

Supplementary

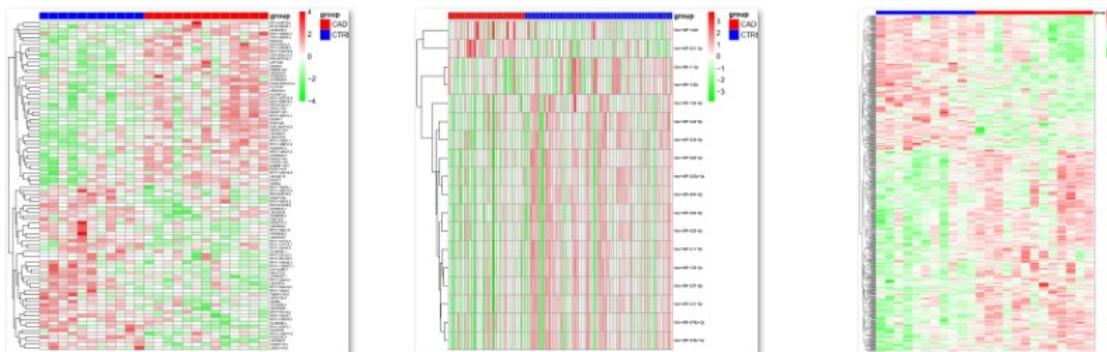


Figure S1 Heat maps. (A) A heat map for differentially expressed lncRNAs. (B) A heat map for differentially expressed miRNAs. (C) A heat map for differentially expressed mRNAs. miRNAs, lncRNAs, and mRNAs, are presented from left to right. The top red bar indicates the CAD samples while the blue bar indicates the control samples. CAD, coronary artery disease; lncRNA, long non-coding RNA; miRNA, micro RNA; mRNA, messenger RNA.

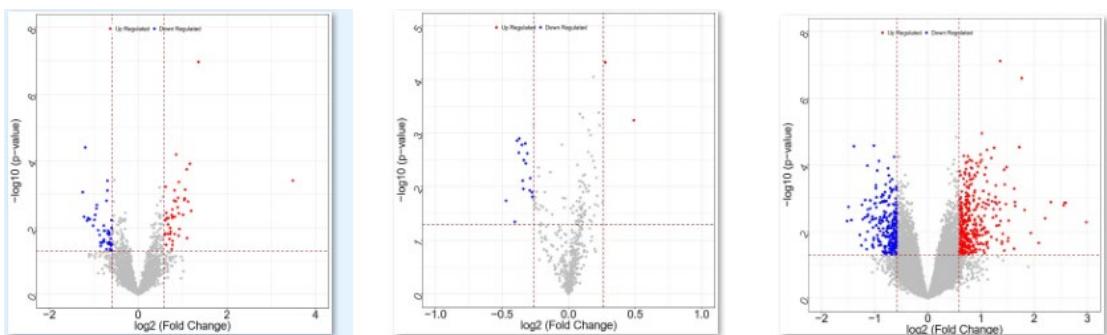


Figure S2 Volcano plots. (A) Volcano plot for differentially expressed lncRNAs. (B) Volcano plot for differentially expressed miRNAs. (C) Volcano plot for differentially expressed mRNAs. miRNAs, lncRNAs, and mRNAs, are displayed from left to right. Red indicates up-regulation, blue indicates down-regulation, and grey indicates no significant change in expression. lncRNA, long non-coding RNA; miRNA, micro RNA; mRNA, messenger RNA.

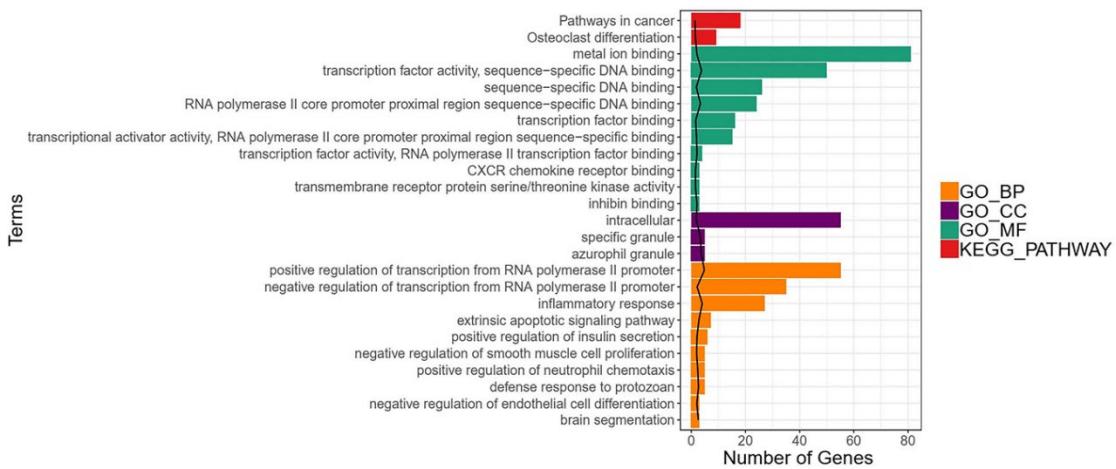


Figure S3 GO and KEGG pathway enrichment analysis. Black lines indicate $-\log_{10}(P \text{ value})$. Bar length indicates the number of enriched genes. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

Table S1 Go and KEGG pathway enrichment analysis of differential genes

Category	Term	Count	P value
KEGG_PATHWAY	hsa04380: Osteoclast differentiation	9	2.82E-02
KEGG_PATHWAY	hsa05200: Pathways in cancer	18	4.33E-02
GOTERM_MF	GO: 0003700~transcription factor activity, sequence-specific DNA binding	50	1.77E-04
GOTERM_MF	GO: 0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding	24	4.40E-04
GOTERM_MF	GO: 0001076~transcription factor activity, RNA polymerase II transcription factor binding	4	7.53E-03
GOTERM_MF	GO: 0034711~inhibin binding	3	8.38E-03
GOTERM_MF	GO: 0046872~metal ion binding	81	8.79E-03
GOTERM_MF	GO: 0001077~transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	15	1.16E-02
GOTERM_MF	GO: 0043565~sequence-specific DNA binding	26	1.32E-02
GOTERM_MF	GO: 0008134~transcription factor binding	16	2.39E-02
GOTERM_MF	GO: 0004675~transmembrane receptor protein serine/threonine kinase activity	3	2.79E-02
GOTERM_MF	GO: 0045236~CXCR chemokine receptor binding	3	2.79E-02
GOTERM_CC	GO: 0042582~azurophil granule	5	2.18E-04
GOTERM_CC	GO: 0042581~specific granule	5	4.50E-04
GOTERM_CC	GO: 0005622~intracellular	55	1.28E-02
GOTERM_BP	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	55	1.47E-05
GOTERM_BP	GO: 0006954~inflammatory response	27	9.45E-05
GOTERM_BP	GO: 0097191~extrinsic apoptotic signaling pathway	7	1.55E-03
GOTERM_BP	GO: 0042832~defense response to protozoan	5	2.23E-03
GOTERM_BP	GO: 0035284~brain segmentation	3	2.69E-03
GOTERM_BP	GO: 0090023~positive regulation of neutrophil chemotaxis	5	3.93E-03
GOTERM_BP	GO: 0000122~negative regulation of transcription from RNA polymerase II promoter	35	7.00E-03
GOTERM_BP	GO: 0032024~positive regulation of insulin secretion	6	7.58E-03
GOTERM_BP	GO: 0045602~negative regulation of endothelial cell differentiation	3	8.60E-03
GOTERM_BP	GO: 0048662~negative regulation of smooth muscle cell proliferation	5	1.08E-02

GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.