

Supplementary Figures

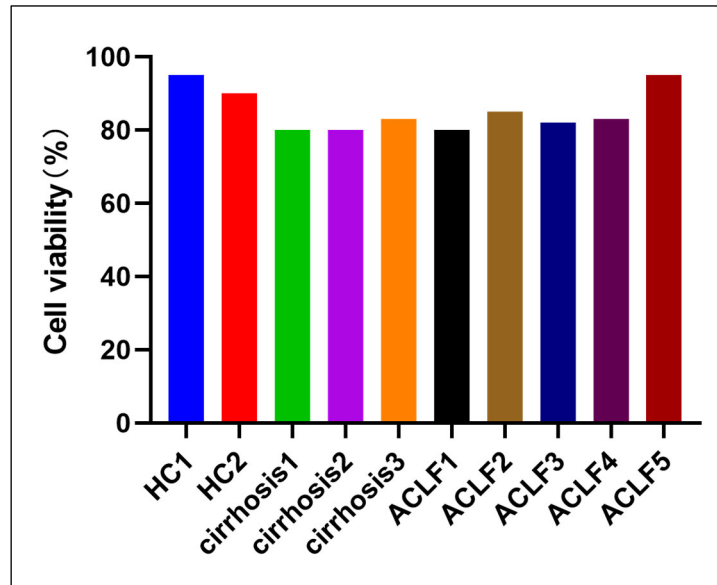


Figure S1 The cell viability for each liver

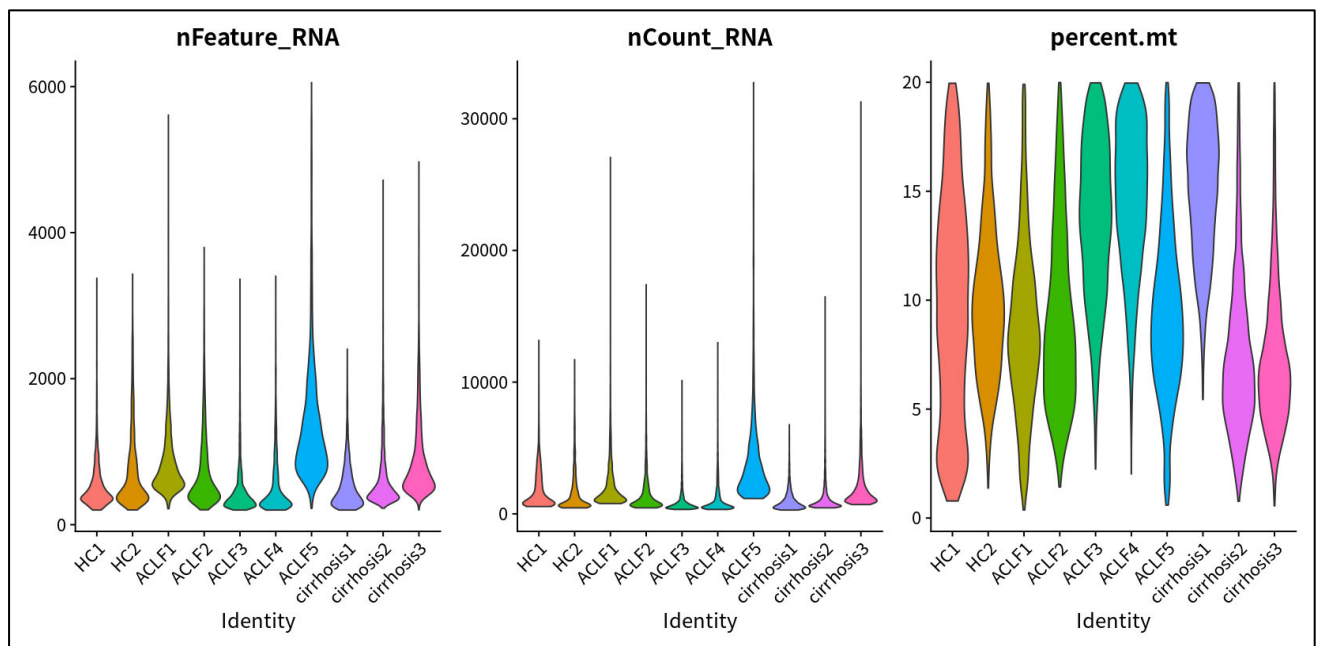


Figure S2 The quality control for scRNA-seq

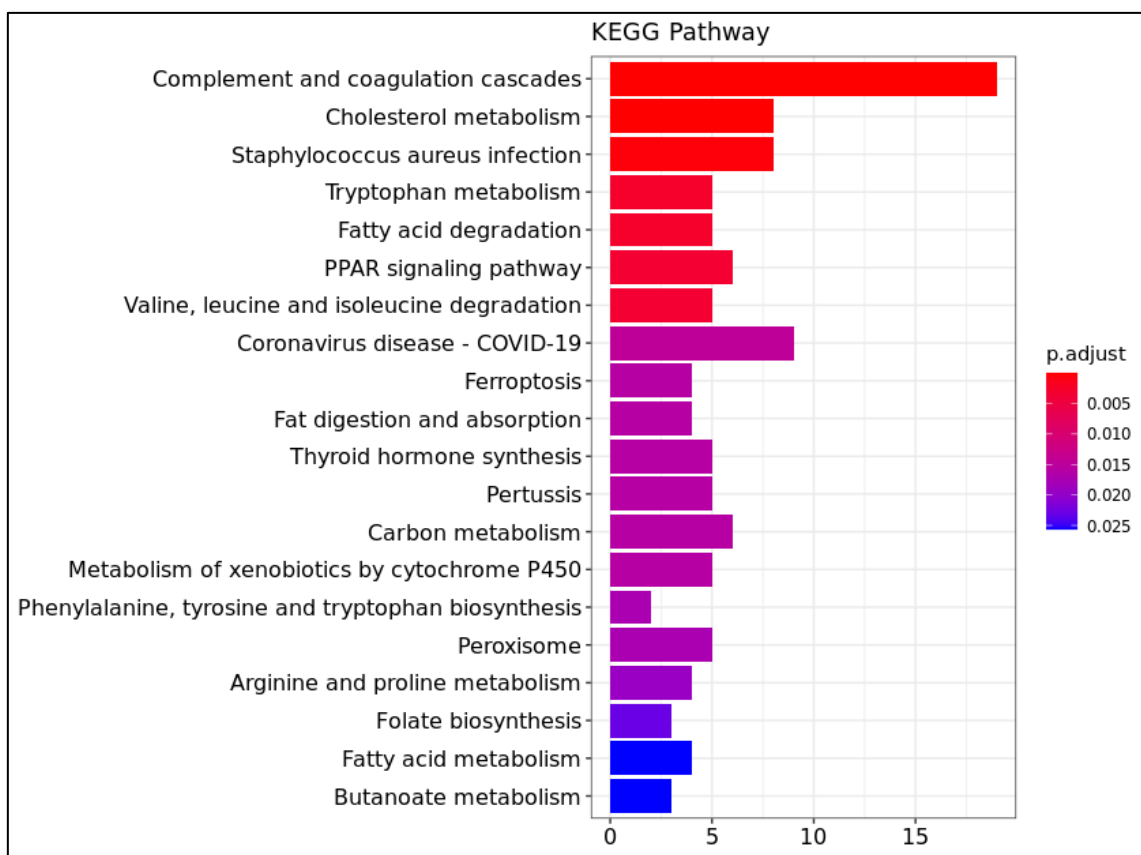


Figure S3 KEGG analyses for high expression genes ($p < 10^{-50}$) of E7 clusters showed a series of metabolic related pathways

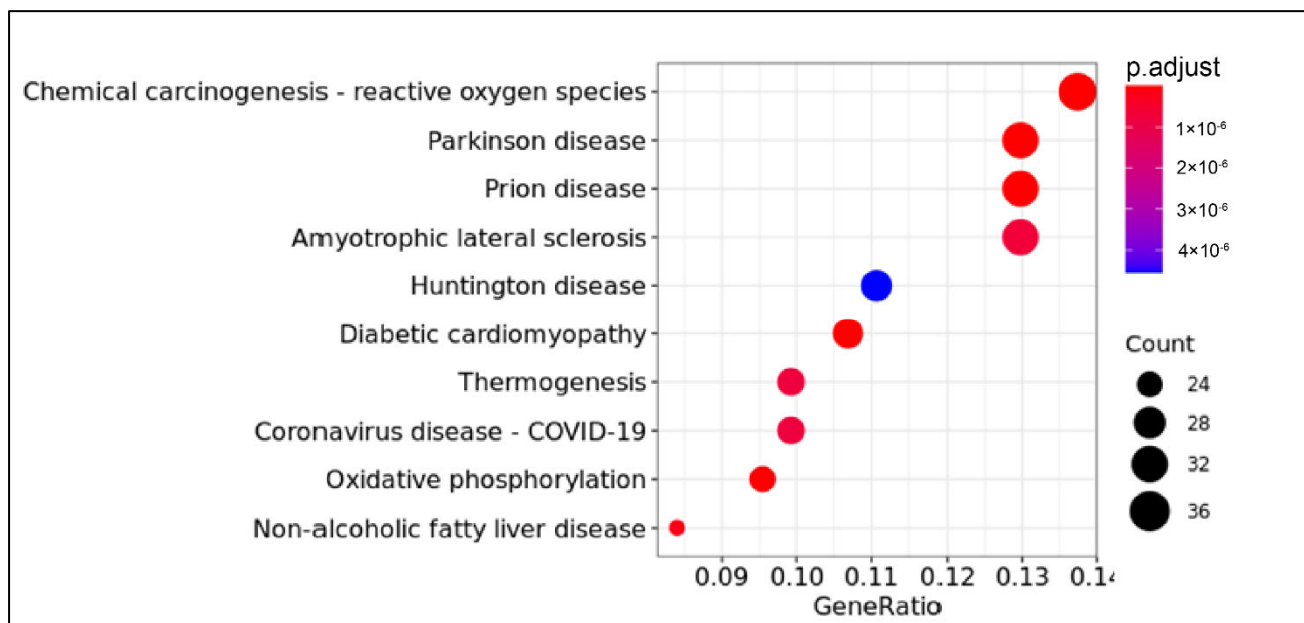


Figure S4 KEGG analyses for high expression genes ($p < 10^{-10}$) of LyEC1 clusters

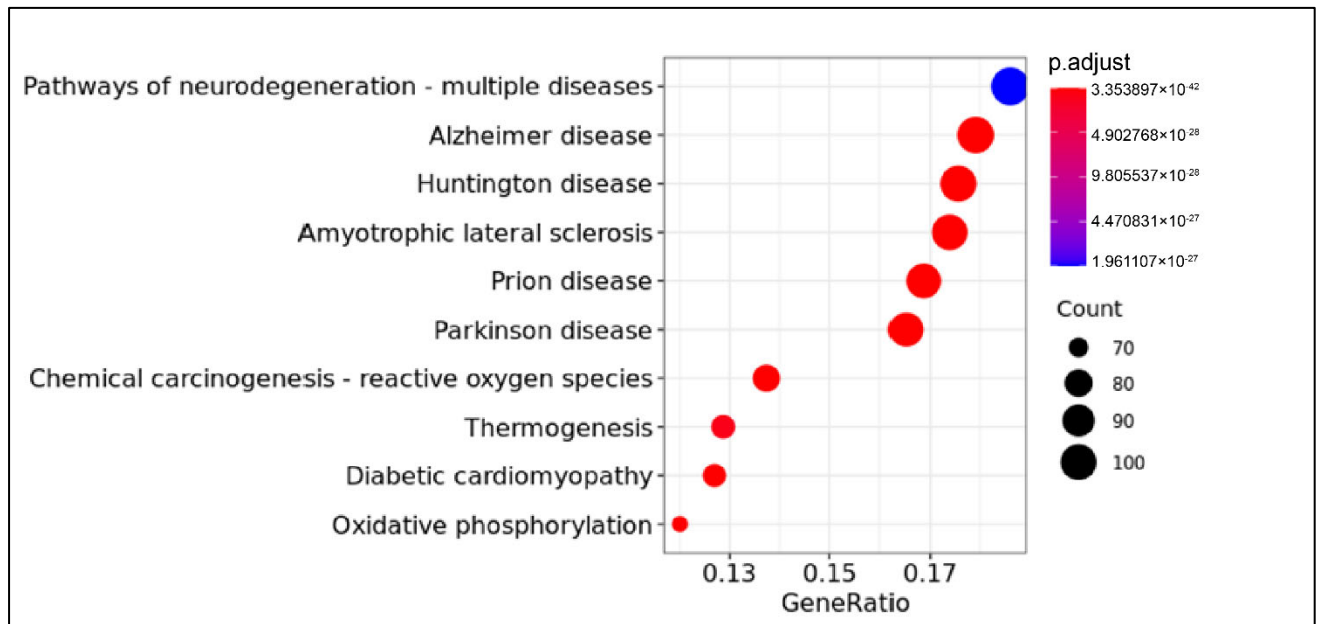


Figure S5 KEGG analyses for high expression genes ($p < 10^{-10}$) of LyEC2 clusters

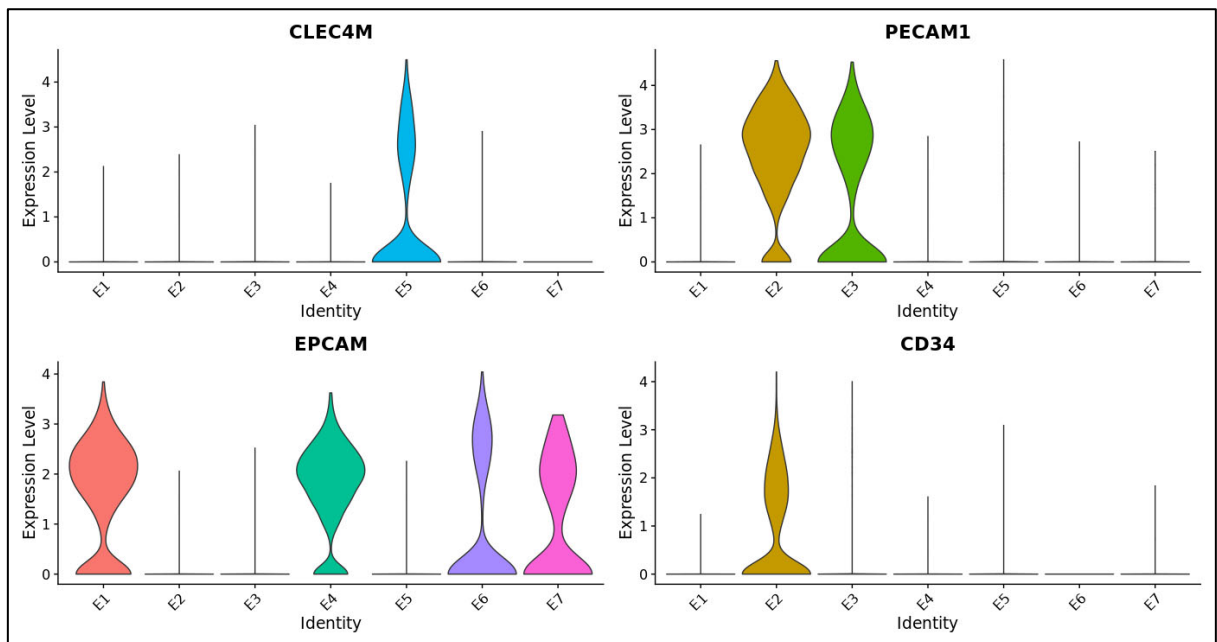


Figure S6 the classical marker for each endothelial cells and epithelial cells cluster. CLEC4M expressed in liver sinusoidal endothelial cells (LsECs), PECAM1 expressed in vascular endothelial cells (VECs), EPCAM expressed in both lymphatic vessels cells (LyECs), epithelial cells and hepatocytes, CD34 expressed in vascular endothelial cells (VECs).

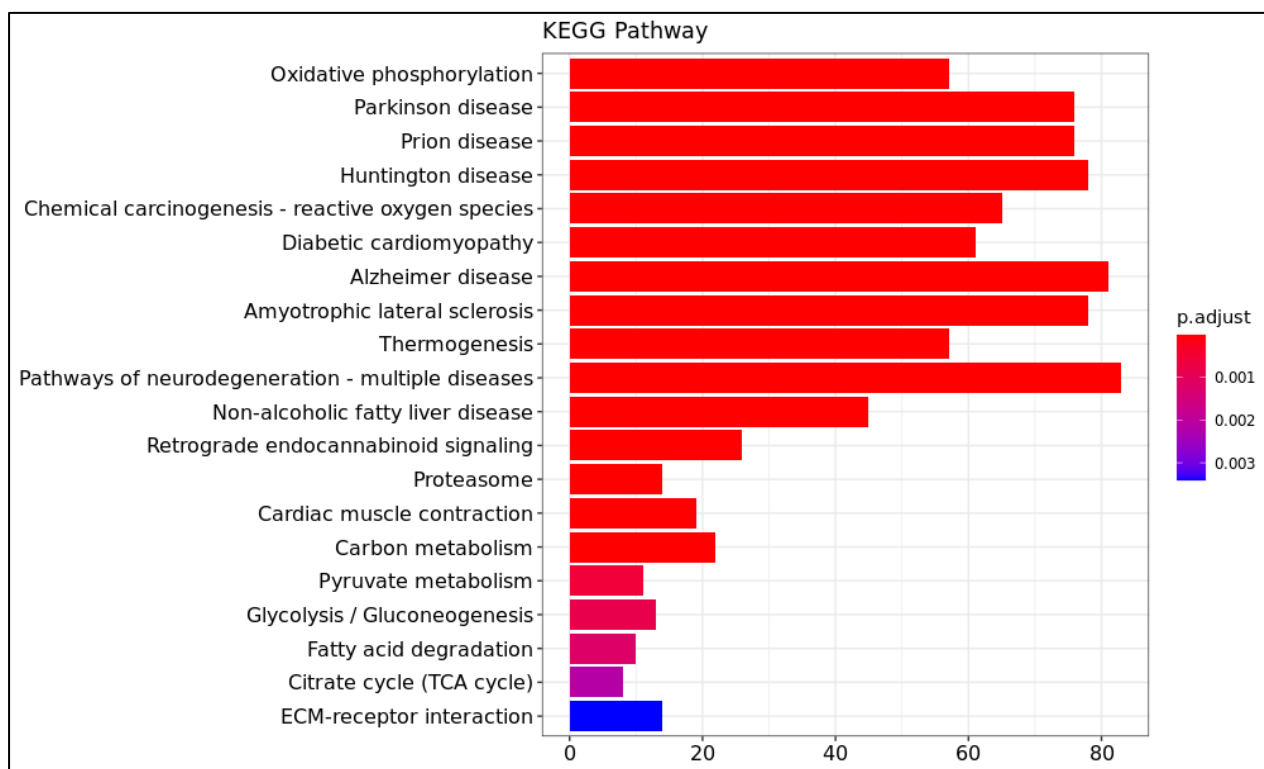


Figure S7 KEGG analyses for high expression genes ($p < 10^{-50}$) of LyEC2 clusters showed an oxidative phosphorylation pathway

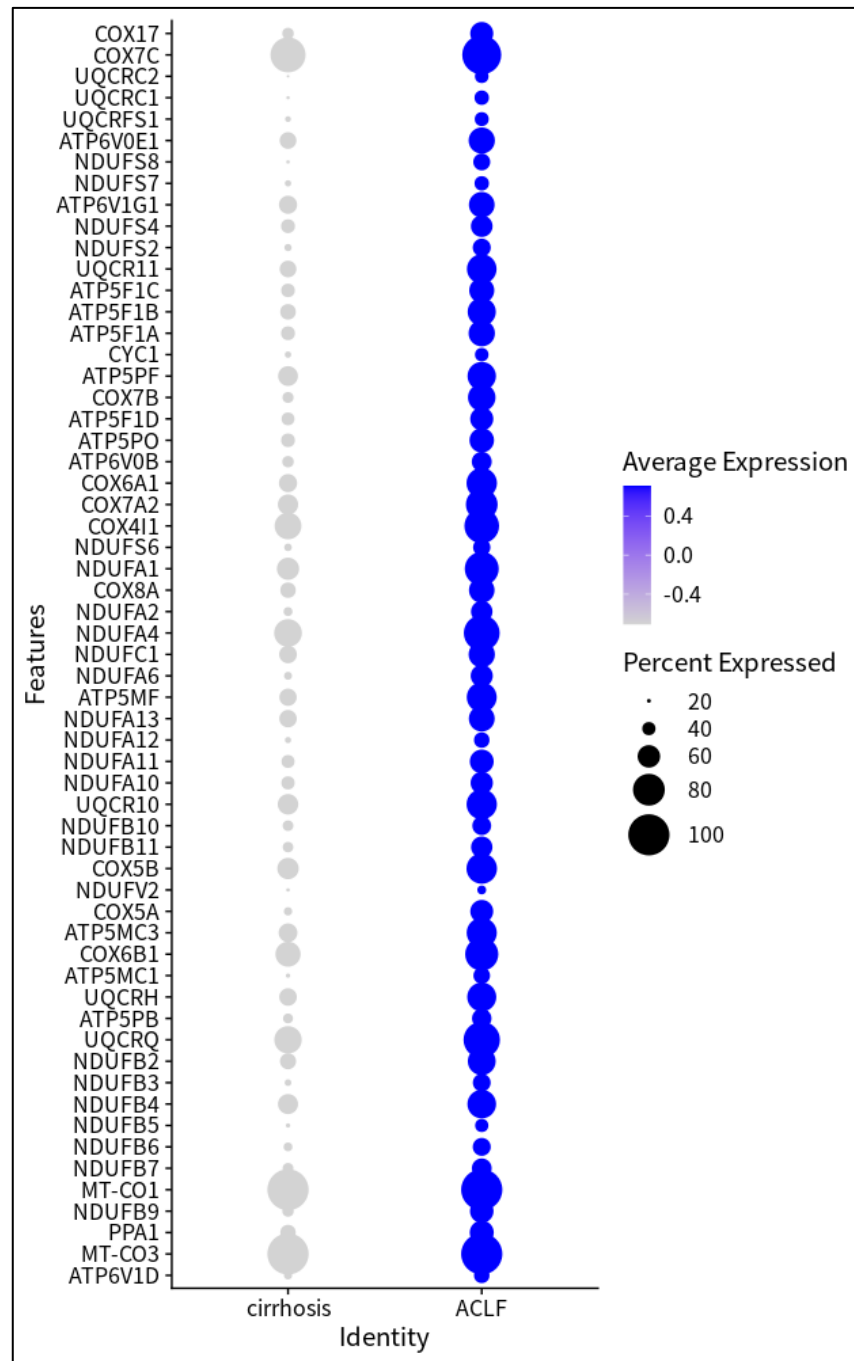


Figure S8 The expression of genes related to oxidative phosphorylation pathway in ACLF and cirrhosis group

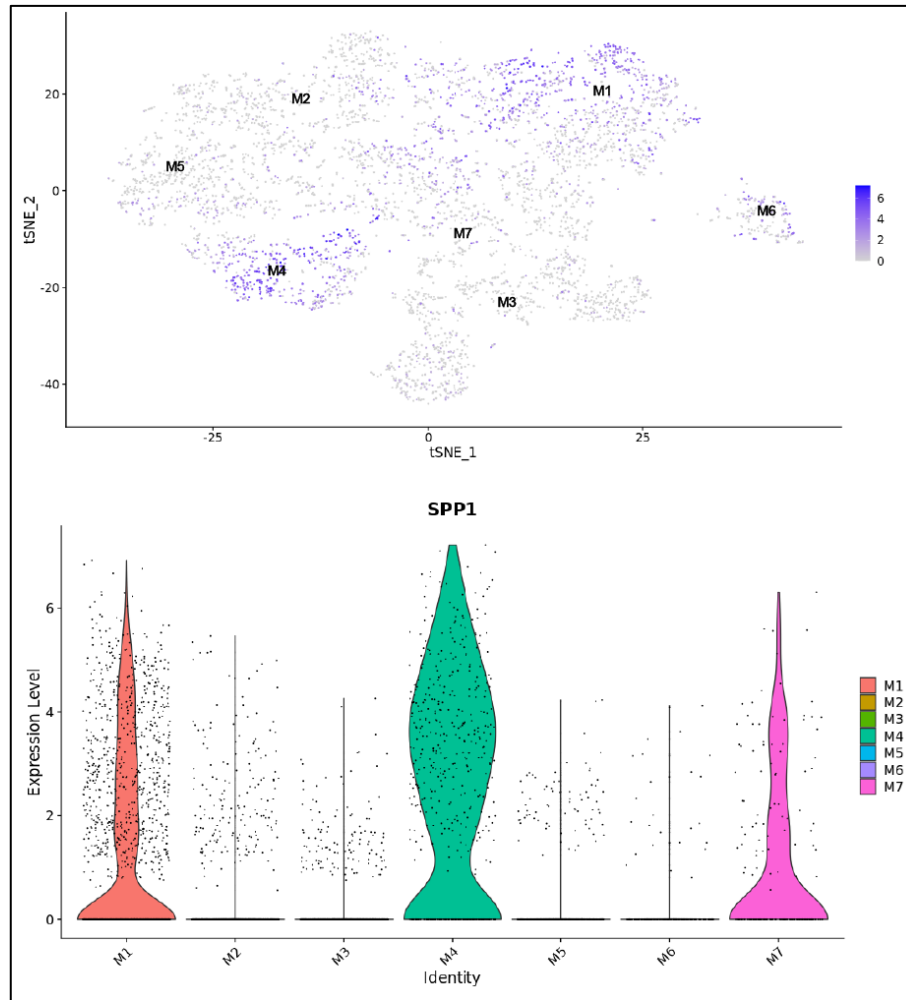


Figure S9 The tSNE and violin plotting of SPP1 in monocyte/macrophages

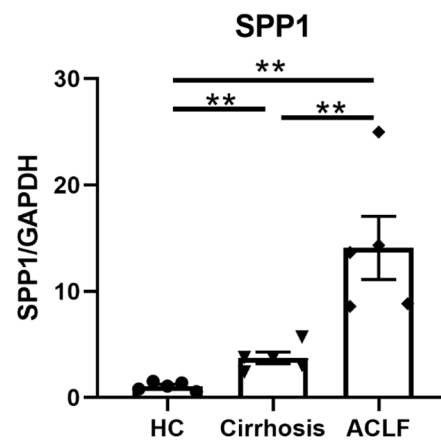


Figure S10 Increased mRNA level of SPP1 was found in cirrhosis and ACLF liver compared with HC (** $p < 0.01$)