

Supplementary Tables

Table S1. MIR100HG transcripts detected in RNA-seq

Transcript ID	Transcript name	Transcript locus	Log2FoldChange	P-value	Padj
ENST00000668776	MIR100HG-280	11:122089353-122204363	10.71881125	3.02E-21	3.43E-20
ENST00000532315	MIR100HG-215	11:122091417-122105942	9.96623511	1.16E-16	9.54E-16
ENST00000656682	MIR100HG-251	11:122061998-122100470	9.100688883	6.14E-12	3.58E-11
ENST00000648209	MIR100HG-231	11:122089186-122157113	7.772098416	1.61E-06	5.95E-06
ENST00000670374	MIR100HG-285	11:122366811-122367974	5.054670009	0.139844617	0.227911
ENST00000647967	MIR100HG-227	11:122199119-122203003	0.97710488	0.704873373	0.817465
ENST00000530072	MIR100HG-209	11:122089110-122101687	-4.633759828	0.264705882	0.386228
ENST00000650497	MIR100HG-239	11:122089144-122156371	-7.457146612	1.27E-05	4.25E-05
ENST00000660329	MIR100HG-263	11:122174358-122309424	-11.41627415	6.74E-26	1.06E-24

Table S2. TSS and promoter on MIR100HG gene

Number	Promoter position (upstream 2000-5000bp)	TSS	Transcript ID
Cluster11	122,037,058-122,041,534	122,037,057	ENST00000666485
		122,039,534	ENST00000648163
		122,069,648	ENST00000648213
	122,069,649-122,72,156	122,069,648	ENST00000531470
		122,070,156	
Cluster10	122,100,439-122,103,832	122,100,438	ENST00000701811
		122,100,447	ENST00000524376
		122,100,448	ENST00000636654
		122,100,448	ENST00000669306
		122,100,448	ENST00000690151

122,100,451	ENST00000656682
122,100,470	ENST00000656793
122,100,470	ENST00000647591
122,100,475	ENST00000660148
122,100,482	ENST00000532319
122,100,492	ENST00000667484
122,100,532	ENST00000649544
122,100,539	ENST00000649626
122,100,539	ENST00000656226
122,101,509	ENST00000656387
122,101,509	ENST00000689894
122,101,509	ENST00000531629
122,101,686	ENST00000688615
122,101,686	ENST00000690198
122,101,686	ENST00000693154
122,101,686	ENST00000530072
122,101,687	ENST00000657554
122,101,689	ENST00000657990
122,101,689	ENST00000647749
122,101,697	ENST00000530955
122,101,702	ENST00000661432
122,101,733	ENST00000661695

		122,101,733	ENST00000670198
		122,101,832	ENST00000670374
		122,101,832	
Cluster9	122,102,122-122,107,942		ENST00000665519
		122,102,121	ENST00000529823
		122,102,166	ENST00000531381
		122,102,178	ENST00000531071
		122,102,194	ENST00000654519
		122,102,194	ENST00000654571
		122,102,194	ENST00000665673
		122,102,203	ENST00000534195
		122,105,169	ENST00000690059
		122,105,544	ENST00000658364
		122,105,616	ENST00000532315
		122,105,942	
Cluster8	122,156,343-122,159,113		ENST00000663296
		122,156,342	ENST00000650497
		122,156,371	ENST00000653167
		122,156,371	ENST00000660603
		122,157,108	ENST00000648209
		122,157,113	
Cluster7	122,180,439-122,182,632		ENST00000534297
		122,180,438	ENST00000666085
		122,180,632	
Cluster6	122,203,004-122,206,363		ENST00000647967
		122,203,003	ENST00000648082

		122,203,003	ENST00000653565
		122,203,003	ENST00000665305
		122,203,003	ENST00000532350
		122,203,087	ENST00000532890
		122,203,087	ENST00000534782
		122,203,087	ENST00000664908
		122,203,110	ENST00000668776
		122,204,363	
Cluster5	122,309,338-122,311,507		ENST00000660311
		122,309,337	ENST00000659378
		122,309,424	ENST00000648734
		122,309,451	ENST00000662950
		122,309,451	ENST00000686059
		122,309,474	ENST00000686772
		122,309,474	ENST00000666347
		122,309,478	ENST00000690515
		122,309,478	ENST00000691884
		122,309,478	ENST00000692610
		122,309,478	ENST00000529804
		122,309,487	ENST00000660329
		122,309,507	
Cluster4	122,367,606-122,369,988		ENST00000649293
		122,367,605	ENST00000648084
		122,367,658	ENST00000669472

		122,367,760	ENST00000528381
		122,367,815	ENST00000528986
		122,367,815	ENST00000529733
		122,367,815	ENST00000654629
		122,367,882	ENST00000663802
		122,367,905	ENST00000656868
		122,367,909	ENST00000527474
		122,367,973	ENST00000665051
		122,367,974	ENST00000670843
		122,367,974	ENST00000649216
		122,367,977	ENST00000661848
		122,367,988	
Cluster3	122,421,832-122,424,871		ENST00000670951
		122,421,831	ENST00000648576
		122,422,839	ENST00000658452
		122,422,849	ENST00000659296
		122,422,849	ENST00000658183
		122,422,850	ENST00000669993
		122,422,857	ENST00000670520
		122,422,860	ENST00000526674
		122,422,871	
Cluster2	122,453,690-122,455,731		ENST00000670396
		122,453,689	ENST00000655814
		122,453,706	ENST00000655138

		122,453,719	ENST00000655232
		122,453,719	ENST00000655288
c		122,453,719	ENST00000637700
		122,453,731	
Cluster1	122,556,722-122,558,721		ENST00000533109
		122,556,721	

Table S3. KEGG enriched pathway terms

Statistic method: hypergeometric test

FDR correction method: Benjamini and Hochberg

Term	Description	cnumber	P-value	FDR
hsa04110	Cell cycle	95	3.91E-10	1.28E-07
hsa03040	Spliceosome	96	8.77E-07	0.000144
hsa04114	Oocyte meiosis	72	1.69E-06	0.000185
hsa03030	DNA replication	26	5.99E-06	0.000491
hsa03420	Nucleotide excision repair	35	7.76E-06	0.000509
hsa04512	ECM-receptor interaction	40	4.21E-05	0.0023
hsa04261	Adrenergic signaling in cardiomyocytes	61	5.51E-05	0.002581
hsa03013	Nucleocytoplasmic transport	70	0.000107	0.004246
hsa03050	Proteasome	32	0.000116	0.004246
hsa03018	RNA degradation	42	0.000184	0.006021
hsa04151	PI3K-Akt signaling pathway	131	0.000494	0.014724
hsa05165	Human papillomavirus infection	123	0.000567	0.015495
hsa04720	Long-term potentiation	31	0.000624	0.015746
hsa04912	GnRH signaling pathway	41	0.000714	0.016739
hsa03008	Ribosome biogenesis in eukaryotes	50	0.000845	0.018137
hsa04962	Vasopressin-regulated water reabsorption	22	0.000885	0.018137
hsa03440	Homologous recombination	21	0.000958	0.018346
hsa04510	Focal adhesion	95	0.001007	0.018346
hsa03015	mRNA surveillance pathway	49	0.001123	0.019381
hsa04728	Dopaminergic synapse	50	0.001369	0.021567
hsa04218	Cellular senescence	69	0.001381	0.021567
hsa05206	MicroRNAs in cancer	62	0.001841	0.027454
hsa04914	Progesterone-mediated oocyte maturation	48	0.002033	0.028342
hsa04310	Wnt signaling pathway	64	0.002152	0.028342
hsa04916	Melanogenesis	38	0.00216	0.028342
hsa04970	Salivary secretion	33	0.002751	0.034705
hsa00970	Aminoacyl-tRNA biosynthesis	21	0.003014	0.036612
hsa04360	Axon guidance	70	0.003218	0.037694
hsa04935	Growth hormone synthesis, secretion and action	45	0.00339	0.038344

hsa04141	Protein processing in endoplasmic reticulum	69	0.00359	0.039255
hsa05231	Choline metabolism in cancer	40	0.003916	0.041437
hsa04072	Phospholipase D signaling pathway	60	0.004329	0.041701
hsa05211	Renal cell carcinoma	35	0.004418	0.041701
hsa04810	Regulation of actin cytoskeleton	103	0.00449	0.041701
hsa04211	Longevity regulating pathway	36	0.004621	0.041701
hsa04750	Inflammatory mediator regulation of TRP channels	36	0.004621	0.041701
hsa05031	Amphetamine addiction	27	0.004704	0.041701
hsa03060	Protein export	16	0.004961	0.042668
hsa04918	Thyroid hormone synthesis	28	0.005073	0.042668
hsa04371	Apelin signaling pathway	56	0.005345	0.043826
hsa01522	Endocrine resistance	38	0.00584	0.04672
hsa04152	AMPK signaling pathway	47	0.007087	0.055233
hsa04911	Insulin secretion	31	0.007241	0.055233
hsa01521	EGFR tyrosine kinase inhibitor resistance	36	0.007455	0.055573
hsa04024	cAMP signaling pathway	75	0.008114	0.058886
hsa05146	Amoebiasis	40	0.008258	0.058886
hsa03430	Mismatch repair	16	0.008731	0.060929
hsa04625	C-type lectin receptor signaling pathway	39	0.009311	0.061268
hsa03266	Virion - Herpesvirus	6	0.009587	0.061268
hsa04020	Calcium signaling pathway	86	0.009687	0.061268
hsa04015	Rap1 signaling pathway	83	0.009983	0.061268
hsa00020	Citrate cycle (TCA cycle)	19	0.01008	0.061268
hsa01250	Biosynthesis of nucleotide sugars	17	0.010087	0.061268
hsa03020	RNA polymerase	17	0.010087	0.061268
hsa05224	Breast cancer	52	0.010603	0.06323
hsa03410	Base excision repair	24	0.012214	0.070437
hsa04928	Parathyroid hormone synthesis, secretion and action	39	0.01224	0.070437
hsa04144	Endocytosis	113	0.012684	0.071728
hsa04010	MAPK signaling pathway	102	0.013815	0.076804
hsa04924	Renin secretion	27	0.014126	0.077223
hsa05166	Human T-cell leukemia virus 1 infection	89	0.016486	0.088648
hsa05163	Human cytomegalovirus infection	77	0.017695	0.093611
hsa04724	Glutamatergic synapse	39	0.01801	0.093767
hsa04926	Relaxin signaling pathway	45	0.018452	0.094565
hsa04921	Oxytocin signaling pathway	63	0.018753	0.09463
hsa00280	Valine, leucine and isoleucine degradation	20	0.020351	0.100338
hsa05214	Glioma	29	0.020496	0.100338
hsa04071	Sphingolipid signaling pathway	43	0.025745	0.122563
hsa04725	Cholinergic synapse	39	0.025783	0.122563
hsa04213	Longevity regulating pathway - multiple species	27	0.026276	0.123124

hsa04062	Chemokine signaling pathway	60	0.030135	0.139214
hsa04713	Circadian entrainment	34	0.032239	0.143608
hsa04925	Aldosterone synthesis and secretion	35	0.032316	0.143608
hsa05169	Epstein-Barr virus infection	73	0.032399	0.143608
hsa04142	Lysosome	49	0.033702	0.147392
hsa04722	Neurotrophin signaling pathway	44	0.035031	0.151187
hsa04923	Regulation of lipolysis in adipocytes	22	0.036706	0.156358
hsa05161	Hepatitis B	54	0.038364	0.161328
hsa05218	Melanoma	26	0.039352	0.163385
hsa04390	Hippo signaling pathway	63	0.043523	0.178442
hsa05219	Bladder cancer	18	0.044988	0.181442
hsa04014	Ras signaling pathway	83	0.045361	0.181442
hsa04380	Osteoclast differentiation	41	0.048153	0.190082
hsa05207	Chemical carcinogenesis - receptor activation	65	0.049101	0.190082
hsa04730	Long-term depression	22	0.049259	0.190082
hsa05142	Chagas disease	34	0.050646	0.19316

Table S4. Proteins specifically binding to MIR100HG-L identified by mass spectrometry

Protein	Description	Gene	PSMs
Q8TBR3	Fusion (Involved in t(1216) in malignant liposarcoma)	FUS	7
Q5T5C7	serine--tRNA ligase	SARS1	6
B5MCF9	Pescadillo homolog	PES1	8
E9PK91	Bcl-2-associated transcription factor 1	BCLAF1	11
Q9BQG0	Myb-binding proteiccn 1A	MYBBP1A	5
Q9Y3F4	Serine-threonine kinase receptor-associated protein	STRAP	11
Q7Z478	ATP-dependent RNA helicase DHX29	DHX29	3
A0A8I5QKQ5	Protein disulfide-isomerase	PDIA3	11
Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2	HNRNPUL2	9
P62906	60S ribosomal protein L10a	RPL10A	4
A0A8Q3WLD1	H/ACA ribonucleoprotein complex subunit DKC1	DKC1	4
Q9NZB2	Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	-
Q9Y295	Developmentally-regulated GTP-binding protein 1	DRG1	10
Q9NVV4	Poly(A) RNA polymerase, mitochondrial	MTPAP	6
P05109	Protein S100-A8	S100A8	2
Q9H6F5	Coiled-coil domain-containing protein 86	CCDC86	4
Q6I9V5	ADP/ATP translocase	SLC25A6	11
P13929	Beta-enolase	ENO3	1
A0A8I5KWU3	La ribonucleoprotein domain family, member 1, isoform CRA_a	LARP1	10
P63267	Actin, gamma-enteric smooth muscle	ACTG2	16
B4DRY2	rRNA adenine N(6)-methyltransferase	DIMT1	3
Q15393	Splicing factor 3B subunit 3	SF3B3	5
A0A3B3IS54	Aspartate--tRNA ligase, mitochondrial	DARS2	4

A0A0D9SGE8	PHD finger protein 6	PHF6	1
K9MS24	Spectrin beta chain	SPTBN1	2
K7EL20	Eukaryotic translation initiation factor 3 subunit G (Fragment)	EIF3G	2
F8W6C2	SPATS2-like protein (Fragment)	SPATS2L	3
Q9BZ93	Prosome P27K protein (Fragment)	PSMA6	1
Q9HAU5	Regulator of nonsense transcripts 2	UPF2	1
Q9HC35	Echinoderm microtubule-associated protein-like 4	EML4	1
A0A384MR33	Structural maintenance of chromosomes protein	SMC1L1	3
A0A7P0T997	Acetyltransferase component of pyruvate dehydrogenase complex	DLAT	1

Table S5. KEGG enriched pathway terms of MIR100HG-L binding proteins

Statistic method: hypergeometric test

FDR correction method: Benjamini and Hochberg

Term	Description	number	P-value	FDR
hsa03040	Spliceosome	35	9.54E-15	2.03271E-12
hsa03010	Ribosome	30	6.64E-14	7.06669E-12
hsa05171	Coronavirus disease - COVID-19	32	1.21E-11	8.60103E-10
hsa03015	mRNA surveillance pathway	15	2.5E-06	0.000133057
hsa03008	Ribosome biogenesis in eukaryotes	19	5.41E-06	0.000230533
hsa00970	Aminoacyl-tRNA biosynthesis	12	7.38E-06	0.000261947
hsa03018	RNA degradation	11	0.000215	0.006533509
hsa03030	DNA replication	7	0.000936	0.024911078
hsa01200	Carbon metabolism	12	0.001203	0.028469774
	Protein processing in endoplasmic			
hsa04141	reticulum	15	0.001506	0.032079058
hsa03013	Nucleocytoplasmic transport	10	0.008167	0.158151755
hsa04216	Ferroptosis	6	0.009897	0.171677028
hsa01230	Biosynthesis of amino acids	8	0.010478	0.171677028
hsa03410	Base excision repair	6	0.013262	0.196670751
hsa05203	Viral carcinogenesis	14	0.015082	0.196670751
hsa00020	Citrate cycle (TCA cycle)	5	0.015169	0.196670751
hsa05205	Proteoglycans in cancer	14	0.015697	0.196670751
hsa00010	Glycolysis / Gluconeogenesis	7	0.020868	0.237525402
hsa04530	Tight junction	12	0.021188	0.237525402
hsa05014	Amyotrophic lateral sclerosis	20	0.026974	0.287268892
hsa01212	Fatty acid metabolism	6	0.036519	0.370408019
hsa05164	Influenza A	11	0.050781	0.491653694
hsa03450	Non-homologous end-joining	3	0.064378	0.57406264
hsa00620	Pyruvate metabolism	5	0.064683	0.57406264
hsa04110	Cell cycle	10	0.068436	0.583074318

Table S6. KEGG enriched pathway terms of MIR100HG-L-5p-1254nt binding proteins

Statistic method: hypergeometric test

FDR correction method: Benjamini and Hochberg

Term	Description	ccnumber	P-value	FDR
hsa03460	Fanconi anemia pathway	9	5.41E-07	8.47E-05
hsa03440	Homologous recombination	7	8.74E-06	0.000855
hsa01100	Metabolic pathways	45	1.57E-05	0.001291
hsa05131	Shigellosis	8	2.36E-05	0.001714
hsa05168	Herpes simplex virus 1 infection	20	0.000174	0.008016
hsa04520	Adherens junction	7	0.000228	0.009626
hsa04150	mTOR signaling pathway	10	0.000244	0.010169
hsa03040	Spliceosome	9	0.00043	0.015009
hsa05166	Human T-cell leukemia virus 1 infection	11	0.000999	0.028421
hsa05100	Bacterial invasion of epithelial cells	6	0.001531	0.038327
hsa03450	Non-homologous end-joining	3	0.001778	0.041838
hsa04215	Apoptosis - multiple species	4	0.002504	0.050777
hsa04146	Peroxisome	6	0.002636	0.052194
hsa04666	Fc gamma R-mediated phagocytosis	6	0.004692	0.071087
hsa00471	D-Glutamine and D-glutamate metabolism	2	0.004771	0.071087
hsa05221	Acute myeloid leukemia	5	0.004917	0.072568
hsa00230	Purine metabolism	7	0.005624	0.079266
hsa03013	RNA transport	8	0.005754	0.080731
hsa04210	Apoptosis	7	0.007066	0.087737
hsa04015	Rap1 signaling pathway	9	0.007454	0.089787
hsa00565	Ether lipid metabolism	4	0.007996	0.089861
hsa04330	Notch signaling pathway	4	0.008559	0.094629
hsa00520	Amino sugar and nucleotide sugar metabolism	4	0.008559	0.094629
hsa05412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	5	0.008978	0.097498
hsa00592	alpha-Linolenic acid metabolism	3	0.009067	0.097498
hsa00563	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	3	0.009067	0.097498
hsa04151	PI3K-Akt signaling pathway	12	0.012465	0.114495
hsa00240	Pyrimidine metabolism	4	0.014804	0.124191
hsa01523	Antifolate resistance	3	0.015471	0.126722
hsa00310	Lysine degradation	4	0.016498	0.128939
hsa00130	Ubiquinone and other terpenoid-quinone biosynthesis	2	0.016665	0.128939
hsa05205	Proteoglycans in cancer	8	0.017585	0.134201
hsa03410	Base excision repair	3	0.018046	0.136389
hsa00561	Glycerolipid metabolism	4	0.018308	0.137704
hsa04068	FoxO signaling pathway	6	0.020808	0.148909
hsa00564	Glycerophospholipid metabolism	5	0.021371	0.150831
hsa04010	MAPK signaling pathway	10	0.0214	0.150831
hsa04810	Regulation of actin cytoskeleton	8	0.023015	0.155563

hsa05231	Choline metabolism in cancer	5	0.023019	0.155563
hsa05200	Pathways in cancer	15	0.024077	0.162018
hsa04120	Ubiquitin mediated proteolysis	6	0.024274	0.162103
hsa05142	Chagas disease (American trypanosomiasis)	5	0.026556	0.170275
hsa05211	Renal cell carcinoma	4	0.02675	0.170443
hsa00604	Glycosphingolipid biosynthesis - ganglio series	2	0.027898	0.170443
hsa04072	Phospholipase D signaling pathway	6	0.033206	0.187709
hsa04014	Ras signaling pathway	8	0.034277	0.187709
hsa03320	PPAR signaling pathway	4	0.035767	0.194975
hsa00511	Other glycan degradation	2	0.03781	0.199841
hsa02010	ABC transporters	3	0.038189	0.200154
hsa03018	RNA degradation	4	0.040106	0.209082
hsa05165	Human papillomavirus infection	10	0.04041	0.209691
hsa04510	Focal adhesion	7	0.042183	0.214259
hsa04144	Endocytosis	8	0.043575	0.218852
hsa04722	Neurotrophin signaling pathway	5	0.044061	0.220938
hsa00670	One carbon pool by folate	2	0.04505	0.22129
hsa05135	Yersinia infection	5	0.046637	0.227064
hsa04630	Jak-STAT signaling pathway	6	0.047326	0.229941
hsa04142	Lysosome	5	0.049302	0.234802
hsa04611	Platelet activation	5	0.050667	0.240207

Table S7. Primers, siRNA, sgRNA, ASO and probe used in this study

qRT-PCR Primers	
GAPDH-Forward	GTCAAGGCTGAGAACGGGAA
GAPDH-Reverse	AAATGAGCCCCAGCCTTCTC
U6-Forward	ATTGGAACGATACAGAGAAGATT
U6-Reverse	GGAACGCTTCACGAATTTG
MIR100HG- ENST00000532315- Forward	ATTCCGATGGGGGAGGGAAA
MIR100HG- ENST00000532315- Reverse	AATTGTCCTACCTGGCCGTC
MIR100HG- ENST00000656682- Forward	GCTCCGCTTCGAATGGATACAG
MIR100HG- ENST00000656682- Reverse	CTCTGTGTGTTTTCCCCCTTTC
MIR100HG- ENST00000648209-	CTGGATGTGCCTCTTTTGTGA

Forward	
MIR100HG- ENST00000648209- Reverse	TGGTCTCCTACAGCTTTTCAGT
MIR100HG- ENST00000650497- Forward	GCTGTGGTGGAGAGGCATAG
MIR100HG- ENST00000650497- Reverse	CCTTGCACTGGGGAGACATT
MIR100HG- ENST00000660329- Forward	TCCTCAGACCCCTGCAAACA
MIR100HG- ENST00000660329- Reverse	ATCCCACCAAAGTGCCATCTC
MIR100HG- ENST00000530072- Forward	GGAAAGCCCCACTTCCAGTC
MIR100HG- ENST00000530072- Reverse	AATCACCAAGAGCGAGCACC
MIR100HG- ENST00000647967- Forward	GGCAACTGTTACAAAACCCA
MIR100HG- ENST00000647967- Reverse	CCTACTCCTTTGGTGAGAACG
MIR100HG- ENST00000670374- Forward	AGCTGATGTAGCCGTAATGGTC
MIR100HG- ENST00000670374- Reverse	AGCCTCAAAGCTCACCAAAAG
MIR100HG-L-Forward	GTGCGAGCACTCTTCTCTCG
MIR100HG-L-Reverse	GCGCTTCCAAAATTCGCA
TGFβ1-Forward	CCTGAACCCGTGTTGCTCTC
TGFβ1-Reverse	GTAGTGAACCCGTGATGTCC
MIR100HG-L- Promoter#1-Forward	CCTAAACGAGGTGGGTCGAAG
MIR100HG-L- Promoter#1-Reverse	GTTACTGTCTCGGGAGTGTCTG
MIR100HG-L- Promoter#2-Forward	GGGGAAACCTAACCGTCTCG

MIR100HG-L-Promoter#2-Reverse	GACTTCGACCCACCTCGTTT
MIR100HG-L-Promoter#3-Forward	AGTGTCTCCCCCTCGGTTAG
MIR100HG-L-Promoter#3-Reverse	CTGGAGGAGGACGTGGCATA
MIR100HG-S-Forward	AACTTGGCTTCCTCGCTTCT
MIR100HG-S-Reverse	CTTTGTCCTTGCACTGGGGA
MIR100HG-L-5p-1254nt-Forward	AGGTGGGGAGCAGTATGTGT
MIR100HG-L-5p-1254nt-Reverse	TGTTCCGAGAGGTAAGGCGT
BCLAF1-Forward	TTAGAGGCAGAGGAAGAGCCA
BCLAF1-Reverse	CACGTTGAAAAGTACCACGACC
IKBKB-Forward	GCTGGATCAGGGCAGTCTTT
IKBKB-Reverse	GTCCACCTCACTCTTCTGCC
AKT2-Forward	AAGAAGGCTGGCTCCACAAG
AKT2-Reverse	ATCCACTCCTCCCTCTCGTC
FAS-Forward	GCATCTGGACCCTCCTACCT
FAS-Reverse	GAGGACAGGGCTTATGGCAG
CTSB-Forward	AGACCGTACTCCATCCCTCC
CTSB-Reverse	GCCATGATGTCCTTCTCGCT
BCL2L11-Forward	GCTACCAGATCCCCGCTTTT
BCL2L11-Reverse	GCAAGGAGGACTTGGGGTTT
BIRC6-Forward	GGACACTCTGTTTCCTGCAGTT
BIRC6-Reverse	TTGACCCCACCACCTTTCAC
Bax-Forward	CAGGATGCGTCCACCAAGAA
Bax-Reverse	CCTTGAGCACCAGTTTGCTG
MDM2-Forward	CTTTGCAGTAAAATATGCCCTT
MDM2-Reverse	GCAAACCTTATTCGGCTCT
ATM-Forward	GCCGTGATGACCTGAGACAA
ATM-Reverse	TTGGCACTGAAAGGCACTGA
ATM Exon20-Forward	TTTCTTACAGTAATTGGAGCATTTG
ATM Exon21-Reverse	GGCAATTTACTAGGGCCATTC
ATM Intron20-Reverse	CAAGCGACTGAGGGAAACAC
THRAP3-Forward	ACCCAGTGGCTTATTGGCTC
THRAP3-Reverse	GGAGGAGGATCTGGACCTGT
RACE Primers	
5'RACE-Reverse	CTCCCCCTTGTGGGAGATGTGGGGCATAGC
3'RACE-Forward	ACATCTCCCACAAGGGGGAGCCGCCGGAGG
siRNA sequences	

siSMAD2#1	GAAUUGAGCCACAGAGUAAAdTdT
siSMAD2#2	GCCCUCACUCACUGUAGAUdTdT
siSMAD3#1	CGUCAACACCAAGUGCAUCdTdT
siSMAD3#2	CCGCAUGAGCUUCGUCAAAdTdT
siBCLAF1#1	CUAGAUUACUUCAGUGAUAdTdT
siBCLAF1#2	UAGUAGAGAUCGUAUGUAUdTdT
siTHRAP3#1	UUCUCCGAACGUGUCACGUdTdT
siTHRAP3#2	CCCGTTCTTCCTCCAACCATA
sgRNA sequences	
Top-MIR100HG-L sg#1	CACCGAAATGAGGAGGAGGAGGAGG
bottom-MIR100HG-L sg#1	AAACCCTCCTCCTCCTCCTCATTTC
Top-MIR100HG-L sg#2	CACCGGAAAGGCCAAGTGTCCACGG
bottom-MIR100HG-L sg#2	AAACCCGTGGACACTTGGCCTTTCC
Top-MIR100HG-S sg#1	CACCGAGATTTCTTTGTTGCAATGA
bottom-MIR100HG-S sg#1	AAACTCATTGCAACAAAGAAATCTC
Top-MIR100HG-S sg#2	CACCGAAAACCAGTTACAGGACAGG
bottom-MIR100HG-S sg#2	AAACCCTGTCCTGTAACTGGTTTTTC
ASO sequences	
MIR100HG-L ASO#1	AUACGTCACAAACCACAUGC
MIR100HG-L ASO#2	UAAGCCTGCATGGCTUACGC
MIR100HG-L ASO#3	UAUCAGCTGTGTTTCUCGCC
FISH probe sequences	
MIR100HG-L	UACUGCUCCCACCUUAGUGAAAACAGACUGUAUGUCC AAAUAGUAUC

Table S8. Antibodies used in this study

Antibodies	Source	Catalog	Application	Dilution
SMAD2/3	Cell Signaling Technology	5678S	WB	1:1000
		cc	ChIP	1:50
Cyclin D1	proteintech	26939-1-AP	WB	1:1000
GAPDH	proteintech	60004-1-Ig	WB	1:1000
Caspase 3	proteintech	19677-1-AP	WB	1:1000
Cleaved Caspase 3	proteintech	25128-1-AP	WB	1:1000
β -catenin	proteintech	51067-2-AP	WB	1:1000
Histone H3	proteintech	17168-1-AP	WB	1:1000
HNRNPA2B1	proteintech	14813-1-AP	WB	1:1000

BCLAF1		abcam	ab181240	IF	1:500
				WB	1:1000
				RIP	1:10
				co-IP	1:100
FLAG tag		proteintech	80010-1-RR	WB	1:1000
				RIP	1:10
THRAP3		proteintech	19744-1-AP	WB	1:1000
SNW1		proteintech	25926-1-AP	WB	1:1000
EIF4A3		proteintech	17504-1-AP	WB	1:1000
IgG Rabbit		abcam	ab172730	ChIP	1:50
				RIP	1:10
				co-IP	1:100
HRP-conjugated	Mouse	Abbkine	A25022	WB	1:10000
Anti-Rabbit IgG LCS					
HRP-conjugated Goat Anti-		proteintech	SA00001-1	WB	1:10000
Mouse IgG					
