

Figure S1. Gene ontology analysis of differentially expressed genes in each cell type.

FB: fibroblast; EC: endothelial cell; TC: T cell; BC: B cell; CM: cardiomyocyte.

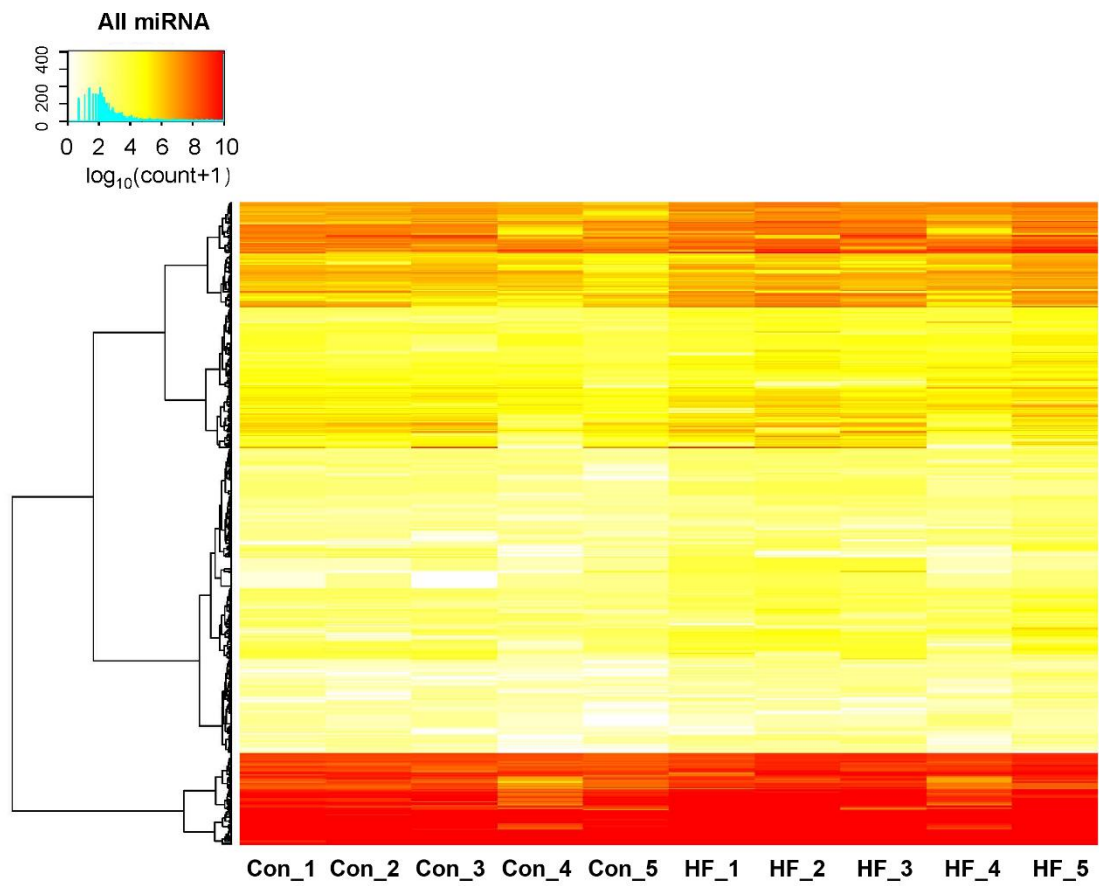


Figure S2. Heatmap of miRNA-seq analysis in control and heart failure (HF) mice.

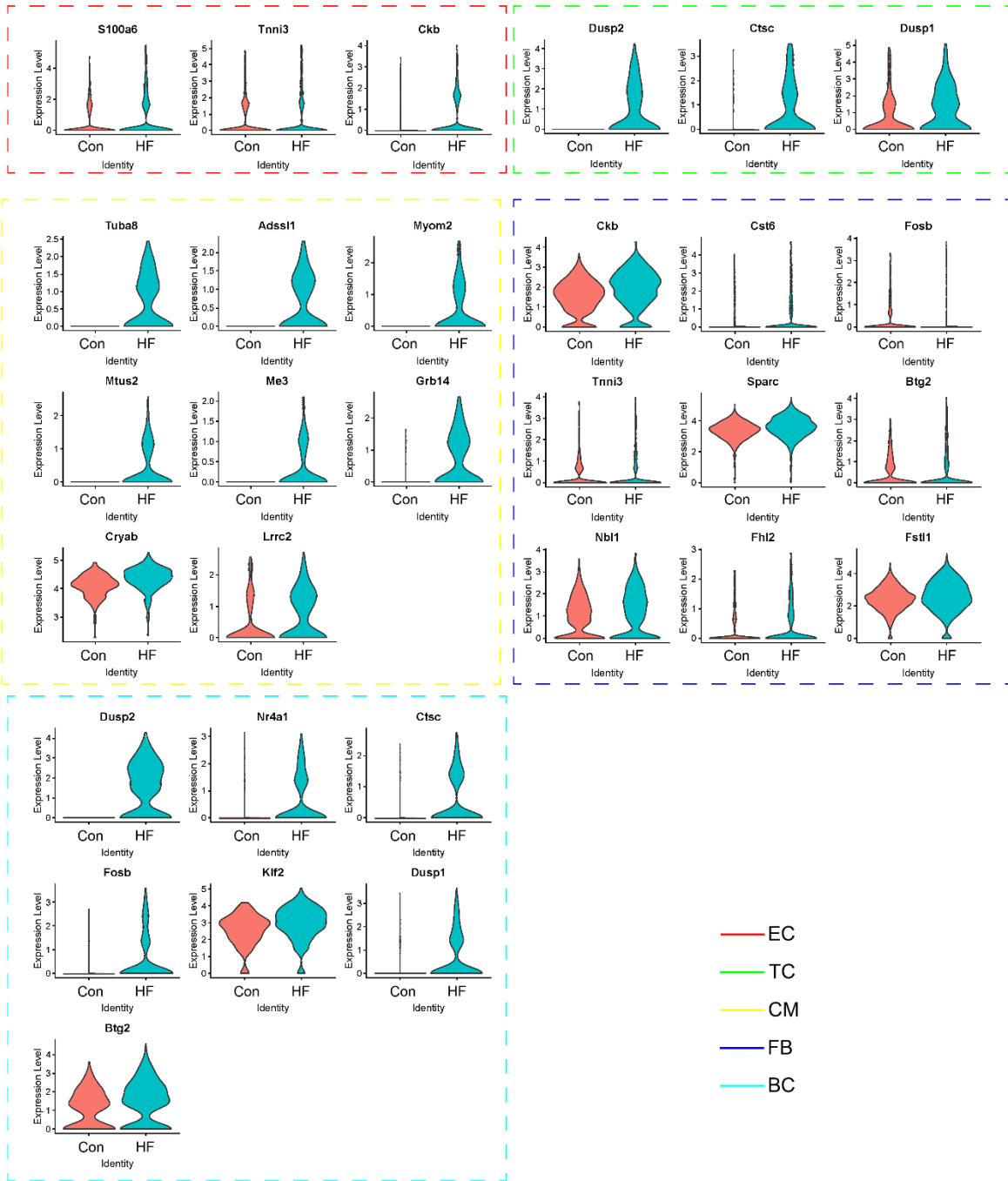


Figure S3. Upregulated genes in individual cell types of failing hearts with increased promoter accessibility. EC: endothelial cell; TC: T cell; CM: cardiomyocyte; FB: fibroblast; BC: B cell.

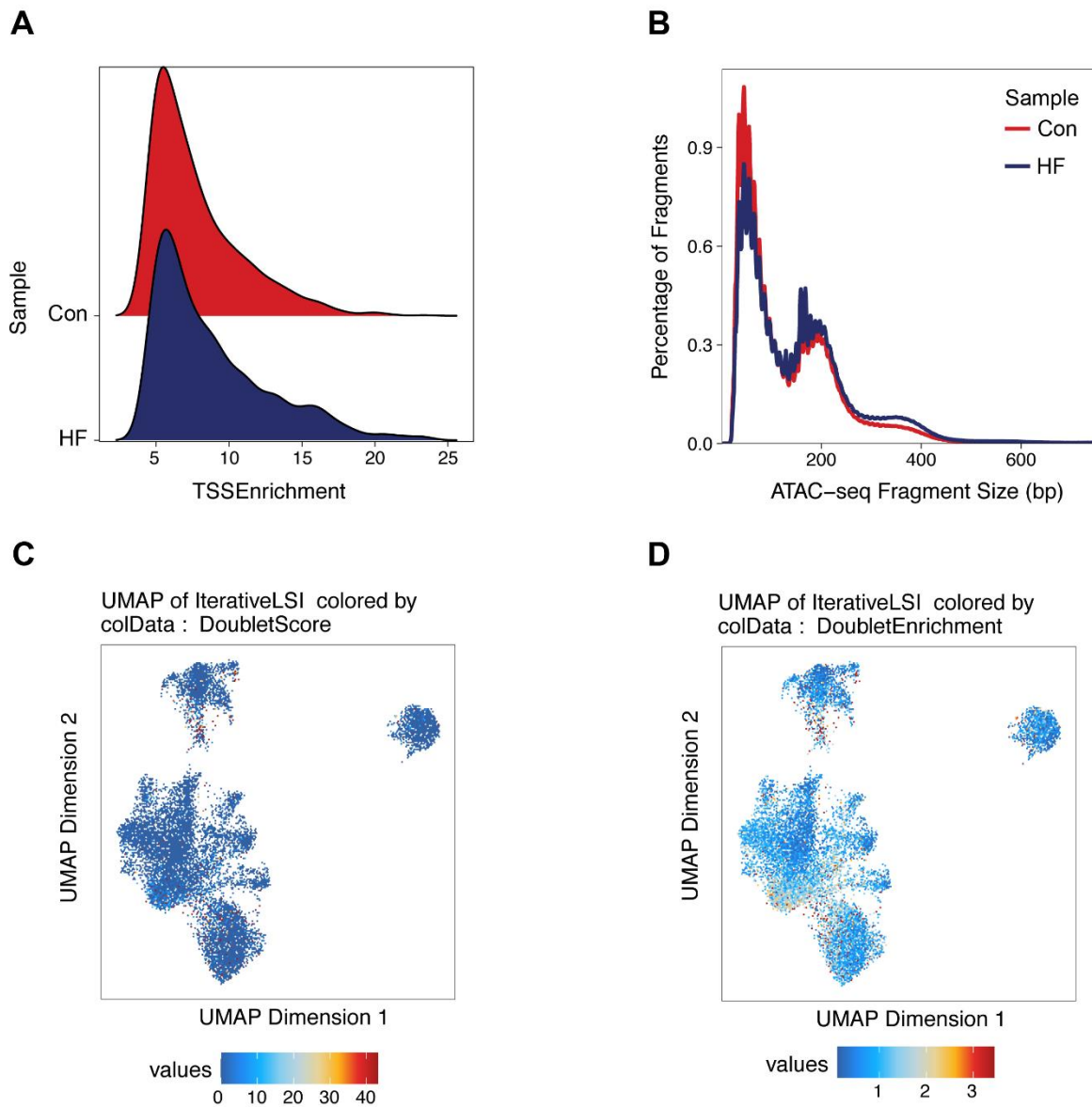


Figure S4. Quality control of scATAC-seq data. (A, B) The distribution of TSS enrichment and fragment size in control and heart failure (HF) mice. (C, D) The doublet score and doublet enrichment of cells passing filters.

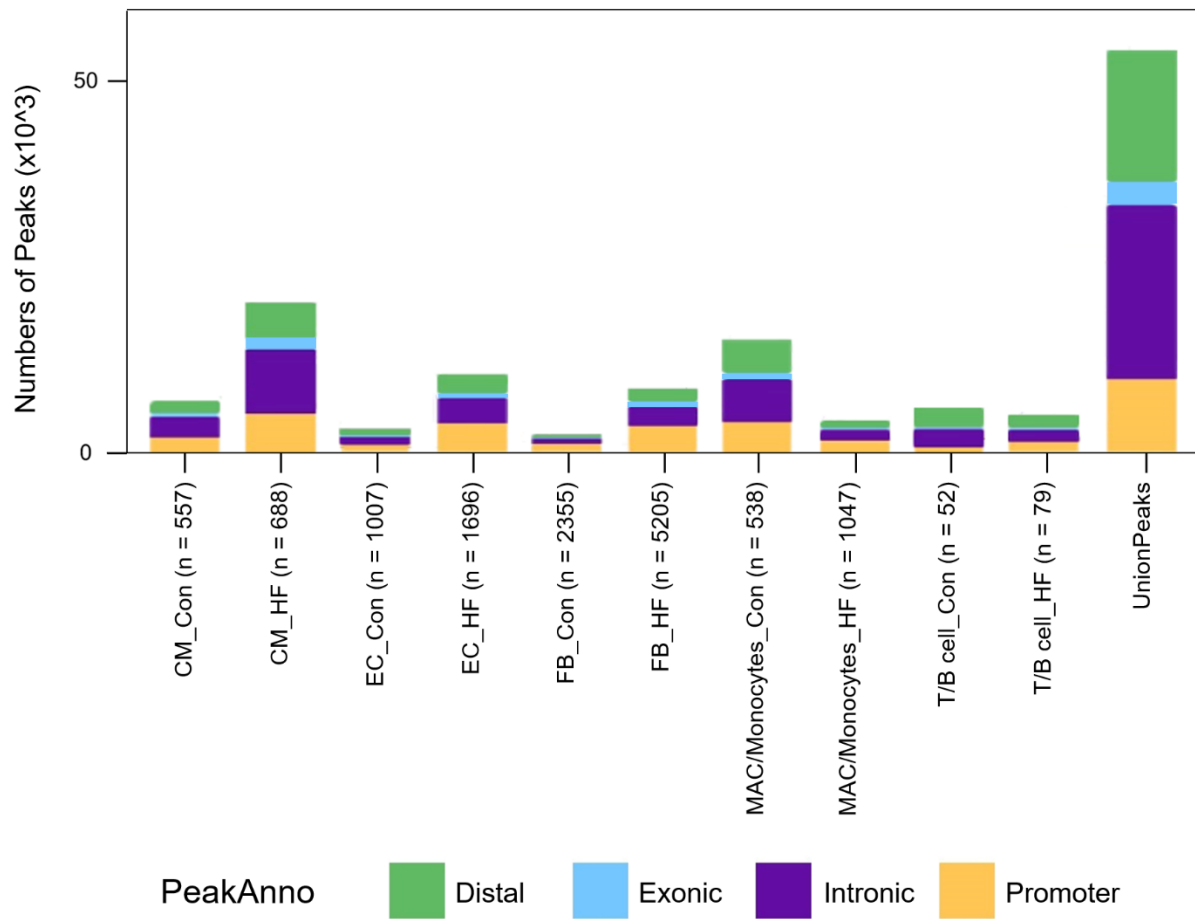


Figure S5. Peak calling of scATAC-seq data in control and heart failure (HF) samples.