



## Corrigendum: Human primitive brain displays negative mitochondrial-nuclear expression correlation of respiratory genes

Gilad Barshad, Amit Blumberg, Tal Cohen, et al.

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## Corrigendum

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### **Corrigendum: Human primitive brain displays negative mitochondrial-nuclear expression correlation of respiratory genes**

Gilad Barshad, Amit Blumberg, Tal Cohen, and Dan Mishmar

In the above-mentioned article, the authors would like to clarify the details of how the gene expression normalization was calculated.

The following corrections have been made in the revised article and the Revised [Supplemental Material](#) online:

A. In the Methods subsection entitled “Control for age, gender, and cause of death,” the text has been changed as follows:

#### **Control for age, gender, and cause of death**

To control for the possible contribution of age, gender, and cause of death to gene expression patterns, we normalized for these factors using linear regression (see below), such that the calculated residual expression per gene reflected age-/gender-/cause-of-death-independent gene expression. To this end we first divided the RPKM values of each sample by the sum of RPKM values associated with a given gene across all samples. In this way, we defined the expression value of each gene in a given sample as a fraction of its expression out of the sum of its expression values in all available samples. Hence, when calculating correlation of gene expression, we asked whether changes in the residual relative expression of genes are correlated.

For gene “*i*” in sample “*S*”, the relative gene expression is calculated as follows:

$$\text{Relative Expression} = \frac{\text{RPKM}(\text{Gene}_i)_{(S)}}{\sum \text{RPKM}(\text{Gene}_i)}$$

B. In the Methods subsection entitled “Analysis of co-expression,” the second sentence has been changed as follows:

Then, we sampled 50 samples from each tissue and calculated Spearman’s rank correlation coefficients ( $\rho_s$ ) between pairs of genes/transcripts according to their 2400 ( $50 \times 48$ ) residual relative expression value vectors.

C. The “RPKM to TPM conversion in RNA-seq data” subsection of the [Supplemental Methods](#) has been removed. Additionally, [Supplemental Figure S1](#) has been revised.

D. Points 3–5 in the README file within [Supplemental Data Set S4](#) have been added to facilitate the use of the code. The revised [Supplemental Data Set S4](#) files have been updated on GitHub ([https://github.com/dmishmar/Barshad\\_2018](https://github.com/dmishmar/Barshad_2018)) and as Revised [Supplemental Material](#).

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