The authors would like to apologise for errors in some of the data shown in Figure 3 of this article. These have mainly arisen from lack of conversion of some standard error of the mean (SEM) values to standard deviations (SD) during entry of the data for meta-analysis, inconsistency in incorporating new values communicated by individual authors and genuine clerical errors in data entry and labelling.

In the text below we have described the amendments with respect to each of the relevant primary papers included in the meta-analysis. All values have been rechecked and means and SDs have been rounded up to two decimal places. A single post-decimal figure is shown where the value of the second is zero.

**Oliver et al. (2012)**

DNA methylation at H19, IGF2, SNRPN and KvDMR: SEMs were accidentally used in place of SDs in the original publication. We converted SEMs into SDs in this amended version of the figure. Mean difference was not affected, whereas the confidence interval changed slightly (but did not influence the overall findings).

**Rancourt et al. (2012)**

DNA methylation at H19: Values (means, SDs and participant numbers) were re-checked against data received following e-mail communication with the authors and supplementary tables available in the original paper by Rancourt et al. (2012). We also noted that values for IVF/ICSI (cases) and spontaneous conception (controls) were transposed and have amended this. This did not affect the overall result for the H19 gene, the difference is thus still not statistically significant, as suggested in the original publication.

DNA methylation at PEG1/MEST: We re-checked and amended all the values related to the study using data received following direct communication from the authors. This did not change the overall result for methylation at PEG1/MEST gene.

DNA methylation at GRB10: We re-checked all the values related to this study and made a small change to one of the SD values (1.31 instead of 1.32, - which was a clerical mistake).

DNA methylation at GRB10, IGF2, SNRPN, KvDMR: The numbers of participants who provided cord blood samples were amended using data from the supplementary tables from the original Rancourt et al. (2012) publication.

For clarity, both types of samples from Rancourt et al. (2012) publication – cord blood and placental tissue samples – were annotated as such in the footnotes.

**Puumala et al. (2012)**

DNA methylation at IGF2: We converted SEMs into SDs in this amended version of the figure.

DNA methylation at KvDMR: The number of participants was entered incorrectly in our original publication; this has now been amended according to the data in the original Puumala et al. (2012) publication. All footnotes have been amended to reflect the fact that the study did not analyse placental tissue.

The authors would like to reassure the readers this does not affect the other content or the conclusions of the article.
Figure 3  Forest plot analyses for weighted mean difference (95% confidence intervals) in methylation percent between IVF/ICSI versus spontaneously conceived children for (A) H19, (B) PEG1/MEST, (C) GRB10, (D) IGF2, (E) SNRPN, (F) KvDMR/KCNQ10T1 and (G) PEG3.
References

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