Supplementary data:

Expression patterns of *FLAGELLIN SENSING 2* map to bacterial entry sites in plant shoots and roots

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Supplement Table*:*

Table 1: Flg22 up-regulated genes in roots, microarray data

Supplement Figures*:*

Fig S1: Prediction of *FLS2* promoter motifs 1000bp upstream of At5g46330

(A) Visualization of promoter motifs 1000 bp upstream of ATG. **(B)** Details of predicted promoter motifs 1000 bp upstream of ATG.

Prediction with Athena: a resource for rapid visualization and systematic analysis of Arabidopsis promoter sequences (O'Connor *et al.,* 2005; http://www.bioinformatics2.wsu.edu/Athena).

Figure S2: *FLS2* promoter activity during plant development

pFLS2::*GUS* is ubiquitously expressed in **(A)** 2 days-old seedling, in **(B)** 8 days-old seedling cotyledons and **(C)** hypocotyl; and highly expressed in **(D)** flower sepals and **(E)** stamen, in **(F)** pod dehiscence zone in mature siliques and **(G)** stipules.

Figure S3: *FLS2* promoter activity during leaf development, wound stress and biotic stress

(A) Definition of different leaf stages; **(B)** GUS staining of *pFLS2*::*GUS* in different leaf stages. Insert shows hydathodes. **(C)** Wound-induced promoter activity in different leaf stages. Insert shows hydathodes. **(D)** Hypocotyl after *Pto* DC3000 incubation with enhanced promoter activity in stomata (arrows), compared to mock treated (10mM $MgCl_2$) hypocotyl; bar = 100 µm.

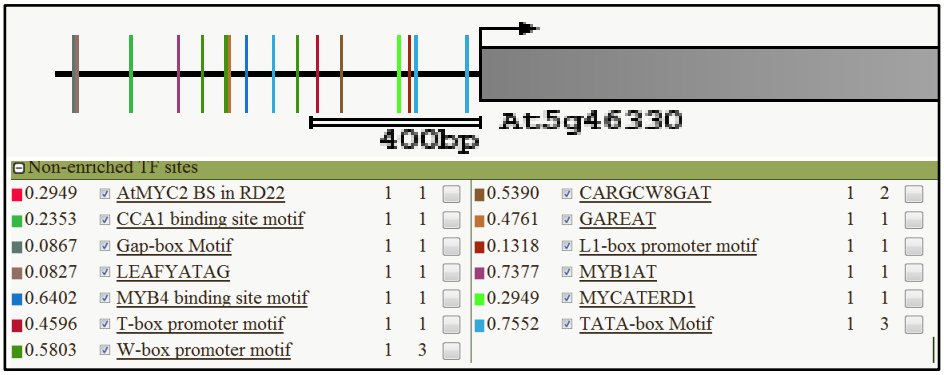
Figure S4: *Pto* DC3000-GFP localization on leaves and roots

(A) Confocal micrographs showing *Pto* DC3000-GFP (green) on Col-0 leaves, upper panel shows bacteria on epidermis, encircled are stomata, lower panel shows bacteria (arrow heads) in the apoplast of mesophyll cells (block arrows); chloroplast autofluorescence is represented in red. **(B)** Confocal micrographs showing DC3000-GFP (green) bacteria on Col-0 roots stained with propidium iodide (red); note the accumulation of bacteria (arrow heads) at outgrowing LR (block arrows).

Figure S5: *FLS2* promoter activity in non-sterile grown roots and flg22 dependent inhibition of root growth

(A) *pFLS2*::*GUS* activity in 14 days-old seedlings grown on soil, white arrow shows inner vasculature, black arrows mark expansion of GUS staining, bar = 50 µm. **(B)** Cross section of roots grown on soil, arrows mark expanded GUS activity in endodermis, bar = 10 µm. **(C)** Graph depicts root length of 12 days-old Col-0 or *fls2* treated with 1 µM flg22 or without (same seedlings as used for 3F, bars represent average of 3 independent experiments, error bars represent SD, statistical significance represented with student t-test (p-value >0.001).

A



B

At5g46330		
Motifs		
AtMYC2 BS in RD22		**CACATG**
189 -184	(-)	CATGTG
CARGCW8GAT		**CWWWWWWWWG**
329 -320	(+)	CATAAATAAG
329 -320	(-)	CATAAATAAG
CCA1 binding site motif		**AAMAATCT**
826 -819	(-)	AGATTGTT
GAREAT		**TAACAAR**
593 -587	(+)	TAACAAA
Gap-box Motif		**CAAATGAA**
962 -955	(-)	TTCATTTG
L1-box promoter motif		**TAAATGYA**
164 -157	(-)	TACATTTA
LEAFYATAG		**CCAATGT**
953 -947	(+)	CCAATGT
MYB1AT		**WAACCA**
710 -705	(+)	AAACCA
MYB4 binding site motif		**AMCWAMC**
550 -544	(-)	GTTTGTT
MYCATERD1		**CATGTG**
189 -184	(+)	CATGTG
T-box promoter motif		**ACTTTG**
381 -376	(+)	ACTTTG
TATA-box Motif		**TATAAA**
484 -479	(+)	TATAAA
29 -24	(+)	TATAAA
151 -146	(-)	TTTATA
W-box promoter motif		**TTGACY**
601 -596	(+)	TTGACC
432 -427	(+)	TTGACT
655 -650	(-)	AGTCAA
EIN3 binding sites		**ATGTATCT**
325-317		ATGAATaT
304-297		AcATACAT
285-278		ATGAATaT

Figure S1

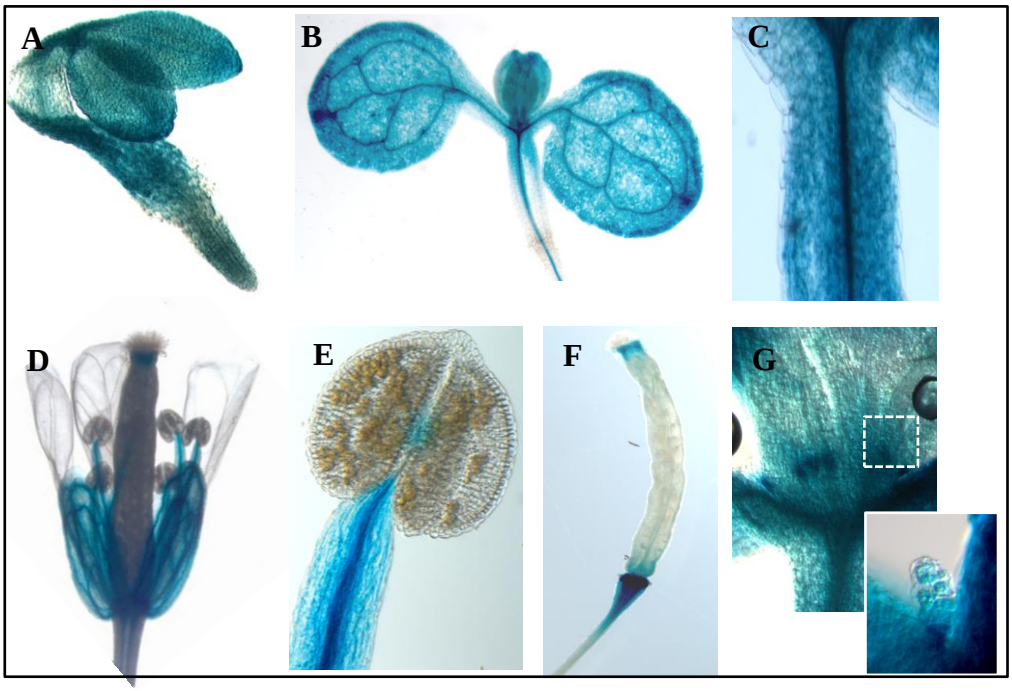


Figure S2

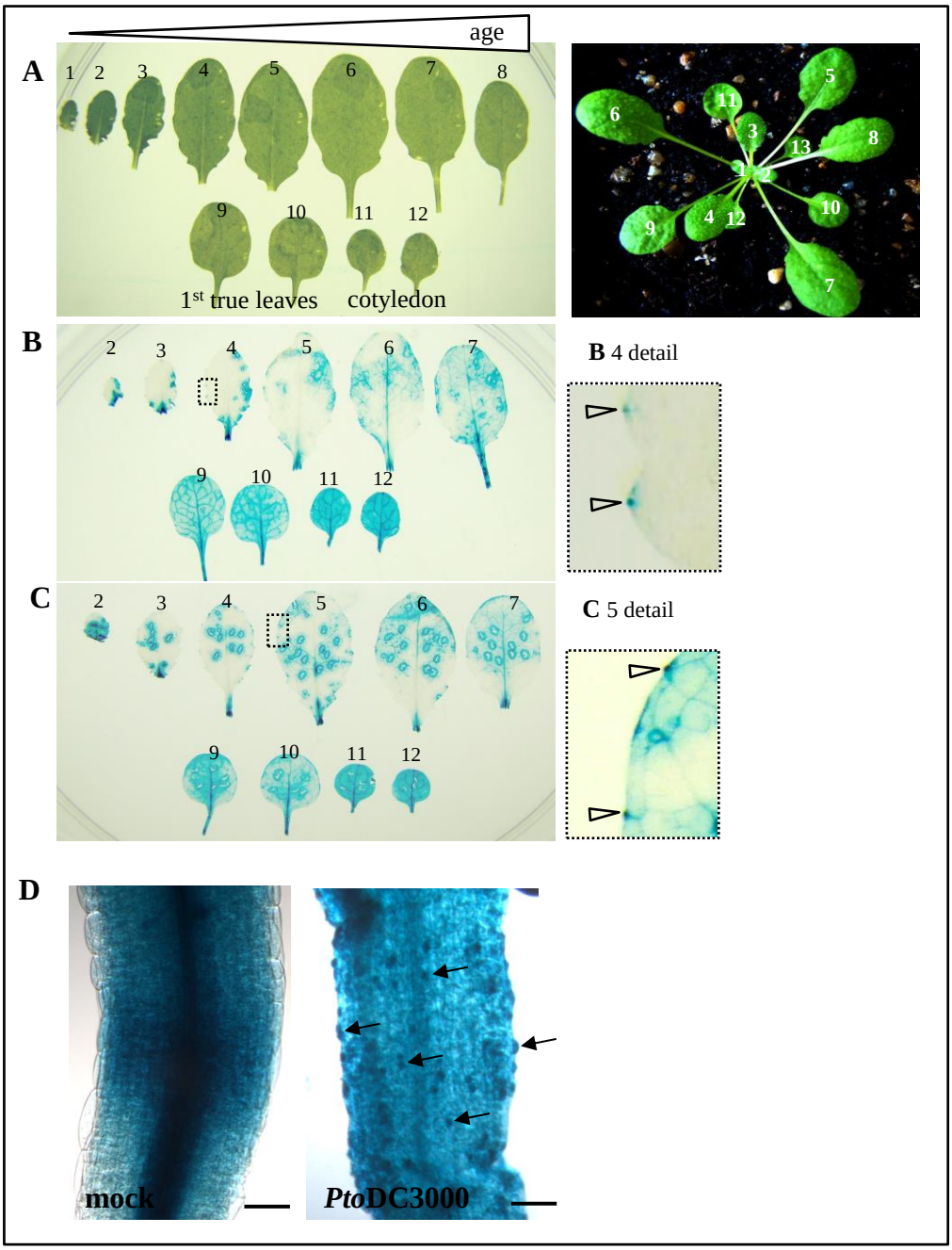

A
age
1 2 3 4 5 6 7 8
9 10 11 12
1st true leaves
cotyledon
B
2 3 4 5 6 7
9 10 11 12
B 4 detail
C
2 3 4 5 6 7
9 10 11 12
C 5 detail
D
mock
PtoDC3000

Figure S3

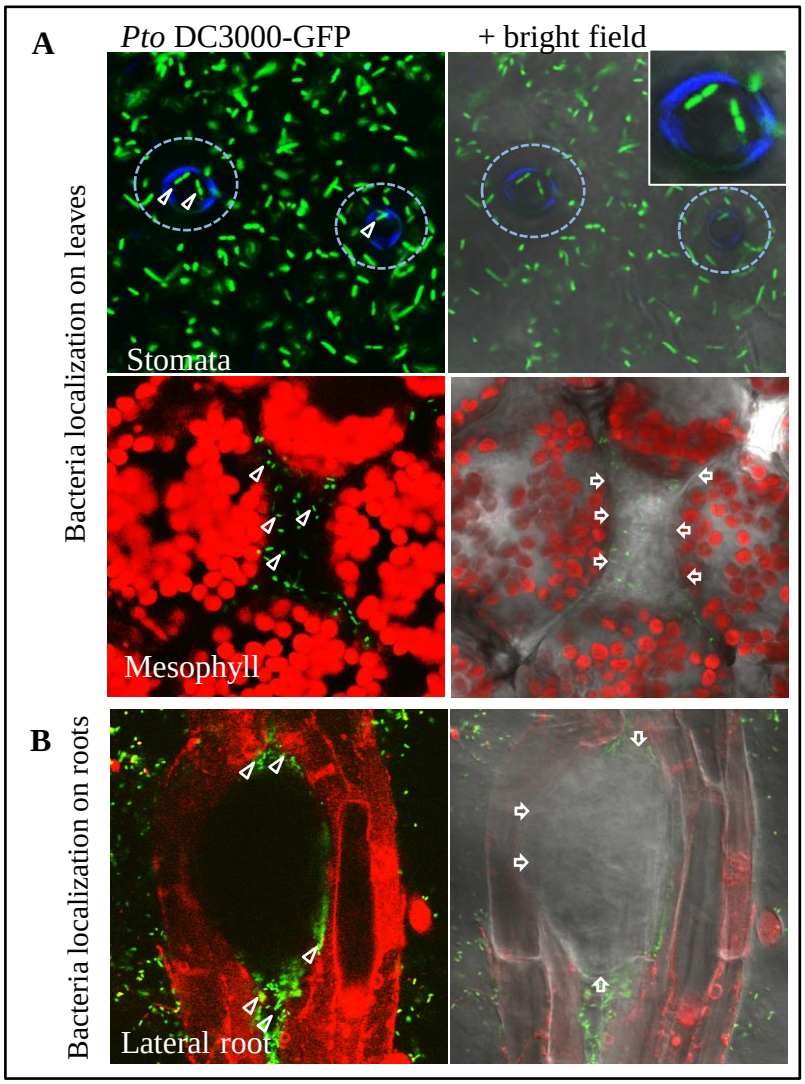
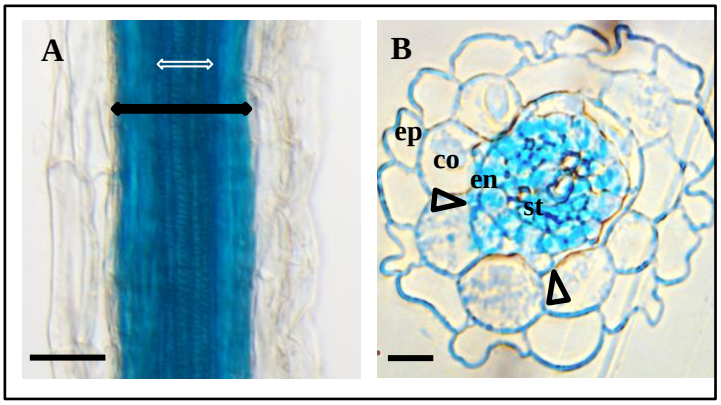

A
Pto DC3000-GFP
+ bright field
Bacteria localization on leaves
Stomata
Mesophyll
B
Bacteria localization on roots
Lateral root

Figure S4


A
B
ep
co
en
st

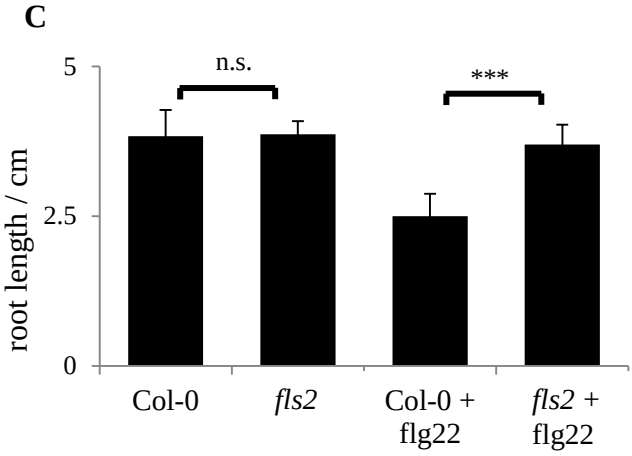

C
n.s.
***
5
2.5
0
root length / cm
Col-0
fls2
Col-0 + flg22
fls2 + flg22

Figure S5