



## OPEN ACCESS

## EDITED AND REVIEWED BY

Lei Dong,  
Beijing Institute of Technology, China

## \*CORRESPONDENCE

Zuhui Pu,  
✉ pupeter190@163.com  
Yong Ni,  
✉ szniyong@sina.com  
Lisha Mou,  
✉ lishamou@gmail.com

<sup>†</sup>These authors have contributed equally to this work

RECEIVED 15 September 2022

ACCEPTED 11 October 2023

PUBLISHED 23 October 2023

## CITATION

Yao F, Zhan Y, Li C, Lu Y, Chen J, Deng J, Wu Z, Li Q, Song Y, Chen B, Chen J, Tian K, Pu Z, Ni Y and Mou L (2023), Corrigendum: Single-cell RNA sequencing reveals the role of phosphorylation-related genes in hepatocellular carcinoma stem cells. *Front. Cell Dev. Biol.* 11:1045260. doi: 10.3389/fcell.2023.1045260

## COPYRIGHT

© 2023 Yao, Zhan, Li, Lu, Chen, Deng, Wu, Li, Song, Chen, Chen, Tian, Pu, Ni and Mou. This is an open-access article distributed under the terms of the [Creative Commons Attribution License \(CC BY\)](https://creativecommons.org/licenses/by/4.0/). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.

# Corrigendum: Single-cell RNA sequencing reveals the role of phosphorylation-related genes in hepatocellular carcinoma stem cells

Fuwen Yao<sup>1,2†</sup>, Yongqiang Zhan<sup>1†</sup>, Changzheng Li<sup>3†</sup>, Ying Lu<sup>2</sup>, Jiao Chen<sup>2</sup>, Jing Deng<sup>2</sup>, Zijing Wu<sup>2</sup>, Qi Li<sup>2</sup>, Yi'an Song<sup>2</sup>, Binhua Chen<sup>1</sup>, Jinjun Chen<sup>1</sup>, Kuifeng Tian<sup>1</sup>, Zuhui Pu<sup>4\*</sup>, Yong Ni<sup>1\*</sup> and Lisha Mou<sup>1,2\*</sup>

<sup>1</sup>Department of Hepatopancreatobiliary Surgery, Shenzhen Institute of Translational Medicine, Health Science Center, Shenzhen Second People's Hospital, The First Affiliated Hospital of Shenzhen University, Shenzhen, China, <sup>2</sup>Shenzhen Xenotransplantation Medical Engineering Research and Development Center, Shenzhen Institute of Translational Medicine, The First Affiliated Hospital of Shenzhen University, Shenzhen Second People's Hospital, Shenzhen, China, <sup>3</sup>Key Laboratory of Stem Cells and Tissue Engineering, Zhongshan School of Medicine, Sun Yat-sen University, Ministry of Education, Guangzhou, China, <sup>4</sup>Imaging Department, Shenzhen Institute of Translational Medicine, Health Science Center, Shenzhen Second People's Hospital, The First Affiliated Hospital of Shenzhen University, Shenzhen, China

## KEYWORDS

AURKA, EZH2, tyrosine kinase inhibitors, TKI, protein kinases, cell cycle, single-cell RNA sequencing, hepatocellular carcinoma

## A Corrigendum on

### Single-cell RNA sequencing reveals the role of phosphorylation-related genes in hepatocellular carcinoma stem cells

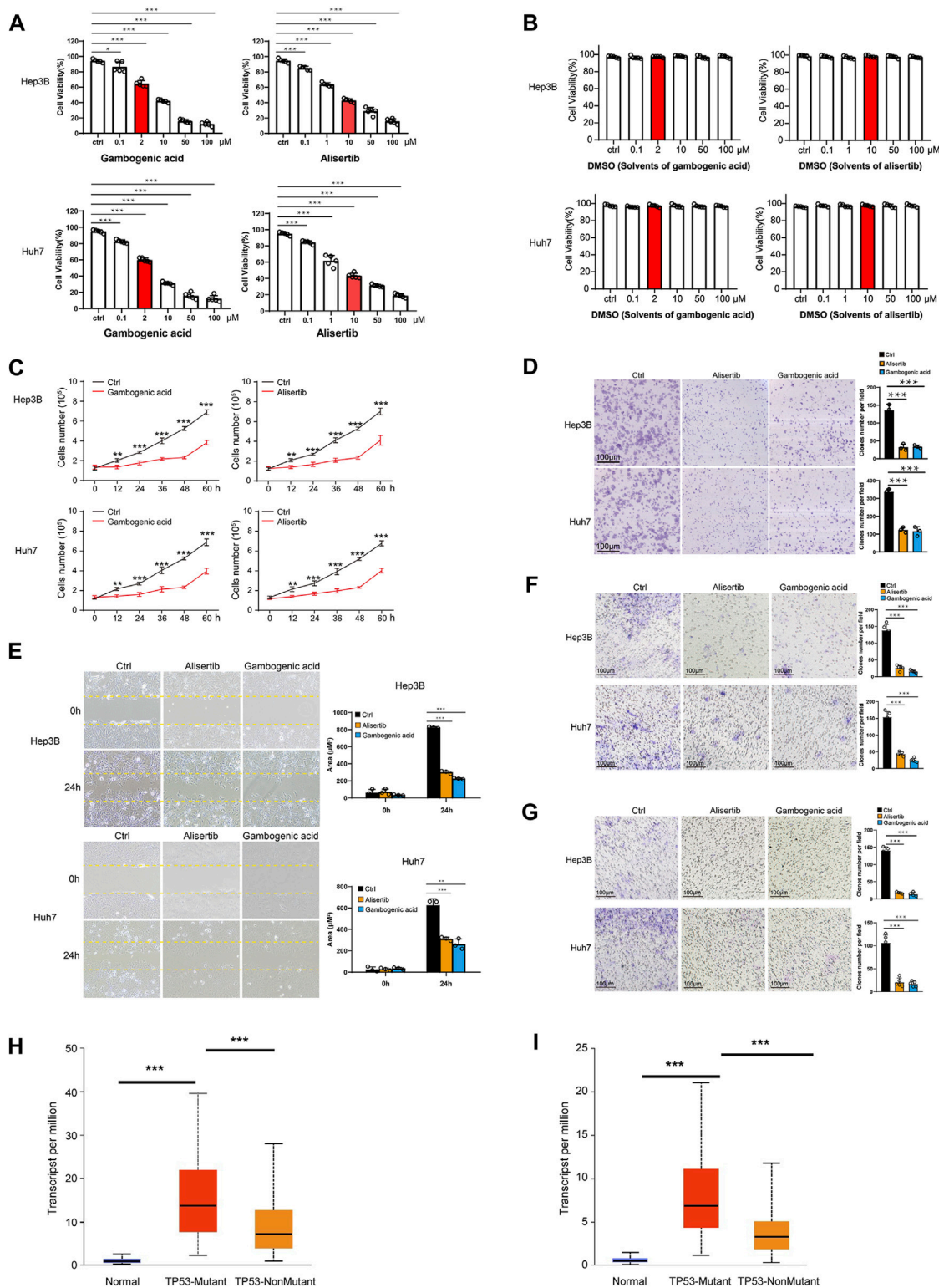
by Yao F, Zhan Y, Li C, Lu Y, Chen J, Deng J, Wu Z, Li Q, Song Y, Chen B, Chen J, Tian K, Pu Z, Ni Y and Mou L (2022). *Front. Cell Dev. Biol.* 9:734287. doi: 10.3389/fcell.2021.734287

In the published article, there was an error in [Figure 7C](#) as published. The red label and black label were reversed. The corrected [Figure 7C](#) and its caption is as follows: “(C) Hep3B and Huh7 cells were treated with gambogic acid (EZH2 inhibitor, 2  $\mu$ M) or alisertib (AURKA inhibitor, 10  $\mu$ M) for 0, 12, 24, 32, 48, and 60 h, and cell viability was determined by Calcein-AM/PI staining assays.”

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

## Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.



**FIGURE 7**

Gambogic acid (EZH2 inhibitor) and alisertib (AURKA inhibitor) inhibit HCC cell proliferation, migration, and invasion. **(A)** Hep3B and Huh7 cells were treated with gambogic acid (EZH2 inhibitor) or alisertib (AURKA inhibitor) at different concentrations (0–100  $\mu\text{M}$ ) for 48 h, and cell viability was determined by Calcein–AM/PI staining assays. **(B)** Hep3B and Huh7 cells were treated with DMSO (solvents of gambogic acid and alisertib) at different concentrations (0–100  $\mu\text{M}$ ) for 48 h, and cell viability was determined by Calcein–AM/PI staining assays. **(C)** Hep3B and Huh7 cells were treated with gambogic acid (EZH2 inhibitor, 2  $\mu\text{M}$ ) or alisertib (AURKA inhibitor, 10  $\mu\text{M}$ ) for 0, 12, 24, 32, 48, and 60 h, and cell viability was determined by Calcein–AM/PI staining assays. **(D)** Colony formation assays were conducted to analyze Hep3B and Huh7 cell proliferation with gambogic acid (2  $\mu\text{M}$ ) or alisertib (10  $\mu\text{M}$ ) treatment. **(E, F)** Wound healing assays were performed to detect the cell migratory abilities of Hep3B and Huh7 cells treated with gambogic acid (2  $\mu\text{M}$ ) or alisertib (10  $\mu\text{M}$ ). **(G)** Transwell assays were performed to detect the cell invasion abilities of Hep3B and Huh7 cells treated with gambogic acid (2  $\mu\text{M}$ ) or alisertib (10  $\mu\text{M}$ ). Data are expressed as the means  $\pm$  s.d. Differences were considered statistically significant if  $p < 0.05$ . ns, no significance, \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ . **(H, I)** Expression of AURKA **(H)** and EZH2 **(I)** in TCGA–LIHC based on TP3 mutation status.