

CORRECTION

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Correction: hsa_circ_0007919 induces LIG1 transcription by binding to FOXA1/TET1 to enhance the DNA damage response and promote gemcitabine resistance in pancreatic ductal adenocarcinoma

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Following publication of the original article [1], the authors found that the grouping tags in Fig. 1A was mis-labeled and led to completely opposite representations, so they would like to correct the picture. The correct figure is given below.

Reference

1. Xu L, Ma X, Zhang X, et al. hsa_circ_0007919 induces LIG1 transcription by binding to FOXA1/TET1 to enhance the DNA damage response and promote gemcitabine resistance in pancreatic ductal adenocarcinoma. *Mol Cancer*. 2023;22:195. <https://doi.org/10.1186/s12943-023-01887-8>.

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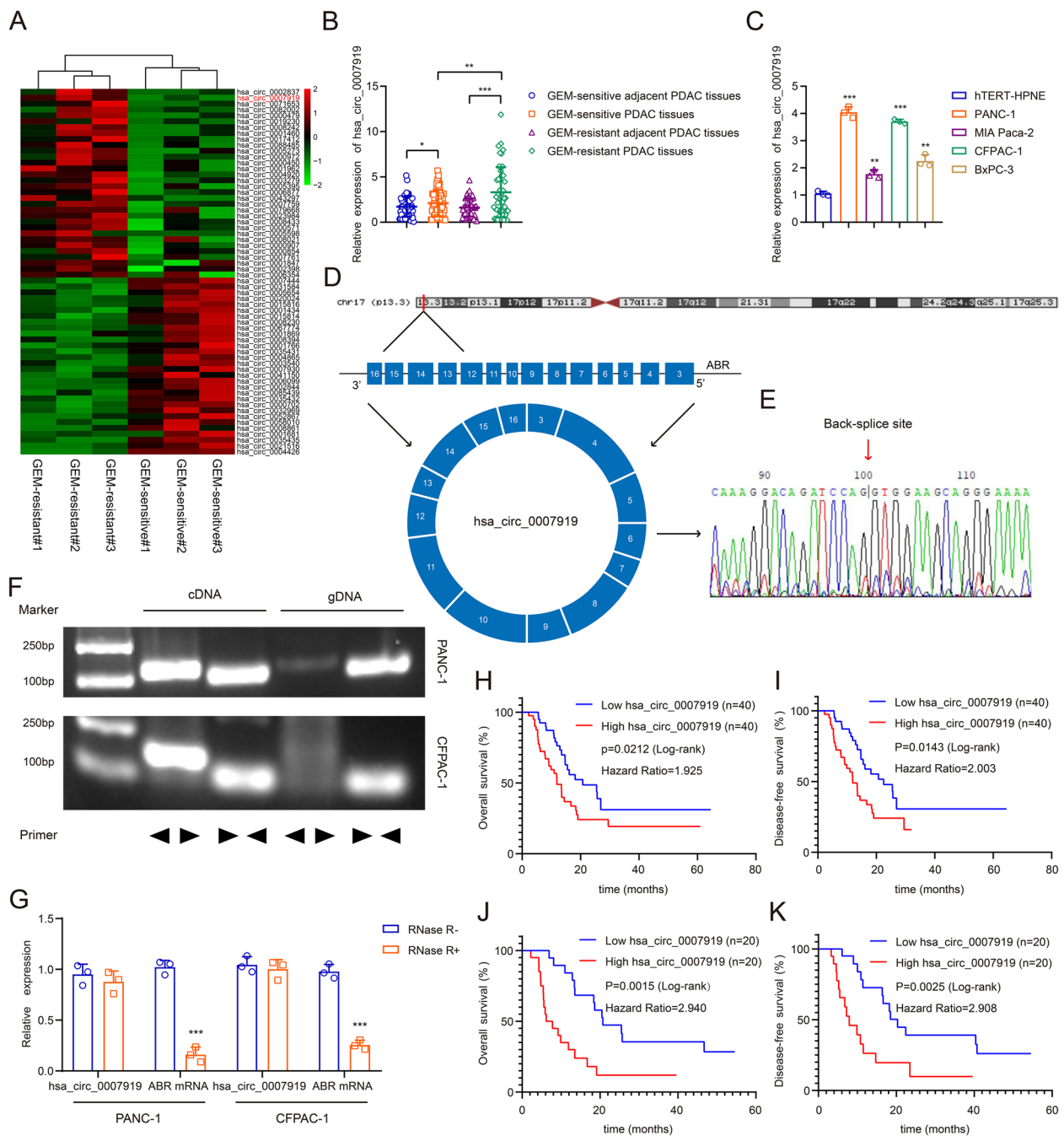


Fig. 1 hsa_circ_0007919 is upregulated in GEM-resistant PDAC and predicts poor prognosis. **(A)** Hierarchical clustering showing differentially expressed circRNAs in GEM-sensitive and GEM-resistant PDAC tissues ($FC > 1$ or < -1 , $p < 0.05$). **(B)** The relative expression of hsa_circ_0007919 in GEM-sensitive and GEM-resistant PDAC tissues and corresponding adjacent PDAC tissues. **(C)** The relative expression of hsa_circ_0007919 in PDAC cells and normal pancreatic cells. **(D)** The genomic location and back-splicing of hsa_circ_0007919. **(E)** The splicing site of hsa_circ_0007919 validated by Sanger-seq. **(F)** PCR and agarose gel electrophoresis analysis of the presence of hsa_circ_0007919 and ABR in cDNA and gDNA samples from PDAC cells. **(G)** Expression of hsa_circ_0007919 and ABR in PDAC cells with or without RNase R treatment. **(H-I)** Kaplan–Meier analysis of the OS rate and DFS rate in PDAC patients with high or low expression of hsa_circ_0007919. **(J-K)** Kaplan–Meier analysis of the OS rate and DFS rate in GEM-resistant PDAC patients with high or low expression of hsa_circ_0007919. Data are the means \pm SDs ($n = 3$ independent experiments), * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$