

Name	Arm	Mature miRNA sequence	Cloning frequency	Pre-miRNA genomic coordinates	Pre-miRNA secondary structure	SVM score	Homologs (mismatches<6)
MP-5	3	AAUUGCACUUAGCAAUGGUG	5(h), 3(m)	chr3, 128025558-128025632, +	<pre> -           CA      C      UUGAA AGG CCGUCACUGUUGCUAA  UGCAA UCUG   U UCC GGUAGUGGUAACGAUU  ACGUU AGGU   A A           UC      A      UAAAG </pre>	0.78	hsa-mir-367(0)
MP-24	5	AUGGUGGCACGGAGUC	1(m)	chr10, 127120840-127120960, +	<pre> .-.AAAA - - U U --- C U UA CCUCUCUCCC   CUA AA CA GGA CUA CAU  GGUGGCA GGAG CAGC \ GGAGAGGAGGG   GAUUU GU CCU GAU GUG  CUAUCGU UCUC GUUG  G \ --- U A U C UCC - U UA </pre>	0.9	hsa-mir-205(5) mmu-miR-205(5) rno-mir-205(5) RN-3(5)
MP-28	5	AAACCGUUACCAUUACUGA	6(h), 5(m)	chr11, 77685721-77685807, +	<pre> U   U---- AU   GA   A GGCAC   UGGGA  GCGGAG  AACCGUUACCAUUACUG  G CCGUG   ACCCU  UCGUUC  UUGGCAAUGGUAAUGAU  U A   UCAAAC   CG   UC   U </pre>	1.19	hsa/mmu/rno- mir-451(0) HP-61(0) RP-66(0)
MP-33	3	AGGUCAGAGGUCGAUCCUGG	2(m)	chr12, 104334262-104334328, +	<pre> A   AC   U   G-  A UGGGCC AGGGUC  CCUCUGAC  CUGU  GCC \ AUCCGG UCCUAG  GGAGACUG  GACA  UGG  A G   CU   -   GA  G </pre>	0.18	RP-30(0)
MP-34	5	GCUCGACUCAUGGUUUGAACC	3(m)	chr12, 104342700-104342775, +	<pre> A-  C  CUC  UG  UACU UUGAACCA  AG  UCGA  AUGGUU  AACCAU  U AGCUUGGU  UC  AGCU  UACCAA  UUGGUG  A CC - CAC  GU  CUUA </pre>	0.61	mmu-mir-434(0) RN-4(0)
	3	UUUGAACCAUCACUCGACUC	1(m)				
MP-35	3	UGAAACAUAACACGGGAAACCU	1(m)	chr12, 104463492-104463576, +	<pre> U   U   GU   -  C  -  UUUA UGAUACU  GAAGGAGAGGUU  CCGUGU  UGU  UUC  UC  \ ACUAUGA  UUUUUUCUCCAA  GGCACA  ACA  AAG  AG  U A   -   AG   U   -  U  UAUU </pre>	1.89	hsa-mir-494(0) HP-35(0) RP-33(0)
MP-37	3	AAACAUUCGCGGUGCACUUCU	1(m)	chr12, 104465432-104465507, +	<pre> U   U   U   -  --  -  UUU GCU AA  GAGAAGU  GC  CCGCG  UGUUUU  UCGC  \ CGA UU  UUCUUA  CG  GCGCG  ACAAAAG  AGUG  A A   C  U   -  U   UU   C  UAU </pre>	0.41	HN-6(0) RP-35(0)
MP-38	3	AACAUAAGAGGAAAUUCACG	2(m)	chr12, 104470892-104470977, +	<pre> U   GU  U   G   UA   U   --  UU UUU  AUU  AAAA  GUGGA  UUCCU  CUAUGUUUA  UGC  \ AAC  UGA  UUUU  CACUU  AAGGA  GAUACAAAU  GUG  U A   UG  C   G   UA   -   UA  UU </pre>	0.91	hsa-mir-368(2) RP-37(0)
MP-39	3	AAUCGUACAGGGUCAUCCACU	3(m)	chr12, 104475507-104475588, +	<pre> U   UG   UUAU  CCUC  -  UUCA GGUACU  GAGAGUGG  CCCUGU  UUUC  C  \ CUAUGA  UUUUCACC  GGGACA  AAGC  G  C A   CU   UACU  UGCU  C  UACU </pre>	0.89	HP-40(0) RP-41(0)
MP-40	5	GGAGAAUUUACCUUGGUGUGU	2(h)	chr12, 104476303-104476376, +	<pre> UG           G   UUGGC  UU UACU  AGGAGAAUUUACCUUG  UGUG  UC  \ AUGA  UUUUUUUAAUAGGAAC  AUAC  AG  U GU           -  UAAGU  GU </pre>	1.03	HP-41(0) RP-42(0)
MP-42	5	AGAGGCUGGCCGUGAUGAAUUC	1(m)	chr12, 104483072-104483152, +	<pre> U   U   CU   -  A  AUUCA GAUACU  GGAGAGAGG  GGCCGUG  AUGA  UUCG  \ CUGUGA  CUUCUCUCC  UCGGCAC  UACU  GAGC  U A   U   UC   A   -  AAAUC </pre>	1.68	mmu-mir-485(0) hsa-mir-485(0) HP-45(0) RP-46(0)

MP-44	5	AAGGGAUUCUGAUGUUGGUCACA	6(m)	chr12, 104490583-104490672, +	<pre> A U AAG A G ----- C GCCA AA CAGAG GGAAUUCUG UGUU GUCAC ACUC \ CGGU UU GUCUC CCUAAGAC ACAA CGGUG UGAG A A C AUA - G AGUAAAAUUU A </pre>	0.49	RP-49(0)
MP-45	5	AGAUCGACCGUGUUUAUUCG	2(h), 1(m)	chr12, 104491592-104491670, +	<pre> U AG UA CUU C GGUACU GA GGAGAUCGACCGUGU UAUUCG GG U CUAUGA CU UUUCUAGUUGGUACA AUAAGC UC G - CU UA U-- A </pre>	0.76	hsa-mir-369(0) RP-51(0)
	3	AAUAAUACAUGGUUGAUCUU	2(h), 1(m)				
MP-56	5	CAAAGUGCUCAUAGUGCAGGUA	5(h), 6(m)	chrX, 45088040-45088119, -	<pre> C U CA- G G UUUUUA CUAG AGUGC AAGUGCUGUA UGCAG UAG \ GGUC UCAUG UUCACGAGUGU ACGUC AUC U - C AUC G - UCACCA </pre>	0.24	hsa-mir-20b(0) HN-14(0) RP-100(0)
MP-58	5	UUUUGCGAUGUGUCCUAAU	1(h)	chrX, 45572542-45572610, -	<pre> UUU U UACU GAACUUA UGCGA GUGUCCUAAUUG \ CUUGGUA ACGUU CGUAGGGUUUAU A CUU U GAGU </pre>	0.44	hsa-mir-450-1/2(0) mmu-mir-450(0) rno-mir-450(0) HP-86(0)
MP-59	5	CUCGGGGAUCAUCUGUCACG	2(h), 1(m), 2(r)	chrX, 45573646-45573730, -	<pre> A GUC GG UCA A- C GG UCUCAGAC UCGG AUCA UGUCACGAG UAC A CC AGGGUCUG AGUC UAGU ACAGUGUUC GUG C G GAA AA UAG CC U </pre>	0.42	RP-101(0)
	3	UGUGACAGAUUGAUACUGAAA	1(h), 1(m)				
MP-60	5	UAGCAGCGGGAACAGUACUGC	6(m),4(r)	chrX, 45578227-45578297, -	<pre> UA C G UGA GUU UGCCC GCAG GGGAAACAGUACU CAG GU \ AUGGG CGUC CCUUUGUUUAUGA GUC CG U UC A G C-- UGG </pre>	0.6	hsa-mir-503(1) HP-87(1) RP-103(0)
MP-61	3	CUUGGUACAUCUUUGAGUGA	3(m)	chrX, 59554721-59554798, -	<pre> A A UG CC UUAAC GUGUG UGU UCACU AGGAUGUACCA CAU A CACAC AUA AGUGA UUCUACAUGGU GUA G A G GU UC CAAAG </pre>	0.92	
MP-63	5	AACUGUUUGCAGAGGAAACUGA	1(h)	chrX, 63820617-63820683, -	<pre> UUACAA G G A UUUAU CU UUUGCAGA GA ACUGAGAC \ GA AAACGUCU CU UGACUCUG A AAUG-- G A C UAUCA </pre>	0.04	mmu-mir-452(0) hsa-mir-452(0) HP-88(0)
MP-66	5	GAUCAAGUGGAGGCCUCUC	4(m)	chrUn_random, 95645494-95645572, -	<pre> UGU U G C C- GG ACAUACAG CGA CAAAGUGGA GC CU UCCGC C UGUGUGUC GUU GUUUUACCU CG GA GGGCG U UCU U A U AA GU </pre>	1.14	mmu-mir-291(1) rno-mir-291(1) mmu-mir-294(3)
	3	AAAGUGCAUCCAUUUUGUUUGUC	2(m)				