Methylation dynamics during folliculogenesis and early embryo development in sheep

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The journal and the authors regret an error in this article published in the May (vol 153, issue 5 pp 605–619) issue of the journal. Figures 1 and 2 were erroneously repeated although the legends were correct. Figure 2 and its legend is correct as published and the correct Figure 1 is published below with the correct legend. The journal apologises for this error.

**Figure 1** Relative expression of DNMT1, DNMT3A, DNMT3B, TET1, TET2, TET3, MBD1, MBD3 and MBD4 in ovine growing oocytes (GO) at different diameter derived from pre-pubertal animals: 70–90 (small; S GO), 90–110 (medium; M GO) or 110–130 µM (large; L GO) diameter. The relative quantification of all transcripts was performed after normalization against luciferase mRNA levels and the number of oocytes and embryos (Su et al. 2007, Ohsugi et al. 2008, Evsikov et al. 2009). Relative abundance values are expressed as ΔCq (Y axis) and show the mean value ± S.E.M. of five replicates for each stage (each replicate = pool of 30 oocytes). Different letters indicate a significant difference in relative mRNA abundance (ANOVA P < 0.05) among the groups.