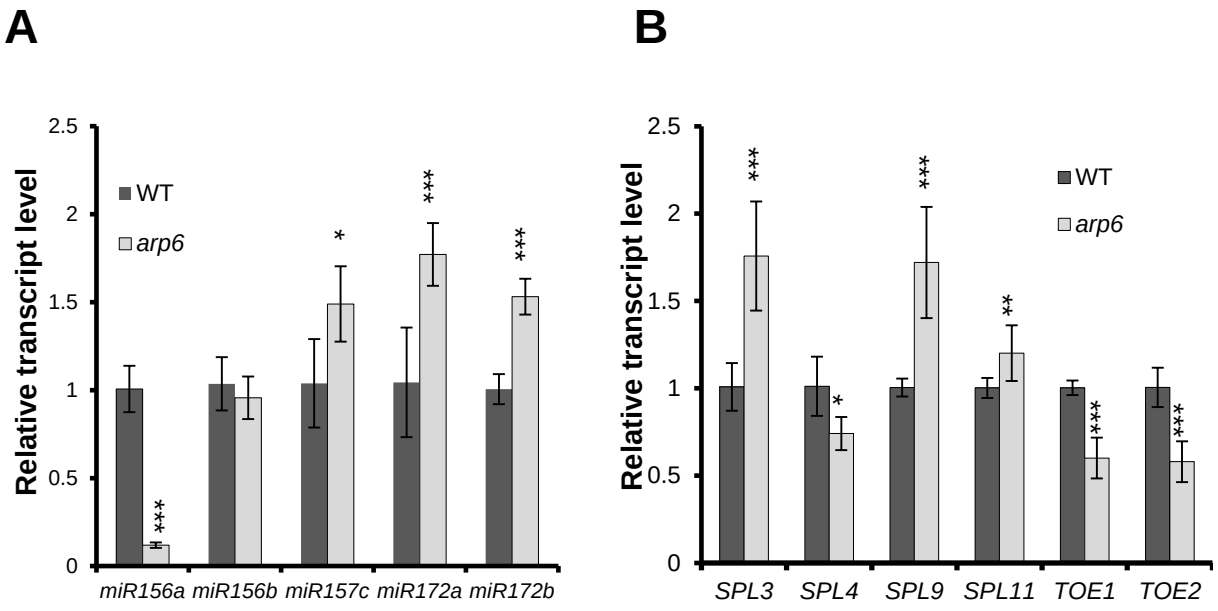
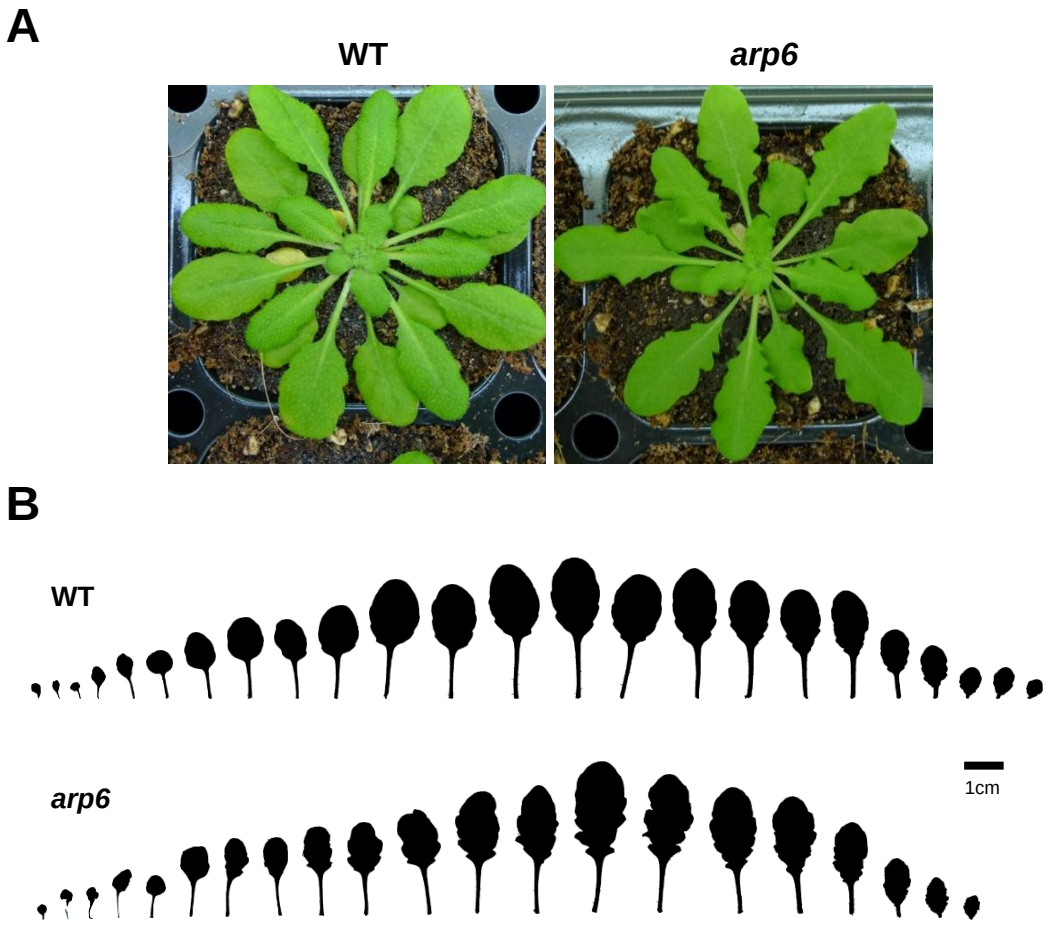
Supplemental Figure S1



Supplemental Figure S1. (A) Transcription levels of *pri-miR156* and *pri-miR172* in *arp6* and WT grown for 20 d under short-day conditions. (B) Transcription levels of miR156 and miR172-regulated genes in *arp6* and WT under short-day conditions. RT-qPCR was performed and analyzed in the same manner shown in Figure 1.

Supplemental Figure S2



Supplemental Figure S2. Comparison of leaf shape in *arp6* and wild type (WT). (A) Images of leaves from WT plants and *arp6* mutants grown under short-day conditions (B) Leaves of WT (upper) and *arp6* (lower) were displayed from first leaf (left) to 21st leaf (right).

Supplemental Figure S3

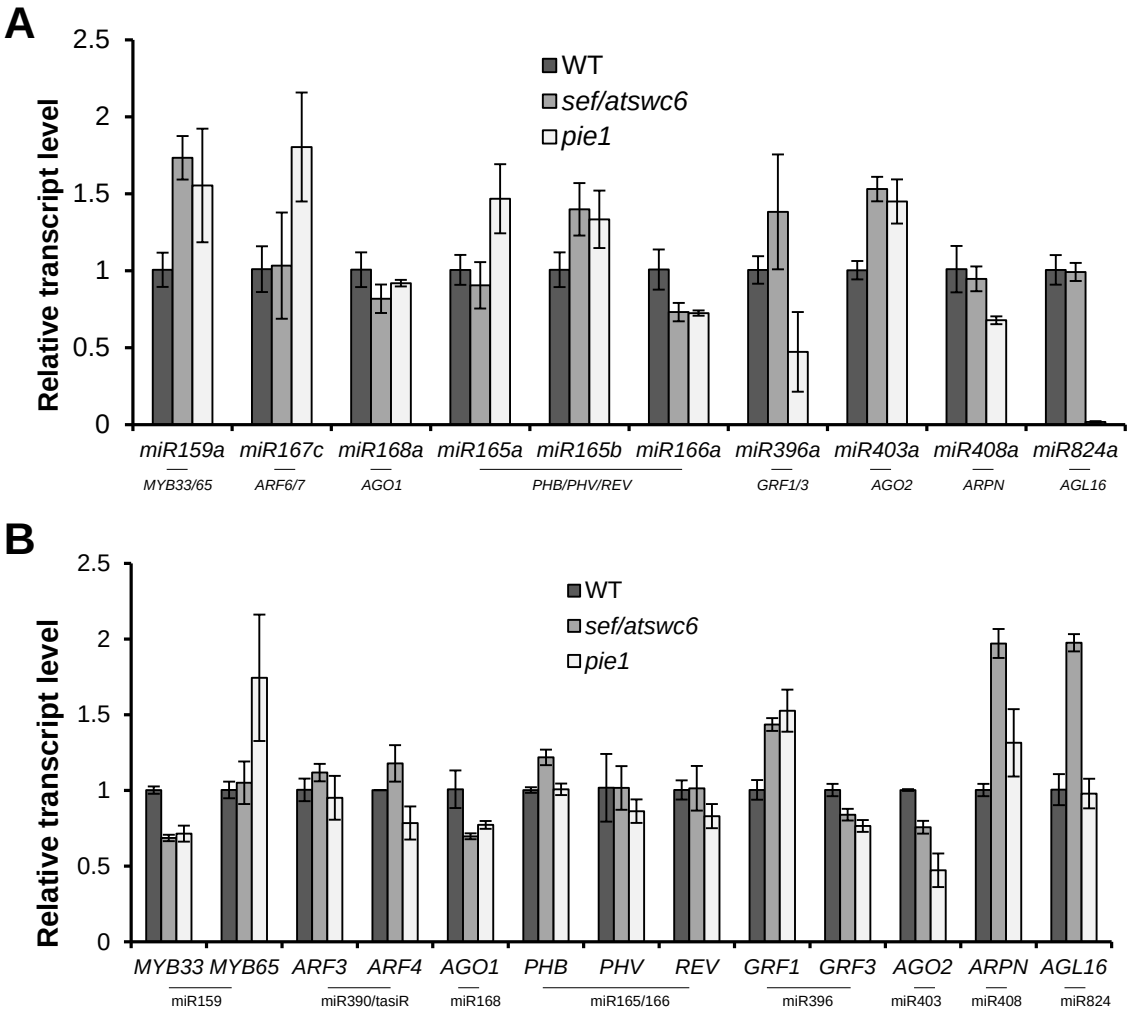
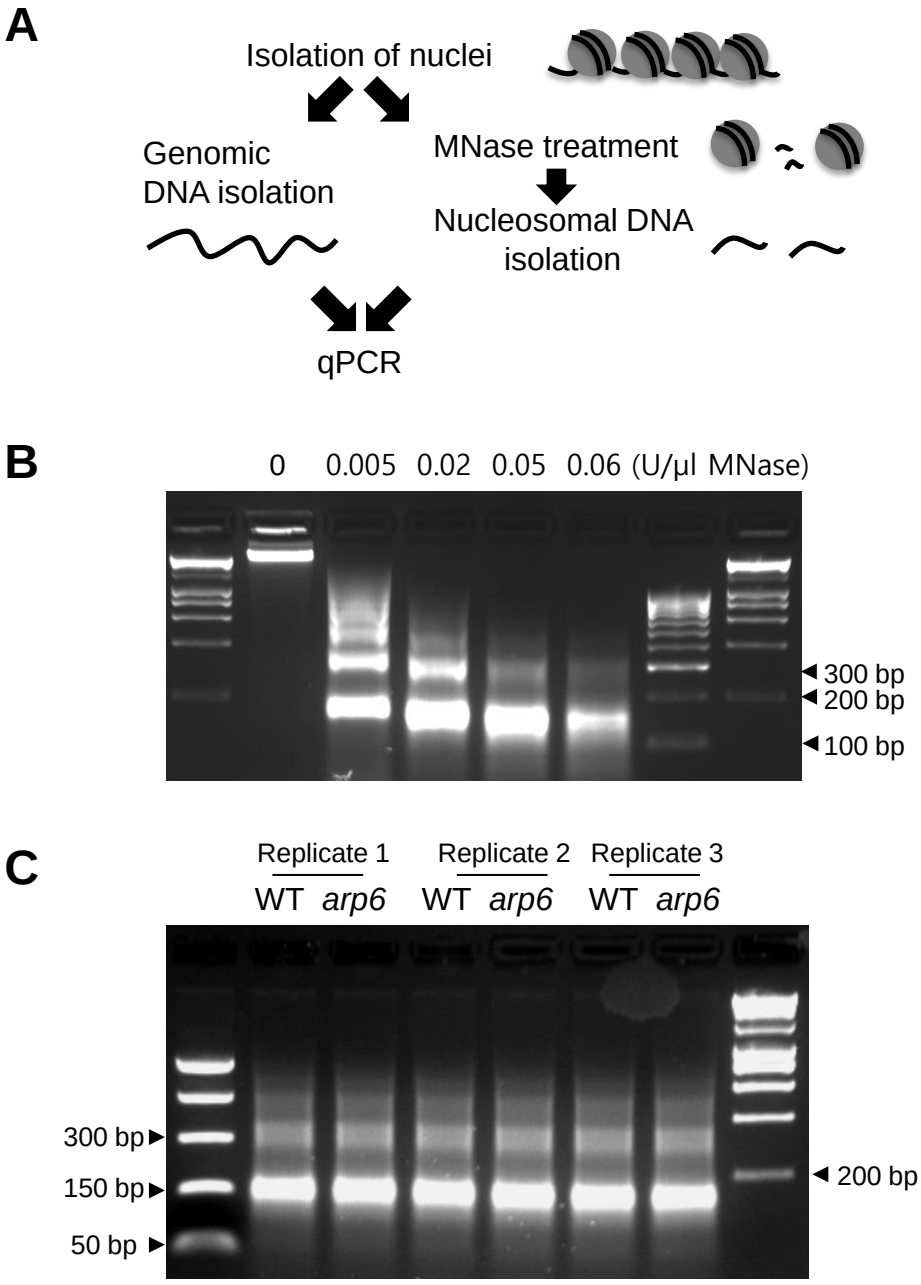


Figure 6. Effect of *sef* and *pie1* on the transcript levels of pri-miRNA and miRNA target genes . (A) Transcript levels of *pri-miRNAs* in *sef* and *pie1*. (B) Transcript levels of the genes regulat ed by miRNAs in *sef* and *pie1*. The matching miRNAs and the miRNA regulated genes are sho wn between lines. TUB was used as a reference gene for normalization of RT-qPCR

Supplemental Figure S4



Supplemental Figure S4. MNase-qPCR assay in *arp6*. (A) Procedure of MNase-qPCR assay. (B) Nucleosomal DNAs digested with MNase. Isolated nuclei were treated with different concentrations of MNase (0, 0.005, 0.02, 0.05, and 0.06 U/ µl) at 37℃ for 10 min. (C) Nucleosomal DNAs used for qPCR. The MNase (0.05 U/µl)-treated nucleosomal DNAs of three biological duplicates in wild type and *arp6* were run with ladders.