



**Figure S2. Differential chromatin accessibility dictates distinct transcription initiation patterns** **A)** Graph representing RNA expression (RNA-seq) read counts overlapping DOCRs that significantly increase (GAIN) and decrease (LOST) accessibility. Reads from RNA-seq are within the region +/- 250 bp of the DOCR center. N= DOCR regions with detectable RNA, e.g., for GAIN ALL 2129 of 2487 (90%). **B)** Heatmap showing average H3K27ac signal near genic TSS pairs within GAIN and LOST regions. Signal is ranked based on distance between TSS pairs. N is the number of genic TSS within each DOCR **C)** Violin plots comparing the distance between divergent GAIN and LOST TSS pairs. **D)** Violin plots comparing the distance between bidirectional (head-to-head) vs PROMPT TSS pairs. **E)** Browser tracks showing examples of bidirectional (head-head) and PROMPT TSS pairs around GAIN and LOST DOCRs. Tracks show read coverage of chromatin accessibility (ATAC), differential ATAC (DIFF), H3K27ac, start RNA hits, strand, Ser5P RANPII, RNA expression. Chromosome start coordinate for each TSS is shown. Names of TSS gene pairs are indicated. Track Control (0), MG24H (24H). Box highlights DOCR region and TSS hits.