

CORRECTION

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# Correction: MethylC-analyzer: a comprehensive downstream pipeline for the analysis of genome-wide DNA methylation

Rita Jui-Hsien Lu<sup>1,2†</sup>, Pei-Yu Lin<sup>1†</sup>, Ming-Ren Yen<sup>1†</sup>, Bing-Heng Wu<sup>1</sup> and Pao-Yang Chen<sup>1\*</sup> 

**Correction:** *Botanical Studies* (2023) 64:1  
<https://doi.org/10.1186/s40529-022-00366-5>

In the original publication of the article (Lu et al. 2023) Fig. 3 was incorrectly published. The corrected Fig. 3 is given below.

The original article (Lu et al. 2023) has been corrected.

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<sup>†</sup>Rita Jui-Hsien Lu, Pei-Yu Lin and Ming-Ren Yen have equal contribution.

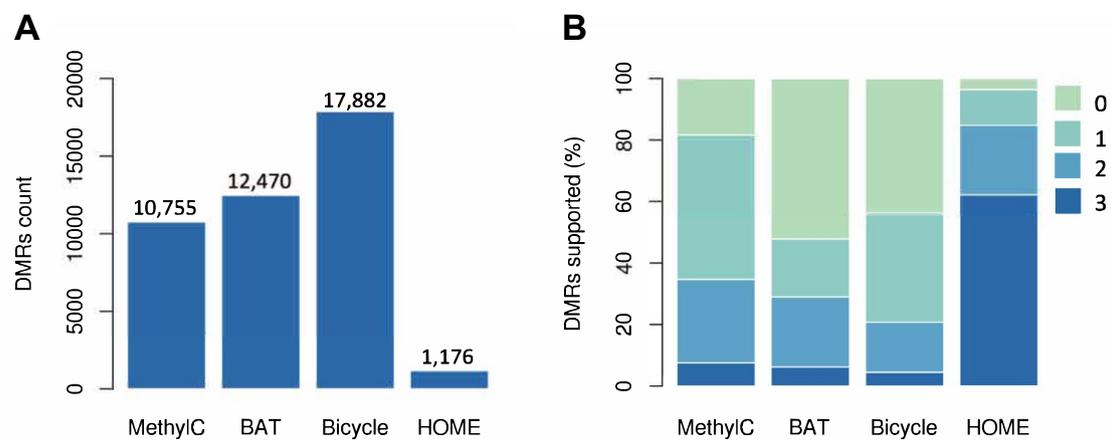
The original article can be found online at <https://doi.org/10.1186/s40529-022-00366-5>.

\*Correspondence:

Pao-Yang Chen  
paoyang@gate.sinica.edu.tw

<sup>1</sup> Institute of Plant and Microbial Biology, Academia Sinica, Taipei 115, Taiwan

<sup>2</sup> Department of Medicine, Washington University in St. Louis, St. Louis, MO, USA



**Fig. 3** DMR calling comparison. **A** Number of CG DMRs called by MethyIC-analyzer, BAT, Bicycle, and HOME using the Arabidopsis WGBS data. **B** The percentage of DMRs confirmed by the DMRs calling tools. The color key indicated the number of other DMR tools detected the same DMR. For example, "0" is the set of DMRs predicted by only one caller, and "3" is the set of DMRs predicted by all callers

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#### Reference

Lu RJH, Lin PY, Yen MR, Wu BH, Chen PY (2023) MethyIC-analyzer: a comprehensive downstream pipeline for the analysis of genome-wide DNA methylation. *Bot Stud* 64:1. <https://doi.org/10.1186/s40529-022-00366-5>

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