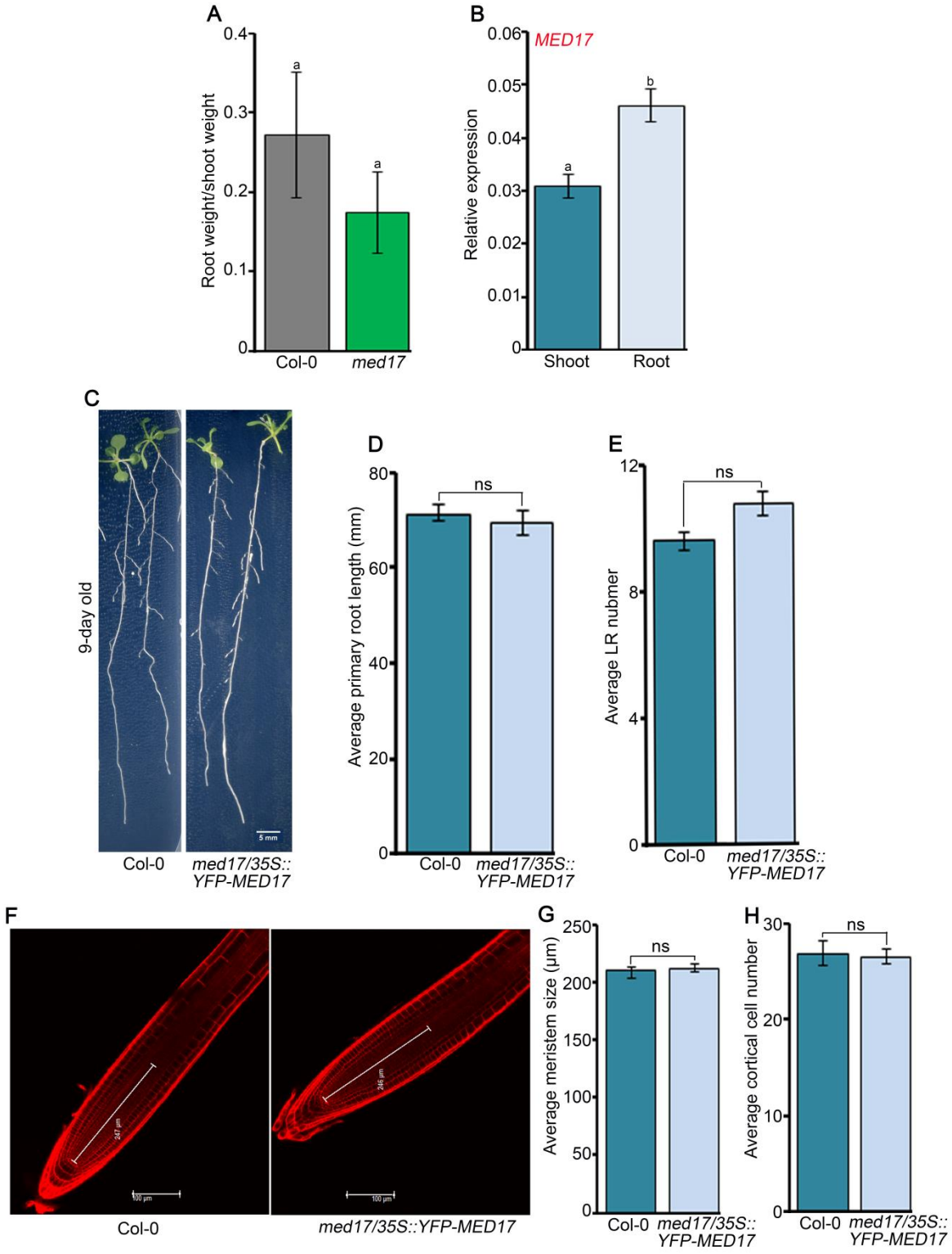
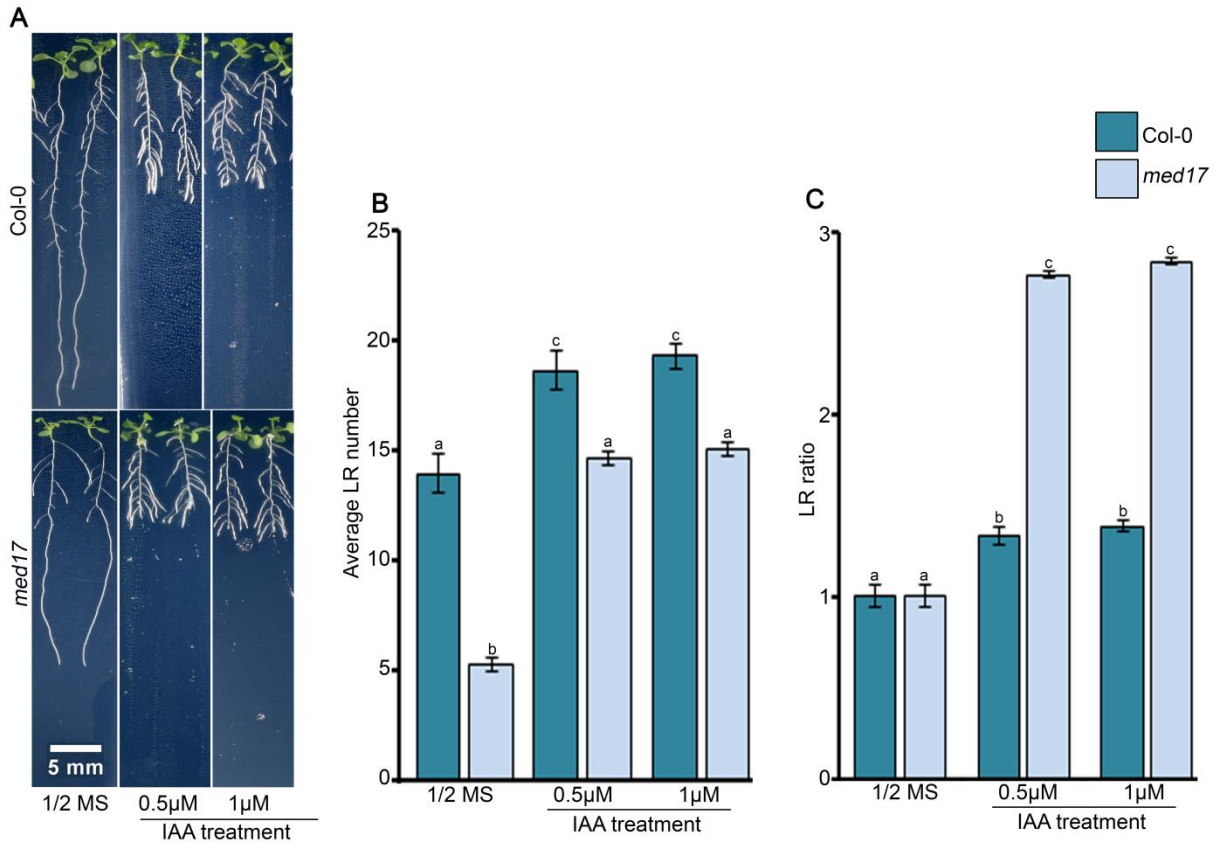
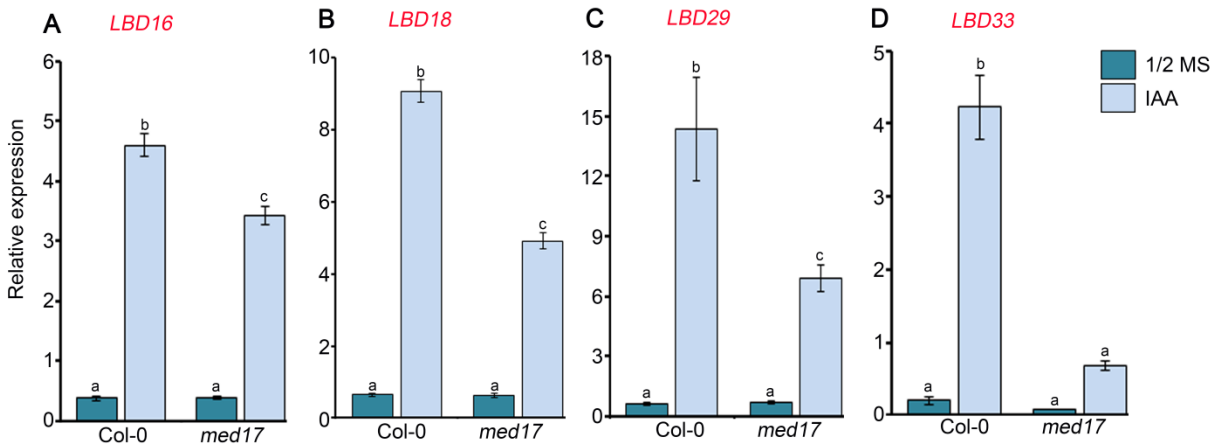


Supplemental Figure S1. Root phenotype of *med17* is rescued by its complementation with *35S::YFP-MED17*. A, Ratio of root and shoot biomass of 7-days old Col-0 and *med17* seedlings. Weight of root and shoot of 7-days old seedlings were measured for calculating the ratio. Quantification was performed on three independent biological replicates (n=3). Bar plots represent mean values and the error bars denote SE.

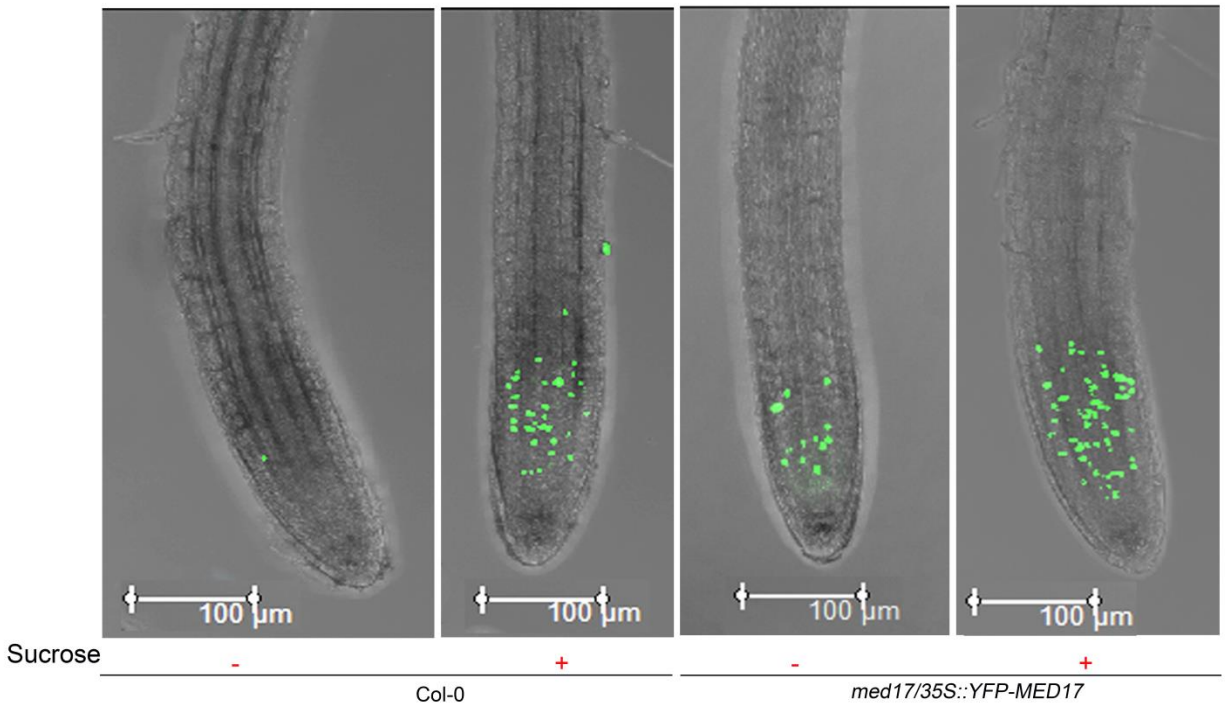
Statistical difference has been depicted by *p* value as assessed by paired ttest. **B,** RT-qPCR showing expression of *MED17* in the shoot and root parts of 7-days old Col-0 seedlings. **C,** Root phenotype of Col-0 and *med17/35S::YFP-MED17* seedlings. Length of the scale bar in the image is 5 mm. **D,** Graph showing the length of primary roots in Col-0 and *med17/35S::YFP-MED17* seedlings. **E,** Graph showing the number of lateral roots (LR) in Col-0 and *med17/35S::YFP-MED17* seedlings. **In C-E,** seedlings were grown on ½ MS for nine-days. Lengths of primary roots were measured using ImageJ. Data shown are average of three independent biological replicates containing at least 15 seedlings. Bar plots represent mean values and error bars denote SE. Statistical difference has been depicted by *p* value as assessed by one-way ANOVA and Tukey's HSD posthoc test. **F,** Col-0 and *med17/35S::YFP-MED17* root tips stained with PI. White line shows the length of the meristematic zone. Length of the scale bar in the image is 100 µm. **G,** Graph showing size of root meristem. **H,** Graph showing cortical cell numbers. **In F-H,** seedlings were grown on ½ MS for four-days and then processed for confocal imaging. Meristem length and cortical cell number were counted using ImageJ. Data shown are average of three independent biological replicates containing at least 10 seedlings. Bar plots represent mean values and error bars denote SE. Statistical difference has been depicted by *p* value as assessed by one-way ANOVA and Tukey's HSD posthoc test. For all the graphs, *p*-value of 0.05 or lower ($p \leq 0.05$) was considered statistically significant, whereas *p* value greater than 0.05 ($p > 0.05$) was considered non-significant (ns).



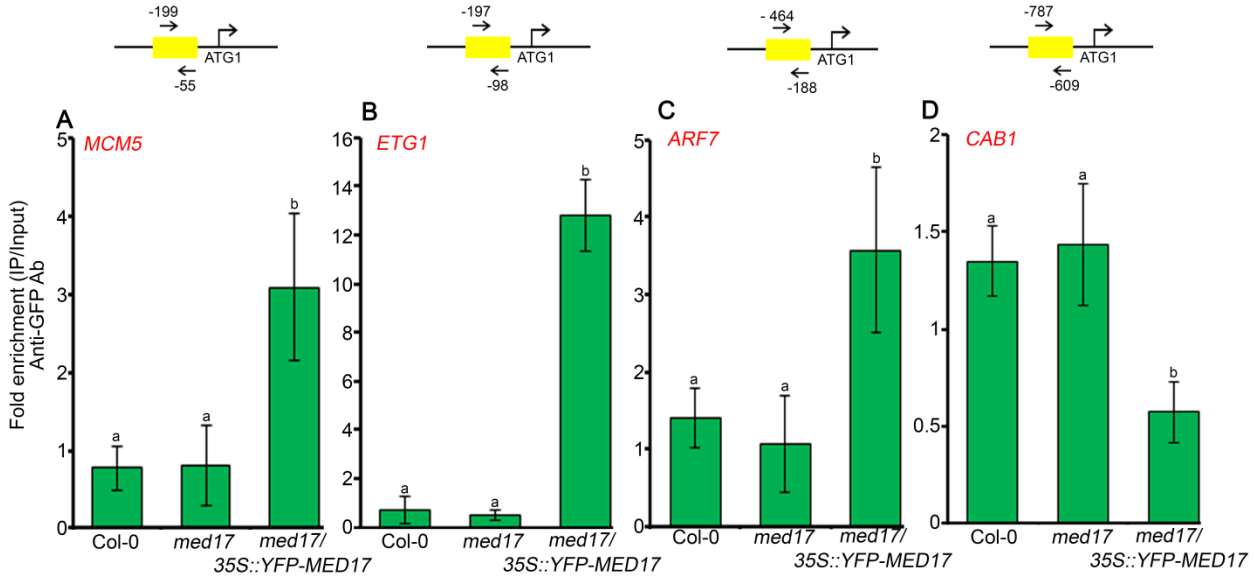
Supplemental Figure S2. Effect of exogenous auxin on lateral roots. A, Root phenotype of Col-0 and *med17* seedlings after treatment with IAA. Length of the scale bar in the image is 5 mm. **B,** Graph showing lateral roots (LRs) number in the Col-0 and *med17* after exogenous auxin treatment. **C,** Graph showing LR ratio in the Col-0 and *med17* after exogenous auxin treatment. **B-C,** Four-day old Col-0 and *med17* seedlings were transferred to ½ MS plates containing different concentration of IAA (0.5 µM and 1 µM) for another 4-days and LR numbers were counted. For plotting LR ratio total number of LRs after auxin treatment was divided by total number of LRs on ½ MS. Four-day old seedlings were transferred to ½ MS plates containing different concentration of IAA (0.5 µM and 1 µM) for another 4-day and LR numbers were counted. Data shown are average of three independent biological replicates containing at least 20 seedlings. Bar plots represent mean values and error bars denote SE. Statistical difference has been depicted by *p* value as assessed by one-way ANOVA and Tukey's HSD posthoc test. For all the graphs, *p*-value of 0.05 or lower ($p \leq 0.05$) was considered statistically significant, whereas *p* value greater than 0.05 ($p > 0.05$) was considered non-significant (ns).



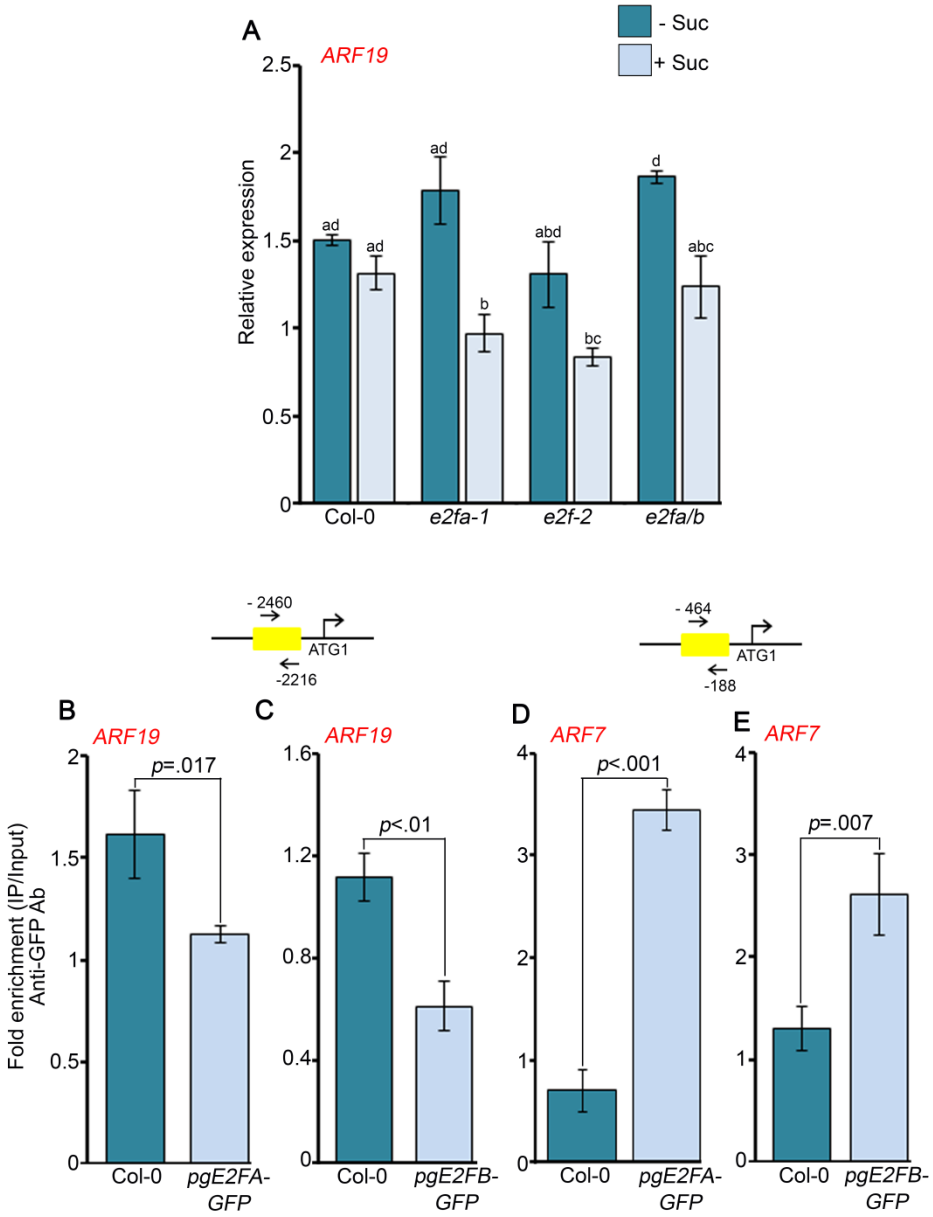
Supplemental Figure S3. MED17 regulates expression of auxin-responsive *LBD* genes. A-D, Reverse transcriptase-quantitative PCR (RT-qPCR) analysis showing expression of *LBD* genes (*LBD16*, *LBD18*, *LBD29*, *LBD33*) after IAA treatment **(Related to Figure 2E-H)**. Seven-day old Col-0 and *med17* seedlings were treated with IAA (10 µM) for 3 hr. Gene expression values were calculated as ΔCt. RT-qPCR analysis was performed on three independent biological replicates (n=3). Bar plots represent mean values and error bars denote SE. Statistical difference has been depicted by *p* value as assessed by one-way ANOVA and Tukey's HSD posthoc test. For all the graphs, *p*-value of 0.05 or lower ($p \leq 0.05$) was considered statistically significant, whereas *p* value greater than 0.05 ($p > 0.05$) was considered non-significant (ns).



Supplemental Figure S4. Defective root meristem activation of *med17* is rescued by *35S::YFP-MED17*. Confocal images showing EDU staining of nuclei. Four-day old Col-0 and *med17/35S::YFP-MED* seedlings were treated with (90 mM) or without (0 mM) sucrose for 3 hr followed by EDU staining and confocal imaging. Length of the scale bar in the image is 100 µm. Data shown are representative of three biological replicates (n=3).

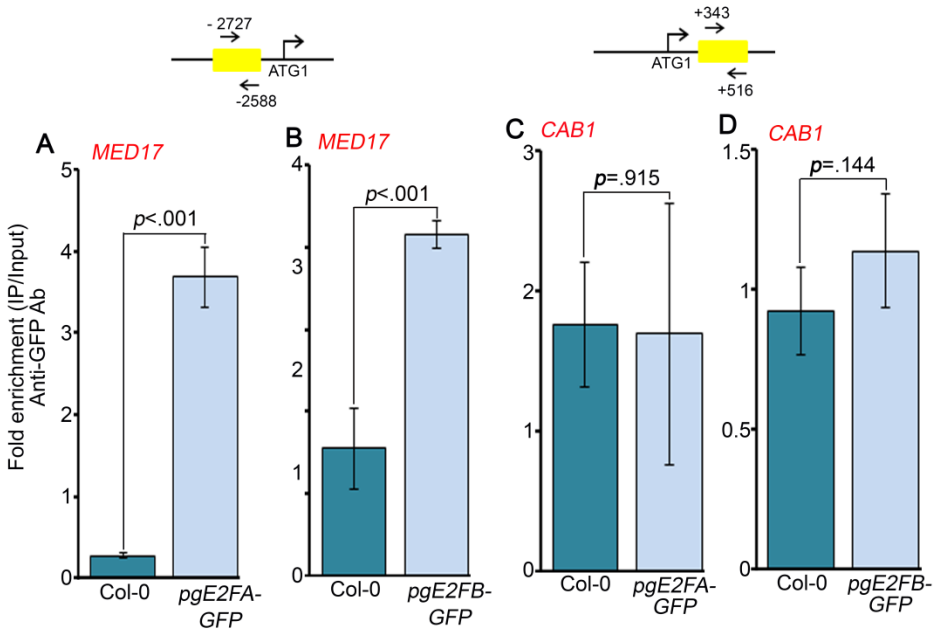


Supplemental Figure S5. Second biological replicate showing enrichment of MED17 at the promoters of *ARF7* and cell-cycle genes. **A-D,** ChIP-qPCR showing enrichment of YFP-MED17 at the promoters of *MCM5*, *ETG1*, *ARF7* and *CAB1* in seven-day-old Col-0 and *med17/35S:YFP-MED17* seedlings **(related to 4E-G and 5G)**. Amplicon positions relative to ATG are shown in the upper panel. Amount of immunoprecipitated DNA was quantified by comparing samples treated with or without anti-GFP antibody. Ct values with and without antibody samples were normalized to input control. Untransformed Col-0 and *med17* seedlings were taken as negative control. *CAB1*, which does not possess any E2F binding motifs in its promoter, was used as a negative control. YFP-MED17 binding on promoters was calculated as fold enrichment. ChIP-qPCR analysis was performed on three technical replicates (n=3) from a single representative experiment. Experiments were independently repeated twice (biological replicates; n=2). Bar plots represent mean values and error bars denote SD. Statistical difference has been depicted by *p* value as assessed by one-way ANOVA and Tukey's HSD posthoc test. For all the graphs, *p*-value of 0.05 or lower ($p \leq 0.05$) was considered statistically significant, whereas *p* value greater than 0.05 ($p > 0.05$) was considered non-significant (ns).

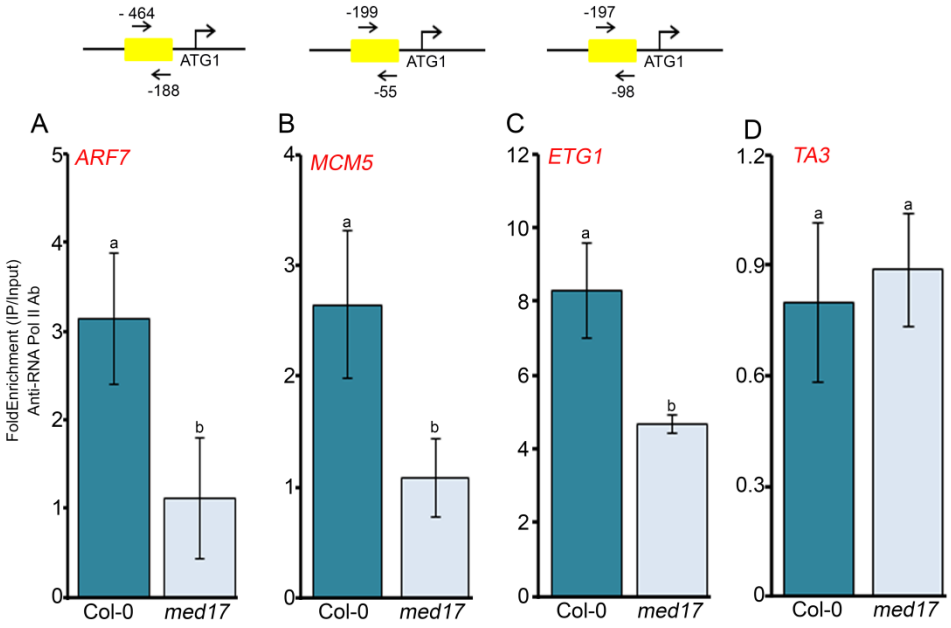


Supplemental Figure S6. Second biological replicate showing enrichment of E2FA and E2FB at the promoters of auxin responsive TF genes. A, RT-qPCR showing expression of *ARF19* in Col-0, *e2fa-1*, *e2fb-2* and *e2fa/b* seedlings after sucrose treatment. 7-day old seedlings were treated with 90 mM sucrose for 3 hr. Gene expression values were calculated as ΔCt. RT-qPCR analysis was performed on three independent biological replicates (n=3). Bar plots represent mean values and error bars denote SE. Statistical difference has been depicted by *p* value as assessed by one-way ANOVA and Tukey's HSD posthoc test. **B-E,** ChIP-qPCR showing enrichment of E2FA-GFP and E2FB-GFP at the promoter of *ARF7* **(related to Figure 7B-C)** but not at the promoter of *ARF19* in seven-day-old seedlings. Amplicon positions relative to ATG are shown in the upper panel. Amount of immunoprecipitated DNA was quantified by comparing samples treated with or without anti-GFP antibody. Ct values with and without antibody samples were normalized to input control. Untransformed Col-0 seedlings were taken as negative control. Binding of E2FA-GFP and E2FB-GFP on the promoters was calculated as fold enrichment. ChIP-qPCR analysis was performed on three technical replicates (n=3) from a single representative

experiment. Experiments were independently repeated twice (biological replicates; n=2). Bar plots represent mean values and error bars denote SD. Statistical difference has been depicted by *p* value as assessed by paired ttest. For all the graphs, *p*-value of 0.05 or lower ($p \leq 0.05$) was considered statistically significant, whereas *p* value greater than 0.05 ($p > 0.05$) was considered non-significant (ns).



Supplemental Figure S7. Second biological replicate showing enrichment of E2FA and E2FB at the promoter of *MED17*. A-D, ChIP-qPCR showing enrichment of E2FA-GFP and E2FB-GFP at the promoter of *MED17* and *CAB1* in seven-day-old Col-0, *pgE2FA-GFP*, and *pgE2FB-GFP* seedlings **(related to figure 9E)**. Amplicon positions relative to ATG are shown in the upper panel. Amount of immunoprecipitated DNA was quantified by comparing samples treated with or without anti-GFP antibody. Ct values with and without antibody samples were normalized to input control. Untransformed Col-0 seedlings were taken as negative control. *CAB1*, which does not possess any E2F binding motifs in its promoter, was used as a negative control. E2FA and E2FB binding on promoters was calculated as fold enrichment. ChIP-qPCR analysis was performed on three technical replicates (n=3) from a single representative experiment. Experiments were independently repeated twice (biological replicates; n=2). Bar plots represent mean values and error bars denote SD. Statistical difference has been depicted by *p* value as assessed by paired ttest. For all the graphs, *p*-value of 0.05 or lower ($p \leq 0.05$) was considered statistically significant, whereas *p* value greater than 0.05 ($p > 0.05$) was considered non-significant (ns).



Supplemental Figure S8. MED17 is required for enrichment of RNA Pol II on the promoters of *ARF7* and cell cycles genes. A-D, ChIP-qPCR showing enrichment of RNA Pol II at the promoters of *ARF7*, *MCM5* and *ETG* genes in seven-day-old Col-0 and *med17* seedlings. *TA3* was used as negative control. Amount of immunoprecipitated DNA was quantified by comparing samples treated with or without anti-RNA Pol II antibody. Ct values with and without antibody samples were normalized to input control. RNA Pol II binding on promoters was calculated as fold enrichment. ChIP-qPCR analysis was performed on three technical replicates (n=3) from a single representative experiment. Experiments were independently repeated twice (biological replicates; n=2). Bar plots represent mean values and error bars denote SD. Statistical difference has been depicted by *p* value as assessed by paired ttest. For all the graphs, *p*-value of 0.05 or lower ($p \leq 0.05$) was considered statistically significant, whereas *p* value greater than 0.05 ($p > 0.05$) was considered non-significant (ns).

Supplemental Table S1. Primers used in this study.

RT-qPCR	
qRT_LBD16FP	TCCGGTCTCGCCACAGA
qRT_LBD16RP	ACGTCACTGCTCGTGTTGCT
qRT_LBD18FP	CCGTACTTTGACTCCGAGCAA
qRT_LBD18RP	CTGGCTCCGAACACTTTATGC
qRT_LBD29FP	GTCATGAACAAGGAGCTTCACACT
qRT_LBD29RP	AGAAGCATTGCTAGCTCCAAAGA
qRT_LBD33FP	TGACTATGGCCACGACCAATT
qRT_LBD33RP	TCCGTCGGCATTGTTCAA
qRT_MCM5FP	CAATTCGCCAGCCTTATATCCGAGT
qRT_MCM5RP	GGAGCGATCTTGGTGCAAATGTTC
qRT_MCM7FP	GCCGACGCTAATGGCAGATCTAA
qRT_MCM7RP	GCGGCGGAGAAAATTGAAACATATC
qRT_ETG1F	CCCACGCCTCCATTGTCTTATCC
qRT_ETG1RP	GAACTGTGCGGCAATGTGATCATTC
qRT_ORC6FP	CGCCGCCACTAGGTTGCAGATTA
qRT_ORC6RP	ACAGCCAAATTGAACCGCCAATTC
qRT_ARF7FP	TGACGGTGATTCCAGGAACA
qRT_ARF7RP	CAGGCACAAAGCCATTATCAAC
qRT_ARF19FP	TGGAGGACTGTGGCCCAAT
qRT_ARF19RP	ACCCTCGTTTTTGAACCTTTGTAT
qRT_MED17FP	CCCGTGATGATTCTCCAACAG
qRT_MED17RP	CGTCCGTGCTTCCTCCAGTA
18S_FP	TGCAACAAACCCCGACTTATG
18S_RP	CCCGCGTCGACCTTTTATC
GAPC2_FP	TGCCATCCCTCAATGGAAA
GAPC2_RP	GAGACATCAACGGTTGGAACAC
ChIP-qPCR	
ChIP_MED17FP	GTAATTTGAGTATCAATTGGGTG
ChIP_MED17RP	ACTATTGGCCATGTTATCAAC
ChIP_CAB1FP	TCCCTGAGCTTTTGGCTAGA
ChIP_ CAB1RP	AACGGCTCCCATCAAAATAA
ChIP_Pro_CAB1_FP	GGAATTGGCTTATTAGTTGTG
ChIP_Pro_CAB1_RP	CTTAATTAGCACCTGTATTGACC
ChIP_MCM5FP	AGAAAGAAAGACCCAATAACCAAC
ChIP_ MCM5RP	TCTAAACGAAGAGAGAGAGTGGG
ChIP_ETG1FP	GTTGGAAGTTGGAGAATGGG
ChIP_ ETG1RP	CGAATTAAGGGCAATGTCAA
ChIP_ARF7FP	GATTTCTTTTTATAGAAACCCGTCTC
ChIP_ ARF7RP	CTCAGCTTTTTATCTCCGACAG
ChIP_ ARF19FP	GAGACATAGAGGCATACACTCA
ChIP_ ARF19RP	ATACGCATGCACCATATATAAC
ChIP_TA3_FP	CTGCGTGGAAGTCTGTCAAA

ChIP_TA3_RP	CTATGCCACAGGGCAGTTTT
Cloning	
Pentr_Med17 Δ1_FP	CACCATGGATAGCGACATGGAA
Pentr_Med17 Δ1_RP	CCCAGCAACTGTTACTGC
Pentr_Med17 Δ2_FP	CACCATGACCAGACCTAAGCCG
Pentr_Med17 Δ2_RP	CTCATTGCTGGCATTTGAAG
Pentr_Med17 Δ3_FP	CACCATGCTGGCCATTAATGTA
Pentr_Med17 Δ3_RP	TCCACTTATGTTGAATCC
Pentr_Med17 Δ4_FP	CACCATGGAAATGAGCATCGGC
Pentr_Med17 Δ4_RP	GCGATTAGGGAACCCTAG
Pentr_ARF7 FP	CACCATGAAAGCTCCTTCATCAAATG
Pentr_ARF7 RP	CCGGTTAAACGAAGTGGC
Pentr_E2FA_FP	CACCATGTCCGGTGTCGTACGATC
Pentr_E2FA_RP	TCTCGGGGTTGAGTCAACAG
Pentr_E2FB_FP	CACCATGTCTGAAGAAGTACCTCAACAATTC
Pentr_E2FB_RP	GCTACCTGTAGGTGATCTCGTAGC
Petr_ProARF7_FP	CACCCATGAACGCTAGTTTATGAAACTC
Petr_ProARF7_RP	GATCACTCAACTTTACTTTCTCTGAAG