

Figure S11

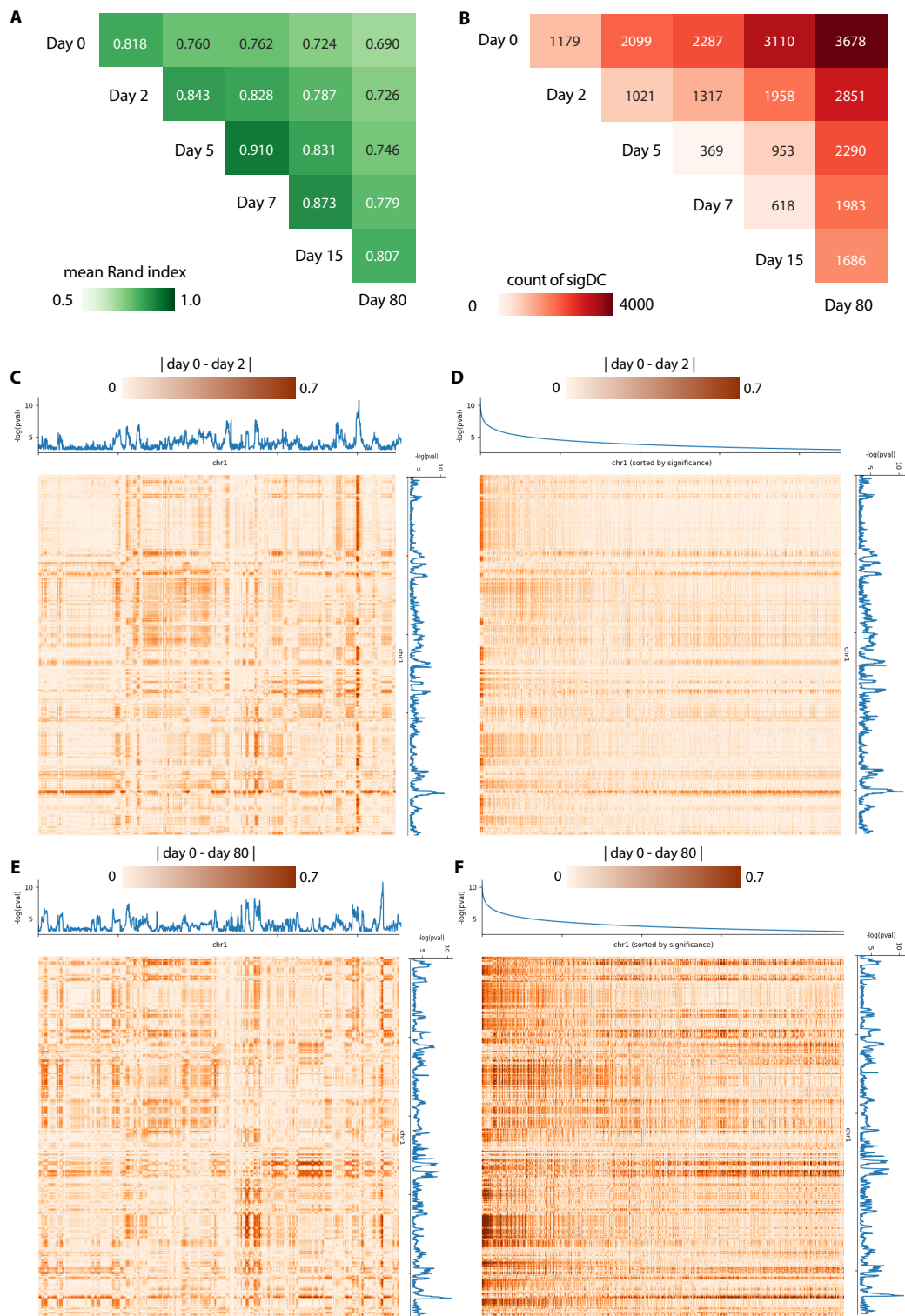


Figure S11. Characterizing TGIF clusters and sigDC from applying TGIF-DC on cardiomyocyte differentiation data. **(A)** Similarity of compartment assignments for every pair of timepoints/states measured by Rand index. **(B)** Count of significantly differential compartmental regions (sigDC) for every pair of timepoints/states. **(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 = $\text{corr}(O/E)_{\text{day } 0} - \text{corr}(O/E)_{\text{day } 2}$. The lineplot shows $-\log(\text{adjusted p-value})$ from TGIF-DC used for detecting significantly differential compartment regions between day 0 and day 2. **(D)** Same information as in **(C)**, 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). **(E)** Same visualization as **(C)**, but for finding sigDC between day 0 and day 80. **(F)** Same visualization as **(D)**, but for finding sigDC between day 0 and day 80.