Supplemental material

Zhao et al., http://www.jcb.org/cgi/content/full/jcb.201501073/DC1

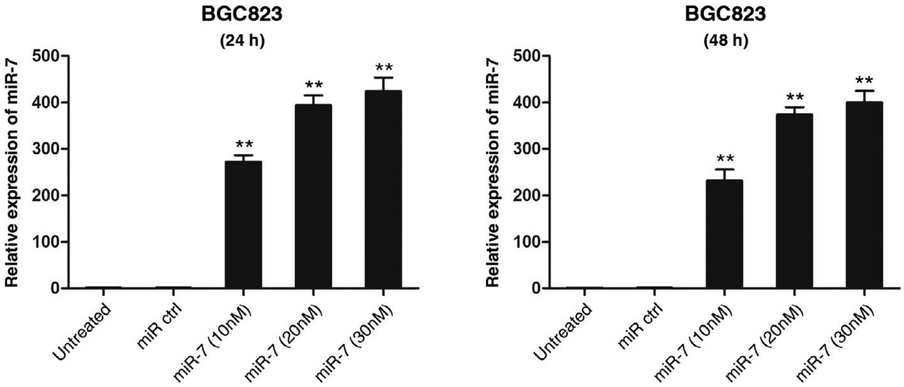

Figure S1. **The transfection efficiency of an miR-7 mimic in BGC823 cells.** Real-time PCR analysis for miR-7 expression in BGC823 cells after miR-7 mimic (miR-7) or miRNA mimic negative control (miR ctrl) transfection for 24 and 48 h (*n* = 3). Means ± SD (error bars) of three experiments performed in triplicates are shown. **, P < 0.01.

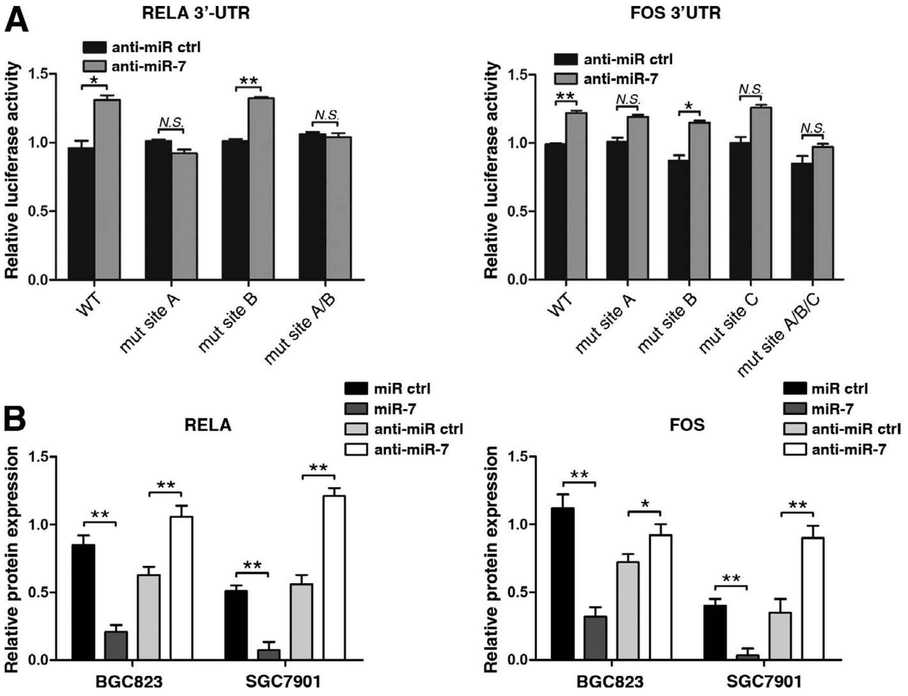

Figure S2. **miR-7 directly targets RELA and FOS 3′-UTR.** (A) Relative luciferase activity levels in BGC823 cells cotransfected with miR-7 inhibitor (anti–miR-7) or miRNA inhibitor negative control (anti-miR ctrl) and wild-type (WT) or mutant (mut) *RELA* and *FOS* 3′-UTR vectors. Means ± SD (error bars) of three experiments performed in triplicates are shown. (B) The densitometric analysis of Western blot bands for Fig. 2 C and the ratios of the protein/β-actin intensities were plotted. Means ± SD of three independent experiments are shown. *, P < 0.05; **, P < 0.01; *N.S.*, not significant (P > 0.05).

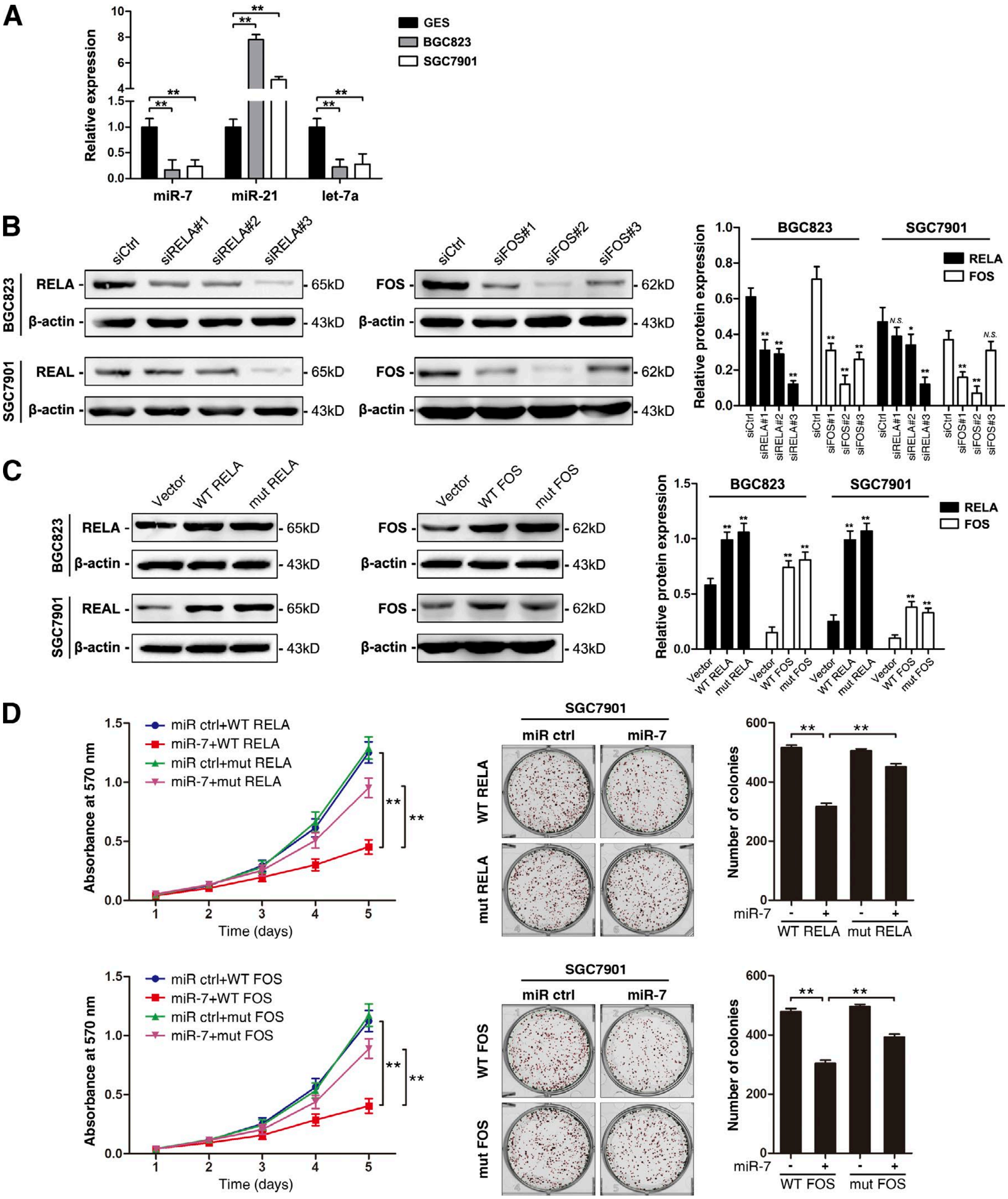

Figure S3. **Knockdown and overexpression of RELA and FOS and their effects on the growth of GC cells.** (A) Real-time PCR analysis of miR-7, miR-21, and let-7a expression in GES, BGC823, and SGC7901 cells. Means ± SD (error bars) of three experiments performed in triplicates are shown. (B, left) Transfection of RELA or FOS siRNAs significantly decreased RELA or FOS protein levels in BGC823 and SGC7901 cells. (right) The ratios of the protein/β-actin intensities were plotted. Means ± SD of three independent experiments are shown. (C, left) Transfection of RELA or FOS vectors containing wild-type or mutant 3′-UTR increased RELA or FOS protein levels in BGC823 and SGC7901 cells. (right) The ratios of the protein/β-actin intensities were plotted. Means ± SD of three independent experiments are shown. (D) Growth curves and colony formation assays of SGC7901 cells transfected with RELA or FOS vectors containing wild-type or mutant 3′-UTR and then treated with miR-7 mimic (miR-7)–transfected and miRNA mimic negative control (miR ctrl)–transfected BGC823 cells. Means ± SD of a representative experiment (*n* = 3) performed in triplicates are shown. *, P < 0.05; **, P < 0.01; *N.S.*, not significant (P > 0.05).

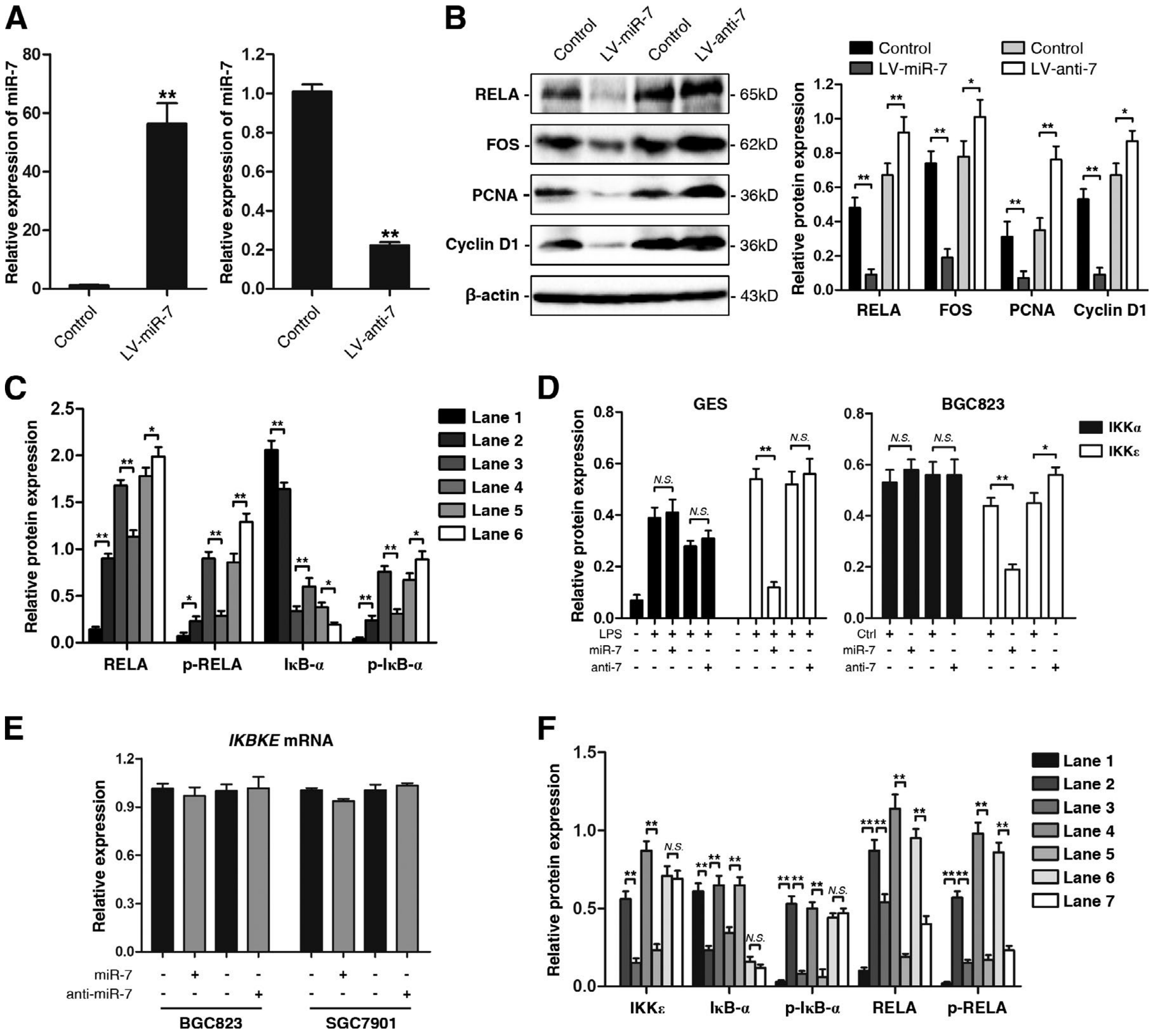

Figure S4. **miR-7 inhibits GC cell growth in vivo and regulates RELA activation by modulating IKKε.** (A) Real-time PCR analysis of miR-7 expression in BGC823 cells after infection with the indicated lentiviral vectors. Means ± SD (error bars) of three experiments performed in triplicates are shown. (B, left) The levels of RELA, FOS, PCNA, and cyclin D1 in the xenograft tumors were analyzed by Western blot. (right) The ratios of the protein/β-actin intensities were plotted. Means ± SD of three independent experiments are shown. (C and D) The densitometric analysis of Western blot bands and the ratios of the protein/β-actin intensities were plotted for Fig. 6 A (C) and Fig. 6 C (D). Means ± SD of three independent experiments are shown. (E) *IKBKE* mRNA expression in BGC823 and SGC7901 cells with the indicated transfection. Means ± SD of three experiments performed in triplicates are shown. (F) The densitometric analysis of Western blot bands and the ratios of the protein/β-actin intensities were plotted for Fig. 6 E. *, P < 0.05; **, P < 0.01; *N.S.*, not significant (P > 0.05).

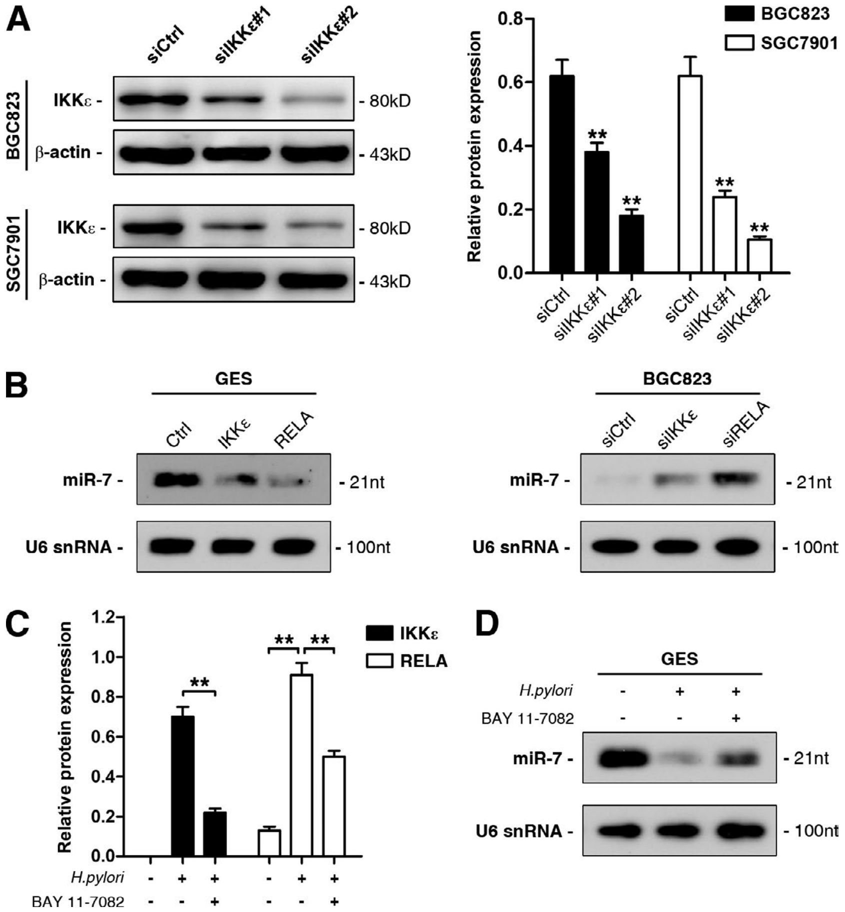

Figure S5. **The knockdown effects of IKKε siRNAs on the protein levels of IKKε in GC cells and the expression of mature miR-7 after modulating IKKε and RELA expression.** (A, left) Transfection of IKKε siRNAs significantly decreased IKKε protein levels in BGC823 and SGC7901 cells. (right) The ratios of IKKε/β-actin intensities were plotted. Means ± SD (error bars) of three independent experiments are shown. (B) Northern blot analysis of mature miR-7 levels in the indicated cells after the overexpression or silencing of IKKε and RELA. (C) The densitometric analysis of Western blot bands for Fig. 7 E. The ratios of the protein/β-actin intensities were plotted. Means ± SD of three independent experiments are shown. (D) Northern blot analysis of mature miR-7 levels after *H. pylori* infection or together with BAY 11-7082 pretreatment in GES cells. **, P < 0.01.

Table S1. **Transcripts down-regulated by miR-7 overexpression in BGC823 cells**

Gene symbol	Replicate 1 Log$_2$ RNA ratio	Replicate 2 Log$_2$ RNA ratio	Mean RNA fold change
REG4	−5.03	−4.88	−4.95
DMBT1	−4.33	−4.53	−4.43
REG1A	−3.73	−4.04	−3.89
CDKN1C	−3.69	−3.82	−3.75
LGALS4	−3.45	−3.42	−3.44
CLRN3	−3.33	−3.32	−3.32
DACT1	−3.09	−3.08	−3.08
PRSS35	−3.07	−3.01	−3.04
FOS	−3.63	−2.39	−3.01
MYH13	−3.03	−2.91	−2.97
MYH1	−3.41	−2.50	−2.96
FAM151A	−2.73	−2.71	−2.72
C11orf86	−2.37	−3.05	−2.71
CYP2B7P1	−2.57	−2.81	−2.69
PLA2G2A	−2.64	−2.72	−2.68
CEACAM6	−2.59	−2.67	−2.63
CXCR7	−2.57	−2.68	−2.63
CNDP1	−2.35	−2.86	−2.60
CYP2B6	−2.57	−2.49	−2.53
LOC100128893	−3.43	−1.55	−2.49
MMP9	−2.52	−2.44	−2.48
CDH17	−2.54	−2.38	−2.46
HEPH	−2.65	−2.23	−2.44
ABCG2	−2.67	−2.13	−2.40
NRAP	−2.09	−2.70	−2.40
CLEC3B	−2.27	−2.48	−2.37
KLK1	−2.44	−2.29	−2.36
S100A9	−1.90	−2.80	−2.35
REG1B	−2.43	−2.22	−2.33
MYH8	−2.17	−2.47	−2.32
SLPI	−2.30	−2.24	−2.27
SNCAIP	−2.30	−2.24	−2.27
PDZRN3	−2.45	−1.85	−2.15
RELA	−1.94	−2.27	−2.10
DNAH8	−2.30	−1.88	−2.09
SYTL2	−2.12	−1.99	−2.06
UST	−2.11	−1.98	−2.04
HSD3B1	−2.02	−2.04	−2.03
SPTA1	−2.07	−2.00	−2.03
RELN	−2.23	−1.83	−2.03
MCHR2	−1.59	−2.44	−2.01
F5	−2.53	−1.48	−2.00
TDGF1	−1.35	−2.63	−1.99
AK4	−1.97	−1.97	−1.97
APOD	−1.72	−2.14	−1.93
KCNJ2	−1.83	−2.03	−1.93
LYZ	−1.81	−2.03	−1.92
REG3A	−1.73	−2.06	−1.90
ACSL6	−2.03	−1.74	−1.89
C19orf77	−2.02	−1.73	−1.88
CCND1	−1.99	−1.69	−1.84
POLE4	−1.80	−1.87	−1.83
BDKRB1	−1.93	−1.68	−1.81
BDKRB2	−1.82	−1.78	−1.80
C6orf223	−1.31	−2.28	−1.80
PRICKLE1	−1.41	−2.18	−1.79
ALPI	−1.81	−1.75	−1.78
ST6GALNAC3	−1.76	−1.77	−1.77
LINC00312	−2.48	−1.05	−1.76
KCNK10	−2.11	−1.42	−1.76
MYOM1	−1.65	−1.84	−1.74

Table S1. **Transcripts down-regulated by miR-7 overexpression in BGC823 cells** *(Continued)*

Gene symbol	Replicate 1 Log_2 RNA ratio	Replicate 2 Log_2 RNA ratio	Mean RNA fold change
GRK5	−1.75	−1.72	−1.73
GRAMD1B	−2.21	−1.24	−1.72
SEMA3F	−1.69	−1.73	−1.71
SLC12A2	−1.72	−1.65	−1.68
VTN	−1.73	−1.62	−1.68
FGFBP1	−1.65	−1.70	−1.68
PGM1	−1.66	−1.69	−1.67
DES	−1.80	−1.54	−1.67
F10	−1.58	−1.75	−1.67
RASL11A	−1.69	−1.64	−1.66
WDFY4	−1.50	−1.80	−1.65
CTSE	−1.74	−1.56	−1.65
AIF1	−1.60	−1.67	−1.64
PIK3R3	−1.44	−1.83	−1.63
SPINK1	−1.85	−1.41	−1.63
ZNF169	−1.70	−1.52	−1.61
GPA33	−1.49	−1.71	−1.60
HS3ST1	−1.46	−1.72	−1.59
YY1	−1.68	−1.47	−1.58
DAPK2	−1.65	−1.50	−1.57
SYNE1	−1.60	−1.54	−1.57
PLA2G2E	−1.25	−1.86	−1.56
HR	−1.82	−1.27	−1.54
C10orf116	−1.63	−1.45	−1.54
VIPR1	−1.66	−1.39	−1.52
LGR5	−1.62	−1.42	−1.52
CDHR5	−1.61	−1.43	−1.52
CREG2	−1.61	−1.42	−1.52
VRTN	−1.37	−1.66	−1.51
PIP5K1B	−1.53	−1.46	−1.49
FAM124B	−1.48	−1.50	−1.49
KLF2	−1.54	−1.43	−1.49
PDGFRA	−1.46	−1.49	−1.48
CCRL2	−1.47	−1.48	−1.47
LOC100505633	−1.35	−1.59	−1.47
PDZK1IP1	−1.55	−1.39	−1.47
ATP1B1	−1.41	−1.53	−1.47
SLC5A1	−1.56	−1.37	−1.46
DNAH2	−1.48	−1.45	−1.46
LIPG	−1.41	−1.50	−1.46
SEMA3B	−1.51	−1.38	−1.45
CCND2	−1.52	−1.37	−1.44
ANXA1	−1.54	−1.35	−1.44
IL1B	−1.59	−1.30	−1.44
FAM113B	−1.76	−1.12	−1.44
SULT2A1	−1.27	−1.60	−1.43
TM4SF5	−1.38	−1.49	−1.43
MUC13	−1.48	−1.38	−1.43
MAN1C1	−1.44	−1.42	−1.43
FCAMR	−1.48	−1.37	−1.43
HOXA7	−1.17	−1.68	−1.42
VSIG2	−1.58	−1.27	−1.42
CEACAM7	−1.55	−1.29	−1.42
ITLN1	−1.73	−1.10	−1.41
MYO15B	−1.60	−1.20	−1.40
FCGR2A	−1.72	−1.06	−1.39
RNF186	−1.05	−1.73	−1.39
BCL2L1	−1.40	−1.37	−1.39
CHRNA7	−1.38	−1.39	−1.38
TFF1	−1.71	−1.02	−1.37
FGB	−1.09	−1.63	−1.36

Table S1. **Transcripts down-regulated by miR-7 overexpression in BGC823 cells** *(Continued)*

Gene symbol	Replicate 1 $\mathrm{Log_2}$ RNA ratio	Replicate 2 $\mathrm{Log_2}$ RNA ratio	Mean RNA fold change
DEFB1	−1.58	−1.14	−1.36
ST6GALNAC1	−1.54	−1.17	−1.35
LOC145837	−1.51	−1.19	−1.35
RGN	−1.30	−1.40	−1.35
EFNB2	−1.31	−1.34	−1.33
KRT6B	−1.35	−1.30	−1.32
KLK10	−1.37	−1.25	−1.31
SLCO2A1	−1.14	−1.48	−1.31
GPR162	−1.23	−1.38	−1.31
KIF26B	−1.31	−1.30	−1.31
MGAT3	−1.27	−1.33	−1.30
HOTTIP	−1.04	−1.53	−1.29
CALML4	−1.23	−1.32	−1.28
TBX4	−1.32	−1.22	−1.27
APOA2	−1.26	−1.28	−1.27
CYP2F1	−1.26	−1.27	−1.27
SAMD11	−1.49	−1.04	−1.26
H19	−1.23	−1.29	−1.26
SLC39A10	−1.14	−1.36	−1.25
MIRLET7BHG	−1.33	−1.16	−1.25
ASGR2	−1.37	−1.12	−1.24
EGFR	−1.18	−1.28	−1.23
IGF1	−1.23	−1.22	−1.23
NEURL3	−1.19	−1.27	−1.23
PAQR8	−1.20	−1.25	−1.22
MPP1	−1.39	−1.05	−1.22
FZD9	−1.30	−1.14	−1.22
SH3TC1	−1.09	−1.36	−1.22
IL17RE	−1.41	−1.02	−1.21
CDX2	−1.42	−1.00	−1.21
LOC100507039	−1.32	−1.08	−1.20
TJP3	−1.19	−1.21	−1.20
FLRT3	−1.31	−1.08	−1.20
AMICA1	−1.13	−1.26	−1.19
THRA	−1.21	−1.17	−1.19
FAM109A	−1.19	−1.15	−1.17
MBIP	−1.16	−1.18	−1.17
ATP8A1	−1.29	−1.05	−1.17
SLC39A4	−1.03	−1.30	−1.17
LYPD6B	−1.10	−1.20	−1.15
C9orf150	−1.08	−1.18	−1.13
ACSM3	−1.12	−1.13	−1.12
SELENBP1	−1.08	−1.16	−1.12
BAIAP3	−1.01	−1.22	−1.12
SARM1	−1.06	−1.17	−1.11
PCSK9	−1.08	−1.14	−1.11
PIWIL2	−1.11	−1.09	−1.10
MGC4294	−1.10	−1.06	−1.08
IGF2BP2	−1.06	−1.10	−1.08
GALC	−1.06	−1.08	−1.07
OAT	−1.02	−1.11	−1.07
CASP4	−1.12	−1.01	−1.06
CYP17A1	−1.09	−1.03	−1.06
TMC5	−1.00	−1.10	−1.05
ODAM	−1.05	−1.04	−1.04
HYAL1	−1.02	−1.06	−1.04
AMIGO2	−1.03	−1.05	−1.04
TSPAN8	−1.01	−1.05	−1.03

Table S2. **Proteins down-regulated by miR-7 overexpression in BGC823 cells**

Gene symbol	Replicate 1 Log$_2$ protein ratio	Replicate 2 Log$_2$ protein ratio	Mean protein fold change
CTSE	−2.73	−2.64	−2.69
TDGF1	−2.40	−2.28	−2.34
N4BP2L2	−2.26	−2.22	−2.24
MUC13	−2.06	−2.02	−2.04
PLA2G2E	−2.01	−1.93	−1.97
ZNF169	−1.96	−1.89	−1.92
SELENBP1	−1.89	−1.93	−1.91
CLEC3B	−1.82	−1.84	−1.83
SIN3B	−1.85	−1.80	−1.83
MAN1C1	−1.80	−1.83	−1.81
MLLT1	−1.77	−1.79	−1.78
MAP3K8	−1.74	−1.78	−1.76
PIWIL2	−1.75	−1.73	−1.74
TACC2	−1.73	−1.70	−1.72
IGF1	−1.71	−1.71	−1.71
IGF2BP2	−1.69	−1.71	−1.70
SLC12A4	−1.67	−1.68	−1.68
SLC39A4	−1.64	−1.66	−1.65
DES	−1.66	−1.63	−1.65
CDC45	−1.61	−1.63	−1.62
SLC5A1	−1.60	−1.61	−1.61
BCL2L1	−1.60	−1.58	−1.59
C16orf71	−1.58	−1.59	−1.59
EGFR	−1.58	−1.57	−1.57
SLPI	−1.57	−1.58	−1.57
F10	−1.56	−1.55	−1.56
IGHMBP2	−1.55	−1.53	−1.54
PEX1	−1.52	−1.56	−1.54
IL17RE	−1.53	−1.54	−1.54
CEACAM7	−1.53	−1.55	−1.54
DDX19B	−1.48	−1.52	−1.50
IGF1R	−1.51	−1.47	−1.49
ANXA1	−1.46	−1.50	−1.48
EXD2	−1.42	−1.48	−1.45
CASP4	−1.40	−1.47	−1.44
KCNJ2	−1.45	−1.39	−1.42
USP1	−1.38	−1.39	−1.39
S100A9	−1.36	−1.39	−1.38
MYH8	−1.35	−1.38	−1.37
NAGLU	−1.36	−1.37	−1.36
AK4	−1.35	−1.37	−1.36
KDM4B	−1.32	−1.33	−1.33
SYTL2	−1.31	−1.34	−1.33
IFT140	−1.30	−1.35	−1.32
CDX2	−1.31	−1.33	−1.32
RELA	−1.34	−1.31	−1.32
VTN	−1.32	−1.31	−1.32
FAM124B	−1.28	−1.35	−1.32
C1D	−1.34	−1.29	−1.31
YY1	−1.30	−1.31	−1.30
DNAH8	−1.28	−1.32	−1.30
MNX1	−1.29	−1.30	−1.29
GON4L	−1.28	−1.30	−1.29
CCRL2	−1.31	−1.27	−1.29
DUS1L	−1.27	−1.28	−1.27
PANK4	−1.26	−1.28	−1.27
IKBKE	−1.25	−1.28	−1.27
C4orf27	−1.29	−1.24	−1.27
PRC1	−1.27	−1.26	−1.26
ACAP2	−1.26	−1.27	−1.26
C1orf131	−1.23	−1.29	−1.26

Table S2. **Proteins down-regulated by miR-7 overexpression in BGC823 cells** *(Continued)*

Gene symbol	Replicate 1 Log$_2$ protein ratio	Replicate 2 Log$_2$ protein ratio	Mean protein fold change
MBIP	−1.25	−1.26	−1.26
GRAMD1B	−1.26	−1.25	−1.26
KRT9	−1.27	−1.24	−1.26
MORC3	−1.23	−1.24	−1.24
PIK3R3	−1.24	−1.23	−1.24
ZNF431	−1.24	−1.22	−1.23
CDH17	−1.20	−1.25	−1.23
FLRT3	−1.20	−1.24	−1.22
KRT10	−0.80	−1.20	−1.00
DDX51	−0.77	−0.79	−0.78
FAM134A	−0.73	−0.79	−0.76
SCAF8	−0.70	−0.77	−0.73
PANK1	−0.68	−0.71	−0.69
ATP11A	−0.63	−0.70	−0.67

Table S3. **39 genes reduced at protein and RNA levels by miR-7 overexpression**

Gene symbol	Mean protein fold change (log$_2$)	Mean RNA fold change (log$_2$)	Prediction algorithms
CTSE	−2.69	−1.65	–
TDGF1	−2.34	−1.99	–
MUC13	−2.04	−1.43	TargetScan[a] (1)[b], miRanda[c] (2)
SELENBP1	−1.91	−1.12	–
CLEC3B	−1.83	−2.37	–
MAN1C1	−1.81	−1.43	–
PIWIL2	−1.74	−1.10	–
IGF1	−1.71	−1.23	–
IGF2BP2	−1.70	−1.08	TargetScan (1), miRanda (1)
SLC39A4	−1.65	−1.17	–
DES	−1.65	−1.67	TargetScan (1), miRanda (1)
ZNF169	−1.61	−1.92	miRanda (1)
SLC5A1	−1.61	−1.46	TargetScan (1), miRanda (1)
BCL2L1	−1.59	−1.39	TargetScan (1), miRanda (2)
EGFR	−1.57	−1.23	TargetScan (3), miRanda (4)
SLPI	−1.57	−2.27	–
F10	−1.56	−1.67	–
PLA2G2E	−1.56	−1.97	–
IL17RE	−1.54	−1.21	TargetScan (1), miRanda (2)
CEACAM7	−1.54	−1.42	miRanda (1)
ANXA1	−1.48	−1.44	–
CASP4	−1.44	−1.06	–
KCNJ2	−1.42	−1.93	TargetScan (1), miRanda (1), PicTar[d] (1)
S100A9	−1.38	−2.35	miRanda (1)
MYH8	−1.37	−2.32	–
AK4	−1.36	−2.10	–
SYTL2	−1.33	−2.06	–
CDX2	−1.32	−1.21	miRanda (2)
RELA	−1.32	−2.10	TargetScan (2), miRanda (2)
VTN	−1.32	−1.68	–
FAM124B	−1.32	−1.49	miRanda (3)
YY1	−1.30	−1.58	TargetScan (1), miRanda (1)
DNAH8	−1.30	−2.09	–
CCRL2	−1.29	−1.47	–
MBIP	−1.26	−1.17	–
GRAMD1B	−1.26	−1.72	–
PIK3R3	−1.24	−1.63	TargetScan (1), miRanda (4)
CDH17	−1.23	−2.46	–
FLRT3	−1.22	−1.20	–

[a] Grimson et al., 2007.

[b] The number of putative miR-7 binding sites predicted by the indicated algorithm is shown in parentheses.

[c] John et al., 2004.

[d] Krek et al., 2005.

Table S4. **Transcripts up-regulated by miR-7 overexpression in BGC823 cells**

Gene symbol	Replicate 1 Log$_2$ RNA ratio	Replicate 2 Log$_2$ RNA ratio	Mean RNA fold change
MT1B	2.40	4.45	3.43
CST7	3.89	2.92	3.40
UBD	3.02	3.38	3.20
VTCN1	3.12	3.16	3.14
FST	2.77	3.36	3.06
LOC643401	2.58	3.46	3.02
ANGPT2	3.02	2.72	2.87
TPO	2.31	3.41	2.86
TXNRD3	3.02	2.69	2.86
TRPC3	2.83	2.88	2.86
CCL4	2.77	2.90	2.84
NPPB	3.29	2.15	2.72
VCX	2.60	2.71	2.66
MATN2	2.08	3.17	2.63
VCX3A	2.60	2.65	2.62
TTYH1	2.70	2.51	2.60
C2orf54	2.72	2.46	2.59
VCX2	2.60	2.55	2.57
CST6	1.88	3.25	2.57
MT1H	2.52	2.58	2.55
MT1L	2.57	2.52	2.55
MT1G	2.47	2.58	2.52
MT1E	2.28	2.70	2.49
ALPP	2.57	2.40	2.49
C6orf15	2.45	2.52	2.49
MT1X	2.38	2.55	2.46
LYG2	1.78	3.12	2.45
NCF2	2.46	2.40	2.43
FLJ26850	2.39	2.46	2.42
HTRA3	2.34	2.46	2.40
DEFB103B	2.39	2.41	2.40
CCL3	2.57	2.21	2.39
FGF9	2.43	2.32	2.38
HBG1	1.40	3.34	2.37
LOC100131138	2.58	2.16	2.37
ANKRD1	2.50	2.24	2.37
MT2A	2.28	2.40	2.34
LOC100506689	2.19	2.37	2.28
KRTAP3-1	2.24	2.28	2.26
MT1F	2.17	2.24	2.21
RSAD2	2.12	2.20	2.16
FHOD3	2.06	2.25	2.16
MT1A	2.14	2.09	2.12
ME1	2.43	1.62	2.02
CCL3L3	2.38	1.61	2.00
PAEP	1.66	2.33	2.00
LOC730755	2.29	1.69	1.99
GPR110	1.91	2.02	1.97
VCY	2.18	1.71	1.94
TNNT2	2.01	1.87	1.94
SIGLEC6	2.03	1.86	1.94
GZMB	2.19	1.60	1.89
ZBED2	2.02	1.76	1.89
COX7B2	1.81	1.94	1.87
SPANXD	1.97	1.77	1.87
MIA	1.85	1.88	1.87
PLAC1	1.99	1.73	1.86
RNF128	1.63	1.94	1.79
SPANXB2	2.16	1.36	1.76
KSR1	1.74	1.78	1.76
MAGEC1	1.55	1.96	1.76

Table S4. **Transcripts up-regulated by miR-7 overexpression in BGC823 cells** *(Continued)*

Gene symbol	**Replicate 1 Log$_2$ RNA ratio**	**Replicate 2 Log$_2$ RNA ratio**	**Mean RNA fold change**
SPANXA1	1.72	1.79	1.76
CXorf51A	1.61	1.82	1.71
ZNF114	1.60	1.77	1.68
ASAP1-IT1	1.39	1.97	1.68
ULBP2	1.54	1.81	1.67
LOC728485	1.44	1.87	1.65
SLC2A3	1.69	1.50	1.60
KRT34	1.33	1.85	1.59
SUSD2	1.55	1.58	1.57
XG	1.51	1.55	1.53
RGL1	1.67	1.38	1.52
C16orf73	1.17	1.88	1.52
VGLL1	1.60	1.44	1.52
KRT7	1.72	1.31	1.51
PRKCH	1.59	1.44	1.51
CRIP2	1.24	1.77	1.51
LOC100506262	1.96	1.04	1.50
SCHIP1	1.49	1.50	1.49
HLA-DQB1	1.34	1.62	1.48
GLI2	1.07	1.82	1.44
LY6K	1.29	1.59	1.44
CCND3	1.47	1.40	1.43
MYH7B	1.44	1.39	1.42
MAP1B	1.41	1.42	1.41
CT45A1	1.35	1.48	1.41
CRYAB	1.42	1.38	1.40
SLC2A12	1.02	1.75	1.39
AQP1	1.51	1.26	1.39
AGPAT9	1.40	1.36	1.38
ABAT	1.35	1.41	1.38
MYBL1	1.36	1.38	1.37
NBPF11	1.48	1.24	1.36
SLC2A14	1.31	1.40	1.36
CYFIP2	1.27	1.44	1.35
KRT13	1.50	1.20	1.35
IFIT3	1.43	1.26	1.34
IL2RG	1.29	1.39	1.34
NBPF10	1.52	1.12	1.32
DDX60	1.39	1.25	1.32
SERPINF1	1.40	1.24	1.32
IFIT1	1.26	1.37	1.31
TAS2R10	1.52	1.10	1.31
PRF1	1.32	1.29	1.31
WWC2	1.51	1.08	1.29
LOC100507218	1.20	1.37	1.28
PADI1	1.17	1.35	1.26
C10orf114	1.34	1.19	1.26
GLS2	1.16	1.34	1.25
RGS9	1.39	1.10	1.25
COL13A1	1.27	1.21	1.24
CST1	1.37	1.12	1.24
IFI44	1.09	1.39	1.24
TKTL1	1.29	1.18	1.23
CST2	1.28	1.18	1.23
GADD45B	1.24	1.21	1.23
CCDC19	1.22	1.21	1.22
HEG1	1.18	1.19	1.18
ABHD6	1.30	1.07	1.18
ABCA1	1.20	1.15	1.18
PSG9	1.05	1.30	1.18
NR2F1	1.08	1.27	1.18

Table S4. **Transcripts up-regulated by miR-7 overexpression in BGC823 cells** *(Continued)*

Gene symbol	**Replicate 1 Log_2 RNA ratio**	**Replicate 2 Log_2 RNA ratio**	**Mean RNA fold change**
CSRP2	1.20	1.15	1.18
ADAMTS14	1.33	1.01	1.17
SYTL3	1.13	1.21	1.17
DKK1	1.22	1.11	1.17
C5orf46	1.29	1.04	1.16
TPM2	1.12	1.21	1.16
SLC16A6	1.11	1.22	1.16
CT45A5	1.01	1.32	1.16
KIF17	1.23	1.10	1.16
CNTNAP3	1.09	1.19	1.14
OASL	1.10	1.17	1.14
LOC84856	1.13	1.12	1.13
ATF3	1.09	1.15	1.12
RFPL1	1.05	1.19	1.12
SHANK2	1.12	1.12	1.12
DHX58	1.08	1.16	1.12
RTP4	1.20	1.02	1.11
MAP2K7	1.06	1.15	1.11
SLCO1B3	1.18	1.00	1.09
MSMB	1.10	1.08	1.09
ACTA2	1.02	1.16	1.09
IFIT2	1.01	1.17	1.09
SAMD4A	1.12	1.03	1.07
NEDD9	1.01	1.14	1.07
MAGEA1	1.13	1.01	1.07
DKFZP586B0319	1.10	1.02	1.06
OBFC2A	1.06	1.07	1.06
GAST	1.01	1.07	1.04
IFFO2	1.01	1.01	1.01

Table S5. **Proteins up-regulated by miR-7 overexpression in BGC823 cells**

Gene Symbol	Replicate 1 $\mathrm{Log_2}$ protein ratio	Replicate 2 $\mathrm{Log_2}$ protein ratio	Mean protein fold change
FAM111A	2.33	3.88	3.10
FAM103A1	2.24	2.92	2.58
CXCL12	2.14	2.78	2.46
STK17A	2.18	2.72	2.45
RPL32P3	2.01	2.84	2.42
LOC339352	2.01	2.77	2.39
METTL18	2.10	1.85	1.97
DCTN2	1.96	1.80	1.88
C7	2.06	1.45	1.75
MCM3AP	1.93	1.55	1.74
C12orf10	1.73	1.65	1.69
OR6K2	1.84	1.48	1.66
NAA25	1.78	1.50	1.64
ALPL	1.51	1.64	1.57
APOO	1.52	1.50	1.51
DDX11	1.40	1.62	1.51
LILRP2	1.45	1.50	1.47
SMN1	1.64	1.22	1.43
ZNF813	1.40	1.43	1.41
LOC729852	1.30	1.52	1.41
GPR115	1.56	1.24	1.40
TMEM8A	1.51	1.25	1.38
UTP11L	1.31	1.39	1.35
MAP2	1.37	1.25	1.31
BBS9	1.39	1.21	1.30
SNRPD1	1.41	1.18	1.29
AIFM2	1.33	1.25	1.29
LYZL1	1.27	1.29	1.28
SYNRG	1.21	1.31	1.26
PHOSPHO2-KLHL23	1.26	1.22	1.24
RRP1	1.21	1.25	1.23
CHTF18	1.43	0.99	1.21
GJB2	1.33	1.10	1.21
ACBD7	1.28	1.12	1.20
DYNLRB1	1.09	1.29	1.19
ERAP1	1.38	1.00	1.19
RPS18	1.13	1.25	1.19
RGP1	1.18	1.18	1.18
IFIT2	1.03	1.31	1.17
CAT	1.37	0.97	1.17
LOC100506334	1.05	1.28	1.16
SOX9	1.17	1.11	1.14
MNAT1	1.08	1.16	1.12
FLJ43826	1.22	1.02	1.12
CST1	1.17	1.07	1.12
IFT81	1.12	1.08	1.10
THOC7	1.20	1.00	1.10
LOC100506455	1.29	0.91	1.10
UROD	1.19	1.01	1.10
LSG1	1.09	1.10	1.09
PAGE5	1.14	1.02	1.08
ZNF468	1.11	1.05	1.08
ZNF587	0.87	1.25	1.06
DHRS7	1.03	1.04	1.03
ULK4	1.15	0.91	1.03
EZR	1.04	1.03	1.03
HTR7	1.19	0.87	1.03
TMED7-TICAM2	1.19	0.85	1.02

Table S6. **Sequences for primers and siRNAs used in this study**

Primers for 3′-UTR mutagenesis	**Sequences**
RELA mutant site A (forward)	5′-TCCAACTGCCCCCAACTTTGTGGATCAGAAGGTTGGAGGGGGGAGCCATATTTTATT-3′
RELA mutant site A (reverse)	5′-AATAAAATATGGCTCCCCCCTCCAACCTTCTGATCCACAAAGTTGGGGGCAGTTGG-3′
RELA mutant site B (forward)	5′-TTGAGCCCACAAAGCCTTATCAAGTCAGAAGGATCATGGATTCATTACAGCTTAATC-3′
RELA mutant site B (reverse)	5′-GATTAAGCTGTAATGAATCCATGATCCTTCTGACTTGATAAGGCTTTGTGGGCTCAA-3′
FOS mutant site A (forward)	5′-TACAGAGAGGAGAAACACAGAGGAACTAGAGGGTTCCTGTAGAC-3′
FOS mutant site A (reverse)	5′-GTCTACAGGAACCCTCTAGTTCCTCTGTGTTTCTCCTCTCTGTA-3′
FOS mutant site B (forward)	5′-GTCTCTTTTCTCTTTCTCCTGCAGTGGTGCATAGCATTAACTAATCT-3′
FOS mutant site B (reverse)	5′-AGATTAGTTAATGCTATGCACCACTGCAGGAGAAAGAGAAAAGAGAC-3′
FOS mutant site C (forward)	5′-CTGAATGTTCTGACATTAACGACCCCTCATGAAAACGTTTTATTGTG-3′
FOS mutant site C (reverse)	5′-CACAATAAAACGTTTTCATGAGGGGTCGTTAATGTCAGAACATTCAG-3′
IKBKE mutant (forward)	5′-GTCAAACGACCTCATCACATGAGGAATTCCTCTTCAAGCGTTTCA-3′
IKBKE mutant (reverse)	5′-TGAAACGCTTGAAGAGGAATTCCTCATGTGATGAGGTCGTTTGAC-3′
ChIP primers	
NF-κB #1 (forward)	5′-TGGAAAGCGGGTACTACCAG-3′
NF-κB #1 (reverse)	5′-GCGGTTTCACAGGGCTCTCG-3′
NF-κB #2 (forward)	5′-GGTCCCTGGGCAGCGCAACT-3′
NF-κB #2 (reverse)	5′-TTCTCGTTCGCGCACTCACTAG-3′
NF-κB #3 (forward)	5′-AGACGCCATTATCCTCTGTTTC-3′
NF-κB #3 (reverse)	5′-GCGACGGAGGAGGCGACAAC-3′
NF-κB #4 (forward)	5′-AGGTCTCAGTTTTCTACAGCTG-3′
NF-κB #4 (reverse)	5′-CTCTATCCAGAATGGGGGTG-3′
NF-κB #5 (forward)	5′-CAGGATATTGTGGCTTTTGC-3′
NF-κB #5 (reverse)	5′-GGTAAGCAGAGCAGGAAGAG-3′
NF-κB #6 (forward)	5′-TGAGTCAACGCACCTGGCTG-3′
NF-κB #6 (reverse)	5′-TCAGGCCAGGACAAAAGTGAAG-3′
NF-κB #7 (forward)	5′-TTGGAGCTCAGGAACCCAGG-3′
NF-κB #7 (reverse)	5′-CCAATGGGATTCCGCCTCAG-3′
Real-time PCR primers	
RelA (forward)	5′-TAAGCAGAAGCATTAACTTCTCTGGA-3′
RelA (reverse)	5′-CCTGCTTCTGTCTCTAGGAGAGTA-3′
Fos (forward)	5′-TAGTTAGTAGCATGTTGAGCCAGG-3′
Fos (reverse)	5′-ACCACCTCAACAATGCATGA-3′
IKKε (forward)	5′-TGCGTGCAGAAGTATCAAGC-3′
IKKε (reverse)	5′-TACAGGCAGCCACAGAACAG-3′
Bcl-xL (forward)	5′-TCCTTGTCTACGCTTTCCACG-3′
Bcl-xL (reverse)	5′-GGTCGCATTGTGGCCTTT-3′
Cyclin D1 (forward)	5′-GGATGCTGGAGGTCTGCGAGGAAC-3′
Cyclin D1 (reverse)	5′-GAGAGGAAGCGTGTGAGGCGGTAG-3′
c-Myc (forward)	5′-TCAAGAGGCGAACACACAAC-3′
c-Myc (reverse)	5′-GGCCTTTTCATTGTTTTCCA-3′
Cox-2 (forward)	5′-TTCAAATGAGATTGTGGGAAAAT-3′
Cox-2 (reverse)	5′-AGATCATCTCTGCCTGAGTATCTT-3′
Tumor necrosis factor (forward)	5′-CGGGACGTGGAGCTGGCCGAGGAG-3′
Tumor necrosis factor (reverse)	5′-CACCAGCTGGTTATCTCACAGCTC-3′
interleukin-6 (forward)	5′-TCTCCACAAGCGCCTTCG-3′
interleukin-6 (reverse)	5′-CTCAGGGCTGAGATGCCG-3′
interleukin-1β (forward)	5′-AAACAGATGAAGTGCTCCTTCCAGG-3′
interleukin-1β (reverse)	5′-TGGAGAACACCACTTGTTGCTCCA-3′
GAPDH (forward)	5′-ATTCCACCCATGGCAAATTC-3′
GAPDH (reverse)	5′-TGGGATTTCCATTGATGACAAG-3′
siRNAs	
siRELA #1 (sense)	5′-GCUGCAGUUUGAUGAUGAATT-3′
siRELA #1 (antisense)	5′-UUCAUCAUCAAACUGCAGCTT-3′
siRELA #2 (sense)	5′-CCUCCUUUCAGGAGAUGAATT-3′
siRELA #2 (antisense)	5′-UUCAUCUCCUGAAAGGAGGTT-3′
siRELA #3 (sense)	5′-GGACAUAUGAGACCUUCAATT-3′
siRELA #3 (antisense)	5′-UUGAAGGUCUCAUAUGUCCTT-3′
siFOS #1 (sense)	5′-GGGAUAGCCUCUCUUACUATT-3′
siFOS #1 (antisense)	5′-UAGUAAGAGAGGCUAUCCCTT-3′
siFOS #2 (sense)	5′-GACAGACCAACUAGAAGAUTT-3′
siFOS #2 (antisense)	5′-AUCUUCUAGUUGGUCUGUCTT-3′

Table S6. **Sequences for primers and siRNAs used in this study** *(Continued)*

Primers for 3′-UTR mutagenesis	Sequences
siFOS #3 (sense)	5′-CAAGGUGGAACAGUUAUCUTT-3′
siFOS #3 (antisense)	5′-AGAUAACUGUUCCACCUUGTT-3′
siIKBKE #1 (sense)	5′-GCAUCAUCGAACGGCUAAATT-3′
siIKBKE #1 (antisense)	5′-UUUAGCCGUUCGAUGAUGCTT-3′
siIKBKE #2 (sense)	5′-GCUGUUUGGACAAGAUGAATT-3′
siIKBKE #2 (antisense)	5′-UUCAUCUUGUCCAAACAGCTT-3′

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