Genome Biology

CORRECTION　　　　　　　　　　　　　　　　　　　　　　　　　　**Open Access**

Author Correction: Feature selection and dimension reduction for single-cell RNA-Seq based on a multinomial model

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Following publication of the original paper [1], an error was identified. In the original version of this manuscript, we referred to the Zheng 10x datasets as FACS-purified. However, based on Supplemental Table 8 of the Zheng et al. (2017) publication, the cells were actually purified by cell-type specific isolation kits that did not involve sorting by fluorescence. The authors thank Miriam Shiffman for identifying this error.

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1.　Townes FW, Hicks SC, Aryee MJ, et al. Feature selection and dimension reduction for single-cell RNA-Seq based on a multinomial model. Genome Biol. 2019;20:295. https://doi.org/10.1186/s13059-019-1861-6.

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