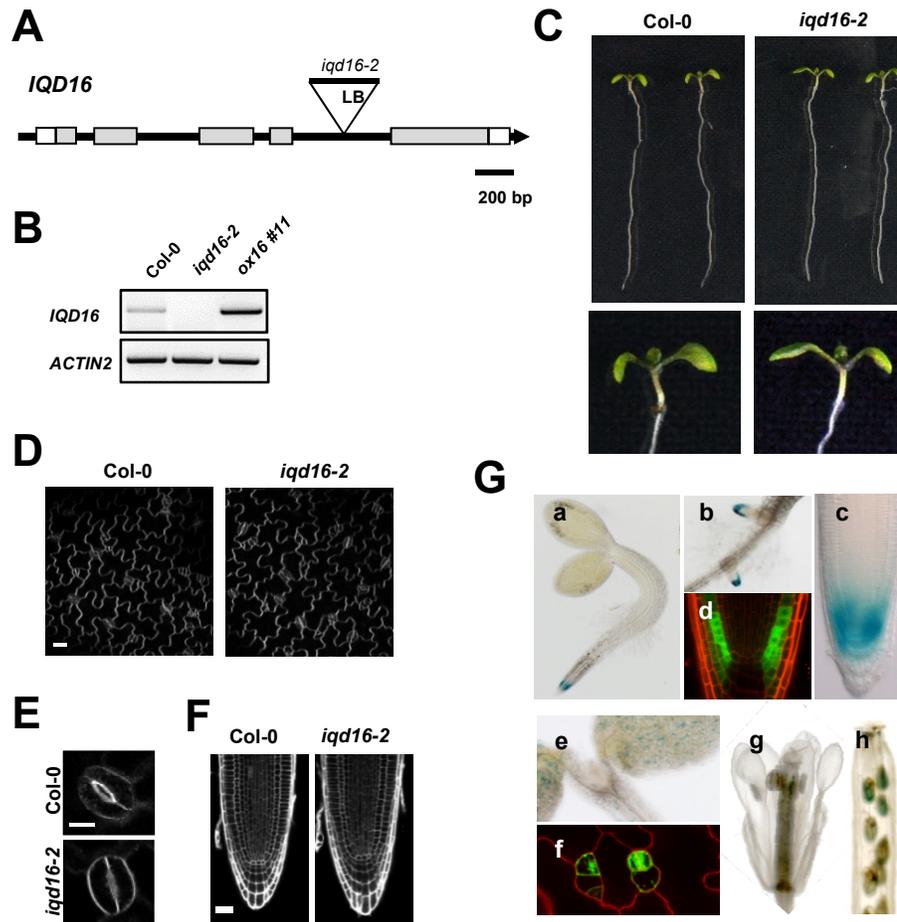


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Supplemental Figure 3. Phenotypes of *iqd16* Lines and Expression Analysis of *ProIQD16:GFP-GUS*.

A, Gene structure of *IQD16* with insertion site and orientation of the T-DNA. White boxes represent the 5'UTR and 3'UTR, grey boxes the exons, black line the introns and intergenic regions. LB, left border. B, RT-PCR amplification of *IQD16* transcripts in wild-type (Col-0), *iqd16-2*, and *p35S::IQD16* #11 seedlings relative to *ACTIN2*. C-E) Phenotype of 5-day-old wild-type (Col-0) and *iqd16-2* seedlings grown on ATS media under long-day condition. C, Complete seedlings (upper panels), and close-up of hypocotyls and cotyledons (lower panels), D-F) Single optical sections. Cell walls were visualized by PI staining. D, Epidermis pavement cells of the adaxial site of cotyledons. Scale bars represent 20 μ m. E, Individual stomata. Scale bars represent 5 μ m. F, Longitudinal sections of primary root tips. Scale bars represent 20 μ m. G, a-c, e, g, h) Histochemical localization of *IQD16* promoter driven GUS expression in 2-day-old seedlings (a), in lateral roots (b), in the primary root tip (c), and in cotyledons and the hypocotyl of 5-day-old seedlings (e), in flowers (g), and in siliques of 5-week-old plants (h). d, f) Fluorescence microscopic analysis of *IQD16* promoter driven GFP expression (green), cell walls were stained with PI (red). Primary root tip (d), and epidermis and stomata cells in cotyledons of 4-day-old seedling (f).