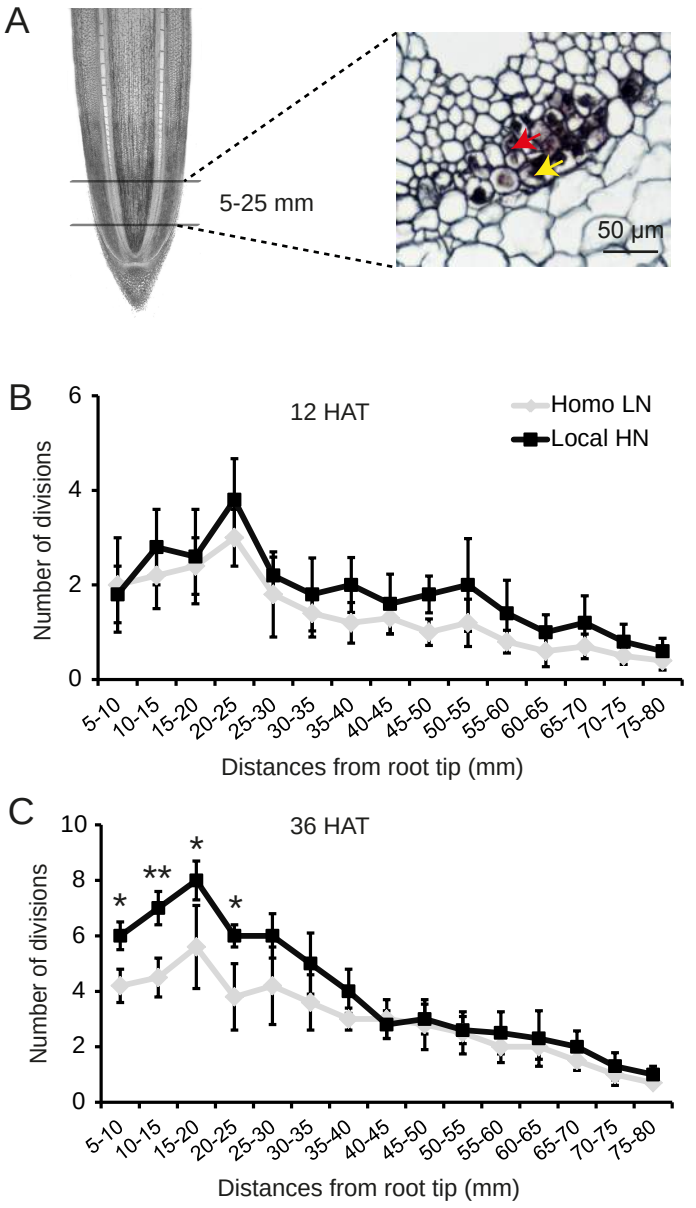
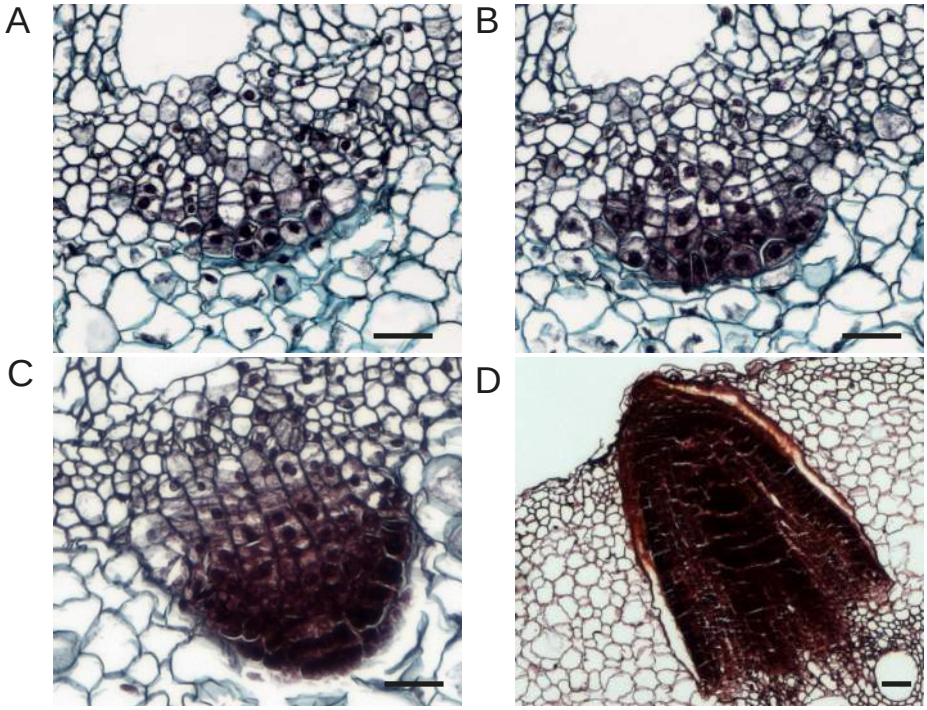
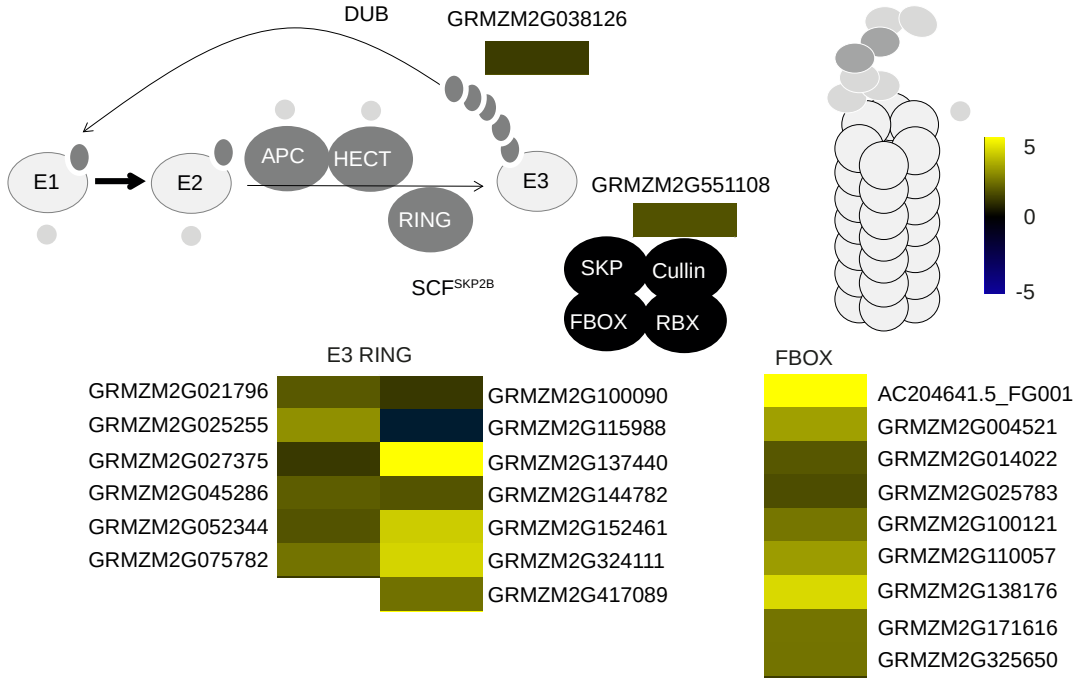


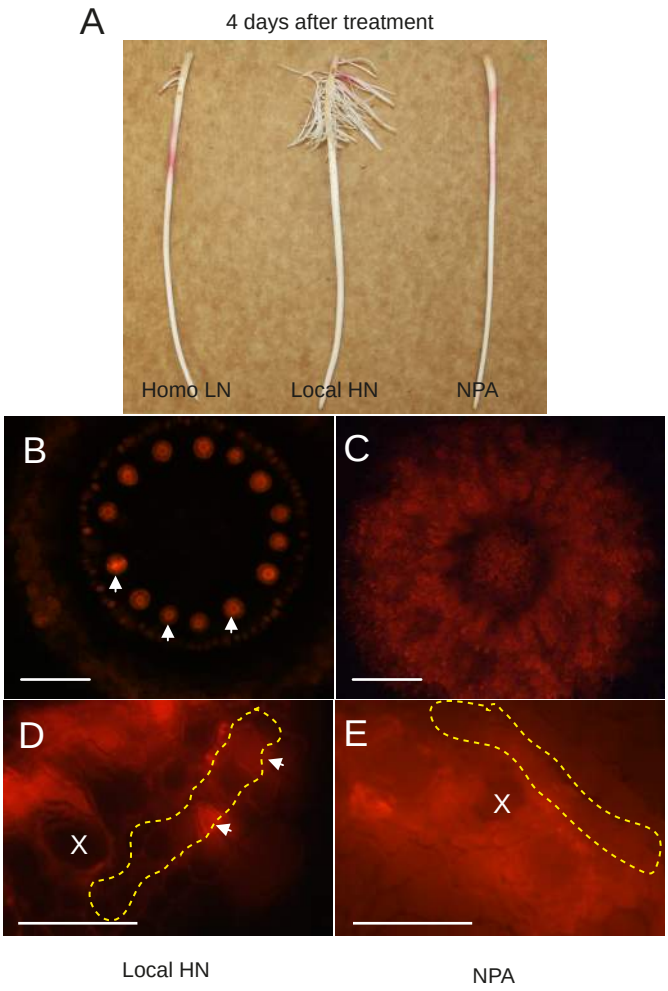
Supplemental Figure 1. Early pericycle cell divisions in shoot-borne roots. (A) Longitudinal section of a shoot-borne root and the first anticlinal divisions of pericycle (red arrows) and endodermis cells (yellow arrows). In the region 5-25 mm proximal of the root tip, peak differences of early pericycle cell divisions (see Figure 1D) were monitored between homogeneous low nitrate (homo LN) and local high nitrate (local HN) treatments. Scale bar: 50 µm. Early pericycle cell divisions in shoot-borne roots 12 (B) and 36 (C) hours after local high nitrate treatment (HAT). Error bars represent SE for four biological replicates. Asterisks denote a significant difference according to paired Student's *t* test (*: $p \leq 0.05$; **: $p \leq 0.01$). Homogeneous low nitrate: homo LN; local high nitrate: local HN.



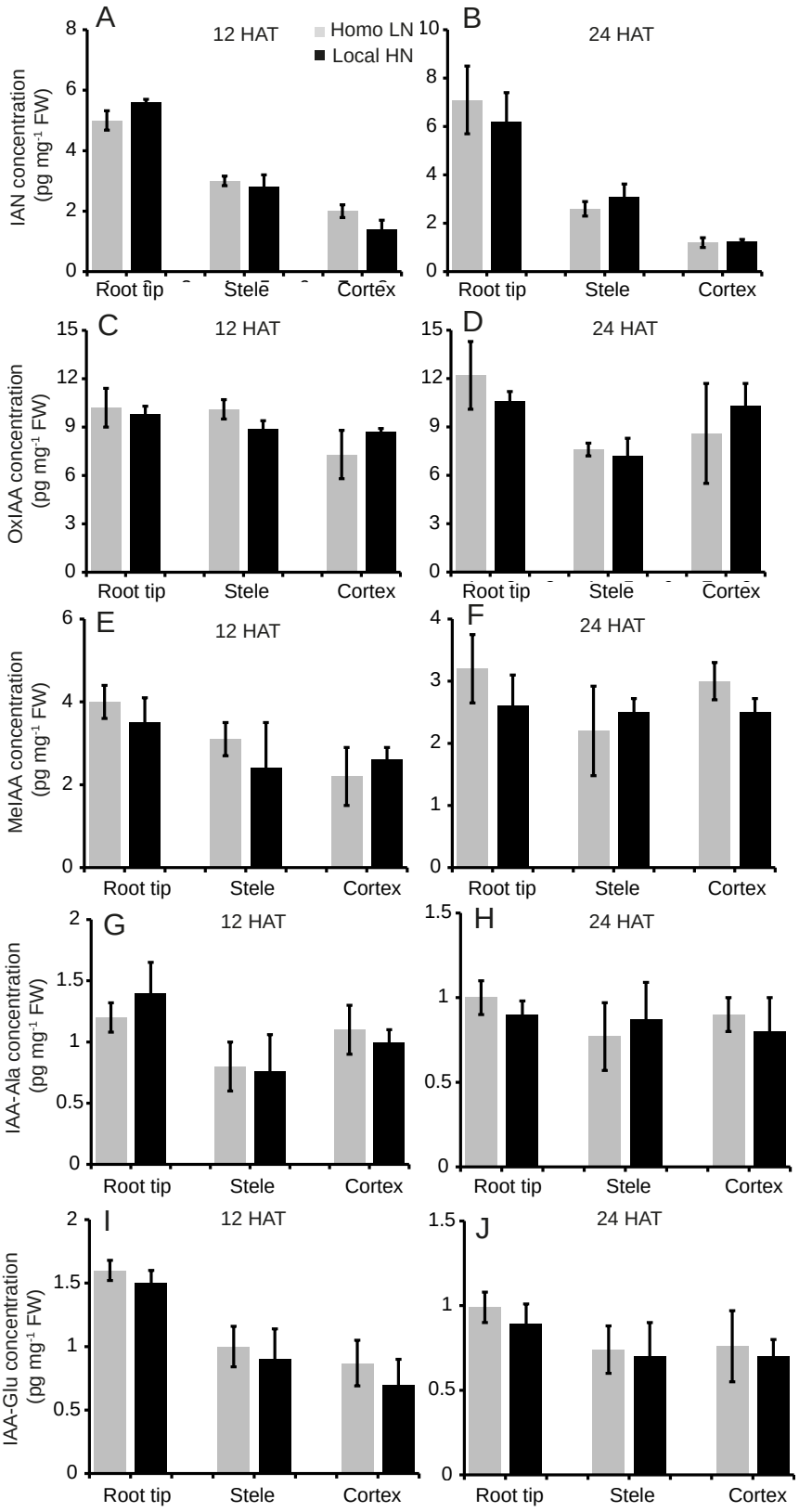
Supplemental Figure 2. Different stages of lateral root primordium formation are illustrated by representative images: (A) I-III, (B) IV-V, (C) VI-VII, (D) VIII. Scale bar: 50 µm.



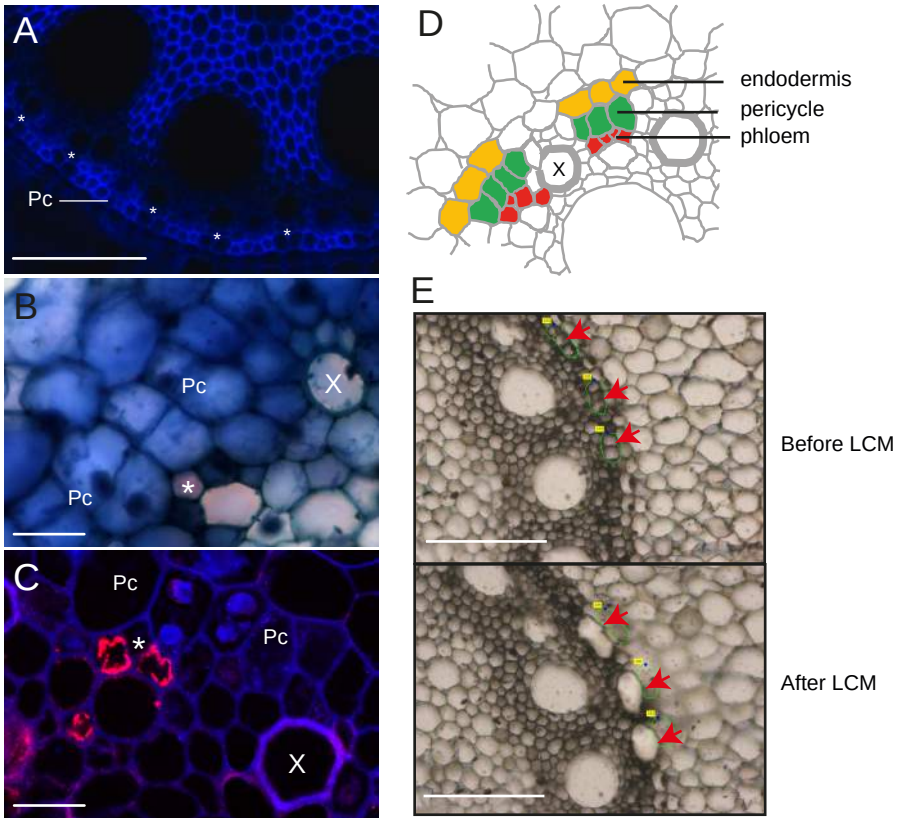
Supplemental Figure 3. Schematic overview of the components of the ubiquitin-dependent degradation system (SCF^{SKP2B} complex) induced in response to local high nitrate. Log_2-fold changes of gene expression (local HN versus homo LN) are illustrated by MapMan. DUB, deubiquitinating enzyme; E1, ubiquitin-activating enzymes; E2, Ubiquitin-conjugating enzymes; RING, C3HC4 RING-domain-containing ubiquitin E3 ligase; HECT, HECT type E3; APC, anaphase-promoting complex; E3, Ubiquitin ligases; Cullin, SKP, FBOX and RBX, subunit of the E3 ligase. Homogeneous low nitrate: homo LN; local high nitrate: local HN.



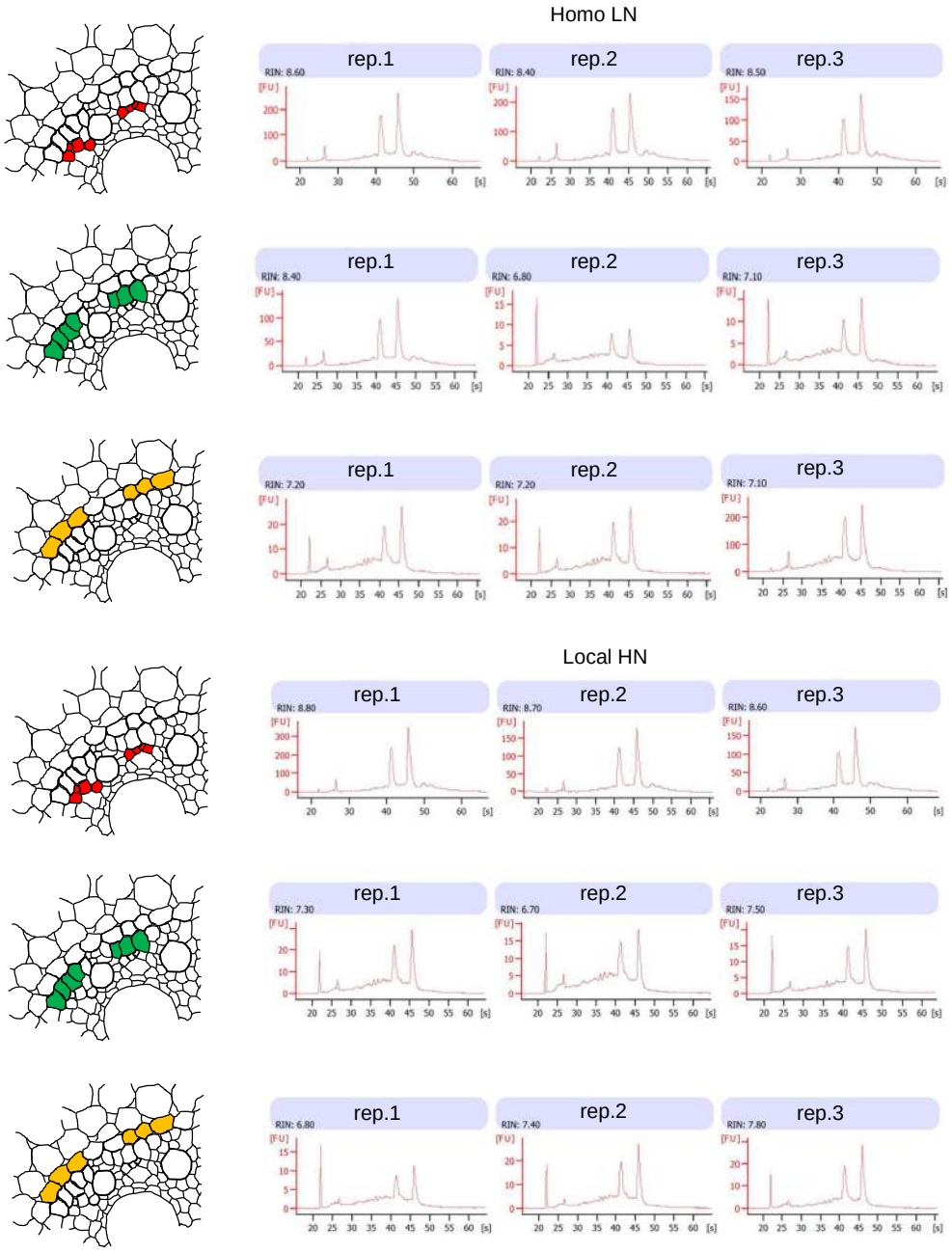
Supplemental Figure 4. Inhibition of lateral root formation and auxin response by NPA treatment. (A) Shoot-borne roots grown in homogeneous low nitrate, local high nitrate and NPA solution for 4 days. Comparison of vascular differentiation and auxin response between local high nitrate (B) and NPA (C) treatment. White arrows indicate auxin signal in the late meta-xylem. Auxin maxima signal in dividing pericycle cells (D) and those after NPA treatment (E). Yellow dotted boxes indicate the pericycle cell layer. X represents a xylem cell. Scale bar = 150 μm (B, C), 50 μm (D, E). Homogeneous low nitrate: homo LN; local high nitrate: local HN.



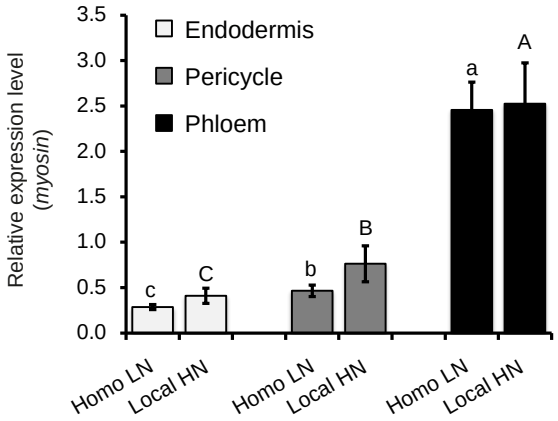
Supplemental Figure 5. MeIAA (A, B), IAN (C, D), OxIAA (E, F), IAA-Ala (G, H), IAA-Glu (I, J) concentrations in root tip, stele and cortex of shoot-borne roots induced by homogeneous low and local high nitrate 12 hours after treatment (HAT) and 24 HAT. Error bars represent SE for four biological replicates.



Supplemental Figure 6. Pericycle cells dividing at the phloem poles and illustration of LCM-microdissected cell types. Heterogeneous arrangements of pericycle cells alternated by phloem and xylem poles are shown by autofluorescence (A). (B) Lateral roots originating from early divisions of competent pericycle cells at the phloem poles illustrated by toluidine blue staining. (C) Auxin maxima and pericycle cell divisions are highlighted by DR5::RFP fluorescence and DAPI counterstaining. Pc: pericycle cell; asterisk: phloem, X: xylem cell. Scale bars: 150 µm (A), 20 µm (B, C). (D) Color-coded scheme of three cell types (endodermis, pericycle and phloem) isolated by LCM. X: meta-xylem vessel. (E) As an example micrographs taken before and after capturing pericycle cells are shown (red arrows).



Supplemental Figure 7. RNA quality of LCM-dissected cell types evaluated by the RNA integrity number (RIN). Color codes indicate phloem (red), pericycle (green), and endodermis (yellow) cells. Homogeneous low nitrate: homo LN; local high nitrate: local HN.



Supplemental Figure 8. Relative expression level of *ZmPIN1c* in three cell-types related to lateral root initiation. Different letters indicate significant differences among means when given a single homogeneous low nitrate (lower case letters) or local high nitrate (capital letters) treatment ($p \leq 0.05$ by one-way ANOVA analysis). Homogeneous low nitrate: homo LN; local high nitrate: local HN.

Supplemental Table 1. Comprehensively enriched GO terms obtained by singular enrichment analyses among differentially expressed genes in pair-wise comparisons between local high nitrate and homogeneous low nitrate treatments. [a]

GO term	Ontology	Description	Number in input list	Number in BG/Ref
GO:0006979	P	response to oxidative stress	37	227
GO:0042221	P	response to chemical stimulus	41	432
GO:0050896	P	response to stimulus	81	2128
GO:0006950	P	response to stress	74	1883
GO:0007050	P	cell cycle arrest	5	7
GO:0022402	P	cell cycle process	6	27
GO:0007049	P	cell cycle	6	35
GO:0016684	F	oxidoreductase activity, acting on peroxide as acceptor	38	243
GO:0004601	F	peroxidase activity	38	243
GO:0016209	F	antioxidant activity	38	257
GO:0005506	F	iron ion binding	53	858
GO:0020037	F	heme binding	46	664
GO:0046906	F	tetrapyrrole binding	46	665
GO:0016491	F	oxidoreductase activity	77	2115
GO:0009055	F	electron carrier activity	49	1046
GO:0030291	F	protein serine/threonine kinase inhibitor activity	5	7
GO:0004860	F	protein kinase inhibitor activity	5	7
GO:0004861	F	cyclin-dependent protein kinase inhibitor activity	5	7
GO:0019210	F	kinase inhibitor activity	5	7
GO:0016538	F	cyclin-dependent protein kinase regulator activity	5	10
GO:0019887	F	protein kinase regulator activity	5	12
GO:0019207	F	kinase regulator activity	5	12
GO:0005576	C	extracellular region	22	458
GO:0031224	C	intrinsic to membrane	48	1591
GO:0016021	C	integral to membrane	48	1574
GO:0044425	C	membrane part	50	1975

[a] SEA was performed with agriGO (http://bioinfo.cau.edu.cn/agriGO/analysis.php) comparing the differentially expressed genes to all expressed genes. GO terms were declared enriched when FDR ≤0.01. Differentially expressed genes were compared between local high nitrate and homogeneous low nitrate at 24 h treatments (513 of 582 differentially expressed genes were annotated).

Supplemental Table 2. Determination of overrepresented and underrepresented functional classes among differentially expressed genes (Fc ≥2; FDR ≤5%) that were functionally annotated by MapMan. Fold changes (local HN vs homo LN) are given as logarithmic (log_2) values. Homogeneous low nitrate: homo LN; local high nitrate: local HN.

Bin[a]	Functional group	Expressed genes[b]	Differentially expressed genes[c]	Representation[d]	*p*-value
1	**Photosynthesis**	157	5		
2	**Major CHO metabolism**	119	3		
3	**Minor CHO metabolism**	139	5		
4	**Glycolysis**	90	1		
5	**Fermentation**	20	4		
6	**Gluconeogenesis/ glyoxylate cycle**	12	1		
7	**OPP**	33	3		
8	**TCA / org. transformation**	74			
9	**Mitochondrial e-transport / ATP synthesis**	126			
10	**Cell wall**	327	21		
11	**Lipid metabolism**	376	13	+	0.0102
12	**N-metabolism**	41	7		
13	**Amino acid metabolism**	317	11	+	0.0192
14	**S-assimilation**	10	5		
15	**Metal handling**	63	4		
16	**Secondary metabolism**	300	13		
17	**Hormone metabolism**	417	21		
18	**Co-factor and vitamine met.**	73	1		
19	**Tetrapyrrole synthesis**	49	2		

Bin[a]	Functional group	Expressed genes[b]	Differentially expressed genes[c]	Representation[d]	*p*-value
20	**Stress**	734	32	+	0.0082
21	**Redox regulation**	214	10		
22	**Polyamine metabolism**	15			
23	**Nucleotide metabolism**	176	1		
24	**Biodegradation of Xenobiotics**	30	1		
25	**C1-metabolism**	25			
26	**Miscelleanous**	1043	60		
27	**RNA**	3071	50	-	<0.0001
28	**DNA**	526	2		
29	**Protein**	3551	93	+	<0.0001
30	**Signalling**	1235	20	-	<0.0001
31	**Cell**	870	31	+	0.0001
32	**MicroRNA, natural antisense**	1			
33	**Development**	526	5		
34	**Transport**	1023	46	+	0.0028
35	**Not assigned**	9281	151	-	<0.0001
	MapMan Sum	**25064**	**622**		
	Expressed DEG Sum	**22796**	**582**		

[a] Each Bin consists of genes of similar biological function.

[b] All genes expressed in shoot-borne root treated by local high nitrate or homogeneous low nitrate.

[c] Subset of expressed genes that are differentially expressed between local high nitrate and homogeneous low nitrate treatment (Fc ≥2; FDR ≤5%).

[d] Over (+) or underrepresentation (-) of differentially expressed genes in functional groups relative to the distribution of all expressed genes.

Supplemental Table 3. Gene list of the ubiquitin-dependent protein degradation pathway extracted from bin29 of the MapMan analysis.

BinCode	BinName	Gene ID	Description	log_2Fc
29.5.11.4.2	**protein.degradation. ubiquitin.E3.RING**	GRMZM2G021796	E3 ubiquitin-protein ligase EL5	1.75
29.5.11.4.2	**protein.degradation. ubiquitin.E3.RING**	GRMZM2G025255	zinc finger (C3HC4-type RING finger) family protein	2.84
29.5.11.4.2	**protein.degradation. ubiquitin.E3.RING**	GRMZM2G027375	armadillo/beta-catenin repeat family protein / U-box domain-containing protein	1.12
29.5.11.4.2	**protein.degradation. ubiquitin.E3.RING**	GRMZM2G045286	zinc finger (C3HC4-type RING finger) family protein	1.84
29.5.11.4.2	**protein.degradation. ubiquitin.E3.RING**	GRMZM2G052344	zinc finger (C3HC4-type RING finger) family protein	1.64
29.5.11.4.2	**protein.degradation. ubiquitin.E3.RING**	GRMZM2G075782	zinc finger (C3HC4-type RING finger) family protein	2.26
29.5.11.4.2	**protein.degradation. ubiquitin.E3.RING**	GRMZM2G100090	armadillo/beta-catenin repeat family protein / U-box domain-containing protein	1.1
29.5.11.4.2	**protein.degradation. ubiquitin.E3.RING**	GRMZM2G115988	protein protein binding protein	-1.25
29.5.11.4.2	**protein.degradation. ubiquitin.E3.RING**	GRMZM2G137440	zinc finger (C3HC4-type RING finger) family protein	5.4
29.5.11.4.2	**protein.degradation. ubiquitin.E3.RING**	GRMZM2G144782	zinc finger (C3HC4-type RING finger) family protein	1.66
29.5.11.4.2	**protein.degradation. ubiquitin.E3.RING**	GRMZM2G152461	zinc finger (C3HC4-type RING finger) family protein	4.01
29.5.11.4.2	**protein.degradation. ubiquitin.E3.RING**	GRMZM2G324111	protein RING-H2 finger protein ATL5H precursor	4.17
29.5.11.4.2	**protein.degradation. ubiquitin.E3.RING**	GRMZM2G417089	protein zinc finger, RING-type	2.23
29.5.11.4.3.2	**protein.degradation. ubiquitin.E3.SCF.FBOX**	AC204641.5_FG001	kelch repeat-containing F-box family protein	5.12
29.5.11.4.3.2	**protein.degradation. ubiquitin.E3.SCF.FBOX**	GRMZM2G004521	kelch repeat-containing F-box family protein	3.14
29.5.11.4.3.2	**protein.degradation. ubiquitin.E3.SCF.FBOX**	GRMZM2G014022	protein F-box domain containing protein	1.72
29.5.11.4.3.2	**protein.degradation. ubiquitin.E3.SCF.FBOX**	GRMZM2G025783	kelch repeat-containing F-box family protein	1.51

BinCode	BinName	Gene ID	Description	log_2Fc
29.5.11.4.3.2	**protein.degradation.ubiquitin.E3.SCF.FBOX**	GRMZM2G100121	FBL17; ubiquitin-protein ligase	2.33
29.5.11.4.3.2	**protein.degradation.ubiquitin.E3.SCF.FBOX**	GRMZM2G110057	protein F-box protein interaction domain containing protein	3.07
29.5.11.4.3.2	**protein.degradation.ubiquitin.E3.SCF.FBOX**	GRMZM2G138176	SKP2B; F-box domain, cyclin-like; protein F-box/ Leucine-rich repeat protein	4.27
29.5.11.4.3.2	**protein.degradation.ubiquitin.E3.SCF.FBOX**	GRMZM2G171616	FBL6 | EBF1 (EIN3-BINDING F BOX PROTEIN 1); protein binding / ubiquitin-protein ligase	2.29
29.5.11.4.3.2	**protein.degradation.ubiquitin.E3.SCF.FBOX**	GRMZM2G325650	kelch repeat-containing F-box family protein	2.27
29.5.11.4.3.3	**protein.degradation.ubiquitin.E3.SCF.cullin**	GRMZM2G551108	ubiquitin-protein ligase	1.18
29.5.11.4.5.2	**protein.degradation.ubiquitin.E3.BTB/POZ Cullin3.BTB/POZ**	GRMZM2G428119	ATBPM4 (BTB-POZ and MATH domain 4); protein binding	1.64
29.5.11.5	**protein.degradation.ubiquitin.ubiquitin protease**	GRMZM2G038126	protein 26S protease regulatory subunit 6B	1.62

Supplemental Table 4. Gene list of cell cycle related genes extracted from bin31 of the MapMan analysis.

BinCode	BinName	Gene ID	Description	log_2Fc
31.2	**cell.division**	GRMZM2G068193	CDKB2;1 (cyclin-dependent kinase B2;1)	1.45
31.2	**cell.division**	GRMZM2G070115	CDKB2;2 (cyclin-dependent kinase B2;2)	2.55
31.2	**cell.division**	GRMZM2G495626	CDKB1;1 (cyclin-dependent kinase B 1;1)	3.83
31.3	**cell.cycle**	GRMZM2G005619	CYCB1;3 (cyclin-dependent protein kinase regulator), G2/mitotic-specific cyclin 1	5.07
31.3	**cell.cycle**	GRMZM2G025200	CYCB1;2 (cyclin-dependent protein kinase regulator), G2/mitotic-specific cyclin 1	1.14
31.3	**cell.cycle**	GRMZM2G034647	CYCB1;2 (cyclin-dependent protein kinase regulator), G2/mitotic-specific cyclin 1	3.59
31.3	**cell.cycle**	GRMZM2G062453	CYCB1;4 (cyclin-dependent protein kinase regulator), G2/mitotic-specific cyclin 1	1.53
31.3	**cell.cycle**	GRMZM2G073003	CYCB1;6 (cyclin-dependent protein kinase regulator), G2/mitotic-specific cyclin 1	5.1
31.3	**cell.cycle**	GRMZM2G073671	CYCB2;1 (cyclin-dependent protein kinase regulator), G2/mitotic-specific cyclin 2	1.73
31.3	**cell.cycle**	GRMZM2G138886	CYCB2;2 (cyclin-dependent protein kinase regulator), G2/mitotic-specific cyclin 2	3.97
31.3	**cell.cycle**	GRMZM2G310115	CYCB1;1 (cyclin-dependent protein kinase regulator), G2/mitotic-specific cyclin 1	3.25
31.3	**cell.cycle**	GRMZM2G037926	KRP4, ICK6 | cyclin-dependent protein kinase inhibitor	-1.14
31.3	**cell.cycle**	GRMZM2G084570	KRP2; cyclin-dependent protein kinase inhibitor	-1.8
31.3	**cell.cycle**	GRMZM2G101613	cyclin-dependent protein kinase inhibitor	-1.45
31.3	**cell.cycle**	GRMZM2G116885	KRP3, ICK6 | cyclin-dependent protein kinase inhibitor	-2.94
31.3	**cell.cycle**	GRMZM2G157510	KRP3, ICK6 | cyclin-dependent protein kinase inhibitor	-4.16
31.3	**cell.cycle**	GRMZM5G854731	KRP1; cyclin-dependent protein kinase inhibitor	-2.2

Supplemental Table 5 Internal standards used in the IAA detection by UPLC-ESI-MS/MS analysis.

Name	Abbreviation	Molecular mass	Ionization mode	Quantification ion	First target ion	Second target ion
Indole-3-acetonitrile	IAN	156.2	ESI+	89.9	117.0	130.0
Indole-3-acetamide	IAM	174.2	ESI+	77.0	103.0	130.4
Indole-3-acetic acid	IAA	175.2	ESI+	77.0	103.0	130.5
[$^2H_5$] Indole-3-acetic acid	D-IAA	180.2	ESI+	106.3	180.2	-
Indole-3-acetic acid methylester	IAAMe	189.2	ESI+	76.9	103.0	130.0
Indole-3-acetic acid ethylester	IAAEt	203.2	ESI+	77.0	103.0	130.0
Indole-3-L-alanine	IAAla	247.0	ESI+	89.9	103.0	130.0
Indole-3-L-isoleucin	IAiLeu	288.4	ESI+	86.0	103.0	130.0
Indole-3-L-tryptophan	IATrp	361.4	ESI+	130.0	188.1	205.1
Indole-3-L-glutamic acid	IAGlu	304.3	ESI+	103.0	130.0	147.9
2-oxindole-3-acetic acid	OxIAA	191.2	ESI+	128.0	132.0	146.0

Supplemental Text 1 Detailed procedure of MS data processing using TargetLynx V4.1 SCN 904.

The column temperature was set to 40 °C and the autosampler was set to 4 °C. The mobile phases were H_2O containing 0.1 % FA (A), MeOH containing 0.1 % FA. The mobile phase flow was 0.4 ml min^{-1}. The gradient conditions were as follows: A, 90 % in 0 – 0.3 min; 90 – 80 % in 0.3 – 0.7 min; 80 – 40 % in 0.7 – 8 min; 40 – 1 % in 8 – 8.5 min; 1 % in 8.5 – 8.9 min; 1 – 90 % in 8.9 – 9.0 min; 90 % in 9.0 – 10.0 min.

The Xevo TQ MS operated in both ESI+ and ESI- ion mode. The electrospray capillary voltage was 2.45 kV with a cone voltage of 20 V. The cone and desolvation gas flows were set to 20 and 1000 L h^{-1}. The cone and desolvation gas flows were set to 50 and 1000 L h^{-1}. The source and desolvation temperature were 150 and 650 °C. The collision energy of the MS-MS was between 10 and 50 eV. For the quantification of the analytes we used three fragment ions one for quantification two for qualification and for the internal standards two fragment ions were used (Tab. S1). MS data processing was done by using TargetLynx V4.1 SCN 904.