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

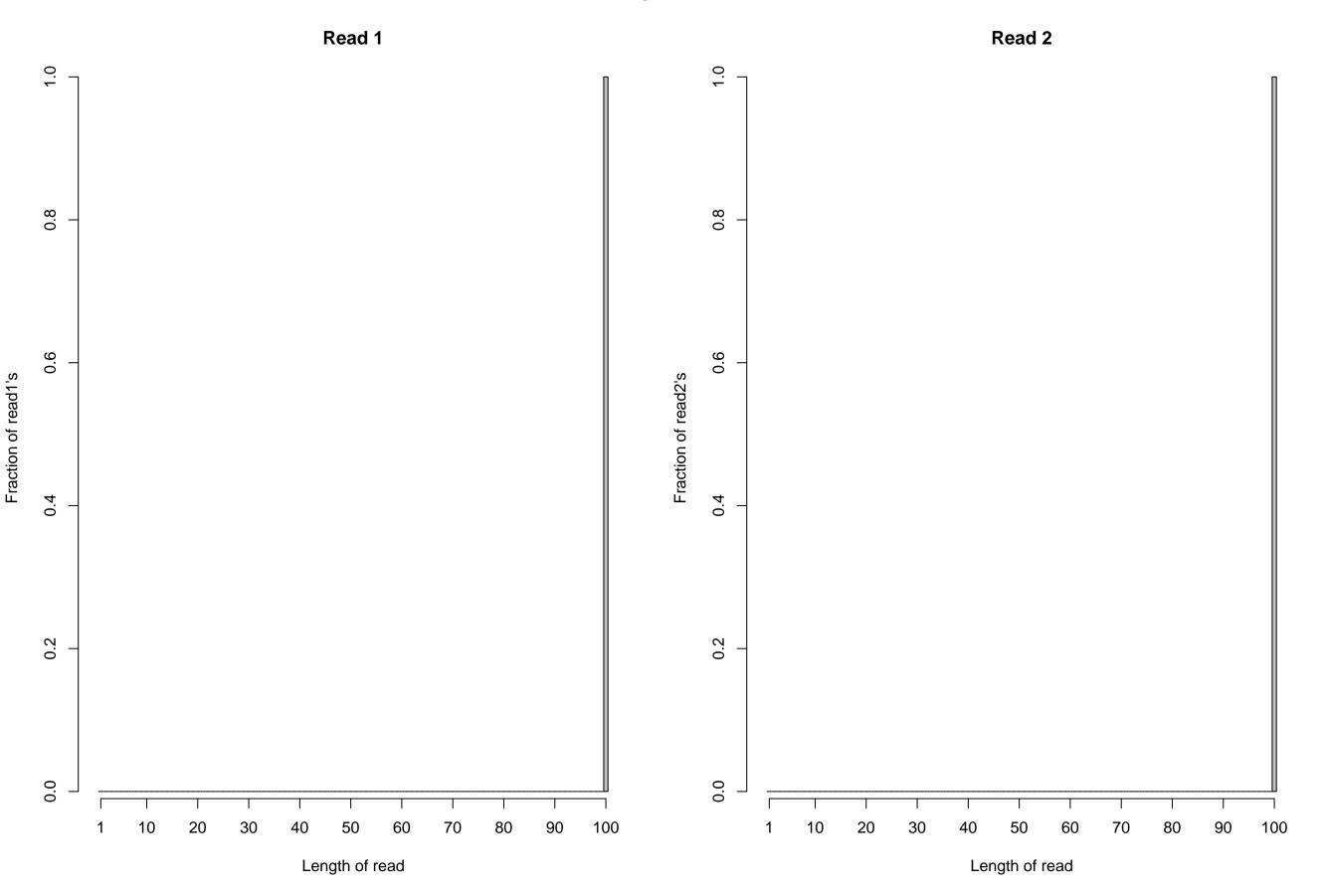
QC-failed bases: 0

Number of bases in single-fragments: 0

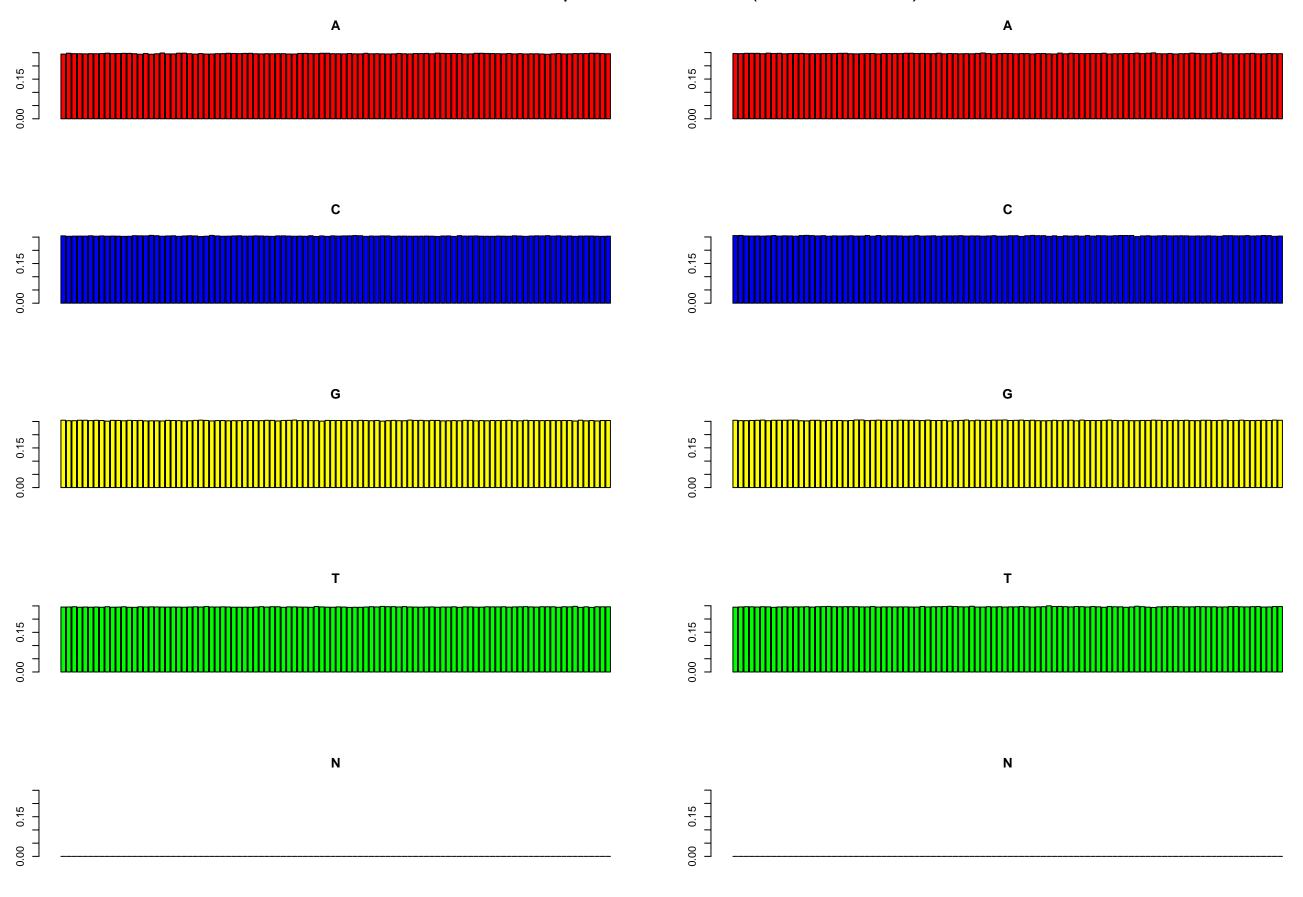
Number of bases paired in sequencing: 50,000,000

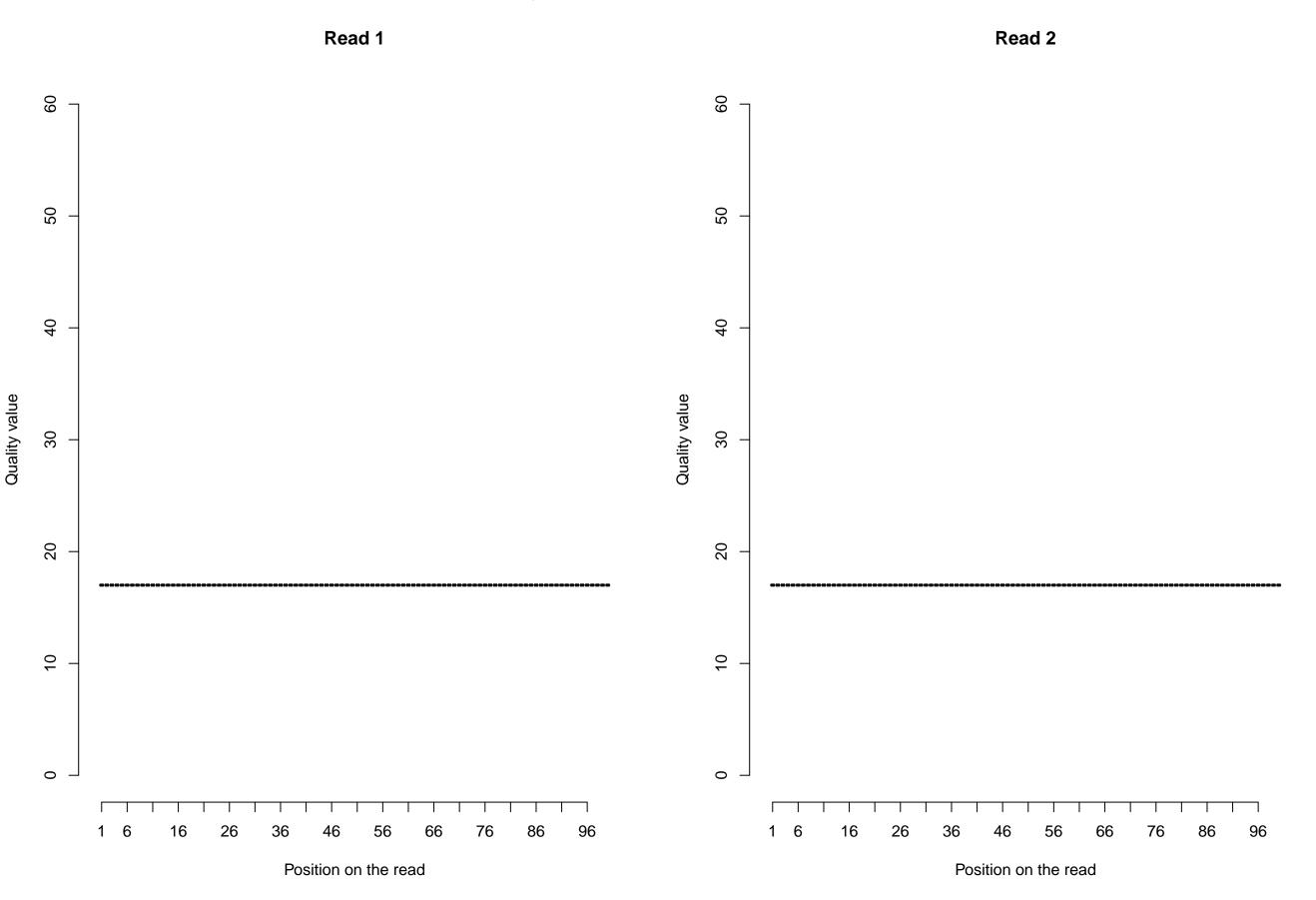
Duplicate bases : 0 (0.00%)

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

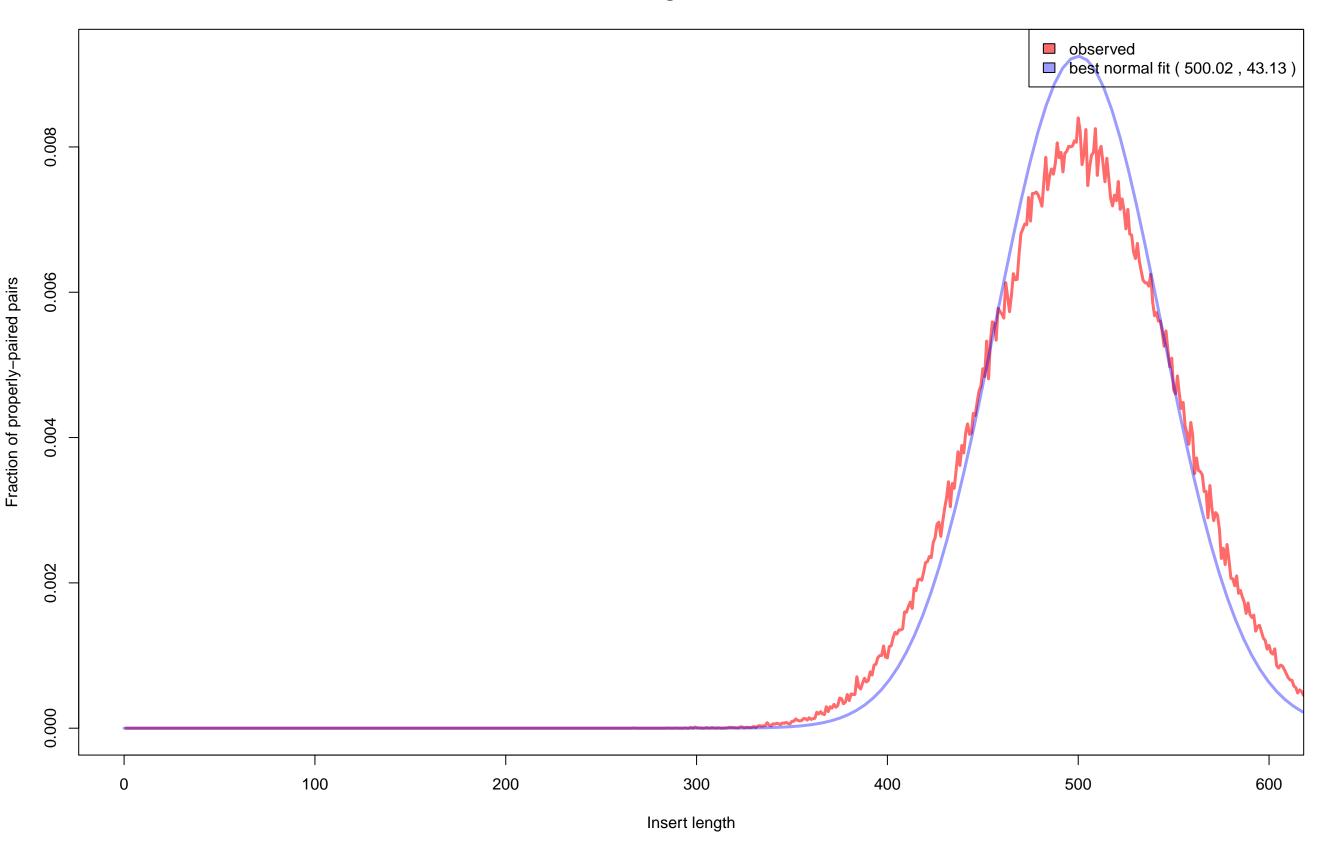


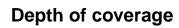
Nucleotide composition variation (Read1, Read2)

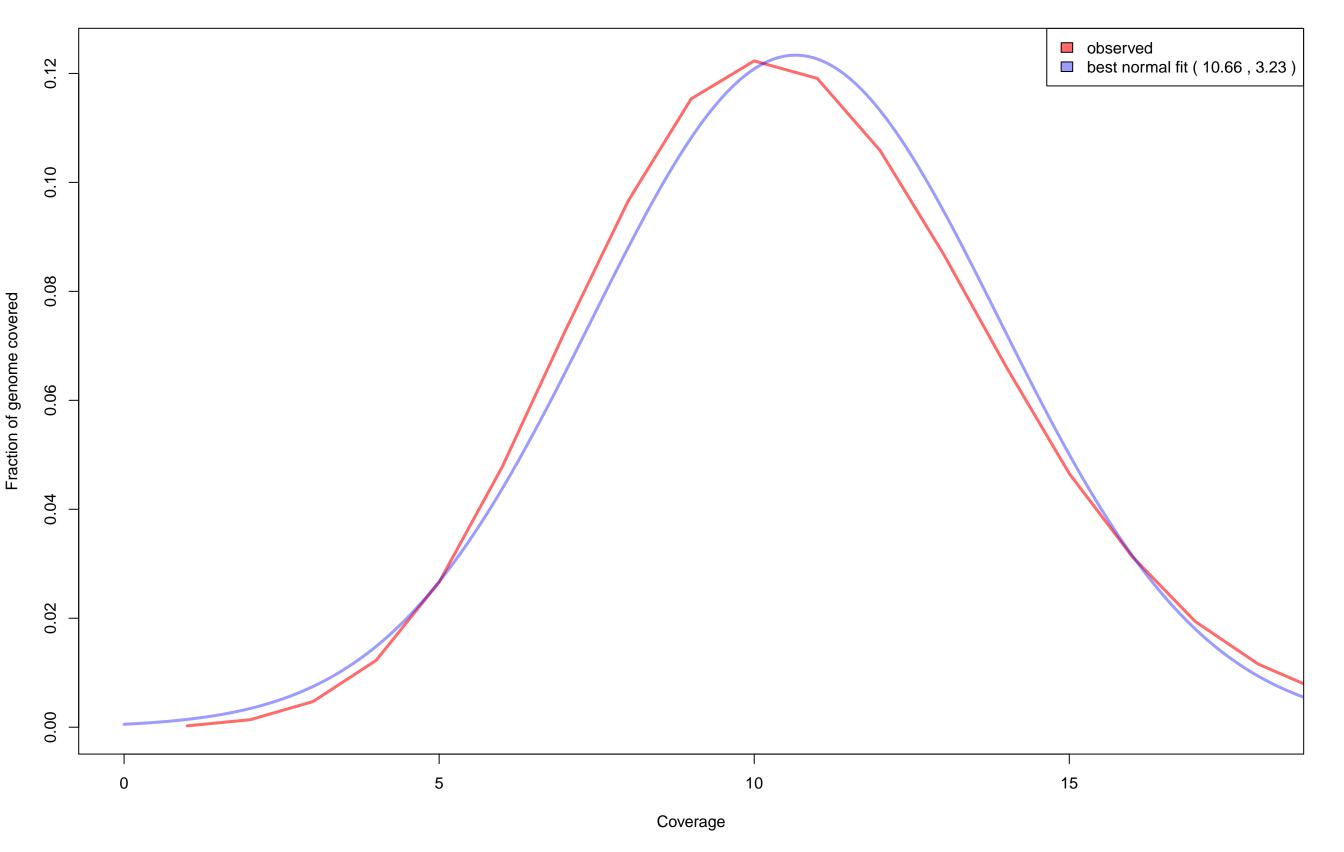


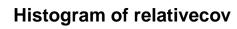


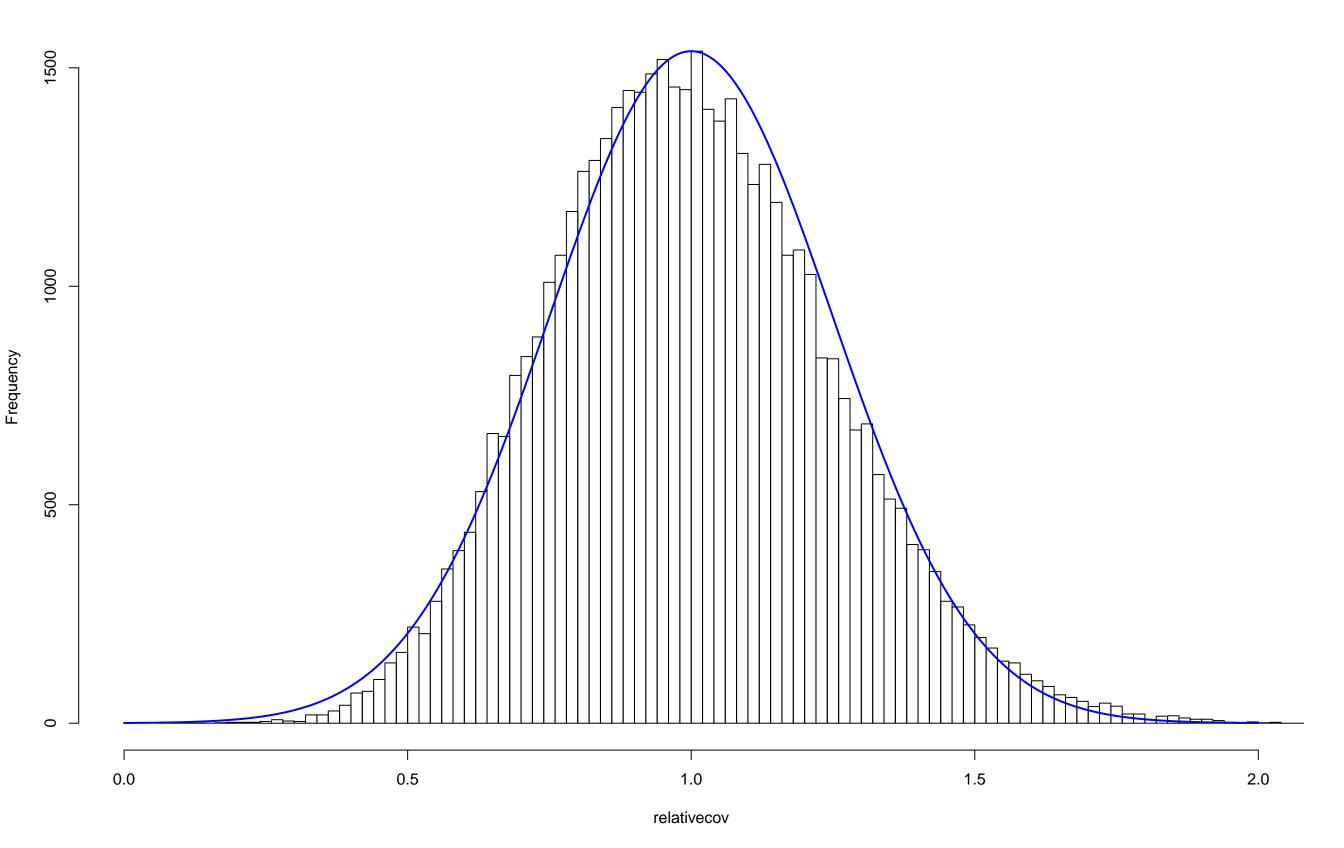
Insert length distribution











GC content vs Coverage from aligned reads

