Correction to: Detect tissue heterogeneity in gene expression data with BioQC

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Correction

After the publication of this work [1], a mistake was noticed in the Eq. 1. Given an \( m \times n \) expression matrix with \( m \) genes and samples of \( n \) tissues, the correct definition of the Gini index for gene \( i \) is:

\[
G_i = \frac{1}{n} \left( \frac{1}{n+1} \left( \frac{\sum_{j=1}^{n}(n+1-j)x_{ij}}{\sum_{j=1}^{n}x_{ij}} \right) \right),
\]

(1)

where \( x_{ij} \) is the \( j \)th value in the non-descending ordered vector of \( x_{i} (i = 1, \ldots, m, j = 1, \ldots, n) \). In the original version of the manuscript, the variable \( j \) in the parentheses of the nominator was erroneously written as \( i \).

The authors apologize for the mistake and thank Mr. Tao Fang for pointing out this mistake.

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Reference

1. Zhang JD, et al. Detect tissue heterogeneity in gene expression data with BioQC. BMC Genomics. 2017;18:277. https://doi.org/10.1186/s12864-017-3661-2.

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