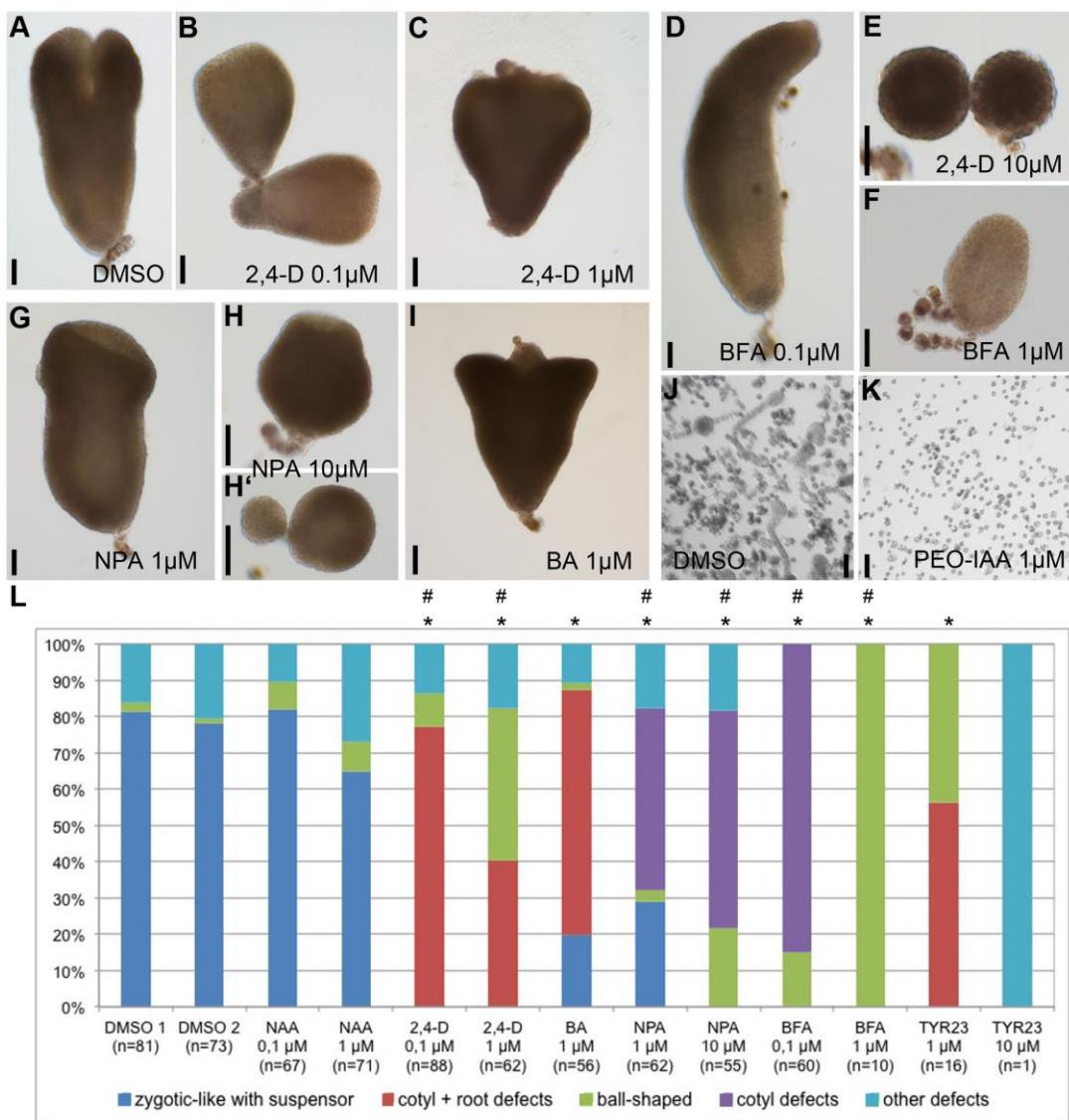


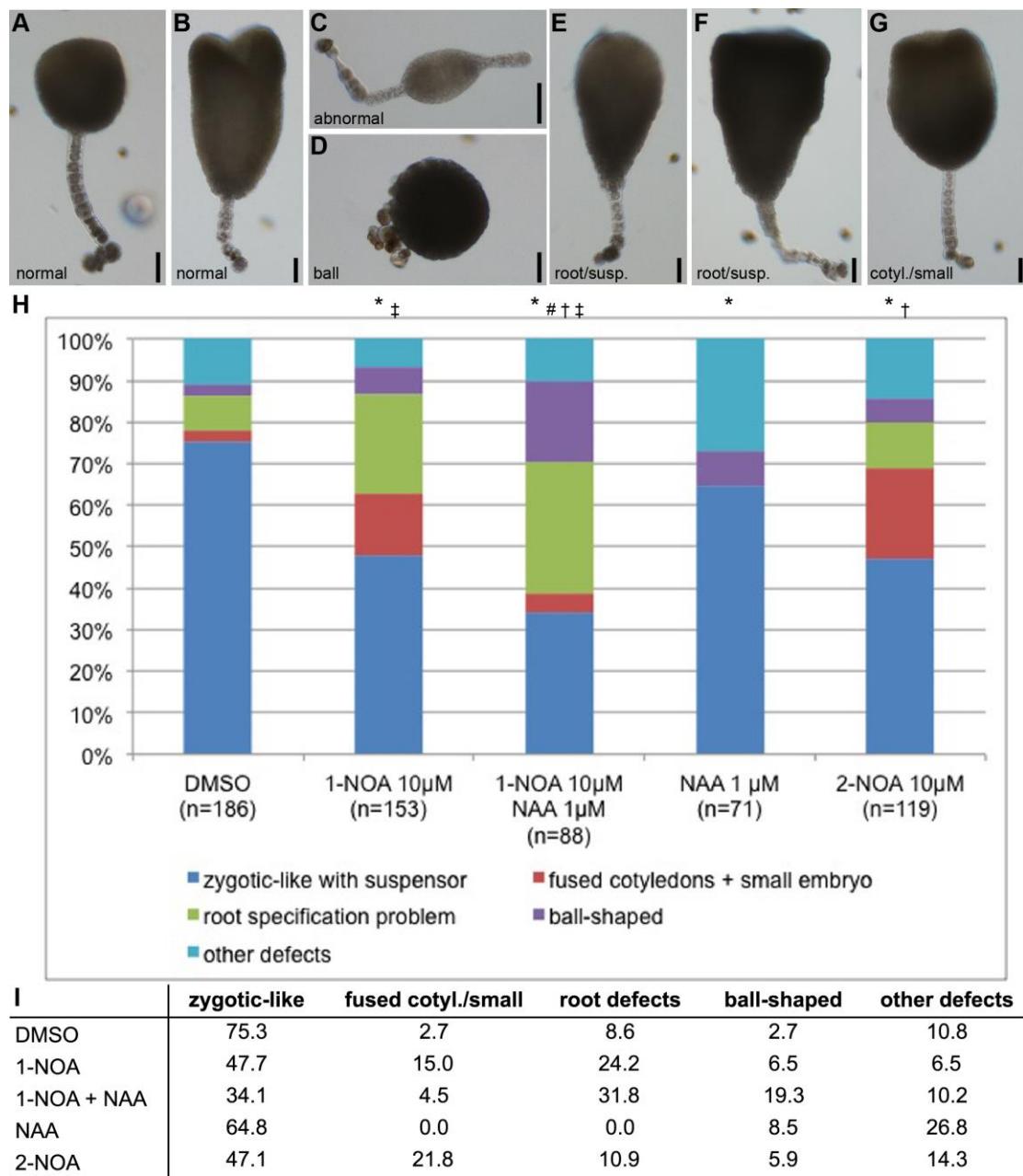
Supplementary material Figure S1. Zygotic development of *Brassica napus* microspore-induced embryos

Brassica napus microspore-induced embryogenesis follows a zygotic embryo development from pollen grain (A). After heat shock, the pollen grain divides (B) and germinates a suspensor-like structure. The apical cell divides vertically (C, arrowhead) and follows a zygotic embryogenesis development: 8-cell (D), 16-cell (E), globular (F, the arrowhead shows the hypophysis), late globular (G, H) and heart stages (I). Scale bars represent 30 µm in A-G and 60 µm in H-I.



Supplementary material Figure S2. Treatments of *Brassica napus* microspore-induced embryos

Brassica napus microspore-induced embryos were treated 5 days after heat shock with DMSO (A) for control, with 2,4-D at 0.1 µM (B), 1 µM (C) and 10 µM (E), brefeldin A (BFA) at 0.1 µM (D) and 1 µM (F), with NPA at 1 µM (G) and 10 µM (H, H'), and with the cytokinin BA at 1 µM (I). Microspore did not germinate when treated with PEO-IAA at 1 µM (K, DMSO for control in J). In L, a graph summarizes the observed phenotypes for the presented treatments (A-I), in addition to NAA at 0.1 µM and 1 µM and to tyrphostin A23 (TyrA23) at 1 µM and 10 µM. Scale bars represent 50 µm. Significant difference ($P < 0.03$) between DMSO controls and the treatment (*) or between the two concentrations of one compound (#) is indicated above the graph (L).

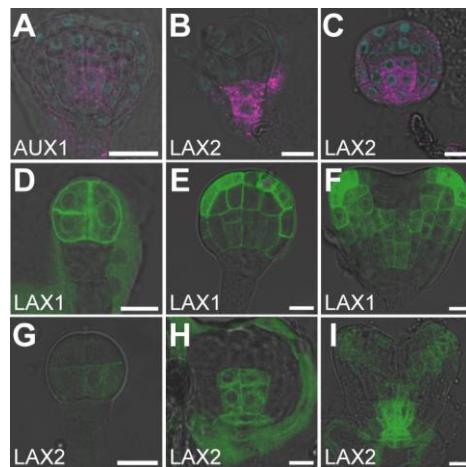


Supplementary material Figure S3. Blocking auxin influx in *Brassica napus* microspore-induced embryos

Five days after heat-shock induction several compounds were added to *Brassica napus* microspore-induced embryos: 1-NOA at 10 µM, NAA at 1 µM, 1-NOA at 10 µM and NAA at 1 µM together or 2-NOA at 10 µM with DMSO as control.

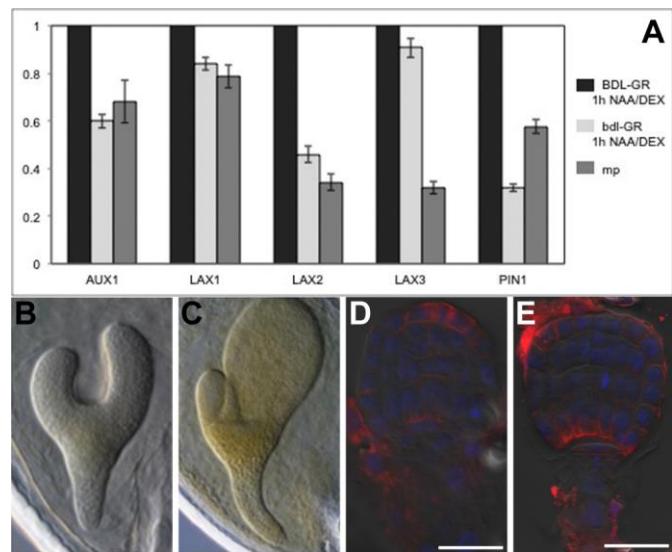
Embryonic phenotypes were scored in the following categories: zygotic-like embryos with suspensor (e.g. normal, A, B, dark blue in H), abnormal embryos or with other defects (C, light blue in H), ball-shaped embryos (D, purple in H), embryos with root

or suspensor specification problem (E, F, green in H), embryos with fused cotyledons or smaller size (G, red in H). The quantification is summarized in graph (H) and table (I). Scale bars represent 50 μm . Significant difference ($P < 0.03$) compared DMSO controls (*), to 1-NOA (†), to 2-NOA (‡) and to NAA (#) is indicated above the graph (H).



Supplementary material Figure S4. Expression patterns of *AUX1*, *LAX1* and *LAX2*

Immuno-localization using anti-HA in *pAUX1::AUX1-HA* embryos (A) and anti-LAX2 in WT embryos (B, C) indicated that *AUX1* is expressed in provascular cells (A) and that *LAX2* in suspensor at early globular stage (B) and in provascular cells from late globular onward (C). The signal is displayed in magenta, nuclei, in cyan, are counter-stained by DAPI. Expression patterns of *LAX1* and *LAX2* are shown after confocal imaging of embryos of *pLAX1::LAX1-Venus* (D-F) and of *pLAX2::LAX2-Venus* (G-I) plants. Signal is at the plasma membrane with noticeable intracellular signal, putatively at the endoplasmic reticulum. Also antibodies against LAX2 give a strong background noise signal. Scale bars represent 10 μ m.



Supplementary material Figure S5. MP/BDL transcriptional pathway regulates *AUX1*, *LAX2* and *PIN1* expression

(A) Graph reporting qRT-PCR results testing *AUX1*, *LAX1*, *LAX2*, *LAX3* and *PIN1* expressions in *pRPS5A::BDL-GR* and *pRPS5A::bdl-GR* roots, after 1 h of co-incubation of dexamethasone (DEX) and NAA, and *mp*^{B4149} seedlings. (B) *mp*^{B4149} embryo. (C) *aux1 lax1 lax2* embryo. (D, E) PIN1 immunolocalization of PIN1 (red signal) in wild type (D) and in *pMP::PIN1 PWii30* (E) embryos. The intensity of PIN1 signal is higher in *pMP::PIN1* embryos (9/15) compared to wild type. Nuclei are stained by DAPI in blue. Scale bars represent 20 μ m.

Supplementary material Table S1. Quantification of all mutant embryonic phenotypes.

Experiment/Ghent Line	n	normal (%)	defects (%)				
			cotyl.	root	cotyl+root	mp-like	total
<i>pin1-201/+</i>	189	81.5	18.0	0.5	0	0	18.5
<i>pin4-2</i>	186	88.2	0	0	11.8	0	11.8
<i>aux1 lax1 lax2</i>	443	73.8	9.5	4.3	9.9	2.5	26.2
<i>pin1-201/+ aux1 lax1 lax2</i>	213	55.9	21.6	8.9	10.8	2.8	44.1
<i>pin4-2 aux1 lax1 lax2</i>	123	60.2	0	0	39.8	0	39.8
Experiment/Brno							
Col	188	100	0	0	0	0	0
<i>pin1-201/+</i>	353	87.5	12.5	0	0	0	12.5
<i>pin4-2</i>	140	97.9	2.1	0	0	0	2.1
<i>pin4-3</i>	195	97.4	2.6	0	0	0	2.6
<i>aux1 lax1 lax2</i>	459	92	1.1	7	0	0	8.1
<i>pin1-201/+ aux1 lax1 lax2</i>	129	86.1	12.4	1.6	0	0	14
<i>pin4-2 aux1 lax1 lax2</i>	304	95.1	1	3.9	0	0	4.9
<i>pin4-3 aux1 lax1 lax2</i>	136	88.2	3.7	8.1	0	0	11.8
<i>pin1-201/+ pin4-2 aux1 lax1 lax2</i>	1424	73.6	25.8	0.6	0	0	26.4
<i>PIN1 pin4-2 aux1 lax1 lax2</i> (from <i>pin1/+ pin4 aux1 lax1 lax2</i>)	432	94.9	4.1	1	0	0	5.1

Embryos were scored from globular to heart stages in two to three biological repeats per growth locations.

Statistic table related to data in Table S1

Fisher Exact test	Chi-square	df	P	Significant difference
<i>aux1 lax1 lax2</i> Ghent vs Brno	99.2	4	0	yes
Col vs <i>aux1 lax1 lax2</i> Brno	16.1	2	0	yes
Col vs <i>pin1</i> Brno	25.5	1	0	yes
Col vs <i>pin4-2</i> Brno	4.07	1	0.044	yes
Col vs <i>pin4-3</i> Brno	4.88	1	0.027	yes
<i>pin4-2</i> vs <i>pin4-3</i> Brno	0.062	1	0.803	no
<i>pin1</i> vs <i>pin1 aux1 lax1 lax2</i> Ghent	50.2	4	0	yes
<i>pin1</i> vs <i>pin1 aux1 lax1 lax2</i> Brno	5.5	2	0.064	no
<i>aux1 lax1 lax2</i> vs <i>pin1 aux1 lax1 lax2</i> Ghent	28	4	0	yes
<i>aux1 lax1 lax2</i> vs <i>pin1 aux1 lax1 lax2</i> Brno	4.6	2	0	yes
<i>pin4-2</i> vs <i>pin4-2 aux1 lax1 lax2</i> Ghent	32.8	1	0	yes
<i>pin4-2</i> vs <i>pin4-2 aux1 lax1 lax2</i> Brno	6.55	2	0.038	yes
<i>pin4-3</i> vs <i>pin4-3 aux1 lax1 lax2</i> Brno	16.8	2	0	yes
<i>aux1 lax1 lax2</i> vs <i>pin4-2 aux1 lax1 lax2</i> Ghent	74.9	4	0	yes
<i>aux1 lax1 lax2</i> vs <i>pin4-2 aux1 lax1 lax2</i> Brno	3.11	2	0.211	no
<i>aux1 lax1 lax2</i> vs <i>pin4-3 aux1 lax1 lax2</i> Brno	4.52	2	0.104	no
<i>pin4-2 aux1 lax1 lax2</i> vs <i>pin4-3 aux1 lax1 lax2</i> Brno	7.29	2	0.026	yes
<i>pin4-2 aux1 lax1 lax2</i> Ghent vs Brno	83.7	1	0	yes
<i>aux1 lax1 lax2</i> vs <i>pin1 pin4 aux1 lax1 lax2</i> Brno	186	2	0	yes
<i>pin1</i> vs <i>pin1 pin4 aux1 lax1 lax2</i> Brno	31.1	2	0	yes

<i>pin1 aux1 lax1 lax2</i> vs <i>pin1 pin4 aux1 lax1 lax2</i> Brno	12.4	2	0.002	yes
<i>pin4 aux1 lax1 lax2</i> vs <i>pin1 pin4 aux1 lax1 lax2</i> Brno	109	2	0	yes
<i>PIN1 pin4 aux1 lax1 lax2</i> vs <i>pin1 pin4 aux1 lax1 lax2</i> Brno	94.2	2	0	yes
<i>pin4 aux1 lax1 lax2</i> vs <i>PIN1 pin4 aux1 lax1 lax2</i> Brno	13.8	2	0.001	yes

Supplementary material Table S2. Quantification of seedling phenotypes in all mutants

Experiment/Ghent Line	n	normal	cotyl. defects with normal root (%)				mp-like (%)	
			tricot	monocot	no cotyl/stub	other		
<i>pin1-201/+</i>	302	91.7	3.3	1	0	4	8.3	0
<i>pin4-2</i>	382	98.5	0.5	0	0	1	1.5	0
<i>aux1 lax2</i>	360	100	0	0	0	0	0	0
<i>aux1 lax1 lax2</i>	406	88.2	1.2	4.2	0.5	2.2	8.1	3.7
<i>pin1-201/+ aux1 lax1 lax2</i>	322	69.2	1.2	8.4	18.4	1.6	29.6	1.2
<i>pin4-2 aux1 lax2</i>	210	95.6	0	1.9	0.5	1	3.4	1
<i>pin4-2 aux1 lax1 lax2</i>	366	93	0.5	3.6	0	1.6	5.7	1.3
<hr/>								
Experiment/Brno								
Col	440	100	0	0	0	0	0	0
<i>pin1-201/+</i>	458	94.8	3.7	1.3	0	0.2	5.2	0
<i>pin4-2</i>	173	99.4	0	0.6	0	0	0.6	0
<i>pin4-3</i>	437	100	0	0	0	0	0	0
<i>aux1 lax1 lax2</i>	289	91.7	0.3	2.8	0	0.3	3.5	4.8
<i>pin1-201/+ aux1 lax1 lax2</i>	554	71.5	0	7.6	19.9	0.5	28	0.5
<i>pin4-2 aux1 lax1 lax2</i>	349	95.1	0	2.9	1.1	0.3	4.3	0.6
<i>pin1-201/+ pin4-2 aux1 lax1 lax2</i>	1978	81.4	0.1	4.9	12.6	0.9	18.5	0.1
<i>PIN1 pin4-2 aux1 lax1 lax2</i> (from <i>pin1/+ pin4 aux1 lax1 lax2</i>)	424	94.7	0.2	3.3	0.7	0.9	5.1	0.2

Statistic table related to data in Table S2

Fisher Exact test 3x2	Chi-square	df	P	Significant difference
<i>aux1 lax1 lax2</i> Brno vs Ghent	6.7	2	0.035	yes
<i>pin1</i> vs <i>pin1 aux1 lax1 lax2</i> Ghent	50.1	2	0	yes
<i>pin1</i> vs <i>pin1 aux1 lax1 lax2</i> Brno	92.3	2	0	yes
<i>aux1 lax1 lax2</i> vs <i>pin1 aux1 lax1 lax2</i> Ghent	58.9	2	0	yes
<i>aux1 lax1 lax2</i> vs <i>pin1 aux1 lax1 lax2</i> Brno	85.7	2	0	yes
<i>pin4-2</i> vs <i>pin4-2 aux1 lax1 lax2</i> Ghent	14.8	2	0.001	yes
<i>pin4-2</i> vs <i>pin4-2 aux1 lax1 lax2</i> Brno	6.43	2	0.04	yes
<i>aux1 lax1 lax2</i> vs <i>pin4-2 aux1 lax1 lax2</i> Ghent	6.07	2	0.048	yes
<i>aux1 lax1 lax2</i> vs <i>pin4-2 aux1 lax1 lax2</i> Brno	12	2	0.003	yes
<i>aux1 lax1 lax2</i> vs <i>pin1 pin4 aux1 lax1 lax2</i> Brno	118	2	0	yes
<i>PIN1 pin4 aux1 lax1 lax2</i> vs <i>pin1 pin4 aux1 lax1 lax2</i> Brno	45.6	2	0	yes

Supplementary material Table S3. Quantification of *mp*^{S319} phenotypes in aux/lax background

Embryonic defects/Ghent	n	% defects	P from contingency table X ² tests compared to		
Line			Col	<i>mp</i> ^{S319} /+	aux/lax
Col	340	0.0			
<i>aux1</i> -21	87	2.3	0.005		
<i>aux1 lax2</i>	260	1.5	0.022		
<i>aux1 lax1 lax2</i>	56	21.4	0.000		
<i>mp</i> ^{S319} /+	281	6.1	0.000		
<i>mp</i> /+ <i>aux1</i>	393	7.4	0.000	0.5	0.081
<i>mp</i> /+ <i>aux1 lax2</i>	450	13.6	0.000	0.001	0.000
<i>mp</i> /+ <i>aux1 lax1 lax2</i>	216	27.3	0.000	0.000	0.371
Seedlings defects/Ghent	n	% rootless seedlings	% total defective seedlings	Col	<i>mp</i> ^{S319} /+
Col	285	0.0	0.0		
<i>aux1</i>	465	0.0	0.0	/	
<i>aux1 lax1</i>	643	0.6	2.3	0.009	
<i>aux1 lax2</i>	635	0.0	0.0	/	
<i>aux1 lax1 lax2</i>	502	3.6	8.7	0.000	
<i>mp</i> ^{S319} /+	821	4.6	5.2	0.000	
<i>mp</i> /+ <i>aux1</i>	1018	6.1	7.5	0.000	0.000
<i>mp</i> /+ <i>aux1 lax1</i>	465	10.5	17.4	0.000	0.000
<i>mp</i> /+ <i>aux1 lax2</i>	678	9.0	10.4	0.000	0.000
<i>mp</i> /+ <i>aux1 lax1 lax2</i>	504	14.2	22.0	0.000	0.000

Embryos were scored from globular to heart stages. All deviations to the wild-type embryo development are collected.

Seedling defects include aberrant number and symmetry of cotyledons (monocot., tricot., no cotyledons, one smaller cotyledon) and rootless seedlings similar to *mp* typical phenotype (see Fig. 5G) with three, two, one or no cotyledons.

Contingency table X² statistical tests were performed for statistical analysis. Mutants were tested against Col. Lines resulting of the crosses with *mp*/+ were tested against Col and against corresponding *aux/lax* mutant combinations. Significant difference is observed for P < 0.05.

Supplementary material Table S4. Analysis of lines with *MP*-driven expression of *PIN1*, *AUX1* and *LAX2* in *mp* alleles

Line in T2	% rootless in T2/Ghent (n)	% rootless in T3 homoz./Brno (n)	qPCR results
ASi29	18.3 (120)		1.99 ± 0.14
ASi36	18.4 (87)	21.7 (507)	
ASi17	20.8 (125)		
ASi25	21.6 (134)		
ASi26	21.9 (137)		
ASi2	23.4 (124)		
ASiii1	23.5 (81)		
ASiii2	23.8 (84)		
ASi17	24.1 (108)		
ASi6	24.5 (106)		
ASi4	25.0 (116)		
ASiii5	25.5 (145)		
ASi32	26.3 (156)		
ASi42	26.4 (106)		
ASi3	26.5 (121)		
ASi14	26.5 (102)		
ASi30	26.6 (143)		1.47 ± 0.13
ASiii9	27.4 (135)		
ASiii7	27.9 (154)	22.5 (608)	2.01 ± 0.19
ASi9	28 (168)		
ASiii6	28.2 (156)	25.2 (1440)	3.91 ± 0.40
ASi23	28.2 (131)		
ASi24	29 (138)		
ASi11	29.5 (210)		
ASiii4	31.4 (153)		
ASiii3	32.3 (155)		
ASi39	32.6 (129)		
LSii45	12.7 (63)		
LSii39	18.2 (66)		
LSi51	18.7 (75)		
LSii22	19.8 (91)		
LSii41	20.5 (83)		
LSi48	21.1 (71)		
LSii48	21.1 (71)		
LSii38	22. (77)		
LSi50	22.9 (70)		
LSii7	23.3 (103)		
LSii44	24.4 (78)		
LSii40	24.7 (73)		
LSii26	24.7 (81)		
LSii16	25 (80)		
LSii21	25.7 (113)		
LSii34	25.7 (66)		
LSii14	26.2 (84)		

LSii32	26.8 (71)	29 (965)	9.32 ± 0.60
LSii3	27.3 (77)		
LSii15	27.4 (102)	23 (643)	11.20 ± 0.73
LSii42	27.5 (80)		
LSii28	27.8 (72)		6.84 ± 0.39
LSii9	28.1 (64)		
LSii5	28.7 (150)		
LSii17	29.1 (86)		
LSi46	29.8 (67)	22 (723)	4.40 ± 0.31
LSii13	30.6 (98)		
LSii25	31.9 (94)		
LSii12	32.6 (86)		
LSii8	33.3 (75)		
LSi49	33.8 (77)		
PSiii26	12.2 (82)		
PSiii17	15.7 (70)	24.5 (1687)	4.13 ± 0.18
PSiii21	20.5 (73)		
PSiii10	21.6 (74)	26.9 (659)	6.29 ± 0.34
PSiii23	21.8 (78)		1.55 ± 0.21
PSiii14	23.3 (60)		
PSiii18	24.1 (83)		
PSiii19	25 (52)		1.35 ± 0.07
PSiii22	25.7 (74)		
PSiii13	25.7 (70)		
PSiii15	26.9 (78)		
PSiii25	29.1 (55)		
PSiii16	29.7 (64)		
AWv10	3.8 (106)		
AWiv1	4.1 (172)	6.2 (64)	3.12 ± 0.29
AWiv15	5.8 (257)		
AWv37	5.9 (101)		
AWv43	6 (100)		
AWv9	6.2 (160)		
AWiv21	7 (157)		
AWv24	7 (156)		
AWv36	7.1 (99)		
AWv35	7.1 (211)		
AWv25	7.6 (171)		
AWv4	7.8 (128)		
AWiv4	7.9 (152)		
AWiv18	8.1 (271)		
AWiv11	8.1 (184)		
AWv49	8.2 (97)		
AWiv20	8.3 (133)		2.25 ± 0.15
AWv38	8.3 (72)		
AWiv13	8.8 (193)		
AWiv11	9.3 (216)		
AWv26	9.7 (144)		

AWv42	10.3 (126)		
AWv34	10.4 (144)		
AWiv19	10.5 (295)		
AWv41	11.0 (154)		
AWv50	11.1 (280)		
AWv45	11.3 (141)	15.4 (635)	2.85 ± 0.18
AWiv6	11.5 (226)		
AWv21	11.9 (118)		
AWv40	13.3 (105)	13.5 (1061)	2.14 ± 0.17
AWv14	13.8 (130)		
AWv12	17.4 (167)	8.3 (779)	
AWiv12	18.9 (185)	5.9 (477)	3.06 ± 0.20
LWv7	1.7 (59)		
LWvi17	3.7 (81)		
LWvi42	4.6 (65)		
LWv8	4.8 (84)		
LWvi4	7.5 (67)		
LWiv31	7.8 (115)		
LWv3	8.6 (81)		
LWvi46	10 (60)		
LWvi44	11.1 (72)	5.2 (306)	3.16 ± 0.23
LWvi6	11.1 (72)		
LWvi21	11.6 (112)		
LWvi24	12 (108)		
LWvi9	12.2 (90)		
LWvi50	13.4 (67)		
LWvi23	14.4 (90)		
LWv4	15.1 (73)		
LWv1	15.4 (78)		7.23 ± 0.51
LWv6	15.8 (57)		
LWvi18	15.8 (82)		
LWvi1	16 (50)	12.9 (923)	
LWv5	16.7 (42)		
LWvi14	16.7 (66)		
LWvi5	17.1 (41)		
LWvi37	17.3 (75)		
LWvi32	19.2 (78)		
LWv2	19.6 (51)	19 (231)	3.29 ± 0.27
LWvi13	21.3 (61)		1.54 ± 0.07
LWvi49	26.9 (67)		
LWvi2	30.8 (65)	24.8 (459)	
PWii33	4.2 (215)		
PWvii51	5 (139)		
PWvii7	5.1 (158)		
PWii36	6 (218)		
PWii32	6.5 (138)		
PWvii21	6.5 (138)		
PWvii12	6.6 (121)		

PWvii41	6.9 (116)	
PWvii24	7.5 (147)	
PWvii14	7.8 (166)	
PWiii37	8 (175)	
PWvii1	8.3 (109)	1.40 ± 0.11
PWvii2	8.3 (133)	1.68 ± 0.1
PWvii13	9.4 (138)	
PWvii30	9.5 (116)	14.99 ± 0.68
PWvii32	10 (110)	
PWvii19	10.2 (137)	
PWvii18	10.3 (146)	
PWiii35	11.3 (194)	
PWiii30	11.5 (148)	8.7 (681)
PWvii36	11.5 (139)	
PWiii29	11.6 (147)	
PWvii15	13.7 (122)	
PWvii39	13.7 (139)	10.5 (153)
PWvii31	14.4 (118)	
PWiii41	16.3 (147)	
PWvii23	19 (105)	3.60 ± 0.20
PWvii22	19.3 (93)	

A = MP::AUX1

L = MP::LAX2

P = MP::PIN1

S = $mp^{B4149}/+$ background

W = $mp^{S319}/+$ background

i-vii = tray number of the T1

1-51 = plant number of the T1

Supplementary material Table S5. Results of crosses between *MP::PIN1* and *MP::AUX1* or *MP::LAX2* in *mp^{B4149}* strong allele. Analysis done in Brno.

Lines			n	cot. defects with normal root (%)			mp-like seedlings (%)				
maternal	x	paternal		normal	monocot.	other defects/stub	total	dicot.	monocot.	fused cot.	total
AS	x	PS	538	71.6	0	3.9	3.9	12.1	11.1	1.3	24.5
AS	x	mp	26	69.2	0	7.7	7.7	19.2	3.9	0	23.1
AS	x	AS	2769	72.4	0.1	3.1	3.2	17.2	6.3	0.9	24.4
LS	x	PS	166	71.8	0.6	6	6.6	10.2	9.6	1.8	21.6
LS	x	mp	100	71	0	8	8	11	10	0	21
LS	x	LS	1230	73.4	0.4	2.4	2.8	17.2	5.7	0.9	23.8
PS	x	PS	903	77.1	0	0.2	0.2	15.3	7.4	0	22.7

At least two independent T3 homozygous lines for each *pMP:xx* lines ectopically expressing *AUX1* (AS), *LAX2* (LS) and *PIN1* (PS) in *mp^{B4149}* strong allele (*S*) background were crossed to each other (*PIN1* to *AUX1*, AS x PS and *PIN1* to *LAX2*, LS x PS). Control crosses are selfed *pMP::AUX1* (AS x AS), *pMP::LAX2* (LS x LS), *pMP::PIN1* (PS x PS) and backcrosses to *mp^{B4149}* (AS x mp, LS x mp). Seedling phenotypes were scored 5 days after germination. Contingency table X² statistical tests were performed for statistical analysis.

3x2 contingency table	Chi-square	df	P	Significant difference
AS x PS vs AS x mp	0.914	2	0.633	no
AS x PS vs AS x AS	0.367	2	0.832	no
AS x PS vs PS x PS	30.5	2	0	yes
LS x PS vs LS x mp	0.0537	2	0.974	no
LS x PS vs LS x LS	9.37	2	0.009	yes
LS x PS vs PS x PS	53.3	2	0	yes
AS x PS vs LS x PS	3.63	2	0.163	no

Supplementary material Table S6. Results of crosses between *MP::PIN1* and *MP::AUX1* or *MP::LAX2* in *mp^{S319}* weak allele. Analysis done in Brno.

maternal	x	paternal	n	normal	cot. defects with normal root (%)	mp-like seedlings (%)			
						dicot.	monocot.	fused cot.	total
<i>AW</i>	x	<i>PW</i>	766	83.3	0.4	12.1	3.9	0.3	16.3
<i>PW</i>	x	<i>AW</i>	764	81.3	0.8	11.6	5.5	0.8	17.9
<i>AW</i>	x	<i>mp</i>	292	94.9	1	3.4	0.7	0	4.1
<i>mp</i>	x	<i>AW</i>	367	83.9	1.4	12	1.1	1.6	14.7
<i>AW</i>	x	<i>AW</i>	656	84.1	0.3	14.2	1.1	0.3	15.5
<i>LW</i>	x	<i>PW</i>	519	79.6	0.6	9.6	9.8	0.4	19.8
<i>PW</i>	x	<i>LW</i>	861	83.6	0.6	8.1	6.3	1.4	15.8
<i>LW</i>	x	<i>mp</i>	279	83.9	0.7	8.6	5.4	1.4	15.4
<i>mp</i>	x	<i>LW</i>	353	90.9	0.3	4.5	3.7	0.6	8.8
<i>LW</i>	x	<i>LW</i>	430	85.8	0.2	11.9	2.1	0	14
<i>PW</i>	x	<i>mp</i>	240	75	0	18.8	5.4	0.8	25
<i>mp</i>	x	<i>PW</i>	360	82.7	0.3	10.8	5.6	0.6	17
<i>PW</i>	x	<i>PW</i>	731	82.4	1.9	9	5.7	1	15.7
<i>mp</i>	x	<i>mp</i>	580	89.1	0.2	9	1.7	0	10.7

At least two independent T3 homozygous lines for each *pMP:xx* lines ectopically expressing *AUX1* (*AW*), *LAX2* (*LW*) and *PIN1* (*PW*) in *mp^{S319}* weak allele (*W*) background were crossed to each other (*PIN1* to *AUX1*, *AW* x *PW* and *PIN1* to *LAX2*, *LW* x *PW*). Control crosses are selfed *pMP::AUX1* (*AW* x *AW*), *pMP::LAX2* (*LW* x *LW*), *pMP::PIN1* (*PW* x *PW*), *mp* and backcrosses to *mp^{S319}* (*AW* x *mp*, *mp* x *AW*, *LW* x *mp*, *mp* x *LW*, *PW* x *mp*, *mp* x *PW*). Seedling phenotypes were scored 5 days after germination. Contingency table X² statistical tests were performed for statistical analysis.

3x2 contingency table	Chi-square	df	P	Significant difference
<i>AW</i> x <i>PW</i> vs <i>PW</i> x <i>AW</i>	1.78	2	0.411	no
<i>AW</i> x <i>mp</i> vs <i>mp</i> x <i>AW</i>	20.6	2	0	yes
<i>AW</i> x <i>PW</i> vs <i>AW</i> x <i>mp</i>	29.1	2	0	yes
<i>PW</i> x <i>AW</i> vs <i>mp</i> x <i>pAW</i>	2.58	2	0.275	no
<i>AW</i> x <i>PW</i> vs <i>AW</i> x <i>AW</i>	0.238	2	0.888	no
<i>PW</i> x <i>AW</i> vs <i>AW</i> x <i>AW</i>	2.99	2	0.225	no
<i>AW</i> x <i>mp</i> vs <i>AW</i> x <i>AW</i>	26.6	2	0	yes
<i>mp</i> x <i>AW</i> vs <i>AW</i> x <i>AW</i>	3.96	2	0.138	no
<i>AW</i> x <i>PW</i> vs <i>mp</i> x <i>mp</i>	9.38	2	0.009	yes
<i>PW</i> x <i>AW</i> vs <i>mp</i> x <i>mp</i>	16.5	2	0	yes
<i>AW</i> x <i>PW</i> vs <i>PW</i> x <i>PW</i>	7.77	2	0.021	yes
<i>PW</i> x <i>AW</i> vs <i>PW</i> x <i>PW</i>	4.69	2	0.096	no

<i>LW x PW vs PW x LW</i>	3.71	2	0.156	no
<i>LW x mp vs mp x LW</i>	7.35	2	0.025	yes
<i>LW x PW vs LW x mp</i>	2.42	2	0.298	no
<i>PW x LW vs mp x LW</i>	11	2	0.004	yes
<i>LW x PW vs LW x LW</i>	6.53	2	0.038	yes
<i>PW x LW vs LW x LW</i>	1.55	2	0.46	no
<i>LW x mp vs LW x LW</i>	1.26	2	0.532	no
<i>mp x LW vs LW x LW</i>	5.06	2	0.08	no
<i>LW x PW vs mp x mp</i>	19.5	2	0	yes
<i>PW x LW vs mp x mp</i>	9.19	2	0.01	yes
<i>LW x PW vs PW x PW</i>	7.22	2	0.027	yes
<i>PW x LW vs PW x PW</i>	5.98	2	0.05	yes
<i>AW x AW vs mp x mp</i>	6.59	2	0.037	yes
<i>LW x LW vs mp x mp</i>	2.53	2	0.282	no
<i>PW x PW vs mp x mp</i>	16.4	2	0	yes
<i>AW x AW vs LW x LW</i>	0.577	2	0.749	no
<i>AW x AW vs PW x PW</i>	7.91	2	0.019	yes
<i>LW x LW vs PW x PW</i>	6.89	2	0.032	yes

Supplementary material Table S7. Primers

Genotyping

Gene/alleles		
<i>lax1</i>	Forward primer	ATATGGTGCAGGTGGCACA
	Reverse primer	GTAACCGGAAAGCTGCA
	Border primer	AAGCACGACGGCTGTAGAATAG
<i>lax2</i>	Forward primer	ATGGAGAACGGTGAGAAAGCAGC
	Reverse primer	CGCAGAAGGCAGCGTTAGCG
	Border primer	AAGCACGACGGCTGTAGAATAG
<i>lax3</i>	Forward primer	TACTTCACCGGAGGCCACCA
	Reverse primer	TGATTGGTCCGAAAAAGG
	Border primer	AAGCACGACGGCTGTAGAATAG
<i>pin1-201</i>	Forward primer	CAAAAACACCCCCAAAATTTC
	Reverse primer	AATCATCACAGCCACTGATCC
	Border primer	TGGTTCACGTAGTGGGCCATCG
<i>pin4-2</i>	Forward primer	AACCGGTACGGGTGTTCAACTA
	Reverse primer	GCCATTCCAAGACCAGCATCT
	Border primer	GAGCGTCGGTCCCCACACTTCTATAC
<i>pin4-3</i>	Forward primer	AACCGGTACGGGTGTTCAACTA
	Reverse primer	GCCATTCCAAGACCAGCATCT
	Border primer	GAGCGTCGGTCCCCACACTTCTATAC
<i>mp</i> ^{B4149}	Forward primer	CTCTCAGCGGATAGTATGCACATCGG
	Reverse primer	ATGGATGGAGCTGACGTTGAGTTTC
	Resctriction	MseI, cut in <i>mp</i> ^{B4149}
<i>mp</i> ^{S319}	Forward primer	GATTTCCAGATAATTCTGGA
	Reverse primer	ATGAATATAGTTCAGGTCTC
	Border primer	ATTTGCCGATTCGGAAC

Cloning primers (attB cassettes underlined)

attB4_MP_FOR	<u>GGGGACAAC</u> TTGTATAGAAAAGTTGCCGACGTGTGAATTACCAAGGCG
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attB1R_MP_REV	<u>GGGGACTGCTTTTGACAAACTGCCATCATACAGAGAGATTTCATG</u>
attB1_PIN1_FOR	<u>GGGGACAAGTTGTACAAAAAAGCAGGCTTCATGATTACGGCGCGGACTTCTACCACG</u>
attB2R_PIN1_REV	<u>GGGGACCACTTGTACAAGAAAGCTGGGTGT</u> CATAGACCCAAGAGAATGTAGTAGAG
attB1_AUX1_FW	<u>GGGGACAAGTTGTACAAAAAAGCAGGCTTCATGTCGGAAGGAGTAGAAGCGATAGTAGC</u>
attB2R_AUX1_RV	<u>GGGGACCACTTGTACAAGAAAGCTGGGTGT</u> CAAAGACGGTGGTGTAAAGCGGAGACC
attB1_LAX2_FW	<u>GGGGACAAGTTGTACAAAAAAGCAGGCTTCATGGAGAACGGTGAGAAAGCAGC</u>
attB2R_LAX2_RV	<u>GGGGACCACTTGTACAAGAAAGCTGGGTGT</u> CAAAGGCCGTGAGTGTGATTGAAG

qPCR/RNA *in situ* probe

<i>AUX1-ISH</i>	Forward Reverse	CCAAGCTTCTAATACGACTCACTATAGGGAGATGCAGCCGCCGC ACATGC GTTCATGGTAAAATAGTTATATAAG
<i>AUX1-qPCR</i>	Forward Reverse	ATGACAACGGAACAGATCAG GTGCCATAGGAAATTGCTTAG
<i>LAX1-qPCR</i>	Forward Reverse	TACTCCGAGACCTTCCAAC TACG TCCACCGCCACCACTTCC
<i>LAX2-qPCR</i>	Forward Reverse	GGAGAACGGTGAGAAAGC TCAGATAGCTTAGATTGATGTC
<i>PIN1-qPCR</i>	Forward Reverse	TACTCCGAGACCTTCCAAC TACG TCCACCGCCACCACTTCC
<i>EEF1a4</i>	Forward Reverse	CTGGAGGTTTGAGGCTGGTAT CCAAGGGTGAAAGCAAGAAGA
<i>CDKA</i>	Forward Reverse	ATTGCGTATTGCCACTCTCATAGG TCCTGACAGGGATACCGAATGC