# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 21:01:10*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094018.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_ERR2094018 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094018_1.fastq.gz ERR2094018_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Aug 26 21:01:09 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | ERR2094018.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 38,580 |
| Mapped reads | 6,319 / 16.38% |
| Unmapped reads | 32,261 / 83.62% |
| Mapped paired reads | 6,319 / 16.38% |
| Mapped reads, first in pair | 3,031 / 7.86% |
| Mapped reads, second in pair | 3,288 / 8.52% |
| Mapped reads, both in pair | 5,884 / 15.25% |
| Mapped reads, singletons | 435 / 1.13% |
| Secondary alignments | 0 |
| Supplementary alignments | 39 / 0.1% |
| Read min/max/mean length | 30 / 151 / 74.19 |
| Duplicated reads (estimated) | 5,939 / 15.39% |
| Duplication rate | 28.4% |
| Clipped reads | 1,562 / 4.05% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 210,553 / 25.74% |
| Number/percentage of C's | 154,963 / 18.95% |
| Number/percentage of T's | 241,313 / 29.5% |
| Number/percentage of G's | 211,011 / 25.8% |
| Number/percentage of N's | 37 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 44.75% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0003 |
| Standard Deviation | 0.8667 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 5.7 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 47,799.51 |
| Standard Deviation | 2,374,083.22 |
| P25/Median/P75 | 237 / 237 / 237 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 3.19% |
| Mismatches | 25,588 |
| Insertions | 116 |
| Mapped reads with at least one insertion | 1.39% |
| Deletions | 240 |
| Mapped reads with at least one deletion | 3.77% |
| Homopolymer indels | 45.22% |

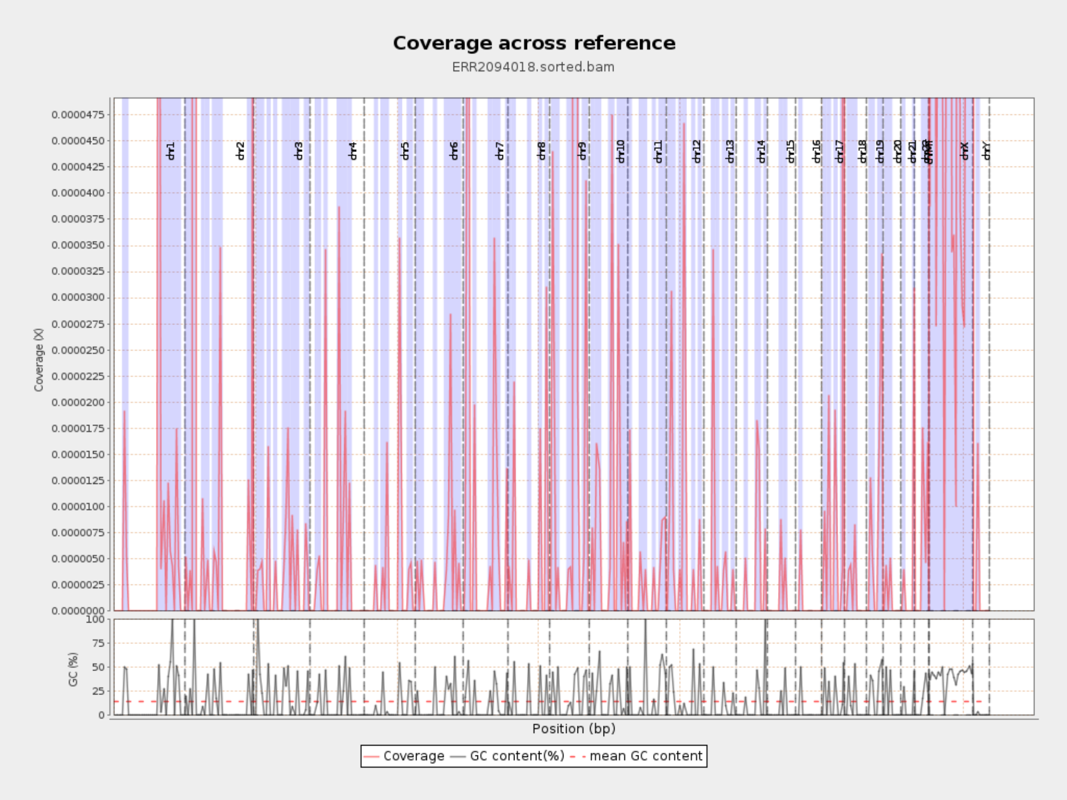
## 2.7. Chromosome stats

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

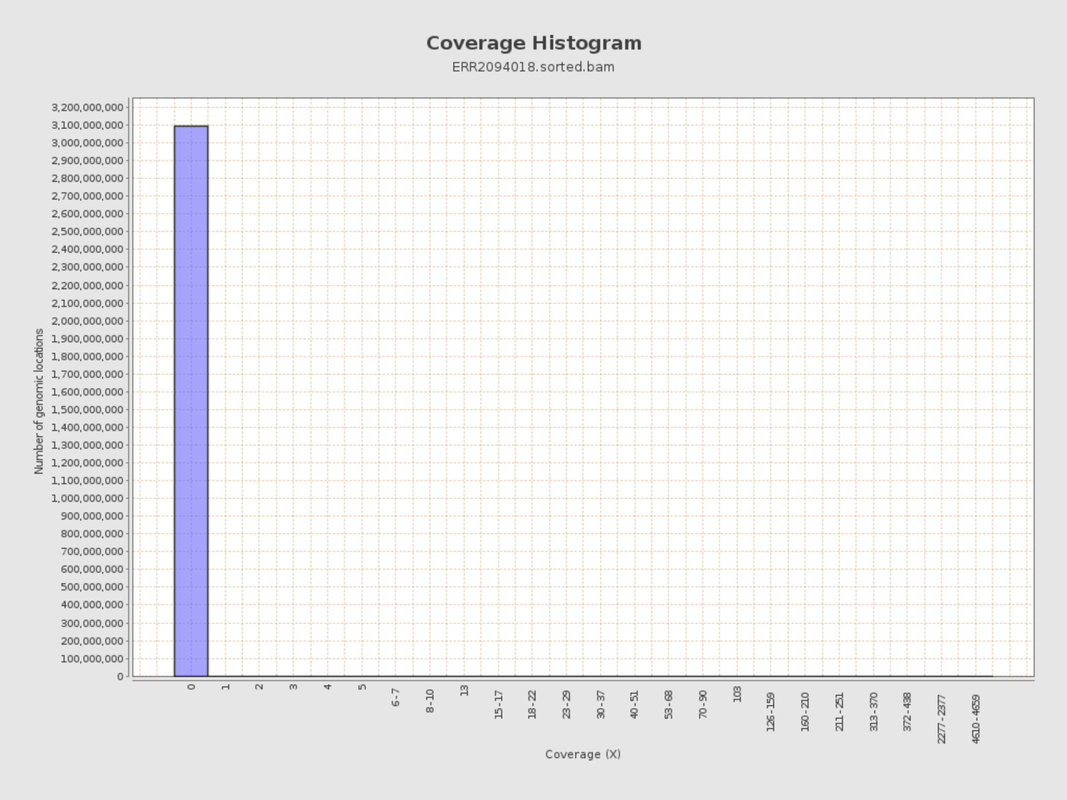
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 1581 | 0 | 0.0048 |
| chr2 | 243199373 | 37362 | 0.0002 | 0.155 |
| chr3 | 198022430 | 721 | 0 | 0.002 |
| chr4 | 191154276 | 952 | 0 | 0.0028 |
| chr5 | 180915260 | 534 | 0 | 0.002 |
| chr6 | 171115067 | 541 | 0 | 0.0019 |
| chr7 | 159138663 | 1499 | 0 | 0.0054 |
| chr8 | 146364022 | 616 | 0 | 0.0032 |
| chr9 | 141213431 | 44146 | 0.0003 | 0.3266 |
| chr10 | 135534747 | 1055 | 0 | 0.0051 |
| chr11 | 135006516 | 408 | 0 | 0.0017 |
| chr12 | 133851895 | 828 | 0 | 0.0039 |
| chr13 | 115169878 | 406 | 0 | 0.0024 |
| chr14 | 107349540 | 361 | 0 | 0.0024 |
| chr15 | 102531392 | 107 | 0 | 0.001 |
| chr16 | 90354753 | 60 | 0 | 0.0012 |
| chr17 | 81195210 | 3233 | 0 | 0.025 |
| chr18 | 78077248 | 128 | 0 | 0.0016 |
| chr19 | 59128983 | 507 | 0 | 0.0029 |
| chr20 | 63025520 | 73 | 0 | 0.0011 |
| chr21 | 48129895 | 183 | 0 | 0.0026 |
| chr22 | 51304566 | 296 | 0 | 0.0026 |
| chrMT | 16571 | 698791 | 42.1695 | 370.4505 |
| chrX | 155270560 | 25707 | 0.0002 | 0.0843 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 124 | 0 | 0.002 |

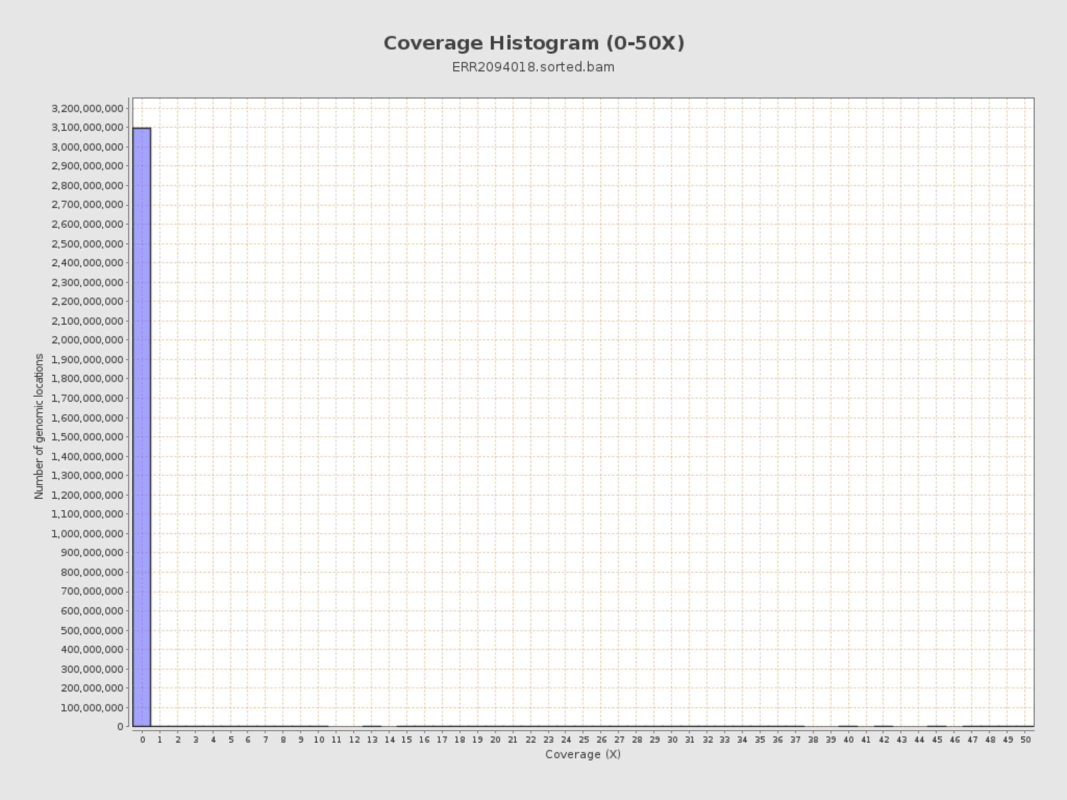
# 3. Results : Coverage across reference



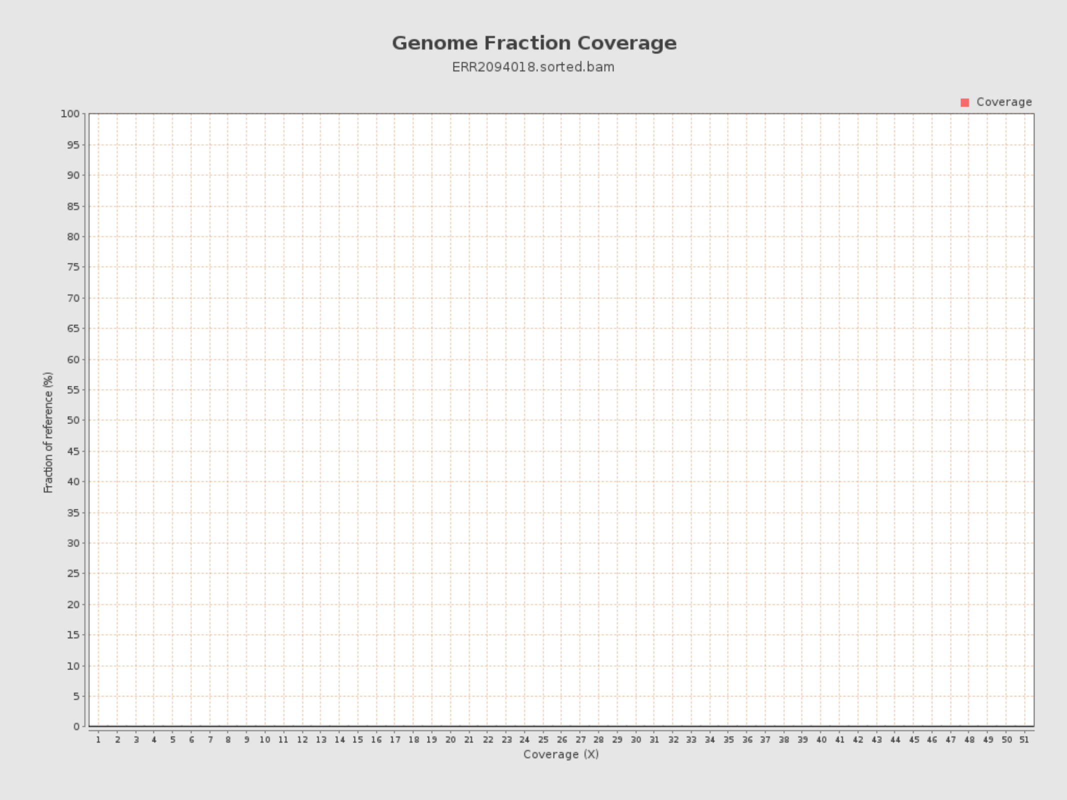
# 4. Results : Coverage Histogram



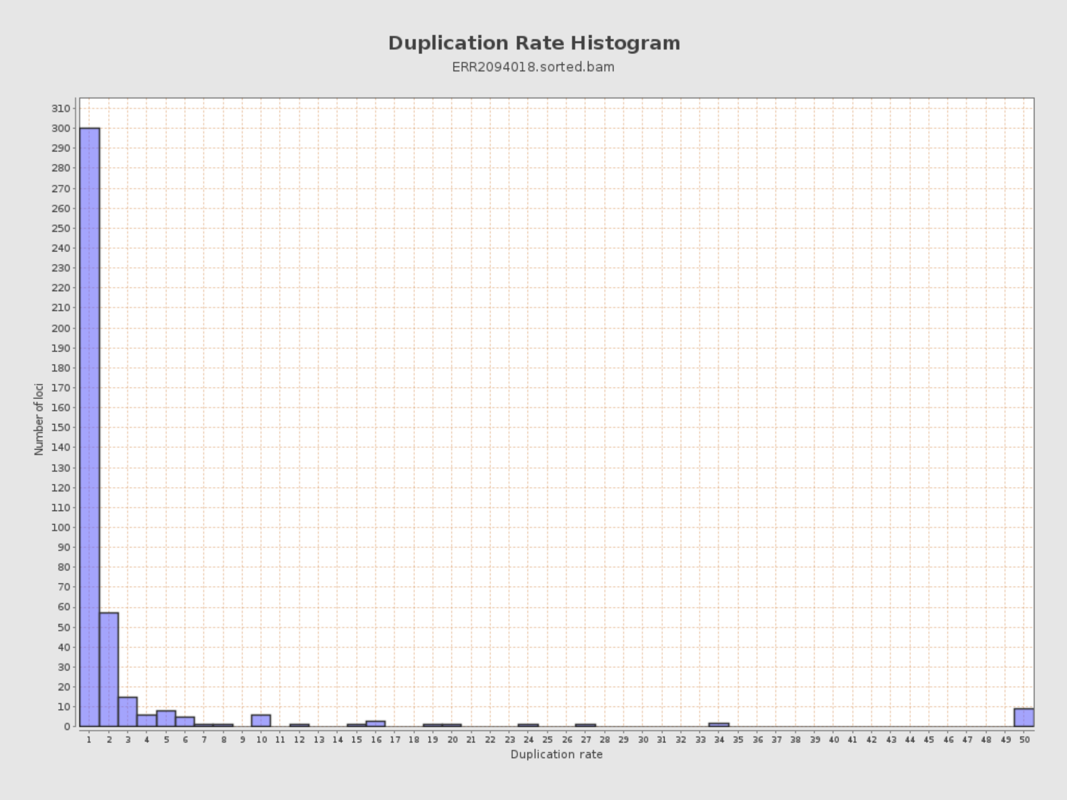
# 5. Results : Coverage Histogram (0-50X)



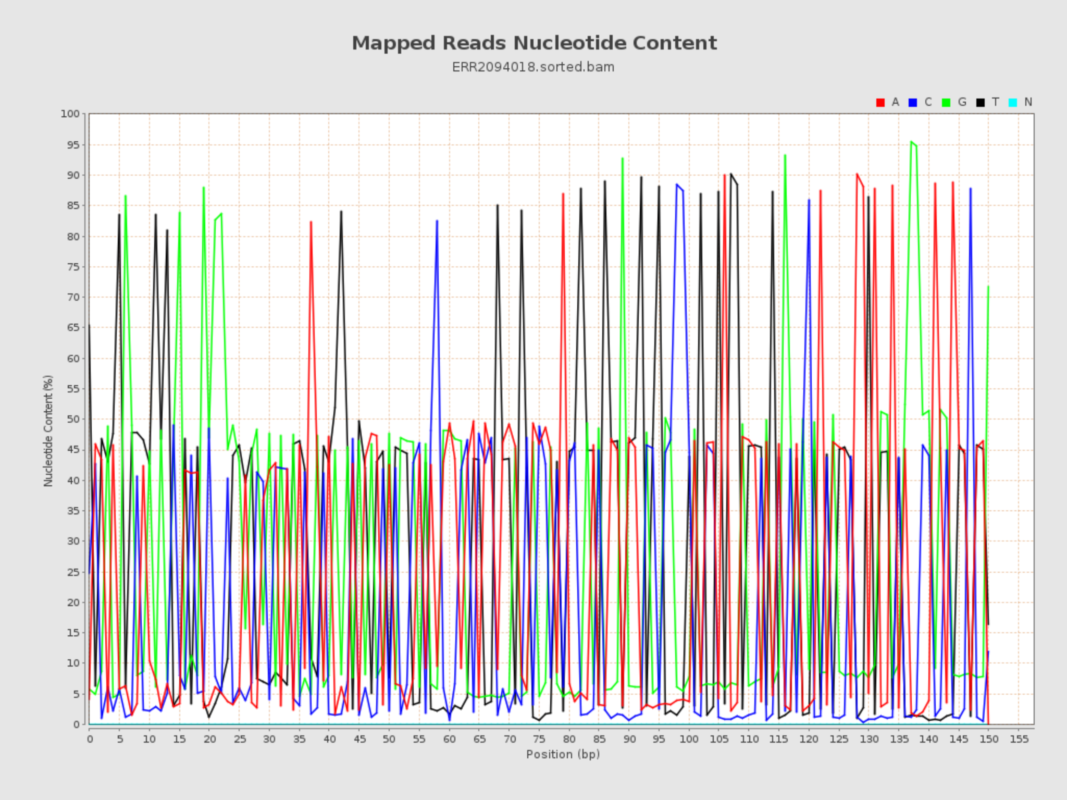
# 6. Results : Genome Fraction Coverage



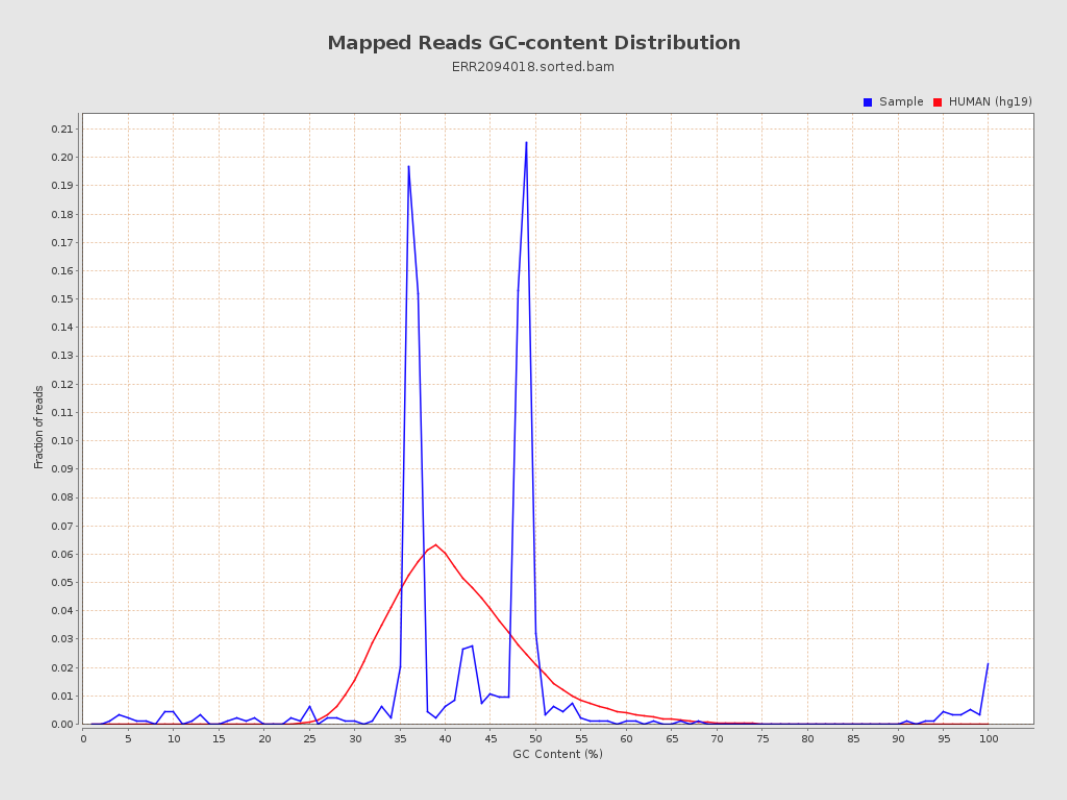
# 7. Results : Duplication Rate Histogram



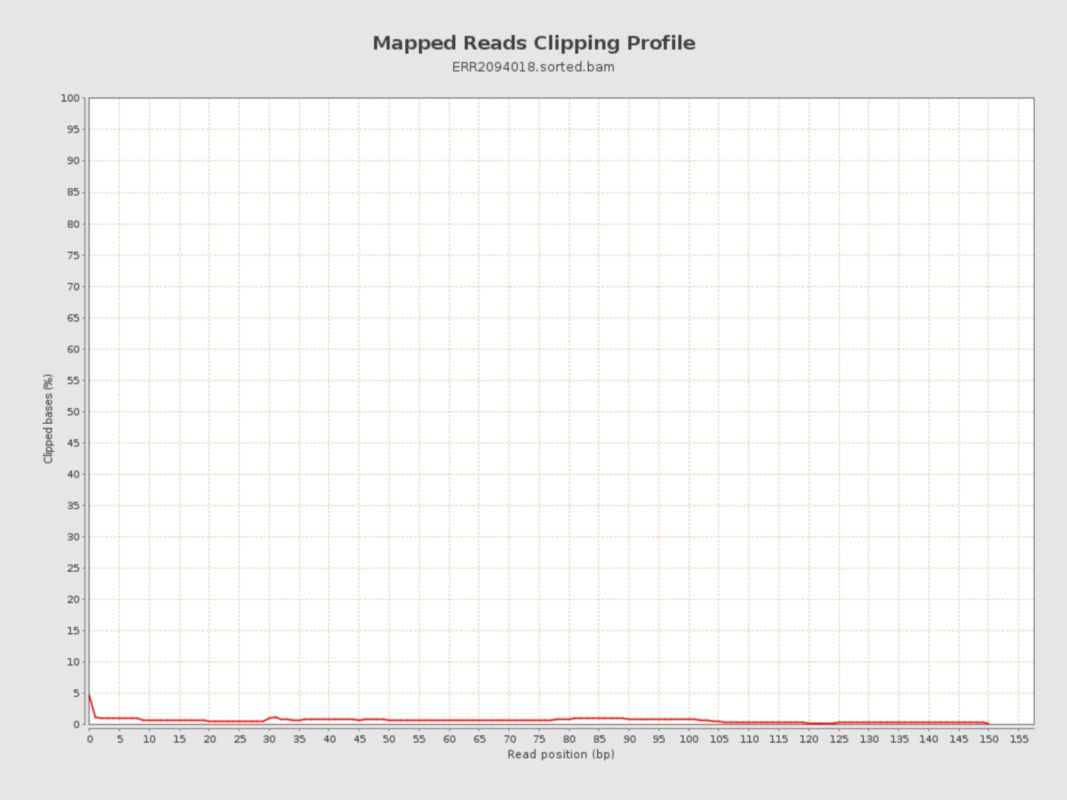
# 8. Results : Mapped Reads Nucleotide Content



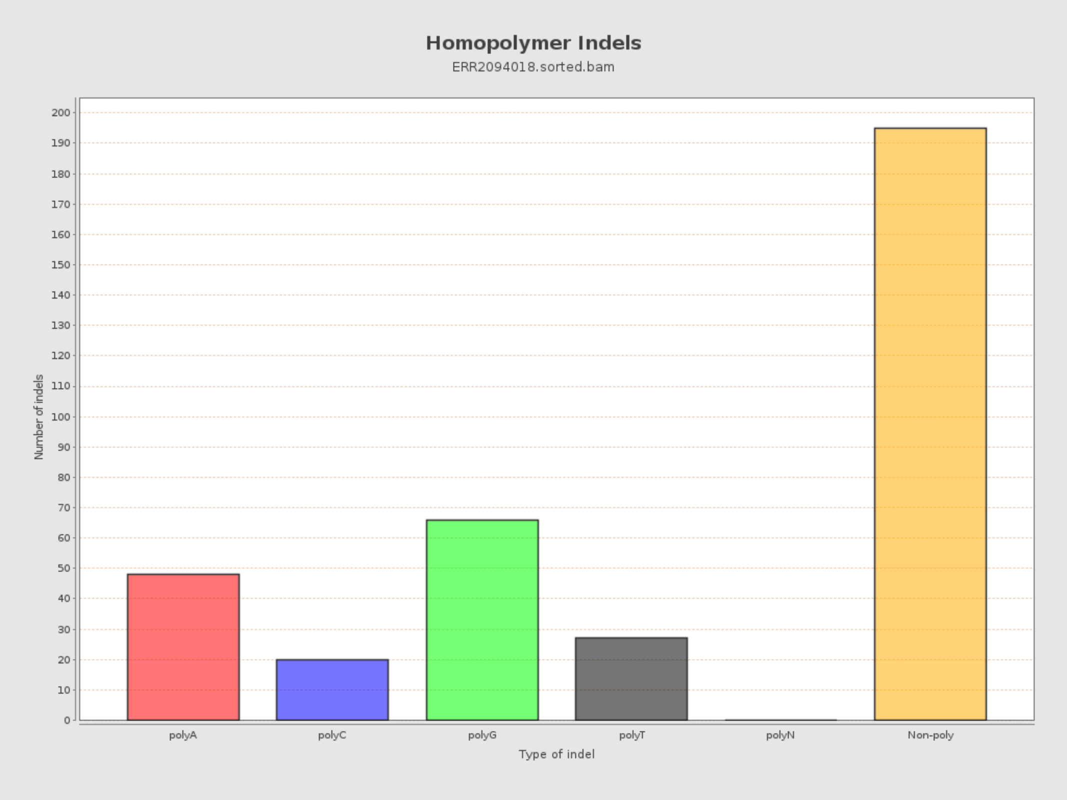
# 9. Results : Mapped Reads GC-content Distribution



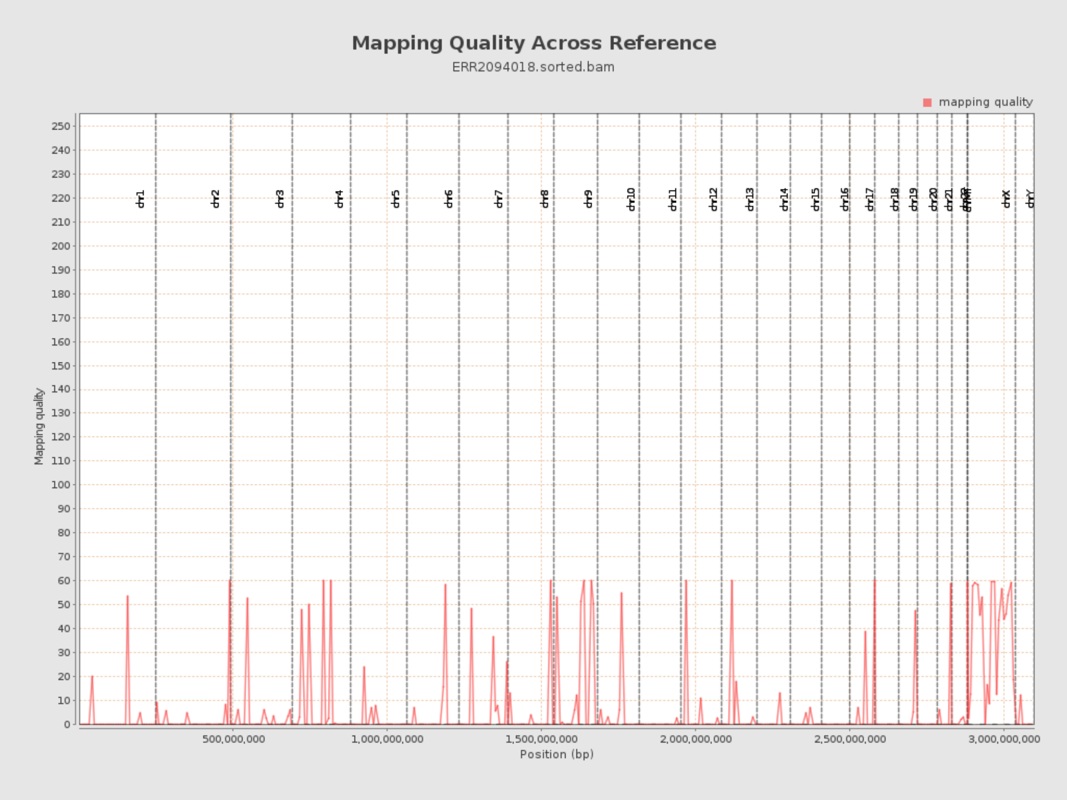
# 10. Results : Mapped Reads Clipping Profile



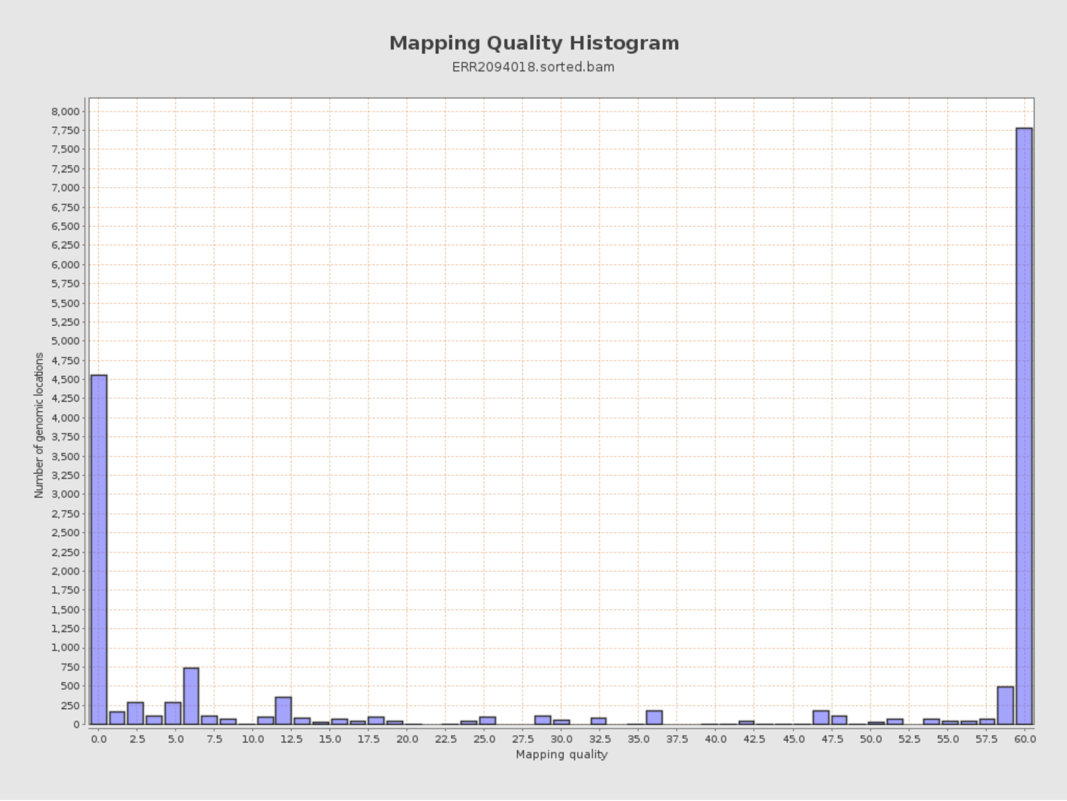
# 11. Results : Homopolymer Indels



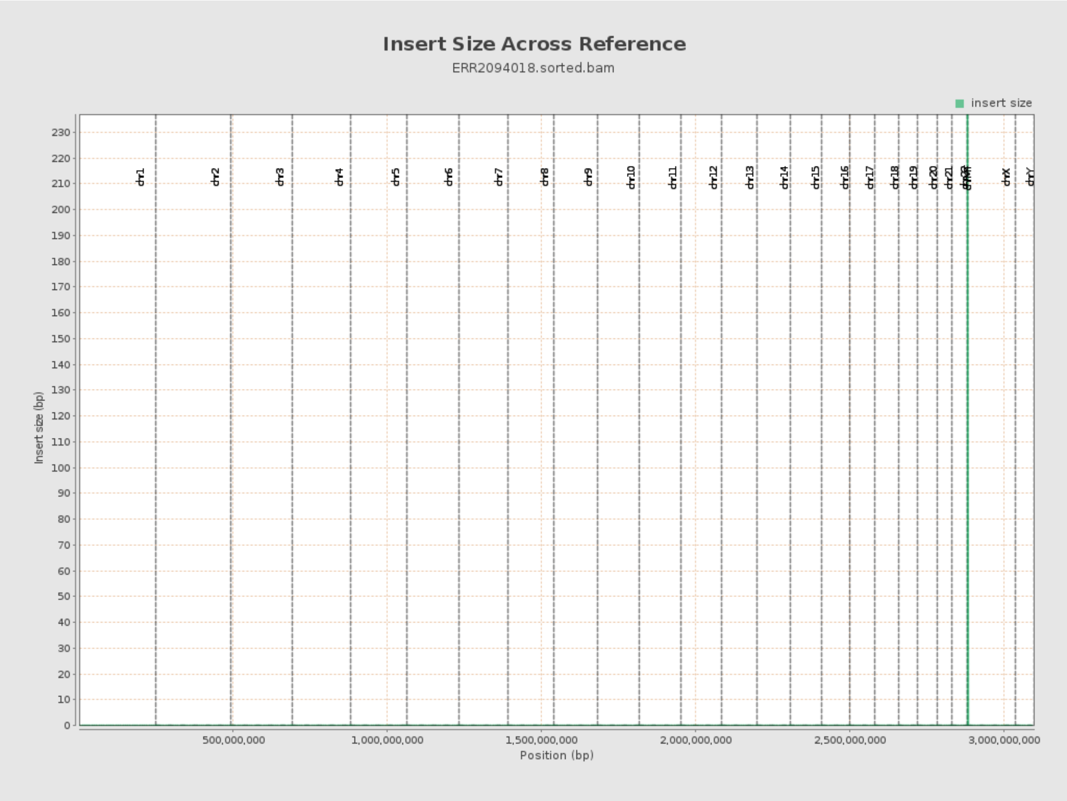
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram