

Name	Arm	Mature miRNA sequence	Cloning frequency	Pre-miRNA genomic coordinates	Pre-miRNA secondary structure	SVM score	Homologs (mismatches<6)
HP-30	3	UGAAGGUUCUACUGUGGCCAG	2(h)	chr14, 100405160-100405230, +	<pre> U CAUUC U GGGCUU GUACAUGGUAGGCUUUCAUU GU U CCCCGA CGUGUGCAUCUGGAAGUGG CA G C CUUA- C </pre>	0.12	hsa-mir-493*(0) RP-29(0) MP-32(0)
HP-31	5	UCUUGGAGUAGGUCAUUGGGU	3(h)	chr14, 100420573-100420666, +	<pre> U - C UCU UA G A UCUAUUU GA CU CUCCAGG UGGAG GGUCAUU GGUGG UCC \ CU GA GAGGUUC ACCUC UCGGUAG UCACC GGG C A A U UGU C- G - UGCAUUC </pre>	1.27	hsa-mir-432(0)
HP-33	3	AACACACCUGGUUAACCUCUU	2(h)	chr14, 100562875-100562954, +	<pre> CU UU UG UUC U AA GGUAC GAAGAGAGG C GGU UGUUUC UU U CUAUG CUUUUCUCCA G CCA ACAAAG AG G AC UU GU C-- C GA </pre>	1.29	HP-34(0) hsa-mir-329-1(0) mmu-mir-329(4) rno-mir-329(4)
HP-34	3	AACACACCUGGUUAACCUCUU	2(h)	chr14, 100563199-100563264, +	<pre> UU UG UUC U AU GAAGAGAGG C GGU UGUUUC UU U CUUUUCUCCA G CCA ACAAAG AG G UU GU C-- C GA </pre>	0.25	HP-33(0) hsa-mir-329-2(0) mmu-mir-329(4) rno-mir-329(4)
HP-35	3	UGAAACAUCACGGGAAACCU	1(h)	chr14, 100565724-100565804, +	<pre> C GU - C - UUUU GAUACU GAAGGAGAGG CCGUGU UGU UUC UC \ CUAUGA UUUUUUCCCAA GGCACA ACA AAG AG G - AG U - U UAUU </pre>	1.4	hsa-mir-494(0) MP-35(0) RP-33(0)
HP-37	3	AUCAUAGAGGAAAAUCCACG	1(h)	chr14, 100576159-100576238, +	<pre> U G A U -- GU GGUAUU AAAA GU GAUUUCCU CUAUGGUUA CGU \ CUAUGA UUUU CA CUAAAAGGA GAUACUAAU GUA U C G C - UG GU </pre>	1.31	hsa-mir-376a(0) mmu-mir-376a(1) RP-39(1)
HP-40	3	AAUCGUACAGGGUCAUCCACUU	3(h)	chr14, 100582545-100582628, +	<pre> U UG UUAU CCU UUUUG UGGUACU GAGAGUGG CCCUGU GUUCG C ACUAUGA UUUUCACC GGGACA UAAGC U A CU UACU UGC UGUAC </pre>	1.28	MP-39(0) RP-41(0)
HP-41	5	GGAGAAUUAUCCUUGGUGUGU	2(h)	chr14, 100583411-100583488, +	<pre> UG A G - C UAU AUACU AGGAGAAUU UCCUUG UGUG UUCG UU \ UAUGA UUUUCUUUAA AGGAAC AUAC AAGU AG U GU C - U - UAU </pre>	1.17	MP-40(0) RP-42(0)
HP-42	3	AUUCUGCAUUUUUAGCAAGU	1(h)	chr14, 100584748-100584838, +	<pre> AUUUU CUA U - U GA- C CAUCAC GGA CUUGUUAAAAA GCAGA UCU UU A GUAGUG CUCU GAACGAUUUUU CGUCU AGA AG G UAAUC AA- U A U ACC G </pre>	0.3	MP-41(1) RP-43(1)
HP-44	3	AAUCAUACAGGGACAUCCAGU	1(h)	chr14, 100588536-100588615, +	<pre> U G UUA C - C AU GGUACU GAAGA UGG UCCUG UGUG UUCG UUA \ CUAUGA UUUU ACC AGGGAC AUAC AAGC AGU U C G UAC - U - AU </pre>	1.11	hsa-mir-487(0) HP-40(3) MP-39(3) RP-38/41(3)
HP-45	5	AGAGGCUGGCCGUGAUGAAUUC	1(m)	chr14, 100591505-100591585, +	<pre> U GU UG CU - A AUUCA G ACU GAGAGAGG GGCCGUG AUGA UUCG \ C UGA UUCUCUCC UCGGCAC UACU GAGC U A UG UU UC A - GAAAC </pre>	1.41	hsa-mir-485(0) mmu-mir-485(0) MP-42(0) RP-46(0)

HP-47	5	AGGUUACCCGAGCAACUUUG	3(h)	chr14, 100601390-100601468, +	U U GG A AC - CA UG GGUAC CG GAG GGUU CCGAGCAAC UUUG UC \ CUAUG GC UUC CCAA GGCUCGUUG AAGC AG G A - UU C GU U -- CA	0.74	hsa-mir-409(0) mmu-mir-409(0) RP-50(0)
	3	CGAAUGUUGCUCGGUGAACCCC	1(h), 1(m)		A C U AA - U GGAUGG UGGU GACCAG UGG AGUA AUUG U CCUGCC AUCA CUGGUC ACU UCAU UAAU U G C C -- G C		
HP-48	3	UUCACCCUGGUCACUAGCC	1(m)	chr14, 100601548-100601614, +	C G UG A A C UUA GGUAC UGAGAA AGGU UCUGUG UG GUUCG UU U CCAUG ACUUUU UCCG AGACAC AU UAAGC AG U - G GU A A - UAA	0.78	hsa-mir-410(0) mmu-mir-410(0) RN-8(0)
HP-49	3	AAUAUAACACAGAUGGCCUG	3(h), 1(m)	chr14, 100602002-100602081, +	GU U GU G A AG UUAU GUG CUCAGAA CGGG UUUGAGGC AG UG U \ UAC GGGUUUU GCCC AAACUCCCG UC AC A G UG C UG G A CU UUUU	1.25	hsa-mir-193b(0) mmu-mir-193(4) rno-mir-193(4)
HP-61	5	AAACCGUUACCAUUACUGAGU	6(h), 5(m)	chr17, 24212514-24212583, -	U A GA A UGGG AUGGCAAG AACCGUUACCAUUACUG G ACCC UAUCGUUC UUGGUAUUGGUAUUGAU U G A UC U	0.83	hsa/mmu/mo- mir-451(0) MP-28(0) RP-66(0)
HP-77	5	AAUCCUUGGAACCUAGGUGUGA	1(h), 1(m)	chrX, 49476605-49476676, +	- ACC A- UG AU CCUCUU GAUCCUUGGA UAGGUGUG G CU \ GGAGAA CUUAGGAACUU AUCCACAC C GA U A --- AA GU CU	0.32	hsa-mir-362(0) MN-9(0)
HP-80	3	AUCAGCAAACAUUUAUUGUGUG	2(h)	chrX, 73289960-73290065, -	CCCAG ---- A -- CU- A A AUAAAA CCUG GC CAU UAGUAGGC CAGUAAAUUUU UU GAUGA \ GGAC CG GUG AUCGUCCG GUUAUUUACAAA GA CUACU G ----- ACCU A AA UGU C - CAGUAA	2.01	HN-9(5)
HP-85	5	CGGGUGGAUCACGAUGCAAUUU	1(h)	chrX, 133028921-133029009, -	U GU CA A GAUGAGUA GUUUUGC GUU CGGGUGGAU CG UGCAAUUUU U CAGGACG CAA GUCUACCUA GC ACGUUA AAA C C AU UG - AGAGGAUA	1.14	hsa-mir-363(0) mmu-mir-363(0) MN-8(0) RP-99(0)
	3	AAUUGCACGGUAUCCAUCUGU	5(h), 1(m)		U UUU U AAU GAUGC AAACUAU UGCGA GUGUUCUAAUAUGU \ CUAUG UUUGAUA ACGUU UACAGGGUUUUGUA A U CUU U AAU		
HP-86	5	UUUUGCGAUGUGUUCUAAU	1(h)	chrX, 133400068-133400148, -	A U G GU AU UGCCCU GCAGCGGGAACAGU CU CA GAGCG \ AUGGGA CGUCGCUUUUGUUA GG GU CUCGU C C U G -- GG	0.8	hsa-mir-503(0) MP-60(1) RP-103(1)
HP-87	5	UAGCAGCGGGAACAGUUCUG	3(h)	chrX, 133405878-133405948, -	AA GU G A UUUGU AGCACUUAC CU UUGCAGA GA ACUGAGAC \ UCUGAAUG GA AACGUCU CU UGACUCUG A AA -- A C UAUCA	1.02	hsa-mir-452(0) mmu-mir-452(0) MP-63(0)