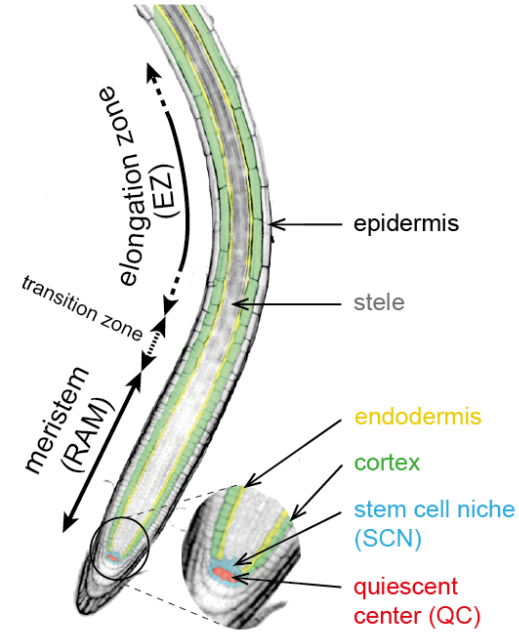
Supplementary Information

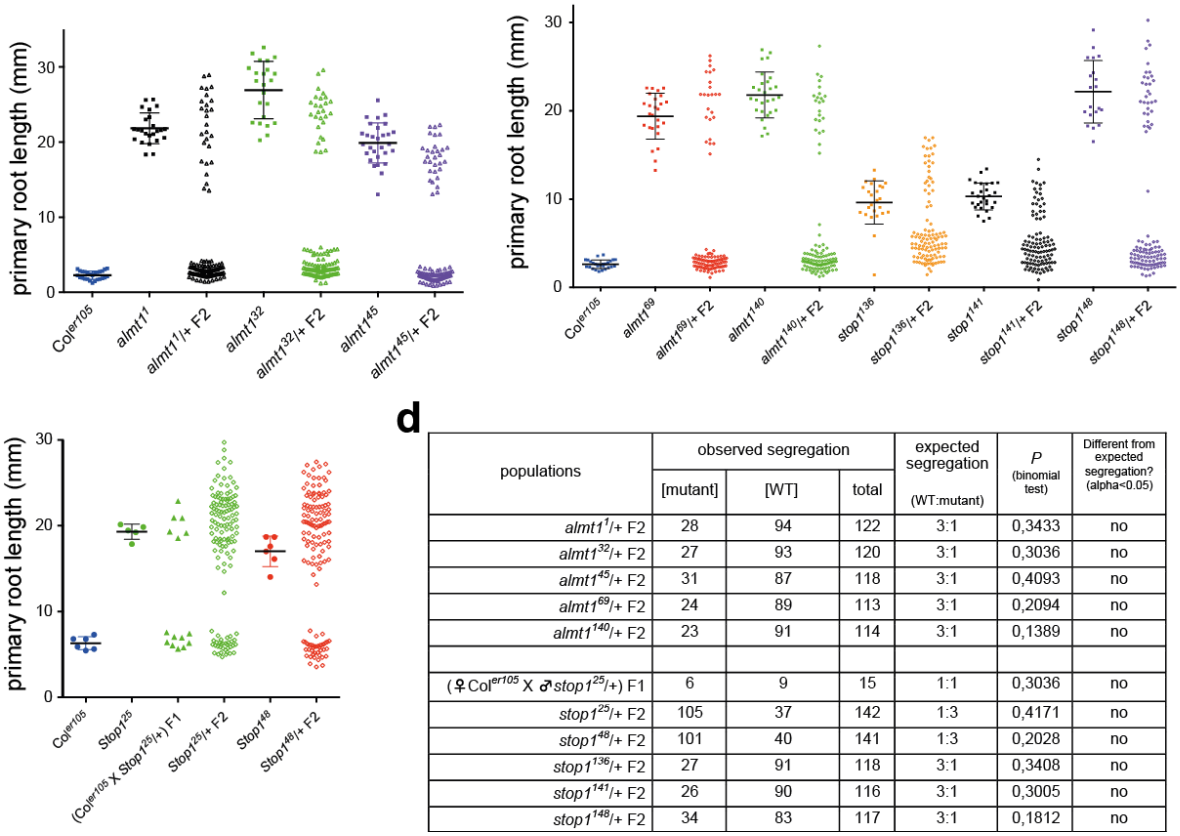
a



b

Lab number	Genomic position from ATG	prediction
almt1 alleles		
almt1^{1}	G974A	Defective splicing of intron 3 (3')
almt1^{32}	G1201A	W255stop
almt1^{45}	G334A	G71E
almt1^{51}	G881A	Defective splicing of intron 3 (5')
almt1^{61}	C471T	Q117stop
almt1^{69}	G3A	M1I (translational frameshift at next ATG
almt1^{140}	G782A	C176Y
almt1^{154}	G816A	W187stop
stop1 alleles		
Stop1^{25}	C1207T	Q403stop
Stop1^{48}	C1297T	Q433stop
stop1^{60}	G36A	W12stop
stop1^{67}	G36A	W12stop
stop1^{90}	C322A	Q108stop
stop1^{115}	G122A	W41stop
stop1^{136}	C784T	H262Y
stop1^{139}	G1057A	E353K
stop1^{141}	C934T	Q312stop
stop1^{148}	G793A	G265R

c



d

populations	observed segregation			expected segregation	*P* (binomial test)	Different from expected segregation? (alpha<0.05)
	[mutant]	[WT]	total	(WT:mutant)		
almt1^{1}/+ F2	28	94	122	3:1	0,3433	no
almt1^{32}/+ F2	27	93	120	3:1	0,3036	no
almt1^{45}/+ F2	31	87	118	3:1	0,4093	no
almt1^{69}/+ F2	24	89	113	3:1	0,2094	no
almt1^{140}/+ F2	23	91	114	3:1	0,1389	no
(♀Col^{er105} X ♂*stop1*^{25}/+) F1	6	9	15	1:1	0,3036	no
stop1^{25}/+ F2	105	37	142	1:3	0,4171	no
stop1^{48}/+ F2	101	40	141	1:3	0,2028	no
stop1^{136}/+ F2	27	91	118	3:1	0,3408	no
stop1^{141}/+ F2	26	90	116	3:1	0,3005	no
stop1^{148}/+ F2	34	83	117	3:1	0,1812	no

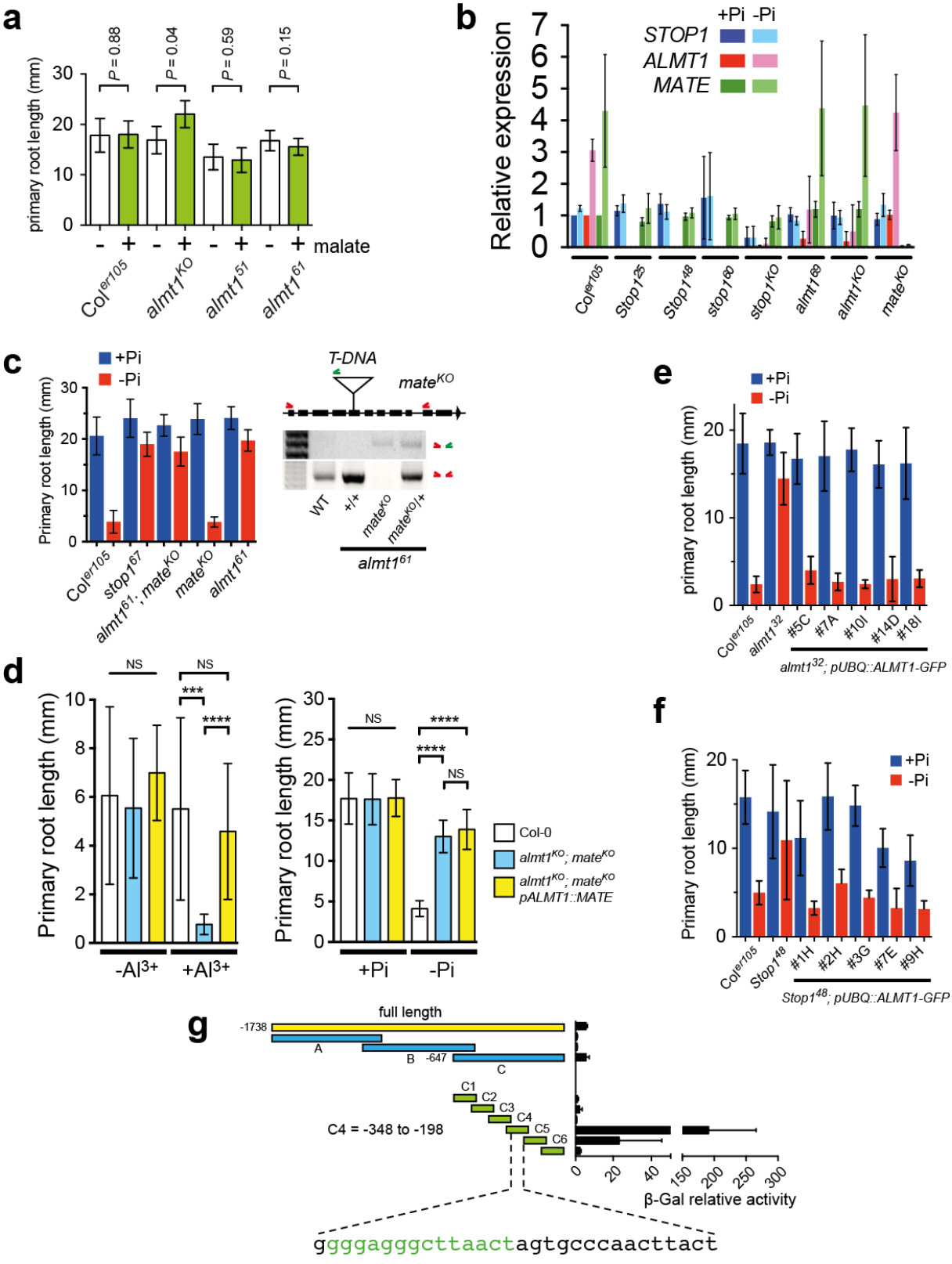
Supplementary Figure 1: Genetic analysis of *almt1* and *stop1* mutations.

(a) Scheme depicting the different cell types of the primary root tip.

(b-d) Genetic analysis of the *almt1* and *stop1* mutations.

(b) Table of the molecular lesions of *almt1* and *stop1* alleles.

(c, d) Segregation pattern of the mutant phenotypes in F1 or F2 populations from a cross between mutant and WT (+). Seedlings were grown for 7 days under –Pi prior to measuring the primary root length (mean (not for segregating populations) +/- s.d., *n* = 5–29 seedlings per line) (b), and statistical analysis of segregation patterns (c).



Supplementary Figure 2: Expression of *STOP1*, *ALMT1* and *MATE*, and complementation analysis.

(a) Under +Pi, exogenous malate does not inhibit primary root growth. WT and *almt1* seedlings grown under +Pi for 2 days were transferred for 6 days to +Pi with or without 200 μM malate (mean +/- s.d., *n* = 7–10 seedlings per condition).

(b) Gene expression analysis. Seedlings of the indicated genotypes were grown for 5 days under +Pi and transferred for 24 h to +Pi or –Pi medium and roots collected for RNA extraction followed by qRT-PCR on *STOP1*, *ALMT1* and *MATE* genes (mean +/- s.d., *n* = 3 independent experiments, each with three technical replicates). Expression levels are normalized relatively to the WT (Col^{er105}) control grown under +Pi.

(c) Analysis of the *mate*^{KO} lines under –Pi.
Top: Primary root length of the *mate*^{KO} and *almt1*^{61};*mate*^{KO} mutants. Seedlings were grown for 5 days under +Pi or –Pi (mean +/- s.d., *n* = 8–18 seedlings per line and condition). The experiment was performed twice with consistent results; one experiment is shown. Bottom: genotyping of the *mate*^{KO} mutant. PCR results with the indicated primers (red and green arrowheads; see Supplementary Tab. 1 for sequences) on genomic DNA from the WT (Col^{er105}) and from *almt1*^{61} lines with the indicated genotypes at the *MATE* locus (+/+, WT; *mate*^{KO}, homozygous KO mutant; *mate*$^{KO/+}$, heterozygous).

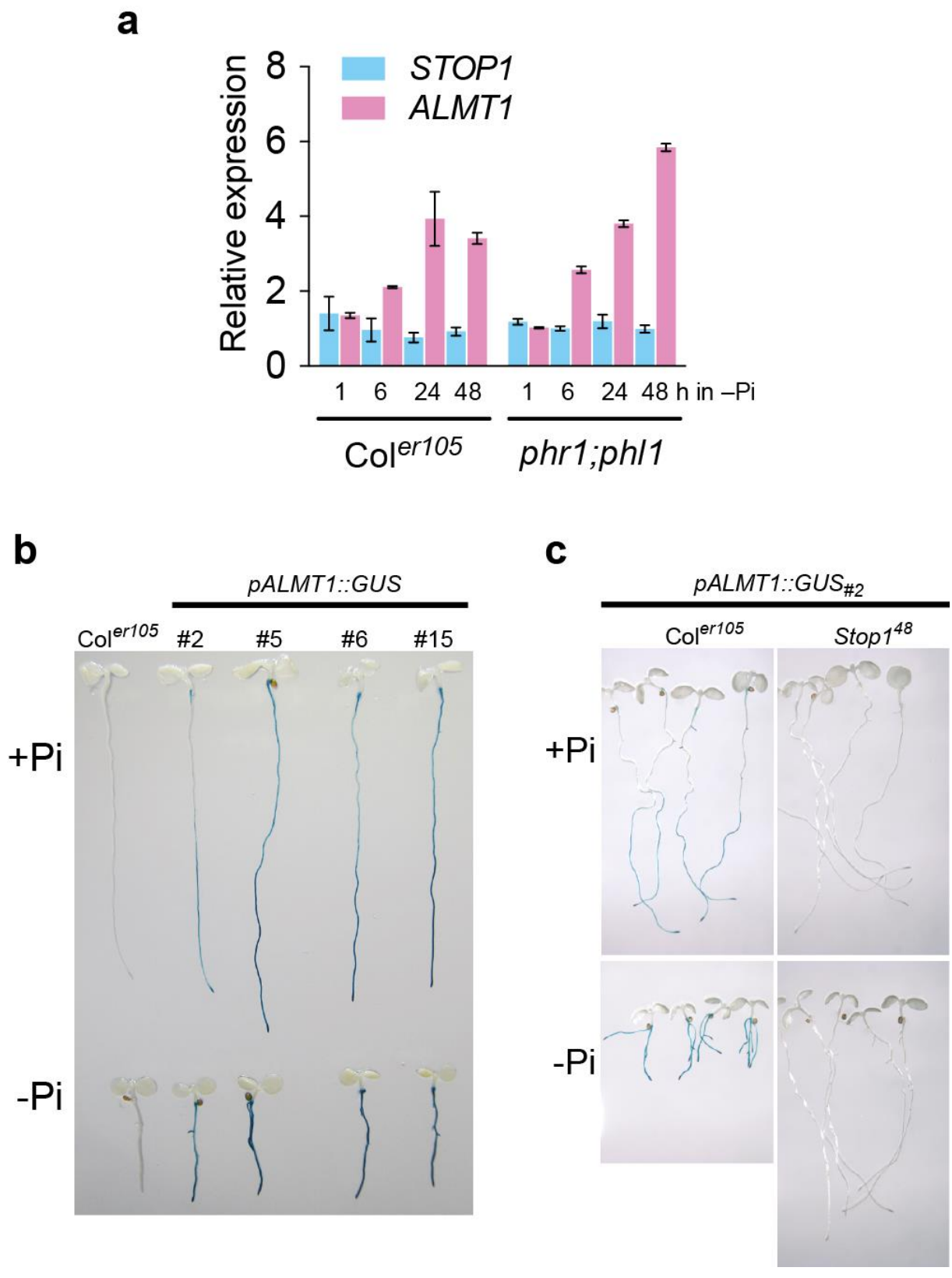
(d) *pALMT1::MATE* rescues the *almt1*^{KO};*mate*^{KO} double mutant for resistance to Al^{3+} but not for the response to –Pi. Left: seedlings were grown five days in 0 or 4 μM Al^{3+} (*n* = 10-18). Right: seedlings were grown six days in + or –Pi (*n* = 33-39). Mean +/- s.d.; two-tailed *t*-test, **** P < 0.0001; *** P < 0.001; NS, not significant. The experiment was performed twice with consistent results; one experiment is shown.

(e) Complementation of *almt1*^{32} mutant with the *pUBQ::ALMT1-GFP* construct (five independent transgenic lines). Seedlings were grown for 5 days under –Pi and the primary root lengths measured (mean +/- s.d., *n* = 11–16 seedlings per line and condition). The experiment was performed twice with consistent results; one experiment is shown.

(f) Complementation of *Stop1*^{48} mutant with the *pUBQ::ALMT1-GFP* construct

(five independent transgenic lines). Seedlings were grown for 5 days under –Pi and the primary root lengths measured (mean +/- s.d., *n* = 4–8 seedlings per line and condition).

(g) Yeast one-hybrid assay of STOP1 and *pALMT1*. Coloured bars represent parts of *pALMT1* fused to LacZ used in the assay; they are numbered with respect to first ATG of the *ALMT1* coding sequence. β-Gal activity is calculated relatively to the density of cells (see Methods) (mean +/- s.d., *n* = 3 independent experiments, each with two biological replicates per condition). The sequence in green indicates the STOP1-binding site found previously[28].

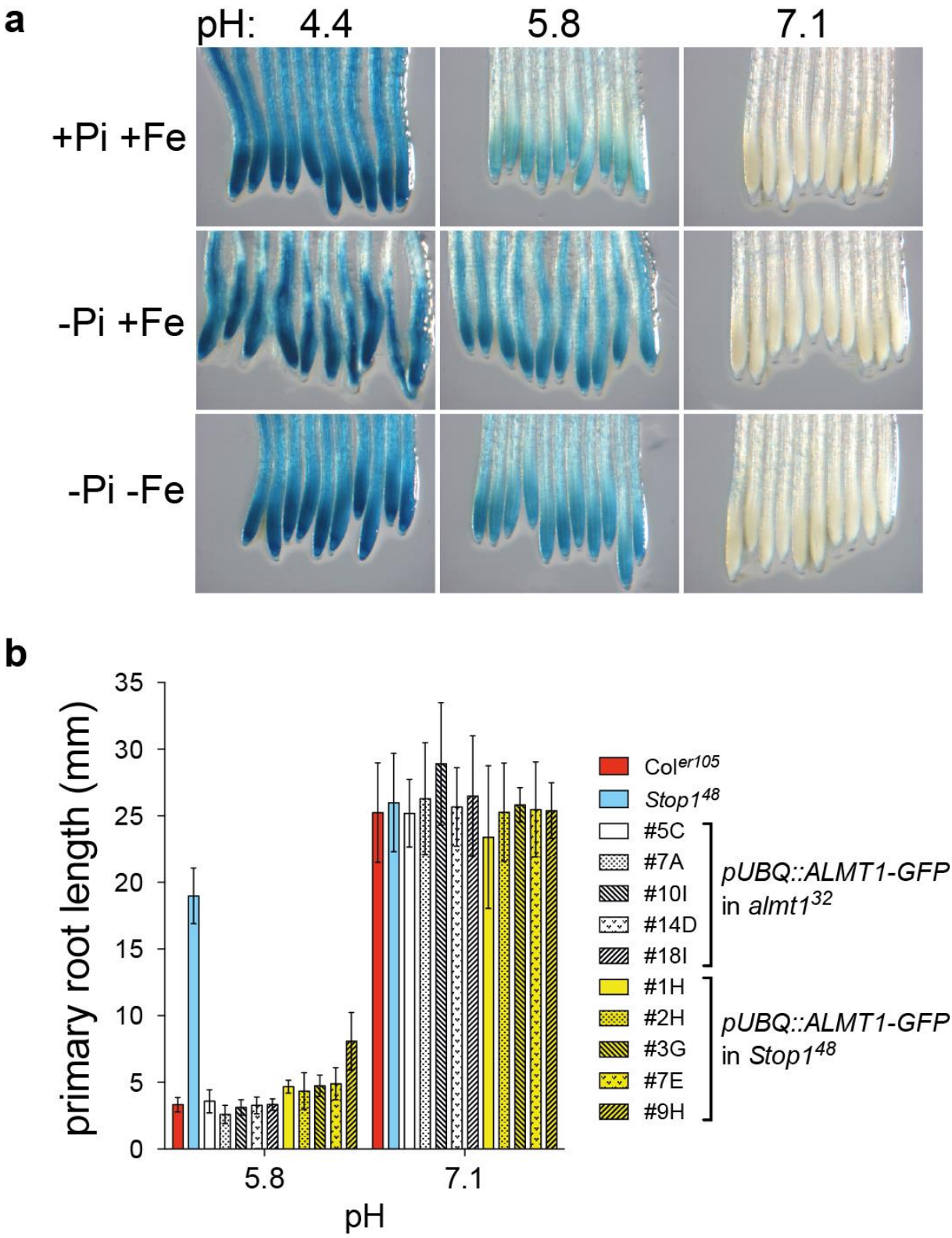


Supplementary Figure 3: *ALMT1* expression in different genetics backgrounds.

(a) Kinetics of *STOP1* and *ALMT1* expression (RT-qPCR) in WT and the *phr1*;*phl1* double mutant. Seedlings grown 5 days under +Pi were transferred for 1 to 48 h to –Pi. (mean +/- s.d.).

(b,c) Pattern of *ALMT1* expression in the primary root.
(b) Representative seedlings of four independent lines homozygous for the *pALMT1::GUS* construct were grown for 6 days under +Pi or –Pi prior the GUS staining (1h). Untransformed WT (Col^{er105}) is shown as a negative control of the GUS staining. Two independent experiments were performed with consistent results and one representative experiment is shown.

(c) *Stop1*^{48} abolishes the expression of *ALMT1*. WT (Col^{er105}) and *Stop1*^{48} seedlings homozygous for the *pALMT1::GUS*$_{\#2}$ construct were grown for 6 days under +Pi or –Pi prior the GUS staining. Two independent experiments were performed with consistent results and one representative experiment is shown.

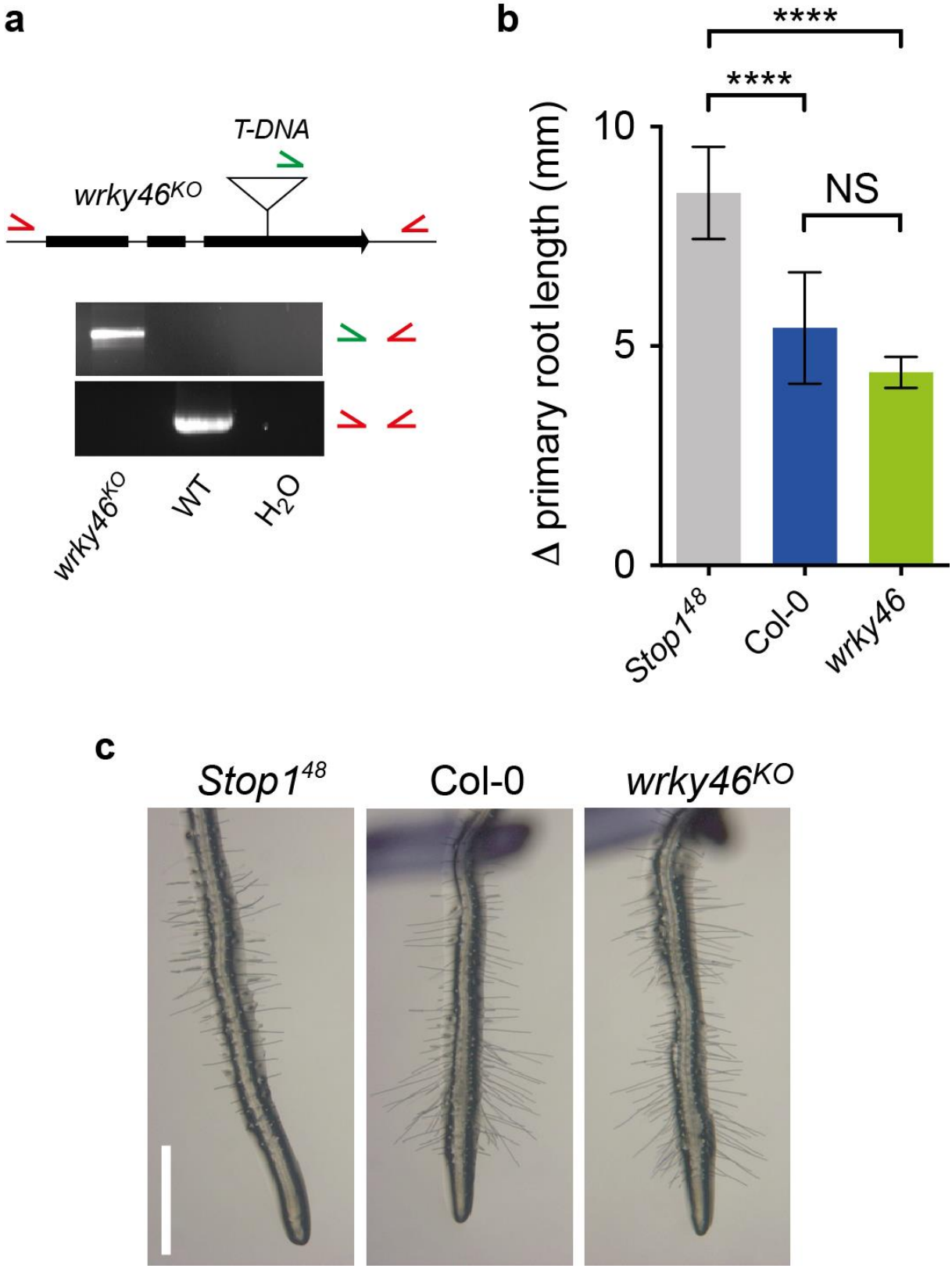


Supplementary Figure 4: Effect of the pH on the expression of *ALMT1* and on the primary root growth under –Pi.

(a) *pALMT1::GUS* expression at different pH.

Four-day old *pALMT1::GUS*$_{\#2}$ seedlings grown under +Pi at pH 7.1 were transferred 48 h in + or –Pi at the indicated pH before GUS staining. Two independent experiments were performed with consistent results and one representative experiment is shown.

(b) At pH 7.1, the constitutive expression of *ALMT1* does not promote a short root under –Pi. The *UBQ::ALMT1-GFP* construct has been introduced in the *almt1*[32] and *Stop1*[48] mutants and five independent transgenic lines selected. Homozygous seedlings were sown on –Pi+Fe plates at pH 5.8 or 7.1 and the primary root lengths measured after 6 days (mean +/- s.d., *n* = 8-15). Note that at pH 5.8, the *UBQ::ALMT1-GFP* construct complements both the *almt1*[32] and *Stop1*[48] mutants, but it does not confer a short primary root at pH 7.1.

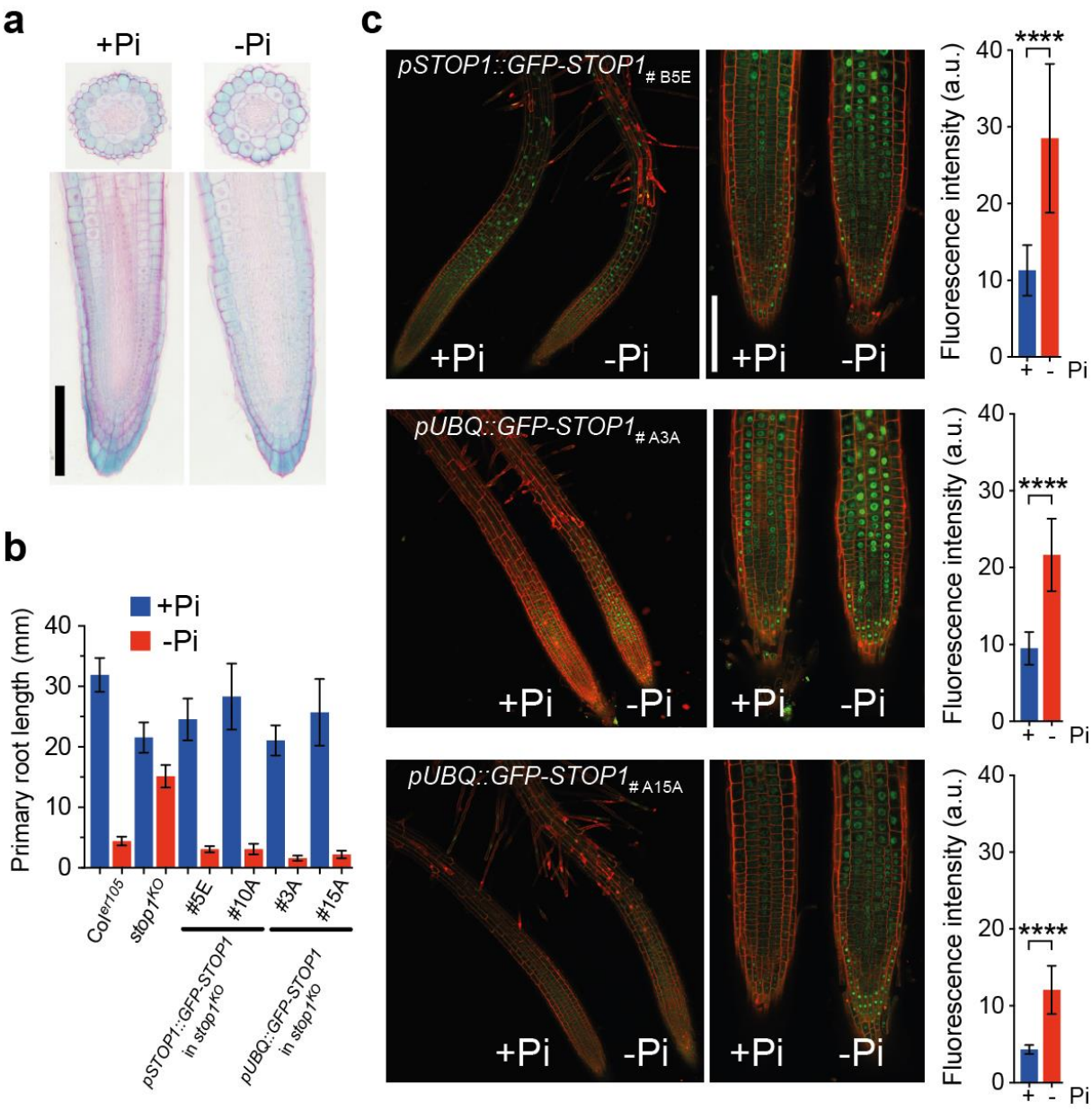


Supplementary Figure 5: Analysis of the *wrky46*^{KO} mutant under –Pi.

(a) Genotyping of the *wrky46*^{KO} mutant. PCR results with the indicated primers (red and green arrowheads; see Supplementary Tab. 1 for sequences) on genomic DNA from the WT (Col-0) and the *wrky46*^{KO} mutant.

(b) Δ primary root length of the *Stop1*^{48}, WT (Col-0) and *wrky46*^{KO} lines. Four-day old seedlings grown under +Pi were transferred 48 h under –Pi before measuring root length and photographing the root tip (mean +/-s.d., n = 5-10; two-tailed *t*-test; **** *P*<0.0001; NS, not significant).

(c) Pictures of the root tip of the indicated lines grown in (b). Scale, 1mm.

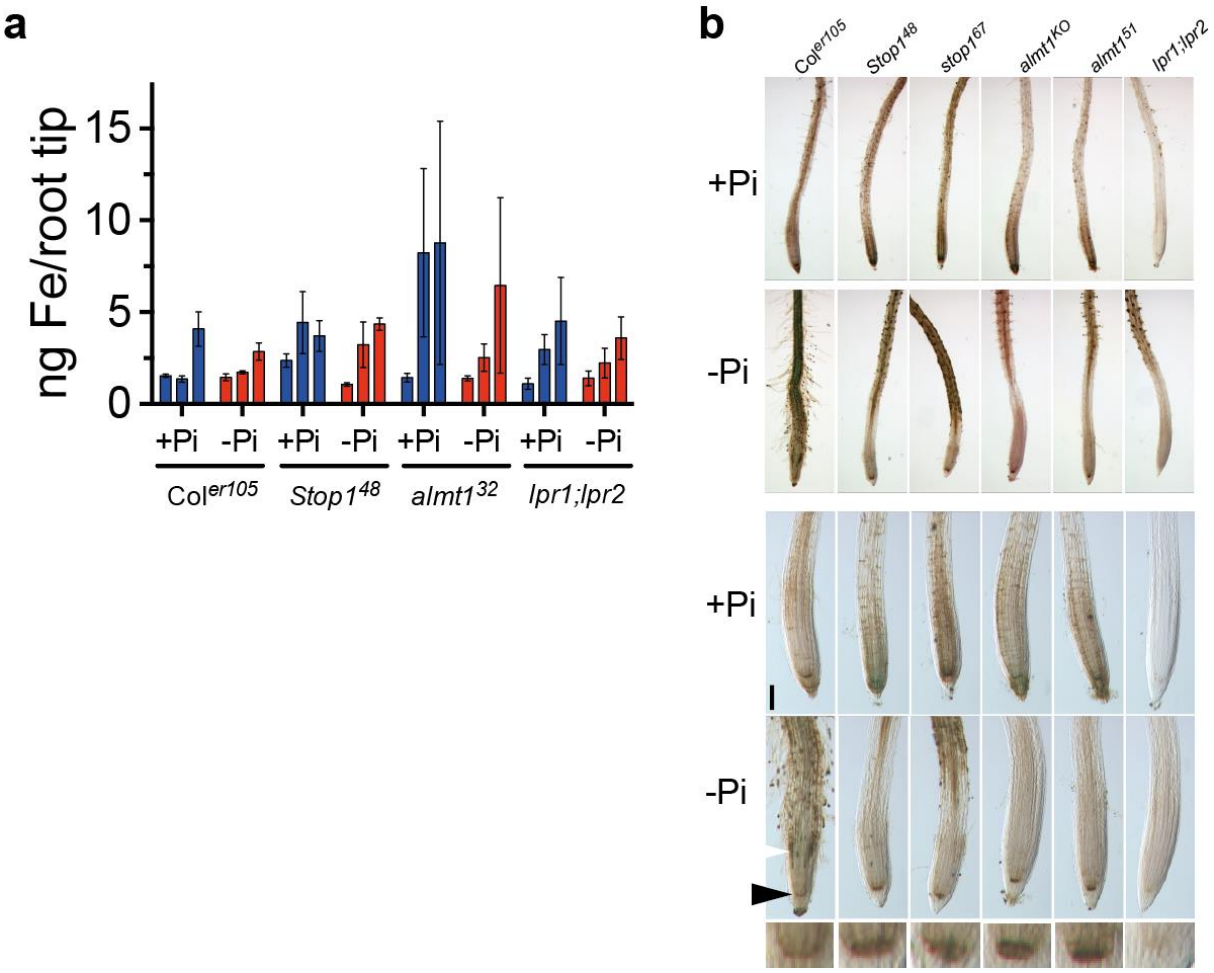


Supplementary Figure 6: Expression of STOP1.

(a) Pattern of *STOP1* expression in the primary root tip. Transverse (top) and longitudinal (bottom) sections of the root tip of *pSTOP1::GUS* (in WT). Seedlings were grown for 5 days under +Pi and transferred for 48 h to +Pi or –Pi prior GUS staining. Two independent experiments were performed with consistent results and one representative experiment is shown. Scale bar, 100 μm.

(b) Complementation of the *stop1*^{KO} mutant with *pSTOP1::GFP-STOP1* or *pUBQ::GFP-STOP1* constructs (2 independent transgenic lines per construct). Seedlings were grown for 6 days to +Pi or –Pi medium and the primary root lengths measured (mean +/- s.d., *n* = 10–15 seedlings per line and condition).

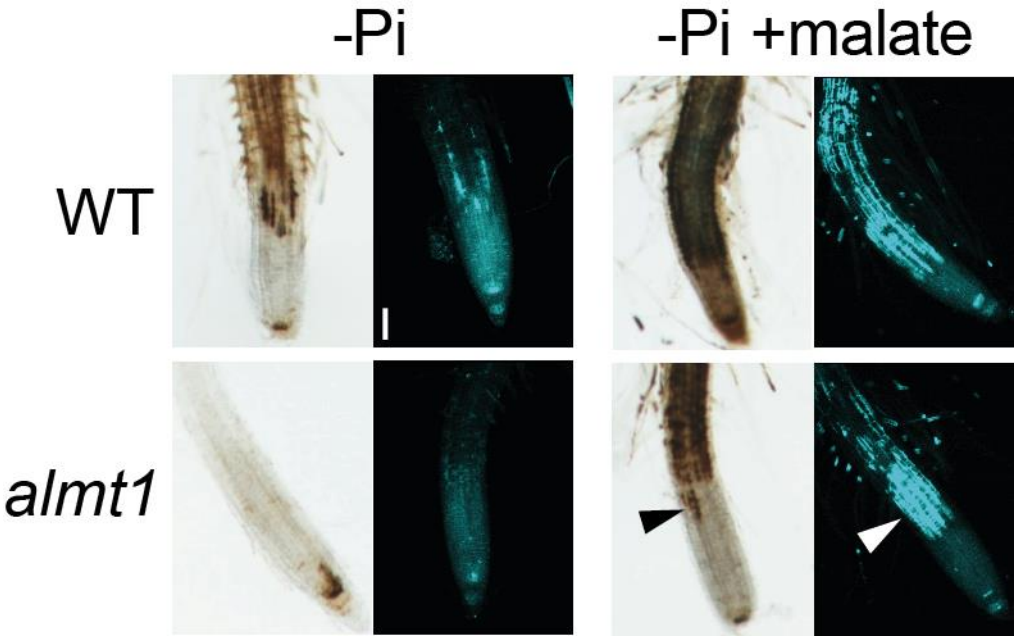
(c) GFP-fluorescence of GFP-STOP1 in the primary root tip. Five day-old *stop1*^{KO};*pSTOP1::GFP-STOP1* (1 line, independent from that in Fig. 1g) and *stop1*^{KO};*pUBQ::GFP-STOP1* (2 independent lines) seedlings grown under +Pi were transferred for 24 h +Pi or –Pi plates and GFP-fluorescence pictured with confocal microscope. All pictures were taken with same microscope and camera settings as in Fig.1g. Left pictures: the two roots were mounted side by side on the same microscope slide. Middle pictures: magnification of the root tips. Three independent experiments were performed with consistent results and one representative experiment is shown. Right panels: intensity of the GFP-fluorescence (a.u., arbitrary units) in nuclei of the root tip (mean +/- s.d., n = 29-60 nuclei; two-tailed t-test; **** P<0.0001). Scale bar, 100 μm.



Supplementary Figure 7: Fe localisation in root tips.

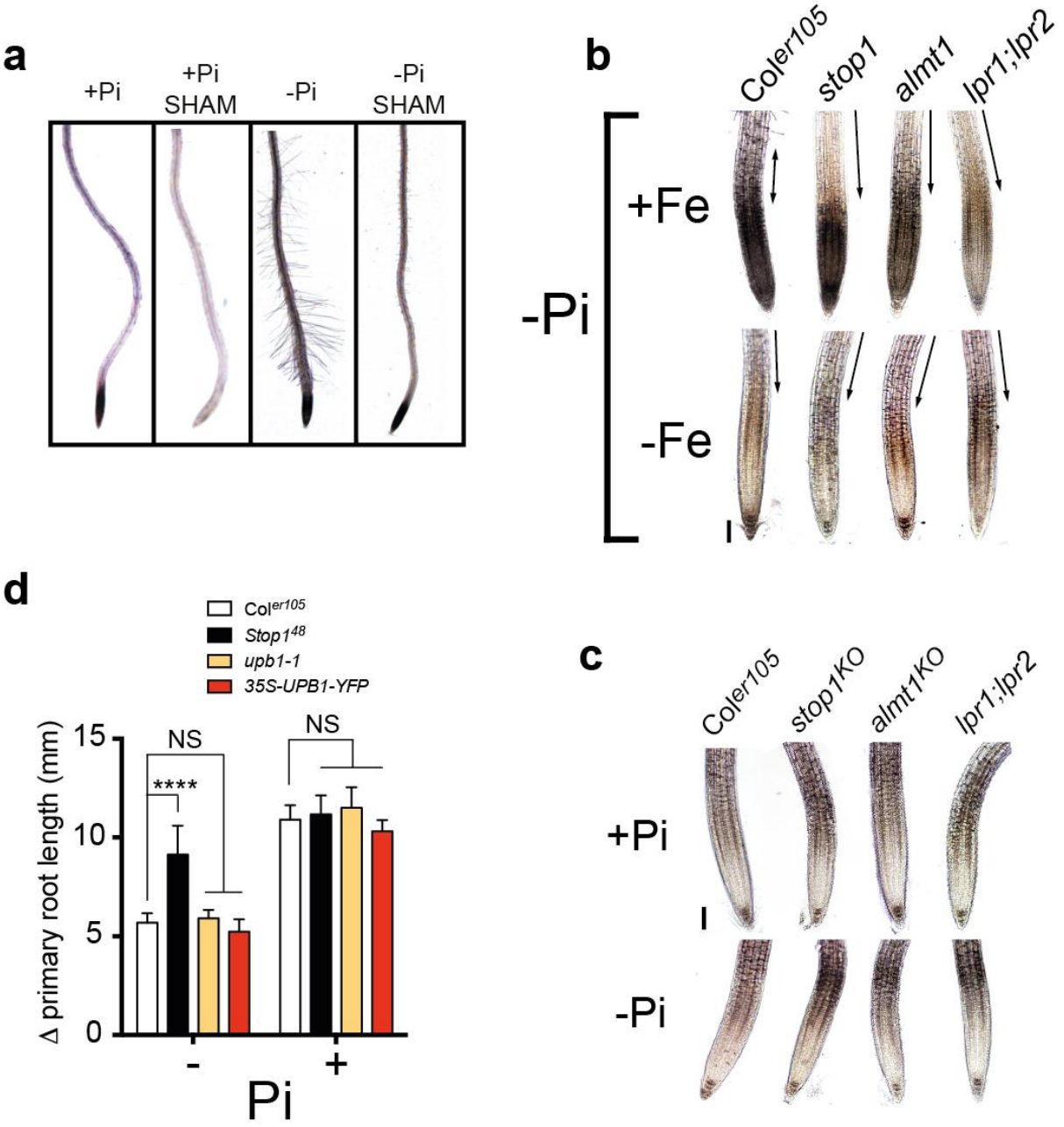
(a) Iron content in the primary root tip. Seedlings of the indicated genotypes were grown for 5 days under +Pi and transferred for 24 h to +Pi or –Pi prior to harvesting root tips (≈5 mm) for ICP-MS measurements of iron (mean +/-s.e.m., *n* = 3 independent experiments, each with 3 biological replicates of 60 root tips each).

(b) Histochemical detection of Fe accumulation and distribution in the primary root of WT and mutants (top panel) and the apex, with magnification of the SCN under –Pi (bottom panels). Three-day old seedlings of the indicated genotypes were transferred 48 h in + or –Pi plates prior to Perls/DAB staining. Note the accumulation of Fe in the elongation zone of the WT (white arrowhead) and in the SCN (black arrowhead). Three independent experiments were performed with consistent results and one representative experiment is shown. Scale bar, 100 μm.



Supplementary Figure 8: Malate complementation of the *almt1* mutant.

Four-day old WT and *almt1* seedlings grown under +Pi were transferred 1 day under -Pi or -Pi supplemented with 250 µM malate before staining iron (left panels) or callose (right panels). Note the accumulation of iron (black arrowhead) and callose (white arrowhead) in the elongation zone of the *almt1* grown under –Pi+malate. Scale bar, 100 µm.



Supplementary Figure 9: Peroxidase activity in the primary root of mutants.

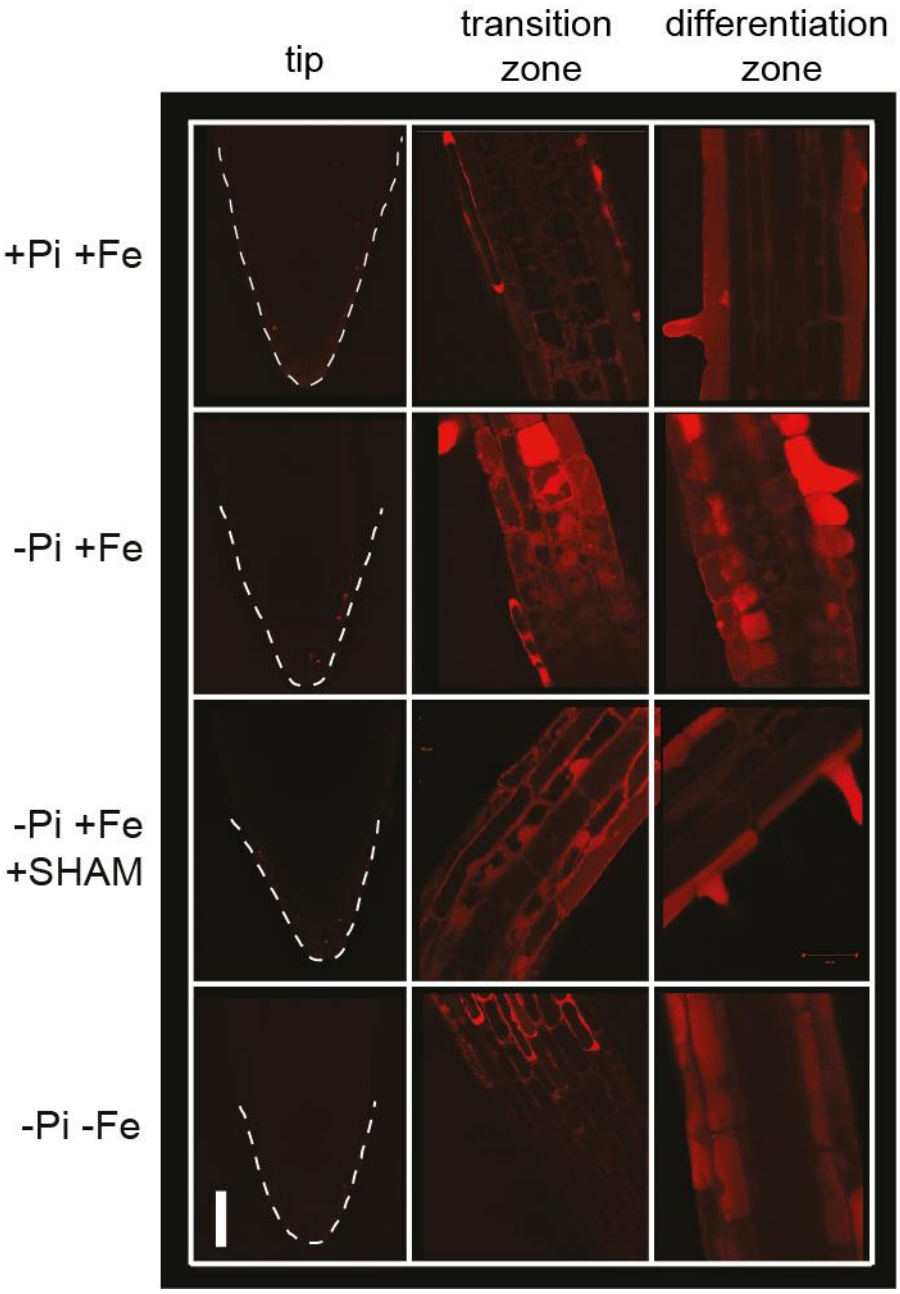
(a) Histochemical detection of peroxidase activity in the WT primary root. Four-day-old WT seedlings were transferred for 48 h to +Pi or –Pi plates, with or without 15 μM SHAM prior to staining with 4-chloro-1-naphtol.

(b) Effect of iron on the peroxidase activity in the primary root tip. Seedlings of the indicated genotypes grown for 6 days under +Pi were transferred for 24 h to –Pi, +Pi or -10 μM Fe, prior staining with 4-chloro-1-naphtol. Arrows indicate the position of

the elongation zone. The experiment was performed three times with consistent results; one representative experiment is shown. Scale bar, 100 μm.

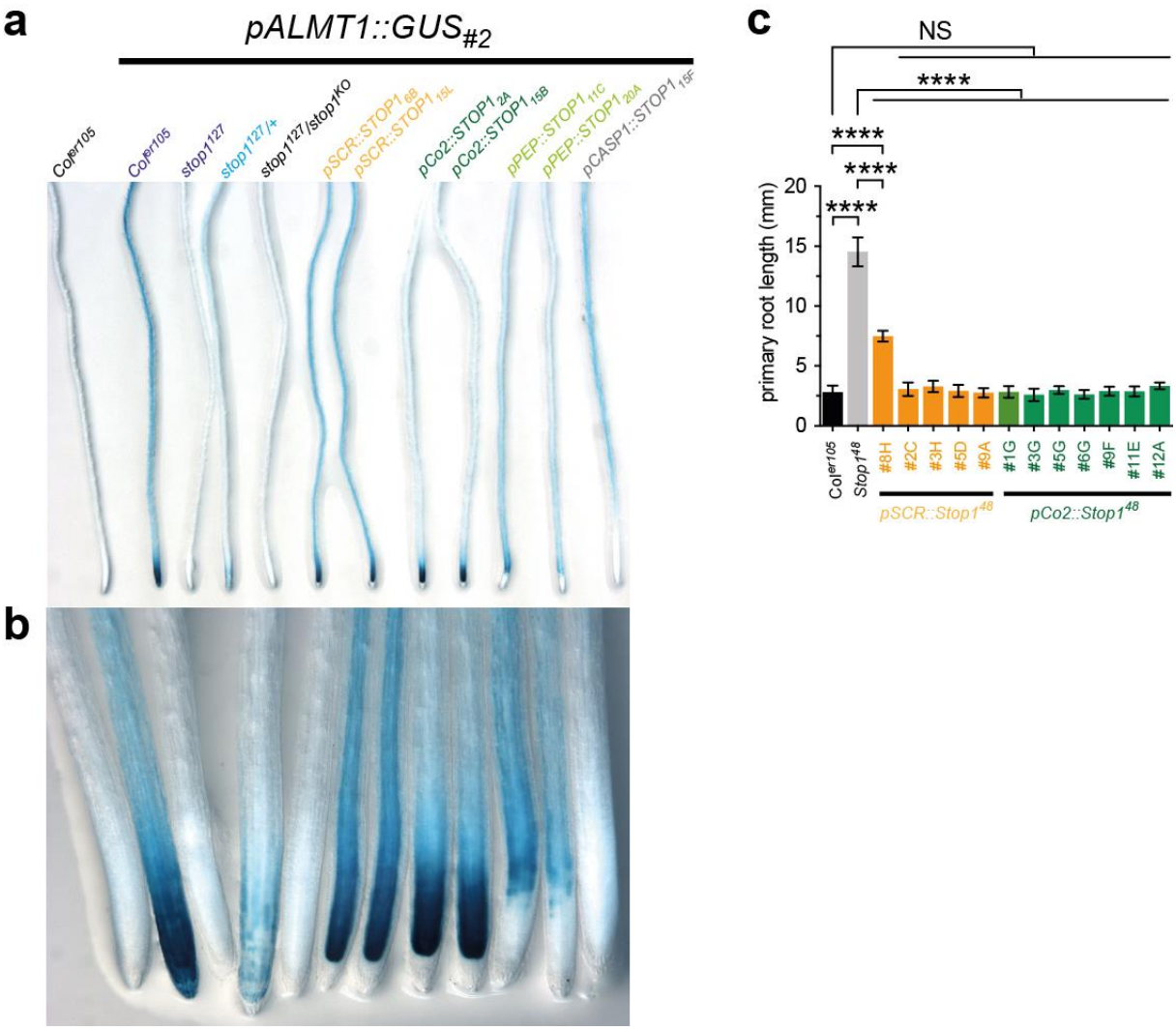
(c) Effect of neutral pH on the peroxidase activity in the primary root tip. Four-day-old seedlings of the indicated genotypes were transferred for 48 h to +Pi or –Pi, pH 7.1 plates prior staining with 4-chloro-1-naphtol. The same lines grown at pH 5.8 are shown in Fig. 4k. The experiment was performed three times with consistent results; one representative experiment is shown. Scale bar, 100 μm.

(d) Primary root length of *upb1-1* and *35S-UPB1-YFP* lines. Three-day-old seedlings were transferred for 2 days to +Pi or –Pi, (mean +/- s.d., n = 8–10 seedlings per line and condition; two-way ANOVA, multiple comparisons; **** P<0.0001).



Supplementary Figure 10: ROS detection in the root tip.

Six-day old Col^{er105} seedlings grown under +Pi were transferred for 24 h in the indicated conditions before staining ROS with CM-H2DCFDA. SHAM was at 15 μM. Pictures were taken in the root tip (left), in the transition zone (middle) and in the differentiation zone (right). The dashed white lines indicate position of the root tips. Scale bar, 50 μm.

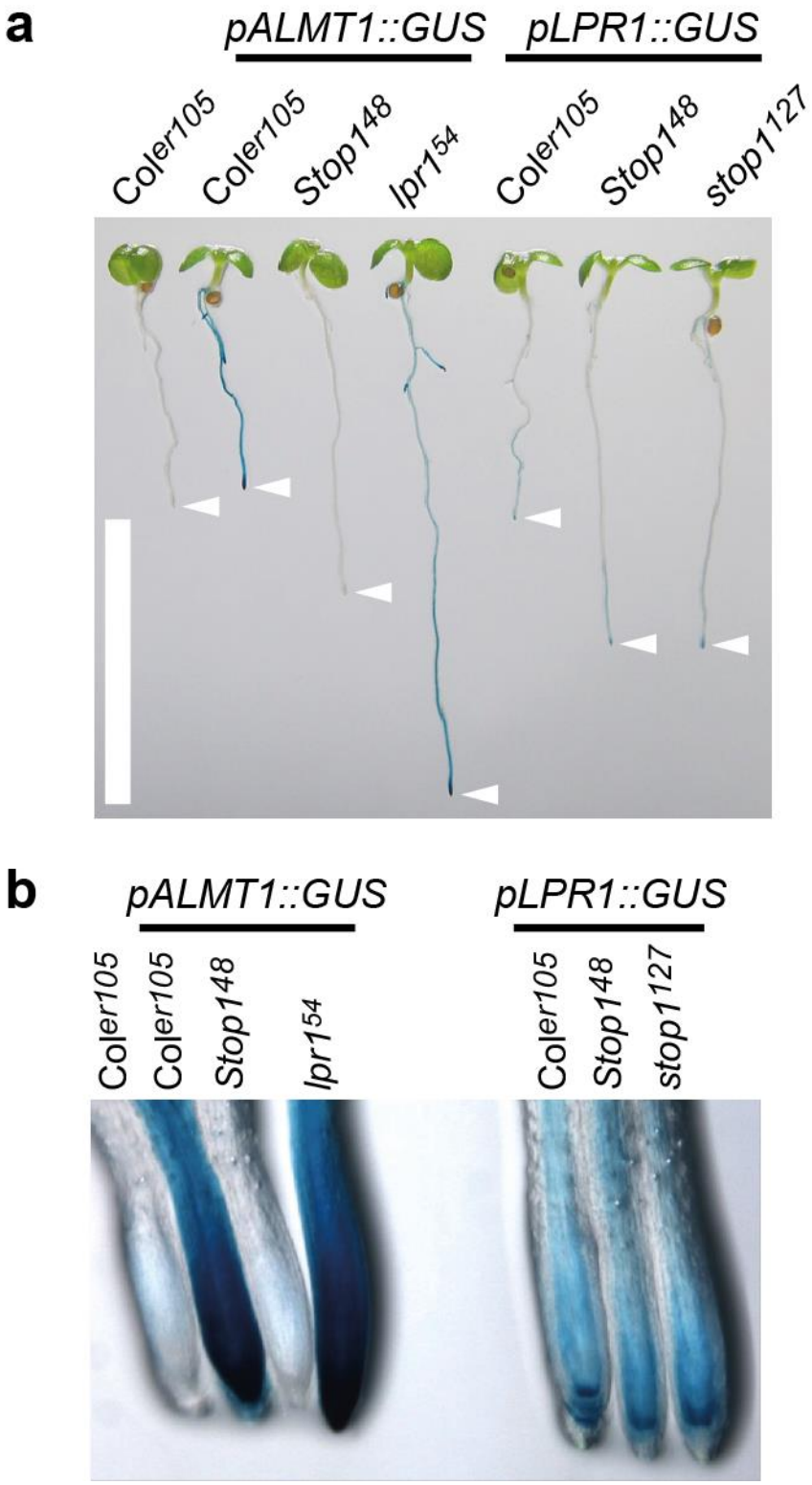


Supplementary Figure 11: Expression of *pALMT1::GUS* in *stop1^{KO}* lines expressing WT *STOP1* in specific cell-types, and root length of WT lines expressing the dominant negative *Stop1^{48}* in the endodermis or in the cortex.

(a,b) GUS-staining from *pALMT1::GUS*. Seedlings were grown for 5 days under +Pi prior to GUS staining (1 h). *pX::STOP1* constructs are in a *stop1^{127}/stop1^{KO}* background (F1 progeny from the cross of *stop1^{127}*; *pALMT1::GUS$_{\#2}$* with *stop1^{KO}*; *pX::STOP1*); seedlings are heterozygous for *pALMT1::GUS$_{\#2}$* except Col^{er105} and *stop1^{127}* that are homozygous. Pictures show the primary roots (a) and magnification of the corresponding root tips (b). Three independent experiments were performed with consistent results; one representative experiment is shown.

(c) Seedlings of the indicated genotypes were grown for 6 days under –Pi and the primary root length measured. Respectively 5 and 7 independent transgenic lines for

the *pSCR::Stop1*^{48} and *pCo2::Stop1*^{48} constructs (in the WT Col^{er105} background) are shown. The experiment has been performed three times with consistent results; one representative experiment is shown (mean +/- s.d., n = 12–15 seedlings per line; one-way ANOVA; **** P<0.0001; NS, not significant).



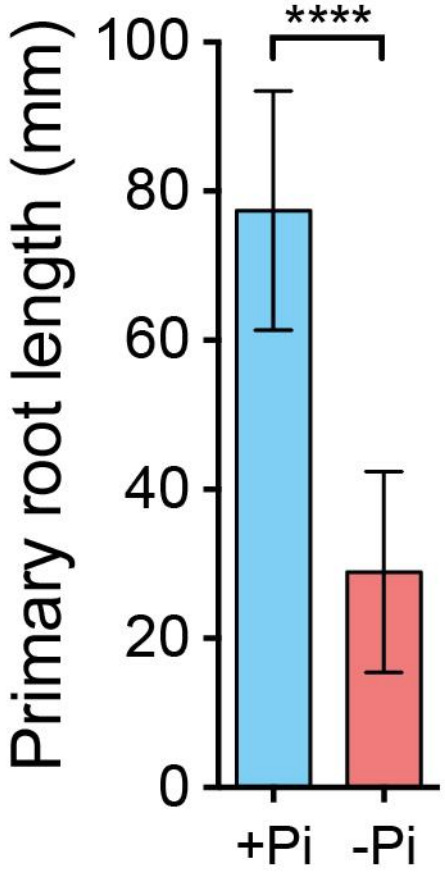
Supplementary Figure 12: Expression of *pALMT1::GUS* in *lpr1* mutant and *pLPR1::GUS* in *stop1* mutants.

(a) Seedlings were grown for 6 days under –Pi prior to GUS staining. The *pLPR1::GUS* (Müller et al., 2015) and *pALMT1::GUS* constructs have been

introgressed by crossing in the indicated genetics backgrounds. Arrowheads indicate the root tips. Scale bar, 1 cm.

(b) Higher magnification of the root tip.
Note that the expression of *ALMT1* is not altered in *lpr1* mutant, neither *LPR1* in *stop1* mutants. Three independent experiments were performed with consistent results; one representative experiment is shown.

a



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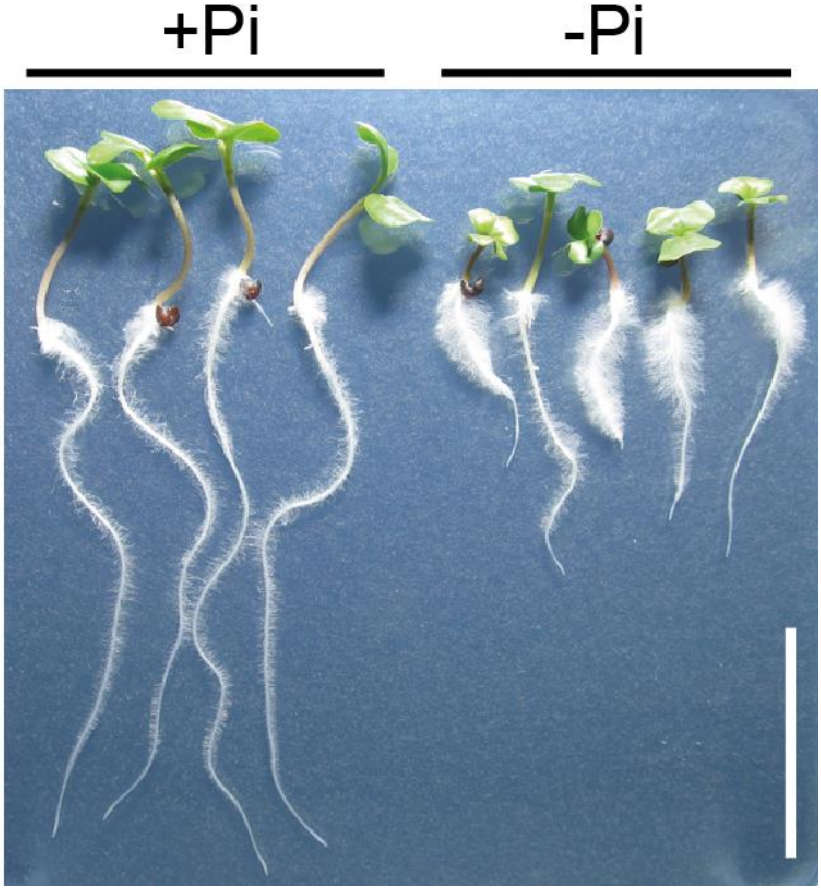

Supplementary Figure 13: –Pi inhibits primary root growth of rapeseed seedlings.

(a) Germinating seeds were transferred from +Pi to + or –Pi plates for 3 days before measuring the primary root length (mean +/- s.d., *n* = 75 for +Pi and 83 for –Pi; two-tailed *t*-test; **** *P*<0.0001). Scale bar, 3 cm.

(b) Picture of representative seedlings.

Three independent experiments were performed with consistent results and one representative experiment is shown.

Supplementary Table 1 : Primers

name	purpose	sequence (5'>3')
MSAT1-2.62-F	mapping *almt1*^{32}	CAACATCTGGACTTCCTTCCA
MSAT1-2.62-R	mapping *almt1*^{32}	TGCATGTTTCATGATGACTCC
PMSha-2.78-F	mapping *almt1*^{32}	ACAAATACGGCACCCATAGC
PMSha-2.78-R	mapping *almt1*^{32}	TCTTCTGTCATTAGCACCCTCA
HRM1:1949448F	mapping *almt1*^{32}	TGGTCTGCTGGTTGTGTACTGGCAGAGCTT
HRM1:1949448R	mapping *almt1*^{32}	ACGGCTGTAGAGAGAGAGAGACTGGCTT
HRM1:2589882F	mapping *almt1*^{32}	AGCGGCTGCTTCAGAGTAAGCACCGGG
HRM1:2589882R	mapping *almt1*^{32}	AGCGCCGCCGCACGAGTTCCA
HRM1:3010815F	mapping *almt1*^{32}	ACACTCTCTAGTGGCAGAGGCCTTATCCGTG
HRM1:3010815R	mapping *almt1*^{32}	ACCGGAACGTGAGACCCAAGAAAGCAACT
HRM1:2745575L	mapping *almt1*^{32}	CCCGGATGGCACGAACAGAGCAGCC
HRM1:2745575R	mapping *almt1*^{32}	AGACCGACAGATGCGATGCGAGAAGCA
MSAT1-12,22-F	mapping *almt1*^{48}	TGTCCGGGACTGCCTTTAGC
MSAT1-12,22-R	mapping *almt1*^{48}	CGCATACGTGTCACCGTGAG
CWI1-F	mapping *almt1*^{48}	ACATTTTCTCAATCCTTACTC
CWI1-R	mapping *almt1*^{48}	GAGAGCTTCTTTATTTGTGAT
23010cDNAF	screening *lpr1* alleles with ENDO1	CTCTCACCCGAAGTTAATAATTCAG
23010R2	screening *lpr1* alleles with ENDO1	CCTACGTCGGACGTTTAATC
23010F4	screening *lpr1* alleles with ENDO1	CCCTTTCAGCTACCTACTGGC
RT10R	screening *lpr1* alleles with ENDO1	CACCATCAAAACTTCGCAGAGATCGA
ALMT1F1	sequencing *ALMT1*	GAAAGTAATCAGAGAATCAG
ALMT1F2	sequencing *ALMT1*	TTGGTCATGTTGGTCTTTG
ALMT1F3	sequencing *ALMT1*	AGTGAATGTGAAATTGGCAG
ALMT1F4	sequencing *ALMT1*	TATGTTTCTGGTTAACGTG
ALMT1F5	sequencing *ALMT1*	GATCTCATTGATGACGACTG
ALMT1R1	sequencing *ALMT1*	CTTGGAAACGCATGGTAATC
ALMT1R2	sequencing *ALMT1*	TTCCTCTTCTCCACTACTTTG
ALMT1R3	sequencing *ALMT1*	TAAATATGCAAACACCTAACA
ALMT1R4	sequencing *ALMT1*	GAGAATCTATTGGCATGGC
ALMT1R5	sequencing *ALMT1*	CTCTATAATCTTGCGGGTAC
STOP1F1	sequencing *STOP1*	GTATGATGAACTTTGAGCTGG
STOP1F2	sequencing *STOP1*	ATTTGCCTAAGCCGGTTCTT
STOP1R1	sequencing *STOP1*	ACTAGAACATCTTACATAAC
STOP1R2	sequencing *STOP1*	ATGCCCTCTCATATGCATCC
LBb1.3	genotyping *stop1*^{KO}	ATTTTGCCGATTTCGGAAC
pSTOP1Fw	genotyping *stop1*^{KO}	CGGTTGAGATTAATGGG
pSTOP1-Fw 4	genotyping *stop1*^{KO}	CCATTGGTGCTCTCCAAGTT
SK3573_LP	genotyping *mate*^{KO}	GACGCGGAGAGAGTTACACAG
SK3573_RP	genotyping *mate*^{KO}	TCAACAATCCAACTGAGGAAAC
pSKI015_LP	genotyping *mate*^{KO}	TCGTGAAGTTTCTCATCTAAGC
WRKY46-F	genotyping *wrky46*^{KO}	CCCACCAATCTCACTCAAAAGAAAA
WRKY46-R	genotyping *wrky46*^{KO}	CCCTGCTGAAAAACAATGAAAAAGG
LBb1.3	genotyping *wrky46*^{KO}	ATTTTGCCGATTTCGGAAC
UPB1-F	genotyping *upb1-1*	TGAATGGGAAGAAAGTTGGTG
UPB1-R	genotyping *upb1-1*	TTTCACAGCCCAACGTTAAAC
LBb1	genotyping *upb1-1*	GCGTGGACCGCTTGCTGCAACT
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attB1rpUBI10	cloning *pUBQ*	GGGGACTGCTTTTTTGTACAAACTTGCCTGTTAATCAGAAAAACTCAG
attB4pALMT1	cloning *pALMT1*	GGGGACAACTTTGTATAGAAAAGTTGCCTCCTTTTGGTTGTCTAAGCTAGACC
attB1rpALMT1	cloning *pALMT1*	GGGGACTGCTTTTTTGTACAAACTTGCAACACCTTTTGATGGTCACTCAGC
attB4pSTOP1	cloning *pSTOP1*	GGGGACAACTTTGTATAGAAAAGTTGCCGGCGAAGAAGTAACTAAGGGTTGA
attB1rpSTOP1	cloning *pSTOP1*	GGGGACTGCTTTTTTGTACAAACTTGCTTTTTAGTTCAAGATCTTGTTTTTCA
TopoALMT1Fw	cloning *ALMT1*	CACCATGGAGAAAGTGAGAGAGATAGTG
TopoALMT1pasSTOPRv	cloning *ALMT1*	CTGAAGATGCCCATTACTTAATG
attB2rALMT1	cloning *ALMT1*	GGGGACAGCTTTCTTGTACAAAGTGGCCATGGAGAAAGTGAGAGAGATAGTG
AttB3ALMT1	cloning *ALMT1*	GGGGACAACTTTGTATAATAAAGTTGCTTACTGAAGATGCCCATTACTTAATG

attB2rSTOP1	cloning *STOP1*	GGGGACAGCTTTCTTGTACAAAGTGGCCATGGAAACTGAAGACGATTTGTG
AttB3STOP1	cloning *STOP1*	GGGGACAACTTTGTATAATAAAGTTGCTTAGAGACTAGTATCTGAAACAG
TopoSTOP1Fw	cloning *STOP1*	CACCATGGAAACTGAAGACGATTTGTG
TopoSTOP1Rv	cloning *STOP1*	GAGACTAGTATCTGAAACAG
Topo-GUS-Fw	cloning *GUS*	CACCATGTTACGTCCTGTAGAAACC
Topo-GUS-Rv	cloning *GUS*	TCATTGTTTGCCTCCCTGCTGC
ROC3-F	qRT-PCR	ATCGTGATGGAGCTTTACGC
ROC3-R	qRT-PCR	TCGGTGAAAGCTTGATCCTT
STOP1-F	qRT-PCR	AAGTGGCTTTGTTCCTGTGG
STOP1-R	qRT-PCR	GGCTGTGTGGTTTCTTGGTT
ALMT1-F	qRT-PCR	GGCAGTGTGCCTACAGGATT
ALMT1-R	qRT-PCR	CGATTCCGAGCTCATTCTTC
MATE-F	qRT-PCR	GCATAGGACTTCCGTTTGTGGCA
MATE-R	qRT-PCR	CGAACACAAACGCTAAGGCA
SPX1-F	qRT-PCR	CGGGTTTTGAAGGAGATCAG
SPX1-R	qRT-PCR	GCGGCAATGAAAACACACTA
STOP1-Fw	Yeast one-hybrid	CTTATGGGTGCTCCTCCAAAAAAGAAGAGAAAGGTAGAAACTGAAGACGATTTGTG
STOP1-Rv	Yeast one-hybrid	CTTATTTAATAATAAAAATCATAAATCATAAGAAATTCGCTTAGAGACTAGTATCTGAAAC
pALMT1-Fw	Yeast one-hybrid	ATTAGAGCTTCAATTTAATTATATCAGTTATTACCCGGGTCCTTTTGGTTGTCTAAGC
pALMT1-Rv	Yeast one-hybrid	CAGAAATAAGGCTAAAAAACTAATCGCATTATCATCCCTCGACAACACCTTTGATGGTCACT
pALMT1-R1	Yeast one-hybrid	CAGAAATAAGGCTAAAAAACTAATCGCATTATCATCCCTCGACCAACATACCAAAATATGATAAAC
pALMT1-F2	Yeast one-hybrid	ATTAGAGCTTCAATTTAATTATATCAGTTATTACCCGGGATAGGCGGCTTCTCAGGTCG
pALMT1-R2	Yeast one-hybrid	CAGAAATAAGGCTAAAAAACTAATCGCATTATCATCCCTCGACATGTTCGAATGATCTTTGCC
pALMT1-F3	Yeast one-hybrid	ATTAGAGCTTCAATTTAATTATATCAGTTATTACCCGGGGGACTCAGTAAAAGAG
pALMTC1-Rv	Yeast one-hybrid	CAGAAATAAGGCTAAAAAACTAATCGCATTATCATCCCTCGACTTCTGTAATCGACAAGATTAG
pALMT1C2-Fw	Yeast one-hybrid	ATTAGAGCTTCAATTTAATTATATCAGTTATTACCCGGGCGAACATTGGAGCCCAAGTG
pALMT1C2-Rv	Yeast one-hybrid	CAGAAATAAGGCTAAAAAACTAATCGCATTATCATCCCTCGACCTTAGTGAATTGTATATAGTG
pALMT1C3-Fw	Yeast one-hybrid	ATTAGAGCTTCAATTTAATTATATCAGTTATTACCCGGGATTCCTTAATCAAAATGTATCATGC
pALMT1C3-Rv	Yeast one-hybrid	CAGAAATAAGGCTAAAAAACTAATCGCATTATCATCCCTCGACTTAATTGGAGCGACGCGTGAG
pALMT1C4-Fw	Yeast one-hybrid	ATTAGAGCTTCAATTTAATTATATCAGTTATTACCCGGGTCTAACTAATCCAGCTCAGC
pALMT1C4-Rv	Yeast one-hybrid	CAGAAATAAGGCTAAAAAACTAATCGCATTATCATCCCTCGACATTTCAGGGTTAAAGTCTTAAAG
pALMT1C5-Fw	Yeast one-hybrid	ATTAGAGCTTCAATTTAATTATATCAGTTATTACCCGGGGGGCTAGGTTCGACTCCG
pALMT1C5-Rv	Yeast one-hybrid	CAGAAATAAGGCTAAAAAACTAATCGCATTATCATCCCTCGACGGATCGATGTATTTATAAAGACC
pALMT1C6-Fw	Yeast one-hybrid	ATTAGAGCTTCAATTTAATTATATCAGTTATTACCCGGGCATGAGTCCTAAACAAGAGTC