Key gene regulatory sequences with distinctive ontological signatures associate with differentially endonuclease-accessible mouse sperm chromatin

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The authors and journal apologize for an error in the above paper, which appeared in volume 142 part 1, pages 73–86. The captions of Tables 2 and 3 should state that gene ontology was tested against a list of background genes from the mouse genome, rather than human genome as published. The correct captions are shown below.

Table 2 Probes associated with promoter sequences returning log₂R values >0.5 or <−0.5 were submitted to the DAVID Gene Ontology web server at <http://david.abcc.ncifcrf.gov/> against a background list of the mouse genome. Only the top five bioprocess 'FAT' categories following Benjamini correction are shown for the target categories and sorted by false discovery rate (FDR). Significantly enriched categories are shown in bold and based on both Benjamini *P* value and the number of genes in each category.

Table 3 Probes associated with promoter sequences returning log₂R values >0.5 or <−0.5 were submitted to the DAVID Gene Ontology web server at <http://david.abcc.ncifcrf.gov/> against a background list of the mouse genome. Only the top five bioprocess 'ALL' categories following Benjamini correction (significantly enriched) are shown for the target categories and sorted by false discovery rate (FDR). Significantly enriched categories are shown in bold and based on both Benjamini *P* value and the number of genes in each category.