Supplementary

Table S1 Information of the screened drugs

Drug	Biological activity	Target (IC ₅₀)	Molecular genetics
Cyclophosphamide	Immunosuppressant	AChE (511 μM)	Cyclophosphamide promotes the proliferation inhibition of mouse ovarian granulosa cells and premature ovarian failure by activating the IncRNA-Meg3-p53-p66Shc pathway
Zoledronate	Bisphosphonate		Zoledronic acid inhibits osteoclast differentiation and function through the regulation of NF- κ B and JNK signaling pathways
Fulvestrant	Antiestrogen	Estrogen receptor (9.4 nM)	Fulvestrant-treated breast cancer cells increased the expression of IncRNA H19 and regulated drug resistance
JAK1	TYK2/JAK1 inhibitor	Tyk2 (6 nM)	JAK1 shows anti-inflammatory effect by regulating the expression of related TYK2/JAK1-regulated genes, as well as the formation of Th1, Th2, and Th17 cells
Sinularin	Natural products	SK-HEP-1 cells (10 μM)	Sinularin, an Anti-Cancer Agent-Causing Mitochondria-Modulated Apoptosis and Cytoskeleton Disruption in Human Hepatocellular Carcinoma
Leflunomide	Pyrimidine synthesis inhibitor	Protein tyrosine kinases (30–100 mM)	Leflunomide prevents the expansion of activated and autoimmune lymphocytes by interfering with cell cycle progression due to insufficient rUMP production and utilizing mechanisms involving p53
XAV939	Tankyrase inhibitor	TNKS1 (5 nM); TNKS2 (2 nM); ARTD2 (479 nM); ARTD1 (5,500 nM)	XAV-939 inhibited Wnt/ β -catenin signaling and promoted the expression of SFRP3 and SFRP4
BMS-345541	Selective inhibitor of the catalytic subunits of IKK	IKK-1 (4 μM); IKK-2 (0.3 μM)	BMS-345541 inhibited LPS-stimulated tumor necrosis factor- α , interleukin-1 β , interleukin-8 and interleukin-6 in THP-1 cells
Entinostat	Selective class I HDAC inhibitor	HDAC1 (243 nM); HDAC2 (453 nM); HDAC3 (248 nM)	Entinostat can induce autophagy and apoptosis
BMS-754807	IGF-1R/IR inhibitor	IR (1.7 nM); IGF-1R (1.8 nM)	BMS-754807 inhibits the activities of IGF-1R and IR by inhibiting the catalytic domain of IGF-1R, and induces apoptosis of tumor cells
Cytochalasin-b	Cell-permeable mycotoxin	F-actin, with Mg^{2+} (2.2 nM); F-actin, with Mg^{2+}/K^{+} (1.4 nM)	Cytochalasin B binds to the barbed ends of actin filaments, disrupting actin polymer formation and preventing cell migration
Linifanib	Multi-target inhibitor of VEGFR and PDGFR family	PDGFRβ (66 nM); FLT3 (4 nM)	Linifanib is a specific miR-10b inhibitor that blocks miR-10b biogenesis

 Table S2 The primers for qRT-PCR

Gene	Primer sequence (5'-3')	Fragment length (bp)	Annealing temperature (°C)
Nova1			
M-Nova1-S	CACAGCAGGTCTGATAATAGGGAA	257	60
M-Nova1-A	GATTGGAATTTGCCACTGGAC		60
Trib3			
M-Trib3-S	CTCTTCCGGCAGATGGCTAG	111	60
M-Trib3-A	CAGCTTCGTCCTCTCACAGTTG		60
UQCRH			
M-UQCRH-S	AGGACGAACGAAAGATGCTCAC	165	60
M-UQCRH-A	ACCGGGAAGACACGCGATT		60
Psmb5			
M-Psmb5-S	CAATAAGGAACGCATCTCGGT	291	60
M-Psmb5-A	CTGTAGGTGGCTTGGTAGATGG		60
dio3os			
M-dio3os-S	GTACAGGGGAGCCCACTTTC	103	60
M-dio3os-A	ATGCATCTGCTGAACAGGCT		60
Aox1			
M-Aox1-S	ACAGCATAAACCCAGCCCTTG	143	60
M-Aox1-A	GGCAGGAATCTTGTATTGGTTTG		60
Mfap4			
M-Mfap4-S	TGGCTATACCCTCTACGTGGCT	187	60
M-Mfap4-A	GTAGAAACCGTTGAGATTGGCG		60
Abca9			
M-Abca9-S	TGTGGTGGATCTGGGACGTGT	287	60
M-Abca9-A	CTGAATGGTCTTTGTGCTCTTTTGT		60
Ackr1			
M-Ackr1-S	GGGAACTGTCTGTATCCGGTG	261	60
M-Ackr1-A	CCAGTGGAAGAAAGGTCTGAGAAT		60

 Table S3 Positive correlations of upregulated genes

Table 55 Fositive correlations of upregulated genes						
LNCRNA	mRNA	Cor	P value			
C5orf66-AS2	CATSPER3	0.509696	1.47E-10			
C5orf66-AS2	C5orf66	0.707206	0			
LNC-SPARCL1-1	IGSF21	0.608896	1.78E-15			
LNC-SPARCL1-1	ANTXR1	0.549008	2.6E-12			
LNC-SPARCL1-1	RFX8	0.50423	2.48E-10			
LNC-SPARCL1-1	DSPP	0.89977	0			
LNC-SPARCL1-1	DMP1	0.889198	0			
LNC-SPARCL1-1	SPP1	0.515024	8.78E-11			
LNC-SPARCL1-1	ANKH	0.515271	8.57E-11			
LNC-SPARCL1-1	SPOCK1	0.508871	1.59E-10			
LNC-SPARCL1-1	SPARC	0.511337	1.26E-10			
LNC-SPARCL1-1	BGN	0.52355	3.76E-11			
LNC-SPARCL1-1	COL5A1	0.523121	3.93E-11			
LNC-SPARCL1-1	HTRA1	0.517772	6.7E-11			
LNC-SPARCL1-1	DACT1	0.50686	1.93E-10			
LNC-SPARCL1-1	ITGA11	0.508346	1.68E–10			

 ${\bf Table \ S4} \ {\rm Negative \ correlations \ of \ downregulated \ genes}$

LNCRNA	mRNA	Cor	P value	LNC-SPARCLI-I	GENPX	-0.49062	8.72677E-10
HCG23	MRPL15	-0.41402	4.05359E-07	LNC-SPARCL1-1	LRRC45	-0.40081	1.01171E-06
HCG23	DNASE2	-0.40578	7.20416E-07	LNC-SPARCL1-1	NKG7	-0.4738	3.83715E-09
		_0 /1552	3.64601E_07				
DI0303		-0.41552	1.77705E 07				
010305	UQCRH	-0.42547	1.77705E-07	Table S6 Positive co	rrelations of do	ownregulated ge	nes
DIO3OS	TRIB3	-0.40021	1.05369E-06	LNCRNA	mRNA	Cor	P value
FZD10-DT	PRDX1	-0.42051	2.5499E-07	HCG23	ATP8B2	0.5000602	3.66569E-10
FZD10-DT	TAF13	-0.41259	4.48652E-07	HCG23	CADM3	0.52913812	2.13465E-11
FZD10-DT	WDR77	-0.43712	7.44162E-08	HCG23	ABI3BP	0.502657558	2.87427E-10
FZD10-DT	ATP5PB	-0.46532	7.85466E-09	HCG23	ADCY5	0.548352468	2.79643E-12
FZD10-DT	MTHFD2	-0.45937	1.28381E-08	HCG23	TSBP1	0.892610128	0
-ZD10-DT	PSMB5	-0.40872	5.87782E-07	HCG23	BTNL2	0.659407047	0
ZD10-DT	EIF2S1	-0.40906	5.74165E-07	HCG23	KHDRBS2	0.522317301	4.26135E-1 ⁻
ZD10-DT	SLIRP	-0.42985	1.2859E-07	HCG23	TCEAL7	0.52108787	4.81897E-1 ⁻
	ΔΤΡ5ΜΡΙ	_0 /1513	3 7/811E_07	HCG23	C12orf/2	0 5058/5005	2 126/1E_1
		0.40202	0.19190E 07	110020		0.5000-5000	7 400055 10
	PIGW	-0.40393	6.16169E-07	HCG23		0.53927766	7.42095E-12
-2010-01	CCDC43	-0.43319	1.00186E-07	HCG23	PGNX1	0.568192021	2.97984E-13
-ZD10-DT	PHB	-0.41705	3.26825E-07	HCG23	MEG9	0.530534476	1.84941E-1
ZD10-DT	NME1	-0.46377	8.93715E-09	HCG23	MFAP4	0.530668393	1.8241E-11
ZD10-DT	CCDC47	-0.4302	1.25269E-07	HCG23	CCL14	0.513876728	9.81619E-1
ZD10-DT	PSMD12	-0.43357	9.73759E-08	HCG23	ABCA9	0.528933815	2.17981E-1
ZD10-DT	NOL11	-0.45425	1.94502E-08	HCG23	ADAM33	0.502315304	2.96823E-10
ZD10-DT	C17orf58	-0.4212	2.4263E-07	HCG23	CLEC17A	0.544515069	4.24016E-12
ZD10-DT	ATP5PD	-0.40232	9.12955F-07	HCG23	NIBAN3	0.524990576	3.25595F_1
	FAM210A	-0 10021	5 67016E_07		ΔΟΥ1	0 540285704	2 52500E 1
		-0.40924				0.049200/94	1 545005
INC-FUXU1-2	SNURA/3B	-0.43636	1.88089E-08		ANKRU30A	0.50918/22	1.54538E-1(
_NC-FOXO1-2	UQCRH	-0.4335	9.78491E-08	DIO3OS	NOVA1	0.533113982	1.41651E-1
NC-FOXO1-2	ATP5PB	-0.42252	2.20455E-07	DIO3OS	DIO3	0.745693945	0
NC-FOXO1-2	JTB	-0.41076	5.09806E-07	FZD10-DT	AHNAK	0.50341473	2.67651E-10
_NC-FOXO1-2	TIMM17A	-0.4139	4.08965E-07	FZD10-DT	FZD10	0.826659645	0
NC-FOXO1-2	SNRPE	-0.49511	5.79659E-10	FZD10-DT	STRA6	0.53572286	1.07914E-1
NC-FOXO1-2	SF3B6	-0.45021	2.68805E-08	LNC-FOXO1-2	IL1R1	0.642097678	0
NC-FOXO1-2	SAP30	-0.42708	1.57883E-07	LNC-FOXO1-2	ARHGAP24	0.515107207	8.70422E-1
NC-FOXO1-2	COX7C	-0.4345	9.07874E-08	LNC-FOXO1-2	SFRP2	0.561513974	6.43929E-13
NC-FOXO1-2	LIOCBO	-0 46326	9.32172E-09	I NC-FOXO1-2	FBF1	0 509436091	1 50887E-1(
	SNORA80D	_0 40167	9.54302E_07		ΔΚΔΡ12	0 510085168	1 41751E_1
		-0.40107	9.545022-07			0.510005100	
	RPA3	-0.40821	6.0921E-07		LRRC32	0.524547344	3.40505E-1
_NC-FOXO1-2	NDUFA4	-0.42578	1.73721E-07	LNC-FOXO1-2	ADRA2A	0.544269747	4.35385E-12
NC-FOXO1-2	COX7B	-0.46491	8.12856E-09	LNC-FOXO1-2	ACACB	0.527895508	2.42393E-1
NC-FOXO1-2	NDUFA1	-0.44568	3.84136E-08	LNC-FOXO1-2	LHFPL6	0.528704263	2.23164E-1
_NC-FOXO1-2	RPL30	-0.41047	5.20268E-07	LNC-FOXO1-2	FOXO1	0.757753107	0
NC-FOXO1-2	RIDA	-0.45019	2.69164E-08	LNC-FOXO1-2	MEG3	0.522486575	4.18963E-1
NC-FOXO1-2	COX6C	-0.45814	1.42025E-08	LNC-FOXO1-2	CRISPLD2	0.510221869	1.39897E-1
NC-FOXO1-2	MRPL13	-0.41568	3.6045E-07	LNC-FOXO1-2	NLRP1	0.528264031	2.3344E-11
_NC-FOXO1-2	DMAC1	-0.42007	2.63322E-07	LNC-FOXO1-2	MYH13	0.537080137	9.35874E-1;
NC-FOXO1-2	TXN	-0 43712	7 43997E_08	INC-FOX01-2	TSH72	0 580477754	6 88338E-1
	TIMM8B	_0 //312	4 68937E_08		BOC	0 520804034	4 91309E_1
		-0.44312	4.00937E-00	LINC-IMIMD-4	BUC	0.520694034	4.91309E-1
	AIG101	-0.4245			EPHB3	0.005335209	4.15223E-10
NC-FOXO1-2	GPN3	-0.40334	8.51404E-07	LNC-MMD-4	HLF	0.855960113	0
NC-FOXO1-2	RN7SL1	-0.43083	1.19552E-07	LNC-MMD-4	GNG7	0.508352811	1.67414E-10
NC-FOXO1-2	ERH	-0.40015	1.05786E-06	LNC-MMD-4	ZNF784	0.50673934	1.95314E-10
NC-FOXO1-2	SLIRP	-0.40592	7.13717E-07	LNC-TMEM106C-6	RAPGEF3	0.531315537	1.70637E-1
NC-FOXO1-2	SNORD3A	-0.40375	8.28049E-07	LNC-TMEM106C-6	SLC48A1	0.562447768	5.78648E-1
NC-FOXO1-2	OXLD1	-0.41169	4.77676E-07				
NC-FOXO1-2	MICOS13	-0.44261	4.87753E-08				
NC-F0X01-2	RPS19RP1	-0.42813	1 46069E-07				
		0.46835	6.00301E.00				
		-0.40005	0.09391E-09				
INC-MIMD-4	RAB42	-0.40005	1.06456E-06				
NC-MMD-4	LRP8	-0.40343	8.46545E-07				
NC-MMD-4	DEPDC1	-0.41686	3.31447E-07				
.NC-MMD-4	C1orf43	-0.40516	7.51865E-07				
NC-MMD-4	CCT3	-0.41465	3.87654E-07				
NC-MMD-4	EPRS1	-0.41872	2.90195E-07				
NC-MMD-4	BPNT1	-0.42119	2.42766E-07				
NC-MMD-4	BROX	-0.40179	9.46227E-07				
_NC-MMD-4	CNIH4	-0.41761	3.14049E-07				
NC-MMD-4	TXNDC9	-0.40578	7.20666F-07				
		_0 /0702	6 61069E 07				
		-0.40703	5.01000E-U/				
INC-IVIIVID-4	NOP10	-0.44087	0.00341E-08				
	10107-1	o :o	0.075505				
NC-MMD-4	KNSTRN	-0.42335	2.07552E-07				
_NC-MMD-4 _NC-MMD-4	KNSTRN EIF3J	-0.42335 -0.40473	2.07552E-07 7.74242E-07				

Table S5 Negative correlations of upregulated genes

LNCRNA	mRNA	Cor	P value
LNC-SPARCL1-1	PLA2G2D	-0.4471	3.4357E-08
LNC-SPARCL1-1	LCK	-0.43086	1.19272E-07
LNC-SPARCL1-1	CD48	-0.40328	8.55037E-07
LNC-SPARCL1-1	SLAMF7	-0.4162	3.47292E-07
LNC-SPARCL1-1	CD247	-0.40177	9.48039E-07
LNC-SPARCL1-1	SNRPE	-0.40199	9.33799E-07
LNC-SPARCL1-1	FANCL	-0.40909	5.72899E-07
LNC-SPARCL1-1	MDH1	-0.40862	5.92075E-07
LNC-SPARCL1-1	DUSP2	-0.4118	4.73946E-07
LNC-SPARCL1-1	PLCXD2	-0.40584	7.17304E-07
LNC-SPARCL1-1	CD38	-0.44127	5.41154E-08
LNC-SPARCL1-1	MIR1244-2	-0.40216	9.23239E-07
LNC-SPARCL1-1	NCF1C	-0.44491	4.08097E-08
LNC-SPARCL1-1	SH2D1A	-0.40548	7.35249E-07
LNC-SPARCL1-1	IFNG	-0.41545	3.66371E-07
LNC-SPARCL1-1	GZMB	-0.42897	1.37313E-07
LNC-SPARCL1-1	PHB	-0.41264	4.46865E-07
LNC-SPARCL1-1	OXLD1	-0.45355	2.0587E-08
LNC-SPARCL1-1	CENPX	-0.49062	8.72677E-10
LNC-SPARCL1-1	LRRC45	-0.40081	1.01171E-06
LNC-SPARCL1-1	NKG7	-0.4738	3.83715E-09

DIO3OS	TRIB3	-0.40021	1.05369E-06	LNCRNA	mRNA	Cor	P value
FZD10-DT	PRDX1	-0.42051	2.5499E-07	HCG23	ATP8B2	0.5000602	3.66569E-10
FZD10-DT	TAF13	-0.41259	4.48652E-07	HCG23	CADM3	0.52913812	2.13465E-11
FZD10-DT	WDR77	-0.43712	7.44162E-08	HCG23	ABI3BP	0.502657558	2.87427E-10
FZD10-DT	ATP5PB	-0.46532	7.85466E-09	HCG23	ADCY5	0.548352468	2.79643E-12
FZD10-DT	MTHFD2	-0.45937	1.28381E-08	HCG23	TSBP1	0.892610128	0
FZD10-DT	PSMB5	-0.40872	5.87782E-07	HCG23	BTNL2	0.659407047	0
FZD10-DT	EIF2S1	-0.40906	5.74165E-07	HCG23	KHDRBS2	0.522317301	4.26135E-11
FZD10-DT	SLIRP	-0.42985	1.2859E-07	HCG23	TCEAL7	0.52108787	4.81897E-11
FZD10-DT	ATP5MPL	-0.41513	3.74811E-07	HCG23	C12orf42	0.505845995	2.12641E-10
FZD10-DT	PIGW	-0.40393	8.18189E-07	HCG23	LRFN5	0.53927768	7.42095E-12
FZD10-DT	CCDC43	-0.43319	1.00186E-07	HCG23	PCNX1	0.568192021	2.97984E-13
FZD10-DT	PHB	-0.41705	3.26825E-07	HCG23	MEG9	0.530534476	1.84941E-11
FZD10-DT	NME1	-0.46377	8.93715E-09	HCG23	MFAP4	0.530668393	1.8241E-11
FZD10-DT	CCDC47	-0.4302	1.25269E-07	HCG23	CCL14	0.513876728	9.81619E-11
FZD10-DT	PSMD12	-0.43357	9.73759E-08	HCG23	ABCA9	0.528933815	2.17981E-11
FZD10-DT	NOL11	-0.45425	1.94502E-08	HCG23	ADAM33	0.502315304	2.96823E-10
FZD10-DT	C17orf58	-0.4212	2.4263E-07	HCG23	CLEC17A	0.544515069	4.24016E-12
FZD10-DT	ATP5PD	-0.40232	9.12955E-07	HCG23	NIBAN3	0.524990576	3.25595E-11
FZD10-DT	FAM210A	-0.40924	5.67016E-07	DIO3OS	AOX1	0.549285794	2.52509E-12
LNC-FOXO1-2	SNORA73B	-0.43636	7.88089E-08	DIO3OS	ANKRD30A	0.50918722	1.54538E-10
I NC-FOXO1-2	UQCBH	-0.4335	9.78491F-08	DIO3OS	NOVA1	0.533113982	1.41651F-11
LNC-F0X01-2	ATP5PB	-0 42252	2 20455E-07			0 745693945	0
LNC-FOX01-2	JTB	-0.41076	5.09806E-07	FZD10-DT	AHNAK	0 50341473	2 67651E-10
LNC-FOX01-2		_0 /139	4 08965E_07	FZD10-DT	F7D10	0.826659645	0
LNC-FOX01-2	SNRPE	_0.4100	5 79659E_10		STRAG	0.53572286	1 07914E_11
LNC-FOX01-2	SE3B6	-0.45021	2 68805E-08			0.642097678	0
	SAP30	-0.40021	1.57883E_07			0.515107207	8 70/22E_11
		-0.4345	9.07874E-08		SERD2	0.56151307/	6 /3020E_13
LNC-F0X01-2	LIOCBO	-0.4343	9.32172E_00		ERE1	0.500/36001	1 50887E_10
LNC-F0X01-2	SNORASOD	-0.40320	9.54302E_07			0.510085168	1.00007E-10
LNC-F0X01-2	RPA3	-0.40107	6.0921E_07			0.524547344	3.40505E_11
		-0.40021	1 73721E 07			0.524547544	4 25285E 12
		-0.42378	8 12856E 00			0.527205502	4.0000L-12
		0.40491	3.84136E 08			0.528704262	2.423930-11
LINC FOXO1-2		-0.44506	5.04130E-00			0.520704205	2.23104E-11
LINC-FOXO1-2	RPLOU	-0.41047	5.20208E-07		FUXUI	0.757753107	U
LINC-FOXO1-2	RIDA	-0.45019	2.09104E-08			0.522460575	4.10903E-11
LNC-FOX01-2		-0.45814	1.42025E-08	LNC-FOXOT-2		0.510221869	1.39897E-10
LNC-FOX01-2	MRPL13	-0.41568	3.6045E-07	LNC-FOX01-2	NLRP1	0.528264031	2.3344E-11
LNC-FOX01-2	DMACT	-0.42007	2.63322E-07	LNC-FOX01-2	MYH13	0.537080137	9.35874E-12
LNC-FOX01-2		-0.43712	7.43997E-08	LNC-FOX01-2	ISHZ2	0.580477754	6.88338E-14
LNC-FOX01-2		-0.44312	4.68937E-08	LNC-MMD-4	BOC	0.520894034	4.91309E-11
LNC-FOXO1-2	AIG101	-0.4245	1.90848E-07	LNC-MMD-4	EPHB3	0.565335209	4.15223E-13
LNC-FOXO1-2	GPN3	-0.40334	8.51404E-07	LNC-MMD-4	HLF	0.855960113	0
LNC-FOXO1-2	RN7SL1	-0.43083	1.19552E-07	LNC-MMD-4	GNG7	0.508352811	1.67414E-10
LNC-FOXO1-2	ERH	-0.40015	1.05786E-06	LNC-MMD-4	ZNF784	0.50673934	1.95314E-10
LNC-FOXO1-2	SLIRP	-0.40592	7.13717E-07	LNC-TMEM106C-6	RAPGEF3	0.531315537	1.70637E-11
LNC-FOXO1-2	SNORD3A	-0.40375	8.28049E-07	LNC-TMEM106C-6	SLC48A1	0.562447768	5.78648E-13
LNC-FOXO1-2	OXLD1	-0.41169	4.77676E-07				
LNC-FOXO1-2	MICOS13	-0.44261	4.87753E-08				
LNC-FOXO1-2	RPS19BP1	-0.42813	1.46069E-07				
LNC-FOXO1-2	TSPO	-0.46835	6.09391E-09				
LNC-MMD-4	RAB42	-0.40005	1.06456E-06				
LNC-MMD-4	LRP8	-0.40343	8.46545E-07				
LNC-MMD-4	DEPDC1	-0.41686	3.31447E-07				
LNC-MMD-4	C1orf43	-0.40516	7.51865E-07				
LNC-MMD-4	CCT3	-0.41465	3.87654E-07				
LNC-MMD-4	EPRS1	-0.41872	2.90195E-07				
LNC-MMD-4	BPNT1	-0.42119	2.42766E-07				
LNC-MMD-4	BROX	-0.40179	9.46227E-07				
LNC-MMD-4	CNIH4	-0.41761	3.14049E-07				
LNC-MMD-4	TXNDC9	-0.40578	7.20666E-07				
LNC-MMD-4	MAD2L1	-0.40703	6.61068E-07				
LNC-MMD-4	NOP10	-0.44087	5.58341E-08				
LNC-MMD-4	KNSTRN	-0.42335	2.07552E-07				
LNC-MMD-4	EIF3J	-0.40473	7.74242E-07				
LNC-MMD-4	MOCOS	-0.51269	1.10139E-10				



Figure S1 Gene Ontology enrichment analysis. (A) GO analysis was used to determine the significant enrichment pathways of mRNAs (upregulated lncRNA: r>0.5 and P<0.01); (B) GO analysis was used to determine the significant enrichment pathways of mRNAs (downregulated lncRNA: r<-0.4 and P<0.01); (C) GO analysis was used to determine the significant enrichment pathways of mRNAs (upregulated lncRNA: r<-0.5 and P<0.01); (D) GO analysis was used to determine the significant enrichment pathways of mRNAs (downregulated lncRNA: r<-0.4 and P<0.01); (D) GO analysis was used to determine the significant enrichment pathways of mRNAs (downregulated lncRNA: r<-0.4 and P<0.01); (D) GO analysis was used to determine the significant enrichment pathways of mRNAs (downregulated lncRNA: r<-0.4 and P<0.01). mRNA, messenger RNA; GO, Gene Ontology.