Supporting Information

Chang *et al.* 10.1073/pnas.0809151105

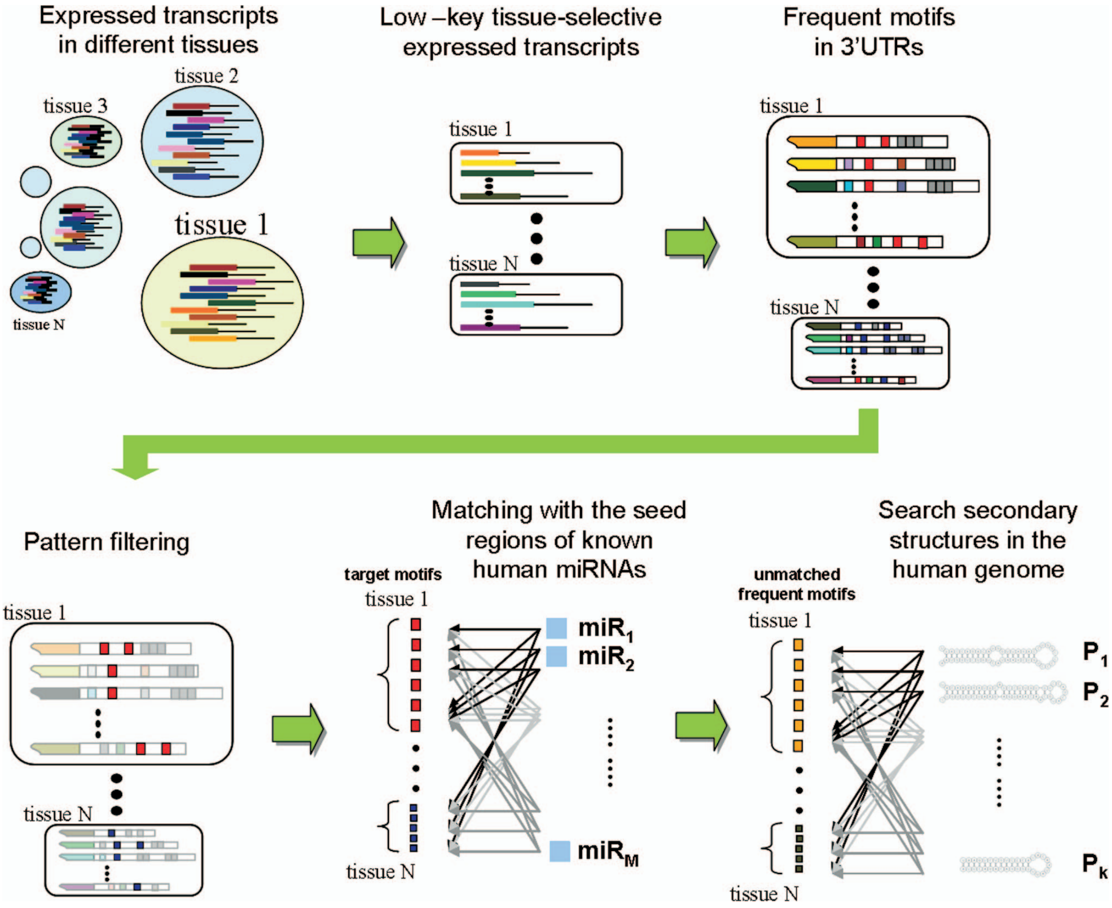


Fig. S1. Flowchart of the proposed method.

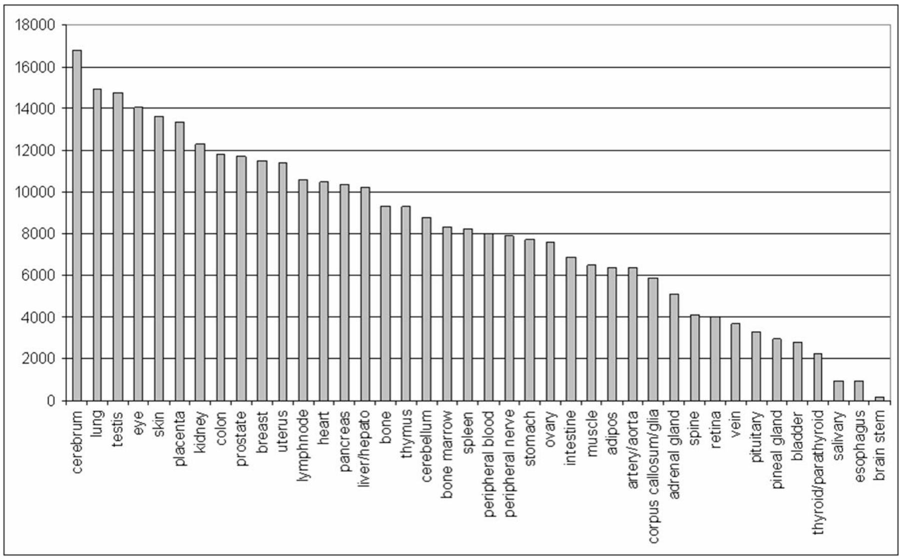


Fig. S2. Distribution of 18,021 human Ensemble genes in 40 tissues from BodyMap-Xs database.

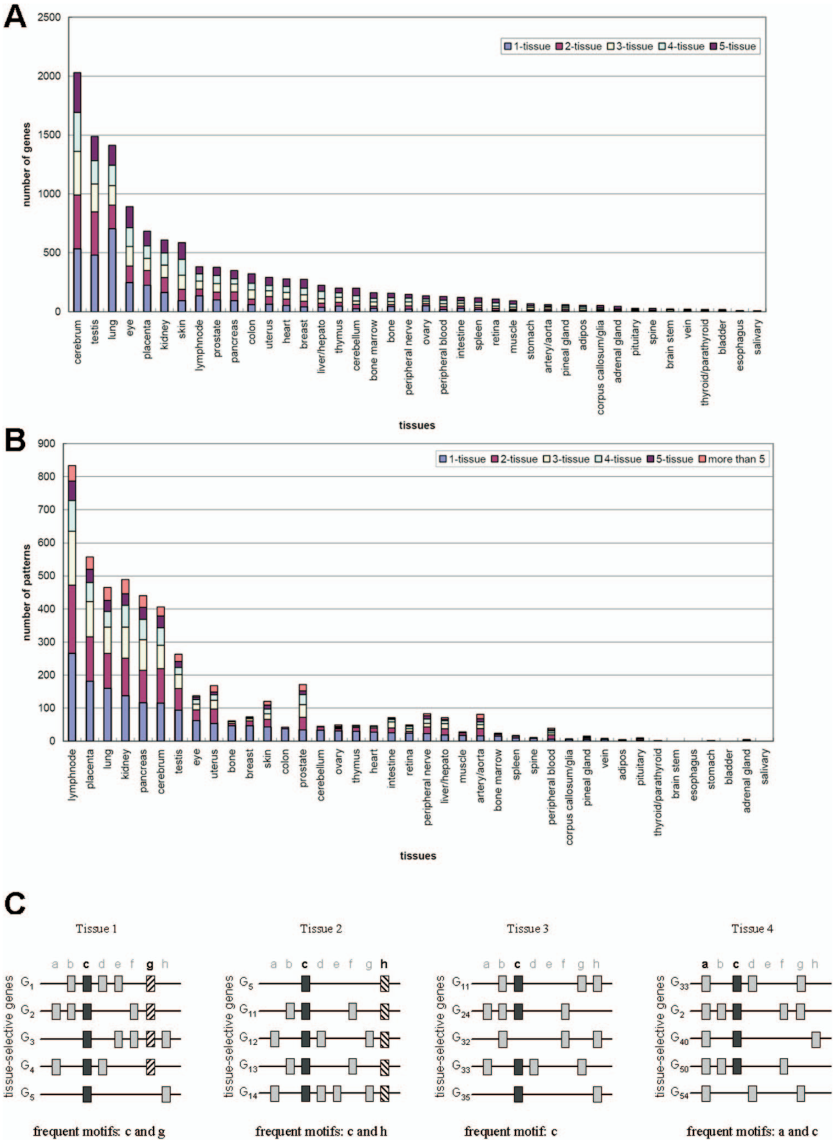


Fig. S3. (*A*) Distribution of low-key tissue-selective genes in 40 tissues. (*B*) Distribution of frequent tissue-selective motifs in 40 tissues. For an explanation of why the tissue number of a frequent motif may appear in more than five tissues, see *C*. (*C*) An example to show that the number of tissues in which a frequent motif appears can be higher than the total number of tissues in which the tissue-selective genes are expressed. In this example, each tissue-selective gene is expressed in ≤2 tissues but motif *c* can be found in 4 tissues. Note that tissue-selective motifs cannot be present in many tissues because we have used a statistical approach to exclude those motifs that appear in many tissues.

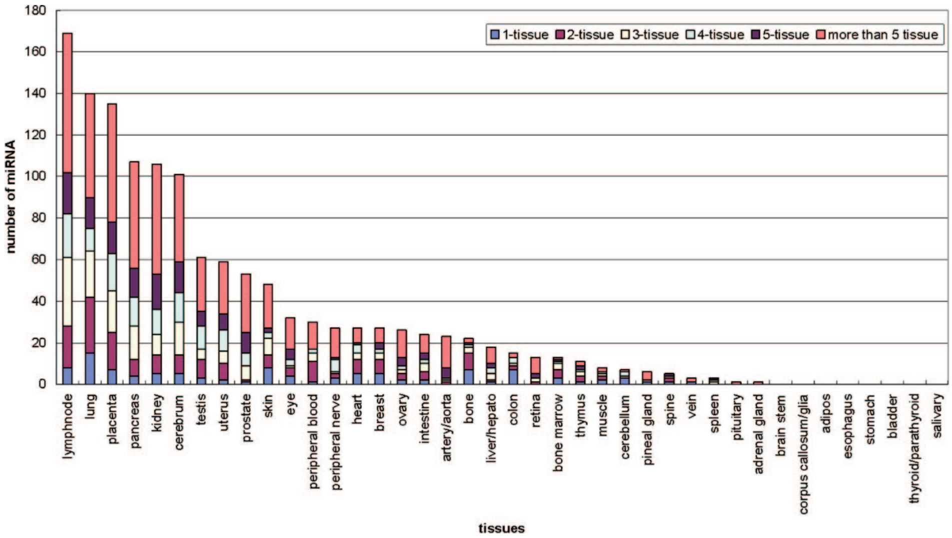


Fig. S4. Distribution of the known miRNAs whose seed regions match our predicted tissue-selective motifs in 40 tissues.

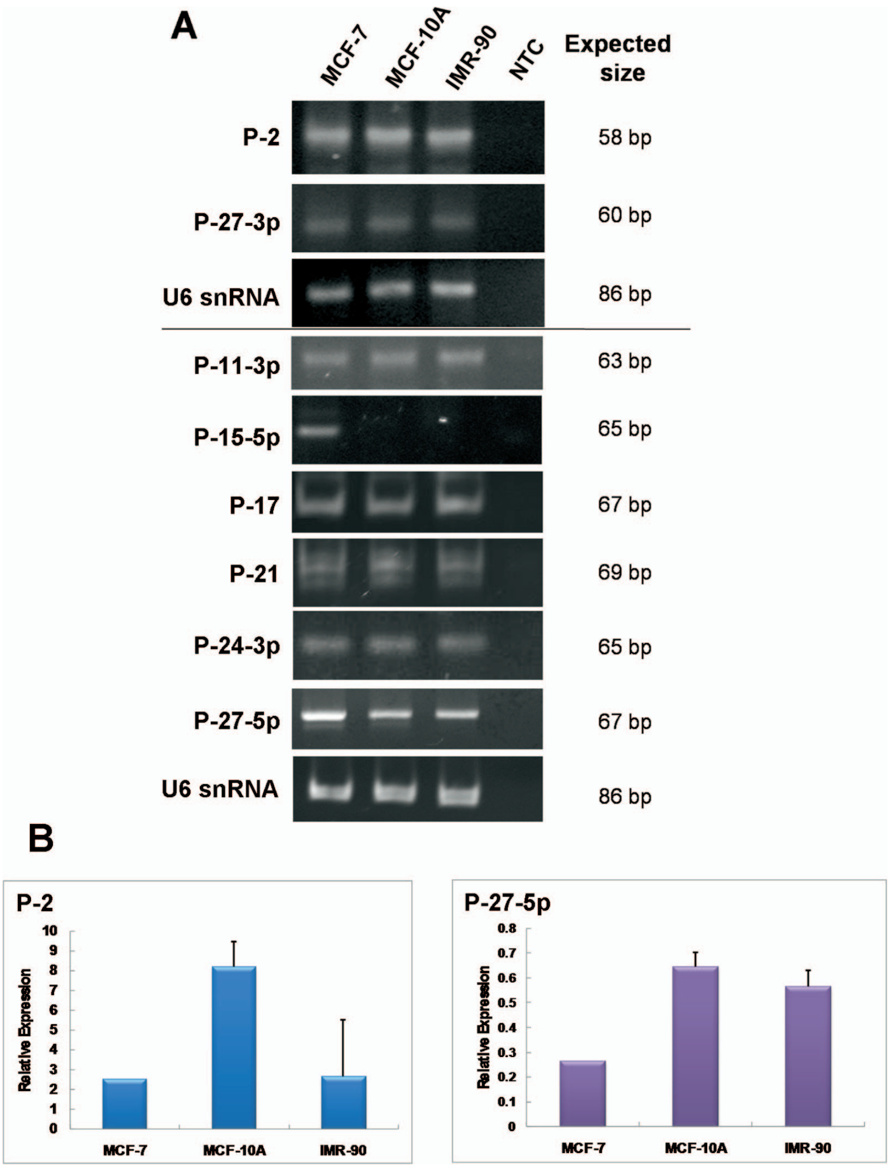
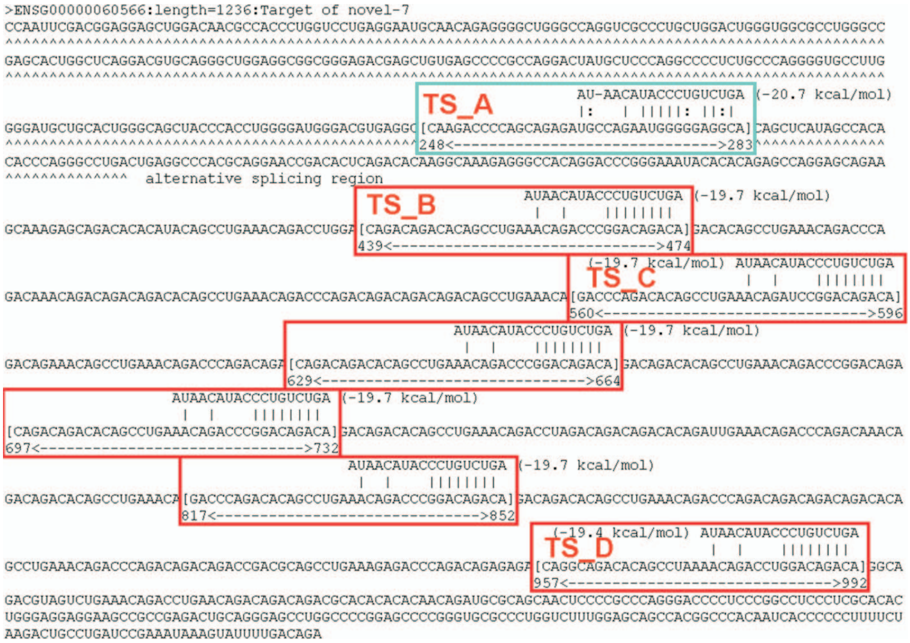


Fig. S5. PCR amplification of eight novel mature miRNAs and their endogenous expression levels. (*A*) Gel electrophoresis bands of eight novel mature miRNAs amplified by PCR. U6 snRNA was used as an internal standard. (*B*) Relative gene expression levels for P-2 and P-27–5p by real-time PCR analysis with respect to U6 small nuclear RNA expression levels. P-17, P-21, and P-24-3p have been registered as hsa-miR-2052, hsa-miR-2054, and hsa-miR-2053-3p, respectively.



```
>ENSG00000060566:length=1236:Target of novel-7
CCAAUUCGACGGAGGAGCUGGACAACGCCACCCUGGUCCUGAGGAAUGCAACAGAGGGGCUGGGCCAGGUCGCCCUGCUGGACUGGGUGGCGCCUGGGCC
^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^
GAGCACUGGCUCAGGACGUGCAGGGCUGGAGGCGGCGGGAGACGAGCUGUGAGCCCCGCCAGGACUAUGCUCCCAGGCCCCUCUGCCCAGGGGUGCCUUG
^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^
                                                                 AU-AACAUACCCUGUCUGA (-20.7 kcal/mol)
                                                                 |:   | |||||: ||:|
GGGAUGCUGCACUGGGCAGCUACCCACCUGGGGAUGGGACGUGAGGC[CAAGACCCCAGCAGAGAUGCCAGAAUGGGGGAGGCA]CAGCUCAUAGCCACA
^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^248<------------------------------>283^^^^^^^^^^^^^^^
CACCCAGGGCCUGACUGAGGCCCACGCAGGAACCGACACUCAGACACAAGGCAAAGAGGGCCACAGGACCCGGGAAAUACACACAGAGCCAGGAGCAGAA
^^^^^^^^^^^^  alternative splicing region
                                                           AUAACAUACCCUGUCUGA (-19.7 kcal/mol)
                                                            |  |    ||||||||
GCAAAGAGCAGACACACAUACAGCCUGAAACAGACCUGGA[CAGACAGACACAGCCUGAAACAGACCCGGACAGACA]GACACAGCCUGAAACAGACCCA
                                        439<------------------------------>474
                                                                  (-19.7 kcal/mol) AUAACAUACCCUGUCUGA
                                                                                    |  |    ||||||||
GACAAACAGACAGACAGACACAGCCUGAAACAGACCCAGACAGACAGACAGACAGCCUGAAACA[GACCCAGACACAGCCUGAAACAGAUCCGGACAGACA]
                                                                560<------------------------------->596
                                                   AUAACAUACCCUGUCUGA (-19.7 kcal/mol)
                                                    |  |    ||||||||
GACAGAAACAGCCUGAAACAGACCCAGACAGA[CAGACAGACACAGCCUGAAACAGACCCGGACAGACA]GACAGACACAGCCUGAAACAGACCCGGACAGA
                                629<------------------------------>664
                   AUAACAUACCCUGUCUGA (-19.7 kcal/mol)
                    |  |    ||||||||
[CAGACAGACACAGCCUGAAACAGACCCGGACAGACA]GACAGACACAGCCUGAAACAGACCUAGACAGACAGACACAGAUUGAAACAGACCCAGACAAACA
697<------------------------------>732
                                       AUAACAUACCCUGUCUGA (-19.7 kcal/mol)
                                        |  |    ||||||||
GACAGACACAGCCUGAAACA[GACCCAGACACAGCCUGAAACAGACCCGGACAGACA]GACAGACACAGCCUGAAACAGACCCAGACAGACAGACAGACACA
                    817<------------------------------>852
                                                              (-19.4 kcal/mol) AUAACAUACCCUGUCUGA
                                                                                |  |    ||||||||
GCCUGAAACAGACCCAGACAGACAGACCGACGCAGCCUGAAAGAGACCCAGACAGAGAGA[CAGGCAGACACAGCCUAAAACAGACCUGGACAGACA]GGCA
                                                            957<------------------------------>992
GACGUAGUCUGAAACAGACCUGAACAGACAGACAGACGCACACACACAACAGAUGCGCAGCAACUCCCCGCCCAGGGACCCCUCCCGGCCUCCCUCGCACAC
UGGGAGGAGGAAGCCGCCGAGACUGCAGGGAGCCUGGCCCCGGAGCCCCGGGUGCGCCCUGGUCUUUGGAGCAGCCACGGCCCACAAUCACCCCCCUUUUCU
AAGACUGCCUGAUCCGAAAUAAAGUAUUUUGACAGA
```

Fig. S6. Seven possible P-2 TSs on *CREB3L3* 3′ UTR. TS_A, TS_B, TS_C, and TS_D are four selected putative TSs for functional validation. TS_B has three exact copies, and TS_C has two highly similar copies, whereas TS_A and TS_D have only one copy in the 3′ UTR.

Table S1. Predicted novel miRNAs with no G/U pairing in the seed match

Frequent motif	Tissues of motif identified	Predicted novel miRNA	Predicted miRNA mature sequence	Genomic coordinates (NCBI 36.1)	Gene located
AUGCAAA	Artery/aorta, uterus	P-1	AUUUGCAUAAUGGAUGC	Chr2:205539433–205539449	ENSG00000116117
GACAGAC	Intestine, liver/hepato, pituitary, breast	P-2	AGUCUGUCCCAUACAAUA	Chr6:44077683–44077700	ENSG00000181577
GGACAGA	Breast		GUCUGUCCCAUACAAUAU	Chr6:44077684–44077701	
AGCUGAA	Peripheral nerve	P-3	UUUCAGCUCAUAAAA	Chr5:82856771–82856785	ENSG00000038427
UAAUUGG	Ovary	P-4	UCCAAUUAAGUCUUUUAAAU	Chr8:83086984–83087003	
UUCAAAG	Liver/hepato	P-5	CCUUUGAAAAUAUAAAAUC	Chr8:35236713–35236732	ENSG00000156687
UUUCAAA	Cerebrum, intestine, liver/hepato, pancreas		CUUUGAAAAUAUAAAAUC	Chr8:35236714–35236732	
UCAAUUU	Kidney	P-6–3p	UAAAUUGAGGUGGAUCCUGU	Chr15:57977629–57977648	
AAAUUGA	Lymph node	P-6–5p	CUCAAUUUAUUCCUAGAAACA	Chr15:57977582–57977602	
UAAAUUG	Placenta		UCAAUUUAUUCCUAGAAACAG	Chr15:57977583–57977603	
AAUUGAG	Kidney		UCUCAAUUUAUUCCUAG	chr15:57977581–57977597	
GCAAUUU	Peripheral nerve	P-7–3p	AAAUUGCCAUAAAGUG	Chr9:80472606–80472621	
AUGUUCA	Artery/aorta	P-8	AUGAACAUCUGAUUAUU	Chr11:132066843–132066859	ENSG00000183715
CCAUUCA	Retina	P-9–3p	UUGAAUGGCGCCACUAGGGUU	ChrX:109185270–109185290	ENSG00000157600
UUGUGCA	Lymph node	P-9–5p	CUGCACAACCCUAGGAGAGGG	ChrX:109185228–109185248	(hsa-miR-652)
ACAAAUC	Cerebrum	P-10	UGAUUUGUUCAAGAUGAUGA	Chr7:27256727–27256746	
GGUCUUG	Lung	P-11–3p	UCAAGACCUACUUAUCUACC	Chr15:81221851–81221870	
AUCUACC	Testis	P-11–5p	GGUAGAUAGAACAGGUCUUG	Chr15:81221817–81221836	
AUGCAUU	Lymph node	P-12–3p	AAAUGCAUGAAAUAGAU	Chr1:158032773–158032789	
AUAAUGA	Cerebrum	P-13–5p-1	UCAUUAUAAAAUGUGAUAAUGU	Chr15:51019585–51019606	
AAUGUCA	Placenta	P-13–3p	GUGACAUUAUGACAUUACAUU	Chr15:51019643–51019663	
CUAAUUA	Retina	P-14	UUAAUUAGCAAAAAGGCU	Chr1:208493640–208493657	
GCUAAUU	Thymus, testis, liver/hepato		UAAUUAGCAAAAAGGCU	Chr1:208493641–208493657	
UGUUAAU	Placenta	P-15–3p	AAUUAACAGAAUAUUAU	Chr5:146055768–146055784	ENSG00000156475
AUUAACA	Cerebrum, lymph node, placenta, lung, pancreas	P-15–5p	UUGUUAAUCAAAAAACUAU	Chr5:146055739–146055757	
UGAAUAU	Cerebrum, pineal gland, peripheral blood	P-16–5p	UAUAUUCACAUUUAUUGGAU	Chr7:146609661–146609680	ENSG00000174469
UCAAAAC	Placenta, lung	P-17	UGUUUUGAUAACAGUAAUGU	Chr8:75780484–75780503	
UAAUUUC	Kidney	P-18–1	UGAAAUUAUAUUACCAACA	Chr10:128235007–128235025	
AAUUUCA	Lymph node, placenta, testis, kidney, pancreas		UUGAAAUUAUAUUACCAACA	Chr10:128235006–128235025	
UUGUAGU	Lymph node	P-19–1	GACUACAACUCCCAAGGUA	Chr1:153246074–153246092	ENSG00000160685
GGAGUUG	Vein	P-19–2	ACAACUCCCAAGGUACAUACA	Chr1:153246078–153246098	
AUUAUCU	Lymph node	P-20–1	UAGAUAAUUUGCACAUUAU	Chr14:72223490–72223508	ENSG00000205683
AUUACAG	Cerebrum, lymph node, uterus, muscle, lung, kidney, pancreas	P-21	CUGUAAUAUAAAUUUAAUUUAUU	Chr4:126647864–126647886	
UUUUAAC	Cerebrum, lymph node	P-22	UGUUAAAAAAAGAAAAACAA	Chr3:85884941–85884960	ENSG00000175161
UUUAACA	Placenta, prostate, pancreas		UUGUUAAAAAAAGAAAAACAA	Chr3:85884940–85884960	
CAAUAUA	Cerebrum, prostate, lung	P-23	GUAUAUUGUGACAUACAUGU	Chr1:1463389–1463408	
AAUUAAC	Placenta	P-24–3p	GUGUUAAUUAAACCUCUAUUUAC	Chr8:113724958–113724980	ENSG00000164796
AUUUACA	Placenta	P-24–5p	AUGUAAAUACAGAUUUAAUUAAC	Chr8:113724904–113724926	
UAUUUAC	Cerebrum, placenta, kidney		UGUAAAUACAGAUUUAAUUAACA	Chr8:113724905–113724927	
UUUACAU	Lymph node, placenta, kidney, pancreas		CAUGUAAAUACAGAUUUAAUUAA	Chr8:113724902–113724924	
AAAUUAC	Lymph node, placenta	P-25	AGUAAUUUUCGAUAAAGCCCUU	Chr10:129082297–129082318	ENSG00000150760
GAAAAUU	Cerebrum, placenta, prostate, testis, lung, pancreas		UAAUUUUCGAUAAAGCCCUU	Chr10:129082299–129082318	
UCAUGUU	Placenta	P-26	CCAACAUGAUGCUAAUAAAU	Chr17:73293262–73293281	
AAUCUUU	Lymph node, placenta, prostate, lung, pancreas	P-27–5p	CAAAGAUUCAUCCUUGUGU	Chr21:36014906–36014929	ENSG00000159216 (hsa-miR-802)
UCCUUGU	Ovary, breast	P27–3p	AACAAGGAGAAUCUUUGUCACU	Chr21:36014934–36014955	
CUAAUAA	Lymph node, placenta	P-28	UUUAUUAGUGCCAUAUAAUA	Chr2:219696897–219696916	ENSG00000187736

Frequent motif	Tissues of motif identified	Predicted novel miRNA	Predicted miRNA mature sequence	Genomic coordinates (NCBI 36.1)	Gene located
AUCAAUA	Cerebrum, testis	P-29–3p	UUAUUGAUCAGCGUAGCAAACA	Chr5:3508678–3508699	
UCAAUAA	Prostate, testis, adrenal gland		CUUAUUGAUCAGCGUAGCAA	Chr5:3508677–3508697	
UUGAUCA	Lymph node	P-29–5p-1	CUGAUCAAUAAUAAGAUUGAU	Chr5:3508628–3508648	
UUAUUGA	Lymph node, kidney	P-29–5p-2	AUCAAUAAUAAGAUUGAUAC	Chr5:3508631–3508650	
UAAACUG	Lymph node	P-30	CCAGUUUAUUUUGUAAAUAUA	Chr1:60826128–60826148	
AUAAACU	Pancreas		CAGUUUAUUUUGUAAAUAUA	Chr1:60826129–60826148	
AAAUAUG	Cerebrum, lymph node, pancreas	P-31	UCAUAUUUUCUAUCUCUUUGCUU	Chr4:39795271–39795293	ENSG00000078177
UUCCUUA	Placenta	P-32–1	UUAAGGAAAUUAUGCUGAAC	Chr4:21498378–21498397	ENSG00000185774
AAUUUUC	Lymph node	P-33	AGAAAAUUAGGUUGAUA	Chr6:37530191–37530212	ENSG00000137200
UUCAAAA	Cerebrum	P-34	CUUUUUGAGUUUUGAGGAAG	Chr9:99359944–99359963	ENSG00000136842
UUACAGC	Placenta	P-35	AGCUGUAAACAGCUCUCCA	Chr17:69079331–69079349	
GAAUAAU	Cerebrum, eye, lymph node, ovary, lung, kidney	P-36	AUUAUUCUUUUUAUAAAA	Chr2:144691036–144691053	ENSG00000121964
UAUAAAC	Liver/hepato, pancreas	P-37	UGUUUAUAGUAAUGGGAGAUA	Chr9:127702054–127702074	ENSG00000167081
CAAAUAU	Peripheral nerve, placenta, kidney	P-38	AAUAUUUGGAAACAUCCA	Chr9:13932445–13932467	

---

[*] P-9 (3p and 5p), [†]P-11 (3p and 5p), and [‡]P-27 (3p and 5p) are alternative mature forms of hsa-miR-652, cfa-miR-1839, and hsa-miR-802, respectively; however, no human version of cfa-miR-1839 is found in miRbase. The coordinates and the located gene identification numbers of these predicted mature miRNAs are given in the last two columns. P-17, P-21, P-24-3p, and P-24-5p have been registered as hsa-miR-2052, hsa-miR-2054, hsa-miR-2053-3p and hsa-miR-2053-5p, respectively. Chr, chromosome; NCBI, National Center for Biotechnology Information.

Table S2. Predicted novel miRNAs with 1 G/U pairing in the seed match

Frequent motif	Tissues of motif identification	Predicted novel miRNA	Predicted miRNA mature sequence	Genomic coordinates (NCBI 36.1)	Gene located
UCCAUCU	Retina	P-6–3p	GAGGUGGAUCCUGUUCCAAUU	Chr15:57977635–57977655	
AAUUUGU	Lymph node	P-7–3p	UGCAAAUUGCCAUAAAGUG	Chr9:80472603–80472621	
UAAAGUG	Prostate, testis	P-7–5p	CAUUUUAUGGCAAUUUGUU	Chr9:80472560–80472583	
UGAAAUA	Placenta, testis, liver/hepato, kidney, pancreas	P-12–5p	CUAUUUUAUGCAUUCUA	Chr1:158032753–158032774	
UUACAUU	Lymph node, uterus, placenta, prostate, kidney, pancreas	P-13–5p-2	AAAUGUGAUAAUGUCAUUGC	Chr15:51019593–51019612	
UUAACAG	Placenta, pancreas	P-15–5p	CUUGUUAAUCAAAAAACUAU	Chr5:146055738–146055757	ENSG00000156475
UGGAUAU	Cerebrum	P-16–3p	UAUAUUCAUGAAUAUAU	Chr7:146609695–146609711	ENSG00000174469
GAUAUAU	Lymph node, prostate, lung, pancreas		AAUAUAUUCAUGAAUAUAU	Chr7:146609693–146609711	
UGAUAUA	Kidney	P-18–2	UUAUAUUACCAACAGAAAU	Chr10:128235012–128235030	
AGAUUAU	Lymph node	P-20–2	GAUAAUUUGCACAUUAU	Chr14:72223492–72223508	ENSG00000205683
AACAUUU	Lymph node, ovary, kidney, pancreas	P-24–3p	UAAGUGUUAAUUAAACCUCUA	Chr8:113724955–113724975	ENSG00000164796
UAACAUU	Cerebrum, skin, placenta		AAGUGUUAAUUAAACCUCUAUU	Chr8:113724956–113724977	
UGAUUUC	Bone, lung	P-32–2	GGAAAUUAUGCUGAACUCAUUU	Chr4:21498382–21498403	ENSG00000185774
UAAUGUU	Artery/aorta	P-39	UGACAUUAGUUCAUUU	Chr2:56002041–56002056	ENSG00000115380
UUUUAAG	Lymph node, skin, placenta, lung, pancreas	P-40	GCUUAGAAAAGUGACCUAGA	Chr2:77350845–77350864	ENSG00000176204
GCUGUUU	Lung	P-41	AAAGCAGCGUGAAGAUGC	Chr2:105075146–105075163	ENSG00000135972
UGCAUAU	Peripheral nerve, placenta, pancreas	P-42	UAUAUGUAGAUGUAGCUAUAU	Chr2:192552553–192552573	ENSG00000144339
AGAUUAU	Lymph node	P-43	AUAAUUUAUUAGAACAAUUAG	Chr3:60801997–60802017	ENSG00000189283
AGUAAUU	Lymph node	P-44	UAAUUAUUUUUCUCCAUC	Chr3:62045270–62045287	ENSG00000144724
GUAAUUA	Lymph node, kidney, pancreas		UUAAUUAUUUUUCUCCAUC	Chr3:62045269–62045287	
UUCAAUU	Lymph node	P-45	UAAUUGGAAAUUUCAUUU	Chr4:146917406–146917423	ENSG00000151612
GCACAUU	Lung	P-46	UAAUGUGUAAUGCUGUAGUUU	Chr4:153150954–153150974	
GUCUAUA	Lymph node, lung	P-47	AUGUAGACAAAACAUCCAGAUAA	Chr5:15476433–15476455	
UGUCUAU	Lung		UGUAGACAAAACAUCCAGAU	Chr5:15476434–15476453	
GAAUAAU	Cerebrum, eye, lymph node, ovary, lung, kidney	P-48	AUUAUUUUAGUAAUUCAACAG	Chr5:36750623–36750643	
AAUAACU	Lymph node, placenta, lung, pancreas	P-49	AAGUUGUUUCUGCAUAAA	Chr5:104185237–104185254	
AGAGUUA	Cerebrum, skin, placenta	P-50	UAACUUUUAAUGUAAGCCUGG	Chr6:50426012–50426032	
UAAGAGU	Placenta, pancreas		AACUUUUAAUGUAAGCC	Chr6:50426013–50426029	
GCAAAAU	Cerebrum, retina, placenta, prostate	P-51	UGUUUUGCCAGCAUGUGGUUG	Chr9:72221811–72221831	
UAAGUGA	Cerebrum	P-52	UUCAUUUAAAAUUAGGC	Chr10:13522803–13522819	ENSG00000165626
UUAAGUG	Lymph node, placenta, lung		UCAUUUAAAAUUAGGC	Chr10:13522804–13522819	
UUUAAGU	Lymph node, placenta, kidney		UCAUUUAAAAUUAGGC	Chr10:13522803–13522819	
AAGUGAA	Cerebrum		AUUCAUUUAAAAUUAGGC	Chr10:13522801–13522819	
UUAAGAU	Placenta, lung, pancreas	P-53	CAUCUUGAAAUAAGUCCUCA	Chr11:122110545–122110564	ENSG00000154127
UUUAAGA	Lymph node, uterus, prostate, testis, lung, kidney, pancreas		AUCUUGAAAUAAGUCCUCAU	Chr11:122110546–122110565	
UUUUAAG	Lymph node, skin, placenta, lung, pancreas		UCUUGAAAUAAGUCCUCAUC	Chr11:122110547–122110566	
UUGAUUA	Lymph node, lung, pancreas	P-54	AUAAUCAGAAACACUAAUCA	Chr13:6638959–66389614	ENSG00000184226
UAAAUGU	Lymph node, placenta	P-55	UAUAUUUAACAUACACUUG	Chr13:104638844–104638862	
AUUAGUU	Lymph node, kidney	P-56	GAAUUAAUGGUAUUAA	Chr14:56071430–56071448	
UAGUUUA	Placenta	P-57	UAAAUUAAAAUCAAUAUUUU	Chr16:7601200–7601219	ENSG00000078328
GAAUUUC	Skin, placenta	P-58	GGGAAUUCCCACUCUGCAG	Chr17:9233266–9233289	ENSG00000170310
GGAAUUU	Kidney		GGAAUUCCCACUCUGCA	Chr17:9233267–9233288	
AUUCUGA	Kidney	P-59	UUUAGAAUUCUAAUUA	Chr18:26697252–26697267	
GCAAAUU	Lymph node	P-60	UGAUUUGCAUUUUAGU	Chr18:40000232–40000247	
AUGAAGU	Uterus, lung	P-61	UAUUUCAUUUUAAUCUUGA	Chr19:35550032–35550050	
UAGCAAG	Prostate	P-62	CUUGUUAAAAAGCAGAUUCU	Chr14:100584767–100584786	hsa-miR-544
UUUUAGC	Lung		UGUUAAAAAGCAGAUUCUGA	Chr14:100584769–100584788	
UUGUUGA	Kidney	P-63–1	CUCAAUAAGUAUUUGUUGA	ChrX:113793391–113793409	ENSG00000147246
UCAAUAA	Prostate, adrenal gland	P-63–2	UUUGUUGAAAGAAUAAAUAA	ChrX:113793402–113793421	(hsa-miR-1264)

Frequent motif	Tissues of motif identification	Predicted novel miRNA	Predicted miRNA mature sequence	Genomic coordinates (NCBI 36.1)	Gene located
AACUUUU	Cerebrum, lymph node, prostate, intestine, lung, kidney	P-64–1	AAGAGUUCAUUCGGCUGUCCAG	ChrX:113855918–113855939	ENSG00000147246 (hsa-miR-1298)
CUGGGCA	Thymus	P-64–2	CUGUCCAGAUGUAUCCAAGU	ChrX:113855932–113855951	
CUCCUGU	Vein	P-65	AAUAGGAGACUCACAAGUUCCUG	Chr9:28878920–28878942	hsa-miR-873
UCCUGUU	Eye		CAAUAGGAGACUCACAAGUU	Chr9:28878919–28878938	
UCUCCUG	Breast		AUAGGAGACUCACAAGUUCCUG	Chr9:28878921–28878942	
CAUGUUU	Lymph node, placenta	P-66	AAAACGUGGAUAUUCCUUCUAUG	Chr14:100576545–100576567	hsa-miR-376b
GUAUCAA	Pancreas	P-67	UUUGGUACUUAAAGCGAGG	Chr14:100582005–100582023	hsa-miR-381
UAUCAAA	Testis		GUUUGGUACUUAAAGCGAGG	Chr14:100582004–100582023	
CCUUAUU	Lymph node	P-68–1	AAAUGAGGGACUUUUGGGGGCA	Chr16:14310653–14310674	hsa-miR-365
CCUAAAA	Uterus	P-68–2	CUUUUGGGGGCAGAUGUG	Chr16:14310663–14310680	
UAGGAUG	Bone	P-69	ACAUCCUGCAUAGUGCUGCCAG	ChrX:113964286–113964307	ENSG00000147246 (hsa-miR-448)

P-24-3p has been registered as hsa-miR-2053-3p. Chr, chromosome; NCBI, National Center for Biotechnology Information.

Table S3. Primer sequences for PCR amplification of 11 predicted novel miRNAs

Predicted novel miRNA	Mature RNA sequence 5′-3′	Primer	Sequence 5′-3′	Length	Special manipulation
P-2	GUCUGUCCCAUACAAUA	Stem-loop RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTATTGT	50-mer	OPC purification
		Forward	GGCCGCGTCTGTCCCATACAATA	23-mer	
		Reverse	GTGCAGGGTCCGAGGT	16-mer	
P-27–3p	AACAAGGAGAAUCUUUGUCACU	Stem-loop RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACAGTGAC	50-mer	OPC purification
		Forward	CGTTACTCGAAACAAGGAGAATCTTTG	27-mer	
		Reverse	GTGCAGGGTCCGAGGT	16-mer	
P-11–3p	UCAAGACCUACUUAUCUACC	Stem-loop RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGGTAGA	50-mer	OPC purification
		Forward	CGAGCGATCAAGACCTACTTATC	23-mer	
		Reverse	GTGCAGGGTCCGAGGT	16-mer	
P-15–5p	UUGUUAAUCAAAAAACUAU	Stem-loop RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACATAGTT	50-mer	OPC purification
		Forward	GCGAGCGCGATTGTTAATCAAAAAA	25-mer	
		Reverse	GTGCAGGGTCCGAGGT	16-mer	
P-17	UGUUUUGAUAACAGUAAUGU	Stem-loop RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACACATTA	50-mer	OPC purification
		Forward	GCGAGCGATTGTTTTGATAACAGT	24-mer	
		Reverse	GTGCAGGGTCCGAGGT	16-mer	
P-21	CUGUAAUAUAAAUUUAAUUUAUU	Stem-loop RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACAATAAA	50-mer	OPC purification
		Forward	GCGCGTGGGCCTGTAATATAAATTTAATT	29-mer	
		Reverse	GTGCAGGGTCCGAGGT	16-mer	
P-23	GUAUAUUGUGACAUACAUGU	Stem-loop RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACACATGT	50-mer	OPC purification
		Forward	CGCGTGAAGTATATTGTGACATAC	24-mer	
		Reverse	GTGCAGGGTCCGAGGT	16-mer	
P-24–3p	GUGUUAAUUAAACCUCUAUUUAC	Stem-loop RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGTAAAT	50-mer	OPC purification
		Forward	GCTAGCGTGTTAATTAAACCTCTAT	25-mer	
		Reverse	GTGCAGGGTCCGAGGT	16-mer	
P-25	UAAUUUUCGAUAAAGCCCUU	Stem-loop RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACAAGGGC	50-mer	OPC purification
		Forward	CGCCAGGTAATTTTCGATAAAGC	23-mer	
		Reverse	GTGCAGGGTCCGAGGT	16-mer	
P-27–5p	CAAAGAUUCAUCCUUGUGU	Stem-loop RT	GTCGTATCCAGTGCAGGGTCCGAGGATTCGCACTGGATACGACTGGACA	50-mer	OPC purification
		Forward	GGGCAAAGATTCATCCTTGTG	21-mer	
		Reverse	GTGCAGGGTCCGAGGT	16-mer	
P-36	AUUAUUCUUUUUAUAAAA	Stem-loop RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTTTTAT	50-mer	OPC purification
		Forward	GCGAGCGCGATTATTCTTTTTAT	23-mer	
		Reverse	GTGCAGGGTCCGAGGT	16-mer	

OPC, oligonucleotide purification cartridge.