MicroRNA-mediated Feedback and Feedforward Loops are Recurrent Network Motifs in Mammals

Supplementary Data

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Table S1a Negative auto-regulatory loops that are conserved across human/mouse/rat/dog.

Host gene	miRNA	Gene description
NM_005730	miR-26a	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2/nuclear LIM interactor-interacting factor 2/conserved gene amplified in osteosarcoma
NM_016300	miR-128b	cyclic AMP-regulated phosphoprotein
NM_004319	miR-488	astrotactin;cell/neuron adhesion

Table S1b Additional negative auto-regulatory loops based on non-conserved seed-matches.

Host gene	miRNA	Gene description
NM_005455	miR-186	zinc finger protein 265/RNA splicing
NM_002081	miR-149	Glypican 1
NM_007085	miR-198	follistatin-like 1/autoantigen associated with rheumatoid arthritis
NM_016215	miR-126	EGF-like-domain, multiple 7/angiogenesis/blood vessel development
NM_001007471	miR-204	Transient receptor potential cation channel, subfamily M, member 3
NM_021990	miR-224	gamma-aminobutyric acid (GABA) A receptor, epsilon
NM_000390	miR-361	choroideremia (Rab escort protein 1)
NM_017551	miR-346	glutamate receptor, ionotropic, delta 1
NM_002438	miR-511	Mannose receptor, C type 1

Table S1c Additional negative auto-regulatory loops based on Miranda (Enright et al., 2003) with $\Delta G < -20$ kcal/mol

Host gene	miRNA	Gene description
NM_031407	let-7f	HECT, UBA and WWE domain containing 1
NM_007014	miR-140	WW domain containing E3 ubiquitin protein ligase 2
NM_005578	miR-28	LIM domain containing preferred translocation partner in lipoma
NM_004041	miR-326	arrestin, beta 1/dampening of cellular responses to stimuli such as hormones, neurotransmitters, or sensory signals
NM_032350	miR-339	hypothetical protein MGC11257
NM_001033563	miR-423	coiled-coil domain containing 55
NM_000868	miR-448	5-hydroxytryptamine (serotonin) receptor 2C
NM_021990	miR-452	gamma-aminobutyric acid (GABA) A receptor, epsilon
NM_021990	miR-452*	gamma-aminobutyric acid (GABA) A receptor, epsilon

Details of putative target sites predicted by Miranda can be found in the linked page *miranda-report.html* on the Supplementary Information website (note that the miRNAs listed are always embedded in the corresponding target gene.).

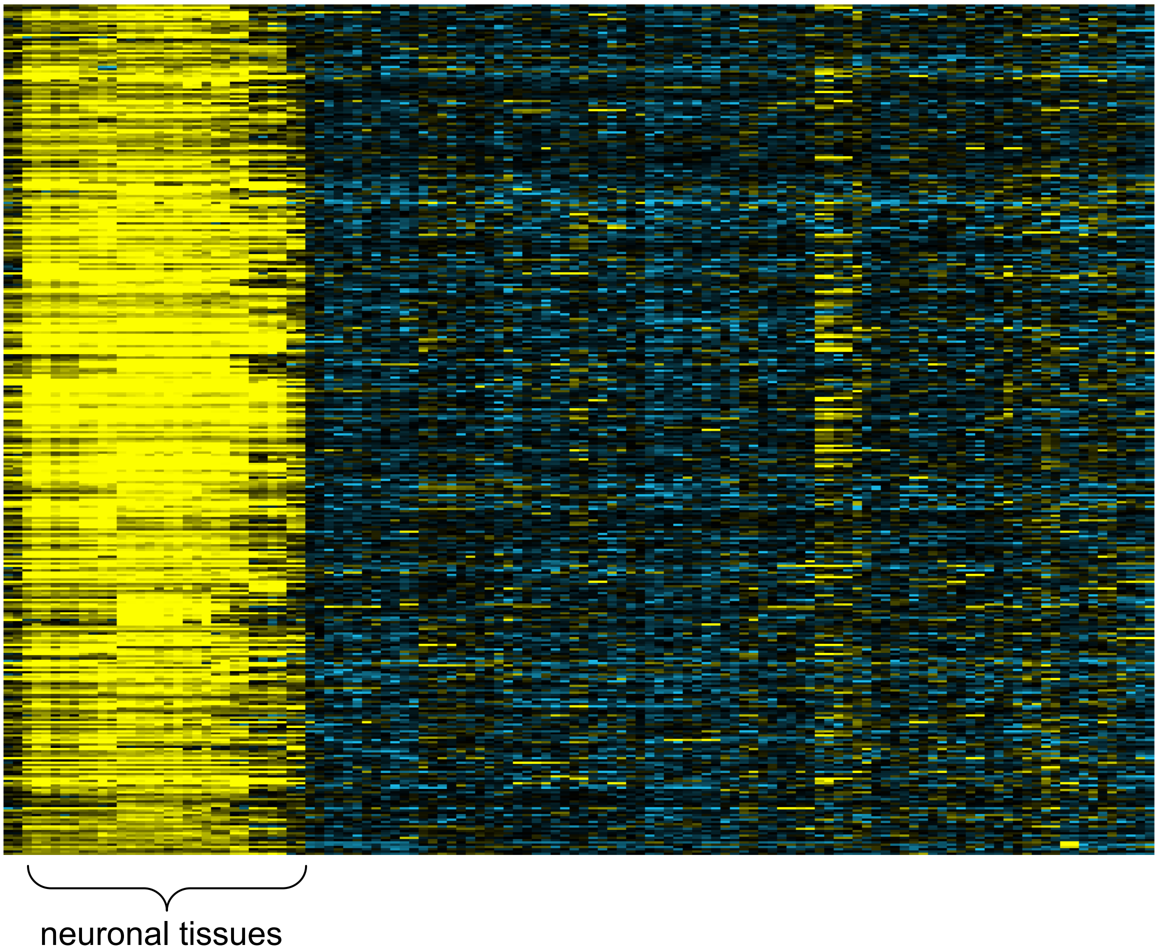

Figure S1 Neuronal-enriched gene cluster (1012 genes) used to identify neuronal-enriched miRNAs using CE analysis.

Host-gene Probe Selection

We used embedded miRNAs that reside in introns and are on the same strand as their host genes. This gave us an initial set of embedded miRNAs along with their host-gene probes. Three different microarray designs were used to generate the four data sets we used: GNF1H/U133A for human, GNF1M for mouse, and Affy-430 for MDEV and NCELL. Since the coverage for RefSeq genes is not uniform among these arrays, a slightly different set of miRNAs was analyzed in each data set.

We removed probes from the initial set of embedded miRNAs based on 1) wrong or inconsistent probes (see below); and 2) probes for miRNAs whose seeds occur at very low frequencies that prevent meaningful statistical analysis. According to the supplied annotations, some host genes are represented by more than one probe on the microarray. In several instances, we found that these annotations are wrong. For instance, some probes were mapped to the opposite strand of a gene, while others cover truncated variants(s) of the gene that typically do not include the intron where the miRNA is embedded. Therefore we first manually examined all probe annotations and removed badly-annotated probes by using the probe alignments in the UCSC Genome Database (genome.ucsc.edu). In addition, different probes could measure the expression of different isoforms resulted from alternative splicing or alternative promoter usage. For host genes with multiple probes in the human and mouse expression atlases, the expression patterns of different probes generally agree with each other (median correlation coefficient > 0.5). A small number of host genes have probes with inconsistent expression patterns; this is likely because different probes measured the expression of different transcript isoforms. Embedded miRNAs could be co-transcribed with different mRNA isoforms, because the intron that contains the miRNA could be included in the pre-mRNA transcript of different mRNA isoforms. Therefore we report CE analysis results for all valid probes because we would like to utilize all potentially meaningful expression patterns of the embedded miRNA(s). The probes removed prior to human and mouse CE analyses are listed in Table S2a-b.

For the MDEV and NCELL data sets, a substantially higher number of host genes have multiple probes, sometimes with different expression patterns. The pairwise correlation between probes that mapped to the same gene ranges from -0.7 to 0.96 (median for MDEV (NCELL) is 0.6 (0.12)). This phenomenon is likely due to the high frequency of alternative splicing in the brain; some probes could also be dysfunctional. To avoid reporting erroneous results due to bad probes, we conservatively removed probes that are likely erroneous by using the following method. For host genes with two probes, we removed the gene if the correlation between the two probes is less than a predefined threshold. For host genes with more than two probes, we tried to detect outliers by first finding the largest group of probes that are consistent with each other in a pairwise manner. Next we removed those probes whose correlation with any probe in the core group is below the threshold. If a unique core group of size at least two can not be found (e.g. if there are two groups that can not be merged due to low correlation between at least one pair of members from each group), the gene is removed from our analysis. We used a relatively low threshold of 0.3 to avoid removing probes that report expression of isoforms. This procedure should eliminate most extreme outliers but retain probes that might correspond to isofroms. Since the MDEV data set tend to have a higher median correlation between probes (0.6), we also tried using higher thresholds (0.6-0.7), but the percentage of miRNAs that exhibit Type I/II bias remained essentially identical to that when a threshold of 0.3 was used. All probes removed prior to MDEV and NCELL CE analyses are listed in Table S2c-d.

Comparison of CE Analysis Results among Data Sets

As discussed in the main text, since different data sets tend to cover different conditions, it is not meaningful to compare CE results across data sets (the human and mouse data sets are somewhat comparable, see below). For instance, the transcription of a miRNA can be regulated by different *cis* regulatory modules under different conditions, or it may not be regulated at all (i.e. constitutively expressed or absent). Two example CE profiles across all four data sets can be found in Figures S2 and S3.

Since a relatively large number of the conditions profiled in the human and mouse data sets are homologous, we tried to compare the type of bias shown by orthologous embedded miRNAs in human and mouse. We defined an embedded miRNA in human to be the ortholog of a mouse embedded miRNA of the same sequence if their host genes are orthologs of each other. Aside from a few exceptions, orthologous miRNAs biased for Type I networks are consistent in the two organisms (12/14). However, a larger number of Type-II-biased miRNAs exhibit bias in only one of human or mouse (with 5/16 being consistent). Closer examination upon the expression pattern of host orthologs indicates that some host-gene's expression pattern have diverged significantly. For instance, miR-103 is significantly upregulated in selected brain tissues in human but not in mouse (Figure S4); miR-326 is ubiquitously upregulated in mouse brain tissues but not in immune cells; but in human it is upregulated in a large number of immune cells and only in a small number of brain tissues (Figure S5). As expected, some of the discrepancies can be attributed to the differences in the conditions profiled. The mouse data set has far less coverage of immue/cancer cell types compared to human, but has extensive coverage of embryonic developmental time-points and tissues (e.g. oocytes and blastocysts), whereas the human data set has none. Hence, miRNAs whose expression signature is characterized by up- or down-regulation in these conditions are likely to only exhibit bias in only one of human or mouse (Figure S6; e.g. miR-93 biased for Type II in mouse only (Table S4 and S3)). The higher level of consistency of Type-I-biased miRNAs is partially due to the fact that a large fraction of them are neuronal-enriched and both data sets have extensive coverage of brain tissues.

Table S2a Human host-gene probes removed prior to CE analysis

miRNA	Host-gene Probe	Reason for removal
128a (chr2)	581	Probe covers a very short version of the host gene (1)
211 (chr5)	8752	Probe covers the opposite strand (2)
26a (chr3)	442	2
149 (chr2)	8488	Probe covers the next gene, so cross-hyb would be possible (3)
15a/16 (chr13)	1686	2
15b/16 (chr3)	408	1
218 (chr5)	10988	The expression pattern of this probe is not consistent with the other two probes (7811 and 7898). It turns out that the expression pattern of this probe resembles that of another copy of miR-218 (chr4, probe 2221), which is embedded in a duplicated copy of the host gene of miR-218-chr5. This is likely due to cross-hybridization.
330 (chr19)	12215	2
9 (chr1)	16739	1
9* (chr1)	16739	1
140 (chr16)	932	1
204 (chr9)	14286	1
26a (chr12)	824	1
489 (chr7)	4479	1
126 (chr9)	3324 (all probes)	Seed-match occurrence frequency is too low for meaningful analysis

Table S2b Mouse host-gene probes removed prior to CE analysis

miRNA	Host-gene Probe	Reason for removal
340 (chr11)	2522	Seed-match occurrence frequency is too low for meaningful analysis

Table S2c Probes removed prior to MDEV CE analysis

miRNA	Host-gene Probe	Reason for removal
Let-7f	34,8694,14599 (all probes)	Probes inconsistent (1)
126-3p	5240,13231,17737,17738 (all probes)	Seed-match occurrence frequency is too low for meaningful analysis.
128b	8048	Probe covers a very short version of the host gene.
140	19938	1
151	6906,11962 (all probes)	1
208	15058,15327	1
28	9344,13455,13587,19323 (all probes)	1
301	7279,13782 (all probes)	1
98	34,8694,14599 (all probes)	1

Table S2d Probes removed prior to NCELL CE analysis

miRNA	Host-gene Probe	Reason for removal
Let-7f	34,8694,14599 (all probes)	Probes inconsistent (1)
106b	351	1
126-3p	5240,13231,17737,17738 (all probes)	Seed-match occurrence frequency is too low for meaningful analysis.
126-5p	5240,13231,17737,17738 (all probes)	1
128b	8048	Probe covers a very short version of the host gene.
140	14658	1
151	6906,11962 (all probes)	1
15b/16	10749,10750,18431 (all probes)	1
207	607,20038 (all probes)	1
208	2033, 15326,15327	1
25	351	1
28	9344,13455,13587,19323 (all probes)	1
483	251,14664 (all probes)	1
93	351	1
301	7279,13782 (all probes)	1
98	34,8694,14599 (all probes)	1

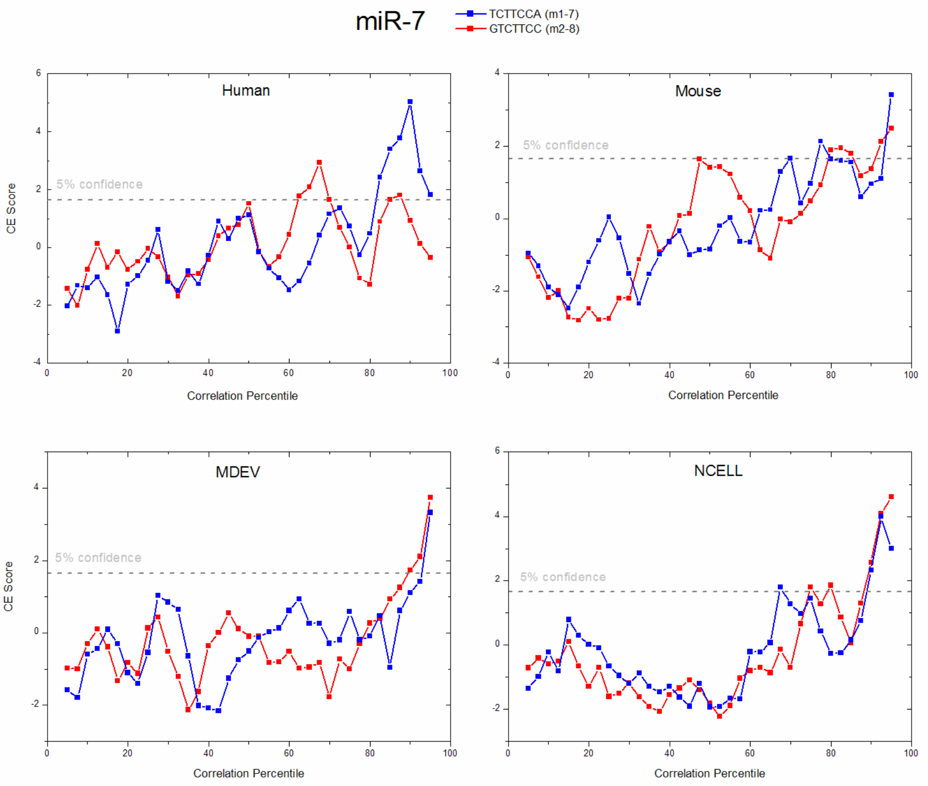

Figure S2. CE profiles of *miR-7* in all four data sets. Note that consistent Type I signatures are present across all data sets.

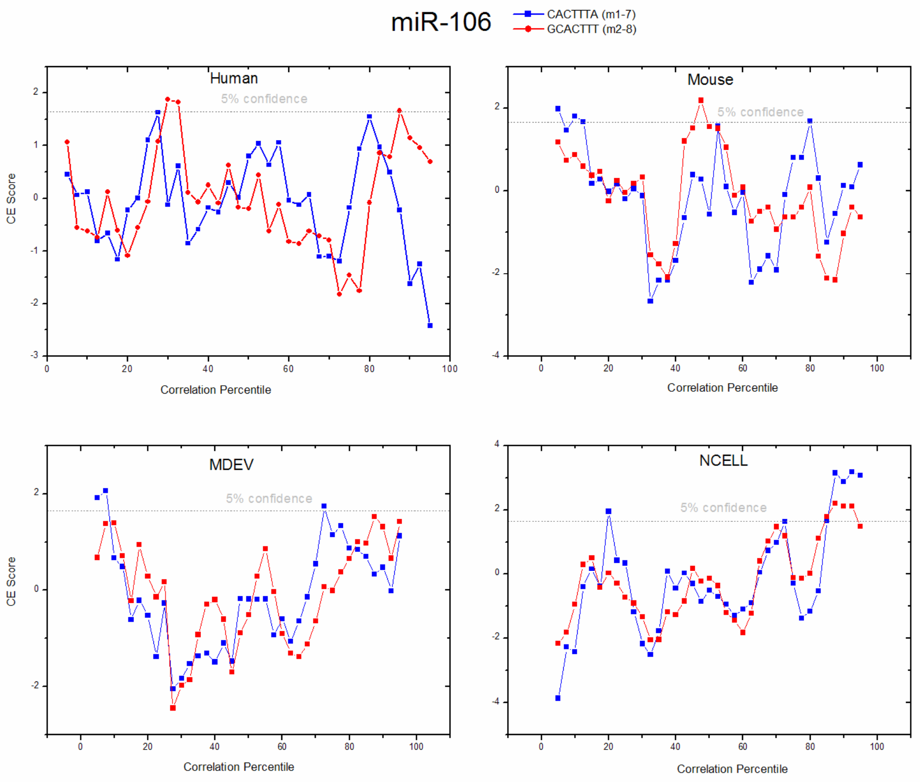

Figure S3. CE profiles of *miR-106* in all four data sets. Note that miR-106 only displays Type I bias in the NCELL data set, even though the trend in the MDEV data set also indicates that Type I bias is likely. In addition, miR-106 shows Type II bias in the mouse and MDEV data sets only.

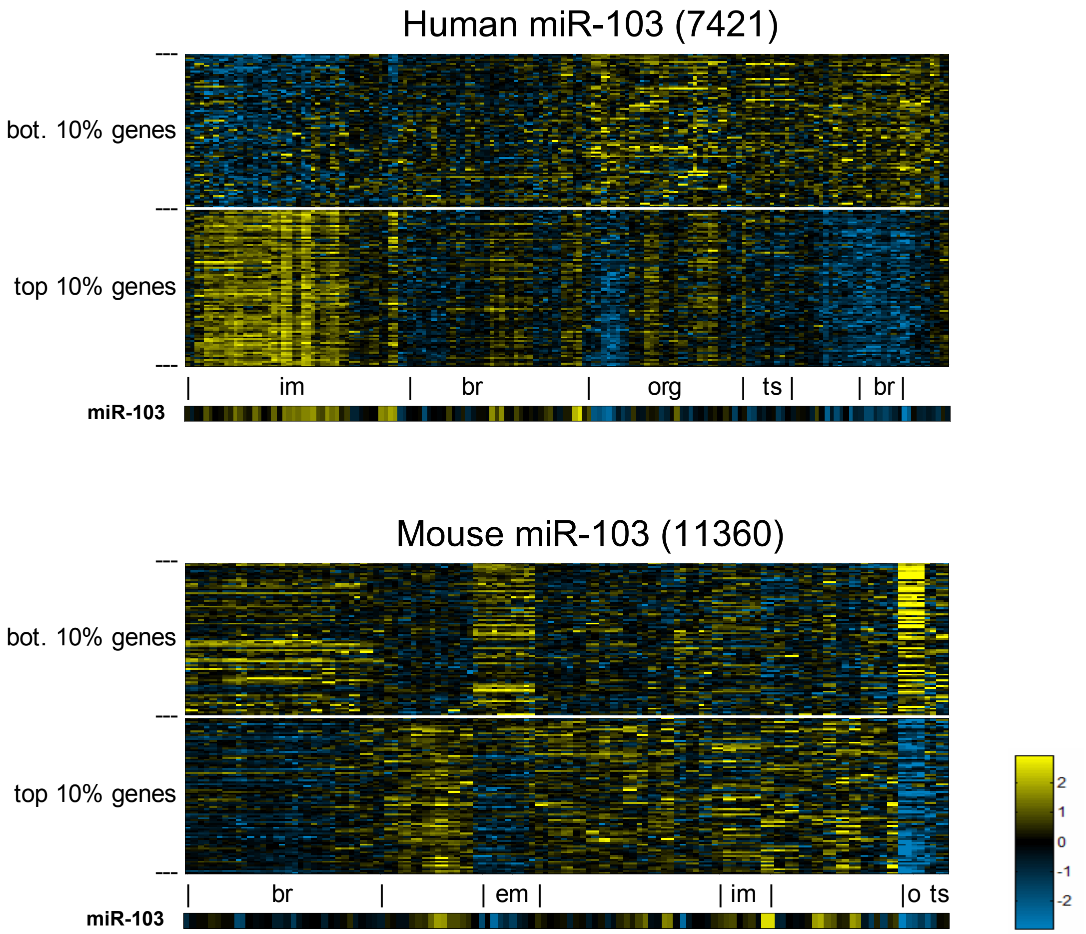

Figure S4. Expression pattern of genes that are highly positively or negatively correlated with *miR-103* in the human and mouse expression atlases. Conditions: **im**=immune/cancer; **br**=brain; **org**= organs; **ts**=testis-related; **o**=oocyte; **em**=embryonic.

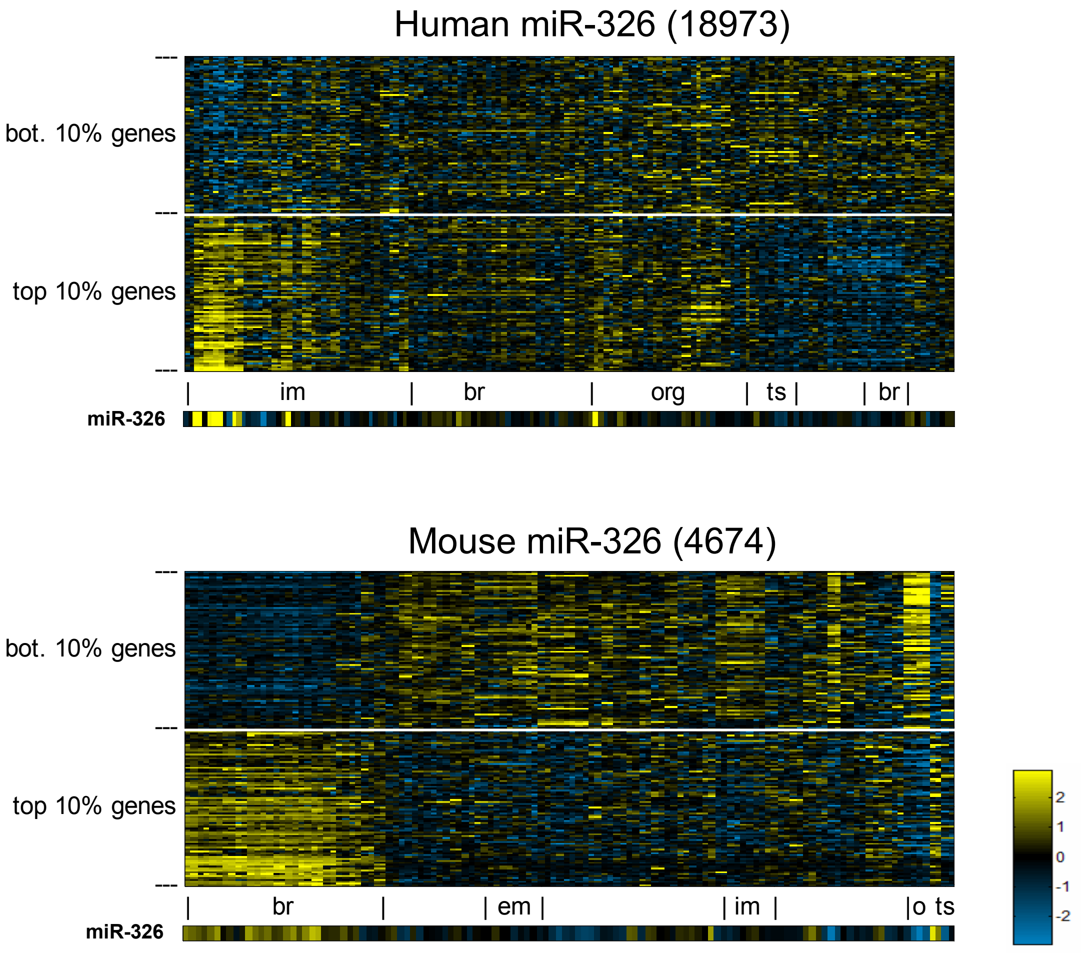

Figure S5. Expression pattern of genes that are highly positively or negatively correlated with *miR-326* in the human and mouse expression atlases. Conditions: **im**=immune/cancer; **br**=brain; **org**= organs; **ts**=testis-related; **o**=oocyte; **em**=embryonic.

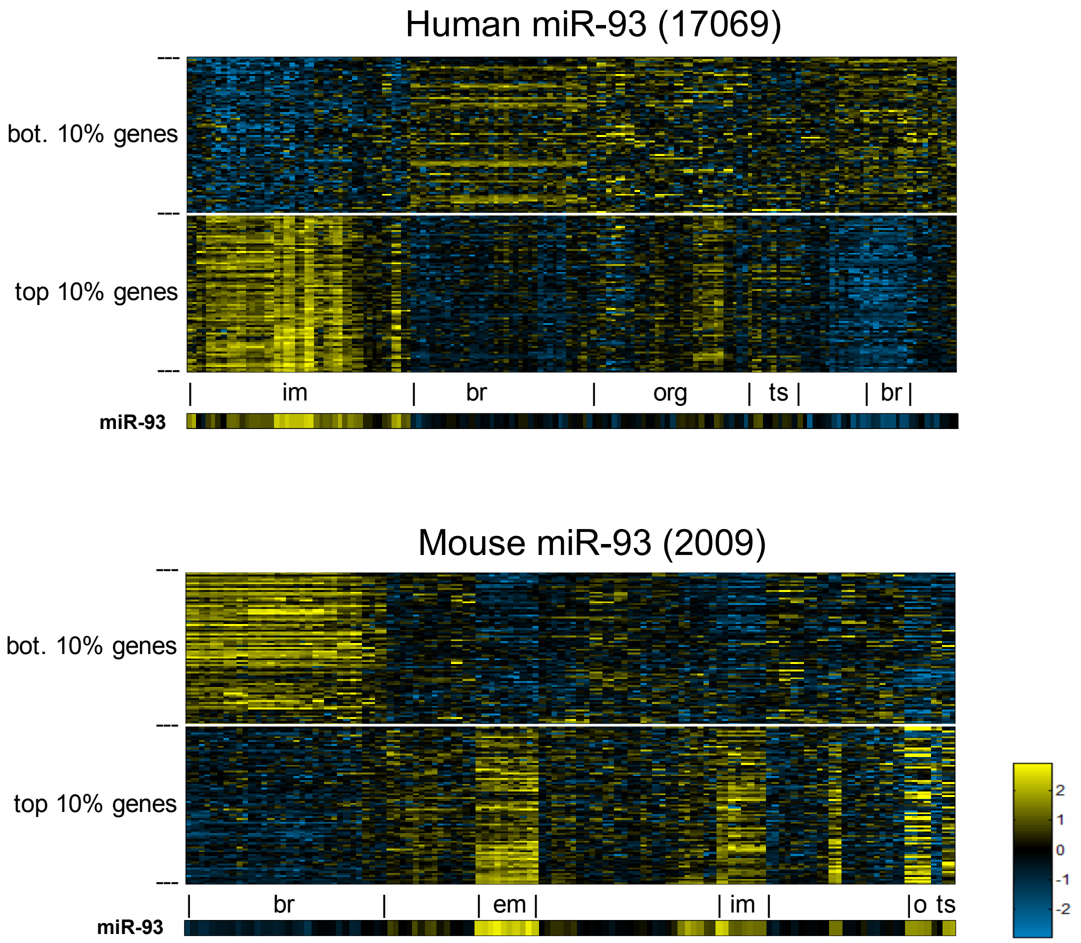

Figure S6. Expression pattern of genes that are highly positively or negatively correlated with *miR-93* in the human and mouse expression atlases. Conditions: **im**=immune/cancer; **br**=brain; **org**= organs; **ts**=testis-related; **o**=oocyte; **em**=embryonic. Note that the expression profile of *mir-93* in mouse is characterized by upregulation in oocyte and embryonic development. But these conditions are not in the human data set.

Table S3 Human CE analysis result

				CE score		
miRNA	**chr**	**seed match**	**probe**	**top 10% set**	**mid 10% set**	**bot. 10% set**
hsa-mir-101	chr9	GUACUGU	6448	-3.43E-02	0.144708667	2.153846342
hsa-mir-101	chr9	UACUGUA	6448	6.46E-03	0.477649176	1.492158046
hsa-mir-103	chr20	AUGCUGC	16412	1.373564491	-1.758397791	-0.563726294
hsa-mir-103	chr20	UGCUGCU	16412	1.789632306	-1.00108365	-0.774265335
hsa-mir-103	chr5	AUGCUGC	7421	2.108463096	-1.122536977	-0.249101792
hsa-mir-103	chr5	UGCUGCU	7421	4.358472479	-0.734517159	-0.958242607
hsa-mir-103	chr5	AUGCUGC	9785	-0.816834662	0.481643486	1.487954698
hsa-mir-103	chr5	UGCUGCU	9785	0.429459833	-2.062941414	0.929440859
hsa-mir-105	chrX	CAUUUGA	17935	0.995697214	-1.027888658	-1.591638863
hsa-mir-105	chrX	GCAUUUG	17935	-0.3940282	-0.256080789	1.37E-02
hsa-mir-106b	chr7	CACUUUA	3161	-2.424367129	0.798307053	0.45107418
hsa-mir-106b	chr7	GCACUUU	3161	0.694150075	-0.195232503	1.06825509
hsa-mir-106b	chr7	CACUUUA	17069	-1.396005511	0.01511622	0.337602669
hsa-mir-106b	chr7	GCACUUU	17069	0.734359105	-1.22043724	0.856008461
hsa-mir-126*	chr9	AAUAAUG	3324	0.016020104	0.854269492	0.410808525
hsa-mir-126*	chr9	UAAUAAU	3324	0.846307279	-1.189667925	0.279668513
hsa-mir-128a	chr2	ACUGUGA	10775	0.548462919	-1.317619508	-1.222927661
hsa-mir-128a	chr2	CACUGUG	10775	3.778439032	-1.739970638	-2.061755286
hsa-mir-128b	chr3	ACUGUGA	4902	2.23522211	-1.833601587	-0.202259896
hsa-mir-128b	chr3	CACUGUG	4902	2.84743495	-1.189737296	1.153799865
hsa-mir-139	chr11	ACUGUAG	6105	1.129995776	0.348843093	-0.029932489
hsa-mir-139	chr11	CUGUAGA	6105	0.775230853	-1.285331058	-0.324052204
hsa-mir-140	chr16	AAACCAC	633	0.800785057	-0.498727546	1.140249574
hsa-mir-140	chr16	AACCACU	633	0.979908015	0.433214945	-0.836974061
hsa-mir-148b	chr12	GCACUGA	11039	0.341774367	0.267290045	1.261098069
hsa-mir-148b	chr12	UGCACUG	11039	-1.070478465	0.692426841	-2.115065639
hsa-mir-149	chr2	AGCCAGA	14955	2.557240659	-1.754264578	-0.951750343
hsa-mir-149	chr2	GAGCCAG	14955	2.824297596	-1.48154765	0.84576229
hsa-mir-151	chr8	AGUCUAG	1953	0.708429892	-1.32903638	-1.32903638
hsa-mir-151	chr8	GUCUAGU	1953	0.562370967	-1.180828378	-1.180828378
hsa-mir-151	chr8	AGUCUAG	17258	1.250448163	0.218654346	-1.32903638
hsa-mir-151	chr8	GUCUAGU	17258	0.146999248	0.106762047	0.842528005
hsa-mir-152	chr17	GCACUGA	12183	-1.998180408	-0.281818358	2.57318448
hsa-mir-152	chr17	UGCACUG	12183	-1.139479892	5.95E-02	1.38637626
hsa-mir-153	chr2	CUAUGCA	7389	2.117392857	1.487070075	-0.589392815
hsa-mir-153	chr2	UAUGCAA	7389	2.019507305	-1.359908138	-0.347374898
hsa-mir-153	chr7	CUAUGCA	907	2.241698373	-1.475813466	-0.363960875
hsa-mir-153	chr7	UAUGCAA	907	2.237159976	-1.100642345	0.171663418
hsa-mir-153	chr7	CUAUGCA	11066	1.728938119	-0.180275591	0.281630952
hsa-mir-153	chr7	UAUGCAA	11066	1.551224287	-1.313565943	0.391411824
hsa-mir-153	chr7	CUAUGCA	13609	2.269498628	-0.117867879	0.335567865
hsa-mir-153	chr7	UAUGCAA	13609	1.211489548	-7.25E-02	-0.994180546
hsa-mir-15a	chr13	GCUGCUA	9834	0.337238482	0.272494156	0.272494156
hsa-mir-15a	chr13	UGCUGCU	9834	2.137937712	-1.240993492	1.737556591
hsa-mir-15b	chr3	GCUGCUA	1744	0.932431937	-0.862811282	0.630746095
hsa-mir-15b	chr3	UGCUGCU	1744	3.167841473	0.104900721	2.85686503
hsa-mir-15b	chr3	GCUGCUA	2413	0.457796883	-1.325115839	0.516756841

hsa-mir-15b	chr3	UGCUGCU	2413	2.759041758	-0.8579839	2.452912457
hsa-mir-16	chr13	GCUGCUA	9834	0.337238482	0.272494156	0.272494156
hsa-mir-16	chr13	UGCUGCU	9834	2.137937712	-1.240993492	1.737556591
hsa-mir-16	chr3	GCUGCUA	1744	0.932431937	-0.862811282	0.630746095
hsa-mir-16	chr3	UGCUGCU	1744	3.167841473	0.104900721	2.85686503
hsa-mir-16	chr3	GCUGCUA	2413	0.457796883	-1.325115839	0.516756841
hsa-mir-16	chr3	UGCUGCU	2413	2.759041758	-0.8579839	2.452912457
hsa-mir-190	chr15	ACAUAUC	5300	0.501149467	0.303956201	0.476293173
hsa-mir-190	chr15	CAUAUCA	5300	1.963658004	-0.96966147	0.162812288
hsa-mir-190	chr15	ACAUAUC	18809	1.768820463	-0.338560988	1.047409883
hsa-mir-190	chr15	CAUAUCA	18809	3.229244855	0.245252907	-3.24E-02
hsa-mir-198	chr3	CUGGACC	1448	4.223604438	0.190191429	-1.507492969
hsa-mir-198	chr3	UCUGGAC	1448	5.277075356	-0.495545909	-0.800632758
hsa-mir-198	chr3	CUGGACC	12019	-1.606299998	1.408681266	0.836928342
hsa-mir-198	chr3	UCUGGAC	12019	-0.822183573	-0.177111966	-1.190205196
hsa-mir-198	chr7	CUGGACC	1448	4.223604438	0.190191429	-1.507492969
hsa-mir-198	chr7	UCUGGAC	1448	5.277075356	-0.495545909	-0.800632758
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hsa-mir-204	chr9	AAGGGAA	5193	0.816343758	-0.585268146	-2.238598107
hsa-mir-204	chr9	AAAGGGA	13109	-1.35143896	-7.78E-02	1.186314943
hsa-mir-204	chr9	AAGGGAA	13109	-1.041537553	-0.639570928	-0.29743713
hsa-mir-208	chr14	CGUCUUA	10152	1.781385007	-0.860204711	0.196431176
hsa-mir-208	chr14	GUCUUAU	10152	-2.076060777	1.377238258	2.296623066
hsa-mir-211	chr15	AAAGGGA	8064	-0.835099143	-5.16E-02	1.253730118
hsa-mir-211	chr15	AAGGGAA	8064	-1.403841986	-0.566758158	0.426520447
hsa-mir-218	chr4	AAGCACA	2221	2.37467716	-1.654968412	-0.910671689
hsa-mir-218	chr4	AGCACAA	2221	1.576519042	-1.371794392	-1.107094427
hsa-mir-218	chr5	AAGCACA	7811	-1.285156772	-0.950903944	2.47075968
hsa-mir-218	chr5	AGCACAA	7811	-0.807101135	-0.54044043	1.658898777
hsa-mir-218	chr5	AAGCACA	7898	0.356644353	-1.035877242	1.238801144
hsa-mir-218	chr5	AGCACAA	7898	-0.299420178	-1.412912833	1.829459636
hsa-mir-22	chr17	GCAGCUU	6070	0.494828806	-0.514093184	0.762428187
hsa-mir-22	chr17	GGCAGCU	6070	0.733863968	-0.84822566	1.589680369
hsa-mir-224	chrX	GUGACUU	17624	-0.220311909	-1.697889846	-0.124499481
hsa-mir-224	chrX	UGACUUG	17624	-0.445310729	8.40E-02	-0.791168129
hsa-mir-23b	chr9	AAUGUGA	9276	1.78526078	0.732607649	0.502213331
hsa-mir-23b	chr9	AUGUGAU	9276	0.931701629	0.209520615	7.44E-02
hsa-mir-24	chr9	CUGAGCC	9276	1.964009397	-0.432916364	1.291936038
hsa-mir-24	chr9	UGAGCCA	9276	2.630122028	-0.567966092	0.855185972
hsa-mir-25	chr7	GUGCAAU	3161	-1.998655335	-0.686835573	-0.23383492
hsa-mir-25	chr7	UGCAAUG	3161	2.098853161	-1.15586382	0.56502904
hsa-mir-25	chr7	GUGCAAU	17069	-1.598880805	-0.644683172	0.230568683
hsa-mir-25	chr7	UGCAAUG	17069	1.487487638	-0.46088286	0.361606576
hsa-mir-26a	chr12	ACUUGAA	17350	-0.337602726	9.81E-02	0.935925462
hsa-mir-26a	chr12	UACUUGA	17350	0.836315949	0.734126137	2.300494472
hsa-mir-26a	chr3	ACUUGAA	8164	0.75469845	1.109449313	-3.330336667
hsa-mir-26a	chr3	UACUUGA	8164	0.983476591	0.187561063	-3.580187074
hsa-mir-26a	chr3	ACUUGAA	8998	-0.389411477	-1.082061812	2.860794683
hsa-mir-26a	chr3	UACUUGA	8998	-1.380268587	-0.482393433	3.654833252
hsa-mir-26a	chr3	ACUUGAA	16468	-6.16E-02	-0.837715775	-2.015858395

hsa-mir-26a	chr3	UACUUGA	16468	1.137644883	-1.53E-02	-0.591721172
hsa-mir-26b	chr2	ACUUGAA	5475	-1.232439845	1.36695187	1.258106818
hsa-mir-26b	chr2	UACUUGA	5475	0.561189531	2.058113912	1.991846904
hsa-mir-27b	chr9	ACUGUGA	9276	1.136867288	0.873402645	0.433272646
hsa-mir-27b	chr9	CUGUGAA	9276	0.526404853	1.416036377	0.458079172
hsa-mir-28	chr3	AGCUCCU	8588	-0.859233934	0.884406855	1.754065712
hsa-mir-28	chr3	GCUCCUU	8588	-1.86E-02	-0.266304076	0.779935788
hsa-mir-28	chr3	AGCUCCU	14077	-1.556889012	-0.753858948	-8.77E-03
hsa-mir-28	chr3	GCUCCUU	14077	0.266593798	-0.474900186	9.93E-02
hsa-mir-30c	chr1	GUUUACA	4066	0.369074172	8.59E-02	0.879438924
hsa-mir-30c	chr1	UGUUUAC	4066	-0.141723149	0.86656161	1.318032398
hsa-mir-30c	chr1	GUUUACA	4542	-0.49597545	-0.107960638	0.700178885
hsa-mir-30c	chr1	UGUUUAC	4542	0.944214585	0.18619829	0.415090822
hsa-mir-30c	chr1	GUUUACA	14965	0.306293201	-9.53E-02	0.156056271
hsa-mir-30c	chr1	UGUUUAC	14965	-0.666181714	1.249163972	1.422838116
hsa-mir-30c	chr1	GUUUACA	19201	-0.250585019	0.482821594	1.204744982
hsa-mir-30c	chr1	UGUUUAC	19201	-2.174226931	1.225464646	2.801847216
hsa-mir-30e-3p	chr1	ACUGAAA	4066	0.475744319	-2.248931028	-0.799438248
hsa-mir-30e-3p	chr1	CUGAAAG	4066	-0.707535199	-0.797974234	-1.363025693
hsa-mir-30e-3p	chr1	ACUGAAA	4542	2.359744491	0.130473101	0.324167269
hsa-mir-30e-3p	chr1	CUGAAAG	4542	0.548638074	-0.593700737	-0.34335051
hsa-mir-30e-3p	chr1	ACUGAAA	14965	2.030415133	-2.266445352	-0.311114815
hsa-mir-30e-3p	chr1	CUGAAAG	14965	0.186767047	-0.623297697	-0.652115789
hsa-mir-30e-3p	chr1	ACUGAAA	19201	2.490683968	-0.363951872	-1.108839105
hsa-mir-30e-3p	chr1	CUGAAAG	19201	-0.946846283	-0.693948505	-0.258268522
hsa-mir-30e-5p	chr1	GUUUACA	4066	0.369074172	8.59E-02	0.879438924
hsa-mir-30e-5p	chr1	UGUUUAC	4066	-0.141723149	0.86656161	1.318032398
hsa-mir-30e-5p	chr1	GUUUACA	4542	-0.49597545	-0.107960638	0.700178885
hsa-mir-30e-5p	chr1	UGUUUAC	4542	0.944214585	0.18619829	0.415090822
hsa-mir-30e-5p	chr1	GUUUACA	14965	0.306293201	-9.53E-02	0.156056271
hsa-mir-30e-5p	chr1	UGUUUAC	14965	-0.666181714	1.249163972	1.422838116
hsa-mir-30e-5p	chr1	GUUUACA	19201	-0.250585019	0.482821594	1.204744982
hsa-mir-30e-5p	chr1	UGUUUAC	19201	-2.174226931	1.225464646	2.801847216
hsa-mir-326	chr11	CCAGAGG	18973	1.816203196	-0.102066616	-0.384483749
hsa-mir-326	chr11	CCCAGAG	18973	0.689465166	-1.445057958	1.090028935
hsa-mir-33	chr22	AAUGCAC	3955	-1.182277697	1.905620573	-2.365243937
hsa-mir-33	chr22	CAAUGCA	3955	-1.610131396	0.132854704	-1.349746277
hsa-mir-33	chr22	AAUGCAC	9716	-0.364892861	-0.192448802	-2.74062521
hsa-mir-33	chr22	CAAUGCA	9716	0.572143884	-0.607317475	-1.664237395
hsa-mir-330	chr19	GCUUUGC	11586	1.085800376	1.856591378	0.774626613
hsa-mir-330	chr19	UGCUUUG	11586	2.183257241	1.26879245	-2.189110425
hsa-mir-330	chr19	GCUUUGC	18833	3.047410196	-0.848272039	-0.475715878
hsa-mir-330	chr19	UGCUUUG	18833	0.519860444	0.461934604	-0.903702408
hsa-mir-335	chr7	CUCUUGA	14117	1.749307997	0.175981939	-0.278275566
hsa-mir-335	chr7	GCUCUUG	14117	0.3045291	-0.585865536	-1.436048801
hsa-mir-342	chr14	GUGUGAG	3585	-0.148595616	-1.619218408	-1.386819352
hsa-mir-342	chr14	UGUGAGA	3585	0.882077331	-1.773075813	-0.268398443
hsa-mir-361	chrX	CUGAUAA	14688	-1.434780455	0.382453284	-1.873787259
hsa-mir-361	chrX	UCUGAUA	14688	-1.281125905	-1.010236934	-0.270427926
hsa-mir-448	chrX	AUAUGCA	12397	0.371637069	-0.551228093	-2.526042621

hsa-mir-448	chrX	UAUGCAA	12397	-5.31E-02	-0.232931575	-0.52574863
hsa-mir-448	chrX	AUAUGCA	19022	1.910236298	-0.244149394	-1.037829724
hsa-mir-448	chrX	UAUGCAA	19022	1.554089077	-0.572549658	0.333688439
hsa-mir-452	chrX	GCAAACA	17624	-0.353498987	3.316853507	0.277147722
hsa-mir-452	chrX	UGCAAAC	17624	0.165354424	2.496373909	0.588406962
hsa-mir-452*	chrX	AGACUGA	17624	1.053261551	1.2134798	1.741671832
hsa-mir-452*	chrX	GAGACUG	17624	0.996187033	0.165440293	2.269998701
hsa-mir-483	chr11	AGGAGUG	1388	0.340326293	-0.204006453	2.314685746
hsa-mir-483	chr11	GGAGUGA	1388	-0.215691823	1.267590956	1.267590956
hsa-mir-483	chr11	AGGAGUG	7321	-0.94073507	1.017069816	3.557070572
hsa-mir-483	chr11	GGAGUGA	7321	-1.415502782	-0.690342312	1.681238829
hsa-mir-483	chr11	AGGAGUG	12401	-1.620187722	0.58254922	2.978170671
hsa-mir-483	chr11	GGAGUGA	12401	-0.737521427	9.28E-02	1.121476533
hsa-mir-488	chr1	AUCUGGG	4472	1.877372578	0.479230492	-0.900570031
hsa-mir-488	chr1	UAUCUGG	4472	-3.41E-02	-1.026215044	-2.322316598
hsa-mir-489	chr7	AUGUCAC	2657	0.736818243	0.069605185	-2.163251374
hsa-mir-489	chr7	UGUCACU	2657	-0.577117425	0.730872688	-1.113720029
hsa-mir-490	chr7	CAGGUUG	3587	0.183631333	1.266844284	-0.486510553
hsa-mir-490	chr7	CCAGGUU	3587	-1.111773215	-0.313877408	0.120114195
hsa-mir-491	chr9	CCCCACU	3814	2.347571234	1.372438782	-0.248125768
hsa-mir-491	chr9	UCCCCAC	3814	1.067443774	-1.599225719	1.108320266
hsa-mir-504	chrX	AGGGUCU	16710	0.840622608	-0.203807703	-0.861411973
hsa-mir-504	chrX	CAGGGUC	16710	0.394375423	1.082938587	-0.83537911
hsa-mir-511	chr10	AAAGACA	33	0.774852508	-1.285497267	0.713030775
hsa-mir-511	chr10	AAGACAC	33	0.939965611	1.153952885	1.583975159
hsa-mir-7	chr9	GUCUUCC	1424	-0.348502501	1.526535198	-1.434700282
hsa-mir-7	chr9	UCUUCCA	1424	1.819179394	1.130960433	-2.039475163
hsa-mir-7	chr9	GUCUUCC	15282	0.105004489	2.215788284	-0.502209734
hsa-mir-7	chr9	UCUUCCA	15282	1.077021075	0.306610903	-1.092765929
hsa-mir-9	chr1	ACCAAAG	2756	3.740852639	-1.700874839	1.166617935
hsa-mir-9	chr1	CCAAAGA	2756	2.64695072	-2.718755781	1.604031247
hsa-mir-9*	chr1	AGCUUUA	2756	4.038434533	0.019772424	-3.211644082
hsa-mir-9*	chr1	UAGCUUU	2756	1.521160395	-0.258016033	-1.770038631
hsa-mir-93	chr7	AGCACUU	3161	1.497903519	0.135700221	-0.527458814
hsa-mir-93	chr7	GCACUUU	3161	0.694150075	-0.195232503	1.06825509
hsa-mir-93	chr7	AGCACUU	17069	1.302675811	-1.262315934	-0.773001306
hsa-mir-93	chr7	GCACUUU	17069	0.734359105	-1.22043724	0.856008461

Table S4 Mouse CE analysis result

				CE score		
miRNA	**chr**	**seed match**	**probe**	**top 10% set**	**Mid 10% set**	**bot. 10% set**
mmu-let-7f	chrX	CUACCUC	3698	2.133981335	-0.679091539	-3.196346252
mmu-let-7f	chrX	UACCUCA	3698	1.739624936	-1.15344594	-1.754266614
mmu-mir-101b	chr19	GUACUGU	15550	1.468836017	-0.470033126	-0.77192534
mmu-mir-101b	chr19	UACUGUA	15550	-0.41684731	0.392328445	-0.522222169
mmu-mir-103	chr11	AUGCUGC	11360	0.758818574	0.284730202	1.064599548
mmu-mir-103	chr11	UGCUGCU	11360	2.148309523	-1.973012567	1.786995722
mmu-mir-106b	chr5	CACUUUA	2009	-0.629479365	1.545394025	1.169930273
mmu-mir-106b	chr5	GCACUUU	2009	0.629001852	-0.564723618	1.980320016
mmu-mir-107	chr19	AUGCUGC	6768	-1.740013946	-0.294022458	1.463952718
mmu-mir-107	chr19	UGCUGCU	6768	-0.987412972	-1.242262741	1.360496961
mmu-mir-10b	chr2	CUACAGG	4451	0.277288463	-1.054574202	-1.799514336
mmu-mir-10b	chr2	UACAGGG	4451	0.282631629	-0.154918652	0.299434635
mmu-mir-10b	chr2	CUACAGG	5528	-0.391271342	-0.771496951	-1.799514336
mmu-mir-10b	chr2	UACAGGG	5528	1.37177194	0.651068277	-0.944557417
mmu-mir-128a	chr1	ACUGUGA	7375	3.024138513	-0.604962256	0.435420171
mmu-mir-128a	chr1	CACUGUG	7375	4.138260142	-0.729309148	-1.505769897
mmu-mir-128b	chr9	ACUGUGA	8538	1.741701215	-1.221957969	-0.183218351
mmu-mir-128b	chr9	CACUGUG	8538	3.104755497	-0.58906666	-1.620261428
mmu-mir-130b	chr16	UGCACUG	4241	1.487685383	0.569955	1.833903627
mmu-mir-130b	chr16	UUGCACU	4241	-2.041204907	0.385170704	1.799432312
mmu-mir-130b	chr16	UGCACUG	6417	-0.694525979	1.347216447	1.722626032
mmu-mir-130b	chr16	UUGCACU	6417	-2.170344238	-1.197846017	3.620171081
mmu-mir-130b	chr18	UGCACUG	4241	1.487685383	0.569955	1.833903627
mmu-mir-130b	chr18	UUGCACU	4241	-2.041204907	0.385170704	1.799432312
mmu-mir-130b	chr18	UGCACUG	6417	-0.694525979	1.347216447	1.722626032
mmu-mir-130b	chr18	UUGCACU	6417	-2.170344238	-1.197846017	3.620171081
mmu-mir-140	chr8	AACCACU	8359	1.968133316	0.229594855	-2.819271033
mmu-mir-140	chr8	ACCACUG	8359	1.323914038	-0.219249147	-2.491596584
mmu-mir-148b	chr15	GCACUGA	14669	0.365400902	0.63704002	3.306207999
mmu-mir-148b	chr15	UGCACUG	14669	1.36722146	2.190627804	1.359776557
mmu-mir-149	chr1	AGCCAGA	8992	1.185198851	-1.875587391	-2.109009328
mmu-mir-149	chr1	GAGCCAG	8992	1.534809261	-1.14511397	0.027790775
mmu-mir-151	chr15	AGUCUAG	9001	0.210371989	-0.192947137	1.027393797
mmu-mir-151	chr15	CAGUCUA	9001	0.350227463	-0.621725072	-0.857349929
mmu-mir-152	chr11	GCACUGA	16072	-2.71E-02	-2.269468121	2.462162872
mmu-mir-152	chr11	UGCACUG	16072	0.432487218	-2.275644923	2.332239991
mmu-mir-153	chr12	CUAUGCA	7200	4.203877717	-1.222418798	-2.09959291
mmu-mir-153	chr12	UAUGCAA	7200	0.678763439	-1.705519719	-2.223948217
mmu-mir-15b	chr3	GCUGCUA	2961	-4.19E-02	-1.571319258	1.770993474
mmu-mir-15b	chr3	UGCUGCU	2961	0.766150301	-2.169111727	2.14880026
mmu-mir-16	chr3	GCUGCUA	2961	-4.19E-02	-1.571319258	1.770993474
mmu-mir-16	chr3	UGCUGCU	2961	0.766150301	-2.169111727	2.14880026
mmu-mir-207	chr4	GAGAAGC	1475	-0.636933864	-0.887841957	1.403624095
mmu-mir-207	chr4	GGAGAAG	1475	-1.155038334	-1.467526537	2.124465435
mmu-mir-208	chr14	CGUCUUA	1530	4.095974693	-0.604149335	-0.604149335
mmu-mir-208	chr14	GUCUUAU	1530	0.20081756	-0.26188709	-0.052224045
mmu-mir-208	chr14	CGUCUUA	13277	3.760251548	-0.604149335	-0.604149335

mmu-mir-208	chr14	GUCUUAU	13277	1.621402011	-0.465196709	1.05E-02
mmu-mir-218	chr5	AAGCACA	2813	2.074397758	-0.866841733	-1.709771672
mmu-mir-218	chr5	AGCACAA	2813	0.966153207	1.883723127	-3.325015452
mmu-mir-218	chr5	AAGCACA	5628	5.006299981	-1.523924842	-1.686068326
mmu-mir-218	chr5	AGCACAA	5628	5.210934325	-2.498629043	-0.894911126
mmu-mir-218	chr5	AAGCACA	11976	3.628492681	-0.102865104	-1.310200987
mmu-mir-218	chr5	AGCACAA	11976	4.810508326	-0.562510492	-2.468090004
mmu-mir-224	chrX	GUGACUU	3923	-2.825566734	-0.946524501	1.791210248
mmu-mir-224	chrX	UGACUUA	3923	-0.886359981	-1.937024479	1.404307513
mmu-mir-25	chr5	GUGCAAU	2009	-1.727344324	-0.753665445	-0.149936338
mmu-mir-25	chr5	UGCAAUG	2009	-1.160455636	0.427668108	0.418236377
mmu-mir-26a	chr9	ACUUGAA	14735	1.680839011	-0.84848527	-2.571214012
mmu-mir-26a	chr9	UACUUGA	14735	1.122812125	-0.232014466	-3.237892447
mmu-mir-26b	chr1	ACUUGAA	12209	1.59468198	-0.158906119	0.983094382
mmu-mir-26b	chr1	UACUUGA	12209	1.117832162	0.786506172	0.832013137
mmu-mir-28	chr16	AGCUCCU	1024	-1.465639731	-0.655384012	0.799269712
mmu-mir-28	chr16	GCUCCUU	1024	-0.268504126	1.660713725	-0.422832153
mmu-mir-301	chr11	UGCACUG	14038	1.128984544	1.184692961	-0.856459077
mmu-mir-301	chr11	UUGCACU	14038	0.291462937	-1.174126548	0.160429224
mmu-mir-30c	chr4	GUUUACA	10024	1.715307342	-1.02820206	0.667938692
mmu-mir-30c	chr4	UGUUUAC	10024	2.27910956	-0.260486256	-0.674577103
mmu-mir-30c	chr4	GUUUACA	10221	0.345922742	-1.662317083	3.334969675
mmu-mir-30c	chr4	UGUUUAC	10221	2.657293728	-2.154549433	0.565801196
mmu-mir-30e	chr4	GUUUACA	10024	1.715307342	-1.02820206	0.667938692
mmu-mir-30e	chr4	UGUUUAC	10024	2.27910956	-0.260486256	-0.674577103
mmu-mir-30e	chr4	GUUUACA	10221	0.345922742	-1.662317083	3.334969675
mmu-mir-30e	chr4	UGUUUAC	10221	2.657293728	-2.154549433	0.565801196
mmu-mir-32	chr4	GUGCAAU	10401	-0.915431714	7.18E-02	-1.52894058
mmu-mir-32	chr4	UGCAAUA	10401	-2.00585798	0.203847848	1.030180914
mmu-mir-326	chr7	CCAGAGG	4674	1.957009489	-0.290828546	-1.748786848
mmu-mir-326	chr7	CCCAGAG	4674	1.579911829	-0.502432942	2.434329379
mmu-mir-335	chr6	CUCUUGA	9548	1.690046699	0.312014257	-0.243595633
mmu-mir-335	chr6	GCUCUUG	9548	0.056262489	0.162306147	-0.289496718
mmu-mir-338	chr11	AUGCUGG	14026	0.708943541	0.138291425	0.826249892
mmu-mir-338	chr11	UGCUGGA	14026	2.842158744	-1.437626589	-1.045174159
mmu-mir-339	chr5	ACAGGGA	4764	1.602229576	-0.868729767	1.850879572
mmu-mir-339	chr5	GACAGGG	4764	1.130614568	-1.342942914	-0.998196226
mmu-mir-342	chr12	GUGUGAG	9770	1.153558555	-1.508131469	2.007232326
mmu-mir-342	chr12	UGUGAGA	9770	0.884381942	-6.58E-02	8.63E-03
mmu-mir-346	chr14	GCAGACA	12224	1.992015326	0.845778381	-0.717847786
mmu-mir-346	chr14	GGCAGAC	12224	1.002964509	1.522842514	-0.378926303
mmu-mir-361	chrX	CUGAUAA	11365	1.934198686	-0.626388389	0.201733899
mmu-mir-361	chrX	UCUGAUA	11365	3.944284032	-1.873657259	-0.506575734
mmu-mir-378	chr18	GUCAGGA	14615	-0.05710494	9.25E-02	-0.583578307
mmu-mir-378	chr18	UCAGGAG	14615	-0.150707689	0.822874892	-0.667928897
mmu-mir-448	chrX	AUAUGCA	2695	0.602381392	-0.039544079	-1.511652012
mmu-mir-448	chrX	UAUGCAA	2695	1.411550372	-0.467390483	-1.594972466
mmu-mir-452	chrX	GCAAACA	3923	-9.90E-03	0.9197392	1.577028484
mmu-mir-452	chrX	UGCAAAC	3923	-0.399633631	-0.085923497	0.376422878
mmu-mir-483	chr7	AGGAGUG	6648	0.687118922	-0.017227769	-0.972140369

mmu-mir-483	chr7	GGAGUGA	6648	-0.882866472	5.58E-02	-0.50927937
mmu-mir-7	chr13	GUCUUCC	15144	2.487877797	1.408531992	-1.049148255
mmu-mir-7	chr13	UCUUCCA	15144	3.425666751	-0.846316617	-0.94722807
mmu-mir-93	chr5	CACUUUG	2009	1.554623114	-0.980944058	-0.103330085
mmu-mir-93	chr5	GCACUUU	2009	0.629001852	-0.564723618	1.980320016
mmu-mir-98	chrX	CUACCUC	3698	2.133981335	-0.679091539	-3.196346252
mmu-mir-98	chrX	UACCUCA	3698	1.739624936	-1.15344594	-1.754266614

Table S5 MDEV CE analysis result

				CE score		
miRNA	**Chr**	**seed match**	**probe**	**top 10% set**	**mid 10% set**	**bot. 10% set**
Mmu-mir-101b	chr19	GUACUGU	1046	-1.893237318	0.629846501	1.235449784
mmu-mir-101b	chr19	UACUGUA	1046	-1.302507466	-0.638618808	2.354354201
mmu-mir-103	chr11	AUGCUGC	9867	2.297403658	-2.404465235	-1.476170264
mmu-mir-103	chr11	UGCUGCU	9867	3.102713398	-1.894411762	-1.612614581
mmu-mir-103	chr11	AUGCUGC	12510	3.516686678	0.351469463	-2.064926714
mmu-mir-103	chr11	UGCUGCU	12510	2.036127714	-0.77835592	-3.033209152
mmu-mir-106b	chr5	CACUUUA	350	1.416736946	-0.516025979	0.676932759
mmu-mir-106b	chr5	GCACUUU	350	1.12391263	-0.19098518	1.918767402
mmu-mir-106b	chr5	CACUUUA	351	1.364203965	0.363924698	6.21E-02
mmu-mir-106b	chr5	GCACUUU	351	0.676813758	0.479737282	1.258476368
mmu-mir-106b	chr5	CACUUUA	14088	1.269484056	-1.729717517	-1.305846936
mmu-mir-106b	chr5	GCACUUU	14088	0.937770196	-0.567473014	1.302317357
mmu-mir-106b	chr5	CACUUUA	14408	1.100638794	-0.35077975	-0.324554232
mmu-mir-106b	chr5	GCACUUU	14408	0.70667383	-1.885180435	1.732990603
mmu-mir-107	chr19	AUGCUGC	2995	1.804930507	-1.075201242	-0.689526229
mmu-mir-107	chr19	UGCUGCU	2995	2.419043695	-0.132895273	-0.984128653
mmu-mir-107	chr19	AUGCUGC	12000	3.360061406	-1.837540169	-2.90108185
mmu-mir-107	chr19	UGCUGCU	12000	3.51634792	0.335803863	-1.673370853
mmu-mir-10b	chr2	CUACAGG	16564	-0.469465565	0.317977649	0.819077877
mmu-mir-10b	chr2	UACAGGG	16564	0.152664666	1.011622264	-1.197125847
mmu-mir-126-5p	chr2	AAUAAUG	5240	-0.028795859	-1.755525809	0.570933876
mmu-mir-126-5p	chr2	UAAUAAU	5240	-1.580970093	4.77E-02	6.01E-02
mmu-mir-126-5p	chr2	AAUAAUG	17737	-0.504811301	-1.37858476	-0.132212521
mmu-mir-126-5p	chr2	UAAUAAU	17737	-1.163242567	1.17061809	1.004962212
mmu-mir-126-5p	chr2	AAUAAUG	17738	-1.600787632	0.64330071	-3.53E-02
mmu-mir-126-5p	chr2	UAAUAAU	17738	-0.788233916	-0.473359228	0.58942191
mmu-mir-128a	chr1	ACUGUGA	12602	-0.439992027	-0.84397336	-1.230475676
mmu-mir-128a	chr1	CACUGUG	12602	-0.243260735	-0.21059224	-3.441060962
mmu-mir-128b	chr9	ACUGUGA	3304	-0.930662266	1.805848939	1.399887305
mmu-mir-128b	chr9	CACUGUG	3304	-0.600782188	9.47E-02	-1.309376667
mmu-mir-128b	chr9	ACUGUGA	17596	-0.827869097	0.460471955	1.755745305
mmu-mir-128b	chr9	CACUGUG	17596	-0.242351565	-3.42E-02	0.736289109
mmu-mir-139	chr7	ACUGUAG	18435	1.125450144	1.283057311	1.5057603
mmu-mir-139	chr7	CUGUAGA	18435	0.854498749	0.259037306	0.675072884
mmu-mir-140	chr8	AACCACU	14657	-0.043746814	-0.588113598	1.264605627
mmu-mir-140	chr8	ACCACUG	14657	-1.56371621	-0.599650932	0.421269478
mmu-mir-140	chr8	AACCACU	14658	-0.269864247	0.82540137	-2.128933518
mmu-mir-140	chr8	ACCACUG	14658	0.475652648	0.421269478	-1.14657258
mmu-mir-148b	chr15	GCACUGA	18093	-0.512735698	-1.039320111	6.05E-02
mmu-mir-148b	chr15	UGCACUG	18093	-0.768534299	-0.999714142	0.596068938
mmu-mir-149	chr1	AGCCAGA	1696	0.41443586	1.105721562	-1.156347375
mmu-mir-149	chr1	GAGCCAG	1696	0.458776911	9.61E-02	-2.760832251
mmu-mir-152	chr11	GCACUGA	2744	0.861242837	1.660255015	0.643902678
mmu-mir-152	chr11	UGCACUG	2744	-0.859937522	2.942808761	-0.15665893
mmu-mir-153	chr12	CUAUGCA	9390	-1.261709681	0.811762954	0.652437946
mmu-mir-153	chr12	UAUGCAA	9390	-1.584515543	-0.57055206	0.367904032
mmu-mir-15b	chr3	GCUGCUA	10749	0.41403527	-0.453947374	1.433672875

mmu-mir-15b	chr3	UGCUGCU	10749	2.30565128	-0.318796815	-0.698986437
mmu-mir-15b	chr3	GCUGCUA	10750	0.321068312	1.04198282	0.447284323
mmu-mir-15b	chr3	UGCUGCU	10750	0.410453364	-0.417321565	-0.206618773
mmu-mir-15b	chr3	GCUGCUA	18431	-0.095783532	0.592852313	0.668944672
mmu-mir-15b	chr3	UGCUGCU	18431	1.864416512	-0.12378576	-0.863961576
mmu-mir-16	chr3	GCUGCUA	10749	0.41403527	-0.453947374	1.433672875
mmu-mir-16	chr3	UGCUGCU	10749	2.30565128	-0.318796815	-0.698986437
mmu-mir-16	chr3	GCUGCUA	10750	0.321068312	1.04198282	0.447284323
mmu-mir-16	chr3	UGCUGCU	10750	0.410453364	-0.417321565	-0.206618773
mmu-mir-16	chr3	GCUGCUA	18431	-0.095783532	0.592852313	0.668944672
mmu-mir-16	chr3	UGCUGCU	18431	1.864416512	-0.12378576	-0.863961576
mmu-mir-186	chr3	AUUCUUU	19231	2.95780647	-0.118169548	-2.509977302
mmu-mir-186	chr3	UUCUUUG	19231	3.176445699	-1.740280562	-1.365463039
mmu-mir-207	chr4	GAGAAGC	607	-6.17E-02	-0.982088924	0.358869678
mmu-mir-207	chr4	GGAGAAG	607	0.563609962	0.673207589	1.027101861
mmu-mir-207	chr4	GAGAAGC	20038	1.623189828	-1.157396111	-0.48782005
mmu-mir-207	chr4	GGAGAAG	20038	0.208838386	-1.603030738	0.918089786
mmu-mir-208	chr14	CGUCUUA	2033	2.648111644	-0.744572843	-0.744572843
mmu-mir-208	chr14	GUCUUAU	2033	-1.379820815	1.225565645	0.733986725
mmu-mir-208	chr14	CGUCUUA	15059	0.709434794	-0.744572843	-0.744572843
mmu-mir-208	chr14	GUCUUAU	15059	-0.525913437	0.92762173	0.775028927
mmu-mir-208	chr14	CGUCUUA	15326	2.163442431	-0.744572843	-0.744572843
mmu-mir-208	chr14	GUCUUAU	15326	-1.445330213	1.338819179	2.426579872
mmu-mir-218	chr5	AAGCACA	8429	4.79E-02	-1.531480009	0.823149755
mmu-mir-218	chr5	AGCACAA	8429	0.919803956	-0.150543518	1.732072723
mmu-mir-218	chr5	AAGCACA	17740	-1.26E-02	0.314890724	1.86763686
mmu-mir-218	chr5	AGCACAA	17740	1.833414385	-1.181500031	1.414228423
mmu-mir-224	chrX	GUGACUU	5524	-0.594505484	0.419372508	1.388227882
mmu-mir-224	chrX	UGACUUA	5524	-0.25961507	0.297916464	1.9302449
mmu-mir-25	chr5	GUGCAAU	350	1.298912705	-0.376095572	0.776560852
mmu-mir-25	chr5	UGCAAUG	350	2.478519602	-1.847693439	-0.389539849
mmu-mir-25	chr5	GUGCAAU	351	1.091837506	-1.828550303	1.009474263
mmu-mir-25	chr5	UGCAAUG	351	2.313251983	-1.261476287	-2.50E-02
mmu-mir-25	chr5	GUGCAAU	14088	0.242369022	-1.245265448	0.354036241
mmu-mir-25	chr5	UGCAAUG	14088	2.512746623	-0.784456447	-1.39086684
mmu-mir-25	chr5	GUGCAAU	14408	0.217085879	-2.06542016	0.593323138
mmu-mir-25	chr5	UGCAAUG	14408	1.381808702	2.280002877	-0.28017833
mmu-mir-26a	chr9	ACUUGAA	6363	-0.281706667	-0.185270229	-0.100025545
mmu-mir-26a	chr9	UACUUGA	6363	1.172565623	-0.406060912	1.840941151
mmu-mir-26b	chr1	ACUUGAA	18303	1.414195349	-2.031443551	1.525697826
mmu-mir-26b	chr1	UACUUGA	18303	0.629304726	-2.49278239	1.449151808
mmu-mir-301	chr11	UGCACUG	7279	0.40287486	-0.378798545	-1.184938964
mmu-mir-301	chr11	UUGCACU	7279	-0.870917957	0.694392025	-1.439864261
mmu-mir-30c	chr4	GUUUACA	15463	-1.386243274	0.433118484	-2.334837922
mmu-mir-30c	chr4	UGUUUAC	15463	0.796759112	0.603173679	-1.43747591
mmu-mir-30e	chr4	GUUUACA	15463	-1.386243274	0.433118484	-2.334837922
mmu-mir-30e	chr4	UGUUUAC	15463	0.796759112	0.603173679	-1.43747591
mmu-mir-32	chr4	GUGCAAU	19397	1.340034021	-0.902219967	9.75E-02
mmu-mir-32	chr4	UGCAAUA	19397	2.21372418	0.341041805	-1.789623874
mmu-mir-326	chr7	CCAGAGG	20278	0.548512167	-0.181500855	-0.422447712

mmu-mir-326	chr7	CCCAGAG	20278	2.444824217	-0.280995662	-0.998895929
mmu-mir-33	chr15	AAUGCAC	10329	-1.872933377	-2.123281709	1.179654512
mmu-mir-33	chr15	CAAUGCA	10329	-0.385578979	-0.81556442	-0.167424601
mmu-mir-33	chr15	AAUGCAC	18413	4.20E-02	0.40205742	-0.887766329
mmu-mir-33	chr15	CAAUGCA	18413	-0.21936612	-0.500289263	-0.797057156
mmu-mir-335	chr6	CUCUUGA	7136	0.844476911	-9.11E-02	-0.395344321
mmu-mir-335	chr6	GCUCUUG	7136	-0.700126374	1.017987226	-1.595928956
mmu-mir-338	chr11	AUGCUGG	1249	0.523695749	-0.980743029	-0.867325631
mmu-mir-338	chr11	UGCUGGA	1249	9.73E-02	0.151779084	-1.202110595
mmu-mir-340	chr11	AGACGGA	11706	-0.604713987	3.882187471	-0.604713987
mmu-mir-340	chr11	GAGACGG	11706	-0.361754495	-0.361754495	-0.361754495
mmu-mir-342	chr12	GUGUGAG	12968	-0.535250571	0.910325735	2.83370329
mmu-mir-342	chr12	UGUGAGA	12968	0.50997243	1.047791633	-1.39684111
mmu-mir-342	chr12	GUGUGAG	16466	-1.063991088	-8.68E-02	3.583932512
mmu-mir-342	chr12	UGUGAGA	16466	0.574709927	-0.527850564	-0.535507891
mmu-mir-346	chr14	GCAGACA	5468	-0.490702254	0.265579583	0.555921033
mmu-mir-346	chr14	GGCAGAC	5468	-0.761963129	-0.628602271	0.792411736
mmu-mir-361	chrX	CUGAUAA	15214	9.44E-02	-0.326945044	0.535843729
mmu-mir-361	chrX	UCUGAUA	15214	0.941053439	0.020863943	0.88014881
mmu-mir-378	chr18	GUCAGGA	16312	1.790080738	-0.444859241	2.457448349
mmu-mir-378	chr18	UCAGGAG	16312	2.312802445	-1.324522588	0.681753891
mmu-mir-448	chrX	AUAUGCA	16820	-1.831465059	1.808033974	-2.106369748
mmu-mir-448	chrX	UAUGCAA	16820	-0.285489458	-0.249856633	-0.333237444
mmu-mir-452	chrX	GCAAACA	5524	-0.027973292	-0.263660199	0.955322624
mmu-mir-452	chrX	UGCAAAC	5524	-1.319775712	0.639263273	0.891217238
mmu-mir-483	chr7	AGGAGUG	251	-0.772159211	1.648589539	-0.788216743
mmu-mir-483	chr7	GGAGUGA	251	-0.546127669	-0.776461641	-1.928131503
mmu-mir-483	chr7	AGGAGUG	14664	0.944960784	-1.197288962	-0.72160772
mmu-mir-483	chr7	GGAGUGA	14664	-1.237129586	-0.350844519	0.412358861
mmu-mir-7	chr13	GUCUUCC	7515	2.646759526	-1.323290917	-1.323290917
mmu-mir-7	chr13	UCUUCCA	7515	3.101139208	-0.441076352	-5.21E-02
mmu-mir-7	chr13	GUCUUCC	14688	3.533916709	-0.326328768	-1.8177193
mmu-mir-7	chr13	UCUUCCA	14688	3.133106444	-0.505821372	-2.590706934
mmu-mir-7	chr13	GUCUUCC	20300	3.749178046	-0.105328654	-0.98092673
mmu-mir-7	chr13	UCUUCCA	20300	3.335188628	-0.511096892	-1.573263311
mmu-mir-93	chr5	CACUUUG	350	0.928715533	-0.937262893	0.525684689
mmu-mir-93	chr5	GCACUUU	350	1.12391263	-0.19098518	1.918767402
mmu-mir-93	chr5	CACUUUG	351	0.801153063	-0.354174517	0.21054887
mmu-mir-93	chr5	GCACUUU	351	0.676813758	0.479737282	1.258476368
mmu-mir-93	chr5	CACUUUG	14088	1.314567733	-1.461354902	8.78E-02
mmu-mir-93	chr5	GCACUUU	14088	0.937770196	-0.567473014	1.302317357
mmu-mir-93	chr5	CACUUUG	14408	0.451790773	4.75E-02	1.558317239
mmu-mir-93	chr5	GCACUUU	14408	0.70667383	-1.885180435	1.732990603

Table S6 NCELL CE analysis result

					CE score	
miRNA	**chr**	**seed match**	**probe**	**top 10% set**	**mid 10% set**	**bot. 10% set**
mmu-mir-101b	chr19	GUACUGU	1046	0.106119653	0.729092524	-0.991032873
mmu-mir-101b	chr19	UACUGUA	1046	-0.681207892	2.839489695	-1.359507427
mmu-mir-103	chr11	AUGCUGC	9867	0.755620731	-1.298341785	-1.289859834
mmu-mir-103	chr11	UGCUGCU	9867	1.320072049	-0.768834782	-1.757576914
mmu-mir-103	chr11	AUGCUGC	12510	2.845365616	-0.719268963	1.342372128
mmu-mir-103	chr11	UGCUGCU	12510	1.446110158	0.722674328	-1.420752671
mmu-mir-106b	chr5	CACUUUA	350	1.478846194	-0.138501496	-2.155844729
mmu-mir-106b	chr5	GCACUUU	350	3.064747706	-0.521932412	-3.872566107
mmu-mir-106b	chr5	CACUUUA	14088	-0.142695308	1.253172966	-2.289009483
mmu-mir-106b	chr5	GCACUUU	14088	-0.379973144	-0.301269495	-2.963304688
mmu-mir-106b	chr5	CACUUUA	14408	0.218241823	0.676932759	-0.145916641
mmu-mir-106b	chr5	GCACUUU	14408	-0.643438409	1.28550566	-1.140135219
mmu-mir-107	chr19	AUGCUGC	2995	-6.63E-02	1.007443828	1.17730495
mmu-mir-107	chr19	UGCUGCU	2995	0.284224532	-1.01977143	0.196003694
mmu-mir-107	chr19	AUGCUGC	12000	-9.03E-02	0.222980852	0.480354643
mmu-mir-107	chr19	UGCUGCU	12000	-0.273897121	1.054291865	1.216334692
mmu-mir-10b	chr2	CUACAGG	16564	-1.133260671	-1.050699091	-0.672291847
mmu-mir-10b	chr2	UACAGGG	16564	-0.921032333	0.370372813	-1.730271943
mmu-mir-128a	chr1	ACUGUGA	12602	2.390187654	-2.718985914	1.399887305
mmu-mir-128a	chr1	CACUGUG	12602	1.219386075	-1.278724998	0.925572611
mmu-mir-128b	chr9	ACUGUGA	3304	0.986544551	-1.250897748	1.26126626
mmu-mir-128b	chr9	CACUGUG	3304	0.581308026	-0.969542939	0.95271655
mmu-mir-128b	chr9	ACUGUGA	17596	2.045735359	0.199369747	0.34703312
mmu-mir-128b	chr9	CACUGUG	17596	1.423248595	-1.223581324	1.409099079
mmu-mir-139	chr7	ACUGUAG	18435	0.323607405	0.829083679	0.59958038
mmu-mir-139	chr7	CUGUAGA	18435	1.887456199	-0.238877615	6.42E-02
mmu-mir-140	chr8	AACCACU	14657	0.22220851	-1.096117256	-1.536252031
mmu-mir-140	chr8	ACCACUG	14657	-0.297901057	0.700278783	-0.9362181
mmu-mir-140	chr8	AACCACU	19938	-0.340685934	-0.162808209	-0.162808209
mmu-mir-140	chr8	ACCACUG	19938	-1.72566609	-0.49547538	-0.69476774
mmu-mir-148b	chr15	GCACUGA	18093	1.699866987	-0.66287414	-1.205915348
mmu-mir-148b	chr15	UGCACUG	18093	0.442035822	0.551193148	-3.393388761
mmu-mir-149	chr1	AGCCAGA	1696	1.667739993	0.574988838	0.841095542
mmu-mir-149	chr1	GAGCCAG	1696	1.505519059	-0.41814038	0.131526459
mmu-mir-152	chr11	GCACUGA	2744	-0.558067405	-1.250358003	0.123918773
mmu-mir-152	chr11	UGCACUG	2744	-0.251113199	-0.525825803	0.113083744
mmu-mir-153	chr12	CUAUGCA	9390	0.193085325	0.493545299	0.500354984
mmu-mir-153	chr12	UAUGCAA	9390	2.101909834	1.724952051	-0.285489458
mmu-mir-186	chr3	AUUCUUU	19231	2.853181435	-0.48004908	-0.198065029
mmu-mir-186	chr3	UUCUUUG	19231	2.710691015	-0.850820124	-3.202181112
mmu-mir-208	chr14	CGUCUUA	15058	1.398175254	1.291037849	-0.744572843
mmu-mir-208	chr14	GUCUUAU	15058	1.787607439	0.1618833	-0.804450541
mmu-mir-208	chr14	CGUCUUA	15059	1.291037849	-0.744572843	-0.744572843
mmu-mir-208	chr14	GUCUUAU	15059	2.261328381	0.557461124	-1.228030748
mmu-mir-218	chr5	AAGCACA	8429	-2.011712852	-0.293819588	1.538811078
mmu-mir-218	chr5	AGCACAA	8429	-0.36569966	7.93E-02	0.789253675
mmu-mir-218	chr5	AAGCACA	17740	1.011061495	-8.77E-02	0.167983895

mmu-mir-218	chr5	AGCACAA	17740	0.128271207	-1.764214582	1.53783454
mmu-mir-224	chrX	GUGACUU	5524	0.110068351	0.27253114	-1.500053939
mmu-mir-224	chrX	UGACUUA	5524	0.487757865	0.777161073	-1.503191272
mmu-mir-25	chr5	GUGCAAU	350	1.331124403	-0.131788671	-0.057369301
mmu-mir-25	chr5	UGCAAUG	350	3.026947923	-0.93277354	-0.978409568
mmu-mir-25	chr5	GUGCAAU	14088	-0.057369301	1.091837506	-0.861165843
mmu-mir-25	chr5	UGCAAUG	14088	-2.618195052	-0.120932609	-2.225251065
mmu-mir-25	chr5	GUGCAAU	14408	-1.600140083	2.462379993	-1.166948287
mmu-mir-25	chr5	UGCAAUG	14408	-2.476896701	1.016536827	5.60E-02
mmu-mir-26a	chr9	ACUUGAA	6363	-0.181659292	0.45886344	0.463237727
mmu-mir-26a	chr9	UACUUGA	6363	-0.341509553	1.271374748	3.423217912
mmu-mir-26b	chr1	ACUUGAA	18303	0.160293674	0.47986946	-1.318707465
mmu-mir-26b	chr1	UACUUGA	18303	-0.929942465	1.460851422	2.022812043
mmu-mir-30c	chr4	GUUUACA	15463	2.107439019	-4.06E-02	-0.19323822
mmu-mir-30c	chr4	UGUUUAC	15463	1.599676545	-1.483466909	-0.210634926
mmu-mir-30e	chr4	GUUUACA	15463	2.107439019	-4.06E-02	-0.19323822
mmu-mir-30e	chr4	UGUUUAC	15463	1.599676545	-1.483466909	-0.210634926
mmu-mir-32	chr4	GUGCAAU	19397	-0.325677263	-0.300564695	0.834464972
mmu-mir-32	chr4	UGCAAUA	19397	3.080759454	-1.077089308	-0.548916832
mmu-mir-326	chr7	CCAGAGG	20278	0.935384282	0.633181148	2.653191013
mmu-mir-326	chr7	CCCAGAG	20278	0.369708533	-0.468805403	-0.245883406
mmu-mir-33	chr15	AAUGCAC	10329	-1.394125091	-1.736334584	0.356800446
mmu-mir-33	chr15	CAAUGCA	10329	-0.332693069	-2.218624572	-0.416197138
mmu-mir-33	chr15	AAUGCAC	18413	0.300229229	2.268400974	-0.805835601
mmu-mir-33	chr15	CAAUGCA	18413	-0.269229978	0.752245817	-0.416197138
mmu-mir-335	chr6	CUCUUGA	7136	-1.039027321	-0.111763699	1.201094697
mmu-mir-335	chr6	GCUCUUG	7136	0.33349199	-1.785947685	0.538749537
mmu-mir-338	chr11	AUGCUGG	1249	-2.027954634	-0.188610694	1.387795522
mmu-mir-338	chr11	UGCUGGA	1249	-0.633123666	-0.480919662	0.743960177
mmu-mir-340	chr11	AGACGGA	11706	-0.604713987	0.770304202	-0.604713987
mmu-mir-340	chr11	GAGACGG	11706	-0.361754495	-0.361754495	2.231412877
mmu-mir-342	chr12	GUGUGAG	12968	0.304710294	-0.34648277	3.260978808
mmu-mir-342	chr12	UGUGAGA	12968	1.047791633	0.1784718	0.397203887
mmu-mir-342	chr12	GUGUGAG	16466	-0.61446563	-0.886304359	1.089834606
mmu-mir-342	chr12	UGUGAGA	16466	-9.05E-02	1.019780217	-1.312319233
mmu-mir-346	chr14	GCAGACA	5468	-0.168517672	0.105451874	-0.448503442
mmu-mir-346	chr14	GGCAGAC	5468	-2.04E-02	-0.68202385	2.062936018
mmu-mir-361	chrX	CUGAUAA	15214	1.498662651	-0.432446997	-0.64644488
mmu-mir-361	chrX	UCUGAUA	15214	1.179596567	-1.098225132	-0.369720087
mmu-mir-378	chr18	GUCAGGA	16312	-0.582025228	1.267737242	0.275262191
mmu-mir-378	chr18	UCAGGAG	16312	-1.335520069	0.172051218	1.474063987
mmu-mir-448	chrX	AUAUGCA	16820	-0.623163055	-0.858952773	0.148645526
mmu-mir-448	chrX	UAUGCAA	16820	-0.913752429	0.826449938	0.826449938
mmu-mir-452	chrX	GCAAACA	5524	-1.832425903	-0.590989502	0.709498645
mmu-mir-452	chrX	UGCAAAC	5524	-0.579346746	-1.217777078	1.136387827
mmu-mir-7	chr13	GUCUUCC	7515	2.157684666	-1.192987018	-1.090284438
mmu-mir-7	chr13	UCUUCCA	7515	2.485215586	-1.654012805	-0.168774251
mmu-mir-7	chr13	GUCUUCC	14688	2.190446789	-1.557540097	-1.486508016
mmu-mir-7	chr13	UCUUCCA	14688	2.666085117	-1.641428468	-0.285842135
mmu-mir-7	chr13	GUCUUCC	20300	4.614843901	-1.826253123	-0.721165263

mmu-mir-7	chr13	UCUUCCA	20300	3.009935984	-1.934229592	-1.350298291
mmu-mir-93	chr5	CACUUUG	350	3.320035868	-0.66819524	-2.372439361
mmu-mir-93	chr5	GCACUUU	350	3.064747706	-0.521932412	-3.872566107
mmu-mir-93	chr5	CACUUUG	14088	-1.057775537	-0.692706662	-6.96E-02
mmu-mir-93	chr5	GCACUUU	14088	-0.379973144	-0.301269495	-2.963304688
mmu-mir-93	chr5	CACUUUG	14408	-0.730599995	-0.460179393	0.819811454
mmu-mir-93	chr5	GCACUUU	14408	-0.643438409	1.28550566	-1.140135219

Linked Excel Tables

Table S7 Mappings between probe IDs and RefSeq genes in human atlas
Table S8 Mappings between probe IDs and RefSeq genes in mouse atlas
Table S9 Mappings between probe IDs and RefSeq genes in MDEV/NCELL
Table S10 & S11 Predicted targets in the top-10 or bottom-10 percentile sets of biased embedded miRNAs in human. If a miRNA is Type-I (-II) biased, predicted targets in its top-10 (bottom-10) percentile set is reported.

References

Enright, A. J., John, B., Gaul, U., Tuschl, T., Sander, C., and Marks, D. S. (2003). MicroRNA targets in Drosophila. Genome Biol *5*, R1.