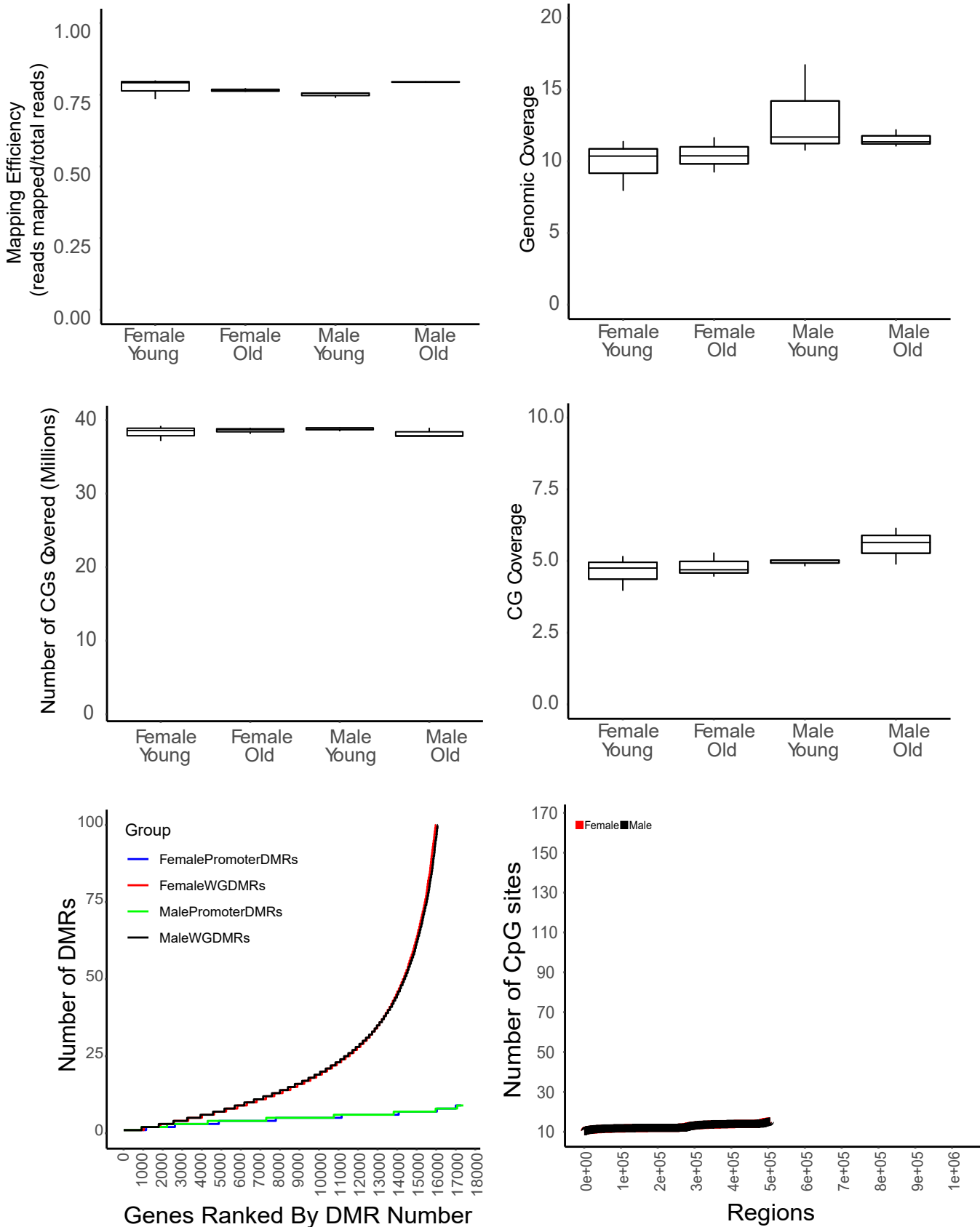




Supplemental Figure 6. Sequencing alignment and differentially methylated region calling summary statistics. A. boxplots representing the mapping efficiency per group. B. Overall genomic sequencing coverage. C. Boxplots showing the number of CpGs covered. D. boxplots representing the average CpG coverage per group. E. Line plot of the number of DMRs mapped to genes (black and red) and gene promoters (green and blue) passed filtering from RNA-sequencing. F. Line plot showing the number of CpG in regions passed filtering for differential methylation.