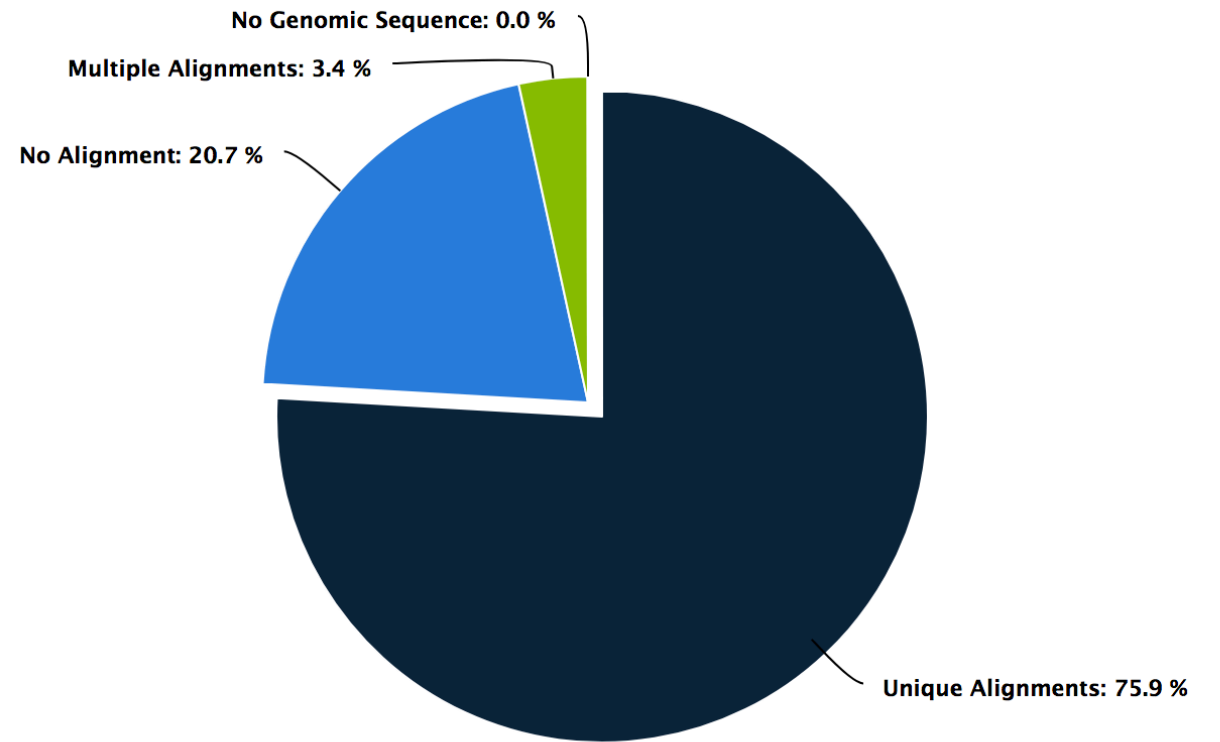


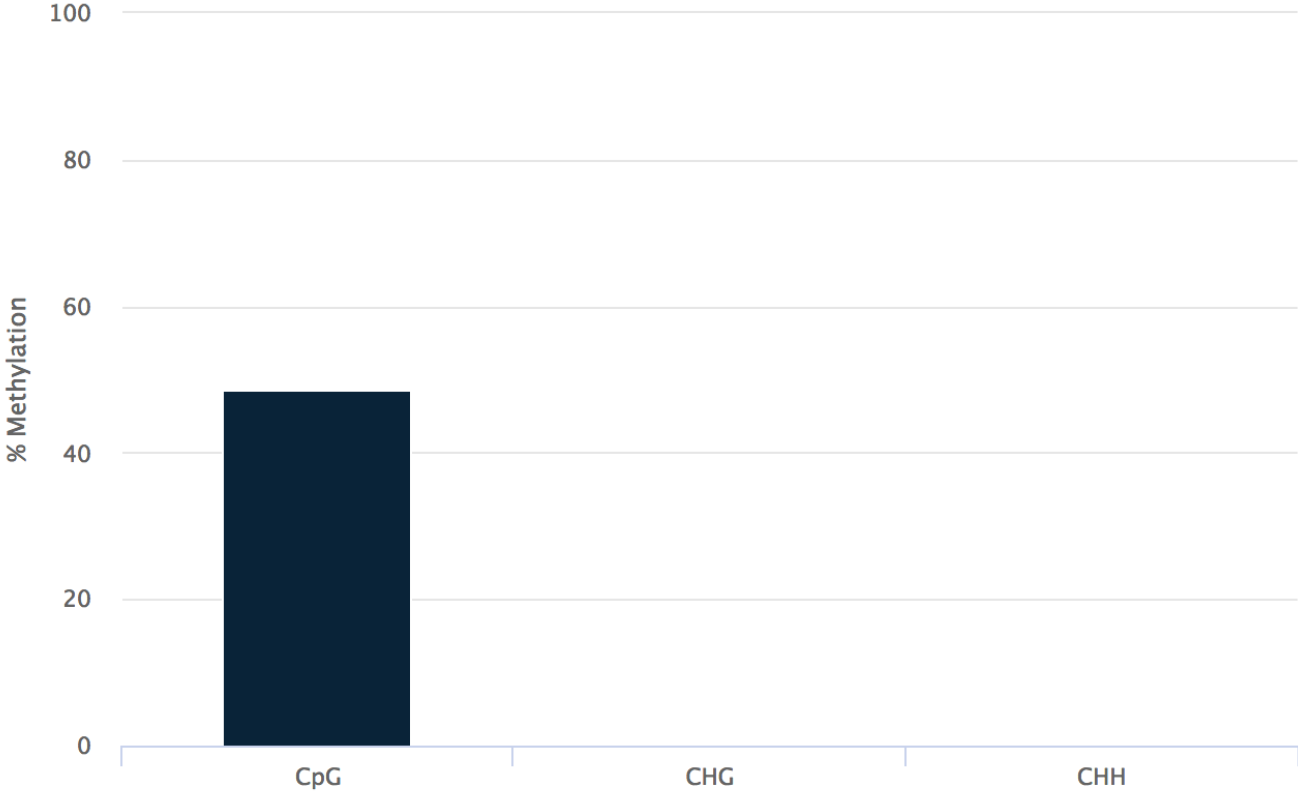
Alignment

Sequence pairs analysed in total	26,172,026
Paired-end alignments with a unique best hit	19,866,626
Pairs without alignments under any condition	5,412,344
Pairs that did not map uniquely	893,056
Genomic sequence context not extractable (edges of chromosomes)	0



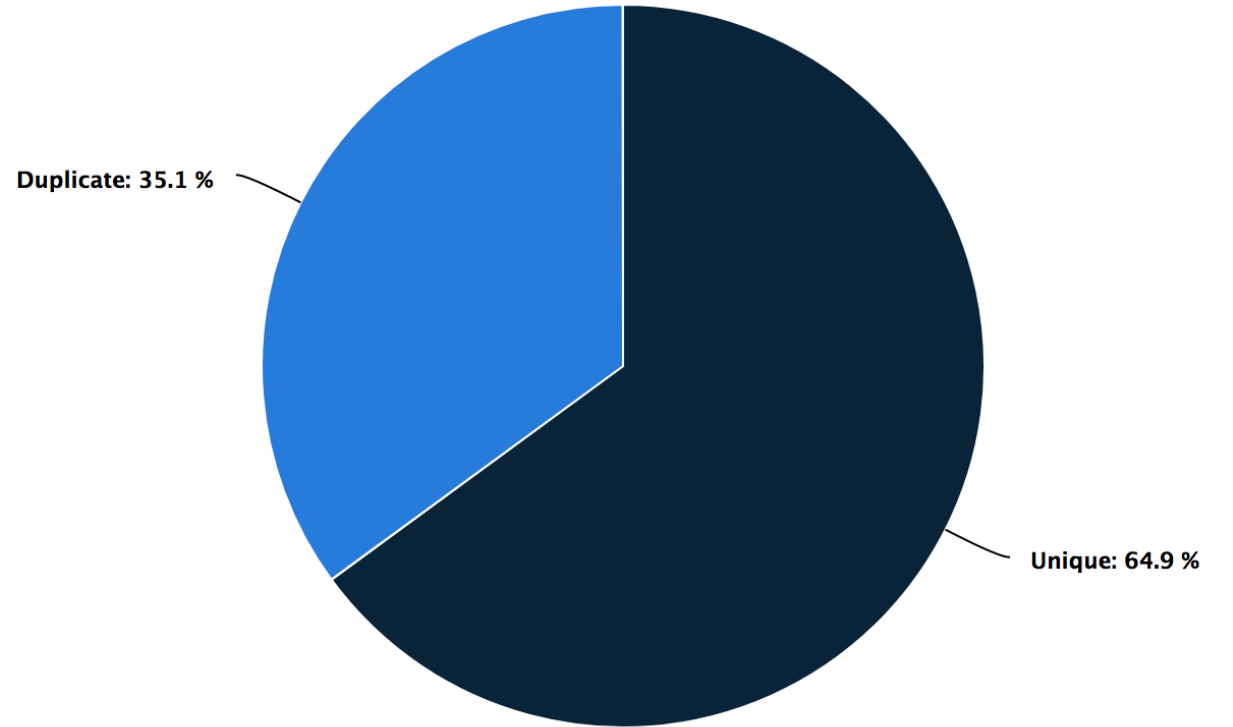
Cytosine Methylation

Total C's analysed	1,192,800,239
Methylated C's in CpG context	54,370,211
Methylated C's in CHG context	645,155
Methylated C's in CHH context	1,651,776
Methylated C's in Unknown context	3,135
Unmethylated C's in CpG context	57,624,737
Unmethylated C's in CHG context	286,457,034
Unmethylated C's in CHH context	792,051,326
Unmethylated C's in Unknown context	244,303
Percentage methylation (CpG context)	48.5%
Percentage methylation (CHG context)	0.2%
Percentage methylation (CHH context)	0.2%
Methylated C's in Unknown context	N/A%



Deduplication

Alignments analysed	19,866,626
Unique alignments	12,902,361
Duplicates removed	6,964,265
Duplicated alignments were found at 4832281 different positions	



M-Bias Plot

