

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
2. bta-miR-101 MIMAT0003520	1909	-10.20	TTTAGTTTAGAAACTTTTACTGTT   :               AAGTCAA--TAGTG-TCATGACAT	3.9E-1
3. bta-miR-21-3p MIMAT0003745	2021	-15.10	ACGCAGGTAAAACTGCCATGCTGTT :    :     :        TCTGTCGG--GTAGCTG--ACGACAA	3.57E-1
4. bta-miR-410 MIMAT0009311	2243	-6.10	TTTTGC--ATGGTGCTTATATA             TGTCCGGTAGACAC-AATATAA	2.61E-1
5. bta-miR-2396 MIMAT0011949	2864	-10.00	CTATT--TTAAACACTGCATGT  : :          GGTAGTTCTGGGGTCACGTACT	1.36E-1
6. bta-miR-410 MIMAT0009311	3495	-16.30	GCAGGATCTTTGGGTGTTATATA :     :  :       TGTC--GGTAG-ACACAATATAA	2.58E-1
7. bta-miR-2285dc MIMAT0046710	5796	-9.50	TAAAAATTGAAACAAACTTTTA     : :        CTTTTGGATT-TATTGAAAAA	2.39E-2
8. bta-miR-2285cr MIMAT0046691	5797	-9.90	AAAAATTGAAACAAACTTTT    :           TCTTGGACTT-GCTTGAAAA	2.39E-2
9. bta-miR-503-3p MIMAT0025558	5897	-11.90	ACGG-AGGTAAGTATTATACTCA     : :  :       GGCCCGTCGTCTTTGTTATGAGG	6.48E-2
10. bta-miR-2406 MIMAT0011964	6171	-13.30	AAGCCATG-AGCAAGCTTCCCTC             TTAGGT-CGAAGGAAGAAGGGAA	3.34E-1
11. bta-miR-219-3p MIMAT0012547	6175	-10.60	CATGAGCAAGCTTCCCTCAATTCT       :          GT-CT--ACAGGTCGGTGTAAAGA	3.34E-1
12. bta-miR-3578 MIMAT0016934	6911	-8.90	TTGGTAAGATCGCACAGTGGATTA :            CTTCA-ACAAGC--ACCACCTAAG	2.28E-1
13. bta-miR-2284t-5p MIMAT0011831	8913	-5.70	CTCTGCTTG-CACTATGTTTG : :        TTTTTGGGCTCACTTACAAAG	2.69E-1
14. bta-miR-21-3p MIMAT0003745	9311	-11.40	TTGCTGGTGCTAT-ACTTGCTGTA :  : :   :        TCTG-TCG-GGTAGCTGACGACAA	2.28E-1

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15. bta-miR-2406 MIMAT0011964	9500	-16.40	ATGCCACGCTTT - -ATTTCCCTT        : :    TTAGGT - CGAAGGAAGAAGGGAA	3.48E-1
16. bta-miR-410 MIMAT0009311	10523	-6.50	AATTGCCCCGTTTCAGGATTATATA             TGTCCGG - -TAGACACAATATAA	8.51E-2
17. bta-miR-2396 MIMAT0011949	11761	-8.70	AATTGCTTGCAACATTTGCATGT :          GGTAGTTCTGGGGT - CACGTACT	3.25E-1
18. bta-miR-17-5p MIMAT0003815	11801	-16.00	TGTGGCAATATTGTA - GCACTTTG :   :         TGATGGACGTGACATTCGTGAAAC	6.2E-2
19. bta-miR-200b MIMAT0003842	11920	-8.80	AGCAAGTGCCCTGACTAGTATTG   :    :     GTAGTAATGG - TCCGTCATAAT	1.75E-1
20. bta-miR-450b MIMAT0024576	12557	-6.60	TATCTGCTACCGCTTTGCAAAA   :         ATAAGTCCTTGTATAACGTTTT	3.29E-1
21. bta-miR-2284t-5p MIMAT0011831	14999	-12.60	TATGACTGG - CAGAATGTTTC :    :           TTTTTGGGCTCACTTACAAAG	9.48E-2
22. bta-miR-455-3p MIMAT0003836	16426	-14.60	TAGCTAGTTGTAAATGGACTGA    :         TCACATATACGGGTACCTGACG	3.57E-1
23. bta-miR-2483-3p MIMAT0012076	16432	-9.50	GTTGTAAATGGACT - GATGTTG    : :    :     AGAGAGTTGGTTGGTCTACAAA	3.57E-1
24. bta-miR-2285bz MIMAT0046646	16731	-7.40	TATCGCGCCACAAC - CACTTATA :               TTTTTG - GGT - TTGCTTGAATAA	8.13E-2
25. bta-miR-450b MIMAT0024576	18487	-7.30	GTCTCCGCTAC - -TTTGCAAAA                 ATAAGTCCTTGTATAACGTTTT	1.95E-1
26. bta-miR-410 MIMAT0009311	18666	-5.30	TCAAGTAATCATGATTTATATT      :              TGTCCGGTAG - ACACAATATAA	2.36E-2
27. bta-miR-3600 MIMAT0016932	19031	-12.80	TTTGTGTATGTTTTGGAAGTGT    :     :         TTCGACGGTCAACTTCTTGACA	2.42E-1
28. bta-miR-3956 MIMAT0025544	19867	-14.80	ATAATGGCGTTTA - CATTTCCACGA    :    :          GGGACTGGAAGTCGT - -AGGTGCA	3.48E-1

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29. bta-miR-345-5p MIMAT0003800	20031	-14.60	TTCGACAGCCTGAGAGTCAGC   :       TCGTGACCTGATCCTCAGTCG	7.09E-2
30. bta-miR-2448-3p MIMAT0012026	20262	-13.70	GTTTATGG-TAATTTCAACCAG :  : :       TGGGTGCCTAGGTTAGTTGGTG	1.95E-1
31. bta-miR-2415-5p MIMAT0011978	20355	-13.40	GAGTTTGTTCATACGACTCCA  :   :      ACCGGCCG-TCCTGGCTGAGGG	1.89E-1
32. bta-miR-450b MIMAT0024576	21169	-5.80	TTTTC-TGCACA-AATGCAAAT                ATAAGTCCTTGTATAACGTTTT	2.01E-1
33. bta-miR-2430 MIMAT0012000	21541	-12.00	TTAATTTTCC--ACTTACCCAGT :    :      GGCCTTTGGGGACGGCTGGGTCT	1.45E-1
34. bta-miR-219-3p MIMAT0012547	21945	-11.40	TTCATAAACAGCATGCAATTCA      :       GTCTACAGGTCG-GTGTTAAGA	9.19E-2
35. bta-miR-2446 MIMAT0012023	22625	-8.00	GGCGAAGGTCAACAAAT-TATTTTT      :            CCG-GGCTA-AAGTTTATATAAAAT	1.86E-1
36. bta-miR-224 MIMAT0009271	24373	-10.10	TATTATGTCTGCCTTTGACTTG              ATTTGCCTTGGTGATCACTGAAC	2.98E-1
37. bta-miR-2284t-5p MIMAT0011831	24935	-11.80	ATTTACCTGCTGCTAATGTTTC    :          TTTTTGGGC-TCACTTACAAAG	9.48E-2
38. bta-miR-2327 MIMAT0011856	25269	-18.49	TACAGGGCCTTACAAGTGCCCCA         :      CGGTCACGAACTCAGAGCGGGGA	1.04E-1
39. bta-miR-2285cr MIMAT0046691	25659	-7.70	CTTAAC--AAACAGAACTTTT             TCTTTGGACTTG-CTTGAAAA	7.54E-2
40. bta-miR-11999 MIMAT0046658	27145	-8.70	GCGAAGGTTAGTCCCGGTCTGT         :       CGGATACTCTTATACCCAGACT	2.14E-1
41. bta-miR-21-3p MIMAT0003745	27825	-17.20	TAATAGCTACCACAATGCCTGCTGTT  :         :       TCTGTCTG--GGT--AGCTGACGACAA	2.25E-1
42. bta-miR-2285cr MIMAT0046691	28049	-7.50	GGTAGACCT-TAT-AACTTTA :    :      :      TC-TTTGGACTTGCTTGAAAA	2.5E-1

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43. bta-miR-455-3p MIMAT0003836	28718	-15.10	ACCAGTTTACACC-TGGACTGC          TCACATATACGGGTACCTGACG	1.17E-2
44. bta-miR-2468 MIMAT0012058	28739	-8.90	TGATGAAGCTATTAAATTCCTAA          :        ACTGTT-AGAAGGTACAAGGATA	1.17E-2
45. bta-miR-2284t-5p MIMAT0011831	28826	-6.40	TACAAGTCGCAGT--ATGTTTG    :           TTTTTGGGC-TACTTACAAAG	1.04E-1
46. bta-miR-2285cr MIMAT0046691	29373	-5.86	AGAAATAATATCTAAACTTTA       :       TCTTTG-GACTTGCTTGAAAA	3.85E-1
47. bta-miR-12030 MIMAT0046723	29852	-20.60	GGCTGATGTCAATACCCCGGC     :            CCGGC--GAGGCCCGGGGCC	1.98E-1
48. bta-miR-2285bu MIMAT0046640	29958	-14.10	ATTGAAGGCTCAGGAAGGTCTG :    :            GGTTTTTCAAGTAAGTCCAGAA	2.01E-1
49. bta-miR-17-5p MIMAT0003815	30467	-7.60	TAGATTTG-ACAGTA--CACTTTC   :                TGATGGACGTGACATTTCGTGAAAC	3.29E-1
50. bta-miR-12006 MIMAT0046667	148	-12.60	CTGTT-AACAG-CTTTCAGCC                   CCCAACTTGTCTCAAAGTCGT	8.51E-2
51. bta-miR-2486-3p MIMAT0012082	1723	-6.82	GTAAAGGA-AACAAATCTCATTT :           :       TTGTGTCTAAAAACGGGGAGTAAA	3.11E-2
52. bta-miR-144 MIMAT0009234	1910	-8.10	TTAGTTTAGAACTTTTACTGTT :      :            GATCATGTAGTAGA-TATGACAT	3.9E-1
53. bta-miR-2284p MIMAT0011885	2940	-8.20	TGATGCCATAGAAGAGAACTTTCT                      TTTTAGG--GCTT--GTTTGAAAGT	2.42E-1
54. bta-miR-2356 MIMAT0011893	3262	-14.90	GTGGAGACATCTGATTCACAAGT       :       GGAGTCTGAGGGAGTAGTGTCT	2.65E-1
55. bta-miR-2284h-5p MIMAT0012019	3430	-7.40	TGCTGGTTGCGATCAGTTTTGGC :            TTTGGGCTTGCT--TGAAAACCC	1.22E-2
56. bta-miR-12050 MIMAT0046753	4798	-13.50	GGGGGCATAGAT-ATATGCAGCCA    :   :       TCATCCTTCCTGCTGT-CGTCGGT	3.16E-1

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57. bta-miR-2284h-5p MIMAT0012019	4815	-11.50	CAGCCAGGATAAAGTTTTTGGT   :       :       :           TTTGGGCTTGCTT-GAAAACCC	3.16E-1
58. bta-miR-2284h-5p MIMAT0012019	5493	-8.90	GGACGCTGTTATG-CATTTTGGT :       :     :           TTTG-GGC-TTGCTTGAAAACCC	2.86E-1
59. bta-miR-374b MIMAT0009302	5893	-10.00	TGTGACGGAGGTAAGTATTATAC                     GTGAATCGTCCA-ACATAATATA	6.48E-2
60. bta-miR-496 MIMAT0009336	5895	-6.30	TGACGGAGGTAAGTATTATACTCA                     CTCTAACCGGTACAT--TATGAGT	6.48E-2
61. bta-miR-2284h-5p MIMAT0012019	6134	-8.90	GGGGTTG-TATTACTTTTGGT : : : : :                 TTTGGGCTTGCTTGAAAACCC	2.14E-1
62. my-mir-noheader-provided-48	8371	-12.00	TGTAAAACTGGTTTGAAACTGAAGCTT   :       :       :           CCGTTCTG-TC--TCTGGTGCTTCGAA	2.69E-1
63. bta-miR-12006 MIMAT0046667	8550	-12.60	ACACAAATCAGATTTTTCAGCT                     CCCAACTTGTCTCAAAGTCGT	5.51E-2
64. bta-miR-9-3p MIMAT0012549	9891	-7.10	TGGTAGTGATGTGCTTTAC :       :     :           GCCAATA-GAT-CGAAATA	1.42E-1
65. bta-miR-2285ai-5p MIMAT0040946	10237	-8.70	CGTACGCCAAAAATATACATTG                     TTTTTTCGGTT-CGCTTGTAATA	1.14E-1
66. bta-miR-2285e MIMAT0024580	10492	-15.10	TATGGTCCTTATAAGGATGCTCAGGTTG   :           :               TAATC-GG-TTTTTCAAGCAAGTCCAAA	8.51E-2
67. bta-miR-16b MIMAT0003525	10564	-12.50	GCATGGCTTTA--TGCTGCTA                     CGGTTATAAATGCACGACGAT	8.51E-2
68. bta-miR-9-3p MIMAT0012549	10685	-7.90	TTGTTATAGATGCTTTAG                     GCCAATA-GATCGAAATA	3.07E-1
69. bta-miR-9-3p MIMAT0012549	11380	-7.60	TGG-ACAACAGCTTTAT :                     GCCAATAGATCGAAATA	1.86E-1
70. bta-miR-2329-3p MIMAT0011859	11436	-10.30	GAATGTT-TTGTATTTACAGA   : : : :             TGAATAGTCGAGTGTAGTGTCT	8.26E-2

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71. bta-miR-2451 MIMAT0012031	11444	-15.60	TGTATTTACAGATATACCTCAA   : : :      :      AGGTGAGAGGTCT- CGTGGAGTA	8.26E-2
72. bta-let-7i MIMAT0003851	11446	-15.50	TATTTACAGAT - - ATACCTCA    : :       TTGTCGTGTTTGATGATGGAGT	8.26E-2
73. bta-miR-2284h-5p MIMAT0012019	11658	-13.20	GCTTAATTTTAAGCTTTTGGG  :      TTTGGGCTTGCTTGAAAACCC	3.07E-1
74. bta-miR-2285ai-5p MIMAT0040946	11760	-9.00	TAATTGCT - TGC - AACATTTG      :          TTTTTCGGTTCGCTTGTAATA	3.25E-1
75. bta-miR-2349 MIMAT0011884	11907	-16.20	AGCTGCTGTGGATAGCAAGTGCCT       :         ACTCAGACTCTGGTC - TTCACGGT	1.75E-1
76. bta-miR-9-3p MIMAT0012549	11975	-6.90	CTGTTTTGCAGGCTTTAC       :    GCCAA - TAGATCGAAATA	2.39E-1
77. bta-miR-12006 MIMAT0046667	13469	-8.10	TAATTGCTGCCG - TTTTCAGCG     :          CCCAAC - TTGTCTCAAAGTCGT	3.76E-1
78. bta-miR-2356 MIMAT0011893	14760	-14.40	GGGTGTATACCGGCATCACAAGT          GGAGTCTGAGGGAGTAGTGTCT	2.35E-1
79. bta-miR-12011 MIMAT0046679	14827	-9.89	AATTTGGAAAAGCCAGGCTCTA    :       ACAAACTCAGAGTACCCGAGAG	6.08E-3
80. bta-miR-2329-3p MIMAT0011859	15514	-10.90	TTGATTCAACCTT - TGTCACAGA       : :        TGAATAGT - CGAGTGTAGTGTCT	3.2E-1
81. bta-miR-2451 MIMAT0012031	15714	-11.90	GACAT - AAACAATGGACCTCAT   :            AGGTGAGAGGTCTCGTGGAGTA	1.15E-2
82. bta-miR-2359 MIMAT0011897	16315	-8.30	GTGAAGATCATAAGCCACAATA :        :         TTTTTCTTTTGTT - - GTGTTAG	1.36E-1
83. bta-miR-453 MIMAT0009325	16723	-14.30	GTGTGTATTATCGCGCCACAACCA  : : :          ACGCTTGAGTGGTGC - CTGTTGGA	8.13E-2
84. bta-miR-2285ai-5p MIMAT0040946	16866	-5.40	AGTGTGCT - - TGAGACATTTT   : :    TTTTTCGGTTCGCTTGTAATA	2.82E-1

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85. bta-miR-2285e MIMAT0024580	19257	-10.21	GATGGC-ATGGATGCTAAGCAGGTTG  :          TAATCGGTTTTTCAAGCAAGTCCAAA	2.46E-1
86. bta-miR-2356 MIMAT0011893	19300	-17.10	CC-GCCACTT--GCATCACAAGA       :               GGAGTCTGAGGGAGTAGTGTCT	2.46E-1
87. bta-miR-2285ai-5p MIMAT0040946	19863	-8.00	TCTAATAATGGCGTTTACATTTTC :               TTTTTCGGTTCGC--TTGTAAAA	3.48E-1
88. bta-miR-12006 MIMAT0046667	20006	-12.40	GGTCAGGATGTCATCTTCAGCC          :             CCCA-ACTTG-TCTCAAAGTCGT	7.09E-2
89. bta-miR-2285bj MIMAT0046391	21549	-10.09	CCACTTACCCAGTTTGAGGGTTT       :               GGTTTTTCAAGTAAG-TCCCAAC	1.45E-1
90. bta-miR-382 MIMAT0009308	21586	-11.60	AAGGTTTAC-AATTTCAACTTC :  :  :               GCTTAGGTGGTGCTTGTTGAAG	1.34E-1
91. bta-miR-2285dg MIMAT0046736	22028	-6.30	TGAAAAG--AAAGATGGTTTTT         :             GGTTTTCAAGTAAAGCCAAAAA	6.99E-2
92. bta-miR-2359 MIMAT0011897	22803	-9.70	TTTATAATGGCTCTGCACAATC :  :  :               TTTTTCTTTTG--TTGTGTTAG	3.25E-1
93. bta-miR-2285e MIMAT0024580	23833	-10.37	AATGGTTACTACCCTACTTCAGGTTTC :  :  :               TAATCGGTTTTTCAAGCAAGTCCAAA	2.86E-1
94. bta-miR-4657 MIMAT0036970	24050	-12.00	GTGTGGTAGTACA--ACCACATA    :  :               TACGGAGTCTGGTGAAGGTGTAA	1.2E-1
95. bta-miR-2285aj-5p MIMAT0040947	24683	-10.10	GGGAACGTA--AGACCTTTTCA :  :  :               TTTTTGGGTTTGCTTGAAAAGT	2.18E-1
96. bta-miR-16b MIMAT0003525	24763	-14.40	AATAATATT--GATGCTGCTA :                       CGGTTATAAATGCACGACGAT	1.75E-1
97. bta-miR-374b MIMAT0009302	24914	-9.80	CAAGTTGTCAGTTGTATTATAA                       GTGAATCGTCCAACATAATATA	9.48E-2
98. bta-miR-16b MIMAT0003525	24929	-16.80	ATTATAATTTACCTGCTGCTA                       CGGTTATAAATGCACGACGAT	9.48E-2

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99. bta-miR-2349 MIMAT0011884	25263	-16.20	TAAATCTACAGGGCCTTACAAGTGCCC     : :        ACTCAGA--CTCTGG--TCTTCACGGT	1.04E-1
100. bta-miR-1777a MIMAT0012032	25272	-25.00	AGGGCCTTACAAGTGCCCCCA    :    :    GGGCGGGGGGT-GGCGGGGGT	1.04E-1
101. bta-miR-2356 MIMAT0011893	25366	-10.00	CCTTGACTTGC-CAACCACAAGC    :            GGAGTCTGAGGGAGT-AGTGTTCT	1.16E-1
102. bta-miR-2284h-5p MIMAT0012019	25378	-13.40	CAACCACAAGC--ATTTTGGG        :   :        TTTGG-GCTTGCTTGAAAACCC	1.16E-1
103. bta-miR-2285bc MIMAT0046377	25628	-8.50	CTAA--TGGTAATCTCTATGGTTTTA  :               GGTTTTCCA-GTAAG--TCCAAAAA	2.65E-1
104. bta-miR-2285dg MIMAT0046736	25628	-7.90	CTAATGGTAATCTCTATGGTTTTA  :   :      :    GGTTTTCA--AGTAAAGCCAAAAA	2.65E-1
105. bta-miR-2329-3p MIMAT0011859	26137	-13.90	GATTATGCAGCATGTAAATCACAGT         :        TGAATA-GTCG--AGTGTAGTGTCT	1.78E-1
106. bta-miR-496 MIMAT0009336	26185	-8.30	GACAAATATTAATGCTATACTCA           CTCTAACC GG TACATTATGAGT	4.38E-2
107. bta-miR-2329-3p MIMAT0011859	26187	-14.10	CAATATTAATGCTATAC-TCACAGA    :       :        TGAATAGT--CGA-GTGTAGTGTCT	4.38E-2
108. bta-miR-2356 MIMAT0011893	26973	-7.90	AGTAAATTTAGTGAGCACAAGC  :  :         GGAGTCTGAG-GGAGTAGTGTCT	3.43E-1
109. bta-miR-935 MIMAT0009385	27253	-8.00	TACTACCCTGAACCCATAACTGG             CGCCATCGCCTTCGCCATTGACC	6.88E-2
110. bta-miR-2285ai-5p MIMAT0040946	27326	-9.50	CGGATGTAATGCTGAACATTTC  :         TTTTTCGGTTCG-CTTGTA AAA	6.88E-2
111. my-mir-noheader-provided-48	27768	-8.90	TACATCCCTTCAATCATGTGAAGCTA  :  :         CCGTTCTGTCTCTGGTG--CTTCGAA	2.11E-1
112. bta-miR-382 MIMAT0009308	29044	-10.60	TCAACCCAGAAACAAACAATTG             GCTTAGGT-GGTGCTTGTTGAAG	3.15E-2



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113. bta-miR-2285bj MIMAT0046391	29331	-8.82	CCA-TCAACCCA-AAAGGGTTC                                    GGTTTTTCAAGTAAGTCCCAAC	3.48E-1
114. bta-miR-362-5p MIMAT0009298	29376	-12.80	AATAATATCTAAACTTTAAGGATG  : :          : :  TGAGTGTGGATCCAAGGTTCTCTAA	3.85E-1
115. bta-let-7i MIMAT0003851	30051	-18.90	TCTGGCAACAGAACCCCTACCTCT :         :               TTGTCGT--GTTTGATGATGGAGT	2.94E-1
116. bta-miR-12036 MIMAT0046731	30204	-15.20	CCCCGC--CAGA--AGAGGAGCCC   :                         CAGGTGCCTGCTCAGTGCCTCGGC	5.91E-3
117. bta-miR-2451 MIMAT0012031	30715	-14.30	CCTATACTGAAGA-CACCTCAG : :                         AGGTGAGAGGTCTCGTGGAGTA	2.39E-1
118. bta-miR-2349 MIMAT0011884	30928	-13.60	GAAGT-AATTGCCGAACAAGTGCCC            : :               ACTCAGACTCTGGT--CTTCACGGT	6.29E-2
119. bta-miR-2285l MIMAT0024587	2210	-10.50	CTGCTCTTGCATTTGCATGGGTTTT                  CGGTTTTTCAAGTACG--CCCAAAA	2.61E-1
120. bta-miR-194b MIMAT0046730	2954	-11.40	AGAAAC--TTTCTCCATGTA                  ACATTGTCGTTGAGGTACAC	2.42E-1
121. bta-miR-2285cf MIMAT0046663	5796	-10.00	TAAAAATTTGAAACAAACTTTT    : :               CTTTTTTGGGCTT-GCTTGAAAC	2.39E-2
122. bta-miR-11997 MIMAT0046653	9640	-13.70	TCTTACTGCAGACAGCTTGGTA    :        :               AGAGCCGGGTGTG-GGAACCAA	2.73E-1
123. bta-miR-2284i MIMAT0011792	9962	-5.04	AAATGGTTAATCCTACTTCTA    :        :              TTTGTGGTCTTGCTTGAAGAG	7.65E-2
124. bta-miR-194b MIMAT0046730	9978	-11.00	TTCTAAGGTAGAACCATGTA : : :              ACATTGTCGTTGAGGTACAC	7.65E-2
125. bta-miR-208a MIMAT0009261	10165	-9.60	CTAAGCCTTACAGTGATGTCTTAT             :        :    TGTTTCG-AAAAACG-AGCAGAATA	3.56E-2
126. bta-miR-2284i MIMAT0011792	11831	-10.20	AAATACT--TGC-CACTTCTG    : :        :               TTTGTGGTCTTGCTTGAAGAG	6.2E-2

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127. bta-miR-2285cy MIMAT0046705	20278	-8.70	ACCAGAAGATTATTGGTGGTTTG   :       :           GTTTTTTC AAGTAA - GACCAAAA	1.95E-1
128. bta-miR-2482 MIMAT0012074	21415	-9.70	TTCTTGAAAAGGGTAAACTAC :        : :       TTTTGCTGTTTCT - TTTGATG	1.45E-1
129. bta-miR-2284i MIMAT0011792	21589	-9.20	GTTTACAATTTT - AACTTCTC :            TTTGTTGGTCTTGCTTGAAGAG	1.34E-1
130. bta-miR-2285cy MIMAT0046705	25627	-6.90	TCTAATGGTAATCTCTATGGTTTT :             GTTTTTTC A - - AGTAAGACCAAAA	2.65E-1
131. bta-miR-2285cf MIMAT0046663	25658	-6.80	ACTTAAC - - AAACAGAACTTTT               CTTTTTGGGCTTG - CTTGAAAC	7.54E-2
132. bta-miR-2285cy MIMAT0046705	27371	-11.90	AGGAAGAGTTGGATCAATGGTTTA : :    :     :          GTTTTTTC AAGTAAG - - ACCAAAA	1.61E-2
133. bta-miR-2285cf MIMAT0046663	28049	-7.10	GGTAGACCT - TAT - AACTTTA   :   :     :   :       CTTTTTGGGCTTGCTTGAAAC	2.5E-1
134. bta-miR-2464-3p MIMAT0012052	28105	-12.90	TAGTAATGGACA - - TCTGGAG :                 GTCAAGACGAGTCGAGACCTC	3.03E-1
135. bta-miR-11997 MIMAT0046653	28227	-13.60	AGAGTTCCTAGTCATGCTTGGTG    :      :       AGAGCCGGGT - - GTGGGAACCAA	2.65E-1
136. bta-miR-2285cf MIMAT0046663	29372	-6.16	GAGAAATAATATCTAAACTTTA    :     :       CTTTTTG - GGCTTGCTTGAAAC	3.85E-1
137. bta-miR-2284i MIMAT0011792	29532	-11.10	AAGCA - AACTGC - TACTTCTC    :    :         TTTGTTGGTCTTGCTTGAAGAG	7.91E-3
138. bta-miR-105b MIMAT0009216	1723	-6.49	GTAAGGAAACAAATCTCATTTGC              TGGTTCCT - - CAGACTCGTAAACT	3.11E-2
139. bta-miR-105b MIMAT0009216	2205	-7.90	TAGCACTGCTCT - TGCATTTGC            TGGTTCCTCAGACTCGTAAACT	2.61E-1
140. bta-miR-2467-3p MIMAT0012057	3449	-23.60	TGGCAGTGATGCAGAACTGCCCTG :                 GTCGGGACT - CG - GAGTGACGGGAG	1.22E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
141. bta-miR-545-3p MIMAT0003807	3523	-14.00	CAGTATAGTCAGTTGTTTGTGAT    : : :        GT-GTGTTA-TTTACAAACAATA	2.58E-1
142. bta-miR-12009 MIMAT0046677	3841	-9.30	AGTGTGTACAAAGC-AGCTTGTG        :        TCAC-C-TCCCTTGAACGAACAA	1.11E-1
143. bta-miR-2341 MIMAT0011876	5118	-13.80	TCAGAAGGAATTGCTTGCCTACTA        : : :  AGTC-GGAAGAA-AGATGGATGAC	9.05E-2
144. bta-miR-2285de MIMAT0046713	5795	-11.50	TTAAAAATTTGAAACAAACTTTT      : :        TCTTTTGGACTTT-CTTGAAAA	2.39E-2
145. bta-miR-2285au MIMAT0046346	5796	-10.00	TAAAAATTTGAAACAAACTTTTA     ::        TCTTTTGGGCTT-GCTTGAAAAA	2.39E-2
146. bta-miR-20a MIMAT0003527	6922	-8.60	GCACAGTGGATTAAGAACAATTTT        :  :        GATG-GACGTGATATTCGTGAAAT	2.28E-1
147. bta-miR-2285au MIMAT0046346	6926	-6.90	AGTGGATTAAGAAC--ACTTTTA    : :             TCTTTTG-GGCTTGCTTGAAAAA	2.28E-1
148. bta-miR-2285au MIMAT0046346	7546	-6.20	TATAAACCAGGTAATACTTTTA      :        TCTTTTGGGCTTGCTTGAAAAA	2.94E-1
149. bta-miR-9851 MIMAT0046371	8175	-15.00	AAGTTGTAATAAATTTGGTGCCA : :  : :        GGTGGCG-GTCACGACCACGGT	3.62E-1
150. bta-miR-2285cv MIMAT0046699	8734	-5.30	GCTGTAGTAGACCAGGATTTTG           TTTTTTCAAGTAAACCTAAAAG	3.52E-1
151. bta-miR-2285au MIMAT0046346	9692	-7.00	AAATGGCTCTTAC-TACTTTTA : :          TCTTTTGGGCTTGCTTGAAAAA	1.98E-1
152. bta-miR-2341 MIMAT0011876	9900	-15.40	TGTGCTTTACCAACCGCTACTG   :          AGTCGGAA-GAAAGATGGATGAC	1.42E-1
153. bta-miR-499 MIMAT0003536	10167	-12.30	AAGCCTTACAGTGATGTCTTAT   :   :          TTTGTAGTGACGTT-CAGAATT	3.56E-2
154. bta-miR-33a MIMAT0009294	10176	-11.02	AGTGATGTCTTATCAAATGCAG      :        ACGTTACG-TTGATGTTACGTG	3.56E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
155. bta-miR-2285c MIMAT0011950	10497	-13.60	TCCTTATAAGGATGCTCAGGTTG                 CGG-TTTTCAAACAAGTCCAAA	8.51E-2
156. bta-miR-376d MIMAT0010199	10692	-10.50	AGATGCTTTAGCTTCTATGAC        :      TACACCTAAAAGGAGATACTA	3.07E-1
157. bta-miR-33a MIMAT0009294	12325	-9.50	GGTTGTGTACCATTG-AATGCAA  : :  :   : :       ACGTTACGT--TGATGTTACGTG	9.78E-2
158. bta-miR-2341 MIMAT0011876	12633	-13.84	TCGACTTGTAATACACCTACTC       :        AGTC-GGAAGAAAGATGGATGAC	2.18E-1
159. bta-miR-2399-3p MIMAT0011955	12880	-7.60	ACAATTTCTTCTACAGTTAGAT                TGTGAAAGACATCAACAATCTT	2.21E-1
160. bta-miR-499 MIMAT0003536	13216	-12.40	AAAGATC-CTGT--GTCTTAT            :       TTTGTAGTGACGTTTCAAAATT	3.29E-1
161. bta-miR-105b MIMAT0009216	13609	-6.20	AACACGATTTCTTTACATTTGA           TGGTTCCTCAGACTCGTAAACT	2.73E-1
162. bta-miR-2341 MIMAT0011876	13765	-8.97	CTGGTTGTGAACAATCCTACTT :  :        AGTCGGAAGAAAGATGGATGAC	1.32E-1
163. bta-miR-26a MIMAT0003516	13922	-5.90	AGGC-ATTTT--AACACTTGAT        :        TCGGATAGGACCTAATGAACTT	3.29E-1
164. bta-miR-2408 MIMAT0011966	15034	-13.10	AAAGTATAGC-AGCTACACGTG     :        GGCCGACTCGAGTG-TGTGCAC	9.48E-2
165. bta-miR-10176-5p MIMAT0040931	18311	-24.40	GGCT-GTGGCTAAAGCTCCTCCT : :               TTGAACGTCTGA--GAGAGGAGGA	2.5E-1
166. bta-miR-376d MIMAT0010199	18934	-11.70	ATTTTGATTTTAAAGTTCTATGAT       :      TACACCTAAAA--GGAGATACTA	2.25E-1
167. bta-miR-12041 MIMAT0046737	20005	-10.50	AGGGTCAGGATGT--CATCTTCAGC       : :      TAAGTCTCC-ACGTTCCGGAAGTCA	7.09E-2
168. bta-miR-20a MIMAT0003527	21521	-8.90	AGACAAGC-CTA--ATCACTTTA                 GATGGACGTGATATTCGTGAAAT	1.45E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
169. bta-miR-545-3p MIMAT0003807	21679	-8.20	AAGACTATAGA - - AGTGTGTGAT           :           GTGTGTTATTTACAAACAATA	2.25E-1
170. bta-miR-376d MIMAT0010199	22099	-7.10	CCACTGATAAGCTAGCTATGAT         :           TACACCTAAAAGG-AGATACTA	3.48E-1
171. bta-miR-1248 MIMAT0009972	22143	-11.70	GTGGTGCGTAAAGAGCTAGAAGAAGGT                 AAATCGTGTCACGAATATGTTCTTCCA	3.85E-1
172. bta-miR-124b MIMAT0013774	22664	-8.50	TTTACGCCTTATC - - ATGCCTTT   :   :           GAACCGTAAGTGGCGCACGGAAT	1.24E-1
173. bta-miR-33a MIMAT0009294	22673	-11.80	TATCATGCCTTTA - AATGCAC         :           ACGTTACGTTGATGTTACGTG	1.24E-1
174. bta-miR-12009 MIMAT0046677	23253	-13.00	ACATGACGGCGGTTGCTTGTC         :           TCACCTCCCTTGAACGAACAA	1.89E-1
175. bta-miR-2285de MIMAT0046713	25657	-7.90	TACTTAAC - AAACAGAACTTTT                 TCTTTTTGGACTTTCTTGAAAA	7.54E-2
176. bta-miR-10176-5p MIMAT0040931	26567	-20.40	CCTCTGCTAGTCTGTTTCCTCCT             :           TTGAACG - TC - GAGAGAGGAGGA	3.46E-2
177. bta-miR-11978 MIMAT0046364	27359	-11.80	TCC - - ATGATTTTAAGGAAGAGT     :                 CGGCCGGCT - CCCTCCCTTCTCA	1.61E-2
178. bta-miR-2285de MIMAT0046713	28048	-8.60	AGGTAGACCT - - TATAACTTTA   :   :             TCTTTTTGGACTTTCTTGAAAA	2.5E-1
179. bta-miR-2285be MIMAT0046380	29025	-11.60	ACTGGAAGTT - GGTGGAGTTTC : :                     GGTTTTTCAAACGAGCTCAAAA	3.15E-2
180. bta-miR-2285de MIMAT0046713	29371	-6.16	TGAGAAATAATATCTAAACTTTA     :     :           TCTTTTTG - GACTTTCTTGAAAA	3.85E-1
181. bta-miR-11978 MIMAT0046364	29504	-16.00	TCAAACC - AGGGGTAGAAGAGC         :           CGGCCGGCTCCCTCCCTTCTCA	7.91E-3
182. bta-miR-2285be MIMAT0046380	29612	-10.10	TCAAAAAG - - GAAAGGAGTTTG :                     GGTTTTTCAAACGAGCTCAAAA	8.64E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
183. bta-miR-33a MIMAT0009294	30219	-12.90	AGC--CCCAATAAACAAATGCAC     :       ACGTTACGTTG-ATGTTACGTG	5.91E-3
184. bta-miR-2368-3p MIMAT0011912	30461	-11.22	TGCA-ATTAGATTTGACAGT     :       CCGTCTCCACCAGACTGTCA	3.29E-1
185. bta-miR-6501 MIMAT0046685	3451	-19.60	GCAGT-GATGCAGAAACTGCCCTGT :    :           TGACAAATGGTGTC-CGACGGGACC	1.22E-2
186. bta-miR-500 MIMAT0009337	8730	-12.10	TGTTGCTGTAGTAGACCAGGATTT   :           AGAGTGGGTCCATC-GTTCCTAAT	3.52E-1
187. bta-miR-2285az MIMAT0046356	8733	-8.60	TGCTGTAGTAGACCAGGATTTT              GGTTTTTCAAGTGAGCCTAAAA	3.52E-1
188. bta-miR-2285az MIMAT0046356	10469	-7.50	GTACTGATTTCAATGGGGATTTT           GGTTTTTCAAGT-GAGCCTAAAA	8.51E-2
189. bta-miR-500 MIMAT0009337	10523	-12.20	AATTGCCC--GT--TCAGGATTA                AGAGTGGGTCCATCGTTCCTAAT	8.51E-2
190. bta-miR-500 MIMAT0009337	13086	-12.80	TGCTACC--ACTAGTCAGGATTC :         :       AGAGTGGGTCCATCGTTCCTAAT	1.38E-1
191. bta-miR-181a MIMAT0003543	14995	-7.80	GTACTATGACTGGC--AGAATGTT :          TTGAGTGGCTGTGCGCAACTTACAA	9.48E-2
192. bta-miR-6501 MIMAT0046685	22521	-16.90	ATATGGACCTTAATCCTGCCCTGT           TGACAAATGG-TGTCCGACGGGACC	3.66E-1
193. bta-miR-181a MIMAT0003543	26995	-7.80	GCTATGGAGAAGGTTAATGAATGTG    :   :       TTGAGTGGCTGTGCG-CAACTTACAA	1.75E-1
194. bta-miR-2373-3p MIMAT0011919	232	-22.70	GGTCTCGAACTAC--ACTGGGCTCC        :    :       CC-GAG-AAGGTGCACGCCCCGAGC	8.01E-2
195. bta-miR-2904 MIMAT0013862	237	-15.80	CGAACTACACTG-GGCTCCA   :    :       CTCCGGT-TGGCTCCGAGGG	8.01E-2
196. bta-miR-217 MIMAT0009267	409	-11.80	AAACAA-GAGT-GTTGTGTGCAGTC         :    :       TAGGTTAGTCAAGGAC-TACGTCAT	1.45E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
197. bta-miR-217 MIMAT0009267	487	-9.50	CTTCAA--GATGCTT--TGCAGTC  :      :          TAGGTTAGTCAAGGACTACGTCAT	3.03E-1
198. bta-miR-2442 MIMAT0012017	2196	-16.40	TTTTACTACTAGC- ACTGCTCT :                ACGTCGGGTGTCGGGGACGAGA	2.61E-1
199. bta-miR-1434-5p MIMAT0012039	2952	-7.70	AGAGA-AACTTTCTCCATGTAA       :              TCTTTAAAAATCAGTAGTACATG	2.42E-1
200. bta-miR-2352 MIMAT0011888	3517	-9.56	AAGCAA-C-AGTATAGTCAGTTG                     GTCGTTAGGACAAGAAAGTCAAA	2.58E-1
201. bta-miR-217 MIMAT0009267	4139	-9.20	TTGCAA--AG--GCTATTGCAGTA                     TAGGTTAGTCAAGGACTACGTCAT	1.02E-1
202. bta-miR-2285dm MIMAT0046758	6055	-12.80	TATAAGGTTACTGAGTGGCCAA                 TTTTATGTCTGA-AAACCGGTT	4.26E-2
203. bta-miR-3602 MIMAT0016937	6062	-13.40	TTACTG-AGTGG--CCAACAG       :      :          AATGGCGCCACTAGGGTTGTG	4.26E-2
204. bta-miR-1284 MIMAT0009955	8252	-13.40	ATTCTGCTAAG-CATGTGCAGG     :                CTTTTCGGTCCCAGACACGTCT	3.07E-1
205. bta-miR-2444 MIMAT0012021	8535	-5.80	GCCCACTTACACAGTACACAAA                 TTTTGTTTTTTTGT--TGTGTTT	5.51E-2
206. bta-miR-106b MIMAT0009218	8798	-11.80	GTTACCATGTGTT-GCACTTTA     :      :            TAGACGTG-ACAGTCGTGAAAT	1.54E-1
207. bta-miR-1284 MIMAT0009955	8831	-10.90	TTTCTGCTGATGG--AGTGCAGT     :                CTTTTCGG-TCCCAGACACGTCT	1.54E-1
208. bta-miR-3533 MIMAT0036975	9922	-13.40	GCTTCCGTTTCA-ACTTCAT       :                TACAGGTGCAGTGTGAAGTA	7.65E-2
209. bta-miR-1603 MIMAT0011823	10295	-13.20	CTGCTTATAACGGCAAACCAC :  :    :              TTTTTTGTGTT-TTGTGTTGGTG	3.62E-1
210. bta-miR-222 MIMAT0003530	10548	-8.02	ATCT-GT-TAATTTTGTAGCA   :  :              TGGGTCATCGGTCTACATCGA	8.51E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
211. bta-miR-1284 MIMAT0009955	16070	-8.13	GAACATGTATTTAAGAAGTGCAGT     :       CTT-TTCG-GTCCCAGACACGTCT	3.52E-1
212. bta-miR-2371 MIMAT0011916	16884	-7.10	CAGAACAATGTTGTGAACATATC  :     : :       TTTTTGGTGTG- - TTTTGATAT	2.82E-1
213. bta-miR-2442 MIMAT0012017	17285	-13.10	TGTTTATATTGGTGATCCTGCTCA :   : :       ACGTCGGGTGTCG- - GGGACGAGA	3.52E-1
214. bta-miR-2405 MIMAT0011963	19156	-12.80	ACAAACATGCATTCCACACT    :          CTCCGGTTTGTGTTGGTGTGT	3.16E-1
215. bta-miR-411a MIMAT0009312	19381	-7.80	CTTAC- - AATACAG-CTACTAC                  GCATGCGATATGCCAGATGATA	3.12E-1
216. bta-miR-2352 MIMAT0011888	20519	-7.10	TGTTGATTTTAAAGATTTTCAGTTC :    :   :       GTCGTTAGGA- - CAAGAAAGTCAAA	3.16E-1
217. bta-miR-106b MIMAT0009218	21523	-5.90	ACAAGC-CT- - AATCACTTTA            TAGACGTGACAGTCGTGAAAT	1.45E-1
218. bta-miR-106b MIMAT0009218	22584	-7.30	TTTTTAGGAGTTTTCACCTTTA    :       TAGACGTGACAGTCGTGAAAT	3.43E-1
219. bta-miR-375 MIMAT0009303	22618	-12.70	TTACAC-AGGCGAAGGTCAACAAAT  :                   AGTGCGCTCGGCTTGC- - TTGTTTT	1.86E-1
220. bta-miR-3533 MIMAT0036975	23837	-7.70	GTTACTAC- - CCTACTTCAG  :    :       TACAGGTGCAGTGTGAAGTA	2.86E-1
221. bta-miR-2371 MIMAT0011916	24798	-9.60	TTTTTCCA-GCATAACTATA     :          TTTTTGGTGTGTTTGTATAT	3.85E-1
222. bta-miR-217 MIMAT0009267	24861	-12.90	GGGCAATTGGGCTATTTGCAGTC      :   :       TAGGTTAGTCAAGGACTACGTCAT	2.32E-1
223. bta-miR-1434-5p MIMAT0012039	26132	-5.50	GTGGTGATTATGCAGCATGTAA              TCTTTAAAATCAGTAGTACATG	1.78E-1
224. bta-miR-1284 MIMAT0009955	26969	-9.30	CACTAGTAAAAATTTAGTGCAGC    :   :       CTTTTCGGTCCCAGACACGTCT	3.43E-1



1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
225. bta-miR-1603 MIMAT0011823	28633	-10.10	TTTACACGATGTAAAACCAC      :        TTTTTGT-GTT-TTGTTTGGTG	1.78E-1
226. bta-miR-2442 MIMAT0012017	29961	-16.50	GAAGGCTCA-GGAAGGTCTGCTCC : :   :  :    ACGTCGGGTGTC--GGGGACGAGA	2.01E-1
227. bta-miR-3533 MIMAT0036975	29985	-12.30	AATTCCAGATC-TACTTCAC        :      TACAGGTGCAGTGTGAAGTA	2.01E-1
228. bta-miR-2378 MIMAT0011924	30301	-15.20	AACTTGGAAGTAGTGACCCACA        :        GGGAAC-GAGTCTGTTGGGTGT	4.98E-2
229. bta-miR-2285dm MIMAT0046758	30376	-13.40	CAAGATTAGA--GTTGGCCAA :          TTTTATGTCTGAAAACCGGTT	1.09E-1
230. bta-miR-1284 MIMAT0009955	30381	-16.70	TTAGAGTTGGCCAAAGTGCAGA  :   :        CTTTTCGGTCCCAGACACGTCT	1.09E-1
231. bta-miR-1603 MIMAT0011823	30555	-12.10	ATGAATATGAGTCCAAAACCAC : :   :  :    TTTTTGTGTTT--TGTTTGGTG	3.66E-2
232. bta-miR-12055 MIMAT0046762	266	-18.90	GGATGTTTGAGGACGCAGAGGAGAA :            TCAAGAGGCTCC--CG-CTCCTCTT	3.03E-1
233. bta-miR-2354 MIMAT0011890	5122	-12.50	AAGGAATTGC-TTGCCTACTA :   :   :        TGATTTGTTGTGTTGGATGAT	9.05E-2
234. bta-miR-10163-3p MIMAT0040910	5862	-13.10	TGAGTATAAACC-TGACTTGTCA             TCTCTCTCTTGGTAC-GAACAGT	6.48E-2
235. bta-miR-671 MIMAT0009365	6168	-14.39	GTTAAGCCATGAGCAAGCTTCCC             GAGGTCGGGGAGGTCCCGAAGGA	3.34E-1
236. bta-miR-671 MIMAT0009365	8555	-14.70	AATCAG-ATTTTCA--GCTTCCC :    :  :        GAGGTCGGGGAGGTCCCGAAGGA	5.51E-2
237. bta-miR-2304 MIMAT0011816	8939	-10.80	CCGATGGTAGTC-CACAACC :          TGTGTGTGTTGGTGTGTTGG	3.62E-1
238. bta-miR-3596 MIMAT0016940	9405	-13.00	TGTTAATGTG-ATTGTGTGGTG     :        ACTCCATCATCCAACACACCAA	1.92E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
239. bta-miR-2354 MIMAT0011890	9959	-8.70	TGAAAATGGTTAATCCTACTT    : :       TGATTGTGTGTTGGATGAT	7.65E-2
240. bta-miR-2354 MIMAT0011890	12637	-14.20	ACT-TGTAATACA-CCTACTC     :   :           TGATTGTGTGTTGGATGAT	2.18E-1
241. bta-miR-2354 MIMAT0011890	13764	-12.90	GCTGGTTGTGAACAATCCTACTT :   : :            TGATT-TGTTGTGTT-GGATGAT	1.32E-1
242. bta-miR-3596 MIMAT0016940	13988	-11.60	TGCAGCCCCAGG--GTGTGGTG           ACTCCATCATCCAACACACCAA	3.48E-1
243. bta-miR-2354 MIMAT0011890	19606	-18.10	ATAATACAACATATCCTACTA        :         TGATTGTGTGTTGGATGAT	5.58E-3
244. bta-miR-664a MIMAT0012078	20024	-17.70	CAGCCA-ATTCG--ACAGCCTG     :       GTAGGTGTGTGTGGGGTCGGAC	7.09E-2
245. bta-miR-664a MIMAT0012078	21655	-14.70	TTGCTATGCTGGATATTCAGCCTG :  ::   : :       GTAGGTGTG--TGTGGGGTCGGAC	2.25E-1
246. bta-miR-10163-3p MIMAT0040910	23252	-15.50	AACATGACGGCGGTTGCTTGTC    :   :       TCTCTCTCTTGGTA-CGAACAGT	1.89E-1
247. bta-miR-2354 MIMAT0011890	23829	-10.00	GCTTAATGGTTACTACCCTACTT :      : :          TGATTGTGTTG-TG-TTGGATGAT	2.86E-1
248. bta-miR-664a MIMAT0012078	24709	-12.10	AATTTTAATATG-AGCAGCCTG   : : :       GTAGGTGTGTGTGGGGTCGGAC	1.75E-1
249. bta-miR-2365 MIMAT0011903	27376	-5.70	GAGTTGGATCAATGGTTTAAAAACC    :      :   :       CT-ATTCT--TTGTCG--TTTTTGA	1.61E-2
250. bta-miR-137 MIMAT0009231	27473	-7.94	ATAGGT--TACAGGAGGCAATAA      : :       GATGCGCATAAGAATTCGTTATT	2.14E-1
251. bta-miR-12024 MIMAT0046717	29969	-6.80	AGGAAGGTCTG-CTCCTAAT                TCACAACAAACCTAGGATTT	2.01E-1
252. bta-miR-1584-5p MIMAT0011969	30207	-20.50	CGCCAGAAGAGGAGCCCCAA              ACGGGGGTCGGGTCGGGGTT	5.91E-3

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
253. bta-miR-12055 MIMAT0046762	30589	-10.40	GTCAGAAGAATGGACAAGGAGAA            TCAAGAGGCTCCC-GCTCCTCTT	4.57E-2
254. bta-miR-664a MIMAT0012078	30673	-15.80	TGACTGCAGAGGACATCAGCCTT      :          GTAGGTGT-GTGTGGGGTCCGAC	1.28E-1
255. bta-miR-29b MIMAT0003828	2237	-13.90	TTCAT--GTTTTGCATGGTGCTT   : :   :       TTGTGACTAAAGTTTACCACGAT	2.61E-1
256. bta-miR-502b MIMAT0009339	2649	-11.40	TAAAAATTTGC-ATTGTGGATA :            CTTAGGAACGGGTCCACCTAA	2.78E-1
257. bta-miR-502b MIMAT0009339	2893	-7.30	GAAGTGGATGATAC-TGTGGATA                CTT-AGGAAC-GGGTCCACCTAA	1.36E-1
258. bta-miR-539 MIMAT0009342	2943	-10.60	TGCCATAGAAGAGAAACTTTCTCC   :                TGTGTG-GTTC-CTATTAAAGAGG	2.42E-1
259. bta-miR-502b MIMAT0009339	3852	-12.40	AGCAGCTTGTGT-TGTGGATG    : :       CTTAGGAACGGGTCCACCTAA	1.11E-1
260. bta-miR-2285w MIMAT0029945	4815	-7.00	CAGCCAGGATAAAGTTTTTGGT  :       :       TTTAGACTTACTT-GAAAACCA	3.16E-1
261. bta-miR-2285w MIMAT0029945	5494	-9.20	GACGCTGTTATG-CATTTTGGT                TTTAGAC-TTACTTGAAAACCA	2.86E-1
262. bta-miR-2404 MIMAT0011961	5647	-11.10	AAGGGTGTAG-GAAGTGCAA :  : : :       CGTCTATGGTACGTCACGTT	9.48E-2
263. bta-miR-2284u MIMAT0011895	5795	-6.60	TTAAAAATTTGAAACAAACTTTT      : :            TCTTTTGG-CTT-GCTTGAAAA	2.39E-2
264. bta-miR-2285w MIMAT0029945	6134	-10.00	GGGGTTG-TATTACTTTTGGT :          TTTAGACTTACTTGAAAACCA	2.14E-1
265. bta-miR-29b MIMAT0003828	6786	-13.00	GAGTGTGGTTGCTAGA-GGTGCTT   :    :  :       TTGTGACTAA-AGTTTACCACGAT	3.52E-1
266. bta-miR-502b MIMAT0009339	9268	-12.90	TTAGCACAGCCT--GTGGATT    :       CTTAGGAACGGGTCCACCTAA	2.28E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
267. bta-miR-29b MIMAT0003828	9298	-13.90	ACTGCTAGTTCATTGCTGGTGCTA :    :                      TTGTGACTAAAGT - - TTACCACGAT	2.28E-1
268. bta-miR-2285w MIMAT0029945	9325	-7.70	CTTGCTGTAATTGTTGTTTGGT                       TTTAGAC - - TTACTTGAAAACCA	2.28E-1
269. bta-miR-33b MIMAT0009295	10177	-11.60	GTGATGTCTTATCAAATGCAG       : :               CGTTACGTTGT - CGTTACGTG	3.56E-2
270. bta-miR-497 MIMAT0004343	10561	-12.10	GTAGCATGGCTTTATGCTGCTA   : :                  ATGTTTGGTGT CACACGACGAC	8.51E-2
271. bta-miR-106a MIMAT0003784	11803	-13.40	TGGCAATATTGTA - GCACTTTG : :                      ATGGACGTGACATT CGTGAAAA	6.2E-2
272. bta-miR-33b MIMAT0009295	12326	-10.10	GTTGTGTACCATTGAATGCAA   : :    :                  CGTTACGTTGT - CGTTACGTG	9.78E-2
273. bta-miR-2285w MIMAT0029945	13958	-7.00	TAAATGGTATGA - - TTTTGGT                         TTTAGACTTACTTGAAAACCA	3.48E-1
274. bta-miR-497 MIMAT0004343	14412	-15.80	GACTTGCTTTTATATGCTGCTG    :   :                   ATGTTTGGTGT CACACGACGAC	7.54E-2
275. bta-miR-11986 MIMAT0046385	14680	-8.70	ATTTGCCAC - CATGGTGACAT :                        TTCCTGATTGAGTA - - ACCTGTT	1.98E-2
276. bta-miR-10169-3p MIMAT0040917	16152	-11.56	AGTTGCAT - CAGAAAGCCTCTTCT :    :                   TACTTGTGCAAGACGAGGAGAAGT	5.43E-2
277. bta-miR-1301 MIMAT0009958	16161	-13.70	AGAAAGCCTCTT - CTTTGCTGCAA     :                     CTTTAGTGAGGATCCGTCGACGTT	5.43E-2
278. bta-miR-1298 MIMAT0009970	17472	-9.00	AATAAGCTTAAGCTAAGAATGAA :    :                   ATGTAGACCTGTCGG - - CTTACTT	3.66E-1
279. bta-miR-12052 MIMAT0046759	18190	-10.90	ATGCCACGCGTGATAGCATTGGG :                         AGAGTCAAACCTTTAGAGTAACCC	2.5E-1
280. bta-miR-1301 MIMAT0009958	20578	-16.40	TCTATC - TTCGTTTGCAAGCTGCAT     :                        CTTTAGTGAGGATCCGT - CGACGTT	2.42E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
281. bta-miR-33b MIMAT0009295	21108	-7.30	ACAGAGTTTCTTGAATGCAG   :  :           CGTTACG-TTG-TCGTTACGTG	3.16E-1
282. bta-miR-11986 MIMAT0046385	21872	-14.20	CAGGA--AATGGATTGGACAT       :       TTCCTGATTGAGTAACCTGTT	2.65E-1
283. bta-miR-1298 MIMAT0009970	22168	-5.94	GTGATCT--TCCCGAGAATGAT              ATGTAGACCTGTCGGCTTACTT	3.85E-1
284. bta-miR-33b MIMAT0009295	22674	-11.10	ATCATGC-CTTTAAATGCAC              CGTTACGTTGTCGTTACGTG	1.24E-1
285. bta-miR-2475 MIMAT0012066	22677	-11.23	ATGCCTTTAAATGCAC-CACTTCT :            GGCG-ACGTCAAAGTGTGTGAAGT	1.24E-1
286. bta-miR-2285al-5p MIMAT0040949	22947	-7.30	AGTATATCGTAC-CACTTTGT :            ATTTTGGGCTTGTTTGAAACA	2.39E-1
287. bta-miR-6529a MIMAT0025565	25625	-6.09	ATTCT--AATGGTAATCTCTA  :            TGAGACGCGGAGACTAGAGAG	2.65E-1
288. bta-miR-2284u MIMAT0011895	25657	-8.00	TACTTAACAAACAGAACTTTT            TCTTTTGGCTTGCTTGAAAA	7.54E-2
289. bta-miR-10178-5p MIMAT0040933	27467	-20.40	AAATG-AATAGGTTACAGGAGG    :            ACGACGGAGTCCAGGGTCCTCC	2.14E-1
290. bta-miR-10178-5p MIMAT0040933	27681	-13.69	TGATTATACTGGACACCAGGAGT              ACGACGGAGTCC-AGGGTCCTCC	2.21E-1
291. bta-miR-2284u MIMAT0011895	28048	-8.60	AGGTAGACCTTAT-AACTTTA   :  :       :       TCTTTTGGCTTGCTTGAAAA	2.5E-1
292. bta-miR-2284u MIMAT0011895	29371	-5.74	TGAGAAATAATATCTAAACTTTA   :     :       TCTTTTGG--GCTTGCTTGAAAA	3.85E-1
293. bta-miR-10178-5p MIMAT0040933	29540	-19.30	TGCTACTTCTCAGCTACCATCAGGAGG      :               ACGA--CGGAGTC-CAGG--GTCCTCC	7.91E-3
294. bta-miR-196a MIMAT0009255	30051	-18.90	TCTGGCAACA-GAACCCCTACCTC :   :                 GGGTTGTTGTACTT--TGATGGAT	2.94E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
295. bta-miR-33b MIMAT0009295	30220	-12.50	GC--CCCAATAAACAATGCAC              :           CGTTACGTTGT-CGTTACGTG	5.91E-3
296. bta-miR-106a MIMAT0003784	30469	-7.60	GATTTG-ACAGTA--CACTTTC  ::                   ATGGACGTGACATTCGTGAAAA	3.29E-1
297. bta-miR-411c-5p MIMAT0025545	206	-9.60	TCACAATGT-CGAAGATCAACA                   TTACATACAAGAGACTAGTTGG	8.01E-2
298. bta-miR-10179-5p MIMAT0040937	1123	-13.40	CGTTATGTTATGAGACTGCAGA :   :            GGTGTCGGATGTTGGGACGTCT	1.69E-1
299. bta-miR-2285a MIMAT0011797	3429	-9.10	TTGCTGTTGCGATCAGTTTTG  :       GGTTCTTAAAGTAAGTCAAAAA	1.22E-2
300. bta-miR-2449 MIMAT0012027	3454	-15.20	GTGATGC-AGAACTGCCCT  :                     CGGGACGACAGAGGACGGGT	1.22E-2
301. bta-miR-299 MIMAT0009274	6138	-14.20	TTGTATTACTTTTGGTAAACCT                 :       TACATACACCCTGCCATTTGGT	2.14E-1
302. bta-miR-142-5p MIMAT0003790	8803	-8.00	CATGTGTT--GCACTTTATT    :           CATCACGAAAGATGAAATAC	1.54E-1
303. bta-miR-130a MIMAT0009223	8809	-13.50	TTGCACTTTATTACACATGCACTT                           TACGGGAAA-ATTGT-AACGTGAC	1.54E-1
304. bta-miR-454 MIMAT0009326	8813	-10.00	ACTTTAT-TACA--CATGCACTT   : :                    TGGGATATTCGTTATAACGTGAT	1.54E-1
305. bta-miR-130a MIMAT0009223	8905	-15.00	GTGCTTTCCTCTGC-TTGCACTA :    : :          :            TACGGGA-AAATTGTAACGTGAC	2.69E-1
306. bta-miR-142-5p MIMAT0003790	9497	-5.20	TTTATGC--CACGCTTTATT            :       CATCACGAAAGATGAAATAC	3.48E-1
307. bta-miR-2287 MIMAT0011794	10048	-16.30	GATAAGGTCTACT-GTCCAG  :   :       TTCACGACGGTGGTCAGGGTC	1.75E-1
308. bta-miR-107 MIMAT0003785	10560	-18.50	TGTAGC-ATG-GCTTTATGCTGCT :          :            CTATCGGGACATG--TTACGACGA	8.51E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
309. bta-miR-411c-5p MIMAT0025545	12065	-12.70	CTAGTG-GTTCTGCTAATCAACA   :                TTACATACAAGA-GACTAGTTGG	3.46E-2
310. bta-miR-2488 MIMAT0012084	12067	-7.26	AGTGGTTCTGCTAATCAACAG             TCTCC-CTTATCCTAGTTGTA	3.46E-2
311. bta-miR-129-5p MIMAT0009221	12714	-5.50	TGATGGTCTTAAGTATACAAAAAT :  :          TCGTTCCGGG--TCTGGCGTTTTTC	3.34E-1
312. bta-miR-107 MIMAT0003785	14412	-15.40	GACTTGCTTT-TATA-TGCTGCT      :    :        CT-ATCGGGACATGTTACGACGA	7.54E-2
313. bta-miR-133c MIMAT0029949	15916	-6.00	ACCACGAAAATGAAGAATACCAAAA                CGACCATTTTAC--CT--TGGTTTA	2.69E-2
314. bta-miR-485 MIMAT0009328	16150	-16.50	GCAGTTGCATCA--GAAAGCCTCT  :                  GCTTAA-GTAGTGCCGGTCGGAGA	5.43E-2
315. bta-miR-107 MIMAT0003785	16162	-17.80	GAAAGCCT-CTTCTTTGCTGCA        :         CTATCGGGACATGTTACGACGA	5.43E-2
316. bta-miR-133c MIMAT0029949	16264	-11.60	GTGATGTAAATGATGTTACCAAAT  :       :          CG-ACCATT--TTACCTTGGTTTA	1.36E-1
317. bta-miR-411c-5p MIMAT0025545	16890	-9.80	AATGT-TGTGAACT-ATCAACA                 TTACATACAAGAGACTAGTTGG	2.82E-1
318. bta-miR-3065 MIMAT0046741	18240	-16.10	TCCA-CAGGAATTGATTTTGTGT                 AGGTCGT-AGTCACTAAAACAACT	2.14E-1
319. bta-miR-152 MIMAT0009238	20418	-12.80	AGTAAG-AGTGTT-TGCACTGT :        :       GGGTTCAAGACAGTACGTGACT	2.21E-1
320. bta-miR-411c-5p MIMAT0025545	21967	-9.00	ATTATAAAATCACT-ATCAACC            TTACATACAAGAGACTAGTTGG	9.19E-2
321. bta-miR-11971 MIMAT0046336	21973	-19.80	AAATCACTATCAACCCCTCA              AAGAGTGAGAGACGGGGAGT	9.19E-2
322. bta-miR-11983 MIMAT0046376	23060	-13.10	TCTACTGAAACCATTACCACTGGTT :  :             GGGTG--TCCG--AGCGTGACCAG	7.42E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
323. bta-miR-216a MIMAT0009265	28112	-10.50	GGACATCTGGAGACCTGAGATTA              AGTGTCAAC - GGTCGACTCTAAT	3.03E-1
324. bta-miR-142-5p MIMAT0003790	28272	-5.40	GCTACACTCACT - CTTTATG             CATCACGAAAGATGAAATAC	6.2E-2
325. bta-miR-411c-5p MIMAT0025545	29316	-8.80	GGTAATTACCGACTGCCATCAACC           TTACATACAAGAGAC - -TAGTTGG	3.48E-1
326. bta-miR-129-5p MIMAT0009221	29599	-10.10	GAATTACTCAG - TTTCAAAAAG   :     :       TCGTTTCGGGTCTGGCGTTTTTC	8.64E-2
327. bta-miR-2287 MIMAT0011794	29657	-20.30	TATTGC - ACCAGGAGTCCAG               TTCACGACGGTGGTCAGGGTC	2.69E-1
328. bta-miR-2345 MIMAT0011880	29690	-10.60	GGGGTACTGGTACAGACACAAC   :      :       CTTTAT - TCT - TTTGTGTGTTG	2.01E-1
329. bta-miR-107 MIMAT0003785	29733	-17.90	GATGGCAACCAGCGT - CAACTGCTGCC     :             CTATCG - -GG - -ACATGTT - ACGACGA	1.11E-1
330. bta-miR-130a MIMAT0009223	30218	-19.80	GAGCCCCAATAAACAATGCACTG               TACGGG - AAAATTGTAACGTGAC	5.91E-3
331. bta-miR-152 MIMAT0009238	30222	-16.44	CCCAA - -TAAACAATGCACTGT           GGGTTCAAGACAGTACGTGACT	5.91E-3
332. bta-miR-2488 MIMAT0012084	30522	-7.90	AATTTGAATGCATATCAACAA     :       TCTCCCTTAT - CCTAGTTGTA	2.11E-1
333. bta-miR-2284e MIMAT0012080	222	-8.60	CAACAAATACGGTCTCGAACTA        :       CCTTTT TAGGCT - -TGCTTGAA	8.01E-2
334. bta-miR-2285bi MIMAT0046389	233	-14.50	GTCTCGAACTACA - CTGGGCTC   :             CGGTTTTTCAAGTAGACCCGAA	8.01E-2
335. bta-miR-2285y MIMAT0029944	2214	-11.90	TCTTGCAATTTGCATGGGTTTT           TTTTTTCAAACAAACCCAAAA	2.61E-1
336. bta-miR-2284ab MIMAT0030437	5797	-13.00	AAAAATTTGAAACAAACTTTTA     : :       TTTTTGGGTT - GGTGTGAAAT	2.39E-2



1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
337. bta-miR-2284ab MIMAT0030437	7546	-9.10	TATAAACCAGGTAATACTTTTA    : :         TTTTTGGGTGGTT-TGAAAAT	2.94E-1
338. bta-miR-2463 MIMAT0012050	8808	-13.90	GTTGCACTTTATTACACATGCAC :      :       GTCTGTAAAG-GTGGTGTACGTC	1.54E-1
339. bta-miR-940 MIMAT0009386	9261	-12.10	TAAAGGT-TTAGCACAGCCTG :  :          CGCCTCGCCCCGGGTCGGAA	2.28E-1
340. bta-miR-2284ab MIMAT0030437	9693	-8.30	AATGGCTCTTACT--ACTTTTA ::  :   :       TTTTTGGG-TTGGTTTGAAAAT	1.98E-1
341. bta-miR-10020 MIMAT0040419	14821	-10.50	TTAATAAATTTGAAAAGCCAG  : :        GCGGTACAAGGTTTCTTCGGTG	6.08E-3
342. bta-miR-2463 MIMAT0012050	15413	-7.30	TGTATGTGCTTTAATGTCATGCAA  :    :         GTCTGTA-AAGGT-GGTGTACGTC	7.31E-2
343. bta-miR-10020 MIMAT0040419	16602	-12.84	GAGATTGAAAAAGTGAAGCCAC          GCGGTACAAGGTTTCTTCGGTG	3.48E-1
344. bta-miR-2428 MIMAT0011998	17010	-18.80	GTATACACTGCG-GCCAGCCA    :  :       TGGAGGCGGCGTGAGGTCGGT	3.2E-1
345. bta-miR-2463 MIMAT0012050	17016	-16.90	ACTGCG--GCCAGC-CATGCAG :  :             GTCTGTAAAGGTGGTGTACGTC	3.2E-1
346. bta-miR-30f MIMAT0009282	17149	-8.20	CCACTCGTAAGTA-TGTGTTTACT            TCGACTCTCACATCCCACAAATGT	3.39E-1
347. bta-miR-12038 MIMAT0046733	17730	-15.20	ATATATTCACAG--ACTGCAGA :  :              TCCGTGACTGTCTGAAGACGTCT	1.09E-1
348. bta-miR-2463 MIMAT0012050	19147	-11.40	TGTATGTTAACA-AACATGCAT  :               GTCTGTAAAGGTGGTGTACGTC	3.16E-1
349. bta-miR-329b MIMAT0009289	20107	-13.00	GTAATGATGCTCTGGCAACCTCC    :  :   :       TTTGTCTTTGGGTCTTTTGGAGA	2.82E-1
350. bta-miR-760-5p MIMAT0009372	21548	-9.54	TCCAATTACCCAGTTTGAGGGT   : :       GCCCAGACCACCTGACTCCCC	1.45E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
351. bta-miR-940 MIMAT0009386	21657	-13.70	GCTATGCTGGATATTCAGCCTG       :       CGCCTCGCCC - CCGGGTCGGAA	2.25E-1
352. bta-miR-2285cc MIMAT0046652	25627	-7.60	TCTAATGGTAATCTCTATGGTTTAA                 AGTTTTCCA - -AGTAAGTCCAAAAA	2.65E-1
353. bta-miR-2285n MIMAT0025531	25628	-7.00	CTAATGGTAATCTCTATGGTTTAA   :    :             GGTTTTCA - -AGTAAGCCCAAAAA	2.65E-1
354. bta-miR-11994 MIMAT0046647	26803	-8.40	AACTTATTGCA - ACAACTCTCT :          GTAGGTCTTGTCCCTTGAGAGT	3.34E-1
355. bta-miR-12038 MIMAT0046733	30660	-12.50	AAGAGTAGAGAGTTGACTGCAGA    :       TCCGTGACTGTCTGA - AGACGTCT	1.28E-1
356. bta-miR-940 MIMAT0009386	30671	-16.10	GTTGACTGCAGAGGACATCAGCCTT   :          :       CGCCT - -CGCCCC - -GGGTCGGAA	1.28E-1
357. bta-miR-3154 MIMAT0025529	30675	-15.60	ACTGCAGAGGACATCAGCCTTCTT                  AGACG - AGGCTG - AG - GGGAAGAC	1.28E-1
358. bta-miR-2440 MIMAT0012015	2860	-9.90	AATACTATTTTAAACACTGCA   : :       AGGTCCCAGAGT - AGTGACGT	1.36E-1
359. bta-miR-7859 MIMAT0030434	3429	-11.10	TTGCTGGTTGCGATCAGTTTTG    :       AATGTACTTCGACGGTCAAAAA	1.22E-2
360. bta-miR-11986b MIMAT0046621	3639	-5.90	GCAGTGTGTTGCATACTGGAAAT    : :       TTTCCTG - ATTGAGTAACCTTTT	3.34E-1
361. bta-miR-10174-3p MIMAT0040928	3653	-12.70	ACTGGAATGC - ATTAAATGTGAT               GCACCATTAGGGACCGTTACACTA	3.34E-1
362. bta-miR-22-3p MIMAT0012536	3840	-12.40	TAGTGTGTACAA - -AGCAGCTT :               GTCA - AGAAGTTGACCGTCGAA	1.11E-1
363. bta-miR-7859 MIMAT0030434	4808	-11.00	ATATATGCAGCCAGGATAAAGTTTTT    :               AATGTACTTCG - -AC - -GGTCAAAAA	3.16E-1
364. bta-miR-186 MIMAT0003818	5091	-8.30	GGCT - GTAAG - -AAGTTCTTTT :    :     :       TCGGGTTTTCTCTTAAGAAAC	1.95E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
365. bta-miR-2285cw MIMAT0046702	5795	-11.70	TTAAAAATTTGAAACAAACTTTT    :::          TCTTTTGGACTT-GATTGAAAA	2.39E-2
366. bta-miR-2284l MIMAT0011824	5797	-12.00	AAAAATTTGAAACAAACTTTT    :::          TTTTTGGGCTT-GGTTGAAAA	2.39E-2
367. bta-miR-155 MIMAT0009241	6793	-8.10	GTTGCTA--GAGGTGCTTGCAATTAT ::       :           TGGGGATAGTGCTA--ATCGTAATT	3.52E-1
368. bta-miR-2377 MIMAT0011923	8254	-13.90	TCTGCTAAG-CATGTGCAGG   :              TCTCGGATCCAGACACGTCA	3.07E-1
369. bta-miR-7859 MIMAT0030434	8449	-12.20	CTTAAAGGGGGTGC-AGTTTTT  ::              AATGTACTTCGACGGTCAAAAA	3.29E-1
370. bta-miR-302b MIMAT0009280	8794	-10.30	TATGGTTACCATGTGTTGCACTTT               GATGATTTTGTAC-CTTCGTGAAT	1.54E-1
371. bta-miR-2377 MIMAT0011923	8833	-14.40	TCTGCTGATGG--AGTGCAGT   :              TCTCGG-ATCCAGACACGTCA	1.54E-1
372. bta-miR-494 MIMAT0009334	9597	-10.30	ATATATATCTGTTGT-TGTTTCA : :                CTCCAAAGGGCA-CATACAAAGT	6.88E-2
373. bta-miR-186 MIMAT0003818	9732	-11.20	TTGTAAGCTTAAGAATTCTTTG                 TCGGGTTTTCTCTTAAGAAAC	2.82E-1
374. bta-miR-562 MIMAT0009349	10068	-8.10	ACATGTGATATGTTCTGCTTC :       :           CATTTACCATG-TCGACGAAA	1.75E-1
375. bta-miR-2284ac MIMAT0030447	11758	-9.00	CTTAATTGCT-TGC-AACATTT       :              CCTTTTTTCGGTTCGCTTGTAAC	3.25E-1
376. bta-miR-302b MIMAT0009280	11800	-9.90	TTGTGGCAATATTGTAGCACTTT   :                GATGATTTTGTACCTTCGTGAAT	6.2E-2
377. bta-miR-2459 MIMAT0012044	11834	-10.30	TACTTGCCACTTCTGATCTGGG       :             TTAGTCGAGGG-TAGTAGACCG	6.2E-2
378. bta-miR-429 MIMAT0009315	11918	-14.70	ATAGCAAGTGCTGACTAGTATTG       :              TGCCGT-AATGGTCTG-TCATAAT	1.75E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
379. bta-miR-656 MIMAT0009361	11993	-6.80	AGAG--TGAATTTGT-TAATATG                    TCTCCAAC--GACATATTATAA	2.39E-1
380. bta-miR-562 MIMAT0009349	12113	-8.40	GTAATATTGCTAAATCTGCTTA                    CATT--TACCATGTCGACGAAA	3.46E-2
381. bta-miR-2917 MIMAT0012885	13304	-9.60	ACACTACTGTTTCAGTCAA  :            TCAGGT-ACA-GTCAGTA	3.12E-1
382. bta-miR-155 MIMAT0009241	14842	-18.60	GGCTCTATTATGA--AGCATTAT : :    : :        TGGGGATAGTGCTAATCGTAATT	6.08E-3
383. bta-miR-190a MIMAT0009251	15778	-6.90	ACGATGTCTATCTTCCATATCC            TGGATTATATAGTTTGTATAGT	2.69E-1
384. bta-miR-186 MIMAT0003818	16155	-9.20	TGCATCAGAAAGCCTCTTCTTTG   : :            TCG-GGTTTCTCTTAAGAAAC	5.43E-2
385. bta-miR-10166-5p MIMAT0040913	16157	-10.29	CATCAGAAAGCCTCTTCTTTGCTGCAA                 GT-GTC--AGACACTAG--TCGACGTG	5.43E-2
386. bta-miR-494 MIMAT0009334	16217	-11.00	TAAATATGTTTGTAGTGTTTCA   :      CTCCAAAGGGCACATACAAAGT	1.69E-1
387. bta-miR-10174-3p MIMAT0040928	16245	-10.40	GTGTGTAACGCACCAGG--ATGTGAT                GCACCATT--AGGGACCGTTACACTA	1.36E-1
388. bta-miR-155 MIMAT0009241	17834	-9.00	GCAGTTGTT-TGA--AGCATTAC : : : :        TGGGGATAGTGCTAATCGTAATT	2.98E-1
389. bta-miR-190a MIMAT0009251	19601	-7.40	TATTAATA-ATACAACATATCC :           TGGATTATATAGTTTGTATAGT	5.58E-3
390. bta-miR-574 MIMAT0024577	20365	-24.00	CATACGACTC-CA-GCATACTCT  :         : :        GTGTG-TGAGTGTGTGTGTGAGT	1.89E-1
391. bta-miR-24 MIMAT0009250	20831	-16.30	ACCGGGTCTGCAGTTC-TTAGGCAG   :     :        TG-ACTA--TAGTCGAGTCATCCGTG	2.78E-1
392. bta-miR-2486-5p MIMAT0012081	21585	-9.10	AAAGGTTTACAATTTCAACTTCTCG : :            GGGTGGGATGT--GGCACGAAGAGG	1.34E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
393. bta-miR-494 MIMAT0009334	24196	-11.10	TGGGATACAGGTGT-TGTTTCC         CTCCAAAGGGCACATACAAAGT	3.8E-1
394. bta-miR-10174-3p MIMAT0040928	24226	-11.40	AAGCGTAATTTTCACATATGATGTGAA         :     GCACCATTAGGG--ACCGTTACACTA	1.36E-1
395. bta-miR-2285bo MIMAT0046627	24684	-9.10	GGAAC--GTAAGACCTTTTCA :            TTTTGAGCTTGCTTGAAAAGT	2.18E-1
396. bta-miR-656 MIMAT0009361	24750	-5.00	CTCATTTACTTGTAATAATATT :         TCTCCAACGACAT-ATTATAA	1.75E-1
397. bta-miR-494 MIMAT0009334	24933	-9.40	TAATTTACCTGCTGCTAATGTTTCT    :        CTCCAAAGGGC-AC--ATACAAAGT	9.48E-2
398. bta-miR-2440 MIMAT0012015	26508	-10.70	CAAAGTGTTGCCTCCACTGCT       :        AGGTCCCAG-AGTAGTGACGT	2.42E-2
399. bta-miR-2377 MIMAT0011923	26971	-9.30	CTAGTAAAATTTAGTGCAGC    :    :     TCTCGGATCCAGACACGTCA	3.43E-1
400. bta-miR-365-5p MIMAT0012539	27139	-14.44	GTCA-CTGCGAAGGTTAGTCCCG            GTGTAGACGGGGTTTTTCAGGGA	2.14E-1
401. bta-miR-2284ac MIMAT0030447	27324	-9.50	GCCGGATGTAATGCTGAACATTT   :        CCTTTTTTCGGTTCG-CTTGTA	6.88E-2
402. bta-miR-10174-3p MIMAT0040928	27764	-12.10	ATATTACATCCCTTCAATCATGTGAA             GCACCATTAGGGA--CCGTTACACTA	2.11E-1
403. bta-miR-2285cw MIMAT0046702	28048	-11.30	AGGTAGACCT--TATAACTTTA    :    :         TCTTTTGGACTTGATTGAAAA	2.5E-1
404. bta-miR-2284l MIMAT0011824	28050	-9.10	GTAGACCT--TATAACTTTA   :     :     TTTTTGGGCTTGTTGAAAA	2.5E-1
405. bta-miR-155 MIMAT0009241	28053	-12.50	GACCTTATAACTTTAAGCATTAT    :            TGGGGATAGTGCTAATCGTAATT	2.5E-1
406. bta-miR-2459 MIMAT0012044	28102	-11.90	CCCTAGTAATGGACATCTGGA :    : :     TGTGCGAGGGTAGTAGACCG	3.03E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
407. bta-miR-2284ac MIMAT0030447	28673	-5.30	ACGTTTAGTTAATCCAAACATTA   :          CCTTTTTCGGTT-CGCTTGTAAG	1.64E-1
408. bta-miR-10174-3p MIMAT0040928	29196	-8.40	TCAGATTTGCC--AGCTTATGTGAC           GCACCATTAGGGACCG-TTACACTA	2.11E-1
409. bta-miR-656 MIMAT0009361	29365	-5.70	CATTGTTGA-GAAATAATATC                 TCTCCAACGACATATTATAA	3.85E-1
410. bta-miR-2486-5p MIMAT0012081	29529	-15.60	CCCA-AGCAAACGCTACTTCTCA           :           GGGTGGGATGTGGC-ACGAAGAGG	7.91E-3
411. bta-miR-365-5p MIMAT0012539	29654	-22.20	GCCTATTGC-ACCAGGAGTCCCA :         :           GTGTAGACGGGGGTTTTTCAGGGA	2.69E-1
412. bta-miR-8549 MIMAT0037488	30056	-14.70	CAACAGAACCC-CCTACCTC                 TATG--GTGGATGATGGAG	2.94E-1
413. bta-miR-2377 MIMAT0011923	30383	-14.44	AGAGTTGGCCAAAGTGCAGA         : :           TCTCGGATCCAGACACGTCA	1.09E-1
414. bta-miR-656 MIMAT0009361	30606	-5.90	GGAG--AAAATG-ATAATATA :                     TCTCCAACGACATATTATAA	4.57E-2
415. bta-miR-211 MIMAT0009263	30937	-10.20	GCCGAACAAGTGCCCAAGGGAA   :     :               CCGTTT-CCTACTGTTTCCCTT	6.29E-2
416. bta-miR-1179 MIMAT0009957	1309	-6.10	GATGCAGTTG--TAAATGCTT :                 GGTTGGTTACTTTCTTACGAA	3.57E-1
417. bta-miR-2464-5p MIMAT0012051	5103	-8.30	TTCTTTTAATTTTG-ATCAGAAGG   :     :               CAGAAGGTCCAGACGTCGTCTTCA	9.05E-2
418. bta-miR-2285cl MIMAT0046681	5797	-8.90	AAAAATTTGAAACAAACTTTT         : : :             TTTTTGGGCTT-ACTTGAAAT	2.39E-2
419. bta-miR-7691 MIMAT0029952	6273	-11.70	TGGT--GGTGATATCTCAGA   :       :           ATCAATAATCTGGAGAGTCG	3.52E-1
420. bta-miR-1179 MIMAT0009957	7708	-8.10	ACATATGATGATGTTAATGCTA     : :                 GGTTGGTTACT-TTCTTACGAA	2.18E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
421. bta-miR-2285cu MIMAT0046698	9615	-10.26	TTCAAATCATGCTTTTGGGTAT :        :       CGGTTT-TCCAAGCAGACCCATA	6.88E-2
422. bta-miR-12057 MIMAT0046764	10046	-13.00	GTGATAAGGTCTACTGTCCCAGA    :          CCGAGAGGAAGGTG--AGGGTCA	1.75E-1
423. bta-miR-677 MIMAT0012003	10162	-12.20	CGTCTAAGC--CTTA-CAGTGAT       :         CAGTCTTCGACGAGTAGTCACTC	3.56E-2
424. bta-miR-503-5p MIMAT0025557	10562	-12.00	TAGCATGGCTTTATGCTGCTA :      :    : :       GTCATG-ACAAGGCGACGAT	8.51E-2
425. bta-miR-2372 MIMAT0011917	16121	-9.80	CTGCTC-TTCTCAAACATCATTA :   :    :       ACTGGGTTAGG-AAAGTAGTAAG	5.43E-2
426. bta-miR-483 MIMAT0009327	17104	-13.90	CCAAGGTCAGG-GTGGAGTGC             TTCTGCCCTCCTCTCCTCACT	3.76E-1
427. bta-miR-2388-3p MIMAT0011941	17778	-13.60	TTCAATGTTGCTATTACTCGAGC             AGTAGAGGTCCA--AGGAGCTCG	2.86E-1
428. bta-miR-323 MIMAT0009284	19038	-11.30	ATGTTTGGAACTGTAATGTGG   : :       TCTCCAGCTGGCACATTACACG	2.42E-1
429. bta-miR-2285br MIMAT0046636	19389	-11.11	ACAG-CTACTACAGCAGGTTTT             TGTCTTTCAAGTAAGTCCAAAA	3.12E-1
430. bta-miR-1814c MIMAT0011984	19876	-10.60	TTTACATTTCCACGACAAAAG     :    :       TTTTGTTTGGGT-TTGTTTTG	3.48E-1
431. bta-miR-2464-5p MIMAT0012051	20262	-8.30	GTTT--ATGGTAATTTCAACCAGAAGA    :              CAGAAGGTCCA--GACGT-CGTCTTCA	1.95E-1
432. bta-miR-451 MIMAT0009323	21151	-10.50	ATTTTGCATTTTGG--ACGGTTT             TTTGAGTCATTACCATTGCCAAA	2.01E-1
433. bta-miR-1179 MIMAT0009957	21172	-7.50	TCTGCACAAATG--CAAAATGCTT :   :             GGTTG--GTTACTTTCTTACGAA	2.01E-1
434. bta-miR-503-5p MIMAT0025557	24930	-16.70	TTATAATTTACCTGCTGCTA    :       GTCATGACAAGGCGACGAT	9.48E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
435. bta-miR-2285cl MIMAT0046681	25659	-5.40	CTTAAC-AAACAGAACTTTT           TTTTTGGGCTTACTTGAAAT	7.54E-2
436. bta-miR-2464-5p MIMAT0012051	26193	-8.50	TAATGCTA-TACT-CA-CAGAAGT  :           CAGAAGGTCCAGACGTCGTCTTCA	4.38E-2
437. bta-miR-502a MIMAT0009338	27152	-17.50	TTAGTCCCGGTCT--GTGCATT  :     :        ACTTAGGAACGGGTCCACGTAA	2.14E-1
438. bta-miR-2285cl MIMAT0046681	28050	-8.10	GTAGACCT-TAT-AACTTTA  :   :          TTTTTGGGCTTACTTGAAAT	2.5E-1
439. bta-miR-7691 MIMAT0029952	28154	-9.90	CGGTT-TTA-ATGTCTCAGA :         :       ATCAATAATCTGGAGAGTCG	3.71E-1
440. bta-miR-148c MIMAT0016933	29044	-5.10	TCAACCCAGAAACAAACAACTTGA                 AGTCACGT-ACTGT--CTTGAACC	3.15E-2
441. bta-miR-7691 MIMAT0029952	29534	-16.00	GCAAACTGCTACTTCTCAGC   :      ATCAATAATCTGGAGAGTCG	7.91E-3
442. bta-miR-12057 MIMAT0046764	29660	-10.10	TGC--ACC-AGGAGTCCCAGC               CCGAGAGGAAGGTGAGGGTCA	2.69E-1
443. bta-miR-12026 MIMAT0046719	29849	-18.50	CCAGGCTGATGTCAATACCCCGGC       :          GGACCGG--TC-GT-CAGGGGCCC	1.98E-1
444. bta-miR-2464-5p MIMAT0012051	30195	-6.40	TTGAATAAGCCCCGC--CAGAAGA               CAGAAGGTCCAGACGTCGTCTTCA	5.91E-3
445. bta-miR-148c MIMAT0016933	30288	-8.50	GGAG-AAATGTTAAACTTGG       :        AGTCACGTACTGTCTTGAACC	4.98E-2
446. bta-miR-2285ck MIMAT0046676	30373	-11.30	GATCAAGATTAGA-GTTGGCCA           TGACTTTGTTTCTAAAACCGGT	1.09E-1
447. bta-miR-2439-3p MIMAT0012014	2546	-10.00	TAAAAGGTTCTG-GTTCTGATT :          AGACGGATGGACAGAAGACTAT	2.65E-2
448. bta-miR-34c MIMAT0003854	3448	-14.00	TTGGCAGTGATGCAGAACTGCCC    : :        GTTAGTCG-ATTG-ATGTGACGGA	1.22E-2



1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
449. bta-miR-495 MIMAT0009335	3523	-8.50	CAGTATAGT-CAGT-TGTTTGTTG           :       TTC--TTCACGTGGTACAAACAAA	2.58E-1
450. bta-miR-2284a MIMAT0011906	5797	-8.50	AAAAATTTGAAACAAACTTTT      :::           TTTTTGGG-GTTGCTTGAAAA	2.39E-2
451. bta-miR-6528 MIMAT0025562	6174	-14.50	CCATGAGCAAGCTTCCCTCA            GGAGGAAGGGAGAAGGGAGA	3.34E-1
452. bta-miR-2285dk MIMAT0046749	7190	-7.69	TGTTTGCTCTTATTAGTATTCAGA   : :    TCAACCGGTTTACAAGTAAGTCC	2.98E-1
453. bta-miR-495 MIMAT0009335	7488	-11.40	TAATGGTGGCACTGGCTTTTGTTT :        ::       TTCTTCAC-GTGGT-ACAAACAAA	2.95E-2
454. bta-miR-2439-3p MIMAT0012014	7878	-7.84	AATGGTTGATAAAAAATCTGATA    : :       AGACGGATGGACAGAAGACTAT	3.48E-1
455. bta-miR-19a MIMAT0004336	8794	-8.20	TATGGTTACCATG-TGTTGCACT    :       AGTCAAAACGTATCTAAACGTGT	1.54E-1
456. bta-miR-302d MIMAT0009279	8796	-10.30	TGGTTACCATGTGTTGCACTTT              TGATTTTGTAC-CTTCGTGAAT	1.54E-1
457. bta-miR-302d MIMAT0009279	8815	-7.70	TTTATTACA--CATGCACTTT :              TGATTTTGTACCTTCGTGAAT	1.54E-1
458. bta-miR-2370-5p MIMAT0011914	9499	-14.30	TATGCCACGCTTT--ATTTCCCT :     :           TATTGGT-TGAAAGTAAAAGGGT	3.48E-1
459. bta-miR-2439-3p MIMAT0012014	10664	-9.10	TTAGCCAAGTT-AAGTCTGATC       :        AGACGGATGGACAGAAGACTAT	3.07E-1
460. bta-miR-2317 MIMAT0011838	11434	-12.70	GTGAATGTTTTGTATTTACAGAT              ATAGTCCATAACA-GTAGTGCTC	8.26E-2
461. bta-let-7g MIMAT0003838	11446	-12.90	TATTTACAGAT--ATACCTCA    : :       TTGACATGTTTGATGATGGAGT	8.26E-2
462. bta-miR-302d MIMAT0009279	11802	-9.90	GTGGCAATATTGTAGCACTTT   :          TGATTTTGTACCTTCGTGAAT	6.2E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
463. bta-miR-19a MIMAT0004336	11805	-12.50	GCAATATTGTAGCACTTTGCACA    :        AGTCAAACGTATCTAAACGTGT	6.2E-2
464. bta-miR-2439-3p MIMAT0012014	11832	-15.30	AATACTTGCC - - ACTTCTGATC  : :        AGACGGATGGACAGAAGACTAT	6.2E-2
465. bta-miR-12027 MIMAT0046720	13168	-14.10	GGGTTGTGCAAATTACGCGGCA    :       TGTGGTCCCTTTGTCGCGCCGT	1.34E-1
466. bta-miR-2414 MIMAT0011977	13913	-10.00	AGGCTTAGTAGGCATTTTAACACT ::  :     :       ATTGTGGTAGGCGTG - - ATTGTGT	3.29E-1
467. bta-miR-495 MIMAT0009335	14308	-15.10	TGGATGGTGTGCC - - TTTTGTGTG :    :             TTCT - TCACGTGGTACAAACAAA	3.62E-1
468. bta-miR-2317 MIMAT0011838	17721	-9.84	GATTATGTTATATATTACAGAC   :           ATAGTCCATAACAGTAGTGTCTC	1.09E-1
469. bta-miR-2347 MIMAT0011882	18856	-15.10	TTAAAGCTGCCATGCTCTGCA    :         CAAGTCGGAACAAGGAGACGT	6.11E-2
470. bta-miR-19a MIMAT0004336	20411	-9.10	TGGTGGTAGTAAGAGTGTTCGCACT  :     :    AGTCAAACGT - ATC - TAAACGTGT	2.21E-1
471. bta-miR-2285u MIMAT0031094	21192	-9.20	TCTTCTAGTGAAGGGTTTTTA          TTTCAAGCA - AGCCAAAAAG	2.01E-1
472. bta-miR-19a MIMAT0004336	21871	-10.80	CCAGGAAATGGATTGGACATTGCACC          :        AGTC - AAAACGTA - TCT - AAACGTGT	2.65E-1
473. bta-miR-2285da MIMAT0046707	22028	-7.44	TGAAAAG - - AAAGATGGTTTTT :             TTTTTTC AAGTAAGTCCAAAAG	6.99E-2
474. bta-miR-660 MIMAT0004344	22107	-15.50	AAGCT - AGCTATGATTATGGGTT                 GTCGAGGCTATAC - GTTACCCAT	3.48E-1
475. bta-miR-1256 MIMAT0009960	23221	-10.80	TTCACGGTGGAA - - CAATGCCA   :          TAGATCTCTCTTCAGTTACGGA	1.89E-1
476. bta-miR-2439-3p MIMAT0012014	23230	-7.80	GAACAATGCCAGGCAGTCTGATA            AGACGGATGGAC - AGAAGACTAT	1.89E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
477. bta-miR-2450b MIMAT0012029	23608	-8.30	TAGGCTGCATGATGCTTAGACCATA  :             GTGTACGTGGAGATGA - - CTGGTAC	3.29E-1
478. bta-miR-2285dk MIMAT0046749	24722	-10.50	GCAGCCTGATGTCTTTTATTTCAGG   :       TCAACCGGTTTACAAAGTAAGTCC	1.75E-1
479. bta-miR-2285u MIMAT0031094	25026	-5.30	TCAACCTGT-AGGTGTTTTTA :                   TTTCAAGCAAGCC- CAAAAAG	2.46E-1
480. bta-miR-2393 MIMAT0011946	25250	-5.60	ACCCCATTTACATCTAAATCTA              TTTTCTTTTGT- TTTTATAGAT	1.04E-1
481. bta-miR-2893 MIMAT0013851	26506	-14.30	ATCAAAGTGTT- GCCTCCAC :       :             GGGGCCCGTAAGAGGAGGTG	2.42E-2
482. bta-miR-2347 MIMAT0011882	26555	-18.20	CTTTGGCT- GCCACCTCTGCT        :          CAAGTCGGAACAAGGAGACGT	3.46E-2
483. bta-miR-2284a MIMAT0011906	28050	-9.50	GTAGACCTTA- - TAACTTTA  :    : :           TTTTTGGGGTTGCTTGAAAA	2.5E-1
484. bta-miR-495 MIMAT0009335	28826	-18.60	TACAAGTCGCAGTATGTTTGTTT            :       TTCTTCA- CGTGGTACAAACAAA	1.04E-1
485. bta-miR-599 MIMAT0009354	29694	-12.10	TACTGGTA- - CAGACACAAC   :             CAAACATTTGACTGTGTTG	2.01E-1
486. bta-miR-6122-5p MIMAT0024594	29730	-9.10	GCCGATGGCAACCAGCGTCAACTGC                          CG- TGACC- TATTTC- ATGTTGACT	1.11E-1
487. bta-let-7g MIMAT0003838	30052	-17.10	CTGGCAACAGAACCCCTACCTCT    :            TTGACATGTTT- GATGATGGAGT	2.94E-1
488. bta-let-7d MIMAT0003810	30054	-16.20	GGCAACAGAACC- CCTACCTCT              TTGATACGTTGGATGATGGAGA	2.94E-1
489. bta-miR-2414 MIMAT0011977	30065	-12.10	CCCTACC- TCTGGTGTAACACC :         :            ATTGTGGTAGGCGTGATTGTGT	2.94E-1
490. bta-miR-2411-3p MIMAT0011973	2496	-8.30	TTTAACCATGCCTAGTCAAGTTCAGA                   CCTACACCCTCATTCCTGT- CAAGTCG	2.65E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
491. bta-miR-10a MIMAT0003786	4286	-14.50	CTGATGCGAGGA - C - ACAGGGTA             GTGTTTAAGCCTAGATGTCCCAT	1.75E-1
492. bta-miR-320a MIMAT0003534	5711	-11.40	GTGAACAGTCTTATCAGCTTTA :       :       AGCGGGAGAGTTGGGTCGAAAA	1.62E-1
493. bta-miR-2284n MIMAT0011846	5797	-10.70	AAAAATTTGAAACAAACTTTTA       : :           TTTTTGGGCTT - ATTTGAAAAA	2.39E-2
494. bta-miR-2284c MIMAT0011926	5798	-8.90	AAAATTTGAAACAAACTTTTA       :             TTTT - GGTTTGTCTTGAAAAA	2.39E-2
495. bta-miR-320a MIMAT0003534	6738	-7.20	TAAGCTTGTAGCTTTAGCTTTT : :         AGCGGGAGAGTTGGGTCGAAAA	4.7E-2
496. bta-miR-2284c MIMAT0011926	6928	-6.80	TGGATTAAGA - ACACCTTTTA : :   :         TTTTGGTTTTGCTTGAAAAA	2.28E-1
497. bta-miR-371 MIMAT0009301	7478	-20.80	ATGCT - ATGGCTAATGGTGGCACTG :     : :       :         TGTGAGTTTGTG - - TACCGCCGTGAA	2.95E-2
498. bta-miR-2284n MIMAT0011846	7546	-6.80	TATAAACCAGGTAATACTTTTA     :           TTTTTGGGCTTATT - TGAAAAA	2.94E-1
499. bta-miR-2284c MIMAT0011926	7548	-8.30	TAAACCAGGTAATACTTTTA       : :         TTTTTGGTTTTGCTTGAAAAA	2.94E-1
500. bta-miR-2285aa MIMAT0030435	8447	-12.50	GTCTTAAAGGGGGT - GCAGTTTT   : :                 CGGGTTTTCAAGCAAGGTCAAAA	3.29E-1
501. bta-miR-2284n MIMAT0011846	9693	-5.40	AATGGCTC - TTAATACTTTTA : :   :         TTTTTGGGCTTATTGAAAAA	1.98E-1
502. bta-miR-2447 MIMAT0012024	10050	-17.00	TAAGGTC - TACTG - - TCCCAGA :   :     :           TCGTCGGTTTGGCCAAGGGTCT	1.75E-1
503. bta-miR-2411-3p MIMAT0011973	10515	-7.54	GGTTGT - - CCAATTGCCCCTCAGG                 CCTACACCCTCATTCTGTCAAGTCG	8.51E-2
504. bta-miR-2355-3p MIMAT0011892	11367	-9.70	TGGTACTTACA - CATGGACAAC                 TAGAGGTTTGTCTTCCTGTTA	1.86E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
505. bta-miR-2355-3p MIMAT0011892	11952	-13.20	CGACGATTAC-GCAAAGGACAAT               TAGAGGTTTGTCTT-CCTGTTA	2.39E-1
506. bta-miR-1251 MIMAT0009963	12086	-16.50	AGCAGTT-AAAACAGCTAGAGA      :       TCG-CGGAAACCGTCGATCTCA	3.46E-2
507. bta-miR-2401 MIMAT0011958	12275	-15.50	GTAAGTTAGATAATCAAGCTCT :    :         GTCGGGATCTGT--GTTTCGAGA	2.14E-1
508. bta-miR-22-5p MIMAT0003826	14334	-13.50	ATTGGCT-ACCATTATAAAGAACT :        :         ATTTCGAACGGTGA--CTTCTTGA	3.9E-1
509. bta-miR-320a MIMAT0003534	14425	-18.50	ATGCT-GCT-GATCCAGCTTTG :  :     :       AGCGGGAGAGTTGGGTCGAAAA	7.54E-2
510. bta-miR-22-5p MIMAT0003826	16055	-6.10	TGAGTCCTTTTAC--AAGAACA : :          ATTTCGAACGGTGACTTCTTGA	3.52E-1
511. bta-miR-708 MIMAT0009367	16793	-15.20	AGTAGCTAATTTAAGTGCTCCTA :               GGGTCGATCTAACATTCGAGGAA	1.34E-1
512. bta-miR-654 MIMAT0009359	16864	-6.70	ATAGTG-TG-CTTG-AGACATT                TTCCACTACCAGTCGTCTGTAT	2.82E-1
513. bta-miR-2355-3p MIMAT0011892	18194	-15.40	CACGCGTGATAGCATTGGGACAAA :  :     :       TAGAGGTTTGTCTT--TCCTGTTA	2.5E-1
514. bta-miR-708 MIMAT0009367	18308	-15.70	AAAGGCTGTGGCTAAAGCTCCTC :  : :       GGGTCGATCTAACATTCGAGGAA	2.5E-1
515. bta-miR-2401 MIMAT0011958	18310	-15.10	AGGCTGTGG-CTAAAGCTCC :  :  :         GTCGGGATCTGTGTTTCGAGA	2.5E-1
516. bta-miR-148a MIMAT0003522	20417	-10.90	TAGTAAGAGTGT-TTGCACTGT           TGTTTCAAGACATCACGTGACT	2.21E-1
517. bta-miR-22-5p MIMAT0003826	20989	-7.20	ATGACCCTATTACT-AAGAACA : :           ATTTCGAACGGTGACTTCTTGA	3.8E-1
518. bta-miR-12064 MIMAT0046771	23829	-12.30	GCT--TAATGG-TTACTACCC  :          CGGTGTGATCCTTATGATGGT	2.86E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
519. bta-miR-2402 MIMAT0011959	25173	-15.10	TATAGGCACTTGTCTGCAGGTAC                 ACGACCGT-CTCA--CCGTCCATA	1.89E-1
520. bta-miR-654 MIMAT0009359	25498	-9.20	CAAAAAATCAAACA-CAGACATA          TTCCACTACCAGTCGTCTGTAT	2.95E-2
521. bta-miR-412 MIMAT0009313	27769	-9.00	ACATCCCTTCAATCATGTGAAGC  :          TGTCGATCACCTGGTCCAATTCA	2.11E-1
522. bta-miR-2299-5p MIMAT0011807	29406	-9.20	ACTCCTGGTAAGCAATCCAGT    :        AAAGTCTCTTTACTTAGGTCA	3.16E-1
523. bta-miR-708 MIMAT0009367	29961	-16.80	GAAGGCTCAGGAAGGTCTGCTCCTA :     :            GGGTCA--TCTAACATTCGAGGAA	2.01E-1
524. bta-miR-2285ag-3p MIMAT0040923	30283	-15.90	GTGGTGGAGAAATGTTAAAACTTGGA  :  :  :          AATCGGTTTTT--CAA--GTGAACCT	4.98E-2
525. bta-miR-2375 MIMAT0011921	227	-19.50	AATACGGTCTCGAACTA-CACTGGG        :       CTAGTCTGGAG--AGGTAGTGACCC	8.01E-2
526. bta-miR-2363 MIMAT0011901	3265	-11.90	GAGACATCTGATTACAAAGTTGA   :       TTTATAAGG-AACTGGTTCAACT	2.65E-1
527. bta-miR-449a MIMAT0009320	3450	-16.90	GGCAGTGATGCAG-AAACTGCC :    :  :       TGGTCG-ATTGTTATGTGACGGT	1.22E-2
528. bta-miR-23b-3p MIMAT0003852	3654	-12.70	CTGGAAATGC-ATTAAATGTGAT                 CACCATTAGGGACCGTTACACTA	3.34E-1
529. bta-miR-2285bk MIMAT0046622	5795	-9.80	TTAAAAATTTGAAACAACTTTT      : :            TCTTTTGTGAG-TTTGCTTGAAAA	2.39E-2
530. bta-miR-374a MIMAT0004342	5893	-8.50	TGTGACGGAGGTAAGTATTATAC            GTGAATAGTCCA-ACATAATATT	6.48E-2
531. bta-miR-12019 MIMAT0046708	6695	-13.30	ATAAAGTAATTTAC--ACCACAGA   :  :          AGACTCG--AGGTGGTAGGTGTCT	1.06E-1
532. bta-miR-2351 MIMAT0011887	7884	-5.70	TGATAAAAAATCTGATAACTAC :  :     :    TTTGT-GTTATGTTATTGATA	3.48E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
533. bta-miR-2284z MIMAT0025559	9610	-7.80	GTTGTTTCAAATCATGCTTTTTG : :          :       TTTTTGGGTTT - GTTTGAAAAAA	6.88E-2
534. bta-let-7a-5p MIMAT0003844	11441	-11.40	TTTTGTATTTACAGATATACCTCA :   :   :             TTGATATG - - TTG - GATGATGGAGT	8.26E-2
535. bta-miR-154b MIMAT0025547	15709	-14.22	AAAATGACATAAAACAATGGACCTCA             : :           GCTTAC - GTG - GTACCTTCTGGAGA	1.15E-2
536. bta-miR-23b-3p MIMAT0003852	16246	-10.40	TGTGTAACGCACCAGG - - ATGTGAT                         CACCATT - - AGGGACCGTTACACTA	1.36E-1
537. bta-miR-2485 MIMAT0012079	18383	-7.50	GGATGTTGTTAGA - CCTAGAAT :   :                 TGATGGACG - TCTAAGATCTTT	2.5E-1
538. bta-miR-2313-3p MIMAT0011830	19029	-17.10	GGTTTGTGTATGTTTTGGAAGTGT     : :   :     :               CCG - - TACGT - CG - CACCTTGACC	2.42E-1
539. bta-miR-25 MIMAT0003853	19305	-10.40	ACTTGC - ATCACAAGATGCAATT :                         AGTCTGGCTCTGTTC - ACGTTAC	2.46E-1
540. bta-miR-2363 MIMAT0011901	19546	-7.80	CCATTATAAATGATAAAGTTGT     :                     TTTATAAGGAAGTGGTTCAACT	1.92E-1
541. bta-miR-2370-3p MIMAT0011915	21498	-14.50	TTAAGAATGG - CAGTTGCTTA                                 ACCTCTTTCCTTTCAACGAAT	1.45E-1
542. bta-miR-346 MIMAT0009297	21501	-21.10	AGAATGGCAG - - TTGCTTATGCAGACA                                 TCT - - CCGTCCGTACG - - CCCGTCTGT	1.45E-1
543. bta-miR-25 MIMAT0003853	21942	-5.70	GATTCATAAACAGCATGCAATT     :                     AGTCTGGCTCTGTT - CACGTTAC	9.19E-2
544. bta-miR-2400 MIMAT0011956	22011	-15.80	ATAGTT - AAGCT - - TGGTGCTGA :     :                         AGTCAGGCTCGACGGACACGACC	6.99E-2
545. bta-miR-124a MIMAT0003811	22664	-8.50	TTTACGCCTTATC - - ATGCCTTT   : :                     GAACCGTAAGTGGCGCACGGAAT	1.24E-1
546. bta-miR-193a-3p MIMAT0003795	24103	-12.80	TTAGAGATCTCTGTTTGCCAGTA                             TGACCCT - GAAACATCCGGTCAA	3.07E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
547. bta-miR-23b-3p MIMAT0003852	24227	-11.40	AGCGTAATTTACATATGATGTGAA         :         CACCATTAGGG - - ACCGTTACACTA	1.36E-1
548. bta-miR-2375 MIMAT0011921	24299	-10.40	ATGCATATTTT-ACAGACACTGGT    : :   :            CTAGTCTGGAGAGGT-AGTGACCC	2.18E-1
549. bta-miR-346 MIMAT0009297	24728	-11.70	TGATGTCTTTTATT CAGGCAGACT      : :              TCTCCG-TCCGTACGCCCGTCTGT	1.75E-1
550. bta-miR-16a MIMAT0009242	24762	-14.40	TAATAATATT - - GATGCTGCTA :                   GTGGTTATAAATGCACGACGAT	1.75E-1
551. bta-miR-2351 MIMAT0011887	24797	-5.70	GTTTTTCCAGCA-TAACTAT :              TTTGTGTTATGTTATTGATA	3.85E-1
552. bta-miR-2351 MIMAT0011887	24875	-7.90	ATTTGCAGTCTTTTAACTAT :    :   :           TTTGTGTTATGTTATTGATA	2.32E-1
553. bta-miR-374a MIMAT0004342	24914	-10.70	CAAGTTGTCAGTTGTATTATAA                   GTGAATAGTCCAACATAATATT	9.48E-2
554. bta-miR-16a MIMAT0009242	24928	-17.90	TATTATAATTTACCTGCTGCTA :   :                     GTGGTTATAAATGCACGACGAT	9.48E-2
555. bta-miR-25 MIMAT0003853	25752	-9.90	TCGGA - - ATATTAAATGCAATT    :    :            AGTCTGGCTCTGTT CACGTTAC	2.5E-1
556. bta-miR-2375 MIMAT0011921	25938	-13.30	TCGTAGAGCGATT-ACCACTGGT :        :         CTAGTCTGGAGAGGTAGTGACCC	2.05E-1
557. bta-miR-12047 MIMAT0046750	26567	-12.40	CCTCTGCTAGTCTGTTTCCTC :             TCCGTTTCCAGGACAAAGGAC	3.46E-2
558. bta-miR-425-5p MIMAT0003832	27000	-10.90	GGAGAAGGTTAATGAATGTGTCAA       :         AGTTGCCC - - TCACTAGCACAGTA	1.75E-1
559. bta-miR-23b-3p MIMAT0003852	27765	-12.10	TATTACATCCCTTCAATCATGTGAA                 CACCATTAGGGA - - CCGTTACACTA	2.11E-1
560. bta-miR-2285bk MIMAT0046622	28048	-5.70	AGGTAGAC-CTTAT-AACTTTA    :   :      :         TCTTTTGTGAGTTTGCTTGAAAA	2.5E-1



1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
561. bta-miR-23b-3p MIMAT0003852	29197	-8.40	CAGATTG GCC - - AGCTTATGTGAC             CACCATTAGGGACCG - TTACACTA	2.11E-1
562. bta-miR-2285bk MIMAT0046622	29371	-5.06	TGAGAAATAATATCTAAACTTTA   :   :       TCTTTTGG - AGTTTGCTTGAAAA	3.85E-1
563. bta-miR-592 MIMAT0009353	29689	-7.70	AGGGGTACTGGTACAGACACAAC :          TGTAGTAGCGTATAACTGTGTTA	2.01E-1
564. bta-let-7a-5p MIMAT0003844	30054	-15.00	GGCAACAGAAC - CCTACCTCT              TTGATATGTTGGATGATGGAGT	2.94E-1
565. bta-miR-12019 MIMAT0046708	30130	-17.50	GCAAGGATGCCACTAAGCCACAGC :       :         AGACTC - GAGGTGGT - AGGTGTCT	2.72E-2
566. bta-miR-12019 MIMAT0046708	30302	-10.60	ACTTGGAAGTAGTGACCCACAGT    :    :         AGACTCGAGGTGG - TAGGTGTCT	4.98E-2
567. bta-miR-12019 MIMAT0046708	30560	-17.90	TATGAG - TCCAAAA - CCACAGC                   AGACTCGAGGTGGTAGGTGTCT	3.66E-2
568. bta-miR-449d MIMAT0011962	30676	-23.60	CTGCAGAGGACATCAGCCTTC                   GAGGTGTCGTGT - GTCGGAAG	1.28E-1
569. bta-miR-12004 MIMAT0046664	30942	-19.40	ACAAGTGCCCAAGGG - AAGAGCCAG         :         TCCTC - CG - TCTCTCGGTCTCGGTC	6.29E-2
570. bta-miR-2397-3p MIMAT0011952	2197	-15.70	TTTACTACTAGC - ACTGCTCTT             TACGCAAGAACGGTGACGAGAC	2.61E-1
571. bta-miR-1434-3p MIMAT0012040	3100	-8.60	CCTGAAGAT - GATGACTTCTTG        :          GGA - GTCTGGAATCT - AAAGAAG	1.72E-1
572. bta-miR-2284q MIMAT0011957	3433	-11.90	TGGTTGCGATCAGTTTGGCA :           AGGCTTGCT - TGAAAAACCGG	1.22E-2
573. bta-miR-2429 MIMAT0011999	4814	-9.00	GCAGCCAGGATAAAAGTTTTT           TTTTTTTCCCTTTTCAAAAA	3.16E-1
574. bta-miR-2285bt MIMAT0046639	5796	-5.70	TAAAAATTGAAACAAACTTTTA   : :          TCTGTTGGGTTT - ACTTGAAAAA	2.39E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
575. bta-miR-200c MIMAT0003823	7186	-5.90	CCATTGTTTGCTCTTATTAGTATTC : :           :      AGGTAGTAATGGG--CCGTCATAAT	2.98E-1
576. bta-miR-2285bt MIMAT0046639	7545	-7.30	TTATAAACCAGGTAATACTTTTA    :                 TCTGTTGGGTTTA-CTTGAAAAA	2.94E-1
577. bta-miR-6120-3p MIMAT0024591	8177	-14.70	GTTGTAATAAC-TTGGTGCCAACATA  : :                                    CGATA--GGTGCAAC--AGGTTGTAT	3.62E-1
578. bta-miR-2429 MIMAT0011999	8449	-12.40	CTTAAAGGGGGTGCAGTTTTT    :   :                  TTTTTTTCCCT-TTCAAAAA	3.29E-1
579. bta-miR-1434-3p MIMAT0012040	9271	-15.50	GCACAG-CCTGTGGATTCTTG            :        GGAGTCTGGA-ATCTAAAGAAG	2.28E-1
580. bta-miR-3120 MIMAT0024572	9312	-25.10	TGCTGGTGCTATACTTGCTGTA    :         :        ACGGACA-GATGTGAACGACAC	2.28E-1
581. bta-miR-2285bt MIMAT0046639	9692	-8.10	AAATGGCTC-TTACTACTTTTA    : :                 TCTGTTGGGTTTACTTGAAAAA	1.98E-1
582. bta-miR-1949 MIMAT0046755	9933	-15.20	AACTTCATTCTTGCAATCTGGTATT                        :        TTGA--TACGACCGTAGGACCATAT	7.65E-2
583. bta-miR-8548 MIMAT0037487	9958	-9.10	GTGAAAATGGTTAATCCTA  :~                 CGTGGTT-CCA-TTAGGAA	7.65E-2
584. bta-miR-12022 MIMAT0046715	10504	-10.80	AAGGATGCTCAGGT--TGTCCAA   :   ::                TTTCAGTGA--ACAGCACAGGTT	8.51E-2
585. bta-miR-195 MIMAT0004335	10560	-14.30	TGTAGCATGGCTTTATGCTGCTA   :    :   :           ACG-GTTATAAAGACACGACGAT	8.51E-2
586. bta-miR-2461-3p MIMAT0012048	10665	-12.50	TAGC-CA-AGTT--AAGTCTGA          :           TCCGTGTGACGAGAGTCAGACT	3.07E-1
587. bta-miR-200c MIMAT0003823	11918	-12.00	ATAGCAAGTGCCTGACTAGTATTG  : :   :      AGGTAGTAATGGGC-CGTCATAAT	1.75E-1
588. bta-miR-2284o MIMAT0012068	14337	-7.64	GGCTACCATTATAAAGAACTTG  :                     CTTTTGG--GGCTTGCTTGAAA	3.9E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
589. bta-miR-3431 MIMAT0017394	16507	-20.30	AAACGCAAAAGGC - GACTGAGG             TGTAGGTGTTCCGACTGACTCC	2.39E-1
590. bta-miR-12022 MIMAT0046715	18677	-13.80	TGATTTATATTGTAGTGTCCAT  : :             TTTCAGTG - AACAGCACAGGTT	2.36E-2
591. bta-miR-2397-3p MIMAT0011952	18852	-20.00	ATGCTTAAAGCTGCCA - TGCTCTG                           TACG - - CAAGAACGGTGACGAGAC	6.11E-2
592. bta-miR-6120-3p MIMAT0024591	19599	-6.39	TTTATT - - AATAATACAACATA  : :       CGATAGGTGCAACAGGTTGTAT	5.58E-3
593. bta-miR-219b-3p MIMAT0040926	20012	-6.70	GGATGTCATCTTCAGC - CAATTCG   :  :        TGACTAACAGG - TTTGCGTTAAGA	7.09E-2
594. bta-miR-6120-3p MIMAT0024591	20749	-8.54	AATATCTGAATACTACAACATT    : :       CGATAGGTGCAACAGGTTGTAT	1.92E-1
595. bta-miR-2429 MIMAT0011999	21445	-7.60	ATACAAATAAAGAAGTTTTT  :        TTTTTTTCCCTTTTCAAAAA	1.45E-1
596. bta-miR-219b-3p MIMAT0040926	21943	-9.70	ATTTCATAAACAGCATGCAATTCA   :  :        TGACTAACAGGTT - TGCCTTAAGA	9.19E-2
597. bta-miR-2461-3p MIMAT0012048	23228	-19.50	TGGAACAATGCCAGGCAGTCTGA                  TCCGTGTGACG - AGAGTCAGACT	1.89E-1
598. bta-miR-3120 MIMAT0024572	23666	-11.00	TACC - AATGGCTTTTGCTGTT         :  :        ACGGACAGATGTGAACGACAC	1.12E-1
599. bta-miR-2284x MIMAT0017395	24682	-9.30	TGGGAACGTAAGACCTTTTCA ::             TTTTGGGCTTGCTTGAAAAGT	2.18E-1
600. bta-miR-195 MIMAT0004335	24760	-15.20	TGTAATAATATT - - GATGCTGCTA   : :              ACG - - GTTATAAAGACACGACGAT	1.75E-1
601. bta-miR-195 MIMAT0004335	24926	-13.30	TGTATTATAATTTACCTGCTGCTA   :               ACG - GTTAT - AAAGACACGACGAT	9.48E-2
602. bta-miR-2284o MIMAT0012068	25654	-8.80	GACTACTTAACAAACAGAACTTT      : :           CTTTTGGG - - GCTTG - CTTGAAA	7.54E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
603. bta-miR-2397-3p MIMAT0011952	26510	-21.20	AAGTGTTCCTCCACTGCTCTC   :           TACGCAAGAACGGTGACGAGAC	2.42E-2
604. bta-miR-2461-3p MIMAT0012048	26558	-16.80	TGGCTGCCAC - - CTCTGCTAGTCTGT             :       TCCG - - TGTGACGAGA - - GTCAGACT	3.46E-2
605. bta-miR-2397-3p MIMAT0011952	26696	-12.50	ATGCATTT - - AACAAATGCTCTT        :          TACGCAAGAACGGTGACGAGAC	1.72E-1
606. bta-miR-12062 MIMAT0046769	27758	-13.00	GACGATATA - TTACATCCCT    :   :       TCACTGTGTCCTGGTAGGGT	2.11E-1
607. bta-miR-193a-5p MIMAT0003794	27781	-17.30	TCATGTGAAGCTAATTATAAGACCCA          :       AGTAGA - - GCGG - - GCGTTTCTGGGT	2.11E-1
608. bta-miR-3120 MIMAT0024572	27829	-10.80	AGCTACCACAATGCCTGCTGTT    :     : :       ACGG - ACAGATGTGAACGACAC	2.25E-1
609. bta-miR-138 MIMAT0003813	29728	-16.30	CAGCC - GAT - GGCA - - ACCAGCG         :          GCCGGACTAAGTGTGTGGTCTGA	1.11E-1
610. bta-miR-219b-3p MIMAT0040926	30033	-9.10	TCGCGTAGT - AGAGC - CAATTCT    :   :       TGACTAACAGGTTTGCGTTAAGA	2.94E-1
611. bta-miR-544b MIMAT0009345	3444	-14.80	AGTTTTGGCAGTGATGCAGAAA :        :       CTTGAACAATCTTTACGTCTTA	1.22E-2
612. bta-miR-2360 MIMAT0011898	3450	-16.10	GGCAGTGATGCAG - AAAGTGCCTT : :     :             TTG - CG - GAGGTCGGAGGACGGGC	1.22E-2
613. bta-miR-2357 MIMAT0011894	4167	-10.72	ACAGCA - GTTTGTTAAAGAGACCAC :      : :       GAGTGTACGAG - ACACGGTCTGGTT	3.62E-1
614. bta-miR-2285db MIMAT0046709	5795	-12.20	TTAAAAATTTGAAACAAACTTTT         :           TCTTTTGTAGACTT - GCTTGAAAA	2.39E-2
615. bta-miR-2285bx MIMAT0046644	5795	-7.70	TTAAAAATTTGAAACAAACTTTT         :           TCCTTTTGTAGCTT - GCTTGAAAA	2.39E-2
616. bta-miR-2284b MIMAT0011983	5797	-8.20	AAAAATTTGAAACAAACTTTT     :           CTTTTGTGGTTTGCTTGAAAA	2.39E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
617. bta-miR-2285am-5p MIMAT0040950	5797	-9.50	AAAAATTTGAAACAAACTTTTA      :        TTTTTGATTT-GATTGAAAAA	2.39E-2
618. bta-miR-27b MIMAT0003546	5986	-14.60	ATAGGAC-ACACCGTCTGTGAT :   :      :     CGTCTTGAATCGGT-GACACTT	2.94E-1
619. bta-miR-147 MIMAT0009237	6908	-11.10	TTGT--TGGTAAGATCGCACAG   : :  :   :     ATCGTCTTCGTAAAGGCGTGTG	2.28E-1
620. bta-miR-2285ch MIMAT0046671	7057	-6.20	GATAATTATAAAG-CCATTGAT           CGACCGGTTTTTCAAGTAACTA	2.42E-1
621. bta-miR-2333 MIMAT0011866	7516	-12.50	CATCAATGGA-ATTGCATTGA       :     CCCCGGACCTCAGACGTAACG	2.95E-2
622. bta-miR-2333 MIMAT0011866	9274	-16.40	CAGCCTGTGGATTTCTTGGCATTGA     :           CCCCGG-ACCT-CAGA--CGTAACG	2.28E-1
623. bta-miR-12008 MIMAT0046675	10400	-10.60	TAATAATGGGTGATTGTGTTAAAT   :           GGGTTTTCTACT-TCTCAATTTT	3.24E-2
624. bta-miR-182 MIMAT0009244	11671	-11.60	CTTTTGGGTATTGGAGGTGTGCCAAT   :    :  : :     TCACACTCAAGATGGT--AACGGTTT	3.07E-1
625. bta-miR-1264 MIMAT0046656	12620	-16.90	ATAGTGGTCCAGATCAGACTTG  :       :        TGTCACGAGTTTATTCTGAAC	2.18E-1
626. bta-miR-2335 MIMAT0011868	14843	-5.90	GCTCTATTATGAAGCATTATCA             TAAGTCAATCAGTAGTAATAGA	6.08E-3
627. bta-miR-3660 MIMAT0025555	15671	-11.40	AAATAACGTTTTTATGTCAGA  :  :   :     AATTTTACGAGAGGACAGTCA	1.45E-1
628. bta-miR-544b MIMAT0009345	17731	-9.70	TATATTCACAGA-CTGCAGAAA          CTTGAACAATCTTTACGTCTTA	1.09E-1
629. bta-miR-490 MIMAT0009331	19259	-22.70	TGGCATGGA-TGCTAAGCAGGTTG :              GTCGTACCTCAGGA--GGTCCAAC	2.46E-1
630. bta-miR-2338 MIMAT0011872	20006	-20.30	GGGTCAGGATGTCATCTTCAGCCA :     : :  :     TGCAGTC-GGGGACAGGAGTCGGA	7.09E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
631. bta-miR-490 MIMAT0009331	20796	-10.90	TTGCATTTAG - -GTGCAGGTTC                 GTCGTACCTCAGGAGGTCCAAC	2.61E-1
632. bta-miR-6534 MIMAT0025570	20832	-14.40	CCGGGTTCTG - CAGTTCTTAGG :           :           TAGGCAGGACTGACGAGAATCT	2.78E-1
633. bta-miR-11980 MIMAT0046368	20844	-15.70	GTTC - TTAGGCAGTGGTTGCCT   :   : :               GAGGCGGTTTCG - -GGCAACGGA	2.78E-1
634. bta-miR-544b MIMAT0009345	21111	-15.40	GAGTTTCTTGGAATGCAGAAT         :               CTTGAACAATCTTTACGTCTTA	3.16E-1
635. bta-miR-2338 MIMAT0011872	21653	-14.60	TCTTGCTATGCTGGATATTCAGCCT :       :           TGCAGTCGGGGAC - -AGGAGTCGGA	2.25E-1
636. bta-miR-2324 MIMAT0011853	21970	-15.90	ATAAAATCACT - -ATCAACCCCT         :           TGTCGGTGTGACGGGGTTGGGGT	9.19E-2
637. bta-miR-2357 MIMAT0011894	23607	-11.80	CTAGGCTGCATGATGCTTAGACCAT       :           GAGTGTACGAGACACGG - TCTGGTT	3.29E-1
638. bta-miR-490 MIMAT0009331	23835	-11.97	TGGTTACTACCCTACTTCAGGTTC :   :     :           GTCG - -TACCTCAGGAGGTCCAAC	2.86E-1
639. bta-miR-299-2 MIMAT0046669	24052	-18.30	GTGGTAGTAC - -AACCACATAC :                       TACCA - AATGGCAGGGTGTATG	1.2E-1
640. bta-miR-182 MIMAT0009244	25360	-9.50	GGTAATCCTTGTA - -TGCCAAC       :           TCACACTCAAGATGGTAACGGTTT	1.16E-1
641. bta-miR-2285db MIMAT0046709	25655	-6.90	ACTACTTAACAAACAGAACTTTT                     TCTTTTGTAGACTTG - CTTGAAAA	7.54E-2
642. bta-miR-2285bx MIMAT0046644	25655	-6.90	ACTACTTAACAAACAGAACTTTT                     TCCTTTTGTAGCTTG - CTTGAAAA	7.54E-2
643. bta-miR-2284b MIMAT0011983	25656	-10.40	CTACTTAACAAACAGAACTTTT                     CTTTTTTGGTTTG - CTTGAAAA	7.54E-2
644. bta-miR-12059 MIMAT0046766	26061	-16.30	TATAGGTA - ATATGGAGGAGT       :             TCCTCCGTCCACCTCCTCT	3.76E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
645. bta-miR-27b MIMAT0003546	26167	-13.60	GAATATGGTAGCTTCTGTGAC    :       CGTCTTGAATCGGTGACACTT	4.38E-2
646. bta-miR-11980 MIMAT0046368	26503	-11.90	GGTATCAAAGT - -GTTGCCT    :       GAGGCGGTTTCGGGCAACGGA	2.42E-2
647. bta-miR-12048 MIMAT0046751	26569	-16.60	TCTG-CTAGTCTGTTTCCTCCTTT       :       AGACCACGAAG-TGGAGGAGGAAC	3.46E-2
648. bta-miR-3660 MIMAT0025555	26577	-11.40	TCTGTTTCCTCCTTTGTCAGC    :       AATTTTACGAGAGGACAGTCA	3.46E-2
649. bta-miR-2474 MIMAT0012065	27142	-15.50	ACTGC-GAAGGTTAGTCCCGGTC      :          AGAGGAAGGTCGACC-GGGCCAT	2.14E-1
650. bta-miR-2333 MIMAT0011866	27153	-21.30	TAGTCCCGGTCTGTGCATTGC  :            CCCGGGACCTCAGACGTAACG	2.14E-1
651. bta-miR-2284b MIMAT0011983	28048	-7.60	AGGTAGACCTTAT-AACTTTA  :       :       CTTTTTTGGTTTGCTTGAAAA	2.5E-1
652. bta-miR-182 MIMAT0009244	28062	-10.80	ACTTTAAGCATTATTAATTGCCAAA    :  :        TCACACTCAAGATGGT-AACGGTTT	2.5E-1
653. bta-miR-3660 MIMAT0025555	29181	-9.50	ACTGGCTATTCTT-TGTCAGA :     :       AATTTTACGAGAGGACAGTCA	2.11E-1
654. bta-miR-2285bx MIMAT0046644	29370	-5.44	TTGAGAAATAATATCTAAACTTTA   :           TCCTTTTTA--GCTTGCTTGAAAA	3.85E-1
655. bta-miR-2285db MIMAT0046709	29371	-5.86	TGAGAAATAATATCTAAACTTTA   :           TCTTTTTA-GACTTGCTTGAAAA	3.85E-1
656. bta-miR-182 MIMAT0009244	29778	-12.10	CTTG-GAACAGGACCGCATGCCAAA         :       TCACACTCAAGATGGT-AACGGTTT	1.83E-1
657. bta-miR-2338 MIMAT0011872	30669	-15.30	GAGTTGACTGCAGAGGACATCAGCCT   :  :         TGCAATCGGGG--ACAGG-AGTCGGA	1.28E-1
658. bta-miR-362-3p MIMAT0012548	3626	-9.80	CCTTATGTGATTGGCAGTGTGTT     :         CTTAGGAAGTTATC--CACACAA	3.34E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
659. bta-miR-2284g MIMAT0011847	5797	-7.30	AAAAATTTGAAACAAACTTTT       :           TTTTTCGGCTT - GCTTGAAAA	2.39E-2
660. bta-miR-2891 MIMAT0013849	6297	-14.20	TGCTAA - AGAACCCAAAGAA :            TTGATTGGATCGGGTTTCTA	7.07E-3
661. bta-miR-199a-3p MIMAT0003746	7884	-10.00	TGATAAAAAATCTGATACTACTGC   : :              ATTG - - GTTACACGTCTGATGACA	3.48E-1
662. bta-miR-2395 MIMAT0011948	8180	-12.79	GTAATAACTTGGTGCCAACAT            CAGACTCTCTCGACGGTTGTC	3.62E-1
663. bta-miR-2315 MIMAT0011835	8240	-13.90	TTCTGATTCAAAA - TTCTGCT    :            GGTCATAGGTTTTTAAGACGA	3.07E-1
664. bta-miR-2315 MIMAT0011835	8820	-8.40	TACACATGCA - - CTTTCTGCT             GGTCATAGGTTTTTAAGACGA	1.54E-1
665. bta-miR-362-3p MIMAT0012548	9410	-11.20	ATGTGATTG - TGTGGTGTGTA :             CTTAGGAAGTTATCCACACAA	1.92E-1
666. bta-miR-2315 MIMAT0011835	10064	-14.50	CCAGACATGTGATATGTTCTGCT         : :       GGTC - ATAGGTT - TTTAAGACGA	1.75E-1
667. bta-miR-2315 MIMAT0011835	12058	-14.70	GCGTGTTCTAGTGGTTCTGCT    : :       GGTCATAGGTTTTTAAGACGA	3.46E-2
668. bta-miR-11998 MIMAT0046654	12087	-14.50	GCAGTTAAAAACA - GCTAGAGAA       :       CAACCCTTTTGTGTGATCTCTT	3.46E-2
669. bta-miR-129 MIMAT0009220	12714	-5.50	TGATGGTCTTAAGTATACAAAAAT :   : :          TCGTTTCGGG - - TCTGGCGTTTTTC	3.34E-1
670. bta-miR-148d MIMAT0046670	14335	-9.00	TTGGCTACCATTATAAAGAACTTG    :    :       TCAGTCACGTGATG - - TCTTGAAA	3.9E-1
671. bta-miR-2484 MIMAT0012077	16411	-9.30	ATGATTTTAA - - TCGT - ATAGCTA     : :    :       TACGTTAGTTTCAGTAGTATCGAG	3.57E-1
672. bta-miR-32 MIMAT0009283	19300	-9.30	CCGCCACTTGCATCACAAGATGCAATT         :            TACGTTGAAT - CAGT - - AC - ACGTTAT	2.46E-1



1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
673. bta-miR-2285cg MIMAT0046665	20279	-9.20	CCAGAAG-ATTATTGGTGGTTTG   :      :           AGTTTTCAAAGTAA-GACCAAAA	1.95E-1
674. bta-miR-2435 MIMAT0012007	20775	-10.30	GTACCTGTTAATATGCGAGTTT :          CGGTTTCTCAAGTAAGCTCAAA	2.61E-1
675. bta-miR-2315 MIMAT0011835	21158	-8.00	ATTTTGGACGG-TTTTCTGCA  :  :       GGTCATAGGTTTTTAAGACGA	2.01E-1
676. bta-miR-11998 MIMAT0046654	21422	-13.60	AAAGGGTAAACTACTTGTTAGAGAT            :       CAACCCTTTTG-TG--TGATCTCTT	1.45E-1
677. bta-miR-2285dd MIMAT0046712	22028	-7.44	TGAAAAG--AAAGATGGTTTTT :             ATTTTCAAGTAAGTCCAAAAG	6.99E-2
678. bta-miR-759 MIMAT0009371	23227	-13.90	GTGGAACAATGCCAGGCAGTCTGA   :          CAGTTT-TAAC-AAACGTCAGACG	1.89E-1
679. bta-miR-142-3p MIMAT0003791	24515	-9.50	GTGAGATTAAGTGTAAACACT    :       GTAGGTATTCATCCTTTGTGA	5.76E-2
680. bta-miR-199a-3p MIMAT0003746	24532	-9.50	ACACTATCTATAGCACCATCTACTGG   :             ATTGGT--TACACGT--CTGATGACA	5.76E-2
681. bta-miR-424-5p MIMAT0013593	24762	-11.40	TAATAATATTGA--TGCTGCTA   :          AGTTTTGTA-CTTAACGACGAC	1.75E-1
682. bta-miR-199a-3p MIMAT0003746	25475	-9.40	GTACTA-CTTGT--TCTACTGA   :    :       ATTGGTTACACGTCTGATGACA	2.95E-2
683. bta-miR-2285cg MIMAT0046665	25627	-7.20	TCTAATGGTAATCTCTATGGTTTT   :          AG-TTTTCA-AAGTAAGACCAAAA	2.65E-1
684. bta-miR-148d MIMAT0046670	25655	-10.70	ACTACTTAACAAACAGAACTTT       TCAGTCACGTGATGTCTTGAAA	7.54E-2
685. bta-miR-2284g MIMAT0011847	25657	-6.90	TACTTAACAAACAGAACTTTT           TTTTTCGGCTTG-CTTGAAAA	7.54E-2
686. bta-miR-2285cg MIMAT0046665	27372	-9.82	GGAAGAGTTGGATCAATGGTTTA   :           AGTTTTCAA-AGTAAGACCAAAA	1.61E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
687. bta-miR-876 MIMAT0009380	28279	-7.60	TCACTCTTTATGG-CAAATCCA   :  :       ACCACTAAGTGTTTCTTTAGGT	6.2E-2
688. bta-miR-32 MIMAT0009283	28796	-6.40	TTTTATTACAATCATATTGCAATT           TACGTTGAATCAGTA-CACGTTAT	1.04E-1
689. bta-miR-129 MIMAT0009220	29599	-10.10	GAATTACTCAG-TTTCAAAAAG  :    :       TCGTTCCGGTCTGGCGTTTTTC	8.64E-2
690. bta-miR-199a-3p MIMAT0003746	29661	-14.30	GCACCAGGAGTCCCAG-CTACTGA    :              ATTGGTT-ACA-CGTCTGATGACA	2.69E-1
691. bta-miR-507b MIMAT0046744	30252	-12.40	TTTGGGAAGAGAGGCCCCAATCA   :        AGGTGAGATTCTTCATGGTTAGT	4.98E-2
692. bta-miR-2441 MIMAT0012016	354	-14.90	AACAGGCGGAATTTGTCTCTGA :  : :       GAGGGTG-ACAGGACAGGACA	1.54E-1
693. bta-miR-105a MIMAT0009217	1722	-5.59	TGTAAAGGAAACAAATCTCATTTGC           TGGTGTCTCT--CAGACTCGTAAACT	3.11E-2
694. bta-miR-2285cz MIMAT0046706	2213	-7.40	CTCTTGCATTTGCATGGGTTTT    : : :       TGTTTTTTAAGTAAGCCCCAAC	2.61E-1
695. bta-miR-2285j MIMAT0024585	2214	-6.90	TCTTGCATTTGCATGGGTTTTA   :        GTTTTTCAAGCAAGACCAAAAA	2.61E-1
696. bta-miR-2284j MIMAT0011827	5798	-10.80	AAAATTTGAAACAAACTTTTA    : :           TTTTGGACTT-GCTTGAAAAG	2.39E-2
697. bta-miR-105a MIMAT0009217	5932	-6.97	GCC-CA--ATTTAAACATTTGA :             TGGTGTCTCTCAGACTCGTAAACT	6.48E-2
698. bta-miR-11991 MIMAT0046631	6923	-10.00	CACAGT--GGATTAAGAACAC    :   :           ATGTTAGTTCTATGTCTTGTA	2.28E-1
699. bta-miR-2284j MIMAT0011827	7548	-5.50	TAAACCAGGTAATACTTTTA      :       TTTTGGACTTGCTTGAAAAG	2.94E-1
700. bta-miR-2285bm MIMAT0046624	8451	-6.80	TAAAGGGGGTGC--AGTTTTTA :    : :   : :       GTTTTTCAGGTGAGCCAAAAAA	3.29E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
701. bta-miR-2419-3p MIMAT0011986	9897	-15.20	TGATGTGCTTTACCAACCGCCTA     :              ACTA-GCATAATCGTGGGCGGAC	1.42E-1
702. bta-miR-584 MIMAT0009352	10298	-14.80	CTTA-TAAC-GGCAAACCA   :             GAGTCAGGGTCCGTTTGGT	3.62E-1
703. bta-miR-2296 MIMAT0011804	10502	-21.10	ATAAGGATGCTCAGGTTGTCCA               TCGTCCTTGGAGTC-AACAGGT	8.51E-2
704. bta-miR-376a MIMAT0009946	10692	-10.50	AGATGCTTTAGCTTCTATGAC        :       TGCACCTAAAAGGAGATACTA	3.07E-1
705. bta-miR-2353 MIMAT0011889	11967	-19.20	GGACAATACTGTTTTGCAGGCTT     :       GGTCAGGAGACATGACGTCCGAT	2.39E-1
706. bta-miR-2452 MIMAT0012033	12069	-8.30	TGGTTCTGCTAATCAACAGCAG   :       TTTTTTCCTTTTGTTCGTG	3.46E-2
707. bta-miR-2471-5p MIMAT0012061	13203	-8.90	GCCTGTAGGTATAAAAGATCCTG  :       GGAGACTCTAATCTGTCTAGGAG	3.29E-1
708. bta-miR-105a MIMAT0009217	13609	-8.30	AACACG-ATTTCTTTACATTTGA    :           TGGTGTCCCTCAGACTCGTAAACT	2.73E-1
709. bta-miR-181b MIMAT0003793	14994	-12.40	AGTACTATGACTGGCA--GAATGTT :     :           TTGGGTGGCTG-TCGTTACTTACAA	9.48E-2
710. bta-miR-433 MIMAT0009318	15721	-11.50	ACA--ATGGA-CC--TCATGAA                  TGTGGCTCCTCGGGTAGTACTA	1.15E-2
711. bta-miR-30e-5p MIMAT0003799	17144	-9.60	TGACACCACTCGTAAGTATGTGTTTACT     :     :       TCGAAGGT--CAGTTC--CTACAAATGT	3.39E-1
712. bta-miR-2285cz MIMAT0046706	17660	-11.80	AGCTAGGCGCGTTTTGGGTTTG   :       TGTTTTTTAAGTAAGCCCAAAC	3.29E-1
713. bta-miR-433 MIMAT0009318	18660	-9.90	TCTTTATCAAGT-AATCATGAT   :       TGTGGCTCCTCGGGTAGTACTA	2.36E-2
714. bta-miR-376a MIMAT0009946	18934	-11.70	ATTTTGATTTTAAGTTCTATGAT         :       TGCACCTAAAA--GGAGATACTA	2.25E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
715. bta-miR-12035 MIMAT0046728	19514	-15.90	TTATACAGGACAGG - - CTGGTGA :      :         AGACCCCTCTGTTTCAGGACCACA	1.98E-1
716. bta-miR-2325a MIMAT0011854	19876	-6.90	TTTACATTTCCACGACAAAAG :     :       CTTTTTTTGGGT - TTGTTTTG	3.48E-1
717. bta-miR-105a MIMAT0009217	20286	-13.00	ATTATTGGTGGTTT - - GCATTTGT   : :     :   :         TGGTGTCC - TCAGACTCGTAAACT	1.95E-1
718. bta-miR-11991 MIMAT0046631	20988	-5.90	TATGACCCTATTACTAAGAACAT           ATGTTAGTTCTATG - - TCTTGTA	3.8E-1
719. bta-miR-2285j MIMAT0024585	21153	-5.80	TTTGCATTTTGGAC - GGTTTTTC    :           GTTTTTCAAGCAAGACCAAAAA	2.01E-1
720. bta-miR-2285j MIMAT0024585	22028	-9.50	TGAAAAAGAAAG - - ATGGTTTTT :               GTTTTTCAAGCAAGACCAAAAA	6.99E-2
721. bta-miR-376a MIMAT0009946	22099	-7.10	CCACTGATAAGCTAGCTATGAT       :       TGCACCTAAAAGG - AGATACTA	3.48E-1
722. bta-miR-15b MIMAT0003792	24760	-15.90	TGTAA - TAATATTGATGCTGCTA                ACATTTGGTACTAC - ACGACGAT	1.75E-1
723. bta-miR-2285j MIMAT0024585	25628	-6.20	CTAATGGTAATCTCTATGGTTTTA :            GTTTTTCA - - AGCAAGACCAAAAA	2.65E-1
724. bta-miR-2284j MIMAT0011827	25660	-7.70	TTAAC - - AAACAGAACTTTTA              TTTTGGACTTG - CTTGAAAAG	7.54E-2
725. bta-miR-181b MIMAT0003793	26995	-10.70	GCTATGGAGAAGGTTAATGAATGTG    :   :       TTGGGTGGCTGTCTG - TTAATTACAA	1.75E-1
726. bta-miR-2386 MIMAT0011938	27386	-12.20	AATGGTTTAAAAACCAACA         CCTTTTGCTTTTGGTTTGT	1.61E-2
727. bta-miR-2386 MIMAT0011938	28283	-9.20	TCTTTATGGCAAATCCAAACA   :   :           CCTTTTGCTTTT - GGTTTGT	6.2E-2
728. bta-miR-1247-3p MIMAT0025550	30307	-17.80	GAAGTAGTGACCC - ACAGTTCCCC   :                  CGAGGTCA - - GGGCTG - CAAGGGC	4.98E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
729. bta-miR-763 MIMAT0009374	30336	-18.70	GCAGAACT--CGCACCCACAGCTGG                CG--GTGACCAAGGAGG-GTCGACC	4.98E-2
730. bta-miR-2367-3p MIMAT0011910	30468	-6.50	AGATTTGACAGTACACTTTCAG :                GAAGGACATTCACG-GAAAGTT	3.29E-1
731. bta-miR-2461-5p MIMAT0012047	1128	-16.00	TGTTATGAGAC--TGCAGAGTGC   :        :       ACGGTCCTAGGCTCTGTCTCACC	1.69E-1
732. bta-miR-374c MIMAT0046394	1708	-7.10	GGTTGCAAGG--CTATTGTAA   :           TGAATAGTCCAACATAACATT	3.11E-2
733. bta-miR-363 MIMAT0003855	5646	-11.30	TAAGGGTGTAGGAAGTGCAAA :   :         GCGTCTACCTATGGCACGTTA	9.48E-2
734. bta-miR-2376 MIMAT0011922	6268	-17.70	GACGATGGTGGTGATATCTCAGAGA    :         TCGC--GGATCGTTCTAGAGTCTCC	3.52E-1
735. bta-miR-11974 MIMAT0046353	6785	-19.60	GGAGTGTGGTTGC-TAG-AGGTGCT        :   :       CGACAC-CCCCTGTGTCTGTCCACGA	3.52E-1
736. bta-miR-210 MIMAT0003824	6904	-16.60	ACTTTTGTGGTAAGATCGCACAGT : :           AGTCGGCGAC--AGTGTGCGTGTCA	2.28E-1
737. bta-miR-2358 MIMAT0011896	8185	-13.80	AACTTGGTGCCAACATATTTGA :   :         AGGTGCTAGGGTTG-ATAAACC	3.62E-1
738. bta-miR-19b MIMAT0004337	8794	-10.00	TATGGTTACCATG-TGTTGCACT           AGTCAAAACGTACCTAAACGTGT	1.54E-1
739. bta-miR-2285z MIMAT0029950	8816	-10.20	TTATTACACATGCACTTTCTGC            TCCTGGACTTACTTGAAAGACC	1.54E-1
740. bta-miR-12017 MIMAT0046697	8893	-11.92	GCTAGTGGCTGTGTGCTTTCTCTGC :             CAAGTAC-AGTTTTTCG--AGGAGACA	2.69E-1
741. bta-miR-221 MIMAT0003529	10546	-11.60	CAATCT-GTTAATTTTGTAGCA   :   :   :       TTTGGGTCGTCTGTTACATCGA	8.51E-2
742. bta-miR-19b MIMAT0004337	11805	-12.50	GCAATATTGTAGCACTTTCACACA     :         AGTCAAAACGTACCTAAACGTGT	6.2E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
743. bta-miR-92b MIMAT0009384	12327	-7.50	TTGTGTACCATTGAATGCAATC   : :          CCTCCGGCCCTGCTCACGTTAT	9.78E-2
744. bta-miR-2385-5p MIMAT0011935	13977	-16.90	GAC - TATGTTATTGCAGCCCCAG :      : ::  :         TTGCATGAGGTGA - -ACGGGGTC	3.48E-1
745. bta-miR-10164-3p MIMAT0040911	14512	-11.30	GCGGTGTAAAAATTTCAAACAGTTA   :   :    :  :         CGTCG - GTTCGGAGGATTGTCAAC	5.76E-2
746. bta-miR-2319b MIMAT0011843	16083	-19.50	AGAAGTGCAGTTATGCAGAGTG         :       GATTCACG - GATTATGTCTCAT	3.52E-1
747. bta-miR-12054 MIMAT0046761	20113	-15.30	ATGC - TCTGGCAACCTCCAC       :       CACGTAGG - -GGTGGAGGTC	2.82E-1
748. bta-miR-2461-5p MIMAT0012047	20393	-15.40	TATCA - CTGATGAGA - AGAGTGG :    :           ACGGTCCTAGGCTCTGTCTCACC	2.21E-1
749. bta-miR-19b MIMAT0004337	20410	-10.10	GTGGTGGTAGTAAGAGTGTTCGACT :       :     :       AGTCAAAA - CGTAC - C - TAAACGTGT	2.21E-1
750. bta-miR-2313-5p MIMAT0011829	21155	-13.60	TGCATTTTGGACGGTTTCTGCACA          :       ACG - -GAACC - AGGAGTCGACGTGA	2.01E-1
751. bta-miR-2358 MIMAT0011896	21214	-9.60	TTGGC - AT - -AAATTATTTGG   : :      :       AGGTGCTAGGGTTGATAAACC	2.01E-1
752. bta-miR-10164-3p MIMAT0040911	21281	-11.40	GTTTTGGAGAAATTCC - -ACAGTTT   : : :    :          CGTCGGTTC - -GGAGGATTGTCAAC	7.65E-2
753. bta-miR-19b MIMAT0004337	21871	-13.10	CCAGGAAATGGATTGGACATTGCACC                    AGTC - AAAACGTA - CCT - AAACGTGT	2.65E-1
754. bta-miR-2358 MIMAT0011896	24860	-11.50	TGGGCAATTTGGGCTATTTGC :     : :       AGGTGCTAGGGTTGATAAACC	2.32E-1
755. bta-miR-10164-3p MIMAT0040911	26221	-8.30	CTACTTGA - C - -ACTACACAGTTG :              CGTCGGTTCGGAGGAT - TGTCAAC	1.95E-1
756. bta-miR-12017 MIMAT0046697	26550	-11.10	ATACACTTTGGCTGCCACCTCTGC      :          CAAGTACAGTTTTCG - AGGAGACA	3.46E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
757. bta-miR-12054 MIMAT0046761	27347	-16.80	CAACA-CCCAACCTCCAT              CACGTAGGGGTGGAGGTC	6.88E-2
758. bta-miR-12017 MIMAT0046697	30051	-10.10	TCTGGCAACAGAACCCCTACCTCTGG   :           CAAGTACAGTTTT- - CGA-GGAGACA	2.94E-1
759. bta-miR-10164-3p MIMAT0040911	30304	-8.00	TTGGAACTAGTGACC- CACAGTTC :    :          CGTC-GGTTCGGAGGATTGTCAAC	4.98E-2
760. bta-miR-12037 MIMAT0046732	240	-7.00	ACTACACTGGG- CTCCAGAATT       :        TGAT- - TTCTCTTCTGTCTTAC	8.01E-2
761. bta-miR-205 MIMAT0003545	1030	-12.30	AAGACATTGCAAGAAATGAAGGC     :          GTCTGAGGC- CACCTTACTTCCT	2.35E-1
762. bta-miR-2285bp MIMAT0046633	1673	-8.00	AGTCTTATGACGGTTTGGTTTA     :        TGTGTTTCAAGCAAGACCAAAA	3.11E-2
763. bta-miR-545-5p MIMAT0003806	1912	-10.10	AGTTTAG- AAACTTTTACTGT : :: :           GTAGGTTATTTGTAAATGACT	3.9E-1
764. bta-miR-2285h MIMAT0024583	2214	-7.20	TCTTGCATTTGCATGGGTTTTTA   :          GTATTTCAAGCAAAGCCAAAAG	2.61E-1
765. bta-miR-2285af MIMAT0031057	3431	-9.10	GCTGGTTGCGATCAGTTTTGGC : :          TTGGACTTGTT- CGAAAAACCG	1.22E-2
766. bta-miR-2285cx MIMAT0046704	3492	-15.10	TTTGCAAGATC- TTTGGGTGTT  :           AGTTTTTCAAGTAAACCCACAA	2.58E-1
767. bta-miR-2320-3p MIMAT0011845	3906	-15.30	TAAACAAATTGATGATCATCGT        :        TTTTGTGTCCCTGGTAGTAGCT	4.64E-2
768. bta-miR-1306 MIMAT0009974	6788	-12.90	GTGTGGTTGC- - TAGAGGTGC   :              CCTGCAAACGTCCCTCCACC	3.52E-1
769. bta-miR-96 MIMAT0009388	8176	-13.80	AGTTGTAATAACTTGGTGCCAAC   :      :        TCGTTTTTACACGATCACGGTTT	3.62E-1
770. bta-miR-2285af MIMAT0031057	8738	-11.10	TAGTAGACCAGG- ATTTTGGC     :        TTGGACTTGTTGAAAAACCG	3.52E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
771. bta-miR-2294 MIMAT0011802	9261	-11.70	TAAAGGT-TTAGC-ACAGCCTG   : ::        TCGTCTACGGGAGATGTCGGAG	2.28E-1
772. bta-miR-2285af MIMAT0031057	9614	-11.40	TTTCAAATCATGCTTTTGGG          TTGGACTTGTTCGAAAAACCG	6.88E-2
773. bta-miR-324 MIMAT0009285	10488	-14.30	TTTTTATGGTCCTTATAAGGATGCT  :          TGTGGTTACGGGA--TCCCCTACGC	8.51E-2
774. bta-miR-383 MIMAT0009309	10666	-20.30	AGCCA-AGTTA-AGTCTGATCT        : :        TCGGTGTTAGTGGAAGACTAGA	3.07E-1
775. bta-miR-543 MIMAT0009344	11422	-17.50	AAGTGGGTTGCCGTGAATGTTT :   :      TTCTTCACGTGGCGCTTACAAA	8.26E-2
776. bta-miR-1306 MIMAT0009974	11672	-13.40	TTTTG--GGTATTGGAGGTGT :   :        CCTGCAAACGTCCCCTCCACC	3.07E-1
777. bta-miR-12002b MIMAT0046694	12482	-10.50	CAAATAAGCAGTTGCATGAGA     :       TCGATTCTAAGGTGTACTCC	2.14E-1
778. bta-miR-543 MIMAT0009344	12639	-6.20	TTGTAATACACCTACTCAATGTTA            TTCTTCACGTGG--CGCTTACAAA	2.18E-1
779. bta-miR-2379 MIMAT0011925	13976	-11.20	TGACTATGTT--ATTGCAGCCC              TTTTTATAGAAGAGGTCTGTCGGA	3.48E-1
780. bta-miR-12037 MIMAT0046732	14994	-10.90	AGTACTATGACTGGCAGAATG     :      TGATTTCTCT-TCTGTCTTAC	9.48E-2
781. bta-miR-543 MIMAT0009344	14995	-10.20	GTACTATG-ACTGGCAGAATGTTT      :        TTCTTCACGTGGC--GCTTACAAA	9.48E-2
782. bta-miR-543 MIMAT0009344	15010	-5.80	GAATGTTTCATCAAAAATGTTT   :        TTCTTCACGTGGCGCTTACAAA	9.48E-2
783. bta-miR-543 MIMAT0009344	17749	-11.80	AAACAGCGCATTCTGTAAATGTTA         :        TTCTTCACGT--GGCGCTTACAAA	1.09E-1
784. bta-miR-2285af MIMAT0031057	19029	-5.10	GTTTTGTGTA--TGTTTTGGA ::    :        TTGGACTTGTTCGAAAAACCG	2.42E-1



1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
785. bta-miR-2294 MIMAT0011802	20019	-19.00	ATCTTCAGCCAATTCGACAGCCTG              TCGTCTACGG - - GAGATGTCGGAG	7.09E-2
786. bta-miR-2285bp MIMAT0046633	20278	-5.30	ACCAGAAGATTATTGGTGGTTTG    :             TGTGTTTC - AAGCAAGACCAAAA	1.95E-1
787. bta-miR-200a MIMAT0003822	20407	-6.80	AGAGTGGT - GGTAAGAGTGT :      : :          TTGTAGCAATGGTC - - TGTACAAT	2.21E-1
788. bta-miR-12037 MIMAT0046732	21114	-9.70	TTTTCTTGAATGCAGAAATT :     :       TGATTTCTCTTCTGTCTTAC	3.16E-1
789. bta-miR-2285h MIMAT0024583	21153	-10.80	TTTGCATTTTG - GACGGTTTTT    :         GTATTTCAAGCAAAGCCAAAAG	2.01E-1
790. bta-miR-205 MIMAT0003545	21186	-12.00	AATGCTTC - TTCTAGTGAAGGG :    :   :       GTCTGAGGCCACCTTACTTCCT	2.01E-1
791. bta-miR-2294 MIMAT0011802	21655	-12.90	TTGCTATGCTGGATATTCAGCCTG     :       TCGTCTACGG - - GAGATGTCGGAG	2.25E-1
792. bta-miR-2285bp MIMAT0046633	22027	-7.30	CTGAAAAGAAAG - - ATGGTTTT             TGTGTTTCAAGCAAGACCAAAA	6.99E-2
793. bta-miR-127 MIMAT0003787	23497	-8.60	ACCTATTTGT - GTGTATGATCCGC   :   :         TCGGT - - TCGAGTCTGCCTAGGCT	3.48E-1
794. bta-miR-543 MIMAT0009344	24934	-11.30	AATTTACCTGCTGCTAATGTTT :   :          TTCTTCACGTGGCGCTTACAAA	9.48E-2
795. bta-miR-2285bp MIMAT0046633	25627	-6.20	TCTAATGGTAATCTCTATGGTTTT :             TGTGTTTCA - - AGCAAGACCAAAA	2.65E-1
796. bta-miR-12001 MIMAT0046660	26142	-9.60	TGCAGCATG - - TAAATCACAGT                 AGGTCCCACTTCGGGAGTGTC	1.78E-1
797. bta-miR-2285bp MIMAT0046633	27371	-10.40	AGGAAGAGTTGGATCAATGGTTTA   :                TGTGTTTCAAGCAAG - - ACCAAAA	1.61E-2
798. bta-miR-2337 MIMAT0011870	27384	-7.40	TCAATGGTTTAA - AAACCAA             TTTTTCCTTATTCTTTGGTG	1.61E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
799. bta-miR-2337 MIMAT0011870	28635	-9.20	TTACAACGATGTAAAACCAC :  :       TTTTTCCTTATTCTTTGGTG	1.78E-1
800. bta-miR-2337 MIMAT0011870	29492	-5.30	ATCTAGAAATGTTCAAACCAG       :       TTTTTCCTTAT-TCTTTGGTG	7.91E-3
801. bta-miR-2337 MIMAT0011870	30557	-8.50	GAATATGAGTCCAAAACCAC   :        TTTTTCCTTATTCTTTGGTG	3.66E-2
802. bta-miR-760-3p MIMAT0022951	30947	-18.40	TGCCCCAGGG- -AAGAGCCA        : :       AGGGGTGTCTGGGTCTCGGC	6.29E-2
803. bta-miR-665 MIMAT0009363	1681	-15.00	GACGGT-TTGGTTTATACTGGA   :  : :       TCCCCGGAGCCG- -GATGACCA	3.11E-2
804. bta-miR-665 MIMAT0009363	3640	-11.00	CAGTGTGTTG- CATACTGGA  :  :          TCCCCGGAGCCGGATGACCA	3.34E-1
805. bta-miR-448 MIMAT0009319	5490	-9.60	TGTGGACG- CT- -GTTATGCAT    :  :       TACCTGTAGGATGTATACGTT	2.86E-1
806. bta-miR-2285cq MIMAT0046688	5795	-12.00	TTAAAAAATTGAAACAACTTTT      :              TCTTTTGTGACCTT-GTTTGAAAA	2.39E-2
807. bta-miR-2285av MIMAT0046347	5797	-10.90	AAAAAATTGAAACAACTTTT      : :            TTTTTGGGCTT-GCTTGAAAA	2.39E-2
808. bta-miR-758 MIMAT0009370	5867	-11.90	ATAAACCTGACT-TGTCACAAT    :       CCAATCACCTGGTCCAGTGTTT	6.48E-2
809. bta-miR-3613b MIMAT0029948	7492	-7.10	GGTGGCACT- -GGCTTTTGTTT              CAAC-ATGAAAAAAAAACAAG	2.95E-2
810. bta-miR-2285av MIMAT0046347	7547	-6.20	ATAAACCCAGGTAATACTTTT      :       TTTTTGGGCTTGCTTGAAAA	2.94E-1
811. bta-miR-448 MIMAT0009319	7771	-7.00	AAGAGTGTGCCTA-ATATGCAT           TACCTGTAGGATGTATACGTT	8.64E-2
812. bta-miR-1271 MIMAT0009975	8177	-17.10	GTTGTAATAACTTGGTGCCAAC               ACTCATGAATGATCCACGGTTC	3.62E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
813. bta-miR-2284aa MIMAT0025560	9611	-7.80	TTGTTTCAAATCATGCTTTTGT : :        :       TTTTGGGTTT-GTTTGAAAAA	6.88E-2
814. bta-miR-448 MIMAT0009319	10415	-9.40	GTGTAAATTTGTGTATATGCAT :       :   :       TACCCT-GTAGGATGTATACGTT	3.24E-2
815. bta-miR-2285q MIMAT0025574	10478	-13.80	TCAATGGGGATTTTTATGGTCCTT :     :     :       GGTCTTCAAGTAAGT-CCAGGAA	8.51E-2
816. bta-miR-1271 MIMAT0009975	11675	-18.70	TGGGTATT-GGAGGTGTGCCAAT   :     :   :       ACTCATGAATGATC-CACGGTTC	3.07E-1
817. bta-miR-216b MIMAT0009266	16552	-6.63	CAGCA-ACAATACAAGAGATTG :           AGTGTAACGGACGTCTCTAAA	2.36E-2
818. bta-miR-29a MIMAT0003518	17101	-16.80	CTGCCAAGGTCAGGGTGGAGTGCTAT :         :         ATTGGCTAAAGTCT--AC-CACGATC	3.76E-1
819. bta-miR-2285ay MIMAT0046355	21549	-10.09	CCACTTACCCAGTTTGAGGGTTT     :   :         GGTTTTCCAAGTAAG-TCCCAA	1.45E-1
820. bta-miR-2285ce MIMAT0046657	22027	-7.44	CTGAAAAG--AAAGATGGTTTTT :                 AGTTTTTCAAGTAAGTCCAAAAG	6.99E-2
821. bta-miR-6519 MIMAT0025537	24930	-16.70	TTATAATTTACCTGCTGCTA   :           AAAGAGACAAGGGCGACGAT	9.48E-2
822. bta-miR-2285ce MIMAT0046657	25627	-5.70	TCTAATGGTAATCTCTATGGTTTTA     :               AGTTTTTCA--AGTAAGTCCAAAAG	2.65E-1
823. bta-miR-2285av MIMAT0046347	25659	-7.70	CTTAAC--AAACAGAACTTTT                   TTTTTGGGCTTG-CTTGAAAA	7.54E-2
824. bta-miR-181d MIMAT0009243	26996	-9.30	CTATGGAGAAGGTTAATGAATGTG     :             TGGGTGGCT-GTTGTACTTACAA	1.75E-1
825. bta-miR-2285bb MIMAT0046375	28048	-12.10	AGGTAGACCTTA--TAACTTTA   :   :     : :         TCTTTTTGGGGTTGTTTGAAAG	2.5E-1
826. bta-miR-2285av MIMAT0046347	28050	-6.80	GTAGACCT-TAT-AACTTTA   :     :   :         TTTTTGGGCTTGCTTGAAAA	2.5E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
827. bta-miR-1271 MIMAT0009975	28064	-10.70	TTTAAGCATTATTAATTGCCAAA :       :           ACTCATG-AATGATCCACGGTTC	2.5E-1
828. bta-miR-2285bb MIMAT0046375	29371	-9.10	TGAGAAATAATATCTAAACTTTA     :     : :   :         TCTTTTGGGGT-TGTTTGAAAG	3.85E-1
829. bta-miR-2285cq MIMAT0046688	29371	-7.30	TGAGAAATAATATCTAAACTTTA     :     : :           TCTTTTGG-ACCTTGTTTGAAAA	3.85E-1
830. bta-miR-2390 MIMAT0011943	29690	-10.70	GGGGTACTGGTACAGACACAAC     : :                 CCTTTTGTTTTGG--TGTGTTG	2.01E-1
831. bta-miR-28 MIMAT0009272	29966	-17.20	CTCA--GGAAGGTCTGCTCCTA       :               GAGTTATCTGACACTCGAGGAA	2.01E-1
832. bta-miR-204 MIMAT0004338	30937	-9.80	GCCGAACAAGTGCCCAAGGGAA :                 TCCGTATCCTACTGTTTCCCTT	6.29E-2
833. bta-miR-2285ao MIMAT0046360	2212	-12.50	GCTCTTGCATTTGCATGGGTTT     :     :             CGGTTTTTCAAGCAGACCCAAA	2.61E-1
834. bta-miR-2285df MIMAT0046729	2214	-8.40	TCTTGCATTTGCATGGGTTTTA   :     : :           GGTTTTTCAGACAAGTCCAAAAA	2.61E-1
835. bta-miR-12039 MIMAT0046734	3453	-12.90	AGTGATGCAGAACTGCCCTGT                     TCTCTTCTTCGGTCCCGGGACC	1.22E-2
836. bta-miR-329a MIMAT0009288	3625	-11.20	ACCTTATGTGATTGGCAGTGTGTT :   :               TTTTTCCAATTGGTC--CACACAA	3.34E-1
837. bta-miR-10b MIMAT0003839	4284	-13.40	ACCTGATGCGAGGAC-ACAGGGTA :                     GTGTTTAAGC-CAAGATGTCCCAT	1.75E-1
838. bta-miR-140 MIMAT0003789	7779	-10.50	GCCTAATATGCATGTTGTGGTA   : :             AGGCACCAAGATGGGACACCAT	8.64E-2
839. bta-miR-2480 MIMAT0012072	10531	-6.70	GTT-CAGGATTATATACAAT     :   :             CAGTATTCTTTGTTATGTTA	8.51E-2
840. bta-let-7c MIMAT0004332	11441	-10.90	TTTTGTATTTTACAGATATACCTCA :     :               TTGGTATG--TTG-GATGATGGAGT	8.26E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
841. bta-miR-376c MIMAT0009947	12447	-6.77	ATGGCAGATTCAAACATATCCAA : :                   ATTTGTATCTTCCTTATAGGTG	2.14E-1
842. bta-miR-2471-3p MIMAT0012062	16143	-15.10	CGTTGTGGCAGTT-GCATCAGA   :          :             TCGTC-CCGACAGAAGTAGTCT	5.43E-2
843. bta-miR-2480 MIMAT0012072	16547	-11.60	TGCATCAGCAACAATACAAG                             CAGTATTCTTTGTTATGTTA	2.36E-2
844. bta-miR-2480 MIMAT0012072	17045	-5.80	ATTGTGTGAAAAAGCATACAAA   :                      CAGTATTCTTT - - GTTATGTTA	2.54E-1
845. bta-miR-329a MIMAT0009288	17308	-13.50	AATTGCCAGCACCACGTGTGTT                         TTTTTCCAATTGGTCCACACAA	3.52E-1
846. bta-miR-2418 MIMAT0011982	18337	-15.10	AACAATTTAAGCATCTCATCCCT :                         GCTGGTGCGGTGT-GAGTAGGGT	3.39E-1
847. bta-miR-2310 MIMAT0011822	19875	-10.60	GTTTACATTTCCACGACAAAAG      :      :             TCTTTGTTTGGGT-TTGTTTTG	3.48E-1
848. bta-miR-2285df MIMAT0046729	21153	-6.20	TTTGCATTTTGGAC-GGTTTTTC   :                     GGTTTTTCAGACAAGTCCAAAAA	2.01E-1
849. bta-miR-2285df MIMAT0046729	21188	-9.60	TGCTTCTTCTAGTGAAGGGTTTTT         :                   GGTTTTTCAGA-CA-AGTCCAAAAA	2.01E-1
850. bta-miR-2285df MIMAT0046729	22028	-6.14	TGAAAAG - - AAAGATGGTTTTT                            GGTTTTTCAGACAAGTCCAAAAA	6.99E-2
851. bta-miR-2285ao MIMAT0046360	22109	-10.31	GCTAG-CTATGATTATGGGTTA    :   :                   CGGTTTTTCAAGCAGACCCAAA	3.48E-1
852. bta-miR-12039 MIMAT0046734	22525	-11.84	GGACCTTAATCC - - TGCCCTGT :                            TCTCTTCTTCGGTCCCGGGACC	3.66E-1
853. bta-miR-2292 MIMAT0011800	24731	-19.80	TGTCTTTTATTCAG - - GCAGACTC    :      : :      :             ACGGAAG - - GAGTTAGAGTCTGAG	1.75E-1
854. bta-miR-15a MIMAT0004334	24760	-12.10	TGTAATAATATTGATGCTGCTA    :                         TGTTTGGTAATAC-ACGACGAT	1.75E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
855. bta-miR-2285ah-5p MIMAT0040945	25271	-21.70	CAGGGCCTTACAAGTGCCCCCAA    :     :      AGGACGGG-TGGAGATGGGGGTT	1.04E-1
856. bta-miR-2285df MIMAT0046729	25628	-8.70	CTAATGGTAATCTCTATGGTTTTA  :    :            GGTTTTTCAGACAAG--TCCAAAAA	2.65E-1
857. bta-miR-2284f MIMAT0011905	25656	-6.00	CTACTTAACAAAACAGAACTTT           CTTTTTAGGCTTG-CTTGAAA	7.54E-2
858. bta-miR-2418 MIMAT0011982	27754	-15.10	TCCTGACGATATATTACATCCCT     : :        GCTGGTGCGGTGTGA-GTAGGGT	2.11E-1
859. bta-miR-320b MIMAT0011991	29660	-17.82	TGCACC-AGGAGTCCCAGCT           TGGTGGGAGAGTTGGGTCTGA	2.69E-1
860. bta-let-7c MIMAT0004332	30054	-15.00	GGCAACAGAACCCCTACCTCT              TTGGTATGTTGGATGATGGAGT	2.94E-1
861. bta-miR-11995 MIMAT0046648	30666	-13.30	AGAGAGTTGACTGCAGAGGACAT   :           TCTGTGCGACT-CTTCATCCTGTT	1.28E-1
862. bta-miR-12018 MIMAT0046701	397	-12.40	CGCCGAC-TTCTTAAACAAGAG         :       AGTTCTGTAAGAGCCTGTTCTA	1.45E-1
863. bta-miR-2297 MIMAT0011805	400	-7.30	CGACTTCTTAAACAAGAGTG           TCCTTATTCTTTTTTCTCAC	1.45E-1
864. bta-miR-17-3p MIMAT0003816	1122	-10.40	ACGTTATGTTATGAGACTGCAGA   :   :       TGT-TCACGG--AAGTGACGTCA	1.69E-1
865. bta-miR-2285bv MIMAT0046642	2873	-10.60	ACACTGCATGT-GGAGTGTTTG              TTTTACAAACAAGCTCACAAAA	1.36E-1
866. bta-miR-2285cb MIMAT0046651	3493	-14.40	TTGCAGGATC-TTTGGGTGTT  :     :       GGTTTTCAAGTAGGCCACAA	2.58E-1
867. bta-miR-655 MIMAT0009360	5904	-5.20	TAAGTATTATACTCAGCGTATTAT             TCTCTCCAATTG-GT-ACATAATA	6.48E-2
868. bta-miR-2455 MIMAT0012037	6905	-12.10	CTTTTGTGGTAAGATCGCACAGT :::   : :          AGGGACGGAGGGGCT--CGTGTCT	2.28E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
869. bta-miR-1721 MIMAT0011849	9587	-7.80	TTTGTTCGCTATATATATCTGTT : :    :          AGAGTCTTAGTGTA - GTAGACAC	6.88E-2
870. bta-miR-17-3p MIMAT0003816	9632	-11.90	GGGTATTTTCTTACTGCAGA :   :            TGTTACGGAAGTGACGTCA	2.73E-1
871. bta-miR-2437 MIMAT0012011	10296	-11.90	TGCTTATAACGGCAAACCACA     : :             TTTCCTTTTGTTTTTTGGTGT	3.62E-1
872. bta-miR-2285cd MIMAT0046655	10498	-15.10	CCTTATAAGGATGCTCAGGTTGTC               : :             GG - TTTTCAAGTAGGTCCAACAA	8.51E-2
873. bta-miR-1721 MIMAT0011849	10531	-19.80	G TTCAGGATTATATACAATCTGTT :       :     :           AGAGTCTTAGTGTA - - GTAGACAC	8.51E-2
874. bta-miR-6119-5p MIMAT0024588	11443	-7.50	TTGTATTTTCACAGATATACCTCA :                           TCAGTTTAGTTAAAAAATGGAGA	8.26E-2
875. bta-miR-2285cd MIMAT0046655	12827	-9.60	ACCTTTATTTTGTAAGGTTGTA                        GGTTTTTCAAGTA - GGTCCAACAA	3.34E-1
876. bta-miR-2285cd MIMAT0046655	13751	-8.30	TCTCTCTATATATGCTGGTTGTG :                GGTTTTTCAAGTAGGTCCAACAA	1.32E-1
877. bta-miR-532 MIMAT0003848	13905	-11.70	GTGGAGGTAGGCTTAGTAGGCATT    :     :           TGCCAGGATGTGAGT - - TCCGTAC	3.29E-1
878. bta-miR-2285cb MIMAT0046651	13979	-10.54	CTATGTTATTGCAGCCCCAGGGTGTG   :                            GGT - - TTTCAAGT - - AGG - CCCACAA	3.48E-1
879. bta-miR-12003 MIMAT0046662	15735	-17.10	GAATTCTGTTCAACATACAATGCT     :     :                            CTTG - GATACCGGTTG - - GGTTACGA	1.15E-2
880. bta-miR-628 MIMAT0009356	16537	-8.40	AGCAGAGT - TATGCATCAGCAA           :                GGAGATCATTTATACAGTCGTA	2.36E-2
881. bta-miR-30c MIMAT0003850	17150	-6.70	CACTCGTAAGTA - TGTGTTTACT        :             CGACTCTCACATCCTACAAATGT	3.39E-1
882. bta-miR-582 MIMAT0009351	19033	-9.20	TGTG - TATGTTTTGGAAGTGTAA    :               :             TCATTGACCAACTTGTGACATT	2.42E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
883. bta-miR-2285bn MIMAT0046625	19389	-8.91	ACAG-CTACTACAGCAGGTTTT    :       TGTTTTTCAAGTAAGTCCAAAA	3.12E-1
884. bta-miR-190b MIMAT0009252	19600	-7.70	TTATTAATAATACAACATATCC ::   :        TTGGGTTATAGT-TTGTATAGT	5.58E-3
885. bta-miR-2297 MIMAT0011805	20406	-10.70	AAGAGTGGTGGTAGTAAGAGTG   : :: :       TCCTTATT-CT-TTTTTCTCAC	2.21E-1
886. bta-miR-2285bv MIMAT0046642	20410	-12.00	GTGGTGGTAGTAAGAGTGTTTG ::            TTTTACAAACAAGCTCACAAAA	2.21E-1
887. bta-miR-148b MIMAT0003814	20414	-12.60	TGGTAGTAAGAGTGTTCACACTGT               TGTTTCA-AGACAC-TACGTGACT	2.21E-1
888. bta-miR-12003 MIMAT0046662	23218	-11.80	TGATTCACGGTGGA-ACAATGCC   :        CTTGGATACCGTTGGGTACGA	1.89E-1
889. bta-miR-2285bv MIMAT0046642	25024	-6.40	CCTCAACCTGT--AGGTGTTTT    :       TTTTACAAACAAGCTCACAAAA	2.46E-1
890. bta-miR-12003 MIMAT0046662	26689	-10.30	ATTGCTAATGCATTTAACAATGCT              CTTGGATACCG-GTTGGGTACGA	1.72E-1
891. bta-miR-12018 MIMAT0046701	26839	-9.60	ATAAGTTCCTTCTT-TACAAGAA :       :       AGTTCTGTAAGAGCCTGTTCTA	3.25E-1
892. bta-miR-2297 MIMAT0011805	27361	-7.90	CATGATTTTAAGGAAGAGTT   :        TCCTTATTCTTTTTTCTCAC	1.61E-2
893. bta-miR-12003 MIMAT0046662	27821	-13.20	ATTATAATAGCTA-CCACAATGCC   :           CTTGGATACCGTTGG-GTTACGA	2.25E-1
894. bta-miR-2437 MIMAT0012011	28635	-8.60	TTACAACGATGTAAAACCACC : ::       TTTCCTTTTGTTTTTTGGTGT	1.78E-1
895. bta-miR-2374 MIMAT0011920	30205	-25.36	CCCGCCAGAAGAGGAGCCCCAA             GGGCGG-AGAGGGGTCGGGGTT	5.91E-3
896. bta-miR-12018 MIMAT0046701	30526	-7.90	TGAATGCATATCAACAACAAGAT :             AGTTCTGTA-AGAGCCTGTTCTA	2.11E-1



1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
897. bta-miR-17-3p MIMAT0003816	30663	-11.60	AGTAGAGAGTTGACTGCAGA           TGTTACCGGAAGTGACGTCA	1.28E-1
898. bta-miR-6529b MIMAT0029947	266	-17.80	GGATGTTTGAGGACGCAGAGG           TCTCTAGTCTCC-GCGTCTCA	3.03E-1
899. bta-miR-29e MIMAT0009953	479	-10.90	AGGTGCT-ACTTCAA--GATGCTT :           TTTGTGACTAAAGTTTACTACGAT	3.03E-1
900. bta-miR-6529b MIMAT0029947	1125	-14.10	TTATGTTATGAGACTGCAGAGT :   :       :           TCTCTAGT-CTC-CGCGTCTCA	1.69E-1
901. bta-miR-2469 MIMAT0012059	2783	-15.30	AGG-AACAG--CCTACAGTAA   :                   TTCGGCGTCCGGGATGTCATT	2.9E-1
902. bta-miR-2284k MIMAT0011907	3982	-6.20	TTTTCAATGACT--ACTTTTG :     :           TTTTTGGGCTGGCTTGAAAAG	2.11E-1
903. bta-miR-2284k MIMAT0011907	5797	-9.60	AAAAATTTGAAACAACTTTTA         : :             TTTTTGGGCT-GGCTTGAAAAG	2.39E-2
904. bta-miR-2469 MIMAT0012059	7067	-13.80	AAGCCATTGATGTAGTACAGTAT         :           TTCGG--CGTCCGGGATGTCATT	2.42E-1
905. bta-miR-2285bs MIMAT0046637	7749	-8.20	TAATTTGCTACATTCTAAGGTTAA       :           GGTTTTTCAAGTAGG--TCCAATC	2.98E-1
906. bta-miR-767 MIMAT0009375	8174	-13.10	AAAGTTGTAATAACT-TGGTGCC   :   :     :           GTACGAGTCTGTTGGTACCACGT	3.62E-1
907. bta-miR-484 MIMAT0003535	9258	-10.00	GTTTAAAGGTTTAGCACAGCCTGT       :           TAGCCCTCC--CCTGACTCGGACT	2.28E-1
908. bta-miR-2284k MIMAT0011907	9693	-6.00	AATGGCTCTTACT--ACTTTTA : :   :     :           TTTTTGGG-CTGGCTTGAAAAG	1.98E-1
909. bta-miR-29e MIMAT0009953	10488	-8.50	TTTTTATGGTCCTTATAAGGATGCTC     :     :           TTTGTGACTA-AAGT-TTACTACGAT	8.51E-2
910. bta-miR-2285bs MIMAT0046637	11394	-5.80	ATCTATGGCTGCAGCAAAGGTTAT :                   GGTTTTTC-AAGT-AGGTCCAATC	1.15E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
911. bta-let-7b MIMAT0004331	11446	-14.10	TATTTACAG - -ATATACCTCA   :     :       TTGGTGTGTTGGATGATGGAGT	8.26E-2
912. bta-miR-2364 MIMAT0011902	11975	-16.80	CTGTTTTCAGGC - TTTACAGAGT     : :      : :       GACG - GGTGTAGGTAGGTGTCTCT	2.39E-1
913. bta-miR-424-3p MIMAT0015304	13464	-8.40	AAAGTTAATTGCTGC - CGTTTTTC    : :    :         TATCG - -TCGCGGAGTGCAAAAC	3.76E-1
914. bta-miR-6529b MIMAT0029947	16083	-15.70	AGAAGTGCAGTTATGCAGAGT           :       TCTCTA - GTCTCCGCGTCTCA	3.52E-1
915. bta-miR-2285bf MIMAT0046382	16217	-6.10	TAAATATGTTT - TGAGTGTTTC :               GTTT - TTCAAACAAGCACAAAA	1.69E-1
916. bta-miR-2285bf MIMAT0046382	17149	-5.80	CCACTCGTAAGTATGTGTTTA       :       GTTTTTCAAACAAGCACAAAA	3.39E-1
917. bta-miR-2477 MIMAT0012069	19151	-13.80	TGTTA - AC - AAACATGCATTCCAC :    :             GCAGTCTGAATAGTA - GTAAGGTG	3.16E-1
918. bta-miR-29e MIMAT0009953	19250	-14.70	GTATATGGATGGCA - TGGATGCTA   :   :              TTTGTGACTAAAGTTTACTACGAT	2.46E-1
919. bta-miR-370 MIMAT0009300	19260	-13.20	GGCATGG - -ATGCT - AAGCAGGT :       : :       TGGT - CCAAGGTGGGGTCGTCCG	2.46E-1
920. bta-miR-484 MIMAT0003535	20024	-13.20	CAGCCAATTCGAC - -AGCCTGA           TAGCCCTCCCCTGACTCGGACT	7.09E-2
921. bta-miR-2477 MIMAT0012069	21276	-8.20	TATTTGTTTGGAGAAATTCAC :    :       GCAGTCTGAATAGTAGTAAGGTG	7.65E-2
922. bta-miR-2469 MIMAT0012059	21460	-10.90	TTTTTGTTGGT - -GACAGTAT : :   :    :       TTCGGCGTCCGGGATGTCATT	1.45E-1
923. bta-miR-484 MIMAT0003535	21656	-13.50	TGCTATGCTGGATATTCAGCCTGA     :       TAGCCCTCCCCTG - -ACTCGGACT	2.25E-1
924. bta-miR-767 MIMAT0009375	22006	-12.40	TTGAAATAGTTAAGCT - TGGTGCT :      :       GTACGAGTC - TGTGGTACCACGT	6.99E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
925. bta-miR-7862 MIMAT0030442	24531	-13.70	AACACTATCTA - - TAGCACCA   :        CGAGTCGAGGTCCCTCGTGGT	5.76E-2
926. bta-miR-29e MIMAT0009953	24753	-9.50	ATTTACTTGTAAATAATATTGATGCTG :    :  :         TTTGTGACTAAAGTT - - TACTACGAT	1.75E-1
927. bta-miR-2285bf MIMAT0046382	25023	-6.60	GCCTCAACCTGTAGGTGTTTT           GTTTTTCAAACAAGCACAAAA	2.46E-1
928. bta-miR-11987 MIMAT0046387	26566	-23.80	ACCTCTGCTAGTCTGTTTCCTCC        :           TGGAGGTGGTC - - TCTAAGGAGC	3.46E-2
929. bta-miR-2285ct MIMAT0046695	28048	-7.10	AGGTAGA - CC - TTATAACTTTA   :  :           TCTTTTAGGTTTGATTGAAAG	2.5E-1
930. bta-miR-6529b MIMAT0029947	29624	-12.90	GGAG - TTTGAATTTGCAGAGG :       :    TCTCTAGTCT - CCGCTCTCA	8.64E-2
931. bta-miR-2299-3p MIMAT0011808	29851	-19.30	AGGCTGATGTCAATACCCCGGC        :            TGCGAC - CTAGGTAAGGGGCCT	1.98E-1
932. bta-miR-2392 MIMAT0011945	29992	-19.20	GATCTACTTCACGCGCATCCAG   :            ACGTGGGGAGTGGGGGTAGGTA	2.01E-1
933. bta-let-7b MIMAT0004331	30054	-19.30	GGCAACAGAAC - CCTACCTCT : :                 TTGGTGTGTTGGATGATGGAGT	2.94E-1
934. bta-miR-2469 MIMAT0012059	30460	-8.80	GTGCAATTAGATTTGACAGTAC    :   :       TTCG - GCGTCCGGGATGTCATT	3.29E-1
935. bta-miR-29d-3p MIMAT0009275	2236	-13.70	TTTCATGTTTTGCATGGTGCTT :    : :       ATTAGCTAAAGTTTACCACGAT	2.61E-1
936. bta-miR-23a MIMAT0003827	3655	-17.10	TGGAAATGC - ATTAAATGTGAT                ACCTTTAGGGACCGTTACACTA	3.34E-1
937. bta-miR-29d-3p MIMAT0009275	6787	-12.30	AGTGTGGTTGCTAGA - GGTGCTT : :   : :        ATTAGCTAA - AGTTTACCACGAT	3.52E-1
938. bta-miR-11979 MIMAT0046367	8176	-9.50	AGTTGTAATAAC - - TTGGTGCC         :          TCCTCACTGGTGCCACCACGT	3.62E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
939. bta-miR-302c MIMAT0009281	8794	-10.30	TATGGTTACCATGTGTTGCACTTT              GGTGACTTTGTAC-CTTCGTGAAT	1.54E-1
940. bta-miR-302c MIMAT0009281	8811	-9.50	GCACTTTATTACA--CATGCACTTT                 GGTGA--CTTTGTACCTTCGTGAAT	1.54E-1
941. bta-miR-301a MIMAT0009276	8905	-15.80	GTGCTTT-CCTCTGCT--TGCACTA :         :          TACGAAACTGTTATGATAACGTGAC	2.69E-1
942. bta-miR-2285ak-5p MIMAT0040948	8943	-8.70	TGG-TAGTCC--AC-AACCTTA                  TCCTTTTGGGCTTGCTTGGAAA	3.62E-1
943. bta-miR-11979 MIMAT0046367	9301	-16.70	GCTAGT-TCCATTGCTGGTGCT          :         TCCTCACTGGTGCCCAACACGT	2.28E-1
944. bta-miR-487a MIMAT0003805	9697	-6.94	GCTCTTACTACTTTTATGATT :      :         TGACCTACAGGGACATACTAA	1.98E-1
945. bta-let-7e MIMAT0004333	11442	-11.40	TTTGTATTTACAGATATACCTCA :   :    :          TGATATG--TTG-GAGGATGGAGT	8.26E-2
946. bta-miR-98 MIMAT0003809	11446	-10.70	TATTTACAG--ATATACCTCA     :       TTGTTATGTTGAATGATGGAGT	8.26E-2
947. bta-miR-302c MIMAT0009281	11800	-9.90	TTGTGGCAATATTGTAGCACTTT    :            GGTGACTTTGTACCTTCGTGAAT	6.2E-2
948. bta-miR-487a MIMAT0003805	14022	-6.70	TCTTATTATTCTTATATGATG   : :         TGACCTACAGGGACATACTAA	2.42E-1
949. bta-miR-1287 MIMAT0009971	14418	-23.50	CTTTTATATGCTGCTGATCCAGCT :   :         CTGAGT--TTGGTGACTAGGTCGT	7.54E-2
950. bta-miR-2318 MIMAT0011841	15733	-7.10	ATGAATTCTGTTCAACATACAA :              CCAGTCTATTAAGT--AGTATGTG	1.15E-2
951. bta-miR-23a MIMAT0003827	16249	-8.60	GTAACGCACCAGG--ATGTGAT            ACCTTTAGGGACCGTTACACTA	1.36E-1
952. bta-miR-2318 MIMAT0011841	17044	-5.30	CATTGTGTGAAAAAGCATACAA :   :         CCAGTCTATTAAGTAGTATGTG	2.54E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
953. bta-miR-2285d MIMAT0011815	19260	-10.70	GGCATGGATGCTAAGCAGGTTG       :             CGGTTTTTAAAGCAAGTCCAAA	2.46E-1
954. bta-miR-2318 MIMAT0011841	20362	-9.00	TTTCATACGACTCCAGCATACAC                     CCAGTCTATTAAG- TAGTATGTG	1.89E-1
955. bta-miR-29d-3p MIMAT0009275	21298	-12.00	CAGTTTGGAAACGGG- GGTGCTT   : :           ATTAGCTAAAGTTTACCACGAT	7.65E-2
956. bta-miR-2285bd MIMAT0046379	21554	-9.10	TACCCAGTTTG- -AGGGTTT       : :           GTTTTTCAAGTAGTCCAAA	1.45E-1
957. bta-miR-11979 MIMAT0046367	22010	-8.90	AATAGT- TAAGC- - TTGGTGCT       :           TCCTCACTGGTGCCACCACGT	6.99E-2
958. bta-miR-669 MIMAT0013838	22083	-12.50	TTTGAATAT- AATCCACCCACT   :               GTGCGTGTACGTGTGTGGGTGT	3.48E-1
959. bta-miR-487a MIMAT0003805	22101	-8.60	ACTGATAAGCTAGCTATGATT         :           TGACCTACAGGGACATACTAA	3.48E-1
960. bta-miR-215 MIMAT0003797	22616	-7.40	AATTACACAG- GCGAAGGTCAA     :   :           ACAGACAGTTAAGTATCCAGTA	1.86E-1
961. bta-miR-2288 MIMAT0011795	23290	-11.80	TTTTCGTAATTCTACTACCA :   : :   :           TTTGGTGTGTGGATGATGGA	2.01E-1
962. bta-miR-2288 MIMAT0011795	23827	-11.80	TTGCTTAATGGTTACTACCC :   :   : :           TTTGGTGTGTGGATGATGGA	2.86E-1
963. bta-miR-23a MIMAT0003827	24228	-7.40	GCGTAATTTACATATGATGTGAA         :           ACCTTTAGGG- -ACCGTTACACTA	1.36E-1
964. bta-miR-23a MIMAT0003827	25868	-7.00	GTGTTGTTC- -AAACATGTGAT :   :             ACCTTTAGGGACCGTTACACTA	1.98E-1
965. bta-miR-23a MIMAT0003827	27766	-12.10	ATTACATCCCTTCAATCATGTGAA                     ACCTTTAGGGA- -CCGTTACACTA	2.11E-1
966. bta-miR-26b MIMAT0003531	29046	-6.40	AACCCAGAAACAAACAACCTTGAT                     TTGG- ATAGGACTTAATGAACTT	3.15E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
967. bta-miR-23a MIMAT0003827	29197	-10.70	CAGATTG GCC - AGCTTATGTGAC                    ACCTTTAGGGACCG - TTACACTA	2.11E-1
968. bta-miR-2410 MIMAT0011968	29509	-13.60	CCAGGGGT - - AGAAGAGCTCAA    :                  AGTGTCCAGGAGGAGTCGAGTC	7.91E-3
969. bta-miR-98 MIMAT0003809	30052	-13.10	CTGGCAACAGAACCCCTACCTCT      :                 TTGTTATGTT - GAATGATGGAGT	2.94E-1
970. bta-let-7e MIMAT0004333	30055	-20.30	GCAACAGAACC - CCTACCTCT                     TGATATGTTGGAGGATGGAGT	2.94E-1
971. bta-miR-301a MIMAT0009276	30215	-12.10	GAGGAGCCCCAATAACAATGCACTG                     TACGAAACTGTTAT - GATAACGTGAC	5.91E-3
972. bta-miR-669 MIMAT0013838	30333	-20.80	CTTG CAGA - ACTCGCACCCACA :          :               GTGCGTGTACGTGTGTGGGTGT	4.98E-2
973. bta-miR-11979 MIMAT0046367	30341	-15.70	ACTCGCACCCACAGCTGGTGCG                     TCCTCACTGGTGCCACCACGT	4.98E-2
974. bta-miR-2290 MIMAT0011798	267	-11.50	GATGTTTGAGGACGCAGAGGA :                    TGTTTGGCTGGTG - GTCTCCG	3.03E-1
975. bta-miR-12058 MIMAT0046765	3106	-12.50	GATGATGACTTTCTTGAAGAAA                     CGTGTACTGA - TGACCTTCTTG	1.72E-1
976. bta-miR-449b MIMAT0009321	3450	-18.50	GGCAGTGATGCAG - AAAGTGCCC       : :   :           CGGTCG - ATTGTTATGTGACGGA	1.22E-2
977. bta-miR-2450a MIMAT0012030	3454	-15.80	GTGATGCA - - GAAAGTGCCCT                     GTGTACGTGGAGATGACGGGT	1.22E-2
978. bta-miR-369-3p MIMAT0003802	5904	-8.20	TAAGTATTATACTCAGCGTATTATT         :                 TTTC - TAGT - TG - GT - ACATAATAA	6.48E-2
979. bta-miR-11993 MIMAT0046634	6064	-21.10	ACTGAGTGGCCAACAGCTACAGGTG                     GTACTCACATGT - - GCG - TGTCCAG	4.26E-2
980. bta-miR-93 MIMAT0003837	8812	-12.30	CAC TTTATTACACATGCACTTTC                     ATGGACGTGCTTGT - CGTGAAAC	1.54E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
981. bta-miR-2420 MIMAT0011987	8940	-12.00	CGATGGTAGTC-CACAACCT : :    :         TTTCTTATTTGTGTGTTGGA	3.62E-1
982. bta-miR-12028 MIMAT0046721	10049	-18.60	ATAAGGTCTACTGTCCCAGACA : :          TCTCTTAG-CCCCAGGGTCTGT	1.75E-1
983. bta-miR-12058 MIMAT0046765	11320	-8.50	GGTTCTAACTTAGAGGAAGAAA           CGTGTACTGA-TGACCTTCTTG	2.73E-1
984. bta-miR-93 MIMAT0003837	11802	-12.20	GTGGCAATATTGTAGCACTTTG :       ATGGACGTGCTTGTCTGTAAC	6.2E-2
985. bta-miR-20b MIMAT0003796	11803	-16.00	TGGCAATATTGT-AGCACTTTG : :           ATGGACGTGACACTCGTGAAC	6.2E-2
986. bta-miR-12058 MIMAT0046765	11927	-12.40	GC-C-TGACTAGTATTGAAGAAG                    CGTGTACTGATGA--CCTTCTTG	1.75E-1
987. bta-miR-380-3p MIMAT0003804	13607	-6.10	TGAACACGATTTCTTTACATT       :         TCTGCACCTGGTGTAATGTAT	2.73E-1
988. bta-miR-376e MIMAT0025543	13962	-7.30	TGGTATGATTTTGGTGACTATGTT             TTACACCTAAAA--GGAGATACAA	3.48E-1
989. bta-miR-381 MIMAT0009307	16270	-6.00	TAAATGATGTT-ACCAAATTGTATC      :            TGTCTCT-CGAACGG--GAACATAT	1.36E-1
990. bta-miR-2420 MIMAT0011987	16726	-10.80	TGTATTATCGCGCCACAACCA : :         TTTCTTATTTGTG-TGTTGGA	8.13E-2
991. bta-miR-92a MIMAT0009383	19305	-13.00	ACTTGC-ATCACAAGATGCAATT                   TGTCCGGCCCTGTTC-ACGTTAT	2.46E-1
992. bta-miR-6525 MIMAT0025554	20639	-12.70	TAAGTATTTGAATTCCCCAA : :          GAGTGAGGACGAAAGGGGTC	3.25E-1
993. bta-miR-668-3p MIMAT0040936	21454	-10.40	AAGAAGTTTTTGTG-TGACAG       :         CCCATCA--CCCGGCTCACTGTA	1.45E-1
994. bta-miR-20b MIMAT0003796	21522	-6.00	GACAAGC-CT--AATCACTTTA               ATGGACGTGACACTCGTGAAC	1.45E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
995. bta-miR-93 MIMAT0003837	21522	-5.80	GACAAGC-CTAAT--CACTTTA           :       ATGGACGTGCTTGTCGTGAAAC	1.45E-1
996. bta-miR-92a MIMAT0009383	21942	-5.70	GATTTCATAAACAGCATGCAATT    :       TGTCGGGCCCTGTT-CACGTTAT	9.19E-2
997. bta-miR-12058 MIMAT0046765	22150	-7.80	GTA-AAGA--GCTAGAAGAAG  :     :       CGTGTACTGATGACCTTCTTG	3.85E-1
998. bta-miR-2450a MIMAT0012030	22520	-21.40	TATATGGACCTTAATCCTGCCCT  :        :       GTGTACGTGGAG--ATGACGGGT	3.66E-1
999. bta-miR-369-3p MIMAT0003802	22983	-7.00	TTTTGTGCAATACAAAGTATTATG :   :          TTTCTAGTT--GGT-ACATAATAA	3.76E-1
1000. bta-miR-380-3p MIMAT0003804	25243	-9.00	ACTCCCGACCC-CATTACATC          TCTGCACCTGGTGTAATGTAT	1.04E-1
1001. bta-miR-769 MIMAT0009376	29215	-13.10	TGACTGTTGCT--AAGGTCTCA :  :       TCGAGTCTTGGGCCTCCAGAGT	2.11E-1
1002. bta-miR-2290 MIMAT0011798	29624	-9.20	GGAGTTTGAATTTGCAGAGGG :  :          TGTTTGGCT-GGTGGTCTCCG	8.64E-2
1003. bta-miR-6525 MIMAT0025554	30313	-13.70	GTGAC-CCACAGTTCCCCAT              GAGTGAGGACGAAAGGGGTC	4.98E-2
1004. bta-miR-20b MIMAT0003796	30469	-6.20	GATTTG-ACAGT--ACACTTTC  :  :            ATGGACGTGACACTCGTGAAAC	3.29E-1
1005. bta-miR-323b-3p MIMAT0040935	1705	-10.60	GTAGGTTGCAAGGCTATTGTA    :  :          TCTCCGGCTGGCACATAACAC	3.11E-2
1006. bta-miR-7864 MIMAT0030449	2905	-15.80	ACTGTGGAT--ATGGAGGAAT    :  :  :       AGACGGTTGGCCTTCTCCTTC	1.36E-1
1007. bta-miR-7864 MIMAT0030449	3145	-11.30	GATGT-AGAAGG-TGAGGAAA   :          AGACGGTTGGCCTTCTCCTTC	2.73E-1
1008. bta-miR-2425-5p MIMAT0011994	3453	-14.70	AGT-GATGCAGAAAC-TGCCCTGT                    TCAAGTAC--CTAGGCACGGGACC	1.22E-2



1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
1009. bta-miR-11986c MIMAT0046638	3516	-5.50	TAAGCAACAGTATAGTCAGTTG   :       AGAAAAGGTTTCCTGAGTCAAG	2.58E-1
1010. bta-miR-10184-3p MIMAT0040943	3650	-9.10	CATACTGG--AAATGCATTAAA   :       GGTAACCCAAAAGATGTAATTT	3.34E-1
1011. bta-miR-2284v MIMAT0011937	3980	-6.00	CATTTTCAA-TGACTACTTTTG :    :       TTTGGGGTTTGCT-TGAAAAA	2.11E-1
1012. bta-miR-2284d MIMAT0011836	5796	-8.30	TAAAAATTGAAACAACTTTTA     ::       CTTTTGGG-ATTGCTTGAAAAA	2.39E-2
1013. bta-miR-2284v MIMAT0011937	5799	-10.30	AAATTTGAAACAACTTTTA     ::       TTTGGGGTTTGCTTGAAAAA	2.39E-2
1014. bta-miR-2284d MIMAT0011836	6130	-5.60	GAAAGGGTGTATTACTTTTG     ::  :       CTTTTGGGATTGCTTGAAAAA	2.14E-1
1015. bta-miR-2284v MIMAT0011937	6929	-6.00	GGATTAAGAAC--ACTTTTA :: :::       TTTGGGGTTTGCTTGAAAAA	2.28E-1
1016. bta-miR-2284v MIMAT0011937	7547	-6.10	ATAAACCAAGTAATACTTTTA    :::       TTTGGGGTTTGCT-TGAAAAA	2.94E-1
1017. bta-miR-323b-3p MIMAT0040935	8944	-7.40	GGTAGTCCACAACCTTATTGTT :    :          TCTCCGGCTG-GCACATAACAC	3.62E-1
1018. bta-miR-2284d MIMAT0011836	9692	-8.50	AAATGGCTCTTAC-TACTTTTA :: :          CTTTTGGGATTGCTTGAAAAA	1.98E-1
1019. bta-miR-2284v MIMAT0011937	9695	-7.60	TGGCTCT-TAC-TACTTTTA :: :          TTTGGGGTTTGCTTGAAAAA	1.98E-1
1020. bta-miR-12005 MIMAT0046666	9921	-9.50	TGCTTCCGTTT--CAACTTCAT    :          TGGGAGGGGAATTCCTGAAGTA	7.65E-2
1021. bta-miR-323b-3p MIMAT0040935	9941	-14.00	TCTTGCAATCTG-GTATTGTG     :       TCTCCGGCTGGCACATAACAC	7.65E-2
1022. bta-miR-323b-3p MIMAT0040935	9981	-16.60	TAAGGTAGAACCATGTATTGTC    :          TCTCCGGCT-GGCACATAACAC	7.65E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
1023. bta-miR-208b MIMAT0009262	10165	-13.30	CTAAGCCTTACAGTGATGTCTTAT   :        :        TGTTTGGAA-AACA-AGCAGAATA	3.56E-2
1024. bta-miR-7864 MIMAT0030449	11320	-13.50	GGTTCTAACT--TAGAGGAAG :   :       AGACGGTTGGCCTTCTCCTTC	2.73E-1
1025. bta-miR-302a MIMAT0009278	11800	-9.90	TTGTGGCAATATTGTAGCACTT   :          AGTGATTTTGTACCTTCGTGAA	6.2E-2
1026. bta-miR-11986c MIMAT0046638	11860	-13.90	GCTTTTGAAAAGCTTGCTCAGTTG            :        AGAAAAGGTTTC--CTGAGTCAAG	1.67E-1
1027. bta-miR-6715 MIMAT0046369	11911	-15.90	GCTGTGGAT-AGCAAGTGCCTGA     :  :         CGA-GTTTGACCG-GCACGGACA	1.75E-1
1028. bta-miR-323b-3p MIMAT0040935	16296	-8.60	GGTGGTATGTCATATTATTGTG     : :          TCTCCG-GCTGGCACATAACAC	1.36E-1
1029. bta-miR-134 MIMAT0009227	16942	-17.60	GACCTCCTGGTACAGGAAAGTCACA             :       GGTGAG-ACCA-GTT-GGTCAGTGT	1.11E-1
1030. bta-miR-1388-3p MIMAT0013591	17172	-14.50	ACTATAAATGCATTACCTGAGAT :          ACGCCC GACTGT-TTGGACTCTA	3.39E-1
1031. bta-miR-10180-3p MIMAT0040938	18311	-22.80	GGCTGTGGCTAAAGCTCCTCCTG :    :      :      TCG-TGTCG--CGCGGGGAGGAG	2.5E-1
1032. bta-miR-323b-3p MIMAT0040935	18671	-5.60	TAATCATGATT-TATATTGTA :   :         TCTCCGCTGGCACATAACAC	2.36E-2
1033. bta-miR-10180-3p MIMAT0040938	18704	-22.10	AGCACA-TGT-TGCCTCCTC       :  :         TCGTGTGCGCGGGGAGGAG	2.36E-2
1034. bta-miR-1388-3p MIMAT0013591	20025	-16.10	AGCCAATTCGACAG-CCTGAGAG         :       ACG-CCCGACTGTTTGGACTCTA	7.09E-2
1035. bta-miR-2308 MIMAT0011820	20048	-16.60	CAGCTCT--AACCAGAGCCCAC :     :       AATGAGAGACGACGTTCTGGGTT	7.09E-2
1036. bta-miR-11986c MIMAT0046638	20521	-13.40	TTGATTTTAAAGATTTTCAGTTC   :     :       AGAAAAGGTTTC-CTGAGTCAAG	3.16E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
1037. bta-miR-6715 MIMAT0046369	20846	-17.70	TCTTAGGCAGTGGT - -TGCCTGC   : ::     :       CGAGTTTG - -ACCGGCACGGACA	2.78E-1
1038. bta-miR-2457 MIMAT0012042	21198	-16.20	AGTGAAGGGTTTT-TAATTGGCAT   :    : :  :        TCGC - -GCCGAGACGTCAACCGTT	2.01E-1
1039. bta-miR-2285ba MIMAT0046373	21549	-11.59	CCACTTACCCAGTTTGAGGGTTT        :       GGTTTTTCAAGCAAG-TCCCAAA	1.45E-1
1040. bta-miR-2403 MIMAT0011960	22161	-15.70	GAAGAAGGTGATCTTCCCGAG  :       TTCCGGTCGATCGAAGGGCTC	3.85E-1
1041. bta-miR-653 MIMAT0009358	22620	-9.60	ACACAGGCGA - -AGGTCAACAA    :          GTTGTCT-CTAACAAAGTTGTG	1.86E-1
1042. bta-miR-10180-3p MIMAT0040938	26571	-16.30	TGC-TAGTCTGTTTCCTCCTT    :  : : ::       TCGTGTCGCGCGG-GGAGGAG	3.46E-2
1043. bta-miR-653 MIMAT0009358	27332	-10.20	TAATGCTGAACATTTCAACAC :   ::          GTTGTCTCTAACAAAGTTGTG	6.88E-2
1044. bta-miR-12051 MIMAT0046754	27468	-14.90	AATGAATAGGT - -TACAGGAGG    :   :        AGCCTTGCTCTACGACGTCCTCA	2.14E-1
1045. bta-miR-1388-3p MIMAT0013591	28112	-18.20	GGACATCTGG-AGACCTGAGAT    :  :      ACGCCCCACTGTTTGGA CTCTA	3.03E-1
1046. bta-miR-12051 MIMAT0046754	29650	-12.90	GTGTGCCTATTGCACCAGGAGT           AGCCTTGCTCTACGACGTCCTCA	2.69E-1
1047. bta-miR-12005 MIMAT0046666	29979	-10.40	GCTCCTAATTCCAGATCTACTTCAC :       :         TG-GGA - -GGGGAATTCTGAAGTA	2.01E-1
1048. bta-miR-2366 MIMAT0011904	30298	-15.80	TAAAACTTGGA ACTAGTGACCCA   ::          GGTCTGGGAGAAGA-CACTGGGT	4.98E-2
1049. bta-miR-29c MIMAT0003829	2236	-13.70	TTTCATGTTTTGCATGGTGCTT :    :         ATTGGCTAAAGTTTACCACGAT	2.61E-1
1050. bta-miR-2399-5p MIMAT0011954	3443	-21.60	CAGTTTTGGCAGTGATGCAGAAAC    : :  :  :      ATCAAGGTTGTCG - -ATGTCTTTC	1.22E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
1051. bta-miR-2367-5p MIMAT0011909	4284	-17.00	ACCTGATG-C-GAGGACACAGGGT                  GAGACTACCGACTC-AATGTCCCA	1.75E-1
1052. bta-miR-2284m MIMAT0011976	5798	-14.00	AAAATTGAAACAACTTTTA    ::        TTTTGGGCTT-GTTTGAAAAG	2.39E-2
1053. bta-miR-2330-5p MIMAT0011861	5916	-14.30	TCAG-C-GTATTATTAAAGCCCA :      :   :       GGTCAGGAGTGACGGGTTCGGGT	6.48E-2
1054. bta-miR-197 MIMAT0009257	6260	-15.00	ATGATGTTGACGATGGTGGTGAT             CGACCCACCT-CTTCCACCACTT	3.52E-1
1055. bta-miR-29c MIMAT0003829	6787	-12.30	AGTGTGGTTGCTAGA-GGTGCTT :   :   :         ATTGGCTAA-AGTTTACCACGAT	3.52E-1
1056. bta-miR-2362 MIMAT0011900	6908	-13.20	TTGTTGGTAAGATCG-CACAGTG :   :       CCAGTCTTGCGAGGTAGTGTCAC	2.28E-1
1057. bta-miR-2284m MIMAT0011976	6928	-5.40	TGGATTAAAGAAC--ACTTTTA : :   :            TTTTG-GGCTTGTTTGAAAAG	2.28E-1
1058. bta-miR-2284m MIMAT0011976	7548	-6.20	TAAACCAGGTAATACTTTTA      :       TTTTGGGCTTGTTTGAAAAG	2.94E-1
1059. bta-miR-2362 MIMAT0011900	8530	-7.60	TTAATGCCCACTT--ACACAGTA     :       CCAGTCTTGCGAGGTAGTGTCAC	5.51E-2
1060. bta-miR-761 MIMAT0009373	8817	-11.00	TATTACACATGCACTTTCTGCTGA        :       ACACAGTCAAAGTGG--GACGACG	1.54E-1
1061. bta-miR-29c MIMAT0003829	9299	-14.60	CTGCTAGTTCCATTGCTGGTGCTA :   :             ATTGGCTAAAGT--TTACCACGAT	2.28E-1
1062. bta-miR-2284m MIMAT0011976	9694	-7.50	ATGGCTCTTAC-TACTTTTA : :   :          TTTTGGGCTTGTTTGAAAAG	1.98E-1
1063. bta-miR-2355-5p MIMAT0011891	9932	-7.60	CAACTTCATTC-TTGCAATCTGGT :             CGTATAACAGGTAAC-ATAGACCC	7.65E-2
1064. bta-miR-194 MIMAT0009254	9990	-9.30	ACCATGTATTGTCAGTGTACC     : :            AGGTGTACCTCAACGACAATGT	7.65E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
1065. bta-miR-2330-3p MIMAT0011862	10303	-15.04	AACGGCAAACCACAAGGAGC             CTGCCGGTCCCCATTCTCA	3.62E-1
1066. bta-miR-2285x MIMAT0029946	10472	-6.30	CTGA--TTTCAATGGGGATTTTTA           :       GGTTTTCAAGT-AAGTCTAAAAAG	8.51E-2
1067. bta-miR-376b MIMAT0009945	10691	-12.00	TAGATGCTTTAGCTTCTATGAC         :       TTGTACCTAAAAGGAGATACTA	3.07E-1
1068. bta-miR-2355-5p MIMAT0011891	11832	-13.90	AATACTTG-CCACTTCTGATCTGGG               CGTATAACAGGT--AACATAGACCC	6.2E-2
1069. bta-miR-10165-5p MIMAT0040912	11969	-15.10	ACAATACTGTT--TTGCAGGCT :    : :       CACAGGAGCAGTGGACGTCCGA	2.39E-1
1070. bta-miR-194 MIMAT0009254	16174	-13.00	TTTGC-TGCAAGTGTGTTACG   :         :       AGGTGTACCTCAACGACAATGT	5.43E-2
1071. bta-miR-2399-5p MIMAT0011954	17731	-16.00	TATATTCA-CAGACTGCAGAAAC   :           :       ATCAAGGTTGTC-GATGTCTTTC	1.09E-1
1072. bta-miR-6516 MIMAT0030443	18857	-10.20	TAAAGCTGCCATG-CTCTGCAAC :   :             CAAGTG-TGG-ACAATGACGTTT	6.11E-2
1073. bta-miR-376b MIMAT0009945	18933	-11.70	GATTTTGATTTTAAGTTCTATGAT       :       TTGTACCTAAAA--GGAGATACTA	2.25E-1
1074. bta-miR-197 MIMAT0009257	19514	-14.50	TTATACAGGA-CAGGCTGGTGAA               CGACCCACCTCTTCC-ACCACTT	1.98E-1
1075. bta-miR-154c MIMAT0025542	20733	-11.70	TATACTCAGTTATGTCAATATCT     : :          TCTCTAGTTGGCAC-GTTATAGA	1.92E-1
1076. bta-miR-2330-3p MIMAT0011862	20808	-14.50	GCAGGTTTCAG-AAAAAGGAGT    :           CTGCCG-GTCCCCATTCTCA	2.61E-1
1077. bta-miR-2362 MIMAT0011900	21286	-9.60	GG--AGAA--ATTCT--CACAGTT           :       CCAGTCTTGCGAGGTAGTGTAC	7.65E-2
1078. bta-miR-29c MIMAT0003829	21298	-12.00	CAGTTTGAACGGG-GGTGCTT   : :       ATTGGCTAAAGTTTACCACGAT	7.65E-2

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
1079. bta-miR-2285ar MIMAT0046337	21552	-9.10	CTTACCCAGTTTG - -AGGGTTT    :  CGGTTTTTCAAGTAGTCCCAA	1.45E-1
1080. bta-miR-376b MIMAT0009945	22098	-7.40	CCCACTGATAAGCTAGCTATGAT    :  TTGTACCTAAAAGG-AGATACTA	3.48E-1
1081. bta-miR-2362 MIMAT0011900	25873	-11.90	GTTCAAACATGTGATCTCACAGTA    :  CCAGT-CTTGCGAGGTAGTGTAC	1.98E-1
1082. bta-miR-2362 MIMAT0011900	26141	-15.40	ATGCAGCATGT-AAATCACAGTT    :  CCAGTCTTGCGAGGTAGTGTAC	1.78E-1
1083. bta-miR-2285ar MIMAT0046337	29330	-13.12	GCCA-TCAACCCAAAAGGGTTC    :  CGGTTTTTCAAGTAGTCCCAA	3.48E-1
1084. bta-miR-761 MIMAT0009373	29737	-19.00	GCAACCAGCGTCA-ACTGCTGC    :  ACACAGTCAAAGTGGGACGACG	1.11E-1
1085. bta-miR-2399-5p MIMAT0011954	30173	-6.90	CAAAGAAATCAG--ACAGAAAA    :  ATCAAGGTTGTCGATGTCTTTC	5.91E-3
1086. bta-miR-2330-5p MIMAT0011861	30185	-14.60	ACAGAAAATTTTGAATAAGCCCC    :  GGTCAGGAGTGACGGGTTCGGGT	5.91E-3
1087. bta-miR-2362 MIMAT0011900	30302	-13.00	ACTTGGAAGTAGTGACC--CACAGTT    :  CCAGTCTTG--CG-AGGTAGTGTAC	4.98E-2
1088. bta-miR-2399-5p MIMAT0011954	30719	-8.50	TACTGAAGACACCT-CAGAAAT :   :  ATCAAGGTTGTCGATGTCTTTC	2.39E-1
1089. bta-miR-194b-3p MIMAT0040934	245	-10.80	ACTGGGCTCCAGAATTTCCATGG    :  GCTAACATTGTCGTTGAGGTACA	8.01E-2
1090. bta-miR-2898 MIMAT0013856	319	-16.30	GATATAGTATGCTCCACCA :   :  AGGGGCCGTA-GAGGTGGT	1.54E-1
1091. bta-miR-450a MIMAT0003834	325	-9.32	GTATGCTCCACCACTGCGCAAAA :   :  TATA-ATCCTTGTGTAGCGTTTT	1.54E-1
1092. bta-miR-2285dj MIMAT0046747	2944	-8.20	GCCATAGA--AGAG-AAACTTTC : : :  CCCTGTTTGACTTGTTTGAAAG	2.42E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
1093. bta-miR-194b-3p MIMAT0040934	2950	-11.40	GAAGAGAAAC - - TTTCTCCATGT           GCTAACATTGTCGTTGAGGTACA	2.42E-1
1094. bta-miR-2285ae MIMAT0030448	3094	-11.70	ACAGCTCCTGAAGATGATGACTTTCT    :             CTTTTTGGATT - - TACT - - TGAAAGA	1.72E-1
1095. bta-miR-544a MIMAT0009346	3445	-11.50	GTTTTGGC - AGTGATGCAGAAA    :    CTTGAACGATTTTACGTCTTA	1.22E-2
1096. my-mir-noheader- provided-33	3448	-12.49	TTGGCAGTGATGCAGAAACTGCCC    :       GTTAGTCG - - ATTAATGTGACGGA	1.22E-2
1097. bta-miR-3613a MIMAT0024574	5125	-6.85	GAATTGCTTGCCACTACAACA    :       CTTGTTTTTTTTTCATGTTGT	9.05E-2
1098. bta-miR-27a-3p MIMAT0003532	5987	-12.00	TAGGAC - ACACCGTCTGTGAT  :   :  GCCTTGAATCGGT - GACACTT	2.94E-1
1099. bta-miR-2422 MIMAT0011989	6172	-14.80	AGCCATGAGC - - AAGCTTCCCTCAA    :   :  GAGG - - CGTGGAGTC - AGGGGAGTT	3.34E-1
1100. bta-miR-1343-3p MIMAT0011840	8728	-11.90	GTTGTTGCTGTAGTAGACCAGGAT      :  CTCTCACG - - CCCG - - GGGTCCTC	3.52E-1
1101. bta-miR-2285ae MIMAT0030448	8814	-9.50	CTTTATTACACATGCACTTTCT           CTTTTTGGATTTACTTGAAAGA	1.54E-1
1102. bta-miR-2286 MIMAT0011793	8896	-14.90	AGTGGCTGTGTGCTTTC - CTCTGCTTG  :  :   :   :  TAATTGTGTAGC - AAGGCGGGACGAAG	2.69E-1
1103. bta-miR-130b MIMAT0009224	8903	-19.60	GTGTGCTTTCCTCTGCTTGCACTA :   :   :  TACGGGAAAGTAG - - TAACGTGAC	2.69E-1
1104. bta-miR-2285bh MIMAT0046388	8944	-7.00	GG - - TAGTCC - - AC - AACCTTA :          TCTTTTTGGGCTTGCTTGAAAA	3.62E-1
1105. bta-miR-2286 MIMAT0011793	10064	-19.20	CCAGACATGT - GATATGTTCTGCTTC :   :  :   :  TAATTGTGTAGCAAGGCGGGACGAAG	1.75E-1
1106. bta-miR-2301 MIMAT0011812	10295	-8.60	CTGCTTATAACGGCAAACCAC     :    TTCTCCCTTGGT - TTTGGTG	3.62E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
1107. bta-miR-153 MIMAT0009239	10416	-13.60	TGTTAAATTTGTGTATATGCAT :   :                     CTAGTGAAAACACTGATACGTT	3.24E-2
1108. bta-miR-1814b MIMAT0011908	10530	-12.70	CGTTCAGGATTATATACAATCT   :     : :   :             GTTTGTTTTGAT - - TTGTTAGA	8.51E-2
1109. bta-miR-507-3p MIMAT0040915	11676	-15.40	GGGTATTGGAGGTGTGCCAAT   : :   :           AAGTAAGGTTCTGTACGGTTA	3.07E-1
1110. bta-miR-2286 MIMAT0011793	12110	-10.50	CCTGTAATATTG - CTAAATCTGCTTA   :   :   :             TAATTGTGTAGCAAGGCGGGACGAAG	3.46E-2
1111. bta-miR-6520 MIMAT0025538	12635	-7.20	AGACTTGTAAATACACCTACTCAA     :                   CGAGAG - AGACTGT - TATGAGTT	2.18E-1
1112. bta-miR-7857-3p MIMAT0040925	13759	-14.90	TATATGCT - GGTG - TGAACAAT     :                     TTTCTCGGTCCAACCTCTTGTTA	1.32E-1
1113. bta-miR-12021 MIMAT0046714	16114	-7.90	GCGTGGTCTGCTCTTCTCAA     :                   TCGACCGTCTAAAAAGAGTT	5.43E-2
1114. bta-miR-2346 MIMAT0011881	16142	-12.20	ACGTTGTGGCAGTTGCATCAGA : :                   CGGTTTGGTGGAAGTGTAGTCA	5.43E-2
1115. bta-miR-1343-3p MIMAT0011840	16243	-12.70	ATGTGTGTAACGCACCAGGAT     :                   CTCTCACG - CCCGGGGTCCTC	1.36E-1
1116. bta-miR-1814b MIMAT0011908	16369	-8.80	TTGGTCTATATAAACAATCT                       GTTTGTTTTGATTGTGTTAGA	3.57E-1
1117. bta-miR-7857-3p MIMAT0040925	16872	-8.40	CTTGAGACA - - TTTCAGAACAAT                         TTTCTCGGTCCAACCTCTTGTTA	2.82E-1
1118. bta-miR-30b-5p MIMAT0003547	17151	-6.70	ACTCGTAAGTA - TGTGTTTACT       :               TCGACTCACATCCTACAAATGT	3.39E-1
1119. bta-miR-544a MIMAT0009346	17730	-9.10	ATATATTCACAGACTGCAGAAA   :                   CTTGAACGATTTTACGTCTTA	1.09E-1
1120. bta-miR-568 MIMAT0009350	19769	-13.20	TGGTGTCTGCATGTATACAG           :             CACACATATGTAAATATGTA	2.61E-1



1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
1121. bta-miR-130b MIMAT0009224	20413	-11.30	GTGGTAGTAAGAGTGTTCACACTG :    : :                TACGG - - GAAAGTAGTAACGTGAC	2.21E-1
1122. bta-miR-3613a MIMAT0024574	20748	-5.80	CAATATCTGAA - TACTACAACA    : :                   CTTGTTTTTTTTTTCATGTTGT	1.92E-1
1123. bta-miR-338 MIMAT0009292	20849	-13.20	TAGGCAGTGGTTGC - - CTGCTGGT : :    : :                   AGTTGTT - TTAGTGACTACGACCT	2.78E-1
1124. bta-miR-544a MIMAT0009346	21111	-16.30	GAGTTTTCTTGAATGCAGAAT          :                      CTTGAACGATTTTACGTCCTTA	3.16E-1
1125. bta-miR-2422 MIMAT0011989	21972	-16.60	AAAATCACTATCA - ACCCCTCAT     :                       GAGGCGTGG - AGTCAGGGGAGTT	9.19E-2
1126. bta-miR-425-3p MIMAT0003833	22159	-13.40	TAGAAGAAGGTGATCTTCCCGAG    :    :                      CCCGCCT - GTGCTGTAAGGGCTA	3.85E-1
1127. bta-miR-1814b MIMAT0011908	22806	-9.70	ATAATGGCTCTGCACAATCT    :    :                      GTTTGTTTTGATTGTGTTAGA	3.25E-1
1128. bta-miR-361 MIMAT0003830	23235	-13.40	ATGCC - - AGG - CAGTCTGATAA   :                               CATGGGGACCTCTAAGACTATT	1.89E-1
1129. bta-miR-2285bh MIMAT0046388	25596	-9.20	TTATAATAGTTGGCAGAACCTTT : :                               TCTTTTTTGGGCTTG - CTTGGAAA	2.65E-1
1130. bta-miR-27a-3p MIMAT0003532	26168	-13.60	AATATGGTAGCTTCTGTGAC     :                            GCCTTGAATCGGTGACACTT	4.38E-2
1131. bta-miR-489 MIMAT0009942	27124	-13.30	GTC - CCTACTAAGT - ATGTCAC                                   CAGCGGTATATACACTACAGTG	2.14E-1
1132. bta-miR-194b-3p MIMAT0040934	27341	-11.80	ACATTTCAACACCCAACCTCCATGA                                   GCTAACATTGT - CGTTG - AGGTACA	6.88E-2
1133. bta-miR-1343-3p MIMAT0011840	27683	-14.60	ATTATACTGGACACCAGGAG :                               CTCTCACGCCCCGGGGTCCCTC	2.21E-1
1134. bta-miR-2285dj MIMAT0046747	28048	-10.90	AGG - TAGACCT - - TATAACTTTA    : :                               CCCTGTTTGACTTGTTTGAAAG	2.5E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
1135. bta-miR-507-3p MIMAT0040915	28068	-7.84	AGCATT - -ATTAATTGCCAAA             AAGTAAGGTTCTGTACGGTTA	2.5E-1
1136. bta-miR-2285b MIMAT0011833	29181	-7.10	ACTGGCTATTCTTTGTCAGATTG            GGTTTTTCAAG - -TGAGTCTAAAA	2.11E-1
1137. bta-miR-2285di MIMAT0046746	29330	-12.60	GCCA - -TCAACCCAAAAGGGTTC :               TGGTTTTACAAGGAAGTCCCAA	3.48E-1
1138. bta-miR-2285dj MIMAT0046747	29370	-6.90	TTGAGAAATAATATCTAACTTTA        : :       CCCTGTTTG - GACTTGTGTTGAAAG	3.85E-1
1139. bta-miR-2346 MIMAT0011881	29541	-13.00	GCTACTTCTCAGCTAC - CATCAGG    :                 CGGT - TTG - GTGGAAGTGTAGTCA	7.91E-3
1140. bta-miR-196b MIMAT0009256	30050	-21.20	TTCTGGCAACAGAACCCCTACCTC   :   :             AGGGTTGTTGTC - CTTTGATGGAT	2.94E-1
1141. bta-let-7f MIMAT0003519	30052	-12.40	CTGGCAACAGAACCCCTACCTCT     :         TTGATATGTT - AGATGATGGAGT	2.94E-1
1142. bta-miR-507-3p MIMAT0040915	30157	-11.70	TAAC TAAGCAGAC - TGCCAAA             AAGTAAGGTTCTGTACGGTTA	5.91E-3
1143. bta-miR-130b MIMAT0009224	30218	-17.02	GAGCCCCAATAAAACAATGCACTG                TACGGG - AAAGTAGTAACGTGAC	5.91E-3
1144. bta-miR-544a MIMAT0009346	30383	-14.80	AGAGTTGGCCAAAGTGCAGAAT :           :       CTTGAACGATTTTACGTCTTA	1.09E-1
1145. bta-miR-2285b MIMAT0011833	30453	-6.60	TATAATGGTGCAATTAGATTTG        :       GGTTTTTCAAGTGAGTCTAAAA	3.29E-1
1146. bta-miR-2285ae MIMAT0030448	30465	-5.70	ATTAGATTTGACAGTACACTTTCA   : : :         CTTTTTTGATT - -TACTTGAAAGA	3.29E-1
1147. bta-miR-2301 MIMAT0011812	30557	-15.70	GAATATGAGTCCAAAACCAC    :       TTCTCCCTTGGTTTGGTG	3.66E-2
1148. bta-miR-2346 MIMAT0011881	30671	-13.60	GTTGA - CTGCAGAGGACATCAGC   :             CGGTTTGGTG - GAAGTGTAGTCA	1.28E-1

1. miR Name	leftmost position of predicted target site	folding energy (in - Kcal/mol)	heteroduplex	p value
1149. bta-miR-2285bh MIMAT0046388	30734	-17.50	AGAAATATAAGAGAATGAACCTTA        :    :        TCTTTTGG--GGCTTGCTTGAAAA	2.39E-1