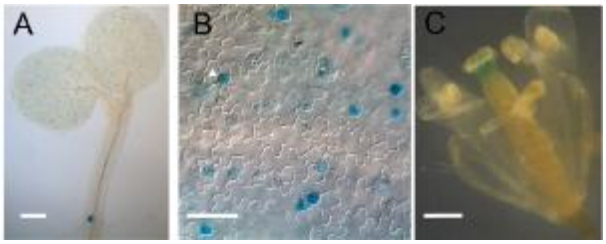


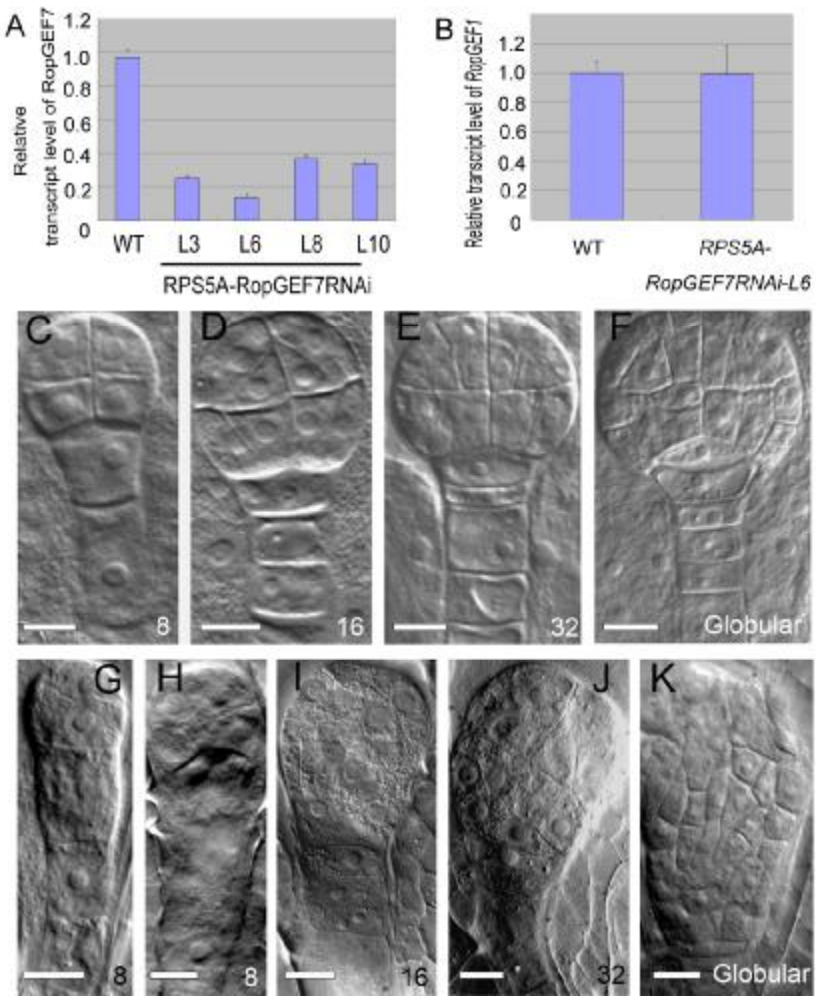
Supplemental Figure 1. *RopGEF7* expression pattern analysis

(A) *RopGEF7-GUS* expression in 5-d-old seedlings, GUS staining was for 16 h in (**A**)-(**C**).

(B) GUS activity was detected in meristemnoids and guard cells of 5-d-old seedlings, arrowhead indicates meristemnoid.

(C) GUS activity was detected in the style of the flowers.

Scale bars for **(A)** and **(C)**, 200 μm. Scale bar for **(B)**, 20 μm.



Supplemental Figure 2. Early embryo phenotypes are observed in the *RopGEF7RNAi* lines

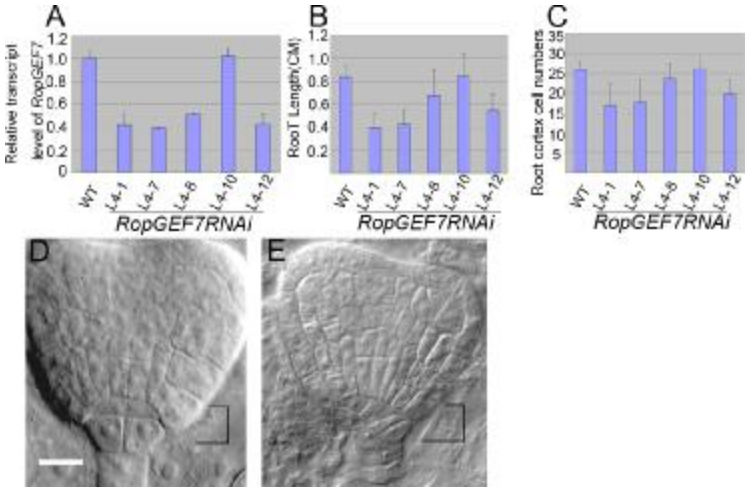
(**A**) Relative transcript level of *RopGEF7* detected by qRT-PCR in embryos of four *RPS5A-RopGEF7RNAi* transgenic lines.

(**B**) Relative transcript level of *RopGEF1* was not affected in embryos of the *RPS5A-RopGEF7RNAi*-L6 line.

(C) - (F) Wild-type embryos at 8-cells (C), 16-cells (**D**), 32-cells (**E**), and globular stage (**F**), respectively.

(**G**)-(**K**) Defects in *RPS5A-RopGEF7RNAi* embryos at corresponding stages as compared to wild-type. Figures at right bottom indicate the number of embryo cells.

Scale bars for (**C**)- (**K**), 20 μm.



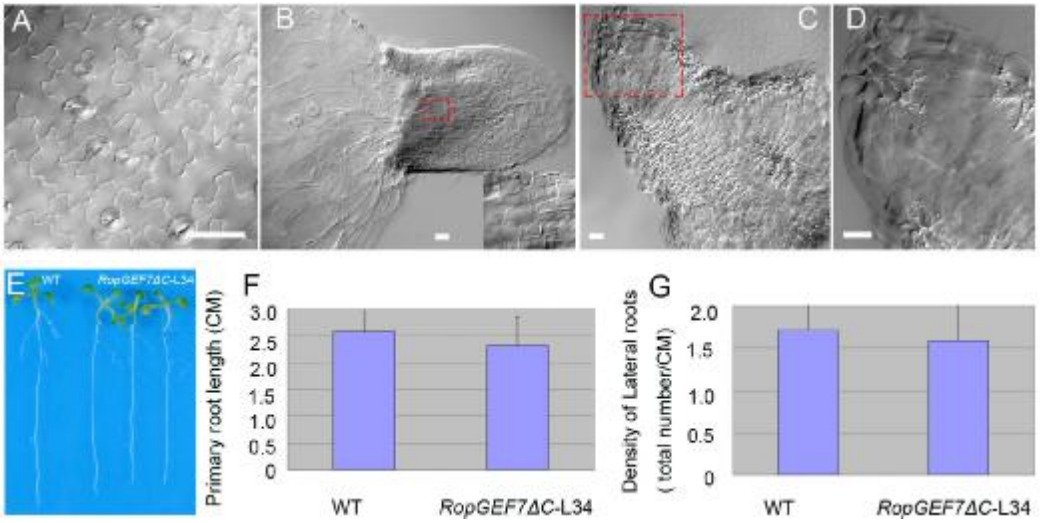
Supplemental Figure 3. Analysis of *RopGEF7 RNAi* transgenic lines

(A) Identification of *35S-RopGEF7 RNAi* transgenic lines L4-1, L4-7, L4-8, L4-10, L4-12 by qRT-PCR analysis. qRT-PCR analysis revealed four lines with various levels of reduced *RopGEF7* transcripts compared with the wild-type.

(B)-(C) 5-d-old *RopGEF7* down-regulated lines show reduced root length **(B)** and smaller root meristem size compared with the wild type **(C).** Data presented are average and SD (n=40 to 60).

(D)-(E) Comparison of embryo phenotype from wild-type **(D)** and *35S-RopGEF7RNAi* **(E)**-L1-9 line at heart stage. Bracketed area is the basal cell region.

Scale bars for (**D**)- (**E**), 20 μm.



Supplemental Figure 4 Analysis of *RopGEF7△C* overexpressing transgenic plants

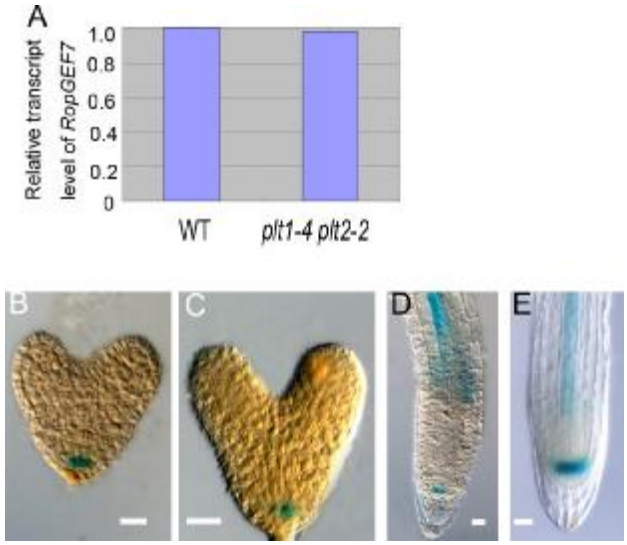
(A) Cotyledon epidermal cells of 7-d-old wild-type seedlings.

(B)-(D) Analysis of cell morphology in *RPS5A-RopGEF7△C* root-like structures, red dotted area in (**B**) indicate the root cell files that enlarged in insets, red dotted area in (**C**) indicates the root columella-like cells, **(D)** shows magnification of the tip region of the root-like structure in **(C)**.

(E) Comparison of 8-d old seedlings in *RPS5A-RopGEF7△C* –L34 line and the wild-type.

(F)-(G) Analysis of root length **(F)** and lateral roots **(G)** in 8-d-old seedlings between *RPS5A-RopGEF7△C* –L34 line and the wild-type. Data presented are average and SD (n=40 to 60).

Scale bars for **(A)** to **(D),** 50 μm.



Supplemental Figure 5. Expression of *RopGEF7* in *plt1-4 plt2-2* double mutant

(A) Relative expression levels of *RopGEF7* detected by q-RT-PCR in 7-d-old seedlings of *plt1-4 plt2-2* compared with the wild-type.

(**B**)-(**E**) *RopGEF7-GUS* expression in embryos and 6-d-old seedlings of wild-type (**B** and **D**) and *plt1-4 plt2-2* (**C** and **E**), GUS staining was for 16 h in embryos, 6 h in seedlings.

Scale bars for **(B)** to **(E),** 20 μm.

Supplemental Table 1: Primers used in the study

Vector constructions	GEF7promoter-F	5'-AAGCTTCTTCATTCATCCATCCCACCT -3'
	GEF7promoter-R	5'-TCTAGACGTGCTTGAATCGCATTACAT -3'
	GEF7RNAi-F	5'-AAGCTTCTTACAAGACATTCATCGGA-3'
	GEF7RNAi-R	5'-GTCGACATCTCAAAGTCAAAGCCCAT-3'
	YFP-GEF7-F	5'-GAATTCATGGATGGTTCGTCGGAAAAT-3'
	YFP-GEF7-R	5'-GTCGACGTCAAAGCCCATCTTTCCAA-3'
	YFP-GEF7ΔC-F	5'-AAGCTTATGGATGGTTCGTCGGAAAA -3'
	YFP-GEF7ΔC-R	5'-GTCGACTCATCTTGTAAGATCATCAACAAAGAG-3'
	YFP-AtRAC1-F	5'-CTGCAGTCCATTTCTGGTGGAGAAGG -3'
	YFP- AtRAC1-R	5'-GTCGACTTGTTCCAGAGTTCGTTGTGA -3'
	GEF7OX-F	5'-GAATTCTAATGCGATTCAAGCACGAG-3'
	GEF7OX-R	5'-GTCGACGTCAAAGCCCATCTTTCCAA-3'
	GEF7ΔCOX-F	5'-GTCGACATGGATGGTTCGTCGGAAAA -3'
	GEF7ΔCOX-R	5'-GAATTCTCATCTTGTAAGATCATCAACAAAGAG-3'
	cYFP-GEF7-F	5'-GAATTCCATGGATGGTTCGTCGGAAAATT-3'
	cYFP-GEF7-R	5'-GTCGACGTCAAAGCCCATCTTTCCAA-3'
	cYFP-GEF7ΔC-F	5'-GAATTCATGGATGGTTCGTCGGAAAA -3'
	cYFP-GEF7ΔC-R	5'-GAATTCTCATCTTGTAAGATCATCAACAAAGAG-3'
	nYFP- AtRAC1-F	5'-GAATTCAGGAAGAAGAAGAGAAATGAGCG-3'
	nYFP- AtRAC1-R	5'-GTCGACTCACAACGAACTCTGGAACAAT -3'
	RPS5A-F	5'- AGCAGCAGGAGATCTATCAGTGCA -3'
	RPS5A-R	5'- GGCTGTGGTGAGAGAAACAGAGC -3'
In situ hybridization	PLT1insitu-F	5'-ACGAAAACCAATCCAACCAC -3'
	PLT1insitu-R	5'-CCTAGACTGGCCTTCCCTTC -3'
RT-PCR analysis of *RopGEF7* expression	GEF7-F	5'-ATTCAACATTGTTGCACGCAT -3'
	GEF7-R	5'-CGGCTCGATCTTTCTAAAGGA-3'
	ACTIN2-F	5'-ATGGCTGAGGCTGATGATATTCAAC-3'
	ACTIN2-R	5'-TACAAGGAGAGAACAGCTTGGATG-3'
RT-qPCR analysis	GEF7qPCR-F	5'-CTGTACGGAGGATTTCACGGC-3'
	GEF7qPCR-R	5'-CTTCTCCAAGCAGCAGTTTCGA-3'
	GEF1qPCR-F	5'- CGGCGGCAAAGATGTGGTC-3'
	GEF1qPCR-R	5'-GATTGGTGATGGCGTTGGAGAT-3'
	ACTIN7qPCR-F	5'-AGCGATGGCTGGAACAGAAC-3'
	ACTIN7qPCR-R	5'-CCTTCGTCTTGATCTTGCGG-3'

Supplemental Table 2 Frequencies of embryo defects in RPS5A-RopGEF7RNAi plants

Genotype	Stage	Defects(def./tot.)	Percentage(%)
WT(Col.)	Before Heart[1]	0/248	0
	Heart	0/127	0
RPS5A-RopGEF7RNAi-L6	Before Heart[1]	16/332	4.8%
	Heart	30/156	19.2%[2]

[1]Embryos were analyzed at proembryo, globular and triangular stages.

[2]Note that the frequency of RNAi heart embryos (in L6 line) with the basal defects is comparable to that of *plt1*$^{-/-}$*plt2*$^{+/-}$*plt3*$^{-/-}$*bbm3*$^{-/-}$ mutants (Galinha et al., 2007).