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

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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.

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

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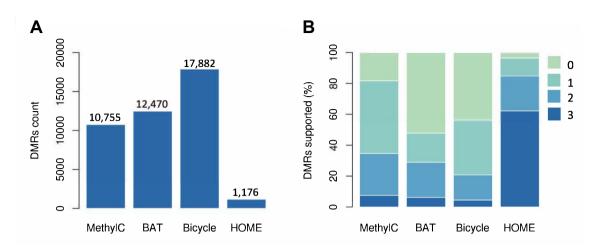


Fig. 3 DMR calling comparison. **A** Number of CG DMRs called by MethylC-analyzer, BAT, Bicycle, and HOME using the Arabidopsis WGBS data. **B** The percentage of DMRs confirmed by the DMRs calling tools. The color key indicated the number of other DMR tools detected the same DMR. For example, "0" is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

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