

## miR-483-5p regulates NSCLC apoptosis through RBM5

**Supplementary Table 1.** Identify potential miRNAs target on RBM5 by MicroCosm Targets Version 5

Rfam ID	Score	Energy	Base P	Poisson P	Org P	Start	End
hsa-miR-708*	19.7566	-27.34	1.206870e-03	1.206140e-03	1.206140e-03	443	465
hsa-miR-30b	19.1088	-17.81	3.551940e-03	3.551940e-03	3.551940e-03	261	282
mmu-miR-743b-3p	19.1088	-16.89	6.585360e-03	6.585360e-03	8.905870e-04	371	392
hsa-miR-151-3p	18.8798	-19.4	1.671550e-03	1.670150e-03	7.352520e-04	442	462
hsa-miR-220c	18.7849	-25.33	6.739570e-03	6.716910e-03	2.321480e-03	390	411
hsa-miR-30c	18.3729	-17.24	6.535670e-03	4.544030e-03	4.544030e-03	260	282
hsa-miR-499-3p	18.2451	-19	5.360300e-03	5.345960e-03	5.345960e-03	367	388
hsa-miR-938	18.2451	-21.56	2.982260e-03	2.977820e-03	3.621500e-04	65	86
hsa-miR-140-5p	18.2451	-22.92	5.230800e-03	3.462110e-03	3.462110e-03	104	124
hsa-miR-578	18.1202	-24.04	8.773450e-03	8.735080e-03	7.653250e-03	19	39
mmu-miR-466e-5p	17.5974	-18.3	1.974680e-02	2.829100e-03	1.660680e-03	409	431
hsa-miR-7-1*	17.4894	-15.13	1.846800e-02	1.846800e-02	1.846800e-02	360	381
mmu-miR-705	17.4531	-26.73	5.971710e-02	5.796900e-02	2.559340e-02	131	150
hsa-miR-568	17.4531	-17.41	3.060590e-02	3.014230e-02	7.623440e-05	404	423
mmu-miR-694	17.4416	-13.94	3.674870e-02	3.608170e-02	8.266160e-04	440	457
mmu-miR-743a	17.3815	-12.28	2.395220e-02	2.366760e-02	8.905870e-04	371	392
mmu-miR-466a-5p	17.3815	-17.86	2.534490e-02	2.829100e-03	1.660680e-03	409	431
mmu-miR-466c-5p	17.2735	-17.79	2.654290e-02	2.829100e-03	1.660680e-03	409	431
mmu-miR-466b-5p	17.2735	-18.3	2.601580e-02	2.829100e-03	1.660680e-03	409	431
hsa-let-7a*	17.2522	-23.1	2.207760e-02	1.000000e-06	1.000000e-06	226	246
hsa-miR-641	17.2197	-13.47	2.429780e-02	2.400500e-02	2.237180e-03	368	391
hsa-miR-423-5p	17.191	-21.85	3.781790e-02	3.711170e-02	3.711170e-02	292	316
hsa-miR-30e	17.1655	-10.83	2.424060e-02	4.544030e-03	4.544030e-03	261	282
hsa-miR-30a	17.1655	-12.39	2.019310e-02	4.544030e-03	4.544030e-03	261	282
hsa-miR-323-3p	17.1437	-13.26	8.490540e-03	1.993120e-03	1.990160e-04	251	271
hsa-miR-206	17.0576	-18.51	2.777060e-02	2.738850e-02	2.738850e-02	303	323
hsa-miR-10b	16.8687	-21.32	1.207400e-02	1.207400e-02	1.207400e-02	117	138
hsa-miR-141*	16.8417	-13.99	3.023350e-02	2.978100e-02	1.561300e-02	431	452
hsa-miR-19a	16.7612	-13.16	3.106540e-02	3.106540e-02	2.556480e-04	400	422
hsa-miR-28-3p	16.7337	-14.97	1.524580e-02	1.513020e-02	1.872960e-03	442	464
hsa-miR-7-2*	16.6257	-12.43	3.089910e-02	3.042660e-02	3.042660e-02	360	381
hsa-miR-194	16.6257	-13.3	2.290410e-02	2.264380e-02	1.575790e-03	46	67
hsa-miR-371-5p	16.5804	-15.9	2.757080e-02	2.719420e-02	2.719420e-02	316	335
hsa-miR-574-5p	16.5463	-18.81	5.550450e-02	5.399220e-02	4.922530e-02	410	433
hsa-let-7f-1*	16.5178	-18.62	3.600690e-02	1.000000e-06	1.000000e-06	225	246
hsa-miR-125a-5p	16.471	-17.34	3.510410e-02	3.449510e-02	3.449510e-02	92	115
hsa-miR-182	16.471	-13.88	3.639680e-02	3.950610e-03	3.950610e-03	450	470
hsa-miR-221	16.4389	-14.82	3.075830e-02	3.029010e-02	3.029010e-02	252	274
hsa-miR-132	16.4098	-17.94	2.285870e-02	2.259940e-02	7.641820e-04	223	244
mmu-miR-290-5p	16.4098	-17.59	3.224690e-02	3.173250e-02	7.835090e-03	314	335
hsa-miR-30b	16.4098	-15.3	3.615520e-02	4.544030e-03	4.544030e-03	226	247
hsa-miR-15a*	16.4098	-18.09	3.991920e-02	3.913290e-02	3.913290e-02	170	193
hsa-miR-378	16.3842	-16.4	3.651900e-02	3.586020e-02	3.565170e-02	443	463
hsa-miR-30d	16.3019	-11.46	3.615340e-02	4.544030e-03	4.544030e-03	261	282
mmu-miR-467e	16.3019	-13.7	5.730700e-02	5.569590e-02	1.330220e-02	412	434
hsa-miR-489	16.3019	-20.56	2.473160e-02	2.442830e-02	2.442830e-02	368	390
hsa-miR-422a	16.3019	-16.54	3.935780e-02	3.859330e-02	3.859330e-02	442	463
mmu-miR-669b	16.3019	-16.47	7.163400e-02	6.912850e-02	1.063610e-02	421	442

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hsa-miR-523	16.224	-19.33	7.510560e-03	7.482430e-03	7.482430e-03	257	279
hsa-miR-597	16.1939	-18.62	2.853030e-02	2.812720e-02	2.812720e-02	337	358
hsa-miR-483-5p	16.1939	-19.56	4.333250e-02	4.240710e-02	2.684530e-02	55	76
hsa-miR-30c	16.1166	-18.96	4.557700e-02	4.544030e-03	4.544030e-03	225	247
hsa-let-7f-2*	16.0859	-23.31	4.756710e-02	1.000000e-06	1.000000e-06	225	246
hsa-miR-139-5p	16.0859	-17.84	3.916460e-02	3.840760e-02	1.196310e-02	322	344
hsa-miR-122	16.0859	-19.92	5.868850e-02	5.699950e-02	7.693060e-03	228	252
hsa-miR-222	16.0586	-13.25	3.519270e-02	2.619020e-03	2.619020e-03	254	274
hsa-miR-103	16.0091	-13.45	6.562630e-02	6.351920e-02	5.060710e-03	320	342
hsa-miR-10a	16.0091	-20.38	3.347260e-02	3.291860e-02	3.291860e-02	117	138
hsa-miR-125b-2*	15.978	-20.19	4.404400e-02	1.431440e-03	1.431440e-03	75	96
hsa-let-7b*	15.978	-16.05	4.098600e-02	1.000000e-06	1.000000e-06	225	246
hsa-miR-448	15.978	-18.22	6.458340e-02	6.254210e-02	8.293750e-04	267	289
hsa-miR-581	15.9501	-17.93	5.561530e-02	5.409700e-02	3.804150e-02	17	37
hsa-miR-625	15.9501	-16.57	9.789560e-02	4.490230e-03	4.490230e-03	148	167
hsa-miR-625	15.9501	-17.75	9.789560e-02	4.490230e-03	4.490230e-03	124	144
hsa-miR-624	15.9501	-16.93	7.486800e-02	7.213400e-02	2.851940e-02	76	95
hsa-miR-19b	15.9017	-11.53	5.681900e-02	5.523490e-02	2.556480e-04	400	422
hsa-miR-125b-2*	15.7621	-24.53	5.448420e-02	1.431440e-03	1.431440e-03	196	216
hsa-miR-363	15.7621	-11.84	4.781370e-02	4.668860e-02	2.999670e-02	249	269
hsa-let-7a*	15.7331	-5	7.506170e-02	1.000000e-06	1.000000e-06	402	423
hsa-miR-573	15.7223	-11.62	9.268000e-02	8.851490e-02	3.088200e-02	105	127
hsa-let-7f-1*	15.6541	-12.02	7.291150e-02	1.000000e-06	1.000000e-06	391	413
hsa-miR-212	15.6246	-13.74	4.961960e-02	4.840870e-02	1.514810e-03	224	244
hsa-miR-182	15.5084	-15.05	9.163510e-02	3.950610e-03	3.950610e-03	378	401
hsa-miR-187*	15.4382	-20.81	4.466080e-02	4.367820e-02	4.367820e-02	282	303
hsa-miR-140-3p	15.4076	-18.86	8.561200e-02	3.462110e-03	3.462110e-03	283	303
mmu-miR-466f-5p	15.3302	-21.78	7.717470e-02	2.829100e-03	1.660680e-03	266	288
hsa-miR-222	15.2991	-19.54	7.418050e-02	2.619020e-03	2.619020e-03	457	477
hsa-miR-551b	15.2991	-18.81	4.878480e-02	4.878480e-02	1.371850e-02	158	178
hsa-miR-532-5p	15.2223	-18.9	9.010240e-02	8.616240e-02	1.220840e-02	69	88
hsa-let-7b*	15.1143	-4.91	8.572380e-02	1.000000e-06	1.000000e-06	402	423
hsa-miR-885-5p	15.1143	-13.88	6.352070e-02	6.154530e-02	1.529340e-03	250	271
hsa-miR-30d	15.1143	-15.21	9.850000e-02	4.544030e-03	4.544030e-03	228	247
hsa-miR-323-3p	15.0821	-13.78	6.450520e-02	1.993120e-03	1.990160e-04	367	388
hsa-miR-365	15.0064	-9.56	5.455920e-02	5.309750e-02	4.090480e-02	68	89
hsa-let-7d*	15.0064	-20.3	4.145360e-02	1.000000e-06	1.000000e-06	331	352
hsa-miR-100	15.0064	-16.99	3.207400e-02	3.156510e-02	7.920160e-04	154	176
mmu-miR-463	15.0064	-14.67	8.764440e-02	8.391340e-02	1.241210e-03	286	308
hsa-miR-551a	14.9736	-19.46	7.006370e-02	6.766560e-02	1.371850e-02	158	178
hsa-miR-369-5p	14.4666	-11.88	5.133330e-02	1.588800e-03	8.026500e-04	28	49
hsa-let-7d*	14.4666	-18.64	7.021790e-02	1.000000e-06	1.000000e-06	224	246
hsa-let-7i*	14.3586	-17.39	8.965440e-02	1.000000e-06	1.000000e-06	391	413
hsa-miR-369-5p	14.3586	-12.86	5.745760e-02	1.588800e-03	8.026500e-04	287	308
hsa-let-7i*	14.2506	-20.04	9.997960e-02	1.000000e-06	1.000000e-06	78	98
hsa-miR-99a	14.1427	-12.61	8.309590e-02	7.973710e-02	8.334790e-04	154	176

Hsa-miR-483-5p is highlighted in the Yellow background. \* = Previous mature sequence ID.