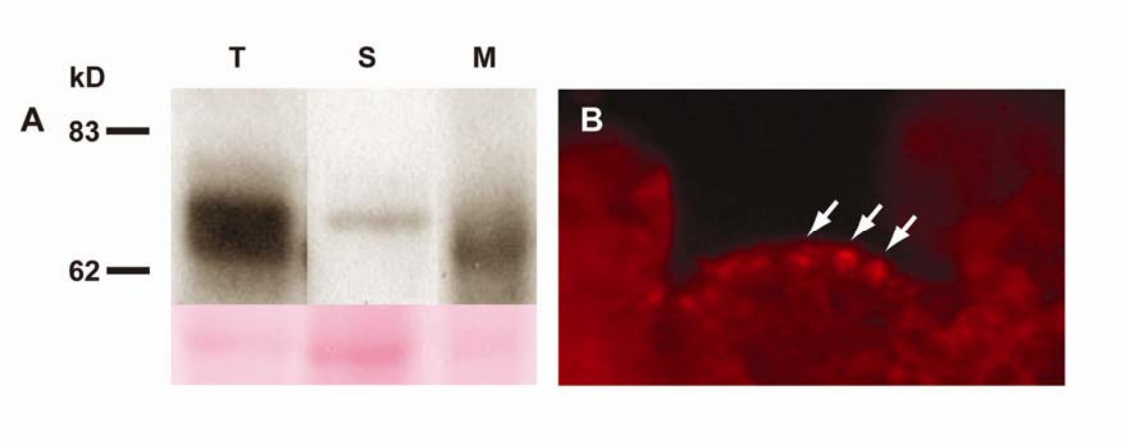
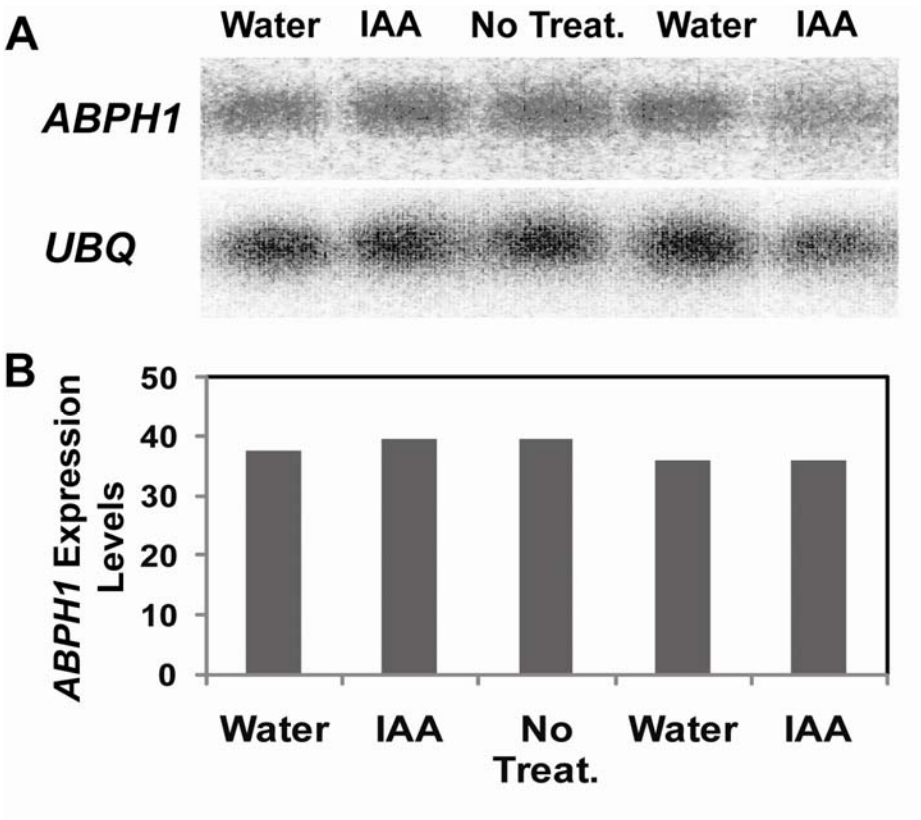
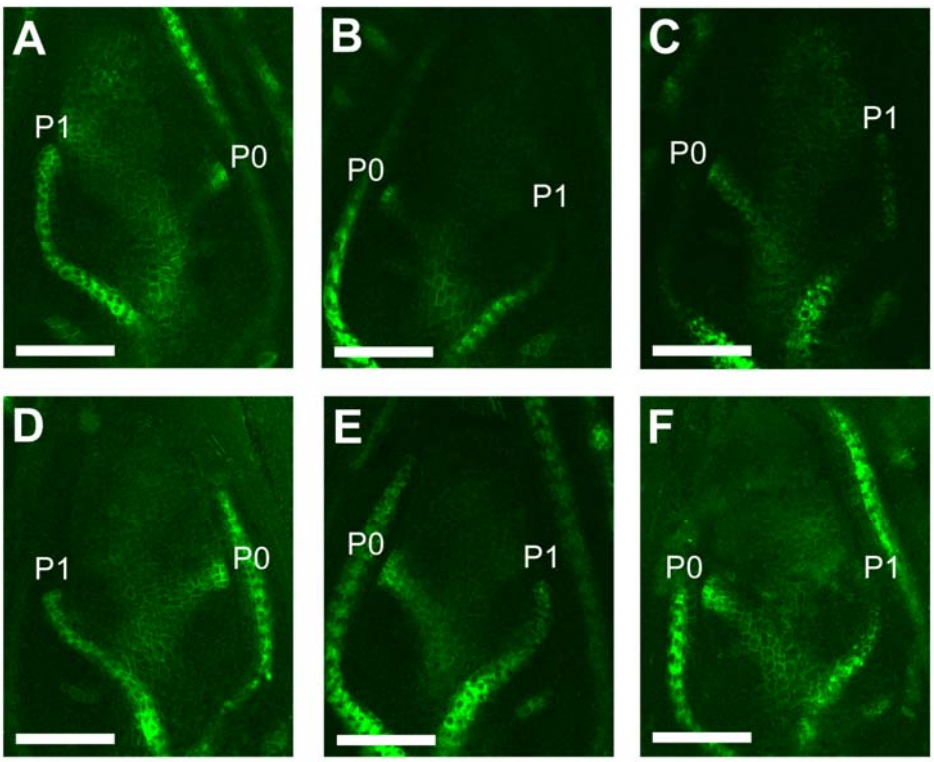


Supplemental Figure S1. Maize PIN1 is detected by an Arabidopsis PIN1 antiserum. A, Immunodetection of maize PIN1 by Arabidopsis PIN1 antiserum. Maize proteins were extracted from shoot apices. T, total fraction; S, soluble fraction; M, membrane fraction. Ponceau S membrane staining is to show equal loading. B, Arabidopsis PIN1 immunolocalization showing expression in L1 layer (White arrows).



Supplemental Figure S2. *ABPH1* is not induced by auxin. A, Roots were removed from two week old seedlings by excising at the shoot-root junction. The shoots were then stood in 10^{-5} M IAA solution or water control for 2 h. Total RNAs were extracted from apices from each treatment. Semi-quantitative RT-PCR and DNA blotting were carried out as described previously (Giulini et al., 2004). Results from two biological replicates are shown. No Treat., No treatment, time zero control; UBQ, ubiquitin as a loading control. B, Quantification of *ABPH1* expression levels shown in (A). *ABPH1* expression levels were normalized relative to ubiquitin expression, and are expressed in arbitrary units.



Supplemental Figure S3. Cytokinin treatment induces ZmPIN1a-YFP in the P_0 leaf primordium. Seedlings expressing ZmPIN1-YFP were excised at the shoot-root junction and treated with either 100 µM kinetin or a control solution for 4 h. Median longitudinal sections were taken through the SAM and imaged by confocal microscopy. A-C, SAMs of seedlings treated with control solution. D-F, SAMs of seedlings treated with kinetin. Scale bars = 100 µm.

Supplemental Table S1. Contents of cytokinins, auxin and related compounds in normal and *abph1* embryos

Hormone and Compound	normal		*abph1*	
	Average	S.E.	Average	S.E.
IAA	1091.89	326.73	421.37	47.33
IAAsp	268.58	23.91	169.57	23.78
tZ	3.00	0.50	3.23	0.26
tZR	15.34	1.82	14.32	0.23
tZRMP	89.75	7.62	96.72	4.89
cZR	2.49	0.33	2.81	0.31
cZRMP	0.89	0.23	0.76	0.03
DZR	0.44	0.11	0.66	0.19
iPR	4.09	0.67	3.47	0.20
iPRMP	69.43	6.10	98.46	0.87
tZ7G	10.60	1.42	12.58	0.77
tZ9G	200.04	25.04	426.17	20.68
tZROG	1.24	0.17	1.24	0.24
IP9G	1.63	0.16	3.24	0.50

Unit= pmole/Fresh weight (g)

Averages were calculated from three independent biological pools of ~10 embryos. S.E., standard error

IAA, indole-3-acetic acid; IAAsp, indole-3-acetylaspartic acid; tZ, trans-zeatin; tZR, tZ riboside; tZRMP, tZR 5'-monophosphate; cZR, cis-zeatin riboside; cZRMP, cZR 5'-monophosphate; DZR, dihydrozeatin riboside; iPR, *N*6-(Δ2-isopentenyl)adenine riboside; iPRMP, iPR 5'-monophophate; tZ7G, tZ N7-glucoside; tZ9G, tZ N9-glucoside; tZROG, tZR O-glucoside; iP9G, iP N9-glucoside

Supplemental Table S2. Quantification of ZmPIN1a-YFP fluorescence in the SAM of kinetin treated and control seedlings

Treatment	Area P_0 (μm^2)	Mean intensity in entire P_0	Integrated density	Mean intensity in center of P_0	N
Control	579 (31)	48 (3)	27143 (2009)	56 (4)	16
Kinetin	703 (33)	57 (5)	40344 (4156)	70 (7)	14
P-value	0.014	0.088	0.006	0.095	

Seedlings expressing the ZmPIN1a-YFP construct were treated for 4 h with 100 µM kinetin or control solution. Median longitudinal hand sections of each SAM were imaged by confocal microscopy, and fluorescence was quantified using ImageJ software. For each section, the P_0 site of leaf initiation, marked by high PIN1-YFP expression, was selected using the polygon tool. Mean fluorescence intensity (on a scale of 0-255) and the area of the P_0 were calculated for the selected region. Integrated density was calculated by multiplying the mean fluorescence intensity by the area. Mean fluorescence intensity was also quantified for a square with a set area of 225 μm^2 (15 µm x 15 µm) that was centred on the P_0 leaf primordium of each sample. The values obtained were compared using a student's t-test. Numbers in brackets = standard error, N = sample size.