Bismark Processing Report

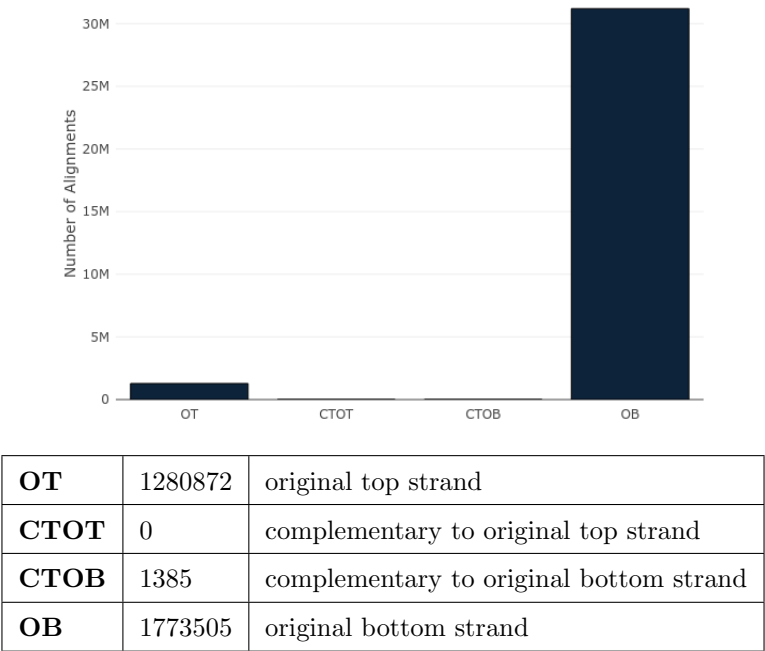|	
Sample ID	id
Run Folder	folder
Reference Genome	genome
Paired End	false

1 Alignment Stats
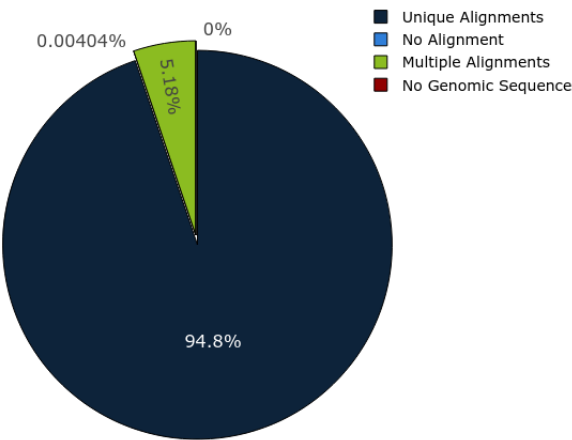
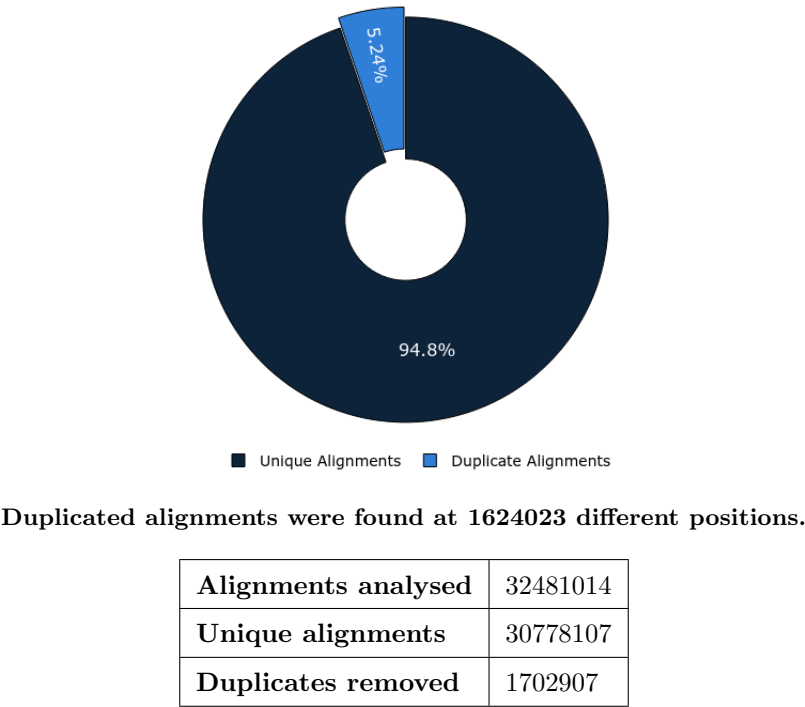|	
Sequence pairs analyzed in total	34255904
Paired-end alignments with a unique best hit	32481014
Pairs without alignments under any condition	1385
Pairs that did not map uniquely	1773505
Genomic sequence context not extractable (edges of chromosomes)	0

2 Cytosine Methylation
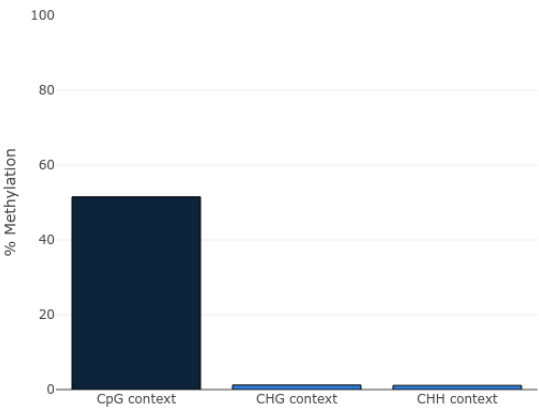
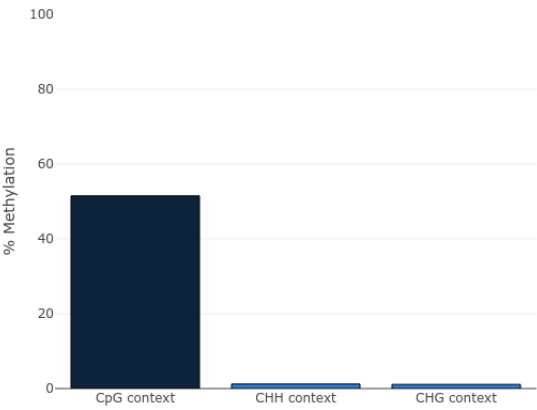| Total C's analysed	771899036
Methylated C's in CpG context	42878888
Methylated C's in CHG context	2229378
Methylated C's in CHH context	5611294
Methylated C's in Unknown context	1781
Unmethylated C's in CpG context	40323331
Unmethylated C's in CHG context	186572497
Unmethylated C's in CHH context	494283648
Unmethylated C's in Unknown context	364151
Percentage methylation (CpG context)	51.5%
Percentage methylation (CHG context)	1.2%
Percentage methylation (CHH context)	1.1%
Methylated C's in Unknown context	N/A%

# 3 Alignment to Individual Bisulfite Strands

OT	1280872	original top strand
CTOT	0	complementary to original top strand
CTOB	1385	complementary to original bottom strand
OB	1773505	original bottom strand

4 Deduplication

Duplicated alignments were found at 1624023 different positions.

Alignments analysed	32481014
Unique alignments	30778107
Duplicates removed	1702907

5 Cytosine Methylation after Extraction

Total C's analysed	728818685
Methylated C's in CpG context	40365434
Methylated C's in CHG context	2103572
Methylated C's in CHH context	5299122
Unmethylated C's in CpG context	38076494
Unmethylated C's in CHG context	176007533
Unmethylated C's in CHH context	466966530
Percentage methylation (CpG context)	51.5%
Percentage methylation (CHG context)	1.2%
Percentage methylation (CHH context)	1.1%

6   M-Bias Plot
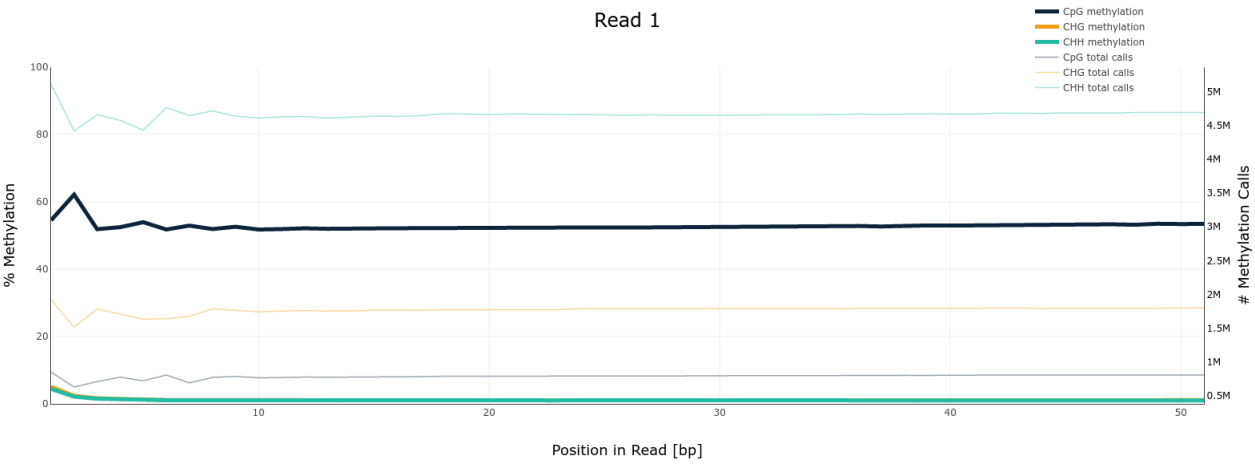
M-Bias Plot of Read 1

M-bias plot of read 2