

## Global loss of imprinting leads to widespread tumorigenesis in adult mice

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Figure 2D in the paper consists of three COBRA analyses (Snrpn, Peg3, and Igf2) and one Southern analysis (Igf2r). In the COBRA analyses, the upper band represents the unmethylated allele and the lower bands represent the methylated allele, whereas in the Southern analysis the upper band represents the methylated allele and the lower band represents the unmethylated allele. After publication, we noticed that an incorrect gel was inadvertently displayed for the Peg3 methylation analysis in the final assembly of the figure, which occurred because of a mistake in labeling the primary data. The bands on the original figure were labeled as if they were a Southern assay, and we drew the conclusion that Peg3 was unmethylated in the IF cells. Once we noticed this error, we repeated the Peg3 analysis using the COBRA assay to verify the original findings. The new figure shows that the CTL cells have both unmethylated and methylated alleles, whereas the IF cells have only unmethylated alleles (Figure 1). This result is entirely consistent with our original conclusion. We regret this error. We also noted that the reference for the primers used for the Igf2 methylation analysis in Figure 2D was omitted. The primers were described in [Olek et al. \(1996\)](#).

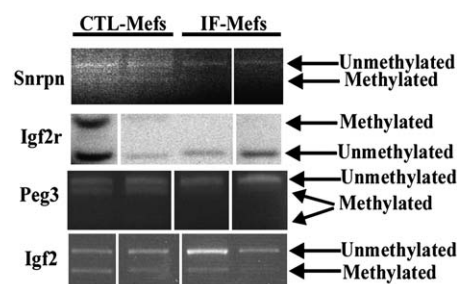


Figure 1. Corrected Figure 2D

### Reference

Olek, A., Oswald, J., and Walter, J. (1996). A modified and improved method for bisulphite based cytosine methylation analysis. *Nucleic Acids Res.* 24, 5064–5066.

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