

Supplementary Figures

Impact of HCMV infection on host transcription by RNA Polymerases I, II, and III

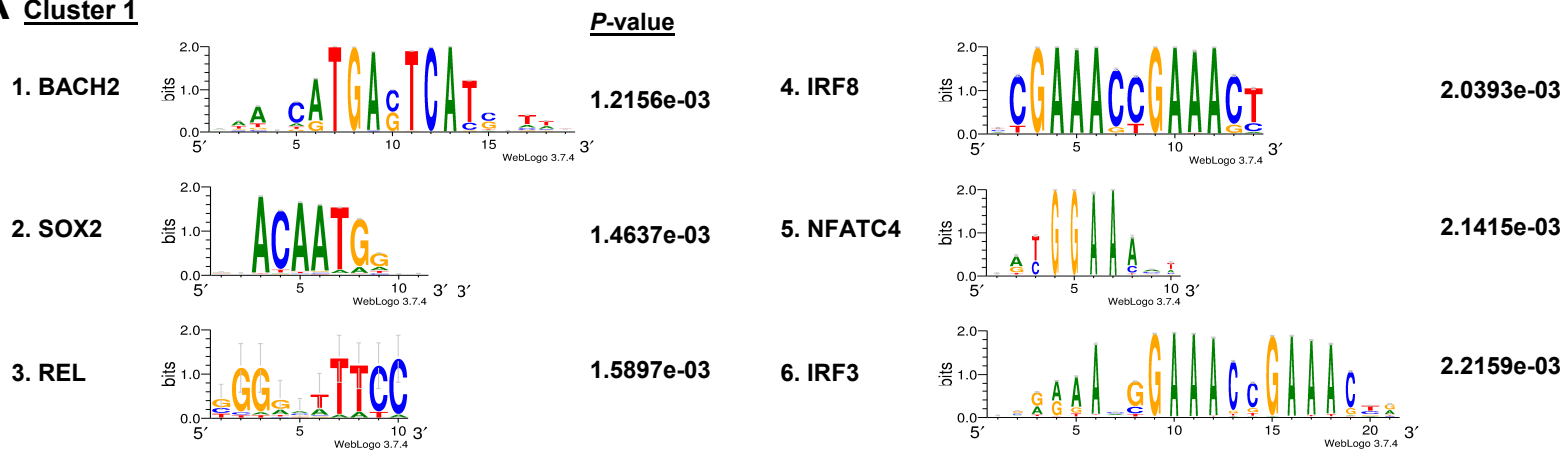
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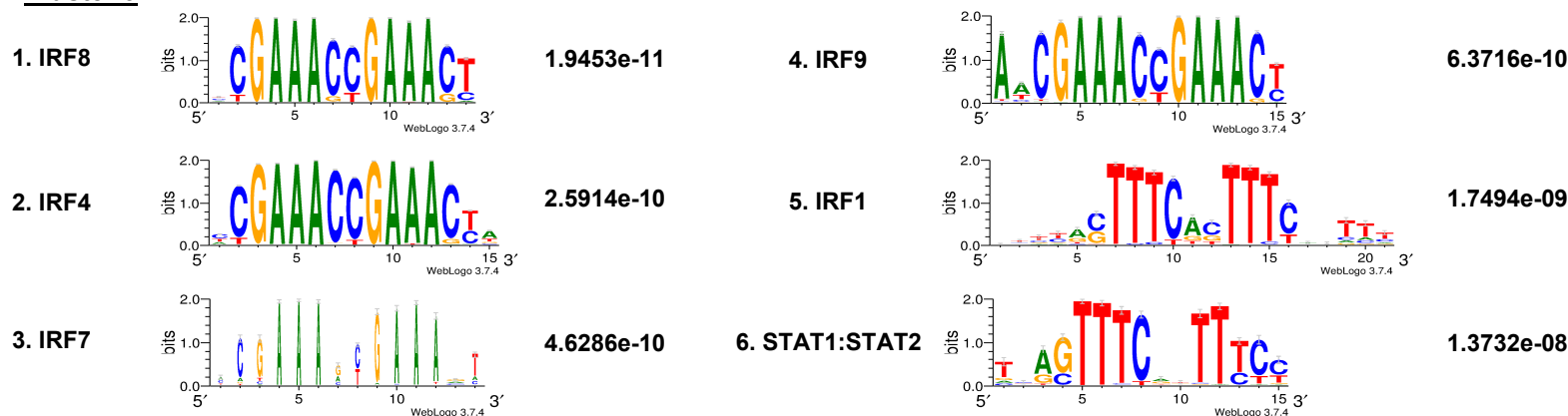
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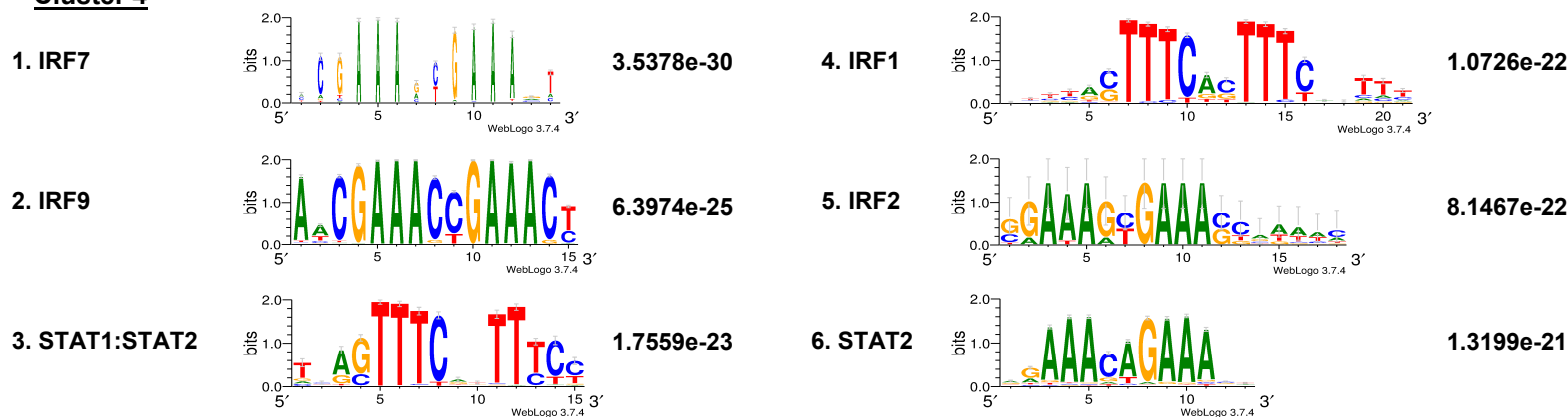
A Cluster 1



B Cluster 3



C Cluster 4



D Cluster 8



Figure S1. Related to Figure 1. (A-D) Top 6 transcription factor motifs identified from motif enrichment analysis performed with promoter regions (150 bp pause region -200 bp and + 50 bp) for genes in clusters 1, 3, 4, and 8, respectively. The JASPAR motif for each transcription factor is shown, and to the right the P-value of enrichment (Fisher's exact test).

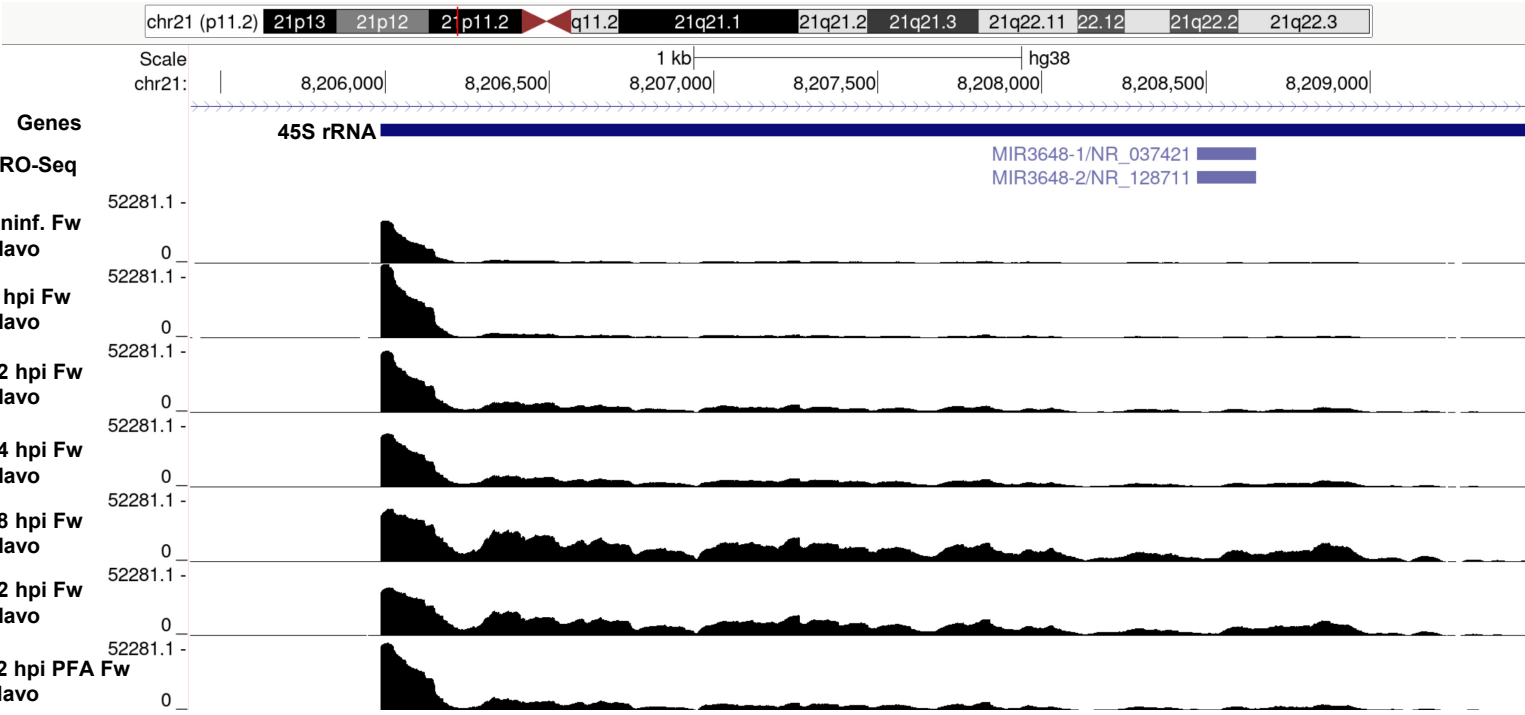


Figure S2. Related to Figure 4. Genome browser snapshot displaying Flavo PRO-Seq data along the infection time course at the 45S promoter region and upstream portion of the 45S rRNA that is not retained as a mature transcript.

Figure S3. Related to Figure 5. (A) UCSC Genome browser snapshot of forward-strand PRO-Seq data at the tRNA-GCC-1-2 gene, which shows an abundance of PRO-Seq 5' ends at the mature tRNA 5' end and associated 3' ends within the tRNA gene body. (B) Plot of length and density of 3' ends associated with either the mature 5' end (blue) or all upstream TSSs (orange). (C) Correlation analysis of read coverage at the 5' upstream position for the uninfected and 48 hpi (DMSO) datasets, the mock infected-datasets +/- Flavo, and time-matched infection points +/- Flavo. The r value represents the Pearson's correlation coefficient. (D) Plots of read coverage at the base downstream 3' position in uninfected HFF and HFF infected for 4, 12, 24, 48, or 72 h, and 72 h + PFA. In each plot, the read coverage for each tRNA in the uninfected HFF is displayed with the data for the infection time point, and the data are sorted by lowest to highest read coverage in the uninfected cells. Data are plotted on a log₁₀ scale.

PIC
Nuc

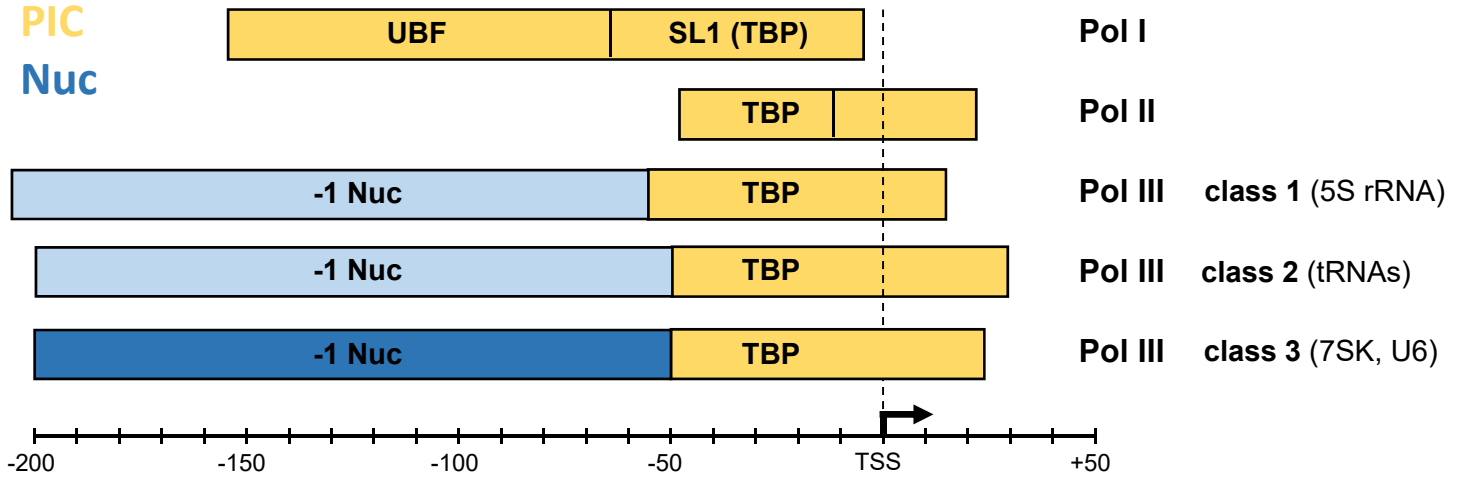


Figure S4. Related to Figure 6. Schematic depicting the regions protected by DFF-ChIP for TBP at Pol I, Pol II, and Pol III promoters (including Class I, II, and III sub-types). At Pol III promoters, the approximate position of the upstream -1 nucleosome associated with the PIC is indicated. The occupancy of the nucleosome relative to the PIC indicated by shading. At Class I and II Pol III promoters, an upstream nucleosome is detected in association with a fraction of Pol III PICs, whereas at Class III promoters, the PIC and upstream nucleosome exhibit approximately 100% co-occupancy.