

Bismark Summary Report

Samples	id
Run Folder	folder
Reference Genome	genome
Paired End	false

1 Alignment Statistics

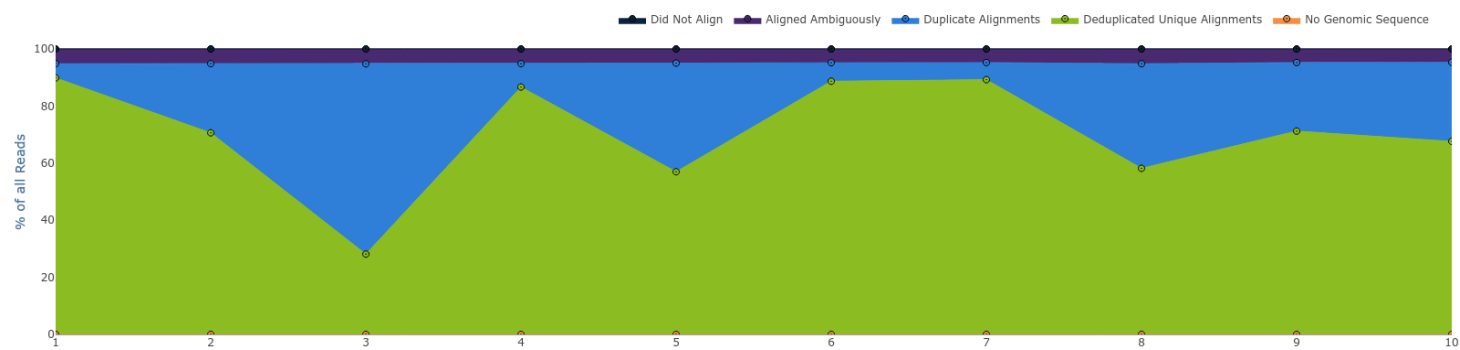


Figure 1. Alignment statistics by percentages of all reads

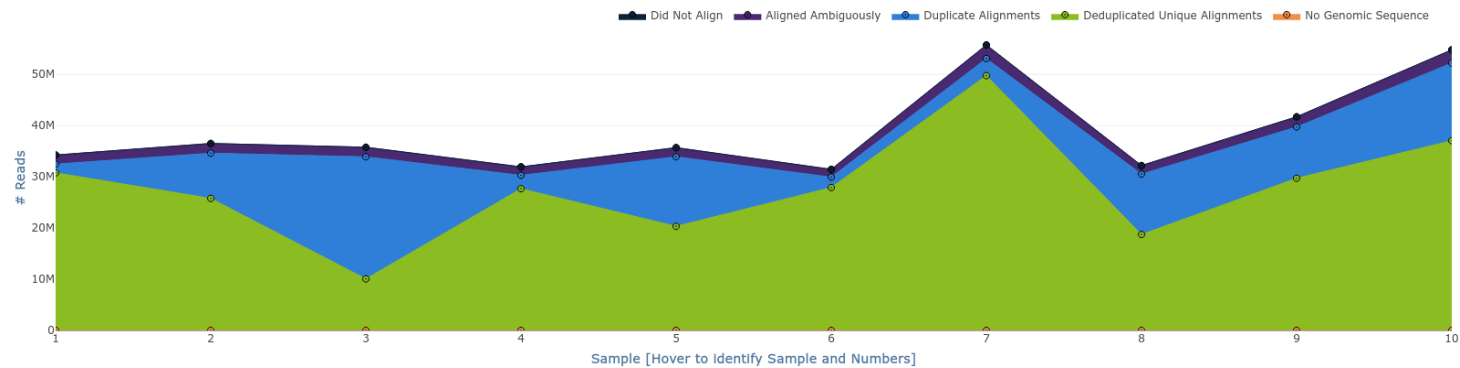


Figure 2. Alignment statistics by number of reads

2 Cytosine Methylation

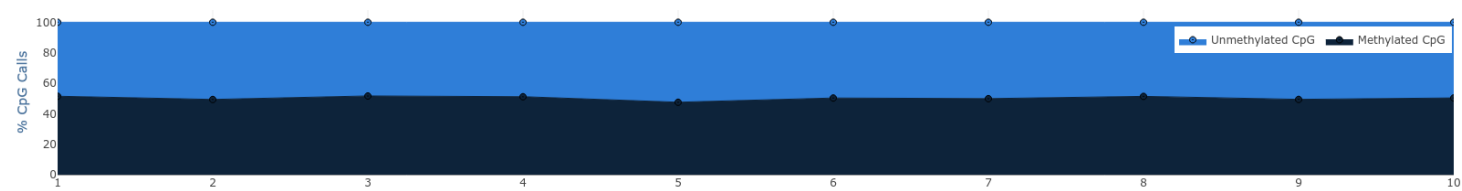


Figure 3. CpG methylation summary

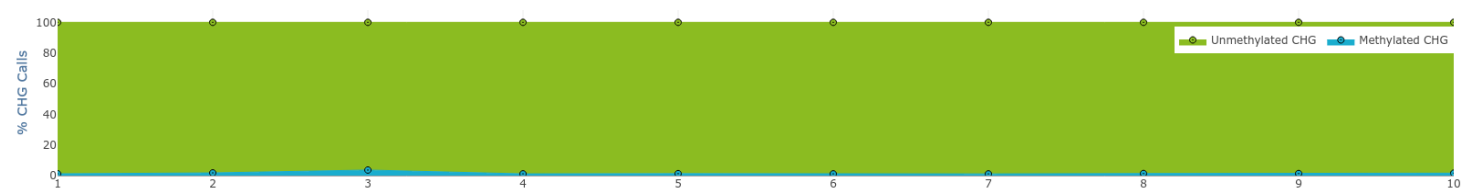


Figure 4. CHG methylation summary

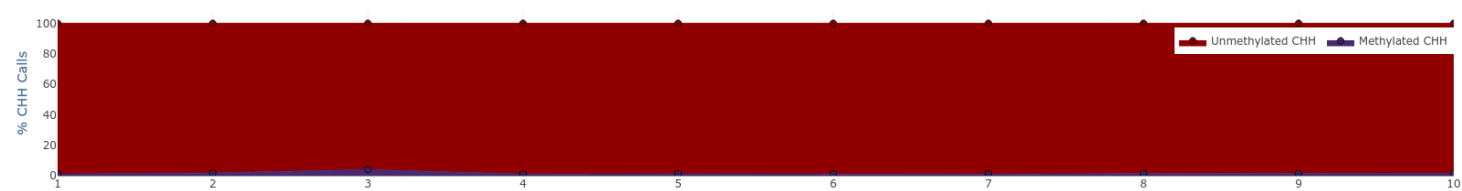


Figure 5. CHH methylation summary