

Table S1. GO biological processes analysis of DE lncRNAs co-location of targeted DE mRNAs (15 terms).

Term	Database	ID	Input number	Background number	P-Value	Corrected P-Value	Input
protein binding	Gene Ontology	GO:0005515	7	11779	0.001296	0.019351	<i>SQSTM1</i> <i>RRAD</i> <i>ZNF148</i> <i>ATF3</i> <i>TNNI1</i> <i>SERPINE1</i> <i>CANX</i>
regulation of striated muscle contraction	Gene Ontology	GO:0006942	1	8	0.001833	0.019351	<i>TNNI1</i>
negative regulation of smooth muscle cell migration	Gene Ontology	GO:0014912	1	13	0.00285	0.019459	<i>SERPINE1</i>
apolipoprotein binding	Gene Ontology	GO:0034185	1	16	0.00346	0.019573	<i>CANX</i>
skeletal muscle contraction	Gene Ontology	GO:0003009	1	26	0.00549	0.022185	<i>TNNI1</i>
regulation of I-kappaB kinase/NF-kappaB signaling	Gene Ontology	GO:0043122	1	29	0.006099	0.022361	<i>SQSTM1</i>
negative regulation of endothelial cell apoptotic process	Gene Ontology	GO:2000352	1	31	0.006504	0.022996	<i>SERPINE1</i>
calcium channel regulator activity	Gene Ontology	GO:0005246	1	35	0.007314	0.023411	<i>RRAD</i>
cardiac muscle contraction	Gene Ontology	GO:0060048	1	44	0.009136	0.024652	<i>TNNI1</i>
cellular response to amino acid starvation	Gene Ontology	GO:0034198	1	44	0.009136	0.024652	<i>ATF3</i>
skeletal muscle cell differentiation	Gene Ontology	GO:0035914	1	45	0.009338	0.024652	<i>ATF3</i>
gluconeogenesis	Gene Ontology	GO:0006094	1	45	0.009338	0.024652	<i>ATF3</i>
small GTPase mediated signal transduction	Gene Ontology	GO:0007264	1	94	0.019201	0.03553	<i>RRAD</i>
muscle contraction	Gene Ontology	GO:0006936	1	105	0.021403	0.037173	<i>TNNI1</i>
cellular response to lipopolysaccharide	Gene Ontology	GO:0071222	1	158	0.031953	0.047569	<i>SERPINE1</i>

Table S2. KEGG analysis of DE lncRNAs co-location of targeted DE mRNAs (15 pathways).

Term	Database	ID	Input number	Background number	P-Value	Corrected P-Value	Input
Cellular senescence	KEGG PATHWAY	hsa04218	2	160	0.000466	0.019351	<i>SQSTM1</i> <i>SERPINE1</i>
Mitophagy - animal	KEGG PATHWAY	hsa04137	1	65	0.013374	0.030091	<i>SQSTM1</i>
p53 signaling pathway	KEGG PATHWAY	hsa04115	1	72	0.014783	0.031986	<i>SERPINE1</i>
Thyroid hormone synthesis	KEGG PATHWAY	hsa04918	1	74	0.015185	0.031986	<i>CANX</i>
Antigen processing and presentation	KEGG PATHWAY	hsa04612	1	77	0.015789	0.032564	<i>CANX</i>
Complement and coagulation cascades	KEGG PATHWAY	hsa04610	1	79	0.01619	0.032711	<i>SERPINE1</i>
AGE-RAGE signaling pathway in diabetic complications	KEGG PATHWAY	hsa04933	1	100	0.020402	0.036393	<i>SERPINE1</i>
Chagas disease (American trypanosomiasis)	KEGG PATHWAY	hsa05142	1	103	0.021003	0.036801	<i>SERPINE1</i>
HIF-1 signaling pathway	KEGG PATHWAY	hsa04066	1	109	0.022203	0.037897	<i>SERPINE1</i>
Osteoclast differentiation	KEGG PATHWAY	hsa04380	1	128	0.025994	0.042164	<i>SQSTM1</i>
Apelin signaling pathway	KEGG PATHWAY	hsa04371	1	137	0.027785	0.044011	<i>SERPINE1</i>
Fluid shear stress and atherosclerosis	KEGG PATHWAY	hsa05418	1	139	0.028182	0.044248	<i>SQSTM1</i>
Phagosome	KEGG PATHWAY	hsa04145	1	152	0.030764	0.047097	<i>CANX</i>
Hippo signaling pathway	KEGG PATHWAY	hsa04390	1	154	0.03116	0.047097	<i>SERPINE1</i>
Necroptosis	KEGG PATHWAY	hsa04217	1	162	0.032745	0.047772	<i>SQSTM1</i>
Protein processing in endoplasmic reticulum	KEGG PATHWAY	hsa04141	1	165	0.033339	0.047772	<i>CANX</i>
Human T-cell leukemia virus 1 infection	KEGG PATHWAY	hsa05166	1	219	0.043973	0.060462	<i>CANX</i>

Table S3. GO biological processes analysis of DE lncRNAs co-expression of targeted DE mRNAs (15 terms).

Term	Database	ID	Input number	Background number	P-Value	Corrected P-Value	Input
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protein phosphorylation	Gene Ontology	GO:0006468	15	451	6.12E-07	7.71E-05	<i>SQSTM1 TBK1 BUB1B ERCC2 SIK2 PIK3CD GRK3 HSPB8 MYLK HIPK3 MAPK1 CFL1 IRAK2 DAPK2 NRBP1</i>
positive regulation of NF-kappaB transcription factor activity	Gene Ontology	GO:0051092	9	159	1.98E-06	0.00017554	<i>TRIM37 MAP3K7 IL6 TFRC CAPN3 FLOT1 FLOT2 IRAK2 CLU</i>
positive regulation of gene expression	Gene Ontology	GO:0010628	12	391	1.79E-05	0.00118926	<i>UXT TFRC ACTC1 PIK3CD WARS IL6 MAPK1 TNRC6B CLU LMNA CD3E UBR5</i>
muscle contraction	Gene Ontology	GO:0006936	6	105	9.96E-05	0.003907848	<i>TNNT3 MYH7 MYLK TLN1 SLMAP TNNI1</i>
glucose transmembrane transport	Gene Ontology	GO:1904659	3	24	0.000742	0.015709511	<i>SLC5A10 MFSD4B SLC2A12</i>
positive regulation of smooth muscle cell proliferation	Gene Ontology	GO:0048661	4	58	0.000769	0.01600441	<i>IL6 NR4A3 NAMPT STAT1</i>
cellular response to lipopolysaccharide	Gene Ontology	GO:0071222	6	158	0.000811	0.016444566	<i>UXT ANKRD1 CD274 DAB2IP IL6 SERPINE1</i>
skeletal muscle contraction	Gene Ontology	GO:0003009	3	26	0.000917	0.016882827	<i>TNNT3 MYH7 TNNI1</i>
ubiquitin-dependent protein catabolic process	Gene Ontology	GO:0006511	8	292	0.000924	0.016882827	<i>SQSTM1 BUB1B USP45 USP14 SPSB2 RNF34 UHRF1 PSMC6</i>
regulation of myoblast differentiation	Gene Ontology	GO:0045661	2	6	0.001186	0.019716713	<i>CAPN3 FLOT2</i>
activation of MAPK activity	Gene Ontology	GO:0000187	5	123	0.001656	0.023049353	<i>IRAK2 PHB2 MAPK1 PLCE1 MAP3K7</i>
regulation of striated muscle contraction	Gene Ontology	GO:0006942	2	8	0.001889	0.023559435	<i>TNNT3 TNNI1</i>
lipid biosynthetic process	Gene Ontology	GO:0008610	2	14	0.004909	0.041627664	<i>AGPS ACSL1</i>
regulation of cell population proliferation	Gene Ontology	GO:0042127	5	169	0.006153	0.046561629	<i>CLU TFRC SQLE STAT1 STAT6</i>
phosphatidylinositol phosphate binding	Gene Ontology	GO:1901981	2	16	0.006204	0.046561629	<i>RNF34 DENND1A</i>

Table S4. KEGG analysis of DE lncRNAs co-expression of targeted DE mRNAs (15 pathways).

Term	Database	ID	Input number	Background number	P-Value	Corrected P-Value	Input
AGE-RAGE signaling pathway in diabetic complications	KEGG PATHWAY	hsa04933	6	100	7.71E-05	0.003296	STAT1 PIK3CD IL6 MAPK1 PLCE1 SERPINE1
Toll-like receptor signaling pathway	KEGG PATHWAY	hsa04620	6	104	9.47E-05	0.003843	TBK1 STAT1 PIK3CD MAP3K7 IL6 MAPK1
HIF-1 signaling pathway	KEGG PATHWAY	hsa04066	6	109	0.000121	0.004575	TFRC PFKFB3 PIK3CD IL6 MAPK1 SERPINE1
Thyroid hormone signaling pathway	KEGG PATHWAY	hsa04919	6	119	0.000191	0.006134	MYH7 STAT1 PIK3CD MAPK1 PLCE1 SIN3A
NOD-like receptor signaling pathway	KEGG PATHWAY	hsa04621	7	178	0.000245	0.007019	STAT1 TBK1 CTSB NAMPT MAP3K7 IL6 MAPK1
Osteoclast differentiation	KEGG PATHWAY	hsa04380	6	128	0.000278	0.007837	SQSTM1 STAT1 PIK3CD CSF1R MAP3K7 MAPK1
Apoptosis	KEGG PATHWAY	hsa04210	6	136	0.00038	0.009668	PIK3CD CTSB DAB2IP MAPK1 LMNA LAMB2
Cellular senescence	KEGG PATHWAY	hsa04218	6	160	0.000863	0.016841	SQSTM1 PIK3CD HIPK3 IL6 MAPK1 SERPINE1
Th17 cell differentiation	KEGG PATHWAY	hsa04659	5	107	0.000914	0.016883	IL6 STAT6 MAPK1 CD3E STAT1
Fructose and mannose metabolism	KEGG PATHWAY	hsa00051	3	33	0.001732	0.023432	ARL1 PFKFB3 GMDS
Insulin signaling pathway	KEGG PATHWAY	hsa04910	5	137	0.002604	0.029681	MAPK1 PIK3CD PRKAR1A FLOT2 FLOT1
ECM-receptor interaction	KEGG PATHWAY	hsa04512	4	86	0.003049	0.033334	AGRN TNXB CD47 FRAS1
IL-17 signaling pathway	KEGG PATHWAY	hsa04657	4	93	0.003989	0.03783	IL6 MAPK1 MAP3K7 TBK1
Jak-STAT signaling pathway	KEGG PATHWAY	hsa04630	5	162	0.005187	0.042965	IL6 STAT6 STAM PIK3CD STAT1
T cell receptor signaling pathway	KEGG PATHWAY	hsa04660	4	103	0.005646	0.045355	MAPK1 PIK3CD CD3E MAP3K7

Table S5. The primers used for the validation of lncRNAs and mRNAs.

Primer Name	Sequence(5'to3')	Tm/°C	Product Size/bp
<i>GAPDH</i> -F	GCCAAAAGGGTCATCATCTC	53.6	287
<i>GAPDH</i> -R	GTAGAGGCAGGGATGATGTTC	55.2	
<i>ZNF148</i> -F	AGTCGGTGCTTCAAGATCGG	60.11	132
<i>ZNF148</i> -R	TCACTGTCTCCTCATGGACC	58.44	
<i>STAT6</i> -F	CAGCCCAGATATGGTGTCCC	59.89	108
<i>STAT6</i> -R	TCCTGGAAGGCTGACAACAC	59.89	
<i>ACTB</i> -F	CTCTTCCAGCCCTCCTTCCT	59.32	177
<i>ACTB</i> -R	GGCCGTGATCTCCTTCTGCAT	60.25	
<i>CMYA5</i> -F	GCCACTGAGACCTACACT	53.83	175
<i>CMYA5</i> -R	CTTCACTCTGTTCACTTGTC	50.35	
<i>FHOD3</i> -F	TTCCACCTCTTCTCCTATGA	51.58	137
<i>FHOD3</i> -R	CGGAAGTTGTAAGGTTCAGA	51.58	
LNC_000040-F	CGAATCTCCTCGTCCTGCTC	58.05	158
LNC_000040-R	ATTGTCCCAAGCAGCGGTAA	57.05	
LNC_004737-F	GCAAGTGCATTAAGGGCTCG	57.26	169
LNC_004737-R	TGGGTTCATTAAGCTCGCGT	56.95	
LNC_006333-F	ACGGGTACTGGCATTGTT	57.06	196
LNC_006333-R	AAGGGAAAGTTGGGCACACA	57.28	
LNC_008264-F	TTCTAATTCGCAACCTGAGA	50.43	163

LNC_008264-R	CAAGCCCTAGTAGCCATT	51.73	
LNC_002605-F	GCCTCTGATTCACTTGACT	51.58	
LNC_002605-R	AATGCTGCTGGACTGTTC	52.67	205
