

Table S24. Local sequence alignment and similar secondary structures motifs of lincRNAs of human chromosome 18.

Local sequence alignment*											Protein interactors**		
LINC01916				LINC01415				Score	%id	P-Value	E-Value	PABPC1 MBNL1 RBMX KHDRBS3 ELAVL1 SFRS13A	
Rank	Start	Stop	Strand	Start	Stop	Strand							
1	826	1018	+	5544	5736	+	454	45	6.40E-02	6.60E-02			
..... 1 2 3 4 5 6 AUUGAAUUUUAAUAUUUAUAUUAUGAAAUGAUCUGCCACUGUUUUUGUAAGUGUACCUG AUUUCUAUCGAAUCUUUAUGCAAUUAGGUUACUGAACUUUUGAAAUCAAAGGAGGAAAUC ..(((((((.....((.....)).....((.....)))).....)) ..EEEEEE.CCCCC.....AA.....aa.....BB.BBBB.....bbbb.....bb													
..... 7 8 9 0 1 2 CUAUUAUGACUAUAUUUUCAGUUAAGAUUCAUGACGUUUUUGUGAGAAAAUAUUU- UA AGAUUUUGUGGUUUUGCCCAGUAUACUAUAGAAUGUCAAUUUUGUUCUAUUUAUAAAAUA ..))))))((((.....)))))).....)))))).....(((((((.....((.....)).....)) .ccccccDDDD.....dddd.....eeeeeee.JJJJFFFFFFFF.....FF.....ff.f f													
..... 3 4 5 6 7 8 AAAACUUGU- UAAUUUUUUCAGAUUAACUACAAAAAAUCUAUUGUAAAAUUUAUAAAAU AUAUUCUAUAUAUUUAUUCUUAUA- - UUGAACAACUAUUCUAUAUAUAAUAUGCUA ..)))).....(((.....((((.....((.....)))))).....)))).....((..... ffffff.....IIII.....GGGGG...GGGGG.....ggggg...ggggg.HH....													
..... 9 ACUAAUAUAUAAGUC AUAUAAGAAUAAGAC ..)).....)).....)) ..hh.....iiii.jjj													
Актив													
LINC01916				LINC01415				Score	%id	P-Value	E-Value		Pum2 KHDRBS3
Rank	Start	Stop	Strand	Start	Stop	Strand							
2	599	657	+	4381	4440	+	447	57	7.45E-02	7.74E-02			
..... 1 2 3 4 5 6 UAUAUGUCAUGAUUAAUGUUAUCUAU- AAUGAGUGUAUUAGGGAUACAUAUAAUUAUCACA UACAUAUAAAAUGUUAAGAUAUAUUUAGAUAAAUGUAUCAAGUAUUUUUUAUUUUUUUA(((((((.....((.....)))))).....)))).....)))).....((.....AAA.AA.AAAAAAA.AAAA.....AAAA.....aaaa.....aaaaa.....aaa													

LINC02564				LINC01919				Score	%id	P-Value	E-Value	a2bp1 EIF4B MBNL1 Vts1 RBMX KHDRBS3
Rank	Start	Stop	Strand	Start	Stop	Strand						
1	65	265	+	212	408	+	645	34	2.50E-03	2.50E-03		
..... 1 2 3 4 5 6												
GCGGGCGGUCCAGGGCCGCCUGGCGCAGCAGCCUGUCCAGCCGCGGUCCCCUGCAGUCCCU												
UUUUUCUUCUGAAACCUCUGCAGUGGUAG- - CAAUGCACUGAAGUUUGAUUAAAAGUUU												
((((((((.....((((((((((((.....((.....))).....)))((((.....((.....))).....)))												
IIIGGGG.....GGGGGGEEAAA..AA.....aaaDD...BB.....												
..... 7 8 9 0 1 2												
CCCUGGCGGCGUGCGCAGCCGUCCACGACAGGGGCCAUAAACUCUCCAG- AGCGGAAAGC												
ACUGGUCAUUCUGCCAUGAGAGAUGAUAGAGAAUAUCACCACAGUGUGACUUGCUUC												
))(((.....))).....)).....)).....)).....(((((.....))).....))												
bbCCC.CC.....cccc..dd.....ee.....FFFF..FFFF...f												
..... 3 4 5 6 7 8												
CGCACCCUGGUGGCCCGGCCCGCGCCAGACCUGGCGGCGCGUGGCACCUGACCCGCGUG												
AAGGCAGCAUGGUUUC AUGCAGAGGAUCUAAACUGGGGACCAUGUGC- - - UGGGCUGCAA												
)).....))).....)).....)).....(((((.....((.....((.....))).....))												
fff...fffffgggggg.....ggggg...HH.HHHHHH..HH...HHH.....hhh.												
..... 9 0 ..												
CAUGGGUCUCCAGGGAGCUCGC												
AAGGGCUGUGCAGUGCCUAAAA												
.....)).....)).....)).....)).....))												
... hhhh... hhhh... hhi i i												
Актив												
LINC02564				LINC01919				Score	%id	P-Value	E-Value	MBNL1 RBMX ELAVL1 KHDRBS3
Rank	Start	Stop	Strand	Start	Stop	Strand						
2	617	718	+	386	485	+	416	48	8.06E-02	8.41E-02		
..... 1 2 3 4 5 6												
AAGUAGCUGGAACUACAGAUGUGCACUGCCAUGCCAGGCUUGUCUAACAUAU- UUUAUGUG												
AAAGGGCUGUGCAG- - - UGCCUAAAUGUUAUGCAAAAUUUUAUAAAGGUAGGUCAUGUA												
((.....(((.....(((.....(((.....((.....))).....))).....((.....((.....))).....)))												
EE.CCCC...CCC...AAAAA.AA..AAA.....aaaaa...aaaaa...BBB..												
..... 7 8 9 0 ..												
UUGCUCACUCCAGUUUGCUAGAGUUUUUGGAGAUUUCUGUCUU												
UUGCUCCAUUGAUGCUGCCCUUAUUC AUGAUGAUUAAAGCCUU												
.....)).....)).....)).....((.....((.....)).....)).....))												
..... bbb...ccc.ccccDDD.DD.....dd.ddd...ee												

[illegible]

[illegible]

**web-based tool ‘linc2function’ [S2] (<https://bioinformatics-lab.erc.monash.edu/linc2function>) was used for prediction of proteins, interacting with motifs of lincRNAs: modes – ‘ANN’ and ‘full model’, species – ‘Homo sapiens’.

Abbreviations:

a2bp1, RNA binding fox-1 homolog 1;

EIF4B, eukaryotic translation initiation factor 4B;

ELAVL1, ELAV like RNA binding protein 1;

FUS, FUS RNA binding protein;

KHDRBS3, KH RNA binding domain containing, signal transduction associated 3;

KHSRP, KH-type splicing regulatory protein;

MBNL1, muscleblind like splicing regulator 1;

PABPC1, poly(A) binding protein cytoplasmic 1;

Pum2, pumilio RNA binding family member 2;

RBMX RNA binding motif protein X-linked;

SFRS1, serine and arginine rich splicing factor 1;

SFRS13A, serine and arginine rich splicing factor 10;

SFRS9, serine and arginine rich splicing factor 9.

References

[S1] Sundfeld D, Havgaard JH, de Melo AC, Gorodkin J. Foldalign 2.5: multithreaded implementation for pairwise structural RNA alignment. *Bioinformatics*. 2016;32(8):1238-40. doi: 10.1093/bioinformatics/btv748.

[S2] Ramakrishnaiah Y, Morris AP, Dhaliwal J, Philip M, Kuhlmann L, Tyagi S. Linc2function: A Comprehensive Pipeline and Webserver for Long Non-Coding RNA (lncRNA) Identification and Functional Predictions Using Deep Learning Approaches. *Epigenomes*. 2023;7(3):22. doi: 10.3390/epigenomes7030022