

Genome-wide characterization of light-regulated genes in *Neurospora crassa*

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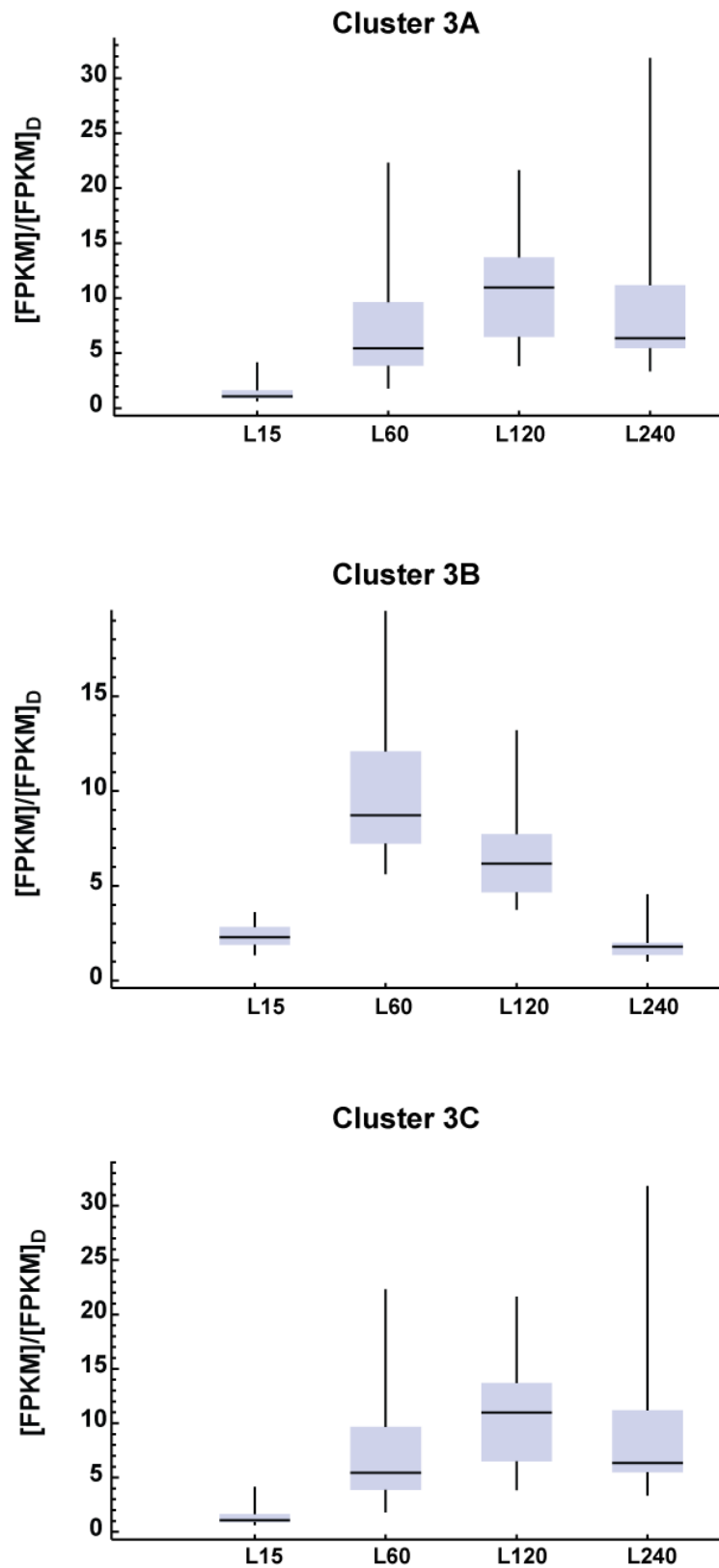


Figure S1 Expression-changes for transcripts in each of Cluster 3 subclusters A, B, and C demarcated in (Figure 3). Values for each time-point (L15, L60, L120 and L240) are normalized to expression in the dark. The horizontal black bar is the median, the box top and bottom are the 75% and 25% quantiles, and the whiskers extend to the maximum and minimum values.

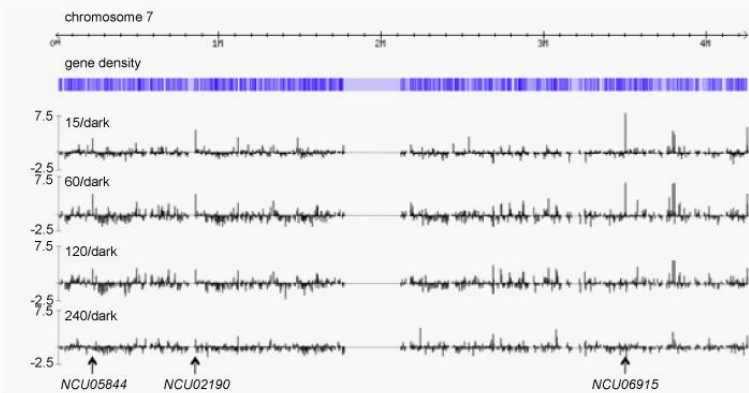
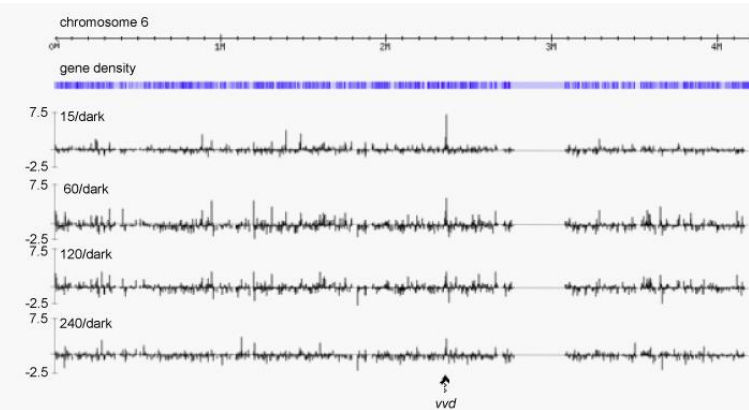
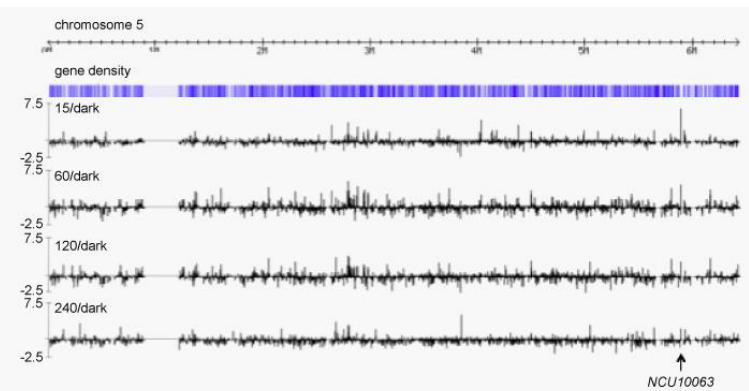
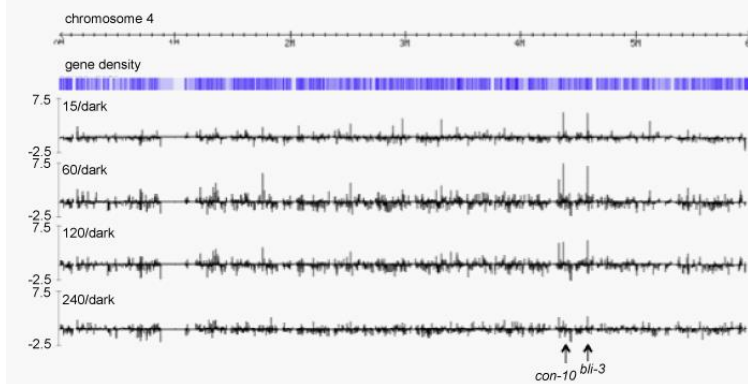
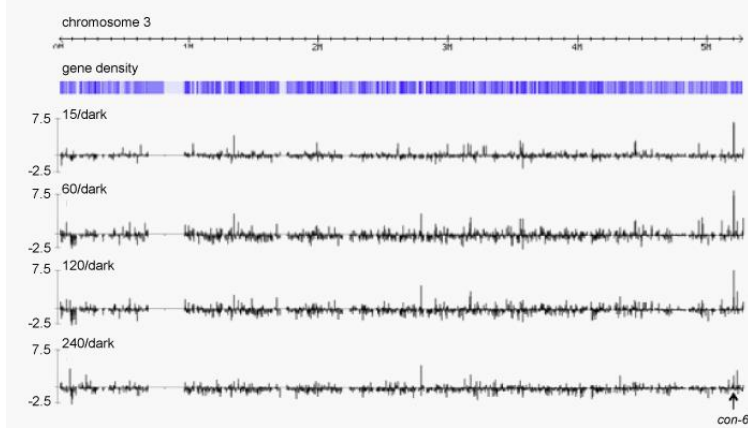
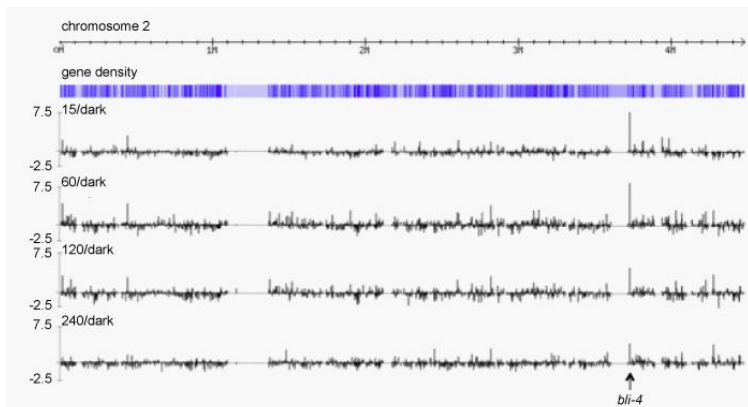


Figure S2 Pattern of light-regulation of genes on Linkage Groups II-VII (Chromosomes 2-7). The log-2 change in expression in the light versus the dark is given on the Y-axis for each time-point in the light (15, 60, 120 and 240 min).

Tables S1-S14

Available for download as Excel files at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.114.012617/-/DC1>

Table S1 CuffDiff analyses of FPKM (fragments per kilobase per million reads) for the combined RNA-seq datasets from two biological replicates. The ratio values given are the \log_2 ratio values. The q-value represents an adjusted p-value that is calculated with a consideration of the false discovery rate of 0.05.

Table S2 CuffDiff analyses of FPKM for biological replicate 1. The ratio values given are the \log_2 ratio values.

Table S3 CuffDiff analyses of FPKM for biological replicate 2. The ratio values given are the \log_2 ratio values.

Table S4 Predicted genes that are not expressed in the combined biological replicates (FPKM<1) that are not designated as hypothetical proteins.

Table S5 FunCat analyses for predicted genes that are highly expressed in the dark in the combined biological replicates (FPKM>400 and FPKM>1000).

Table S6 CuffDiff analyses for the subset of transcripts determined to be regulated 2-fold in response to light.

Table S7 FunCat analysis of the 999 mRNAs most up-regulated in response to light.

Table S8 FunCat analysis of the 999 mRNAs most down-regulated in response to light.

Table S9 CuffDiff analyses for the subsets of transcripts determined to respond to light with $q \leq 0.2$, 0.1 or 0.05. The ratio values given are the \log_2 ratio values.

Table S10 Gene Ontology (GO) analyses of genes that were 2-fold regulated by light and genes whose light-regulation met the $q \leq 0.2$ stringency requirement.

Table S11 FunCat and GO enrichment analyses of the 5 major clusters delineated in Figure 3A.

Table S12 RNA-seq data (extracted from Table S1) for the 27 TFs analyzed as WCC targets in (SMITH et al. 2010). The ratio values given are the \log_2 ratio values.

Table S13 FunCat analysis of mRNAs whose levels change more than 16-fold in response to light (Table 1).

Table S14 Summary of read-depth from Illumina RNA-seq.