

Name	Arm	Mature miRNA sequence	Cloning frequency	Pre-miRNA genomic coordinates	Pre-miRNA secondary structure	SVM score	Homologs (mismatches<6)
RP-29	3	UGAAGGUCUACUGUGGCCAG	2(h)	chr6, 134176527-134176610, +	<pre> CUC      U      CAU  U GGC CAGGGCCU GUACAUGGUAGGCUUUCAUU  UGU  U CCG  GUCCCCGA  CUGUGUCUAUCUGGAAGUGG  ACA  G U--      C      CUU  C </pre>	1.69	hsa-mir-493*(0) HP-30(0) MP-32(0)
RP-30	3	AGGUCAGAGGUCGAUCCUGG	2(m)	chr6, 134183220-134183303, +	<pre> UG  C  A  AC  U  G-  A CCC GGG UGGGCC AGGGUC CCUCUGAC CUGU GCC \ GGG CUC AUCCGG UCCTUAG GGAGACUG GACA UGG A GU  -  G  CU  -  GA  G </pre>	0.58	MP-33(0)
RP-31	3	GCCUGCUGGGUGGAACCUGG	3(h),3(m)	chr6, 134216381-134216459, +	<pre> G      CA  GU  U  U  A  GC AGACAGA AGACCAGGU C  CUC GCAG UAC CA \ UCUGUCU UUU<u>GGUCCA</u> G  GGG CGUC GUG GU  U G      AG  UG  U  C  A  AC </pre>	0.77	hsa-mir-370(0) mmu-mir-370(0)
RP-32	5	UGGUAGACUAUGGAACGUA	3(h),4(m)	chr6, 134394385-134394469, +	<pre> U  UUC  C  G  A  GA  -  UUAU GG  CUG  AGAG  UGGU  GACUAUG  ACGUAGG  CG  \ CC  GAC  UCUC  AUCA  CUGGUAC  UGUAUCC  GU  G A  UAU  -  A  C  AA  A  CUUU </pre>	0.27	hsa-mir-379(0) mmu-mir-379(0)
RP-33	3	UGAAACAUCACGGGAACCU	1(h)	chr6, 134401055-134401137, +	<pre> U      U      GU  -  C  -  UUAU GAUACU GAAGGAGAGGU  CCGUGU UGU UUC UC  \ CUAUGA UUUUUUC<u>CCAA</u>  GGCACA ACA AAG AG  U A  -  AG  U  -  U  UAUU </pre>	1.57	hsa-mir-494(0) HP-35(0) MP-35(0)
RP-35	3	AAACAUCGCGGUGCACUUCU	1(m)	chr6, 134403345-134403424, +	<pre> U  U  U  -  -  -  UUU GGUGCU AA GAGAAGU GC CCGCG UGUUUU UCGC \ CUACGA UU <u>UCUUCA</u> CG GCGCG <u>ACAAAG</u> AGUG  A C  U  -  U  UU  C  UAU </pre>	1.12	HN-6(0) MP-37(0)
RP-37	3	AACAUGAGGAAAUUUCACG	2(m)	chr6, 134409711-134409794, +	<pre> U  GU  U  G  UA  U  UGGUUAU UG  AUU  AAAA  GUGGA  UUCCU  CUAUGUUUA  \ AC  UGA  UUUU  <u>CACUU</u>  <u>AAGGA</u>  GAUACAAU  U A  UG  C  G  UA  -  UAGUAU </pre>	1.2	hsa-mir-368(2) MP-38(0)
RP-38	5	GUGGAUUAUCCUUAUGGUU	2(m)	chr6, 134410367-134410452, +	<pre> U      U      A      U      CGUGCU UUGGUAUU AAAAG<u>GUGGAU</u> UUCCU CUAUGGUUA  \ AACUAUGA UUUU<u>CACCUA</u> AAGGA GAUACUAAU  U A      C      C      -  AGGUCC </pre>	1.88	mmu-mir-376b(0) hsa-mir-376a(2)
	3	AUCAUAGAGGAACAUCCACU	1(m)				
RP-39	5	GGUAGAUUUCUUCUAUGAG	1(h),1(m)	chr6, 134410877-134410958, +	<pre> U      U  G  A  C  U  GUACAUAU GAUAUU AAAA GU GAUU UCCU CUAUGA  \ CUAUGA UUUU CA CUAA AGGA GAUGCU  U A      C  G  C  A  -  AAUCAGUAA </pre>	0.92	hsa-mir-376a(1) mmu-mir-376a(0) HP-37(1)
	3	AUCGUAGAGGAAAUCCACG	2(m)				
RP-40	3	UAUACAAGGCAAGCUCUC	1(h)	chr6, 134413887-134413947, +	<pre> C  G  U  G  UUA AG GAG UUGCCCUU GUUAUUC GU  U UC  CUC  AACGGGA  CAUAUAGG UA  U U  G  -  G  CAG </pre>	0.08	hsa/mmu-mir-381(0) mmu/mo-mir-300(1)
RP-41	3	AAUCGUACAGGUCAUCCACU	3(h)	chr6, 134414396-134414477, +	<pre> U  UG  UUAU  CCUC  -  UUCA GGUACU GAGAGUGG  CCGUGU  UUCG C  \ CUAUGA UUUU<u>CACC</u>  GGCACA  AAGC G  C A  CU  <u>UACU</u>  <u>UGCU</u>  C  UAUU </pre>	0.89	HP-40(0) MP-39(0)
RP-42	5	GGAGAAAUUAUCCUUGGUGUGU	2(h)	chr6, 134415104-134415179, +	<pre> G  -  CU  U AUACUUGA<u>GGAGAAAUUAUCCUUG</u> UGUG UUG  C  U UAUGAGCUUUUCUUAAUUGGGAAC AUAC AAGU  G  U -  U  AG  U </pre>	1.12	HP-41(0) MP-40(0)
RP-45	5	GAAGUUGUUCUGGUGGAUUC	1(h), 2(m)	chr6, 134421450-134421529, +	<pre> U      A-      UG  CU  C GGUACU GAAGAGA  GUUGUUCGUGG  GAUUCG  UUA  U CCAUGA CUUUUUU  CAACAGGCACU  CUAAGC  AGU  U -      CA      UA      -  G </pre>	0.81	hsa-mir-382(0) mmu-mir-382(0)

RP-46	5	AGAGGCUGGCCGUGAUGAAUUC	1(m)	chr6, 134422571-134422649, +	U CU - A AUUCA GAUACU GGAGAGAGG GGGCGUG AUGA UUCG \\ CUGUGA CUUCUCUCC UCGGCAC UACU GAGC U U UC A - AAAUC	1.61	hsa-mir-485(0) mmu-mir-485(0) HP-45(0) MP-42(0)
RP-48	5	AGAGGUUGCCCUUGGUGAAUU	1(h)	chr6, 134427956-134428039, +	U U UG G C - A - UUUU UGAU CU A CAGAGGUUGCC UUG GUGA UUCG C \\ ACUA GA U GUUUCAACGG AAC CACU AAGU G U A U GU G A A - U UAGU	1.46	HP-45(4),MP-42(4) RP-46(4)
	3	AAUCACACAAGGCAACUUUU	3(h),1(m)		hsa-mir-377(1) mmu-mir-377(1)		
RP-49	5	AAGGGAUUCUGAUGUUGGUCACA	6(m)	chr6, 134429927-134430016, +	A U AAG A G ACUCCAAGAA GCCA AA CAGAG GGAUUCUG UGUU GUCAC \\ CGGU UU GUCUC CCUAAGAC ACAA CGGUG U A C AUA - G AGUAAAAUUU	1.39	MP-44(0)
RP-50	5	AGGUUACCCGAGCAACUUUG	3(h)	chr6, 134430691-134430767, +	U A AC - CA UG GGUAC CCGAGAG GGUU CCGAGCAAC UUG UC \\ CUAUG GCUUUUU CCAA GGCUCGUG AAGC AG G - C GU U -- GA	0.77	hsa-mir-409(0) mmu-mir-409(0) HP-47(0)
	3	AAUGUUGCUCGGUGAACCCC	1(h),1(m)				
RP-51	5	AGAUCGACCGUGUUAUUUCG	2(h),1(m)	chr6, 134430965-134431043, +	U AG UA CUU C GGUACU GA GGAGAUCGACCGUGU UAUUCG AG U CUAUGA CU UUUUAGUUGGUACA AUAAGC UC G - CU UA U-- A	0.67	hsa-mir-369(0) MP-45(0)
	3	AAUAAUACAUGGUUGAUCUU	2(h),1(m)				
RP-62	3	UUUGGUCCCUUCAACCAGC	1(m),1(r)	chr9, 19403192-19403268, +	C CA C A U G C CCUUCU UGGCUGGU AA GG ACCAAG CC UCUC \\ GGGACGA AUCGACCA UU CC UGGUUU GG AGAG C C AC C C - U	1	hsa/mmu/rno- mir-133a(0) hsa/mmu-mir-133b(0)
RP-66	5	AAACCGUUACCAUUCUGAG	6(h),5(m)	chr10, 64143143-64143210, +	U AU GA A GGGA GCGGAG AACCGUUACCAUUCUG G CCCU UCGUUC UUGGUAAUGGUAAUGAU U A CG UC U	0.56	hsa/mmu/rno- mir-451(0) HP-61(0) MP-28(0)
RP-79	5	GCACAUACUUUUUAUGUACCC	1(m)	chr18, 2191671-2191757, -	C AC UGAACA UGCCUACUCAGAG ACAUACUUUUUAUGU CCAUA U AUGGAUGGGUUUU UGUGAAGAAAUGUA GGUAU A A A- CGUAG	1.89	mmu-mir-1-2*(0)
RP-97	5	AUAUAAUACAACCUGCUAAGU	3(h),5(m), 2(r)	chrX, 91637005-91637072, -	UG AU C U CUCGGA G AUAUACAAC UGCUAAGUGU C GAGCCU U UAUUAGUUG ACGAUUCACG U GU AU C A	1.05	hsa-mir-374(2)
RP-99	5	CGGGUGGAUCACGAUGCAAUUU	1(h)	chrX, 139814084-139814170, -	U AU CA A GA-- GA UUUUGC GUU CGGGUGGAU CG UGCAAUUU UUA G AGGACG CAA GUCUACCUA GC ACGUUAAAG GGU U C AU UG - AGAG AA	0.88	hsa-mir-363(0) mmu-mir-363(0) HP-85(0) MN-8(0)
	3	AAUUGCAGCGUAUCCAUCUGU	5(h),1(m), 1(r)				
RP-100	5	CAAAGUCUCAUAGUCAGGU	4(h),5(m)	chrX, 139814504-139814575, -	GU - G G - UUU AGUGCCA AAGUGCUDAUA UGCAG UAG GU G UCAUGGU UUCACGAGUGU ACGUC AUC CA C C- C G - U CGU	1.01	hsa-mir-20b(0) HN-14(0) MP-56(0)
	3	ACUGCAGUGUGAGCACUUCUG	3(r)				
RP-101	5	CUCGGGAUCAUGUACACG	2(h),1(m), 2(r)	chrX, 140069623-140069701, -	GUC GG UCA AUACCA UCUCAGAC UCGG AUCA UGUCACGAG \\ AGGGUCUG AGUC UAGU ACAGUGUUC C GAA AA UAG ACGCGU	0.53	MP-59(0)
	3	UGUGACAGAUUGAUAACUGAA	1(h),1(m)				
RP-103	5	UAGCAGCGGGAACAGUACUG	6(m),4(r)	chrX, 140073303-140073373, -	UA G UGA GUU UGCC GCAGCGGGAACAGUACU CAG GU \\ AUGGG CGUCGCCUUUGUUAUGA GUC CG U UC G C-- UGG	0.78	hsa-mir-503(1) HP-87(1) MP-60(0)