

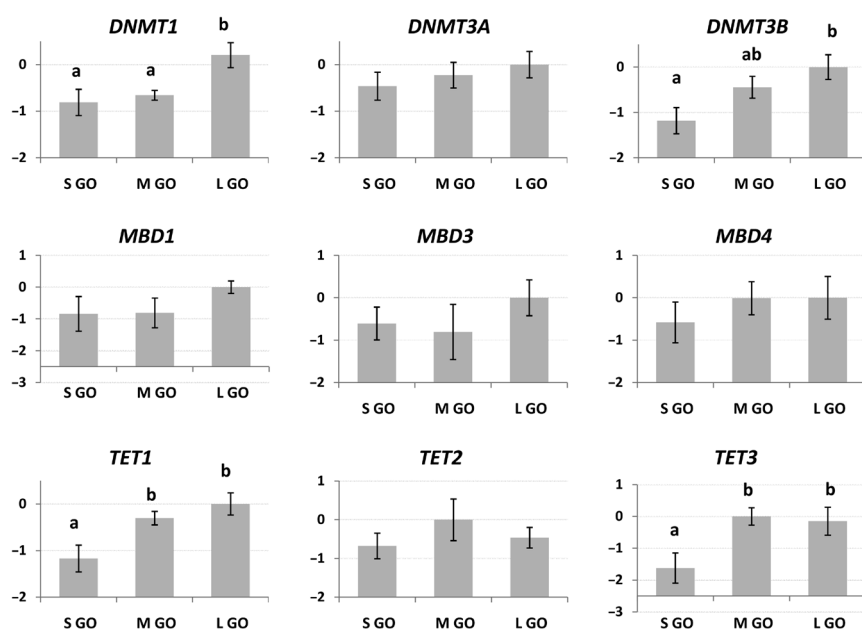
## Methylation dynamics during folliculogenesis and early embryo development in sheep

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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  $\Delta Cq$  (Y axis) and show the mean value  $\pm$  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.