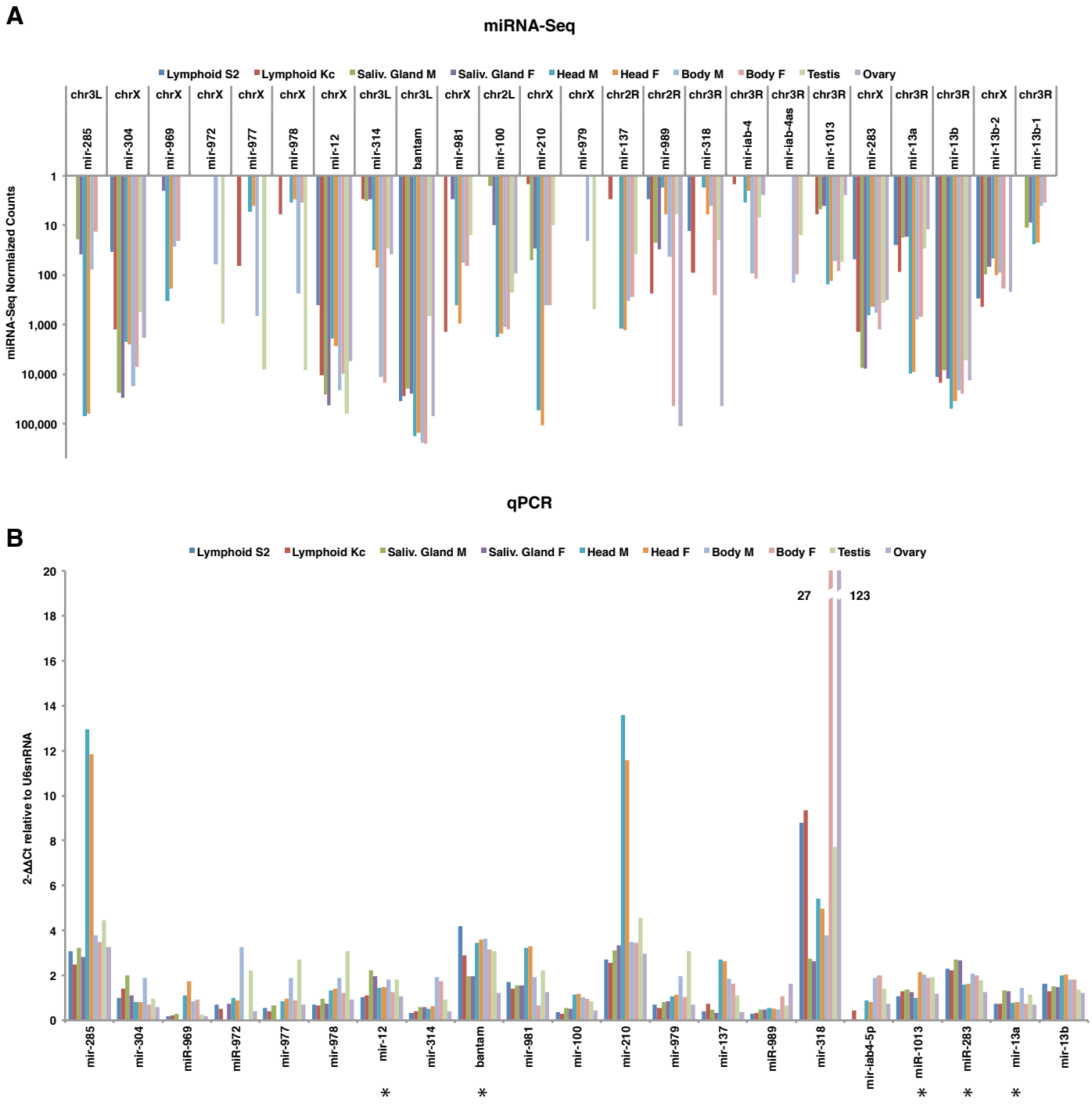

FIGURE S1: **qPCR validation of the expression levels of 22 miRNAs across all samples**. The trends of miRNA expression levels and relative abundance across all samples by miRNA-Seq (A) and qPCR (B) are similar for 16 miRNAs. Five additional miRNAs showing differences between miRNA-Seq and qPCR trends in one or more tissues (miR-12, bantam, miR-1013, miR-283, and miR-13a) are denoted with an asterisk. The genome presents several copies of mature miR-13b undistinguishable by qPCR: mir-13b and mir-13b-1 on chr3R, and mir-13b-2 on chrX. MiRNA normalized reads are reported in (A). qPCR assays were performed with at least two independent biological replicates and gave similar trends in (B). M: male ; F: female.

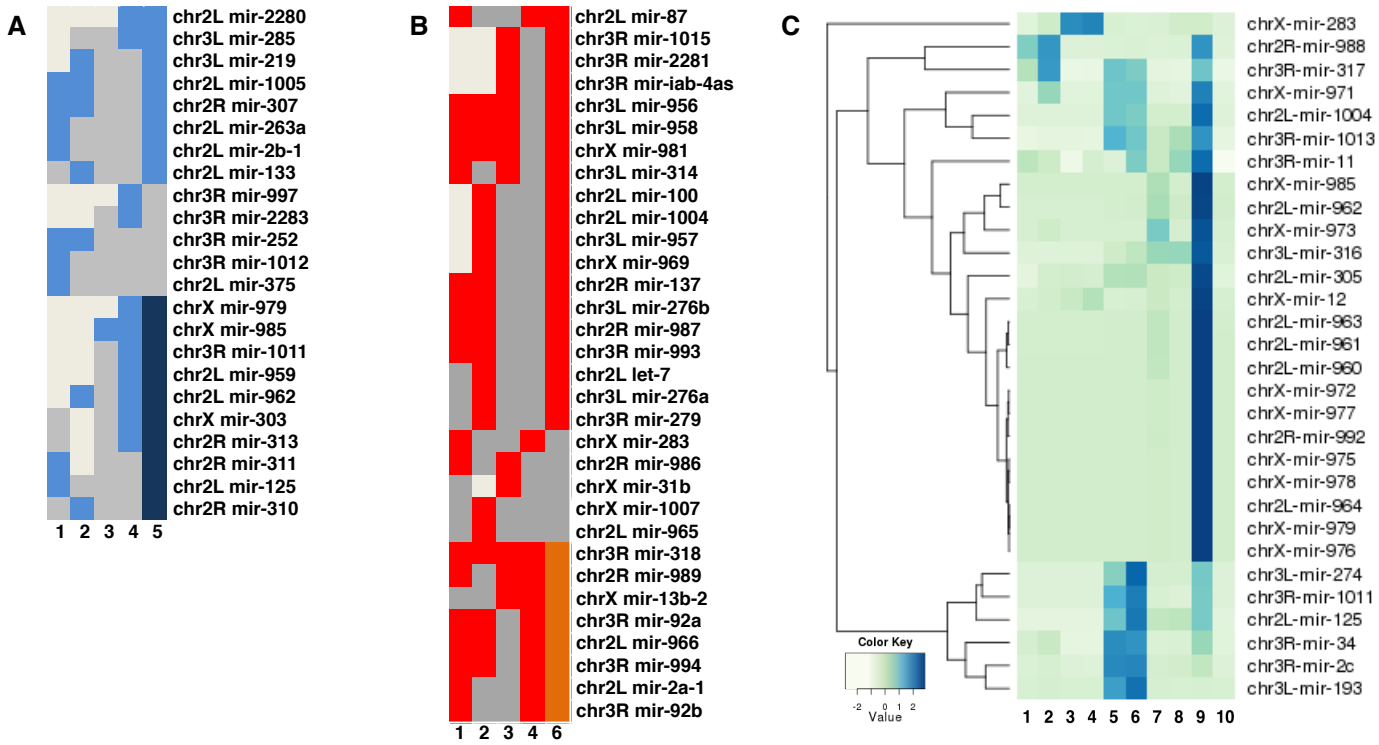

Figure S2: Male-enriched, female-enriched and X-linked testis-enriched miRNAs. (A) 23 miRNAs enriched in male somatic tissues in pairwise comparisons of S2 vs. Kc cells (1), male vs. female salivary glands (2), heads (3), and decapitated body (4). Colors indicate male-enriched miRNAs (light blue), miRNAs present at similar levels in both sexes (grey), poorly expressed miRNAs (white) and whether these miRNAs are more abundant in the male body (light blue) or testis (dark blue) in (5). (B) 32 female-enriched miRNAs in somatic tissues. Colors indicate female-enriched miRNAs (red), miRNAs present at similar levels in both sexes (grey), poorly expressed miRNAs (white) in somatic tissues [tissues (1) to (4) as in (A)], and whether these miRNAs are more abundant in the female body (red) or ovary (orange) in (6). (C) Relative abundance across all sexed tissues of the 30 miRNAs enriched exclusively in testis compared to the male body and not enriched in ovaries in females. 11 of the 30 testis-enriched miRNAs reside on the X chromosome. These miRNAs are highly and almost exclusively expressed in testis. S2 cells (1), Kc cells (2), male (3) and female (4) salivary glands, heads [male (5), female (6)], body [male (7), female (8)], testis (9), ovary (10).

TABLE S1: PCR primers used in this study

2S rRNA depletion:

5'-AGTCTTACAACCCTCAACCATATGTAGTCCAAGCAGCACT-3'

qPCR (miScript assay):

bantam-fwd	5'-GAGATCATTTTGAAAGCTGATT-3'	
miR-12-fwd	5'-GAGTATTACATCAGGTACTGGT-3'	
mir-13b-1-2-fwd	5'-TATCACAGCCATTTTGACGAGT-3'	
mir-13a-fwd	5'-TATCACAGCCATTTTGATGAGT-3'	
mir-283-fwd	5'-TAAATATCAGCTGGTAATTCT-3'	
mir-304-fwd	5'-AATCTCAATTTGTAAATGTGAG-3'	
mir-210-fwd	5'-TTGTGCGTGTGACAGCGGCTA-3'	
mir-iab-4-5p-fwd	5'-ACGTATACTGAATGTATCCTGA-3'	
mir-iab-4-3p-fwd	5'-GTATACCTTCAGTATACGTAAC-3'	
mir-318-fwd	5'-TCACTGGGCTTTGTTTATCTCA-3'	
mir-985-fwd	5'-CAAATGTTCCAATGGTCGGGCA-3'	
mir-979-fwd	5'-TTCTTCCCGAACTCAGGCTAA-3'	
mir-981-fwd	5'-TTCGTTGTCGACGAAACCTGCA-3'	
mir-977-fwd	5'-TGAGATATTCACGTTGTCTAA-3'	
mir-285-fwd	5'-TAGCACCATTCGAAATCAGTGC-3'	
mir-969-fwd	5'-GAGTTCCACTAAGCAAGTTTT-3'	
mir-972-fwd	5'-TGTACAATACGAATATTTAGGC-3'	
mir-978-fwd	5'-TGTCCAGTGCCGTAAATTGCAG-3'	
mir-314-fwd	5'-TATTCGAGCCAATAAGTTCGG-3'	
mir-100-fwd	5'-AACCCGTAAATCCGAACTTGTG-3'	
mir-137-Fwd	5'-TATTGCTTGAGAATACACGTAG-3'	
mir-989-fwd	5'-ATGTGATGTGACGTAGTGGAAC-3'	
mir-1013-fwd	5'-AATAAAAGTATGCCGAACTCG-3'	
mir-Spike-fwd	5'-CTCAGGATGGCGGAGCGGTGT-3'	external reference
U6snRNA-fwd	5'-ATTGGAACGATACAGAGAAGATTAG-3'	reference
Dspt-4-fwd	5'-TTGACGCGATACCCAAGGAT-3'	reference
Dspt4-rev	5'-CTAGTGTGATCATAGACATTGTCCTTGTT-3'	

qPCR on sex-specific transcripts:

RpL32-fwd	5'-AAGATGACCATCCGCCCAGC-3'	endogenous control
RpL32-rev	5'-GTCGATACCCTTGGGCTTGC-3'	
Esg-fwd	5'-CGCCCATGAGATCTGAAATC-3'	
Esg rev	5'-GGTCTTGTCACAATCCTTGC-3'	(Chau *et al.* 2009)
DsxM fwd	5'-TCCTTGGGAGCTGATGCCAC-3'	
DsxM rev	5'-GGCTACAGTGCGATTTATT-3'	
Yp1-fwd	5'-TGAGCGTCTGGAGAACATGAA-3'	
Yp1-rev	5'-GCGACAGGTGGTAGACTTGCT-3'	
tra1-fwd	5'-GGAACCCAGCATCGAGATTC-3'	
tra1-rev	5'-ATCGCCCATGGTATTCTCTTTC-3'	
Sxl-fwd	5'-ACAACGACAGCAGCAGGCCA-3'	
Sxl-rev	5'-TTGTAACCACGACGCGACGAT-3'	(Hashiyama *et al.* 2011)

TABLE S2: Late embryo-derived Lymphoid S2 (male) and Kc (female) cells biased miRNAs

S2 biased

chrom	miRNA	S2 reads	Kc reads	M/M+F	F/M+F	Sum reads	% miRNA
chr3R	dme-mir-252	13294	205	0.98479	0.01521	**13499**	1.1771
chr2R	dme-mir-307	932	33	0.96584	0.03416	**965**	0.0841
chr2L	dme-mir-263a	66	4	0.93623	0.06377	**70**	0.0061
chrX	dme-mir-980	1534	453	0.77219	0.22781	**1987**	0.1732
chr3L	dme-mir-282	13543	4622	0.74557	0.25443	**18165**	1.5839
chr2R	dme-mir-311	8	3	0.72746	0.27254	**11**	0.001
chr3R	dme-mir-1012	164	63	0.72266	0.27734	**227**	0.0198
chr2L	dme-mir-2b-1	498	207	0.70658	0.29342	**705**	0.0615
chr2L	dme-mir-125	10	4	0.68986	0.31014	**14**	0.0013
chr2R	dme-mir-286	43	21	0.67209	0.32791	**64**	0.0056

Kc biased

chrom	miRNA	S2	Kc reads	M/M+F	F/M+F	Sum reads	% miRNA
chrX	dme-mir-971	0	52	0	1	**52**	0.0046
chrX	dme-mir-973	0	12	0	1	**12**	0.001
chrX	dme-mir-982	0	16	0	1	**16**	0.0014
chrX	dme-mir-981	1	1427	0.00070	0.99930	**1428**	0.1245
chr3R	dme-mir-1000	1	1299	0.00077	0.99923	**1300**	0.1134
chr3R	dme-mir-92a	13	2215	0.00584	0.99416	**2228**	0.1943
chr3R	dme-mir-1010	1	106	0.00931	0.99069	**107**	0.0094
chr2R	dme-mir-989	3	237	0.01251	0.98749	**240**	0.0209
chrX	dme-mir-977	1	66	0.01494	0.98506	**67**	0.0058
chr3L	dme-mir-276b	5	187	0.02600	0.97400	**192**	0.0168
chrX	dme-mir-304	34	1260	0.02627	0.97373	**1294**	0.1129
chr2L	dme-mir-932	5	177	0.02750	0.97250	**182**	0.0159
chr2R	dme-mir-278	47	1647	0.02775	0.97225	**1694**	0.1477
chr3R	dme-mir-92b	20	670	0.02899	0.97101	**690**	0.0602
chr3L	dme-mir-193	3	96	0.03033	0.96967	**99**	0.0086
chrX	dme-mir-283	48	1394	0.03330	0.96670	**1442**	0.1257
chr3L	dme-mir-958	1	28	0.03393	0.96607	**29**	0.0026
chr3R	dme-mir-10	1	27	0.03575	0.96425	**28**	0.0024
chrX	dme-mir-12	415	10569	0.03778	0.96222	**10984**	0.9578
chr2R	dme-mir-986	3	43	0.06457	0.93543	**46**	0.0041
chr2L	dme-mir-124	8	94	0.07812	0.92188	**102**	0.0089
chr4	dme-mir-954	11	91	0.10741	0.89259	**102**	0.0089
chr3R	dme-mir-994	5	40	0.10998	0.89002	**45**	0.004
chr2R	dme-mir-8	4003	27812	0.12582	0.87418	**31815**	2.7742
chr3R	dme-mir-318	13	90	0.12632	0.87368	**103**	0.009
chr2L	dme-mir-9b	2463	11885	0.17166	0.82834	**14348**	1.2511
chr2L	dme-mir-2a-2	2015	9699	0.17202	0.82798	**11714**	1.0214
chrX	dme-mir-984	25	102	0.19700	0.80300	**127**	0.0111
chr2L	dme-mir-966	15	58	0.20424	0.79576	**73**	0.0064
chr2L	dme-mir-2b-2	431	1648	0.20727	0.79273	**2079**	0.1813
chr2L	dme-mir-2a	7839	29779	0.20838	0.79162	**37618**	3.2803
chr2R	dme-mir-31a	5	18	0.21756	0.78244	**23**	0.002

chr2L	dme-mir-1	23	82	0.21817	0.78183	**105**	0.0092
chr3R	dme-mir-13a	25	85	0.22641	0.77359	**110**	0.0096
chr3L	dme-mir-276	4524	15417	0.22687	0.77313	**19941**	1.7389
chr2L	dme-mir-305	3321	10310	0.24364	0.75636	**13631**	1.1886
chr2R	dme-mir-312	3	9	0.25018	0.74982	**12**	0.001
chr2L	dme-mir-9c	1896	5648	0.25132	0.74868	**7544**	0.6578
chr2R	dme-mir-1008	94	262	0.26386	0.73614	**356**	0.0311
chr2L	dme-mir-275	461	1247	0.26994	0.73006	**1708**	0.1489
chr3L	dme-mir-190	171	462	0.27033	0.72967	**633**	0.0552
chr2L	dme-mir-79	2043	5420	0.27374	0.72626	**7463**	0.6508
chr3L	dme-mir-9a	49	124	0.28262	0.71738	**173**	0.0151
chr2L	dme-mir-1006	58	145	0.28521	0.71479	**203**	0.0177
chr2L	dme-mir-306	2500	6128	0.28977	0.71023	**8628**	0.7523
chr3R	dme-mir-317	9157	21083	0.30281	0.69719	**30240**	2.6369
chr3R	dme-mir-999	247	560	0.30590	0.69410	**807**	0.0704
chr2R	dme-mir-1009	4	9	0.30790	0.69210	**13**	0.0011
chrX	dme-mir-983	6	13	0.30790	0.69210	**19**	0.0017
chr2L	dme-mir-2a-1	173	388	0.30831	0.69169	**561**	0.0489
chr3R	dme-mir-2c	9	19	0.31600	0.68400	**28**	0.0025
chr3L	dme-mir-33	1927	4040	0.32294	0.67706	**5967**	0.5203
chr2L	dme-mir-2b	9981	20837	0.32387	0.67613	**30818**	2.6874
chr2R	dme-mir-184	54062	109778	0.32997	0.67003	**163840**	14.2868

At least 10 normalized reads in the summed normalized reads were required. S2: Male (M); Kc: Female (F).
A ratio (F/M+F) >=0.66 is female biased. A ratio (M/M+F) >=0.66 is male biased.

TABLE S3: Male and female biased miRNAs in L3 larval salivary glands

Male biased

chrom	miRNA	Male S. Gland reads	Female S. Gland reads	M/M+F	F/M+F	Sum Reads	% miRNA
chr2L	dme-mir-275	21773	2588	0.89376	0.10624	**24361**	2.63097
chr2R	dme-mir-1009	8	2	0.80000	0.20000	**10**	0.00108
chr2R	dme-mir-278	1275	526	0.70797	0.29203	**1801**	0.19453
chr2L	dme-mir-133	10	4	0.70588	0.29412	**14**	0.00147
chr2L	dme-mir-1005	26	11	0.69945	0.30055	**37**	0.00395
chr3R	dme-mir-252	1330	644	0.67369	0.32631	**1974**	0.21315

Female biased

chrom	miRNA	Male S. Gland reads	Female S. Gland reads	M/M+F	F/M+F	Sum Reads	% miRNA
chr2L	dme-mir-100	2	10	0.13793	0.86207	**12**	0.00125
chr3L	dme-mir-282	6635	31936	0.17202	0.82798	**38571**	4.1657
chr2L	dme-let-7	48	219	0.17978	0.82022	**267**	0.02884
chr3R	dme-mir-279	514	1492	0.25608	0.74392	**2006**	0.21661
chr2L	dme-mir-965	210	567	0.26989	0.73011	**777**	0.08387
chr2R	dme-mir-987	14	36	0.28571	0.71429	**50**	0.00544
chr2L	dme-mir-305-as	3	7	0.31373	0.68627	**10**	0.0011
chr3R	dme-mir-92a	3	7	0.31373	0.68627	**10**	0.0011
chr3L	dme-mir-957	3	7	0.31373	0.68627	**10**	0.0011
chr2R	dme-mir-307-as	8	17	0.32000	0.68000	**25**	0.0027
chr3L	dme-mir-276a	1853	3728	0.33200	0.66800	**5581**	0.60273
chr3L	dme-mir-285	19	38	0.33566	0.66434	**57**	0.00618

At least 10 normalized reads in the summed normalized reads were required. M: male ; F: female.
A ratio (F/M+F) >=0.66 is female biased in salivary glands (S. glands). A ratio(M/M+F) >=0.66 is male biased.

TABLE S4: Male and female biased miRNAs in adult heads

Male biased

chrom	miRNA	Male Head reads	Female Head reads	M/M+F	F/M+F	Sum Reads	% miRNA
chrX	dme-mir-974	9	2	0.81405	0.18595	**11**	0.000247
chr3L	dme-mir-190	2189	634	0.77540	0.22460	**2823**	0.06472
chr2L	dme-mir-305-as	21	8	0.72426	0.27574	**29**	0.000665
chr3L	dme-mir-276	119752	58112	0.67328	0.32672	**177864**	4.077941
chr2R	dme-mir-1008	208	104	0.66707	0.33293	**312**	0.007162

Female biased

chrom	miRNA	Male Head reads	Female Head reads	M/M+F	F/M+F	Sum Reads	% miRNA
chr3L	dme-mir-958	5	29	0.15336	0.84664	**34**	0.000785
chrX	dme-mir-31b	12	44	0.21788	0.78212	**56**	0.00129
chr2L	dme-mir-964	12	41	0.23015	0.76985	**53**	0.001221
chr3L	dme-mir-956	7	20	0.25938	0.74062	**27**	0.000619
chrX	dme-mir-980	611	1464	0.29450	0.70550	**2075**	0.047577
chrX	dme-mir-981	404	968	0.29472	0.70528	**1372**	0.031468
chr3L	dme-mir-274	24301	55708	0.30373	0.69627	**80009**	1.834398
chr3L	dme-mir-314	32	72	0.30448	0.69552	**104**	0.002373
chr2L	dme-mir-961	9	20	0.30448	0.69552	**29**	0.000659
chr2L	dme-mir-963	9	20	0.30448	0.69552	**29**	0.000659
chr3R	dme-mir-284	907	2009	0.31105	0.68895	**2916**	0.066857
chr2R	dme-mir-286	7	15	0.31831	0.68169	**22**	0.000504
chr2L	dme-mir-275	1170	2503	0.31849	0.68151	**3673**	0.084205
chrX	dme-mir-13b-2	47	101	0.31885	0.68115	**148**	0.0034
chr2R	dme-mir-986	475	1006	0.32052	0.67948	**1481**	0.033945
chrX	dme-mir-210	54115	106957	0.33597	0.66403	**161072**	3.692947
chr3R	dme-mir-11	10872	21450	0.33637	0.66363	**32322**	0.741065
chr2L	dme-mir-960	53	103	0.33776	0.66224	**156**	0.003566
chr2L	dme-mir-133	8468	16473	0.33953	0.66047	**24941**	0.571834

At least 10 normalized reads in the summed normalized reads were required.

A ratio (F/M+F) >=0.66 is female biased in the head. A ratio(M/M+F) >=0.66 is male biased. F: female; M: Male.

TABLE S5: Male vs. female biased miRNAs in the adult body

Male body biased

chrom	miRNA	Male Body reads	Female Body reads	M/M+F	F/M+F	Sum Reads	% miRNA
chrX	dme-mir-972	61	0	1	0	**61**	0.001355886
chrX	dme-mir-975	33	0	1	0	**33**	0.000733512
chrX	dme-mir-977	680	0	1	0	**680**	0.015114796
chrX	dme-mir-979	21	0	1	0	**21**	0.00046678
chr3R	dme-mir-997	184	0	1	0	**184**	0.004089886
chrX	dme-mir-978	241	3	0.98597	0.01403	**244**	0.00543307
chrX	dme-mir-974	236	3	0.98568	0.01432	**239**	0.005321932
chrX	dme-mir-976	380	7	0.98227	0.01773	**387**	0.008598921
chr2L	dme-mir-959	478	10	0.97894	0.02106	**488**	0.010853439
chrX	dme-mir-303	142	3	0.97642	0.02358	**145**	0.003232534
chrX	dme-mir-985	214	7	0.96895	0.03105	**221**	0.004909133
chrX	dme-mir-983	724	24	0.96791	0.03209	**748**	0.016626275
chrX	dme-mir-984	551	24	0.95826	0.04174	**575**	0.012780893
chrX	dme-mir-973	76	3	0.95683	0.04317	**79**	0.00176551
chr2L	dme-mir-963	368	21	0.94706	0.05294	**389**	0.008637026
chr2R	dme-mir-991	120	7	0.94595	0.05405	**127**	0.002819735
chr2L	dme-mir-960	1717	117	0.93642	0.06358	**1834**	0.040755964
chr2R	dme-mir-992	45	3	0.92920	0.07080	**48**	0.001076453
chr2L	dme-mir-964	437	34	0.92725	0.07275	**471**	0.010475569
chrX	dme-mir-982	118	10	0.91982	0.08018	**128**	0.002851489
chr2L	dme-mir-961	177	17	0.91170	0.08830	**194**	0.004315337
chr3L	dme-mir-285	76	14	0.84713	0.15287	**90**	0.001994137
chr2R	dme-mir-1009	38	10	0.78698	0.21302	**48**	0.001073277
chr3L	dme-mir-193	12	3	0.77778	0.22222	**15**	0.000342941
chr2L	dme-mir-962	401	134	0.74993	0.25007	**535**	0.011885434
chrX	dme-mir-304	17186	7227	0.70396	0.29604	**24413**	0.542652738
chrX	dme-mir-12	21306	9603	0.68930	0.31070	**30909**	0.687043433
chr2R	dme-mir-313	59	27	0.68264	0.31736	**86**	0.001921103

Female body biased

chrom	miRNA	Male Body reads	Female Body reads	M/M+F	F/M+F	Sum Reads	% miRNA
chr2R	dme-mir-989	44	45010	0.00098	0.99902	**45054**	1.001449337
chr3R	dme-mir-318	4	261	0.01512	0.98488	**265**	0.005880792
chr3R	dme-mir-994	4	261	0.01512	0.98488	**265**	0.005880792
chr3R	dme-mir-92b	42	233	0.15265	0.84735	**275**	0.006115771
chr2L	dme-mir-966	5	21	0.19553	0.80447	**26**	0.000568392
chr2L	dme-mir-2a-1	21	75	0.21778	0.78222	**96**	0.002143378
chr3L	dme-mir-190	162	579	0.21850	0.78150	**741**	0.016480193
chr3L	dme-mir-276	47955	128270	0.27212	0.72788	**176225**	3.917056396
chr2L	dme-mir-275	1122	2616	0.30016	0.69984	**3738**	0.083086855
chr3R	dme-mir-92a	254	579	0.30477	0.69523	**833**	0.018525136
chrX	dme-mir-283	577	1245	0.31676	0.68324	**1822**	0.040489204
chrX	dme-mir-13b-2	92	189	0.32790	0.67210	**281**	0.006236436

chr2L	dme-mir-87	908	1834	0.33111	0.66889	**2742**	0.060954495

At least 10 normalized reads in the summed normalized reads were required.
A ratio (F/M+F) >=0.66 is female biased. A ratio (M/M+F) >=0.66 is male biased. F: female; M: male.

TABLE S6: Testis and Ovary biased miRNAs

Testis biased

chrom	miRNA	Testes reads	Ovary reads	T/Ov+T	Ov/T+Ov	Sum Reads	% miRNA
chr2L	dme-mir-1004	144	0	1	0	**144**	0.01472903
chr2R	dme-mir-137	38	0	1	0	**38**	0.003886827
chrX	dme-mir-210	10	0	1	0	**10**	0.001022849
chr3L	dme-mir-263b	13	0	1	0	**13**	0.001329704
chr3L	dme-mir-315	12	0	1	0	**12**	0.001227419
chr2L	dme-mir-375	1491	0	1	0	**1491**	0.152506835
chrX	dme-mir-971	33	0	1	0	**33**	0.003375403
chrX	dme-mir-972	961	0	1	0	**961**	0.098295821
chrX	dme-mir-973	51	0	1	0	**51**	0.005216532
chrX	dme-mir-974	82	0	1	0	**82**	0.008387364
chrX	dme-mir-975	2134	0	1	0	**2134**	0.218276047
chrX	dme-mir-976	7525	0	1	0	**7525**	0.76969412
chrX	dme-mir-977	8100	0	1	0	**8100**	0.828507956
chrX	dme-mir-978	8457	0	1	0	**8457**	0.865023677
chrX	dme-mir-979	497	0	1	0	**497**	0.050835612
chrX	dme-mir-981	16	0	1	0	**16**	0.001636559
chr2R	dme-mir-992	395	0	1	0	**395**	0.040402548
chr3R	dme-mir-997	59	0	1	0	**59**	0.006034811
chr3R	dme-mir-iab-4as	16	0	1	0	**16**	0.001636559
chr2L	dme-mir-959	17252	10	0.99943	0.00057	**17262**	1.765620246
chr2L	dme-mir-964	10115	12	0.99879	0.00121	**10127**	1.035862826
chr3L	dme-mir-274	7928	12	0.99846	0.00154	**7940**	0.812165678
chr2L	dme-mir-963	926	2	0.99737	0.00263	**928**	0.094965994
chr2L	dme-mir-960	5436	27	0.99508	0.00492	**5463**	0.558772501
chrX	dme-mir-985	321	2	0.99244	0.00756	**323**	0.033083609
chr3L	dme-mir-9a	6846	98	0.98591	0.01409	**6944**	0.710248489
chr2L	dme-mir-124	151	2	0.98406	0.01594	**153**	0.015695171
chr3R	dme-mir-277	9542	213	0.97819	0.02181	**9755**	0.997765528
chr2L	dme-mir-961	477	12	0.97501	0.02499	**489**	0.050040643
chr3R	dme-mir-1013	54	2	0.95667	0.04333	**56**	0.005773532
chr3R	dme-mir-252	990	51	0.95068	0.04932	**1041**	0.106515149
chr2L	dme-mir-133	38	2	0.93953	0.06047	**40**	0.004136973
chr2R	dme-mir-991	127	10	0.92848	0.07152	**137**	0.01399077
chr2R	dme-mir-988	6587	523	0.92640	0.07360	**7110**	0.727282088
chr2R	dme-mir-310	3356	289	0.92082	0.07918	**3645**	0.372785458
chrX	dme-mir-12	62228	5576	0.91776	0.08224	**67804**	6.935319591
chr2L	dme-mir-932	45	5	0.90196	0.09804	**50**	0.005103114
chr3R	dme-mir-1010	168	20	0.89569	0.10431	**188**	0.019185036
chr2R	dme-mir-278	2426	286	0.89450	0.10550	**2712**	0.277410324
chr3R	dme-mir-2c	19	2	0.88596	0.11404	**21**	0.00219356
chrX	dme-mir-983	6732	1010	0.86954	0.13046	**7742**	0.791892449
chr2R	dme-mir-311	3582	582	0.86022	0.13978	**4164**	0.425919368
chr2L	dme-mir-962	471	81	0.85372	0.14628	**552**	0.05643102
chr2L	dme-mir-125	3331	614	0.84439	0.15561	**3945**	0.403497747

chr3L	dme-mir-316	4417	814	0.84433	0.15567	**5231**	0.535091153
chr2L	dme-let-7	11559	2179	0.84139	0.15861	**13738**	1.405191589
chr2R	dme-mir-1008	11	2	0.81811	0.18189	**13**	0.00137528
chr3R	dme-mir-999	673	179	0.79034	0.20966	**852**	0.087098415
chr3R	dme-mir-317	4489	1294	0.77628	0.22372	**5783**	0.591484276
chr2L	dme-mir-305	18583	6588	0.73826	0.26174	**25171**	2.574654122
chr3L	dme-mir-956	54	22	0.71043	0.28957	**76**	0.0077747
chr2L	dme-mir-100	226	93	0.70861	0.29139	**319**	0.032621941
chr3R	dme-mir-13a	29	12	0.70341	0.29659	**41**	0.004216993
chrX	dme-mir-31b	875	416	0.67790	0.32210	**1291**	0.132024129

Ovary biased

chrom	miRNA	Testes reads	Ovary reads	T/Ov+T	Ov/T+Ov	Sum Reads	% miRNA
chr2R	dme-mir-989	6	111853	0.00005	0.99995	**111859**	11.44153945
chr3R	dme-mir-318	20	44135	0.00045	0.99955	**44155**	4.516429825
chr3R	dme-mir-994	19	18298	0.00104	0.99896	**18317**	1.873535481
chr2L	dme-mir-2b-1	2	460	0.00433	0.99567	**462**	0.04723201
chrX	dme-mir-13b-2	1	218	0.00457	0.99543	**219**	0.022365275
chr3R	dme-mir-996	348	36033	0.00957	0.99043	**36381**	3.72124572
chr3L	dme-bantam	687	69609	0.00977	0.99023	**70296**	7.190174187
chr2R	dme-mir-184	540	38992	0.01366	0.98634	**39532**	4.043561038
chr2R	dme-mir-1009	5	220	0.02221	0.97779	**225**	0.023024561
chr2L	dme-mir-965	9	355	0.02475	0.97525	**364**	0.037191728
chr2L	dme-mir-79	219	8506	0.02510	0.97490	**8725**	0.892408047
chr2L	dme-mir-263a	245	8899	0.02679	0.97321	**9144**	0.935340954
chr3L	dme-mir-33	166	5092	0.03157	0.96843	**5258**	0.537783186
chr2L	dme-mir-2b-2	40	1091	0.03538	0.96462	**1131**	0.115656495
chr2R	dme-mir-308	30	790	0.03659	0.96341	**820**	0.083865693
chr2L	dme-mir-275	605	15923	0.03660	0.96340	**16528**	1.690582725
chr3L	dme-mir-276	123	3194	0.03708	0.96292	**3317**	0.33927167
chr2R	dme-mir-281-2	21	430	0.04652	0.95348	**451**	0.046173672
chr3R	dme-mir-995	228	4654	0.04670	0.95330	**4882**	0.499348725
chr2L	dme-mir-1	241	3788	0.05981	0.94019	**4029**	0.41212676
chr2R	dme-mir-307	42	599	0.06551	0.93449	**641**	0.065581727
chr3R	dme-mir-998	84	986	0.07854	0.92146	**1070**	0.109400756
chr2L	dme-mir-87	12	139	0.07926	0.92074	**151**	0.015485739
chr2L	dme-mir-2a-1	13	149	0.08016	0.91984	**162**	0.016588608
chr2L	dme-mir-1005	3	34	0.08056	0.91944	**37**	0.003808898
chr2R	dme-mir-281-1	143	1277	0.10073	0.89927	**1420**	0.145202936
chr2L	dme-mir-966	6	51	0.10461	0.89539	**57**	0.005866775
chr2L	dme-mir-2a-2	112	829	0.11902	0.88098	**941**	0.096255393
chr3R	dme-mir-929	4	29	0.11995	0.88005	**33**	0.003410891
chr2R	dme-mir-313	370	1538	0.19389	0.80611	**1908**	0.195187234
chrX	dme-mir-1007	6	24	0.19701	0.80299	**30**	0.003115169
chr3R	dme-mir-284	16	56	0.22146	0.77854	**72**	0.007389916
chr2R	dme-mir-7	863	2981	0.22450	0.77550	**3844**	0.393199821
chr3L	dme-mir-190	13	44	0.22799	0.77201	**57**	0.005832331
chr2L	dme-mir-2b	6058	20095	0.23163	0.76837	**26153**	2.675091471

chr2L	dme-mir-2a	14216	47031	0.23211	0.76789	**61247**	6.264639548
chrX	dme-mir-304	556	1817	0.23430	0.76570	**2373**	0.24272887
chr2L	dme-mir-9c	2050	5715	0.26399	0.73601	**7765**	0.794275219
chr2L	dme-mir-306	951	2472	0.27779	0.72221	**3423**	0.350170536
chr3R	dme-mir-13b	5212	13392	0.28015	0.71985	**18604**	1.902908343
chr2R	dme-mir-986	309	736	0.29566	0.70434	**1045**	0.106899978
chr3R	dme-mir-1012	46	98	0.31984	0.68016	**144**	0.014710945
chr2R	dme-mir-312	1704	3546	0.32457	0.67543	**5250**	0.537005167
chr2L	dme-mir-9b	6727	13372	0.33469	0.66531	**20099**	2.055868849

At least 10 normalized reads in the summed normalized reads in male and female gonads are required.
A ratio (Testis/Ovary+Testis) >=0.66 is Testis biased. A ratio(Ovary/Ovary +Testis) >=0.66 is Ovary biased
T: Testis; Ov: Ovaries

TABLE S7: miRNAs with testis vs. male body biases

Male Body (male somatic tissues) biased miRNAs

chrom	miRNA	Male Body reads	Testis reads	BM/BM+T	Testis/BM+T	Sum reads	% miRNA
chr3R	dme-mir-1014	248	0	1	0	**248**	0.007666282
chr3L	dme-mir-285	76	0	1	0	**76**	0.002349344
chr2R	dme-mir-5	14	0	1	0	**14**	0.000432774
chrX	dme-mir-927	41	0	1	0	**41**	0.001267409
chr3L	dme-mir-957	839	0	1	0	**839**	0.025935526
chrX	dme-mir-969	27	0	1	0	**27**	0.000834636
chr2L	dme-mir-1	496888	844	0.99831	0.00169	**497732**	15.38608851
chr3R	dme-mir-993	1448	4	0.99759	0.00241	**1452**	0.044869387
chr3R	dme-mir-1000	875	4	0.99602	0.00398	**879**	0.027156567
chr3L	dme-mir-958	7379	32	0.99575	0.00425	**7411**	0.229076539
chr3R	dme-mir-929	1810	14	0.99232	0.00768	**1824**	0.056384267
chr3L	dme-mir-314	11627	102	0.99135	0.00865	**11729**	0.362556399
chr3L	dme-mir-276	47955	431	0.99110	0.00890	**48386**	1.495713233
chr3L	dme-bantam	244113	2405	0.99025	0.00975	**246518**	7.620454209
chr2L	dme-mir-2b-1	623	7	0.98889	0.01111	**630**	0.019474829
chr2R	dme-mir-987	803	11	0.98709	0.01291	**814**	0.025147259
chr2R	dme-mir-281-2	5100	74	0.98579	0.01421	**5174**	0.159925441
chr3L	dme-mir-276b	530	11	0.98057	0.01943	**541**	0.016708167
chr2L	dme-mir-965	1129	32	0.97286	0.02714	**1161**	0.035873872
chr2R	dme-mir-281-1	17602	501	0.97235	0.02765	**18103**	0.559592219
chr3R	dme-mir-10	19132	599	0.96967	0.03033	**19731**	0.609917652
chrX	dme-mir-13b-2	92	4	0.96335	0.03665	**96**	0.002952137
chr3L	dme-mir-263b	1144	46	0.96175	0.03825	**1190**	0.036770333
chr3R	dme-mir-996	29997	1218	0.96098	0.03902	**31215**	0.964931435
chr3L	dme-mir-219	84	4	0.96000	0.04000	**88**	0.002704837
chr3L	dme-mir-956	4342	189	0.95829	0.04171	**4531**	0.140064211
chr2L	dme-mir-87	908	42	0.95579	0.04421	**950**	0.029366807
chr2R	dme-mir-308	1864	105	0.94667	0.05333	**1969**	0.060866571
chr3L	dme-mir-33	9633	581	0.94312	0.05688	**10214**	0.315739544
chr2L	dme-mir-79	12143	767	0.94063	0.05937	**12910**	0.399063995
chr3R	dme-mir-1001	106	7	0.93805	0.06195	**113**	0.003493104
chr2R	dme-mir-307	2063	147	0.93348	0.06652	**2210**	0.068316467
chr2L	dme-mir-263a	11829	858	0.93241	0.06759	**12687**	0.392170527
chrX	dme-mir-210	409	35	0.92117	0.07883	**444**	0.013725119
chr2L	dme-mir-1005	122	11	0.92075	0.07925	**133**	0.004095897
chr3L	dme-mir-276a	90583	7868	0.92008	0.07992	**98451**	3.043359558
chr3R	dme-mir-284	523	56	0.90328	0.09672	**579**	0.017898297
chr3R	dme-mir-1015	62	7	0.89855	0.10145	**69**	0.002132958
chrX	dme-mir-304	17186	1946	0.89829	0.10171	**19132**	0.591416607
chr2R	dme-mir-184	15336	1890	0.89028	0.10972	**17226**	0.53249752
chr2L	dme-mir-133	1065	133	0.88898	0.11102	**1198**	0.037033091
chr2L	dme-mir-1006	415	53	0.88770	0.11230	**468**	0.014451561
chr3R	dme-mir-13a	797	102	0.88703	0.11297	**899**	0.027774818
chr3R	dme-mir-1017	25	4	0.87719	0.12281	**29**	0.000881004

chr2R	dme-mir-31a	24842	3969	0.86224	0.13776	**28811**	0.890618047
chrX	dme-mir-980	2995	539	0.84748	0.15252	**3534**	0.109244532
chr2L	dme-mir-124	2863	529	0.84417	0.15583	**3392**	0.104839511
chr2L	dme-mir-2b-2	615	140	0.81457	0.18543	**755**	0.023338886
chr3R	dme-mir-iab-4	94	25	0.79325	0.20675	**119**	0.003663123
chr3R	dme-mir-998	1074	294	0.78509	0.21491	**1368**	0.042288209
chr3L	dme-mir-190	162	46	0.78072	0.21928	**208**	0.00641433
chr2R	dme-mir-1008	106	39	0.73356	0.26644	**145**	0.004466847
chr3R	dme-mir-279	14571	5439	0.72819	0.27181	**20010**	0.618557825
chr2L	dme-mir-2a-2	1047	392	0.72759	0.27241	**1439**	0.044482994
chr3R	dme-mir-iab-4as	144	56	0.72000	0.28000	**200**	0.006182487
chr2R	dme-mir-137	341	133	0.71941	0.28059	**474**	0.014652494
chr3L	dme-mir-955	59	25	0.70659	0.29341	**84**	0.002581188
chr3R	dme-mir-277	76053	33397	0.69487	0.30513	**109450**	3.383366128
chr2R	dme-mir-8	447346	198170	0.69301	0.30699	**645516**	19.95447212
chrX	dme-mir-1007	47	21	0.69118	0.30882	**68**	0.002102046
chr2R	dme-mir-1009	38	18	0.68468	0.31532	**56**	0.00171564
chr2R	dme-mir-989	44	21	0.67692	0.32308	**65**	0.002009308

Testis enriched miRNAs

chrom	miRNA	Male Body reads	Testis reads	BM/BM+T	Testis/BM+T	Sum Reads	% miRNA
chrX	dme-mir-975	33	7469	0.00440	0.99560	**7502**	0.231905256
chr2R	dme-mir-310	55	11746	0.00466	0.99534	**11801**	0.36479791
chr2R	dme-mir-311	68	12537	0.00539	0.99461	**12605**	0.389651525
chr2L	dme-mir-959	478	60382	0.00785	0.99215	**60860**	1.881332152
chrX	dme-mir-978	241	29600	0.00808	0.99192	**29841**	0.922443182
chrX	dme-mir-979	21	1740	0.01193	0.98807	**1761**	0.054421381
chr2L	dme-mir-964	437	35403	0.01219	0.98781	**35840**	1.107887009
chrX	dme-mir-976	380	26338	0.01422	0.98578	**26718**	0.825903573
chr2R	dme-mir-312	95	5964	0.01568	0.98432	**6059**	0.187298577
chr3R	dme-mir-92b	42	2615	0.01581	0.98419	**2657**	0.082118942
chrX	dme-mir-972	61	3364	0.01781	0.98219	**3425**	0.105859709
chrX	dme-mir-977	680	28350	0.02342	0.97658	**29030**	0.897388622
chrX	dme-mir-983	724	23562	0.02981	0.97019	**24286**	0.750739922
chr2R	dme-mir-992	45	1383	0.03152	0.96848	**1428**	0.044127532
chrX	dme-mir-971	4	116	0.03347	0.96653	**120**	0.003694039
chr2R	dme-mir-988	876	23055	0.03661	0.96339	**23931**	0.739750538
chr2R	dme-mir-313	59	1295	0.04357	0.95643	**1354**	0.041855466
chr3R	dme-mir-92a	254	4984	0.04849	0.95151	**5238**	0.161919445
chr3R	dme-mir-318	4	70	0.05405	0.94595	**74**	0.002287522
chr3R	dme-mir-994	4	67	0.05674	0.94326	**71**	0.002179328
chr2R	dme-mir-3	2	28	0.06667	0.93333	**30**	0.000927374
chrX	dme-mir-984	551	7704	0.06675	0.93325	**8255**	0.255166864
chr2L	dme-mir-1004	44	504	0.08029	0.91971	**548**	0.016940025
chr2L	dme-mir-960	1717	19026	0.08277	0.91723	**20743**	0.641217054
chr3R	dme-mir-1011	1	11	0.08696	0.91304	**12**	0.000355493
chrX	dme-mir-12	21306	217798	0.08911	0.91089	**239104**	7.391291592
chr2L	dme-mir-961	177	1670	0.09586	0.90414	**1847**	0.057079847

chr2L	dme-mir-963	368	3241	0.10197	0.89803	**3609**	0.111563048
chr3L	dme-mir-274	3593	27748	0.11464	0.88536	**31341**	0.968827221
chr3R	dme-mir-317	2370	15712	0.13107	0.86893	**18082**	0.558943528
chr2L	dme-mir-9b	4263	23545	0.15330	0.84670	**27808**	0.859598032
chrX	dme-mir-985	214	1124	0.16000	0.84000	**1338**	0.041345405
chr2L	dme-mir-305	13965	65041	0.17676	0.82324	**79006**	2.442253734
chr4	dme-mir-954	50	217	0.18727	0.81273	**267**	0.008253625
chr3R	dme-mir-34	9383	40124	0.18953	0.81047	**49507**	1.530382746
chr2L	dme-mir-966	5	21	0.19231	0.80769	**26**	0.000803724
chr2L	dme-mir-962	401	1649	0.19566	0.80434	**2050**	0.063355069
chr2R	dme-mir-991	120	445	0.21258	0.78742	**565**	0.017450079
chr3R	dme-mir-1013	52	189	0.21577	0.78423	**241**	0.007449901
chrX	dme-mir-982	118	420	0.21933	0.78067	**538**	0.016630899
chr2L	dme-mir-306	1152	3329	0.25711	0.74289	**4481**	0.13850323
chr3L	dme-mir-316	5546	15460	0.26403	0.73597	**21006**	0.649331456
chrX	dme-mir-303	142	396	0.26419	0.73581	**538**	0.016615442
chr3R	dme-mir-2c	27	67	0.28877	0.71123	**94**	0.002890314
chrX	dme-mir-973	76	179	0.29862	0.70138	**255**	0.007867218
chr3R	dme-mir-11	14438	32372	0.30844	0.69156	**46810**	1.446996236
chr2L	dme-mir-125	5238	11659	0.31000	0.69000	**16897**	0.522312177
chrX	dme-mir-283	577	1257	0.31470	0.68530	**1834**	0.056677973
chr2L	dme-mir-2a-1	21	46	0.31579	0.68421	**67**	0.002055678
chr3L	dme-mir-193	12	25	0.32877	0.67123	**37**	0.001128304

At least 10 normalized reads in the summed normalized reads were required. A ratio (BodyM/BodyM+Testis) >=0.66 is male body biased. A ratio (Testis/Body M+Testis) >=0.66 is testis biased. BM: Body Male; T: testis

TABLE S8: Adult Female Body vs. Ovary biased miRNAs

Female Body (female somatic tissues) biased:

chrom	miRNA	Female Body reads	Ovary reads	BF/BF+Ov	BF/BF+Ov	Sum Reads	% miRNA
chr3R	dme-mir-1000	206	0	1	0	**206**	0.016796842
chr3R	dme-mir-1001	29	0	1	0	**29**	0.002364604
chr2L	dme-mir-1004	13	0	1	0	**13**	0.001059995
chr3R	dme-mir-1014	66	0	1	0	**66**	0.005381513
chr3R	dme-mir-1015	15	0	1	0	**15**	0.001223071
chr2R	dme-mir-137	80	0	1	0	**80**	0.006523046
chrX	dme-mir-210	121	0	1	0	**121**	0.009866106
chr3L	dme-mir-219	21	0	1	0	**21**	0.001712299
chr3L	dme-mir-263b	263	0	1	0	**263**	0.021444512
chr3L	dme-mir-276b	112	0	1	0	**112**	0.009132264
chr2L	dme-mir-375	811	0	1	0	**811**	0.066127374
chr3L	dme-mir-957	307	0	1	0	**307**	0.025032187
chr3L	dme-mir-958	2103	0	1	0	**2103**	0.171474559
chrX	dme-mir-981	19	0	1	0	**19**	0.001549223
chr2R	dme-mir-987	308	0	1	0	**308**	0.025113725
chr3R	dme-mir-993	314	0	1	0	**314**	0.025602954
chr3R	dme-mir-iab-4as	28	0	1	0	**28**	0.002283066
chr2L	dme-mir-124	470	2	0.99590	0.00410	**472**	0.038480513
chr2L	dme-mir-133	300	2	0.99360	0.00640	**302**	0.024619041
chr3L	dme-mir-314	4449	31	0.99310	0.00690	**4480**	0.365284793
chr3L	dme-mir-274	1179	10	0.99187	0.00813	**1189**	0.096921485
chr3R	dme-mir-277	19989	168	0.99166	0.00834	**20157**	1.643577423
chr3L	dme-mir-9a	8813	77	0.99130	0.00870	**8890**	0.724899812
chr3L	dme-mir-956	1393	17	0.98766	0.01234	**1410**	0.115001112
chr3R	dme-mir-10	6256	79	0.98749	0.01251	**6335**	0.51656459
chr2L	dme-mir-1	199357	2994	0.98520	0.01480	**202351**	16.4993386
chr3R	dme-mir-929	819	23	0.97246	0.02754	**842**	0.068671122
chr3R	dme-mir-252	1420	41	0.97221	0.02779	**1461**	0.119094084
chr3R	dme-mir-13a	202	10	0.95434	0.04566	**212**	0.017258791
chr2R	dme-mir-1008	36	2	0.94904	0.05096	**38**	0.003092991
chr2L	dme-mir-932	70	4	0.94766	0.05234	**74**	0.006022905
chr3R	dme-mir-iab-4	35	2	0.94766	0.05234	**37**	0.003011453
chr3L	dme-mir-276	37412	2525	0.93678	0.06322	**39937**	3.256354306
chr3L	dme-mir-955	26	2	0.93080	0.06920	**28**	0.00227761
chr2L	dme-mir-1006	101	8	0.92889	0.07111	**109**	0.008865826
chr3R	dme-mir-1013	24	2	0.92546	0.07454	**26**	0.002114534
chr3L	dme-mir-276a	31855	2710	0.92159	0.07841	**34565**	2.818378803
chr2R	dme-mir-278	2040	226	0.90020	0.09980	**2266**	0.184779232
chrX	dme-mir-980	908	106	0.89518	0.10482	**1014**	0.082705681
chr2R	dme-mir-31a	11038	1703	0.86633	0.13367	**12741**	1.038880662
chr3R	dme-mir-1010	92	15	0.85610	0.14390	**107**	0.008762464
chr3R	dme-mir-999	771	141	0.84529	0.15471	**912**	0.074372131
chr2R	dme-mir-281-1	5351	1009	0.84134	0.15866	**6360**	0.518587988
chr3R	dme-mir-2c	10	2	0.83801	0.16199	**12**	0.000973001

chr2R	dme-mir-281-2	1730	340	0.83566	0.16434	**2070**	0.168802027
chr2L	dme-mir-100	366	73	0.83285	0.16715	**439**	0.035832503
chr3L	dme-mir-190	169	35	0.82926	0.17074	**204**	0.016617099
chr2L	dme-mir-87	535	110	0.82922	0.17078	**645**	0.052607222
chr2L	dme-let-7	8023	1722	0.82326	0.17674	**9745**	0.794619587
chr2R	dme-mir-8	191101	44755	0.81024	0.18976	**235856**	19.23123099
chr2L	dme-mir-125	1718	485	0.77977	0.22023	**2203**	0.17964509
chr3R	dme-mir-279	4143	1208	0.77422	0.22578	**5351**	0.436324888
chr3L	dme-mir-316	1713	644	0.72686	0.27314	**2357**	0.192162262
chr3R	dme-mir-284	116	44	0.72292	0.27708	**160**	0.013083682

Ovary enriched miRNAs:

chrom	miRNA	Female Body reads	Ovary reads	BF/BF+Ov	Ov/BF+Ov	Sum Reads	% miRNA
chr3R	dme-mir-318	76	34886	0.00217	0.99783	**34962**	2.850769902
chrX	dme-mir-984	7	1378	0.00505	0.99495	**1385**	0.112954019
chr3R	dme-mir-994	76	14463	0.00523	0.99477	**14539**	1.185511752
chr2R	dme-mir-313	8	1216	0.00654	0.99346	**1224**	0.099795454
chrX	dme-mir-303	1	128	0.00778	0.99222	**129**	0.010484476
chrX	dme-mir-983	7	798	0.00869	0.99131	**805**	0.065667938
chr2R	dme-mir-312	40	2803	0.01407	0.98593	**2843**	0.231810914
chr2R	dme-mir-1009	3	174	0.01695	0.98305	**177**	0.014430438
chr2R	dme-mir-311	13	460	0.02748	0.97252	**473**	0.038573619
chrX	dme-mir-982	3	89	0.03264	0.96736	**92**	0.007495147
chr2R	dme-mir-310	9	228	0.03796	0.96204	**237**	0.019333034
chr2L	dme-mir-275	763	12586	0.05716	0.94284	**13349**	1.088479123
chr3R	dme-mir-92b	68	990	0.06429	0.93571	**1058**	0.086246167
chr3R	dme-mir-92a	169	1514	0.10044	0.89956	**1683**	0.137196605
chr3R	dme-mir-995	459	3679	0.11093	0.88907	**4138**	0.337377347
chr2L	dme-mir-966	6	41	0.12877	0.87123	**47**	0.003799254
chr2R	dme-mir-989	13128	88414	0.12929	0.87071	**101542**	8.279510048
chr2L	dme-mir-9b	1608	10570	0.13204	0.86796	**12178**	0.99298085
chr2L	dme-mir-2a-1	22	118	0.15723	0.84277	**140**	0.011408674
chr2L	dme-mir-306	499	1954	0.20340	0.79660	**2453**	0.200041589
chr2R	dme-mir-184	7879	30821	0.20359	0.79641	**38700**	3.155536026
chr4	dme-mir-954	11	43	0.20550	0.79450	**54**	0.004364565
chr3R	dme-mir-996	8051	28482	0.22038	0.77962	**36533**	2.978840048
chrX	dme-mir-13b-2	55	172	0.24224	0.75776	**227**	0.018512798
chr2L	dme-mir-79	2196	6723	0.24621	0.75379	**8919**	0.727260898
chr2L	dme-mir-2b-2	319	862	0.27007	0.72993	**1181**	0.096309284
chr2L	dme-mir-959	3	8	0.27953	0.72047	**11**	0.000875095
chr2R	dme-mir-7	928	2356	0.28254	0.71746	**3284**	0.267806437
chr3L	dme-mir-33	1974	4025	0.32907	0.67093	**5999**	0.48912155
chr3R	dme-mir-34	3245	6344	0.33839	0.66161	**9589**	0.781900759

At least 10 normalized reads in summed normalized reads were required. A ratio (BodyF/BodyF+Ovary) >=0.66 is female body biased and a ratio (Ovary/Body M+Ovary) >=0.66 is ovary biased. BF: Body Female; Ov: Ovary.

TABLE S9: Raw Counts miRNA-Seq

		Late Embryo Lymphoid Cells		L3 Larvae Salivary Glands		Adult Head		Adult Body		Adult Gonads	
Chrom	miRNA	S2 (M)	Kc (F)	S. Glands M	S. Glands F	Head M	Head F	Body M	Body F	Testis	Ovary
chr3L	dme-bantam	35460	18240	12348	24423	103920	152727	244113	72941	28463	687
chr2L	dme-let-7	5	5	30	219	20606	51163	28931	8023	891	11559
chr2L	dme-let-7-as	0	0	0	0	0	0	0	0	0	0
chr2L	dme-mir-1	23	55	679	1503	126814	175008	496888	199357	1549	241
chr3R	dme-mir-10	1	18	199	395	3730	4794	19132	6256	41	171
chr2L	dme-mir-100	0	0	1	10	1004	1527	1103	366	38	226
chr3R	dme-mir-1000	1	867	13	27	18668	25776	875	206	0	1
chr3R	dme-mir-1001	0	0	0	0	162	208	106	29	0	2
chr2L	dme-mir-1002	0	0	0	0	0	0	0	0	0	0
chr3R	dme-mir-1003	1487	902	34	30	107	228	124	34	16	63
chr2L	dme-mir-1004	0	0	0	1	157	253	44	13	0	144
chr2L	dme-mir-1004-as	0	0	0	0	1	0	0	0	0	0
chr2L	dme-mir-1005	1	0	16	11	101	332	122	44	14	3
chr2L	dme-mir-1006	58	97	71	107	315	519	415	101	4	15
chr2L	dme-mir-1006-as	0	0	0	0	0	0	0	0	0	0
chrX	dme-mir-1007	13	5	0	4	109	125	47	19	10	6
chr2R	dme-mir-1008	94	175	8	9	119	104	106	36	1	11
chr2R	dme-mir-1009	4	6	5	2	30	85	38	3	90	5
chr3R	dme-mir-1010	1	71	1	0	851	1677	319	92	8	168
chr3R	dme-mir-1011	0	0	0	0	8	19	1	0	0	3
chr3R	dme-mir-1012	164	42	230	346	374	623	215	79	40	46
chr3R	dme-mir-1013	1	4	3	4	90	131	52	24	1	54
chr3R	dme-mir-1014	0	0	0	0	0	0	248	66	0	0
chr3R	dme-mir-1015	0	0	0	0	0	1	62	15	0	2
chr2R	dme-mir-1016	5	4	3	4	35	76	18	8	0	6
chr3R	dme-mir-1017	0	0	0	0	183	278	25	6	0	1
chr3R	dme-mir-11	15690	9328	5007	12439	6209	21450	14438	5606	3338	9249
chrX	dme-mir-12	415	7053	16391	43021	1117	2682	21306	2801	2280	62228
chr2L	dme-mir-124	8	63	10	16	29849	48896	2863	470	1	151
chr2L	dme-mir-124-as	0	0	0	0	0	0	0	0	0	0
chr2L	dme-mir-125	10	3	23	63	7175	20670	5238	1718	251	3331
chrX	dme-mir-12-as	0	0	0	0	0	0	0	0	0	0
chr2L	dme-mir-133	5	3	6	4	4836	16473	1065	300	1	38
chr2R	dme-mir-137	0	2	0	1	701	1301	341	80	0	38
chr3R	dme-mir-13a	25	57	11	17	5608	9074	797	202	5	29
chr3R	dme-mir-13b	11557	9820	5207	12399	27953	34823	21017	7131	5476	5212
chr3R	dme-mir-13b-1	0	0	7	9	14	22	4	1	0	0
chrX	dme-mir-13b-2	299	300	62	70	27	101	92	55	89	1
chr2R	dme-mir-14	182756	130160	2602	2658	31243	68581	26146	5504	1571	6722
chr2R	dme-mir-14-as	0	0	0	0	2	1	0	0	0	0
chr2R	dme-mir-184	54062	73256	810	1085	51441	89330	15336	7879	15944	540
chr3L	dme-mir-190	171	308	130	168	1250	634	162	169	18	13
chr3L	dme-mir-193	3	64	0	4	1978	4491	12	1	1	7
chr2L	dme-mir-1-as	0	0	0	0	0	0	0	0	0	0
chrX	dme-mir-210	1	1	31	29	30904	106957	409	121	0	10
chr3L	dme-mir-219	0	0	1	0	259	437	84	21	0	1
chr2RHet	dme-mir-2279	8	9	2	5	7	16	12	3	0	3
chr2RHet	dme-mir-2279-as	0	1	0	1	0	0	0	0	0	0
chr2L	dme-mir-2280	0	0	0	0	0	0	1	0	0	0
chr3R	dme-mir-2281	0	0	0	0	0	1	4	1	0	0
chr3L	dme-mir-2282	1	3	0	0	0	0	0	0	0	0
chr3R	dme-mir-2283	0	0	0	0	3	3	4	0	0	1
chr3R	dme-mir-252	13294	137	831	644	14416	37717	4036	1420	21	990
chr2L	dme-mir-263a	66	3	27399	39275	17316	25950	11829	3892	3639	245
chr2L	dme-mir-263a-as	0	0	0	0	0	0	0	0	0	0
chr3L	dme-mir-263b	1	2	2	6	3141	6005	1144	263	0	13
chr3L	dme-mir-274	1	0	12	16	13878	55708	3593	1179	5	7928
chr2L	dme-mir-275	461	832	13608	2588	668	2503	1122	763	6511	605
chr2L	dme-mir-275-as	0	0	0	1	1	1	0	0	0	0
chr3L	dme-mir-276	4524	10288	1946	5840	68388	58112	47955	37412	1306	123
chr3L	dme-mir-276a	9143	7257	1158	3728	73713	163232	90583	31855	1402	2248
chr3L	dme-mir-276b	5	125	1	8	7324	16746	530	112	0	3
chr3R	dme-mir-277	3703	1688	807	1660	59156	104947	76053	19989	87	9542
chr2R	dme-mir-278	47	1099	797	526	2829	9122	4966	2040	117	2426
chr3R	dme-mir-279	16526	10095	321	1492	8345	13021	14571	4143	625	1554
chr3R	dme-mir-279-as	0	0	0	0	0	0	0	0	0	0
chr2R	dme-mir-281-1	179	132	55	118	260	557	17602	5351	522	143
chr2R	dme-mir-281-2	34	23	53	84	277	439	5100	1730	176	21
chr3L	dme-mir-282	13543	3084	4147	31936	6842	6760	23325	12554	3427	11072
chr3L	dme-mir-282-as	0	0	0	0	0	0	0	0	0	0
chrX	dme-mir-283	48	930	4683	7791	370	448	577	363	133	359
chr3R	dme-mir-284	0	5	2	1	518	2009	523	116	23	16
chr3L	dme-mir-285	0	0	12	38	40821	63213	76	4	0	0
chr2R	dme-mir-286	43	14	23	31	4	15	5	1	0	0
chr2L	dme-mir-287	0	0	0	0	0	0	0	1	0	0
chr3L	dme-mir-289	0	0	0	0	0	0	0	1	0	0
chr2L	dme-mir-2a	7839	19872	7976	9677	40963	62518	42678	21855	19231	14216
chr2L	dme-mir-2a-1	173	259	16	27	34	64	21	22	61	13
chr2L	dme-mir-2a-2	2015	6472	112	164	1780	4486	1047	363	339	112
chr2L	dme-mir-2b	9981	13905	6378	7854	43346	58488	18220	8986	8217	6058
chr2L	dme-mir-2b-1	498	138	461	465	1684	1927	623	328	188	2
chr2L	dme-mir-2b-2	431	1100	189	177	714	1184	615	319	446	40
chr3R	dme-mir-2c	9	13	3	0	163	287	27	10	1	19
chr2R	dme-mir-3	15	8	1	1	3	5	2	1	3	8
chrX	dme-mir-303	7	8	0	0	1	3	142	1	66	113
chrX	dme-mir-304	34	841	15014	30430	1286	2492	17186	2108	743	556
chrX	dme-mir-304-as	0	0	0	0	0	0	0	0	0	0
chr2L	dme-mir-305	3321	6880	7165	9763	11336	20428	13965	3692	2694	18583
chr2L	dme-mir-305-as	0	3	2	7	12	8	0	1	1	0
chr2L	dme-mir-306	2500	4089	1067	1144	752	2067	1152	499	1011	951
chr2R	dme-mir-307	932	22	1	0	5587	15933	2063	482	245	42
chr2R	dme-mir-307-as	1	0	5	17	0	3	6	1	0	0

chr2R	dme-mir-308	1483	1685	2781	5046	1048	1674	1864	684	323	30
chr2R	dme-mir-309	4	3	1	0	0	1	0	0	0	0
chr2R	dme-mir-310	8	4	1	0	2	2	55	9	118	3356
chr2R	dme-mir-311	8	2	0	0	1	2	68	13	238	3582
chr2R	dme-mir-312	3	6	0	0	8	9	95	40	1450	1704
chr2R	dme-mir-313	2	2	0	0	4	4	59	8	629	370
chr3L	dme-mir-314	0	2	2	3	18	72	11627	4449	16	29
chr3L	dme-mir-314-as	0	0	0	0	0	0	0	1	0	0
chr3L	dme-mir-315	0	0	0	0	1204	2424	24	7	0	12
chr3L	dme-mir-316	0	0	8	14	1119	3236	5546	1713	333	4417
chr3L	dme-mir-316-as	0	0	0	0	0	0	1	0	0	0
chr3R	dme-mir-317	9157	14069	718	1536	8974	14533	2370	561	529	4489
chr3R	dme-mir-317-as	0	0	0	0	0	0	0	1	0	0
chr3R	dme-mir-318	13	60	0	1	1	6	4	76	18047	20
chr2R	dme-mir-31a	5	12	521	763	11606	22138	24842	11038	881	1134
chrX	dme-mir-31b	3	3	0	0	7	44	2068	447	170	875
chr3L	dme-mir-33	1927	2696	1239	2256	1864	3555	9633	1974	2082	166
chr3R	dme-mir-34	13980	15190	1643	2983	45375	77345	9383	3245	3282	11464
chr2L	dme-mir-375	1	0	18745	34030	57	182	4698	811	0	1491
chr2R	dme-mir-4	6	2	1	6	3	5	2	0	0	0
chr2R	dme-mir-5	14	9	18	26	7	22	14	4	4	0
chr2R	dme-mir-6-1	7	1	0	0	0	0	0	0	0	0
chr2R	dme-mir-6-2	1	1	0	0	0	0	0	0	0	0
chr2R	dme-mir-6-3	2	1	0	0	0	0	0	0	0	0
chr2R	dme-mir-6-3-as	0	0	0	0	0	0	0	0	0	0
chr2R	dme-mir-7	332	243	176	270	13849	20729	3010	928	1219	863
chr2L	dme-mir-79	2043	3617	1604	3518	7700	13318	12143	2196	3478	219
chr2R	dme-mir-8	4003	18559	84972	180692	184826	244757	447346	191101	23152	56620
chr2L	dme-mir-87	0	2	2	4	2344	4107	908	535	57	12
chrX	dme-mir-927	0	1	0	0	662	994	41	9	0	0
chr3R	dme-mir-929	1	2	20	39	12012	13343	1810	819	12	4
chr3R	dme-mir-929-as	0	0	0	0	0	0	2	0	0	0
chr3R	dme-mir-92a	13	1478	2	7	1421	2484	254	169	783	1424
chr3R	dme-mir-92a-as	0	0	0	0	0	0	0	0	0	0
chr3R	dme-mir-92b	20	447	31	64	54	68	42	68	512	747
chr2L	dme-mir-932	5	118	4	2	3614	8766	276	70	2	45
chr4	dme-mir-954	11	61	1	1	59	124	50	11	22	62
chr3L	dme-mir-955	0	0	0	0	54	84	59	26	1	7
chr3L	dme-mir-956	0	1	0	1	4	20	4342	1393	9	54
chr3L	dme-mir-957	0	0	2	7	6154	12255	839	307	0	0
chr3L	dme-mir-958	1	19	0	1	3	29	7379	2103	0	9
chr2L	dme-mir-959	0	0	0	0	7	18	478	3	4	17252
chr2L	dme-mir-960	0	1	0	2	30	103	1717	34	11	5436
chr2L	dme-mir-961	0	0	0	0	5	20	177	5	5	477
chr2L	dme-mir-962	0	0	1	0	28	55	401	39	33	471
chr2L	dme-mir-963	0	1	0	0	5	20	368	6	1	926
chr2L	dme-mir-964	0	0	0	0	7	41	437	10	5	10115
chr2L	dme-mir-965	559	608	131	567	361	613	1129	201	145	9
chr2L	dme-mir-966	15	39	1	4	8	12	5	6	21	6
chr2L	dme-mir-967	10	7	0	1	4	2	3	0	0	0
chr2L	dme-mir-967-as	0	0	0	0	0	0	0	1	0	0
chr2L	dme-mir-968	0	0	0	0	2	3	0	0	0	0
chrX	dme-mir-969	0	0	0	2	194	192	27	6	0	0
chrX	dme-mir-970	1140	1185	177	198	1442	3119	656	205	59	100
chrX	dme-mir-971	0	35	0	1	40	70	4	0	0	33
chrX	dme-mir-972	0	0	0	0	0	1	61	0	0	961
chrX	dme-mir-973	0	8	0	0	0	0	76	1	0	51
chrX	dme-mir-974	0	2	0	0	5	2	236	1	0	82
chrX	dme-mir-975	0	3	0	0	0	0	33	0	0	2134
chrX	dme-mir-976	0	1	0	0	0	2	380	2	0	7525
chrX	dme-mir-977	1	44	0	0	3	4	680	0	0	8100
chrX	dme-mir-978	1	4	0	0	2	3	241	1	0	8457
chrX	dme-mir-979	0	0	0	0	0	0	21	0	0	497
chrX	dme-mir-980	1534	302	3	3	349	1464	2995	908	55	154
chrX	dme-mir-981	1	952	0	3	231	968	56	19	0	16
chrX	dme-mir-981-as	1	4	0	0	1	1	0	0	0	0
chrX	dme-mir-982	0	11	0	0	1	3	118	3	46	120
chrX	dme-mir-983	6	9	0	0	9	16	724	7	413	6732
chrX	dme-mir-983-1	0	0	0	0	0	0	1	0	2	1
chrX	dme-mir-984	25	68	0	0	10	11	551	7	713	2201
chrX	dme-mir-985	0	0	0	0	1	0	214	2	1	321
chr2R	dme-mir-986	3	29	211	226	271	1006	1880	510	301	309
chr2R	dme-mir-987	0	3	9	36	14710	16043	803	308	0	3
chr2R	dme-mir-988	13800	15082	558	539	620	1460	876	280	214	6587
chr2R	dme-mir-988-as	1	0	0	0	0	0	0	0	0	0
chr2R	dme-mir-989	3	158	14	30	1	6	44	13128	45737	6
chr2R	dme-mir-990	0	0	0	0	382	430	8	2	0	0
chr2R	dme-mir-991	0	0	0	0	0	1	120	2	4	127
chr2R	dme-mir-992	2	4	0	0	0	1	45	1	0	395
chr3R	dme-mir-993	0	1	0	2	982	1433	1448	314	0	1
chr3R	dme-mir-994	5	27	0	2	2	3	4	76	7482	19
chr3R	dme-mir-995	3761	3754	1631	3220	2255	3287	909	459	1903	228
chr3R	dme-mir-995-as	0	0	0	0	0	0	1	0	0	0
chr3R	dme-mir-996	23117	10275	2982	6077	10447	27396	29997	8051	14734	348
chr3R	dme-mir-997	0	0	0	0	0	0	184	0	0	59
chr3R	dme-mir-998	3118	3965	2123	5021	4751	5610	1074	459	403	84
chr3R	dme-mir-999	247	374	27	35	7193	10562	1464	771	73	673
chr3L	dme-mir-9a	49	83	1540	2193	12061	32808	28787	8813	40	6846
chr2L	dme-mir-9b	2463	7931	1257	1648	1557	3726	4263	1608	5468	6727
chr2L	dme-mir-9c	1896	3769	737	920	2615	5475	5508	2430	2337	2050
chr3R	dme-mir-iab-4	0	1	0	0	2	2	94	35	1	7
chr3R	dme-mir-iab-4as	0	0	0	0	0	1	144	28	0	16

S. Glands: Salivary Glands; M: Male; F: Female

TABLE S10: Normalized read counts in libraries

Chrom	miRNA	S2	Kc	S. Glands M	S. Glands F	Head M	Head F	Body M	Body F	Testis	Ovary	SUM
chr3L	dme-bantam	35460	27334	19757	24423	181971	152727	244113	250083	2405	55022	**993293**
chr2L	dme-let-7	5	7	48	219	36082	51163	28931	27507	40457	1722	**186142**
chr2L	dme-let-7-as	0	0	0	0	0	0	0	0	0	0	**0**
chr2L	dme-mir-1	23	82	1086	1503	222060	175008	496888	683509	844	2994	**1583998**
chr2L	dme-mir-1-as	0	0	0	0	0	0	0	0	0	0	**0**
chr3R	dme-mir-10	1	27	318	395	6531	4794	19132	21449	599	79	**53326**
chr2L	dme-mir-100	0	0	2	10	1758	1527	1103	1255	791	73	**6519**
chr3R	dme-mir-1000	1	1299	21	27	32689	25776	875	706	4	0	**61398**
chr3R	dme-mir-1001	0	0	0	0	284	208	106	99	7	0	**704**
chr2L	dme-mir-1002	0	0	0	0	0	0	0	0	0	0	**0**
chr3R	dme-mir-1003	1487	1352	54	30	187	228	124	117	221	31	**3830**
chr2L	dme-mir-1004	0	0	0	1	275	253	44	45	504	0	**1121**
chr2L	dme-mir-1004-as	0	0	0	0	2	0	0	0	0	0	**2**
chr2L	dme-mir-1005	1	0	26	11	177	332	122	151	11	27	**857**
chr2L	dme-mir-1006	58	145	114	107	552	519	415	346	53	8	**2316**
chrX	dme-mir-1007	13	7	0	4	191	125	47	65	21	19	**493**
chr2R	dme-mir-1008	94	262	13	9	208	104	106	123	39	2	**960**
chr2R	dme-mir-1009	4	9	8	2	53	85	38	10	18	174	**400**
chr3R	dme-mir-1010	1	106	2	0	1490	1677	319	315	588	15	**4514**
chr3R	dme-mir-1011	0	0	0	0	14	19	1	0	11	0	**45**
chr3R	dme-mir-1012	164	63	368	346	655	623	215	271	161	77	**2943**
chr3R	dme-mir-1013	1	6	5	4	158	131	52	82	189	2	**630**
chr3R	dme-mir-1014	0	0	0	0	0	0	248	226	0	0	**474**
chr3R	dme-mir-1015	0	0	0	0	0	1	62	51	7	0	**121**
chr2R	dme-mir-1016	5	6	5	4	61	76	18	27	21	0	**224**
chr3R	dme-mir-1017	0	0	0	0	320	278	25	21	4	0	**648**
chr3R	dme-mir-11	15690	13979	8011	12439	10872	21450	14438	19221	32372	6453	**154924**
chrX	dme-mir-12	415	10569	26226	43021	1956	2682	21306	9603	217798	4407	**337984**
chr2L	dme-mir-124	8	94	16	16	52268	48896	2863	1611	529	2	**106303**
chr2L	dme-mir-125	10	4	37	63	12564	20670	5238	5890	11659	485	**56620**
chr2L	dme-mir-133	5	4	10	4	8468	16473	1065	1029	133	2	**27193**
chr2R	dme-mir-137	0	3	0	1	1228	1301	341	274	133	0	**3281**
chr3R	dme-mir-13a	25	85	18	17	9820	9074	797	693	102	10	**20640**
chr3R	dme-mir-13b	11557	14716	8331	12399	48948	34823	21017	24449	18242	10586	**205067**
chr3R	dme-mir-13b-1	0	0	11	9	25	22	4	3	0	0	**74**
chrX	dme-mir-13b-2	299	450	99	70	47	101	92	189	4	172	**1522**
chr2R	dme-mir-14	182756	195051	4163	2658	54709	68581	26146	18871	23527	3037	**579498**
chr2R	dme-mir-184	54062	109778	1296	1085	90077	89330	15336	27014	1890	30821	**420688**
chr3L	dme-mir-190	171	462	208	168	2189	634	162	579	46	35	**4653**
chr3L	dme-mir-193	3	96	0	4	3464	4491	12	3	25	2	**8099**
chrX	dme-mir-210	1	1	50	29	54115	106957	409	415	35	0	**162012**
chr3L	dme-mir-219	0	0	2	0	454	437	84	72	4	0	**1052**
chr2RHet	dme-mir-2279	8	13	3	5	12	16	12	10	11	0	**91**
chr2RHet	dme-mir-2279-as	0	1	0	1	0	0	0	0	0	0	**2**
chr2L	dme-mir-2280	0	0	0	0	0	0	1	0	0	0	**1**
chr3R	dme-mir-2281	0	0	0	0	0	1	4	3	0	0	**8**
chr3L	dme-mir-2282	1	4	0	0	0	0	0	0	0	0	**5**
chr3R	dme-mir-2283	0	0	0	0	5	3	4	0	4	0	**16**
chr3R	dme-mir-252	13294	205	1330	644	25243	37717	4036	4869	3465	41	**90843**
chr2L	dme-mir-263a	66	4	43838	39275	30321	25950	11829	13344	858	7035	**172520**
chr3L	dme-mir-263b	1	3	3	6	5500	6005	1144	902	46	0	**13610**
chr3L	dme-mir-274	1	0	19	16	24301	55708	3593	4042	27748	10	**115438**
chr2L	dme-mir-275	461	1247	21773	2588	1170	2503	1122	2616	2118	12586	**48183**
chr2L	dme-mir-275-as	0	0	0	1	2	1	0	0	0	0	**4**
chr3L	dme-mir-276	4524	15417	3114	5840	119752	58112	47955	128270	431	2525	**385939**
chr3L	dme-mir-276a	9143	10875	1853	3728	129076	163232	90583	109217	7868	2710	**528285**
chr3L	dme-mir-276b	5	187	2	8	12825	16746	530	384	11	0	**30697**
chr3R	dme-mir-277	3703	2530	1291	1660	103586	104947	76053	68534	33397	168	**395869**
chr2R	dme-mir-278	47	1647	1275	526	4954	9122	4966	6994	8491	226	**38248**

chr3R	dme-mir-279	16526	15128	514	1492	14613	13021	14571	14205	5439	1208	**96716**
chr2R	dme-mir-281-1	179	198	88	118	455	557	17602	18346	501	1009	**39053**
chr2R	dme-mir-281-2	34	34	85	84	485	439	5100	5931	74	340	**12606**
chr3L	dme-mir-282	13543	4622	6635	31936	11981	6760	23325	43042	38752	6625	**187220**
chrX	dme-mir-283	48	1394	7493	7791	648	448	577	1245	1257	257	**21157**
chr3R	dme-mir-284	0	7	3	1	907	2009	523	398	56	44	**3949**
chr3L	dme-mir-285	0	0	19	38	71480	63213	76	14	0	0	**134840**
chr2R	dme-mir-286	43	21	37	31	7	15	5	3	0	0	**162**
chr2L	dme-mir-287	0	0	0	0	0	0	0	3	0	0	**3**
chr3L	dme-mir-289	0	0	0	0	0	0	0	3	0	0	**3**
chr2L	dme-mir-2a	7839	29779	12762	9677	71729	62518	42678	74931	49756	37175	**398844**
chr2L	dme-mir-2a-1	173	388	26	27	60	64	21	75	46	118	**997**
chr2L	dme-mir-2a-2	2015	9699	179	164	3117	4486	1047	1245	392	655	**22999**
chr2L	dme-mir-2b	9981	20837	10205	7854	75902	58488	18220	30809	21203	15884	**269383**
chr2L	dme-mir-2b-1	498	207	738	465	2949	1927	623	1125	7	363	**8901**
chr2L	dme-mir-2b-2	431	1648	302	177	1250	1184	615	1094	140	862	**7704**
chr3R	dme-mir-2c	9	19	5	0	285	287	27	34	67	2	**735**
chr2R	dme-mir-3	15	12	2	1	5	5	2	3	28	6	**79**
chrX	dme-mir-303	7	12	0	0	2	3	142	3	396	128	**692**
chrX	dme-mir-304	34	1260	24022	30430	2252	2492	17186	7227	1946	1436	**88286**
chr2L	dme-mir-305	3321	10310	11464	9763	19850	20428	13965	12658	65041	5208	**172008**
chr2L	dme-mir-305-as	0	4	3	7	21	8	0	3	0	2	**49**
chr2L	dme-mir-306	2500	6128	1707	1144	1317	2067	1152	1711	3329	1954	**23008**
chr2R	dme-mir-307	932	33	2	0	9783	15933	2063	1653	147	474	**31019**
chr2R	dme-mir-307-as	1	0	8	17	0	3	6	3	0	0	**38**
chr2R	dme-mir-308	1483	2525	4450	5046	1835	1674	1864	2345	105	624	**21951**
chr2R	dme-mir-309	4	4	2	0	0	1	0	0	0	0	**11**
chr2R	dme-mir-310	8	6	2	0	4	2	55	31	11746	228	**12081**
chr2R	dme-mir-311	8	3	0	0	2	2	68	45	12537	460	**13124**
chr2R	dme-mir-312	3	9	0	0	14	9	95	137	5964	2803	**9034**
chr2R	dme-mir-313	2	3	0	0	7	4	59	27	1295	1216	**2613**
chr3L	dme-mir-314	0	3	3	3	32	72	11627	15254	102	31	**27126**
chr3L	dme-mir-315	0	0	0	0	2108	2424	24	24	42	0	**4622**
chr3L	dme-mir-316	0	0	13	14	1959	3236	5546	5873	15460	644	**32745**
chr3R	dme-mir-317	9157	21083	1149	1536	15714	14533	2370	1923	15712	1023	**84200**
chr3R	dme-mir-318	13	90	0	1	2	6	4	261	70	34886	**35333**
chr2R	dme-mir-31a	5	18	834	763	20323	22138	24842	37845	3969	1703	**112439**
chrX	dme-mir-31b	3	4	0	0	12	44	2068	1533	3063	329	**7055**
chr3L	dme-mir-33	1927	4040	1982	2256	3264	3555	9633	6768	581	4025	**38031**
chr3R	dme-mir-34	13980	22763	2629	2983	79455	77345	9383	11126	40124	6344	**266132**
chr2L	dme-mir-375	1	0	29992	34030	100	182	4698	2781	5219	0	**77002**
chr2R	dme-mir-4	6	3	2	6	5	5	2	0	0	0	**29**
chr2R	dme-mir-5	14	13	29	26	12	22	14	14	0	8	**152**
chr2R	dme-mir-6	10	4	0	0	0	0	0	0	0	0	**14**
chr2R	dme-mir-7	332	364	282	270	24251	20729	3010	3182	3021	2356	**57796**
chr2L	dme-mir-79	2043	5420	2566	3518	13483	13318	12143	7529	767	6723	**67511**
chr2R	dme-mir-8	4003	27812	135955	180692	323642	244757	447346	655203	198170	44755	**2262335**
chr2L	dme-mir-87	0	3	3	4	4105	4107	908	1834	42	110	**11116**
chrX	dme-mir-927	0	1	0	0	1159	994	41	31	0	0	**2227**
chr3R	dme-mir-929	1	3	32	39	21034	13343	1810	2808	14	23	**39107**
chr3R	dme-mir-92a	13	2215	3	7	2488	2484	254	579	4984	1514	**14541**
chr3R	dme-mir-92b	20	670	50	64	95	68	42	233	2615	990	**4845**
chr2L	dme-mir-932	5	177	6	2	6328	8766	276	240	158	4	**15962**
chr4	dme-mir-954	11	91	2	1	103	124	50	38	217	43	**680**
chr3L	dme-mir-955	0	0	0	0	95	84	59	89	25	2	**353**
chr3L	dme-mir-956	0	1	0	1	7	20	4342	4776	189	17	**9354**
chr3L	dme-mir-957	0	0	3	7	10776	12255	839	1053	0	0	**24933**
chr3L	dme-mir-958	1	28	0	1	5	29	7379	7210	32	0	**14686**
chr2L	dme-mir-959	0	0	0	0	12	18	478	10	60382	8	**60908**
chr2L	dme-mir-960	0	1	0	2	53	103	1717	117	19026	21	**21040**
chr2L	dme-mir-961	0	0	0	0	9	20	177	17	1670	10	**1902**
chr2L	dme-mir-962	0	0	2	0	49	55	401	134	1649	64	**2353**

chr2L	dme-mir-963	0	1	0	0	9	20	368	21	3241	2	**3662**
chr2L	dme-mir-964	0	0	0	0	12	41	437	34	35403	10	**35937**
chr2L	dme-mir-965	559	911	210	567	632	613	1129	689	32	280	**5622**
chr2L	dme-mir-966	15	58	2	4	14	12	5	21	21	41	**192**
chr2L	dme-mir-967	10	10	0	1	7	2	3	0	0	0	**33**
chr2L	dme-mir-968	0	0	0	0	4	3	0	0	0	0	**7**
chrX	dme-mir-969	0	0	0	2	340	192	27	21	0	0	**581**
chrX	dme-mir-970	1140	1776	283	198	2525	3119	656	703	350	114	**10864**
chrX	dme-mir-971	0	52	0	1	70	70	4	0	116	0	**313**
chrX	dme-mir-972	0	0	0	0	0	1	61	0	3364	0	**3426**
chrX	dme-mir-973	0	12	0	0	0	0	76	3	179	0	**270**
chrX	dme-mir-974	0	3	0	0	9	2	236	3	287	0	**540**
chrX	dme-mir-975	0	4	0	0	0	0	33	0	7469	0	**7507**
chrX	dme-mir-976	0	1	0	0	0	2	380	7	26338	0	**26728**
chrX	dme-mir-977	1	66	0	0	5	4	680	0	28350	0	**29106**
chrX	dme-mir-978	1	6	0	0	4	3	241	3	29600	0	**29857**
chrX	dme-mir-979	0	0	0	0	0	0	21	0	1740	0	**1761**
chrX	dme-mir-980	1534	453	5	3	611	1464	2995	3113	539	106	**10823**
chrX	dme-mir-981	1	1427	0	3	404	968	56	65	56	0	**2980**
chrX	dme-mir-982	0	16	0	0	2	3	118	10	420	89	**658**
chrX	dme-mir-983	6	13	0	0	16	16	724	24	23562	798	**25160**
chrX	dme-mir-983-1	0	0	0	0	0	0	1	0	4	4	**8**
chrX	dme-mir-984	25	102	0	0	18	11	551	24	7704	1378	**9812**
chrX	dme-mir-985	0	0	0	0	2	0	214	7	1124	2	**1348**
chr2R	dme-mir-986	3	43	338	226	475	1006	1880	1749	1082	582	**7383**
chr2R	dme-mir-987	0	4	14	36	25758	16043	803	1056	11	0	**43726**
chr2R	dme-mir-988	13800	22601	893	539	1086	1460	876	960	23055	414	**65683**
chr2R	dme-mir-989	3	237	22	30	2	6	44	45010	21	88414	**133789**
chr2R	dme-mir-990	0	0	0	0	669	430	8	7	0	0	**1114**
chr2R	dme-mir-991	0	0	0	0	0	1	120	7	445	8	**580**
chr2R	dme-mir-992	2	6	0	0	0	1	45	3	1383	0	**1440**
chr3R	dme-mir-993	0	1	0	2	1720	1433	1448	1077	4	0	**5684**
chr3R	dme-mir-994	5	40	0	2	4	3	4	261	67	14463	**14848**
chr3R	dme-mir-995	3761	5626	2610	3220	3949	3287	909	1574	798	3679	**29411**
chr3R	dme-mir-996	23117	15398	4771	6077	18293	27396	29997	27603	1218	28482	**182353**
chr3R	dme-mir-997	0	0	0	0	0	0	184	0	207	0	**391**
chr3R	dme-mir-998	3118	5942	3397	5021	8319	5610	1074	1574	294	779	**35128**
chr3R	dme-mir-999	247	560	43	35	12595	10562	1464	2643	2356	141	**30647**
chr3L	dme-mir-9a	49	124	2464	2193	21120	32808	28787	30216	23961	77	**141799**
chr2L	dme-mir-9b	2463	11885	2011	1648	2726	3726	4263	5513	23545	10570	**68350**
chr2L	dme-mir-9c	1896	5648	1179	920	4579	5475	5508	8331	7175	4518	**45229**
chr3R	dme-mir-iab-4	0	1	0	0	4	2	94	120	25	2	**247**
chr3R	dme-mir-iab-4as	0	0	0	0	0	1	144	96	56	0	**297**
SUM_Norm_Reads_in_libr		**476512**	**670269**	**419331**	**506593**	**2221284**	**2140318**	**1943944**	**2554945**	**1290996**	**481225**	

TABLE S11: Abundance of miRNAs in *msl3* mutant salivary glands

	Genotype	Exp.	Average Ct [a]	Corrected amount [b]	Fold Difference (FD)[c]	log2 (FD)	Average log2(FD)	SD [d]	p value [e]
Dspt4	msl3-/msl3+	1	23.5091	95.762	1.000	0.000	0.000	0.000	
		2	23.7935	200.048	1.000	0.000			
	msl3-/msl3-	1	23.2659	106.222					
		2	23.2766	250.610					
mir-283	msl3-/msl3+	1	24.9728	89.769	0.514	-0.961	-0.901	0.086	0.00045
		2	24.7449	185.152	0.559	-0.840			
	msl3-/msl3-	1	26.4340	57.172					
		2	26.1674	129.580					
mir-304	msl3-/msl3+	1	29.9743	100.663	0.338	-1.564	-1.631	0.095	0.00070
		2	30.2644	203.835	0.308	-1.698			
	msl3-/msl3-	1	32.2164	37.754					
		2	32.3252	78.686					
mir-12	msl3-/msl3+	1	21.5294	88.515	0.406	-1.300	-1.284	0.022	0.00006
		2	21.8149	182.599	0.415	-1.269			
	msl3-/msl3-	1	23.8153	39.885					
		2	24.1442	94.941					
mir-979	msl3-/msl3+	1	36.2751	149.915	0.833	-0.263	-0.749	0.687	0.24047
		2	35.4645	209.309	0.425	-1.235			
	msl3-/msl3-	1	36.5484	138.570					
		2	37.5508	111.399					
mir-210	msl3-/msl3+	1	28.5830	100.340	1.425	0.511	0.384	0.180	0.07654
		2	29.1231	202.647	1.195	0.257			
	msl3-/msl3-	1	27.8037	158.625					
		2	28.3154	303.278					
U6	msl3-/msl3+	1	17.1883	100.088	0.611	-0.710	-0.627	0.117	0.01472
		2	17.7507	184.333	0.686	-0.544			
	msl3-/msl3-	1	18.0034	67.880					
		2	18.2684	158.374					

a. Dilution series were prepared in the control sample to construct standard curves for the Dspt4 autosomal gene reference and for each miRNA. C_T values measured in replicates for the target miRNA and Dspt4 reference in mutant and heterozygous mutant control samples respectively are averaged in individual experiments (Exp.1 and 2) and the corrected amount of target miRNA and Dspt4 reference inferred from the standard curve in b.

c. The amounts of miRNA are normalized in the mutant sample and in the heterozygous mutant control sample by dividing the calculated amount of miRNA by the amount of the Dspt4 reference. The fold difference (FD) or relative expression level of a miRNA corresponds to the

ratio of the normalized abundance of the miRNA in the mutant relative to the heterozygous mutant control sample, that is the ratio [miRNA/Dspt4] Mutant / [miRNA/Dspt4] Control; the average of the base 2 logarithm of the fold difference is plotted in Figure 2B,C.
d. SD is the standard deviation of the difference.
e. p-values are established in a two tailed Students t-test comparing the means of the normalized amounts of target miRNA in the mutant and in the heterozygous mutant control samples. *p<0.05, **p<0.005. ***p<0.0005

TABLE S12: Abundance of miRNAs in *msl3* mutant L3 larvae

	Genotype	Exp.	Average Ct [a]	Corrected amount [b]	Fold Difference (FD) [c]	log2 (FD)	Average log2(FD)	SD [d]	p value [e]
Dspt4	msl3-/msl3+	1	25.9974	34.628	1.000	0.000			
		2	25.6265	92.801	1.000	0.000			
	msl3-/msl3-	1	24.8854	54.398					
		2	24.7720	132.066					
mir-283	msl3-/msl3+	1	26.9201	49.324	0.756	-0.403	-0.253	0.213	0.18885
		2	27.2713	98.504	0.932	-0.102			
	msl3-/msl3-	1	26.3534	58.590					
		2	26.1358	130.596					
mir-304	msl3-/msl3+	1	31.2445	57.627	0.356	-1.488	-1.475	0.019	0.03552
		2	31.5988	109.348	0.363	-1.462			
	msl3-/msl3-	1	32.5782	32.271					
		2	33.0699	56.492					
mir-12	msl3-/msl3+	1	22.7659	57.656	0.455	-1.136	-1.040	0.136	0.00881
		2	22.9153	134.505	0.520	-0.943			
	msl3-/msl3-	1	23.7208	41.214					
		2	23.9739	99.544					
mir-979	msl3-/msl3+	1	31.1498	1044.716	0.760	-0.396	-0.259	0.193	0.38647
		2	31.4659	927.357	0.918	-0.123			
	msl3-/msl3-	1	30.6831	1247.539					
		2	30.7420	1211.981					
mir-210	msl3-/msl3+	1	27.5383	185.744	1.197	0.259	0.065	0.275	0.38641
		2	27.5514	461.878	0.914	-0.129			
	msl3-/msl3-	1	26.4166	349.245					
		2	26.9873	600.996					
U6	msl3-/msl3+	1	17.1512	101.819	0.694	-0.526	-0.444	0.117	0.14280
		2	17.5728	194.135	0.778	-0.362			
	msl3-/msl3-	1	16.9733	111.054					
		2	17.2156	215.036					

a-e as in Table S11.

TABLE S13: Abundance of miRNAs in *msl3* mutant salivary glands

	Genotype	Exp.	Average Ct [a]	Corrected amount [b]	Fold Difference (FD)[c]	log2 (FD)	Average log2(FD)	SD [d]	p value [e]
Dspt4	msl3-/msl3+	1	24.216	100.872	1.000	0.000	0.000	0.000	
		2	24.262	99.102	1.000	0.000			
	msl3-/msl3-	1	23.663	124.744					
		2	24.150	103.457					
mir-314	msl3-/msl3+	1	31.225	100.048	2.258	1.175	1.149	0.037	0.0667
		2	30.498	152.880	2.178	1.123			
	msl3-/msl3-	1	29.463	279.422					
		2	29.089	347.564					
mir-981	msl3-/msl3+	1	32.920	117.805	0.958	-0.061	0.197	0.366	0.2414
		2	33.704	84.927	1.372	0.456			
	msl3-/msl3-	1	32.513	139.636					
		2	32.844	121.608					
mir-13b	msl3-/msl3+	1	23.450	122.437	0.411	-1.282	-0.884	0.564	0.0703
		2	24.218	81.676	0.714	-0.485			
	msl3-/msl3-	1	24.733	62.257					
		2	24.774	60.919					
mir-100	msl3-/msl3+	1	29.324	99.987	1.185	0.245	0.545	0.425	0.0596
		2	29.977	75.275	1.796	0.845			
	msl3-/msl3-	1	28.447	146.492					
		2	28.532	141.148					
mir-1013	msl3-/msl3+	1	31.660	84.010	1.176	0.234	-0.137	0.524	0.3233
		2	31.010	119.016	0.704	-0.507			
	msl3-/msl3-	1	30.962	122.159					
		2	31.585	87.439					
U6	msl3-/msl3+	1	18.097	100.004	0.726	-0.462	-0.418	0.061	0.0046
		2	18.127	98.736	0.771	-0.375			
	msl3-/msl3-	1	18.352	89.811					
		2	18.643	79.476					

a-e as in Table S11.

TABLE S14: Abundance of miRNAs in *msl3* mutant L3 larvae

	Genotype	Exp.	Average Ct [a]	Corrected amount [b]	Fold Difference (FD) [c]	log2 (FD)	Average log2(FD)	SD [d]	p value [e]
Dspt4	msl3-/msl3+	1	26.1455	48.078	1.000	0.000			
		2	26.1633	47.750	1.000	0.000			
	msl3-/msl3-	1	24.995	74.796					
		2	25.335	65.635					
mir-314	msl3-/msl3+	1	21.1699	35123.558	0.350	-1.514	-1.441	0.104	0.0003
		2	21.2272	33969.861	0.388	-1.367			
	msl3-/msl3-	1	22.213	19128.386					
		2	22.307	18104.321					
mir-981	msl3-/msl3+	1	29.5758	476.005	0.655	-0.609	-0.290	0.452	0.1481
		2	30.2449	359.989	1.021	0.030			
	msl3-/msl3-	1	29.529	485.377					
		2	29.433	505.205					
mir-13b	msl3-/msl3+	1	21.4858	344.693	0.540	-0.889	-0.905	0.022	0.0079
		2	21.5918	325.964	0.528	-0.921			
	msl3-/msl3-	1	21.817	289.481					
		2	22.199	236.640					
mir-100	msl3-/msl3+	1	26.8667	291.331	0.208	-2.262	-2.062	0.284	0.0032
		2	27.1654	255.822	0.275	-1.861			
	msl3-/msl3-	1	29.455	94.471					
		2	29.398	96.819					
mir-1013	msl3-/msl3+	1	29.240	142.324	0.573	-0.803	-0.610	0.273	0.0861
		2	28.286	126.568	0.749	-0.417			
	msl3-/msl3-	1	29.365	126.899					
		2	29.391	130.301					
U6	msl3-/msl3+	1	17.259	307.518	0.601	-0.734	-1.024	0.410	0.0125
		2	17.538	512.989	0.402	-1.314			
	msl3-/msl3-	1	17.532	287.625					
		2	17.469	283.612					

a-e as in Table S11.

TABLE S15: Abundance of miRNAs in *mle* mutant salivary glands

	Genotype	Exp.	Average Ct [a]	Corrected amount [b]	Fold Difference (FD)[c]	log2 (FD)	Average log2(FD)	SD [d]	p value [e]
Dspt4	mle-/mle+	1	24.693	102.093	1.000	0.000			
		2	24.533	100.668	1.000	0.000			
	mle-/mle-	1	23.901	170.434					
		2	23.827	158.044					
mir-283	mle-/mle+	1	25.142	100.816	0.740	-0.435	-0.430	0.008	0.0040
		2	24.812	102.914	0.745	-0.425			
	mle-/mle-	1	24.788	124.474					
		2	24.510	120.380					
mir-304	mle-/mle+	1	30.746	96.522	0.636	-0.652	-0.739	0.123	0.0031
		2	31.004	99.139	0.564	-0.826			
	mle-/mle-	1	30.568	102.559					
		2	31.168	87.778					
mir-12	mle-/mle+	1	21.652	101.133	0.532	-0.910	-0.946	0.051	0.0003
		2	21.533	100.745	0.506	-0.983			
	mle-/mle-	1	21.869	89.833					
		2	21.882	80.045					
mir-979	mle-/mle+	1	36.290	101.068	0.730	-0.454	-0.635	0.257	0.0203
		2	35.292	102.616	0.568	-0.817			
	mle-/mle-	1	36.064	123.209					
		2	35.753	91.460					
mir-210	mle-/mle+	1	29.642	107.507	0.782	-0.355	-0.182	0.244	0.2301
		2	29.573	109.561	0.994	-0.009			
	mle-/mle-	1	29.288	140.360					
		2	29.094	170.943					
U6	mle-/mle+	1	18.185	99.069	0.883	-0.180	0.098	0.393	0.3556
		2	18.095	99.106	1.298	0.376			
	mle-/mle-	1	17.555	146.012					
		2	17.022	201.962					

a-e as in Table S11.

TABLE S16: Abundance of miRNAs in *mle* mutant L3 larvae

	Genotype	Exp.	Average Ct [a]	Corrected amount [b]	Fold Difference (FD) [c]	log2 (FD)	Average log2(FD)	SD [d]	p value [e]
Dspt4	mle-/mle+	1	25.034	81.970	1.000	0.000			
		2	24.991	76.150	1.000	0.000			
	mle-/mle-	1	25.047	81.265					
		2	24.697	90.724					
mir-283	mle-/mle+	1	26.352	48.723	0.807	-0.309	-0.165	0.204	0.2143
		2	26.170	46.630	0.986	-0.021			
	mle-/mle-	1	26.717	38.996					
		2	25.887	54.769					
mir-304	mle-/mle+	1	33.859	16.253	1.264	0.338	0.117	0.313	0.2913
		2	33.412	15.797	0.930	-0.104			
	mle-/mle-	1	33.445	20.368					
		2	33.277	17.510					
mir-12	mle-/mle+	1	24.132	19.072	0.892	-0.165	-0.164	0.002	0.0126
		2	24.135	18.169	0.894	-0.162			
	mle-/mle-	1	24.311	16.868					
		2	24.037	19.341					
mir-979	mle-/mle+	1	32.007	1533.669	1.972	0.980	0.550	0.607	0.3187
		2	31.470	404.038	1.088	0.121			
	mle-/mle-	1	30.972	2998.693					
		2	30.760	523.538					
mir-210	mle-/mle+	1	26.990	1098.538	1.579	0.659	0.484	0.247	0.3002
		2	26.722	2357.685	1.239	0.309			
	mle-/mle-	1	26.467	1719.262					
		2	26.347	3479.985					
U6	mle-/mle+	1	16.909	227.810	1.506	0.591	0.559	0.046	0.3274
		2	16.978	208.576	1.440	0.526			
	mle-/mle-	1	16.296	340.231					
		2	16.160	357.836					

a-e as in Table S11.

Table S17: Levels of let-7 miRNA in adult females and males

Tissue		C_T *let±7* ± StDev	C_T *2SrRNA* ± StDev	ΔC_T (ΔC_T *let-7* - ΔC_T *2SrRNA*) [a]	$\Delta\Delta C_T$ (ΔC_T - ΔC_T ^{control}) [b]	Average $\Delta\Delta C_T$ ± StDev	Fold Difference [c]
Female carcasses	Exp 1	25.33±0.30	6.14±0.24	19.19±0.39	0.00±0.39	0.00±0.28	1.00 (0.82 - 1.22)
	Exp 2	26.35±0.30	8.29±0.36	18.06±0.47	0.00±0.47		
Germaria	Exp 1	22.18±0.18	6.29±0.09	15.90±0.20	3.29±0.20	-2.24±0.11	4.72 (4.38 - 5.09) $p=7.76x10^{-6***}$
	Exp 2	22.35±0.05	7.72±0.11	14.63±0.12	3.43±0.12		
Male carcasses	Exp 1	22.71±0.11	7.10±0.03	15.61±0.12	3.58±0.12	-1.92±0.09	3.79 (3.57 – 4.02) $p=1.55x10^{-6***}$
	Exp 2	23.68±0.08	7.80±0.12	15.88±0.14	2.18±0.14		
Testes	Exp 1	21.14±0.26	6.56±0.03	14.58±0.26	4.61±0.26	-2.89±0.12	7.43 (6.84 - 8.07) $p=7.73x10^{-8***}$
	Exp 2	22.40±0.05	8.41±0.09	13.99±0.10	4.07±0.10		

a: ΔC_T was determined by subtracting the average *2SrRNA* C_T value from the average Experimental C_T value. The standard deviation of the difference is calculated from the standard deviation of the Experimental and *2SrRNA* values using the formula $s = \sqrt{(s_1^2 + s_2^2)}$ where s = standard deviation

b: $\Delta\Delta C_T$ is calculated by subtracting the ΔC_T control value (ΔC_T of female carcasses). The standard deviation is the same as for ΔC_T

c: the fold difference between the Experimental Sample and the control is calculated by: $2^{\pm\Delta\Delta CT}$ with $\Delta\Delta C_T$ -s and $\Delta\Delta C_T$ –s where s is the standard deviation of $\Delta\Delta C_T$ value The fold difference of the experimental values was compared to the respective control. P-value was calculated using the two tailed Students t-test. *p<0.05. **p<0.005. ***p<0.0005

Table S18: Levels of sex specific mRNAs in *Δlet-7* females and males

Genotype		C_T *SxlF* ± StDev	C_T *RpL32* ± StDev	ΔC_T (ΔC_T *SxlF*- ΔC_T *RpL32*) [a]	$\Delta\Delta C_T$ (ΔC_T- ΔC_T ^{control}) [b]	Fold Difference [c]
Females	**Control:** *let-7-C* Rescue	16.15±0.22	11.32±0.12	4.83±0.25	0.00±0.25	1.00 (0.840-1.190)
	Δ let-7	15.95±0.03	11.16±0.09	4.78±0.25	-0.05±0.09	1.033 (0.969-1.102) p=0.70
Males	**Control:** *let-7-C* Rescue	21.48±0.12	12.28±0.16	9.21±0.20	0.00±0.20	1.00 (0.872-1.147)
	Δ let-7	18.89±0.09	12.20±0.22	6.69±0.23	-2.51±0.23	5.704 (4.853-6.705) $1.73x10^{-4}$***
Genotype		C_T *tra1* ± StDev	C_T *RpL32* ± StDev	ΔC_T (ΔC_T *tra1*- ΔC_T *RpL32*) [a]	$\Delta\Delta C_T$ (ΔC_T- ΔC_T ^{control}) [b]	Fold Difference [c]
Females	**Control:** *let-7-C* Rescue	21.30±0.13	11.32±0.12	9.98±0.17	0.00±0.17	1.00 (0.886-1.129)
	Δ let-7	20.72±0.14	11.16±0.09	9.56±0.16	-0.42±0.16	1.334 (1.190-1.495) p=0.06
Males	**Control:** *let-7-C* Rescue	29.84±0.03	12.28±0.16	17.57±0.16	0.00±0.16	1.00 (0.896-1.116)
	Δ let-7	29.66±0.09	12.20±0.22	17.46±0.23	-0.11±0.23	1.079 (0.917-1.270) p=0.40
Genotype		C_T *DsxM* ± StDev	C_T *RpL32* ± StDev	ΔC_T (ΔC_T *DsxM*- ΔC_T *RpL32*) [a]	$\Delta\Delta C_T$ (ΔC_T- ΔC_T ^{control}) [b]	Fold Difference [c]
Females	**Control:** *let-7-C* Rescue	25.23±0.09	11.32±0.12	13.90±0.15	0.00±0.15	1.00 (0.900-1.111)
	Δ let-7	25.69±0.05	11.16±0.09	14.52±0.10	0.62±0.10	0.649 (0.605-0.697) $p=1.83x10^{-3}$**
Males	**Control:** *let-7-C* Rescue	17.89±0.33	12.28±0.16	5.61±0.37	0.00±0.37	1.00 (0.950-1.052)
	Δ let-7	17.94±0.03	12.20±0.22	5.74±0.22	0.30±0.17	0.914 (0.786-1.062) 0.75

Genotype		C_T *Yp1* ± StDev	C_T *RpL32* ± StDev	ΔC_T (ΔC_T *Yp1*- ΔC_T *RpL32*) [a]	$\Delta\Delta C_T$ (ΔC_T- ΔC_T control) [b]	Fold Difference [c]
Females	**Control:** *let-7-C* Rescue	10.33±0.07	11.32±0.12	-1.00±0.14	0.00±0.14	1.00 (0.908-1.101)
	Δ let-7	12.93±0.10	11.16±0.09	1.77±0.13	2.76±0.13	0.147 (0.134-0.162) $p=3.29x10^{-6}$***
Males	**Control:** *let-7-C* Rescue	25.99±0.05	12.28±0.16	13.71±0.16	0.00±0.16	1.00 (0.894-1.119)
	Δ let-7	25.01±0.13	12.20±0.22	12.81±0.25	-0.90±0.25	1.867 (1.568-2.223) $p=9.85x10^{-4}$**

a: ΔC_T was determined by subtracting the average *RpL32* C_T value from the average Experimental C_T value. The standard deviation of the difference is calculated from the standard deviation of the Experimental and *RpL32* values using the formula $s = \sqrt{(s_1^2 + s_2^2)}$ where s = standard deviation

b: $\Delta\Delta C_T$ is calculated by subtracting the ΔC_T control. The standard deviation is the same as for ΔC_T

c: the fold difference between the Experimental Sample and the control is calculated by: $2^{-\Delta\Delta CT}$ with $\Delta\Delta C_T$ +s and $\Delta\Delta C_T$ –s where s is the standard deviation of $\Delta\Delta C_T$ value. The fold difference of the experimental values was compared to the respective control. P-value was calculated using the two tailed Students t-test. *p<0.05, **p<0.005. ***p<0.0005

Table S19: let-7 expression depends on ecdysone signaling in adult ovaries and testes

	Genotype, conditions	C_T *let-7* ± StDev[a]	C_T *RpL32* ± StDev	ΔC_T (ΔC_T *let-7* - ΔC_T *RpL32*)[a]	$\Delta\Delta C_T$ (ΔC_T-$\Delta C_T^{control}$)[b]	Fold Difference[c]	Relative change of *let-7* levels[d]
Females	*OregonR*, 4d at 18°C	25.88±0.16	14.13±0.21	11.74±0.06	0.00±0.06	1.00 (0.96-1.04)	1.00 (0.88-1.13)
	OregonR, 4d at 29°C	25.00±0.04	14.39±0.17	10.58±0.18	-1.16±0.18	2.24 (1.98-2.54) $p=2.01x10^{-5}$***	
	$ecd1^{ts\,4210}$, 4d at 18°C	24.07±0.04	13.42±0.28	10.65±0.05	0.00±0.05	1.00 (0-97-1.03)	0.38 (0.37.0.38) $p=2.44x10^{-4}$***
	$ecd1^{ts\,4210}$, 4d at 29°C	24.80±0.15	13.96±0.45	10.92±0.001	0.27±0.001	0.84 (0.84-0.84) p=0.14	
	Genotype, conditions	**C_T *let-7* ± StDev**	**C_T *S2rRNA* ± StDev**	**ΔC_T (ΔC_T *let-7* - ΔC_T *S2rRNA*)[a]**	**$\Delta\Delta C_T$ (ΔC_T-$\Delta C_T^{control}$)[b]**	**Fold Difference[c]**	**Relative change of *let-7* levels[d]**
Males	*OregonR*, 4d at 18°C	22.90±0.03	8.41±0.11	14.49±0.13	0.00±0.13	1.00 (0.91-1.09)	1.00 (0.92-1.08)
	OregonR, 4d at 29°C	22.55±0.03	8.35±0.12	14.20±0.12	-0.29±0.12	1.23 (1.14-1.33) p=0.02*	
	$ecd1^{ts\,4210}$, 4d at 18°C	22.13±0.55	8.33±0.09	13.80±0.15	0.00±0.15	1.00 (0.90-1.11)	0.24 (0.23-0.25) $p=1.77x10^{-4}$***
	$ecd1^{ts\,4210}$, 4d at 29°C	23.49±0.02	7.87±0.11	15.64±0.08	1.85±0.08	0.29 (0.28-0.31) $p=3.59x10^{-4}$***	

a: ΔC_T values were determined by subtracting the average *RpL32* or *2SrRNA* C_T value from the average Experimental C_T value. The standard deviation of the difference is calculated from the standard deviation of the Experimental and *RpL32* or *2SrRNA* values using the formula $s = \sqrt{(s_1^2 + s_2^2)}$ where s = standard deviation

b: $\Delta\Delta C_T$ is calculated by subtracting the ΔC_T control value (ΔC_T of the respective genotype at 18°C). The standard deviation is the same as for ΔC_T

c: the fold difference between the Experimental Sample and the control is calculated by: $2^{-\Delta\Delta CT}$ with $\Delta\Delta C_T$ +s and $\Delta\Delta C_T$ –s where s is the standard deviation of $\Delta\Delta C_T$ value. The fold difference of the experimental values was compared to the respective control. P-value between ΔC_T values of the experiments was calculated using the two tailed Students t-test

d: The relative changes of *let-7* levels were calculated by dividing the fold difference ranges of $ecd1^{ts}$ and *OrR*. Students T-test was used to compare the relative changes *p<0.05, **p<0.005

Table S20: Levels of sex specific mRNAs are misregulated upon ecdysone deficit

Genotype, conditions			C_T *DsxM* ± StDev	C_T *Rpl32* ± StDev	ΔC_T (ΔC_T *DsxM*- ΔC_T *Rpl32*) [a]	$\Delta\Delta C_T$ (ΔC_T-ΔC_T $_{control}$) [b]	Fold Difference [c]
Females	**Control**: *OrR*	18°C	26.20±0.07	15.40±0.20	10.80±0.21	0.00±0.21	1.00 (0.866-1.155)
	OrR	29°C	26.34±0.01	13.95±0.03	12.39±0.03	1.58±0.03	0.334 (0.326-0.341) p=3.73x10^{-3}**
	Control: *ecd1^{ts}*	18°C	26.41±0.07	13.69±0.07	12.72±0.10	0.00±0.10	1.00 (0.935-1.070)
	ecd1^{ts}	29°C	25.88±0.12	14.36±0.07	11.52±0.14	-1.20±0.14	2.299 (2.081-2.539) 2.59x10^{-4}***
Males	**Control**: OrR	18°C	17.84±0.04	15.67±0.15	2.17±0.16	0.00±0.16	1.00 (0.896-1.116)
	OrR	29°C	18.17±0.06	15.45±0.29	2.72±0.30	0.55±0.30	0.681 (0.553-0.838) p=0.06
	Control: *ecd1^{ts}*	18°C	18.40±0.02	15.77±0.20	2.63±0.20	0.00±0.20	1.00 (0.868-1.152)
	ecd1^{ts}	29°C	18.04±0.05	14.60±0.14	3.45±0.25	0.81±0.15	0.569 (0.511-0.633) p=7.97x10^{-3}*

Genotype, conditions			C_T *Esg* ± StDev	C_T *Rpl32* ± StDev	ΔC_T (ΔC_T *Esg*- ΔC_T *Rpl32*) [a]	$\Delta\Delta C_T$ (ΔC_T-ΔC_T $_{control}$) [b]	Fold Difference [c]
Females	**Control**: *OrR*	18°C	29.30±0.09	15.40±0.20	13.90±0.22	0.00±0.22	1.00 (0.862-1.161)
	OrR	29°C	27.90±0.08	13.95±0.03	13.94±0.09	0.04±0.09	0.970 (0.912-1.032) p=0.81
	Control: *ecd1^{ts}*	18°C	24.39±0.28	13.69±0.07	10.70±0.28	0.00±0.28	1.00 (0.821-1.218)
	ecd1^{ts}	29°C	24.69±0.22	14.36±0.07	10.33±0.24	-0,37±0.24	1.293 (1.097-1.523) p=0.07
Males	**Control**: OrR	18°C	26.86±0.05	15.67±0.15	11.19±0.16	0.00±0.16	1.00 (0.894-1.119)
	OrR	29°C	27.48±0.003	15.45±0.29	12.03±0.29	0.84±0.29	0.559 (0.456-0.685) p=0.55
	Control: *ecd1^{ts}*	18°C	25.89±0.02	15.77±0.20	10.12±0.20	0.00±0.20	1.00 (0.868-1.152)
	ecd1^{ts}	29°C	25.34±0.13	14.60±0.14	10.75±0.20	0.63±0.20	0.648 (0.566-0.742) p=8.77x10^{-3}*

Genotype, conditions			C_T *SxlFl1* ± StDev	C_T *Rpl32* ± StDev	ΔC_T (ΔC_T *SxlFl1*- ΔC_T *Rpl32*) [a]	$\Delta\Delta C_T$ (ΔC_T-ΔC_T $_{control}$) [b]	Fold Difference [c]
Females	**Control**: *OrR*	18°C	17.81±0.08	15.40±0.20	2.41±0.21	0.00±0.21	1.00 (0.864-1.158)
	OrR	29°C	15.96±0.16	13.95±0.03	2.00±0.16	-0.41±0.16	1.330 (1.189-1.487) p=5.00x10^{-2}*
	Control: *ecd1^{ts}*	18°C	16.02±0.04	13.69±0.07	2.33±0.08	0.00±0.08	1.00 (0.947-1.056)
	ecd1^{ts}	29°C	16.18±0.16	14.36±0.07	1.82±0.17	-0.51±0.17	1.424 (1.262-1.607) p=1.64x10^{-3}**
Males	**Control**: OrR	18°C	21.05±0.12	15.67±0.15	5.38±0.20	0.00±	1.00 (0.873-1.146)
	OrR	29°C	21.44±0.07	15.45±0.29	5.99±0.30	0.61±	0.653 (0.530-0.805) p=0.15
	Control: *ecd1^{ts}*	18°C	22.24±0.12	15.77±0.20	6.47±0.24	0.00±	1.00 (0.848-1.179)
	ecd1^{ts}	29°C	19.38±0.07	14.60±0.14	4.78±0.16	-1.69±	3.222 (2.883-3.600) p=9.13x10^{-3}**

Genotype, conditions			C_T *tra1* ± StDev	C_T *Rpl32* ± StDev	ΔC_T (ΔC_T *tra1*- ΔC_T *Rpl32*) [a]	$\Delta\Delta C_T$ (ΔC_T-ΔC_T $_{control}$) [b]	Fold Difference [c]
Females	**Control**: *OrR*	18°C	21.04±0.05	15.40±0.20	5.64±0.20	0.00±0.20	1.00 (0.868-1.152)
	OrR	29°C	19.87±0.11	13.95±0.03	5.92±0.11	0.28±0.11	0.826 (0.765-0.891) p=0.14
	Control: *ecd1^{ts}*	18°C	20.01±0.08	13.69±0.07	6.32±0.11	0.00±0.11	1.00 (0.927-1.079)
	ecd1^{ts}	29°C	20.69±0.11	14.36±0.07	6.33±0.13	0.008±0.13	0.994 (0.909-1.088) p=0.93
Males	**Control**: OrR	18°C	28.84±0.09	15.67±0.15	13.18±0.18	0.00±0.18	1.00 (0.885-1.129)
	OrR	29°C	28.67±0.05	15.45±0.29	13.22±0.30	0.05±0.30	0.969 (0.789-1.190) p=0.73
	Control: *ecd1^{ts}*	18°C	28.69±0.12	15.77±0.20	12.92±0.23	0.00±0.23	1.00 (0.850-1.176)
	ecd1^{ts}	29°C	23.68±0.06	14.60±0.14	9.08±0.16	-3.84±0.16	14.277 (12.801-15.924) p=1.76x10^{-5}***

Genotype, conditions			C_T *Yp1* ± StDev	C_T *Rpl32* ± StDev	ΔC_T (ΔC_T *Yp1*- ΔC_T *Rpl32*) [a]	$\Delta\Delta C_T$ (ΔC_T-ΔC_T $_{control}$) [b]	Fold Difference [c]
Females	**Control**: *OrR*	18°C	12.33±0.14	15.40±0.20	-3.07±0.24	0.00±0.24	1.00 (0.846-1.182)
	OrR	29°C	11.21±0.23	13.95±0.03	-2.74±0.23	0.33±0.23	0.794 (0.678-0.930) p=0.12
	Control: *ecd1^{ts}*	18°C	10.86±0.31	13.69±0.07	-2.82±0.32	0.00±0.32	1.00 (0.800-1.249)
	ecd1^{ts}	29°C	11.24±0.20	14.36±0.07	-3.12±0.21	-0.30±0.21	1.231 (1.061-1.428) p=0.15
Males	**Control**: OrR	18°C	26.15±0.11	15.67±0.15	10.48±0.19	0.00±0.19	1.00 (0.876-1.142)
	OrR	29°C	25.57±0.03	15.45±0.29	10.12±0.29	-0.36±0.29	1.285 (1.048-1.576) p=0.14
	Control: *ecd1^{ts}*	18°C	24.63±0.08	15.77±0.20	8.86±0.22	0.00±0.22	1.00 (0.86-1.163)
	ecd1^{ts}	29°C	16.76±0.06	14.60±0.14	2.16±0.16	-6.702±0.16	104.080 (93.395-115.987) p=3.22x10^{-6}***

a: ΔC_T was determined by subtracting the average *RpL32* C_T value from the average Experimental C_T value. Since the same set of samples was used for all PCRs, the same *RpL32* C_T values are used as internal control. The standard deviation of the difference is calculated from the standard deviation of the Experimental and *RpL32* values using the formula $s = \sqrt{(s_1^2 + s_2^2)}$ where s = standard deviation.
b: $\Delta\Delta C_T$ is calculated by subtracting the ΔC_T control value (ΔC_T of the sample of the respective sex and genotype at 18°C). The standard deviation is the same as for ΔC_T.
c: the fold difference between the Experimental Sample and the control is calculated by: $2^{-\Delta\Delta CT}$ with $\Delta\Delta C_T$ +s and $\Delta\Delta C_T$ –s where s is the standard deviation of $\Delta\Delta C_T$ value. The fold difference of the experimental values was compared to the respective control. P-value was calculated using the two tailed Students t-test. *p<0.05, **p<0.005. ***p<0.0005.

Table S21. Ecdysteroid deficit leads to differentiation defects in the CySC lineage cells in adult testes

Genotype, conditions	Clustering of somatic cyst cells				Appearance of epithelium-like clusters			
	< 5 cells	≥ 5 cells	> 10 cells	P value	None	Apical	Lateral	P value
Control: *ecd*^{1ts,} 5 days, 18°	40%	60%	0%		100%	0%	0%	
ecd^{1ts,} 5 days, 29°	7%	57%	36%	0.0368*	43%	43%	14%	0.0137*
Control: *ecd*^{1ts,} 11 days, 18°	50%	50%	0%		83%	17%	0%	
ecd^{1ts,} 11 days, 29°	17%	8%	75%	0.0113*	0%	50%	50%	0.0001***

To calculate the significance two-way tables and chi-squared test with 2 degrees of freedom were used. The frequencies of the testes with the somatic cell clustering phenotype (<5, ≥ 5 or >10 somatic cell in the cluster) and the frequencies of the testes with epithelial sheets (none, apical or lateral) acquired by induction of ecdysone deficit for 5d or 11d at the restrictive temperature (29°) were compared to the frequencies of the same phenotypes in flies with the same genotype but kept for the same periods of time (5d or 11d) at the permissive temperature (18°). N=10-20 testes for each genotype. *p<0.05, **p<0.005. ***p<0.0005.

TABLE S22: Ranked abundance of miRNAs in each sexed library (Complete list)

	Late embryo Lymphoid Cells				L3 Larvae Salivary Glands				Adult Head				Adult Body				Adult Gonads			
					S. Gland M		S. Gland F										Testis			
Chrom	miRNA	S2 M (%)	miRNA	Kc F (%)	miRNA	(%)	miRNA	(%)	miRNA	Head M (%)	miRNA	Head F (%)	miRNA	Body M (%)	miRNA	Body F (%)	miRNA	(%)	miRNA	Ovary (%)
chr2R	mir-14	38.35286	mir-14	29.10042	mir-8	32.42188	mir-8	35.66808	mir-8	14.57004	mir-8	11.43554	mir-1	25.56082	mir-1	26.75240	mir-12	16.87054	mir-989	18.37262
chr2R	mir-184	11.34536	mir-184	16.37821	mir-263a	10.45437	mir-12	8.49222	mir-1	9.99692	mir-1	8.17673	mir-8	23.01229	mir-8	25.64450	mir-8	15.35016	bantam	11.43364
chr3L	bantam	7.44158	mir-2a	4.44288	mir-375	7.15235	mir-263a	7.75277	bantam	8.19215	mir-276a	7.62653	bantam	12.55761	bantam	9.78819	mir-305	5.03802	mir-8	9.30021
chr3R	mir-996	4.85129	mir-8	4.14932	mir-12	6.25415	mir-375	6.71742	mir-276a	5.81087	bantam	7.13572	mir-276a	4.65975	mir-276	5.02046	mir-959	4.67717	mir-2a	7.72512
chr3R	mir-279	3.46812	bantam	4.07801	mir-304	5.72874	mir-282	6.30407	mir-276	5.39112	mir-210	4.99725	mir-277	3.91230	mir-276a	4.27473	mir-2a	3.85408	mir-318	7.24950
chr3R	mir-11	3.29268	mir-34	3.39610	mir-275	5.19227	mir-304	6.00679	mir-277	4.66334	mir-277	4.90334	mir-276	2.46689	mir-2a	2.93279	let-7	3.13374	mir-184	6.40474
chr3R	mir-34	2.93382	mir-988	3.37195	bantam	4.71150	bantam	4.82103	mir-184	4.05515	mir-184	4.17368	mir-2a	2.19543	mir-277	2.68239	mir-34	3.10799	mir-996	5.91867
chr2R	mir-988	2.89604	mir-317	3.14547	mir-2a	3.04332	mir-11	2.45542	mir-34	3.57697	mir-34	3.61372	mir-996	1.54310	mir-989	1.76169	mir-282	3.00171	mir-2b	3.30079
chr3L	mir-282	2.84211	mir-2b	3.10880	mir-305	2.73388	mir-13b	2.44753	mir-2b	3.41702	mir-14	3.20424	let-7	1.48826	mir-282	1.68466	mir-964	2.74226	mir-994	3.00554
chr3R	mir-252	2.78986	mir-276	2.30014	mir-2b	2.43359	mir-305	1.92719	mir-2a	3.22916	mir-285	2.95344	mir-9a	1.48086	mir-31a	1.48123	mir-277	2.58692	mir-275	2.61547
chr3R	mir-13b	2.42533	mir-996	2.29723	mir-13b	1.98678	mir-2a	1.91021	mir-285	3.21797	mir-2a	2.92097	mir-14	1.34500	mir-2b	1.20586	mir-11	2.50748	mir-13b	2.19972
chr2L	mir-2b	2.09460	mir-279	2.25699	mir-11	1.91047	mir-2b	1.55036	mir-14	2.46292	mir-2b	2.73268	mir-31a	1.27792	mir-9a	1.18265	mir-978	2.29276	mir-9b	2.19650
chr3R	mir-317	1.92167	mir-13b	2.19551	mir-283	1.78685	mir-283	1.53792	mir-210	2.43620	mir-276	2.71511	mir-282	1.19988	mir-996	1.08039	mir-977	2.19598	mir-263a	1.46179
chr3L	mir-276a	1.91873	mir-11	2.08551	mir-282	1.58233	mir-996	1.19958	mir-124	2.35303	mir-274	2.60279	mir-12	1.09602	let-7	1.07663	mir-274	2.14935	mir-79	1.39712
chr2L	mir-2a	1.64508	mir-9b	1.77317	mir-996	1.13781	mir-276	1.15280	mir-13b	2.20357	let-7	2.39044	mir-13b	1.08115	mir-184	1.05731	mir-976	2.04009	mir-282	1.37663
chr3L	mir-276	0.94940	mir-276a	1.62248	mir-308	1.06112	mir-308	0.99607	let-7	1.62439	mir-124	2.28452	mir-10	0.98418	mir-13b	0.95693	mir-9a	1.85601	mir-11	1.34088
chr2R	mir-8	0.84006	mir-12	1.57688	mir-14	0.99282	mir-998	0.99113	mir-1000	1.47162	mir-252	1.76221	mir-2b	0.93727	mir-10	0.83951	mir-983	1.82510	mir-34	1.31839
chr3R	mir-995	0.78928	mir-305	1.53819	mir-998	0.81005	mir-276a	0.73590	mir-263a	1.36504	mir-13b	1.62700	mir-281-1	0.90548	mir-11	0.75229	mir-9b	1.82375	mir-305	1.08218
chr3R	mir-277	0.77711	mir-2a-2	1.44698	mir-276	0.74252	mir-79	0.69444	mir-987	1.15961	mir-9a	1.53286	mir-304	0.88408	mir-14	0.73860	mir-14	1.82239	mir-9c	0.93878
chr2L	mir-305	0.69694	mir-306	0.91420	mir-34	0.62690	mir-995	0.63562	mir-252	1.13643	mir-996	1.28000	mir-184	0.78891	mir-281-1	0.71807	mir-988	1.78579	mir-12	0.91588
chr3R	mir-998	0.65434	mir-998	0.88647	mir-995	0.62232	mir-34	0.58884	mir-274	1.09402	mir-263a	1.21244	mir-279	0.74956	mir-314	0.59703	mir-2b	1.64237	mir-33	0.83634
chr2L	mir-306	0.52465	mir-9c	0.84265	mir-79	0.61202	mir-14	0.52468	mir-7	1.09173	mir-1000	1.20431	mir-11	0.74272	mir-279	0.55596	mir-960	1.47375	mir-995	0.76444
chr2L	mir-9b	0.51688	mir-995	0.83930	mir-9a	0.58760	mir-275	0.51086	mir-9a	0.95078	mir-31a	1.03433	mir-305	0.71838	mir-263a	0.52228	mir-13b	1.41302	mir-14	0.63107
chr2L	mir-79	0.42874	mir-79	0.80867	mir-9b	0.47962	mir-33	0.44533	mir-929	0.94692	mir-11	1.00219	mir-79	0.62466	mir-305	0.49544	mir-317	1.21701	mir-1	0.62224
chr2L	mir-2a-2	0.42286	mir-282	0.68950	mir-33	0.47275	mir-9a	0.43289	mir-31a	0.91492	mir-7	0.96850	mir-263a	0.60851	mir-34	0.43546	mir-316	1.19749	mir-312	0.58247
chr3L	mir-33	0.40440	mir-33	0.60276	mir-276a	0.44185	mir-277	0.32768	mir-305	0.89363	mir-125	0.96574	mir-314	0.59811	mir-12	0.37588	mir-311	0.97111	mir-276a	0.56319
chr2L	mir-9c	0.39789	mir-277	0.37739	mir-306	0.40712	mir-9b	0.32531	mir-996	0.82355	mir-305	0.95444	mir-33	0.49554	mir-9c	0.32609	mir-310	0.90984	mir-276	0.52462
chrX	mir-980	0.32192	mir-308	0.37672	mir-252	0.31708	mir-317	0.30320	mir-317	0.70743	mir-276b	0.78241	mir-34	0.48268	mir-79	0.29469	mir-125	0.90306	mir-7	0.48967
chr3R	mir-1003	0.31206	mir-92a	0.33044	mir-184	0.30906	mir-1	0.29669	mir-279	0.65784	mir-133	0.76965	mir-958	0.37959	mir-304	0.28288	mir-278	0.65771	mir-306	0.40612
chr2R	mir-308	0.31122	mir-970	0.26494	mir-277	0.30792	mir-279	0.29452	mir-79	0.60700	mir-987	0.74956	mir-316	0.28530	mir-958	0.28221	mir-276a	0.60945	let-7	0.35792
chrX	mir-970	0.23924	mir-2b-2	0.24593	mir-278	0.30410	mir-306	0.22582	mir-276b	0.57736	mir-307	0.74442	mir-9c	0.28334	mir-278	0.27375	mir-984	0.59671	mir-31a	0.35390
chr2R	mir-307	0.19559	mir-278	0.24571	mir-9c	0.28121	mir-184	0.21418	mir-999	0.56703	mir-317	0.67901	mir-125	0.26945	mir-33	0.26490	mir-975	0.57855	mir-92a	0.31453
chr2L	mir-965	0.11731	mir-981	0.21284	mir-317	0.27396	mir-9c	0.18161	mir-125	0.56561	mir-929	0.62341	mir-281-2	0.26235	mir-281-2	0.23215	mir-9c	0.55577	mir-304	0.29846
chr2L	mir-2b-1	0.10451	mir-283	0.20792	mir-1	0.25908	mir-31a	0.15061	mir-282	0.53936	mir-79	0.62224	mir-278	0.25546	mir-125	0.23054	mir-312	0.46197	mir-984	0.28641
chr2L	mir-275	0.09674	mir-1003	0.20166	mir-988	0.21291	mir-252	0.12712	mir-11	0.48946	mir-279	0.60837	mir-375	0.24167	mir-316	0.22987	mir-279	0.42130	mir-313	0.25267
chr2L	mir-2b-2	0.09045	mir-1000	0.19384	mir-31a	0.19879	mir-965	0.11192	mir-957	0.48513	mir-957	0.57258	mir-956	0.22336	mir-9b	0.21578	mir-375	0.40422	mir-279	0.25106
chrX	mir-12	0.08709	mir-304	0.18803	mir-2b-1	0.17590	mir-988	0.10640	mir-13a	0.44209	mir-999	0.49348	mir-9b	0.21930	mir-252	0.19055	mir-92a	0.38606	mir-317	0.21250
chr2R	mir-7	0.06967	mir-275	0.18601	mir-279	0.12248	mir-278	0.10383	mir-307	0.44043	mir-278	0.42620	mir-252	0.20762	mir-956	0.18693	mir-31a	0.30744	mir-281-1	0.20969
chrX	mir-13b-2	0.06275	mir-965	0.13593	mir-1012	0.08776	mir-2b-1	0.09179	mir-133	0.38123	mir-13a	0.42396	mir-274	0.18483	mir-274	0.15821	mir-252	0.26840	mir-92b	0.20567
chr3R	mir-999	0.05184	mir-92b	0.09994	mir-986	0.08051	mir-10	0.07797	mir-998	0.37453	mir-932	0.40957	mir-7	0.15484	mir-7	0.12453	mir-972	0.26054	mir-2b-2	0.17916
chr2R	mir-281-1	0.03756	mir-999	0.08362	mir-10	0.07593	mir-1012	0.06830	mir-10	0.29404	mir-282	0.31584	mir-980	0.15407	mir-980	0.12185	mir-306	0.25782	mir-983	0.16590
chr2L	mir-2a-1	0.03631	mir-190	0.06886	mir-2b-2	0.07211	mir-7	0.05330	mir-932	0.28490	mir-263b	0.28057	mir-124	0.14728	mir-929	0.10990	mir-963	0.25105	mir-998	0.16189
chr3L	mir-190	0.03589	mir-980	0.06752	mir-970	0.06754	mir-986	0.04461	mir-263b	0.24761	mir-998	0.26211	mir-317	0.12192	mir-375	0.10883	mir-31b	0.23722	mir-2a-2	0.13618
chr3R	mir-1012	0.03442	mir-13b-2	0.06707	mir-7	0.06715	let-7	0.04323	mir-278	0.22301	mir-9c	0.25580	mir-31b	0.10638	mir-999	0.10346	mir-7	0.23397	mir-316	0.13377
chr2R	mir-1008	0.01973	mir-2a-1	0.05791	mir-965	0.04998	mir-970	0.03908	mir-9c	0.20614	mir-10	0.22399	mir-307	0.10612	mir-275	0.10239	mir-92b	0.20252	mir-308	0.12975
chr2L	mir-263a	0.01385	mir-7	0.05433	mir-190	0.04960	mir-2b-2	0.03494	mir-87	0.18478	mir-193	0.20983	mir-986	0.09671	mir-308	0.09179	bantam	0.18625	mir-986	0.12091
chr2L	mir-1006	0.01217	mir-1008	0.03913	mir-2a-2	0.04273	mir-190	0.03316	mir-995	0.17776	mir-2a-2	0.20960	mir-308	0.09589	mir-317	0.07528	mir-999	0.18246	mir-125	0.10083
chr3L	mir-9a	0.01028	mir-989	0.03532	mir-1006	0.02709	mir-2a-2	0.03237	mir-193	0.15593	mir-87	0.19189	mir-929	0.09311	mir-87	0.07179	mir-275	0.16402	mir-307	0.09842
chrX	mir-283	0.01007	mir-2b-1	0.03085	mir-13b-2	0.02366	mir-281-1	0.02329	mir-33	0.14694	mir-9b	0.17409	mir-960	0.08833	mir-986	0.06844	mir-304	0.15074	mir-311	0.09560
chr2R	mir-278	0.00986	mir-252	0.03063	mir-281-1	0.02099	mir-1006	0.02112	mir-2a-2	0.14032	mir-33	0.16610	mir-999	0.07531	mir-306	0.06696	mir-184	0.14640	mir-988	0.08596
chr2R	mir-286	0.00902	mir-281-1	0.02951	mir-281-2	0.02022	mir-281-2	0.01658	mir-2b-1	0.13275	mir-995	0.15358	mir-993	0.07449	mir-307	0.06468	mir-979	0.13474	mir-2b-1	0.07552
chr2R	mir-281-2	0.00714	mir-276b	0.02795	mir-1003	0.01297	mir-13b-2	0.01382	mir-9b	0.12274	mir-316	0.15119	mir-306	0.05926	mir-124	0.06307	mir-961	0.12932	mir-281-2	0.07070
chrX	mir-304	0.00714	mir-932	0.02638	mir-210	0.01183	mir-92b	0.01263	mir-970	0.11367	mir-970	0.14573	mir-263b	0.05885	mir-995	0.06159	mir-962	0.12769	mir-31b	0.06829
chr3R	mir-13a	0.00525	mir-1006	0.02169	mir-92b	0.01183	mir-125	0.01244	mir-92a	0.11202	mir-12	0.12531	mir-965	0.05808	mir-998	0.06159	mir-992	0.10709	mir-965	0.05825
chrX	mir-984	0.00525	mir-9a	0.01856	let-7	0.01145	mir-929	0.00770	mir-304	0.10138	mir-275	0.11695	mir-275	0.05772	mir-31b	0.05998	mir-313	0.10031	mir-283	0.05343
chr2L	mir-1	0.00483	mir-1010	0.01587	mir-999	0.01030	mir-285	0.00750	mir-190	0.09854	mir-304	0.11643	mir-100	0.05674	mir-100	0.04911	mir-283	0.09733	mir-310	0.04740
chr3R	mir-92b	0.00420	mir-984	0.01520	mir-125	0.00878	mir-987	0.00711	mir-315	0.09491	mir-92a	0.11606	mir-998	0.05525	mir-283	0.04871	mir-996	0.09435	mir-278	0.04700
chr2R	mir-3	0.00315	mir-193	0.01431	mir-286	0.00878	mir-999	0.00691	mir-316	0.08821	mir-315	0.11325	mir-133	0.05479	mir-2a-2	0.04871	mir-985	0.08703	mir-1009	0.03615
chr2L	mir-966	0.00315	mir-124	0.01409	mir-929	0.00763	mir-286	0.00612	mir-12	0.08805	mir-306	0.09657	mir-2a-2	0.05386	mir-2b-1	0.04402	mir-986	0.08377	mir-13b-2	0.03575
chr2R	mir-5	0.00294	mir-954	0.01364	mir-5	0.00687	mir-1003	0.00592	mir-308	0.08262	mir-284	0.09386	mir-995	0.04676	mir-2b-2	0.04281	mir-263a	0.06642	mir-277	0.03495
chrX	mir-1007	0.00273	mir-318	0.01341	mir-1005	0.00610	mir-989	0.00592	mir-100	0.07915	mir-2b-1	0.09003	mir-87	0.04671	mir-993	0.04214	mir-1	0.06534	mir-999	0.02932
chr3R	mir-318	0.00273	mir-13a	0.01274	mir-2a-1	0.00610	mir-210	0.00572	mir-993	0.07741	mir-1010	0.07835	mir-988	0.04506	mir-987	0.04133	mir-995	0.06181	mir-303	0.02651
chr3R	mir-92a	0.00273	mir-1	0.01230	mir-989	0.00534	mir-1000	0.00533	mir-1010	0.06709	mir-308	0.07821	mir-1000	0.04501	mir-957	0.04120	mir-100	0.06127	mir-2a-1	0.02450
chr4	mir-954	0.00231	mir-977	0.00984	mir-1000	0.00496	mir-2a-1	0.00533	mir-306	0.05928	mir-100	0.07134	mir-957	0.04316	mir-133	0.04026	mir-79	0.05937	mir-970	0.02370
chr2L	mir-125	0.00210	mir-1012	0.00939	mir-274	0.00458	mir-5	0.00513	mir-2b-2	0.05629	mir-980	0.06840	mir-987	0.04131	mir-988	0.03757	mir-10	0.04636	mir-87	0.02290
chr2R	mir-6	0.00210	mir-966	0.00872	mir-285	0.00458	mir-13a	0.00336	mir-137	0.05526	mir-988	0.06821	mir-13a	0.04100	mir-263b	0.03529	mir-1010	0.04555	mir-980	0.02209
chr2L	mir-967	0.00210	mir-971	0.00783	mir-13a	0.00420	mir-307-as	0.00336	mir-275	0.05266	mir-993	0.06695	mir-983	0.03724	mir-1000	0.02764	mir-33	0.04500	mir-982	0.01848
chr3R	mir-2c	0.00189	mir-986	0.00648	mir-124	0.00382	mir-124	0.00316	mir-927	0.05219	mir-137	0.06079	mir-977	0.03498	mir-970	0.02751	mir-980	0.04175	mir-10	0.01647
chr2L	mir-124	0.00168	mir-994	0.00604	mir-987	0.00343	mir-274	0.00316	mir-988	0.04888	mir-2b-2	0.05532	mir-970	0.03375	mir-13a	0.02711	mir-124	0.04094	mir-1012	0.01607
chr2RHet	mir-2279	0.00168	mir-281-2	0.00514	mir-1008	0.00305	mir-316	0.00276	mir-284	0.04083	mir-986	0.04700	mir-2b-1	0.03205	mir-965	0.02697	mir-1004	0.03904	mir-9a	0.01607
chr2R	mir-310	0.00168	mir-307	0.00492	mir-316	0.00305	mir-1005	0.00217	mir-990	0.03011	mir-927	0.04644	mir-2b-2	0.03164	mir-190	0.02268	mir-281-1	0.03877	mir-100	0.01526
chr2R	mir-311	0.00168	mir-958	0.00425	mir-13b-1	0.00267	mir-100	0.00197	mir-1012	0.02948	mir-981	0.04523	mir-283	0.02968	mir-92a	0.02268	mir-991	0.03443	mir-962	0.01326
chrX	mir-303	0.00147	mir-10	0.00402	mir-133	0.00229	mir-1008	0.00178	mir-283	0.02917	mir-190	0.02962	mir-984	0.02834	mir-210	0.01624	mir-276	0.03335	mir-284	0.00924
chr2R	mir-4	0.00126	mir-286	0.00313	mir-1009	0.00191	mir-13b-1	0.00178	mir-965	0.02846	mir-1012	0.02911	mir-276b	0.02726	mir-284	0.01557	mir-982	0.03253	mir-954	0.00884
chrX	mir-983	0.00126	mir-2c	0.00291	mir-307-as	0.00191	mir-276b	0.00158	mir-980	0.02751	mir-965	0.02864	mir-284	0.02690	mir-276b	0.01503	mir-303	0.03064	mir-252	0.00844
chr2L	let-7	0.00105	mir-31a	0.00268	mir-932	0.00153	mir-305-as	0.00138	mir-1006	0.02483	mir-281-1	0.02602	mir-959	0.02459	mir-1006	0.01355	mir-2a-2	0.03036	mir-966	0.00844
chr2R	mir-1016	0.00105	mir-982	0.00246	mir-1013	0.00114	mir-92a	0.00138	mir-281-2	0.02184	mir-1006	0.02425	mir-964	0.02248	mir-1010	0.01235	mir-970	0.02711	mir-190	0.00723
chr2L	mir-133	0.00105	mir-2279	0.00201	mir-1016	0.00114	mir-957	0.00138	mir-986	0.02136	mir-283	0.02093	mir-1006	0.02135	mir-137	0.01074	mir-998	0.02277	mir-1003	0.00643
chr3L	mir-276b	0.00105	mir-5	0.00201	mir-2c	0.00114	mir-263b	0.00118	mir-281-1	0.02050	mir-281-2	0.02051	mir-210	0.02104	mir-1012	0.01060	mir-974	0.02223	mir-314	0.00643
chr2R	mir-31a	0.00105	mir-983	0.00201	mir-980	0.00114	mir-4	0.00118	mir-219	0.02042	mir-219	0.02042	mir-962	0.02063	mir-318	0.01020	mir-1003	0.01708	mir-1005	0.00562
chr2L	mir-932	0.00105	mir-3	0.00179	mir-2279	0.00076	mir-2279	0.00099	mir-981	0.01821	mir-990	0.02009	mir-976	0.01955	mir-994	0.01020	mir-954	0.01681	mir-929	0.00482
chr3R	mir-994	0.00105	mir-303	0.00179	mir-263b	0.00076	mir-1007	0.00079	mir-969	0.01529	mir-1005	0.01551	mir-963	0.01893	mir-932	0.00939	mir-997	0.01600	mir-960	0.00442
chr2R	mir-1009	0.00084	mir-973	0.00179	mir-284	0.00076	mir-1013	0.00079	mir-1017	0.01443	mir-2c	0.01341	mir-137	0.01754	mir-92b	0.00913	mir-1013	0.01464	mir-1007	0.00402
chr2R	mir-309	0.00084	mir-967	0.00157	mir-305-as	0.00076	mir-1016	0.00079	mir-2c	0.01285	mir-1017	0.01299	mir-1010	0.01641	mir-1014	0.00886	mir-956	0.01464	mir-956	0.00362
chr3L	mir-193	0.00063	mir-1009	0.00134	mir-314	0.00076	mir-133	0.00079	mir-1001	0.01277	mir-1004	0.01182	mir-932	0.01420	mir-13b-2	0.00738	mir-973	0.01383	mir-1010	0.00321
chr2R	mir-312	0.00063	mir-312	0.00134	mir-87	0.00076	mir-193	0.00079	mir-1004	0.01238	mir-1003	0.01065	mir-92a	0.01307	mir-1005	0.00590	mir-1012	0.01247	mir-13a	0.00201
chrX	mir-31b	0.00063	let-7	0.00112	mir-92a	0.00076	mir-87	0.00079	mir-1008	0.00938	mir-1001	0.00972	mir-1014	0.01276	mir-312	0.00537	mir-932	0.01220	mir-274	0.00201
chr2R	mir-986	0.00063	mir-1007	0.00112	mir-957	0.00076	mir-966	0.00079	mir-1007	0.00859	mir-969	0.00897	mir-978	0.01240	mir-962	0.00523	mir-307	0.01139	mir-961	0.00201

chr2R	mir-989	0.00063 mir-284	0.00112 mir-100	0.00038 mir-314	0.00059 mir-1003	0.00843 mir-375	0.00850 mir-974	0.01214 mir-1008	0.00483 mir-2b-2	0.01084 mir-964	0.00201
chr2R	mir-313	0.00042 mir-1013	0.00089 mir-1010	0.00038 mir-980	0.00059 mir-1005	0.00796 mir-1013	0.00612 mir-1012	0.01106 mir-iab-4	0.00470 mir-133	0.01030 mir-1006	0.00161
chr2R	mir-992	0.00042 mir-1016	0.00089 mir-219	0.00038 mir-981	0.00059 mir-1013	0.00709 mir-1007	0.00584 mir-985	0.01101 mir-1003	0.00456 mir-137	0.01030 mir-5	0.00161
chr3R	mir-10	0.00021 mir-310	0.00089 mir-276b	0.00038 mir-1009	0.00039 mir-954	0.00465 mir-954	0.00579 mir-997	0.00947 mir-960	0.00456 mir-971	0.00895 mir-959	0.00161
chr3R	mir-1000	0.00021 mir-978	0.00089 mir-3	0.00038 mir-932	0.00039 mir-375	0.00449 mir-1008	0.00486 mir-961	0.00911 mir-1001	0.00389 mir-308	0.00813 mir-991	0.00161
chr2L	mir-1005	0.00021 mir-992	0.00089 mir-307	0.00038 mir-960	0.00039 mir-92b	0.00426 mir-960	0.00481 mir-190	0.00833 mir-iab-4as	0.00376 mir-13a	0.00786 mir-3	0.00121
chr3R	mir-1010	0.00021 mir-125	0.00067 mir-309	0.00038 mir-969	0.00039 mir-955	0.00426 mir-13b-2	0.00472 mir-iab-4as	0.00741 mir-955	0.00349 mir-314	0.00786 mir-932	0.00080
chr3R	mir-1013	0.00021 mir-133	0.00067 mir-310	0.00038 mir-993	0.00039 mir-971	0.00315 mir-1009	0.00397 mir-303	0.00730 mir-1013	0.00322 mir-281-2	0.00569 mir-983-1	0.00080
chrX	mir-210	0.00021 mir-2282	0.00067 mir-4	0.00038 mir-994	0.00039 mir-1016	0.00276 mir-955	0.00392 mir-1003	0.00638 mir-2a-1	0.00295 mir-318	0.00542 mir-1008	0.00040
chr3L	mir-2282	0.00021 mir-263a	0.00067 mir-954	0.00038 mir-1004	0.00020 mir-2a-1	0.00268 mir-1016	0.00355 mir-1005	0.00628 mir-219	0.00282 mir-2c	0.00515 mir-1013	0.00040
chr3L	mir-263b	0.00021 mir-305-as	0.00067 mir-962	0.00038 mir-137	0.00020 mir-1009	0.00236 mir-314	0.00336 mir-991	0.00617 mir-1007	0.00255 mir-994	0.00515 mir-124	0.00040
chr3L	mir-274	0.00021 mir-309	0.00067 mir-966	0.00038 mir-2279-as	0.00020 mir-960	0.00236 mir-971	0.00327 mir-982	0.00607 mir-981	0.00255 mir-284	0.00434 mir-133	0.00040
chr2R	mir-307-as	0.00021 mir-31b	0.00067 let-7-as	0.00000 mir-275-as	0.00020 mir-962	0.00221 mir-92b	0.00318 mir-1001	0.00545 mir-1015	0.00201 mir-981	0.00434 mir-193	0.00040
chr2L	mir-375	0.00021 mir-6	0.00067 mir-1-as	0.00000 mir-284	0.00020 mir-13b-2	0.00213 mir-2a-1	0.00299 mir-1008	0.00545 mir-1004	0.00174 mir-iab-4as	0.00434 mir-2c	0.00040
chr3R	mir-929	0.00021 mir-975	0.00067 mir-1001	0.00000 mir-3	0.00020 mir-314	0.00142 mir-962	0.00257 mir-312	0.00489 mir-311	0.00174 mir-1006	0.00407 mir-305-as	0.00040
chr3L	mir-958	0.00021 mir-987	0.00067 mir-1002	0.00000 mir-318	0.00020 mir-13b-1	0.00110 mir-31b	0.00206 mir-iab-4	0.00484 mir-954	0.00148 mir-190	0.00352 mir-955	0.00040
chrX	mir-977	0.00021 mir-137	0.00045 mir-1004	0.00000 mir-954	0.00020 mir-305-as	0.00095 mir-964	0.00192 mir-13b-2	0.00473 mir-2c	0.00134 mir-263b	0.00352 mir-963	0.00040
chrX	mir-978	0.00021 mir-263b	0.00045 mir-1004-as	0.00000 mir-956	0.00020 mir-984	0.00079 mir-958	0.00135 mir-219	0.00432 mir-964	0.00134 mir-2a-1	0.00352 mir-985	0.00040
chrX	mir-981	0.00021 mir-311	0.00045 mir-1007	0.00000 mir-958	0.00020 mir-983	0.00071 mir-13b-1	0.00103 mir-285	0.00391 mir-310	0.00121 mir-315	0.00325 mir-iab-4	0.00040
chr2L	let-7-as	0.00000 mir-313	0.00045 mir-1011	0.00000 mir-967	0.00020 mir-1011	0.00063 mir-5	0.00103 mir-973	0.00391 mir-927	0.00121 mir-87	0.00325 let-7-as	0.00000
chr2L	mir-1-as	0.00000 mir-314	0.00045 mir-1014	0.00000 mir-971	0.00020 mir-312	0.00063 mir-956	0.00093 mir-311	0.00350 mir-1016	0.00107 mir-1008	0.00298 mir-1-as	0.00000
chr2L	mir-100	0.00000 mir-4	0.00045 mir-1015	0.00000 let-7-as	0.00000 mir-966	0.00063 mir-961	0.00093 mir-1015	0.00319 mir-313	0.00107 mir-210	0.00271 mir-1000	0.00000
chr3R	mir-1001	0.00000 mir-87	0.00045 mir-1017	0.00000 mir-1-as	0.00000 mir-2279	0.00055 mir-963	0.00093 mir-972	0.00314 mir-315	0.00094 mir-958	0.00244 mir-1001	0.00000
chr2L	mir-1002	0.00000 mir-929	0.00045 mir-137	0.00000 mir-1001	0.00000 mir-31b	0.00055 mir-1011	0.00089 mir-313	0.00304 mir-983	0.00094 mir-965	0.00244 mir-1002	0.00000
chr2L	mir-1004	0.00000 mir-974	0.00045 mir-193	0.00000 mir-1002	0.00000 mir-5	0.00055 mir-959	0.00084 mir-955	0.00304 mir-984	0.00094 mir-3	0.00217 mir-1004	0.00000
chr2L	mir-1004-as	0.00000 mir-210	0.00022 mir-2279-as	0.00000 mir-1004-as	0.00000 mir-959	0.00055 mir-2279	0.00075 mir-981	0.00288 mir-1017	0.00081 mir-193	0.00190 mir-1004-as	0.00000
chr3R	mir-1011	0.00000 mir-2279-as	0.00022 mir-2280	0.00000 mir-1010	0.00000 mir-964	0.00055 mir-983	0.00075 mir-310	0.00283 mir-963	0.00081 mir-955	0.00190 mir-1011	0.00000
chr3R	mir-1014	0.00000 mir-927	0.00022 mir-2281	0.00000 mir-1011	0.00000 mir-961	0.00039 mir-286	0.00070 mir-1013	0.00267 mir-966	0.00081 mir-iab-4	0.00190 mir-1014	0.00000
chr3R	mir-1015	0.00000 mir-956	0.00022 mir-2282	0.00000 mir-1014	0.00000 mir-963	0.00039 mir-966	0.00056 mir-954	0.00257 mir-969	0.00081 mir-1007	0.00163 mir-1015	0.00000
chr3R	mir-1017	0.00000 mir-960	0.00022 mir-2283	0.00000 mir-1015	0.00000 mir-974	0.00039 mir-984	0.00051 mir-1007	0.00242 mir-961	0.00067 mir-1016	0.00163 mir-1016	0.00000
chr2R	mir-137	0.00000 mir-963	0.00022 mir-275-as	0.00000 mir-1017	0.00000 mir-286	0.00032 mir-312	0.00042 mir-992	0.00231 mir-285	0.00054 mir-966	0.00163 mir-1017	0.00000
chr3R	mir-13b-1	0.00000 mir-976	0.00022 mir-287	0.00000 mir-219	0.00000 mir-313	0.00032 mir-305-as	0.00037 mir-1004	0.00226 mir-5	0.00054 mir-989	0.00163 mir-137	0.00000
chr3L	mir-219	0.00000 mir-993	0.00022 mir-289	0.00000 mir-2280	0.00000 mir-956	0.00032 mir-318	0.00028 mir-989	0.00226 mir-1009	0.00040 mir-1009	0.00136 mir-13b-1	0.00000
chr2RHet	mir-2279-as	0.00000 mir-iab-4	0.00022 mir-303	0.00000 mir-2281	0.00000 mir-967	0.00032 mir-989	0.00028 mir-92b	0.00216 mir-2279	0.00040 mir-929	0.00108 mir-210	0.00000
chr2L	mir-2280	0.00000 let-7-as	0.00000 mir-311	0.00000 mir-2282	0.00000 mir-2283	0.00024 mir-3	0.00023 mir-927	0.00211 mir-959	0.00040 mir-1005	0.00081 mir-219	0.00000
chr3R	mir-2281	0.00000 mir-1-as	0.00000 mir-312	0.00000 mir-2283	0.00000 mir-3	0.00024 mir-4	0.00023 mir-1009	0.00195 mir-982	0.00040 mir-1011	0.00081 mir-2279	0.00000
chr3R	mir-2283	0.00000 mir-100	0.00000 mir-313	0.00000 mir-287	0.00000 mir-4	0.00024 mir-313	0.00019 mir-975	0.00170 mir-976	0.00027 mir-2279	0.00081 mir-2279-as	0.00000
chr2L	mir-275-as	0.00000 mir-1001	0.00000 mir-315	0.00000 mir-289	0.00000 mir-958	0.00024 mir-977	0.00019 mir-2c	0.00139 mir-985	0.00027 mir-276b	0.00081 mir-2280	0.00000
chr3R	mir-284	0.00000 mir-1002	0.00000 mir-318	0.00000 mir-2c	0.00000 mir-977	0.00024 mir-2283	0.00014 mir-969	0.00139 mir-990	0.00027 mir-987	0.00081 mir-2281	0.00000
chr3L	mir-285	0.00000 mir-1004	0.00000 mir-31b	0.00000 mir-303	0.00000 mir-310	0.00016 mir-303	0.00014 mir-1017	0.00129 mir-991	0.00027 mir-1001	0.00054 mir-2282	0.00000
chr2L	mir-287	0.00000 mir-1004-as	0.00000 mir-6	0.00000 mir-307	0.00000 mir-968	0.00016 mir-307-as	0.00014 mir-315	0.00123 mir-13b-1	0.00013 mir-1015	0.00054 mir-2283	0.00000
chr3L	mir-289	0.00000 mir-1005	0.00000 mir-927	0.00000 mir-309	0.00000 mir-978	0.00016 mir-968	0.00014 mir-2a-1	0.00108 mir-193	0.00013 mir-2b-1	0.00054 mir-263b	0.00000
chr2L	mir-305-as	0.00000 mir-1011	0.00000 mir-955	0.00000 mir-310	0.00000 mir-994	0.00016 mir-978	0.00014 mir-979	0.00108 mir-2281	0.00013 mir-1000	0.00027 mir-275-as	0.00000
chr3L	mir-314	0.00000 mir-1014	0.00000 mir-956	0.00000 mir-311	0.00000 mir-iab-4	0.00016 mir-982	0.00014 mir-1016	0.00093 mir-286	0.00013 mir-1017	0.00027 mir-276b	0.00000
chr3L	mir-315	0.00000 mir-1015	0.00000 mir-958	0.00000 mir-312	0.00000 mir-1004-as	0.00008 mir-994	0.00014 mir-5	0.00072 mir-287	0.00013 mir-13b-2	0.00027 mir-285	0.00000
chr3L	mir-316	0.00000 mir-1017	0.00000 mir-959	0.00000 mir-313	0.00000 mir-275-as	0.00008 mir-310	0.00009 mir-193	0.00062 mir-289	0.00013 mir-219	0.00027 mir-286	0.00000
chr2L	mir-87	0.00000 mir-13b-1	0.00000 mir-960	0.00000 mir-315	0.00000 mir-303	0.00008 mir-311	0.00009 mir-2279	0.00062 mir-3	0.00013 mir-2283	0.00027 mir-287	0.00000
chrX	mir-927	0.00000 mir-219	0.00000 mir-961	0.00000 mir-31b	0.00000 mir-311	0.00008 mir-967	0.00009 mir-990	0.00041 mir-303	0.00013 mir-983-1	0.00027 mir-289	0.00000
chr3L	mir-955	0.00000 mir-2280	0.00000 mir-963	0.00000 mir-6	0.00000 mir-318	0.00008 mir-974	0.00009 mir-307-as	0.00031 mir-305-as	0.00013 mir-993	0.00027 mir-307-as	0.00000
chr3L	mir-956	0.00000 mir-2281	0.00000 mir-964	0.00000 mir-927	0.00000 mir-982	0.00008 mir-976	0.00009 mir-286	0.00026 mir-307-as	0.00013 let-7-as	0.00000 mir-309	0.00000
chr3L	mir-957	0.00000 mir-2283	0.00000 mir-967	0.00000 mir-955	0.00000 mir-985	0.00008 mir-iab-4	0.00009 mir-966	0.00026 mir-973	0.00013 mir-1-as	0.00000 mir-315	0.00000
chr2L	mir-959	0.00000 mir-274	0.00000 mir-968	0.00000 mir-959	0.00000 mir-989	0.00008 mir-1015	0.00005 mir-13b-1	0.00021 mir-974	0.00013 mir-1002	0.00000 mir-375	0.00000
chr2L	mir-960	0.00000 mir-275-as	0.00000 mir-969	0.00000 mir-961	0.00000 let-7-as	0.00000 mir-2281	0.00005 mir-2281	0.00021 mir-978	0.00013 mir-1004-as	0.00000 mir-4	0.00000
chr2L	mir-961	0.00000 mir-285	0.00000 mir-971	0.00000 mir-962	0.00000 mir-1-as	0.00000 mir-275-as	0.00005 mir-2283	0.00021 mir-992	0.00013 mir-1014	0.00000 mir-6	0.00000
chr2L	mir-962	0.00000 mir-287	0.00000 mir-972	0.00000 mir-963	0.00000 mir-1002	0.00000 mir-309	0.00005 mir-318	0.00021 let-7-as	0.00000 mir-13b-1	0.00000 mir-927	0.00000
chr2L	mir-963	0.00000 mir-289	0.00000 mir-973	0.00000 mir-964	0.00000 mir-1014	0.00000 mir-972	0.00005 mir-971	0.00021 mir-1-as	0.00000 mir-2279-as	0.00000 mir-957	0.00000
chr2L	mir-964	0.00000 mir-307-as	0.00000 mir-974	0.00000 mir-968	0.00000 mir-1015	0.00000 mir-991	0.00005 mir-994	0.00021 mir-1002	0.00000 mir-2280	0.00000 mir-958	0.00000
chr2L	mir-968	0.00000 mir-315	0.00000 mir-975	0.00000 mir-972	0.00000 mir-2279-as	0.00000 mir-992	0.00005 mir-967	0.00015 mir-1004-as	0.00000 mir-2281	0.00000 mir-967	0.00000
chrX	mir-969	0.00000 mir-316	0.00000 mir-976	0.00000 mir-973	0.00000 mir-2280	0.00000 mir-iab-4as	0.00005 mir-3	0.00010 mir-1011	0.00000 mir-2282	0.00000 mir-968	0.00000
chrX	mir-971	0.00000 mir-375	0.00000 mir-977	0.00000 mir-974	0.00000 mir-2281	0.00000 let-7-as	0.00000 mir-4	0.00010 mir-2279-as	0.00000 mir-275-as	0.00000 mir-969	0.00000
chrX	mir-972	0.00000 mir-955	0.00000 mir-978	0.00000 mir-975	0.00000 mir-2282	0.00000 mir-1-as	0.00000 mir-1011	0.00005 mir-2280	0.00000 mir-285	0.00000 mir-971	0.00000
chrX	mir-973	0.00000 mir-957	0.00000 mir-979	0.00000 mir-976	0.00000 mir-287	0.00000 mir-1002	0.00000 mir-2280	0.00005 mir-2282	0.00000 mir-286	0.00000 mir-972	0.00000
chrX	mir-974	0.00000 mir-959	0.00000 mir-981	0.00000 mir-977	0.00000 mir-289	0.00000 mir-1004-as	0.00000 mir-983-1	0.00005 mir-2283	0.00000 mir-287	0.00000 mir-973	0.00000
chrX	mir-975	0.00000 mir-961	0.00000 mir-982	0.00000 mir-978	0.00000 mir-307-as	0.00000 mir-1014	0.00000 let-7-as	0.00000 mir-275-as	0.00000 mir-289	0.00000 mir-974	0.00000
chrX	mir-976	0.00000 mir-962	0.00000 mir-983	0.00000 mir-979	0.00000 mir-309	0.00000 mir-2279-as	0.00000 mir-1-as	0.00000 mir-309	0.00000 mir-305-as	0.00000 mir-975	0.00000
chrX	mir-979	0.00000 mir-964	0.00000 mir-983-1	0.00000 mir-982	0.00000 mir-6	0.00000 mir-2280	0.00000 mir-1002	0.00000 mir-4	0.00000 mir-307-as	0.00000 mir-976	0.00000
chrX	mir-982	0.00000 mir-968	0.00000 mir-984	0.00000 mir-983	0.00000 mir-972	0.00000 mir-2282	0.00000 mir-1004-as	0.00000 mir-6	0.00000 mir-309	0.00000 mir-977	0.00000
chrX	mir-983-1	0.00000 mir-969	0.00000 mir-985	0.00000 mir-983-1	0.00000 mir-973	0.00000 mir-287	0.00000 mir-2279-as	0.00000 mir-967	0.00000 mir-4	0.00000 mir-978	0.00000
chrX	mir-985	0.00000 mir-972	0.00000 mir-990	0.00000 mir-984	0.00000 mir-975	0.00000 mir-289	0.00000 mir-2282	0.00000 mir-968	0.00000 mir-5	0.00000 mir-979	0.00000
chr2R	mir-987	0.00000 mir-979	0.00000 mir-991	0.00000 mir-985	0.00000 mir-976	0.00000 mir-6	0.00000 mir-275-as	0.00000 mir-971	0.00000 mir-6	0.00000 mir-981	0.00000
chr2R	mir-990	0.00000 mir-983-1	0.00000 mir-992	0.00000 mir-990	0.00000 mir-979	0.00000 mir-973	0.00000 mir-287	0.00000 mir-972	0.00000 mir-927	0.00000 mir-987	0.00000
chr2R	mir-991	0.00000 mir-985	0.00000 mir-993	0.00000 mir-991	0.00000 mir-983-1	0.00000 mir-975	0.00000 mir-289	0.00000 mir-975	0.00000 mir-957	0.00000 mir-990	0.00000
chr3R	mir-993	0.00000 mir-990	0.00000 mir-994	0.00000 mir-992	0.00000 mir-991	0.00000 mir-979	0.00000 mir-305-as	0.00000 mir-977	0.00000 mir-967	0.00000 mir-992	0.00000
chr3R	mir-997	0.00000 mir-991	0.00000 mir-997	0.00000 mir-997	0.00000 mir-992	0.00000 mir-983-1	0.00000 mir-309	0.00000 mir-979	0.00000 mir-968	0.00000 mir-993	0.00000
chr3R	mir-iab-4	0.00000 mir-997	0.00000 mir-iab-4	0.00000 mir-iab-4	0.00000 mir-997	0.00000 mir-985	0.00000 mir-6	0.00000 mir-983-1	0.00000 mir-969	0.00000 mir-997	0.00000
chr3R	mir-iab-4as	0.00000 mir-iab-4as	0.00000 mir-iab-4as	0.00000 mir-iab-4as	0.00000 mir-iab-4as	0.00000 mir-997	0.00000 mir-968	0.00000 mir-997	0.00000 mir-990	0.00000 mir-iab-4as	0.00000
SUM_Norm_Reads_in_lib		**476512.00**	**670268.57**	**419331.00**	**506593.00**	**2221284.28**	**2140318.00**	**1943944.00**	**2554945.07**	**1290996.29**	**481224.84**

The number of reads matching each miRNA in a given library is given in decreasing order as a percentage of all reads in that library. miRNAs representing less than 0.01% of each library are shaded in grey. S. Glands: Salivary glands; M: Male; F: Female.