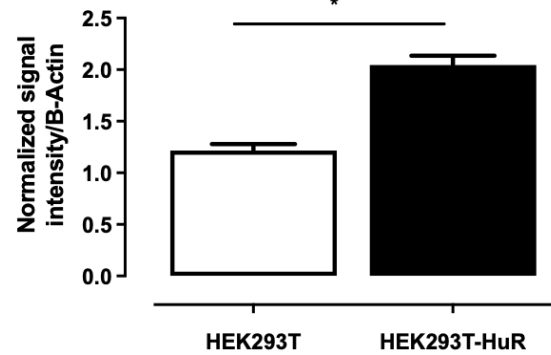
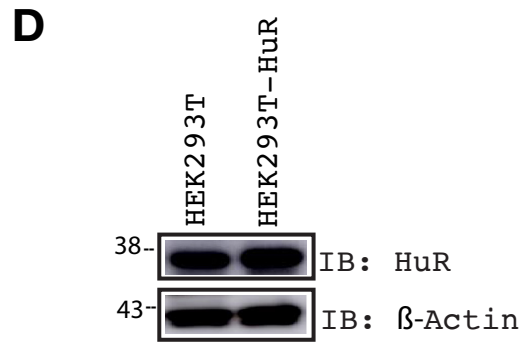
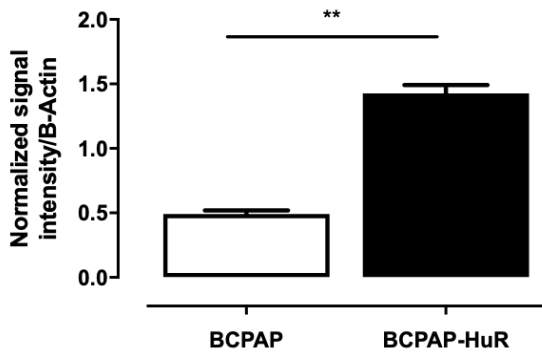
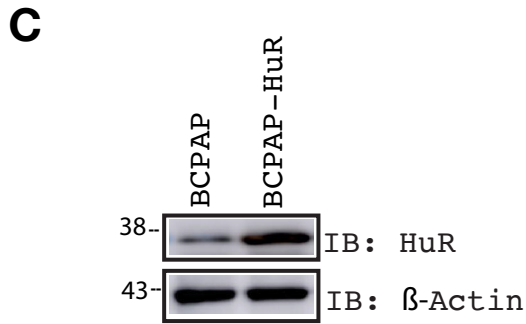
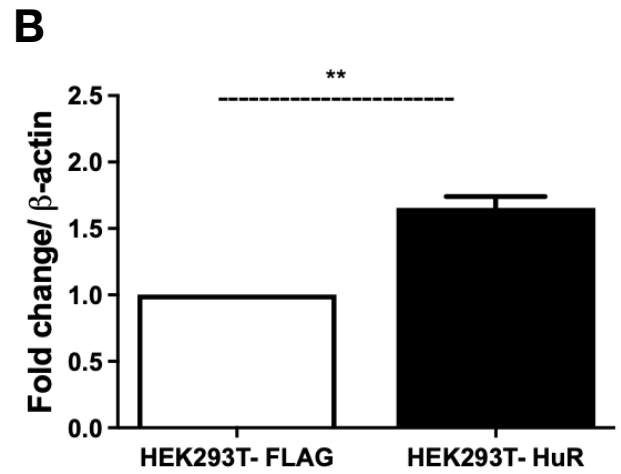
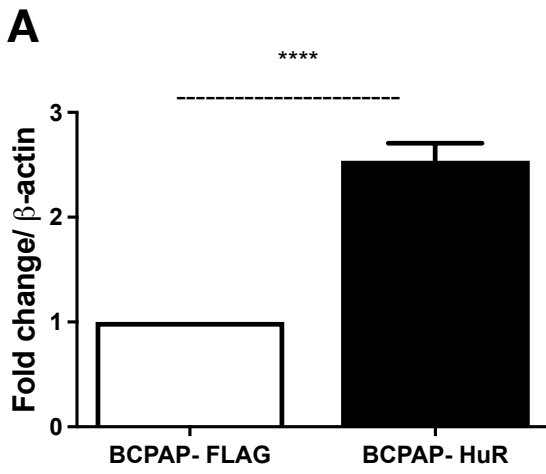


## **Supplementary Material**

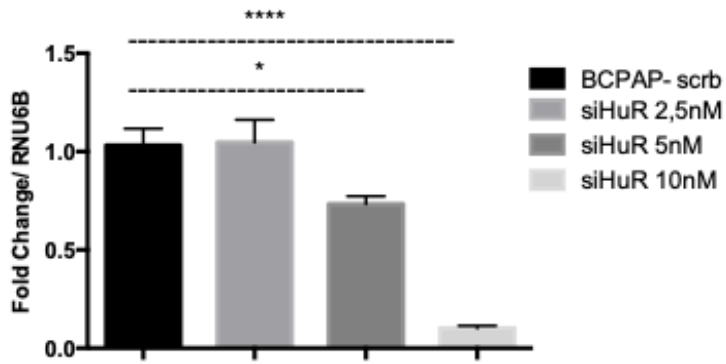
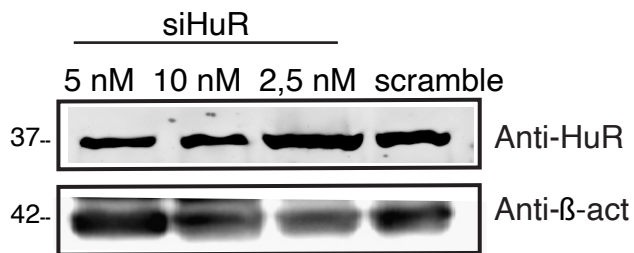
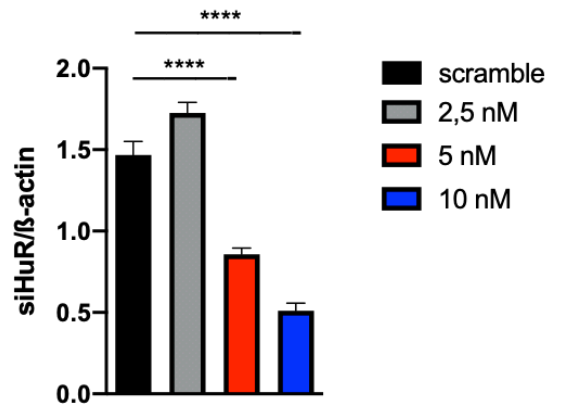
# **Human Antigen R (HuR) Facilitates miR-19 Synthesis and Affects Cellular Kinetics in Papillary Thyroid Cancer**

Guilherme Henrique Gatti da Silva   Maria Gabriela Pereira dos Santos   Helder Yudi Nagasse  
Patricia Pereira Coltri

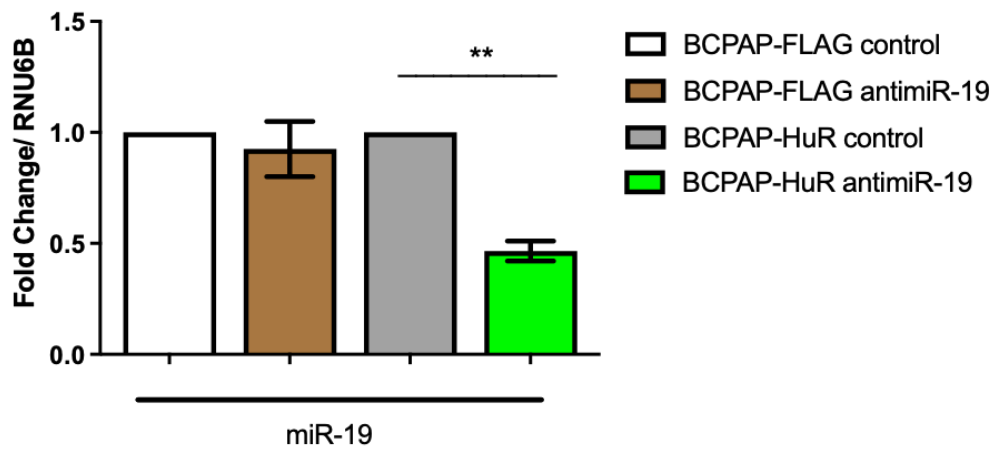
Departamento de Biologia Celular e do Desenvolvimento, Instituto de Ciências Biomédicas, Universidade de São Paulo,  
São Paulo, Brazil



**Supplementary Figure 1.** Confirmation of FLAG-HuR over-expression in (A, C) BCPAP and (B, D) HEK-293T cells using qPCR and western blot. (A, B) Cell lines transfected with empty pFLAG were used as controls (white bars). The amplification of  $\beta$ -actin was used to normalize Ct values. The y-axis represents the fold change of expression calculated after normalization. Error bars represent standard deviations calculated from three independent measurements. (C, D) Western blot using anti-HuR and anti- $\beta$ -actin were performed with the control and HuR over-expression cell lines, and optical densitometry was calculated using Image J software. The y-axis shows the signal intensity after  $\beta$ -actin normalization. \* $P < 0.05$ , \*\* $P < 0.005$ , \*\*\* $P < 0.0005$ .

**A****B****C**

**Supplementary Figure 2.** Confirmation of HuR knockdown. (A) qPCR analysis of HuR mRNA knockdown in BCPAP cells using siRNA-HuR (siHuR) at 2.5, 5, and 10 nM concentrations. HuR mRNA levels were assessed by qPCR with specific primers and normalization was performed with RNU6B amplification; BCPAP transfected with scrambled siRNA was used as a control (BCPAP-scrb). (B) HuR protein knockdown was analyzed after the use of 2.5, 5 and 10 nM siHuR by western blot using anti-HuR (30 kDa) and anti- $\beta$ -actin as endogenous control (42 kDa). Cells transfected with scrambled siRNA were used as a control. (C) Optical densitometry was calculated using Image J software. The y-axis shows the signal intensity after  $\beta$ -actin normalization; \*\*\*\*  $P < 0.0005$ ; \* $P < 0.05$ .



**Supplementary Figure 3.** Confirmation of *miR-19a* inhibition in BCPAP-HuR cells. qRT-PCR analysis of *miR-19a* using BCPAP-FLAG (white), BCPAP-FLAG anti*miR-19a* (brown), BCPAP-HuR (grey), and BCPAP-HuR anti*miR-19a* (green). *miR-19a* levels were assessed using SYBR Green and specific primers. The y-axis represents the fold change of expression calculated after normalization with RNU6B primers. BCPAP-FLAG and BCPAP-HuR were used as controls to calculate *miR-19a* levels on the respective groups after anti*miR-19a* transfection. Error bars represent standard deviations calculated from three independent measurements. **\*\* $P < 0.005$ .**

**Supplementary Table S1.** Oligonucleotide sequences used in this work

<b>Oligo</b>	<b>Sequence (5'-3')</b>	<b>Source</b>
miR-17a - F	ATAGCCTCGAGGTCAGAATAATG	this work
miR-17a - R	ATGATAAGCTTGTCACCATAATG	this work
miR-18 - F	ATAGCCTCGAGTGTCTAAGG	[1]
miR-18 - R	ATGATAAGCTTTGCCAGAAGG	[1]
miR-19a - F	ATAGCCTCGAGGCAGTCCTCTGTTAG	[1]
miR-19a - R	ATGATAAGCTTGCAGGCCACCATCAG	[1]
miR-92 - F	ATAGCCTCGAGCTTTCTACAC	this work
miR-92 - R	ATGATAAGCTTCCAAACTCAAC	this work
RNU6B - F	CTCGCTTCGGCAGCACATATAC	this work
RNU6B- R	GGAACGCTTCACGAATTTGCGTG	this work
HuR - F	GACTACAGGTTTGTCCAGAG	this work
HuR - R	GGGGGTTTATGACCATTGAA	this work
B-actin - F	ACCTTCTACAATGAGCTGCG	this work
B- actin - R	CCTGGATAGCAACGTACATGG	this work
hsa-miR19a	UGUGCAAUUAUGCAAACUGA	Thermo
hsa-miR19b	UGUGCAAUCCAUGCAAACUGA	Thermo
hsa-miR18	UAAGGUGCAUCUAGUGCAGAUAG	Thermo
hsa-miR423	AGCUCGGUCUGAGGCCCCUCAGU	Thermo
anti-miR-19a	commercial	Ambion cat# 4464084
anti-miR-negative control #1	commercial	Ambion cat# 4464076
siHuR	UGAACUACGUGACCGCAATT	Thermo cat# 4390824
siRNA-negative control	commercial	Thermo cat# 4390843

1. Paiva MM, Kimura ET, Coltri PP: miR18a and miR19a Recruit Specific Proteins for Splicing in Thyroid Cancer Cells. *Cancer Genomics Proteomics* 2017;14(5):373-381.