

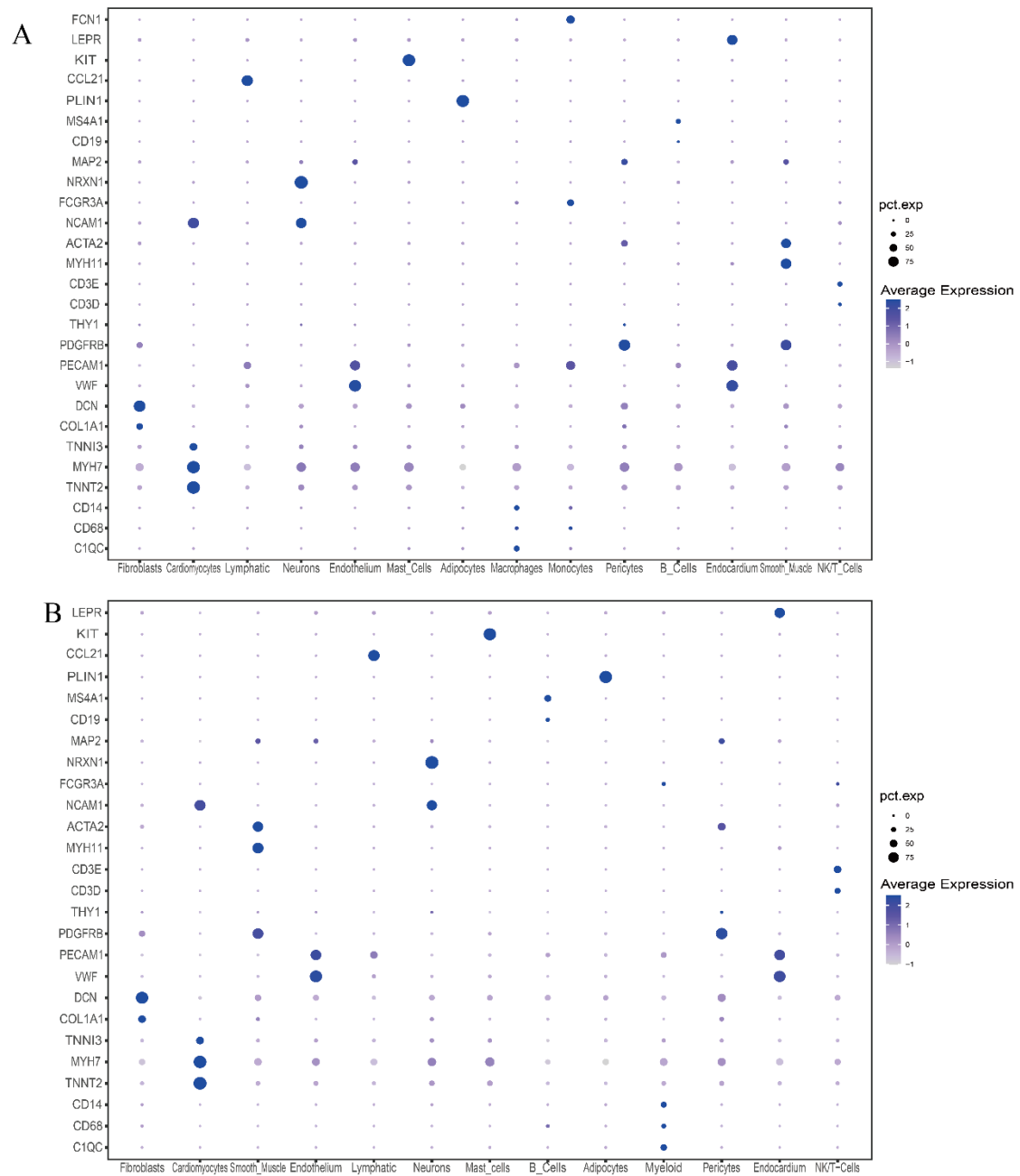


Fig.S1 Dop plots show marker genes of each identified cell clusters in single-cell analysis. (A) Cell markers of single-nucleus RNA sequencing data (snRNA-seq) from GSE183852. (B) Cell markers of the integrated data combining snRNA-seq and single-cell RNA sequencing (scRNA-seq) data from GSE183852.

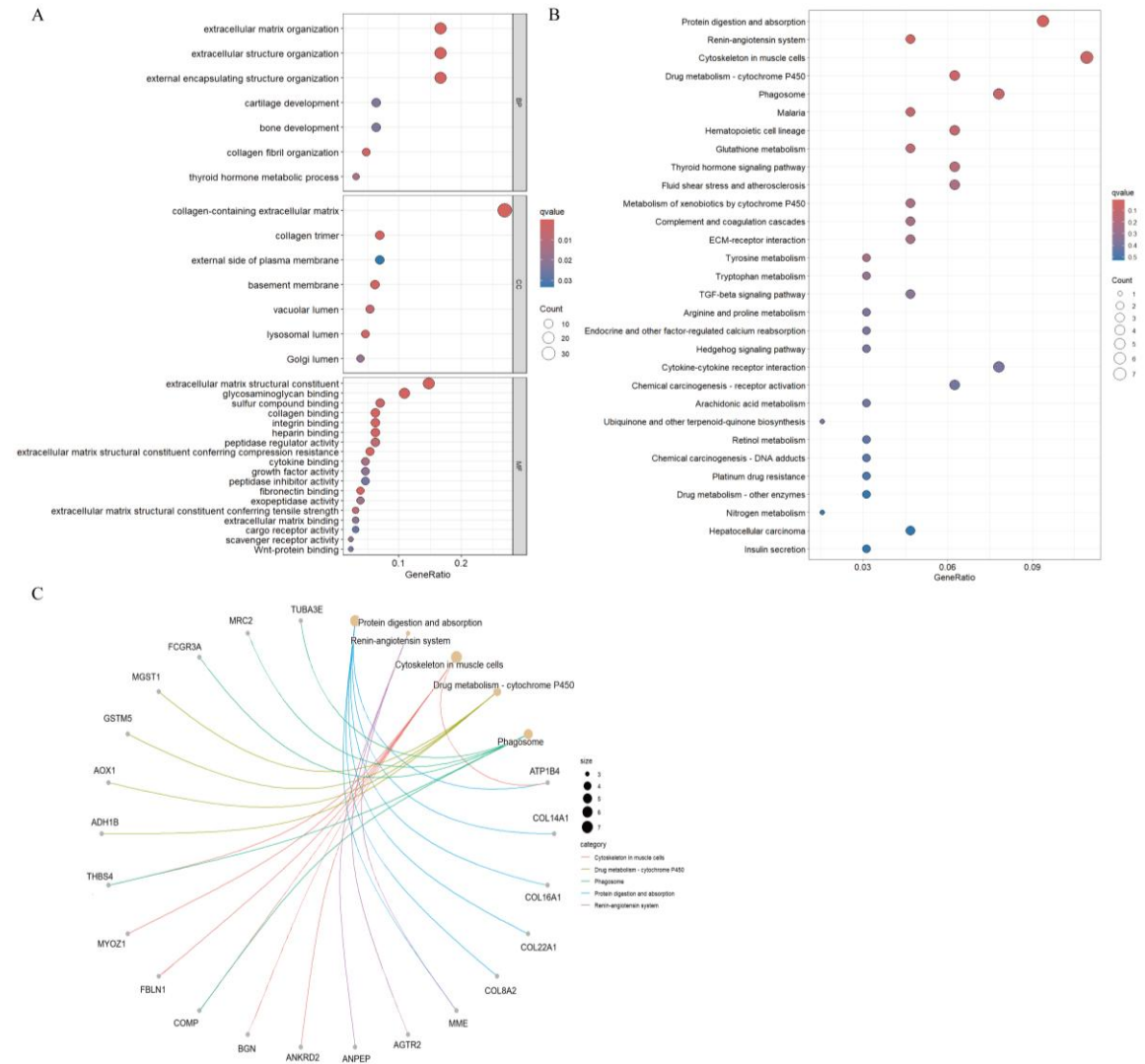


Fig.S2 Functional enrichment analysis of 138 intersection genes. (A)Gene Ontology (GO) enrichment analysis. (B,C) Kyoto Encyclopedia of Genes (KEGG) enrichment analysis.

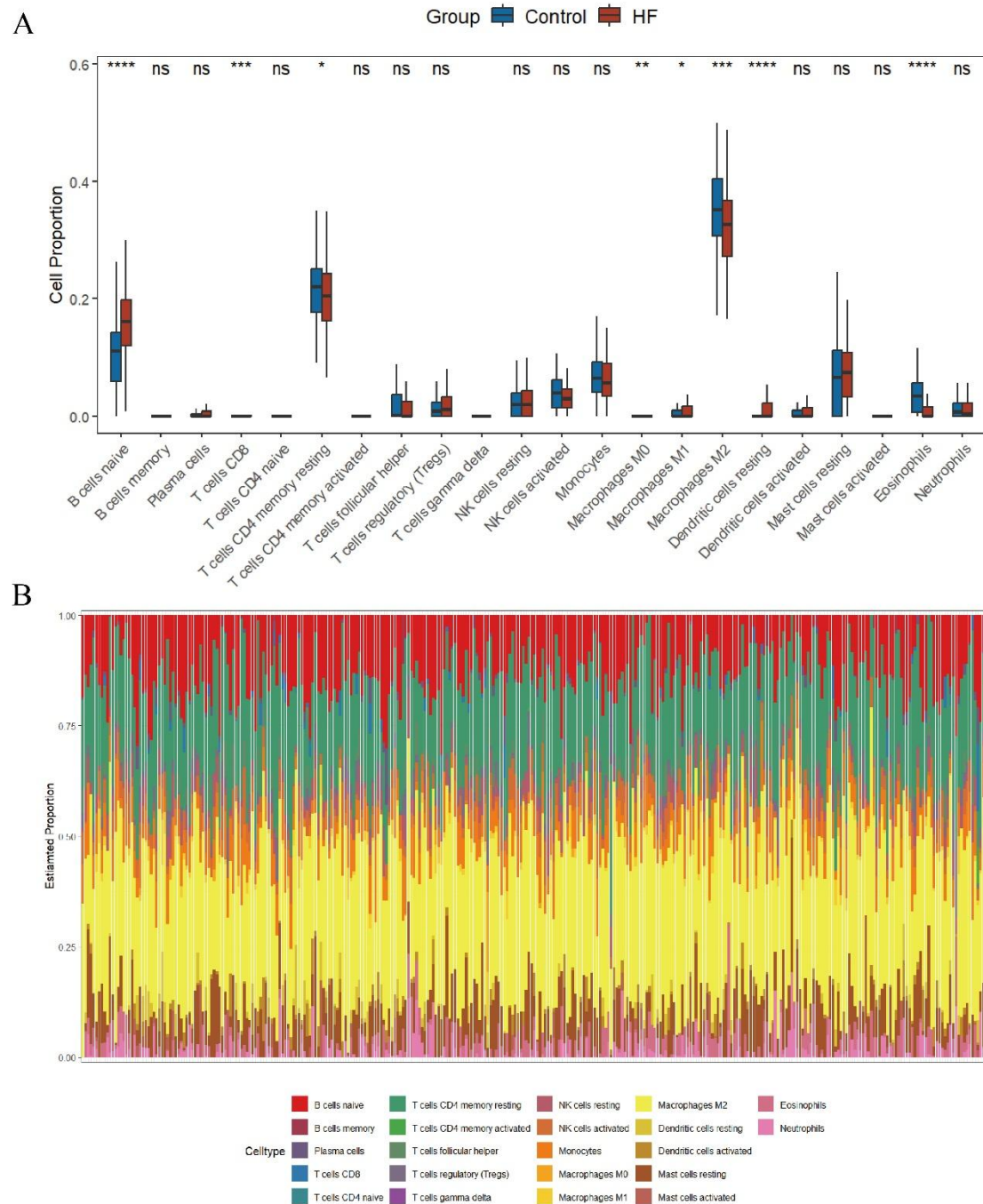


Fig.S3 Immune infiltration analysis. (A) The estimated proportion of immune cells; (B) Immune infiltration analysis between groups. "*" indicates $P < 0.05$, "***" indicates $P < 0.01$, "****" indicates $P < 0.001$, "*****" indicates $P < 0.0001$.

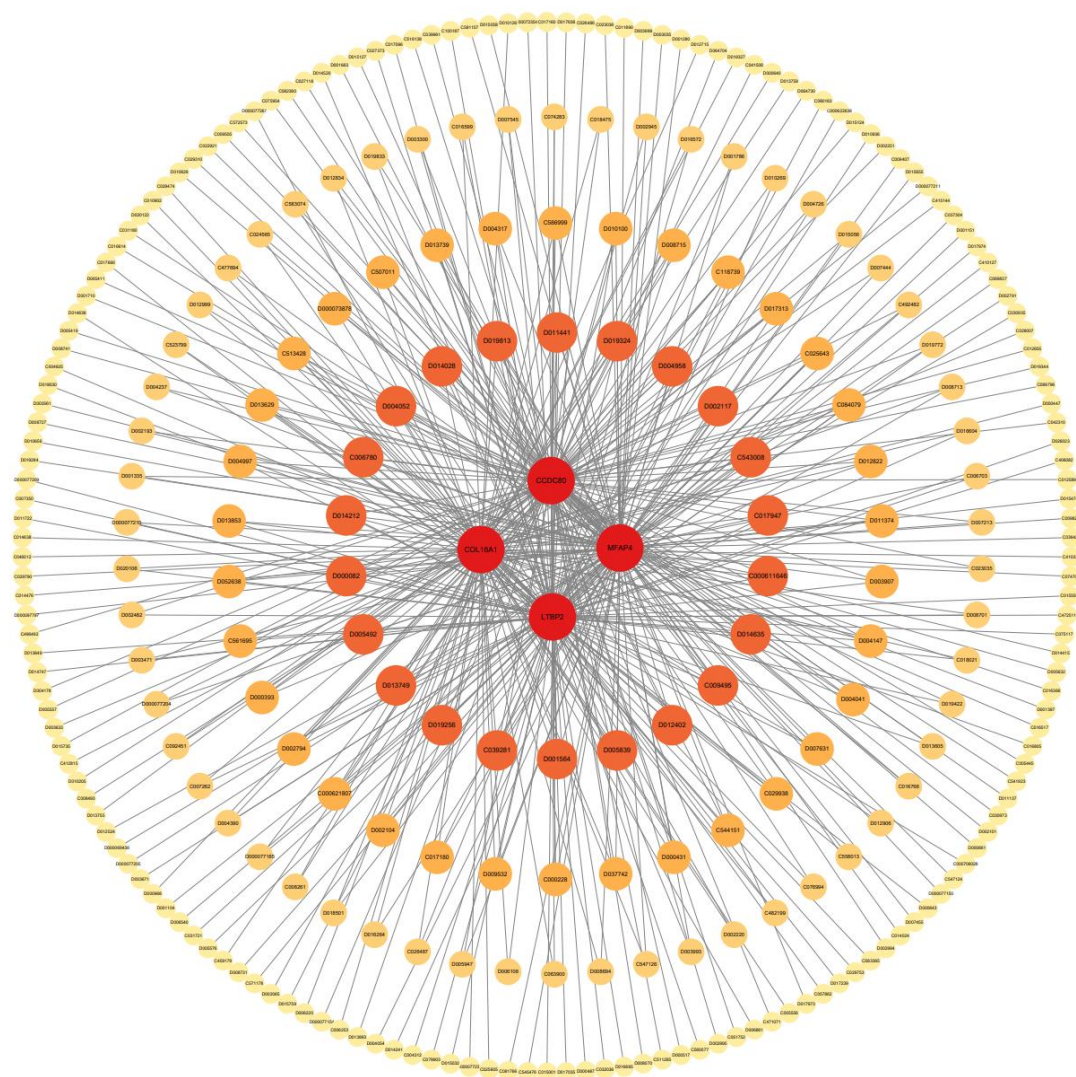


Fig.S4 Chemical-gene network

TableS1 Demographic and baseline clinical characteristics of the study population in GSE17800

	Level	Control (n=8)	DCM-induced HF (n=40)	p
Gender	female	2 (25.0%)	12 (30.0%)	1.000
	male	6 (75.0%)	28 (70.0%)	
Age (years)		43.12 ± 14.76	50.21 ± 9.35	0.084
Left Ventricular Inner Diameter				
at Diastole (mm) ± SD		51.38 ± 3.11	69.80 ± 8.00	<0.001
BMI (kg/m ²) ± SD		26.32 ± 5.26	27.88 ± 4.57	0.394
Left Ventricular Ejection				
Fraction (%) ±SD		59.75 ± 8.05	33.27 ± 6.41	<0.001

TableS2 Demographic and baseline clinical characteristics of the study population in GSE116250

	Level	Control (n=14)	DCM-induced HF (n=37)	p
Gender	Female	3 (21.4%)	7 (18.9%)	1.000
	Male	11 (78.6%)	30 (81.1%)	
Race	Black or African American	0 (0.0%)	3 (8.1%)	0.537
	Caucasian	13 (92.9%)	31 (83.8%)	
	Unknown	1 (7.1%)	3 (8.1%)	
Age (years) ± SD		49.07 ± 8.61	48.78 ± 13.29	0.941

TableS3. Specific primer sequences for RT-qPCR.

Genes	Forward (5'to3')	Reverse (5'to3')
MFAP4	GCAACCCCTGGACTGTGATG	TTGTCATGTCGCAGAAGACGG
CCDC80	CGTGAGATGGTCCGAGATGA	CCAGCTCACAATACACGTCG
LTBP2	AACAGCACCAACCACTGTATC	CCTGGCATTCTGAGGGTCAAA
COL16A1	AGGCCCTATTGGGCTTCAAG	GCCAGTGTATCCTCGCTCTC