

Description of Additional Supplementary Files:

Supplementary Dataset 1. Transcriptomic analysis of genome-wide PhANGs in de-etiolated mutants. Relative transcript levels of the 149 PhANGs in dark-grown seedlings of pifq (4-d-old), det1-1 (4-d-old), ein3/eil1 (2.5-d old), cop1-4 (4-d-old), and spaq (3-d-old) are shown as fold-changes between the levels in the mutants and their respective Col-0 controls. Genes that are significantly upregulated in the mutants by at least twofold are labeled in magenta. The accession numbers of the RNA-seq data used in this study and their references are listed in Supplementary Table 2.

Supplementary Dataset 2. Transcriptomic analysis of genome-wide PhANGs in 2-d-old and 4- d-old dark-grown pifq seedlings. Relative transcript levels of the 149 PhANGs in dark-grown seedlings of 2-d-old pifq and 4-d-old pifq are shown as fold-changes between the levels in pifq and their respective Col-0 controls. Genes that are significantly upregulated in the mutants by at least twofold are labeled in magenta. The accession numbers of the RNA-seq data used in this study and their references are listed in Supplementary Table 2.