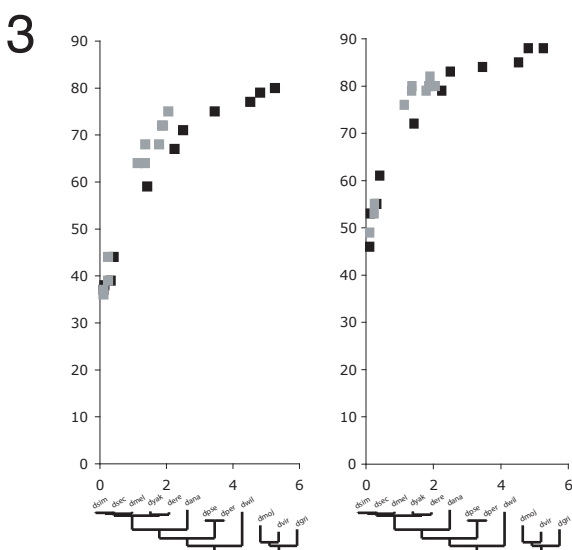


[illegible]

Supplemental Figures

Supplemental Table 2: miRNA hairpin features

Feature	Range (5% - 95%)			Known enrichment
	Known miRNAs	miRNA-like hairpins	Random hairpins	
Correlation to average conservation profile of known miRNAs	0.75 - 0.97	-0.28 - 0.7	-0.28 - 0.77	327.54
Match fraction for the less conserved arm	5.9 - 12	1.8 - 8.9	1.6 - 8.1	42.32
Z-score of the minimum free energy (MFE) with respect to the length and GC content	2.7 - 6.2	0.11 - 3.4	-2.5 - 2.5	39.25
Match fraction for the more conserved arm	6.1 - 12	2.5 - 10	2.5 - 10	16.14
Mismatch fraction for the region flanking the more conserved arm	1.9 - 6.4	0.05 - 3.7	0.05 - 3.7	13.38
Mismatch fraction for the loop	0.33 - 5.5	0 - 2.2	0 - 2.1	10.87
Number genomes the hairpin is present in (range 2..12)	7 - 12	3 - 12	3 - 12	9.56
Mismatch fraction for the region flanking the less conserved arm	2.4 - 6.2	0.1 - 4.6	0.09 - 4.7	6.56
MFE of the consensus fold	-41 - -20	-30 - -2.5	-27 - -1.6	6.32
Average difference between the MFE of the consensus fold and the individual fold	0.59 - 9.4	1.9 - 22	1.3 - 21	6.24
(less conserved arm conservation)/(loop conservation)	0.99 - 1.7	0.63 - 1.2	0.53 - 1.2	5.18
Number of bases conserved in the longest stretch of perfectly conserved base pairs in an arm	20 - 39	5 - 29	1 - 22	5.00
Match fraction for the region flanking the less conserved arm	3.9 - 8.6	1.7 - 7.9	1.7 - 7.6	4.68
(more conserved arm conservation)/(loop conservation)	1 - 1.8	0.86 - 1.4	0.87 - 1.3	4.11
Match fraction for the loop	4.1 - 12	2 - 10	2.2 - 9.7	3.94
(MFE of consensus fold/average MFE of the individual ortholog folds)	0.68 - 1	0.15 - 0.96	0.12 - 0.97	3.74
Match fraction for the region flanking the more conserved arm	3.9 - 8.7	2 - 8.8	1.9 - 8.6	3.37
Mismatch fraction in less conserved arm	0.036 - 1.8	0.19 - 3.4	0 - 4.4	3.28
(# of symmetric bulges)/(# of asymmetric bulges)	0.33 - 7	0.000025 - 3	0.00005 - 10000	3.01
Mismatch fraction in more conserved arm	0 - 1.3	0 - 1.4	0 - 1.8	2.60
Number of paired bases in the best stretch of 22 base pairs	18 - 22	16 - 21	3 - 19	2.56
Indel fraction for the loop	0 - 0.16	0 - 0.17	0 - 0.14	2.44
Percent of arm bases that are paired	0.77 - 0.9	0.72 - 0.86	0.67 - 1	2.32
Number of bases that need to be removed to make all internal bulges symmetric	1 - 7	1 - 13	0 - 10	1.99
Indel fraction for the region flanking more conserved arm	0.012 - 0.17	0 - 0.14	0 - 0.15	1.97
Less conserved arm length	31 - 47	21 - 52	3 - 42	1.72
More conserved arm length	31 - 47	21 - 52	3 - 42	1.72
Indel fraction for the less conserved arm	0 - 0.036	0 - 0.23	0 - 0.26	1.66
Indel fraction for the region flanking less conserved arm	0.018 - 0.17	0 - 0.2	0 - 0.2	1.49
Loop length	4 - 26	4 - 64	4 - 110	1.37
Structure length	73 - 100	65 - 120	47 - 120	1.36
Number of substructures	0 - 0	0 - 1	0 - 2	1.36
Indel fraction for the more conserved arm	0 - 0.02	0 - 0.078	0 - 0.07	1.21
Number of internal bulges	3 - 8	2 - 9	0 - 6	1.20

Supplemental Table 3: Mature miRNA features

Feature	Range (5% - 95%) or Faction 1 (for binary features)		Known Enrichment
	Known 5'	Other positions	
Target 7mer conservation profile correlation	-0.12 - 0.94	-0.49 - 0.65	15.2
Target 7mer conservation score	5.9 - 110	-0.54 - 24	11.04
Target 7mer avoidance score	-1.5 - 4.6	-3.5 - 3.7	4.11
Length of perfect conservation that follows, including start	15 - 32	0 - 32	3.54
20mer conservation	0.99 - 1	0.83 - 1	2.85
0/1 presence of U	0.78	0.30	2.62
0/1 start of perfect 20mer conservation	0.95	0.42	2.24
0/1 start of perfectly conserved 8-mer followed by a 95%- conserved 12-mer	0.97	0.45	2.15
Size of symmetric loop	0 - 2	0 - 2	1.9
Distance from terminal loop	0 - 9	-5 - 20	1.46
Distance from start of the hairpin	3 - 16	-2 - 23	1.43
Overlap length with the loop region	0 - 0	0 - 5	1.24
0/1 loop at 1 position	0.27	0.22	1.21
Number of paired bases in window of 7	3 - 7	2 - 7	1.18
0/1 loop at 2 position	0.08	0.21	1.16
0/1 loop at -2 position	0.18	0.26	1.11
Size of overlapping bulged loop	0 - 0	0 - 6	1.08
0/1 loop at -1 position	0.22	0.25	1.04
Number of paired bases in window of 3	1 - 3	0 - 3	1.03
Number of paired bases in window of 5	2 - 5	1 - 5	1.02
0/1 loop at current position	0.23	0.23	1

[illegible]

1.0000 L	ZL 9950419 9950518 -	mir-87	
GCACACATCTTCATGCGCCCTGTATCTCTGAAACCCTGCACATATGCGCAACCTCCGTGTGACCAAAATTCAGTGTTGTGAAGATGTTTATGC			+ 1
TGGCGCTCTATCTCTCTGAC			+ 1
TGGCGCTCTATCTCTCTGAC			+ 3
TTTGACCAAAATTCAGTGTTG			+ 3
TTTGACCAAAATTCAGTGTTG			+ 8
TTTGACCAAAATTCAGTGTTG			+ 11
TTTGACCAAAATTCAGTGTTG			+ 8
TTTGACCAAAATTCAGTGTTG			+ 24
TTTGACCAAAATTCAGTGTTG			+ 1
TTTGACCAAAATTCAGTGTTG			+ 7

1.0000 HM 2R 15175570 15175671 - miR-6-3*
ATTGAAAATGGTACAAAAGAAAGGGAACGGGTGCTGATGATGTAGTTTGAAACCTCTCACAATTTATATCACAGTGGCCTTCTCTTTTGGTTGGCAATCGAT

1.0000 HM 2R 15175862 15175950 = miR-6-1*

GCCTTTAATGTAGAGGGAAATAGTCTGCTGCTGTAAAGTTAATATACCATATCTATATACAGTGGCTGTTCTTTTGTACCTAAAGTGC

1.0000 L 2R 15176008 15176098 - miR-5*
GGGCCATTCGCTAAAGGAACGATCGTTGTGATATGAGTTGTTTCTAACATATCACAGTGATTTCCTTTATAAAGCATGTTTAAAGTCC
TATCACAGTGATTTCCTTTAT + 1 1

1.0000 H 2R 15176151 15176233 - mir-4*
GTTGCAATTAGTTCTTTGTCGTGACGCTAGGTGATTCTTCGGCTATAAGCTAGACAACCATTTGAAGTTCGTTGTGCG
ATAAAGCTAGACAACCATTTGA + 1 1

1.0000 HM 2R 15176285 15176387 - mir-286*
GTTTAAATAGTGAATGCGGATGTCGTGATGATGCTCTCTTTCAAGAAAGGTTTGATTAAGGCGAAGTGTAGACGACCACTGCTGTATATTTAAAT
TGACTAGACGACCACTGCTG + 1
TGACTAGACGACCACTGCTG + 2

1.0000	H	2R	4824837	4824929	-	Novel-1/miR-987		
TOTTGACATCTGTTTAAAGTAAGTATGCTGGATTGATGAAGTGCATTCGAAATTCATCAACAGGCATTTCCTCACTGCAGTTTGAACA								
				TAAAGTAAATAGCTGGATTG			+ 1	1
				TAAAGTAAATAGCTGGATTGA			+ 1	1
				TAAAGTAAATAGCTGGATTGAT			+ 1	1
				TAAAGTAAATAGCTGGATTGATG			+ 1	1
				TAAAGTAAATAGCTGGATTGATGA			+ 2	1
						CATCAACAGGCATTACTTCAA	+ 1	1

[illegible]

1	00000	LM	ZR	5131062	5131153	-	mir-307*		
1	TTCTTCCT	1	CTCTTCACTTCACTCTGCTGATGATGATTTTCTTGATGATATTCACACGAGAACTCTCTGATGATGACGATACAGACAGAGA					+1	1
			ATCTCTCACTCACTGGTGT					+1	1
			ATCTCTCACTCACTGGTGTGTA					+1	1
			ATCTCTCACTCACTGGTGTGTT					+1	1
			ATCTCTCACTCACTGGTGTGTTG					+1	1
				TCGCAAACTCTCTTGATGTA				+1	1
				TCGCAAACTCTCTTGATGTTA				+9	1
				TCGCAAACTCTCTTGATGAGAGG				+10	1
				TCGCAAACTCTCTTGATGAGAGG				+16	1
				TCGCAAACTCTCTTGATGAGAGG				+6	1
				TCGCAAACTCTCTTGATGAGAGG				+1	1
				CAGCAACTCTCTTGATGAGAGCA				+12	1

[illegible]

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	1																																																																																								

[illegible]

TACTTCAGGTAAGATGT	+ 11	1
TACTTCAGGTAAGATGTC	+ 10	1
ACTTCAGGTAAGAT	+ 2	1
ACTTCAGGTAAGATG	+ 4	1
ACTCTCAGGTAAGATGT	+ 16	1
ACTTCAGGTAAGATGTC	+ 17	1
CTVTCAGGTAAGATG	+ 5	1
CTVTCAGGTAAGATGT	+ 13	1
CTVTCAGGTAAGATGTC	+ 22	1

[illegible][illegible][illegible]

0.9980 BB	3L 625742 625820 +	bantam*		
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CGGTTTCGATTTGCTTGGTT			+ 8	1
CGGTTTCGATTTGCTTGGTT			+ 16	1
CGGTTTCGATTTGCTTGGTT			+ 82	1
CGGTTTCGATTTGCTTGGTTACT			+ 200	1
CGGTTTCGATTTGCTTGGTTAC			+ 31	1
CGGTTTCGATTTGCTTGGTTACT			+ 1	1
GTTCGATTTGCTTGGTTAC			+ 2	1
TTTCGATTTGCTTGGTTAC			+ 1	1
	TGAGATCATTTGAAA		+ 1	1
	TGAGATCATTTGAAG		+ 1	1
	TGAGATCATTTGAAGC		+ 5	1
	TGAGATCATTTGAAGCT		+ 9	1
	TGAGATCATTTGAAGCTG		+ 86	1
	TGAGATCATTTGAAGACTGA		+ 171	1
	TGAGATCATTTGAAGACTGA		+ 160	1
	TGAGATCATTTGAAGACTGATT		+ 1066	1
	TGAGATCATTTGAAGACTGATT		+ 4	1
	GAGATCATTTGAAGCTGA		+ 1	1
	ATCATTTGAAGACTGATT		+ 5	1
	TGATTTGAAGACTGATT		+ 2	1
	TCATTTGAAGACTGATT		+ 1	1
	CTTTGAAGACTGATT		+ 3	1
	ATTGAAGACTGATT		+ 3	1

009800 BM	3R	11243121	11242306	- mir-13b-1*		
TTTCTATACATGCTGCTTAAATGATTTTGATGATTTATATGATGACATATACAGACACCTTTTGAGGTTTGGTGAAGAAA						
				CTATGACAGACACCTTTTGAGGTTTGGTGAAGAAA	+ 1	2
				ATATACAGACACCTTTTGAGGTTTGGTGAAGAAA	+ 1	2
				ATATACAGACACCTTTTGAGGTTTGGTGAAGAAA	+ 2	3
				TATACAGACACCTTTTGAGGTTTGGTGAAGAAA	+ 24	2
				TATACAGACACCTTTTGAGGTTTGGTGAAGAAA	+ 12	2
				TATACAGACACCTTTTGAGGTTTGGTGAAGAAA	+ 2	3
				TATACAGACACCTTTTGAGGTTTGGTGAAGAAA	+ 26	2
				TATACAGACACCTTTTGAGGTTTGGTGAAGAAA	+ 299	2
				TATACAGACACCTTTTGAGGTTTGGTGAAGAAA	+ 4249	2
				TATACAGACACCTTTTGAGGTTTGGTGAAGAAA	+ 18375	2
				TATACAGACACCTTTTGAGGTTTGGTGAAGAAA	+ 281	2
				ATACAGACACCTTTTGAGGTTTGGTGAAGAAA	+ 7	2
				ATACAGACACCTTTTGAGGTTTGGTGAAGAAA	+ 45	2
				TACAGACACCTTTTGAGGTTTGGTGAAGAAA	+ 21	2
				TACAGACACCTTTTGAGGTTTGGTGAAGAAA	+ 45	2
				TACAGACACCTTTTGAGGTTTGGTGAAGAAA	+ 1	2
				CGACAGACCTTTTGAGGTTTGGTGAAGAAA	+ 1	2
				CGACAGACCTTTTGAGGTTTGGTGAAGAAA	+ 10	2
				AGACACCTTTTGAGGTTTGGTGAAGAAA	+ 7	2
				AGACACCTTTTGAGGTTTGGTGAAGAAA	+ 107	2
				AGACACCTTTTGAGGTTTGGTGAAGAAA	+ 1	2

OTC_9960_Lm	Zl_19565824	19565903	- mir-2a-1*		
ATGTCGACCTCTCAAAATGGTGTGTAAGGACCTCTCCCTTCCTGAGGCGACATCTCACAGCAACTTGTAGAGCTTAGGCT				+ 1	1
CTCTCAAAATGGTGTGTAAGG				+ 2	1
CTCTCAAAATGGTGTGTAAGG				+ 27	1
ATATACACAGCAACTCTGTAGAG				+ 6	2
ATATACACAGCAACTCTGTAGAGC				+ 6	2
ATATACACAGCAACTCTGTAGAGC				+ 3	2
TATCACACAGCAACTCTTGA				+ 4	5
TATCACACAGCAACTCTTGA				+ 63	3
TATCACACAGCAACTCTTGA				+ 327	3
TATCACACAGCAACTCTTGTAGA				+ 1753	2
TATCACACAGCAACTCTTGTAGAC				+ 10821	2
TATCACACAGCAACTCTTGTAGAC				+ 8214	2
TATCACACAGCAACTCTTGTAGAC				+ 2129	2
TATCACACAGCAACTCTGTAGACTT				+ 69	1

[illegible]

6,9920	HM	3L	1031917	1031929	+ mis-276*		
TGGTTTTCCTCATGCTGCTGCTCATGCTCATGCTCATGAGACCTCATCATGCTGCTCTCTGAGACCA						+1	2
ACGCGATATATAGAGTCTC						+1	2
ACGCGATATATAGAGTCTTC						+1	2
ACGCGATATATAGAGTCTCTA						+1	2
ACGCGATATATAGAGTCTTAC						+66	2
ACGCGATATATAGAGTCTTAC						+118	2
ACGCGATATATAGAGTCTTACATCT						+15	2
ACGCGATATATAGAGTCTTACATCT						+15	2
ACGCGATATATAGAGTCTTACAG						+3	2
CAGCGATATAGAGTCTTACAG						+1	2
GAGCGATATAGAGTCTTACAG						+2	2
AGCGATATATAGAGTCTTACAG						+1	2
GTAGGAGACCTCATCATGCTCTCT						+1	1

[illegible]

GGGGGTCACCTCTGTGCCTGTGC + 155 1

0.9680 H 3R 17447616 17447730 - Hovel-29/miR-998
TCATTGGGAACCTGAATCTCTGGGTGCTGACCTGACACCTGACCGCTCCAGGCGAAATGTCATTCTGGAAATGGAATCTCTGTAGCACCAGTGATCTCAGCTCTGGCTGGA
ACTGGAATCTCTGGGTGCTG
ACTGGAATCTCTGGGTGCTG
ACTGGAATCTCTGGGTGCTG
ACTGGAATCTCTGGGTGCTG
CTGGAATCTCTGGGTGCTGCA
TCTCTGGGTGCTGCA

Q9460	HM	3R	16561652	16561725	+ Movel-10nR-995		
ACC	CGAC	CGCCAAATATAT	TGGAGAGCTGGCC	CCCTTCCATTCGATGAC	CACACATCATATGGCTGCTGGTGGT		
						+ 1	1
GCC	CAATATATAT	TGGAGAGCTGG					
						+ 3	1
CCG	CAATATATAT	TGGAGAGCTGG					
						+ 3	1
CCG	CAATATATAT	TGGAGAGCTGG					
						+ 9	1
TAG	CACACATATAT	TGGAGAGCTGG				+ 57	1
TAG	CACACATATAT	TGGAGAGCTGG				+ 94	1
TAG	CACACATATAT	TGGAGAGCTGG				+ 1259	1
TAG	CACACATATAT	TGGAGAGCTGG				+ 3	1
TAG	CACACATATAT	TGGAGAGCTGG				+ 2	1
CGC	ACATATATAT	TGGAGAGCTGG				+ 2	1
CAC	ACATATATAT	TGGAGAGCTGG				+ 1	1

95460	HM	3R	21477135	21477201	+ mir-92b*		
TGTAGAGCTGCGACCGCTATTGTGTGCATTTCGAAATCAAGATCAATGCTAGTCCGCCGCGTCA						+ 1	1
AGGCGCTCCCGACCGCTTATTT						+ 6	1
AGGCGCTCCCGACCGCTTATTT						+ 7	1
AGGCGCTCCCGACCGCTTATTT						+ 86	1
AGGCGCTCCCGACCGCTTATTTGT						+ 2	1
GCGCTCCCGACCGCTTATTTGT						+ 1	1
TTCGATTCTTGAATATACA						+ 1	1
TTCGATTCTTGAATATACA						+ 8	1
AAATTCGCTAGTATGCCCGGCTGT						+ 8	1
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AATTCGCTAGTATGCC						+ 1	1
AATTCGCTAGTATGCCGCT						+ 27	1
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AATTCGCTAGTATGCCCGCTGT						+ 1905	1
AATTCGCTAGTATGCCCGCTGT						+ 4943	1
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ATTCGCTAGTATGCCCGCTGT						+ 12	1
ATTCGCTAGTATGCCCGCTGT						+ 46	1
ATTCGCTAGTATGCCCGCTGTA						+ 1	1
TTCGCTAGTATGCCCGCTGT						+ 1	1
TTCGCTAGTATGCCCGCTGT						+ 30	1
TTCGCTAGTATGCCCGCTGT						+ 3	1
TTCGCTAGTATGCCCGCTGT						+ 8	1
GCATATGCCCGCTGT						+ 7	1
GCATATGCCCGCTGT						+ 8	1

0.9620 X 15110474 15110559 + Novel-32
ATACAAACACACTCAAAGTGAAANTGGAAAAAGTTTCAATGGTTTTATCATGTTTACITTTATTGTGTCACTGAGTGGTTGTAT

0.9600 X 18015331 18015398 = Novel-34
GGCGACGTCATATTGTGTTGGCAATCGTTGCGATAAGCCAACTACATAATGTCTCTGTAGGCC

TGAGTATGATAGTTATAT	+ 74	1
TGAGTATGATAGTTATAT	+ 116	1
TGAGTATGATAGTTATATG	+ 1441	1
TGAGTATGATAGTTATATAGT	+ 6939	1
TGAGTATGATAGTTATATAGTA	+ 1497	1
TGAGTATGATAGTTATATAGTAG	+ 2	1
AGAGTATGATAGTTATATAG	+ 5	1
AGAGTATGATAGTTATATAGT	+ 4	1
AGAGTATGATAGTTATATAGTA	+ 2	1
AGATGATAGTTATATATAG	+ 2	1
AGATGATAGTTATATATAGT	+ 2	1
AGATGATAGTTATATAGTAG	+ 2	1
GTATGATAGTTATATAGT	+ 3	1
GTATGATAGTTATATAGT	+ 4	1
GTATGATAGTTATATAGTA	+ 1	1
TATATGATAGTTATATAG	+ 1	1
TATATGATAGTTATATAGT	+ 1	1
TATATGATAGTTATATAGTA	+ 1	1
	+ 2	1
	+ 1	1
	+ 3	1
	+ 28	1
	+ 238	1
	+ 1	1

0.9580 2R 13077473 13077566 + Novel-36
CCTTCTCCAGGACTGGCTCATTGTTCTCTCCATTTCTGACTCGTTCTAGGTGCGAATCCGGAACGGGAATGAGGACAGTGTAGCCAAAGCCAGAAGG

0.9780	3R	8377236	8377341	-	mir-284				
ATGTTGGTCGATGCTTCGGATGATGCTGATGCTGTTGAGCTGTAAGCGAGGACGCTGATGATATGCTCTGATGCTAGTGAAGCAACTGATTCAAGCAAGTTCGGCGCCGAT									
								3	1
CTCGAATTAAGTCTACTGCTG								+3	
CTCGAATTAAGTCTACTGTG								+1	1
CTCGAATTAAGTCTACTGTCGAC								+1	21
CTCGAATTAAGTCTACTGTTAGCC								+8	1
CTCGAATTAAGTCTACTGTTAGCTG								+1	1
CTCGAATTAAGTCTACTGTTAGCTG								+1	1
						GTGAGCACTTATTCTGAC		+2	1
						GTGAGCACTTATTCTGACCA		+5	1
						GTGAGCACTTATTCTGACGA		+4	1

0.9760 3R 24822601 24822689 - Novel-25
GCTCGAGTTGCATTTAAGCCAAATTAGCATAGGTAACAAAAACATTTGAGTGAGCCAGCCAAAGTGCTTGCGGTTGAGTGC GGCTCTGGGC

0.9740 3L 7188122 7188227 - Novel-27
GACGAATTCCTTGAGTCGGCCACGCGAACTATTGTGAACATCATGGGACGCCGAAGGGGAGGCCATCGTCTCTGAGTCCTTTCAC TGCCCACTCAAGGATCGTT

[illegible]

[illegible]

0.9220 HM X 136993 137094 - Novel-64/miR-980
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0.4400 L 2L 18467369 18467437 + miR-100
ACAGAAACCOTAAATCCGAACTTGTGCTGTTTTATATCTGTTACAAAGACCGGCATATGGGAGCTGT
TATTCAGACTTCCCGGCT + 41 1
TATTCAGACTTCCCGGCT + 329 1
TATTCAGACTTCCCGGCT + 786 1
TATTCAGACTTCCCGGCT + 4591 1
TATTCAGACTTCCCGGCTTAA + 862 1
TATTCAGACTTCCCGGCTTAA + 144 1
TATTCAGACTTCCCGGCTTAA + 40 1
ATTGCACTTCCCGGCTTT + 9 1
ATTGCACTTCCCGGCTTT + 1 1
ATTGCACTTCCCGGCTTTAA + 2 1
TTGCACTTCCCGGCTTT + 9 1
TTGCACTTCCCGGCTTT + 3 1
TTGCACTTCCCGGCTTTAA + 1 1
GCAGACTTCCCGGCTTT + 1 1

0.4600 L 2L 18467369 18467437 + miR-100
ACAGAAACCOTAAATCCGAACTTGTGCTGTTTTATATCTGTTACAAAGACCGGCATATGGGAGCTGT
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TATTCAGACTTCCCGGCT + 2 1
TATTCAGACTTCCCGGCTTTAA + 1 1
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TATTCAGACTTCCCGGCTTTAA + 9 1
TATTCAGACTTCCCGGCTTTAA + 3 1
TATTCAGACTTCCCGGCTTTAA + 1 1
TATTCAGACTTCCCGGCTTTAA + 1 1

0.3620 HM X 8838541 8838640 - miR-31b*
TGGCAGATGTGGGATAGCTGAGGACGACGCGATCGAATTTATGTCGCGGAAATGTGATATTTTGGAAAGCGGTATGCTCATCTAGTCA
TGGCAGATGTGGGATAG + 1 1
TGGCAGATGTGGGATAG + 17 1
TGGCAGATGTGGGATAG + 53 1
TGGCAGATGTGGGATAG + 374 1
TGGCAGATGTGGGATAG + 458 1
TGGCAGATGTGGGATAG + 89 1
TGGCAGATGTGGGATAG + 1 1

0.1660 HM 2R 16698739 16988824 - miR-311*
TCTGAGCATTTTTCGAGCGGTATGAGGATGAGTCTGATTTGTCGAGATATATGACATTCACCGGCTGAAATATCAGAA
CGACGATATATGAGTTAA + 11 1
CGACGATATATGAGTTAA + 9 1
CGACGATATATGAGTTAA + 4 1
CGACGATATATGAGTTAA + 20 1
CGACGATATATGAGTTAA + 29 1
CGACGATATATGAGTTAA + 2 1
ATATTCAGATTCACCGGCT + 1 1
ATATTCAGATTCACCGGCT + 7 1
ATATTCAGATTCACCGGCT + 4 1
TATTCAGATTCACCGGCT + 24 1
TATTCAGATTCACCGGCT + 51 1
TATTCAGATTCACCGGCT + 398 1
TATTCAGATTCACCGGCT + 1015 1
TATTCAGATTCACCGGCT + 5148 1
TATTCAGATTCACCGGCT + 1271 1
TATTCAGATTCACCGGCTGAAA + 363 1
TATTCAGATTCACCGGCTGAAA + 40 1
TATTCAGATTCACCGGCTGAAA + 1 1
ATTCAGATTCACCGGCT + 1 1
ATTCAGATTCACCGGCT + 8 1
ATTCAGATTCACCGGCT + 47 1
ATTCAGATTCACCGGCTGAA + 35 1
ATTCAGATTCACCGGCTGAA + 6 1
ATTCAGATTCACCGGCTGAAA + 1 1
TTCAGATTCACCGGCTGAA + 11 1
TTCAGATTCACCGGCTGAA + 2 1
TTCAGATTCACCGGCTGAA + 2 1
TTCAGATTCACCGGCTGAA + 1 1
GCATTCACCGGCTGAA + 4 1

0.0480 3L 13594772 13594863 + miR-289
TTTACATTAATAATATTTAGGAGGAGCTCGGAGCTGATGCTTCTGAGCTGAGGAGTAAAGTCACTGAGGCTTTGTTGAGCAGTAAA

0.0180 HM 3L 11746959 11747048 + miR-314*
TGTAACTGTGTGAGCTGAGCTTACCTAGTGGAGGAAACTCCCATGTGTGAGATTTGTATGACCTGTGATTTGAGCCAAATAGTTGCG
TATTCGAGCCAAATAGTT + 2 1
TATTCGAGCCAAATAGTT + 7 1
TATTCGAGCCAAATAGTT + 13 1

0.0120 HM 2R 16699047 16999130 - miR-313
GCCACACATTTTCTGCTCGGATGCGGCGGAGTACTGTTTTTAAACATTGAGTATGCACTTTTCACAGCCCGGAAATGTTAGC
CTGCTCGGATGCGGCGGAGCA + 7 1
CTGCTCGGATGCGGCGGAGCA + 1 1
CTGCTCGGATGCGGCGGAGTAC + 4 1
CTGCTCGGATGCGGCGGAGTAC + 7 1
TCTGCTCGGATGCGGCGGAGC + 1 2
TCTGCTCGGATGCGGCGGAGC + 11 1
TCTGCTCGGATGCGGCGGAGT + 1 1
TCTGCTCGGATGCGGCGGAGT + 3 1
TCTGCTCGGATGCGGCGGAGT + 15 1
TCTGCTCGGATGCGGCGGAGT + 44 1
TCTGCTCGGATGCGGCGGAGT + 8 1
TCTGCTCGGATGCGGCGGAGT + 19 1
GTATTCAGATTTTCACAGCCG + 11 1
GTATTCAGATTTTCACAGCCG + 1 1
GTATTCAGATTTTCACAGCCG + 4 1
TATTCAGATTTTCACAGCCG + 3 1
TATTCAGATTTTCACAGCCG + 59 1
TATTCAGATTTTCACAGCCG + 721 1
TATTCAGATTTTCACAGCCG + 32 1
TATTCAGATTTTCACAGCCG + 33 1
TATTCAGATTTTCACAGCCG + 3 1
TATTCAGATTTTCACAGCCG + 1 1
TTCAGATTTTCACAGCCG + 1 1
TTCAGATTTTCACAGCCG + 2 1
TTCAGATTTTCACAGCCG + 1 1

0.0000 L X 4211411 4211490 - miR-303*
TGATATCTGTTTTAGTTTCACAGGAACTGGTTAATACGAAACTAGTTTCTTAAATCTTATCGAGAGTCA
TTAGTTTCACAGGAACTG + 1 1
TTAGTTTCACAGGAACTG + 4 1
TTAGTTTCACAGGAACTG + 2 1
TTAGTTTCACAGGAACTG + 1 1
TTAGTTTCACAGGAACTG + 4 1

TAGTTTCACAGGAACTGTT + 4 1
TAGTTTCACAGGAACTGTT + 53 1
TAGTTTCACAGGAACTGTT + 7 1
TAGTTTCACAGGAACTGTT + 2 1
GTTTCACAGGAACTGTT + 1 1
TTTCACAGGAACTGTT + 2 1
ACTAGTTTCTCTTAAATCTCTA + 1 1
CTAGTTTCTCTTAAATCTCTA + 2 1
CTAGTTTCTCTTAAATCTCTA + 7 1
CTAGTTTCTCTTAAATCTCTA + 11 1
CTAGTTTCTCTTAAATCTCTA + 9 1
TAGTTTCTCTTAAATCTCTA + 2 1
TAGTTTCTCTTAAATCTCTA + 1 1