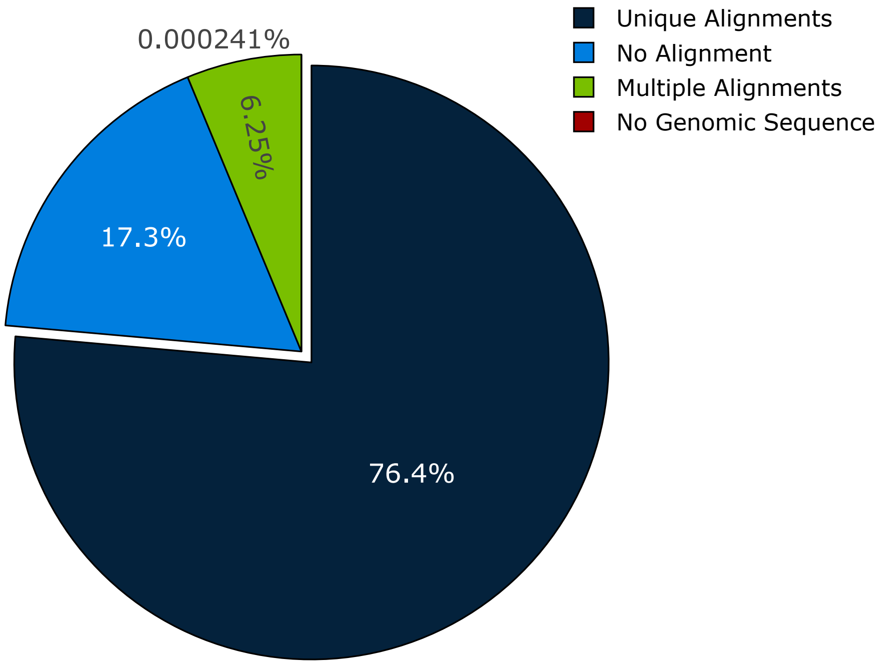
Bismark Processing Report

M6.R1_val_1.fq.gz and M6.R2_val_2.fq.gz

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

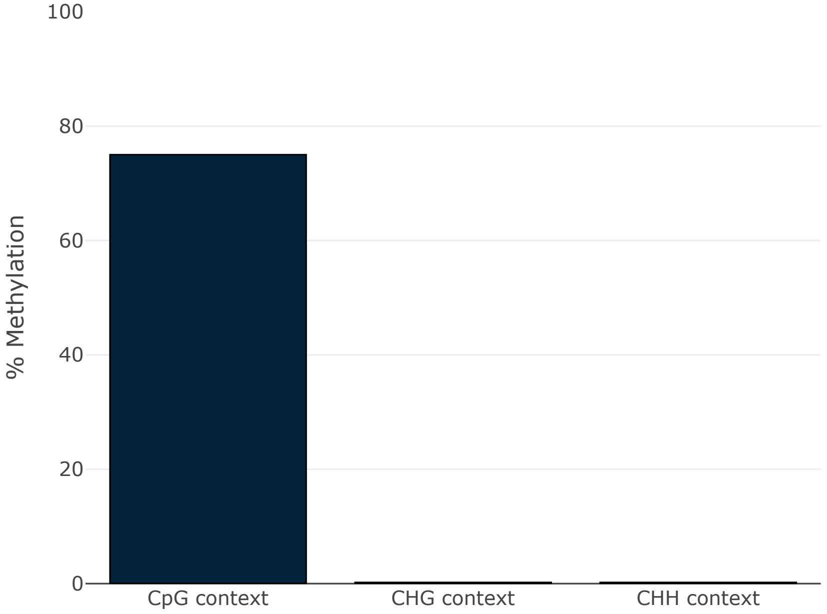
Alignment Stats

Sequence pairs analysed in total	334213888
Paired-end alignments with a unique best hit	255343860
Pairs without alignments under any condition	57978368
Pairs that did not map uniquely	20891660
Genomic sequence context not extractable (edges of chromosomes)	805



Cytosine Methylation

Total C's analysed	12883512537
Methylated C's in CpG context	399106184
Methylated C's in CHG context	4363337
Methylated C's in CHH context	17505908
Methylated C's in Unknown context	20151
Unmethylated C's in CpG context	133347657
Unmethylated C's in CHG context	2753986289
Unmethylated C's in CHH context	9575203162
Unmethylated C's in Unknown context	1223542
Percentage methylation (CpG context)	75.0%
Percentage methylation (CHG context)	0.2%
Percentage methylation (CHH context)	0.2%
Methylated C's in Unknown context	1.6%



Alignment to Individual Bisulfite Strands

OT	127957638	original top strand
CTOT	0	complementary to original top strand
CTOB	0	complementary to original bottom strand
OB	127385417	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