



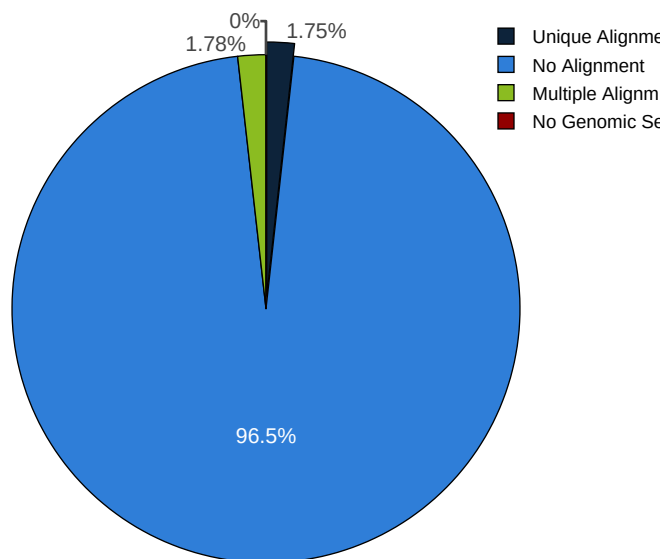
Bismark Processing Report

subset_1.fastq and subset_2.fastq

Data processed at 15:13:33 on 2021-08-13

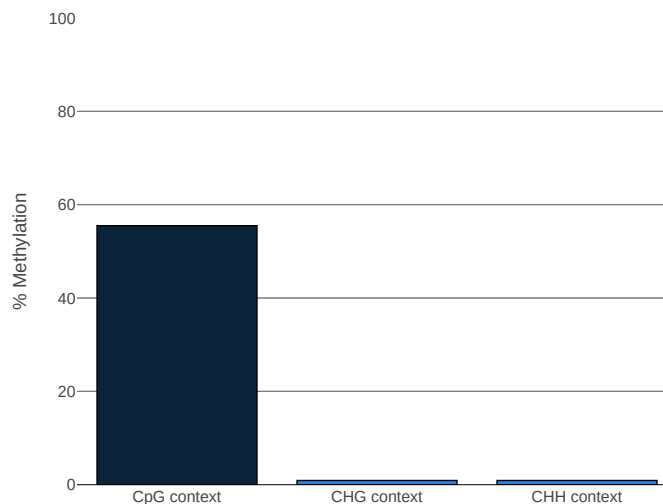
Alignment Stats

Sequence pairs analysed in total	458003
Paired-end alignments with a unique best hit	8032
Pairs without alignments under any condition	441797
Pairs that did not map uniquely	8174
Genomic sequence context not extractable (edges of chromosomes)	0



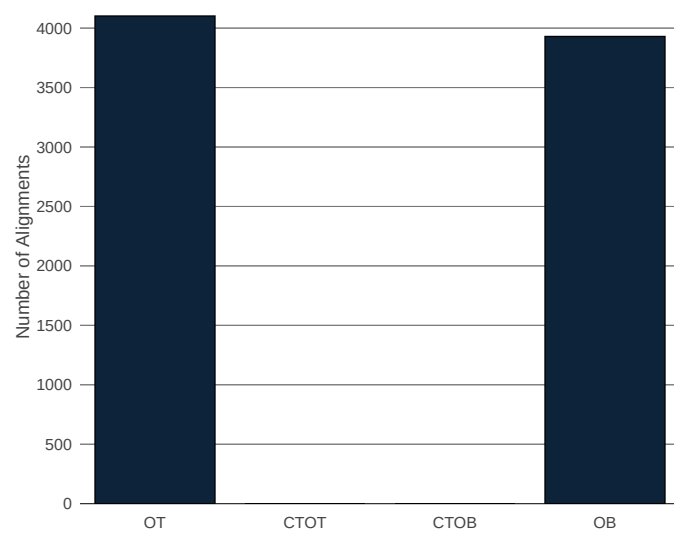
Cytosine Methylation

Total C's analysed	398669
Methylated C's in CpG context	13430
Methylated C's in CHG context	848
Methylated C's in CHH context	2426
Methylated C's in Unknown context	8
Unmethylated C's in CpG context	10750
Unmethylated C's in CHG context	93879
Unmethylated C's in CHH context	277336
Unmethylated C's in Unknown context	150
Percentage methylation (CpG context)	55.5%
Percentage methylation (CHG context)	0.9%
Percentage methylation (CHH context)	0.9%
Methylated C's in Unknown context	N/A%



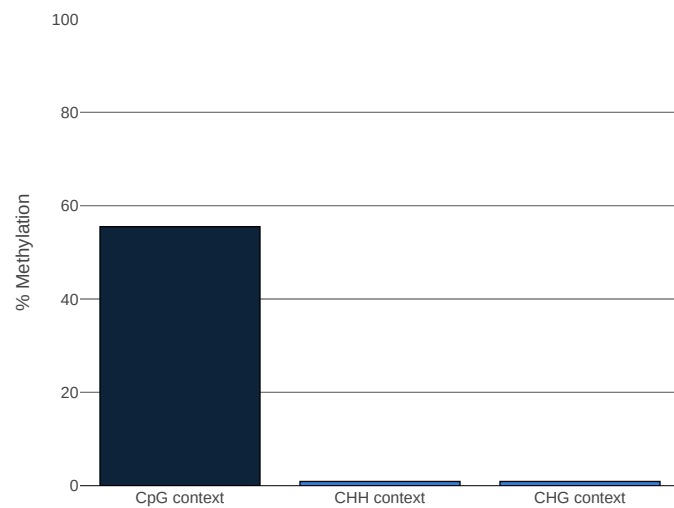
Alignment to Individual Bisulfite Strands

OT	4102	original top strand
CTOT	0	complementary to original top strand
CTOB	0	complementary to original bottom strand
OB	3930	original bottom strand



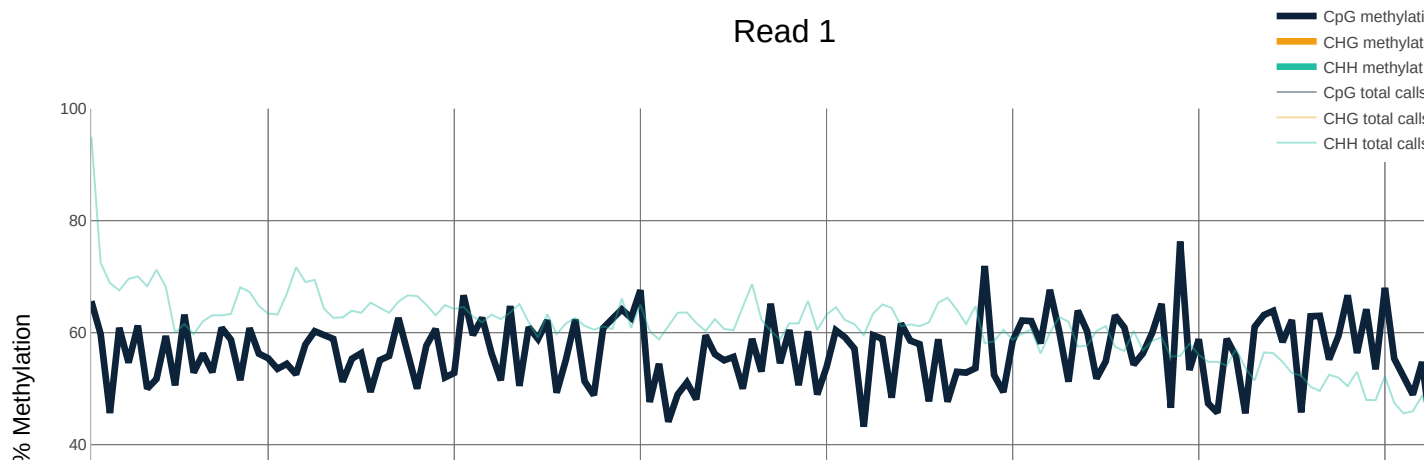
Cytosine Methylation after Extraction

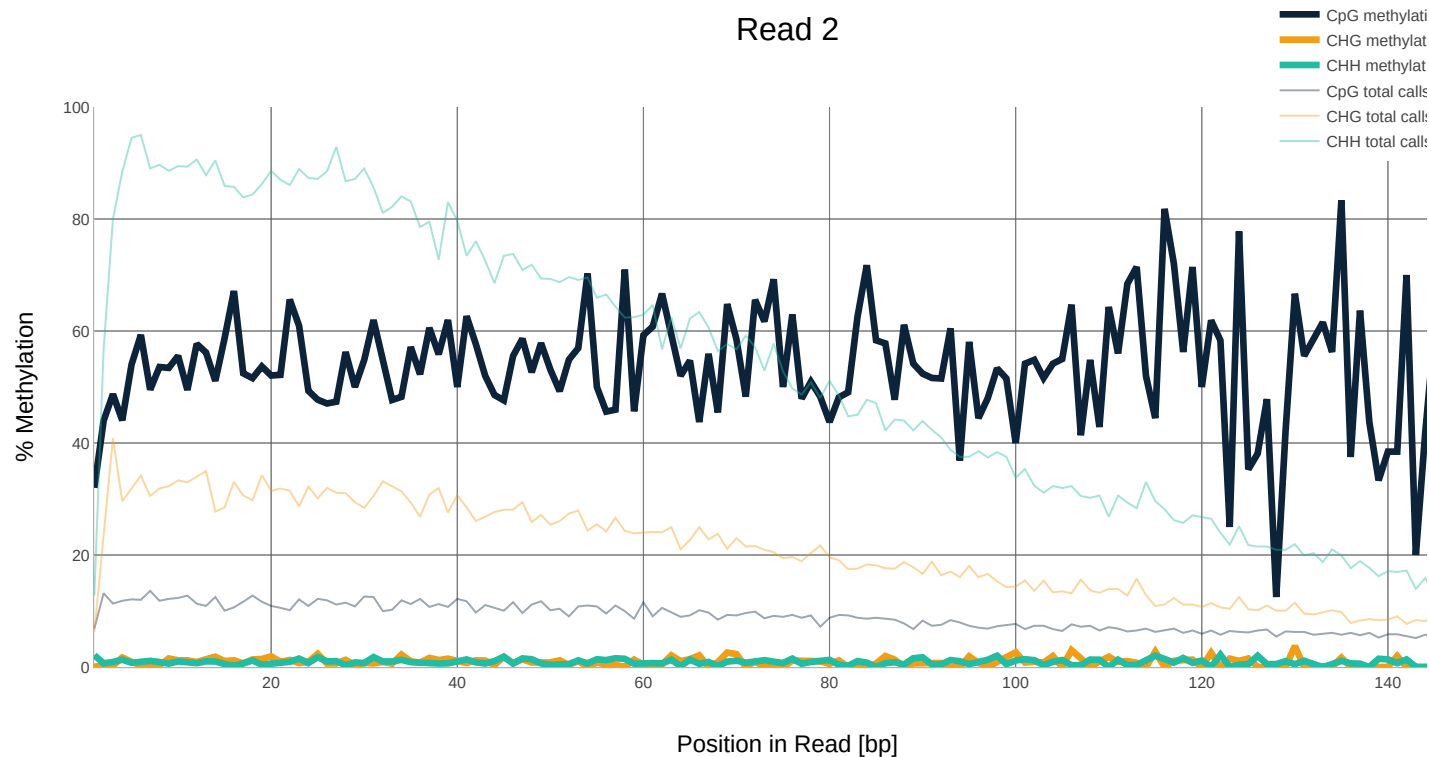
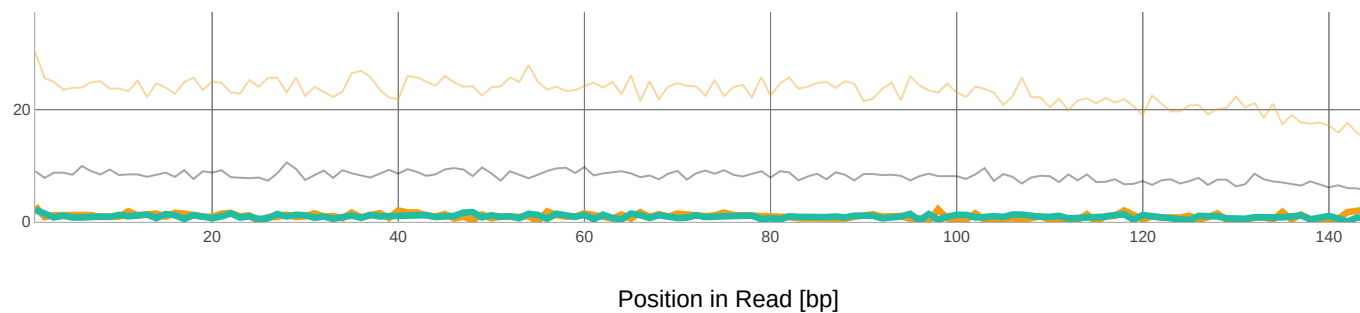
Total C's analysed	316985
Methylated C's in CpG context	10754
Methylated C's in CHG context	713
Methylated C's in CHH context	2009
Unmethylated C's in CpG context	8607
Unmethylated C's in CHG context	74641
Unmethylated C's in CHH context	220261
Percentage methylation (CpG context)	55.5%
Percentage methylation (CHG context)	0.9%
Percentage methylation (CHH context)	0.9%



M-Bias Plot

Read 1





Analysis produced by **Bismark** (version v0.23.1) - a tool to map bisulfite converted sequence reads and determine cytosine methylation states

Report graphs rendered using plot.ly, design last changed 07 Aug 2018