

Name	Arm	Mature miRNA sequence	Cloning frequency	Pre-miRNA genomic coordinates	Pre-miRNA secondary structure	SVM score	Homologs (mismatches<6)	Other predictions
RN-1	5	ACUCAAAUGUGGGCACACUU	1(m)	chr1, 64350964-64351026, -	<pre> G U - AC GAUU GA ACUCAAA GUGG GGCAC UU CUG \ CU UGGGUUU CAUC UCGUG AAGAU A G U A A- GCGU </pre>	-0.33	mmu-mir-295*(0)	L290
RN-2	3	ACCAGGAGGCUGAGGUCCUU	1(m)	chr6, 134183482-134183559, +	<pre> U - U AUCCA A CU GGUC CCU UGAGGGGCCUC GCCUCU GG UUAU U CCGG GGA AUUCCUGGAG CGGAGG CC AGUA U C C U A---- - UU </pre>	-0.03	HN-4(1) MN-6(0)	
RN-3	5	AUCAUGAUGGGCUCUCGGUG	2(h), 1(m)	chr6, 134189465-134189537, +	<pre> GA---- UGA - C---- UC- AGG UCA UGGGCU CCU GGUGU UCC \ GGU GCCCGA GGA CCACA AGG U CUAGGAA UAG C AGUA CCA CGA </pre>	-1.81	hsa/mmu/rno- mir-433-3P(0) MP-24(5)	
RN-4	5	GCUCGACUCAUGGUUUGAACC	4(m)	chr6, 134192432-134192513, +	<pre> U CUCU UG - CUC UC U GUCGA UGA UGGUU AACCAC AG GAC AUGGU U CAGCU ACU ACCAA UUGGUG UC CUG UA CCA G C ---- GU C AAA U- A </pre>	-0.06	mmu-mir-434(0) MP-34(0)	
RN-5	5	AUAGUAGACCGUAUAGCGUAC	2(h), 4(m)	chr6, 134395538-134395603, +	<pre> AGA A AUA C UAU GAG UAGU GACCGU GCGUACG UU \ CUC AUCA CUGGCA UGUUAGC AG C CCA C CAA - UGU </pre>	-0.5	mmu-mir-411(0) HN-5(0)	
	3	UAUGUAACACGGUCCACUAA	1(m)					
RN-6	5	AUGGUAGACCAUAGAACAUGC	1(m)	chr6, 134397179-134397245, +	<pre> A GUU GA C U GA AAGAUG GACCAUA ACAUCCG UAC U CU UUCUAC CUGGUAU UGUUAGC GUG C C AC- GA U U </pre>	-0.81	hsa-mir-380(0) mmu-miR-380(0)	
RN-7	3	GGCUGCAGCUGAUCGCCUG	2(m)	chr6, 134403226-134403284, +	<pre> A-- - GAG - AG AGCGGGC CG GCUGU AGCCCC CU G UCGUCCG GU CGACG UCGGGG GA U CUA G --- C CA </pre>	-2.11	MN-7(0)	
RN-8	3	AAUAUAACACAGAUGGCCUGU	3(h), 1(m)	chr6, 134431273-134431338, +	<pre> G UG A A C UAU GAGGA AGGU UCUGUG UG GUUCG UU \ CUUUU UCCG AGACAC AU UAAGC AG U G GU A A - UAA </pre>	-0.39	HP-49(0) hsa-mir-410(0) mmu-mir-410(0)	X26
RN-9	5	GAUGGAAACUGAGAGGA	1(m)	chr9, 22136907-22136975, +	<pre> U UU C A AAAC AG G GGGG GGAGG UG UGG UGAGAGG GAUU \ CCCC CCUCC AC ACC ACUCUUC UUAG C A U- - - C--- GU U </pre>	-2.01	hsa/mmu/rno- mir-184(4)	
RN-10	5	AGCAGCACACUGUGGUUUGUA	2(m)	chr10, 57087471-57087528, +	<pre> G C U -- AC AGCA CACA UGUGGUUG AC GGC U UUUGU GUGU ACACCAAAC UG CCG G G C C CA GU </pre>	-0.06	hsa-mir-497(0) HN-9(0) MN-5(0)	X43
RN-11	5	CUUACAGUCAGGUA	1(h)	chrX, 139814891-139814942, -	<pre> A G CU U AAGUCU CAGUCAG UAG UC U UUACGAA GUCACGUC AUC AG G C - U- A </pre>	-0.22	hsa/mmu/rno-mir-17(0) hsa/mmu/rno-mir-20(1) hsa-mir-106a(0) mm-mir-106a(1)	B971