



Corrigendum: Transcriptome-Wide Annotation of m⁵C RNA Modifications Using Machine Learning

Jie Song^{1,2†}, Jingjing Zhai^{1†}, Enze Bian^{3†}, Yujia Song³, Jiantao Yu³ and Chuang Ma^{1,2*}

¹ State Key Laboratory of Crop Stress Biology for Arid Areas, Center of Bioinformatics, College of Life Sciences, Northwest A&F University, Shaanxi, China, ² Key Laboratory of Biology and Genetics Improvement of Maize in Arid Area of Northwest Region, Ministry of Agriculture, Northwest A&F University, Shaanxi, China, ³ College of Information Engineering, Northwest A&F University, Shaanxi, China

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Giovanni Nigita,
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*Correspondence:

Chuang Ma
chuangma2006@gmail.com

[†]These authors have contributed
equally to this work

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A corrigendum on

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by Song, J., Zhai, J., Bian, E., Song, Y., Yu, J., and Ma, C. (2018). *Front. Plant Sci.* 9:519.
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In the original article, there was an error, the word “reversible” is misleading. A correction has been made to the Abstract and the Introduction, paragraph 2.

Though high-throughput experimental technologies have been developed and applied to profile m⁵C modifications under certain conditions, transcriptome-wide studies of m⁵C modifications are still hindered by the dynamic nature of m⁵C and the lack of computational prediction methods.

Second, because of the dynamic nature of m⁵C (Wang and He, 2014), existing high-throughput sequencing technologies can only capture a snapshot of RNA modifications under certain experimental conditions, and cover just a small fraction of the whole transcriptome of a given sample (Zhou et al., 2016), resulting in the generation of significant numbers of false negatives (non-detected true m⁵C modifications).

The authors apologize for the mistake. This error does not change the scientific conclusions of the article in any way. The original article has been updated.

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Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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