

ERRATUM

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Erratum to: Deep sequencing and de novo assembly of the mouse oocyte transcriptome define the contribution of transcription to the DNA methylation landscape

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After the publication of this work [1], we noticed that in Figure 2 the legends for panels 'd' and 'e' were accidentally interchanged. The correct legends are given below:

'd' should be: Venn diagram representing the numbers of upstream TSSs of reference genes identified in our transcriptome assembly, in PGCs, early embryos and somatic tissues

'e' should be: Pie charts representing the proportion of TSSs overlapping CGIs, TEs or neither (NA) for reference genes, novel upstream TSSs of reference genes and novel genes. For each category, the proportion of each TE family is displayed as a bar graph

The original article was corrected.

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Received: 21 October 2015 Accepted: 21 October 2015

Published online: 03 December 2015

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