# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/27 02:55:34*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094134.sorted.bam -c -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| Command line: | /home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_ERR2094134 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094134_1.fastq.gz ERR2094134_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Aug 27 02:55:30 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | ERR2094134.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 538,374 |
| Mapped reads | 521,592 / 96.88% |
| Unmapped reads | 16,782 / 3.12% |
| Mapped paired reads | 521,592 / 96.88% |
| Mapped reads, first in pair | 261,744 / 48.62% |
| Mapped reads,  second in pair | 259,848 / 48.27% |
| Mapped reads, both in pair | 519,076 / 96.42% |
| Mapped reads, singletons | 2,516 / 0.47% |
| Secondary alignments | 0 |
| Supplementary alignments | 9,502 / 1.76% |
| Read min/max/mean length | 30 / 151 / 146.92 |
| Duplicated reads (estimated) | 520,945 / 96.76% |
| Duplication rate | 40.54% |
| Clipped reads | 118,545 / 22.02% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 21,148,639 / 28.12% |
| Number/percentage of C's | 16,076,939 / 21.37% |
| Number/percentage of T's | 21,359,254 / 28.4% |
| Number/percentage of G's | 16,634,488 / 22.11% |
| Number/percentage of N's | 1,014 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 43.49% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0244 |
| Standard Deviation | 34.9468 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 23.55 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 138,286.85 |
| Standard Deviation | 3,331,410.79 |
| P25/Median/P75 | 212 / 229 / 256 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 1.73% |
| Mismatches | 1,253,790 |
| Insertions | 28,852 |
| Mapped reads with at least one insertion | 5.46% |
| Deletions | 64,621 |
| Mapped reads with at least one deletion | 12.09% |
| Homopolymer indels | 54.51% |

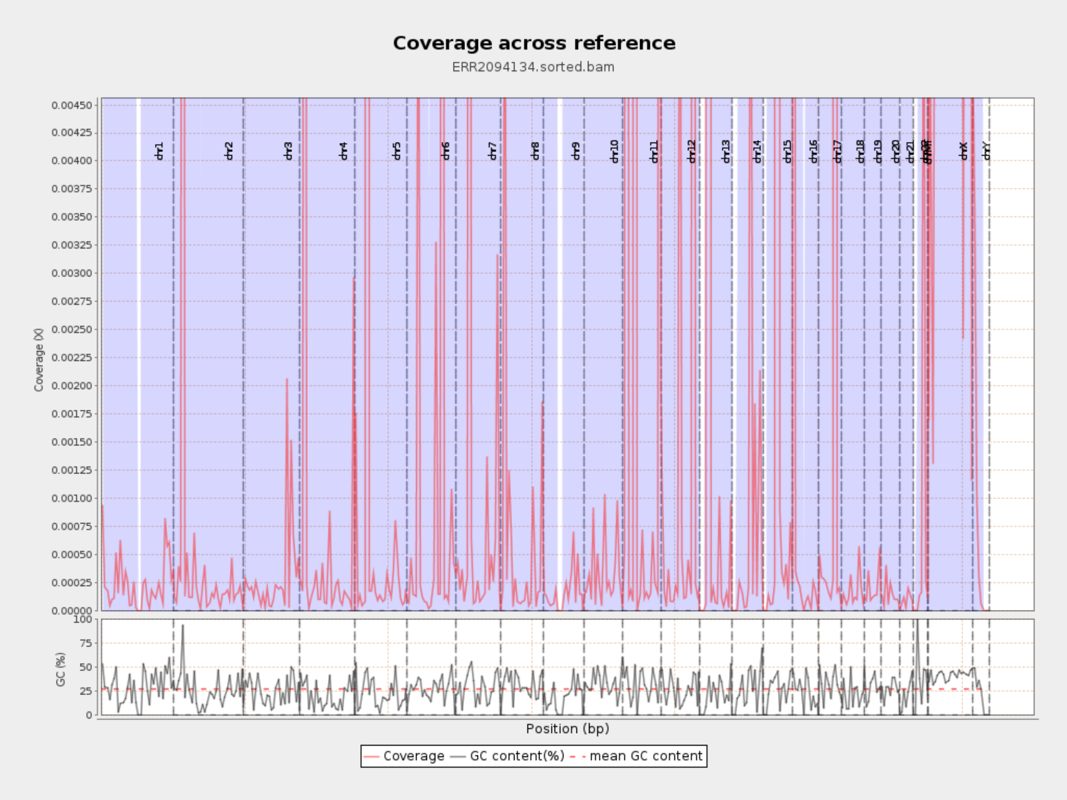
## 2.7. Chromosome stats

| **Name** | **Length** | **Mapped** | **Mean** | **Standard** |
|---|---|---|---|---|

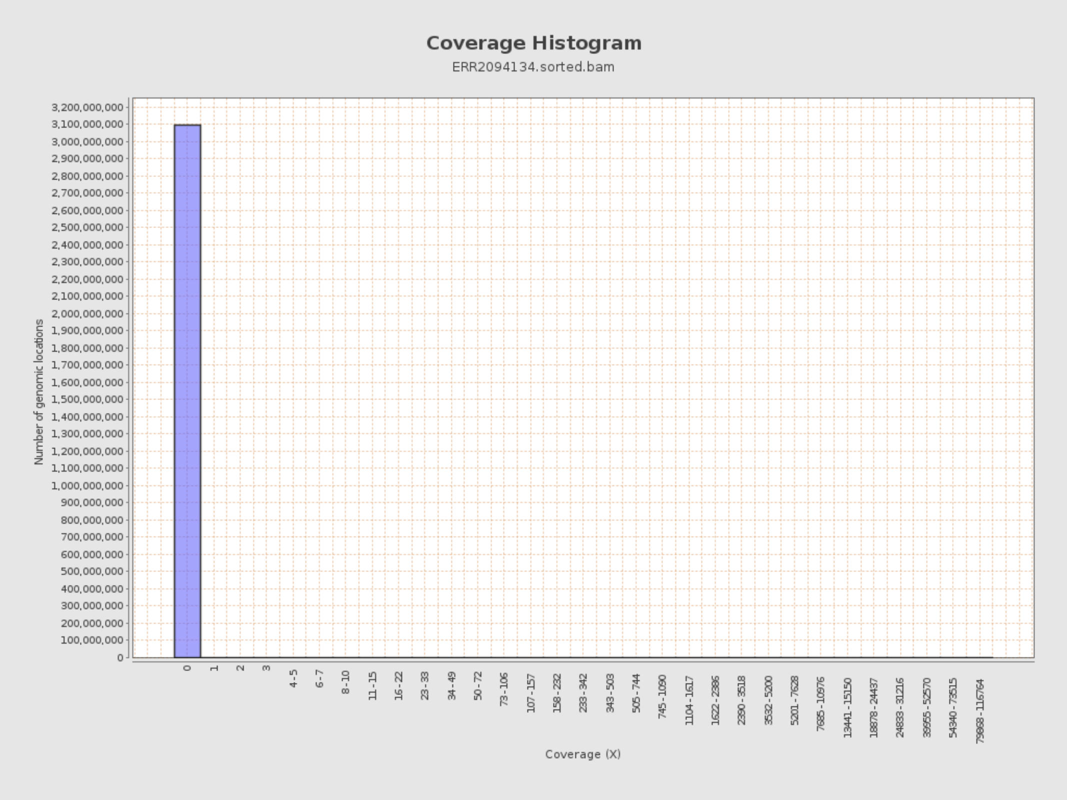
|  |  | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 60894 | 0.0002 | 0.0653 |
| chr2 | 243199373 | 255567 | 0.0011 | 0.804 |
| chr3 | 198022430 | 61967 | 0.0003 | 0.1132 |
| chr4 | 191154276 | 196414 | 0.001 | 0.6783 |
| chr5 | 180915260 | 600501 | 0.0033 | 2.9746 |
| chr6 | 171115067 | 312447 | 0.0018 | 1.3735 |
| chr7 | 159138663 | 254728 | 0.0016 | 0.8362 |
| chr8 | 146364022 | 104998 | 0.0007 | 0.4743 |
| chr9 | 141213431 | 24064 | 0.0002 | 0.0416 |
| chr10 | 135534747 | 46699 | 0.0003 | 0.0908 |
| chr11 | 135006516 | 1800604 | 0.0133 | 6.095 |
| chr12 | 133851895 | 458608 | 0.0034 | 2.3041 |
| chr13 | 115169878 | 2426743 | 0.0211 | 16.7426 |
| chr14 | 107349540 | 105560 | 0.001 | 0.3239 |
| chr15 | 102531392 | 1976401 | 0.0193 | 16.0917 |
| chr16 | 90354753 | 236305 | 0.0026 | 2.2707 |
| chr17 | 81195210 | 745826 | 0.0092 | 4.9311 |
| chr18 | 78077248 | 13737 | 0.0002 | 0.0609 |
| chr19 | 59128983 | 12300 | 0.0002 | 0.036 |
| chr20 | 63025520 | 9489 | 0.0002 | 0.0267 |
| chr21 | 48129895 | 4736 | 0.0001 | 0.0169 |
| chr22 | 51304566 | 56055 | 0.0011 | 0.5385 |
| chrMT | 16571 | 58282498 | 3,517.1383 | 14,508.6064 |
| chrX | 155270560 | 7293525 | 0.047 | 10.9116 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 65002 | 0.0011 | 0.4334 |

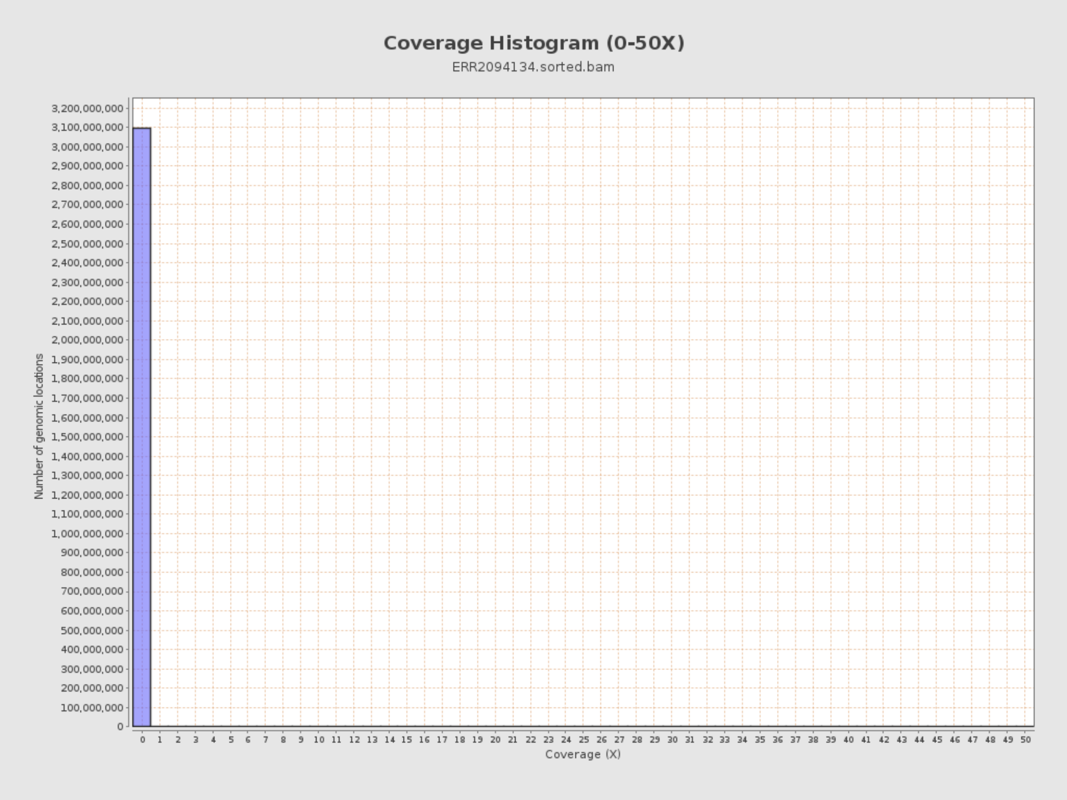
# 3. Results : Coverage across reference



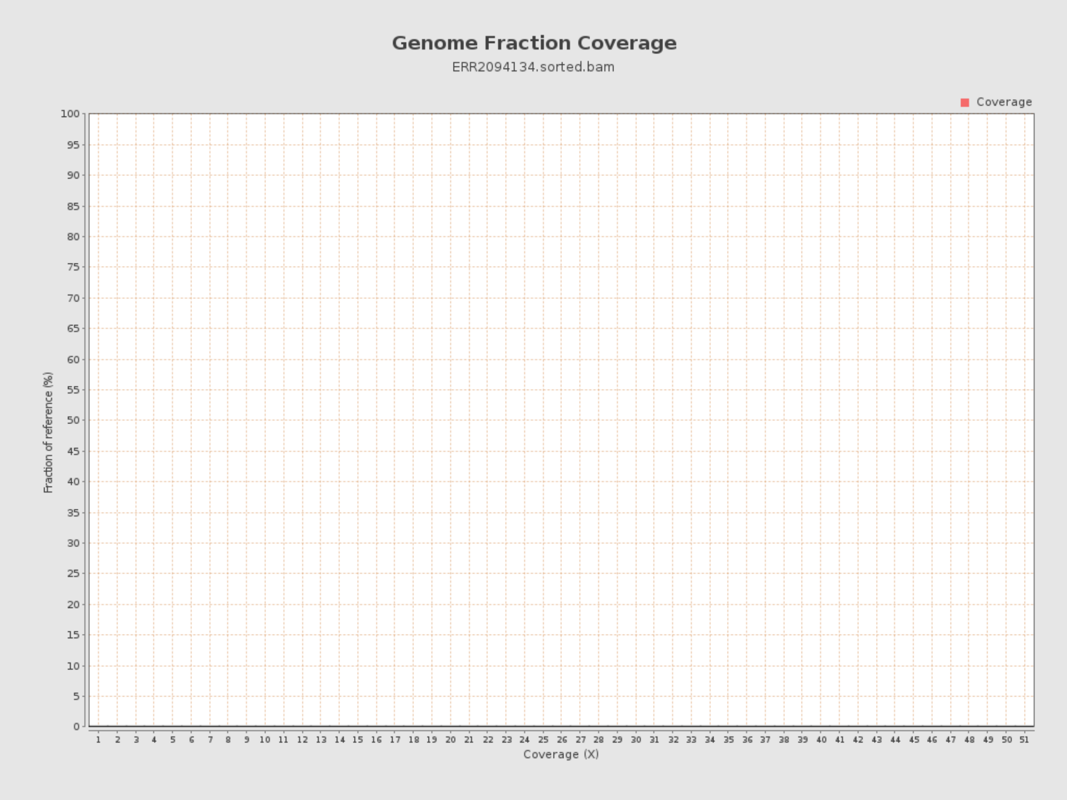
# 4. Results : Coverage Histogram



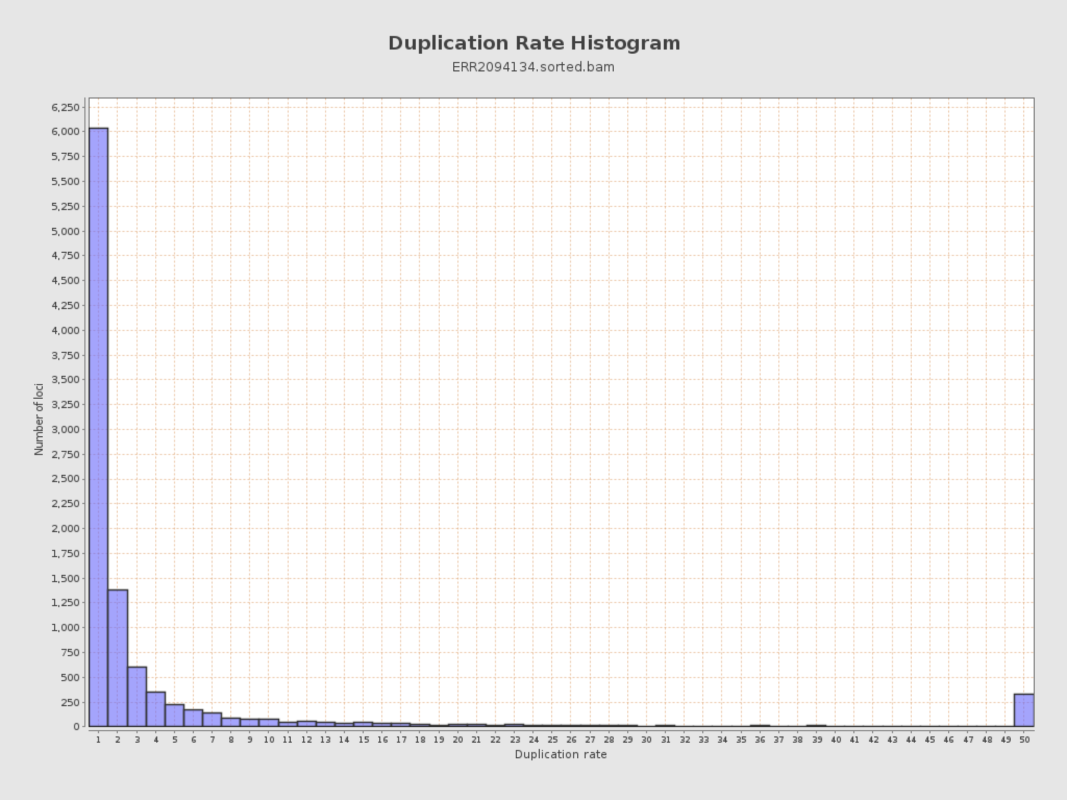
# 5. Results : Coverage Histogram (0-50X)



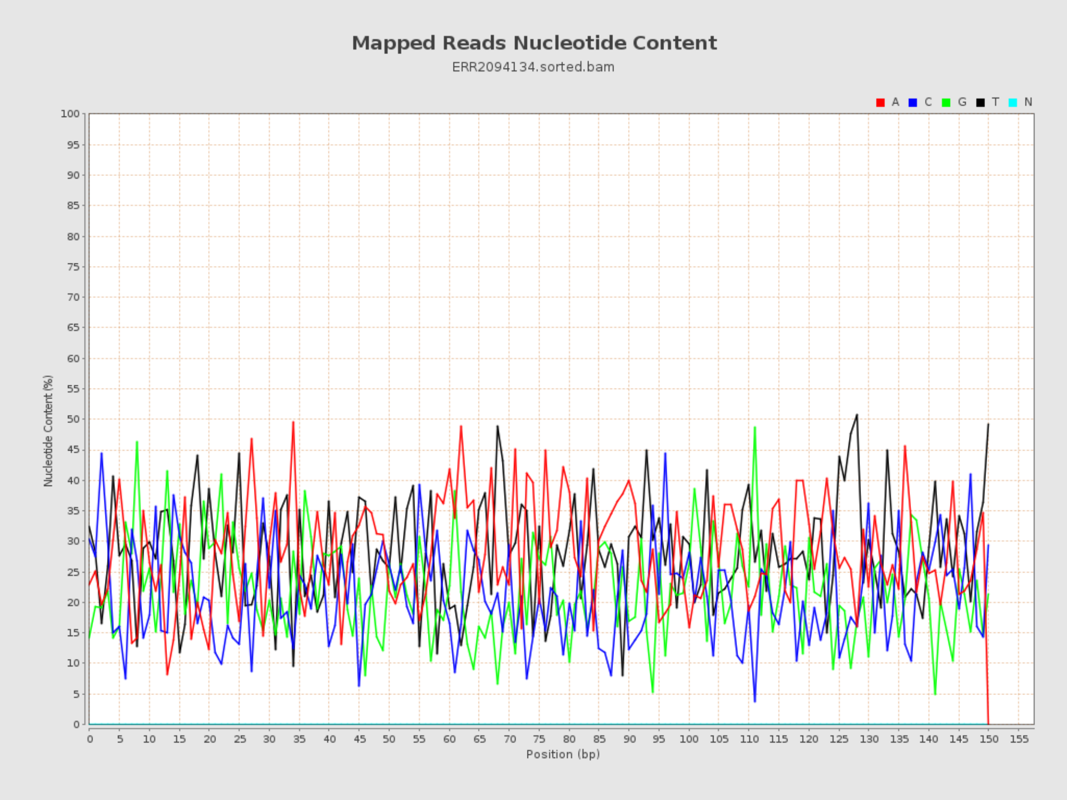
# 6. Results : Genome Fraction Coverage



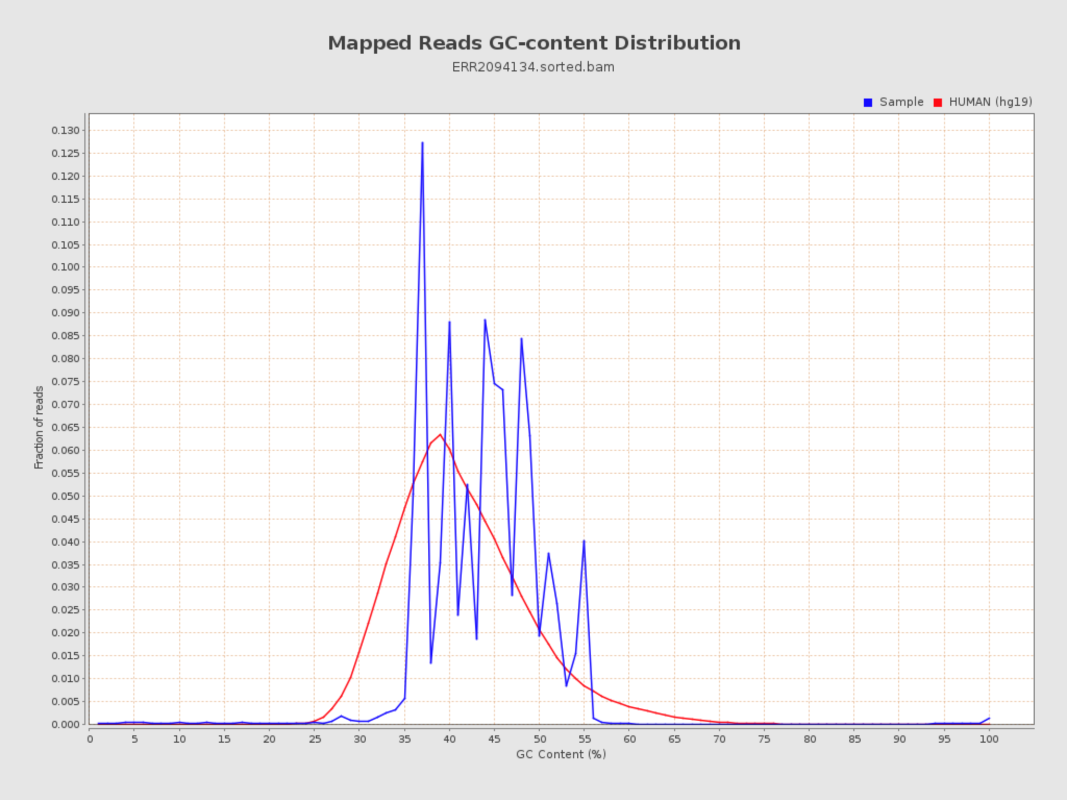
# 7. Results : Duplication Rate Histogram



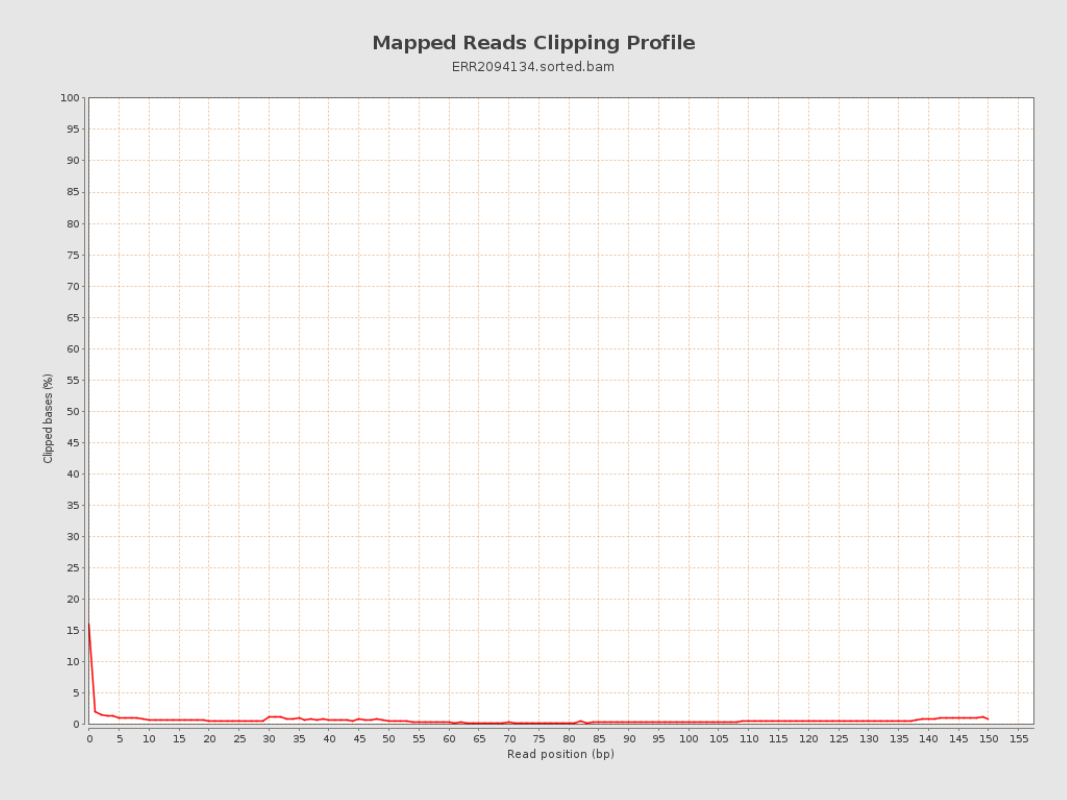
# 8. Results : Mapped Reads Nucleotide Content



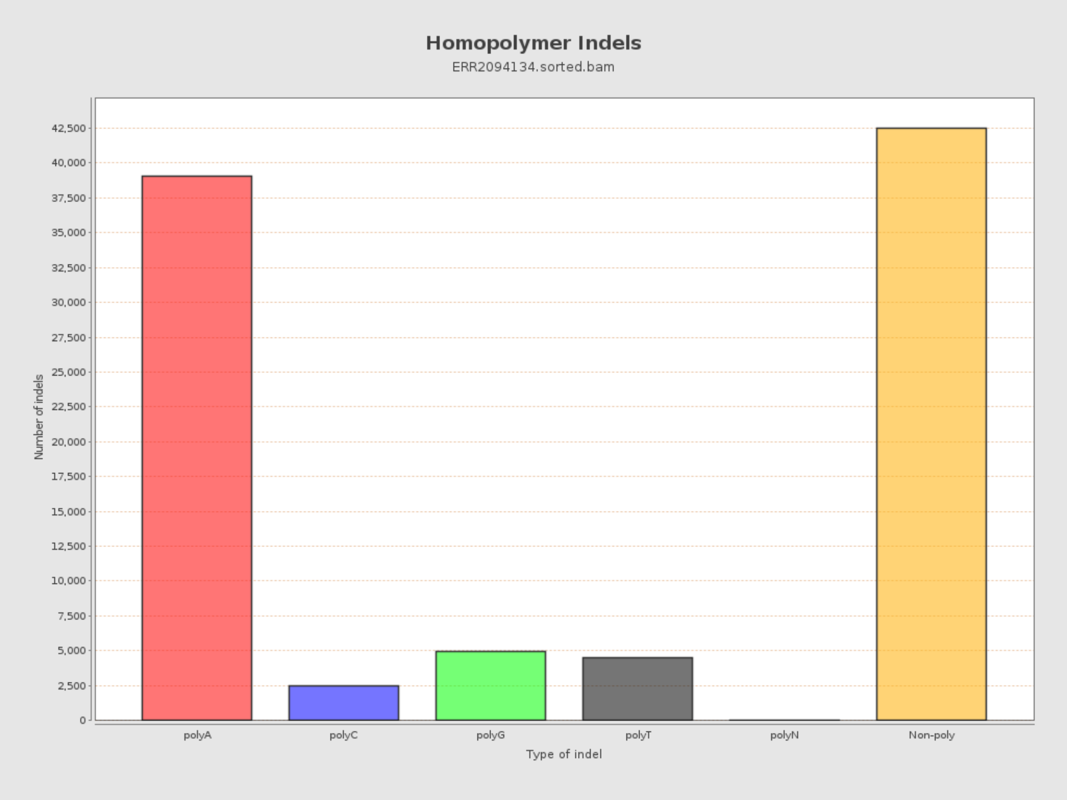
# 9. Results : Mapped Reads GC-content Distribution



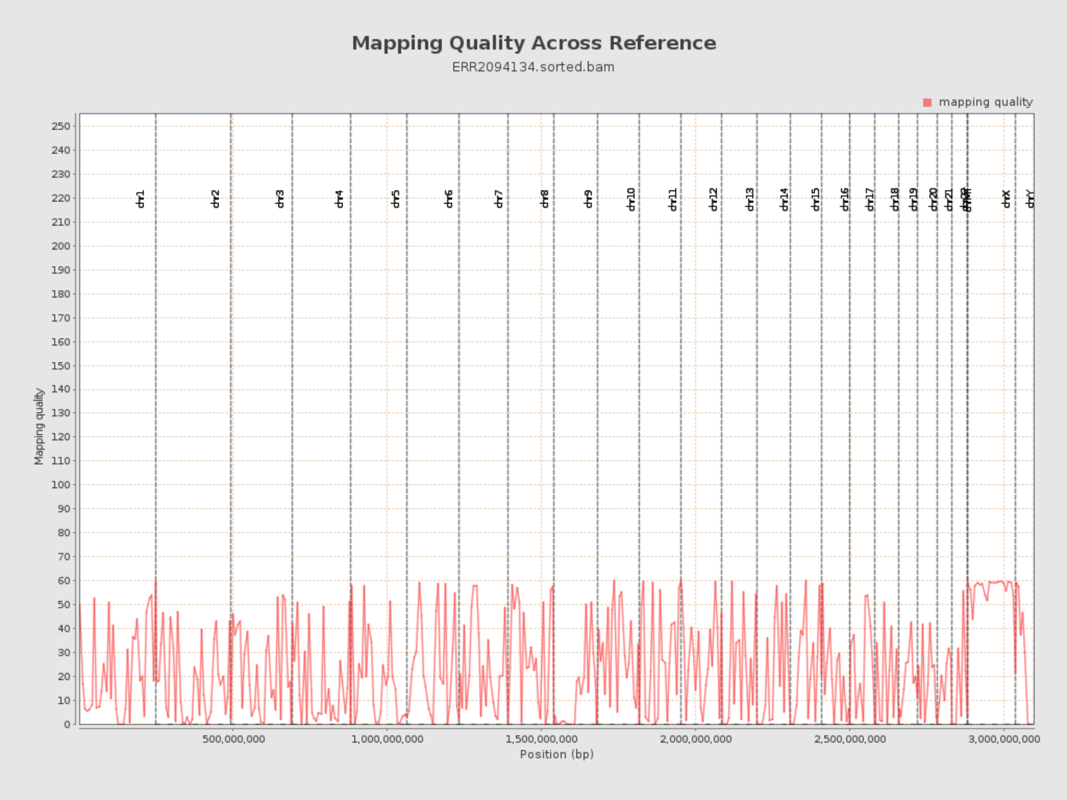
# 10. Results : Mapped Reads Clipping Profile



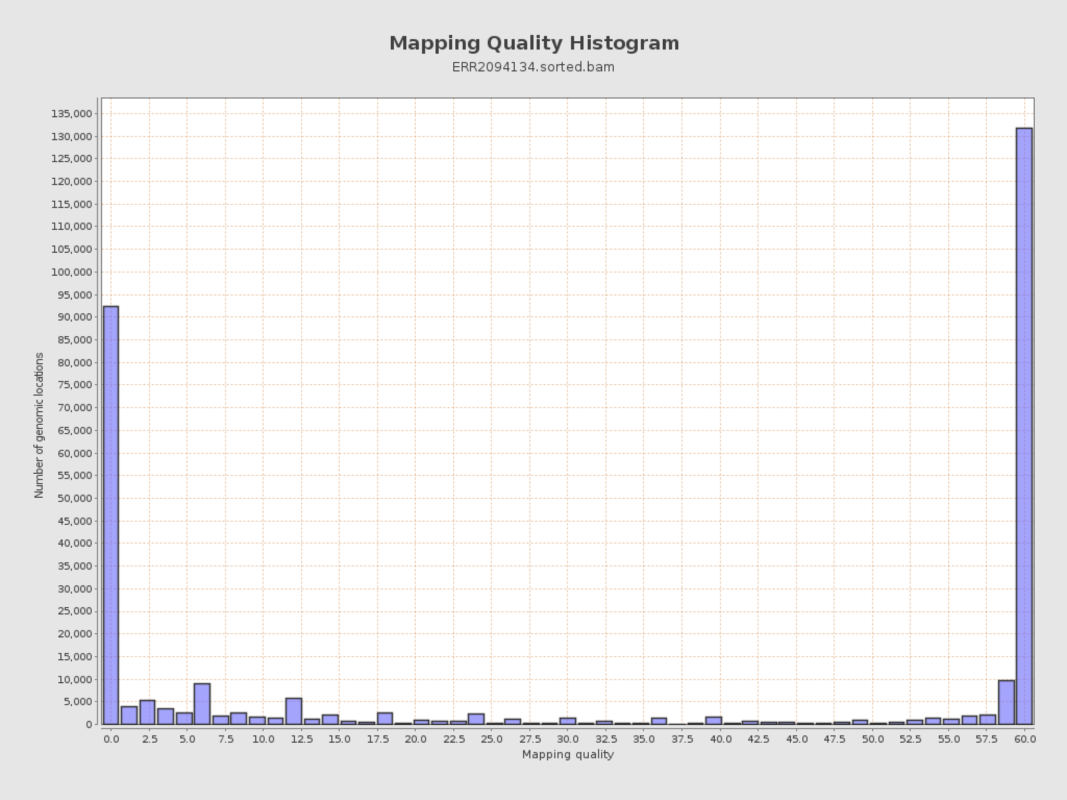
# 11. Results : Homopolymer Indels



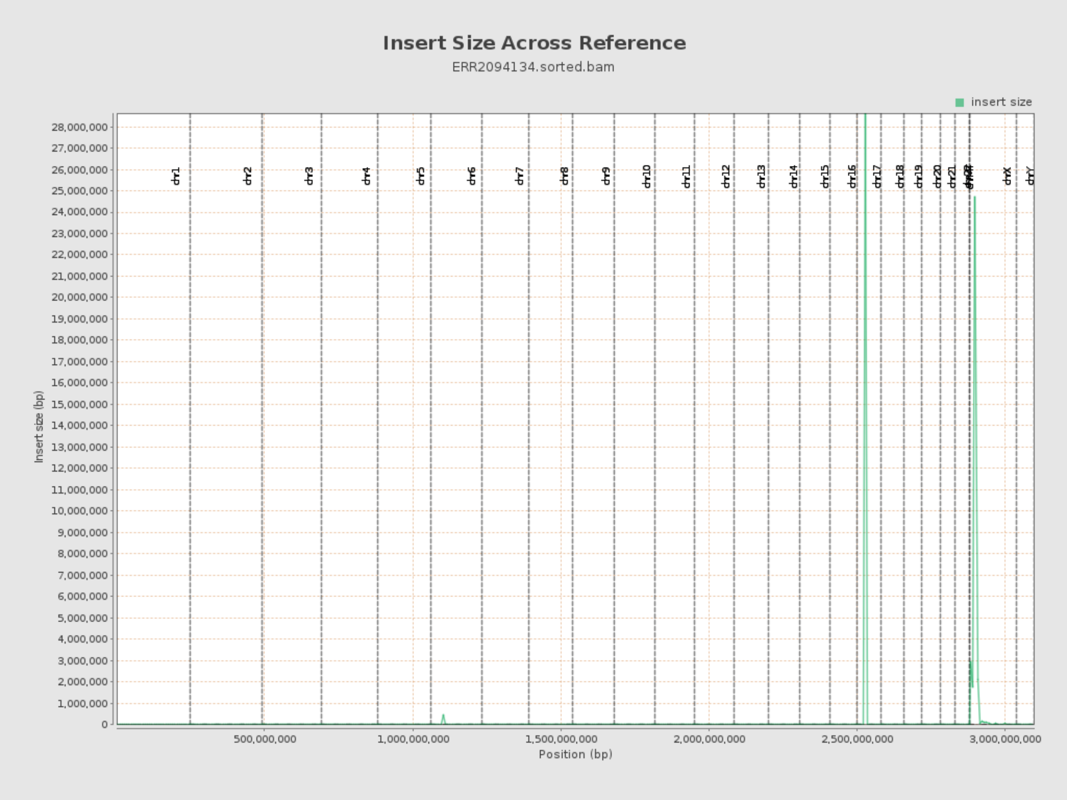
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram