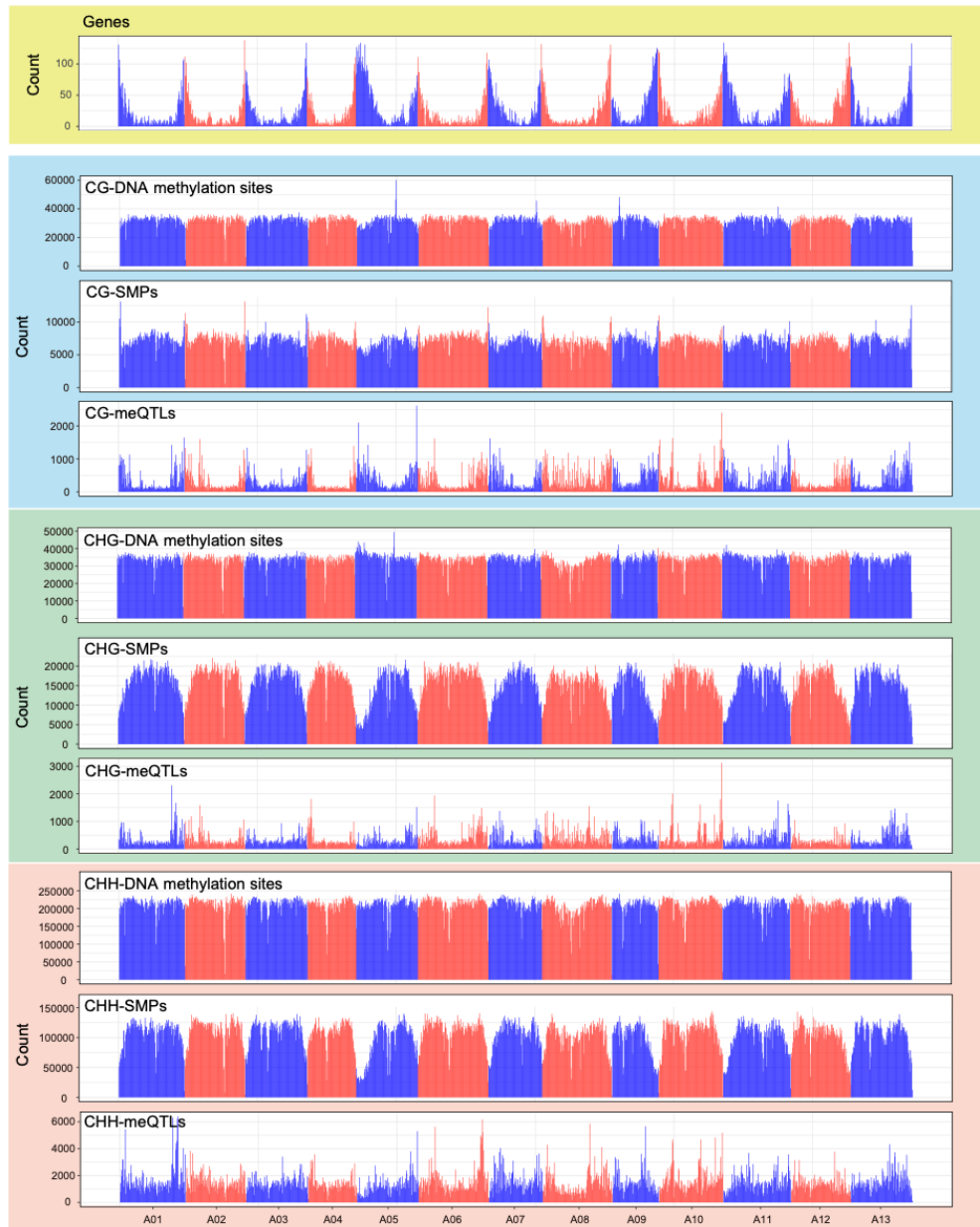




Supplementary information, Fig. S6. The *cis*-meQTLs were enriched in the gene-rich region on chromosome. Distribution of meQTL across the genome. From top to bottom, is counts of genes, counts of CG DNA methylation sites, CG-SMP, CG-meQTL, counts of CHG DNA methylation sites, CHG-SMP, CHG-meQTL, counts of CHH DNA methylation sites, CHH-SMP, CHH-meQTL, respectively. Each type of data was measured in 1-Mb windows.