Fig. S1 Plant nutritional status influences meristem function.

a to c. Rosette weight (a), meristem size (b) and plastochron ratio (c) of WT plants grown on soils of different nutritive quality (1/3 soil 2/3 sand: n=17, ½ soil ½ sand: n=22, 2/3 soil 1/3 sand: n=23, 1/1 soil: n=21, 1/1 soil + fertilizer: n=26, pool of 2 independent experiments). Note that as the plastochron ratio is the average area between successive primordia, this parameter is more variable for meristems producing few organs as it is averaged on a smaller number of measurements. d. Number of flowers produced by the main inflorescence within the first 15 days of flowering of WT plants grown on soils of different nutritive quality (1/3 soil 2/3 sand: n=34, ½ soil ½ sand: n=32, 2/3 soil 1/3 sand: n=33, 1/1 soil: n=34, 1/1 soil + fertilizer: n=18, pool of 2 independent experiments).

Fig. S2 Automatic analysis of gene expression domains in the SAM

In order to detect the expression domain, a maximal intensity z-projection of the stack (here from a meristem expressing *WUS-GFP*) is performed and the resulting image is blurred (Gaussian filter of radius: 5 µm). The GFP domain is then automatically detected using a binary transformation of the image resulting from an Otsu thresholding. To extract the size and the total fluorescence level of the detected domain, a blurred (Gaussian filter of radius: 5 µm) z-projection of the stack summing the signal in each slice is performed. Then, the average signal of the domain is extracted at a defined distance from the center of such domain, which shows a curve with a stretched exponential decay. In order to extract the characteristic length of such domain, an exponential fit is applied to the extracted intensity data. The characteristic length of the domain is defined as the domain radius so that the GFP signal – with the autofluorescence levels subtracted - has decreased a factor 1/e from its maximum. Finally, the total GFP signal (after removal of the autofluorescence signal) is then measured. C_0: background signal, C_1: maximum signal without background, L_0: characteristic length, e: e number (See supplementary experimental procedures). Scale bars: 50 µm.

Fig. S3 Plant nutritional status influences gene expression in the SAM

a. Characteristic size domain of expression of *pWUS::GFP* in WT plants grown on soils of different nutritive quality from the same experiment as Fig1.c (n=57). b. Expression of *pWUS::GFP* in WT plants grown on soils of different nutritive quality from an independent experiment different from the one shown in Figure 1c and Supplementary Figure 3a (n=52). c. Expression of *WUS-GFP* in WT plants grown on soils of different nutritive quality (1^{st} replicate, n=54; 2^{nd} replicate, n=42: scale bar: 50 µm). Red arrows point to the center of the SAM. d. Expression of *pCLV3::dsRED* in WT plants grown on soils of different nutritive quality (1^{st} replicate: n=65, 2^{nd} replicate: n=50, 3^{rd} replicate: n=44, scale bar: 50 µm). Red arrows point to the center of the SAM. e. Characteristic size of the domain of expression of *pTCSn::GFP* in WT plants grown on soils of different nutritive quality from the same experiment as Fig. 1c (n=55). f. Expression of *pTCSn::GFP* in WT plants grown on soils of different nutritive quality levels from an independent experiment different from the one shown in Figure 1d and Supplementary Figure 3e (n=52).

Fig. S4 Phenotype of the cytokinin-associated mutants and impact of mineral nutrition on cytokinin levels

a. to d. Rosette weight at bolting stage (a), meristem size (b), plastochron ratio (c) and number of flowers produced by the main inflorescence within the first 15 days of flowering (d) of WT and CK-associated mutants grown on soil with fertilizer (2 independent experiments, the numbers of replicates are displayed in the Figure). Each green p-value corresponds to the result of a Student's t-test between a given mutant and the WT (Col-0). e. Expression of *WUS* revealed by *in situ* hybridization in meristems of Col-0 wild type plants and cytokinin-associated mutants at bolting stage and grown on soil with fertilizer (scale bars: 10 µm). *WUS* domain sizes were compared to Col-0 using Welch's t-test (the numbers of replicates are displayed in the Figure) f. Concentration of cytokinin species in

inflorescences of plants grown on soil without or with fertilizer in two different experimental repeats and measured by liquid chromatography mass spectrometry (n=3 inflorescences x 3 replicates). Data were compared using Student tests. The error bars correspond to the standard errors.

Fig. S5 Cytokinin precursors act as long in range signals in the control of SAM homeostasis

a. Plastochron ratio of the inflorescence meristem of WT and cytokinin-associated mutant plants self-grafted or grafted with a WT root and grown in soil supplied with fertilizer (pool of two independent experiments). Data were compared using Student's t-test. b. Meristems of WT and cytokinin-associated mutant plants self-grafted or grafted with a WT scion and grown in soil supplied with fertilizer (Scale bar: 50 µm). c and d. Meristem size (c) and plastochron ratio (d) of WT and cytokinin-associated mutant plants self-grafted or grafted with a WT scion and grown in soil supplied with fertilizer (pool of two independent experiments). Data were compared using Student's t-test, in green is displayed the *p-value* when comparing a given grafted plants with the self-grafted WT and in red is displayed the *p*-value when comparing a given grafted plants with the corresponding self-grafted mutant.

Fig. S6 *IPT3* is sufficient to maintain cytokinin signalling and WUS expression *in-vitro*

Effect of an induction of *IPT3* using an estradiol inducible system under the control of the *p35S* on the expression of *pTCS::GFP* (a) or p*WUS::GFP* (b) in cut meristems grown *in vitro* without addition of extrinsic cytokinin (scale bars: 50 µm, pools of two independent experiments, *pTCS::GFP*: n=17, *pWUS::GFP*: n=12). Red arrows point to the center of each inflorescence meristem. Data were compared using Student tests.

Fig. S7 Nitrate modulates meristem homeostasis through cytokinins

Effect of the nitrate treatment on the expression of *pTCSn::GFP* (a), the expression of *pWUS::GFP* (b), the size of the meristem (c) and the plastochron ratio (d) from independent experiments different from the ones presented in Fig.4. The treatments were performed after day 0 and different meristems were dissected and imaged each day (n=8-12). The different conditions were compared using Student's t-test.

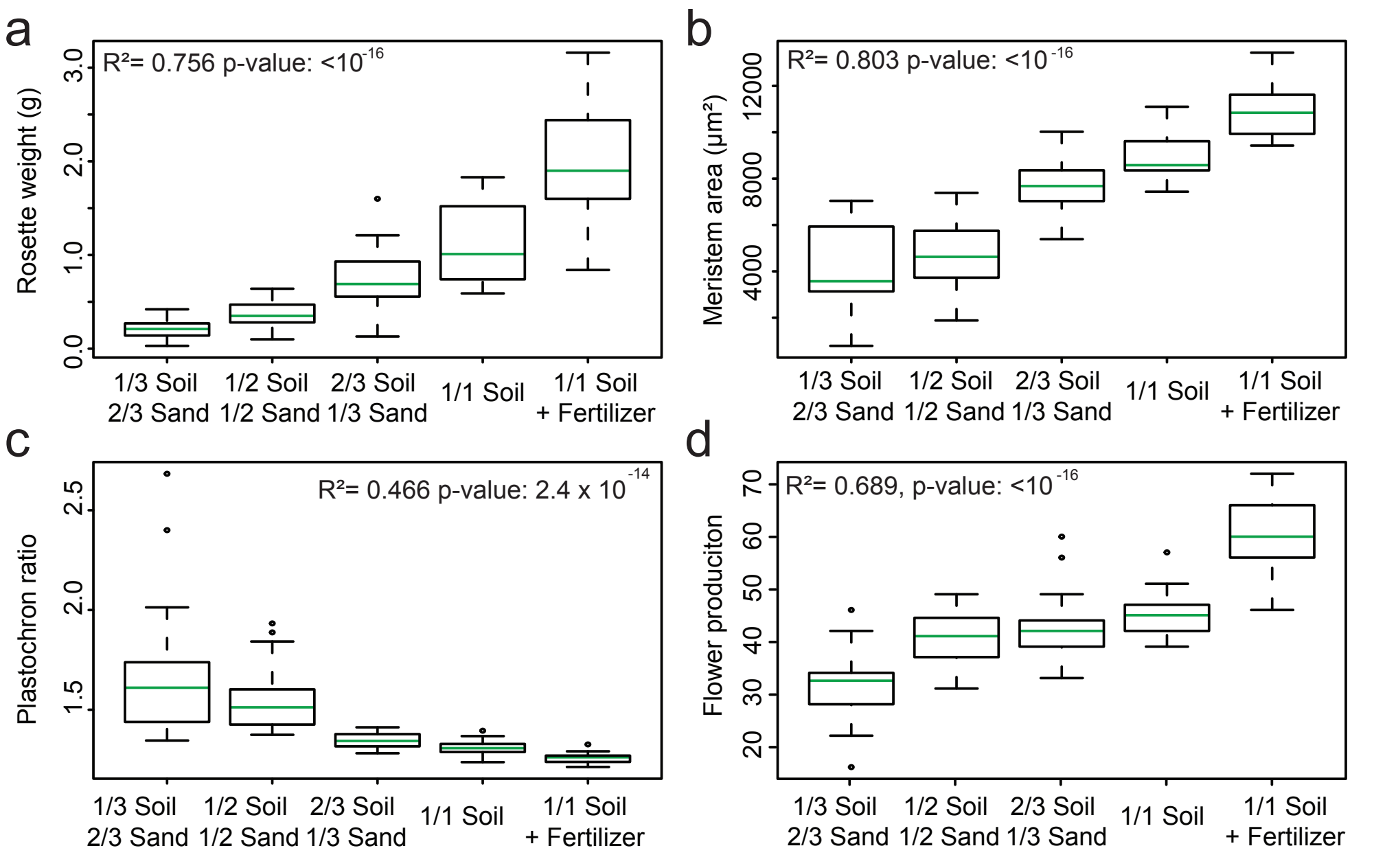
Fig. S8 Cytokinin biosynthesis and levels are influenced by nitrate levels

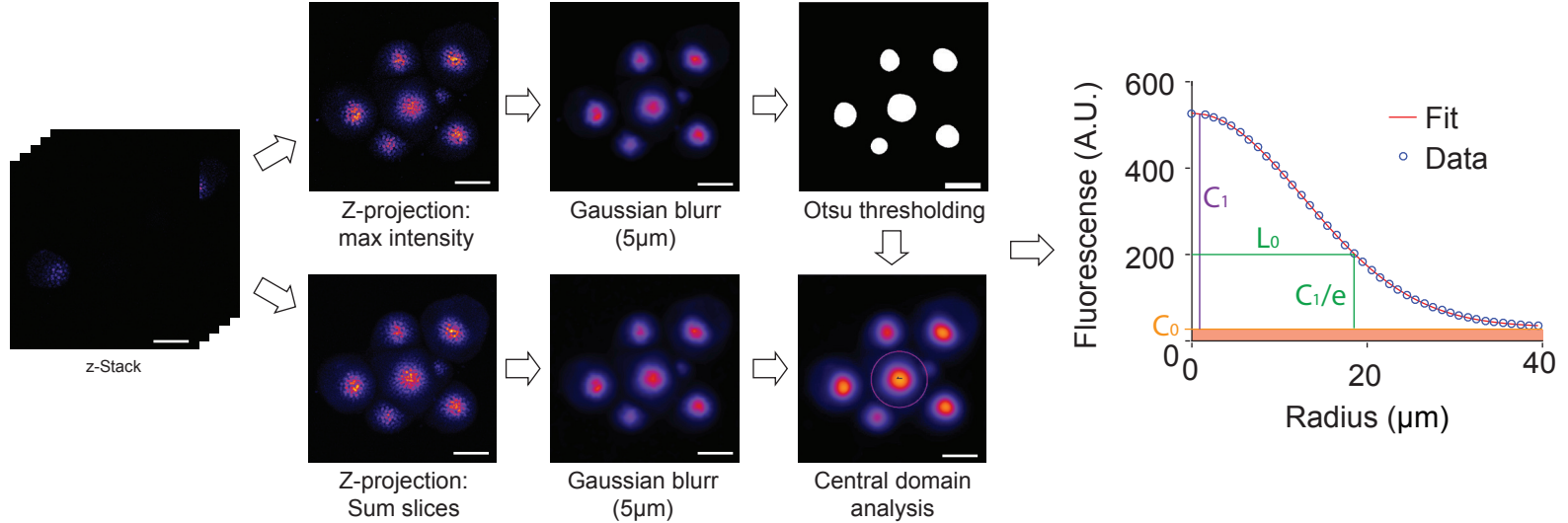
a. Effect of the nitrate resupply on the expression of *NIA1* (a nitrate responsive gene), *IPT3* and *IPT5* in root tissues (3 biological replicates of 3 meristems). The different conditions were compared using Student's t-test. b. Concentration of various cytokinin species in root, leaf or inflorescence tissues measured 2 days after a treatment with a nutritive solution containing either 0mM of NO_3 or 9mM of NO_3 and measured by liquid chromatography mass spectrometry (3 biological replicates of 3 inflorescences). Data were compared using Student's t-test; error bars correspond to the standard errors.

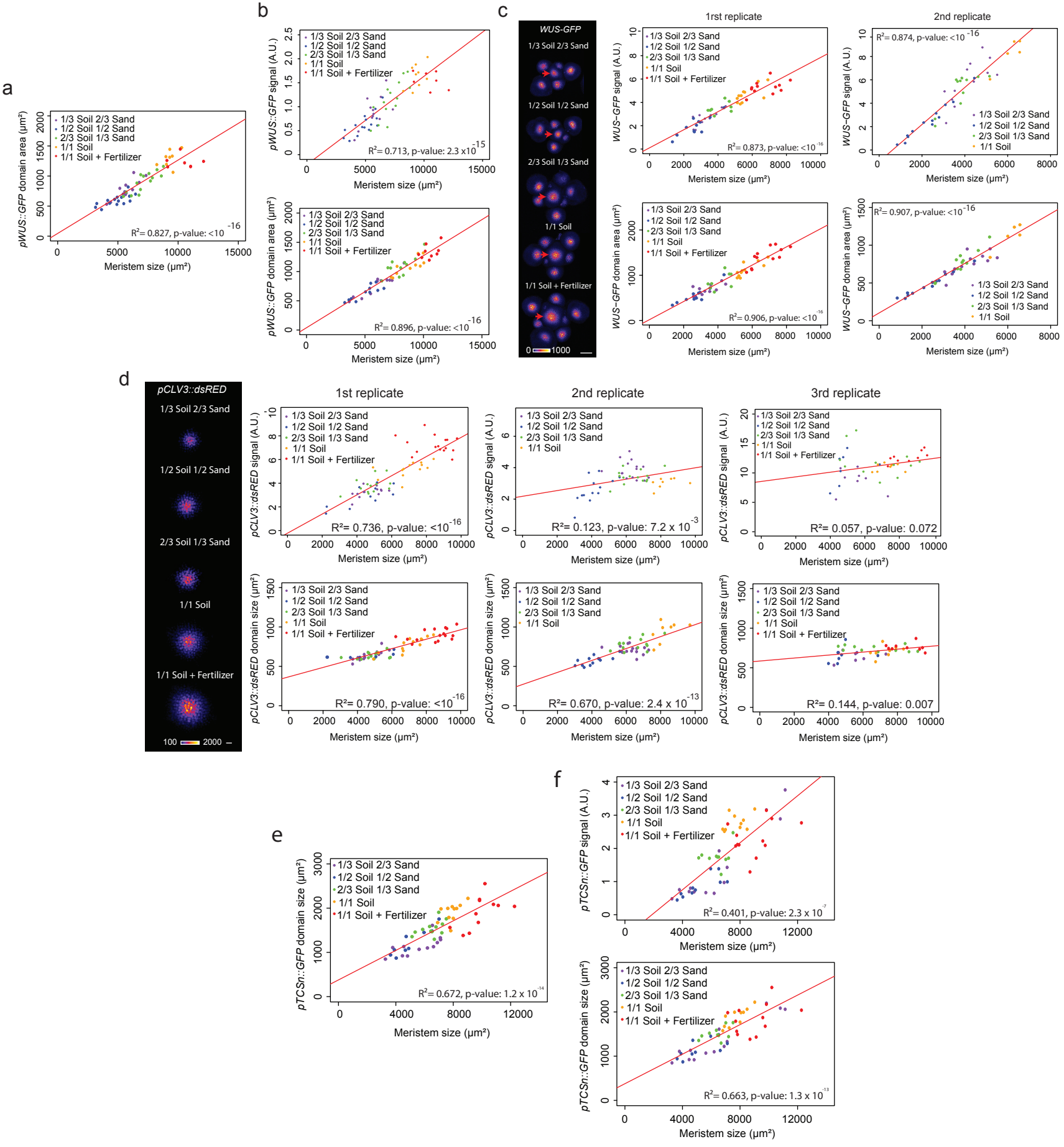
Fig.S9 The response of the SAM to NO_3 is reduced in *ipt3.5.7* mutant

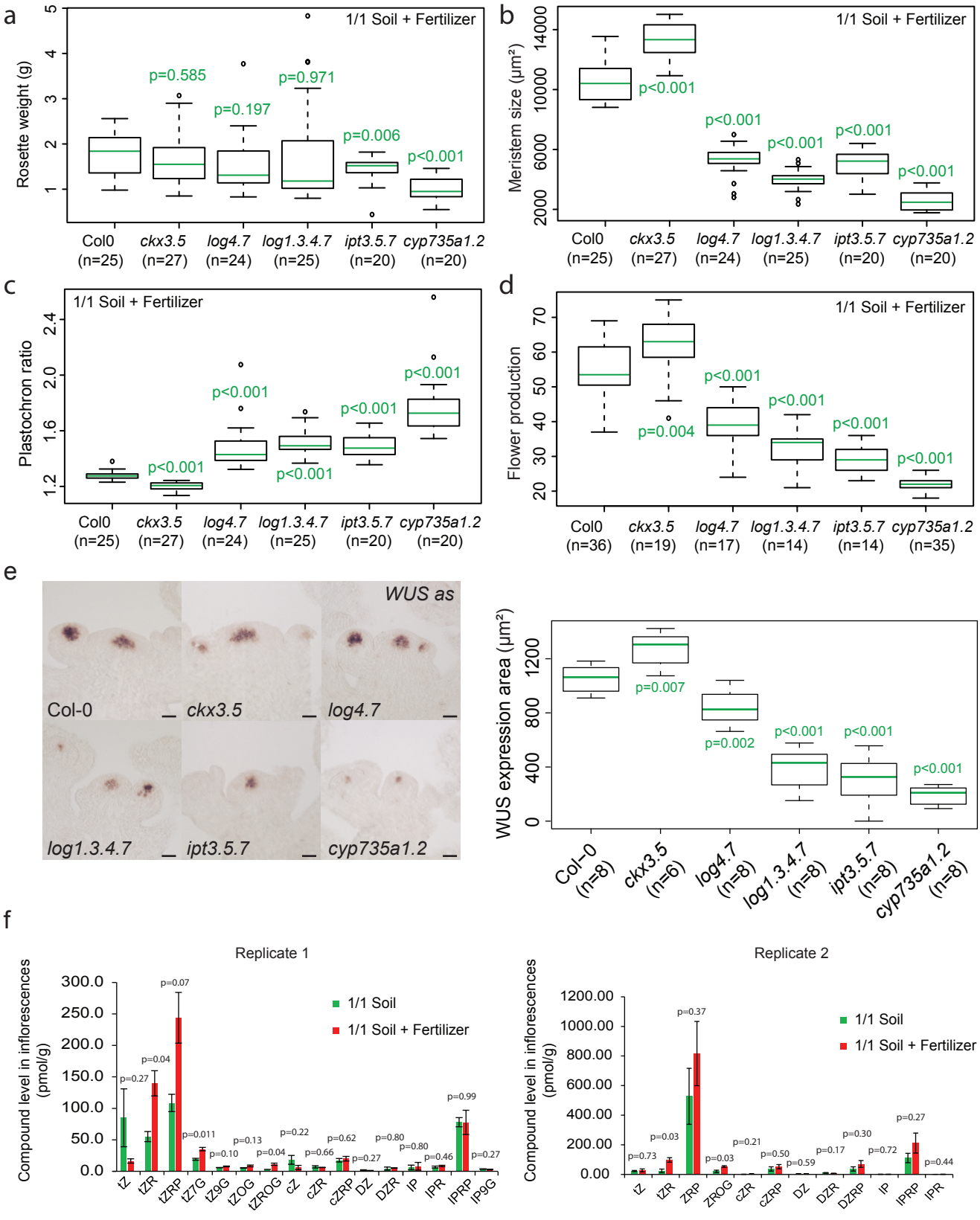
Meristem size and plastochron ratio of WT and cytokinin-associated mutants three days after treatment with a nutritive solution containing either 0 mM (g) or 9 mM of NO_3 (r) from an independent experiment different from the one shown in Fig.4d (Col-0: n= 15 (g) and 15 (r), *ckx3.5*: n= 16 (g) and 15 (r), *log4.7*: n= 18 (g) and 14 (r), *log1.3.4.7*: n= 13 (g) and 15 (r), *ipt3.5.7*: n= 12 (g) and 13 (r), *cyp735a1.2*: n= 7 (g) and 8 (r)). Conditions were compared using Student's t-test.

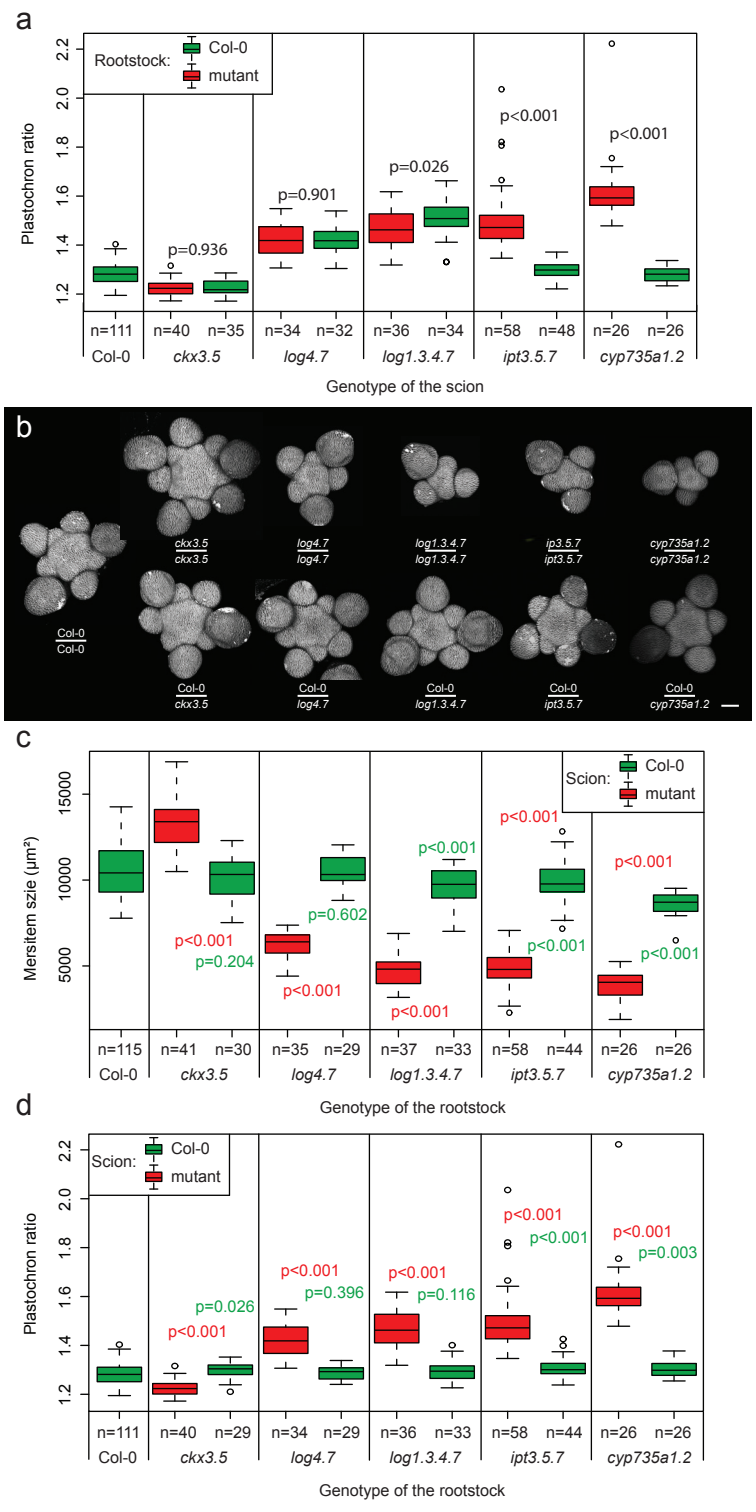
Fig. S10 An integrative and mechanistic model of the modulation of meristem function by nitrate

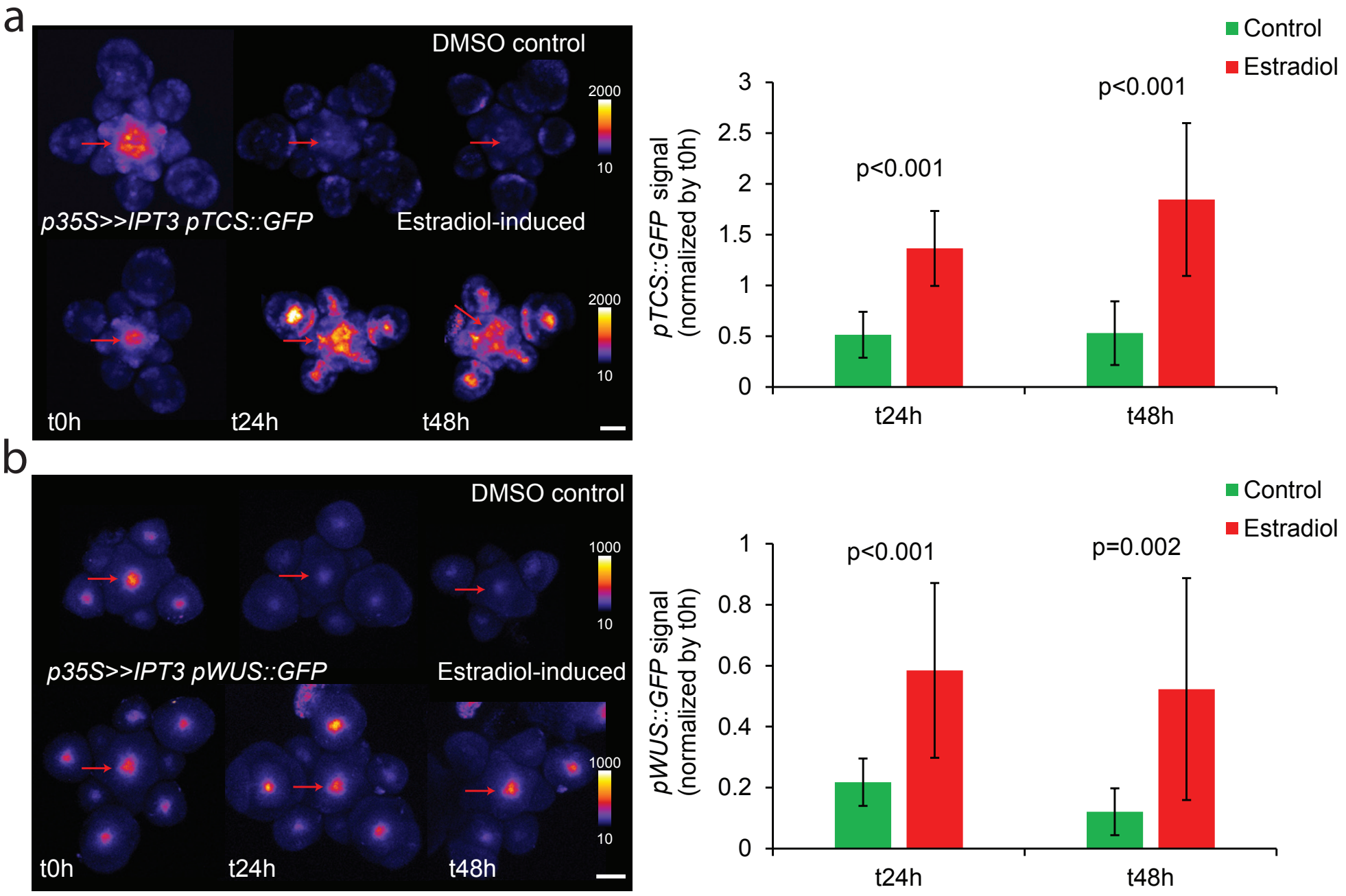

a
Rosette weight (g)
0.0
1.0
2.0
3.0
R²= 0.756 p-value: <10-16
1/3 Soil 2/3 Sand
1/2 Soil 1/2 Sand
2/3 Soil 1/3 Sand
1/1 Soil
1/1 Soil + Fertilizer
b
Meristem area (µm²)
4000
8000
12000
R²= 0.803 p-value: <10-16
1/3 Soil 2/3 Sand
1/2 Soil 1/2 Sand
2/3 Soil 1/3 Sand
1/1 Soil
1/1 Soil + Fertilizer
c
Plastochron ratio
1.5
2.0
2.5
R²= 0.466 p-value: 2.4 x 10-14
1/3 Soil 2/3 Sand
1/2 Soil 1/2 Sand
2/3 Soil 1/3 Sand
1/1 Soil
1/1 Soil + Fertilizer
d
Flower produciton
20
30
40
50
60
70
R²= 0.689, p-value: <10-16
1/3 Soil 2/3 Sand
1/2 Soil 1/2 Sand
2/3 Soil 1/3 Sand
1/1 Soil
1/1 Soil + Fertilizer

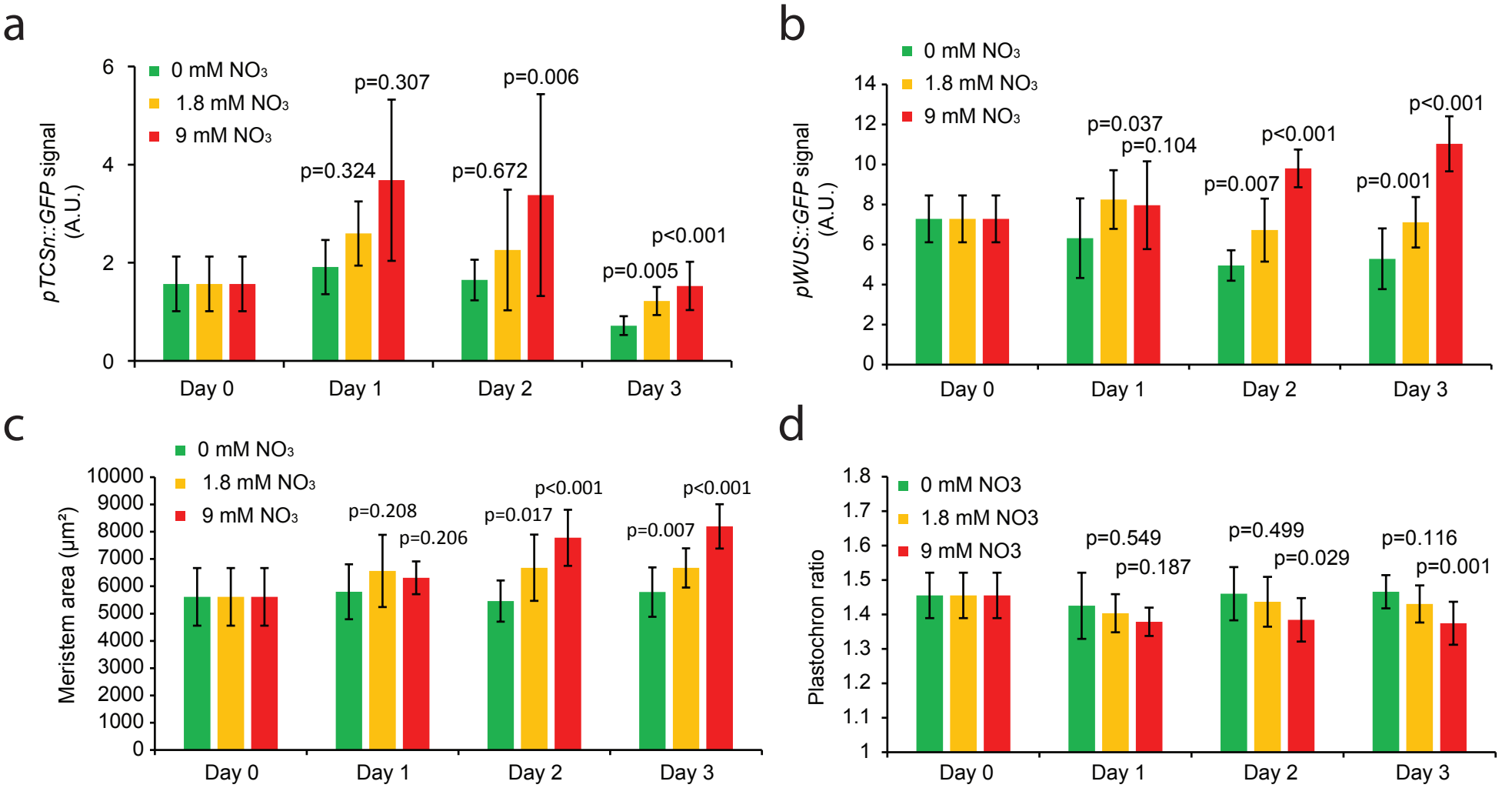

z-Stack
Z-projection:
max intensity
Gaussian blurr
(5µm)
Otsu thresholding
Z-projection:
Sum slices
Gaussian blurr
(5µm)
Central domain
analysis
Fluorescense (A.U.)
600
400
200
0
0
20
40
Radius (µm)
Fit
Data
C1
L0
C1/e
C0

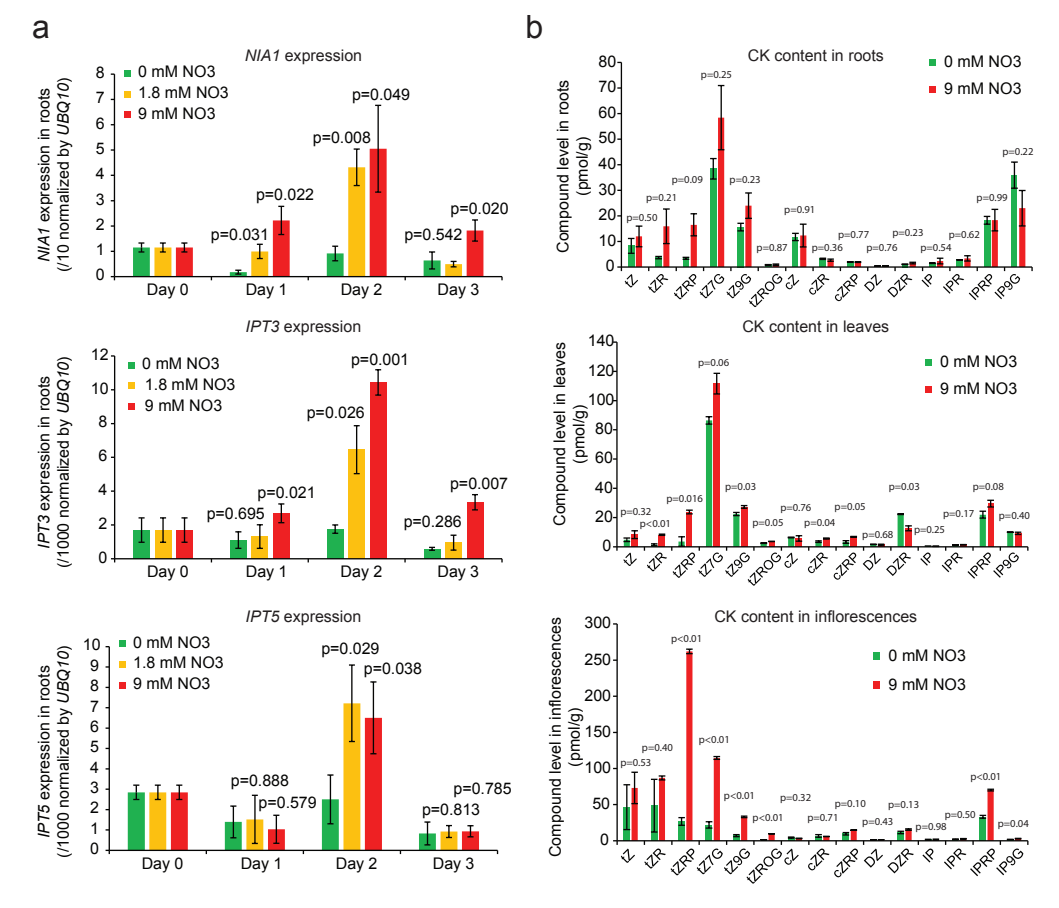

a
b
c
d
e
f
1/3 Soil 2/3 Sand
1/2 Soil 1/2 Sand
2/3 Soil 1/3 Sand
1/1 Soil
1/1 Soil + Fertilizer
pWUS::GFP domain area (µm²)
pWUS::GFP signal (A.U.)
Meristem size (µm²)
R²= 0.827, p-value: <10 -16
R²= 0.713, p-value: 2.3 x10-15
R²= 0.896, p-value: <10-16
WUS-GFP
1rst replicate
2nd replicate
WUS-GFP signal (A.U.)
WUS-GFP domain area (µm²)
R²= 0.873, p-value: <10-16
R²= 0.874, p-value: <10-16
R²= 0.906, p-value: <10-16
R²= 0.907, p-value: <10-16
pCLV3::dsRED
1st replicate
2nd replicate
3rd replicate
pCLV3::dsRED signal (A.U.)
pCLV3::dsRED domain size (µm²)
R²= 0.736, p-value: <10-16
R²= 0.123, p-value: 7.2 x 10-3
R²= 0.057, p-value: 0.072
R²= 0.790, p-value: <10-16
R²= 0.670, p-value: 2.4 x 10-13
R²= 0.144, p-value: 0.007
pTCSn::GFP domain size (µm²)
pTCSn::GFP signal (A.U.)
R²= 0.672, p-value: 1.2 x 10-14
R²= 0.401, p-value: 2.3 x 10-7
R²= 0.663, p-value: 1.3 x 10-13

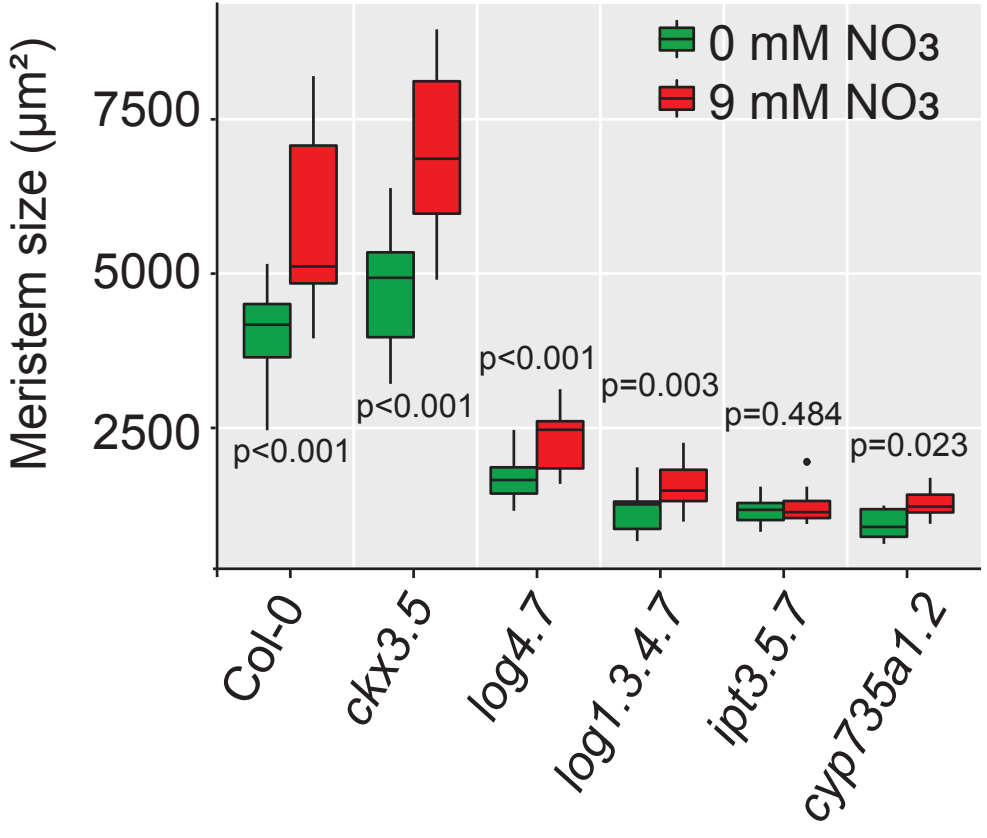

a
1/1 Soil + Fertilizer
Rosette weight (g)
p=0.585
p=0.197
p=0.971
p=0.006
p<0.001
Col0 (n=25)
ckx3.5 (n=27)
log4.7 (n=24)
log1.3.4.7 (n=25)
ipt3.5.7 (n=20)
cyp735a1.2 (n=20)
b
1/1 Soil + Fertilizer
Meristem size (µm²)
p<0.001
p<0.001
p<0.001
p<0.001
p<0.001
Col0 (n=25)
ckx3.5 (n=27)
log4.7 (n=24)
log1.3.4.7 (n=25)
ipt3.5.7 (n=20)
cyp735a1.2 (n=20)
c
1/1 Soil + Fertilizer
Plastochron ratio
p<0.001
p<0.001
p<0.001
p<0.001
p<0.001
Col0 (n=25)
ckx3.5 (n=27)
log4.7 (n=24)
log1.3.4.7 (n=25)
ipt3.5.7 (n=20)
cyp735a1.2 (n=20)
d
1/1 Soil + Fertilizer
Flower production
p=0.004
p<0.001
p<0.001
p<0.001
p<0.001
Col0 (n=36)
ckx3.5 (n=19)
log4.7 (n=17)
log1.3.4.7 (n=14)
ipt3.5.7 (n=14)
cyp735a1.2 (n=35)
e
WUS as
Col-0
ckx3.5
log4.7
log1.3.4.7
ipt3.5.7
cyp735a1.2
WUS expression area (µm²)
p=0.007
p=0.002
p<0.001
p<0.001
p<0.001
Col-0 (n=8)
ckx3.5 (n=6)
log4.7 (n=8)
log1.3.4.7 (n=8)
ipt3.5.7 (n=8)
cyp735a1.2 (n=8)
f
Replicate 1
Compound level in inflorescences (pmol/g)
1/1 Soil
1/1 Soil + Fertilizer
p=0.27
p=0.04
p=0.07
p=0.011
p=0.10
p=0.13
p=0.04
p=0.22
p=0.66
p=0.62
p=0.27
p=0.80
p=0.80
p=0.46
p=0.99
p=0.27
tZ
tZR
tZRP
tZ7G
tZ9G
tZOG
tZROG
cZ
cZR
cZRP
DZ
DZR
IP
IPR
IPRP
IP9G
Replicate 2
Compound level in inflorescences (pmol/g)
1/1 Soil
1/1 Soil + Fertilizer
p=0.73
p=0.03
p=0.37
p=0.03
p=0.21
p=0.50
p=0.59
p=0.17
p=0.30
p=0.72
p=0.27
p=0.44
tZ
tZR
ZRP
ZROG
cZR
cZRP
DZ
DZR
DZRP
IP
IPRP
IPR

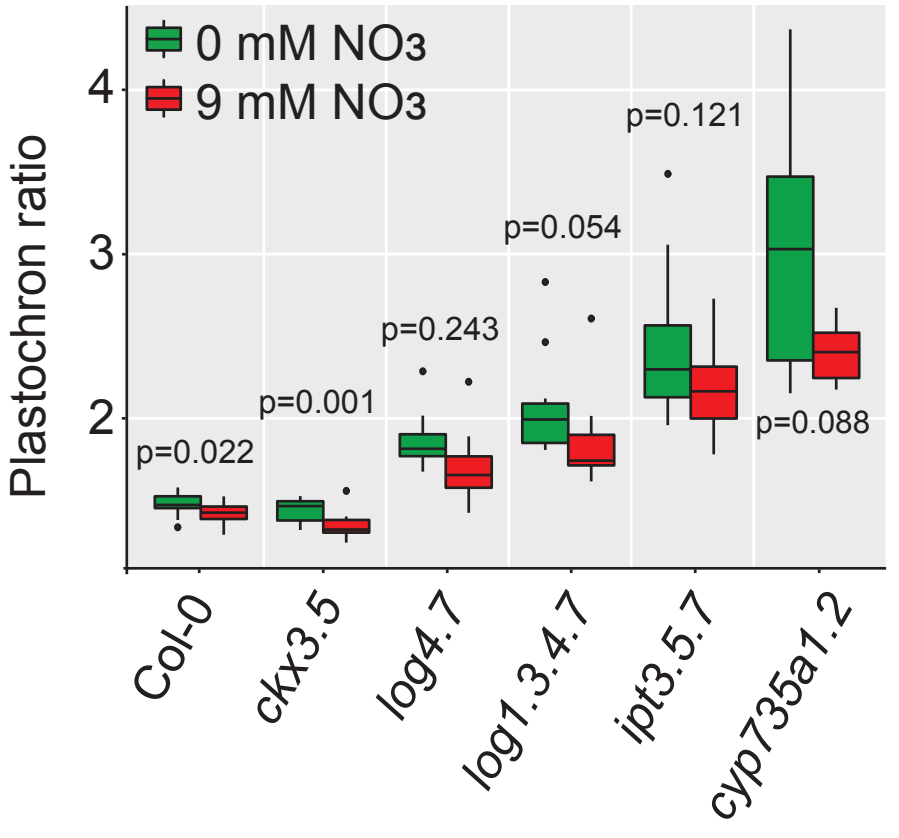

a
Rootstock:
Col-0
mutant
Plastochron ratio
p=0.936
p=0.901
p=0.026
p<0.001
p<0.001
n=111
n=40
n=35
n=34
n=32
n=36
n=34
n=58
n=48
n=26
n=26
Col-0
ckx3.5
log4.7
log1.3.4.7
ipt3.5.7
cyp735a1.2
Genotype of the scion
b
Col-0 / Col-0
ckx3.5 / ckx3.5
log4.7 / log4.7
log1.3.4.7 / log1.3.4.7
ip3.5.7 / ipt3.5.7
cyp735a1.2 / cyp735a1.2
Col-0 / ckx3.5
Col-0 / log4.7
Col-0 / log1.3.4.7
Col-0 / ipt3.5.7
Col-0 / cyp735a1.2
c
Scion:
Col-0
mutant
Mersitem szie (µm²)
p<0.001
p=0.204
p=0.602
p<0.001
p<0.001
p<0.001
p<0.001
p<0.001
p<0.001
p<0.001
n=115
n=41
n=30
n=35
n=29
n=37
n=33
n=58
n=44
n=26
n=26
Col-0
ckx3.5
log4.7
log1.3.4.7
ipt3.5.7
cyp735a1.2
Genotype of the rootstock
d
Scion:
Col-0
mutant
Plastochron ratio
p=0.026
p<0.001
p<0.001
p=0.396
p<0.001
p=0.116
p<0.001
p<0.001
p<0.001
p=0.003
n=111
n=40
n=29
n=34
n=29
n=36
n=33
n=58
n=44
n=26
n=26
Col-0
ckx3.5
log4.7
log1.3.4.7
ipt3.5.7
cyp735a1.2
Genotype of the rootstock

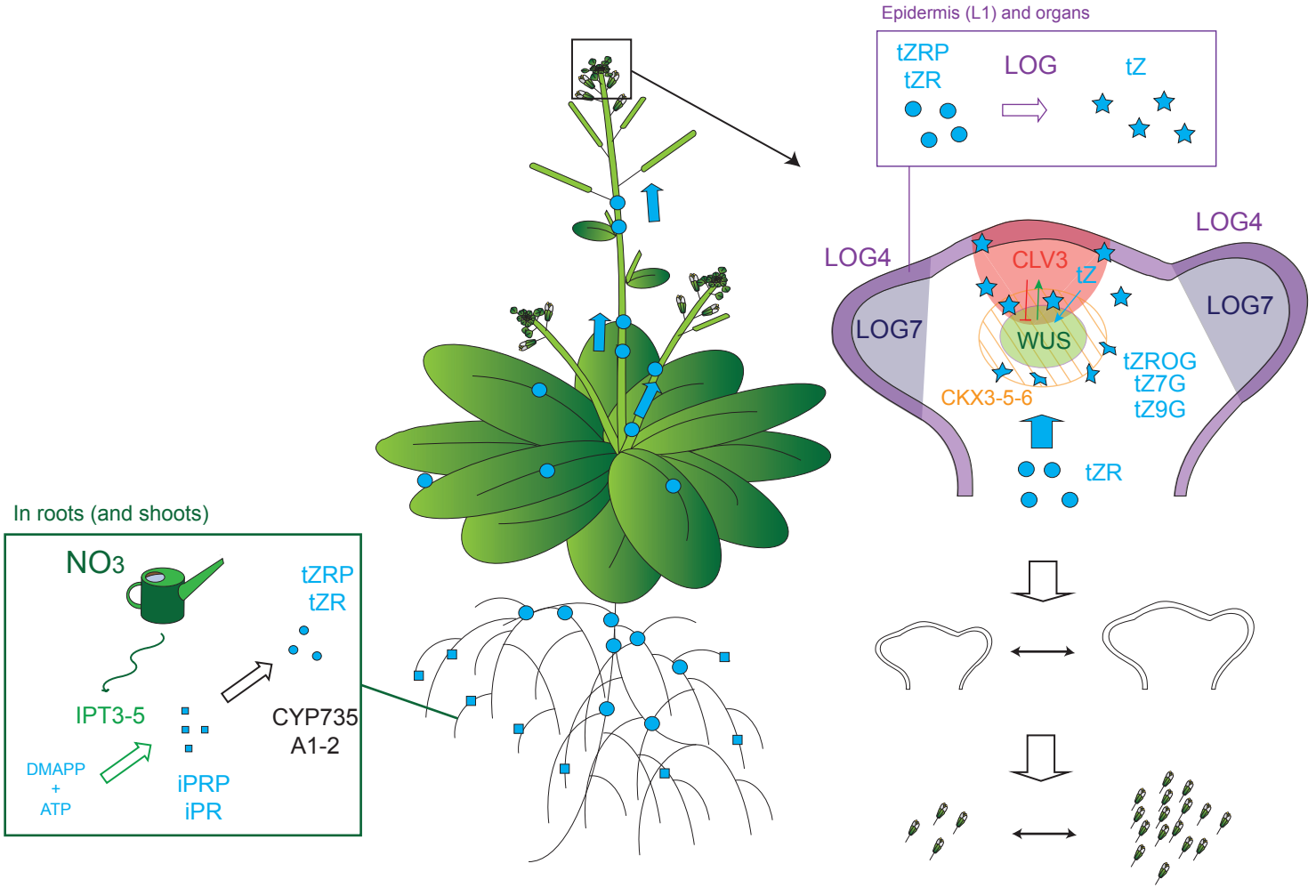

a
DMSO control
2000
10
p35S>>IPT3 pTCS::GFP
Estradiol-induced
2000
10
t0h
t24h
t48h
Control
Estradiol
pTCS::GFP signal
(normalized by t0h)
3
2.5
2
1.5
1
0.5
0
p<0.001
p<0.001
t24h
t48h
b
DMSO control
1000
10
p35S>>IPT3 pWUS::GFP
Estradiol-induced
1000
10
t0h
t24h
t48h
Control
Estradiol
pWUS::GFP signal
(normalized by t0h)
1
0.8
0.6
0.4
0.2
0
p<0.001
p=0.002
t24h
t48h


a
0 mM NO3
1.8 mM NO3
9 mM NO3
pTCSn::GFP signal (A.U.)
p=0.324
p=0.307
p=0.672
p=0.006
p=0.005
p<0.001
Day 0
Day 1
Day 2
Day 3
b
0 mM NO3
1.8 mM NO3
9 mM NO3
pWUS::GFP signal (A.U.)
p=0.037
p=0.104
p=0.007
p<0.001
p=0.001
p<0.001
Day 0
Day 1
Day 2
Day 3
c
0 mM NO3
1.8 mM NO3
9 mM NO3
Meristem area (µm²)
p=0.208
p=0.206
p=0.017
p<0.001
p=0.007
p<0.001
Day 0
Day 1
Day 2
Day 3
d
0 mM NO3
1.8 mM NO3
9 mM NO3
Plastochron ratio
p=0.549
p=0.187
p=0.499
p=0.029
p=0.116
p=0.001
Day 0
Day 1
Day 2
Day 3


a
NIA1 expression
0 mM NO3
1.8 mM NO3
9 mM NO3
NIA1 expression in roots
(/10 normalized by UBQ10)
p=0.031
p=0.022
p=0.008
p=0.049
p=0.542
p=0.020
Day 0
Day 1
Day 2
Day 3
IPT3 expression
IPT3 expression in roots
(/1000 normalized by UBQ10)
p=0.695
p=0.021
p=0.026
p=0.001
p=0.286
p=0.007
IPT5 expression
IPT5 expression in roots
(/1000 normalized by UBQ10)
p=0.888
p=0.579
p=0.029
p=0.038
p=0.813
p=0.785
b
CK content in roots
Compound level in roots
(pmol/g)
p=0.50
p=0.21
p=0.09
p=0.25
p=0.23
p=0.87
p=0.91
p=0.36
p=0.77
p=0.76
p=0.23
p=0.54
p=0.62
p=0.99
p=0.22
tZ
tZR
tZRP
tZ7G
tZ9G
tZROG
cZ
cZR
cZRP
DZ
DZR
IP
IPR
IPRP
IP9G
CK content in leaves
Compound level in leaves
(pmol/g)
p=0.32
p<0.01
p=0.016
p=0.06
p=0.03
p=0.05
p=0.76
p=0.04
p=0.05
p=0.68
p=0.03
p=0.25
p=0.17
p=0.08
p=0.40
CK content in inflorescences
Compound level in inflorescences
(pmol/g)
p=0.53
p=0.40
p<0.01
p<0.01
p<0.01
p<0.01
p=0.32
p=0.71
p=0.10
p=0.43
p=0.13
p=0.98
p=0.50
p<0.01
p=0.04


Meristem size (µm²)
7500
5000
2500
0 mM NO3
9 mM NO3
p<0.001
p<0.001
p<0.001
p=0.003
p=0.484
p=0.023
Col-0
ckx3.5
log4.7
log1.3.4.7
ipt3.5.7
cyp735a1.2


Plastochron ratio
4
3
2
0 mM NO3
9 mM NO3
p=0.022
p=0.001
p=0.243
p=0.054
p=0.121
p=0.088
Col-0
ckx3.5
log4.7
log1.3.4.7
ipt3.5.7
cyp735a1.2


Epidermis (L1) and organs
tZRP
tZR
LOG
tZ
LOG4
LOG4
CLV3
tZ
LOG7
LOG7
WUS
tZROG
tZ7G
tZ9G
CKX3-5-6
tZR
In roots (and shoots)
NO3
tZRP
tZR
IPT3-5
CYP735
A1-2
DMAPP
+
ATP
iPRP
iPR