Supplementary data legends

Supplementary Figure 1- Dose response curves for inhibitors utilized in microarray experiments.

Supplementary Figure 2- q-RT-PCR validation of microarray results.

Supplementary File 1- Gene lists from SAM, GO ontology analysis, TAGGIT ontology analysis and selected output from the seed eFP Browser.

Supplementary File 2- GO and TAGGIT ontology analyses of SAM selected germination responsive transcripts.

Supplementary File 3- Selected output from the seed eFP Browser. eFP output for genes mentioned in the text are presented in this file.

Supplementary File 4- Germination signature of Arabidopsis seeds. Venn intersections of the germination-responsive transcripts with the germinating and dormant transcriptional signatures (Carrera et al. 2007), and the ABA-responsive transcripts determined by SAM under the same conditions.

Supplementary File 5- Effects of the individual drug treatments based on genes showing a two-fold change or more in transcript abundance. TAGGIT ontological analysis of the genes affected by the individual drug treatments.

Supplementary File 6- Gene lists of nuclear-encoded components of photosynthesis that show an increase in transcript abundance during seed germination.

Supplementary File7- qRT-PCR primers and reaction conditions