



Figure S4

Figure S4. Biological processes affected by MG132 treatment

A) cNet-plot showing GO biological processes that were significantly enriched for genes closest to genic and nongenic TSS. The color of gene node represents the most enriched DOCR as per legend, genes in each node are organized based on direction of expression, border color of the dot identifies genes UP (red) or DOWN (blue) ($\log_2FC \leq 1$, $FDR=0.05$) in cells treated for 24H. **B)** Enriched hallmark pathways. Dot plot showing the degree of enrichment for genes closest to DOCRs split by category. Dot size represents the number of genes in each hallmark pathway. **C)** cNet-plot showing hallmark pathways enriched for genes closest to genic and non-genic TSS. Key genes in each pathway are shown. **D)** Transcriptional cofactors predicted to regulate genes closest to genic and nongenic TSS. Dot plot showing the degree of enrichment for genes closest to DOCRs split by category. Dot size represents the number of genes predicted to be regulated by each cofactor as determined from GTRD (gene transcription regulation database). **E)** cNet-plot showing GTRD factors whose targets are enriched for genes closest to genic and non-genic TSS.