Supporting Information

Lujambio et al. 10.1073/pnas.0803055105

SI Materials and Methods

RNA Isolation and miRNA Expression Analysis. Total RNA was isolated from SW620, IGR37, and SIHN-011B cells, before and after 5-aza-2'-deoxycytidine treatment, by TRIzol extraction (Invitrogen). miRNA microarray profiling was conducted as described (1). Briefly, 5 μ g of total RNA was used for hybridization on a custom miRNA microarray platform containing quadruplicates of 389 human microRNA probes. These arrays contain gene-specific 40-mer oligonucleotide probes, spotted by contacting technologies and covalently attached to a polymeric matrix (1). The hybridized biotinylated transcripts were detected by streptavidin-Alexa Fluor 647 conjugation, scanned on an Axon 4000B microarray scanner, and analyzed by using GENE-PIX PRO 6.0 (Axon Instruments). After background subtraction and normalization of average values of replicate spots of each miRNA, those that were differentially expressed in treated and nontreated cells were identified from significant t tests (Significance Analysis of Microarrays). Principal component analysis (PCA; Partek Genomic Suite) was performed to classify samples.

DNA Methylation Analyses. The miRNA sequences were analyzed by using miRBase (http://microrna.sanger.ac.uk/) and the University of California at Santa Cruz Human Genome Browser (http://genome.cse.ucsc.edu). The CpG Island Searcher Program (2) was used to determine which miRNAs were embedded in a CpG island, because it has been predicted that >90% of the human miRNA promoters are located 1,000 bp upstream of the mature miRNA (3). DNA methylation status was established by PCR analysis of bisulfite-modified genomic DNA, which induces chemical conversion of unmethylated, but not methylated, cytosine to uracil. Two procedures were used. First, methylation status was analyzed by bisulfite genomic sequencing of both strands of the corresponding CpG islands. Eight independent clones were analyzed. The second analysis used methylationspecific PCR with primers specific for either the methylated or modified unmethylated DNA (Table S5).

Quantification of miRNAs with Real-Time PCR. TaqMan MicroRNA assays were used to quantify the level of mature miRNAs as described previously (4). Each reverse transcriptase (RT) reaction contained 6 ng of purified and DNase-treated (turbo DNA-free, Ambion) total RNA. Real-time PCRs included 2 μ l of diluted RT product (1:15 dilution). Reactions were incubated in an Applied Biosystems 7900HT Fast Real-Time PCR system in 384-well plates. RNU19 was used to normalize the data. Total RNA was extracted from two independent experiments, and the real-time PCRs for each miRNA (10 μ l) were performed in triplicate.

RACE. RACE was developed as previously described (5). We used the 5' RACE System for Rapid Amplification of cDNA Ends Version 2.0 from Invitrogen according to the manufacturer's instruction. Briefly, 5 μ g of total RNA from 5'-aza-2deoxycytidine treated cells was reverse-transcribed into cDNA using SuperScript II RT reverse transcriptase and specific reverse primers (GSP1). cDNAs were amplified by PCR using Elongase Amplification System (Invitrogen) and other specific primers, first GSP2 and afterward GSP3, for nested amplification (Table S5). Specific PCR products were cloned into pGEMT vector (Promega), and, after transformation, multiple clones were sequenced. **Chromatin Immunoprecipitation Assay.** Standard chromatin immunoprecipitation assays were developed as previously described (6). In brief, cells were treated with 1% formaldehyde for 15 min. Then, chromatin was sheared with a Bioruptor (Diagenode) to an average length of 0.4-0.8 kb for this analysis. The following antibodies were used: anti-trimethyl-K4 histone H3 (ab8580/ab1220; Abcam) and anti-acetyl H4 (06-598; Upstate Biotechnologies). PCR amplification was developed in 20 μ l with specific primers for each of the analyzed promoters. Primers used are described in Table S5.

Mouse Xenograft and Metastasis Models. Four- to 5-week-old male athymic nu/nu mice (Charles River) were used in this study. Mice were anesthetized, and tumor cells were s.c. injected. A total of 3×10^{6} cells of the c-shRNA-SIHN-011B cell line or those stably transfected with miR-148a or miR-34b/c were injected s.c. in both flanks of each animal (n = 12 for paired control/miR-148a, and n = 10 for control/miR-34b/c), respectively. Mice were weighed, and tumor width and length were measured every 5 days. Mice were killed 30 days after injection, and tumors from both groups were excised and weighed. The mean volume or tumor mass \pm SEM were calculated. For experimental metastasis assays, 1×10^6 of c-shRNA control or stably miR-148a or miR-34b/c transfected cells were injected intravenously via the lateral tail vein (n = 10, 4- to 5-week-old male athymic nude mice per group). Mice were killed 40 days after injection, and the presence of macroscopic lung metastases was analyzed by H&E tissue staining.

Expression Analyses of miRNA Target Genes by Western Blot and Immunohistochemistry. Information of base-pairing comparison among miR-34b, miR-34c, and miR-148a and their targets sites in the 3' UTR of c-MYC, E2F3, CDK6, and TGIF2 mRNA is available at Targetscan (www.targetscan.org/). Western blot was done as previously described (6). The membranes were immunoprobed with antibodies against C-MYC (1:500; Santa Cruz Biotechnology), E2F3 (1:1,000; Abcam), CDK6 (1:1,000; Cell Signaling), and TGIF2 (1:500; Abcam). An antibody against β -actin (1:5,000; Sigma) or nucleolin (1:1,000; Santa Cruz Biotechnology) was used as a loading control. C-MYC and CDK6 were immunohistochemically stained with a 1:1,500 dilution. Tissue microarrays were read and scored by a pathologist who had no knowledge of the clinical features.

Luciferase Reporter Assay. Standard luciferase reporter assays were developed as previously described (6). Luciferase constructs were made by ligating oligonucleotides containing the wild-type or mutant putative target site of the C-MYC, E2F3, CDK6, and TGIF2 3' UTR into the multicloning site of the p-MIR Reporter Luciferase vector (Ambion). Cells were cotransfected in 24-well plates using Lipofectamine 2000 (Invitrogen) with 0.4 μ g of firefly luciferase reporter vector containing the wild-type or mutant oligonucleotides, 0.04 μ g of control vector (pRL-TK vector; Promega) containing Renilla luciferase, and 100 ng of miR-34b, miR-34c, or miR-148a precursor (Ambion). Firefly and Renilla luciferase activities were measured consecutively 48 h after transfection using Renilla for normalization in dual-luciferase assays (Promega). The experiments were performed in quadruplicate in three independent experiments. The mean luciferase levels \pm SEM were calculated for each group.

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- Zhou X, Ruan J, Wang G, Zhang W (2007) Characterization and identification of microRNA core promoters in four model species. *PLoS Comput Biol* 3:e37.

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Fig. S1. Bisulfite genomic sequencing analyses of illustrative miRNAs that show a methylated CpG island in normal and cancer cells. Eight single clones are represented for each sample. The CpG island is depicted, and each vertical bar illustrates a single CpG. Black and white squares represent methylated and unmethylated CpG, respectively. NL, normal lymphocytes; NC, normal colon; NS, normal skin.



Fig. 52. Bisulfite genomic sequencing analyses of miR-9-1 and miR-9-2 that show cancer-specific CpG island hypermethylation. Eight single clones are represented for each sample. The CpG island is depicted, and each vertical bar represents a single CpG. Black and white squares represent methylated and unmethylated CpG, respectively. NL, normal lymphocytes; NC, normal colon; NS, normal skin.

DNAS

S A ZO



100bp

Fig. 53. 5' RACE analyses of the five miRNAs in 5-aza-2'-deoxycytidine-treated cells. Black arrows represent the putative transcriptional start site. Red lines indicate the position of the mature miRNAs, and gray lines represent the location of the bisulfite sequencing primers. Blue lines depict the CpG islands.

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Fig. 54. Bisulfite genomic sequencing analyses of CR612213 and BC021736 5' ends. Eight single clones are represented for each sample. Each vertical bar represents a single CpG. The black arrow represents the transcriptional start site. Black and white squares represent methylated and unmethylated CpGs, respectively. NL, normal lymphocytes.



Fig. S5. Chromatin immunoprecipitation assay for histone modification marks in the miRNA-associated CpG islands (examples in miR-9-1, miR-9-3, and miR-34b/c) in untreated (c) and 5-aza-2'-deoxycytidine-treated (A) cells. The presence of miRNA methylation is associated with the lack of histone modifications linked to transcriptional activity, such as acetylation of histones H4 (AcH4) and trimethylation of Lys-4 of histone H3 (3mK4H3), whereas the opposite scenario is observed when DNA demethylation events are present by pharmacologic treatment with a DNA-demethylating agent. No AB, no antibody.



Fig. S6. (*A*) Bisulfite genomic sequencing analyses of the five miRNAs that show cancer-specific CpG island hypermethylation, before and after treatment with trichostatin A (TSA) in the corresponding cell lines. Eight single clones are represented for each sample. The CpG island is depicted, and each vertical bar illustrates a single CpG. Black and white squares represent methylated and unmethylated CpG, respectively. The percentage of methylation and the significance after χ^2 test are represented. There are no significant differences in the DNA methylation levels. (*B*) Expression analyses of mature miRNAs by qRT-PCR in methylated metastatic cell lines in untreated cells (c) and upon treatment with TSA. No significant differences were observed.



Fig. 57. Complementary sites between miR-34b and CDK6 and C-MYC, between miR-34c and E2F3, and between miR-148 and TGIF2. The capital and bold letters identify perfect base matches according to the TARGETSCAN 4.1 software. The base pairing between the miRNAs and the mutant target site is also shown.

S. A

Table S1. Fifty-seven different miRNAs up-regulated ≥2-fold
with minimal basal expression in untreated cells

miRNA	SW620	IGR37	11B
nsa-miR-100		2.2	
nsa-miR-101-1		2.57	
nsa-miR-101-2		2.57	
nsa-miR-106a		2.16	
nsa-miR-126	2.9	2.3	2.8
nsa-miR-126*	2.4	2.5	2.6
nsa-miR-132	2	4.26	
nsa-miR-135-1			2.28
nsa-miR-145	8.17		
nsa-miR-147			2.08
nsa-miR-148a		2.8	
nsa-miR-148b		2.56	
nsa-miR-150			3.56
nsa-miR-151			2.05
nsa-miR-152		2.58	
nsa-miR-155	30	2.05	
nsa-miR-15b		2.14	
nsa-miR-17		3.25	
nsa-miR-181a		2.27	
nsa-miR-192		2 19	2 07
nsa-miR-193a		2.15	2.55
nsa-miR-193b		2.2	2.55
nsa-miR-196-1		2.2	3 47
nsa-miR-19a		2.4	5.47
nsa-miR-205		2.4	2 1 2
nsa-miR-200		3 23	2.12
nsa-miR-210		2.25	
nsa-miR-210		2.5	2 22
nsa-miR-212		5.05	2.22
nsa-miR-215			3.07
nsa-miR-218-2		5 58	2.47
nsa-miR-210-2	2 15	2.50	2.22
nsa-miR-219-1	2.15	2.47	
nsa-miR-220	2.57	2.15	
nsa-miR-220		2.05	
nsa-miR-221		2.37	
nsa-miR-27b		2.1	
nsa miP 20h 2		2.03	
nsa miR 201	2.1	2.45	2.24
nsa-miR 20a	5.1	2.4	5.24
nco miP 22		2.4	2 20
nsa-miR.22	דס ר	2.00	2.29
nsa-miP 24h	2.07		2.71
nsa miR 24c			5.9
nsd-mik-54C	2.22		5.50
nsa-mik-36 i	2.32		
nsa-miR-373	2.46		
nsa-miR-3/3 [^]	3.4		2.24
nsa-miR-425	2.4		2.21
nsa-mik-429	2.1		6.97
nsa-miK-494			2.04
nsa-miR-516		2.55	2.86
nsa-miR-7-2		2.29	
nsa-miR-9-1			2.54
nsa-miR-92	2.56		
nsa-miR-9-2		4.42	
nsa-miR-9-3	2	2.87	
nsa-miR-96		3.46	2.46

Table S3A. Frequency of CpG island hypermethylation of the metastasis-associated miRNAs in human malignancies and normal tissues

Cells	miR-148A	miR-34b/c	miR-9-1	miR-9-2	miR-9-3
		Tumor t	уре		
Colon	14/36 (39)	13/37 (35)	12/37 (32)	6/37 (16)	31/37 (84)
Lung	20/36 (56)	34/63 (54)	22/42 (52)	26/47 (55)	31/58 (53)
Breast	38/71 (53)	50/72 (69)	23/40 (57)	22/40 (56)	42/72 (58)
Head and neck	4/17 (24)	1/12 (8)	8/17 (47)	4/9 (44)	5/15 (33)
Melanoma	29/59 (49)	18/72 (25)	32/89 (36)	55/86 (64)	11/65 (17)
Normal					
Lymphocytes	0/5 (0)	0/5 (0)	0/5 (0)	0/5 (0)	0/5 (0)
Colon	0/8 (0)	0/15 (0)	0/16 (0)	0/12 (0)	2/13 (15)
Lung	0/4 (0)	0/4 (0)	0/4 (0)	1/4 (25)	0/4 (0)
Breast	0/4 (0)	0/4 (0)	0/4 (0)	0/4 (0)	0/4 (0)
Skin	0/2 (0)	0/2 (0)	0/2 (0)	0/2 (0)	0/2 (0)
Melanocytes	0/1 (0)	0/1 (0)	0/1 (0)	0/1 (0)	0/1 (0)

Data in parentheses are percentages.

Table S3B. The distribution of cases related to methylation and positive immunostaining

Target gene	Staining	miR-34b/c unmethylated	miR-34b/c methylated	<i>P</i> value
C-MYC	-	34	5	0.0001
	+	6	20	
CDK6	-	21	4	0.040
	+	10	8	

P value was calculated by using Pearson's χ^2 test.

Table S5. Primers used in this study

miRNA	Sequence
Primers used for genomic bisulfite se	quencing (BS) and methylation-specific PCR (MSP) analyses
BS-219-1-s	GGGGATAAGATGTTTATTAGGG
BS-219-1-as	CTTTAACTCTCCCTAAACCCTC
BS-210-s	TGGTTGAGGGATTAGGTTATTT
BS-210-as	AAAAATTAACCCCACCCC
BS-152-s	GAGAGGAGGTTTGTTTTGAGTT
BS-152-as	ACTCCACTCCCAAACAAATATT
BS-92-s	TGGGGATATTTGAYGTTAG
BS-92-as	
D3-423-5 RS-425-as	
BS-132/212-s	YGGGTYGTTTTTAGTAATAGTT
BS-132/212-as	TAAACTATTACCTCCAATTCCC
BS-9-1-s	GGTTTTTGTYGTGTTTGTATT
BS-9-1-as	ΤΑΑCTTTATAAAAACTCCACACCA
BS-9-2-s	YGGAATAAATTTTGAAGGTAAT
BS-9-2-as	ΤΑΑCΤΤΤΑΤΑΑΑΑΑCCAATACACTCA
BS-9-3-s	GTGTTTTAYGTGAGTTTYGG
BS-9-3-as	
BS-34b/c-s	
BS-34D/C-dS BS-1/8a-c	
BS-148a-as	ΤΓΓΓΓΟΑΑΑΑΑΤΤΤΟΤΤΟΟΤΑΟ
BS-373-s	TTGGGGAAGGGAAGGGGGTTTT
BS-373-as	CCTACCTCAACCTCCCAAATAAC
BS-220-s	TTATGTTGTTGGGGATTTATTG
BS-220-as	ΑCCAACTAAACACCAACCTACA
BS-219-2-s	GATTTTAGGTTGGGGGTAGG
BS-219-2-as	CACAAATATCCAACCACAATTC
BS-7-2-s	AGTTGGAGTGAGTTGTGATTGT
BS-7-2-as	
D3-90-5 RS-96-35	
BS-27h-s	GGGATTTTGTTTTTAAGGGTTA
BS-27b-as	ΑζΑΑΑΤζΑΑζΑΤΑζζΑΑΑΑΑζζ
BS-126-s	TAAATAGTTTTGGTTGTGTTTGG
BS-126-as	CRTCTTCCAAAATACTACRCT
BS-193b-s	TTTGGTATTTTGGTGAGATGAA
BS-193b-as	СТАТССААААТААССССААААА
BS-193a-s	TYGTGTAATTTTTGGAGGGT
BS-193a-as	AACTITATAAACCAATTAATCCRACA
BS-218-2-S	
D3-210-2-d5 RS_/19/Lc	GAAGGTTGTTTGGATTTATGG
BS-494-as	ATCACCTCCAAAAAAATTCC
BS-192-s	TAGTTTTGGTTGGGAAAGAAAT
BS-192-as	ΑΑΑΑΤΑΤΟΟΟΑΤΑΟΟΑΟ
MSP-9-1-ms	TTTTATTTCGTTGACGGGC
MSP-9-1-mas	CCCGCCTCCTAACTACTATCG
MSP-9-1-us	TTTTTTATTTTGTTGATGGGT
MSP-9-1-uas	
MSP-9-2-ms	
MSD 0.2 up	
MSP-9-2-us MSP-9-2-uas	ζαδαδατοςτταςζαζατιτιαστι
MSP-9-3-ms	GGTGTTAGGACGTACGGAAC
MSP-9-3-mas	TACCCGAATCCTAAAACGC
MSP-9-3-us	GGTGTTAGGATGTATGGAAT
MSP-9-3-uas	TACCCAAATCCTAAAACAC
MSP-34b/c-ms	TTTAGTTACGCGTGTTGTGC
MSP-34b/c-mas	
MSP-34b/c-us	
NISP-34D/C-Uas	
17107-140d-1115 MSP-148a-mas	
MSP-148a-us	TTTTAGGGGAGGTTTTGTAAAGT

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Sequence

Primers used for cloning the flanking regions of selected miRNAs and containing BamHI and Hindill restriction sites pSIL-148a-s AAAAAGCTTCGGGGCTGGGAGCAGG pSIL-34b/c-s AAAAAGCTTCGCGGCTGGGGGCGCG pSIL-34b/c-s AAAAAGCTTCGCGGCCGGGGGCGGG Primers used for obtaining the WT or mutant (mut) target site of target genes, containing MUI and Hindill restriction sites pLUC-myc-WT-s CGCGTGAAAGTTTTGCCCATATGTGATAGCACAGG pLUC-myc-WT-s CGCGTGAAAGTTTTTGCCGGTGCTGAAAACTGCCTGAAATGT pLUC-myc-WT-s CGCGTGAAAGTTTTTGCCGCGCTGAAAACTGCCTGAAAACTGCCTGAAATGT pLUC-myc-WT-s CGCGTGAAAGTTTTTGCCGCTGGAAAACTGCCGCAGAACAAGTACTTGCGGGCAAACAGAATG pLUC-t2F3-WT-s CGCGTATAGCAATTAATTTGTAAACCTGCCAGAGAAACTTCTCA pLUC-t2F3-WT-s CGCGTATAGCAATTAAGTGGCAGGGTGAAACTGCCAGAAACTACTTCCAGCGCGCA pLUC-t2F3-WT-s CGCGTAGAAGAGTATCTGCGCGGAATACCTTCCAGGCAACAACAATTATTGCTGCATA pLUC-t2F3-WT-s CGCGTGGAACTGGGAATTCCCCCGGCGGGGTGGAAATCCTCCACAGCGCA pLUC-t2F3-WT-s CGCGTGGGAATTCCCCGGGGGAATTCCCACAGGGGGAAACCCCCA pLUC-CDKE-WT-s CGCGTGGGAATTCCCGGGGGGAAATCCCCACAGGGACAACACCCACAGGGGGAAATCCCCA pLUC-CDKE-WT-s CGCGTGGGATTTCCCCGCGGGCAATTCCGGGGGAAATCCCA pLUC-TDKE-WT-s CGCGTGGGATTTCCCCGCGGGGAAATCCCACAGACCCCA pLUC-CDKE-WT-s CGCGTGGGATTTCCCCGCGGATTGGGGGGAAATCCCA pLUC-CDKE-WT-s CGCGTGGGATTTCCCGCGGATTGGGGGGAGGAAATCCCA pLUC-TDKE-WT-s CGCGGGATTG	Primers used for cloning the flanking regions of selected miRNAs and containing BamHi and Hindill restriction sites pSIL-148a-s AAAAAGCTCCGACCGTCGGAGCACTG pSIL-34b/c-s AAAAAAGCTTCTGGCGCTCGGAGCACTG pSIL-34b/c-s AAAAAGCTTCCGACGTCGGAGCACTG pSIL-34b/c-s AAAAAGCTTCCGACTGGAGCACTG PLIC-myc-WT-s CGGCTGAAACTTTTGATGCCACAAGG PLUC-myc-WT-s CGGCTGAAACTTTTGCACCTCAAGCGCTCGATGGCAAACTGCTCCAAATA PLUC-myc-WT-s CGGCTGAAACTTTTGCACCACAGCCCTGTGGAAACTGCTCCAAATA PLUC-myc-WT-s CGGCTAAACGCATGTGGAAACTGCTCCACAGGCCTGGTGACAACTGC PLUC-myc-WT-s CGGCTAAGCAAACGTTTGCACCAGGCCTGGTGGAAACTGCCCAAATA PLUC-223-WT-s CGGCTAGGAAACGAAGCATGTGGGAAATCACTGCCCAAATAGCTGCCACAA PLUC-223-WT-s CGGCTAGGAAACGCAGGGGGAAATCACTGCCACGAAATTAGTGCCACA PLUC-223-WT-s CGGCTAGGAAACAGCAGTGGGAAATCACTGCCAGGACAA PLUC-223-WT-s CGGCTAGGAAAACAGCAGGTGGGAAATCACTGCTGGAACAC PLUC-223-WT-s CGGCTAGGAAAGCAGGTGGGAAATCACCGCGCCGCACAA PLUC-20K-WT-s CGGCTAGGAAAGCAGGAGGAAAATCCCCAAGGCCCCGCTGGAAATGGGACAA PLUC-DKF-WT-s CGGCTGGGACTTGCCCCCCGCCGGAAATCGGGGGAAAATCCCA PLUC-DKF-WT-s CGGCTGGGACTTGCCCCCCGGGGGGAAAATCCCCA PLUC-DKF-WT-s CGGCTGGGACTTGCCCCCCCCGGGGGGGGAAATCCCCA PLUC-DKF-WT-s CGGCTGGGGACTTGCCCCCCCCCGGGGGGGGGAAATCCCCA PLUC-DKF-WT-s CGGCTGGGCCCCCCCCCCCGGCTGGGGGGGGAAATCCCCA <th>MSP-148a-uas</th> <th>ΑCACAAAAACAAATATTCAAAACT</th>	MSP-148a-uas	ΑCACAAAAACAAATATTCAAAACT
psli-148a-s psli-34b/cs AAAAGGATICGGCACACACCTGCGGGAGGAG psli-34b/cs AAAAAGGTTICGCACATTGACGACGTG psli-34b/cs AAAAAGGTTICGCACATTGACGACGCG psli-34b/cs AAAAAGGTTICGCACATTGACGACGCCGGGAGGAGTG psli-34b/cs AAAAAGGTTICGCACATTGACGATCACACGG psli-34b/cs AGCTATTGAGGCATAATGTAAACTGCCTCAAATG pLUC-myc-WT-s CGCGTGAAAGATTTGACGATAAGGCCTAAATGTAAACTGCCTCAAATG pLUC-myc-WT-s CGCGTGAAAGATTTGACGCATAAGGCCTGAGGAAACTAATG pLUC-myc-WT-s CGCGTGAAAGATTTGACGCTGAGGCAAACTAATGT pLUC-myc-WT-s CGCGTGAAAGATTTTGCCACAGGCCTGTGGAAAACTAATG pLUC-g273-WT-s CGCGTAAGAAATTTTGTACGCACGCGCGAGAAACTAATG pLUC-g273-WT-s CGCGTAAGAAATTTTGTACGCACGGCGAGGAAAATTAATT	psl.148a-s; AAAAGGATCGAACACCTGCAGGAAGAA psl.148a-s; AAAAAGCTTGCGGCGCTGGAGCACTG psl.34br-s; AAAAAGCTTGCGGCGCTGGGAGCACG psl.34br-s; AAAAAGCTTGCGGACGTCGGGAGCAGG psl.34br-s; AAAAAGCTTGCGCACTTGATGATGCACGG psl.34br-s; CGGGTGAAAGATTTAGCCACATGGTAAACTGCTCAAATA pulc-mye-WT-s; CGGGTGAAAGATTTAGCCACATGGAAACACTGCT pulc-mye-WT-s; CGGGTGAAAGATTTAGCCACAAGGCCGTGGAAAAATTA pulc-mye-WT-s; CGGGTGAAGATTTAGGCGAGTGAAAACTTCCA pulc-gr3WT-s; CGGGTAAGATTATTGGTGACAAGGCCGTGGAAAAATTA pulc-gr3WT-s; CGGGTAAGGATTAATTGGTGAAAACATTGCCACAAATGA pulc-gr3WT-s; CGGGTAAGGATTAATTGTTGGCAAAAAATTAATTGGTATA pulc-gr3WT-s; CGGGTAAGGATTAATTGTTGGCAAAAAATTGCTATA pulc-gr3WT-s; CGGGTAAGGATTAATTGTTGGCAGAAAAATTGCTATA pulc-gr3WT-s; CGGGTAAGGATTAATTGTTGGGAAATACATTTGCGCGAAA pulc-QDK-WT-s; CGGGTAAGGATTAATTGTGGGAAATACATTGCGGGAAAA pulc-QDK-WT-s; CGGTAAGAAGACGGTGGAAAACATGCTGGGAAAAACTTCTGCAGGA pulc-QDK-WT-s; CGGTAAGAAGACGGTGGAAATGCGTGGAAATACTTCTGCAGGAAA pulc-QDK-WT-s; CGGTAAGAAGACGGTGGAAATCCCCCCGTGGACAA pulc-QDK-WT-s; CGGTGAGAGAGCGTGGAATTCCCCCGCGGACAA pulc-QDK-WT-s; CGGTGGGGAGTTCCCCCCCCCAGAGCCAATGGGGAAA pulc-GDK-WT-s; CGGTGGGGGAGTTCCCCCCCCCCAGGGCCAATGGGGAAA pulc-GDK-WT-s; CGGTGGGGGACTGCGAGAAGCGGGAAAATCCCCA pulc-GTGF2-WT-s; CGGTGGGGGGGTGGGGGGGGGGAAATCCCCA pulc-GTGF2-WT-s; CGGTGGGGGGGTGGGGGGGGGGGGGGGGGGGGGGGGGG	Primers used for cloning the flanking r	egions of selected miRNAs and containing BamHI and HindIII restriction sites
pSIL-148a-as AAAAAAGCTTCTGGCGTTTGGACACTG pSIL-34b/c-s AAAAAAGCTTCGACGGCGTCGGGGGG pSIL-34b/c-s AAAAAAGCTTCGACATGATGACGGCG pSIL-34b/c-s AAAAAAGCTTCGACATGATGACGCACAGG Primers used for obtaining the WT or mutant (mult) target site of target genes, containing Milu and Hindlll restriction sites pLUC-myc-WT-s CGCGTGAAAGATTTTGCACATGGCACAAGGACAATA pLUC-myc-WT-s CGCGTGAAAGATTTTGCCATAAGGCCTTGATGGCAAACAAA	pSIL-148a-as pSIL-34b/cs pSIL-	pSII -148a-s	ΑΑΑΑGGATCCGAACACACCTGCAGGAAGAA
pSII-34b/c-s AAAAGCATCCGGACCGTCCGGGAGCTG pSII-34b/c-s AAAAAGCATCCGGACCGTCCGGGAGCTG pSII-34b/c-s AAAAGCATCCGGACCGTCCGGGAGCTG pSII-34b/c-s Catalong the WT or mutant (mut) target site of target genes, containing Mlul and Hindill restriction sites pLUC-myc-WT-s CGCGTGAAAGCTTTAGCCATAATGAAACGTCGCCAAATA pLUC-myc-WT-s AAGCTTATTTGAGGCAGGTTTAGCGCAAAACATA pLUC-myc-mut-s CGCGTGAAAGCTTTGCCACAAGGGCCTGGGAAAACATTA pLUC-myc-mut-s AGCTTATTTGTTTGCCATCAAGGCCTGGGAAAACATTAC pLUC-223-WT-s CGCGTAAGGAAGCTATACTTGGCAGTGTACAAATTATTGTGAAA pLUC-223-WT-s CGCGTAAGGAAGCAGTGGGGAAAACCTTCCCGAGAATACTTTCGTCATA pLUC-223-WT-s CGCGTAAGGAAGCAGTGTGGAAACCATGCCAGAAATAATTGCTATA pLUC-223-WT-s CGCGTAAGGAAGCAGTGTGGAAATTCATGCGCGGGGACAA pLUC-223-WT-s CGCGTAAGAAGCAGTGTGGAAATTCATGCGCGGGGACAA pLUC-2056-WT-s CGCGTAAGAAGCAGTGTGGAAATTCACGGCGCGGGACAA pLUC-CDK6-WT-s CGCGTAAGAAGCAGTGTGGAAATTCACGGCGCGGGACAA pLUC-CDK6-WT-s CGCGTGAGAAGCAGTGTGGGAATTCCACACTGGTTCTA pLUC-CDK6-WT-s CGCGTGAGAAGCAGTGTGGGAACTCCCACACTGGTGCTA pLUC-CDK6-WT-s CGCGTGAGAAGCAGTGTGGGAACTCCCACACTGGTGCTTA pLUC-CDK6-WT-s CGCGTGAGAATTCCCACACTGGCGGGAGAAATCCCA pLUC-CDK6-WT-s CGCGTGGGATTTCCCCCCCACAGTGCGGGGAGAAATCCCA pLUC-TGIF2-WT-s CGCGTGGGATTTCCCCCCCACAGTGCGGGGAGAAATCCCA pLUC-TGIF2-WT-s CGCGTGGGATTTCCCTCCCCACAGTGGGGGAGAAATCCCA pLUC-TGIF2-WT-s CGCGTGGGATTTCCCTCCCCACAGTGGGGGAGAAATCCCA pLUC-TGIF2-WT-s CGCGTGGGATTTCCCTCCCCACAGTGGGGGAGAAATCCCA pLUC-TGIF2-WT-S CGCGTGGAATTCCCCCCCACAGTGGGGAAATCCCA pLUC-TGIF2-WT-S CGCGTGGAAGTGGAGTTG miR-91-GSP1 AAGGGACACGAGTGGAGTG miR-91-GSP1 CCGCACGACGGAGAGAAA miR-92-GSP3 CGGCTAAAACATCCAAGGA miR-92-GSP3 CGGCTAAAACATCCAAGGA miR-93-GSP3 CGGCTAAAACATCCAAGGA miR-93-GSP3 CGGCTAAAACATCCAAGGA miR-93-GSP3 CGGCTAGACACCACAC miR-93-GSP3 CGGCTAGACACCACACACACACACACACACACACACACAC	pSIL:33bics AAAAGCATTCGGGACGTTCGGGACGTG pSIL:34bics AAAAAGCTTCGCACATTGATGCACAGG pSIL:34bics AAAAAGCTTCGCACATTGATGCACAGG pSIL:34bics AAAAAGCTTCGCACATTGATGCACAGG pSIL:34bics ACGTATTTTGGCACATTGATGTAAATGCTCAAATA pLUC-myc-WT-s CGGTGAAAGATTTAGCCATAAGTGCTGAAATA pLUC-myc-WT-s AGGTTATTTTGAGGCAGTTACAAGGCTGTGAAAAACATTCCCCAAAATA pLUC-myc-WT-s AGGTTATTTTTGAGCGACATAATTGGTGAAAAACTTCCA pLUC-g23-WT-s CGGTAAAGATTAATTGTTGGAGAATAATTGGAGAAACTTTCA pLUC-g23-WT-s CGGTAAGCATTAAGCATTAATTGGAGAAAACTTTCA pLUC-g23-WT-s CGGTAAGCATAATTGTTGGAGAGAAAACTTTCA pLUC-g23-WT-s CGGTAAGAAGCAGTGGGAAATAATTGGGAGAAAACTTTCA pLUC-g23-WT-s CGGTAAGAAGCAGTGGGAAATAATTGGGAGAAAACTTTCA pLUC-g23-WT-s CGGTAAGAAGCAGTGGGAAATAATTGGGAGAAAACTTCACGCGGACAA pLUC-DK6-WT-s CGGTAAGAAGCAGTGGGAAATCACTGGCGGACAA pLUC-DK6-WT-s CGGTAAGAAGCAGTGGGAGAATCGGGGACAA pLUC-DK6-WT-s CGGTGAAGGATTCCCCACAGTCGAGCAATCGGGAGAAACCCCA pLUC-DK6-WT-s CGGTGAGGGTTGACCCCCCCCCACAGATCGGGGACAATCCCA pLUC-TGF2-WT-s CGGTGAGGGTGAAGGAGGAGAAAACCCCA pLUC-TGF2-WT-s CGGTGAGGGTGAAGGAGGAGAAAA pLUC-TGF2-WT-s CGGTGAGGGTGAAGGAGGAGAAAA pLUC-TGF2-WT-s CGGTGAGGTGAAGAGGAGGAGAAAA pLUC-TGF2-WT-s CGGTGAGGTGAAG	pSIL-148a-as	AAAAAGCTTCTGGCGTCTGGAGCACTG
psll-34b/c-as AAAAAAGCTTGCACATTGATGATGCACAGG Primers used for obtaining the WT or mutant (mut) target site of target genes, containing Mlul and Hindlll restriction sites plUC-myc-WT-s CGGGTGAAAGATTTAGCTATAATGCAAAATGCTCCAAATA plUC-myc-WT-s AGCTTATTTGCAGCAGCGCTTGAAAAACTTTCA plUC-myc-WT-s CGGGTAGAGATTTAGCCATAATGGCCAGAAACAAATA plUC-myc-mut-s AGCTTATTTGCAGCTAGAAGAACGATTTGCAGAAACAAATA plUC-t2F3-WT-s CGGGTATAGCAATAATTTGTGCAGCAGGCAGGAAAACAATTAATT	pSIL-34b/c-as AAAAAAGCTTIGCACATIGATGCACAGG Primers used for obtaining the WT or mutant (mut) target site of target genes, containing Mlul and Hindli restriction sites pLUC-myc-WT-s CGCGTGAAAGATTTAGCCATAATGTGCACAACTGCCTCAAATA pLUC-myc-WT-s AGCTTATTTGAGGCAGTTTACATTATGGCTAAACTTCTC pLUC-myc-WT-s CGCGTGAAAGATTTGCCACGAGCACGCAACAAATA pLUC-myc-mut-s AGCTTATTGTGCACATGGCACACGCAACGAAATA pLUC-E2F3-WT-s CGCGTAAAGAATTTGTGCCACGCAGCAACGAATTCACGCCAGAATACATTCGCACGACGAACGA	pSIL-34b/c-s	AAAAGGATCCGGACCGTCCGGGAGCTG
Primers used for obtaining the WT or mutant (mut) target site of target genes, containing Mlul and Hindill restriction sites PLUC-my-WT-3 CGCGTGAAAGATTAGCCATAATGTAAACTGCTCAAATA PLUC-my-WT-3s AGCTTATTTGAGCAGTTTAAATTAGGCAAAAATA PLUC-my-mut-s CGCGTGAAAGATTATTGGCGAAACAATA PLUC-gt3-WT-3s CGCGTGAAAGCATTAATTGGCAGAAACAAATA PLUC-E2F3-WT-3s CGCGTAAGCAATAATTGTGAAACACTGGCAAAAATAATTGGTGATA PLUC-E2F3-WT-3s CGCGTAAGCAACTAATTGTGGCAGTGTGAAAATTTGGCAGTGTGAAAATTTGGTAATA PLUC-E2F3-WT-3s CGCGTAAGCAAGCAGTGGGAAATTCAATGCGGGAGGAAACAATTAATT	Primers used for obtaining the WT or mutant (mut) target site of target genes, containing MIU and HindIII restriction sites PUC-myc-WT-3 CGCGTGAAASATTTAGCCATAATGTAAACTGCCTCAAATG PUC-myc-WT-35 AGCTTATTTGAGCGACATTAATGTGAAACTGCCTCAAATG PUC-myc-mut-3 AGCTTATTTGAGCGACATCAAGGCCTTGAGAAACAAATA PUC-E2F3-WT-5 CGCGTATAGCAATTAATTTGTTGACCACGGAGTGAAAACTTCTCA PUC-E2F3-WT-5 CGCGTATAGCAATTAATTTGTTGAAACTGCCCAGAGATACTTTCTAGCTGCA PUC-E2F3-WT-5 CGCGTAAGAAGTATCTGCACGAGGGATTACATACTTGCTAGCTGCA PUC-E2F3-mut-3 AGCTTGCAGCTGAAAAGTATCTGCCAGGGAATACCTTTCTAGCTGCA PUC-E2F3-mut-3 CGCGTAGAAAGTATCTGCCAGGGAATACATTCTCAGCTGCAA PUC-CDKF-WT-3 CGCGTAGAAAGGAGTGGAAATTCCCACAGCGACAA PUC-CDKF-WT-3 CGCGTGGAATTGGGGGAATCCCACCACGACAA PUC-CDKF-WT-3 AGCTTCGCAGGCAGTGGAAATTCCACACTGCTCTA PUC-CDKF-WT-3 AGCTTCCATGCCCCGATTCCGTGGGAAGGCAAAATCCCA PUC-CDKF-WT-3 AGCTTCCATTGCCCCGATTCGTGGGGAGGGAAAATCCCA PUC-TGF2-WT-3 AGCTTCCATTGCCCCGATTCGTGGGGAGGGAAAATCCCA PUC-TGF2-WT-3 AGCTTCCATTGCCCCGGATTCGTGGGGAGGGAAAATCCCA PUC-TGF2-WT-3 AGCTTCCATTGCCCGGATTCGTGGGGAGGGAAAATCCCA PUC-TGF2-WT-3 AGCTTCCATTGCCGGATTCGTGGGGAGGGAAAATCCCA PUC-TGF2-WT-3 AGCTCCCATGCCCGATTCGTGGGGAGGGAAAATCCCA PUC-TGF2-WT-3 AGCGCGCATGCCCGATTCGTGGGGAGGGAAAATCCCA PUC-TGF2-WT-3 AGCGCGCATGCCAAGACACGGGGG	pSIL-34b/c-as	AAAAAGCTTGCACATTGATGATGCACAGG
pLUC-myc-WT-sCGCGTGAAAGATTTAGCCATAATGTGAAACTGCCTCAAATApLUC-myc-WT-ssAGCTTATTTGAGCGCATTACATTATGCTCAAATApLUC-myc-mut-sCGCGTAAGCATTAATTGTTGCCATCAAGCCTTGATGAAAACATTApLUC-E2F3-WT-sCGCGTATAGCAATTAATTTGTAAACACTGCCAAAATAATTCTTCAGCTGCApLUC-E2F3-WT-ssAGCTTGCAGCTAGAAAGATTAATTGTGAAAACACTGCAGAAATACTTTCTAGCTGCApLUC-E2F3-WT-ssCGCGTATAGCAATTAATTGTGAAAACTACTTCAGCAAAATTAATT	pLUC-myc-WT-sCGCGTGAAAGATTAGCCATAATGTAAACTGCCTCAAATApLUC-myc-WT-asAGCTTATTGAGGCAGATTAGCCATAAAGATTApLUC-myc-Wt-asAGCTTATTGAGGCAGAGCCTAGAAAGAATApLUC-t2P3-WT-sCGCGTAAGAAAGTATTTGTACCACTGCCAGAATGACTTCACpLUC-t2P3-WT-sAGCTTAGCAATTAAGCAATTAATTGGACAACTGCAGAAATAATTGTGTAGAATTAATT	Primers used for obtaining the WT or mut	ant (mut) target site of target genes, containing Mlul and HindIII restriction sites
pLUC-myc.WT-as AGCTTATTGAGGCAGTTACATTATGGCTAAATCTTTC pLUC-myc.mut-s CGCGTGAAAGTTTTTCACAGGCCTTGAGAAACAAATA pLUC-myc.mut-as AGCTTATTGATTGTTTCCACAGGCGCTGAAAACATTCA pLUC-E2F3-WT-s CGCGTATAGCAATTAATTTGCAACAGGCCAGGCAAATTCATTC	pLUC-myc-WT-as AGCTTATTGAGGCAGTTTACATTATGGCTAAATGTTTC pLUC-myc-mut-as AGCTTATTGGTTGACAGGCCTGTGAAAAACTTTCA pLUC-t2F3-WT-s CGCGTATAGCAATTAATTGTGAAACACTGCCAGAATAATTTCAGCTGGCA pLUC-t2F3-WT-s AGCTTATTGGTTGCCAGCAGAAGAAGTATTCCAGCGCAGAATACTTTCAGCTGCA pLUC-t2F3-WT-s CGCGTATAGCAATTAATTGTGGAAGAAGTAATTCATGCCAGAATTAATT	pLUC-mvc-WT-s	CGCGTGAAAGATTTAGCCATAATGTAAACTGCCTCAAATA
pLUC-myc-mut-sCGCGTGAAAGTTTTCACAGGCCTGTGGGAAACAATApLUC-myc-mut-asAGCTTATTGTTGCCATCAAGGCCTGTGAAAAACTTTCApLUC-E2F3-WT-sCGCGTATAGCAATTAATTGTGAAACACTGCCAGAATACTTTCTAGCTGCApLUC-E2F3-WT-sCGCGTATGCAGCTAGAAAGTATTCTGCCAGTAAAATCTTTCAGCTGCApLUC-E2F3-Wt-sCGCGTAAGAAGTATTCTGGCTAGTTAATCGGTGAATACTTTCTGGCAATAATTGTGTAAATGGGCAAATCATCAGCTGAGpLUC-E2F3-wt-sAGCTTGCCAGCTAGAAAGTATTCCGCTAGTAAATACTGGTCAACAApLUC-E2F3-wt-sCGCGTAAGAAGTGTGGAAATTCCACGCGGGACAApLUC-E2F3-wt-sCGCGTAAGAAGCAGTGGGAATTCCACGCGCGGACAApLUC-CDK6-WT-sCGCGTAAGAAGCAGTGGGAATTCCACACTGCTTCTApLUC-CDK6-WT-sCGCGTGGGATTTCCCCCCCACAGTGGAATCCACACTGCTTCTApLUC-CDK6-WT-sCGCGTGGGATTTCCCCCCCACAGTGGAATCCACACTGGCACAApLUC-CDK6-WT-sCGCGTGGGATTTTCCCTCCCCACAGTGCACTGGACAATGGApLUC-TGIF2-WT-sCGCGTGGGATTTTCCCTCCCCACAGTGCACTGGACAATGGApLUC-TGIF2-WT-sCGCGTGGGATTTTCCCTCCCCACAGTGGCACTGGACAATGGApLUC-TGIF2-WT-sCGCGTGGGATTTTCCCTCCCCACAGAATCGGGGGAGGAAAATCCCApLUC-TGIF2-WT-sCGCGTGGGAGTGAAGAGCAAApLUC-TGIF2-WT-sCGCGGGAGGCGCCCCATTGGCACTGTGGGAGGAGAAATCCCApLUC-TGIF2-WT-sCGGGAGGGCGCGCATCCATGGCACCCAACGACAmiR-91-GSP1AAGGGACCCGATGGCAGAAAACGGGCATGGAmiR-91-GSP1AAGGGACACGACGGAAAAGGGmiR-91-GSP1CAGGGACGGCAGAAAAGGGmiR-92-GSP2CGGCAGGAGCACCCAACAGAAAAGGGmiR-92-GSP3CGGCAGGACACGACAAAAGGGmiR-92-GSP3CGGCAGGGCATCCAAGGAmiR-93-GSP1GAGGGGATGGACCCCATCCAACGAAAATCGGGTmiR-94-GSP2CGGCAGGGCATCCCTGGTmiR-94-GSP2CGGCAGAGACACCCCCTT	ILUC-mycmut-sCGCGTGAAGAGTTTTCACAGGCCTTGATGGCAACAAACTAPLUC-mycmut-ssAGCTTATTTGTTGCCATGAGCCTGGAAAACATTCAPLUC-E2F3-WT-sCGCGTATAGCAATTAATTGTAAACACTGCCAGAATTATTGTGATAPLUC-E2F3-WT-sCGCGTATAGCAATTAATTGGCAGTGTTACAAATTAATTGGTATAPLUC-E2F3-WT-sCGCGTAGAGAAGCAGTGGGAAATTCATGCTGGGAGGGCAAPLUC-E2F3-WT-sCGCGTAGGAAGTATTCATCCGTGGGAACGCAATTAATTGGTATAPLUC-EXF-WT-sCGCGTAGAAGAGCAGTGGGAATTCCAACAATTAATTGGTATAPLUC-CDK6-WT-sCGCGTAGAAGAGCAGTGGGAATTCCAACAATTCAATGCGTGGGAAGPLUC-CDK6-WT-sCGCGTAGAAGAGCAGTGGGAATTCCCACGCGGGGCAAPLUC-CDK6-mut-sAGCTTTGTCCCCGATTCCCAGGCAGTGGGAAGGGGAAATCCGAPLUC-CDK6-mut-sCGCGTGGGATTTCCCAGGCGGGGGGGGAAATCCCAPLUC-TGIF2-WT-sCGCGTGGGGAGTTTCCCAGTGCCTGGGGGGGGGGAAATCCAPLUC-TGIF2-WT-sCGCGTGGGGAGTTGCCCGATTCTGGGGGGGGGGGAAATCCCAPLUC-TGIF2-WT-sCGCGTGGGGGGGGGGGGGGGGGGGGGAAATCCCAPLUC-TGIF2-WT-sCGCGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	pLUC-myc-WT-as	AGCTTATTTGAGGCAGTTTACATTATGGCTAAATCTTTC
pLUC-myc-mut-asAGCTTATTTGTTTGCCATCAAGGCCTGGAAAAACTTTCApLUC-E2F3-WT-sCGCGTATAGCAATTAATTTGTAATACACTGCCAGAATAATTTATTGCTATApLUC-E2F3-WT-sAGCTTGCAGCTAGAAAGTATTCTGGAGTGTTTAACAAATTAATT	pLUC-Epris-WT-sCGCGTATAGCATTAATTGTAAACACTGCCAGAAAACTTTCApLUC-E2F3-WT-sCGCGTATAGCAATTAATTTGTAAACACTGCCAGAATTAATT	pLUC-myc-mut-s	CGCGTGAAAGTTTTTCACAGGCCTTGATGGCAAACAAATA
pLUC-E2F3-WT-sCGCGTATAGCAATTAATTTGTAAACAGTGCCAGCAATAACTTTCAGCTGCApLUC-E2F3-WT-sAGCTTGCAGCTAGAAAGTAATTCTGCGAGTGTTACAAATTAATT	PLUC-E2F3-WT-sCGCGTATAGCAATTAATTTGTAAACACTGCCAGAATACTTTCTAGCTGCAPLUC-E2F3-mut-sCGCGTATAGCAAAGTATTCTGTGCAGTAGCAAAGTATTCATGCGCAGGAATTAATT	pLUC-myc-mut-as	AGCTTATTTGTTTGCCATCAAGGCCTGTGAAAAACTTTCA
pLUC-E2F3-WT-asAGCTTGCAGCTAGAAAGTATTCTGGCAGTGTTTACAAATTAATT	PLUC-E2F3-WT-asAGCTTGCAGCTAGAAAGTATTCTGCGCAGTTAATGCTTATAATTGCTATAPLUC-E2F3-mut-asAGCTTGCAGCTAGAAAGTATTCTGCAGTAATACTTGTCAGCTGCAPLUC-E2F3-mut-asAGCTTGCAGGCAGGAATTCATCCCCGTGCGACAAPLUC-CDK6-WT-asCGCGTAAGCAAGCAGTGGGAATTCCACACTGCTTCTAPLUC-CDK6-mut-sCGCGTGGGATTGCACGCAGTGGATTCCACACTGCTCTTAPLUC-CDK6-mut-sCGCGTGGGATTTCCCCCCCACAGTGCGACTGGACAATCGAGGAATGACTCTGAPLUC-CDK6-mut-sCGCGTGGGATTTTCCCTCCCCCACAGTGCGACTGGAGCAAPLUC-TGIF2-WT-sCGCGTGGGATTTTCCCTCCCCACAGTGCACTGGGGAATGGAPLUC-TGIF2-WT-sCGCGTGGGATTTTCCCTCCCCACAGTGCGACTGGAGCAATGGAPLUC-TGIF2-mut-sCGCGTGGGATTTTCCCTCCCCACAGTGGGAGGAAAATCCCAPLUC-TGIF2-mut-sCGGGAAGGCGGAAGAGCAmiR-9-1-GSP1AAGGGACACGAGTGGAGTGmiR-9-1-GSP1AAGGGACACGAGTGGAGTGGAAGGAGAAAmiR-9-1-GSP1AAGGGACACGAGTGGAAGAGAAAmiR-9-1-GSP1AAGGGACACGAGTGGAAGAGAAAmiR-9-1-GSP1CGGCTAAGACGGCGAAAAGGmiR-9-1-GSP2GGGGAAGGCGGAAAAGGGmiR-9-1-GSP3CGGCTAAGACGGCGAAAAGGGmiR-9-1-GSP4CGGCTAAGACACCGAATGGAmiR-9-2-GSP2TACTTGGCCGCTAAACAGGAmiR-9-3-GSP3CGGCTAAGACGGCCCCCTTAGmiR-9-3-GSP3CGGCAATGGACAGCACACmiR-94-GSP3CTCCTTCCTCCTCCTCCTmiR-94-GSP3CGGCAATGGACGACACACmiR-94-GSP3CTCCTGCCCGCCCTTAGmiR-94-GSP3CGGCAATGGACGACACACmiR-94-GSP3CGGCAACGGGATGGACAGACACCmiR-94-GSP3CGGCAACAGCACCACCACCACCchip-miR-9-1-SGGGCACGGGGATGGACAGACACACchip-miR-9-1-SGGGCACGGGGATGGACAGACACAC<	pLUC-E2F3-WT-s	CGCGTATAGCAATTAATTTGTAAACACTGCCAGAATACTTTCTAGCTGCA
pLUC-E2F3-mut-asCGCGTATAGCAATTAATTGGTGAAATTAATTGGAGAATACTTTCTCACACAAAATTAATT	PLUC-E2F3-mut-s CGCGTATAGCAATTAATTGCTGACAAATTAATTGCTGACAAATTAATT	pLUC-E2F3-WT-as	AGCTTGCAGCTAGAAAGTATTCTGGCAGTGTTTACAAATTAATT
pLUC-E2F3-mut-asAGCTTGCAGCTAGAAAGTATTCCCACTATAACAACAAATTAATT	PLUC-E2F3-mut-as AGCTTGCAGCTAGAAAGTATTCTCCATTAATCAACAAATTAATT	pLUC-E2F3-mut-s	CGCGTATAGCAATTAATTTGTTGATTAATGGAGAATACTTTCTAGCTGCA
pLUC-CDK6-WT-s CGCGTAAGAAGCAGTGTGGGAAATTCACTGCTGGGACAA pLUC-CDK6-mut-s CGCGTAAGAAGCAGTGTGGATTCCAGGACTGTA pLUC-CDK6-mut-s CGCGTAAGAAGCAGTGTGGATTCCAGGACATGGGACAA pLUC-CDK6-mut-s CGCGTGGGATTTCCAGGACACACTGACTTCTA pLUC-CDK6-mut-s CGCGTGGGATTTCCAGGGACCACACGTGGGACGAAATCCCA pLUC-TGIF2-WT-s CGCGTGGGATTTTCCATGCACAGAATCGGGGGGAAATCCCA pLUC-TGIF2-mut-s CGCGTGGGATTTTCCATGGCACAGAATCGGGGGACAATGGA pLUC-TGIF2-mut-s CGCGTAGGACACGAGTGGGAGAAAATCCCA pLUC-TGIF2-mut-s CGGCGAGGGGAAGAGACGAGGGGGAAAATCCCA gene-specific primers (GSPs) used for 5' RACE analyses GGGGACGGGAAGGGGAAGAGACGAAGAAGAGA miR-9-1-GSP1 AAGGGACACGAAGTCCAGAGTC miR-9-1-GSP2 GGGGAAGACCGAAGACCGAAAAAAGG miR-9-2-GSP1 CTCTTGCCAGACTCCAAGAA miR-9-2-GSP2 TACTTGCCGCGCTAAAACAGGA miR-9-2-GSP3 CGGCTAAAACATCCAAACGA miR-9-3-GSP3 GAGGGGATGGACAGAACACA miR-9-3-GSP3 CGAGCAATCATGGT miR-148a-GSP1 ACCAAACGGCTGTCTTAG miR-148a-GSP1 CCCAAATCATGGTGT miR-93-GSP3 GAGGGATGACACACAC miR-94a-GSP2 CCGATTCACCGTCTCT miR-148a-GSP3 CTTCCTTCCCCCTATGGT <td>pLUC-CDK6-WT-s CGCGTAAGAAGCAGTGTGGGAATTCCATGCCTGGGACAA pLUC-CDK6-mut-s AGCTTTGTCCCCGAGGCAGTGAATTTCCACACTGGCTTCTTA pLUC-CDK6-mut-s AGCTTTGTCCCCCGATTTCCAGGACTCACACTGGCTTCTA pLUC-TGIF2-WT-s CGCGTGGGATTTTCCCTCCCACAGTGGCACTGAGCAATTGACACATGGA pLUC-TGIF2-WT-s CGCGTGGGATTTTCCCTCCCCACAGTGGCACTGAGCAATTGACACTGA pLUC-TGIF2-WT-s CGCGTGGGATTTGCCTCCCCACAGGGAGGAAAATCCCA pLUC-TGIF2-WT-s CGCGTGGGAGTGGAAGAGGGGGAGGAAAATCCCA pLUC-TGIF2-WT-s AGGTTCCATTGCCCCCACATTGTGTGGGGAGGGAAAATCCCA pLUC-TGIF2-WT-s AGGTCACGGGGATTGGCAGGGGGAGGAAAATCCCA pLUC-TGIF2-WT-s AGGGGGAGGGGAAGAGGGGAGAGAA miR-91-GSP1 AAGGGACAGGAGGGGGAGAGAAA miR-91-GSP2 GGGGAAGGGGGAAAAAGGG miR-91-GSP3 ACGACAGAGACCGAAAAAGG miR-92-GSP3 CGGCTAAAACATCCAAGGT miR-93-GSP2 AGAAACGGGCCTTCCTTAG miR-93-GSP3 GAGGGATGGACAGACACACA miR-148a-GSP1 ACGACACGACACACACAC miR-148a-GSP1 CCGATTCGACCCGTTCCT miR-148a-GSP2 CCGATTCGACCCGTTTCAC miR-148a-GSP3 CTCGGACCGGAATTCATCGGT miR-148a-GSP3 CTCGGACCGTGTCTCCT miR-148a-GSP3 CTCGGACCCCCATTTCAC <!--</td--><td>pLUC-E2F3-mut-as</td><td>AGCTTGCAGCTAGAAAGTATTCTCCATTAATCAACAAATTAATT</td></td>	pLUC-CDK6-WT-s CGCGTAAGAAGCAGTGTGGGAATTCCATGCCTGGGACAA pLUC-CDK6-mut-s AGCTTTGTCCCCGAGGCAGTGAATTTCCACACTGGCTTCTTA pLUC-CDK6-mut-s AGCTTTGTCCCCCGATTTCCAGGACTCACACTGGCTTCTA pLUC-TGIF2-WT-s CGCGTGGGATTTTCCCTCCCACAGTGGCACTGAGCAATTGACACATGGA pLUC-TGIF2-WT-s CGCGTGGGATTTTCCCTCCCCACAGTGGCACTGAGCAATTGACACTGA pLUC-TGIF2-WT-s CGCGTGGGATTTGCCTCCCCACAGGGAGGAAAATCCCA pLUC-TGIF2-WT-s CGCGTGGGAGTGGAAGAGGGGGAGGAAAATCCCA pLUC-TGIF2-WT-s AGGTTCCATTGCCCCCACATTGTGTGGGGAGGGAAAATCCCA pLUC-TGIF2-WT-s AGGTCACGGGGATTGGCAGGGGGAGGAAAATCCCA pLUC-TGIF2-WT-s AGGGGGAGGGGAAGAGGGGAGAGAA miR-91-GSP1 AAGGGACAGGAGGGGGAGAGAAA miR-91-GSP2 GGGGAAGGGGGAAAAAGGG miR-91-GSP3 ACGACAGAGACCGAAAAAGG miR-92-GSP3 CGGCTAAAACATCCAAGGT miR-93-GSP2 AGAAACGGGCCTTCCTTAG miR-93-GSP3 GAGGGATGGACAGACACACA miR-148a-GSP1 ACGACACGACACACACAC miR-148a-GSP1 CCGATTCGACCCGTTCCT miR-148a-GSP2 CCGATTCGACCCGTTTCAC miR-148a-GSP3 CTCGGACCGGAATTCATCGGT miR-148a-GSP3 CTCGGACCGTGTCTCCT miR-148a-GSP3 CTCGGACCCCCATTTCAC </td <td>pLUC-E2F3-mut-as</td> <td>AGCTTGCAGCTAGAAAGTATTCTCCATTAATCAACAAATTAATT</td>	pLUC-E2F3-mut-as	AGCTTGCAGCTAGAAAGTATTCTCCATTAATCAACAAATTAATT
pLUC-CDK6-WT-as AGCTTTGTCCCAGGCAGTGAGTTTCCACACTGCTTCTTA pLUC-CDK6-mut-as CGCGTAGAGAGCGTGGGATCCTGGAAATCGGGGGACAA pLUC-CDK6-mut-as AGCTTTGTCCCCAGGTCCACAGTGCACTGAGCAATGGA pLUC-TGIF2-WT-s CGCGTGGGATTTTCCCTCCCCACAGGGACAGTCGA pLUC-TGIF2-mut-s CGCGTGGGATTTTCCCTCCCCACAGGGAAATCCCA pLUC-TGIF2-mut-s CGCGTGGGATTTCCCTCCCCACAGGGACAGTGGA pLUC-TGIF2-mut-s CGCGTGGGAGTGGAGTTG miR-91-GSP1 AAGGGCACAGGGGGAGAGACGGAAAATCCCA miR-91-GSP2 GGGGAGGGGAAAACCGAAAGGG miR-91-GSP3 ACGACAGAGGTGAAAGAGAAA miR-92-GSP1 CTCTTGCCAGGCTCAAGGAGTG miR-92-GSP1 CGCTTGTGGCACTCAAACG miR-92-GSP2 TACTTGCCGGCGTTAAGAGTT miR-93-GSP1 GGCTCTGTGGCACTCAAACA miR-93-GSP2 AGAAACGGCCTCCTTAG miR-93-GSP3 GGGGAGAGCAGCACACA miR-148a-GSP3 CTTCGTCCCCTTAG miR-148a-GSP3 CTTCGTCCCCCTTAG miR-148a-GSP3 CTCGGATCCAGCCCCCTTAG miR-148a-GSP3 CTCGGACCCCATTCCC miR-148a-GSP3 CTCGGACCCCATTCGGC miR-148a-GSP3 CTCGGGCACCCCATTCGCC miR-148a-GSP3 CTCGGGCATCCACCCCCCCCCC	pLUC-CDK6-WT-as AGCTTTGTCCCAGGCAGTGAATTCCCACACTGCTTCTTA pLUC-CDK6-mut-as CGCGTAGACAGCAGTGGGATCCTGGGAAATCGGGGGACAA pLUC-CTGIP2-WT-s CGCGTGGGATTTTCCCTCCCACACTGGTGGAAAATCCCA pLUC-TGIP2-WT-s CGCGTGGGATTTTCCCTCCCCACAGTGGGAGAGAAATCCCA pLUC-TGIP2-WT-s CGCGTGGGATTTTCCCTCCCCACAGAGGGGAAAATCCCA pLUC-TGIP2-mut-s CGCGTGGGACTTGCCCCCGGATTGCGGGGGGGAAAATCCCA rgene-specific primers (GSPs) used for S' RACE analyses miR-9-1-GSP3 miR-9-1-GSP1 AAGGGACACGAGTGAAGAGAAAA miR-9-1-GSP3 ACGACAGAGACCGAAAAAAGG miR-9-2-GSP1 CTCTTGCCAGACTCCAAGGT miR-9-2-GSP3 CGGCTAAAACACCAAAGG miR-9-3-GSP3 GGGCTCCTGTGGCACTCATACA miR-9-3-GSP3 GAGGGAATGGACAGACACACA miR-9-3-GSP3 GAGGGAATGGACAGACACACAC miR-9-3-GSP3 GAGGGAATGGACAGACACACAC miR-148a-GSP3 CTCCTTCCTGTGCGCCTCTAG miR-148a-GSP3 CTCCTTCCTCCCCCTTCC miR-9-1-S CTGCGACCCACATTCCC miR-9-1-S CTGCGCACCCACTTCCC miR-9-1-S TGCCCTCCCTCCTCCTCC miR-9-1-S CGCCCACACACACACACACACACACACACACACACACAC	pLUC-CDK6-WT-s	CGCGTAAGAAGCAGTGTGGAAATTCACTGCCTGGGACAA
pLUC-CDK6-mut-sCGCGTAAGAAGCAGTGTGGAATCCTGGAAATCGGGGACAApLUC-CDK6-mut-asAGCTTTGCCCGGATTTCCAGGATCCTACACTGCTTTApLUC-TGIF2-WT-sCGCGTGGGATTTCCCTCCCCACAGTGCACATGGApLUC-TGIF2-WT-asAGCTTCCATTGCCCCCCACTGAGGGAGGGAAAATCCCApLUC-TGIF2-mut-sCGCGTGGGATTCCATTGCCCCCCACAGAATCGGGGGAGGGA	pLUC-CDK6-mut-s CGCGTAAGAAGCAGTGTGGACTCGGGAAATCGGGGACAA pLUC-CDK6-mut-as AGCTTGCCCCGGATTCCAGGGACTCAACATGGA pLUC-TGIF2-WT-as CGCGTGGGATTTTCCCTCCCCACAGATCGGGGGGAAAATCCCA pLUC-TGIF2-mut-as CGCGTGGGATTTTCCCTCCCCACAGATCGGGGGGGAGAAAATCCCA pLUC-TGIF2-mut-as CGCGTGGAGTTTTCCCTCCCCACAGATCGGGGGGGAGAAAATCCCA Gene-specific primers (GSPs) used for 5' RACE analyses GGGAAGGGTGAAGAGAGAGAA miR-9-1-GSP1 AAGGGACACGAGTGGAGGTG miR-9-1-GSP2 GGGGAGGGTGAAGAGAGAAA miR-9-1-GSP3 ACGACAGAGACCGAGTCCAGGTC miR-9-2-GSP1 CTCTTGCCAGGCTCAAAACGA miR-9-2-GSP3 CGGCTAAAACATCCAAACGA miR-9-3-GSP1 GGCTCTGTGGCACTCATACA miR-9-3-GSP3 GAGAGGCTTGGACATCCAACGA miR-9-3-GSP3 GAGAGGCTTCCTGGCACTCATACA miR-9-3-GSP3 GAGGGATGGACGACACAC miR-148a-GSP3 CTCGGATCGACAAATCGAACGA miR-148a-GSP3 CTCGGATCCACCCTTCC miR-148a-GSP3 CTCGGATCCACGCTCCCTTCA miR-148a-GSP3 CTCGGACCCCATTCACC miR-148a-GSP3 CTCGGACCCCATTCACC miR-148a-GSP3 CTCGGACCCCATTCACC miR-148a-GSP3 CTCGGACCCCATTCACC miR-148a-GSP3 </td <td>pLUC-CDK6-WT-as</td> <td>AGCTTTGTCCCAGGCAGTGAATTTCCACACTGCTTCTTA</td>	pLUC-CDK6-WT-as	AGCTTTGTCCCAGGCAGTGAATTTCCACACTGCTTCTTA
pLUC-CDK6-mut-asAGCTTTGTCCCCGATTGCAGGATCCACAGTGCATTGAGpLUC-TGIF2-WT-sCGCGTGGATTTTCCCTCCCCCACAGATGGACAATGGApLUC-TGIF2-mut-sCGCGTGGGATTTCCCCCCCACAGAATCGGGGGCAATGGApLUC-TGIF2-mut-sCGCGTGGGATTGCCCCCCACAGAATCGGGGGCAATGGApLUC-TGIF2-mut-sGGGGACGGTGGAGTGGAGTGGAGGGAAGAATCCCAGene-specific primers (GSPs) used for 5' RACE analysesmiR-9-1-GSP1AAGGGACACGAGTGGAGTGmiR-9-1-GSP3ACGACAGAGCGAAAAAGGmiR-9-1-GSP3ACGACAGAGCGAAAAAGGmiR-9-2-GSP1CTCTTGCCAGAGTCCAAGGTmiR-9-2-GSP2TACTTGCCGGCTTAAGAATTmiR-9-2-GSP3CGGCTAAAACATCCAAACGAmiR-9-3-GSP1GGTCTGTGGCACTCATACAmiR-9-3-GSP3GGGCTGGACAGAGACACACCmiR-9-3-GSP3GGGCTGGACAGAACACCmiR-9-3-GSP3GAGGGATGGACAGACACACmiR-148a-GSP1ACCAAACGGCGTCTCCTTAGmiR-148a-GSP1CCGATTCCACCGTCCTCmiR-148a-GSP1CCGGACCCCATTCGACACACmiR-148a-GSP2CCGATTCGACACATTCATGGTmiR-34b/c-GSP3CTCGGACCCCATTCCCmiR-34b/c-GSP3CTCGGCCCCCTTCTCmiR-34b/c-GSP3CTCGGACCCCATTCACCCmiR-34b/c-GSP3CTCGGACCCCATTCACCCmiR-34b/c-GSP3CTCGGACCCCATTCACCCchip-miR-9-1-sTGTCCCTTCCTCCCchip-miR-9-1-sGGCACCAGACACACACACACACACACACACACACACACA	pLUC-CDK6-mut-as AGCTTTGTCCCGATTTCCAGACTGCCACAGTGCAATGGA pLUC-GIR2-WT-as CGCGTGGGATTTTCCCTCCCCACAGTGCAATGGA pLUC-TGIR2-WT-as CGCGTGGGATTTCCCTCCCCCACAGTGCAATGGA pLUC-TGIR2-WT-as CGCGTGGGATTTCCCCCCCCAGGGCAATGGA pLUC-TGIR2-WT-as CGCGTGGGATTTCCCCCCCCCGGGAAATCCCA pLUC-TGIR2-WT-as CGCGTGGGAGGGAGGAGTTG miR-91-GSP1 AAGGGACACGAGTGGAGTGG miR-91-GSP2 GGGGAGGGTGAAGAGAAA miR-91-GSP3 ACGACCGAATGCAGGGCT miR-91-GSP3 ACGACCGACTGAGGAGGAGAAA miR-92-GSP3 CGGCTAAAACATCCAAACGG miR-92-GSP3 CGGCTCTGTGGCACTCATACA miR-93-GSP3 GAGGGAGGGCCTCCCTTAG miR-93-GSP3 GAGGGAGGCGCTCCTTAG miR-93-GSP3 GAGGGAGGCGCCTCCTTAG miR-94-GSP1 ACCAAACGTGCACAGACACAC miR-148a-GSP3 CTCCTGCCACCGTCCTGGT miR-148a-GSP3 CTCCTTCCCACCGGTCCCTTAG miR-148a-GSP1 ACCAAACGTGCTGCTTG miR-148a-GSP1 CAGGCACTTCCTTGGT miR-148a-GSP2 CGGATTCCACCACTCA miR-148a-GSP2 CGGATCTCCTCCTCCTGGT miR-148a-GSP2 CCGATCCCCACACAAACAGAA miR-148a-GSP2 C	pLUC-CDK6-mut-s	CGCGTAAGAAGCAGTGTGGATCCTGGAAATCGGGGACAA
pLUC-TGIF2-WT-sCGCGTGGGATTTTCCCTCCCCACAGTGCACTGAGCAATGGApLUC-TGIF2-wtr-sCGCGTGGGATTTCCCTCCCCCACAGAATCGGGGAAGAATCCCApLUC-TGIF2-wtr-sCGCGTGGGATTTCCCTCCCCCACAGAATCGGGACGGAAAATCCCArene-specific primers (GSPs) used for 5' RACE analysesmiR-9-1-GSP1AAGGGACACGAGTGGAGTTGmiR-9-1-GSP2GGGAAGGTGAAGAGAGAAAmiR-9-1-GSP3ACGACAGAGACCGAAAAAGGmiR-9-2-GSP1CTCTTGCCAGACTCCAAGGTCmiR-9-2-GSP2TACTTGCCGCGCTTAAGATTmiR-9-2-GSP3CGGCTAAAACTCCAAACGAmiR-9-3-GSP2GAGGGGCTCCCTTAGmiR-9-3-GSP3GAGGGGCTCGTGTGGCACTCATACAmiR-9-3-GSP3GAGGGGCTCGTGTGCCCCTTAGmiR-148a-GSP1ACCAAACGGGCTTCCTCCTmiR-148a-GSP1ACCAAACGTGCTGTCTCCTmiR-148a-GSP2CCGATTCGACACACACAmiR-148a-GSP3CTTCCTTCCTCCCCCTTAGmiR-148a-GSP3CTTCCTTCTCCTCCTmiR-34b/c-GSP2CAGGCATTCTCTCCCCCTTAGmiR-34b/c-GSP2CAGGCACTCCATCCCmiR-34b/c-GSP2CAGGCACTCCATCCCmiR-34b/c-GSP3CTTCCTTCCTCCCCCTCTCCmiR-34b/c-GSP3CTTCCTTCCTCCCCCTCTCCCmiR-34b/c-GSP3CTCCGTCCCCCCTCTCCCCCCCCCCCCCCCCCCCCCCC	pLUC-TGIF2-WT-s CGCGTGGGATTTTCCCTCCCCACAGTGCACTGAGCAATGGA pLUC-TGIF2-WT-s CGCGTGGGATTTTCCCTTCCCACAGTGCAGGGAAGAATGCCA pLUC-TGIF2-mut-s CGCGTGGGATTTTCCCTCCCCACAGAATCGGGGAAGAATCCCA Gene-specific primers (GSPs) used for 5' RACE analyses GGGGAGGGTGAAGAGAGAAA miR-9-1-GSP1 AAGGGACACGAGTGGAGTG miR-9-1-GSP2 GGGGAGGGTGAAGAGAGAAA miR-9-1-GSP3 ACGACAGAGACCGAATGGAGTG miR-9-2-GSP3 CGGCTAAAGCAGCACAGGACTCCAGGTC miR-9-2-GSP3 CGGCTAAACATCCAACGA miR-9-3-GSP1 GGCTCTGTGGCACTCCATACA miR-9-3-GSP3 GAGGGGATGGACAGAACACCAAC miR-9-3-GSP3 GAGGGGATGGACAGAACACCAAC miR-9-3-GSP3 GAGGGGATTGGCACTCCATACA miR-9-3-GSP3 GAGGGATTGGACAGACACAC miR-148a-GSP1 ACCAAACGTGCTGCTCCT miR-148a-GSP3 CTTCCTTCACCCGTCCT miR-148a-GSP3 CTTCCTTCTACCGTGCTC miR-148a-GSP3 CTGCTCTCTCTCCTACCG miR-34b/c-GSP1 CAGGCACTTCCTTCGTAAGA miR-34b/c-GSP3 CTGCGCCTACACCACACACACACACACACACACACACACA	pLUC-CDK6-mut-as	AGCTTTGTCCCCGATTTCCAGGATCCACACTGCTTCTTA
pLUC-TGIF2-WT-asAGCTTCCATTGCCACTGTGGGGAGGGAAAATCCCApLUC-TGIF2-mut-asCGCGTGGGATTTCCCTCCCCCACAGAATCGGGGGCAATGGApLUC-TGIF2-mut-asAGCTTCCATTGCCCCCGATTCTGTGGGGAGGGAAAATCCCAGene-specific primers (GSPs) used for 5' RACE analysesmiR-9-1-GSP1AAGGGACACGAGTGGAGTTGmiR-9-1-GSP3ACGACAGAGGCGAAAAGGmiR-9-1-GSP3ACGACAGAGACCGAAAAGGmiR-9-2-GSP1CTCTTGCCAGACTCCAGGTCmiR-9-2-GSP1CTCTTGCCAGACTCCAAGGAmiR-9-2-GSP2TACTTGCCGGCCTTAAGATTmiR-9-2-GSP3CGGCTAAAACATCCCAAACGAmiR-9-3-GSP3GGCTCTGTGGCACTCCATACAmiR-9-3-GSP3GAGGGGATGGACAGACACACCAmiR-9-3-GSP3GAGGGGATGGACAGACACACCAmiR-148a-GSP1CCCGATTCGACGTCTCTCTmiR-148a-GSP3CTTCCTTCCTACCCGTCCTmiR-34b/c-GSP1CAGGCATTCATTGGTmiR-34b/c-GSP1CAGGCATTCATTGGTGAGGmiR-34b/c-GSP2CAGGCATTCATCGCAGCCCCTmiR-34b/c-GSP3CTTCCTTCCTACCCGTCCTmiR-34b/c-GSP3CTTCCTTCCTACCCGTCCTmiR-34b/c-GSP3CTTCCTTCCTACCCGTCCTmiR-34b/c-GSP3CTTCCTTCCTACCCGTCCTmiR-34b/c-GSP3CTTCCTTCCTACCCGTCCTchip-miR-9-1-sTGTAGACACACACACACACAGGAchip-miR-9-1-sCGGCATCACCACACACACACACAGGAchip-miR-9-1-sCGGCGCACGGGAGAAATGchip-miR-9-3-sGGGGGGGGGAGAAATGchip-miR-9-3-sGGGGGGGGGGAGAAATGchip-miR-9-3-sCGACCAGGGATGGACAGACACACCchip-miR-148a-asCCCACACAAAAAGGTGGTchip-miR-148a-sCCCACACAGAAAATGGTGTTTchip-miR-148a-sCCC	pLUC-TGIF2-WT-as AGCTTCCATTGCTCATGCCATGGGGGGGGAGAAATCCCA pLUC-TGIF2-mut-s CGCGTGGGATTTTCCCTCCCCACAGAATGGGGGGGAAAATCCCA Gene-specific primers (GSPs) used for 5' RACE analyses GGGGAGGGGAAAAGGG miR-91-GSP1 AAGGGACACGAGGGGAAAAGG miR-91-GSP2 GGGGAGGGTGAAAAGGG miR-91-GSP3 ACGACCAGAGGCCCAAAAAGG miR-92-GSP1 CTCTTGCCAGGCTCAAGAGTT miR-92-GSP2 TACTTGCCGGCTTAAAACTCCAAACGA miR-92-GSP3 CGGCTAAAACTCCCAAACGA miR-93-GSP1 GGCTCTGGGCACTCCATACA miR-93-GSP3 GAGGGGATGGACAGACACAC miR-93-GSP3 GAGGGACTCCTTAG miR-148a-GSP1 CCGATTCGACAAATTCTGGT miR-148a-GSP2 CCGATTCGACAAATTCTGGT miR-148a-GSP3 CTTCCTTCCTACCCGTCCT miR-148a-GSP2 CGGGCACCCCATTTCAC miR-148a-GSP2 CGGGCACCCCATTTCACC miR-34b/c-GSP2 CAGGCAATTCATTGTGTGAG miR-34b/c-GSP2 CGGGACACCCACATTCATCGT miR-34b/c-GSP2 CGGCACCCCATTCACC primers used for CHP analyses Chip-miR-91-s chip-miR-91-s CGCCCTTCCCCCCACACAAAACGGACACAC chip-miR-92-s CGCACACACAAAAACGGACACAC <t< td=""><td>pLUC-TGIF2-WT-s</td><td>CGCGTGGGATTTTCCCTCCCCACAGTGCACTGAGCAATGGA</td></t<>	pLUC-TGIF2-WT-s	CGCGTGGGATTTTCCCTCCCCACAGTGCACTGAGCAATGGA
pLUC-TGIF2-mut-sCGCGTGGGATTTTCCCTCCCCACAGAATCGGGGGCAATGGApLUC-TGIF2-mut-asAGCTTCCATTGCCCCGATTCTGTGGGGAGGGAAAATCCCAGene-specific primers (GSPs) used for 5' RACE analysesmiR-9-1-GSP1AAGGGACACGAAGAGAGAAAmiR-9-1-GSP2GGGGAGGGTGAAGAGAGAAAAGGmiR-9-1-GSP3ACGACAGACCGAAAAAAGGmiR-9-1-GSP3CTCTTGCCAGACTCCAGGTCmiR-9-2-GSP1CTCTTGCCAGACTCCAAGCAmiR-9-2-GSP2TACTTGCCGGCTTAAGATTmiR-9-2-GSP3CGGCTAAAACATCCAAACGAmiR-9-3-GSP1GGCTCTGTGGCACTCCATACAmiR-9-3-GSP3GAGGGGATGGACAGACACACmiR-9-3-GSP3GAGGGGATGGACAGACACACmiR-148a-GSP1ACCAAACGTGCTCTTCTmiR-148a-GSP2CCGATTCGACAAATTCTGGTmiR-34b/c-GSP1CAGGCAATTCATTGGTTGAGmiR-34b/c-GSP2CAGGCATCTCTCCTCCCCCTCmiR-34b/c-GSP3CTCGCGACCCCATTTCACCmiR-34b/c-GSP3CTCGGACCCCATTTCACCmiR-34b/c-GSP3CTCGGACCCCATTCCCCchip-miR-9-1-sTGTCCCTCCCTCCTCACTCCchip-miR-9-1-sCGGCACTCCCCCCCCCCCCCCchip-miR-9-1-sCGCCACACACACAAACAGAAAchip-miR-9-3-sGGGAGCAGGGAGAAATGchip-miR-9-3-sGGGAGCAGGGAGAAATGchip-miR-9-3-sGGGAGCAGGGATGACACACCACchip-miR-9-3-sGCCCAACACACAAACAGAAAATGGTGTTTchip-miR-9-3-sCGACCAGCAGGGATGGACAGACACCchip-miR-9-3-sGCCCAACAGGAATGGGTTCTAAchip-miR-9-3-sCGCCCAACAGGAATGGTGTTTchip-miR-94-sCTGCCTGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	pLUC-TGIF2-mut-s CGCGTGGGATTTTCCCTCCCACAGAATCGGGGGAAATCGGA pLUC-TGIF2-mut-as AGCTTCCATTGCCCCCGATTCTGGGGAGGGGAAAATCCCA Gene-specific primers (GSPs) used for 5' RACE analyses miR-9-1-GSP1 AAGGGACACGAGTGGAAAAAGGA miR-9-1-GSP3 ACGACAGAGACCAAAAAAGG miR-9-2-GSP1 CTCTTGCCAGACTCCAGGTC miR-9-2-GSP3 CGGCTAAAAACATCCAAACGAA miR-9-2-GSP3 CGGCTAAAAACATCCAAACGAA miR-9-3-GSP3 GGGCTCTGTGGCACTCATACA miR-9-3-GSP3 GGGGATGAACAGACACAC miR-9-3-GSP3 GAGGGATGACACAGACACAC miR-148a-GSP1 ACCAAACGTGCTGTTCCT miR-148a-GSP1 CCGATTCGACAAATTCTGGT miR-34b/c-GSP1 CAGGCAATTCATTGGTTGAG miR-34b/c-GSP1 CAGGCAATTCATTGGTTGAG miR-34b/c-GSP1 CAGGCAATTCATTGGTTGAG miR-34b/c-GSP3 CTCCTCCCCTCT miR-34b/c-GSP3 CGCACACACACACACACACACACACACACACACACACAC	pLUC-TGIF2-WT-as	AGCTTCCATTGCTCAGTGCACTGTGGGGAGGGAAAATCCCA
pLUC-TGIF2-mut-as AGCTTCCATTGCCCCGATTCTGTGGGGAGGGAAAATCCCA Gene-specific primers (GSPs) used for 5' RACE analyses miR-9-1-GSP1 AAGGGACACGAGGGGAGAAA miR-9-1-GSP2 GGGGAGGGTGAAGAGAGAAAA miR-9-1-GSP3 ACGACAGAGACCGAAAAAGG miR-9-2-GSP1 CTCTTGCCAGACTCCAGGTC miR-9-2-GSP2 TACTTGCCGCGCTTAAGATT miR-9-2-GSP3 CGGCTAAAACATCCAAACGA miR-9-3-GSP1 GGCTCTGTGGCACTCATACA miR-9-3-GSP3 GAGGGGATGGACAGACACAC miR-9-3-GSP3 GAGGGGATGGACGACACAC miR-9-3-GSP3 GAGGGGATGGTCTCTTAG miR-9-3-GSP3 GAGGGATGGTCTGTGTCTCCT miR-148a-GSP1 ACCAAACGTGCTGCTCT miR-148a-GSP1 ACCAAACATTCATGGT miR-148a-GSP2 CCGATTCCTACCCGTCTC miR-148a-GSP3 CTTCCTTCCTACCCGTCTC miR-34b/c-GSP1 CAGGCAATTCATTGTTGAG miR-34b/c-GSP3 CTCGGACCCCATTTCACC miR-34b/c-GSP3 CTCGGACCCCATTCACC miR-34b/c-GSP3 CTCGGACCCCATTCACC miR-9-1-s TGTCCTTCCTCCTCCTCCTCC miR-9-1-s CTGCGACTCCACACACACACAAA chip-miR-9-1-as TGCACTCCCCACTCA chip-miR-9-2-s CGGCACAGCAGGGAGAAAGA chip-miR-9-3-s GGGGAGGAGACGACACAC chip-miR-9-3-s GGGAGCAGGACGACACACAC	pLUC-TGIF2-mut-as AGCTTCCATTGCCCCCGATTCTGGGGAGGGAAAATCCCA Gene-specific primers (GSPs) used for 5' RACE analyses miR-9-1-GSP1 AAGGGACACGAAGTGGAGTTG miR-9-1-GSP3 ACGACAGAGGACCGAAAAAGG miR-9-1-GSP3 ACGACAGAGACCGAAAAAGG miR-9-2-GSP2 TACTTGCCGCGCTTAAGATT miR-9-2-GSP3 CGGCTAAAACATCCAAACGA miR-9-3-GSP1 GGCTCTGTGGCACTCATACA miR-9-3-GSP3 GGAGGGCTCCCTTAG miR-9-3-GSP3 GAGGGGATGGACAGACACAC miR-148a-GSP1 ACCAAACGTGCTGTCTCCT miR-148a-GSP3 CTTCCTCCTACCGTTCCT miR-148a-GSP3 CTTCCTTCCTACCGTCCC miR-34b/c-GSP1 CAGGCATTCATCCTGGT miR-34b/c-GSP3 CTCGGACCCCATTCCTC miR-34b/c-GSP3 CTCGGACCCCATTCCC miR-34b/c-GSP3 CTCGGACCCCATTCCC miR-34b/c-GSP3 CTCCGGACTCCATCCC miR-9-1-s TGCAAGACTCCAGGCT chip-miR-9-1-s TGCACACACCACCACCACCACCACCACC chip-miR-9-1-s GGCACAGGGACAGACACAC chip-miR-9-1-s GGCCACAGCACACACACAAACAGAAA chip-miR-9-1-s GGCCACACACACACACACACACACACACACACACACACA	pLUC-TGIF2-mut-s	CGCGTGGGATTTTCCCTCCCACAGAATCGGGGGCAATGGA
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miR-9-1-GSP3ACGACAGAGACCGAAAAAGGmiR-9-2-GSP1CTCTTGCCAGACTCCAGGTCmiR-9-2-GSP2TACTTGCCGCGCTTAAAACATCCAAACGAmiR-9-2-GSP3CGGCTAAAACATCCAAACGAmiR-9-3-GSP1GGCTCTGTGGCACTCATACAmiR-9-3-GSP2AGAAACGGGCCTCCCTTAGmiR-9-3-GSP3GAGGGATGGACAGACACACAmiR-148a-GSP1ACCAAACGTGCTGTCTCCTmiR-148a-GSP2CCGATTCGACAAATTCTGGTmiR-148a-GSP3CTTCCTTCCTACCCGTCCTmiR-34b/c-GSP1CAGGCAATTCATTGGTTGAGmiR-34b/c-GSP2CAGGCAATTCATCGGTGTGTGAGmiR-34b/c-GSP2CAGGCAATTCATCGGTmiR-34b/c-GSP3CTTCGGACCCCATTTCACCmiR-34b/c-GSP3CTTCGGACCCCATTTCACCchip-miR-9-1-sTGCCCTCCCTCCTCCchip-miR-9-1-sTGCACACACAAAAAGAAAchip-miR-9-2-sCGCACACACACAAAAAGGAAAAchip-miR-9-3-asGGAGCAGGGAGAGAGACACACchip-miR-9-3-asGAGCGAGTGGACAGACACACchip-miR-148a-asCCCCAACAGAAATGGTGTTTchip-miR-148a-asCCGCACACACAGAAATGGGGTCTAAchip-miR-148a-asCCGCACACACAGAAATGGGTGTTAAchip-miR-148a-asCCGCACACACAGAAATGGGTGTTAAchip-miR-148a-asCCGCACACACAGAAATGGGGTCTAAchip-miR-148a-asCCGCACACAGAAATGGGTGTTAAchip-miR-148a-asCCGCCACACAGAAATGGGTGTTAAchip-miR-148a-asCCGCCACACAGAAATGGGTGTTAAchip-miR-148a-asCCGCCACACAGAAATGGGTGTTAAchip-miR-148a-asCCGCCACACAGAAATGGGTGTTAAchip-miR-148a-asCCGCCACACAGAAATGGGTGTTAAchip-miR-148a-asCCGCCACACAGAAATGGGTGTTAchip-miR-148a-as <td< td=""><td>miR-91-GSP3 ACGACAGAGACCGAAAAAGG miR-92-GSP1 CTGCCAGACTCCAGGTC miR-92-GSP3 CGGCTAAAACATCCAAACGA miR-93-GSP1 GGCTCTGTGGCACTCATACA miR-93-GSP2 AGAAACGGGCCTCCCTTAG miR-93-GSP3 GAGGGATGGACAGACACAC miR-148a-GSP1 ACCAAACGTGCTGTCTTCCT miR-148a-GSP2 CCGATTCGACAAATTCTGGT miR-34b/c-GSP1 CCAGCAAATTCCTGGT miR-34b/c-GSP2 CCGATTCGACAAGTCCCCCCCC miR-34b/c-GSP3 CTTCGCACAAGTCCCCCCCCCCCCCCCCCCCCCCCCCCC</td><td>miR-9-1-GSP2</td><td>GGGGAGGGTGAAGAGAGAAA</td></td<>	miR-91-GSP3 ACGACAGAGACCGAAAAAGG miR-92-GSP1 CTGCCAGACTCCAGGTC miR-92-GSP3 CGGCTAAAACATCCAAACGA miR-93-GSP1 GGCTCTGTGGCACTCATACA miR-93-GSP2 AGAAACGGGCCTCCCTTAG miR-93-GSP3 GAGGGATGGACAGACACAC miR-148a-GSP1 ACCAAACGTGCTGTCTTCCT miR-148a-GSP2 CCGATTCGACAAATTCTGGT miR-34b/c-GSP1 CCAGCAAATTCCTGGT miR-34b/c-GSP2 CCGATTCGACAAGTCCCCCCCC miR-34b/c-GSP3 CTTCGCACAAGTCCCCCCCCCCCCCCCCCCCCCCCCCCC	miR-9-1-GSP2	GGGGAGGGTGAAGAGAGAAA
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mik-34b/c-GSP3 CTCGGACCCCATTICACC Primers used for ChIP analyses chip-miR-9-1-s TGTCCCTTCCCTACTCC chip-miR-9-1-as TGAAGACTCCACACCACTCA chip-miR-9-2-s CGCACACACACACAAACAGAAA chip-miR-9-2-as CTCTTGCCAGGCGAGAGAAATG chip-miR-9-3-s GGGAGCAGGGGAGAAATG chip-miR-9-3-as CGACCACAGAAACAGCACC chip-miR-148a-s CGACCAAGAAATGGGTTCTAA chip-miR-148a-as GCCCCAACAGAAATGGGGTTT chip-miR-34b-s CTGGCGTGAAGGAAGTGG	mix-340/c-GSP3 CTCGGACCCCATTICACC Primers used for ChIP analyses chip-miR-9-1-s TGTCCCTTCCTCCTACTCC chip-miR-9-1-as TGAAGACTCCACACCACACCACACACACACACACACACAC	miR-34b/c-GSP2	
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chip-miR-9-1-sIGICCCITCCCIACICCchip-miR-9-1-asTGAAGACTCCACACCACTCAchip-miR-9-2-sCGCACACACACACACACACAAACAGAAAchip-miR-9-2-asCTCTTGCCAGACTCCAGGTCchip-miR-9-3-sGGGAGCAGGGGAGAAATGchip-miR-9-3-asGAGGGGATGGACAGACACACCchip-miR-148a-sCGACCAGGAATGGGTTCTAAchip-miR-148a-asGCCCAACAGAAATGGTTTTchip-miR-34b-sCTGGCGGAAGGAAGTGGchip-miR-34b-sCTGGCGGAAGGAAGTGGGchip-miR-34b-sCTGGCGGAAGGAAGTGGG	chip-miR-9-1-sIGICCCITCCCIACICCchip-miR-9-1-asTGAAGACTCCACCACCACCACCACCACACAchip-miR-9-1-asCGCACACACACACACACACAAACAGAAAchip-miR-9-2-asCGCACACCACACACACAGACAchip-miR-9-3-asGGGAGCAGGGGAGAAATGchip-miR-9-3-asGAGGGGATGGACAGACACACchip-miR-148a-sCGACCAGGAATGGGTTTAAchip-miR-148a-asGCCCACAGAAATGGTGTTTchip-miR-34b-sCTGGCGTGAAGGAAGTGGchip-miR-34b-asCCATGACCCCCAGGAATGGGchip-miR-34b-asCCATGACCCCCAGGAGTGBS-CR612216-sTTGAAAGATTGTGGAAATTAAAABS-CR612216-asATATATTTCTCCCACTTCCACABS-BC021736-sTTGAGATGGAGTTTGGBS-BC021736-sTTGAGATGGAGTTTGG		
Cnip-miR-9-1-asIGAAGACICCACACCACICAchip-miR-9-2-sCGCACACACACACACACACACACACACACACACACACAC	Chip-miR-9-1-asIGAAGACICCACACACACACACACACACACACACACACAC	cnip-miR-9-1-s	
cmip-min-9-2-sCGCACACACACACACACACACACACACACACACACACAC	chip-miR-9-2-sCGCACACACACACACACAAACAGAAAchip-miR-9-2-asCTCTTGCCAGACTCCAGGTCchip-miR-9-3-asGGGAGCAGGGGAGAAATGchip-miR-9-3-asGAGGGGATGGACAGACACACchip-miR-148a-sCGACCAGGAATGGGTTCTAAchip-miR-148a-asGCCCAACAGAAATGGTGTTTchip-miR-34b-sCTGGCGTGAAGGAAGTGGchip-miR-34b-asCCATGACCCCCAGGAATGGGACchip-miR-34b-asCCATGACCCCCAGGAGTGPrimers used for genomic bisulfite sequencing of CR612216 and BC021736BS-CR612216-asATATATTTCTCCCACTTCCACABS-CR612216-asATATATTTCTCCCACTTCCACABS-BC021736-sTTGAAAGATGGAGTTTTGBS-CR012736-sTTGAAAGATGGAGTTTTGTTTGBS-CR012736-sTTGAAAGATGGAAGTTTGTCCCACTS-BC021736-sTTGAAAGATGAAAAAACAAAAAAAAAAAAAAAAAAAAAA	cnip-mik-9-1-as	
cnip-min-9-2-asCTCTTGCCAGACTCCAGGTCchip-miR-9-3-sGGGAGCAGGGGAGAAATGchip-miR-9-3-asGAGGGGATGGACAGACACACchip-miR-148a-sCGACCAGGAATGGGTTCTAAchip-miR-148a-asGCCCAACAGAAATGGTGTTTchip-miR-34b-sCTGGCGTGAAGGAAGTGGchip-miR-34b-sCCGATCAGCAGCACGCC	Chip-min-9-2c-asCTCLTGCCAGACTCCAGGTCchip-miR-9-3-sGGGAGGCAGGGAGAAATGchip-miR-9-3-asGAGGGGATGGACAGACACACchip-miR-148a-ssCGACCAGGAATGGGTTCTAAchip-miR-148a-asGCCCAACAGAAATGGTGTTTchip-miR-34b-sCTGGCGTGAAGGAAGTGGchip-miR-34b-asCCATGACCCCCAGGAGTGPrimers used for genomic bisulfite sequencing of CR612216 and BC021736BS-CR612216-sTTGAAAGATTGTGGAAATTAAAABS-CR612216-asATATATTTCTCCCACTTCCACABS-BC021736-sTTGAAAGATGGAGTTTTGBS-BC021736-s	cnip-mik-9-2-s	
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chip-miR-9-3-as GAGGGGATGGACAGACAGACACAC chip-miR-148a-ss CGACCAGGAATGGGTTCTAA chip-miR-34b-s GCCCAACAGAAATGGTGTTT chip-miR-34b-s CTGGCGTGAAGGAAGTGG	chip-miR-9-3-as GAGGGGATGGACAGACACAC chip-miR-148a-s CGACCAGGAATGGGTTCTAA chip-miR-148a-as GCCCACAGAAATGGTGTTT chip-miR-34b-s CTGGCGTGAAGGAAGTGG chip-miR-34b-as CCATGACCCCCAGGAGTG Primers used for genomic bisulfite sequencing of CR612216 and BC021736 BS-CR612216-as TTGAAAGATTGTGGAAATTAAAA BS-CR612216-as ATATATTTCTCCCACTTCCACA BS-BC021736-s TTGAGATGGAGTTTTG BS-BC021736-s TTCCAACACTTTAAAAAATCAA	chip-mik-9-3-s	
chip-miR-14ba-as GCCAACAGAATGGGTTTAA chip-miR-34b-s CTGGCGTGAAGGGAGGG chip-miR-34b-s CTGGCGTGAAGGGAGGG	Chip-min-14aa-s CGACCAGGAATGGGTTGTAA chip-miR-148a-as GCCCAACAGAAATGGGTGTTT chip-miR-34b-s CTGGCGTGAAGGAAGTGG chip-miR-34b-as CCATGACCCCAGGAGTG Primers used for genomic bisulfite sequencing of CR612216 and BC021736 BS-CR612216-s TTGAAAGATTGTGGAAATTAAAA BS-CR612216-as ATATATTTCTCCCACTTCCACA BS-BC021736-s TTTGAGATGGAGTTTTGTTTTG BS-BC021736-as TCCCAACACTTTAAAAAATCAA	chip-miP 1495 c	
chip-miR-34b-s CTGGCGGGAAGTGG	chip-miR-34b-s CTGGCGTGAAGGAAGTGG chip-miR-34b-as CCATGACCCAGGAGG Primers used for genomic bisulfite sequencing of CR612216 and BC021736 BS-CR612216-s TTGAAAGATTGTGGAAATTAAAA BS-CR612216-as ATATATTTCTCCCACTTCCACA BS-BC021736-s TTGAGATGGAGTTTTGTTTTG BS-BC021736-s TCCCAGCACTTTAAAAAATCAA	chip-miR-140a-s	GCCCAACAGAATGGTGTTT
CIUDCHICAADDAADDD	chip-miR-34b-as CCATGACCCCCAGGAGTG Primers used for genomic bisulfite sequencing of CR612216 and BC021736 BS-CR612216-as TTGAAAGATTGTGGAAATTAAAA BS-BC021736-s TTTGAGATGGAGTTTTGTTTTG BS-BC021736-as TCCCAACACTTTAAAAAATCAA	chip-miR-34b-s	
$(\Delta)(\Delta)(\Delta)(\Delta)(\Delta)(\Delta))$	Primers used for genomic bisulfite sequencing of CR612216 and BC021736 BS-CR612216-as ATATATTTCTCCCACTTCCACA BS-BC021736-s TTTGAGATGGAGTTTTGTTTTG BS-BC021736-as TCCCACACACTTTAAAAAATCAA	chip-miR-34b-as	CLATGACCCCAGGAGTG
Primers used for genomic bisulfite sequencing of CR612216 and BC021736	BS-CR612216-s TTGAAAGATTGTGGAAATTAAAA BS-CR612216-as ATATATTTCTCCCACTTCCACA BS-BC021736-s TTTGAGATGGAGTTTTGTTTTG BS-BC021736-as TCCCAACACTTTAAAAAAATCAA	Primers used for a	enomic bisulfite sequencing of CR612216 and BC021736
	BS-CR612216-as ATATATTCCCACTTCCACA BS-BC021736-as TTGAGATGGAGTTTGTTTG BS-BC021736-as TCCCAACACTTAAAAAATCAA	RS_CR612216_c	TIGAAAGATTGIGGAAATTAAAA
	BS-BC021736-s TTTGAGATGGAGTTTTG BS-BC021736-as TCCCAACACTTTAAAAAAATCAA	BS-CR612210-S RS-CR612216-ac	ΛΤΑΤΑΤΤΤΓΓΓΓΓΑΓΑ
	ΒS-BC(21736-as ΤC(CAACACTTTAAAAAAATCAA	BS-BC021736-s	TTTGAGATGGAGTTTTGTTTTG
BS-BC021736-s TTTGAGATGGAGTTTTGTTTTG		BS-BC021736-as	ТСССААСАСТТТААААААТСАА
RS-RC021736-s TTTGAGATGGAGTTTTGTTTG		BS-BC021736-as	ΤΓΓΓΔΑΓΑΓΤΤΔΑΔΑΔΑΤΓΔΑ

Other Supporting Information Files

Table S2 (PDF) Table S4 (PDF)