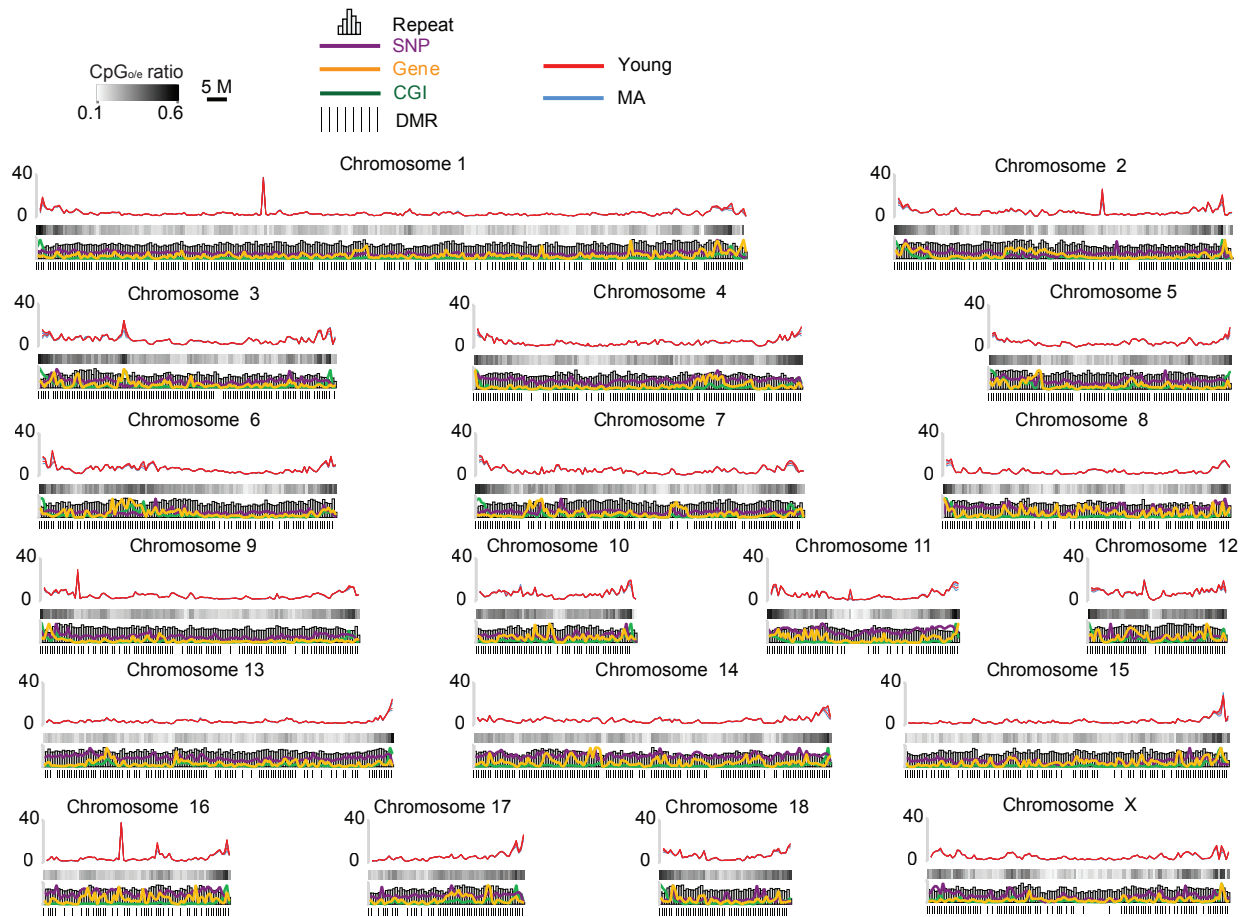




Additional file 4: Genome-wide distribution of the DNA methylation levels. To compare the DNA methylation state between samples, the read depth was normalized to the overall average number of reads in each group. The CpG_{O/e} ratio, SNPs density, numbers of genes, repeats and CGIs were all calculated over 1 M Mb sliding windows.