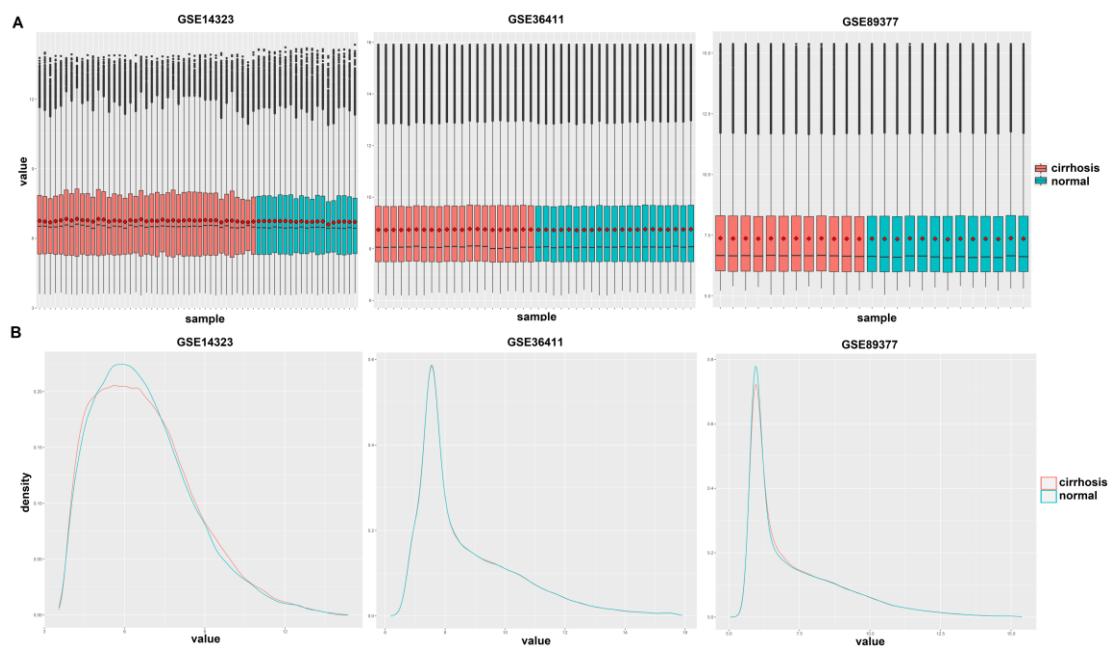
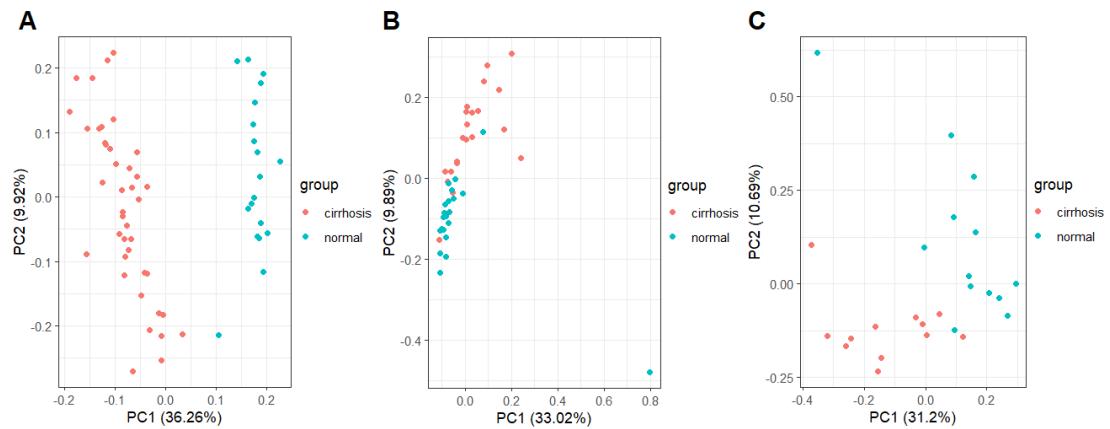


Supplementary Table 1 Sequences of synthesized primers used for qRT-PCR assays (designed with mouse genome mm10)

Name	Forward primer	Reverse primer
<i>Cyclophilina</i>	CAAATGCTGGACCAAACACAA	GCCATCCAGCCATTCACT
<i>Cxcl9</i>	AGTCCGCTGTTCTTCCTC	TGAGGTCTTGAGGGATTGTAG
<i>Cxcl10</i>	TCAGCACCATGAACCCAAG	CTATGGCCCTCATTCTCACTG
<i>Cxcr4</i>	TGTTGCCATGGAACCGATCA	TGGTGGGCAGGAAGATCCTA
<i>Dcn</i>	TGTCAACCACCTAGTAAAGCGT	GTTCGGCGGCATTGACTTT
<i>Dpt</i>	AGACAATGGAAC TACGCCTG	GAAGTAGCGGCTCTGGAATC
<i>Lama2</i>	CCTGTCCACTCAATATCCCATC	AGAGGGTTGTCCAAAATAGCC
<i>Lum</i>	GATCAAGCATCTGCGCTTGG	CCCCACATTCCAACCATGA
<i>Mfap4</i>	CTGGAATGACTACAAGCTGGG	CTTCTGCTTCAGTGTCAAGGAG
<i>Pdgfra</i>	CATGGTGAAATGCTGGAACAG	GCAGGATGGTCACTCTTCAG
<i>Sox9</i>	GAGGAGCACTGACTCCTTGC	CTATCCACGGCACACACACTTG



Supplementary Figure 1 The analysis of gene expression levels between cirrhotic and healthy groups in each sample of three profiles (GSE14323, GSE36411 and GSE89377). Orange is the cirrhosis group and cyan is the normal group. The position of the red diamond is the average value of each sample in (A).



Supplementary Figure 2 Principal component analysis results between cirrhotic and healthy groups in each sample of three profiles (GSE14323, GSE36411 and GSE89377). Orange is the cirrhosis group and cyan is the normal group. The X-axis represents the first principal component and the Y-axis represents the second principal component.