# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 21:20:37*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094026.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_ERR2094026 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094026_1.fastq.gz ERR2094026_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Aug 26 21:20:36 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | ERR2094026.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 420,060 |
| Mapped reads | 389,959 / 92.83% |
| Unmapped reads | 30,101 / 7.17% |
| Mapped paired reads | 389,959 / 92.83% |
| Mapped reads, first in pair | 195,898 / 46.64% |
| Mapped reads, second in pair | 194,061 / 46.2% |
| Mapped reads, both in pair | 385,976 / 91.89% |
| Mapped reads, singletons | 3,983 / 0.95% |
| Secondary alignments | 0 |
| Supplementary alignments | 19,516 / 4.65% |
| Read min/max/mean length | 30 / 151 / 139.7 |
| Duplicated reads (estimated) | 362,227 / 86.23% |
| Duplication rate | 47.35% |
| Clipped reads | 179,978 / 42.85% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 13,575,138 / 27.49% |
| Number/percentage of C's | 11,010,692 / 22.29% |
| Number/percentage of T's | 13,182,015 / 26.69% |
| Number/percentage of G's | 11,619,003 / 23.53% |
| Number/percentage of N's | 596 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 45.82% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0163 |
| Standard Deviation | 4.8998 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.41 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 729,509.71 |
| Standard Deviation | 7,788,081.47 |
| P25/Median/P75 | 129 / 169 / 208 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 3.62% |
| Mismatches | 1,722,263 |
| Insertions | 30,541 |
| Mapped reads with at least one insertion | 7.71% |
| Deletions | 124,846 |
| Mapped reads with at least one deletion | 30.88% |
| Homopolymer indels | 28.54% |

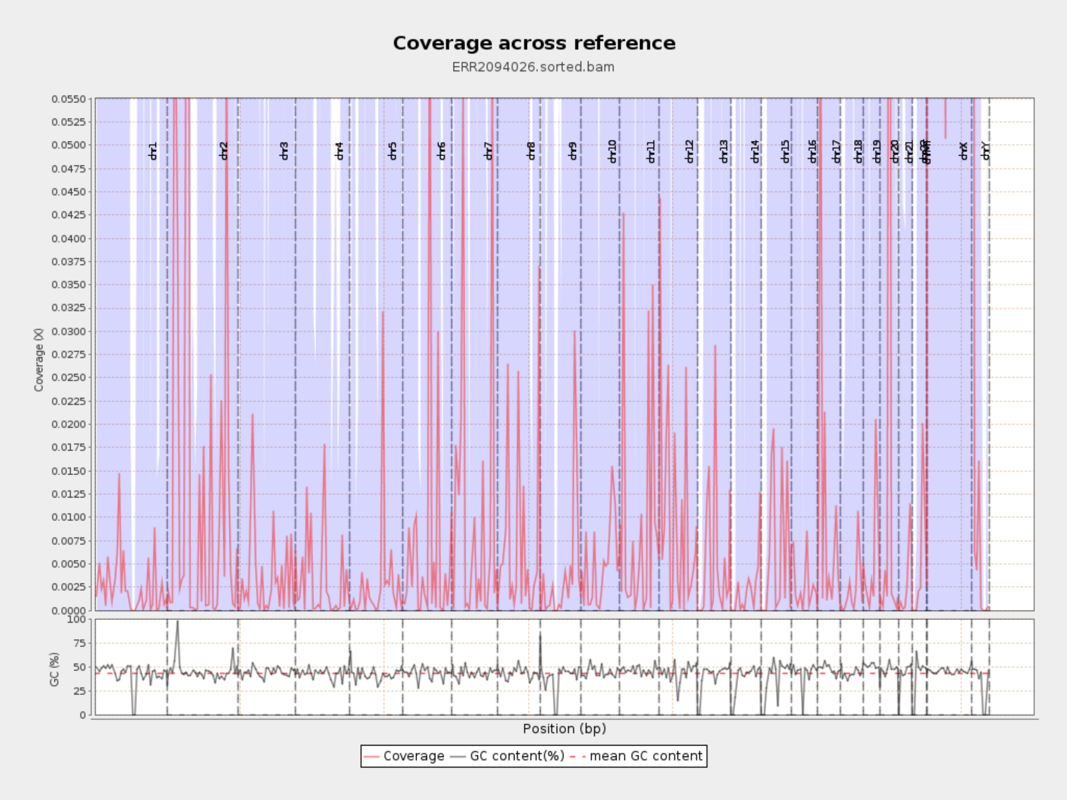
## 2.7. Chromosome stats

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

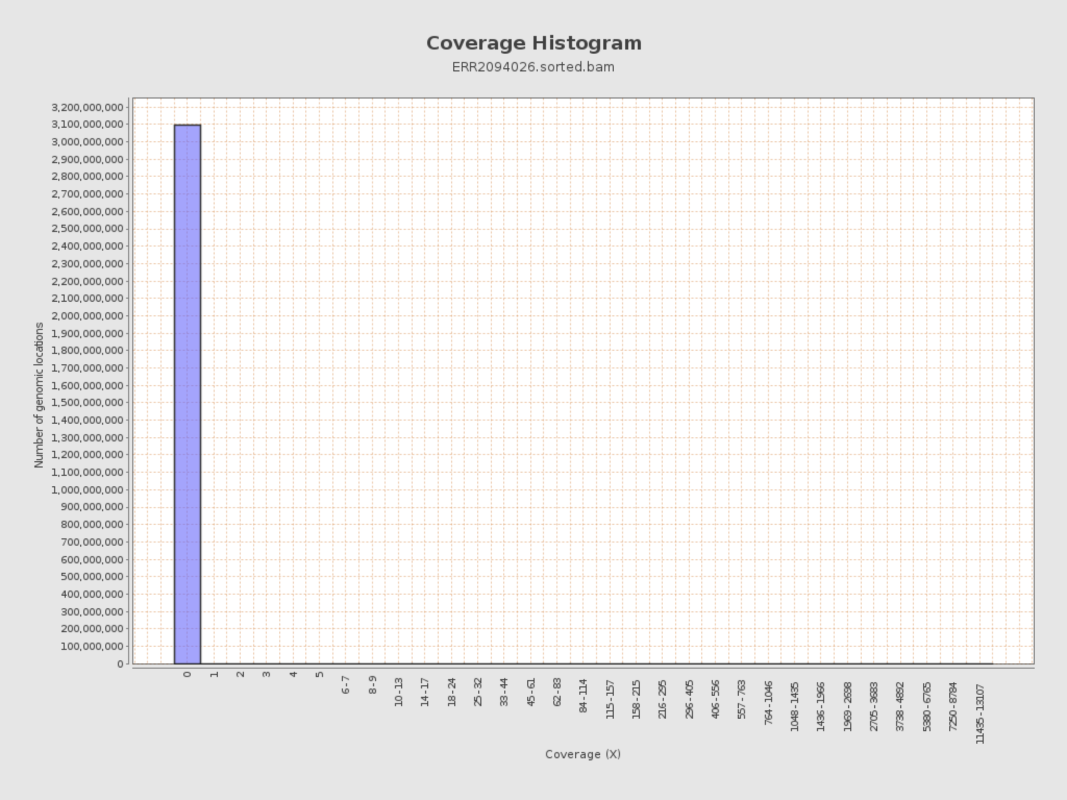
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 658701 | 0.0026 | 0.9076 |
| chr2 | 243199373 | 3809396 | 0.0157 | 5.0815 |
| chr3 | 198022430 | 726879 | 0.0037 | 0.8395 |
| chr4 | 191154276 | 682676 | 0.0036 | 0.9397 |
| chr5 | 180915260 | 548833 | 0.003 | 1.5791 |
| chr6 | 171115067 | 1257520 | 0.0073 | 2.9591 |
| chr7 | 159138663 | 1660158 | 0.0104 | 2.9755 |
| chr8 | 146364022 | 1078642 | 0.0074 | 2.3011 |
| chr9 | 141213431 | 588370 | 0.0042 | 1.3143 |
| chr10 | 135534747 | 673758 | 0.005 | 0.9588 |
| chr11 | 135006516 | 1275703 | 0.0094 | 2.7448 |
| chr12 | 133851895 | 1393377 | 0.0104 | 2.4412 |
| chr13 | 115169878 | 593500 | 0.0052 | 1.7423 |
| chr14 | 107349540 | 255424 | 0.0024 | 0.4025 |
| chr15 | 102531392 | 664287 | 0.0065 | 1.5689 |
| chr16 | 90354753 | 261772 | 0.0029 | 0.6352 |
| chr17 | 81195210 | 987005 | 0.0122 | 2.9574 |
| chr18 | 78077248 | 194116 | 0.0025 | 0.7759 |
| chr19 | 59128983 | 297560 | 0.005 | 1.0815 |
| chr20 | 63025520 | 1054260 | 0.0167 | 6.5825 |
| chr21 | 48129895 | 157834 | 0.0033 | 0.4788 |
| chr22 | 51304566 | 251679 | 0.0049 | 1.0893 |
| chrMT | 16571 | 5926630 | 357.6507 | 1,489.0027 |
| chrX | 155270560 | 24342424 | 0.1568 | 10.0035 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1030399 | 0.0174 | 6.526 |

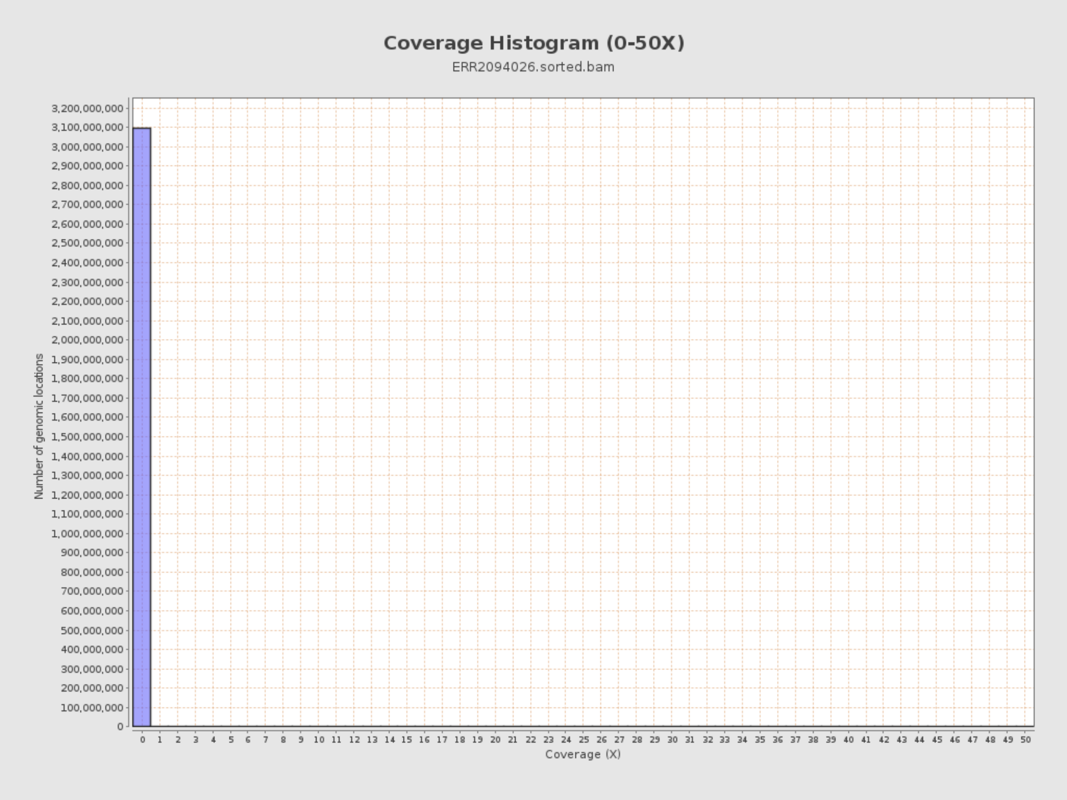
# 3. Results : Coverage across reference



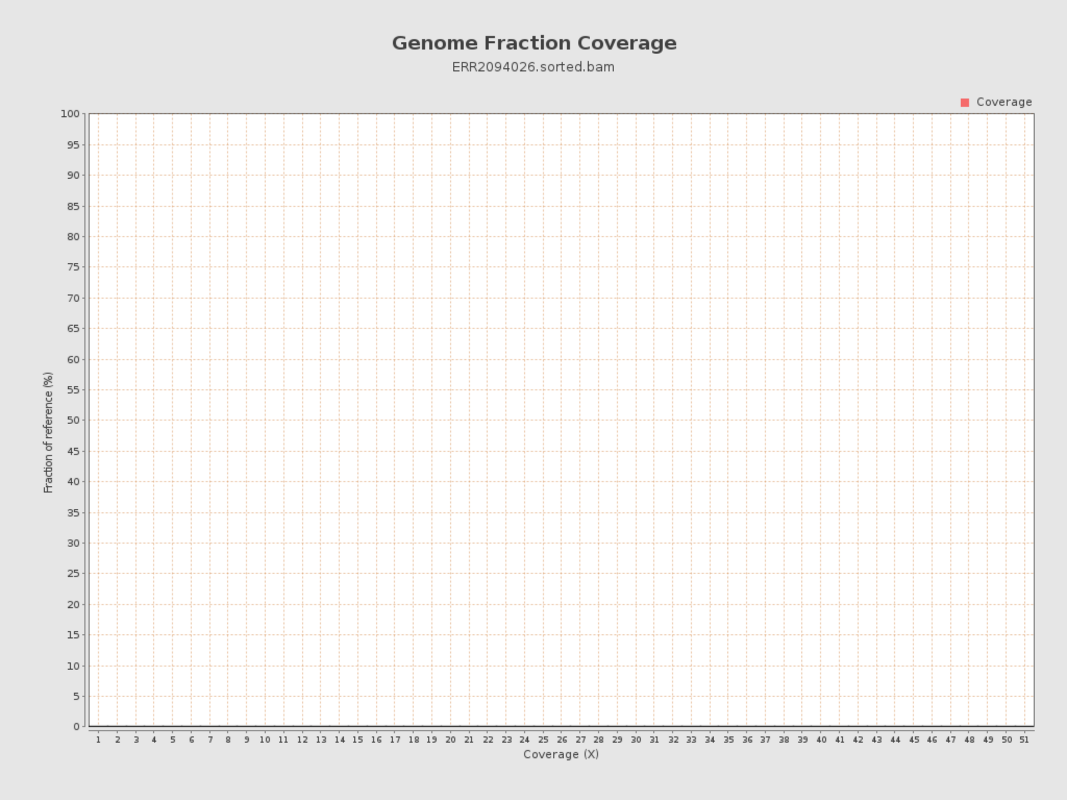
# 4. Results : Coverage Histogram



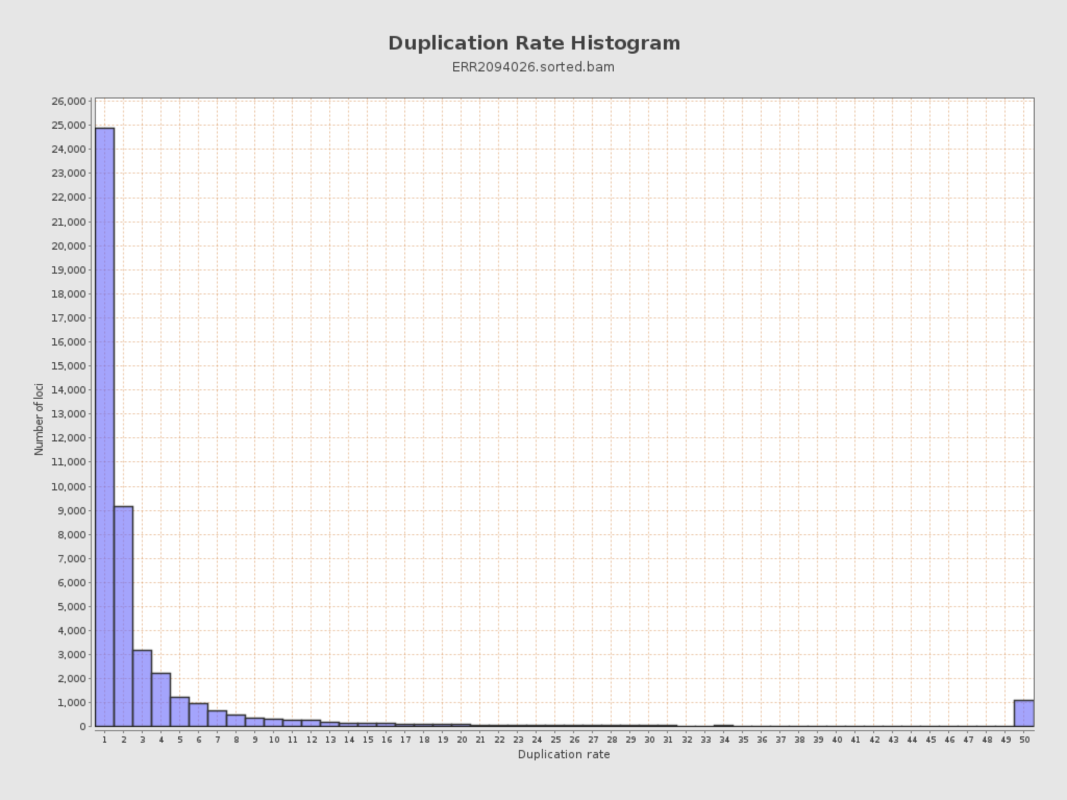
# 5. Results : Coverage Histogram (0-50X)



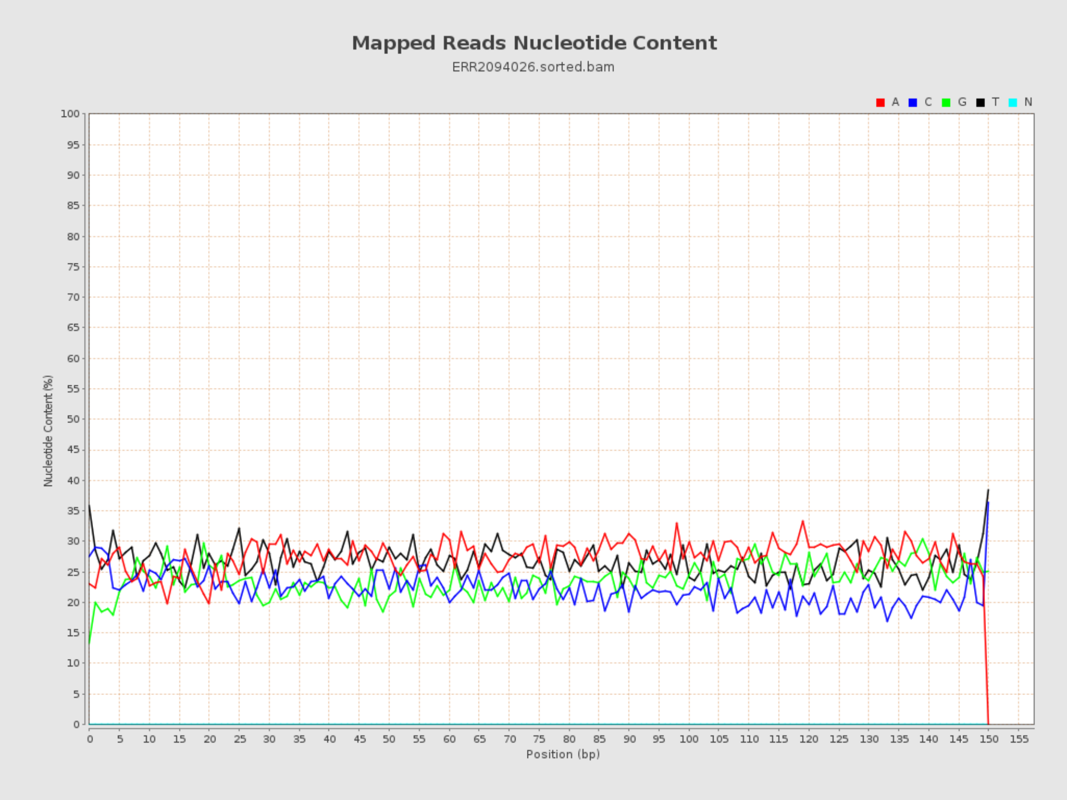
# 6. Results : Genome Fraction Coverage



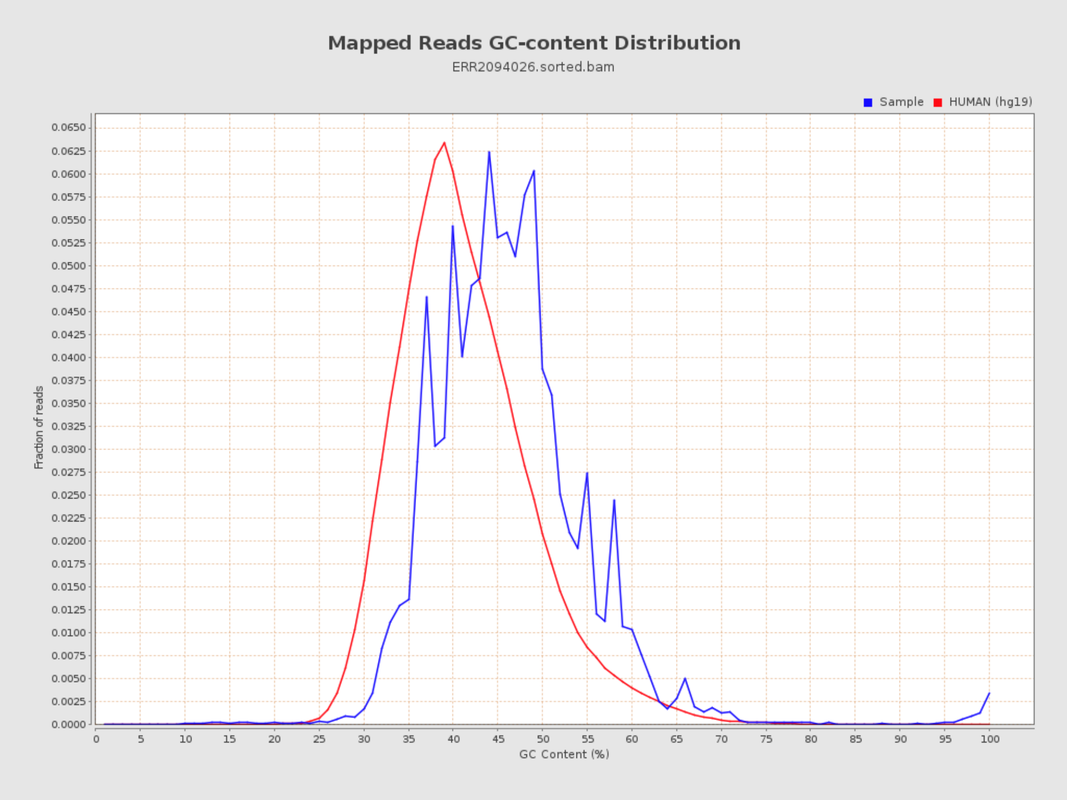
# 7. Results : Duplication Rate Histogram



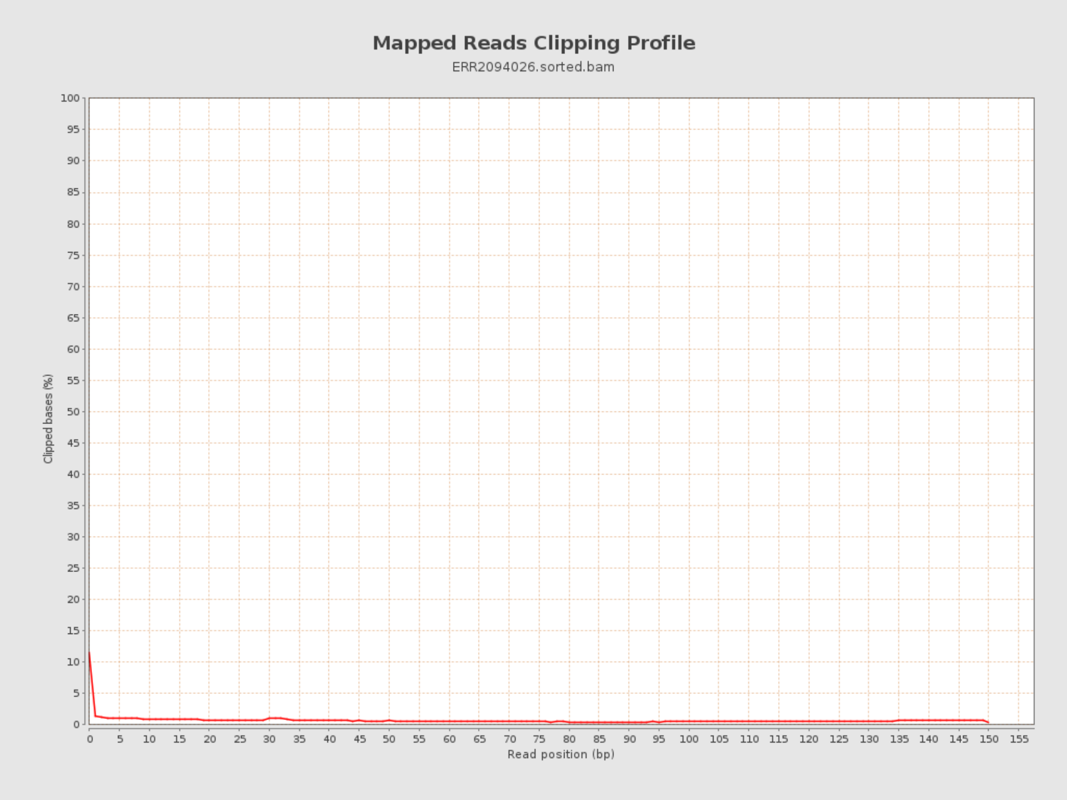
# 8. Results : Mapped Reads Nucleotide Content



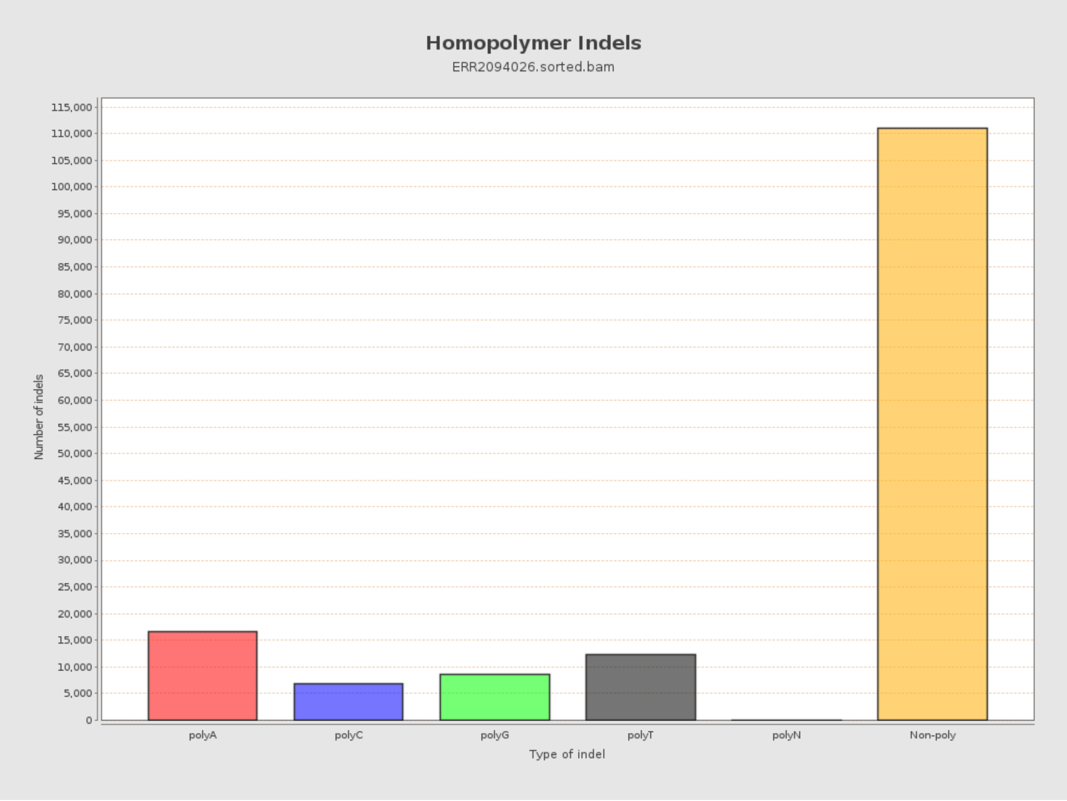
# 9. Results : Mapped Reads GC-content Distribution



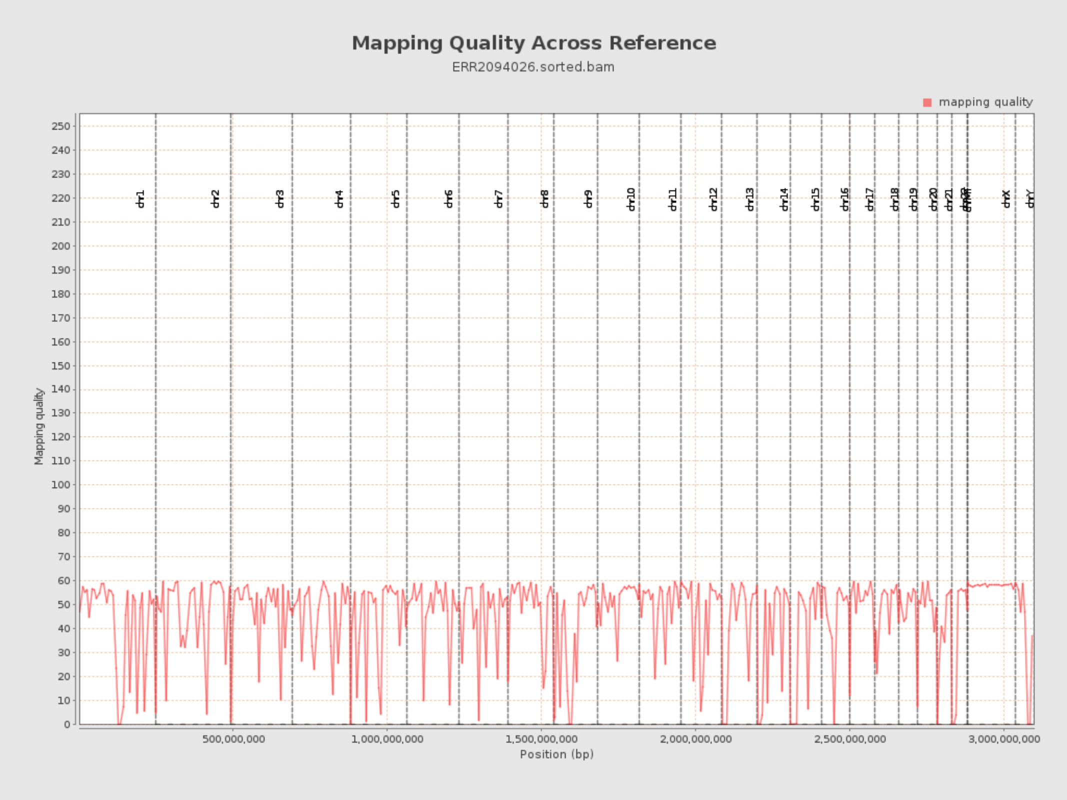
# 10. Results : Mapped Reads Clipping Profile



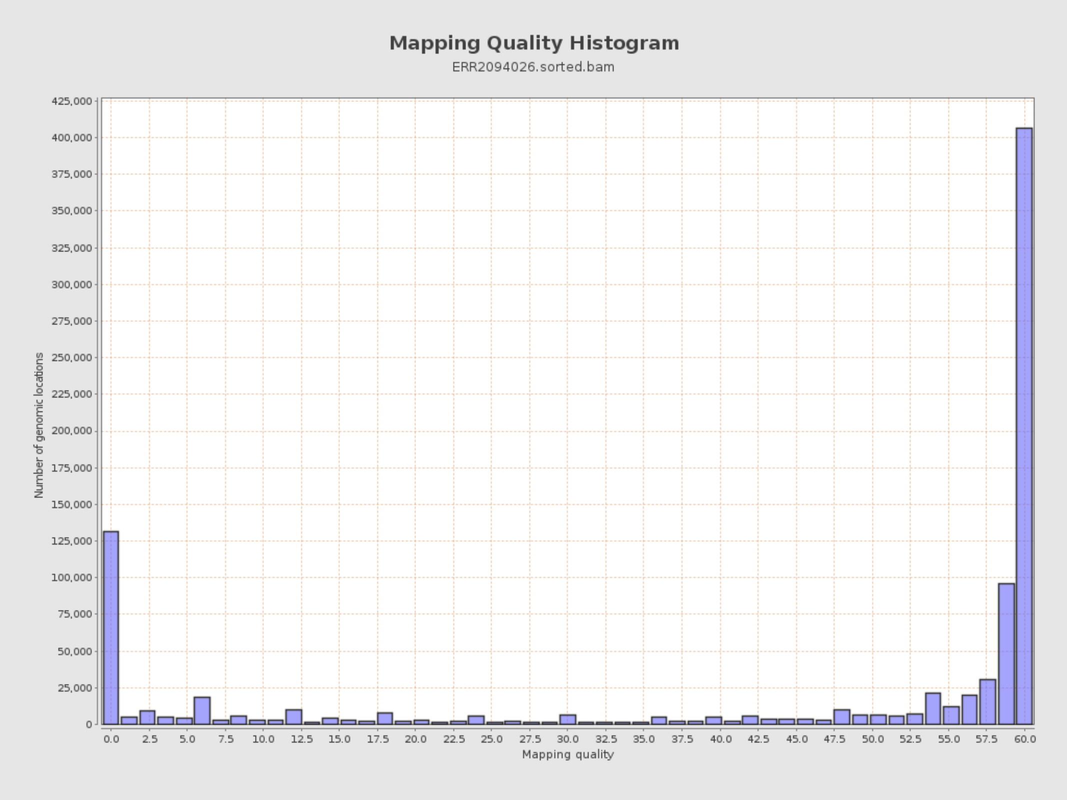
# 11. Results : Homopolymer Indels



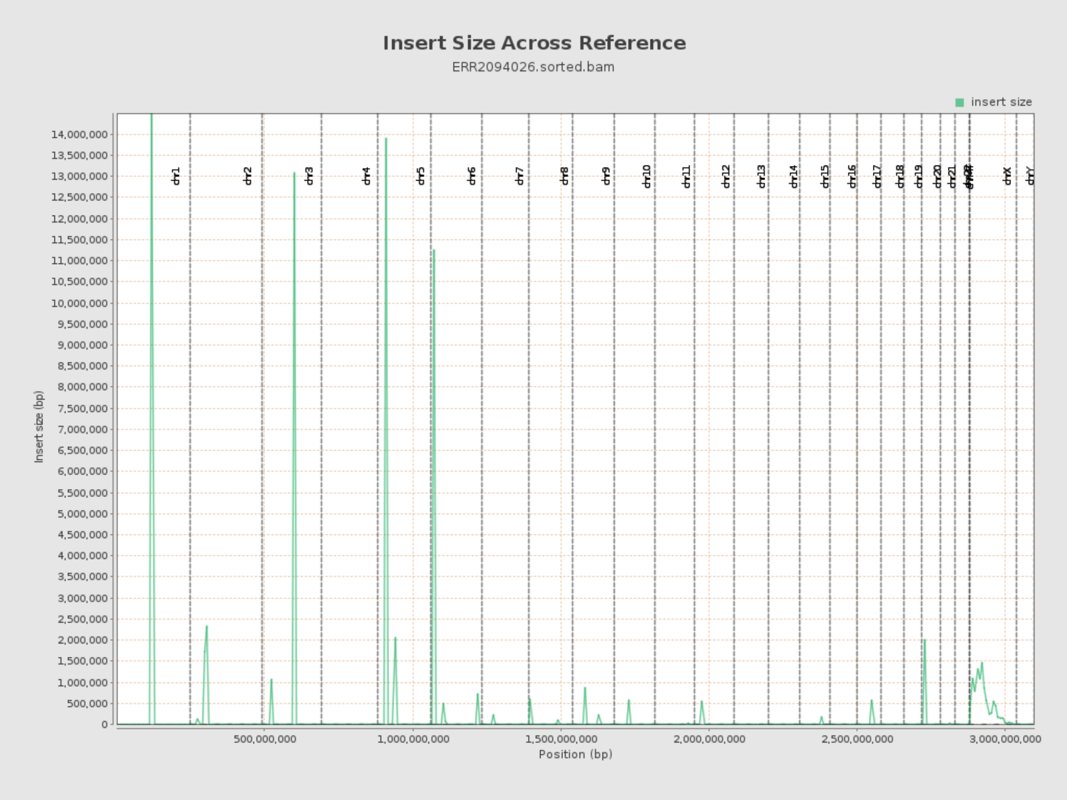
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram