Figure S3

Figure S3. Proteasome inhibition drives non-genic transcription that is largely non-coding.
A) Heatmap showing H3K27ac signal at nongenic TSS. H3K27ac signal is sorted descending order based on total start-TSS read signal. N is the number of nongenic TSS within each DOCR. **B)** Scatter plot showing correlation between expression of nongenic TSS (start-seq) and closest gene (RNA-seq) read counts. **C)** Graph showing expression of different classes of noncoding RNAs nearby genic and nongenic TSS. **D)** Browser tracks showing examples of nongenic TSS in the gene body and intergenic GAIN and LOST DOCRs. Tracks show read coverage of chromatin accessibility (ATAC), Differential ATAC (DIFF), H3K27ac, start RNA hits, strand, Ser5P and RNA expression. Chromosome start coordinate for each TSS is shown. Gene names closest to the nongenic TSS in gene body are indicated. Tracks: Control (0), MG24H (24H).