

Fig. S1. Accumulation of *TMO5-LIKE1* transcripts during embryogenesis of *Arabidopsis*. (A-F) Accumulation of *TMO5-LIKE1* transcripts in wild-type embryos (A-C) and *lhw* mutant embryos (D-F). Scale bars: 50 μm.

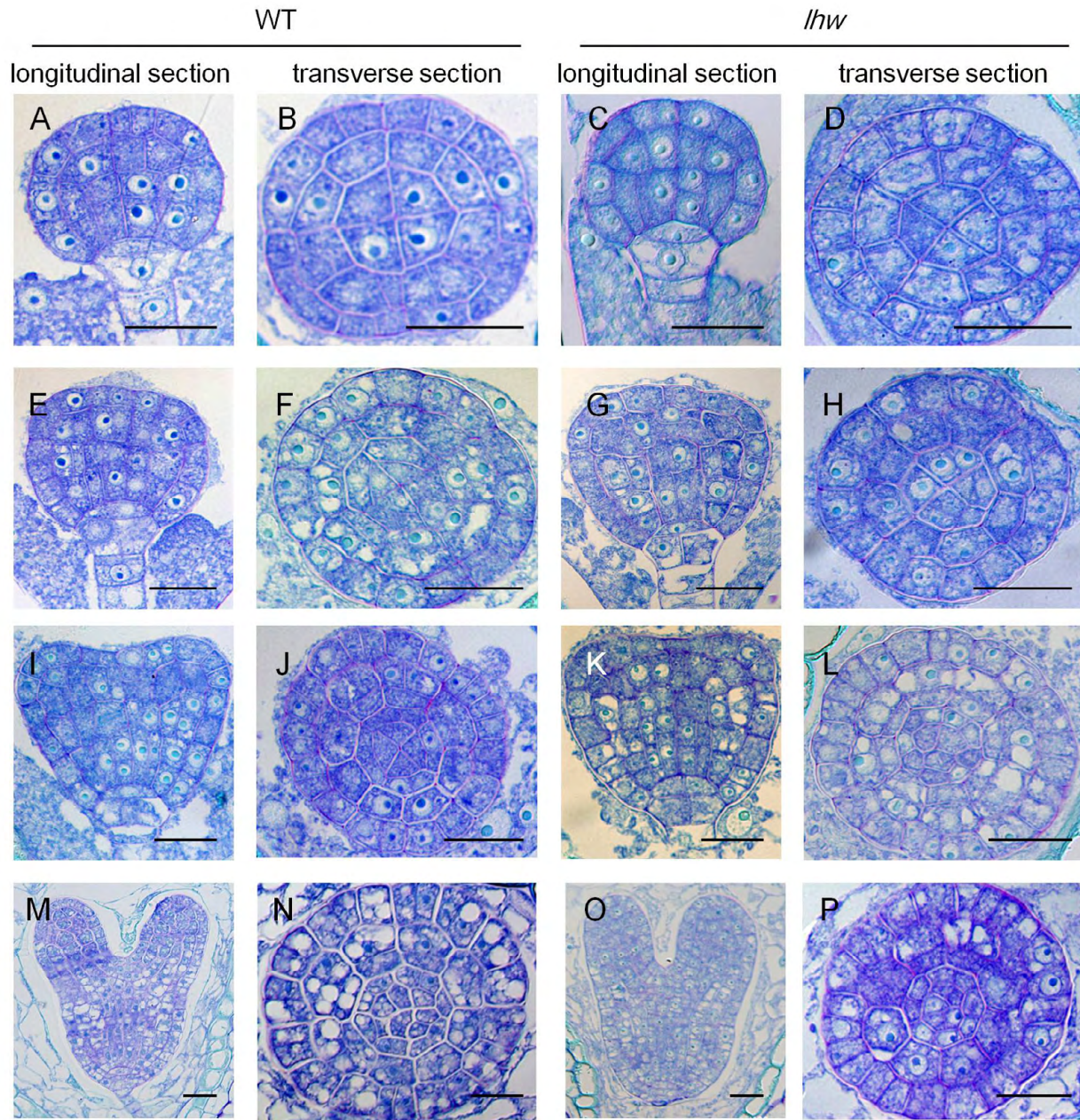


Fig. S2. Anatomical analysis of wild-type and *lhw* embryos. (A-D) Globular-stage embryos of wild type (A,B) and *lhw* (C,D). (E-H) Transition stage embryos of wild-type (E,F) and *lhw* (G,H). (I-L) Early heart stage embryos of wild type (I,J) and *lhw* (K,L). (M-P) Late heart stage embryos of wild type (M,N) and *lhw* (O,P). Scale bars: 20 μ m.

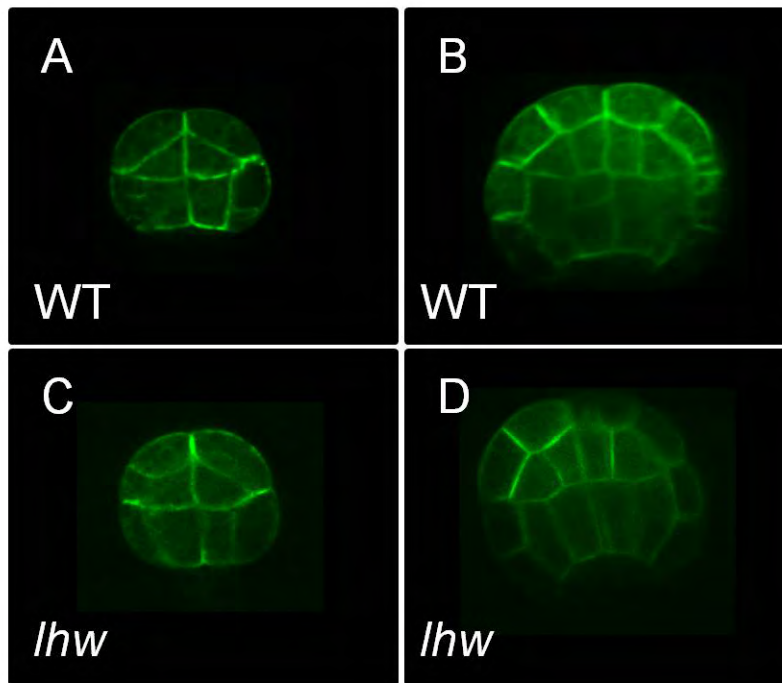


Fig. S3. Expression patterns of *PIN1::PIN1-GFP* during early embryogenesis. (A,B) Wild-type embryos; (C,D) *lhw* embryos.

A

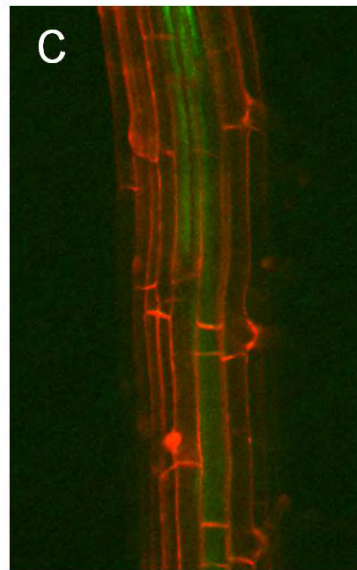
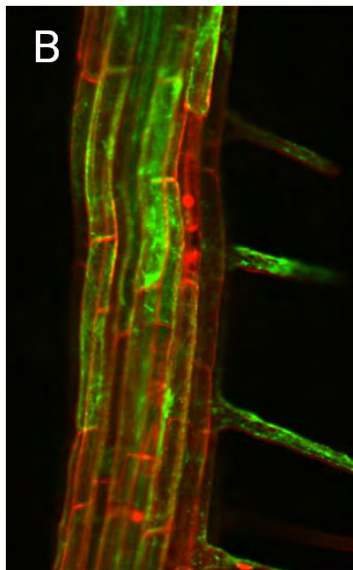
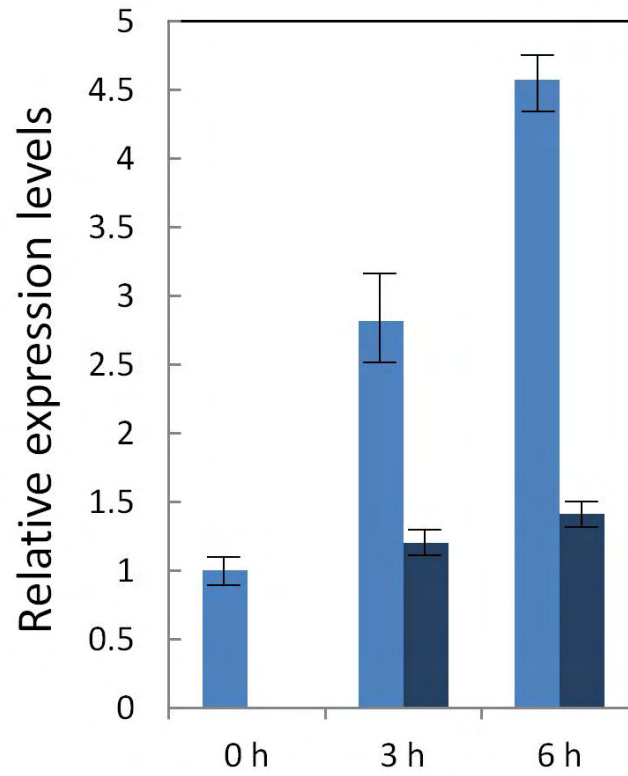


Fig. S4. Analysis of estrogen-inducible *LHW* plants. (A) Relative expression levels of *LHW* mRNA 0, 3 and 6 hours after the addition of estrogen (blue) and without estrogen (dark blue). Bars indicate s.d. (B,C) *DR5::GFP* signal in estrogen-inducible *LHW* roots 24 hours after the addition of estrogen (B) or DMSO (C).

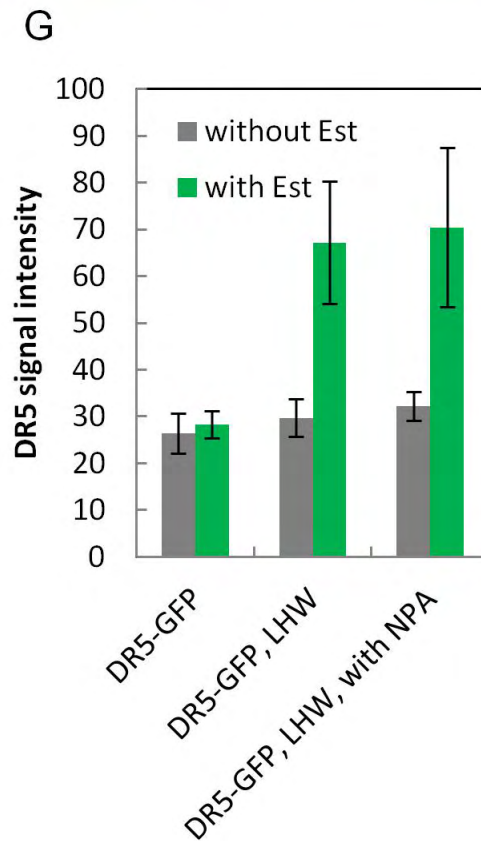
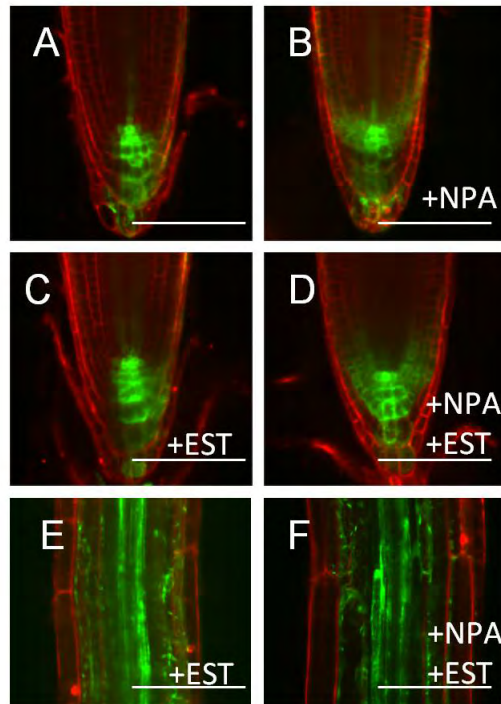


Fig. S5. Effects of NPA treatment on *DR5::GFP* expression. (A-F) *DR5::GFP* signal in estrogen-inducible *LHW* roots with or without NPA and estrogen. Images were taken 24 hours after these treatments. (G) *DR5::GFP* signal intensity in estrogen-inducible *LHW* plants with NPA treatment. *DR5::GFP* signal intensity in the differentiation zone of roots was measured at 24 hours after the induction of *LHW* with or without 10 μ M NPA.

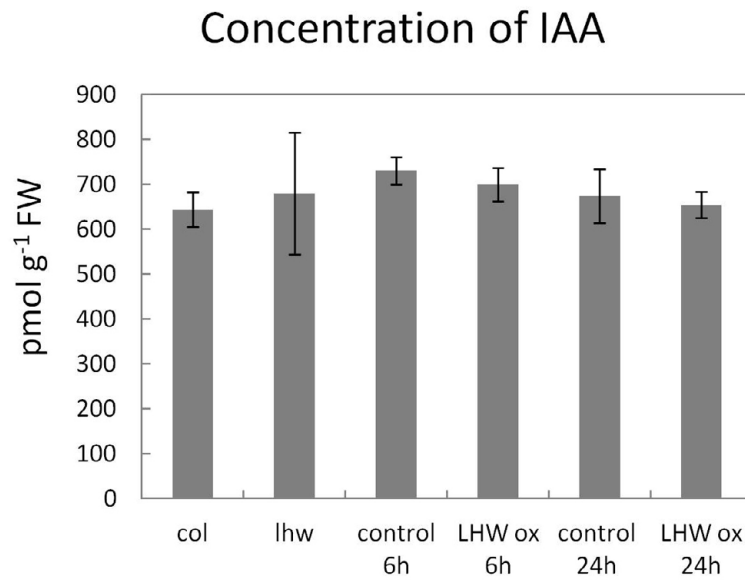


Fig. S6. Concentration of IAA in wild-type, *lhw* and *LHW*-overexpressing roots.

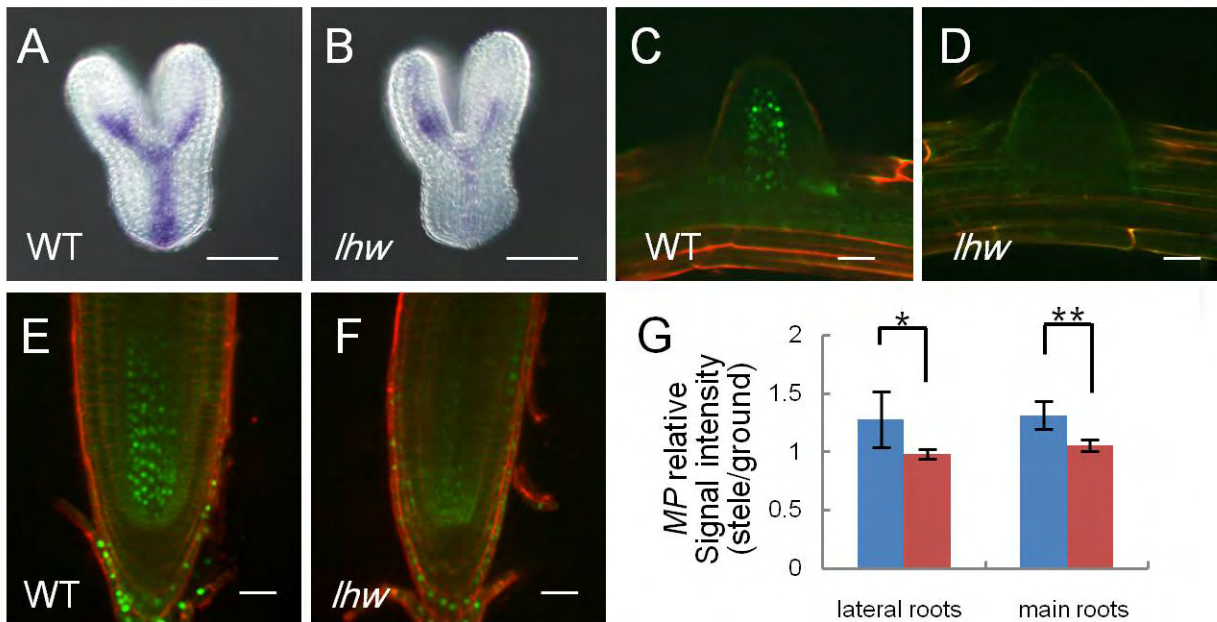


Fig. S7. LHW induces *MP* expression in the vascular region. (A,B) Whole-mount *in situ* hybridization using *MP* probe on wild-type (A) and *lhw* (B) embryos. (C,D) *MP::YFP-NLS* expression in lateral root primordia of wild-type (C) and *lhw* (D). (E,F) *MP::YFP-NLS* expression in root apical region of wild-type (E) and *lhw* (F). (G) Relative *MP::YFP-NLS* signal intensity at stele versus ground tissue region in wild-type (blue) and *lhw* (red) roots. Bars indicate s.d. $n=5$, $*P<0.05$, $**P<0.01$ (*t*-test). Scale bars: 50 μm in A,B; 20 μm in C-F.

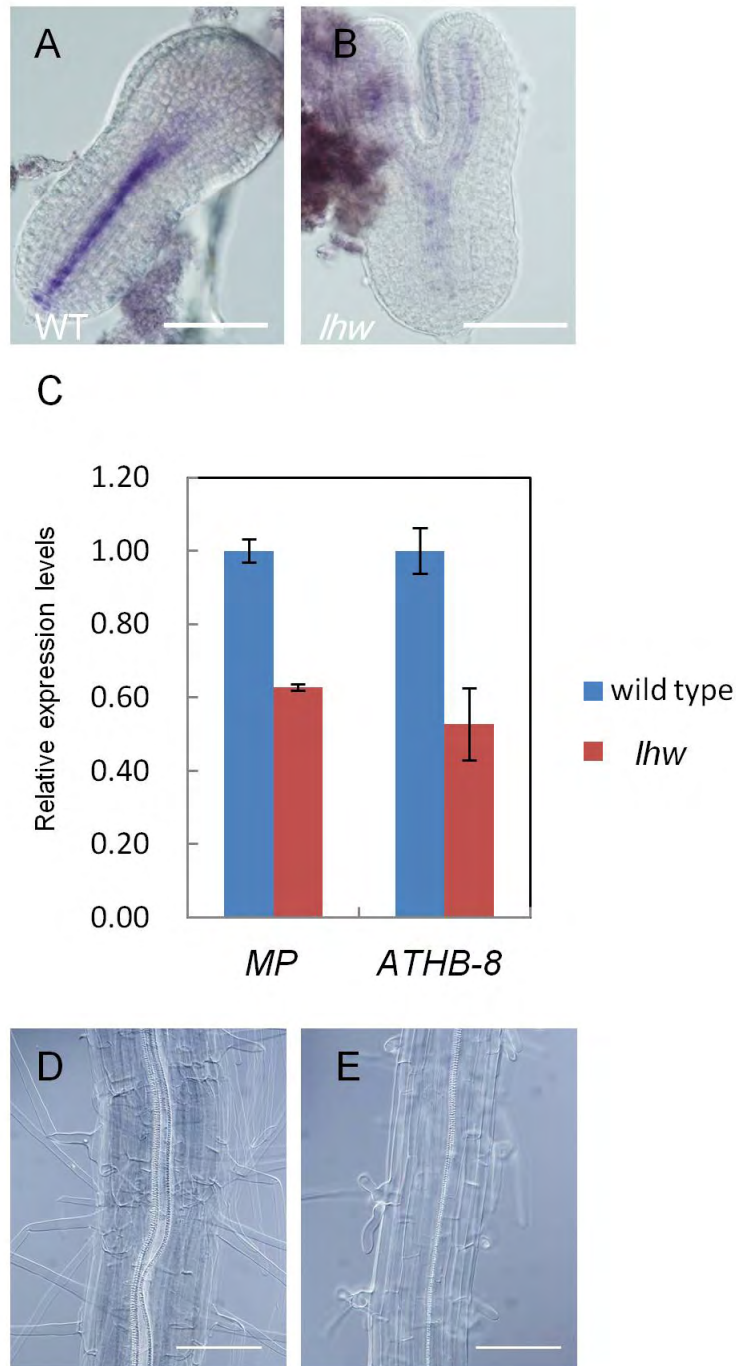


Fig. S8. Analysis of transcription factors related to auxin signalling. (A,B) mRNA accumulation patterns of *ATHB-8* in wild-type (A) and *lhw* (B) embryos. Scale bars: 50 μ m. (C) Quantitative RT-PCR of *MP* and *ATHB-8* transcripts. Total RNA isolated from wild-type and *lhw* roots was used for the analysis. Wild type (blue) and *lhw* (red). (D,E) DIC images of *lhw* roots harbouring *SHR::ATHB-8^r* (D) and *SHR::PHB^r* (E). Scale bars: 200 μ m.

Table S1. The list of primers used for this study

Purpose	Name	Sequences
RNA probe	LHW(1554)-F	GGAATCCAAGATTATGAAAGAGGACG
RNA probe	LHW-R1	TTACATTGAACAGCCACCAGTAAC
RNA probe	TMO5(651)-F	CTTGGTGATAAGAGCATCCTTTTGCT
RNA probe	TMO5-R	CTAATTATAACATCGATTCACCATC
RNA probe	At1G68810(650)-F	ACATGTGAAAGAGTTGAAGAGA
RNA probe	AT1G68810-R	TTACCTCTGATTATATTGTTGTTG
RNA probe	MP-F	CACCATGATGGCTTCATTGTCTTGTG
RNA probe	MP-R	TTATGAAACAGAAGTCTTAAGATC
RNA probe	ATHB-8-F	ATGGGAGGAGGAAGCAATAATA
RNA probe	ATHB-8-R	TCATATAAAAGACCAGTTGAGG
qRT-PCR	LHW-real-F	AAACCGGGGAATCCAAGA
qRT-PCR	LHW-real-R	CCTACTTCGAAAGCCCATGT
qRT-PCR	MP-real-F	TGCCATATGCATCTTCCCTA
qRT-PCR	MP-real-R	GCCTCATCATCATTTTCATAAGC
qRT-PCR	ATHB-8-real-F	TGGGGCACTACCAAGAAGAC
qRT-PCR	ATHB-8-real-R	TGCACATTTGCAGAAGGAAG
qRT-PCR	MBF1A-real-F	TCGAGACCGTCAGAAAATTCA
qRT-PCR	MBF1A-real-R	CATTTTTGTGTTTCAGAGATGTGC
pAtPIN1	pPIN1(-1289)-F	CACCTCATTATATCATCAACCCATTG
	pPIN1(-5)-R	TGTTCCGCCGAGAAGAGA
pMP	pMP(-2050)-F	CACCGTATCCGAATAAGTAGTTATGTTTATATAGATATTCTATCATAAT
	pMP(-1)-R	CACCACAGAGAGATTTTTCAATGTTCTGTTTTGTCTCT
pSHR	pSHR(-2000)-F	CACCACATAAACCAGTAGACATATGGATAAATATGAACACA
	pSHR(-1)-R	CACCTTTTTTTTTTAAATGAATAAGAAAATGAATAGAAGAAAGGGAGAC
ATHB-8orf -mutagenesis	ATHB-8orf-SDM-F	TGGGTCCAAATGCCTGGGATGAAACCGGGCCTGATTCCATAGGAATCG
	ATHB-8orf-SDM-R	CGATTCCATGGAATCAGGCCCGGTTTCATCCCAGGCATTTGGACCCA
PHBorf -mutagenesis	PHBorf-SDM-F	TGGGTTCCAGATGATTGGGATGAAACCGGGCCTGATTCTATTGGCATAG
	PHBorf-SDM-R	CTATGCCAATAGAATCAGGCCCGGTTTCATCCCAATCATCTGAACCCA
pENTR-LHW	LHW-F	CACCATGGGAGTTTTACTAAGAGAAGCTT
	LHW-R	CACCATGGGAGTTTTACTAAGAGAAGCTT

Table S2. Quantification of phytohormones (pmol g⁻¹ FW)

	col	lhw	Control 6h	LHW _{ox} 6h	Control 24h	LHW _{ox} 24h
auxin						
IAA	643.67±39.05	680.29±135.9	730.56±30.25	699.55±37.05	673.91±59.75	654.13±29.42
IAAla	3.041±0.761	3.524±0.776	3.503±0.329	3.107±0.452	6.095±0.140	4.835±1.740
cytokinin						
tZ	0.549±0.168	0.743±0.095	0.864±0.093	0.691±0.063	0.950±0.116	1.348±0.302
tZR	1.753±0.091	4.395±1.006	2.273±0.165	2.506±0.426	3.257±0.538	6.015±0.111
tZRP _s	6.074±0.194	8.056±1.627	6.259±0.731	7.414±0.934	7.752±0.931	16.014±1.413
cZ	0.703±0.109	0.967±0.092	1.035±0.146	0.615±0.032	0.683±0.069	0.486±0.065
cZR	1.529±0.174	1.774±0.186	1.726±0.373	1.380±0.204	1.236±0.205	1.432±0.128
cZRP _s	4.154±0.435	4.335±0.861	3.982±0.985	3.336±1.166	2.296±0.188	3.394±0.507
iP	1.224±1.530	0.442±0.031	0.265±0.021	0.294±0.019	0.262±0.029	0.289±0.029
iPR	0.160±0.009	0.159±0.016	0.200±0.028	0.201±0.011	0.225±0.046	0.222±0.002
iPRP _s	8.864±0.193	10.804±0.340	7.245±1.890	9.631±1.587	8.584±0.788	9.940±0.334
tZ7G	2.940±0.146	3.452±0.237	5.905±0.434	5.989±0.515	6.421±1.367	5.525±0.205
tZ9G	2.812±0.165	3.327±0.108	4.698±0.232	4.919±0.212	5.387±0.751	4.659±0.129
tZOG	4.076±0.506	5.464±0.340	5.219±0.411	6.197±0.776	7.428±1.143	6.387±0.503
cZOG	2.971±0.181	4.501±0.064	2.340±0.298	2.716±0.201	2.628±0.321	1.895±0.148
tZROG	0.039±0.007	-	0.051±0.023	0.040±0.002	0.057±0.011	0.078±0.021
cZROG	0.164±0.048	0.264±0.073	0.184±0.033	0.188±0.022	0.193±0.025	0.224±0.018
iP7G	4.065±0.114	5.796±0.124	4.474±0.175	4.662±0.051	4.200±0.181	4.102±0.105
iP9G	0.905±0.085	1.448±0.058	0.889±0.058	0.894±0.030	0.862±0.104	0.815±0.082
others						
GA19	0.967±0.152	1.397±0.202	0.874±0.154	0.990±0.186	0.739±0.199	0.824±0.107
GA20	1.433±0.033	1.822±0.003	1.353±0.091	1.339±0.105	1.145±0.051	1.337±0.147
GA24	0.999±0.112	0.771±0.031	-	0.910±0.134	-	-
GA53	0.841±0.092	1.610±0.077	1.057±0.068	1.124±0.116	0.900±0.157	0.962±0.277
SA	12,355±71.69	19,778±2,400	29,806±14,511	23,794±3,475	26,853±6,758	23,367±2,692
JA	142.52±19.32	226.66±28.18	126.038±25.87	145.57±17.98	104.30±6.348	119.94±13.60
ABA	33.592±3.319	63.785±10.175	32.009±2.986	39.418±1.787	27.896±5.100	31.421±5.654

Concentrations of auxin, cytokinin, gibberellin, SA, JA and ABA in roots. Data are the means±s.d.

(n=3).