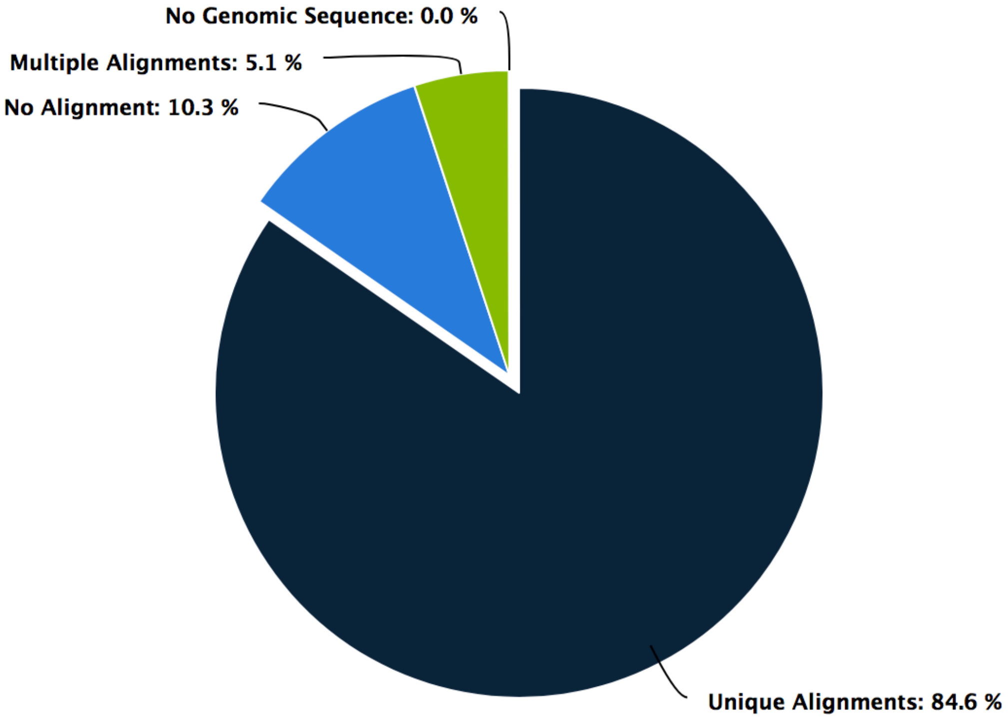
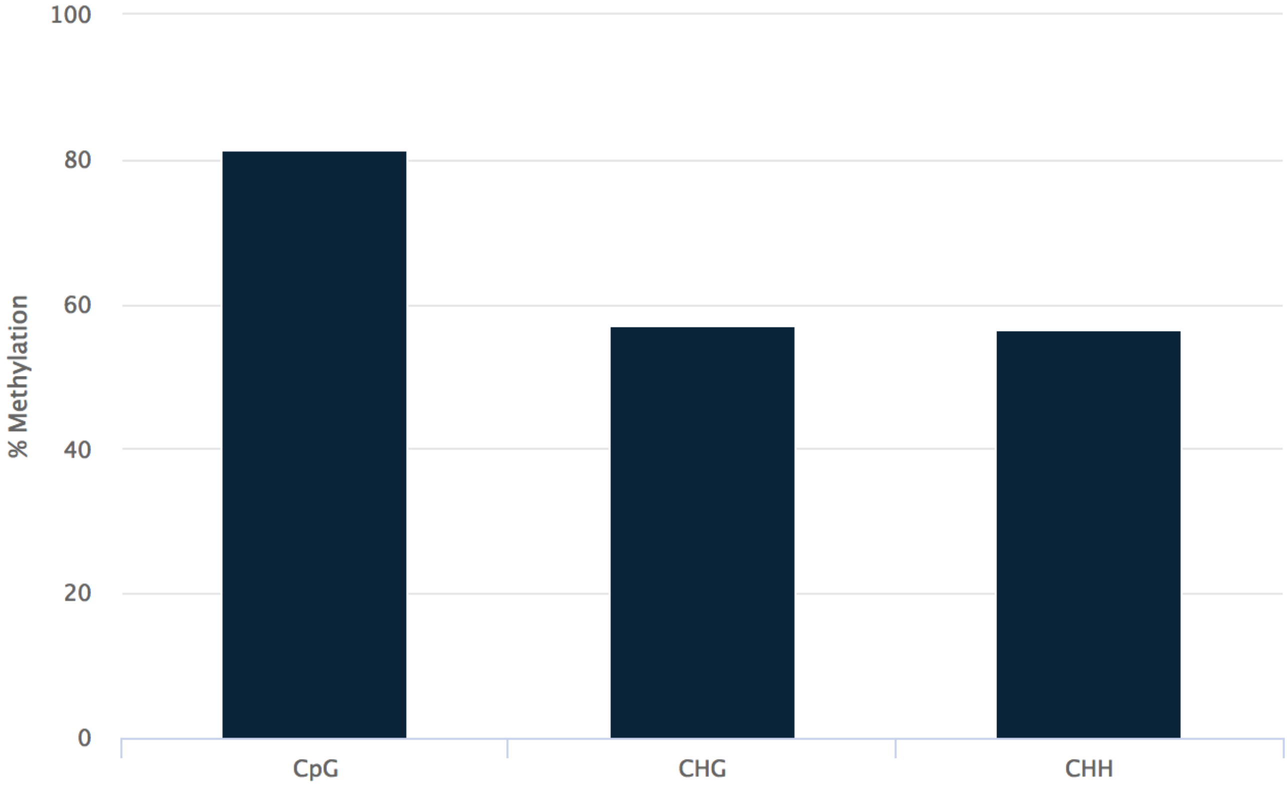
Alignment

Sequence pairs analysed in total	27,969,335
Paired-end alignments with a unique best hit	23,674,565
Pairs without alignments under any condition	2,880,261
Pairs that did not map uniquely	1,414,509
Genomic sequence context not extractable (edges of chromosomes)	0



Cytosine Methylation

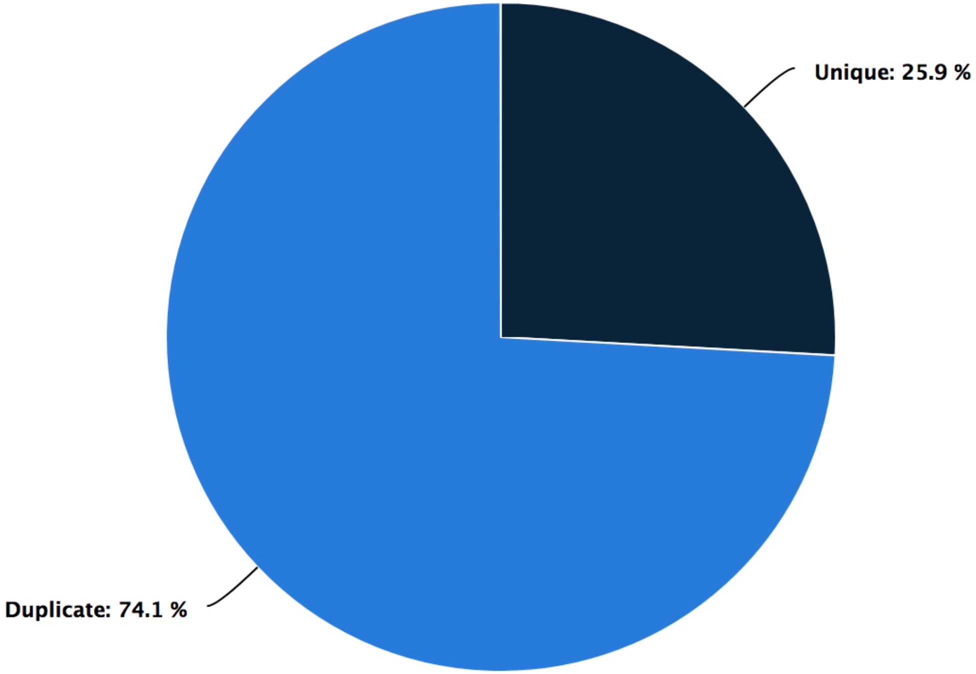
Total C's analysed	1,434,012,062
Methylated C's in CpG context	118,157,109
Methylated C's in CHG context	194,100,620
Methylated C's in CHH context	537,224,660
Methylated C's in Unknown context	56,867
Unmethylated C's in CpG context	27,151,741
Unmethylated C's in CHG context	145,986,557
Unmethylated C's in CHH context	411,391,375
Unmethylated C's in Unknown context	74,234
Percentage methylation (CpG context)	81.3%
Percentage methylation (CHG context)	57.1%
Percentage methylation (CHH context)	56.6%
Methylated C's in Unknown context	N/A%



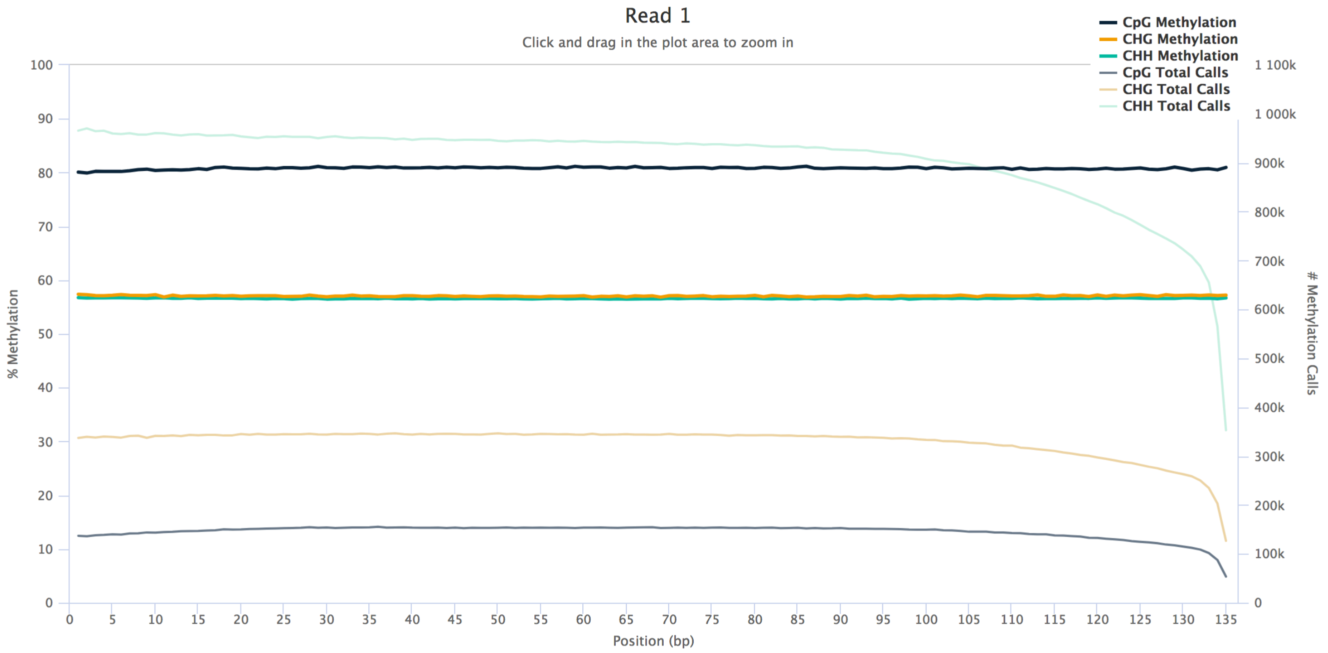
Deduplication

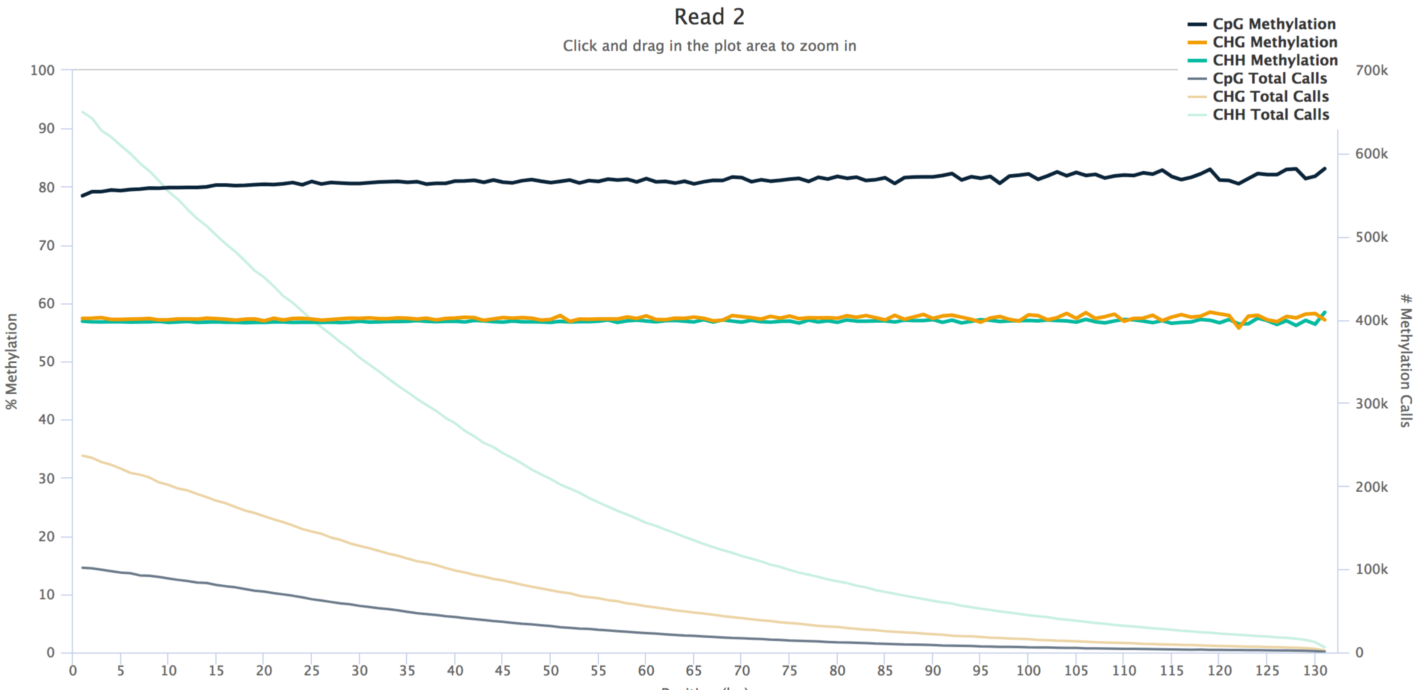
Alignments analysed	23,674,565
Unique alignments	6,125,868
Duplicates removed	17,548,697

Duplicated alignments were found at **5093996** different positions



M-Bias Plot


Read 1
Click and drag in the plot area to zoom in
CpG Methylation
CHG Methylation
CHH Methylation
CpG Total Calls
CHG Total Calls
CHH Total Calls
% Methylation
100
90
80
70
60
50
40
30
20
10
0
Methylation Calls
1 100k
1 000k
900k
800k
700k
600k
500k
400k
300k
200k
100k
0
Position (bp)
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
105
110
115
120
125
130
135


Read 2
Click and drag in the plot area to zoom in
CpG Methylation
CHG Methylation
CHH Methylation
CpG Total Calls
CHG Total Calls
CHH Total Calls
% Methylation
100
90
80
70
60
50
40
30
20
10
0
Methylation Calls
700k
600k
500k
400k
300k
200k
100k
0
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
105
110
115
120
125
130