

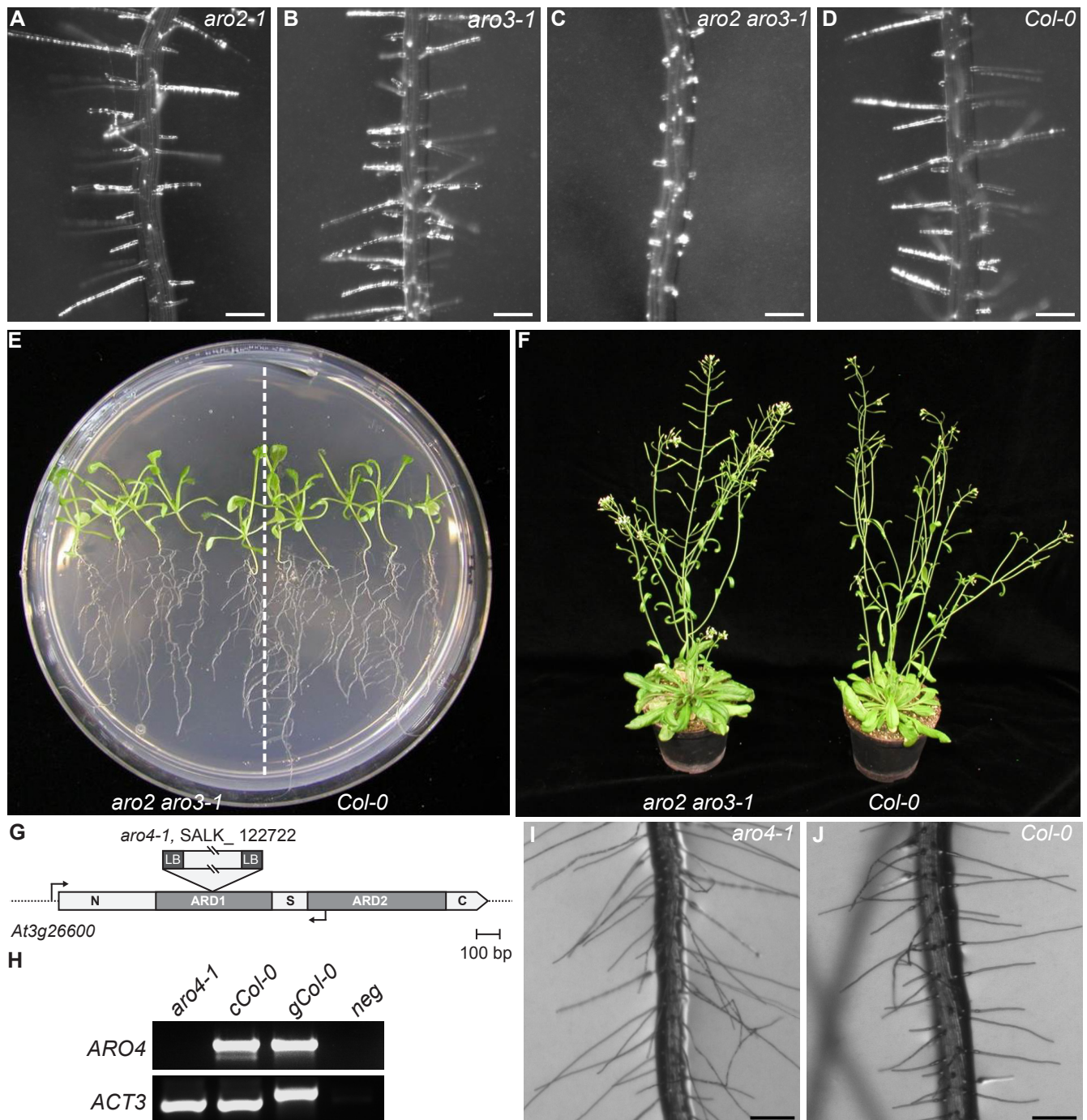


Figure S3.2 | Characterization of single and double *aro* knockout lines.

(A) Root hair morphology of the *aro2-1* single knockout line. **(B)** Root hair morphology of the *aro3-1* single knockout line. **(C)** Altered root hair morphology of the *aro2 aro3-1* double knockout line. **(D)** Wild-type root hair morphology. **(E)** and **(F)** No morphological differences in root system organization or in any areal parts are observed between the double mutant and wild-type. **(G)** Genomic structure of the *ARO4* gene. Armadillo repeat domains according to Gebert et al. (2008) are indicated by light grey boxes. The position of a tandem-inverse integrated T-DNA is indicated for the *aro4-1* insertions. Arrows indicate genotyping and expression analysis primer positions and dashed lines 5' and 3' UTR sequences. N, N-terminal domain; ARD, armadillo repeat domain; S, spacer region; C, C-terminal domain. Bar = 100 base pairs. **(H)** RT-PCR using cDNA generated from leaf mRNA isolated from the *aro4-1* single T-DNA insertion line as well as from wild-type. Wild-type gDNA and water were used as PCR controls. Gene specific primers for *ARO4* were used as well as gene-specific, intron-spanning primers for *Actin 3* (*ACT3*) which results in a larger *ACT3* amplicon on gDNA. **(I)** and **(J)** No altered root hair morphology is observed for the *aro4-1* T-DNA insertion line when compared with wild-type. Bars = 200 μ m in (A) to (D) and (I) and (J).