

### Mtar 2: Positive Dataset

SL. No	Target gene	miRNA mature_ID	microRNA sequence (5'-3')	Target site_position	Length of binding sites (mRNA)
1	ABCA1	hsa-miR-758	UUUGUGACCUGGUCCACUAACC	8677	23
2	ABCA1	hsa-miR-758	UUUGUGACCUGGUCCACUAACC	10447	23
3	ACVR1B	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	2571	27
4	ACVR1B	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	2027	23
5	ADCY6	hsa-miR-96	UUUGGCACUAGCACAUUUUUGCU	4969	22
6	ADCY6	hsa-miR-96	UUUGGCACUAGCACAUUUUUGCU	6376	22
7	ADCY6	hsa-miR-96	UUUGGCACUAGCACAUUUUUGCU	5440	22
8	ADCY6	hsa-miR-96	UUUGGCACUAGCACAUUUUUGCU	5002	22
9	ADCY6	hsa-miR-96	UUUGGCACUAGCACAUUUUUGCU	5113	22
10	ADCY6	hsa-miR-96	UUUGGCACUAGCACAUUUUUGCU	4780	22
11	ADCY6	hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	5113	22
12	ADCY6	hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	5440	22
13	ADCY6	hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	4505	22
14	ADCY6	hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	4780	22
15	AGTR1	hsa-miR-155	UUAAUGCUAAUCGUGAUAGGGGU	1432	22
16	API5	hsa-miR-224	CAAGUCACUAGUGGUUCCGUU	1941	21
17	API5	hsa-miR-224	CAAGUCACUAGUGGUUCCGUU	3511	21
18	API5	hsa-miR-224	CAAGUCACUAGUGGUUCCGUU	2773	21
19	AURKB	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	1142	22
20	BACE1	hsa-miR-107	AGCAGCAUUGUACAGGGCUAUCA	2240	23
21	BACE1	hsa-miR-29a	UAGCACCAUCUGAAAU CGGUUA	2818	21
22	BACE1	hsa-miR-29b	UAGCACCAUUUGAAAU CAGUGUU	2818	29
23	BACE1	hsa-miR-124	UAAGGCACGCGGUGAAUGCC	5271	23
24	BACH1	hsa-miR-155	UUAAUGCUAAUCGUGAUAGGGGU	4640	24
25	BAK1	hsa-miR-125b	UCCCUGAGACCCUAA CUUGUGA	1573	22
26	BBC3	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	942	25
27	BBC3	hsa-miR-222	AGCUACAU CUGGCUACUGGGU	942	25
28	BCL2	hsa-miR-15a	UAGCAGCACAUAAUGGUUUGUG	3749	22
29	BCL2	hsa-miR-16	UAGCAGCACGUAAAUAUUGGCG	3749	22
30	BCL2	hsa-miR-16	UAGCAGCACGUAAAUAUUGGCG	3749	22
31	BCL2	hsa-miR-34a	UGGCAGUGUCUUA GCUGGUUGU	1422	22
32	BCL2	hsa-miR-15b	UAGCAGCACAUCAUGGUUUACA	3749	21
33	Bcl-2	hsa-miR-143	UGAGAUGAAGCACUGUAGCUC	5719	23
34	BDNF	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	2635	24
35	BIM	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	4944	20
36	BIM	hsa-miR-222	AGCUACAU CUGGCUACUGGGU	4944	18
37	BMF	hsa-miR-125b	UCCCUGAGACCCUAA CUUGUGA	2336	23
38	BMF	hsa-miR-125b	UCCCUGAGACCCUAA CUUGUGA	1126	23
39	BMI1	hsa-miR-708	AAGGAGCUUACAAUCUAGCUGGG	2722	25
40	BMI1	hsa-miR-302b	UAAGUGCUUCCAUGUUUUAGUAG	1009	23

41	BMPR1B	hsa-miR-125b	UCCUGAGACCCUAACUUGUGA	1932	34
42	BMPR2	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	11582	22
43	BMPR2	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	11767	23
44	BMPR2	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	5232	23
45	BMPR2	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	4815	24
46	BRCA1	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	6631	22
47	C21orf33	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	801	21
48	C6orf134	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	1207	17
49	CAPRIN1	hsa-miR-16	UAGCAGCACGUAAAUAUUGGCG	3399	22
50	CASP9	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	767	22
51	CASP9	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	1166	21
52	CASP9	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	167	22
53	CASP9	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	1549	23
54	CASP9	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	907	22
55	CCNA2	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	2047	22
56	CCND1	hsa-miR-20a	UAAAGUGCUUAUAGUGCAGGUAG	2127	30
57	CCND1	hsa-miR-17	CAAAGUGCUUACAGUGCAGGUAG	2127	30
58	CCND1	hsa-miR-17	CAAAGUGCUUACAGUGCAGGUAG	2117	30
59	CCND1	hsa-miR-20a	UAAAGUGCUUAUAGUGCAGGUAG	2117	30
60	CCND1	hsa-miR-302a	UAAGUGCUUCCAUGUUUUGGUGA	680	22
61	CCND1	hsa-miR-302c	UAAGUGCUUCCAUGUUUUGAGUGG	3488	20
62	CCND2	hsa-miR-302b	UAAGUGCUUCCAUGUUUUGAGUAG	2113	31
63	CCND2	hsa-miR-302d	UAAGUGCUUCCAUGUUUGAGUGU	2127	23
64	CCND2	hsa-miR-302d	UAAGUGCUUCCAUGUUUGAGUGU	3474	27
65	CCNE1	hsa-miR-16	UAGCAGCACGUAAAUAUUGGCG	1674	26
66	CCNE1	hsa-miR-16	UAGCAGCACGUAAAUAUUGGCG	1910	33
67	CCNE1	hsa-miR-16	UAGCAGCACGUAAAUAUUGGCG	1670	26
68	CCNE1	hsa-miR-16	UAGCAGCACGUAAAUAUUGGCG	1908	33
69	CCNE1	hsa-miR-503	UAGCAGCGGGAACAGUUCUGCAG	1649	23
70	CCNE1	hsa-miR-503	UAGCAGCGGGAACAGUUCUGCAG	1887	23
71	CCNG1	hsa-miR-122	UGGAGUGUGACAAUGGUGUUUG	1861	22
72	CD276	hsa-miR-29a	UAGCACCAUCUGAAAUCGGUUA	2531	28
73	CD44	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	1855	24
74	CD44	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	3399	23
75	CDC2	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	1807	22
76	CDC25A	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	2567	26
77	CDC25A	hsa-miR-503	UAGCAGCGGGAACAGUUCUGCAG	2476	26
78	CDC42	hsa-miR-29a	UAGCACCAUCUGAAAUCGGUUA	999	23
79	CDC42	hsa-miR-29a	UAGCACCAUCUGAAAUCGGUUA	590	23
80	CDC42	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	599	23
81	CDC42	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	999	23
82	CDK2	hsa-miR-302d	UAAGUGCUUCCAUGUUUGAGUGU	1222	22
83	CDK2	hsa-miR-302d	UAAGUGCUUCCAUGUUUGAGUGU	1869	22
84	CDK4	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	1228	22

85	CDK6	hsa-miR-124	UAAGGCACGCGGUGAAUGCC	3029	22
86	CDK6	hsa-miR-137	UUAUUGCUUAAGAAUACGCGUAG	8522	20
87	CDK6	hsa-miR-124	UAAGGCACGCGGUGAAUGCC	7760	23
88	CDK6	hsa-miR-124	UAAGGCACGCGGUGAAUGCC	1670	23
89	CDKN1B	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	1343	23
90	CDKN1B	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	1270	23
91	CDKN1B	hsa-miR-222	AGCUACAUUGGCUACUGGGU	1343	23
92	CDKN1B	hsa-miR-222	AGCUACAUUGUCUGCUGGGUUUC	1667	24
93	CDKN1B	hsa-miR-222	AGCUACAUUGGCUACUGGGU	1343	23
94	CDKN1B	hsa-miR-222	AGCUACAUUGGCUACUGGGU	1270	23
95	CDKN1C	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	1148	23
96	CDKN1C	hsa-miR-222	AGCUACAUUGGCUACUGGGU	1148	23
97	CDKN1C	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	1148	23
98	CDKN1C	hsa-miR-222	AGCUACAUUGGCUACUGGGU	1148	23
99	CDKN2A	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	1369	22
100	CDKN2A	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	854	22
101	CDKN1B	hsa-miR-148a	UCAGUGCACUACAGAACUUUGU	1182	22
102	CLOCK	hsa-miR-141	U AACACUGUCUGGUAAAGAUGG	3111	19
103	COL1A1	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	5583	19
104	COL1A1	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	5408	19
105	COL1A1	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	5451	20
106	col2a1	hsa-miR-29a	UAGCACCAUCUGAAAUCGGUUA	4993	23
107	col2a1	hsa-miR-29b	UAGCACCAUUUGAAAUCAGUGUU	4993	23
108	COL3A1	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	4767	18
109	COL3A1	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	5207	20
110	COL3A1	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	5133	19
111	CREB1	hsa-miR-103	AGCAGCAUUGUACAGGGCUAUGA	2048	22
112	CTLA-4	hsa-miR-155	UUAAUGCUAAUUCGUGAUAGGGGU	1070	23
113	CXCL12	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	1818	21
114	CXCR4	hsa-miR-146a	UGAGAACUGAAUCCAUGGGUU	1596	22
115	DDIT4	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	1119	23
116	DDIT4	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	1172	23
117	DHFR	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	1265	25
118	DHFR	hsa-miR-215	AUGACCUAUGAAUUGACAGAC	3494	22
119	DICER1	hsa-miR-107	AGCAGCAUUGUACAGGGCUAUGA	7572	22
120	DLL1	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	2846	22
121	DLL1	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	2942	20
122	DLL1	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	3005	20
123	DNMT1	hsa-miR-148a	UCAGUGCACUACAGAACUUUGU	5134	22
124	DNMT3A	hsa-miR-29a	UAGCACCAUCUGAAAUCGGUUA	3865	22
125	DNMT3A	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	3865	21
126	DNMT3B	hsa-miR-148a	UCAGUGCACUACAGAACUUUGU	2651	28
127	DNMT3B	hsa-miR-148b	UCAGUGCAUCACAGAACUUUGU	2651	28
128	DNMT3B	hsa-miR-29a	UAGCACCAUCUGAAAUCGGUUA	4033	23

129	DNMT3B	hsa-miR-29a	UAGCACCAUCUGAAAUCGGUUA	3062	22
130	DNMT3B	hsa-miR-29a	UAGCACCAUCUGAAAUCGGUUA	3899	23
131	DNMT3B	hsa-miR-29c	UAGCACCAUUUGAAAUCGGUUA	4033	22
132	E2F2	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	3164	22
133	E2F3	hsa-miR-125b	UCCCUGAGACCCUAAACUUGUGA	2895	23
134	E2F6	hsa-miR-193a-3	AACUGGCCUACAAAGUCCAGU	1273	20
135	EGFR	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	4255	19
136	EGFR	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	4626	21
137	EGFR	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	4343	22
138	EGR2	hsa-miR-150	UCUCCCAACCCUUGUACCAGUG	2176	23
139	ERBB2	hsa-miR-125b	UCCCUGAGACCCUAAACUUGUGA	4050	26
140	ERBB3	hsa-miR-125b	UCCCUGAGACCCUAAACUUGUGA	4248	19
141	ERK5	hsa-miR-143	UGAGAUGAAGCACUGUAGCUC	2932	21
142	ESR1	hsa-miR-206	UGGAAUGUAAGGAAGUGUGUGG	3317	31
143	ESR1	hsa-miR-206	UGGAAUGUAAGGAAGUGUGUGG	2266	23
144	ESR1	hsa-miR-222	AGCUACAUCUGGCUACUGGGU	2275	23
145	ETS1	hsa-miR-155	UUAAUGCUAAUCGUGAUAGGGGU	4592	23
146	EZH2	hsa-miR-124	UAAGGCACGCGGUGAAUGCC	2467	20
147	FBXW11	hsa-miR-103	UAGCAGCACGUAAAUAUUGGCG	4312	17
148	FBXW7	hsa-miR-27a	CGCUUGAAUCGGUGACACUU	3652	23
149	FEN1	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	2164	22
150	FGFR1	hsa-miR-16	UAGCAGCACGUAAAUAUUGGCG	3338	23
151	FOS	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	1558	23
152	FSCN1	hsa-miR-145	GUCCAGUUUUUCCAGGAAUCCCU	1980	23
153	FSCN1	hsa-miR-145	GUCCAGUUUUUCCAGGAAUCCCU	1719	22
154	FSCN1	hsa-miR-145	GUCCAGUUUUUCCAGGAAUCCCU	2332	22
155	FSCN1	hsa-miR-145	GUCCAGUUUUUCCAGGAAUCCCU	2743	23
156	FSCN1	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	2348	22
157	G6PD	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	2101	22
158	GJA1	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	3015	23
159	GRIA2	hsa-miR-181b	GGGUGGCUGUCGUUACUUACA	2768	20
160	HCN2	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	3381	22
161	HCN2	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	2783	22
162	HCN4	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	4219	22
163	HES1	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	1080	22
164	HES1	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	1191	22
165	HES1	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	1367	22
166	HMGA1	hsa-miR-16	UAGCAGCACGUAAAUAUUGGCG	9447	38
167	HMGA2	hsa-let-7b	UGAGGUAGUAGGUUGUGUGGUU	1169	24
168	HMGA2	hsa-let-7b	UGAGGUAGUAGGUUGUGUGGUU	2766	22
169	HMGA2	hsa-let-7b	UGAGGUAGUAGGUUGUGUGGUU	2815	20
170	HMGA2	hsa-let-7b	UGAGGUAGUAGGUUGUGUGGUU	2254	23
171	HMGA2	hsa-let-7b	UGAGGUAGUAGGUUGUGUGGUU	2405	28
172	HMGA2	hsa-let-7b	UGAGGUAGUAGGUUGUGUGGUU	3699	23

173	HMGA2	hsa-let-7e	UGAGGUAGGAGGUUGUAUAGUU	1169	19
174	HMGA2	hsa-let-7e	UGAGGUAGGAGGUUGUAUAGUU	3699	25
175	HMGA2	hsa-let-7e	UGAGGUAGGAGGUUGUAUAGUU	2254	21
176	HMGA2	hsa-let-7e	UGAGGUAGGAGGUUGUAUAGUU	2766	21
177	HMGA2	hsa-let-7e	UGAGGUAGGAGGUUGUAUAGUU	2405	20
178	HMGA2	hsa-let-7e	UGAGGUAGGAGGUUGUAUAGUU	2815	19
179	HMGA2	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	2254	22
180	HMGA2	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	2403	21
181	HMGA2	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	2815	21
182	HMGA2	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	3688	21
183	HMGA2	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	1169	22
184	HMGA2	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	2766	21
185	HMGA2	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	3668	21
186	HMGA2	hsa-let-7c	UGAGGUAGUAGGUUGUAUGGUU	1169	22
187	HMGA2	hsa-let-7c	UGAGGUAGUAGGUUGUAUGGUU	2766	21
188	HMGA2	hsa-let-7c	UGAGGUAGUAGGUUGUAUGGUU	2254	22
189	HMGA2	hsa-let-7c	UGAGGUAGUAGGUUGUAUGGUU	3668	21
190	HMGA2	hsa-let-7c	UGAGGUAGUAGGUUGUAUGGUU	2403	21
191	HMGA2	hsa-let-7c	UGAGGUAGUAGGUUGUAUGGUU	2815	21
192	HMGA2	hsa-let-7c	UGAGGUAGUAGGUUGUAUGGUU	3688	22
193	HMGA2	hsa-let-7g	UGAGGUAGUAGUUUGUACAGUU	1169	22
194	HMGA2	hsa-let-7g	UGAGGUAGUAGUUUGUACAGUU	2403	21
195	HMGA2	hsa-let-7g	UGAGGUAGUAGUUUGUACAGUU	2815	21
196	HMGA2	hsa-let-7g	UGAGGUAGUAGUUUGUACAGUU	3688	21
197	HMGA2	hsa-let-7g	UGAGGUAGUAGUUUGUACAGUU	2254	22
198	HMGA2	hsa-miR-98	UGAGGUAGUAAGUUGUAUUGUU	2816	23
199	HMGA2	hsa-miR-98	UGAGGUAGUAAGUUGUAUUGUU	2254	21
200	HMGA2	hsa-miR-98	UGAGGUAGUAAGUUGUAUUGUU	3669	24
201	HMGA2	hsa-miR-98	UGAGGUAGUAAGUUGUAUUGUU	3688	31
202	HMGA2	hsa-miR-98	UGAGGUAGUAAGUUGUAUUGUU	2404	32
203	HMGA2	hsa-miR-98	UGAGGUAGUAAGUUGUAUUGUU	1169	22
204	HOXA11	hsa-miR-181a	AACAUUCAACGCUGUCGGUGAGU	2240	30
205	HOXA7	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	1286	22
206	HOXA7	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	1171	22
207	HOXA7	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	1134	21
208	HOXA7	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	1304	21
209	HOXB8	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	1399	22
210	HOXB8	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	1399	22
211	HOXC8	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	2017	21
212	HOXC8	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	2017	21
213	HSPA1A	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAAU	2177	22
214	HSPD1	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAAU	2081	22
215	HuR	hsa-miR-125b	UCCCUGAGACCCUAAAUUGUGA	1840	22
216	ICAM1	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	2338	23

217	ICOS	hsa-miR-103	AGCAGCAUUGUACAGGGCUAUGA	2263	23
218	IKBKB	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	3752	32
219	IKBKB	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	2722	33
220	IKBKB	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	2507	22
221	IRF-5	hsa-miR-146a	UGAGAACUGAAUCCAUGGGUU	2554	21
222	IRS1	hsa-miR-145	GUCCAGUUUUCCCAGGAUCCCU	4947	26
223	IRS1	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	5664	20
224	IRS2	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	6126	22
225	IRS2	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	6845	23
226	JAG1	hsa-miR-141	UAACACUGUCUGGUAAGAUGG	4255	30
227	JAK1	hsa-miR-17	CAAAGUGCUUACAGUGCAGGUAG	5010	25
228	KCNE1	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	1079	22
229	KCNE1	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	3157	22
230	KCNE1	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	2688	22
231	KCNH2	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	1608	22
232	KCNH2	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	1629	22
233	KCNH2	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	2931	22
234	KCNH2	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	2316	22
235	KCNH2	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	2891	22
236	KCNH2	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	2019	22
237	KCNJ2	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	2750	22
238	KCNQ1	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	1920	23
239	KCNQ1	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	2283	22
240	KCNQ1	hsa-miR-133a	UUUGGUCCCCUUAACCAGCUG	1803	24
241	KGF	hsa-miR-155	UUAUUGCUAAUCGUGAUAGGGGU	1294	22
242	KGF	hsa-miR-155	UUAUUGCUAAUCGUGAUAGGGGU	2022	19
243	KLF13	hsa-miR-302d	UAAGUGCUUCCAUGUUUGAGUGU	3922	22
244	KLF13	hsa-miR-372	AAAGUGCUGCGACAUUUGAGCGU	2150	29
245	KLF13	hsa-miR-372	AAAGUGCUGCGACAUUUGAGCGU	3806	37
246	KLF4	hsa-miR-137	UUAUUGCUUAAAGAAUACGCGUAG	2695	23
247	KRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	3900	28
248	KRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	2571	19
249	KRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	925	25
250	KRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	3270	21
251	KRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	3970	28
252	KRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	2708	25
253	KRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	3246	24
254	KRAS	hsa-miR-143	UGAGAUGAAGCACUGUAGCUC	2479	21
255	KRAS	hsa-miR-143	UGAGAUGAAGCACUGUAGCUC	4531	29
256	KRAS	hsa-miR-181c	AACAUUCAACCGUCGGUGAGU	1189	20
257	KRT5	hsa-miR-196a	UAGGUAGUUUCAUGUUGUUGGG	1959	20
258	LIN28	hsa-let-7b	UGAGGUAGUAGGUUGUGUGGUU	1656	23
259	LIN28	hsa-miR-125b	UCCCUGAGACCCUAAUUGUGA	1552	18
260	LIN28	hsa-miR-125b	UCCCUGAGACCCUAAUUGUGA	1534	17

261	LMO2	hsa-miR-223	UGUCAGUUUGUCAAAUACCCCA	1765	21
262	MAP2K1	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	2237	23
263	MAPK14	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	2035	18
264	MBNL2	hsa-miR-302d	UAAGUGCUUCCAUGUUUGAGUGU	4512	33
265	MBNL2	hsa-miR-372	AAAGUGCUGCGACAUUUGAGCGU	4510	25
266	MCL1	hsa-miR-29b	UAGCACCAUUUGAAAUCAGUGUU	2523	23
267	MCL1	hsa-miR-29b	UAGCACCAUUUGAAAUCAGUGUU	2523	23
268	MCP2	hsa-miR-146a	UGAGAACUGAAUCCAUGGGUU	1136	19
269	MeCP2	hsa-miR-155	UUAAUGCUAAUCGUGAUAGGGGU	4700	23
270	MeCP2	hsa-miR-155	UUAAUGCUAAUCGUGAUAGGGGU	6328	23
271	MEIS1	hsa-miR-155	UUAAUGCUAAUCGUGAUAGGGGU	2366	23
272	MET	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	836	23
273	MET	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	521	23
274	MET	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	6532	23
275	MET	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	4418	23
276	MET	hsa-miR-206	UGGAAUGUAAGGAAGUGUGUGG	5181	23
277	MET	hsa-miR-206	UGGAAUGUAAGGAAGUGUGUGG	4866	23
278	MET	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	5181	23
279	MET	hsa-miR-1	UGGAAUGUAAAGAAGUAUGUAU	4866	23
280	MET	hsa-miR-23b	AUCACAUUGCCAGGGAUUACC	5386	21
281	MET	hsa-miR-23b	AUCACAUUGCCAGGGAUUACC	5809	21
282	MET	hsa-miR-23b	AUCACAUUGCCAGGGAUUACC	6432	20
283	MET	hsa-miR-23b	AUCACAUUGCCAGGGAUUACC	4937	21
284	MITF	hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	4323	22
285	MITF	hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	4382	22
286	MITF	hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	4050	22
287	MITF	hsa-miR-182	UUUGGCAAUGGUAGAACUCACACU	4165	22
288	MMP1	hsa-miR-222	AGCUACAUCUGGCUACUGGGU	1721	22
289	MTAP	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	2778	25
290	MUC1	hsa-miR-145	GUCCAGUUUUUCCAGGAAUCCCU	1169	19
291	MUC4	hsa-miR-150	UCUCCCAACCCUUGUACCAGUG	3591	23
292	MYB	hsa-miR-150	UCUCCCAACCCUUGUACCAGUG	3097	22
293	MYB	hsa-miR-150	UCUCCCAACCCUUGUACCAGUG	3054	22
294	MYC	hsa-miR-145	GUCCAGUUUUUCCAGGAAUCCCU	2042	24
295	MYC	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	1969	22
296	MYC	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	1957	22
297	MYC	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	2166	22
298	MYC	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	2052	22
299	MYC	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	2358	23
300	MYC	hsa-miR-24	UGGCUCAGUUCAGCAGGAACAG	2006	22
301	MYCN	hsa-miR-101	UACAGUACUGUGAUAAACUGAA	2196	23
302	MYCN	hsa-miR-101	UACAGUACUGUGAUAAACUGAA	2265	18
303	MYCN	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	2283	23
304	MYCN	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	1725	21

305	NCOA3	hsa-miR-17	CAAAGUGCUUACAGUGCAGGUAG	5783	22
306	NCOA3	hsa-miR-17	CAAAGUGCUUACAGUGCAGGUAG	656	24
307	NFIB	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	2147	23
308	NFKB1	hsa-miR-9	UCUUUGGUUAUCUAGCUGUAUGA	3413	23
309	NLK	hsa-miR-181b	GGGUGGCUGUCGUUACUUAACA	3013	25
310	Notch-1	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	3867	23
311	Notch-1	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	8584	20
312	NOTCH2	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	1897	22
313	NOTCH4	hsa-miR-181c	AACAUUCAACCGUCGGUGAGU	6284	22
314	NR1I2	hsa-miR-148a	UCAGUGCACUACAGAACUUUGU	3275	28
315	NRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	1103	18
316	NRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	1048	26
317	NRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	1942	28
318	NRAS	hsa-let-7a	UGAGGUAGUAGGUUGUAUAGUU	1018	25
319	NTRK3	hsa-miR-9	UCUUUGGUUAUCUAGCUGUAUGA	2842	28
320	NTRK3	hsa-miR-125b	UCCUGAGACCCUAAAUUGUGA	2851	26
321	Osx	hsa-miR-637	U	1992	28
322	PARP8	hsa-miR-145	GUCCAGUUUUCCCAGGAAUCCCU	2737	21
323	PDCD4	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	1902	22
324	PDCD4	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	1902	23
325	PDCD4	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	1906	22
326	PDCD4	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	249	22
327	PIK3R1	hsa-miR-29a	UAGCACCAUCUGAAAU CGGUUA	1925	23
328	PIK3R1	hsa-miR-221	AGCUACAUUGUCUGCUGGGUUUC	3262	23
329	PITX3	hsa-miR-133b	UUUGGUCCCCUUAACCAGCUA	1290	21
330	PLAU	hsa-miR-23b	AUCACAUUGCCAGGGAUUACC	2007	21
331	PLAU	hsa-miR-23b	AUCACAUUGCCAGGGAUUACC	2363	20
332	POU4F2	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	1658	25
333	POU4F2	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	3141	29
334	POU4F2	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	1587	21
335	POU4F2	hsa-miR-23a	AUCACAUUGCCAGGGAUUUCC	1948	22
336	PRDM1	hsa-miR-9	UCUUUGGUUAUCUAGCUGUAUGA	2330	28
337	PRDM1	hsa-miR-9	UCUUUGGUUAUCUAGCUGUAUGA	1465	21
338	PTBP2	hsa-miR-133b	UUUGGUCCCCUUAACCAGCUA	2690	20
339	PTEN	hsa-miR-19a	UGUGCAAUUCUAUGCAAACUGA	3471	21
340	PTEN	hsa-miR-19a	UGUGCAAUUCUAUGCAAACUGA	2661	23
341	PTEN	hsa-miR-19a	UGUGCAAUUCUAUGCAAACUGA	4502	25
342	PTEN	hsa-miR-494	UGAAACAUACACGGGAAACCUC	5048	23
343	PTEN	hsa-miR-494	UGAAACAUACACGGGAAACCUC	4563	23
344	PTEN	hsa-miR-29a	UAGCACCAUCUGAAAU CGGUUA	2904	23
345	PTEN	hsa-miR-29a	UAGCACCAUCUGAAAU CGGUUA	3969	23
346	PUMA	hsa-miR-296	AGGGCCCCCCCUCAAUCCUGU	1284	21
347	PUMA	hsa-miR-296	AGGGCCCCCCCUCAAUCCUGU	1447	23
348	RAF1	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	3021	22



349	RAF1	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	2999	23
350	RECK	hsa-miR-16	ACAUUUGGUACUACACGACGAU	3820	19
351	RECK	hsa-miR-372	AAAGUGCUGCGACAUUUGAGCGU	4284	32
352	RERE	hsa-miR-429	UAAUACUGUCUGGUAAAACCGU	5675	15
353	RERE	hsa-miR-429	UAAUACUGUCUGGUAAAACCGU	7024	34
354	RERE	hsa-miR-429	UAAUACUGUCUGGUAAAACCGU	6768	22
355	RHOA	hsa-miR-155	UUAUUGCUAAUCGUGAUAGGGGU	1471	23
356	RHOA	hsa-miR-133a	UUUGGUCCCCUUAACACGACUG	1330	30
357	RHOB	hsa-miR-223	UGUCAGUUUGUCAAAUACCCCA	1631	22
358	RHOB	hsa-miR-223	UGUCAGUUUGUCAAAUACCCCA	2266	21
359	RHOC	hsa-miR-138	AGCUGGUGUUGUGAAUCAGGCCG	1254	22
360	ROCK2	hsa-miR-138	AGCUGGUGUUGUGAAUCAGGCCG	4979	23
361	RTKN	hsa-miR-145	GUCCAGUUUUCCCAGGAUCCCU	2482	25
362	RUNX1	hsa-miR-17	CAAAGUGCUUACAGUGCAGGUAG	3577	20
363	SERPINB5	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	2456	21
364	SFRS1	hsa-miR-10a	UACCCUGUAGAUCCGAAUUUGUG	1749	17
365	SIP1	hsa-miR-141	UAACACUGUCUGGUAAAGAUGG	4382	23
366	SIP1	hsa-miR-141	UAACACUGUCUGGUAAAGAUGG	4949	23
367	SIRT1	hsa-miR-34a	UGGCAGUGUCUAGCUGGUUGU	3736	26
368	SMAD1	hsa-miR-26a	UUCAAGUAAUCCAGGAUAGGCU	1924	19
369	SMO	hsa-miR-125b	UCCUGAGACCCUAAAUUGUGA	2873	23
370	SNCA	hsa-miR-7	UGGAAGACUAGUGAUUUUGUUGU	813	23
371	SOX5	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	2830	29
372	SPI1	hsa-miR-155	UUAUUGCUAAUCGUGAUAGGGGU	1089	21
373	STAT1	hsa-miR-146a	UGAGAACUGAAUCCAUGGGUU	3436	21
374	STAT3	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	4326	23
375	STAT5A	hsa-miR-222	AGCUACAUCUGGCUACUGGGU	3190	21
376	STMN1	hsa-miR-223	UGUCAGUUUGUCAAAUACCCCA	833	19
377	Survivin	hsa-miR-708	AAGGAGCUUACAAUCUAGCUGGG	1106	24
378	Survivin	hsa-miR-708	AAGGAGCUUACAAUCUAGCUGGG	1854	23
379	Survivin	hsa-miR-708	AAGGAGCUUACAAUCUAGCUGGG	1344	26
380	TBP	hsa-miR-146a	UGAGAACUGAAUCCAUGGGUU	1667	27
381	TCL1A	hsa-miR-29b	UAGCACC AUUUGAAAU CAGUGUU	925	23
382	TCL1A	hsa-miR-181b	AACAUUCAUUGCUGUCGGUGGGU	1154	24
383	TGFB2	hsa-miR-141	UAACACUGUCUGGUAAAGAUGG	1542	22
384	TIMP3	hsa-miR-222	AGCUACAUCUGGCUACUGGGU	2443	23
385	TIMP3	hsa-miR-181b	UGGGUGGCUGUCGUUACUACAA	3499	23
386	TIMP3	hsa-miR-181b	UGGGUGGCUGUCGUUACUACAA	3573	23
387	TPM1	hsa-miR-21	UAGCUUAUCAGACUGAUGUUGA	1239	22
388	TPPP3	hsa-miR-16	UAGCAGCACGUAAAUAUUGGCG	1077	17
389	TYMS	hsa-miR-215	AUGACCUAUGAAUUGACAGAC	1317	21
390	UBE2I	hsa-miR-30e	UGUAAACAUCUUGACUGGAAG	640	23
391	UBE2I	hsa-miR-30c	UGUAAACAUCUACACUCUCAGC	1134	25
392	UBE2Q1	hsa-miR-338-3p	UCCAGCAUCAGUGAUUUUGUUG	1653	36

393	UBE2Q1	hsa-miR-338-3p	UCCAGCAUCAGUGAUUUUGUUG	1751	33
394	UBE2Q1	hsa-miR-338-3p	UCCAGCAUCAGUGAUUUUGUUG	1594	20
395	VEGF	hsa-miR-16	UAGCAGCACGUAAAUAUUGGCG	1713	23
396	VEGFA	hsa-miR-17	CAAAGUGCUUACAGUGCAGGUAG	1914	23
397	VEGFA	hsa-miR-34a	UGGCAGUGUCUUAGCUGGUUGU	1829	24
398	VEGFA	hsa-miR-372	AAAGUGCUGCGACAUUUGAGCGU	2578	29
399	VEGFR2	hsa-miR-16	UAGCAGCACGUAAAUAUUGGCG	4404	22
400	VSNL1	hsa-miR-181b	AACAUUCAUUGCUGUCGGUGGGU	1725	23
401	WNK1	hsa-miR-215	AUGACCUAUGAAUUGACAGAC	7588	22
402	ZEB1	hsa-miR-200b	UAAUACUGCCUGGUAAUGAUGA	3871	23
403	ZEB1	hsa-miR-200b	UAAUACUGCCUGGUAAUGAUGA	3777	23
404	ZEB2	hsa-miR-708	AAGGAGCUUACAAUCUAGCUGGG	704	25