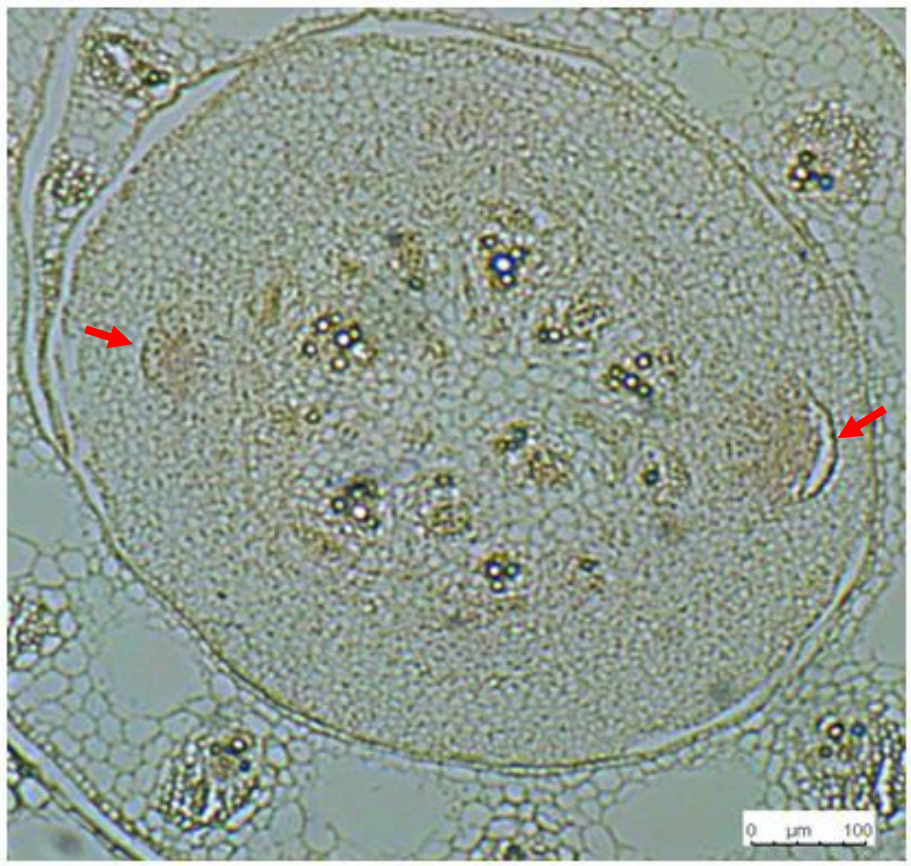
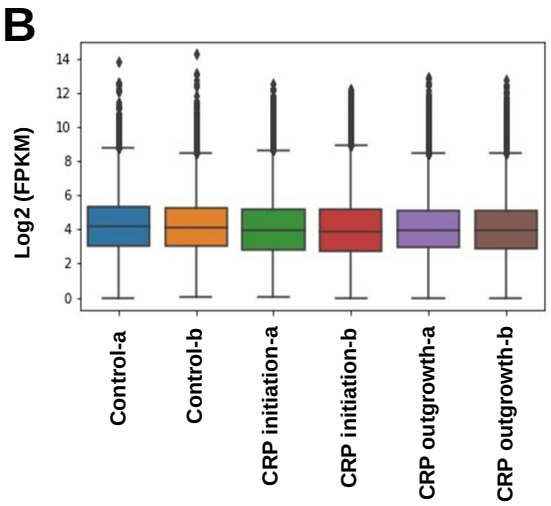


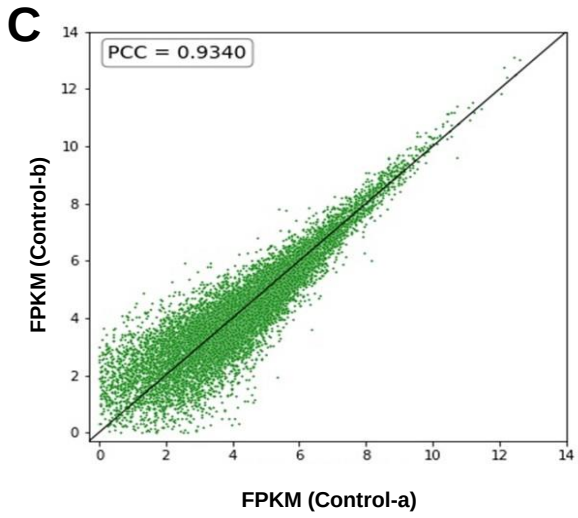
YFP (as)/wild-type

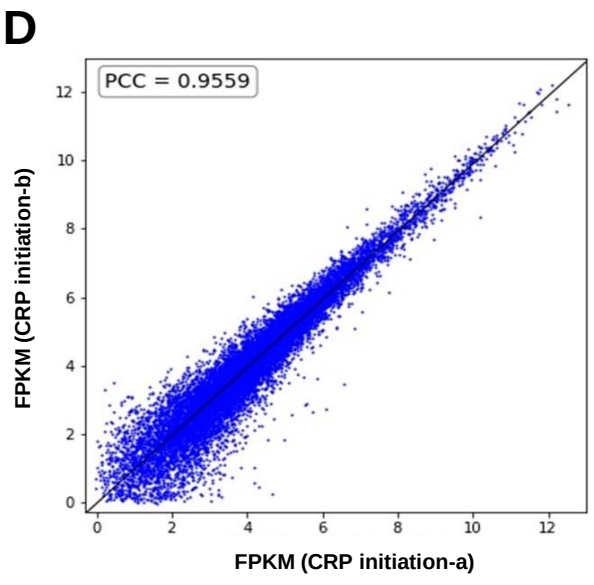
Fig. S1. Negative control for auxin response analysis. RNA *in situ* hybridization using antisense YFP riboprobes on the cross section of stem base of 6-day old wild-type plant as a control. Read arrows mark crown root primordia (CRP). Bars= 100 µm.

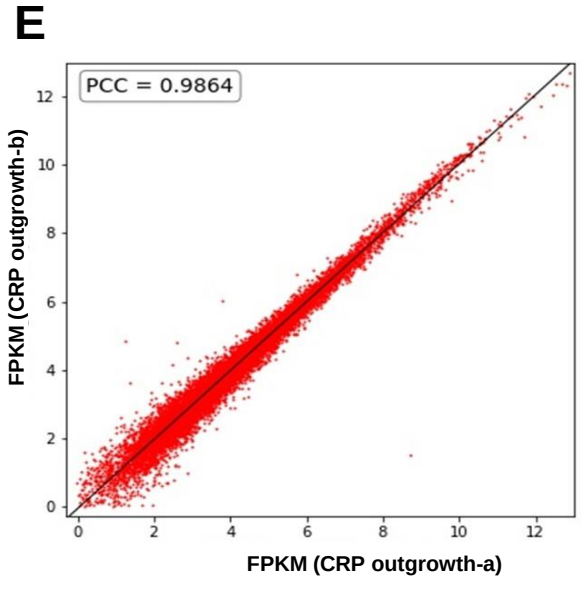
A

Samples	Total RNA obtained (ng)	RNA used for RiboZero (ng)	Library Size (bp)	Total reads
CRP initiation-a	13	13	366	39,723,434
CRP initiation-b	10	10	382	42,734,522
CRP outgrowth-a	163	50	367	40,354,596
CRP outgrowth-b	192	50	371	40,598,166
Control-a	8	8	285	40,522,100
Control-b	20	20	336	62,463,600









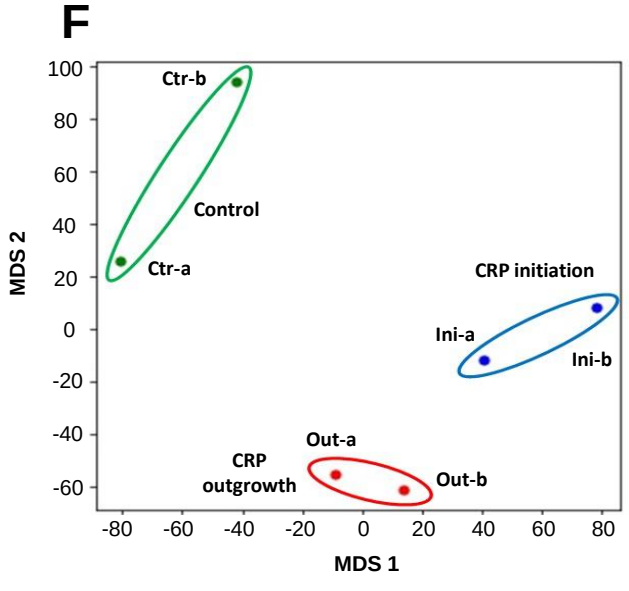


Fig. S2. LCM-seq data quality control. (A) Data QC of library and RNA seq data. RNA quantity, library size and total reads are given in the table. (B) Box plot showing the range of log2 FPKM values for the replicates. (C-E) Scatter plots depicting the Pearson's correlation coefficient (PCC) values between $\log_2$ transformed FPKM values of two replicates of control (C), CRP initiation (D), and CRP outgrowth (E). PCC values (0.93-0.99) indicate high correlation between the replicates for each stage. (F) Multidimensional scaling plots of all replicates of control, CRP initiation and CRP outgrowth, showing low divergence between the replicates.

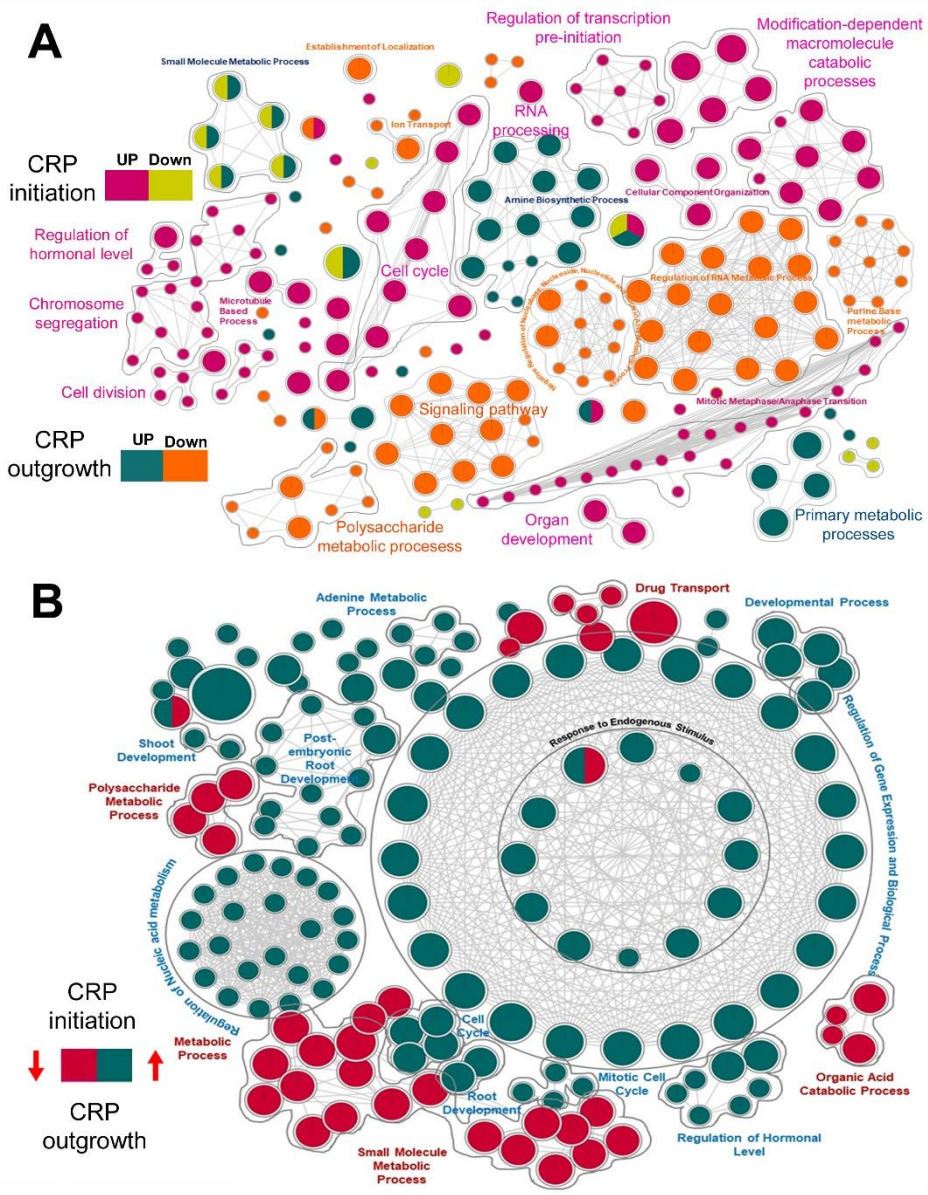
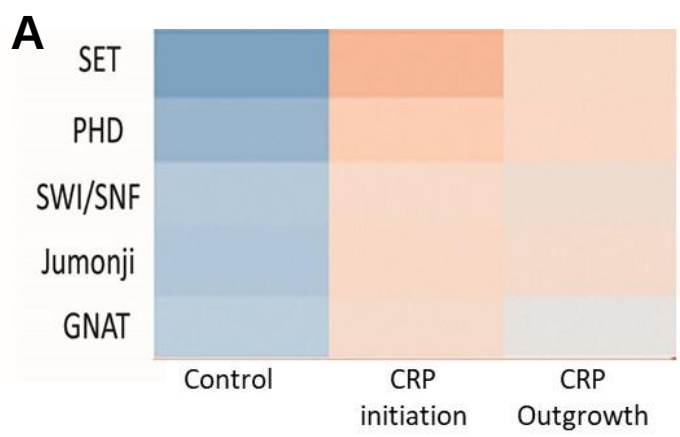
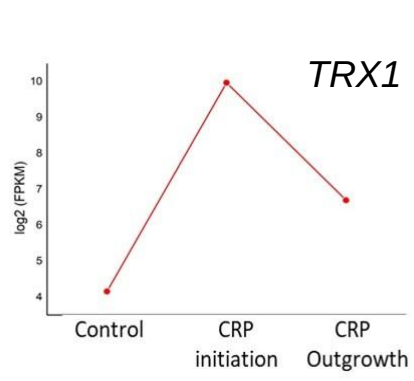
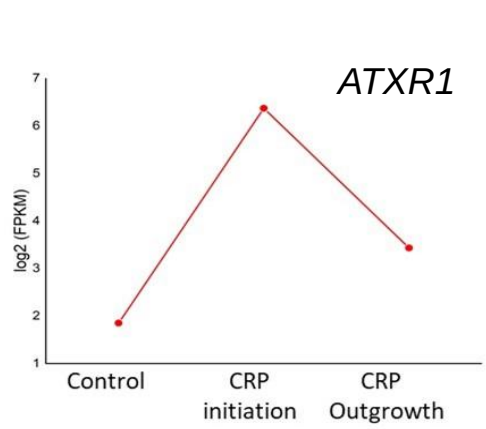
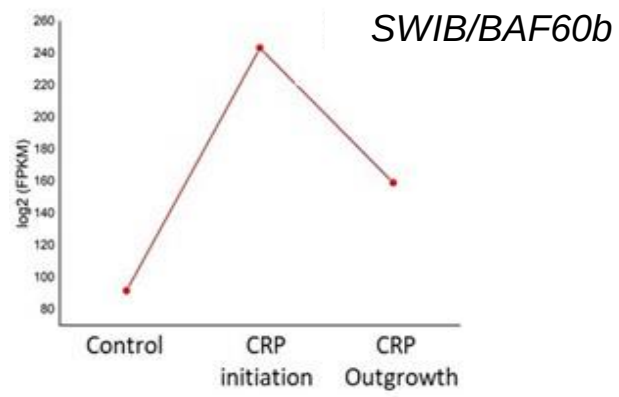


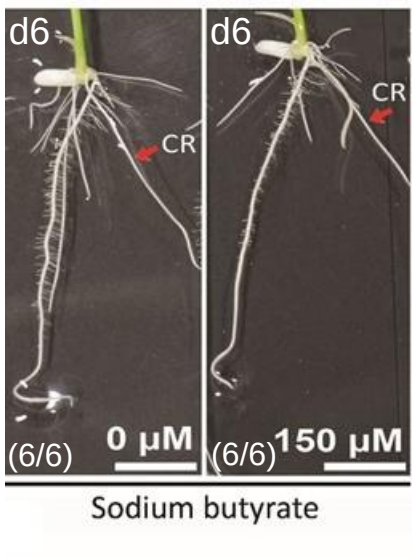
Fig. S3. Gene ontology analysis of DEGs. (A) GO terms associated with genes specifically de-regulated during CRP initiation and outgrowth. (B) GO analysis of DEGs when CRP progress from initiation to outgrowth stage.











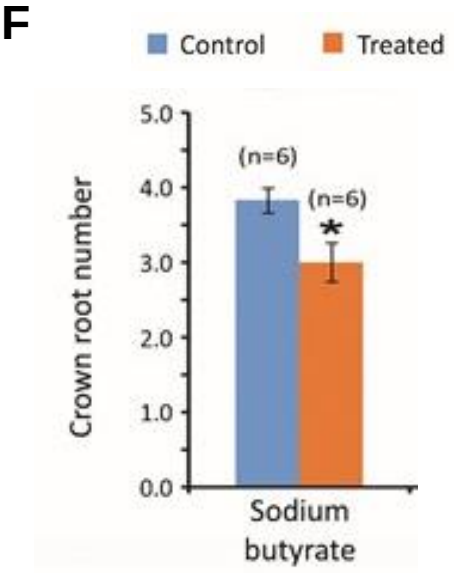


Fig. S4. Epigenetic regulation of CRP development. (A) Geneset enrichment analysis of putative epigenetic regulators.(B-D) LCM-seq expression pattern of selected putative epigenetic modifiers (i.e. *TRX1, ATXR6,* and *SWIB/BAF60b*) during CRP initiation and outgrowth. (E,F) CR number was decreased when histone acetylation was interfered for 6 days using sodium butyrate. The mean of CR number is plotted with s.e.m. (*$p \leq 0.05$; two-tailed, unpaired Student's *t*-test). Sample size (n) is mentioned in the panels (E) and (F). Scale bars=1 cm (E).

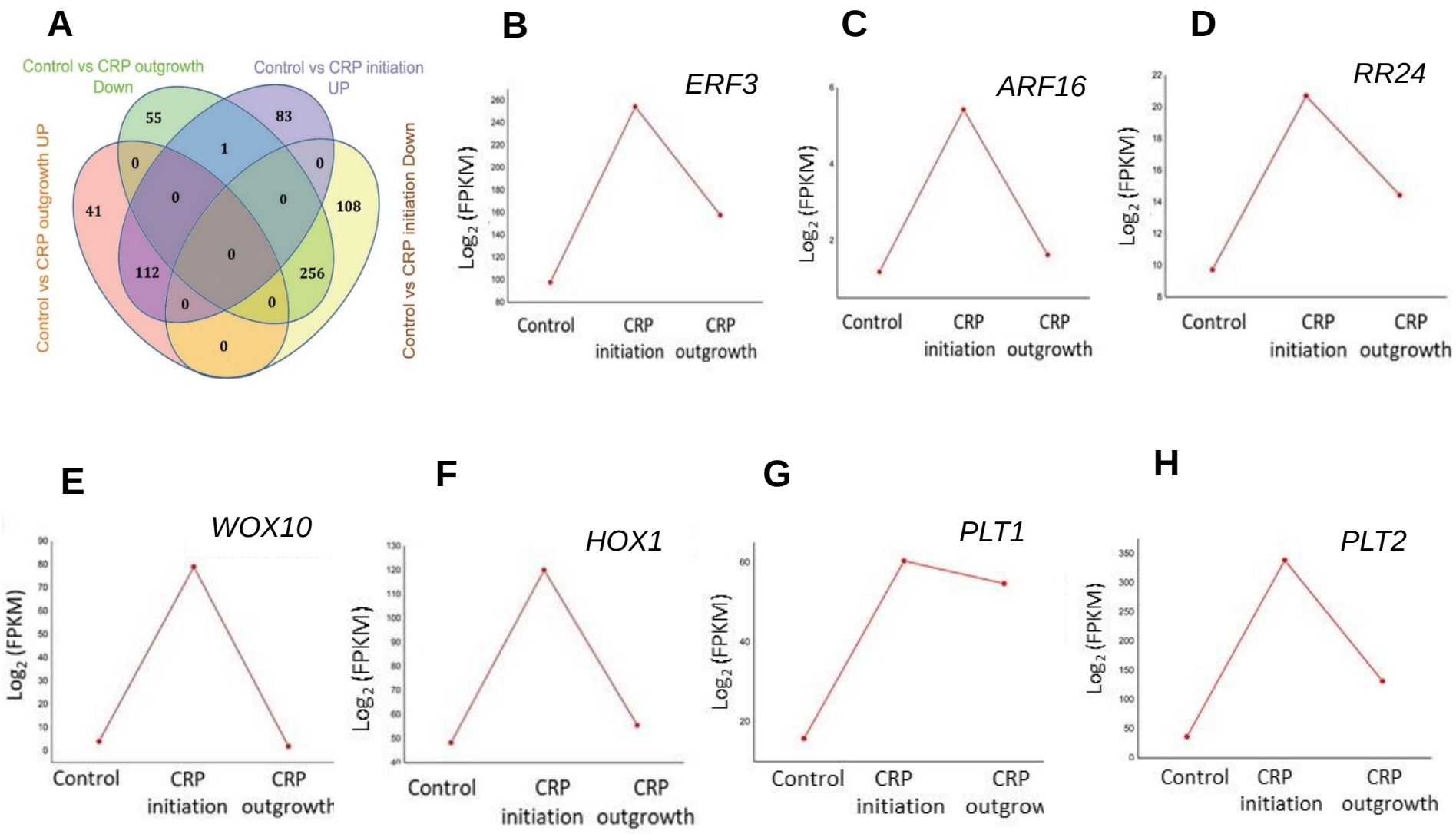


Fig. S5. Differentially regulated transcription factors (TFs). (A) Venn diagram showing common and unique differentially expressed TFs during CRP initiation and outgrowth. (B-H) LCM-seq data for selected TFs (*ERF3, ARF16*, *RR24, WOX10, HOX1, PLT1,* and *PLT2*) during CRP initiation and outgrowth.

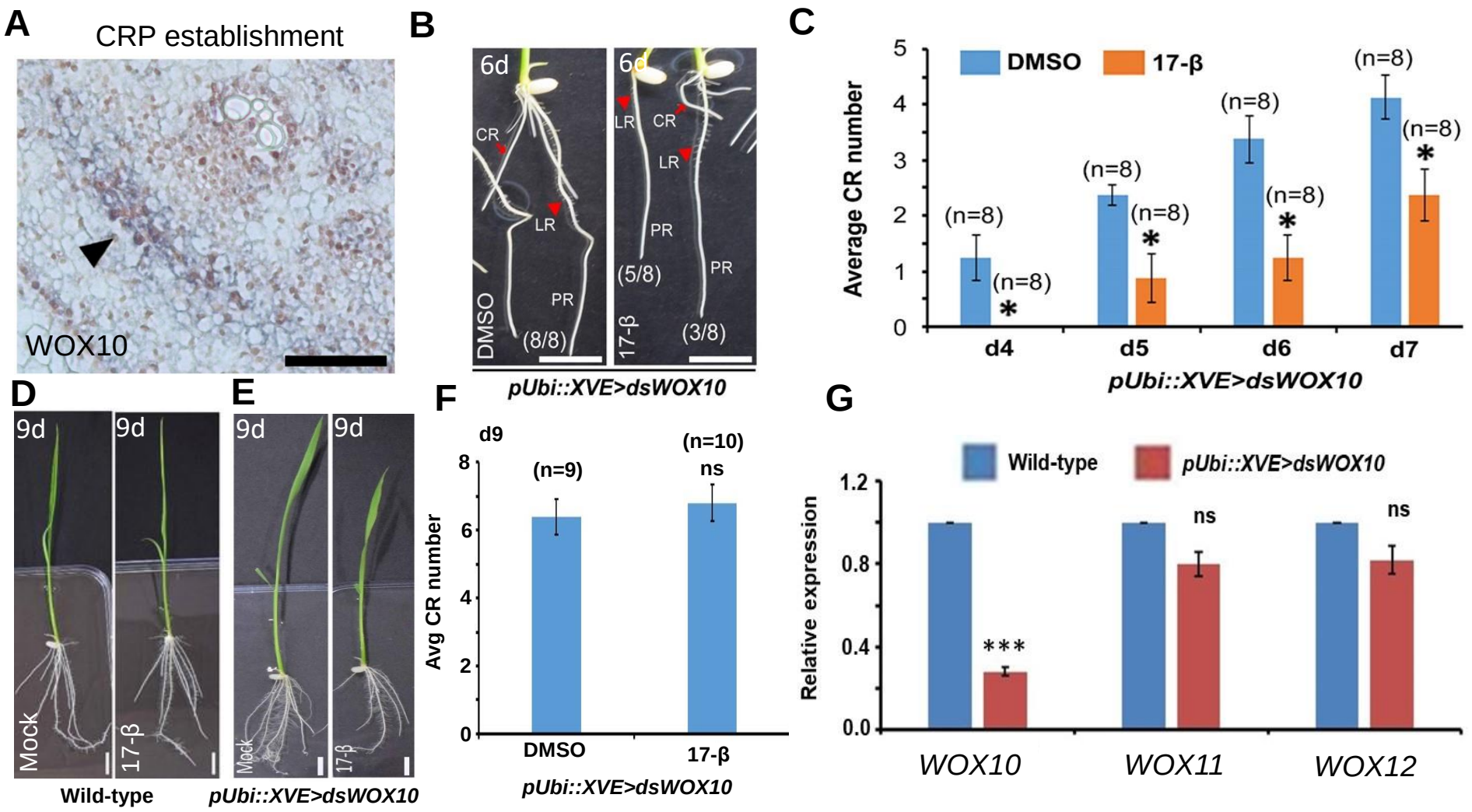


Fig. S6. Functional and molecular characterization of *WOX10* down-regulation lines. (A*) WOX10* expression is initiated in the CR founder cell. (B) CR number is reduced when *WOX10* is down-regulated upon 10 µM 17β-estradiol treatment in 6-day old pUbi::*XVE>dsWOX10* lines (right panel) as compared to mock-treated plant (left panel). (C) Quantitative representation of CR number. The mean of CR number is plotted with s.e.m. (*$p \leq 0.05$; two-tailed, unpaired Student's *t*-test). Sample size (n) is mentioned in the panels (B,C). (D,E) Plant morphology of 9-day old wild-type (D) and pUbi::XVE>ds*WOX10* lines (E) upon mock (left) and 17-β estradiol (right) treatment. No significant effect was observed in wild-type plants. (F) CR number is not significantly altered in 9-day old *WOX10* down-regulated lines. (G) Down-regulation of *WOX10* upon 17β-estradiol treatment. Expression level of related WOX-genes, *WOX11* and *WOX12* was not affected upon *WOX10* down-regulation. Relative expression (fold change) is plotted with ±s.e.m. The p-value is calculated from three experiments (ns, not significant; $p > 0.05$; ***$p \leq 0.001$; two-tailed, unpaired Student's *t*-test). Scale bars = 25 µm (A); 1 cm (B,D,E).

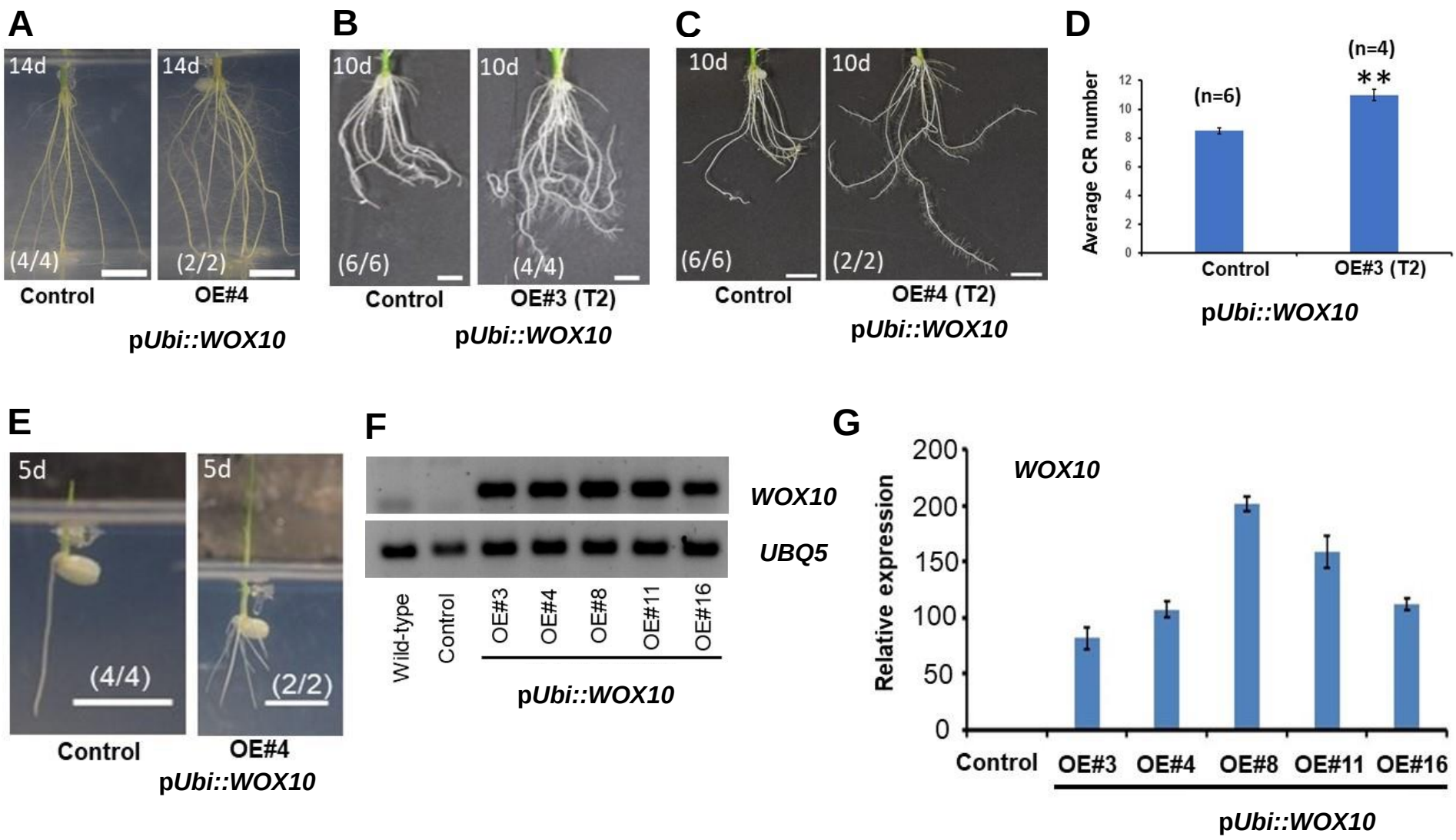


Fig. S7. Functional and molecular characterization of *WOX10* over-expression lines. (A-C) Root architecture of *WOX10* over-expression line OE#4 (T1), OE#3 (T2), and OE#4 (T2). (D) Quantitative representation of CR number. The mean of CR number of 10-day old plantds is plotted with s.e.m. (**$p \leq 0.005$; two-tailed, unpaired Student's *t*-test). (E) Precocious rooting in 5-day old *WOX10* over-expression line (right), than wild-type (left). Sample size (n) is mentioned in the panels (A-E). (F,G) Over-expression of *WOX10* in multiple p*Ubi::WOX10* lines, measured by semi-quantitative (F), and qRT-PCR (G). Age of the plants are mentioned at top left side of the panels in (A-C; E). Scale bars = 1 cm (A-C; E).

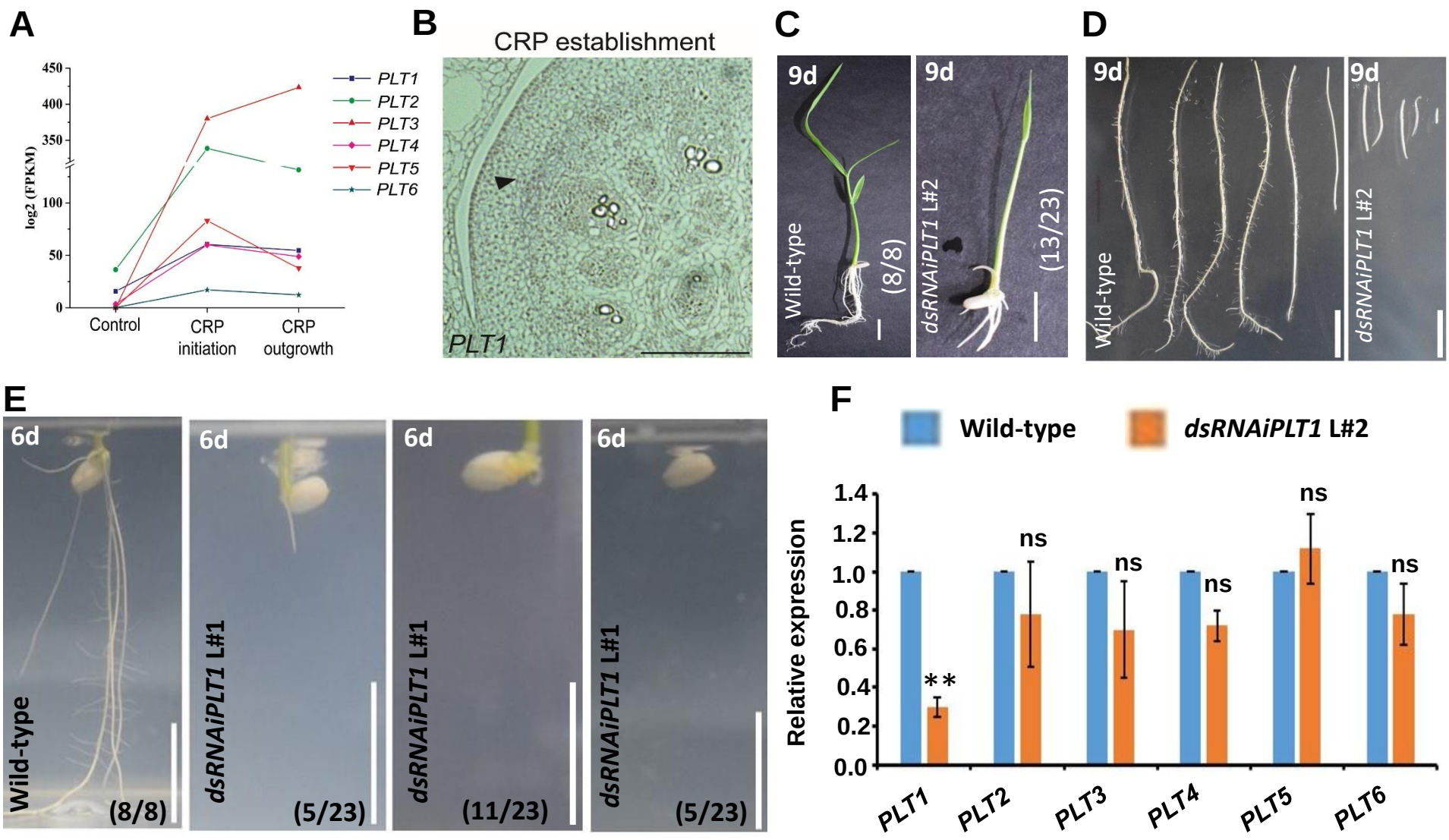


Fig. S8. Phenotypic and molecular characterization of *OsPLT1* down-regulated lines. (A) LCM-seq data for the expression pattern of rice *PLETHORA* genes during CRP initiation and outgrowth. (B) Onset of *PLT1* expression during CRP establishment. (C) Morphology of 9-day old wild-type (left) and *dsRNAiPLT1* L#2 plant (right). (D) LR phenotype of *dsRNAiPLT1* L#2. (E) Phenotypes of 6-day old *dsRNAiPLT1* L#1 plants. Sample size (n) is mentioned in the panels (C,E). (F) Expression level of PLT genes, in *dsRNAiPLT1* line. Relative expression (fold change) is plotted with ±s.e.m. The p-value is calculated from three experiments (**p<0.005; ns, not significant; p>0.05; two-tailed, unpaired Student's t-test). Scale bars= 100 µm (B); 1 cm (C-E).

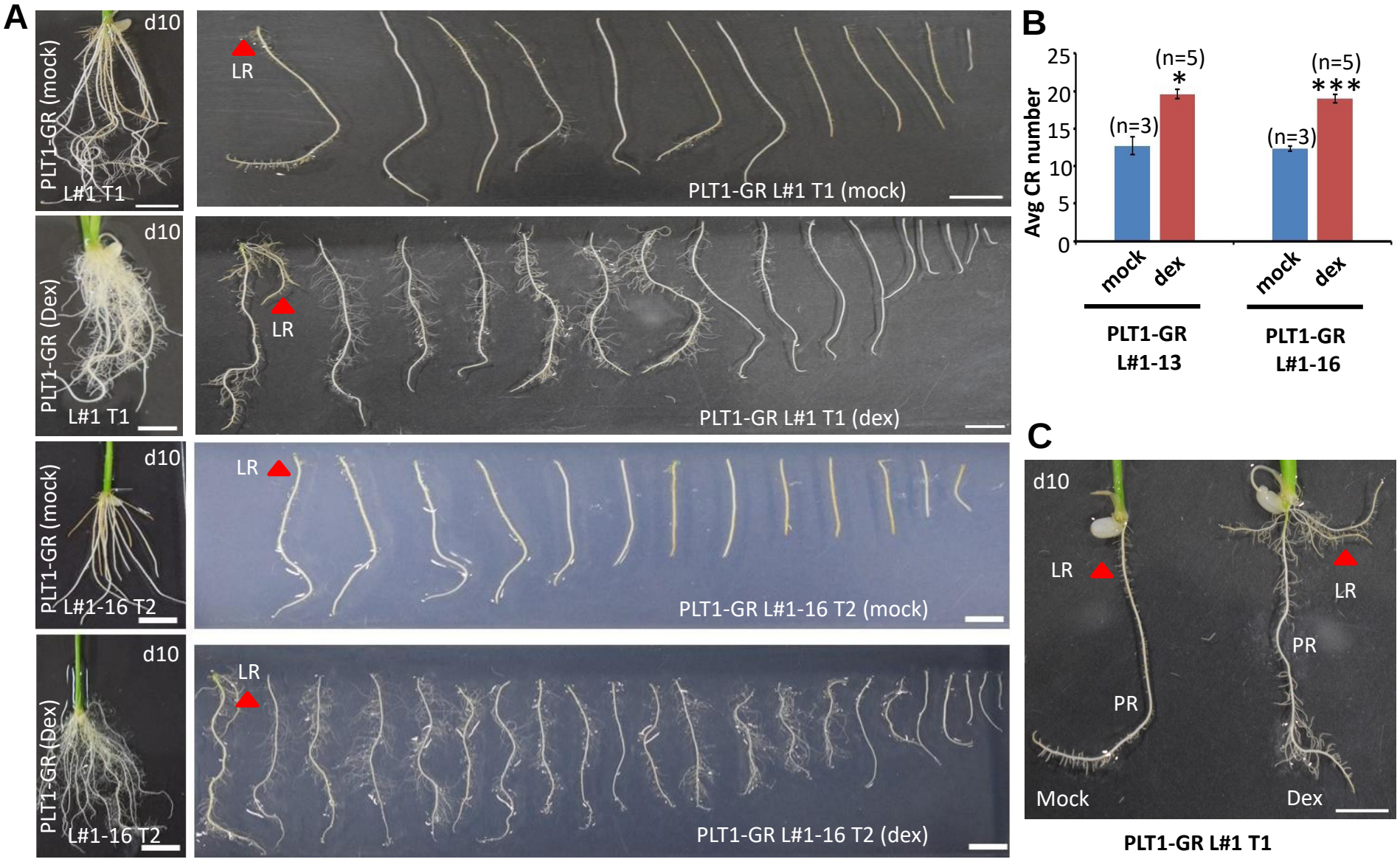


Fig. S9. Phenotypic characterization of *PLT1* over-expression lines. (A) Root architecture (left panel) and LRs phenotypes (right panel) of 10-day old mock (first row) and 5 µM dex (second row) treated *PLT1-GR1* L#1 (T1) plants. Similarly, mock (third row) and dex (fourth row) treated *PLT1-GR* L#1 in T2 generation. Number of CRs and LRs are increased upon dex treatment. (B) Quantitative representation of CR number upon dex treatment for 10 days. The mean of CR number is plotted with s.e.m. (*$p \leq 0.05$; ***$p \leq 0.001$; two-tailed, unpaired Student's *t*-test) in two independent T2 lines. Sample size (n) is mentioned in (B). (C) LR phenotypes on PR of mock (left) and dex (right) treated plants. CRs are removed. Scale bars= 1 cm (A,C).

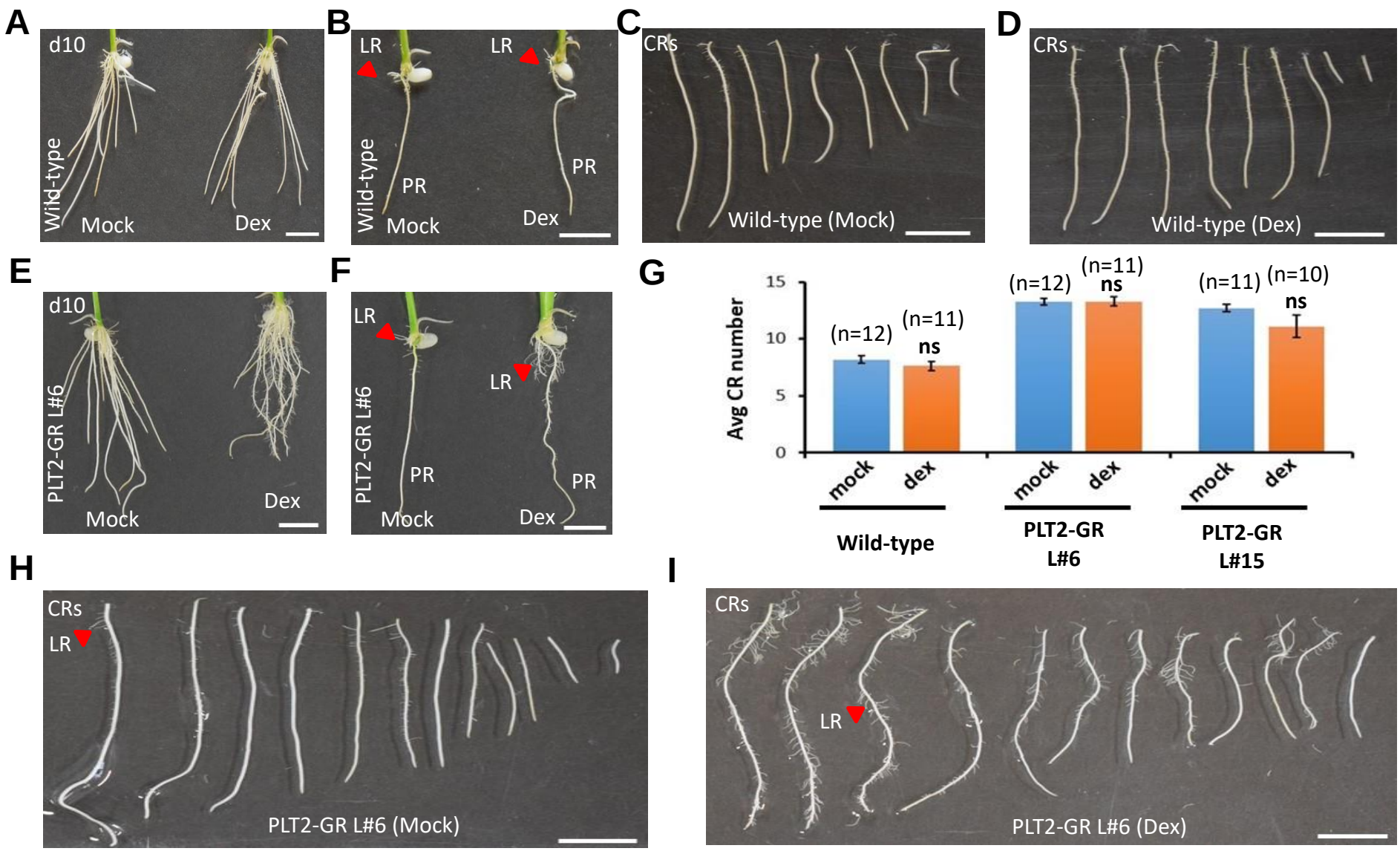


Fig. S10. Phenotypic characterization of *PLT2* over-expression lines. (A) Root architecture upon mock (left) and 5 µM dex (right) treated 10-day old wild-type plants. (B-D) Dex treatment does not affect LR development on PR (B) and CRs (C,D) of wild-type plants. (E) Root architecture phenotypes of 10-day old *PLT2-GR* L#6. (F) Number and growth of LRs are increased in PR upon dex treatment (right) as compared to mock (left) treated *PLT2-GR* L#6 plants. CRs are removed in (B,F). (G) CR number is not affected *PLT2-GR* lines. The mean of CR number is plotted with s.e.m. (ns, $p>0.05$; two-sample t-test). Sample size (n) is mentioned in (G). (H-I) LR number and growth are increased on the CRs of *PLT2-GR* L#6 upon 5 µM dex treatment. Scale bars= 1 cm (A-F; H,I).

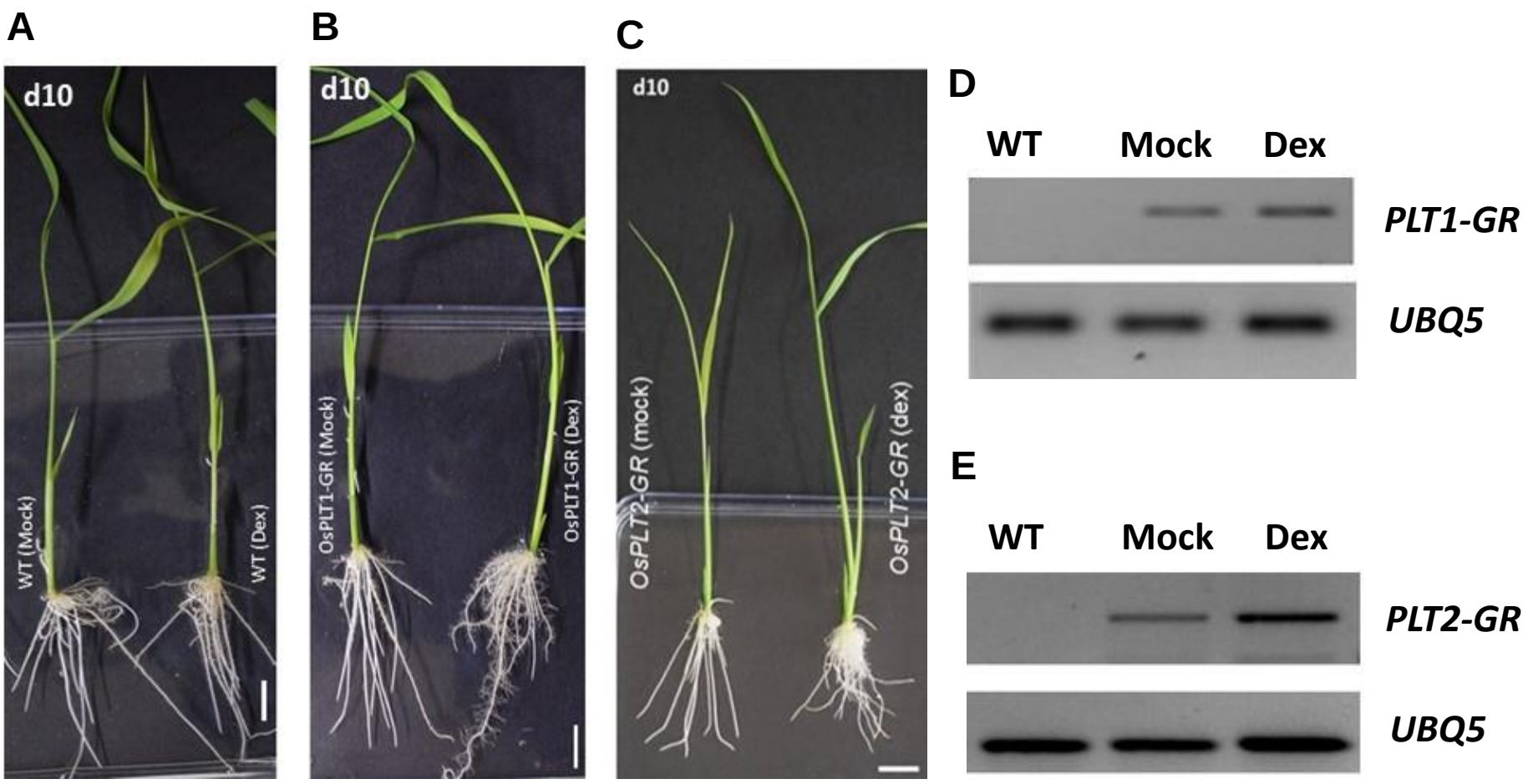


Fig. S11. Molecular and phenotypic characterization of *PLT1* and *PLT2* over-expression lines. (A-C) Plant morphology of 10-day old wild-type (A), PLT1-GR1 (B) and PLT2-GR lines (C) upon 5 µM dex treatment (right), as compared to mock treated plants (left). No significant effect was seen on the gross morphology of wild-type plants upon dex treatment. (D,E) RT-PCR analysis of PLT1-GR and PLT2-GR lines, respectively, showing expression of fusion transcripts. Scale bars= 1 cm (A,C).

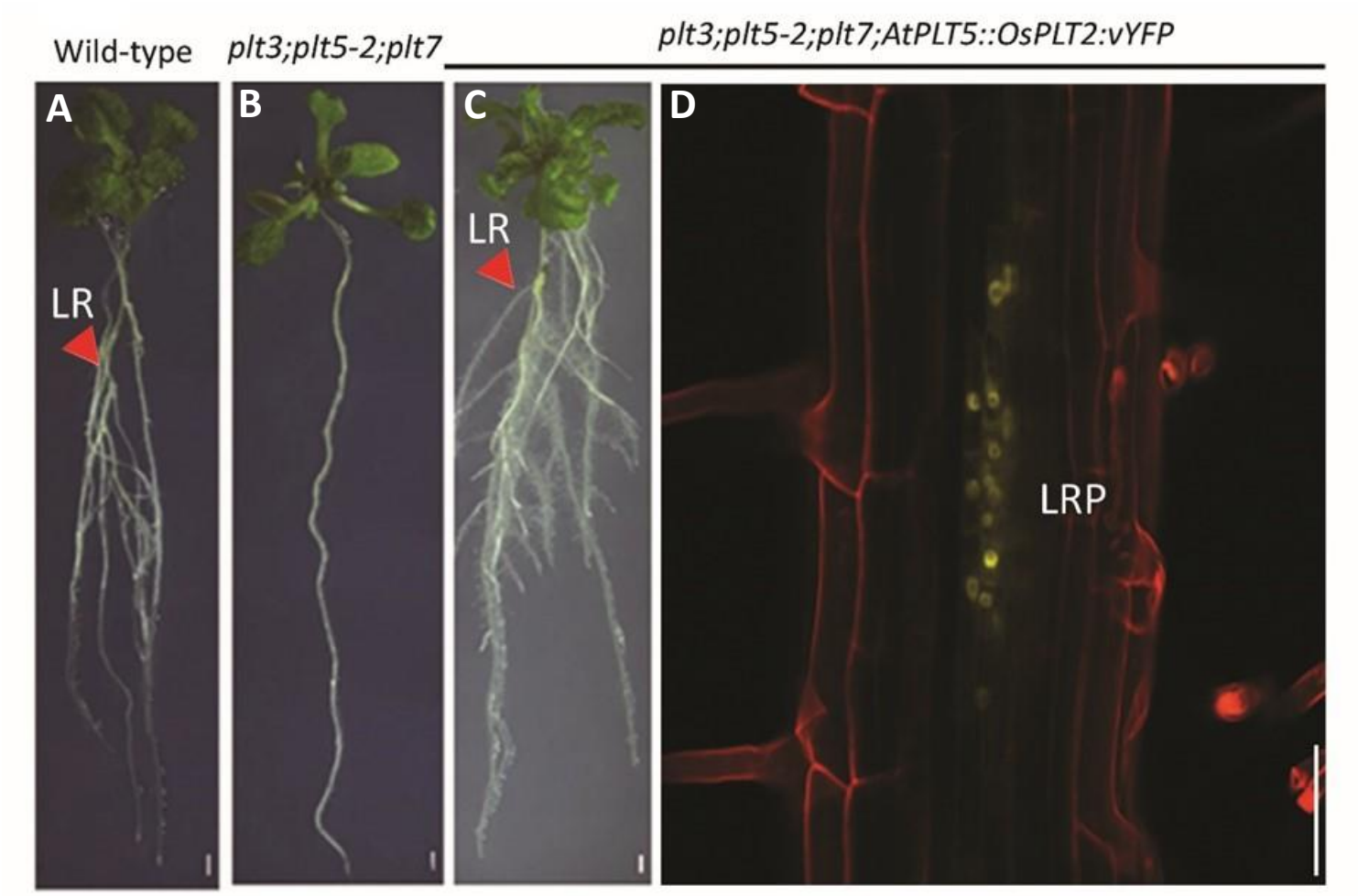


Fig. S12. Expression of *OsPLT2* in lateral root primordia (LRP) of *plt3;plt5-2;plt7* defective in LRP outgrowth rescued LRP outgrowth. Stereo images of 8-dpg wild-type plant (A), *plt3;plt5-2;plt7* (B), and *plt3;plt5-2;plt7;AtPLT5::OsPLT2:vYFP* (C). Confocal images showing expression of *OsPLT2:vYFP* in the LRP of *plt3;plt5-2;plt7;AtPLT5::OsPLT2:vYFP* (D). Red colour in (D) represents propidium iodide staining. (LRP, lateral root primordia; red arrowhead marks LR, lateral root). Scale Bars = 1 mm (A,C); 50 µm (D).

Table S1. Stage-specific differential expression of known regulators during CRP development

Click here to download Table S1

Table S2. List of eight annotated clusters of genes with distinct expression pattern during CRP development.

Click here to download Table S2

Table S3. List of differentially expressed genes during CRP initiation and outgrowth.

Click here to download Table S3

Table S4. List of specifically and commonly expressed genes during CRP initiation and outgrowth.

Click here to download Table S4

Table S5. List of putative epigenetic modifiers differentially expressed during CRP development.

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Table S6. List of genes selected for validation in this study.

Click here to download Table S6

Table S7. List of differentially expressed transcription factors during CRP initiation and CRP outgrowth.

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Table S8. List of primers used in this study

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