

Appendix Table S1 Primers for Q-PCR

Primer name	Sequence (5'→3')
rno-miR-3075	TGTCTGGGAGCAGCCAAGGACA
RT-DRG-3075	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTGTCCT
Forward-DRG-3075	TCAGTTGTCTGGGAGCAGCCA
DRG-REVERSE	GTGCAGGGTCCGAGGT
rno-miR-3099	TAGGCTAGAAAGAGGTTGGGA
RT-DRG-3099	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTCCCA
Forward-DRG-3099	CCGTGCTAGGCTAGAAAGAGGT
DRG-REVERSE	GTGCAGGGTCCGAGGT
rno-miR-3102-5p.2	GGTGGTGCAGGCAGGAGAGCC
RT-DRG-3102-5p.2	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGGCTCT
Forward-DRG-3102-5p.2	AGCGTGGTGGTGCAGGCAGGA
DRG-REVERSE	GTGCAGGGTCCGAGGT
rno-miR-1247*	CGGGAACGTCGAGACTGGAGC
RT-DRG-1247*	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGCTCCA
Forward-DRG-1247*	CTTGCGGGAACGTCGAGACT
DRG-REVERSE	GTGCAGGGTCCGAGGT
rno-miR-sc1	GGAGTTGGAGGTGATCGTGAGC
RT-sc1	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGCTCAC
Forward-sc1	TGGGTGGAGTTGGAGGTGATC
REVERSE	GTGCAGGGTCCGAGGT
rno-miR-sc2	TGGGGCACTCAGGAGGCTGCAG
RT-sc2	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCTGCAG
Forward-sc2	GTGAGAGGGGCACTCAGGAGGC
REVERSE	GTGCAGGGTCCGAGGT
rno-miR-sc3	ATGTAAGTGTGTATGTATATG
RT-sc3	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCATATA
Forward-sc3	CCGTCGCGTAAAGTGTGTATGTATAT
REVERSE	GTGCAGGGTCCGAGGT
rno-miR-sc4	TGTGGGTAGAATGACAGAGCAGA
RT-sc4	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTCTGCT
Forward-sc4	CCGCGTGTGGGTAGAATGACA
REVERSE	GTGCAGGGTCCGAGGT
rno-miR-sc5	CATAAGTGTAGAGAGTCTGTAGT
RT-sc5	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACACTACA
Forward-sc5	CCGCGCATAAGTGTAGAGAGTC
REVERSE	GTGCAGGGTCCGAGGT
rno-miR-sc6	TGGGGGACAGGGCAAGGTGG
RT-sc6	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCCACCT
Forward-sc6	CCTGTGGGGGACAGGGCAA

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Primer name	Sequence (5'→3')
REVERSE	GTGCAGGGTCCGAGGT
rno-miR-sc7	CAGGGTTACCTGTTGAGCTGC
RT-sc7	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGCAGCT
Forward-sc7	CGCAGAGGGTTACCTGTTGA
REVERSE	GTGCAGGGTCCGAGGT
rno-miR-sc8	TGAGGATTACGAAGAGGATGGT
RT-sc8	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACACCATC
Forward-sc8	CGGTGAGGATTACGAAGAGGA
REVERSE	GTGCAGGGTCCGAGGT
rno-miR-sc9	CACAGCGGAGCTGGGCACTGGCGT
RT-sc9	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACACGCCA
Forward-sc9	AGTACACAGCGGAGCTGGGCA
REVERSE	GTGCAGGGTCCGAGGT
rno-miR-sc10	TGTGTTTTGTGTGTGTACATGTG
RT-sc10	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCACATG
Forward-sc10	CCGCTGTGTTTTGTGTGTGTAC
REVERSE	GTGCAGGGTCCGAGGT
rno-miR-sc11	GGTGACAGTAAGCTGTAGTTGC
RT-sc11	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGCAACT
Forward-sc11	CCGCAGGTGACAGTAAGCTGTA
REVERSE	GTGCAGGGTCCGAGGT
rno-miR-sc12	ATGGTAATGGTGGTGGTGATG
RT-sc12	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCCATCA
Forward-sc12	GCTGATGGTAATGGTGGTGGT
REVERSE	GTGCAGGGTCCGAGGT
rno-miR-sc13	AATGTGACTCAGCTATCTGAAC
RT-sc13	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGTTTCAG
Forward-sc13	GCCGAATGTGACTCAGCTATC
REVERSE	GTGCAGGGTCCGAGGT
rno-miR-sc14	AACAGGTGATCTTCAAGTAGA
RT-sc14	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTCTACT
Forward-sc14	CGCTCACAGGTGATCTTCAAGT
REVERSE	GTGCAGGGTCCGAGGT
rno-miR-sc15	TGGGGGCAGGCCGGATCTAGTG
RT-sc15	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCACTAG
Forward-sc15	TTAATGGGGGCAGGCCGGAT
REVERSE	GTGCAGGGTCCGAGGT
rno-miR-sc16	TGACTTTCCAGAGAACCCTTGA
RT-sc16	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTCAAGG
Forward-sc16	CGCGCTGACTTTCCAGAGAAC
REVERSE	GTGCAGGGTCCGAGGT
U6-forward-p	CTCGCTTCGGCAGCACA
U6-reverse-p	AACGCTTCACGAATTGCGT

Appendix Table S2 The categories of rat small RNAs

Yield								
	total reads		clean reads		clean/total (%)			
0 h	11115161		10518910		97.49			
1 d	10389441		9825421		98.05			
4 d	10654339		9851345		96.33			
7 d	12983557		12183086		95.56			
14 d	10688245		9775473		94.5			

The composition of Solexa sequencing of various lengths (%)								
	19	20	21	22	23	24	25	Others
0 h	1.94	9.46	18.12	48.49	14.89	2.89	0.81	3.4
1 d	1.64	9.12	16.86	50.24	13.26	3.73	1.03	4.12
4 d	2.04	9.36	14.99	46.87	14.55	5.07	1.57	5.55
7 d	1.82	7.28	16.91	39.29	22.33	6.7	1.34	4.33
14 d	0.79	6.63	15.62	46.47	13.68	4.12	0.89	11.8

Mapping summary						
	unique sequence number			total reads number		%
	total	match	match/total(%)	total	total	
0 h	318323	83329	26.18	10518910	8213858	78.09
1 d	316625	95369	31.12	9825421	7770977	79.09
4 d	477007	198039	41.52	9851345	7852278	79.71
7 d	456322	170362	37.33	12183086	9850603	80.85
14 d	295773	102544	34.67	9775473	7684960	78.61

Annotation of sRNAs from Solexa sequencing					
	unique sequence number			total reads number	
	type	count	%	count	%
0 h	total	318323		10518910	
	rRNA	32150	10.1	177500	1.687
	snRNA	938	0.295	5371	0.051
	snoRNA	9	0.003	21	0.0002
	tRNA	2055	0.646	22983	0.218
	other	283171	88.96	10313035	98.04
1 d	total	316625		9825421	
	rRNA	22941	7.25	197197	2
	snRNA	1224	0.387	9456	0.096
	snoRNA	12	0.004	22	0.0002
	tRNA	2364	0.747	21071	0.214
	other	290084	91.62	9597675	97.26
4 d	total	477007		9851345	
	rRNA	19343	4.055	146414	1.486
	snRNA	1034	0.217	8545	0.087
	snoRNA	13	0.0027	40	0.0004
	tRNA	2041	0.428	28101	0.285
	other	454576	95.3	9668245	98.14
7 d	total	456322		12183086	
	rRNA	16964	3.718	122625	1
	snRNA	1551	0.34	12598	0.103

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		unique sequence number		total reads number	
14 d	snoRNA	13	0.0028	24	0.0002
	tRNA	3086	0.676	44505	0.365
	A				
	other	434708	95.263	12003334	98.52
	total	295773		9775473	
	rRNA	16061	5.43	99508	0.017
	snRNA	993	0.336	8877	0.091
	snoRNA	16	0.005	121	0.0012
	tRNA	2228	0.753	51422	0.526
	other	276475	93.475	9615545	98.37

Appendix Table S3 The data of known miRNAs

The number of known miRNAs		
	miRNAs number	miRNA* number
0 h	259	55
1 d	261	56
4 d	262	56
7 d	266	56
14 d	259	52

Known miRNAs and their reads number after rat sciatic nerve transection

miRNA	Reads				
	0 h	1 d	4 d	7 d	14 d
rno-let-7a	942371.2	642961	642961	496244.4	642961
rno-let-7b	642961	496244.4	302073	642961	496244.4
rno-let-7b*	13.5	24.8	14.2	17	38.7
rno-let-7c	1822639	1822639	1822639	942371.2	1822639
rno-let-7d	54465	79692.4	89954.8	43579.8	71545.6
rno-let-7d*	917.8	1358.8	832	901	986.6
rno-let-7e	38732	46908.4	65239.8	28640	65239.8
rno-let-7e*	15.2	14.5	15.2	11.3	13.6
rno-let-7f	496244.4	942371.2	942371.2	428397	942371.2
rno-let-7i	17243	20235	24001.4	11901.6	24001.4
rno-let-7i*	22.7	26.6	12.7	6.3	0.2
rno-miR-1	397124.8	230172.6	22927.2	24504.2	89954.8
rno-miR-100	52101	33839.6	33839.6	59647.8	31103.8
rno-miR-101a	12265.8	9699	11213.4	13690	9015.4
rno-miR-101a*	12.5	6.2	6.2	12.6	15.2
rno-miR-101b	12484.6	10976.4	15413.4	22927.2	15413.4
rno-miR-103	100320	54465	49881.8	77264.4	49881.8
rno-miR-106b	1245.2	798.4	1055.4	2394	1221
rno-miR-106b*	178.6	357.4	405	361.6	357.4
rno-miR-107	689.6	342.6	327.8	328.6	283.2
rno-miR-10a-3p	52.4	38.2	34.4	49	46.8
rno-miR-10a-5p	65239.8	52101	79692.4	100320	79692.4
rno-miR-10b	124613.6	110873	100320	110873	110873
rno-miR-122	61.2	181.4	28.3	10.8	33.6
rno-miR-124	154.6	337.2	234.6	72.6	68.4
rno-miR-124*	1.5	4.9	0	0	0.2
rno-miR-125a-3p	191.8	212.2	283.8	163.8	327.8
rno-miR-125a-5p	11901.6	11213.4	7302.6	12484.6	10976.4
rno-miR-125b*	5500.6	4150.2	3432.4	3343.8	2394

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miRNA	Reads				
rno-miR-125b-3p	2457.4	2530.6	1697.4	811.6	622.8
rno-miR-125b-5p	43579.8	35790.6	31103.8	49881.8	24504.2
rno-miR-126	59647.8	59647.8	59647.8	79692.4	59647.8
rno-miR-126*	3432.4	2457.4	2394	4150.2	2344.2
rno-miR-127	19147.6	18616.8	17243	18616.8	16363.6
rno-miR-128	497.8	689.6	488.8	566.4	493.3
rno-miR-129	159.4	194.6	194.6	181.4	111
rno-miR-129*	0	1.4	1	0.9	0.2
rno-miR-130a	1037.7	1020	867	697.4	1111
rno-miR-130b	13.5	64.5	102.4	89.8	60
rno-miR-132	88.4	105.4	244.8	337.2	201.6
rno-miR-133a	840	467.2	53.1	69.2	361.6
rno-miR-133b	82.8	68.4	5.2	6.3	12.7
rno-miR-134	7302.6	6290.6	9699	12265.8	7877.2
rno-miR-135a	25.2	9.1	15.2	15.2	8.6
rno-miR-135a*	2.2	1.4	6.2	1.4	0.2
rno-miR-135b	0	0	0	0.2	0.2
rno-miR-136	283.2	142.6	145.8	293.2	252.6
rno-miR-136*	147.8	132.4	117.2	172.2	142.6
rno-miR-137	337.2	376.8	357.4	459.2	133.4
rno-miR-138	15413.4	16363.6	9994.4	7877.2	4568.6
rno-miR-138*	246.6	206.8	136.2	123.2	81.7
rno-miR-139-3p	405	744.8	768	284.4	778.8
rno-miR-139-5p	175.6	136.2	171.4	162.6	162.6
rno-miR-140	2344.2	1737.4	1638.2	2156.8	2457.4
rno-miR-140*	40946.4	43579.8	52101	86065	38732
rno-miR-141	3.4	6.2	6.2	8.2	3.2
rno-miR-142-3p	986.6	2075	1805.4	3927	1805.4
rno-miR-142-5p	856	2032	1414.8	1414.8	840
rno-miR-143	428397	428397	397124.8	302073	302073
rno-miR-144	8.6	29.7	4.4	8.2	3.2
rno-miR-145	276.8	446.8	283.8	311.2	416.5
rno-miR-146a	10976.4	9015.4	7877.2	9699	13690
rno-miR-146b	86065	142892.8	230172.6	397124.8	252720
rno-miR-147	0	3.8	7.6	5.6	0.2
rno-miR-148b-3p	13690	17785.8	13690	8252.2	9994.4
rno-miR-148b-5p	867	941	778.8	446.8	798.4
rno-miR-150	197.8	283.2	105.4	183.8	284.4
rno-miR-151	2762.4	3021	2940.6	2633.2	3343.8
rno-miR-151*	20235	28640	40946.4	24001.4	33839.6
rno-miR-152	71545.6	49881.8	54465	65239.8	54465
rno-miR-153	1.5	3.8	1	0	0.2
rno-miR-154	21.4	15.2	8.9	11.3	15.2
rno-miR-15b	446.8	497.8	811.6	744.8	917.8
rno-miR-16	18616.8	24504.2	28640	14705.2	26911.2
rno-miR-17-3p	117.2	109.5	183.8	170.6	173.9
rno-miR-17-5p	2156.8	1805.4	2344.2	3781.2	2762.4
rno-miR-181a	33839.6	26911.2	21725.2	26911.2	22927.2
rno-miR-181a*	163.2	145.8	154.6	191.8	182.6
rno-miR-181b	9994.4	7877.2	6290.6	9994.4	6290.6
rno-miR-181c	1805.4	1189.6	622.8	867	856
rno-miR-181d	3781.2	3343.8	2244	3432.4	4150.2

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miRNA	Reads				
rno-miR-182	28640	65239.8	71545.6	35790.6	46908.4
rno-miR-183	35790.6	71545.6	77264.4	37096.4	35790.6
rno-miR-184	419.2	811.6	3927	1221	3927
rno-miR-185	1485.6	1245.2	901	1189.6	811.6
rno-miR-186	3021	3516	2633.2	2849.2	2633.2
rno-miR-187	45.3	19.1	25.6	34.4	16.2
rno-miR-188	15.2	7.6	17.1	29.2	0.2
rno-miR-18a	23.6	67.2	117.2	142.6	74
rno-miR-190	150	79.5	82.8	97	106.7
rno-miR-190b	19.9	22.7	44.4	69.2	46.8
rno-miR-191	37096.4	40946.4	43579.8	40946.4	37096.4
rno-miR-192	3516	2633.2	2156.8	1805.4	1569.2
rno-miR-193	1.5	4.9	4.4	3.4	3.2
rno-miR-193*	70.7	95	76.4	61.2	86.9
rno-miR-194	476	329.4	230.4	304.4	307.8
rno-miR-195	3343.8	5402	6105	1605.4	8252.2
rno-miR-196a	46908.4	37096.4	38732	52101	43579.8
rno-miR-196a*	19.9	17	12.7	23.6	8.6
rno-miR-196b	24504.2	22927.2	24504.2	17785.8	19147.6
rno-miR-196c	252.6	361.6	530.8	276.8	252.6
rno-miR-199a-3p	17785.8	13297.2	17785.8	31103.8	21725.2
rno-miR-199a-5p	1474	697.4	1358.8	2244	1605.4
rno-miR-19a	9.1	17	17.1	30.2	17.1
rno-miR-19b	68.4	91.6	127.4	136.2	163.8
rno-miR-200a	3.4	1.4	2.7	3	4.7
rno-miR-200b	4.6	7.6	2.7	4.6	8.6
rno-miR-200c	304.4	592.4	697.4	497.8	493.3
rno-miR-203	1037.7	867	753.2	1153.4	832
rno-miR-204	488.8	530.8	376.8	530.8	744.8
rno-miR-204*	133.4	217.6	267.5	101.4	241.4
rno-miR-205	116	132.4	64.8	91.6	189.2
rno-miR-206	166843	124613.6	46908.4	46908.4	100320
rno-miR-20a	1325.2	1605.4	2075	3021	1697.4
rno-miR-20a*	15.2	15.2	25.6	13.5	21.4
rno-miR-20b-3p	234.6	170.6	150	178.6	191.8
rno-miR-20b-5p	2530.6	1474	1325.2	2344.2	1638.2
rno-miR-21	77264.4	252720	428397	1822639	397124.8
rno-miR-21*	4.6	56.3	72.6	76	10.8
rno-miR-210	224.6	159.4	142.6	152.4	126.2
rno-miR-211	0	0	1	0	0.2
rno-miR-212	7.6	9.1	15.2	17.2	28.8
rno-miR-214	396	409.4	1111	430.8	1485.6
rno-miR-215	34.4	49	34.4	55	28.8
rno-miR-216a	11.2	22.7	8.9	8.9	10.8
rno-miR-217	299.2	327.8	267.5	269.6	194.6
rno-miR-218	1221	1055.4	840	768	669
rno-miR-218*	5.7	4.9	2.7	4.9	4.7
rno-miR-219-1-3p	28.2	29.7	7.6	19.9	10.8
rno-miR-219-2-3p	39.2	12.6	11.3	24.8	4.7
rno-miR-22	4150.2	5010.6	2762.4	3166.6	2156.8
rno-miR-22*	103.9	126.2	111	128.6	131.4
rno-miR-221	467.2	768	1153.4	1638.2	941

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miRNA	Reads				
rno-miR-222	209.5	476	669	856	530.8
rno-miR-223	76.4	409.4	293.2	224.6	173.9
rno-miR-224	53.8	32.8	70	111	101.4
rno-miR-23a	3166.6	3781.2	3021	3516	5010.6
rno-miR-23a*	1.5	3.8	2.7	5.6	8.6
rno-miR-23b	2849.2	3166.6	1737.4	2457.4	3516
rno-miR-24	89954.8	89954.8	124613.6	89954.8	77264.4
rno-miR-24-1*	42	14.5	22.7	26.6	28.8
rno-miR-24-2*	1569.2	1221	941	1569.2	867
rno-miR-25	1737.4	1638.2	1485.6	1896.6	2075
rno-miR-25*	152.4	293.2	361.6	159.4	548.4
rno-miR-26a	79692.4	100320	86065	54465	86065
rno-miR-26b	11213.4	15413.4	11901.6	5500.6	12265.8
rno-miR-26b*	7.6	4.9	1	6.8	6.4
rno-miR-27a	21725.2	21725.2	19147.6	33839.6	9699
rno-miR-27a*	778.8	986.6	856	1020	768
rno-miR-27b	49881.8	38732	37096.4	71545.6	52101
rno-miR-28	1896.6	1569.2	2032	1737.4	2032
rno-miR-28*	2032	1697.4	1569.2	2530.6	1737.4
rno-miR-292-3p	0	3.1	0	0	0.2
rno-miR-292-5p	0	1.4	0	0.2	0.2
rno-miR-296	111	64.5	131.4	243	121.2
rno-miR-296*	4.6	4.9	4.4	7.6	1.7
rno-miR-298	97	101.9	162.6	85.4	269.6
rno-miR-299	13.5	12.6	10.3	12.6	25.6
rno-miR-29a	5899.6	5899.6	6916	9015.4	6105
rno-miR-29a*	29.2	52.4	64.2	77.6	72.8
rno-miR-29b	85.4	147.8	251	217.6	230.4
rno-miR-29b-1*	108	121.2	189.2	234.6	102.4
rno-miR-29b-2*	25.2	12.6	20.2	22.4	25.6
rno-miR-29c	128.6	101.9	97	95	99.6
rno-miR-29c*	10.2	10.6	15.2	27.4	4.7
rno-miR-300-3p	622.8	548.4	459.2	592.4	430.8
rno-miR-300-5p	0	0	0	0.2	3.2
rno-miR-301a	103.9	45.3	49.8	46.5	68.4
rno-miR-301b	3.4	3.8	4.4	9.8	1.7
rno-miR-30a	252720	166843	166843	252720	166843
rno-miR-30a*	24001.4	31103.8	35790.6	16363.6	40946.4
rno-miR-30b-3p	669	669	566.4	413.8	592.4
rno-miR-30b-5p	1358.8	1153.4	689.6	986.6	1037.7
rno-miR-30c	6916	8252.2	4150.2	7302.6	6916
rno-miR-30c-1*	30.5	45.3	53.1	15.4	52.4
rno-miR-30c-2*	5402	6105	5010.6	2762.4	5500.6
rno-miR-30d	302073	302073	252720	230172.6	230172.6
rno-miR-30d*	55	20.2	28.3	36.8	50.6
rno-miR-30e	31103.8	24001.4	26911.2	38732	28640
rno-miR-30e*	9699	12484.6	13297.2	6290.6	17243
rno-miR-31	11.2	251	1896.6	669	1325.2
rno-miR-32	361.6	224.6	201.6	175.6	170.6
rno-miR-320	8252.2	7302.6	5899.6	5402	7302.6
rno-miR-322	1697.4	778.8	1245.2	2032	1414.8
rno-miR-322*	2075	1414.8	2457.4	1474	3166.6

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miRNA	Reads				
rno-miR-323	78.4	116.6	79.5	102.4	78.4
rno-miR-323*	17	22.7	17.1	16.2	15.2
rno-miR-324-3p	136.2	56.3	68.4	145.8	76.4
rno-miR-324-5p	126.2	97	68.4	73.5	60
rno-miR-325-3p	64.8	84.1	85.4	58.2	106.7
rno-miR-325-5p	68.4	76	30.8	42	56.3
rno-miR-326	30.5	34.4	22.7	18.6	12.4
rno-miR-328	239.8	230.4	159.4	147.8	212.2
rno-miR-329	6.6	7.6	10.3	3.4	8.6
rno-miR-33	170.6	72.6	38.2	64.5	17.1
rno-miR-330	182.6	183.8	117.2	82.8	97
rno-miR-330*	697.4	840	446.8	328.6	416.5
rno-miR-331	13.5	10.6	1	3.4	1.7
rno-miR-335	744.8	1111	1189.6	917.8	1245.2
rno-miR-337	5.7	1.4	1	2.2	1.7
rno-miR-338	5010.6	4568.6	3781.2	2940.6	2849.2
rno-miR-338*	22927.2	17243	12265.8	17243	13297.2
rno-miR-339-3p	131.4	116.6	108	108	95
rno-miR-339-5p	73.5	72.6	95	88.4	56.3
rno-miR-340-3p	243	175.6	123.2	121.2	123.2
rno-miR-340-5p	1189.6	2156.8	2849.2	840	2244
rno-miR-341	329.4	241.4	244.8	299.2	42
rno-miR-342-3p	163.2	154.6	178.6	265.4	276.8
rno-miR-342-5p	201.6	267.5	497.8	357.4	566.4
rno-miR-344-3p	1.5	1.4	0	1.6	1.7
rno-miR-345-3p	1111	753.2	396	488.8	146.8
rno-miR-345-5p	61.2	22.7	13.6	32.8	38.7
rno-miR-346	1.5	4.9	1	0.9	1.7
rno-miR-34a	252.6	201.6	212.2	239.8	241.4
rno-miR-34b	0	0	0	0.9	4.7
rno-miR-34c	2633.2	3927	8252.2	11213.4	5899.6
rno-miR-34c*	0	0	12.7	1.6	12.7
rno-miR-350	37.5	52.4	23.6	39.2	68.4
rno-miR-351	530.8	419.2	476	548.4	697.4
rno-miR-352	3.4	1.4	1	0	4.7
rno-miR-361	142.6	128.6	90.7	150	159.4
rno-miR-363	3927	2940.6	3166.6	4568.6	3021
rno-miR-363*	5.7	3.1	2.7	1.4	0.2
rno-miR-365	2.2	3.1	2.7	0.2	1.7
rno-miR-369-3p	342.6	283.2	413.8	689.6	293.2
rno-miR-369-5p	230.4	162.6	197.8	197.8	217.6
rno-miR-370	592.4	299.2	548.4	832	342.6
rno-miR-374	327.8	283.2	311.2	419.2	337.2
rno-miR-375	15.2	11.4	2.7	4.1	10.8
rno-miR-376a	49	60	79.5	58.2	64.5
rno-miR-376a*	28.2	17	30.2	28.3	25.6
rno-miR-376b-3p	46.8	38.2	49.8	52.4	44.4
rno-miR-376b-5p	293.2	189.2	239.8	194.6	234.6
rno-miR-376c	90.7	79.5	99.6	99.6	76.4
rno-miR-377	26.6	15.2	39.2	38.2	42
rno-miR-378	230172.6	397124.8	496244.4	142892.8	428397
rno-miR-378*	73.5	42.4	42.4	44.4	46.8

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(Continued)

miRNA	Reads				
rno-miR-379	110873	77264.4	142892.8	124613.6	142892.8
rno-miR-379*	68.4	68.4	67.2	42	72.8
rno-miR-380	2244	2344.2	1605.4	1697.4	1896.6
rno-miR-381	76.4	17	57.6	50.6	28.8
rno-miR-382	6290.6	5500.6	5402	6916	3781.2
rno-miR-382*	97	109.5	175.6	117.2	153.5
rno-miR-383	1638.2	2244	1474	1055.4	1153.4
rno-miR-384-3p	50.6	74	60	46.5	53.8
rno-miR-384-5p	194.6	234.6	133.4	212.2	224.6
rno-miR-409-3p	798.4	856	798.4	1245.2	689.6
rno-miR-409-5p	72.6	89.1	88.4	77.6	64.5
rno-miR-410	267.5	311.2	304.4	342.6	265.4
rno-miR-411	7877.2	9994.4	16363.6	5899.6	20235
rno-miR-412	0	1.4	0	1.6	4.7
rno-miR-421	0	1.4	0	2.2	0.2
rno-miR-423	1605.4	1325.2	986.6	1358.8	1189.6
rno-miR-425	566.4	566.4	430.8	622.8	446.8
rno-miR-429	3.4	1.4	2.7	0.9	0.2
rno-miR-431	37.5	29.7	21.4	25.6	28.8
rno-miR-433	172.2	172.2	171.4	154.6	150
rno-miR-434	9015.4	11901.6	10976.4	10976.4	11213.4
rno-miR-448	5.7	9.1	8.9	9.8	1.7
rno-miR-449a	9.1	6.2	4.4	19.9	8.6
rno-miR-450a	941	488.8	744.8	1111	753.2
rno-miR-451	548.4	1485.6	592.4	467.2	299.2
rno-miR-455	101.4	76.8	127.4	206.8	376.8
rno-miR-463	1.5	0	7.6	4.6	4.7
rno-miR-466b	2.2	0	6.2	8.9	10.8
rno-miR-466c	10.2	3.1	10.3	14.5	8.6
rno-miR-483	1.5	1.4	0	1.6	0.2
rno-miR-484	11.2	13.5	11.3	13.5	13.6
rno-miR-485	768	901	1020	396	1037.7
rno-miR-487b	28.2	29.7	25.6	30.8	23.3
rno-miR-488	22.7	41.6	46.5	23	19.6
rno-miR-489	10.2	1.4	10.3	2.2	1.7
rno-miR-493	182.6	152.4	181.4	201.6	182.6
rno-miR-494	376.8	304.4	467.2	798.4	459.2
rno-miR-495	15.2	19.1	28.3	21.4	21.4
rno-miR-497	459.2	267.5	276.8	476	476
rno-miR-499	413.8	396	329.4	246.6	206.8
rno-miR-500	122.2	99.6	72.6	131.4	136.2
rno-miR-501	0	0	1	0.9	6.4
rno-miR-503	1414.8	832	2530.6	2075	1474
rno-miR-505	61.2	60	55	64.5	91.6
rno-miR-532-3p	90.7	89.1	76.4	73.5	117.2
rno-miR-532-5p	2940.6	2394	3516	5010.6	3432.4
rno-miR-539	70.7	84.1	41.6	53.8	86.9
rno-miR-540	217.6	163.8	299.2	283.2	246.6
rno-miR-541	14705.2	13690	20235	21725.2	18616.8
rno-miR-542-3p	4568.6	2762.4	5500.6	6105	5402
rno-miR-542-5p	430.8	246.6	217.6	405	396
rno-miR-543	3.4	0	2.7	2.2	4.7

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(Continued)

miRNA	Reads				
rno-miR-543*	12.5	28.2	34.4	28.3	23.3
rno-miR-551b	0	0	1	0	0.2
rno-miR-598-3p	267.5	241.4	206.8	189.2	153.5
rno-miR-598-5p	0	1.4	0	0.2	0.2
rno-miR-652	1153.4	917.8	917.8	1325.2	901
rno-miR-664	8.6	8.2	2.7	4.1	17.1
rno-miR-671	42	26.6	28.3	15.2	17.1
rno-miR-672	357.4	254.2	337.2	376.8	329.4
rno-miR-673	80.6	38.2	46.5	67.2	71.4
rno-miR-674-3p	57.6	70	90.7	80.6	89.8
rno-miR-674-5p	45.3	52.4	72.6	69.2	81.7
rno-miR-708	209.5	150	147.8	230.4	307.8
rno-miR-708*	17	8.2	17.1	12.6	36.8
rno-miR-743a	0	1.4	12.7	7.6	4.7
rno-miR-743b	1.5	1.4	8.9	3.4	13.6
rno-miR-758	4.6	0	19.6	14.5	8.6
rno-miR-760-3p	311.2	191.8	152.4	105.4	116
rno-miR-770	7.6	3.8	4.4	4.9	1.7
rno-miR-7a	753.2	2849.2	4568.6	941	2530.6
rno-miR-7a*	4.6	9.1	6.2	5.6	15.2
rno-miR-7b	18.6	46.8	101.4	17	21.4
rno-miR-871	1.5	0	1	0	0.2
rno-miR-872	13297.2	12265.8	14705.2	19147.6	17785.8
rno-miR-872*	811.6	459.2	419.2	753.2	467.2
rno-miR-873	6.6	10.6	5.2	3.4	6.4
rno-miR-874	32.8	26.6	15.2	9.8	28.8
rno-miR-877	97	178.6	224.6	116	197.8
rno-miR-878	0	0	1	0	0.2
rno-miR-879	17	13.5	0	0	0.2
rno-miR-880	0	0	0	0.9	3.2
rno-miR-881	3.4	10.6	60	10.4	33.6
rno-miR-9	16363.6	14705.2	12484.6	13297.2	14705.2
rno-miR-9*	284.4	430.8	342.6	126.2	405
rno-miR-92a	901	1896.6	1221	1485.6	1358.8
rno-miR-92b	832	622.8	254.2	251	146.8
rno-miR-93	6105	6916	9015.4	15413.4	11901.6
rno-miR-96	122.2	197.8	163.8	133.4	128.6
rno-miR-98	2394	3432.4	3343.8	778.8	2940.6
rno-miR-99a	26911.2	19147.6	18616.8	20235	12484.6
rno-miR-99a*	145.8	72.6	74	69.2	67.2
rno-miR-99b	142892.8	86065	110873	166843	124613.6
rno-miR-99b*	189.2	123.2	191.8	254.2	178.6

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(Continued)

MFE	Sequence
-18	aacagaggaataggggtctcaggaactgtagatacttgcactgttaagaatttggtttgtctttgtcactggcatgtctgtgtgtga
-20.2	atgattcatatattgttgaggagatgtggaatggcacctgatctcacctcacaaaaggaggtga
-24.1	aaaaccatagtgtaagatgtaggcagggtgccatattgcatgcccttaattgctttcactgggggcta
-36.2	cgacccctgctccctgcccagtcactcagctggggctctgcacagcgtggtgctgtggctgtggaggcggaggctgt
-34.4	ccggctgtcctgggtgaggagacaaggccagtcgccaggtgtgctgacctgtctcccaccagggggtccag
-34.8	ggcatttgtctcagagagatgagagacaagcagggaacctccccgctccctgctcaccattccctctgcaggtggaccagtcggcct
-31.2	tgggtggcattgagcaccccaaccatccagggaatattgtagtagccatgctgggggttgccgtgtagggtgtgggtgccgagg
-46.9	tgggagggggaggccagagcagcgggttctgctgggctctcagaggcctgctctgagccccgcctcctctctc
-34.9	ccggttctctgtctgtctccgttgcttccgaggtgaaagggtggcctggatgggaacctggtagcgaggatgcggcagtcacca
-22.2	gggacttagtggaggatgaggagtcagtggtcttgatattgtaactgtccttccctccacaggctct
-30	cagccttgaaatgtgggtgggtgaagtagagagaccagcatgggtctctgactcttgcctccacagaagacctg
-34.5	ccccagccctccttgggtcctccccgctcctccggcgacgagacagccagggaactgtggcgagcagtggtgtgtggg
-27.04	ccctcctgctcaggaggagatttggaggtatctgagccactccacatttctcctccagggtgtgt
-29.86	ctgaggcgagaggggatgagtagagcagacagccctcctctccagtgtctgacctccatccaccttagg
-21.2	gaggcgggtcccaactgttccctcaaccggcagaatgcactataccagtcctgtcacgaagatgagaatgattgtgcagaccatctcg
-22.84	catcgcgctcagaggatcctgggagtgtaggcttaatcgtggtctctagctagactccgggattttcctcttctctctctc
-30	agagagcaatggaagggtgtgtgttgggaagacagcagtgcttctccctgacaaggcctccacactgttggtctg
-32.3	tgggtctccagtttttctgcttctgctctgtggtgtgtggtgctggttccagaggcgagtggaactgtggcctttag
-30.1	tagtggtagtactctgctgtgtgcccgcagcaacctcgggtcgaatccgagtcacggcattgtggcaacaatggcacgcaaggcgctt
-29.1	aaaggctctcctaaggcaggcagactcagtggttcccatttctcagttctctgaagcttctacctccaaggcgctt
-24	gagcagagacatggacaggcaaggtgaatcacaagccatcgtaaagtgttttccctgtctgttccacagacccaaagtaccatgcag
-29.9	agactggaaactcggagggtgtgagtgctcacagaacagagcccacttggccccttcaggactaggaca
-41.5	tgtctgggacnacctgtagcaggtgtgctgggacacctgtaccagctgtgctnggacacctgtaccagctgtgctgggacacctgtagcagatgcagca
-40.2	tgcgtccgcggggggggcggggctcgcgcggacgcgcggcgggggcggggaagcagctagctgtcgggatcggcgcgcggggcacaggacgtg
-24.66	cttggttccccaagcccttgatgtcagcatccagcaagcatgaggtctcggcatagagggttttttttcttc
-21.8	aaaatggacaacatgattggagatgggagaagtcagaattgctgggtgcttccaactccaatgcgggcattaa
-31.9	ctgcgtgaggtgggagagcagtgaggggcagggtggtggcacaggaaagcctcacaccaactgattattctctaccttcccgtt
-35.3	ccggggcggtcagctacccgtgctccgcggcgccgcatcttgacctgaaacaccgggtcaggtctagggcatacttcccgt
-24.2	atggttttggtagtcttgacggtgagggcagcagctgtgctggaagcaactgtctcttgggtaggtagctatctctcctc
-30.5	gtgtcagaagggtttgactcctggttcttgggtgacctctgttggcagtaggcaagctatggcaggtagatcagagtgcctgttgacag
-32.5	tggccaagtggtaaggcgtcgtctcgttaaacgaagatcgcgggttcgaacccgtcctgctgctgttgggaacgatgtgttgcgtgtgttt
-30.26	ttggagcatctacaagggtgggtccccatatgtaaatcttctcatcttgaggggccttgccttgcagagcatgga
-29.24	tcagatggggttggaaagcattgtgaaggtgtcattccgtctgccagccatcttcacagagtttccacctttagggtcttc
-27.5	cctgacaggaaaggagatcaaaagctgcaggagcttctgctgtgcagacctgtgttccaacctgttgt
-37	ccctctgtagtggcgaggctgcggggcagccgcttgcgtggccgaagctcctcctctcctctccgttaccgggt
-41.61	atatctgggtggggacaaggcagagaagatggcgctcttgaccaatggcttcttctctgctgacctccccagcccttcgggtgatgg
-26.6	tagggaaaggtaggggcaggggcaagggtattcaagtgccttcaaggaaacattgaccagcctctgttccccag
-30.6	cgcggcgctcctgcgttcgcgggcattaccgtgtagtagctgaaggagacggcgatgactgtgaaccagaacaagctgcc
-31.9	tggctcagcctctggagttggagagccggaaggagacagctcaacacttcttctgacttttccccagggcctatcaaccgtgaaatcgccac
-36.2	ctgctagaacttgggagagtgaaagggaaggcactggcactcagcctgtctcctatttctctcaggtgatatttatttccggaagaaggatgggca
-22.84	catcgcgctcagaggatcctgggagtgtaggcttaatcgtggtctctagctagactccgggattttcttctctctctc
-33.2	atggcgggtggcgactacaggaaagctgtccagtgttgaggagtggtgctgacagcttccctgtgtctgtgaccaccttcc
-28	catgtggcggtagggggttgagtgatgaaagcatltaagtttgaccacacgctcctcactgtggcctacaggtgtccctgtataagctgtg
-40.5	ggcatgccggtcaggaggggacacggagtgacaggcactcaccactggcctcctcctgtcctcctgcaggagatccg
-22.7	gtaaatagagtcgtagatccaagggaataagactcgggtctcctcagcttgtgacttgggttccagcattgtgaaa
-25.9	cccttgggtttgagggtcaggagctggttgagtgactaaagattaaactcagcttctcatgtctcagggccatcac

Appendix Table S6 The MEF and pre-miRNA sequences of novel predicted miRNAs

IDs	MFE	pre-miRNA sequence
rno-miR-3075	-36.9	cggtttttacTGTCTGGGAGCAGCCAAGGACAagttacctcttctctctgcttggccttctaggtgtccaagctcacgcaggctgggagcca
rno-miR-3099b	-41.6	atcgatccccatcccagcttctccagcccttgatgtttcagtagcacaTAGGCTAGAAAAGAGGTTGGGGAAtggggaaga
rno-miR-3102-5p.2	-42.54	gggtgggctgGGTGGTGCAGGCAGGAGAGCCattgatctattgctgggctctactcctgccccagccagagacccttg
rno-miR-1247*	-39.2	gccgccggcgccagcccgcttctgctccccggacgttgctctctgcccCGGGAACGTCGAGACTGGAGCgccccgaactg
rno-miR-sc1	-37.82	agcgtgagctGGAGTTGGAGGTGATCGTGAGCgtgaagactgtgttgccacaagcacttccaactgcagagccacgctctgc
rno-miR-sc2	-42.9	gggtggccgagTGGGGCACTCAGGAGGCTGCAGcgaccggctccttctgctgctctccagcacccttctgctccct
rno-miR-sc3-1	-36.4	atgtgtgtatATGTAAGTGTGTATGTATATGgttttatgaatatacatataactacacacacacacacgcaa
rno-miR-sc3-2	-33.4	gtgtgcaATGTAAGTGTGTATGTATATGgtgcatatgagtagtgtgtgcatgtgtgtgtgtacatgtgagtgcatgtgcatgtg
rno-miR-sc4	-32.62	cggattcacTGTGGGTAGAATGACAGAGCAGAcagagactagagagctctgtttgccatctcttgcaggcatgtgcct
rno-miR-sc5	-31.3	gatgtgtgtgagacacagcttctcttacttattatttcttcttataatCATAAGTGTAGAGAGTCTGTAGTcaccacccat
rno-miR-sc6	-43.41	gaggccagtTGGGGGACAGGGCAAGGTGGcagtagctgacagcctgtttacacttgcctttttcccgagctatgttcggtgtggcaga
rno-miR-sc7	-31.3	agacacccggCAGGGTTACCTGTTGAGCTGCagcagaaggtgaatgcagcctctgtgaccttccccagatgtca
rno-miR-sc8	-47.6	taaaacggagTGAGGATTACGAAGAGGATGGTgtgctttaattagaaactttacagcatcctcttataacttttactcgttttac
rno-miR-sc9	-39.2	catcctgaccCACAGCGAGCTGGGCACTGGCGTcacgcagctcctgttggcacccttgctctgtgagctcagggtcgg
rno-miR-sc10-1	-38	catgtgtgtaTGTGTTTTGTGTGTGTACATGTGgtatgtgaagacacatatacatgcacataagcacacacacgcagt
rno-miR-sc10-2	-38	catgtgtgtaTGTGTTTTGTGTGTGTACATGTGgtatgtgaagacacatatacatgcacataagcacacacacgcaag
rno-miR-sc10-3	-49	catgtgtgtaTGTGTTTTGTGTGTGTACATGTGgtatgtgaagacacatatacatgcacataagcacacacacgcaagcacactcacatga
rno-miR-sc10-4	-33.8	gcattgtgtaTGTGTTTTGTGTGTGTACATGTGgtatgtgaagacacatatacatgcacataagcacacactcaagca
rno-miR-sc10-5	-40.3	catgtgtgtaTGTGTTTTGTGTGTGTACATGTGgtatgtgaagacacatatacatgcacataagcacacactcaagcacactcacaagta
rno-miR-sc10-6	-47.1	catgtgtgtaTGTGTTTTGTGTGTGTACATGTGgtatgtgaagacacatatacatgcacataagcacacacacgcaagcacactcacatga
rno-miR-sc11	-38.7	atggtgacagtaagctacagttgctctgctcacttgcctctcgcgaGGTGACAGTAAGCTGTAGTTGCTctgtccttt
rno-miR-sc12	-44.9	atcatcatcatcatcatcatcatcatcatcatcatcgaagtATGGTAATGGTGGTGGTGTATGgtggagatga
rno-miR-sc13	-44.3	gacagtttgcAATGTGACTCAGCTATCTGAACagtcaccccaatgtcagacagctgagtcactctgcaaatgtcac
rno-miR-sc14	-22.6	caattctgaaAACAGGTGATCTTCAAGTAGAaaaaacacaaaaaggcagttttctattgaagtcatctcttccctttaa
rno-miR-sc15	-42.9	cctcagctcccTGGGGGACAGCCGGATCTAGTGgtgacgagagagccctagatgtggtcctcgcccatagacaggtgagc
rno-miR-sc16	-56.1	aagtggaaacttaagggttctctgaaagtcggtgtgtgtgatgtgtgtgcTGACTTTCCAGAGAACCCTTGAgtttctacct
rno-miR-sc17	-45.9	tgcgcacagtcacccagcgcgaagggtgctgtgtgtatctcaATGCCACCTTTTCGCGTTGTGGAttttacagca
rno-miR-sc18	-37.9	gcagaccctgccaggcagccctgcctgtcagcactgtgcataatctgTTGACAGGCTGTGAAGTGCAGGCccagctctga
rno-miR-sc19	-39.5	aagactgttttagcttctcgcagtcggcgttagagattgtccgtcTGGTCTAGACTGTGGAGAGCTGTtccgctgtct
rno-miR-sc20	-31.8	ccacagaacACTGGGCTCTGAGATTTCGGCTACagggaaatccccctgcgcccccttctccagccataatctctttaa
rno-miR-sc21	-34.6	tcgctcgacACTAGACGGTCTGTGCTCTCCAtggtgcacgtcaaggcaggcagacccgtctctgtgttctgctc
rno-miR-sc22	-54.3	gctttgtgacccgggctctgtttcccccggcgttggcgaccgCGGGCGGAACGCGGAGACCTGGCgtcgcgggag
rno-miR-sc23	-32.3	ttccagttcaTTGGGAGGAGCAGCTGAGGGATgcttttaactttccctgtggaatctgctctccaggtggagt
rno-miR-sc24	-67.6	agtctggatgccaaaggagtcaccaactttaagcttctgtgagcctctgggcacaaagcttAAAGGTTGAGGACTCCTTGGGCaatctaaata
rno-miR-sc25	-41.3	tggtcgggcaTCTCCAGCTGTGACTGACAAGCctcgaggtgcttggtacagcgggttgtgtttcagctggccttttagctac
rno-miR-sc26	-36.8	aggatcattaACGGAGAAGGCCGAGGGGGGgtcgtcgtcccttccctcttggcctgtgtgagtggtctc
rno-miR-sc27	-32.3	atggtgttgAGGGACGGTGGCTCGGTTGTGAtttgattgtacagtcactcaatcatggtcgggcatttttccactaggtagtt
rno-miR-sc28	-24.4	cctcgtgagtATAAGACCAAGAAGTGTGCAAAAGtggaagacaattttccagtgagcttgcgttaagaatgcatggca
rno-miR-sc29	-38.8	acagacacacTAAGGGAGGGAGAGAATGAGTGTgtatgtctctctctctctctctctctctctctctctgtgtgtgtg
rno-miR-sc30	-47.1	gtccaggacTGACGGACAGGACGGAGGGAGGGCAaagtgagctgcgatctcagactgaccgcccccttctctccgcagcctgccaccggcc
rno-miR-sc31	-37.6	catgagctgtTCCTGGCAGGGGACACGAGGACatttgtaaagctctctgaagctgccagaacagctcaag
rno-miR-sc32	-34.7	aggacctgggTAAGGGTAGCAAGAGTAGGTGGccagggaacccccacttgacttgatccctctcagacctg
rno-miR-sc33	-43.91	tgtggaagagGTGAGGGGACACGTCATGCTGGGgactcagagaggctgcatgtctgtctgtgggtgacctgccccatccatctaggt
rno-miR-sc34	-55.9	cacgtgactCAGACTGAGCACTGGGCAGAAAgaccccttacttctgttctgccagtggtcagctgaagtacacctgtgc
rno-miR-sc35	-31.9	ctgcgctgagTGGGAGAGCAGTGAGGGGCAgggctgggcacaggaagcctcacaccaacctgattatctctcacttcccggtt
rno-miR-3072*	-37.7	tgtgagtgtAGGGACCCGAGGGAGGGCAGGctgccccaggccctgccccctccagggaagccttctgtctccag
rno-miR-sc36	-32.1	ctctagtgtTGGTCTGTGAGCCTTACGGTCTgtgtacacttagtgtgtgtgtgtgagccttatgtctgtgtacactcagtt
rno-miR-sc37	-31.8	cttctctcagGTAGGTTCCGCCAGTAGGAGTtttgaaatttgggaattccctggcctggctctcaccgcaactctgt
rno-miR-3082b	-31.1	cccggtggacagagtgtgtgtgtgtgtggagagacagaggtgcccACATGGCGCTCAACTCTGCAGgataataaca
rno-miR-sc38	-34.6	tcctgccattccaggtccactctgtgagcactgtgacatcaccacTGCTTTCGAGTGTTCCTGTGCctggtctggg

(To be continued on the next page)

(Continued)

IDs	MFE	pre-miRNA sequence
rno-miR-sc39	-37.3	gggctgtgccATGAGACTCAGTGGCACTCTGGAaggtgtccagaggccactgtgctctgataatgccgagctct
rno-miR-sc40	-39.6	ccatctctcACTTGCATGTACACTTTCCTGAaggccctctcaaacccaggaggtgtgcatgcaggaaaggagcgt
rno-miR-sc41	-40.6	cccagccagccctggaatccctgcaggcacaccagagtcggtatgTGGCCTGGTGGGATTGCTGTTGGcatgctgtg
rno-miR-sc42	-39.29	gcgctggaagcaggccctggttgccttctcccaaggagagctgtggAAGGTCGGCCAAGCAGGGCAGAAaacaagcaa
rno-miR-sc43	-26.4	aagcttaaccATGGAGATATTCTGTTGGTTGGGttttgatagcccttttactgaataatccataattaccatt
rno-miR-sc44	-32.3	taggcagctacTGGGGTAGCTTGGGAATTTGACcaggcctagatcaactttccctctgccaccaggataccactacgtctgcctgc
rno-miR-sc45	-29.4	actgagacctgggccccggacttgcctgtagtagtaccgctaTCGGAGACCGAGACCTGGGGCCCgggacttgcct
rno-miR-sc46	-29.4	actgagacctgggccccggacttgcctgtagtagtaccgctaTCGGAGACCGAGACCTGGGGCCCgggacttgcct
rno-miR-sc47	-47.62	gagggattggggctggggcctccctcttctgtctaaagactgttaacaTAAAGGGGGGCCAGGCTCTGAGCctgggtccct
rno-miR-sc48	-33.2	ggtgcaggtacATGTTCCACTCACTCTCAGAcgaaaacagagaggtctgggagaggtgtggaccagctacctccct
rno-miR-sc49	-29.5	ctttgcgttgATTACAGATGGGCAGATTGGGAAGtagtctttgcacatgatgtagtctcccttctgaataatctgaagtaatat
rno-miR-sc50	-29	taaccgtatgAGTGCTAGGAACCAAACTCTGTgcttacagatgatcagagttcaattccagcaccacacggggg
rno-miR-sc51-1	-35.3	acactcagaacctgtgacagtgtgtgaacccagggtgacactcagaacctgtgacagtgtgtTCAACCCAGGGCAGACACTCAGAcctgagact
rno-miR-sc51-2	-31.6	acagtgtgtTCAACCCAGGGCAGACACTCAGAcctgtgacagtgtgtgtcaaccagggtagacactcagaacctgtg
rno-miR-sc52	-29.2	gtccttgggATGACAGAGAATCTCCTGACGctgttttcttctccgctgaggatgctctctctccacacgctgtc
rno-miR-sc53	-29.2	tgtatatgtatgtgcatgtgtgtgtgtgtgtgtgtgtgtgtgtgtGTGTGATGTGTGTATGTATATGTATatgatgtat
rno-miR-sc54	-28.2	taacaacttcTACAACACAGAGACAAGCAGAAcattgtactaaccaggaactgttttctgcatcagtggttgaagtaactc
rno-miR-sc55	-31.7	tttctaccacAGAGATGGTGGGATATGTGGAaagaacacaaaactagaacgtccacatctctgaccacctccgtgtgtgact
rno-miR-sc56	-25.12	ctttggcttcTAAACAGAAACCAACAGATTGGCtttctgtgtttatggaagagctaatcccaatttctcatctgtttatgaatagtatgc
rno-miR-sc57	-45.3	ggggccctgtgtctctactgtgtgtccctcaacaagtcctgtgtgtgtgtgtgtgtgtTAGGGATGAAGTGTGGGACTGCcagagggtc
rno-miR-sc58	-30.4	caggcttaccAGAGGGATTCTGGGTACAGAAGCagtgactgtgacagcttttctctctctctctccctcagctag
rno-miR-sc59	-36.4	gtctgtgtgcAGTTGGTTCAGGATCCGTCTGATGgtaataccaagtcacagaaagatcctgccacctgagcggga
rno-miR-sc60	-33.3	agaggacaactttcaggagaccattctacccttccacttgaggcagtgactcttttctgtcTTATGTGAAGTTGGGATGAGTctctgtctc
rno-miR-sc61	-53.1	atgaggcttgcctccgaaggttcttctctgtattgtgtgtgtgtgtgtgtgtTACACATGGTACAGAAGGAAGAccttctctca
rno-miR-sc62	-32	gagaagatccTGTAGGAAAGGAGTGTGGAGACtttctgagaagtgactccagctcttcttcttcttggcccttttcc
rno-miR-sc63	-31.4	ctgggtaacaTGGTCATGGTTCATGAAGTGGAGCgggtccatcgtgtgtgtgtccagttcaacctgttccctgttccctta
rno-miR-sc64	-30.8	atgccgtccCGGACCATGTGAACCAGAGTGCaggctctcacttccctctgttcttctcgttccaggtacggctg
rno-miR-466e	-34.14	catgtgtgtaTGTGTTTTGTGTATGTACATGgtgtgtatgaagaacatatacatacataagcacacacacaag
rno-miR-sc65	-34.7	gaggggtctcTTGGAGTGGGGACCGTGCAGAGAaatgtgtaacaactgagccctgtatggacacacttcaggaaatcaagaacgccgactcga
rno-miR-sc66	-31.8	acaacaacaactactacaacaacaactactactactactactactagtTGTAGTTGTTATTGTTGTTGCTgttgcgtgtg
rno-miR-sc67	-33.8	gtgctttccaggatagggttctttagctctgtgtgtcagttgtgtcTCAAGAGTTCTGAAGTCACTGGTctctgagcag
rno-miR-sc68	-30.5	tctgattcccTCTGATTATATACATACGTGCatgctgtgtgtgctgcatgcatgtgtgttaacttttgaatctat
rno-miR-sc69	-30.67	gatcagcagCAGGTGTTGGAGATTGTATGGGAtactactactaacttctccacttctcttaccctcaggttgggtgatg
rno-miR-sc70	-63.7	gctctctctctgtcagcccgaagctccctatgaggaagcttggacccaaggcagagaaatctTAGGGAGCTTCGGGCTGACAGCaggagagctcc
rno-miR-sc71	-32	tctagccctgTGGCTCACTGACCTCTACTTTGCAagttagttgcaaaagtacagttagttgagcttctgggacgggt
rno-miR-sc72	-47.8	gccggctgtgtccgcagcaccctcagaccccgaggcctctgatcgcGGGGGTCTAGAGGTGCATGGTccaaccccg
rno-miR-sc73	-40.5	gtgtgtatatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtTACATACCTACATACACAGAcagaagcaca
rno-miR-sc74	-28.19	gttgtgagtcGGTGTGGGTAGCAAAGGTAGATCTaatcatagtaaaactgaccttcttgccttccacagttagccatctct
rno-miR-sc75	-34.2	gcctcccacagcctccagcactggacatgagtcagtcagtcTGCTCTGTCCAGAGTTAGGGAGAccttgggtggg
rno-miR-sc76	-45	ctgctgcccaCCCAACTAGGTGGGAGGTGAGCagagagtgcccacaggtcctgctgcccaccaactaggtgggaggtgagcagcgga
rno-miR-sc77	-29.5	tttgcgttgATTACAGATGGGCAGATTGGGAAGtagtctttgcacatgatgtagtcttcttctgaataatctgtagaagttaatat
rno-miR-sc78	-47.4	agaggagctggattcacaggcagtgagatgccgagagggaatgagcctTCATTCTGCTGCTCTGGAGTcctgtcttc
rno-miR-sc79	-32.8	caggggtttgCTGGGGACAGATGGCTGGCTGAgagtcaactcttgaatctccgggaggtttgtgccatcaattccccc
rno-miR-sc80	-38.9	caagaggccaGAAGAGGGCGTTGGGTTTATGTgagacctatctgctgtcacagaaccacagctccctcaggttcggcctctgtgg
rno-miR-sc81	-36.4	cctgtgagcgAGGTGCTGTGGAGAGGTCTGctgattgttctcggaggagcagaacctcggccagagcacactctgggttg
rno-miR-sc82	-47.2	gaggaggctTGAGGTGACCTGAGAACCTAAGGcggttaggtgtggccagccttaggactctgtcatcttggctcttcaccc
rno-miR-sc83	-48.5	ctgaatgagcAGGGAGAGATAAGGGGACACTGTagtgcgaaactgaggcacagtgctccctcactctctctgctcattcaa
rno-miR-sc84	-48.6	gaccaggactgtctctctctcctcctccctcgccggcgaggacactactacgccCGCGGGTGTGGAGGGAGTGAGCtagaggggt

a) Mature miRNAs are showed using capital letters. MFE means Minimum Free Energy and the same below.

Appendix Table S7 Mature sequences and genome location of the novel miRNAs

IDs	Best homologue	Mature miRNA sequence	Length	Chr	From	Strand
rno-miR-3075	mmu-miR-3075	TGTCTGGGAGCAGCCAAGGACA	22	16	1112128	+
rno-miR-3099b	mmu-miR-3099	TAGGCTAGAAAGAGGTTGGGGA	22	1	65425859	-
rno-miR-3102-5p.2	mmu-miR-3102-5p.2	GGTGGTGCAGGCAGGAGAGCC	21	1	158330166	-
rno-miR-1247*	mmu-miR-1247*	CGGGAACGTCGAGACTGGAGC	21	6	1586560	-
rno-miR-sc1	no	GGAGTTGGAGGTGATCGTGAGC	22	10	57458838	+
rno-miR-sc2	no	TGGGGCACTCAGGAGGCTGCAG	22	11	85512681	-
rno-miR-sc3-1	no	ATGTAAGTGTGTATGTATATG	21	17	79253055	-
rno-miR-sc3-2	no	ATGTAAGTGTGTATGTATATG	21	18	62168312	-
rno-miR-sc4	no	TGTGGGTAGAATGACAGAGCAGA	23	19	14316669	+
rno-miR-sc5	no	CATAAGTGTAGAGAGTCTGTAGT	23	1	131079839	+
rno-miR-sc6	no	TGGGGGACAGGGCAAGGTGG	20	1	63873991	-
rno-miR-sc7	no	CAGGGTTACCTGTTGAGCTGC	21	3	106571996	-
rno-miR-sc8	no	TGAGGATTACGAAGAGGATGGT	22	5	130346817	+
rno-miR-sc9	no	CACAGCGAGCTGGGCACTGGCGT	24	5	156425084	+
rno-miR-sc10-1	no	TGTGTTTTGTGTGTGTACATGTG	23	17	79276506	+
rno-miR-sc10-2	no	TGTGTTTTGTGTGTGTACATGTG	23	17	79264423	-
rno-miR-sc10-3	no	TGTGTTTTGTGTGTGTACATGTG	23	17	79281787	-
rno-miR-sc10-4	no	TGTGTTTTGTGTGTGTACATGTG	23	17	79268513	-
rno-miR-sc10-5	no	TGTGTTTTGTGTGTGTACATGTG	23	17	79275714	-
rno-miR-sc10-6	no	TGTGTTTTGTGTGTGTACATGTG	23	17	79283453	-
rno-miR-sc11	no	GGTGACAGTAAGCTGTAGTTGC	22	7	141082914	+
rno-miR-sc12	no	ATGGTAATGGTGGTGGTGATG	21	8	64686683	+
rno-miR-sc13	no	AATGTGACTCAGCTATCTGAAC	22	8	55466028	-
rno-miR-sc14	no	AACAGGTGATCTTCAAGTAGA	21	x	58440590	+
rno-miR-sc15	no	TGGGGGCAGGCCGATCTAGTG	22	x	52534678	-
rno-miR-sc16	no	TGACTTTCAGAGAACCCTTGA	22	x	56289684	-
rno-miR-sc17	no	ATGCCACCTTTCGCGTTGTGGA	22	12	19854273	+
rno-miR-sc18	no	TTGACAGGCTGTGAACTGCAGGC	23	5	170773055	+
rno-miR-sc19	no	TGGTCTAGACTGTGGAGAGCTGT	23	8	38458926	-
rno-miR-sc20	no	ACTGGGCTCTGAGATTCGGCTAC	22	9	86782104	-
rno-miR-sc21	no	ACTAGACGCTCTGTGCTCTCCA	21	11	85049838	-
rno-miR-sc22	no	CGGGCGGAACGCGGAGACCTGGC	23	16	47746083	-
rno-miR-sc23	no	TTGGGAGGAGCAGCTGAGGGAT	21	2	203996313	-
rno-miR-sc24	no	AAAGGTTGAGGACTCCTTGGGC	22	3	4200066	+
rno-miR-sc25	no	TCTCCCAGCTGTGACTGACAAGC	22	3	141306409	-
rno-miR-sc26	no	ACGGAGAAGGCCGAGGGGGGG	20	Un	23405571	+
rno-miR-sc27	no	AGGGACGGTGGCTCGGTTGTGA	21	10	56485872	-
rno-miR-sc28	no	ATAAGACCAAGAACTGTGCAAAG	22	15	40339290	+
rno-miR-sc29	no	TAAGGGAGGGAGAGAAATGAGTGT	22	1	225038257	+
rno-miR-sc30	no	TGACGGACAGGACGGAGGGAGGGC	23	1	21329832	-
rno-miR-sc31	no	TCCTGGCAGGGGACACGAGGAC	20	1	263581638	-
rno-miR-sc32	no	TAAGGGTAGCAAGAGTAGGTGG	20	7	127462100	-
rno-miR-sc33	no	GTGAGGGGACACGTCATGCTGGGG	22	8	60894087	+
rno-miR-sc34	no	CAGACTGAGCACTGGGCAGAAA	20	8	69404005	+
rno-miR-sc35	no	GTGGGAGAGCAGTGAGGGGCA	19	9	10025878	+
rno-miR-3072*	mmu-miR-3072*	AGGGACCCCCAGGGAGGGCAGG	22	6	134429903	+
rno-miR-sc36	no	TGGTCTGTGAGCCTTACGGTCC	22	6	136567294	+
rno-miR-sc37	no	GTAGGTTCCGGCCAGTAGGAGT	20	10	15660172	+
rno-miR-3082b	mmu-miR-3082-3p	ACACATGGCGCTCAACTCTGCAG	21	10	15096852	-
rno-miR-sc38	no	TGCTTTCGGAGTGTTCCTGTGC	20	11	32819350	+
rno-miR-sc39	no	ATGAGACTCAGTGGCACTCTGG	20	12	3495278	+

(To be continued on the next page)

(Continued)

IDs	Best homologue	Mature miRNA sequence	Length	Chr	From	Strand
rno-miR-sc40	no	ACTTGCATGTACACTTTCCTGA	20	12	9954876	+
rno-miR-sc41	no	TGGCCTGGTGGGATTGCTGTTGG	23	15	36545467	+
rno-miR-sc42	no	AAGGTCGGCCAAGCAGGGCAGA	22	16	18769788	+
rno-miR-sc43	no	ATGGAGATATTCTGTTGGTTGG	22	1	232955460	+
rno-miR-sc44	no	TGGGGTAGCTTGGGAATTTGAC	22	1	209632377	-
rno-miR-sc45	no	TCGGAGACCGAGACCTGGGCC	22	2	250065840	+
rno-miR-sc46	no	TCGGAGACCGAGACCTGGGCC	22	2	4119161	-
rno-miR-sc47	no	TAAAGGGGGCCAGGCTCTGAGC	22	3	77734878	-
rno-miR-sc48	no	CATGTTCCACTCACTCTCAGA	21	3	112617829	-
rno-miR-sc49	no	ATTCAGATGGGCAGATTGGGAA	22	4	66067987	+
rno-miR-sc50	no	AGTGCTAGGAACCAAACCTCTGT	22	5	58830005	-
rno-miR-sc51-1	no	TCAACCCAGGGCAGACACTCAGA	23	7	22452860	-
rno-miR-sc51-2	no	TCAACCCAGGGCAGACACTCAGA	23	7	22452903	-
rno-miR-sc52	no	ATGACAGAGAATCTCCTGACGC	22	9	107106533	-
rno-miR-sc53	no	TGTGATGTGTGTATGTATATGTA	23	4	180422914	-
rno-miR-sc54	no	TACAACACAGAGACAAGCAGAA	22	18	57044317	+
rno-miR-sc55	no	AGAGATGGTGGGATATGTGGA	21	2	158043965	+
rno-miR-sc56	no	TAAACAGAACCAACAGATTGGC	23	3	103222079	+
rno-miR-sc57	no	TAGGGATGAAGTGTGGGACTGC	22	3	170371876	-
rno-miR-sc58	no	AGAGGGATTCTGGGTACAGAAGC	23	5	60017268	-
rno-miR-sc59	no	AGTTGGTTCAGGATCCGTCTGATG	24	1	136294736	-
rno-miR-sc60	no	TTATGTGAAGTGGGATGAGT	21	4	152107700	-
rno-miR-sc61	no	TACACATGGTACAGAAGGAAGA	22	11	45809420	+
rno-miR-sc62	no	TGTAGGAAAGGAGTGTGGAGAC	22	9	32551189	-
rno-miR-sc63	no	TGGTCAATGGTTCATGAACCTGGAGC	24	5	80236398	+
rno-miR-sc64	no	CGGACCATGTGAACCAGAGTGC	22	16	83149225	+
rno-miR-466e	466c	TGTGTTTTGTGTATGTACATG	21	17	79257816	-
rno-miR-sc65	no	TTGGAGTGGGGACCGTGCAGAGA	23	8	113973029	+
rno-miR-sc66	no	TGTAGTTGTTATTGTTGTTGCT	22	2	79766143	-
rno-miR-sc67	no	CAAGAGTTCTGAAGTCACTGGT	22	3	6924198	+
rno-miR-sc68	no	TCTGATTATATACATACGTGC	21	3	52723037	-
rno-miR-sc69	no	CAGGTGTTGGAGAGTTGATGGGA	23	4	125665141	+
rno-miR-sc70	no	TAGGGAGCTTCGGGCTGACAGC	22	5	51584116	-
rno-miR-sc71	no	TGGCTCACTGACCTCTACTTTGC	23	7	118462256	+
rno-miR-sc72	no	GGGGGGTCTAGAGGTGCATGGT	22	7	137640187	+
rno-miR-sc73	no	TACATACCTACATACACACAGA	22	17	79263835	-
rno-miR-sc74	no	GGTGTGGGTAGCAAAGGTAGATCT	24	1	221154333	-
rno-miR-sc75	no	TGCTCTGTCCAGAGTTAGGGAGA	23	18	24709106	+
rno-miR-sc76	no	CCCAACTAGGTGGGAGGTGAGC	22	18	44995707	+
rno-miR-sc77	no	TTCAGATGGGCAGATTGGGAAGT	23	4	66067988	+
rno-miR-sc78	no	TCATTCTCGCTGCTCTGGAGT	21	17	40031892	+
rno-miR-sc79	no	CTGGGGACAGATGGCTGGCTGA	22	2	228812992	-
rno-miR-sc80	no	GAAGAGGGCGTTGGGTTTATGT	22	12	33751957	-
rno-miR-sc81	no	AGGTGCTGTGGAGAGGTCTGC	21	11	69295029	-
rno-miR-sc82	no	TGAGGTGACCTGAGAACCTAAGG	23	17	15980057	-
rno-miR-sc83	no	AGGGAGAGATAAGGGGACACTGT	23	11	17109063	-
rno-miR-sc84	no	CGCGGGTGTGGAGGGAGTGAGC	22	5	142721898	-

Appendix Table S8 Expression pattern clustering of miRNA with significant change using the Short Time-series Expression Miner (STEM)

micRNAs	Profiles	0 h	1 d	4 d	7 d	14 d
rno-miR-sc17	7	10	0	0	0	0
rno-miR-sc18	7	7	0	0	0	0
rno-miR-sc19	7	5	0	0	0	0
rno-miR-sc20	7	5	0	0	0	0
rno-miR-sc7	7	69	42	32	31	17
rno-miR-sc26	4	0	21	0	0	0
rno-miR-sc22	4	0	9	0	0	0
rno-miR-sc24	4	0	9	0	0	0
rno-miR-sc23	4	0	7	0	0	0
rno-miR-sc21	4	0	6	0	0	0
rno-miR-sc25	4	0	6	0	0	0
rno-miR-sc80	4	9	16	7	0	6
rno-miR-3102-5p.2	4	47	72	56	41	42
rno-miR-sc30	0	0	0	14	0	0
rno-miR-sc28	0	0	0	8	0	0
rno-miR-sc32	0	0	0	8	0	0
rno-miR-sc31	0	0	0	7	0	0
rno-miR-sc27	0	0	0	6	0	0
rno-miR-sc29	0	0	0	6	0	0
rno-miR-sc33	0	0	0	6	0	0
rno-miR-sc34	0	0	0	5	0	0
rno-miR-1247*	0	7	68	157	111	79
rno-miR-sc5	3	224	304	428	771	317
rno-miR-sc49	3	0	0	0	13	0
rno-miR-sc3	3	9	12	11	37	5
rno-miR-sc75	3	0	5	0	15	0
rno-miR-sc48	3	0	0	0	10	0
rno-miR-sc43	3	0	0	0	9	0
rno-miR-sc79	3	8	13	0	18	0
rno-miR-sc38	3	0	0	0	7	0
rno-miR-sc53	3	0	0	0	7	0
rno-miR-3072*	3	0	0	0	6	0
rno-miR-sc36	3	0	0	0	6	0
rno-miR-sc37	3	0	0	0	6	0
rno-miR-3082b	3	0	0	0	6	0
rno-miR-sc44	3	0	0	0	6	0
rno-miR-sc47	3	0	0	0	6	0
rno-miR-sc39	3	0	0	0	5	0
rno-miR-sc40	3	0	0	0	4	0
rno-miR-sc41	3	0	0	0	4	0
rno-miR-sc42	3	0	0	0	4	0
rno-miR-sc45	3	0	0	0	4	0
rno-miR-sc46	3	0	0	0	4	0
rno-miR-sc50	3	0	0	0	4	0
rno-miR-sc51	3	0	0	0	4	0
rno-miR-sc52	3	0	0	0	4	0
rno-miR-3075	3	16	19	32	91	25
5rno-miR-sc10	3	17	32	46	76	16

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micRNAs	Profiles	0 h	1 d	4 d	7 d	14 d
rno-miR-sc16	3	5	7	16	39	9
rno-miR-sc66	3	7	0	0	10	0
rno-miR-sc72	3	6	0	0	9	0
rno-miR-sc13	3	302	273	357	467	225
rno-miR-sc15	3	47	42	62	80	49
rno-miR-sc14	6	104	49	107	83	174
rno-miR-sc58	6	0	0	0	0	11
rno-miR-3099b	6	22	60	37	47	65
rno-miR-sc55	6	0	0	0	0	6
rno-miR-sc56	6	0	0	0	0	6
rno-miR-sc57	6	0	0	0	0	6
rno-miR-sc76	6	0	0	0	0	8
rno-miR-sc54	6	0	0	0	0	5

Appendix Table S9 GO Biological Process (FDR<0.01) of target genes in expression profile 7 (high expression of miRNA at 0 h) after sciatic nerve resection

GO-BP-ID	Term	FDR	Biological Process categories
GO:0051179	localization	2.94×10^{-7}	localization
GO:0048522	positive regulation of cellular process	0.001134	cellular process
GO:0007275	multicellular organismal development	0.001134	developmental process
GO:0048869	cellular developmental process	0.002877	developmental process

Appendix Table S10 GO Biological Process (FDR<0.01) of target genes in expression profile 4 (high expression of miRNA at 1 d) after sciatic nerve resection

GO-BP-ID	Term	FDR	Biological Process categories
GO:0007275	multicellular organismal development	1.99×10^{-14}	developmental process
GO:0007155	cell adhesion	9.48×10^{-6}	cellular process
GO:0048522	positive regulation of cellular process	1.62×10^{-5}	cellular process
GO:0051649	establishment of localization in cell	4.28×10^{-5}	localization
GO:0048513	organ development	4.28×10^{-5}	developmental process
GO:0009719	response to endogenous stimulus	0.00013049	response to stimulus
GO:0009891	positive regulation of biosynthetic process	0.000141906	metabolic process
GO:0065008	regulation of biological quality	0.000198547	biological regulation
GO:0031325	positive regulation of cellular metabolic process	0.000217163	metabolic process
GO:0019222	regulation of metabolic process	0.0004319	metabolic process
GO:0007156	homophilic cell adhesion	0.000504964	cellular process
GO:0007399	nervous system development	0.00052965	developmental process
GO:0051254	positive regulation of RNA metabolic process	0.000672376	metabolic process
GO:0008104	protein localization	0.000746548	localization
GO:0045941	positive regulation of transcription	0.001004216	biological regulation
GO:0043062	extracellular structure organization	0.001004216	cellular component organization or biogenesis
GO:0051674	localization of cell	0.001004216	localization
GO:0046903	secretion	0.001405247	cellular process
GO:0009653	anatomical structure morphogenesis	0.001716318	developmental process
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	0.001716318	biological regulation
GO:0007268	synaptic transmission	0.00177658	signaling
GO:0051094	positive regulation of developmental process	0.001836297	developmental process
GO:0043067	regulation of programmed cell death	0.001836297	death
GO:0007242	intracellular signaling cascade	0.001836297	signaling
GO:0007398	ectoderm development	0.002957777	developmental process

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GO-BP-ID	Term	FDR	Biological Process categories
GO:0048523	negative regulation of cellular process	0.002982192	cellular process
GO:0051128	regulation of cellular component organization	0.003914323	cellular component organization or biogenesis
GO:0008219	cell death	0.004064015	death
GO:0048699	generation of neurons	0.004064015	developmental process
GO:0051270	regulation of cell motion	0.004064015	biological regulation
GO:0030335	positive regulation of cell migration	0.004611457	biological regulation
GO:0051047	positive regulation of secretion	0.004611457	biological regulation
GO:0051591	response to cAMP	0.005612569	response to stimulus
GO:0048545	response to steroid hormone stimulus	0.005612569	response to stimulus
GO:0030154	cell differentiation	0.006170003	developmental process
GO:0000904	cell morphogenesis involved in differentiation	0.006241565	cellular component organization or biogenesis
GO:0006950	response to stress	0.006403524	response to stimulus
GO:0009792	embryonic development ending in birth or egg hatching	0.006403524	developmental process
GO:0021700	developmental maturation	0.007114151	developmental process
GO:0032355	response to estradiol stimulus	0.007212287	response to stimulus
GO:0040012	regulation of locomotion	0.007793866	locomotion
GO:0022603	regulation of anatomical structure morphogenesis	0.008034602	developmental process
GO:0031326	regulation of cellular biosynthetic process	0.008341154	biological regulation
GO:0048646	anatomical structure formation	0.008341154	developmental process
GO:0051234	establishment of localization	0.009452016	localization

Appendix Table S11 GO Biological Process (FDR<0.01) of target genes in expression profile 0 (high expression of miRNA at 4 d) after sciatic nerve resection

GO-BP-ID	Term	FDR	Biological Process categories
GO:0019222	regulation of metabolic process	6.93×10^{-11}	metabolic process
GO:0048869	cellular developmental process	1.58×10^{-10}	developmental process
GO:0031325	positive regulation of cellular metabolic process	7.69×10^{-10}	metabolic process
GO:0009891	positive regulation of biosynthetic process	1.29×10^{-9}	metabolic process
GO:0045941	positive regulation of transcription	2.13×10^{-9}	biological regulation
GO:0051254	positive regulation of RNA metabolic process	2.62×10^{-8}	metabolic process
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	3.18×10^{-8}	biological regulation
GO:0010646	regulation of cell communication	3.18×10^{-8}	signaling
GO:0065009	regulation of molecular function	3.52×10^{-7}	biological regulation
GO:0009790	embryonic development	3.52×10^{-7}	developmental process
GO:0007242	intracellular signaling cascade	7.11×10^{-7}	signaling
GO:0051246	regulation of protein metabolic process	7.11×10^{-7}	metabolic process
GO:0051179	localization	1.32×10^{-6}	localization
GO:0031326	regulation of cellular biosynthetic process	1.39×10^{-6}	metabolic process
GO:0010605	negative regulation of macromolecule metabolic process	1.65×10^{-6}	metabolic process
GO:0051239	regulation of multicellular organismal process	1.72×10^{-6}	biological regulation
GO:0048522	positive regulation of cellular process	2.23×10^{-6}	cellular process
GO:0000904	cell morphogenesis involved in differentiation	5.05×10^{-6}	cellular component organization or biogenesis
GO:0048666	neuron development	5.87×10^{-6}	developmental process
GO:0048534	hemopoietic or lymphoid organ development	6.91×10^{-6}	developmental process
GO:0010556	regulation of macromolecule biosynthetic process	8.50×10^{-6}	metabolic process
GO:0051094	positive regulation of developmental process	9.29×10^{-6}	developmental process
GO:0010468	regulation of gene expression	9.29×10^{-6}	biological regulation
GO:0019219	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.53×10^{-5}	metabolic process
GO:0043067	regulation of programmed cell death	2.23×10^{-5}	death

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GO-BP-ID	Term	FDR	Biological Process categories
GO:0016477	cell migration	2.23×10^{-5}	cellular process
GO:0022008	neurogenesis	2.23×10^{-5}	developmental process
GO:0032990	cell part morphogenesis	2.98×10^{-5}	developmental process
GO:0044238	primary metabolic process	4.23×10^{-5}	metabolic process
GO:0040011	locomotion	4.23×10^{-5}	locomotion
GO:0009967	positive regulation of signal transduction	4.42×10^{-5}	signaling
GO:0008219	cell death	5.30×10^{-5}	death
GO:0009653	anatomical structure morphogenesis	7.30×10^{-5}	developmental process
GO:0035150	regulation of tube size	7.49×10^{-5}	biological regulation
GO:0008284	positive regulation of cell proliferation	8.79×10^{-5}	biological regulation
GO:0007507	heart development	9.91×10^{-5}	developmental process
GO:0051338	regulation of transferase activity	0.000101	biological regulation
GO:0006950	response to stress	0.000103	response to stimulus
GO:0003018	vascular process in circulatory system	0.000103	multicellular organismal process
GO:0010604	positive regulation of macromolecule metabolic process	0.000114	metabolic process
GO:0030030	cell projection organization	0.000128	cellular component organization or biogenesis
GO:0043085	positive regulation of catalytic activity	0.000164	biological regulation
GO:0051093	negative regulation of developmental process	0.000204	developmental process
GO:0065008	regulation of biological quality	0.000288	biological regulation
GO:0048704	embryonic skeletal system morphogenesis	0.000307	developmental process
GO:0016044	membrane organization	0.000355	cellular component organization or biogenesis
GO:0007389	pattern specification process	0.000372	developmental process
GO:0033674	positive regulation of kinase activity	0.000479	biological regulation
GO:0045859	regulation of protein kinase activity	0.0005	biological regulation
GO:0046903	secretion	0.0005	cellular process
GO:0007417	central nervous system development	0.0005	developmental process
GO:0016192	vesicle-mediated transport	0.000539	localization
GO:0035295	tube development	0.000553	developmental process
GO:0048731	system development	0.000664	developmental process
GO:0045596	negative regulation of cell differentiation	0.000675	developmental process
GO:0009605	response to external stimulus	0.000793	response to stimulus
GO:0048771	tissue remodeling	0.000799	multicellular organismal process
GO:0007409	axonogenesis	0.000856	cellular component organization or biogenesis
GO:0001666	response to hypoxia	0.000923	response to stimulus
GO:0032269	negative regulation of cellular protein metabolic process	0.001056	metabolic process
GO:0031668	cellular response to extracellular stimulus	0.001082	response to stimulus
GO:0048523	negative regulation of cellular process	0.001115	biological regulation
GO:0043066	negative regulation of apoptosis	0.001115	death
GO:0009890	negative regulation of biosynthetic process	0.001149	metabolic process
GO:0001944	vasculature development	0.001417	developmental process
GO:0042060	wound healing	0.001887	response to stimulus
GO:0043009	chordate embryonic development	0.002495	developmental process
GO:0048513	organ development	0.002495	developmental process
GO:0044248	cellular catabolic process	0.002495	metabolic process
GO:0042592	homeostatic process	0.002578	biological regulation
GO:0032774	RNA biosynthetic process	0.002798	metabolic process
GO:0006928	cell motion	0.002944	cellular process
GO:0042310	vasoconstriction	0.003293	multicellular organismal process
GO:0046907	intracellular transport	0.003432	localization
GO:0030029	actin filament-based process	0.003432	cellular process

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GO-BP-ID	Term	FDR	Biological Process categories
GO:0009952	anterior/posterior pattern formation	0.003537	multicellular organismal process
GO:0009057	macromolecule catabolic process	0.003904	metabolic process
GO:0030900	forebrain development	0.003906	developmental process
GO:0043412	biopolymer modification	0.00452	metabolic process
GO:0043467	regulation of generation of precursor metabolites and energy	0.004634	metabolic process
GO:0051240	positive regulation of multicellular organismal process	0.004972	biological regulation
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	0.005082	signaling
GO:0030163	protein catabolic process	0.005191	metabolic process
GO:0046777	protein amino acid autophosphorylation	0.00548	metabolic process
GO:0051050	positive regulation of transport	0.005563	localization
GO:0008283	cell proliferation	0.005746	cell proliferation
GO:0006461	protein complex assembly	0.00672	cellular component organization or biogenesis
GO:0047496	vesicle transport along microtubule	0.006921	localization
GO:0031324	negative regulation of cellular metabolic process	0.006921	metabolic process
GO:0030522	intracellular receptor-mediated signaling pathway	0.006939	signaling
GO:0007517	muscle development	0.007063	developmental process
GO:0032879	regulation of localization	0.007063	localization
GO:0021700	developmental maturation	0.008516	developmental process
GO:0032270	positive regulation of cellular protein metabolic process	0.009084	metabolic process
GO:0000003	reproduction	0.009236	reproduction
GO:0033036	macromolecule localization	0.009675	localization

Appendix Table S12 GO Biological Process (FDR<0.01) of target genes in expression profile 3 (high expression of miRNA at 7 d) after sciatic nerve resection

GO-BP-ID	Term	FDR	Biological Process categories
GO:0048869	cellular developmental process	1.02×10^{-40}	developmental process
GO:0051179	localization	5.61×10^{-26}	localization
GO:0065008	regulation of biological quality	2.02×10^{-25}	biological regulation
GO:0048523	negative regulation of cellular process	3.59×10^{-22}	cellular process
GO:0043412	biopolymer modification	9.18×10^{-22}	metabolic process
GO:0022008	neurogenesis	1.45×10^{-20}	developmental process
GO:0010605	negative regulation of macromolecule metabolic process	1.45×10^{-20}	metabolic process
GO:0008219	cell death	1.78×10^{-20}	death
GO:0009889	regulation of biosynthetic process	6.46×10^{-20}	metabolic process
GO:0048522	positive regulation of cellular process	5.92×10^{-18}	cellular process
GO:0043067	regulation of programmed cell death	5.92×10^{-18}	death
GO:0009887	organ morphogenesis	1.58×10^{-17}	developmental process
GO:0010628	positive regulation of gene expression	2.85×10^{-17}	biological regulation
GO:0008104	protein localization	3.75×10^{-17}	localization
GO:0031323	regulation of cellular metabolic process	2.26×10^{-16}	metabolic process
GO:0048878	chemical homeostasis	4.05×10^{-16}	biological regulation
GO:0010557	positive regulation of macromolecule biosynthetic process	1.14×10^{-15}	metabolic process
GO:0031328	positive regulation of cellular biosynthetic process	1.19×10^{-15}	metabolic process
GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.82×10^{-15}	metabolic process
GO:0040011	locomotion	1.18×10^{-13}	locomotion
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	2.89×10^{-13}	biological regulation
GO:0048534	hemopoietic or lymphoid organ development	3.85×10^{-13}	developmental process

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GO-BP-ID	Term	FDR	Biological Process categories
GO:0048731	system development	1.47×10^{-12}	developmental process
GO:0051649	establishment of localization in cell	3.27×10^{-12}	localization
GO:0051252	regulation of RNA metabolic process	3.30×10^{-12}	metabolic process
GO:0009790	embryonic development	4.13×10^{-12}	developmental process
GO:0032502	developmental process	6.96×10^{-12}	developmental process
GO:0032774	RNA biosynthetic process	7.42×10^{-12}	metabolic process
GO:0051338	regulation of transferase activity	8.84×10^{-12}	biological regulation
GO:0019725	cellular homeostasis	1.29×10^{-11}	biological regulation
GO:0006796	phosphate metabolic process	3.30×10^{-11}	metabolic process
GO:0032990	cell part morphogenesis	3.30×10^{-11}	developmental process
GO:0051093	negative regulation of developmental process	1.64×10^{-10}	developmental process
GO:0000904	cell morphogenesis involved in differentiation	1.78×10^{-10}	cellular component organization or biogenesis
GO:0034960	cellular biopolymer metabolic process	1.78×10^{-10}	metabolic process
GO:0009653	anatomical structure morphogenesis	2.48×10^{-10}	developmental process
GO:0010646	regulation of cell communication	2.92×10^{-10}	biological regulation
GO:0006873	cellular ion homeostasis	4.42×10^{-10}	cellular process
GO:0045859	regulation of protein kinase activity	5.71×10^{-10}	biological regulation
GO:0030030	cell projection organization	5.75×10^{-10}	cellular component organization or biogenesis
GO:0001501	skeletal system development	7.79×10^{-10}	developmental process
GO:0070271	protein complex biogenesis	8.52×10^{-10}	cellular component organization or biogenesis
GO:0001568	blood vessel development	1.06×10^{-9}	developmental process
GO:0048666	neuron development	1.15×10^{-9}	developmental process
GO:0009967	positive regulation of signal transduction	1.18×10^{-9}	signaling
GO:0033674	positive regulation of kinase activity	5.12×10^{-9}	biological regulation
GO:0007242	intracellular signaling cascade	1.44×10^{-8}	signaling
GO:0040012	regulation of locomotion	3.29×10^{-8}	locomotion
GO:0001666	response to hypoxia	3.70×10^{-8}	response to stimulus
GO:0008285	negative regulation of cell proliferation	4.17×10^{-8}	developmental process
GO:0043065	positive regulation of apoptosis	6.27×10^{-8}	death
GO:0002682	regulation of immune system process	9.59×10^{-8}	immune system process
GO:0031644	regulation of neurological system process	1.05×10^{-7}	biological regulation
GO:0007268	synaptic transmission	1.66×10^{-7}	signaling
GO:0007389	pattern specification process	2.29×10^{-7}	developmental process
GO:0019220	regulation of phosphate metabolic process	2.31×10^{-7}	metabolic process
GO:0000122	negative regulation of transcription from RNA polymerase II promoter	2.31×10^{-7}	biological regulation
GO:0007267	cell-cell signaling	2.36×10^{-7}	signaling
GO:0018193	peptidyl-amino acid modification	2.48×10^{-7}	metabolic process
GO:0065009	regulation of molecular function	3.65×10^{-7}	biological regulation
GO:0007420	brain development	3.66×10^{-7}	developmental process
GO:0008284	positive regulation of cell proliferation	3.74×10^{-7}	biological regulation
GO:0022603	regulation of anatomical structure morphogenesis	3.74×10^{-7}	developmental process
GO:0007626	locomotory behavior	4.45×10^{-7}	response to stimulus
GO:0007507	heart development	4.82×10^{-7}	developmental process
GO:0016044	membrane organization	5.92×10^{-7}	cellular component organization or biogenesis
GO:0043085	positive regulation of catalytic activity	6.17×10^{-7}	metabolic process
GO:0051094	positive regulation of developmental process	8.34×10^{-7}	developmental process
GO:0032270	positive regulation of cellular protein metabolic process	8.42×10^{-7}	metabolic process
GO:0051049	regulation of transport	9.09×10^{-7}	localization
GO:0006605	protein targeting	9.28×10^{-7}	localization
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	1.19×10^{-6}	signaling

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GO-BP-ID	Term	FDR	Biological Process categories
GO:0006916	anti-apoptosis	1.21×10^{-6}	death
GO:0006812	cation transport	1.46×10^{-6}	localization
GO:0065003	macromolecular complex assembly	1.48×10^{-6}	cellular component organization or biogenesis
GO:0033002	muscle cell proliferation	1.53×10^{-6}	cellular proliferation
GO:0048661	positive regulation of smooth muscle cell proliferation	1.77×10^{-6}	cellular process
GO:0007156	homophilic cell adhesion	2.45×10^{-6}	cellular process
GO:0016477	cell migration	3.48×10^{-6}	localization
GO:0016337	cell-cell adhesion	3.64×10^{-6}	cellular process
GO:0035295	tube development	3.75×10^{-6}	developmental process
GO:0016192	vesicle-mediated transport	5.11×10^{-6}	cellular process
GO:0000003	reproduction	5.72×10^{-6}	reproduction
GO:0002696	positive regulation of leukocyte activation	6.67×10^{-6}	immune system process
GO:0009628	response to abiotic stimulus	6.78×10^{-6}	response to stimulus
GO:0048468	cell development	7.24×10^{-6}	developmental process
GO:0007517	muscle development	7.61×10^{-6}	developmental process
GO:0009612	response to mechanical stimulus	9.09×10^{-6}	response to stimulus
GO:0032269	negative regulation of cellular protein metabolic process	9.96×10^{-6}	metabolic process
GO:0030003	cellular cation homeostasis	1.11×10^{-5}	cellular process
GO:0014070	response to organic cyclic substance	1.46×10^{-5}	response to stimulus
GO:0010562	positive regulation of phosphorus metabolic process	1.48×10^{-5}	metabolic process
GO:0007167	enzyme linked receptor protein signaling pathway	1.55×10^{-5}	signaling
GO:0032940	secretion by cell	1.64×10^{-5}	cellular process
GO:0008283	cell proliferation	1.75×10^{-5}	biological regulation
GO:0051098	regulation of binding	1.89×10^{-5}	biological regulation
GO:0006874	cellular calcium ion homeostasis	2.10×10^{-5}	cellular process
GO:0055065	metal ion homeostasis	2.13×10^{-5}	biological regulation
GO:0043687	post-translational protein modification	2.43×10^{-5}	metabolic process
GO:0055066	di-, tri-valent inorganic cation homeostasis	2.43×10^{-5}	cellular process
GO:0050808	synapse organization	2.46×10^{-5}	cellular component organization or biogenesis
GO:0051241	negative regulation of multicellular organismal process	2.54×10^{-5}	biological regulation
GO:0045137	development of primary sexual characteristics	2.62×10^{-5}	developmental process
GO:0001508	regulation of action potential	2.85×10^{-5}	biological regulation
GO:0030335	positive regulation of cell migration	3.20×10^{-5}	cellular process
GO:0045449	regulation of transcription	3.25×10^{-5}	biological regulation
GO:0001816	cytokine production	3.34×10^{-5}	multicellular organismal process
GO:0046660	female sex differentiation	3.77×10^{-5}	developmental process
GO:0007411	axon guidance	3.98×10^{-5}	developmental process
GO:0002521	leukocyte differentiation	4.55×10^{-5}	developmental process
GO:0051239	regulation of multicellular organismal process	4.78×10^{-5}	multicellular organismal process
GO:0007155	cell adhesion	5.22×10^{-5}	cellular process
GO:0030036	actin cytoskeleton organization	6.36×10^{-5}	cellular component organization or biogenesis
GO:0019915	lipid storage	6.42×10^{-5}	localization
GO:0051129	negative regulation of cellular component organization	6.82×10^{-5}	cellular component organization or biogenesis
GO:0042493	response to drug	7.30×10^{-5}	response to stimulus
GO:0016043	cellular component organization	9.19×10^{-5}	cellular component organization or biogenesis
GO:0006897	endocytosis	0.0001073	cellular process
GO:0030278	regulation of ossification	0.0001242	biological regulation
GO:0030098	lymphocyte differentiation	0.000127	immune system process
GO:0034103	regulation of tissue remodeling	0.0001301	biological regulation
GO:0001934	positive regulation of protein amino acid phosphorylation	0.0001347	metabolic process

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GO-BP-ID	Term	FDR	Biological Process categories
GO:0009952	anterior/posterior pattern formation	0.0001499	developmental process
GO:0048167	regulation of synaptic plasticity	0.0001607	biological regulation
GO:0051960	regulation of nervous system development	0.0001626	developmental process
GO:0032147	activation of protein kinase activity	0.0001757	metabolic process
GO:0008542	visual learning	0.0001842	response to stimulus
GO:0050865	regulation of cell activation	0.0001918	cellular process
GO:0051169	nuclear transport	0.0001926	localization
GO:0051291	protein heterooligomerization	0.0002017	cellular component organization or biogenesis
GO:0070201	regulation of establishment of protein localization	0.0002017	localization
GO:0001822	kidney development	0.0002164	developmental process
GO:0016197	endosome transport	0.0002789	localization
GO:0006886	intracellular protein transport	0.0002984	localization
GO:0006082	organic acid metabolic process	0.0003065	metabolic process
GO:0040018	positive regulation of multicellular organism growth	0.0003175	multicellular organismal process
GO:0050852	T cell receptor signaling pathway	0.0003175	signaling
GO:0007417	central nervous system development	0.0004722	developmental process
GO:0002053	positive regulation of mesenchymal cell proliferation	0.0005175	cellular process
GO:0032101	regulation of response to external stimulus	0.00052	response to stimulus
GO:0017038	protein import	0.00052	localization
GO:0051899	membrane depolarization	0.00052	cellular process
GO:0051240	positive regulation of multicellular organismal process	0.0005208	multicellular organismal process
GO:0040007	growth	0.0006006	growth
GO:0051048	negative regulation of secretion	0.0006063	localization
GO:0010604	positive regulation of macromolecule metabolic process	0.0006063	metabolic process
GO:0045892	negative regulation of transcription, DNA-dependent	0.0006063	biological regulation
GO:0018108	peptidyl-tyrosine phosphorylation	0.0006162	metabolic process
GO:0021954	central nervous system neuron development	0.0006188	developmental process
GO:0001701	in utero embryonic development	0.0007081	developmental process
GO:0007162	negative regulation of cell adhesion	0.0007902	cellular process
GO:0048754	branching morphogenesis of a tube	0.0007902	multicellular organismal process
GO:0007409	axonogenesis	0.0008536	cellular component organization or biogenesis
GO:0033554	cellular response to stress	0.0008536	response to stimulus
GO:0016071	mRNA metabolic process	0.0008536	metabolic process
GO:0048193	Golgi vesicle transport	0.0008536	localization
GO:0003001	generation of a signal involved in cell-cell signaling	0.0009119	signaling
GO:0034284	response to monosaccharide stimulus	0.0009119	response to stimulus
GO:0043550	regulation of lipid kinase activity	0.0010612	metabolic process
GO:0045597	positive regulation of cell differentiation	0.0011952	biological regulation
GO:0009611	response to wounding	0.0011952	response to stimulus
GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	0.0012215	metabolic process
GO:0001558	regulation of cell growth	0.001292	cellular process
GO:0050885	neuromuscular process controlling balance	0.001393	multicellular organismal process
GO:0008361	regulation of cell size	0.0014001	biological regulation
GO:0006468	protein amino acid phosphorylation	0.0014215	metabolic process
GO:0015031	protein transport	0.0014347	localization
GO:0043524	negative regulation of neuron apoptosis	0.0014393	death
GO:0045321	leukocyte activation	0.0014393	immune system process
GO:0016481	negative regulation of transcription	0.0014459	biological regulation
GO:0016050	vesicle organization	0.0015353	cellular component organization or biogenesis
GO:0022403	cell cycle phase	0.0015978	cellular process

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GO-BP-ID	Term	FDR	Biological Process categories
GO:0006979	response to oxidative stress	0.0016469	response to stimulus
GO:0051128	regulation of cellular component organization	0.0016488	cellular component organization or biogenesis
GO:0033077	T cell differentiation in the thymus	0.0016488	immune system process
GO:0048593	camera-type eye morphogenesis	0.0016488	developmental process
GO:0042445	hormone metabolic process	0.0016508	metabolic process
GO:0006470	protein amino acid dephosphorylation	0.0016789	metabolic process
GO:0048608	reproductive structure development	0.0016789	developmental process
GO:0046777	protein amino acid autophosphorylation	0.0017556	metabolic process
GO:0006810	transport	0.0019143	localization
GO:0031344	regulation of cell projection organization	0.0020479	cellular process
GO:0045740	positive regulation of DNA replication	0.0021014	biological regulation
GO:0060021	palate development	0.0021014	developmental process
GO:0009416	response to light stimulus	0.0021154	response to stimulus
GO:0032446	protein modification by small protein conjugation	0.0021232	metabolic process
GO:0050708	regulation of protein secretion	0.0022374	biological regulation
GO:0006813	potassium ion transport	0.0022449	localization
GO:0045664	regulation of neuron differentiation	0.0022899	developmental process
GO:0045893	positive regulation of transcription, DNA-dependent	0.0022899	biological regulation
GO:0019233	sensory perception of pain	0.0023206	multicellular organismal process
GO:0051130	positive regulation of cellular component organization	0.0023388	cellular component organization or biogenesis
GO:0048609	reproductive process in a multicellular organism	0.0023388	multicellular organismal process
GO:0044249	cellular biosynthetic process	0.0023388	metabolic process
GO:0001525	angiogenesis	0.0024417	developmental process
GO:0042551	neuron maturation	0.0024694	developmental process
GO:0009914	hormone transport	0.0025044	biological regulation
GO:0006090	pyruvate metabolic process	0.002597	metabolic process
GO:0051050	positive regulation of transport	0.002597	localization
GO:0007272	ensheathment of neurons	0.0026972	developmental process
GO:0032946	positive regulation of mononuclear cell proliferation	0.0026972	cellular process
GO:0042060	wound healing	0.0027006	response to stimulus
GO:0034645	cellular macromolecule biosynthetic process	0.0027737	metabolic process
GO:0019221	cytokine-mediated signaling pathway	0.0028529	signaling
GO:0006575	amino acid derivative metabolic process	0.0028698	metabolic process
GO:0015837	amine transport	0.0028698	localization
GO:0032787	monocarboxylic acid metabolic process	0.00288	metabolic process
GO:0009749	response to glucose stimulus	0.0028814	response to stimulus
GO:0006111	regulation of gluconeogenesis	0.0028975	metabolic process
GO:0006509	membrane protein ectodomain proteolysis	0.0030732	metabolic process
GO:0031110	regulation of microtubule polymerization or depolymerization	0.0030732	cellular component organization or biogenesis
GO:0045576	mast cell activation	0.0030732	immune system process
GO:0048584	positive regulation of response to stimulus	0.0031198	response to stimulus
GO:0008015	blood circulation	0.0031762	developmental process
GO:0010627	regulation of protein kinase cascade	0.0031762	signaling
GO:0015833	peptide transport	0.0031762	localization
GO:0051170	nuclear import	0.0031762	localization
GO:0045927	positive regulation of growth	0.0031762	biological regulation
GO:0045787	positive regulation of cell cycle	0.0031762	cellular process
GO:0046852	positive regulation of bone remodeling	0.0032516	biological regulation
GO:0006906	vesicle fusion	0.0032661	cellular process
GO:0051270	regulation of cell motion	0.0033365	biological regulation
GO:0046661	male sex differentiation	0.0033365	developmental process

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GO-BP-ID	Term	FDR	Biological Process categories
GO:0010033	response to organic substance	0.003422	response to stimulus
GO:0007264	small GTPase mediated signal transduction	0.0034959	signaling
GO:0060255	regulation of macromolecule metabolic process	0.0038513	metabolic process
GO:0030336	negative regulation of cell migration	0.0038792	biological regulation
GO:0051384	response to glucocorticoid stimulus	0.0038792	response to stimulus
GO:0006935	chemotaxis	0.0039896	response to stimulus
GO:0008202	steroid metabolic process	0.0039896	metabolic process
GO:0007049	cell cycle	0.0040156	cellular process
GO:0043542	endothelial cell migration	0.0040573	localization
GO:0016358	dendrite development	0.0040573	developmental process
GO:0006936	muscle contraction	0.0041309	multicellular organismal process
GO:0030879	mammary gland development	0.0044114	developmental process
GO:0009888	tissue development	0.0044488	developmental process
GO:0006915	apoptosis	0.0044488	death
GO:0000096	sulfur amino acid metabolic process	0.0044488	metabolic process
GO:0030199	collagen fibril organization	0.0044488	cellular component organization or biogenesis
GO:0030509	BMP signaling pathway	0.0045726	signaling
GO:0007243	protein kinase cascade	0.0046048	signaling
GO:0021700	developmental maturation	0.0047604	developmental process
GO:0030072	peptide hormone secretion	0.0048533	signaling
GO:0003018	vascular process in circulatory system	0.004899	multicellular organismal process
GO:0030324	lung development	0.004917	developmental process
GO:0042110	T cell activation	0.004917	immune system process
GO:0048169	regulation of long-term neuronal synaptic plasticity	0.0050593	biological regulation
GO:0048646	anatomical structure formation	0.0050643	developmental process
GO:0030501	positive regulation of bone mineralization	0.0053295	biological regulation
GO:0048041	focal adhesion formation	0.0053295	cellular process
GO:0009880	embryonic pattern specification	0.0053687	developmental process
GO:0044237	cellular metabolic process	0.005444	metabolic process
GO:0000165	MAPKKK cascade	0.005444	signaling
GO:0009100	glycoprotein metabolic process	0.0057477	metabolic process
GO:0050678	regulation of epithelial cell proliferation	0.0057543	cellular process
GO:0042552	myelination	0.0057916	developmental process
GO:0045596	negative regulation of cell differentiation	0.0057916	developmental process
GO:0007398	ectoderm development	0.0058802	developmental process
GO:0051090	regulation of transcription factor activity	0.0059688	biological regulation
GO:0051261	protein depolymerization	0.0060909	cellular component organization or biogenesis
GO:0035150	regulation of tube size	0.0060909	biological regulation
GO:0021537	telencephalon development	0.0060978	developmental process
GO:0019538	protein metabolic process	0.0061486	metabolic process
GO:0042102	positive regulation of T cell proliferation	0.0061499	immune system process
GO:0042058	regulation of epidermal growth factor receptor signaling pathway	0.0061765	signaling
GO:0030182	neuron differentiation	0.0062773	developmental process
GO:0007265	Ras protein signal transduction	0.0063596	signaling
GO:0007612	learning	0.0067524	response to stimulus
GO:0032355	response to estradiol stimulus	0.0067618	response to stimulus
GO:0044057	regulation of system process	0.0068041	biological regulation
GO:0001657	ureteric bud development	0.007	developmental process
GO:0046632	alpha-beta T cell differentiation	0.007	developmental process
GO:0051259	protein oligomerization	0.007063	cellular component organization or biogenesis
GO:0044248	cellular catabolic process	0.007063	metabolic process

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GO-BP-ID	Term	FDR	Biological Process categories
GO:0048741	skeletal muscle fiber development	0.0071582	developmental process
GO:0043244	regulation of protein complex disassembly	0.0077517	biological regulation
GO:0048008	platelet-derived growth factor receptor signaling pathway	0.0077517	signaling
GO:0045639	positive regulation of myeloid cell differentiation	0.0078177	developmental process
GO:0010469	regulation of receptor activity	0.0079797	signaling
GO:0006725	cellular aromatic compound metabolic process	0.0079797	metabolic process
GO:0000902	cell morphogenesis	0.0083955	cellular component organization or biogenesis
GO:0055086	nucleobase, nucleoside and nucleotide metabolic process	0.0083955	metabolic process
GO:0008344	adult locomotory behavior	0.0088622	response to stimulus
GO:0030518	steroid hormone receptor signaling pathway	0.0089886	signaling
GO:0016331	morphogenesis of embryonic epithelium	0.0092356	developmental process
GO:0030099	myeloid cell differentiation	0.0092356	developmental process
GO:0051216	cartilage development	0.0092356	developmental process
GO:0030258	lipid modification	0.0096857	metabolic process
GO:0007346	regulation of mitotic cell cycle	0.0097028	cellular process
GO:0045471	response to ethanol	0.0097028	response to stimulus
GO:0051495	positive regulation of cytoskeleton organization	0.0099263	cellular process
GO:0070167	regulation of biomineral formation	0.0099263	biological regulation

Appendix Table S13 GO Biological Process (FDR<0.01) of target genes in expression profiles 6 (high expression of miRNA at 14 d) after sciatic nerve resection

GO-BP-ID	Term	FDR	Biological Process categories
GO:0007275	multicellular organismal development	3.04×10^{-23}	developmental process
GO:0045941	positive regulation of transcription	5.49×10^{-18}	biological regulation
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	6.91×10^{-18}	biological regulation
GO:0051254	positive regulation of RNA metabolic process	1.81×10^{-17}	metabolic process
GO:0031325	positive regulation of cellular metabolic process	1.81×10^{-17}	metabolic process
GO:0009891	positive regulation of biosynthetic process	1.81×10^{-17}	metabolic process
GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.20×10^{-15}	metabolic process
GO:0006355	regulation of transcription, DNA-dependent	1.75×10^{-13}	biological regulation
GO:0032774	RNA biosynthetic process	1.75×10^{-13}	metabolic process
GO:0048699	generation of neurons	1.89×10^{-9}	developmental process
GO:0040011	locomotion	1.21×10^{-8}	locomotion
GO:0009890	negative regulation of biosynthetic process	2.22×10^{-8}	metabolic process
GO:0009792	embryonic development ending in birth or egg hatching	5.28×10^{-8}	developmental process
GO:0009887	organ morphogenesis	6.02×10^{-8}	developmental process
GO:0034960	cellular biopolymer metabolic process	6.07×10^{-8}	metabolic process
GO:0016481	negative regulation of transcription	9.02×10^{-8}	biological regulation
GO:0051094	positive regulation of developmental process	4.32×10^{-7}	developmental process
GO:0009059	macromolecule biosynthetic process	4.32×10^{-7}	metabolic process
GO:0002520	immune system development	7.35×10^{-7}	immune system process
GO:0048667	cell morphogenesis involved in neuron differentiation	7.38×10^{-7}	developmental process
GO:0031324	negative regulation of cellular metabolic process	9.17×10^{-7}	metabolic process
GO:0006464	protein modification process	9.65×10^{-7}	metabolic process
GO:0007399	nervous system development	1.19×10^{-6}	developmental process
GO:0048468	cell development	1.23×10^{-6}	developmental process
GO:0010467	gene expression	1.52×10^{-6}	metabolic process
GO:0043067	regulation of programmed cell death	1.74×10^{-6}	death

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GO-BP-ID	Term	FDR	Biological Process categories
GO:0051674	localization of cell	1.83×10^{-6}	localization
GO:0048858	cell projection morphogenesis	1.88×10^{-6}	developmental process
GO:0051234	establishment of localization	4.86×10^{-6}	localization
GO:0006796	phosphate metabolic process	5.43×10^{-6}	metabolic process
GO:0051239	regulation of multicellular organismal process	5.44×10^{-6}	multicellular organismal process
GO:0034961	cellular biopolymer biosynthetic process	6.38×10^{-6}	metabolic process
GO:0022603	regulation of anatomical structure morphogenesis	9.18×10^{-6}	developmental process
GO:0000902	cell morphogenesis	1.10×10^{-5}	cellular component organization or biogenesis
GO:0001568	blood vessel development	1.22×10^{-5}	developmental process
GO:0010605	negative regulation of macromolecule metabolic process	2.08×10^{-5}	metabolic process
GO:0048878	chemical homeostasis	2.46×10^{-5}	biological regulation
GO:0008219	cell death	3.99×10^{-5}	death
GO:0007049	cell cycle	4.27×10^{-5}	cellular process
GO:0051246	regulation of protein metabolic process	4.30×10^{-5}	metabolic process
GO:0051253	negative regulation of RNA metabolic process	4.39×10^{-5}	metabolic process
GO:0048523	negative regulation of cellular process	5.57×10^{-5}	cellular process
GO:0048522	positive regulation of cellular process	5.57×10^{-5}	cellular process
GO:0031175	neurite development	8.51×10^{-5}	developmental process
GO:0060348	bone development	0.00010246	developmental process
GO:0048513	organ development	0.00014382	developmental process
GO:0001701	in utero embryonic development	0.00014382	developmental process
GO:0070271	protein complex biogenesis	0.00015566	cellular component organization or biogenesis
GO:0015031	protein transport	0.00018538	localization
GO:0051093	negative regulation of developmental process	0.00020109	developmental process
GO:0048856	anatomical structure development	0.00020109	developmental process
GO:0030154	cell differentiation	0.00020109	developmental process
GO:0065009	regulation of molecular function	0.00024247	biological regulation
GO:0007243	protein kinase cascade	0.0002562	signaling
GO:0051130	positive regulation of cellular component organization	0.0002562	cellular component organization or biogenesis
GO:0007389	pattern specification process	0.0002562	developmental process
GO:0006873	cellular ion homeostasis	0.00031898	cellular process
GO:0051347	positive regulation of transferase activity	0.00032172	biological regulation
GO:0009653	anatomical structure morphogenesis	0.00032172	developmental process
GO:0021700	developmental maturation	0.00042316	developmental process
GO:0009952	anterior/posterior pattern formation	0.00043603	developmental process
GO:0045648	positive regulation of erythrocyte differentiation	0.00049545	immune system process
GO:0046777	protein amino acid autophosphorylation	0.00055993	metabolic process
GO:0034101	erythrocyte homeostasis	0.00060436	biological regulation
GO:0046545	development of primary female sexual characteristics	0.00060655	developmental process
GO:0022414	reproductive process	0.00060655	reproduction
GO:0051056	regulation of small GTPase mediated signal transduction	0.00086415	signaling
GO:0019725	cellular homeostasis	0.00086415	biological regulation
GO:0065003	macromolecular complex assembly	0.00087586	cellular component organization or biogenesis
GO:0008406	gonad development	0.00102982	developmental process
GO:0051128	regulation of cellular component organization	0.0012023	cellular component organization or biogenesis
GO:0051716	cellular response to stimulus	0.0012023	response to stimulus
GO:0007242	intracellular signaling cascade	0.0012023	signaling
GO:0043065	positive regulation of apoptosis	0.0012023	death
GO:0051960	regulation of nervous system development	0.00121532	developmental process

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GO-BP-ID	Term	FDR	Biological Process categories
GO:0048598	embryonic morphogenesis	0.00121532	developmental process
GO:0045860	positive regulation of protein kinase activity	0.00136536	biological regulation
GO:0002682	regulation of immune system process	0.00136536	immune system process
GO:0009968	negative regulation of signal transduction	0.00139111	signaling
GO:0043170	macromolecule metabolic process	0.00145313	metabolic process
GO:0007548	sex differentiation	0.00158449	developmental process
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	0.00169263	signaling
GO:0048869	cellular developmental process	0.00169263	developmental process
GO:0006996	organelle organization	0.00177575	cellular component organization or biogenesis
GO:0043549	regulation of kinase activity	0.00200121	biological regulation
GO:0016477	cell migration	0.00208441	localization
GO:0009628	response to abiotic stimulus	0.00211072	response to stimulus
GO:0000122	negative regulation of transcription from RNA polymerase II promoter	0.00211072	biological regulation
GO:0007507	heart development	0.00211072	developmental process
GO:0009057	macromolecule catabolic process	0.00220163	metabolic process
GO:0044248	cellular catabolic process	0.00226036	metabolic process
GO:0043583	ear development	0.00252467	developmental process
GO:0008104	protein localization	0.0025652	localization
GO:0016043	cellular component organization	0.00264561	cellular component organization or biogenesis
GO:0019395	fatty acid oxidation	0.00265184	metabolic process
GO:0048762	mesenchymal cell differentiation	0.00265184	cellular process
GO:0016202	regulation of striated muscle development	0.00265184	developmental process
GO:0001816	cytokine production	0.00265184	multicellular organismal process
GO:0009967	positive regulation of signal transduction	0.00267009	signaling
GO:0008284	positive regulation of cell proliferation	0.00293015	biological regulation
GO:0007610	behavior	0.00318542	response to stimulus
GO:0031323	regulation of cellular metabolic process	0.00371715	metabolic process
GO:0042698	ovulation cycle	0.00384016	multicellular organismal process
GO:0032504	multicellular organism reproduction	0.00392997	cellular component organization or biogenesis
GO:0016192	vesicle-mediated transport	0.00412413	localization
GO:0060255	regulation of macromolecule metabolic process	0.0041409	metabolic process
GO:0030509	BMP signaling pathway	0.00415437	signaling
GO:0001525	angiogenesis	0.00490259	developmental process
GO:0021953	central nervous system neuron differentiation	0.00500279	developmental process
GO:0044238	primary metabolic process	0.00500279	metabolic process
GO:0030900	forebrain development	0.00500562	developmental process
GO:0045840	positive regulation of mitosis	0.00505125	cellular process
GO:0007611	learning or memory	0.00524509	response to stimulus
GO:0051641	cellular localization	0.00570766	localization
GO:0009889	regulation of biosynthetic process	0.00570766	metabolic process
GO:0007346	regulation of mitotic cell cycle	0.00571471	cellular process
GO:0042127	regulation of cell proliferation	0.00580779	biological regulation
GO:0010564	regulation of cell cycle process	0.00580779	cellular process
GO:0007417	central nervous system development	0.00580779	developmental process
GO:0001541	ovarian follicle development	0.0059557	developmental process
GO:0030278	regulation of ossification	0.00644127	biological regulation
GO:0016071	mRNA metabolic process	0.00644127	metabolic process
GO:0045165	cell fate commitment	0.00652412	developmental process
GO:0032350	regulation of hormone metabolic process	0.00694006	metabolic process
GO:0010604	positive regulation of macromolecule metabolic process	0.00727124	metabolic process

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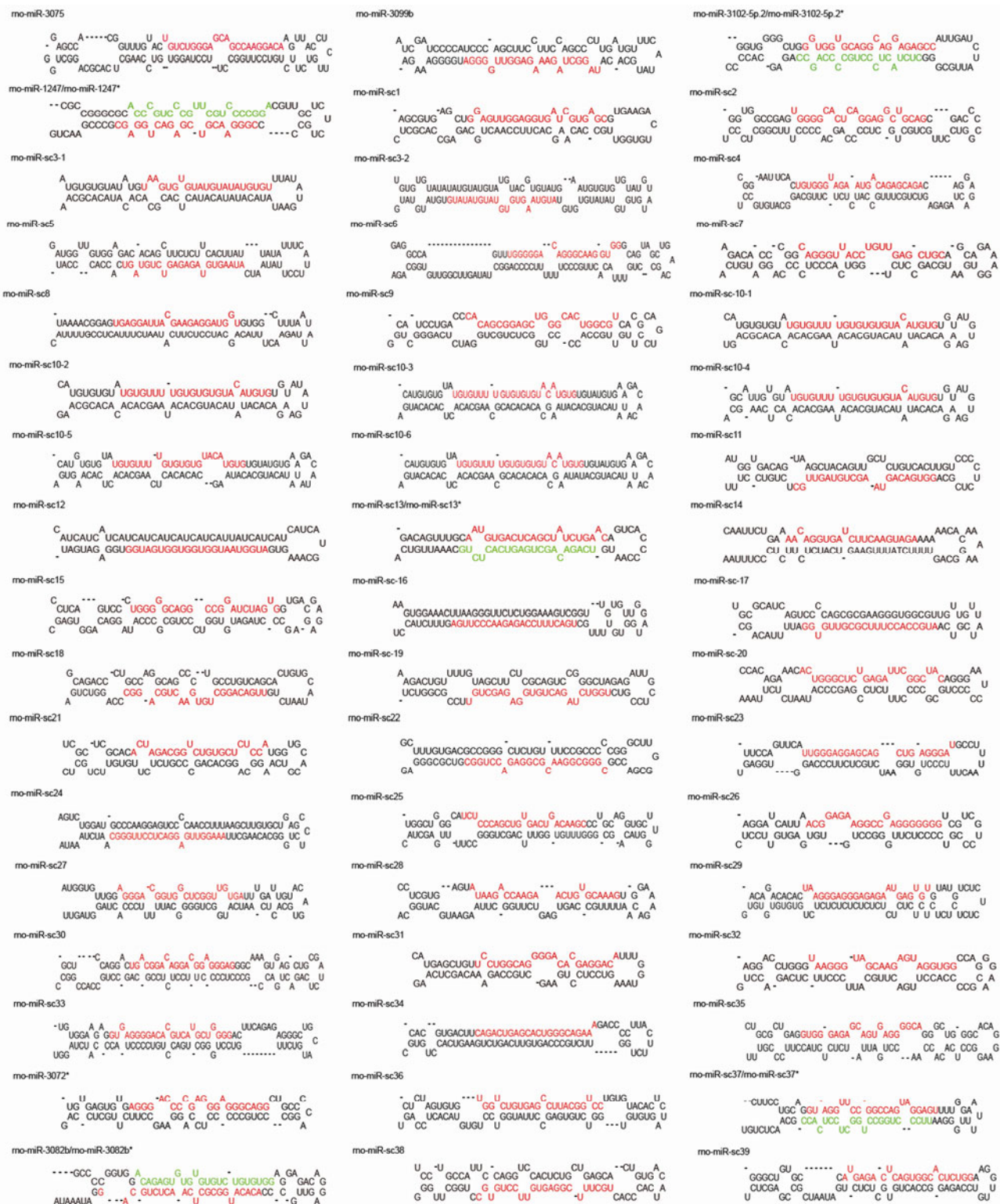
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GO-BP-ID	Term	FDR	Biological Process categories
GO:0007268	synaptic transmission	0.00744549	signaling
GO:0048806	genitalia development	0.00744549	developmental process
GO:0009880	embryonic pattern specification	0.00828867	developmental process
GO:0045321	leukocyte activation	0.00829778	immune system process
GO:0003013	circulatory system process	0.00829778	multicellular organismal process
GO:0045669	positive regulation of osteoblast differentiation	0.00834457	developmental process
GO:0006468	protein amino acid phosphorylation	0.00839634	metabolic process
GO:0048771	tissue remodeling	0.00858096	multicellular organismal process
GO:0016358	dendrite development	0.00858096	developmental process
GO:0046852	positive regulation of bone remodeling	0.00858857	biological regulation
GO:0045664	regulation of neuron differentiation	0.00872952	developmental process
GO:0030326	embryonic limb morphogenesis	0.00872952	developmental process
GO:0051240	positive regulation of multicellular organismal process	0.00878448	multicellular organismal process
GO:0043062	extracellular structure organization	0.00879179	cellular component organization or biogenesis
GO:0048705	skeletal system morphogenesis	0.00901526	developmental process
GO:0008104	multicellular organismal development	3.04×10^{-23}	developmental process
GO:0016043	positive regulation of transcription	5.49×10^{-18}	biological regulation
GO:0019395	positive regulation of transcription from RNA polymerase II promoter	6.91×10^{-18}	biological regulation
GO:0048762	positive regulation of RNA metabolic process	1.81×10^{-17}	metabolic process
GO:0016202	positive regulation of cellular metabolic process	1.81×10^{-17}	metabolic process
GO:0001816	positive regulation of biosynthetic process	1.81×10^{-17}	metabolic process
GO:0009967	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.20×10^{-15}	metabolic process
GO:0008284	regulation of transcription, DNA-dependent	1.75×10^{-13}	biological regulation
GO:0007610	RNA biosynthetic process	1.75×10^{-13}	metabolic process
GO:0031323	generation of neurons	1.89×10^{-9}	developmental process
GO:0042698	locomotion	1.21×10^{-8}	locomotion
GO:0032504	negative regulation of biosynthetic process	2.22×10^{-8}	metabolic process
GO:0016192	embryonic development ending in birth or egg hatching	5.28×10^{-8}	developmental process
GO:0060255	organ morphogenesis	6.02×10^{-8}	developmental process
GO:0030509	cellular biopolymer metabolic process	6.07×10^{-8}	metabolic process
GO:0001525	negative regulation of transcription	9.02×10^{-8}	biological regulation
GO:0021953	positive regulation of developmental process	4.32×10^{-7}	developmental process
GO:0044238	macromolecule biosynthetic process	4.32×10^{-7}	metabolic process
GO:0030900	immune system development	7.35×10^{-7}	immune system process
GO:0045840	cell morphogenesis involved in neuron differentiation	7.38×10^{-7}	developmental process
GO:0007611	negative regulation of cellular metabolic process	9.17×10^{-7}	metabolic process
GO:0051641	protein modification process	9.65×10^{-7}	metabolic process
GO:0009889	nervous system development	1.19×10^{-6}	developmental process
GO:0007346	cell development	1.23×10^{-6}	developmental process
GO:0042127	gene expression	1.52×10^{-6}	metabolic process
GO:0010564	regulation of programmed cell death	1.74×10^{-6}	death
GO:0007417	localization of cell	1.83×10^{-6}	localization
GO:0001541	cell projection morphogenesis	1.88×10^{-6}	developmental process
GO:0030278	establishment of localization	4.86×10^{-6}	localization
GO:0016071	phosphate metabolic process	5.43×10^{-6}	metabolic process
GO:0045165	regulation of multicellular organismal process	5.44×10^{-6}	multicellular organismal process
GO:0032350	cellular biopolymer biosynthetic process	6.38×10^{-6}	metabolic process
GO:0010604	regulation of anatomical structure morphogenesis	9.18×10^{-6}	developmental process
GO:0007268	cell morphogenesis	1.10×10^{-5}	cellular component organization or biogenesis
GO:0048806	blood vessel development	1.22×10^{-5}	developmental process

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GO-BP-ID	Term	FDR	Biological Process categories
GO:0009880	negative regulation of macromolecule metabolic process	2.08×10^{-5}	metabolic process
GO:0045321	chemical homeostasis	2.46×10^{-5}	biological regulation
GO:0003013	cell death	3.99×10^{-5}	death
GO:0045669	cell cycle	4.27×10^{-5}	cellular process
GO:0006468	regulation of protein metabolic process	4.30×10^{-5}	metabolic process
GO:0048771	negative regulation of RNA metabolic process	4.39×10^{-5}	metabolic process
GO:0016358	negative regulation of cellular process	5.57×10^{-5}	cellular process
GO:0046852	positive regulation of cellular process	5.57×10^{-5}	cellular process
GO:0045664	neurite development	8.51×10^{-5}	developmental process
GO:0030326	bone development	0.00010246	developmental process
GO:0051240	organ development	0.00014382	developmental process
GO:0043062	in utero embryonic development	0.00014382	developmental process
GO:0048705	protein complex biogenesis	0.00015566	cellular component organization or biogenesis
GO:0001816	protein transport	0.00018538	localization
GO:0009967	negative regulation of developmental process	0.00020109	developmental process
GO:0008284	anatomical structure development	0.00020109	developmental process
GO:0007610	cell differentiation	0.00020109	developmental process
GO:0031323	regulation of molecular function	0.00024247	biological regulation
GO:0042698	protein kinase cascade	0.0002562	signaling
GO:0032504	positive regulation of cellular component organization	0.0002562	cellular component organization or biogenesis
GO:0016192	pattern specification process	0.0002562	developmental process
GO:0060255	cellular ion homeostasis	0.00031898	cellular process
GO:0030509	positive regulation of transferase activity	0.00032172	biological regulation
GO:0001525	anatomical structure morphogenesis	0.00032172	developmental process
GO:0021953	developmental maturation	0.00042316	developmental process
GO:0044238	anterior/posterior pattern formation	0.00043603	developmental process
GO:0030900	positive regulation of erythrocyte differentiation	0.00049545	immune system process
GO:0045840	protein amino acid autophosphorylation	0.00055993	metabolic process
GO:0007611	erythrocyte homeostasis	0.00060436	biological regulation
GO:0051641	development of primary female sexual characteristics	0.00060655	developmental process
GO:0009889	reproductive process	0.00060655	reproduction
GO:0007346	regulation of small GTPase mediated signal transduction	0.00086415	signaling
GO:0042127	cellular homeostasis	0.00086415	biological regulation
GO:0010564	macromolecular complex assembly	0.00087586	cellular component organization or biogenesis
GO:0007417	gonad development	0.00102982	developmental process
GO:0001541	regulation of cellular component organization	0.0012023	cellular component organization or biogenesis
GO:0030278	cellular response to stimulus	0.0012023	response to stimulus
GO:0016071	intracellular signaling cascade	0.0012023	signaling
GO:0045165	positive regulation of apoptosis	0.0012023	death
GO:0032350	regulation of nervous system development	0.00121532	developmental process
GO:0010604	embryonic morphogenesis	0.00121532	developmental process
GO:0007268	positive regulation of protein kinase activity	0.00136536	biological regulation
GO:0048806	regulation of immune system process	0.00136536	immune system process
GO:0009880	negative regulation of signal transduction	0.00139111	signaling
GO:0045321	macromolecule metabolic process	0.00145313	metabolic process
GO:0003013	sex differentiation	0.00158449	developmental process
GO:0045669	transmembrane receptor protein tyrosine kinase signaling pathway	0.00169263	signaling
GO:0006468	cellular developmental process	0.00169263	developmental process
GO:0048771	organelle organization	0.00177575	cellular component organization or biogenesis
GO:0016358	regulation of kinase activity	0.00200121	biological regulation
GO:0046852	cell migration	0.00208441	localization
GO:0045664	response to abiotic stimulus	0.00211072	response to stimulus
GO:0030326	negative regulation of transcription from RNA polymerase II promoter	0.00211072	biological regulation
GO:0051240	heart development	0.00211072	developmental process
GO:0043062	macromolecule catabolic process	0.00220163	metabolic process
GO:0048705	cellular catabolic process	0.00226036	metabolic process



Appendix Figure S1 The predicted stem-loop structures of rat-specific miRNAs. The secondary structure of pre-miRNA was predicted by MIREAP. The mature miRNAs are marked in red while miRNA* are marked in green.

