Erratum to: Imprinting disorders: a group of congenital disorders with overlapping patterns of molecular changes affecting imprinted loci

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Erratum
Unfortunately, after publication of the original version of this article [1], it was noticed that there were some errors in Fig. 3 and Fig. 4:

- In Fig. 3, the methylation of H19/IGF2:IG-DMR hypomethylation is not correctly illustrated: the lolly pops should be empty (=unmethylated).
- In Fig. 4, the methylation of both H19/IGF2:IG-DMR hypermethylation and KCNQ1OT1:TSS-DMR hypomethylation are not correctly illustrated: in case of the H19/IGF2:IG-DMR hypermethylation the lolly pops should be filled (=methylated), and for the KCNQ1OT1:TSS-DMR, they should be empty (=unmethylated).

The corrected Fig. 3 and Fig. 4 have been included in this erratum.

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Reference
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Fig. 3 The 11p15.5 cluster can be divided in two functional domains whose imprinting is dependent on distinct imprinting control regions (H19/IGF2: IG DMR and KCNQ1OT1: TSS DMR). Mainly hypomethylation of the KCNQ1OT1: TSS DMR is responsible for SRS.
Fig. 4 Epimutations and mutations in 11p15.5 are also responsible for BWS