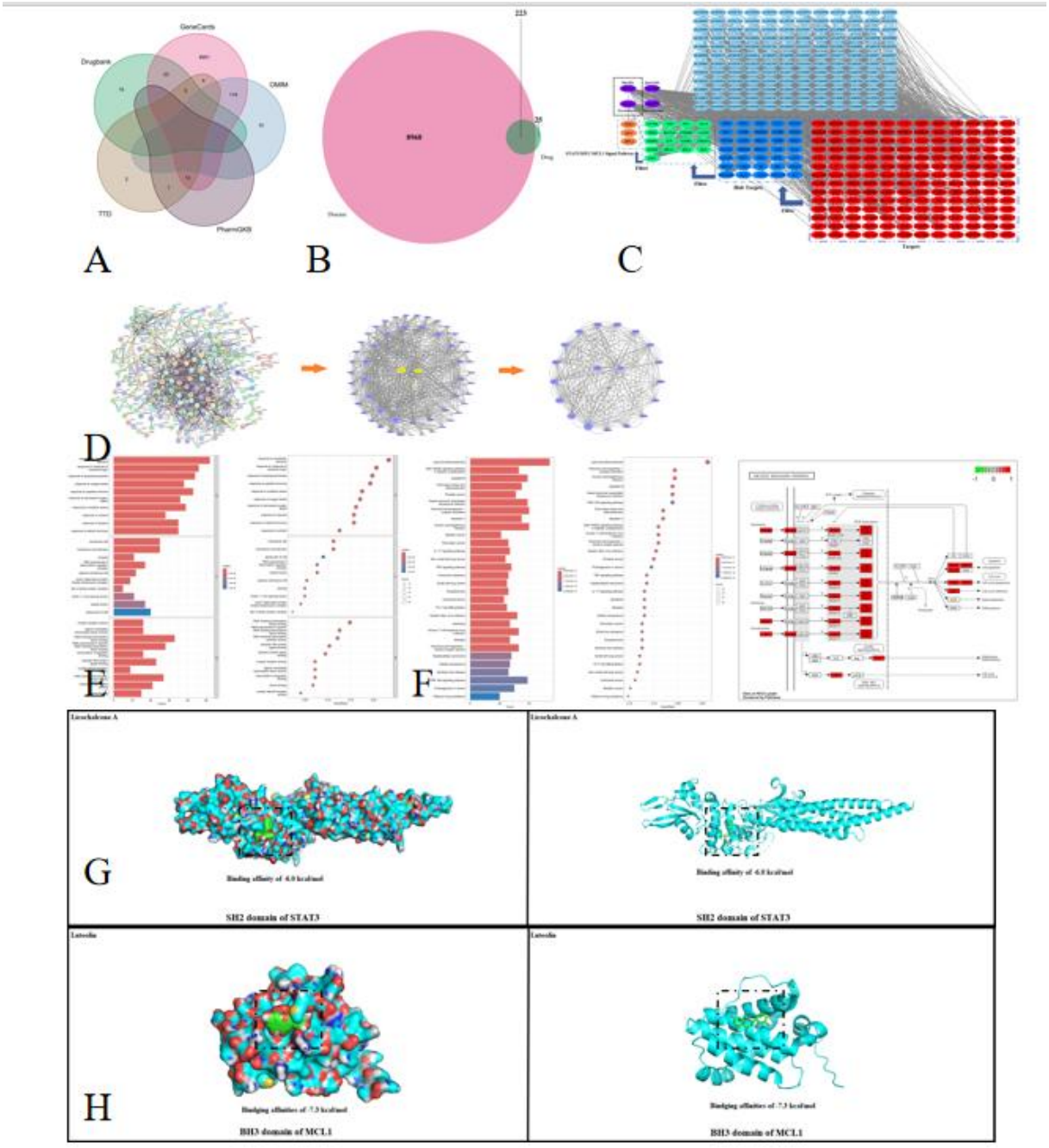
Supplementary Table 1 The baseline of the included scRNA-seq patients

Variable	JHF Group(n=3)	Control Group(n=3)	*P*-value
Sex(Male/Female)	3/0	3/0	NA
Age	30.67 ± 15.01	39.00 ± 9.17	0.44
Etiology			0.60
HLD	3	2	
HBV	0	1	
Pre-treatment			
ALT(U/L)	53.47 ± 0.81	54.00 ± 1.00	0.43
TBIL(μmol/L)	42.75 ± 2.11	43.56 ± 1.70	0.62
PT(s)	12.90 ± 1.54	13.87 ± 0.97	0.37
HA(ng/mL)	139.35 ± 54.85	153.56 ± 37.28	0.72
LN(ng/mL)	285.73 ± 147.75	115.14 ± 76.35	0.14
PIIINP(ng/mL)	114.54 ± 11.16	90.12 ± 36.32	0.32
CIV(ng/mL)	69.79 ± 44.83	86.78 ± 32.52	0.57
Liver Stiffness(kPa)	12.46 ± 2.98	12.37 ± 2.87	0.97
Shear Wave Velocity(m/s)	2.00 ± 0.23	1.98 ± 0.22	0.92



Supplement Figure 1 Network Pharmacology Analysis of Jianpi Huoxue Formula in Liver Fibrosis

(A) Venn diagram of disease-related genes from GeneCards, TTD, DrugBank, OMIM, and PharmGKB. (B) Intersection genes were identified between active compound targets and disease targets. (C) A "herbal-compound-gene target" network was constructed. (D) The protein–protein interaction network was analyzed. (E) GO analyses of intersection genes were constructed. (F) KEGG analyses of intersection genes were constructed. (G) Molecular docking of Licochalcone A with the STAT3 protein. (H) Molecular docking of luteolin with the MCL-1 protein.