ERRATUM

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Erratum to: DNA methylome profiling of human tissues identifies global and tissue-specific methylation patterns

Kaie Lokk^{1,2,3}, Vijayachitra Modhukur⁴, Balaji Rajashekar⁴, Kaspar Märtens⁴, Reedik Mägi⁵, Raivo Kolde⁴, Marina Koltšina¹, Torbjörn K. Nilsson⁶, Jaak Vilo⁴, Andres Salumets^{7,8,9*} and Neeme Tönisson^{1,2,5*}

Erratum

After the publication of this work [1] it was noticed that Additional file 1 is the same as Additional file 2. Additional file 1 has now been correctly replaced.

Additional file

Additional file 1: Methylation calidation using Sanger sequencing. For validation of the methylation data from BeadChip, 17 genes were chosen, including unmethylated sites (n = 1), fully methylated sites (n = 2), and genes with tDMRs (n = 14) representing 36 CpG sites altogether. The x-axis shows DNA methylation beta-values obtained from BeadChip, and the y-axis shows beta values from Sanger sequencing. (PDF 24 kb)

Author details

¹Institute of Molecular and Cell Biology, University of Tartu, Tartu, Estonia. ²Department of Genetics, United Laboratories, Tartu University Hospital, Tartu, Estonia. ³Estonian Biocentre, Tartu, Estonia. ⁴Institute of Computer Science, University of Tartu, Tartu, Estonia. ⁵Estonian Genome Center, University of Tartu, Tartu, Estonia. ⁶Department of Medical Biosciences, Clinical Chemistry, Umeå University, Umeå, Sweden. ⁷Competence Centre on Reproductive Medicine and Biology, Tartu, Estonia. ⁹Institute of Bio- and Translational Medicine, University of Tartu, Tartu, Estonia.

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Reference

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* Correspondence: andres.salumets@ccrmb.ee; neemet@ut.ee

⁷Competence Centre on Reproductive Medicine and Biology, Tartu, Estonia ¹Institute of Molecular and Cell Biology, University of Tartu, Tartu, Estonia



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