Supplementary Material

Identification of miRNAs involved in intracranial aneurysm rupture in cigarette smoking patients

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Supplementary Table 1 Differentially expressed miRNAs between smoking IA patients and healthy controls.

miR name	miR sequence	up/down	fold_change	log2(fold_change)	P value
hsa-miR-92b-5p_R-2	AGGGACGGGACGCGGTGCAG	down	0.02	-5.72	1.08484E-10
hsa-miR-107_R-2	AGCAGCATTGTACAGGGCTAT	down	0.14	-2.85	1.60212E-09
mmr-miR-1839_L+1R-1	AAGGTAGATAGAACAGGTCTTG	down	0.15	-2.73	4.94069E-09
hsa-miR-126-3p_R-1	TCGTACCGTGAGTAATAATGC	down	0.35	-1.50	1.70747E-08
hsa-mir-1304-p5	CGGTTTGAGGCTACAGTGAGAT	down	0.13	-2.97	1.70821E-08
PC-5p-49096_267	AGCCTGGAAGCTGGAGCCTGCAG	down	0.07	-3.85	2.61249E-08
hsa-miR-324-3p_L-3R+1	ACTGCCCCAGGTGCTGCTGGA	down	0.07	-3.86	3.15182E-08
hsa-mir-8086-p3_1ss11AG	AGGCTGGAGTGCAGTGGC	down	0.02	-5.47	3.38742E-08
hsa-miR-223-5p_R+2	CGTGTATTTGACAAGCTGAGTTGG	down	0.21	-2.23	8.03675E-08
hsa-miR-103a-3p	AGCAGCATTGTACAGGGCTATGA	down	0.19	-2.42	8.29712E-08
hsa-miR-95-3p_R-1	TTCAACGGGTATTTATTGAGC	down	0.04	-4.82	1.01821E-07
hsa-miR-6735-5p_R-4	CAGGGCAGAGGGCACAGGAAT	down	0.10	-3.33	1.05287E-07
PC-5p-42143_323	TTAGTGGCTCCCTCTGCCTGCA	down	0.07	-3.88	1.38295E-07
hsa-miR-1285-3p_R-2	TCTGGGCAACAAAGTGAGAC	down	0.13	-2.98	1.6504E-07
hsa-miR-576-3p_R-1	AAGATGTGGAAAAATTGGAAT	down	0.09	-3.43	1.72125E-07
hsa-let-7c-5p_R-4	TGAGGTAGTAGGTTGTAT	down	0.26	-1.95	1.76247E-07
mmu-miR-2137_L-2_1ss16AG	CGGCGGGAGCCCCGGGGAG	down	0.06	-3.95	1.83002E-07
hsa-miR-320a-3p	AAAAGCTGGGTTGAGAGGGCGA	down	0.21	-2.25	2.01609E-07
mmu-miR-2137_L-2R-1_1ss16AG	CGGCGGGAGCCCCGGGGA	down	0.13	-2.89	2.04631E-07
hsa-miR-550a-3-5p	AGTGCCTGAGGGAGTAAGAG	down	0.09	-3.47	3.42866E-07
hsa-miR-3140-3p_R-1	AGCTTTTGGGAATTCAGGTAG	down	0.10	-3.39	3.63602E-07
hsa-miR-3127-5p	ATCAGGGCTTGTGGAATGGGAAG	down	0.04	-4.73	4.80872E-07

hsa-miR-363-3p_R-1	AATTGCACGGTATCCATCTGT	down	0.18	-2.43	4.82696E-07
hsa-miR-598-3p	TACGTCATCGTTGTCATCGTCA	down	0.17	-2.55	4.83891E-07
hsa-miR-511-5p	GTGTCTTTTGCTCTGCAGTCA	down	0.00	-8.38	4.90864E-07
PC-3p-2703_5627	TTTGGGGATTCTAAGAGGAAG	down	0.08	-3.66	5.20708E-07
hsa-miR-361-3p_R+1	TCCCCCAGGTGTGATTCTGATTTG	down	0.14	-2.82	5.32283E-07
hsa-miR-190b-5p	TGATATGTTTGATATTGGGTTG	down	0.02	-5.45	5.94992E-07
hsa-miR-21-5p	TAGCTTATCAGACTGATGTTGA	down	0.19	-2.36	6.89989E-07
hsa-miR-106b-5p_R-1	TAAAGTGCTGACAGTGCAGA	down	0.06	-4.18	7.31391E-07
hsa-miR-25-3p	CATTGCACTTGTCTCGGTCTGA	down	0.08	-3.58	7.32155E-07
hsa-miR-1180-3p_R-2	TTTCCGGCTCGCGTGGGTGT	down	0.15	-2.76	9.19536E-07
hsa-miR-199b-5p_R-1	CCCAGTGTTTAGACTATCTGTT	down	0.13	-2.91	9.24587E-07
hsa-miR-542-3p_R-2	TGTGACAGATTGATAACTGA	down	0.11	-3.18	9.29355E-07
hsa-let-7i-5p	TGAGGTAGTAGTTTGTGCTGTT	down	0.19	-2.39	1.06339E-06
hsa-miR-532-5p	CATGCCTTGAGTGTAGGACCGT	down	0.09	-3.44	1.36228E-06
ocu-miR-502b-3p_R-3	AATGCACCTGGGCAAGGATTT	down	-inf	-inf	1.76924E-06
hsa-miR-660-5p_R+1	TACCCATTGCATATCGGAGTTGT	down	0.04	-4.53	3.1283E-06
hsa-miR-210-3p	CTGTGCGTGTGACAGCGGCTGA	down	0.08	-3.59	3.52357E-06
hsa-miR-106b-3p_R-2	CCGCACTGTGGGTACTTGCT	down	0.20	-2.33	3.53265E-06
hsa-miR-92a-1-5p	AGGTTGGGATCGGTTGCAATGCT	down	0.12	-3.06	3.77561E-06
hsa-miR-16-5p	TAGCAGCACGTAAATATTGGCG	down	0.11	-3.12	4.07521E-06
hsa-miR-6866-5p_R-2	TTAGAGGCTGGAATAGAGATT	down	0.09	-3.50	4.15803E-06
hsa-miR-4732-5p	TGTAGAGCAGGGAGCAGGAAGCT	down	0.13	-2.92	4.16916E-06
hsa-miR-652-3p_R+1	AATGGCGCCACTAGGGTTGTGT	down	0.51	-0.98	4.49954E-06
hsa-miR-140-3p_R+1	TACCACAGGGTAGAACCACGGA	down	0.12	-3.02	4.78143E-06
hsa-miR-181b-5p_R-2	AACATTCATTGCTGTCGGTGG	down	0.23	-2.10	4.83834E-06
hsa-miR-18a-5p	TAAGGTGCATCTAGTGCAGATAG	down	0.13	-2.89	5.05749E-06

hsa-miR-7-5p_R-1	TGGAAGACTAGTGATTTTGTTGT	down	0.10	-3.38	5.21475E-06
hsa-miR-500a-3p_L+1R-1_1ss22TA	AATGCACCTGGGCAAGGATTCA	down	0.25	-2.02	5.25802E-06
hsa-miR-502-3p	AATGCACCTGGGCAAGGATTCA	down	0.25	-2.02	5.25802E-06
hsa-miR-3200-3p_R-1	CACCTTGCGCTACTCAGGTCT	down	0.04	-4.56	5.56206E-06
hsa-miR-424-5p_R-1	CAGCAGCAATTCATGTTTTGA	down	0.10	-3.35	6.6359E-06
hsa-miR-15a-5p_R-1	TAGCAGCACATAATGGTTTGT	down	0.09	-3.47	6.66011E-06
hsa-miR-10b-5p_R-1	TACCCTGTAGAACCGAATTTGT	down	0.17	-2.54	8.13965E-06
hsa-miR-451a_R-1	AAACCGTTACCATTACTGAGT	down	0.13	-2.90	8.97423E-06
hsa-miR-4772-3p	CCTGCAACTTTGCCTGATCAGA	down	0.02	-5.80	8.98577E-06
mmu-miR-92a-3p_R+1	TATTGCACTTGTCCCGGCCTGA	down	0.18	-2.48	9.21432E-06
bta-mir-2887-1-p5_1ss5CA	GGGAAACGGGGCGCGGCC	down	0.08	-3.71	9.24033E-06
hsa-miR-150-3p_R-2	CTGGTACAGGCCTGGGGGAC	down	0.09	-3.42	9.27176E-06
hsa-miR-32-3p_R-1	CAATTTAGTGTGTGTGATATT	down	0.10	-3.35	9.6495E-06
hsa-miR-5010-5p	AGGGGGATGGCAGAGCAAAATT	down	0.13	-2.95	9.7424E-06
hsa-miR-326_R+1	CCTCTGGGCCCTTCCTCCAGT	up	5.85	2.55	1.02372E-05
hsa-miR-130a-3p	CAGTGCAATGTTAAAAGGGCAT	down	0.32	-1.65	1.0416E-05
hsa-miR-942-3p	CACATGGCCGAAACAGAGAAGT	down	0.03	-5.16	1.08226E-05
hsa-miR-214-3p_R-1	ACAGCAGGCACAGACAGGCAG	down	0.04	-4.67	1.10697E-05
hsa-mir-451a-p3	TTTAGTAATGGTAATGGTTCT	down	0.06	-4.02	1.1414E-05
hsa-miR-33a-5p_R-1	GTGCATTGTAGTTGCATTGC	down	0.02	-5.87	1.19204E-05
hsa-miR-185-5p	TGGAGAGAAAGGCAGTTCCTGA	down	0.06	-4.03	1.20408E-05
hsa-miR-106a-3p_L+2R-3	TACTGCAATGTAAGCACTTCT	down	0.09	-3.52	1.20674E-05
PC-3p-39847_345	ACATATAGTGAATTCTGGGATT	down	0.07	-3.91	1.21495E-05
hsa-miR-101-5p_L+1R-1	TCAGTTATCACAGTGCTGATGC	down	0.03	-4.97	1.27642E-05
hsa-miR-3909	TGTCCTCTAGGGCCTGCAGTCT	down	0.10	-3.28	1.31832E-05
hsa-miR-30e-5p_R+2	TGTAAACATCCTTGACTGGAAGCT	down	0.39	-1.36	1.39977E-05

hsa-let-7i-3p_R-1	CTGCGCAAGCTACTGCCTTGC	down	0.10	-3.32	1.44451E-05
hsa-miR-503-5p_R-2_1ss21CA	TAGCAGCGGGAACAGTTCTGA	down	0.10	-3.30	1.47992E-05
hsa-miR-342-5p	AGGGGTGCTATCTGTGATTGA	down	0.17	-2.57	1.51845E-05
hsa-miR-15b-3p_R-1	CGAATCATTATTTGCTGCTCT	down	0.18	-2.45	1.54743E-05
hsa-miR-942-5p_L-2R+1	TTCTCTGTTTTGGCCATGTGT	down	0.26	-1.92	1.5824E-05
hsa-miR-31-5p_R-2	AGGCAAGATGCTGGCATAG	down	-inf	-inf	1.62293E-05
hsa-miR-4772-5p	TGATCAGGCAAAATTGCAGACT	down	0.05	-4.32	1.80286E-05
hsa-miR-424-3p	CAAAACGTGAGGCGCTGCTAT	down	0.22	-2.17	1.92314E-05
hsa-miR-29c-3p_R-1	TAGCACCATTTGAAATCGGTT	down	0.15	-2.77	1.97776E-05
hsa-miR-34c-5p	AGGCAGTGTAGTTAGCTGATTGC	down	-inf	-inf	2.01481E-05
hsa-miR-30a-3p_R-1	CTTTCAGTCGGATGTTTGCAG	down	0.19	-2.40	2.0875E-05
hsa-miR-93-5p	CAAAGTGCTGTTCGTGCAGGTAG	down	0.12	-3.11	2.12153E-05
hsa-miR-20b-3p_R-3	ACTGTAGTATGGGCACTTC	down	0.10	-3.32	2.17505E-05
hsa-miR-486-5p	TCCTGTACTGAGCTGCCCCGAG	down	0.22	-2.16	2.18094E-05
hsa-let-7g-5p	TGAGGTAGTAGTTTGTACAGTT	down	0.15	-2.73	2.23756E-05
mmu-miR-2137_L-1R-1_1ss16AG	CCGGCGGGAGCCCCGGGGA	down	0.10	-3.38	2.27005E-05
hsa-mir-619-p5_1ss3AG	AAGTGCTGGGATTACAGG	down	0.08	-3.67	2.29723E-05
hsa-miR-450a-5p_R-2	TTTTGCGATGTGTTCCTAAT	down	0.33	-1.60	2.4688E-05
hsa-miR-642a-3p_R-1	AGACACATTTGGAGAGGGAAC	down	0.04	-4.54	2.4886E-05
hsa-miR-3912-3p	TAACGCATAATATGGACATGT	down	-inf	-inf	2.70745E-05
hsa-miR-582-5p_R-1	TTACAGTTGTTCAACCAGTTAC	down	0.11	-3.15	2.96624E-05
hsa-miR-497-5p	CAGCAGCACACTGTGGTTTGT	down	0.03	-5.26	3.00718E-05
hsa-miR-197-5p_R-2	CGGGTAGAGAGGGCAGTGGGA	down	0.02	-5.32	3.09763E-05
hsa-miR-132-5p	ACCGTGGCTTTCGATTGTTACT	down	0.02	-5.41	3.31751E-05
hsa-miR-610	TGAGCTAAATGTGTGCTGGGA	down	0.07	-3.87	3.51409E-05
hsa-miR-16-2-3p_L+1R-2	ACCAATATTACTGTGCTGCTT	down	0.22	-2.16	3.76187E-05

hsa-miR-425-5p	AATGACACGATCACTCCCGTTGA	down	0.42	-1.25	3.79344E-05
hsa-miR-3913-5p	TTTGGGACTGATCTTGATGTCT	down	0.14	-2.79	4.00854E-05
hsa-miR-188-5p_R+1	CATCCCTTGCATGGTGGAGGGT	down	-inf	-inf	4.01972E-05
pal-mir-9993a-p3_1ss2GA	AAATCTCGGTGGGACCTC	down	-inf	-inf	4.32534E-05
hsa-miR-340-5p	TTATAAAGCAATGAGACTGATT	down	0.41	-1.28	4.68301E-05
hsa-miR-2110_R+1	TTGGGGAAACGGCCGCTGAGTGA	down	0.34	-1.57	4.69082E-05
hsa-mir-5100-p3_1ss17TC	ATCCCAGCGGTGCCTCCA	down	0.04	-4.75	4.73183E-05
hsa-miR-20b-5p	CAAAGTGCTCATAGTGCAGGTAG	down	0.03	-5.16	4.74926E-05
hsa-miR-320e_L+1R+3_1ss17AG	AAAAGCTGGGTTGAGAGGGTGA	down	0.20	-2.29	4.97585E-05
hsa-miR-499a-5p	TTAAGACTTGCAGTGATGTTT	down	0.07	-3.84	5.04029E-05
hsa-miR-30c-2-3p	CTGGGAGAAGGCTGTTTACTCT	down	0.17	-2.56	5.07818E-05
hsa-miR-3164	TGTGACTTTAAGGGAAATGGCG	down	-inf	-inf	5.52437E-05
hsa-miR-6815-5p_R-2	TAGGTGGCGCCGGAGGAGTCA	down	0.14	-2.80	5.52543E-05
hsa-miR-32-5p_R-2	TATTGCACATTACTAAGTTG	down	0.18	-2.51	5.74948E-05
hsa-miR-629-5p	TGGGTTTACGTTGGGAGAACT	down	0.09	-3.45	5.91126E-05
hsa-miR-15b-5p	TAGCAGCACATCATGGTTTACA	down	0.33	-1.62	6.13089E-05
hsa-miR-3934-5p	TCAGGTGTGGAAACTGAGGCAG	down	-inf	-inf	6.21003E-05
hsa-miR-92a-3p	TATTGCACTTGTCCCGGCCTGT	down	0.30	-1.76	6.42886E-05
hsa-miR-6805-5p	TAGGGGGCGGCTTGTGGAGTGT	down	0.01	-6.22	6.88969E-05
hsa-miR-128-3p	TCACAGTGAACCGGTCTCTTT	down	0.38	-1.41	7.06564E-05
hsa-miR-548ak_L-1_1ss9CT	AAAGTAATTGCGGTTTTTGA	down	0.10	-3.36	7.45441E-05
hsa-miR-1255b-5p	CGGATGAGCAAAGAAAGTGGTT	down	0.06	-3.97	7.63209E-05
hsa-miR-22-3p	AAGCTGCCAGTTGAAGAACTGT	down	0.14	-2.85	7.85996E-05
hsa-miR-6513-5p	TTTGGGATTGACGCCACATGTCT	down	0.09	-3.47	7.86044E-05
hsa-miR-363-5p	CGGGTGGATCACGATGCAATTT	down	0.02	-5.35	8.56723E-05
hsa-miR-4508_L+2R-1	AAGCGGGGCTGGGCGCGC	down	0.16	-2.64	8.60579E-05

mmu-miR-6238_L-1R-2_1ss12TC	TATTAGTCAGCGGAGGAAA	down	-inf	-inf	8.79199E-05
hsa-miR-29b-3p_R-3	TAGCACCATTTGAAATCAGT	down	0.23	-2.14	8.96515E-05
hsa-miR-17-5p	CAAAGTGCTTACAGTGCAGGTAG	down	0.11	-3.21	9.01134E-05
hsa-miR-106a-5p_1ss1AC	CAAAGTGCTTACAGTGCAGGTAG	down	0.11	-3.21	9.01134E-05
bta-miR-1246_L+1R-2	AAATGGATTTTTGGAGCA	down	-inf	-inf	9.22023E-05
hsa-miR-196b-5p_R-1	TAGGTAGTTTCCTGTTGTTGG	down	0.18	-2.44	9.43642E-05
hsa-miR-651-5p_R-1	TTTAGGATAAGCTTGACTTTT	down	0.17	-2.59	9.4942E-05
hsa-miR-130b-3p	CAGTGCAATGATGAAAGGGCAT	down	0.12	-3.08	9.80967E-05
hsa-miR-1976_R+2	CCTCCTGCCCTCCTTGCTGTAG	down	0.24	-2.06	0.000103276
hsa-miR-1273c_R-1	GGCGACAAAACGAGACCCTGT	down	0.22	-2.20	0.000105249
hsa-miR-143-3p	TGAGATGAAGCACTGTAGCTC	down	0.36	-1.46	0.000112498
hsa-miR-548ay-5p_R-1	AAAAGTAATTGTGGTTTTTG	down	0.14	-2.84	0.000113348
ppy-miR-548a	AAAAGTAATTGTGGTTTTTG	down	0.14	-2.84	0.000113348
hsa-miR-548ad-5p	AAAAGTAATTGTGGTTTTTG	down	0.14	-2.84	0.000113348
hsa-miR-18a-3p_1ss23GA	ACTGCCCTAAGTGCTCCTTCTGA	down	0.21	-2.28	0.000121698
hsa-miR-29a-3p_R-1	TAGCACCATCTGAAATCGGTT	down	0.10	-3.39	0.000123064
hsa-miR-548bc	AAAAACTGTGATTACTTTTGC	down	0.05	-4.21	0.000124707
hsa-miR-1294_R-2	TGTGAGGTTGGCATTGTTGT	down	0.08	-3.65	0.000127528
hsa-let-7b-5p	TGAGGTAGTAGGTTGTGTGGTT	down	0.23	-2.13	0.000128104
hsa-miR-101-3p_R+1	TACAGTACTGTGATAACTGAAG	down	0.06	-4.06	0.00012996
hsa-miR-450b-5p_R-1	TTTTGCAATATGTTCCTGAAT	down	0.11	-3.23	0.000132441
hsa-miR-486-3p	CGGGGCAGCTCAGTACAGGAT	down	0.15	-2.79	0.000134294
PC-3p-81170_138	TGGCAAGGGCTGTGAAGAGA	down	0.03	-5.23	0.000139892
hsa-miR-20a-5p	TAAAGTGCTTATAGTGCAGGTAG	down	0.09	-3.41	0.000144961
hsa-miR-28-5p_R-1	AAGGAGCTCACAGTCTATTGA	down	0.30	-1.75	0.000146627
hsa-miR-6780a-5p_L-1R+2	TGGGAGGGAAGACAGCTGGAGAGT	down	0.03	-5.16	0.000149219

hsa-miR-3143_R-4	ATAACATTGTAAAGCGCTTCT	down	0.15	-2.76	0.000150339
hsa-miR-150-5p	TCTCCCAACCCTTGTACCAGTG	down	0.17	-2.58	0.000151282
hsa-miR-19b-3p	TGTGCAAATCCATGCAAAACTGA	down	0.18	-2.44	0.000155629
hsa-let-7d-5p	AGAGGTAGTAGGTTGCATAGTT	down	0.27	-1.88	0.00016187
hsa-miR-183-5p_L-1	ATGGCACTGGTAGAATTCACT	down	0.16	-2.65	0.000167171
hsa-miR-6842-3p	TTGGCTGGTCTCTGCTCCGCAG	down	0.09	-3.49	0.000171886
hsa-miR-4488_L+2R-1	GGAGGGGGCGGGCTCCGGC	down	0.03	-4.92	0.000172589
mmu-miR-3964_L+1_1ss6GA	CATAAAGTAGAAAGCACTAAA	down	-inf	-inf	0.000177503
hsa-miR-182-5p_R-4	TTTGGCAATGGTAGAACTCA	down	0.11	-3.12	0.000182013
hsa-miR-3150b-3p	TGAGGAGATCGTCGAGGTTGG	down	-inf	-inf	0.000182708
bta-miR-11987_L-2R-1_1ss8TA	AGGAAACTCTGGTGGAGG	down	0.04	-4.48	0.000188308
hsa-mir-3665-p5_1ss2CA	GAGGGCGGCGGCGGCGGC	down	-inf	-inf	0.000205891
hsa-miR-3944-5p	TGTGCAGCAGGCCAACCGAGA	down	-inf	-inf	0.000220135
hsa-miR-18b-5p_R-3	TAAGGTGCATCTAGTGCAGT	down	0.15	-2.71	0.000223971
PC-5p-37928_367	TGAGGGGAGAGAGCGAGACT	down	0.02	-5.47	0.000227953
hsa-miR-4732-3p	GCCCTGACCTGTCCTGTTCTG	down	0.24	-2.05	0.000231939
hsa-miR-625-5p_R-1	AGGGGGAAAGTTCTATAGTC	down	0.14	-2.86	0.000232995
hsa-miR-19a-3p	TGTGCAAATCTATGCAAAACTGA	down	0.14	-2.84	0.000235482
hsa-miR-1268b_R-2	CGGGCGTGGTGGTGGGGG	down	-inf	-inf	0.000241138
hsa-miR-1268a	CGGGCGTGGTGGTGGGGG	down	-inf	-inf	0.000241138
hsa-miR-148b-3p	TCAGTGCATCACAGAACTTTGT	down	0.52	-0.95	0.000260204
hsa-miR-10a-3p_R-1	CAAATTCGTATCTAGGGGAAT	down	0.01	-6.13	0.000260251
hsa-miR-1246_L-2R+1	TGGATTTTTGGAGCAGGG	down	0.02	-5.86	0.000261333
hsa-miR-548ac_L-1	AAAAACCGGCAATTACTTTTG	down	0.02	-5.88	0.000266219
pal-miR-9993a-3p_1ss11GA	ATCTCGGTGGAACCTCCA	down	0.31	-1.69	0.000266323
pal-miR-9995-3p	ATCTCGGTGGAACCTCCA	down	0.31	-1.69	0.000266323

hsa-miR-514a-3p_R-1	ATTGACACTTCTGTGAGTAG	down	-inf	-inf	0.000273831
hsa-miR-22-5p_R-1	AGTTCTTCAGTGGCAAGCTTT	down	0.10	-3.39	0.000283163
hsa-miR-144-3p_R-1	TACAGTATAGATGATGTAC	down	0.29	-1.79	0.000285132
bta-miR-1246_L+1R+3	AAATGGATTTTTGGAGCAGGGAG	down	0.02	-5.55	0.000290931
PC-5p-60328_204	AGAATATGGGAGTCTGTGGCT	down	0.15	-2.76	0.000293917
hsa-miR-9-3p	ATAAAGCTAGATAACCGAAAGT	down	0.10	-3.28	0.000315379
hsa-miR-345-5p_R+1	GCTGACTCCTAGTCCAGGGCTCT	down	0.48	-1.06	0.000319448
hsa-miR-501-5p_R+2	AATCCTTTGTCCCTGGGTGAGAGT	down	0.01	-6.45	0.000324049
hsa-mir-6511a-3-p5	CTGCAGGCAGAAGTGGGGCTGA	down	-inf	-inf	0.000326857
hsa-mir-6511b-1-p5	CTGCAGGCAGAAGTGGGGCTGA	down	-inf	-inf	0.000326857
hsa-miR-203a-3p_R-2	GTGAAATGTTTAGGACCACT	down	0.18	-2.48	0.0003504
hsa-miR-548at-5p_R-2	AAAAGTTATTGCGGTTTTGG	down	0.03	-5.14	0.000350577
hsa-miR-9985_R-1_1ss16CT	TTCACAGTGGCTAAGTTA	down	0.03	-5.03	0.000353695
hsa-miR-5581-3p	TTCCATGCCTCCTAGAAGTTCC	down	-inf	-inf	0.000356248
hsa-miR-3124-5p	TTCGCGGGCGAAGGCAAAGTC	down	0.08	-3.61	0.000362379
bta-miR-1246_L+1R-1	AAATGGATTTTTGGAGCAG	down	0.14	-2.80	0.000363923
bta-miR-150	TCTCCCAACCCTTGTACCAGTGT	down	0.22	-2.19	0.000379353
hsa-miR-338-3p_R+1	TCCAGCATCAGTGATTTTGTTGA	down	0.20	-2.34	0.000383316
bta-miR-11987_L-2_1ss8TA	AGGAAACTCTGGTGGAGGT	down	0.05	-4.45	0.000383475
hsa-miR-3130-3p	GCTGCACCGGAGACTGGGTAA	down	0.09	-3.52	0.000402804
hsa-miR-1290_1ss13TG	TGGATTTTTGGAGCAGGGA	down	0.08	-3.63	0.000403901
hsa-miR-7706_R-1	TGAAGCGCCTGTGCTCTGCCGAG	down	0.37	-1.44	0.000408641
hsa-miR-29b-2-5p_R+1	CTGGTTTCACATGGTGGCTTAGA	down	0.17	-2.54	0.00041214
hsa-miR-548au-5p_R-1	AAAAGTAATTGCGGTTTTTG	down	0.17	-2.55	0.000412952
hsa-miR-548am-5p_R-2	AAAAGTAATTGCGGTTTTTG	down	0.17	-2.55	0.000412952
hsa-miR-574-5p	TGAGTGTGTGTGTGTGAGTGTGT	down	0.18	-2.47	0.000413532

hsa-miR-16-1-3p	CCAGTATTAACTGTGCTGCTGA	down	0.21	-2.24	0.000415088
mmu-miR-146a-5p_R+1	TGAGAACTGAATTCCATGGGTTT	up	3.75	1.91	0.000440424
hsa-miR-618_R-2	AAACTCTACTTGTCCTTCTGA	down	-inf	-inf	0.000442692
hsa-miR-26a-5p	TTCAAGTAATCCAGGATAGGCT	up	3.79	1.92	0.000454235
hsa-miR-3202_L+2R-3	TATGGAAGGGAGAAGAGCTTT	down	-inf	-inf	0.000465686
hsa-miR-450a-2-3p_L-1	TTGGGGACATTTTGCATTCAT	down	0.02	-5.75	0.000496953
hsa-miR-215-5p_R-1	ATGACCTATGAATTGACAGA	down	0.01	-7.23	0.000537576
mml-miR-378d_L-1R+1_1ss21CG	CTGGACTTGGAGTCAGAAGGAG	down	-inf	-inf	0.000569743
mmu-miR-6238_L-1R-3_1ss12TC	TATTAGTCAGCGGAGGAA	down	-inf	-inf	0.000584533
hsa-miR-423-5p	TGAGGGGCAGAGAGCGAGACTTT	down	0.55	-0.86	0.000602025
hsa-miR-183-3p_L-1	TGAATTACCGAAGGGCCATAA	down	0.10	-3.37	0.000604478
hsa-miR-3611_R-2	TTGTGAAGAAAGAAATTCT	down	0.04	-4.69	0.000607847
hsa-miR-362-5p_R-2	AATCCTTGGAACCTAGGTGTGA	down	0.17	-2.59	0.000608832
hsa-miR-3688-3p_R-2	TATGGAAAGACTTTGCCACT	down	0.21	-2.28	0.000613947
PC-5p-120168_84	GGCAGAGAGGAGGAGAGAATTG	down	-inf	-inf	0.000615084
hsa-mir-3922-p3	TGTGGGACTTCTGGCCTTGA	down	0.07	-3.74	0.000634045
hsa-miR-548q_L-1R+1	CTGGTGCAAAAGTAATGGCGGT	down	-inf	-inf	0.000643992
hsa-miR-30a-5p_R+2	TGTAAACATCCTCGACTGGAAGCT	down	0.18	-2.44	0.000650598
hsa-miR-152-3p	TCAGTGCATGACAGAACTTGG	down	0.35	-1.50	0.000681248
hsa-miR-550a-5p_R-2	AGTGCCTGAGGGAGTAAGAGC	down	0.22	-2.16	0.000689858
hsa-miR-10b-3p_L-1	CAGATTCGATTCTAGGGGAAT	down	0.10	-3.28	0.000695003
hsa-miR-548e-5p	CAAAAGCAATCGCGGTTTTTGC	down	0.18	-2.44	0.000701408
hsa-miR-1303_R-2	TTTAGAGACGGGGTCTTGCT	down	0.01	-6.15	0.000708581
hsa-miR-4433b-5p_R+1	ATGTCCCACCCCCACTCCTGTT	up	14.54	3.86	0.000714369
hsa-miR-3615_R+1	TCTCTCGGCTCCTCGCGGCTCG	down	0.40	-1.32	0.000714975
hsa-miR-4466_R+2	GGGTGCGGGCCGGCGGGGTC	down	-inf	-inf	0.000718557

hsa-miR-3064-5p	TCTGGCTGTTGTGGTGTGCAA	down	0.12	-3.01	0.0007615
hsa-mir-3196-p5_1ss4GT	GGGTCGGGGCGGCAGGGGCC	down	0.01	-7.50	0.000768424
hsa-miR-142-3p_R-1	TGTAGTGTTTCCTACTTTATGG	down	0.33	-1.62	0.000787849
pal-mir-10001-p5_1ss1AT	TGGGCGGGCGGGGCCGGGGG	down	0.00	-9.96	0.000792689
hsa-miR-7-1-3p	CAACAAATCACAGTCTGCCATA	down	0.29	-1.77	0.000798761
hsa-miR-147b-3p	GTGTGCGGAAATGCTTCTGCT	down	-inf	-inf	0.000837268
hsa-miR-181a-5p	AACATTCAACGCTGTCGGTGAGT	down	0.64	-0.64	0.000838619
hsa-miR-450a-1-3p	ATTGGGAACATTTTGCATGTAT	down	0.02	-5.46	0.000842992
bta-miR-150_1ss10CT	TCTCCCAACTCTTGTACCAGTGT	down	-inf	-inf	0.000855105
hsa-let-7a-5p	TGAGGTAGTAGGTTGTATAGTT	down	0.25	-2.02	0.000862466
mdo-miR-106-5p	AAAAGTGCTTATAGTGCAGGTAG	down	-inf	-inf	0.000866975
hsa-miR-335-5p	TCAAGAGCAATAACGAAAAATGT	up	1.92	0.94	0.000872125
hsa-mir-5684-p3_1ss16CG	TGCCCAGGCTGGAGTGCAG	down	-inf	-inf	0.000872613
hsa-miR-580-3p	TTGAGAATGATGAATCATTAGG	down	-inf	-inf	0.000942594
hsa-miR-624-5p_R-1	TAGTACCAGTACCTTGTGTTC	down	0.28	-1.86	0.000945669
hsa-miR-151b_R+2	TCGAGGAGCTCACAGTCTAG	down	0.48	-1.07	0.000995322
hsa-miR-6503-3p_L-1R-1_1ss7AG	GGACTGGGATGCAGACCTC	down	0.01	-7.18	0.001015093
hsa-miR-371b-5p	ACTCAAAAGATGGCGGCACTTT	down	0.20	-2.35	0.00102028
hsa-miR-1250-5p	ACGGTGCTGGATGTGGCCTTT	down	0.17	-2.57	0.001033156
hsa-miR-3942-5p_L-1	AGCAATACTGTTACCTGAAAT	down	0.18	-2.46	0.001062149
bta-miR-1246_L-1R+3	ATGGATTTTTGGAGCAGGGAG	down	0.02	-5.62	0.001062681
hsa-miR-5001-3p_R-1	TTCTGCCTCTGTCCAGGTCCT	down	0.20	-2.33	0.001068956
hsa-miR-676-3p_R+1	CTGTCCTAAGGTTGTTGAGTTT	down	-inf	-inf	0.001106478
ssc-mir-4332-p5_1ss9CT	GGGTGGGGTCGGCGGGGG	down	0.00	-7.97	0.001110239
hsa-miR-1301-3p_R+1	TTGCAGCTGCCTGGGAGTGACTTCT	up	3.45	1.79	0.001126926
mmu-mir-6236-p3_1ss2AG_2	CGGCCGTCGCCGGCAGTC	down	0.17	-2.59	0.001137489

mmu-mir-6236-p3_1ss2AG_1	AGCTAGCCCTGAAAATGGAT	down	0.17	-2.59	0.001137489
hsa-miR-509-3p	TGATTGGTACGTCTGTGGGTAG	down	-inf	-inf	0.001144557
PC-5p-35367_398	ACAGGATGCAGTGCTCAGTGA	down	0.02	-5.42	0.001178901
hsa-miR-616-3p_L+1R-3	AAGTCATTGGAGGGTTTGAG	down	0.05	-4.24	0.001202079
hsa-miR-6852-5p	CCCTGGGGTTCTGAGGACATG	up	5.12	2.36	0.001272002
hsa-miR-659-5p	AGGACCTTCCCTGAACCAAGGA	down	-inf	-inf	0.001307356
pal-miR-9993a-3p	ATCTCGGTGGGACCTCCA	down	0.19	-2.40	0.00131013
hsa-miR-362-3p_1ss22AT	AACACACCTATTCAAGGATTCT	down	-inf	-inf	0.001324293
hsa-miR-6764-5p	TCCCAGGGTCTGGTCAGAGTTG	down	-inf	-inf	0.001348013
hsa-mir-3199-1-p5	ACTGCCTTAGGAGAAAGTTTCT	down	-inf	-inf	0.001353807
hsa-mir-3199-2-p5	ACTGCCTTAGGAGAAAGTTTCT	down	-inf	-inf	0.001353807
hsa-miR-628-5p	ATGCTGACATATTTACTAGAGG	down	0.18	-2.51	0.001380983
hsa-miR-582-3p	TAACTGGTTGAACAACTGAACC	down	0.04	-4.70	0.00139723
hsa-miR-205-5p_R-1	TCCTTCATTCCACCGGAGTCT	down	0.16	-2.65	0.001425488
PC-3p-62500_195	AAATCTCGCTGGGGCCTCCA	down	-inf	-inf	0.001438588
hsa-miR-4511_R+1	GAAGAACTGTTGCATTTGCCCTG	down	0.03	-5.29	0.001464203
hsa-miR-548n	CAAAAGTAATTGTGGATTTTGT	down	0.19	-2.40	0.001480629
hsa-miR-3200-5p	AATCTGAGAAGGCGCACAAGGT	down	0.10	-3.31	0.001494014
hsa-miR-10400-5p_R-3_1ss12GA	CGGCGGCGGCGACTCTGG	down	-inf	-inf	0.001552286
hsa-miR-26b-5p_R+1	TTCAAGTAATTCAGGATAGGTT	down	0.29	-1.78	0.001570283
hsa-miR-516a-5p_R-1	TTCTCGAGGAAAGAAGCACTTT	down	0.01	-6.50	0.001580756
hsa-mir-2110-p3	CACCGCGGTCTTTTCCTCCCACT	up	32.66	5.03	0.001624901
hsa-miR-4672	TTACACAGCTGGACAGAGGCA	down	-inf	-inf	0.001631834
PC-5p-273115_36	TGTGAGGAAGCTGTTGTTGCT	down	0.11	-3.12	0.001746197
hsa-miR-744-5p_R-1	TGCGGGGCTAGGGCTAACAGC	up	2.94	1.56	0.00176165
hsa-miR-660-3p_R-2	ACCTCCTGTGTGCATGGAT	down	-inf	-inf	0.001846501

hsa-miR-1306-3p_R+4	ACGTTGGCTCTGGTGGTGATGT	down	0.34	-1.55	0.001850341
hsa-miR-204-3p	GCTGGGAAGGCAAAGGGACGT	down	0.01	-6.17	0.002012073
ppy-mir-1268-p3_1ss8TC	AGCTACTCGGGAGGCTGA	down	-inf	-inf	0.00204359
hsa-miR-2277-3p_R+1	TGACAGCGCCCTGCCTGGCTCG	down	0.08	-3.60	0.002061216
hsa-miR-2115-3p	CATCAGAATTCATGGAGGCTAG	down	-inf	-inf	0.002074986
PC-5p-146_367656	TTCCTCTTTCCGGCACCA	up	326.24	8.35	0.002090502
hsa-miR-30c-5p_R+1	TGTAAACATCCTACACTCTCAGCT	up	2.13	1.09	0.002157759
hsa-miR-5000-3p_R-1	TCAGGACACTTCTGAACTTGG	down	-inf	-inf	0.002158351
PC-5p-31521_454	TTGCAAGCAACACTCTGTGG	down	0.20	-2.30	0.002207087
PC-3p-111035_92	TAAAAACCGTGACTACTTCT	down	0.02	-5.57	0.002241571
hsa-miR-1228-5p	GTGGGCGGGGGCAGGTGTGTG	down	-inf	-inf	0.002260147
PC-3p-228736_42	ACGGAAACGGAAACAAAGCTTT	down	-inf	-inf	0.002296962
hsa-miR-124-3p_R-3	TAAGGCACGCGGTGAATGC	down	-inf	-inf	0.002309275
hsa-miR-548az-5p_L-2R+1_1ss8GA	AAAGTAATTGTGGTTTTTGCT	down	0.01	-7.29	0.002310638
hsa-mir-548ac-p5_1ss6TA	AAAGTAATTGTGGTTTTTGCT	down	0.01	-7.29	0.002310638
hsa-miR-155-5p_R-1	TTAATGCTAATCGTGATAGGGGT	down	0.47	-1.08	0.002388473
bta-miR-378_L-2R+1	TGGACTTGGAGTCAGAAGGCT	down	0.10	-3.32	0.002430625
bta-mir-1246-p3_1ss18AG_2	TGGATTTTTGGAGCAGGGAG	down	0.01	-6.21	0.002435808
bta-mir-1246-p3_1ss18AG_1	AAATGGATTTTTGGAGCGG	down	0.01	-6.21	0.002435808
hsa-miR-3146_R+1	CATGCTAGGATAGAAAGAATGGG	down	-inf	-inf	0.002537175
pal-miR-9995-3p_1ss15TA	ATCTCGGTGGAACCACCA	down	0.02	-6.01	0.002542022
ssc-mir-4332-p5_1ss12CT	CGGGGGTGGGGTCGGCGGGGG	down	0.09	-3.55	0.002571338
hsa-miR-4646-5p	ACTGGGAAGAGGAGCTGAGGGA	down	0.12	-3.03	0.002581087
hsa-miR-126-5p	CATTATTACTTTTGGTACGCG	up	1.63	0.71	0.002612256
hsa-miR-191-5p	CAACGGAATCCCAAAAGCAGCTG	up	5.69	2.51	0.002616433
hsa-miR-15a-3p_1ss22AT	CAGGCCATATTGTGCTGCCTCT	down	0.25	-1.98	0.002640489

hsa-miR-4639-5p	TTGCTAAGTAGGCTGAGATTGA	down	-inf	-inf	0.002846895
hsa-miR-675-3p_R+2	CTGTATGCCCTCACCGCTCAGC	down	-inf	-inf	0.00286346
PC-5p-386146_24	TTTAGCACGGACATGGTTCT	down	-inf	-inf	0.002865472
hsa-miR-4440_R+1	TGTCGTGGGGCTTGCTGGCTTGA	down	-inf	-inf	0.002890446
hsa-miR-7850-5p	GTTTGGACATAGTGTGGCTGG	down	-inf	-inf	0.002900266
hsa-miR-4498_R+1	TGGGCTGGCAGGGCAAGTGCTGC	down	-inf	-inf	0.002949151
pal-miR-9993b-3p_1ss1AT	TTCTCGCTGGGGCCTCCA	down	0.19	-2.42	0.002952461
hsa-mir-3929-p3_1ss19TG	AGCACTTTGGGAGGCTGAG	down	-inf	-inf	0.002959226
hsa-miR-96-5p_R-2	TTTGGCACTAGCACATTTTTG	down	0.29	-1.80	0.00297723
hsa-miR-202-3p	AGAGGTATAGGGCATGGGAA	down	-inf	-inf	0.002987385
hsa-miR-3157-3p	CTGCCCTAGTCTAGCTGAAGCT	down	0.19	-2.43	0.00299454
hsa-miR-29a-5p_R-1	ACTGATTTCTTTTGGTGTTCA	down	0.06	-4.07	0.003023378
hsa-miR-584-3p_R-2	TCAGTTCCAGGCCAACCAGG	down	-inf	-inf	0.003028548
hsa-miR-98-5p	TGAGGTAGTAAGTTGTATTGTT	down	0.45	-1.17	0.003091851
hsa-miR-1260b_1ss9AG	ATCCCACCGCTGCCACCAT	up	5.60	2.48	0.003129626
hsa-miR-3136-5p_R-1	CTGACTGAATAGGTAGGGTCAT	down	-inf	-inf	0.003185159
cja-miR-3135_L-1_1ss10CG	AGGCTGGAGTGCAGTGGCG	down	-inf	-inf	0.003203611
hsa-miR-370-3p	GCCTGCTGGGGTGGAACCTGGT	up	10.79	3.43	0.003206543
PC-3p-54257_235	GTTCGACTCCCGGTATGGGAACCA	down	0.17	-2.52	0.003210127
hsa-miR-130b-5p_R+1	ACTCTTTCCCTGTTGCACTACT	up	10.91	3.45	0.003236588
PC-5p-189265_50	TTGTGGTCTGGGGTCTTGGGC	down	-inf	-inf	0.003310691
hsa-miR-4797-3p_L-2R+2	TCAGTAAGTGGCACTCTGTCT	down	-inf	-inf	0.003321988
hsa-miR-127-3p	TCGGATCCGTCTGAGCTTGGCT	up	27.12	4.76	0.003354275
hsa-miR-4667-5p_R-2	ACTGGGGAGCAGAAGGAGAA	down	0.20	-2.34	0.003390368
hsa-miR-4742-3p_R-1	TCTGTATTCTCCTTTGCCTGCA	down	0.23	-2.13	0.00340597
hsa-miR-151a-5p	TCGAGGAGCTCACAGTCTAGT	up	1.94	0.96	0.00352844

mmu-miR-8117_L-1R-1_1ss15GA	CTCGTGTGGAACAAAAGGG	down	0.13	-2.93	0.003536616
bta-mir-1246-p5_1ss16AG	GATTTTTGGAGCAGGGAG	down	0.01	-6.62	0.00353788
hsa-miR-3117-3p_R+1	ATAGGACTCATATAGTGCCAGG	down	-inf	-inf	0.003564807
mmu-mir-6236-p3_1ss16GC	ATGGCGCTGGAGCGTCGGG	down	-inf	-inf	0.003584861
hsa-miR-11401_R+1	TCACGTCTGCGGCTGTCACGT	down	0.11	-3.24	0.003622872
hsa-miR-589-5p_R-1	TGAGAACCACGTCTGCTCTGA	down	0.49	-1.02	0.003623274
PC-5p-73128_158	GGCGGGCCATCACTGTTGGAG	down	-inf	-inf	0.00368543
mdo-miR-22-3p	AAGCTGCCAGTTGAAGAACTGC	down	0.18	-2.44	0.003716117
hsa-miR-409-3p	GAATGTTGCTCGGTGAACCCCT	up	4.27	2.10	0.003718992
hsa-miR-378j_R+1_1ss14CT	ACTGGATTTGGAGTCAGAAG	down	-inf	-inf	0.003722753
hsa-mir-548al-p3_1ss7GC	AAAAACCGCAATGACTTTTG	down	0.04	-4.83	0.003729868
hsa-miR-329-3p	AACACACCTGGTTAACCTCTTT	up	4.46	2.16	0.003737157
mmu-miR-452-3p_1ss20GA	TCAGTCTCATCTGCAAAGAAGT	down	0.02	-5.69	0.003769591
hsa-miR-6500-3p	ACACTTGTTGGGATGACCTGC	down	0.09	-3.52	0.003783276
hsa-miR-328-3p	CTGGCCCTCTCTGCCCTTCCGT	up	8.84	3.14	0.003801632
hsa-mir-597-p3	AGTGGTTCTCTTGTGGCTCA	down	-inf	-inf	0.003822119
hsa-miR-452-5p_R+1	AACTGTTTGCAGAGGAAACTGAG	down	0.23	-2.12	0.00386016
hsa-miR-508-3p_R-3	TGATTGTAGCCTTTTGGAGT	down	-inf	-inf	0.003884399
PC-3p-37476_372	ATGTTATGATGATGGGCGAAA	down	-inf	-inf	0.003888273
PC-3p-29103_499	CTTGAGACTCTGGGTCAGT	down	-inf	-inf	0.003901713
hsa-miR-4637	TACTAACTGCAGATTCAAGTGA	down	-inf	-inf	0.003934464
eca-mir-8969-p3_1ss14GT	GGTGGTTCAGTGGTAGAA	down	0.07	-3.80	0.004010694
hsa-let-7f-5p	TGAGGTAGTAGATTGTATAGTT	down	0.34	-1.58	0.004015423
hsa-miR-3064-3p_L+1R-4	TTTGCCACACTGCAACACCT	down	-inf	-inf	0.004016411
hsa-miR-4999-5p	TGCTGTATTGTCAGGTAGTGA	down	-inf	-inf	0.004032134
pal-mir-9226-p5_1ss18CT	TCCCTGTTCGGGCGCCATT	up	4.29	2.10	0.004115545

hsa-miR-4755-3p	AGCCAGGCTCTGAAGGGAAAGT	down	-inf	-inf	0.004151231
hsa-miR-1224-5p_R+2	GTGAGGACTCGGGAGGTGGAG	down	0.09	-3.45	0.004221213
hsa-mir-3648-2-p5	GGGGGAGCCGCGGGGATC	down	0.09	-3.50	0.004354447
PC-3p-33579_423	TTCGCTGGGAATTCAGCCTCT	down	0.06	-4.17	0.004360602
hsa-miR-7704_R-1	CGGGGTCGGCGGCGACGT	down	0.24	-2.07	0.004409855
hsa-mir-653-p5	TTGAAACAATCTCTACTGAAC	down	-inf	-inf	0.004420893
hsa-miR-30b-5p	TGTAAACATCCTACACTCAGCT	up	2.18	1.12	0.004473191
PC-3p-23817_616	TTGCTGGGAAAGGGAGAAGTTC	down	0.19	-2.40	0.004503405
hsa-miR-6767-5p	TCGCAGACAGGGACACATGGAGA	down	0.07	-3.89	0.00456342
hsa-miR-378a-5p	CTCCTGACTCCAGGTCCTGTGT	down	0.18	-2.44	0.004569989
hsa-miR-340-3p_R+1	TCCGTCTCAGTTACTTTATAGCC	up	11.29	3.50	0.004579682
hsa-miR-643	ACTTGTATGCTAGCTCAGGTAG	down	0.07	-3.77	0.004585324
hsa-miR-671-5p_R+1	AGGAAGCCCTGGAGGGGCTGGAGG	down	0.06	-4.04	0.004589911
hsa-miR-139-5p	TCTACAGTGCACGTGTCTCCAGT	down	0.44	-1.18	0.004687775
hsa-miR-501-3p	AATGCACCCGGGCAAGGATTCT	down	0.49	-1.04	0.004726515
hsa-miR-516b-5p	ATCTGGAGGTAAGAAGCACTTT	down	-inf	-inf	0.004727218
hsa-miR-11400_1ss20TC	TCGGCTGTGTATCTCTGTGCC	up	3.87	1.95	0.004928951
hsa-miR-550b-2-5p_L-3_1ss21CG	TGCCTGAGGGAGTAAGAGA	down	0.06	-4.02	0.004939498
PC-5p-62477_195	CAGAGTGGGGTTTTGCAGTC	down	0.13	-2.93	0.004959317
hsa-miR-199a-5p	CCCAGTGTTCAGACTACCTGTTC	up	9.81	3.29	0.004965905
PC-3p-129317_77	TAGGTCACTGGGGTCAGAG	down	0.19	-2.42	0.005004825
hsa-miR-873-3p_L-1	GAGACTGATGAGTTCCCGGGA	down	0.01	-6.27	0.005024181
hsa-miR-548b-5p_R-4	AAAAGTAATTGTGGTTTT	down	0.03	-4.97	0.005185825
hsa-miR-4326_R+3	TGTTCCTCTGTCTCCCAGACTCT	down	0.35	-1.51	0.005196965
bta-miR-378_R+1_1ss22CA	ACTGGACTTGGAGTCAGAAGGAT	down	0.00	-10.07	0.005233455
hsa-miR-6509-5p_R-1	ATTAGGTAGTGGCAGTGGAA	down	-inf	-inf	0.005284102

hsa-miR-3691-5p_L+1R-2	TAGTGGATGATGGAGACTCGGT	down	-inf	-inf	0.005325661
hsa-miR-513c-5p_R-2	TTCTCAAGGAGGTGTCGTTT	down	-inf	-inf	0.005360135
hsa-miR-30d-5p_R+2	TGTAAACATCCCCGACTGGAAGCT	down	0.72	-0.47	0.005415705
PC-5p-190163_50	TTAAGTGGGAAACGATGTG	down	-inf	-inf	0.005587299
hsa-miR-335-3p	TTTTTCATTATTGCTCCTGACC	up	18.45	4.21	0.005699661
hsa-miR-214-5p_1ss22CA	TGCCTGTCTACACTTGCTGTGA	down	0.20	-2.35	0.005722329
hsa-miR-3682-3p	TGATGATACAGGTGGAGGTAG	down	-inf	-inf	0.005728604
hsa-miR-548ai_R-2	AAAGGTAATTGCAGTTTTTC	down	-inf	-inf	0.005847297
eca-miR-451_R-2	AAACCGTTACCATTACTGTG	down	0.18	-2.44	0.005867644
mmu-mir-3535-p3	CCTCTAGATAGTCAAGTTCTGATC	down	-inf	-inf	0.00589662
hsa-miR-146a-5p	TGAGAACTGAATTCCATGGGTT	up	3.30	1.72	0.006033463
PC-5p-104097_99	TGGAGAAAGGACTTCAGGGAGT	down	-inf	-inf	0.006136062
hsa-miR-378c_R-5	ACTGGACTTGGAGTCAGAAG	down	0.03	-5.03	0.006245196
hsa-miR-222-5p_R-1	CTCAGTAGCCAGTGTAGATCC	down	0.07	-3.94	0.006267183
hsa-miR-218-5p_R-1	TTGTGCTTGATCTAACCATG	down	0.22	-2.18	0.006270965
hsa-miR-181c-3p_L-1R+1	ACCATCGACCGTTGAGTGGACC	up	3.95	1.98	0.006277796
hsa-miR-6884-5p	AGAGGCTGAGAAGGTGATGTTG	down	-inf	-inf	0.006330237
hsa-miR-320d_R-1	AAAAGCTGGGTTGAGAGG	down	0.07	-3.93	0.006434751
hsa-miR-548l_R-1	AAAAGTATTTGCGGGTTTTGT	down	0.28	-1.86	0.006564142
hsa-miR-194-5p_R-1	TGTAACAGCAACTCCATGTGG	down	0.05	-4.43	0.006729091
hsa-miR-873-5p_L+1R-3	TGCAGGAACTTGTGAGTCT	down	0.02	-5.46	0.006942793
efu-miR-9226_L-2_1ss22GA	AAGTCCCTGTTCGGGCGCCA	down	-inf	-inf	0.007010783
PC-5p-295297_33	ACAGCGAGAGGCAGCTCTGG	down	0.19	-2.39	0.007173272
hsa-miR-1289_R-1	TGGAGTCCAGGAATCTGCATTT	down	0.13	-2.91	0.007265983
hsa-miR-190a-5p_R+1	TGATATGTTTGATATATTAGGTT	down	0.02	-6.01	0.00743068
PC-3p-147533_66	TAACTTGTGTGACTTTGGGCGA	down	-inf	-inf	0.007459496

hsa-miR-125a-5p_R-2	TCCCTGAGACCCTTTAACCTGT	up	2.64	1.40	0.007505459
hsa-miR-500b-5p_L+1R+3	TAATCCTTGCTACCTGGGTGAG	down	0.03	-4.94	0.007536963
mmu-miR-5126_L-4_1ss18CT	GCGGGGCCGGGGGTGGGG	down	-inf	-inf	0.007543519
hsa-miR-378a-3p	ACTGGACTTGGAGTCAGAAGGC	down	0.05	-4.41	0.00756731
hsa-miR-223-3p_R+1	TGTCAGTTTGTCAAATACCCCAA	down	0.57	-0.81	0.00759517
hsa-miR-5010-3p_R+1	TTTTGTGTCTCCCATTCCCCAGT	down	0.12	-3.03	0.007636142
PC-5p-278729_35	AGGCAGGGTCGGGTAGGGGGCA	down	-inf	-inf	0.007810898
mmu-miR-501-3p_R-1	AATGCACCCGGGCAAGGATTT	down	0.10	-3.31	0.007841223
hsa-miR-320c_R-1	AAAAGCTGGGTTGAGAGGG	down	0.12	-3.06	0.008007438
hsa-miR-548ar-5p_R-1_1ss10TC	AAAAGTAATCGCAGTTTTTG	down	-inf	-inf	0.008227982
hsa-miR-548x-5p_L-3_1ss13TC	AAAAGTAATCGCAGTTTTTG	down	-inf	-inf	0.008227982
hsa-miR-548h-5p_R-2_1ss13GA	AAAAGTAATCGCAGTTTTTG	down	-inf	-inf	0.008227982
hsa-mir-548f-1-p5_1ss11AG	AAAAGTAATCGCAGTTTTTG	down	-inf	-inf	0.008227982
hsa-mir-548i-1-p5	TTAGGTTGGTGCAAAAGTAA	down	-inf	-inf	0.008233578
hsa-mir-548f-4-p5	TTAGGTTGGTGCAAAAGTAA	down	-inf	-inf	0.008233578
hsa-mir-548y-p5	TTAGGTTGGTGCAAAAGTAA	down	-inf	-inf	0.008233578
hsa-miR-423-3p	AGCTCGGTCTGAGGCCCCTCAGT	up	1.71	0.77	0.008332745
hsa-miR-4781-3p_L-2R+3	TGTTGGAATCCTCGCTAGAGCGT	down	0.07	-3.92	0.008337751
hsa-miR-3163_R-1	TATAAAATGAGGGCAGTAAGA	down	-inf	-inf	0.008357575
hsa-miR-4489	TGGGGCTAGTGATGCAGGACG	down	-inf	-inf	0.008385017
hsa-mir-548v-p5	AAAAGTAATTGCGGTTTT	down	0.03	-4.84	0.008385348
PC-5p-64281_188	AGCAGCATTGTACAGGGAAA	down	-inf	-inf	0.008498819
hsa-miR-654-3p_R-2	TATGTCTGCTGACCATCACC	up	16.93	4.08	0.008503838
hsa-miR-429	TAATACTGTCTGGTAAAACCGT	down	0.05	-4.40	0.008712457
PC-5p-4861_2738	GCCTGTACTCTTTATCCT	up	19.66	4.30	0.008730005
PC-3p-4861_2738	GCCTGTACTCTTTATCCT	up	19.66	4.30	0.008730005

hsa-miR-145-5p_R-1	GTCCAGTTTTCCCAGGAATCCC	down	0.40	-1.33	0.008737173
hsa-miR-1270	CTGGAGATATGGAAGAGCTGTGT	down	0.18	-2.48	0.008744543
hsa-miR-4474-3p_R-2	TTGTGGCTGGTCATGAGGCT	down	0.03	-4.91	0.008766563
hsa-miR-6875-5p	TGAGGGACCCAGGACAGGAGA	down	-inf	-inf	0.008813581
hsa-miR-374a-3p	CTTATCAGATTGTATTGTAATT	down	0.33	-1.62	0.008857548
hsa-miR-27a-5p	AGGGCTTAGCTGCTTGTGAGCA	down	0.30	-1.75	0.008884418
hsa-mir-600-p5	CATAGGAAGGCTCTTGTCTGT	down	-inf	-inf	0.008907558
mml-miR-378d_L-1R-1_1ss21CT	CTGGACTTGGAGTCAGAAGT	down	-inf	-inf	0.009059891
hsa-miR-3176_R+2	ACTGGCCTGGGACTACCGGGA	down	0.12	-3.01	0.009062435
hsa-miR-151a-3p	CTAGACTGAAGCTCCTTGAGG	up	1.42	0.51	0.009113039
hsa-mir-3929-p5_1ss5AT	CACCTGTAATCCCAGCACTT	down	-inf	-inf	0.009279969
hsa-miR-7976_R+1	TGCCCTGAGACTTTTGCTCT	down	0.36	-1.46	0.009308272
mml-miR-378d_R-1_1ss21CT	ACTGGACTTGGAGTCAGAAGT	down	0.01	-6.37	0.009350738
hsa-miR-148a-3p	TCAGTGCACTACAGAACTTTGT	down	0.25	-2.01	0.009379144
hsa-miR-6750-5p_L-1R-3	AGGGAACAGCTGGGTGAGCT	down	0.02	-5.60	0.00939065
hsa-miR-576-5p	ATTCTAATTTCTCCACGTCTTT	down	0.30	-1.74	0.009422867
hsa-miR-331-5p_R-2	CTAGGTATGGTCCCAGGGAT	down	0.57	-0.82	0.009473956
PC-5p-87005_125	GAAGAAGGCTAGGGGACAG	down	-inf	-inf	0.009518621
mmu-miR-5119_L+1R-2	TCATCTCATCCTGGGGCT	up	16.16	4.01	0.009560608
hsa-miR-320b_R-2	AAAAGCTGGGTTGAGAGGGC	down	0.16	-2.66	0.009598398
hsa-miR-6862-5p	CGGGCATGCTGGGAGAGACTTT	down	-inf	-inf	0.009659058
mmu-miR-146a-5p_R+2	TGAGAACTGAATTCCATGGGTTAA	up	2.65	1.40	0.009791564
hsa-mir-5695-p5	TCTAGATTCTTCTTGGCCTCT	down	0.20	-2.36	0.00992675
hsa-miR-125b-1-3p_R-2	ACGGGTTAGGCTCTTGGGAG	down	0.03	-5.26	0.010010017
PC-3p-136753_72	TGTCTAGACAAGGCTGGGGAA	down	0.06	-3.98	0.010034156
hsa-miR-4479_R-1	CGCGCGGCCGTGCTCGGAGCA	down	-inf	-inf	0.01011644

PC-3p-143720_68	ATTTGGCCTTTTATGTTCTTGA	down	-inf	-inf	0.010200788
hsa-miR-485-3p	GTCATACACGGCTCTCCTCTCT	up	15.92	3.99	0.01023646
PC-3p-128622_77	TCTTGACTAGCTTGCTGTTT	down	-inf	-inf	0.010277156
hsa-miR-548h-3p_R-1_1ss4AG	CAAGAACCGCAATTACTTTTGC	down	0.30	-1.74	0.010307196
hsa-miR-125b-5p_R-2	TCCCTGAGACCCTAACTTGT	down	0.40	-1.33	0.010459053
hsa-miR-3605-3p_R-2	CCTCCGTGTTACCTGTCCTCT	down	0.28	-1.82	0.010470439
hsa-miR-3173-3p_L-1	AAGGAGGAAATAGGCAGGCCA	down	0.12	-3.01	0.010494915
PC-3p-82011_136	TCCTGGAGCTGGGCAGATGGGA	down	0.10	-3.26	0.010515913
hsa-miR-2115-5p_R-2	AGCTTCCATGACTCCTGATG	down	-inf	-inf	0.010555463
hsa-miR-132-3p	TAACAGTCTACAGCCATGGTCG	down	0.33	-1.62	0.010586861
hsa-miR-219a-5p	TGATTGTCCAAACGCAATTCT	down	-inf	-inf	0.010596858
hsa-miR-4731-5p_R-1	TGCTGGGGGCCACATGAGTGT	down	-inf	-inf	0.010684256
hsa-miR-378g_R+2	ACTGGGCTTGGAGTCAGAAGGC	down	0.05	-4.27	0.010837116
hsa-miR-1273h-3p	CTGCAGACTCGACCTCCCAGGC	up	4.74	2.24	0.010876503
hsa-miR-4659a-3p	TTTCTTCTTAGACATGGCAACG	down	0.31	-1.67	0.010883123
hsa-miR-4484_L+2R-4	AAAAAAGGCGGGAGAAGC	down	0.11	-3.22	0.01092867
PC-3p-365143_26	TTGAGGTCGGACATGGTGGCTT	down	-inf	-inf	0.010977239
hsa-miR-518e-5p_R-1	CTCTAGAGGGAAGCGCTTTCT	down	-inf	-inf	0.010985773
hsa-miR-708-3p_R-2	CAACTAGACTGTGAGCTTCT	down	-inf	-inf	0.01123105
PC-5p-146020_66	AGGGACGGCCGGGGGCAAG	down	-inf	-inf	0.011262946
PC-3p-126191_79	TCTCTGGGGGTGACTGTCCGT	down	-inf	-inf	0.011318607
hsa-miR-4516_R+1	GGGAGAAGGGTCGGGGCG	down	-inf	-inf	0.011332419
hsa-mir-3159-p3_1ss21TC	TCACGCCTGTAATCCCAGCACT	down	0.08	-3.64	0.011423422
PC-5p-111666_91	TGGAGAGAAAGGCAGTTAG	down	0.05	-4.41	0.011546117
hsa-miR-425-3p_L+1R-1	CATCGGGAATGTCGTGTCCGCC	up	1.93	0.95	0.011556862
hsa-miR-1262	ATGGGTGAATTTGTAGAAGGAT	down	-inf	-inf	0.011623409

hsa-miR-3155b_R+3	CCAGGCTCTGCAGTGGGAACT	down	0.04	-4.71	0.011660596
hsa-miR-193a-5p	TGGGTCTTTGCGGGCGAGATGA	down	0.04	-4.59	0.011709687
hsa-miR-6514-5p_R-1	TATGGAGTGGACTTTCAGCTGG	down	0.07	-3.89	0.011917295
hsa-miR-3135a_R+1	TGCCTAGGCTGAGACTGCAGTGA	down	0.16	-2.63	0.012344809
hsa-miR-4492_L+1	CGGGGCTGGGCGCGCGCC	down	-inf	-inf	0.012515868
PC-5p-481280_16	TATGATGGCTGTAACAAGAAATTT	down	-inf	-inf	0.01264186
PC-3p-366052_26	ATTTGCTGTTAAGATATGGGAT	down	-inf	-inf	0.012859622
bta-miR-11971_R-1	TGAGGGGCAGAGAGTGAGA	down	-inf	-inf	0.012866422
mmu-miR-5100_R-1	TCGAATCCCAGCGGTGCCTC	down	0.23	-2.14	0.013180537
hsa-let-7f-1-3p_1ss22CT	CTATACAATCTATTGCCTTCCT	down	0.29	-1.78	0.013226436
hsa-miR-627-3p	TCTTTTCTTTGAGACTCACT	up	6.24	2.64	0.013534682
PC-3p-41831_326	AATCCTCTCGCCCCGACC	up	220.31	7.78	0.013689904
hsa-miR-6783-5p	TAGGGGAAAAGTCCTGATCCGG	down	-inf	-inf	0.013827488
hsa-miR-135a-5p	TATGGCTTTTTATTCCTATGTGA	down	0.10	-3.29	0.013912366
PC-3p-90463_119	AACAGCGGGGAAAGAAGAC	down	-inf	-inf	0.014153839
hsa-miR-6807-5p	GTGAGCCAGTGGAATGGAGAGG	down	-inf	-inf	0.014199506
hsa-miR-1296-5p	TTAGGGCCCTGGCTCCATCTCC	up	5.28	2.40	0.014244124
hsa-miR-4467_R-1	TGGCGGCGGTAGTTATGGGCT	down	0.02	-5.61	0.014573936
hsa-miR-1287-5p	TGCTGGATCAGTGGTTCGAGTC	down	0.46	-1.13	0.014593124
hsa-miR-127-5p_R+1	CTGAAGCTCAGAGGGCTCTGATT	down	0.32	-1.65	0.014690381
hsa-miR-181b-2-3p_L+1R+1	ACTCACTGATCAATGAATGCAA	down	0.16	-2.68	0.015056383
hsa-miR-548ay-3p_R-1	CAAAACCGCGATTACTCTTGC	down	0.20	-2.29	0.015146434
hsa-miR-222-3p_R+3	AGCTACATCTGGCTACTGGGTCTC	up	1.62	0.69	0.015267023
hsa-miR-4503_R-1	TTTAAGCAGGAAATAGAATTT	down	-inf	-inf	0.015451393
PC-3p-4764_2788	GAGGGCGCGCGGGTCGGG	down	0.05	-4.36	0.015534764
hsa-miR-202-5p_R-1	TTCCTATGCATATACTTCTTT	down	-inf	-inf	0.015569007

hsa-miR-6763-5p_L+2R+1	TCCTGGGGAGTGGCTGGGGAGC	down	0.08	-3.59	0.015614703
hsa-miR-4448_R-2_1ss6CG	GGCTCGTTGGTCTAGGGG	down	0.25	-2.03	0.01572049
efu-mir-9277-p5	TCGTGGCCGAGTGGTTAAG	down	-inf	-inf	0.016204134
hsa-miR-584-5p_R-1	TTATGGTTTGCCTGGGACTGA	up	1.99	0.99	0.016323484
hsa-miR-1291_L+1R-2	GTGGCCCTGACTGAAGACCAGCA	down	0.10	-3.34	0.016346945
hsa-miR-548j-5p	AAAAGTAATTGCGGTCTTTGGT	down	0.36	-1.49	0.016412353
hsa-miR-361-5p	TTATCAGAATCTCCAGGGGTAC	up	4.96	2.31	0.016561934
PC-3p-120076_84	CAAAGAATTCCCCTTGGGCT	down	0.08	-3.62	0.016594813
mmu-mir-3968-p3_1ss11AT	ATCCCACTCCTGACACCAT	up	83.98	6.39	0.016718618
hsa-miR-4753-5p_L-1R+1	AAGGCCAAAGGAAGAGAACAGA	down	-inf	-inf	0.016719616
hsa-miR-100-5p_R-1	AACCCGTAGATCCGAACTTGT	down	0.20	-2.30	0.016722529
PC-3p-164403_58	AATAATCAGCGGGGAAAGA	down	0.08	-3.65	0.016894818
hsa-miR-3680-3p_R-1	TTTTGCATGACCCTGGGAGTAG	down	-inf	-inf	0.016980168
mmu-miR-5100_L-1R-1_1ss15TG	CGAATCCCAGCGGGGCCTC	down	-inf	-inf	0.017023771
hsa-miR-197-3p	TTCACCACCTTCTCCACCCAGC	up	3.93	1.97	0.017043153
PC-5p-55154_230	GAAGGGCTAGGATTCTAA	down	-inf	-inf	0.017187726
hsa-miR-4444_L+4R+1	TGAACTCGAGTTGGAAGAGGCGA	down	-inf	-inf	0.017338091
hsa-miR-1228-3p_R+1	TCACACCTGCCTCGCCCCCCA	down	-inf	-inf	0.017543936
cja-mir-3135-p3_1ss7GT	GCGCGATCTCGGCTCACTGCA	down	-inf	-inf	0.017588124
hsa-mir-599-p5	TTTGATAAGCTGACATGGGAC	down	-inf	-inf	0.017755908
hsa-miR-1278_R-2	TAGTACTGTGCATATCATCT	down	0.04	-4.76	0.017794045
hsa-miR-627-5p_1ss2TG	GGGAGTCTCTAAGAAAAGAGGA	down	0.01	-6.72	0.017829004
hsa-miR-3158-3p_R-1	AAGGGCTTCCTCTCTGCAGGA	down	0.26	-1.94	0.018054803
hsa-miR-4683_R-1	TGGAGATCCAGTGCTCGCCCGA	down	-inf	-inf	0.018190619
hsa-miR-4286_R+1	ACCCCACTCCTGGTACCA	up	24.23	4.60	0.01834938
hsa-miR-574-3p	CACGCTCATGCACACACCCACA	up	4.58	2.20	0.018664146

PC-5p-505426_15	TCCTGGCTGGGTTTATGGAG	down	-inf	-inf	0.018749855
hsa-miR-219a-1-3p_R+1	AGAGTTGAGTCTGGACGTCCCGA	down	0.06	-4.15	0.018806711
PC-5p-517991_14	GTAGTTTGACTGGGGTGGT	down	-inf	-inf	0.018863518
hsa-miR-483-3p_L-1R+2	CACTCCTCTCCTCCCGTCTTCT	down	0.08	-3.64	0.01889646
hsa-miR-1908-5p	CGGCGGGGACGGCGATTGGTC	up	3.13	1.65	0.018925133
hsa-miR-3960_L-2_1ss12AC	CGGCGGCGGCGGCGGGGG	down	0.44	-1.18	0.018953894
hsa-let-7g-3p	CTGTACAGGCCACTGCCTTGC	down	0.12	-3.07	0.018984429
mmu-mir-6236-p5_1ss11CG	CCTGCCGAATGAACTAGCCCT	up	21.61	4.43	0.019074181
hsa-miR-154-5p	TAGGTTATCCGTGTTGCCTTCG	down	-inf	-inf	0.019105205
hsa-miR-3179_L+1R-1	TAGAAGGGGTGAAATTTAAACG	down	-inf	-inf	0.019399212
hsa-miR-6793-5p_L+2R-3	ACTGTGGGTTCTGGGTTGGGG	down	-inf	-inf	0.01942121
hsa-miR-548am-3p_R-2	CAAAAACTGCAGTTACTTTT	down	0.03	-5.16	0.019482918
PC-5p-514458_14	AGCTGAAGTGTAAGAGGTTGA	down	-inf	-inf	0.019635008
hsa-miR-671-3p	TCCGGTTCTCAGGGCTCCACC	up	17.88	4.16	0.020019226
hsa-mir-548aw-p3_1ss22TC	AAAACCGCGATGACTTTTGCAC	down	-inf	-inf	0.021011928
bta-miR-2478_L-1_1ss2TA	AATCCCACTTCTGACACCA	up	22.55	4.50	0.021067609
ssc-mir-1285-p5_1ss22TC	CGCGCCTGTGAATAGCCACTGCA	up	4.13	2.05	0.021786372
ocu-miR-194-3p_R-2	CCAGTGGAGATGCTGTTACT	down	-inf	-inf	0.021922135
mmu-mir-6236-p3_1ss14CG	TCACCTGCCGAATGAACT	up	32.50	5.02	0.022218713
hsa-miR-378i_R+1_1ss9AT	ACTGGACTTGGAGTCAGAAGGT	down	0.07	-3.90	0.022229132
pal-miR-339b-5p_R+1	TCCCTGTCCTCCAGGAGCTT	down	0.13	-2.91	0.022637841
pal-miR-9993b-3p_L+1_1ss2AT	TTTCTCGCTGGGGCCTCCA	down	-inf	-inf	0.022818569
mmu-miR-3968_L-2_1ss14AT	AATCCCACTCCTGACACCA	up	179.14	7.48	0.022955832
PC-3p-170351_55	GTGGGAGGCTTTGAAACC	down	-inf	-inf	0.022960298
PC-3p-8405_1605	TAGTTGTTGGGGATTACT	up	18.24	4.19	0.022981024
hsa-miR-1304-3p_1ss13CA	TCTCACTGTAGCATCGAACCCC	up	3.68	1.88	0.023445285

hsa-miR-29b-1-5p_R-4	GCTGGTTTCATATGGTGGTT	down	-inf	-inf	0.023457583
mmu-miR-6239_R-2_1ss6TG	TAGCGGTGGATCACTCGG	down	-inf	-inf	0.023590013
hsa-miR-342-3p_R+1	TCTCACACAGAAATCGCACCCGTC	up	2.56	1.35	0.023660474
PC-5p-370386_26	ATTGATGGCATCGAACCAGG	down	-inf	-inf	0.023818849
hsa-miR-548ab_L+1R-3	CAAAAGTAATTGTGGATTTT	down	0.22	-2.19	0.02430114
hsa-miR-2278_L-1R+1	AGAGCAGTGTGTGTTGCCTGGG	down	-inf	-inf	0.024461221
hsa-miR-509-3-5p	TACTGCAGACGTGGCAATCATG	down	-inf	-inf	0.02455571
PC-5p-153646_63	GCCATCGGGGCGAGTGCG	down	-inf	-inf	0.024931778
hsa-miR-3139_R-1	TAGGAGCTCAACAGATGCCTGT	down	-inf	-inf	0.02509119
hsa-miR-512-3p_R-2	AAGTGCTGTCATAGCTGAGG	down	-inf	-inf	0.025145688
hsa-miR-511-3p_R+2	AATGTGTAGCAAAAGACAGAAT	down	-inf	-inf	0.02518683
hsa-miR-18b-3p_L+3R-5	TACTGCCCTAAATGCCCCTT	down	0.18	-2.49	0.025199508
hsa-miR-5090_L+1R-4	CCCGGGGCAGATTGGTGTAG	down	-inf	-inf	0.025314798
hsa-miR-548d-3p	CAAAAACCACAGTTTCTTTTGC	down	-inf	-inf	0.025470246
mmu-miR-3535	TGGATATGATGACTGATTACCTGAGA	down	0.26	-1.93	0.025600473
PC-3p-1495_12859	CGAGTCCCATCAGCCACCCCA	up	13.95	3.80	0.025714033
mmu-miR-3968_L-3_1ss14AT	ATCCCACTCCTGACACCA	up	133.70	7.06	0.025946135
PC-5p-299757_33	CACACTGACACAGAGAGAGAGA	down	-inf	-inf	0.026031909
hsa-miR-4804-5p_L+1R-1_1ss7CG	TTTGGAGGGTAAGGTTAAGCA	down	0.05	-4.33	0.026047222
PC-3p-1467_13126	ATCCCTCCGTCTCCGCCA	up	57.57	5.85	0.026393727
hsa-miR-26a-2-3p	CCTATTCTTGATTACTTGTTTC	down	0.26	-1.92	0.02645758
hsa-miR-339-5p	TCCCTGTCCTCCAGGAGCTCACG	up	2.16	1.11	0.026522456
hsa-miR-4635_R-1	TCTTGAAGTCAGAACCCGCA	down	-inf	-inf	0.026733744
PC-5p-311599_32	ACTGCTGCAGATGGAAAAGTTC	down	-inf	-inf	0.027657208
PC-5p-310574_32	TTTGAGAGAACTTCGCCCTTGT	down	-inf	-inf	0.027784086
hsa-miR-199a-3p	ACAGTAGTCTGCACATTGGTTA	down	0.63	-0.67	0.02783789

hsa-miR-3198	GTGGAGTCCTGGGGAATGGAGA	down	0.11	-3.16	0.027998666
PC-3p-47036_282	GGATGTTGGCTTAGAAGC	up	15.77	3.98	0.028146088
hsa-mir-548p-p3	CAAAAACTGCAGTTACTTTTGC	down	0.23	-2.10	0.028242716
hsa-miR-548ah-3p	CAAAAACTGCAGTTACTTTTGC	down	0.23	-2.10	0.028242716
hsa-miR-4661-5p_R-1	AACTAGCTCTGTGGATCCTGA	down	-inf	-inf	0.028406731
hsa-miR-5009-5p_L-1	TGGACTTTTTCAGATTTGGGGAT	down	-inf	-inf	0.028472485
hsa-miR-4747-5p_R-3	AGGGAAGGAGGCTTGGTCT	down	0.21	-2.27	0.02856317
hsa-miR-889-3p	TTAATATCGGACAACCATTGT	up	4.25	2.09	0.028739468
PC-3p-5835_2265	GTAGGTAATCTTCAGGCT	up	77.49	6.28	0.02909039
PC-5p-6976_1912	AGAGCGTTCTGTAAGCCT	up	9.02	3.17	0.029121916
PC-3p-52541_245	ATTCAAACTCTTGGCACCA	up	94.93	6.57	0.029619934
hsa-miR-1276	TAAAGAGCCCTGTGGAGACA	down	0.13	-2.92	0.029755677
PC-3p-6927_1922	GAGGTTGGCTTAGAAGCAGC	up	13.57	3.76	0.029828702
hsa-miR-375-3p	TTTGTTCGTTCGGCTCGCGTGA	down	0.20	-2.35	0.029850579
hsa-mir-6820-p5	TCTGCGGCAGAGCTGGGGT	down	-inf	-inf	0.030221053
hsa-miR-186-3p_L-2R+1	CCAAAGGTGAATTTTTTGGGA	down	-inf	-inf	0.030405299
PC-3p-101409_103	AAACAGGATAGGCACTAAATGG	down	0.27	-1.86	0.030512679
hsa-miR-454-3p	TAGTGCAATATTGCTTATAGGGT	down	0.04	-4.58	0.030521751
PC-5p-180544_52	TAACTCTTAGAATCCCCAAAG	down	0.03	-4.85	0.031010368
hsa-miR-4669_R-1	TGTGTCCGGGAAGTGGAGGAG	down	0.10	-3.35	0.031085397
hsa-miR-23b-3p_R+1	ATCACATTGCCAGGGATTACCACT	up	1.62	0.70	0.031358138
hsa-miR-590-5p	GAGCTTATTCATAAAAGTGCAG	down	-inf	-inf	0.031361877
PC-5p-61866_198	AGTCCGGCCTCACTCACCA	up	223.87	7.81	0.031721984
PC-3p-4291_3123	ATCCCGTCTGCCTCACCA	up	203.47	7.67	0.031725451
hsa-miR-7854-3p	TGAGGTGACCGCAGATGGGAA	down	0.28	-1.85	0.032029597
hsa-miR-4676-3p_L-1	ACTGTTTCACCACTGGCTCTT	down	0.29	-1.78	0.032466957

bta-miR-11987_L-1R-1_1ss8TA	GAGGAAACTCTGGTGGAGG	down	0.29	-1.78	0.032620049
hsa-miR-1910-3p	GAGGCAGAAGCAGGATGACA	down	-inf	-inf	0.032670608
bta-miR-378_L-1R+1	CTGGACTTGGAGTCAGAAGGCT	down	0.24	-2.04	0.032834515
hsa-mir-4485-p3_1ss1CT	TGTTTAACGGCCGCGGTAC	up	7.88	2.98	0.033006497
chi-miR-16b-5p	TAGCAGCACGTAAATATTGGGG	down	-inf	-inf	0.033070927
PC-3p-48697_270	ATCCCCTCTGCCTCCACCA	up	243.65	7.93	0.033746373
hsa-miR-3614-5p_R-1	CCACTTGGATCTGAAGGCTGCC	down	0.15	-2.76	0.033959312
hsa-miR-191-3p_L-1	CTGCGCTTGGATTTCGTCCCC	up	4.84	2.27	0.034273271
hsa-miR-133a-3p_R+1	TTTGGTCCCCTTCAACCAGCTGT	up	4.62	2.21	0.034393006
hsa-miR-5003-3p	TACTTTTCTAGGTTGTTGGGG	down	-inf	-inf	0.034406533
hsa-miR-548ap-5p_L+1	CAAAAGTAATTGCGGTCTTT	down	-inf	-inf	0.03494639
PC-5p-9698_1413	GCAGGAAAAGAAATCAACC	up	15.70	3.97	0.035326994
hsa-miR-221-5p_R+2	ACCTGGCATACAATGTAGATTTCT	up	2.79	1.48	0.035340126
PC-5p-17547_833	CCCACCAGGAGCCTGGCACTGT	up	20.95	4.39	0.035404353
mmu-miR-5100_R-1_1ss15TG	TCGAATCCCAGCGGGGCCTC	down	-inf	-inf	0.036310696
hsa-miR-4446-3p	CAGGGCTGGCAGTGACATGGGT	up	6.29	2.65	0.03635323
efu-miR-9226_L-1R-1	CAAGTCCCTGTTCGGGCGCC	down	-inf	-inf	0.03665765
hsa-mir-7851-p5_1ss12AT	AGTAGCTGGGATTACAGG	down	-inf	-inf	0.036712453
PC-3p-262158_37	TATCATCTTGGGCGTGGTTGA	down	-inf	-inf	0.036879614
rno-miR-3590-3p_R+1	TAGCACAATGTGAAAAGAGCTCT	down	-inf	-inf	0.037148113
hsa-miR-6779-5p_L+1R-1	TCTGGGAGGGGCTGGGTTTGG	down	-inf	-inf	0.037690838
hsa-miR-4727-3p	ATAGTGGGAAGCTGGCAGATTC	down	-inf	-inf	0.037896358
PC-3p-27930_522	AGACTCTTCTCCCGCTCCA	up	49.02	5.62	0.037973702
PC-5p-224026_43	GTTGGAGGTTGGAGGTTGA	down	-inf	-inf	0.038166369
hsa-mir-4473-p5	CACTTGTAATGGAGAACACT	down	0.11	-3.24	0.038314456
hsa-miR-139-3p	TGGAGACGCGGCCCTGTTGGAGT	up	2.33	1.22	0.03858276

mdo-miR-200a-3p_R+2	TAACACTGTCTGGTAACGATGTTT	down	-inf	-inf	0.038845112
hsa-miR-4504	TGTGACAATAGAGATGAACATG	down	0.20	-2.34	0.038905676
hsa-miR-135a-3p_L+1R-1	ATATAGGGATTGGAGCCGTGGC	down	-inf	-inf	0.038953639
PC-3p-392001_24	TGCAGAGGGACTGGCAGGAAG	down	-inf	-inf	0.039134929
hsa-miR-374b-5p_R-1	ATATAATACAACCTGCTAAGT	up	7.22	2.85	0.039255217
PC-5p-494846_15	ATCTGAAATCTGATGAGAAAT	down	-inf	-inf	0.039309258
PC-3p-656119_10	TCACCGCCCTTCCCGCCCGCG	down	-inf	-inf	0.039900881
PC-5p-73747_156	GCCGCGGCGGCCGTCGGGTGT	down	0.38	-1.39	0.039999446
PC-3p-367049_26	ATATAGATATCATCAGAGCTGT	down	-inf	-inf	0.040269803
hsa-miR-7705_R-1	AATAGCTCAGAATGTCAGTTCT	down	-inf	-inf	0.040285581
PC-5p-80013_140	TAGGGAAAATGTACAGAAATGG	down	-inf	-inf	0.040877921
hsa-mir-3143-p3	CAACTCTTTACAATGTTTCT	down	-inf	-inf	0.041148095
hsa-miR-561-5p	ATCAAGGATCTTAAACTTTGCC	down	0.08	-3.61	0.041179238
PC-5p-335457_29	GTCGGCGGGGGCCCCGGGA	down	-inf	-inf	0.041617844
hsa-mir-497-p3_1ss5CA	AGAGAGAGGGTGGGGGAG	down	-inf	-inf	0.041764909
hsa-miR-1179_R+1	AAGCATTCTTTCATTGGTTGGT	down	-inf	-inf	0.041870402
hsa-miR-4686_R-4	TATCTGCTGGGCTTTCTGG	down	-inf	-inf	0.041920978
ptr-miR-6131_R-1_1ss15GT	GGCTGGTCGGATGGTAGT	down	-inf	-inf	0.042012476
mmu-miR-8112_L+1R-1	CTCTCCGCCACCTCCACCGC	down	-inf	-inf	0.042012743
PC-3p-85981_127	AAGGTCAGCTCAATGAGAA	up	17.89	4.16	0.042173359
mmu-miR-3968_L-2R-1_1ss14AT	AATCCCACTCCTGACACC	up	108.58	6.76	0.0422171
hsa-miR-6730-5p_L-2	AAAGGTGGAGGGGTTGTCAGA	down	-inf	-inf	0.042356541
hsa-miR-6858-5p_L-1	TGAGGAGGGGCTGGCAGGGAC	down	-inf	-inf	0.042490007
PC-5p-358054_27	TTGGAGAACTCTCCTTCCCGG	down	-inf	-inf	0.04280781
hsa-miR-6131_R-1_1ss15GT	GGCTGGTCAGATGGTAGT	down	-inf	-inf	0.042850394
hsa-mir-12136-p3_1ss20TC	TCGATTCCTTCCTTTTTTGCC	up	12.54	3.65	0.043024236

hsa-miR-642b-3p_R-3	AGACACATTTGGAGAGGGA	down	-inf	-inf	0.043522428
hsa-miR-4659b-5p_R+3	TTGCCATGTCTAAGAAGAAAAT	down	-inf	-inf	0.043665226
hsa-miR-144-5p	GGATATCATCATATACTGTAAG	down	0.03	-5.02	0.043761351
PC-3p-10362_1335	CAGCCCGAAGTGTGACCCA	up	172.34	7.43	0.043816448
mmu-mir-6236-p5_1ss4CG_1	AATGAACTAGCCCTGAAA	up	32.75	5.03	0.044025653
mmu-mir-6236-p5_1ss4CG_3	AATGAACTAGCCCTGAAAATGG	up	32.75	5.03	0.044025653
mmu-mir-6236-p5_1ss4CG_2	AATGAACTAGCCCTGAAAA	up	32.75	5.03	0.044025653
hsa-miR-99b-5p	CACCCGTAGAACCGACCTTGCG	up	5.28	2.40	0.044089942
hsa-miR-6803-3p_R-1	TCCCTCGCCTTCTCACCCTCA	down	0.05	-4.32	0.044112311
hsa-miR-138-5p	AGCTGGTGTTGTGAATCAGGCCG	down	-inf	-inf	0.04412647
PC-3p-154505_62	CTTGACTGGAGGATTCGT	down	-inf	-inf	0.044153261
hsa-miR-628-3p	TCTAGTAAGAGTGGCAGTCGA	up	1.58	0.66	0.044155683
cfa-mir-8903-p3_1ss9AG	TCTGGGGTGGGGCCTGGGAAT	down	-inf	-inf	0.044416104
hsa-miR-3158-5p_R-1	CCTGCAGAGAGGAAGCCCTT	down	-inf	-inf	0.044551092
PC-5p-310347_32	TGCAAAAATAATTGTGGTTTTGA	down	-inf	-inf	0.044621886
PC-5p-579051_12	AGTGAAGCTGGCCTAAATGTT	down	-inf	-inf	0.04484443
hsa-miR-4454_L-2	ATCCGAGTCACGGCACCA	up	13.34	3.74	0.044847902
hsa-miR-140-5p	CAGTGGTTTTACCCTATGGTAG	down	0.47	-1.09	0.04495751
hsa-miR-3928-3p	GGAGGAACCTTGGAGCTTCGGC	up	3.60	1.85	0.045291905
PC-3p-855779_7	CCTCACTCCTGCCCACACCCCTC	down	-inf	-inf	0.045609671
hsa-miR-3160-3p_R-2	AGAGCTGAGACTAGAAAGCC	down	-inf	-inf	0.045680709
mmu-miR-106a-5p	CAAAGTGCTAACAGTGCAGGTAG	down	-inf	-inf	0.045709257
hsa-miR-7851-3p_R+1	TACCTGGGAGACTGAGGTTGGAT	down	-inf	-inf	0.046248244
PC-5p-318577_31	TTTGTCTGGGGCCTGGTGAGT	down	-inf	-inf	0.046621829
hsa-miR-502-5p_L+1R-1	AATCCTTGCTATCTGGGTGCT	down	-inf	-inf	0.046767438
hsa-miR-6787-5p_1ss22CT	TGGCGGGGGTAGAGCTGGCTGT	down	-inf	-inf	0.046981061

hsa-mir-548ak-p3_1ss12TG	AAAACCGCAATGACTTTTG	down	-inf	-inf	0.046983043
hsa-miR-331-3p_L-1R+1	CCCCTGGGCCTATCCTAGAAT	up	5.92	2.57	0.047240549
hsa-miR-378d_R-2	ACTGGACTTGGAGTCAGA	down	0.03	-5.06	0.04781347
hsa-miR-103a-1-5p_R+1	GGCTTCTTTACAGTGCTGCCTTGT	down	-inf	-inf	0.047833282
hsa-miR-4690-3p_R-1	GCAGCCCAGCTGAGGCCTCT	down	0.07	-3.74	0.047938744
hsa-miR-92b-3p	TATTGCACTCGTCCCGGCCTCC	up	2.10	1.07	0.048120631
hsa-miR-323b-3p_R-1	CCCAATACACGGTCGACCTCT	up	2.57	1.36	0.048200354
hsa-miR-5188_L-1R+1	ATCGGACCCATTTAAACCGGAGA	down	-inf	-inf	0.048343481
PC-5p-127875_78	TGGCAAAGGAGGTGAGAGTG	down	-inf	-inf	0.048711104
hsa-miR-548s_R-1	ATGGCCAAAACTGCAGTTATTT	down	0.16	-2.63	0.048781578
eca-mir-1543-p5_1ss21GA	TTTGCACCTCTGAGAGTGGAAT	down	0.11	-3.13	0.048911956
eca-mir-1543-p3_1ss21GA	TTTGCACCTCTGAGAGTGGAAT	down	0.11	-3.13	0.048911956
hsa-miR-4700-5p	TCTGGGGATGAGGACAGTGTGT	down	-inf	-inf	0.048989049
mmu-miR-30f_L+1R-1_1ss17AG	TGTAAACATCCGACTGGAAGCT	down	0.04	-4.61	0.04922045
cja-miR-151_R+2	TCGAGGAGCTCACAGTCTAGTT	up	6.93	2.79	0.049547736
hsa-miR-372-3p_R-1	AAAGTGCTGCGACATTTGAGCG	down	-inf	-inf	0.049552237
PC-3p-836782_7	CAGCCTCTGCAGCTCCCCGG	down	-inf	-inf	0.049865151
PC-5p-23414_626	AAAGTAGGTCATGTCAGACT	up	28.91	4.85	0.049923367
PC-3p-11702_1197	AAAGTGGACGTATAGGGT	up	7.03	2.81	0.049931679

Supplementary Table 2. Differentially expressed miRNAs between smoking IA and non-smoking IA group.

miR name	miR sequence	up/down	fold_change	log2(fold_change)	P value
hsa-miR-378a-3p	ACTGGACTTGGAGTCAGAAGGC	down	0.27	-1.87	1.16E-05
hsa-miR-574-5p	TGAGTGTGTGTGTGTGAGTGTGT	down	0.18	-2.45	2.33E-05
hsa-miR-28-3p	CACTAGATTGTGAGCTCCTGGA	down	0.51	-0.97	3.85E-05
hsa-miR-361-3p_R+1	TCCCCCAGGTGTGATTCTGATTTG	down	0.20	-2.34	3.96E-05
hsa-miR-340-5p	TTATAAAGCAATGAGACTGATT	down	0.19	-2.40	4.08E-05
hsa-miR-374a-3p	CTTATCAGATTGTATTGTAATT	down	0.12	-3.06	4.95E-05
hsa-miR-130b-3p	CAGTGCAATGATGAAAGGGCAT	down	0.19	-2.39	7.26E-05
hsa-miR-223-3p_R+1	TGTCAGTTTGTCAAATACCCCAA	down	0.28	-1.81	7.99E-05
hsa-miR-1250-5p	ACGGTGCTGGATGTGGCCTTT	down	0.03	-5.10	8.46E-05
hsa-miR-199a-3p	ACAGTAGTCTGCACATTGGTTA	down	0.16	-2.60	8.77E-05
hsa-miR-185-5p	TGGAGAGAAAGGCAGTTCCTGA	down	0.22	-2.17	8.80E-05
hsa-miR-128-3p	TCACAGTGAACCGGTCTCTTT	down	0.24	-2.06	8.91E-05
hsa-miR-629-5p	TGGGTTTACGTTGGGAGAACT	down	0.31	-1.69	1.01E-04
hsa-miR-152-3p	TCAGTGCATGACAGAACTTGG	down	0.18	-2.46	1.04E-04
hsa-miR-151a-3p	CTAGACTGAAGCTCCTTGAGG	down	0.55	-0.85	1.15E-04
hsa-miR-142-3p_R-1	TGTAGTGTTTCCTACTTTATGG	down	0.07	-3.94	1.15E-04
hsa-miR-20b-5p	CAAAGTGCTCATAGTGCAGGTAG	down	0.09	-3.50	1.27E-04
hsa-miR-126-3p_R-1	TCGTACCGTGAGTAATAATGC	down	0.22	-2.16	1.29E-04
hsa-miR-28-5p_R-1	AAGGAGCTCACAGTCTATTGA	down	0.08	-3.62	1.44E-04
hsa-miR-103a-3p	AGCAGCATTGTACAGGGCTATGA	down	0.10	-3.38	1.81E-04
PC-3p-23817_616	TTGCTGGGAAAGGGAGAAGTTC	down	0.09	-3.54	1.87E-04
hsa-miR-22-5p_R-1	AGTTCTTCAGTGGCAAGCTTT	down	0.11	-3.19	1.88E-04
hsa-miR-93-5p	CAAAGTGCTGTTCGTGCAGGTAG	down	0.11	-3.19	2.26E-04
hsa-miR-30e-3p_1ss22CT	CTTTCAGTCGGATGTTTACAGT	down	0.36	-1.46	2.27E-04

hsa-miR-140-5p	CAGTGGTTTTACCCTATGGTAG	down	0.11	-3.23	2.38E-04
hsa-miR-17-5p	CAAAGTGCTTACAGTGCAGGTAG	down	0.05	-4.33	2.51E-04
hsa-miR-106a-5p_1ss1AC	CAAAGTGCTTACAGTGCAGGTAG	down	0.05	-4.33	2.51E-04
hsa-miR-101-3p_R+1	TACAGTACTGTGATAACTGAAG	down	0.15	-2.76	2.62E-04
hsa-miR-221-3p	AGCTACATTGTCTGCTGGGTTTC	down	0.20	-2.29	2.66E-04
hsa-miR-20a-5p	TAAAGTGCTTATAGTGCAGGTAG	down	0.04	-4.51	2.78E-04
hsa-miR-21-5p	TAGCTTATCAGACTGATGTTGA	down	0.09	-3.54	3.22E-04
PC-3p-10623_1306	CAGTTCAATGGTGTTCAGCAGA	down	0.03	-5.25	3.39E-04
hsa-miR-1307-3p_R+1	ACTCGGCGTGGCGTCGGTCGTGG	down	0.32	-1.65	3.49E-04
mmr-miR-1839_L+1R-1	AAGGTAGATAGAACAGGTCTTG	down	0.28	-1.81	3.56E-04
hsa-miR-363-5p	CGGGTGGATCACGATGCAATTT	down	0.08	-3.60	4.08E-04
mml-miR-378d_R-1_1ss21CT	ACTGGACTTGGAGTCAGAAGT	down	0.02	-5.52	4.13E-04
hsa-miR-548j-5p	AAAAGTAATTGCGGTCTTTGGT	down	0.09	-3.42	4.51E-04
hsa-miR-7851-3p_R+1	TACCTGGGAGACTGAGGTTGGAT	down	-inf	-inf	4.54E-04
hsa-miR-652-3p_R+1	AATGGCGCCACTAGGGTTGTGT	down	0.49	-1.03	4.69E-04
hsa-miR-132-5p	ACCGTGGCTTTCGATTGTTACT	down	0.08	-3.67	4.70E-04
hsa-miR-301b-3p	CAGTGCAATGATATTGTCAAAGC	down	0.03	-4.95	4.86E-04
hsa-miR-26b-5p_R+1	TTCAAGTAATTCAGGATAGGTT	down	0.25	-2.00	4.89E-04
PC-5p-35367_398	ACAGGATGCAGTGCTCAGTGA	down	0.03	-4.89	5.16E-04
hsa-miR-548n	CAAAAGTAATTGTGGATTTTGT	down	0.10	-3.26	5.18E-04
hsa-miR-548ag_1ss4GA	AAAAGTAATTGTGGTTTCTGC	down	0.05	-4.44	5.30E-04
hsa-miR-148b-3p	TCAGTGCATCACAGAACTTTGT	down	0.33	-1.59	5.36E-04
hsa-miR-107_R-2	AGCAGCATTGTACAGGGCTAT	down	0.42	-1.26	5.45E-04
hsa-miR-181b-5p_R-2	AACATTCATTGCTGTCGGTGG	down	0.22	-2.16	5.61E-04
bta-miR-378_R+1_1ss22CA	ACTGGACTTGGAGTCAGAAGGAT	down	0.01	-7.59	5.70E-04
hsa-mir-597-p3	AGTGGTTCTCTTGTGGCTCA	down	-inf	-inf	5.87E-04

hsa-miR-548bc	AAAAACTGTGATTACTTTTGC	down	0.11	-3.23	6.59E-04
hsa-miR-181d-5p_R+1	AACATTCATTGTTGTCGGTGGGTT	down	0.23	-2.10	6.84E-04
hsa-miR-1273h-5p_R+2	CTGGGAGGTCAAGGCTGCAGTGT	down	0.15	-2.71	7.32E-04
cja-miR-151_R+1	TCGAGGAGCTCACAGTCTAGC	down	0.11	-3.24	7.78E-04
hsa-miR-15a-5p_R-1	TAGCAGCACATAATGGTTTGT	down	0.28	-1.86	8.17E-04
hsa-miR-598-3p	TACGTCATCGTTGTCATCGTCA	down	0.14	-2.81	8.47E-04
hsa-miR-628-5p	ATGCTGACATATTTACTAGAGG	down	0.06	-4.15	8.48E-04
hsa-miR-33a-5p_R-1	GTGCATTGTAGTTGCATTGC	down	0.00	-8.45	8.55E-04
hsa-miR-2355-3p_L-2R+2	TGTCCTTGCTGTTTGGAGATAA	down	0.17	-2.52	8.76E-04
bta-miR-199c_L-1R+4	ACAGTAGTCTGCACATTGGTTTC	down	-inf	-inf	9.17E-04
hsa-miR-2277-3p_R+1	TGACAGCGCCCTGCCTGGCTCG	down	0.07	-3.78	9.75E-04
hsa-miR-29b-2-5p_R+1	CTGGTTTCACATGGTGGCTTAGA	down	0.14	-2.83	9.89E-04
hsa-miR-1287-5p	TGCTGGATCAGTGGTTCGAGTC	down	0.30	-1.75	1.01E-03
hsa-miR-3064-5p	TCTGGCTGTTGTGGTGTGCAA	down	0.06	-4.06	1.03E-03
hsa-miR-501-5p_R+2	AATCCTTTGTCCCTGGGTGAGAGT	down	0.04	-4.49	1.04E-03
hsa-miR-219a-1-3p_R+1	AGAGTTGAGTCTGGACGTCCCGA	down	0.06	-3.99	1.04E-03
hsa-miR-3124-5p	TTCGCGGGCGAAGGCAAAGTC	down	0.07	-3.89	1.05E-03
hsa-miR-18a-5p	TAAGGTGCATCTAGTGCAGATAG	down	0.10	-3.33	1.07E-03
mdo-miR-200a-3p_R+2	TAACACTGTCTGGTAACGATGTTT	down	-inf	-inf	1.12E-03
hsa-miR-378c_R-5	ACTGGACTTGGAGTCAGAAG	down	0.16	-2.61	1.15E-03
hsa-miR-3120-3p	CACAGCAAGTGTAGACAGGCA	down	0.26	-1.96	1.15E-03
hsa-miR-6513-5p	TTTGGGATTGACGCCACATGTCT	down	0.11	-3.22	1.16E-03
hsa-miR-32-3p_R-1	CAATTTAGTGTGTGTGATATT	down	0.05	-4.19	1.24E-03
hsa-miR-338-3p_R+1	TCCAGCATCAGTGATTTTGTTGA	down	0.15	-2.71	1.25E-03
PC-3p-83127_133	CCAGGCTCTTGGTTATGTTTT	down	0.06	-4.10	1.25E-03
hsa-miR-140-3p_R+1	TACCACAGGGTAGAACCACGGA	down	0.61	-0.72	1.31E-03

PC-5p-14422_992	ACTTGACTGCTCTGACCA	down	0.03	-5.03	1.32E-03
hsa-mir-4422-p3	GCCCTTCTTGATGCTCTTGATT	down	-inf	-inf	1.32E-03
hsa-miR-106b-5p_R-1	TAAAGTGCTGACAGTGCAGA	down	0.14	-2.88	1.32E-03
hsa-miR-580-3p	TTGAGAATGATGAATCATTAGG	down	-inf	-inf	1.36E-03
hsa-miR-497-5p	CAGCAGCACACTGTGGTTTGT	down	0.04	-4.48	1.40E-03
hsa-miR-6876-5p	CAGGAAGGAGACAGGCAGTTCA	down	0.10	-3.29	1.41E-03
hsa-miR-22-3p	AAGCTGCCAGTTGAAGAACTGT	down	0.48	-1.07	1.42E-03
hsa-miR-454-3p	TAGTGCAATATTGCTTATAGGGT	down	0.02	-5.49	1.42E-03
PC-5p-80013_140	TAGGGAAAATGTACAGAAATGG	down	-inf	-inf	1.44E-03
hsa-miR-4523	GACCGAGAGGGCCTCGGCTGT	down	-inf	-inf	1.45E-03
hsa-miR-127-5p_R+1	CTGAAGCTCAGAGGGCTCTGATT	down	0.09	-3.44	1.51E-03
hsa-miR-3136-5p_R-1	CTGACTGAATAGGTAGGGTCAT	down	-inf	-inf	1.52E-03
hsa-miR-671-5p_R+1	AGGAAGCCCTGGAGGGGCTGGAGG	down	0.05	-4.32	1.55E-03
bta-miR-199c_L-1R+2	ACAGTAGTCTGCACATTGGCT	down	0.06	-4.08	1.58E-03
hsa-miR-7151-3p_L+1	CCTACAGGCTGGAATGGGCTCA	down	-inf	-inf	1.65E-03
hsa-miR-4999-5p	TGCTGTATTGTCAGGTAGTGA	down	-inf	-inf	1.68E-03
hsa-miR-450a-2-3p_L-1	TTGGGGACATTTTGCATTCAT	down	0.06	-3.99	1.81E-03
hsa-miR-4676-3p_L-1	ACTGTTTCACCACTGGCTCTT	down	0.17	-2.52	1.81E-03
PC-5p-133941_74	AAATTTGACTGGCTATTTT	down	-inf	-inf	1.88E-03
hsa-let-7f-5p	TGAGGTAGTAGATTGTATAGTT	down	0.32	-1.64	1.88E-03
hsa-miR-12136_R+8	GAAAAAGTCATGGAGGCCATGGGGTT	down	0.19	-2.37	1.89E-03
hsa-miR-135a-3p_L+1R-1	ATATAGGGATTGGAGCCGTGGC	down	-inf	-inf	1.90E-03
hsa-miR-9-5p	TCTTTGGTTATCTAGCTGTATGA	down	0.05	-4.45	1.94E-03
hsa-miR-382-5p	GAAGTTGTTCGTGGTGGATTCG	down	0.17	-2.59	1.95E-03
hsa-miR-3065-3p	TCAGCACCAGGATATTGTTGGAG	down	-inf	-inf	1.97E-03
hsa-miR-651-5p_R-1	TTTAGGATAAGCTTGACTTTT	down	0.24	-2.06	1.98E-03

PC-5p-121193_83	AAAAGTAATTGTGGTTTTTGTGT	down	-inf	-inf	1.99E-03
hsa-miR-4804-5p_L+1R-1_1ss7CG	TTTGGAGGGTAAGGTTAAGCA	down	0.11	-3.19	2.00E-03
hsa-miR-5010-3p_R+1	TTTTGTGTCTCCCATTCCCCAGT	down	0.09	-3.48	2.02E-03
hsa-miR-6514-5p_R-1	TATGGAGTGGACTTTCAGCTGG	down	0.08	-3.66	2.05E-03
hsa-miR-3164	TGTGACTTTAAGGGAAATGGCG	down	-inf	-inf	2.08E-03
hsa-miR-429	TAATACTGTCTGGTAAAACCGT	down	0.19	-2.42	2.09E-03
hsa-miR-142-5p_L+2R-3	CCCATAAAGTAGAAAGCACT	up	2.35	1.23	2.20E-03
hsa-miR-499a-5p	TTAAGACTTGCAGTGATGTTT	down	0.22	-2.18	2.21E-03
hsa-miR-210-3p	CTGTGCGTGTGACAGCGGCTGA	down	0.14	-2.87	2.21E-03
hsa-miR-503-5p_R-2_1ss21CA	TAGCAGCGGGAACAGTTCTGA	down	0.31	-1.70	2.30E-03
mdo-miR-106-5p	AAAAGTGCTTATAGTGCAGGTAG	down	-inf	-inf	2.33E-03
mdo-miR-153-1-5p_L+1	GTCATTTTTGTGATCTGCAGCT	down	0.07	-3.80	2.41E-03
hsa-let-7i-5p	TGAGGTAGTAGTTTGTGCTGTT	down	0.53	-0.90	2.50E-03
hsa-miR-514a-3p_R-1	ATTGACACTTCTGTGAGTAG	down	-inf	-inf	2.50E-03
hsa-miR-5187-5p	TGGGATGAGGGATTGAAGTGGA	down	0.18	-2.45	2.51E-03
hsa-miR-380-5p_L+1R-1	ATGGTTGACCATAGAACATGCG	down	-inf	-inf	2.54E-03
hsa-let-7g-5p	TGAGGTAGTAGTTTGTACAGTT	down	0.36	-1.47	2.64E-03
hsa-miR-450a-1-3p	ATTGGGAACATTTTGCATGTAT	down	0.03	-5.07	2.70E-03
hsa-mir-1302-1-p5_1ss9AG	GAATTTCAGGTAAACAATGAAT	down	0.08	-3.67	2.73E-03
hsa-miR-181a-5p	AACATTCAACGCTGTCGGTGAGT	down	0.63	-0.68	2.74E-03
PC-3p-147694_66	AAGACTTTTTCTCTGACCT	down	-inf	-inf	2.79E-03
PC-5p-38571_359	AATCCTCACTTTGAATCCATGT	down	0.07	-3.76	2.81E-03
rno-miR-539-5p_R+2	GGAGAAATTATCCTTGGTGTGTTT	down	0.04	-4.59	2.82E-03
hsa-miR-3191-3p_R-1_1ss22AT	TGGGGACGTAGCTGGCCAGACT	down	-inf	-inf	2.83E-03
hsa-miR-20a-3p_R+1	ACTGCATTATGAGCACTTAAAGT	down	0.05	-4.23	2.84E-03
hsa-miR-338-5p_R-1	AACAATATCCTGGTGCTGAGT	up	2.10	1.07	2.90E-03

hsa-miR-542-3p_R-2	TGTGACAGATTGATAACTGA	down	0.14	-2.87	2.91E-03
hsa-miR-616-3p_L+1R-3	AAGTCATTGGAGGGTTTGAG	down	0.11	-3.15	2.94E-03
hsa-mir-5100-p3_1ss17TC	ATCCCAGCGGTGCCTCCA	down	0.05	-4.38	2.94E-03
mmu-miR-106a-5p	CAAAGTGCTAACAGTGCAGGTAG	down	-inf	-inf	2.98E-03
hsa-miR-190b-5p	TGATATGTTTGATATTGGGTTG	down	0.16	-2.60	3.09E-03
hsa-miR-452-5p_R+1	AACTGTTTGCAGAGGAAACTGAG	down	0.12	-3.03	3.14E-03
hsa-miR-190a-5p_R+1	TGATATGTTTGATATATTAGGTT	down	0.00	-8.17	3.22E-03
hsa-miR-4645-3p_L+2R-1	CGAGACAGTAGTTCTTGCCTGGT	down	0.16	-2.60	3.25E-03
mdo-miR-181a-5p_R+3_2	AACATTCAACGCTGTCGGTGAGTTTT	down	0.10	-3.36	3.30E-03
mdo-miR-181a-5p_R+3_1	AACATTCAACGCTGTCGGTGAGTTAT	down	0.10	-3.36	3.30E-03
eca-mir-8969-p3_1ss14GT	GGTGGTTCAGTGGTAGAA	down	0.15	-2.72	3.32E-03
hsa-miR-660-5p_R+1	TACCCATTGCATATCGGAGTTGT	down	0.34	-1.54	3.43E-03
PC-5p-49096_267	AGCCTGGAAGCTGGAGCCTGCAG	down	0.17	-2.57	3.48E-03
hsa-miR-590-3p	TAATTTTATGTATAAGCTAGT	down	0.17	-2.54	3.49E-03
hsa-miR-219b-5p	AGATGTCCAGCCACAATTCTCG	down	0.12	-3.04	3.60E-03
hsa-miR-125a-5p_R-2	TCCCTGAGACCCTTTAACCTGT	up	3.49	1.80	3.69E-03
hsa-miR-27b-5p	AGAGCTTAGCTGATTGGTGAAC	down	0.23	-2.12	3.77E-03
hsa-miR-4750-5p_R+1	CTCGGGCGGAGGTGGTTGAGTGT	down	0.03	-5.10	3.80E-03
hsa-miR-154-5p	TAGGTTATCCGTGTTGCCTTCG	down	-inf	-inf	3.84E-03
hsa-miR-11401_R+1	TCACGTCTGCGGCTGTCACGT	down	0.23	-2.13	3.85E-03
hsa-miR-1278_R-2	TAGTACTGTGCATATCATCT	down	0.10	-3.37	3.90E-03
mml-miR-378d_L-1R-1_1ss21CT	CTGGACTTGGAGTCAGAAGT	down	-inf	-inf	3.93E-03
PC-3p-128672_77	TTGGGGAGTTTACTGGAGGAAG	down	-inf	-inf	4.10E-03
hsa-miR-135a-5p	TATGGCTTTTTATTCCTATGTGA	down	0.03	-4.85	4.15E-03
hsa-miR-19a-3p	TGTGCAAATCTATGCAAAACTGA	down	0.31	-1.67	4.17E-03
hsa-miR-1-3p	TGGAATGTAAAGAAGTATGTAT	down	0.17	-2.53	4.28E-03

hsa-miR-5585-3p	CTGAATAGCTGGGACTACAGGT	down	-inf	-inf	4.42E-03
hsa-miR-335-5p	TCAAGAGCAATAACGAAAAATGT	up	1.61	0.68	4.47E-03
hsa-miR-130a-3p	CAGTGCAATGTTAAAAGGGCAT	down	0.29	-1.79	4.50E-03
hsa-miR-548az-5p_L-2R+1_1ss8GA	AAAGTAATTGTGGTTTTTGCT	down	0.02	-5.40	4.55E-03
hsa-mir-548ac-p5_1ss6TA	AAAGTAATTGTGGTTTTTGCT	down	0.02	-5.40	4.55E-03
cgr-miR-1260_L-1R+2_5	TCCCACCGCTGCCACCATA	down	-inf	-inf	4.58E-03
cgr-miR-1260_L-1R+2_1	TCCCACCGCTGCCACCAAA	down	-inf	-inf	4.58E-03
cgr-miR-1260_L-1R+2_3	TCCCACCGCTGCCACCAAT	down	-inf	-inf	4.58E-03
cgr-miR-1260_L-1R+2_4	TCCCACCGCTGCCACCAGA	down	-inf	-inf	4.58E-03
cgr-miR-1260_L-1R+2_2	TCCCACCGCTGCCACCAAG	down	-inf	-inf	4.58E-03
hsa-miR-223-5p_R+2	CGTGTATTTGACAAGCTGAGTTGG	down	0.28	-1.83	4.60E-03
hsa-miR-3174_R-1	TAGTGAGTTAGAGATGCAGAGC	down	0.05	-4.43	4.75E-03
hsa-miR-6764-5p	TCCCAGGGTCTGGTCAGAGTTG	down	-inf	-inf	4.78E-03
hsa-miR-3691-5p_L+1R-2	TAGTGGATGATGGAGACTCGGT	down	-inf	-inf	5.09E-03
hsa-miR-4533_R+2	TGGAAGGAGGTTGCCGGACGCTGT	down	-inf	-inf	5.24E-03
hsa-miR-5581-3p	TTCCATGCCTCCTAGAAGTTCC	down	-inf	-inf	5.27E-03
hsa-miR-224-5p_L-1	CAAGTCACTAGTGGTTCCGTTTAG	down	0.32	-1.67	5.49E-03
hsa-miR-379-5p	TGGTAGACTATGGAACGTAGG	down	0.19	-2.41	5.50E-03
hsa-miR-532-5p	CATGCCTTGAGTGTAGGACCGT	down	0.48	-1.06	5.66E-03
hsa-miR-6842-3p	TTGGCTGGTCTCTGCTCCGCAG	down	0.05	-4.26	5.74E-03
PC-3p-103492_100	GAAATAATCTATTCTGAGGCTTT	down	0.14	-2.82	5.81E-03
hsa-miR-30e-5p_R+2	TGTAAACATCCTTGACTGGAAGCT	down	0.67	-0.57	5.82E-03
cgr-miR-130b-3p_R+2	CAGTGCAATGATGAAAGGGCATTT	down	-inf	-inf	5.83E-03
PC-3p-92753_115	AATTTGACTGGCTTATTT	down	0.05	-4.21	5.90E-03
hsa-miR-4799-5p	ATCTAAATGCAGCATGCCAGTC	down	-inf	-inf	6.09E-03

hsa-miR-4662a-5p	TTAGCCAATTGTCCATCTTTAG	down	0.13	-2.90	6.20E-03
hsa-miR-1179_R+1	AAGCATTCTTTCATTGGTTGGT	down	-inf	-inf	6.21E-03
ggo-mir-1277-p5	TATATATATATATGTACGTAT	down	0.08	-3.60	6.21E-03
mmu-miR-107-5p_R+1	AGCTTCTTTACAGTGTTGCCTTGT	down	-inf	-inf	6.29E-03
hsa-miR-6755-5p	TAGGGTAGACACTGACAACGTT	down	-inf	-inf	6.32E-03
PC-3p-62500_195	AAATCTCGCTGGGGCCTCCA	down	-inf	-inf	6.38E-03
hsa-miR-6516-5p_R-1	TTTGCAGTAACAGGTGTGAGC	down	0.21	-2.24	6.38E-03
hsa-miR-6866-5p_R-2	TTAGAGGCTGGAATAGAGATT	down	0.17	-2.54	6.44E-03
hsa-miR-34c-5p	AGGCAGTGTAGTTAGCTGATTGC	down	-inf	-inf	6.52E-03
hsa-miR-539-5p	GGAGAAATTATCCTTGGTGTGT	down	0.03	-4.93	6.67E-03
mmu-miR-452-3p_1ss20GA	TCAGTCTCATCTGCAAAGAAGT	down	0.01	-6.60	6.73E-03
hsa-miR-23a-3p_R+1	ATCACATTGCCAGGGATTTCCA	down	0.52	-0.93	6.73E-03
mmu-let-7j_1ss8TG	TGAGGTAGTAGTTTGTGCTGTTAT	down	0.28	-1.85	6.91E-03
mmu-miR-421-5p	CTCATTAAATGTTTGTTGAAT	down	-inf	-inf	6.92E-03
mmu-miR-1839-3p	AGACCTACTTATCTACCAACAGC	down	0.25	-2.01	7.01E-03
PC-5p-124265_81	CTCGCTGTAGCATCGAACCCCT	down	0.12	-3.09	7.07E-03
hsa-miR-19b-1-5p	AGTTTTGCAGGTTTGCATCCAGC	down	-inf	-inf	7.10E-03
hsa-miR-4742-5p	TCAGGCAAAGGGATATTTACAGA	down	0.16	-2.67	7.21E-03
PC-3p-103652_100	AGGTTGTAGGATGCTAAACAGA	down	-inf	-inf	7.24E-03
hsa-miR-376a-3p	ATCATAGAGGAAAATCCACGT	down	0.08	-3.62	7.39E-03
hsa-miR-4743-5p	TGGCCGGATGGGACAGGAGGCAT	down	-inf	-inf	7.44E-03
hsa-miR-6505-5p	TTGGAATAGGGGATATCTCAGC	down	-inf	-inf	7.52E-03
PC-5p-146_367656	TTCCTCTTTCCGGCACCA	up	5.58	2.48	7.74E-03
hsa-miR-4676-5p	GAGCCAGTGGTGAGACAGTGA	down	-inf	-inf	7.94E-03
hsa-miR-511-5p	GTGTCTTTTGCTCTGCAGTCA	down	0.08	-3.72	8.33E-03
hsa-miR-4659b-5p_R+3	TTGCCATGTCTAAGAAGAAAAT	down	-inf	-inf	8.38E-03

hsa-miR-6862-5p	CGGGCATGCTGGGAGAGACTTT	down	-inf	-inf	8.41E-03
hsa-miR-324-3p_L-3R+1	ACTGCCCCAGGTGCTGCTGGA	down	0.16	-2.67	8.45E-03
PC-3p-84256_131	CGCGTGGCCTGCTGGGAGTTGT	down	-inf	-inf	8.78E-03
PC-3p-168185_56	TCCCCAACCCCTGCCCGCAGT	down	-inf	-inf	9.19E-03
hsa-miR-19b-3p	TGTGCAAATCCATGCAAAACTGA	down	0.47	-1.08	9.24E-03
hsa-miR-4638-5p	ACTCGGCTGCGGTGGACAAGT	down	0.12	-3.08	9.26E-03
PC-3p-76092_150	CGCCTGTCTCATTCTCTGCAGT	down	0.19	-2.43	9.65E-03
hsa-miR-3617-5p	AAAGACATAGTTGCAAGATGGG	down	0.01	-6.32	9.68E-03
tch-let-7a-5p	TAAGGTAGTAGATTGTATAGTT	down	0.13	-2.96	9.72E-03
PC-5p-388722_24	TAAGGCCATCGTAAGTTGAAA	down	-inf	-inf	9.87E-03
hsa-miR-1306-3p_R+4	ACGTTGGCTCTGGTGGTGATGT	down	0.22	-2.17	9.95E-03
mdo-miR-181b-5p_R+3	AACATTCATTGCTGTCGGTGGGTTGT	down	-inf	-inf	1.03E-02
hsa-miR-329-5p	GAGGTTTTCTGGGTTTCTGTTTC	down	-inf	-inf	1.03E-02
pal-miR-9993b-3p_L+1_1ss2AT	TTTCTCGCTGGGGCCTCCA	down	-inf	-inf	1.06E-02
hsa-miR-29c-5p_R-1	TGACCGATTTCTCCTGGTGTT	down	0.32	-1.65	1.08E-02
PC-5p-203106_47	AAATGTAACTGCAGTTTTTGGA	down	-inf	-inf	1.10E-02
dno-miR-146a-5p_L-5	ACTGAATTCCATGGGTTT	down	0.04	-4.67	1.10E-02
hsa-miR-548ay-5p_R-1	AAAAGTAATTGTGGTTTTTG	down	0.38	-1.40	1.11E-02
ppy-miR-548a	AAAAGTAATTGTGGTTTTTG	down	0.38	-1.40	1.11E-02
hsa-miR-548ad-5p	AAAAGTAATTGTGGTTTTTG	down	0.38	-1.40	1.11E-02
hsa-miR-3611_R-2	TTGTGAAGAAAGAAATTCT	down	0.13	-2.97	1.13E-02
hsa-miR-92b-5p_R-2	AGGGACGGGACGCGGTGCAG	down	0.08	-3.69	1.18E-02
hsa-miR-5698	TGGGGGAGTGCAGTGATTGTGG	down	-inf	-inf	1.19E-02
bta-miR-20b_R+1	CAAAGTGCTCACAGTGCAGGTAG	down	-inf	-inf	1.20E-02
hsa-miR-627-5p_1ss2TG	GGGAGTCTCTAAGAAAAGAGGA	down	0.02	-5.37	1.20E-02
cgr-miR-532-5p_R+2_2	CATGCCTTGAGTGTAGGACCGTTA	down	-inf	-inf	1.21E-02

cgr-miR-532-5p_R+2_1	CATGCCTTGAGTGTAGGACCGTAA	down	-inf	-inf	1.21E-02
PC-3p-43735_309	CCCGCCCCTCCGCGCCCCCCAT	down	0.03	-5.15	1.22E-02
hsa-miR-181d-3p_1ss21CT	CCACCGGGGGATGAATGTCAT	down	-inf	-inf	1.22E-02
hsa-miR-196b-5p_R-1	TAGGTAGTTTCCTGTTGTTGG	down	0.32	-1.63	1.22E-02
hsa-miR-7843-5p	GAGGGCAGAGCCAGCTTCCTGA	down	-inf	-inf	1.23E-02
hsa-miR-449a	TGGCAGTGTATTGTTAGCTGGT	down	-inf	-inf	1.26E-02
PC-3p-146542_66	CAACAGGCCTTGCTCTGCTCACA	down	0.09	-3.42	1.26E-02
hsa-miR-92b-3p	TATTGCACTCGTCCCGGCCTCC	up	3.51	1.81	1.27E-02
hsa-miR-548ax_R-1	AGAAGTAATTGCGGTTTTGCC	down	0.20	-2.34	1.28E-02
hsa-miR-342-3p_R+1	TCTCACACAGAAATCGCACCCGTC	up	3.24	1.70	1.28E-02
mmu-miR-5126_L-4_1ss18CT	GCGGGGCCGGGGGTGGGG	down	-inf	-inf	1.29E-02
hsa-miR-155-5p_R-1	TTAATGCTAATCGTGATAGGGGT	down	0.44	-1.20	1.29E-02
hsa-miR-4521_R+1	GCTAAGGAAGTCCTGTGCTCAGT	down	0.21	-2.23	1.29E-02
hsa-miR-30b-3p	CTGGGAGGTGGATGTTTACTTC	down	0.25	-2.01	1.30E-02
cgr-miR-1260_R+1_2	ATCCCACCGCTGCCACCAG	down	-inf	-inf	1.31E-02
cgr-miR-1260_R+1_1	ATCCCACCGCTGCCACCAA	down	-inf	-inf	1.31E-02
hsa-miR-301a-3p	CAGTGCAATAGTATTGTCAAAGC	down	0.25	-2.02	1.32E-02
PC-3p-94741_112	CCAGGTGTCTTCCATTCTGTCC	down	0.07	-3.80	1.33E-02
hsa-miR-3190-3p_L-2R+2	TGGAAGGTAGACGGCCAGAGAGT	down	0.23	-2.10	1.36E-02
hsa-miR-501-3p	AATGCACCCGGGCAAGGATTCT	up	4.54	2.18	1.36E-02
hsa-miR-2278_L-1R+1	AGAGCAGTGTGTGTTGCCTGGG	down	-inf	-inf	1.37E-02
hsa-miR-378i_R+1_1ss9AT	ACTGGACTTGGAGTCAGAAGGT	down	0.37	-1.42	1.39E-02
bta-miR-378_1ss4GT	ACTTGACTTGGAGTCAGAAGGC	down	-inf	-inf	1.41E-02
pal-miR-9995-3p_1ss15TA	ATCTCGGTGGAACCACCA	down	0.02	-5.89	1.42E-02
hsa-miR-186-5p	CAAAGAATTCTCCTTTTGGGCT	up	1.72	0.78	1.43E-02
hsa-miR-7-5p_R-1	TGGAAGACTAGTGATTTTGTTGT	down	0.41	-1.28	1.43E-02

hsa-miR-181a-2-3p	ACCACTGACCGTTGACTGTACC	up	1.77	0.83	1.45E-02
PC-5p-4861_2738	GCCTGTACTCTTTATCCT	up	7.38	2.88	1.47E-02
PC-3p-4861_2738	GCCTGTACTCTTTATCCT	up	7.38	2.88	1.47E-02
hsa-miR-191-5p	CAACGGAATCCCAAAAGCAGCTG	up	2.51	1.33	1.51E-02
hsa-miR-584-5p_R-1	TTATGGTTTGCCTGGGACTGA	down	0.66	-0.61	1.52E-02
bta-miR-191b_1ss2AG	GGACGAAATCCAAGCGCAGCTG	down	-inf	-inf	1.52E-02
hsa-miR-3913-5p	TTTGGGACTGATCTTGATGTCT	down	0.27	-1.91	1.53E-02
hsa-miR-6892-5p	GTAAGGGACCGGAGAGTAGGA	down	-inf	-inf	1.54E-02
hsa-miR-410-3p	AATATAACACAGATGGCCTGT	down	0.29	-1.80	1.56E-02
hsa-miR-378d_R-2	ACTGGACTTGGAGTCAGA	down	0.21	-2.26	1.57E-02
hsa-miR-423-3p	AGCTCGGTCTGAGGCCCCTCAGT	down	0.71	-0.49	1.58E-02
hsa-miR-590-5p	GAGCTTATTCATAAAAGTGCAG	down	-inf	-inf	1.59E-02
hsa-miR-3661_R+1	TGACCTGGGACTCGGACAGCTGT	down	0.11	-3.13	1.59E-02
hsa-miR-127-3p	TCGGATCCGTCTGAGCTTGGCT	up	3.85	1.94	1.59E-02
hsa-miR-143-5p_R-1	GGTGCAGTGCTGCATCTCTGG	down	0.12	-3.07	1.64E-02
hsa-miR-490-5p	CCATGGATCTCCAGGTGGGT	down	-inf	-inf	1.65E-02
PC-3p-4847_2746	GAAGTGGGGTTGTGGGAAT	up	9.11	3.19	1.70E-02
hsa-miR-7110-5p_R+1	TGGGGGTGTGGGGAGAGAGAGT	down	-inf	-inf	1.72E-02
PC-3p-151959_63	CCTACAGGCTGGAATGGGCTCAT	down	-inf	-inf	1.75E-02
hsa-miR-9983-3p	TTTTTTGCTGGAACATTTCTGG	down	-inf	-inf	1.76E-02
PC-3p-243877_40	TGCAGCATAGGGCAGTTAGGA	down	-inf	-inf	1.77E-02
PC-5p-207873_46	AAATATGATTTGGAAGATTGTG	down	-inf	-inf	1.77E-02
hsa-miR-627-3p	TCTTTTCTTTGAGACTCACT	up	4.87	2.29	1.78E-02
hsa-miR-98-5p	TGAGGTAGTAAGTTGTATTGTT	down	0.48	-1.05	1.80E-02
hsa-mir-548ag-2-p3	CAAGAACCTCAATTACCTTTGC	down	0.22	-2.21	1.81E-02
hsa-miR-330-3p	GCAAAGCACACGGCCTGCAGAGA	down	0.44	-1.18	1.81E-02

PC-3p-129011_77	TGAGCTCTCTGCACTCCCAGG	down	0.11	-3.18	1.83E-02
hsa-miR-151a-5p	TCGAGGAGCTCACAGTCTAGT	down	0.69	-0.53	1.85E-02
dno-miR-134-5p_R+1_1ss22CA	TGTGACTGGTTGACCAGAGGGAT	down	0.16	-2.67	1.86E-02
eca-miR-8986a_R-1_1ss1TG	GAGTGTGCTAGAGTCCTCGAAGA	down	-inf	-inf	1.87E-02
hsa-miR-664b-3p	TTCATTTGCCTCCCAGCCTACA	down	-inf	-inf	1.88E-02
hsa-miR-29a-5p_R-1	ACTGATTTCTTTTGGTGTTCA	down	0.08	-3.71	1.90E-02
mmu-mir-1983-p5_1ss1GA	AAAAGCATGCTCCAGTGGCGC	down	-inf	-inf	1.92E-02
hsa-miR-378e_R+1_1ss18GA	ACTGGACTTGGAGTCAGAAC	down	-inf	-inf	1.92E-02
hsa-miR-433-3p	ATCATGATGGGCTCCTCGGTGT	down	0.37	-1.43	1.95E-02
eca-mir-191b-p3_1ss23CT	CTGCTTTTGGGATTCCGTTGCCT	down	-inf	-inf	1.96E-02
hsa-miR-194-3p_R-1	CCAGTGGGGCTGCTGTTATCT	down	-inf	-inf	1.96E-02
hsa-miR-200c-3p	TAATACTGCCGGGTAATGATGGA	down	0.45	-1.17	2.02E-02
PC-5p-135472_73	TGGGGTGGAGTAGGGCAGGAA	down	0.10	-3.37	2.06E-02
pal-miR-9993a-3p	ATCTCGGTGGGACCTCCA	down	0.32	-1.63	2.06E-02
hsa-miR-6819-5p	TTGGGGTGGAGGGCCAAGGAGC	down	-inf	-inf	2.09E-02
hsa-miR-222-5p_R-1	CTCAGTAGCCAGTGTAGATCC	down	0.16	-2.65	2.09E-02
PC-5p-247305_39	CCATCCTGACTCTACCTGGCTGT	down	-inf	-inf	2.10E-02
hsa-miR-3127-5p	ATCAGGGCTTGTGGAATGGGAAG	down	0.10	-3.31	2.10E-02
PC-5p-234738_41	GTTCCTCTTCTTAACACCA	down	-inf	-inf	2.13E-02
hsa-miR-552-5p_L+1	TGTTTAACCTTTTGCCTGTTGG	down	0.04	-4.65	2.14E-02
hsa-miR-3675-5p_L-1	ATGGGGCTTCTGTAGAGATTTC	down	0.07	-3.80	2.15E-02
hsa-miR-99b-3p_R+1	CAAGCTCGTGTCTGTGGGTCCGT	down	0.33	-1.58	2.15E-02
hsa-miR-6767-5p	TCGCAGACAGGGACACATGGAGA	down	0.09	-3.42	2.15E-02
PC-3p-82011_136	TCCTGGAGCTGGGCAGATGGGA	down	0.15	-2.75	2.21E-02
bta-miR-2478_L-1_1ss2TA	AATCCCACTTCTGACACCA	up	17.87	4.16	2.24E-02
PC-3p-136753_72	TGTCTAGACAAGGCTGGGGAA	down	0.07	-3.92	2.24E-02

PC-3p-8405_1605	TAGTTGTTGGGGATTACT	up	19.52	4.29	2.27E-02
PC-5p-6976_1912	AGAGCGTTCTGTAAGCCT	up	16.59	4.05	2.29E-02
hsa-miR-509-3p	TGATTGGTACGTCTGTGGGTAG	down	-inf	-inf	2.31E-02
PC-5p-99555_105	TTAGTCTAGCACCTGGTCAATTC	down	0.12	-3.07	2.32E-02
hsa-miR-376b-3p_R-1	ATCATAGAGGAAAATCCATGT	down	-inf	-inf	2.33E-02
hsa-miR-1268b_R-2	CGGGCGTGGTGGTGGGGG	down	-inf	-inf	2.34E-02
hsa-miR-1268a	CGGGCGTGGTGGTGGGGG	down	-inf	-inf	2.34E-02
PC-3p-17720_825	TGCACAGTACGAGAGGAAC	up	8.18	3.03	2.36E-02
PC-3p-133316_74	TCACTCTAGGGTTGGGGACAGT	down	0.18	-2.50	2.38E-02
hsa-mir-3922-p3	TGTGGGACTTCTGGCCTTGA	down	0.21	-2.22	2.38E-02
hsa-miR-340-3p_R+1	TCCGTCTCAGTTACTTTATAGCC	up	2.99	1.58	2.39E-02
PC-3p-106369_97	AGTTGGATCTTGGGAGAAA	down	-inf	-inf	2.41E-02
hsa-miR-374b-3p	CTTAGCAGGTTGTATTATCATT	down	0.31	-1.70	2.43E-02
hsa-miR-4661-5p_R-1	AACTAGCTCTGTGGATCCTGA	down	-inf	-inf	2.43E-02
hsa-miR-491-3p	CTTATGCAAGATTCCCTTCTAC	down	-inf	-inf	2.45E-02
hsa-miR-11400_1ss20TC	TCGGCTGTGTATCTCTGTGCC	down	0.60	-0.74	2.49E-02
PC-3p-164451_58	TTGGTCAATGTATTGGTCTGCAT	down	0.17	-2.56	2.51E-02
mmu-let-7c-5p_R+2	TGAGGTAGTAGGTTGTATGGTTAT	down	0.14	-2.82	2.52E-02
PC-3p-6927_1922	GAGGTTGGCTTAGAAGCAGC	up	25.62	4.68	2.55E-02
hsa-miR-548d-3p	CAAAAACCACAGTTTCTTTTGC	down	-inf	-inf	2.55E-02
hsa-miR-4765	TGAGTGATTGATAGCTATGTTC	down	-inf	-inf	2.58E-02
mmu-miR-339-5p_R+2	TCCCTGTCCTCCAGGAGCTCACGAA	down	0.18	-2.49	2.60E-02
hsa-miR-551b-3p_R+1	GCGACCCATACTTGGTTTCAGT	down	0.21	-2.28	2.61E-02
hsa-miR-96-5p_R-2	TTTGGCACTAGCACATTTTTG	up	12.11	3.60	2.62E-02
hsa-miR-3198	GTGGAGTCCTGGGGAATGGAGA	down	0.10	-3.35	2.64E-02
hsa-miR-6803-3p_R-1	TCCCTCGCCTTCTCACCCTCA	down	0.06	-3.99	2.65E-02

mmu-miR-1187_R-2_1ss8GA	TATGTGTATGTGTATGTGTGT	down	-inf	-inf	2.66E-02
PC-3p-1495_12859	CGAGTCCCATCAGCCACCCCA	up	12.76	3.67	2.67E-02
hsa-miR-4508_L+2R-1	AAGCGGGGCTGGGCGCGC	up	3.87	1.95	2.70E-02
hsa-miR-362-3p_1ss22AT	AACACACCTATTCAAGGATTCT	down	-inf	-inf	2.71E-02
mmu-miR-431-5p_R-1	TGTCTTGCAGGCCGTCATGC	down	0.29	-1.79	2.71E-02
hsa-miR-7705_R-1	AATAGCTCAGAATGTCAGTTCT	down	-inf	-inf	2.72E-02
hsa-miR-769-3p_L-1R+1	TGGGATCTCCGGGGTCTTGGTTT	down	0.28	-1.85	2.75E-02
hsa-miR-487a-3p	AATCATACAGGGACATCCAGTT	down	0.24	-2.05	2.76E-02
hsa-miR-548ba	AAAGGTAACTGTGATTTTTGCT	down	-inf	-inf	2.78E-02
hsa-miR-324-5p_R+1	CGCATCCCCTAGGGCATTGGTGT	down	0.46	-1.14	2.82E-02
hsa-miR-1185-1-3p	ATATACAGGGGGAGACTCTTAT	down	0.32	-1.63	2.82E-02
hsa-miR-144-3p_R-1	TACAGTATAGATGATGTAC	up	9.16	3.20	2.84E-02
hsa-miR-4473_R-1	CTAGTGCTCTCCGTTACAAGT	down	-inf	-inf	2.86E-02
PC-3p-29103_499	CTTGAGACTCTGGGTCAGT	down	-inf	-inf	2.92E-02
hsa-miR-376c-5p_L-1R+2	GTGGATATTCCTTCTATGTTTA	down	-inf	-inf	2.93E-02
hsa-miR-376b-5p_L-1R+1	GTGGATATTCCTTCTATGTTTA	down	-inf	-inf	2.93E-02
hsa-let-7a-5p	TGAGGTAGTAGGTTGTATAGTT	down	0.57	-0.81	3.00E-02
PC-5p-131452_76	AGATGGGGAGAACTCAATCCT	down	0.15	-2.74	3.02E-02
hsa-miR-493-5p	TTGTACATGGTAGGCTTTCATT	down	0.43	-1.22	3.06E-02
hsa-miR-548au-5p_R-1	AAAAGTAATTGCGGTTTTTG	down	0.22	-2.18	3.09E-02
hsa-miR-548am-5p_R-2	AAAAGTAATTGCGGTTTTTG	down	0.22	-2.18	3.09E-02
pal-miR-9993a-3p_1ss11GA	ATCTCGGTGGAACCTCCA	down	0.43	-1.21	3.09E-02
pal-miR-9995-3p	ATCTCGGTGGAACCTCCA	down	0.43	-1.21	3.09E-02
PC-5p-61866_198	AGTCCGGCCTCACTCACCA	up	inf	inf	3.11E-02
hsa-miR-30c-5p_R+1	TGTAAACATCCTACACTCTCAGCT	up	1.56	0.64	3.12E-02
hsa-miR-654-3p_R-2	TATGTCTGCTGACCATCACC	up	3.82	1.93	3.12E-02

pal-miR-9993b-3p_L+1_1	AATCTCGCTGGGGCCTCCA	down	0.29	-1.79	3.17E-02
pal-miR-9993b-3p_L+1_2	CATCTCGCTGGGGCCTCCA	down	0.29	-1.79	3.17E-02
pal-miR-9993b-3p_L+1_3	GATCTCGCTGGGGCCTCCA	down	0.29	-1.79	3.17E-02
hsa-miR-100-5p_R-1	AACCCGTAGATCCGAACTTGT	up	7.86	2.98	3.23E-02
hsa-miR-181b-2-3p_L+1R+1	ACTCACTGATCAATGAATGCAA	down	0.21	-2.24	3.29E-02
pal-miR-9995-3p_1ss1AG	GTCTCGGTGGAACCTCCA	down	0.16	-2.63	3.29E-02
PC-3p-11702_1197	AAAGTGGACGTATAGGGT	up	20.71	4.37	3.33E-02
PC-3p-85981_127	AAGGTCAGCTCAATGAGAA	up	599.05	9.23	3.37E-02
hsa-miR-5587-5p_R+2	ATGGTCACCTCCGGGACTCT	down	-inf	-inf	3.37E-02
hsa-miR-484	TCAGGCTCAGTCCCCTCCCGAT	up	1.35	0.43	3.39E-02
hsa-miR-199a-5p	CCCAGTGTTCAGACTACCTGTTC	up	2.56	1.36	3.41E-02
hsa-miR-6500-3p	ACACTTGTTGGGATGACCTGC	down	0.23	-2.13	3.42E-02
hsa-miR-99a-5p_R-1	AACCCGTAGATCCGATCTTGT	up	4.54	2.18	3.45E-02
hsa-miR-487b-3p	AATCGTACAGGGTCATCCACTT	down	0.32	-1.66	3.49E-02
hsa-miR-379-3p_R-1	TATGTAACATGGTCCACTAAC	down	0.31	-1.68	3.63E-02
hsa-miR-1249-3p	ACGCCCTTCCCCCCCTTCTTCA	down	0.27	-1.90	3.69E-02
hsa-miR-5588-5p	ACTGGCATTAGTGGGACTTTT	down	-inf	-inf	3.69E-02
hsa-miR-655-3p	ATAATACATGGTTAACCTCTTT	down	0.19	-2.40	3.79E-02
hsa-miR-3120-5p_R-1	CCTGTCTGTGCCTGCTGTAC	down	0.15	-2.73	3.83E-02
hsa-miR-548b-3p	CAAGAACCTCAGTTGCTTTTGT	down	0.18	-2.45	3.85E-02
hsa-miR-361-5p	TTATCAGAATCTCCAGGGGTAC	up	2.92	1.55	3.93E-02
hsa-miR-3146_R+1	CATGCTAGGATAGAAAGAATGGG	down	-inf	-inf	3.94E-02
hsa-miR-7-1-3p	CAACAAATCACAGTCTGCCATA	down	0.39	-1.34	3.97E-02
hsa-miR-139-5p	TCTACAGTGCACGTGTCTCCAGT	down	0.47	-1.08	3.98E-02
hsa-miR-7856-5p	TTTTAAGGACACTGAGGGATC	down	0.12	-3.02	4.01E-02
hsa-miR-424-5p_R-1	CAGCAGCAATTCATGTTTTGA	down	0.35	-1.51	4.02E-02

cja-miR-556_R+1	GATGAGCTCATTGTAATATGAA	down	-inf	-inf	4.06E-02
hsa-miR-6809-5p_L+1R-1	TTGGCAAGGAAAGAAGAGGATC	down	0.25	-1.98	4.10E-02
mmu-miR-101c_L+1R+2	TACAGTACTGTGATAACTGATC	down	-inf	-inf	4.10E-02
hsa-miR-370-3p	GCCTGCTGGGGTGGAACCTGGT	up	2.58	1.37	4.11E-02
PC-5p-17547_833	CCCACCAGGAGCCTGGCACTGT	up	11.93	3.58	4.13E-02
hsa-miR-30d-3p	CTTTCAGTCAGATGTTTGCTGC	down	0.54	-0.90	4.14E-02
ppy-mir-1268-p3_1ss8TC	AGCTACTCGGGAGGCTGA	down	-inf	-inf	4.15E-02
mmu-miR-6238_L-1R-2_1ss12TC	TATTAGTCAGCGGAGGAAA	down	-inf	-inf	4.17E-02
hsa-miR-941	CACCCGGCTGTGTGCACATGTGC	up	2.59	1.37	4.18E-02
hsa-miR-147b-3p	GTGTGCGGAAATGCTTCTGCT	down	-inf	-inf	4.20E-02
hsa-miR-6502-5p	AGCTCTAGAAAGATTGTTGACC	down	-inf	-inf	4.21E-02
hsa-miR-6770-3p_L+1R-1	CCTGGCGGCTGTGTCTTCACA	down	-inf	-inf	4.24E-02
hsa-miR-552-3p	AACAGGTGACTGGTTAGACAA	down	-inf	-inf	4.24E-02
hsa-miR-125b-5p_R-2	TCCCTGAGACCCTAACTTGT	up	2.36	1.24	4.27E-02
hsa-miR-4685-3p_R-2	TCTCCCTTCCTGCCCTGGCT	up	16.78	4.07	4.31E-02
mmu-miR-3964_L+1_1ss6GA	CATAAAGTAGAAAGCACTAAA	down	-inf	-inf	4.33E-02
hsa-miR-181b-3p	CTCACTGAACAATGAATGCAA	down	0.31	-1.71	4.34E-02
hsa-miR-3960_L-2_1ss12AC	CGGCGGCGGCGGCGGGGG	up	17.32	4.11	4.38E-02
hsa-miR-4761-3p_R-1	GAGGGCATGCGCACTTTGTC	down	-inf	-inf	4.48E-02
hsa-miR-942-3p	CACATGGCCGAAACAGAGAAGT	down	0.23	-2.14	4.50E-02
PC-3p-137989_71	TTTTATAATATGGACCCTTCTGT	down	0.12	-3.11	4.50E-02
hsa-miR-3165	AGGTGGATGCAATGTGACCTCA	down	-inf	-inf	4.52E-02
hsa-miR-548ar-3p_R-1	TAAAACTGCAGTTATTTTTG	down	-inf	-inf	4.54E-02
mmu-mir-6236-p5_1ss4CG_1	AATGAACTAGCCCTGAAA	up	26.12	4.71	4.56E-02
mmu-mir-6236-p5_1ss4CG_3	AATGAACTAGCCCTGAAAATGG	up	26.12	4.71	4.56E-02
mmu-mir-6236-p5_1ss4CG_2	AATGAACTAGCCCTGAAAA	up	26.12	4.71	4.56E-02

hsa-mir-548aw-p3_1ss22TC	AAAACCGCGATGACTTTTGCAC	down	-inf	-inf	4.56E-02
PC-5p-196353_48	AAAGGTAATTGAGGTCTTTGA	down	-inf	-inf	4.57E-02
mmu-miR-5119_L+1R-2	TCATCTCATCCTGGGGCT	up	3.68	1.88	4.66E-02
PC-3p-10362_1335	CAGCCCGAAGTGTGACCCA	up	44.62	5.48	4.68E-02
hsa-miR-1537-3p	AAAACCGTCTAGTTACAGTTGT	down	-inf	-inf	4.68E-02
hsa-miR-891a-5p	TGCAACGAACCTGAGCCACTGA	down	-inf	-inf	4.68E-02
mmu-miR-30f_L+1R-1_1ss17AG	TGTAAACATCCGACTGGAAGCT	down	0.16	-2.65	4.77E-02
hsa-miR-4524a-3p	TGAGACAGGCTTATGCTGCTAT	down	-inf	-inf	4.79E-02
PC-3p-59915_206	TTGAGGGGAGAAATGCTGTGT	down	0.28	-1.82	4.82E-02
hsa-miR-192-5p	CTGACCTATGAATTGACAGCC	up	4.42	2.15	4.82E-02
hsa-miR-369-5p_R-1	AGATCGACCGTGTTATATTCG	down	0.26	-1.97	4.86E-02
hsa-miR-134-5p	TGTGACTGGTTGACCAGAGGGG	down	0.45	-1.16	4.87E-02
PC-3p-114333_89	TACTGGGATATTTGGAGCTTCT	down	0.20	-2.31	4.93E-02
hsa-miR-183-5p_L-1	ATGGCACTGGTAGAATTCACT	up	3.63	1.86	4.93E-02
PC-5p-142741_68	GAGAAAGCTCACAGGAACT	down	-inf	-inf	4.99E-02

Supplementary Material 3. Differentially expressed miRNAs between non-smoking IA and healthy controls.

miR name	miR sequence	up/down	Fold change	log2(fold_change)	P value
mmu-miR-146a-5p_R+1	TGAGAACTGAATTCCATGGGTTT	up	3.29	1.72	3.00E-09
hsa-miR-107_R-2	AGCAGCATTGTACAGGGCTAT	down	0.33	-1.59	2.35E-08
hsa-miR-195-5p_R+1	TAGCAGCACAGAAATATTGGCA	down	0.27	-1.89	5.07E-08
hsa-miR-584-5p_R-1	TTATGGTTTGCCTGGGACTGA	up	3.03	1.60	7.97E-08
hsa-mir-8086-p3_1ss11AG	AGGCTGGAGTGCAGTGGC	down	0.02	-5.43	1.05E-07
hsa-mir-1304-p5	CGGTTTGAGGCTACAGTGAGAT	down	0.27	-1.90	1.47E-07
hsa-miR-191-5p	CAACGGAATCCCAAAAGCAGCTG	up	2.27	1.18	1.83E-07
hsa-miR-92b-5p_R-2	AGGGACGGGACGCGGTGCAG	down	0.25	-2.02	2.11E-07
hsa-miR-2110_R+1	TTGGGGAAACGGCCGCTGAGTGA	down	0.25	-1.98	2.83E-07
hsa-miR-3605-3p_R-2	CCTCCGTGTTACCTGTCCTCT	down	0.14	-2.81	3.32E-07
hsa-miR-95-3p_R-1	TTCAACGGGTATTTATTGAGC	down	0.02	-5.91	5.27E-07
hsa-miR-511-5p	GTGTCTTTTGCTCTGCAGTCA	down	0.04	-4.65	5.34E-07
hsa-miR-3140-3p_R-1	AGCTTTTGGGAATTCAGGTAG	down	0.13	-2.96	7.01E-07
hsa-miR-320a-3p	AAAAGCTGGGTTGAGAGGGCGA	down	0.33	-1.59	7.18E-07
hsa-miR-331-5p_R-2	CTAGGTATGGTCCCAGGGAT	down	0.30	-1.72	7.33E-07
hsa-miR-28-3p	CACTAGATTGTGAGCTCCTGGA	up	2.70	1.43	7.63E-07
PC-5p-42143_323	TTAGTGGCTCCCTCTGCCTGCA	down	0.15	-2.78	8.21E-07
hsa-miR-1285-3p_R-2	TCTGGGCAACAAAGTGAGAC	down	0.08	-3.56	8.23E-07
hsa-miR-363-3p_R-1	AATTGCACGGTATCCATCTGT	down	0.07	-3.79	9.21E-07
hsa-miR-146a-5p	TGAGAACTGAATTCCATGGGTT	up	2.56	1.36	9.40E-07
oga-miR-100_R+1	AACCCGTAGATCCGAACTTGTGA	down	0.10	-3.36	1.13E-06
hsa-miR-320e_L+1R+3_1ss17AG	AAAAGCTGGGTTGAGAGGGTGA	down	0.06	-4.00	1.33E-06

hsa-miR-1180-3p_R-2	TTTCCGGCTCGCGTGGGTGT	down	0.06	-4.09	1.59E-06
hsa-miR-550a-3-5p	AGTGCCTGAGGGAGTAAGAG	down	0.09	-3.42	1.62E-06
hsa-miR-190b-5p	TGATATGTTTGATATTGGGTTG	down	0.14	-2.85	1.73E-06
ocu-miR-502b-3p_R-3	AATGCACCTGGGCAAGGATTT	down	-inf	-inf	1.77E-06
hsa-miR-6815-5p_R-2	TAGGTGGCGCCGGAGGAGTCA	down	0.00	-8.71	1.86E-06
hsa-miR-423-3p	AGCTCGGTCTGAGGCCCCTCAGT	up	2.39	1.26	1.90E-06
PC-3p-2703_5627	TTTGGGGATTCTAAGAGGAAG	down	0.01	-7.36	2.15E-06
hsa-miR-1976_R+2	CCTCCTGCCCTCCTTGCTGTAG	down	0.20	-2.31	2.52E-06
hsa-mir-4472-2-p3_1ss11CT	AGTCTTGCTCTGTCGCCCAGG	down	-inf	-inf	2.53E-06
hsa-miR-576-3p_R-1	AAGATGTGGAAAAATTGGAAT	down	0.16	-2.66	2.56E-06
hsa-miR-500a-3p_L+1R-1_1ss22TA	AATGCACCTGGGCAAGGATTCA	down	0.12	-3.09	2.65E-06
hsa-miR-502-3p	AATGCACCTGGGCAAGGATTCA	down	0.12	-3.09	2.65E-06
hsa-let-7c-5p_R-4	TGAGGTAGTAGGTTGTAT	down	0.40	-1.33	2.94E-06
hsa-miR-16-2-3p_L+1R-2	ACCAATATTACTGTGCTGCTT	down	0.07	-3.93	3.27E-06
hsa-miR-26a-5p	TTCAAGTAATCCAGGATAGGCT	up	2.80	1.48	3.47E-06
hsa-miR-7706_R-1	TGAAGCGCCTGTGCTCTGCCGAG	down	0.18	-2.47	3.54E-06
hsa-miR-25-3p	CATTGCACTTGTCTCGGTCTGA	down	0.14	-2.83	4.27E-06
hsa-miR-424-3p	CAAAACGTGAGGCGCTGCTAT	down	0.30	-1.73	4.38E-06
hsa-miR-4732-3p	GCCCTGACCTGTCCTGTTCTG	down	0.12	-3.04	5.11E-06
PC-3p-15389_938	CTTTGGGGATTCTAAGAGTT	down	0.01	-6.42	5.23E-06
PC-5p-15389_938	CTTTGGGGATTCTAAGAGTT	down	0.01	-6.42	5.23E-06
hsa-miR-92a-3p	TATTGCACTTGTCCCGGCCTGT	down	0.25	-1.99	5.24E-06
mmu-miR-92a-3p_R+1	TATTGCACTTGTCCCGGCCTGA	down	0.09	-3.47	5.33E-06
hsa-miR-4732-5p	TGTAGAGCAGGGAGCAGGAAGCT	down	0.03	-5.27	6.09E-06
hsa-miR-501-3p	AATGCACCCGGGCAAGGATTCT	down	0.11	-3.22	6.14E-06

hsa-miR-10b-5p_R-1	TACCCTGTAGAACCGAATTTGT	down	0.04	-4.75	6.90E-06
hsa-miR-199b-5p_R-1	CCCAGTGTTTAGACTATCTGTT	down	0.25	-1.99	7.17E-06
hsa-miR-532-5p	CATGCCTTGAGTGTAGGACCGT	down	0.19	-2.38	7.26E-06
hsa-miR-660-5p_R+1	TACCCATTGCATATCGGAGTTGT	down	0.13	-2.99	7.57E-06
hsa-miR-18b-5p_R-3	TAAGGTGCATCTAGTGCAGT	down	0.17	-2.54	7.81E-06
hsa-miR-151a-3p	CTAGACTGAAGCTCCTTGAGG	up	2.56	1.36	8.00E-06
hsa-miR-16-5p	TAGCAGCACGTAAATATTGGCG	down	0.13	-2.94	8.15E-06
hsa-miR-3200-3p_R-1	CACCTTGCGCTACTCAGGTCT	down	0.01	-6.74	9.44E-06
hsa-let-7i-5p	TGAGGTAGTAGTTTGTGCTGTT	down	0.36	-1.49	9.59E-06
hsa-miR-4772-3p	CCTGCAACTTTGCCTGATCAGA	down	0.01	-7.42	1.00E-05
hsa-miR-30c-2-3p	CTGGGAGAAGGCTGTTTACTCT	down	0.25	-2.02	1.07E-05
hsa-miR-342-5p	AGGGGTGCTATCTGTGATTGA	down	0.13	-2.94	1.07E-05
hsa-miR-451a_R-1	AAACCGTTACCATTACTGAGT	down	0.02	-5.33	1.08E-05
hsa-miR-486-5p	TCCTGTACTGAGCTGCCCCGAG	down	0.07	-3.83	1.09E-05
hsa-miR-140-3p_R+1	TACCACAGGGTAGAACCACGGA	down	0.20	-2.30	1.21E-05
hsa-miR-151a-5p	TCGAGGAGCTCACAGTCTAGT	up	2.82	1.49	1.24E-05
hsa-miR-7-5p_R-1	TGGAAGACTAGTGATTTTGTTGT	down	0.23	-2.10	1.30E-05
hsa-miR-150-3p_R-2	CTGGTACAGGCCTGGGGGAC	down	0.03	-4.84	1.35E-05
hsa-miR-942-5p_L-2R+1	TTCTCTGTTTTGGCCATGTGT	down	0.36	-1.49	1.39E-05
bta-mir-2887-1-p5_1ss5CA	GGGAAACGGGGCGCGGCC	down	0.06	-4.06	1.42E-05
mmu-let-7j_R-2	TGAGGTATTAGTTTGTGCTGTT	down	0.26	-1.93	1.60E-05
hsa-miR-4667-5p_R-2	ACTGGGGAGCAGAAGGAGAA	down	0.13	-2.97	1.61E-05
hsa-miR-106b-3p_R-2	CCGCACTGTGGGTACTTGCT	down	0.27	-1.89	1.61E-05
hsa-miR-3960_L-2_1ss12AC	CGGCGGCGGCGGCGGGGG	down	0.03	-5.29	1.62E-05
hsa-miR-214-3p_R-1	ACAGCAGGCACAGACAGGCAG	down	0.01	-6.15	1.67E-05
hsa-miR-31-5p_R-2	AGGCAAGATGCTGGCATAG	down	0.01	-6.94	1.71E-05

hsa-miR-27a-5p	AGGGCTTAGCTGCTTGTGAGCA	down	0.20	-2.31	1.94E-05
hsa-mir-451a-p3	TTTAGTAATGGTAATGGTTCT	down	0.02	-5.71	2.00E-05
hsa-miR-11400_1ss20TC	TCGGCTGTGTATCTCTGTGCC	up	6.47	2.69	2.01E-05
mmu-miR-2137_L-1R-1_1ss16AG	CCGGCGGGAGCCCCGGGGA	down	-inf	-inf	2.03E-05
hsa-miR-144-3p_R-1	TACAGTATAGATGATGTAC	down	0.03	-4.99	2.18E-05
hsa-miR-3909	TGTCCTCTAGGGCCTGCAGTCT	down	0.05	-4.29	2.29E-05
hsa-miR-942-3p	CACATGGCCGAAACAGAGAAGT	down	0.12	-3.02	2.30E-05
PC-3p-39847_345	ACATATAGTGAATTCTGGGATT	down	0.02	-5.40	2.33E-05
hsa-miR-29c-3p_R-1	TAGCACCATTTGAAATCGGTT	down	0.15	-2.77	2.38E-05
hsa-let-7i-3p_R-1	CTGCGCAAGCTACTGCCTTGC	down	0.06	-4.07	2.46E-05
hsa-miR-20b-3p_R-3	ACTGTAGTATGGGCACTTC	down	0.02	-5.80	2.60E-05
hsa-miR-744-5p_R-1	TGCGGGGCTAGGGCTAACAGC	up	3.59	1.85	2.67E-05
hsa-miR-4772-5p	TGATCAGGCAAAATTGCAGACT	down	0.01	-6.60	2.70E-05
hsa-miR-582-5p_R-1	TTACAGTTGTTCAACCAGTTAC	down	0.01	-7.61	2.79E-05
hsa-miR-15b-5p	TAGCAGCACATCATGGTTTACA	down	0.33	-1.60	2.92E-05
hsa-miR-642a-3p_R-1	AGACACATTTGGAGAGGGAAC	down	0.00	-7.99	3.12E-05
hsa-miR-27a-3p	TTCACAGTGGCTAAGTTCCGC	down	0.54	-0.88	3.27E-05
hsa-miR-425-5p	AATGACACGATCACTCCCGTTGA	down	0.39	-1.34	3.31E-05
hsa-mir-619-p5_1ss3AG	AAGTGCTGGGATTACAGG	down	0.04	-4.83	3.33E-05
hsa-miR-34c-5p	AGGCAGTGTAGTTAGCTGATTGC	down	0.10	-3.37	3.34E-05
hsa-miR-576-5p	ATTCTAATTTCTCCACGTCTTT	down	0.23	-2.13	3.49E-05
mmu-miR-2137_L-2_1ss16AG	CGGCGGGAGCCCCGGGGAG	down	0.14	-2.88	3.51E-05
hsa-miR-10a-5p_R-1	TACCCTGTAGATCCGAATTTGT	down	0.25	-2.00	3.58E-05
hsa-miR-3143_R-4	ATAACATTGTAAAGCGCTTCT	down	0.08	-3.58	3.59E-05

bta-miR-1246_L+1R-1	AAATGGATTTTTGGAGCAG	down	-inf	-inf	3.63E-05
hsa-miR-548l_R-1	AAAAGTATTTGCGGGTTTTGT	down	0.40	-1.31	3.66E-05
hsa-miR-199a-5p	CCCAGTGTTCAGACTACCTGTTC	up	3.83	1.94	3.78E-05
hsa-miR-4755-5p	TTTCCCTTCAGAGCCTGGCTTT	down	0.12	-3.10	3.93E-05
hsa-miR-196a-5p_R-1	TAGGTAGTTTCATGTTGTTGG	down	0.05	-4.42	4.06E-05
hsa-miR-195-3p_R-1	CCAATATTGGCTGTGCTGCTC	down	0.03	-4.95	4.23E-05
pal-mir-9993a-p3_1ss2GA	AAATCTCGGTGGGACCTC	down	-inf	-inf	4.33E-05
hsa-miR-106a-3p_L+2R-3	TACTGCAATGTAAGCACTTCT	down	0.15	-2.71	4.47E-05
hsa-miR-3615_R+1	TCTCTCGGCTCCTCGCGGCTCG	down	0.23	-2.12	4.58E-05
hsa-miR-4508_L+2R-1	AAGCGGGGCTGGGCGCGC	down	0.04	-4.59	4.66E-05
hsa-miR-188-5p_R+1	CATCCCTTGCATGGTGGAGGGT	down	0.04	-4.81	4.69E-05
hsa-miR-29b-3p_R-3	TAGCACCATTTGAAATCAGT	down	0.14	-2.86	4.83E-05
hsa-miR-424-5p_R-1	CAGCAGCAATTCATGTTTTGA	down	0.28	-1.84	5.05E-05
hsa-miR-532-3p_R-1	CCTCCCACACCCAAGGCTTGC	down	0.25	-2.00	5.41E-05
hsa-miR-548h-3p_R-1_1ss4AG	CAAGAACCGCAATTACTTTTGC	down	0.18	-2.46	5.47E-05
PC-5p-30483_473	TAGGGGTGAAAGGCTAAACA	down	0.10	-3.33	5.83E-05
hsa-miR-1273c_R-1	GGCGACAAAACGAGACCCTGT	down	0.34	-1.54	6.00E-05
hsa-miR-203a-3p_R-2	GTGAAATGTTTAGGACCACT	down	0.06	-4.02	6.29E-05
hsa-miR-3934-5p	TCAGGTGTGGAAACTGAGGCAG	down	0.02	-5.44	6.43E-05
hsa-miR-610	TGAGCTAAATGTGTGCTGGGA	down	0.08	-3.71	6.52E-05
hsa-miR-106b-5p_R-1	TAAAGTGCTGACAGTGCAGA	down	0.41	-1.30	6.58E-05
hsa-miR-142-5p_L+2R-3	CCCATAAAGTAGAAAGCACT	down	0.31	-1.69	6.62E-05
PC-5p-49096_267	AGCCTGGAAGCTGGAGCCTGCAG	down	0.41	-1.28	6.65E-05
hsa-miR-6805-5p	TAGGGGGCGGCTTGTGGAGTGT	down	0.02	-5.88	6.88E-05
bta-miR-2478_1ss2TA	GAATCCCACTTCTGACACCA	down	0.13	-2.97	7.11E-05

hsa-miR-185-5p	TGGAGAGAAAGGCAGTTCCTGA	down	0.28	-1.86	7.15E-05
hsa-miR-548ak_L-1_1ss9CT	AAAGTAATTGCGGTTTTTGA	down	0.04	-4.53	7.55E-05
hsa-miR-15a-5p_R-1	TAGCAGCACATAATGGTTTGT	down	0.33	-1.61	7.62E-05
hsa-miR-5010-5p	AGGGGGATGGCAGAGCAAAATT	down	0.29	-1.81	7.86E-05
hsa-miR-6852-5p	CCCTGGGGTTCTGAGGACATG	up	5.25	2.39	8.64E-05
hsa-miR-624-5p_R-1	TAGTACCAGTACCTTGTGTTC	down	0.12	-3.05	8.83E-05
hsa-miR-183-5p_L-1	ATGGCACTGGTAGAATTCACT	down	0.04	-4.52	8.88E-05
hsa-miR-150-5p	TCTCCCAACCCTTGTACCAGTG	down	0.07	-3.75	9.12E-05
hsa-miR-15b-3p_R-1	CGAATCATTATTTGCTGCTCT	down	0.31	-1.70	9.31E-05
mmr-miR-1839_L+1R-1	AAGGTAGATAGAACAGGTCTTG	down	0.53	-0.91	9.37E-05
hsa-miR-30a-3p_R-1	CTTTCAGTCGGATGTTTGCAG	down	0.29	-1.78	9.55E-05
bta-miR-1246_L+1R-2	AAATGGATTTTTGGAGCA	down	0.01	-7.40	9.56E-05
hsa-miR-3688-3p_R-2	TATGGAAAGACTTTGCCACT	down	0.04	-4.74	9.82E-05
hsa-miR-4448_R-2_1ss6CG	GGCTCGTTGGTCTAGGGG	down	0.11	-3.20	1.08E-04
hsa-miR-615-3p_R-1	TCCGAGCCTGGGTCTCCCTCT	down	0.03	-5.03	1.09E-04
hsa-miR-503-5p_R-2_1ss21CA	TAGCAGCGGGAACAGTTCTGA	down	0.33	-1.60	1.13E-04
PC-3p-101409_103	AAACAGGATAGGCACTAAATGG	down	-inf	-inf	1.17E-04
pal-miR-9993a-3p_L+1R-1	AATCTCGGTGGGACCTCC	down	0.24	-2.04	1.19E-04
hsa-miR-218-5p_R-1	TTGTGCTTGATCTAACCATG	down	-inf	-inf	1.19E-04
hsa-miR-371b-5p	ACTCAAAAGATGGCGGCACTTT	down	0.01	-6.32	1.37E-04
hsa-miR-32-5p_R-2	TATTGCACATTACTAAGTTG	down	0.25	-2.00	1.39E-04
hsa-miR-182-5p_R-4	TTTGGCAATGGTAGAACTCA	down	0.06	-4.08	1.42E-04
hsa-miR-636_R-1	TGTGCTTGCTCGTCCCGCCCGC	down	0.02	-5.45	1.50E-04
hsa-miR-1294_R-2	TGTGAGGTTGGCATTGTTGT	down	0.09	-3.50	1.56E-04
hsa-let-7b-5p	TGAGGTAGTAGGTTGTGTGGTT	down	0.23	-2.11	1.59E-04

hsa-miR-4488_L+2R-1	GGAGGGGGCGGGCTCCGGC	down	-inf	-inf	1.59E-04
hsa-miR-589-5p_R-1	TGAGAACCACGTCTGCTCTGA	down	0.42	-1.26	1.60E-04
mmu-miR-3535	TGGATATGATGACTGATTACCTGAGA	down	0.11	-3.19	1.61E-04
hsa-miR-15a-3p_1ss22AT	CAGGCCATATTGTGCTGCCTCT	down	0.08	-3.68	1.70E-04
hsa-miR-214-5p_1ss22CA	TGCCTGTCTACACTTGCTGTGA	down	-inf	-inf	1.71E-04
bta-miR-11987_L-2R-1_1ss8TA	AGGAAACTCTGGTGGAGG	down	0.02	-5.39	1.73E-04
hsa-miR-151b_R+2	TCGAGGAGCTCACAGTCTAG	down	0.36	-1.49	1.76E-04
PC-3p-81170_138	TGGCAAGGGCTGTGAAGAGA	down	0.07	-3.84	1.81E-04
hsa-miR-3150b-3p	TGAGGAGATCGTCGAGGTTGG	down	0.01	-6.59	1.94E-04
hsa-miR-1323	TCAAAACTGAGGGGCATTTTCT	down	0.04	-4.69	1.95E-04
hsa-miR-29a-3p_R-1	TAGCACCATCTGAAATCGGTT	down	0.15	-2.73	2.03E-04
hsa-mir-3665-p5_1ss2CA	GAGGGCGGCGGCGGCGGC	down	-inf	-inf	2.06E-04
hsa-miR-182-3p_R-1	TGGTTCTAGACTTGCCAACT	down	0.05	-4.33	2.14E-04
hsa-miR-486-3p	CGGGGCAGCTCAGTACAGGAT	down	0.18	-2.48	2.19E-04
PC-5p-37928_367	TGAGGGGAGAGAGCGAGACT	down	0.01	-6.24	2.26E-04
hsa-miR-4446-3p	CAGGGCTGGCAGTGACATGGGT	up	7.17	2.84	2.34E-04
hsa-miR-3164	TGTGACTTTAAGGGAAATGGCG	down	0.21	-2.24	2.39E-04
hsa-miR-548ac_L-1	AAAAACCGGCAATTACTTTTG	down	-inf	-inf	2.44E-04
hsa-miR-3944-5p	TGTGCAGCAGGCCAACCGAGA	down	0.03	-5.22	2.44E-04
mmu-miR-3964_L+1_1ss6GA	CATAAAGTAGAAAGCACTAAA	down	0.06	-4.15	2.51E-04
hsa-miR-216a-5p	TAATCTCAGCTGGCAACTGTGA	down	-inf	-inf	2.52E-04
hsa-miR-197-5p_R-2	CGGGTAGAGAGGGCAGTGGGA	down	0.21	-2.25	2.55E-04
hsa-mir-937-p3	CCCATCCGCGCTCTGACTCT	down	0.04	-4.62	2.58E-04
hsa-miR-1250-5p	ACGGTGCTGGATGTGGCCTTT	up	5.76	2.53	2.61E-04

hsa-miR-579-3p	TTCATTTGGTATAAACCGCGATT	down	0.20	-2.35	2.66E-04
hsa-miR-199a-3p	ACAGTAGTCTGCACATTGGTTA	up	3.82	1.93	2.68E-04
hsa-miR-550a-5p_R-2	AGTGCCTGAGGGAGTAAGAGC	down	0.09	-3.41	2.71E-04
hsa-miR-450b-5p_R-1	TTTTGCAATATGTTCCTGAAT	down	0.17	-2.58	2.72E-04
hsa-miR-5001-3p_R-1	TTCTGCCTCTGTCCAGGTCCT	down	0.03	-4.89	2.74E-04
mmu-miR-6238_L-1R-2_1ss12TC	TATTAGTCAGCGGAGGAAA	down	0.18	-2.44	2.80E-04
hsa-miR-1307-3p_R+1	ACTCGGCGTGGCGTCGGTCGTGG	up	3.53	1.82	2.83E-04
bta-miR-1246_L+1R+3	AAATGGATTTTTGGAGCAGGGAG	down	0.02	-6.00	2.85E-04
hsa-miR-18a-3p_1ss23GA	ACTGCCCTAAGTGCTCCTTCTGA	down	0.30	-1.76	2.91E-04
hsa-miR-1246_L-2R+1	TGGATTTTTGGAGCAGGG	down	0.05	-4.40	2.95E-04
hsa-miR-22-3p	AAGCTGCCAGTTGAAGAACTGT	down	0.29	-1.78	2.99E-04
hsa-miR-1290_1ss13TG	TGGATTTTTGGAGCAGGGA	down	0.03	-5.23	3.09E-04
hsa-miR-96-5p_R-2	TTTGGCACTAGCACATTTTTG	down	0.02	-5.39	3.15E-04
PC-3p-8050_1668	GAAAAGTTAGGGGATGAGC	down	0.11	-3.21	3.22E-04
mmu-miR-5100_R-1	TCGAATCCCAGCGGTGCCTC	down	0.02	-5.56	3.29E-04
bta-miR-11987_L-2_1ss8TA	AGGAAACTCTGGTGGAGGT	down	0.00	-8.55	3.34E-04
hsa-miR-125a-3p_R-1	ACAGGTGAGGTTCTTGGGAGC	down	0.23	-2.11	3.37E-04
hsa-miR-3940-3p_R-1	CAGCCCGGATCCCAGCCCACT	down	0.18	-2.49	3.39E-04
hsa-miR-142-3p_R-1	TGTAGTGTTTCCTACTTTATGG	up	4.98	2.32	3.51E-04
hsa-miR-132-5p	ACCGTGGCTTTCGATTGTTACT	down	0.30	-1.74	3.64E-04
hsa-miR-4659a-3p	TTTCTTCTTAGACATGGCAACG	down	0.17	-2.59	3.66E-04
hsa-miR-205-5p_R-1	TCCTTCATTCCACCGGAGTCT	down	0.01	-7.34	3.67E-04
hsa-miR-7976_R+1	TGCCCTGAGACTTTTGCTCT	down	0.09	-3.55	3.68E-04
rno-miR-1843b-3p_R+1	TCTGATCGTTCCCCTCCATACA	up	7.51	2.91	3.72E-04
hsa-miR-30e-3p_1ss22CT	CTTTCAGTCGGATGTTTACAGT	up	2.56	1.36	3.77E-04

PC-5p-16110_898	ATGGGGTGCAAGCTCTTGA	down	0.16	-2.69	3.86E-04
hsa-miR-183-3p_L-1	TGAATTACCGAAGGGCCATAA	down	0.01	-6.53	3.92E-04
hsa-miR-186-5p	CAAAGAATTCTCCTTTTGGGCT	down	0.57	-0.82	3.93E-04
hsa-miR-6780a-5p_L-1R+2	TGGGAGGGAAGACAGCTGGAGAGT	down	0.17	-2.58	3.94E-04
hsa-miR-10b-3p_L-1	CAGATTCGATTCTAGGGGAAT	down	0.01	-7.09	4.14E-04
hsa-miR-181d-5p_R+1	AACATTCATTGTTGTCGGTGGGTT	up	6.10	2.61	4.17E-04
bta-miR-2478_L-1R-1_1ss2TA	AATCCCACTTCTGACACC	down	0.03	-4.97	4.20E-04
hsa-miR-4685-3p_R-2	TCTCCCTTCCTGCCCTGGCT	down	0.11	-3.22	4.22E-04
hsa-miR-126-5p	CATTATTACTTTTGGTACGCG	up	1.75	0.81	4.24E-04
hsa-miR-629-5p	TGGGTTTACGTTGGGAGAACT	down	0.30	-1.75	4.26E-04
hsa-miR-374b-5p_R-1	ATATAATACAACCTGCTAAGT	up	3.50	1.81	4.27E-04
bta-miR-11987_L-1R-2_1ss8TA	GAGGAAACTCTGGTGGAG	down	0.11	-3.13	4.46E-04
hsa-miR-200b-5p_R-1	CATCTTACTGGGCAGCATTGG	down	0.06	-4.09	4.50E-04
hsa-miR-3202_L+2R-3	TATGGAAGGGAGAAGAGCTTT	down	-inf	-inf	4.66E-04
hsa-miR-618_R-2	AAACTCTACTTGTCCTTCTGA	down	0.01	-6.96	4.66E-04
hsa-miR-30e-5p_R+2	TGTAAACATCCTTGACTGGAAGCT	down	0.58	-0.79	4.72E-04
mmu-miR-5124a_L-1R-1_1ss5CA	GTCAAGTGACTAAGAGCA	down	0.13	-2.90	4.75E-04
hsa-miR-221-3p	AGCTACATTGTCTGCTGGGTTTC	up	3.84	1.94	5.02E-04
hsa-mir-6511a-3-p5	CTGCAGGCAGAAGTGGGGCTGA	down	0.08	-3.57	5.02E-04
hsa-mir-6511b-1-p5	CTGCAGGCAGAAGTGGGGCTGA	down	0.08	-3.57	5.02E-04
hsa-let-7g-5p	TGAGGTAGTAGTTTGTACAGTT	down	0.42	-1.26	5.07E-04
hsa-miR-3158-3p_R-1	AAGGGCTTCCTCTCTGCAGGA	down	0.02	-5.50	5.16E-04
hsa-miR-20b-5p	CAAAGTGCTCATAGTGCAGGTAG	down	0.31	-1.67	5.40E-04

hsa-miR-3130-3p	GCTGCACCGGAGACTGGGTAA	down	0.10	-3.26	5.44E-04
hsa-let-7a-3p	CTATACAATCTACTGTCTTTC	down	0.32	-1.64	5.53E-04
hsa-miR-3120-3p	CACAGCAAGTGTAGACAGGCA	up	5.52	2.47	5.55E-04
hsa-miR-324-3p_L-3R+1	ACTGCCCCAGGTGCTGCTGGA	down	0.44	-1.20	5.57E-04
hsa-miR-215-5p_R-1	ATGACCTATGAATTGACAGA	down	0.01	-6.35	5.60E-04
hsa-mir-1285-1-p5_1ss12AG	AGGCTGGTCTCGAACTCC	down	0.24	-2.08	5.80E-04
hsa-miR-330-3p	GCAAAGCACACGGCCTGCAGAGA	up	5.02	2.33	5.80E-04
hsa-miR-9985_R-1_1ss16CT	TTCACAGTGGCTAAGTTA	down	0.11	-3.23	5.85E-04
PC-5p-83623_132	GGGCTAGTGACTGGAGTGAA	down	0.02	-6.02	5.87E-04
PC-5p-31521_454	TTGCAAGCAACACTCTGTGG	down	0.17	-2.60	5.92E-04
cja-miR-151_R+1	TCGAGGAGCTCACAGTCTAGC	up	11.79	3.56	6.03E-04
hsa-miR-3127-5p	ATCAGGGCTTGTGGAATGGGAAG	down	0.37	-1.43	6.03E-04
PC-5p-120168_84	GGCAGAGAGGAGGAGAGAATTG	down	-inf	-inf	6.15E-04
mml-miR-378d_L-1R+1_1ss21CG	CTGGACTTGGAGTCAGAAGGAG	down	0.02	-5.72	6.34E-04
hsa-miR-499a-5p	TTAAGACTTGCAGTGATGTTT	down	0.32	-1.66	6.44E-04
PC-5p-18835_776	GGTGGTTCTGTATGGAAG	down	0.19	-2.39	6.52E-04
hsa-miR-548at-5p_R-2	AAAAGTTATTGCGGTTTTGG	down	0.11	-3.16	6.54E-04
hsa-miR-1301-3p_R+1	TTGCAGCTGCCTGGGAGTGACTTCT	up	3.38	1.76	6.59E-04
hsa-miR-3942-5p_L-1	AGCAATACTGTTACCTGAAAT	down	0.23	-2.14	6.72E-04
bta-mir-2904-2-p5	AGCCTCGGTTGGCCTCGGAT	down	0.27	-1.87	6.97E-04
hsa-miR-30a-5p_R+2	TGTAAACATCCTCGACTGGAAGCT	down	0.18	-2.47	7.01E-04
eca-miR-451_R-2	AAACCGTTACCATTACTGTG	down	-inf	-inf	7.05E-04
PC-3p-10623_1306	CAGTTCAATGGTGTTCAGCAGA	up	7.40	2.89	7.07E-04
hsa-mir-5695-p5	TCTAGATTCTTCTTGGCCTCT	down	-inf	-inf	7.33E-04

bta-miR-11987_L-1R-1_1ss8TA	GAGGAAACTCTGGTGGAGG	down	0.08	-3.73	7.43E-04
PC-5p-273115_36	TGTGAGGAAGCTGTTGTTGCT	down	-inf	-inf	7.45E-04
hsa-miR-548ag_R+1_1ss4GA	AAAAGTAATTGTGGTTTCTGCC	up	6.98	2.80	7.47E-04
hsa-mir-3196-p5_1ss4GT	GGGTCGGGGCGGCAGGGGCC	down	0.01	-7.16	7.77E-04
PC-5p-24850_590	GGGCGTTGGATATTTGAA	down	0.07	-3.90	7.89E-04
bta-miR-2478_L-1	TATCCCACTTCTGACACCA	down	0.15	-2.73	8.10E-04
hsa-miR-500b-3p_L+3R-1	AGTGCACCCAGGCAAGGATTCT	down	0.10	-3.34	8.16E-04
hsa-miR-140-5p	CAGTGGTTTTACCCTATGGTAG	up	4.42	2.14	8.19E-04
hsa-miR-28-5p_R-1	AAGGAGCTCACAGTCTATTGA	up	3.66	1.87	8.23E-04
hsa-miR-409-3p	GAATGTTGCTCGGTGAACCCCT	up	4.10	2.04	8.24E-04
hsa-miR-548q_L-1R+1	CTGGTGCAAAAGTAATGGCGGT	down	0.04	-4.55	8.38E-04
PC-5p-37527_371	GGGAGACAGACATCGGGT	down	0.04	-4.82	8.41E-04
pal-mir-10001-p5_1ss1AT	TGGGCGGGCGGGGCCGGGGG	down	0.01	-6.38	8.53E-04
bta-miR-150_1ss10CT	TCTCCCAACTCTTGTACCAGTGT	down	-inf	-inf	8.55E-04
hsa-miR-766-3p	ACTCCAGCCCCACAGCCTCAGC	up	10.36	3.37	8.65E-04
hsa-miR-3157-3p	CTGCCCTAGTCTAGCTGAAGCT	down	0.08	-3.70	8.67E-04
hsa-miR-363-5p	CGGGTGGATCACGATGCAATTT	down	0.30	-1.75	8.79E-04
hsa-miR-1303_R-2	TTTAGAGACGGGGTCTTGCT	down	0.05	-4.35	8.94E-04
hsa-miR-374a-3p	CTTATCAGATTGTATTGTAATT	up	2.71	1.44	9.05E-04
hsa-miR-744-3p_R-1	CTGTTGCCACTAACCTCAACC	up	5.86	2.55	9.13E-04
hsa-miR-3200-5p	AATCTGAGAAGGCGCACAAGGT	down	0.02	-5.98	9.14E-04
PC-3p-83127_133	CCAGGCTCTTGGTTATGTTTT	up	inf	inf	9.33E-04
hsa-mir-5684-p3_1ss16CG	TGCCCAGGCTGGAGTGCAG	down	0.01	-6.40	9.38E-04
hsa-miR-9-3p	ATAAAGCTAGATAACCGAAAGT	down	0.21	-2.23	9.44E-04
hsa-miR-1234-3p_R+1	TCGGCCTGACCACCCACCCCACT	down	0.08	-3.72	9.47E-04

PC-3p-32854_434	CAAAGGGTAACGGAGGAG	down	0.18	-2.49	9.57E-04
hsa-miR-6503-3p_L-1R-1_1ss7AG	GGACTGGGATGCAGACCTC	down	-inf	-inf	9.72E-04
hsa-miR-4742-3p_R-1	TCTGTATTCTCCTTTGCCTGCA	down	0.38	-1.39	9.90E-04
hsa-miR-129-5p	CTTTTTGCGGTCTGGGCTTGC	down	0.05	-4.36	1.01E-03
hsa-miR-4429_R+1_1ss11CT	AAAAGCTGGGTTGAGAGGCGA	down	0.16	-2.69	1.02E-03
hsa-miR-340-5p	TTATAAAGCAATGAGACTGATT	up	2.18	1.12	1.03E-03
hsa-miR-1273h-5p_R+2	CTGGGAGGTCAAGGCTGCAGTGT	up	5.70	2.51	1.03E-03
cja-miR-1895_L-4_1ss14CG	TGAGGAGGAGGAGGAGGA	down	0.04	-4.56	1.04E-03
PC-3p-24862_589	AGGGACGCACCGCTGGTG	down	0.05	-4.19	1.05E-03
PC-3p-76092_150	CGCCTGTCTCATTCTCTGCAGT	up	inf	inf	1.05E-03
bta-miR-1246_L-1R+3	ATGGATTTTTGGAGCAGGGAG	down	0.02	-5.88	1.05E-03
hsa-miR-625-5p_R-1	AGGGGGAAAGTTCTATAGTC	down	0.29	-1.80	1.07E-03
bta-mir-1264-p3_1ss5AT	AAGATTAAGAGAACCAACA	up	65.53	6.03	1.10E-03
hsa-miR-676-3p_R+1	CTGTCCTAAGGTTGTTGAGTTT	down	-inf	-inf	1.11E-03
hsa-miR-1268b_R-2	CGGGCGTGGTGGTGGGGG	down	0.21	-2.24	1.11E-03
hsa-miR-1268a	CGGGCGTGGTGGTGGGGG	down	0.21	-2.24	1.11E-03
hsa-miR-326_R+1	CCTCTGGGCCCTTCCTCCAGT	up	4.82	2.27	1.14E-03
PC-3p-95714_110	CAGCGGCTGCGCATCTCGGG	down	-inf	-inf	1.15E-03
hsa-miR-374b-3p	CTTAGCAGGTTGTATTATCATT	up	2.93	1.55	1.15E-03
hsa-miR-125b-5p_R-2	TCCCTGAGACCCTAACTTGT	down	0.17	-2.57	1.17E-03
hsa-miR-30b-5p	TGTAAACATCCTACACTCAGCT	up	1.88	0.91	1.17E-03
hsa-miR-145-5p_R-1	GTCCAGTTTTCCCAGGAATCCC	down	0.32	-1.64	1.19E-03
hsa-miR-582-3p	TAACTGGTTGAACAACTGAACC	down	0.01	-6.34	1.23E-03
hsa-miR-98-3p_1ss22CT	CTATACAACTTACTACTTTCCT	up	2.64	1.40	1.23E-03
hsa-miR-484	TCAGGCTCAGTCCCCTCCCGAT	down	0.61	-0.72	1.24E-03

bta-miR-378_L-2R+1	TGGACTTGGAGTCAGAAGGCT	down	-inf	-inf	1.26E-03
hsa-miR-659-5p	AGGACCTTCCCTGAACCAAGGA	down	-inf	-inf	1.31E-03
hsa-miR-4646-5p	ACTGGGAAGAGGAGCTGAGGGA	down	0.03	-5.00	1.32E-03
hsa-miR-548ay-5p_R-1	AAAAGTAATTGTGGTTTTTG	down	0.37	-1.44	1.32E-03
ppy-miR-548a	AAAAGTAATTGTGGTTTTTG	down	0.37	-1.44	1.32E-03
hsa-miR-548ad-5p	AAAAGTAATTGTGGTTTTTG	down	0.37	-1.44	1.32E-03
bta-miR-150	TCTCCCAACCCTTGTACCAGTGT	down	0.20	-2.34	1.32E-03
PC-5p-14422_992	ACTTGACTGCTCTGACCA	up	35.22	5.14	1.32E-03
hsa-let-7d-5p	AGAGGTAGTAGGTTGCATAGTT	down	0.44	-1.19	1.34E-03
hsa-miR-625-3p	GACTATAGAACTTTCCCCCTCA	up	2.27	1.18	1.37E-03
hsa-miR-7849-3p_R+2	GACAATTGTTGATCTTGGGCCTGA	up	10.67	3.42	1.38E-03
hsa-miR-19b-3p	TGTGCAAATCCATGCAAAACTGA	down	0.39	-1.36	1.41E-03
mmu-mir-6236-p3_1ss2AG_2	CGGCCGTCGCCGGCAGTC	down	0.31	-1.69	1.41E-03
mmu-mir-6236-p3_1ss2AG_1	AGCTAGCCCTGAAAATGGAT	down	0.31	-1.69	1.41E-03
hsa-miR-181c-5p_R+2	AACATTCAACCTGTCGGTGAGTTT	up	2.50	1.32	1.42E-03
mdo-miR-22-3p	AAGCTGCCAGTTGAAGAACTGC	down	0.17	-2.57	1.42E-03
hsa-miR-6516-5p_R-1	TTTGCAGTAACAGGTGTGAGC	up	6.37	2.67	1.43E-03
hsa-miR-6859-5p_R-2	GAGAGGAACATGGGCTCAGGA	down	0.16	-2.68	1.46E-03
mmu-miR-486a-5p_R+2	TCCTGTACTGAGCTGCCCCGAGGT	down	0.14	-2.85	1.46E-03
hsa-miR-409-5p	AGGTTACCCGAGCAACTTTGCAT	up	4.11	2.04	1.48E-03
hsa-miR-338-5p_R-1	AACAATATCCTGGTGCTGAGT	down	0.49	-1.03	1.49E-03
hsa-miR-223-3p_R+1	TGTCAGTTTGTCAAATACCCCAA	up	2.01	1.01	1.52E-03
hsa-miR-516a-5p_R-1	TTCTCGAGGAAAGAAGCACTTT	down	0.00	-7.67	1.52E-03
PC-5p-36522_384	TCTTAGGAAGCGAAGCAAT	down	0.08	-3.56	1.53E-03
eca-mir-8986a-p5_1ss1GA	ATCGAGGCTAGAGTCACGCTTGG	down	0.54	-0.90	1.54E-03
mmu-miR-1983	CTCACCTGGAGCATGTTTTCT	up	2.97	1.57	1.56E-03

hsa-miR-4466_R+2	GGGTGCGGGCCGGCGGGGTC	down	0.11	-3.17	1.59E-03
hsa-miR-5695_L-1R+1	CTCCAAGAAGAATCTAGACAGA	down	-inf	-inf	1.60E-03
bta-miR-199c_L-1R+4	ACAGTAGTCTGCACATTGGTTTC	up	10.45	3.39	1.62E-03
hsa-miR-4672	TTACACAGCTGGACAGAGGCA	down	-inf	-inf	1.63E-03
hsa-mir-3199-1-p5	ACTGCCTTAGGAGAAAGTTTCT	down	0.03	-4.85	1.68E-03
hsa-mir-3199-2-p5	ACTGCCTTAGGAGAAAGTTTCT	down	0.03	-4.85	1.68E-03
hsa-miR-10401-3p_L+1R-1	GACCTCGCCGTCCCGCCCGCC	down	0.39	-1.35	1.71E-03
PC-3p-103492_100	GAAATAATCTATTCTGAGGCTTT	up	inf	inf	1.71E-03
ssc-mir-4332-p5_1ss12CT	CGGGGGTGGGGTCGGCGGGGG	down	0.02	-5.88	1.72E-03
hsa-miR-548ag_1ss4GA	AAAAGTAATTGTGGTTTCTGC	up	5.27	2.40	1.73E-03
bta-miR-199c_L-1R+2	ACAGTAGTCTGCACATTGGCT	up	14.09	3.82	1.75E-03
hsa-miR-147b-3p	GTGTGCGGAAATGCTTCTGCT	down	0.12	-3.08	1.79E-03
bta-mir-1264-p5_1ss5AT	AAGATTAAGAGAACCAAC	up	inf	inf	1.83E-03
hsa-miR-362-3p_1ss22AT	AACACACCTATTCAAGGATTCT	down	0.05	-4.26	1.85E-03
PC-5p-60328_204	AGAATATGGGAGTCTGTGGCT	down	0.34	-1.56	1.88E-03
PC-5p-133941_74	AAATTTGACTGGCTATTTT	up	inf	inf	1.88E-03
PC-5p-41840_326	TTGGTCTTCTCTGCCCTCCAGT	up	11.39	3.51	1.91E-03
hsa-miR-6772-3p	TTGCTCCTGACTCTGTGCCCACA	up	inf	inf	1.99E-03
PC-5p-121193_83	AAAAGTAATTGTGGTTTTTGTGT	up	inf	inf	1.99E-03
hsa-miR-301b-3p	CAGTGCAATGATATTGTCAAAGC	up	4.90	2.29	2.06E-03
hsa-miR-2115-3p	CATCAGAATTCATGGAGGCTAG	down	-inf	-inf	2.07E-03
hsa-miR-4523	GACCGAGAGGGCCTCGGCTGT	up	15.41	3.95	2.08E-03
hsa-miR-501-5p_R+2	AATCCTTTGTCCCTGGGTGAGAGT	down	0.26	-1.96	2.11E-03
hsa-miR-769-5p	TGAGACCTCTGGGTTCTGAGCT	up	1.61	0.69	2.13E-03
hsa-miR-548j-5p	AAAAGTAATTGCGGTCTTTGGT	up	3.80	1.93	2.13E-03

mdo-miR-181a-5p_R+3_2	AACATTCAACGCTGTCGGTGAGTTTT	up	36.43	5.19	2.14E-03
mdo-miR-181a-5p_R+3_1	AACATTCAACGCTGTCGGTGAGTTAT	up	36.43	5.19	2.14E-03
hsa-miR-5000-3p_R-1	TCAGGACACTTCTGAACTTGG	down	-inf	-inf	2.16E-03
PC-3p-111035_92	TAAAAACCGTGACTACTTCT	down	0.02	-5.99	2.18E-03
PC-3p-97333_108	TTAGAGGTTCGGGGGATGT	down	0.03	-5.07	2.20E-03
hsa-miR-27b-5p	AGAGCTTAGCTGATTGGTGAAC	up	4.06	2.02	2.22E-03
rno-miR-539-5p_R+2	GGAGAAATTATCCTTGGTGTGTTT	up	inf	inf	2.24E-03
hsa-miR-1228-5p	GTGGGCGGGGGCAGGTGTGTG	down	-inf	-inf	2.26E-03
PC-5p-295297_33	ACAGCGAGAGGCAGCTCTGG	down	0.10	-3.32	2.26E-03
PC-3p-228736_42	ACGGAAACGGAAACAAAGCTTT	down	-inf	-inf	2.30E-03
hsa-miR-124-3p_R-3	TAAGGCACGCGGTGAATGC	down	-inf	-inf	2.31E-03
hsa-miR-5187-5p	TGGGATGAGGGATTGAAGTGGA	up	5.56	2.48	2.31E-03
hsa-miR-509-3p	TGATTGGTACGTCTGTGGGTAG	down	0.11	-3.19	2.32E-03
hsa-mir-1273c-p3	CAGAGTCTCGTTCTGTTGCC	down	0.45	-1.16	2.34E-03
hsa-miR-324-5p_R+1	CGCATCCCCTAGGGCATTGGTGT	up	3.44	1.78	2.36E-03
PC-3p-56114_225	TCAGGTGGGGAGTTTGGCTG	down	0.03	-5.16	2.39E-03
hsa-miR-12136_R+8	GAAAAAGTCATGGAGGCCATGGGGTT	up	4.45	2.15	2.42E-03
PC-3p-29968_482	CAGAAACCAGAATTACTTTTGC	up	6.20	2.63	2.44E-03
bta-mir-1246-p3_1ss18AG_2	TGGATTTTTGGAGCAGGGAG	down	0.01	-6.12	2.45E-03
bta-mir-1246-p3_1ss18AG_1	AAATGGATTTTTGGAGCGG	down	0.01	-6.12	2.45E-03
hsa-miR-1224-5p_R+2	GTGAGGACTCGGGAGGTGGAG	down	0.01	-6.53	2.57E-03
hsa-miR-5581-3p	TTCCATGCCTCCTAGAAGTTCC	down	0.26	-1.92	2.62E-03
hsa-mir-3648-2-p5	GGGGGAGCCGCGGGGATC	down	0.01	-7.04	2.63E-03

hsa-miR-6740-5p_L-2R+2	TTTGGGATGGAGAGAGGAGAAA	down	-inf	-inf	2.69E-03
hsa-miR-145-3p_L-2R+1	ATTCCTGGAAATACTGTTCTT	down	0.34	-1.55	2.69E-03
hsa-miR-33a-5p_R-1	GTGCATTGTAGTTGCATTGC	up	5.99	2.58	2.70E-03
hsa-miR-660-3p_R-2	ACCTCCTGTGTGCATGGAT	down	0.06	-3.96	2.73E-03
hsa-miR-1296-5p	TTAGGGCCCTGGCTCCATCTCC	up	2.22	1.15	2.78E-03
PC-3p-147694_66	AAGACTTTTTCTCTGACCT	up	inf	inf	2.79E-03
hsa-miR-339-5p	TCCCTGTCCTCCAGGAGCTCACG	up	2.53	1.34	2.85E-03
hsa-miR-675-3p_R+2	CTGTATGCCCTCACCGCTCAGC	down	-inf	-inf	2.86E-03
hsa-miR-222-3p_R+3	AGCTACATCTGGCTACTGGGTCTC	up	1.80	0.85	2.87E-03
PC-5p-386146_24	TTTAGCACGGACATGGTTCT	down	-inf	-inf	2.87E-03
hsa-miR-4440_R+1	TGTCGTGGGGCTTGCTGGCTTGA	down	-inf	-inf	2.89E-03
hsa-miR-7850-5p	GTTTGGACATAGTGTGGCTGG	down	-inf	-inf	2.90E-03
hsa-miR-139-3p	TGGAGACGCGGCCCTGTTGGAGT	up	2.19	1.13	2.91E-03
hsa-miR-340-3p_R+1	TCCGTCTCAGTTACTTTATAGCC	up	3.77	1.91	2.93E-03
hsa-mir-3929-p3_1ss19TG	AGCACTTTGGGAGGCTGAG	down	-inf	-inf	2.96E-03
hsa-miR-1260b_1ss9AG	ATCCCACCGCTGCCACCAT	up	8.96	3.16	2.97E-03
hsa-miR-202-3p	AGAGGTATAGGGCATGGGAA	down	-inf	-inf	2.99E-03
hsa-miR-132-3p	TAACAGTCTACAGCCATGGTCG	down	0.65	-0.62	2.99E-03
oga-miR-28b_R+3_1	TCGAGGAGCTCACAGTCTAGTAGT	up	14.22	3.83	3.00E-03
oga-miR-28b_R+3_2	TCGAGGAGCTCACAGTCTAGTTTT	up	14.22	3.83	3.00E-03
hsa-miR-584-3p_R-2	TCAGTTCCAGGCCAACCAGG	down	-inf	-inf	3.03E-03
PC-3p-24564_597	CGTGAAATCCTGTCTGAA	down	0.16	-2.62	3.03E-03
hsa-miR-380-5p_L+1R-1	ATGGTTGACCATAGAACATGCG	up	31.17	4.96	3.04E-03
hsa-miR-1289_R-1	TGGAGTCCAGGAATCTGCATTT	down	-inf	-inf	3.09E-03
hsa-miR-101-3p_R+1	TACAGTACTGTGATAACTGAAG	down	0.41	-1.29	3.15E-03
hsa-miR-548ab_L+1R-3	CAAAAGTAATTGTGGATTTT	down	0.05	-4.39	3.15E-03

hsa-miR-204-3p	GCTGGGAAGGCAAAGGGACGT	down	0.09	-3.54	3.16E-03
mmu-mir-6236-p3_1ss18GA_2	GAAAATGGATGGCGCTGAA	down	0.05	-4.26	3.17E-03
mmu-mir-6236-p3_1ss18GA_1	GAAAATGGATGGCGCTGA	down	0.05	-4.26	3.17E-03
ssc-mir-4332-p5_1ss9CT	GGGTGGGGTCGGCGGGGG	down	0.14	-2.85	3.18E-03
hsa-miR-301a-3p	CAGTGCAATAGTATTGTCAAAGC	up	4.62	2.21	3.20E-03
cja-miR-3135_L-1_1ss10CG	AGGCTGGAGTGCAGTGGCG	down	-inf	-inf	3.20E-03
hsa-miR-224-5p_L-1	CAAGTCACTAGTGGTTCCGTTTAG	up	3.83	1.94	3.24E-03
hsa-miR-4511_R+1	GAAGAACTGTTGCATTTGCCCTG	down	0.15	-2.78	3.28E-03
PC-3p-33579_423	TTCGCTGGGAATTCAGCCTCT	down	0.01	-7.39	3.28E-03
PC-5p-189265_50	TTGTGGTCTGGGGTCTTGGGC	down	-inf	-inf	3.31E-03
hsa-miR-605-3p	AGAAGGCACTATGAGATTTAGA	up	8.23	3.04	3.37E-03
hsa-miR-494-3p_R+1	TGAAACATACACGGGAAACCTCT	up	3.33	1.74	3.40E-03
hsa-miR-10400-5p_R-3_1ss12GA	CGGCGGCGGCGACTCTGG	down	0.13	-2.98	3.47E-03
PC-3p-48185_274	AAGCCTCTGTCCCCACCCCAGT	up	5.28	2.40	3.48E-03
bta-mir-1246-p5_1ss16AG	GATTTTTGGAGCAGGGAG	down	0.01	-6.86	3.51E-03
hsa-let-7b-3p_1ss22CT	CTATACAACCTACTGCCTTCCT	down	0.38	-1.38	3.54E-03
hsa-miR-3117-3p_R+1	ATAGGACTCATATAGTGCCAGG	down	-inf	-inf	3.56E-03
PC-3p-85981_127	AAGGTCAGCTCAATGAGAA	down	0.03	-5.07	3.58E-03
PC-5p-38571_359	AATCCTCACTTTGAATCCATGT	up	9.35	3.22	3.60E-03
hsa-miR-3191-3p_R-1_1ss22AT	TGGGGACGTAGCTGGCCAGACT	up	22.64	4.50	3.63E-03
hsa-miR-12135_1ss9TC	TAAAGGTTCGTTTGTAAA	up	43.61	5.45	3.65E-03
pal-mir-9226-p5_1ss18CT	TCCCTGTTCGGGCGCCATT	up	4.72	2.24	3.70E-03

hsa-miR-378j_R+1_1ss14CT	ACTGGATTTGGAGTCAGAAG	down	-inf	-inf	3.72E-03
hsa-miR-570-3p	CGAAAACAGCAATTACCTTTGC	down	0.12	-3.08	3.73E-03
hsa-miR-508-3p_R-3	TGATTGTAGCCTTTTGGAGT	down	-inf	-inf	3.88E-03
hsa-miR-4637	TACTAACTGCAGATTCAAGTGA	down	-inf	-inf	3.93E-03
PC-3p-187469_50	GGCGCCCGGGGAGAACTGC	down	-inf	-inf	3.99E-03
hsa-miR-3064-3p_L+1R-4	TTTGCCACACTGCAACACCT	down	-inf	-inf	4.02E-03
hsa-miR-450a-5p_R-2	TTTTGCGATGTGTTCCTAAT	down	0.57	-0.80	4.08E-03
PC-3p-4847_2746	GAAGTGGGGTTGTGGGAAT	down	0.23	-2.12	4.11E-03
mmu-mir-6236-p3_1ss16GC	ATGGCGCTGGAGCGTCGGG	down	0.03	-5.29	4.15E-03
hsa-miR-154-3p	AATCATACACGGTTGACCTATT	up	6.65	2.73	4.18E-03
hsa-mir-1976-p5_1ss21CT	CAGCAAGGAAGGCAGGGGTCT	down	0.03	-4.97	4.19E-03
hsa-miR-450a-2-3p_L-1	TTGGGGACATTTTGCATTCAT	down	0.29	-1.77	4.19E-03
hsa-miR-4665-5p	CTGGGGGACGCGTGAGCGCGAGC	up	4.66	2.22	4.22E-03
hsa-miR-329-3p	AACACACCTGGTTAACCTCTTT	up	2.98	1.57	4.25E-03
hsa-miR-671-3p	TCCGGTTCTCAGGGCTCCACC	up	5.05	2.34	4.26E-03
mmu-miR-501-3p_R-1	AATGCACCCGGGCAAGGATTT	down	-inf	-inf	4.26E-03
PC-3p-37476_372	ATGTTATGATGATGGGCGAAA	down	0.02	-5.89	4.28E-03
hsa-miR-382-5p	GAAGTTGTTCGTGGTGGATTCG	up	3.84	1.94	4.29E-03
PC-3p-29103_499	CTTGAGACTCTGGGTCAGT	down	0.02	-5.73	4.36E-03
hsa-miR-6818-5p	TTGTGTGAGTACAGAGAGCATC	down	0.40	-1.32	4.42E-03
hsa-mir-653-p5	TTGAAACAATCTCTACTGAAC	down	-inf	-inf	4.42E-03
hsa-miR-514a-3p_R-1	ATTGACACTTCTGTGAGTAG	down	0.34	-1.56	4.46E-03
cgr-miR-1260_L-1R+2_5	TCCCACCGCTGCCACCATA	up	inf	inf	4.58E-03
cgr-miR-1260_L-1R+2_1	TCCCACCGCTGCCACCAAA	up	inf	inf	4.58E-03
cgr-miR-1260_L-1R+2_3	TCCCACCGCTGCCACCAAT	up	inf	inf	4.58E-03
cgr-miR-1260_L-1R+2_4	TCCCACCGCTGCCACCAGA	up	inf	inf	4.58E-03

cgr-miR-1260_L-1R+2_2	TCCCACCGCTGCCACCAAG	up	inf	inf	4.58E-03
hsa-miR-3176_R+2	ACTGGCCTGGGACTACCGGGA	down	0.02	-5.44	4.64E-03
hsa-miR-6866-5p_R-2	TTAGAGGCTGGAATAGAGATT	down	0.51	-0.96	4.64E-03
PC-3p-89469_121	TGCCCACAGAACCCTCTAA	up	inf	inf	4.65E-03
hsa-miR-873-3p_L-1	GAGACTGATGAGTTCCCGGGA	down	-inf	-inf	4.67E-03
hsa-miR-548b-5p_R-4	AAAAGTAATTGTGGTTTT	down	0.01	-6.21	4.68E-03
cja-miR-151_R+2	TCGAGGAGCTCACAGTCTAGTT	up	4.15	2.05	4.69E-03
hsa-miR-516b-5p	ATCTGGAGGTAAGAAGCACTTT	down	-inf	-inf	4.73E-03
mdo-miR-200a-3p_R+2	TAACACTGTCTGGTAACGATGTTT	up	4.86	2.28	4.76E-03
PC-3p-46468_286	AACTGCATCGTGATGGGGA	down	0.16	-2.60	4.79E-03
hsa-miR-200a-5p_R-1	CATCTTACCGGACAGTGCTGG	down	0.08	-3.72	4.83E-03
PC-3p-31070_462	TTCATCGGCGTAGGGTGA	down	0.31	-1.67	4.92E-03
hsa-let-7d-3p	CTATACGACCTGCTGCCTTTCT	down	0.68	-0.55	4.93E-03
hsa-mir-4422-p3	GCCCTTCTTGATGCTCTTGATT	up	6.90	2.79	4.98E-03
hsa-miR-2355-3p_L-2R+2	TGTCCTTGCTGTTTGGAGATAA	up	2.75	1.46	5.08E-03
hsa-miR-3173-3p_L-1	AAGGAGGAAATAGGCAGGCCA	down	0.03	-5.18	5.11E-03
hsa-miR-152-3p	TCAGTGCATGACAGAACTTGG	up	1.95	0.96	5.12E-03
hsa-miR-3065-3p	TCAGCACCAGGATATTGTTGGAG	up	6.74	2.75	5.15E-03
hsa-miR-133a-3p_R+1	TTTGGTCCCCTTCAACCAGCTGT	up	5.11	2.35	5.20E-03
hsa-miR-939-5p_R-1	TGGGGAGCTGAGGCTCTGGGGGT	down	0.47	-1.10	5.24E-03
hsa-miR-493-3p	TGAAGGTCTACTGTGTGCCAGG	up	2.73	1.45	5.26E-03
hsa-miR-3611_R-2	TTGTGAAGAAAGAAATTCT	down	0.30	-1.72	5.33E-03
hsa-miR-941	CACCCGGCTGTGTGCACATGTGC	down	0.31	-1.71	5.40E-03
hsa-miR-3065-5p	TCAACAAAATCACTGATGCTGGA	up	3.96	1.98	5.45E-03
hsa-miR-4747-5p_R-3	AGGGAAGGAGGCTTGGTCT	down	-inf	-inf	5.48E-03
hsa-miR-3920	ACTGATTATCTTAACTCTCTGA	up	5.11	2.35	5.48E-03

hsa-miR-301a-5p	GCTCTGACTTTATTGCACTACT	up	3.32	1.73	5.50E-03
hsa-miR-628-3p	TCTAGTAAGAGTGGCAGTCGA	up	1.34	0.42	5.52E-03
mmu-miR-106a-5p	CAAAGTGCTAACAGTGCAGGTAG	up	9.77	3.29	5.55E-03
PC-5p-190163_50	TTAAGTGGGAAACGATGTG	down	-inf	-inf	5.59E-03
hsa-miR-345-5p_R+1	GCTGACTCCTAGTCCAGGGCTCT	down	0.59	-0.76	5.63E-03
bta-mir-2478-p5_1ss20GA_1	ATCCCACTTCTGACACCATA	up	inf	inf	5.66E-03
bta-mir-2478-p5_1ss20GA_2	ATCCCACTTCTGACACCATAT	up	inf	inf	5.66E-03
hsa-miR-100-5p_R-1	AACCCGTAGATCCGAACTTGT	down	0.03	-5.28	5.68E-03
hsa-miR-19a-3p	TGTGCAAATCTATGCAAAACTGA	down	0.44	-1.17	5.73E-03
hsa-miR-3682-3p	TGATGATACAGGTGGAGGTAG	down	-inf	-inf	5.73E-03
hsa-miR-539-5p	GGAGAAATTATCCTTGGTGTGT	up	138.15	7.11	5.78E-03
hsa-miR-493-5p	TTGTACATGGTAGGCTTTCATT	up	2.89	1.53	5.80E-03
hsa-mir-548ag-2-p3	CAAGAACCTCAATTACCTTTGC	up	4.47	2.16	5.81E-03
hsa-miR-548ai_R-2	AAAGGTAATTGCAGTTTTTC	down	-inf	-inf	5.85E-03
mmu-mir-3535-p3	CCTCTAGATAGTCAAGTTCTGATC	down	-inf	-inf	5.90E-03
hsa-miR-487b-3p	AATCGTACAGGGTCATCCACTT	up	6.71	2.75	5.90E-03
hsa-miR-513c-5p_R-2	TTCTCAAGGAGGTGTCGTTT	down	0.02	-5.74	5.95E-03
hsa-let-7a-5p	TGAGGTAGTAGGTTGTATAGTT	down	0.43	-1.21	5.96E-03
hsa-miR-6509-5p_R-1	ATTAGGTAGTGGCAGTGGAA	down	0.02	-5.53	5.96E-03
hsa-miR-18b-3p_L+3R-5	TACTGCCCTAAATGCCCCTT	down	-inf	-inf	5.98E-03
hsa-miR-551b-3p_R+1	GCGACCCATACTTGGTTTCAGT	up	10.86	3.44	5.98E-03
hsa-miR-4755-3p	AGCCAGGCTCTGAAGGGAAAGT	down	0.06	-3.95	6.04E-03
hsa-mir-548ba-p3	CAAAAACTGCAATTACTTT	down	0.18	-2.51	6.04E-03
hsa-miR-548aq-3p_R-3	CAAAAACTGCAATTACTTT	down	0.18	-2.51	6.04E-03
hsa-miR-548ae-3p_R-2	CAAAAACTGCAATTACTTT	down	0.18	-2.51	6.04E-03
hsa-miR-4645-3p_L+2R-1	CGAGACAGTAGTTCTTGCCTGGT	up	3.80	1.93	6.10E-03

hsa-miR-548a-3p	CAAAACTGGCAATTACTTTTGC	up	3.30	1.72	6.14E-03
hsa-miR-320d_R-1	AAAAGCTGGGTTGAGAGG	down	0.06	-4.06	6.23E-03
mmu-miR-107-5p_R+1	AGCTTCTTTACAGTGTTGCCTTGT	up	inf	inf	6.29E-03
PC-3p-129317_77	TAGGTCACTGGGGTCAGAG	down	0.28	-1.83	6.30E-03
PC-3p-92753_115	AATTTGACTGGCTTATTT	up	15.50	3.95	6.30E-03
hsa-miR-1-3p	TGGAATGTAAAGAAGTATGTAT	up	4.27	2.09	6.52E-03
hsa-miR-3135a_R+1	TGCCTAGGCTGAGACTGCAGTGA	down	0.13	-2.98	6.53E-03
mmu-miR-6412_R-2_1ss15AT	TCGAAACCATCCTCTGCTAC	down	0.27	-1.86	6.54E-03
hsa-miR-873-5p_L+1R-3	TGCAGGAACTTGTGAGTCT	down	0.01	-6.11	6.63E-03
hsa-miR-191-3p_L-1	CTGCGCTTGGATTTCGTCCCC	up	2.13	1.09	6.68E-03
hsa-miR-6876-5p	CAGGAAGGAGACAGGCAGTTCA	up	3.58	1.84	6.73E-03
hsa-miR-543	AAACATTCGCGGTGCACTTCTT	up	3.33	1.74	6.82E-03
hsa-miR-16-1-3p	CCAGTATTAACTGTGCTGCTGA	down	0.45	-1.15	6.91E-03
mmu-miR-421-5p	CTCATTAAATGTTTGTTGAAT	up	inf	inf	6.92E-03
hsa-mir-548v-p5	AAAAGTAATTGCGGTTTT	down	-inf	-inf	6.93E-03
hsa-miR-127-5p_R+1	CTGAAGCTCAGAGGGCTCTGATT	up	3.46	1.79	7.00E-03
hsa-miR-1908-5p	CGGCGGGGACGGCGATTGGTC	up	2.58	1.37	7.09E-03
hsa-miR-196b-5p_R-1	TAGGTAGTTTCCTGTTGTTGG	down	0.57	-0.81	7.12E-03
hsa-miR-6515-5p	TTGGAGGGTGTGGAAGACATC	up	3.66	1.87	7.15E-03
ggo-miR-1277_R+1	TACGTAGATATATATGTATTTT	up	4.86	2.28	7.18E-03
hsa-miR-628-5p	ATGCTGACATATTTACTAGAGG	up	3.11	1.64	7.22E-03
hsa-miR-4781-3p_L-2R+3	TGTTGGAATCCTCGCTAGAGCGT	down	0.04	-4.54	7.26E-03
hsa-miR-6884-5p	AGAGGCTGAGAAGGTGATGTTG	down	0.03	-5.32	7.27E-03
hsa-mir-3159-p3_1ss21TC	TCACGCCTGTAATCCCAGCACT	down	-inf	-inf	7.27E-03
hsa-miR-3913-5p	TTTGGGACTGATCTTGATGTCT	down	0.54	-0.88	7.33E-03

bta-miR-1260b_R+2_1ss9AG	ATCCCACCGCTGCCACCACT	up	5.69	2.51	7.35E-03
hsa-mir-3922-p3	TGTGGGACTTCTGGCCTTGA	down	0.35	-1.52	7.37E-03
hsa-mir-548al-p3_1ss7GC	AAAAACCGCAATGACTTTTG	down	0.14	-2.81	7.38E-03
hsa-miR-194-5p_R-1	TGTAACAGCAACTCCATGTGG	down	0.06	-3.99	7.40E-03
hsa-miR-320c_R-1	AAAAGCTGGGTTGAGAGGG	down	0.11	-3.22	7.41E-03
hsa-miR-6747-3p_R-1	TCCTGCCTTCCTCTGCACCA	down	0.07	-3.81	7.41E-03
PC-5p-104097_99	TGGAGAAAGGACTTCAGGGAGT	down	0.04	-4.83	7.45E-03
PC-3p-147533_66	TAACTTGTGTGACTTTGGGCGA	down	-inf	-inf	7.46E-03
hsa-miR-4498_R+1	TGGGCTGGCAGGGCAAGTGCTGC	down	0.13	-2.97	7.67E-03
hsa-miR-21-5p	TAGCTTATCAGACTGATGTTGA	up	2.27	1.18	7.72E-03
hsa-miR-490-3p_R+1	CAACCTGGAGGACTCCATGCTGT	up	8.88	3.15	7.74E-03
PC-5p-100312_104	ATTGGACTTTGAACAGATC	down	-inf	-inf	7.78E-03
hsa-miR-4797-3p_L-2R+2	TCAGTAAGTGGCACTCTGTCT	down	0.14	-2.86	7.79E-03
hsa-miR-5193	TCCTCCTCTACCTCATCCCAGT	up	5.16	2.37	7.80E-03
PC-5p-278729_35	AGGCAGGGTCGGGTAGGGGGCA	down	-inf	-inf	7.81E-03
PC-3p-81713_137	AGGCGGGGTTGTGGGAGAG	down	-inf	-inf	7.85E-03
hsa-miR-590-3p	TAATTTTATGTATAAGCTAGT	up	3.03	1.60	8.09E-03
hsa-miR-20a-3p_R+1	ACTGCATTATGAGCACTTAAAGT	up	4.94	2.30	8.14E-03
bta-miR-2887_L-6R+4	CGGGGTCCGGTGCGGAGT	down	0.25	-2.02	8.31E-03
hsa-miR-3163_R-1	TATAAAATGAGGGCAGTAAGA	down	-inf	-inf	8.36E-03
PC-3p-23817_616	TTGCTGGGAAAGGGAGAAGTTC	up	2.21	1.15	8.36E-03
hsa-miR-4489	TGGGGCTAGTGATGCAGGACG	down	-inf	-inf	8.39E-03
hsa-miR-6750-5p_L-1R-3	AGGGAACAGCTGGGTGAGCT	down	-inf	-inf	8.41E-03
cgr-miR-130b-3p_R+2	CAGTGCAATGATGAAAGGGCATTT	up	15.39	3.94	8.41E-03
PC-3p-71053_164	AATAAGCGGAGGAAAAGAAA	down	-inf	-inf	8.41E-03
PC-5p-64281_188	AGCAGCATTGTACAGGGAAA	down	-inf	-inf	8.50E-03

hsa-miR-548ax_R-1	AGAAGTAATTGCGGTTTTGCC	up	5.81	2.54	8.52E-03
hsa-miR-664a-3p	TATTCATTTATCCCCAGCCTACA	up	2.77	1.47	8.56E-03
hsa-miR-500b-5p_L+1R+3	TAATCCTTGCTACCTGGGTGAG	down	0.06	-4.15	8.63E-03
hsa-miR-181b-3p	CTCACTGAACAATGAATGCAA	up	3.21	1.68	8.67E-03
hsa-miR-125b-1-3p_R-2	ACGGGTTAGGCTCTTGGGAG	down	-inf	-inf	8.72E-03
PC-3p-84256_131	CGCGTGGCCTGCTGGGAGTTGT	up	inf	inf	8.78E-03
hsa-miR-379-5p	TGGTAGACTATGGAACGTAGG	up	3.87	1.95	8.89E-03
dno-miR-146a-5p_L-5	ACTGAATTCCATGGGTTT	up	inf	inf	8.89E-03
hsa-miR-1271-5p_R-1	CTTGGCACCTAGCAAGCACTC	up	1.79	0.84	8.89E-03
PC-3p-94741_112	CCAGGTGTCTTCCATTCTGTCC	up	inf	inf	8.91E-03
hsa-mir-600-p5	CATAGGAAGGCTCTTGTCTGT	down	-inf	-inf	8.91E-03
hsa-miR-423-5p	TGAGGGGCAGAGAGCGAGACTTT	down	0.69	-0.53	9.01E-03
mdo-miR-153-1-5p_L+1	GTCATTTTTGTGATCTGCAGCT	up	4.18	2.06	9.03E-03
hsa-miR-1291_L+1R-2	GTGGCCCTGACTGAAGACCAGCA	down	-inf	-inf	9.08E-03
hsa-miR-320b_R-2	AAAAGCTGGGTTGAGAGGGC	down	0.15	-2.75	9.09E-03
hsa-miR-556-3p_R-1	ATATTACCATTAGCTCATCTT	up	3.43	1.78	9.13E-03
mmu-miR-6238_L-1R-3_1ss12TC	TATTAGTCAGCGGAGGAA	down	0.28	-1.85	9.25E-03
hsa-mir-3929-p5_1ss5AT	CACCTGTAATCCCAGCACTT	down	-inf	-inf	9.28E-03
hsa-miR-433-3p	ATCATGATGGGCTCCTCGGTGT	up	3.05	1.61	9.44E-03
PC-5p-87005_125	GAAGAAGGCTAGGGGACAG	down	-inf	-inf	9.52E-03
hsa-miR-23b-3p_R+1	ATCACATTGCCAGGGATTACCACT	up	1.67	0.74	9.55E-03
hsa-mir-548i-1-p5	TTAGGTTGGTGCAAAAGTAA	down	0.03	-5.04	9.69E-03
hsa-mir-548f-4-p5	TTAGGTTGGTGCAAAAGTAA	down	0.03	-5.04	9.69E-03
hsa-mir-548y-p5	TTAGGTTGGTGCAAAAGTAA	down	0.03	-5.04	9.69E-03
PC-5p-388722_24	TAAGGCCATCGTAAGTTGAAA	up	inf	inf	9.87E-03

hsa-miR-4533_R+2	TGGAAGGAGGTTGCCGGACGCTGT	up	9.31	3.22	9.90E-03
hsa-miR-17-5p	CAAAGTGCTTACAGTGCAGGTAG	up	2.16	1.11	1.01E-02
hsa-miR-106a-5p_1ss1AC	CAAAGTGCTTACAGTGCAGGTAG	up	2.16	1.11	1.01E-02
PC-3p-143650_68	TTCCTGTTTGGGCTCTGCTAT	up	inf	inf	1.02E-02
hsa-miR-4750-5p_R+1	CTCGGGCGGAGGTGGTTGAGTGT	up	5.48	2.45	1.02E-02
hsa-miR-30b-3p	CTGGGAGGTGGATGTTTACTTC	up	4.22	2.08	1.02E-02
PC-5p-111666_91	TGGAGAGAAAGGCAGTTAG	down	0.03	-5.32	1.02E-02
hsa-mir-4485-p3_1ss1CT	TGTTTAACGGCCGCGGTAC	up	2.78	1.48	1.03E-02
PC-3p-128622_77	TCTTGACTAGCTTGCTGTTT	down	-inf	-inf	1.03E-02
hsa-miR-181a-3p	ACCATCGACCGTTGATTGTACC	up	1.98	0.99	1.04E-02
hsa-miR-3155b_R+3	CCAGGCTCTGCAGTGGGAACT	down	0.02	-5.89	1.04E-02
hsa-miR-103a-3p	AGCAGCATTGTACAGGGCTATGA	up	1.94	0.96	1.04E-02
hsa-miR-6764-5p	TCCCAGGGTCTGGTCAGAGTTG	down	0.29	-1.80	1.04E-02
PC-3p-120076_84	CAAAGAATTCCCCTTGGGCT	down	-inf	-inf	1.05E-02
hsa-miR-2115-5p_R-2	AGCTTCCATGACTCCTGATG	down	-inf	-inf	1.06E-02
hsa-miR-548ay-3p_R-1	CAAAACCGCGATTACTCTTGC	down	0.29	-1.80	1.06E-02
hsa-miR-219a-5p	TGATTGTCCAAACGCAATTCT	down	-inf	-inf	1.06E-02
hsa-miR-4731-5p_R-1	TGCTGGGGGCCACATGAGTGT	down	-inf	-inf	1.07E-02
hsa-miR-381-3p	TATACAAGGGCAAGCTCTCTGT	up	1.95	0.96	1.07E-02
PC-3p-164403_58	AATAATCAGCGGGGAAAGA	down	-inf	-inf	1.09E-02
hsa-miR-193a-5p	TGGGTCTTTGCGGGCGAGATGA	down	0.03	-5.15	1.09E-02
PC-5p-203106_47	AAATGTAACTGCAGTTTTTGGA	up	inf	inf	1.10E-02
PC-3p-365143_26	TTGAGGTCGGACATGGTGGCTT	down	-inf	-inf	1.10E-02
hsa-miR-518e-5p_R-1	CTCTAGAGGGAAGCGCTTTCT	down	-inf	-inf	1.10E-02
hsa-miR-551a	GCGACCCACTCTTGGTTTCCA	down	0.02	-5.83	1.11E-02
hsa-mir-548ax-p3	CAAAAACCGTAATTACTTTTGT	up	2.43	1.28	1.11E-02

mdo-miR-26-5p_R+3	TTCAAGTAATCCAGGATAGGCTAG	up	3.61	1.85	1.11E-02
hsa-miR-6730-3p_1ss22AT	CCTGACACCCCATCTGCCCTCT	down	-inf	-inf	1.12E-02
PC-5p-99555_105	TTAGTCTAGCACCTGGTCAATTC	up	inf	inf	1.12E-02
hsa-miR-30d-3p	CTTTCAGTCAGATGTTTGCTGC	up	1.73	0.79	1.13E-02
PC-5p-146020_66	AGGGACGGCCGGGGGCAAG	down	-inf	-inf	1.13E-02
PC-5p-22651_648	CATCTCATCCTGGGGCTGTA	down	0.41	-1.29	1.13E-02
PC-3p-126191_79	TCTCTGGGGGTGACTGTCCGT	down	-inf	-inf	1.13E-02
hsa-miR-4516_R+1	GGGAGAAGGGTCGGGGCG	down	-inf	-inf	1.13E-02
hsa-miR-1185-1-3p	ATATACAGGGGGAGACTCTTAT	up	3.64	1.87	1.13E-02
hsa-miR-181a-2-3p	ACCACTGACCGTTGACTGTACC	down	0.62	-0.69	1.15E-02
mmu-miR-92a-3p_R+2_2	TATTGCACTTGTCCCGGCCTGAG	down	0.30	-1.73	1.16E-02
mmu-miR-92a-3p_R+2_1	TATTGCACTTGTCCCGGCCTGAA	down	0.30	-1.73	1.16E-02
hsa-miR-1262	ATGGGTGAATTTGTAGAAGGAT	down	-inf	-inf	1.16E-02
PC-5p-70731_165	TAAGAGGGACGGAGGAGG	down	0.04	-4.61	1.17E-02
hsa-miR-4474-3p_R-2	TTGTGGCTGGTCATGAGGCT	down	0.08	-3.57	1.17E-02
hsa-miR-23a-5p	GGGGTTCCTGGGGATGGGATTT	up	2.05	1.04	1.18E-02
hsa-miR-20a-5p	TAAAGTGCTTATAGTGCAGGTAG	up	2.15	1.10	1.19E-02
hsa-miR-6875-5p	TGAGGGACCCAGGACAGGAGA	down	0.06	-4.17	1.19E-02
hsa-miR-3617-5p	AAAGACATAGTTGCAAGATGGG	up	19.10	4.26	1.20E-02
bta-miR-2478_L-2R+1_1	ATCCCACTTCTGACACCAA	up	2.53	1.34	1.21E-02
bta-miR-2478_L-2R+1_3	ATCCCACTTCTGACACCAT	up	2.53	1.34	1.21E-02
bta-miR-2478_L-2R+1_2	ATCCCACTTCTGACACCAG	up	2.53	1.34	1.21E-02
PC-3p-96428_109	TAGAGGTTCGGGGGATGT	down	-inf	-inf	1.22E-02
PC-5p-148359_65	ACCAGGCAAGAACTACTGTCT	down	0.06	-4.13	1.23E-02
hsa-miR-19b-1-5p	AGTTTTGCAGGTTTGCATCCAGC	up	10.84	3.44	1.24E-02
hsa-miR-1914-5p_R+1	CCCTGTGCCCGGCCCACTTCTGC	up	inf	inf	1.26E-02

mmu-miR-2137_L-2R-1_1ss16AG	CGGCGGGAGCCCCGGGGA	down	0.25	-1.98	1.26E-02
PC-5p-481280_16	TATGATGGCTGTAACAAGAAATTT	down	-inf	-inf	1.26E-02
hsa-miR-99a-5p_R-1	AACCCGTAGATCCGATCTTGT	down	0.07	-3.83	1.27E-02
PC-3p-366052_26	ATTTGCTGTTAAGATATGGGAT	down	-inf	-inf	1.29E-02
bta-miR-11971_R-1	TGAGGGGCAGAGAGTGAGA	down	-inf	-inf	1.29E-02
hsa-miR-3140-5p	ACCTGAATTACCAAAAGCTTT	down	0.17	-2.53	1.29E-02
hsa-miR-3157-5p_R-2	TTCAGCCAGGCTAGTGCAGT	down	0.13	-2.93	1.29E-02
hsa-miR-190a-5p_R+1	TGATATGTTTGATATATTAGGTT	up	4.47	2.16	1.31E-02
PC-3p-4764_2788	GAGGGCGCGCGGGTCGGG	down	0.02	-5.95	1.31E-02
ptr-mir-618-p3	TCAGGAGACAAGCAGGGTTAC	down	-inf	-inf	1.32E-02
hsa-miR-556-5p_R-1	GATGAGCTCATTGTAATATGA	up	6.65	2.73	1.32E-02
hsa-miR-4660_R+1	TGCAGCTCTGGTGGAAAATGGAGA	down	-inf	-inf	1.32E-02
hsa-miR-708-3p_R-2	CAACTAGACTGTGAGCTTCT	down	0.03	-5.00	1.32E-02
hsa-miR-548az-5p_L-2R+1_1ss8GA	AAAGTAATTGTGGTTTTTGCT	down	0.27	-1.89	1.35E-02
hsa-mir-548ac-p5_1ss6TA	AAAGTAATTGTGGTTTTTGCT	down	0.27	-1.89	1.35E-02
PC-3p-11702_1197	AAAGTGGACGTATAGGGT	down	0.34	-1.56	1.35E-02
hsa-miR-4659b-3p_L+1R-1	TTTTCTTCTTAGACATGGCAGC	up	1.89	0.92	1.39E-02
hsa-miR-5584-5p	CAGGGAAATGGGAAGAACTAGA	up	2.98	1.58	1.40E-02
ggo-mir-1277-p5	TATATATATATATGTACGTAT	up	4.91	2.30	1.41E-02
PC-3p-90463_119	AACAGCGGGGAAAGAAGAC	down	-inf	-inf	1.42E-02
hsa-miR-4504	TGTGACAATAGAGATGAACATG	down	0.10	-3.32	1.42E-02
hsa-miR-485-5p_R+1	AGAGGCTGGCCGTGATGAATTCG	up	2.77	1.47	1.44E-02
hsa-miR-296-3p_L-1R-2	AGGGTTGGGTGGAGGCTCT	down	0.41	-1.29	1.47E-02
hsa-miR-654-5p	TGGTGGGCCGCAGAACATGTGC	up	3.28	1.71	1.48E-02

PC-3p-143720_68	ATTTGGCCTTTTATGTTCTTGA	down	0.07	-3.87	1.48E-02
bta-miR-378_R+1_1ss22CA	ACTGGACTTGGAGTCAGAAGGAT	down	0.18	-2.48	1.49E-02
hsa-miR-766-5p_R+1	AGGAGGAATTGGTGCTGGTCTTT	up	1.87	0.91	1.50E-02
hsa-miR-323b-3p_R-1	CCCAATACACGGTCGACCTCT	up	2.11	1.08	1.50E-02
hsa-miR-5094_L-1R+1	ATCAGTGAATGCCTTGAACCTA	down	0.27	-1.87	1.50E-02
hsa-miR-361-5p	TTATCAGAATCTCCAGGGGTAC	up	1.70	0.76	1.51E-02
hsa-miR-362-5p_R-2	AATCCTTGGAACCTAGGTGTGA	down	0.45	-1.16	1.51E-02
bta-miR-191b_1ss2AG	GGACGAAATCCAAGCGCAGCTG	up	inf	inf	1.52E-02
hsa-miR-3614-5p_R-1	CCACTTGGATCTGAAGGCTGCC	down	0.01	-6.71	1.54E-02
mmu-miR-339-5p_R-1_1ss22CT	TCCCTGTCCTCCAGGAGCTCAT	up	4.43	2.15	1.54E-02
hsa-miR-4503_R-1	TTTAAGCAGGAAATAGAATTT	down	-inf	-inf	1.55E-02
hsa-miR-375-3p	TTTGTTCGTTCGGCTCGCGTGA	down	0.09	-3.45	1.55E-02
hsa-miR-378a-3p	ACTGGACTTGGAGTCAGAAGGC	down	0.17	-2.55	1.55E-02
hsa-miR-1270	CTGGAGATATGGAAGAGCTGTGT	down	0.29	-1.77	1.56E-02
hsa-miR-202-5p_R-1	TTCCTATGCATATACTTCTTT	down	-inf	-inf	1.56E-02
hsa-miR-378c_R-5	ACTGGACTTGGAGTCAGAAG	down	0.19	-2.42	1.57E-02
bta-miR-339b_R+3_1	TCCCTGTCCTCCAGGAGCTCAAT	up	8.89	3.15	1.57E-02
bta-miR-339b_R+3_3	TCCCTGTCCTCCAGGAGCTCAGT	up	8.89	3.15	1.57E-02
bta-miR-339b_R+3_2	TCCCTGTCCTCCAGGAGCTCACT	up	8.89	3.15	1.57E-02
hsa-miR-4433b-5p_R+1	ATGTCCCACCCCCACTCCTGTT	up	16.21	4.02	1.59E-02
cgr-miR-1260_R+2_5	ATCCCACCGCTGCCACCATA	up	3.93	1.98	1.61E-02
cgr-miR-1260_R+2_4	ATCCCACCGCTGCCACCACA	up	3.93	1.98	1.61E-02
cgr-miR-1260_R+2_3	ATCCCACCGCTGCCACCAAT	up	3.93	1.98	1.61E-02
cgr-miR-1260_R+2_2	ATCCCACCGCTGCCACCAAG	up	3.93	1.98	1.61E-02
cgr-miR-1260_R+2_1	ATCCCACCGCTGCCACCAAA	up	3.93	1.98	1.61E-02

hsa-miR-548bc	AAAAACTGTGATTACTTTTGC	down	0.51	-0.97	1.61E-02
hsa-miR-6734-5p	TTGAGGGGAGAATGAGGTGGAGA	down	0.49	-1.03	1.61E-02
hsa-miR-23a-3p_R+1	ATCACATTGCCAGGGATTTCCA	up	1.56	0.64	1.62E-02
hsa-miR-1276	TAAAGAGCCCTGTGGAGACA	down	0.04	-4.67	1.63E-02
mmu-miR-146a-5p_R+2	TGAGAACTGAATTCCATGGGTTAA	up	1.70	0.77	1.63E-02
PC-5p-135472_73	TGGGGTGGAGTAGGGCAGGAA	up	16.56	4.05	1.64E-02
mmu-miR-5126_L-4_1ss18CT	GCGGGGCCGGGGGTGGGG	down	0.14	-2.84	1.64E-02
hsa-mir-3166-p5	GAGGCCAGTAGGCATTGTCTGC	up	7.32	2.87	1.64E-02
PC-5p-67594_176	ACTGCCACTTGTAGTCTTCCTTT	up	3.76	1.91	1.64E-02
hsa-miR-3188_1ss23GT	AGAGGCTTTGTGCGGATACGGGT	up	5.45	2.44	1.66E-02
hsa-miR-432-5p_1ss23GT	TCTTGGAGTAGGTCATTGGGTGT	up	2.21	1.14	1.66E-02
PC-3p-129011_77	TGAGCTCTCTGCACTCCCAGG	up	10.16	3.34	1.66E-02
bta-miR-378_L-1R+1	CTGGACTTGGAGTCAGAAGGCT	down	0.14	-2.89	1.67E-02
hsa-miR-4753-5p_L-1R+1	AAGGCCAAAGGAAGAGAACAGA	down	-inf	-inf	1.67E-02
hsa-miR-148a-3p	TCAGTGCACTACAGAACTTTGT	down	0.33	-1.59	1.68E-02
hsa-miR-3680-3p_R-1	TTTTGCATGACCCTGGGAGTAG	down	-inf	-inf	1.70E-02
mmu-miR-5100_L-1R-1_1ss15TG	CGAATCCCAGCGGGGCCTC	down	-inf	-inf	1.70E-02
hsa-miR-7110-5p_R+1	TGGGGGTGTGGGGAGAGAGAGT	up	inf	inf	1.72E-02
hsa-miR-4444_L+4R+1	TGAACTCGAGTTGGAAGAGGCGA	down	-inf	-inf	1.73E-02
mmu-let-7j_1ss8TG	TGAGGTAGTAGTTTGTGCTGTTAT	up	2.40	1.26	1.74E-02
hsa-miR-411-3p_R-1	TATGTAACACGGTCCACTAAC	up	3.05	1.61	1.75E-02
hsa-miR-1228-3p_R+1	TCACACCTGCCTCGCCCCCCA	down	-inf	-inf	1.75E-02
hsa-miR-6783-5p	TAGGGGAAAAGTCCTGATCCGG	down	0.05	-4.41	1.76E-02
hsa-miR-9983-3p	TTTTTTGCTGGAACATTTCTGG	up	inf	inf	1.76E-02

hsa-miR-4639-5p	TTGCTAAGTAGGCTGAGATTGA	down	0.26	-1.97	1.76E-02
PC-3p-243877_40	TGCAGCATAGGGCAGTTAGGA	up	inf	inf	1.77E-02
hsa-mir-599-p5	TTTGATAAGCTGACATGGGAC	down	-inf	-inf	1.78E-02
hsa-miR-6807-5p	GTGAGCCAGTGGAATGGAGAGG	down	0.05	-4.45	1.79E-02
PC-5p-62128_197	ATGTTCATGGACTGAAAGACT	down	0.22	-2.21	1.80E-02
efu-mir-9277-p5	TCGTGGCCGAGTGGTTAAG	down	0.02	-5.56	1.80E-02
hsa-miR-128-3p	TCACAGTGAACCGGTCTCTTT	up	1.57	0.65	1.80E-02
hsa-miR-6733-5p_L+1	TTGGGAAAGACAAACTCAGAGTT	down	0.03	-5.12	1.80E-02
hsa-let-7f-1-3p_1ss22CT	CTATACAATCTATTGCCTTCCT	down	0.40	-1.34	1.81E-02
hsa-mir-7849-p5	TGTTGAACATCAGACTCAAGGC	up	10.95	3.45	1.81E-02
hsa-miR-126-3p_R-1	TCGTACCGTGAGTAATAATGC	up	1.57	0.65	1.81E-02
hsa-miR-4484_L+2R-4	AAAAAAGGCGGGAGAAGC	down	0.18	-2.45	1.83E-02
hsa-miR-1185-5p_R+1	AGAGGATACCCTTTGTATGTTC	up	7.02	2.81	1.84E-02
hsa-miR-196b-3p_R+1	TCGACAGCACGACACTGCCTTCA	down	0.09	-3.40	1.86E-02
hsa-miR-5004-3p_R+1	CTTGGATTTTCCTGGGCCTCAGT	up	inf	inf	1.87E-02
hsa-miR-130a-5p	GCTCTTTTCACATTGTGCTACT	up	inf	inf	1.87E-02
PC-5p-505426_15	TCCTGGCTGGGTTTATGGAG	down	-inf	-inf	1.87E-02
PC-5p-517991_14	GTAGTTTGACTGGGGTGGT	down	-inf	-inf	1.89E-02
hsa-miR-1260a_R+3_1ss9TG	ATCCCACCGCTGCCACCAAAA	up	4.28	2.10	1.92E-02
hsa-miR-6793-5p_L+2R-3	ACTGTGGGTTCTGGGTTGGGG	down	-inf	-inf	1.94E-02
PC-5p-514458_14	AGCTGAAGTGTAAGAGGTTGA	down	-inf	-inf	1.96E-02
hsa-miR-4669_R-1	TGTGTCCGGGAAGTGGAGGAG	down	0.01	-6.26	1.97E-02
hsa-miR-328-3p	CTGGCCCTCTCTGCCCTTCCGT	up	6.43	2.68	1.97E-02
PC-3p-33359_426	GGAGGAACCTTGGAGCTTCGGCT	up	3.70	1.89	1.99E-02
hsa-miR-758-3p_R-1	TTTGTGACCTGGTCCACTAAC	up	4.10	2.04	1.99E-02
hsa-miR-487a-3p	AATCATACAGGGACATCCAGTT	up	4.02	2.01	1.99E-02

mml-miR-607_L-1R+1_1ss2TA	ATATAGATCTGGATTGGAACC	down	-inf	-inf	2.02E-02
hsa-miR-3177-3p	TGCACGGCACTGGGGACACGT	up	2.25	1.17	2.05E-02
bta-miR-2478_L-1_1ss11TC	TATCCCACTCCTGACACCA	up	6.78	2.76	2.05E-02
hsa-miR-432-3p_L+1	ACTGGATGGCTCCTCCATGTCT	up	inf	inf	2.06E-02
hsa-miR-378g_R+2	ACTGGGCTTGGAGTCAGAAGGC	down	0.17	-2.58	2.07E-02
hsa-mir-641-p3	TGACTGTCCTATGTCTTTCCT	up	3.08	1.62	2.09E-02
PC-5p-234738_41	GTTCCTCTTCTTAACACCA	up	inf	inf	2.13E-02
hsa-miR-154-5p	TAGGTTATCCGTGTTGCCTTCG	up	3.73	1.90	2.19E-02
ocu-miR-194-3p_R-2	CCAGTGGAGATGCTGTTACT	down	-inf	-inf	2.19E-02
PC-5p-34098_416	TGGGGGAAGGGAGCTAGCCTGACT	up	4.71	2.24	2.20E-02
PC-3p-386754_24	CTTCACTGCATACTCCAGCCT	down	-inf	-inf	2.21E-02
hsa-miR-411-5p	TAGTAGACCGTATAGCGTACG	up	3.05	1.61	2.21E-02
hsa-miR-4683_R-1	TGGAGATCCAGTGCTCGCCCGA	down	0.04	-4.50	2.26E-02
hsa-miR-369-5p_R-1	AGATCGACCGTGTTATATTCG	up	4.97	2.31	2.27E-02
hsa-miR-221-5p_R+2	ACCTGGCATACAATGTAGATTTCT	up	1.82	0.87	2.27E-02
hsa-miR-655-3p	ATAATACATGGTTAACCTCTTT	up	8.68	3.12	2.28E-02
hsa-miR-410-3p	AATATAACACAGATGGCCTGT	up	2.86	1.51	2.29E-02
PC-3p-170351_55	GTGGGAGGCTTTGAAACC	down	-inf	-inf	2.30E-02
hsa-miR-206	TGGAATGTAAGGAAGTGTGTGG	down	0.01	-7.61	2.30E-02
PC-3p-103652_100	AGGTTGTAGGATGCTAAACAGA	up	5.46	2.45	2.31E-02
hsa-miR-93-3p_R+1	ACTGCTGAGCTAGCACTTCCCGA	down	0.65	-0.62	2.31E-02
hsa-miR-1185-2-3p	ATATACAGGGGGAGACTCTCAT	up	2.74	1.45	2.34E-02
hsa-miR-29b-1-5p_R-4	GCTGGTTTCATATGGTGGTT	down	-inf	-inf	2.35E-02
mmu-miR-3963_R+2_1ss1TC	CGTATCCCACTTCTGACACCA	down	0.13	-2.98	2.36E-02
hsa-miR-125b-2-3p_L-2	ACAAGTCAGGCTCTTGGGAC	down	0.01	-6.37	2.38E-02

PC-5p-370386_26	ATTGATGGCATCGAACCAGG	down	-inf	-inf	2.38E-02
hsa-miR-548j-3p	CAAAAACTGCATTACTTTTGC	up	3.40	1.77	2.41E-02
PC-3p-106369_97	AGTTGGATCTTGGGAGAAA	up	inf	inf	2.41E-02
hsa-miR-197-3p	TTCACCACCTTCTCCACCCAGC	up	2.20	1.14	2.41E-02
hsa-miR-487a-5p	GTGGTTATCCCTGCTGTGTTCG	up	3.24	1.70	2.41E-02
hsa-miR-3130-5p_R+1_1ss12CT	TACCCAGTCTCTGGTGCAGCCT	down	0.06	-4.06	2.42E-02
hsa-miR-335-3p	TTTTTCATTATTGCTCCTGACC	up	8.18	3.03	2.44E-02
hsa-miR-509-3-5p	TACTGCAGACGTGGCAATCATG	down	-inf	-inf	2.46E-02
mmu-mir-6240-p3_1ss10CT_1	ATTTCTGCCTAGTGCTCTGA	down	-inf	-inf	2.47E-02
mmu-mir-6240-p3_1ss10CT_2	GATTTCTGCTCAGTGCTCT	down	-inf	-inf	2.47E-02
rno-miR-1843b-5p_L+1R-2_1ss19AG	TATGGAGGTCTCTGTCTGGCTT	up	1.45	0.54	2.47E-02
hsa-miR-2355-5p_R+1	ATCCCCAGATACAATGGACAAT	up	2.08	1.05	2.49E-02
hsa-miR-3691-5p_L+1R-2	TAGTGGATGATGGAGACTCGGT	down	0.26	-1.96	2.51E-02
hsa-miR-512-3p_R-2	AAGTGCTGTCATAGCTGAGG	down	-inf	-inf	2.51E-02
hsa-miR-6892-5p	GTAAGGGACCGGAGAGTAGGA	up	11.01	3.46	2.52E-02
hsa-miR-511-3p_R+2	AATGTGTAGCAAAAGACAGAAT	down	-inf	-inf	2.52E-02
hsa-miR-30c-1-3p_R-2	CTGGGAGAGGGTTGTTTACT	up	3.23	1.69	2.52E-02
PC-5p-173008_55	CAGACACAGGTATGGCTGGCTCC	up	inf	inf	2.53E-02
hsa-miR-148b-3p	TCAGTGCATCACAGAACTTTGT	up	1.56	0.65	2.53E-02
hsa-miR-5090_L+1R-4	CCCGGGGCAGATTGGTGTAG	down	-inf	-inf	2.53E-02
oga-miR-100_R+2	AACCCGTAGATCCGAACTTGTGAA	down	-inf	-inf	2.54E-02
hsa-miR-4717-3p	ACACATGGGTGGCTGTGGCCT	down	0.05	-4.26	2.55E-02

hsa-miR-652-5p_L+1R-1	ACAACCCTAGGAGAGGGTGCCATTC	up	3.47	1.79	2.60E-02
PC-5p-127847_78	ATTGGCACTGCACATGATTG	down	-inf	-inf	2.60E-02
PC-3p-164451_58	TTGGTCAATGTATTGGTCTGCAT	up	5.79	2.53	2.60E-02
PC-5p-299757_33	CACACTGACACAGAGAGAGAGA	down	-inf	-inf	2.60E-02
hsa-miR-548am-3p_R-2	CAAAAACTGCAGTTACTTTT	down	0.09	-3.54	2.61E-02
hsa-miR-4479_R-1	CGCGCGGCCGTGCTCGGAGCA	down	0.17	-2.58	2.61E-02
PC-5p-232230_41	TAGGACAAAGGGCCCCGGGTGC	down	0.04	-4.61	2.62E-02
hsa-miR-210-3p	CTGTGCGTGTGACAGCGGCTGA	down	0.61	-0.72	2.63E-02
hsa-miR-629-3p	GTTCTCCCAACGTAAGCCCAGC	down	0.25	-2.01	2.63E-02
hsa-miR-758-5p_L-1R+1	ATGGTTGACCAGAGAGCACACG	up	5.10	2.35	2.63E-02
PC-5p-373569_25	TTGGGAAATGGTAGTGAAGGA	down	-inf	-inf	2.64E-02
hsa-miR-210-5p	AGCCCCTGCCCACCGCACACTG	up	inf	inf	2.65E-02
PC-5p-180544_52	TAACTCTTAGAATCCCCAAAG	down	-inf	-inf	2.65E-02
hsa-let-7g-3p	CTGTACAGGCCACTGCCTTGC	down	0.19	-2.43	2.66E-02
hsa-miR-4635_R-1	TCTTGAAGTCAGAACCCGCA	down	-inf	-inf	2.67E-02
hsa-miR-4467_R-1	TGGCGGCGGTAGTTATGGGCT	down	0.14	-2.85	2.68E-02
hsa-miR-548s_R-1	ATGGCCAAAACTGCAGTTATTT	down	0.07	-3.77	2.71E-02
hsa-miR-6813-5p	CAGGGGCTGGGGTTTCAGGTTCT	up	2.56	1.36	2.75E-02
hsa-miR-369-3p	AATAATACATGGTTGATCTTT	up	2.90	1.54	2.76E-02
hsa-miR-146b-5p_R+1	TGAGAACTGAATTCCATAGGCTGT	up	1.34	0.42	2.77E-02
PC-5p-311599_32	ACTGCTGCAGATGGAAAAGTTC	down	-inf	-inf	2.77E-02
PC-5p-310574_32	TTTGAGAGAACTTCGCCCTTGT	down	-inf	-inf	2.78E-02
hsa-miR-548ba	AAAGGTAACTGTGATTTTTGCT	up	inf	inf	2.78E-02
hsa-miR-377-5p	AGAGGTTGCCCTTGGTGAATTC	up	5.06	2.34	2.79E-02

mdo-miR-26-5p_R+1_1ss10TC	TTCAAGTAACCCAGGATAGGCT	up	1.95	0.96	2.80E-02
hsa-miR-548at-3p_L+1	CCAAAACCGCAGTAACTTTTGT	down	0.04	-4.73	2.81E-02
mdo-miR-181b-5p_R+3	AACATTCATTGCTGTCGGTGGGTTGT	up	5.83	2.54	2.82E-02
hsa-miR-379-3p_R-1	TATGTAACATGGTCCACTAAC	up	2.78	1.48	2.84E-02
hsa-miR-5009-5p_L-1	TGGACTTTTTCAGATTTGGGGAT	down	-inf	-inf	2.85E-02
hsa-mir-1302-1-p5_1ss9AG	GAATTTCAGGTAAACAATGAAT	up	3.17	1.66	2.86E-02
hsa-miR-429	TAATACTGTCTGGTAAAACCGT	down	0.25	-1.98	2.87E-02
hsa-miR-33a-3p_R-1	CAATGTTTCCACAGTGCATCA	up	4.74	2.24	2.91E-02
hsa-miR-497-5p	CAGCAGCACACTGTGGTTTGT	down	0.58	-0.78	2.92E-02
hsa-miR-149-5p_R-3	TCTGGCTCCGTGTCTTCACT	down	0.23	-2.14	2.92E-02
hsa-miR-4638-5p	ACTCGGCTGCGGTGGACAAGT	up	3.96	1.99	2.96E-02
hsa-miR-361-3p_R+1	TCCCCCAGGTGTGATTCTGATTTG	down	0.72	-0.48	2.96E-02
hsa-miR-376a-3p	ATCATAGAGGAAAATCCACGT	up	3.30	1.72	2.97E-02
mdo-miR-152-3p_R+3	TCAGTGCATGACAGAACTTGGGTTT	up	16.94	4.08	2.98E-02
mmu-mir-6240-p5_1ss21GT	TTTCTGCCCAGTGCTCTGAATGTC	down	0.38	-1.38	2.99E-02
hsa-miR-25-5p_R+2	AGGCGGAGACTTGGGCAATTGCT	down	0.58	-0.79	3.02E-02
hsa-mir-6820-p5	TCTGCGGCAGAGCTGGGGT	down	-inf	-inf	3.02E-02
hsa-miR-216b-5p	AAATCTCTGCAGGCAAATGTGA	down	-inf	-inf	3.05E-02
hsa-miR-3139_R-1	TAGGAGCTCAACAGATGCCTGT	down	0.04	-4.53	3.06E-02
hsa-miR-382-3p_R+1	AATCATTCACGGACAACACTTT	up	2.60	1.38	3.07E-02
PC-5p-153646_63	GCCATCGGGGCGAGTGCG	down	0.05	-4.46	3.07E-02
hsa-miR-490-5p	CCATGGATCTCCAGGTGGGT	up	8.84	3.14	3.10E-02
mmu-miR-431-5p_R-1	TGTCTTGCAGGCCGTCATGC	up	2.85	1.51	3.11E-02
efu-miR-9226_L-2_1ss22GA	AAGTCCCTGTTCGGGCGCCA	down	0.24	-2.08	3.14E-02

PC-5p-224252_43	GTGGGACAAAAGCGTGGG	down	0.11	-3.17	3.15E-02
hsa-miR-130b-3p	CAGTGCAATGATGAAAGGGCAT	down	0.62	-0.70	3.17E-02
hsa-miR-494-5p_R-1	AGGTTGTCCGTGTTGTCTTCTC	up	inf	inf	3.18E-02
hsa-miR-6500-3p	ACACTTGTTGGGATGACCTGC	down	0.38	-1.39	3.19E-02
hsa-miR-1249-3p	ACGCCCTTCCCCCCCTTCTTCA	up	3.84	1.94	3.20E-02
hsa-miR-433-5p	TACGGTGAGCCTGTCATTATTC	up	inf	inf	3.21E-02
pal-miR-9993b-3p_1ss1AT	TTCTCGCTGGGGCCTCCA	down	0.50	-1.01	3.22E-02
PC-3p-403857_23	TGGCCCAAGACCTCAGACCACT	down	0.03	-4.87	3.23E-02
hsa-miR-3179_L+1R-1	TAGAAGGGGTGAAATTTAAACG	down	0.11	-3.25	3.25E-02
hsa-miR-135a-5p	TATGGCTTTTTATTCCTATGTGA	up	2.94	1.56	3.26E-02
hsa-miR-1910-3p	GAGGCAGAAGCAGGATGACA	down	-inf	-inf	3.27E-02
chi-miR-16b-5p	TAGCAGCACGTAAATATTGGGG	down	-inf	-inf	3.31E-02
hsa-miR-141-3p_R-1	TAACACTGTCTGGTAAAGATG	down	0.05	-4.36	3.31E-02
pal-miR-339b-5p_R+1	TCCCTGTCCTCCAGGAGCTT	down	0.23	-2.14	3.35E-02
hsa-miR-143-5p_R-1	GGTGCAGTGCTGCATCTCTGG	up	3.97	1.99	3.35E-02
hsa-miR-4743-5p	TGGCCGGATGGGACAGGAGGCAT	up	4.11	2.04	3.40E-02
hsa-miR-146a-3p_L+1R-2	ACCTCTGAAATTCAGTTCTTC	up	3.16	1.66	3.43E-02
hsa-miR-6837-3p	CCTTCACTGTGACTCTGCTGCAG	up	2.25	1.17	3.47E-02
hsa-miR-539-3p	ATCATACAAGGACAATTTCTTT	up	2.76	1.46	3.50E-02
hsa-miR-3174_R-1	TAGTGAGTTAGAGATGCAGAGC	up	3.73	1.90	3.53E-02
PC-3p-248853_39	TGCCCATGAGCTCCACCTGCCT	down	0.05	-4.47	3.55E-02
cgr-miR-1260_R+4	ATCCCACCGCTGCCACCAAAAA	up	2.96	1.56	3.55E-02
hsa-miR-3064-5p	TCTGGCTGTTGTGGTGTGCAA	up	2.07	1.05	3.56E-02
mmu-miR-5100_R-1_1ss15TG	TCGAATCCCAGCGGGGCCTC	down	-inf	-inf	3.63E-02
hsa-miR-299-3p	TATGTGGGATGGTAAACCGCTT	up	2.24	1.17	3.66E-02

efu-miR-9226_L-1R-1	CAAGTCCCTGTTCGGGCGCC	down	-inf	-inf	3.67E-02
PC-5p-73128_158	GGCGGGCCATCACTGTTGGAG	down	0.32	-1.63	3.70E-02
rno-miR-3590-3p_R+1	TAGCACAATGTGAAAAGAGCTCT	down	-inf	-inf	3.71E-02
hsa-miR-152-5p	AGGTTCTGTGATACACTCCGACT	up	2.84	1.50	3.75E-02
PC-5p-292156_34	TTGTGTCCAGTTGTTGGGGGAA	down	-inf	-inf	3.76E-02
PC-5p-140549_70	TCTGGGAGAGAGCTACCGCT	down	-inf	-inf	3.77E-02
hsa-miR-4727-3p	ATAGTGGGAAGCTGGCAGATTC	down	-inf	-inf	3.79E-02
PC-3p-43735_309	CCCGCCCCTCCGCGCCCCCCAT	up	4.35	2.12	3.80E-02
hsa-miR-4485-5p_L+1R+2	CACCGCCTGCCCAGTGACA	up	7.80	2.96	3.81E-02
PC-5p-224026_43	GTTGGAGGTTGGAGGTTGA	down	-inf	-inf	3.82E-02
hsa-miR-6721-5p_R+1	TGGGCAGGGGCTTATTGTAGGAGT	up	8.62	3.11	3.86E-02
hsa-miR-378i_R+1_1ss9AT	ACTGGACTTGGAGTCAGAAGGT	down	0.18	-2.47	3.86E-02
hsa-miR-616-3p_L+1R-3	AAGTCATTGGAGGGTTTGAG	down	0.47	-1.09	3.86E-02
hsa-miR-6736-5p	CTGGGTGAGGGCATCTGTGGT	up	6.45	2.69	3.88E-02
hsa-miR-147b-5p_R-2	TGGAAACATTTCTGCACAAA	down	-inf	-inf	3.89E-02
hsa-miR-26a-1-3p	CCTATTCTTGGTTACTTGCACG	up	7.99	3.00	3.90E-02
PC-3p-392001_24	TGCAGAGGGACTGGCAGGAAG	down	-inf	-inf	3.91E-02
PC-5p-494846_15	ATCTGAAATCTGATGAGAAAT	down	-inf	-inf	3.93E-02
PC-3p-264097_37	ATGCTCTCGGCCTATTCTCA	down	-inf	-inf	3.95E-02
PC-5p-270602_36	TGCACAGTTCTGGGAGAGAC	down	0.10	-3.35	3.97E-02
hsa-miR-186-3p_L-2R+1	CCAAAGGTGAATTTTTTGGGA	down	0.06	-4.05	3.99E-02
PC-3p-656119_10	TCACCGCCCTTCCCGCCCGCG	down	-inf	-inf	3.99E-02
bta-miR-185_L+2	TCTGGAGAGAAAGGCAGTTCCTGA	down	-inf	-inf	3.99E-02
PC-3p-367049_26	ATATAGATATCATCAGAGCTGT	down	-inf	-inf	4.03E-02
hsa-miR-4690-3p_R-1	GCAGCCCAGCTGAGGCCTCT	down	0.04	-4.66	4.07E-02
hsa-miR-4435	ATGGCCAGAGCTCACACAGAGG	up	1.98	0.99	4.09E-02

hsa-miR-496_L-2R+1	AGTATTACATGGCCAATCTCT	up	2.63	1.40	4.09E-02
hsa-miR-548n	CAAAAGTAATTGTGGATTTTGT	up	1.82	0.86	4.11E-02
PC-3p-114333_89	TACTGGGATATTTGGAGCTTCT	up	4.46	2.16	4.11E-02
hsa-mir-4473-p5	CACTTGTAATGGAGAACACT	down	0.13	-2.99	4.12E-02
bta-miR-1260b_1ss9AG	ATCCCACCGCTGCCACCA	up	6.56	2.71	4.13E-02
cgr-miR-1260	ATCCCACCGCTGCCACCA	up	6.56	2.71	4.13E-02
PC-5p-131452_76	AGATGGGGAGAACTCAATCCT	up	5.46	2.45	4.14E-02
PC-5p-335457_29	GTCGGCGGGGGCCCCGGGA	down	-inf	-inf	4.16E-02
PC-5p-255905_38	ACACTCATCAACTGTGCCTGA	down	-inf	-inf	4.16E-02
hsa-mir-497-p3_1ss5CA	AGAGAGAGGGTGGGGGAG	down	-inf	-inf	4.18E-02
hsa-miR-4686_R-4	TATCTGCTGGGCTTTCTGG	down	-inf	-inf	4.19E-02
ptr-miR-6131_R-1_1ss15GT	GGCTGGTCGGATGGTAGT	down	-inf	-inf	4.20E-02
hsa-miR-103a-2-5p_R+1	AGCTTCTTTACAGTGCTGCCTTGT	up	2.45	1.29	4.22E-02
PC-3p-400812_23	AGTCTAAACAAACCTGGAA	down	-inf	-inf	4.22E-02
hsa-miR-29c-5p_R-1	TGACCGATTTCTCCTGGTGTT	up	1.92	0.94	4.23E-02
hsa-miR-552-3p	AACAGGTGACTGGTTAGACAA	up	inf	inf	4.24E-02
hsa-miR-6858-5p_L-1	TGAGGAGGGGCTGGCAGGGAC	down	-inf	-inf	4.25E-02
PC-5p-358054_27	TTGGAGAACTCTCCTTCCCGG	down	-inf	-inf	4.28E-02
hsa-mir-7851-p5_1ss12AT	AGTAGCTGGGATTACAGG	down	0.04	-4.73	4.30E-02
sha-mir-199a-p5	CCCAGTGTTCAGACTACCTGTCC	up	3.05	1.61	4.33E-02
hsa-miR-495-3p	AAACAAACATGGTGCACTTCTT	up	1.77	0.82	4.34E-02
hsa-miR-642b-3p_R-3	AGACACATTTGGAGAGGGA	down	-inf	-inf	4.35E-02
hsa-miR-138-5p	AGCTGGTGTTGTGAATCAGGCCG	down	-inf	-inf	4.41E-02
PC-3p-154505_62	CTTGACTGGAGGATTCGT	down	-inf	-inf	4.42E-02
hsa-miR-3158-5p_R-1	CCTGCAGAGAGGAAGCCCTT	down	-inf	-inf	4.46E-02

hsa-miR-548ar-5p_R-1_1ss10TC	AAAAGTAATCGCAGTTTTTG	down	0.28	-1.85	4.46E-02
hsa-miR-548x-5p_L-3_1ss13TC	AAAAGTAATCGCAGTTTTTG	down	0.28	-1.85	4.46E-02
hsa-miR-548h-5p_R-2_1ss13GA	AAAAGTAATCGCAGTTTTTG	down	0.28	-1.85	4.46E-02
hsa-mir-548f-1-p5_1ss11AG	AAAAGTAATCGCAGTTTTTG	down	0.28	-1.85	4.46E-02
hsa-miR-505-3p_R+2	CGTCAACACTTGCTGGTTTCCTCT	up	1.51	0.59	4.47E-02
ssc-miR-339_R+1_1ss21AT	TCCCTGTCCTCCAGGAGCTCTT	up	8.56	3.10	4.48E-02
PC-3p-151959_63	CCTACAGGCTGGAATGGGCTCAT	up	6.37	2.67	4.49E-02
PC-5p-469533_17	CTGCCGGAAGATTAAATGA	down	-inf	-inf	4.50E-02
hsa-miR-1255b-5p	CGGATGAGCAAAGAAAGTGGTT	down	0.33	-1.61	4.51E-02
PC-3p-84661_130	CTTCTGGGGTAGAGCACT	down	-inf	-inf	4.51E-02
PC-3p-42568_319	CTGGCGGCTGTGTCTTCACAGT	up	2.45	1.29	4.54E-02
hsa-miR-7856-5p	TTTTAAGGACACTGAGGGATC	up	7.05	2.82	4.54E-02
mmu-miR-3963_L-1_1ss3TA	GAATCCCACTTCTGACAC	down	-inf	-inf	4.55E-02
PC-3p-855779_7	CCTCACTCCTGCCCACACCCCTC	down	-inf	-inf	4.56E-02
hsa-miR-30d-5p_R+2	TGTAAACATCCCCGACTGGAAGCT	down	0.79	-0.35	4.56E-02
hsa-miR-3160-3p_R-2	AGAGCTGAGACTAGAAAGCC	down	-inf	-inf	4.57E-02
PC-3p-227929_42	GGTTAGAGCACTGTCATGG	down	-inf	-inf	4.57E-02
hsa-miR-144-5p	GGATATCATCATATACTGTAAG	down	0.04	-4.52	4.60E-02
PC-3p-259469_38	TTCCTGTTTGGGCTCTGCTAC	up	inf	inf	4.60E-02
PC-5p-318577_31	TTTGTCTGGGGCCTGGTGAGT	down	-inf	-inf	4.66E-02
hsa-miR-891a-5p	TGCAACGAACCTGAGCCACTGA	up	inf	inf	4.68E-02
PC-5p-132114_75	AAAAAGATTGAGGCCATGGTAG	down	-inf	-inf	4.69E-02
bta-miR-2478_1ss2TG	GGATCCCACTTCTGACACCA	down	0.17	-2.53	4.70E-02

hsa-miR-6787-5p_1ss22CT	TGGCGGGGGTAGAGCTGGCTGT	down	-inf	-inf	4.70E-02
hsa-mir-548ak-p3_1ss12TG	AAAACCGCAATGACTTTTG	down	-inf	-inf	4.70E-02
hsa-miR-1287-5p	TGCTGGATCAGTGGTTCGAGTC	up	1.55	0.63	4.72E-02
hsa-miR-6852-3p_L+4R+1	CTGATGTCCTCTGTTCCTCAGA	up	inf	inf	4.74E-02
hsa-miR-7852-3p_R-1	TATGTAGTAGTCAAAGGCATT	up	inf	inf	4.76E-02
hsa-miR-7855-5p	TTGGTGAGGACCCCAAGCTCGG	down	0.25	-2.00	4.79E-02
hsa-miR-337-3p_L-1	TCCTATATGATGCCTTTCTTC	up	2.65	1.41	4.81E-02
hsa-miR-5188_L-1R+1	ATCGGACCCATTTAAACCGGAGA	down	-inf	-inf	4.83E-02
PC-5p-226840_42	GTTGATAGGCCGGGTGTG	down	0.10	-3.38	4.87E-02
hsa-miR-1908-3p_R+1	CCGGCCGCCGGCTCCGCCCCGT	up	8.11	3.02	4.88E-02
hsa-miR-590-5p	GAGCTTATTCATAAAAGTGCAG	up	4.53	2.18	4.88E-02
hsa-miR-4700-5p	TCTGGGGATGAGGACAGTGTGT	down	-inf	-inf	4.90E-02
hsa-miR-330-5p_R-2	TCTCTGGGCCTGTGTCTTAG	up	1.85	0.89	4.95E-02
PC-3p-167202_57	CTCTGAGGGTTGGGCCTAGG	down	0.02	-5.62	4.95E-02
hsa-miR-372-3p_R-1	AAAGTGCTGCGACATTTGAGCG	down	-inf	-inf	4.96E-02
hsa-miR-192-5p	CTGACCTATGAATTGACAGCC	down	0.03	-5.15	4.97E-02
PC-3p-836782_7	CAGCCTCTGCAGCTCCCCGG	down	-inf	-inf	4.99E-02
hsa-miR-889-3p	TTAATATCGGACAACCATTGT	up	1.89	0.92	4.99E-02

Supplementary Material 4. The target genes of indemnified DE miRNAs

non-smoking IA vs ctrl	smoking IA vs ctrl	smoking IA vs non-smoking IA
ARF5	ARF5	ARF5
M6PR	M6PR	M6PR
ESRRA	ESRRA	ESRRA
FKBP4	FKBP4	FKBP4
CYP26B1	CYP26B1	CYP26B1
NDUFAF7	NDUFAF7	NDUFAF7
FUCA2	FUCA2	FUCA2
DBNDD1	DBNDD1	DBNDD1
HS3ST1	HS3ST1	HS3ST1
SEMA3F	SEMA3F	SEMA3F
CFTR	CFTR	CFTR
CYP51A1	CYP51A1	CYP51A1
USP28	USP28	USP28
STPG1	STPG1	STPG1
NIPAL3	NIPAL3	NIPAL3
TMEM176A	TMEM176A	TMEM176A
SLC7A2	SLC7A2	SLC7A2
HSPB6	HSPB6	HSPB6
ZNF195	ZNF195	PDK4
PDK4	PDK4	CCL26
CCL26	CCL26	USH1C
USH1C	USH1C	RALA
RALA	RALA	BCAP29
BCAP29	BCAP29	BAIAP2L1
BAIAP2L1	BAIAP2L1	CACNG3
CACNG3	CACNG3	TMEM132A
TMEM132A	TMEM132A	DVL2
DVL2	DVL2	GGCT
GGCT	GGCT	RPAP3
RPAP3	RPAP3	UPP2
UPP2	UPP2	PRSS21
PRSS21	PRSS21	HOXA11
HOXA11	HOXA11	CX3CL1
CX3CL1	CX3CL1	PRR5
PRR5	PRR5	TRAPPC6A
TRAPPC6A	TRAPPC6A	SPATA20
SPATA20	SPATA20	CEACAM7
CEACAM7	CEACAM7	CD79B
CD79B	CD79B	RHBDD2
RHBDD2	RHBDD2	RPUSD1

RPUSD1	RPUSD1	TSR3
TSR3	TSR3	OSBPL7
OSBPL7	OSBPL7	ARHGAP33
ARHGAP33	ARHGAP33	NDUFAB1
NDUFAB1	NDUFAB1	YBX2
YBX2	YBX2	PDK2
PDK2	PDK2	ITGA3
ITGA3	ITGA3	LRRC23
LRRC23	LRRC23	IL32
IL32	IL32	TFAP2D
TFAP2D	TFAP2D	SPRTN
SPRTN	SPRTN	CRY1
CRY1	CRY1	PGLYRP1
PGLYRP1	PGLYRP1	STARD3NL
STARD3NL	STARD3NL	CAMK1G
CAMK1G	CAMK1G	CD9
CD9	CD9	CD74
CD74	CD74	RPS20
RPS20	DYRK4	DYRK4
DYRK4	MGST1	MGST1
MGST1	CPA1	CPA1
CPA1	SYPL1	SYPL1
SYPL1	RANBP9	RANBP9
RANBP9	CD4	CD4
CD4	PLEKHG6	PLEKHG6
PLEKHG6	SS18L2	SS18L2
SS18L2	VPS13D	VPS13D
VPS13D	TSPAN9	TSPAN9
TSPAN9	CYP4F2	CYP4F2
CYP4F2	QPCTL	QPCTL
QPCTL	HIVEP2	HIVEP2
HIVEP2	PPP5C	PPP5C
PPP5C	NME1	NME1
NME1	UBR7	UBR7
UBR7	MAP4K5	MAP4K5
MAP4K5	INMT	INMT
INMT	ABHD5	ERCC1
ERCC1	GPRC5A	ABHD5
ABHD5	HEBP1	GPRC5A
GPRC5A	DNASE1L1	HEBP1
HEBP1	COX15	DNASE1L1
DNASE1L1	MS4A12	COX15
COX15	RGPD5	MS4A12
MS4A12	XYLT2	RGPD5

RGPD5	FTSJ1	XYLT2
XYLT2	SCTR	FTSJ1
FTSJ1	RALBP1	SCTR
SCTR	PSD	RALBP1
RALBP1	SYT13	PSD
PSD	SNAI2	SYT13
SYT13	VDAC3	SNAI2
SNAI2	GABRA1	VDAC3
VDAC3	RTF2	SLC7A9
SLC7A9	SLC45A4	GABRA1
GABRA1	RB1CC1	RTF2
RTF2	AKAP11	SLC45A4
SLC45A4	STRAP	RB1CC1
RB1CC1	PIGQ	AKAP11
AKAP11	CDH17	STRAP
STRAP	RNASET2	PIGQ
PIGQ	B4GALT7	CDH17
CDH17	SLC39A9	RNASET2
RNASET2	FAM13B	B4GALT7
B4GALT7	RANBP3	SLC39A9
SLC39A9	CHPF2	FAM13B
FAM13B	GABARAPL2	RANBP3
RANBP3	MYOC	CHPF2
CHPF2	FAM136A	GABARAPL2
GABARAPL2	NSMAF	MYOC
MYOC	OTC	FAM136A
FAM136A	TTC17	NSMAF
NSMAF	HOXC8	OTC
OTC	MRI1	TTC17
TTC17	BOD1L1	HOXC8
HOXC8	TARBP1	MRI1
MRI1	RIPOR1	BOD1L1
BOD1L1	BEST2	TARBP1
TARBP1	RTN4R	RIPOR1
RIPOR1	PSMA4	BEST2
BEST2	RIPOR3	RTN4R
RTN4R	ZPBP	PSMA4
PSMA4	CTNS	RIPOR3
RIPOR3	LCP2	ZPBP
ZPBP	GOPC	CTNS
CTNS	DCN	LCP2
LCP2	TNFRSF17	GOPC
GOPC	MRPS10	DCN
DCN	GRN	TNFRSF17

TNFRSF17
MRPS10
GRN
THAP3
VAMP3
RCN1
RFC2
PPP1R3F
NEXMIF
ARHGEF5
NFE2L3
TNIP3
SIKE1
TLL1
CBLN4
CLDN11
FAM168A
RELT
CDC27
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ST6GALNAC1	PSMC4	MBD3
MBD3	FNDC8	LMCD1
LMCD1	CAMKK1	PSMC4
PSMC4	DERL2	FNDC8
FNDC8	NOX3	CAMKK1
CAMKK1	ANO8	ACAP1
ACAP1	KDM4B	DERL2
DERL2	PANX2	NOX3
NOX3	CAMSAP3	ANO8
ANO8	CTTNBP2	KDM4B
KDM4B	ACTL6B	PANX2
PANX2	CIC	ICAM3
ICAM3	KIF22	CAMSAP3
CAMSAP3	PRSS22	CTTNBP2
CTTNBP2	CEACAM1	ACTL6B
ACTL6B	YTHDC2	CIC
CIC	TMEM161A	KIF22
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PRSS22	FOXJ2	CEACAM1
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CABP7	PHF5A	TAB1
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SYNGR1	PMM1	PNPLA3
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PNPLA5	BRD1	TXN2
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SGCG	CCDC113	NTHL1
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ACSM2A	PSMD7	ZNF205
NTHL1	SETD6	ORC6
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ZNF205	SMPD3	LYRM1
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CORO1A	FA2H	ARL2BP
LYRM1	CMC2	PLLP
NUTF2	PDIA2	CCL22
CBLN1	ARHGDIG	DHODH
ARL2BP	HSDL1	CCL17
PLLP	WFDC1	ACD
CCL22	USP10	POLR2C
DHODH	TSC2	PARD6A
CCL17	ZNF500	MMP15
ACD	NME4	USB1
POLR2C	DECR2	CCDC113
PARD6A	METRN	PRSS54
MMP15	STUB1	NME3
USB1	RHBDL1	PSMD7
CCDC113	MEFV	SETD6
PRSS54	CRYM	SLC38A7
NME3	CAPN15	HAS3
PSMD7	AQP8	SMPD3
SETD6	USP31	SLC7A6
SLC38A7	HMOX2	PLA2G15
HAS3	TOX3	FA2H
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PLA2G15	BCKDK	ARHGDIG
FA2H	TMC5	MPG

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WFDC1
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STUB1
RHBDL1
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TOX3
MAZ
CDIPT
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KAT8
TMC5
SLC6A2
KNOP1
MGA
AQP9
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RASL12
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VPS18
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PAG1
TG
BRF2
ZFAND1
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RIPK2
CPQ
DECR1
SFRP1
PLAT
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EPOR
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PIK3R2
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ERF
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SIPA1L3
CADM4

COMP
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ERF
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ZNF574
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LAMB1
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BET1
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TWISTNB
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ITGB8
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SP4
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MPP6
OGDH
NPVF
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CAV2
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LFNG
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PON1
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AIMP2
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MOGAT3
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PLOD3
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GLCCI1
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NRF1
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VIM
BLNK

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GIT1
RUNDC3A
CSF3
SUPT4H1
WNT3
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LTA4H
ELK3
ITFG2
PRR4
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SCNN1A
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RERGL
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VDR
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PRKAB1
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OAS3
ART4

LTBR
OGFOD2
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ART4
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HINT3
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SLC44A4
FBXO5
OPRM1
FANCE
TULP1
MAPK14
STK38
HLA-DOA
MCM3
RNF8
SAYSD1
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CAP2
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KIF6
CAP2
GPR63
FBXL4
GPLD1
ACOT13
B3GAT2
GMNN
SNX3
ZBTB24
FIG4
ADGRG6
UNC93A
C6orf118
MDFI
TFEB
BYSL
TBP
GUCA1B
PRPH2
PPP2R5D
MRPL2
PTK7
DNPH1
BYSL
TBP
GUCA1B
PRPH2
PPP2R5D
PTK7
DNPH1
EXOC2
TMEM30A
VEGFA
TTK
LAMA4
ENPP5
LY86
PRSS16
MEP1A
MTREX
ISL1
SLC6A7
HARS2
NUDT12
TENT4A
GHR
DAP
BRD8
HBEGF
LOX
GZMK
CDH9
SPARC
HAND1
PCDHB3
PCDHB5
PCDHB6
PCDHB7
PCDHB15
GRM6
THG1L
IL12B
BTNL8
TTC1
C1QTNF3
IRX4
LNPEP
ADTRP
ASF1A
HINT3
NCOA7
ULBP1
SLC44A4
FBXO5
OPRM1
FANCE
TULP1
MAPK14
STK38
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RNF8
SAYSD1
KIF6
CAP2
GPR63
FBXL4
GPLD1
ACOT13
B3GAT2
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SNX3
ZBTB24
FIG4
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UNC93A
C6orf118
MDFI
TFEB
BYSL
TBP
GUCA1B
PRPH2
PPP2R5D
MRPL2
PTK7
DNPH1
EXOC2
TMEM30A
VEGFA
TTK

EXOC2	AGXT2	CCN6
TMEM30A	PRLR	LAMA4
VEGFA	IL4	ENPP5
TTK	IL5	LY86
CCN6	ST8SIA4	PRSS16
LAMA4	PCDH12	MEP1A
ENPP5	NUP155	MTREX
LY86	NR3C1	ISL1
PRSS16	C5orf15	SLC6A7
MEP1A	TRIM23	HARS2
MTREX	TRAPPC13	NUDT12
ISL1	RARS1	TENT4A
SLC6A7	CDX1	GHR
HARS2	BNIP1	DAP
NUDT12	SLC7A14	BRD8
TENT4A	SEMA3G	HBEGF
GHR	ZMYND10	LOX
DAP	LTF	GZMK
BRD8	MLH1	CDH9
HBEGF	EHHADH	SPARC
LOX	CRBN	HAND1
GZMK	HRG	PCDHB3
CDH9	BCL6	PCDHB5
SPARC	FAM162A	PCDHB6
HAND1	RBP2	PCDHB7
PCDHB3	RBP1	PCDHB15
PCDHB5	PFKFB4	GRM6
PCDHB6	HES1	THG1L
PCDHB7	ECT2	IL12B
PCDHB15	GNAT1	BTNL8
GRM6	TUSC2	TTC1
THG1L	NPRL2	C1QTNF3
IL12B	CYB561D2	IRX4
BTNL8	C3orf14	LNPEP
TTC1	GNB4	AGXT2
C1QTNF3	MORC1	PRLR
IRX4	UMPS	IL4
LNPEP	ABTB1	IL5
AGXT2	KLHL18	ST8SIA4
PRLR	HEMK1	PCDH12
IL4	AADAC	NUP155
IL5	EIF1B	NR3C1
ST8SIA4	ZBTB47	C5orf15
PCDH12	TNNC1	TRIM23

NUP155
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C5orf15
TRIM23
TRAPPC13
RARS1
CDX1
BNIP1
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ZMYND10
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MLH1
EHHADH
CRBN
HRG
BCL6
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RBP1
PFKFB4
HES1
ECT2
GNAT1
TUSC2
NPRL2
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C3orf14
GNB4
MORC1
UMPS
ABTB1
KLHL18
HEMK1
RRP9
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NKTR
SPCS1
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SPCS1
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CPS1
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DDX1
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MDH1
MAPRE3
TMSB10
MSH2
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APOB
RTKN
INO80B
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FAHD2A
SF3B6
CENPA
SLC30A3
MPV17
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SNX17
REEP6
APC2
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REG1A
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CPS1
DAZAP1
DDX1

EIF2AK2
CPS1
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DDX1
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MAPRE3
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INO80B
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PCGF1
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IGFBP5
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MOB4
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IGFBP5
KCNJ13
GGCX
MOB4
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PRKAG3
WNT6
IL1RL1
IL18R1
SLC9A2
AZU1
PPP1R7
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PROC
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ODC1
PLEKHB2
GREB1
GORASP2
CEBPZ
PRKD3
RMDN2
DLX2
SLC1A4
ORC2
COX7A2L
PPP3R1
PLEK
PRTN3
KISS1R
GRIN3B
VAX2
ATP6V1B1
MSH6
PLEKHA3
SPR
ENO1
CDC7
SARS1
CLCA1
BCL9
TPSG1
FKBP7
HEATR5B
MDH1
MAPRE3
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MSH2
NCK2
TFPI
NDUFS1
SLC11A1
APOB
RTKN
INO80B
TTL
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SF3B6
CENPA
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SNX17
REEP6
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RPS15
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WNT6

HSPE1
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WNT6
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IL18R1
SLC9A2
AZU1
PPP1R7
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ORC2
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GRIN3B
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SARS1
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WDR77
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WARS2
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SYF2
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STAG1
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MMP8
APOA1
SLC8A2
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TNNT2
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SLC9A2
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ORC2
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C1orf21
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RGS2
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VAMP4
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TNP1
FASTKD2
FCGR2B
FCRLA
EEF1B2
ATIC
TNP1
FASTKD2
TTR
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DOP1A
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SPACA1
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TBPL1
FBXO30
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PMFBP1
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RPN2
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PKD2
ABCG2
SPP1
STBD1
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LDAH
FGF23
ELL2
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NDUFB3
ZFAND5
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ECRG4
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RGS2
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WARS2
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DOP1A

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ABCG2
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ALG2
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ACOT2
FLVCR2
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ZC2HC1C
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RHOQ
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YIPF4
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MFSD13A
SLF2
PPP1R3C
MXI1
HELLS
PRLHR
HOXB8
HOXB5
HOXB7
HOXB1
DUSP1
PANK3
FILIP1
UBE3D
SPACA1
SGIP1
TBPL1
ZC2HC1B
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RPN2
SOGA1
PKD2
ABCG2
SPP1
STBD1
ADH6
CCNI
RARRES1
LDAH
FGF23
ELL2
GLRX
NDUFB3
ZFAND5
GDA
ECRG4
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LIPF
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HOXB7
HOXB1
DUSP1
PANK3
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IFNA7
LRP11

MSX2
INSL4
IFNA7
LRP11
CCDC170
ARAP3
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PCDHB10
PCDHB14
PCDHB12
SLC25A2
PRRX1
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MSANTD2
PDZD11
NUDCD1
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MTRF1
CCDC169
UFM1
ELF1
EXOSC8
FAM53C
MYOT
EGR1
PFN2
SERP1
MTERF2
NFYB
WASHC3
FZD3
SLC39A14
DUSP4
SORBS3
PPP3CC
RNF170
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PRAMEF2
RDH10
LUC7L3
DLX4
COIL
TBX2

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ACYP1
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HOXB1
DUSP1
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CCDC170
ARAP3
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MTRF1
CCDC169
UFM1
ELF1
ALG5
EXOSC8
FAM53C
MYOT
EGR1
PFN2
SERP1
MTERF2
NFYB
WASHC3
FZD3
SLC39A14
DUSP4
SORBS3
PPP3CC
RNF170
TARDBP
PRAMEF2
RDH10
LUC7L3
DLX4
COIL
TBX2
SLC35B1
TBX4
TEX14
SLC35B1
TBX4
TEX14
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TMEM131L
MND1
ZNF141
TSHZ3
PLBD1
KLRK1
PRB1
PYROXD1
IAPP
KCNJ8
ZNF549
ZSCAN18
ZNF211
TFG
KALRN
NAA50
MAPK8IP1
PEX16
DEPDC7
CAT
ACHE
FBXO24
GJB6
GJA3
GHSR
TNFSF10
SLITRK3
CPXM2
CSMD2
GSTM2
ADORA3
GTDC1
CXCR4
ACVR2A
POLK
FLT3
RASL11A
FYTTD1
MTERF4
PCDHB10
PCDHB14
PCDHB12
SLC25A2
PRRX1
TNN
TTLL2
MSANTD2
PDZD11
NUDCD1
CCDC77
MTRF1
CCDC169
UFM1
ELF1
ALG5
EXOSC8
FAM53C
MYOT
EGR1
PFN2
SERP1
MTERF2
NFYB
WASHC3
FZD3
DUSP4
SORBS3
PPP3CC
RNF170
TARDBP
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RDH10
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DLX4
COIL
TBX2
SLC35B1
TBX4
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NCAPH
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MND1

FAM117A
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MRPS2
MYOG
COPA
PRM2
OPN4
AHR
SCRN1
ETV1
BBS9
OCM
EEPD1
WIPF3
NPY
HOXA7
INHBA
FKBP9
POLM
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MRM2
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CLTA
TAF1L
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DNAI1
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ZC3HAV1
AKR1D1
NEUROG3
SRGN
EGR2
FAM149B1
UNG
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IFT81
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HVCN1
RNF11
BHLHE41
SSPN
STX10
DDX39A
PKN1
TRIR

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PRB1
PYROXD1
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GSTM2
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GTDC1
CXCR4
ACVR2A
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FLT3
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FYTTD1
MTERF4
MRPS2
MYOG
COPA
PRM2
OPN4
AHR

MYOG	ADGRE5	SCRN1
COPA	ZNF442	ETV1
PRM2	KLHL24	BBS9
OPN4	CCDC70	OCM
AHR	EBPL	EEPD1
SCRN1	ATP7B	WIPF3
ETV1	ZC3H13	NPY
BBS9	CENPK	HOXA7
OCM	NEUROD4	INHBA
EEPD1	PFDN5	FKBP9
WIPF3	ORMDL2	POLM
NPY	NR4A1	RAMP3
HOXA7	PDE1B	MRM2
INHBA	HOXC13	TWIST1
FKBP9	LRP1	SLC25A51
POLM	HOXC11	CLTA
RAMP3	HOXC12	TAF1L
MRM2	HOXC6	PHF24
TWIST1	FAAH	DNAI1
SLC25A51	RSRP1	DCAF10
CLTA	IL13RA2	ZC3HAV1
TAF1L	COL10A1	AKR1D1
PHF24	SEC61A1	NEUROG3
DNAI1	TCEAL3	SRGN
DCAF10	RAB9B	EGR2
ZC3HAV1	NRK	FAM149B1
AKR1D1	MAGEA9	UNG
NEUROG3	RIF1	DYNLL1
SRGN	TTC21B	IFT81
EGR2	NMI	ACADS
FAM149B1	TNFAIP6	HVCN1
UNG	ACVR1C	RNF11
DYNLL1	SLC36A1	BHLHE41
IFT81	BATF3	SSPN
ACADS	KCNJ2	ITPR2
HVCN1	EXOSC9	STX10
RNF11	PLA2G12A	DDX39A
BHLHE41	SNRPA	PKN1
SSPN	B9D2	TRIR
ITPR2	COQ8B	ADGRE5
STX10	ZNF468	ZNF442
DDX39A	ZNF415	KLHL24
PKN1	ZNF350	CCDC70
TRIR	RAB38	EBPL

ADGRE5	GPR83	ATP7B
ZNF442	HAUS3	ZC3H13
KLHL24	CHPF	CENPK
CCDC70	INHA	NEUROD4
EBPL	FAM124B	PFDN5
ATP7B	SP140L	ORMDL2
ZC3H13	ENKD1	NR4A1
CENPK	UBE2C	PDE1B
NEUROD4	SLC35C2	HOXC13
PFDN5	ACTR5	LRP1
ORMDL2	CTCFL	HOXC11
NR4A1	SYS1	HOXC12
PDE1B	PI3	HOXC6
HOXC13	WFDC3	FAAH
LRP1	SLC12A5	RSRP1
HOXC11	ATP5F1E	IL13RA2
HOXC12	PLCG1	COL10A1
HOXC6	SRSF6	SEC61A1
FAAH	RAB22A	TCEAL3
RSRP1	PTGIS	RAB9B
IL13RA2	CDH26	NRK
COL10A1	SNAI1	MAGEA9
SEC61A1	MOCS3	RIF1
TCEAL3	RNF114	TTC21B
RAB9B	MAGEA10	NMI
NRK	PEPD	TNFAIP6
MAGEA9	IL9R	ACVR1C
RIF1	NAGK	SLC36A1
TTC21B	MCEE	BATF3
NMI	PAIP2B	KCNJ2
TNFAIP6	SNRNP27	EXOSC9
ACVR1C	MPHOSPH10	PLA2G12A
SLC36A1	IL17C	SNRPA
BATF3	LIPE	B9D2
KCNJ2	PSG9	COQ8B
EXOSC9	PSG4	ZNF468
PLA2G12A	PSG1	ZNF415
SNRPA	HIF3A	ZNF350
B9D2	IRGC	RAB38
COQ8B	LYPD3	GPR83
ZNF468	CEACAM8	HAUS3
ZNF415	RNF39	CHPF
ZNF350	DST	INHA
RAB38	FBXO9	FAM124B

GPR83
HAUS3
CHPF
INHA
FAM124B
SP140L
ENKD1
UBE2C
SLC35C2
ACTR5
GCNT7
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SAFB2
NCAN
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BST2
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USHBP1
COLGALT1
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PGLS
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RSPH3
MAS1
MLLT1
FUT5
BMP15
ACTN4
NDUFA10
ZNF655
EPO
CACNG6
ZSWIM6
FCHO1
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ZNF747
PXDN
GDF15
PGPEP1
LSM4
JUND
HRC
TRPM4
ZNF557
OLFM1
NUMBL
TNNI2
ATXN10
TUBGCP2

TRPM4
ZNF557
OLFM1
NUMBL
TNNI2
ATXN10
TUBGCP2
CALY
CYP2E1
HBZ
MNX1
ZNF337
ALKBH6
CEP85
TAF4
GATA5
RBBP8NL
LAMA5
ADRM1
PRDM12
UBE2M
TRIM28
YIPF2
EIF2S3
TMEM160
ZC3H4
GMFG
MAP3K10
SESN2
CCDC62
HIP1R
MRPL4
PPAN
EIF3G
ANGPTL6
SHFL
ZNF426
SLC6A8
ZNF331
ZNF236
SLC7A10
LRP3
C12orf65
GRWD1
HIGD1B
ATP6V1E1
CCL25
COX4I1
EMC8
GSE1
C16orf95
GINS2
FAM153B
F12
NFATC1
IDO1
ABCB7
HAUS8
ADGRE3
MRPS25
TBC1D5
CAPN7
C3orf20
RBSN
NAPSA
NR1H2
PDLIM4
GFPT2
PSMC3IP
VPS25
RAMP2
AOC2
G6PC
PCDHAC1
DIAPH1
PCDHGA3
NDFIP1
EXOC4
PPFIA1
FLYWCH1
TMEM204
THOC6
BARX1
WDR44
CKMT2
ZCCHC9
KRT15
TNS4
CALY
CYP2E1
HBZ
MNX1
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GATA5
RBBP8NL
LAMA5
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TMEM160
ZC3H4
GMFG
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SESN2
CCDC62
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MRPL4
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SLC7A10
LRP3
C12orf65
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PKDREJ
NUTM2F
SLC35D2
PPIL4
AKAP12

NOL11
UBE4B
PKDREJ
NUTM2F
SLC35D2
PPIL4
AKAP12
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BPIFA2
RBM39
DEFB118
ACSS2
ARHGEF9
C1QL1
GFAP
HIGD1B
ATP6V1E1
CCL25
COX4I1
EMC8
GSE1
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IDO1
ABCB7
HAUS8
ADGRE3
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TBC1D5
CAPN7
C3orf20
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NR1H2
PDLIM4
GFPT2
PSMC3IP
VPS25
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AOC2
RARA
KRTAP9-8
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FMO5
PRKAB2
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FSHB
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USP29
CHSY1
SNRPA1
NR0B2
LIN28A
ADCY7
THAP1
RHPN2
FAAP24
LRRC9
ACTR10
LGALS3
PODNL1
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DNAJB1
ZSWIM4
RFX1
DCAF15
SDC1
TRIM21
WDR7
SMARCC1
SLC6A11
NUP210
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ARFIP2
RRP8
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MRPL35
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ILKAP
PER2
LATS1
BPIFB1
BPIFA2
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GFAP
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NDFIP1
EXOC4
PPFIA1
FLYWCH1

G6PC
PCDHAC1
DIAPH1
PCDHGA3
NDFIP1
EXOC4
PPFIA1
FLYWCH1
TMEM204
THOC6
BARX1
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CKMT2
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TNS4
RARA
KRTAP9-8
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FMO5
PRKAB2
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FSHB
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SNRPA1
NR0B2
LIN28A
ADCY7
THAP1
RHPN2
FAAP24
LRRC9
ACTR10
LGALS3
PODNL1
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SDC1
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SCLY
PTPRE
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RPA1
SERPINF1
EEFSEC
TMEM128
COQ3
POPDC3
LANCL2
GRSF1
JCHAIN
UTP3
WBP2
H3-3B
TRIM47
ZRANB2
KDM6B
ASGR2
SLC52A1
GUCY2D
CLEC10A
RIDA
MATN2
REEP2
PCBD2
ERAL1
NIP7
TERF2
VPS4A
JAG1
HSPA12B
SNAP25
BTBD3
NXT1
RIN2
SSTR4
CRP
HAPLN2
APCS
IGHMBP2
TMEM204
THOC6
BARX1
WDR44
CKMT2
ZCCHC9
KRT15
TNS4
RARA
KRTAP9-8
PPP1R1B
FMO5
PRKAB2
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FSHB
ZNF132
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NR0B2
LIN28A
ADCY7
THAP1
RHPN2
FAAP24
LRRC9
ACTR10
LGALS3
PODNL1
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DNAJB1
ZSWIM4
RFX1
DCAF15
SDC1
TRIM21
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SMARCC1
SLC6A11
NUP210
HSD17B7
EMILIN2
ARFIP2
RRP8

WDR7
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SLC6A11
NUP210
HSD17B7
EMILIN2
ARFIP2
RRP8
TIMM10B
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MRPL35
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ILKAP
PER2
RAMP1
SCLY
PTPRE
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RAP1GAP2
MYBBP1A
RPA1
SERPINF1
EEFSEC
TMEM128
COQ3
POPDC3
LANCL2
GRSF1
JCHAIN
UTP3
WBP2
H3-3B
TRIM47
ZRANB2
KDM6B
ASGR2
SLC52A1
GUCY2D
CLEC10A
RIDA
MATN2
ACY3
TESMIN
DPH2
ZSWIM3
OSER1
SERINC3
DMGDH
BHMT2
AP3B1
ZBED3
SYT4
SLC14A2
NMUR2
PDE6A
ATP8A2
USPL1
XPO4
TPTE2
RNF17
CHRM3
MYH4
SCO1
CHI3L1
MYBPH
CHIT1
LGR6
DCLK1
CCNA1
RFXAP
STARD13
MORC4
RNF128
PCDH19
C17orf80
SLC39A11
BTBD2
KMT5C
ZNF414
PDE6B
HSPBP1
CSNK1G2
RTTN
MACROD1
LGALS12
TIMM10B
EFR3A
OC90
PTCD3
IMMT
MRPL35
IQCA1
ILKAP
PER2
RAMP1
SCLY
PTPRE
CARD6
RAP1GAP2
MYBBP1A
RPA1
SERPINF1
EEFSEC
TMEM128
COQ3
POPDC3
LANCL2
GRSF1
JCHAIN
UTP3
WBP2
H3-3B
TRIM47
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KDM6B
ASGR2
SLC52A1
GUCY2D
CLEC10A
RIDA
MATN2
REEP2
PCBD2
ERAL1
NIP7
TERF2
VPS4A
JAG1
HSPA12B

REEP2	PLAAT4	SNAP25
PCBD2	PLAAT2	BTBD3
ERAL1	CEP20	NXT1
NIP7	MED10	RIN2
TERF2	CCDC134	SSTR4
VPS4A	SLC2A11	CRP
JAG1	SEC14L4	HAPLN2
HSPA12B	PI4KA	APCS
SNAP25	GIMAP4	IGHMBP2
BTBD3	MKRN1	ACY3
NXT1	ACTR3B	TESMIN
RIN2	NTS	DPH2
SSTR4	BTG1	ZSWIM3
CRP	DYDC2	OSER1
HAPLN2	TMTC1	SERINC3
APCS	KRAS	DMGDH
IGHMBP2	IPO8	BHMT2
ACY3	SPINK5	AP3B1
TESMIN	PMP2	ZBED3
DPH2	FABP4	SYT4
ZSWIM3	IMPA1	SLC14A2
OSER1	E2F5	NMUR2
SERINC3	CCDC59	PDE6A
DMGDH	LYVE1	ATP8A2
BHMT2	MICAL2	USPL1
AP3B1	SBF2	XPO4
ZBED3	RRAS2	TPTE2
SYT4	TEX15	RNF17
SLC14A2	SARAF	CHRM3
NMUR2	RNF122	MYH4
PDE6A	DUSP26	PEMT
ATP8A2	ERG28	SCO1
USPL1	DGLUCY	CHI3L1
XPO4	UNC79	MYBPH
TPTE2	CATSPERB	CHIT1
RNF17	VRTN	LGR6
CHRM3	SYNJ2BP	DCLK1
MYH4	TTC9	CCNA1
PEMT	MED6	RFXAP
SCO1	EIF2S1	STARD13
CHI3L1	ADAM20	MORC4
MYBPH	ELP3	RNF128
CHIT1	ADAMDEC1	PCDH19