

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.

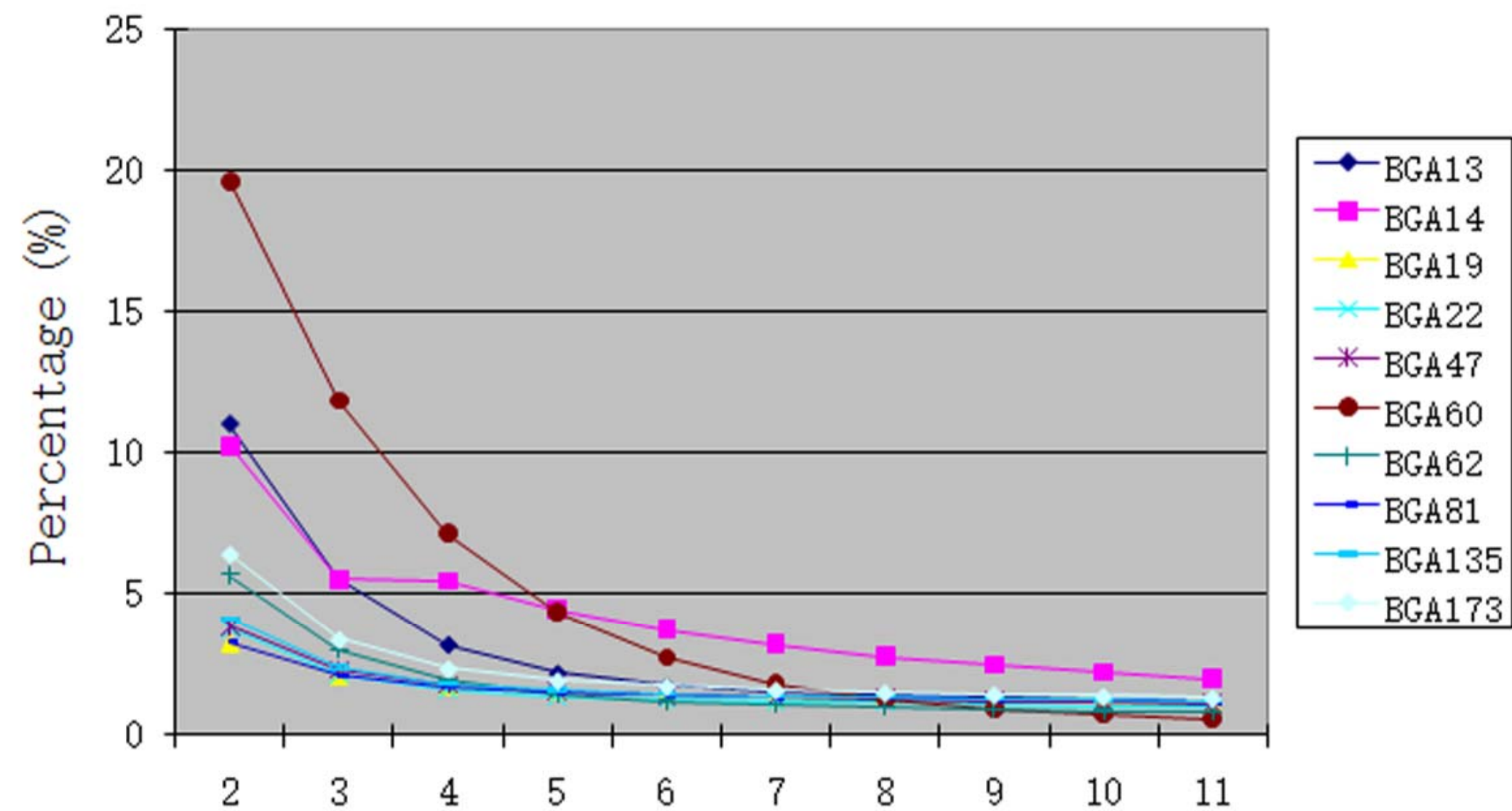
Figure S5. Methylation levels for different repetitive sequences. Note: the error bar represents the standard deviation among the 10 tissues.

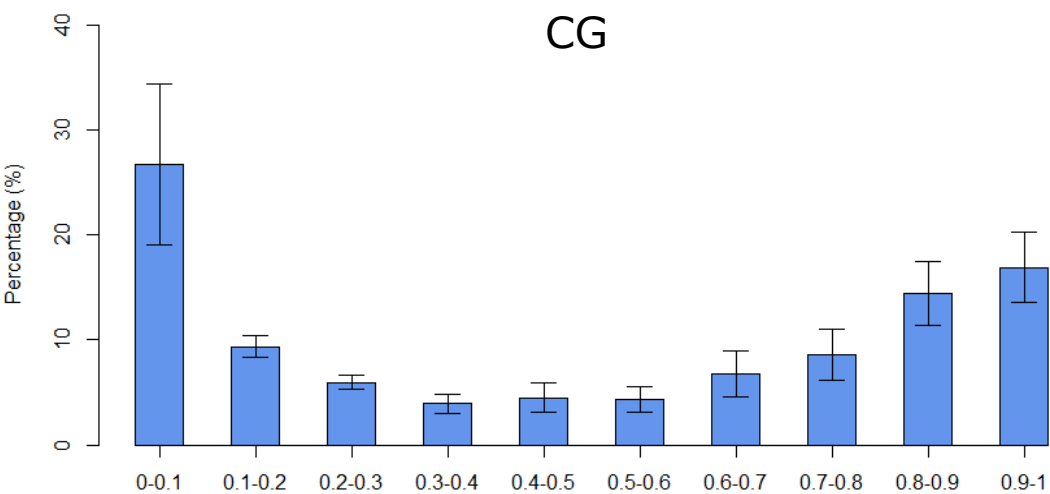
Figure S6. Methylation distributions of the 3 methylation contexts in genic regions and CG islands for oocyte overlapped with the RRBS data.

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.

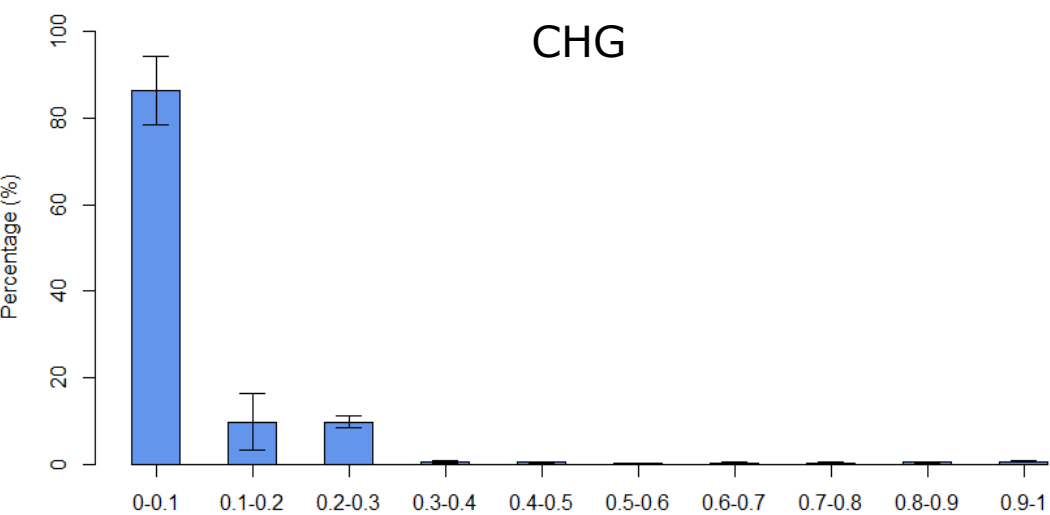
Figure S8. CG island methylations in cattle somatic tissues. (a) Average methylation levels of CG islands, CG island shores and non-CG island regions. (b) Distribution of CG islands at different methylation levels. (c) CG island methylation levels within every window of 10% length of all chromosomes. 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).

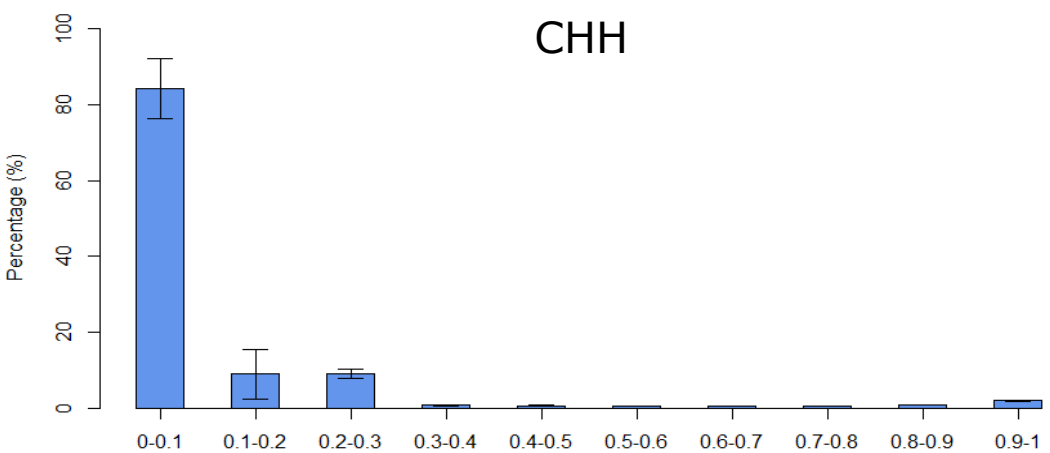




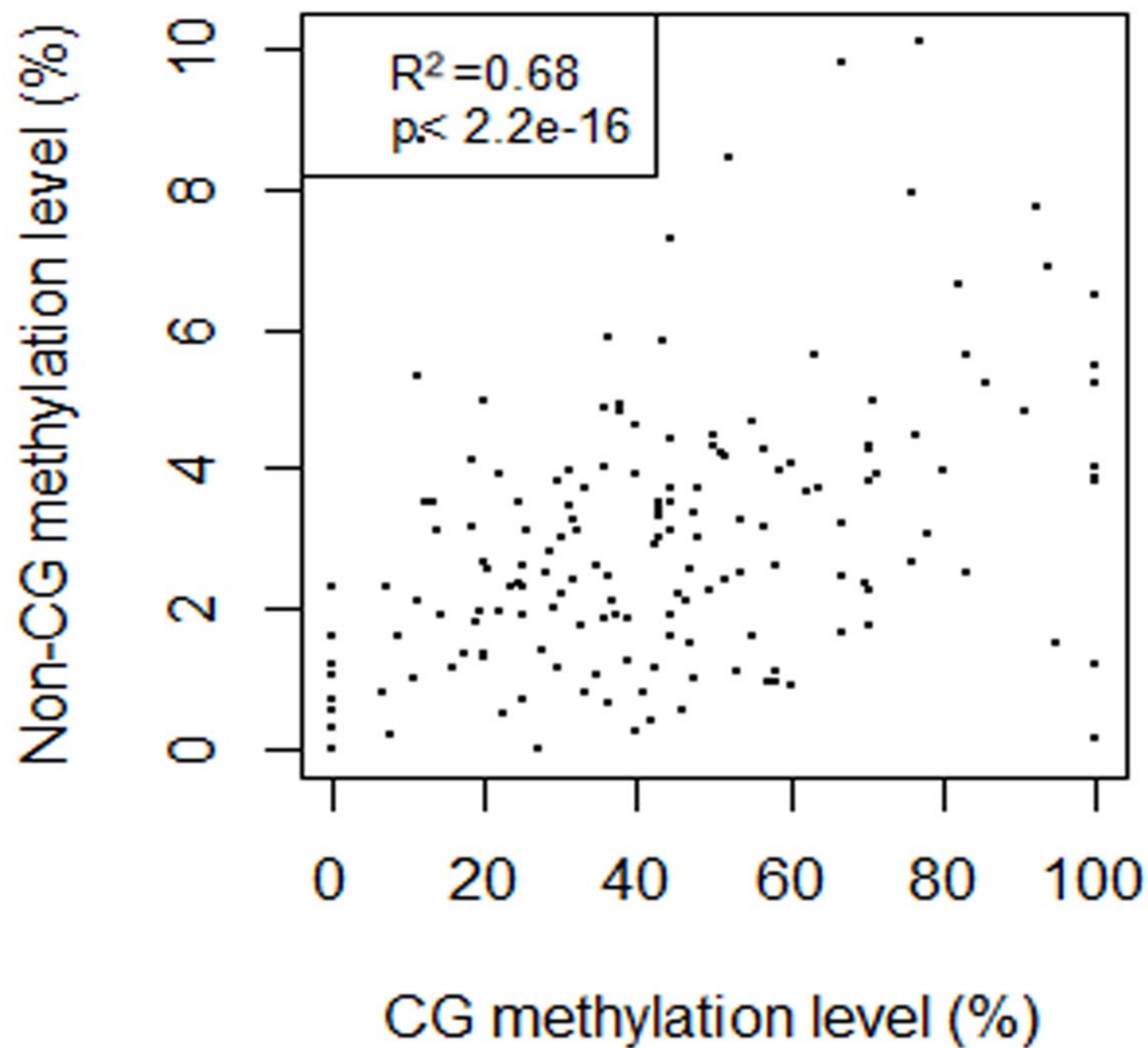
(a)

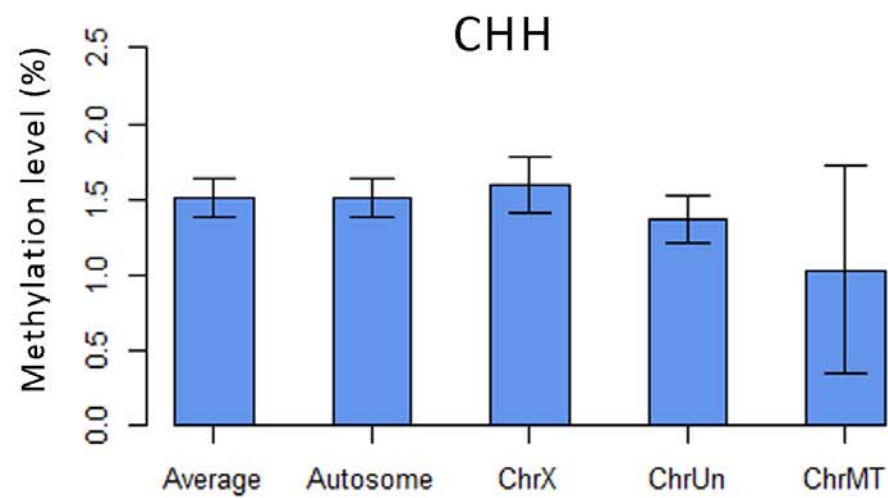
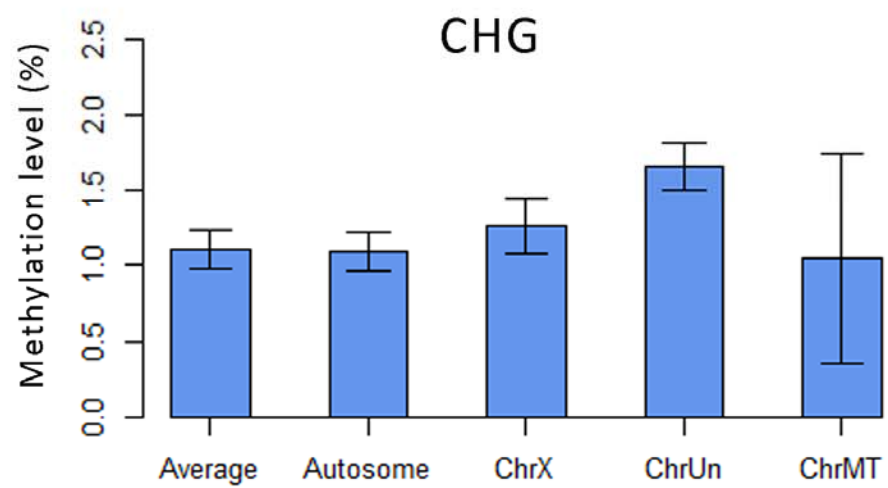
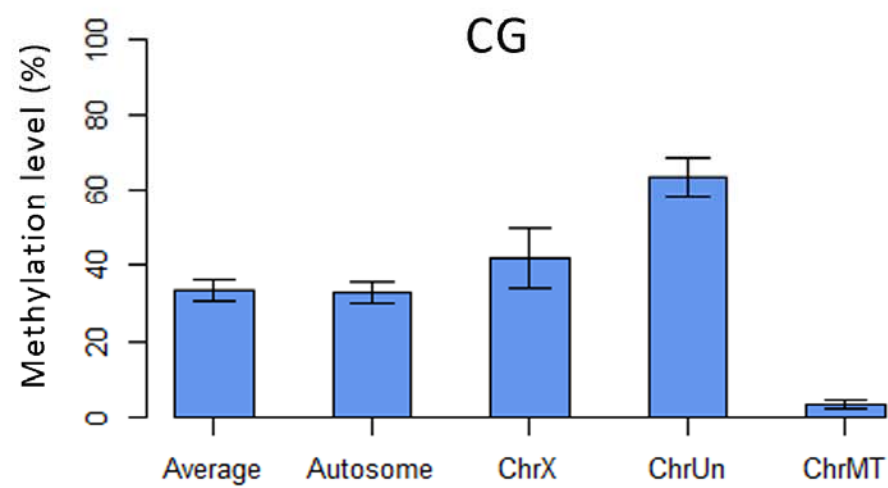


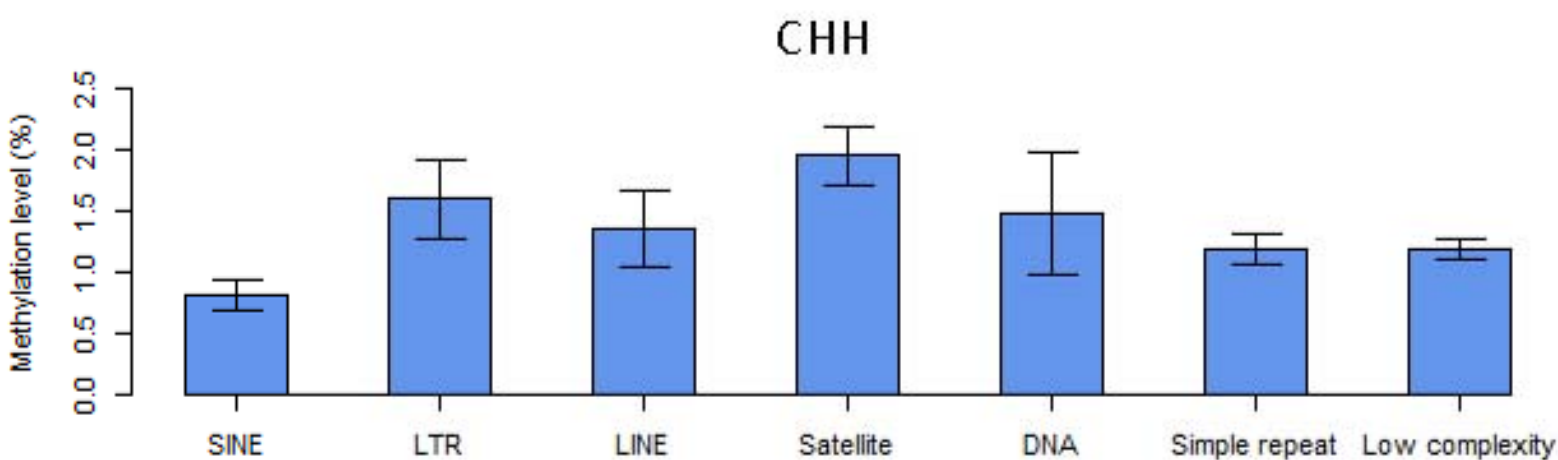
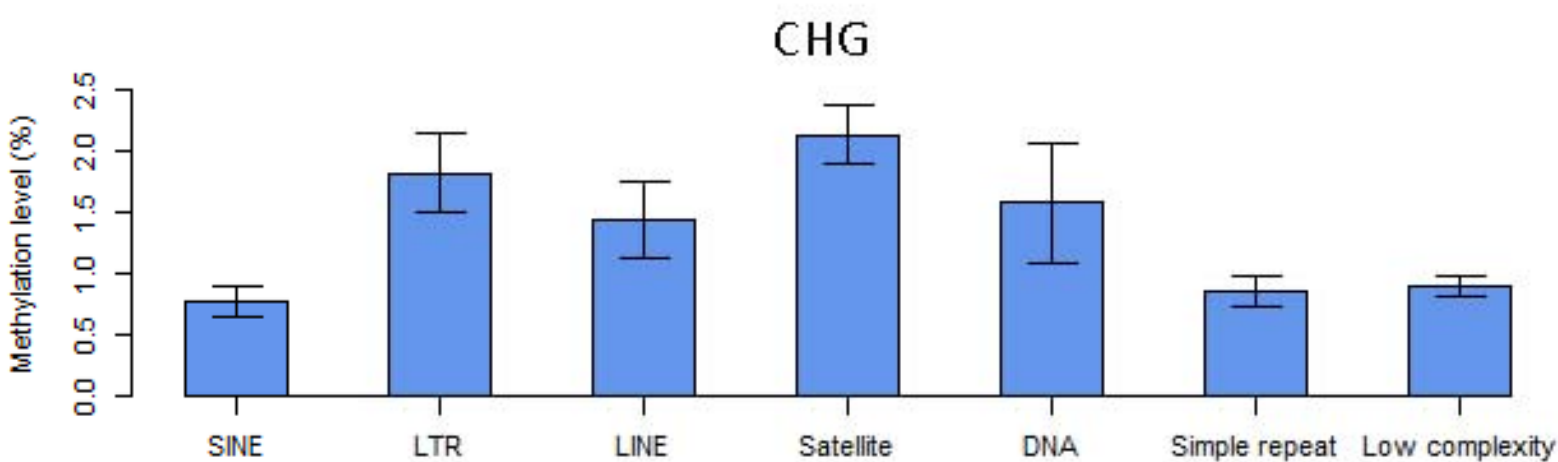
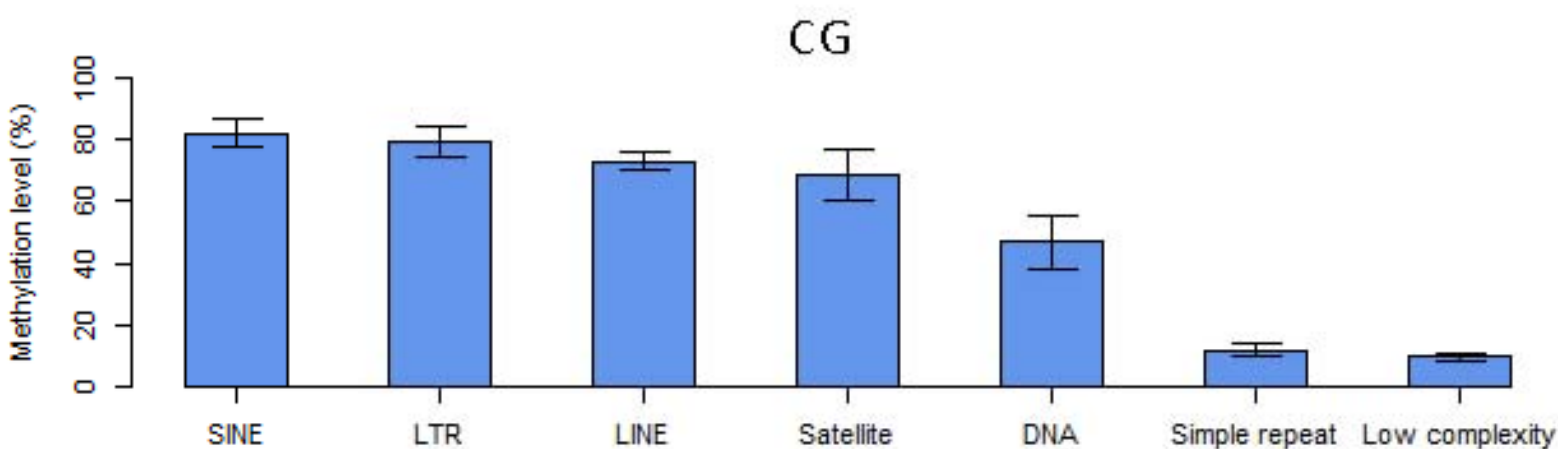
(b)

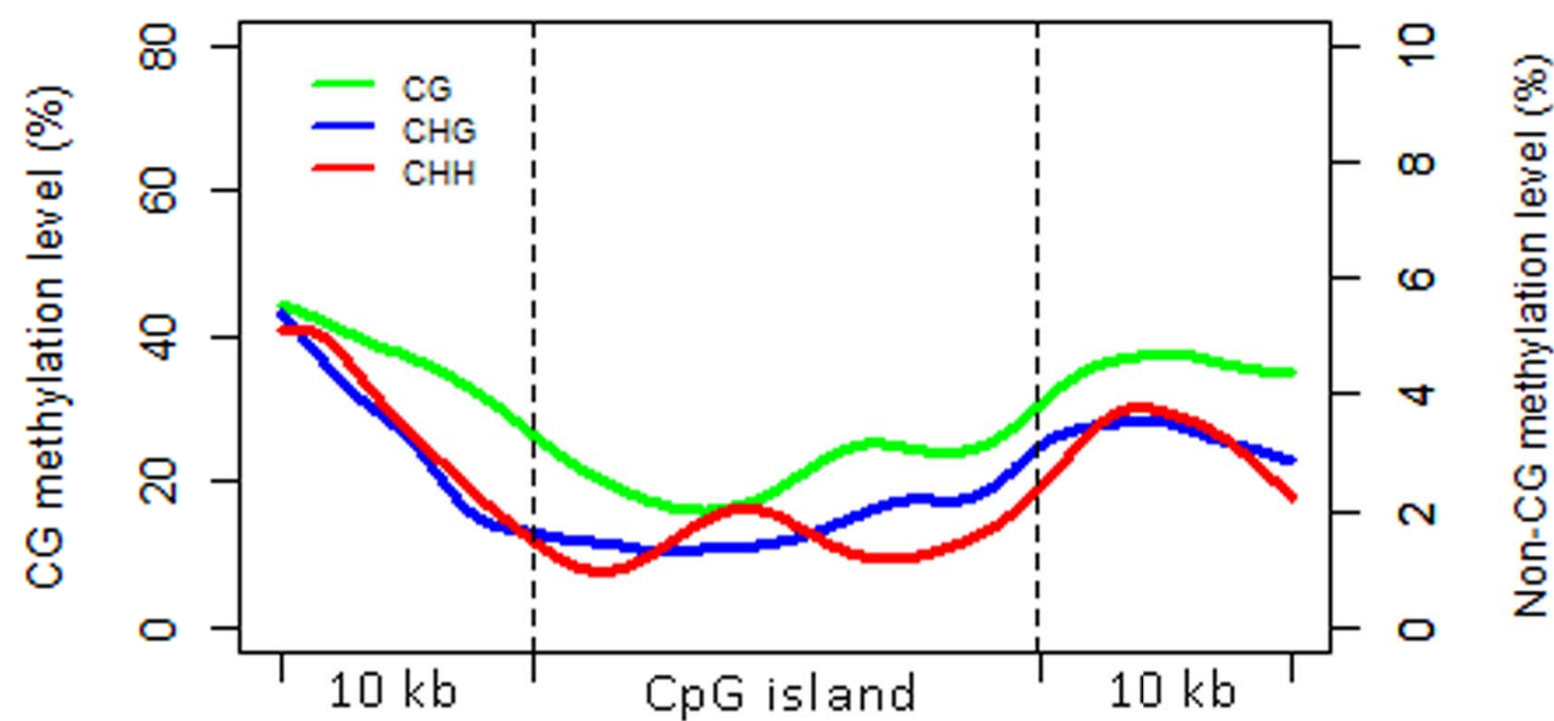
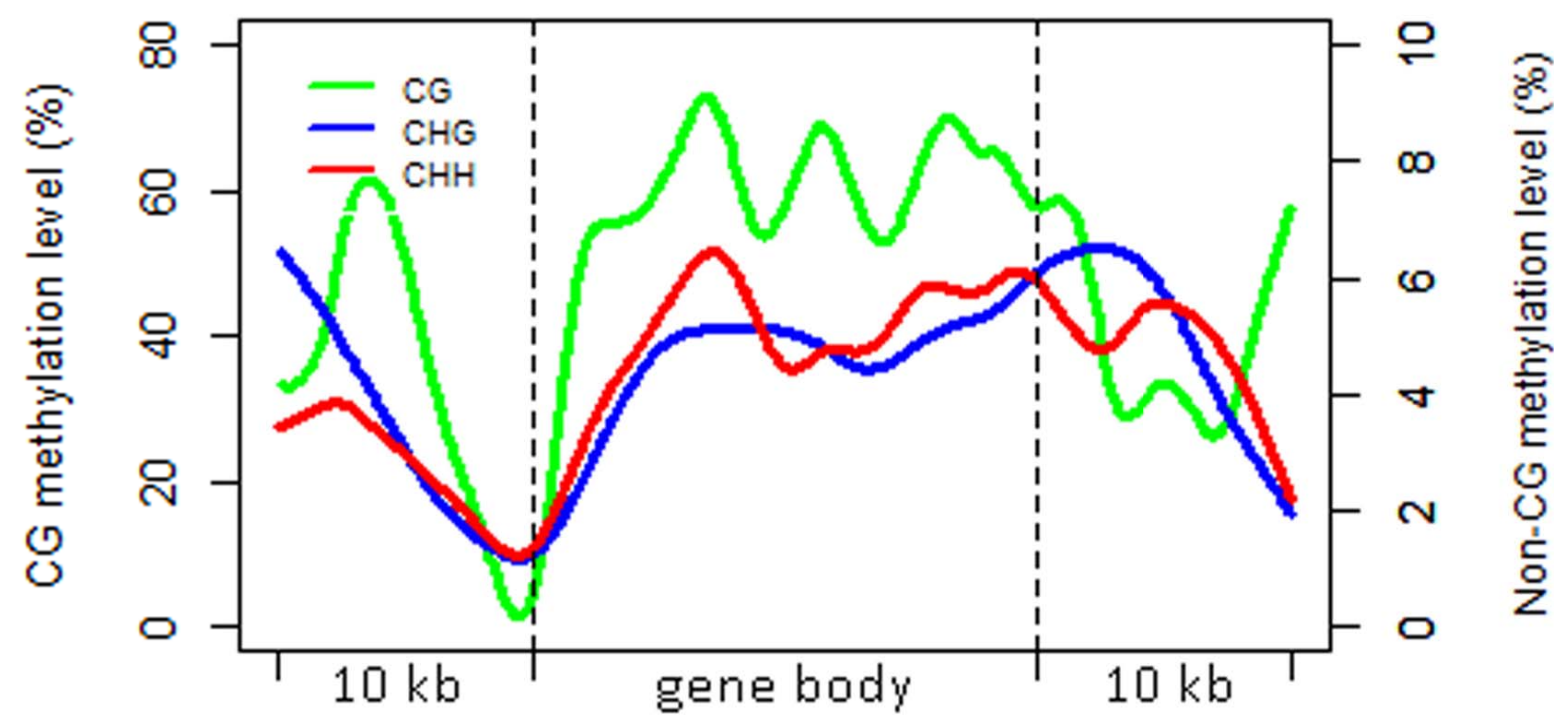


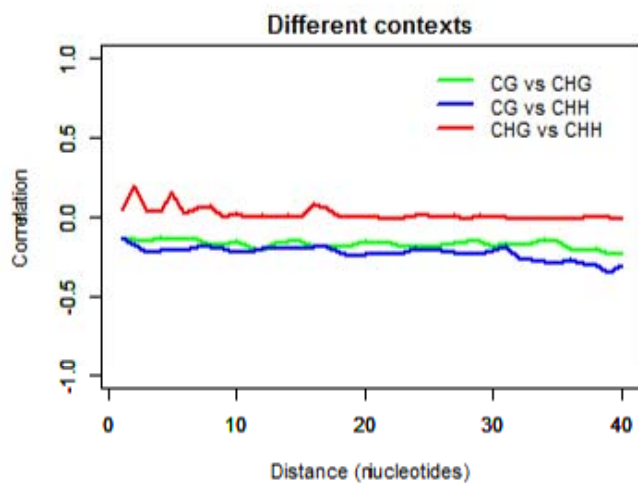
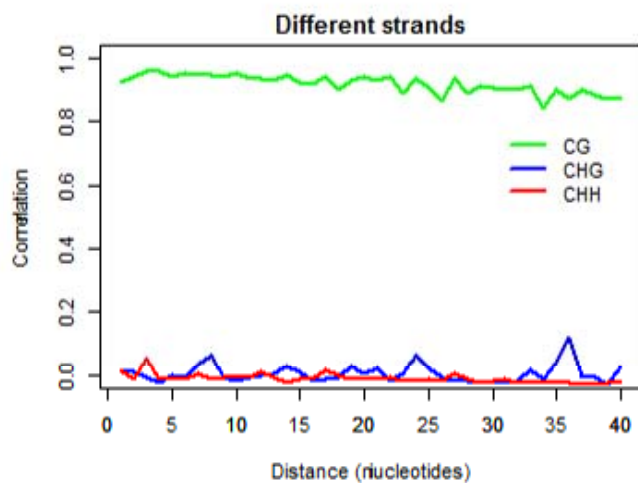
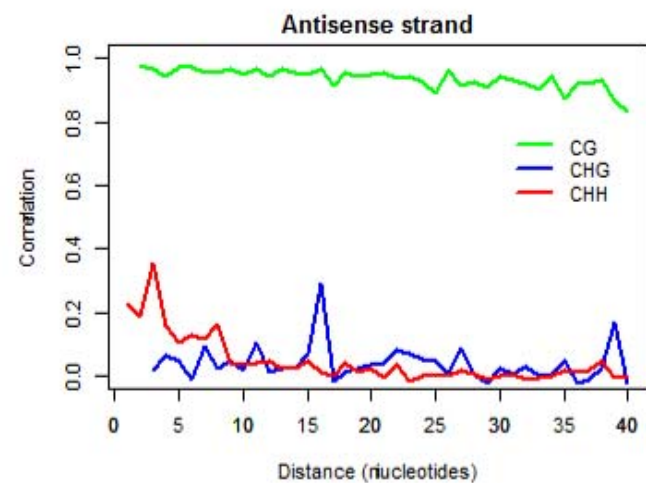
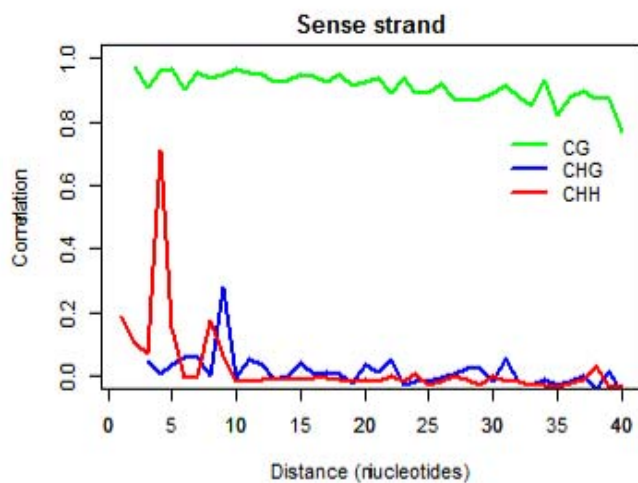
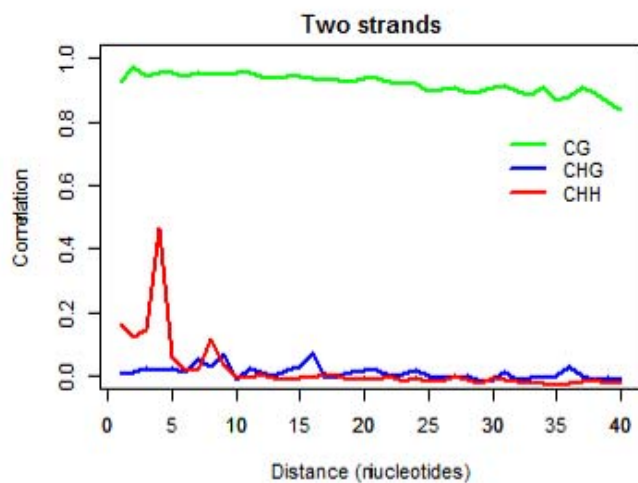
(c)

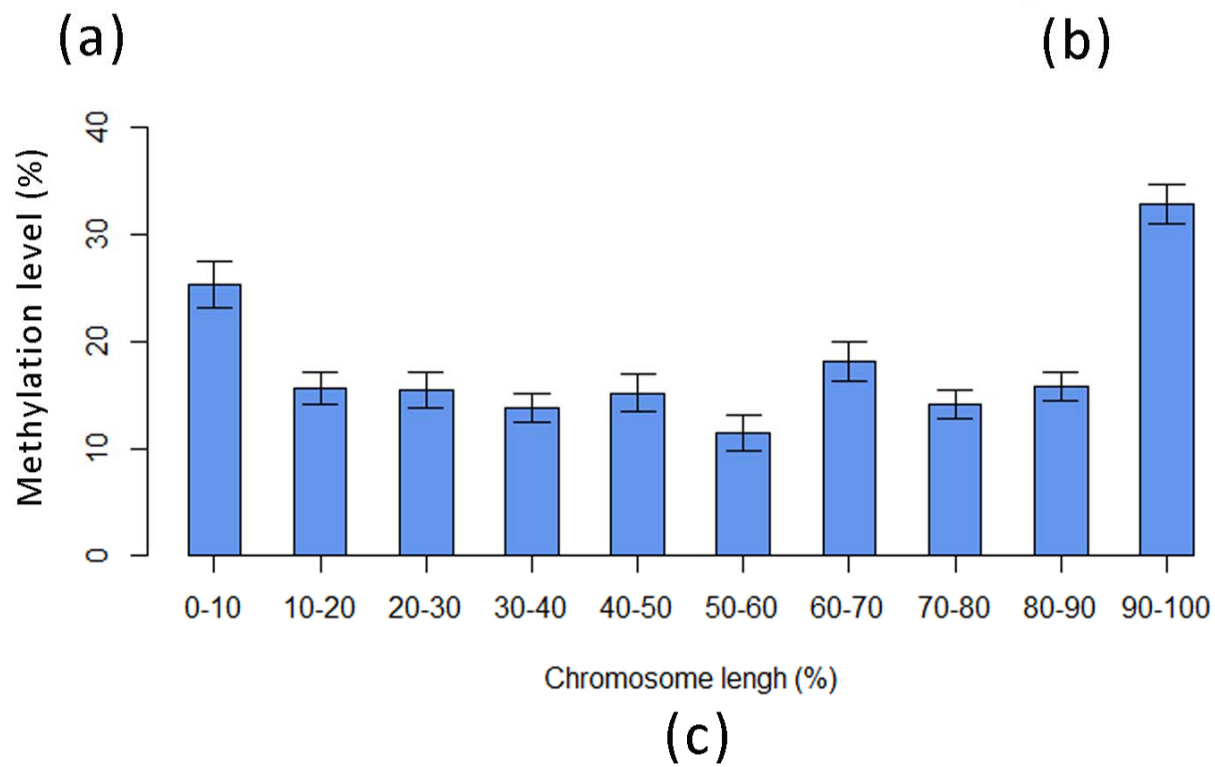
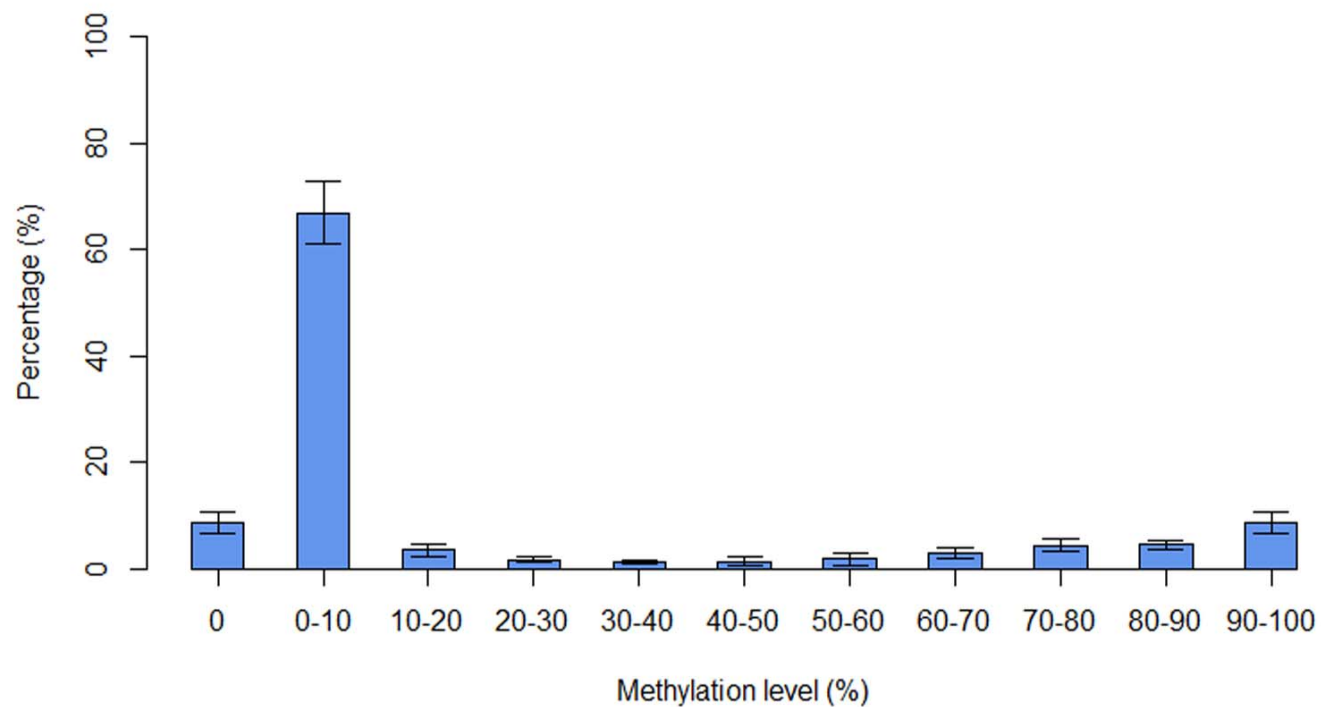
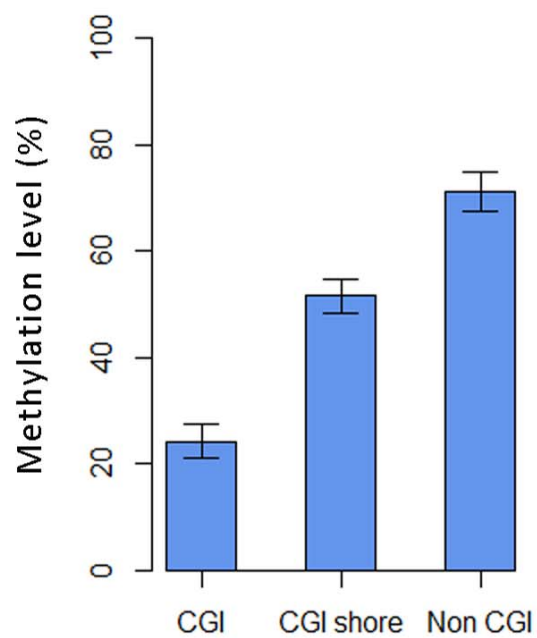










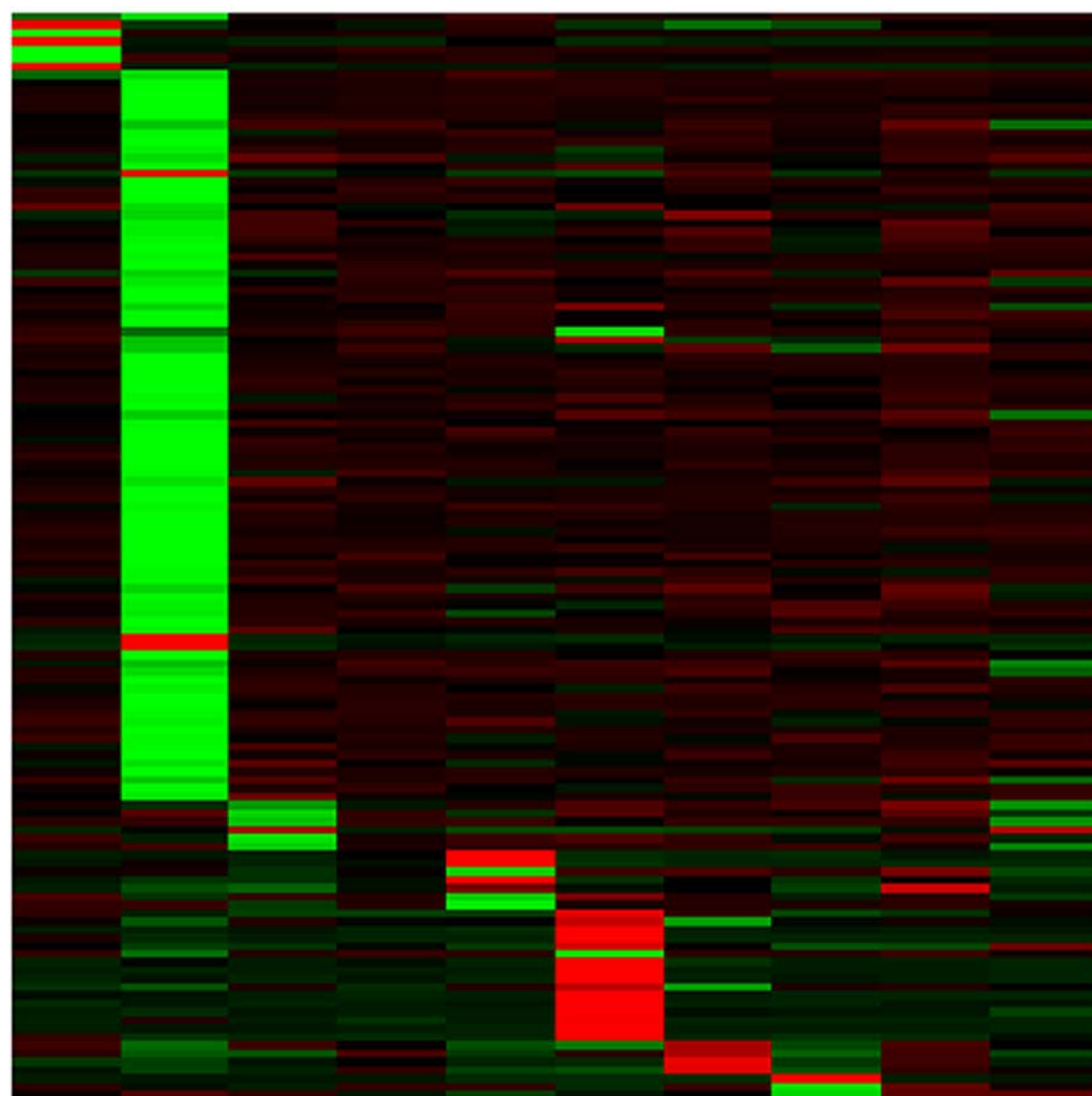


Color Key



-2 0 2

Row Z-Score



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BGA14

BGA19

BGA22

BGA47

BGA60

BGA62

BGA81

BGA135

BGA173