

MTar 2: Negative Dataset

SL. No	Target gene	miRNA mature_ID	microRNA sequence (5'-3')	mRNA
1	HCN2	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	CGGAUGGAAAAAGGACCUGAUC
2	HCN2	hsa-miR-133a	UUUGGUCCCCUUCACCAGCUG	CUAAAACAAUAGUUUAUAAAU
3	HMGA2	hsa-let-7e	UGAGGUAGGAGGUUGUAUAGUU	AGAUAGCUCAUUUCAUUAAGUU
4	HMGA2	hsa-let-7b	UGAGGUAGUAGGUUGUGUGGUU	CUCUAAUUAAUCCAACUGUAC
5	AGTR1	hsa-miR-155	UUA AUGCUAAUCGUGAUAGGGGU	UUUUGAAAAGCCAGUGAUGAUCU
6	BACE1	hsa-miR-29a	UAGCACCAUCUGAAAUCGGUUA	AAACAUGUUUAUAAAUGAACAGG
7	BACE1	hsa-miR-107	AGCAGCAUUGUACAGGGCUAUC	AUACUUUGAUCUCAUUUAUGUAC
8	BBC3	hsa-miR-221	AGCUACAUUGUCUGCGGGUUUC	CCUGUGGCUGAAAAAGAGAAAGC
9	BCL2	hsa-miR-16	UAGCAGCACGUAAAUAUUGGCG	CACAAAGAAGGAAGUGUUUAUA
10	BMI1	hsa-miR-302b	UAAGUGCUUCCAUGUUUAUAGUAG	UGCUCAGGACAGGAGCGGCAGCC
11	CASP9	hsa-miR-133a	UUUGGUCCCCUUCACCAGCUG	ACUAGCAAAGUCCGAGAUGAAUG
12	CCNE1	hsa-miR-503	UAGCAGCGGGAACAGUUCUGCAG	GAACAUUUUAGAAAAGGU AUGUC
13	CD44	hsa-miR-34a	UGGCAGUGUCUAGCUGGUUGU	UGUGAAUUUUCUCCUGGACUCCC
14	CDC25A	hsa-miR-503	UAGCAGCGGGAACAGUUCUGCAG	GAUAUCAGCGAUCUUCUCUACUU
15	CDC42	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	AAAACAUUAUCUUGUCACUGUAG
16	CDK6	hsa-miR-124	UAAGGCACGCGGUAAUGCC	AAGUUUUCAGAAUAACCAGAACU
17	CDKN1B	hsa-miR-222	AGCUACAUUGUCUGCGGGUUUC	UGAGAAACAUUUUGAAGUUUGUG
18	CDKN1C	hsa-miR-222	AGCUACAUCUGGCUACUGGGU	GAAGCACCUCAAUUUAGUUCAAA
19	COL3A1	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	GGGUGGGAGGGAGGAAGAAUUU
20	COL3A1	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	UUUUUUUUUAAAUAUUUAUGGG
21	CXCL12	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	AAGAAUUUUUAAAUGUAAAACAU
22	DLL1	hsa-miR-34a	UGGCAGUGUCUAGCUGGUUGU	AGGGAAGGAACAGAGGCCUGGG
23	DNMT1	hsa-miR-148a	UCAGUGCACUACAGAACUUUGU	UUUGUUUUAAAUAUUUUUAAGUG
24	ETS1	hsa-miR-155	UUA AUGCUAAUCGUGAUAGGGGU	AUAUGUGAUCUUUGUUUAUUG
25	HCN4	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	CAAAGGACAUUUGUUGGAGGGGU
26	HES1	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	ACUGGCCACUGAGGAGCUUUGUU
27	HES1	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	UGGGGCAUUAAAAAAAAAUCAA
28	HMGA2	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	ACAAAAAAAAGUUCAGGUGUG
29	HMGA2	hsa-miR-98	UGAGGUAGUAAGUUGUAUUGUU	CAGCAAUUCACUGUAAAGCUGGA
30	HMGA2	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	GCACAUCCAAUAAAUAAGCUGGA
31	HXA7	hsa-miR-196a	UAGGUAGUUCAUGUUGUUGGG	CUGAAAGGGAAGGUGGAAGCCGU
32	HSPD1	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	ACAAAAAGGGAGUAACUAUUCCC
33	ICAM1	hsa-miR-221	AGCUACAUUGUCUGCGGGUUUC	UGUCCAUUUGUUUAUUGUUGUU
34	ICOS	hsa-miR-103	AGCAGCAUUGUACAGGGCUAUGA	CCUCUCCUCGGCUUCUCCUGAA
35	KCNE1	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	CUCUCUAAAUGAAGUGCCACU
36	KCNH2	hsa-miR-133a	UUUGGUCCCCUUCACCAGCUG	GAAGAAAGAAGCACUCUGCUGGC
37	KLF13	hsa-miR-372	AAAGUGCUGCGACAUUUGAGCGU	UGAAAAAUGACUGUCCAUUCUC
38	MCL1	hsa-miR-29b	UAGCACCAUUUGAAAUCAGUGUU	ACCAGAGGCAGCUGUCCAGCACA
39	MET	hsa-miR-23b	AUCACAUUGCCAGGGAUUACC	GACUGAUCCUGAACAAGAAAGAG

40	MET	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	GGGACCAGGGAAGCCGCCACCGG
41	MET	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	UGAACCACCCUUUAUUCUACAUA
42	MET	hsa-miR-23b	AUCACAUUGCCAGGGAUUACC	UGGUUGCAGCCUGACCAAAAGUG
43	MUC4	hsa-miR-150	UCUCCCAACCCUUGUACCAGUG	UAAAAACAAGAAUACUGAGUCAGU
44	MYC	hsa-miR-145	GUCCAGUUUUCCAGGAAUCCCU	AUUUAGCCAUAUAUGUAAACUGCC
45	MYC	hsa-miR-145	GUCCAGUUUUCCAGGAAUCCCU	CUGCUGCCACCCCGCCCCUGUC
46	MYC	hsa-miR-200b	UAAUACUGCCUGGUAUGAUGA	GGUCUUUGUGAUUUUAUCAAAAA
47	MYC	hsa-miR-200b	UAAUACUGCCUGGUAUGAUGA	UCCCUUCUUAAACUGUAACUCAAC
48	MYC	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	UUCUUCCCCUCCCCGCUCCUAAU
49	MYC	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	UUUUGAUGACGUUUGGGCCGGGU
50	MYCN	hsa-miR-101	UACAGUACUGUGAUAAACUGAA	GCGCCUGCCUCCCCACUGCUCUG
51	NTRK3	hsa-miR-125b	UCCUGAGACCCUAACUUGUGA	UUUUGAUGACGUUUGGGCCGGGU
52	PARP8	hsa-miR-145	GUCCAGUUUUCCAGGAAUCCCU	GCGCCUGCCUCCCCACUGCUCUG
53	PTBP2	hsa-miR-133b	UUUGGUCCCCUUAACCAGCUA	AUUGGGUUUAGUCAAUACACUGCA
54	PTEN	hsa-miR-29a	UAGCACCAUCUGAAAUCGGUUA	CGCAGGGUGGGGGGAAGAGGAGG
55	PTEN	hsa-miR-19a	UGUGCAAUUCUAUGCAAAACUGA	UUCUAAUCAUCUGCAGUUCUUUU
56	PUMA	hsa-miR-296	AGGGCCCCCUCAAUCCUGU	CCAAGUCGCUCCUAGGUUCUUA
57	RAF1	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	CAGGAGUAAUAAUUUACUCACA
58	RAF1	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	UGAGGUGGGAGGAGCGAAAUCUA
59	RHOA	hsa-miR-155	UUAUUGCUAAUCGUGAUAGGGGU	UUCCGAAGUGCUCGCGGUGCCCG
60	RHOB	hsa-miR-223	UGUCAGUUUGUCAAUACCCCA	AAUCAAAAAUUGUGUUUUUAAG
61	RHOC	hsa-miR-138	AGCUGGUGUUGUGAAUCAGGCCG	UAGGUUCUUAAGGAUAAUUUCC
62	STAT3	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	AUUUUUGUAAUUGUCUCAACCA
63	UBE2I	hsa-miR-30c	UGUAAACAUCUACACUCUCAGC	AAGAUUUAGCCAUAUUGUAAACU
64	VEGFR2	hsa-miR-16	UAGCAGCACGUAAAUUUGGCG	GAGACACCGCCACCACCAGCAG
65	VSNL1	hsa-miR-181b	AACAUUCAUUGCUGCGGUGGGU	UUUUUUUUUUCUUUAACAGAUUU
66	ABCA1	hsa-miR-758	UUUGUGACCUGGUCCACUAACC	AAGAAAGGGUGGAUGGAUUGAAAA
67	ABCA1	hsa-miR-758	UUUGUGACCUGGUCCACUAACC	UUAAAUGAAAACUAAAAUAGAC
68	ACVR1B	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	UGUACUGGAAAUUAGGGGAAUGA
69	ADCY6	hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	GAAAAUUUGUAUGAAUAAUUUAG
70	ADCY6	hsa-miR-96	UUUGGCACUAGCACAUUUUUGCU	GAGGAUAUAAAUUUGAUUUAAA
71	ADCY6	hsa-miR-96	UUUGGCACUAGCACAUUUUUGCU	GAGUUUUUUUUUGCAUAGGGUGU
72	ADCY6	hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	UGUUAUUUAAAUUACUGGAUUCUA
73	API5	hsa-miR-224	CAAGUCACUAGUGGUUCCGUU	GGUAGAGCAAAGAAAGGGUGGAUG
74	AURKB	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	GAGAAAAAAGAGAUCCACAAAGAA
75	BACE1	hsa-miR-29b	UAGCACCAUUUGAAAUCAGUGUU	UAGGACACUUCUGAGAAAUUCAUC
76	BCL2	hsa-miR-15a	UAGCAGCACAUAAUGGUUUGUG	CUUUUUCAUGUUAGAUGGGAUCCU
77	BDNF	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	AAAAAAGAGAUCCACAAAGAAGGA
78	BMF	hsa-miR-125b	UCCUGAGACCCUAACUUGUGA	AAAACUUUUUGGGAGUUUAUUUU
79	BMF	hsa-miR-125b	UCCUGAGACCCUAACUUGUGA	UCGAUAUUCUUUGCUCUUGCCAAA
80	BMI1	hsa-miR-708	AAGGAGCUUACAAUCUAGCUGGG	UUUAACUGGAAAUUACCUAAACAG
81	BMPR2	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	CAUAGGAAGAGGGCAUUUUGGUUG
82	BMPR2	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	CUUACCAGAAGACACAAGGAAUUG
83	BMPR2	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	UUUAAGGACUUGUAUUGUUAUUUA

84	C6orf134	hsa-miR-23a	AUCACAUUGCCAGGGAUUUC	AUAUGAGAAAAUUUUGUUAGGCC
85	CAPRIN1	hsa-miR-16	UAGCAGCACGUAAAUUUGGCG	CUCAAUGGGCAAUAGAAAUGUACU
86	CASP9	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	UGCAAGAAACUGUAUGCUGGAUGA
87	CCND1	hsa-miR-302c	UAAGUGCUUCCAUGUUUCAGUGG	AUCCACAAAGAAGGAAGUGUUUAA
88	CCND1	hsa-miR-17	CAAAGUGCUUACAGUGCAGGUAG	GAAAAACCUGAAUUCAGUUAGUGU
89	CCND1	hsa-miR-20a	UAAAGUGCUUUAUAGUGCAGGUAG	GCUUGUAAGUGCCCGAAGUGUAAG
90	CCND2	hsa-miR-302d	UAAGUGCUUCCAUGUUUGAGUGU	AACAUUCCUUUUAAAUGUUUGUU
91	CCND2	hsa-miR-302d	UAAGUGCUUCCAUGUUUGAGUGU	CAGAAAACUCAGAAGAGAUAGUAA
92	CCNE1	hsa-miR-16	UAGCAGCACGUAAAUUUGGCG	UGAGAGGAGGCGGGGAGGCGCGGA
93	CCNG1	hsa-miR-122	UGGAGUGUGACAAUGGUGUUUG	UCACACAAGAAUAUACAGGUUCUG
94	CD276	hsa-miR-29a	UAGCACCAUCUGAAAUUCGGUUA	AUCUAUAUCCACCUUCAUUAAGG
95	CDC42	hsa-miR-29a	UAGCACCAUCUGAAAUUCGGUUA	CAUGUGUGCAUUCUUCAUCAAUA
96	CDC42	hsa-miR-29c	UAGCACCAUUUGAAAUUCGGUUA	UAAAAAAGCCCCAAAAGGAGAAG
97	CDK6	hsa-miR-124	UAAGGCACGCGUGAAUGCC	GGAGGAGCUCUUCAGGGACGGGU
98	CDKN1B	hsa-miR-222	AGCUACAUCUGGCUACUGGGU	AAGAGUGACAGUGGAUUGCAUUUC
99	CDKN1B	hsa-miR-222	AGCUACAUCUGGCUACUGGGU	UUUCUUCAGUUUAGAAUCAGCCU
100	CDKN1C	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	CAUCUGUUUCUAAAUGUUUAUUUAU
101	CDKN2A	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	CAGUCCUCUGUAUGUACUCCUCUU
102	DDIT4	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	AUUUUCUUUAUUGUUAAAAACAUG
103	DNMT3A	hsa-miR-29a	UAGCACCAUCUGAAAUUCGGUUA	CAUCUGCAUCUUAACUGCUCUUUA
104	DNMT3B	hsa-miR-29a	UAGCACCAUCUGAAAUUCGGUUA	AAAAAGAUUUUAUUUAUUUAAGACA
105	E2F2	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	CACUGUAGUUUGGUUUUAUUUGAA
106	E2F3	hsa-miR-125b	UCCUGAGACCCUAACUUGUGA	UAAUAAUAAGACUGUAGUGUAGA
107	EGFR	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	AAAUAGUCUCUAAUUGUAAUUGAA
108	EGFR	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	CUCUGGAACUUGAGGAAGUGAACA
109	ERBB2	hsa-miR-125b	UCCUGAGACCCUAACUUGUGA	CACAGAAUUAAGGAAGCACCUCAA
110	ESR1	hsa-miR-206	UGGAUGUAAGGAAGUGUGUGG	AUUUGGAUCUUUCAGGGAUUUUUU
111	ESR1	hsa-miR-206	UGGAUGUAAGGAAGUGUGUGG	GUUGGAGGGGUGGGAGGGAGGAAG
112	EZH2	hsa-miR-124	UAAGGCACGCGUGAAUGCC	AUUUUUAAGCAAAUAUUUUUUUA
113	FOS	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	CAGACCCACCCAGAGCCCUCUCG
114	FSCN1	hsa-miR-145	GUCCAGUUUCCAGGAUCCCU	AUUUUAGCAUUUUUAACAUAUCA
115	FSCN1	hsa-miR-145	GUCCAGUUUCCAGGAUCCCU	CAGGGAACAGAAUGAUCAGACCUU
116	FSCN1	hsa-miR-145	GUCCAGUUUCCAGGAUCCCU	CUCAACUAGUCAUUUUUUUCUCCU
117	FSCN1	hsa-miR-145	GUCCAGUUUCCAGGAUCCCU	GAAAAAUUAGGAAGUGAUUAUAAA
118	G6PD	hsa-miR-1	UGGAUGUAAAGAAGUAUGUAU	UGCAGGCUGUUUAAGAAAAAUAA
119	GJA1	hsa-miR-1	UGGAUGUAAAGAAGUAUGUAU	AAAAGGAACUUGACAGAGGAUCA
120	GRIA2	hsa-miR-181b	GGGUGGCUGUCGUUACUUACA	GACUUUCUUAUCACUUUAAGUUAG
121	HES1	hsa-miR-23a	AUCACAUUGCCAGGGAUUUC	AUUUCAUUAAGUUUUUCCUCCAA
122	HMGA1	hsa-miR-16	UAGCAGCACGUAAAUUUGGCG	CCCCAGAAAAUAACUUAAGCAA
123	HMGA2	hsa-let-7e	UGAGGUAGGAGGUUGUAUAGUU	AAAAACAGGAAAGGUCGAAAUAC
124	HMGA2	hsa-let-7g	UGAGGUAGUAGUUUGUACAGUU	AAAAAUAAAGUACAGUGUGAGUA
125	HMGA2	hsa-let-7e	UGAGGUAGGAGGUUGUAUAGUU	AACUAGUCAUUUUUUUCUCCUCUU
126	HMGA2	hsa-let-7e	UGAGGUAGGAGGUUGUAUAGUU	ACAAUACUUAUAAUAAUACGUG
127	HMGA2	hsa-miR-98	UGAGGUAGUAAGUUGUAUUGUU	AUGAUGUAGUAAGGUUUUUGGAUU

128	HMGA2	hsa-let-7e	UGAGGUAGGAGGUUGUAUAGUU	CCAUCAAAACUCCUGUCUUUGGAA
129	HMGA2	hsa-let-7c	UGAGGUAGUAGGUUGUAUGGUU	CUACCUAAGAAAAACCUGGAUGUC
130	HMGA2	hsa-let-7e	UGAGGUAGGAGGUUGUAUAGUU	CUUCCAGUUUAGAAUCAGCCUUGA
131	HMGA2	hsa-let-7b	UGAGGUAGUAGGUUGUGUGGUU	GGGGUUUUUGUUACCUGGUUUUAAU
132	HMGA2	hsa-let-7b	UGAGGUAGUAGGUUGUGUGGUU	UAAGGAAAUUAGGGAGUCAGUUGA
133	HMGA2	hsa-miR-98	UGAGGUAGUAAGUUGUAUUGUU	UACCAUCCCAAGUCCUUUGUAGCU
134	HMGA2	hsa-let-7c	UGAGGUAGUAGGUUGUAUGGUU	UAUAUUUUGGAUACGCACCCCCCA
135	HMGA2	hsa-let-7b	UGAGGUAGUAGGUUGUGUGGUU	UCAUUUUGGAUCUUUCAGGGAUUU
136	HMGA2	hsa-let-7g	UGAGGUAGUAGUUUGUACAGUU	UGGACCUAGUACCCACUGAGAUUU
137	HMGA2	hsa-let-7b	UGAGGUAGUAGGUUGUGUGGUU	UUCUUUUGGGGAAGCUUUCUUUUG
138	HMGA2	hsa-let-7b	UGAGGUAGUAGGUUGUGUGGUU	UUUCUUAUCACUUAUAGUUAGUAA
139	HMGA2	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	UUUUCUCUGGGAAGGAUGGCGCA
140	HOXA7	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	AUUCUGACACCACUGACUCUGAUC
141	HOXA7	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	UCAAGUUUUUGAGAAGCCUUGCU
142	HOXB8	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	AAUACCAUAUGAUGUGUACAGGA
143	HOXC8	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	UUAGGGAAUUUUACUUGAAUACUG
144	IKBKB	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	GUCUUUCAUAAAAGCUGAAAAUUG
145	IRS1	hsa-miR-145	GUCCAGUUUCCAGGAUCCCU	UUCCCCUCCCGCUCCUAAUGGUA
146	IRS2	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	UCAUUUUCUAAAUUUGCAGGGGAU
147	JAG1	hsa-miR-141	UAACACUGUCUGGUAAGAUGG	AAUUUUGGUGAUGUAAAACAGAAU
148	KCNE1	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	ACAUUCCACAGACAGAUGAGUCAA
149	KCNE1	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	UUCUCCACUCACUGCAUUUGGGGC
150	KCNH2	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	AGAGAAGAAAGAAGCACUCUCUG
151	KCNH2	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	AGGAGAUCAUUUAGUUGGGUCUGA
152	KCNH2	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	UCAUUUUCAUUUUCUAAAUUUGCA
153	KCNQ1	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	ACCUCUUCUUAUCUAAUCCUAAAA
154	KCNQ1	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	UUCUUUUCUUAUUUCAGAAGUAC
155	KGF	hsa-miR-155	UUAAUGCUAAUCGUGAUAGGGGU	AUUGUCUCUAUCUGAACCACCCUU
156	KLF13	hsa-miR-372	AAAGUGCUGCGACAUUUGAGCGU	ACCUGUAGGAAACAGAAAAGAGAA
157	KLF13	hsa-miR-302d	UAAGUGCUUCCAUGUUUGAGUGU	AGGGAGUACAAAGACAGGGAAUAG
158	KLF4	hsa-miR-137	UUAUUGCUUAAGAAUACGCGUAG	GUAGGAGUAAAGAUAAAAGGAUAG
159	KRAS	hsa-miR-143	UGAGAUGAAGCACUGUAGCUC	AAUGAGGAAGAAUCCAUCUGUGAG
160	KRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	AGAAGGAAAAGAGUAUCAAGGCA
161	KRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	CAGAAAAGAGAAGAAAGAAGCACU
162	KRAS	hsa-miR-181c	AACAUUCAACCUGUCGGUGAGU	UCCUGAGAAGCCACCAGCACCACC
163	LIN28	hsa-miR-125b	UCCUGAGACCCUUAACUUGUGA	CUGUAAACCUAUUGUCUGUAUAAA
164	LMO2	hsa-miR-223	UGUCAGUUUGUCAAUACCCCA	AGGGGGAUUAGCUAGACUAGGAGA
165	MAP2K1	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	ACAGGAAAUUUGUCCCCCCCUAAC
166	MET	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	ACAACAGCUUCUUGCUUGUAAAAA
167	MET	hsa-miR-206	UGGAAUGUAAGGAAGUGUGUGG	CAUAAAACAAGAAUACUGAGUCA
168	MITF	hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	AAUUUAAGUCGGGAAAUUCUGCUG
169	MITF	hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	GGGUCGCCAACACUUGUGUUGCUU
170	MITF	hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	UUCCUGCCCCAAAAUUUAAACUC
171	MITF	hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	UUUUUUUUUUUUUUUACUCCUUGG

172	MMP1	hsa-miR-222	AGCUACAUCUGGCUACUGGGU	AUUAAAAUCCAGCAUCCCAAGAUC
173	MYC	hsa-miR-145	GUCCAGUUUCCAGGAAUCCCU	AAAAUAAAAUACUGGCAAAUUAU
174	MYC	hsa-miR-200b	UAAUACUGCCUGGUAUGAUGA	AAUAAGUUUACAUGUAUUUGAACU
175	MYC	hsa-miR-200b	UAAUACUGCCUGGUAUGAUGA	ACUUUUUAUCAAAGAAGGAUUUUUCA
176	MYC	hsa-miR-200b	UAAUACUGCCUGGUAUGAUGA	AGAUGGGAUUUUUCAUUUUUAUUA
177	MYC	hsa-miR-200b	UAAUACUGCCUGGUAUGAUGA	AUUCAUUUAAUUUUAGGUCAAUA
178	MYC	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	CCAGGUGCCUGUGGGAGAGCAAC
179	MYC	hsa-miR-145	GUCCAGUUUCCAGGAAUCCCU	CGGCAGCGGUGGAAGGCCUUUUG
180	MYC	hsa-miR-145	GUCCAGUUUCCAGGAAUCCCU	CUAUGAACUUGUUUCAAUUGCAUG
181	MYC	hsa-miR-200b	UAAUACUGCCUGGUAUGAUGA	CUGCAGCCUCAUGAAAACAUAGUC
182	MYC	hsa-miR-200b	UAAUACUGCCUGGUAUGAUGA	GAAUUCACAUGGGGAAAAAAUAUA
183	MYC	hsa-miR-200b	UAAUACUGCCUGGUAUGAUGA	UACUCUCCACACGCUUAGUUCU
184	MYC	hsa-miR-200b	UAAUACUGCCUGGUAUGAUGA	UCUGUACUUUUAGAGAGUUUCCU
185	MYC	hsa-miR-200b	UAAUACUGCCUGGUAUGAUGA	UUCAAUUAUCCCUCCCCACAAAGA
186	MYCN	hsa-miR-34a	UGGCAGUGUCUAGCUGGUUGU	UCGAAGAAAGGUCAGCUUCCUCGC
187	NLK	hsa-miR-181b	GGGUGGCGUCGUUACUUAACA	GGUUGAUACCCCAACUCCUCUAC
188	NOTCH2	hsa-miR-34a	UGGCAGUGUCUAGCUGGUUGU	ACCCUCUCCUCUGUCUCCAGAAG
189	NRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	CUUUGGUUUUAAUAAUAAUUUUGA
190	PDCD4	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	UCGAAGAAAGGUCAGCUUCCUCGC
191	PITX3	hsa-miR-133b	UUUGGUCCCCUACAACCAGCUA	GGUUGAUACCCCAACUCCUCUAC
192	POU4F2	hsa-miR-23a	AUCACAUUGCCAGGGAUUUC	ACCCUCUCCUCUGUCUCCAGAAG
193	POU4F2	hsa-miR-23a	AUCACAUUGCCAGGGAUUUC	CUUUGGUUUUAAUAAUAAUUUUGA
194	PRDM1	hsa-miR-9	UCUUUGGUUAUCUAGCUGUAUGA	CAAUCACUGCACUGCAUGCAAACA
195	PTEN	hsa-miR-19a	UGUGCAAUUCUAGCAAACUGA	CCGCCAGCUCGCGCUCGCCCCGCC
196	PTEN	hsa-miR-29a	UAGCACCAUCUGAAAUCCGUUA	UCUCUGCUAGAUUUCUACAUUAAC
197	RECK	hsa-miR-372	AAAGUGCUGCGACAUUUGAGCGU	AUGCAAGAAAAAACUUAUCUGGGU
198	RERE	hsa-miR-429	UAAUACUGUCUGGUAUAAACCGU	AACUUAUCUGGGUAGGUGAUUCUAA
199	RHOA	hsa-miR-133a	UUUGGUCCCCUACAACCAGCUG	ACUGUUUUCUUUUUUCUUAACCUA
200	ROCK2	hsa-miR-138	AGCUGGUGUUGUGAAUCAGGCCG	CAAUUUAAAAAGCAAAAAAAAAA
201	RTKN	hsa-miR-145	GUCCAGUUUCCAGGAAUCCCU	UAAAUUUCUUUUGCUAUGUUAUA
202	RUNX1	hsa-miR-17	CAAAGUGCUUACAGUGCAGGUAG	CUCAUUUUUCAUACUGAAAAAAA
203	SFRS1	hsa-miR-10a	UACCUGUAGAUCCGAUUUUGUG	UUUGAGUGUCUUCUAAUUUAUUC
204	SIP1	hsa-miR-141	UAACACUGUCUGGUAAGAUGG	UAAAUAAUAAUAAAUAAAGCC
205	SOX5	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	ACAUAAAGACUGGACAUUUAACUUU
206	SPI1	hsa-miR-155	UUAAUGCUAAUCGUGAUAGGGGU	GAUUUCUACAUUAACUUGAAAAUU
207	Survivin	hsa-miR-708	AAGGAGCUUACAAUCUAGCUGGG	GAAAACAAUGAAAAGGCCCCCAAG
208	Survivin	hsa-miR-708	AAGGAGCUUACAAUCUAGCUGGG	GGACUUUGGGCAUAAAAGACUUU
209	TGFB2	hsa-miR-141	UAACACUGUCUGGUAAGAUGG	AUCCUUAAAAAGCCACAGCAUAC
210	TIMP3	hsa-miR-222	AGCUACAUCUGGCUACUGGGU	AACGUUAGCUUCACCAACAGGAAC
211	TIMP3	hsa-miR-181b	UGGGUGGCUGUCGUUACUUAACA	CAGCUACGGAACUCUUGUGCGUAA
212	TPM1	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	CCCACCCGCCCGUGUCCCUAGC
213	UBE2Q1	hsa-miR-338-3p	UCCAGCAUCAGUGAUUUUGUUG	UAGCCAUAUUGUAAACUGCCUCAA
214	VEGF	hsa-miR-16	UAGCAGCACGUAAAUUUGGCG	CAAGACUCCAGCGCCUUCUCUCCG
215	VEGFA	hsa-miR-372	AAAGUGCUGCGACAUUUGAGCGU	CACAGCAAACCUCCUCACAGCCCA

216	VEGFA	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	UAUUUAAGAAUUGUUUUUAAAAA
217	WNK1	hsa-miR-215	AUGACCUAUGAAUUGACAGAC	AGAAUUGUUUUUAAAAAUUUUA
218	ACVR1B	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	GAAGAAGAUACGAAGAUCCAUUG
219	ADCY6	hsa-miR-96	UUUGGCACUAGCACAUUUUUGCU	GAAAAAGAGAAAGCAAUUAAAGAU
220	ADCY6	hsa-miR-96	UUUGGCACUAGCACAUUUUUGCU	UAAAGGUGAAGUGUUAAGUUGGA
221	ADCY6	hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	UUUUUAAUGAUUAGAGAAAAUUUU
222	API5	hsa-miR-224	CAAGUCACUAGUGGUUCCGUU	AGAGCAAAGAAAGGGUGGAUGGAU
223	API5	hsa-miR-224	CAAGUCACUAGUGGUUCCGUU	UGGGUUUUUCCUGUGGCUGAAAAAG
224	BAK1	hsa-miR-125b	UCCUGAGACCCUAAUUGUGA	GGAAUGCCUGAGCGGGACAUGGACU
225	BBC3	hsa-miR-222	AGCUACAUCUGGCUCACUGGGU	UUUUCACACAAGAAUAAUCAGGUUC
226	BCL2	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	AAAUUACCUAAACAGUGGGAAUUCU
227	BCL2	hsa-miR-16	UAGCAGCACGUAUAAUUGGCG	CAGAACAGGCCACUCAUUUAGAAUU
228	BCL2	hsa-miR-15b	UAGCAGCACAUCAUGGUUUACA	UACUAAAAGGUUCAUUGGUUCCAAU
229	Bcl-2	hsa-miR-143	UGAGAUGAAGCACUGUAGCUC	UGUGUUUAAGCCUUUUGAAAAGCCA
230	BIM	hsa-miR-222	AGCUACAUCUGGCUCACUGGGU	UAAAAUGUUUAUUUUUAAUGAUU
231	BIM	hsa-miR-221	AGCUACAUUGUCUGCGGGUUUC	UUAAUGAUUAGAGAAAAUUUUGUU
232	BMPR1B	hsa-miR-125b	UCCUGAGACCCUAAUUGUGA	GGGGAGUUUUUUUUGCAUUGGGU
233	BMPR2	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	CUCUAAUUCAGAGAUAAUCUGUUGU
234	CASP9	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	UGGGGACUCUGAUUAUCCAGUCCA
235	CCNA2	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	AAAUUUCAUUUCGAAUGAGACUCAU
236	CCND1	hsa-miR-17	CAAAGUGCUUACAGUGCAGGUAG	GCAUUAGGGUGUGUUUUUUGUUAAG
237	CCND2	hsa-miR-302b	UAAGUGCUUCCAUGUUUUGUAG	CAUUUUGUACAUAUCCUGUGUUU
238	CCNE1	hsa-miR-16	UAGCAGCACGUAUAAUUGGCG	AAAGAAGGAAGUGUUUAAUUAUACUU
239	CCNE1	hsa-miR-16	UAGCAGCACGUAUAAUUGGCG	CAAAACUUGAAUUCUGGGUUGAAUU
240	CDC2	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	AAUGGUUUCAAUGAAUCUGUAGAC
241	CDK2	hsa-miR-302d	UAAGUGCUUCCAUGUUUUGUUGU	AUUUGGAUCUUUCAGGGAUUUUUUU
242	CDK4	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	UAUGUACAUAACAGAAAAAAUUUU
243	CDK6	hsa-miR-137	UUAUUGCUUAGAAUACGCGUAG	AGAAAAAAUUUUUUAUAAUUUAAGC
244	CDK6	hsa-miR-124	UAAGGCACGCGGUGAAUGCC	CCUACUCUAUCAGAGAAAAACAGGA
245	CDKN1B	hsa-miR-221	AGCUACAUUGUCUGCGGGUUUC	AUACCUUCUUAAGUUUUAACCAAG
246	CDKN1C	hsa-miR-222	AGCUACAUCUGGCUCACUGGGU	AGGAAAGUAAAAUUUUAAGCUACCA
247	CDKN2A	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	UUCUGAGACUAUUAUAAUUAAGAC
248	CLOCK	hsa-miR-141	UAACACUGUCUGGUAAAGAUGG	GGAGGGGUGGGAGGGAGGAAGAAUU
249	COL1A1	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	AGAAGAUGGGAACACUGGUGGAGGA
250	COL1A1	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	UUUGAAAACCUGACAAAAAAAAGU
251	col2a1	hsa-miR-29a	UAGCACCAUCUGAAAUCGGUUA	CCAAAGGGAAAUAUCAUUUAUUUUU
252	COL3A1	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	UGGGAAAAUUUAGGAAGUGAUUAUA
253	CREB1	hsa-miR-103	AGCAGCAUUGUACAGGGCUAUGA	UUACAUAUUUAAGAAAAAAGAUUU
254	CTLA-4	hsa-miR-155	UUAAUGCUAAUCGUGAUAGGGGU	UAAAGAAGUAACAAAAGAAGUGACA
255	CXCR4	hsa-miR-146a	UGAGAACUGAAUCCAUGGGUU	AAAUUUUUUUUUCUCCAGUUUAGA
256	DHFR	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	GAAAUCCUCCUAAUUUUUACUCCCU
257	DHFR	hsa-miR-215	AUGACCUAUGAAUUGACAGAC	UCAGAGAAAAACAGGAAAGGCUCGA
258	DICER1	hsa-miR-107	AGCAGCAUUGUACAGGGCUAUCA	GUGGGAGGGAGGAAGAAUUUUUAAA
259	DNMT3B	hsa-miR-148b	UCAGUGCAUCACAGAACUUUGU	AUGAAAAACAGUCCUCUGUAUGUA

260	DNMT3B	hsa-miR-148a	UCAGUGCACUACAGAACUUUGU	CGAAGGACAGCGAUGGGAAAAAUGC
261	DNMT3B	hsa-miR-29c	UAGACCAUUUGAAAUCGGUUA	UCUGUAUGUACUCCUUUUACACUG
262	E2F6	hsa-miR-193a-3	AACUGGCCUACAAAGUCCAGU	GAAAAUUAGGAAGUGAUUUAAAAU
263	EGFR	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	GAGAGUGAUAAUACAAGUCCUUUAG
264	EGR2	hsa-miR-150	UCUCCCAACCCUUGUACCAGUG	AUAUGUGAUCUUUGUUUUUUUAGUA
265	ERBB3	hsa-miR-125b	UCCUGAGACCCUAAUUGUGA	GAACCUCCUCGGCCCUCCAGUCCC
266	ERK5	hsa-miR-143	UGAGAUGAAGCACUGUAGCUC	AGCAUUUUAGCAAUUUUAUACAAU
267	FBXW11	hsa-miR-103	UAGCAGCACGUAAAUAUUGGCG	CGCGCCCCCGGGGGCCGCCCCGCA
268	FBXW7	hsa-miR-27a	CGCUUGAAUCGGUGACACUU	AAAUUCUGAGACUAAUAAUAAUAA
269	FEN1	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	UGGCCUAUACACUAAUUGUGAGCAA
270	FGFR1	hsa-miR-16	UAGCAGCACGUAAAUAUUGGCG	UGGAAAAAGUCACAUUGCCAUAUAA
271	FSCN1	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	GAUACGCACCCCCAACUCCCAAUA
272	HMGA2	hsa-miR-98	UGAGGUAGUAAGUUGUAUUGUU	AGUGCCUCGUUUACCUUUAAUACU
273	HMGA2	hsa-let-7c	UGAGGUAGUAGGUUGUAUGGUU	AUAUUAACAAUACUACUAAUAAUA
274	HMGA2	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	AUUUAUACAAUAUCAUCCAGUACCU
275	HMGA2	hsa-let-7c	UGAGGUAGUAGGUUGUAUGGUU	CCUCCUCGCCCCUCCAGUCCUCG
276	HMGA2	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	GAAACUGAAUUGGAGAGUGAAUUA
277	HMGA2	hsa-let-7c	UGAGGUAGUAGGUUGUAUGGUU	GGAGGGGUGGGAGGGAGGAAGAAUU
278	HMGA2	hsa-let-7g	UGAGGUAGUAGUUUGUACAGUU	UGUAAAACAUUAUCUUGUCACUGUA
279	HMGA2	hsa-let-7c	UGAGGUAGUAGGUUGUAUGGUU	UGUUUGAGAUUUUUUAUCUCUUGAUU
280	HMGA2	hsa-let-7g	UGAGGUAGUAGUUUGUACAGUU	UUCCUUAUUGUUAAAAACAUGUUAG
281	HMGA2	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	UUCCUUGUCUGUCUAGUUAUUAUUG
282	HMGA2	hsa-miR-98	UGAGGUAGUAAGUUGUAUUGUU	UUUUUUUUUAAAUGUGCAGUGUUGA
283	HOXA11	hsa-miR-181a	AACAUUCAACGCUGUCGGUGAGU	AUGCUGCACAGAAUUUUUCAAUUUG
284	HOXA7	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	AAUUUUUAAAGGCACAAGAGGCCCU
285	HOXB8	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	UAGACUUGACCUAAUUAUUUCCAAA
286	HOXC8	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	UGUAGGUAAUCUCUGAGUUUCUGGA
287	HSPA1A	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAAU	ACCUUCUGCAACAUCUUAAGAUCCA
288	IKBKB	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	AUAAACUUUCAGAACUGCUACCAUG
289	IRF-5	hsa-miR-146a	UGAGAACUGAAUUCUAGGGUU	CCCCACCCACAAAUGCCUCUGCCU
290	JAK1	hsa-miR-17	CAAAGUGCUUACAGUGCAGGUAG	CCUUCGCAUCACCAUCCUUCGCA
291	KCNH2	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	GAAAGGAGAUCAUUUAGUUGGGUCU
292	KCNH2	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	UGAGCGUUAACACAGUAAAAUUAUC
293	KCNJ2	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAAU	AAGAGAAAUGAGGAAGAAUCCAUCU
294	KRAS	hsa-miR-143	UGAGAUGAAGCACUGUAGCUC	AAAACUAGAUUGACUAAUUUAUACAA
295	KRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	AACUCUAGUUUUUACUUGUUUAAU
296	KRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	AGGACAGGAAAUUGUCCCCCCCUA
297	KRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	AUUGGUAAUAUAAUAAUGUCCUUUC
298	LIN28	hsa-let-7b	UGAGGUAGUAGGUUGUGUGGUU	AGACAAAGAAGGAAAAGAGUAUCAA
299	LIN28	hsa-miR-125b	UCCUGAGACCCUAAUUGUGA	CCACUAAGAAGUUCACUUAACACA
300	MAPK14	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	AGAGCAAGUGAUUUUAUAAUUUGAA
301	MBNL2	hsa-miR-302d	UAAGUGCUUCCAUGUUUGAGUGU	AUUCUGUAAACCUAAUGUCUGUAUA
302	MCL1	hsa-miR-29b	UAGACCAUUUGAAAUCAGUGUU	CCAGGUAAAAACCUAAAAUUAAGA
303	MeCP2	hsa-miR-155	UUAAGUCUAAUCGUGAUAGGGGU	AUAAUGUCCUUUCCUGGAGUCAGU

304	MeCP2	hsa-miR-155	UUA AUGCUAAUCGUGAUAGGGGU	UUUUAGGUCCAGAAUGGAAAAAA
305	MEIS1	hsa-miR-155	UUA AUGCUAAUCGUGAUAGGGGU	ACCUGAGGGGCAAGUCGGGGCAGGG
306	MET	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	AACUUUCUUGCUUCAAAAAUAAAA
307	MET	hsa-miR-23b	AUCACAUUGCCAGGGAUUACC	ACUUGGGGGCAGGCGCCAGGGACGG
308	MET	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	CUAGUUUUAGACCUCAUCUCCAAGA
309	MET	hsa-miR-206	UGGAAUGUAAGGAAGUGUGUGG	GAAUUAAAAAAAAAAACUAGAUUGA
310	MET	hsa-miR-23b	AUCACAUUGCCAGGGAUUACC	UGGUGCUGCUUUGGCUGACUGGGAA
311	MTAP	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	AAAAGAGAAGAAAGAAGCACUCUGC
312	MYB	hsa-miR-150	UCUCCAACCCUUGUACCAGUG	UGGCAGAGAAGAGACCAAGCUUGUU
313	MYC	hsa-miR-145	GUCCAGUUUCCAGGAUCCCU	AAUAACUUUAAUAAAACGUUUUAG
314	MYC	hsa-miR-200b	UAAUACUGCCUGGUAAUGAUGA	ACUGUUUUUUAAAAUCCAUACCUA
315	MYC	hsa-miR-200b	UAAUACUGCCUGGUAAUGAUGA	AUGUCUAAUUUUAUUAUUAUACUUU
316	MYC	hsa-miR-200b	UAAUACUGCCUGGUAAUGAUGA	AUUCUGAAAAUUUUUAUACAUGCAA
317	MYC	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	CCUGGAGCCCCUGUCCUGGCCGU
318	MYC	hsa-miR-200b	UAAUACUGCCUGGUAAUGAUGA	CUGCCCAAUAAUAGUUUAUGUA
319	MYC	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	GGGUCCUGAGCUGUUCUUCUGCC
320	MYC	hsa-miR-145	GUCCAGUUUCCAGGAUCCCU	UAAAAGAACUUUUUAUGCUUACCA
321	MYC	hsa-miR-200b	UAAUACUGCCUGGUAAUGAUGA	UCGUUUCUCCUUCUUGAAUGGCAC
322	MYC	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	UGUCUCUGCAGCCUGGAGCCCCU
323	MYC	hsa-miR-145	GUCCAGUUUCCAGGAUCCCU	UUAAAUGUAAAUACUUUAUAAAA
324	MYC	hsa-miR-145	GUCCAGUUUCCAGGAUCCCU	UUAAGAAUUGUUUUUAAAAUUUU
325	MYC	hsa-miR-145	GUCCAGUUUCCAGGAUCCCU	UUUUUUUAUUUAAGUACAUUUUGCUU
326	MYC	hsa-miR-145	GUCCAGUUUCCAGGAUCCCU	UUUUUUUCUUUAACAGAUUUGUAUU
327	MYCN	hsa-miR-34a	UGGCAGUGUCUAGCUGGUUGU	CAUAACUCGAAGAAAGGUCAGCUUC
328	NCOA3	hsa-miR-17	CAAAGUGCUUACAGUGCAGGUAG	CCUAACUCAAAGCAGAUCCAGUAA
329	NCOA3	hsa-miR-17	CAAAGUGCUUACAGUGCAGGUAG	GCCCCUGCGACCCUGACCUGCUGCU
330	NFIB	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	CCUCUCCUCUGUCUCCAGAAGCUUC
331	Notch-1	hsa-miR-34a	UGGCAGUGUCUAGCUGGUUGU	AAGGGAAGGAGUCUGUGUGUGUGU
332	Notch-1	hsa-miR-34a	UGGCAGUGUCUAGCUGGUUGU	UGUUCCUCCUGCUUUGGUUUUAU
333	NOTCH4	hsa-miR-181c	AACAUUCAACUGUCGGUGAGU	GCCAUCCAGGAAAAGGUGUGAAUUC
334	NR1I2	hsa-miR-148a	UCAGUGCACUACAGAACUUUGU	UCUCCGGCCUCCUCCUGAGGAGUU
335	NRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	CCUGGAGCCCCUGUCCUGGCCGU
336	NRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	UGAAGCGGAGGCUGGACCUGGAAAC
337	NRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	UGUCUCUGCAGCCUGGAGCCCCU
338	NTRK3	hsa-miR-9	UCUUUGGUUAUCUAGCUGUAUGA	GGGGUCCUGAGCUGUUCUUCUGCC
339	PDCD4	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	CAUAACUCGAAGAAAGGUCAGCUUC
340	PDCD4	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	CCUAACUCAAAGCAGAUCCAGUAA
341	PDCD4	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	GCCCCUGCGACCCUGACCUGCUGCU
342	PIK3R1	hsa-miR-29a	UAGCACCAUCUGAAAUCCGUUA	CCUCUCCUCUGUCUCCAGAAGCUUC
343	PLAU	hsa-miR-23b	AUCACAUUGCCAGGGAUUACC	AAGGGAAGGAGUCUGUGUGGUGUGU
344	PLAU	hsa-miR-23b	AUCACAUUGCCAGGGAUUACC	UGUUCCUCCUGCUUUGGUUUUAU
345	POU4F2	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	GCCAUCCAGGAAAAGGUGUGAAUUC
346	POU4F2	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	UCUCCGGCCUCCUCCUGAGGAGUU
347	PRDM1	hsa-miR-9	UCUUUGGUUAUCUAGCUGUAUGA	UGAAGCGGAGGCUGGACCUGGAAAC

348	PTEN	hsa-miR-494	UGAAACAUACACGGGAAACCUC	CUAGAUUUCUACAUUAAUUGAAAA
349	RECK	hsa-miR-16	ACAUUUGGUACUACACGACGAU	CCUCUGUUUAGAACACCAAGAUAA
350	RERE	hsa-miR-429	UAAUACUGUCUGGUAAAACCGU	UUCUUCUCCUCGCUUCCCUCCUC
351	SERPINB5	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	AAGGGAAGUAAGCAAACAAUUAUUG
352	SIP1	hsa-miR-141	UAACACUGUCUGGUAAGAUGG	UGGGCGGGUGAGAAAAACGAAUUG
353	SMAD1	hsa-miR-26a	UUCAAGUAAUCCAGGAUAGGCU	UUUUUAACAUGGUUAUUAACUGG
354	STAT1	hsa-miR-146a	UGAGAACUGAAUCCAUGGGUU	AUGUUUUUUAAUUAAAAUUUUUA
355	STMN1	hsa-miR-223	UGUCAGUUUGUAAAAUACCCCA	GCAUAAAAGAACUUUUUUUAUGCUUA
356	Survivin	hsa-miR-708	AAGGAGCUUACAAUCUAGCUGGG	AAAAACAUCAUCAUCCAGGACUGUA
357	TBP	hsa-miR-146a	UGAGAACUGAAUCCAUGGGUU	UUGGAAAACAAUGAAAAGGCCCCCA
358	TCL1A	hsa-miR-29b	UAGCACCAUUUGAAAUCAGUGUU	GCAACCCUUGCCGCAUCCACGAAAC
359	TCL1A	hsa-miR-181b	AACAUUCAUUGCUGCGGUGGGU	UCCGCAACCCUUGCCGCAUCCACGA
360	TIMP3	hsa-miR-181b	UGGGUGGCUGUCGUUACUACAA	UCCCCAGCCAGCGGUCCGCAACCC
361	UBE2I	hsa-miR-30e	UGUAAACAUCUUGACUGGAAG	UGUGCGUAAGGAAAAGUAAGGAAAA
362	UBE2Q1	hsa-miR-338-3p	UCCAGCAUCAGUGAUUUUGUUG	UCCUACGUUGCGGUCACACCCUUCU
363	UBE2Q1	hsa-miR-338-3p	UCCAGCAUCAGUGAUUUUGUUG	UUUAUAGGUACUUAUAAACCCUAAUUU
364	VEGFA	hsa-miR-17	CAAAGUGCUUACAGUGCAGGUAG	AAGAACUUUUUAUGCUUACCAUCU
365	ZEB2	hsa-miR-708	AAGGAGCUUACAAUCUAGCUGGG	GGCCACAGCAAACCUCCUCACAGCC
366	ADCY6	hsa-miR-96	UUUGGCACUAGCACAUUUUUGCU	AAAGUUUACCACCAAGUCAGAUGUGU
367	ADCY6	hsa-miR-96	UUUGGCACUAGCACAUUUUUGCU	GCAAAGAAAGGGUGGAUGGAUUGAAA
368	ADCY6	hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	UUUUCCAGAAGAUAGUUUCCUAAUU
369	BACE1	hsa-miR-124	UAAGGCACGCGGUGAAUGCC	GAACGUAAAAUGUGUCGCUCCGUUUC
370	BACH1	hsa-miR-155	UUAAUGCUAAUCGUGAUAGGGGU	AGUCCUCUUAACAUCUUAUUAUCCACCU
371	BRCA1	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	UAAUUCACAGAGUAUUGUAAAUGGUG
372	C21orf33	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	UAGUCAUCAUGAAAUUUUAGUUGUC
373	CASP9	hsa-miR-133a	UUUGGUCCCCUUAACACAGCUG	GCUAAUUUUUGUAUUUUUUUGUAGAGA
374	CASP9	hsa-miR-133a	UUUGGUCCCCUUAACACAGCUG	UAGUGUCCCGAGAAUGGUCAUAAAUG
375	CCND1	hsa-miR-20a	UAAAGUGCUUAUAGUGCAGGUAG	AGCCUCCAAAGUGCUAGGAUUACAG
376	CCND1	hsa-miR-302a	UAAGUGCUUCCAUGUUUUGGUGA	UGCUUCAUUCUGUGGAAUUUUGUGCU
377	CCNE1	hsa-miR-16	UAGCAGCACGUAAAUUUGGCG	ACACAUUUCAAUUGGUGGAAAAACAU
378	CCNE1	hsa-miR-503	UAGCAGCGGGAACAGUUCUGCAG	ACCUGGCAUCCUGUGCUCCUGUUUA
379	CD44	hsa-miR-34a	UGGCAGUGUCUAGCUGGUUGU	GAAAACUAAAAUAAGACAAGUAAUU
380	CDC25A	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	UCUCAUUUAUGUACAUAAUCCUGUGU
381	CDC42	hsa-miR-29a	UAGCACCAUCUGAAAUCGGUUA	AGAAGACACAAGGAUUUGUACUGAAG
382	CDK2	hsa-miR-302d	UAAGUGCUUCCAUGUUUUGAGUGU	AAUCAUAGGAAAGUAUUUUUUUAAGC
383	CDKN1B	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	CUCAACUAGUCAUUUUUUUUCUCCUCU
384	CDKN1B	hsa-miR-222	AGCUACAUCUGGCUACUGGGU	GUAAGGAUACUUUACAUGGUUAAGGU
385	CDKN1C	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	AAAAUCAUUUUAAUGGAGUCAGUUUG
386	CDNK1B	hsa-miR-148a	UCAGUGCACUACAGAACUUUGU	AGAAAAUUCUGAGACUAAUAAUAAU
387	COL1A1	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	CAUUUAAUUCAUUGGUUAUUCAGGAUUA
388	col2a1	hsa-miR-29b	UAGCACCAUUUGAAAUCAGUGUU	UGGAGGAUGGAAAGGCUCGCUCAAUC
389	DDIT4	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	UUUUUACAUAUUUAAGAAAAAAGAU
390	DLL1	hsa-miR-34a	UGGCAGUGUCUAGCUGGUUGU	AUUUUCAUACUUUUACCUUCCAUGGC
391	DLL1	hsa-miR-34a	UGGCAGUGUCUAGCUGGUUGU	CCAUCAAACUCCUGUCUUUGGAAAU

392	DNMT3A	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	GUUUUCUGUUUGAGAUUUUUAUCUCU
393	DNMT3B	hsa-miR-29a	UAGCACCAUCUGAAAUCGGUUA	AAAAUAAGUGUACAAUAAGUGUUUU
394	DNMT3B	hsa-miR-29a	UAGCACCAUCUGAAAUCGGUUA	CAUUAUUAAAGAAAAAAGAUUUUUUU
395	ESR1	hsa-miR-222	AGCUACAUCUGGCUACUGGGU	GGGAGAAGGUGUUCAUUCACUUGCAU
396	HMGA2	hsa-miR-98	UGAGGUAGUAAGUUGUAUUGUU	ACCCACCCAGAGCCCUCCUGCCCUCC
397	HMGA2	hsa-let-7g	UGAGGUAGUAGUUUGUACAGUU	ACUUUCCUUGUCUGUCUAGUUAUAU
398	HMGA2	hsa-let-7c	UGAGGUAGUAGGUUGUAUGGUU	CUGUAAACAUAGAUUCGCUUCCAUG
399	HMGA2	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	UUGGAGAGUGAUAAUACAAGUCCUUU
400	HuR	hsa-miR-125b	UCCUGAGACCCUAACUUGUGA	UGACCAAUCUUGUUUUACCCUAUACA
401	IKBKB	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	GACAGUAACAUUUCAUUAACCAAAGA
402	IRS1	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	AGAAGAGACCAAGCUUGUUUCCUGC
403	IRS2	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	UGGCAGAGAAGAGACCAAGCUUGUUU
404	KCNQ1	hsa-miR-133a	UUUGGUCCCCUUAACACAGCUG	UAAACAAGCCUAACAUUGGUGCAAAG
405	KGF	hsa-miR-155	UUAUAGCUAAUCGUGAUAGGGGU	CAUGGAGGAUUUGGGACCUUGGUUUG
406	KRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	AAACCUAAAAUUAGAAGUACAAUAA
407	KRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	ACUGUAUAAACAAGCCUAACAUUGGU
408	KRT5	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	GUCUCUAUCUGAACCACCCUUUAUUC
409	MBNL2	hsa-miR-372	AAAGUGCUGCGACAUUUGAGCGU	UGUAGCGGGCUCCGGAUCCAGCCUC
410	MCP2	hsa-miR-146a	UGAGAACUGAAUCCAUGGGUU	AUCAGCCUAUUUUUUUUUAAAGAAA
411	MET	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	UUUGCUUUAGAGACAGGGACUGUAUA
412	MUC1	hsa-miR-145	GUCCAGUUUCCAGGAUCCCU	UUUCUUUCUUUACUCCUUUGGCUUCA
413	MYB	hsa-miR-150	UCUCCCAACCCUUGUACCAGUG	UCACCAUCCUCCGCAGCAAUACCUG
414	MYC	hsa-miR-200b	UAAUACUGCCUGGUAUUGAUGA	AACUCAACUAUUCUGUAUUCAAUGAC
415	MYC	hsa-miR-200b	UAAUACUGCCUGGUAUUGAUGA	ACAAAAGCUAGUAGCAUCAGUUUAGA
416	MYC	hsa-miR-200b	UAAUACUGCCUGGUAUUGAUGA	AGGCUAACAAAACCUUCCAUUUUAC
417	MYC	hsa-miR-200b	UAAUACUGCCUGGUAUUGAUGA	UAAGAAAAUACAGGUGACUCAUCU
418	MYCN	hsa-miR-101	UACAGUACUGUGAUAAUCUGAA	AGAAGUCCAAGAACCACAUCCAGUGG
419	NFKB1	hsa-miR-9	UCUUUGGUUAUCUAGCUGUAUGA	GUCCCACAAGGCCAGGGCAGUGCCU
420	Osx	hsa-miR-637	ACUGGGGGCUUUCGGGCUCUGCGU	AGAAGUCCAAGAACCACAUCCAGUGG
421	PIK3R1	hsa-miR-221	AGCUACAUUGUCUGUGGGUUUC	GUCCCACAAGGCCAGGGCAGUGCCU
422	PTEN	hsa-miR-19a	UGUGCAAUUCUAUGCAAAACUGA	GUUAUACAUCAAUUUAAAAAGCAAAA
423	PTEN	hsa-miR-494	UGAAACAUACACGGGAAACCUC	UACUACCUCUGAAUGUUACAACGAU
424	PUMA	hsa-miR-296	AGGGCCCCCUCAAUCCUGU	UAGGAAGAACGCGGUGUGUAACACUG
425	RECE	hsa-miR-429	UAAUACUGUCUGGUAUAAACCGU	AUAUAGGAAGAACGCGGUGUGUAACA
426	RHOB	hsa-miR-223	UGUCAGUUUGUCAAUACCCCA	CUCAACCAGAUUUUUUUUAAACGCUU
427	SIRT1	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	GAGAAAAGUAUCAAGACGUUUAACUG
428	SMO	hsa-miR-125b	UCCUGAGACCCUAACUUGUGA	UAGUACUGAAGCCAAUUGAAACUCAA
429	SNCA	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	UUGAAGCUUUGUAGGUGAGAUACAAC
430	STAT5A	hsa-miR-222	AGCUACAUCUGGCUACUGGGU	UGUUAACUGUGCGUUAAAUAAGCAAA
431	TPPP3	hsa-miR-16	UAGCAGCACGUAAAUAUUGGCG	CGGGCGGGCACUUUGCACUGGAACUU
432	TYMS	hsa-miR-215	AUGACCUAUGAAUUGACAGAC	GCUGCGGGCGUCCUGGGAAGGGAGAU
433	ZEB1	hsa-miR-200b	UAAUACUGCCUGGUAUUGAUGA	GUUAUCCUUAAAAAGCCACAGCAUA
434	ZEB1	hsa-miR-200b	UAAUACUGCCUGGUAUUGAUGA	UAAAUAUUGCCAUUAAAUGUAAUAA