Supplementary Tables

Supplementary Table S1: Predicted miRNA binding sites on the human and mouse *MYC* CDS by RNA22

MicroRNAs	Heteroduplex in human	Heteroduplex in mouse	Position in human/mouse
MiR-125a-3p	`TGCTGCCCA--CCCCGCCCCTGT` ` ||| |||| ||	|||||` `CCGA-GGGTTCTTGGAGTGGACA`	`TGCTTCCCA--CCCCGCCCCTGT` ` ||| |||| ||	|||||` `CCGA-GGGTTCTTGGAGTGGACA`	164/164

	`GGTGAACCA-GAGTTTCATCTGC`
	`||:    ||| ||: |||:|||`
	`CCG-AGGGTTCTTGGAGTGGACA`
		`GGTGAACCA-GAGCTTCATCTGC`
		`||:    ||| ||:|:|||:|||`
		`CCG-AGGGTTCTTGGAGTGGACA`
			330/333

	`ACCTCCTCACAGCC-CACTGGT` ` ||||:	|:|| |||: ||` `CCGAGGGTTCTTGGAGTGGACA`	`ACCTCCGCA-CAGCC-CACTGGT` `  |||| || |:|| |||: ||` `CCGAGG-GTTCTTGGAGTGGACA`	867/867

MiR-138-5p	`AGG-AGGA-GAACTTCTACCAGCA`
	` ||   ||   ||  :||||||`
	`GCCGGACTAAGTG-TTGTGGTCGA`
		`AGGAAGAGAATTTC-TATCACCAGCA`
		` ||    ||  |||   |||||||`
		`GCC-GGACT--AAGTGTTGTGGTCGA`
			80/80

	`GCGTCTG-CTC-CACCTCCAGCT` ` |:||| || ||	||||||` `GCCGGACTAAGTGTTGTGGTCGA`	`GCGTCTG-CTC-CACCTCCAGCC` ` |:||| || ||	|||||` `GCCGGACTAAGTGTTGTGGTCGA`	506/509

	`GTGCCACGTCTCCACA-CATCAGCA`
	` |||      |||| ||:||||`
	`GCCGG--ACTAAGTGTTGTGGTCGA`
		`GTGCCACGTCTCCAC-TCACCAGCA`
		` |||       |||  |||||||`
		`GCCGG--ACTAAGTGTTGTGGTCGA`
			897/897

MiR-139-3p	`TCCTCAAGAGGTGCCACGTCTCCA`
	`      || ||| ||||||||`
	`TGAGGTTGTCC-CGGCGCAGAGGT`
		`CCTCAAGAGGTGCCACGTCTCCA`
		`|   ||| ||| ||| ||||||||`
		`GAGGTTGTCC-CGGCGCAGAGGT`
			887/888

MiR-503-5p	`CTGGAAGAA--ATTCGAGCTGCTG` ` ||  ||||    |||  ||||||:` `GAC-GTCTTGACAAGGGCGACGAT`	`CTGGAAGA-AATTCGAGCTGCTT` `|||		||| ||||||` `GACGTCATGACAAGGGCGACGAT`	147/147

MiR-744-5p	`AGCTG-CTGCCC--ACCCCGCC`
	`||||    ||||   ||||||`
	`ACGACAATCGGGATCGGGGCGT`
		`AGCTG-CTTCCC--ACCCCGCC`
		`||||    |||   ||||||`
		`ACGACAATCGGGATCGGGGCGT`
			161/161

For the heteroduplex, the top strand denotes the MRE sequence in the 5′ - 3′ direction, while the bottom strand denotes the miRNA sequence in the 3′ - 5′ direction.

Supplementary Table S2: Predicted miR-138 MREs on the human and mouse *MYC* CDS by RNA22

MREs	Heteroduplex (Human)	Heteroduplex (Mouse)	Leftmost position (Human/Mouse)

A	`AGG-AGGA-GAACTTCTACCAGCA`
	`  ||    ||    ||   :||||||`
	`GCCGGACTAAGTG-TTGTGGTCGA`
		`AGGAAGAGAATTTC-TATCACCAGCA`
		`  ||      ||   |||     |||||||`
		`GCC-GGACT--AAGTGTTGTGGTCGA`
			80/80

B	`GCGTCTG-CTC-CACCTCCAGCT`
	`  |:|||   || || |  ||||||`
	`GCCGGACTAAGTGTTGTGGTCGA`
		`GCGTCTG-CTC-CACCTCCAGCC`
		`  |:|||   || || |  |||||`
		`GCCGGACTAAGTGTTGTGGTCGA`
			506/509

C	`GTGCCACGTCTCCACA-CATCAGCA`
	`  |||        |||| ||:||||`
	`GCCGG--ACTAAGTGTTGTGGTCGA`
		`GTGCCACGTCTCCAC-TCACCAGCA`
		`  |||       |||  |||||||`
		`GCCGG--ACTAAGTGTTGTGGTCGA`
			897/897

For the heteroduplex, the top strand denotes the MRE sequence in the 5′ - 3′ direction, while the bottom strand denotes the miRNA sequence in the 3′ - 5′ direction. Red font indicates the different nucleotides between the human and mouse *MYC* sequences.

Supplementary Table S3: Predicted miR-138 MREs on the human *MYC* CDS by STarMir

Sites	Predicted Bindings
| 1 | ```
5'->3'        A   AG    GA    UUC        A
Target   81   GG    GA    AC    UACCAGC    100
              ||    ||    ||    |||||||
miRNA    23   CC    CU    UG    GUGGUCG    1
3'->5'        G   GGA   AAG   UU         A
``` |
| 2 | ```
5'->3'        U    GG   GCUUCUC       CG        G
Target   268  GGC  GA         CACGGC  ACCAGCU   296
              |||  ||         ||||||  |||||||
miRNA    23   CCG  CU         GUGUUG  UGGUCGA   1
3'->5'        G    GA   AA
``` |
| 3 | ```
5'->3'        C    ACGA GA   CC        CAAA        N
Target   356  CGG      C  GA  UUCAU    AACAUCA     385
              |||      |  ||  |||||    |||||||
miRNA    23   GCC      G  CU  AAGUG    UUGUGGU     1
3'->5'             G      A                    CGA
``` |
| 4 | ```
5'->3'        U   U   CAA   GGUGC    UCUCCAC        A
Target   885  GG CCU    GA       CACG        ACAUCAGC   919
              || |||    ||       ||||        ||||||||
miRNA    23   CC GGA    CU       GUGU        UGUGGUCG   1
3'->5'        G            AA                         A
``` |

Site 1 is the same site as MRE_A predicted by RNA22 and site 1 predicted by miRDB.

Supplementary Table S4: List of primers for *MYC* 3′ RACE

Primer Names	Primer Sequences (5′-3′)
MYC 3′ RACE outer	GTCCAAGCAGAGGAGCAAAA
MYC 3′ RACE inner	CCCAAGCTTGGGAAGAGGACTTGTTGCGGAAA

Supplementary Table S5: Primers for RT-qPCR

Gene Names	Forward Primers (5′-3′)	Reverse Primers (5′-3′)
MYC	TTCGGGTAGTGGAAAACCAG	CAGCAGCTCGAATTTCTTCC
GAPDH	AGCCACATCGCTCAGACAC	GCCCAATACGACCAAATCC
ROCK2	GAGGTCTACAGATGAAGGCAGA	CCTTGTGACGAACCAACTGC
LYPLA1	GAGATACTGGGCACGGATGG	TGTAACAGGCCTAACAGGCG
PTK2	GTGCTCTTGGTTCAAGCTGGAT	ACTTGAGTGAAGTCAGCAAGATGTGT
SOX4	GGTCTCTAGTTCTTGCACGCTC	CGGAATCGGCACTAAGGAG
P27	ACTCGCCGTGTCAATCATTT	AACACCCCGAAAAGACGAG
CDK4	TTGTCCGGCTGATGGAC	GGGTGCCTTGTCCAGATA
CDK6	CCACTTACTTGGATAAAGTTCCAGA	CAGAATGTTCTGTGGTTTTAGATCG

Supplementary Table S6: Oligonucleotides for cloning miR-138 MREs into psiCHECK-2

Oligo Names	Oligonucleotide Sequences	Restriction Sites
MRE A Forward	TCGAGAGGAGGAGAACTTCTACCAGCAGC	XhoI
MRE A Reverse	GGCCGCTGCTGGTAGAAGTTCTCCTCCTC	NotI
MRE B Forward	TCGAGGCGTCTGCTCCACCTCCAGCTGC	XhoI
MRE B Reverse	GGCCGCAGCTGGAGGTGGAGCAGACGCC	NotI
MRE C Forward	TCGAGGTGCCACGTCTCCACACATCAGCAGC	XhoI
MRE C Reverse	GGCCGCTGCTGATGTGTGGAGACGTGGCACC	NotI
RC Forward	TCGAGCGGCCTGATTCACAACACCAGCTGC	XhoI
RC Reverse	GGCCGCAGCTGGTGTTGTGAATCAGGCCGC	NotI
CDK6 WT Forward	TCGAGCTTGTTTTGTTTTATCACCAGCAGC	XhoI
CDK6 WT Reverse	GGCCGCTGCTGGTGATAAAACAAAACAAGC	NotI
CDK6 Mutant Forward	TCGAGCTTGTTTTGTTTTATATATATAAGC	XhoI
CDK6 Mutant Reverse	GGCCGCTTATATATATAAAACAAAACAAGC	NotI

Supplementary Table S7: Primers for site-directed mutagenesis (SDM)

Target Sites	Primer Sequences (5′-3′)
MRE A	GAGGAGGAGAACTTCT**TGGTCG**AGCAGCAGCAGAGCGA
MRE C	AGGTGCCACGTCTCCACAC**TAGTCG**ACAACTACGCAGC
Rluc+ MRE A	TGCTGAAGAACGAGCAGCG**AGGAGGAGAACTTCTACCAGCA**TAATTCTAGGCGATCGC
Rluc+ MYC CDS	TGCTGAAGAACGAGCAGCTCAACGTTAGCTTCAC

The bold font indicates the mutated nucleotides on the MRE sequence to which the miR-138 seed region binds. The SDM for MRE A and MRE B was performed on the ATG-less *MYC* CDS construct cloned into the psiCHECK-2 vector. The SDM for Rluc+ MRE A was performed to insert the MRE A (red bold font) into the *Renilla luciferase* gene, right before the stop codon. The SDM for Rluc+ MYC CDS was performed to fuse the Renilla luciferase gene and the ATG-less *MYC* CDS.