

Figure S2. Locations, structures, sequences and scores of tested mammalian miRNA target sites and mutants and lin-41 controls.

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miRNA: mir-26a
Human predicted target: ENSG00000170365
Mouse predicted target: ENSMUSG00000031681
Rat predicted target: ENSRNOG00000018483
Hs Gene description: MOTHERS AGAINST DECAPENTAPLEGIC HOMOLOG 1 (SMAD 1) (MOTHERS
AGAINST DPP HOMOLOG 1) (MAD-RELATED PROTEIN 1) (
TRANSFORMING GROWTH FACTOR- BETA SIGNALING PROTEIN-1) (BSP-1) (HSMAD1) (JV4-1)
mir-26a ENSG00000170365 2160 nt UTR      2 hits 46 103
-1--1-----
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>ENSG00000170365 hs-mir-26a      46      53
UUCAAGUAAUCCAGGAUAGGCU&GCAUCUGCCUCUGGAAAACUAUUGAGCCUUGCAUGUACUUGAAG
(((((((((((((...((((&.....)))))))))).....)))))))). -21.80
>ENSG00000170365 hs-mir-26a     103     110
UUCAAGUAAUCCAGGAUAGGCU&GACACGAUUGAGAACUGACAAAGGAGCCUUGAUAAUACUUGAC
.(((((((((((.....((((&.....))))))))))..)))). -17.00
mir-26a ENSMUSG00000031681      3248 nt UTR      2 hits 46 103
-1--1-----
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-
>ENSMUSG00000031681 hs-mir-26a   46      53
UUCAAGUAAUCCAGGAUAGGCU&GCUUCCGUCUCUUGCAAACUAUCGAGCCUUGCAUGUACUUGAAG
(((((((((((...((((&.....)))))))))).....)))))))). -19.50
>ENSMUSG00000031681 hs-mir-26a   103     110
UUCAAGUAAUCCAGGAUAGGCU&GACAGGAUGGAGACCUGACGAAGGAGCCACGAUAAUACUUGAC
.(((((((((((.....((((&.....))))))))))..)))). -15.60
mir-26a ENSRNOG00000018483      2285 nt UTR      2 hits 49 102
-1--1-----
-----
>ENSRNOG00000018483 hs-mir-26a   49      56
UUCAAGUAAUCCAGGAUAGGCU&GCUUCUGUCUCUUGCAAACUAUUGGGCCUUGCAUGUACUUGAAG
(((((((((((...((((&.....)))))))))).....)))))))). -19.50
>ENSRNOG00000018483 hs-mir-26a   102     109
UUCAAGUAAUCCAGGAUAGGCU&GUCAGACAGGAUGGGGAGCUGUAAAGGAGCCGUGAUACUUGAC
.(((((((((((...((((&.....)))))))))).....)))))))). -16.20
Wild type PCR fragment:
CACAAcGagctcGGCATCTGCCTCTGGAAAAC TATTGAGCCTTGCATGTACTTGAAGGATGGATGAGTCAGACACGATTG
AGA ACTGACAAAGGAGCCTTGATAA TACTTGA CCTCTGtctagaGTTGTG
Mutant PCR fragment:
GGCATCTGCCTCTGGAAAAC TATTGAGCCTTGCATGTtCgTtAAGGATGGATGAGTCAGACACGATTGAGA ACTGACAAA
GGAGCCTTGATAA TtCgTtA CCTCTG

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miRNA: mir-23a
Human predicted target: ENSG00000107562
Mouse predicted target: ENSMUSG00000030130
Rat predicted target: ENSRNOG00000013589
Hs Gene description: STROMAL CELL-DERIVED FACTOR 1 PRECURSOR (SDF-1) (CXCL12)
(PRE-B CELL GROWTH STIMULATING FACTOR) (PBSF) (HIRH)
mir-23a ENSG00000107562 3504 nt UTR 3 hits 1387 1452 1976
-----1--1-----
1-----
>ENSG00000107562 hs-mir-23a 1387 1394

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AUCACAUUGCCAGGGAUUUC&ACUGGCAAUUUGUAAAAGAAUAUAUAUGAUUAUAAAUGUGAUU
((((((((((((((.....&)))))).....)))))))). -17.65
>ENSG00000107562 hs-mir-23a 1452 1459
AUCACAUUGCCAGGGAUUUC&CAGUGUAUUUUUCACUUGUACUAAAAUUGUAUCAAAUGUGAC
.((((((((.....(((((..&.....))))))..))))).. -13.00
>ENSG00000107562 hs-mir-23a 1976 1983
AUCACAUUGCCAGGGAUUUC&UAAAUCAUUAAAUACCAUUCAGCUUGAAUCAUUUUAAUGUGAC
.((((((((.....(((((..&.....))))))..))))).. -15.10
mir-23a ENSMUSG00000030130 3486 nt UTR 3 hits 830 1888 2470
-----1-----1-----
-----1-----1-----
>ENSMUSG00000030130 hs-mir-23a 830 837
AUCACAUUGCCAGGGAUUUC&GGCCUCCUGUAGAAUGGAGCCAGACCAUCCUGGAUAAUGUGAG
.((((((((((((((((.....&.....))))))..))))).. -24.00
>ENSMUSG00000030130 hs-mir-23a 1888 1895
AUCACAUUGCCAGGGAUUUC&UAAAUCAUUAAAUACCAUUCAGCUUGAAUCAUUUUAAUGUGAC
.((((((((.....(((((..&.....))))))..))))).. -15.10
>ENSMUSG00000030130 hs-mir-23a 2470 2477
AUCACAUUGCCAGGGAUUUC&GUGGGAACUGAGAUAGAUACACUCCUCUAUGUUGCAAUGUGAUU
(((((((((((((((((((((&..)))))).....))))))..)).. -20.56
mir-23a ENSRNOG00000013589 3497 nt UTR 3 hits 847 1895 2465
-----1-----1-----
-----1-----1-----
>ENSRNOG00000013589 hs-mir-23a 847 854
AUCACAUUGCCAGGGAUUUC&GGCCUCCUGUAGAAUGGAGCCAGCCCCUCCUGGAUAAUGUGAG
.((((((((((((((((.....&.....))))))..))))).. -23.80
>ENSRNOG00000013589 hs-mir-23a 1895 1902
AUCACAUUGCCAGGGAUUUC&UAAAUCAUUAAAUACCAUUCAGCUUGAAUCAUUUUAAUGUGAC
.((((((((.....(((((..&.....))))))..))))).. -15.10
>ENSRNOG00000013589 hs-mir-23a 2465 2472
AUCACAUUGCCAGGGAUUUC&GUGGGAACUGAGAGAGAUACCCUCCCAUUGUUGCAAUGUGAUU
(((((((((((((((((((((&.....))))))..)))))..)).. -24.40

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Wild type PCR fragment:

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AAACTACTGGCAATTTGTAAAGAAATATATATGATATATAAATGTGATTGCGAGCTTTTCAATGTTAGCCACAGTGTATTT
TTTCACTTGTACTAAAATTGTATCAAAATGTGACATTATATGCACTAGCAATAAAATGCTAATTGTTTCATGGTATAAACG
TCCTACTGTATGTGGGAATTTATTTACCTGAAATAAAATTCATTAGTTGTTAGTGATGGAGCTTATAGACGTTTCTGGTT
TATATAGTTAAGCCTGCCTGCAGTCAGGTGTCTGAGACCCCTCTCACAGCCCATGTGTGACAGTGTATGGGCTTTTCTC
ACGAGCAGATTAGATCTGCAGCTCAAGTTTTTGGATCTTTTTTTTTTTTTTTTAAACCCGATTGAAATAGCAGTGTGCTGGTT
TTCTGAAGAATAATATTTGACTCACTAATTCGTCTCCCTCCCTCCTCCTTGGTTCTCCTAACTTCCCCATGTAATC
CCCAGAGACTCAACCCTAGTAATATCAACCTTTTACATTTTCCCATGTAAAAATCCCATGACTCCAGGCCATGGTTAATA
TGAAGCTTTTACAGGGACAGGTGGCCTCACCCATAAATCATTAAATACCATTTCAGCTTGAATCATTTTAATGTGACAGT
CA

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Mutant PCR fragment:

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AAACTACTGGCAATTTGTAAAGAAATATATATGATATATAAgTcTtATTGCGAGCTTTTCAATGTTAGCCACAGTGTATTT
TTTCACTTGTACTAAAATTGTATCAAAATGTGACATTATATGCACTAGCAATAAAATGCTAATTGTTTCATGGTATAAACG
TCCTACTGTATGTGGGAATTTATTTACCTGAAATAAAATTCATTAGTTGTTAGTGATGGAGCTTATAGACGTTTCTGGTT
TATATAGTTAAGCCTGCCTGCAGTCAGGTGTCTGAGACCCCTCTCACAGCCCATGTGTGACAGTGTATGGGCTTTTCTC
ACGAGCAGATTAGATCTGCAGCTCAAGTTTTTGGATCTTTTTTTTTTTTTTTTAAACCCGATTGAAATAGCAGTGTGCTGGTT
TTCTGAAGAATAATATTTGACTCACTAATTCGTCTCCCTCCCTCCTCCTTGGTTCTCCTAACTTCCCCATGTAATC
CCCAGAGACTCAACCCTAGTAATATCAACCTTTTACATTTTCCCATGTAAAAATCCCATGACTCCAGGCCATGGTTAATA
TGAAGCTTTTACAGGGACAGGTGGCCTCACCCATAAATCATTAAATACCATTTCAGCTTGAATCATTTTAgTcTtACAGT
CA

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miRNA: mir-23a
Human predicted target: ENSG00000151615
Mouse predicted target: ENSMUSG00000031688

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UACAGUACUGUGUAACUGA&CUCUGAAACAGCUGCCUAGCUUCAGGAACCUUGAGUACUGUGG
(((((((((((((...((((&.....)))))).....)))))))). -20.20
>ENSG00000106462 hs-mir-101 114 121
UACAGUACUGUGUAACUGA&AAAGAACAUGCAGUUUGAAAUUCUGAAUUUGCAAAGUACUGUAA
(((((((((((((...((((&.....)))))).....)))))))). -19.77
mir-101 ENSMUSG00000029687 2260 nt UTR 2 hits 59 114
--1-1-----
-----
>ENSMUSG00000029687 hs-mir-101 59 66
UACAGUACUGUGUAACUGA&CUCUGAAACAGCUGCCUAGCUUCAGGAACCUUGAGUACUGUGG
((((((((((.....((((&.....)))))).....)))))))). -18.76
>ENSMUSG00000029687 hs-mir-101 114 121
UACAGUACUGUGUAACUGA&AACGGAAAUGCAGUUUGAAAUUCUGAAUUUGCAAAGUACUGUAA
(((((((((((((...((((&.....)))))).....)))))))). -19.77
mir-101 ENSRNOG00000006048 2000 nt UTR 2 hits 60 115
--1-1-----
-----
>ENSRNOG00000006048 hs-mir-101 60 67
UACAGUACUGUGUAACUGA&CUCUCAACAGCUGCCUAGCUUCAGGAACCUUGAGUACUGUGG
((((((((((.....((((&.....)))))).....)))))))). -18.76
>ENSRNOG00000006048 hs-mir-101 115 122
UACAGUACUGUGUAACUGA&AAAGGAAAUGCAGUUUGAAAUUUUGAAUUUGCAAAGUACUGUAA
(((((((((((((...((((&.....)))))).....)))))))). -19.77
Wild type PCR fragment:
CACAAAGcagctcTTAGCTTCAGGAACCTCGAGTACTGTGGGCAATTTAGAAAAAGAACATGCAGTTTGAAATTCTGAATT
TGCAAAGTACTGTAAGAATAtctagaGTTGTG
Mutant PCR fragment:
TTAGCTTCAGGAACCTCGAGgAgTtTGGGCAATTTAGAAAAAGAACATGCAGTTTGAAATTCTGAATTTGCAAAGgAgTt
TAAGAATA

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miRNA: mir-101

Human predicted target: ENSG00000134323

Mouse predicted target: ENSMUSG00000037169

Rat predicted target: ENSRNOG00000006308

Hs Gene description: N-MYC PROTO-ONCOGENE PROTEIN

NOTE: N-MYC is also a predicted target of miR-202. The construct below was designed to potentially test the ability of both miRNAs to regulate N-MYC. Thus it contains two seed matches each to miR-101 and miR-202, and one seed hit of each was mutated in the mutant PCR fragment. However, because miR-202 does not appear to be expressed in HeLa cells (i.e. it has never been cloned from HeLa cells), we have not yet tested the ability of miR-202 to regulate to N-MYC UTR.

mir-101 ENSG00000134323 2907 nt UTR 2 hits 494 563

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-----1--1-----
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>ENSG00000134323 hs-mir-101 494 501
UACAGUACUGUGUAACUGA&UUGCGGCCAGUAUUGAGCUGGAAGUUCAUACCUAAGUACUGUAA
(((((((((((((((...(((...&.....)))))).....)))))))). -17.90
>ENSG00000134323 hs-mir-101 563 570
UACAGUACUGUGUAACUGA&GUUUUGUAUACAAUAUAUUGUUAUUCUCUGUUAUGUACUGUAC
(((((((((((...(((...(((...&.....)))))).....)))))))). -17.00
mir-101 ENSMUSG00000037169 2911 nt UTR 3 hits 489 556 2017
-----1--1-----
1-----
>ENSMUSG00000037169 hs-mir-101 489 496
UACAGUACUGUGUAACUGA&UUGCGGCCAGUAUUGAGCUGGAAGUUCACACCUAAGUACUGUAA
(((((((((((((((...(((...&.....)))))).....)))))))). -19.70
>ENSMUSG00000037169 hs-mir-101 556 563

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UACAGUACUGUGUAACUGA&AUGUUUUUGUAUACAAUUAUUGUUAUCUGUUAUGUACUGUAC  
(((((((.....&.....)))))))). -17.50  
>ENSMUSG00000037169 hs-mir-101 2017 2024  
UACAGUACUGUGUAACUGA&AGCCCAAGGUCACAGACAGCUUUGCUUGUGUGGCUGUACUGUC  
.(((((((.....&.....)))))). -17.30  
mir-101 ENSRNOG00000006308 2915 nt UTR 4 hits 484 551 1414 1481  
-----1--1-----1--1-----

>ENSRNOG00000006308 hs-mir-101 484 491  
UACAGUACUGUGUAACUGA&CUCGGGCCAGUAUAGACUGGAAGUUCACACCUAAGUACUGUAA  
((((((((.....&.....)))))))). -19.70  
>ENSRNOG00000006308 hs-mir-101 551 558  
UACAGUACUGUGUAACUGA&AUGUUUUUGUAUACAAUACAUGUUAUCUGUUAUGUACUGUAC  
((((((((.....&.....)))))))). -17.50  
>ENSRNOG00000006308 hs-mir-101 1414 1421  
UACAGUACUGUGUAACUGA&CUCGGGCCAGUAUAGACUGGAAGUUCACACCUAAGUACUGUAA  
((((((((.....&.....)))))))). -19.70  
>ENSRNOG00000006308 hs-mir-101 1481 1488  
UACAGUACUGUGUAACUGA&AUGUUUUUGUAUACAAUACAUGUUAUCUGUUAUGUACUGUAC  
((((((((.....&.....)))))))). -17.50

Wild type PCR fragment:  
AGACTGGAAGTTCATACCTAAG**GTACTGT**AATAATACCTCAATGTTTGAGGAGCATGTTTTGTATACAAATATATTGTTAA  
TCTCTGTTAT**GTACTGT**ACTAATTCCTTACACTGCCTGTATACTTTAGTATGACGCTGATACATAACTAAATTTGATACTT  
ATATTTTCGTATGAAAATGAGTTGTGAAAGTTTTGAGTAGATATTACTTTTATCACTTTTTGAACTAAGAACTTTTGTAA  
AGAAATTTACTATATATATATATGCCTTTTTCCTAGCCTGTTTCTTCTGTAAATGTATTTGTTCATGTTTGGTGCATAGAA  
CTGGGTAAATGCAAAGTTCGTGTTTAATTCTTCAAAATGTATATATTTAGTGCTGCATCTTATAGCACTTTGAAATAC  
CTCATGTTT

Mutant PCR fragment:  
AGACTGGAAGTTCATACCTAAG**GgAgTtT**AATAATACCTCAATGTTTGAGGAGCATGTTTTGTATACAAATATATTGTTAA  
TCTCTGTTAT**GTACTGT**ACTAATTCCTTACACTGCCTGTATACTTTAGTATGACGCTGATACATAACTAAATTTGATACTT  
ATATTTTCGTATGAAAATGAGTTGTGAAAGTTTTGAGTAGATATTACTTTTATCACTTTTTGAACTAAGAACTTTTGTAA  
AGAAATTTACTATATATATATATGCCTTTTTCCTAGCCTGTTTCTTCTGTAAATGTATTTGTTCATGTTTGGTGCATAGAA  
CTGGGTAAATGCAAAGTTCGTGTTTAATTCTTCAAAATGTATATATTTAGTGCTGCATCTTATAGCACTTTGAAaAc  
TcCATGTTT

miRNA: mir-19a  
Human predicted target: ENSG00000106004  
Mouse predicted target: ENSMUSG00000038253  
Rat predicted target: ENSRNOG00000006466  
Hs Gene description: HOMEBOX PROTEIN HOX-A5 (HOX-1C)  
mir-19a ENSG00000106004 2458 nt UTR 2 hits 583 1350  
-----1-----1-----

>ENSG00000106004 hs-mir-19a 583 590  
UGUGCAAUAUCUAAACUGA&CAAGCGGUGUGUCCUGCGUCCUUUAUGACCCUUUGCACGA  
((((((((.....&.....)))))))). -18.12  
>ENSG00000106004 hs-mir-19a 1350 1357  
UGUGCAAUAUCUAAACUGA&GAAACUCCUCAGAGCAGCUAAAGCGCAACUAGAGAUUUGCACAU  
((((((((.....&.....)))))))). -22.53  
mir-19a ENSMUSG00000038253 2827 nt UTR 2 hits 603 1344  
-----1-----1-----

>ENSMUSG00000038253 hs-mir-19a 603 610  
UGUGCAAUAUCUAAACUGA&CAAGCGGUGUGUCCUGCGUCCUUUAUGACCCUUUGCACGA  
((((((((.....&.....)))))))). -18.20  
>ENSMUSG00000038253 hs-mir-19a 1344 1351

UGUGCAAUCUAUGCAAACUGA&GAAACUCCUCAGAGCAGCUAAAGCCCAACUAGAGAUUUGCACAU  
 ((((((((((((((((.....(((&.....)))))).....))))))))). -22.53  
 mir-19a ENSRNOG00000006466 2000 nt UTR 3 hits 619 1367 1798  
 -----1-----1-----1-----  
 >ENSRNOG00000006466 hs-mir-19a 619 626  
 UGUGCAAUCUAUGCAAACUGA&CAAGCGGUGUGUCCUCGUGCCUUUGUAGGACCCUUUGCACGA  
 ((((((((((((((((.....&.....)))))))).....))))). -18.20  
 >ENSRNOG00000006466 hs-mir-19a 1367 1374  
 UGUGCAAUCUAUGCAAACUGA&GAAACUCCUCAGAGCAGCUAAAGCCCAACUAGAGAUUUGCACAU  
 ((((((((((((((((.....(((&.....)))))).....))))))))). -22.53  
 >ENSRNOG00000006466 hs-mir-19a 1798 1805  
 UGUGCAAUCUAUGCAAACUGA&CCAUGUUAAGGUUAGCUCGCCUCCUUGAGUUUUUUUGCACC  
 .(((((((((((((.....&.....)))).....)))))). -15.60

Wild type PCR fragment:

CCCTGCGTGCCTTTATAGGACCC**TTTGCAC**GAACTCTGGAAGTGGCTCTTATAAGCGCAGCTTCAGTGATGTATGTTTTT  
 GTGAACAAAGTTACAAATATTGTCCAAGTCTGGCTGTTTTAAGCAAACCTGTGATCAGCTTTTTTTTTTTTTTTTTTTTTT  
 TTGTATTTGTTTTTAAGGAAAAAATACTGACTGGAACAAAAAATAAACTTTCTATTGTAAGTTCTCTTGGTCTGGTTTTGT  
 GCCAAATAGTGAGCGGCTCTGTCTGCTTTTCTGTCTGTCTGTGCAGTCTTGAAGCTGTTGGGTCTGAGGCTACCTGAGC  
 AGATGACCTGTGCAGGGAGACCTCATACCAACACTGTCCCATCGCTTCCCTACCTCTGACCCATTGCAAAGTTCAGGGCA  
 GAAGGTGGAAAAAGCTGTAGGCTGTTCCAAAGCCCCAGAACACCCTGTCCATCTCTGAGGAAACCAAGTTAACTTGCTGG  
 GTACAAAAAAGAGAGAAAGAGCAAGAAAAAAGGAGAAAAAACCAGGGCTTTGTTAGCCGCCCTCAGGCCACACAGATCC  
 TGCCTCTTTCCCTAAGGCTGTCCCTAGGCCTCCACTTGCTGAAGACGCTGCTATGTCTGTCTGTGGACCCCAAACCCTCTGC  
 CCTTAACCCATCCCAGCACCCCTTCCCCACTCTTCAACCCGGGACCCAGTTGGCTTCTTTTGCTACAATTAATTTGCTACA  
 AATTGAAGGTACTTACCCCATCTTAGCTCGATTGGGAAACTCCTCAGAGCAGCTAAAGCGCAACTAGAGAT**TTTGCAC**ATT  
 TACC

Mutant PCR fragment:

CCCTGCGTGCCTTTATAGGACCC**TgTtCtC**GAACTCTGGAAGTGGCTCTTATAAGCGCAGCTTCAGTGATGTATGTTTTT  
 GTGAACAAAGTTACAAATATTGTCCAAGTCTGGCTGTTTTAAGCAAACCTGTGATCAGCTTTTTTTTTTTTTTTTTTTTTT  
 TTGTATTTGTTTTTAAGGAAAAAATACTGACTGGAACAAAAAATAAACTTTCTATTGTAAGTTCTCTTGGTCTGGTTTTGT  
 GCCAAATAGTGAGCGGCTCTGTCTGCTTTTCTGTCTGTCTGTGCAGTCTTGAAGCTGTTGGGTCTGAGGCTACCTGAGC  
 AGATGACCTGTGCAGGGAGACCTCATACCAACACTGTCCCATCGCTTCCCTACCTCTGACCCATTGCAAAGTTCAGGGCA  
 GAAGGTGGAAAAAGCTGTAGGCTGTTCCAAAGCCCCAGAACACCCTGTCCATCTCTGAGGAAACCAAGTTAACTTGCTGG  
 GTACAAAAAAGAGAGAAAGAGCAAGAAAAAAGGAGAAAAAACCAGGGCTTTGTTAGCCGCCCTCAGGCCACACAGATCC  
 TGCCTCTTTCCCTAAGGCTGTCCCTAGGCCTCCACTTGCTGAAGACGCTGCTATGTCTGTCTGTGGACCCCAAACCCTCTGC  
 CCTTAACCCATCCCAGCACCCCTTCCCCACTCTTCAACCCGGGACCCAGTTGGCTTCTTTTGCTACAATTAATTTGCTACA  
 AATTGAAGGTACTTACCCCATCTTAGCTCGATTGGGAAACTCCTCAGAGCAGCTAAAGCGCAACTAGAGAT**TgTtCtC**ATT  
 TACC

miRNA: mir-19a

Human predicted target: ENSG00000169057

Mouse predicted target: ENSMUSG00000031393

Rat predicted target: ENSRNOG00000019947

Hs Gene description: METHYL-CPG-BINDING PROTEIN 2 (MECP-2 PROTEIN) (MECP2)

mir-19a ENSG00000169057 10554 nt UTR 4 hits 239 975 5757 8723

-----1-----1-----1-----  
 -----1-----  
 -----1-----  
 -----1-----

>ENSG00000169057 hs-mir-19a 239 246  
 UGUGCAAUCUAUGCAAACUGA&GUCAGGUUGAAGACCUAACCAGGGCCAGAAGUAGCUUUGCACU  
 .(((((((((((((.....(((&.....)))))).....))))))))). -19.90  
 >ENSG00000169057 hs-mir-19a 975 982  
 UGUGCAAUCUAUGCAAACUGA&CUUUCCAAUUCUCCUUUAGGGACAGCUUAGAAUUUUUGCACU  
 .(((((((((((((.....(((&.....)))))).....))))))))). -17.80

>ENSG00000169057 hs-mir-19a 5757 5764  
UGUGCAAUUAUGCAAACUGA&UGCCAGGUGAAGGAGGCUCCAGGCAGCACCCAGGUUUUGCACU  
.(((((((((((.....(((&.....)))))).....)))))))). -19.40  
>ENSG00000169057 hs-mir-19a 8723 8730  
UGUGCAAUUAUGCAAACUGA&CAAAGAAUACUCAGCAUGCCUUUCUAAGUGACGCGUUUGCACC  
.((((((((.....((...(((&.....)))))).....)))))))). -15.61  
mir-19a ENSMUSG00000031393 10591 nt UTR 4 hits 238 946 5093 8754  
-----1-----1-----  
-----1-----  
-----1-----  
-----1-----  
-----1-----

>ENSMUSG00000031393 hs-mir-19a 238 245  
UGUGCAAUUAUGCAAACUGA&GUCAGGUUGAAGACCUAACCAGGGCCAGAAGUAGCUUUUGCACU  
.(((((((((((.....(((&.....)))))).....)))))))). -19.90  
>ENSMUSG00000031393 hs-mir-19a 946 953  
UGUGCAAUUAUGCAAACUGA&CUUUCAGUUCUCCUUUAGGGACAGCUUAGAAUUUUUGCACU  
.(((((((((((.....(((&.....)))))).....)))))))). -17.80  
>ENSMUSG00000031393 hs-mir-19a 5093 5100  
UGUGCAAUUAUGCAAACUGA&AAAAAGGCUCUGGGAGAAAGACAGCCUCCUAGGCUUUUGCACAA  
((((((((((((.....(((&.....)))))).....)))))))). -17.90  
>ENSMUSG00000031393 hs-mir-19a 8754 8761  
UGUGCAAUUAUGCAAACUGA&CAAAGAAUACUCAGCAUGCCUUUCUAAGUGAUGCGUUUGCACC  
.((((((((.....((...(((&.....)))))).....)))))))). -18.30  
mir-19a ENSRNOG00000019947 2028 nt UTR 2 hits 241 951  
-----1-----1-----  
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>ENSRNOG00000019947 hs-mir-19a 241 248  
UGUGCAAUUAUGCAAACUGA&GUCAGGUUGAAGACCUAACCAGGGCCAGAAGUAGCUUUUGCACU  
.(((((((((((.....(((&.....)))))).....)))))))). -19.90  
>ENSRNOG00000019947 hs-mir-19a 951 958  
UGUGCAAUUAUGCAAACUGA&CUUUCAGUUCUCCUUUAGGGACAGCUUAGAAUUUUUGCACU  
.(((((((((((.....(((&.....)))))).....)))))))). -17.80

Wild type PCR fragment:  
ACCTAACCAGGGCCAGAAGTAGC**TTTGCAC**TTTTCTAAACTAGGCTCCTTCAACAAGGCTTGCTGCAGATACTACTGACC  
AGACAAGCTGTTGACCAGGCACCTCCCCTCCCGCCCAAACCTTCCCCCATGTGGTTCGTTAGAGACAGAGCGACAGAGCA  
GTTGAGAGGACACTCCCCTTTTCGGTGCCATCAGTGCCCGTCTACAGCTCCCCCAGCTCCCCCACCTCCCCACTCCC  
AACCACGTTGGGACAGGGAGGTGTGAGGCAGGAGACAGTTGGATTCTTTAGAGAAGATGGATATGACCAGTGGCTATG  
GCCTGTGCGATCCCACCCGTGGTGGCTCAAGTCTGGCCCCACACCAGCCCCAATCCAAAACCTGGCAAGGACGCTTCACAG  
GACAGGAAAGTGGCACCTGTCTGCTCCAGCTCTGGCATGGCTAGGAGGGGGGAGTCCCTTGAACACTGGGTGTAGACTG  
GCCTGAACCACAGGAGAGGATGGCCAGGGTGGGTGGCATGGTCCATTCTCAAGGGACGTCCTCCAACGGGTGGCGCTA  
GAGGCCATGGAGGCAGTAGGACAAGGTGCAGGCAGGCTGGCTGGGGTCAGGCCGGGCAGAGCACAGCGGGGTGAGAGGG  
ATTCTAATCACTCAGAGCAGTCTGTGACTTAGTGGACAGGGGAGGGGGCAAAGGGGGAGGAGAAGAAAATGTTCTTCCA  
GTTACTTTCCAATTCTCCTTTAGGGACAGCTTAGAATTA**TTTGCAC**TATTGAG

Mutant PCR fragment:  
ACCTAACCAGGGCCAGAAGTAGC**TgTtCtC**TTTTCTAAACTAGGCTCCTTCAACAAGGCTTGCTGCAGATACTACTGACC  
AGACAAGCTGTTGACCAGGCACCTCCCCTCCCGCCCAAACCTTCCCCCATGTGGTTCGTTAGAGACAGAGCGACAGAGCA  
GTTGAGAGGACACTCCCCTTTTCGGTGCCATCAGTGCCCGTCTACAGCTCCCCCAGCTCCCCCACCTCCCCACTCCC  
AACCACGTTGGGACAGGGAGGTGTGAGGCAGGAGACAGTTGGATTCTTTAGAGAAGATGGATATGACCAGTGGCTATG  
GCCTGTGCGATCCCACCCGTGGTGGCTCAAGTCTGGCCCCACACCAGCCCCAATCCAAAACCTGGCAAGGACGCTTCACAG  
GACAGGAAAGTGGCACCTGTCTGCTCCAGCTCTGGCATGGCTAGGAGGGGGGAGTCCCTTGAACACTGGGTGTAGACTG  
GCCTGAACCACAGGAGAGGATGGCCAGGGTGGGTGGCATGGTCCATTCTCAAGGGACGTCCTCCAACGGGTGGCGCTA  
GAGGCCATGGAGGCAGTAGGACAAGGTGCAGGCAGGCTGGCTGGGGTCAGGCCGGGCAGAGCACAGCGGGGTGAGAGGG  
ATTCTAATCACTCAGAGCAGTCTGTGACTTAGTGGACAGGGGAGGGGGCAAAGGGGGAGGAGAAGAAAATGTTCTTCCA  
GTTACTTTCCAATTCTCCTTTAGGGACAGCTTAGAATTA**TgTtCtC**TATTGAG

miRNA: mir-19a

Human predicted target: ENSG00000171862

Mouse predicted target: ENSMUSG00000013663

Rat predicted target: ENSRNOG00000020723

Hs Gene description: PHOSPHATIDYLINOSITOL-3,4,5-TRISPHOSPHATE 3-PHOSPHATASE PTEN (EC 3.1.3.67) (MUTATED IN MULTIPLE ADVANCED CANCERS 1)

mir-19a ENSG00000171862 2904 nt UTR 3 hits 411 1221 2252

-----1-----1-----

>ENSG00000171862 hs-mir-19a 411 418  
UGUGCAAUUAUGCAAACUGA&AGAGCUUUGUGAUUAUCUGGUUCACAUCUACCCUUGCACU  
.(((((((.....&.....)))))))). -13.00

>ENSG00000171862 hs-mir-19a 1221 1228  
UGUGCAAUUAUGCAAACUGA&GACCUUACACAUUCUAUUACAAUGAAUUUGCAGUUUGCACAU  
(((((((.....&.....)))))))). -21.80

>ENSG00000171862 hs-mir-19a 2252 2259  
UGUGCAAUUAUGCAAACUGA&GGGCCAGGUCAUAAAUAUUGACAUUAUAAUGGGCUUUGCACU  
.(((((((.....&.....)))))))). -15.20

mir-19a ENSMUSG00000013663 2073 nt UTR 2 hits 425 1236  
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>ENSMUSG00000013663 hs-mir-19a 425 432  
UGUGCAAUUAUGCAAACUGA&GAAGAGCUCUGAUUCCGGGUUCACGUCCUACCCUUGCACU  
.(((((((.....&.....)))))))). -13.00

>ENSMUSG00000013663 hs-mir-19a 1236 1243  
UGUGCAAUUAUGCAAACUGA&GACCUUACACAUUCUAUUACAAUGAGUUUGCAGUUUGCACAU  
(((((((.....&.....)))))))). -26.00

mir-19a ENSRNOG00000020723 3882 nt UTR 2 hits 1184 2564  
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>ENSRNOG00000020723 hs-mir-19a 1184 1191  
UGUGCAAUUAUGCAAACUGA&GACCUUACACAUUCUAUUACAAUGAGUUUGCAGUUUGCACAU  
(((((((.....&.....)))))))). -26.00

>ENSRNOG00000020723 hs-mir-19a 2564 2571  
UGUGCAAUUAUGCAAACUGA&GACCUUACACAUUCUAUUACAAUGAGUUUGCAGUUUGCACAU  
(((((((.....&.....)))))))). -26.00

Wild type PCR fragment:

GGCTAAAGAGCTTTGTGATATACTGGTTCACATCCTACCCC**TTTGAC**TTGTGGCAACAGATAAGTTTGCAGTTGGCTAA  
GAGAGTTTCCGAAGGGTTTTGCTACATTCCTAATGCATGTATTTCGGGTTAGGGGAATGGAGGGAATGCTCAGAAAGGAAA  
TAATTTTATGCTGGACTCTGGACCATATACCATCTCCAGCTATTTACACACACCTTTCTTTAGCATGCTACAGTTATTAA  
TCTGGACATTCGAGGAATTGGCCGCTGTCACCTGCTTGTGTTTGCGCATTTTTTTTTTAAAGCATATTGGTGTAGAAAAG  
GCAGCTAAAGGAAGTGAATCTGTATTGGGGTACAGGAATGAACCTTCTGCAACATCTTAAGATCCACAAATGAAGGGATA  
TAAAATAATGTCATAGGTAAGAAACACAGCAACAATGACTTAACCATATAAATGTGGAGGCTATCAACAAAGAATGGGC  
TTGAAACATTATAAAAATTGACAATGATTTATTAATATGTTTCTCAATTGTAACGACTTCTCCATCTCCTGTGTAATC  
AAGGCCAGTGTGATGCTTACATGCTGTAGTACCTACATCAGTCAACAACCTTACACTTATTTTACTAGTTTCAATCAT  
AATACCTGCTGTGGATGCTTACATGCTGCCTGCAAGCTTCTTTTTTCTCATTAAATATAAAAATTTTGTAAATGCTGCA  
CAGAAATTTTCAATTTGAGATTTACAGTAAGCGTTTTTTTTCTTTGAAGATTTATGATGCACCTATTCAATAGCTGTCA  
GCCGTTCCACCCTTTTGACCTTACACATTCATTACAATGAATTTTGCAGT**TTTGAC**ATTTTTT

Mutant PCR fragment:

GGCTAAAGAGCTTTGTGATATACTGGTTCACATCCTACCCC**TgTtCtC**TTGTGGCAACAGATAAGTTTGCAGTTGGCTAA  
GAGAGTTTCCGAAGGGTTTTGCTACATTCCTAATGCATGTATTTCGGGTTAGGGGAATGGAGGGAATGCTCAGAAAGGAAA  
TAATTTTATGCTGGACTCTGGACCATATACCATCTCCAGCTATTTACACACACCTTTCTTTAGCATGCTACAGTTATTAA  
TCTGGACATTCGAGGAATTGGCCGCTGTCACCTGCTTGTGTTTGCGCATTTTTTTTTTAAAGCATATTGGTGTAGAAAAG  
GCAGCTAAAGGAAGTGAATCTGTATTGGGGTACAGGAATGAACCTTCTGCAACATCTTAAGATCCACAAATGAAGGGATA  
TAAAATAATGTCATAGGTAAGAAACACAGCAACAATGACTTAACCATATAAATGTGGAGGCTATCAACAAAGAATGGGC  
TTGAAACATTATAAAAATTGACAATGATTTATTAATATGTTTCTCAATTGTAACGACTTCTCCATCTCCTGTGTAATC



AAGGCCAGTGCTAAAATTCAGATGCTGTTAGTACCTACATCAGTCAACAACCTTACACTTATTTTACTAGTTTTCAATCAT  
AATACCTGCTGTGGATGCTTCATGTGCTGCCTGCAAGCTTCTTTTTCTCATTAAATATAAAAATATTTTGTAAATGCTGCA  
CAGAAATTTTCAATTTGAGATTCTACAGTAAGCGTTTTTTTTCTTTGAAGATTTATGATGCACCTTATTCAATAGCTGTCA  
GCCGTTCCACCCTTTTGACCTTACACATTCTATTACAATGAATTTTGCAGT**TgTtCtC**ATTTTTTT

miRNA: mir-34

Human predicted target: ENSG00000112577

Mouse predicted target: ENSMUSG00000014773

Rat predicted target: ENSRNOG00000014667

Hs Gene description: DELTA-LIKE PROTEIN 1 PRECURSOR (DROSOPHILA DELTA HOMOLOG 1)  
(DELTA1) (H-DELTA-1)

mir-34 ENSG00000112577 2661 nt UTR 3 hits 197 293 356

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>ENSG00000112577 hs-mir-34 197 204  
UGGCAGUGUCUUAGCUGGUUGU&CUGCCGACAGCCUGUCGCGGCCCGCCCGCCUGCGGCACUGCCU  
.(((((((((((((.(.((((&.....)))))))).)))..)))))))). -31.30

>ENSG00000112577 hs-mir-34 293 300  
UGGCAGUGUCUUAGCUGGUUGU&UAAAUGGGUGAACUGAAUUACGCAUAAGAAGCAUGCACUGCCU  
.(((((((((((((.(.((((&.....)))))))).)))..)))))))). -22.80

>ENSG00000112577 hs-mir-34 356 363  
UGGCAGUGUCUUAGCUGGUUGU&UAUGAGCCAGUCUUUCUUGAAUUAGAAACACAAACACUGCCU  
.(((((((((((((.(.((((&.....)))))))).)))..)))))))). -24.35

mir-34 ENSMUSG00000014773 2675 nt UTR 3 hits 165 290 1214

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>ENSMUSG00000014773 hs-mir-34 165 172  
UGGCAGUGUCUUAGCUGGUUGU&AAGCUGGUUCUCUCAGAGUUAGCAGAGGCCCGCCGACACUGCCAG  
(((((((((((((.(.((((&.....)))))))).)))..)))))))). -29.20

>ENSMUSG00000014773 hs-mir-34 290 297  
UGGCAGUGUCUUAGCUGGUUGU&AAUGGACGAGUGACUUGAUUCAUAUAGGAAGCACGCACUGCCC  
.(((((((((((((.(.((((&.....)))))))).)))..)))))))). -22.00

>ENSMUSG00000014773 hs-mir-34 1214 1221  
UGGCAGUGUCUUAGCUGGUUGU&UGACAGGAGAGAAAAUGGAGUUAGUGGGUGAAGUCACUGCCAC  
(((((((((((((.(.((((&.....)))))))).)))..)))))))). -25.10

mir-34 ENSRNOG00000014667 2366 nt UTR 2 hits 170 295

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>ENSRNOG00000014667 hs-mir-34 170 177  
UGGCAGUGUCUUAGCUGGUUGU&GAGCUGGUUCUCCGGAGUUAGCAGAGGCCCGCCGACACUGCCAG  
(((((((((((((.(.((((&.....)))))))).)))..)))))))). -31.00

>ENSRNOG00000014667 hs-mir-34 295 302  
UGGCAGUGUCUUAGCUGGUUGU&AAUGGACGAGUGACUUGAUUCACACAGGAAGCACGCACUGCCGG  
(((((((((((((.(.((((&.....)))))))).)))..)))))))). -24.90

Wild type PCR fragment:

CGCGGCCCGGCCCGCTGCGG**CACTGCC**TTCCGTGACGTGCGCGTTGCACTATGGACAGTTGCTCTTAAGAGAATATATAT  
TTAAATGGGTGAAGTGAATTACGCATAAGAAGCATG**CACTGCC**TGAGTGTATATTTTGGATTCTTATGAGCCAGTCTTTT  
CTTGAATTAGAAACACAAA**CACTGCC**TTTATT

Mutant PCR fragment:

CGCGGCCCGGCCCGCTGCGG**CtCaGgC**TTCCGTGACGTGCGCGTTGCACTATGGACAGTTGCTCTTAAGAGAATATATAT  
TTAAATGGGTGAAGTGAATTACGCATAAGAAGCATG**CACTGCC**TGAGTGTATATTTTGGATTCTTATGAGCCAGTCTTTT  
CTTGAATTAGAAACACAAA**CtCaGgC**TTTATT

miRNA: mir-34

Human predicted target: ENSG00000148400

Mouse predicted target: ENSMUSG00000026923

Rat predicted target: ENSRNOG00000019322  
 Hs Gene description: NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (NOTCH 1) (HN1) (TRANSLOCATION-ASSOCIATED NOTCH PROTEIN TAN-1)  
 mir-34 ENSG00000148400 3627 nt UTR 4 hits 909 2299 2398 2714

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 >ENSG00000148400 hs-mir-34 909 916  
 UGGCAGUGUCUUAGCUGGUUGU&CACACGGAGGCAUCCUACCCUUUUUCUGGGGAAAGACACUGCCU  
 .((((((((((((((..(..&.....)).....)).....)).....)).....)).....)).....). -25.90  
 >ENSG00000148400 hs-mir-34 2299 2306  
 UGGCAGUGUCUUAGCUGGUUGU&GCCAGCCUCACACAAGGGUGGGCCCCUUCUCUCCCCACUGCCU  
 .((((((((((((((..(..&.....)).....)).....)).....)).....)).....)).....). -21.86  
 >ENSG00000148400 hs-mir-34 2398 2405  
 UGGCAGUGUCUUAGCUGGUUGU&GUGGGGAGUCUGAGAUCCCUCUUUGGAUUGCAAAGCACUGCCU  
 .((((((((((((((((..(..(&..)..)).....)).....)).....)).....)).....)).....). -21.55  
 >ENSG00000148400 hs-mir-34 2714 2721  
 UGGCAGUGUCUUAGCUGGUUGU&CAUCACUCAGUACAGCCACAGACAGCCUGAGCGUCCACUGCCAA  
 ((((((((((.(((((((.(((((((&.....)).....)).....)).....)).....)).....)).....)).....). -28.20  
 mir-34 ENSMUSG00000026923 3625 nt UTR 3 hits 187 458 800

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 >ENSMUSG00000026923 hs-mir-34 187 194  
 UGGCAGUGUCUUAGCUGGUUGU&AGUAUUUAUUUAUGUACUUUAUUUUCCACAGAAACACUGCCU  
 .(((((((((((.(((((((.(((((((&.....)).....)).....)).....)).....)).....)).....)).....). -21.60  
 >ENSMUSG00000026923 hs-mir-34 458 465  
 UGGCAGUGUCUUAGCUGGUUGU&AACUGCCAUGGCCAGAAUUGCCCCUCCCCACACUCACUGCCC  
 .((((((((.....(((((((.(((((((&.....)).....)).....)).....)).....)).....)).....)).....). -23.57  
 >ENSMUSG00000026923 hs-mir-34 800 807  
 UGGCAGUGUCUUAGCUGGUUGU&UAAGCCAUGCAGGGUGUGGCCUCCUAGAGAAAACACUGCCU  
 .(((((((((((.(((((((.(((((((&..)..)).....)).....)).....)).....)).....)).....)).....). -25.05  
 mir-34 ENSRNOG00000019322 2384 nt UTR 3 hits 193 523 890

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 -----  
 >ENSRNOG00000019322 hs-mir-34 193 200  
 UGGCAGUGUCUUAGCUGGUUGU&AGUAUUUAUUUAUGUACUUUAUUUUCCACAGAAACACUGCCU  
 .(((((((((((.(((((((.(((((((&.....)).....)).....)).....)).....)).....)).....)).....). -21.60  
 >ENSRNOG00000019322 hs-mir-34 523 530  
 UGGCAGUGUCUUAGCUGGUUGU&AGAUUUUUUUUUUCCCGAUGCCUGCUACCCACACUCACUGCCC  
 .((((((((.....(((((((.(((((((&.....)).....)).....)).....)).....)).....)).....)).....). -23.50  
 >ENSRNOG00000019322 hs-mir-34 890 897  
 UGGCAGUGUCUUAGCUGGUUGU&AAGCCAAGUGGGGUGUGGCUCCUGGAGAAUGACACUGCCU  
 .((((((((((((((..(..(&.....)).....)).....)).....)).....)).....)).....). -25.50

Wild type PCR fragment:

AGAGCTGCCAGCCTCACACAAGGGTGGGCCCCTTCTCTCCC**CACTGCC**TGGGCCTCTGCCAGCCCCAGACCTTCAGGGC  
 AGGCCAGTGGCTTCAAACCAGAGCGGTGGGGAGTCTGAGATCCCTCTTTGGATTGCAAAG**CACTGCC**TGCCCTGGGCCCA  
 GTCTCTCCAAGGAGGGATGTGAGCCCCGAGCCCTACTATGGCTGGGGCTGCGTCTGCCAGCCAGCGCTGGGCACCAGG  
 ACCAGGAGGGGCCACCGTGGAACTGCAGTGCAGTGCAGTGGCCTGACTCTTGCTTTCAAAGGGGGTGACCCAGCCGGAGTCTGCC  
 CATAAAACTCCCAGCACCTGAAATTCACCTCTGGGGTCTGTCCGAAAGAAGTGAAAACAGGGACTCAAACAAACGCA  
 CGTGGCCACTTGCTGTCCCGGCATCACTCAGTACAGCCACAGACAGCCTGAGCGTCC**CACTGCC**AACGACG

Mutant PCR fragment:

AGAGCTGCCAGCCTCACACAAGGGTGGGCCCCTTCTCTCCC**CtCaGgC**TGGGCCTCTGCCAGCCCCAGACCTTCAGGGC  
 AGGCCAGTGGCTTCAAACCAGAGCGGTGGGGAGTCTGAGATCCCTCTTTGGATTGCAAAG**CACTGCC**TGCCCTGGGCCCA  
 GTCTCTCCAAGGAGGGATGTGAGCCCCGAGCCCTACTATGGCTGGGGCTGCGTCTGCCAGCCAGCGCTGGGCACCAGG  
 ACCAGGAGGGGCCACCGTGGAACTGCAGTGCAGTGCAGTGGCCTGACTCTTGCTTTCAAAGGGGGTGACCCAGCCGGAGTCTGCC  
 CATAAAACTCCCAGCACCTGAAATTCACCTCTGGGGTCTGTCCGAAAGAAGTGAAAACAGGGACTCAAACAAACGCA  
 CGTGGCCACTTGCTGTCCCGGCATCACTCAGTACAGCCACAGACAGCCTGAGCGTCC**CtCaGgC**AACGACG

miRNA: mir-34

Human predicted target: ENSG00000179036

Mouse predicted target: ENSMUSG00000020894

Rat predicted target: ENSRNOG00000006989

Hs Gene description: VESICLE-ASSOCIATED MEMBRANE PROTEIN 2 (VAMP-2)

(SYNAPTOBREVIN 2). [Source:SWISSPROT;Acc:P19065] NM\_014232

mir-34 ENSG00000179036 3727 nt UTR 6 hits 1129 1256 1309 3456 3583 3636

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>ENSG00000179036 hs-mir-34 1129 1136  
UGGCAGUGUCUUAGCUGGUUGU&AGAGGGGUGGCUACCAGUGUGUGUGGGGGUCAUCACUGCCU  
.(((((((.(.(.(((.(.(&.....)).)))))).....)))). -25.80  
>ENSG00000179036 hs-mir-34 1256 1263  
UGGCAGUGUCUUAGCUGGUUGU&AACCCUCCUCCCCAAUUUGGGGGUGUUGCCCCAUCACUGCCC  
.(((((((.(.(.(((.(.(&.....)).)))))).....)))). -18.70  
>ENSG00000179036 hs-mir-34 1309 1316  
UGGCAGUGUCUUAGCUGGUUGU&ACUGCCCCCCUGAAUUUAGGGUGGGGGUACUAGUCACUGCCAA  
(((((((.(.....(((.(...&.....))))))))) -22.80  
>ENSG00000179036 hs-mir-34 3456 3463  
UGGCAGUGUCUUAGCUGGUUGU&AGAGGGGUGGCUACCAGUGUGUGUGGGGGUCAUCACUGCCU  
.(((((((.(.(.(((.(.(&.....)).)))))).....)))). -25.80  
>ENSG00000179036 hs-mir-34 3583 3590  
UGGCAGUGUCUUAGCUGGUUGU&AACCCUCCUCCCCAAUUUGGGGGUGUUGCCCCAUCACUGCCC  
.(((((((.(.(.(((.(.(&.....)).)))))).....)))). -18.70  
>ENSG00000179036 hs-mir-34 3636 3643  
UGGCAGUGUCUUAGCUGGUUGU&ACUGCCCCCCUGAAUUUAGGGUGGGGGUACUAGUCACUGCCAA  
(((((((.(.....(((.(...&.....))))))))) -22.80  
mir-34 ENSMUSG00000020894 3731 nt UTR 3 hits 1116 1246 1298

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>ENSMUSG00000020894 hs-mir-34 1116 1123  
UGGCAGUGUCUUAGCUGGUUGU&UUUGAGGAGGGGUGGCUCCAGUGUGUGGGGGUCAUCACUGCCU  
.(((((((.(.(.(((.(.(&.....)).)))))).....)))). -24.40  
>ENSMUSG00000020894 hs-mir-34 1246 1253  
UGGCAGUGUCUUAGCUGGUUGU&UCCUCCCCAGUCUGGGGGGGGGUAAUUACCCCCAUCACUGCCC  
.(((((((.(.(.(((.(.(&.....)).)))))).....)))). -25.16  
>ENSMUSG00000020894 hs-mir-34 1298 1305  
UGGCAGUGUCUUAGCUGGUUGU&GACUGCCCCCCUGAAUUUACAGGGUGGGGGUACUAGUCACUGCCAA  
(((((((.(.....(((.(...&.....))))))))) -22.80  
mir-34 ENSRNOG00000006989 4248 nt UTR 4 hits 1629 1761 1813 2899

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>ENSRNOG00000006989 hs-mir-34 1629 1636  
UGGCAGUGUCUUAGCUGGUUGU&UGAGGAGGGGUGGCUCCAGUGUGUGGGGGUCAUCACUGCCU  
.(((((((.(.(.(((.(.(&.....)).)))))).....)))). -21.40  
>ENSRNOG00000006989 hs-mir-34 1761 1768  
UGGCAGUGUCUUAGCUGGUUGU&CCUCCCCAAUCCUGGGGGGGGGUAAUUACCCCCAUCACUGCCC  
.(((((((.(.(.(((.(.(&.....)).)))))).....)))). -21.16  
>ENSRNOG00000006989 hs-mir-34 1813 1820  
UGGCAGUGUCUUAGCUGGUUGU&GACUGCCCCCCUGAAUUUACAGGGUGGGGGUACUAGUCACUGCCAA  
(((((((.(.....(((.(...&.....))))))))) -22.80  
>ENSRNOG00000006989 hs-mir-34 2899 2906  
UGGCAGUGUCUUAGCUGGUUGU&GGUUGCCCUCUGAAUUUACAGGUCAUGAGGGACUAGUCACUGCCAG  
(((((((.(.....(((.(.(&.....)).))))))))) -24.50  
Wild type PCR fragment:

GGGGTGGCTACCAGTGTGTGTGTGGGGGTCAT**CACTGCC**TTGGGGAGGAGTGGGGCAGGGCAGAGAATCCCCCAATTCC  
TGCCTGAAATCTCTGGCCTCACCCCTGCTGGGGGTGGACTGAAAACCTCCTCCCCAATTTGGGGGGTGTGGCCCCATC  
**ACTGCC**CAGCTCCTCTGACTGCCCCCTGAATTTAGGGTGGGGTACTAGT**CACTGCC**AATGTGT

Mutant PCR fragment:

GGGGTGGCTACCAGTGTGTGTGTGGGGGTCAT**CtCaGgC**TTGGGGAGGAGTGGGGCAGGGCAGAGAATCCCCCAATTCC  
TGCCTGAAATCTCTGGCCTCACCCCTGCTGGGGGTGGACTGAAAACCTCCTCCCCAATTTGGGGGGTGTGGCCCCATC  
**ACTGCC**CAGCTCCTCTGACTGCCCCCTGAATTTAGGGTGGGGTACTAGT**CtCaGgC**AATGTGT

miRNA: mir-1b

Human predicted target: ENSG00000160211

Mouse predicted target: ENSMUSG00000031400

Rat predicted target: ENSRNOG00000020508

Hs Gene description: GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE (EC 1.1.1.49) (G6PD)

mir-1b ENSG00000160211 2609 nt UTR 3 hits 97 165 433

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>ENSG00000160211 hs-mir-1b 97 104  
UGGAAUGUAAAGAAGUAUGUAU&GUCGGGAGGACUCCGGGACCAUUGACCUCAGCUGCACAUUCCU  
.(((((((.....&.....)))))). -14.90

>ENSG00000160211 hs-mir-1b 165 172  
UGGAAUGUAAAGAAGUAUGUAU&CCGCCCCUCGUGCUGCUACUACCCGAGCCCAGCUACAUUCCU  
.(((((((.....&.....)))))). -15.84

>ENSG00000160211 hs-mir-1b 433 440  
UGGAAUGUAAAGAAGUAUGUAU&CCUGUGGCCUUGCCCCGCCAGCCUCAGUGCCACUUGACAUUCCU  
.(((((((.....&.....)))))). -18.60

mir-1b ENSMUSG00000031400 2721 nt UTR 2 hits 210 527  
-----1-----1-----  
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>ENSMUSG00000031400 hs-mir-1b 210 217  
UGGAAUGUAAAGAAGUAUGUAU&UGCUGCUGCCACUGCCACCACCAGUAAACCCAGCUACAUUCCU  
.(((((((.....&.....)))))). -14.90

>ENSMUSG00000031400 hs-mir-1b 527 534  
UGGAAUGUAAAGAAGUAUGUAU&CCUGCCCAUGGCCACACUAGCCUCAGUGCUACUAGACAUUCCU  
.(((((((.....&.....)))))). -20.00

mir-1b ENSRNOG00000020508 2000 nt UTR 2 hits 214 535  
-----1-----1-----  
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>ENSRNOG00000020508 hs-mir-1b 214 221  
UGGAAUGUAAAGAAGUAUGUAU&UGCUGCUGCCACUGCCACUACCACUAAGCCCAGCUACAUUCCU  
.(((((((.....&.....)))))). -14.90

>ENSRNOG00000020508 hs-mir-1b 535 542  
UGGAAUGUAAAGAAGUAUGUAU&CCUGCCCAUAGCCACACUAGCCUUAGUGCUACUUGACAUUCCU  
.(((((((.....&.....)))))). -20.90

Wild type PCR fragment:

CCCCGAGTCGGGAGGACTCCGGGACCATTGACCTCAGCTGC**ACATTCC**TGGCCCCGGGCTCTGGCCACCCTGGCCCCGCC  
CTCGCTGCTGCTACTACCCGAGCCCAGCT**ACATTCC**TCAGCTGCCAAGCACTCGAGACCATCCTGGCCCCCTCCAGACCCT  
GCCTGAGCCCAGGAGCTGAGTCACCTCCTCCACTCACTCCAGCCCAACAGAAGGAAGGAGGGGCGCCCATTCGTCTGT  
CCCAGAGCTTATTGGCCACTGGGTCTCACTCCTGAGTGGGGCCAGGGTGGGAGGGAGGGACAAGGGGGAGGAAAGGGGCG  
AGCACCCACGTGAGAGAATCTGCCTGTGGCCTTGCCCGCCAGCCTCAGTGCCACTTG**ACATTCC**TTGTCA

Mutant PCR fragment:

CCCCGAGTCGGGAGGACTCCGGGACCATTGACCTCAGCTGC**AgAaTgC**TGGCCCCGGGCTCTGGCCACCCTGGCCCCGCC  
CTCGCTGCTGCTACTACCCGAGCCCAGCT**ACATTCC**TCAGCTGCCAAGCACTCGAGACCATCCTGGCCCCCTCCAGACCCT  
GCCTGAGCCCAGGAGCTGAGTCACCTCCTCCACTCACTCCAGCCCAACAGAAGGAAGGAGGGGCGCCCATTCGTCTGT  
CCCAGAGCTTATTGGCCACTGGGTCTCACTCCTGAGTGGGGCCAGGGTGGGAGGGAGGGACAAGGGGGAGGAAAGGGGCG  
AGCACCCACGTGAGAGAATCTGCCTGTGGCCTTGCCCGCCAGCCTCAGTGCCACTTG**AgAaTgC**TTGTCA

miRNA: mir-1b  
 Human predicted target: ENSG00000176697  
 Mouse predicted target: ENSMUSG00000048482  
 Rat predicted target: ENSRNOG00000005051  
 Hs Gene description: BRAIN-DERIVED NEUROTROPHIC FACTOR PRECURSOR (BDNF)  
 mir-1b ENSG00000176697 2498 nt UTR 3 hits 220 390 1322

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 >ENSG00000176697 hs-mir-1b 220 227  
 UGGA AUGUAAAGAAGUAUGUAU&ACAGUCAUUUGCGCACACUUAAAAAGUCUGCAUUACAUUCCU  
 .((((((((((((((..(((((.&.....)))))).)).....))))).....)))). -16.51  
 >ENSG00000176697 hs-mir-1b 390 397  
 UGGA AUGUAAAGAAGUAUGUAU&AAACACACACACACACAAAAUUUGAACCAAAACAUUCCGU  
 (((((((((((.....&.....)))))).....))))).....)))). -14.00  
 >ENSG00000176697 hs-mir-1b 1322 1329  
 UGGA AUGUAAAGAAGUAUGUAU&CAAGGUCUAGGUGGAGGUGGGCAUGGUUUUGAGACAUUCCAA  
 (((((((((((((..(((((.&.....)))))).)).....))))).....)))). -20.00  
 mir-1b ENSMUSG00000048482 4854 nt UTR 2 hits 213 1306

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 -----  
 >ENSMUSG00000048482 hs-mir-1b 213 220  
 UGGA AUGUAAAGAAGUAUGUAU&ACAGUCAUUUGCGCACACUUAAAAAGUCUGCAUUACAUUCCU  
 .((((((((((((((..(((((.&.....)))))).)).....))))).....)))). -16.51  
 >ENSMUSG00000048482 hs-mir-1b 1306 1313  
 UGGA AUGUAAAGAAGUAUGUAU&AAGGUCUAGGAUGGAGGUGGGAAUGGUACUUGAGACAUUCCU  
 .((((((((((((((..(((((.&.....)))))).)).....))))).....)))). -18.70  
 mir-1b ENSRNOG00000005051 2266 nt UTR 2 hits 217 1298

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 -----  
 >ENSRNOG00000005051 hs-mir-1b 217 224  
 UGGA AUGUAAAGAAGUAUGUAU&ACAGUCAUUUGCGCACACUUAAAAAGUCUGCAUUACAUUCCU  
 .((((((((((((((..(((((.&.....)))))).)).....))))).....)))). -16.51  
 >ENSRNOG00000005051 hs-mir-1b 1298 1305  
 UGGA AUGUAAAGAAGUAUGUAU&UGAGGUCUAGAUGGAGGUGGGAAUGGUACUUGAGACAUUCCU  
 .((((((((((((((..(((((.&.....)))))).)).....))))).....)))). -18.70

Wild type PCR fragment:  
 CAGTCATTTGCGCACAACTTAAAAAGTCTGCATT**ACATTCC**TTGATAATGTTGTGGTTTGTGCGGTTGCCAAGAAGACTGA  
 AAACATAAAAAGTTAAAAAAAATAATAAATTGCATGCTGCTTTAATTGTGAATTGATAATAAACTGTCCTCTTTTCAGAAA  
 ACAGAAAAAAAACACACACACACACACAAAAATTTGAACCAAAA**ACATTCC**GTTTACATTTTAGACAGTAAGTATCTTCG  
 TTCTTGTTAGTACTATATCTGTTTTACTGCTTTTAACTTCTGATAGCGTTGGAATTAACAATGTCAAGGTGCTGTTGT  
 CATTGCTTTACTGGCTTAGGGGATGGGGGATGGGGGATATTTTTGTTTTGTTTTGTTTTTTTTTCGTTTTGTTTTGTTT  
 TGTTTTTTAGTTCCCACAGGGAGTAGAGATGGGGAAAGAAATCCTACAATATATATTCTGGCTGATAAAAGATACATTTG  
 TATGTTGTGAAGATGTTTGCAATATCGATCAGATGACTAGAAAAGTGAATAAAAAATTAAGGCAACTGAACAAAAAAATGCT  
 CACACTCCACATCCCGTGATGCACCTCCCAGGCCCGCTCATCTTTGGGCGTTGGTCAGAGTAAGCTGCTTTTGACGGA  
 AGGACCTATGTTTGCTCAGAACACATCTTTCCCCCCTCCCCCTCTGGTCTCCTCTTTGTTTTGTTTTAAGGAAGAAAA  
 ATCAGTTGCGCGTTCAGAAATATTTTACCAGTCTGTGAACAAGTGAACACATTTGTGTGCACATCATGCACACTCGTATAAG  
 CATGGAGAACAGTGATTTTTTTTTTAGAACAGAAAAACAACAAAAATAACCCCAAAATGAAGATTATTTTTTATGAGGAGT  
 GAACATTTGGGTAAATCATGGCTAAGCTTAAAAAAACTCATGGTGAGGCTTAACAATGTCTTGTAAGCAAAAGGTAGAG  
 CCCTGTATCAACCCAGAAACACCTAGATCAGAACAGGAATCCACATTGCCAGTGACATGAGACTGAACAGCCAAATGGAG  
 GCTATGTGGAGTTGGCATTGCATTTACCGGCAGTGCGGGAGGAATTTCTGAGTGCCATCCCAAGGTCTAGGTGGAGGTG  
 GGGCATGGTATTTGAG**ACATTCC**AAAACGA

Mutant PCR fragment:  
 CAGTCATTTGCGCACAACTTAAAAAGTCTGCATT**AgAaTgC**TTGATAATGTTGTGGTTTGTGCGGTTGCCAAGAAGACTGA  
 AAACATAAAAAGTTAAAAAAAATAATAAATTGCATGCTGCTTTAATTGTGAATTGATAATAAACTGTCCTCTTTTCAGAAA  
 ACAGAAAAAAAACACACACACACACACAAAAATTTGAACCAAAA**ACATTCC**GTTTACATTTTAGACAGTAAGTATCTTCG  
 TTCTTGTTAGTACTATATCTGTTTTACTGCTTTTAACTTCTGATAGCGTTGGAATTAACAATGTCAAGGTGCTGTTGT

CATTGCTTTACTGGCTTAGGGGATGGGGGATGGGGGATATATTTTTGTTTGTGTTTTGTTTTCGTTTGTGTTT  
TGTTTTTTAGTTCCCACAGGGAGTAGAGATGGGGAAAGAATTCCTACAATATATATTTCTGGCTGATAAAAGATA  
TATGTTGTGAAGATGTTTGCATATCGATCAGATGACTAGAAAGTGAATAAAAATTAAGGCAACTGAACAAAAA  
CACACTCCACATCCCCTGATGCACCTCCCAGGCCCGCTCATTCTTTGGGCGTTGGTCAGAGTAAGCTGCTTTT  
AGGACCTATGTTTGTCTAGAACACATTCTTTCCCCCCCCCTCCCCCTCTGGTCTCCTCTTTGTTTTGTTTTA  
ATCAGTTGCGCGTTCTGAAATATTTTACCCTGCTGTGAACAAGTGAACACATTGTGTACATCATGACACTCGT  
CATGGAGAACAGTGATTTTTTTTTTAGAACAGAAAAACAACAAAAATAACCCCAAAATGAAGATTATTTTTT  
GAACATTTGGGTAAATCATGGCTAAGCTTAAAAAACTCATGGTGAGGCTTAAACAATGTCTTGTAAAGCAA  
CCCTGTATCAACCCAGAAACACCTAGATCAGAACAGGAATCCACATTGCCAGTGACATGAGACTGAACAGCC  
GCTATGTGGAGTTGGCATTTCACCGCAGTGCGGGAGGAATTTCTGAGTGGCCATCCCAAGGTCTAGGTGGAG  
GGGCATGGTATTTGAG**AgAaTgC**AAAAACGA

miRNA: mir-130

Human predicted target: ENSG00000130164

Mouse predicted target: ENSMUSG00000032193

Rat predicted target: ENSRNOG00000009946

Hs Gene description: LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (LDL RECEPTOR)

mir-130 ENSG00000130164 2207 nt UTR 4 hits 813 871 1970 2161

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>ENSG00000130164 hs-mir-130 813 820  
CAGUGCAAUGUUAAAAGGGC&CCCGACCCCUACCCACUCCAUUCCCGUGGUCUCCUUGCACUU  
.(((((((.(.....((.&.....)))))))). -17.22  
>ENSG00000130164 hs-mir-130 871 878  
CAGUGCAAUGUUAAAAGGGC&GUACACUGUGUACAUUUGGCAUUUGUGUUUUUUUGCACUGU  
(((((((((((.(.(&.....).)))))))). -17.93  
>ENSG00000130164 hs-mir-130 1970 1977  
CAGUGCAAUGUUAAAAGGGC&GACUUCAGGUUCUUCUGAAAUCGCCGUGUACUGUUGCACUGA  
(((((((((((.(.((.&.....).)))))))). -24.00  
>ENSG00000130164 hs-mir-130 2161 2168  
CAGUGCAAUGUUAAAAGGGC&GUCCUGUACAGAUAGUGGGGAUUUUUUUGUUAUGUUUGCACUU  
.(((((((((((.(.((.&..)))).)))). -16.75

mir-130 ENSMUSG00000032193 3530 nt UTR 2 hits 571 642

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>ENSMUSG00000032193 hs-mir-130 571 578  
CAGUGCAAUGUUAAAAGGGC&GUCCUGUGCCCAGCCCCGAGUCUCCGAGUGAGGCUUGCACUU  
.(((((((((((.(.((.&.....)))))))). -17.59  
>ENSMUSG00000032193 hs-mir-130 642 649  
CAGUGCAAUGUUAAAAGGGC&UGGGCACCCACGUGGCCACAUUUGUACUCCUAGGUUGCACUGA  
(((((((((((.(.((.&.....)))))))). -20.20

mir-130 ENSRNOG00000009946 2000 nt UTR 2 hits 1479 1548

-----1-1-----

>ENSRNOG00000009946 hs-mir-130 1479 1486  
CAGUGCAAUGUUAAAAGGGC&CGUCUCAUGCCCAGCCCCUACUGUCCAUUGGAGAUUUGCACUU  
.(((((((((((.(.((.&.....)))))))). -17.20  
>ENSRNOG00000009946 hs-mir-130 1548 1555  
CAGUGCAAUGUUAAAAGGGC&UGGGCACCCACGUGGCCGUCUGUACUCCUAGGUUGCACUGU  
(((((((((((.(.((.&.....)))))))). -22.21

Wild type PCR fragment:

TTCCATTCCCGTGGTCTCC**TTGCACT**TTCTCAGTTCAGAGTTGTACTGTGTACATTTGGCATTGTGTTATTATT**TTG**  
**CACT**GTTTTCT

Mutant PCR fragment:

TTCCATTCCCGTGGTCTCC**TaGgAgT**TTCTCAGTTCAGAGTTGTACTGTGTACATTTGGCATTGTGTTATTATT**TaG**  
**gAgT**GTTTTCT

miRNA: mir-130  
Human predicted target: ENSG00000184371  
Mouse predicted target: ENSMUSG00000014599  
Rat predicted target: ENSRNOG00000018659  
Hs Gene description: MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) (M-CSF). [Source:SWISSPROT;Acc:P09603] NM\_17  
2211

mir-130 ENSG00000184371 4161 nt UTR 2 hits 800 1064  
-----1-----1-----  
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>ENSG00000184371 hs-mir-130 800 807  
CAGUGCAAUGUAAAAGGGC&AGGCCAAGCAGAGGCUCCCCUCAUGAAGGAAGCCAUUGCACUGU  
((((((((((((((..(((.&.....)))))).....)))))))). -23.01

>ENSG00000184371 hs-mir-130 1064 1071  
CAGUGCAAUGUAAAAGGGC&CUUUAGGCUGUGUUCGCCAGGUUUCUGCAUCUUGCACUU  
.((((((((((((((..(((.&.....)))))).....)))))))). -20.50

mir-130 ENSMUSG00000014599 4102 nt UTR 3 hits 787 896 1057  
-----1---1-----1-----  
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>ENSMUSG00000014599 hs-mir-130 787 794  
CAGUGCAAUGUAAAAGGGC&UUGCCCAGCAGAGGCACCCUCAUGAAGGAAGCCAUUGCACUGU  
((((((((((((((((..(((.&.....)))))).....)))))))). -23.01

>ENSMUSG00000014599 hs-mir-130 896 903  
CAGUGCAAUGUAAAAGGGC&UGUUCUCCCACUCCUUCAGCCUCUCCUCGGCUUCUUGCACUGA  
((((((((((((((((..(((.&.....)))))).....)))))))). -21.60

>ENSMUSG00000014599 hs-mir-130 1057 1064  
CAGUGCAAUGUAAAAGGGC&CUUUAGGCUGUGUUCUCCUUGCCCAGGUUUCUGCAUCUUGCACUU  
.((((((((((((((((..(((.&.....)))))).....)))))))). -20.20

mir-130 ENSRNOG00000018659 3232 nt UTR 3 hits 831 940 1100  
-----1---1-----1-----  
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>ENSRNOG00000018659 hs-mir-130 831 838  
CAGUGCAAUGUAAAAGGGC&UUUGCCAGCAGAGGCACCCUCAUGAAGGAAGCCAUUGCACUGU  
((((((((((((((((..(((.&.....)))))).....)))))))). -23.01

>ENSRNOG00000018659 hs-mir-130 940 947  
CAGUGCAAUGUAAAAGGGC&UGUUCUCCCACUCCUUCACCCUCCUCAGCUUCUUGCACUGA  
((((((((((((((((..(((.&.....)))))).....)))))))). -19.30

>ENSRNOG00000018659 hs-mir-130 1100 1107  
CAGUGCAAUGUAAAAGGGC&CUUUAGGCUGUGUUCUACCCAGGUUUUUGCAUCUUGCACUU  
.((((((((((((((((..(((.&.....)))))).....)))))))). -18.30

Wild type PCR fragment:

GAGGCTCCCCTCATGAAGGAAGCCA**TTGCACT**GTGAACACTGTACCTGCCTGCTGAACAGCCTGCCCCGTCATCCATG  
AGCCAGCATCCGTCCGTCCCTCCACTCTCCAGCCTCTCCCCAGCCTCCTGCACTGAGCTGGCCTCACCAGTCGACTGAGGG  
AGCCCCTCAGCCCTGACCTTCTCCTGACCTGGCCTTTGACTCCCCGGAGTGGAGTGGGGTGGGAGAACCCTCCTGGGCCG  
CAGCCAGAGCCGGTCTTTAGGCTGTGTTGTTTCGCCAGGTTTCTGCATC**TTGCACT**TTGAC

Mutant PCR fragment:

GAGGCTCCCCTCATGAAGGAAGCCA**TaGgAgT**GTGAACACTGTACCTGCCTGCTGAACAGCCTGCCCCGTCATCCATG  
AGCCAGCATCCGTCCGTCCCTCCACTCTCCAGCCTCTCCCCAGCCTCCTGCACTGAGCTGGCCTCACCAGTCGACTGAGGG  
AGCCCCTCAGCCCTGACCTTCTCCTGACCTGGCCTTTGACTCCCCGGAGTGGAGTGGGGTGGGAGAACCCTCCTGGGCCG  
CAGCCAGAGCCGGTCTTTAGGCTGTGTTGTTTCGCCAGGTTTCTGCATC**TaGgAgT**TTGAC

*lin-41* CONTROL (known target of *C. elegans let-7* RNA)

miRNA:let-7

*Lin-41* full-length wildtype

CACTTTCTTCTTGCTCTTTACCCATTTTCAGATTGTTTTTAAAAATAATCTTTTGATCCCTTGATCCTTCTTGATCTAGAGTACAGTTCAACTTGACTTTCTTTCTTTTCCCCACTCCTAGTCGATGATCGGCCCCATCAAATCGGGCGCAAAGCACACACATTCAGAAATGTTCCCTTTTTTCCCCCGAGTATTGTCTTTTCCCTTTTCTACACAGGTTAATTAAGAGTTATGTATTTTCATATAGTATTTGTGTAATGTTTATTTTCCGTGCTTCTACCCGGTAGAACATCCAAAAAGCTCCCCCGTCCCCCAAATCCATGTTCCATCTGTATATCCCAGTTTTTTGTCTGTTTTATCTTCTCTCGAGCGCTTCAGCCAAATCCCCTTCCCTCGTAATTATCCTTGTTTTTTCATACATTTATGCAAGTTTTCTCTCACCATTTTTAATGGTTTTCCCATCCATTCATATGGCTCCGCCCCCTCCCTGTGCACTTTTTTATCTGAAAATCTTTGATATTTAGAGAAATTTGAGAATATTTTCGATGAGATTCA TGTAGGTTTTTCCAAAAATCGAACGAATTTGTGCGGAATATTTGAAATCTCAGGAAAAGTCTAAAGAATTAACACCCACAATAGCACCTCTTTTCCCAAATTCACCAACTCAAGTATACCTTTTATACAACCGTTCTACACTCAACGCGATGTAAATATCGCAATCCCTTTTTTATACAACCATTTCTGCCTCTGAACCATTGAAACCTTCTCCCGTACTCCCACCAATAGATTATGCACTTTTCTGAGAGTTTTTCTGTGTTGGAATCATAATTTCTAAACTGATTTCGCATAATTTCCAACACTGAAAACTTTCTCAACACCTCTGGTGACTATTTTCTTTTCCGGTGTTAATTGTCCCAATTGCCTAATGTCCCCAGTGTTTCATTTAAGCTCCCATTTATTTTTATTTCACTGTCTTGTTTTTGTGCCCTAGCGCTAAATATTGTTTTATTTAATGCATGCTTCCCTGCA CGCCCCCTCCCCCTTCTTGCGCACCCAATTTTACAACAATTTGTAATTTAAATTCGCAAATTTCACTGCGAAATTTGAAAT ATATTGCTGATAACATAATTGGAATAAATGTTTTTTTTTAAAAAAAAAAAAAAAAAAAAA

*Lin-41* full-length mutant

CACTTTCTTCTTGCTCTTTACCCATTTTCAGATTGTTTTTAAAAATAATCTTTTGATCCCTTGATCCTTCTTGATCTAGAGTACAGTTCAACTTGACTTTCTTTCTTTTCCCCACTCCTAGTCGATGATCGGCCCCATCAAATCGGGCGCAAAGCACACACATTCAGAAATGTTCCCTTTTTTCCCCCGAGTATTGTCTTTTCCCTTTTCTACACAGGTTAATTAAGAGTTATGTATTTTCATATAGTATTTGTGTAATGTTTATTTTCCGTGCTTCTACCCGGTAGAACATCCAAAAAGCTCCCCCGTCCCCCAAATCCATGTTCCATCTGTATATCCCAGTTTTTTGTCTGTTTTATCTTCTCTCGAGCGCTTCAGCCAAATCCCCTTCCCTCGTAATTATCCTTGTTTTTTCATACATTTATGCAAGTTTTCTCTCACCATTTTTAATGGTTTTCCCATCCATTCATATGGCTCCGCCCCCTCCCTGTGCACTTTTTTATCTGAAAATCTTTGATATTTAGAGAAATTTGAGAATATTTTCGATGAGATTCA TGTAGGTTTTTCCAAAAATCGAACGAATTTGTGCGGAATATTTGAAATCTCAGGAAAAGTCTAAAGAATTAACACCCACAATAGCACCTCTTTTCCCAAATTCACCAACTCAAGTATACCTTTTATACAtCCGTTCTcaACTCAACGCGATGTAAATATCGCAATCCCTTTTTTATACA tCCATTCTcgCTCTGAACCATTGAAACCTTCTCCCGTACTCCCACCAATAGATTATGCACTTTTCTGAGAGTTTTTCTGTGTTGGAATCATAATTTCTAAACTGATTTCGCATAATTTCCAACACTGAAAACTTTCTCAACACCTCTGGTGACTATTTTCTTTTCCGGTGTTAATTGTCCCAATTGCCTAATGTCCCCAGTGTTTCATTTAAGCTCCCATTTATTTTTATTTCACTGTCTTGTTTTTGTGCCCTAGCGCTAAATATTGTTTTATTTAATGCATGCTTCCCTGCA CGCCCCCTCCCCCTTCTTGCGCACCCAATTTTACAACAATTTGTAATTTAAATTCGCAAATTTCACTGCGAAATTTGAAAT ATATTGCTGATAACATAATTGGAATAAATGTTTTTTTTTAAAAAAAAAAAAAAAAAAAAA

*lin-41* segment wildtype

TTTCTCAAATTCACCAACTCAAGTATACCTTTTATACAACCGTTCTACACTCAACGCGATGTAAATATCGCAATCCCT  
TTTTATACAACCATTTCTGCCTCTGAACCATTGAAACCTTCTCCC

*lin-41* segment mutant

TTTCTCAAATTCACCAACTCAAGTATACCTTTTATACA tCCGTTCTcaACTCAACGCGATGTAAATATCGCAATCCCT  
TTTTATACAtCCATTCTcgCTCTGAACCATTGAAACCTTCTCCG