Supporting Information

SI Methods

Library preparation for RNA-seq

Total RNA was extracted by using Trizol reagent (Invitrogen) according to the manufacturer's instructions. The concentration and quality of total RNA were measured by Nanodrop and verified by gel electrophoresis. The Ribo-minus transcriptome libraries were constructed with TruSeq Ribo Profile Library Prep Kit (Illumina), according to the manufacturer's instructions. The libraries were then subjected to 150-nt paired-end sequencing generating ~100 million read pairs with an Illumina Nextseq 500 system (Novogene, China) or a BGISEQ-500 system (BGITech, China).

Clinical samples preparation

All fresh GC patient tumor samples and adjacent tissues were collected from the First Affiliated Hospital of Anhui Medical University, which was approved by the Human Research Ethics Committee of Anhui Medical University. Written informed consent was obtained from each patient for this study. All samples were rinsed with PBS after the operation, and then were cut into small pieces with RNAhold (TransGen, EH101-01) immersed. All samples were stored at -80°C until the time of analysis.

Cell culture

Human GC cell line AGS was purchased from the Culture Collection of Chinese Academy of Sciences (Chinese Academy of Sciences, Shanghai). Human GC cell lines SGC7901, BGC823, MGC803 and MKN45 were kindly provided by Dr. Chunwei Peng (Department of General Surgery, the First Affiliated Hospital of Anhui Medical University). AGS cells are derived from untreated tumor fragments belong to poor differentiated GC cells. SGC7901 cells are derived from lymph node metastasis of gastric cancer, which are moderately differentiated GC cells. MGC803, MKN45 and BGC823 cells were all derived from poorly differentiated adenocarcinomas. All the cells were maintained under standard culture conditions with DMEM containing 10% FBS at 37°C and 5% CO_2. Two GC cell lines (AGS and SGC7901) were authenticated by short-tandem-repeat (STR) profiling. All cells were checked for mycoplasma by a PCR-based method as well as DAPI staining, to ensure the absence of contamination.

Plasmids construction and cell transfection

All plasmids were constructed with restriction-enzyme digestion and ligation or with recombinant methods (Vazyme c113-02). The backbone vector of p3×FLAG-Myc was used for constructing FLAG-tagged hnRNPM, its truncations and VEGFA isoforms. For *circURI1* overexpression, the third and fourth exons of *URI1* and the endogenous flanking sequence including the complementary *Alu* element pairs was inserted into the backbone vector of pcDNA3, while *circURI1-M19* was constructed with the mutation of the 19-nt hnRNPM binding site in *circURI1*. Further information about these plasmids is available upon request. Transfection of plasmid and siRNAs was carried out with Lipofectamine 2000 according to the manufacturer's protocol. 2-O-methyl RNA/DNA antisense oligonucleotides (ASOs), which were modified by changing the five nucleotides at the 5′ and 3′ ends into 2′-O-methyl ribonucleotides, were synthesized by RiboBio (Guangzhou, China). Oligonucleotide sequences for primers used in plasmid construction, probe preparation, siRNA and biotin-labeled nucleic acids were listed in Table S5.

Fluorescence in situ hybridization (FISH)

RNA probes were generated with a Transcript Aid T7 High Yield Transcription Kit (Thermo Scientific), with the corresponding insertion in the T vector as a template, and then labeled with Alexa Fluor488, by using a ULYSIS Nucleic Acid Labeling Kit (Invitrogen), which added a fluor on every G in the probe to amplify the fluorescence intensity. The primers for the amplification of the FISH antisense probe were listed in Table S5. Fixed cells and RNA probes were denatured at 80 °C for 10 min and then incubated at 42 °C for 15-17 h with 30 ng/μl human Cot-1 DNA (Life Technologies) and 500 ng/μl yeast total RNA (Ambion). For tissues, the slides were treated with 1 mg/ml proteinase K (Roche) for 1 h at 37 °C before denaturation and incubation. Slides were washed with 2× SSC at 45 °C for 10 min. For data collection, images were taken with an AndoriXonEM+ DV897KEM CCD camera mounted on an Andor Revolution XD laser confocal microscope system (Andor Technology), with Andor IQ 10.1 software.

Nuclear/cytosolic fractionation

Cellular fractionation was performed as described previously with minor modifications (16). Briefly, cells were washed twice with PBS and incubated with hypotonic buffer (25 mM Tris (pH 7.4), 1 mM $MgCl_2$, 5 mM KCl, 1% NP-40 and 50 U/mL RNase inhibitor (Promega)) on ice for 20 min. Samples were then centrifuged at 1000g for 3 min at 4 °C, and the supernatant was collected as the cytoplasmic fraction. The pellets were resuspended in nucleus resuspension buffer (20 mM HEPES (pH 7.9), 400 mM NaCl, 1 mM EDTA, 1 mM EGTA, 1 mM DTT and 1 mM PMSF), and incubated at 4°C for 30 min. Nuclear fraction was collected after removing insoluble membrane debris by centrifugation at 12000 g for 10 min.

Quantification of RNA copy number per cell

The DNA fragment corresponding to *circURI1* was amplified with cDNA, and then The Ct values and the amount of the purified product were used to plot standard curves through real-time PCR on a PikoReal 96 real-time PCR system (Thermo Scientific) according to standard procedures. Total RNAs of AGS and SGC7901 cells were extracted from 100,000 cells, and cDNA was then synthesized. The copy numbers per cell in each cell line were calculated on the basis of cell numbers and the Ct value by using the standard curve.

***CircURI1* knockout via CRISPR-Cas9 technique**

To knockout *circURI1* in AGS cells, four single-guide RNAs (sgRNAs) were designed based on potential off-target sites using the algorithm described at http://crispr.mit.edu targeted the fourth intron of human *URI1*, which resulted in the deletion of the complementary repeat sequences. Firstly, AGS cells were seeded into 6-well plates at a density of 400,000 cells per well and transfected 2μg of the Cas9- and sgRNA- expressing plasmid (PX330) which was engineered with expressing mCherry and a puromycin selectable marker using Lipofectamine 2000 (Life Technologies). Then, the efficient transfection was verified by examining mCherry expression after 24h and the media was replaced with 1 μg/ml puromycin for selection after 48h. Four days later, we generated hundreds of individual colonies expressing mCherry in 96-well plates through the BD FACSAria™ III cell sorting system. After ten days, the colonies were split into two identical plates and one plate was harvested for further confirmation of genotype. Finally, we extracted genomic DNA, performed PCR using primers spanning the deleted sequence using PrimeSTAR Max (Takara) and confirmed the corresponding bands by Sanger sequencing. The primer sequences are presented in Table S5.

Construction of stable cell line for *circURI1* knockdown

Oligonucleotides specific for short hairpin RNAs (shRNAs) against the junction site of *circURI1* were inserted into the backbone vector of pLKO.1 (Sigma). The primer sequences are presented in Table S5. Lentiviral constructs including lentivirus-shRNA for knocking down *circURI1* (sh-KD) and the negative control (sh-NC) were co-transfected with packaging plasmids psPAX2 and pMD2G into 293T cells. Infectious lentiviruses were harvested at 48h after transfection, followed with concentration by ultracentrifugation. Stable AGS cell lines were obtained by the selection with 1 μg/ml puromycin for 2 weeks.

PCR reactions

RNA was extracted with TRIzol reagent (Invitrogen) according to the manufacturer's protocol. For RT-PCR, cDNA was synthesized from RNA with a GoScript Reverse Transcription System (Promega) according to the manufacturer's protocol. For PCR with template of gDNA, gDNA was isolated with phenol/chloroform extraction. Real-time quantitative PCR (RT-qPCR) was performed with GoTaq SYBR Green qPCR Master Mix (Promega) on a PikoReal 96 real-time PCR system (Thermo Scientific) according to standard procedures. For semi-quantitative RT-PCR gels, 25-30 cycles of PCR were always performed. All PCR products were sequenced for confirmation. All primer information is included in Table S5.

Cell cycle and apoptosis analysis

Cells were seeded in 6-well plates at a density of 2×10^5 cells per well. For cell cycle analysis, AGS and SGC7901 cells were harvested after treatment with siRNAs for 48 h and fixed in 70% ethanol at -20 °C overnight, followed by the staining with phycoerythrin. Cells were then analyzed for cell cycle distribution by flow cytometry. For cell apoptosis assay, 10^5 cells were collected and washed twice with ice-cold PBS, resuspended in binding buffer, treated with Annexin V-FITC and 7-AAD (BD Biosciences) and incubated in the dark for 15 min. Flow cytometry analysis was performed within 1 h to measure Annexin V-FITC positive cells (BD FACVerse).

iCLIP-seq and the bioinformatics

The iCLIP experiment was carried out as described with minor modifications (38, 39). Briefly, 5×10^6 AGS cells expressing FLAG-hnRNPM were ultraviolet crosslinked to a total of 0.4 J/cm^2 in a UV cross-linker and harvested in ice-cold lysis buffer (10 mM HEPES (pH 7.4), 200 mM NaCl, 30 mM EDTA, 0.5% Triton-X 100, 1.5 mM DTT and 1× Protease-inhibitor cocktail (Roche, 04693116001)). Then, cells were sonicated for 5 min with a Sonics Vibra-Cell, and the cell supernatant was collected after centrifugation at 12,000 g for 15 min at 4 °C. The hnRNPM-binding complexes were isolated by anti-FLAG (Sigma, F1804) coupled with Protein G Dynabeads (Life Technology, 10004D) and partially digested with 0.1U/μl RNase I (Thermo Scientific, EN0601) for 3 min at 37 °C. After washing once with lysis buffer, twice with high salt lysis buffer (10 mM HEPES (pH 7.4), 500 mM NaCl, 30 mM EDTA, 0.5% Triton-X 100, 1.5 mM DTT, 1× Protease-inhibitor cocktail, 50 U/ml RNasin (Promega, N2111SV)), RNAs were dephosphorylated by T4 PNK (NEB, M0201L) for 20 min at 37 °C and then ligated at the 3' ends to a preadenylated DNA linker (5'-rApp-AGATCGGAAGAGCACACGTCTGAAC/AzideT/CCAGTCAC-3') with T4 RNA ligase I (NEB, M0204) for 60 min at 25 °C. The IR800CW dye conjugated to the NHS-Azide modification (/AzideT/) was visualized using a near infrared imager (39). SDS-PAGE separation, visualization, protein-RNA complexes isolation, proteinase K treatment, and overnight RNA precipitation were performed as previously described (39). For iCLIP cDNA library preparation, the isolated RNAs were reverse transcribed with barcoded primers. The cDNA library was purified by PAGE, circularized by CircLigase II (Lucigen, CL9021K), PCR-amplified by NEBNext Ultra II Q5 Master Mix (NEB, M0544S) for ~25 cycles and then subjected to high-throughput sequencing using an Illumina HiSeq2000 platform with a 50-nt run length. Sequences of all primers were listed in Table S5. For iCLIP data analysis, the randomers were registered and the 2-nt barcodes for identifying PCR duplicates were removed, followed by trimming relevant sequencing adapters. Trimmed reads were aligned to the human genome (hg19) allowing one mismatch using Bowtie (-v 1 -m 1 -a --best --strata). The genomic location of

5' end of each aligned cDNA read was considered as the cross-link nucleotide, and the cDNA counts for each cross-link nucleotide were calculated. A custom BED file was created for a window of 15 bases up and downstream of the cross-link nucleotide and a 30bp window surrounding the cross-link nucleotides was then used to identify peaks using Piranha (-b 30 -s -p 0.05). To evaluate the distribution of hnRNPM binding sites on *circURI1*, iCLIP reads were aligned to the *circURI1* sequence with Bowtie (-v 0 --best).

Individual-CLIP

Individual crosslinking immunoprecipitation (individual-CLIP) was performed with the specific modifications below (39). The 5×10^6 AGS cells were covered with ice-cold PBS buffer and irradiated in a UV cross-linker (254 nm, 400 mJ/cm^2, 2 min). Upon PBS buffer removal, cells were harvested in 1ml ice-cold lysis buffer (10 mM HEPES (pH 7.4), 200 mM NaCl, 30 mM EDTA, 0.5 % Triton-X 100, 1.5 mM DTT, 1× Protease-inhibitor cocktail (Roche, 04693116001) and 50 U/ml RNasin (Promega, N2111SV)). The lysate was sonicated for 5 min with a Sonics Vibra-Cell, and the cell supernatant was collected for immunoprecipitation (IP) after centrifugation at 12,000 g for 15 min at 4 °C.

For hnRNPM IP, 50 µl Protein G-coated Dynabeads (Life Technology, 10004D) were washed with 500 µl lysis buffer twice, resuspended in 200 µl lysis buffer with 1 µg hnRNPM antibody (OriGene, TA301557). After rotation for 60 min, the antibody-Protein G beads were washed with lysis buffer twice, resuspended in 1ml cell supernatant and incubated overnight at 4 °C. The antibody-Protein G bead complexes were washed with lysis buffer once and high-salt lysis buffer (10 mM HEPES (pH 7.4), 500 mM NaCl, 30 mM EDTA, 0.5% Triton-X 100, 1.5 mM DTT, 1× Protease-inhibitor cocktail and 50 U/ml RNasin Inhibitor) twice.

The antibody-Protein G bead complexes were separated on 8 % SDS-PAGE gel in 1× MOPS running buffer (50 mM MOPS, 50 mM Tris-HCl (pH 7.7), 1 mM EDTA, 0.1% SDS). The complexes with a molecular weight corresponding to ~75–150 kD were excised and eluted overnight in 200 µl elution buffer (100 mM Tris-HCl (pH 7.8), 10 mM EDTA, 1 % SDS, 50 U/ml RNasin Inhibitor). The elution was then treated with 1 mg/ml proteinase K (Roche, 3115828001) for 10 min at 37 °C, mixed with 300 µl RNA phenol/chloroform (pH 4.2) and incubated for 5 min at 37 °C. After centrifugation for 10 min at 12,000 rpm at 4 °C, 300 µl aqueous phase was transferred into a new microtube, and mixed with 0.5 µl Glycogen (Thermo Scientific, R0551), 30 µl 3 M sodium acetate (pH 4.5) and 1 ml 100 % EtOH for overnight at -80 °C. The cross-linked RNAs were precipitated by centrifugation for 30 min at 15,000 rpm and 4 °C, washed with 500 µl 80 % EtOH and resuspended in 12 µl nuclease-free H_2O.

For reverse transcription (RT), 1 µl *circURI1*-specific antisense primers were mixed with 12 µl RNA, preheated for 5 min at 70 °C and then cooled on ice. 7 µl RT mix (4 µl 5× RT buffer, 1 µl 10 mM dNTPs, 1 µl 0.1 M DTT, 0.5 µl RNasin and 0.5 µl Superscript III reverse transcriptase (Thermo Scientific, 18080051)) was added, mixed by pipetting and RT was performed with the following program: 10 min at 42 °C, 40 min at 50 °C, 10 min at 55 °C. In order to remove RNA, the RT products were treated with RNaseH (Thermo Scientific, EN0201) for 10 min at 37 °C. After mixing with 80 µl H_2O, 0.5 µl Glycogen, 10 µl 3 M sodium acetate (pH 4.5) and 350 µl 100 % EtOH for overnight at -80 °C, the cDNA was precipitated by centrifugation for 30 min at 15,000 rpm and 4 °C, washed with 500 µl 80 % EtOH and resuspended in 14 µl H_2O.

For poly(A) addition, 14 µl purified cDNA was mixed with 4 µl 5× reaction buffer, 1 µl dATP, 1 µl Terminal Deoxynucleotidyl Transferase (Thermo Scientific, EP0161), and incubated for 30 min at 37 °C. Then, the reaction was stopped by heating for 10 min at 70 °C and the products were used for two successive rounds of PCR as followed.

The first PCR amplification was primed by a *circURI1*-specific antisense oligonucleotide and an oligo(dT) primer, which contained a specific sequence at the 5’ and a poly(T) tract at the 3’ end (CGCTCCCGCTGAATTGGAATTTTTTTTTTTTTTTT) for about 20 cycles. The second nested PCR was primed by a *circURI1*-specific antisense oligonucleotide internal to the first, and the specific sequence at the 5' of the oligo(dT) primer (CGCTCCCGCTGAATTGGAAT), based on the template of the first PCR products. The products amplified in the second PCR were isolated, cloned and subjected to Sanger sequencing (totally 24 bacterial clones of PCR products were obtained with poly(T) readings). All primer information is included in Table S5 and the raw sequences obtained from these clones were included in Table S3.

Only readings with poly(T) were used for analysis of the binding sites from hnRNPM individual-CLIP in *circURI1*. Firstly, we trimmed poly(T) of the inserted sequences of the clones and aligned the sequences to *circURI1*. The first nucleotide in the upstream of the sequence mapped to *circURI1* was defined as the crosslink nucleotide. Multiple occurrences at the same crosslink nucleotide were counted only once. Five crosslink nucleotides of *circURI1* were identified from 24 clones and the region with 2 crosslink nucleotides at a distance of no more than 15 nucleotides was deduced as the hnRNPM binding sequence.

Pull down of biotinylated circRNAs

RNA pulldown was carried out as previously described, with minor modifications (60). In brief, 10^7 cells were lysed in 4 mL of RNA immunoprecipitation (RIP) buffer (150 mM KCl, 25 mM Tris (pH 7.4), 5 mM EDTA, 0.5 mM DTT, 0.5% NP-40, and 1×Protease-inhibitor cocktail (Roche)) for 30 min. After sonication for 10 min, cell lysates were cleared of cell debris by centrifugation at 13000 rpm for 20 min. Ten picomoles of biotinylated circRNAs were heated for 10 min to 60 °C and slow-cooled over the course of 40 min to 4 °C. RNA was mixed with 1 mg of cell lysate in RIP buffer supplemented with 0.1 mg/mL yeast total RNA, 5 mM $MgCl_2$, and 1 U/mL RNase inhibitor (Promega) and incubated for 2 h at 4°C with gentle rotation. Twenty-five microliters of washed M280 Streptavidin magnetic Dynabeads (Invitrogen) were added to each binding reaction and further incubated for 4 h at 4 °C. Beads were harvested for the following studies after washing with supplemented RIP buffer once and supplemented RIP buffer with 500 mM NaCl twice.

Figure S1

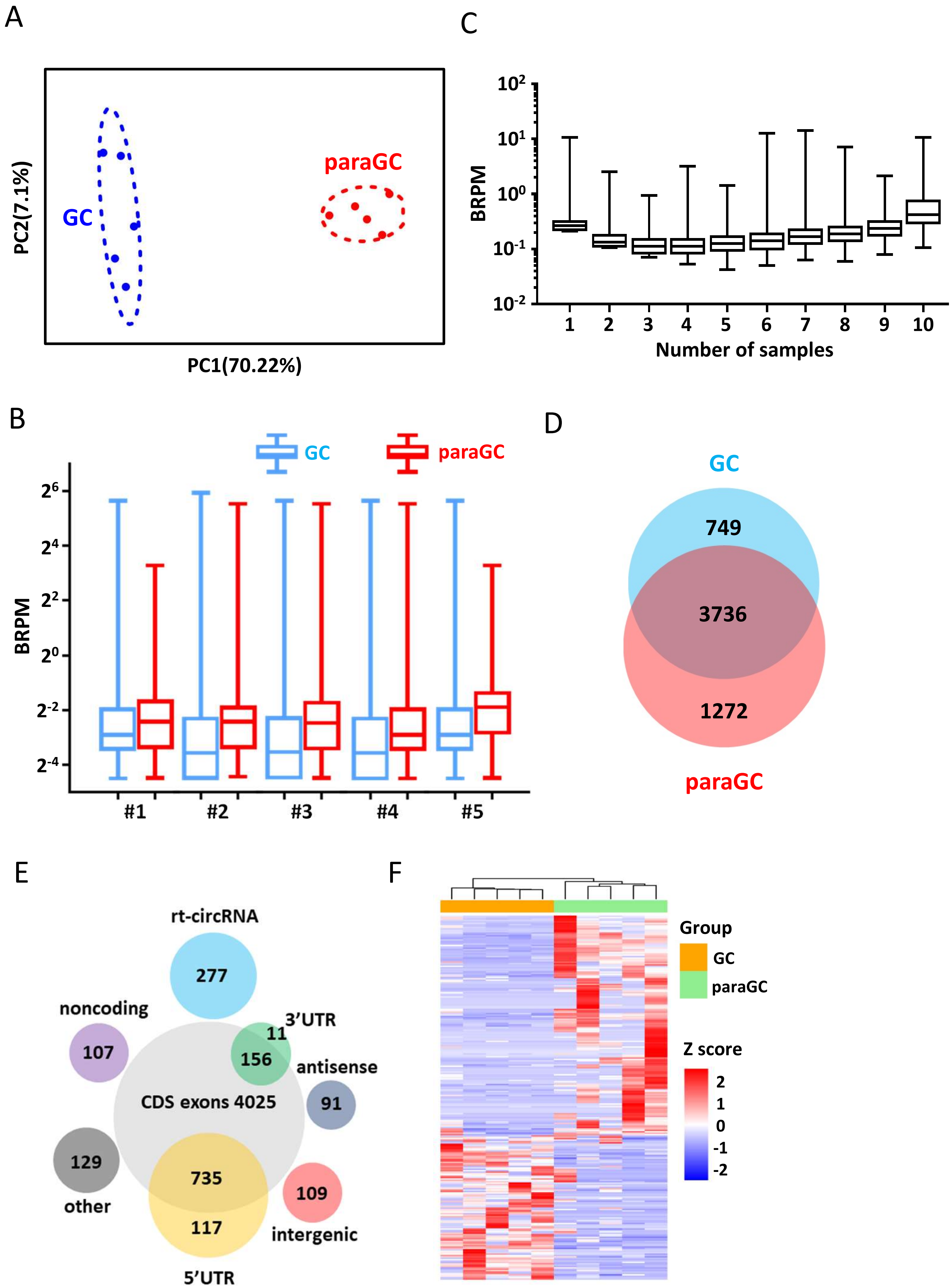
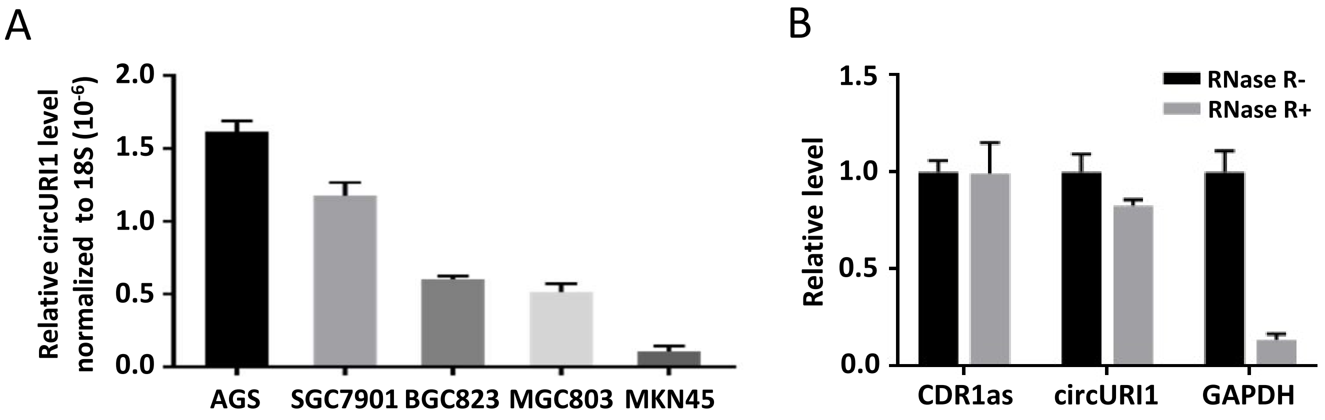
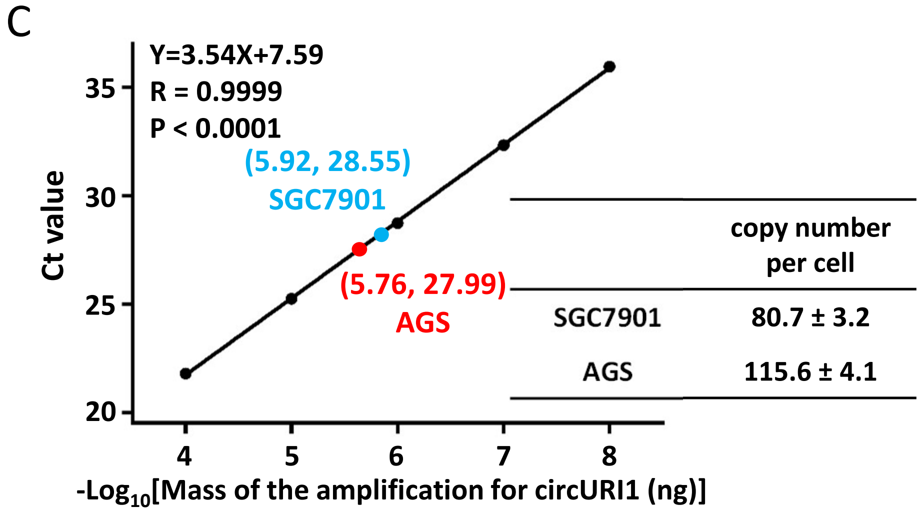

A
PC2(7.1%)
PC1(70.22%)
GC
paraGC
C
BRPM
10^{2}
10^{1}
10^{0}
10^{-1}
10^{-2}
1
2
3
4
5
6
7
8
9
10
Number of samples
B
GC
paraGC
BRPM
2^{6}
2^{4}
2^{2}
2^{0}
2^{-2}
2^{-4}
#1
#2
#3
#4
#5
D
GC
749
3736
1272
paraGC
E
rt-circRNA
277
noncoding
107
3'UTR
11
156
antisense
91
CDS exons 4025
129
other
735
117
5'UTR
109
intergenic
F
Group
GC
paraGC
Z score
2
1
0
-1
-2

Fig. S1. GC circRNA profiling. (*A*) PCA plots of the RNA-seq dataset showing the similarities/differences between five paired GC and paraGC samples. Percentages represent variance captured by each principal component 1 and 2 in each analysis. The back-spliced reads of circRNAs and reads that mapped to annotated linear genes were counted for PCA analysis. (*B*) Tremendously various circRNA expression levels of 5-paired GC and paraGC samples. (*C*) The distribution of expression levels for circRNAs detected in ten samples. (*D*) Venn diagram revealing the overlap of circRNAs identified from GC and paraGC samples. (*E*) Genomic origin of circRNAs identified in GC samples. Greater than 95% of circRNAs overlapped with known transcripts. (*F*) Hierarchical cluster analysis of the differentially expressed circRNAs in 5-paired GC and paraGC samples. Red indicates a high expression level, and blue indicates a low expression level.

Figure S2





	copy number per cell
SGC7901	80.7 ± 3.2
AGS	115.6 ± 4.1

D

	Human URI1 mRNA
Mouse	81.1%
Fish	No ortholog
Fly	No ortholog
Worm	No ortholog

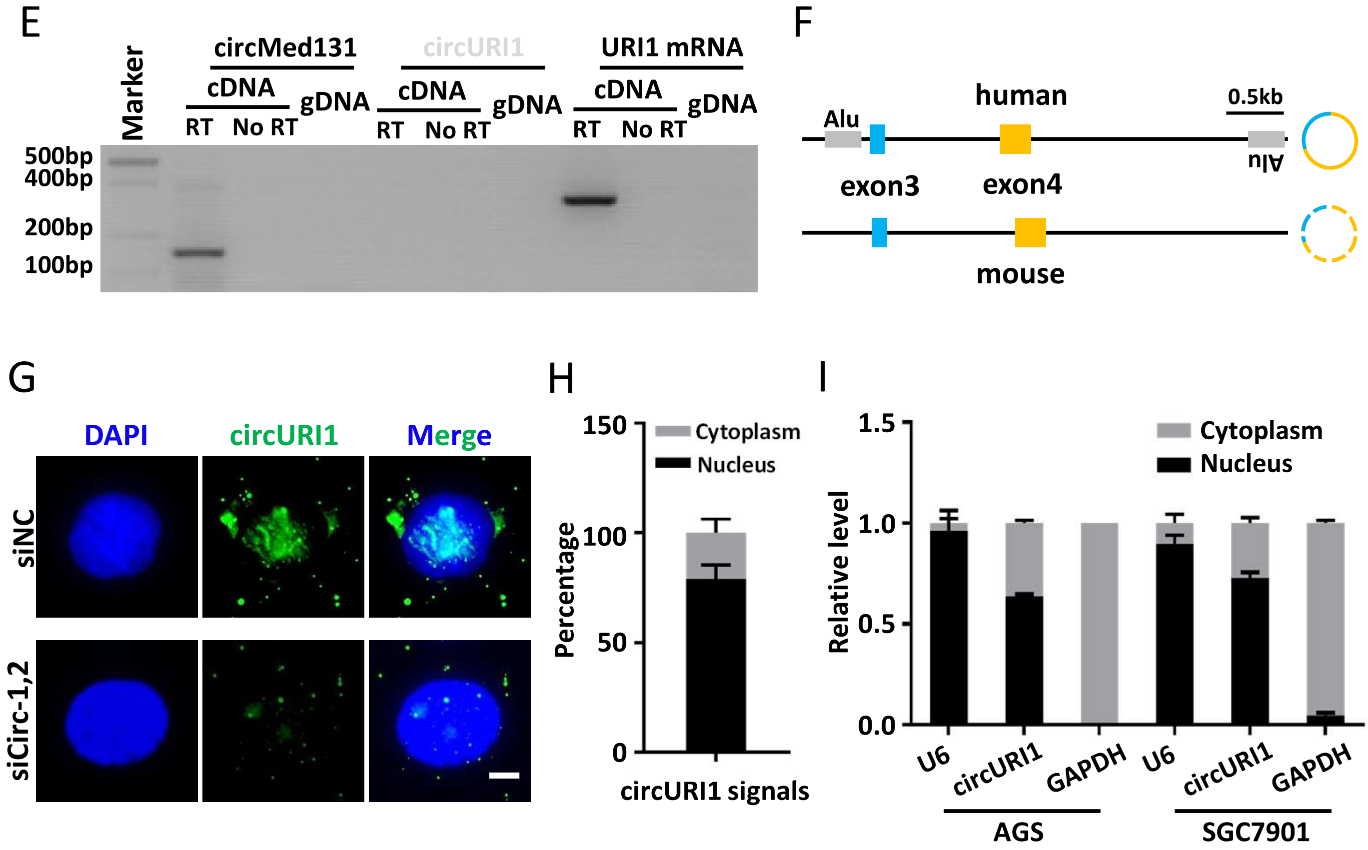


Fig. S2. Detection of *circURI1* in human GC. (*A*) *CircURI1* expression levels examined by RT-qPCR in 5 GC cell lines. (*B*) RT-qPCR analysis of *circURI1* after RNase R treatment in AGS cells. *CDR1as* was a positive control, while *GAPDH* mRNA was a negative control. (*C*) Quantification of *circURI1* copy numbers in AGS and SGC7901 cell lines. The Ct values and the amount of purified dsDNA fragments corresponding to *circURI1* amplicon were plotted to generate a standard curve by RT-qPCR. R represents Spearman's correlation coefficient and the P value was calculated by Spearman's correlation test. The red and blue dots present the Ct values and the amount of *circURI1* from the cDNA used in AGS and SGC7901 cells, respectively. The inset presents the copy numbers of *circURI1* in AGS and SGC7901 cells. More experimental details are available in the Methods section. (*D*) Homology of URI1 across species from the UCSC database. (*E*) RT-PCR detection of *circURI1* in mice. *URI1* mRNA and *circMed131* (termed mmu_circ_0001396 in circBase) were both positive controls. NRC, no RT control. (*F*) The genomic locus of URI1 exons 3-4 in humans and mice. (*G*) RNA FISH of *circURI1* (green) with the probe antisense to the back-spliced junction in AGS cells treated with siRNAs against *circURI1*. siNC, siRNA with scrambled sequences; siCirc-1,2, two siRNAs (siCirc-1, siCirc-2) against the junction sites of *circURI1*. (*H*) Quantification of FISH signals in AGS cells. (*I*) RT-qPCR analysis of *circURI1* in the nuclear and cytoplasmic fractions of AGS and SGC7901 cells. Error bars, S.E.M. from three independent experiments.

Figure S3

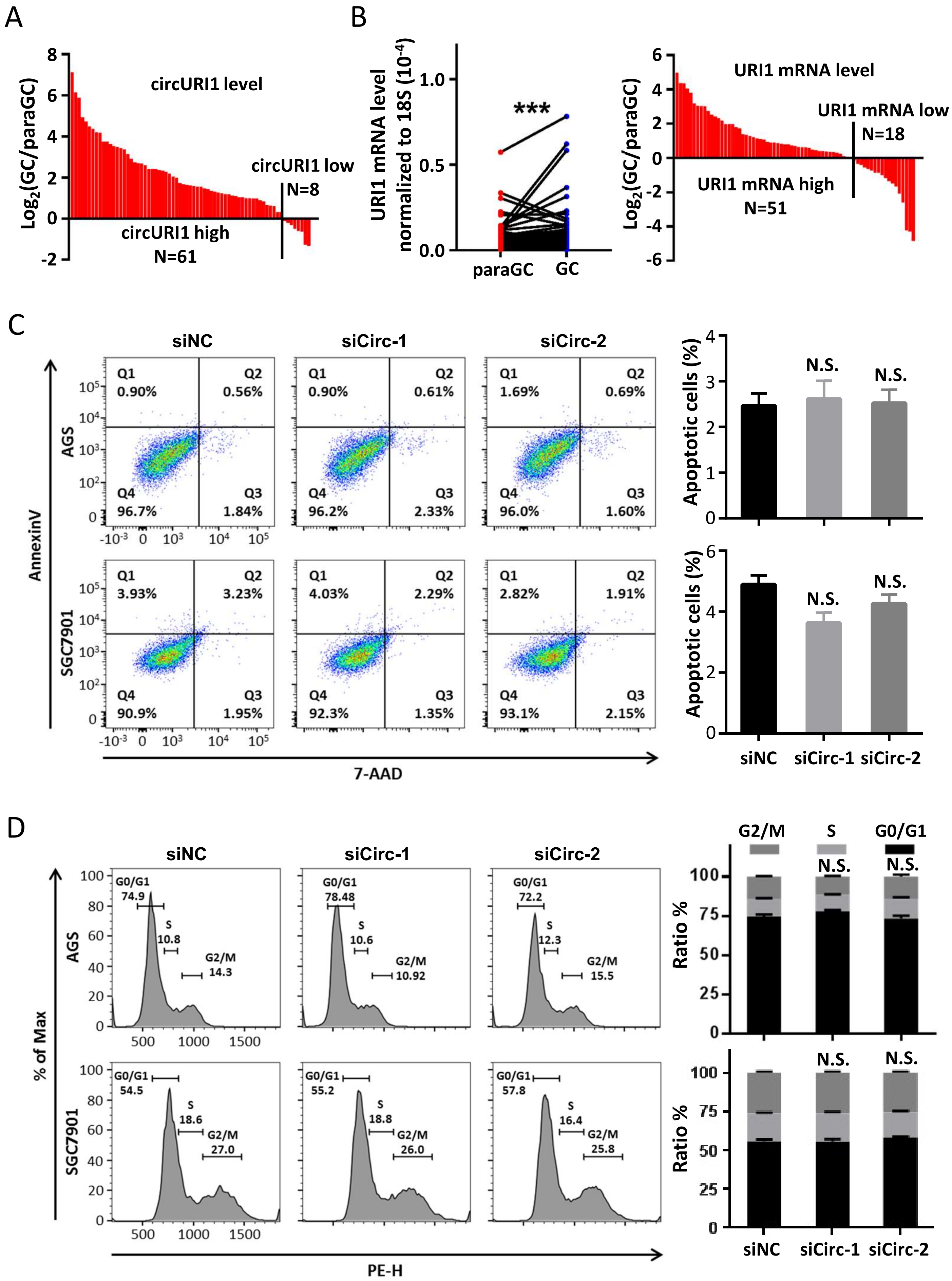

A
Log$_2$(GC/paraGC)
circURI1 level
circURI1 low
N=8
circURI1 high
N=61
8
6
4
2
0
-2
B
URI1 mRNA level normalized to 18S (10^{-4})
***
1.0
0.5
0.0
paraGC
GC
URI1 mRNA level
URI1 mRNA low
N=18
URI1 mRNA high
N=51
Log$_2$(GC/paraGC)
6
4
2
0
-2
-4
-6
C
siNC
siCirc-1
siCirc-2
AnnexinV
AGS
SGC7901
Q1 0.90%
Q2 0.56%
Q4 96.7%
Q3 1.84%
Q1 0.90%
Q2 0.61%
Q4 96.2%
Q3 2.33%
Q1 1.69%
Q2 0.69%
Q4 96.0%
Q3 1.60%
Q1 3.93%
Q2 3.23%
Q4 90.9%
Q3 1.95%
Q1 4.03%
Q2 2.29%
Q4 92.3%
Q3 1.35%
Q1 2.82%
Q2 1.91%
Q4 93.1%
Q3 2.15%
10^5
10^4
10^3
10^2
0
-10^3
7-AAD
Apoptotic cells (%)
N.S.
4
3
2
1
0
6
4
2
0
siNC
siCirc-1
siCirc-2
D
siNC
siCirc-1
siCirc-2
% of Max
AGS
SGC7901
G0/G1 74.9
S 10.8
G2/M 14.3
G0/G1 78.48
S 10.6
G2/M 10.92
G0/G1 72.2
S 12.3
G2/M 15.5
G0/G1 54.5
S 18.6
G2/M 27.0
G0/G1 55.2
S 18.8
G2/M 26.0
G0/G1 57.8
S 16.4
G2/M 25.8
100
80
60
40
20
0
500
1000
1500
PE-H
G2/M
S
G0/G1
N.S.
Ratio %
100
75
50
25
0
siNC
siCirc-1
siCirc-2

Fig. S3. Effects of *circURI1* on cell cycle and apoptosis. (*A*) RT-qPCR analysis of *circURI1* expression levels in 69-paired GC and paraGC tissues. The fold changes in each paired sample are arranged from high to low. The minimum change in upregulated *circURI1* in GC was 1.24 compared to paraGC. (*B*) RT-qPCR analysis of *URI1* mRNA in 69-paired GC and paraGC samples. 18S rRNA was used as the internal control. (*C*) Assessment of apoptosis by flow cytometry in AGS and SGC7901 cells treated with siRNAs against *circURI1*. (*D*) Effects on cell cycle progression analyzed by flow cytometry after depleting *circURI1* in AGS and SGC7901 cells. Error bars, S.E.M. from three independent experiments. N.S., not significant; ***P< 0.001 by two-tailed Student's *t*-test.

Figure S4

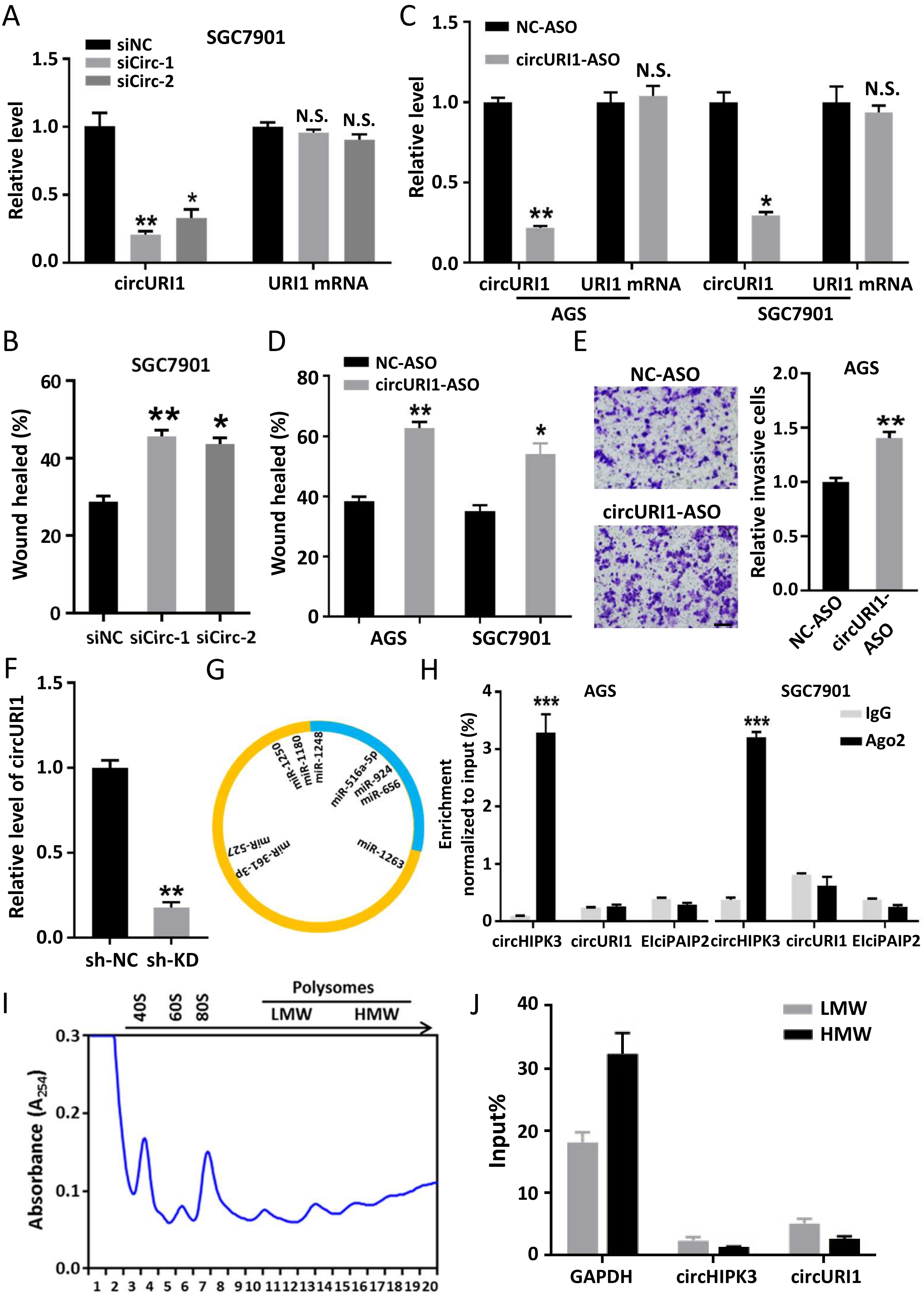

A
SGC7901
siNC
siCirc-1
siCirc-2
Relative level
1.5
1.0
0.5
0.0
**
*
N.S.
N.S.
circURI1
URI1 mRNA
B
SGC7901
Wound healed (%)
60
40
20
0
**
*
siNC
siCirc-1
siCirc-2
C
NC-ASO
circURI1-ASO
Relative level
1.5
1.0
0.5
0.0
**
N.S.
*
N.S.
circURI1
URI1 mRNA
AGS
circURI1
URI1 mRNA
SGC7901
D
NC-ASO
circURI1-ASO
Wound healed (%)
80
60
40
20
0
**
*
AGS
SGC7901
E
NC-ASO
circURI1-ASO
AGS
Relative invasive cells
2.0
1.5
1.0
0.5
0.0
**
NC-ASO
circURI1-ASO
F
Relative level of circURI1
1.5
1.0
0.5
0.0
**
sh-NC
sh-KD
G
miR-1250
miR-1180
miR-1248
miR-516a-5p
miR-924
miR-656
miR-1263
miR-361-3p
miR-527
H
AGS
SGC7901
IgG
Ago2
Enrichment normalized to input (%)
4
3
2
1
0
***
***
circHIPK3
circURI1
ElciPAIP2
circHIPK3
circURI1
ElciPAIP2
I
40S
60S
80S
Polysomes
LMW
HMW
Absorbance (A_{254})
0.3
0.2
0.1
0.0
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
J
LMW
HMW
Input%
40
30
20
10
0
GAPDH
circHIPK3
circURI1

Fig. S4. Effects of *circURI1* on cell migration and invasion, and *circURI1* functions beyond miRNA sponge and translation. (*A*) RT-qPCR analysis of *circURI1* and *URI1* mRNA expression in SGC7901 cells treated with two independent siRNAs against *circURI1*. siNC, siRNA with scrambled sequences; siCirc-1 and siCirc-2, two siRNAs against the junction sites of *circURI1*. (*B*) Wound-healing assays of SGC7901 cells treated with siRNAs targeting *circURI1*. (*C*) RT-qPCR analysis of *circURI1* and *URI1* mRNA expression in AGS and SGC7901 cells treated with ASO against *circURI1*. NC-ASO, ASO with scrambled sequences. (*D*) Wound-healing assays of AGS and SGC7901 cells treated with ASO of *circURI1*. (*E*) Transwell assays of AGS cells treated with ASO of *circURI1*. Scale bars, 100 μm. (*F*) Knockdown efficiency lentivirus-shRNA to knockdown *circURI1* (sh-KD) in stable cell lines. sh-NC is the negative control for knockdown *circURI1*. (*G*) Predicted putative binding miRNAs of *circURI1* with CircInteractome. (*H*) Ago2 RNA IP assay for detection of *circURI1* in AGS and SGC7901 cells. *CircHIPK3* acted as a miRNA sponge was a positive control, while *EIciPAIP2* was a negative control. (*I*) The curve of ribosome profiling. LMW, low molecular weight fraction; HMW, high molecular weight fraction. (*J*) RT-qPCR analysis of *circURI1* in either LMW or HMW in AGS cells. *GAPDH* mRNA was a positive control, while *circHIPK3* was a negative control. Error bars, S.E.M. from three independent experiments. N.S., not significant; *P< 0.05; **P< 0.01; ***P< 0.001 by two-tailed Student's *t*-test.

Figure S5

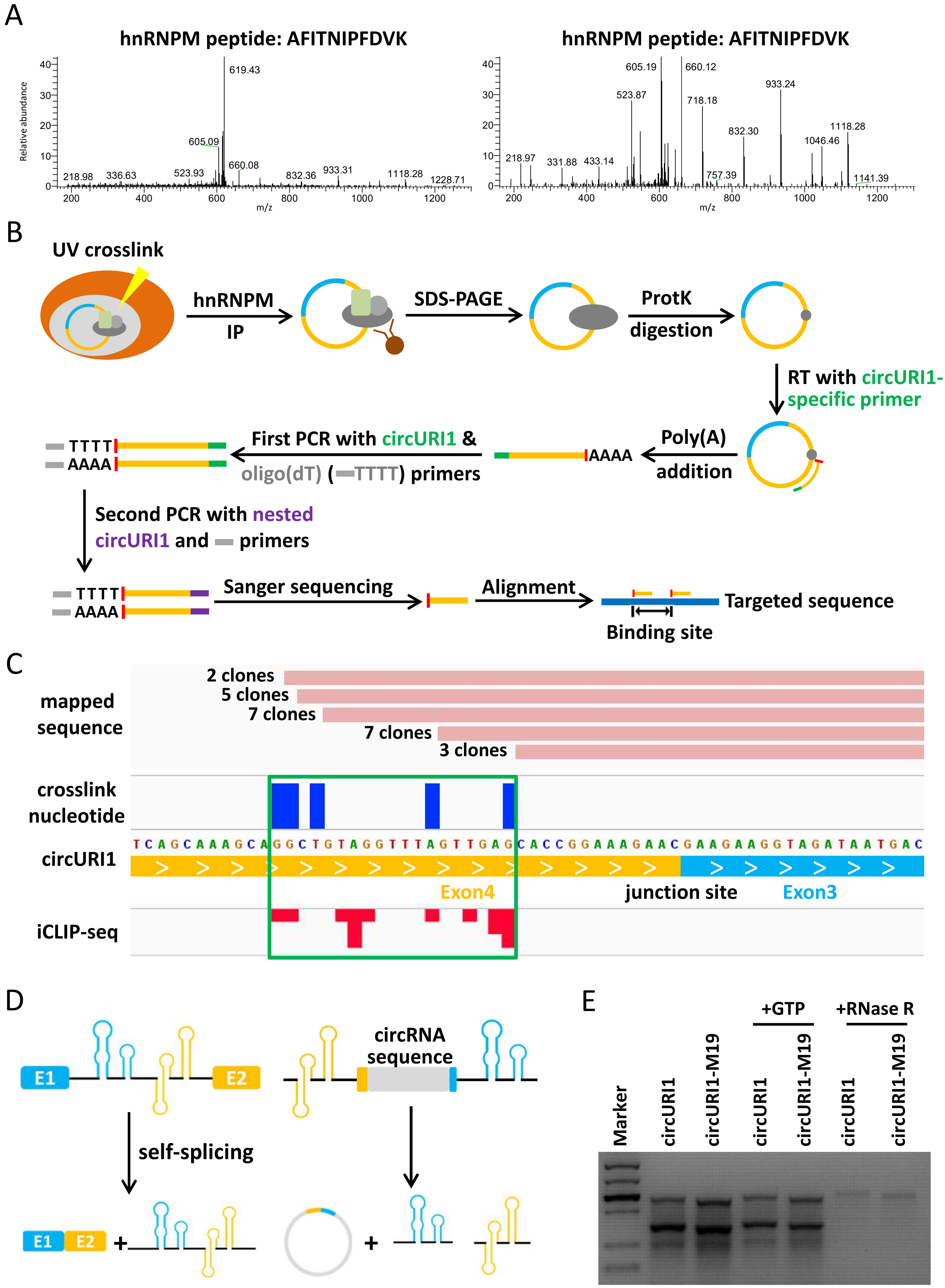

A
hnRNPM peptide: AFITNIPFDVK
Relative abundance
40
30
20
10
0
619.43
605.09
660.08
218.98
336.63
523.93
832.36
933.31
1118.28
1228.71
200
400
600
800
1000
1200
m/z
hnRNPM peptide: AFITNIPFDVK
605.19
660.12
933.24
523.87
718.18
832.30
1118.28
1046.46
218.97
331.88
433.14
757.39
1141.39
m/z
B
UV crosslink
hnRNPM
IP
SDS-PAGE
ProtK
digestion
RT with circURI1-specific primer
Poly(A)
addition
AAAA
First PCR with circURI1 &
oligo(dT) (TTTT) primers
TTTT
AAAA
Second PCR with nested
circURI1 and primers
TTTT
AAAA
Sanger sequencing
Alignment
Targeted sequence
Binding site
C
mapped
sequence
2 clones
5 clones
7 clones
7 clones
3 clones
crosslink
nucleotide
circURI1
TCAGCAAAGCAGGCTGTAGGTTTAGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGAC
Exon4
junction site
Exon3
iCLIP-seq
D
E1
E2
self-splicing
circRNA
sequence
E1
E2
+
+
E
+GTP
+RNase R
Marker
circURI1
circURI1-M19
circURI1
circURI1-M19
circURI1
circURI1-M19

Fig. S5. Analysis of hnRNPM individual-CLIP and the circularization of *circURI1 in vitro*. (*A*) The identified peptides of hnRNPM from MS assay. (*B*) Scheme of individual-CLIP for the identification of hnRNPM binding site in *circURI1*. Briefly, the covalently linked protein-RNA complexes were separated with SDS-PAGE and partially digested with proteinase K (ProtK), followed by co-immunoprecipitated with anti-hnRNPM after UV crosslinking. Incomplete ProtK digestion left the covalently bound polypeptide fragment on the RNA binding site of hnRNPM protein. Reverse transcription (RT) with a *circURI1*-specific primer (in green) stopped at the cross-link site. Red bar, the RT-stop nucleotide. The synthesized cDNA molecules were polyadenylated at the 3' ends, used as templates for two successive rounds of PCR and subjected to Sanger sequencing. oligo(dT) primer, a specific sequence at the 5' and oligo(dT) at the 3' end. For analysis, only readings with poly(T) were mapped to the *circURI1* sequence and the first nucleotide in the upstream of the sequence was defined as the crosslink nucleotide. (*C*) Five crosslink nucleotides of *circURI1* were identified from 24 clones and the binding site of hnRNPM individual-CLIP in *circURI1* is depicted as the green rectangle, consistent with the binding site identified by hnRNPM iCLIP-seq. (*D*) The principle of circularization *in vitro.* This method was based on self-spliced intron. (*E*) Agarose gel of synthesized *circURI1* and *circURI1-M19 in vitro*. *CircURI1-M19*, *circURI1* with the mutation of the 19-nt sequence.

Figure S6

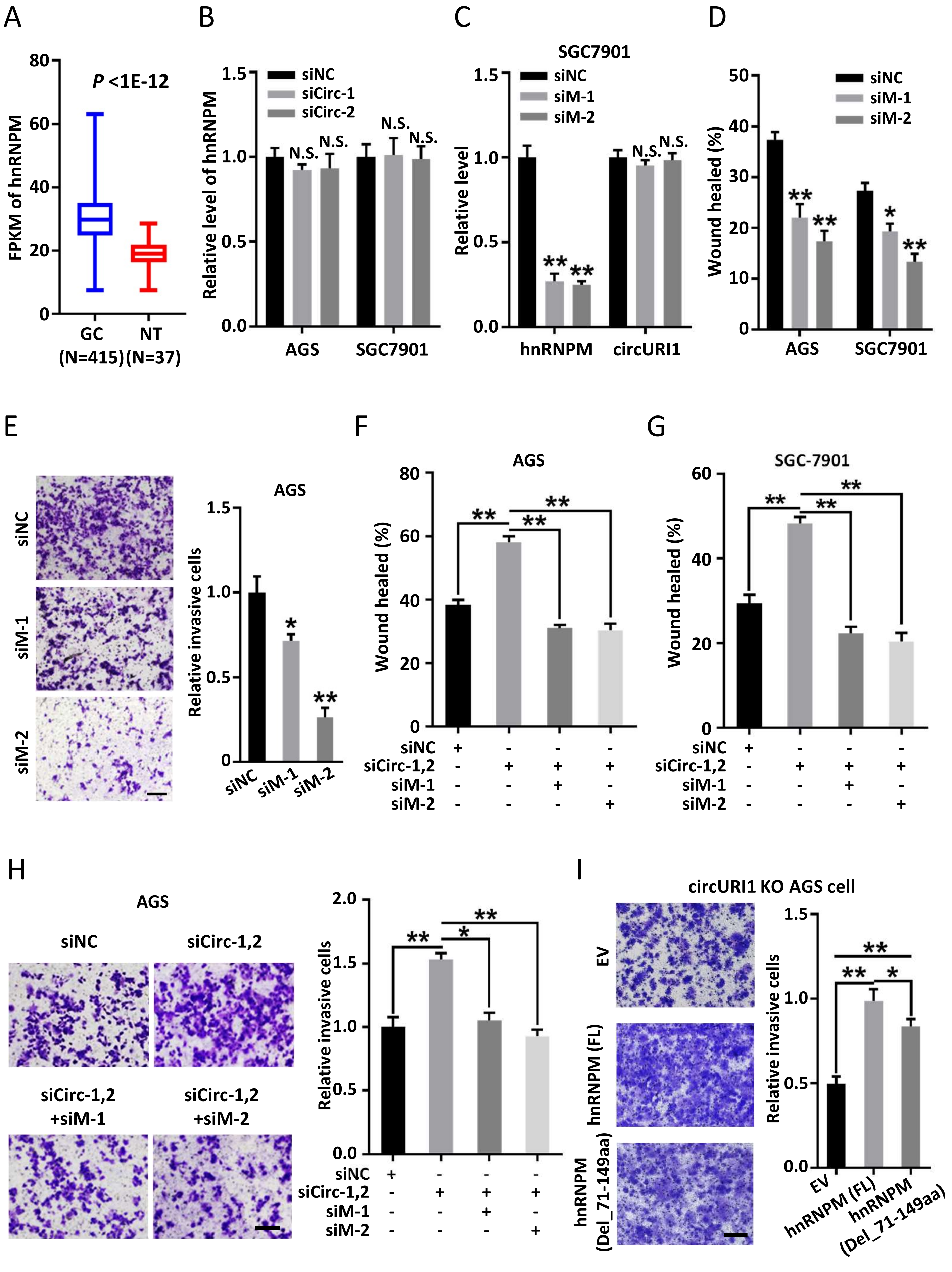
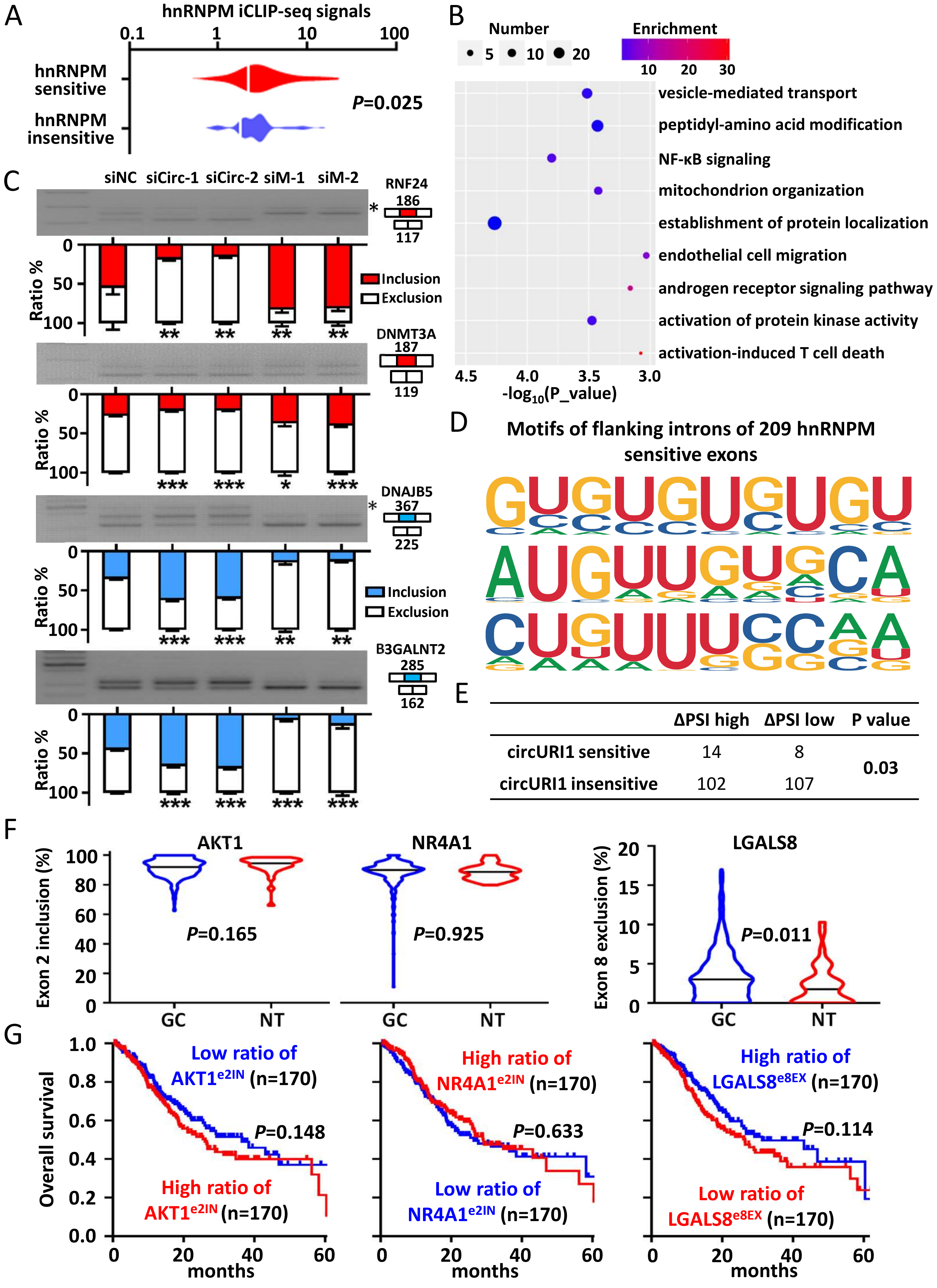

A
FPKM of hnRNPM
P <1E-12
80
60
40
20
0
GC
(N=415)
NT
(N=37)
B
Relative level of hnRNPM
siNC
siCirc-1
siCirc-2
N.S.
N.S.
N.S.
N.S.
1.5
1.0
0.5
0.0
AGS
SGC7901
C
SGC7901
Relative level
siNC
siM-1
siM-2
**
**
N.S.
N.S.
1.5
1.0
0.5
0.0
hnRNPM
circURI1
D
Wound healed (%)
siNC
siM-1
siM-2
**
**
*
**
50
40
30
20
10
0
AGS
SGC7901
E
siNC
siM-1
siM-2
AGS
Relative invasive cells
*
**
1.5
1.0
0.5
0
siNC
siM-1
siM-2
F
AGS
Wound healed (%)
**
**
**
80
60
40
20
0
siNC + - - -
siCirc-1,2 - + + +
siM-1 - - + -
siM-2 - - - +
G
SGC-7901
Wound healed (%)
**
**
**
60
40
20
0
siNC + - - -
siCirc-1,2 - + + +
siM-1 - - + -
siM-2 - - - +
H
AGS
siNC
siCirc-1,2
siCirc-1,2
+siM-1
siCirc-1,2
+siM-2
Relative invasive cells
**
*
**
2.0
1.5
1.0
0.5
0.0
siNC + - - -
siCirc-1,2 - + + +
siM-1 - - + -
siM-2 - - - +
I
circURI1 KO AGS cell
EV
hnRNPM (FL)
hnRNPM
(Del_71-149aa)
Relative invasive cells
**
**
*
1.5
1.0
0.5
0.0
EV
hnRNPM (FL)
hnRNPM
(Del_71-149aa)

Fig. S6. Effects of hnRNPM on cell migration and invasion in GC. (*A*) The expression levels of hnRNPM analyzed from TCGA database in GC. NT, normal tissue. (*B*) RT-qPCR analysis of hnRNPM expression upon *circURI1* silencing in AGS and SGC7901 cells. siNC, siRNA with scrambled sequences; siCirc-1 and siCirc-2, two siRNAs against the junction sites of *circURI1*. (*C*) RT-qPCR analysis of hnRNPM and *circURI1* expression after treatment with two independent siRNAs against hnRNPM in SGC7901 cells. siNC, siRNA with scrambled sequences; siM-1 and siM-2, two independent siRNAs against hnRNPM. (*D*) Wound-healing assays of AGS and SGC7901 cells upon hnRNPM knockdown. (*E*) Transwell assays of AGS cells treated with siRNAs targeting hnRNPM. Scale bars, 100 µm. (*F* and *G*) Wound-healing assays of AGS and SGC7901 cells treated with siRNAs targeting *circURI1* or co-transfected with siRNAs targeting hnRNPM. siNC, siRNA with scrambled sequences; siCirc-1,2, two siRNAs (siCirc-1, siCirc-2) against the junction sites of *circURI1*. (*H*) Transwell assays of AGS cells treated with siRNAs targeting *circURI1* or co-transfected with siRNAs targeting hnRNPM. Scale bars, 100 µm. (*I*) Transwell assays of AGS *circURI1* KO cells overexpressing hnRNPM truncated forms including full length hnRNPM (hnRNPM (FL)) and hnRNPM without the RRM1 domain (hnRNPM (Del_71-149aa)). EV, empty vector. Scale bars, 100 µm. Error bars, S.E.M. from three independent experiments. N.S., not significant; $^{*}P< 0.05$; $^{**}P< 0.01$ by two-tailed Student's *t*-test.

Figure S7



	ΔPSI high	ΔPSI low	P value
circURI1 sensitive	14	8	0.03
circURI1 insensitive	102	107	

Fig. S7. Analysis of alternative splicing caused by hnRNPM loss in AGS cells and TCGA analysis of alternative splicing. (*A*) Violin plots showing hnRNPM iCLIP-seq signals in the flanking introns of the hnRNPM sensitive and insensitive exons. (*B*) Gene ontology analysis of 231 hnRNPM sensitive targets analyzed by Gorilla. (*C*) Semi-quantitative RT-PCR gels. For RNF24 and DNAJB5, unspecific bands are also amplified (indicated with a star). siNC, siRNA with scrambled sequences; siCirc-1 and siCirc-2, two siRNAs against the junction sites of *circURI1*; siM-1 and siM-2, two independent siRNAs against hnRNPM. *P<0.05; **P<0.01; ***P<0.001 by two-tailed Student's *t*-test. (*D*) The enriched motifs of introns flanked by 209 hnRNPM sensitive exons analyzed by HOMER (-len 10). (*E*) Distribution of the changes for 22 circURI1-sensitive exons in 231 hnRNPM-sensitive exons. The changes of PSI (ΔPSI) for all exons sensitive to hnRNPM are arranged from high to low. ΔPSI high, the top 50% exons; ΔPSI low, the bottom 50% exons. P value was calculated by Chi-square test. (*F*) Violin plots depicting the ratios of $AKT1^{e2IN}$, $NR4A1^{e2IN}$ and $LGALS8^{e8EX}$ in GC patients and controls analyzed from TCGA database. NT, normal tissue. $AKT1^{e2IN}$, exon 2 inclusion of AKT1; $NR4A1^{e2IN}$, exon 2 inclusion of NR4A1; $LGALS8^{e8EX}$, exon 8 exclusion of LGALS8. P values were calculated by two-tailed Student's *t*-test. (*G*) Kaplan-Meier analysis of overall survival for GC patients with $AKT1^{e2IN}$, $NR4A1^{e2IN}$ and $LGALS8^{e8EX}$. P value was calculated by log-rank test. Error bars, S.E.M. from three independent experiments.

Table S1. Differentially expressed circRNAs in GC.

#chrom	Start	Stop	Strand	Log2FC(GC/paraGC)	P value
chr7	134222331	134260679	+	8.76	0.008644453
chr22	22681864	22764194	+	8.66	0.04300031
chr7	134216659	134253077	+	7.26	0.015298981
chr1	1572769	1635783	-	6.99	2.35E-06
chr4	100205555	100264212	-	6.77	0.020609079
chr14	106109959	106208132	-	6.2	0.026791931
chr19	42265156	42301880	+	6.18	0.000902785
chr21	34804483	34805178	+	6.07	0.000275168
chr10	124348459	124358613	+	6.02	0.037791341
chr7	48541721	48542148	+	5.89	0.04073598
chr1	89523674	89579979	-	5.83	0.005214303
chr9	90343499	90388160	+	5.78	0.000486664
chr12	49491348	49491888	-	5.34	0.019235087
chr6	26368792	26443670	+	5.25	0.014067792
chr1	155182175	155202636	+	5.17	0.015602036
chr5	137288316	137290065	-	5.15	0.004011448
chr9	115013208	115060196	-	5.08	0.026928525
chr1	111690263	111703918	+	4.94	0.024339698
chr1	232649602	232669329	-	4.91	0.034285789
chr13	21305979	21306260	-	4.86	0.009601477
chr16	53907697	53922863	+	4.86	0.026700685
chr14	35331249	35331528	-	4.85	0.039222862
chr1	151089867	151090615	+	4.84	0.039439288
chrX	134679347	134690225	+	4.78	0.014821815
chr17	60111147	60112969	-	4.77	0.024162691
chr17	27778472	27778698	+	4.76	0.022544179
chr1	231506307	231509845	-	4.75	0.029688738
chr2	230723487	230744844	-	4.73	0.028832165
chrX	77270158	77275895	+	4.68	0.034255988
chr9	134305476	134308181	+	4.64	0.007747359
chr2	32735592	32738221	+	4.64	0.027119487
chr13	41892941	41910892	+	4.55	0.026208224
chr3	196118683	196129890	-	4.54	0.037515345
chr16	83940591	83945972	+	4.52	0.010434323
chr4	39915230	39927553	-	4.52	0.0357726
chr3	179131199	179137293	-	4.51	0.011460949
chr2	15601324	15651474	-	4.51	0.011461935
chr12	133357383	133359079	-	4.49	0.034386269
chr16	24043456	24046868	+	4.49	0.041045313
chr1	21327691	21329301	-	4.49	0.041051858
chr4	106832305	106832889	+	4.4	0.042577566
chr7	133821775	133848292	+	4.38	0.047566238
chr2	200233327	200298237	-	4.37	0.019693797
chr19	50902107	50902741	+	4.36	0.038019195

chr10	111883774	111890244	+	4.35	0.039974013
chr8	124089350	124096580	+	4.35	0.045048164
chr1	1423242	1459777	+	4.23	0.049071767
chr1	104108056	104152972	+	4.22	0.02497363
chr1	161479609	161559609	+	4.21	0.000634754
chr19	55175636	55208843	+	4.21	0.028824637
chr2	191765289	191789319	+	4.21	0.030688108
chr4	169812072	169837178	+	4.2	0.047194124
chr2	69575302	69590802	-	4.2	0.04904088
chr12	66597490	66622150	+	4.1	0.012003239
chr10	124340381	124358613	+	4.06	0.001710737
chr14	91947919	91952074	-	4.04	0.033921106
chr1	155896466	155896947	-	4.04	0.039752065
chr7	43679047	43680248	-	4.03	0.009442163
chr15	101775286	101775782	-	3.91	0.003961356
chr10	31661946	31750166	+	3.7	0.00165616
chr8	128902834	128903244	+	3.7	0.014794205
chr6	144858717	144864006	+	3.66	0.008606594
chr3	197541778	197547301	+	3.66	0.027262821
chr1	161480623	161561188	+	3.6	0.025322291
chr15	67524151	67529158	-	3.58	0.016705296
chr8	99718694	99719539	-	3.37	0.02642291
chr16	31392217	31435524	+	3.36	0.005586221
chr9	128419929	128434922	-	3.35	0.041855082
chr12	10561987	10588009	-	3.3	0.049571796
chr1	65243305	65255197	+	3.29	0.049844037
chr15	44907560	44912601	-	3.26	0.047609224
chr19	45419446	45430290	+	3.23	0.000447381
chr1	145323653	145327665	+	3	0.044750977
chr9	4286037	4286523	-	2.91	0.031438846
chr11	108098321	108100050	+	2.87	0.023294112
chr10	34558584	34573173	-	2.68	0.034256054
chr4	128842678	128861152	-	2.61	0.043051776
chr1	196682864	196749103	+	2.56	0.009852882
chr19	30476129	30477324	+	2.55	0.0224366
chr9	90343164	90387913	+	2.23	0.000287188
chr12	9251976	9333728	-	2.22	0.00175949
chr1	89477429	89521911	-	2.18	0.036733544
chr1	31465236	31468067	-	2.12	0.039056807
chr11	104901056	104936972	-	2.08	0.002060441
chr16	18852886	18856973	-	1.99	0.037903909
chr5	176370335	176385155	-	1.88	0.037771319
chr12	9268359	9356547	-	1.8	0.001214883
chr7	35942685	36006136	+	1.78	0.034711244
chr12	94562928	94580249	+	1.68	0.029732262
chr2	40655612	40657444	-	1.39	0.001123669

chr12	49525080	49580616	-	1.27	0.013939526
chr12	9246060	9317963	-	1.25	0.022238707
chr15	43873424	43973156	-	1.02	0.005182414
chr6	7176887	7189555	+	-1.21	0.034518945
chr3	171965322	171969331	+	-1.22	0.009089271
chr6	158703294	158735300	+	-1.31	0.034002904
chr12	32751430	32764217	+	-1.53	0.001750767
chr2	227729319	227779067	+	-1.63	0.006300266
chr5	145176004	145205763	-	-1.66	0.028043138
chr17	20107645	20109225	+	-1.72	0.003113621
chr16	56660791	56717142	+	-1.82	0.024427608
chr16	56643174	56717142	+	-1.9	0.003699757
chr16	85667519	85667738	+	-1.93	0.002845673
chr6	158733082	158735300	+	-1.98	0.000566279
chr16	56643174	56673241	+	-1.99	0.000161069
chr4	37633006	37640126	-	-2.02	0.03358793
chr16	56660791	56667317	+	-2.02	0.04582683
chr2	233651863	233660935	+	-2.14	0.03276043
chr6	161455290	161471011	+	-2.16	0.028745588
chr16	56660791	56692652	+	-2.25	0.006246202
chr3	169694733	169706147	+	-2.3	0.011898539
chr1	59787207	59812070	+	-2.39	0.031065243
chr4	187627716	187630999	-	-2.51	0.003094547
chr15	100871093	100874385	-	-2.51	0.032270326
chr16	56660791	56704483	+	-2.56	0.035548444
chr16	56660791	56670416	+	-2.59	0.0089101
chr7	97820039	97823884	+	-2.63	0.010846862
chr1	95609446	95616975	+	-2.66	0.04273992
chr1	19595065	19609386	-	-2.68	0.005822795
chr16	56660791	56673241	+	-2.71	0.000206145
chr6	52657653	52712830	-	-2.71	0.020628369
chr17	18110128	18111689	+	-2.76	0.037936617
chr2	63206322	63223901	+	-2.79	0.004689665
chr13	33109905	33111164	-	-2.8	0.007661046
chr1	19612381	19633904	-	-2.86	0.005962385
chr3	169831147	169840532	-	-2.87	0.04740725
chr10	12123470	12162266	+	-2.87	0.04877325
chr3	3819408	3830758	-	-2.89	0.00949252
chrX	24190831	24197887	+	-2.89	0.01518267
chr1	213290658	213303232	+	-2.95	0.043058649
chr12	12672795	12674397	-	-2.96	0.001919718
chr4	108603170	108622441	-	-2.96	0.014927722
chr20	47570092	47580435	+	-3.01	0.036663069
chr18	42529845	42533305	+	-3.03	0.003704764
chr16	11114049	11154879	+	-3.05	0.006216082
chr4	40596274	40598817	-	-3.06	0.030915288

chr12	32729199	32764217	+	-3.11	0.002993519
chr12	32734893	32764217	+	-3.14	0.025521296
chr2	223765391	223773868	+	-3.18	0.010886125
chr5	132426884	132428481	+	-3.35	0.009632904
chr15	57730182	57734676	+	-3.35	0.020750542
chr1	59787207	59844509	+	-3.36	0.048897712
chr3	71064699	71102924	-	-3.41	0.030287317
chr7	151900018	151904513	-	-3.58	0.048601931
chr16	30490411	30490782	+	-3.65	0.032343127
chr6	73005639	73043538	+	-3.72	0.001859961
chr2	120885263	120932580	+	-3.74	0.000330623
chr2	183993014	183995273	+	-3.87	0.027617684
chr4	140810510	140812121	-	-3.96	0.009947137
chr16	56643174	56660443	+	-4.03	0.001376818
chr6	35586872	35614627	-	-4.07	0.010622024
chr4	40892380	40937156	-	-4.13	0.04391518
chr5	123974825	124036962	-	-4.14	0.031438754
chr2	170487283	170488443	+	-4.16	0.046354645
chr14	67431907	67525503	+	-4.16	0.046357118
chr1	95609446	95639445	+	-4.16	0.046359591
chr5	127474288	127488497	+	-4.17	0.003779461
chr7	102453723	102462650	-	-4.25	0.029638
chr1	118035768	118045592	+	-4.26	0.048137215
chr15	66021409	66048810	-	-4.26	0.048140666
chr5	112327850	112339774	+	-4.26	0.048144117
chr2	113057425	113089859	+	-4.27	0.000321254
chr2	27822449	27824309	+	-4.27	0.022525463
chr14	71209067	71209308	-	-4.28	0.024112161
chr16	57238415	57250947	+	-4.28	0.02411516
chr14	95056377	95081421	+	-4.29	0.036048221
chr2	173423435	173435552	+	-4.38	0.025166377
chr20	18278628	18287037	+	-4.39	0.018199893
chr1	14057494	14075982	+	-4.39	0.041182107
chr19	57706136	57755417	+	-4.39	0.041185221
chr16	16101672	16150152	+	-4.41	0.041279032
chr4	103610730	103651893	-	-4.41	0.04128217
chr17	65906992	65909303	+	-4.44	0.041189245
chr8	94798450	94828743	+	-4.44	0.0430133
chr5	145044816	145083858	-	-4.48	0.045976523
chr2	73761950	73800551	+	-4.51	0.01235442
chr10	1118055	1151207	+	-4.52	0.032652927
chr10	88212976	88220253	-	-4.54	0.039422549
chr17	29483000	29497015	+	-4.56	0.032714133
chr2	214174782	214215369	+	-4.56	0.032716628
chr4	2659529	2661781	+	-4.56	0.03673529
chr10	75142932	75143448	-	-4.56	0.038131621

chr6	158922709	158925210	+	-4.56	0.048224519
chr2	165548730	165552343	-	-4.56	0.048229556
chr5	139574030	139574237	+	-4.62	0.027169074
chr1	213037066	213061936	+	-4.64	0.029640687
chr1	235950499	235964397	-	-4.66	0.044543821
chr12	32729199	32778713	+	-4.66	0.044550643
chr19	12503416	12542794	-	-4.66	0.044557468
chr9	33953282	33956144	-	-4.66	0.044564295
chr1	180953812	180974599	-	-4.67	0.029243026
chr3	17549965	17628049	-	-4.67	0.029244653
chr11	67934448	67957619	-	-4.67	0.042893384
chr8	124089350	124117704	+	-4.68	0.043863151
chr17	11984672	11999011	+	-4.68	0.043871105
chr2	205521864	205551005	+	-4.72	0.023560349
chr18	77488906	77496521	+	-4.72	0.023565649
chr17	74287095	74290102	-	-4.72	0.02357095
chr9	111819470	111826847	-	-4.75	0.00497201
chr6	134349518	134350859	-	-4.75	0.00600937
chr2	15415607	15417225	-	-4.75	0.030342735
chr1	203680004	203691817	+	-4.75	0.030349078
chr3	111828389	111831992	+	-4.77	0.024197941
chr6	111493897	111527938	+	-4.78	0.039775568
chr12	18715636	18719991	+	-4.82	0.005721344
chr1	215342541	215345526	+	-4.83	0.004253443
chr8	73117533	73123790	-	-4.84	0.022957082
chr7	141759655	141785761	+	-4.84	0.022962645
chr14	74360499	74370813	+	-4.84	0.02297377
chr15	73408880	73428368	+	-4.85	0.006815048
chr11	60971980	61009403	+	-4.86	0.01132546
chr3	47777523	47814426	-	-4.86	0.035841824
chr1	236966727	236969533	+	-4.87	0.022225199
chr1	76205664	76216231	+	-4.87	0.02223067
chr1	52237741	52238395	+	-4.87	0.022236141
chr9	79115831	79142811	+	-4.9	0.021894332
chr1	32502510	32504220	+	-4.94	0.024145546
chr8	17541836	17613470	-	-4.96	0.019609646
chr12	18434937	18478032	+	-4.96	0.019613134
chr22	39438941	39473383	+	-4.99	0.017523254
chr10	90427043	90433491	+	-5.03	0.010244453
chr3	183361267	183382827	+	-5.05	0.007263108
chr2	48065997	48066908	-	-5.08	0.015442617
chr4	187584452	187630999	-	-5.09	0.001281834
chr20	32996456	33001685	+	-5.1	0.014985992
chr14	31596990	31641328	-	-5.11	0.002436026
chr4	2951660	2955372	-	-5.11	0.002620583
chr3	185316199	185331196	+	-5.14	0.014384253

chr15	41961025	41991357	+	-5.27	0.011963139
chr14	38218143	38266152	+	-5.27	0.011967449
chr8	61707544	61714152	+	-5.31	0.000806553
chr1	16358204	16378906	+	-5.35	0.011523233
chr2	175324605	175346715	-	-5.51	0.001197123
chr15	57743697	57754090	+	-5.6	0.000195385
chr11	60971980	60990577	+	-5.63	0.001162448
chr18	51686134	51731527	-	-5.64	0.001851611
chr16	29916172	29917280	+	-5.69	0.004217829
chr15	45777354	45778619	-	-5.75	0.038474549
chr4	37633006	37636745	-	-5.81	0.005726359
chr15	57730182	57754090	+	-5.83	0.000208886
chr15	73995112	73996338	+	-6.02	0.032042203
chr7	91924202	91981956	+	-6.19	0.004170394
chr2	120885263	120932576	+	-6.38	0.005896768
chr11	60974814	60993643	-	-6.58	0.002569343
chr14	106208229	106235896	-	-9.16	0.049547775

FC=Fold Change. P values were generated by DEseq2.

Table S2.

The binding sites of hnRNPM iCLIP-seq

#chrom	start	stop	strand	signals
chr1	28833872	28833931	+	39
chrM	1858	1875	+	35
chrM	2222	2276	+	33
chr1	109642920	109642955	+	28
chr13	45911662	45911706	-	25
chrM	3071	3115	+	19
chr15	25274053	25274068	+	17
chrUn_gl000220	118160	118204	+	16
chr1	28835090	28835122	+	15
chr11	62620423	62620462	-	15
chr11	93464201	93464241	-	15
chrM	3133	3143	+	15
chr19	30477292	30477311	+	14
chr1	28835148	28835177	+	14
chr3	186505100	186505135	+	14
chr9	35657822	35657852	-	14
chr3	39449877	39449892	+	13
chr1	28833952	28833986	+	12
chr3	39452586	39452608	+	12
chr1	93306301	93306320	+	11
chrM	729	734	+	11
chr1	93306272	93306276	+	10
chr3	186739528	186739536	+	10
chr6	15275372	15275394	+	10
chr9	130210845	130210861	-	10
chr11	62310632	62310640	-	9
chr11	65271948	65271977	+	9
chr11	68255702	68255706	+	9
chr15	25232318	25232340	+	9
chr15	25251200	25251208	+	9
chr15	25295317	25295321	+	9
chr15	25311811	25311828	+	9
chr15	57229961	57229977	+	9
chr17	7478027	7478045	+	9
chr3	186505432	186505439	+	9
chr6	8086732	8086741	-	9
chr6	133138382	133138386	+	9
chr7	6415333	6415337	+	9
chrM	2042	2050	+	9
chrM	2351	2356	+	9

chrUn_gl000220	117875	117881	+	9
chr11	65192876	65192890	+	8
chr11	65269041	65269049	+	8
chr11	65272234	65272251	+	8
chr15	25232250	25232256	+	8
chr15	25294821	25294825	+	8
chr15	25311054	25311061	+	8
chr17	37009171	37009188	-	8
chr17	62223693	62223699	+	8
chr17	62223723	62223730	+	8
chr17	74494643	74494655	-	8
chr19	8517608	8517614	+	8
chr19	17973425	17973441	+	8
chr20	21116004	21116010	+	8
chr20	57468131	57468136	+	8
chr3	39449911	39449921	+	8
chr3	39452545	39452572	+	8
chr3	186504462	186504473	+	8
chr5	110430681	110430686	+	8
chr14	62247602	62247608	+	7
chr15	25249957	25249975	+	7
chr15	25311273	25311278	+	7
chr15	25338215	25338224	+	7
chr15	49307976	49307984	-	7
chr3	185536271	185536282	-	7
chr7	33458226	33458245	+	7
chr7	138157031	138157035	+	7
chr8	48975778	48975781	+	7
chrX	24780158	24780162	+	7
chr1	1412413	1412417	+	6
chr1	13911106	13911109	+	6
chr1	91412278	91412283	-	6
chr1	162134502	162134506	+	6
chr1	171471881	171471884	+	6
chr1	223145923	223145927	+	6
chr1	224853485	224853487	+	6
chr10	12140881	12140883	+	6
chr10	114717415	114717420	+	6
chr10	114852686	114852690	+	6
chr11	8705771	8705773	+	6
chr11	75129933	75129937	+	6
chr12	16145365	16145369	+	6
chr12	52354919	52354924	+	6

chr12	109541290	109541294	+	6
chr13	46109369	46109373	+	6
chr13	111876560	111876564	+	6
chr14	38667318	38667322	+	6
chr14	70086989	70086993	+	6
chr14	99972764	99972766	+	6
chr14	104191212	104191216	+	6
chr15	25232615	25232620	+	6
chr15	25276146	25276148	+	6
chr15	80420769	80420773	+	6
chr15	84265025	84265029	+	6
chr16	1724327	1724331	+	6
chr16	28309510	28309514	+	6
chr16	28313235	28313237	+	6
chr16	81574985	81574987	+	6
chr16	84742933	84742937	+	6
chr17	4754005	4754009	+	6
chr17	67525018	67525023	+	6
chr18	56623103	56623107	+	6
chr18	56630560	56630565	+	6
chr19	2198503	2198507	+	6
chr19	34878751	34878755	+	6
chr2	44620762	44620772	+	6
chr2	122360625	122360633	-	6
chr2	135702639	135702641	+	6
chr2	207026980	207026986	+	6
chr2	210868762	210868766	+	6
chr2	238582411	238582416	+	6
chr2	239357553	239357555	+	6
chr20	31351058	31351060	+	6
chr20	60758201	60758203	+	6
chr20	62654800	62654804	+	6
chr3	15872384	15872394	-	6
chr3	61553064	61553068	+	6
chr3	61734437	61734441	+	6
chr3	61756689	61756691	+	6
chr3	76284932	76284936	+	6
chr3	122929898	122929902	+	6
chr3	172005771	172005775	+	6
chr3	186504546	186504550	+	6
chr3	192613116	192613123	-	6
chr3	196851930	196851934	-	6
chr4	6919530	6919534	+	6

chr4	8475493	8475497	+	6
chr4	119200387	119200389	+	6
chr4	129732994	129733010	+	6
chr5	98132251	98132253	+	6
chr6	15257992	15257995	+	6
chr6	15276939	15276945	+	6
chr6	44383308	44383312	+	6
chr6	111843679	111843683	+	6
chr7	2153382	2153388	-	6
chr7	5635392	5635396	+	6
chr7	26245411	26245413	+	6
chr7	90695245	90695249	+	6
chr7	93278529	93278533	+	6
chr7	95764348	95764353	-	6
chr8	1007746	1007748	+	6
chr8	143624181	143624183	+	6
chr9	132880174	132880178	+	6
chrM	13900	13902	+	6
chrX	2795965	2795969	+	6
chrX	9489421	9489425	+	6
chrX	21966159	21966163	+	6
chrX	47056880	47056884	+	6
chr1	1558314	1558318	+	5
chr1	2163803	2163817	+	5
chr1	2165077	2165081	+	5
chr1	33283449	33283451	+	5
chr1	64961983	64961985	+	5
chr1	225192598	225192602	+	5
chr1	230282161	230282163	+	5
chr1	237266427	237266431	+	5
chr10	72240374	72240376	+	5
chr11	314523	314526	+	5
chr11	65212495	65212499	+	5
chr11	69461203	69461207	+	5
chr11	74684456	74684460	+	5
chr11	75304154	75304156	+	5
chr11	100656371	100656375	+	5
chr11	118342964	118342966	+	5
chr11	118771467	118771471	-	5
chr12	12972589	12972593	+	5
chr12	51798774	51798776	+	5
chr12	56552626	56552630	+	5
chr12	98989470	98989474	+	5

chr12	98993517	98993524	+	5
chr12	121137042	121137046	+	5
chr12	132536827	132536831	+	5
chr13	28240712	28240716	+	5
chr13	28716214	28716219	+	5
chr13	29690901	29690905	+	5
chr13	43621966	43621968	+	5
chr13	49793290	49793294	-	5
chr13	100210284	100210286	+	5
chr13	103307002	103307004	+	5
chr13	111908912	111908916	+	5
chr13	114163016	114163020	+	5
chr13	114182742	114182746	+	5
chr15	25229853	25229856	+	5
chr15	25233884	25233888	+	5
chr15	25315313	25315317	+	5
chr15	25330824	25330827	+	5
chr15	25333499	25333502	+	5
chr15	49930933	49930937	+	5
chr15	62689996	62690000	+	5
chr15	99275017	99275022	+	5
chr16	2814818	2814820	+	5
chr16	13118264	13118268	+	5
chr16	81570442	81570444	+	5
chr16	84787963	84787968	+	5
chr16	89202787	89202791	+	5
chr17	2501630	2501632	+	5
chr17	40627114	40627118	+	5
chr17	65374656	65374660	+	5
chr17	75404164	75404168	+	5
chr17	78860442	78860446	+	5
chr18	8627205	8627207	+	5
chr18	55909617	55909621	+	5
chr19	38409790	38409794	+	5
chr2	982199	982201	+	5
chr2	42891311	42891315	+	5
chr2	44780790	44780794	+	5
chr2	105673748	105673752	+	5
chr2	168188475	168188479	+	5
chr2	231742918	231742933	+	5
chr2	236451853	236451857	+	5
chr20	18727469	18727473	+	5
chr20	30702455	30702459	+	5

chr21	17233508	17233512	+	5
chr21	46908258	46908262	+	5
chr22	17897581	17897585	+	5
chr3	32936582	32936584	+	5
chr3	61568709	61568711	+	5
chr3	110791482	110791486	+	5
chr3	173128660	173128662	+	5
chr3	174476413	174476415	+	5
chr4	2066871	2066873	+	5
chr4	25370238	25370242	+	5
chr4	39721097	39721101	+	5
chr4	40941747	40941750	-	5
chr4	93788818	93788822	+	5
chr4	113894575	113894577	+	5
chr4	120162523	120162525	+	5
chr4	123763753	123763755	+	5
chr4	146656969	146656971	+	5
chr4	152443338	152443340	+	5
chr4	184034442	184034446	+	5
chr4	186590490	186590495	-	5
chr5	1806411	1806415	+	5
chr5	7807266	7807270	+	5
chr5	43163532	43163536	+	5
chr5	60808704	60808708	+	5
chr5	71490943	71490945	+	5
chr5	93697767	93697772	-	5
chr5	112178391	112178395	+	5
chr6	4819176	4819181	+	5
chr6	15319629	15319633	+	5
chr6	33611407	33611411	+	5
chr6	57256332	57256340	+	5
chr7	2285791	2285795	+	5
chr7	127315958	127315962	+	5
chr7	128850854	128850858	+	5
chr8	589803	589808	-	5
chr8	1777786	1777789	+	5
chr8	35118345	35118349	+	5
chr8	103955526	103955530	+	5
chr8	144674705	144674709	-	5
chr9	21905573	21905577	+	5
chr9	91966267	91966271	+	5
chr9	108357791	108357793	+	5
chr9	128521584	128521588	+	5

chr9	131356179	131356181	+	5
chr9	133917787	133917789	+	5
chr9	134280889	134280893	+	5
chr9	134292575	134292579	+	5
chrM	1701	1707	+	5
chrX	18478364	18478368	+	5
chrX	73186096	73186100	+	5
chr1	10502444	10502448	+	4
chr1	19932220	19932222	+	4
chr1	32511825	32511827	+	4
chr1	45216668	45216672	+	4
chr1	174871423	174871427	+	4
chr1	182847814	182847816	+	4
chr1	243954504	243954506	-	4
chr10	83849179	83849183	+	4
chr10	84557456	84557458	+	4
chr11	60699629	60699633	+	4
chr11	76245399	76245403	+	4
chr11	82618402	82618406	+	4
chr12	11843065	11843069	+	4
chr12	117182406	117182408	+	4
chr12	133129579	133129581	+	4
chr13	107928713	107928717	-	4
chr15	25277718	25277724	+	4
chr16	25792607	25792611	+	4
chr16	57502773	57502777	+	4
chr17	2539293	2539297	+	4
chr17	16962925	16962929	+	4
chr17	40696103	40696107	+	4
chr19	9273519	9273523	+	4
chr19	45412501	45412505	+	4
chr2	44669814	44669818	+	4
chr2	197615847	197615851	+	4
chr2	233069702	233069706	+	4
chr20	21358354	21358358	+	4
chr22	20113953	20113955	+	4
chr22	39801776	39801778	+	4
chr22	50921837	50921839	+	4
chr3	32862234	32862236	+	4
chr3	50952519	50952521	+	4
chr3	61568262	61568269	+	4
chr3	162885867	162885871	+	4
chr4	183152170	183152174	+	4

chr5	132406859	132406863	+	4
chr6	15253163	15253167	+	4
chr6	15317846	15317850	+	4
chr6	15411586	15411590	+	4
chr6	21805739	21805741	+	4
chr6	89451990	89451992	-	4
chr6	149111641	149111645	+	4
chr7	8011777	8011781	+	4
chr7	127452637	127452641	+	4
chr7	127540896	127540900	+	4
chr8	26179827	26179830	+	4
chr8	30339339	30339343	+	4
chr9	88630451	88630453	+	4
chr9	115551068	115551072	+	4
chrUn_gl000220	117847	117860	+	4
chrUn_gl000220	118063	118065	+	4

Table S3. The sequence of 24 clones from hnRNPM individual-CLIP in circURI1

	No.	Sequence	
2 clones	1	TTTTTTTTTTGCTGTAGGTTTAGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	2	TTTTTTTTTTGCTGTAGGTTTAGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
5 clones	3	TTTTTTTTTTCTGTAGGTTTAGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	4	TTTTTTTTTTCTGTAGGTTTAGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	5	TTTTTTTTTTCTGTAGGTTTAGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	6	TTTTTTTTTTCTGTAGGTTTAGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	7	TTTTTTTTTTCTGTAGGTTTAGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
7 clones	8	TTTTTTTTTTGTAGGTTTAGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	9	TTTTTTTTTTGTAGGTTTAGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	10	TTTTTTTTTTGTAGGTTTAGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	11	TTTTTTTTTTGTAGGTTTAGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	12	TTTTTTTTTTGTAGGTTTAGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	13	TTTTTTTTTTGTAGGTTTAGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	14	TTTTTTTTTTGTAGGTTTAGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
7 clones	15	TTTTTTTTTTGTTGAGCACCGGAAAGAACGGAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	16	TTTTTTTTTTGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	17	TTTTTTTTTTGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	18	TTTTTTTTTTGTTGAGCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	19	TTTTTTTTTTGTTGAGCACCGGAAAGAACGGAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	20	TTTTTTTTTTGTTGAGCACCGGAAAGAACGGAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	21	TTTTTTTTTTGTTGAGCACCGGAAAGAACGGAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
3 clones	22	TTTTTTTTTTCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
	23	TTTTTTTTTTCACCGGAAAGAACGAAGAAGGTAGATAATGACTATAATGCCCTTC	GAGAAAGACTCAGCACCTTG
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circURI1-specific primer was highlighted in gray; Oligo(dT) sequence located on the left.

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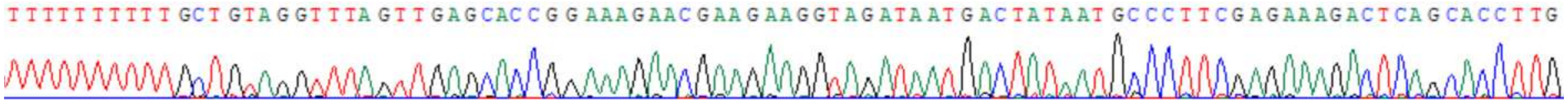

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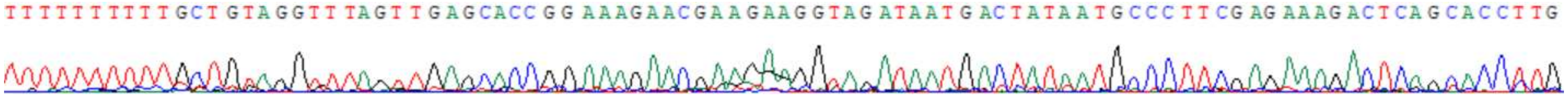

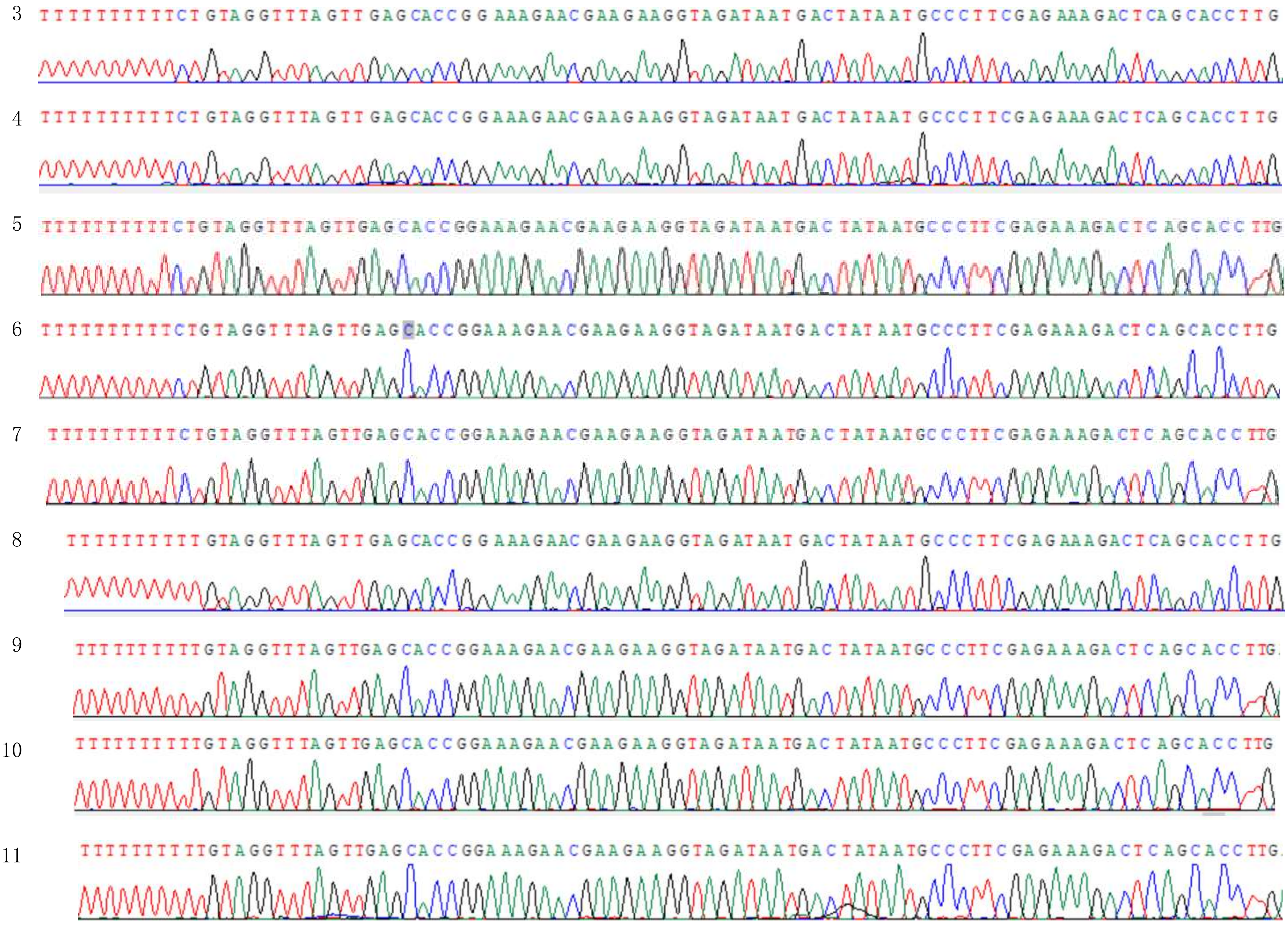
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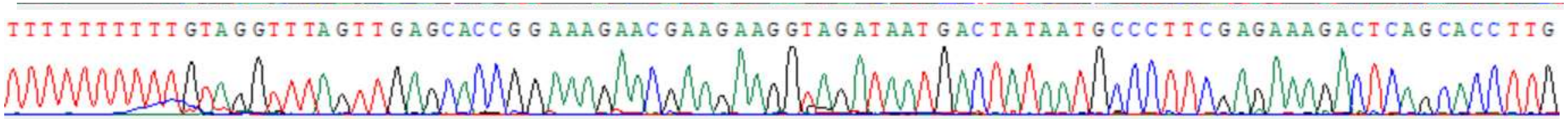

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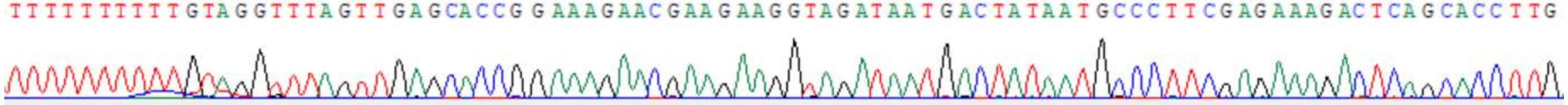

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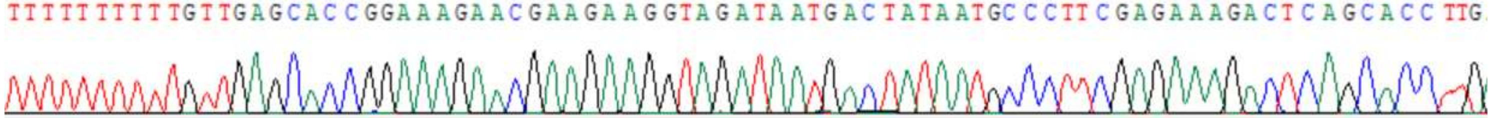

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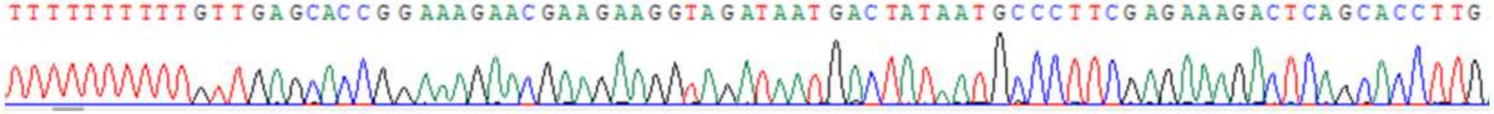

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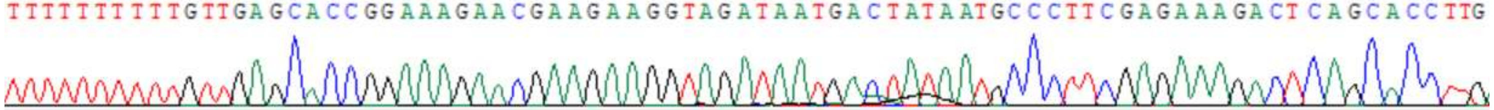

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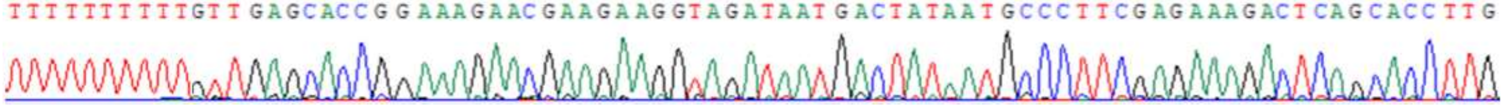

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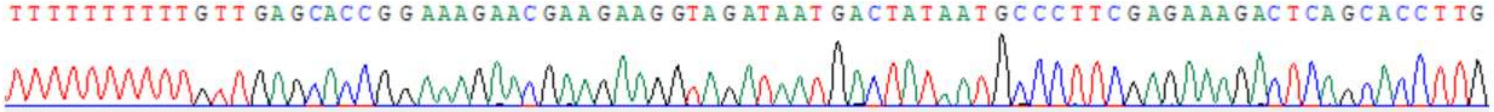

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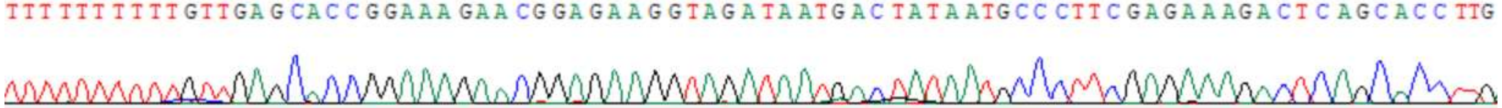

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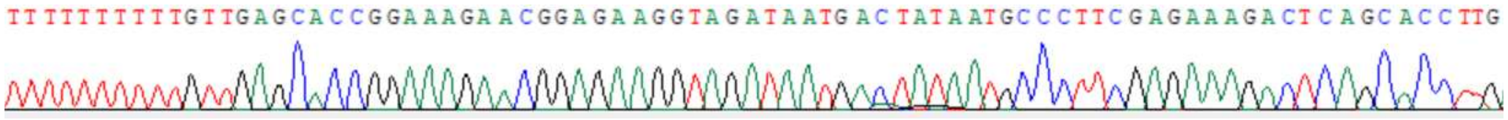
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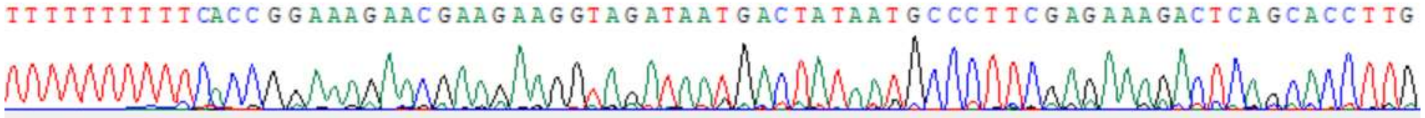
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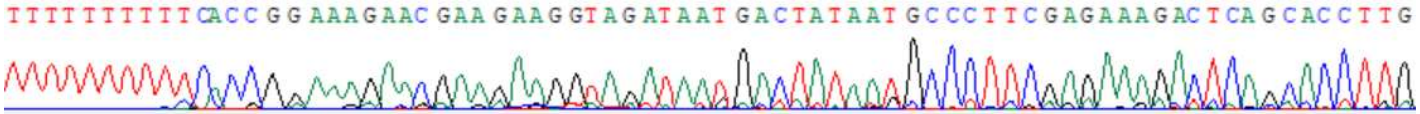
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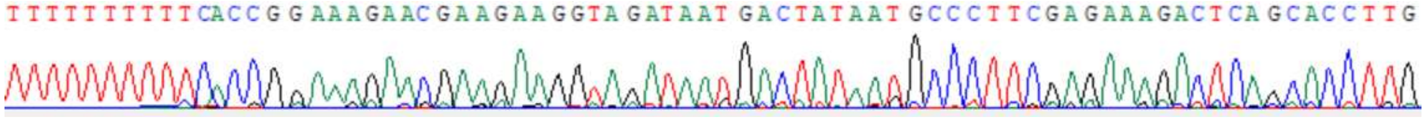
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Table S4.
Differential analysis of alternative splicing upon circURI1 knockdown.

Gene	Chrom	Exon start	Exon stop	PSI of siNC	PSI of siCirc-1	P value (siCirc-1 vs siNC)	PSI of siCirc-2	P value (siCirc-2 vs siNC)
GMPR2	chr14	24703312	24703447	0.758	0.861	1.06171E-07	0.909	2.02025E-08
DNMT3A	chr2	25472525	25472593	0.222	0.583	0.036546341	0.556	0.010636855
SENP1	chr12	48482945	48483076	0.750	0.935	1.40519E-05	0.892	0.011066885
KIAA1217	chr10	24831621	24831699	0.118	0.333	0.038112373	0.308	0.025347319
AKT1	chr14	105259463	105259547	0.212	0.344	0.000161485	0.366	0.038867104
RAB11FIP1	chr8	37728795	37730697	0.420	0.560	0.046118177	0.484	0.084234195
NR4A1	chr12	52446279	52446429	0.498	0.583	6.25588E-06	0.579	0.012806798
RNF24	chr20	3954978	3955047	0.492	0.614	0.016421754	0.595	3.16642E-07
ARMC8	chr3	137907242	137907372	0.500	0.714	0.035938931	0.640	0.042602365
VEGFA	chr6	43749692	43749824	0.164	0.225	6.15097E-29	0.298	1.71857E-43
DNAJB5	chr9	34990664	34990809	0.889	0.769	0.047338026	0.731	0.044299419
B3GALNT2	chr1	235659495	235659618	0.574	0.496	0.030427426	0.474	0.005031573
SCEL	chr13	78167648	78167708	0.167	0.000	0	0.063	0.009823275
LGALS8	chr1	236706214	236706340	0.214	0.135	2.04572E-05	0.136	0.000754764
EPB41	chr1	29385100	29385157	0.541	0.375	8.83413E-10	0.364	1.57637E-05
RGS5	chr1	163288971	163289081	0.231	0.100	0.042602365	0.056	0.008705089
ARRB1	chr11	74982744	74982768	0.824	0.545	0.000708557	0.600	0.038613801
FAM135A	chr6	71195869	71195947	0.603	0.514	4.3795E-08	0.466	0.005296283
LPIN1	chr2	11916211	11916319	0.600	0.550	0.024618761	0.526	0.036410438
PEX2	chr8	77900542	77900574	0.217	0.087	0.026416147	0.100	0.033894854
SS18L1	chr20	60729336	60729521	0.140	0.348	0.001073771	0.342	5.20345E-05
ZCCHC10	chr5	132358532	132358598	0.659	0.455	0.004329928	0.484	0.002606079
SLC25A26	chr3	66354876	66354961	0.839	0.740	0.009252698	0.540	3.3456E-08
FXYD3	chr19	35610071	35610155	0.600	0.417	0.011458046	0.375	0.028459737
NBPF15	chr1	148577071	148577251	0.263	0.000	0	0.105	0.024920361
SUPT20H	chr13	37584688	37584792	0.438	0.500	8.11407E-06	0.492	4.03193E-06
BCAR1	chr16	75298248	75298499	0.877	0.962	0.000402703	0.932	0.018326089
TRAF3	chr14	103296670	103296809	0.069	0.226	0.046970956	0.161	0.038857633
RNF146	chr6	127607194	127607322	0.260	0.336	0.037372988	0.390	1.71911E-05

PSI=Percentage Spliced In. P-values were calculated by Chi-square test.

Differential analysis of alternative splicing upon hnRNPM knockdown.

Gene	Chrom	Exon start	Exon stop	PSI of siNC	PSI of siM-1	P value (siM-1 vs siNC)	PSI of siM-2	P value (siM-2 vs siNC)
KIAA1217	chr10	24831621	24831699	0.118	0.000	0	0.000	0
DNAJB5	chr9	34990664	34990809	0.889	1.000	0	1.000	0
DTYMK	chr2	242619643	242619734	0.169	0.059	1.14013E-27	0.072	5.95984E-23
DBF4B	chr17	42809545	42809633	0.652	0.194	1.8445E-19	0.230	4.86043E-10
CTTN	chr11	70267575	70267686	0.304	0.196	3.44657E-19	0.218	1.27894E-10
GANAB	chr11	62401781	62401847	0.665	0.765	5.55723E-19	0.723	1.37836E-06
CD59	chr11	33752969	33753014	0.562	0.692	5.3305E-18	0.642	1.27685E-10
CHCHD4	chr3	14163416	14163586	0.441	0.784	3.58255E-17	0.750	2.12131E-27
ENC1	chr5	73933318	73933443	0.744	0.367	5.10074E-16	0.194	1.17083E-32
CHKA	chr11	67848870	67848924	0.198	0.078	1.1634E-15	0.090	4.32804E-24
YPEL5	chr2	30371110	30371171	0.762	0.943	1.36799E-15	0.888	5.6609E-05
KLHL5	chr4	39064178	39064655	0.888	0.697	3.24449E-15	0.604	3.80366E-18
CD55	chr1	207523482	207523567	0.980	0.771	1.26575E-14	0.798	4.46806E-13
ANKRD11	chr16	89497663	89497734	0.970	0.839	1.32624E-14	0.912	2.36742E-33
ST6GALNAC6	chr9	130660234	130660289	0.301	0.145	4.60037E-14	0.146	6.08397E-25
SMG7	chr1	183481971	183482003	0.349	0.068	5.21586E-13	0.133	4.60887E-05
KRBOX4	chrX	46330576	46330620	0.903	0.360	1.09076E-12	0.536	1.3356E-05
VEGFA	chr6	43749692	43749824	0.164	0.113	2.36952E-12	0.114	6.62788E-05
UCHL5	chr1	192989436	192989511	0.294	0.524	2.42116E-12	0.506	0.000217641
PPP6R3	chr11	68350510	68350597	0.303	0.131	3.2782E-12	0.190	7.12221E-05
ZDHHC20	chr13	21952799	21952877	0.595	0.871	5.2137E-12	0.825	3.47568E-12
RHOC	chr1	113247721	113247790	0.318	0.229	7.43772E-12	0.152	1.08133E-71
NEK6	chr9	127055127	127055292	0.878	0.957	1.29153E-11	0.932	0.004408606
GMPR2	chr14	24703312	24703447	0.758	0.375	3.98937E-11	0.333	9.69145E-25
HPS5	chr11	18339297	18339454	0.423	0.111	1.90426E-10	0.167	5.47399E-11
ASNS	chr7	97501030	97501308	0.388	0.512	1.92667E-10	0.494	5.11327E-10
CD40	chr20	44751764	44751858	0.147	0.048	2.41289E-10	0.059	1.77499E-05
B3GALNT2	chr1	235659495	235659618	0.474	0.636	4.71742E-10	0.637	1.25321E-05
MCAT	chr22	43533086	43533304	0.220	0.067	5.45038E-10	0.115	0.000399911
WASF1	chr6	110499800	110499945	0.404	0.545	1.53977E-09	0.484	0.001509759
SLC25A26	chr3	66286967	66287124	0.311	0.392	1.56343E-09	0.545	9.01972E-19
UMAD1	chr7	7715732	7715839	0.410	0.800	1.85057E-09	0.679	2.39177E-06

SLC2A8	chr9	130160183	130160390	0.150	0.066	5.02326E-09	0.071	2.01377E-22
CTBP2	chr10	126822080	126822181	0.927	0.514	6.26164E-09	0.536	5.58999E-11
CTAGE5	chr14	39790131	39790260	0.194	0.286	9.24004E-09	0.297	3.38264E-05
IKBKB	chr8	42177102	42177164	0.286	0.063	1.00408E-08	0.135	0.010599544
ZNF507	chr19	32838150	32838244	0.375	0.061	1.04372E-08	0.167	0.006169899
RHOT1	chr17	30499955	30500079	0.925	0.615	1.21515E-08	0.447	4.33026E-10
FIP1L1	chr4	54280781	54280889	0.286	0.483	1.39527E-08	0.402	0.00035504
PRKAR1A	chr17	66511127	66511260	0.713	0.547	1.51013E-08	0.504	5.63103E-17
TLK2	chr17	60601596	60601692	0.500	0.243	2.0761E-08	0.381	0.001223625
FHL2	chr2	106013103	106013154	0.349	0.225	2.20611E-08	0.219	2.11093E-10
CYB561D2	chr3	50389439	50389477	0.205	0.057	3.34737E-08	0.058	1.05951E-14
NFIX	chr19	13198802	13198950	0.659	0.861	8.12373E-08	0.764	0.016935158
MLH3	chr14	75500121	75500193	0.406	0.159	8.37991E-08	0.286	0.015045679
SNX7	chr1	99128252	99128372	0.689	0.375	1.03132E-07	0.556	0.000655982
NCOR2	chr12	124858958	124859009	0.462	0.244	2.62292E-07	0.351	0.025144461
C16orf13	chr16	685611	685774	0.208	0.269	3.02041E-07	0.266	4.76745E-26
ADNP	chr20	49521302	49521386	0.804	0.938	3.18636E-07	0.905	0.012236223
ZNF74	chr22	20749622	20749708	0.429	0.083	3.75138E-07	0.118	0.000789113
MARK2	chr11	63671457	63671619	0.059	0.182	4.41724E-07	0.131	3.02935E-06
CREB1	chr2	208425842	208425884	0.718	0.635	4.60696E-07	0.512	0.011423173
UQCRH	chr1	46774772	46774799	0.307	0.220	5.96763E-07	0.220	8.80442E-09
CAMTA2	chr17	4885383	4885455	0.281	0.071	6.20928E-07	0.160	0.011154874
SAR1A	chr10	71922445	71922515	0.896	0.950	6.32018E-07	0.957	7.84952E-11
SAMD4A	chr14	55251057	55251165	0.516	0.839	1.0435E-06	0.857	2.5903E-07
GIPC1	chr19	14603668	14603724	0.211	0.106	1.20777E-06	0.074	1.00198E-48
MAP3K7	chr6	91254270	91254351	0.308	0.208	1.34939E-06	0.220	0.001163536
TRMU	chr22	46739158	46739265	0.142	0.071	1.44123E-06	0.066	0.00058588
ZNF195	chr11	3394806	3394886	0.435	0.167	1.73637E-06	0.225	0.00115391
TMEM51	chr1	15536985	15537058	0.312	0.212	1.84848E-06	0.211	6.1847E-05
SPOP	chr17	47753256	47753378	0.821	0.455	4.63296E-06	0.737	0.016156931
NR4A1	chr12	52446279	52446429	0.558	0.373	4.88463E-06	0.426	0.004468199
C11orf49	chr11	47008758	47008861	0.375	0.079	4.94843E-06	0.087	0.000207502
FAM173B	chr5	10235322	10235373	0.250	0.198	5.51953E-06	0.163	9.68865E-05
ADAM15	chr1	155033890	155033965	0.908	0.787	5.64764E-06	0.847	7.95764E-10
POC1A	chr3	52130584	52130728	0.217	0.149	6.6131E-06	0.138	0.00016232

MR1	chr19	6897438	6897558	0.207	0.095	6.68717E-06	0.104	0.002052116
PML	chr15	74324912	74325056	0.308	0.082	6.97529E-06	0.043	1.76673E-12
RBM6	chr3	50036872	50036946	0.544	0.352	8.65937E-06	0.360	1.37562E-11
RDH13	chr19	55559413	55559625	0.742	0.872	8.97037E-06	0.807	0.008444198
DYRK2	chr12	68043576	68043725	0.088	0.170	9.75871E-06	0.194	3.06872E-16
MAPKAP1	chr9	128268588	128268696	0.423	0.246	1.00924E-05	0.290	0.000572739
SMARCC2	chr12	56566720	56566813	0.742	0.905	1.22653E-05	0.818	0.021876816
CRELD1	chr3	9985585	9985779	0.830	0.946	2.54771E-05	0.935	0.001386145
FNIP1	chr5	131046270	131046354	0.412	0.161	2.74803E-05	0.286	0.033894854
MRPL55	chr1	228296655	228296722	0.246	0.184	2.9852E-05	0.161	0.000674828
LRRC42	chr1	54413460	54413494	0.338	0.438	3.0346E-05	0.409	0.002448565
IFIT1	chr10	91159646	91159760	0.571	0.804	3.95702E-05	0.755	2.6665E-05
PCBP4	chr3	51995956	51996104	0.299	0.409	3.97172E-05	0.375	0.001066541
PUM2	chr2	20526021	20526146	0.226	0.500	4.11373E-05	0.286	0.018305577
ZNF384	chr12	6787828	6787876	0.623	0.490	4.30031E-05	0.565	0.019625855
DNAJA3	chr16	4504811	4504928	0.585	0.479	4.49849E-05	0.431	2.35193E-09
DEDD2	chr19	42708613	42708711	1.000	0.682	4.6151E-05	0.750	0.000132915
ENSA	chr1	150598954	150599002	0.794	0.718	4.84956E-05	0.721	6.43683E-05
CLASP1	chr2	122166599	122166623	0.750	0.667	5.44731E-05	0.516	0.002603112
ABI2	chr2	204276007	204276094	0.288	0.358	5.94442E-05	0.396	0.000395335
AURKA	chr20	54965611	54965721	0.342	0.257	6.18822E-05	0.211	5.43433E-07
ZNF772	chr19	57986391	57986514	0.857	0.528	6.98746E-05	0.444	0.00375221
SLC35B3	chr6	8418976	8419118	0.654	0.767	7.3632E-05	0.761	0.034231239
TNIK	chr3	170846502	170846667	0.018	0.208	7.40179E-05	0.143	7.86269E-11
PTPRA	chr20	2955860	2955887	1.000	0.871	8.00387E-05	0.947	0.015140885
POFUT2	chr21	46685936	46686142	0.723	0.505	8.29332E-05	0.493	9.6504E-07
SEC24B	chr4	110402832	110402937	0.771	0.631	8.48446E-05	0.549	0.001727818
ZNF706	chr8	102216877	102216921	0.778	0.217	0.000106253	0.231	0.000613905
ARHGAP12	chr10	32128564	32128639	0.174	0.349	0.000108367	0.352	0.000111752
PPP2R4	chr9	131890242	131890347	0.747	0.625	0.000118222	0.522	1.83235E-05
RHOT1	chr17	30538134	30538257	0.465	0.735	0.000119319	0.806	2.35112E-12
METTL15	chr11	28349641	28349712	0.553	0.773	0.000129098	0.667	0.008539601
FEZ2	chr2	36787927	36788008	0.849	0.751	0.000151594	0.782	0.002330142
AKT1	chr14	105259463	105259547	0.212	0.091	0.000155865	0.100	0.020481628
DTX2	chr7	76126653	76126794	0.044	0.185	0.000170849	0.215	2.37311E-08

TTC8	chr14	89307768	89307858	0.158	0.500	0.000197246	0.417	0.000435954
MFF	chr2	228207460	228207535	0.786	0.566	0.00022478	0.696	0.009118868
PARD3	chr10	34661425	34661464	0.463	0.590	0.000233469	0.544	0.004960572
AMBRA1	chr11	46534276	46534363	0.079	0.259	0.000234066	0.313	0.000389518
SYNE2	chr14	64682003	64682072	0.656	0.441	0.000236939	0.553	2.13386E-06
RWDD3	chr1	95705332	95705465	0.592	0.371	0.000246702	0.221	6.72129E-09
ZNF195	chr11	3381949	3382018	0.920	0.820	0.000258852	0.804	2.07499E-05
SMARCA4	chr19	11144442	11144541	0.951	0.890	0.000260391	0.900	0.000729737
RTN2	chr19	45996417	45996636	0.153	0.092	0.000315998	0.057	1.8777E-13
TNK2	chr3	195594039	195594129	0.167	0.552	0.000352368	0.316	0.035190714
MAP3K4	chr6	161519309	161519459	0.268	0.538	0.00035375	0.400	0.000101963
TMEM254	chr10	81850135	81850187	0.714	0.929	0.000374794	0.913	0.001828411
FAM60A	chr12	31457915	31458057	0.579	0.504	0.000389311	0.473	2.28588E-06
SIRT2	chr19	39389018	39389065	0.709	0.803	0.000456743	0.793	1.32468E-05
ZNF611	chr19	53233158	53233258	0.407	0.200	0.000465258	0.074	3.75028E-11
ZFYVE21	chr14	104196129	104196183	0.726	0.873	0.000548477	0.875	0.000456439
CPNE1	chr20	34246851	34246904	0.838	0.745	0.0006072	0.697	2.41418E-09
PPP6R2	chr22	50875416	50875497	0.388	0.260	0.000622235	0.269	2.73232E-08
BID	chr22	18232870	18232940	0.082	0.172	0.000644186	0.136	1.83007E-18
TSFM	chr12	58186768	58186856	0.166	0.100	0.00068787	0.087	4.86889E-07
ARMC8	chr3	137907296	137907372	0.559	0.289	0.000751167	0.273	0.000805218
PATZ1	chr22	31724772	31724845	0.688	0.414	0.000811088	0.419	0.001758145
ABLIM3	chr5	148622053	148622101	0.529	0.828	0.000829069	0.750	0.040423979
RAB11FIP1	chr8	37728795	37730697	0.445	0.246	0.000856668	0.328	0.016636286
METTL21B	chr12	58168411	58168550	0.667	0.300	0.000934834	0.529	0.006981285
PI4KB	chr1	151282686	151282731	0.880	0.682	0.001028141	0.750	0.043737503
PLEKHA4	chr19	49360678	49360753	0.256	0.127	0.001046642	0.081	1.44075E-06
ATXN7	chr3	63983296	63983363	0.839	0.955	0.001133793	0.917	0.005792855
PCSK6	chr15	101871855	101871894	0.618	0.353	0.001238627	0.231	4.12846E-07
KDM6A	chrX	44921891	44921993	0.507	0.333	0.001265037	0.436	0.020937475
SCEL	chr13	78167648	78167708	0.167	0.450	0.001271231	0.267	0.018770972
UBAP2	chr9	33956076	33956144	0.278	0.204	0.001312403	0.151	3.67449E-07
DTNBP1	chr6	15660613	15660752	0.900	0.848	0.001314945	0.781	4.68516E-05
CHID1	chr11	908541	908645	0.410	0.551	0.001350014	0.520	0.000510498
TCERG1	chr5	145847903	145847966	0.760	0.898	0.001370346	0.848	0.012878571

REPIN1	chr7	150067848	150067973	0.323	0.520	0.00138839	0.452	0.035166532
ZNF567	chr19	37185703	37185778	0.222	0.383	0.001399164	0.429	0.032679337
SNX11	chr17	46188069	46188129	0.929	0.629	0.001535965	0.605	0.00063928
ZDHHC20	chr13	21956039	21956084	0.806	0.915	0.001541612	0.968	4.89265E-15
ZNF586	chr19	58287910	58288037	0.182	0.119	0.001602601	0.000	0
SENP1	chr12	48482945	48483076	0.750	0.691	0.001632615	0.600	0.045500264
LPIN1	chr2	11916211	11916319	0.600	0.833	0.001745119	0.846	0.038728723
ITGB3BP	chr1	63913235	63913285	0.406	0.588	0.0019083	0.469	0.001802222
NEDD4L	chr18	56002709	56002769	0.617	0.785	0.001915443	0.741	0.01421927
SLC16A4	chr1	110925455	110925588	0.132	0.204	0.001970957	0.196	0.014972993
OPTN	chr10	13150137	13150289	0.471	0.544	0.002030326	0.572	6.9178E-10
BCOR	chrX	39930889	39930943	0.368	0.238	0.002071698	0.250	0.000232413
PIGQ	chr16	632247	632309	0.582	0.719	0.002559506	0.827	1.98313E-10
ADAM15	chr1	155034379	155034593	0.773	0.644	0.002613575	0.677	2.88956E-06
PHB	chr17	47491603	47491695	0.936	0.884	0.00261563	0.886	0.005348308
RGS5	chr1	163288971	163289081	0.231	0.429	0.002699796	0.333	0.002054719
STAU1	chr20	47782533	47782822	0.620	0.735	0.002732628	0.800	4.99753E-06
DSC2	chr18	28648264	28648310	0.966	0.838	0.002829961	0.843	0.006114726
C11orf30	chr11	76165792	76165834	0.684	0.833	0.002851707	0.875	4.01363E-08
PPARG	chr3	12353878	12353952	0.125	0.389	0.003046813	0.448	9.51406E-05
RPRD2	chr1	150414356	150414434	0.238	0.132	0.003083186	0.054	0.000118633
ZNF426	chr19	9645863	9645955	0.240	0.111	0.003431579	0.000	0
NCOA7	chr6	126117825	126117943	0.500	0.792	0.0042626	0.590	0.001213585
RNF24	chr20	3954978	3955047	0.552	0.417	0.004444005	0.361	0.019361888
GLT8D1	chr3	52738739	52738968	0.444	0.364	0.005266097	0.368	0.020497166
PPP3CC	chr8	22396981	22397011	0.582	0.435	0.00601383	0.500	2.60137E-09
TMEM139	chr7	142983033	142983295	0.265	0.450	0.006061304	0.457	0.004977435
PEX2	chr8	77900542	77900574	0.217	0.444	0.006084855	0.467	0.000299834
EHMT2	chr6_cox_hap2	3366499	3366601	0.385	0.296	0.006376191	0.280	0.000843559
RPH3AL	chr17	183549	183725	0.176	0.524	0.006456803	0.429	0.014305878
LGALS8	chr1	236706214	236706340	0.214	0.295	0.006850281	0.323	0.000573799
PI4KB	chr1	151297220	151297393	0.550	0.273	0.00717285	0.250	3.85962E-06
EDC3	chr15	74979431	74979520	0.748	0.843	0.007241681	0.859	1.04835E-05
PPP2R5C	chr14	102384167	102384284	0.667	0.544	0.007288846	0.558	0.000445322
SAR1B	chr5	133967766	133967885	0.813	0.894	0.007439181	0.903	8.1126E-05

RNF121	chr11	71673197	71673335	0.746	0.816	0.00801918	0.843	1.0222E-05
MON2	chr12	62959793	62959811	0.132	0.193	0.00839768	0.262	0.000286281
CPNE1	chr20	34243123	34243266	0.328	0.194	0.008625071	0.148	1.66072E-05
ZFAND6	chr15	80390757	80390920	0.510	0.427	0.009031927	0.416	1.03549E-09
SCML1	chrX	17762190	17762339	0.276	0.435	0.009300969	0.367	0.042242834
C8orf58	chr8	22460073	22460156	0.036	0.182	0.009374768	0.211	0.000576613
STAU2	chr8	74439925	74440039	0.000	0.214	0.009494967	0.467	6.79535E-06
MKNK1	chr1	47025905	47025949	0.438	0.309	0.010619752	0.295	2.58689E-08
ATP2C1	chr3	130613551	130613619	0.469	0.286	0.011519688	0.222	0.001228868
TFIP11	chr22	26907084	26907161	0.860	0.943	0.011541343	1.000	0
ARMC8	chr3	137907242	137907372	0.500	0.379	0.011582142	0.448	0.014943839
CBLL1	chr7	107392989	107393062	0.724	0.596	0.011901583	0.468	8.67111E-06
DDX42	chr17	61852467	61852538	0.938	0.868	0.011939353	0.813	0.000700779
UBE2V1	chr20	48713208	48713348	0.714	0.417	0.012171501	0.500	4.45571E-05
URGCP	chr7	43927388	43927415	0.071	0.250	0.012615667	0.294	2.05964E-05
SCAI	chr9	127828268	127828337	0.682	0.864	0.01295358	0.850	0.018285088
ZMYM5	chr13	20412839	20413125	0.106	0.161	0.013348631	0.181	0.028393576
ARMC6	chr19	19144939	19145047	0.556	0.400	0.013808208	0.378	0.020933765
DNMT3A	chr2	25472525	25472593	0.222	0.059	0.013808208	0.067	0.033894854
NDUFA5	chr7	123186711	123186871	0.481	0.625	0.015785006	0.708	0.004832241
ADAM15	chr1	155034379	155034451	0.575	0.492	0.017388275	0.494	0.005975716
ZCCHC10	chr5	132358532	132358598	0.659	0.478	0.017937194	0.345	2.85326E-05
LRR1	chr14	50074117	50074839	0.332	0.402	0.018403503	0.450	0.000197502
UBXN11	chr1	26627416	26627515	0.087	0.300	0.019630657	0.471	5.96313E-06
PARP11	chr12	3938075	3938196	0.556	0.333	0.020136752	0.364	0.002496909
PCBP4	chr3	51996825	51996908	0.710	0.775	0.022254125	0.821	0.010866887
CD55	chr1	207513735	207513853	0.807	0.752	0.022315349	0.739	5.10856E-06
SS18L1	chr20	60729336	60729521	0.117	0.255	0.023112086	0.299	0.003028156
ZNF461	chr19	37134695	37134764	0.222	0.325	0.023890503	0.472	0.006788201
STRN3	chr14	31398406	31398517	0.242	0.378	0.024117893	0.575	0.000232624
TMED3	chr15	79606882	79606997	0.786	0.840	0.026545566	0.848	0.000103934
NFAT5	chr16	69602397	69602451	0.471	0.561	0.027806895	0.636	4.26305E-07
ARRB1	chr11	74982744	74982768	0.724	0.917	0.028161035	1.000	0
SMEK2	chr2	55805382	55805478	0.279	0.172	0.028442742	0.184	0.006131953
RWDD1	chr6	116894020	116894148	0.837	0.681	0.029015953	0.500	7.55375E-06

ARFIP1	chr4	153711910	153712027	0.888	0.938	0.029936448	0.970	1.94016E-07
USP4	chr3	49348946	49349087	0.255	0.153	0.030913176	0.125	0.00030213
ALCAM	chr3	105270987	105271026	0.156	0.279	0.031981984	0.256	0.044067405
DMTN	chr8	21924595	21924670	0.051	0.132	0.032542321	0.196	3.9763E-08
CEP57	chr11	95528679	95528723	0.960	0.899	0.032988379	0.857	0.000417164
DCP1A	chr3	53372117	53372172	0.815	0.920	0.033044382	1.000	0
RNF121	chr11	71668272	71668310	0.163	0.113	0.033755564	0.108	8.85211E-05
DSN1	chr20	35399827	35399876	0.170	0.103	0.034755584	0.075	0.003667654
ANKRD10	chr13	111546455	111546549	0.236	0.138	0.035833725	0.114	0.000306415
GAS8	chr16	90102040	90102095	0.050	0.175	0.037468157	0.237	0.004103253
EPB41	chr1	29385100	29385157	0.541	0.593	0.038728723	0.706	5.14621E-09
EIF4E2	chr2	233438972	233439051	0.750	0.660	0.038794554	0.563	0.002496909
NIPA2	chr15	23027800	23027922	0.531	0.454	0.03883638	0.410	0.000299885
DDX19B	chr16	70346511	70346560	0.162	0.217	0.038903432	0.305	5.9477E-10
ZNF83	chr19	53119970	53120094	0.143	0.263	0.041111122	0.429	1.09397E-08
FBXO16	chr8	28331288	28331324	0.034	0.176	0.041226833	0.300	0.002117896
CCSER2	chr10	86259630	86259715	0.843	0.911	0.042945123	0.917	0.035557906
RBPMS	chr8	30407016	30407102	0.811	0.686	0.043430363	0.603	0.002451561
FAM135A	chr6	71195869	71195947	0.603	0.714	0.043651274	0.810	9.44195E-07
PREPL	chr2	44586635	44586889	0.100	0.222	0.044546814	0.243	0.00717285
TCF7L2	chr10	114849158	114849299	0.467	0.552	0.047288437	0.675	0.001106063
PARP11	chr12	3973001	3973123	0.412	0.211	0.047809587	0.000	0
DSTYK	chr1	205117332	205117467	0.056	0.132	0.04937601	0.216	1.91394E-06
COG6	chr13	40230962	40231027	0.857	1.000	0	0.978	1.45167E-05

PSI=Percentage Spliced In. P-values were calculated by Chi-square test.

Table S5. Oligos used in the study.

hsa-circURI1-F	GTCCATACTAATGAAGTCAC	For circURI1 qPCR in human	Fig. 1D, 1G, 2A, 2E, 2I, 3B, 3D-E, 4B, 4E et al.
hsa-circURI1-R	CAAGGTGCTGAGTCTTTCTC		
h-URI1-F	TGAAGAACTAGAGAGACAGG	For URI1 mRNA qPCR in human	Fig. 1D, 2A, 2E, 2I, 3D, S3B, S4A
h-URI1-R	GCATCGCATTCACATTTGTG		
Q-18S-F	CGGCGACGACCCATTCGAAC	For 18S qPCR in human	Fig. 1G, 3B, 3D, S2A
Q-18S-R	GAATCGAACCCTGATTCCC		
circURI1-Probe-F	TAATACGACTCACTATAGGGAGAATCAGGCAAGGTGCTGAGT	For circURI1 NB and FISH probes in human	Fig. 1E-G, S2G
circURI1-Probe-R	CCAGGAAAACTTGTCCATAC		
URI1-Probe-F	TAATACGACTCACTATAGGGAGACTCTACTTCGAGACTTCAG	FISH probes for URI1 mRNA	Fig. 1F
URI1-Probe-R	ATGATGATGACGACGACGAC		
CDR1as-F	AACTACCCAGTCTTCCATCA	For CDR1as qPCR in human	Fig. S2B
CDR1as-R	AGACTTGAAGTCGCTGGAAG		
mus-circURI1-F	AAAGTGCTCAGCCAAGCAGG	For circURI1 RT-PCR in mouse	Fig. S2E
mus-circURI1-R	CAAGGTCCTCAGCCTCTCTT		
mus-Uri1-F	AGAAAGAGGAAGCCAAACGG	For URI1 mRNA RT-PCR in mouse	
mus-Uri1-R	GTTCTCTTGGAGTTCGTCCA		
mus-circMed131-R	CTGAAATTATGGGTCCACAGT	For circMED131 RT-PCR in mouse	
mus-circMed131-F	AAGAGCTCTGGATATTCTGGT		
U6-F	CGCTTCGGCAGCACATATAC	For U6 qPCR in human	Fig. S2I
U6-R	TTCACGAATTTGCGTGTCAT		
GAPDH-F	CTTCATTGACCTCAACTACATG	For GAPDH qPCR in human	Fig. S2B, S2I, S4J
GAPDH-R	CTCGCTCCTGGAAGATGGTGA		
circHIPK3-F	ATGTTGGTGGATCCTGTTCG	For circHIPK3 qPCR in human	Fig. S4H
circHIPK3-R	GGGTAGACCAAGACTTGTGA		
EIciPAIP2-F	AGCTCGAGATCTCCCACAAA	For EIciPAIP2 qPCR in human	
EIciPAIP2-R	ACTGCTGCGACTTGGATCTT		
circURI1-Probe	Biotin-TTATCTACCTTCTTCGTTCTTTCCGGTGCT	Antisense oligo of circURI1	Fig. 3A-C
Scramble	Biotin-TTCTCCGAACGTGTCACGTTCGAACGTGTC	Control oligo	
circCDYL-F	GGCCACAGGCTTAGCTGTTA	For circCDYL qPCR in human	Fig. 3D
circCDYL-R	TGTCGTCCTCGCTGTCATAG		
hnRNPM-F	GACATCAAGATGGAGAATGG	For hnRNPM qPCR in human	Fig. 5D-E
hnRNPM-R	CACTCAGCTTCATGCCATTC		
siNC	UUCUCCGAACGUGUCACGU ACGUGACACGUUCGGAGAA	Negative control of siRNAs	Fig. 2A-C, 5E, 6D, 7B-D et al.
siCirc-1	CGGAAAGAACGAAGAAGGUA UACCUUCUUCGUUCUUUCCG	siRNAs of circURI1 in human	Fig. 2A-C, 5E, 6D, 7B-D et al.

siCirc-2	CACCGGAAAGAACGAAGAAG CUUCUUCGUUCUUUCCGGUG		
circURI1-sgRNA1	GTATATTAGCGAAAGAGAAT	sgRNAs for circURI1 knockout construction	Fig. 2D
circURI1-sgRNA2	GAGAGGCTTCGTCTTCAGTA		
circURI1-sgRNA3	GTATTTTTCCTGTTGTTGGG		
circURI1-sgRNA4	GTATGTCTATTAGGTCTAAT		
circURI1 KO check-F	TTGGAGACTCTAATTGCAAA	Check primers for circURI1 KO cells	
circURI1 KO check-R	TACATACATACCTAACAGAG		
circURI1 shRNA-1F	CCGGCGGAAAGAACGAAGAAGGTAGCTCGAGCTACCTTCTTCGTTCTTTCCGTTTTTG	shRNAs for knock down circURI1	Fig. 2L, S4F
circURI1 shRNA-1R	AATTCAAAAACGGAAAGAACGAAGAAGGTAGCTCGAGCTACCTTCTTCGTTCTTTCCG		
circURI1 shRNA-2F	CCGGCACCGGAAAGAACGAAGAAGGCTCGAGCCTTCTTCGTTCTTTCCGGTGTTTTTG		
circURI1 shRNA-2R	AATTCAAAAACACCGGAAAGAACGAAGAAGGCTCGAGCCTTCTTCGTTCTTTCCGGTG		
OE circURI1-F	GCTTGGTACCGAGCTCGGATCCGGTCCAGATAGTCTTGTATC	For circURI1 overexpression in human	Fig. 2H
OE circURI1-R	GTGATGGATATCTGCAGAATTCCTGTAATCTCAGCTACTCAG		
circURI1-M19-F	CAAGCAGTCGGACTAGTCGAACACCGGAAAGAACGTAGG	For overexpressing circURI1 with 19-nt mutation	Fig. 5A-C
circURI1-M19-R	TTCGACTAGTCCGACTGCTTGCTTTGCTGAGCACTTTGC		
NC-ASO	U*U*C*U*C*CGAACGTGTCA*C*G*U*U*	ASO of circURI1 in human	Fig. S4C-E
circURI1-ASO	U*A*C*C*U*TCTTCGTTCTU*U*C*C*G*		
siM-1	GAAGUCCUAAACAAGCAUA UAUGCUUGUUUAGGACUUC	hnRNPM siRNAs in human	Fig. 5E, 6D, 7B-D et al.
siM-2	AUAUGCCAAUCCAACUAAA UUUAGUUGGAUUGGCAUAU		
Flag-hnRNPM-FL-F	AGGATGACGATGACAAGCTTATGGCGGCAGGGGTCGAAGC	Plasmid for full length hnRNPM in human	Fig. 4A
Flag-hnRNPM-FL-R	ATGAGTTTTTGTTCGGATCCTTAAGCGTTTCTATCAATTC		
Flag-hnRNPM-D1-F	TGACAAGCTTTACAGAGCCTTCATTACAAACA	Plasmid for Del_0-70aa truncation of hnRNPM in	
Flag-hnRNPM-D1-R	AGGCTCTGTAAAGCTTGTCAT		

	CGTCATCCTTG	human	
Flag-hnRNPM-D2-F	CAACTAAAAGAGGTGAACATGCCAGGAGAGCA	Plasmid for Del_71-149aa truncation of hnRNPM in human	
Flag-hnRNPM-D2-R	ATGTTCACCTCTTTTAGTTGGATTGGCATATG		
Flag-hnRNPM-D3-F	AGATCCTGATAGCACAGTATTTGTAGCAAATC	Plasmid for Del_150-203aa truncation of hnRNPM in human	
Flag-hnRNPM-D3-R	ATACTGTGCTATCAGGATCTTCTTTGACTTTC		
Flag-hnRNPM-D4-F	AAGACTTGGAGCCTTACCAAAAGGAGATTTCT	Plasmid for Del_204-281aa truncation of hnRNPM in human	
Flag-hnRNPM-D4-R	TTGGTAAGGCTCCAAGTCTTCCAGCCTGTAAT		
Flag-hnRNPM-D5-F	GGATGAGAGGTGCCAGATATTTGTGAGAAATC	Plasmid for Del_282-652aa truncation of hnRNPM in human	
Flag-hnRNPM-D5-R	ATATCTGGCACCTCTCATCCATCTTGACGTGC		
Flag-hnRNPM-D6-F	CAGGAAGGCCGGATCCGAACAAAAACTCATCT	Plasmid for Del_653-729aa truncation of hnRNPM in human	
Flag-hnRNPM-D6-R	GCCACCCGGGGGCCTTCCTGGCCACCCCAGGA		
DNA linker	5’-rApp-AGATCGGAAGAGCACACGTCTGAAC/AzideT/CCAGTCAC-3’	hnRNPM iCLIP-seq	Fig. 4D
RT-primer	NNCAAGTGNAGATCGGAAGAGCGTCGTGTAGGGAAAGAGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT		
First outer-F	CGCTCCCGCTGAATTGGAATTTTTTTTTTTTTTTT	First PCR for individual-CLIP	Fig. S5B-C
First outer-R1	ATCAGGCAAGGTGCTGAGTC		
First outer-R2	GTGACTTCATTAGTATGGAC		
First outer-R3	TTGCTGAGCACTTTGCAAAC		
Second nested-F	CGCTCCCGCTGAATTGGAAT	Second nested PCR for individual-CLIP	
Second nested-R1	TGCTGAGTCTTTCTCGAAGG		
Second nested-R2	GCCAAATGGTACCATTATAT		
Second nested-R3	CAAGGTGCTGAGTCTTTCTC		

circURI1-T7-F	TAATACGACTCACTATAGGGAGAGGTTCTACATAAATGCCTA	Primers for *in vitro* circularization of circURI1	Fig. 4E
circURI1-T7-R	AGTCCTACAATTTAGCACGG		
circURI1-M19-F	GAAAACATGTTCTTTCCGGTGTGCTTTGCTGAGCACTTTGC	Primers for *in vitro* circularization of circURI1-M19	
circURI1-M19-R	CACCGGAAAGAACATGTTTTC		
29 nt in the junction site	ATGTTTTCTTGGGTCTACCGTTTAATATT	Added sequences for circularization	Fig. S5D
GMPR2-AS-F	CATCATTGCTGCCAATATGG	For semi-quantitative RT-PCR check of alternative splicing	Fig. 6D, 7C, S7C
GMPR2-AS-R	GCTATAGTGCTTATGGACAG		
VEGFA-AS-F	AGTTCGAGGAAAGGGAAAGG		
VEGFA-AS-R	CTTTCCTGGTGAGAGATCTG		
SCEL-AS-F	CAGATACATCCACCTAAACC		
SCEL-AS-R	CTGAAGAGACTATCAAGACC		
LGALS8-AS-F	CTAGTCTGGAACTGACAGAG		
LGALS8-AS-R	GCATTTGCATTCACTTCTCC		
DNMT3A-AS-F	CAGCTACTTCCAGAGCTTCA		
DNMT3A-AS-R	TCCACAGCATTCATTCCTGC		
NR4A1-AS-F	GAGTGCACAGAAGAACTTCG		
NR4A1-AS-R	TGGTGTCCCATATTGGGCTT		
RNF24-AS-F	TGACGGTCCCGCACGTCT		
RNF24-AS-R	GTTGAGAGGCAGATTCTGG		
DNAJB5-AS-F	GAGCTGAGTGACAGGAAGAC		
DNAJB5-AS-R	ATCACAGCCACTGGACCAG		
B3GALNT2-AS-F	AAACTGGCTGGTGCTGCTGT		
B3GALNT2-AS-R	CCAACTACCACATCATAGTG		
LPIN1-AS-F	CAGCCTCATACCCTAATTCG		
LPIN1-AS-R	CTTTCCGTGGACTTGCTGAC		
SNX11-AS-F	CTTCTCCTCCTTCTTTGTTC		
SNX11-AS-R	GCCTTCTACTCGGCTGATAG		
GMPR2-pre-AS-F	TTTCATGTCTGCTGCCTGTC	Primers for RNA IP of hnRNPM upon circURI1 knockdown	Fig. 7D
GMPR2-pre-AS-R	GCTGGGATTTGAGTTCAACC		
DNMT3A-pre-AS-F	GAAAGAGTGACTCTGTCTCC		
DNMT3A-pre-AS-R	TTAGGAAACCTTCCTCCCAG		
VEGFA-pre-AS-F	GTAGATTGCAAGCTCAGGAG		
VEGFA-pre-AS-F	CATAAGAGCAGAGAGGACAG		
DNAJB5-pre-AS-F	TCACTGACACGCTGCCATAC		
DNAJB5-pre-AS-F	CACCTCCTTGGACTCTCAGA		
SCEL-pre-AS-F	TGTGTGCCATGAGCTGACAT		
SCEL-pre-AS-R	CAGGTCAATGATAGTCGAGC		
LGALS8-pre-AS-F	GCCTGGGTTATTTCATGTGG		
LGALS8-pre-AS-R	CCTCCTCTATTACTAGGCTG		
SNX11-pre-AS-F	GTGTTACAATTGTAGTGGTCC		

SNX11-pre-AS-R	TCTGTAGAGCTCTTCTACAC		
VEGFA-FL-F	AGGATGACGATGACAAGCTTATGAACTTTCTGCTGTCTTG	Plasmid for VEGFA with exon 7 inclusion	Fig. 7G
VEGFA-FL-R	ATCAGATCTATCGATGAATTCTCACCGCCTCGGCTTGTCAC		
VEGFA-AS-F	ATGTGACAAGCCGAGGCGGT	Plasmid for VEGFA with exon 7 exclusion	
VEGFA-AS-F	ACCGCCTCGGCTTGTCACATACGCTCCAGGACTTATACC		