Table S1: miRNA annotation results in C. elegans

Pre-capped intergenic miRNAs

	mi_name	mi_chrom	mi_strand	mi_start	mi_end	confidence	mature_miRNA	pre-miRNA_capped	pre_cap_reads_num	pre_cap_pvalue	pri_TSS	pri_TSS_position	pri_TSS_reads_number	pri_TSS_pvalue	Conservation
1	cel-mir-235	I	-	6162291	6162387	1	3p	1	20,	8.63e-23,	2	6163239,6164365,	11,5,	3.56e-13,3.60e-04,	Worm specific
2	cel-mir-4932	I	+	9512307	9512416	0	5p	1	5,	1.08e-03,	0	.	.	,	
3	cel-mir-244	I	-	4684316	4684414	1	5p	1	33,	1.34e-51,	1	4684495,	29,	1.73e-37,	Worm specific
4	cel-mir-2207	II	+	11600300	11600383	0	None	1	21,	2.97e-33,	3	11595576,11595763,11595881,	6,16,5,	1.38e-07,2.20e-21,6.82e-06,	Worm specific
5	cel-mir-238	III	-	8867328	8867425	1	3p	1	6,	8.70e-03,	2	8867479,8868502,	17,14,	4.03e-05,1.34e-13,	Worm specific
6	*cel-mir-228	IV	+	5562025	5562122	1	5p	1	91,	7.04e-97,	1	5561898,	369,	<2.2e-308,	Worm specific
7	*cel-mir-51	IV	-	11026013	11026112	1	5p	2	34,56,	1.04e-29,1.45e-28,	1	11026830,	21,	1.16e-5,	Worm specific
8	cel-mir-53	IV	-	11027593	11027691	1	5p	1	239,	3.09e-223,	1	11028153,	25,	1.42e-11,	Worm specific
9	cel-mir-49	X	+	9989282	9989378	1	3p	1	43,	5.14e-64,	4	9985099,9987380,9988327,9989143,	11,27,7,31,	4.21e-11,9.46e-20,1.14e-03,8.52e-29,	Worm specific

*: There is a ncRNA_gene between the miRNA and the upstream primary TIC, but the ncRNA_gene is not expressed according to the small RNA-seq mapping results.
Therefore, the upstream primary TIC is assigned to the miRNA gene.

Intergenic miRNA clusters: 16 clusters, 8 with primary capped TICs

cluster_nu	mi_name	mi_chrom	mi_strand	mi_start	mi_end	confidence	mature_miRNA	pre-miRNA_capped	pre_cap_reads_num	pre_cap_pValue	pri_TSS	pri_TSS_position	pri_TSS_reads_numeer	pri_TSS_pValue
*1	cel-mir-35	II	+	11537608	11537704	1	3p	1	24	3.54E-04	5	11535699,11535906,11536194,11537280,11537526,	22,31,46,7,513,	0.0917201527861,0.0575271881349,8.69038527086e-18,0.916867319088,<2.2e-308
1	cel-mir-36	II	+	11537713	11537809	1	3p	1	176	1.29E-142	5	11535699,11535906,11536194,11537280,11537526,	22,31,46,7,513,	0.0917201527861,0.0575271881349,8.69038527086e-18,0.916867319088,<2.2e-308
1	cel-mir-37	II	+	11537833	11537930	1	3p	1	36	2.44E-09	5	11535699,11535906,11536194,11537280,11537526,	22,31,46,7,513,	0.0917201527861,0.0575271881349,8.69038527086e-18,0.916867319088,<2.2e-308
1	cel-mir-38	II	+	11537933	11538027	1	3p	1	68	1.50E-31	5	11535699,11535906,11536194,11537280,11537526,	22,31,46,7,513,	0.0917201527861,0.0575271881349,8.69038527086e-18,0.916867319088,<2.2e-308
1	cel-mir-39	II	+	11538089	11538175	1	3p	1	21	1.34E-03	5	11535699,11535906,11536194,11537280,11537526,	22,31,46,7,513,	0.0917201527861,0.0575271881349,8.69038527086e-18,0.916867319088,<2.2e-308
1	cel-mir-40	II	+	11538184	11538275	1	3p	1	106	2.76E-67	5	11535699,11535906,11536194,11537280,11537526,	22,31,46,7,513,	0.0917201527861,0.0575271881349,8.69038527086e-18,0.916867319088,<2.2e-308
1	cel-mir-41	II	+	11538308	11538404	1	3p	1	50	3.51E-17	5	11535699,11535906,11536194,11537280,11537526,	22,31,46,7,513,	0.0917201527861,0.0575271881349,8.69038527086e-18,0.916867319088,<2.2e-308
*2	cel-mir-42	II	+	11889811	11889905	1	3p	1	145	2.48E-107	3	11888058,11888392,11889625,	24,93,11,	0.34727907435,2.29284078432e-35,0.16542968745,
2	cel-mir-43	II	+	11889910	11890007	1	3p	1	494	<2.2e-308	3	11888058,11888392,11889625,	24,93,11,	0.34727907435,2.29284078432e-35,0.16542968745,
2	cel-mir-44	II	+	11890023	11890118	1	3p	1	6	9.61E-01	3	11888058,11888392,11889625,	24,93,11,	0.34727907435,2.29284078432e-35,0.16542968745,
*3	cel-mir-229	III	+	2172452	2172566	1	5p	1	10	8.27E-01	1	2172375,	1035,	<2.2e-308,
3	cel-mir-64	III	+	2172848	2172957	1	5p	1	7	9.62E-01	1	2172375,	1035,	<2.2e-308,
3	cel-mir-65	III	+	2173002	2173101	1	5p	1	28	1.75E-05	1	2172375,	1035,	<2.2e-308,
3	cel-mir-66	III	+	2173108	2173206	1	5p	1	9	7.77E-01	1	2172375,	1035,	<2.2e-308,
*4	cel-mir-86	III	-	11936637	11936734	1	5p	1	23	2.38E-20	2	11936993,11937071,	16,70,	1.06063883032e-11,7.87380144283e-86,
4	cel-mir-8211	III	-	11936916	11936980	0	None	0	0	.	2	11936993,11937071,	16,70,	1.06063883032e-11,7.87380144283e-86,
*5	cel-mir-250	V	-	11769917	11770015	1	3p	0	0	.	1	11770221,	39,	1.6112648912e-51,
5	cel-mir-61	V	-	11770060	11770156	1	3p	1	9	2.55E-07	1	11770221,	39,	1.6112648912e-51,
6*	cel-mir-1821	V	-	3042530	3042633	1	3p	0	.	.	1	3042228,		
6*	cel-mir-792	V	-	3042092	3042181	0	None	0	.	.	1	3042228,		
*7	cel-mir-56	X	-	13144691	13144787	1	5p-3p	1	287	5.91E-228	4	13145254,13145358,13146147,13146365,	629,14,52,21,	<2.2e-308,0.718086377362,<2.2e-3080832126157183,0.875610216879,
7	cel-mir-55	X	-	13144827	13144924	1	3p	1	455	<2.2e-308	4	13145254,13145358,13146147,13146365,	629,14,52,21,	<2.2e-308,0.718086377362,<2.2e-3080832126157183,0.875610216879,
7	cel-mir-54	X	-	13144996	13145094	1	3p	1	54	2.86E-11	4	13145254,13145358,13146147,13146365,	629,14,52,21,	<2.2e-308,0.718086377362,<2.2e-3080832126157183,0.875610216879,
*8	cel-mir-73	X	+	2368765	2368863	1	3p	1	24	1.84E-12	2	2367321,2368753,	7,306,	0.349939826396,<2.2e-308,
8	cel-mir-74	X	+	2369043	2369139	1	3p	1	7	7.40E-02	2	2367321,2368753,	7,306,	0.349939826396,<2.2e-308,

Intergenic miRNAs with candidate primary start sites

	mi_name	mi_chrom	mi_strand	mi_start	mi_end	confidence	mature_miRNA	pre-miRNA_capped	pre_cap_reads_num	pre_cap_pvalue	pri_TSS	pri_TSS_position	pri_TSS_reads_number	pri_TSS_pvalue
1	cel-mir-8204	I	+	3710171	3710241	0	None	0	.	,	1	3710095,	67,	2.36e-101,
2	cel-mir-235	I	-	6162291	6162387	1	3p	1	20,	8.63e-23,	2	6163239,6164365,	11,5,	3.56e-13,3.60e-04,
3	cel-mir-1818	I	-	13980858	13980954	0	None	0	.	,	5	13980989,13989672,13992591,13997150,14004323,	19,12,5,12,5,	1.51e-31,2.05e-18,2.26e-09,2.66e-20,1.13e-08,
4	cel-mir-244	I	-	4684316	4684414	1	5p	1	33,	1.34e-51,	1	4684495,	29,	1.73e-37,
5	cel-mir-79	I	+	9332946	9333043	1	3p	0	.	,	3	9331031,9331835,9332806,	12,62,602,	1.73e-01,8.14e-22,<2.2e-308,
6	cel-mir-245	I	+	7887371	7887467	1	3p	0	.	,	2	7886105,7887328,	18,74,	1.57e-12,1.16e-102,
7	cel-mir-1823	I	+	12608619	12608708	1	3p	0	.	,	1	12601770,	7,	1.48e-12,
8	cel-mir-234	II	-	14466263	14466358	1	3p	0	.	,	1	14468883,	15,	6.28e-21,
9	cel-mir-236	II	-	7030180	7030277	1	3p	0	.	,	3	7030340,7031321,7033201,	735,17,5,	<2.2e-308,1.66e-02,1.83e-06,
10	cel-mir-5593-1	II	+	431492	431554	0	None	0	.	,	4	420660,423250,427134,429983,	38,13,14,37,	5.58e-53,2.24e-18,5.06e-21,9.44e-46,
11	cel-mir-45	II	-	11880944	11881039	1	3p	0	.	,	3	11881110,11884361,11886964,	98,56,10,	5.29e-71,3.45e-63,1.00e+00,
12	cel-mir-60	II	-	6328702	6328799	1	3p	0	.	,	1	6328847,	612,	<2.2e-308,
13	cel-mir-261	II	+	5969058	5969156	0	None	0	.	,	1	5967673,	27,	5.49e-36,
14	cel-mir-355	II	-	11833536	11833645	1	5p	0	.	,	1	11833679,	50,	4.78e-84,
15	cel-mir-44	II	+	11890023	11890118	1	3p	0	.	,	6	11887151,11888058,11888392,11889625,11889824,11889993,	15,24,93,11,368,499,	1.42e-06,3.47e-01,2.29e-35,1.65e-01,5.98e-286,<2.2e-308,
16	cel-mir-2207	II	+	11600300	11600383	0	None	1	21,	2.97e-33,	3	11595576,11595763,11595881,	6,16,5,	1.38e-07,2.20e-21,6.82e-06,
17	cel-mir-8186-2	II	-	18637	18697	0	None	0	.	,	2	18932,22945,	39,5,	6.42e-52,5.87e-09,
18	cel-mir-2215	II	-	13333763	13333827	0	None	0	.	,	4	13335024,13335202,13338104,13338764,	16,131,12,17,	3.46e-11,2.79e-170,1.11e-15,2.00e-24,
19	cel-mir-72	II	+	2452838	2452936	1	5p	0	.	,	1	2452695,	150,	4.53e-156,
20	cel-mir-5547	II	+	12238602	12238711	0	None	0	.	,	1	12237814,	35,	1.34e-38,
21	cel-mir-272	III	-	11637966	11638060	0	None	0	.	,	5	11657316,11674565,11675607,11684870,11689384,	9,12,10,5,5,	5.38e-15,1.16e-18,1.15e-16,5.91e-09,1.70e-08,
22	cel-mir-238	III	-	8867328	8867425	1	3p	1	6,	8.70e-03,	2	8867479,8868502,	17,14,	4.03e-05,1.34e-13,
23	cel-mir-46	III	+	13660515	13660611	1	3p	0	.	,	1	13660404,	69,	5.51e-75,
24	cel-mir-76	III	+	3142045	3142141	0	3p	0	.	,	3	3136864,3139322,3140528,	9,15,316,	1.08e-11,1.36e-06,<2.2e-308,
25	cel-mir-2213	III	+	6968870	6968924	0	None	0	.	,	1	6968527,	18,	4.47e-26,
26	cel-mir-5551	IV	+	9757508	9757616	0	None	0	.	,	2	9741430,9757383,	5,9,	3.96e-10,1.63e-13,
27	W08D2.14	IV	-	9825313	9825421	.	.	0	.	,	1	9825518,	6,	4.75e-06,
28	cel-mir-232	IV	-	10994169	10994266	1	3p	0	.	,	3	10994312,10995625,11008387,	54,13,63,	5.54e-94,5.45e-09,1.26e-78,
29	cel-mir-242	IV	+	4274247	4274342	0	None	0	.	,	1	4274173,	20,	6.06e-27,
30	cel-mir-4934	IV	-	9825312	9825421	0	None	0	.	,	1	9825518,	6,	4.75e-06,
31	cel-mir-4937	IV	-	1381705	1381814	0	None	0	.	,	2	1381998,1390313,	12,7,	2.19e-16,4.12e-14,
32	cel-mir-53	IV	-	11027593	11027691	1	5p	1	239,	3.09e-223,	1	11028153,	25,	1.42e-11,
33	cel-mir-59	IV	-	11309154	11309253	1	3p	0	.	,	2	11309320,11310747,	8,15,	3.47e-10,9.31e-21,
34	C07B3.1	IV	-	1381706	1381814	.	.	0	.	,	2	1381998,1390313,	12,7,	2.19e-16,4.12e-14,
35	cel-mir-61	V	-	11770060	11770156	1	3p	0	.	,	7	11770221,11773124,11773636,11774077,11774168,11777938,1177956	39,9,86,17,24,7,12,	1.61e-51,5.17e-06,3.90e-97,7.88e-13,2.80e-21,6.85e-10,1.78e-17,
36	cel-mir-241	V	-	14366188	14366283	1	5p	0	.	,	1	14366610,	6,	1.16e-14,
37	cel-mir-8194	V	-	1221313	1221368	0	None	0	.	,	2	1221457,1222116,	6,5,	9.84e-09,1.20e-06,
38	cel-lsy-6	V	+	10647232	10647304	0	3p	0	.	,	2	10645677,10647182,	38,50,	1.02e-28,9.36e-80,
39	cel-mir-250	V	-	11769917	11770015	1	3p	0	.	,	7	11770221,11773124,11773636,11774077,11774168,11777938,1177956	39,9,86,17,24,7,12,	1.61e-51,5.17e-06,3.90e-97,7.88e-13,2.80e-21,6.85e-10,1.78e-17,
40	cel-mir-255	V	+	5440639	5440748	1	3p	0	.	,	1	5440590,	41,	4.36e-66,
41	cel-mir-259	V	-	10539025	10539125	1	5p	0	.	,	1	10539186,	44,	2.58e-26,
42	cel-mir-792	V	-	3042092	3042181	0	3p	0	.	,	1	3042229,	14,	1.36e-21,
43	cel-mir-8203	X	-	7882764	7882824	0	None	0	.	,	1	7883041,	10,	5.47e-12,
44	cel-mir-788	X	-	8485294	8485371	1	5p	0	.	,	1	8485434,	881,	<2.2e-308,
45	cel-mir-787	X	+	11294708	11294797	1	3p	0	.	,	3	11288996,11290226,11290665,	18,5,159,	1.86e-07,1.30e-02,1.97e-195,
46	cel-mir-47	X	+	13921250	13921346	1	3p	0	.	,	5	13887410,13889362,13917622,13918406,13920855,	5,8,54,13,65,	1.10e-04,3.12e-12,1.03e-68,6.11e-09,1.41e-76,
47	cel-mir-785	X	+	3004668	3004761	0	3p	0	.	,	1	2995849,	15,	5.96e-27,
48	cel-mir-264	X	+	2819254	2819346	0	None	0	.	,	2	2809851,2814606,	16,76,	8.53e-22,4.23e-107,
49	cel-mir-359	X	+	3004291	3004400	0	None	0	.	,	1	2995849,	15,	5.96e-27,
50	cel-mir-63	X	-	17598765	17598868	1	3p	0	.	,	2	17598908,17600216,	214,8,	1.06e-286,6.19e-03,
51	F18E9.9	X	-	8600642	8600734	.	.	0	.	,	1	8601093,	5,	9.12e-08,
52	cel-mir-248	X	-	2262373	2262470	0	None	0	.	,	1	2262525,	152,	2.80e-232,
53	cel-mir-49	X	+	9989282	9989378	1	3p	1	43,	5.14e-64,	4	9985099,9987380,9988327,9989143,	11,27,7,31,	4.21e-11,9.46e-20,1.14e-03,8.52e-29,
54	cel-mir-73	X	+	2368765	2368863	1	3p	0	.	,	2	2367321,2368753,	7,306,	3.50e-01,<2.2e-308,
55	cel-mir-75	X	+	2372453	2372549	1	3p	0	.	,	3	2369581,2370904,2372432,	6,9,11,	1.26e-01,4.22e-03,1.30e-13,
56	cel-mir-800	X	-	380919	380991	1	3p	0	.	,	1	381098,	14,	1.12e-15,
57	cel-mir-251	X	+	11004728	11004824	0	None	0	.	,	2	11003127,11004598,	6,40,	1.25e-05,2.44e-54,
58	cel-mir-392	X	+	13597231	13597340	1	3p	0	.	,	1	13596247,	86,	3.20e-103,
59	cel-mir-799	X	-	8600643	8600735	0	None	0	.	,	1	8601093,	5,	9.12e-08,
60	cel-mir-797	X	+	4757109	4757197	1	5p	0	.	,	7	4741598,4744289,4748911,4750276,4751364,4751655,4752322,	6,10,17,5,8,10,7,	5.74e-08,5.04e-15,1.85e-17,1.27e-04,1.12e-07,1.14e-12,6.14e-09,
61	cel-mir-793	X	+	13857962	13858053	0	None	0	.	,	1	13857900,	55,	4.76e-41,
62	cel-mir-791	X	+	5809349	5809433	1	3p	0	.	,	1	5809275,	15,	1.25e-18,
63	cel-mir-239b	X	-	11791302	11791399	1	5p	0	.	,	1	11791457,	11,	4.59e-12,
64	cel-let-7	X	-	14744173	14744271	1	5p	0	.	,	2	14744481,14747079,	5,85,	3.09e-09,2.30e-139,