Reads Summary
−−−−−−−−−−−−
QC−passed reads : 500,000
QC−failed reads : 0
Number of single−fragments : 0
Number of reads paired in sequencing : 500,000

Duplicate reads : 0 (0.00%)
Number of reads aligned : 500,000 (100.00%)
Number of reads mapped : 468,465 (93.69%)

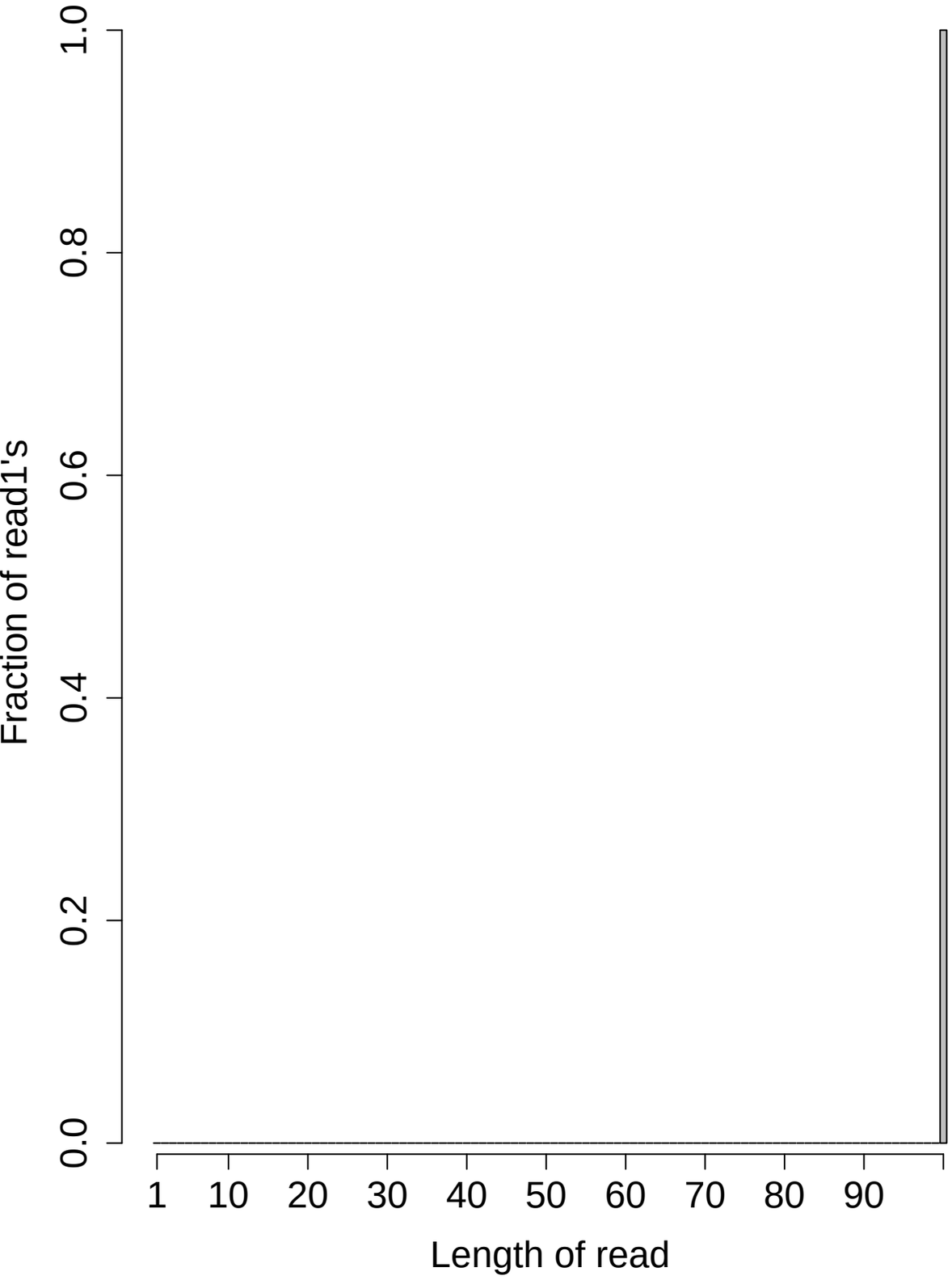
Number of read1's : 250,000
Number of read2's : 250,000
Number of reads properly paired : 499,998 (100.00%)
Number of reads with itself and mate aligned : 500,000 (100.00%)

Bases Summary
−−−−−−−−−−−−
QC−passed bases : 50,000,000
QC−failed bases : 0
Number of bases in single−fragments : 0
Number of bases paired in sequencing : 50,000,000

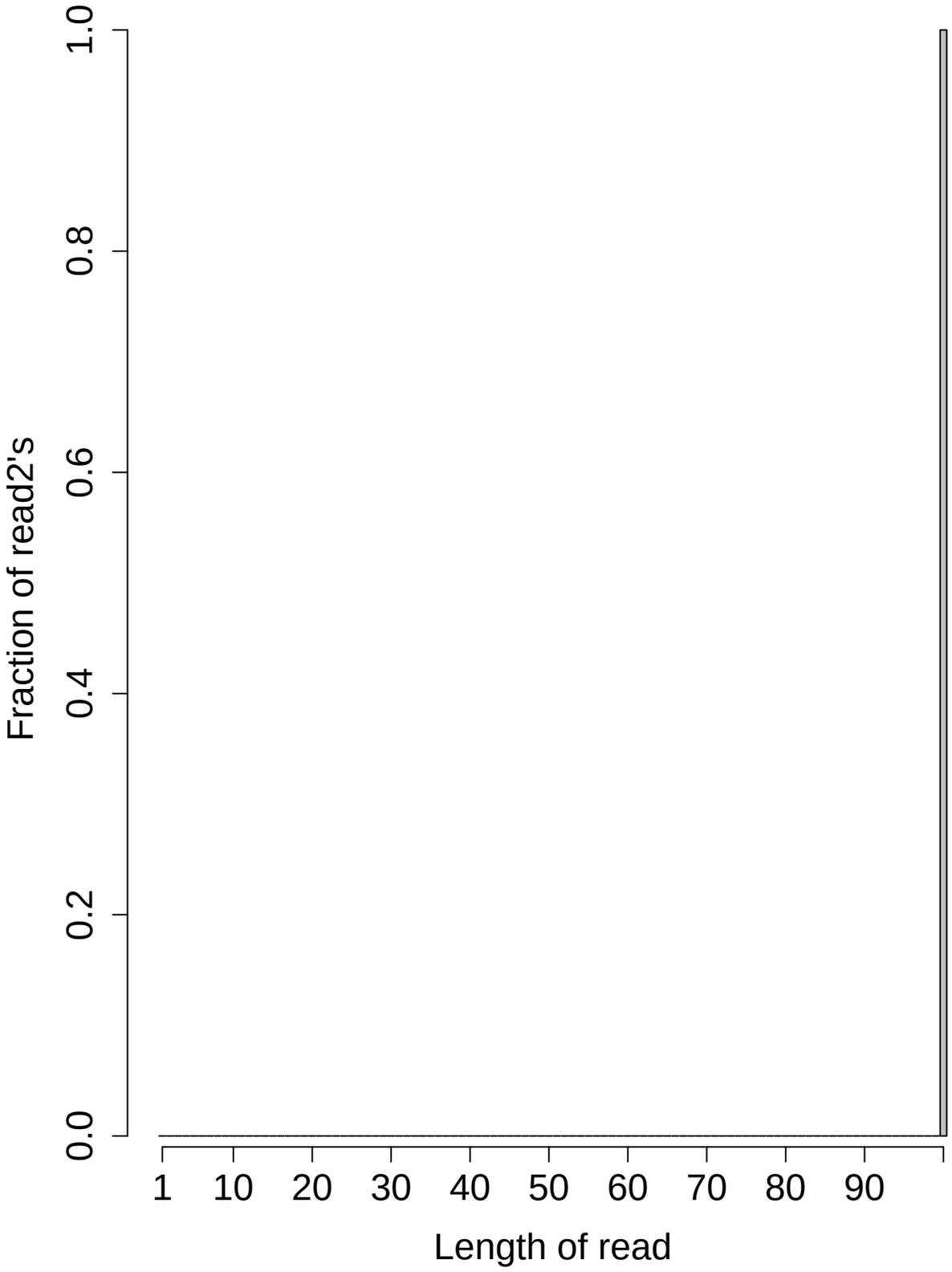
Duplicate bases : 0 (0.00%)
Number of bases aligned : 49,975,689 (99.95%)
Number of bases mapped : 46,823,863 (93.65%)

Read length distribution

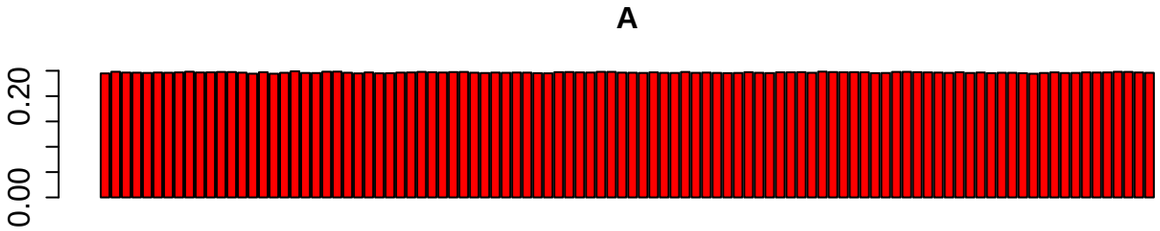
Read 1

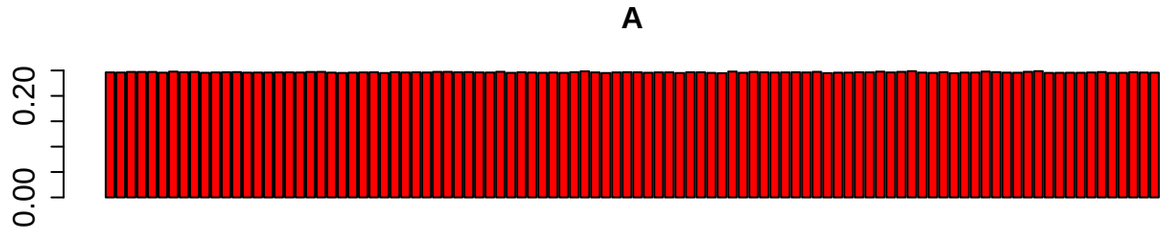


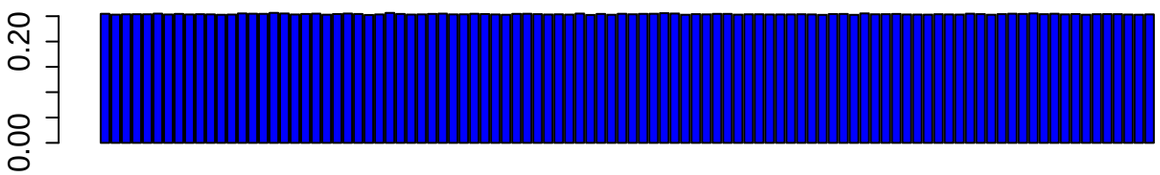
Read 2

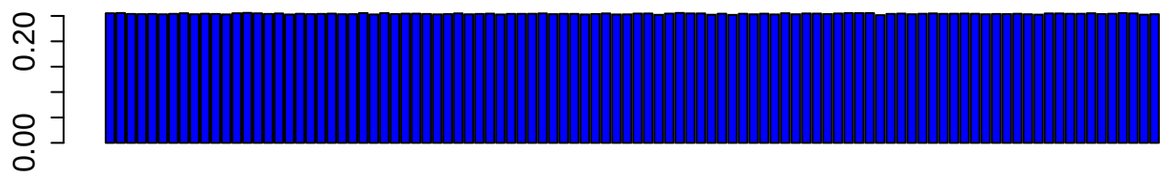


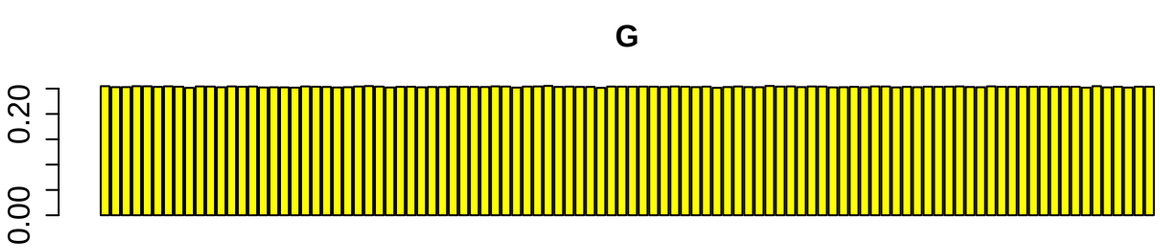
Nucleotide composition variation (Read1, Read2)

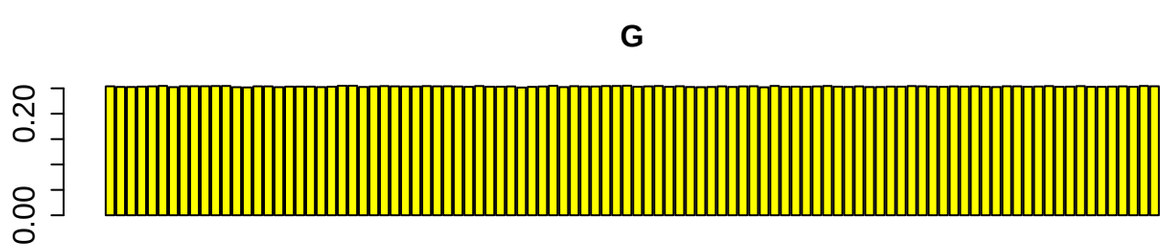


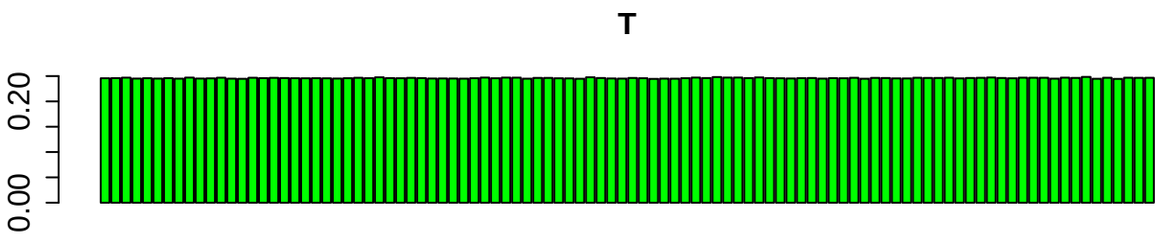


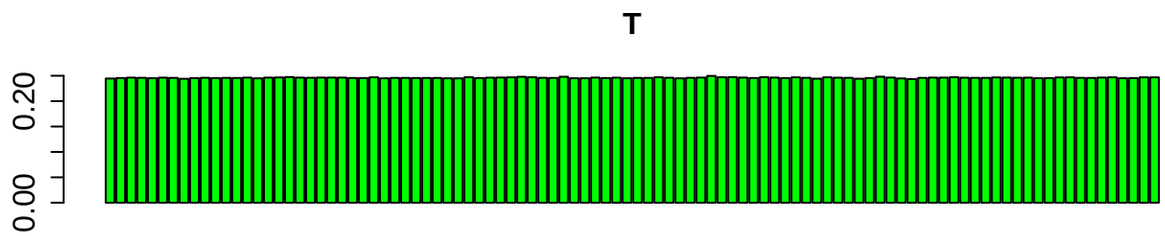


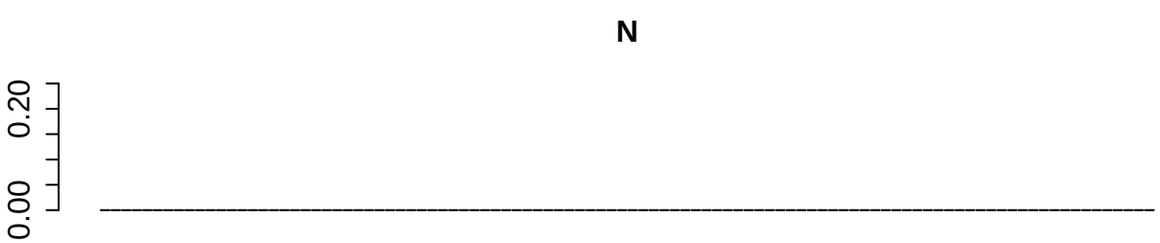


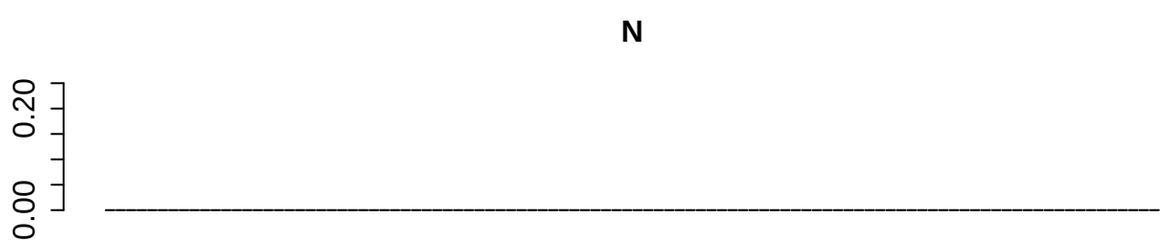






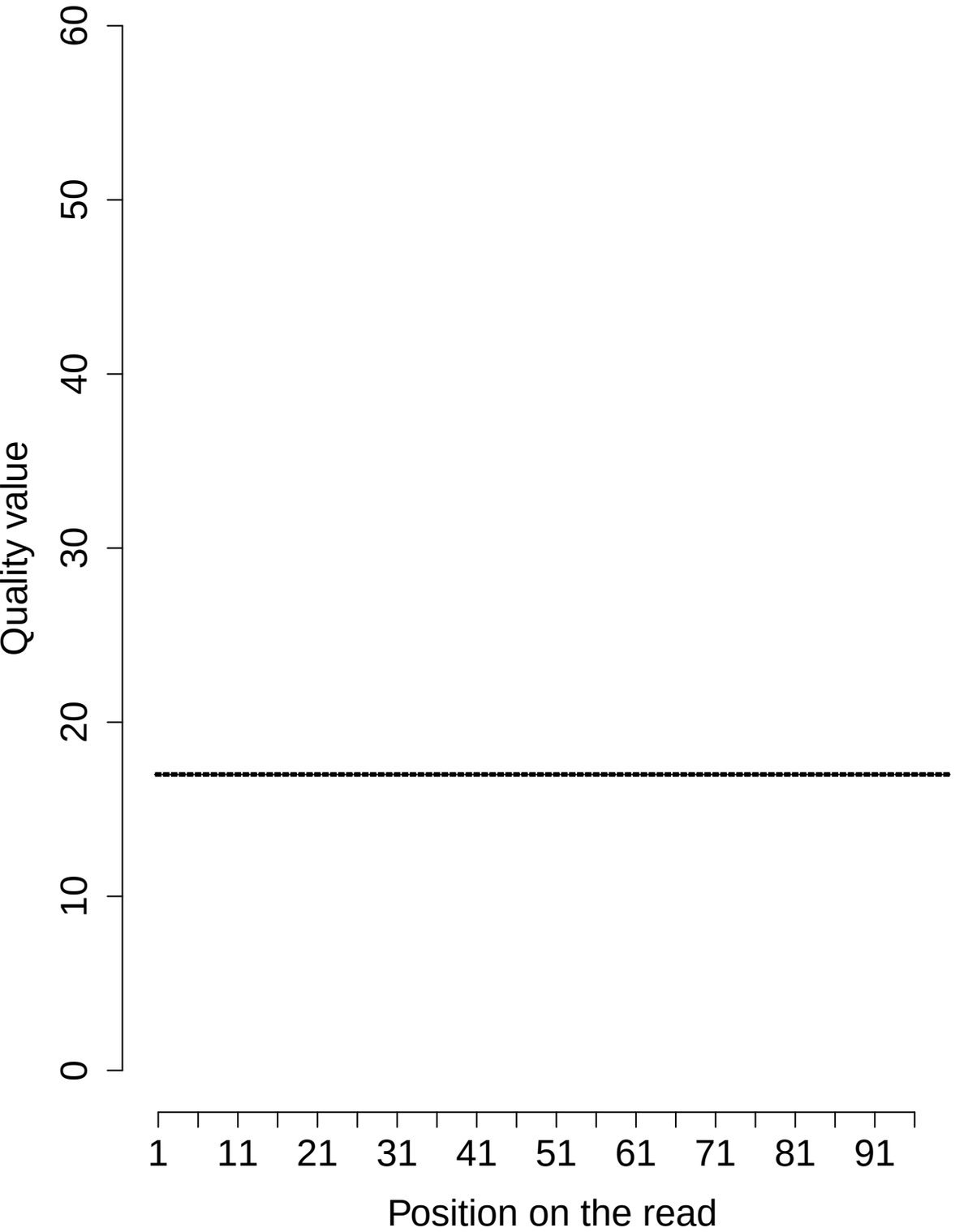




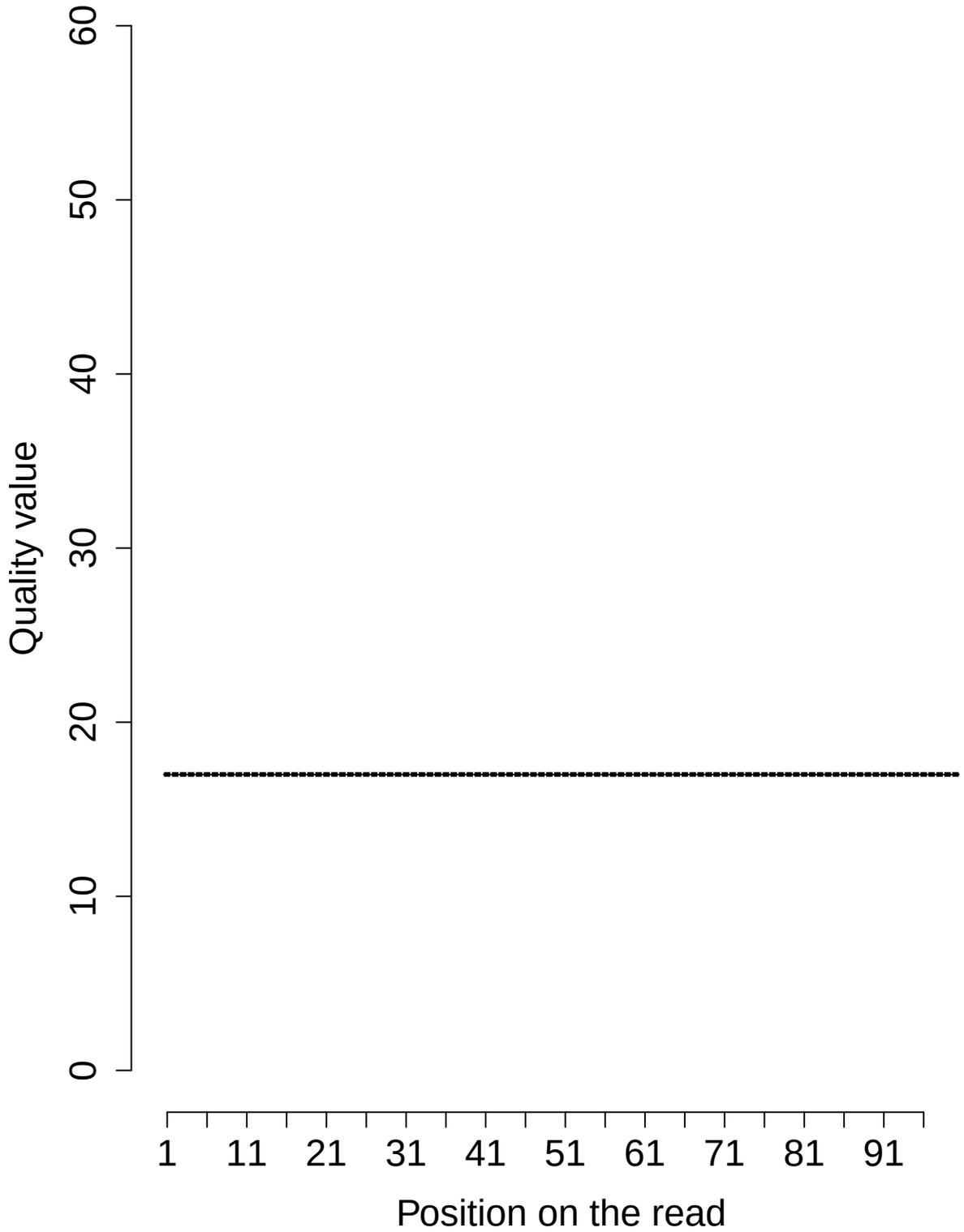


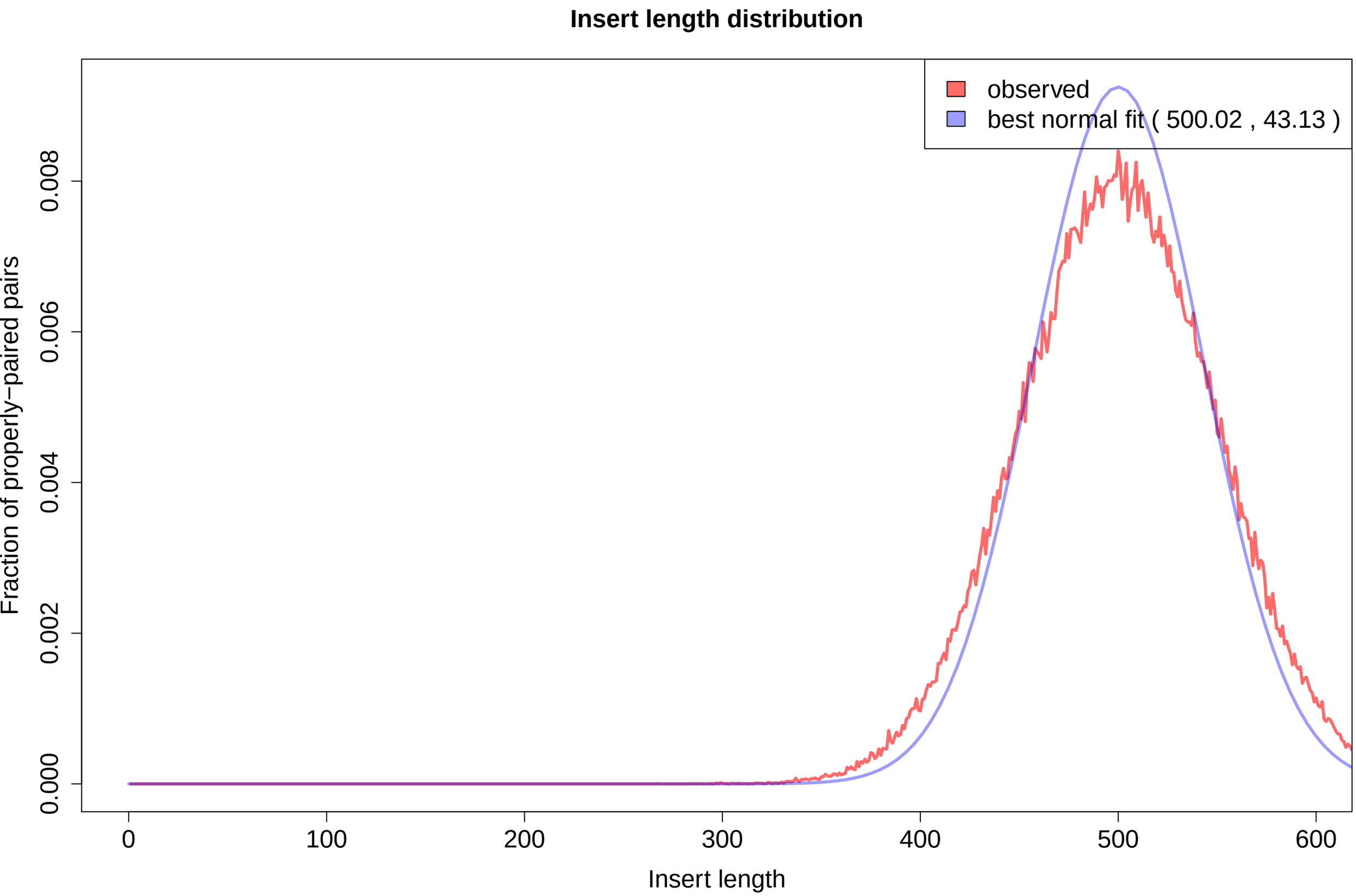
Quality value variation (Read1,Read2)

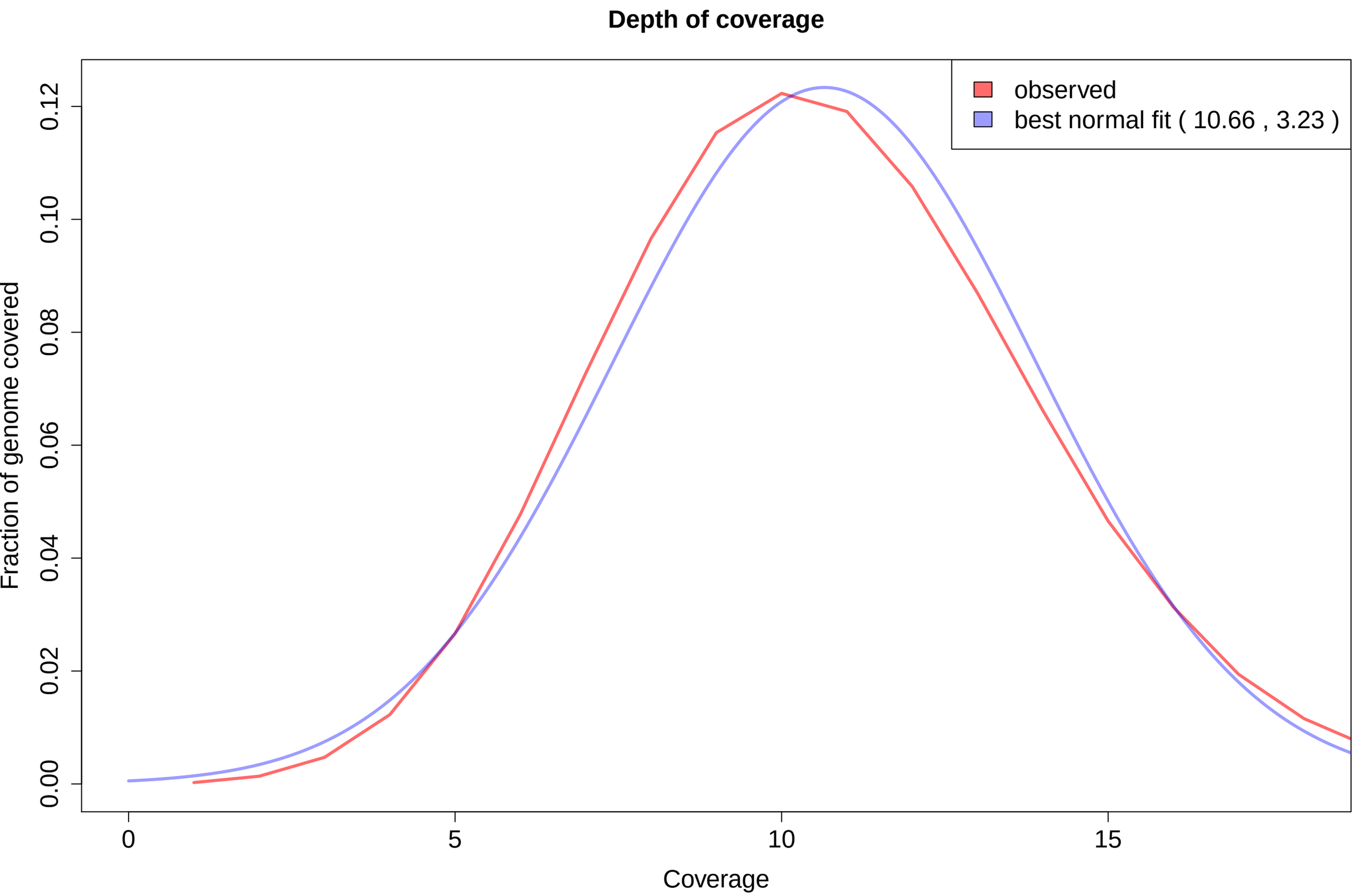
Read 1

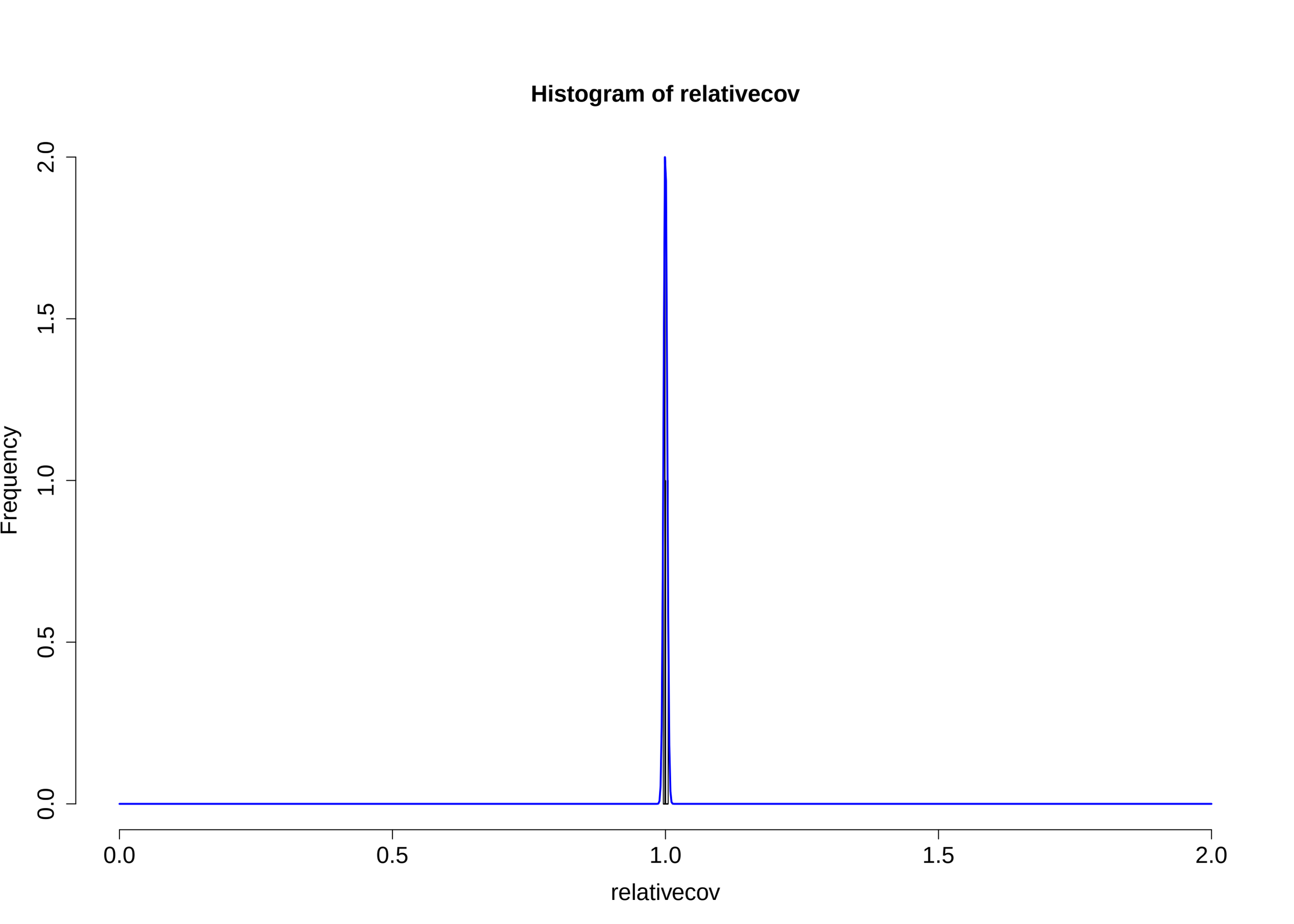


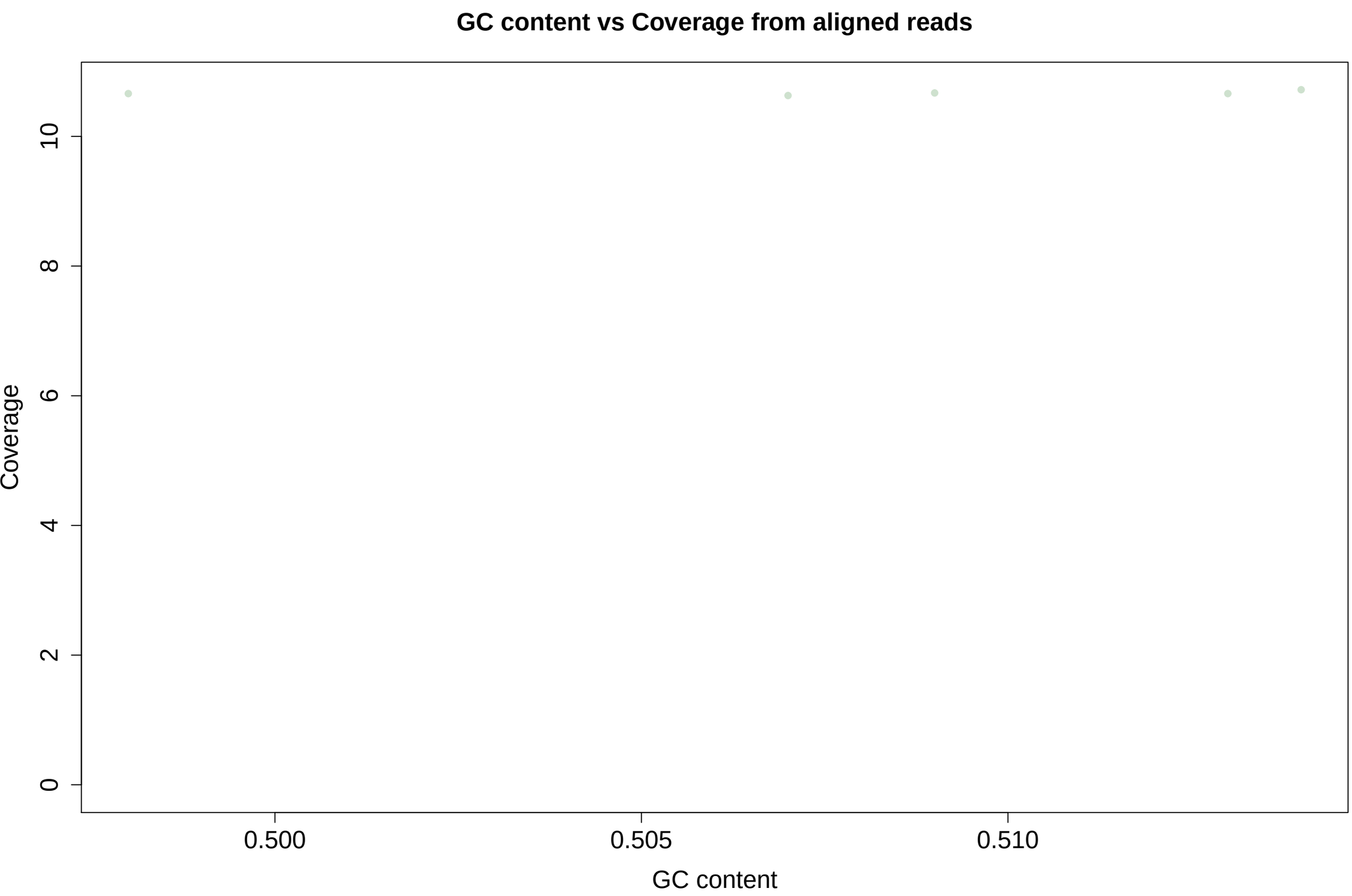
Read 2




Insert length distribution
observed
best normal fit (500.02 , 43.13)
Fraction of properly−paired pairs
0.000
0.002
0.004
0.006
0.008
0
100
200
300
400
500
600
Insert length

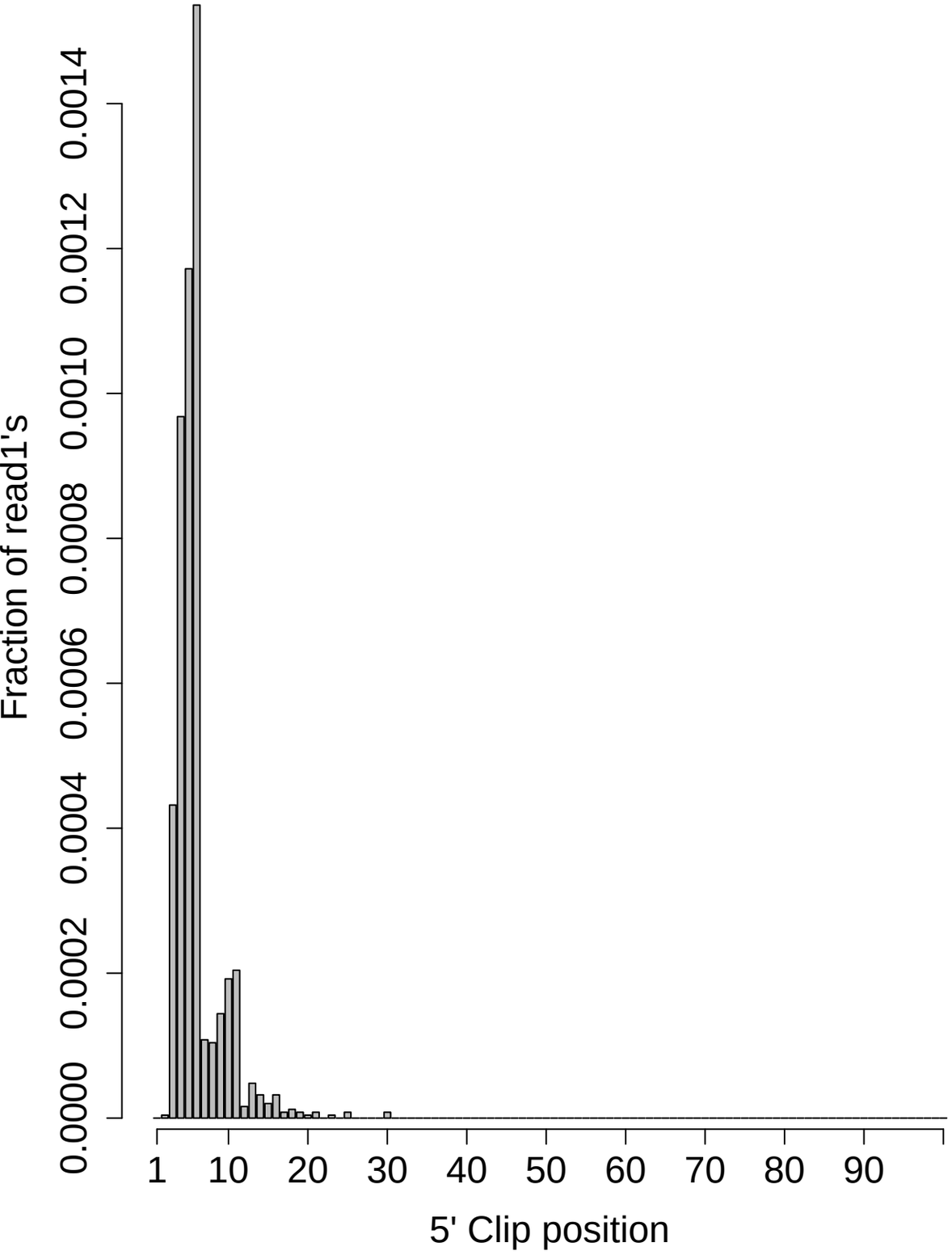

Depth of coverage
observed
best normal fit (10.66 , 3.23)
Fraction of genome covered
0.00
0.02
0.04
0.06
0.08
0.10
0.12
0
5
10
15
Coverage


Histogram of relativecov
Frequency
0.0
0.5
1.0
1.5
2.0
relativecov

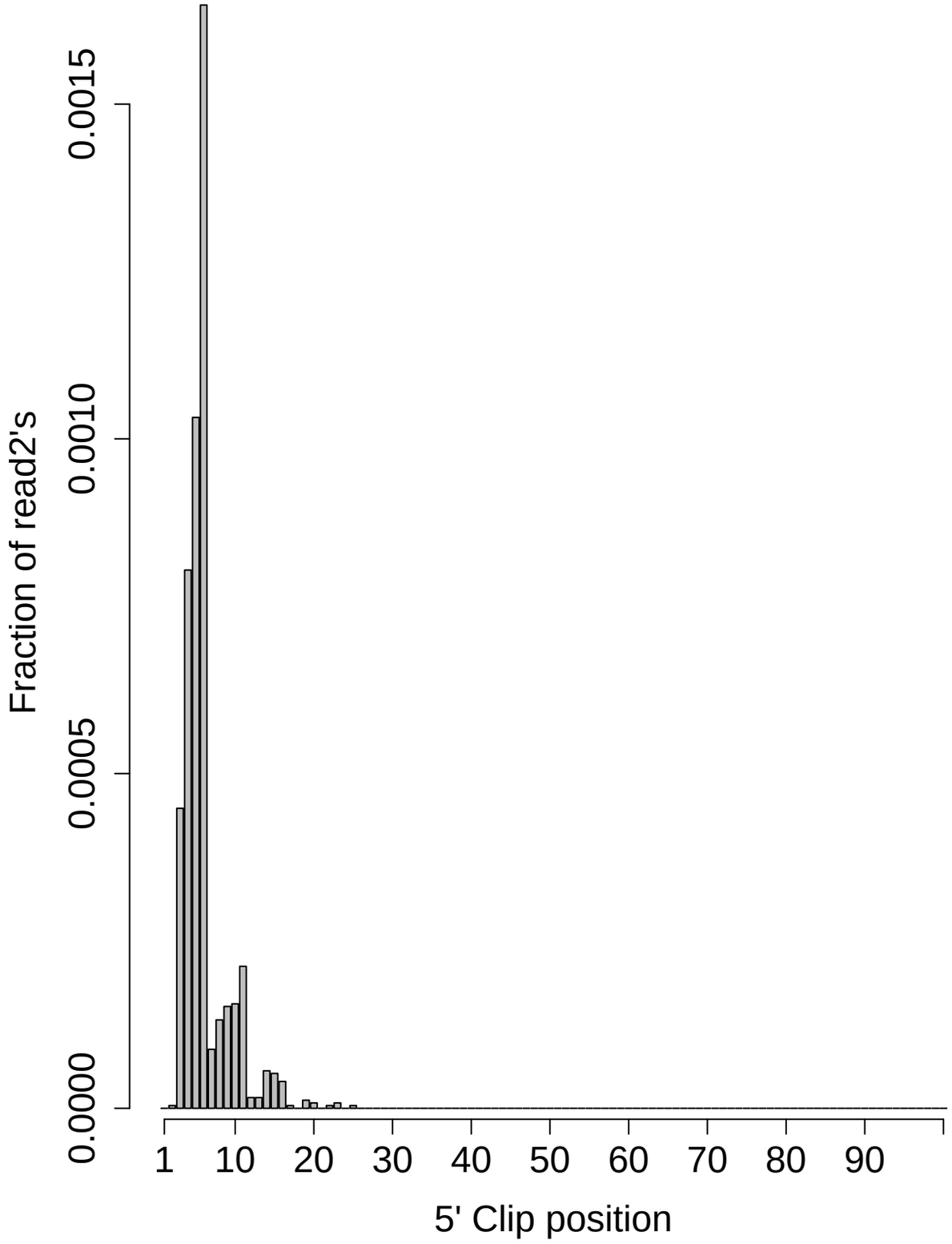

GC content vs Coverage from aligned reads
Coverage
0
2
4
6
8
10
0.500
0.505
0.510
GC content

5' Clipping locations on aligned reads

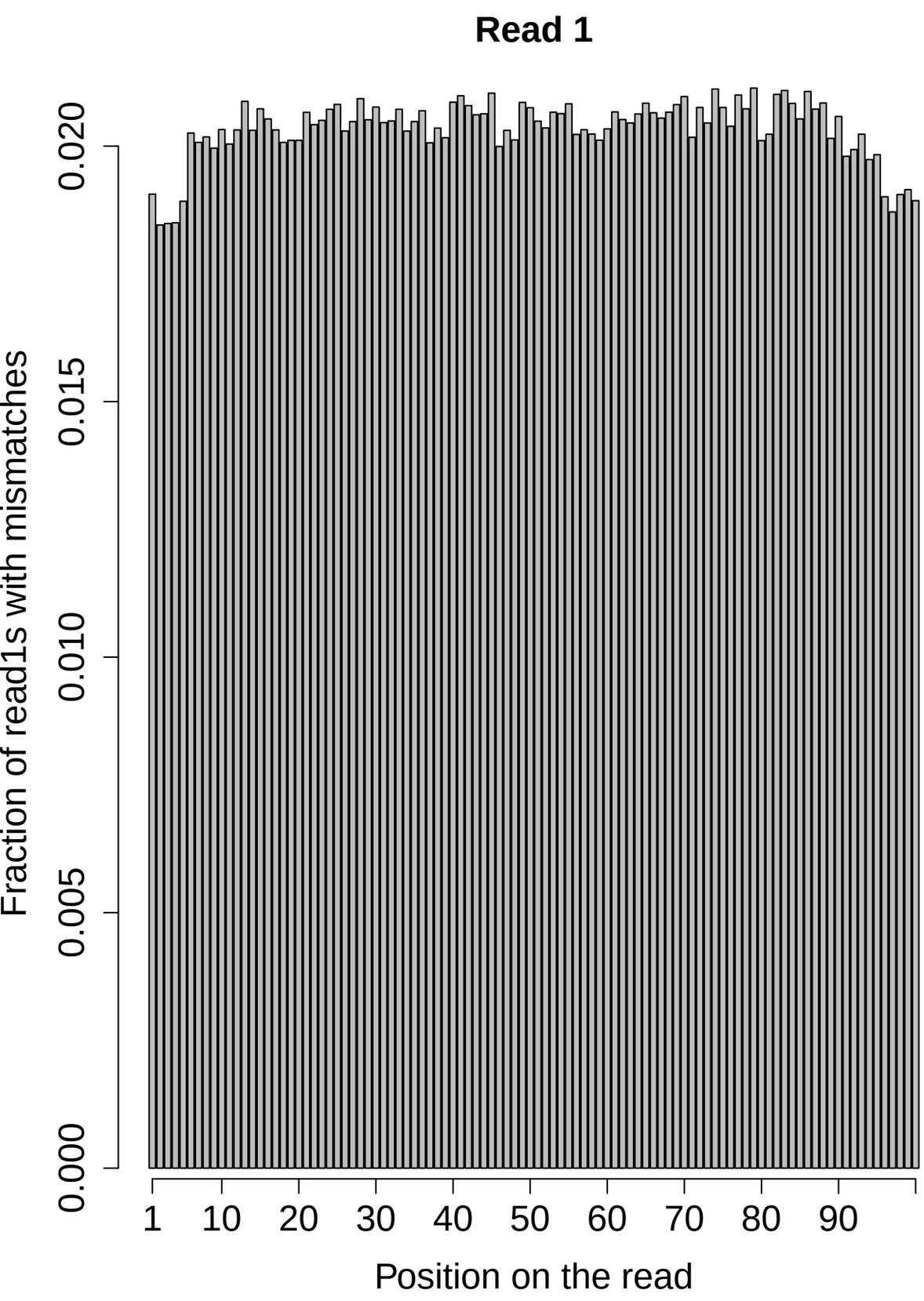
Read 1

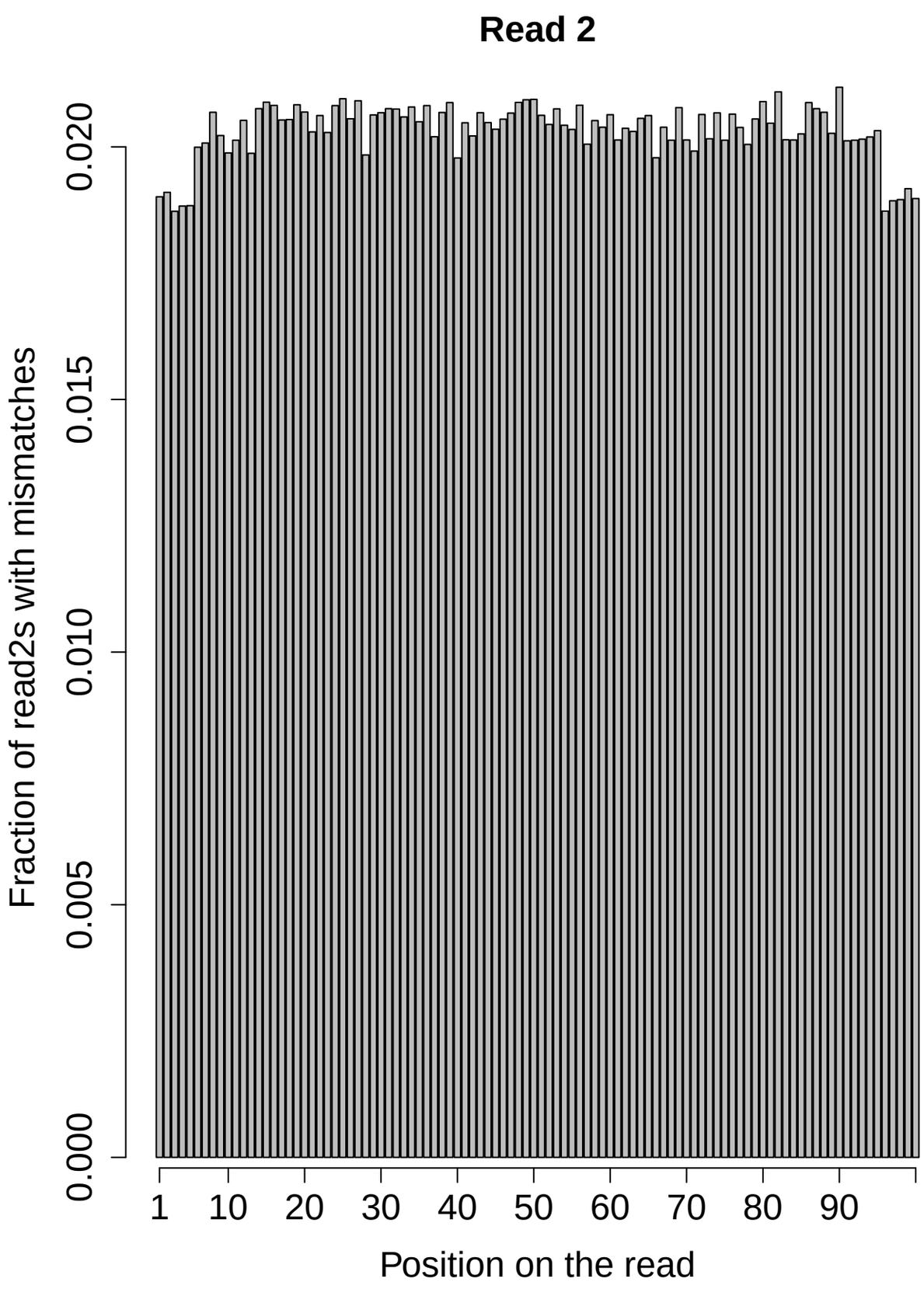


Read 2



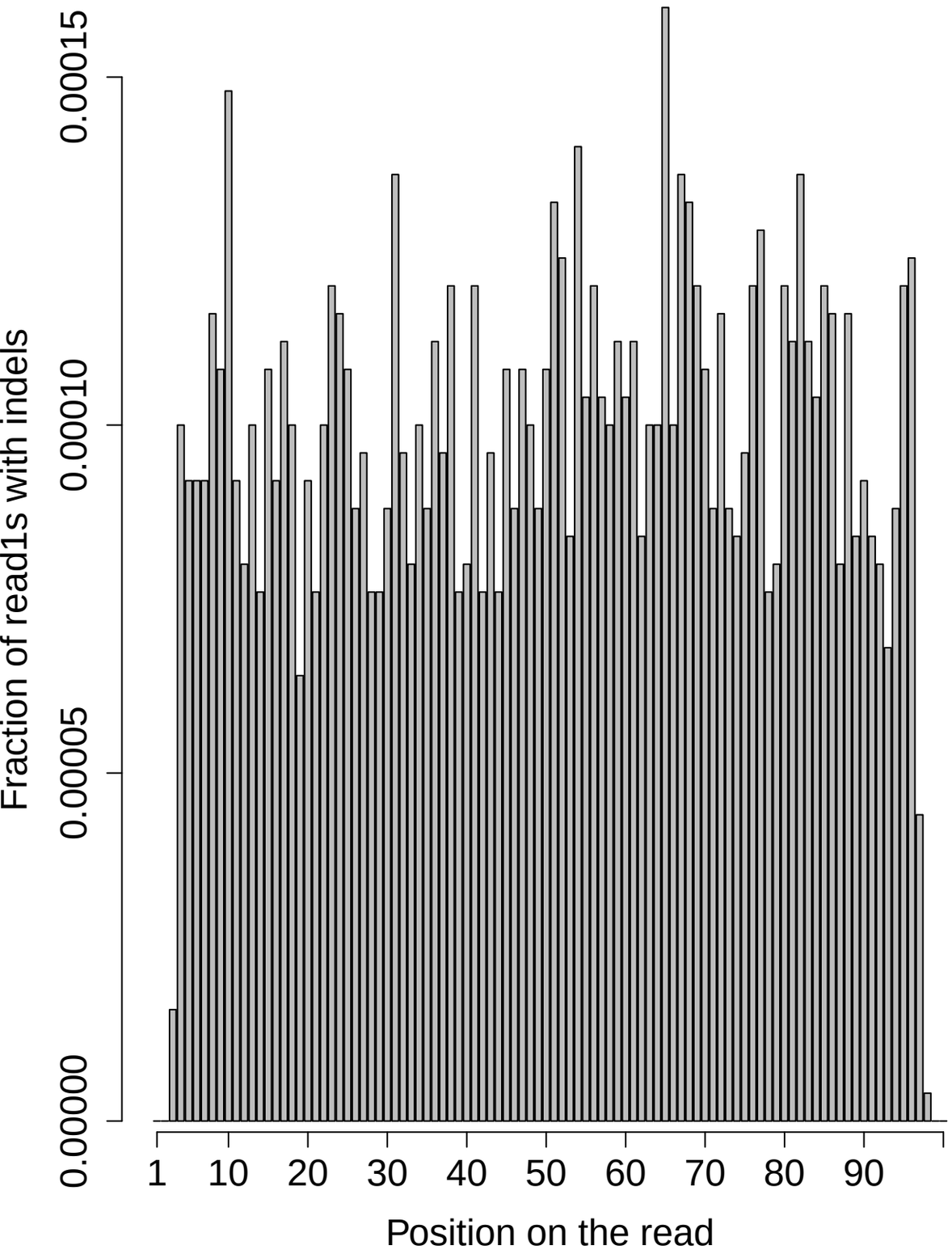
Mismatch positions (vs reference) on aligned reads





Indel positions (vs reference) on the read

Read 1



Read 2