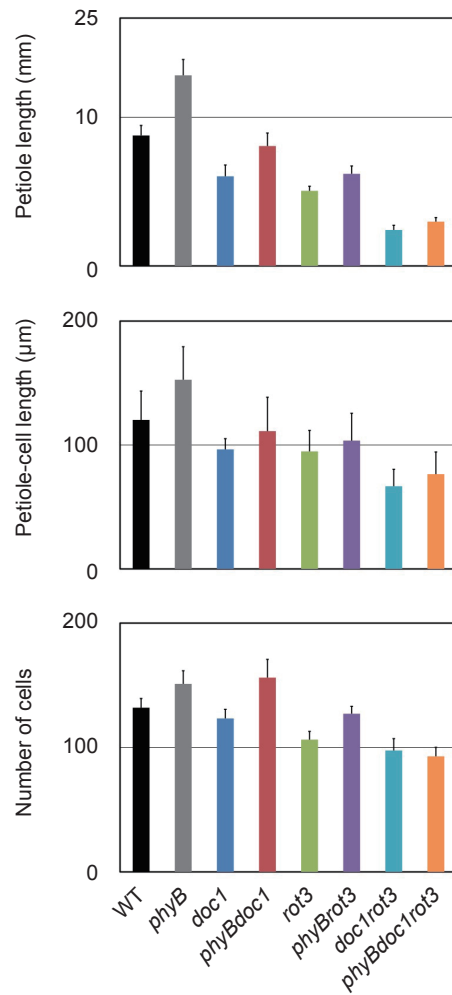
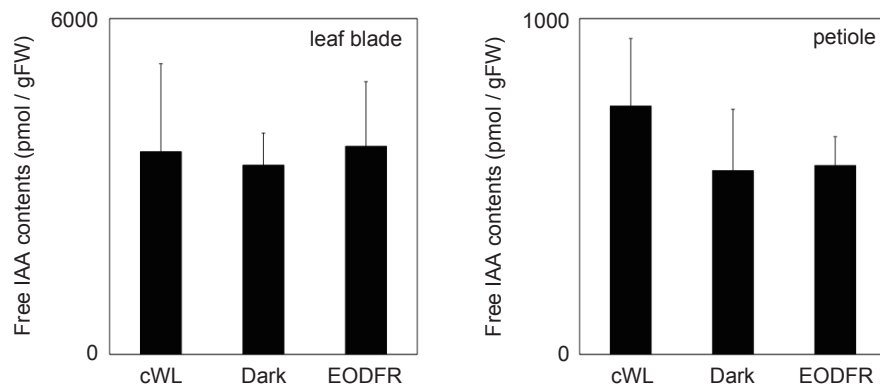


Supplemental Figure S1. Quantitative real-time RT-PCR analysis. The mRNA levels were determined in the leaf blade and petiole after WT, *doc1* and *rot3* plants treated with cWL (W), Dark (D), and EODFR (E) as described in Figure 2A. The transcription levels of *ATHB2*, *HFR1*, *YUC2*, *YUC8*, *YUC9*, *TAA1*, *DOC1/BIG* and *ROT3/CYP90C1* were quantified by real-time RT-PCR and normalized to *UBQ10* (see the Materials and Methods). Data are represented as the means \pm SD (n = 3).



Supplemental Figure S2. The length and number of petiole cells. The total length of petioles (upper), cell length (middle) and cell number (lower) in the fourth rosette leaves. The petiole lengths were determined in WT, *phyB*, *doc1* and *rot3* single and multiple mutants. The petiole lengths are shown as the averages of ≥ 20 leaves \pm SD. The cell lengths are the averages of ≥ 25 cells in the middle part of ≥ 6 petioles. The number of petiole cells was determined in a leaf-length direction of at least 6 petioles.



Supplemental Figure S3. Free IAA levels in the leaf blade and petiole. Seedlings were grown in continuous white light conditions for 19 d before the experimental light treatment, as described in Figure 2A. The free IAA levels were measured from the leaf blade and petiole grown under cWL, Dark and EODFR conditions. Data are represented as the means \pm SD ($n \geq 5$ in leaf blades; $n = 3$ in petioles).