

length	sequence	Neonate	Gut	Gut normalized to Neonate reads by x 3.35	Pupa	Pupa normalized to Neonate reads by x 2.5	Dm_HaMiRNAs_miR-id	Bm_HaMiRNAs_miR-id	Ap_miR-id	tcas_miR-id	aga_miR-id
19	CGACGTGGTAGAAGCGGGC	0	3	10.05	0	0					
22	CGACTTTACTATGACAGATGTA	301	108	361.8	690	1725					
24	CGTACAACCTCCCGCGTATCCGGT	1163	503	1685.05	7	17.5					
22	CGTACACTTTGGAAAAGTCCGA	65	0	0	6	15					
20	CGTGTCCGCCGAGCAGGAGC	2	0	0	0	0					
22	CTAAGTACTAGTGCCGAGGAG	92	0	0	15	37.5	dme-miR-252		Ap-mir-252		
22	CTAGCACTGTGGCTGTACTGT	1	2	6.7	2	5					
21	CTCATCGGCAACATCGGAGCT	2408	4962	16622.7	3765	9412.5					
22	CTCCCTAATCGAGTCAGGTGA	2	0	0	0	0					
22	CTCTCTCGCCTCCATGACCTGA	5	0	0	0	0					
19	CTGCAAACTTTTAGTCGGC	9	37	123.95	0	0					
22	CTGCTGCGTCCGGACAAGCGGG	32	6	20.1	2	5					
20	CTTAGGTGGATTTCCGGCGT	4	8	26.8	1	2.5					
23	CTTGCACTGGGAGAAATTCACAG	35	0	0	11	27.5	dme-miR-263b	bmo-miR-263b	Ap-mir-263b		aga-miR-263b
23	CTTGGTTTGGAAATCGCCTATGAT	13	1	3.35	6	15					
22	GAAGGTACGGAAAGCAGACTCC	5	13	43.55	8	20					
21	GAATTATTCGTTGGCAGACGA	1	0	0	0	0					
21	GACCCGGCCTTTGGACTGTAC	2	3	10.05	0	0					
23	GACCCGTACTTCCGGAGGACAT	14	14	46.9	2	5					
22	GAGCATCAGTTGGACTACGCGC	1	1	3.35	0	0					
22	GAGCCTCGGACAAGTCGGTAT	21	1	3.35	0	0					
19	GATCCGGCTCGAAGGACCA	9	45	150.75	157	392.5					
21	GATGTTTGGGAATCGATGGC	1	9	30.15	0	0					
22	AAGAGAGCTATCCGTCGACAGT	814	824	2760.4	89	222.5			Ap-mir-X7		
20	GCCGCCGGGATCGGCCACA	52	8	26.8	0	0					
23	GGCAAAGCGATCATCGTTGGAC	1	4	13.4	0	0					
24	GGCACTTGTCTTGGAAATGGGGAAC	3	3	10.05	0	0					
20	GGCTACTAGCGCTTGTGCGC	0	1	3.35	0	0					
23	GGGGATGTAACCTCAGTGGTAGAG	182	7	23.45	0	0					
20	GGGGATGTAGCTCAGTGGTA	108	255	854.25	6	15					
20	GGGGCGCGCAGGAACACCTA	0	21	70.35	0	0					
24	GGGGCGGTAGCTCAGATGGTAGAG	1929	121	405.35	92	230					
21	GGTAACTCCACCACCGTTGGC	0	0	0	25	62.5					
20	GGTGAATGCCAACGGATTTT	5	14	46.9	0	0					
24	GGTGCACTCACTGGCTCCGGAACC	1	0	0	0	0					
21	GGTTAACTATACGCGGACGAC	0	6	20.1	0	0					
19	GGTTCAAGTTTCGTCGTGAC	3	11	36.85	0	0					
23	GTAAGTTTCGTCGTTCGGC	1	9	30.15	0	0					
22	AAGGCCACGTAGGTACGTGCA	3	1	3.35	0	0					
20	GTAGCGCGTACGTGAGTGT	31	0	0	0	0					
19	GTCAAGTGGACCGGAGAA	1	0	0	0	0					
22	GTCAGTCAAGAGATCGATCGGC	4	2	6.7	0	0					
23	GTCGGTGACGATCGTTGGGAC	2	9	30.15	0	0					
22	GTGAGCAAATTTTAGGTTGTGT	26	10	33.5	0	0					
21	GTGCATTGTAGTTGCATTGCA	8	588	1969.8	25	62.5				tca-miR-33	
22	GTGCGAAGCAGCTATCGTCGCGC	1	3	10.05	0	0					
22	GTGTGTGGACTACGCGGGCGGA	1	0	0	0	0					
24	GTTAACTGTAGGTCCTCGCTGTC	14	1	3.35	0	0					
20	GTTGAGTGATGACGTAGCGG	3	0	0	0	0					
21	GTTGTTGGACCTTGAAGCGGC	2	4	13.4	0	0					
22	GTTTGTAAGCAGGAGAATTTT	0	3	10.05	0	0					
19	GTTTTCATAAAACGACTGT	0	15	50.25	0	0					
22	TAAATTCGTGAAATCGGACGTT	3005	4244	14217.4	749	1872.5					
21	TAAGGCACCGGTGAATGCCA	498	24	80.4	63	157.5	dme-miR-124	bmo-miR-124	Ap-mir-124	tca-miR-124	aga-miR-124
22	TAAGTAGATTTTGTGATTT	6	0	0	0	0					
24	TAATGTCACTTTGACGGCAAACCA	3	1	3.35	0	0					
22	TACCCTGTAGATCCGAATTTGT	2127	118	395.3	485	1212.5	dme-miR-10	bmo-miR-10	Ap-mir-10	tca-miR-10	aga-miR-10
23	TACCCTGTAGATCCGGCTTTTG	1996	0	0	38	95			Ap-mir-10c		
23	TACCCTGTAGGGCCATGTGGGAT	42	9	30.15	10	25					
23	TACGCAAGCGGTGTGGCTGTCT	0	10	33.5	0	0					
22	TACTGGCCTGCTAAGTCCCAAG	2	0	0	16	40					
22	TAGCACCATGGGATTCAGCTCA	271	37	123.95	40	100					
22	TAGCACCAATCGAATTCAGTGC	163	4	13.4	54	135	dme-miR-285	bmo-miR-285			
22	TAGCCTCTCCTTGGCTTTGTCT	15	1	3.35	2	5				tca-miR-282	
23	TAGCTCAGTCGATATGTATAGCA	1	0	0	0	0					
22	TATCACAGCCACTTTGATGTGG	10	3	10.05	1	2.5					
21	TATCACAGCCAGCTTTGATGA	37	26	87.1	14	35	dme-miR-2a	bmo-miR-13a	Ap-mir-13a	tca-miR-13a	
23	TATCACAGCCAGCTTTGTTGACT	27	8	26.8	9	22.5		bmo-miR-2a	Ap-mir-2a-1a	tca-miR-2	aga-miR-2
23	TATTTCGAGACCTCTGCTGATCCT	77	748	2505.8	28	70		bmo-miR-2b	Ap-mir-2a-1b		
22	TATTGCACCAGTCCGGCCTAT	41	12	40.2	11	27.5					
22	TATTGCTTGAGAATACACGTAG	15	4	13.4	0	0					
22	TATTTGCGACTGTAGTTGGTC	6	0	0	0	0					
21	TCAATTCGCTAGTGACATTGCA	7	1	3.35	0	0	dme-miR-137	bmo-miR-137	Ap-mir-137	tca-miR-137	aga-miR-137
24	TCACAGTCCGATCGCGGGATTAG	10	1	3.35	0	0	dme-miR-932	bmo-miR-932		tca-miR-932	

21	TCCTATGACTTCAAGTAATG	0	2	6.7	0	286	0
22	TCCTGAGACCCTAACTTGTGA	9	0	0	0	0	0
20	TTGGTCCCTTCAACCAGCA	1	0	0	0	0	0
24	TATCACAGCCATTTTTGACGAGTT	27	1	3.35	0	0	0
21	TCAGTCTTTTTCTCTCTCCTA	24	18	60.3	5	5	5
22	TGGACGGAGAACTGATAAGGGT	79	9	30.15	20	20	20
23	GGACGGAGAACTGATAAGGGCTT	0	0	0	3	3	3
24	GCCAACGTCACATACCATGTTGAAA	1	0	0	0	0	0
22	TTGTGCGTGTGACAGCGTTAT	0	0	0	1	1	1
23	TGATTGTCCAACGCAATTCTCG	0	0	0	10	10	10
24	AATGGCACTGAAAGAATTCACGGG	7	0	0	0	0	0
23	TCAGGTACCTGAAGTAGCGCGC	73	3515	11775.25	2698	2698	2698
21	TCAGGTACCTGAAGTAGCGCG	22	3449	11554.15	374	374	374
22	TCAGGTACCTGAAGTAGCGCGC	9	823	2757.05	162	162	162
21	TAGGAACATTCATACCGTGCTC	495	437	1463.95	108	108	108
23	TAGGAACATTCATACCGTGCTCTT	133	144	482.4	58	58	58
23	TAAATGCACTATCTGGTACGACA	74	26	87.1	16	16	16
22	TGCCTAGATCCACACTCATCCA	0	0	0	2	2	2
22	CTGTCATGGAGTTGCTCTCTTT	5	23	77.05	3	3	3
22	TCACAGCCAGCTTTGATGAGCA	132	51	170.85	42	42	42
22	TGTACTTCATCAGGTGCTCTGG	0	1	3.35	0	0	0
23	TCACAACCTCCTTGAGTGAGCGA	9	10	33.5	4	4	4
23	TTTTGATTGTTGCTCAGAAGCGC	0	0	0	146	146	146
23	AGGCAAGAAGTCGGCATAGCTGA	11	9	30.15	1	1	1
22	TTTGTTGTTGCTCGGCTCGAGTTA	0	0	0	494	494	494
22	TGAAAGACATGGGTAGTGAGAT	0	0	0	56	56	56
23	TAATACTGTCAAGTAAAGATGTC	605	250	837.5	900	900	900
21	AAATTGACTCTAGTAGGGAGT	2	0	0	0	0	0
23	TATTGCACTTGTCCCGCCTGTA	4	0	0	10	10	10
22	CTCGGCAGGACTGGGTGACGGC	0	3	10.05	0	0	0
20	CATAAGACACACGCGGCTCT	2	1	3.35	4	4	4
23	GAAGCTCGTCTTACAGGTATCT	596	0	0	7	7	7
23	TCITTTGGTATCCTAGCTGTAGAA	13	3	10.05	16	16	16
21	CGGTATACCTTCAGTATACGT	4	13	43.55	18	18	18
19	TATACTGAATGTATCCTGA	0	1	3.35	0	0	0
23	CAAATTCGGTTCTAGAGAGGTTT	2118	169	566.15	288	288	288
21	AGGCCGGCGGAAACTACTTGC	2	0	0	0	0	0

715	dme-miR-125	bmo-miR-12	tca-miR-125	aga-miR-125	ame-miR-125	
0	dme-miR-133	bmo-miR-133	tca-miR-133	aga-miR-133	ame-miR-133	
0		bmo-miR-13b				
12.5	dme-miR-14	bmo-miR-14	Ap-mir-14	tca-miR-14	aga-miR-14	ame-miR-14
50			Ap-mir-184a		aga-miR-184	
7.5			Ap-mir-184b			
0		bmo-miR-1925				
2.5	dme-miR-210	bmo-miR-210		tca-miR-210		ame-miR-210
25	dme-miR-219		Ap-mir-219	tca-miR-219	aga-miR-219	ame-miR-219
0			Ap-mir-228			
6745	dme-miR-275	bmo-miR-275	Ap-mir-275	tca-miR-275	aga-miR-275	ame-miR-275
935	dme-miR-275	bmo-miR-275	Ap-mir-275	tca-miR-275	aga-miR-275	ame-miR-275
405	dme-miR-275	bmo-miR-275	Ap-mir-275	tca-miR-275	aga-miR-275	ame-miR-275
270	dme-miR-276a		Ap-mir-276a	tca-miR-276	aga-miR-276-3p	ame-miR-276
145	dme-miR-276b		Ap-mir-276a	tca-miR-276	aga-miR-276-3p	ame-miR-276
40	dme-miR-277	bmo-miR-277	Ap-mir-277	tca-miR-277	aga-miR-277	ame-miR-277
5			Ap-mir-279a	tca-miR-279b		
7.5		bmo-miR-281	Ap-mir-281	tca-miR-281		ame-miR-281
105	dme-miR-2c	bmo-miR-2a	Ap-mir-2a-1a	tca-miR-2	aga-miR-2	ame-miR-2
0	dme-miR-305	bmo-miR-305	Ap-mir-305	tca-miR-305	aga-miR-305	ame-miR-305
10	dme-miR-307	bmo-miR-307	Ap-mir-307	tca-miR-307	aga-miR-307	
365	dme-miR-315		Ap-mir315	tca-miR-315	aga-miR-315	ame-miR-315
2.5	dme-miR-31a	bmo-miR-31		tca-miR-31a		ame-miR-31a
1235					aga-miR-375	ame-miR-375
140		bmo-miR-71	Ap-mir-71	tca-miR-71		ame-miR-71
2250	dme-miR-8	bmo-miR-8	Ap-mir-8	tca-miR-8	aga-miR-8	ame-miR-8
0		bmo-miR-929	Ap-mir-929	tca-miR-929		ame-miR-929
25	dme-miR-92a			tca-miR-92b	aga-miR-92a	ame-miR-92a
0						ame-miR-931
10	dme-miR-970			tca-miR-970	aga-miR-970	
17.5	dme-miR-993			tca-miR-993		
40	dme-miR-9c				aga-miR-9c	
45	dme-miR-lab-4-3p	bmo-miR-lab-4-3p		tca-miR-lab-4-3p		
0	dme-miR-lab-4-5p	bmo-miR-lab-4-5p		tca-miR-lab-4-5p	aga-miR-lab-4	ame-miR-lab-4
720			Ap-mir-X3			
0			Ap-mir-X64			