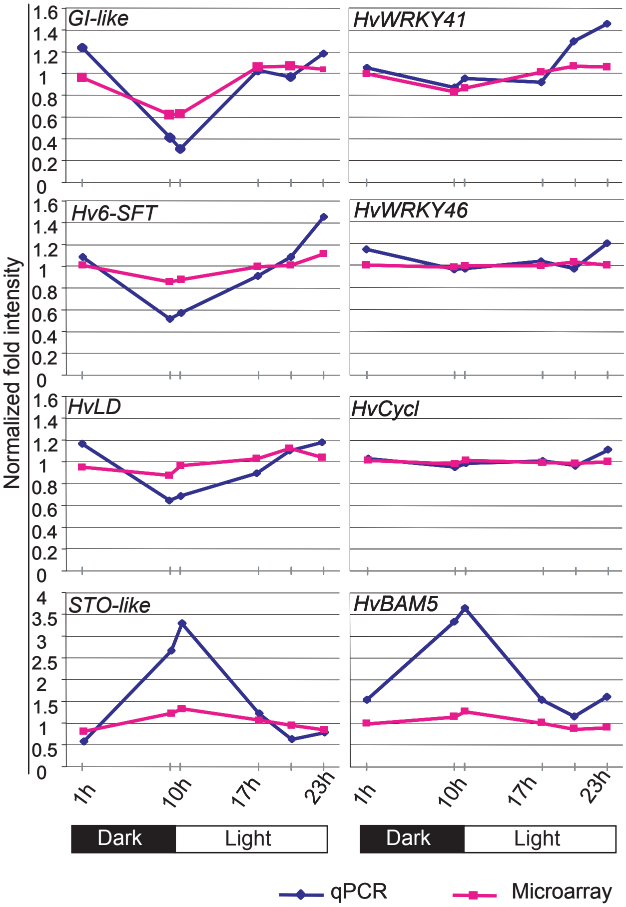

Figure S1. Quantitative real time PCR (qPCR) of selected genes. Transcript levels were normalized to three reference genes. The resulting expression profiles were compared to those obtained from the microarray experiments. The signal intensities are normalized to the mean expression values and are plotted in log-scale. The respective genes are a putative Gigantea ortholog (*GI-like*), the WRKY transcription factor genes *HvWRKY41* and *HvWRKY46*, the sucrose: fructan-6-fructosyltransferase gene (*Hv6-SFT*), the limit dextrinase gene (*HvLD*), a cyclophilin gene (*HvCycl*), a putative ortholog for the salt tolerance gene (*STO-like*) and the beta-amylase 5 gene (*HvBAM5*).