



Corrigendum: A statistical learning method for simultaneous copy number estimation and subclone clustering with single-cell sequencing data

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The authors would like to correct erroneous text in the Discussion and Methods sections, respectively. The corrected text is as follows and has been updated in the revised article online.

In the Discussion section, third paragraph, ninth sentence:

FLCNA uses the observed mean value of each cell across bins as a reference, providing increased sensitivity at detecting CNA signals.

In Methods, first subsection, final sentence:

In the final preprocessing step, FLCNA computes the ratio of the normalized read counts to their sample-specific mean, the logarithm transformation of which (i.e., $\log_2 R$) represents the main signal intensities.

These corrections do not alter the results or conclusions presented in the original article. The authors apologize for the inconvenience.

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