



OPEN ACCESS

EDITED AND REVIEWED BY
Dawei Chen,
University of Kiel, Germany

*CORRESPONDENCE
Xiao Hu,
✉ huxiao202@163.com

†These authors have contributed equally to
this work

RECEIVED 14 January 2025
ACCEPTED 27 January 2025
PUBLISHED 18 February 2025

CITATION

Fu K, Su J, Zhou Y, Chen X and Hu X (2025)
Corrigendum: The role of epigenetic regulation
in pancreatic ductal adenocarcinoma
progression and drug response: an integrative
genomic and pharmacological prognostic
prediction model.
Front. Pharmacol. 16:1560529.
doi: 10.3389/fphar.2025.1560529

COPYRIGHT

© 2025 Fu, Su, Zhou, Chen and Hu. This is an
open-access article distributed under the terms
of the [Creative Commons Attribution License
\(CC BY\)](#). 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: The role of epigenetic regulation in pancreatic ductal adenocarcinoma progression and drug response: an integrative genomic and pharmacological prognostic prediction model

Kang Fu[†], Junzhe Su[†], Yiming Zhou, Xiaotong Chen and Xiao Hu*

Department of Hepatobiliary Pancreatic Surgery, The Affiliated Hospital of Qingdao University, Qingdao, China

KEYWORDS

pancreatic ductal adenocarcinoma, epigenetic regulation, single-cell RNA sequencing, machine learning, prognostic model, tumor microenvironment, drug sensitivity

A Corrigendum on

[The role of epigenetic regulation in pancreatic ductal adenocarcinoma progression and drug response: an integrative genomic and pharmacological prognostic prediction model](#)

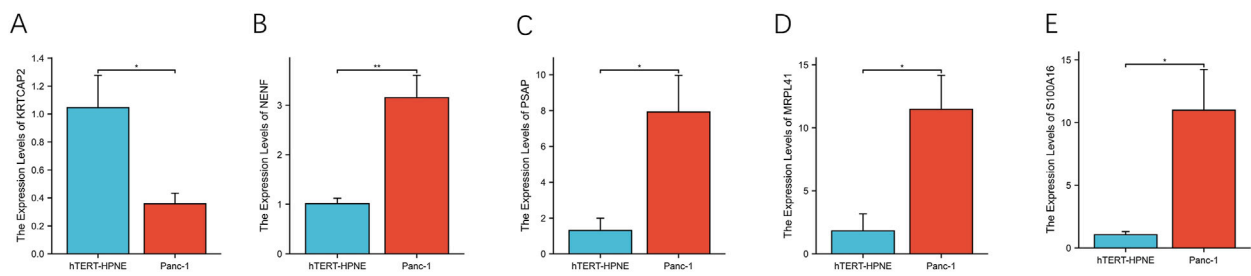
by Fu K, Su J, Zhou Y, Chen X and Hu X (2024). *Front. Pharmacol.* 15:1498031. doi: 10.3389/fphar.2024.1498031

In the published article, there was an error in [Figure 13](#) as published. Due to a data format inconsistency between CSV and TXT files during analysis, an undetected empty row in the header resulted in a misalignment of data. This affected the gene names on the y-axis and cell types on the x-axis, causing a one-row shift in visualization, which led to incorrect matching of color representation with corresponding samples. The corrected [Figure 13](#) and its caption appear below.

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 13**

Differential expression analysis of prognostic genes in pancreatic cell lines (A–E). The relative mRNA expression levels of KRTCAP2, NENF, PSAP, MRPL41, and S100A16 were quantified by qRT-PCR in pancreatic cancer cell line PANC-1 and normal pancreatic epithelial cell line hTERT-HPNE.