



OPEN ACCESS

APPROVED BY
Frontiers Editorial Office,
Frontiers Media SA, Switzerland

*CORRESPONDENCE
Min Chen,
✉ edchen99@gmail.com

[†]These authors have contributed equally
to this work

RECEIVED 02 April 2023
ACCEPTED 24 May 2023
PUBLISHED 10 July 2023

CITATION
Yang J, Xu J, Zhang L, Li Y and Chen M
(2023), Corrigendum: Identifying key
m⁶A-methylated lncRNAs and genes
associated with neural tube defects via
integrative MeRIP and RNA
sequencing analyses.
Front. Genet. 14:1198975.
doi: 10.3389/fgene.2023.1198975

COPYRIGHT
© 2023 Yang, Xu, Zhang, Li and Chen.
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: Identifying key m⁶A-methylated lncRNAs and genes associated with neural tube defects via integrative MeRIP and RNA sequencing analyses

Jing Yang^{1†}, Jing Xu^{2,3†}, Luting Zhang³, Yingting Li³ and
Min Chen^{3*}

¹Department of Obstetrics, Affiliated Xiaoshan Hospital, Hangzhou Normal University, Hangzhou, Zhejiang, China, ²Department of Obstetrics and Gynecology, The First Affiliated Hospital of Kunming Medical University, Kunming, Yunnan, China, ³Department of Obstetrics and Gynecology, Department of Fetal Medicine and Prenatal Diagnosis, Key Laboratory for Major Obstetric Diseases of Guangdong Province, The Third Affiliated Hospital of Guangzhou Medical University, Guangzhou, Guangdong, China

KEYWORDS

neural tube defects, N6-methyladenosine modification, long non-coding RNA, functional enrichment analysis, methylated RNA immunoprecipitation sequencing

A Corrigendum on

Identifying key m⁶A-methylated lncRNAs and genes associated with neural tube defects via integrative MeRIP and RNA sequencing analyses

by Yang J, Xu J, Zhang L, Li Y and Chen M (2022) *Front. Genet.* 13:974357. doi: 10.3389/fgene.2022.974357

In the published article, there was an error in the **author list**. Author Xu J was erroneously excluded. The corrected author list appears below.

“Yang J^{1†}, Xu J^{2†}, Zhang L³, Li Y³, Chen M^{3*}

These authors contributed equally to this work”

The **Author Contribution** statement has also been updated to reflect Xu J’s contribution to the study, and appears below:

“JY, JX, and MC designed the study. LZ and YL performed the experiment. JY and LZ analyzed the data. JY, JX, and MC wrote the manuscript. All authors read and approved the final article.”

In the published article, Xu J’s affiliations were erroneously omitted. As well as having **affiliation 3**, they should also have “Department of Obstetrics and Gynecology, The First Affiliated Hospital of Kunming Medical University, Kunming, Yunnan, China”.

In the published article, there was an error in the **Funding** statement. The funder “Yunnan Province Science and Technology Program (No. 202101AY070001-121)” was erroneously omitted. The correct Funding statement appears below:

“This study was supported by the Guangzhou Science and Technology Program (No. 202102010129), Yunnan Province Science and Technology Program (No. 202101AY070001-121) and the Hangzhou Science and Technology Program (No. 20211231Y121)”.

The authors apologize for these errors and state that they do 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.