Expanded View Figures

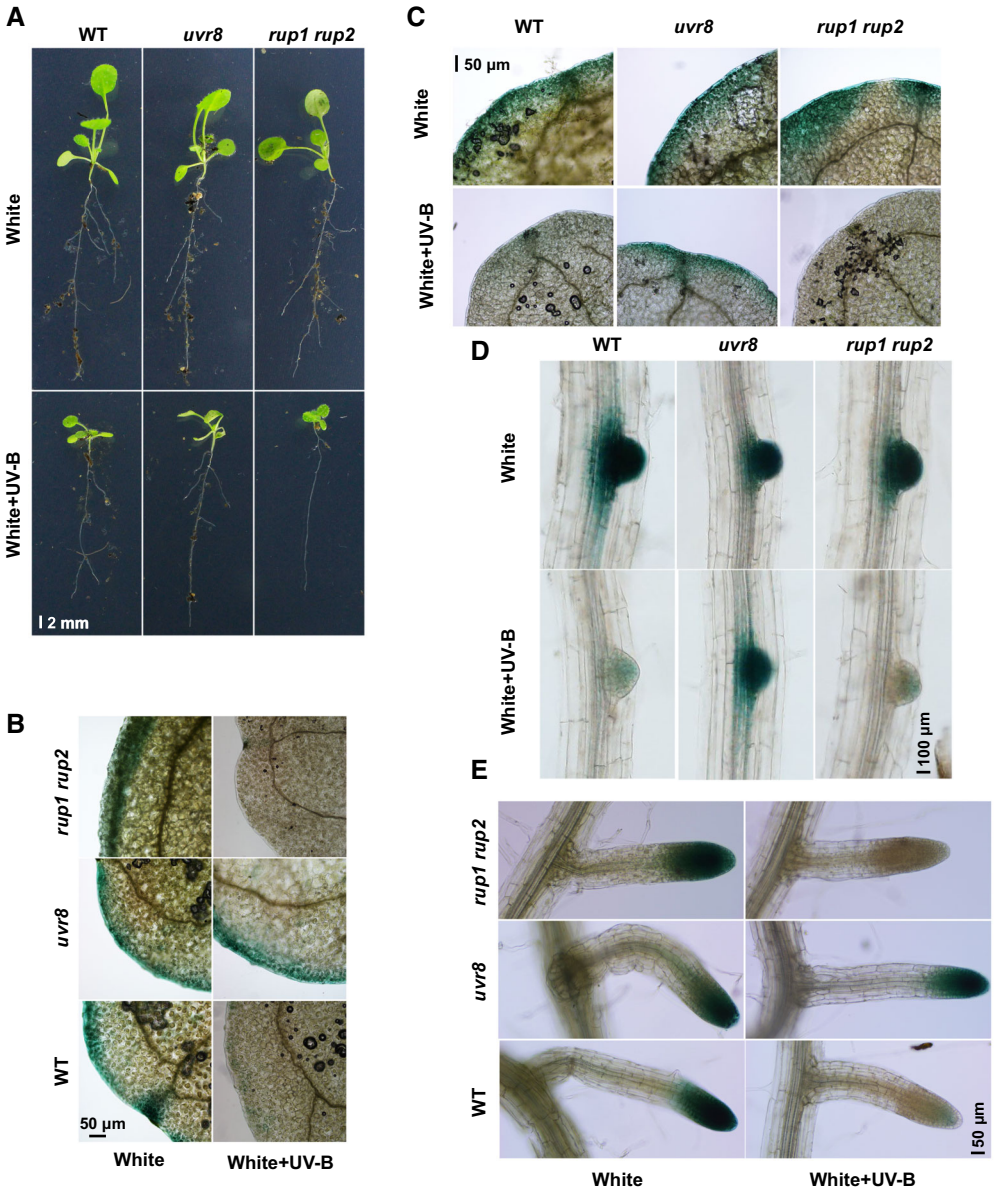

Figure EV1. UV-B inhibits lateral root growth and auxin signaling.

A Phenotypic analysis. Wild-type, *uvr8*, and *rup1 rup2* seedlings were grown in soil in LD condition (16-h light/8-h dark) for 5 days and then transferred to continuous white light or white light plus UV-B (1 W/m^2) for 10 days. Scale bar = 2 mm.

B GUS staining of seedlings expressing the *DR5p::GUS* transgene in the WT, *uvr8*, and *rup1 rup2* background. Seedlings were grown in 1/2 MS with or without UV-B for 2 weeks. Images show leaves; scale bar = 50 µm.

C–E GUS staining of seedlings expressing the *DR5p::GUS* transgene in the WT, *uvr8*, and *rup1 rup2* background. Seedlings of the indicated genotypes were grown in soil under LD conditions for 5 days and then transferred to continuous white light or white light plus UV-B (1 W/m^2) for 10 days. Images show leaves (C), lateral root primordia (D), and lateral roots (E). Scale bars = 50 µm, 100 µm, and 50 µm, respectively.

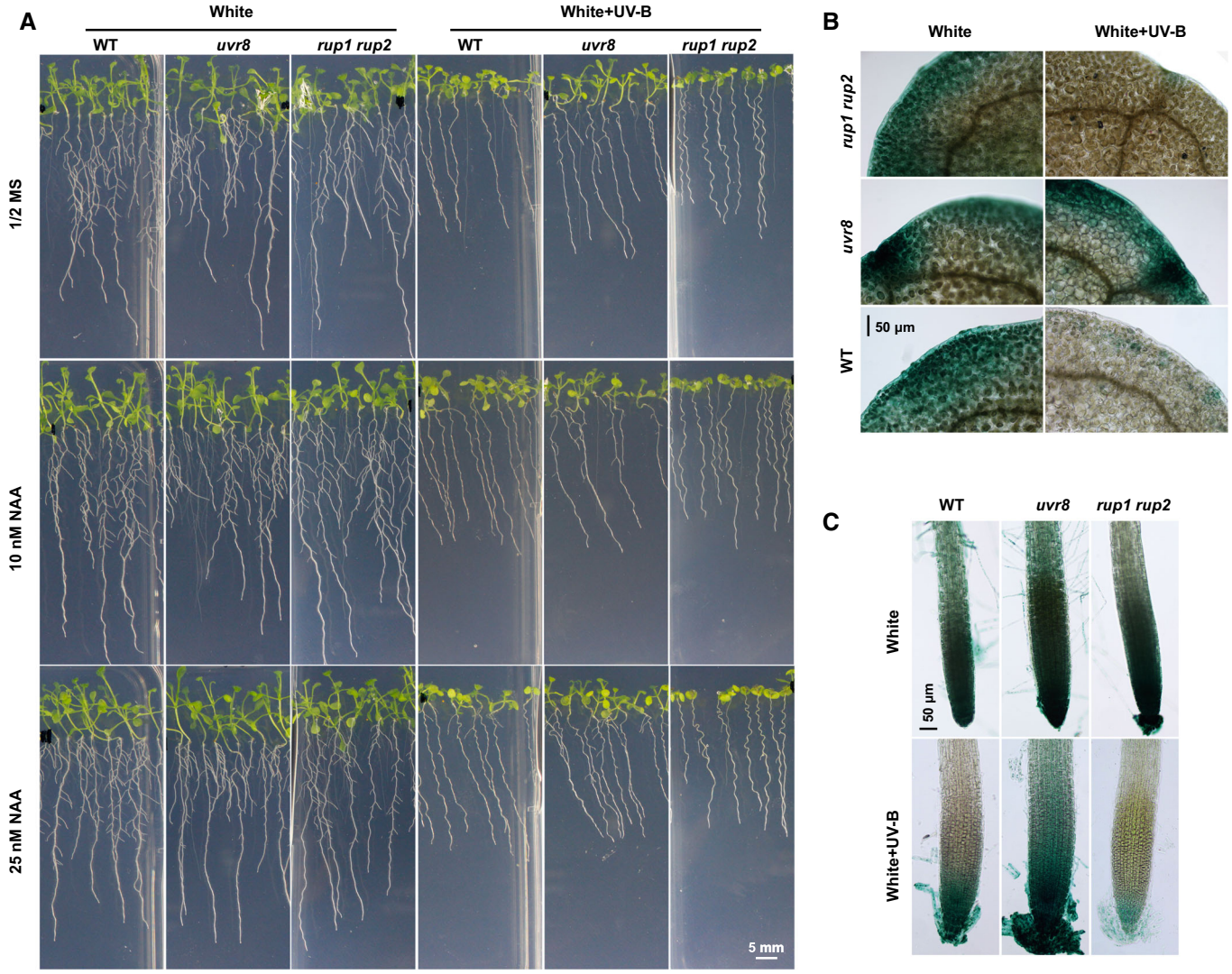

Figure EV2. UV-B represses the auxin responses and inhibits lateral root growth in a UVR8-dependent manner.

A Phenotypic analysis. Seedlings of the indicated genotypes were grown in 1/2 MS with the addition of a series of concentrations of NAA under either continuous white light or white plus UV-B (1 W/m^2) for 2 weeks. Images of representative seedlings are shown; scale bar = 5 mm.

B, C GUS staining of seedlings expressing the *DR5p::GUS* transgene in the WT, *uvr8*, and *rup1 rup2* mutant background. Seedlings of each indicated genotype were grown under LD conditions (16-h light/8-h dark) for 5 days, then transplanted to new medium containing 0.4 μM NAA, and kept in continuous white light or white light plus UV-B (1 W/m^2) for 7 days. Images of leaves (B) and lateral roots (C); scale bars = 50 μm.

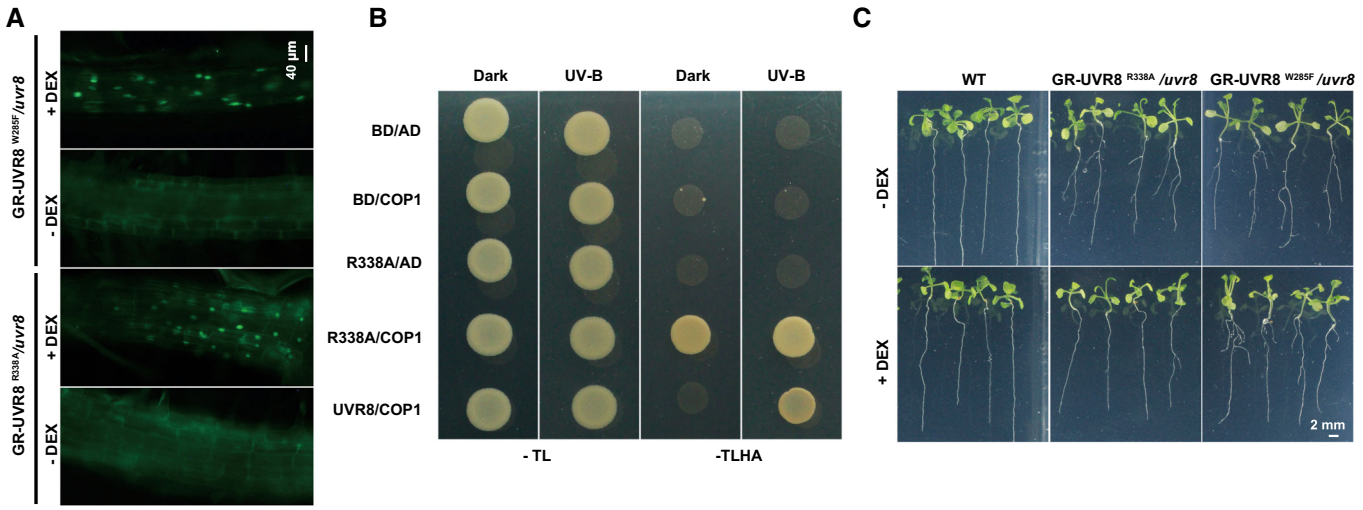

Figure EV3. Monomeric UVR8 inhibits lateral root growth and development.

A DEX treatment induces the nuclear accumulation of GR-UVR8^{R338A} and GR-UVR8^{W285F} in roots. Transgenic plants expressing GR-UVR8^{R338A} or GR-UVR8^{W285F} in the *uvr8* background were grown in LD (16-h light/8-h dark) for 5 days and then transplanted to new medium containing 1 μM IAA and with or without 20 μM DEX. Plants were photographed after 7 days. Scale bar = 40 μm.

B Yeast two-hybrid analysis showed that UVR8^{R338A} could interact with COP1 with or without UV-B.

C Phenotypic analysis. Seedlings of the indicated genotypes were grown in 1/2 MS with or without 20 μM DEX for 2 weeks under UV-B. Scale bar = 2 mm.

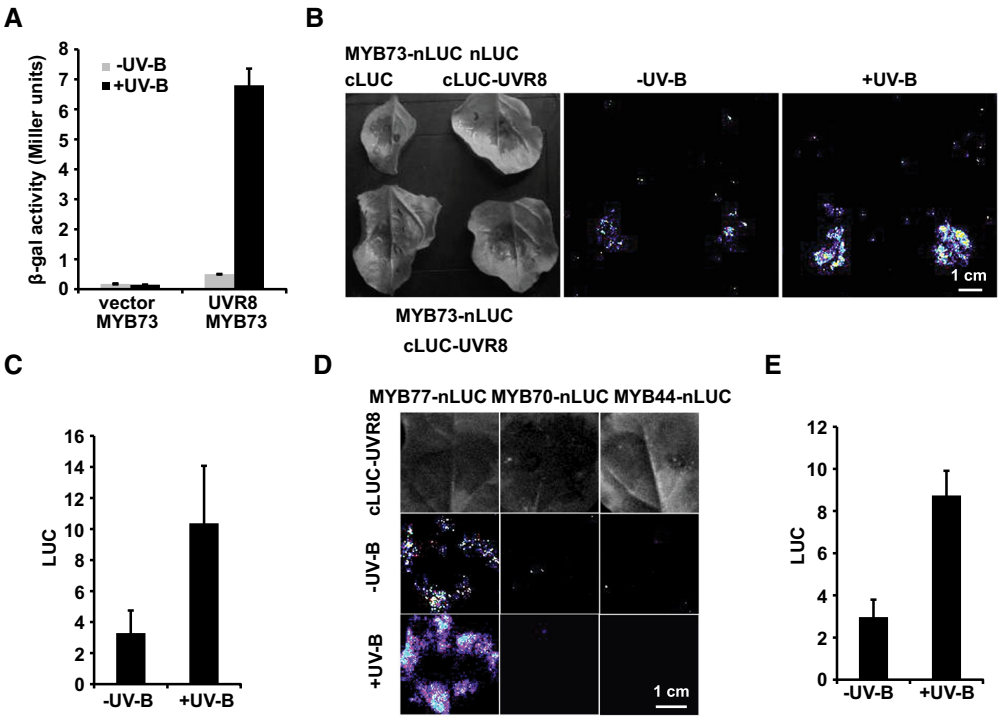

Figure EV4.

Figure EV4. UVR8 physically interacts with MYB73/MYB77 in a UV-B-enhanced manner.

A β-gal assay showing the UV-B-dependent interaction between UVR8 and MYB73. β-gal activity was present in yeast cells expressing UVR8 and MYB73 together in the presence of UV-B and almost absent in yeast cells in the absence of UV-B or expressing MYB73 alone. Error bars, SDs of three biological replicates.

B BiLC assay showing that UV-B treatment promotes the formation of the UVR8–MYB73 complex. Leaf epidermal cells of *N. benthamiana* were co-transformed with MYB73-nLUC and cLUC-UVR8 and treated with or without UV-B (2 W/m^2) for 30 min before being photographed. Scale bar = 1 cm.

C Quantification of luciferase (LUC) activities of MYB73-nLUC + cLUC-UVR8 in (B) with or without UV-B treatment (UV-B + white light versus white light only). Error bars, SDs of three biological replicates.

D BiLC assay showing that UV-B treatment promotes the formation of the UVR8–MYB77 complex. Scale bar = 1 cm.

E Quantification of LUC activities of MYB77-nLUC + cLUC-UVR8 in (D) with or without UV-B treatment. Error bars, SDs of three biological replicates.

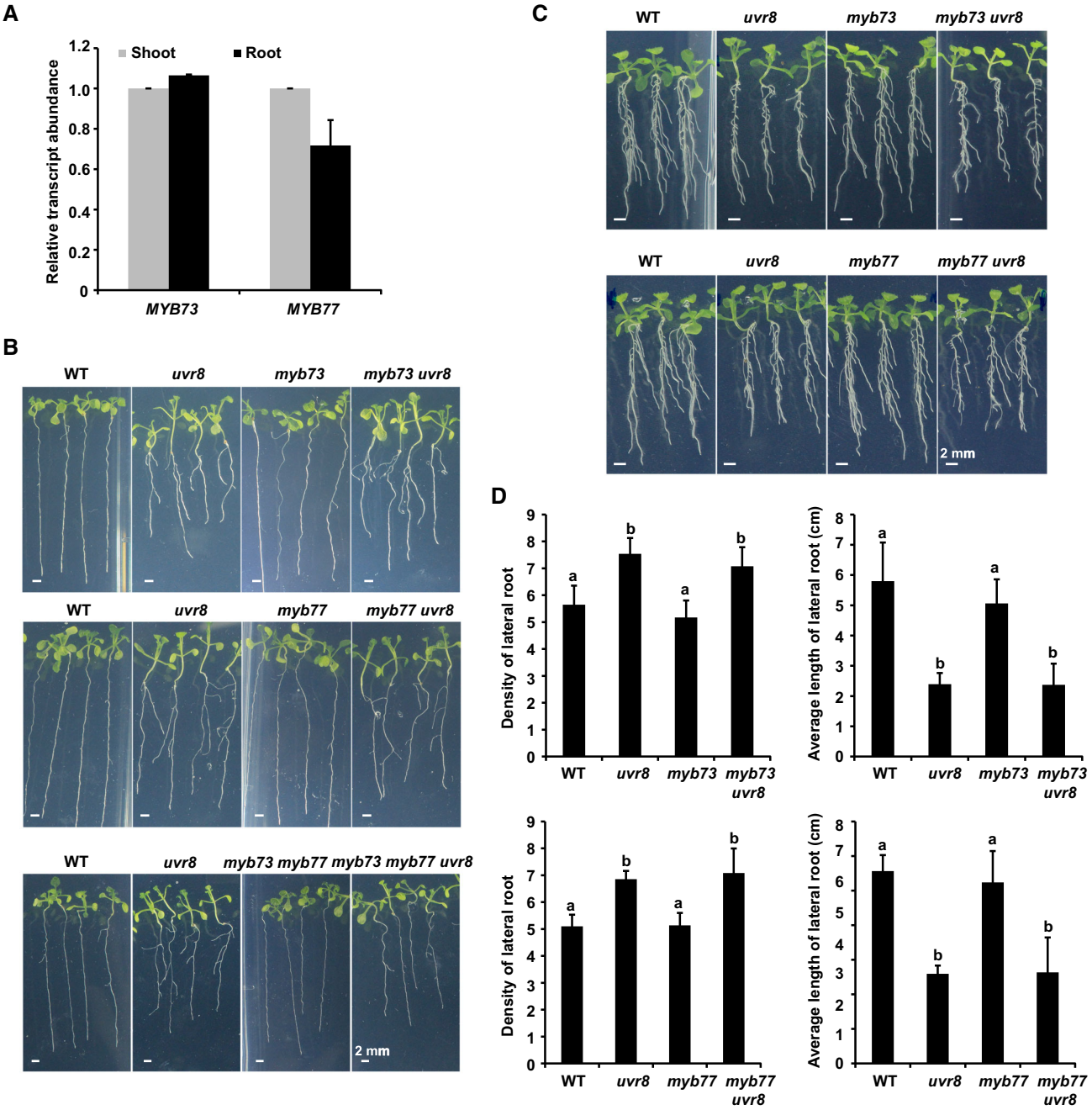

Figure EV5.

Figure EV5. MYB73/MYB77 works redundantly to mediate UVR8-controlled auxin responses.

A qPCR assay showing that *MYB73/MYB77* is expressed in both the shoot and root. Wild-type seedlings were grown in 1/2 MS for 12 days. *ACT7* expression was analyzed as an internal control. Error bars are SD of three biological replicates.

B Phenotypic analysis. Seedlings of the indicated genotypes were grown in 1/2 MS with UV-B treatment for 2 weeks. Scale bars = 2 mm.

C, D Phenotypic analysis. Seedlings of the indicated genotypes were grown in LD (16-h light/8-h dark) conditions for 5 days and then transplanted to new plates containing 0.4 μM NAA with UV-B treatment for 7 days. Images are shown in (C); scale bars = 2 mm. The lateral root density (number of lateral roots/length of primary root) and average length of lateral roots of the indicated genotypes were measured (D). SDs ($n > 8$) are indicated. Letters "a" and "b" indicate statistically significant differences for the indicated values, as determined by analysis of variance (ANOVA), followed by Tukey's least significant difference (LSD) test ($P < 0.05$). There was statistically significant difference between values marked with different letters (for example "a" and "b"), while there was no statistically significant difference between values marked with the same letters (for example "a" and "a").