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**Supplementary Figure 1.** The heat map of top 100 differentially expressed genes in coronary artery disease. Diagram presents the result of a two-way hierarchical clustering of 100 differentially expressed genes and samples. The clustering is constructed using the complete-linkage method together with the Euclidean distance. Each row represents a gene and each column, a sample. The gene clustering tree is shown on the right. The color scale illustrates the relative level of gene expression: red, below the reference channel; green, higher than the reference.

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**Supplementary Figure 2.** The protein-protein interaction network in coronary artery disease. Rhombus and ellipses represent the genes and proteins, respectively. The red and green colors represent up-regulation and down-regulation, respectively. The grey line indicates the interaction between gene and protein.