

Plasma MicroRNAs for GC

hsa-miR-223:

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P _{CT}
Position 439-446 of SP3 3' UTR	5' ... AUUUUUUUUUUUGCAUAAACUGACA... 3' ACCCCAAAACUGU-UUGACUGU	8mer	-0.247	-0.029	-0.073	-0.003	-0.016	0.017	-0.35	97	4.124	0.47

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P _{CT}
Position 265-272 of FBXO8 3' UTR	5' ... UGUUAAACGAAGAUAAACUGACA... 3' ACCCCAAAACUGU-UUGACUGU	8mer	-0.247	0.003	-0.080	-0.047	-0.016	0.017	-0.37	97	1.742	0.47

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P _{CT}
Position 95-101 of SCN3A 3' UTR	5' ... AGGAGGUCCAGGCCAAACUGACU... 3' ACCCCAAAACUGU-UUGACUGU	7mer-8	-0.120	0.003	-0.021	-0.048	-0.011	0.014	-0.18	79	1.936	0.48

hsa-miR-19b-2*

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P _{CT}
Position 167-173 of NME1 3' UTR	5' ... UGUUAGAACAGUGAUUUUGACU... 3' AGUCAAAAACGUACCU-AAACGUGU	7mer-8	-0.120	-0.035	-0.056	-0.050	0.004	0.019	-0.24	88	1.655	0.50

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P _{CT}
Position 1207-1214 of SCN4B 3' UTR	5' ... UUCUCCAGAGCGUUGUUGACACA... 3' AGUCAAAAACGUACCU-AAACGUGU	8mer	-0.247	0.003	0.119	0.191	0.008	0.025	> -0.03	1	1.669	0.70
Position 1207-1214 of SCN4B 3' UTR	5' ... UUCUCCAGAGCGUUGUUGACACA... 3' AGUCAAAAACGUACCU-AAACGUGU	8mer	-0.247	0.003	0.119	0.191	0.008	0.025	> -0.03	1	1.669	0.70

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P _{CT}
Position 141-148 of RHEBL1 3' UTR	5' ... UGUGGCAUCCUUAUG--UUUGCACA... 3' AGUCAAAAACGUACCU-AAACGUGU	8mer	-0.247	-0.018	0.078	-0.079	0.008	0.025	-0.23	87	1.691	0.71
Position 141-148 of RHEBL1 3' UTR	5' ... UGUGGCAUCCUUAUG--UUUGCACA... 3' AGUCAAAAACGUACCU-AAACGUGU	8mer	-0.247	-0.008	0.078	-0.079	0.008	0.025	-0.22	85	1.691	0.71

hsa-miR-194*

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P _{CT}
Position 273-280 of CHD4 3' UTR	5' ... UCCCCACUGUAAAGCCUGUUACA... 3' AGGUGUACCUCAAACGACAAGU	8mer	-0.247	0.003	0.094	-0.045	0.001	0.038	-0.16	81	1.583	0.49

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P _{CT}
Position 38-45 of ARHGAP21 3' UTR	5' ... CAAGUAAAACAAACUUCUUAACA... 3' AGGUGUACCUCAAACGACAAGU	8mer	-0.247	0.034	-0.027	-0.105	0.001	0.038	-0.31	97	1.065	0.21

hsa-miR-141

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P _{CT}
Position 933-939 of ARPC5 3' UTR	5' ... CCCCUGAAAAGUCUUCAGUGUUC... 3' UGUAGCAAUGGUCUGUCACAAU	7mer-8	-0.120	0.003	-0.038	-0.006	0.015	0.020	-0.13	74	1.420	0.22
Position 933-939 of ARPC5 3' UTR	5' ... CCCCUGAAAAGUCUUCAGUGUUC... 3' GGUAGAAAUGGUCUGUCACAAU	7mer-8	-0.120	0.012	-0.038	-0.006	0.015	0.020	-0.12	71	1.420	0.22
Position 1009-1015 of ARPC5 3' UTR	5' ... UUCUGUGUUUUAGCU--CAGUGUUU... 3' GGUAGAAAUGGUCUGUCACAAU	7mer-8	-0.120	-0.025	-0.067	-0.016	0.015	0.020	-0.19	87	1.503	0.24
Position 1009-1015 of ARPC5 3' UTR	5' ... UUCUGUGUUUUAGCU--CAGUGUUU... 3' UGUAGCAAUGGUCUGUCACAAU	7mer-8	-0.120	-0.016	-0.067	-0.016	0.015	0.020	-0.18	86	1.503	0.24

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P _{CT}
Position 1617-1624 of CHD9 3' UTR	5' ... CCUUUUUAGAGACAGUGUUA... 3' GGUAGAAAUGGUCUGUCACAAU	8mer	-0.247	-0.018	-0.069	0.134	0.026	0.026	-0.15	79	1.095	0.26
Position 1617-1624 of CHD9 3' UTR	5' ... CCUUUUUAGAGACAGUGUUA... 3' UGUAGCAAUGGUCUGUCACAAU	8mer	-0.247	-0.018	-0.069	0.134	0.026	0.026	-0.15	79	1.095	0.26

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	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P _{CT}
Position 391-397 of LMO3 3' UTR	5' ... UGCAUUUAGUACAADCAGUGUUU... 3' GGUAGAAAUGGUCU--GUCACAAU	7mer-m8	-0.120	-0.025	-0.112	-0.006	0.015	0.020	-0.23	92	2.073	0.50
hsa-miR-141												
Position 391-397 of LMO3 3' UTR	5' ... UGCAUUUAGUACAAD-CAGUGUUU... 3' UGUAGCAAUGGUCUCACAAU	7mer-m8	-0.120	-0.016	-0.112	-0.006	0.015	0.020	-0.22	92	2.073	0.50
hsa-miR-200a												
Position 608-614 of LMO3 3' UTR	5' ... UGAGUUAGAGUCUADCAGUGUUC... 3' UGUAGCAAUGGUCU--GUCACAAU	7mer-m8	-0.120	-0.016	-0.055	0.024	0.015	0.020	-0.13	76	1.459	0.23
hsa-miR-200a												
Position 608-614 of LMO3 3' UTR	5' ... UGAGUUAGAGUCUADCAGUGUUC... 3' GGUAGAAAUGGUCUCACAAU	7mer-m8	-0.120	-0.007	-0.055	0.024	0.015	0.020	-0.12	73	1.459	0.23
hsa-miR-141												

hsa-miR-1233

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P _{CT}
Position 139-146 of DLGAP4 3' UTR	5' ... AAAUUGACGCCAUACAGGGCUCA... 3' GAGGCCUCCUGUCCCGAGU	8mer	-0.247	0.013	-0.008	-0.079	0.000	-0.146	-0.47	99	2.540	N/A
hsa-miR-1233												

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P _{CT}
Position 111-118 of FMNL2 3' UTR	5' ... ACAAAAUAUUCUUAAGGGCUCA... 3' GAGGCCUCCUGUCCCGAGU	8mer	-0.247	0.045	-0.066	-0.086	0.000	-0.146	-0.50	99	1.386	N/A
hsa-miR-1233												

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P _{CT}
Position 1311-1317 of LRRC57 3' UTR	5' ... GUGCCUUAUUGGUAAGGGCUUC... 3' GAGGCCUCCUGUCCCGAGU	7mer-m8	-0.120	0.003	0.001	-0.027	-0.001	-0.085	-0.23	84	1.562	N/A
hsa-miR-1233												

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P _{CT}
Position 816-823 of PDRG1 3' UTR	5' ... CUUAUGUUCUAUAAGGGCUCA... 3' GAGGCCUCCUGUCCCGAGU	8mer	-0.247	0.024	-0.093	-0.107	0.000	-0.146	-0.57	99	1.308	N/A
hsa-miR-1233												

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile	conserved branch length	P _{CT}
Position 895-901 of STIM1 3' UTR	5' ... CCACAGCCAGAUACAGGGCUUC... 3' GAGGCCUCCUGUCCCGAGU	7mer-m8	-0.120	0.003	0.009	0.011	-0.001	-0.085	-0.18	71	1.508	N/A
hsa-miR-1233												