



Supplemental Figure 2. Expression patterns of *PEX11* genes.

(A) Semiquantitative RT-PCR analysis of *PEX11* transcript levels.

Total RNA was from seedlings subjected to dark to light transition (top panel) and leaves after 2-d induced senescence (bottom panel). Lanes are indicated as untreated (-) and treated (+).

(B) Genes co-expressed with *PEX11d* and *PEX11e*.

Genes that are co-expressed with *PEX11d* and *PEX11e* are displayed as a pie chart with groups of co-expressed genes with similar functions represented by sections of the pie chart. These numbered sections account for a percentage of the total number of genes co-expressed with the respective *PEX11* genes. The results were obtained using the atge0100 Matrix (12200 genes) from DSB.DB (http://csbdb.mpimp-golm.mpg.de/csbdb/dbcor.ath/ath_tsgq.html). Genes listed in the pie charts represent 1509 genes co-expressed with *PEX11d* and 628 genes co-expressed with *PEX11e*, retrieved as positive, significant co-responding genes (after Bonferroni correction) with 95% probability. The two functional categories pertinent to this report are 1, photosynthesis, and 6, gluconeogenesis and the glyoxylate cycle.