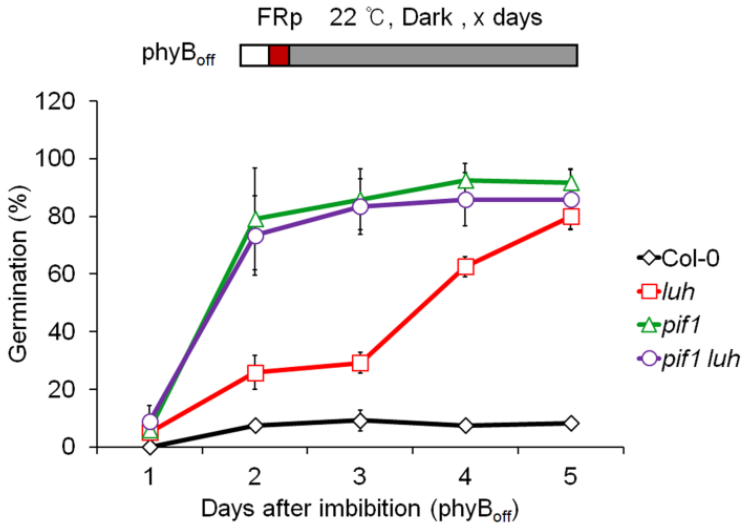
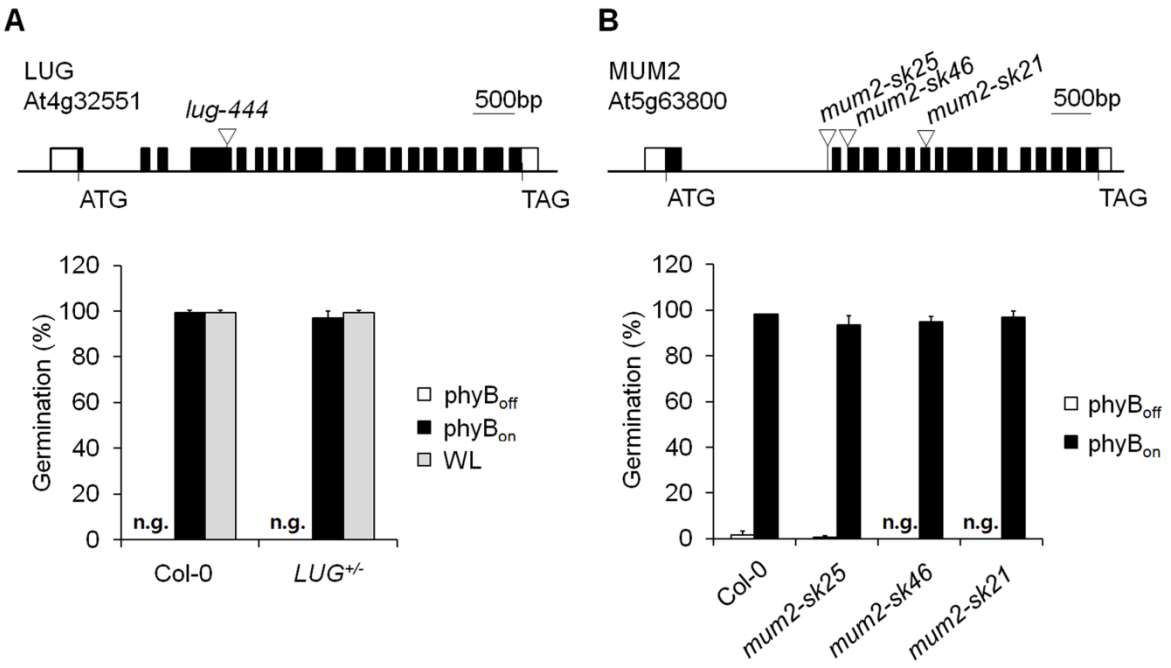
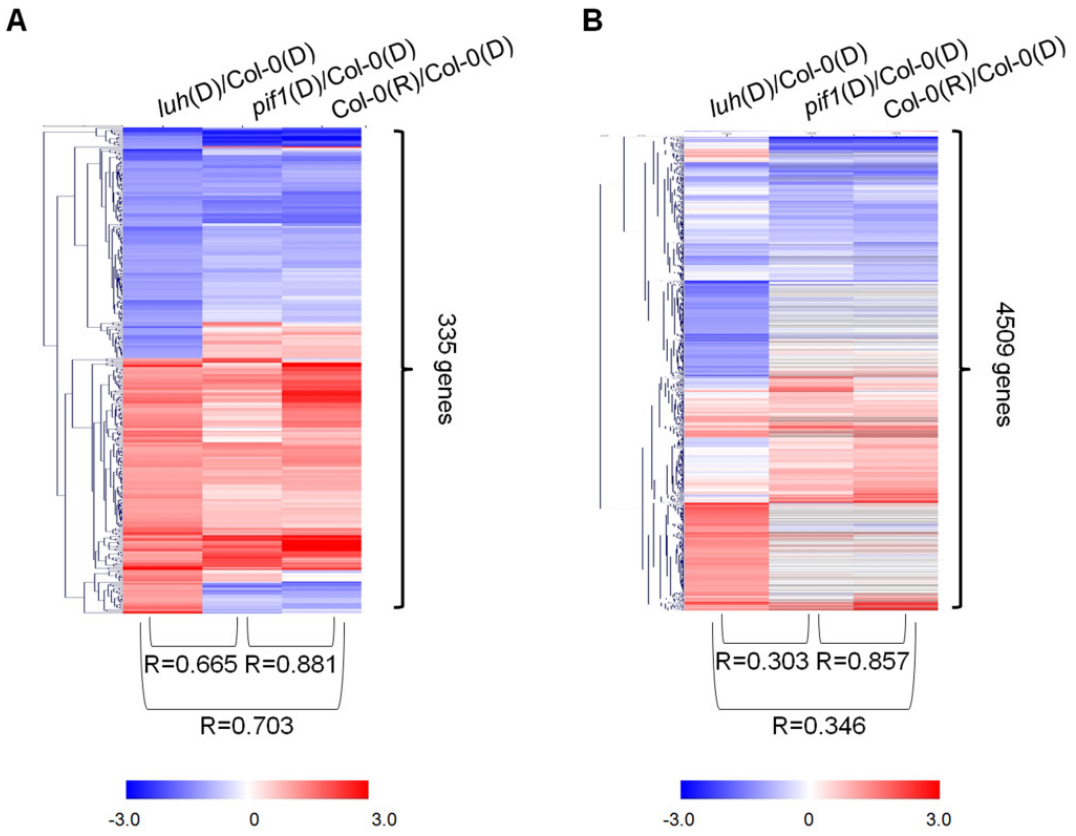


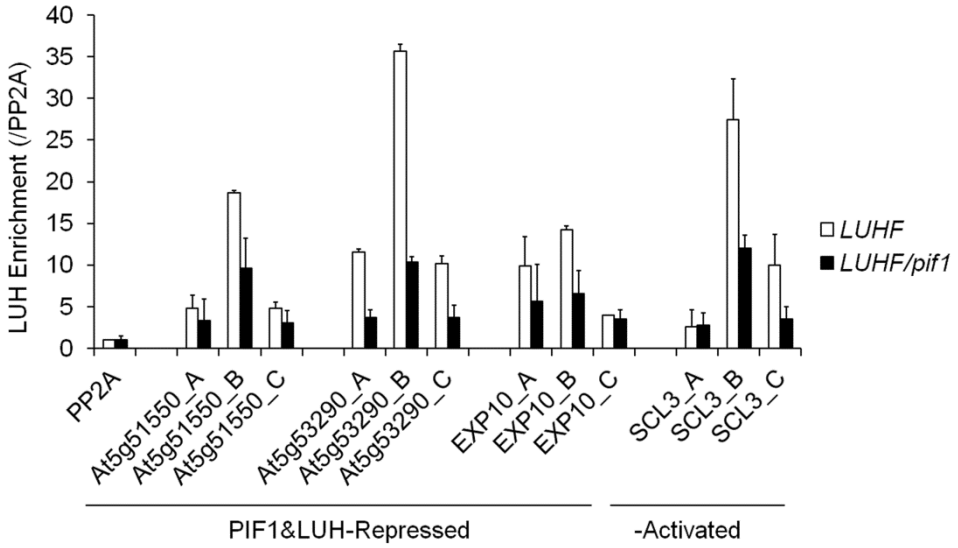
Supplemental Figure 1. *pif1* mutants and *pif1 luh* double mutants have comparable germination kinetics under the phyB$_{off}$ condition. Germination frequencies were counted on different days after a far-red light pulse treatment (SD, n=2 biological replicates).



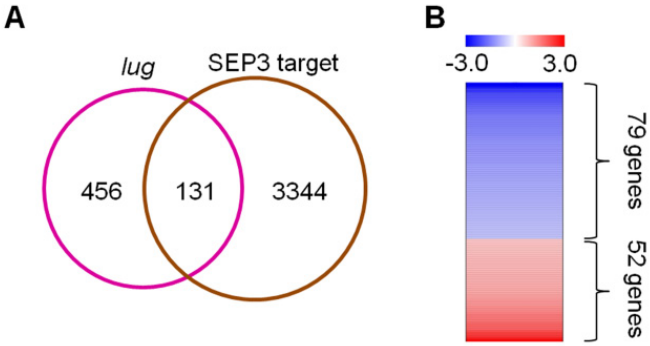
Supplemental Figure 2. Comparable germination frequencies for wild-type seeds and seeds harvested from the *LUG*$^{+/-}$ (A) or *mum2* mutants (B). n.g. indicates 0% germination frequency. Upper diagrams show the structure of *LUG* and *MUM2* with the T-DNA insertion sites indicated by inverted triangles. Exons are indicated with black boxes, UTRs are indicated with white boxes, and translation start and termination sites are indicated with ATG and TAG, respectively. All T-DNA insertion lines were obtained from the Salk collection: *lug-444* (Salk_126444), *mum2-sk25* (Salk_015025), *mum2-sk46* (Salk_022846), and *mum2-sk21* (Salk_060221). (SD, n=3 biological replicates).



Supplemental Figure 3. Heatmap showing a hierarchical clustering analysis of LUH- and PIF1-regulated genes. The overlapping DEGs (A) and the union DEGs (B) of LUH- and PIF1-regulated genes are shown. R indicates each respective correlation coefficient.



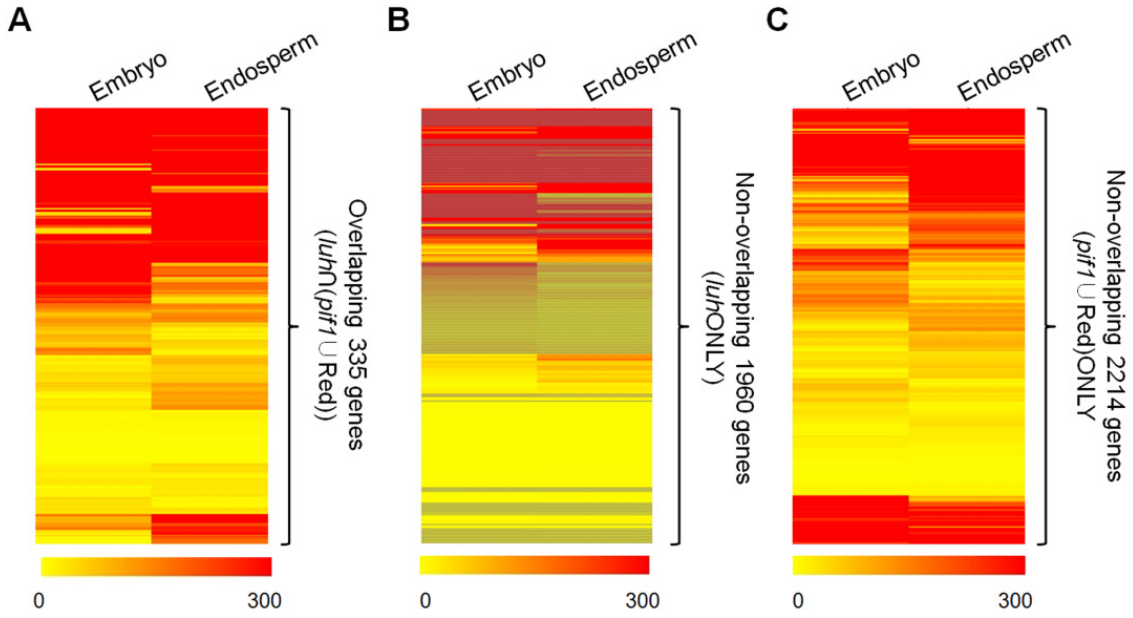
Supplemental Figure 4. LUH-mediated enrichment of promoter fragments in wild type and *pif1* mutants. Imbibed $phyB_{off}$ seeds were incubated for 12 h in the dark. The enrichment of each promoter was normalized both by the level of input DNA and by the ChIP enrichment value of the non-binding *PP2A* promoter. (SE, n=2 biological replicates).



Supplemental Figure 5. LUG regulates SEP3 targets either positively or negatively.

(A) Venn diagram identifying 131 LUG-regulated SEP3 targets (P <5.91x10^{-6}, hypergeometric test).

(B) Log2-transformed expression levels of these 131 genes in the *lug* mutant: 79 are up-regulated and 52 are down-regulated.



Supplemental Figure 6. Expression patterns of LUH- and PIF1-regulated genes in the embryo and endosperm. Expression patterns of overlapping DEGs among LUH- and PIF1-regulated genes (A), non-overlapping LUH-regulated genes (B), and non-overlapping PIF1-regulated genes (C) in the embryo and endosperm. Grey cells indicate genes not included in Affymetrix probe set.