

Figure S7

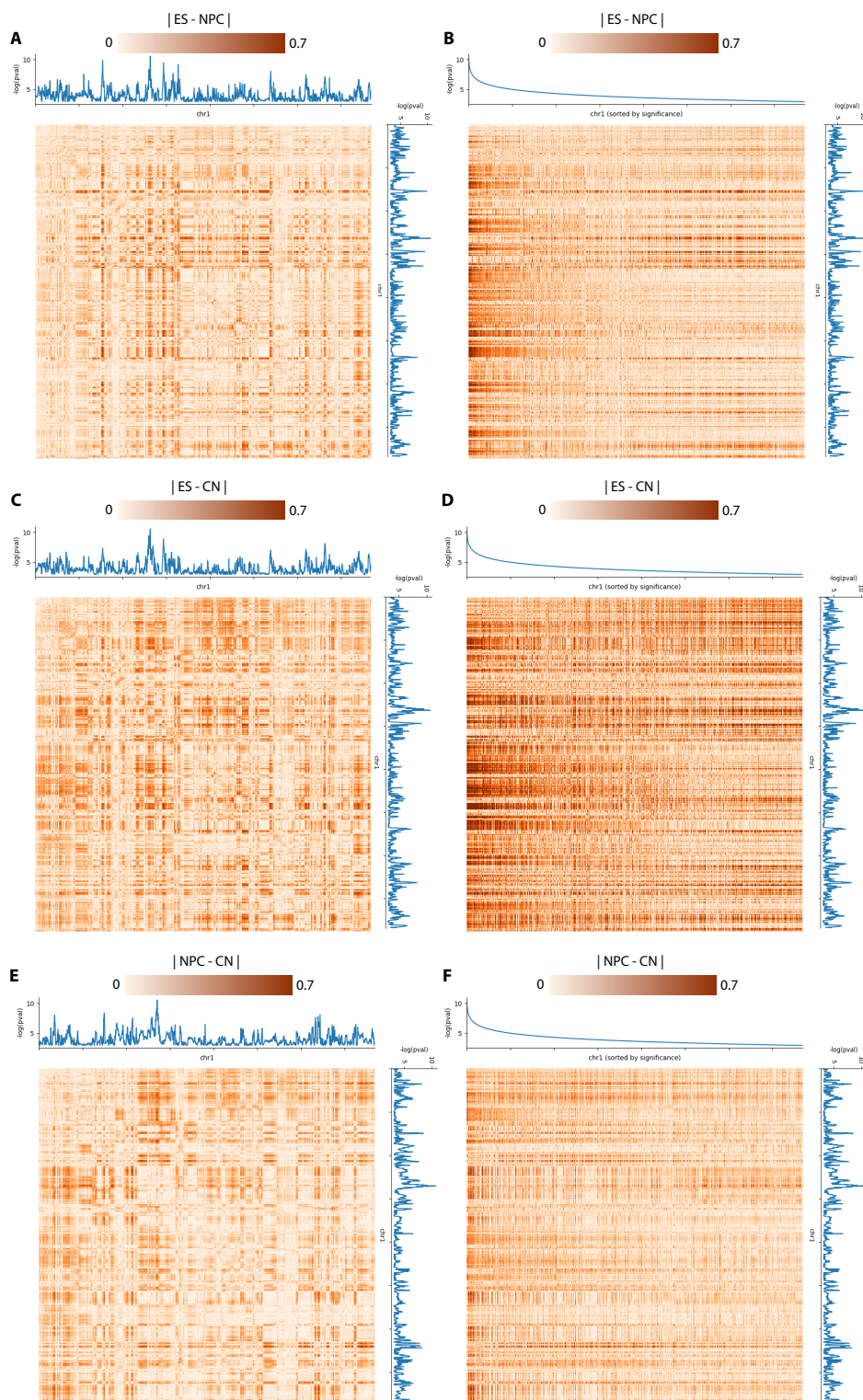


Figure S7. (A) Visualization of the difference in the input matrices (heatmap) and the significance of differences estimated with TGIF-DC (lineplot). Each row and column of the heatmap is a 100kb genomic region of chr1 and each entry in the heatmap = $\text{corr}(\text{O/E})_{\text{ES}} - \text{corr}(\text{O/E})_{\text{NPC}}$. The lineplot shows $-\log(\text{adjusted p-value})$ from TGIF-DC used for detecting significantly differential compartment regions between ES and NPC. (B) Same information as in (A), but only the columns are sorted in descending significance. The sorting of regions by p-value highlights greater differences in count for regions with higher negative log p-values (high significance). (C) Same visualization as (A), but for finding sigDC between ES and CN. (D) Same visualization as (B), but for finding sigDC between ES and CN. (E) Same visualization as (A), but for finding sigDC between NPC and CN. (F) Same visualization as (B), but for finding sigDC between NPC and CN.