

Figure S1

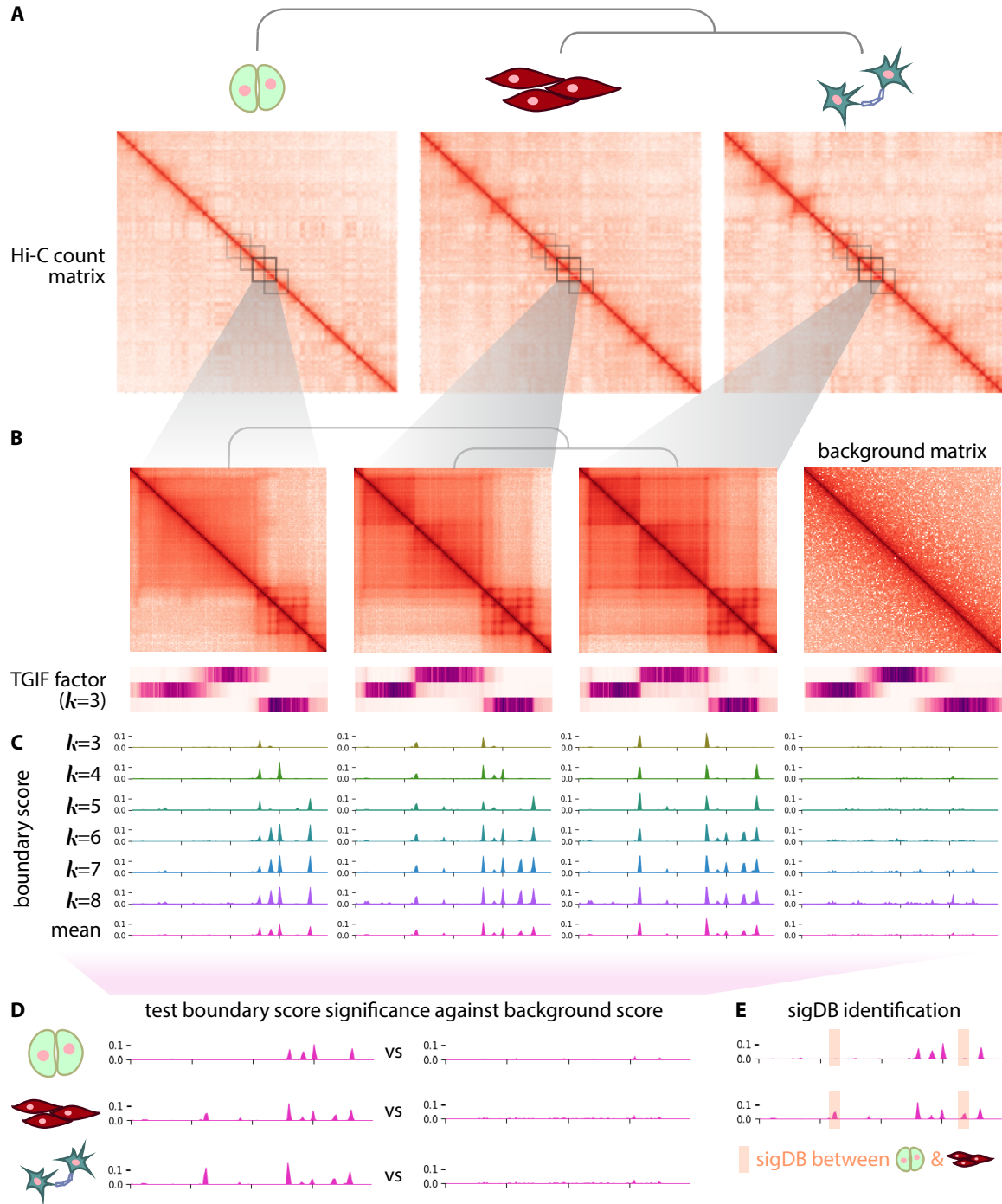


Figure S1. Overview of TGIF-DB. (A) TGIF-DB takes as input a user-specified tree structure that encodes the relationship among the input Hi-C datasets. Shown is an example of a tree encoding a cell lineage across

3 cell types. **(B)** Multitask matrix factorization is performed for submatrices along the diagonal of the input intra-chromosomal Hi-C matrices. **(C)** Within each submatrix, a range of hyper-parameter k values is used to generate boundary scores for TADs at different scales. For each genomic region, the mean boundary score is taken across the range of k s. **(D)** The mean boundary scores are compared to a “null-distribution” boundary scores generated from a randomly shuffled matrix in order to calculate an empirical p-value for each genomic region and to identify significant boundaries. **(E)** Significantly differential boundaries (sigDB) are identified for every pair of input matrices (only 1 pair shown here as example).