

Figure S24

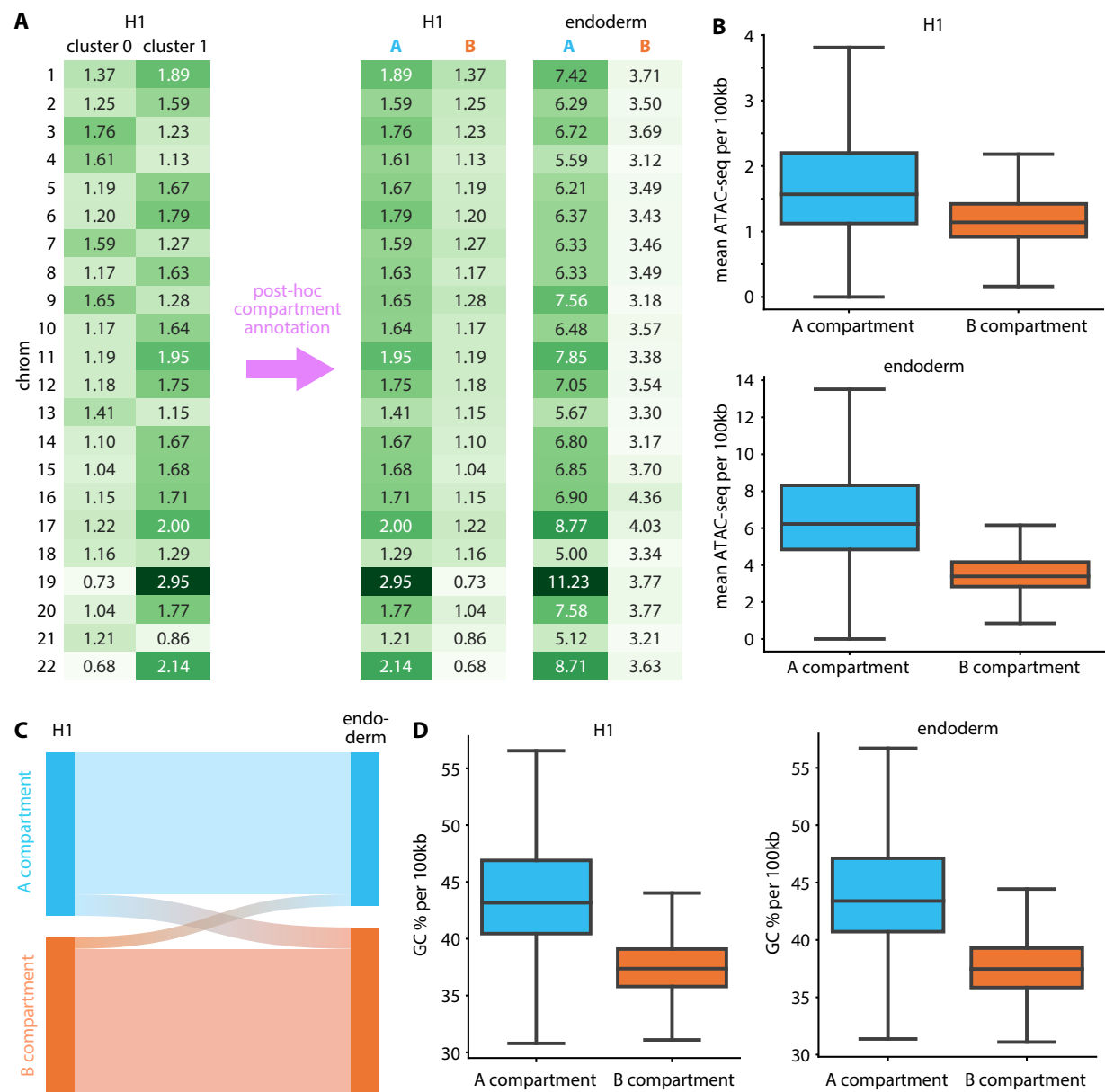


Figure S24. Post-hoc annotation of TGIF-DC clusters into A and B compartments in H1-endoderm dataset using accessibility. **(A)** For each chromosome, mean ATAC-seq signal in each 100kb bin is measured for each TGIF-DC cluster in H1. The cluster with higher mean ATAC-seq signal is annotated as A compartment; the other cluster B compartment. **(B)** Genome-wide mean ATAC-seq signal distribution by compartment in H1 (top) and endoderm (bottom). **(C)** Dynamic compartment assignment pattern from H1 to endoderm. **(D)** Genome-wide mean GC content per 100kb bin by compartment in H1 and endoderm.