



Figure S1, Related to Figure 1: α modifies network graph edge weights to create Louvain clusters that increasingly reflect clone barcode assignments.

A. Output edge weight of the ClonoCluster model for graph edge weights between two cells for different proportions of shared nearest neighbors in transcriptome space with fixed $\beta = 0.1$.

B. Network graphs with modified edge weights and cluster assignments at three α values for simulated data.