

AUTHOR CORRECTION

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Author Correction: Regulatory analysis of single cell multiome gene expression and chromatin accessibility data with scREG

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Following publication of the original paper [1], the authors have reported an error in reference genome version of the HiC data used for validation of the RE-TG interactions. After using the correct version of the HiC anchor locations, the result in Fig. 4D, supplementary Figure S11, and S12 are all improved.



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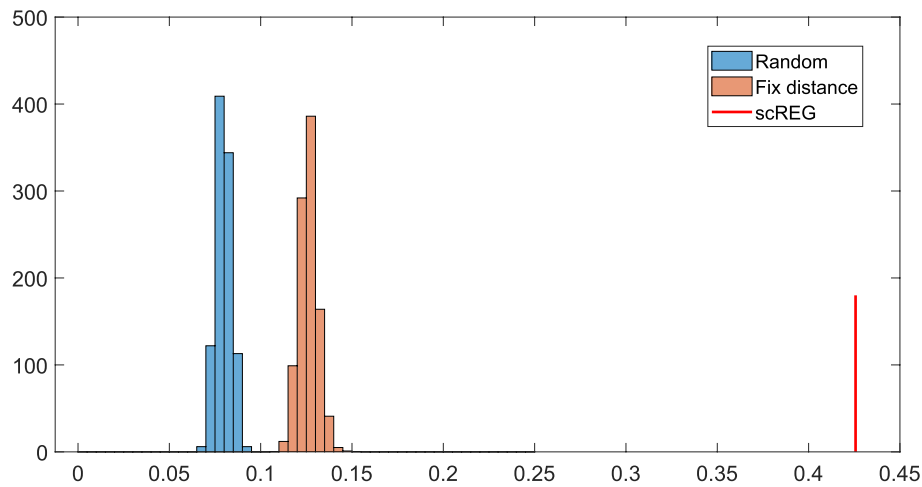


Fig. 4 D. Validation of RE-TG prediction by HiC data on Naïve CD4 T cell

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s13059-022-02786-9>.

Additional file 1: Supplementary Figure S11. Validation of RE-TG prediction by HiC data. Consistency ratio of predicted RE and promoter capture HiC data on different cell types of. We can see in all cell type, scREG predict the greatest number of same RE-TG pairs as previously found promoter capture HiC data. set select distribution distance same with scREG, does improve the performance. **Supplementary Figure S12.** AUROC and AUPR of RE-TG prediction by taking HiC data as ground truth.

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Reference

1. Duren Z, Chang F, Naqing F, Xin J, Liu Q, Wong WH. Regulatory analysis of single cell multiome gene expression and chromatin accessibility data with scREG. *Genome Biol.* 2022;23:114.

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