

name	sequence	precursor	<i>H. sapiens</i>	<i>C. elegans</i>	<i>M. musculus</i>	<i>D. melanogaster</i>	<i>F. rubripes</i>	<i>D. rerio</i>
let-7a-1	UGAGGUAGUAGUUUAUAGUU	UG U UAGG ACA C CAC UGGGA GAGGUAGUAGUUUAUAGUU GUC CCGA C GUG AUCCU UUCUGUCAUCAACAUAUCA UAG GGGU A CA - - - - - A - - - - - C	AC007924 Chr9		3 copies, similar precursors mmtrace: 20316581 49561783 48365244			ti 108513271
let-7a-2	UGAGGUAGUAGUUUAUAGUU	UU G U UAGAAUAC AA AGG GAG UAG AGUUGUUAUAGUU AUC G UCC UUC AUC UCCGCAUUGCAA UAG G U - G C - - - - - AG	AF001359 Chr11					
let-7a-3	UGAGGUAGUAGUUUAUAGUU	U UAGGUAUC GGG GAGGUAGUAGUUUAUAGUU UGGGC \\ UCC UUCUGUCAUCAACAUAUCA UAGGGUAC U	AL049853 Chr22	AF274345 chrX with diff. precursor		AE003659 diff. precursor		
let-7b	UGAGGUAGUAGUUUGUUGUU	U - A - - - - UG CGGG GAGGUAGUAGUUUGUUGUU UC GGCAG \\ GUCC UUCGUCAUCCAACAUAUCA AG CCGUU A - - - - - U AAGCUC	AL049853 Chr22		EST AI481799.1		with slightly diff precursor	ti 106211630
let-7c	UGAGGUAGUAGUUUGUUGUU	A UG G U UA G UA AC GC UCCGG GAG UAG AGUUGUUAUAGUU GA U C \\ CG AGGUUC UUC AUC UCCAACAUGUCA UA A G C - - - - - CU G U - - - - - G G UC	AP001667 Chr21		EST AI614897			ti 107286511
let-7d	AGAGGUAGUAGUUUGUAGUU	A C UUA - - - - GG CCUAGGA GAGGUAGUAGUUUGUAGUU GGCAG \\ GGAUUUC UUCGUCGUCAGC UAUCA CCGUU A - - - - - A UGAGGAACA UU	AC007924.3 Chr9		mmtrace 83587042			
new variant	AGAGGUAGUAGUUUGCAUAGU only predicted, not cloned	G A A U C UUA - - - - G CUA GA GAGGU GAG UAG UAGUU GGCACA \\ GAU UU UUCG CUC AGC UAUCA CCGUU A G - - - - - A C A UUGAUGACA U			EST BB051239			
let-7e	UGAGGUAGUAGUUUAUAGUU	C CU G U GGA - - - - A CC GGG GAG UAGGAGUUUAUAGUU GA GG C GG CCC UUC AUCCCGCAUAUCA CU CC A A CU G - - - - - AGAGAA C	AC018755 Chr19					
let-7f-1	UGAGGUAGUAGUUUAUAGUU	AGU - - - - - UG UCAG GAGGUAGUAGUUUAUAGUU GGGUAG \\ AGUC UUCGUCUAUCAACAUAUCA VCCAAU A CC - - - - - GAGGACUG UU	AC007924 Chr9		mmtrace 64945869			ti 108513271
let-7f-2	UGAGGUAGUAGUUUAUAGUU	U - - - - - UCAU CUGUGGA GAGGUAGUAGUUUAUAGUU UAGGG A GGCACCU UUCUGUCAUCAACAUAUCA GGUUCU C - - - - - UAGA ACCC	AL592046 ChrX		mmtrace 18713911			
let-7g	UGAGGUAGUAGUUUGUAGUA	A U A A UGAGG A - A A CC GCG GAGGUAGU GUUUGUAGUA GUCU UG UACC C GG CCG UUCGUCA CGACAUGUCA UAGA AG AUG C A - - - - - C - - - - - GG - C	precursor identical to mouse in AC092045.2 Chr3		mmtrace 62173215			
let-7h	UGAGGUAGUAGUUUGUAGUA							
let-7i	UGAGGUAGUAGUUUGUCU	U U - - - - - U UGUG CUCCG GAGGUAGUAGUUUGUCU GUV GG CCGU \\ GAUC UUCGUCAUCCAACAUAUCA UAGA AG AUG C - - - - - U UAGAGGU - UUAC	AC048341.22 Chr12 (also AL117383.19) precursor identical to mouse		EST BB661268			
lin-4	UCCUGAGACCUCAAGUGUA	G U - - - - - C U CUA CCG CUG CCC GAGA CUCA GUGUGAG UUA \\ GGC GGC GGG CUCU GGU CACACUU CGU U A CAU C C C - - - - - AGU C.elegans			U01830.1			
miR-1	UGGAAGUAAAGAAUGUAGG	A UUUAGA C A - AUA UUC GCC GUCCAUGCUC UGCAUUC AUA GUU \\ GAG CGG CGAGUUAUGAG AAUGUAAG UAU CGA U - - - - - UCUAAG A G A ACU D.m.			2L.AE003667			
miR-1b	UGGAAGUAAAGAAUGUAGUA	C AC UGA AU UACUCAGAG ACAUACUUCUUUAUGU CCAU \\ AUGGGUUUU UGUUAAGAAAGUA GUAU UG U A - - - - - A - - - - - CG - AC	AL449263.5 Chr20 nt1-21	U97405.1 nt 1-21 (22G)	mmtrace 19673694 (A22U)		ti 30081664	
miR-1c	UGGAAGUAAAGAAUGUAGUAC							
miR-1d	UGGAAGUAAAGAAUGUAGUAAU	C GC UGAACC GCUUGGGA ACAUACUUCUUUAUGU CCAU U CGACAUUU UGUUAAGAAAGUA GUAU G A - - - - - CGAAUC	AL449263.5 Chr20 nt1-22 (23G); AC116916.2 Chr18 (23U) similar precursor		mmtrace 91523974		BF157601.1 with C23 (diff. precursor)	
miR-2a-1	UAUCACGCCAGCUUUGAUGAGC	CGUUGGUC UCAAAG UGUUUGUA AUGC CGC \\ CGAUUCGAG AGUUUC ACCGACACU UACG GCG U U g A - - - - - CG			2L.AE003663			
miR-2a-2	UAUCACGCCAGCUUUGAUGAGC	A C - - - - - GAUAC AUC AGC UCAUCAAG UGUUUGUUAUGU \\ UAG UCG AGUAGUUU ACCGACACUAC C A - - - - - CG GCAAC		miR-2 ortholog in <i>C. elegans</i> (Lau et al. SCIENCE 2001, 294:858)	2L.AE003620			
miR-2b-1	UAUCACGCCAGCUUUGAUGAGC	U UG - - - - - A C - - - - - U CU CAAC UCUUCAAG UGC GUA AUGUG C GG GUUG AGGAGUUUC HCCG CACU UAUAC A C CG G A AUAUA A			2L.AE003663			
miR-2b-2	UAUCACGCCAGCUUUGAUGAGC	A - - - - - A UUU - - - - CUU UUGUGUC UUCUCAAG UGUUUGUA AUG GC U AGGCGAG GAGGAGUUUC ACCGACACU UAC CG U C G A UUAUC UAU			2R.AE003795			
miR-3	UCACUGGGCAAAGUGUGUCA	C C G U UUCA GAUC UGGAGCAU UUGU CAGU AUGU CGC \\ CUAG ACUCUGUGUG AACG GUCA UACA A A - - - - - A G C CUCU			2R.AE003795			
miR-4	AUAAGACUAGACAACCAUUGA	U UU C C C GG UU UUGCAU AGUUUC UGUU GUC AGC UUA UGAUU \\ GGUGUG UUGAAG ACCA CAG UCG AAU ACUGG U C UU A A A - - - - - CC			2R.AE003795			
miR-5	AAAGGAACGACUUGUAGUAG	UA - - - - - AGUGUU GC AAAGGA GAUCGUUGUAGUAG CG UUUUUU UAGUGACACUAUAC U CAAUA - - - - - AAUCCU			2R.AE003795			
miR-6-1	UAUCACAGUGGCUUUCUUUUU	A - - - - - C AG UAAUA UUUA UGUAGAGGAUAGUUGUCUGU UGA U \\ AAAU AUGUUUUUCUGUGGACAC AAUA A U CC CU UACCA			2R.AE003795			
miR-6-2	UAUCACAGUGGCUUUCUUUUU	C UU UG C U - G UAACC AAGGGAAC C CUG UGUAUA UA UU A GUUGG UUUUCUUG G GAC ACUAUUA AU AA A U UC GU - - - - - C C A			2R.AE003795			
miR-6-3	UAUCACAGUGGCUUUCUUUUU	A A UAAC CAA AAGAGGAACGGUUGUCU UGAUUG UG \\ GUUU UUUUUUCUGUGGAC ACUAUUAU AAC U G - - - - - U ACUC			2R.AE003795			
miR-7	UGGAAGACUAGUAGUUUUUGUU	U U U - - - - UGUG GAGUGCAU CCGUA GGAAGC AG GAUUU UGUUUU \\ UUUACGUG GGC AU UUCUC UC CUA A ACAUAU U C - - - - - U C UA UGUGU	EST BF373391		not cloned, but mouse EST predicts precursor similar to human	2R.AE003791		
miR-8	UAUAUCUGCAGGUAAGAUUGC	CUGUUC - G C UCCUU AAGGCAU ACAUCU ACC GGCAG AUUAGA \\ UUCUGUG UGUAGA A UG GUG UAAU A U CCUGC - - - - - A A CAUAU			2R.AE003805			
miR-9	UCUUUGUUUAUCAGCUGUAUGA	- U UAU G - GAU GUA UGUUG GUUGUU CUAGGU UAGA GU A CGAU AUAU GAASCCA GAUGA AUUC CA A U UUC A G AUA	AC005316 Chr15 AC026701 Chr5 each with diff. precursor; AL139130.28 chr1	AF155142.1 chr19 diff. precursor	3L.AE003516	2diff precurs scaffold_38 68 and 2417 U92575.1	ti 102744571	
miR-10a	ACCCUGUAGUCCGAAUUUUU	CU - G U AUUC CCACGU ACC CU UAGA CCGAAUUUUUUU A GGUGUG UGG GA AUUC GCUUAACAGGA G UU A G U AUUC	AF287967 Chr17 HOXB cluster		AC011194 chr.11 diff. precursor	AE001574	ti 123068104	
miR-10b	CCCUUGAAGCCGAUUUUUGUU	A G C UG- AC UAUAU CCU UAGAA CGAAUUUUUGU G C AUUA GGG AUUCU GCUUAGACAC UA C A - - - - - A UGA CA	Chr2 gi 22044651 HOXD cluster		Chr2 U77364.1, intronic location Hoxd4 gene		scaffold_82	

miR-11	CAUCACAGUCUGAGUUCUUCG	U UCU CCC U ACU GCACUUC CAAGAACUU CUGUGA GCG GU U CGUGAGU GUUCUUGAG GACACU GCG CG A U A-- - AAA				3R, AE003735		
miR-12	UGAGUUUAUCAUCAGGUAUCUGU	UG U G - - GCCU UACGGU AGUUA ACAN AGGUACUUGU GU A GUGCCG UCAUA UGUA UUCAUGACCA CA A CA C - - A ACCUA				X, AE003499		
miR-13a	UAUCACAGCCAUUUUGAUGAGU	U C - - A UC-- CU UACG AACUC UCAAG GGUUGUGA AUG GA A GUGC UUGAG AGUUUU CCGACACU UAC CU U U U A UCAU AU				3R, AE003708		
miR-13b-1	UAUCACAGCCAUUUUGAUCAGU	UG- U ACU UUAU CCA UCGUUAAAUG UUGUGA UAGU C GGU AGCAGUUUUAAC GACACU AUAC A UUG C - - - UAAC				3R, AE003708		
miR-13b-2	UAUCACAGCCAUUUUGAUCAGU	G A GCUA UU AAC GUCAAAUG CUGUGA UGUGGA U UUG GCAGUUUUAAC GACACU AUACU G A C - - - - CA				X, AE003446		
miR-14	UCAGUCUUUUUCUCUCUCCUA	C C C GCUU UGUGGAG GAGA GGGGACU ACUGU \\ AUUCCUC CUCU UUUUCUGA UGAUA A U U C AAUU				2R, AE003833		
miR-15a	UAGCAGCACUAUUGGUUUUGU	GAGUAAAGUA UA GA U CCUUG GCAGCACA AUGGUUUGU UUU \\ GGAAC CCUGUGU UACCGGACU AAA G AUA AAAAACUC UA GG A	Chr13, AC069475	mmtrace 72137197	interesting leukemia locus			
miR-15b	UAGCAGCACUAUUGGUUUUA	U C C A A ACA CUG AGCAGCA AU AUGGUUU CAU CU \\ GAU UGUCGU UR UACUAG GUA GA G C U U C - ACU		mmtrace 79105069			ti 42632568	
miR-16-1	UAGCAGCACUAUUGGUUUUGGCG	AG C - - A CGUA UCUA GUCAGC UGC UUAGCAGCAC GU AAUUAUGG AGAU \\ CAGUUG AUG AGUCUGUGU CA UUAUGACC UCUA A GA A U A - - - - - UAAA	Chr13, AC069475	2 genomic hits with	interesting leukemia locus		AL606727	diff precurs
miR-16-2	UAGCAGCACUAUUGGUUUUGGCG	UC CU - - UA C AG AAU GU CACU AGCAGCAGC AAUUAUGG GU UGA A CA GUGA UGUCUGU UUAUAAC CA AUU U GU UU C - - A - AUA		mmtrace 79105069;	nearly ident prec. as in human			
miR-17	ACUCGAGUGAAGGCAUCUUGU	GA CA- A G G - - AUA GUCA AUAUUGU AAGUCUUA CA UGCAG UAG UG \\ CAU UAUUACG UUCACGGA GU ACUGC AU C U GG AUG A G - - U GUG	Chr13, AL138714	Chr14 gi 20882784	with Al1G			
miR-18	UAAGGUCACUAGUUGCAGUA	CU U C U A UGAA AG UGUU AAG GCAN UAG GCAG UAG GU A ACGG UCC CGUG AUC CCUC AUC CG U UC U A C - - UA-- AU	Chr13, AL138714	Chr14 gi 20882784				
miR-19a	UGUGCAAUUCUAUUGAAAUCUGA	U U - - - - - AGA GCAG CC CUGUAGUUUUGCAUG UUGCAC UACA \\ CGUC GG GGUAGUCAAACGUUAC AACGUG AUGU A C U - - - - - UA UG AAG	Chr13, AL138714	Chr14 gi 20882784				
miR-19b-1	UGUGCAAUUCUAUUGAAAUCUGA	UU - - - - - UC UGUGUG CACUC CUUAGUUUUGUUGCA GG UUUCA CAGC \\ GUGAU GGUUCAGUCAAACGU CC AAACGU GUC A - - - - - A U - - - - - UCUAU	Chr13, AL138714	Chr14 gi 20882784	with C11U		G46757 with a U9C	
miR-19b-2	UGUGCAAUUCUAUUGAAAUCUGA	CUAC - - - - - UUCA U ACAUG UUAACAUAUUUGCA GG UUGCAU GCUAUA U UGUAU AGUUUAGUCAAACGU CC AAACGU UGUUAU U - - - - - A U UCGG G	X, AC002407					
miR-20	UAAAAGUCUUAUUGAGCAGGUAG	C A- - - - - G - - UU GUAG ACU AAGUCUUAUUGAGCAG UAG UG U CCUC UGA UUCACAGUAUUCGUC AUC AU A A AA - - - - - U UG	Chr13, AL138714	gi 20882784	[NW_001014 nt 16913861-883] Chr14			
miR-21	UAGCUUAUCAGACUAGUUGA	UUGCGGUAGCUUAC GACU UGUU CUGU G \\ ACAGUCUCUGCGGUG CUGAC ACAAC GUUA C U - - - - - C - - - - - UC	Chr17, AC004686	AL604063	chr11,nearly ident precursor			
miR-22	AAGCUGCCAGUUGAAGAACUGU	U CC - - - - - A U CCUG GGC GAG GCAGUAGUUCUACG UGCC CCUUAU GU \\ CCG CUC CUVUUCAGAAAGUU ACCGU CGAAAU CG A U C- - - - - G - - - - - ACCC	several highly similar ESTs; AR961681 shown	AK008813 (cDNA),prec ident to human				
miR-23a	AUCACAUUGCCAGGAAUUCU	C G - - - - - G CUUC GG CGG UGGGG UCCUGG GAUG GAUUUG C CC GCC ACCUU AGGGACC UUAC CUAAAC U A A U U G A ACUG	Chr19, AC020916	mmtrace 62540691	diff. Precursor		three hits in db	ti 70109732
miR-23b	AUCACAUUGCCAGGAAUUCAC	C U - - - - - C GUGACU GG UGC UGG GUUCCUGGCA UG UGAUU U CC ACG ACC UAGGGACCGU AC ACUAAA G A G AU U - - - - - AUUAGA	AL354893	EST AW124037 and AI848465	cerebellum			ti 45808187
miR-24-1	UGGUCAGUUCAGCAGGAACAG	G G A UA UCUAAU CUCC GU CCU CUGAGCUA UCAU \\ GAGG CA GGA GACUUGACU GGUCA U A A C C- - - - - CACA	Chr9, AF043896	EST AI286629	(thymus): nearly ident. to miR-24-1; EST AA111466			ti 137648976
miR-24-2	UGGUCAGUUCAGCAGGAACAG	CC CG CU- AA-- UU CUCUG UCC UGC ACUGAGCUG ACACAG \\ GGAC AGG ACG UGACUCGGU UGUGUU G A - - - - - ACU CACA UC	Chr19, AC020916					
miR-25	CAUUGCACUUGUCUGGUCUGA	A AG G UU G UG ACG GGCC GUGUUU AGGC AGAC G GCAU CUGG C CCGG CGUGAC UGUC CUCUG C GUAU GGUC U C AG G UU A CG CCG	Chr7, AC073842	predicted in mouse	(EST AI595464), but not cloned		G46757 similar precursor	
miR-26a	UUCAGAAUUCAGGAAUAGGU	- G U U U GCAG AGGCC GUG CCUCUG CAAGUA CCAGGAUAGGCUU G UCCGG CGC GGGGCA GUUCAU GUUUCUACGGUA U G A C - - - - - ACCC	Chr3, AP000497	AC055818.9,mmtrace 88471973	diff. from human		Scaffold_40 97	ti 109895676
miR-26b	UUCAGAAUUCAGGAAUAGGU	GA - - - - - UC CCGG CCC AGU CAAGUAA AGGAUAGGUUG \\ GGCC GGG UCG GUUCAUUA UCUUUGCCGAC C AG C - - - - - CC CUGU	Chr2, AC021016	mmtrace 69866494				
miR-27a	UUCACAGUGGCUAAGUUCGCU	A A A U G UCCAC CUG GG GC GGGCUUAGCUCU GUGAGCA GG \\ GAC CC GG CUUGAAUCGGUGA CACUUUU CU A C C C - - - - - G GAAC	Chr19, AC020916					ti 45777014
miR-27b	UUCACAGUGGCUAAGUUCUG	AGGUACAGAGCUUAGCUG GUGAACAG UGG \\ UCCACGUCUUGAAUCGUG CACUUGUU GCC U GA-- - - - - - UC-- U	XI 098943.1 chr9	Chr13 MGSC mmtrace 44671617	identical precursor			
miR-28	AAGGAGCUCACAGUCUUAUG	C A U - - - - - CC GGU CUUGCCUUC AGGAGCUCACAGUCUA UG AGUUA U UCA GGACGGGAG UCCUGAGGUGUAGAU AC UCAU U C G C CCU CU	Chr3, AC063932					
miR-29a	CUAGCAUUCUGAAUUCGGUU	UUU C UCAAU AUGACUAGUUC UGUUUU AGAG \\ UAUUGCUAAG ACCACGA UCUU A UCU - - - - - UUAUU	AF017104.1 Chr7,	AC024913.32 mouse	miR-29a/29b cluster!			
miR-29b	UAGCACC AUUUGAAUUCAGUUGU	A U U GU UUAUU AGGA GCUGUUUUA AUGUG UUGAU \\ UCUU UGACUAAAGU UACAC GAUCUG A G U - - - - - UUAUG	AL035209.1 Chr1	AL513470.8 Chr1	mouse miR-29b/29c cluster. BG342396 diff. precursor	Scaffold 17670 has 29b/29c cluster and 2nd 29c copy	ti 46254927	ti 46254927
miR-29c	UAGCACC AUUUGAAUUCGGUUA		12. miRNA similar to miR-83					
miR-30a-s	UGUAAACAUCCUCAGUGGAAGC	A UC - - - - - A GCG CUGUAAACAUCC GACUGGAAGCU GUG A CGU GACGUUUUAGG CUGACUUUCG GUAA C	nearly ident fold in	ESTs,mmtrace 68023889	chr6			ti 16009376
miR-30a-as	CUUUCAGUCGGAUUGUUCGAC	A UC - - - - - A GCG CUGUAAACAUCC GACUGGAAGCU GUG A CGU GACGUUUUAGG CUGACUUUCG GUAA C	6, AL035467	mmtrace 85261735				ti 16009376
miR-30b	UGUAAACAUCCUCAGUCAGC	U - - - - - UCAU AUGUAAACAUCC ACA CUCAGCUG C UGCAUUUGUAGG UGU GGGUCGU A - - - - - A UGCU	human AF159227.6	Chr8,different precursor		Scaffold_34 83,diff precursor		ti 15929506

miR-30c	UGUAAACAUCUACUCUCACAGC	UACU U ACA GUGGAA AGA GUAAACA CCU CUCUCAGCU A UCU CAUUUGU GGA GAGGGUCGA G UUCU C A-- AAGAAU	AL136164.8 Chr.6 supported by ESTs (BF594736.1)		Chr4 AL606904.11			ti 100083938
miR-30d	UGUAAACAUCUCCGACUGGAAG	U U CCC GUAAGA GU GU GUAAACAUC GACUGGAAGCU C CA CG CGUUUGUAG CUGACUUUCGA A U U A-- AUCGAC	AF159227.5 Chr8		AC108837.4		Scaffold 3483,diff fold	ti 15929506
miR-30e	UGUAAACAUCUUGACUGGA	UU GUAAGU CUGUAAACAUC GACUGGAAGCU G GACAUUUGUAGG CUGACUUUCGA U -- GGAGAGU	chr1 AL354914.9 ident.precursor		mmtrace 23457381			
miR-31	GGCAAGAUGCUGGCAUAGCUG	GA G C U GAA GGAGG GGCAA AUG UGGCAUAGC GUU C CCUUUC CCGUU UAC ACCGUUUCG CAA U UA A A UC GGG	9, AL353732		Chr4 NW 000209.1 [nt 27207638-618]			
miR-32	UAUUGCACAUUAUAAGUUGC	U -UU C GGAGAUUUGCACAU ACUAAGUUGCAU G GU A CUUUUAUAGUGUGUG UGAUUUACGUA C CG C - A UC G	9, AL354797		Chr4 NW 000208.1 [nt 7525224-204]			
miR-33	GUGCAUUGUAGUUGCAUUG	A UU UUCU UG CUGUGUGCAUUGU G GCAUUGCAUG GG \\ GACACUACGUGACA C UGUUACGUAC CC G C UU ---- AU	22, 299716		Chr15 NW_000106.1 [nt 43886572-590]			G44780 with diff.precurs or
miR-34	AGGCAGUGUGUAGCUGGUUG							
miR-35	UCACCGGUGGAAACUAGCAGU							
miR-36	UCACCGGUGGAAAUUCGCAUG							
miR-37	UCACCGGUGAACACUUGCA							
miR-38	UCACCGGAGAAAAUCUGGAGU							
miR-39	UCACCGGUGGAAAUACAGCUUG							
miR-40	UCACCGGUGUACUACGCUAA							
miR-41	UCACCGGUGGAAAUACCUA							
miR-42	CACCGGUAACAUCUACAG							
miR-43	UAUCACAUUUACUUGCUGUCG							
miR-44	UGACUAGGACACAUUCAGCU							
miR-46	UGUCAUGGAGUCGUCUCUUA							
miR-47	UGUCAUGGAGGCGUCUCUUA							
miR-48	UGAGGUAGGUCACUAGAUUGCA							
miR-49	AAGCACACGAGAAAGCUGCAGA							
miR-50	UGAUUUGUCUGGUUUUCUGGGUU							
miR-51	UACCGUAGCUCUUAUCCAUUUU							
miR-52	CACCGUACAUUGUUUCCGUGCU							
miR-53	CACCGUACAUUUUUUCCGUGCU							
miR-54	UACCGUAUUCUUAUAUCCGAG							
miR-55	UACCGUAUAAGUUUCUGUGAG							
miR-56-s	UACCGUAUUGUUUCCGUGAG							
miR-56-as	UGGCGAUCCAUUUUUGGUGUA							
miR-57	UACCGUAGAUAGCUGUGUGU							
miR-58	UGAGAUUGUUCAGUACGGCAU							
miR-59	UCGAAUCGUUUUACGAGGAUG							
miR-60	UAUUUGCACAUUUUCUAGUUCA							
miR-61	UGACUAGAACGUAUCUACUC							
miR-62	UGAUUUGUAUUCUAGCUUACAG							

The
C.elegans
microRNAs
miR-34 to
miR-86 are
from
Lau, Lim,
Weinstein,
Bartel 2001
SCIENCE
294:858-862

miR-39
predicted
only, con-
firmed by
Northern

miR-63	UAUGACACUGAAGCGUUGGAAA						
miR-64	UAUGACACUGAAGCGUUACCGAA						
miR-65	UAUGACACUGAAGCGUAACCGAA				miR-65 predicted only		
miR-66	CAUGACACUGAUUAGGGAUUGUGA						
miR-67	UCACAACCUCCUAGAAAGAGUAGA						
miR-68	UCGAAGACUCAAAAAGUGUAGA						
miR-69	UCGAAAUAUAAAAGUGUAGA				miR-69 predicted only, con- firmed by Northern		
miR-70	UAAUACGUCGUUGGUGUUCCAU						
miR-71	UGAAAGACAUGGGUAGUGA						
miR-72	AGGCAAGAUGUUGGCAUAGC						
miR-73	UGGCAAGAUGAGGCAGUUCAGU						
miR-74	UGGCAAGAAUGGCAGUCUACA						
miR-75	UUAAGCUACCAACCGCUUCA						
miR-76	UUCGUUGUGAUGAAGCCUUGA						
miR-77	UUCAUCAGCCAUAGGUCUCA						
miR-78	UGGAGGCCUGGUUGUUUGUC						
miR-79	AUAAAGCUAGGUUACCAAGCU	mouse miR-131 potential ortholog					
miR-80	UGAGAUCAUUAUGUAAAGCCGA						
miR-81	UGAGAUCUUCGUGAAAGCUAGU						
miR-82	UGAGAUCUUCGUGAAAGCCAGU						
miR-83	UAGCACCAUUAUUUCAGUAA				miRNA is similar to miR-29		
miR-84	UGAGGUAGUUGUAAUUGUA						
miR-85	UACAAAUAUUUGAAAAGUCGUGC						
miR-86	UAAGUGAAUGCUUUGCCACAGUC						
miR-87	GUGAGCAAAGUUCAGGUGU						
miR-88	UCUUGACGUCGGACUGGAG				miR-87 to miR-90 from Lee, Ambros SCIENCE 2001 294:862-864		
miR-89	AACACUCAUUUCCAUCAAUAAA						
miR-90	UGAUUUGUUGUUGAAUGCCCC						
miR-91	CAAAGUCUUCACUGCAGGUGU very similar to miR-106	Sequences miR-91 to miR-121 are from Mourelatos, Dostie, Paushkin, Sharma, Charroux, Abel, Rappsilber, Mann and Dreyfuss miRNPs: a novel class of ribonucleoproteins containing numerous microRNAs, 2002, Genes & Development, 16:720-728. miR-91, miR-95, miR-99a, miR-99b, miR-101, miR-105 and miR-106 were also cloned in our lab and we adopted the numbers of Mourelatos et al. for these microRNAs.	Chr13 AL138714				ti 45862242
miR-92	UAUUGCACUUGCCCGCCUGU related to miR-25						ti 42820713
miR-93	AAAGUGCUGUUCGUCAGGUG						
miR-94	AAAGUGCUGACAUUCAGAU related to miR-20						
miR-95	UUCACGGGUUUUUUGAGCA		AC097381.3 chr4				
miR-96	UUUGGCAUAGCAUUUUUUGC						ti 45862242
miR-97	UGUAAACUCCUCGACUGGAAGC =miR-30a-s						

miR-98	UGAGGUAGUAGUUGUUGUUGU a let-7 variant							
miR-99a	ACCCGUAGUCCGAUCUUGU variant of miR-100	A UC U G AAG CAUA ACCCGUAGA CGA CUUGUG UG U GUGU UGGGUUUCU GCU GAACGC GC G C UU C - CAG	AP000962.2 Chr21,ident to mouse;[similar to miR-10 and miR- 511	mmtrace 48910714			ti 42883792	
miR-99b	CACCCGUAGAACCGACCUUGCG	CC AC G --- C GGCAC ACCCGUAGA CGA CU UGCGG GG \ CUGUG UGGGUUUCU GCU GA ACGCC CU C CC G C ACAC G U	AC018755.3 chr19; [similar to miR- 10 and miR-51]	mmtrace 92340982				
miR-100	AACCCGUAGUCCGAUCUUGU variant of miR-99a		AF001359.4 chr11				ti 133428833	
miR-101	UACAGUACUGUAUACUGA	A GUCCA UCAGUUUACAGUGUCUGU UGU C U AGUCAAUUGUGUCAUGAC AUGG U - AAUUC	AL158147.17 chr9 diff precursor	AK021368.1 cDNA eyeball. gi 20842708 []		U53213.1 T.fluviatilis	ti 25839635	
miR-102	UAGCACCAUUGAAUACAGU =miR-29b							
miR-103	AGCAGCAUUGUACAGGGCUAUGA variant of miR-107		AC020894.5 chr5					
miR-104	UCAACAUCAGUCUGUAUAGCUA this is just the reverse complement of miR-21		AF480502.1					
miR-105	UCAAAUGUCAGACUCCUGU		ChrX AF274857.2 two copies					
miR-106	AAAAGUCUUACAGUGCAGGUAGC variant of miR-91		ChrX AC002407.1					
miR-107	AGCAGCAUUGUACAGGGCUAUGA variant of miR-103							
miR-108	AUAAGGAUUUUUUGGGGCAUU				Chr11 NW_000039.1 [38206860-940], Chr16 NW_000107.1 [9938964-944]			
miR-109	CUGGUCGAGUCGGCCUGCGC							
miR-110	UCGAGCGCCGACGUCG							
miR-111	UGUGCAAUCUUAUGCAAACUGU =miR-19a							
miR-112	GGUCCUGACAUCACGGAA							
miR-113	UCGAGCCUGGUGCGCCACCA							
miR-114	UAGCUGCACGAAAUUUGGCG 1 nt. Diff. from miR-16							
miR-115	UGAAGCGGAGCUGGAA							
miR-116	UUGAUCCUGGUCAGGACGAACGUG							
miR-117	UUCAGCAGGAACAQU related to miR-24							
miR-118	AUGCCUUGAGUGUAGGAU				chrX gi 20983083:411451- 427706, good precursor, terminal C			
miR-119	AUUCCAGGGAUUACCAU =miR-23b							
miR-120	GGCGGAGCAGCUGUGU							
miR-121	UGAACCACCGUAUCCUUCGGAA							
miR-122a	UGGAGUGUACAAGUGGUUUUGU	GG C - UCC AGCUGU AGUGUGA ABUGGUGUUUG UG \ UCGAUA UCACACU UVACCGCAAAC AC A AA A U CAA	AL355858.14 (nt 1 20)		chr18 NW_000134.1 [nt 62584664-686]		ti 89843692	
miR-122b	UGGAGUGUACAAGUGGUUUUGA				chr18 gi 20881247			
miR-123/miR-126-s	CAUUAUACUUUUGGUACGCG	A A U CGCUG C UGAC GC CAUUAUACUU UGGUACG UGA A ACUG CG GUAAUAUAGAG GCCAUGC ACU C G C U UCAA- U	Chr9 AL590226.23	mmtrace 6108147		Scaffold_32 95	ti 45858477	
miR-126/miR-123-as	UCGUACCGUGAUAAUUAUGC	A A U CGCUG C UGAC GC CAUUAUACUU UGGUACG UGA A ACUG CG GUAAUAUAGAG GCCAUGC ACU C G C U UCAA- U	AL590226.23 chr9	mmtrace 3521597		with diff precursor Scaffold_32 95		
miR-124a	UUAAGGCACGGUGAUAUGCCA	- C A GA UAAUG CUCU G GUGUACAC GCG CCUGAUU U GAGA C CGUAAGUG CGC GGAUUAU C A - G AC CAUAU	nearly ident. precursor in chr8[AC021518] chr20[AL096828]	Found in 272504.1 chrIV intron,diff precursor	mmtrace 21097008,11737241	slightly diff precursor AC009251 chr2L	Scaffold_14 98 ti 110845148	
miR-124b	UUAAGGCACGGUGAUAUGC	CC A GA UAAUG CUCU GUGUACAC GCG CCUGAUU \ GAGA CGUAAGUG CGC GGAUUAU U AC G AC CAUAC	AC021518 chr8,nearly ident chr20 AL096828.29					
miR-125a	UCCUGAGACCCUUUAACUGUG potential lin-4 ortholog	C C UA GG- U CUGGUU CCUGAGA CCUU ACCUGUGA GG C GGUCCG GGUUCU GGAG UGGACACU CC G A U -- GGGA U	ident precu in AC018755.3 chr19	mmtrace 33921945, 48262259				
miR-125b	UCCUGAGACCCUUUAACUGUG potential lin-4 ortholog	UC C A GG- U GCCUAG CCUGAGA CCU ACUUGUGA UAU U CGGAUC GGUUCU GGA UGAACACU AUG U CA U C ACA A	AP001359.4 chr11 AP001667.1 chr21(chr21 like mouse)	mmtrace 83985705	Found in AC006590.11 with diff fold	Scaffold_23 58	ti 89843692	
miR-127	UCGGAUCCUGUGAGUUGGUCU	A U G G C -- AG CC GCC GCU AAGCUCAGA GG UCUGAU UC \ GG UGG CGG UUCGAGUCU CG AGGCUA AG A C U - G U CU AA	human AL117190.6 Chr14 same precurs as in mouse	mmtrace 79514537				

miR-128	UCACAGUGAACCGGUCUCUUU	UUC UAG CU U GUUGA GGGCCG CACUGU GAGAGU U CGACU CUCUGG GUGACA CUCUUUA U UUU CAA -- C	ident. in AC016742.10 chr 2;diff prec in AC016943.7 chr3		mmtrace 51670230		Scaffold_82 8,diff prec	ti 35780267
miR-129	CUUUUUUCGGUCUGGCGUUC	- C CU G UUCU C A GGAU CUUUUUG GGU GGGCUU CUG CU A UCUA GAAAAC CCU CCGAA GAC GA A U C UU G UGAU- C	human AC018662.3 chr7					
miR-129b	CUUUUUUCGGUCUGGCGUUC	- C CU G UUUU C UGGAU CUUUUUG GGU GGGCUU CUG C G AUCUA GAAAAC CCA CCGAA GAC GA A U C UU G UGAU C	similar precurs.in chr7 AC018662.3		mmtrace 13885686		ti 111444617	
miR-130	CAGUGCAUUGUAAAAGGC	- C A GUCUAC GA GCUCUUU ACAUUGUCU CU \\ CU GGGGAAA UGUUACUGUA GA \ G A U C CCAUGU	AP00662.4 chr11		mmtrace 68479278		with diff fold AC091299.2	
miR-131	UAAAGCUAGUAACCGAAAGU	g c g u a GUU UUAU UUUGUUUAUCUGU UAUGG GU U CAA AAUG AAGCCAAUAGAUCA AUACU UG U A A C A C G G	AC005317.2 chr 15 diff. precursor, AC026701.6 chr 5 ident. precurs.		AF155142		ti 70118863	
miR-132	UAACAGUCUACAGCCAUUGUCU	- A UUC G- G GGGC ACCGUGGU GAUUGUUACU UGG \\ CCG UGGUACCGA CUGACAUUGG GC A C CAU AG A	AL137038.5 chr17 diff. precursor from mouse		mmtrace 86984641 U23C		ti 136388144	
miR-133	UUGGUCUUUUAACACCGUCU	A AA U A GCCUC GCUA AGCUGU AA GG ACCAAUC U CGAU UCGACCA UU CC UGGUUUAG U G AC C C GUAAC	AL391221.15 chr6 diff. Precursor(ident to rat L33722.1)		mmtrace 62407955	AC093440.1 diff. Precursor	Scaffold_10 49;precu nearly like mouse	ti 108431634
miR-134	UGUGACUGGUUACACAGAGGA	GU U A- G GCU GC \\ AGGU GUGACUGG UG CCA AGGG GC \\ UCCCA CACUGAUC AC GGU UCCC UG U AC C C G ACU- UC	AL132709.5 chr14 similar precursor		mmtrace 64620311 (A22G)			
miR-135	UAUGGCUUUUUUCCUUAUGGAA	CUAUGGCUUU AUUCCUAUGUA \\ UGUGCCGAGG UAGGUAUAUCU \\ U- CCGUCG	AC092045.2 chr3 AC018659.35 chr12 (ident or siml to mouse)		trace#71495235 (A24U);EST BF780995.1(kidn.,sp leen)		Scaffold_21 25 with similar precurs	ti 124203848
miR-136	ACUCCAUUUUUUUGAUGGA	C UUU UUCU GAGGACU AUUUG UGAUGAUGGA \\ UCUGUAG UAAC UCUCUAUCU U - UCU CGAA	AL117190.6 chr14 ident to mouse		mmtrace 86071753			
miR-137	UAUUGCUAAGAAUACGCGUAG	g g a - g CUUCGU ACG GUUUCUUGGUGU UAUA CG \\ GAGCUG UGC CAUAAAGAUUCGUU AUUGU GC U A G - U AU	AC027691.1 chr1 ident to mouse,nearly ident fish		AI852436.1		Scaffold_18 244 nearly ident to mouse/man	ti 15797384
miR-138	AGCUGGUGUUGUGAAUC	-- UCA AC- C CG CAGCU GGUUUUGGAA GCGC GAG AG C GUUGG CCACAGCACU UCGGC UUC UC A GA UA- CCA - CU	AC006058.1 chr3 precursor diff		EST BB528620.2			
miR-139	UCUACAGUCACGUGUCU	g - U A GUGGC GU UAUUCUA CAG GC CGUUCUCCAGU \\ CA AUGAGGU GUC CG GCGCAGAGGUCG U - U C - GAGGC	AP003065.2 chr11					
miR-140a	AGUGGUUUUACCCUUAUGGUG	- A UUA A UU UC CCU CC GUGUUUUACCCU UGUUAGU ACG A GGAC GG CACCAAGAUGGGA ACCAUCU UG U A C - -- CG	AC026468.8 chr.16,precursor nearly ident.		mm10530393		ti 45759243	
miR-140as	UACCACAGGUGAAGACACGGGA	- G A UU UC UCCUG CCG UGUUUUACCCU UGUUAGG ACG A AGGAC GGC ACCAAGAUGGGA ACCAUCU UGU U A - -- CG	chr16 AC026468.8 nearly ident.precursor		mm10530393		scaffold_ 2083	ti 45759243
miR-141	AACACUCUCUGUAAAAGUG	U -- U AU GAAG GGG CCAUCU CCAG GCAGUUUUG GGUU \\ CCC GGUAGAA GGUU UGUCACAAUC UCGA AU - C- AGUA	AC006512.12 chr12,precursor slightly diff		Chr6 AC002397			
miR-142a	CAUAAAGUAGAAAGCACUAC	AC- CAUAAAGUA AAGCACUAC GUUAUUCAUC UUUGUGAUG GU A GUA C UGGGAG C	AC004687.1 chr17 BCL3/myc translocation locus,like mouse		EST AI153235		ti 90594313	
miR-142as	UGUAGUUUUUCCUUAUUGG	AC- CAUAAAGUA AAGCACUAC GGUAUUCAUC UUUGUGAUG GU A GUA G UGGGAG C			AI153235		ti 90594313	
miR-143	UGAGAUGAAGCACUUGAUGCA UUAUGAAGACACUUGAG	g g u u ag CCUGAG UGCAGUCU CAUUC GG UC U GGACUC AUGUCACGA GUAGAG CU AG U g A U G G	AC008681.7 chr5					
miR-144	UACAGAUAGAUAGUACUAG	g a a- gu GGCUGU AUAUCU UAUCUGUA GUU G CUGAUC UGUAGUG AUAGACAU CAGA A A - CA GU	Chr17 XM_064366.1 precursor nearly ident		EST AA290206.1, mmtrace 2143909		ti 16054574	
miR-145	GUCCAGUUUCCAGGAUCCUU	C UC U C UUGAUG CUCA GG CAGU UU CCAGGAUCCU \\ GAGU UC GUCA AA GGUUUUAGGGG C - UU U A UAGAUA	AC008681.7 chr5 GG->GA;precu nearly like mouse, see 2 positions above		EST BF163348.1		Scaffold 934 similar	ti 30316905
miR-146	UGAGAUCUGAAUCCUAGGGUU	CU GAGAUCUGAAU C AUGGGU UCGA UUCUUGACUUA GUGUCCAG A A C- A ACUGU	AC008388.7 chr5 diff precursor		mmtrace 34639321 (U23A)			
miR-147	GUGUGGAAAUUCUCUGCC	A- CAA ACR--- GA AAUCUA AGA CAUUCUUGCACAC CCA \\ UUAGAU UCU GUAAAGGUGUGUG GGU C CG UC- ACCGAA AU	Chr9 AL592549.7					
miR-148	UCAGUGCACUACAGAACUUUU	- A- CC - AGU GAGCRAAGUUCUG AG CACU GACU CUG \\ CUCUGUUUACAGAC UC GUGA CUGA GAU A A AC -- A AGU	Chr7 AC010719.4		NW_000250.1 chr6 [2957550-529]			
miR-149	UCGUCUCCGUGUCUACUCC	g c g g GGCUGU CUC GU UCUUC CUCU UUU U UCGGGC GAG CA GGAG GAGGG GAG C G A G - AG- C	NE_005472.7 chr2 [399188-167]		mmtrace 85955550			
miR-150	UCUCCAAUCCUUGUACCAUGU	AC U UG- UG CCUGUCUCCCA CCU GUACAG CUG \\ GGGAUAGGGGU GGA CAUGGUC GAC C CC - CCA UC	NT_011109.12 chr19 [6144715- 694](nt1-22)		mmtrace 84721065,10352801 (U23C)		ti 102760037	
miR-151	CUAGACUGAGCCUUGAGGU	C CA UGUCU CCUG CCUCAGAGGCG CAGUCUAGUA U GGAC GGAGUUCUCCGG GUCAGAUCAU C A A- CCCC			mmtrace 88456669			
miR-152	UCAGUGCAUGACAGAACUUG	g a cc CGG C CCGGCCUAGUUCUGU AU CACU GACU GCU U GCCCGGUUCAAGACA UA GUGA CUGA CGA G g c e -- --- g	human chr17 AC004477.1, nearly identical		mmtrace 83700445		ti 91657282	
miR-153	UUGCAUAGUCACAAAAGUGA	- GU A- AAU CAGUG UCAUUUUUGAU UGCAGU GU \\ GUUAC AGUAAAACACUG ACUUGGA CG A U AU CC AGU	AC006372.2 chr7 ident.precursor		mmtrace 87010874		ti 138688365	
miR-154	UAGGUUAUCCGUGUUGCCUUG	U - CCU- UUU GAAGAUUGUA CCGUGU UG UCCG \\ UUUUUAUCCAGU GGCACA AC AGUG A U U UAAGC UUU	AL132709.5 chr14 nearly identical precursor		mmtrace 86715639			
miR-155 [BIC-RNA]	UUAUUGCUAAUUGUAUAGGG	U U A UUGGCC CUGUAAUUGCUAAU G G UAGGGUU \\ GACAAUACGAUUG U C AUCCUAG U - C - UCAGUC	human BIC RNA:AF402776.1 (has U12C)		Chr 16 mouse		ti 43006946	
miR-181	AACAUAUACCGUCUGGUGAGU	U A U CU A GGAUUC CCA GG ACA UCAACG CUGGUGUU \\ GGU CC UGU AGUUGC CAGCCAC CAAA A U A C - -- AAAACAAA	with different precursors in chr9 AL158075.11,chr1 AL136321.5 chr7 AC084864.2		Chr1 NW_000154.1 [19946715-137], Chr2 NW_000175.1 [4948211-233]		scaffold_ 1819	ti 120853346
miR-182	UUUGCAUUGGUAAGUCACA	UU UGG UCA UAAGGU ACCAU UUGGUA UAGACA CACCGA A UGUAU AACCGUU AUCUUG GUGGCC A UC CAG --- CAGGUU	similar precursor		Chr6 NW_000272.1 [27180972-951], mmtrace 88841093		scaffold_ 967	AL590150.2
miR-183	UAUGGACUGGUAAGUACUG	g AC- GA -- AC CUGU UAUGC UGUA AUUCACUG UGA A GACA AUACG GCCAU UAAGUAC ACU G A GGA -- UG CU	chr7 AC084864.2 ident.precursor		Chr6 NW_000272.1 [27184718-696], mmtrace 86029980		scaffold_ 967	AL590150.2

miR-184	UGGACGGAGAACUGUAUAGGGU	U C AG - UG CCU UCCUAUCA UUUUC CCAGC UUUU A GGA GGAUAUGU AAGAG GGUUG GAUA C U C CA U CU	chr15 AC069082.9	Chr9 NW 000355.1 [557587-566], mmtrace 87318220	found	scaffold_3671	ti 42218413
miR-185	UGGAGGAAAAGGCAUGUUC	A G AU UC AGGUAUUGGAG GAAAG CAGUUCUG GG C UUCUGUGUCU CUUUC GUCCGGGAC CC C - G - UC	chr22 AC005664.2 ident.precursor	Chr16 AC012526.32			
miR-186	CAAAAGAAUCCUUUUUGGGCU	U UU UCUCAU ACUUUCCAAAAGAAUUC CCUU GGGCUU U UGAAGGUUUUUUUAAG GGAA CCCGAA U U U- UUUUAU	chr1 AL512443.7 similar prec.	Chr3 NW 000203.1 [2621170-192], mmtrace 86694995			
miR-187	UCGUGUCUUGUGUGCAGCCGG	A G C CGUCUC UC GGCU CAACACAGAGC CGGG U GG CGGA GUGUGUUGUC GCU C - G - U CCGAGU	chr18 NT_010934.10 almost identical precursor	Chr18 NW 000134.1 [2154396-375], mmtrace 51673384		ti 115972602	
miR-188	CAUCCUUGCAUGUGGAGGGU	CA UC GU UGAGCUC G UCU CA CCUUGCAUG GAGGG U AGG GU GGGAGUAC CCUCC C AC UU AC CAAAAGU	chrX AF222886.1 nearly ident. precursor	ChrX NW 042617.1 [419161-140], mmtrace 61928192			
miR-189	GUCCUACUGAGCUGAUCAGU	G G A UA UCUCAU CUCU CCU CUGAGCUGA UCAGU \\ GAGG CA GGA GACUUGACU GGUCA U A A C C CACACU	chr9 XM_098943.1 has C17U;prec.nearly identical to mouse	cDNA A1286629.1, has C17U			
miR-190	UGAUUUGUUGAUUAUUGAGU	U- UA--- UU CUGUG GAUAUGUUUGAUUAU GGUUG \\ GACAU UUAUACGAACUAUAUA CUAU A CC C A UCACU UU	NT_010265.12 [601139-160] different prec.	Chr9 NW 000353.1 [13587064-043], mmtrace 71760450	scaffold_2294	ti 98807991	
miR-191	CAACGGAUCCCAAAGCAGCU	C A A U U - C AGCGG AACGGAUCC AA GCAGCU GU CU C UCGUCC UUGCUUAGG UU CGUCAG UA GA A C - CA CU - C		Chr9 NW 000356.1 [7597852-873], mmtrace 88722637			
miR-192	CUGACCUAUGAAUUGACA	C - A UGUCUC UGACCUAUG AAUUG CAGCCAG G ACUGAUAC UUAAC GUCGGUC U - C C UCCCCUC	chr11 AC000159.6				
miR-193	AACUGCCUACAAGUCCAG	A U C A A AGU GAG CUGGG CUUUG GGGC AG UGAG G CUC UGACCC GBAAG UCCG UC ACUU U C U A G A GAC	chr17 AC003101.1, similar precursor	mmtrace 9555103	scaffold_246	ti 35831698	
miR-194	UGUACAGCAACUCCAUUGUGA	U A G - - U AUCGG GUACAGCA CUCCAU UGGA CUG G UAGUCU CAUUGUCGU GAGGUG ACCU GGC C U U - UA U	chr11 AC000159.6, chr1 AC103590.2; diff.prec.	Chr1 NW 000163.1 [1824200-221]; Chr 19 NW 000140.1 [424960-879]	scaffold_152	ti 15658026	
miR-195	UAGCAGCACAGAAUUAUUGC	U A- UGAG G G AGCAGCACAG AAUAUUGCA GG G UCGUCGUCU UAUAACCGU CU U - - GAG	chr17 NT_010823.10 [1648753-733] precursor similar to mouse	Chr11 NW 000039.1 [28660803-823], mmtrace 47823768			
miR-196	UAGGAGUUUAUUGUUGUGG	A A C G C C C C C GUGAAU GGU GUUU AUGUUGUG U CACUAG CCA CAA UACACAC C C U ACAAGUCU	chr17 AC009789.21	Chr11 AC011194.15, similar precursor	scaffold_18334	AC107365	
miR-197	UUCACCAUUCUCCACCCAGC	C A A CA GA A GGCUGUC GGU GAGAGGG GUGG GGU AAG G CCGGUACG CCA CUCUUC CACU CCA UUC C A G AG UC C U	chr1 AL355310.19				
miR-198	GGUCCAGGGGAGAUAGG	G C G U UUCUC U UCAU G UC A AGGGAGA AGG U AGUA U AG U UCUCUUC UCC G A A A - UUUUA	chr3 AC063952.15				
miR-199-s	CCGAGUUCAGACUACCUUGU	AAC U C U G - - G GCC CCAGUG CAGACUAC UGU CA GAG \\ CGG GGUUACA GUCUGAUG ACA CU C C AUU C - U GUAA U	chr19 AC007229.1; chr1 AL137157.7 similar precursor	Chr1 NW 000158.1 [6126994- 7015]similar prec.; Chr9 [NW_000351.1 [8200855-834]diff. prec.			
miR-199-as	UACAGUAGUCGACAUUGGU	AUC U C - - - - - G GCC CCAGUGU CAGACUAC UGU UCAG A CGG GGUUACA GUCUGAUG ACA GUG G AUU C - UGUACAG G	chr9 AC006312.8	Chr1 NW 000158.1 [6127032-053] similar prec.; Chr9 NW 000351.1 [8200816-795]diff. prec.; Chr2 NW_000174.1 [9865129-150]	scaffold_5830		
miR-200a	UAUAUCGCGUUAUGAUGAC	GGC - C UAGUG GCCGU CAUC UUAUCGGCAG AUUGGA U CGGCA GUAG AAUGGUCGUC UAUAUC C - - - U A CUAGU	chr1 NT_004350.12 [626407-429]	Chr4 NW 000222.1 [8367659-429], mmtrace 72257777	scaffold_2210	ti 98591420	
miR-200b	UAUAUCGCGUUAUGAUGAC	GGC - C UAGUG GCCGU CAUC UUAUCGGCAG AUUGGA U CGGCA GUAG AAUGGUCGUC UAUAUC C - - - U A CUAGU	NT_004350.12 chr1 [626407-429]	NW 000222.1 chr4 [8367659-637]		ti 98591420	
miR-201	UACUCAGUAGGCAUUGUUCU	U U UUC A UAUCUAC CAG AAGGCAUUGUC UAU U AUGGAGU GUC UCCUGACAAG AUA U U U UAA A		ChrX NW 042622.1 [11847560-540]			
miR-202	AGAGGUUAAGCCAUUGGAGA	U A- UG C GUUCC UUUUCCUAGC UAUACUUCU UGGAU \\ CGAGG AGAAGGUUACG AAUUGGAGA AUUCU U U CG - - G		Chr7 NW 000335.1 [895960-939], mmtrace 49754566			
miR-203	UGAAUUGUUUAGGACCAUAGA	U C U G A C U GCC GGUC AGUGUUCU GACA UUCA CAGUU UG \\ CGG CCAG UCACCAAGA UUGU AAGU GUUAA AC A C A U A - C G	chr14 AL136001 ident. precursor	Chr12 NW 000055.1 [8274647-669], mmtrace 18453604		BF157485	
miR-204	UUCCUUUGUCAUCCUAUGCCUG	U A U GAGAUA UGGAC UCCUUUUGUC UCCUA CCUU \\ ACUUG AGGGAACGG AGGGU CGGA U C A - GGAUA	chr9 AL159990.12 identical precursor	Chr 19 NW 000143.1 [13367970-992], mmtrace 91503159	scaffold_725	ti 90539298	
miR-205	UCCUCAUCCACCGAGUCUG	UC G UCUUA CUCUUG CUUCAUCCAC GAGUCUG U GAGGAC GAAGUGAGGUG CUUAGAC G UC A CAACC	XM_036612.4, precursor very similar	XM_149012.1	scaffold_13664	ti 100304320	
miR-206	UGGAAUGUAAGGAGUGUGUGG potential miR-1 homolog	- C U AUUAC CCAAG CCACAUGCUUCUUUAU C CAUAG \\ GGUUU GUGUGUGAAGGAUUGA G GUUAC U U A - ACAGC	chr6 AL391221.15 similar precursor	Chr1 NW 000165.1 [4959909-930], mmtrace 84055510		ti 109888625	
miR-207	GCUUCUCCUGGUCUCCUCCUC	C U UUG GGAG AAGG AAGGG GAGGG CGGAGAGC CGGC G UUCC UCUC CUCUC GUCCUUCUG GUUC C U - UCG C GCGU		Chr4 NW 000206.1 [17744597-621], mtrace 72109322			
miR-208	AUAAGACGAGCAAAAGCUUGU	G C C G C AU UGAC GCGAGCUUUU GC CG UUAUAC UG \\ ACUG UUGUCCGAAA CG GC AAUAUG AC G G A A AG C UC	Chr14 NT_025892.9 [4180272-251]	Chr14 NW 000100.1 [1172468-447]			