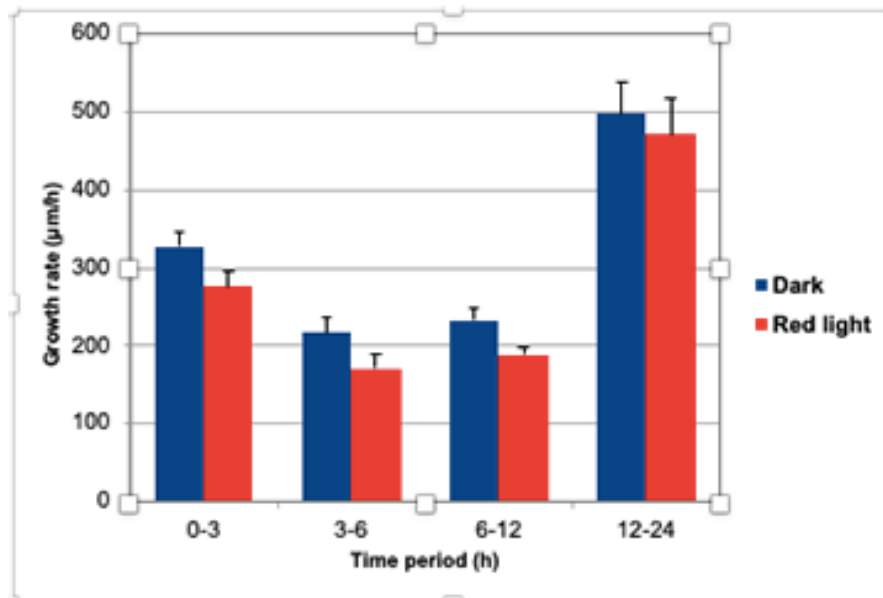
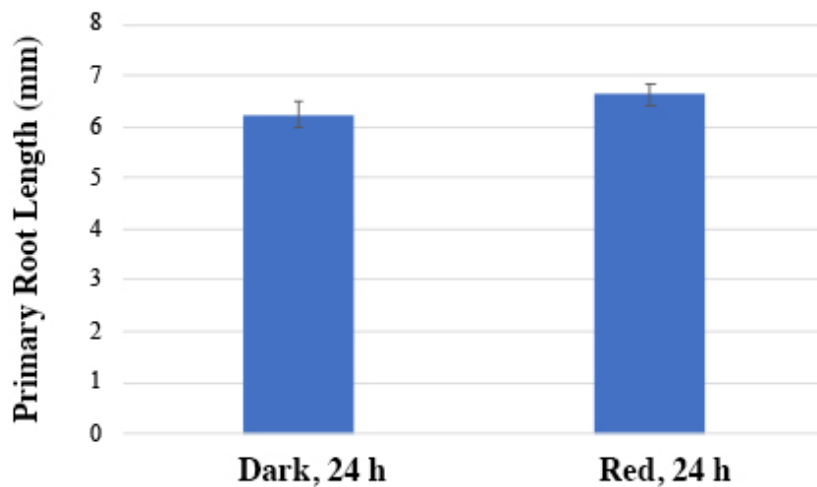


A.

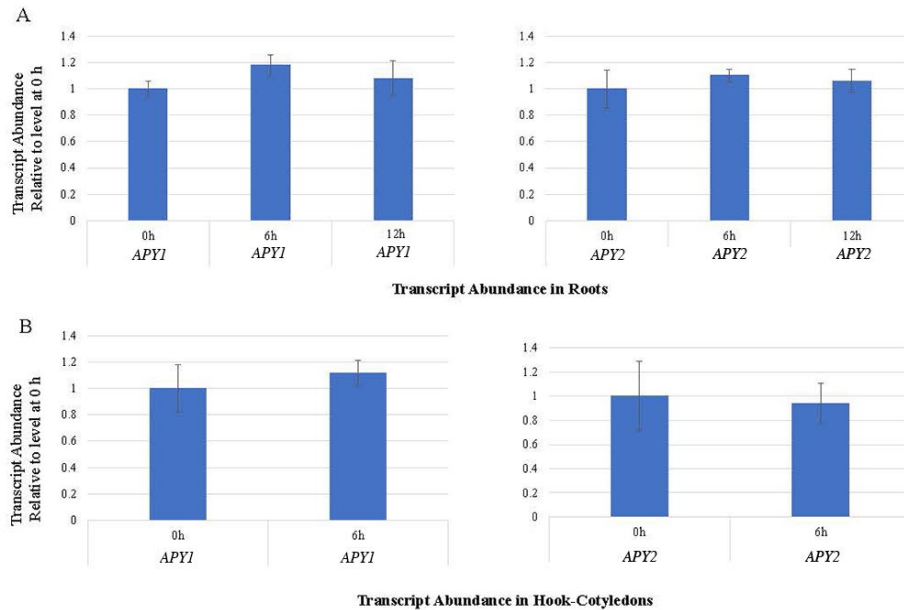


B.

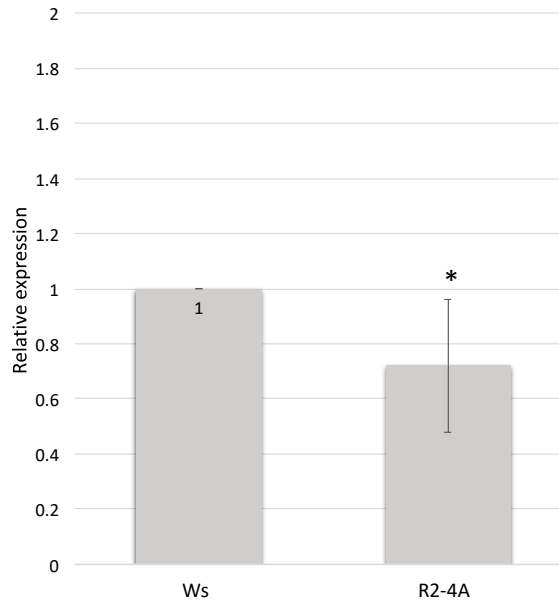


**Supplemental Figure S1.** Root growth rates and lengths of seedlings grown in different periods of darkness or red light. A, Growth rate ( $\mu\text{m/h}$ ) of primary roots of seedlings grown in darkness and in continuous red light in different periods ( $n$  value for each time period was at least 15). Shown are representative results of independent experiments repeated at least twice. The only statistically significant ( $p < 0.05$ ) difference in the growth rate between Dark- and Red light-grown roots is in the 6-12 h time period, in which the  $p$  value was 0.02. B. Length of primary roots after growth for 24 h in darkness or in light. Shown are representative

results of independent experiments repeated 3 times. The root length difference (Dark vs. Red) is insignificant ( $p = 0.22$ ;  $n = 15$ ).



**Supplemental Figure S2.** In roots and hook-cotyledons, *APY1* and *APY2* transcript levels do not significantly change after 6h and 12h of red-light treatment. A, Transcript abundance in roots; B, Transcript abundance in hook-cotyledons. The RT-qPCR samples were from 2.5-days dark-grown WS seedlings that were then exposed to red-light for different times as shown in the figure. Three biological repeats were performed. Relative gene expression levels were normalized using the expression levels of PP2A for RT-qPCR.



**Supplemental Figure S3.** *SAUR50* transcript level in cotyledon-hooks of etiolated seedlings treated with light is significantly lower in R2-4A mutants than in wild-type (Ws) seedlings. Relative fold change in *SAUR50* transcript abundance in R24-A treated with estradiol is compared to wild-type (Ws) after both were treated with 3 h white light. Data represents average of five independent biological replicates, each with an n-value >25, and error bar represents standard deviation. Student t-test was applied. \* Denotes significantly different expression from the calibrator (WT expression level) at  $p < 0.05$ .

**Supplemental Table S1.** Transcript abundance of peroxidase genes in etiolated seedlings of wild-type (WsWT) compared to that in *APY* mutants

<u>Peroxidase</u>	<u>Gene Locus</u>	<u>AtAPY2 OE*</u>	<u>RNAi suppressed Expression*</u>
<b>Prx 15</b>	<b>AT2G18150</b>	<b>-2.6</b>	<b>+ 21.8</b>
<b>Prx 49</b>	<b>AT4G36430</b>	<b>-2.1</b>	<b>+ 11.2</b>
<b>Prx 59</b>	<b>AT5G19890</b>	<b>-2.0</b>	<b>+ 5.4</b>

\*Linear change in transcript abundance in AtAPY2 OE mutants, and in estradiol-induced R2-4A mutants, compared to wild-type (WsWT), In the RNAi suppressed mutants, *APY2* is null and *APY1* is suppressed by 60%. Data taken from Lim et al. (2014).