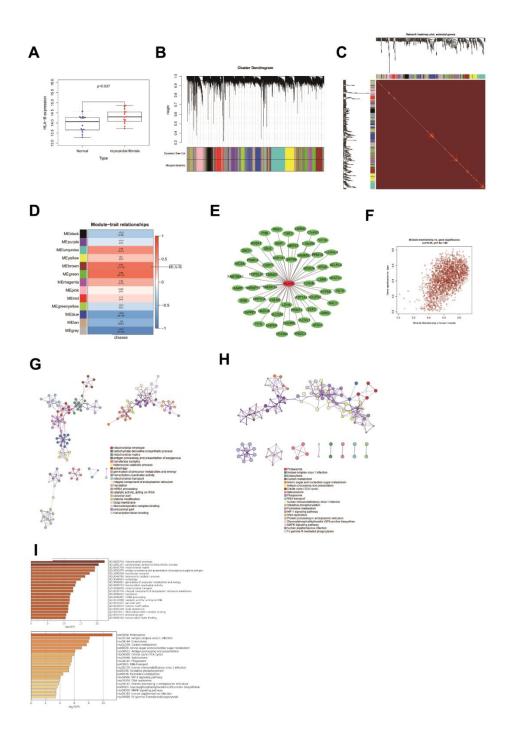
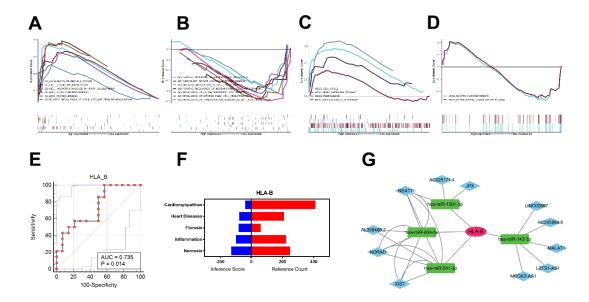
SUPPLEMENTARY FIGURES



Supplementary Figure 1. Differential expression analysis and WGCNA of the genes in the GSE74144 dataset. (A) A box diagram of HLA-B showing differential expression between the ventricular remodeling and control groups. (B) A repeated hierarchical clustering tree of all genes; HLA-B is in the brown module. (C) A dendrogram and heatmap showing all the genes. (D) The associations between clinical traits and the modules and the correlation between the brown module and ventricular remodeling is 0.67. (E) Interrelationships between HLA-B and the genes in the brown module. (F) Module membership in the brown module. (G) GO enrichment analysis of the brown module genes using Metascape. (H) KEGG analysis. (I) A heatmap showing GO and KEGG analyses using Metascape.



Supplementary Figure 2. Gene functional enrichment analysis of HLA-B by GSEA. (A, B) GO analyses by GSEA. (C, D) KEGG analyses by GSEA. (E) ROC curves of HLA-B. (F) Relationships between the ventricular remodeling group and the control group related to HLA-B, based on the CTD. (G) Predicting the ceRNA network mechanism of HLA-B using starBase.