

Supplementary Fig.S1 Microarray quality control chart.

Data after normalization. X-axis: sample; Y-axis: log₂ expression value. Box plot showed the distribution of value data for the samples we selected was median-centered, indicating the data are normalized and cross-comparable. A for GSE5406, B for GSE26887, C for GSE42955 and D for GSE57338.

Supplementary Fig.S2 Display of the overview of pathway network from Reactome online.

Overview of the pathway network of 255 DEGs generated by online Reactome tool. The immune system, signal transduction and metabolism with red circle are the three most enriched categories. Immune system is connected with signal transduction by several pathways.

Supplementary Fig.S3 The topology property of the Cytoscape network.

(A) Degree of distribution; The number of nodes is plotted on y-axis as the node degree on x-axis. The distribution of clustering coefficient decreases as the node degree increases. The number of genes decreased as the node degree increased, reflecting the tendency to contain hub nodes. (B) Average clustering coefficient distribution; The average clustering coefficient is plotted on y-axis as a function of number of neighbours on x-axis. The distribution of clustering coefficient decreases as the node degree increases. The graph exhibits a decreasing tendency of average clustering coefficient as number of neighbours increases. The property follows the power law distribution and suggests a hierarchical organization of the network. (C) neighborhood connectivity distribution; The average neighbourhood connectivity is plotted on y-axis as number of neighbours on x-axis. The chart shows edges between low connected and highly connected nodes prevail in the network. (D) Topological coefficients; The distribution of topological coefficient is plotted on y-axis and the number of neighbours is plotted on x-axis. The graph indicates the tendency of the nodes in the network to have shared neighbors.

Supplementary Fig.S4 Network of seven hub genes

Hub gene located in the center of the network interacted with all the surrounding genes showed. Node size is related to proportional to the edge degree. Edge color suggests the significance according to p value (The brighter the color, the lower the p value). Red node suggests up-regulated genes and blue node suggests down-regulated genes.

Supplementary Table S1. Baseline information of samples from the four datasets.

The characteristic of the subjects enrolled in our study is displayed, including: age, sex, the stage of heart failure. Sampling spot and the way of sample preservation and RNA isolation are listed. Con: non-ischemic heart with normal heart function; ICM: ischemic cardiomyopathy; LV: left ventricle; LVEF: left ventricle ejection fraction; NYHA: New York Heart Association (heart function classification). None: no information was available. # $p>0.05$, there was no significant difference of age between the control and ICM group in GSE 5406. * $p<0.05$, the difference of age between the control and ICM group was statistically significant in GSE26887 and GSE57338.

Supplementary Table S2. List of the common DEGs of the four datasets.

255 differentially expressed genes (DEGs) were identified from four profile datasets, including 93 up-regulated genes and 162 down-regulated genes in ICM compared to normal human heart sample. Genes were arranged according to fold change from the largest to the smallest. Genes in bold represent the key DEGs appeared in PPI network.

Supplementary Table S3. List of DEGs involved in the top ten pathways.

A number of pathways were significantly enriched in the Reactome network analysis ($p<0.05$). Here we clearly present the 10 most significant pathways, the number of genes involved and the gene symbol.

Supplementary Table S4. Primer list of DEGs selected for RT-PCR.

Fig. S1

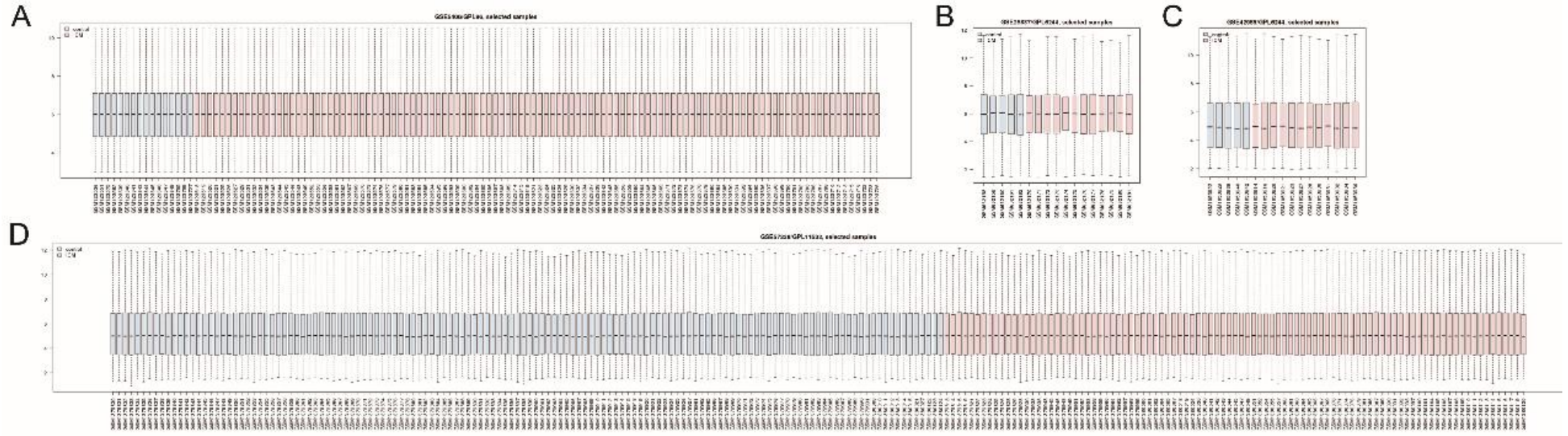


Fig. S2

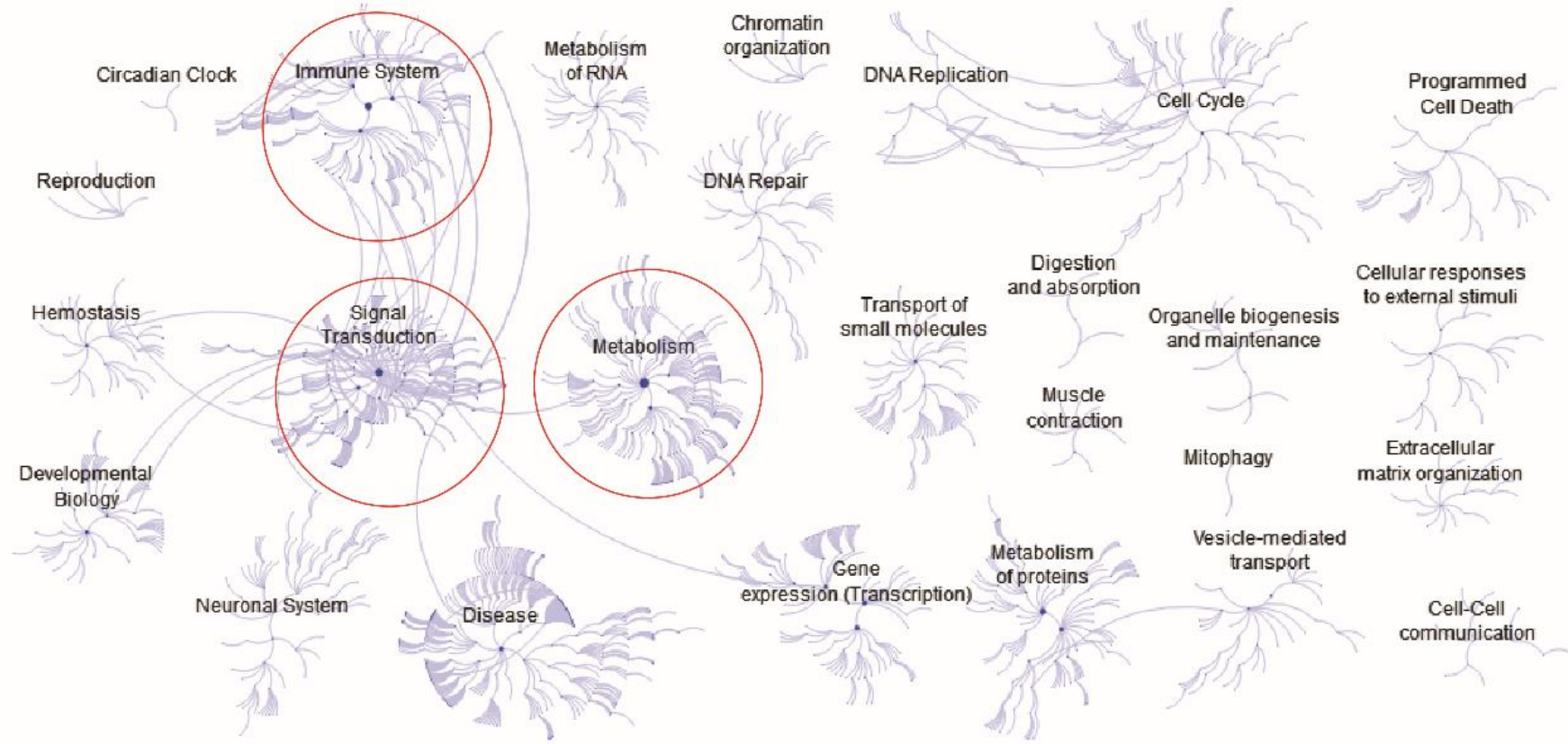


Fig. S3

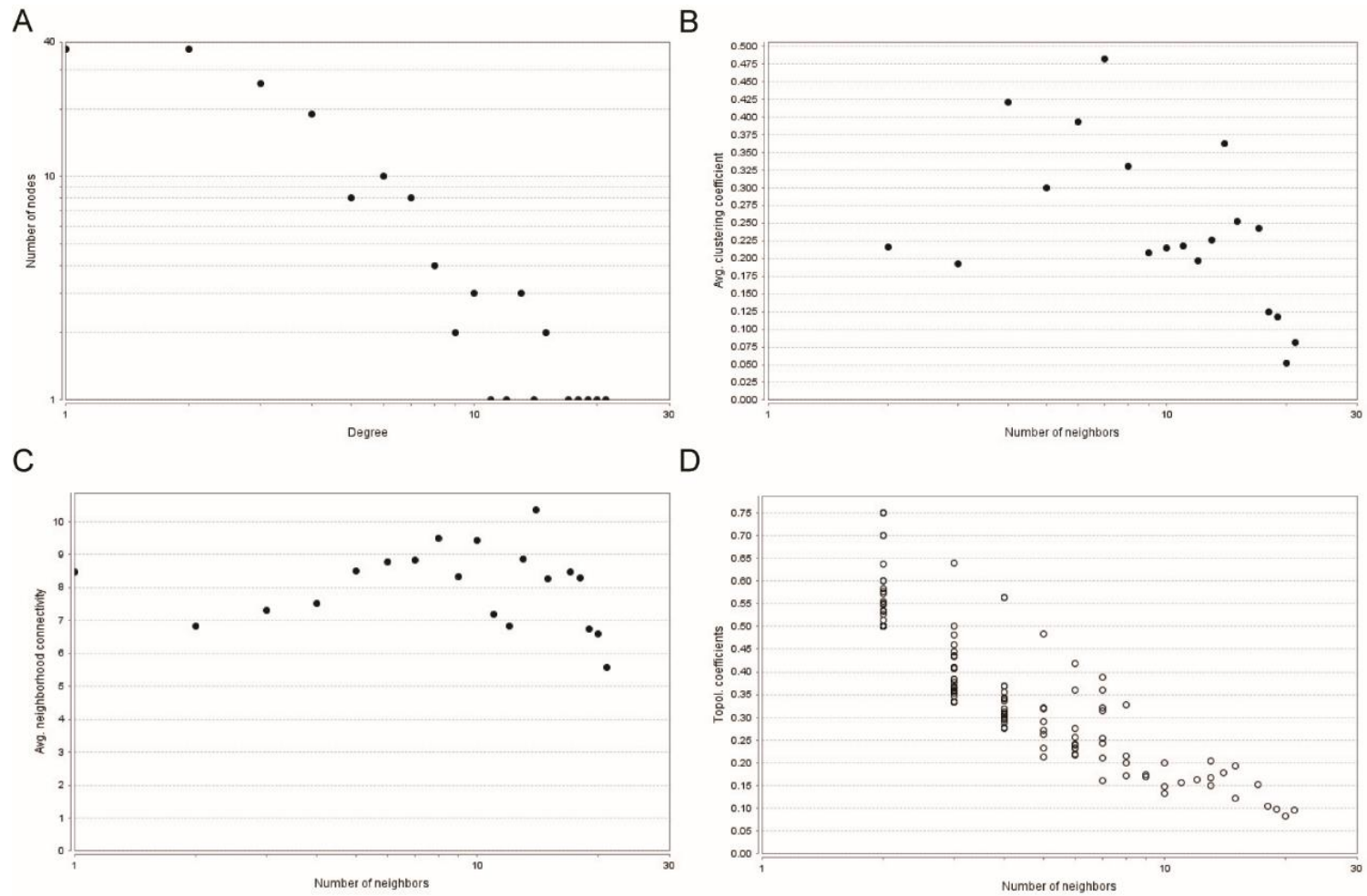


Fig. S4

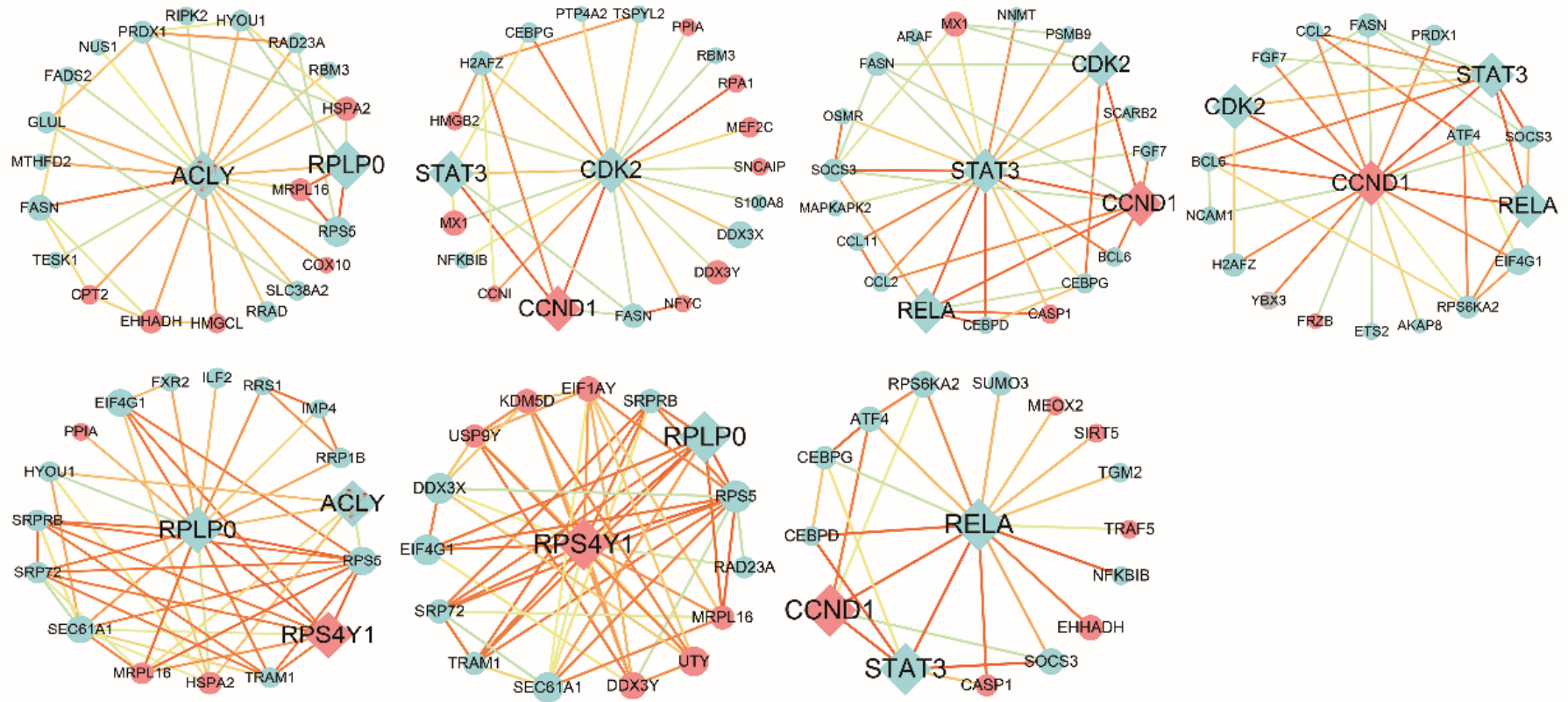


Table S1

	Number of Samples (n)	Cardiac area	Stage of heart failure	Age(year)	Male/female	Sample preservation	RNA isolation	Number of DEGs
GSE5406	Con (n=16)	Non-infarcted LV free wall	LVEF: 56±7%	(54±12)	None	snap-frozen in liquid nitrogen	Trizol (Invitrogen)	3840
	ICM (n=108)		NYHA classIII-IV LVEF: 14±8%	(57±12) #	None			
GSE26887	Con (n=5)	LV, vital and non-infarcted zone	normal LV function	48.4±1.2	2/3	snap frozen at -80°C	Trizol (Invitrogen)	5639
	ICM (n=12)		LVEF 27.6±1.9	60.4±4.3 *	12/0	Samples were immersed in RNAlater (QIAGEN GmbH) and stored at 4°C less than 24h before RNA extraction		
GSE42955	Con (n=5)	The apex of the LV	normal LV function	None	5/0	Stored at -80°C until the RNA extraction	Qiagen RNeasy Mini kit	2137
	ICM (n=12)		None		12/0			
GSE57338	Con (n=136)	LV free-wall tissue	normal LV function	49.4±1.3	74/62	Stored at -80°C until the RNA extraction	Qiagen RNeasy total RNA mini kit	10448
	ICM (n=95)		heart failure undergoing transplantation	59.1±0.7 *	81/14			

Table S3

Pathway name	Gene count	p Value	Genes involved
Cytokine Signaling	35	0.00035	<i>IFITM3</i> <i>CCL11</i> <i>CEBPD</i> <i>RPLP0</i> <i>ARAF</i> <i>IFI6</i> <i>FPR1</i> <i>IFIT1</i> <i>RELA</i> <i>RPS6KA2</i> <i>FGF7</i> <i>CCND1</i> <i>SOCS3</i> <i>CASP1</i> <i>CCL2</i> <i>HLA-DPA1</i> <i>NCAM1</i> <i>TRIM22</i> <i>MTA2</i> <i>IL13RA1</i> <i>IL15RA</i> ; <i>MEF2C</i> <i>RSAD2</i> <i>STAT3</i> <i>MX1</i> ; <i>OSMR</i> <i>PSMB9</i> <i>BCL6</i> <i>HLA-DPB1</i> <i>HNRNPF</i> <i>MAPKAPK2</i> <i>RIPK2</i> <i>PPIA</i> <i>KPNB1</i> <i>EIF4G1</i>
Interleukins Signaling	25	0.00132	<i>CCL11</i> <i>CEBPD</i> <i>RPLP0</i> <i>ARAF</i> <i>FPR1</i> <i>RELA</i> <i>SOCS3</i> <i>FGF7</i> <i>CCND1</i> <i>RPS6KA2</i> <i>CASP1</i> <i>CCL2</i> <i>NCAM1</i> <i>MTA2</i> <i>IL13RA1</i> <i>IL15RA</i> <i>MEF2C</i> <i>RIPK2</i> <i>STAT3</i> <i>OSMR</i> <i>PSMB9</i> <i>BCL6</i> <i>HNRNPF</i> <i>MAPKAPK2</i> <i>PPIA</i>
Neutrophil degranulation	16	0.01252	<i>DDX3Y</i> <i>PYGB</i> <i>SERPINA3</i> <i>DDX3X</i> <i>RAB3A</i> <i>AMD1</i> <i>FPR1</i> <i>ILF2</i> <i>ACLY</i> <i>SERPINB1</i> <i>CD59</i> <i>S100A9</i> <i>PPIA</i> <i>S100A8</i> <i>KPNB1</i> <i>SLC29A1</i>
Interferon Signaling	12	0.01542	<i>IFITM3</i> <i>SOCS3</i> <i>HLA-DPA1</i> <i>MX1</i> <i>IFI6</i> <i>NCAM1</i> <i>IFIT1</i> <i>TRIM22</i> <i>KPNB1</i> <i>HLA-DPB1</i> <i>RSAD2</i> <i>EIF4G1</i>
Unfolded Protein Response (UPR)	8	0.00002	<i>WFS1</i> <i>TSPYL2</i> <i>SEC61A1</i> <i>NFYC</i> <i>SRPRB</i> <i>CCL2</i> <i>HYOU1</i> <i>ATF4</i>
SRP-dependent cotranslational protein targeting to membrane	7	0.01941	<i>TRAM1</i> <i>SEC61A1</i> <i>SRP72</i> <i>RPS5</i> <i>RPLP0</i> <i>SRPRB</i> <i>PS4Y1</i>
Cellular Senescence	7	0.03672	<i>H2AFZ</i> <i>RPS6KA2</i> <i>MAPKAPK2</i> <i>CDK2</i> <i>STAT3</i> <i>ETS2</i> <i>RELA</i>
Regulation of cholesterol biosynthesis	6	0.00354	<i>NFYC</i> <i>FASN</i> <i>SEC24D</i> <i>KPNB1</i> <i>TM7SF2</i> <i>ACLY</i>
Toll Like Receptor Cascade	6	0.02007	<i>MEF2C</i> <i>RPS6KA2</i> <i>MAPKAPK2</i> <i>RIPK2</i> <i>RELA</i> <i>NFKBIB</i>
Senescence-Associated Secretory Phenotype (SASP)	5	0.01586	<i>H2AFZ</i> <i>RPS6KA</i> <i>CDK2</i> <i>STAT3</i> <i>RELA</i>

Table S4.

Primer list of DEGs selected for RT-PCR.

EIF1AY-	CCCACCTGCTGCATCTTAGTTC	SERPINA3-	AAAGTCACCAATCCCAAGCAAG
EIF1AY-	GCTTCCAATCGTCCATTTCCC	SERPINA3-	GGATAAGCAGACAGGGCCACAC
RPS4Y1-	TCGACAGGTCCCCACAAGC	MYOT-F	TTCCCTATTCCTGCCCCTTCC
RPS4Y1-	TGCGGTGAACAGCAAAACG	MYOT-R	TGTGCTTGCCTGTCCATCTACC
DDX3Y-	CTCATAAAGCGCAGGCACAC	CD163-F	CCCCACAAAAGCCACAACAGG
DDX3Y-	AAGAACAGGTCCGCAGAAGG	CD163R	GCCAACAGAACAACCCCAAGGA
USP9Y-	GAAGAGCCTGCATTCCACATAC	FCN3-F	CTGGCTGGGAAATGAGAAT
USP9Y-	CCACTCACAGCCTCATCCATAA	FCN3-R	CGCATAGTGGGCGAAAGTA
UTY-F	AACTAAGTGGTTGGGAGCGGG	S100A8-F	GTTTTTCAGGTGGGGCAAGTC
UTY-R	CATCTGGGAAACTACAGGGAAGG	S100A8-R	ACTGAGGACACTCGGTCTCT

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