

Supplementary Table 3. The hsa_circ_0007444 binding miRNA predicted by miRanda, which were predicted to have at least two binding sites in hsa_circ_0007444.

miRNA	align scor	energy	miRN A	miRN start	miRN A end	gene_ start	gene_ end	miRNA align	alignment	count
hsa-miR-345-3p	132	-16.02	3	19	179	203	3 gaggUCUGGG-GA--GCAAGUCCcg 5		4	
hsa-miR-345-3p	128	-17.06	3	21	348	369	3 gaGGUCUGGGGAGCAAGUCCcg 5	: : : : :	4	
hsa-miR-345-3p	121	-16	3	12	268	288	3 gaggucuggggAGCAAGUCCcg 5		4	
hsa-miR-345-3p	121	-19.31	2	21	361	380	3 gaGGUCUGGGGAGCAAGUCCCg 5		4	
hsa-miR-3116	137	-16.79	2	17	245	267	3 ucagggAUGA--UACAAGGUCCGu 5	: :: :	4	
hsa-miR-3116	130	-17.1	2	21	264	288	3 ucAGGGAUGAUAC--A-AGGUCCGu 5	: :	4	
hsa-miR-3116	122	-23.23	3	21	183	203	3 ucAGGGAUGAUACAAGGUCCgu 5	:	4	
hsa-miR-3116	121	-14.22	2	21	344	369	3 ucAGGGA-UGA--UACA-AGGUCCGu 5	: :	4	
hsa-miR-4468	136	-17.81	2	17	315	332	3 uaGAGUAGGAAGACGAGa 5	:	4	
hsa-miR-4468	132	-14.05	3	17	54	71	3 uaGAGUAGGAAGACGAg a 5	: :	4	
hsa-miR-4468	125	-13.05	3	14	224	241	3 uagagUAGGAAGACGAg a 5	: :	4	
hsa-miR-4468	121	-15.87	2	16	130	146	3 uagAGUAGGAAGACGAGa 5	: :	4	
hsa-miR-4709-3p	137	-20.27	2	22	335	358	3 cgAU-GUCUCGU-GGAGGAGAAGUu 5	:	4	
hsa-miR-4709-3p	136	-19.26	3	22	309	328	3 cgAUGUCUCGUGGAGGAGAAGuu 5	:	4	
hsa-miR-4709-3p	133	-14.9	2	15	152	175	3 cgaugucucGUG-GAGGAGAAGUu 5	: :	4	
hsa-miR-4709-3p	120	-13.93	2	8	263	285	3 cgaugucucguggaggAGAAGUu 5		4	
hsa-miR-6501-3p	134	-15.72	2	11	46	68	3 ugacaauggcgucCGACGAGACc 5	:	4	
hsa-miR-6501-3p	126	-13.83	3	22	153	173	3 ugACAAUGGCGUCCGACGAGAcc 5	: :	4	
hsa-miR-6501-3p	123	-13.42	3	20	355	375	3 ugacAAUGGCGUCCGACGAGAcc 5	:: :	4	
hsa-miR-6501-3p	121	-14.96	2	18	126	148	3 ugacaaUGGCGUCCGACGAGACc 5	: : :	4	
hsa-miR-296-3p	143	-19.84	3	20	273	294	3 ccuCUCGGAGGUGGGUUGGGag 5	: :	3	
hsa-miR-296-3p	124	-15.69	2	19	22	45	3 ccucUCGGAG-GUGG-GUUGGGAg 5	:	3	
hsa-miR-296-3p	120	-15.06	3	9	81	102	3 ccucucggagguggGUUGGGAg 5		3	
hsa-miR-670-5p	130	-20.55	4	19	185	204	3 guGGUGUAUGUGAGUCCcug 5	:	3	
hsa-miR-670-5p	126	-14.23	2	19	270	289	3 guGGUGUAUGUGAGUCCCUg 5	:: : :	3	
hsa-miR-670-5p	122	-18.19	4	19	351	370	3 guGGUGUAUGUGAGUCCcug 5	: : :	3	
hsa-miR-298	142	-20.3	2	21	308	330	3 acccUCUUGGAGGGACGAAGACGa 5	: :	3	
hsa-miR-298	127	-17.32	2	21	48	72	3 acccUCUUGGA-GGGACGAAGACGa 5	: :	3	
hsa-miR-298	122	-17.52	2	20	212	239	3 acccuCUUGGAGGG----ACGAAGACGa 5	:	3	
hsa-miR-875-3p	142	-15.43	2	19	245	265	3 gugUUGGAGUCACAAAGGUCc 5	: : :	3	
hsa-miR-875-3p	137	-15.37	2	16	356	378	3 guguugGAGU-CAC-AAAGGUCc 5	: :	3	
hsa-miR-875-3p	128	-15.98	2	20	189	209	3 guGUUG-GAGUCACAAAGGUCc 5	:: :	3	
hsa-miR-922	146	-19.42	2	16	48	71	3 cugcaucaGGAU-AAGAGACGACg 5	: : :	3	
hsa-miR-922	132	-23.64	2	22	144	168	3 cuGCA-UCAGGAUAAGAG-ACGACg 5	: : :	3	
hsa-miR-922	120	-18.89	4	19	125	146	3 cugcaUCAGGAUAAGAGACGacg 5	: :	3	
hsa-miR-924	146	-14.45	2	19	403	422	3 cgUUCUGUAGUGUUCUGAGa 5	: : :	3	
hsa-miR-924	130	-17.13	2	17	188	206	3 cguuCUGUAGUGUUCUGAGa 5	: : :	3	
hsa-miR-924	121	-12.94	2	19	299	320	3 cgUUCUGUAGUG--UUCUGAGa 5	: ::	3	

hsa-miR-942-3p	159	-19.81	2	21	134	158	3 ugAAGAGAC---AAAGCCGGUACAc 5		3
hsa-miR-942-3p	128	-13.29	3	21	257	278	3 ugAAGAGACAAAGCCGGUACac 5	:	3
hsa-miR-942-3p	122	-21.48	2	20	54	78	3 ugaAGAGACAAAGC--CGGU-ACAc 5	: :	3
hsa-miR-1236-3p	135	-19.53	3	21	388	410	3 gaCCUC-UCUGUUCUUUUUCUcc 5	:	3
hsa-miR-1236-3p	133	-14.75	3	14	366	387	3 gaccucucuGUUUUUUUUCUcc 5	:	3
hsa-miR-1236-3p	125	-12.21	2	14	164	185	3 gaccucucuGUUUUUUUUCUCc 5		3
hsa-miR-1254	138	-19.4	2	17	245	267	3 ugacguccGAGGUCGAAGGUCCGa 5	: :	3
hsa-miR-1254	137	-16.2	2	23	264	288	3 ugACG-UCCGAGGUCGAAGGUCCGa 5	: :	3
hsa-miR-1254	128	-15.61	2	18	345	369	3 ugacgucCGAGGUCGA-AGGUCCGa 5	:	3
hsa-miR-1276	123	-14.98	2	18	217	235	3 acaGAGGUGUUCCCGAGAAu 5	: : : :	3
hsa-miR-1276	122	-13.89	3	19	155	174	3 acAGAGGUGUUCCCGAGAAu 5		3
hsa-miR-1276	121	-13.08	3	19	356	376	3 acAGAGGUGUCC-CGAGAAu 5	: : :: :	3
hsa-miR-1276	121	-13.08	3	19	356	376	3 acAGAGGUGUCC-CGAGAAu 5	: : :	3
hsa-miR-3925-5p	145	-22.34	2	21	121	142	3 ucCGAG-GUGAAAGUCAAGAGAA 5		3
hsa-miR-3925-5p	123	-12.59	3	20	314	335	3 uccGAGGUGAAAGUCAAGAGaa 5		3
hsa-miR-3925-5p	122	-19.3	2	21	350	374	3 ucCGAGGUGA--AAGU-CAAGAGAA 5	: :	3
hsa-miR-4502	135	-18.56	2	21	195	218	3 gaAGUCGU--GGUAGUAGUAGUCg 5	: :	3
hsa-miR-4502	130	-13.21	2	21	323	343	3 gaAGUCGUGGUAGUAGUAGUCg 5	:	3
hsa-miR-4502	122	-13.55	2	16	264	286	3 gaagucgUGGUA-GUAGUAGUCg 5	: :	3
hsa-miR-4524a-5p	151	-18.51	3	21	148	171	3 acUCUGUCC--AAGUACGACGAua 5	:	3
hsa-miR-4524a-5p	124	-12.99	2	15	54	74	3 acucugucCAAGUACGACGAUa 5	:	3
hsa-miR-4524a-5p	121	-15.36	2	18	220	241	3 acucuGUCCAAGUACGACGAUa 5		3
hsa-miR-4773	151	-15.24	2	12	312	333	3 cggaaagauacGAGGACAAGAc 5	:	3
hsa-miR-4773	147	-16.13	2	16	46	67	3 cggaaagAUACGAGGACAAGAc 5	:	3
hsa-miR-4773	123	-14.31	3	20	154	175	3 cggAAAGAUACGAGGACAAGAc 5	:	3
hsa-miR-4778-3p	150	-14.09	2	11	390	411	3 aguugagacguUCCUUCUUCu 5	:	3
hsa-miR-4778-3p	146	-14.41	2	15	376	397	3 aguugagaCGUUUCCUUCUUCu 5		3
hsa-miR-4778-3p	142	-14.63	3	20	366	388	3 aguUGAGACGUU-UCCUUCUUCu 5		3
hsa-miR-4436b-3p	125	-15.44	2	19	148	172	3 aacaGGUGAAGAAG--GACGGGA 5	: : :	3
hsa-miR-4436b-3p	122	-15.05	2	21	313	333	3 aaCAGGUGAAGAAGGACGGGA 5	: :	3
hsa-miR-4436b-3p	120	-17.36	2	13	46	67	3 aacaggugaaGAAGGACGGGA 5	:	3
hsa-miR-6079	126	-14.88	2	23	142	163	3 guCGAUCAACCAGGUUCGAAGGUu 5		3
hsa-miR-6079	125	-15.02	2	14	185	208	3 gucgaucaaccAGGUUCGAAGGUu 5	:	3
hsa-miR-6079	122	-12.79	2	22	53	74	3 gucGAUCAACCAGGUUCGAAGGUu 5	:	3
hsa-miR-6735-5p	125	-23.82	2	14	123	147	3 agucuaaggacaCGGGAGACGGGA 5		3
hsa-miR-6735-5p	122	-21.45	4	21	52	75	3 agucuAAGGACACGGGAGACGGGac 5	: :	3
hsa-miR-6735-5p	120	-19.52	2	13	309	333	3 agucuaaggacacGGGAGACGGGA 5	:	3
hsa-miR-6852-5p	129	-12.09	2	18	456	476	3 guacAGGAGUCUUGGGGUCCc 5	: : :	3
hsa-miR-6852-5p	126	-17.4	2	20	207	229	3 guACAGGAGUCUU--GGGGUCCc 5	:	3
hsa-miR-6852-5p	121	-14.21	4	19	84	105	3 guaCA-GGAGUCUUGGGGUccc 5		3

hsa-miR-7161-3p	134	-15.08	3	25	106	136	3 ggacCUCUGACGGUCUC--AGU-UUCUAGau 5	: 	3
hsa-miR-7161-3p	128	-14.73	2	18	204	233	3 ggaccucugacGGUCUCA--GUUUCUAGau 5	: :	3
hsa-miR-7161-3p	121	-14.52	3	25	392	422	3 ggacCUCU-GACGGUC-UCAG-UUUCUAGau 5	: :	3
hsa-miR-7851-3p	135	-18.08	2	19	248	267	3 agguUGGAGUCAGAGGGUCCAu 5	: : :	3
hsa-miR-7851-3p	130	-18.64	2	19	348	369	3 agguUGGAGUCAGAGGGUCCAu 5	: : : ::	3
hsa-miR-7851-3p	126	-18.38	3	21	210	230	3 agGUUGGAGUCAGAGGGUCCau 5		3
hsa-miR-8060	141	-14.95	2	22	142	165	3 cagGAGGAUGGGUGACGAAGUACc 5	: : :	3
hsa-miR-8060	136	-14.3	3	17	337	360	3 caggaggaUGGGUGACGAAGUAcc 5	: :	3
hsa-miR-8060	121	-19.09	2	21	262	287	3 caggAGGAUGGGUGAC---GAAGUACc 5	 	3
hsa-miR-22-5p	141	-14.73	2	19	365	388	3 auuuCGAACGGUGA--CUUCUUGa 5	: :	2
hsa-miR-22-5p	125	-14.01	2	19	163	186	3 auuuCGAACGGU--GACUUCUUGa 5	: ::	2
hsa-miR-23a-3p	152	-12.17	2	17	161	181	3 ccuuuAGGGACCGUUACACUa 5	:	2
hsa-miR-23a-3p	123	-14.78	3	17	59	80	3 ccuuuAGG-GACCGUUACACUa 5	: : :	2
hsa-miR-29a-3p	124	-18.44	2	21	250	270	3 auUGGC-UAAAGUCUACCACGAu 5	:	2
hsa-miR-29a-3p	120	-12.15	2	8	351	372	3 auuggcuaaagucuaCCACGAu 5		2
hsa-miR-92a-2-5p	134	-14.77	2	21	172	192	3 caUUACGUUGUUUAGGGGUGGg 5	: : : :	2
hsa-miR-92a-2-5p	120	-16.28	2	8	275	296	3 cauucguuguuuagGGGUGGg 5		2
hsa-miR-29b-3p	129	-22.05	2	22	249	270	3 uuGUGAC-UAAAGUUUACCACGAu 5	:	2
hsa-miR-29b-3p	120	-14.59	2	8	350	372	3 uugugacuaaaguuaaCCACGAu 5		2
hsa-miR-103a-2-5p	143	-15.78	3	22	377	398	3 guUCCGUCGUGACAUUUCUUCga 5	: : :	2
hsa-miR-103a-2-5p	132	-16.18	2	22	297	320	3 guUCCGUCGUGAC-AUUUCUUCGa 5	: :	2
hsa-miR-103a-3p	158	-21.26	2	20	146	169	3 aguaUCGGGAC-AUGUUACGACGa 5	:	2
hsa-miR-103a-3p	125	-14.35	2	22	50	72	3 agUAUCGGGACAUGUUACGACGa 5	: : :	2
hsa-miR-105-3p	136	-13.6	3	13	329	350	3 aucguguacgAGUUUGUAGGca 5	:	2
hsa-miR-105-3p	120	-13.45	2	8	197	218	3 aucguguacgaguuuGUAGGCa 5		2
hsa-miR-107	158	-21.26	2	20	146	169	3 acuaUCGGGAC-AUGUUACGACGa 5	:	2
hsa-miR-107	125	-14.35	2	22	50	72	3 acUAUCGGGACAUGUUACGACGa 5	: : :	2
hsa-miR-34a-5p	128	-20.9	2	21	52	73	3 ugUUGGUCGAUUCUGUGACGGu 5	: :	2
hsa-miR-34a-5p	127	-17.7	3	20	237	258	3 uguUGGUCGAUUCUGUGACGGu 5	: : :	2
hsa-miR-214-3p	142	-21.21	2	19	52	71	3 ugacGGACAGACACGGACGACa 5	: :	2
hsa-miR-214-3p	122	-16.21	2	20	148	168	3 ugaCGG-ACAGACACGGACGACa 5	:	2
hsa-miR-200b-3p	128	-14.92	2	21	291	312	3 agUAGUAAUGGUCCGUCAUAAu 5	:	2
hsa-miR-200b-3p	126	-13.74	3	19	190	213	3 aguaGUAAUGGUCC----GUCAUAau 5	 	2
hsa-miR-15b-5p	163	-25.93	2	21	146	170	3 acAUUUGGUACUA---CACGACGAu 5	: 	2
hsa-miR-15b-5p	135	-14.59	2	21	47	70	3 acAUUUG--GUACUACACGACGAu 5	: 	2

hsa-miR-23b-3p	155	-12.17	2	20	161	181	3 ccAUUAGGGACCGUUACACUa 5	: :	2
hsa-miR-23b-3p	126	-14.78	3	20	59	80	3 ccAUUAGG-GACCGUUACACua 5	: : : :	2
hsa-miR-141-3p	136	-14.71	2	21	291	312	3 ggUAGAAAUGGUCUGUCACAAu 5		2
hsa-miR-141-3p	128	-14.5	3	19	59	79	3 gguaGAAAUGGUCUGUCACAau 5	: : :	2
hsa-miR-145-3p	121	-14.32	2	19	184	206	3 ucuuGUCA-UAAAGGUCCUUAGg 5	:	2
hsa-miR-145-3p	120	-13.09	2	18	259	281	3 ucuugUCAU-AAAGGUCCUUAGg 5	: :	2
hsa-miR-195-5p	163	-20.7	2	20	150	170	3 cgGUUAUAAAAGACACGACGAu 5	: : :	2
hsa-miR-195-5p	137	-14.83	2	19	48	70	3 cggUUAU-AAAGACACGACGAu 5		2
hsa-miR-200c-3p	129	-12.26	3	22	192	213	3 agGU-AGUAAUGGGCCGUCAUAau 5	: :	2
hsa-miR-200c-3p	125	-15.31	2	22	290	312	3 agGUAGUAAUGGGCCGUCAUAAu 5	:	2
hsa-miR-106b-3p	130	-14.4	2	15	58	79	3 cgucguucAUGGGUGUCACGCc 5	: : :	2
hsa-miR-106b-3p	125	-23.22	2	19	360	382	3 cgucGUUCAUG-GGUGUCACGCc 5	: : :	2
hsa-miR-34c-5p	123	-13.6	2	22	52	73	3 cgUUAGUCGAUUGAUGUGACGGa 5	: :	2
								::	
hsa-miR-34c-5p	120	-16.27	2	22	240	263	3 cgUUAGUCGAU-UGAUGUGACGGa 5	: :	2
hsa-miR-135b-5p	140	-12.48	2	9	134	156	3 aguguaucuuacuuUUCGGUAu 5		2
hsa-miR-135b-5p	120	-14.32	2	8	254	276	3 aguguaucuuacuuUUCGGUAu 5		2
hsa-miR-452-3p	129	-12.56	3	19	247	269	3 gugaAUGAAG-AAACGUCUACuc 5	:	2
hsa-miR-452-3p	122	-12.56	3	21	351	371	3 guGAAUGAAGAAACGUCUACuc 5	: :	2
hsa-miR-410-5p	137	-18.63	2	15	271	292	3 gcuugagUAG-UGUCUGUUGGa 5	:	2
hsa-miR-410-5p	123	-17.06	2	18	327	349	3 gcuuGAGU-AGU-GUCUGUUGGa 5	: :	2
hsa-miR-483-5p	124	-12.77	2	9	1	16	3 gagggaagaaggaGGGCAGaA 5	:	2
hsa-miR-483-5p	120	-19.28	2	21	317	338	3 gaGGGAAGAAAGGAGGGCAGaA 5	:	2
								: : : :	
hsa-miR-500a-3p	139	-17.71	3	20	249	270	3 gucUUAGGAACGGGUCCACGua 5	:	2
hsa-miR-500a-3p	136	-17.96	3	18	350	372	3 gucuuAG-GAACGGGUCCACGua 5	: : :	2
hsa-miR-502-3p	129	-16.86	2	19	351	373	3 acuuAG-GAACGGGUCCACGuaA 5	: : :	2
hsa-miR-502-3p	124	-17.54	4	21	250	271	3 acUUAGGAACGGGUCCACGuaa 5	:	2
hsa-miR-503-5p	138	-16.44	2	15	148	170	3 gacgucuugACAAGGGCGACGAu 5	:	2
hsa-miR-503-5p	126	-18.93	3	17	52	73	3 gacgucuUGACAAGGGCGACGau 5	: : :	2
hsa-miR-573	153	-16.87	2	22	335	358	3 gacUAGUCA AUGUGUAGUGAAGUc 5	:	2
								:	
hsa-miR-573	125	-14.11	3	22	240	263	3 gacUAGUCA AUGUGUAGUGAAGuc 5	:	2
hsa-miR-573	125	-14.11	3	22	240	263	3 gacUAGUCA AUGUGUAGUGAAGuc 5	:	2
								:	
hsa-miR-550a-5p	135	-19.3	3	22	269	290	3 ccCGAGAAUGAGGGAGUCCGUga 5	: :	2
hsa-miR-550a-5p	131	-16.59	2	22	350	371	3 ccCGAGAAUGAGGGAGUCCGUga 5	:	2
								: : : :	
hsa-miR-605-3p	132	-12.21	2	17	152	173	3 agauuuAGAGUAUCACGGAAGa 5	: : : : : :	2
hsa-miR-605-3p	121	-12.83	2	16	355	375	3 agauuuAGAGUAUCACGGAAGa 5	: : : : :	2
hsa-miR-619-3p	154	-17.19	2	21	245	267	3 ugacCCGUGUUUGUACAGGUCCAg 5	: :	2
hsa-miR-619-3p	129	-13.21	2	14	346	369	3 ugacccguguuUGUACAGGUCCAg 5	: :	2
hsa-miR-642a-5p	126	-13.95	2	21	363	383	3 guUCUGUGUAAACCUCUCCCUg 5	:	2
hsa-miR-642a-5p	120	-13.3	4	21	105	126	3 guUCUGUGUAAACCUCUCCcug 5		2
hsa-miR-661	127	-17.82	3	20	207	230	3 ugcgGUCUCCGGUCUCUGGGUCCgu 5		2
hsa-miR-661	125	-26.7	2	23	263	288	3 ugCGCGUCCGGUCUCU--GGGUCCGu 5	: :	2
								::	
hsa-miR-654-5p	137	-18.13	3	19	108	130	3 cgugUACAAGA-CGCCGGGUGgu 5		2

hsa-miR-654-5p	125	-17.92	2	19	274	296	3 cgugUACAAG-ACGCCGGGUGGu 5		2
hsa-miR-550a-3-5p	134	-17.12	3	19	271	290	3 gaGAAUGAGGGAGUCCGUga 5	: :	2
hsa-miR-550a-3-5p	129	-16.59	2	19	351	371	3 gaGAA-UGAGGGAGUCCGUGa 5	: : : :	2
hsa-miR-449c-5p	125	-16.51	2	23	234	259	3 uguCGGCGAUCGU-UAUGUGACGGAu 5	: :	2
hsa-miR-449c-5p	121	-19.23	2	23	141	171	3 uguCGGCGAUCGUUA-----UGUGACGGAu 5	:	2
hsa-miR-670-3p	134	-13.36	2	20	385	407	3 agGACUUACU--UAUACUCCUUu 5	:	2
hsa-miR-670-3p	131	-13.15	3	20	409	429	3 agGACUUACUUUAUACUCCUuu 5	: :	2
hsa-miR-450b-5p	134	-12.81	2	21	417	437	3 auAAGUCCUUGUAUAACGUUUu 5	: : :	2
hsa-miR-450b-5p	127	-15.62	2	20	397	418	3 auaAGUCCUUGUAUAACGUUUu 5	: :	2
hsa-miR-891b	138	-13.27	2	19	40	61	3 aguuACUGAGUCCAUAUCAACGu 5	:	2
hsa-miR-891b	134	-17.19	3	21	391	415	3 agUUACUG-AGUCC--AUUCAACgu 5	: :	2
hsa-miR-541-5p	130	-19.14	2	21	212	235	3 ucaccCUGGCUGUCGUCUUAGGAAa 5		2
hsa-miR-541-5p	122	-12.09	2	15	326	351	3 ucaccuggcuGUCGUCU-UAGGAAa 5	: :	2
hsa-miR-541-3p	120	-17.1	3	9	109	130	3 ucaggucuaagacaCGGGUGgu 5	:	2
hsa-miR-541-3p	120	-18.27	2	8	275	296	3 ucaggucuaagacacGGGUGGu 5		2
hsa-miR-889-5p	129	-14.11	2	20	253	276	3 cugGU-AUGAUGC-CUGUCGGUAa 5		2
hsa-miR-889-5p	120	-14.81	2	8	135	156	3 cugguaugaugccugUCGGUAa 5	:	2
hsa-miR-873-5p	131	-12.51	2	16	315	335	3 uccucuGAGUGUUCAAGGACg 5		2
hsa-miR-873-5p	126	-23.05	2	20	118	143	3 ucCUCUGAGUGUU----CAAG-GACg 5	:	2
hsa-miR-543	136	-14.83	2	21	411	432	3 uuCUUCACGUGGCGCUUACAAa 5	: :	2
hsa-miR-543	130	-13	2	20	260	283	3 uucUUCACG--UGGCGCUUACAAa 5	: :	2
hsa-miR-936	130	-12.98	2	17	51	71	3 gacgcuAAGGAGGGAGAUGACa 5	: : :	2
hsa-miR-936	125	-17.46	2	14	308	329	3 gacgcuaagGAGGGAGAUGACa 5		2
hsa-miR-939-3p	126	-21.23	4	15	110	130	3 gaccccuCGUCUCCGGGUccc 5		2
hsa-miR-939-3p	120	-14.42	2	8	209	229	3 gaccccuçgucuccGGGUCCc 5	:	2
hsa-miR-1229-5p	158	-20.06	2	22	206	227	3 gcgAGAGGGGGUUUGGGAUGGGUg 5		2
hsa-miR-1229-5p	129	-22.13	2	23	251	275	3 gcGA-GAGGGGGUUUGGGAUGGGUg 5	:: ::	2
hsa-miR-1287-5p	128	-16.82	3	21	347	368	3 cuGAGCUUGGUGACUAGGUCgu 5		2
hsa-miR-1287-5p	121	-18.92	3	15	179	202	3 cugagcuuGGUGAC--UAGGUCgu 5	: : :	2
hsa-miR-1293	145	-24.49	2	20	203	226	3 cgUGUUUAGAGGUCUGGUGGGu 5	:	2
hsa-miR-1293	140	-29.32	2	21	272	293	3 aggGAGUGU--GUCUUAAGGUCuu 5	: :	2
hsa-miR-1299	150	-24.99	3	20	187	210	3 agggagUGUGUC-UUAAGGUCUu 5	:	2
hsa-miR-1243	121	-12.52	3	21	347	368	3 guGAG-GAUAUUAACUAGGUCaa 5	: :	2
hsa-miR-1243	120	-13.61	2	8	189	210	3 gugaggauauuaacuAGGUCAa 5	: :	2
hsa-miR-1270	141	-19.11	2	22	242	264	3 ugUGUCGAGAAGGUUAUAGAGGUc 5	:	2
hsa-miR-1270	137	-20.97	2	21	259	285	3 uguGUCGA-GA-AGGUA--UAGAGGUc 5		2

hsa-miR-664a-5p	128	-16.55	3	18	249	276	3 uagguuaGUA AAAAG---GGAUCGGUca 5		2
hsa-miR-664a-5p	127	-17.09	2	23	203	228	3 uaGGUUAGU AAAAGG---GAUCGGUCa 5	:	2
hsa-miR-2278	136	-18.33	2	13	151	172	3 gguccguuguGUGUGACGAGAg 5	: :	2
hsa-miR-2278	132	-14.02	2	21	312	333	3 ggUCCGUUGUGUGUGACGAGAg 5	:	2
hsa-miR-2682-3p	133	-17.57	2	21	106	125	3 ccUUCUGUCGCGACUUCUCCGc 5	:	2
hsa-miR-2682-3p	122	-12.26	2	17	167	187	3 ccuucuGUCGCGACUUCUCCGc 5	:	2
hsa-miR-3132	121	-18.69	2	18	123	146	3 aggagacUCGAGGAAGAGAUGGGu 5	:	2
hsa-miR-3132	120	-18.69	2	8	203	226	3 aggagacucgaggaagaGAUGGGu 5		2
hsa-miR-3074-5p	135	-17.64	2	20	364	384	3 gaCCGAGUCAAGUCGUCCUu 5	: :	2
hsa-miR-3074-5p	120	-13	2	8	387	407	3 gaccgagucaagucGUCCUu 5		2
hsa-miR-323b-5p	136	-16.25	2	22	273	292	3 acGCUUGAGUGGUGCCUGUUGGa 5	: :	2
hsa-miR-323b-5p	120	-16.64	2	8	78	100	3 acgcuagagugguccUGUUGGa 5		2
hsa-miR-3065-3p	139	-17.33	3	16	249	271	3 gagguuguUAUAGGACCACGAcu 5		2
hsa-miR-3065-3p	138	-19.09	3	15	351	373	3 gagguuguuAUAGGACCACGAcu 5	:	2
hsa-miR-4320	131	-13.72	2	16	171	188	3 uccUUCGAUGUCUUAGGg 5	: :	2
hsa-miR-4320	121	-12.04	2	17	215	233	3 ucCUUCGAU--GUCUUAGGg 5	:	2
hsa-miR-4254	131	-18.66	2	22	262	287	3 cuCUACCACC--U-CAUCGAGGUCCg 5	: :	2
hsa-miR-4254	128	-17.79	2	13	244	266	3 cucuaccaccuCAUCGAGGUCCg 5	:	2
hsa-miR-4327	131	-17.69	2	16	135	153	3 ggucAGGGGGUACGUUCGg 5	: :	2
hsa-miR-4327	121	-19.68	2	18	255	273	3 ggUCAGGGGGUACGUUCGg 5	: :	2
hsa-miR-3612	128	-17.89	2	21	354	375	3 agGUA AAGAGUUCUACGGAGGa 5	:	2
hsa-miR-3612	123	-16.52	2	21	151	173	3 agGUA-AAGAGUUCUACGGAGGa 5	: :	2
hsa-miR-3614-5p	140	-16.45	2	17	246	268	3 cccgucgGAAGUCUAGGUUCACc 5	:	2
hsa-miR-3614-5p	127	-16.69	2	17	346	370	3 cccgucgGAAGU--CUAGGUUCACc 5	: :	2
hsa-miR-3619-5p	137	-16.9	2	18	50	71	3 cgacgUGGUCGGACGGACGACu 5	: : :	2
hsa-miR-3619-5p	126	-20	2	21	144	168	3 cgACGU--GGU-CGGACGGACGACu 5	: :	2
hsa-miR-3653-5p	145	-24.31	3	19	387	407	3 cuUCUUCUU-AGUAGUCCUcc 5	: :	2
hsa-miR-3653-5p	124	-12.47	4	17	270	289	3 cuucUUCUUAGUAGUCCucc 5		2
hsa-miR-3660	131	-18.46	2	16	55	75	3 aguuuuACGAGAGGACAGUCa 5	:	2
hsa-miR-3660	125	-18.25	2	20	127	152	3 agUUUUA-CGAGAG---GACAGUCa 5	: :	2
hsa-miR-3662	145	-15.2	3	23	337	362	3 guAGUCAGU--GAUGAGUAGUAAAag 5		2
hsa-miR-3662	129	-12.57	2	18	288	311	3 guagucaGUGAUGAGUAGUAAAag 5	: :	2
hsa-miR-3663-3p	124	-14.68	2	9	351	373	3 cgcgggccggacacaCCACGAGu 5	:	2
hsa-miR-3663-3p	121	-12.31	3	19	248	271	3 cgcggGCCGGACA-CACCACGAGu 5		2
hsa-miR-3689a-5p	135	-12.23	3	18	384	404	3 aggggCCUUGGUACUAUAGUGu 5		2
hsa-miR-3689a-5p	124	-18.97	2	21	195	215	3 agGGUCCU-UGGUACUAUAGUGu 5	:	2
hsa-miR-3689b-5p	135	-12.23	3	18	384	404	3 aggggCCUUGGUACUAUAGUGu 5		2
hsa-miR-3689b-5p	124	-18.97	2	21	195	215	3 agGGUCCU-UGGUACUAUAGUGu 5	:	2
hsa-miR-676-5p	127	-18.32	2	17	7	28	3 acguuCAGGA-CUCCAACUUCu 5	:	2
hsa-miR-676-5p	120	-13.52	2	20	298	316	3 acGUUCAGGACUCCAACUUCu 5	: :	2

hsa-miR-3940-5p	141	-17.45	2	19	274	294	3 guCUCGGGCG-GGGUUGGGUg 5	:	2
hsa-miR-3940-5p	121	-13.1	3	18	83	102	3 gucUCGGGCGGGGUUGGGug 5	: : :	2
hsa-miR-4417	134	-18.33	2	11	112	129	3 gggaggccCUUCGGGUGg 5	:	2
hsa-miR-4417	128	-21.6	2	17	278	295	3 ggGAGGCCCUUCGGGUGg 5	:	2
hsa-miR-4422	137	-12.02	2	14	354	374	3 acccaugaAGGACUACGAAAa 5	: :	2
hsa-miR-4422	132	-13.1	2	19	153	172	3 accCAUGAAGGACUACGAAAa 5	:	2
hsa-miR-4436a	133	-16.64	2	14	48	68	3 uaggugaaGACGGACAGGACg 5	:	2
hsa-miR-4436a	124	-15.66	3	13	1	18	3 uaggugaagACGGACAGGAcg 5	:	2
hsa-miR-4456	135	-12.58	3	16	282	298	3 uuUCCUUCGGUGGUcc 5	:	2
hsa-miR-4456	120	-14.71	2	8	459	475	3 uuuuccuucgGUGGUCc 5		2
hsa-miR-3689e	135	-12.23	3	18	384	404	3 agggguCCUUGGUACUAUAGUgu 5		2
								:	
hsa-miR-3689e	124	-18.97	2	21	195	215	3 agGGUCCU-UGGUACUAUAGUGu 5	: :	2
hsa-miR-3689f	143	-16.73	3	18	384	404	3 agggguCCUUCGUGCUAUAGUgu 5		2
								:	
hsa-miR-3689f	126	-16.19	2	21	195	215	3 agGGUCCUUCGUGCUAUAGUGu 5	: :	2
hsa-miR-4524a-3p	138	-16.41	2	15	1	17	3 uaucgucgUAUUCGGACAGAGu 5	:	2
hsa-miR-3978	146	-17.87	2	21	153	175	3 ugugGGACCUACGUACGAAAGGUg 5	:: :	2
							3 uguGGGACCUACGU--ACGAAAGGUg 5	:	
hsa-miR-3978	140	-13.62	2	22	352	377	5	:	2
								::	
hsa-miR-4632-5p	135	-26.76	2	21	148	172	3 aggCGGUGU--GGGUGCGACGGGAg 5	:: : :	2
hsa-miR-4632-5p	124	-20.1	2	18	310	333	3 aggcgguGUGGGUG-CGACGGGAg 5	: :	2
hsa-miR-4646-5p	130	-14.48	2	17	242	265	3 agggagUCGAGGA-G-AAGGGUCa 5	:	2
hsa-miR-4646-5p	120	-17.98	2	20	359	378	3 aggGAGUCGAGGAGAAGGGUCa 5	: :	2
								: : :	
hsa-miR-4647	132	-20.51	2	22	135	159	3 aaGGAGUCGUGUCGU--GGUAGAAg 5		2
								: : :	
hsa-miR-4647	124	-14.2	2	22	303	326	3 aaGGAGUCGUGUC-GUGGUAGAAg 5		2
hsa-miR-4654	126	-16.13	2	19	171	191	3 ggucUACGGAGGUC-UAGGGUGu 5	:	2
								: :	
hsa-miR-4654	124	-24.54	2	19	270	295	3 ggucUAC--GGAGGUC--UAGGGUGu 5		2
								::	
hsa-miR-4688	127	-25.21	2	21	151	173	3 ggGUCCAGGAG-ACGACGGGGAu 5	::	2
hsa-miR-4688	123	-20.69	2	20	313	334	3 gggUCCAGGAGACGACGGGGAu 5	::	2
								: : :	
hsa-miR-4692	122	-13.39	2	21	55	75	3 uaGACUAUGGGUGUGACGGACu 5		2
hsa-miR-4692	121	-13.58	3	18	151	172	3 uagacUAUGGGUGUGACGGACu 5	: :: : :	2
								: :	
hsa-miR-4693-5p	125	-16.01	2	22	189	211	3 acACUGUCACUUUAAGUGUCAUa 5		2
								: :	
hsa-miR-4693-5p	123	-12.85	2	22	14	38	3 acACUGUC-ACUUU-AAGUGUCAUa 5		2
hsa-miR-4711-5p	133	-18.62	2	22	7	29	3 gaGUACAGAAGACCGGACUACGu 5		2
								:	
hsa-miR-4711-5p	131	-14.35	2	21	49	72	3 gagUACAGAA-GACCGGACUACGu 5		2
hsa-miR-451b	132	-12.65	2	14	218	240	3 uuaccauuaCCAAG-AGAACGAu 5	:	2
hsa-miR-451b	125	-12.53	2	16	147	167	3 uuaccauUACCAAGAGAACGAu 5	:	2
hsa-miR-4727-3p	138	-19.93	2	21	173	193	3 cuUAGACGGUCGAAGGGUGAUa 5	:	2
hsa-miR-4727-3p	132	-19.58	2	21	276	297	3 cuUAGACGGUCGAAGGGUGAUa 5	:	2
hsa-miR-4757-5p	155	-19.51	2	16	104	126	3 uguggcacUGCAGUGUCUCCGGa 5	::	2
hsa-miR-4757-5p	125	-14.63	2	19	298	321	3 uguggCACU-GCAGUGUCUCCGGa 5	:	2

hsa-miR-4766-5p	139	-16.79	2	18	359	378	3 uuguGGUUGACGAGAAAGUCu 5	: : :	2
hsa-miR-4766-5p	123	-14.88	2	18	182	201	3 uuguGGUUGACGAGAAAGUCu 5		2
hsa-miR-4766-3p	142	-14.49	2	20	292	313	3 aaGGU-UUUCUCGUUAACGAUa 5	: :	2
hsa-miR-4766-3p	120	-12.32	2	8	221	241	3 aagguuuucucguuAACGAUa 5		2
hsa-miR-4769-5p	124	-14.97	2	9	168	191	3 gaguauggaagagaggUAGGGUGg 5	:	2
hsa-miR-4769-5p	123	-22.79	2	23	271	295	3 gaGUA--UGGAAGAGAGGUAGGGUGg 5	:	2
hsa-miR-4436b-5p	135	-16.32	2	16	394	415	3 ccgucceGUCCGUCUUCACCUg 5		2
hsa-miR-4436b-5p	132	-15.33	2	17	371	392	3 ccguccCGUCCGUCUUCACCUg 5	:	2
hsa-miR-2467-3p	128	-14.22	2	13	123	144	3 ggacucggagAGACGGAGACGa 5	:	2
hsa-miR-2467-3p	120	-17.21	2	19	310	330	3 ggacUCGGAGAGACGGAGACGa 5	: :	2
hsa-miR-4793-5p	123	-17.56	3	21	181	205	3 ggagACGG-GACACCUCGUCCUAca 5		2
hsa-miR-4793-5p	120	-12.75	3	9	209	232	3 ggagacgggacaccucGUCCUAca 5		2
hsa-miR-4794	129	-12.7	3	19	254	276	3 ugucAGAGCACU-CUAUCGGUcu 5	: :	2
hsa-miR-4794	123	-12.68	2	21	205	228	3 ugUCAGAGCA--CUCUAUCGGUCu 5		2
hsa-miR-4799-3p	129	-13.38	2	18	188	209	3 auauUUUACGUCGUACGGUCa 5		2
hsa-miR-4799-3p	120	-14.17	2	8	54	75	3 auauuuuacgucguACGGUCa 5		2
hsa-miR-5003-3p	133	-12.72	2	16	167	186	3 gggguuGUUGGAUCUUUUCa 5	: :	2
hsa-miR-5009-5p	128	-15.59	3	23	167	189	3 uaGGGGUUUAGACUUUUUCAGGuu 5	::::	2
hsa-miR-5009-5p	122	-16.76	4	23	96	119	3 uaGGGGUUUAGACUUUUUCAGguu 5	:	2
hsa-miR-5011-3p	127	-14.29	2	21	257	279	3 acAAUAUAUAUG-UCGGUACGUg 5	: :	2
hsa-miR-5011-3p	121	-12.16	3	16	139	159	3 acaauauAUAUGUCGGUACGug 5	:	2
hsa-miR-5089-5p	133	-20.29	2	20	164	190	3 cuACGAUGAGU----CU--UUAGGGUg 5	:	2
hsa-miR-5089-5p	129	-15.82	2	20	189	208	3 cuACGAUGAGUCUUUAGGGUg 5	: :	2
hsa-miR-5093	147	-13.52	2	18	242	263	3 cgaggaUCGGUCGGAGUAAAGGa 5	: :	2
hsa-miR-5093	120	-16.12	4	22	344	363	3 cgAGGAUCGGUCGGAGUAAAgga 5	: :	2
hsa-miR-5197-3p	146	-12.07	2	22	308	328	3 uaAGCUACUGAGUCAGAGAAGa 5	:	2
hsa-miR-5197-3p	123	-13.41	3	22	353	377	3 uaAGCUACUGAGU-CA-GAGAAgaa 5	:	2
hsa-miR-4524b-5p	142	-15.62	3	20	149	171	3 cuCUGUCCGAA--UACGACGAua 5	:	2
hsa-miR-4524b-5p	121	-13.38	2	19	52	74	3 cucUGUCCG--AAUACGACGAUa 5		2
hsa-miR-4524b-3p	142	-12.9	2	14	1	16	3 aucgucgUACUUGGACAGAg 5		2
hsa-miR-5682	152	-18.99	2	18	245	271	3 uggaaUAGGACGU-----UCCACGAUg 5		2
hsa-miR-5682	135	-15.69	3	21	351	373	3 ugGAA-UAGGACGUUCCACGAug 5	:: :	2
hsa-miR-5693	131	-17.2	2	18	290	310	3 cucaaGUAAGUCUCGGUGACg 5	: :	2
hsa-miR-5693	120	-15.79	2	8	172	193	3 cucaaguaagucucGGUGACg 5		2
hsa-miR-5706	134	-16.94	2	21	428	448	3 ucGAAGUCGUACAAUAGGUCUu 5	:	2
hsa-miR-5706	129	-16.59	2	21	346	368	3 ucGAAGU--CGUACAAUAGGUCUu 5	:	2

hsa-miR-6078	134	-13.64	2	17	353	370	3 gguGUCGAUCGAGUCCGCc 5	: :	2
hsa-miR-6078	121	-16.11	3	10	271	289	3 ggugucgaucGAGUCCGcc 5	:	2
hsa-miR-6128	154	-17.7	2	17	188	209	3 aaaACUG-AGGU--UAAGGUCa 5	:	2
hsa-miR-6128	130	-13.85	2	15	247	265	3 aaaacUGAGGUUAAGGUCa 5		2
hsa-miR-6165	133	-16.87	2	15	51	70	3 gagggGAGUGG-AGGACGAc 5	:: :	2
hsa-miR-6165	125	-16	2	18	319	337	3 gaGGGGAGUGGAGGACGAc 5	: : :	2
hsa-miR-6505-3p	136	-12.5	2	13	393	413	3 gaaaccuucUCCAUCUUCAGu 5	:	2
hsa-miR-6505-3p	122	-16.67	4	20	376	399	3 gaAACCUUCU---CCAUCUUCagu 5		2
hsa-miR-6507-5p	146	-17.95	2	15	314	334	3 uguuucagGGAGGAUAAGAAg 5	: : :	2
hsa-miR-6507-5p	123	-12.23	3	20	48	68	3 ugUUUCAGGGAGGAUAAGAag 5	: :	2
								: :	
hsa-miR-6513-5p	123	-17.51	2	22	80	104	3 ucUGUA-CACCGCA-GUUAGGGUuu 5		2
hsa-miR-6513-5p	120	-13.57	3	20	171	191	3 ucugUACACCGCAGUUAGGGUuu 5	:	2
hsa-miR-6720-3p	136	-14.09	2	19	351	371	3 agauGGUCAAGGACGUCCGCGc 5	: : :	2
								: ::	
hsa-miR-6720-3p	134	-16.75	2	21	249	269	3 agAUGGUCAAGGACGUCCGCGc 5	:	2
							3 acAAGAC--GGAGAAA-GG--	: :	
hsa-miR-6747-5p	127	-20.47	2	23	322	350	UGUGGGGa 5	: :	2
hsa-miR-6747-5p	120	-15.74	2	13	78	101	3 acaagacggagaAAGGUGUGGGGa 5	::	2
								:	
hsa-miR-6748-5p	122	-22.59	3	21	202	228	3 uuAGGUCA-GGAAG----GGUGGGUgu 5	:	2
hsa-miR-6748-5p	120	-17.55	2	8	274	295	3 uuaggucaggaaggUGGGUGu 5		2
hsa-miR-6759-5p	141	-18.02	3	18	275	296	3 ugucuGAAGACGGGUGGGUGuu 5		2
hsa-miR-6759-5p	128	-17.88	2	21	109	130	3 ugUCUGAAGACGGGUGGGUGUu 5	:	2
hsa-miR-6765-3p	140	-17.41	2	9	248	268	3 gaccgccccggucGUCCACu 5		2
hsa-miR-6765-3p	128	-15.74	2	13	350	370	3 gaccgccccGGUCGGUCCACu 5	:: :	2
							3 gaGUUAUUCUAGA----CG-	:	
hsa-miR-6766-5p	126	-21.14	3	23	270	297	AGGGUGGgc 5		2
								:	
hsa-miR-6766-5p	124	-18.66	3	23	171	193	3 gaGUUAUUCUAGACGAGGGUGGgc 5	:	2
hsa-miR-6776-5p	135	-27.64	2	17	182	201	3 uugGGGGUGAC-GUGGGUCu 5	: ::	2
hsa-miR-6776-5p	129	-20.62	2	18	210	228	3 uuGGGGGUGACGUGGGUCu 5	: : :	2
hsa-miR-6783-3p	140	-14.55	2	9	209	230	3 gaugucuccucucGGGUCCUu 5		2
hsa-miR-6783-3p	120	-12.77	2	8	456	477	3 gaugucuccucucgGUCCUu 5		2
hsa-miR-6786-5p	136	-24	3	18	275	297	3 ugcgGGGAGGCCG--GGGUGGcg 5	: :	2
hsa-miR-6786-5p	130	-18.45	2	11	173	193	3 ugcggggaggcCGGGUGGCg 5	: :	2
hsa-miR-6796-5p	126	-22.05	2	19	108	130	3 gucggUCGAGAGGUUGGGGUGUu 5	: :	2
hsa-miR-6796-5p	124	-16.98	4	17	83	105	3 gucggucGAGAGGUUGGGGUGuu 5	: :	2
								: :	
hsa-miR-6804-5p	140	-25.21	2	20	302	324	3 gcAGUGGACGA---CUGUGGGAGu 5	:	2
								:::	
hsa-miR-6804-5p	122	-17.49	2	20	330	351	3 gcAGUGGA-CGACUGUGGGAGu 5	: :	2
								: :	
hsa-miR-6805-5p	144	-22.88	2	21	304	325	3 ugUGAGGUGUUCGGCGGGGGAu 5	:	2
hsa-miR-6805-5p	124	-27.58	2	18	120	142	3 ugugaGGUGUUC-GGCGGGGGAu 5	: : :	2
hsa-miR-6808-5p	126	-12.73	2	11	1	16	3 guaccaggguggAGGGACGGAc 5	:	2
hsa-miR-6830-3p	141	-14.18	2	19	397	420	3 gacguUCCUCUC-UCUUCUUCUGu 5	:	2
								: :	
hsa-miR-6830-3p	127	-16.74	3	21	372	396	3 gacGUUCCUCUCUU--CUUUCUgu 5	:	2
hsa-miR-6838-5p	151	-16.75	2	18	150	170	3 uccucAGAACGGUGACGACGAa 5	:	2
hsa-miR-6838-5p	139	-20.43	3	17	50	73	3 uccucaGAACGGU--GACGACGaa 5	::	2

hsa-miR-6847-5p	140	-19.84	2	21	121	143	3 cgaGUGUGAGGUGACAGGAGACa 5	:	2
hsa-miR-6847-5p	129	-16.06	2	14	307	329	3 cgagugugagGUGACAGGAGACa 5	:	2
hsa-miR-6853-5p	126	-21.55	2	20	330	354	3 gacugAAGUA-CCUGUAGGGUGCGa 5	: : :	2
hsa-miR-6853-5p	125	-18.67	4	21	276	297	3 gacuGAAGUACCUGUAGGGUGcga 5	:	2
hsa-miR-6855-5p	152	-19.88	2	24	79	103	3 cgUUACAGACGUGGGGU-UUGGGGUu	: : ::	2
							5		
hsa-miR-6855-5p	125	-16.51	2	24	445	474	3 cgUUACAG---ACGUGGGG--	: :::	2
							UUUGGGGUu 5		
hsa-miR-6856-3p	143	-18.57	2	20	410	431	3 gacCUUUCUAGUGUCCCGACAu 5	: ::	2
hsa-miR-6856-3p	123	-15.3	2	20	128	149	3 gacCUUUCUAGUGUCCCGACAu 5		2
hsa-miR-6861-5p	155	-20.81	2	16	207	228	3 ggaccucGGGUGGAUGGGUCA 5	:	2
hsa-miR-6861-5p	132	-23.8	2	17	346	367	3 ggaccuCGGGUGGAUGGGUCA 5	:: : ::	2
hsa-miR-6864-5p	131	-13.86	2	21	333	358	3 ccguAUAGACUGAA--CAGGGAAGUu 5		2
							3 ccGUAUAGACUGAAC-A-GGGAAGUu	:: :	
hsa-miR-6864-5p	122	-14.59	2	23	151	175	5	:::	2
hsa-miR-6871-3p	120	-16.19	2	8	249	270	3 gacaccucggugucCCACGA 5		2
hsa-miR-6871-3p	120	-16.28	2	8	351	372	3 gacaccucggugucCCACGA 5		2
hsa-miR-6875-3p	150	-16.72	2	11	389	410	3 uaccucgguccGUCCUUCUu 5		2
hsa-miR-6875-3p	147	-17.47	2	12	366	387	3 uaccucgguccGUCCUUCUu 5	: :	2
hsa-miR-6879-5p	126	-20.53	2	15	126	147	3 gagagggUGGAAGGACGGGA 5	:	2
hsa-miR-6879-5p	123	-18.7	2	17	311	333	3 gagaggUGGAAG-GGACGGGA 5	: : : ::	2
hsa-miR-6894-5p	136	-19.89	2	23	325	352	3 agACCGGGUCGAG-AG---GUAGGAGGa	: : : :	2
							5	:	
hsa-miR-6894-5p	120	-18.19	3	22	261	285	3 agaCCG-GGUCGAGAGGUAGGAGga 5	: :	2
hsa-miR-7515	124	-14.16	2	14	339	357	3 cagugGUA-GAAGGGAAGa 5		2
hsa-miR-7515	120	-19.52	2	17	315	332	3 caGUGGUAGAAGGGAAGa 5	: : :	2
hsa-miR-7706	123	-17.94	2	12	351	374	3 agagccgucucguGUCCGCGAAGu 5	: :	2
hsa-miR-7706	120	-17.62	2	8	334	357	3 agagccgucucguguccGCGAAGu 5		2
hsa-miR-8073	149	-28.44	3	19	54	76	3 ugcUGCGAGGGACGACGGUCca 5	: ::	2
hsa-miR-8073	123	-15.4	3	20	252	273	3 ugcUGCGAGGGACGACGGUCca 5	: : : :	2
hsa-miR-4524a-3p	136	-13.91	3	18	9	30	3 uaucgUCGUAAU--CGGACAGAg 5		2
hsa-miR-5003-3p	121	-12.59	3	18	1	17	3 ggggUUGUUGGAUCUUUUCau 5	:	2
hsa-miR-4524b-3p	143	-12.88	2	17	10	30	3 aucgUCGUACUU--GGACAGAg 5		2
hsa-miR-6808-5p	126	-12.5	2	11	10	30	3 guaccagguggAGGGACGGAc 5	:	2