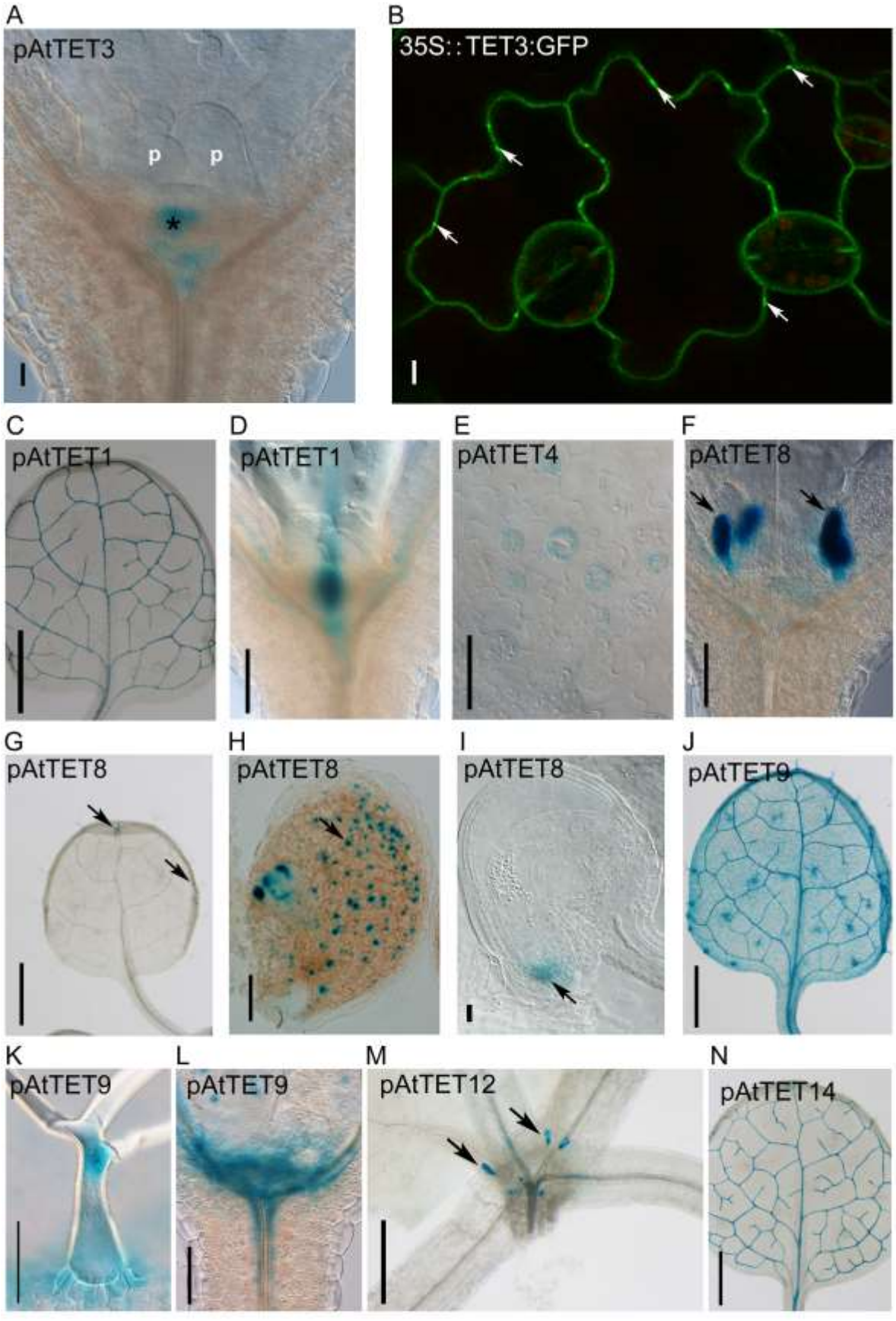
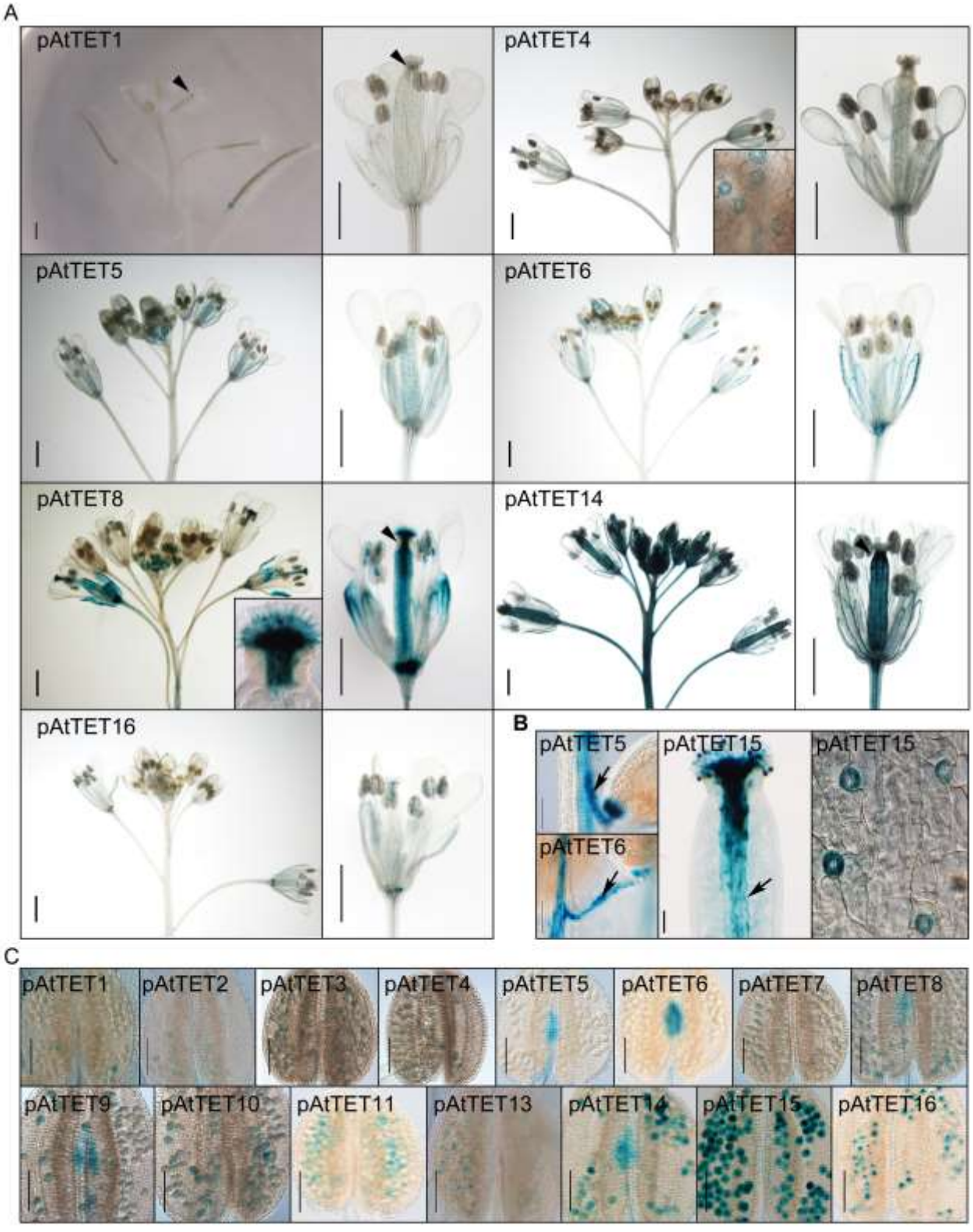
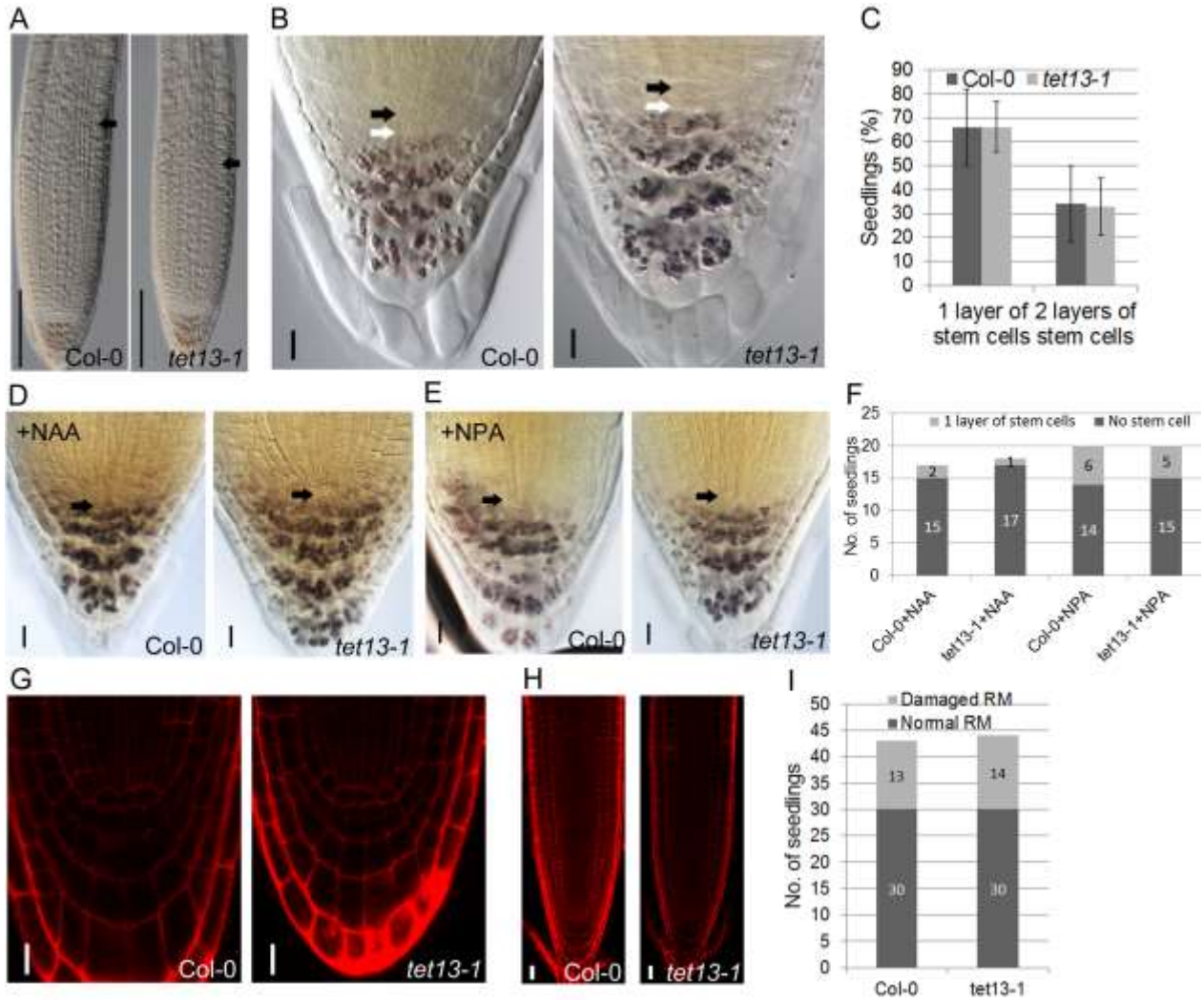

A
pAtTET3
p
p
*
B
35S::TET3:GFP
C
pAtTET1
D
pAtTET1
E
pAtTET4
F
pAtTET8
G
pAtTET8
H
pAtTET8
I
pAtTET8
J
pAtTET9
K
pAtTET9
L
pAtTET9
M
pAtTET12
N
pAtTET14

Supplemental Figure S1. *TET* expression in seedlings, seeds and TET3 protein localization. Transgenic plants shown are: *pAtTET1::NLS-GFP/GUS* (C and D), *pAtTET3::NLS-GFP/GUS* (A), *p35S::TET3:GFP* (B), *pAtTET4::NLS-GFP/GUS* (E), *pAtTET8::NLS-GFP/GUS* (F-I), *pAtTET9::NLS-GFP/GUS* (J-L), *pAtTET12::NLS-GFP/GUS* (M), and *pAtTET14::NLS-GFP/GUS* (N). A, *TET3* expression in the SAM. p, primordia. Asterisk indicates the *TET3* expression in the SAM organizing center of layer 3. B, TET3 protein localization at the plasmodesmata of cotyledons. Arrows indicate plasmodesmata. C and D, *TET1* expression in the leaf vascular tissue and in the SAM, respectively. E, *TET4* expression in the stomatal guard cells. F-I, *TET8* expression in the stipules, hydathodes, endosperm and presumably synergid cells, respectively, as indicated by arrows in each panel. J-L, *TET9* expression in the leaf, trichome and SAM, respectively. M, *TET12* expression in the stipules, as indicated by arrows. N, *TET14* expression in the leaf vascular tissue. Scale bars represent 5 μm (A and B), 1 mm (C, G, J and N), 0.1 mm (D, F, H, K and L), 0.05 mm (E), 0.01 mm (I), and 0.5 mm (M).

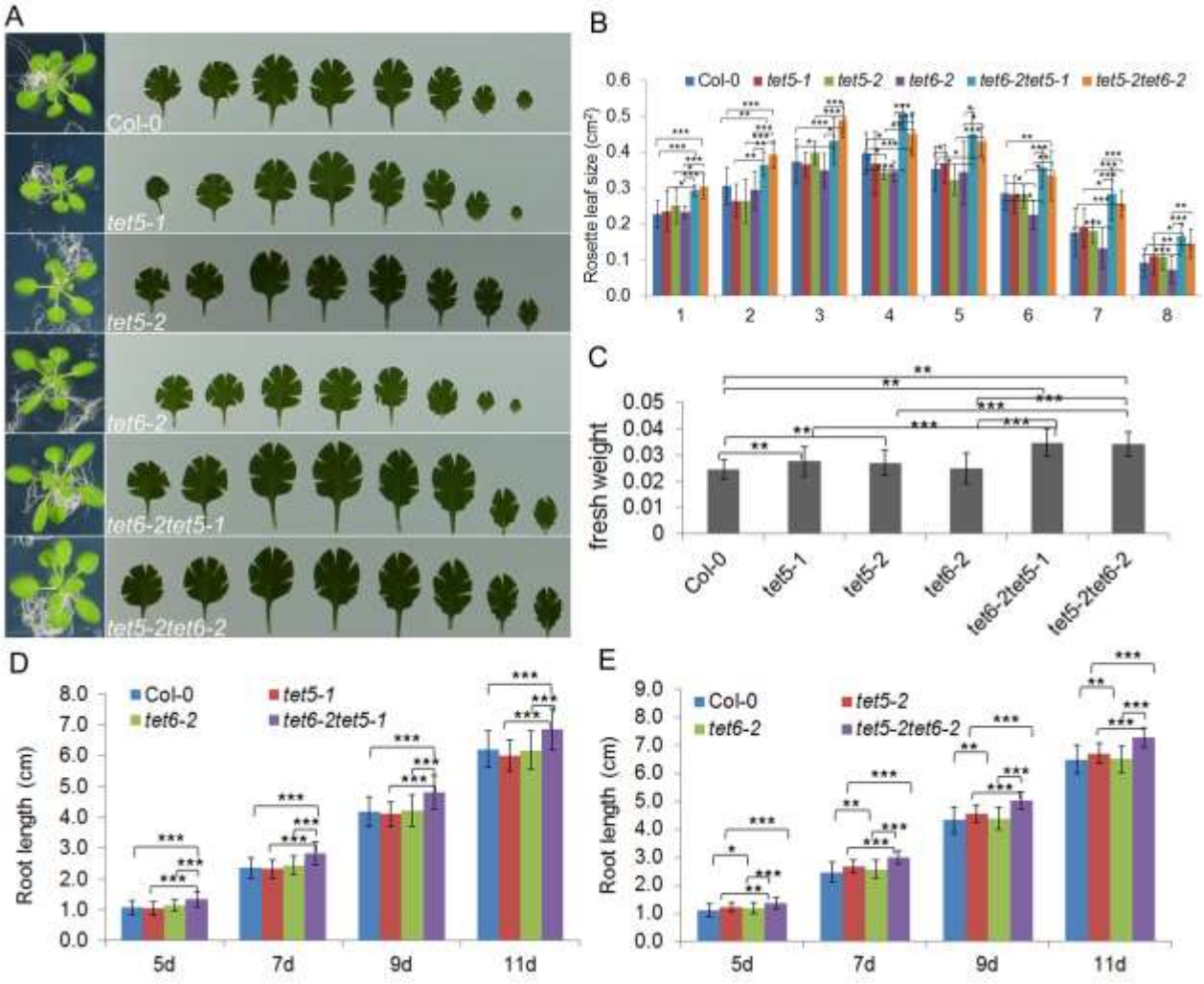

A
pAtTET1
pAtTET4
pAtTET5
pAtTET6
pAtTET8
pAtTET14
pAtTET16
B
pAtTET5
pAtTET15
pAtTET15
pAtTET6
C
pAtTET1
pAtTET2
pAtTET3
pAtTET4
pAtTET5
pAtTET6
pAtTET7
pAtTET8
pAtTET9
pAtTET10
pAtTET11
pAtTET13
pAtTET14
pAtTET15
pAtTET16

Supplemental Figure S2. *TET* expression in flower organs. Transgenic plants shown are: *pAtTET1::NLS-GFP/GUS* (A and C), *pAtTET2::NLS-GFP/GUS* (C), *pAtTET3::NLS-GFP/GUS* (C), *pAtTET4::NLS-GFP/GUS* (A and C), *pAtTET5::NLS-GFP/GUS* (A-C), *pAtTET6::NLS-GFP/GUS* (A-C), *pAtTET7::NLS-GFP/GUS* (C), *pAtTET8::NLS-GFP/GUS* (A and C), *pAtTET9::NLS-GFP/GUS* (C), *pAtTET10::NLS-GFP/GUS* (C), *pAtTET11::NLS-GFP/GUS* (C), *pAtTET13::NLS-GFP/GUS* (C), *pAtTET14::NLS-GFP/GUS* (A and C), *pAtTET15::NLS-GFP/GUS* (B and C), and *pAtTET16::NLS-GFP/GUS* (A and C). A, Overview of whole inflorescences and single flowers. Arrowheads indicate the stigma transmitting tract. Insets in *pAtTET4* and *pAtTET8* show stomatal guard cells at the anther, and the magnification of the stigma and transmitting tissue, respectively. B, *TET5* and *TET6* expression in the funiculus. *TET15* activity in the pollen tube and stomatal guard cells of the sepal. C, *TET* expression in the pollen and stamen filament tissues. Scale bars represent 1 mm (A), and 0.1 mm (B and C).

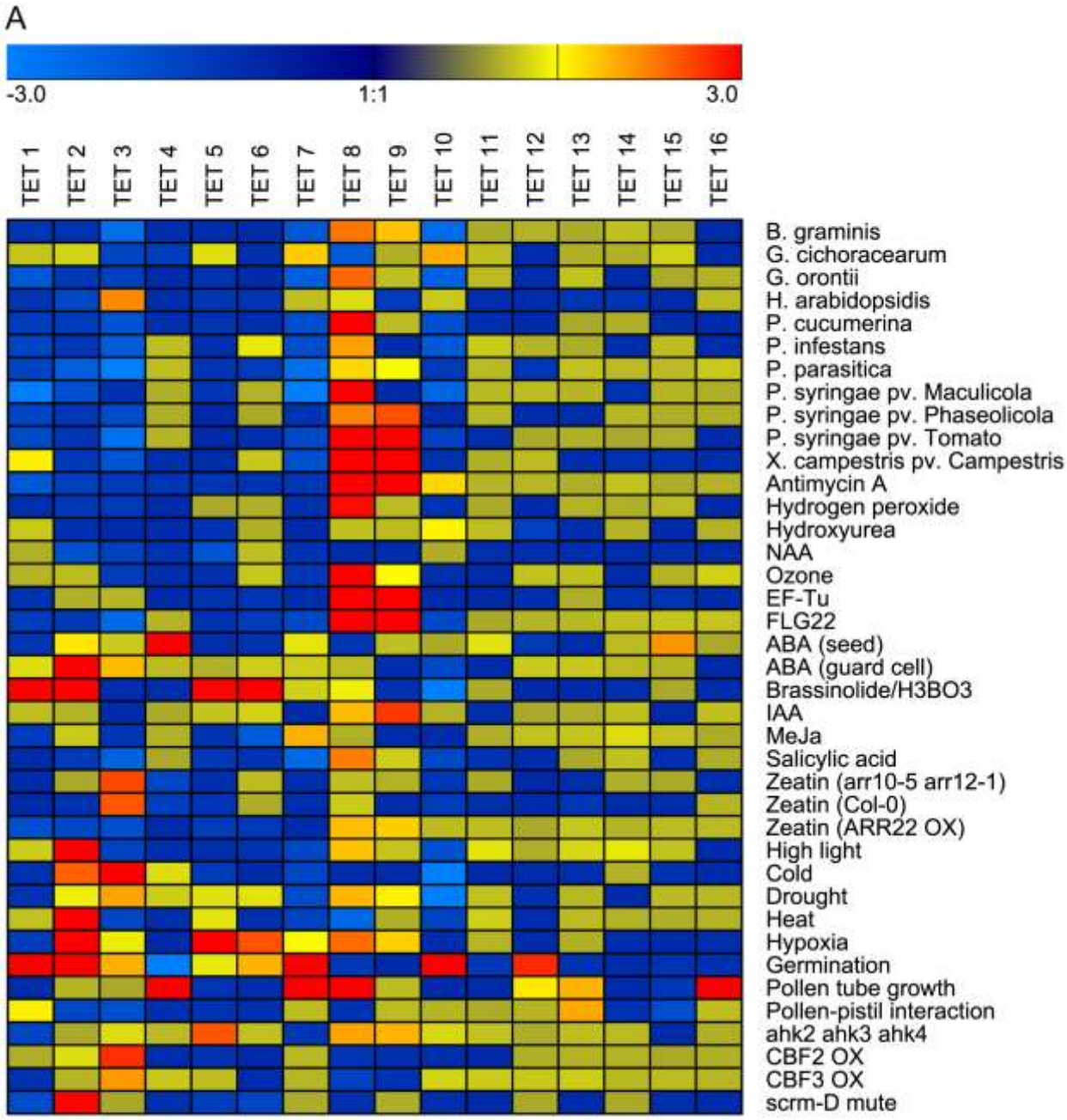


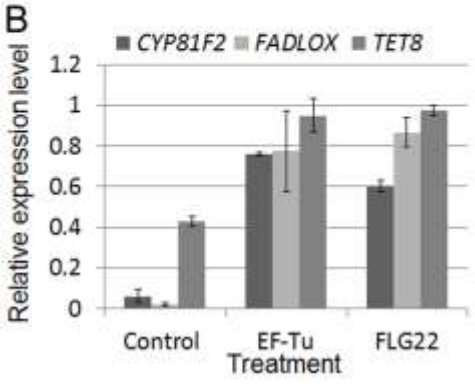
Supplemental Figure S3. *tet13-1* primary root morphology. A, Root meristem size of 6-d-old seedlings. Means are presented ± sd (n=28-39). Arrows indicate the boundary between the root meristem and the transition zone. B and C, Lugol solution staining of starch in differentiated columella cells (B) and quantification of seedlings showing one or two layers of stem cells (C). Means are presented ± sd (n=125-130). Black and white arrows indicate QC and the columella initial cells, respectively. D-F, Lugol solution staining of starch in differentiated columella cells after treatment with NAA (D) or NPA (E) and quantification of seedlings showing one or no layer of stem cells (F). Five-d-old seedlings growing under 24-h light conditions were transferred onto medium containing 1 μM NAA or 1 μM NPA for 24 h. Black arrows indicate the QC. G, Organization of QC and columella cells. The root was counterstained with propidium iodide. H

and I, Root meristem (H) and quantification of seedlings showing dead cells in the RM (I) after hydroxyurea treatment. Six-d-old seedlings growing under 24-h light conditions were transferred onto medium containing 1mM hydroxyurea for 24 h. The root was counterstained with propidium iodide. Scale bars represent 0.1 mm (A and G), 0.01 mm (B, D and E), and 0.02 mm (H).



Supplemental Figure S4. *tet5* and *tet6* single and double mutant phenotypes in other alleles. A, Rosette and leaf series of 21-d-old seedlings. From left to right were leaf 1 to leaf 8, incisions were made to make the leaves fully expanded when necessary. B, Quantification of the rosette leaf size in A. Means are presented ± sd (n=8-10). C, Fresh weight of 21-d-old seedlings. Only rosette leaves were used for the experiment. D and E, Primary root growth kinetics (root length). Means are presented ± sd (n=31-39). Asterisks in all graphs mark significant differences: *p < 0.05, **p < 0.01 and ***p < 0.001.


A
-3.0
1:1
3.0
TET 1
TET 2
TET 3
TET 4
TET 5
TET 6
TET 7
TET 8
TET 9
TET 10
TET 11
TET 12
TET 13
TET 14
TET 15
TET 16
B. graminis
G. cichoracearum
G. orontii
H. arabidopsidis
P. cucumerina
P. infestans
P. parasitica
P. syringae pv. Maculicola
P. syringae pv. Phaseolicola
P. syringae pv. Tomato
X. campestris pv. Campestris
Antimycin A
Hydrogen peroxide
Hydroxyurea
NAA
Ozone
EF-Tu
FLG22
ABA (seed)
ABA (guard cell)
Brassinolide/H3BO3
IAA
MeJa
Salicylic acid
Zeatin (arr10-5 arr12-1)
Zeatin (Col-0)
Zeatin (ARR22 OX)
High light
Cold
Drought
Heat
Hypoxia
Germination
Pollen tube growth
Pollen-pistil interaction
ahk2 ahk3 ahk4
CBF2 OX
CBF3 OX
scrm-D mute


B
CYP81F2
FADLOX
TET8
Relative expression level
1.2
1
0.8
0.6
0.4
0.2
0
Control
EF-Tu
FLG22
Treatment

Supplemental Figure S5. Heat map of *TET* response to different perturbations and *TET8* expression levels after elicitors treatment. A, The perturbations were collected from the dataset in Genevestigator. Orange/yellow and blue colors represent up- and down-regulation, respectively. Color scale represents fold-change between -3.0 and 3.0, the values beyond this range are shown in the same color as -3.0 and 3.0. B, *TET8* expression levels measured by qRT-PCR after 2-h mock or elicitor treatment at the concentration of 1 µM. *CYP81F2* and *FADLOX* genes were used as positive control (Denoux et al., 2008). Means are presented ± sd.

Supplemental Table S1. *tet* mutants collected in this study. Only the GT line of *TET13* is a transposon insertion mutant, the rest are T-DNA insertions. SALK and GABI lines are in the Columbia (Col) background and ordered from NASC (http://arabidopsis.info/), FLAG lines are in the Wassilewskija (Ws) background and ordered from INRC (http://publiclines.versailles.inra.fr/), the GT line is in the Landsberg *erecta* (L*er*) background and ordered from CSHL (http://genetrap.cshl.edu/TrHome.html). GABI lines' second insertion information is obtained according to the segregation analysis from the GABI website (http://www.gabi-kat.de/). Plant samples harvested for qRT-PCR in this study were 7-d-old seedlings growing vertically under 24-h light conditions, except for *tet13-2*, for which inflorescences were harvested. pro, promoter. HM, homozygous. HZ, heterozygous. S, sensitive to plant selective antibiotics (SALK and GT: kanamycin 50 mg/L, GABI: sulfadiazin 7.5 mg/L, FLAG: DL-phosphinothricin 50 μM/L.). KO, knock-out. D, down-regulated. U, up-regulated. NC, no change. B, results from Boavida *et al.*, 2013. E, embryo. R, root. C, cotyledon. L, rosette leaf. F, flower. LR, lateral root. LRP, lateral root primordia.

AGI code	Gene	Seed stock	Allele	T-DNA insertion	Pedigree and antibiotic resistance	qRT-PCR result	Gene expression	Phenotype
AT5G46700	*TET1*	GK-254G01.02	*trn2-7*	exon 1			E, R, C, L, F.	Altered leaf patterning and symmetry
AT2G19580	*TET2*	GK-967G02.01	*tet2-1*	intron 2	HM	KO	C, L, F, meristemoid, stomatal guard cell.	Narrow leaves, reduced leaf area
		SALK_101340C	*tet2-2*	intron 2	HM. S	D		No phenotype in leaf
AT3G45600	*TET3*	SALK_116766C	*tet3-1*	intron	HM. S	D	E, R, F, SAM organizing center.	No phenotype in primary root length, flowering time or leaf morphology under normal condition
		GK-026G04.01	*tet3-2*	intron	HM, 2nd insertion	U		No phenotype in primary root length, flowering time or leaf morphology under normal condition

		FLAG_306C01	*tet3-3*	exon 1	HM	KO[B]		No phenotype in flowering time or leaf morphology under normal condition
		FLAG_421H09	*tet3-4*	exon 1	HM	KO[B]		No phenotype in flowering time or leaf morphology under normal condition
AT5G60220	*TET4*	SALK_076971C		prom	HM. S	D	E, R, C, F.	No phenotype in primary root length
AT4G23410	*TET5*	GK-290A02.01	*tet5-1*	prom	HM	D	E, R, C, L, F.	No phenotype in seedling
		SALK_148216	*tet5-2*	exon 1	HM	KO		No phenotype in seedling
		SALK_020009C	*tet5-3*	exon 2	HM	KO		No phenotype in seedling
AT3G12090	*TET6*	SALK_139305	*tet6-2*	prom	HM	D	R, C, L, F.	No phenotype in seedling
AT2G23810	*TET8*	SALK_136039C	*tet8-1*	exon 1	HM. S	D; KO[B]	E, R, C, L, F.	No phenotype in primary root length
AT4G30430	*TET9*	GK-207H01.01	*tet9-1*	3' UTR	HM	U	R, C, L, F, trichome precusors, trichome.	No trichome morphology phenotype
AT1G63260	*TET10*	SALK_120966C		prom	HM	U	E, R, F.	No phenotype in primary root length
AT2G03840	*TET13*	SALK_011012C	*tet13-1*	exon 1	HM	KO[B]	F, QC, LR founder cell, LRP.	Reduced primary root length, root apical meristem size and LR density
		GT8699	*tet13-2*	exon 1	HM	U		No root phenotype
AT5G57810	*TET15*	GK-513E06.01		exon 2	HM	U	E, R, F.	No phenotype in primary root length

Supplemental Table S2. *TET cis*-regulatory element information

See Supplemental Table S2.xlsx file.

FDR, false discovery rate. DH, DNase I hypersensitive site. "SRP" and "GSE" codes refer to Heyndrickx et al., 2014; strong positions in the matrix are in upper case.

Supplemental Table S3. Primers used in the study.

Primer Name	Sequence (5'-3')	Purpose
pAtTET1attB4F	GGGGACAACTTTGTATAGAAAAGTTGGAATAGTAATTAAGTTATAAATTAGTACACTTG	promoter cloning
pAtTET1attB1R	GGGGACTGCTTTTTTGTACAAACTTGTCTTTTTTGGGAGAGATGAGAG	promoter cloning
pAtTET2attB4F	GGGGACAACTTTGTATAGAAAAGTTGGAGATGCATCTGGAATTTGACG	promoter cloning
pAtTET2attB1R	GGGGACTGCTTTTTTGTACAAACTTGTTAAATTTTCTCTCTCTCTCTCTCT	promoter cloning
pAtTET3attB4F	GGGGACAACTTTGTATAGAAAAGTTGGATAGAAATGTGTGTATTCAGTAAGG	promoter cloning
pAtTET3attB1R	GGGGACTGCTTTTTTGTACAAACTTGTAGCTTAGGGTTTTGAGGTTTTC	promoter cloning
pAtTET4attB4F	GGGGACAACTTTGTATAGAAAAGTTGGACTACATTTTCCAGGAAAAGCTAATG	promoter cloning
pAtTET4attB1R	GGGGACTGCTTTTTTGTACAAACTTGTGGCGATTTTGTTTTTGTTGAATATG	promoter cloning
pAtTET5attB4F	GGGGACAACTTTGTATAGAAAAGTTGGAAGTTTCCTACATATTCTCTG	promoter cloning
pAtTET5attB1R	GGGGACTGCTTTTTTGTACAAACTTGTTTTCCTTCTCTCTCCTTTTTT	promoter cloning
pAtTET6attB4F	GGGGACAACTTTGTATAGAAAAGTTGGATGCCTCTTCTTTGTTTTTAAATG	promoter cloning
pAtTET6attB1R	GGGGACTGCTTTTTTGTACAAACTTGTAGTAGTAATGTTATCAAGAAG	promoter cloning
pAtTET7attB4F	GGGGACAACTTTGTATAGAAAAGTTGGATTCACACAAGAATCTCTCTT	promoter cloning
pAtTET7attB1R	GGGGACTGCTTTTTTGTACAAACTTGTCGCTTTTTGTTCCGGCGG	promoter cloning
pAtTET8attB4F	GGGGACAACTTTGTATAGAAAAGTTGGAAAATTTAAAATAGTGCTTCAAAG	promoter cloning
pAtTET8attB1R	GGGGACTGCTTTTTTGTACAAACTTGTGGTTTAGATTCAGAGAGAAAG	promoter cloning
pAtTET9attB4F	GGGGACAACTTTGTATAGAAAAGTTGGACCGTGACTATTATTATTATTTTTA	promoter cloning
pAtTET9attB1R	GGGGACTGCTTTTTTGTACAAACTTGTGGTGATGATTGAAGAAG	promoter cloning
pAtTET10attB4F	GGGGACAACTTTGTATAGAAAAGTTGGATAGAAGAATCAAAGAGAG	promoter cloning
pAtTET10attB1R	GGGGACTGCTTTTTTGTACAAACTTGTTTTTTCAAGGTTGTTGCTTTTG	promoter cloning
pAtTET11attB4F	GGGGACAACTTTGTATAGAAAAGTTGGATTTCATTTTTCCATATCAAATG	promoter cloning
pAtTET11attB1R	GGGGACTGCTTTTTTGTACAAACTTGTTTTTGGAAATTTGCTTTCTCC	promoter cloning
pAtTET12attB4F	GGGGACAACTTTGTATAGAAAAGTTGGAATAGTCATATGGAAATTATTTG	promoter cloning
pAtTET12attB1R	GGGGACTGCTTTTTTGTACAAACTTGTTGTTTATCGGCGGTTATTTG	promoter cloning
pAtTET13attB4F	GGGGACAACTTTGTATAGAAAAGTTGGAAAACATTATATTATTTCAAAATA	promoter cloning
pAtTET13attB1R	GGGGACTGCTTTTTTGTACAAACTTGTTATCGTGTAAAGAGAAAGGG	promoter cloning

pAtTET14attB4F	GGGGACAACTTTGTATAGAAAAGTTGGATGCTTCTTTTTCAAAGAGTG	promoter cloning
pAtTET14attB1R	GGGGACTGCTTTTTTGTACAAACTTGTTATTGGAGAGCTTCAAGGACAG	promoter cloning
pAtTET15attB4F	GGGGACAACTTTGTATAGAAAAGTTGGAGGCTGATCTGATCAATGAATTG	promoter cloning
pAtTET15attB1R	GGGGACTGCTTTTTTGTACAAACTTGTGTGAAAGTGAAAGAAAG	promoter cloning
pAtTET16attB4F	GGGGACAACTTTGTATAGAAAAGTTGGAATTAAAAATCTTTCCGG	promoter cloning
pAtTET16attB1R	GGGGACTGCTTTTTTGTACAAACTTGTTGTTAAGAACCCTGTTCG	promoter cloning
pAtTET17attB4F	GGGGACAACTTTGTATAGAAAAGTTGGAAGAAAATCTTACCTGCAAATCTCAG	promoter cloning
pAtTET17attB1R	GGGGACTGCTTTTTTGTACAAACTTGTTGTTGTTTTTTGGTATAGACCTG	promoter cloning
qPP2A_F	TAACGTGGCCAAAATGATGC	qRT-PCR
qPP2A_R	GTTCTCCACAACCGCTTGGT	qRT-PCR
qUBC_F	CTGCGACTCAGGGAATCTTCTAA	qRT-PCR
qUBC_R	TTGTGCCATTGAATTGAACCC	qRT-PCR
TET5 qPCR_F	TACTGTGTTGGCTGTTGCG	qRT-PCR
TET5 qPCR_R	GACTGTTCCCATCCAGGTCT	qRT-PCR
TET6 qPCR_F	CAGCTCATCCTTACCATCCA	qRT-PCR
TET6 qPCR_R	CCACCAGTAATAGTCCCAACG	qRT-PCR
TET3 attB1F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAGAAGGAGATAGAACCATGAGAACAAGCAACCATCTCATAG	gene cloning
TET3 attB2R	GGGGACCACTTTGTACAAGAAAGCTGGGTCAAGATGGAAATGACTAGGATGTG	gene cloning
TET13 attB1F	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAGAAGGAGATAGAACCATGGCGAGAGATAAAGAAGATC	gene cloning
TET13 attB2R	GGGGACCACTTTGTACAAGAAAGCTGGGTCCTATTTCTGACTTTCTCGAAGG	gene cloning
Bar_F	GCCACCGAGGCGGACATG	genotyping
Bar_R	GGGCAGCCCGATGACAGC	genotyping

Supplemental Movie S1. TET3-GFP movement on the plasma membrane.

See Supplemental Movie S1.avi file.

Supplemental Reference

Denoux C, Galletti R, Mammarella N, Gopalan S, Werck D, De Lorenzo G, Ferrari S, Ausubel FM, Dewdney J (2008) Activation of defense response pathways by OGs and Flg22 elicitors in *Arabidopsis* seedlings. Mol Plant **1:** 423-445