

Name	Arm	Mature miRNA sequence	Cloning frequency	Pre-miRNA genomic coordinates	Pre-miRNA secondary structure	SVM score	Homologs (mismatches<6)	Other predictions
HN-1	3	ACCAACAUGGUGAAACCCU	1(m)	chr3, 37995864-37995931, +	<pre> UG UGGA - A- AUUUCA GAGG GG UCACC UG GGUCAGG \ CUCU CC AGUGG AC CCA GUCC A GU CAA- U AA GACCAG </pre>	-1.26	HN-3(0)	
HN-2	5	CAGGGUUUCACCAUGUUGG	1(m)	chr3, 52284705-52284776, -	<pre> GUA A UUCAC UU CU CU GAGGC GGGU CAUG GGUCAGG GGU \ CUCCG CCCA GUGC CUAGUCC UCA U CGA - UCUA- U- -- AG </pre>	-1.9	hsa-mir-196a(4) mmu-miR-196a(4) rno-mir-196a(4)	
HN-3	3	ACCAACAUGGUGAAACCCU	1(m)	chr4, 8133205-8133274, -	<pre> U UGGA UGA-- A-- C GAGGCAGG UCAUU GGUCAGG GUU \ CUCUGUCC AGUGG CCA GUCC CAG A A CAA- UACAA GAC A </pre>	-2.01	HN-1(0)	
HN-4	3	ACCAGGAGGCGUAGGCCCC	2(h)	chr14, 100411130-100411185, +	<pre> U ACC- G CU GAGGGGUCU GCCUCU CA GA \ CUCCCCGAG CGGAGG GU CU C U ACCA A UU </pre>	-1.42	MN-6(1) RN-2(1)	
HN-5	5	UAGUAGACCGUAUAGCGUAC	1(h), 2(m)	chr14, 100559430-100559483, +	<pre> A AUA C UAU UAGU GACCGU GCGUAC GU \ AUCA CUGGCA UGU AUGC AG C C CAA - UGU </pre>	-0.78	mmu-mir-411*(0) RN-5(0)	
HN-6	3	AAACAUUCCGGUGCACUUCU	1(m)	chr14, 100568085-100568144, +	<pre> U - U-- U UUU GAGAAGU GC CCGUG UUUU UCGC \ UUCUUA CG GGC GC AAAG AGUG A - U UUAC C UUU </pre>	-1.63	MP-37(0) RP-35(0)	B210, X202
HN-7	5	UGGUGGGCCGCAGAACAUUG	1 (h)	chr14, 100576319-100576381, +	<pre> A GCC A - - A AAAG UGGUGG GCAGA CAUGUG C UG G UUUC ACUACC CGUCU GUAUAC G GC U C AGU - C U U </pre>	-0.13	hsa-mir-380-5p(5) mmu-miR-380-5p(5)	
	3	UAUGUCUGCUGACCAUCAC	1 (h)					
HN-8	5	AGGUUGUCCGUGGUGAGUUCGC	1 (h)	chr14, 100592317-100592383, +	<pre> U GUGAGUUC U GGAGGGAGGUUG CCGUG GCAUUUU \ CUUUUCUCCAGC GGCAC CGUAGUA U U AUAACC- - A </pre>	-1.17	hsa-mir-453-3P(0) RP-45/48(5)	ANMH-52
HN-9	5	GCAGCACACUGUGGUUUG	2(m)	chr17, 6861984-6862041, -	<pre> G C U -- AC AGCA CACA UGUGGUUUU AC GGC U UUGU GUGU ACACCAAAC UG CCG G G C C CA GU </pre>	-0.06	hsa-mir-497(0) MN-5(0) RN-10(0)	X43, ANMH64
HN-10	3	CAGUGCAAUGAUUUGCAAAGC	3(h)	chr22, 20331820-20331903, +	<pre> - G C G-- A GUGCU GCUGG CC CAGGUCU UGACGA GUUGCACU CU \ CGACC GG GUCUA CGA ACUGUU UAACGUGA GA C A - A AUAG C AGAGU </pre>	-0.75	hsa/mmu/rno-mir-301(2)	X220, ANMH76
HN-11	5	UAUCCUUGCUACCUUGGGUGAG	1 (h)	chrX, 49476075-49476158, +	<pre> CCC U- UAC UG AGAG UGUC GCUC CUCUC AAUCCUUGC C GGUG UGC \ CGAG GAGAG UAAGGAACG G CCAC ACG U AGC UC --- GU GUA- UAAG </pre>	-0.33	hsa-mir-500(0) HN-12-5(0)	
HN-12	5	UAUCCUUGCUACCUUGGGUGAG	1 (h)	chrX, 49478315-49478394, +	<pre> CUCU- UAC AGAG UUUC UCCCCCU AAUCCUUGC CUGGUG UGC \ AGGGGGA UAAGGAACG GACCAC ACG U ACGUC --- GUG- UAAG </pre>	-0.33	hsa-mir-500(0) HN-11-5(0)	

HN-13	5	UA CC CAUUGCAUAUCGGAGUUG	2(h)	chrX, 49480881-49480976, +	<pre> U ACU- C CAUAC- U C U GAAUU GA GCUC UUCUCC CCAU GCAUUAU GGAG UGU \ CU CGAG GGGAGG GGUA CGUGUG CCUC ACA C A GUUC U ACAUUA - U C AAACU </pre>	-0.55		
HN-14	5	CAAAGUGCUCUAUAGUGCAGGUA	5(h), 6(m)	chrX, 133029352-133029435, -	<pre> U U CA- G GU- UUG GUCC AG AGUAC AAGUGCUCUAU UGCAG AGUU \ UAGG UC UCAUG UUCACGGGUUUA AUGUC UCAG G U - ACC G AUC UAC </pre>	-0.91	hsa-mir-20b(0) MP-56(0) RP-100(0)	X216
	3	ACUGUAGUAUGGGCACUCCAG	1 (h)					