

ORIGINAL ARTICLE

lncRNA LUCAT1 acts as a Potential Biomarker and Demonstrates Malignant Biological Behaviors in Gastric Cancer

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SUMMARY

Background: Gastric cancer (GC) remains the fourth-leading malignancy worldwide and has a high mortality rate. Accumulating evidence reveals that long noncoding RNAs (lncRNAs) play essential roles in tumorigenesis and metastasis and can be used as potential biomarkers for diagnosis and prognosis.

Methods: We downloaded gene expression profiles from the National Center of Biotechnology Information Gene Expression Omnibus (GEO), screened lncRNAs differentially expressed in gastric cancer tissues and adjacent tissues, and then constructed a lncRNA-miRNA-mRNA network. Seventy patients with gastric cancer were divided into two groups according to different clinical characteristics. The expression of lncRNA LUCAT1 in gastric cancer was detected by reverse transcription polymerase chain reaction (RT-PCR). The AGS and SGC-7901 cell lines were used in CCK8 assay, apoptosis, cell cycle test, transwell assay, and wound healing assay.

Results: The expression level of LUCAT1 was associated with tumor diameter ($p < 0.001$), tissue differentiation grade ($p = 0.026$), and LNM status ($p = 0.020$) in GC. The results showed that the lncRNA LUCAT1 could promote the proliferation, invasion, and migration of GC cells, inhibit the apoptosis of GC cells, and affect the process of cell cycles.

Conclusions: The lncRNA LUCAT1 may be used as a potential biomarker for early signs of LNM in GC and may play a crucial role in the development of GC.

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Supplementary Tables and Figures

Table S1.

ID	adj.P.Val	p-value	t	B	logFC	SPOT_ID	GB_ACC	Gene_name	Gene ID
A_21_P0006541	1	0.03291	-2.27245	-4.57	-2.86372	A_23_P160167	NM_005727	TSPAN1	
A_21_P0001708	1	0.02241	-2.4513	-4.56	-2.44077	A_23_P110276	NR_026892	AFAP1-ASI	AFAP1-ASI
A_21_P0001889	1	0.0483	-2.08783	-4.57	-2.29531	A_33_P3888629	NM_001164000	MECOM	
A_19_P00319226	1	0.03727	-2.21334	-4.57	-2.05351	A_19_P00319226	NR_026867	ZNF300P1	
A_21_P0012445	1	0.0287	-2.33684	-4.57	-2.02126	A_33_P3387493			
A_32_P8925	1	0.04628	-2.1087	-4.57	-1.69229	A_33_P3300600	NM_001005192	OR7G1	
A_23_P335981	1	0.04436	-2.12938	-4.57	-1.4214	A_24_P458479	BC119676	FAM27E2	
A_21_P0010304	1	0.04946	2.076195	-4.57	1.026391	A_23_P24543	NM_152315	NXPE1	
A_21_P0010223	1	0.04833	2.08748	-4.57	1.053399	A_33_P3296427	NR_015407	LINC01139	
A_21_P0003012	1	0.04405	2.132745	-4.57	1.096889	A_33_P3289093			
A_33_P3293773	1	0.04244	2.150872	-4.57	1.107536	tc[THC2603124 linc TCONS_I2_00019353 linc TCONS_I2_00019352		TCONS_I2_00019353	
A_21_P0005504	1	0.04952	2.075507	-4.57	1.129195	linc TCONS_00013857		TCONS_00013857	XLOC_006488
A_33_P3289093	1	0.03701	2.216644	-4.57	1.140108	linc TCONS_00028974		TCONS_00028974	XLOC_013881
A_21_P0003415	1	0.03638	2.224805	-4.57	1.140182	tc[THC276827 linc TCONS_00026416		TCONS_00026416	XLOC_012761
A_33_P3877992	1	0.03577	2.232901	-4.57	1.157382	A_23_P151598	NM_006032	CPNE6	
A_33_P3236122	1	0.02923	2.328269	-4.57	1.157746	A_33_P3877992	NR_038881	LACTB2-ASI	LACTB2-ASI
A_21_P0013894	1	0.04268	2.14808	-4.57	1.173078	linc TCONS_00021809		TCONS_00021809	XLOC_010409
A_33_P3224916	1	0.04334	2.140626	-4.57	1.174682	ens ENST00000488173 linc TCONS_I2_00020247		TCONS_I2_00020247	XLOC_010409

Table S1. Continued.

ID	adj.P.Val	p-value	t	B	logFC	SPOT_ID	GB_ACC	Gene_name	Gene ID
A_24_P246777	1	0.04361	2.137647	-4.57	1.186531	A_23_P315991	NM_178168	OR10A5	
A_21_P0001075	1	0.03956	2.184755	-4.57	1.197285	A_21_P0013124	BC030116	LOC105374928	
A_21_P0008478	1	0.04912	2.079542	-4.57	1.197859	A_33_P3812027	BC032033	LOC414300	
A_33_P3888629	1	0.04711	2.100063	-4.57	1.200496	linc TCONS_12_00030929		TCONS_12_00030929	
A_24_P166397	1	0.04823	2.088556	-4.57	1.204929	ens ENST0000556662 tc THC2629038 linc TCONS_00023004 linc TCONS_00022533		TCONS_00022533	
A_33_P3357738	1	0.03372	2.260969	-4.57	1.212273	A_33_P3289401	NM_001001916	OR52J3	
A_33_P3313125	1	0.04363	2.137455	-4.57	1.223741	ens ENST0000505781 linc TCONS_00007656		TCONS_00007656	
A_21_P0008514	1	0.0466	2.105386	-4.57	1.229895	A_33_P3356637			
A_21_P0012418	1	0.03611	2.228349	-4.57	1.23054	A_24_P246777			
A_33_P3300600	1	0.04231	2.152268	-4.57	1.256353	linc TCONS_00004514 linc TCONS_00004513		TCONS_00004513	
A_23_P303101	1	0.0461	2.110568	-4.57	1.264424	A_21_P0006982	BX093705	#N/A	
A_33_P3293307	1	0.03515	2.241277	-4.57	1.285013	A_21_P0014207	XR_108853	#N/A	
A_33_P3296427	1	0.04751	2.095841	-4.57	1.28661	A_33_P3224916			
A_21_P0006083	1	0.02946	2.324558	-4.57	1.298075	A_21_P0014679	XR_111377	#N/A	
A_33_P3356637	1	0.04268	2.148139	-4.57	1.317682	linc TCONS_12_00006715 linc TCONS_12_00006716		TCONS_12_00006715	
A_21_P0012554	1	0.03423	2.253854	-4.57	1.341518	linc TCONS_00011020		TCONS_00011020	
A_21_P0008902	1	0.04246	2.150579	-4.57	1.351572	A_32_P225345	NM_207430	C11orf88	
A_23_P160167	1	0.03502	2.243038	-4.57	1.352745	A_21_P0010304	NM_052997	ANKRD30A	

Table S1. Continued.

ID	adj.P.Val	p-value	t	B	logFC	SPOT_ID	GB_ACC	Gene_name	Gene ID
A_21_P0002525	1	0.02747	2.357285	-4.57	1.3677	ens ENST00000453878 linc TCONS_00002957		TCONS_00002957	
A_21_P0009825	1	0.04803	2.090519	-4.57	1.397668	ens ENST00000429567			
A_24_P233078	1	0.04166	2.159795	-4.57	1.40342	A_21_P0009427	BC034583	LOC400655	
A_33_P3812027	1	0.04817	2.089097	-4.57	1.416447	linc TCONS_00006165		TCONS_00006165	XLOC_002770
A_23_P68436	1	0.01974	2.509346	-4.56	1.42638	A_33_P3250695	NM_031856	PCDHA8	
A_21_P0004422	1	0.02795	2.349236	-4.57	1.427438	A_21_P0003568	NM_018088	Fam90a1	
A_32_P225345	1	0.02874	2.336163	-4.57	1.427711	linc TCONS_00017353		TCONS_00017353	XLOC_008198
A_21_P0011122	1	0.02955	2.323183	-4.57	1.428092	ens ENST00000502209 linc TCONS_00009606		TCONS_00009606	
A_33_P3282641	1	0.02378	2.424089	-4.56	1.475788	A_33_P3381621	BC065041	PLB1	
A_21_P0006982	1	0.04083	2.169477	-4.57	1.479707	ens ENST00000397864 linc TCONS_00015839		TCONS_00015839	
A_33_P3718274	1	0.02119	2.476985	-4.56	1.48383	A_33_P3718274	DB296219	#N/A	
A_21_P0013124	1	0.0351	2.24186	-4.57	1.499509	A_33_P3262449	XM_002343322	#N/A	
A_33_P3387493	1	0.03612	2.228273	-4.57	1.502378	A_33_P3264528	NM_005523	HOXA11	
A_21_P0014679	1	0.04487	2.123823	-4.57	1.518346	A_24_P365015	NM_006361	HOXB13	
A_23_P110276	1	0.02239	2.451724	-4.56	1.523808	A_32_P8925	NM_001012970	C1orf100	
A_23_P161458	1	0.02426	2.414968	-4.56	1.535502	A_23_P161458	NM_001039702	OLAH	
A_21_P0007576	1	0.04892	2.081496	-4.57	1.546523	ens ENST0000049270 tc THC2613461 linc TCONS_00027899		TCONS_00027899	
A_21_P0003568	1	0.04775	2.093435	-4.57	1.557132	A_33_P3276856	NM_001198542	HYDIN	

Table S1. Continued.

ID	adj.P.Val	p-value	t	B	logFC	SPOT_ID	GB_ACC	Gene_name	Gene ID
A_23_P136870	1	0.01938	2.517644	-4.56	1.562185	A_23_P303101	NM_032406	PCDHGC4	
A_33_P3262449	1	0.04659	2.105469	-4.57	1.591172	A_33_P3293773	NM_173651	FSIP2	
A_21_P0011394	1	0.03923	2.188777	-4.57	1.591176	ens ENST00000425104		RP5-827C21.2	
A_21_P0009427	1	0.01018	2.804401	-4.55	1.602312	ens ENST0000430921 tc THC2690712 linc TCONS_00000419		TCONS_00000419	KIAA1383
A_33_P3276630	1	0.02152	2.469865	-4.56	1.602773	A_33_P3357738	BC021736	LOC728196	
A_33_P3882624	1	0.04603	2.111371	-4.57	1.639767	A_21_P0003941	XR_108596	#N/A	
A_23_P24543	1	0.04936	2.077151	-4.57	1.663931	tc THC2706764 linc TCONS_00020462		TCONS_00020462	XLOC_009793
A_33_P3260974	1	0.00948	2.835171	-4.55	1.722622	A_33_P3276630	BC054892	DYNLRB2	
A_21_P0012672	1	0.04991	2.071715	-4.57	1.735129	linc TCONS_I2_00021193		TCONS_I2_00021193	
A_23_P315991	1	0.03629	2.226088	-4.57	1.79353	linc TCONS_00024321		TCONS_00024321	XLOC_011635
A_21_P0008070	1	0.0313	2.296122	-4.57	1.879631	linc TCONS_00010403 linc TCONS_00010984 linc TCONS_00010402		TCONS_00010403	
A_21_P0009524	1	0.01575	2.611307	-4.56	1.891136	A_24_P233078	NR_003064	PYY2	
A_21_P0004571	1	0.03119	2.297777	-4.57	1.919218	A_24_P215240	NM_145010	ENKUR	
A_33_P3276856	1	0.04345	2.139458	-4.57	1.93555	linc TCONS_I2_00019040		TCONS_I2_00019040	
A_33_P3285456	1	0.01343	2.682353	-4.56	1.948986	linc TCONS_00022841		TCONS_00022841	XLOC_011107
A_23_P151598	1	0.0322	2.282783	-4.57	1.954324	A_23_P136870	NM_175868	MAGEA6	XLOC_004924
A_33_P3381621	1	0.04208	2.154977	-4.57	2.013106	A_33_P3285456	NM_001024679	C1orf68	
A_21_P0004102	1	0.04936	2.077183	-4.57	2.027513	A_24_P166397	NM_014809	KIAA0319	

Table S1. Continued.

ID	adj.P.Val	p-value	t	B	logFC	SPOT_ID	GB_ACC	Gene_name	Gene ID
A_19_P00802433	1	0.01782	2.555701	-4.56	2.131947	A_33_P3282641	NR_033752	NMRAL2P	
A_33_P3250695	1	0.01781	2.555794	-4.56	2.132315	A_33_P3260974	DA734158	#N/A	
A_21_P0014207	1	0.01785	2.555022	-4.56	2.150539	A_23_P335981	NM_173860	HOXC12	
A_33_P3264528	1	0.03814	2.202271	-4.57	2.285512	A_33_P3306207	NM_198508	KLRG2	
A_21_P0003941	1	0.04071	2.170902	-4.57	2.311821	A_33_P3293307			
A_24_P215240	1	0.04017	2.177401	-4.57	2.317817	A_33_P3882624	NM_015450	POT1	
A_33_P3306207	1	0.00837	2.889351	-4.55	2.427084	A_23_P398449	NR_028291	#N/A	
A_23_P398449	1	0.04524	2.119748	-4.57	2.465621	A_21_P0011394	AK309255	HERC2P2	
A_33_P3289401	1	0.03161	2.291476	-4.57	2.668751	A_23_P68436	NM_080869	WFDC12	
A_24_P365015	1	0.03868	2.195571	-4.57	3.300579	ens ENST0000448327 tc THC 2716204 tc THC2649843 linc TCONS_00012509		TCONS_00012509	
A_24_P458479	1	0.03813	2.20238	-4.57	3.990047	linc TCONS_00002202		TCONS_00002202	

Table S2.

miRNA	mRNA
hsa-let-7a-5p	HMGA2, KRAS, PAK1, TNFRSF10B
hsa-let-7f-5p	CCL7, COPS8, CYP19A1, KLK10, KLK6
hsa-let-7i-5p	ASCL1, COPS8, IGF1, TLR4
hsa-miR-126-5p	MMP7
hsa-miR-143-3p	CD44, COL3A1, FHIT, IGF1R, KRAS, PTGS2, SERPINE1,
hsa-miR-214-3p	JAG1, LTF, LZTS1, PAPP, PLXNB1, POU4F2
hsa-miR-218-5p	BIRC5, DKK2, HOXB3, LEF1, MTF, PDGFRA, ROBO1, RUNX2, SFRP2, TFF1
hsa-miR-24-3p	ACVR1B, CDK1, CHEK1, JPH2, MAP3K9, MAPK14, MMP14, NOS3, PTPN9, TACC3, TRIB3, WNT4
hsa-miR-27a-3p	HIPK2, HOXA10, IGF1, KRAS, LDLR, NFE2L2, PAX3, PDS5B, PPARG, SEMA7A, SLC7A11, ZBTB10
hsa-miR-27b-3p	ADORA2B, CYP3A4, EDNRA, PAX3, PAX7, PPARG, THBS1, THBS2, VEGFC
hsa-miR-335-5p	BIRC5, FMNL3, FOXA2, IGF1R, PTPRN2, RUNX2, TFF2, TNC, ZEB2
hsa-miR-375	ADIPOR2, IGF1R, PDK1, PHLPP1
hsa-miR-377-3p	PAK1
hsa-miR-665	CNR2

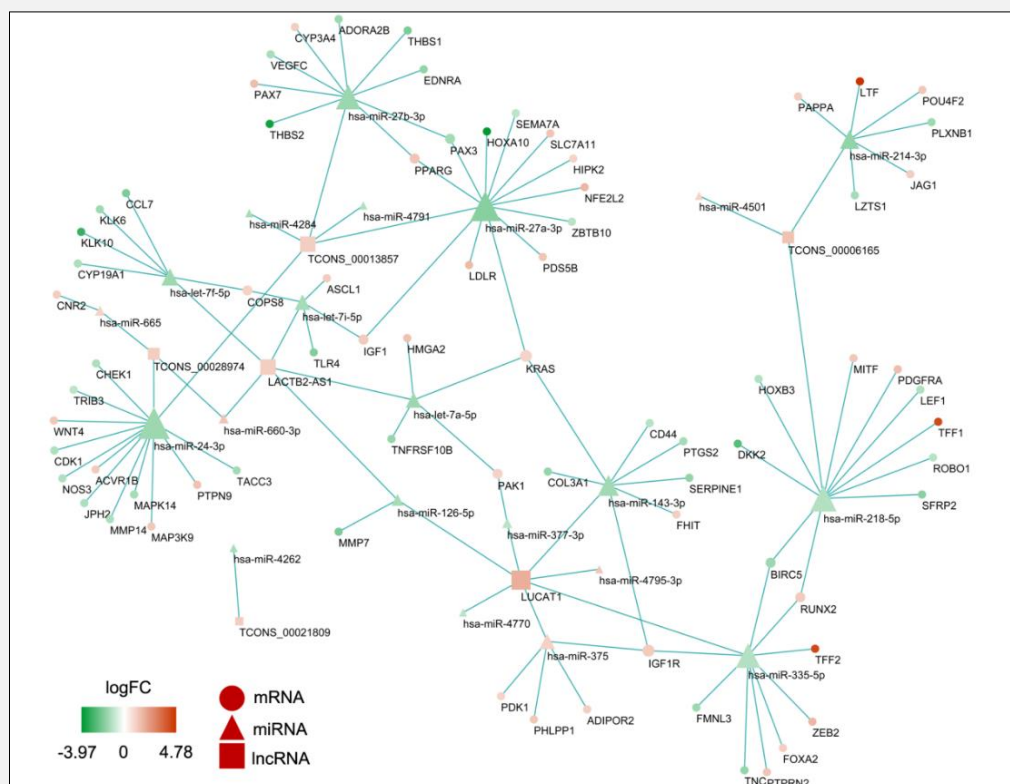


Figure S1. LncRNA-miRNA-mRNA regulatory network in GC.

The circular nodes represent mRNAs, the round rectangular nodes represent lncRNAs, and the triangular nodes represent miRNAs. The red nodes represent upregulated genes, and the green nodes represent downregulated genes. Node size represents the degrees, with a larger node corresponding to more degrees.

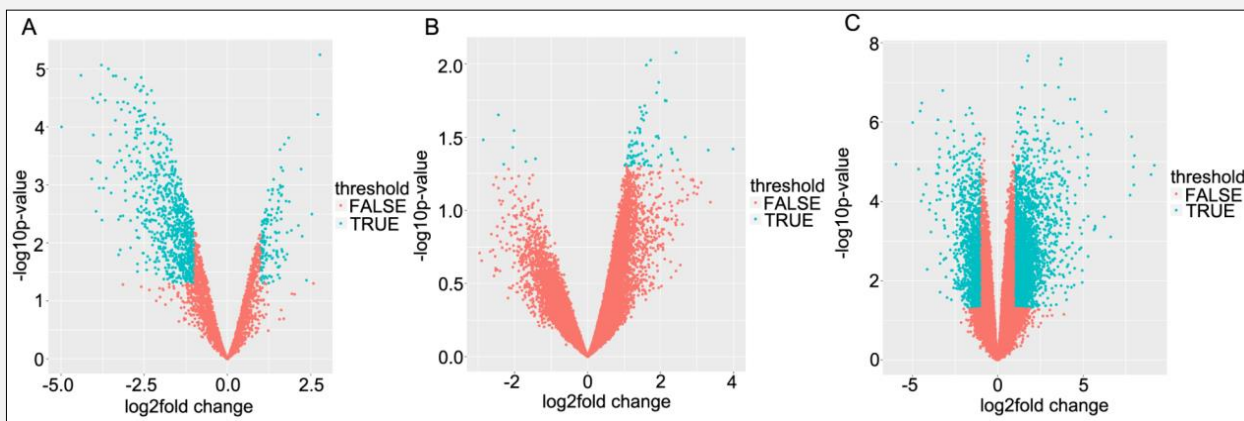


Figure S2. Differentially expressed genes in GC.

The volcano plots of miRNA expression data from GSE93415 (A), lncRNA expression data from GSE84787 (B) and mRNA expression data from GSE79973 (C) are shown separately. The horizontal axis represents \log_2 (fold change), and the vertical axis represents $-\log_{10}$ (p-value). The blue dots represent the selected differentially expressed genes.

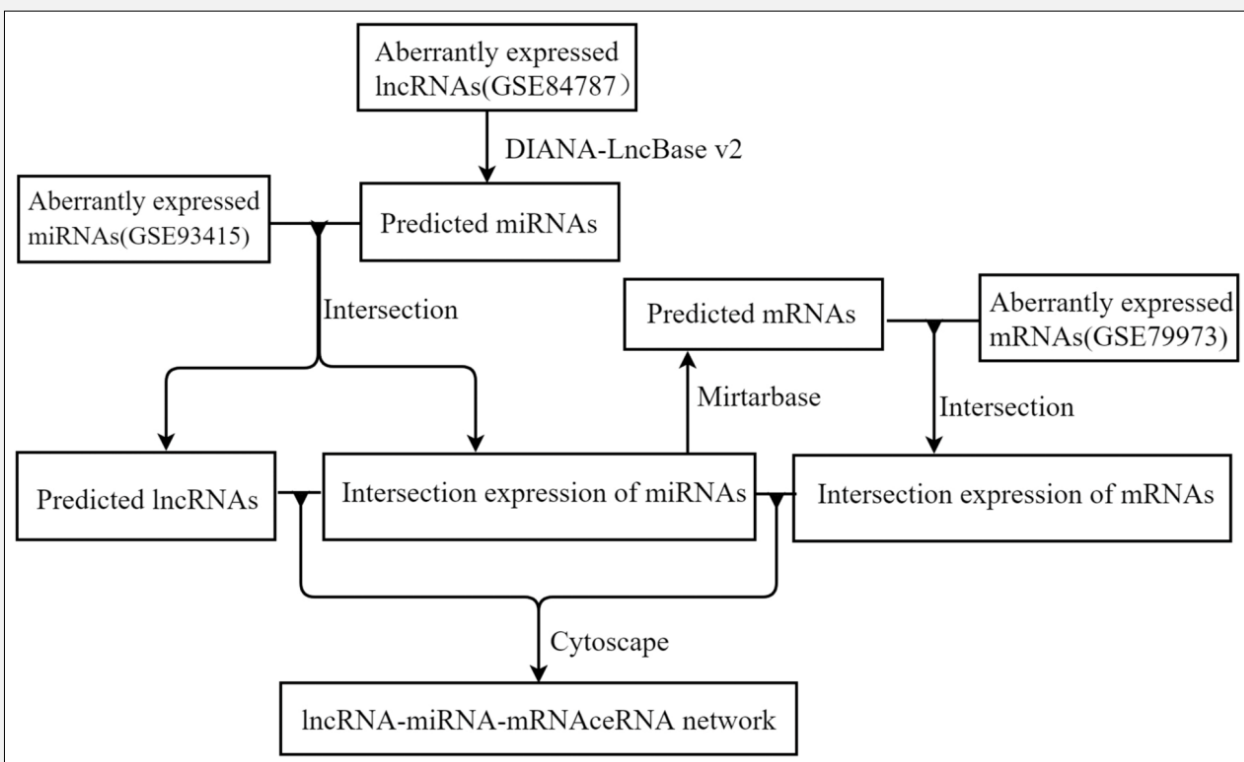


Figure S3. Flow chart detailing the ceRNA network analysis.