Table S1 The list of top 50 differentially expressed mRNAs.

Symbol	FDR	Regulation	Symbol	FDR	Regulation
NETO2	0	Up-regulation	SORT1	0	Down-regulation
TTYH3	0	Up-regulation	RBM47	0	Down-regulation
RFC4	0	Up-regulation	PGM5	0	Down-regulation
PLAU	0	Up-regulation	GPX3	0	Down-regulation
NEK2	0	Up-regulation	PDCD4	0	Down-regulation
WDR53	0	Up-regulation	GCHFR	0	Down-regulation
WDR66	0	Up-regulation	PLEKHA6	0	Down-regulation
COL10A1	0	Up-regulation	CFD	0	Down-regulation
RSAD2	1.41E-13	Up-regulation	TM7SF2	1.41E-13	Down-regulation
PTHLH	1.41E-13	Up-regulation	ACADVL	1.41E-13	Down-regulation
RAD51AP1	2.69E-13	Up-regulation	SSBP2	1.24E-12	Down-regulation
RAB32	3.84E-13	Up-regulation	ZFAND2B	1.36E-12	Down-regulation
FZD6	4.90E-13	Up-regulation	SYNGR1	1.56E-12	Down-regulation
MTHFD2	1.06E-12	Up-regulation	VSIG2	2.98E-12	Down-regulation
PARP14	1.36E-12	Up-regulation	OGN	4.60E-12	Down-regulation
STIL	1.56E-12	Up-regulation	FAM189A2	4.84E-12	Down-regulation
HOMER3	2.26E-12	Up-regulation	ETFDH	5.15E-12	Down-regulation
ADAR	2.46E-12	Up-regulation	EDN3	6.11E-12	Down-regulation
PLXNA1	2.65E-12	Up-regulation	TCEA3	9.23E-12	Down-regulation
MB21D2	2.65E-12	Up-regulation	TJP3	1.27E-11	Down-regulation
MCM5	2.74E-12	Up-regulation	MKNK2	2.18E-11	Down-regulation
LAMP3	3.76E-12	Up-regulation	CEACAM7	2.54E-11	Down-regulation
GMPS	4.19E-12	Up-regulation	ISOC1	6.46E-11	Down-regulation

DCBLD1	5.29E-12	Up-regulation	ABI3BP	8.49E-11	Down-regulation
STC2	8.52E-12	Up-regulation	SERPINB6	9.21E-11	Down-regulation

FDR false discovery rate

Table S2 The top 15 significantly enriched GO-BP/CC terms and all significantly enriched GO-MF terms and KEGG pathways by target DEmRNAs of DEmiRNAs.

Terms/Pathways	**GO-ID**	**Description**	**No.**	**FDR**
GO-BP terms	GO:0006260	DNA replication	54	2.71E-07
	GO:0051052	regulation of DNA metabolic process	68	4.49E-06
	GO:0030198	extracellular matrix organization	57	7.08E-05
	GO:0097191	extrinsic apoptotic signaling pathway	42	7.08E-05
	GO:0018209	peptidyl-serine modification	51	7.08E-05
	GO:0006261	DNA-dependent DNA replication	32	7.08E-05
	GO:0043062	extracellular structure organization	62	8.86E-05
	GO:0018105	peptidyl-serine phosphorylation	48	1.10E-04
	GO:0090068	positive regulation of cell cycle process	48	1.51E-04
	GO:0051054	positive regulation of DNA metabolic process	40	1.60E-04

	GO:0002009	morphogenesis of an epithelium	69	1.60E-04
	GO:0000086	G2/M transition of mitotic cell cycle	37	2.10E-04
	GO:0048285	organelle fission	66	2.41E-04
	GO:0044839	cell cycle G2/M phase transition	39	2.48E-04
	GO:2001233	regulation of apoptotic signaling pathway	57	8.50E-04
GO-CC terms	GO:0098589	membrane region	52	4.82E-05
	GO:0098857	membrane microdomain	49	1.20E-04
	GO:0098687	chromosomal region	53	1.27E-04
	GO:0045121	membrane raft	48	1.32E-04
	GO:0000151	ubiquitin ligase complex	44	2.09E-04
	GO:0016323	basolateral plasma membrane	36	4.25E-04
	GO:0000775	chromosome, centromeric region	33	7.91E-04
	GO:0030667	secretory granule membrane	44	8.16E-04

	GO:0061695	transferase complex, transferring phosphorus-containing groups	40	8.16E-04
	GO:0005657	replication fork	16	2.28E-03
	GO:0043596	nuclear replication fork	12	2.55E-03
	GO:0070820	tertiary granule	27	5.27E-03
	GO:0000793	condensed chromosome	33	6.26E-03
	GO:0032154	cleavage furrow	13	6.80E-03
	GO:0032155	cell division site part	14	8.90E-03
GO-MF terms	GO:0030020	extracellular matrix structural constituent conferring tensile strength	13	3.70E-03
	GO:0003725	double-stranded RNA binding	18	1.21E-02
	GO:0008094	DNA-dependent ATPase activity	19	1.53E-02
	GO:0046332	SMAD binding	18	1.53E-02
	GO:0019838	growth factor binding	25	2.12E-02

	GO:0004674	protein serine/threonine kinase activity	60	2.22E-02
	GO:0004386	helicase activity	26	2.61E-02
	GO:0042623	ATPase activity, coupled	49	2.61E-02
KEGG pathways	hsa05160	Hepatitis C	30	1.06E-02
	hsa04974	Protein digestion and absorption	20	3.09E-02
	hsa04668	TNF signaling pathway	22	3.09E-02
	hsa05164	Influenza A	29	3.23E-02
	hsa05132	Salmonella infection	33	3.23E-02
	hsa04512	ECM-receptor interaction	18	3.23E-02
	hsa03030	DNA replication	10	3.90E-02
	hsa04151	PI3K-Akt signaling pathway	49	4.39E-02
	hsa04066	HIF-1 signaling pathway	20	4.68E-02

GO-BP: Gene Ontology-Biological Process; GO-MF: Gene Ontology-Molecular Function; GO-CC: Gene Ontology-Cellular Component; KEGG: Kyoto Encyclopedia of Genes and Genomes; FDR: false discovery rate; DEmRNAs: differentially expressed mRNAs; DEmiRNAs: differentially expressed miRNAs.

Table S3 The top 15 significantly enriched GO-BP/CC terms by target mRNAs of DElncRNAs.

Terms/Pathways	**GO-ID**	**Description**	**No.**	**FDR**
GO-BP terms	GO:0006342	chromatin silencing	5	2.61E-02
	GO:0072599	establishment of protein localization to endoplasmic reticulum	5	2.61E-02
	GO:0045814	negative regulation of gene expression, epigenetic	5	2.61E-02
	GO:0090150	establishment of protein localization to membrane	7	2.61E-02
	GO:0046677	response to antibiotic	7	2.61E-02
	GO:0042542	response to hydrogen peroxide	5	2.61E-02
	GO:0071236	cellular response to antibiotic	5	2.61E-02
	GO:0070972	protein localization to endoplasmic reticulum	5	2.61E-02
	GO:0097237	cellular response to toxic substance	6	2.61E-02
	GO:0007411	axon guidance	6	3.51E-02

	GO:0097485	neuron projection guidance	6	3.51E-02
	GO:0061564	axon development	8	3.51E-02
	GO:0070301	cellular response to hydrogen peroxide	4	3.55E-02
	GO:0071103	DNA conformation change	6	4.25E-02
	GO:0006614	SRP-dependent cotranslational protein targeting to membrane	4	4.25E-02
GO-CC terms	GO:0022625	cytosolic large ribosomal subunit	4	1.73E-02
	GO:0043209	myelin sheath	5	2.92E-02
	GO:0005903	brush border	4	2.92E-02
	GO:0044391	ribosomal subunit	5	2.92E-02
	GO:0031965	nuclear membrane	6	2.92E-02
	GO:0022626	cytosolic ribosome	4	2.92E-02
	GO:0015934	large ribosomal subunit	4	3.02E-02
	GO:0005635	nuclear envelope	7	3.39E-02

	GO:0031143	pseudopodium	2	3.92E-02
	GO:0098862	cluster of actin-based cell projections	4	3.92E-02
	GO:0044445	cytosolic part	5	3.92E-02
	GO:0005766	primary lysosome	4	3.92E-02
	GO:0042582	azurophil granule	4	3.92E-02
	GO:0000792	heterochromatin	3	3.92E-02
	GO:0005925	focal adhesion	6	3.92E-02

GO-BP: Gene Ontology-Biological Process; GO-CC: Gene Ontology-Cellular Component; FDR: false discovery rate; DElncRNAs: differentially expressed lncRNAs.

Table S4 The subcellular localization of 17 DElncRNA in ceRNA network.

lncRNA	Cytoplasm	Nucleus	Ribosome	Cytosol	Exosome	Prediction
AL121839.2	0.898567425	0.027368317	0.016199798	0.05616501	0.00169945	Cytoplasm
ZNF503-AS1	0.065571121	0.007297334	0.065213781	0.860225527	0.001692237	Cytosol
LINC02147	0.882511665	0.022524054	0.018746987	0.07491883	0.001298464	Cytoplasm
AL354956.1	0.050204498	0.009913713	0.45061779	0.481260048	0.008003952	Cytosol
AC079328.2	0.891630473	0.029240892	0.01546238	0.061445438	0.002220817	Cytoplasm
DGCR9	0.020287168	0.003389453	0.422625984	0.548115946	0.005581449	Cytosol
AC006064.2	0.058025191	0.01718853	0.022731075	0.898034757	0.004020447	Cytosol
AC078778.1	0.031874003	0.002329916	0.576596174	0.383435925	0.005763982	Ribosome
AC004943.2	0.870423462	0.02514308	0.020469637	0.08228416	0.001679661	Cytoplasm
AC007620.2	0.33969809	0.023268489	0.106271377	0.526745101	0.004016943	Cytosol
MELTF-AS1	0.053285586	0.010370459	0.030361157	0.849757583	0.056225216	Cytosol

AC084024.3	0.034785426	0.001951721	0.575239461	0.376074836	0.011948556	Ribosome
AC024267.6	0.034795943	0.005628238	0.032254044	0.849819168	0.077502607	Cytosol
AP001439.1	0.132908462	0.048022511	0.076161224	0.719412465	0.023495339	Cytosol
AC106820.5	0.050361069	0.020344449	0.025777076	0.868887382	0.034630024	Cytosol
HMGA2-AS1	0.871585334	0.018370052	0.017041894	0.091145443	0.001857277	Cytoplasm
DGCR5	0.020015199	0.003428247	0.094134182	0.87042668	0.011995692	Cytosol

DElncRNAs: differentially expressed lncRNAs; ceRNA: competing endogenous RNA.