YMTHE, Volume *27*

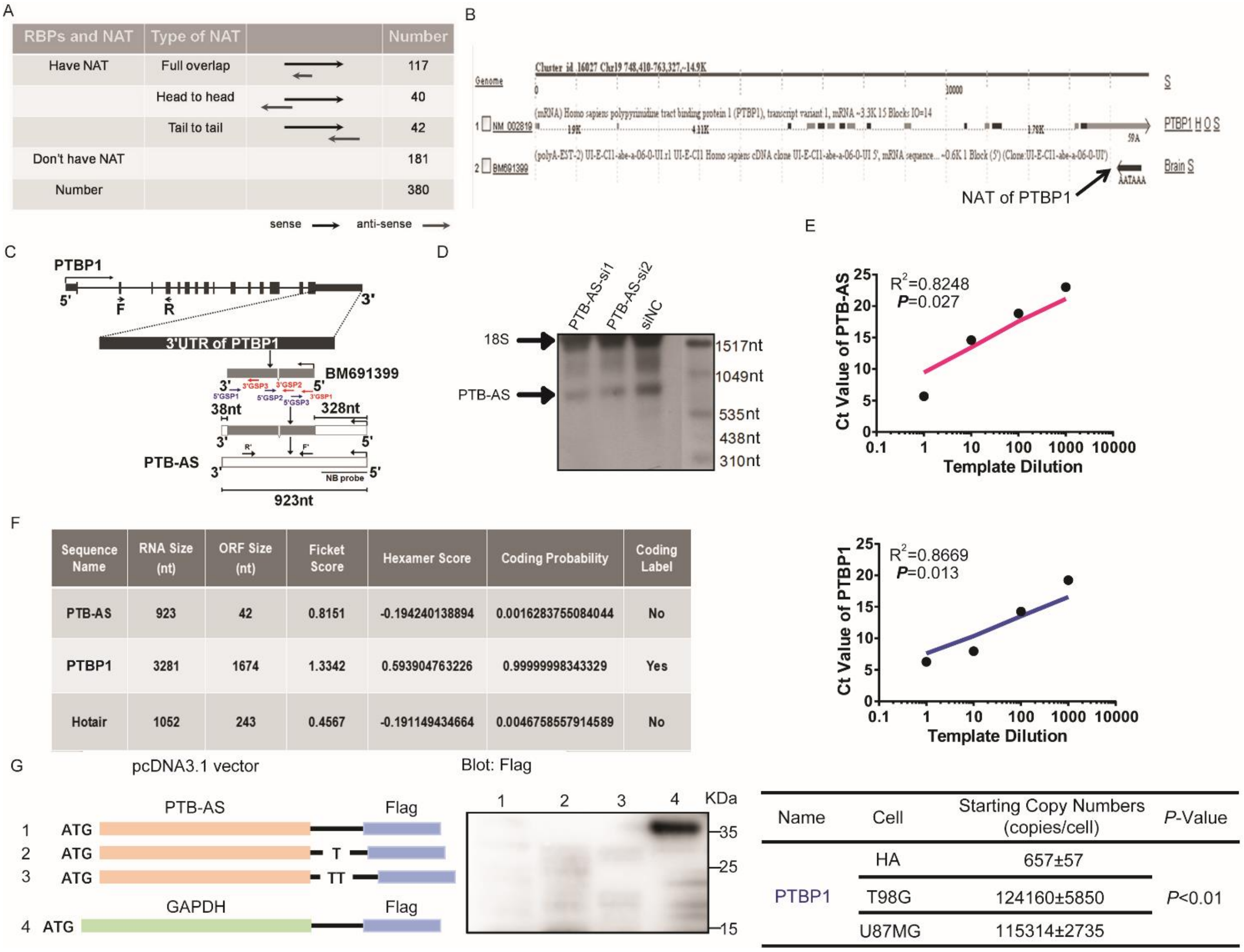
Supplemental Information

PTB-AS, a Novel Natural Antisense Transcript, Promotes Glioma Progression by Improving PTBP1 mRNA Stability with SND1

Liyuan Zhu, Qunfang Wei, Yingjiao Qi, Xiangbin Ruan, Fan Wu, Liang Li, Junjie Zhou, Wei Liu, Tao Jiang, Jing Zhang, Bin Yin, Jiangang Yuan, Boqin Qiang, Wei Han, and Xiaozhong Peng

Supplemental Figures and Figure Legends

Figure S1



RBPs and NAT	Type of NAT		Number
Have NAT	Full overlap		117
	Head to head		40
	Tail to tail		42
Don't have NAT			181
Number			380

Sequence Name	RNA Size (nt)	ORF Size (nt)	Ficket Score	Hexamer Score	Coding Probability	Coding Label
PTB-AS	923	42	0.8151	-0.194240138894	0.0016283755084044	No
PTBP1	3281	1674	1.3342	0.593904763226	0.99999998343329	Yes
Hotair	1052	243	0.4567	-0.191149434664	0.0046758557914589	No

Name	Cell	Starting Copy Numbers (copies/cell)	*P*-Value
PTBP1	HA	657±57	*P*<0.01
	T98G	124160±5850	
	U87MG	115314±2735	

Suppl Figure S1: The overview of screening results for RBPs associated NATs and identification of PTBP1 NAT.

A. The statistics of the screening results for RBPs and the subtype of the NATs.

B. NAT of PTBP1 was located in the 3'UTR of PTBP1 and owns the poly (A) tail. The black stick which had been directed by arrow indicated the NAT of PTBP1.

C. U87MG cell was transfected with PTB-AS-siRNA or siNC and the total RNA was extracted for northern blot. The amount of total RNA each lane was equivalent. The sharp band directed by the subjacent arrow was PTB-AS.

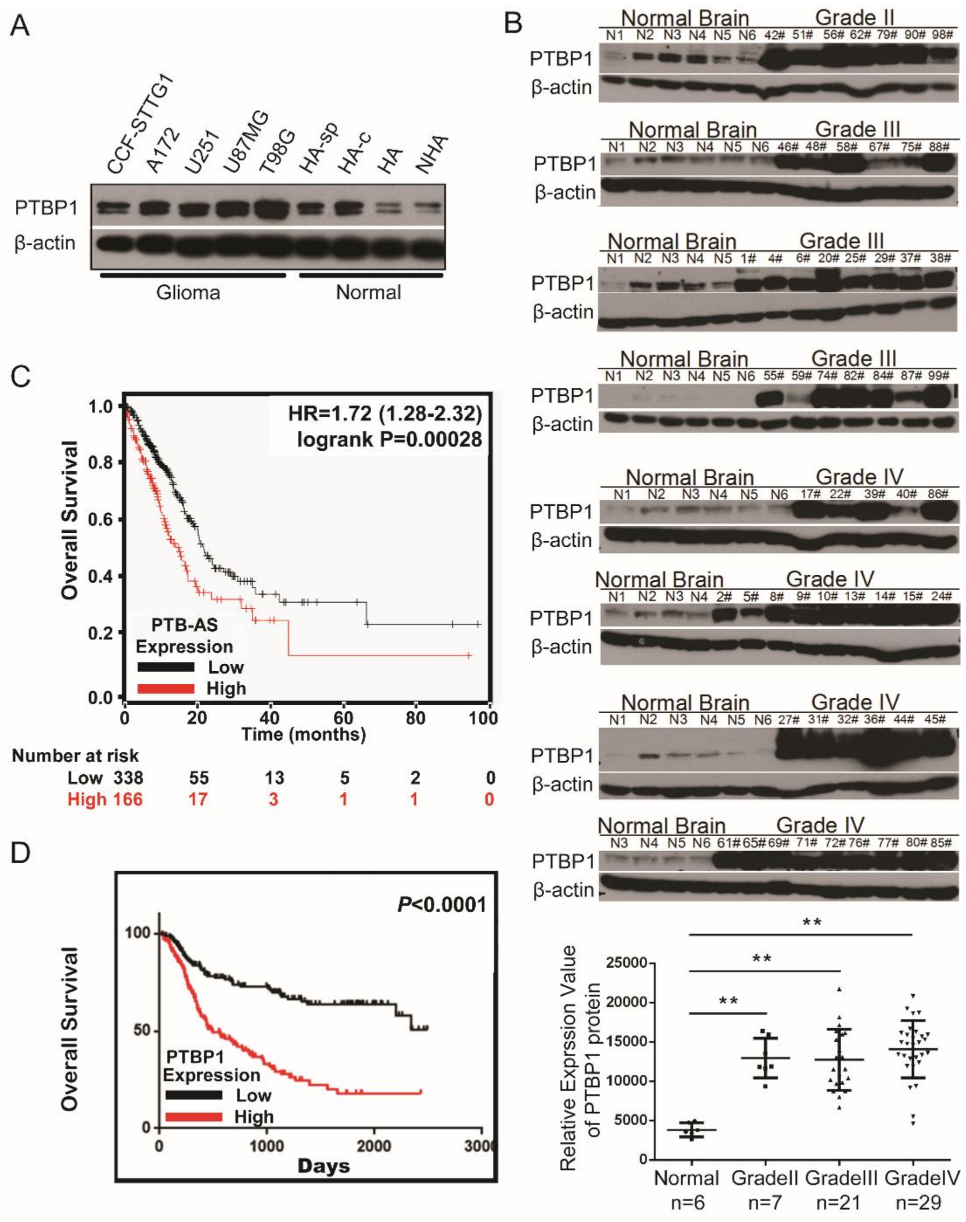
D. The relative genomic locus of PTB-AS and PTBP1. The raw transcript of PTB-AS, BM691399, was totally overlapped by PTBP1-3'UTR. By using 5'& 3' RACE, the full length of PTB-AS was identified as 923nt. NB probe indicated the real position of probe for Northern Blot.

E. The starting copy number was detected and calculated to quantify the expression of PTBP1 in HA, T98G or U87MG cell lines using absolute Quantification PCR. The standard curve was made according to the starting cycle value of PTB-AS and PTBP1, respectively.

F. Coding potential prediction for PTB-AS using CPC and CPAT software. PTBP1 and HOTAIR acted as coding and non-coding transcript positive controls, respectively.

G. Full-length PTB-AS was cloned into pcDNA3.1 (with N-terminal start codon ATG and C-terminal Flag tag) in all three coding patterns and subsequently transfected into HEK293T cells separately. GAPDH (the mRNA length was close to PTB-AS) with Flag tag severs as a positive control. Western blot was performed to detect the Flag-tagged protein after 48 hours. Data are representative of three independent experiments.

Figure S2



Suppl Figure S2: The raw data of PTBP1 which expressed and functioned in glioma.

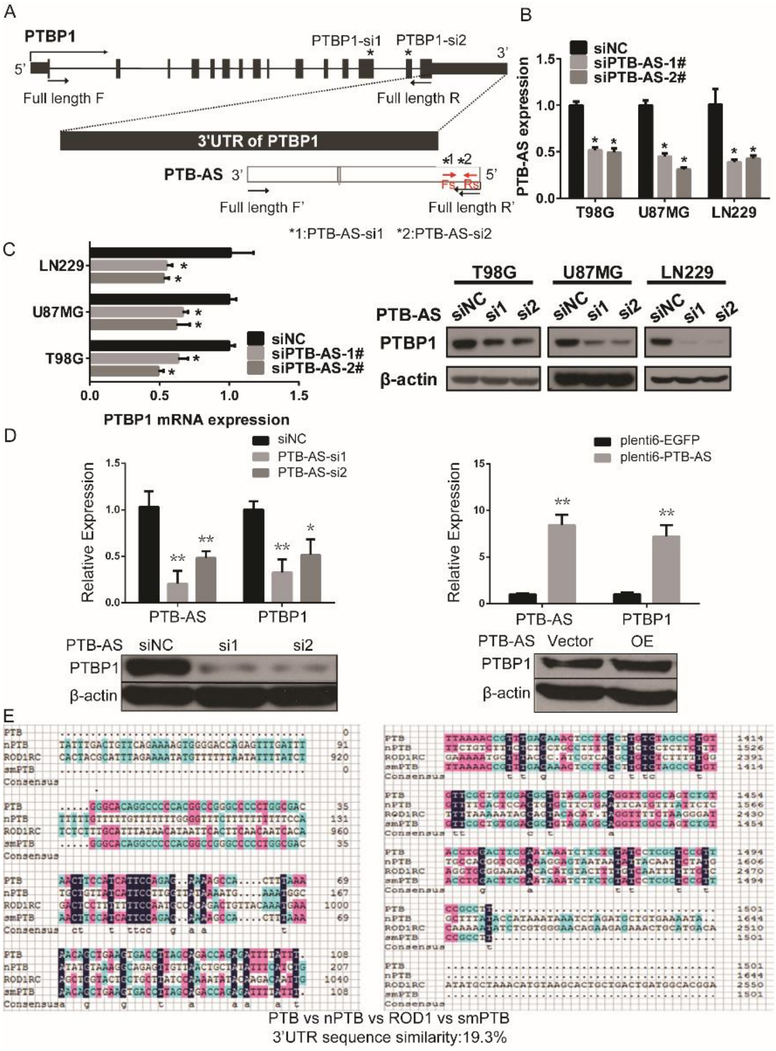
A. Western blotting result showed the expression level of PTBP1 protein in 5 glioma cell lines and 4 human astrocyte cell lines.

B. Relative expression level of PTBP1 protein in 6 control brain tissues, representative 7 grade II, 21 grade III, and 29 grade IV glioma tissues by western blotting (β-actin was used as the internal parameters) and analysis the value of grey scale scanning the corresponding bands after western blotting. The protein expression levels of PTBP1 are relatively expressed as the mean ± SD, n = 3. **P*< 0.05; ***P*<0.01 (Student's t test).

C. The Kaplan–Meier curve analysis on the impact of PTB-AS expression on overall survival. *P* value was calculated by Log Rank test.

D. The differential overall survival curve of high or low PTBP1 expressed patients. Kaplan–Meier curve analysis on the impact of PTBP1 expression. P value was calculated by Log Rank test.

Figure S3



Suppl Figure S3: The target site of stealth siRNAs of PTB-AS and PTBP1.

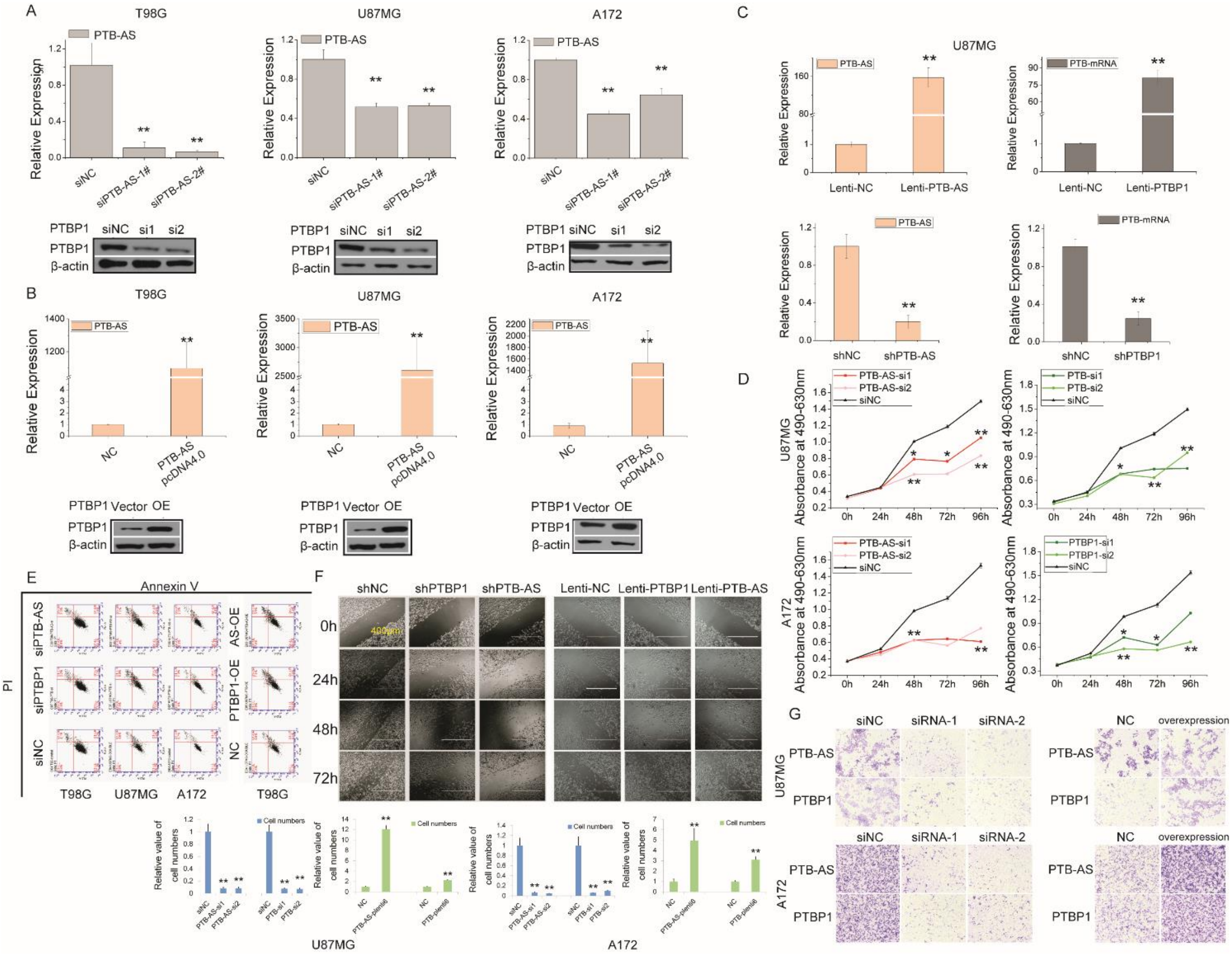
A. The detail graph which shown the target site (marked *) of stealth siRNAs of PTB-AS and PTBP1, as well as the position of primers (Full length F&R, F'&R') for PTB-AS or PTBP1 overexpression. The specific primers Fs&Rs of PTB-AS were used for qRT-PCR. The target of siRNAs for PTB-AS located in the non-overlapped area with PTBP1-3'UTR in order to avoid off-target effect.

B&C. Changes in PTB-AS level alter PTBP1 mRNA and protein levels. T98G, U87MG or LN229 cells were infected with two different siRNAs (PTB-AS si1 or PTB-AS si2) to knock down. PTB-AS (using Fs&Rs primer pair) and PTBP1 mRNA level were measured by qRT-PCR. PTBP1 protein level was measured by western blot. n=3. *P<0.05 (Student's t test).

D. A172 cells were transfected with two different PTB-AS siRNAs, siNC or PTB-AS-plenti6 plasmid, plenti6-EGFP, separately. Then total RNA of differential treatment cells was extracted for reverse transcription. Following qRT-PCR and western blotting were performed to test the expression changes of PTBP1 in RNA and protein level after knocking down PTB-AS. The expression of PTBP1 in RNA level is relatively showed as the mean ± SD, n = 3. *P< 0.05; **P<0.01 (Student's t test).

E. Alignment of 3'UTR of PTBP1 family members using DNAman. The bases in dark blue indicated the absolutely similar sequence of the four members, the pink one indicated three members had this base in the same position, and the light green one indicated that only two members share the same base.

Figure S4



Suppl Figure S4: The biological function of PTB-AS and PTBP1 in glioma

A, B and C. Quantitative real-time PCR and western blotting were performed to identify the efficiency of PTB-AS and PTBP1 knocking down or overexpressing in T98G, U87MG and A172 glioma cell lines. The RNA levels of PTB-AS and PTBP1 are relatively expressed as the mean ± SD, n = 3. **P*< 0.05; ***P*<0.01; ****P*<0.001 (Student's t test).

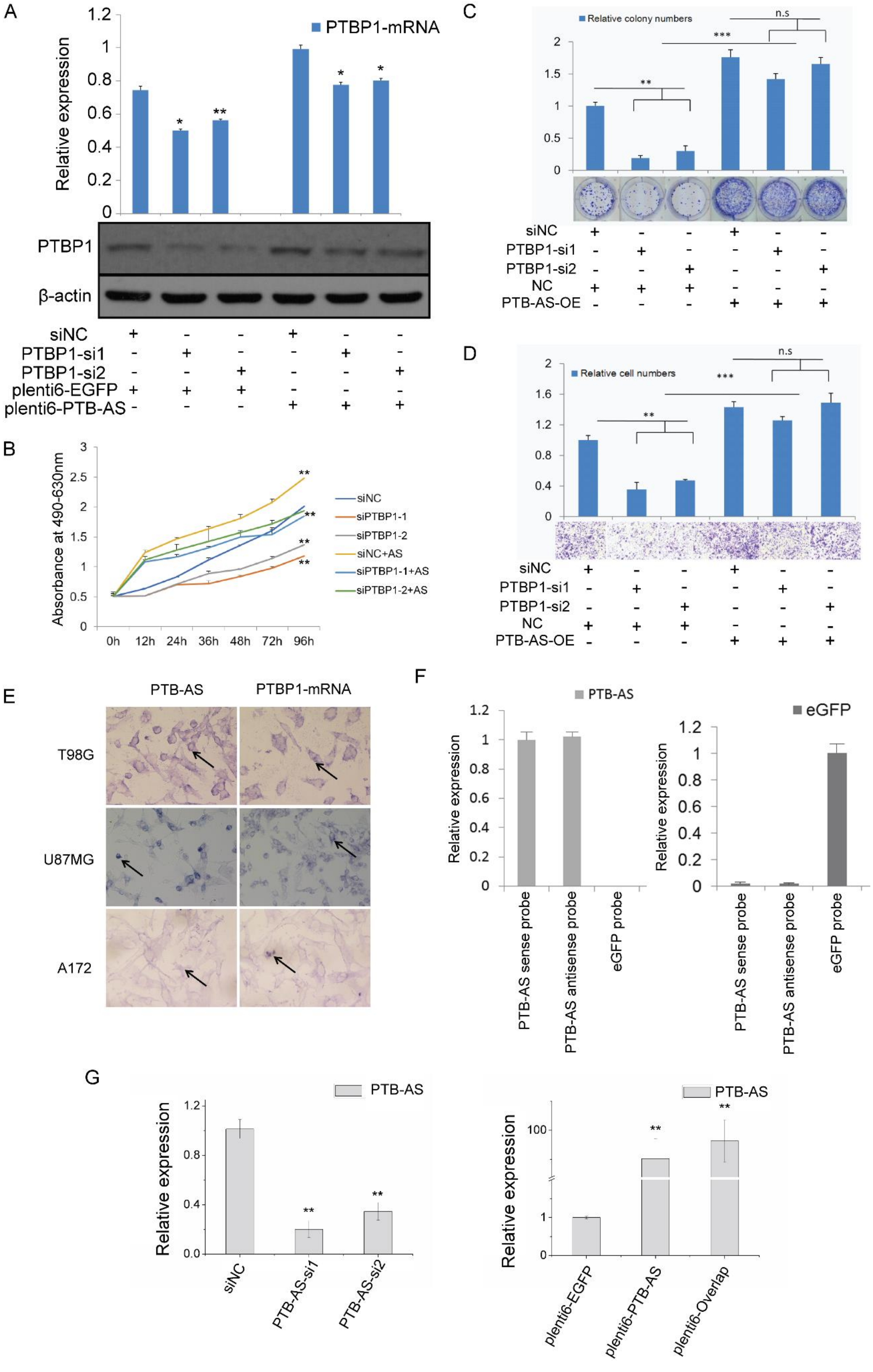
D. MTS assays shown the growth curve of U87MG and A172 cell lines after transfecting siRNAs against PTB-AS or PTBP1, following individually test the absorbance in 490nm and 630nm. Results are expressed as mean ± SD, n = 4. **P* < 0.05; ***P* < 0.01 (Student's t test).

E. Annexin V-FITC and PI co-staining to identify the apoptosis of glioma cells (T98G, U87MG and A172) after transfected with the knocking down or overexpressing materials of PTB-AS or PTBP1, respectively.

F. The wound-healing images, which represents the relative area of the remaining open wound calculated in relation to that at time 0 h after PTB-AS/PTBP1 knockdown or overexpression.

G. Transwell migration assays of U87MG and A172 glioma cell line transfected with siRNAs or plasmids for PTB-AS and PTBP1 knocking down or overexpressing, respectively. Fixation and staining were performed after transfection for 72h. The results are representative of at least three independent experiments. Graphs indicate the average number of cells per field of the indicated cell lines in migration assays. Results show the mean ± SD, **P*<0.05, ***P*<0.01 (Student's t test).

Figure S5


A
PTBP1-mRNA
Relative expression
1.2
1
0.8
0.6
0.4
0.2
0
*
**
*
*
PTBP1
β-actin
siNC + - - + - -
PTBP1-si1 - + - - + -
PTBP1-si2 - - + - - +
plenti6-EGFP + + + - - -
plenti6-PTB-AS - - - + + +
B
Absorbance at 490-630nm
3
2.5
2
1.5
1
0.5
0
0h
12h
24h
36h
48h
72h
96h
**
**
**
**
siNC
siPTBP1-1
siPTBP1-2
siNC+AS
siPTBP1-1+AS
siPTBP1-2+AS
C
Relative colony numbers
2
1.5
1
0.5
0
**
***
n.s
siNC + - - + - -
PTBP1-si1 - + - - + -
PTBP1-si2 - - + - - +
NC + + + - - -
PTB-AS-OE - - - + + +
D
Relative cell numbers
2
1.6
1.2
0.8
0.4
0
**
***
n.s
siNC + - - + - -
PTBP1-si1 - + - - + -
PTBP1-si2 - - + - - +
NC + + + - - -
PTB-AS-OE - - - + + +
E
PTB-AS
PTBP1-mRNA
T98G
U87MG
A172
F
PTB-AS
Relative expression
1.2
1
0.8
0.6
0.4
0.2
0
PTB-AS sense probe
PTB-AS antisense probe
eGFP probe
eGFP
Relative expression
1.2
1
0.8
0.6
0.4
0.2
0
PTB-AS sense probe
PTB-AS antisense probe
eGFP probe
G
PTB-AS
Relative expression
1.2
0.8
0.4
0.0
**
**
siNC
PTB-AS-si1
PTB-AS-si2
PTB-AS
Relative expression
100
1
0
**
**
plenti6-EGFP
plenti6-PTB-AS
plenti6-Overlap

Suppl Figure S5: PTB-AS could rescue the down regulation of PTBP1 through binding to PTBP1-3'UTR in cytoplasm and influenced PTBP1 mRNA stability.

A. The glioma cell U87MG was co-transfected with PTBP1-siRNA and PTB-AS-OE (plenti6-PTB-AS) in order to perform the rescue experiment. SiNC or NC (plenti6-EGFP), as the negative control, was used to make permutation and combination with PTBP1-siRNA or PTB-AS-OE. Following qRT-PCR and western blotting were operated to test the expression changes of PTBP1 in RNA and protein level. The expression of PTBP1 in RNA level is relatively showed as the mean ± SD, n = 3. $^{*}P< 0.05$; $^{**}P<0.01$ (Student's t test).

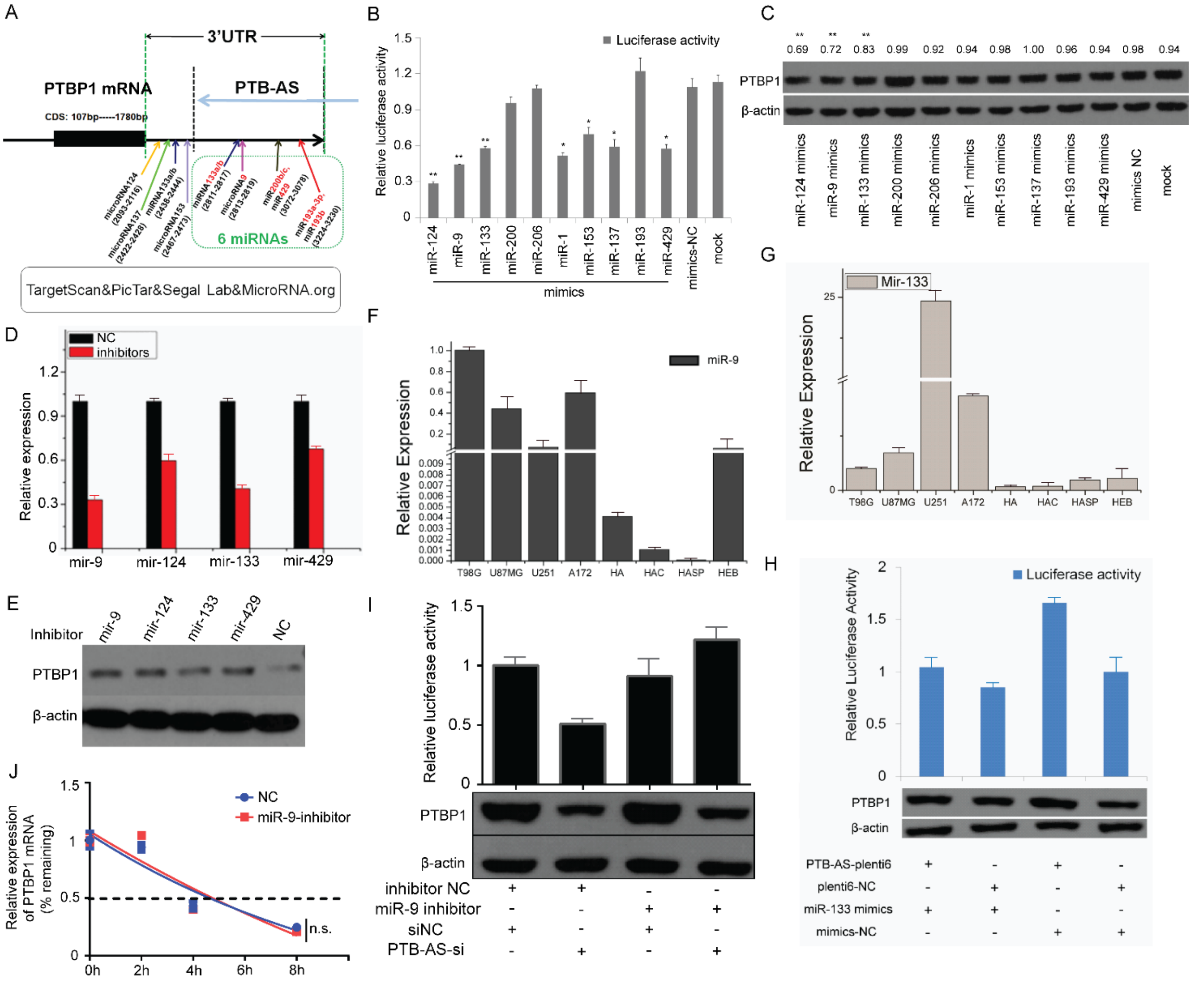
B, C and D. The glioma cell U87MG was co-transfected with PTBP1-siRNA and PTB-AS-OE (plenti6-PTB-AS) in order to perform the rescue experiment. SiNC or NC (plenti6-EGFP), as the negative control, was used to make permutation and combination with PTBP1-siRNA or PTB-AS-OE. Following MTS assays (B), colony formation (C) and transwell migration assays (D) were performed to identify the rescue effect of PTB-AS to PTBP1 in regulating glioma tumorigenesis. Graphs indicate the average number of cells per field of the indicated cell lines in migration assays. The cell colonies were counted by Image-Pro Plus software and plotted. Data were expressed as mean ± SD, n = 5. $^{*}P < 0.05$; $^{**}P < 0.01$ (Student's t test).

E. In situ hybridization for PTB-AS and PTBP1 on slides through T98G, U87MG and A172 cell. All images show the same magnification (40X). PTB-AS and PTBP1-mRNA intracellular localization was visualized in cytoplasm as the arrows directed.

F. U87MG cell were transfected with biotinylated the full length of PTB-AS or biotinylated eGFP as the NC. PTB-AS and eGFP expression levels were analysed by qRT-PCR. Data were expressed as mean ± SD, n = 3.

G. The identification of effect on PTB-AS knocking down or overexpression before half-life assay. QRT-PCR was used to show the expression of PTB-AS. Data are shown as mean ±SD of three independent experiments. $^{**}P<0.01$(Student's t test).

Figure S6



Suppl Figure S6: MiR-9 plays significant role in regulating PTBP1 expression.

A. Potential miRNAs which regulated PTBP1 were predicted using integrated bioinformatics tools and the relative position of binding site for these miRNAs.

B. All of miRNA mimics were separately transfected in U87MG cells and luciferase reporter assays were performed. Relative luciferase activity value was shown as the mean ± SD, n=3. *P<0.05, **P<0.01 (t test).

C. Western blotting experiments were performed after transfection of the mimics. The results of western blotting were quantified by densitometry and are shown as the ratios of PTBP1/β-actin protein levels (the values shown above the blots). Results were from three biological replicates.

D and E. U87MG were transfected with potential miRNAs to identify the effect of miRNAs on expression of PTBP1. Quantitive real-time PCR were performed to validate the changing of miRNAs. Data were expressed as mean ± SD, n = 3. Western blotting experiments were performed to identify the effect of miRNAs inhibitors on expression of PTBP1.

F and G. Relative expression profile of miR-9 or miR-133 in glioma and normal astrocyte cells. Quantitative real-time PCR was performed. Data were expressed as mean ± SD, n = 3.

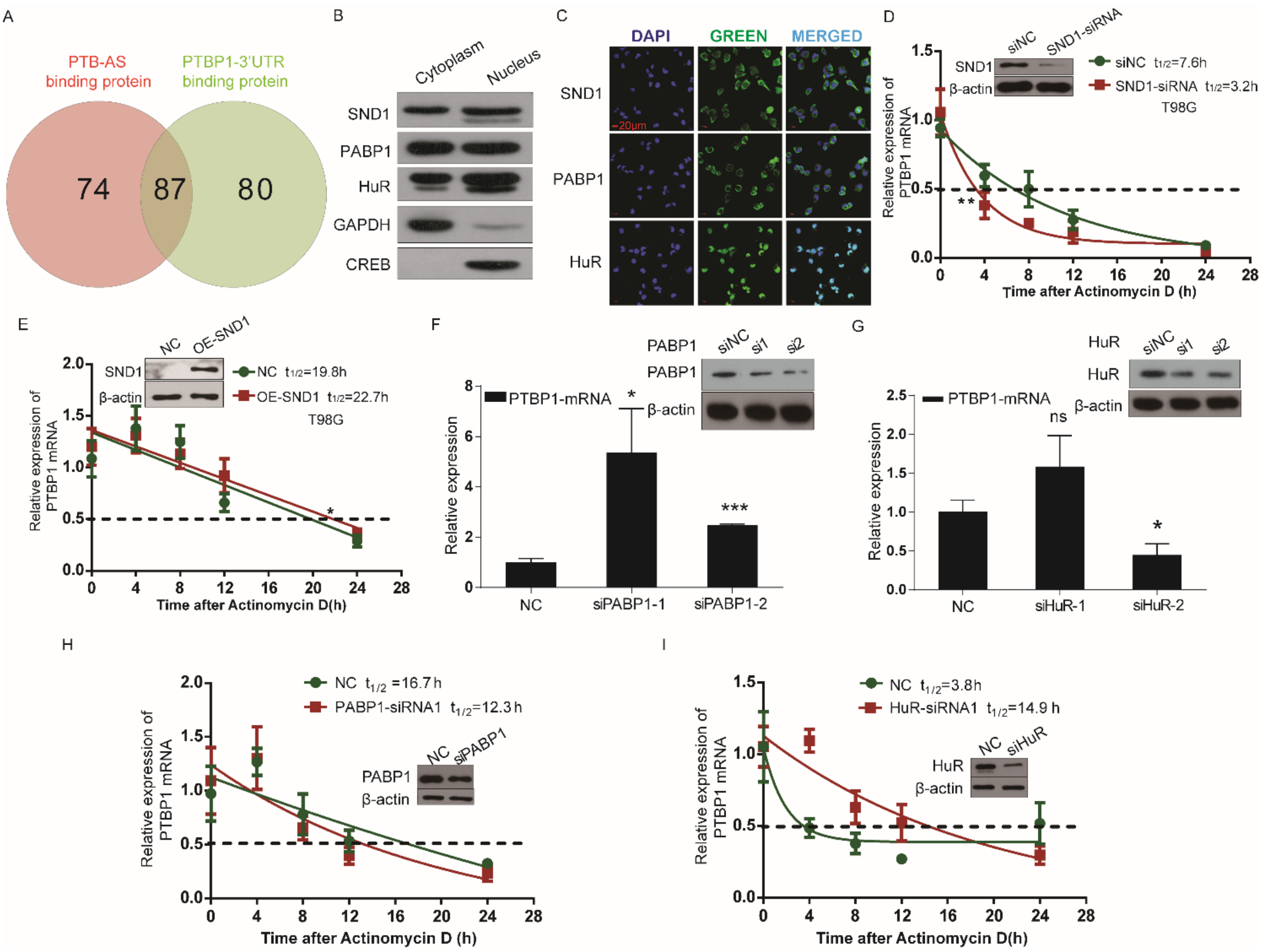
H. Luciferase reporter assays and western blotting experiments were performed to validate the miR-

133 misregulated PTBP1 caused by overexpression of PTB-AS. Data were expressed as mean ± SD, n = 3. Relative luciferase activity value was shown as the best result of two replicates. The results of western blotting were from three biological replicates.

I. U87MG cell were co-transfected with miR-9 inhibitor and PTB-AS-siRNA, and siNC or inhibitor-NC were negative control. Luciferase reporter assays and western blotting experiments were performed to validate the miR-9 re-regulated PTBP1 caused by downregulation of PTB-AS. Data were expressed as mean ± SD, n = 3. Relative luciferase activity value was shown as the best result of two replicates. The results of western blotting were from three biological replicates.

J. Half-life assay for PTBP1 mRNA after inhibiting miR-9 expression. NC or miR-9 inhibitor was transfected into U87MG cells. Transcript decay curves were measured after transfection for 48 h when transcription was blocked by adding actinomycin D (5 μg/mL). Transcripts remaining relative to the control gene were assessed by qRT-PCR. N.S. indicates no significance, and the analyses used nonlinear regression (one phase decay curve fit) to determine the half-life. Error bars show the standard deviation. The results were from three biological replicates.

Figure S7



Suppl Figure S7: Effects of HuR and PABP1 in the expression and half-life of PTBP1 mRNA.

A. Venn diagram showing the overlap of genes occupied by genes pulled down by PTB-AS probe and PTBP1-3'UTR probe at high confidence in T98G cells as determined by mass spectrometry.

B&C. The cytoplasm/nuclear separation experiment and immunofluorescence (IFC) assay show the cellular localization of candidate proteins in glioma cells. GAPDH and CREB act as the positive control indicating cytoplasm or nuclear compositions, respectively. Scale Bar: 20 μ m.

C and D. T98G cells expressing control siRNA or SND1 siRNA / mock-vector (NC) or pcDNA4.0-SND1 plasmid (OE-SND1) were treated with actinomycin D (5 μg/mL) for the indicated periods of time. Total RNA was then analysed by RT-qPCR to examine the mRNA half-life of PTBP1. Half-life was calculated by using one phase decay; Data shown are the mean ± SD (n = 3; $*P<0.05$, $**P<0.01$, two-tailed t-test).

E and F. T98G cells were infected with two different siRNAs ((A) PABP1-siRNA1 or PABP1-siRNA2 and (B) HuR-siRNA1 or HuR-siRNA2) to knock down each gene. PTBP1 mRNA level were calculated by RT-qPCR. Data were expressed as mean ± SD, n = 3. $*P < 0.05$; $**P < 0.01$, $***P < 0.001$ (Student's t test).

G and H. T98G cells expressing target or control siRNAs were treated with actinomycin D (5 μg/mL) for the indicated periods of time. Total RNA was then analyzed by RT-qPCR to examine the half-life of PTBP1 mRNA. Half-life was calculated with linear fitting. Data were expressed as mean ± SD, n = 3. $*P < 0.05$; $**P < 0.01$, $***P<0.001$ (Student's t test).

Supplemental Tables and Table Legends

Supplemental Table S1: List of 380 genes identified as putative RBPs.

RBPs Names	Domain	ISH Profiled?
Fxr2	KH	x
Tdrkh	KH	x
Retrovirus-related gag	other	x
gene model 381	KH	
similar to HPRP18	other, prp18	x
Bicc1	KH	x
cw17	KH	x
Fmr1	KH	x
Refbp1	RRM	x
Cpsf1	RRM	x
Daz1	RRM	x
Elavl3	RRM	x
Ewsh	RRM	x
Nssr	RRM	x
G3bp1	RRM	x
Nsap11	RRM	x
Hnrpa/b	RRM	x
Pabpc4l	RRM	x
Pparg1b	RRM	x

Ptbp2	RRM	x
Rbmy1a1	RRM	x
4921506I22Rik	RRM	x
Msi1h	RRM	x
Silg41	RRM	x
Rbpms2	RRM	x
3000004N20Rik	RRM	x
5730555F13Rik	RRM	x
2810036L13Rik	RRM	x
2610101N10Rik	RRM	x
8030431D03Rik	RRM	x
4932702K14Rik	RRM	x
U2af1	RRM	x
1700012H05Rik	RRM	x
Snrpb2	RRM	x
Rbm28	RRM	x
Snrp70	RRM	x
6330548G22Rik	RRM	x
C330027G06Rik	RRM	x
Rbm18	RRM	x
2610019N13Rik	RRM	x
2610020H08Rik	RRM	x
Rad52b	RRM	x
2610015J01Rik	RRM	x

Rdbp	RRM	x
Drbp1	RRM	x
Refbp2	RRM	x
Sfrs4	RRM	x
Ppargc1	RRM	x
4930565A21Rik	RRM	x
U2af2	RRM	x
LOC381370	RRM	x
LOC225307	RRM	x
2310016K04Rik	dsRM	x
Tarbp2	dsRM	x
Spnr	dsRM	x
Adar3	dsRM	x
Tenr	dsRM	x
Mrlp44	dsRM	x
Dhx30	dsRM	x
2810055E05Rik	other, S1	x
2610029K21Rik	G-patch	x
2010009L17Rik	G-patch	x
1300018I05Rik	G-patch	x
Bat4	G-patch	x
Hrmt1l3	other, arginine N-methyltransferase	x
LOC381813	other, arginine N-methyltransferase	x
Hrmtl16	other, arginine N-methyltransferase	x

LOC215034	**Piwi**	**x**
Top3a	**Zinc Knuckle**	**x**
3110031B13Rik	**Zinc Knuckle**	**x**
BC005685	**other**	**x**
Cnbp2	**Zinc Knuckle**	**x**
Zcchc10	**Zinc Knuckle**	**x**
2700088M22Rik	**RRM**	**x**
1500031H04Rik	**Zinc Knuckle**	**x**
Zcchc4	**Zinc Knuckle**	**x**
Zcchc12	**Zinc Knuckle**	**x**
Rn7sk	**other**	**x**
2610524B01Rik	**other, PHD**	**x**
Rpo2tc1	**other, transcription**	**x**
LOC218298	**other, SKIP**	**x**
AI033314	**Tudor**	**x**
2410004F06Rik	**Tudor**	**x**
Gtrosa26as	**other, THUMP**	**x**
Adam5	**other, Zn dependent metaloproteinase domain**	**x**
Traf6	**RRM**	**x**
D3Wsu161c	**RRM**	**x**
Tlr5	**RRM**	**x**
0610009D07Rik	**RRM**	**x**
5430431G03Rik	**RRM**	**x**

2600016B03Rik	RRM	x
1810073H04Rik	RRM	x
0610033I05Rik	RRM	x
1110007F05Rik	RRM	x
2610024N24Rik	RRM	x
2010015M23Rik	RRM	x
1700009P03Rik	RRM	x
9530027K23Rik	RRM	x
Tdrd7	RRM	x
Rbm16	RRM	x
2610209F03Rik	RRM	x
V1rc17	RRM	x
2210008M09Rik	RRM	x
Pprc1	RRM	x
D8ertd233e	RRM	x
D330023I21Rik	RRM	x
A430091O22Rik	RRM	x
BC013481	RRM	x
5730453I16Rik	RRM	x
4921511I16Rik	dsRM	x
4930403J07Rik	dsRM	x
Snrpe	other, Sm protein	x
2810441A10Rik	other, U5 snRNP associated domain	x
2610031L17Rik	other, HAT	x

Snrpa1	other, LRR	x
Prpf3	other, PWI	x
Sf3a3	other, PRP9	x
Sf3b3	other, CPSF	x
Sf3b4	RRM	x
Nxf2	other, TAP-C	x
Nxf7	other, TAP-C	x
Eif4a1	DEAD, Superfamily II RNA helicase	x
Srrm1	other, PWI	x
Ddx39	DEAD, Superfamily II RNA helicase	x
G430041M01Rik	RRM	x
Lsm6	other, Sm-protein	x
LOC384385	other, prp18	x
MCG1038304	RRM	x
Ascc3l1	DEAD, Superfamily II RNA helicase	x
MCG1027004	RRM	x
BC035291	RRM	x
LOC216024	RRM	x
Rbm11	RRM	x
E030019O05	RRM	x
D11Bwg0517e	RRM	x
9930033H14Rik	RRM	x
1810017N16Rik	RRM	x
Gm761	RRM	x

1700128F08Rik	RRM	x
LOC436185	RRM	x
LOC195154	RRM	x
Gm411	KH	x
Gm1424	KH	x
Nova1	KH	x
Gm381	KH	x
1810003N24Rik	KH	x
Htatsf1	RRM	x
Cpeb4	RRM	x
LOC433054	RRM	
LOC237032	RRM	
Miwi	Piwi	
D8ertd233e	RRM	
Rbmx2	RRM	
MCG51890	RRM	
AA517739	RRM	
B230333C21Rik	RRM	
C330012H03Rik	KH	
C530047H08Rik	RRM	
Cstf2t	RRM	
Oog4	KH	
Rps3	KH	
1810035L17Rik	RRM	

ds8	G-patch	
Khsrp	KH	
Mela	Zinc Knuckle	
C430048L16Rik	RRM	
Cstf2	RRM	
Dppa5	KH	
Sfrs15	RRM	
Raver	RRM	
Rkhd1	KH	
Rkhd2	KH	
Rkhd3	KH	
1700025B16Rik	RRM	
2410104I19Rik	RRM	
2810441O16Rik	RRM	
3100004P22Rik	RRM	
4930562C03Rik	RRM	
4933434H11Rik	RRM	
6430512A10Rik	RRM	
Pcbp2	KH	x
Pcbp4	KH	x
Igf2bp1	KH	x
Fxr1	KH	x
Hnrpk	KH	x
Igf2bp3	KH	x

Khdrbs1	KH	x
Qk	KH	x
Khdrbs2	KH	x
Khdrbs3	KH	x
Ascc1	KH	x
Boll	RRM	x
Brunol4	RRM	x
Mint	RRM	x
Cpeb	RRM	x
Cugbp1	RRM	x
Elavl2	RRM	x
Elavl4	RRM	x
Cugbp2	RRM	x
G3bp2	RRM	x
Hnrpa1	RRM	x
Hnrpc	RRM	x
Hnrph1	RRM	x
Hnrph2	RRM	x
Hnrpr	RRM	x
Raly	RRM	x
Hnrpdl	RRM	x
Ssb	RRM	x
Myef2	RRM	x
Rbm4	RRM	x

Msi2h	**RRM**	**x**
Rbms1	**RRM**	**x**
Cnot4	**RRM**	**x**
Np220	**RRM**	**x**
Nsap1	**RRM**	**x**
Ncl	**RRM**	**x**
Pabpc2	**RRM**	**x**
Kist	**KH**	**x**
Fus	**RRM**	**x**
Pabpn1	**RRM**	**x**
Ptbp1	**RRM**	**x**
Sfpq	**RRM**	**x**
Rbm10	**RRM**	**x**
Rbm3	**RRM**	**x**
Rbm6	**RRM**	**x**
Rbmx	**RRM**	**x**
Rbpms	**RRM**	**x**
Rnps1	**RRM**	**x**
Sart3	**RRM**	**x**
Rbms2	**RRM**	**x**
Rnpc1	**RRM**	**x**
Sfrs10	**RRM**	**x**
Sfrs2	**RRM**	**x**
Snrpa	**RRM**	**x**

U2af1-rs1	RRM	x
U2af1-rs2	RRM	x
Synj2	RRM	x
Tia1	RRM	x
Tial1	RRM	x
Ppil4	RRM	x
Rbm19	RRM	x
Rbm8	RRM	x
Rbm22	RRM	x
Nono	RRM	x
Sfrs6	RRM	x
Sfrs9	RRM	x
Rbm14	RRM	x
Pabpc1	RRM	x
Pspc1	RRM	x
Hnrpm	RRM	x
Rbm12	RRM	x
Nol8	RRM	x
Tnrc6	RRM	x
Rnpc2	RRM	x
Acin1	RRM	x
A2bp1	RRM	x
Ppie	RRM	x
Cirbp	RRM	x

Stau2	dsRM	x
Stau1	dsRM	x
Prkra	dsRM	x
Ilf3	dsRM	x
Adarb1	dsRM	x
Adar	dsRM	x
Prkr	dsRM	x
Ddx9	dsRM	x
Pdcd11	other, S1	x
Supt6h	other, S1	x
Tfip11	G-patch	x
Rbm5	G-patch	x
Pum1	other, PUF	x
Hrmt1l2 (PRMT1)	other, arginine N-methyltransferase	x
Hrmt1l1	other, arginine N-methyltransferase	x
Piwil2	Piwi	x
Eif2c4	Piwi	x
Eif2c3	Piwi	x
Peg10	Zinc Knuckle	x
Cnbp	other, arginine N-methyltransferase	x
Zcchc7	Zinc Knuckle	x
Pnpt1	KH	x
Carm1	other, arginine N-methyltransferase	x
Cops5	other, CSN5 domain	x

Scand1	other, LR	x
Ncoa6ip	other, THUMP	x
Ncoa3	other, PAS	x
Ptcd2	other, PPR	x
Ptcd1	other, PPR	x
Akap1	KH	x
Sfrs1	RRM	x
Hnrpd	RRM	x
Son	dsRM	x
Eif2c2 (AGO2)	Piwi	x
Dazap1	RRM	x
Col4a3	RRM	x
Hnrpl	RRM	x
Htf9c	RRM	x
Rbmxrt	RRM	x
Rpo1-2	RRM	x
Eif3s9	RRM	x
Afg3l2	RRM	x
Rbm21	RRM	x
Poldip3	RRM	x
Rbm17	RRM	x
Wdr9	RRM	x
Slc6a8	RRM	x
Hnrpa3	RRM	x

Rbms3	**RRM**	**x**
Cova1	**RRM**	**x**
Rnpep	**RRM**	**x**
Safb	**RRM**	**x**
Rbm27	**RRM**	**x**
Tardbp	**RRM**	**x**
Grsf1	**RRM**	**x**
Rbed1	**RRM**	**x**
Csad	**RRM**	**x**
Lsm4	**other, Sm protein**	**x**
Lsm7	**other, Sm protein**	**x**
Crnkl1	**other, HAT**	**x**
Sf3a1	**other, SWAP**	**x**
Snrpg	**other, Sm protein**	**x**
Cpsf5	**other, mRNA cleavage factor**	**x**
Snrpf	**other, Sm protein**	**x**
Prp17	**other, WD40**	**x**
Sf3b1	**other, U2 snRNP spliceosome subunit**	**x**
Prpf8	**other, JAB/MPN**	**x**
Nxt1	**other, NTF2**	**x**
Nxf1	**other, TAP-C**	**x**
Rpl5	**other, Ribosomal L18p**	**x**
Nup88	**other, nuclear pore**	**x**
Ddx19	**DEAD, Superfamily II RNA helicase**	**x**

Gle1l	other	x
Nup98	other, nuclear pore	x
Lsm3	RRM	x
Sip1	other, SIP1	x
Hnrpf	RRM	x
Hnrpa0	RRM	x
Taf15	RRM	x
Dnd1	RRM	x
Sfrs12	RRM	x
Sfrs7	RRM	x
Pabpc5	RRM	x
Rbm15	RRM	x
Fubp1	KH	x
Hrb2	KH	x
Hdlbp	KH	x
Pcbp3	KH	x
Cpeb2	RRM	x
Ankhd1	KH	x
Dclre1b	KH	x
Rod1	RRM	x
Elavl1	RRM	x
Sfrs5	RRM	x
Thumpd1	other, THUMP	
Lrpprc	other, PPR	

Zfp422	RRM	
Fubp3	KH	
Pum2	other, PUF	
Wbscr1	RRM	
Etohi2	dsRM	
Hnrpa2b1	RRM	
Mki67ip	RRM	
Ncbp2	RRM	
Sfrs3	RRM	
Dscr1l1	RRM	
Eif3s4	RRM	
Anks1	KH	
Cpsf6	RRM	
Dgcr8	dsRM	
Dicer1	dsRM	
Matrin 3	RRM	
Pcbp1	KH	
Safb2	RRM	
Tnrc4	RRM	
Rbm25	RRM	
Rbm7	RRM	
Rbm9	RRM	
Pinx1	G-patch	x
Brunol6	RRM	x

Gpatc1	**G-patch**	**x**
LOC383923	**Piwi**	**x**

(‘x’ means ‘not present’.)

Supplemental Table S2: List of 199 RBPs which exist NATs in their genomic locus.

RBPs Names	Domain	NAT exists?	NAT type	NAT detail	ISH Profiled?
Pcbp4	KH	y	tail to tail	GPR62 G protein-coupled receptor 62	x
Ascc1	KH	y	head to head	AA984891	x
Boll	RRM	y	tail to tail	BC021693	x
Mint	RRM	y	head to head	AK124018	x
Elavl2	RRM	y	full length (small)	AF147374	x
Elavl4	RRM	y	full length	BE218251	x
Hnrpa1	RRM	y	full length	DB552539	x
Hnrpc	RRM	y	full length	BU607926	x
Hnrph1	RRM	y	full length	R05743	x
Hnrph2	RRM	y	full length	CA434430	x
Hnrpr	RRM	y	full length	AW136837	x
Raly	RRM	y	full length	AA074799	x
Hnrpdl	RRM	y	head to head	DA129778	x
Myef2	RRM	y	tail to tail	SLC24A5 solute carrier family 24, member 5	x
Rbm4	RRM	y	full length	BE467850	x

Msi2h	**RRM**	**y**	**full length**	**AI694538**	**x**
Rbms1	**RRM**	**y**	**full length**	**AL704230**	**x**
Cnot4	**RRM**	**y**	**full length**	**CA439725**	**x**
Np220	**RRM**	**y**	**full length**	**BG207090**	**x**
Ncl	**RRM**	**y**	**full length**	**DB339881**	**x**
Pabpc2	**RRM**	**y**	**full length**	**CD364547**	**x**
Kist	**KH**	**y**	**full length**	**AV659210**	**x**
Fus	**RRM**	**y**	**full length**	**DB070270**	**x**
Pabpn1	**RRM**	**y**	**full length**	**BU608633**	**x**
Sfpq	**RRM**	**y**	**full length**	**BG028196**	**x**
Rbm10	**RRM**	**y**	**head to head**	**BE379249**	**x**
Rbm3	**RRM**	**y**	**head to head**	**AK129559**	**x**
Rbm6	**RRM**	**y**	**full length**	**AV759137**	**x**
Rbmx	**RRM**	**y**	**full length**	**AI131042**	**x**
Rbpms	**RRM**	**y**	**head to head**	**CF129999**	**x**
Rnps1	**RRM**	**y**	**full length**	**BQ672813**	**x**
Sart3	**RRM**	**y**	**full length**	**AI023828**	**x**
Rbms2	**RRM**	**y**	**tail to tail**	**AK096412**	**x**

Rnpc1	RRM	y	head to head	AK096426	x
Sfrs10	RRM	y	full length	BU686967	x
Sfrs2	RRM	y	head to head	ET hypothetical protein ET	x
Snrpa	RRM	y	head to head	CX163256	x
Tia1	RRM	y	head to head	T55036	x
Rbm8	RRM	y	tail to tail	GNRHR2 gonadotropin-releasing hormone (type 2) receptor 2	x
Sfrs9	RRM	y	tail to tail	15E1.2 hypothetical protein LOC283459	x
Nol8	RRM	y	head to head	CENPP centromere protein P	x
Acin1	RRM	y	head to head	C14orf119 chromosome 14 open reading frame 119	x
Ppie	RRM	y	tail to tail	BMP8B bone morphogenetic protein 8b (osteogenic protein 2)	x
Adarb1	dsRM	y	head to head	AW294061	x
Prkr	dsRM	y	tail to tail	BG189068	x
Ddx9	dsRM	y	head to head	AK001442	x
Supt6h	other, S1	y	head to head	BQ310438	x

Tfip11	G-patch	y	tail to tail	CTB-1048E9.5 similar to SRR1-like protein	x
Rbm5	G-patch	y	tail to tail	AK125500	x
Hrmt1l2 (PRMT1)	other, arginine N-methyltransferase	y	head to head	IRF3 to BCL2L12	x
Eif2c3	Piwi	y	full length	AW511062	x
Peg10	Zinc Knuckle	y	full length	AW137627	x
Cnbp	other, arginine N-methyltransferase	y	head to head	DB242329	x
Zcchc7	Zinc Knuckle	y	full length	BF512512	x
Pnpt1	KH	y	full length	AW296091	x
Carm1	other, arginine N-methyltransferase	y	tail to tail	BM552692	x
Cops5	other, CSN5 domain	y	tail to tail	CSPP1 to ARFGEF1	x
Scand1	other, LR	y	head to head	DB056200	x
Ncoa6ip	other, THUMP	y	head to head	TMEM68 transmembrane protein 68	x
Ncoa3	other, PAS	y	full length	DB275059	x
Ptcd2	other, PPR	y	full length	AW087699	x
Ptcd1	other, PPR	y	tail to tail	BC001578	x
Akap1	KH	y	full length	BU675476	x
Sfrs1	RRM	y	head to head	DA002141	x

Hnrpd	RRM	y	head to head	DA129778	x
Son	dsRM	y	tail to tail	AI480262	x
Eif2c2 (AGO2)	Piwi	y	head to head	AF426412	x
Dazap1	RRM	y	full length	AK094875	x
Col4a3	RRM	y	tail to tail	AK056332	x
Hnrpl	RRM	y	full length	AA937108	x
Htf9c	RRM	y	head to head	AK097659	x
Rbmxrt	RRM	y	full length	AI131042	x
Rpo1-2	RRM	y	full length	AI223157	x
Eif3s9	RRM	y	full length	BF512712	x
Afg3l2	RRM	y	tail to tail	BC039717	x
Rbm21	RRM	y	tail to tail	AK125351	x
Poldip3	RRM	y	tail to tail	BC031838 SERHL and CTA-126B4.3	x
Rbm17	RRM	y	full length	BP398070	x
Wdr9	RRM	y	full length	AA207251	x
Slc6a8	RRM	y	head to head	BI598085	x
Hnrpa3	RRM	y	tail to tail	BI488549	x

Rbms3	RRM	y	head to head	DA506411	x
Cova1	RRM	y	full length	DB449817	x
Rnpep	RRM	y	head to head	AA150807	x
Safb	RRM	y	full length	BM563776	x
Rbm27	RRM	y	full length	AW298002	x
Tardbp	RRM	y	full length	BU675715	x
Grsf1	RRM	y	full length	BG391541	x
Rbed1	RRM	y	full length	DA107497	x
Csad	RRM	y	head to head	ZNF740 zinc finger protein 740	x
Lsm4	other, Sm protein	y	full length	AI282073	x
Lsm7	other, Sm protein	y	tail to tail	AW057599	x
Crnkl1	other, HAT	y	head to head	C20orf26 chromosome 20 open reading frame 26	x
Sf3a1	other, SWAP	y	head to head	BC018040	x
Snrpg	other, Sm protein	y	full length	EB386723	x
Cpsf5	other, mRNA cleavage factor	y	tail to tail	BF966722	x
Snrpf	other, Sm protein	y	tail to tail	DA746379	x
Prp17	other, WD40	y	full length	CA397410	x

Sf3b1	other, U2 snRNP spliceosome subunit	y	full length	CA502883	x
Prpf8	other, JAB/MPN	y	full length	AA399588	x
Nxt1	other, NTF2	y	head to head	BE891551	x
Nxf1	other, TAP-C	y	full length	DB039117	x
Rpl5	other, Ribosomal L18p	y	head to head	U66589	x
Nup88	other, nuclear pore	y	tail to tail	NM_001212	x
Ddx19	DEAD, Superfamily II RNA helicase	y	full length	BC039497	x
Gle1l	other	y	tail to tail	BG397948	x
Nup98	other, nuclear pore	y	full length	BF309280	x
Lsm3	RRM	y	full length	DB228065	x
Sip1	other, SIP1	y	full length	CA422147	x
Hnrpf	RRM	y	full length	AI133166	x
Taf15	RRM	y	full length	AK130999	x
Dnd1	RRM	y	tail to tail	WDR55 WD repeat domain 55	x
Sfrs12	RRM	y	full length	CA312467	x
Sfrs7	RRM	y	full length	DA568942	x

Pabpc5	RRM	y	full length	DA375776	x
Rbm15	RRM	y	full length	BM999102	x
Fubp1	KH	y	head to head	NEXN to C1orf118	x
Hrb2	KH	y	tail to tail	GLIPR1 GLI pathogenesis-related 1 (glioma)	x
Hdlbp	KH	y	head to head	NM_001008491 SEPT2 septin 2	x
Cpeb2	RRM	y	tail to tail	AI760149	x
Ankhd1	KH	y	full length	BI793092	x
Dclre1b	KH	y	tail to tail	AK123199	x
Rod1	RRM	y	full length	BU607910	x
Elavl1	RRM	y	full length	W37464	x
Sfrs5	RRM	y	tail to tail	T67695	x
Thumpd1	other, THUMP	y	full length	DB543799	
Lrpprc	other, PPR	y	full length	BC031947	
Zfp422	RRM	y	tail to tail	BC026193	
Fubp3	KH	y	full length	DB524448	
Pum2	other, PUF	y	full length	BF513882	
Wbscr1	RRM	y	head to head	AI863284	

Etohi2	dsRM	y	tail to tail	BG219344	
Hnrpa2b1	RRM	y	head to head	CBX3 chromobox homolog 3 (HP1 gamma homolog, Drosophila)	
Mki67ip	RRM	y	tail to tail	AK098264	
Ncbp2	RRM	y	full length	DA277609	
Sfrs3	RRM	y	full length	BX464843	
Dscr1l1	RRM	y	full length	BC043004	
Eif3s4	RRM	y	tail to tail	P2RY11 purinergic receptor P2Y, G-protein coupled, 11	
Anks1	KH	y	full length	AI243659	
Cpsf6	RRM	y	full length	AK098338	
Dgcr8	dsRM	y	full length	CA442060	
Matrin 3	RRM	y	full length	CB242024	
Safb2	RRM	y	full length	BM563776	
Tnrc4	RRM	y	full length	DB535646	
Rbm25	RRM	y	full length	CR739627	
Rbm7	RRM	y	full length	BG196362	
Rbm9	RRM	y	full length	CB267142	
Pinx1	G-patch	y	tail to tail	PINX1 PIN2-interacting protein 1 BC043573	x

Brunol6	RRM	y	tail to tail	BC034424	x
Gpatc1	G-patch	?			x
LOC383923	Piwi	?			x
Pcbp2	KH	y	tail to tail	MAP3K12 mitogen-activated protein kinase kinase kinase 12	x
Igf2bp1	KH	y	head to head	BE044435	x
Fxr1	KH	y	tail to tail	BU686455	x
Hnrpk =hnRNPK	KH	y	full length	AW978702	x
Igf2bp3	KH	y	tail to tail	AK127742	x
Khdrbs1	KH	y	full length	CA417903	x
Qk	KH	y	full length	DB530476	x
Khdrbs2	KH	y	full length	CA391235	x
Khdrbs3	KH	y	full length	CA388804	x
Brunol4	RRM	y	tail to tail	DB209115	x
Cpeb	RRM	y	head to head	BC050629	x
Cugbp1	RRM	y	tail to tail	PTPMT1 and KBTBD4	x
Cugbp2	RRM	y	full length	BM931184	x
G3bp2	RRM	y	full length	BM978447	x

Ssb	RRM	y	tail to tail	METTL5 methyltransferase like 5	x
Nsap1=hnRNP-Q	RRM	y	full length	DA447957	x
Ptbp1	RRM	y	full length	BM691399	x
U2af1-rs1	RRM	y	full length	BU619109	x
U2af1-rs2	RRM	y	full length	BC039434	x
Synj2	RRM	y	full length	BM683410	x
Tial1	RRM	y	full length	DB080956	x
Ppil4	RRM	y	full length	DB542130	x
Rbm19	RRM	y	full length	DA295001	x
Rbm22	RRM	y	full length	DB572704	x
Nono	RRM	y	full length	DA667525	x
Sfrs6	RRM	y	full length	CD243053	x
Rbm14	RRM	y	full length	BE467850	x
Pabpc1	RRM	y	full length	CD364547	x
Pspc1	RRM	y	full length	DR978109	x
Hnrpm	RRM	y	full length	BC045573	x
Rbm12	RRM	y	full length	BM968574	x
Tnrc6	RRM	y	full length	BX495114	x

Rnpc2	RRM	y	full length	BG429761	x
A2bp1	RRM	y	full length	BM669724	x
Cirbp	RRM	y	full length	BM665199	x
Stau2	dsRM	y	full length	CK818592	x
Stau1	dsRM	y	full length	CA439621	x
Prkra	dsRM	y	full length	NEB nebulin	x
Ilf3	dsRM	y	full length	DA854620	x
Adar=adar1	dsRM	y	full length	CD514840	x
Pdcd11	other, S1	y	full length	AY007124	x
Pum1	other, PUF	y	full length	DB521106	x
Hrmt1l1	other, arginine N-methyltransferase	y	full length	BQ017509	x
Piwil2	Piwi	y	full length	BQ448561	x
Eif2c4	Piwi	y	full length	BQ017637	x
Hnrpa0	RRM	y	tail to tail	NM_016603	x
Pcbp3	KH	y	head to head	DA117170	x
Dicer1	dsRM	y	full length	AA931786	
Pcbp1	KH	y	head to head	DA872092	

(‘y’ means ‘Yes’ and ‘x’ means ‘not present’)

Supplemental Table S3: List of 12 NATs which had been perfectly identified by Reverse Transcription-PCR (RT-PCR).

RBPs Names	NAT exists?	NAT type and detail	NAT detail	Domain	ISH Profiled?
Pcbp2	y	tail to tail	MAP3K12 mitogen-activated protein kinase kinase kinase 12	KH	x
Hnrpk =hnRNPK	y	full length	AW978702	KH	x
Ssb	y	tail to tail	METTL5 methyltransferase like 5	RRM	x
Nsap1=hnRNP-Q	y	full length	DA447957	RRM	x
Ptbp1	y	full length	BM691399	RRM	x
Adar=adar1	y	full length	CD514840	dsRM	x
Hnrpa0	y	tail to tail	NM_016603	RRM	x
Pcbp3	y	head to head	DA117170	KH	x
Dicer1	y	full length	AA931786	dsRM	
Pcbp1	y	head to head	DA872092	KH	Present
Cirbp	y	full length	BM665199	RRM	x
Hnrpa1	y	full length	DB552539	RRM	Present

(‘y’ means ‘Yes’ and ‘x’ means ‘not present’)

Supplemental Table S4: List of primers for RACE and PCR.

name	application	Sequence (5'-3')
PTB-AS-5'RACE-GSP1	RACE	GTAATTAAGTCACAGGCAGG
PTB-AS-5'RACE-GSP2	RACE	CACCACGCCTTCACCTGCAG
PTB-AS-5'RACE-GSP3	RACE	GCCTGCCTCTGATGCTGGGAC
PTB-AS-5'RACE-GSP4	RACE	CGTAAAAGCGTGTAACAAGGGTG
PTB-AS-3'RACE-GSP1	RACE	TACTGAGCCTGGAATTGC
PTB-AS-3'RACE-GSP2	RACE	CACCCTTGTTACACGCTTTTACG
PTB-AS-3'RACE-GSP3	RACE	GAGCACAAAGACAGGAGGAGCG
PTB-AS-3'RACE-GSP4	RACE	CTGCAGGTGAAGGCGTGGTG
PTB-AS-3'RACE-GSP5	RACE	CCTGCTCTCTGGAAACTGGGTC
PTB-AS-Northern-probe-F	Northern	CCCAAGCTTGCTCTTGGTCATTCGCTCTGG
PTB-AS-Northern-probe-R	Northern	CGGAATTCCTGTGTTTTGCCTGCCTCTGA
PTB-AS-biotin-probe-F	Biotin pull down	CCCAAGCTTGCTCTTGGTCATTCGCTCTGG
PTB-AS-biotin-probe-R	Biotin pull down	CGGAATTCTGTGGTATTACCTTGTATGCTGTTACT

GAPDH-F	qRT-PCR	GGTCATCCATGACAACTTTGG
GAPDH-R	qRT-PCR	GGCCATCACGCCACAG
PTB-AS-F	qRT-PCR	CAGAGGCAGGCAAAACACAG
PTB-AS-R	qRT-PCR	GACCCAGTTTCCAGAGAGCAG
PTB-F	qRT-PCR	CTGCAGCAAACGGAAATGACAG
PTB-R	qRT-PCR	GTTCATCTCGATGAAGGCCTGG
PTB-AS Reverse Transcript	qRT-PCR	GACCCAGTTTCCAGAGAGCAG
Malat1-F	qRT-PCR	CTTCCCTAGGGGATTTCAGG
Malat1-R	qRT-PCR	GCCCACAGGAACAAGTCCTA
PTB-AS-plenti6-F	overexpression	GAAGATCTGCTCTTGGTCATTCGCTCTGG
PTB-AS-plenti6-R	overexpression	CCGCTCGAGTGTGGTATTACCTTGTATGCTGTTACT
GSP-Reverse Transcript	overexpression	GTGGTATTACCTTGTATGCTG
PTB-3'UTR-luc-F	Luciferase	CCGCTCGAGctccttctccaagtccaccatc
PTB-3'UTR-luc-R	Luciferase	GCTCTAGAGAACGGAGCGAGGATACAGAAG
PTB-plenti6-F	overexpression	CGGGATCCAtggacggcattgtcccag
PTB-plenti6-R	overexpression	CCGCTCGAGCTAGATGGTGGACTTGGAGAAGG

PTB-AS-shRNA-F	Lentivirus	CCGGCAGAAAGAGGAAGCCAGCAACGAAGCTCGAGCTTCGTTGCTGGCTTCCTCTTTCTGTTTTTG
PTB-AS-shRNA-R	Lentivirus	AATTCAAAAACAGAAAGAGGAAGCCAGCAACGAAGCTCGAGCTTCGTTGCTGGCTTCCTCTTTCTG
PTB-3'UTR-RT-F	Half-life	GAAGTGACCTTAGCAGACCAGAG
PTB-3'UTR-RT-R	Half-life	CACAAGGAAGCCAAGTCGTG
PTB-3'UTR-P1	RPA	AGAAGGAGAACGCCCTAGTG
PTB-3'UTR-P2	RPA	TCTGGAAGTTCTTGGAGCCC
PTB-3'UTR-P3	RPA	CAGGCTCAGTATTGTGACCG
PTB-3'UTR-P4	RPA	AACACAGGGCTAGACAAGGG
SND1-F	qRT-PCR	GGTGCCCCAAGATGATGATG
SND1-R	qRT-PCR	GGTATTCTGTGATCACTTTCTGGA
Universe miRNAs Rltm-R	qRT-PCR	GTGCAGGGTCCGAGGT
U6-RT	qRT-PCR	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACAAAATATG
U6-F	qRT-PCR	GCGCGTCGTGAAGCGTTC
mir-9-RT	qRT-PCR	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTCATAC
mir-9-F	qRT-PCR	CGGCCGTCTTTGGTTATCTAGC
mir-133-RT	qRT-PCR	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCAGCTG

mir-133-F	qRT-PCR	GCGCTTTGGTCCCCTTCAAC
PTB-AS-stealth-si1	siRNA	CUUCGUUGCUGGCUUCCUCUUUCUG
PTB-AS-stealth-si2	siRNA	UGCGGGCCAGAGCGAAUGACCAAGA

Supplemental Table S5: Details of candidate proteins

Protein Symbol	Alias	Main Cell Localizations	Function	Reference(Pubmed IDs)
SND1	p100; TDRD11; Tudor-SN	extracellular, nucleus, cytosol	RNA binding	22681889
			nucleic acid binding	
			transcription cofactor activity	7651391
			nuclease activity	
			protein binding	20642132
hnRNP U	SAFA; HNRPU; U21.1; pp120; EIEE54; GRIP120	cytoskeleton, nucleus, extracellular	nucleotide binding	
			RNA polymerase II core binding	10490622
			core promoter binding	
			TFIIH-class transcription factor binding	10490622
			DNA binding	9204873
SFPQ	PSF; POMP100; PPP1R140	nucleus, extracellular	transcription regulatory region sequence-specific DNA binding	
			RNA polymerase II distal enhancer sequence-specific DNA binding	
			core promoter binding	
			nucleic acid binding	
			DNA binding	25765647

LGALS3BP	90K; M2BP; gp90; CyCAP; BTBD17B; MAC-2-BP; TANGO10B	extracellular, nucleus	scavenger receptor activity	
HDLBP	HBP; VGL; PRO2900	plasma membrane, cytosol, extracellular, nucleus	RNA binding	22658674
			protein binding	24725430
			lipid binding	1318310
			cadherin binding	25468996
PTBP1	PTB; PTB2; PTB3; PTB4; pPTB; HNRPI; PTB-1; PTB-T; HNRNPI; HNRNP-I	extracellular, nucleus	nucleic acid binding	
			RNA binding	22658674
			protein binding	10653975
			poly-pyrimidine tract binding	1906036
			pre-mRNA binding	16260624
HNRNPR	HNRPR; hnRNP-R	nucleus	nucleic acid binding	
			RNA binding	9421497
			mRNA 3-UTR binding	
			protein binding	16169070
DHX9	LKP; RHA; DDX9; NDH2; NDHI	cytoskeleton, nucleus, cytosol	RNA polymerase II core binding	11416126
			core promoter binding	11038348
			regulatory region RNA binding	28355180
			RNA polymerase II transcription factor binding	17303075
			RNA polymerase II transcription cofactor activity	11416126

CKAP4	p63; CLIMP-63; ERGIC-63	plasma membrane, extracellular, cytoskeleton, nucleus, endoplasmic reticulum, cytosol	RNA binding	22658674
ELAVL1	HUR; Hua; MelG; ELAV1	nucleus, cytosol	nucleic acid binding RNA binding double-stranded RNA binding mRNA binding mRNA 3-UTR binding	19561594 21266579 10660597
PABPC1	PAB1; PABP; PABP1; PABPC2; PABPL1	extracellular, nucleus, cytosol	nucleic acid binding RNA binding mRNA 3-UTR binding protein binding protein C-terminus binding	25225333 16126846 11051545 15663938
RPL10	QM; L10; NOV; AUTSX5; DXS648; MRXS35; DXS648E	nucleus, cytosol	RNA binding structural constituent of ribosome protein binding translation regulator activity	12962325 10508860 26290468
SLC25A6	ANT; AAC3; ANT3; ANT 2; ANT 3; ANT3Y	extracellular, mitochondrion, nucleus	ATP:ADP antiporter activity protein binding adenine transmembrane transporter activity transmembrane transporter activity	2541251 21370995
RPS2	S2; LLREP3	extracellular, nucleus, cytosol	RNA binding mRNA binding	22658674 18464793

			structural constituent of ribosome	15883184
			protein binding	15473865
			fibroblast growth factor binding	16263090
KHSRP	FBP2; KSRP; FUBP2	nucleus, cytosol	nucleic acid binding	
			DNA binding	
			RNA binding	22658674
			mRNA binding	
			protein binding	16126846
HNRNPC	C1; C2; HNRNP; HNRPC; SNRPC	extracellular, nucleus, cytosol, cytoskeleton	RNA polymerase II proximal promoter sequence-specific DNA binding	16217013
			RNA polymerase II distal enhancer sequence-specific DNA binding	16217013
			nucleic acid binding	
			RNA binding	9731529
			mRNA 3-UTR binding	16010978
RRBP1	RRp; hES; ES130; ES/130	endoplasmic reticulum	RNA binding	22681889
			receptor activity	9628588
HNRNPK	AUKS; CSBP; TUNP; HNRPK	extracellular, nucleus, cytoskeleton	RNA polymerase II proximal promoter sequence-specific DNA binding	20371611
			transcriptional activator activity, RNA polymerase II proximal promoter	20371611

			sequence-specific DNA binding	
			nucleic acid binding	
			DNA binding	
			single-stranded DNA binding	20371611
HSP90B1	ECGP; GP96; TRA1; GRP94; HEL35; HEL-S-125m	extracellular, nucleus, endoplasmic reticulum, cytosol	RNA binding	11958450
			calcium ion binding	10497210
			protein binding	9596688
			ATP binding	
			protein phosphatase binding	19000834
SLC3A2	4F2; CD98; MDU1; 4F2HC; 4T2HC; NACAE; CD98HC	plasma membrane, extracellular, nucleus, cytosol	RNA binding	22658674
			double-stranded RNA binding	21266579
			catalytic activity	
			calcium:sodium antiporter activity	10673541
			protein binding	10506149
MYH9	MHA; FTNS; EPSTS; BDPLT6; DFNA17; NMMHCA; NMHC-II-A; NMMHC-IIA	plasma membrane, extracellular, nucleus, cytosol, cytoskeleton	microfilament motor activity	12237319
			nucleotide binding	
			RNA binding	22681889
			motor activity	12421915
			actin binding	15065866
COPA	AILJK; HEP-COP	extracellular, endoplasmic reticulum, cytosol, golgi apparatus	hormone activity	
			structural molecule activity	

RPL23	L23; rpL17	extracellular, nucleus, cytosol	transcription coactivator binding	19160485
			RNA binding	22658674
			structural constituent of ribosome	12962325
			protein binding	15314173
			ubiquitin protein ligase binding	15314173
HSPB1	CMT2F; HMN2B; HSP27; HSP28; Hsp25; SRP27; HS.76067; HEL-S-102	extracellular, nucleus, cytosol, cytoskeleton	RNA binding	22658674
			protein kinase C binding	
			protein binding	11003656
			protein kinase C inhibitor activity	
			protein kinase binding	8774846
YBX1	YB1; BP-8; CSDB; DBPB; YB-1; CBF-A; CSDA2; EFI-A; NSEP1; NSEP-1; MDR-NF1	extracellular, nucleus, cytosol	RNA polymerase II proximal promoter sequence-specific DNA binding	18809583
			transcriptional activator activity, RNA polymerase II proximal promoter sequence-specific DNA binding	18809583
			nucleic acid binding	
			DNA binding	2977358
			chromatin binding	
RPS8	S8	extracellular, nucleus, cytosol	RNA binding	22658674
			structural constituent of ribosome	
			protein binding	

FUBP3	FBP3	nucleus	RNA polymerase II proximal promoter sequence-specific DNA binding	8940189
			transcriptional activator activity, RNA polymerase II proximal promoter sequence-specific DNA binding	8940189
			nucleic acid binding	
			DNA binding	
			RNA binding	22658674
HADHA	GBP; ECHA; HADH; LCEH; MTPA; LCHAD; TP-ALPHA	extracellular, mitochondrion	fatty-acyl-CoA binding	
			catalytic activity	
			3-hydroxyacyl-CoA dehydrogenase activity	8135828
			acetyl-CoA C-acetyltransferase activity	8135828
			acetyl-CoA C-acyltransferase activity	
EIF2AK2	PKR; PRKR; EIF2AK1; PPP1R83	nucleus, cytosol	RNA binding	22681889
			double-stranded RNA binding	21266579
			protein kinase activity	21123651
			protein serine/threonine kinase activity	1695551
			eukaryotic translation initiation factor 2alpha kinase activity	25329545
RPS16	S16	extracellular, nucleus, cytosol	RNA binding	17881366

			structural constituent of ribosome	
			protein binding	24725412
CCT3	CCTG; PIG48; TRIC5; CCT-gamma; TCP-1-gamma	extracellular, nucleus, cytosol, plasma membrane	RNA binding	22681889
			protein binding	12620389
			ATP binding	
			protein binding involved in protein folding	
			unfolded protein binding	
IGF2BP3	KOC; CT98; IMP3; KOC1; IMP-3; VICKZ3	nucleus, cytosol	RNA binding	22658674
			mRNA 3-UTR binding	20080952
			protein binding	17289661
			translation regulator activity	9891060
			mRNA 5-UTR binding	9891060
MTDH	3D3; AEG1; AEG-1; LYRIC; LYRIC/3D3	plasma membrane, nucleus, endoplasmic reticulum	RNA polymerase II transcription factor binding	18316612
			transcription coactivator activity	18316612
			RNA binding	22658674
			double-stranded RNA binding	21266579
			protein binding	18316612
RPN1	HRD2; NAS1	extracellular, endoplasmic reticulum, cytosol	RNA binding	22658674
			contributes_to dolichyl-diphosphooligosaccharide-protein glycotransferase activity	15835887
			protein binding	22988243

			transferase activity	
			transferase activity, transferring glycosyl groups	
HNRNPL	HNRPL; hnRNP-L; P/OKcl.14	extracellular, nucleus	nucleic acid binding	
			RNA binding	22658674
			protein binding	11809897
			transcription regulatory region DNA binding	11809897
			pre-mRNA intronic binding	25623890
GLUD1	GDH; GDH1; GLUD	mitochondrion	glutamate dehydrogenase (NAD+) activity	11903050
			glutamate dehydrogenase [NAD(P)+] activity	11032875
			protein binding	16959573
			ATP binding	
			GTP binding	11032875
FUBP1	FBP; FUBP; hDH V	nucleus	DNA binding	
			single-stranded DNA binding	8125259
			DNA binding transcription factor activity	8125259
			RNA binding	22658674
			protein binding	21285945
ACLY	ACL; ATPCL; CLATP	extracellular, nucleus, cytosol, plasma membrane	catalytic activity	
			ATP citrate synthase activity	23932781
			protein binding	23932781
			ATP binding	1371749

			transferase activity	
PRKDC	HYRC; p350; DNAPK; DNPK1; HYRC1; IMD26; XRCC7; DNA-PKcs	nucleus, cytosol, extracellular	DNA binding	
			double-stranded DNA binding	22504299
			RNA binding	22658674
			protein kinase activity	22504299
			protein serine/threonine kinase activity	
RPS18	KE3; S18; HKE3; KE-3; D6S218E	nucleus, cytosol, extracellular	nucleic acid binding	
			RNA binding	22658674
			structural constituent of ribosome	
			protein binding	22720776
			rRNA binding	
UQCRC2	QCR2; UQCR2; MC3DN5	extracellular, nucleus, mitochondrion	metalloendopeptidase activity	
			protein binding	21078624
			zinc ion binding	
			protein complex binding	
			metal ion binding	
KRT2	K2e; KRTE; CK-2e; KRT2A; KRT2E	nucleus, cytosol, extracellular, cytoskeleton	structural molecule activity	
			structural constituent of cytoskeleton	1380918
			protein binding	25416956
			cytoskeletal protein binding	
			structural constituent of epidermis	7543090
PABPC4		nucleus, cytosol	RNA binding	22658674

	mRNA binding	
APP1; APP-1; PABP4; iPABP	protein binding	11369516
	poly(A) binding	8524242
	poly(U) RNA binding	8524242