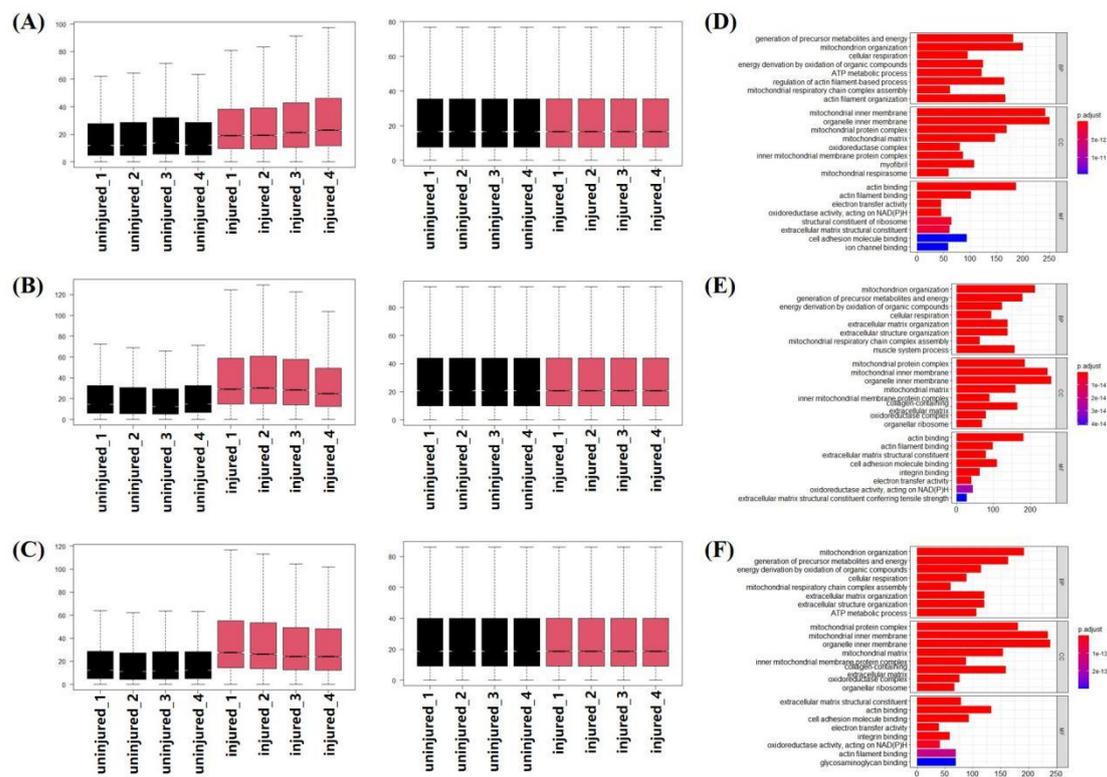


**Figure S1: Gene ontology analysis of DEGs at each time point in scRNA-seq data.**

(A), (B), (C) are bar graphs of GO analysis of significant DEGs on days 1, 3, and 7 post MI, respectively. BP: Biological Process, CC: Cellular Components, MF: Molecular Function, only the first 8 items are displayed in each column.



**Figure S2: mRNA-seq data processing results.** (A) is the comparison before and after normalization of mRNA-seq data on day 3 post MI, (B) represents day 7 post MI, (C) represents day 14 after MI. Black is the control group, red is the MI group, n=4. (D), (E), (F) are bar graphs of GO analysis of significant DEGs on days 3, 7, and 14 post MI, respectively. only the first 8 items are displayed in each column.