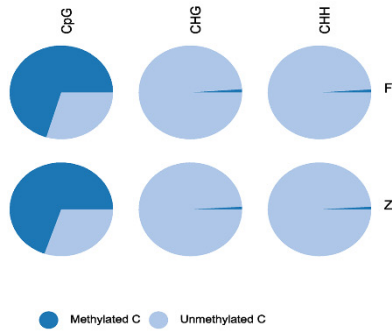
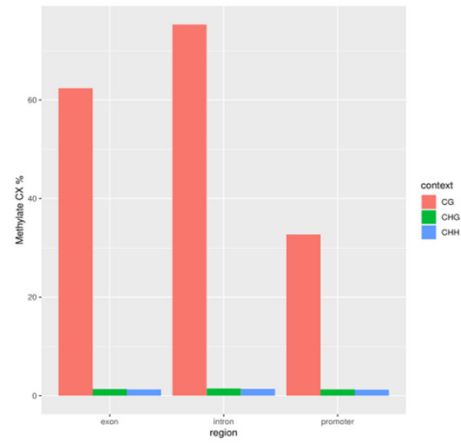


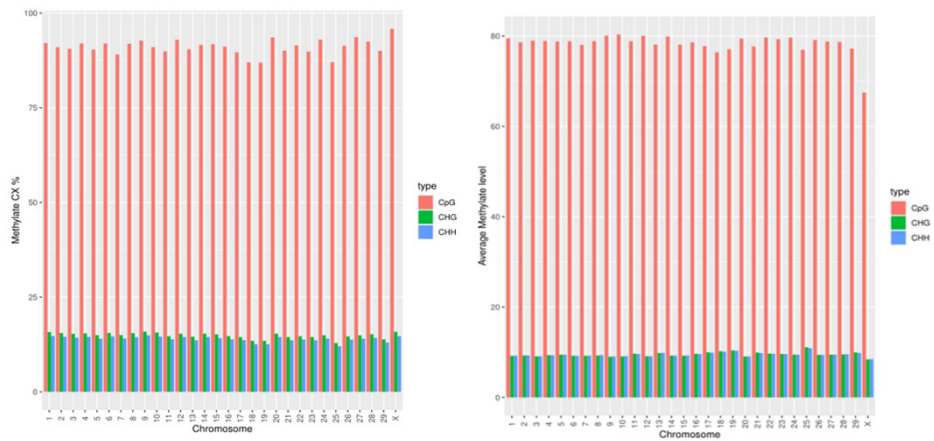
A



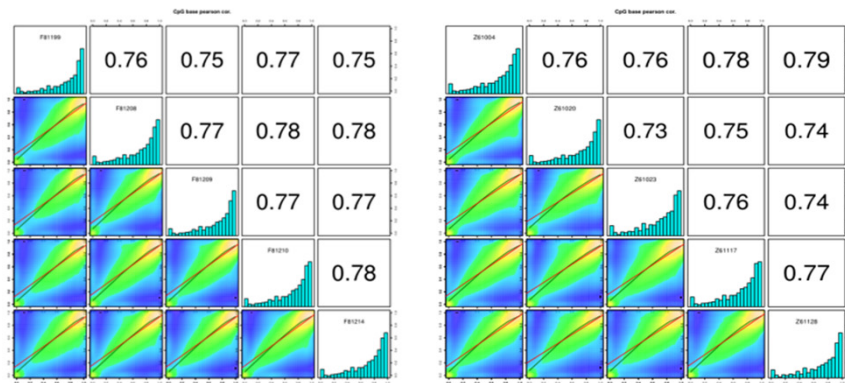
B



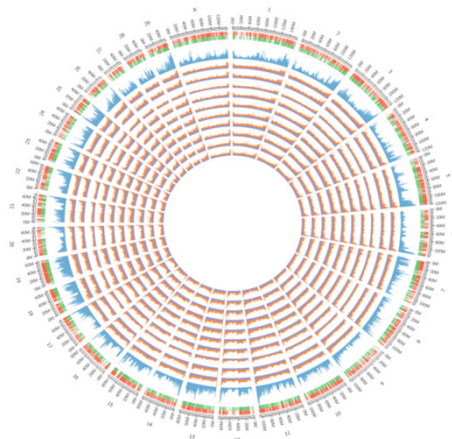
C



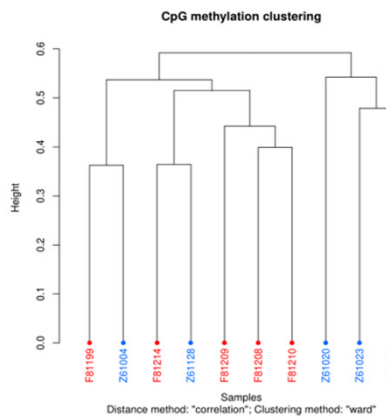
D



E



F



Supplementary Materials S11. Genome-wide DNA methylation profiling. A, Statistics of genome-wide DNA methylation cytosine (CG, CHH and CHG) levels. Distribution of methylation levels of B, C loci in each gene functional region (exons, introns, and promoters). C, The mean methylation level (right) and proportion of methylated C sites (left) for chromosomally distributed methylated C sites. D, Correlation of sample methylation levels in wild-type (F) (left) and *MSTN*^{+/-} edits (Z) (right). E, Methylation circle map. F, Cluster map of sample methylation.

The CG, CHH, and CHG (where H stands for A, C, or T) have different levels of methylation. We found genome-wide methylated cytosines (mC) of $69.74 \pm 1.06\%$ for CG in *MSTN*^{+/-} edited samples, $0.94 \pm 0.21\%$ for CHG, $0.94 \pm 0.21\%$ for CHH, and $70.34 \pm 1.26\%$ for CG in wild-type samples, CHG was $1.12 \pm 0.26\%$, CHH was $1.04 \pm 0.24\%$, and the proportions of these contexts were similar in each group (Supplementary Material S11, A). We analysed the methylation status of three different regions, including promoters, exons and introns. The CG context plays an important role and is most pronounced in introns. The CHG and CHH contexts remain ultra-hypomethylated and stable in all functional elements (Supplementary Material S11, B). Furthermore, the methylation of the CG context is evenly distributed across the genome. The samples were highly correlated (Supplementary Materials S11, C, D, E and F).