

ERRATUM

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Erratum to: Quartz-Seq: a highly reproducible and sensitive single-cell RNA sequencing method, reveals non-genetic gene-expression heterogeneity

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Erratum

After publication of our article [1], we noticed some errors. In this manuscript, we amplified cDNA with 41.67 nmol/l RT primer and 70 nmol/l tagging primer for single-cell Quartz-Seq, and not pmol/l as originally stated. In addition, two mathematical expressions were inadvertently omitted.

Thus, in the section *Whole-transcript amplification for single-cell Quartz-Seq*, the following are correct:

Immediately after the second centrifugation, 0.8 μ l of priming buffer (1.5 \times PCR buffer with MgCl₂ (TaKaRa Bio), 41.67 nmol/l of the RT primer (HPLC-purified; Table 1), 4 U/ μ l of RNase inhibitor (RNasin Plus; Promega Corp., Madison, WI, USA), and 50 μ mol/l dNTPs were added to each tube.

And

We then added 23 μ l of the second-strand buffer (1.09 \times MightyAmp Buffer v2 (TaKaRa), 70 nmol/l tagging primer (HPLC-purified; Table 1), and 0.054 U/ μ l MightyAmp DNA polymerase (TaKaRa)) to each tube.

In the section *Bioinformatics analysis*, the equations should appear as follows:

The MI is considered the Kullback–Leibler distance from the joint probability density to the product of the marginal probability densities as follows:

$$MI(X, Y) = E_{f(x,y)} \left\{ \log \frac{f(x,y)}{f(x)f(y)} \right\} \quad (1)$$

The MI is always non-negative, symmetric, and equal to 0 only if X and Y are independent. The MI can be represented as a summation of entropies:

$$MI(X, Y) = H(X) + H(Y) - H(X, Y) \quad (2)$$

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Reference

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