CORRECTION   **Open Access**

Correction to: ATAC2GRN: optimized ATAC-seq and DNase1-seq pipelines for rapid and accurate genome regulatory network inference

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Correction to: BMC Genomics
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Following the publication of this article [1], the authors informed us of the following typographical errors in the Results section (the changes are marked in bold).

1) The sub-heading "Footprints increase linearly with reads – ChIP-seq recovery yields diminishing returns with read depths greater than 60 million readz" should be "Footprints increase linearly with **reads** – ChIP-seq recovery yields diminishing returns with read depths greater than 60 million **reads**".

2) The sentence "ROC AUC (area under the repeater operating characteristic curve), a measure of a predictor's ability to predict true positives, increased non-linearly as read depths increased (Fig. 2b)" should read "ROC AUC (**area under the receiver operating characteristic curve**), a measure of a predictor's ability to predict true positives, increased non-linearly as read depths increased (Fig. 2b)."

Reference
1. Pranzatelli, et al. ATAC2GRN: optimized ATAC-seq and DNase1-seq pipelines for rapid and accurate genome regulatory network inference. BMC Genomics. 2018;19:563. https://doi.org/10.1186/s12864-018-4943-z.

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