

Supplementary Material

Supplementary Figures and Tables

1.1 Supplementary Tables

Table S1. Sequences of RNA oligos.

Name	Sequence (5'→3')
RBM24 siRNA-383 sense	CCACCUACACCAAGAUCUUTT
RBM24 siRNA-383 antisense	AAGAUCUUGGUGUAGGUGGTT
RBM24 siRNA-857 sense	CCUACGAGCAAUACCCGUATT
RBM24 siRNA-857 antisense	UACGGGUAUUGCUCGUAGGTT
RBM24 siRNA-1017 sense	GCAGACAGAUCGUAUGCAATT
RBM24 siRNA-1017 antisense	UUGCAUACGAUCUGUCUGCTT
MYOD1 siRNA-212 sense	GCCGAUGACUUCUAUGACGTT
MYOD1 siRNA-212 antisense	CGUCAUAGAAGUCAUCGGCTT
MYOD1 siRNA-628 sense	GCAGGAGGAUGCAUACUACTT
MYOD1 siRNA-628 antisense	GUAGUAUGCAUCCUCCUGCTT
MYOD1 siRNA-759 sense	GCUACGACAGCAGCUACUATT
MYOD1 siRNA-759 antisense	UAGUAGCUGCUGUCGUAGCTT
negative siRNA / mimic sense	UUCUCCGAACGUGUCACGUTT
negative siRNA / mimic antisense	ACGUGACACGUUCGGAGAATT
miR-M2-5p mimic sense	GUUGUAUUCUGCCCCGGUAGUCCG
miR-M2-5p mimic antisense	GACUACCGGGCAGAAUACAACUU
mut-miR-M2-5p mimic sense	GGUUGCUUCUGCCCCGGUAGUCCG
mut-miR-M2-5p mimic antisense	GACUACCGGGCAGAAUACAACUU
miR-M2-5p inhibitor	CGGACUACCGGGCAGAAUACAAC
inhibitor negative control	CAGUACUUUUGUGUAGUACAA

Table S2. Primers used for 3'-RACE PCR.

Name	Sequence (5'→3')
miR-M2-5p hybrid-primer	CGGRCTRCCGGGCRGRATACAA
3'-RACE out primer	TACCGTCGTTCCACTAGTGATTT
3'-RACE inner primer	CGCGGATCCTCCACTAGTGATTTCACTATAGG

Note: "R" in the sequence of miR-M2-5p hybrid-primer represents for "A" or "G"

Table S3. Primers and oligonucleotides used for making wild or mutated types of psiCHECK-2-3'UTR plasmids.

Name	Sequence (5'→3')	Location	Length
RBM24-3'UTR-F	CCGCTCGAGCATCCAAATCTTGTTGTTAG	1202-1319	118
RBM24-3'UTR-R	GAATGCGGCCGCTGCTACTCCTGCCACTCT		
MYOD1-3'UTR-F	CCGCTCGAGCAATCCAATCTACCAAGTG	1030-1400	371
MYOD1-3'UTR-R	GAATGCGGCCGCCAGGGGTAATAAGGAGAAG		
RAC1-3'UTR-F	CCGCTCGAGGTTATTTCCAGCCCAGTA	1797-2134	338
RAC1-3'UTR-R	GAATGCGGCCGCTTTAGTGGTCGAAAGGGT		
ADRBK2-3'UTR-F	CCGCTCGAGAGTGGTTGTTCTGCGTATG	4828-4937	110
ADRBK2-3'UTR-R	GAATGCGGCCGCACACGACCACAACACTATTTACT		
APMAP-3'UTR-F	CCGCTCGAGCCTTGGTTTGACTGCTCT	1423-1762	340
APMAP-3'UTR-R	GAATGCGGCCGCATGTTGCTGCCTCTACCA		
WVOX-3'UTR-F	CCGCTCGAGTCATCGTAACTGGTGGGT	1062-1573	512
WVOX-3'UTR-R	GAATGCGGCCGCCCTCCTTGGGTTACACTT		
EMP2-3'UTR-F	CCGCTCGAGTGGCTATTCCTTTGTCTTA	626-1263	638
EMP2-3'UTR-R	GAATGCGGCCGCTTTGCAGAGCAAGTGGTT		
KIF14-3'UTR-F	CCGCTCGAGAAAACACTACCGTATGAGACAAA	6734-7114	381
KIF14-3'UTR-R	GAATGCGGCCGCAAGCAACACCGCACCTCA		
GNB1-3'UTR-F	CCGCTCGAGCAGCGGATTGTTCTGTTA	2737-3052	316
GNB1-3'UTR-R	GAATGCGGCCGCTCATGTCAAACCTGCTTTATT		
ATP8A2-3'UTR-F	CCGCTCGAGTAATGTCCTCTGGTCGTTT	9058-9176	119
ATP8A2-3'UTR-R	GAATGCGGCCGCGCTGTTCAAAGCTACAAATT		
BACE2-3'UTR-F	CCGCTCGAGAGGAAACAACAAAACGAA	2925-3482	558
BACE2-3'UTR-R	GAATGCGGCCGCTGACGGATTGGGAGATTC		
FGD3-3'UTR-F	CCGCTCGAGCACTGACATTCCGTTCCGC	3856-4385	530
FGD3-3'UTR-R	GAATGCGGCCGCCAAATACAAGTGAACAGGAAAA		
PIGG-3'UTR-F	CCGCTCGAGAAAGCTACGTGGAGATACC	2365-2862	498
PIGG-3'UTR-R	GAATGCGGCCGCGTGTAACGCAGGACAAGC		
Mut-RBM24-3'UTR-F	TCGAGGCATCCAAATCTTGTTGTTAGAGGGGAGTGG TTCTCGGCCATGGCTAGTTGC	1201-1250	50
Mut-RBM24-3'UTR-R	GGCCGCAACTAGCCATGGCCGAGAACCACTCCCCT CTAACAAACAAGATTTGGATGCC	1201-1250	50
Mut-MYOD1-3'UTR-F	TCGAGGGAGAATAGGGAACCTGGCTCTTGTTTAGCC AGGAGAAAAGAAATCTACAGC	1311-1360	50
Mut-MYOD1-3'UTR-R	GGCCGCTGTAGATTTCTTTTCTCCTGGCTAAACAAG AGCCAGGTTCCCTATTCTCCC	1311-1360	50
Mut-RAC1-3'UTR-F	TCGAGAATGTTCTGTACATCCTCAGCTGGCAGGATA ACTCTGTTGAACTACACCCTGC	2071-2121	51
Mut-RAC1-3'UTR-R	GGCCGCAGGGTGTAGTTCAACAGAGTTATCCTGCCA GCTGAGGATGTACAGAACATTC	2071-2121	51
Mut-KIF14-3'UTR-F	TCGAGTCTTTTTGCACTTTTTCGGCTTTGGAGGGCAT AGCTTTCATGCTGAACTAGTGC	6950-7000	51

Mut-KIF14-3'UTR-R	GGCCGCACTAGTTCAGCATGAAAGCTATGCCCTCCA AAGCCGAAAAGTGCAAAAAGAC	6950-7000	51
Mut-WWOX-3'UTR-F	TCGAGATGTTAAGTACTAATGGGAAATGGGGATAAC CCCGGGTTAAAGGGACAATGGC	1449-1499	51
Mut-WWOX-3'UTR-R	GGCCGCCATTGTCCCTTTAACCCGGGGTTATCCCCAT TTCCATTAGTACTTAAACATC	1449-1499	51
Mut-EMP2-3'UTR-F	TCGAGTGTACTGTGTTCTTAATATGAAACAGATAACT TAACAAAAACAACCAACAGC	825-875	51
Mut-EMP2-3'UTR-R	GGCCGCTGTTGGTTGTTTTTTGTTAAGTTATCTGTTT CATATTAAGAACACAGTACAC	825-875	51

Table S4. Primers used for qRT-PCR in this study.

Name	Sequence (5'→3')
RT-qPCR-RBM24-F	AGGATCATGCAGCCAGGTTT
RT-qPCR-RBM24-R	GTGGATAGACATAGTGAGCTGGG
RT-qPCR-MYOD1-F	GGCGGCTCAGCAAGGTCAAC
RT-qPCR-MYOD1-R	AGGCTCTCGATGTAGCGGATGG
RT-qPCR-RAC1-F	AGAAGAAGCTGACTCCTATCACCTACC
RT-qPCR-RAC1-R	GCCTCGCTGTGTAAGTGCTGAG
RT-qPCR-WWOX-F	TGGTGGTCGTGTCTCAGAGTC
RT-qPCR-WWOX-R	AAGGCGTCGGTTCAGCTCATTG
RT-qPCR-EMP2-F	GGTCATGCTGTTCCATCTCCATTCC
RT-qPCR-EMP2-R	TAACTTCTTGCCAGTCCTGTTGTGC
RT-qPCR-KIF14-F	TTGAGTTGTTCTTAGGAAGCCAGGAAG
RT-qPCR-KIF14-R	AAGAGGAGATAGCAGCAGCATTATGAC
RT-qPCR-gB-F	TCTAGGGCATGGCACACGAC
RT-qPCR-gB-R	GAATACGGAAACACAGGAGCGG
RT-qPCR-pp38-F	CCGAAAGACAAAACCCAAAT
RT-qPCR-pp38-R	ATGTAACCAGCATATAAGAACGC
RT-qPCR-p63-F	TTCGGCAAGGAACTCATGGCATACT
RT-qPCR-p63-R	TGGTGCTGCTGTTGCTGCTG
RT-qPCR-p21-F	GTGACTGCTGCTGCTGAGGATG
RT-qPCR-p21-R	AACTACAGACTCGGCATTGCTTCG
miR-M2-5p reverse-transcribed	CTCAACTGGTGTCTGGAGTCGGCAATTCAGTTGA GCGGACTAC
miR-M3-5p reverse-transcribed	CTCAACTGGTGTCTGGAGTCGGCAATTCAGTTGA GGCGGGAGA
miR-neg reverse-transcribed	CTCAACTGGTGTCTGGAGTCGGCAATTCAGTTGA GAACGTCTC
gga-miR-1 reverse-transcribed	CTCAACTGGTGTCTGGAGTCGGCAATTCAGTTGA GTACATACT
gga-miR-206 reverse-transcribed	CTCAACTGGTGTCTGGAGTCGGCAATTCAGTTGA GCCACACAC
gga-miR-223 reverse-transcribed	CTCAACTGGTGTCTGGAGTCGGCAATTCAGTTGA GGGGGTATT
U6 reverse-transcribed	CTCAACTGGTGTCTGGAGTCGGCAATTCAGTTGA GAAAAACATGG
RT-qPCR-miR-M2-5p-F	ACACTCCAGCTGGGGTTGTATTCTGCCCGGT
RT-qPCR-miR-M3-5p-F	ACACTCCAGCTGGGATGAAAATGTGAAACCTC
RT-qPCR-miR-neg-F	ACACTCCAGCTGGGGTACTGCGCGTGGA
RT-qPCR-gga-miR-1-F	ACACTCCAGCTGGGTGGAATGTAAGAAG
RT-qPCR-gga-miR-206-F	ACACTCCAGCTGGGTGGAATGTAAGGAAGT
RT-qPCR-gga-miR-223-F	ACACTCCAGCTGGGTGTCAGTTTGTCAA
RT-qPCR-miR-universal-R	CTCAACTGGTGTCTGGAGTCGGCAATTCAG

RT-qPCR-GAPDH-F	GGTAGTGAAGGCTGCTGCTGATG
RT-qPCR-GAPDH-R	AGTCCACAACACGGTTGCTGTATC
U6-F	CTCGCTTCGGCAGCACA
U6-R	AACGCTTCACGAATTTGCGT

Table S5. Putative host mRNA targets for miR-M2-5p acquired by hybrid-PCR

No.	Gene Abb.	Acc. No.	mRNA : miRNA interaction	Location
1	RAC1	XM_015294138.1	5' UCCUCAGCUGGCAGGAAUACAG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
2	ARIH1	NM_001030387.1	5' GGGGCCUGGGACAGAACGCGG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
3	RBM24	NM_001012863.2	5' UUAGAGGGGAGUGGUAGUGCGG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
4	ADRBK2	XM_015275493.1	5' GGGGCUGUUGCAGUGUACAG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
5	APMAP	NM_001006177.1	5' UAUUAAUGGCUGGCCAAUACGG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
6	WVOX	NM_001030574.2	5' UAAUGGGAAAUGGGGAAUACGG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
7	VMA21	NM_001031127.1	5' UCCUUUGUGAAGCAGAACACAA3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
8	EMP2	XM_414935.5	5' CUUAAUUGAAACAGAAUACAA3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
9	MYOD1	NM_204214.2	5' GGAACCGGCUCUUGAAUACGG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
10	TPT1	NM_205398.1	5' GAAAUGUUAACAAUCAAACAU3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
11	PIGG	XM_015280488.1	5' CAAUUGUUGUCAGAGUGCGA3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
12	SET	NM_001030691.2	5' AAAUACCUUGAGCAGAACACAG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
13	ENC1	XM_015277651.1	5' GGCUCCCGUCAGAAAUGGAA3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
14	SIRT7	NM_001291971.1	5' UGCGACGGCUGGUGAGUGCGGG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
15	TBL1XR1	NM_001031369.1	5' GGGACGUAUUUCGCCAAACUU3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
16	KIF14	XM_422190.5	5' UCGGCUUGGAGGGCAAUGCAA3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
17	GPR64	XM_015272778.1	5' UAUGUCUGAGACGGAUACGAC3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR

18	RGMB	XM_424860.5	5' AGGGCCCCAGCUCUGACUGCAG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
19	WNT5A	XM_015292956.1	5' CUGGCUAUCUUUCGAAACACAG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
20	GNB1	NM_001012835.2	5' ACUUCAAGAAAGCUGGAUGCAA3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
21	ATP8A2	XM_004938793.2	5' UUCCCUCCAGACUGAAUACAA3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
22	BACE2	XM_015301191.1	5' UGGACUGACUUCUGAAUACAA3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
23	TDO2	XM_420377.5	5' CUGAAUCUGCUAAGGGU AUGG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
24	CTSO	NM_001031129.1	5' CCAUACCCUAGCAGAUUACAG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
25	FGD3	XM_414331.5	5' UAUACUGCCAACUGGGAUACGA3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	3'UTR
26	SMAD5	XM_015293968.1	5' AAGCGUCCAAGAAAGAAUACAG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	5'UTR
27	UPF2	XM_015297566.1	5' CAGACUUGCCUGGGU AACACAA3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	5'UTR
28	EIF5B	NM_001038496.1	5' AACAAGAGCGAGGACAGUGCAA3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	CDS
29	GTF3A	NM_001113571.1	5' AUGUGGUUGUGACAGAAUGCAA3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	CDS
30	ATP5C1	NM_001278096.1	5' ACCACCAGUGAGCAGAGUGCAA3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	CDS
31	EIF5B	NM_001038496.1	5' AACAAGAGCGAGGACAGUGCAA3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	CDS
32	ANXA11	NM_001012903.3	5' UGGACAUACGUGCAGAAUACAA3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	CDS
33	ANXA4	XM_015297501.1	5' GAGACUGCUCAGGAGACUACAG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	CDS
34	RPL21	XM_001233392.3	5' AGGACU AACGGGAAGGAUCCGG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	CDS
35	LYAR	XM_004936167.2	5' GACAGCACUUUGCAGAAUCAGG3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	CDS
36	ATP5I	NM_001097534.2	5' GAGGAGCUCGAACGGAUUGCAA3' 3' GCCUGAUGGCCCGUCUUAUGUUG5'	CDS

37	ENAH	NM_204300.1	5' ACCCAGUGCCAAUGGAGUACAG3'	CDS
			3' GCCUGAUGGCCCGUCUUAUGUUG5'	
38	HNRNPD	NM_001031143.1	5' ACAACAACUACUACGGAUACAG3'	CDS
			3' GCCUGAUGGCCCGUCUUAUGUUG5'	
39	RPS6	NM_205225.2	5' AAACGCCAGGAGCAGAUUGCGA3'	CDS
			3' GCCUGAUGGCCCGUCUUAUGUUG5'	
40	RTF1	XM_421139.5	5' AGACCCGGCUCGACUGGAGCAA3'	CDS
			3' GCCUGAUGGCCCGUCUUAUGUUG5'	
41	ZNHIT6	XM_422364.5	5' GUCUCCUCGGUCAGAUGUACAA3'	CDS
			3' GCCUGAUGGCCCGUCUUAUGUUG5'	
42	TOP1	NM_205110.1	5' AACACCCGCACAAAGAGCACAA3'	CDS
			3' GCCUGAUGGCCCGUCUUAUGUUG5'	
43	RPL5	NM_204581.4	5' CUCAGGGCCAGGAGCGUGCAG3'	CDS
			3' GCCUGAUGGCCCGUCUUAUGUUG5'	
44	PSMC5	NM_001292069.1	5' GGCUGUUGCCAAGGUGAUGCAG3'	CDS
			3' GCCUGAUGGCCCGUCUUAUGUUG5'	
45	RPL30	XM_015282954.1	5' GUAAAUACGUGCUAGGAUACAA3'	CDS
			3' GCCUGAUGGCCCGUCUUAUGUUG5'	
46	TRIO	XM_015282226.1	5' AUUCUUGUUAAAAACAGUauc3'	CDS
			3' GCCUGAUGGCCCGUCUUAUGUUG5'	
47	CHMP5	NM_001277399.1	5' GAGGGGCCUGCAAAGAAUACAG3'	CDS
			3' GCCUGAUGGCCCGUCUUAUGUUG5'	
48	CMSS1	NM_001285926.1	5' UCUGCUUGCAGCACAUAAUAU3'	CDS
			3' GCCUGAUGGCCCGUCUUAUGUUG5'	
49	GNAS	XM_015296547.1	5' UGACUGUCGGGACAUUAUCAG3'	CDS
			3' GCCUGAUGGCCCGUCUUAUGUUG5'	
50	PIGX	XM_015277133.1	5' ACCACCUCUGUCAGUGGUACAG3'	CDS
			3' GCCUGAUGGCCCGUCUUAUGUUG5'	
51	ITSN1	XM_015299993.1	5' AGCUGGAACGGGCAGAGCAAGA3'	CDS
			3' GCCUGAUGGCCCGUCUUAUGUUG5'	

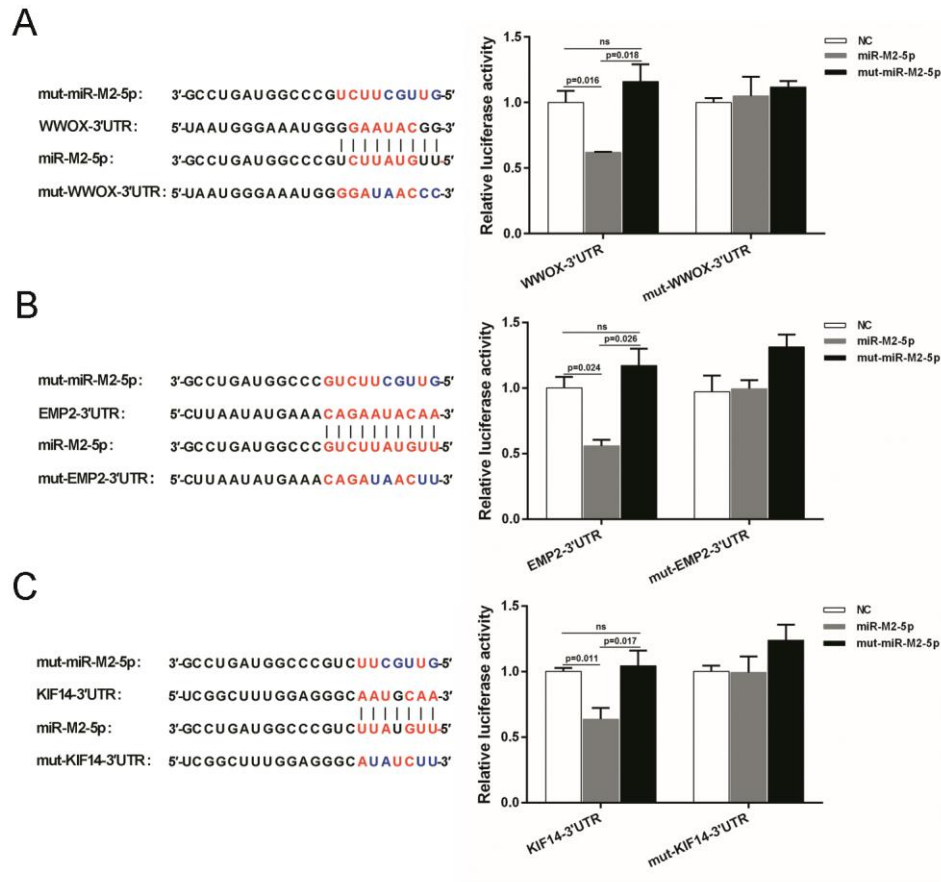
Table S6. Putative host mRNA targets for miR-M2-3p acquired by hybrid-PCR

No.	Gene Abb.	Acc. No.	mRNA : miRNA interaction	Location
1	CCL3	XM_015296023.1	5' ACAATTAGATGCAGCAGTCC 3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
2	PSMA2	NM_001012860.2	5' GGGTGCAAATGCAGCAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
3	RNF14	NM_001030623.2	5' CTGTGCCTTGTGCCAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
4	SIPA1L1	XM_010711501.2	5' TGCATCTCTGCGTGCACTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
5	NFκBIZ	NM_001006254.1	5' CACTGTCAGTCAGGCAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
6	MAPK6	NM_001030549.1	5' AGCTTATTCTGAGGCTATCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
7	ARID4A	XM_015287509.1	5' GTTGAAACTTTGGCAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
8	RFC1	XM_015285652.1	5' TGAGAAAAATGCTGCAGACC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
9	CNEP1R1	NM_001198857.2	5' AGCAATTCTCCGCCCGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
10	CLIC4	XM_015297737.1	5' CTATTCCTGCTCGGTTGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
11	ARIH1	NM_001030387.1	5' GGGACAGAACGCGGAAGTCA3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
12	AKR1E2	NM_001243590.1	5' CTTTCTTAATGCGGCTGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
13	RDH12	XM_421193.5	5' CTATCCATGTACATCAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
14	ZNF385B	XM_013093934.1	5' AGCATCTTTATCTGCAATCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
15	ACADSB	NM_001031240.1	5' GGTCTCTTCATGTGCAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
16	KCTD10	XM_415191.5	5' ACTTTGAGTGAGGGCAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
17	PTBP3	XM_004949517.2	5' TTATCTGTTACGGAAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
18	ZNHIT3	XM_015296154.1	5' AAGCCATTCTGCAGCACCCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR

19	ROCK2	XM_015276087.1	5' TCGTCATCATGGGCAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
20	RCAN1	NM_001278079.1	5' GTTCTGCTTCTGGCAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
21	ABCB10	XM_015284390.1	5' TGCTGATTTTGTGGCAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
22	GUCY1A2	XM_015852224.1	5' GCTAGGAGCAGACCAATTCT3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
23	PSMD1	NM_001012600.3	5' CTGTTCAAGTGCATGCAGCCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
24	CRNKL1	XM_419315.5	5' AAGTTCTATCTGTGCAATCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	3'UTR
25	C5H11ORF58	XM_015286530.1	5' ACACGATGAAGCTGCGGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	CDS
26	PRPF6	XM_417426.5	5' AGCCTGTTCTCAAGCGGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	CDS
27	ZC3H11A	NM_001031030.1	5' ACAAGCTTTCTGTGCAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	CDS
28	MPP4	XM_015289463.1	5' TCAGCTGTTGTCTGCAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	CDS
29	ATF4	NM_204880.2	5' CCTGTGGCTCTGTGCGGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	CDS
30	HNRNPA3	XM_015289584.1	5' ACAGTGGACAGCAGCAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	CDS
31	FAM18B1	NM_001030699.1	5' AGCAGTTTTTGGCGCAGACC3' 3' UUCGAUAAGACGCCGUCAGGC5'	CDS
32	PRKG1	XM_015278708.1	5' GAACTCCTGACTGGCAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	CDS
33	ZC3H11A	NM_001031030.1	5' ACAAGCTTTCTGTGCAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	CDS
34	MRPS2	XM_015279792.1	5' CTTCTATCCTGGACCCTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	CDS
35	PHF3	XM_015284854.1	5' CTGTAATCCTCGGCGCTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	CDS
36	ZFR	XM_015848318.1	5' GGAGGAACCTCAGGCAGTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	CDS
37	RPL27	XM_015299594.1	5' CGGTATTCTGTTGACATTCC3' 3' UUCGAUAAGACGCCGUCAGGC5'	CDS

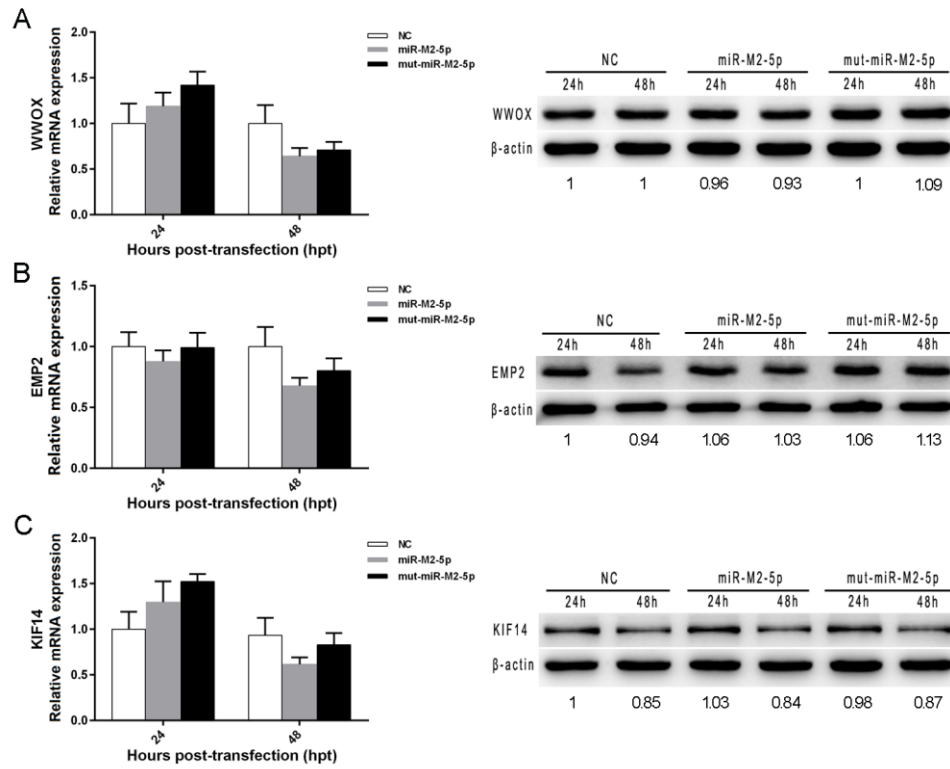
38	ELF1	NM_001006269.1	5' TAGATGATCCTGAGCAGTCC3'	CDS
			3' UUCGAUAAGACGCCGUCAGGC5'	
39	CCDC88C	XM_015287749.1	5' TGAAAGAACAGCACCAGTCC3'	CDS
			3' UUCGAUAAGACGCCGUCAGGC5'	
40	HS6ST1	NM_204482.1	5' AGAGGCTTCTTCACCGGTCC3'	CDS
			3' UUCGAUAAGACGCCGUCAGGC5'	
41	MDH1	NM_001006395.2	5' GGCAATTCTTACGGCGTTCC3'	CDS
			3' UUCGAUAAGACGCCGUCAGGC5'	
42	CCDC91	XM_015292478.1	5' AGGCTTTGATGCAGCAGTCA3'	CDS
			3' UUCGAUAAGACGCCGUCAGGC5'	
43	MAP1A	XM_015292140.1	5' AGCAGAGGAAAAGGCAGTCC3'	CDS
			3' UUCGAUAAGACGCCGUCAGGC5'	
44	AUS6	XM_015280096.1	5' GAAGCTATACGCTGCAGTCC3'	CDS
			3' UUCGAUAAGACGCCGUCAGGC5'	
45	TGFB2	NM_001031045.3	5' CCTCTCCGTGCTGCGTGTCC3'	CDS
			3' UUCGAUAAGACGCCGUCAGGC5'	

1.2 Supplementary Figures

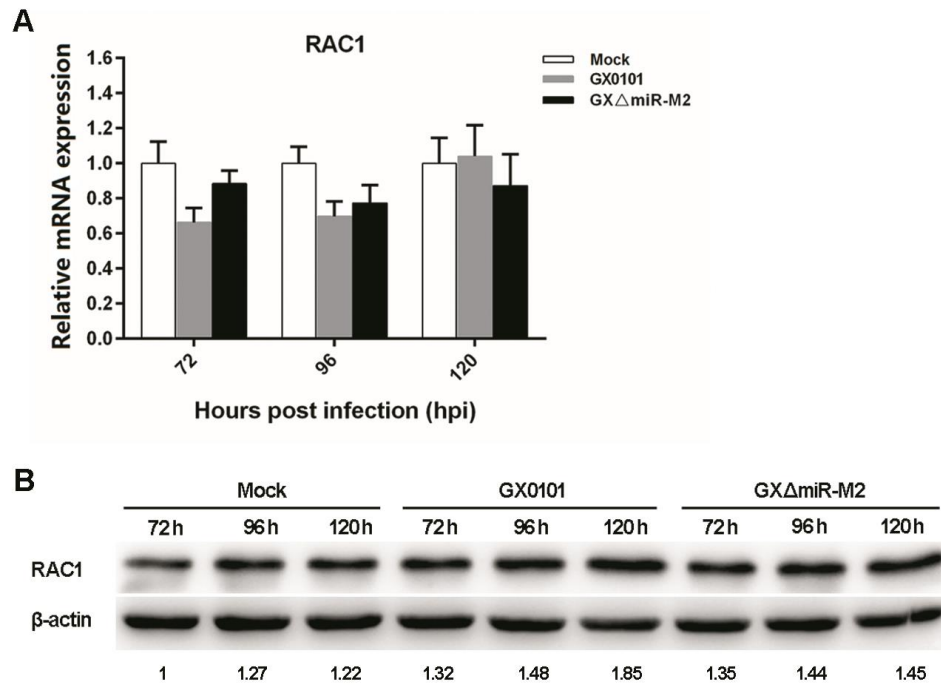


Supplementary Figure 1. Interactions between miR-M2-5p and 3'UTRs of candidate mRNA targets determined by dual luciferase reporter assay (DLRA). (A-C) DLRA performed for confirming the interactions between miR-M2-5p and 3'UTRs of mRNA candidate target genes, *WWOX*, *EMP2* and *KIF14*. The colored seed sequence of miRNA or binding sites of 3'UTRs and the corresponding mutants are shown on the left side. The wild type or mutated 3'UTRs of candidate mRNA targets were cloned into the downstream of *Renilla* luciferase in psiCHECK-2 vector, and then were co-transfected into 293T cells with the miR-M2-5p, mut-miR-M2-5p or miRNA negative control (NC) mimics, respectively. *Firefly* and *Renilla* luciferase activities

were measured at 48 h post-transfection using the dual luciferase reporter system (Promega). *Firefly* luciferase was served as the internal control. For each luciferase assay, relative luciferase activity was normalized with respect to miRNA NC. Results are shown as the mean \pm SD of three independent experiments. Independent sample *t*-test was used to analyze the statistical differences between groups. P values indicated on columns were used for statistical analyses; ns, no significance.

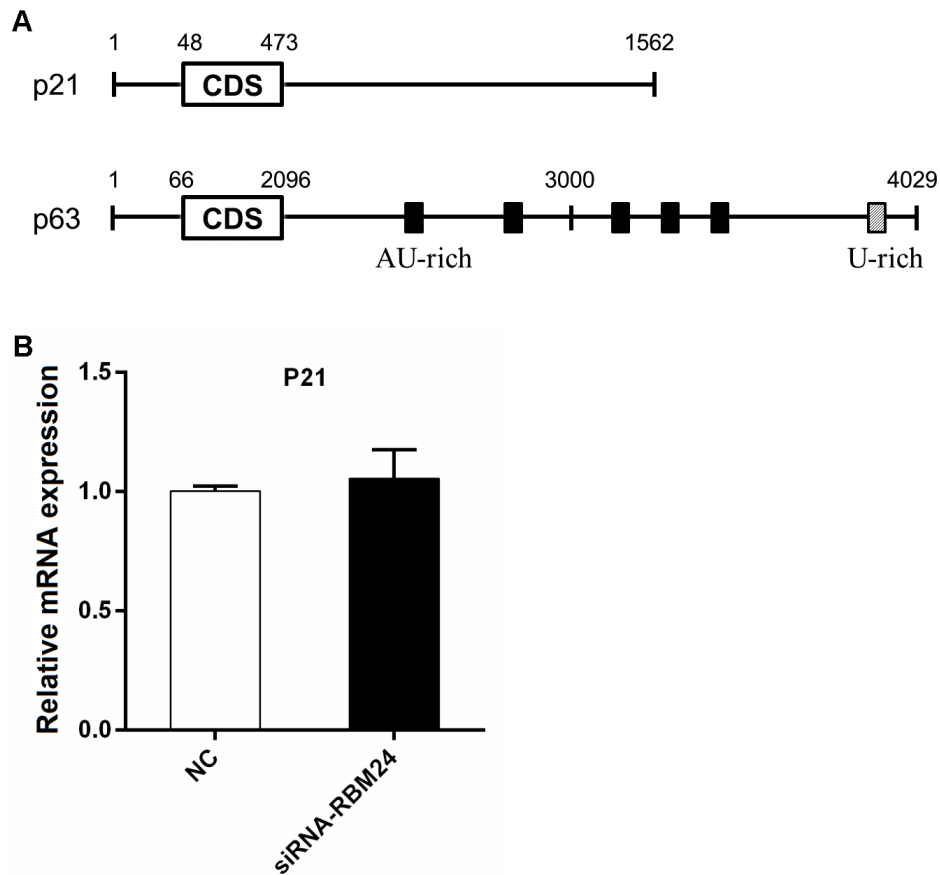


Supplementary Figure 2. (A-C) qRT-PCR and western blot analysis performed to analyze the inhibitory effect of miR-M2-5p on candidate targets WWOX, EMP2, and KIF14 respectively. Numbers below the blots indicate relative band intensity normalized to β -actin. Error bars are derived from three independent replicates.

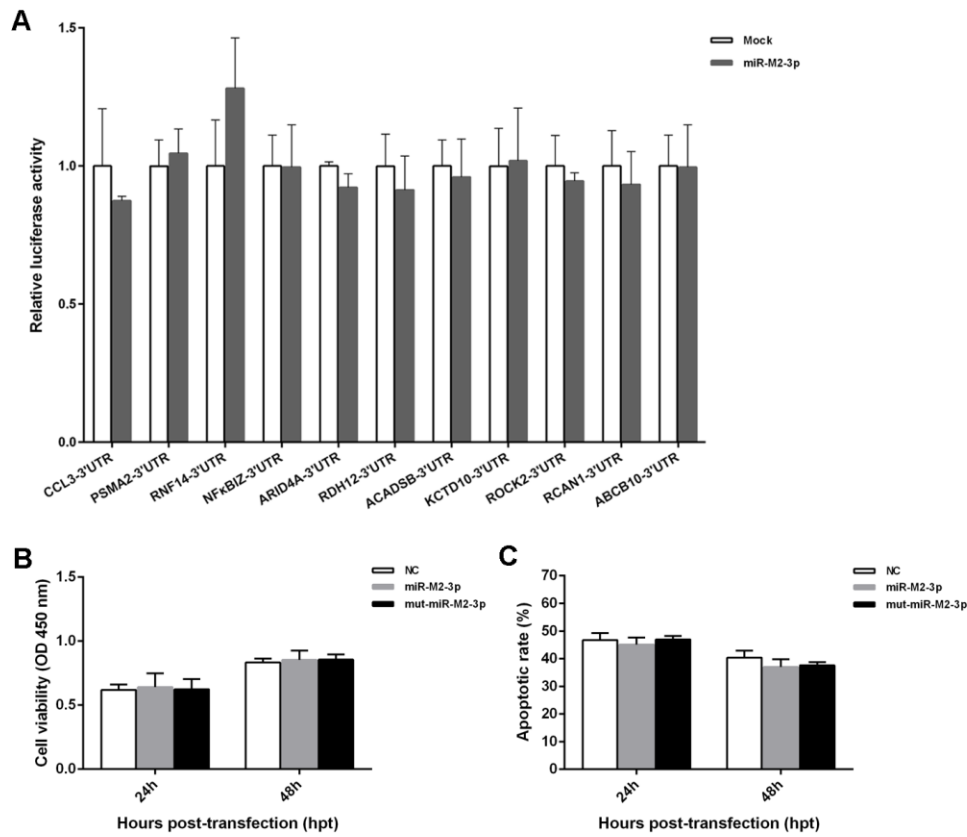


Supplementary Figure 3. Expression levels of RAC1 in CEFs infected with GaHV2.

(A) Expression levels of the RAC1 mRNA genes in virus-infected CEFs determined by qRT-PCR. Results are shown as the mean \pm SD of three independent experiments. Independent sample t-test was used to analyze the statistical differences between groups. (B) Expression levels of the RAC1 proteins in virus-infected CEFs determined by western blot. Numbers below the blots indicate relative band intensity normalized to β -actin.



Supplementary Figure 4. (A) Schematic representations of chicken *p63* and *p21* transcripts. The AU- or U-rich elements were shown in shaded boxes. The sequence comparison was done using the online tool, BLAST. (B) RT-qPCR analysis of *p21* expressions in the RBM24-silenced CEF cells at 48 hours post-transfection. Error bars are derived from three independent replicates.



Supplementary Figure 5. (A) The first round of DLRA for primary analysis of the interactions between miR-M2-3p and 3'UTRs of eleven mRNA containing perfect base pairing to the seed region of miR-M2-3p, including CCL3, PSMA2, RNF14, NFκBIZ, ARID4A, RDH12, ACADSB, KCTD10, ROCK2, RCAN1, and ABCB10. (B & C) Cell viability and apoptosis of miR-M2-3p-overexpressed CEF cells. At different time points post miRNA transfection, the CEF cells were harvested for Annexin V-FITC and propidium iodide (PI) staining for apoptosis analysis using flow cytometry. CCK-8 assay was used to assess cell viability. Error bars are derived from three independent replicates.