

Although LINC01419 and AK021443 show the gene co-expression mode, there is no crosstalk relationship between them. The protein target of LINC01419 and the expression changes of these LINC01419-regulated targets are presented below:

Although LINC01419 and AK021443 show the gene co-expression mode (their expression increased in HCV and HCC patients in comparison to the control group), the correlation between them was found to be non-significant. Moreover, Using LncTar (<http://www.cuilab.cn/lncstar>) an efficient tool for predicting RNA targets of lncRNAs, LINC01419 and AK021443 are not predicted to interact with each other.

LncTar: an efficient tool for predicting RNA targets of lncRNAs

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LncTar Parameters

cutoff of the normalized deltaG (ndG)

Input (Please use IE10+ or other browsers)

Query (LncRNA)(FASTA format): [Use examples](#) [Clear](#)

```
>NR_122034.1
CTTCCACATCGTGGAGCTTTGTCTTTGGCTCTTTGCAATAATCTTGGCTACTGCTCACTCTTTG
GGTCCACCGCTCTTTATGAGCTGTAAACACTCAACCGCGAAGATCTGAGGCTTCACTCCGAGCCA
GCGAGACCACGAACCCACAGAGGAAGAACTCCGAACACATCTGAACATCAGAAAGGCGAGA
CTCCAGACAGCGCCCTTAAGAGCTGTAACACTCACCGCGAGGGTCCACGGCTTCATTCTTGAA
GTCACTGACACCAAGACCCACCAATTCGGACACATTTCTGGCTCTCAGTGGCTTCCATGGGA
AGTCTGCAATCAACCGAGGAGAACCGCTAAACCCAGGAGGCGGAGGTTGCGATGAGCCA
AGTATGCATCACTGCACCTCAGCGCTGGAAGACAGAGTGAGACCGCTGTCTCAACAAATAAATAA
ATAAAAAATAATATTTTCTAAGTATCATCCCTTTTCCAAATCAGGAATTCGCCCTAAGTTTCTCTC
AATTTCGATGGCAATATCTTGCATAGATTCATTAAGAATTGTGCTTTTAAATAAAATAAAGG
```

OR input a file in FASTA format: [Browse](#)

Target (RNA)(FASTA format): [Use examples](#) [Clear](#)

```
>AK021443.1
AATTATAATGGATTGAAATTTGCCCTAACCAAGAGTCACAGACAGAAAAAGGAAGTTAATGATC
TCTTGATCACTGTCAAGATGTGGTATTGAACCTTCAAGATCCTTTTCAGGGAATATGTGAGATCAAA
ATTTTTACTCGGCACTATGATGTATTGGCTTTTCCCTCATATTCAAAAGTGAAAGTGAGATTTTA
CAGAAAGTATATAATGTATGACATCACTGATGGGTAAGAATGTGGCTTGATATCCGAAACTT
TCAGTTCCAATTTCTTCGATCAATGTAATCCTCATAAGTAAAGTTATTTGAGGACCTCAGACATTT
TAAAAATGTAAGGGGGTGGGTGAGGCTCAGTGGCTCATGCCGTGTAATCCAGCATTTTGGAAAG
GCCGAGGCGAAGGATCACTTGAGGCCAGGAGTTTGAACATAGTCTGGTCAACATGTTGAAACC
CGCTTCCACTAAACAAAAAGTTTCTGGATGTGGTGGCACACATACCTGTAATCCAGCTACTT
TTGGTGGCTGAGGCATGAGATCACTTGAACCCAGAGACAGGTTGCAGTGAGCCAGATTGTGC
```

OR input a file in FASTA format: [Browse](#)

Query	Length_Query	Target	Length_Target	dG	ndG	Start_Position_Query	End_Position_Query	Start_Position_Target	End_Position_Target
The LncRNA and mRNA that you submitted are not predicted to interact with each other, suggest you adjust the ndG or try other pairs!									

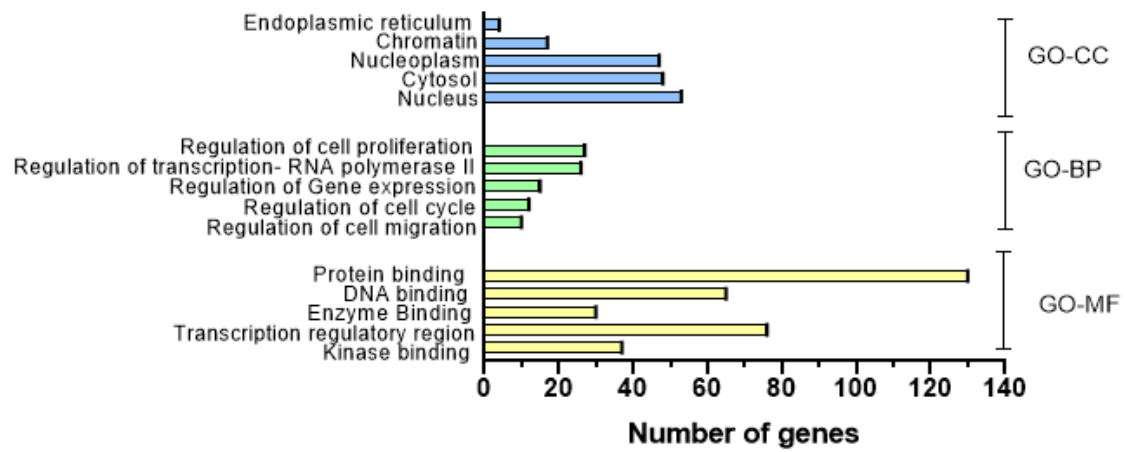
LncRNAs regulate genes expression by sponging various miRNAs. Using TarBase V.8 (<https://dianalab.e-ce.uth.gr/html/diana/web/index.php?r=tarbasev8>) and Incbase V 3 (<https://diana.e-ce.uth.gr/Incbasev3/interactions>) the target miRNAs and genes of high prediction score of LINC01419 were predicted and listed in the table below. miRpath was also used to detect the targeted pathway.

Table S1: Crosstalk relationship between LINC01419 and LINC01419

miRNA	Target genes	Pathway
hsa-let-7i-3p	STAG2, DPYSL5, COL12A1, PAQR3, HNRNPUL2, MYBPC3, USP48, ACTB, ACTB, KCNB1, KDM2A, KLHL15	cellular metabolic process, cellular protein modification process, modification of charged tRNAs
hsa-miR-106b-5p	CCND1, ZNF367, REEP3, TNKS2, ULK1, RAB22A, LDLR, G3BP1, RBBP7, TMEM127, ANKRD52, FAM117B, STYX, RUFY2, REEP5, SEMA7A, ITGB8, AHNAK, EPHA4, LZIC	positive regulation of metabolic process, apoptotic process, protein phosphorylation
hsa-miR-130a-3p	STX6, CSF1, PSAP, PPP6R1, SMARCD2, LDLR, E2F1,E2F2,E2F3,	DNA-binding transcription factor activity, RNA polymerase II-specific

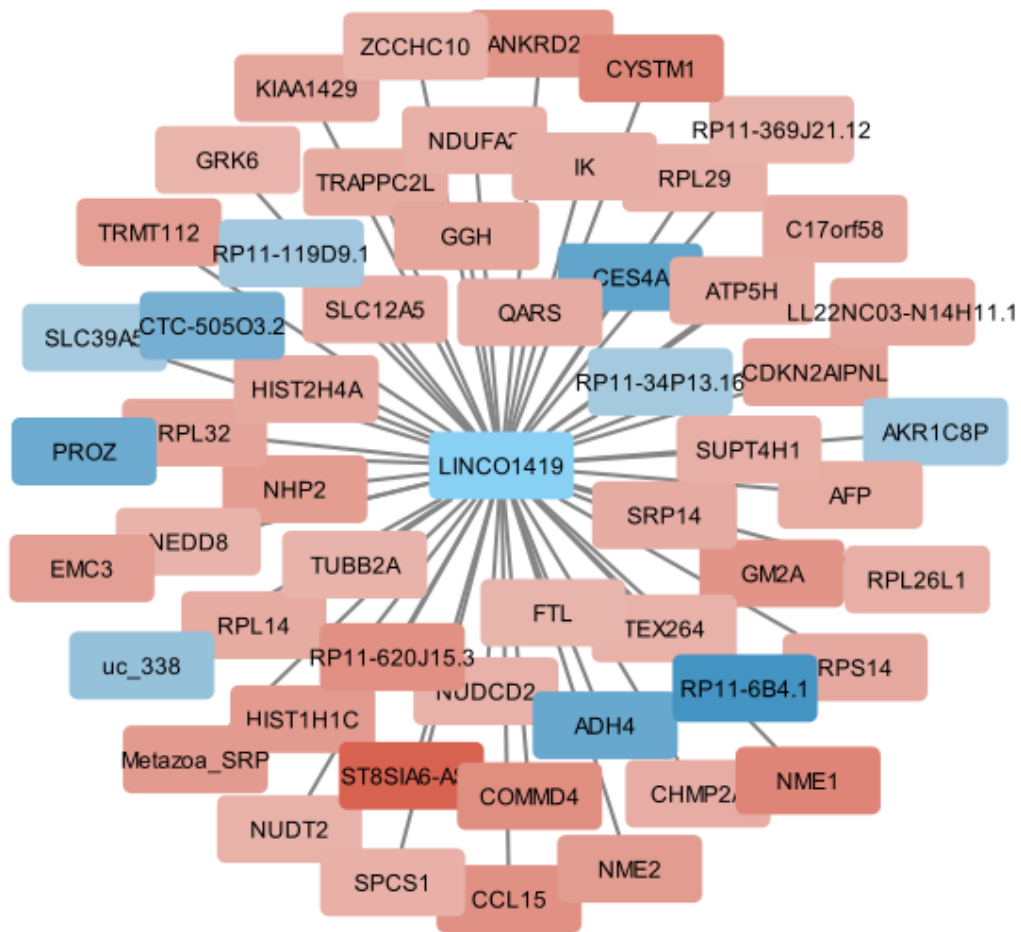
hsa-miR-142-5p	AFF4, MTDH, UBE4A, EFCAB14, ANKIB1, PTPN4, RORA, DNAJB4, CHD9, GLO1	nuclear chromosome, regulation of signaling, cell development, <u>regulation of catalytic activity</u>
hsa-miR-148a-3p	ITGA5, CCKBR, CDKN1B, CAND1, PPP6R1, BTBD3, SBF2, DCP2, TBL1XR1	<u>protein metabolic process</u> , <u>nucleobase-containing compound metabolic process</u> , <u>signal transduction</u>
hsa-miR-155-5p	ZIC3, TSHZ3, FBXO11, IL6R, DHX40, MEF2A, HBP1, IGJ, WHSC1L1	<u>developmental process</u> , <u>positive regulation of cellular metabolic process</u> , <u>regulation of nitrogen compound metabolic process</u>
hsa-miR-191-5p	AMMECR1L, TJP1, ZBTB34, DTD2, FUBP3, TMOD2, TLX3	<u>developmental process</u> , <u>cellular nitrogen compound metabolic process</u> , <u>regulation of nitrogen compound metabolic process</u>
hsa-miR-26a-5p	PDHX, CDK6, SMAD1, FGF9, PTEN, TET1, MAP3K2, HOXA9, PDCD10, GSK3B	<u>DNA binding</u> , <u>gene expression</u> , <u>regulation of cellular component organization</u>
hsa-miR-34a-5p	NOTCH1, MAP2K1, MET, PDGFRA, E2F3, VAMP2, MDM4, PTPN4, E2F5	<u>system development</u> , <u>regulation of cellular protein metabolic process</u> , <u>endomembrane system</u>
hsa-miR-454-3p	C16orf70, RNF41, ANKRD52, PSAP, ARL6IP1, IRF1, PCNX, HPRT1, CLCN5, SMARCD2, TBL1XR1	<u>DNA-binding transcription factor activity</u> , <u>metal ion binding</u> , <u>regulation of catalytic activity</u>
hsa-miR-7-5p	CAND1, DDIT4, FBXO28, H2AFV, PTPNA, SETD8, ZBTB38, NUPL1	<u>metal ion binding</u> , <u>cellular protein modification process</u> , <u>positive regulation of gene expression</u>
hsa-miR-17-5p	STAT3, ETV1, MMP2, TBC1D9, PKD2, SAMD12, PFN2, EIF4G2, MAP3K9	<u>protein phosphorylation</u> , <u>apoptotic process</u> , <u>positive regulation of cellular metabolic process</u>
hsa-miR-302c-3p	ZZNRF33, LATS2, ZBTB7A, RAB22A, MTMR4, C10orf12, KLHL15, ZNF148, ZNF800, NUFIP2	<u>DNA-binding transcription factor activity</u> , <u>nuclear chromosome</u> , <u>nucleotide binding</u> , <u>establishment of localization in cell</u>

The top 15 biological processes identified in Gene Ontology (GO) pathways revealed that mRNAs positively co-expressed with LINC01419 participated in various processes related to cancer regulation as cell proliferation, cell cycle, and migration as shown in the figure below



LINC01419

Moreover, LINC01419 affect the expression of various genes by other mechanisms too. To further investigate the function of LINC01419, we firstly obtained 1,000 co-expression genes of LINC01419 from GEPIA2 in LIHC. Secondly, we selected 55 mRNAs that are up or down regulated in LIHC (Liver hepatocellular carcinoma). Blue and red colors indicate the co expressed genes that are up regulated or down regulated, respectively, in LIHC as shown in the Figure below.



(Figure S1): Co-expression genes of LINC01419 from GEPIA2 in Liver hepatocellular carcinoma.