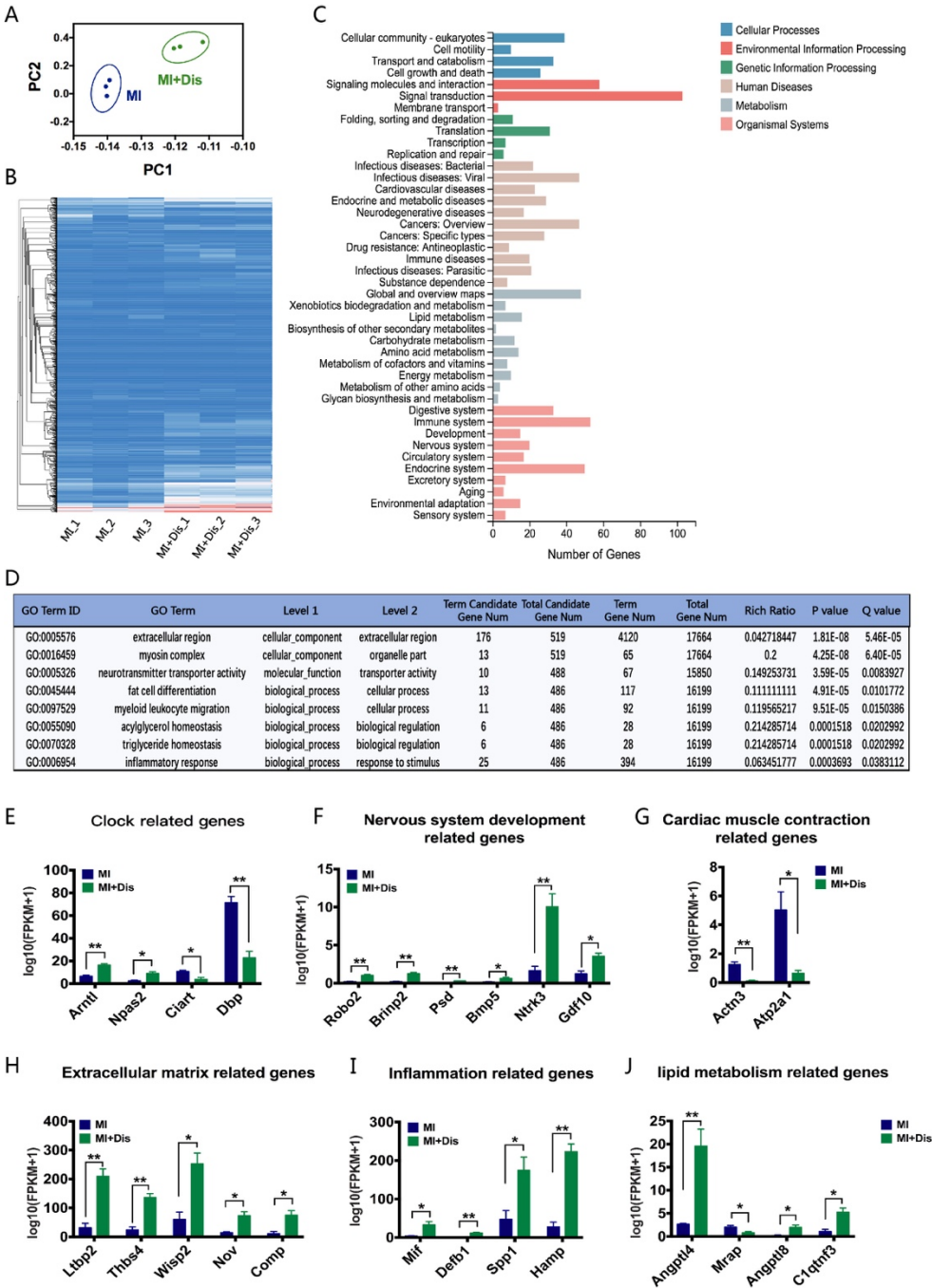# Supplemental Methods

RNA sequencing (RNA-Seq)

The ischemic myocardium of rats was quickly dissected and snap-frozen in liquid nitrogen for storage. The sample quality was assessed using an Agilent 2100 Bioanalyzer with a kit (Agilent RNA 6000 Nano Reagents Part 1), and samples with 28S/18S less than 1.0 or RQN (RNA quality number) less than 7.0 were discarded. Total RNA was enriched using magnetic beads with OligodT, and then a single-stranded circular DNA library was prepared for the following RNA-Seq. Briefly, the sequencing reads were mapped to the rat genome (Rattus_norvegicus, UCSC, rn6) using HISAT (Hierarchical Indexing for Spliced Alignment of Transcripts), and reads were also mapped to rat genes using Bowtie2 (version 2.2.5; -q --phred64 --sensitive –dpad 0 --gbar 99999999 --mp 1,1 --np 1 --score-min L,0,-0.1 -p 16 -k 200). To identify the gene expression levels of samples, Bowtie2 was used for mapping, and RSEM (version1.2.8; default) was used to calculate the expression level. To identify the differential gene expression between groups, the DEGseq2 algorithm was used with the predefined parameters "Fold Change ≥ 2 and Adjusted P-value (Q-value) ≤ 0.001". The Pheatmap function from the R software package was applied to depict these differentially expressed genes as a heatmap. Gene ontology (GO) enrichment and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment were analyzed using the phyper function from the R software package, and the P-value algorithm was given as follows:

$$P = 1 - \sum_{i=0}^{m-1} \frac{\binom{M}{i}\binom{N-M}{n-i}}{\binom{N}{n}}$$

The P-value was adjusted by FDR, and the adjusted P-value was designated as the Q-value. The significance level was set at an FDR ≤ 0.01. More details can be found in supplemental files.

Supplemental Figures

Supplementary Figure S1. Cardiac remodeling at the transcriptional level was aggravated by circadian disruption. Q-values < 0.05. PCA, Principal component analysis; KEGG, Kyoto Encyclopedia of Genes and Genome; GO, Gene Ontology; Q-value, FDR-adjusted P-value; FPKM, fragments per kilobase of transcript per million fragments mapped; $p^* < 0.05$, $p^{**} < 0.01$.

Supplementary Figure S2. Effects of ganglionic blockade on cardiac remodeling at the transcriptional level. $p^* < 0.05$, $p^{**} < 0.01$, $p^{***} < 0.001$.