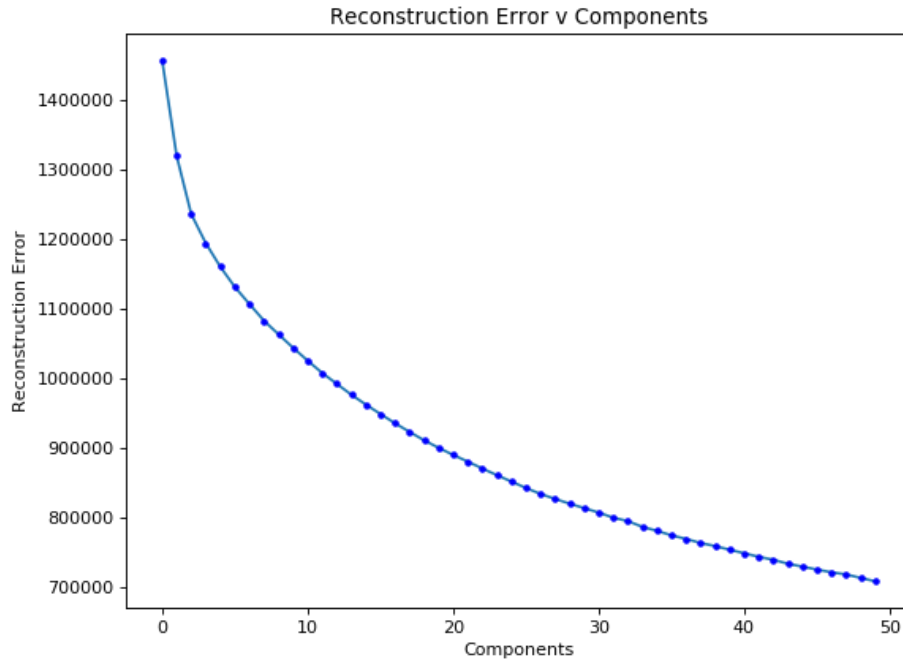
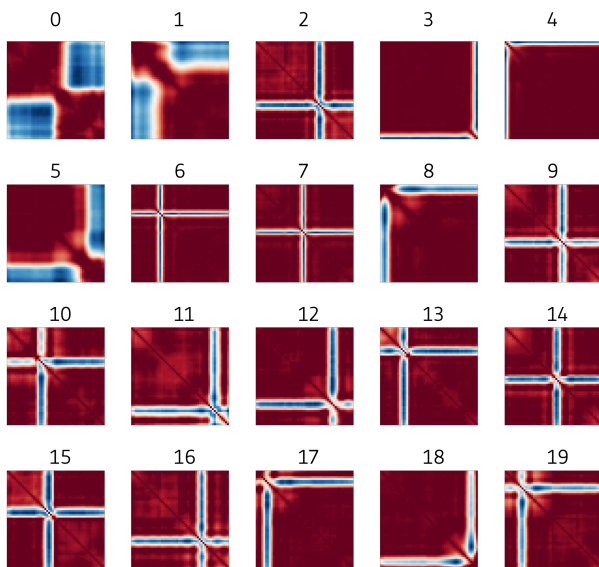


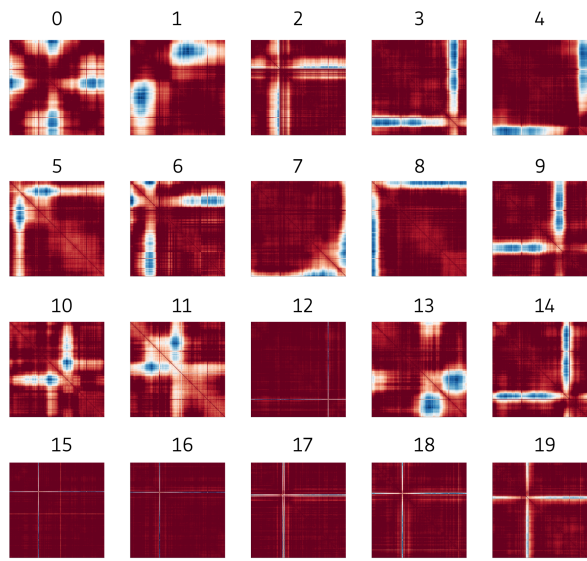
ChromaFactor Supplementary Information



Supplementary Figure 1: Reconstruction error across number of components, k . Reconstruction error, measured by the difference between the original single-cell chromatin folding dataset and the NMF reconstructed approximation, across different values of k components. Adding more components reduces the reconstruction error as NMF can better capture patterns in the data at the expense of interpretability. An elbow is visible around $k=15-20$ where adding additional components leads to diminishing returns in error reduction. We selected $k=20$ components for our analysis to balance reconstruction accuracy and interpretability.



Supplementary Figure 2: Components at BX-C locus. All 20 components generated by applying NMF across the cells at this locus from the Mateo et al. dataset.



Supplementary Figure 3: Components at HLCS locus. All 20 components generated by applying NMF across the cells at this locus from the Su et al. dataset.