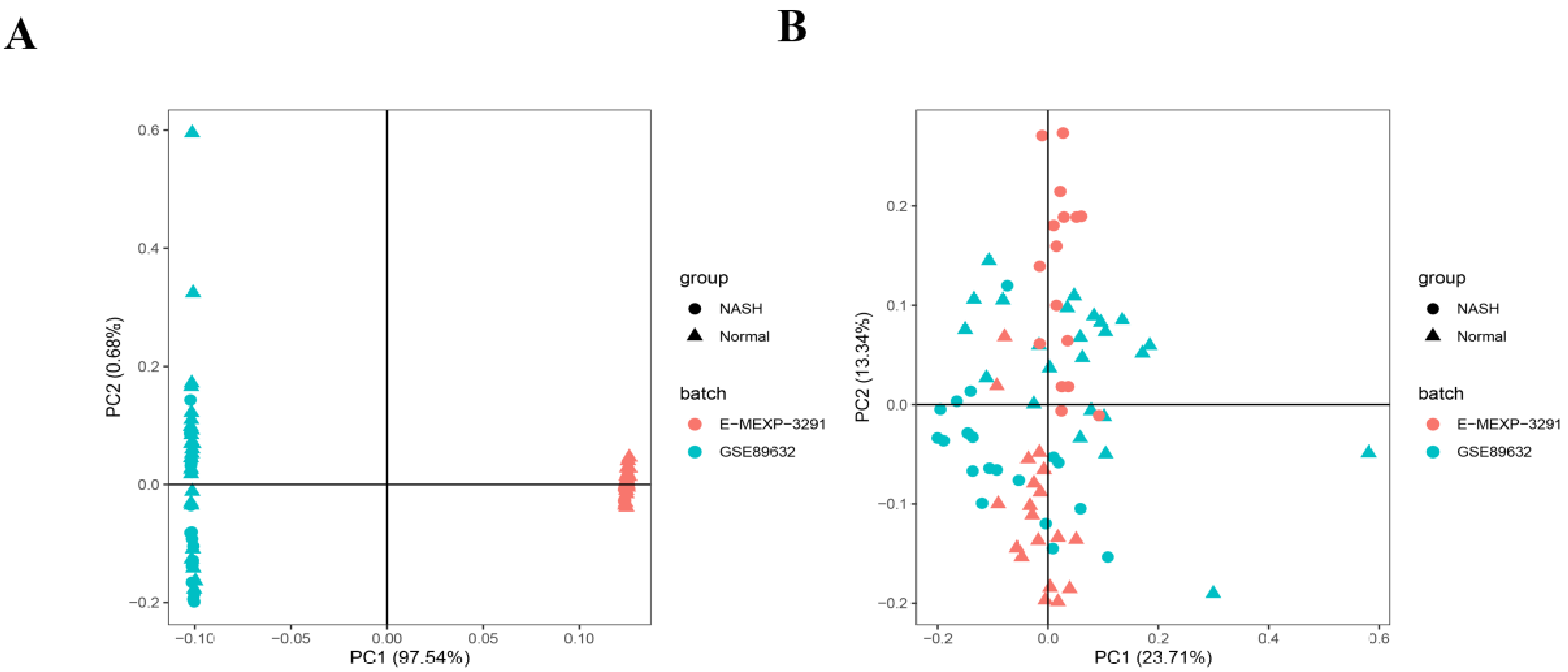
Supplemental Materials

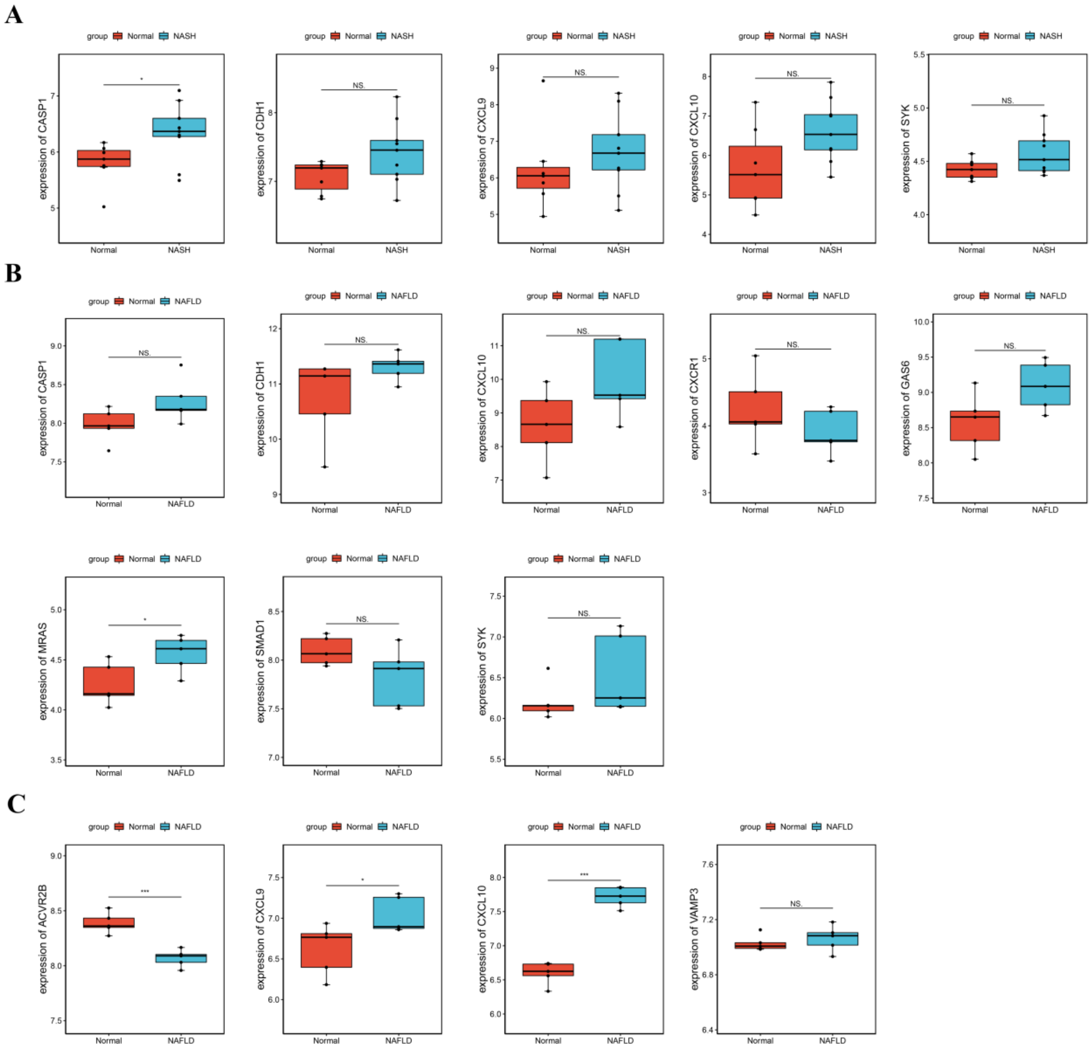


Appendix 1 Principal component analysis (PCA) diagrams before (A) and after (B) removing the batch effect on samples from GSE89632 and E-MEXP-3291 datasets.

Appendix 2. Module mining analysis based on 17 submodules from the PPI network

Submodule	**Score (Density*Nodes)**	**Nodes**	**Edges**	**Genes**
MCODE1	9.667	19	87	*CXCR6, FPR3, SAMD9L, IFIH1, CXCL2, CCR2, CCL5, CXCL10, SAA1, IFIT2, CXCR1, IFIT3, DDX60, IFI44, CCL28, IFI44L, CXCL9, IFIT1, DDX58*
MCODE2	8	8	28	*AP2B1, VAMP3, CD3D, SYNJ2, LRP2, CFTR, FNBP1L, CD3G*
MCODE3	6.333	7	19	*TCTN1, DYNC1I2, CC2D2A, OPTN, CEP290, CEP152, NEDD1*
MCODE4	6	6	15	*NOL6, NOP14, BYSL, POLR1B, DDX56, NOP2*
MCODE5	5	5	10	*PPP2R1B, CLASP2, XPO1, KNTC1, ITGB3BP*
MCODE6	4.5	5	9	*BMPR1B, SMAD1, ACVR2B, BMPR1A, BMP5*
MCODE7	4.444	10	20	*CDH1, CD28, CD2, STAT3, CASP3, SYK, PAK1, IL2RG, VAV3, PIK3CG*
MCODE8	4	4	6	*P2RY10, AVPR1A, CYSLTR1, HTR2B*
MCODE9	4	4	6	*KLHL3, FBXL4, FBXO7, DET1*
MCODE10	4	4	6	*CLUAP1, IFT80, IFT52, KIFAP3*
MCODE11	3.667	7	11	*ACTN1, GAS6, ITGA6, IGF1, LGALS3BP, LAMA4, ITGB6*
MCODE12	3.333	4	5	*APAF1, TNFSF10, FAS, CASP1*
MCODE13	3	3	3	*GZMA, KLRB1, GZMK*
MCODE14	3	3	3	*RASGRP1, RASGRP3, MRAS*
MCODE15	3	7	9	*PLCG1, PDGFRB, PLD1, PLA2G4C, FGFR2, SOS1, LPCAT2*
MCODE16	3	3	3	*CALCA, PTGDR, SCTR*
MCODE17	3	3	3	*S100A12, S100A8, S100A9*

PPI: Protein-protein interaction.



Appendix 3. Validation of the expression of differentially expressed genes (DEGs) in GSE63067, GSE107231, and GSE72756 datasets between normal and non-alcoholic steatohepatitis (NASH) samples. The expression of DEG signatures with corresponding characteristics was further compared between normal and NASH samples from GSE63067 (A), GSE107231 (B), and GSE72756 (C). *P<0.05, ***P<0.005, and NS indicates non-significant.