Figure S1. GO and KEGG enrichment analysis for genes of GSE141910 in black and blue modules. **(A)** GO analysis in black module. **(B)** KEGG pathways analysis in black module. **(C)** GO analysis in blue module. **(D)** KEGG pathways analysis in blue module.
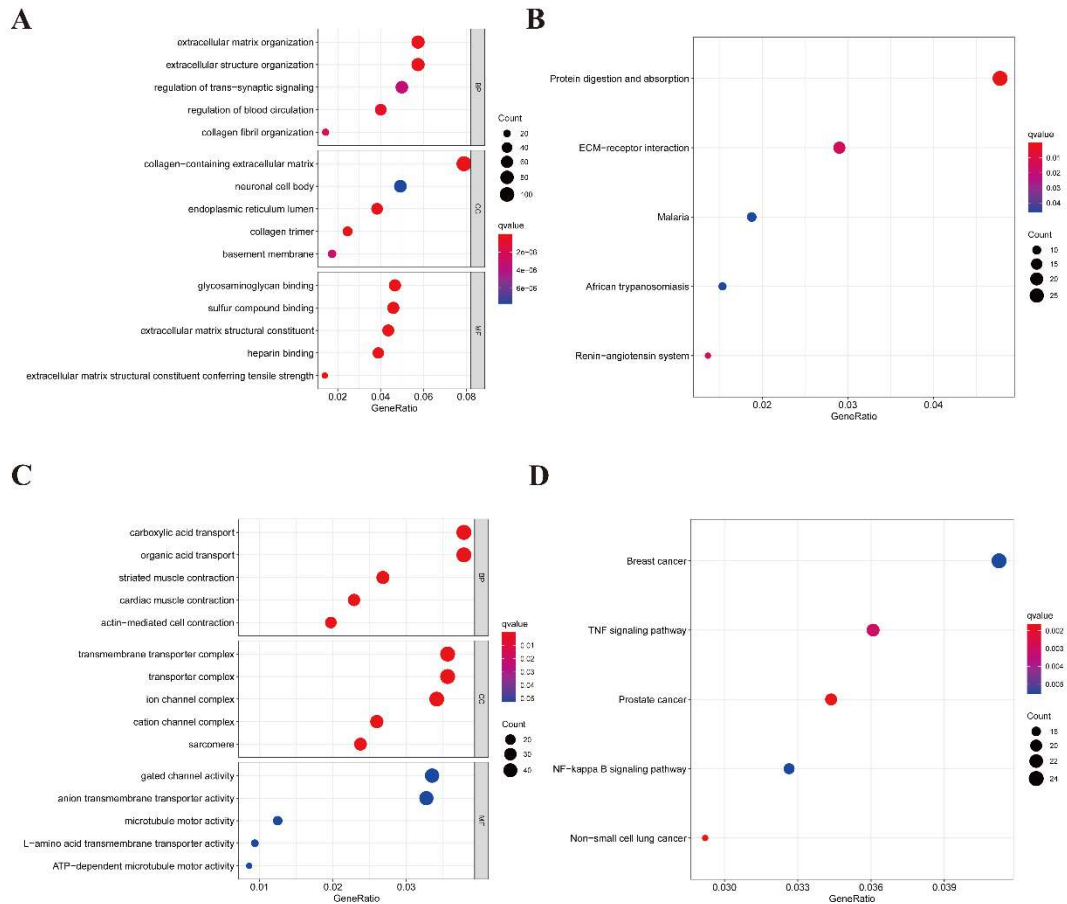
Figure S2. GO and KEGG enrichment analysis for genes of GSE5406 in salmon and tan modules. **(A)** GO analysis in salmon module. **(B)** KEGG pathways analysis in salmon module. **(C)** GO analysis in tan module. **(D)** KEGG pathways analysis in tan module.
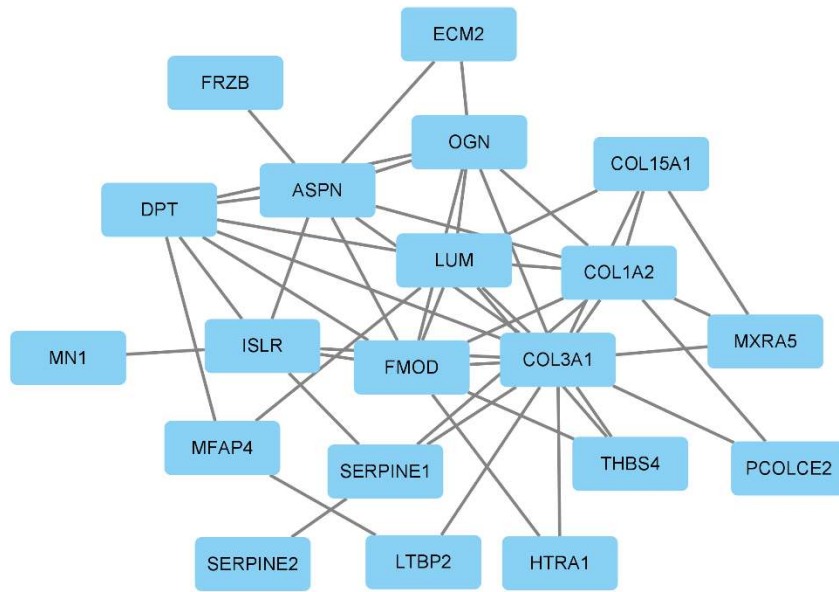
Figure S3. Protein interaction network (PPI) analysis of 30 overlapping genes
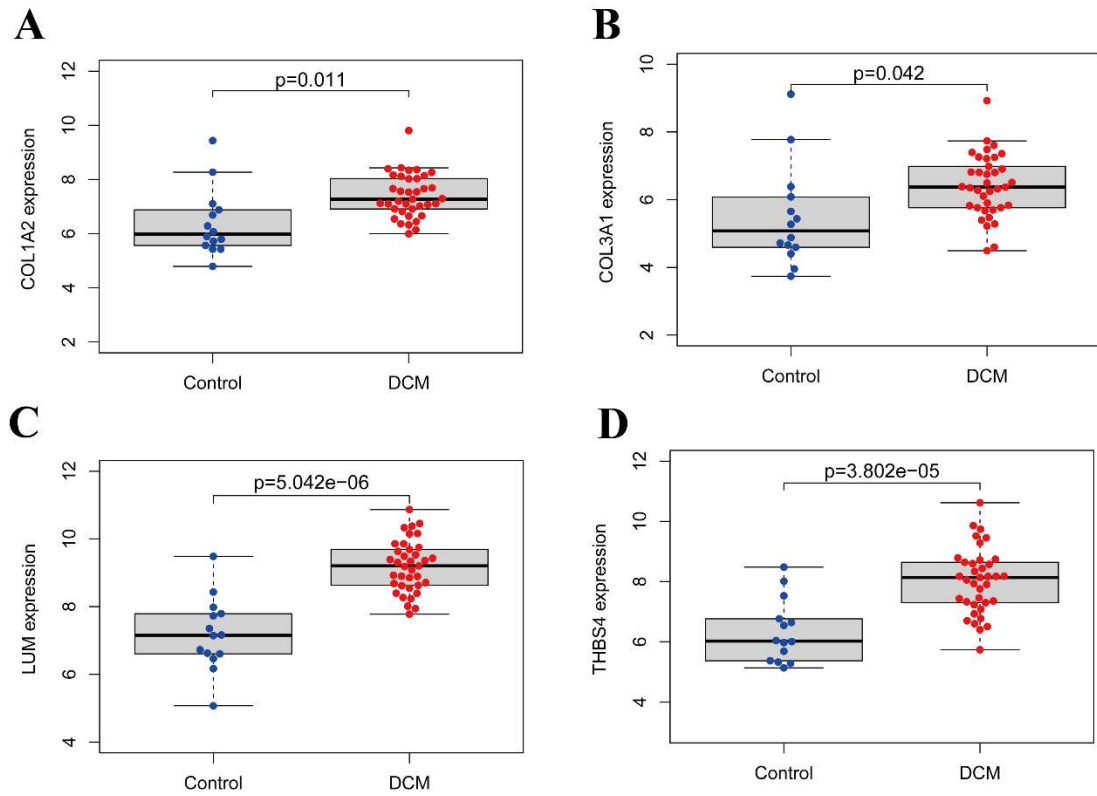
Figure S4. Verification of differential expression of 4 hub genes in GSE116250. **(A-D)** 4 hub genes were upregulated in GSE116250.
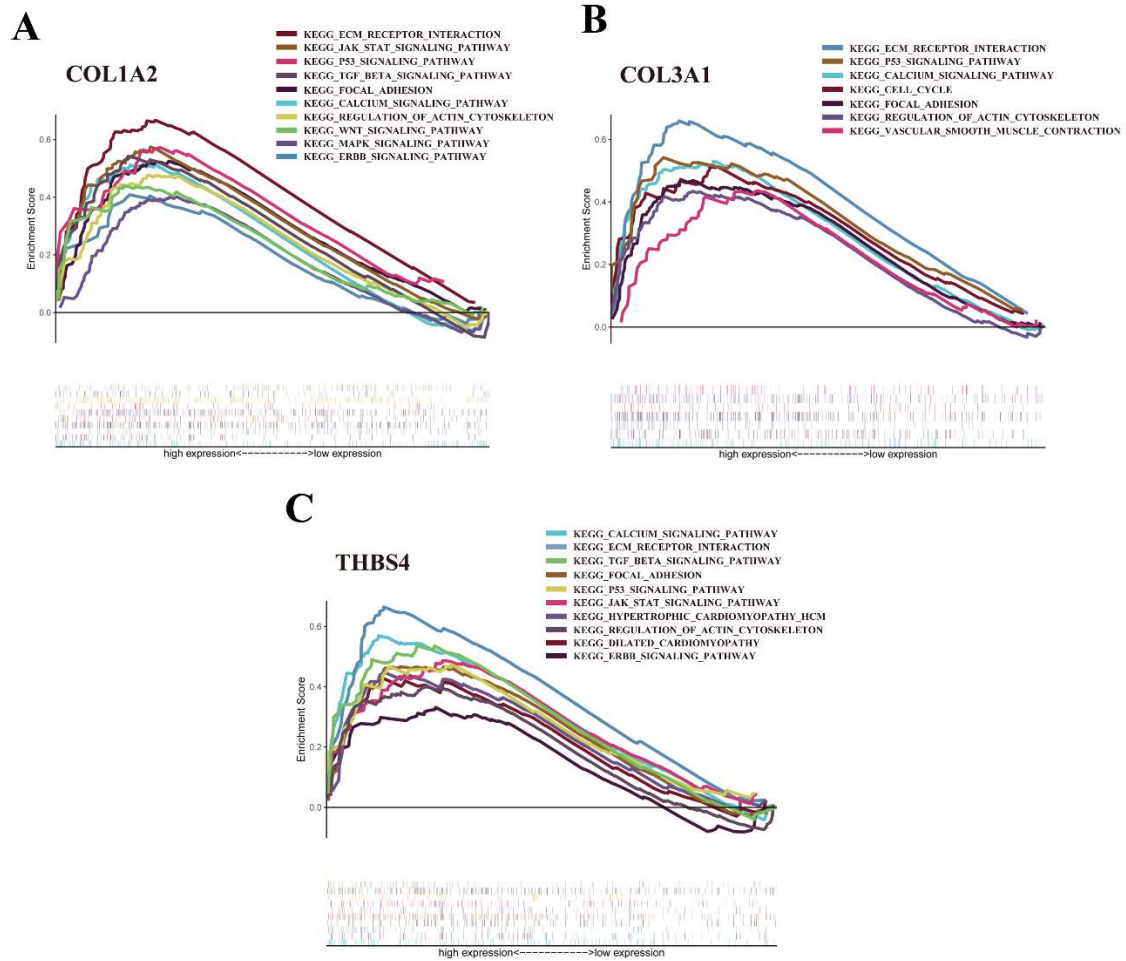
Figure S5. Single-gene GSEA enrichment results of 4 hub genes in GSE141910. **(A-C)** Single-gene enrichment analysis of KEGG pathways.
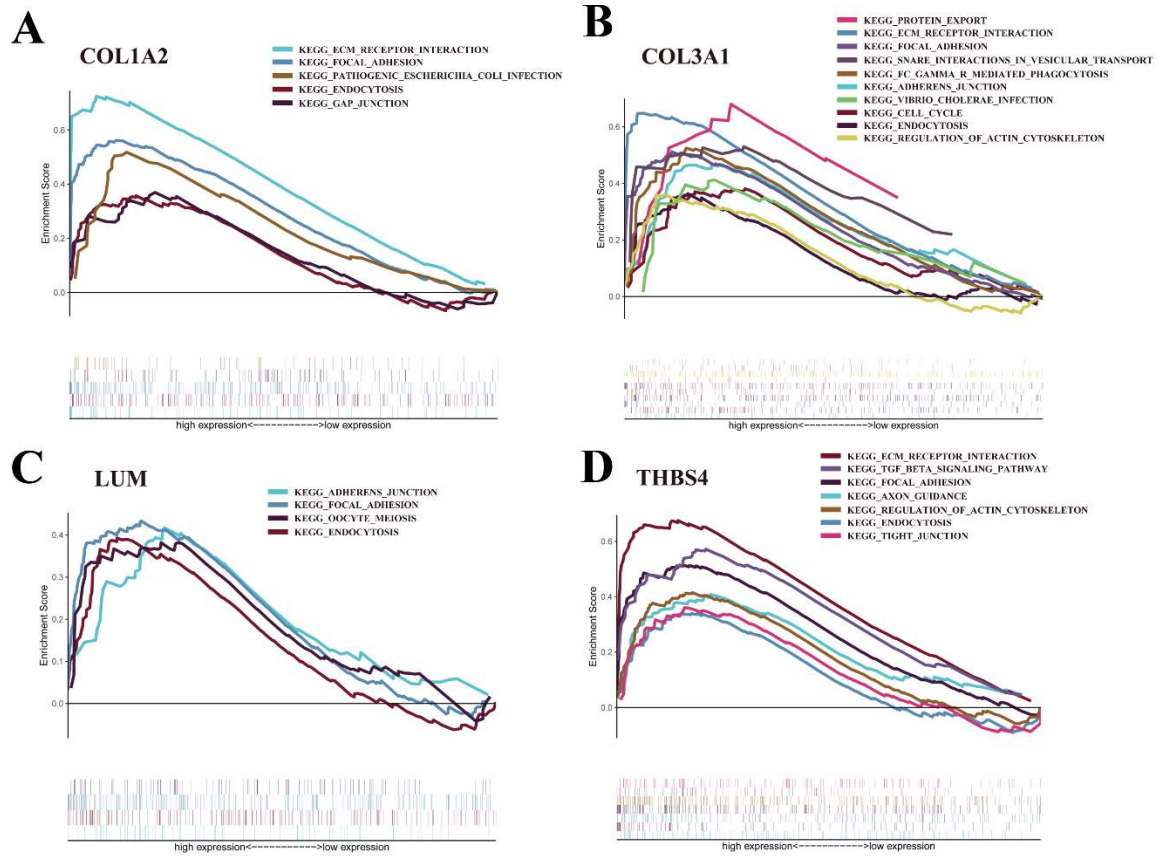
Figure S6. Single-gene GSEA enrichment results of 4 hub genes in GSE5406. **(A-D)** Single-gene enrichment analysis of KEGG pathways.
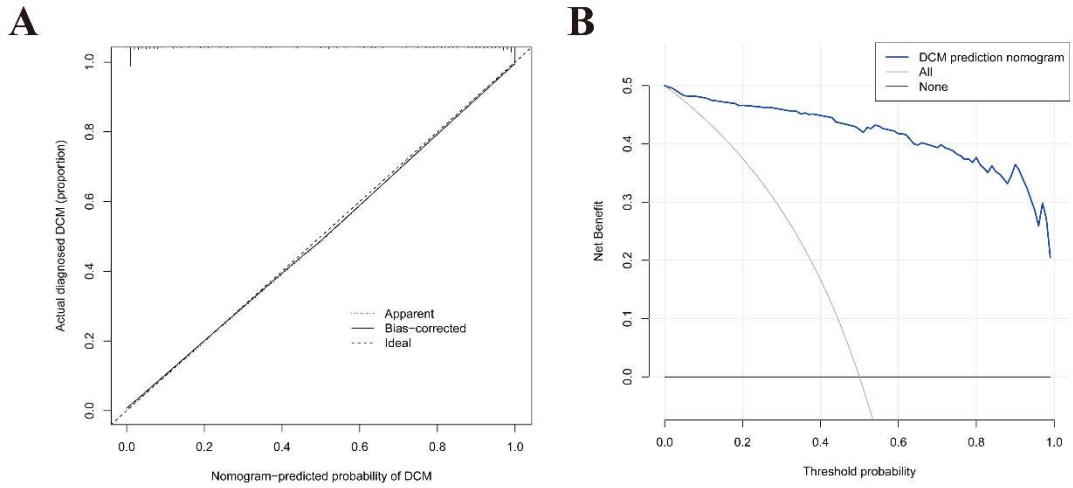
Figure S7. Calibration and decision curve analysis (DCA) for LASSO model. **(A)** Calibration plot. **(B)** DCA analysis.
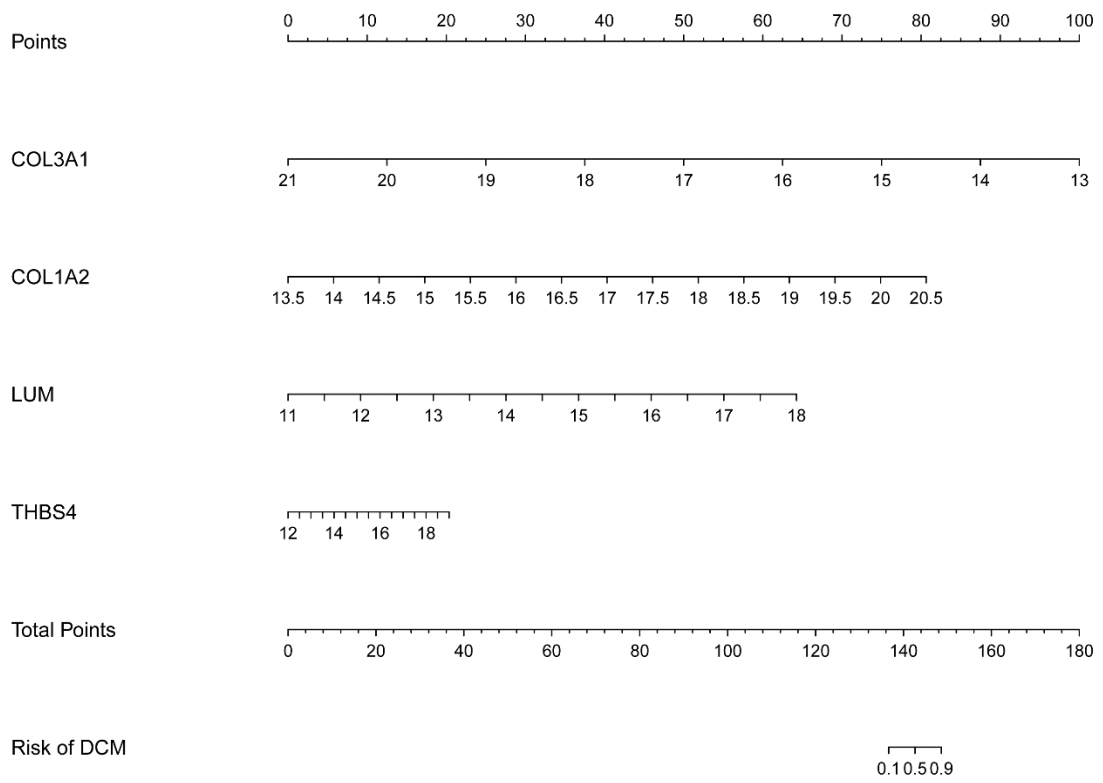
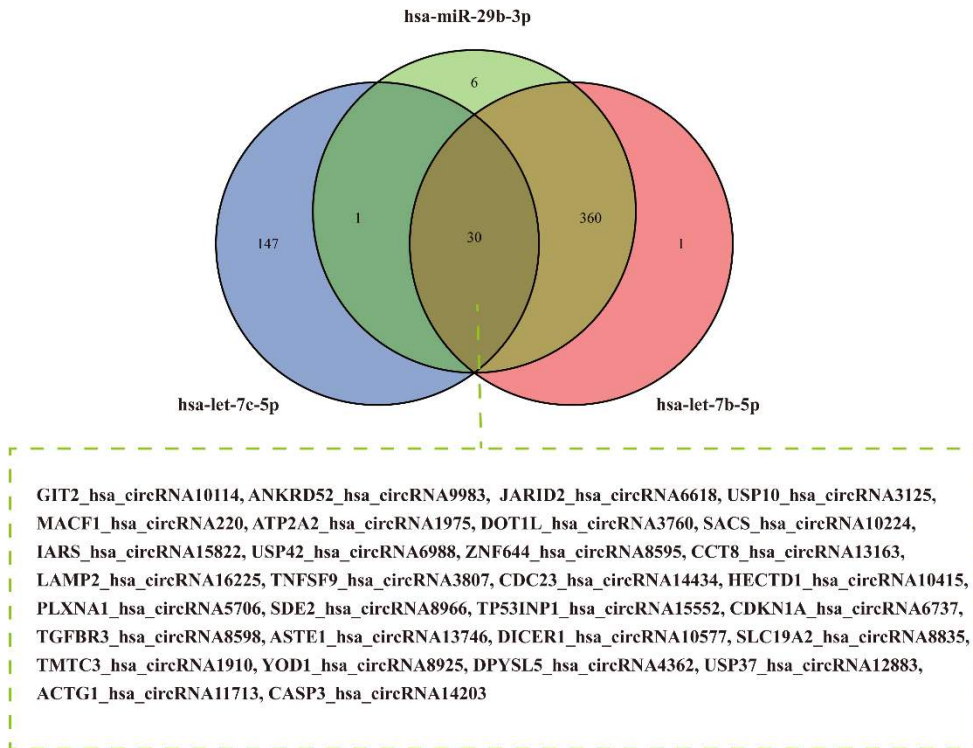**Figure S8.** Nomogram for LASSO model.

Figure S9. The Venn diagram of all targeted circRNAs among three overlapping miRNAs.

Table S1. Predictive performance of gene based model for DCM patients

Cohort	SE	SP	PPV	NPV	Accuracy	AUC
Train	0.9231	0.9316	0.931	0.9237	0.9274	0.9777
Test	1	0.8571	0.875	1	0.9286	0.9917
Total	0.9458	0.9096	0.9128	0.9438	0.9277	0.9811

SE, sensitivity; SP, specificity; PPV, positive predictive value; NPV, negative predictive value; AUC, area under the receiver operating characteristic curve.

Table S2. Potential drugs identified by DGIdb

Gene	Drug	Type	Source	Interaction score
COL3A1	OCRIPLASMIN	None found	ChemblInteractions	0.86
	COLLAGENASE CLOSTRIDIUM HISTOLYTICUM	None found	ChemblInteractions/TEND	2.28
COL1A2	OCRIPLASMIN	None found	ChemblInteractions	0.86
	COLLAGENASE CLOSTRIDIUM HISTOLYTICUM	None found	ChemblInteractions/TEND	2.28
THBS4	VASOPRESSIN	None found	NCI	7.5