

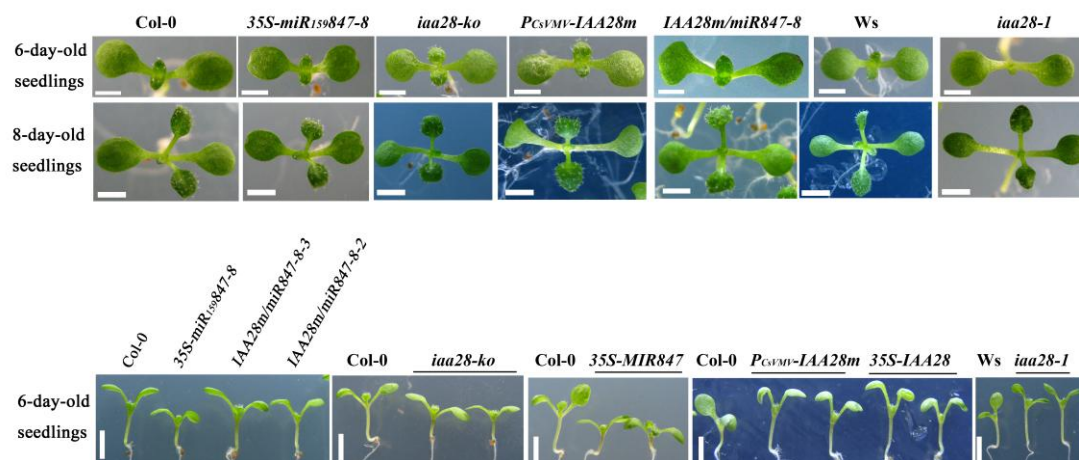
Supplemental Figure 1. Expression pattern of *GUS* transcript in *IAA28-GUS* and *MIR847-GUS* transgenic plants upon auxin treatment

Ten-day-old *IAA28-GUS* and *MIR847-GUS* transgenic seedlings were treated with 20 μM NAA, and samples were collected at the times indicated at top. 30 μg total RNA samples were loaded for hybridization with *GUS*-specific probe. Induction of *IAA1* mRNA was also examined to monitor auxin treatment. Methylene blue-stained rRNA is shown as a loading control.



Supplemental Figure 2. Lateral root development in gain-of-function mutant *iaa28-1* and wild-type control *Wassilewskija*

Early and sustained formation of lateral roots in the gain-of-function mutant *iaa28-1* and its background control *Wassilewskija* (Ws) seedlings. Ws and *iaa28-1* seedlings were grown on MS medium with 3% sucrose. Seedlings were photographed at 9 days and 12 days after germination. Scale bar: 5 mm.



Supplemental Figure 3. Phenotypes of transgenic plants overexpressing miR847 or IAA28, and IAA28 lost-of-function and gain-of-function mutants

Developmental phenotypes of cotyledons (upper panel) and hypocotyls (lower panel) of 6-day- and 8-day-old seedlings of various genotypes as indicated. Transgenic plants overexpressing miR847 resemble the lost-of-function *iaa28-ko*-like phenotypes and were opposite to plants overexpressing *IAA28* mRNA, which resemble the gain-of-function *iaa28-1*-like phenotypes. *35S-MIR847* transgenic plants, in which miR847 was expressed from the *MIR847* precursor backbone, developed shorter hypocotyls similar to that in *35S-MIR₁₅₉847*, in which miR847 was expressed from the *MIR159* precursor backbone. Scale bars: 1 mm (for cotyledons) and 5 mm (for hypocotyls).