Supplementary Figure 1. Comparison of light induction between WT and *frq*^{7}.

(A) Relative microarray readouts of early light-responsive genes. (B) Relative microarray readouts of late light-responsive genes in WT, *frq*^{7} and WT (DD). Median value is shown as a horizontal bar with the 25% to 75% range indicated as a box and extreme values as an extended line. Red arrows indicate where the most obvious difference is in the *frq*^{7} strain. Red dashed lines enclose the 25% to 75% range of the wild-type readout in the first DD time point to facilitate a visual comparison for light induction.

Supplementary Figure 2. Statistically significant clusters identified by a bootstrapping analysis.

A dendrogram was generated using Manhattan distance calculations. The red boxes indicate terminal branches of genes that were differentiated at a 95% or greater level of confidence. The yellow boxes denote the major clusters encompassing at least 10 or more genes. The arrows trace how the clusters were arranged in the heatmap representation. Timing of light treatment is shown to the right (see Fig.1 legend).

Supplementary Figure 3. RT-QPCR validation of novel light-responsive genes.

(A) Microarray readouts of 6 light-responsive transcription factors. Each block of data represents individual readouts from 90 microarrays. For each gene, from left to right, the individual columns correspond to light treatment for 0, 5, 10, 15, 30, 45, 60, 90, 120, 240 minutes, respectively. Square colors as described in Figures 1. Experimental strains: Lane 1, 74A (WT); Lane 2, Δ*phy-1*; Lane 3, Δ*phy-2*; Lane 4, Δ*phy-1*, Δ*phy-2*; Lane 5, *frq*^{7}; Lane 6, Δ*wc-1*; Lane 7, Δ*wc-2*; Lane 8, Δ*wc-1*, Δ*wc-2*; Lane 9, 74A without light treatment. (B) RT-QPCR validation of 5 light-responsive transcription factors. (C)(D)(E)(F) RT-QPCR validation of 4 novel light-responsive genes. The

results obtained by 3 independent replicate experiments are shown. Columns represent mean values ± standard error.

Supplementary Figure 4. Circadian clock phenotypes of the light inducible transcription factor knockout strains.

To facilitate the observation of the underlying circadian rhythm, knockout strains were crossed to strain 324-8 to gain the dominant Ras allele: *ras-1*^{bd}. Race tube data represent mean values of period ± standard error (n ≥ 5). After inoculation, mycelia were grown on race tubes for 2 days in constant light (LL) and then shifted into constant darkness (DD). The growth front was marked every 24 h under red light. Period and phase of the free running clock were analyzed using CHRONO (Roenneberg and Taylor, 2000) and shown next to the race tubes, respectively.

Supplementary Figure 5. Distribution of the ELRE and the LLRE.

(A) Distribution of the ELRE among all ELRGs. (B) Distribution of the LLRE among all LLRGs.

Supplementary Figure 6. SAM analysis of late light responses in knockout strains.

Time points in the light (4 arrays) from wild-type were categorized as class l (Figure 4B, lane 1) in contrast to class ll, the time points from different knockout strains (Figure 4B, lane 2 to lane 8). A two class unpaired test was performed with a T-statistic method and 5% FDR as a cut-off to select for genes showing statistical differences between the two classes. For each knockout strain, the number of genes identified with altered expression relative to the wild type is shown.