Index	miR_name	miR_seq	DSS treated 1	Before treatment 1	Before Treatment 2	Back to normal 1	Back to normal 2	Recovery 2	DSS_treated 2	Recovery 1	Expression level
1	PC-5p-64929_97	CCCTAAGATGAGATCTCT	19	22	28	26	28	0	0	4	middle
2	PC-5p-83204_75	TACAAGCAGATATAGCACT	15	18	11	13	16	6	2	4	middle
3	PC-5p-28717_207	AACATGAGAGTTTGATCCT	164	187	156	104	165	52	9	25	high
4	PC-3p-101610_59	CAAGATGGCTGAGGGGACA	14	21	11	14	14	0	0	0	middle
5	PC-3p-64895_97	GGGACACAGAAGGATAGT	20	39	30	27	30	9	4	10	middle
6	PC-3p-30946_194	AAGGTGAGGTATATGAGC	67	43	48	42	44	13	0	13	middle
7	rno-mir-711-p3_1ss3GT	GGTAAAGCTGGGGACCCT	5	7	11	10	9	0	0	0	middle
8	PC-5p-41107_151	AGGCTAATATCGTTGACT	25	62	72	59	46	0	0	14	middle
9	PC-3p-4173_897	GCTGGAAGGTTAAGAGGA	188	290	336	288	232	100	113	145	high
10	mmu-miR-140-3p_L-1R+2	ACCACAGGGTAGAACCACGGAC	38	7	0	0	0	44	50	58	middle
11	PC-5p-32769_185	GAGATTTGAAGGGAGCTGTC	60	103	84	130	110	43	16	36	middle
12	PC-5p-24662_235	CGTGTTGGCTATGAAACCT	74	128	193	122	152	43	17	43	high
13	PC-5p-59712_106	AAAGCTTTCGGATGACCT	34	31	26	9	27	0	4	5	middle
14	PC-3p-89652_69	GTTGCATGTGAATTCTATC	6	16	22	14	14	0	4	3	middle
15	PC-5p-89052_69	GATGGCGGGCCTCGCTCC	17	12	39	33	34	0	0	0	middle
16	PC-5p-157248_32	GCGGGTAGTTTGACTGGG	6	10	17	9	7	0	0	0	middle
17	PC-3p-67404_94	GTAACTGACACTGAGGCT	23	9	18	30	24	6	2	4	middle
18	PC-5p-56203_113	GTTAAGGAACTCGGCAAGTT	10	19	14	11	9	6	0	2	middle
19	PC-5p-71575_88	GTGTCTGCTAATTCTTCCT	11	21	22	42	24	0	4	0	middle
20	PC-5p-52772_120	GGTGACTGGGGTGAAGTC	16	39	26	33	19	7	5	11	middle
21	mmu-miR-151-3p_R+1	CTAGACTGAGGCTCCTTGAGGA	23	0	7	0	0	22	29	27	middle
22	bta-mir-2904-2-p3_1ss15TC	AGCCTCGGTTGGCCCCGGATAGCC	8	16	12	22	13	3	6	1	middle
23	pal-miR-9226-5p_L-2_1ss4AG	AGGTCCCTGTTCGGGCGCCA	14	7	26	21	17	7	2	0	middle
24	PC-3p-93543_65	GGTGGAGGACCGCACACAC	6	15	17	20	23	7	0	0	middle
25	mmu-mir-5119-p3_1ss6TG	TCATCGCATCCTGGGGCT	17	13	43	24	33	6	0	4	middle
26	PC-5p-100392_60	GAACTATAACCAGAAAACC	6	22	10	11	19	0	4	0	middle
27	PC-5p-19499_284	AAGAACAGAGCAGAACGGC	98	19	78	67	47	13	0	0	middle
28	PC-3p-43069_145	GGTCTCCTACCTACTCTGC	23	43	47	96	68	0	0	15	middle
29	PC-3p-136506_40	CTGCCGTTGAAACTGCATCC	19	12	14	20	21	0	0	8	middle
30	PC-5p-47677_132	GAGATAGCTGGTTCTCCCC	16	27	30	23	38	16	4	7	middle
31	bta-miR-378_R+1	ACTGGACTTGGAGTCAGAAGGCT	25	22	47	13	17	58	50	41	middle
32	aja-mir-671-p3_1ss18GC	AGGGCTCCACCTCTTCCC	27	62	22	36	85	0	0	0	middle
33	PC-5p-73161_86	GAATCAGAATGTCGGGGTG	10	13	29	23	34	10	0	0	middle
34	PC-5p-113008_52	GGAGCCGGTAACTGGGGT	12	12	37	27	19	7	0	4	middle
35	PC-3p-196912_22	AGTGTATTGGTAGAGGAGC	7	0	10	9	7	0	0	0	low
36	PC-3p-116868_49	GTCACATCCCGGGGCTGG	31	25	25	0	24	0	0	3	middle
37	bta-miR-11987_L-2R-1_1ss8TA	AGGAAACTCTGGTGGAGG	3	11	5	9	5	0	2	2	middle
38	PC-3p-84309_74	AGGTTAAGAGGAGAGGTTA	10	13	22	16	20	0	7	8	middle
39	PC-3p-211437_19	TGTAGTATCGGTGAAGATGC	15	19	8	7	9	6	3	0	middle
40	PC-3p-132361_42	GAACTGAAACATCTTAGTA	7	7	7	9	13	0	0	5	middle
41	PC-3p-112124_52	CAATTATGGAGAGTTTGAT	14	7	7	10	11	6	2	0	middle
42	mmu-miR-378a-3p_R+1	ACTGGACTTGGAGTCAGAAGGC	178	262	180	264	162	275	297	290	high
43	PC-5p-82362_76	TGTTAAGGAACTCGGCAA	5	6	13	8	7	0	1	4	middle
44	mmu-miR-99a-5p_R-1	AACCCGTAGATCCGATCTTGT	116	39	60	57	63	110	169	149	high
45	mmu-miR-100-5p_R-1_1ss16AT	AACCCGTAGATCCGATCTTGT	116	39	60	57	63	110	169	149	high
46	PC-5p-82477_75	ATGCGAGGGCTTCACCGCC	55	101	65	7	95	0	0	20	middle
47	PC-3p-9419_502	AGCTGGGTTCAGAACGTC	209	414	407	309	363	156	32	196	high
48	PC-5p-92751_66	GGCATAAGTAGCGAGAGG	44	9	89	39	53	6	0	0	middle
49	mmu-mir-5108-p3_1ss3TA	GGAGGTAGAGCACTGGAT	7	45	34	67	28	11	0	0	middle
50	PC-3p-55588_114	TTGAGTACTGGAGAGGCA	34	70	26	94	48	12	10	15	middle
51	PC-3p-52393_121	GTTCTTGTGCTGTGGATGTC	12	41	52	63	48	0	9	24	middle
52	PC-5p-52393_121	GTTCTTGTGCTGTGGATGTC	12	41	52	63	48	0	9	24	middle
53	PC-5p-15481_342	GGAGGGAAGCGGATGGGGG	36	92	40	113	63	30	12	16	middle
54	mmu-miR-30e-3p	CTTTCAGTCGGATGTTTACAGC	22	9	0	0	0	20	22	19	middle
55	PC-5p-43913_142	AGCACGAGAAATTCTGTC	83	40	55	0	46	0	0	0	middle
56	PC-3p-141420_38	AGGAGAAGAAAACAACAGT	12	16	7	0	10	0	0	0	middle
57	PC-3p-105972_56	GTTCGACTCCCGGTGTGGGAACC	2	7	4	9	16	0	0	0	middle
58	mmu-miR-186-5p	CAAAGAATTCTCCTTTTGGGCT	105	15	37	34	28	89	96	138	middle
59	PC-5p-125445_45	AGGAGTGGAAGTTTGGTGA	12	12	25	33	7	0	0	7	middle
60	PC-5p-138993_39	GGATGACCTGTGGATAGCGG	23	25	10	31	11	11	3	5	middle

61	PC-5p-168746_29	TCTGCCCACAATACTTGGC	5	9	0	11	13	0	0	0	middle
62	PC-3p-71684_88	AGAGGCCGTGAGTTCAAGTCT	16	7	26	9	19	0	6	6	middle
63	PC-3p-137754_39	AGAGATGCGTAGCTGATGG	23	25	0	9	19	0	0	0	middle
64	PC-5p-242185_15	TTAAGAGGAGACGTTAGG	4	7	0	11	10	0	0	0	middle
65	PC-3p-3757_960	TAGTAGGAGGAGGAAAAGA	119	199	145	253	184	246	340	275	high
66	bta-miR-11980_R-1_1ss4CG	AGGGAACGGGCTTGGCGGA	3	15	8	12	15	3	2	5	middle
67	mmu-miR-30e-5p_R+2	TGTAAACATCCTTGACTGGAAGCT	285	135	134	130	130	241	300	241	high
68	PC-5p-7927_569	GAAGCAGATATGAACAAACC	56	113	153	125	154	72	78	46	middle
69	PC-3p-156650_32	GTTCCCTGTCCAACATCCT	0	7	10	10	19	0	0	0	middle
70	PC-3p-95597_64	GGGTAGCCGCGTCTGGGC	23	37	8	10	9	0	0	0	middle
71	PC-3p-144238_37	AGGACCGGGATGGACACA	14	21	25	0	13	0	0	6	middle
72	PC-3p-169435_29	CTGGTCTGCAACTGACACT	5	9	0	9	16	0	0	0	middle
73	hsa-miR-1469_L-4_1ss10GC	GCGCGCGGCGCGGGCTCC	14	7	10	0	9	0	0	4	middle
74	PC-3p-23428_246	AGGTAACACTGACTGGAGGG	77	144	94	89	80	65	2	18	middle
75	mmu-miR-30c-5p_R+1	TGTAAACATCCTACACTCTCAGCT	172	145	118	138	128	236	260	345	high
76	bta-mir-2904-2-p3_1ss12TC	CTCGGTTGGCCCCGGATAGCC	9	30	12	16	29	11	4	4	middle
77	bta-mir-2904-2-p5_1ss12TC	CTCGGTTGGCCCCGGATAGCC	9	30	12	16	29	11	4	4	middle
78	PC-3p-84288_74	ATAGAGGAGACAGACCCAGG	18	0	14	21	17	6	4	0	middle
79	mmu-miR-429-3p	TAATACTGTCTGGTAATGCCGT	123	170	134	179	169	133	97	86	high
80	PC-5p-94450_65	GGTATAGTGCTGATAAACA	0	48	23	54	31	7	6	0	middle
81	PC-3p-10765_453	CCAGGAAGGGAGAATGCC	71	118	332	119	137	67	0	12	high
82	mmu-miR-484	TCAGGCTCAGTCCCCTCCCGAT	15	7	0	9	0	25	41	55	middle
83	mmu-miR-5106_L-3R+1_1ss20CT	TCTGTAGCTCAGTTGGTAGAG	19	67	15	92	34	11	0	3	middle
84	mmu-miR-96-5p	TTTGGCACTAGCACATTTTTGCT	27	61	52	37	33	82	58	63	middle
85	PC-5p-130968_42	GCATAGTGTAGTAGGAAGA	16	0	14	40	20	0	0	0	middle
86	PC-3p-77153_81	AGAAGAGCTTAGAGATAAG	11	13	28	13	7	0	4	8	middle
87	PC-3p-29250_204	GGGAAGATAGGTAGTGCC	49	89	104	41	64	11	36	46	middle
88	mmu-miR-361-5p	TTATCAGAATCTCCAGGGGTAC	0	0	0	0	0	11	17	7	middle
89	PC-5p-141515_38	TTTTTCGAGAGTTTGATC	7	15	28	0	16	0	2	0	middle
90	PC-5p-165416_30	TAGGAGGAAGAGCCATGAAG	0	7	11	11	9	0	0	5	middle
91	mmu-miR-26a-5p	TTCAAGTAATCCAGGATAGGCT	817	404	533	428	390	700	1,024	1,151	high
92	PC-5p-48908_128	AAAACTGTTGGACTTGAGTG	30	10	30	52	27	20	2	7	middle
93	PC-5p-78770_79	GCTTACAAGCACTCAGAGC	13	13	10	17	21	10	0	6	middle
94	PC-3p-58991_107	CAGCCTTGTGAGTTACTAAT	44	51	0	19	53	7	4	11	middle
95	eca-mir-9112-p3_1ss18AC	GTTAGGAGCAGAGATGAC	12	31	52	67	51	8	12	29	middle
96	PC-5p-8347_547	GAGGGCTGGGCACGGGGGT	113	43	249	79	77	40	8	19	high
97	mmu-miR-374c-5p_L+2R-1	ATATAATACAACCTGCTAAGT	6	12	10	7	0	15	30	19	middle
98	mmu-miR-142a-5p_L+2R-3	CCCATAAAGTAGAAAGCACT	403	65	72	74	95	391	239	314	high
99	PC-3p-182654_25	TGAGATTGGTAGGGGAGC	19	0	19	0	17	0	0	0	middle
100	PC-5p-200607_21	CAGTTCAAGTCTGACTACC	8	0	8	0	7	0	0	0	low
101	PC-3p-95788_63	CTCCAGGCATTGAAGAATT	13	7	28	14	7	0	8	4	middle
102	PC-3p-237582_15	AAGGCGCTTGAGAGAACT	7	9	0	0	9	0	0	0	low
103	PC-3p-85446_72	ACTGTGGGTGATAAGGTCC	6	24	10	19	14	10	0	5	middle
104	PC-3p-213436_19	GAAGGTCATGTGGTTCAAA	6	0	0	9	7	0	0	0	low
105	mmu-miR-103-3p	AGCAGCATTGTACAGGGCTATGA	53	42	32	53	22	60	106	115	middle
106	PC-3p-226380_17	GATTTGCTGGACTGTAACT	10	0	7	7	0	0	0	0	low
107	mmu-miR-20a-5p	TAAAGTGCTTATAGTGCAGGTAG	9	10	0	0	0	12	20	9	middle
108	PC-5p-18345_299	TCGCCGAAGCTCAGGGAAGG	46	97	47	126	60	43	12	47	middle
109	PC-5p-52557_120	ACCAGAGAGGGTGAAAGTC	38	10	73	9	23	8	0	0	middle
110	PC-3p-279676_11	ACGGGGAGTTTGACTGGGG	0	9	11	7	0	0	0	0	middle
111	PC-3p-201267_21	AACTCTGTACAGACCGCC	15	0	0	10	11	0	0	0	middle
112	PC-5p-198261_22	ACGAGAAGAAAATTCTAAGA	7	0	11	0	7	0	0	0	middle
113	PC-3p-206796_20	CAGTGGCTCAGTTGGTGGA	0	7	12	9	0	0	0	0	middle
114	PC-5p-276194_11	TGGGAAAGTAGATGGTTGC	5	0	7	9	0	0	0	0	low
115	PC-3p-88143_70	GAAACTGATGTTCTTGAGT	96	15	34	0	44	0	0	0	middle
116	PC-5p-3037_1102	GTGAAGGAAAGGTGAAAAGC	883	1,245	932	1,192	1,132	994	667	734	high
117	PC-3p-193454_23	CTAGAGGCCTATGACGTCT	0	13	7	13	0	0	0	0	middle
118	mmu-mir-6236-p3_1ss9AG	CCATACCCGGCCGTCGCC	0	10	8	0	16	0	0	0	middle
119	PC-5p-110195_53	GCAGGAGCCCAAACCGGA	44	27	32	0	33	0	5	19	middle
120	mmu-miR-30d-5p_R+2	TGTAAACATCCCCGACTGGAAGCT	200	135	142	153	130	271	349	528	high
121	PC-3p-187096_24	AAAGGATGTGTCACTGCT	14	0	10	0	7	0	0	0	middle

122	mmu-miR-425-5p_R-1	AATGACACGATCACTCCCGTTG	39	9	21	27	7	35	28	42	middle
123	PC-3p-51786_122	GAAGGAGTGACGGAGAAGG	15	10	21	29	13	6	12	12	middle
124	PC-3p-217375_18	AAATGGATAAGATAAAGTT	0	10	17	0	7	0	0	0	middle
125	PC-5p-184656_25	GGAGGTGCAAGTCAGCGGT	0	16	23	9	7	0	0	6	middle
126	mmu-miR-128-3p	TCACAGTGAACCGGTCTCTTT	8	0	0	0	0	4	6	11	middle
127	eca-mir-8969-p5_1ss14GT	GGTGGTTCAGTGGTAGAA	3	7	0	16	9	3	0	0	middle
128	PC-5p-168283_29	AGGCAGAGAGCCGCAGATA	0	0	11	10	11	0	3	0	middle
129	PC-3p-242901_15	AGTCGCACTACTCGGACCA	0	15	7	0	7	0	0	0	middle
130	PC-5p-109345_54	GAGGTTAAGGGTAGAGGCC	5	13	8	26	14	8	2	7	middle
131	PC-3p-176876_27	ACACAGGGCTGTGCAAAGT	8	7	0	0	17	0	0	0	middle
132	PC-5p-37319_165	TTTCCGGTGGCCAGGCGGC	56	0	153	0	83	0	0	0	middle
133	bta-miR-11980_R-2_1ss4CG	AGGGAACGGGCTTGGCGG	0	4	0	8	7	0	0	1	low
134	PC-3p-199168_22	AATAAGAAGGGAGAATGCC	4	0	0	10	14	0	0	0	middle
135	PC-3p-157541_32	GGGATAACAGGCTGATTCC	29	0	8	0	20	0	0	0	middle
136	PC-3p-170344_28	CAGACCTGCAGCTAAGGC	14	0	7	0	11	0	2	0	middle
137	mmu-let-7j_R-1_1ss8TG	TGAGGTAGTAGTTTGTGCTGTTA	7	0	3	0	6	6	21	14	middle
138	pal-miR-9995-3p	ATCTCGGTGGAACCTCCA	6	0	11	14	0	0	2	0	middle
139	mmu-miR-125b-5p	TCCCTGAGACCCTAACTTGTGA	40	20	19	14	30	33	78	89	middle
140	mmu-let-7c-5p_1ss19GA	TGAGGTAGTAGGTTGTATAGTT	443	241	300	361	296	478	829	503	high
141	mmu-let-7a-5p	TGAGGTAGTAGGTTGTATAGTT	443	241	300	361	296	478	829	503	high
142	mmu-miR-378c_R+3_1ss21CG	ACTGGACTTGGAGTCAGAAGGCTT	2	0	0	0	0	6	4	1	low
143	PC-3p-47598_132	GTAGGAAATTTGAGAGGAG	22	27	18	30	10	0	9	18	middle
144	eca-mir-9112-p5_1ss3GT	TGTGTTAGGAGCAGAGATG	2	5	13	6	0	0	0	3	middle
145	PC-5p-8572_537	TGGGGAGTTTGGCTGGGGC	608	43	66	72	251	18	0	9	high
146	PC-5p-212023_19	GTAGATAGGGCATGGGTGC	0	0	0	9	0	6	4	5	low
147	PC-5p-262373_12	GAGCAGAGTACTGTGAAGGAA	0	9	8	9	9	6	3	0	low
148	PC-5p-58070_109	CAGGAAGAATTAGCAGACA	6	33	26	31	31	0	19	16	middle
149	PC-5p-79138_79	TTTAGGTGCAGCCTTGTGA	0	49	0	19	28	0	3	4	middle
150	bta-miR-11987_L-1R-2_1ss8TA	GAGGAAACTCTGGTGGAG	0	4	0	6	4	0	0	1	low
151	mmu-miR-148b-3p	TCAGTGCATCACAGAACTTTGT	21	7	0	0	0	15	94	65	middle
152	PC-3p-42663_146	TGAGGGAAAGGTGAAAAGA	4	34	19	36	23	9	11	18	middle
153	mmu-miR-215-3p_R+1	TCTGTCATTCTGTAGGCCAATA	23	7	15	21	20	13	14	9	middle
154	PC-3p-9235_509	GTTCTTAGTTGGTGGAGC	265	27	17	53	112	6	8	30	high
155	mmu-miR-29b-3p	TAGCACCATTTGAAATCAGTGTT	2	0	3	0	4	3	12	8	middle
156	PC-3p-267694_12	CATGAGCAGGATGAAGCAGA	5	0	10	0	16	0	2	0	middle
157	mmu-mir-1983-p3	GTTCGAGCCTCACCTGGA	10	0	0	7	20	0	0	3	middle
158	mmu-miR-23b-3p_R+3	ATCACATTGCCAGGGATTACCACT	44	85	56	89	71	73	122	101	middle
159	PC-3p-51291_123	GCACTGGGAATCAAAGACT	6	18	45	10	26	0	10	13	middle
160	PC-5p-239266_15	ACACGTAGTCGGGTTGAA	0	27	0	7	14	0	0	3	middle
161	PC-5p-83829_74	TGAGTGCAGAAGAGGGAA	28	18	8	39	14	0	10	18	middle
162	mmu-mir-3106-p5_1ss1TC	CTTAGAAGCAGCCATACA	6	62	95	20	56	11	18	32	middle
163	PC-3p-80980_77	TGAAGAGTTTGATCCTGGC	13	21	0	10	37	0	7	9	middle
164	bta-miR-11987_L-1_1ss8TA	GAGGAAACTCTGGTGGAGGT	0	4	10	16	9	0	3	5	middle
165	mmu-let-7i-5p	TGAGGTAGTAGTTTGTGCTGTT	118	36	57	56	30	99	327	168	high
166	mmu-let-7b-5p	TGAGGTAGTAGGTTGTGTGGTT	499	237	290	322	250	497	367	387	high
167	PC-3p-143176_37	GGTGTCTGAATGGGGAAAC	8	19	0	20	0	6	0	0	middle
168	mmu-mir-6240-p3_1ss1GA	AATGTGATTTCTGCCCAGTGCT	4,547	591	396	897	1,837	691	196	305	high
169	PC-3p-49497_127	TTTTGAAAGGAGGTAGCCC	19	28	14	20	24	12	0	19	middle
170	PC-3p-97503_62	CCATACATTCAAAGAGTG	9	68	29	17	9	16	0	7	middle
171	PC-3p-193182_23	GGTAGCTAAGTATGGAAGG	17	0	0	0	17	0	0	0	middle
172	PC-5p-299786_10	ATTAAGTTCAGTAGGTATT	0	7	0	7	0	0	0	0	low
173	ssc-mir-9820-p3_1ss12GC	GTGAGGAGGAGCGAAGAAA	0	4	5	0	0	0	0	0	low
174	mmu-mir-711-p3_1ss4CT	AGGTAAAGCTGGGGACCC	6	0	0	7	0	0	0	0	low
175	PC-3p-259493_13	GAGCACCGTGACTAATGT	10	0	0	0	9	0	0	0	low
176	PC-3p-275999_11	AAAGACTATGAGGTTGATA	0	7	0	0	9	0	0	0	low
177	PC-5p-252515_13	GATTTAGTGGTTGGACATC	0	10	8	0	0	0	0	0	middle
178	PC-5p-157207_32	GAATGATGGAATTGGCAGA	4	15	0	16	0	0	0	4	middle
179	PC-5p-283750_11	GTTAAGGAACTCGGCAAGTTG	0	4	3	0	0	0	0	0	low
180	mml-mir-711-p5_1ss6CT	GCAGGTAAAGCTGGGGACC	5	7	7	0	0	0	0	3	low
181	mmu-mir-8101-p3_1ss17GA	TGGAGGAGCCGTCGAGAA	0	0	0	0	0	0	4	4	low
182	PC-5p-221088_18	AAGGCAGAGTGGTAGAAGA	0	0	0	0	0	0	4	5	low

183	PC-3p-277713_11	AAGGTTAAGGGCTAAAGGC	10	0	0	7	0	0	0	0	low
184	cja-miR-155_R+1	TTAATGCTAATCGTGATAGGGGT	0	0	0	0	0	0	58	63	middle
185	mmu-miR-16-2-3p_R-1_1ss11TC	ACCAATATTACTGTGCTGCTT	0	0	0	0	0	0	3	3	low
186	PC-5p-246458_14	GATACTGGCAAACTAGAA	11	0	8	0	0	0	0	0	middle
187	mmu-miR-365-3p	TAATGCCCCTAAAAATCCTTAT	0	0	0	0	0	0	14	13	middle
188	mmu-miR-1839-5p_R+1	AAGGTAGATAGAACAGGTCTTGT	0	0	0	0	0	0	3	4	low
189	PC-5p-42949_145	CAGGTGGATGAGGAGAGAA	33	30	50	46	26	20	35	25	middle
190	mmu-miR-191-5p_R-1	CAACGGAATCCCAAAAGCAGCT	4,227	857	1,127	1,019	1,045	4,126	2,028	2,837	high
191	mmu-miR-26b-5p_R+1	TTCAAGTAATTCAGGATAGGTT	167	112	103	156	117	156	415	264	high
192	mmu-miR-331-3p_R+1	GCCCCTGGGCCTATCCTAGAAT	0	0	0	0	0	0	9	11	middle
193	mmu-miR-1893_R-4_1ss12TA	GGCGCGGGCGCAGGACGC	6	0	8	0	0	0	0	0	low
194	PC-5p-186306_24	AAAAGAAGTGTGAGAGAC	10	0	0	0	7	0	0	0	middle
195	PC-3p-27627_214	AGGATGTTGGCCCAGAAGC	9	19	26	17	16	26	22	44	middle
196	mmu-miR-23a-3p	ATCACATTGCCAGGGATTTCC	36	48	39	50	30	43	141	106	middle
197	cpo-miR-193a-5p	TGGGTCTTTGCGGGCGAGATGA	0	0	0	0	0	8	6	0	low
198	PC-5p-255861_13	GAATGGCATATGTGACTGC	6	0	0	0	9	0	0	0	low
199	mmu-miR-339-5p_R-3	TCCCTGTCCTCCAGGAGCTC	0	0	0	0	0	0	16	20	middle
200	mmu-miR-342-3p	TCTCACACAGAAATCGCACCCGT	33	0	0	0	0	0	418	470	high
201	mmu-miR-181c-5p_R+1	AACATTCAACCTGTCGGTGAGTT	0	0	0	0	0	0	2	3	low
202	mmu-miR-335-5p	TCAAGAGCAATAACGAAAAATGT	0	0	0	0	0	0	3	4	low
203	mmu-miR-378a-5p	CTCCTGACTCCAGGTCCTGTGT	0	0	0	0	0	0	4	5	low
204	ocu-miR-501-3p_R-1	AATGCACCCGGGCAAGGATTC	0	0	0	0	0	0	2	3	low
205	mmu-miR-28a-3p_R+1_1ss17GC	CACTAGATTGTGAGCTCCTGGAA	4	0	0	0	0	0	38	40	middle
206	mmu-miR-30a-5p_R+2	TGTAAACATCCTCGACTGGAAGCT	120	118	145	172	127	154	787	532	high
207	rno-mir-711-p3_1ss4GT	AGGTAAAGCTGGGGACCCT	0	7	4	0	0	0	0	0	low
208	mmu-miR-221-5p_R-4	ACCTGGCATACAATGTAGATTT	0	0	0	0	0	0	8	11	middle
209	PC-5p-171502_28	GTGTAGGTCACGGAAGTTT	43	0	0	0	26	0	0	0	middle
210	PC-3p-293071_10	CTTGAAGATGGAGAAGCAGGC	4	0	7	0	0	0	0	0	low
211	ssc-miR-1285_L+2R-4	GCCTGGGCAACATAGCGAGACC	89	30	56	47	74	65	199	130	high
212	PC-5p-190700_23	GCGGGGGACAATGTCTGGC	10	0	33	7	54	6	0	11	middle
213	mmu-miR-6538_L-1	GCGGGCTCCGGGGCGGCG	7	0	0	13	0	0	0	0	middle
214	PC-5p-217353_18	GGTGGGAGGCTATGAAGAA	0	0	0	0	0	0	5	4	low
215	PC-5p-99761_60	CTTGGGGTTAAGGACTGC	15	0	56	0	9	0	0	0	middle
216	mmu-let-7b-3p_1ss22CT	CTATACAACCTACTGCCTTCCT	0	0	0	0	0	0	3	4	low
217	mmu-miR-15a-5p_R-1	TAGCAGCACATAATGGTTTGT	17	0	0	7	0	6	14	13	middle
218	PC-3p-251705_14	TAGAGAGAATGAGGTAGAT	6	10	0	0	0	0	0	0	middle
219	PC-5p-7386_598	GAACACGAGGAATTCTGAC	125	106	134	80	77	107	4	36	middle
220	mmu-miR-21a-3p_R-1_1ss6GC	CAACACCAGTCGATGGGCTGT	0	0	0	0	0	0	52	33	middle
221	mmu-miR-195a-5p_R+1	TAGCAGCACAGAAATATTGGCA	0	0	0	0	0	0	2	4	low
222	PC-5p-250485_14	TTGATTTTGATTTCCAGTA	32	0	0	0	17	0	0	0	middle
223	mmu-miR-361-3p_R-3	TCCCCCAGGTGTGATTCTGATT	4	0	0	0	0	0	18	23	middle
224	hsa-miR-941	CACCCGGCTGTGTGCACATGTGC	0	0	0	0	0	0	32	20	middle
225	hsa-miR-664a-3p	TATTCATTTATCCCCAGCCTACA	0	0	0	0	0	0	6	4	low
226	mmu-miR-532-5p	CATGCCTTGAGTGTAGGACCGT	0	0	0	0	0	0	33	20	middle
227	mmu-miR-423-3p	AGCTCGGTCTGAGGCCCCTCAGT	56	12	8	9	13	46	121	295	high
228	mmu-miR-340-3p_R+1	TCCGTCTCAGTTACTTTATAGCC	0	0	0	0	0	0	15	9	middle
229	mmu-miR-6240_L-2R-6	AAAGCATCGCGAAGGCCC	79	226	180	464	204	182	50	143	high
230	PC-3p-276111_11	AAGTGGGAAAGGATGTGACA	4	0	0	9	0	0	0	0	low
231	hsa-miR-511-5p_R+2	GTGTCTTTTGCTCTGCAGTCAGT	0	0	0	0	0	0	6	4	low
232	cja-miR-589_R-1	TGAGAACCACGTCTGCTCTGA	0	0	0	0	0	0	4	6	low
233	mmu-miR-24-3p_R-2	TGGCTCAGTTCAGCAGGAAC	26	39	46	52	33	42	239	140	high
234	PC-3p-205604_20	AGTACCCGCAGGAAGAGAA	0	0	0	0	0	0	11	6	middle
235	mmu-miR-17-5p	CAAAGTGCTTACAGTGCAGGTAG	9	0	0	14	0	8	19	8	middle
236	hsa-miR-4508_L+1R+1	AGCGGGGCTGGGCGCGCGC	8	0	3	0	0	0	0	0	low
237	mmu-miR-93-5p_R-2	CAAAGTGCTGTTCGTGCAGGT	48	10	25	27	33	79	39	37	middle
238	hsa-miR-146b-3p	GCCCTGTGGACTCAGTTCTGGT	0	0	0	0	0	0	25	46	middle
239	chi-miR-1307-5p_R+4	TCGACCGGACCTCGACCGGCT	0	0	0	0	0	0	1	2	low
240	mmu-miR-200c-3p	TAATACTGCCGGGTAATGATGGA	95	195	135	245	142	184	305	200	high
241	ssc-miR-500-3p	ATGCACCTGGGCAAGGATTCT	0	0	0	0	0	0	37	20	middle
242	cja-miR-502b_R-2	ATGCACCTGGGCAAGGATTCT	0	0	0	0	0	0	37	20	middle
243	mmu-miR-146b-5p_R+2	TGAGAACTGAATTCCATAGGCTGT	257	31	28	0	20	13	5,192	2,911	high

244	mmu-let-7g-5p	TGAGGTAGTAGTTTGTACAGTT	267	177	180	222	164	306	1,076	462	high
245	PC-5p-166051_30	GCAGCTGCTCCGTTGAGCT	23	0	0	0	10	0	0	0	middle
246	oan-miR-1386_L+4	TCGGCTCCTGGCTGGCTCGCCA	4	0	0	0	0	0	8	9	low
247	PC-3p-335837_7	ATGGGAGTCGGGAGTGCC	4	0	10	0	0	0	0	0	low
248	PC-5p-7639_584	AGGTCCAGACATAGCAAGG	928	0	0	0	386	0	0	0	high
249	mmu-miR-200a-3p_R+1	TAACACTGTCTGGTAACGATGTT	630	850	709	1,155	748	845	459	491	high
250	mmu-miR-326-3p	CCTCTGGGCCCTTCCTCCAGT	0	0	0	0	0	0	6	3	low
251	mmu-miR-146a-5p	TGAGAACTGAATTCCATGGGTT	54	62	172	160	44	10	1,044	954	high
252	PC-3p-276641_11	CTTTTAAGTGTTTGGGTGAAA	0	0	0	7	0	6	2	4	low
253	PC-3p-105637_56	ATGCACAGACAACTAGGAT	0	7	28	37	30	15	4	11	middle
254	PC-5p-140741_38	AGGACGGTGGTCATGGAA	47	0	0	0	19	0	0	0	middle
255	PC-5p-198429_22	GCTATGGCTCAGCAGGTAGA	0	9	0	23	0	0	0	0	middle
256	cpo-miR-769-5p	TGAGACCTCTGGGTTCTGAGCT	0	0	0	0	0	0	8	4	low
257	PC-5p-1729_1595	GGAACAATGTAGGCAAGGG	2,719	0	7	0	1,034	0	0	0	high
258	PC-5p-131618_42	ATCGAAGCAGTGAAGTGAA	6	0	0	0	7	6	13	4	middle
259	cfa-miR-1301_R-1	TTGCAGCTGCCTGGGAGTGACTTC	0	0	0	0	0	0	6	12	middle
260	eca-mir-9112-p5_1ss2GT	GTGTTAGGAGCAGAGATG	5	19	33	31	16	3	5	22	middle
261	PC-3p-97329_62	GAATTAAAGTAGCGAAGC	70	0	12	0	10	0	0	0	middle
262	PC-3p-166226_29	GAACCCGAAAACCTGTCT	19	24	0	0	0	0	3	0	middle
263	PC-5p-18541_296	GGTGTCCTAAGATGAGCT	449	0	0	0	167	0	0	0	high
264	PC-5p-2906_1133	GTTAAGAAGAGAGAATGCC	388	179	301	208	253	260	187	71	high
265	PC-3p-290201_10	CGTGGATCGCCTCAGCTGC	4	7	7	0	7	6	0	0	low
266	PC-5p-28815_206	GGGAGGCGAAGAGATGGC	26	48	116	16	38	13	38	19	middle
267	PC-3p-120714_47	AAGTGGGCCATTTTTGGTA	27	0	0	0	9	0	0	0	middle
268	PC-5p-145977_36	CTGGAAGGTTAAGGAGAGA	24	0	8	0	0	0	0	0	middle
269	PC-3p-21055_268	GATGGTCCTTGCGGATGCT	218	0	0	0	73	0	0	0	high
270	PC-5p-305844_9	AGCATAGCTGTTGGGACCC	4	0	12	0	0	0	0	0	middle
271	mmu-miR-34c-5p	AGGCAGTGTAGTTAGCTGATTGC	5	0	0	0	0	0	17	34	middle
272	PC-3p-103430_58	GATAGGTGGGAGGCTTGGA	10	0	14	11	7	0	3	9	middle
273	cfa-miR-660_R+1	TACCCATTGCATATCGGAGTTGT	0	0	0	0	0	0	16	6	middle
274	PC-3p-175446_27	GATGGACAACTGGTAGATA	0	0	0	10	0	15	0	20	middle
275	mmu-mir-6236-p5	CACCTGCCGAATCAACTAGCC	10,304	315	475	563	2,658	434	82	312	high
276	PC-5p-184447_25	TTTGAGATTGGTAGGGGAG	27	0	0	0	9	0	0	0	middle
277	PC-3p-7629_584	CCCAGCTTGAGAATTTGGC	414	0	0	9	115	0	0	0	high
278	bta-miR-374a_R-1	TTATAATACAACCTGATAAGT	6	0	0	0	0	0	13	9	middle
279	chi-miR-374a-5p	TTATAATACAACCTGATAAGT	6	0	0	0	0	0	13	9	middle
280	mmu-miR-106b-5p	TAAAGTGCTGACAGTGCAGAT	16	13	8	16	16	0	12	12	middle
281	PC-3p-83099_75	CAAAGTGGCGCAGTTGGTAGC	5	36	26	24	26	25	0	10	middle
282	PC-5p-122085_47	AGCAGGAGAGCTGGGCACT	0	7	11	14	10	7	0	6	middle
283	PC-3p-77658_81	GTCAGGTGGGCAGTTTGA	0	21	14	36	11	8	0	14	middle
284	PC-3p-238558_15	AGTGAAATCTTATGGAGGA	4	0	14	0	0	0	0	0	middle
285	mmu-miR-181a-1-3p	ACCATCGACCGTTGATTGTACC	0	0	0	0	0	0	2	6	low
286	PC-5p-104544_57	AGGTAGACAGGAAGAGGATT	37	37	18	0	10	13	9	9	middle
287	PC-5p-114836_51	GAAGAAGCATTGTTAAGGA	27	0	22	0	20	9	6	4	middle
288	mmu-miR-28a-5p_R-1	AAGGAGCTCACAGTCTATTGA	0	0	0	0	0	0	20	8	middle
289	mmu-miR-340-5p	TTATAAAGCAATGAGACTGATT	18	0	11	13	11	6	37	42	middle
290	mmu-miR-181b-5p_R-1	AACATTCATTGCTGTCGGTGGGT	2	0	0	0	0	0	4	8	low
291	hsa-miR-141-3p_R+2	TAACACTGTCTGGTAAAGATGGCT	4	19	7	7	7	10	0	0	middle
292	mmu-miR-98-5p	TGAGGTAGTAAGTTGTATTGTT	13	0	11	17	11	16	94	32	middle
293	bta-miR-197	TTCACCACCTTCTCCACCCAGC	0	0	0	0	0	0	12	34	middle
294	mmu-miR-29a-3p_R-1	TAGCACCATCTGAAATCGGTT	61	139	155	111	125	71	371	533	high
295	mmu-miR-21a-5p	TAGCTTATCAGACTGATGTTGA	840	1,125	1,031	1,448	896	1,195	6,649	2,783	high
296	PC-3p-172744_28	GGTGTGGAGCCGAAGGGA	0	0	41	0	17	0	4	0	middle
297	PC-5p-21449_264	GAACAGTCAACTCAGAACT	821	0	0	0	202	0	0	0	high
298	mmu-let-7c-5p	TGAGGTAGTAGGTTGTATGGTT	102	137	179	190	174	156	99	127	high
299	PC-5p-83316_75	AACAGAGTGAGGCGAACC	10	39	0	62	19	26	0	0	middle
300	bta-miR-11987_L-2_1ss8TA	AGGAAACTCTGGTGGAGGT	0	7	0	10	0	0	0	2	middle
301	mmu-let-7d-5p	AGAGGTAGTAGGTTGCATAGTT	147	121	149	210	152	151	236	193	high
302	PC-5p-98309_62	GGAAGGTGAGGTATATGGG	12	13	11	14	10	15	0	0	middle
303	mmu-miR-27a-3p	TTCACAGTGGCTAAGTTCCGC	151	233	207	182	182	137	442	546	high
304	mmu-miR-181a-5p	AACATTCAACGCTGTCGGTGAGT	22	14	19	19	13	11	82	184	high

305	cfa-miR-502	AATGCACCTGGGCAAGGATTCA	0	0	0	0	0	0	11	33	middle
306	PC-3p-141105_38	TAAGGAGTGACGTGGAGAC	14	48	8	9	7	6	5	11	middle
307	mmu-miR-16-5p	TAGCAGCACGTAAATATTGGCG	281	98	118	177	119	271	190	176	high
308	PC-3p-205805_20	CTTGAGTACTGGAGAGGCAG	6	0	0	25	11	7	0	0	middle
309	mmu-let-7d-3p	CTATACGACCTGCTGCCTTTCT	10	9	0	14	10	10	21	58	middle
310	mmu-mir-690-p3_1ss1TC	CGTTAAAGGCTAGGCTCACAACC	0	7	0	19	13	22	16	6	middle
311	mmu-miR-34a-5p_R+1	TGGCAGTGTCTTAGCTGGTTGTT	0	0	0	0	0	0	27	8	middle
312	mmu-let-7f-5p	TGAGGTAGTAGATTGTATAGTT	342	182	151	233	154	290	1,761	542	high
313	PC-3p-119791_48	GGGATAACATCACAGGAT	76	0	0	0	14	0	0	0	middle
314	mmu-miR-101a-3p_L+1R-3	GTACAGTACTGTGATAACT	0	0	0	0	0	0	35	9	middle
315	PC-3p-29066_205	CTTGAGGAGAACCGGCACT	55	25	18	7	26	0	25	16	middle
316	PC-5p-115294_50	TTGAGAATTTGGCGGTTGA	72	0	0	0	11	0	0	0	middle
317	PC-5p-159214_32	GAAGTGCGGATGAGATAAA	0	21	8	31	7	11	5	4	middle
318	mmu-miR-25-3p	CATTGCACTTGTCTCGGTCTGA	111	13	32	24	23	102	39	68	middle
319	PC-5p-177603_26	TGGAGCGGCGGGGAGAGAGA	4	0	0	0	0	0	5	15	middle
320	PC-5p-277832_11	CTGTACAGAAGTGAGAATG	0	0	0	0	0	0	2	9	low
321	PC-5p-55648_114	GTTAAGGAACTCGGCAAGT	6	11	19	11	13	3	3	14	middle
322	mmu-miR-221-3p_R-1	AGCTACATTGTCTGCTGGGTTT	4	34	28	17	13	13	44	40	middle
323	mmu-miR-7a-5p_R+1	TGGAAGACTAGTGATTTTGTTGTT	11	0	0	0	0	9	4	3	middle
324	mmu-miR-15b-5p	TAGCAGCACATCATGGTTTACA	101	27	29	24	38	130	48	60	middle
325	PC-5p-77419_81	TACAACGGCAGAAGGCACT	12	25	0	90	31	8	15	18	middle
326	mmu-miR-30a-3p	CTTTCAGTCGGATGTTTGCAGC	13	0	0	0	0	0	31	13	middle
327	mmu-miR-183-5p	TATGGCACTGGTAGAATTCACT	0	0	0	0	0	29	0	6	middle
328	PC-3p-22291_256	AACCCGACTACATGAAGCTG	385	559	702	366	478	547	15	313	high
329	mmu-miR-22-3p	AAGCTGCCAGTTGAAGAACTGT	300	198	284	245	168	178	430	590	high
330	PC-3p-94732_64	GCAAGACCAAGGTTTCCTG	21	45	0	19	30	27	4	0	middle
331	PC-3p-61586_103	AGAATTTGGCGGTTGAATC	78	0	0	0	9	0	0	0	middle
332	PC-5p-181721_25	GACCTAGATCTTCTGTGAAG	65	0	0	0	7	0	0	0	middle
333	mmu-miR-328-3p_R+1	CTGGCCCTCTCTGCCCTTCCGTT	0	0	0	0	0	0	2	11	middle
334	bta-mir-2887-1-p5	GACCGGGGTCCGGTGCGGAGAGCC	170	116	284	97	111	125	145	57	high
335	mmu-miR-92b-3p_R-2	TATTGCACTCGTCCCGGCCT	0	0	0	0	0	0	4	20	middle
336	PC-3p-140750_38	GTGTATATCCAAGGAGCCC	5	0	21	0	10	0	4	4	middle
337	PC-5p-147454_36	AGAGATGTATCAGGTGCC	0	0	0	0	10	0	12	8	middle
338	PC-3p-103407_58	AGTGGAAAAGGATGTGGGG	0	0	26	10	16	7	3	5	middle
339	mmu-miR-126a-5p	CATTATTACTTTTGGTACGCG	0	21	40	42	13	0	25	11	middle
340	PC-3p-175408_27	AGGAGAAGTCAGGGAAACC	10	0	0	0	0	8	12	0	middle
341	mmu-miR-222-3p	AGCTACATCTGGCTACTGGGTCT	4	0	10	10	17	0	28	57	middle
342	PC-3p-78482_80	AGGATAGCTGGAGCTCGAG	120	0	0	0	7	0	0	0	middle
343	mmu-miR-320-3p	AAAAGCTGGGTTGAGAGGGCGA	39	0	22	7	47	31	24	56	middle
344	rno-miR-215	ATGACCTATGATTTGACAGACA	26	10	17	7	20	17	11	7	middle
345	mmu-miR-223-3p	TGTCAGTTTGTCAAATACCCCA	88	0	0	0	10	0	87	73	middle
346	PC-3p-32561_186	TTAGTAGGAGGAGGAAAAG	21	88	45	56	41	35	31	49	middle
347	PC-5p-39705_156	AAGTACCTGGAGGAAAAGA	20	33	12	33	21	25	10	19	middle
348	mmu-miR-194-5p	TGTAACAGCAACTCCATGTGGA	256	411	372	591	379	425	288	278	high
349	mmu-miR-423-5p	TGAGGGGCAGAGAGCGAGACTTT	264	27	26	33	33	188	55	172	high
350	PC-5p-242972_15	CTCTGACCCAGGGTTCCAAGCC	5	0	0	0	23	0	0	3	middle
351	bta-miR-11987_L-1R-1_1ss8TA	GAGGAAACTCTGGTGGAGG	0	7	14	20	13	8	6	8	middle
352	PC-5p-103277_58	AGGAAGAGAATTTTAAGAC	14	7	14	0	11	9	7	3	middle
353	mmu-miR-193b-3p	AACTGGCCCACAAAGTCCCGCT	6	0	0	0	0	0	0	0	low
354	mmu-miR-194-2-3p	CCAGTGGGGCTGCTGTTATCTG	4	0	0	0	0	0	0	0	low
355	mmu-mir-540-p3_1ss7CT	GGTAGATAGGTCAGAGGT	4	0	0	0	0	0	0	0	low
356	mmu-miR-709_L+1	AGGAGGCAGAGGCAGGAGGA	4	0	0	0	0	0	0	0	low
357	mmu-miR-5124a_L-1R-1_1ss5CA	GTCAAGTGACTAAGAGCA	17	0	0	0	0	0	0	0	middle
358	mmu-miR-5126_R-4_1ss18CT	GCGGGCGGGGCCGGGGGT	4	0	0	0	0	0	0	0	low
359	bta-miR-454	TAGTGCAATATTGCTTATAGGGT	4	0	0	0	0	0	0	0	low
360	cfa-miR-1271_R+2	CTTGGCACCTAGTAAGCACTCC	9	0	0	0	0	0	0	0	low
361	PC-5p-304864_9	GCAGAGACAGCCAGGAGGT	7	0	0	0	0	0	0	0	low
362	PC-3p-283416_11	TTTTATTCCCGTGATGACT	9	0	0	0	0	0	0	0	low
363	PC-5p-360872_6	TACTTAAGCACAAGGACA	0	9	0	0	0	0	0	0	low
364	PC-5p-430495_5	AGGAGCCGTTGTTGAAATA	4	0	0	0	0	0	0	0	low
365	PC-3p-427638_5	TCAGGTGGACAGTTTGACT	4	0	0	0	0	0	0	0	low

366	PC-5p-317701_8	AGGACACTTGGAGCTAGCT	6	0	0	0	0	0	0	0	low
367	PC-3p-374647_6	ATCTGAGAGGAGCTGTTCT	5	0	0	0	0	0	0	0	low
368	PC-5p-295737_10	GGACGCCAGTTCCTGAGGA	8	0	0	0	0	0	0	0	low
369	PC-5p-280213_11	TCAAAGTCTTTGGGTTCC	9	0	0	0	0	0	0	0	low
370	PC-3p-293682_10	AAGGAGGTAGGGGTGCAGA	8	0	0	0	0	0	0	0	low
371	PC-3p-399874_5	AAAACTGTTAGACTTGAGT	4	0	0	0	0	0	0	0	low
372	PC-5p-351861_6	AGGCTGAGGACTCTGGCGA	5	0	0	0	0	0	0	0	low
373	PC-5p-225081_17	TTCCGCCAGGAGCACAGCC	14	0	0	0	0	0	0	0	middle
374	PC-3p-308773_9	TTTAGGAGTAAGAGGTAGA	7	0	0	0	0	0	0	0	low
375	PC-3p-310528_8	ACATGACCGAAGAATAAAC	6	0	0	0	0	0	0	0	low
376	PC-3p-341346_7	GCCTCAAGAATAGATTTCC	6	0	0	0	0	0	0	0	low
377	PC-3p-397370_5	CCCATGTCCAGGATGAAGT	4	0	0	0	0	0	0	0	low
378	PC-3p-366779_6	GCTAGCCTTGAACAAGACA	5	0	0	0	0	0	0	0	low
379	PC-5p-326877_7	AAGTATGGAGAGTTTGATC	0	10	0	0	0	0	0	0	middle
380	PC-5p-357506_6	ACTGAATATGACATCTGGGC	0	9	0	0	0	0	0	0	low
381	PC-5p-294905_10	CTGGGCGTAAAGGGAGTGT	12	0	0	0	0	0	0	0	middle
382	PC-5p-409428_5	ACAAACAAGGAGGATATAA	4	0	0	0	0	0	0	0	low
383	PC-3p-404592_5	AGGAGGAGAAAACAAAAGTGA	4	0	0	0	0	0	0	0	low
384	PC-3p-222543_17	CTTAAAGAGAATGAGGTAGA	14	0	0	0	0	0	0	0	middle
385	PC-5p-382494_6	TAAAATCTATACCGAAGCT	5	0	0	0	0	0	0	0	low
386	PC-5p-338454_7	GGAAACGGGCTTGGCAGAA	6	0	0	0	0	0	0	0	low
387	PC-5p-219216_18	TGAGAGAACTATGTTGAA	24	0	0	0	0	0	0	0	middle
388	PC-3p-375076_6	AGGTTGGGTGTGTAAGCAC	5	0	0	0	0	0	0	0	low
389	PC-5p-380828_6	GCACGAGGGTCCCGGCCCC	5	0	0	0	0	0	0	0	low
390	PC-5p-414110_5	GCATTTGAAACTGTTGATC	4	0	0	0	0	0	0	0	low
391	PC-3p-275678_11	AAGTCAGATGTGAAATCCAC	9	0	0	0	0	0	0	0	low
392	PC-5p-462431_5	CTAAAGGAGAAGAATCCAG	4	0	0	0	0	0	0	0	low
393	PC-5p-357292_6	GAGTAGCCCAAACCGGAGAT	5	0	0	0	0	0	0	0	low
394	PC-5p-404698_5	CCATGAGCAGGCTGAAGCA	4	0	0	0	0	0	0	0	low
395	PC-5p-437097_5	CCTTGAAATTAGTAGTTTTC	0	7	0	0	0	0	0	0	low
396	PC-3p-356884_6	AGCAGAAAGGTTTTGGGAAAGC	5	0	0	0	0	0	0	0	low
397	PC-3p-305892_9	ATGGGGTGCCGGGGAGGGT	7	0	0	0	0	0	0	0	low
398	PC-3p-459005_5	CCAGATAAGAAAAAGGTTA	4	0	0	0	0	0	0	0	low
399	PC-3p-225944_17	GCTCTGAGGGCTGGGCACG	7	0	0	0	0	0	0	0	low
400	PC-5p-315146_8	GGGGAGCAAGCTGTGTCAC	6	0	0	0	0	0	0	0	low
401	PC-5p-274645_11	AGCATGGGATAACATCACA	9	0	0	0	0	0	0	0	low
402	PC-3p-434894_5	GTGGGCAGGTTGAAGCAGGA	4	0	0	0	0	0	0	0	low
403	PC-3p-260867_13	GGTCCCGGCCCCAAACTCGT	24	0	0	0	0	0	0	0	middle
404	PC-5p-403915_5	AGCGAAAACAGAAGGAGCA	4	0	0	0	0	0	0	0	low
405	PC-5p-309104_9	ATGTTTTTGGTAGAGGAGC	7	0	0	0	0	0	0	0	low
406	PC-5p-389270_5	TATTCAGCTGACTGGTACT	4	0	0	0	0	0	0	0	low
407	PC-5p-259602_13	TAGGTGACAAATGTGTAGGA	19	0	0	0	0	0	0	0	middle
408	PC-5p-372871_6	AAGGCAGCTCTCTTGGTCT	5	0	0	0	0	0	0	0	low
409	PC-5p-435394_5	AGACCTCAGCCTAACTAGC	4	0	0	0	0	0	0	0	low
410	PC-5p-365834_6	GGAATAATGTAGGCAAGGG	5	0	0	0	0	0	0	0	low
411	PC-3p-249521_14	ATTCCTCAAGAGACCCTGC	11	0	0	0	0	0	0	0	middle
412	PC-3p-334635_7	GCACGAGATAAGTTAGGTA	6	0	0	0	0	0	0	0	low
413	PC-5p-239424_15	GTTTGATTTTGATTTCCAGT	12	0	0	0	0	0	0	0	middle
414	PC-5p-379179_6	GAAGACAGCGAGAAAGATT	0	9	0	0	0	0	0	0	low
415	PC-3p-362836_6	CTGAATACTAGATATGACC	5	0	0	0	0	0	0	0	low
416	PC-3p-324291_7	GGGAACTCAGGAGAGACTG	6	0	0	0	0	0	0	0	low
417	PC-3p-271304_12	CTACACTGATGTATTCAAC	10	0	0	0	0	0	0	0	low
418	PC-5p-262310_12	GGAGGGATAAGAAGAGAGAAT	23	0	0	0	0	0	0	0	middle
419	PC-5p-350850_6	GAAGGCGGGGCTAGTGACT	5	0	0	0	0	0	0	0	low
420	PC-3p-385089_6	GCGCACCCTGGAAATGGCT	5	0	0	0	0	0	0	0	low
421	PC-5p-428556_5	CAGCAGTTGGACATGGGTGA	4	0	0	0	0	0	0	0	low
422	PC-3p-455819_5	CAGAGCAGCTGTTCCAGTT	4	0	0	0	0	0	0	0	low
423	PC-5p-358807_6	AAGAGAAGCAGGTAGATAG	5	0	0	0	0	0	0	0	low
424	PC-5p-124898_45	GGCTGGAGAGGGTGAAAGC	0	0	32	0	11	0	3	4	middle
425	PC-5p-119386_48	AGGAAGCCAGATACCCGTC	10	0	14	0	9	0	5	5	middle
426	mmu-miR-144-5p	GGATATCATCATATACTGTAAGT	18	0	0	0	0	19	6	4	middle

427	mmu-miR-375-3p	TTTGTTCGTTCGGCTCGCGTGA	14	15	18	29	11	16	12	15	middle
428	PC-5p-14992_350	AGTGGATACCAAAGGACAGT	19	40	67	93	58	48	12	54	middle
429	PC-5p-103999_57	CGAAACAGGCAGGCTGGCC	0	0	0	7	0	0	4	25	middle
430	mmu-miR-19b-3p_R-2	TGTGCAAATCCATGCAAAACT	4	6	4	0	4	6	2	11	middle
431	mmu-miR-744-5p_R-1	TGCGGGGCTAGGGCTAACAGC	4	0	0	0	0	0	2	13	middle
432	mmu-miR-29c-3p_R-1	TAGCACCATTTGAAATCGGTT	0	4	3	4	0	0	6	11	middle
433	mmu-miR-652-3p_R+1	AATGGCGCCACTAGGGTTGTGT	22	9	23	27	9	19	18	45	middle
434	PC-3p-50169_125	TGAGTATCGGAGAGGCAGG	4	24	10	53	20	15	4	21	middle
435	mmu-miR-142a-3p_R-1	TGTAGTGTTTCCTACTTTATGG	6	0	0	0	0	0	8	4	low
436	PC-3p-123554_46	GCAGGCAAATCCACCTCTC	5	7	0	13	9	0	2	9	middle
437	PC-5p-209428_20	GGGAAGGCTGGCCAGAGAGG	0	0	7	0	0	7	4	0	low
438	mmu-miR-150-5p	TCTCCCAACCCTTGTACCAGTG	13	0	0	0	0	0	10	209	high
439	PC-5p-16619_324	GTTAGCTTGGAAGCAGCT	14	83	67	125	94	31	40	90	middle
440	PC-5p-160015_31	TTGGAGAGTACGAGGTGGA	6	0	0	66	10	13	0	0	middle
441	PC-5p-161240_31	TAGGATATTTGAAAGGAGC	0	0	12	0	0	7	5	3	middle
442	PC-5p-83409_74	GTGGAGATTCCTGTACTACA	7	9	0	16	7	17	8	8	middle
443	mmu-let-7a-1-3p_1ss22CT	CTATACAATCTACTGTCTTTCT	0	0	0	0	0	0	6	0	low
444	mmu-miR-19a-3p_R-2	TGTGCAAATCTATGCAAAACT	0	0	0	0	0	6	0	0	low
445	mmu-miR-22-5p	AGTTCTTCAGTGGCAAGCTTTA	0	0	0	0	0	0	5	0	low
446	mmu-miR-30c-2-3p	CTGGGAGAAGGCTGTTTACTCT	0	0	0	0	0	0	4	0	low
447	mmu-miR-130b-5p	ACTCTTTCCCTGTTGCACTACT	0	0	0	0	0	7	0	0	low
448	mmu-miR-140-5p	CAGTGGTTTTACCCTATGGTAG	0	0	0	0	0	0	3	0	low
449	mmu-miR-147-5p_R-2	TGGAAACATTTCTGCACAAACT	0	0	0	0	0	0	2	0	low
450	mmu-miR-148b-5p_R-1	GAAGTTCTGTTATACACTCAGGC	0	0	0	0	0	0	2	0	low
451	mmu-miR-223-5p	CGTGTATTTGACAAGCTGAGTTG	0	0	0	0	0	0	4	0	low
452	mmu-mir-466k-p3_1ss3GT	GTTTGTGAGTATGTGAAT	0	0	0	0	0	0	3	0	low
453	mmu-miR-542-3p_R+2	TGTGACAGATTGATAACTGAAAGT	0	0	0	0	0	0	2	0	low
454	mmu-miR-708-5p	AAGGAGCTTACAATCTAGCTGGG	0	0	0	0	0	0	2	0	low
455	rno-miR-224-5p	CAAGTCACTAGTGGTTCCGTTT	0	0	0	0	0	0	2	0	low
456	cgr-miR-362_R-2	AATCCTTGGAACCTAGGTGTGAGT	0	0	0	0	0	0	3	0	low
457	rno-miR-505-3p_R+3	GTCAACACTTGCTGGTTTCCTCT	0	0	0	0	0	0	8	0	low
458	bta-mir-3533-p5_1ss15CT	ATGGAGTCCTGTGGTATCC	0	0	0	0	0	6	0	0	low
459	bta-miR-146a_R-3	TGAGAACTGAATTCCATAGGT	0	0	0	0	0	0	5	0	low
460	bta-miR-339a_R+1	TCCCTGTCCTCCAGGAGCTCACT	0	0	0	0	0	0	4	0	low
461	dno-miR-374a-3p	CTTATCAGATTGTATTGTAATT	0	0	0	0	0	0	3	0	low
462	hsa-miR-511-5p_R-1	GTGTCTTTTGCTCTGCAGTC	0	0	0	0	0	0	2	0	low
463	mml-miR-1271-5p	CTTGGCACCTAGCAAGCACTCA	0	0	0	0	0	0	2	0	low
464	pal-miR-9993b-3p	ATCTCGCTGGGGCCTCCA	0	0	0	0	0	0	2	0	low
465	ssc-miR-24-1-5p	GTGCCTACTGAGCTGAAACACAGT	0	0	0	0	0	0	3	0	low
466	cja-miR-345_R+2	GCTGACTCCTAGTCCAGGGCTC	0	0	0	0	0	0	3	0	low
467	cfa-miR-590	TAATTTTATGTATAAGCTAGT	0	0	0	0	0	0	1	0	low
468	eca-miR-590-3p	TAATTTTATGTATAAGCTAGT	0	0	0	0	0	0	1	0	low
469	bta-miR-1246_L+1	AAATGGATTTTTGGAGCAGG	0	0	0	0	0	0	3	0	low
470	hsa-miR-7977_1ss6AG	TTCCCGGCCAACGCACCA	0	0	0	0	0	0	4	0	low
471	PC-5p-374535_6	TACAAAGAGCATATAGGGG	0	0	0	0	0	3	0	0	low
472	PC-3p-335774_7	AATTGATGGCCTTGGCAGA	0	0	0	0	0	0	3	0	low
473	PC-3p-426196_5	GCAAGTGCGGGGTAGGGGA	0	0	0	0	0	6	0	0	low
474	PC-3p-454111_5	GGAGTGCATTTGGAACTGT	0	0	0	0	0	6	0	0	low
475	PC-3p-350003_6	GGAGGATATTTAAGGGGAGC	0	0	0	0	0	7	0	0	low
476	PC-3p-414155_5	AGCAAGCCAAAGGGACCTG	0	0	0	0	0	6	0	0	low
477	PC-3p-301012_9	GGCCGCAGAGGGTGAAAGC	0	0	0	0	0	10	0	0	middle
478	PC-5p-389468_5	TCAAATGTTAAGACTTACC	0	0	0	0	0	6	0	0	low
479	PC-5p-400136_5	CAGCTAAGGTCCCTAAGTG	0	0	0	0	0	6	0	0	low
480	PC-5p-342950_7	AAGTGAATGGCTAAGAGATT	0	0	0	0	0	0	3	0	low
481	PC-3p-402243_5	TCACCAAAGAATGAAATGTA	0	0	0	0	0	6	0	0	low
482	PC-5p-303205_9	AGGGAAGCCAGTGAATGAC	0	0	0	0	0	0	4	0	low
483	PC-5p-332195_7	GCAGAATGGTTTTGGGAAAG	0	0	0	0	0	0	3	0	low
484	PC-5p-400238_5	TAGGAGGGAGGCTAAGAAGC	0	0	0	0	0	6	0	0	low
485	PC-5p-390489_5	GAAGCATACGAATCTGCACC	0	0	0	0	0	6	0	0	low
486	PC-5p-295224_10	GCGAGAAAGAGGTGAGAAT	0	0	0	0	0	0	4	0	low
487	PC-5p-411016_5	CATGCAGCCTTTTACACCAGG	0	0	0	0	0	6	0	0	low

488	PC-5p-459946_5	AAGATTTCATGGGACGGAG	0	0	0	0	0	6	0	0	low
489	PC-3p-436682_5	GTAACACTAACTGGATGACC	0	0	0	0	0	6	0	0	low
490	PC-3p-402430_5	ACTGGCCCACTCTTTCTTGCC	0	0	0	0	0	6	0	0	low
491	PC-3p-425263_5	CTCTGGAGGGCTGATGTCTC	0	0	0	0	0	6	0	0	low
492	PC-5p-335886_7	AGAGATGTATCAGGTGCCC	0	0	0	0	0	0	3	0	low
493	PC-5p-232503_16	GGATTTTGGAGATAGAAGT	0	0	0	0	0	0	13	0	middle
494	PC-5p-325143_7	AGGAGGAGGTGTGAAGGAAA	0	0	0	0	0	0	6	0	low
495	PC-5p-178727_26	TGGAGAGCATAGAAGAGAGAA	0	0	0	0	0	0	12	0	middle
496	PC-3p-332986_7	AGTGAAAGAGAACCTAAAACC	0	0	0	0	0	8	0	0	low
497	PC-5p-309768_8	GTGGAGAGCATAGAAGAGA	0	0	0	0	0	0	4	0	low
498	PC-3p-339787_7	AGTATAAAATAAGAAAGAGAA	0	0	0	0	0	0	3	0	low
499	PC-5p-420437_5	CCAGTTCAGATTGCAGGCT	0	0	0	0	0	6	0	0	low
500	PC-5p-358438_6	TGTTAAGGAACTCGGCAAGTTG	0	0	0	0	0	3	0	0	low
501	mmu-miR-151-5p	TCGAGGAGCTCACAGTCTAGT	403	48	94	69	74	356	117	191	high
502	PC-3p-222577_17	GAAACAGACCCTGAAATCA	5	0	0	0	9	0	0	3	low
503	PC-5p-209999_20	AGAGGAGAAGTGAGAGCTT	6	9	0	0	0	0	0	4	low
504	cgr-miR-1260	ATCCCACCGCTGCCACCA	0	0	0	7	0	0	4	6	low
505	PC-3p-151544_34	GTAGGGTGAGGAAAAGAA	0	0	15	16	0	0	5	3	middle
506	PC-3p-79797_78	TAGGATGTTGGCTTAGAAG	0	27	37	0	10	11	0	12	middle
507	PC-5p-160315_31	AAGATGGGCACTCTGGAGA	52	0	0	0	0	0	4	0	middle
508	mmu-miR-99b-5p	CACCCGTAGAACCGACCTTGCG	16	31	52	39	26	21	46	79	middle
509	mmu-miR-199b-5p_1ss10TC	CCCAGTGTTCAGACTACCTGTTC	4	0	0	0	0	0	1	19	middle
510	mmu-miR-199a-5p	CCCAGTGTTCAGACTACCTGTTC	4	0	0	0	0	0	1	19	middle
511	PC-5p-151035_34	GTGACAATGGCGGTAGGG	7	10	0	33	0	0	3	11	middle
512	mmu-miR-106b-3p_L+2R-2	TACCGCACTGTGGGTACTTGCT	11	0	0	0	0	0	6	10	middle
513	mmu-miR-125a-5p_R-2	TCCCTGAGACCCTTTAACCTGT	10	28	51	60	36	13	48	267	high
514	PC-3p-147353_36	GGAGAATCAGACTGTCAAG	12	7	11	0	0	30	0	12	middle
515	PC-5p-129669_43	TTTGGGAGAAGGGGTGCC	13	27	30	17	24	0	5	33	middle
516	bta-miR-150	TCTCCCAACCCTTGTACCAGTGT	4	0	0	0	0	0	0	26	middle
517	PC-3p-133086_41	TGCCGGAGGATTACAAAG	4	0	23	0	14	0	4	9	middle
518	mmu-miR-30b-5p	TGTAAACATCCTACACTCAGCT	131	161	117	135	107	181	123	135	high
519	PC-3p-194053_23	GCAGAGTCGTGACGCAGAG	0	0	0	4	0	0	1	7	low
520	mmu-miR-1a-3p	TGGAATGTAAAGAAGTATGTAT	7	0	0	0	0	10	0	2	low
521	mmu-miR-92a-3p_R+1	TATTGCACTTGTCCCGGCCTGT	731	73	115	84	136	638	183	290	high
522	PC-5p-26214_223	ACAATGGCAGGTACAGAGA	23	25	98	19	17	24	0	41	middle
523	mmu-miR-144-3p_R-1	TACAGTATAGATGATGTAC	35	0	10	0	17	46	4	20	middle
524	PC-3p-9044_516	AGACTGACGCTGAGGCAC	156	106	51	62	60	66	204	97	high
525	PC-5p-183753_25	CAGGATAGGTGGGAGGCTGA	0	9	0	13	0	0	0	6	middle
526	PC-5p-11519_431	GTGGAGAGATGTGAAGAGAGA	196	139	216	150	220	29	281	46	high
527	PC-3p-97109_62	GAGGGGAGGCCGCAGAGAA	12	0	0	0	0	0	19	3	middle
528	PC-5p-190381_23	GAAGGAACGGTGAAAAGGA	4	0	0	0	7	0	6	6	low
529	PC-3p-19325_287	ACACAGGTAGACGAGAAGAAA	197	126	304	159	103	208	122	103	high
530	PC-3p-129204_43	CCTGGGCGAGGCTCTCGAGA	5	0	22	0	0	0	20	12	middle
531	bta-miR-2478_L-2	ATCCCACTTCTGACACCA	4	12	0	21	7	0	9	8	middle
532	PC-3p-25177_231	TGGAGAGATGTGAAGAGAGA	14	11	17	16	14	6	21	3	middle
533	PC-5p-59165_107	TAAGAGGAGGGGTCAGGAGA	0	25	17	77	37	49	26	49	middle
534	PC-3p-359_4224	TGATGTGTAGGATAGGCC	360	719	224	451	471	324	615	681	high
535	mmu-miR-203-3p_R+1	GTGAAATGTTTAGGACCACTAGA	30	25	10	16	7	12	8	20	middle
536	PC-5p-192678_23	AGTTCTATCACAGGAGTGA	0	7	0	0	0	0	3	7	low
537	PC-5p-141289_38	GCTGTGCTGGAACTGGTAGA	8	0	15	9	0	9	8	8	middle
538	PC-3p-7141_612	AGAGAGGGACCGAAAGAGA	55	55	52	82	74	46	180	60	high
539	mmu-miR-215-5p_R+1	ATGACCTATGATTTGACAGACC	601	635	646	654	589	692	603	357	high
540	mmu-miR-185-5p	TGGAGAGAAAGGCAGTTCCTGA	316	34	22	27	51	316	81	71	high
541	ssc-mir-9843-p5_1ss5AT_1	AGAATCCTCTGGAAAGTG	132	222	23	52	164	146	43	75	high
542	ssc-mir-9843-p5_1ss5AT_2	AGAATCCTCTGGAAAGTGG	132	222	23	52	164	146	43	75	high
543	mmu-miR-8101_R-3_1ss11GA	GGCGAGCGGAACCGGAGGA	10	0	66	0	0	0	18	0	middle
544	PC-3p-162671_31	GGGAAAGCAGACGAGAAAGG	10	0	0	0	10	20	2	3	middle
545	PC-5p-112241_52	GTCTGGGCAGGATAAGTGC	12	9	0	0	0	6	8	4	middle
546	PC-3p-59976_106	GGAGTCAGGCTGCACGAGA	23	19	72	27	36	26	38	22	middle
547	PC-5p-225587_17	CTGCAAAGCTAGAGTATGA	0	0	0	37	0	8	0	0	middle
548	mmu-miR-31-5p_R+1	AGGCAAGATGCTGGCATAGCTGT	6	28	23	21	0	6	22	5	middle

549	PC-5p-275224_11	GCAAGTCTGAAGTGAAAGG	4	9	0	14	0	6	5	0	middle
550	PC-3p-17270_314	CGAAAGTCTGAGGTTTCCT	81	119	84	103	117	170	6	23	high
551	mmu-miR-27b-3p	TTCACAGTGGCTAAGTTCTGC	535	386	392	298	251	440	177	338	high
552	mmu-miR-24-2-5p	GTGCCTACTGAGCTGAAACAGT	8	0	0	0	0	6	3	0	low
553	mmu-miR-196a-5p	TAGGTAGTTTCATGTTGTTGGG	0	0	4	4	9	3	2	3	low
554	PC-5p-210541_19	GACACTGTTAGGCGGGCAG	6	0	7	0	0	0	0	4	low
555	bta-miR-6529a	GAGAGATCAGAGGCGCAGAGT	2	0	0	0	0	4	0	0	low
556	cpo-miR-6529-5p	GAGAGATCAGAGGCGCAGAGT	2	0	0	0	0	4	0	0	low
557	PC-3p-383358_6	CAGTGCTGGAAGGTTAAGG	0	9	0	0	0	0	2	0	low
558	PC-5p-126272_45	CAGAACTGTGGGGACGTA	10	9	23	13	9	7	2	19	middle
559	PC-3p-273813_11	TTAGGGCTAGCGTTGTATT	0	0	0	30	0	0	2	6	middle
560	PC-5p-265815_12	GATAGGATGCAGGTGTAA	0	9	0	7	0	0	3	4	low
561	PC-5p-112615_52	TTAAGTCAGTTGTGAAAGT	0	18	0	10	11	9	4	5	middle
562	mmu-miR-126a-3p	TCGTACCGTGAGTAATAATGCG	6	15	40	44	47	0	37	110	middle
563	mmu-miR-205-5p_R+1	TCCTTCATTCCACCGGAGTCTGT	4	0	0	7	0	0	0	16	middle
564	mmu-miR-192-5p	CTGACCTATGAATTGACAGCC	2,729	2,045	2,066	1,881	1,613	2,850	2,206	1,734	high
565	mmu-miR-486b-5p_R+1	TCCTGTACTGAGCTGCCCCGAGT	8,227	1,125	1,387	1,353	1,649	7,797	679	3,652	high
566	mmu-miR-378d_1ss6CA	ACTGGACTTGGAGTCAGAAGGT	2	6	0	6	4	6	4	3	low
567	PC-3p-114965_51	GGTTCGACTCCCGGTGTGGGAAC	7	0	11	0	9	16	0	8	middle
568	PC-5p-163628_30	GATGAGGCGTGGGTAGGGGA	0	13	10	30	23	0	0	29	middle
569	PC-3p-181823_25	AAACCGGAGGATTTATTCT	10	0	8	0	0	7	0	0	middle
570	mmu-miR-10b-5p_R-1	TACCCTGTAGAACCGAATTTGT	48	173	379	329	46	34	340	36	high
571	mmu-miR-130a-3p	CAGTGCAATGTTAAAAGGGCAT	4	0	0	7	0	0	0	4	low
572	mmu-let-7e-5p	TGAGGTAGGAGGTTGTATAGTT	9	0	0	10	0	0	5	11	middle
573	PC-3p-212704_19	GCATGGAAGCCAGAAGAAC	0	0	18	0	7	9	0	0	middle
574	PC-3p-101134_59	GTGGGATTGATGACTGGGG	4	30	37	0	7	19	14	25	middle
575	PC-3p-194678_22	AGCAGAAGGGCCTGGAAAGG	26	18	0	0	9	20	0	0	middle
576	mmu-miR-143-3p_R+1	TGAGATGAAGCACTGTAGCTCT	37	21	36	21	48	0	16	147	middle
577	mmu-miR-802-5p	TCAGTAACAAAGATTCATCCTT	12	0	0	0	0	0	6	5	middle
578	PC-3p-281599_11	GTGAGCACGGGAGACAGAGC	5	0	0	0	0	6	0	0	low
579	PC-5p-62023_102	GGGTGTAAAGGGAGTGTAGG	7	16	15	19	16	20	2	14	middle
580	PC-5p-113744_51	AAGATAGAGTAGCGAAGCA	4	55	0	7	28	37	0	0	middle
581	PC-5p-49634_127	AGTTATATTGGCAATGAAGA	11	25	10	31	13	45	23	3	middle
582	ssc-miR-7134-5p	ATGTCCGCGGGTTCCCTATCC	9	0	0	0	0	10	0	0	middle
583	PC-5p-202544_21	CACTGTGGAGGACCGAACC	0	12	0	0	0	7	0	4	middle
584	PC-3p-218573_18	AGGTAGAGCACTGGATTTC	0	9	0	0	9	7	0	0	low
585	PC-5p-104193_57	CAACCGTGAGCTCAGTGAA	23	10	0	0	0	7	3	5	middle
586	PC-5p-227473_17	AGTGGAGAAGGATGTGGGG	0	24	0	0	0	0	0	8	middle
587	mmu-miR-141-3p	TAACACTGTCTGGTAAAGATGG	166	312	354	292	279	185	273	326	high
588	ssc-mir-9843-p3_1ss6AT	TAGAATCCTCTGGAAAGTGG	8	10	0	4	9	22	2	2	middle
589	PC-5p-34704_176	TGTTTGGTGGGTAGTTTGA	23	31	10	13	23	40	12	19	middle
590	PC-5p-83484_74	GTAACTTCGGGATAAAGGGT	12	57	7	26	11	20	14	23	middle
591	PC-5p-273716_11	GACGCATGAGAAAAGATGA	0	7	0	0	0	0	3	0	low
592	mmu-miR-3968_L-3_1ss14AT	ATCCCACTCCTGACACCA	0	10	0	10	11	0	6	20	middle
593	mmu-miR-10a-5p_R-1	TACCCTGTAGATCCGAATTTGT	310	186	390	222	83	229	390	180	high
594	cfa-miR-194_R+1	TGTAACAGCAACTCCATGTGGAT	48	51	63	135	63	75	73	49	middle
595	mmu-miR-5099_L+2R-1	TCTTAGATCGATGTGGTGCTC	0	0	0	7	0	0	7	0	low
596	PC-5p-122887_46	ATGTGAGTGGAAATGCCATC	6	0	10	10	0	0	8	5	middle
597	PC-5p-105512_56	CAGGTAGGCGAGGAGAGAA	12	18	8	0	7	0	13	21	middle
598	PC-3p-122310_47	CAAGGTTAAGTTGAAGAGA	0	0	0	10	11	0	7	9	middle
599	PC-3p-223408_17	GAGAGGGTAATGTAGTAAT	4	0	0	0	9	0	2	4	low
600	PC-3p-171771_28	CGGAGGAAGAGAAAACAACA	6	0	0	0	10	0	3	4	low
601	PC-3p-63973_99	AAAGAAAACAAAAGTGATTGC	24	71	0	19	28	63	0	0	middle
602	bta-miR-2284y_R+1_1ss2AG	AGAAGTTCGTTCGGGTTTTTCT	5	0	0	0	0	2	0	0	low
603	PC-5p-154828_33	AAAGGAAGTAGCGAAGCA	6	12	0	7	0	18	0	3	middle
604	mmu-miR-345-5p_L+1R-1	TGCTGACCCCTAGTCCAGTGCT	0	7	0	0	0	0	0	3	low
605	mmu-miR-200b-5p	CATCTTACTGGGCAGCATTGGA	9	18	0	24	0	20	5	11	middle
606	PC-3p-67324_94	AGTTATGTCGTGGGAGTTC	14	13	11	30	14	0	14	28	middle
607	PC-3p-69490_91	GGTGGAGAGATGTGAAGAGA	6	9	11	10	10	0	29	6	middle
608	PC-5p-177896_26	TCGGAGAGGCAGGCGGAA	0	7	0	10	7	7	0	6	middle
609	PC-3p-230783_16	CGGAAAGGCAAGTCAGAA	0	0	8	11	0	9	0	0	middle

610	PC-5p-185717_24	GCAATGTGTGGAGCTGACA	0	0	0	9	10	7	2	0	low
611	mmu-miR-451a_R-1	AAACCGTTACCATTACTGAGT	2,589	973	1,264	1,052	1,447	2,402	695	837	high
612	oan-miR-429-3p_R+2	TAATACTGTCTGGTAATGCCGTAA	0	0	0	9	0	0	3	4	low
613	PC-5p-231313_16	AACAAGAGAGAATGCCGGA	7	0	0	0	0	0	3	0	low
614	PC-3p-147256_36	GCAGAGTCGTGACGCAGA	0	0	8	14	0	0	6	10	middle
615	PC-5p-204840_20	AAGGGGAGGGCTCAGGGGA	3	0	0	0	0	0	3	0	low
616	PC-5p-115842_50	AAGAAGGCAGGAGAACGGC	0	13	0	9	13	6	0	12	middle
617	mmu-miR-574-3p	CACGCTCATGCACACACCCACA	0	0	0	0	7	0	6	0	low
618	mmu-miR-182-5p_R-1	TTTGGCAATGGTAGAACTCACACC	85	65	99	63	70	118	59	65	middle
619	PC-3p-19277_287	ACAGGTTAGGGGAAAGTGC	49	65	58	79	71	24	114	72	middle
620	PC-5p-151366_34	GAGAATCATTGTTAAGGA	4	10	0	7	0	0	7	5	middle
621	PC-5p-170687_28	CGGAAGAAGGGGTGCCTGC	7	7	0	0	0	0	2	5	low
622	bta-miR-2285ba_1ss7TC	AAACCCCGAACGAACTTTTTGG	7	0	0	0	0	6	0	0	low
623	PC-3p-325246_7	TAAGGTTAGAAGAATTGTGG	4	0	0	0	0	0	3	0	low
624	PC-3p-189725_24	AGGGCACGTTGAAAAGTG	15	10	0	0	7	0	2	15	middle
625	PC-5p-49200_128	ATGAACTGAGGGTGGGGGT	16	55	26	29	21	9	32	41	middle
626	PC-3p-35_15356	AGGATGTTGGCTTGGAAGC	2,066	5,684	6,664	1,742	4,038	3,905	489	9,160	high
627	mmu-miR-139-5p_R+1	TCTACAGTGCACGTGTCTCCAGT	0	12	0	19	0	0	10	11	middle
628	mmu-miR-107-3p_R-5	AGCAGCATTGTACAGGGC	0	3	9	14	4	0	8	12	middle
629	PC-3p-167723_29	GCCGGAGGAAGAGAAAAC	14	0	8	0	0	8	3	4	middle
630	mmu-miR-32-5p_R-1	TATTGCACATTACTAAGTTGC	0	0	0	7	0	0	5	0	low
631	PC-5p-421939_5	TGTGGAGCTGACATGTACT	4	0	0	0	0	0	0	3	low
632	PC-5p-180601_26	AGGTAAGGCTGGGCACTCT	0	7	0	0	13	8	0	3	middle
633	PC-3p-295085_10	ATCTTTGGGGTTCGGACAGC	4	0	7	0	0	6	0	0	low
634	bta-miR-2285f	AAAACCTGAATGAACTTTTTGG	6	0	0	0	0	4	0	0	low
635	mmu-miR-148a-3p	TCAGTGCACTACAGAACTTTGT	144	98	116	93	65	179	40	106	high
636	mmu-miR-466i-5p_L-1R-1	GTGTGTGTGTGTGTGTGT	2	0	0	0	0	0	0	1	low
637	mmu-mir-466k-p5	GTGTGTGTGTGTGTGTGT	2	0	0	0	0	0	0	1	low
638	cpo-miR-1271-5p	CTTGGCACCTAGTAAGCACTCA	31	0	10	13	7	33	0	0	middle
639	mmu-miR-200b-3p_R+1	TAATACTGCCTGGTAATGATGAC	602	680	608	883	617	916	609	470	high
640	PC-3p-249540_14	ATTGGCAATGAAGAAGAGTT	0	16	0	7	0	0	16	0	middle
641	mmu-miR-449a-5p	TGGCAGTGTATTGTTAGCTGGT	4	0	0	0	0	0	3	0	low
642	PC-5p-245451_14	CGAGAGGAAGGTGGGAAT	0	0	18	0	9	0	6	9	middle
643	PC-3p-229624_16	AGGATGTTATCTTGGAAGC	0	9	0	0	0	0	0	6	low
644	PC-3p-163766_30	GGAGGGTCATTGGAAACTG	19	0	0	14	9	13	0	11	middle
645	mmu-miR-31-3p	TGCTATGCCAACATATTGCCATC	5	0	0	0	0	0	3	0	low
646	PC-5p-47156_133	AGGTGGGAGACTAGGAAGC	11	22	40	16	24	31	25	12	middle
647	PC-5p-117670_49	TCAGTGCCGGAGGCGAAGC	4	0	19	0	10	6	5	10	middle
648	PC-3p-157006_32	GAAGAAGGTAGATCGAGAG	0	0	21	11	0	7	5	8	middle
649	PC-5p-45649_137	TGCACAGACAACTAGGAGGT	21	28	44	21	0	10	15	45	middle
650	PC-3p-251106_14	GAGACGAAAGGGAGAGGTA	0	0	0	17	0	0	4	7	middle
651	ssc-mir-1285-p5	ATCGCGCCTGTGAATAGCCACT	151	10	69	7	37	74	50	42	middle
652	PC-3p-184887_25	TCAAAAGGAGAGGTTAGGG	6	0	10	0	0	6	0	4	low
653	PC-3p-211313_19	GTGTGAATGTAAGCAAATC	0	0	0	10	0	0	3	3	middle
654	PC-5p-55135_115	GGGGGTGAAAGGCTAATC	14	21	18	10	9	11	8	23	middle