

Figure S1. Microarray for auxin effect on PIN lateralization identifies PATELLINS as candidate genes.

A. PIN1 and PIN2 are basally localized in endodermis and young cortex cells, respectively, pumping auxin in the direction of the root tip. Auxin is able to modify PIN1 and PIN2 localization to baso-lateral. This effect is dependent on the AXR3-mediated transcription of so far unknown components.

B. Microarray results. Among the auxin-regulated genes in wild type, we selected 245 gene candidates as being auxin inducible but differentially expressed in the dominant negative version of AXR3 (*HS:axr3-1*).

C, D. PATELLINS are auxin-regulated genes in an AXR3-dependent fashion. PATL6 is auxin inducible depending on AXR3. On the other hand, PATL2 and PATL4 are negatively regulated by auxin and in the *HS:axr3-1* mutant background these effects were lost. In D, the Fold Change (FC) and the *P* values for the *PATL* genes obtained in the microarray data.

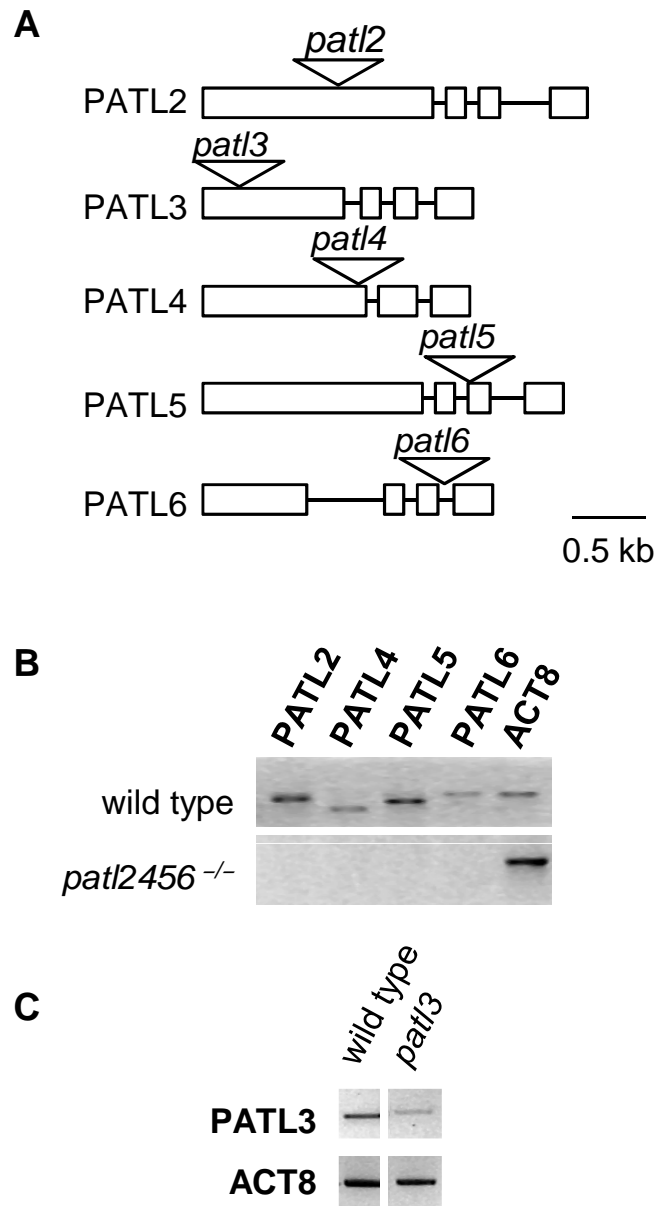


Figure S2. PATELLIN quadruple mutant *patl2456*^{-/-}

A-C. Scheme of *PATL* genes representing exons (boxes) and introns (lines) and the insertion sites of the T-DNA insertions in the *patl* mutants (A). RT-PCR analysis for *PATL* gene expression in wild type and *patl2456*^{-/-} quadruple knockout mutants (B) and *patl3* knockdown mutant (C).

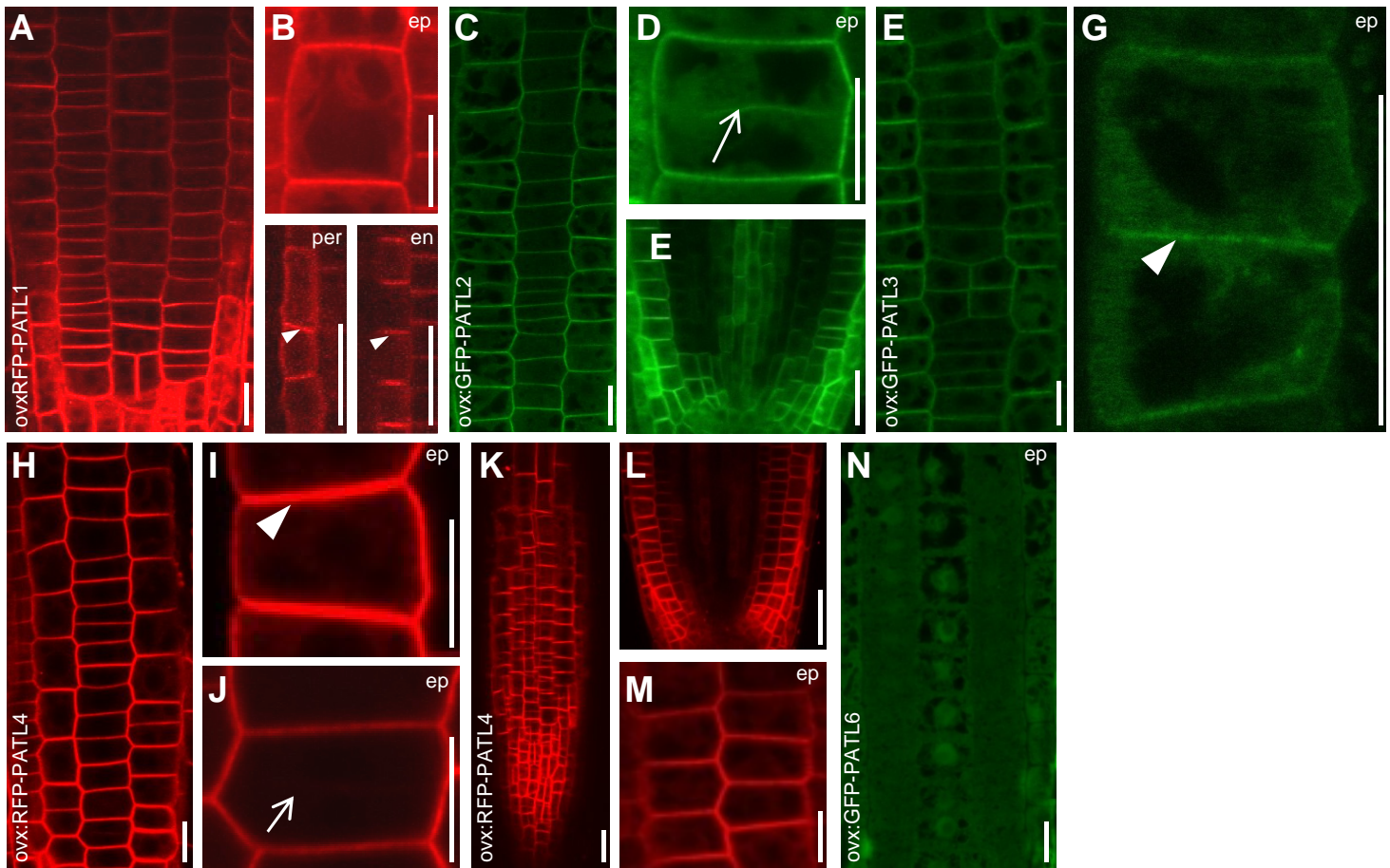


Figure S3. PATELLIN localization in FP-PATL overexpressors lines.

FP-PATL1-5 are localized at the PM or cell plates, and GFP-PATL6 is accumulated at PATL localization was observed in primary roots in GFP-PATL (C to G, N) or RFP-PATL (A, B, H to L) reporter lines expressed in wild type plants using the Cauliflower mosaic virus 35S promoter. Arrowheads are used to highlight asymmetric localization at plasma membranes (B, G), arrowheads depict asymmetric PATL localization at the plasma membrane (C, I, J, O) and arrows indicate cell plate localized PATLs (D, H). . All images are representative of at least 20 different individuals. Bar size= 20 μm.

Table S1. Candidates genes differentially regulated in *HS::axr3-2* compared to auxin-regulated genes in wild type. The gene model description is depicted as it appears in TAIR database. In bold are indicated the candidates that were tested for defects on PIN polarity.

[Click here to Download Table S1](#)

Table S2. Sec14-like proteins in *Arabidopsis*.

Gene model	ATI code	Sec14p homology			Other protein domains
		Identities	+	E value	
AtSFH1/COW1	AT4G34580	102/242	152/242	1e-53	Nodullin ^a
AtSFH2	AT4G39180	102/236	146/236	2e-53	Nodullin ^a
AtSFH3	AT2G21540	104/250	150/250	1e-52	Nodullin ^a
AtSFH4	AT1G19650	103/241	150/241	1e-51	Nodullin ^a
AtSFH5	AT1G75370	101/241	147/241	3e-48	Nodullin ^a
AtSFH6	AT4G39170	97/239	149/239	1e-50	Nodullin ^a
AtSFH7	AT2G16380	102/248	149/248	1e-49	Nodullin ^a
AtSFH8	AT2G21520	97/243	150/243	7e-49	Nodullin ^a
AtSFH9	AT3G24840	100/242	141/242	2e-47	Nodullin ^a
AtSFH10	AT2G18180	89/232	140/232	1e-47	Nodullin ^a
AtSFH11	AT5G47510	95/236	133/236	2e-46	ND
AtSFH12	AT4G36490	91/243	146/243	4e-47	Nodullin ^a
AtSFH13	AT1G55690	90/237	141/237	5e-40	Nodullin ^a
AtSFH14	AT5G56160	90/236	142/236	4e-43	ND
PATL1	AT1G72150	58/221	100/221	2e-11	GOLD; CRAL/Trio
PATL2	AT1G22530	69/221	103/221	3e-11	GOLD; CRAL/Trio
PATL3	AT1G72160	62/216	106/216	4e-17	GOLD; CRAL/Trio
PATL4	AT1G30690	68/224	106/224	2e-16	GOLD; CRAL/Trio
PATL5	AT4G09160	62/217	101/217	2e-15	GOLD; CRAL/Trio
PATL6	AT3G51670	68/232	102/232	1e-14	GOLD; CRAL/Trio
AtPITPs	AT4G36640	75/254	116/254	9e-18	-
	AT5G47730	60/209	99/209	2e-16	-
	AT1G55840	62/209	98/209	4e-16	-
	AT1G01630	66/218	98/218	1e-15	-
	AT1G75170	67/217	102/217	4e-15	-
	AT1G22180	31/96	56/96	7e-08	-
	AT4G08690	56/218	97/218	2e-10	-
	AT1G14820	54/222	96/222	2e-08	-
	AT3G46450	54/213	86/213	2e-06	-
	AT1G05370	41/182	79/182	5e-05	-
	AT5G63060	52/214	88/214	2e-03	-
	AT3G22410	39/183	85/183	5e-04	-

Table S3. Segregation of *patl2* mutant allele in the progeny of a single *patl2*^{+/-} 3456^{-/-} mutant plant.

<i>patl2</i>	<i>n_o</i>	<i>f_o</i>	<i>n_E</i>	<i>f_E</i>
+ / +	14	0.1944	18	0.25
+ / -	51	0.7083	36	0.5
- / -	7	0.0972	18	0.25
TOTAL	72	1	72	1

$$\chi^2 = 13.861$$

$$p = 0.001$$

n_o observed amount; *f_o* observed frequency; *n_E* expected amount; *f_E* expected frequency. Expected values under the assumption of Mendelian traits and no linkage among the different alleles.

Table S4. List of primers used for cloning procedures, *patl* mutant genotyping, amiRNA construct and transcripts level analysis.

Gene	Sequence	Orientation	Application
PATL1	ATGGCTCAAGAGGAAGTAC	Fw	Cloning coding sequence, RT-PCR
PATL1	AGTTTTGAACCTGTAGTAG	Rv	Cloning coding sequence, RT-PCR
PATL2	ATGGCTCAAGAAGAGATAC	Fw	Cloning coding sequence, RT-PCR
PATL2	TGCTTGGGTTTTGGACCTG	Rv	Cloning coding sequence, RT-PCR
PATL3	ATGGCTGAAGAACCTACTAC	Fw	Cloning coding sequence, RT-PCR
PATL3	GAGAGGTTTGACATTGAAC	Rv	Cloning coding sequence, RT-PCR
PATL4	ATGACTGCTGAAGTTAAGG	Fw	Cloning coding sequence, RT-PCR
PATL4	GGAAGAGGATTCAGTCTTG	Rv	Cloning coding sequence, RT-PCR
PATL5	ATGTCTCAAGATTCTGCAAC	Fw	Cloning coding sequence, RT-PCR
PATL5	CTCACAAGCTAAAGGCTTA	Rv	Cloning coding sequence, RT-PCR
PATL6	ATGGATGCTTCATTGTCTCC	Fw	Cloning coding sequence, RT-PCR
PATL6	GACGGTTGTAGTAGATTCCGG	Rv	Cloning coding sequence, RT-PCR
ACTIN8	ACCTTGCTGGTCGTGACCTTACTG	Fw	RT-PCR
ACTIN8	GATCCCGTCATGGAAACGATGTCTC	Rv	RT-PCR
PATL1	GGATTTTTAACGGATCACTC	Fw	Promoter sequence cloning
PATL1	CTTCTTGCTGATTTTAGA	Rv	Promoter sequence cloning
PATL2	TCCGGTTTGACTGGATTTTT	Fw	Promoter sequence cloning
PATL2	GATCACTTGATTCGAAAGGG	Rv	Promoter sequence cloning
PATL3	TTTTACTTGTGCCGTCTTG	Fw	Promoter sequence cloning
PATL3	GCAGGTTTAGGAAACAATTC	Rv	Promoter sequence cloning
PATL4	ATAACTGTTGACTTCAACTA	Fw	Promoter sequence cloning
PATL4	CTTAAAGCCTGTCATTCAGA	Rv	Promoter sequence cloning
PATL5	CCCTAATTCACATTGGTC	Fw	Promoter sequence cloning
PATL5	TTTTTATTGTTCTTGAA	Rv	Promoter sequence cloning
PATL6	TATTTAGCCATAGTGGAAAG	Fw	Promoter sequence cloning
PATL6	TGTTTCTTGAGAGTTTTTC	Rv	Promoter sequence cloning
PATL2	GGAAAAATCTCTTGAGGCTGAA	Right	Genotyping <i>patl</i> mutants
PATL2	CTTGTTGTCGACACCGTGAG	Left	Genotyping <i>patl</i> mutants
PATL3	GTCATTGGATCCAATTCACG	Right	Genotyping <i>patl</i> mutants
PATL3	AACCTTCTCAAGATCATCCAC	Left	Genotyping <i>patl</i> mutants
PATL4	TCTACTGTTTTGAACCCACCG	Right	Genotyping <i>patl</i> mutants
PATL4	CTGAGGCTGTTGTTACCGAAG	Left	Genotyping <i>patl</i> mutants
PATL5	TTTGTAGCTGGTGGTGTTC	Right	Genotyping <i>patl</i> mutants
PATL5	GGCTTTTGTACTACAAGC	Left	Genotyping <i>patl</i> mutants
PATL6	CAAACCCAAGAAAGAAAACCC	Right	Genotyping <i>patl</i> mutants
PATL6	ATTTGTGCGGTTTCTTGAG	Left	Genotyping <i>patl</i> mutants
LBb1+	ATTTTGCCGATTTCCGGAAC		Genotyping <i>patl</i> mutants
LBa1	TGGTTCACGTAGTGGCCATCG		Genotyping <i>patl</i> mutants
PATL1	gaTATAGTGTAGTTTGGCTGGCGTctctctttgtattcc	miR-s	amiRNAa
PATL1	gaCCGCCAGCAAACCTACTATAAtcaaagagaatcaatga	miR-a	amiRNAa
PATL1	gaCCACCAGCAAACCTTCACTATTtcacaggtcgtgatag	miR*s	amiRNAa
PATL1	gaAATAGTGAAGTTTGGCTGGTGGTctcatatataattcct	miR*a	amiRNAa
PATL1	gaTCGAATTGTTTAAACAGCCCGTtctctctttgtattcc	miR-s	amiRNAb
PATL1	gaACGGGCTGTTAAACAATTCGAtcaaagagaatcaatga	miR-a	amiRNAb
PATL1	gaACAGGCTGTTAAAGAATTCGTtcacaggtcgtgatag	miR*s	amiRNAb
PATL1	gaACGAATTCTTTAAACAGCCTGTtcatatataattcct	miR*a	amiRNAb
PATL3	gaTGTCTTATTATAAAGCTCCGTtctctctttgtattcc	miR-s	amiRNAa
PATL3	gaACGGAGCTTTATAATAAGACAtcaaagagaatcaatga	miR-a	amiRNAa
PATL3	gaACAGAGCTTTATATTAAGACTtcacaggtcgtgatag	miR*s	amiRNAa
PATL3	gaAGTCTTAATATAAAGCTCTGTtcatatataattcct	miR*a	amiRNAa
PATL3	gaTACACATAAGATATCTCGCTTtctctctttgtattcc	miR-s	amiRNAb
PATL3	gaAAGCGAGATATCTTATGTGTAtcaaagagaatcaatga	miR-a	amiRNAb
PATL3	gaAAACGAGATATCTAATGTGTTtcacaggtcgtgatag	miR*s	amiRNAb
PATL3	gaAACACATTAGATATCTCGTTTtcatatataattcct	miR*a	amiRNAb