

ERRATUM

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

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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 validation 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)

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Reference

1. Lokk K, Modhukur V, Rajashekar B, Märtens K, Mägi R, Kolde R, et al. DNA methylome profiling of human tissues identifies global and tissue-specific methylation patterns. *Genome Biol.* 2014;15:r54.

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