Bismark Processing Report
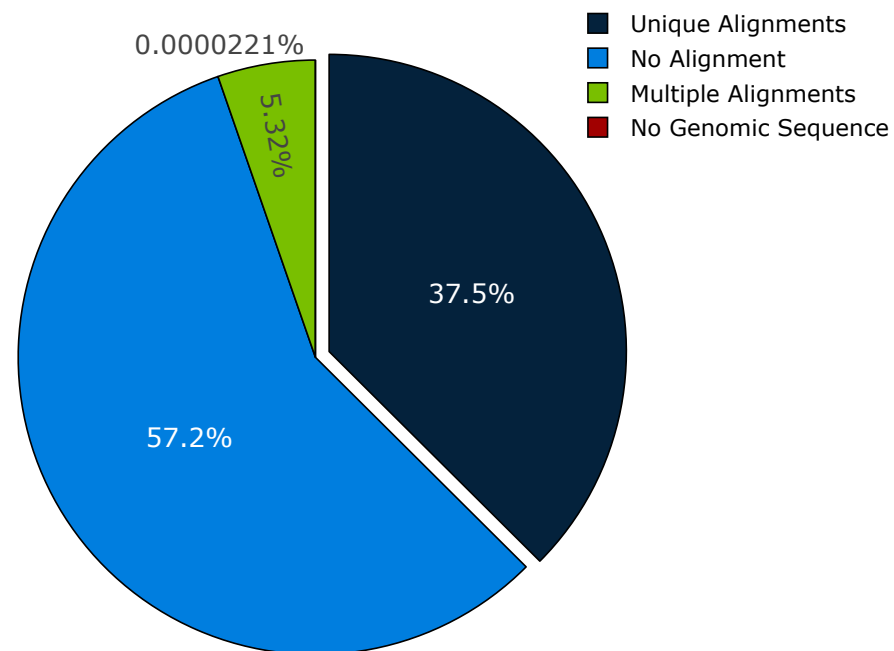
M3.R1_val_1.fq.gz and M3.R2_val_2.fq.gz

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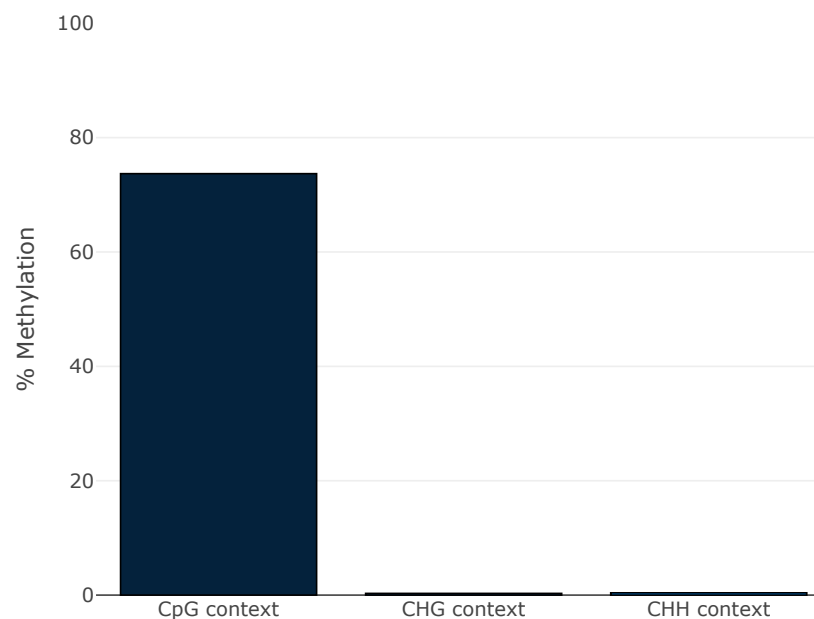
Alignment Stats

Sequence pairs analysed in total	421768182
Paired-end alignments with a unique best hit	157980023
Pairs without alignments under any condition	241366911
Pairs that did not map uniquely	22421248
Genomic sequence context not extractable (edges of chromosomes)	93

Cytosine Methylation

Total C's analysed	7661041387
Methylated C's in CpG context	304255279
Methylated C's in CHG context	4952598
Methylated C's in CHH context	20950926
Methylated C's in Unknown context	36237
Unmethylated C's in CpG context	108568550
Unmethylated C's in CHG context	1706536446
Unmethylated C's in CHH context	5515777588
Unmethylated C's in Unknown context	1746173
Percentage methylation (CpG context)	73.7%
Percentage methylation (CHG context)	0.3%
Percentage methylation (CHH context)	0.4%
Methylated C's in Unknown context	2.0%

Alignment to Individual Bisulfite Strands

OT	80210002	original top strand
CTOT	0	complementary to original top strand
CTOB	0	complementary to original bottom strand
OB	77769928	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