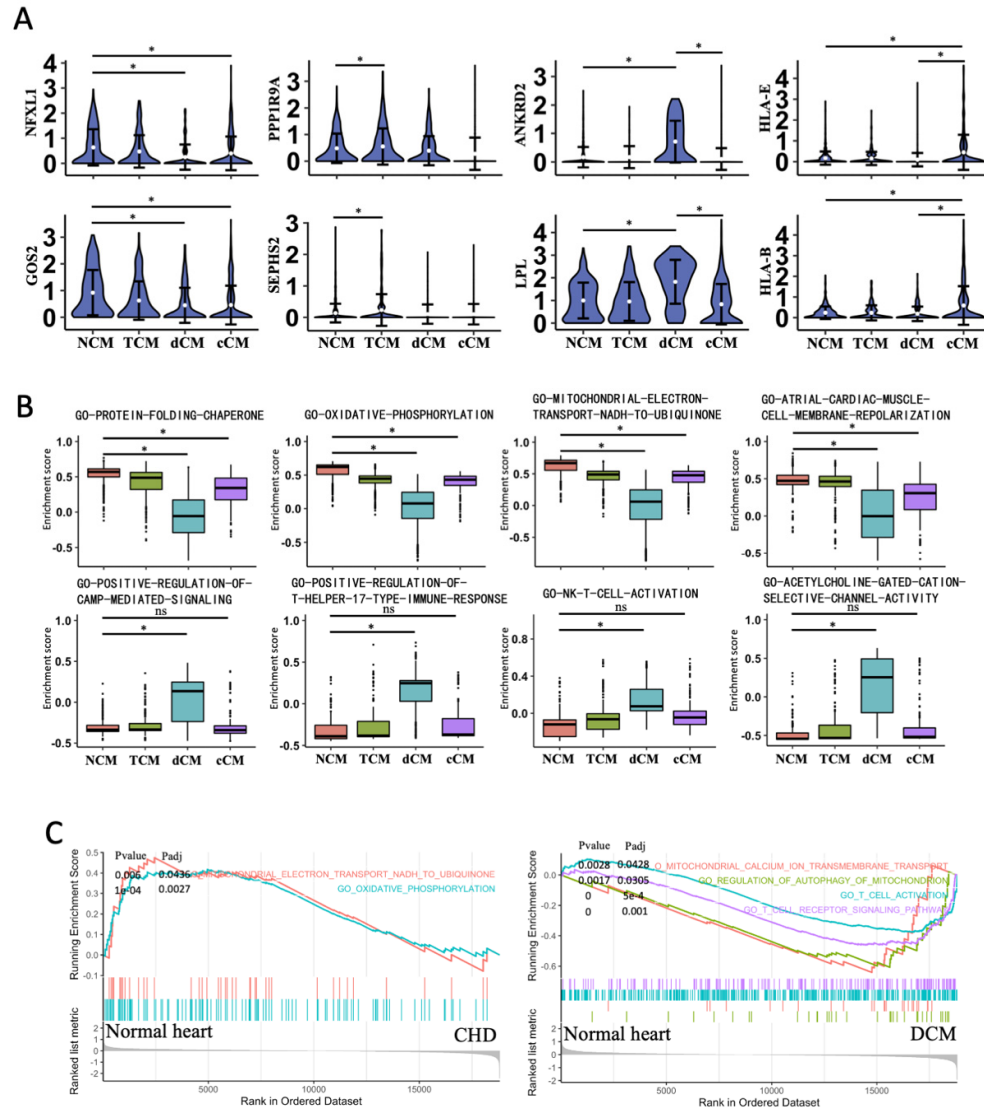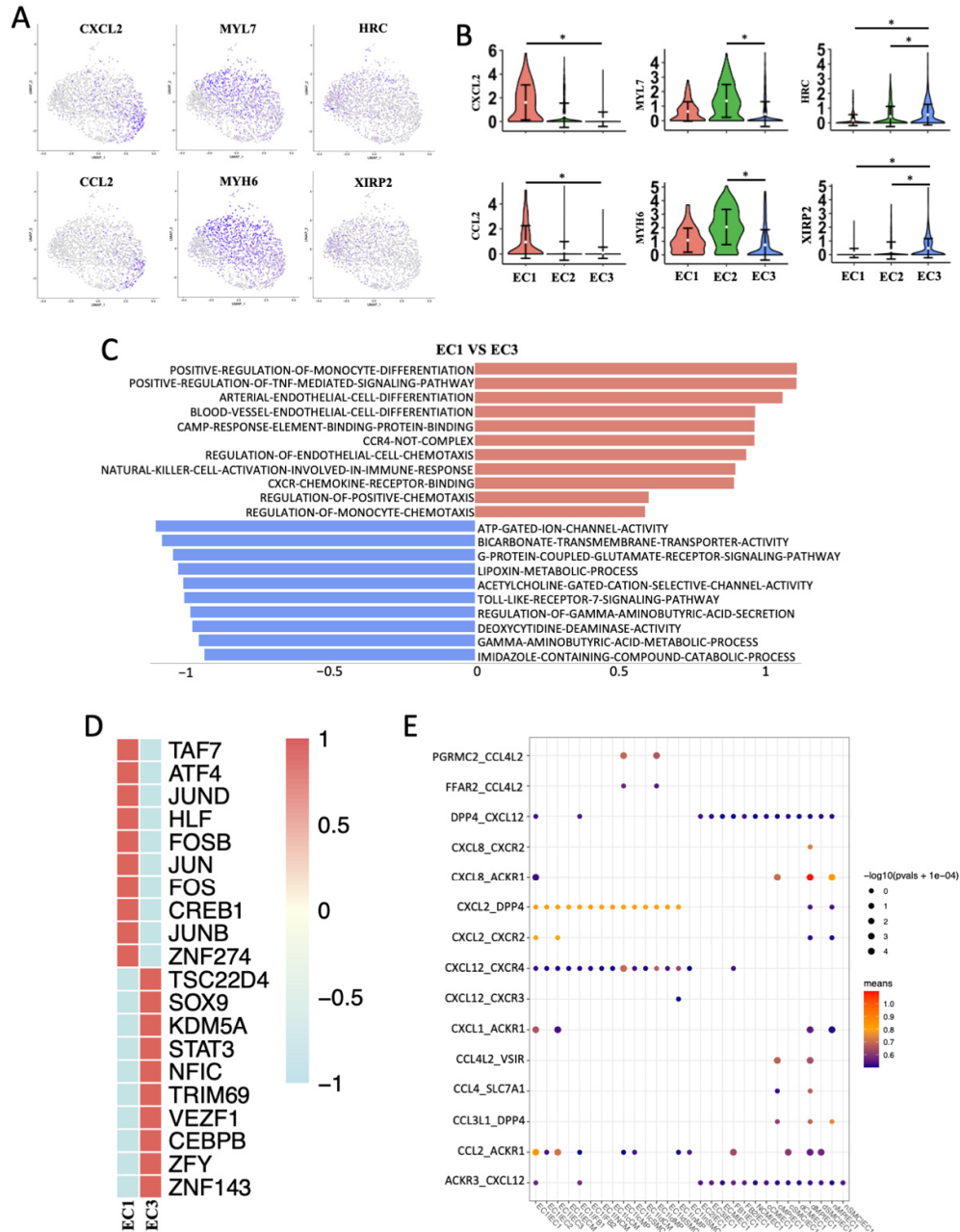**Supplementary Figure S1. Five cell types were identified from Single-cell transcriptome of heart disease. (A)** UMAP plots of five cell types, clusters are color-coded by cell sample. **(B)** proportion of five cell types in each sample. **(C)** UMAP plot of each sample (cHF, dHF and nHF), colored by cell types.
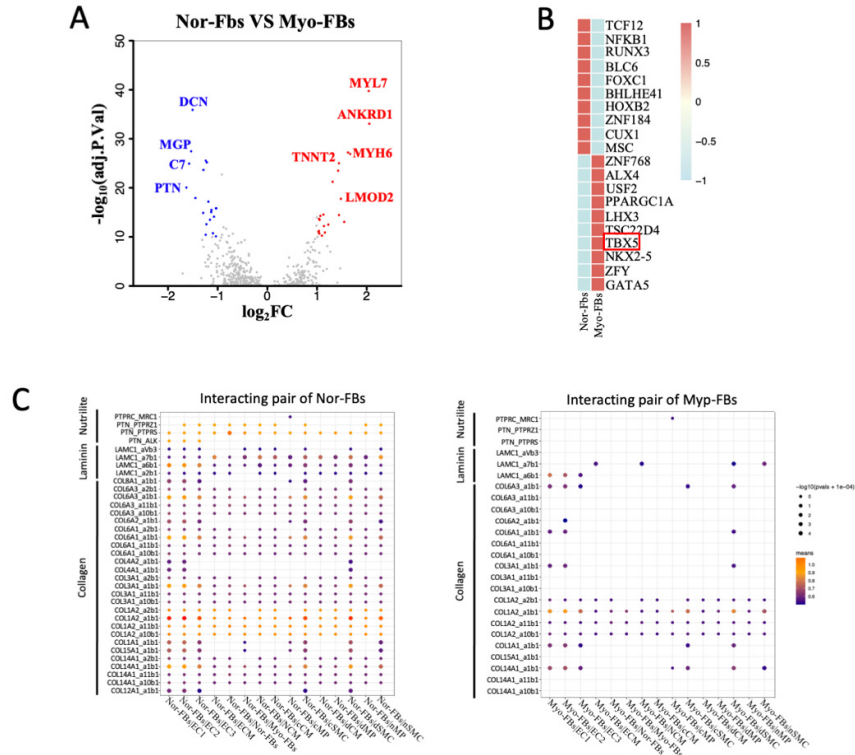
Supplementary Figure S2. Cardiomyocytes (CMs) cluster into 4 distinct phenotypes. (A) violin plots indicate differentially expressed gene in phenotypes of CMs. *Padj < 0.05 Wilcox test. **(B)** Multiple pathway enrichments show the characteristics of the cCM and dCM, as well as the difference between cCM and dCM. Boxplot y axis demonstrates enrichment score of pathways. *padj < 0.05 Wilcox test. **(C)** GSEA results showed the pathway difference between normal heart and ischemic or diluted cardiomyopathy.

Supplementary Figure S3. Endothelial cells in HF have two special disease-related

phenotypes. (A) Expression of marker genes for the phenotypes of ECs defined above

each panel. **(B)** The expression of known cell type discriminating genes in EC1, EC2

and EC3 from 3 samples. *Padj < 0.05 Wilcox test. **(C)** Differences in pathway

enrichment scored by GSVA between EC1 and EC3. **(D)** Differences in TFs active

scored by SCENIC between EC1 and EC3. **(E)** Immunity-related interacting pair

between EC1 and other cell clusters.

Supplementary Figure S4. Fibroblasts transformed into Myofibroblasts. (A)

Volcano show the DEGs (log2FC>1) between Nor-FBs and Myo-FBs. **(B)** Differences

in TFs active scored by SCENIC between Nor-FBs and Myo-FBs. **(C)** Crosstalk of

Nor-FBs or Myo-FBs showed the functional change during the phenotypic

transformation.