Supplemental Figures

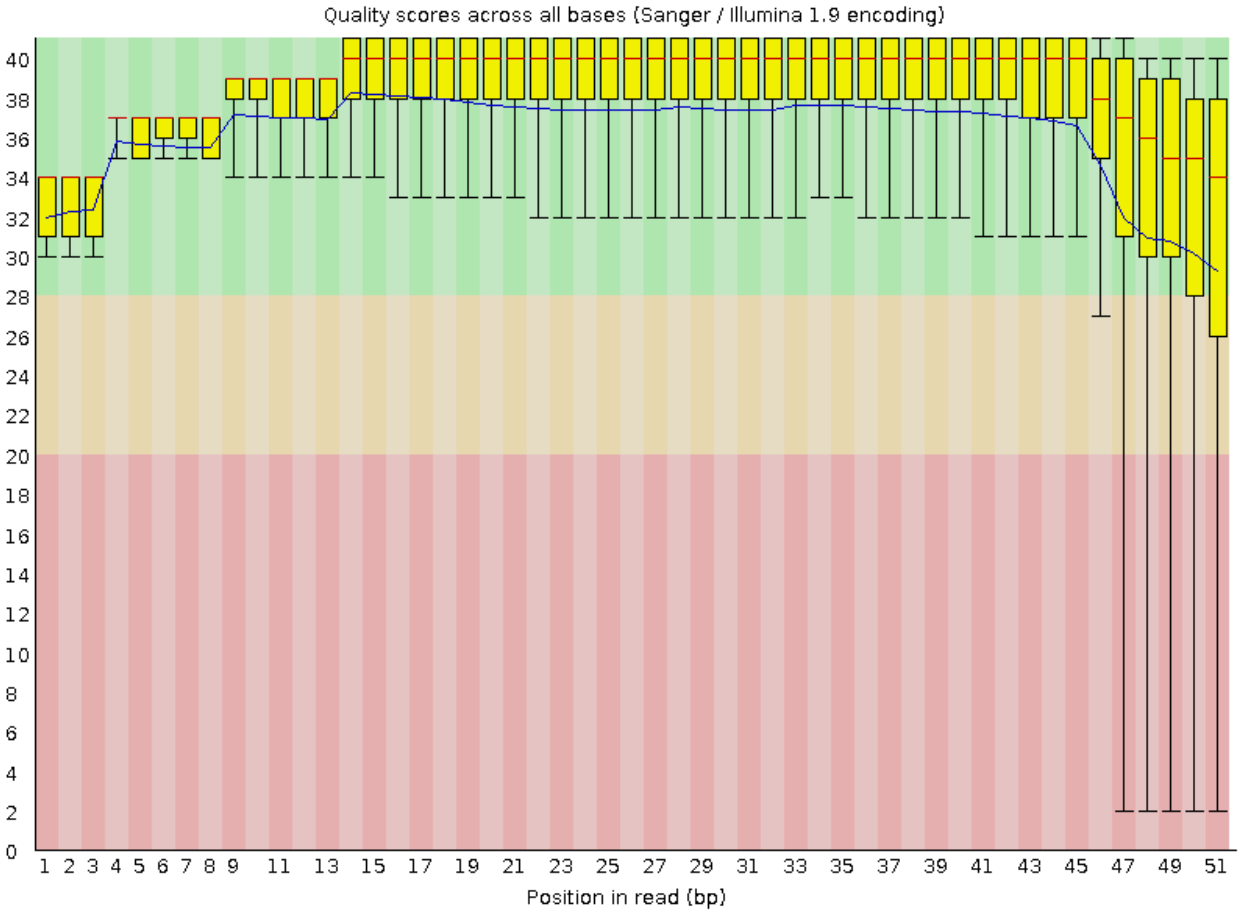

Figure S1. FastQC RNA-Seq Quality Report. Quality control checks on raw sequence data from high throughput sequencing pipelines. The x-axis represents positions of the read in the sequence and the y-axis shows the quality scores for each position.

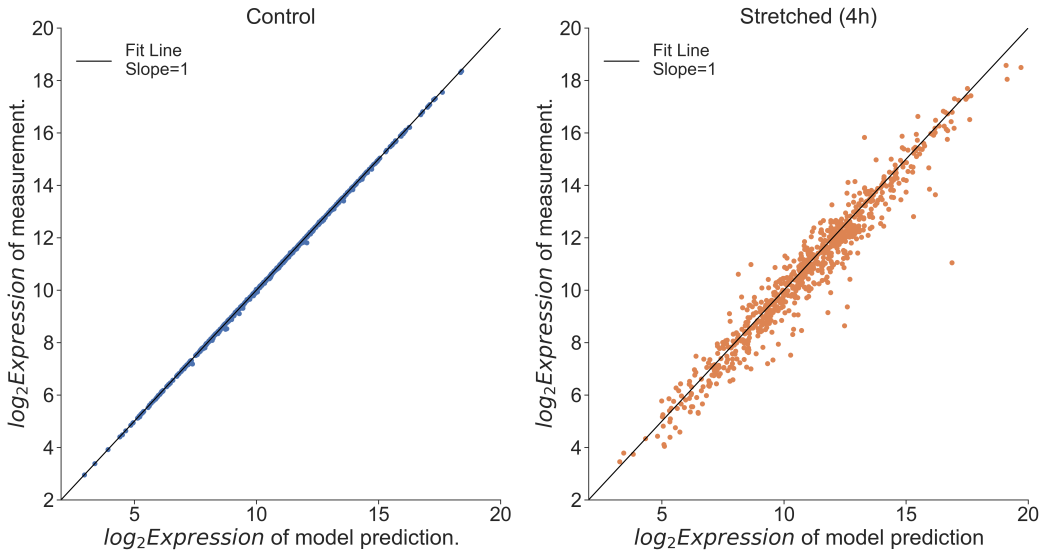

Figure S2. RNA-seq measurements on a $\log_2$(FC) scale regressed against model-predicted mRNA counts.

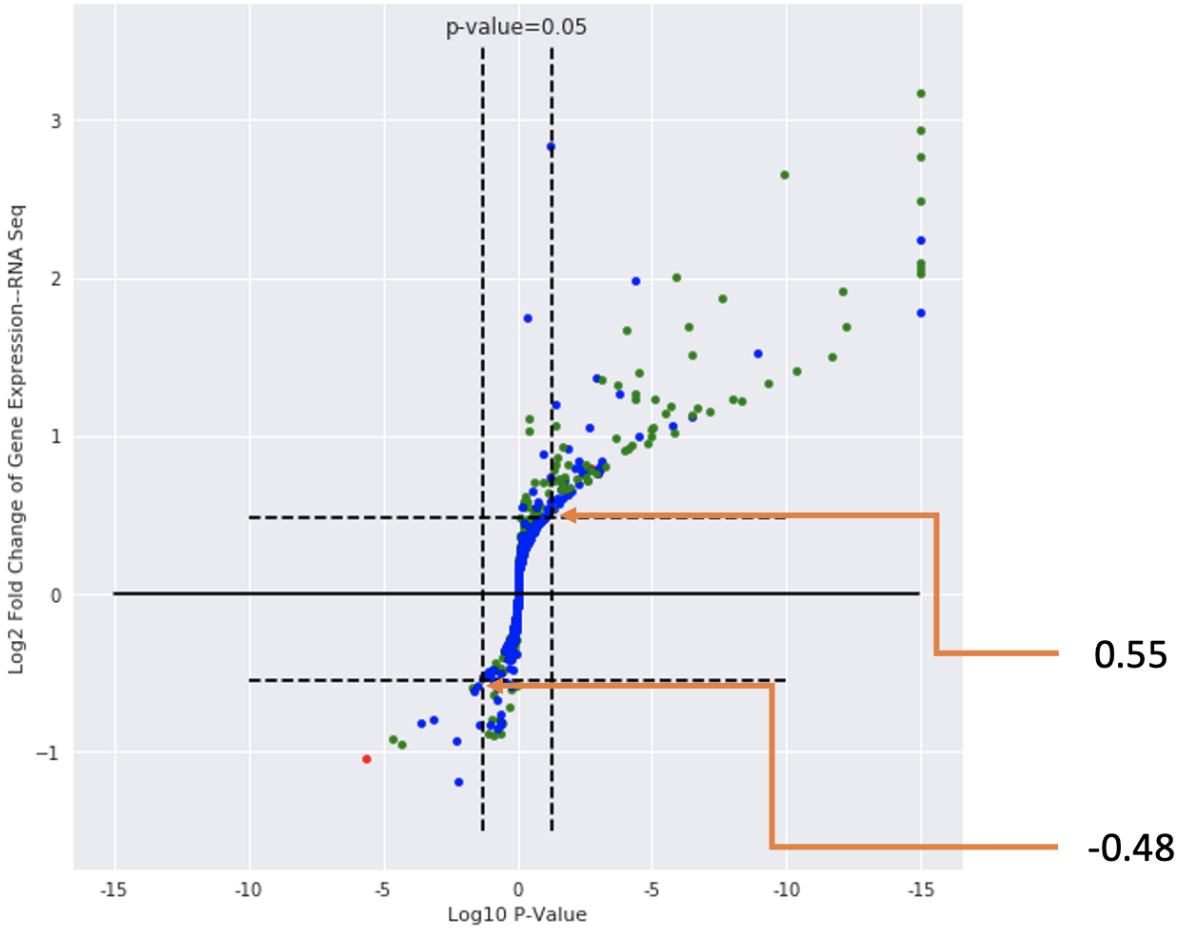

Figure S3. Log_2FC of gene expression *vs.* corrected p-value (FDR) suggesting that a Log_2FC threshold of ± 0.5 is consistent with a statistical threshold of 0.05

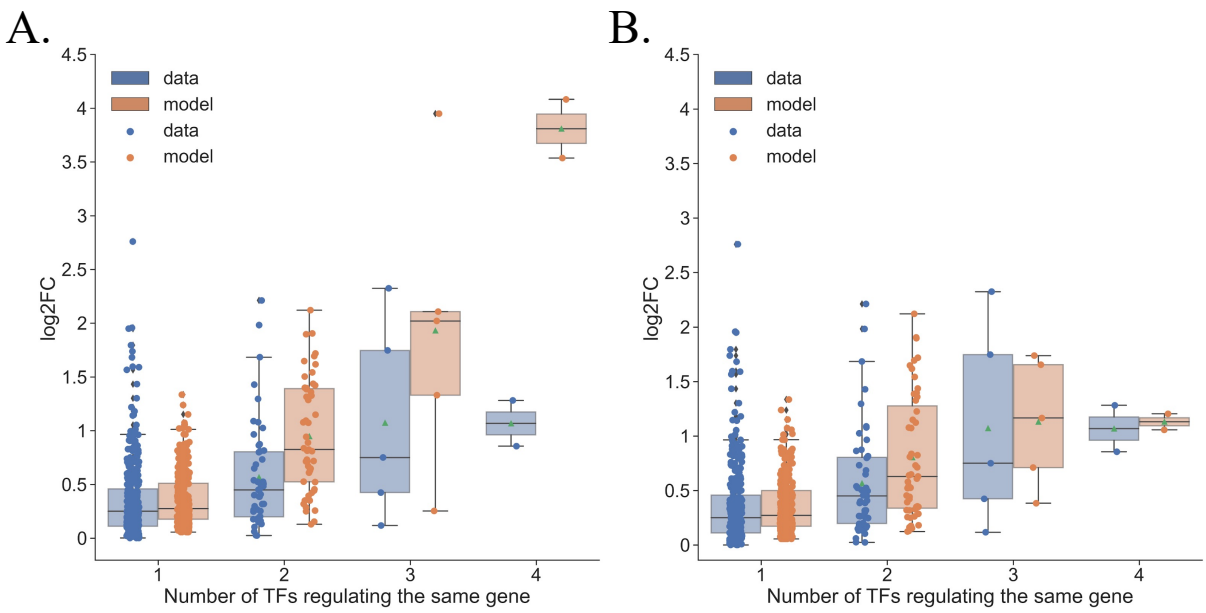

Figure S4. Dependence of Gene Expression on Number of Transcriptional Regulators. Since many genes in the model are regulated by multiple transcription factors and the activation function is mildly cooperative ($n = 1.4$), we compared average predicted and measured expression of genes as a function of the number of transcriptional regulators and found that, as the number of transcription factors regulating a gene increased, the model increasingly over-estimated the transcriptional response compared with the measurements that tended to saturate when there were three or more (Fig. S4A). Decreasing EC_50 network-wide and replacing AND logic with OR logic as the default (when more than one transcription factor regulates the expression of a gene and there no published evidence was found suggesting co-regulation) caused model-predicted expression to saturate for fewer regulators (Fig. S4B). Data in blue and model simulation in orange.

Supplemental Tables

Supplemental Table S1: Primers used for RT-PCR
Supplemental Table S2: Gene regulatory model species and reactions
Supplemental Table S3: Differential expression profiles. RNA-seq measurements of gene expression profiles after processing with bioinformatics packages described in Methods section.