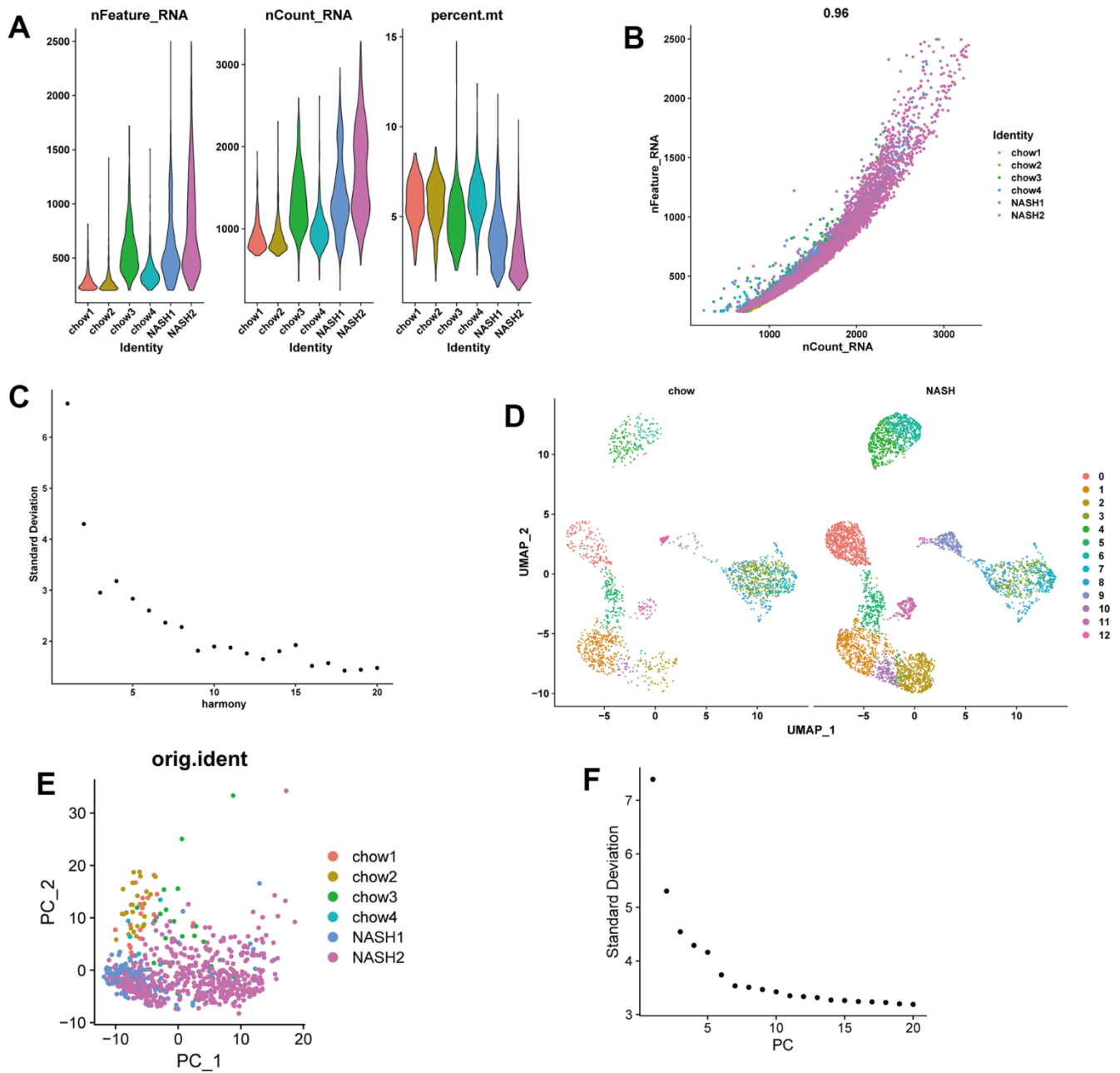
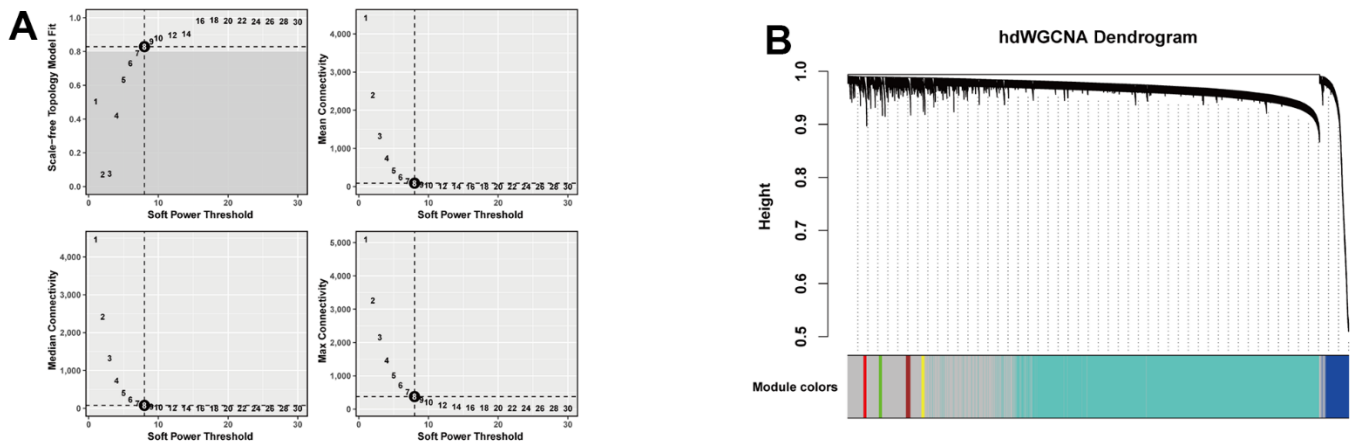


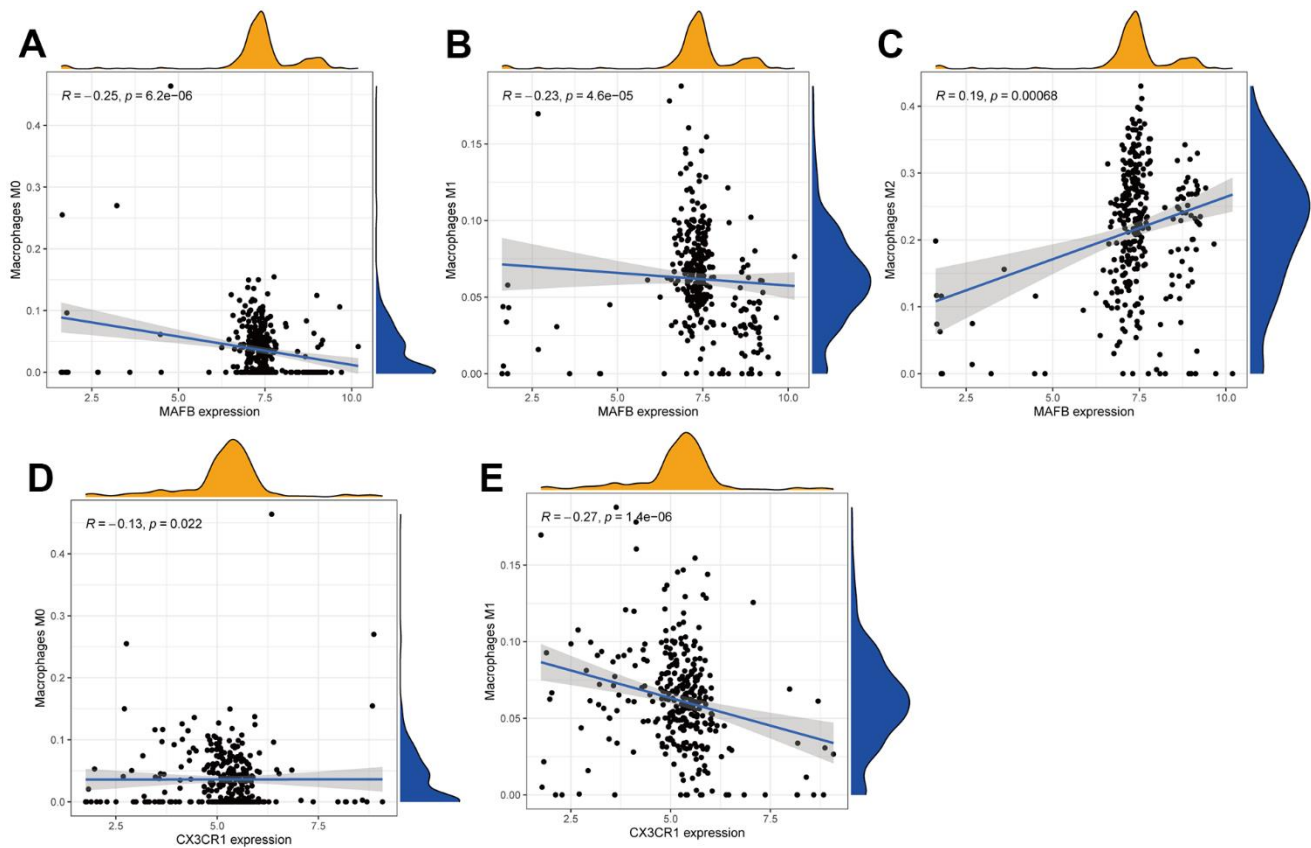
SUPPLEMENTARY FIGURES



Supplementary Figure 1. Preprocessing of scRNA-seq data. (A) The features, counts, and percentages of mitochondrial genes in each of the analyzed samples. (B) The Scatter Plot demonstrates the correlation between cell counts and intracellular gene counts following standardization. (C) Selecting the principal components (PCs) for further analysis. (D) UMAP plot visualizes the clusters in control and NASH mouse livers. (E) PCA dimension reduction of macrophages. (F) Selecting the principal components (PCs) for further analysis.



Supplementary Figure 2. The process of hdWGCNA. (A) Scale-free fit index and mean connectivity plot for various soft threshold powers. (B) The hdWGCNA dendrogram of macrophages.



Supplementary Figure 3. Immune cell infiltration analysis. Correlation between MAFB and M0 macrophages (A), M1 macrophages (B), and M2 macrophages (C); Correlation between CX3CR1 and M0 macrophages (D) and M1 macrophages (E).