

Supplemental material - novel RNA structures in human UTRs

Following table depicts Dialign-2 alignments of highly conserved regions in untranslated regions of mature human mRNAs, their corresponding RNA consensus structure as detected by RNAz and Rfam annotations. The annotation of putative RNA structures was done by using cmsearch of the Infernal toolkit. Each sequence of an alignment has been aligned to each Rfam RNA model and the model had to match completely with a significant bit score in order to get reported.

5' UTR

Description	Sequence/Structure
Alignment 1778 (SVM RNA-class probability: 0.999940; MFE = -47.75)	
ENST00000266746.1 ENSG00000120853.3	GGTCATCTGCAGCAGTAtgtggccacctatcagcagcaggtggtcacCTATCAGCAGCTG
ENST00000299125.3 ENSG00000166104.3	GGTCTTCTGCAGCAGTA-----CTATCAGCAGCTG
RNAz consensus structure	(((((.....)))))).....(((((.....)))))).....(((((.....)))))).....
ENST00000266746.1 ENSG00000120853.3	ACCTCTGAGGAGGAGGCTGCACAacCAGTTACTGCTGCAGACCCAGCTCGTGGACCGG
ENST00000299125.3 ENSG00000166104.3	ATCTCTGAGGAGGAGGCACTGCACAggCAGTTATTTCTGCAGATCCAGCTCGTGGACCAG
RNAz consensus structure	.(((.....)))))).....)))))).....)))))).....)))))).....)))))).....
ENST00000266746.1 ENSG00000120853.3	CTGCAGCagcagaagctCAAAGCAAAGctgtggccaAGATGGGCTGCCAAGAGTTGCGG
ENST00000299125.3 ENSG00000166104.3	CTGCAGCac-----CAGAGAAAAGagtagcag-AGATGGCCTGCCAAGAGTTGCAG
RNAz consensus structure	(((((.....)))))).....)))))).....)))))).....)))))).....)))))).....
ENST00000266746.1 ENSG00000120853.3	GAG
ENST00000299125.3 ENSG00000166104.3	GAG
RNAz consensus structure	...

Rfam match in stockholm format (Bit score: 6.8; negative strang; IRE)

```
<<<<---<<<<_____>>>>->>>>
Model      1 uuUcuCGCuucaACAGUGuUuggaCagAag 30
           U : +GC      :CAGUG+ :   C : A
Query      80 AUAACUGCCUGUGCAGUGCCUCCUCUCAG 109
```

Alignment 1401 (SVM RNA-class probability: 0.992147; MFE = -67.32)

ENST00000306882.2 ENSG00000172352.2	CCAAGCTGTCCCACCGAGTAAGTATGGAGAGGTTTCAGGCACATGGCATAGCTGCTAT
ENST00000306609.2 ENSG00000172288.2	CCAAGCTGTCCCACCGAGTAAGTATGGAGAGGTTTCAGGCACATGGCATAGCTGCTAT
ENST00000250838.2 ENSG00000129873.2	CCAAGCTGTCCCACCGAGTAAGTATGGAGAGGTTTCAGGCACATGGCATAGCTGCTAT
RNAz consensus structure(((.....))))((.....)).....))))((.....)))).....(((((.....)))))).....
ENST00000306882.2 ENSG00000172352.2	TTCGCACAATTTTCACTACACCAGTGGTGACAAAATAGAAGAGTTTCATCCATACACAGA
ENST00000306609.2 ENSG00000172288.2	TTCGCACAATTTTCACTACACCAGTGGTGACAAAATAGAAGAGTTTCATCCATACACAGA
ENST00000250838.2 ENSG00000129873.2	TTCGCACAATTTTCACTACACCAGTGGTGACcAAATAGAAGAGTTTCATCCATACACAGA
RNAz consensus structure	(.....(((((.....)))))).....)))))).....)))))).....)))))).....)))))).....
ENST00000306882.2 ENSG00000172352.2	ACCTGGTGAAGAGCTGGAGGCAGAAAGAAGTGTCTATGTGGAGACGCAACTGAAACAAAG
ENST00000306609.2 ENSG00000172288.2	ACCTGGTGAAGAGCTGGAGGCAGAAAGAAGTGTCTATGTGGAGACGCAACTGAAACAAAG
ENST00000250838.2 ENSG00000129873.2	ACCTGGTGAAGAGCTGGAGGCAGAAAGAAGTGTCTATGTGGAGACGCAACTGAAACAAAG
RNAz consensus structure	..)).....)))))).....)))))).....)))))).....)))))).....)))))).....
ENST00000306882.2 ENSG00000172352.2	GTGGCAGCAACTGTTCCA
ENST00000306609.2 ENSG00000172288.2	GTGGCAGCAACTGTTCCA
ENST00000250838.2 ENSG00000129873.2	GTGGCAGCAACTGTTCCA
RNAz consensus structure)))))).)))))).)))))).....)))))).....)))))).....)))))).....)))))).....

Rfam match in stockholm format (Bit score: 9.89; positive strang; IRE)

```
<<<<---<<<<_____>>>>->>>>
Model      1 uuUcuCGCuucaACAGUGuUuggaCagAag 30
           :UU:UC CU CA:CAGUG :UG ACA:AA:
Query      78 AUUUUCACUACACCAGUG-GUG-ACAAAAU 105
```

Alignment 1487 (SVM RNA-class probability: 0.999621; MFE = -28.65)

ENST00000336053.2|ENSG00000092199.5 CCAGGCTGGTCTCAA...
ENST00000336648.1|ENSG00000159267.5 CCAGGCTGGTTTCGA...
RNaz consensus structure ...(((.....(((.....)))).....))(((.....
ENST00000336053.2|ENSG00000092199.5 TGTTGGGATTACAGGTGTGAGCCACCacacttggccttaaaatatttttaatttccTCAA
ENST00000336648.1|ENSG00000159267.5 TGCTGGGATTACAGGTGTGAGCCACCgcgccctggcctgtattt-----TCAA
RNaz consensus structure ...)))).....)))))).....
ENST00000336053.2|ENSG00000092199.5 TT
ENST00000336648.1|ENSG00000159267.5 TT
RNaz consensus structure ..

Rfam match in stockholm format (Bit score: 6.31; positive strang; IRE)

<<<<---<<<<_>>>>->>>>
Model 1 uuUcuCGCuucaACAGUGuUuggaCagAag 30
U:: C U C:A AGUG+U:GA ::G
Query 42 UCGGCC--UCCCAAAGUGCUGGGAUUACAG 69

3' UTR

Description Sequence/Structure
Alignment 4105 (SVM RNA-class probability: 0.995304; MFE = -51.30)
ENST00000350997.1|ENSG00000134822.6 TGGGTAGGAAAATTAGAAGCAAGCTGGATGca---GTGGCTCATGCCTGTAATCCCAACA
ENST00000319903.3|ENSG00000066294.3 TGGGAATTACAGATAAACGGAAGCCGGCTGgggtgGTGGCTCAGCCTGTAATCCCAACA
RNaz consensus structure .(((.....(((.....(((.....(((.....(((.....(((.....
ENST00000350997.1|ENSG00000134822.6 CTTTtGGGAGGTCCAGGCAGGAGGATCACTTGGGCCAGGAGTcaagcc-----
ENST00000319903.3|ENSG00000066294.3 CTTT-GGGAGGCCAAGGCAGGCGGATCACCTGAGGTGAGGAGTTCgagattagtctggcc
RNaz consensus structure ...)))).....))))))(((.....)))))).....
ENST00000350997.1|ENSG00000134822.6 -----
ENST00000319903.3|ENSG00000066294.3 aacatggtgaaccccatctactaaaaatacgaattagccaggtgtggtggcacaca
RNaz consensus structure(((.....(((.....(((.....(((.....
ENST00000350997.1|ENSG00000134822.6 -----
ENST00000319903.3|ENSG00000066294.3 tctgtagtccagctactctggaggctgagacaggagaatcgcttgaaccaggaagtgg
RNaz consensus structure)))..(((.....)))))).....)))))).....
ENST00000350997.1|ENSG00000134822.6 ----TGCAGCGAGCTGAGATCACACCACTGCACTCCAGCCTGGG-GTGATAGACAAGAC
ENST00000319903.3|ENSG00000066294.3 aggtTGCAGTGAGCTGAGATCACACCACTGCACTCCAGCCTGGGgAGACAGAGTGAGAC
RNaz consensus structure))).....))))((.....)))))).....))))))(((.....)).....
ENST00000350997.1|ENSG00000134822.6 CCTGTCTC
ENST00000319903.3|ENSG00000066294.3 TCCATCTC
RNaz consensus structure)).....

Rfam match in stockholm format (Bit score: 8.24; negative strang; IRE)

<<<<---<<<<_>>>>->>>>
Model 1 uuUcuCGCuucaACAGUGuUuggaCagAag 30
UU: C U C:A AGUGUU:G A :AG
Query 234JUGGCC--UCCCAAAGUGUUGGGAUUACAG 261

Alignment 4861 (SVM RNA-class probability: 0.991040; MFE = -37.55)

ENST00000334271.2|ENSG00000152056.4 AGGGAATAgcttgTAGGCCGGGAGTGGTGGCTTACACCTgTAATCCAGCACTTTGGGA
ENST00000298004.3|ENSG00000165282.3 AGTGAATAaaa--TAGGCCGGGCGTGGTACTTGCACCTaTAATCCAGCACTTTGGGA
RNaz consensus structure(((.....(((.....)))).....(((.....))))))
ENST00000334271.2|ENSG00000152056.4 GGCCGAGGcaGGTGGATCACTTGGAGTTCAGAGCAGCCTGgccAATATGATG

```
ENST00000298004.3|ENSG00000165282.3 GGCAGAGGtgGGAGGATTGCTTGGTCCCAGGAGTTCAAGACCAGCTGtgAACATAACA
RNAz consensus structure )))(((((((.(.(((((((((((((((....)))))))))....))))))

ENST00000334271.2|ENSG00000152056.4 AAACCCCATCTCTACTAAAAATACAAAA
ENST00000298004.3|ENSG00000165282.3 AGACCCCGTCTCTACTATTAAAAAAA
RNAz consensus structure ..))))).....
```

Rfam match in stockholm format (Bit score: 8.26; negative strang; IRE)

```
<<<<<-----<<<<<_>>>>>->>>>>
Model      1 uuUcuCGCuucaACAGUGuUuggaCagAag 30
          : :U  C  U  C:A AGUG+U:G A  A ::
Query      83 UCUGCC--UCCCAAAGUGCUGGGA-UUAUA 109
```

Alignment 5334 (SVM RNA-class probability: 0.999966; MFE = -43.76)

```
ENST00000299866.3|ENSG00000166676.3 TTTATT-----TTTATTTTATTTTTTTTG---AGACACGGTCTCAGCTGT
ENST00000315599.4|ENSG00000090659.4 TTATTT-----TTTAATTACTATTTTTTTTtaaAGATGGGTCTTGCTCTGT
ENST00000305141.2|ENSG00000171596.4 ATCAGT-----CTACCTTTCTTTTTTCTG---AGACAGAGTCTCACTCTGT
ENST00000278379.1|ENSG00000110436.2 AGTAGTagaaaatgcatcTTTTTTTTTTTTTTTTTTT---AGACAGAGTCTTGCTCTGT
RNAz consensus structure .....(((((((....))))))

ENST00000299866.3|ENSG00000166676.3 TGCCCAGGCTGGAGTGCAGTGGCGGATCTCgcCTTACTGCAGCC-----TCGCCTCC
ENST00000315599.4|ENSG00000090659.4 CG-CCAGGCTGGAGTGCAGTGGCGGATCTAGGCTCACTGCAACT-----TCGCCTCC
ENST00000305141.2|ENSG00000171596.4 CGCCCAGGCTAGAGTGCAGTGGCGGATTTGGTCACTGCAACC-----TCGCCTCC
ENST00000278379.1|ENSG00000110436.2 TGCTCAGGCTGGAGTACAGTGGCACGATCTCAGTCACTGCActgcaatgTCCACCTCTC
RNAz consensus structure (((.(((.....)))))).....((((....

ENST00000299866.3|ENSG00000166676.3 AGGTTC AAGCGATTCTCCTGCCTCAGCCTCCTGAGTAGTGGGACTACA-----
ENST00000315599.4|ENSG00000090659.4 GGGTTC AAGCGATTCTCCTGCCTCAGCCTCCCAGTAGTGGGACTccactaaaagtaca
ENST00000305141.2|ENSG00000171596.4 GGGTTC AAGCGATTCTCCTGCCTCAGCCTCCCAGTAGTGGGACTACA-----
ENST00000278379.1|ENSG00000110436.2 TAGTTC AAGCGATTCTCCTGTCTCAGCCTCCCAGTAGTGGGACTACA-----
RNAz consensus structure ..)).....))))))..)).....(((((((.....

ENST00000299866.3|ENSG00000166676.3 -----GGCaTGCGCCACCACCCGGCTAATTTTCAT--ATTTTGTAGTAGAGC
ENST00000315599.4|ENSG00000090659.4 aaaattagctgGGCGTGACCCTGCGCCAGCTAATTTCTTGT--ATTTTGGTAGAGC
ENST00000305141.2|ENSG00000171596.4 -----GGTgAGCCCAACATGCCAGCTAATTTTTTTTAAATTTTGTAGTAGAGC
ENST00000278379.1|ENSG00000110436.2 -----GGCaTGCGCCACCATGCCTGGCTAATTTTTTGTA--TTTGTAGTAGAGC
RNAz consensus structure .....)))))).....))

ENST00000299866.3|ENSG00000166676.3 AGTGTTCCTCCATGTT
ENST00000315599.4|ENSG00000090659.4 GGGTTTCAACATGTT
ENST00000305141.2|ENSG00000171596.4 GGGTTTCAACATGTT
ENST00000278379.1|ENSG00000110436.2 -GGTTTCAATATGTT
RNAz consensus structure ))))...))..))
```

Rfam match in stockholm format (Bit score: 8.28; positive strang; IRE)

```
<<<<<-----<<<<<_>>>>>->>>>>
Model      1 uuUcuCGCuucaACAGUGuUuggaCagAag 30
          U  U  :+   :::ACAGUG  U:::  : A  G
Query      184 UUUAGU--AGAGACAGUG-UUUCU-CCAUG 209
```

Rfam match in stockholm format (Bit score: 12.17; negative strang; REN-SE)

```
<<-<<<<_>>>>>:~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~~::~
Model      1 cuGcuuuGAGGAaaaacagAAUAAAGACUUCAUGUUU 37
          UG:::U +A  AA  A:::A+AA AAAGA U+CAU  UU
Query      187 -UGUCUAAAAAAAAAAAAAAAAAAGAAUGCAUUUUUC 222
```

Alignment 4662 (SVM RNA-class probability: 0.999859; MFE = -78.75)

```
ENST00000336706.1|ENSG00000181894.4 GAAGTCgttctcttaagactgaacaagcagcagatGTGGTGGCTCAGCCTGTAAT
ENST00000350009.1|ENSG00000149451.5 GAAGTCaaagaaagacatgttgctataggc-----GTGGTGGCTCATGCTATAAT
```

RNAz consensus structure ...((((.....(((.....((((.....(((((((.....((((.....(

ENST00000336706.1|ENSG00000181894.4 CCTAGCACTTTGGGAGGCCgaggcgccaGATCACAAggtt--AGGAGTTCAAGACCAGC

ENST00000350009.1|ENSG00000149451.5 CCCAGCACTTTGGGAAGCCgggttaggagGATCACCAGaggccAGCAGGTCCACACCAGC

RNAz consensus structure (((((.....)))))).....))))))....))))))))).....)))))).(((

ENST00000336706.1|ENSG00000181894.4 CTGGCCAGCAatggt--GAAACCCCATCTCTACCAAAAAATacaggAAATTATCTGGGCATA

ENST00000350009.1|ENSG00000149451.5 CTGGCAACAcagcaaGACACCGCATCTACAGAAAAATtta--AAATTAGCTGGGCGTG

RNAz consensus structure (((.....((((.....((((.....((((.....(

ENST00000336706.1|ENSG00000181894.4 GTAGTGTCCTGTAatcccAGCTACTTGGGAAGCTGAGGCAGGAGAATTGCTTGAACC

ENST00000350009.1|ENSG00000149451.5 GTGGTGTGTACCTGTAaggcctAGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCC

RNAz consensus structure ..(((.....)))..)).....)))))(((.....((.....))..((.....))).....

ENST00000336706.1|ENSG00000181894.4 TgggaggtggaggtTGCACTGAGCTAagatcGCACCACTGCACTCCAGCCTGGGTGACAG

ENST00000350009.1|ENSG00000149451.5 Tgagttcaaac--TGCACTGAGCTAatggtgGCACCACTGCACTCCAGCCTGGGTGACAG

RNAz consensus structure))).....)))..(((((((.....)))..)).....))).....))).....(((

ENST00000336706.1|ENSG00000181894.4 AGCGAGACTccatttcaaaa-----AAAAAGAC

ENST00000350009.1|ENSG00000149451.5 AGCAAGACcctgtctctaaataaatttAAAAAGAC

RNAz consensus structure (((.....)))).).....

Rfam match in stockholm format (Bit score: 8.33; positive strang; IRE)

```

                <<<<---<<<<_..____>>>>->>>>
Model      1   uuUcuCGCuucaAC...AGUGuUuggaCagAag 30
           :UU::C  ::CA  AGUGU UG:: ::AA:
Query      163 AUUAUCUGGGCAU-aguAGUGUGUGCCUGAAU 194

```

Alignment 3993 (SVM RNA-class probability: 0.992001; MFE = -54.95)

ENST00000313577.4|ENSG00000181719.4 CTTGCACTGTATTGCTCATCTGCTTTGGAGAACACAGTTTCTAACAGACTTCAACAGA

ENST00000327173.4|ENSG00000180747.4 CTTGCACTGTATTGCTCACCTGCTTTGGAGAACACAGTTTCTAACAGACTTAAACAGA

ENST00000325834.1|ENSG00000178887.2 CTTGCACTGTATTGCTCGTCTGCTTTGGAGAACACAGTTTCTAACAGACTTCAACAGA

RNAz consensus structure ...(((((((.....(((((((.....))))))((.....)))

ENST00000313577.4|ENSG00000181719.4 GGTCTGTATATTTTTACAAGCACATTCTTATGACTATTAATGGTCATTACTGTAGAACAA

ENST00000327173.4|ENSG00000180747.4 GGTCTGTATATTTTTACAAGCACATTCTTATGACTATTAATGGTCATTACTGTAGAACAA

ENST00000325834.1|ENSG00000178887.2 GGTCTGTATATTTTTACAAGCACACTCTTATGACTATTAATGGTCATTACTGTAGAACAA

RNAz consensus structure))))))).....)))((.....(((.....))).....((

ENST00000313577.4|ENSG00000181719.4 AGACCTTATTTTTTGGAGTTTTTTGAAATAGGATTTGTAGTTGGGCAAGCTGGTAAATCCA

ENST00000327173.4|ENSG00000180747.4 AGACCTTATTTTTTGGAGTTTTTTGAAATAGGATTTGTAGTTGGGCAAGCTGGTAAATCCA

ENST00000325834.1|ENSG00000178887.2 AGACCTTATTTTTTGGAGTTTTTTGAAATAGGATTTGTAGTTGGGCAAGCTGGTAAATCCA

RNAz consensus structure (((.....)))..))))).)))))..))))).)))))..((.....))

ENST00000313577.4|ENSG00000181719.4 GAAATCTAACATGCCTGTTTT

ENST00000327173.4|ENSG00000180747.4 GAAATCTAACATGCCTGTTTT

ENST00000325834.1|ENSG00000178887.2 GAAATCTAACATGCCTGTTTT

RNAz consensus structure).....)))..)))))..

Rfam match in stockholm format (Bit score: 10.87; negative strang; SECIS)

```

                <<<<---..--<<<<<<<<<<<<<<<<<<<<<<<<<<--->>>>->>>>>>>>>>>>>>>>>>>>>. -
Model      1   gucuuuuu..uAUGAuGaccucagccuAAAccccuugggGcaggcugagguCuGA U.g 57
           :U::+  UA+  :GACC C+G::+AAA+:C: +U :G:  ::C+G GGUC:: + +
Query      121 CUUGUAAAaaUAUACAGACCUCUGUUGAAAGUCUGUU-AGA---AACUGUGGUCUCC A aA 176
           ---->>>>>
Model      58  cuuggagac 66
           ++ G:::A:
Query      177 GCAGACGAG 185

```

Rfam match in stockholm format (Bit score: 9.19; negative strang; IRE)

```

<<<<<---<<<<<_<<<<<_>>>>>->>>>>
Model      1  uuUcuCGCuucaACAGUGuUuggaCagAag 30
           : :U U+   : : AC GUGUU : : A A : :
Query      152 UCUGUU--AGAAACUGUGUUCUCC-AAAGC 178

```

Alignment 4819 (SVM RNA-class probability: 0.996484; MFE = -50.95)

```

ENST00000343028.1|ENSG00000064115.2 GTGGCTCACACCTGTAATCCCAATACTgggaagccaagGTGGGAGTATCGCTTGAGCCCA
ENST00000332589.1|ENSG00000185753.3 GTGGTTCACGCCTGTAATCCCAGCACT-----GTGGGCGGATCACTTGAGCCCA
RNAz consensus structure                ..(((((((.....((((.....)))))).....))))((.....((((.....((((.....
ENST00000343028.1|ENSG00000064115.2 GGAGTTTGAGACCGACaTGGGCAACATGACAAGACCCCATCTCTACAAAAAAATTaAAAA
ENST00000332589.1|ENSG00000185753.3 GGAGTTTGAGACCAACcTGGGCAAGATGGCGAGACCCCATCTCTACAAAAAAATTtAAAA
RNAz consensus structure                ((.....((((.....)))))).....((((.....((((.....
ENST00000343028.1|ENSG00000064115.2 ATTAGCCAGGCATGGTGGCACATGCCTactcc--CAGCTCCAAGGAGACTGAGATGGGA
ENST00000332589.1|ENSG00000185753.3 ATTACCTGGCATGGTGGCACACACCTttattctCAGTACTCAGGTGGCTGAGGTGGGA
RNAz consensus structure                .....(((((((.....)))))).....(((((((.....)))))).....
ENST00000343028.1|ENSG00000064115.2 GGATCCCTGGAGCC
ENST00000332589.1|ENSG00000185753.3 GGATCCCTTGAGCC
RNAz consensus structure                .)))))))).))))))

```

Rfam match in stockholm format (Bit score: 11.29; negative strang; IRE)

```

<<<<<---<. <<<<<_<<<<<_>>>>>->>>>>
Model      1  uuUcuCGCu.ucaACAGUGuUuggaCagAag 30
           :U : UC      C : ACAGUG+U : G   A : : A :
Query      144 GUGAUC--CgCCCACAGUGCUGGG--AUUAC 170

```

Alignment 5338 (SVM RNA-class probability: 1.000000; MFE = -20.97)

```

ENST00000325722.2|ENSG00000142687.5 TTAAACCTGGGAGGTGGAGGCTGCAGTGAGCCAAGATCGTGCCACTGCACTCCAGCCTGA
ENST00000351666.1|ENSG0000012048.5 TTCAGCCCGGGAGGTGGAGGTTGCAGTGAGCCAAGATCATAACCAGGCACTCCAGCCTGG
ENST00000287263.2|ENSG00000156675.3 TTGAACTTGGGAGATGGAGGCTGCAGcGAGCCAAGATCGTGCCACTGCACTCCAGCCTGG
RNAz consensus structure                ....(((((((.....((((.....((((.....((((.....)))))).....)))))).....))))))
ENST00000325722.2|ENSG00000142687.5 GTGACAGagc---AAGACTCcgTCAAAAAAAAAAAAAAAAAAAAAAAGA
ENST00000351666.1|ENSG0000012048.5 GTGACAGtgagactgtggc---TCAAAAAAAAAAAAAAAAAAAAAAGGAA
ENST00000287263.2|ENSG00000156675.3 GcaagagttttttAAGACTCtt-----AAAAAAAAAGA
RNAz consensus structure                )).....

```

Rfam match in stockholm format (Bit score: 12.51; negative strang; IRE)

```

<<<<<---<<<<<_<<<<<_>>>>>->>>>>
Model      1  uuUcuCGCuucaACAGUGuUuggaCagAag 30
           : :U :U+   U : : AA AGU +UU : : A A : A : :
Query      1  UCUUUU--UUUAAGAGU-CUUAAA-AAAAC 26

```

Supplemental material - novel miRNA targets in human 3'UTRs

3' UTR

Alignment 4929

```

ENST00000339642.1|ENSG00000183850.4 TTGCTGCATAAAAGATATGAGATTCTTTTTT
ENST00000275539.3|ENSG00000181342.4 TTGCTGCATCAAAGATATGAGATTCTTTTTT

```

Miranda match - ENST00000339642.1|ENSG00000183850.4 - hsa-miR-187

Forward: Score: 106.000000 Q:3 to 22 R:3 to 21 Align Len (19) (84.21%) (89.47%)
Query: 3' GCCGACGUUGUGUUCUGUGCU 5'
||| | | : | ||| | | | | | | | |
Ref: 5' TTGCTGC-ATAAAAGATATGA 3'
Z-Score: 11.652
Energy: -21.240000 kCal/Mol

Miranda match - ENST00000275539.3|ENSG00000181342.4 - hsa-miR-187

Forward: Score: 104.000000 Q:3 to 22 R:3 to 21 Align Len (19) (89.47%) (89.47%)
Query: 3' GCCGACGUUGUGUUCUGUGCU 5'
||| | | | | | | | | | | | | | | | |
Ref: 5' TTGCTGCATCA-AAGATATGA 3'
Z-Score: 11.109
Energy: -21.969999 kCal/Mol

RNAhybrid match - ENST00000339642.1|ENSG00000183850.4

11746|align_4929|1:31:hsa-miR-187:21:-25.6:0.000096:2:
U UAA G: GCUGCA AAGAUUGA : CGACGU UUCUGUGCU :GC UGUG

RNAhybrid match - ENST00000275539.3|ENSG00000181342.4

11751|align_4929|2:31:hsa-miR-187:21:-25.8:0.000081:2:
U U G: GCUGCA CA AAGAUUGA : CGACGU GU UUCUGUGCU :GC U G

Alignment 4476

ENST00000184183.1|ENSG00000065371.5 AAAATCAATTTTCTTGTAACAAGGTACACACT
ENST00000251776.1|ENSG00000114547.1 AAAATCAATTTTCTTGTAACAAGGTACACACT

Miranda match - ENST00000184183.1|ENSG00000065371.5 - hsa-miR-134

Forward: Score: 107.000000 Q:1 to 22 R:9 to 32 Align Len (23) (73.91%) (86.96%)
Query: 3' GGGAGACCA-GUUGGUCA-GUGU 5'
: : : | | | | | | | | | | | | | | | | | |
Ref: 5' TTTTCTTGTAACAAGGTACACA 3'
Z-Score: 10.503
Energy: -20.770000 kCal/Mol

Miranda match - ENST00000251776.1|ENSG00000114547.1 - hsa-miR-134

Forward: Score: 107.000000 Q:1 to 22 R:9 to 32 Align Len (23) (73.91%) (86.96%)
Query: 3' GGGAGACCA-GUUGGUCA-GUGU 5'
: : : | | | | | | | | | | | | | | | | | |
Ref: 5' TTTTCTTGTAACAAGGTACACA 3'
Z-Score: 10.503
Energy: -20.770000 kCal/Mol

RNAhybrid match - ENST00000184183.1|ENSG00000065371.5

9018|align_4476|1:33:hsa-miR-134:21:-23.1:0.000914:9:
U U A AC: UUUCU GU CAACUGGU CACA : GGAGA CA GUUGGUCA GUGU :G C

RNAhybrid match - ENST00000251776.1|ENSG00000114547.1

9022|align_4476|2:33:hsa-miR-134:21:-23.1:0.000914:9:
U U A A C: UUUCU GU CAACUGGU CACA : GGAGA CA GUUGGUCA GUGU :G C

Alignment 4435

ENST00000250151.2|ENSG00000129277.3 TTATTGTATTAGGTGTCATTTCCATTATTTATATTAGTTTAGCCAAAGGATAAGTGTCCTCC
ENST00000344580.1|ENSG00000189315.1 TTATTGTATTAGGTGTTATTTCCATTATTTATATTAGTTTAGCCAAAGGATAAGTGTCCTCC
ENST00000250151.2|ENSG00000129277.3 CTATGGGGATGGTCCACT

ENST00000344580.1|ENSG00000189315.1 CTATGGGGATGGTCCACT

Miranda match - ENST00000250151.2|ENSG00000129277.3 - hsa-miR-324-5

Forward: Score: 100.000000 Q:3 to 22 R:50 to 72 Align Len (22) (72.73%) (81.82%)
Query: 3' UGUGGUUAC--GGGAU-CCCCUACGC 5'
|: |:|| | |||| | |||||
Ref: 5' GGATAAGTGTCCCCTATGGGGATGGT 3'
Z-Score: 8.407
Energy: -25.090000 kCal/Mol

Miranda match - ENST00000344580.1|ENSG00000189315.1 - hsa-miR-324-5

Forward: Score: 100.000000 Q:3 to 22 R:50 to 72 Align Len (22) (72.73%) (81.82%)
Query: 3' UGUGGUUAC--GGGAU-CCCCUACGC 5'
|: |:|| | |||| | |||||
Ref: 5' GGATAAGTGTCCCCTATGGGGATGGT 3'
Z-Score: 8.359
Energy: -25.090000 kCal/Mol

RNAhybrid match - ENST00000250151.2|ENSG00000129277.3

12631|align_4435|1:78:hsa-miR-324-5p:23:-30.2:0.000062:41:
A AAGGAUAA UC U G : GCCA GUG CCCUA GGGGAUG : UGGU UAC GGGAU CCCCUAC :UG GC

RNAhybrid match - ENST00000344580.1|ENSG00000189315.1

12638|align_4435|2:78:hsa-miR-324-5p:23:-30.2:0.000062:41:
A AAGGAUAA UC U G : GCCA GUG CCCUA GGGGAUG : UGGU UAC GGGAU CCCCUAC :UG GC

Alignment 4202

ENST00000317128.2|ENSG00000177111.2 TTTACCCACTAGATACATATTTGCCACTGGTTAGTTCTCCATCTAAGCTCAAGAGGTTA
ENST00000324472.1|ENSG00000177990.2 TTTACCCACTAGATACATATTTGCCACTGGTTAGTTCTCCATCTAAGCTCAAGAGGTTA

ENST00000317128.2|ENSG00000177111.2 TTCATCTCTCTTTAGATTCCAGTGGTTTTTCTTTTAACTCCAGGTA
ENST00000324472.1|ENSG00000177990.2 TTCATCTCTCTTTAGATTCCAGTGGCTTTTTCTTTTAACTCCAGGTA

Miranda match - ENST00000317128.2|ENSG00000177111.2 - hsa-miR-184

Forward: Score: 118.000000 Q:1 to 23 R:24 to 47 Align Len (23) (73.91%) (86.96%)
Query: 3' UGG-GAAUAGUCAAGAGGCAGGU 5'
: || || |: ||||| ||||
Ref: 5' GCCACTGGTTAGTTCTCCATCTA 3'
Z-Score: 11.492
Energy: -25.650000 kCal/Mol

Miranda match - ENST00000324472.1|ENSG00000177990.2 - hsa-miR-184

Forward: Score: 118.000000 Q:1 to 23 R:24 to 47 Align Len (23) (73.91%) (86.96%)
Query: 3' UGG-GAAUAGUCAAGAGGCAGGU 5'
: || || |: ||||| ||||
Ref: 5' GCCACTGGTTAGTTCTCCATCTA 3'
Z-Score: 11.033
Energy: -25.650000 kCal/Mol

RNAhybrid match - ENST00000317128.2|ENSG00000177111.2

5688|align_4202|1:110:hsa-miR-184:22:-30.2:0.000143:23:
U A G A A: GCC CU GUUAGUUCUCC UCUA : UGG GA UAGUCAAGAGG AGGU : A C

RNAhybrid match - ENST00000324472.1|ENSG00000177990.2

5701|align_4202|2:110:hsa-miR-184:22:-30.2:0.000143:23:
U A G A A: GCC CU GUUAGUUCUCC UCUA : UGG GA UAGUCAAGAGG AGGU : A C