# Bismark Processing Report

/Volumes/web/seashell/bu-serine-wd/18-04-07/zr2096_1_s1_R1.fastq.gz and /Volumes/web/seashell/bu-serine-wd/18-04-07/zr2096_1_s1_R2.fastq.gz

Data processed at 16:32 on 2018-09-21

Alignment Stats

|	
Sequence pairs analysed in total	100000
Paired-end alignments with a unique best hit	13744
Pairs without alignments under any condition	81302
Pairs that did not map uniquely	4954
Genomic sequence context not extractable (edges of chromosomes)	0

- Unique Alignments
- No Alignment
- Multiple Alignments
- No Genomic Sequence
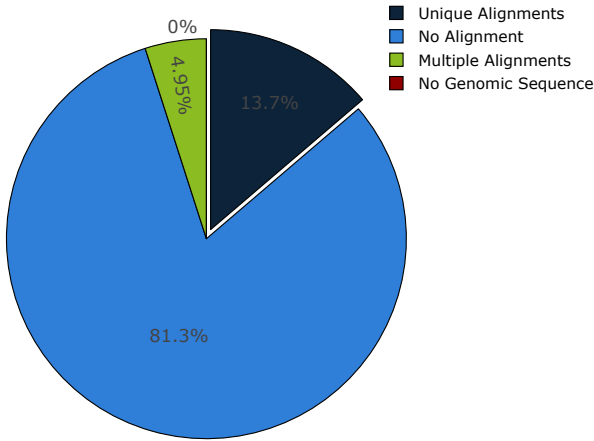
Cytosine Methylation

Total C's analysed	481569
Methylated C's in CpG context	47945
Methylated C's in CHG context	2774
Methylated C's in CHH context	7846
Methylated C's in Unknown context	624
Unmethylated C's in CpG context	17126
Unmethylated C's in CHG context	107925
Unmethylated C's in CHH context	297953
Unmethylated C's in Unknown context	1993
Percentage methylation (CpG context)	73.7%
Percentage methylation (CHG context)	2.5%
Percentage methylation (CHH context)	2.6%
Methylated C's in Unknown context	N/A%
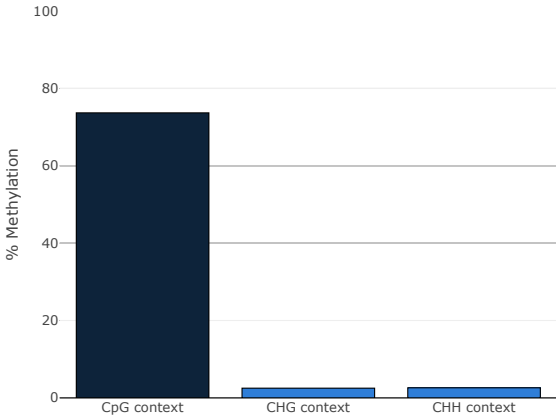
Alignment to Individual Bisulfite Strands
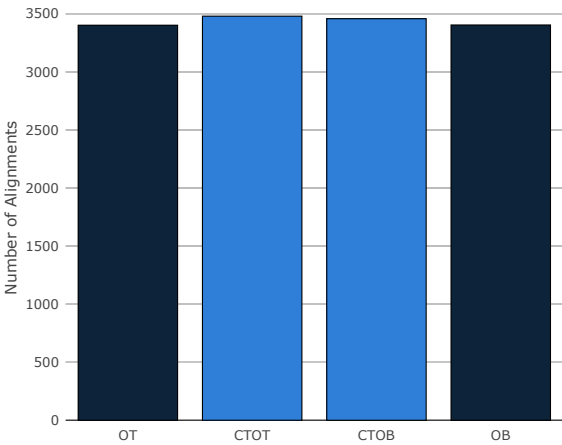
Cytosine Methylation after Extraction

Total C's analysed	304266
Methylated C's in CpG context	29931
Methylated C's in CHG context	1873
Methylated C's in CHH context	5172
Unmethylated C's in CpG context	10904
Unmethylated C's in CHG context	67806
Unmethylated C's in CHH context	188580
Percentage methylation (CpG context)	73.3%
Percentage methylation (CHG context)	2.7%
Percentage methylation (CHH context)	2.7%

M-Bias Plot

Read 2
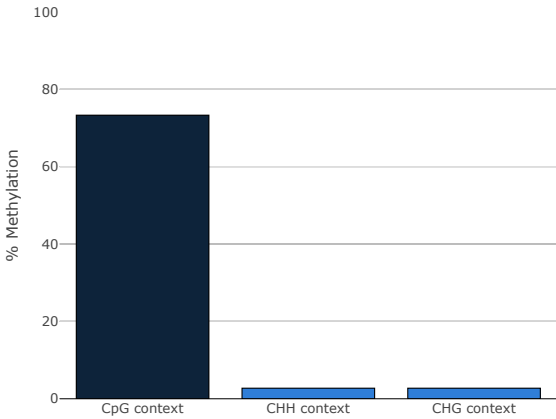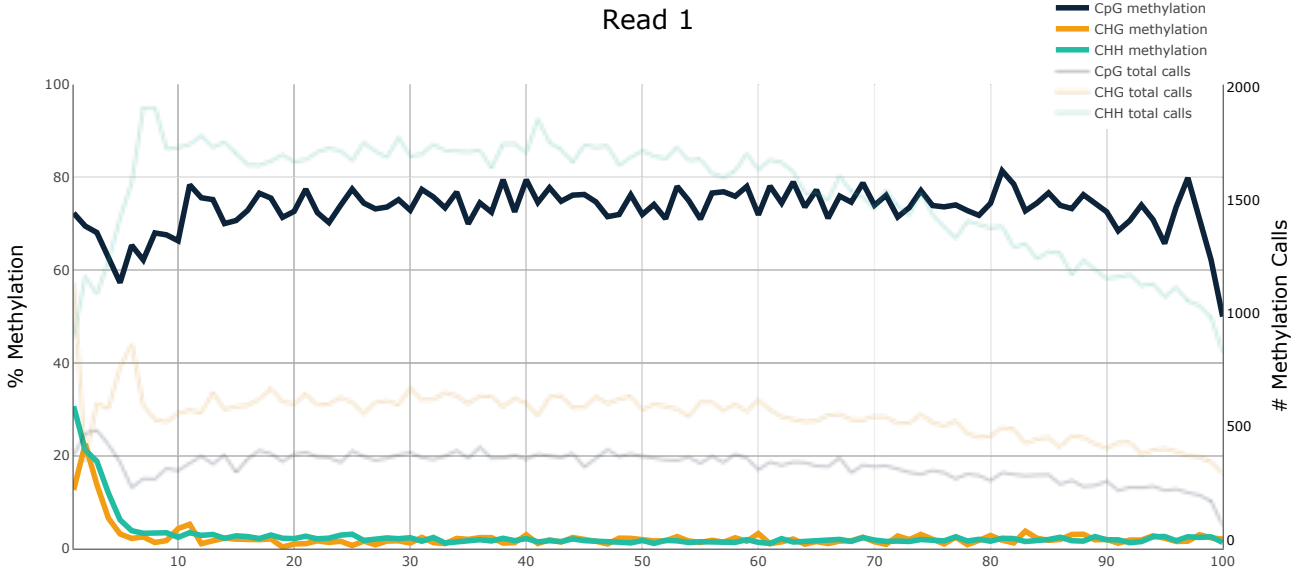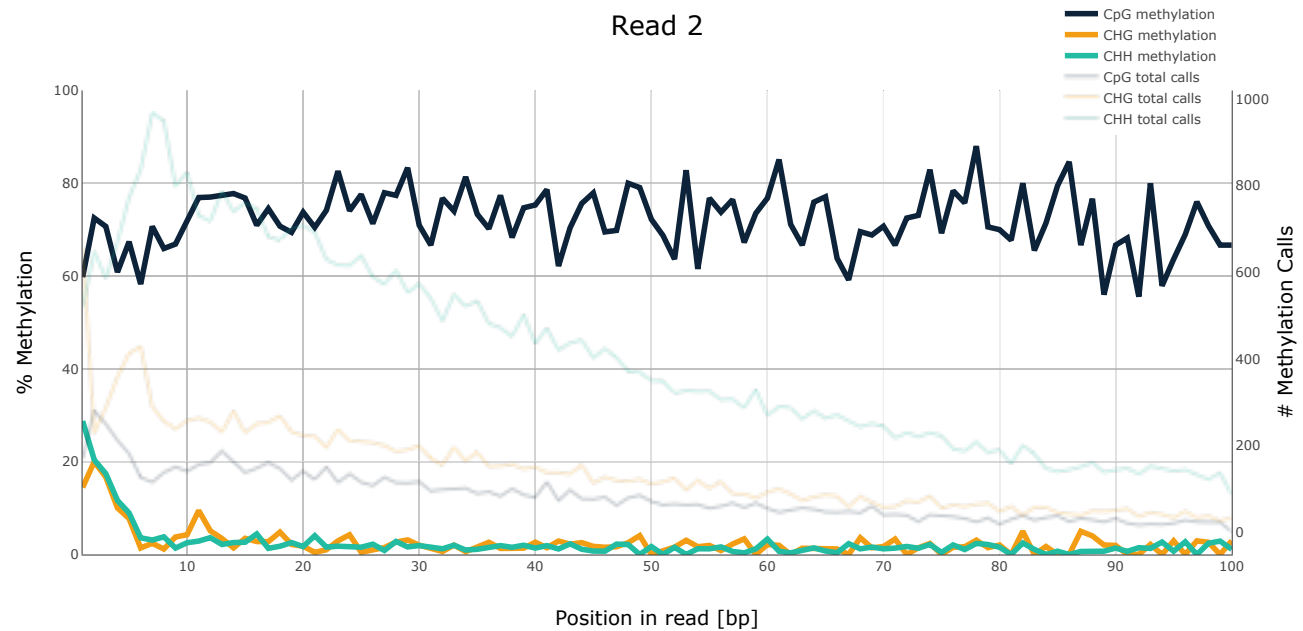
Analysis produced by **Bismark** (version v0.20.0) - a tool to map bisulfite converted sequence reads and determine cytosine methylation states

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

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