



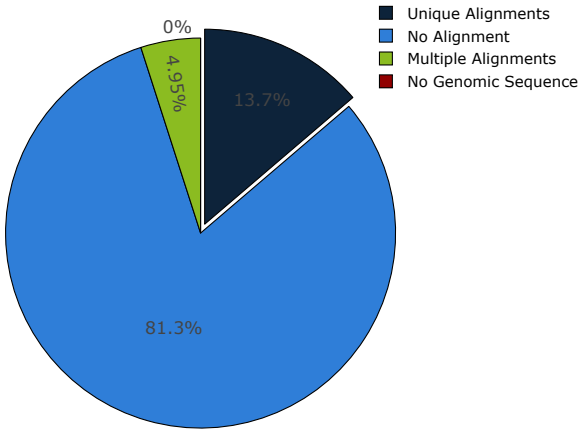
Bismark Processing Report

/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 17:48 on 2018-09-21

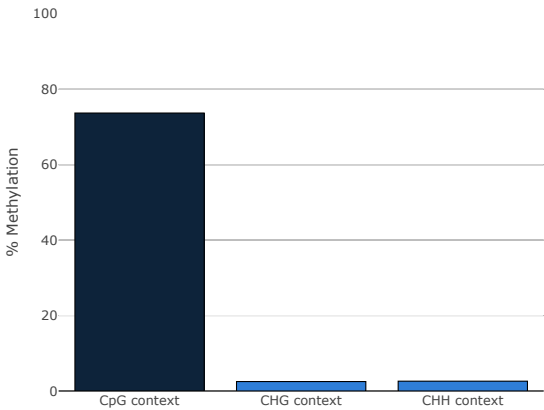
Alignment Stats

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



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

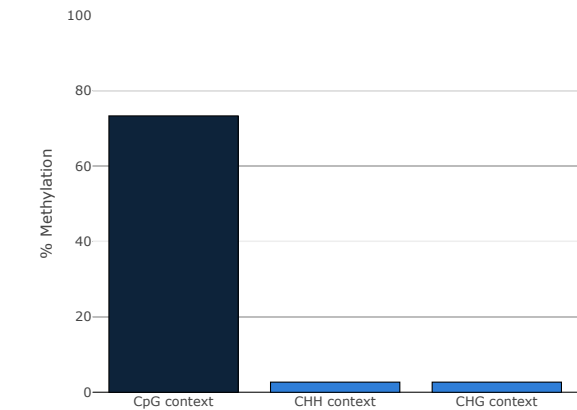
OT	3402	original top strand
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CTOT	3480	complementary to original top strand
CTOB	3458	complementary to original bottom strand
OB	3404	original bottom strand

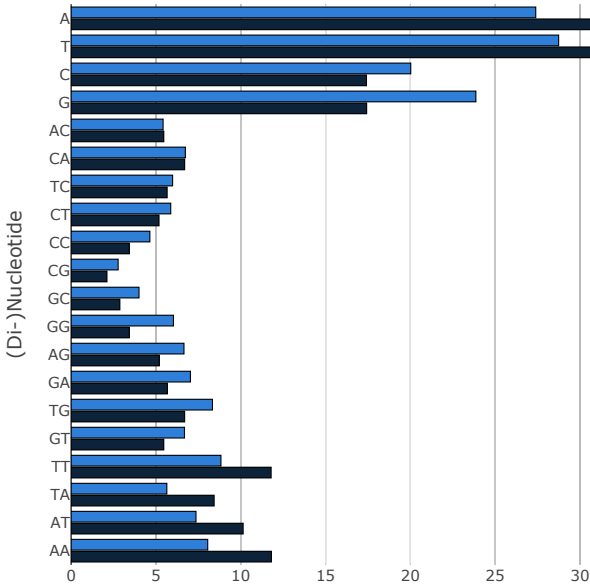
Cytosine Methylation after Extraction

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%

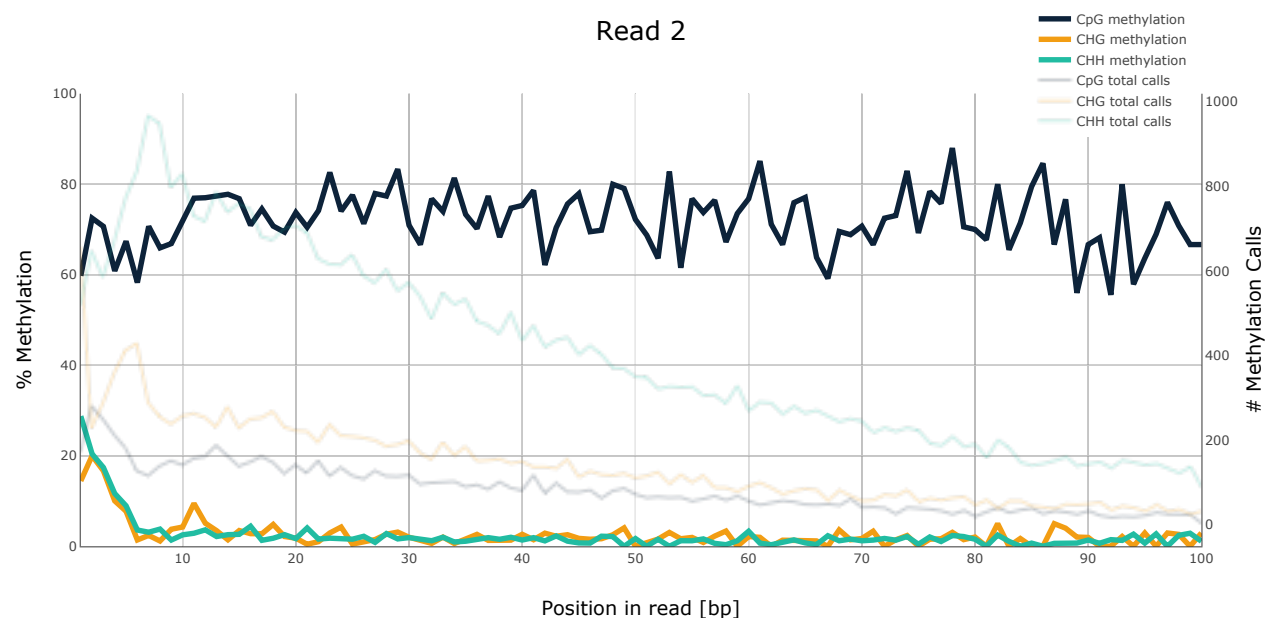
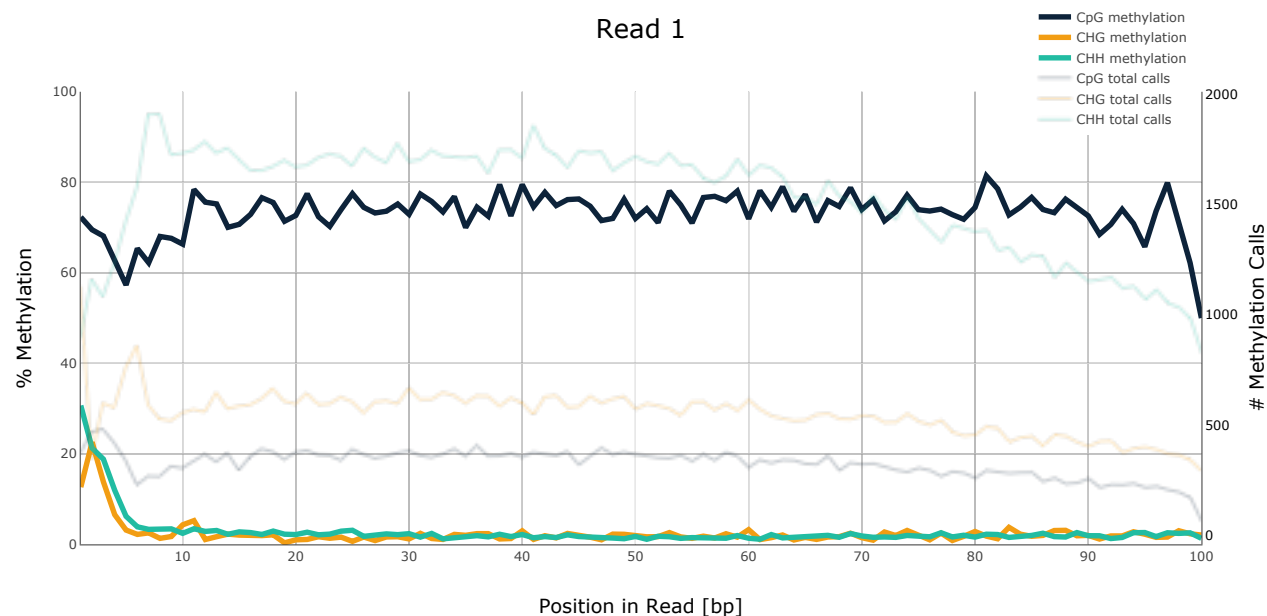


Nucleotide Coverage

Nucleotide Class	Counts Sample	Counts Genome	% in Sample	% in Genome	fold coverage
A	397765	223134775	27.39	32.59	0.002
T	417399	223043757	28.74	32.58	0.002
C	290760	119229119	20.02	17.41	0.002
G	346559	119267677	23.86	17.42	0.003
AC	77775	37359527	5.42	5.46	0.002
CA	96576	45827414	6.73	6.69	0.002
TC	85855	38778132	5.98	5.66	0.002
CT	84353	35498217	5.87	5.18	0.002
CC	66568	23444678	4.64	3.42	0.003
CG	39753	14458703	2.77	2.11	0.003
GC	57424	19646670	4.00	2.87	0.003
GG	86627	23423030	6.03	3.42	0.004
AG	95546	35548672	6.65	5.19	0.003
GA	100972	38810489	7.03	5.67	0.003
TG	119602	45837169	8.33	6.69	0.003
GT	95958	37387368	6.68	5.46	0.003
TT	126771	80726644	8.83	11.79	0.002
TA	80967	57701608	5.64	8.43	0.001
AT	105707	69431301	7.36	10.14	0.002
AA	115616	80795037	8.05	11.80	0.001



M-Bias Plot



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