# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 20:26:28*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094001.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_ERR2094001 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094001_1.fastq.gz ERR2094001_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Aug 26 20:26:26 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | ERR2094001.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 433,806 |
| Mapped reads | 102,141 / 23.55% |
| Unmapped reads | 331,665 / 76.45% |
| Mapped paired reads | 102,141 / 23.55% |
| Mapped reads, first in pair | 49,690 / 11.45% |
| Mapped reads,  second in pair | 52,451 / 12.09% |
| Mapped reads, both in pair | 97,936 / 22.58% |
| Mapped reads, singletons | 4,205 / 0.97% |
| Secondary alignments | 0 |
| Supplementary alignments | 230 / 0.05% |
| Read min/max/mean length | 30 / 151 / 72.15 |
| Duplicated reads (estimated) | 100,885 / 23.26% |
| Duplication rate | 37.48% |
| Clipped reads | 12,064 / 2.78% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 3,999,822 / 28.6% |
| Number/percentage of C's | 2,740,609 / 19.6% |
| Number/percentage of T's | 4,044,326 / 28.92% |
| Number/percentage of G's | 3,200,427 / 22.88% |
| Number/percentage of N's | 180 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 42.48% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0045 |
| Standard Deviation | 11.1092 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 7.63 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 8,138.65 |
| Standard Deviation | 875,640.34 |
| P25/Median/P75 | 217 / 217 / 237 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 1.83% |
| Mismatches | 249,649 |
| Insertions | 2,227 |
| Mapped reads with at least one insertion | 1.92% |
| Deletions | 10,405 |
| Mapped reads with at least one deletion | 9.95% |
| Homopolymer indels | 16.76% |

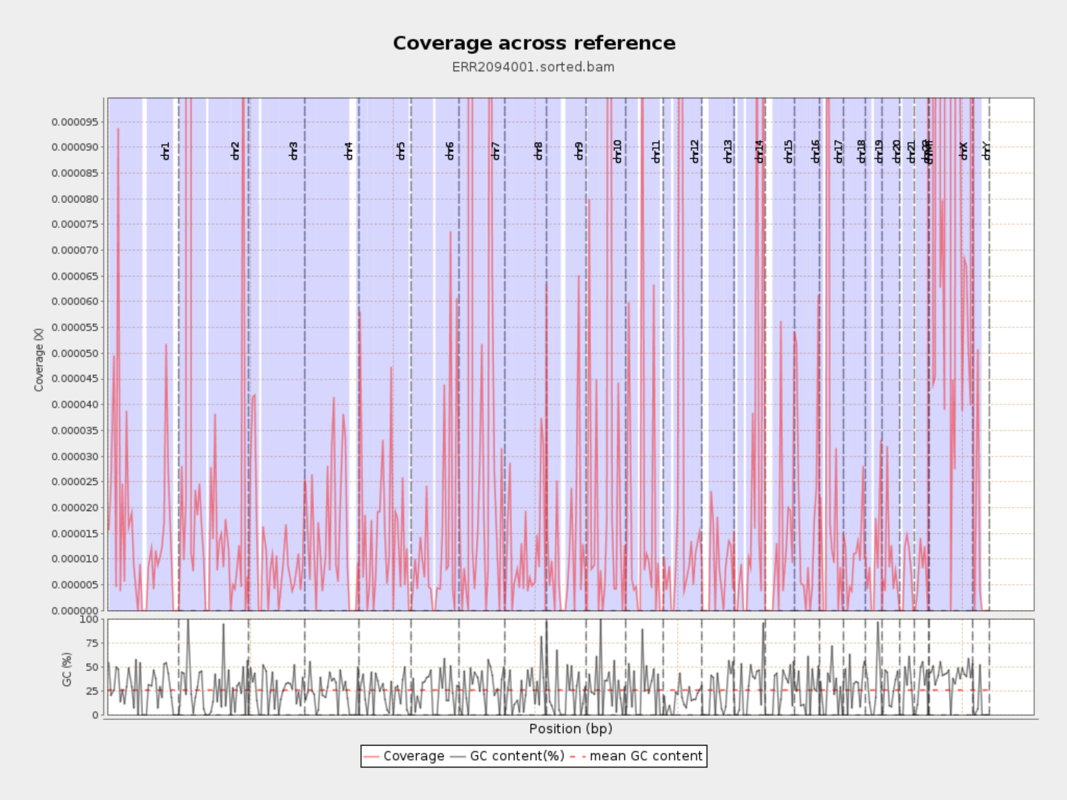
## 2.7. Chromosome stats

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

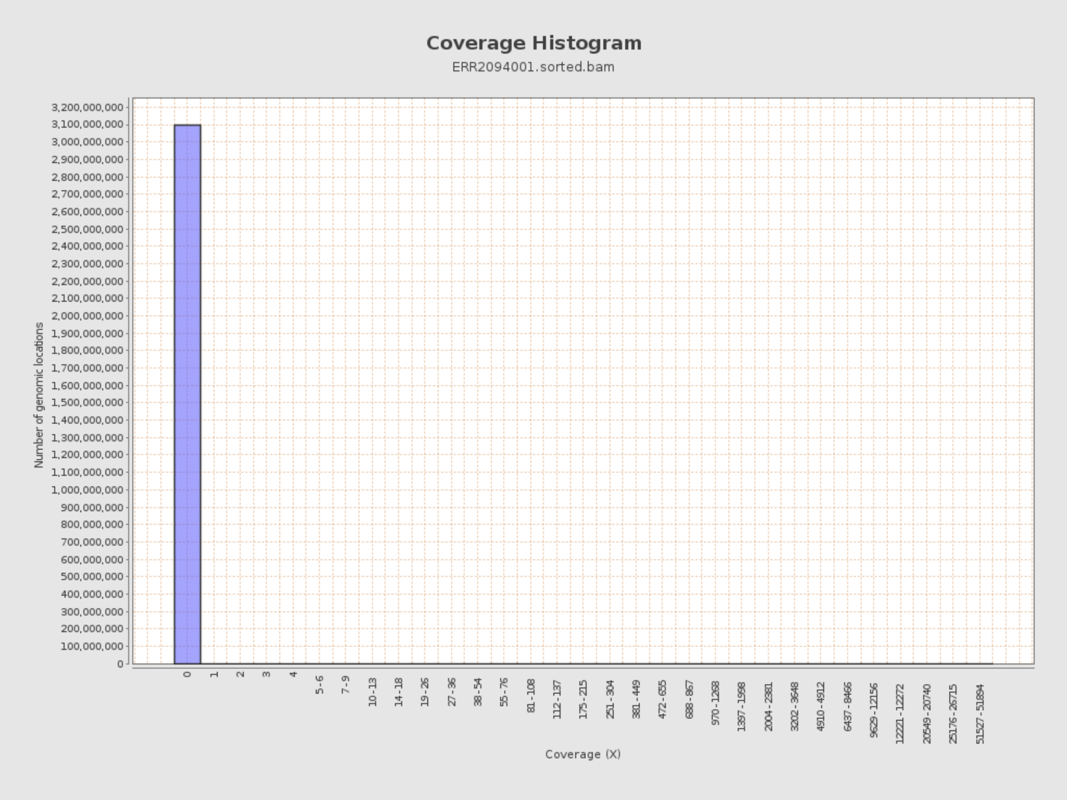
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 3811 | 0 | 0.0081 |
| chr2 | 243199373 | 371739 | 0.0015 | 1.5714 |
| chr3 | 198022430 | 2163 | 0 | 0.0046 |
| chr4 | 191154276 | 2738 | 0 | 0.0048 |
| chr5 | 180915260 | 2673 | 0 | 0.0049 |
| chr6 | 171115067 | 2433 | 0 | 0.009 |
| chr7 | 159138663 | 1273123 | 0.008 | 9.5334 |
| chr8 | 146364022 | 1697 | 0 | 0.0047 |
| chr9 | 141213431 | 1724 | 0 | 0.007 |
| chr10 | 135534747 | 4548 | 0 | 0.0346 |
| chr11 | 135006516 | 2471 | 0 | 0.0133 |
| chr12 | 133851895 | 3263 | 0 | 0.0195 |
| chr13 | 115169878 | 879 | 0 | 0.0033 |
| chr14 | 107349540 | 2670 | 0 | 0.022 |
| chr15 | 102531392 | 1178 | 0 | 0.0064 |
| chr16 | 90354753 | 1816 | 0 | 0.0065 |
| chr17 | 81195210 | 2293 | 0 | 0.0282 |
| chr18 | 78077248 | 832 | 0 | 0.0038 |
| chr19 | 59128983 | 588 | 0 | 0.0033 |
| chr20 | 63025520 | 601 | 0 | 0.004 |
| chr21 | 48129895 | 360 | 0 | 0.003 |
| chr22 | 51304566 | 336 | 0 | 0.0026 |
| chrMT | 16571 | 12226424 | 737.8205 | 4,647.3013 |
| chrX | 155270560 | 108164 | 0.0007 | 0.708 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 455 | 0 | 0.0047 |

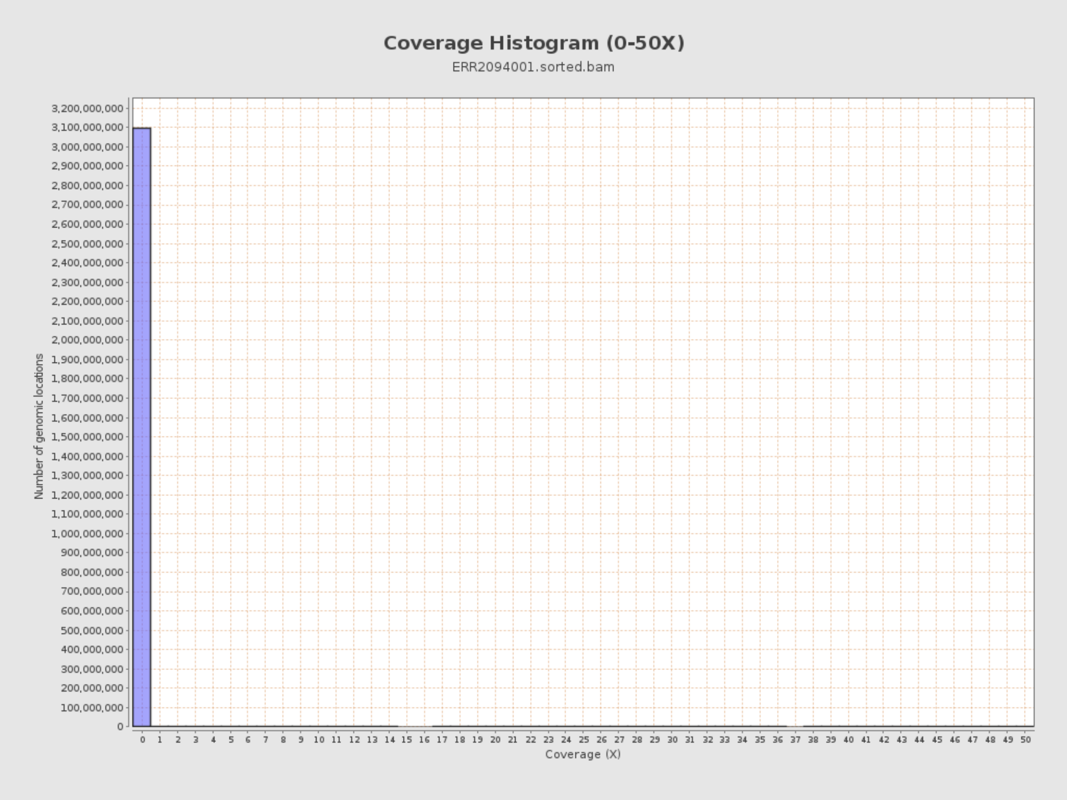
# 3. Results : Coverage across reference



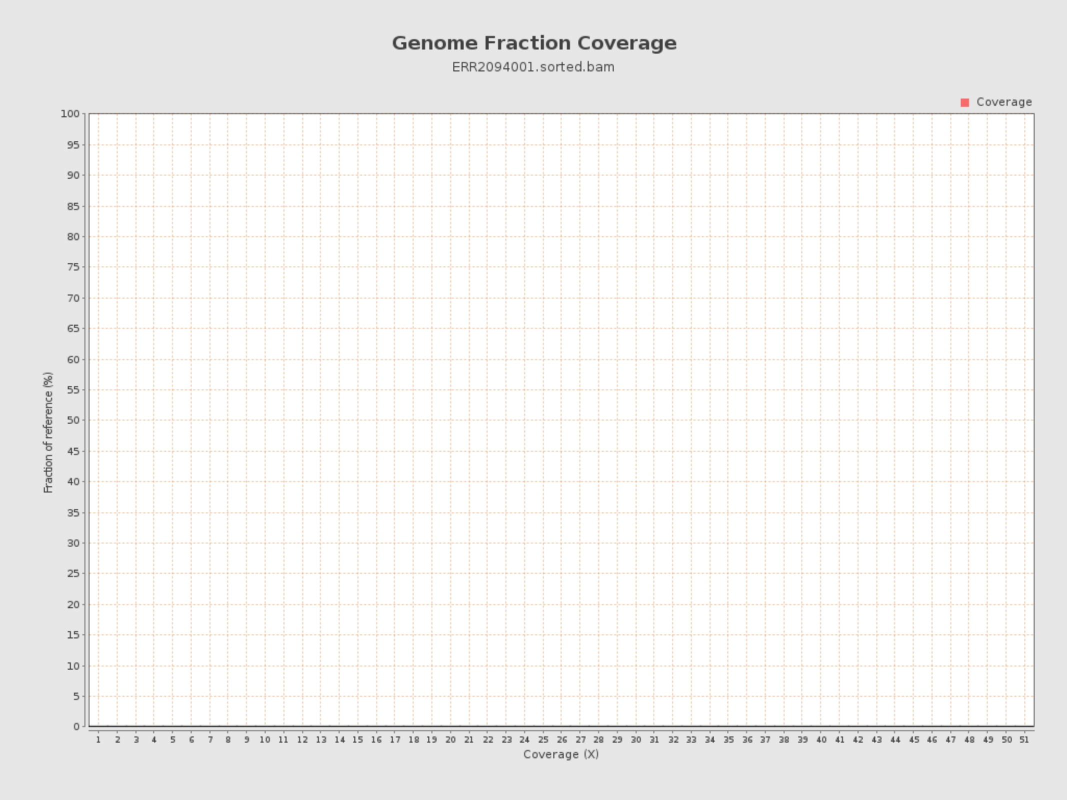
# 4. Results : Coverage Histogram



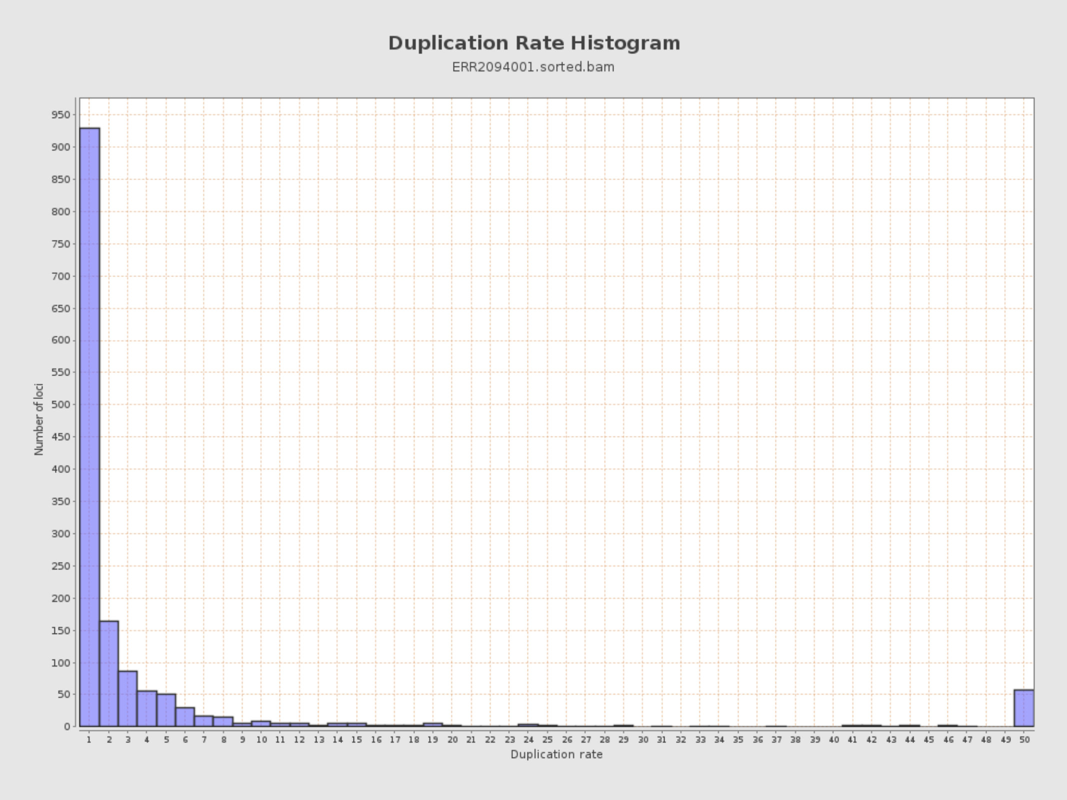
# 5. Results : Coverage Histogram (0-50X)



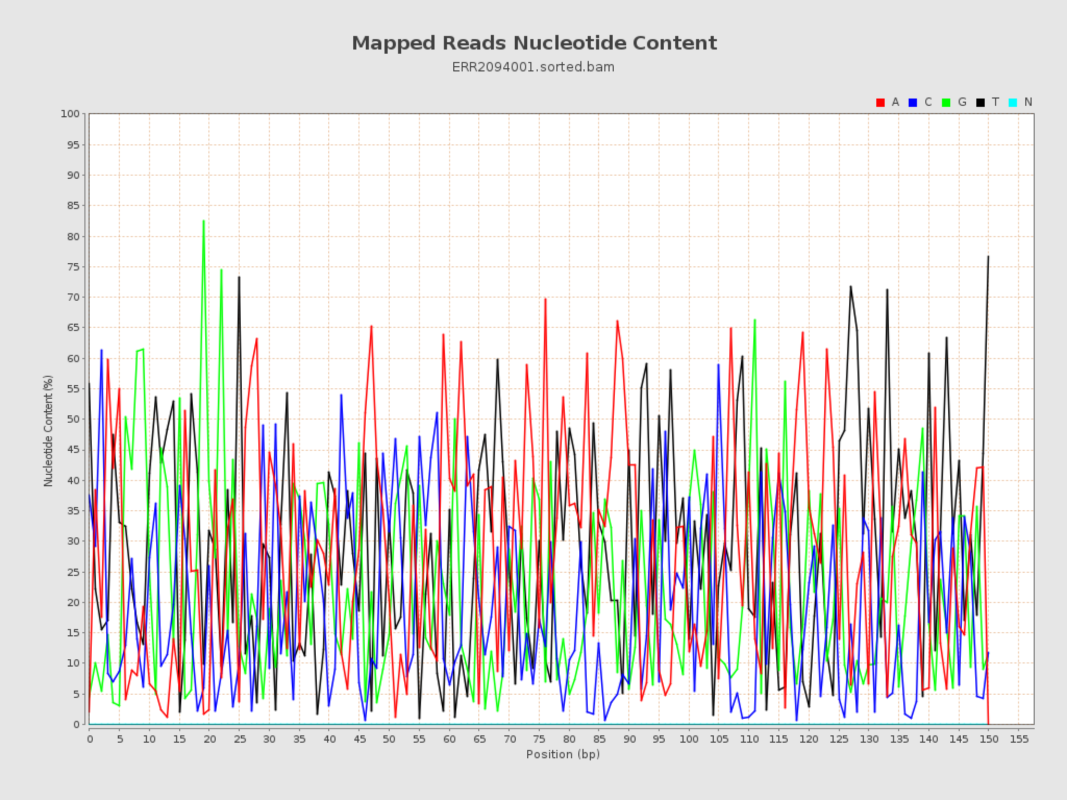
# 6. Results : Genome Fraction Coverage



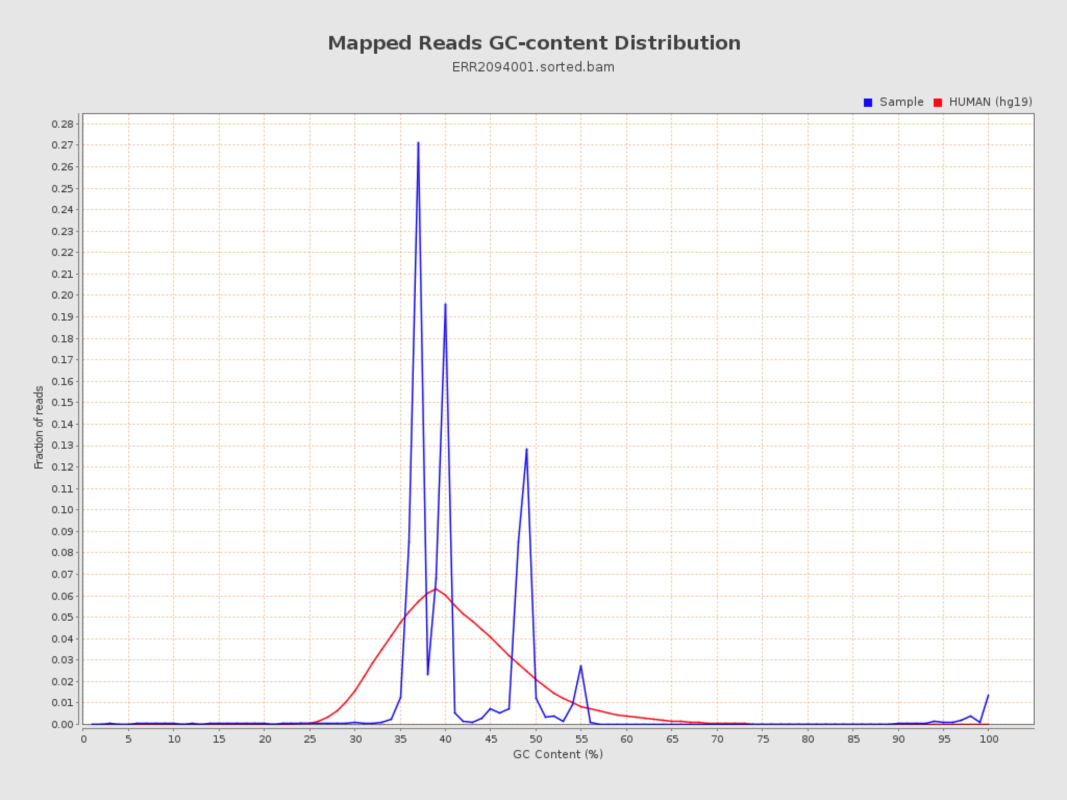
# 7. Results : Duplication Rate Histogram



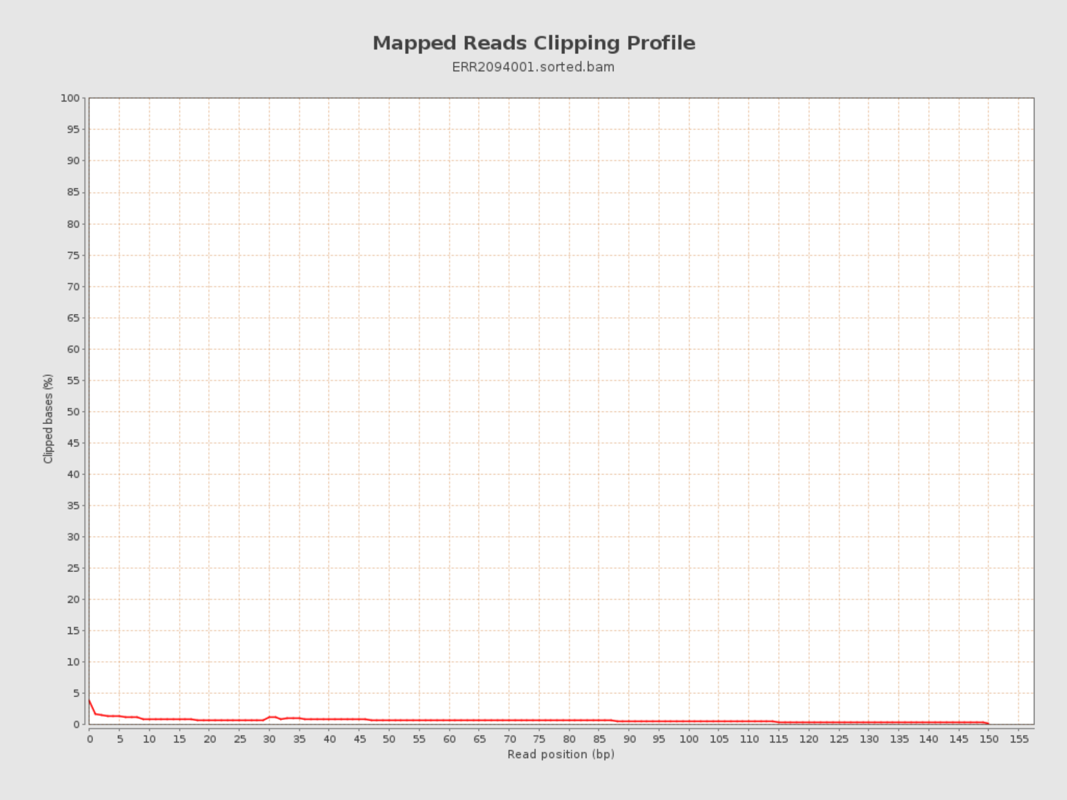
# 8. Results : Mapped Reads Nucleotide Content



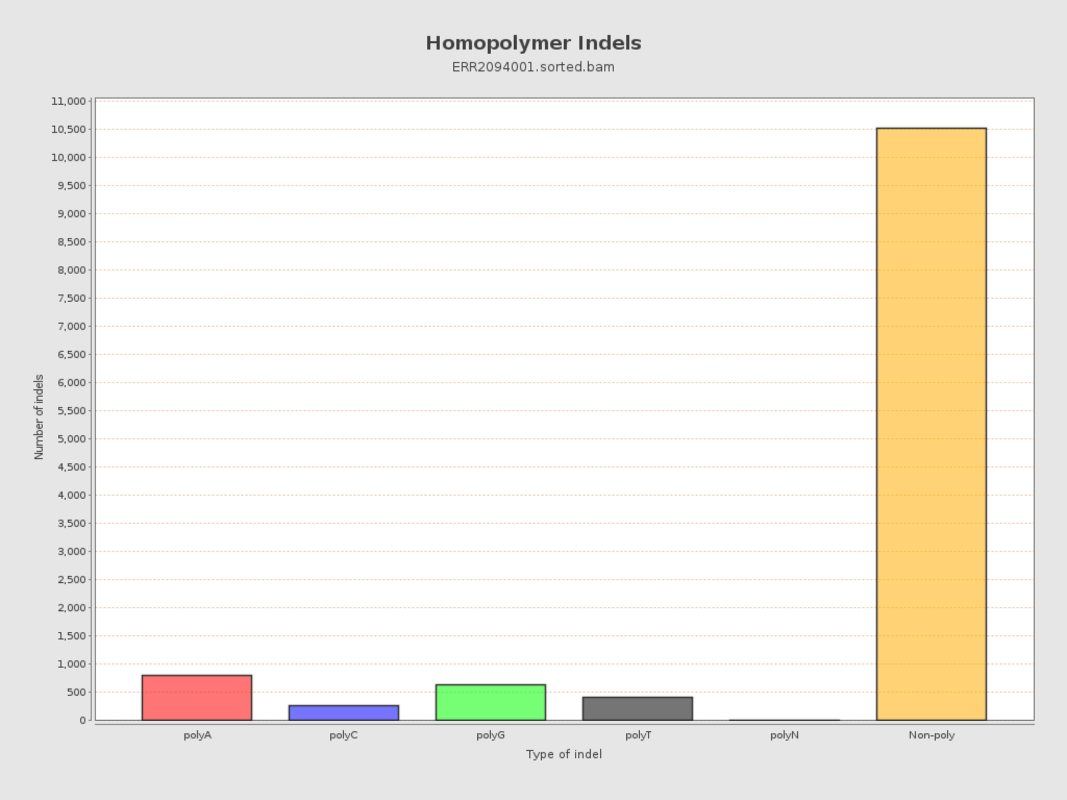
# 9. Results : Mapped Reads GC-content Distribution



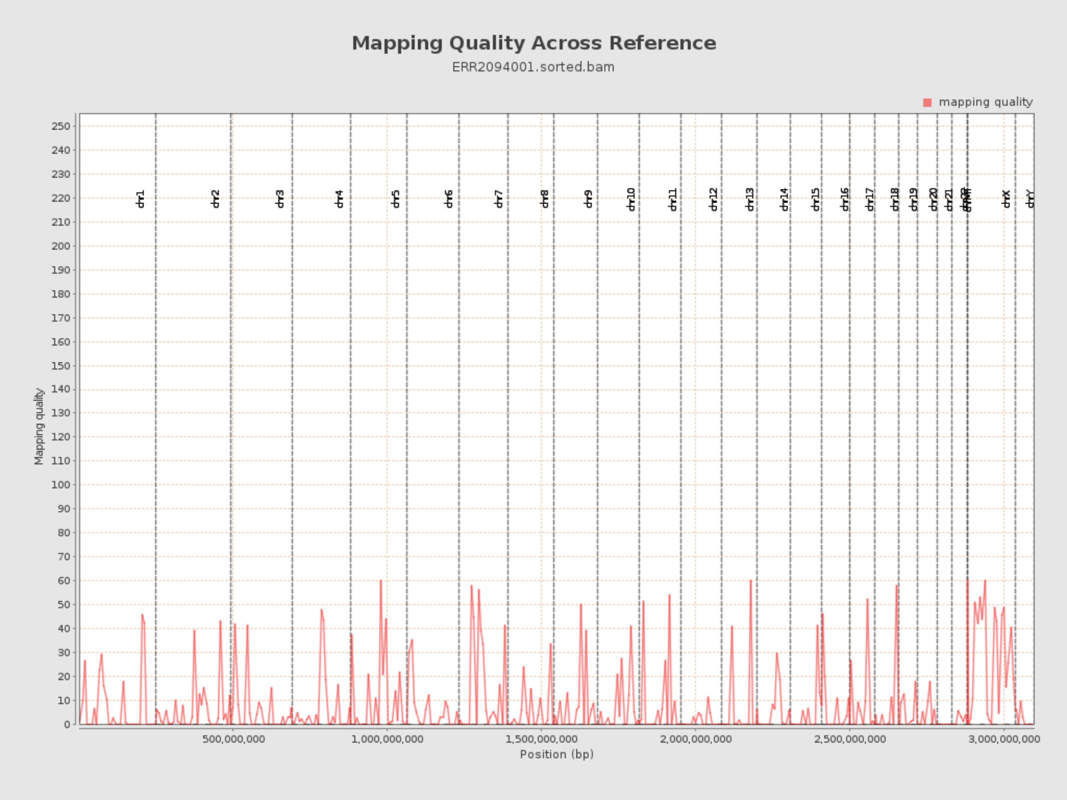
# 10. Results : Mapped Reads Clipping Profile



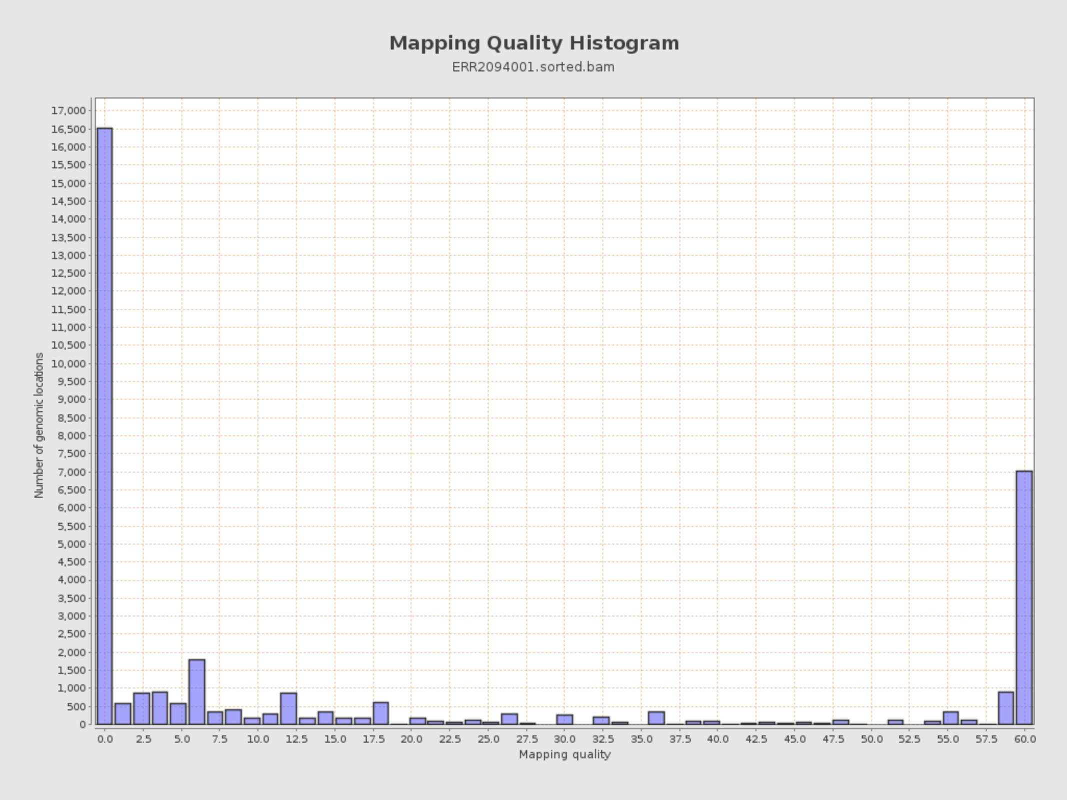
# 11. Results : Homopolymer Indels



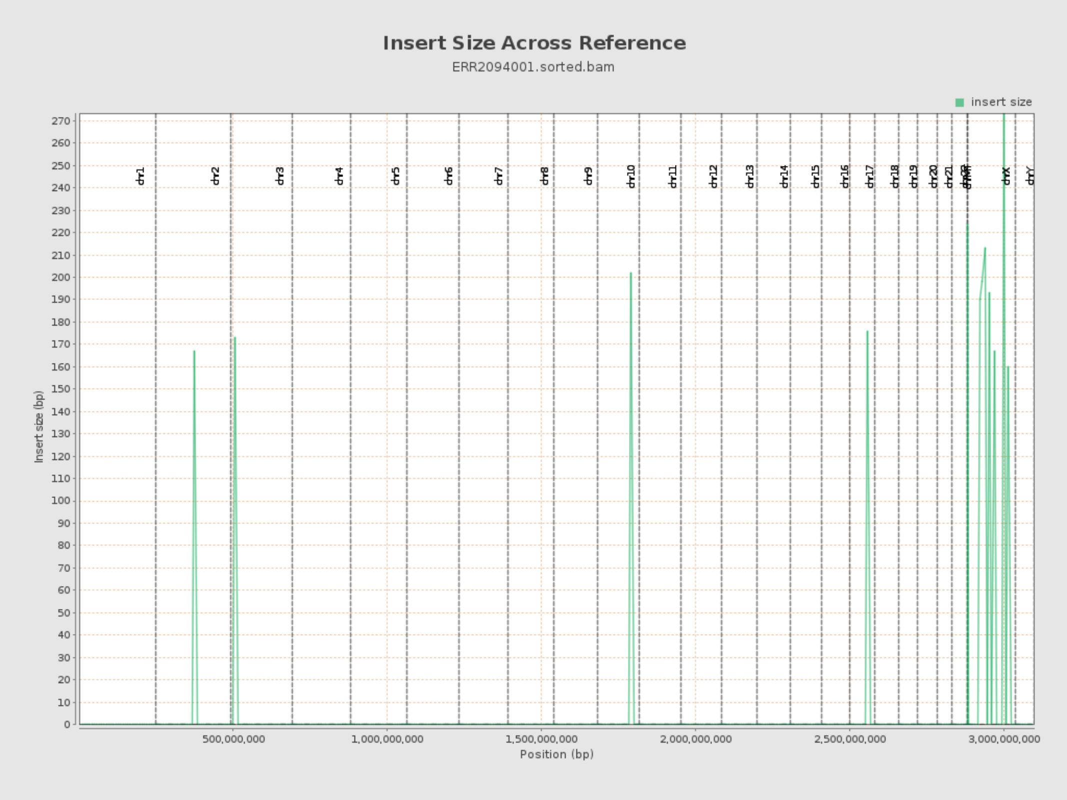
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram