Bismark Processing Report
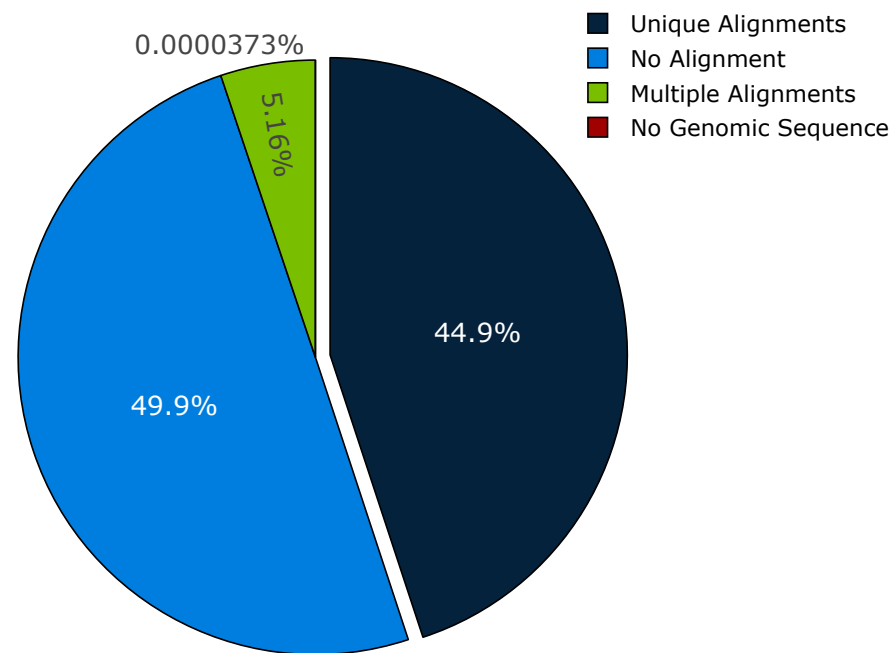
M5.R1_val_1.fq.gz and M5.R2_val_2.fq.gz

Data processed at 03:21:22 on 2024-06-18
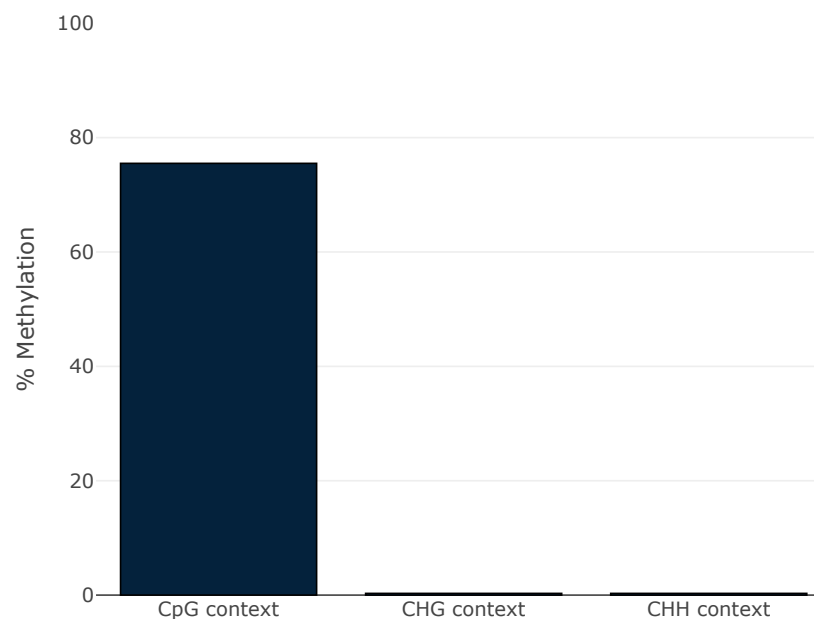
Alignment Stats

Sequence pairs analysed in total	310948683
Paired-end alignments with a unique best hit	139741303
Pairs without alignments under any condition	155171379
Pairs that did not map uniquely	16036001
Genomic sequence context not extractable (edges of chromosomes)	116

Cytosine Methylation

Total C's analysed	7026389776
Methylated C's in CpG context	259884172
Methylated C's in CHG context	4179555
Methylated C's in CHH context	17715123
Methylated C's in Unknown context	23303
Unmethylated C's in CpG context	84544750
Unmethylated C's in CHG context	1527790992
Unmethylated C's in CHH context	5132275184
Unmethylated C's in Unknown context	1227257
Percentage methylation (CpG context)	75.5%
Percentage methylation (CHG context)	0.3%
Percentage methylation (CHH context)	0.3%
Methylated C's in Unknown context	1.9%

Alignment to Individual Bisulfite Strands

OT	70744667	original top strand
CTOT	0	complementary to original top strand
CTOB	0	complementary to original bottom strand
OB	68996520	original bottom strand

Analysis produced by **Bismark** (version v0.24.2) - 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