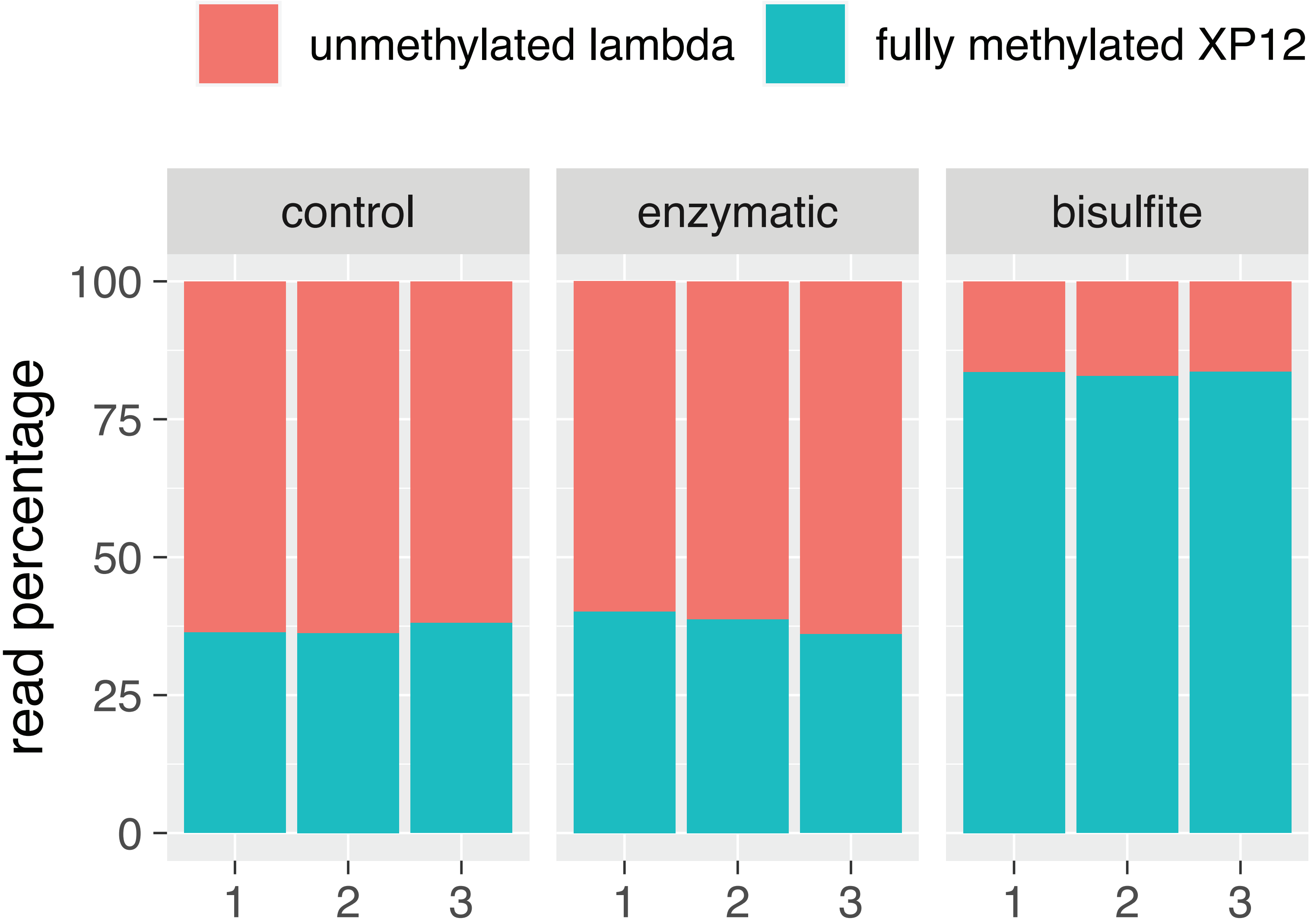

Supplemental Figure 3

Enzymatic deamination method (APOBEC(5mC)) does not introduce additional PCR bias. Lambda (no methylation) and XP12 (fully 5mC methylated) genomic DNA's were mixed 1:1 ratio. 3 libraries (no treatment PCR control; enzymatic treatment and bisulfite treatment) were sequenced on Illumina platform. Each barplot represents the percentage of reads mapping to either Lambda (red) or XP12 (blue). Three replicates were performed for each treatment (1,2 and 3 on the x axis).