

CORRIGENDUM

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Corrigendum: Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells

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The parameters described in the “Identification of DMRs” subsection of the Methods of our Article regarding the identification of the non-CG mega-DMRs (differentially methylated regions) should read as follows: “The average methylation level of mC called (1% FDR) in the mCHG sequence context was determined in 1-kb windows (sW). The genome was scanned considering groups of 50 adjacent windows sW. The set of 50 average values in the H1 sample was compared to the set of 50 average values in the ADS-iPSC sample using the Wilcoxon test.” We thank Mark van de Wiel for bringing this to our attention. Importantly, the specific code used for this analysis can be found in the methylPipe R package on the Bioconductor website (<http://bioconductor.org/>).