

Name	Arm	Mature miRNA sequence	Cloning frequency	Pre-miRNA genomic coordinates	Pre-miRNA secondary structure	SVM score	Homologs (mismatches<6)	Other predictions
MN-1	3	ACUUAGCUCACUUCUU	1(m)	chr1, 23518215-23518296, +	<pre> AAAG AG GG --- ACA-- UCCU AGUGAG GGG AAAGG AGA GAG UGAA \ UCACUU CUC UUUCC UCU CUC ACUU A GA-- GU UU UCA GAUUC CCAG </pre>	-1.75	hsa/mmu/rno-mir-27b(5) hsa/rno-mir-151(5) mmu/rno-mir-329(5) HP-33/34(5)	B463
MN-2	3	UAAGUGCUUCCAUGUUUUAG	1(h), 1(m)	chr3, 128025063-128025120, +	<pre> UU AU U G- UC ACU AACAUGGGA GCUU CU UC \ UGA UUGUACCU UGAA GA AG A UU CG U GA CU </pre>	-0.96	hsa-mir-302b(0) hsa-mir-302a/c/d(1) mmu-mir-302(1)	
MN-3	5	ACAUUCAUUGUUGUCGGUGGGU	1(m)	chr8, 83449175-83449233, -	<pre> G UG GUGA AG ACAUUCAU U UCGGUGGGU GG G UGUAAGUAG G GGCCACCCAG CC C G -- A--- GA </pre>	-0.6	hsa-mir-181d(0) hsa/mmu/rno-mir-181b-1/2(1)	X74
MN-4	3	AGCCAUCUCUCCAGCC	1(h)	chr9, 106092117-106092176, +	<pre> - AC A-- AGG C GCUGGGGCUGG GA UG GCUC UC U CGGCCCGACC CU AC CGAG GG C U CU CGA AA- G </pre>	-1.44	hsa-mir-197(4) rno-mir-349(4)	
MN-5	5	AGCAGCACACUGUGUUUUGUA	2(m)	chr11, 69847287-69847344, +	<pre> G C U -- AC AGCA CACA UGUGUUUG AC GGC U UUGU GUGU ACACCAAAC UG CCG G G C C CA GU </pre>	-0.06	hsa-mir-497(0) HN-9(0) RN-10(0)	X43
MN-6	3	ACCAGGAGGCUAGGUCCCUU	1(m)	chr12, 104334502-104334581, +	<pre> U - U AUCCA A U GGGUC CCU UGAGGGGCUC GCCUCU GG UUAUG U UCCGG GGA AUUCCUGGAG CGGAGG CC AGUAU U C C U A---- - U </pre>	-0.01	HN-4(1) RN-2(0)	
MN-7	3	GGCUGCAGCGUGAUCGCCUG	2(m)	chr12, 104465268-104465345, +	<pre> C - A-- - GAG - AG CCUG GUG GAGCGGC CA GCUGU AGCCCC CU G GGAC CGC CUCGUCCG GU CGACG UCGGGG GA U A A CUA G --- C CA </pre>	-1.58	RN-7(0)	
MN-8	3	AAUUGCACGGUAUCCAUCU	1(h)	chrX, 45087626-45087688, -	<pre> - A A GG GGUG CAGGUGGA AC CG UGCAUUUUU UU U GUCUACCU UG GC ACGUAAAA AG A A - - GG GAUA </pre>	-0.69	mmu-mir-363(0) hsa-mir-363(0) HP-85(0) RP-99(0)	B343, X211
MN-9	5	AAUCCUUGGAACCUAGGUGU	1(m)	chrX, 5530957-5531028, -	<pre> C- ACC AA U U CCUCU GAUCCUUGGA UAGGUGU UGC GC U GGAGA CUUAGGAACUU GUCCACAC ACG UG C AA --- A- - A </pre>	-0.61	hsa-mir-362(0) HP-77(0)	B121, X144
MN-10	5	CAUGCCUUGAGUGUAGGACCG	1(h), 1(m)	chrX, 5537395-5537461, -	<pre> C U A A CC UGACAU UCUU CA GCCUUG GUGU GGA GU \ AGGA GU CGGAAC CACA CCU CA C C U C C CC UUAUU </pre>	-0.13		
	3	CCUCCACACCCAAGGCUUGC	1(h),2(m),1(r)			-0.13		