SUPPLEMENTARY TABLES AND FIGURE

Supplementary Table S1: Putative targeting miRNAs of RBM4

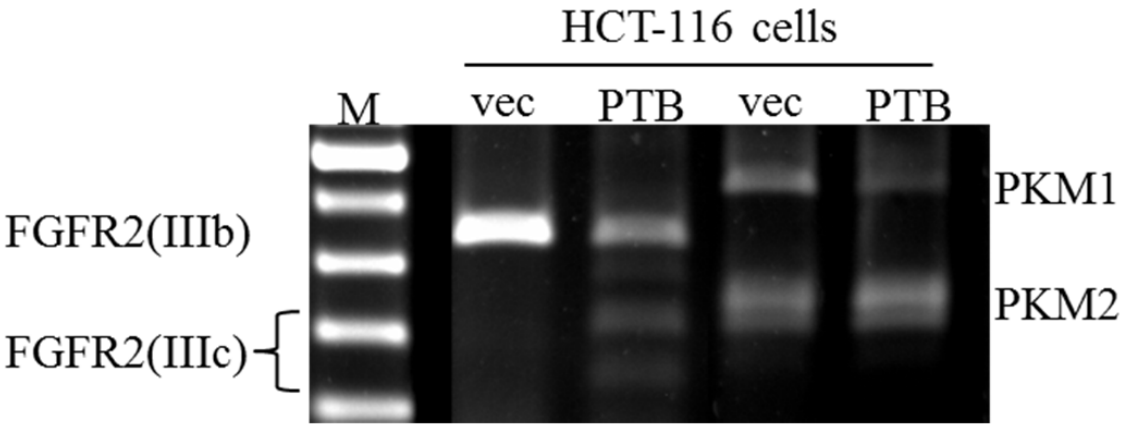
<table>
<thead>
<tr><th>miRNA</th><th>Alignment</th><th>Leftmost position of predicted site</th><th>Folding energy (Kcal/mol)</th><th><i>p</i> Value</th></tr>
</thead>
<tbody>
<tr><td>has-miR-103a</td><td>CAGGAGCTGCTGCCACAGCTGCTGCT
|||: ||| |||: |||||||
AGTATCGG-GAC-ATGTT-ACGACGA</td><td>+837</td><td>–14.0</td><td>5.61E-3</td></tr>
<tr><td>hsa-miR-18a</td><td>CCAGAATACAGC-C-ATGGCCAGT
|||||| ||| | || ||||
GGTCTT-CCTCGTGAATCCCGTCA</td><td>+763</td><td>–15.2</td><td>2.56E-2</td></tr>
<tr><td>hsa-miR-92a</td><td>ACATGGAGCGGGCAGAGGATGCAGTG
||| || |||| | |:| ||||:|:
TGT-CC-GGCCC-TGTTC-ACGTTAT</td><td>+348</td><td>–19.2</td><td>5.23E-2</td></tr>
<tr><td>hsa-miR-23a</td><td>GGAAGGTGCTGG-AATGTGAC
||||: : |||| |||||||
CCTTTAGGGACCGTTACACTA</td><td>+75</td><td>–18.8</td><td>3.21E-1</td></tr>
<tr><td>hsa-miR-139</td><td>GCGCTA-CAGCCCC-AGTCCCCA
:| |:| ||| || ||| |||
TGAGGTTGTCCCGGCGCAGAGGT</td><td>+936</td><td>–14.6</td><td>2.3E-2</td></tr>
<tr><td>hsa-miR-222</td><td>TAGA-AGACAAGACGGCAGCTGAG
|| ||| ||| :|||||
TCCTAGATGT--GACCGATGACTC</td><td>+123</td><td>–14.2</td><td>9.43E-2</td></tr>
<tr><td>hsa-miR-324-5p</td><td>ACAAGACGGCAGCTG-AGGATGCC
||| || ||: ||||||
TGTGGTTACG-GGATCCCCTACGC</td><td>+129</td><td>–14.2</td><td>9.43E-2</td></tr>
<tr><td>hsa-miR-214</td><td>GATGCCTACTACAAGCGCTGCCGT
||||| || |||| ||
TGACGGA-CAGACACG-GACGACA</td><td>+653</td><td>–14.2</td><td>3.47E-1</td></tr>
<tr><td>hsa-miR-25</td><td>ATGGAGCGGGCAGAGGATGCAGTG
:|| ||:| | |:| ||||:||
AGTCTGGCTC-TGTTC-ACGTTAC</td><td>+350</td><td>–18.7</td><td>5.23E-2</td></tr>
<tr><td>hsa-miR-24</td><td>TCCCCACTGTTGGAGAGGGCTA
|||:||:| |:||:|
GACAAGGACGACTTGACTCGGT</td><td>+951</td><td>–16.4</td><td>2.3E-2</td></tr>
<tr><td>hsa-miR-17</td><td>CCGCTGCTGCTGTTACTGCAGC
| ||: |:||||||
GATGTTCACGGAAGTGACGTCA</td><td>+873</td><td>–17.6</td><td>2.92E-2</td></tr>
<tr><td>hsa-miR-17</td><td>CTGCCTCCTGCCT-C-CTGCGGC
||:| ||||| | ||||:|
GATG-TTCACGGAAGTGACGTCA</td><td>+1346 (3‘UTR)</td><td>–24.1</td><td>4.85E-3</td></tr>
</tbody>
</table>

Supplementary Table S2: List of upregulated miRNAs in CRC tissues

Candidates	Reference
miR-92a	Int J Colorectal Dis, 28, 19–24
miR-21	Eur J Cancer, 51, 409–420
miR-29a	Cancer Biomark, 15, 103–113
miR-125	Eur J Cancer, 51, 409–420
miR-196	World J Gastroenterol, 18, 2827–2831.
miR-103	Int J Mol Sci. 2014 May 13;15(5):8458–8472
miR-135b	Am J Cancer Res, 5, 1382–1395
miR-26b	J Cell Mol Med, 15, 1941–1954
miR-182	Oncol Rep, 33, 2592–2598
miR-206	Oncol Rep, 33, 1402–1410
1miR-7	Carcinogenesis, 36, 338–345
miR-320b	Eur J Cancer, 51, 409–420
miR-193a	World J Gastroenterol, 20, 12241–12248
miR-708	Oncol Lett, 8, 1768–1774.
miR-31	Oncol Lett, 8, 1768–1774.
miR-18a	Cancer Biomark, 15, 103–113
miR-155	Tumour Biol, 36, 1619–1625
miR-181a	J Clin Pathol, 67, 198–203
amiR-106a	FEBS Lett, 588, 705–712.
miR-15a-3p	PLoS One, 10, e0132495
miR-19	Mol Cancer Res, pii: molcanres.0466.2014.
miR-23a	Int J Mol Sci, 15, 11713–11729.
miR-224	Br J Cancer, 112, 1480–1490
miR-200b	RNA Biol, 12, 276–289
miR-200c	RNA Biol, 12, 276–289
miR-124	Biochim Biophys Acta,. pii: S0925–4439
miR-30	Mol Cell Biol, 35, 988–1000
miR-214	Hum Mutat, 33, 551–560
miR-455-3p	PLoS One, 9, e109430
miR-17	Oncotarget, 5, 2974–2987
miR-128	Oncotarget, 6, 5412–5425
1miR-130b	Neoplasia, 15, 1218–1231
bmiR-152	Mol Cell Biochem, 345, 283–290
miR-34b	Med Oncol, 31, 894
miR-25	Int J Mol Med, 34, 1286–1292
miR-20b	Hum Immunol, 75, 348–353
miR-24	Eur J Cancer, 51, 409–420
miR-18b	Cancer Res, 70, 8233–8246
miR-93-5p	PLoS One, 8, e83025
miR-324-5p	Unknown
miR-139-3p	Oncol Rep, 25, 739–747
miR-222-5p	Exp Cell Res, 318, 2168–2177

Supplementary Table S3: List of PCR Primers

Gene	Forward	Reverse	cycle
nPTB	gcatttgccaaggagacatcc	cgctgcacatctccataaacac	35
nPTB(minigene)	atcggtaccggcttcctgttgcagctgttc	atcgatatccaagttgtgattggtttcc	30
nPTB(minigene mut)	aaagtctgtttaccggcttcggtatgttattg	caataacataccgaagccggtaaacagacttt	18
hRBM4 (ORF)	atctctagatggtccggtcatcgaatgtg	atcgcggccgcgcgctccgtacgcgttgttg	30
hRBM4 (ORF mut)	cgggcagaggatgcaggggaggccatcaggggc	gcccctgatggcctcccctgcatcctctgcccg	18
miR-92a-2	tattgcacttgtcccggcctgt		
miR-92a-2 (WT)	gtgaattcctgtgtgatattctgctg	ggctcgagtgccaaatctgacacgc	35
miR-92a-2 (m5P)	accccctttctacacatgttgggatcggttgc	gcaaccgatcccaacatgtgtagaaaggggt	10
miR-92a-2 (m3P)	gtgtttctgtatggtcttgcacttgtcccgg	ccgggacaagtgcaagaccatacagaaacac	18
SV40miR-polyA(R)	ttttggaggcctaggctttt	ccgaggcggccgacatgttt	35
FGFR2	ggatcaagcacgtggaaaagaac	ggcgattaagaagacccctatgc	35
PKM1/2	agaaacagccaaaggggact	cattcatggcaaagttcacc	35
GAPDH	cggagtcaacggatttggtcgtatg	agccttctccatggtggtgaagac	30
RBM4	taggatccgcagtgcgtac	ttaaaaggctgagtccgcg	35
16S rRNA	agagtttgatcmtggctcag	ggmtaccttgttacgactt	
Pri-miR-92a-1	ctttctacacaggttg	caaactcaacaggc	
Pri-miR-92a-2	tctccagcactcatgcc	ctttcttccacaggccg	



Supplementary Figure S1: Polypyrimidine tract-binding protein (PTB) modulated the splicing patterns of the *FGFR2* and *PKM* genes HCT-116 cells were transfected with empty vector or PTB expressing vector, followed by total RNA extraction. Splicing profiles of FGFR2 and PKM pre-mRNAs were analyzed as described in "Materials and methods" section.