Genome Biology

AUTHOR CORRECTION

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Author Correction: DNA methylation remodeling and the functional implication during male gametogenesis in rice

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Following publication of the original article [1], the authors identified an error in Fig. 2. In Fig. 2B, a wild type pollen picture was wrongly used to represent cmt3b pollens that in fact are of wild type phenotype.

The incorrect and correct Fig. 2 is published in this correction article and the original article [1] has been updated.

Incorrect figure:

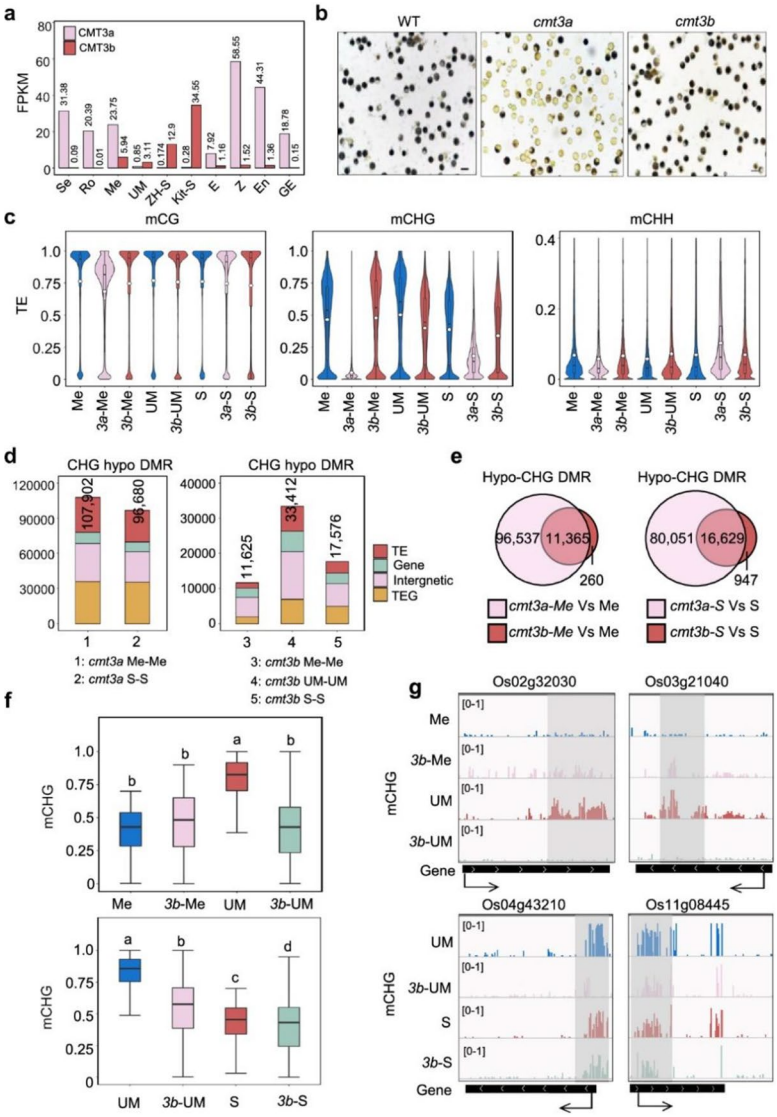
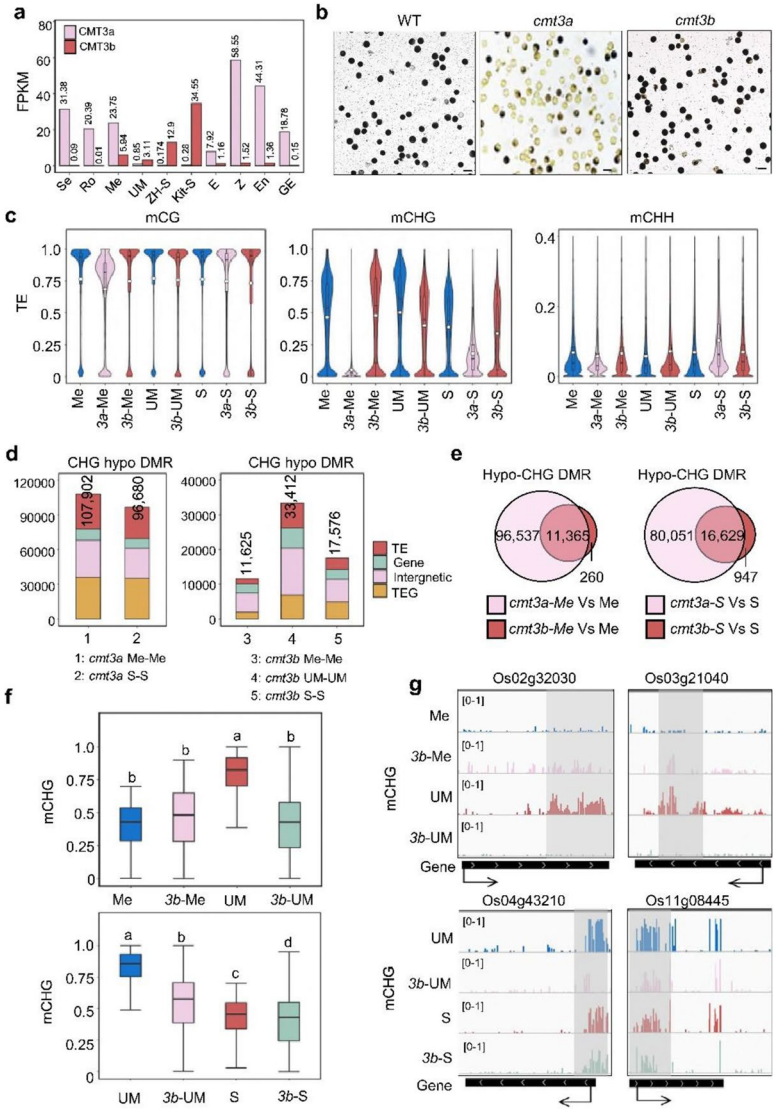


Fig. 2 Effects of *cmt3a* and *cmt3b* mutations on DNA methylation in meiocyte, microspore and sperm. **a** Transcript levels in FPKM of rice CMT3a and CMT3b in seedling (Se), roots (Ro), meiocyte (Me), unicellular microspore (UM), sperm (S), egg (E), zygote (Z), endosperm nuclei (En, 1.5 days after fertilization) and globular embryo (GE, 3 days after fertilization) from RNA-seq data. The sperm (Kit-S) in Kitaake background was reported by Anderson et al., (2013). **b** The pollen grains of wild type and *cmt3a* and *cmt3b* mutants were I2-KI stained. Bars = 50 μm. **c** Violin plots comparing overall cytosine methylation levels of wild type and *cmt3a* and *cmt3b* mutant meiocyte (Me), unicellular microspore (UM) and sperm (S). The average methylation levels (white dots) and median values (black bars) in transposable elements (TE) are shown. Values of the methylomes are averages from the two replicates. **d** Number of differential methylated regions (DMR) in *cmt3a* and *cmt3b* relative to wild type. Relative portions in TE (> 500 bp), TEG, gene, and Intergenic regions are indicated by different colors. **e** Venn diagrams showing overlapping of hypo-CHG DMRs in *cmt3a* and *cmt3b* meiocyte (left) and sperm (right) relative to wild type cells. **f** Box plots of DNA methylation levels of hypo-CHG DMRs in meiocyte (Me) versus microspore (UM) (upper) and sperm (S) relative to microspore (UM) (lower) in wild type, *cmt3a* (3a) and *cmt3b* (3b) cells. The significance was calculated with multiple comparison tests. Different letters on top of the bars indicate a significant difference ($p < 0.05$). **g** Genome Browser screen captures showing high CHG methylation sites in microspore relative to meiocyte and sperm decreased in cmt3b mutants (highlighted by grey)

Correct figure:



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Reference

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