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# Erratum to: DeepCpG: accurate prediction of single-cell DNA methylation states using deep learning

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#### **Erratum**

After publication of this article [1] it was noticed that the legend of Fig. 3 is incorrect. The circles should be labelled as 'De novo' and triangles as 'Annotated'.

The original article has been updated.

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### Reference

 Angermueller C, Lee HJ, Reik W, Stegle O. DeeCpG: accurate prediction of single-cell DNA methylation states using deep learning. Genome Biol. 2017;18:67

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