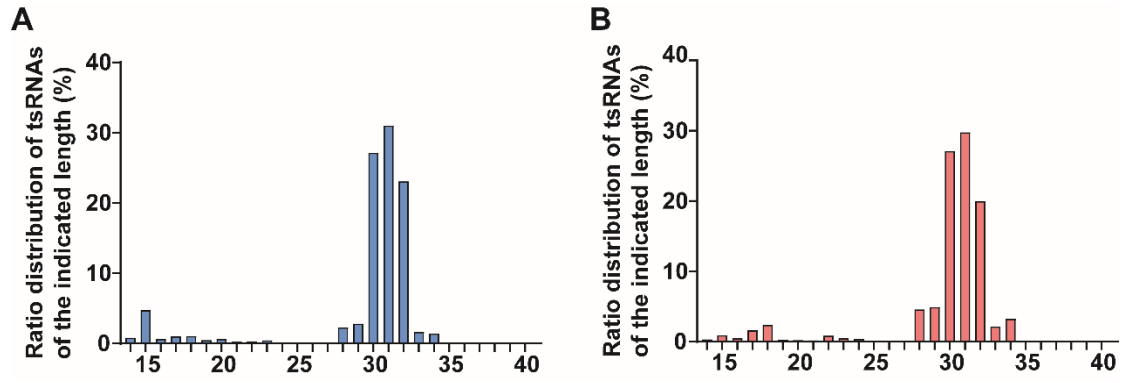


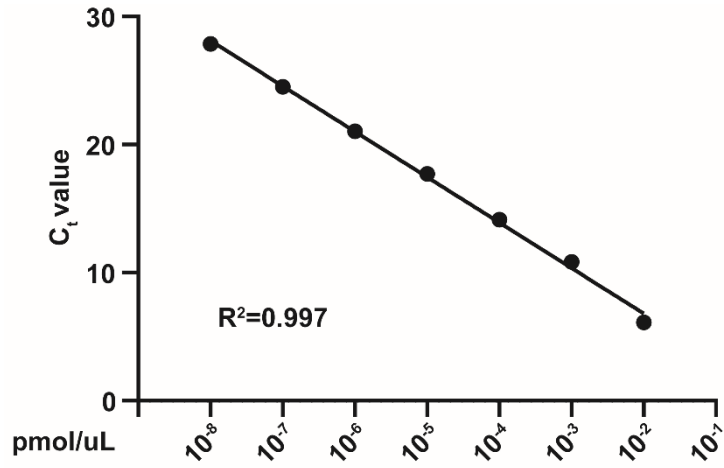
Table s1 The 17 significant differentially expressed tsRNAs in serum

tRF_ID	tRF_Sequence	Type	lg(fold change) (T/N)
tRF-Pro-AGG-004	GGCTCGTTGGTCTAGGGGTATGATTCTCGC	tRF-5c	2.75
tRF-Pro-AGG-002	GGCTCGTTGGTCTAGGGGTATGATTCTC	tRF-5c	1.38
tRF-Leu-CAG-002	ATCCCACTCCTGACACCA	tRF-3a	1.34
tRF-Pro-AGG-005	GGCTCGTTGGTCTAGGGGTATGATTCTCGCT	tRF-5c	1.33
tRF-Gly-CCC-043	TCGATTCCCGGGCGGCCACCA	tRF-3b	1.29
tRF-Ile-AAT-019	TCCCCGTACGGGCCACCA	tRF-3a	1.29
tRF-Thr-CGT-009	GGCCCTGTAGCTCAG	tRF-5a	1.23
tRF-Gln-TTG-006	TAGGATGGGGTGTGATAGGTGG	tRF-5b	1.10
tRF-Leu-AAG-002	GGTAGCGTGGCCGAG	tRF-5a	1.10
tRF-His-GTG-009	GCCGTGATCGTATAGTGGTTAGTACTCTGCGT	tRF-5c	1.05
tRF-Val-CAC-010	GCTTCTGTAGTGTAGTGGTTATCACGTTTCGC	tRF-5c	-1.01
tRF-Pro-TGG-003	AGACTTTTTCTCTGACCA	tRF-3a	-1.03
tRF-Leu-TAA-017	ACCAGAATGGCCGAG	tRF-5a	-1.10
tRF-Val-AAC-004	GTTTCCGTAGTGTA	tRF-5a	-1.24
tRF-Ser-GCT-005	GACGAGGTGGCCGA	tRF-5a	-1.24
tRF-Pro-TGG-010	TCGTGGCTACTGTTTT	tRF-1	-1.36
tRF-Ser-GCT-024	GACGAGGTGGCCGAG	tRF-5a	-1.75

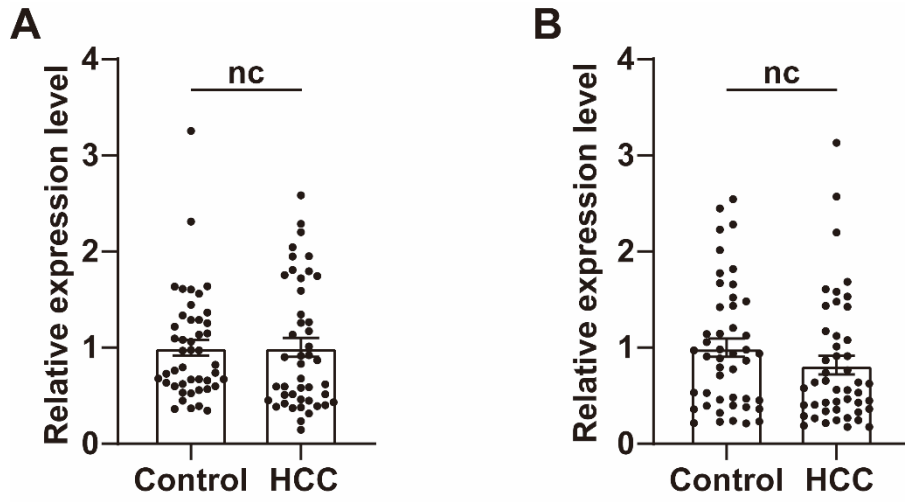
Abbreviations: T/N, CPM-tumor/CPM-control



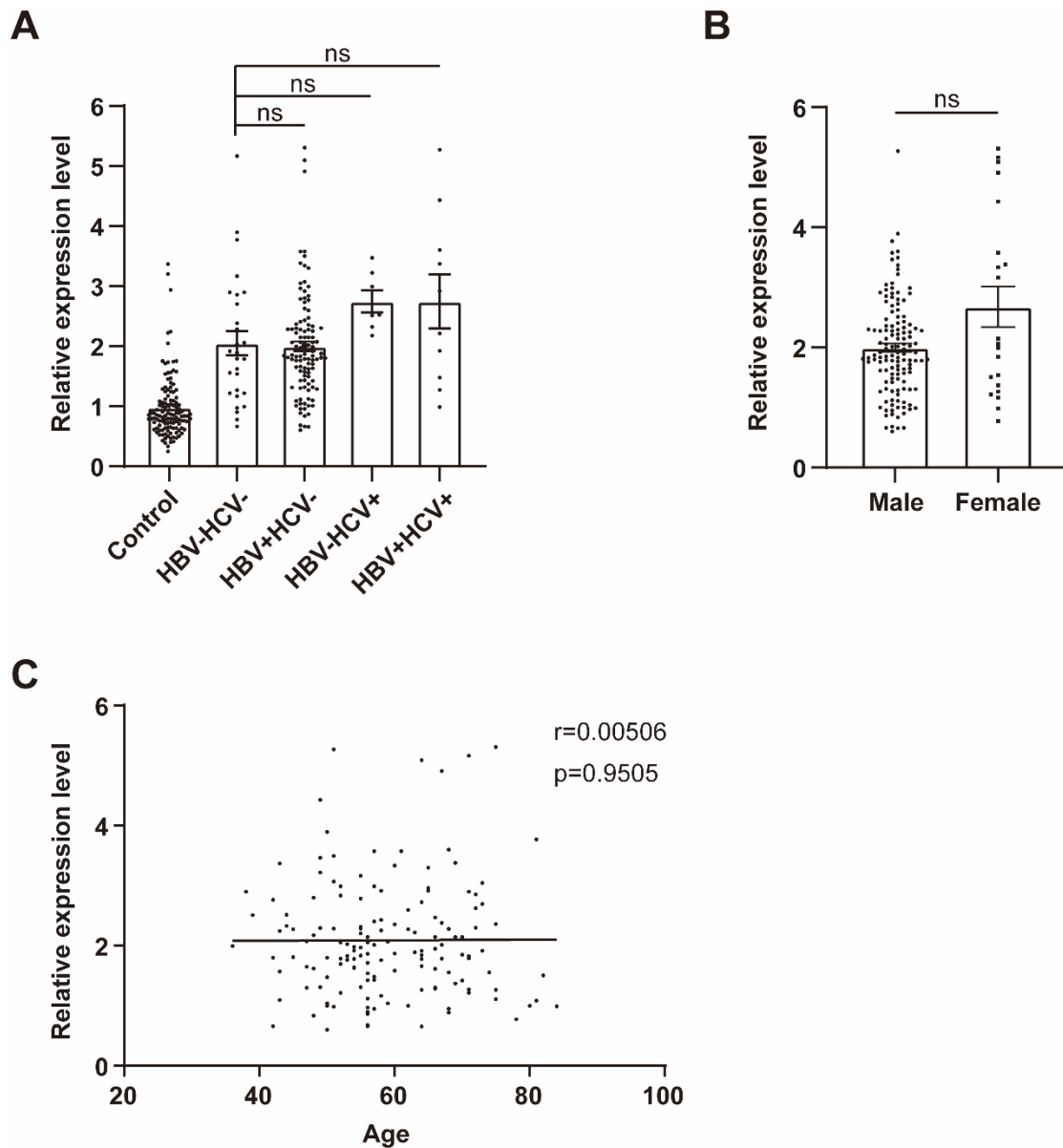
**Fig. S1 Analysis of small RNAs in serum pools of HCC patients and healthy controls.** Length distribution of small RNAs in serum pools from 30 NC patients (A) and 30 HCC controls (B).



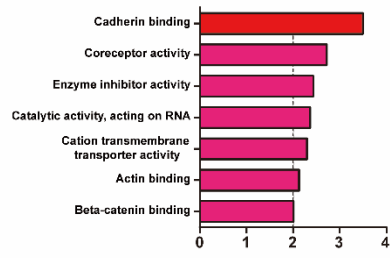
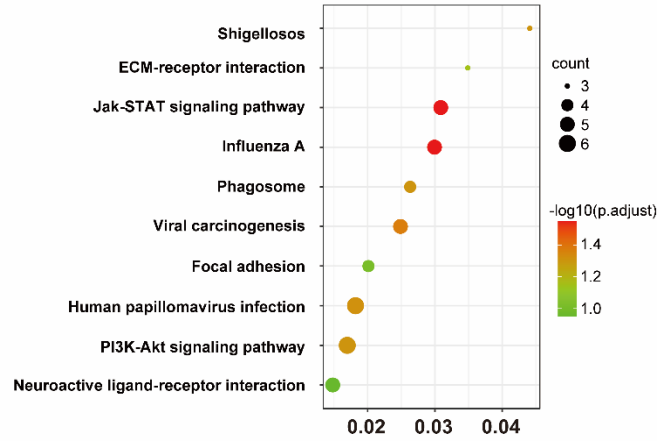
**Fig. S2 Standard curve of tRF-Gln-TTG-006.** The representative standard curve of TaqMan-custom synthesized probe-based RT-qPCR for tRF-Gln-TTG-006. RNA concentration was converted to the actual concentration in serum (R<sup>2</sup>=0.997).



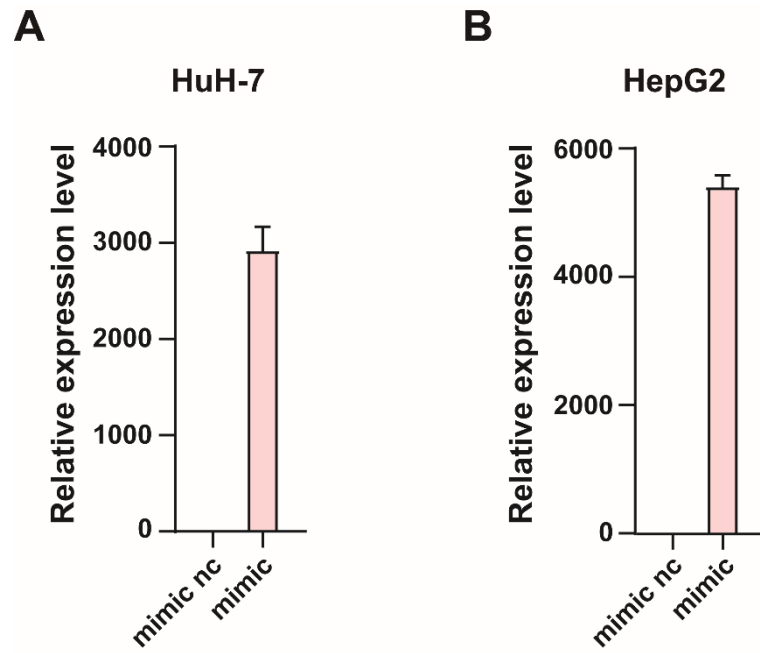
**Fig. S3 qRT-PCR data of tRF-Pro-AGG-005 in serum.** The relative expression of tRF-Pro-AGG-005 in the cohort 1 from The First People's Hospital of Lianyungang (A) and cohort 2 from The Affiliated Drum Tower Hospital of Nanjing University Medical School (B).



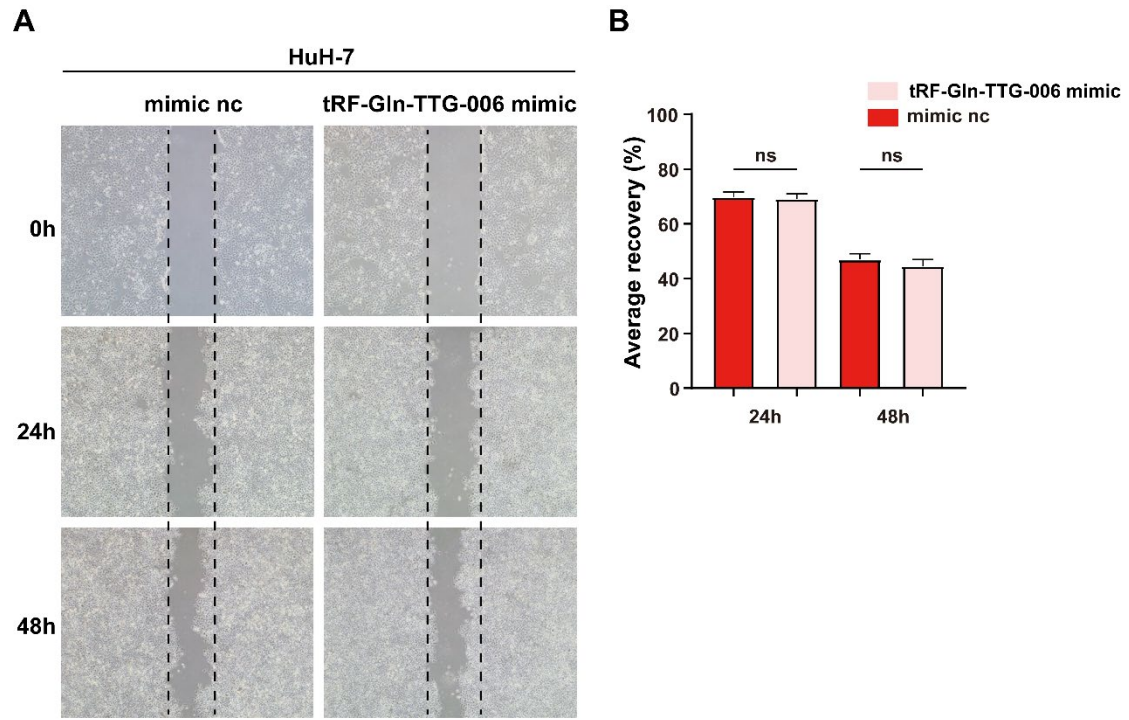
**Fig. S4 Comparison of tRF-Gln-TTG-006 expression level in serum of patients with different factors.** (A) The tRF-Gln-TTG-006 expression level was compared among patients with different virus infection status. (B) The tRF-Gln-TTG-006 expression level was analyzed between male and female HCC patients. (C) The correlation between the age and serum tRF-Gln-TTG-006 level of HCC patients. Negative HBs-Ag, positive HBs-Ag, negative anti-HCV Ab, and positive anti-HCV Ab were defined as HBV-, HBV+, HCC-, and HCV+, respectively.

**A****B**

**Fig. S5 Bioinformatics function assays of tRF-Gln-TTG-006.** (A) Bar plot of GO term of molecular function (target genes of tRF-Gln-TTG-006). (B) A bubble plot of enriched KEGG pathways (target genes of tRF-Gln-TTG-006).



**Fig. S6 Validation of tRF-Gln-TTG-006 mimic transfection efficiency.** qRT-PCR analysis of the expression level of tRF-Gln-TTG-006 in HuH-7 (A) and HepG2 cells (B) that were transfected with mimic nc or tRF-Gln-TTG-006 mimic.



**Fig. S7 Wound healing assays of HuH-7 cells.** Migration ability of HuH-7 cells was analyzed by the wound healing assays (A) and recovery area was calculated (B).