**Figure S1.** Distribution for the percentage of cytosine with 2 to 11 reads.

**Figure S2.** Methylation of different methylation contexts for cattle somatic tissues. (a) CG percentages with different methylation levels; (b) CHG percentages with different methylation levels; (c) CHH percentages with different methylation levels. Note: the error bar represents the standard deviation among the 10 tissues.

**Figure S3.** Correlation analysis of CG and non-CG methylation using 1-Mb non-overlapping windows for oocyte overlapped with the RRBS data. Note: Only the cytosines that overlapped with the RRBS data in oocyte WGBS were used for plotting.

**Figure S4.** Methylation levels for different genomes. Note: the error bar represents the standard deviation among the 10 tissues.

**Figure S5.** Methylation levels for different repetitive sequences. Note: the error bar represents the standard deviation among the 10 tissues.

**Figure S6.** Methylation distributions of the 3 methylation contexts in genic regions and CG islands for oocyte overlapped with the RRBS data.

**Figure S7.** Autocorrelation analysis for different methylation contexts on genome. Chr1 was used to calculate the correlation of different methylation contexts with different distances. Note: all figures for somatic tissues were from the merged data after examining results individually that did not show differences between them.

**Figure S8.** CG island methyllations in cattle somatic tissues. (a) Average methylation levels of CG islands, CG island shores and non-CG island regions. (b) Distribution of CG islands at different methylation levels. (c) CG island methylation levels within every window of 10% length of all chromosomes. The x-axis is the interval of all chromosomes from 5’ to 3’.

**Figure S9.** Clustering of 10 tissues based on 131 tissue-specific DMIs (tDMIs).
The scatter plot shows the relationship between non-CG methylation level (%) and CG methylation level (%). The coefficient of determination ($R^2$) is 0.68, and the p-value is less than $2.2 \times 10^{-16}$. This indicates a strong correlation with statistical significance.
The image contains three bar charts comparing methylation levels across different genomic regions:

### CG
- Average
- Autosome
- ChrX
- ChrUn
- ChrMT

### CHG
- Average
- Autosome
- ChrX
- ChrUn
- ChrMT

### CHH
- Average
- Autosome
- ChrX
- ChrUn
- ChrMT

The y-axis represents the methylation level (%) with values ranging from 0 to 100. The x-axis lists the genomic regions.