

Figure S5

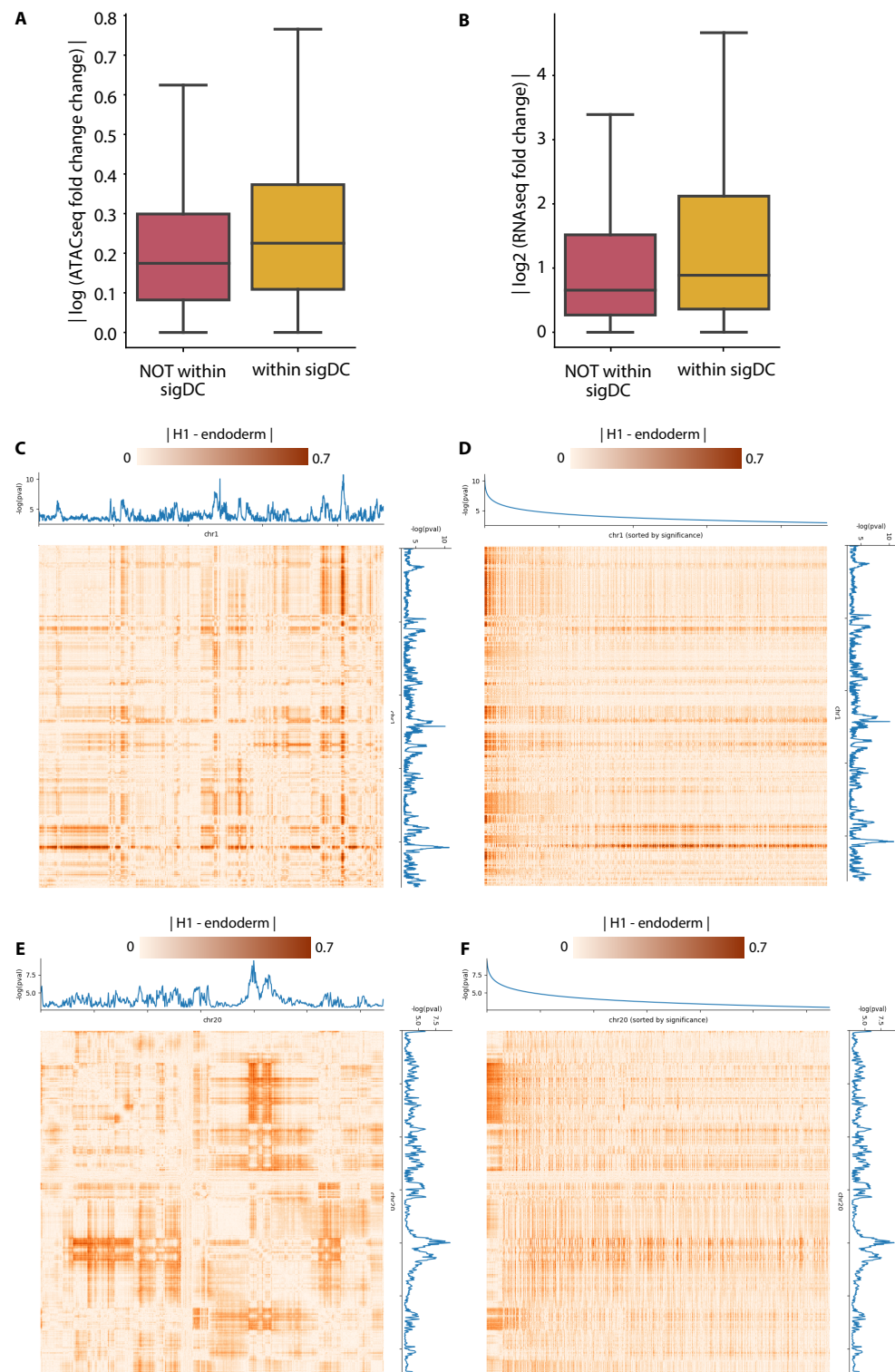


Figure S5. Characterizing sigDC in H1-endoderm differentiation. **(A)** Changes in accessibility within significantly differential compartment regions (sigDC). **(B)** Changes in gene expression level within sigDC. **(C)** Visualization of the difference in the input matrices (heatmap) and the significance of differences estimated with TGIF-DC (lineplot). Each row and column of the heatmap is a 100kb genomic region of chr1 and each entry in the heatmap = $\text{corr}(\text{O/E})_{\text{H1}} - \text{corr}(\text{O/E})_{\text{endoderm}}$. The lineplot shows $-\log(\text{adjusted p-value})$ from TGIF-DC used for detecting significantly differential compartment regions between H1 and endoderm. **(D)** Heatmap shows the same information as in **(C)**, but with columns and rows sorted in decreasing significance, i.e., TGIF-DC's $-\log(\text{adjusted p-value})$. The sorting of regions by p-value highlights greater differences in count for regions with higher negative log p-values (high significance). **(E)** Same visualization as **(C)**, but for chr20. **(F)** Same visualization as **(D)**, but for chr20.