGGTTATATCCACGCACAC
<i>UBIQUITIN 7</i>	<i>qUBI7-F</i>	CTTCGTCAAACCCTCACCGGCAAAA
	<i>qUBI7-R</i>	GAGAAGACCACCCCTAAGAGCAAGA
<i>TPLATE</i>	<i>qTPLATE-F</i>	CAGGCAGCAGTGCTCCAAG
	<i>qTPLATE-R</i>	CGAAGAAACCACACACAACAAAAG
<i>TML</i>	<i>qTML-F</i>	TCGGGATCATGTCTGTGTTTA
	<i>qTML-R</i>	AGCAAAATGTCTGGATCCATT
<i>ACTIN 2</i>	<i>qACTIN2-F</i>	TTGACTACGAGCAGGAGATGG
	<i>qACTIN2-R</i>	AC ACGAGGGCTGGAACAAG
<i>ap-2 mutants</i>		
<i>ap2μ</i> (SALK_083693C)	<i>ap2μ-F</i>	AGCTTCTCCTTTTCTTCACCG
	<i>ap2μ-R</i>	TTCATTAACCTTCCCCGTC
<i>ap2σ</i> (SALK_141555)	<i>ap2σ-F</i>	GATATTGGACCATTTCTTCAGC
	<i>ap2σ-R</i>	TTATCAGTGGAGGACAAAGAAGG
SALK_LBb1		GCGTGGACCGCTTGCTGCAACT

Supplemental Table S4. Information for the AP-2 Antibodies.

Name of antibodies (anti-rabbit)	Peptide location	Sequences
AP1/2 β 1	768-779	CFQNMSAGPPSSL
AP2 μ	260-274	TRFNSEKTVSFVPPDC
AP2 σ	131-142	CIERMSELEKLQ