# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/27 05:21:14*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094149.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_ERR2094149 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094149_1.fastq.gz ERR2094149_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Aug 27 05:21:12 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | ERR2094149.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 428,922 |
| Mapped reads | 414,731 / 96.69% |
| Unmapped reads | 14,191 / 3.31% |
| Mapped paired reads | 414,731 / 96.69% |
| Mapped reads, first in pair | 208,389 / 48.58% |
| Mapped reads, second in pair | 206,342 / 48.11% |
| Mapped reads, both in pair | 411,768 / 96% |
| Mapped reads, singletons | 2,963 / 0.69% |
| Secondary alignments | 0 |
| Supplementary alignments | 14,195 / 3.31% |
| Read min/max/mean length | 30 / 151 / 142.72 |
| Duplicated reads (estimated) | 395,129 / 92.12% |
| Duplication rate | 49.34% |
| Clipped reads | 154,297 / 35.97% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 13,946,107 / 25.69% |
| Number/percentage of C's | 13,122,387 / 24.17% |
| Number/percentage of T's | 13,363,980 / 24.62% |
| Number/percentage of G's | 13,851,243 / 25.52% |
| Number/percentage of N's | 525 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 49.69% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.018 |
| Standard Deviation | 4.821 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 40.22 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 359,705.25 |
| Standard Deviation | 5,445,938.65 |
| P25/Median/P75 | 141 / 171 / 201 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 4.21% |
| Mismatches | 2,252,092 |
| Insertions | 29,244 |
| Mapped reads with at least one insertion | 6.96% |
| Deletions | 176,053 |
| Mapped reads with at least one deletion | 40.52% |
| Homopolymer indels | 27.57% |

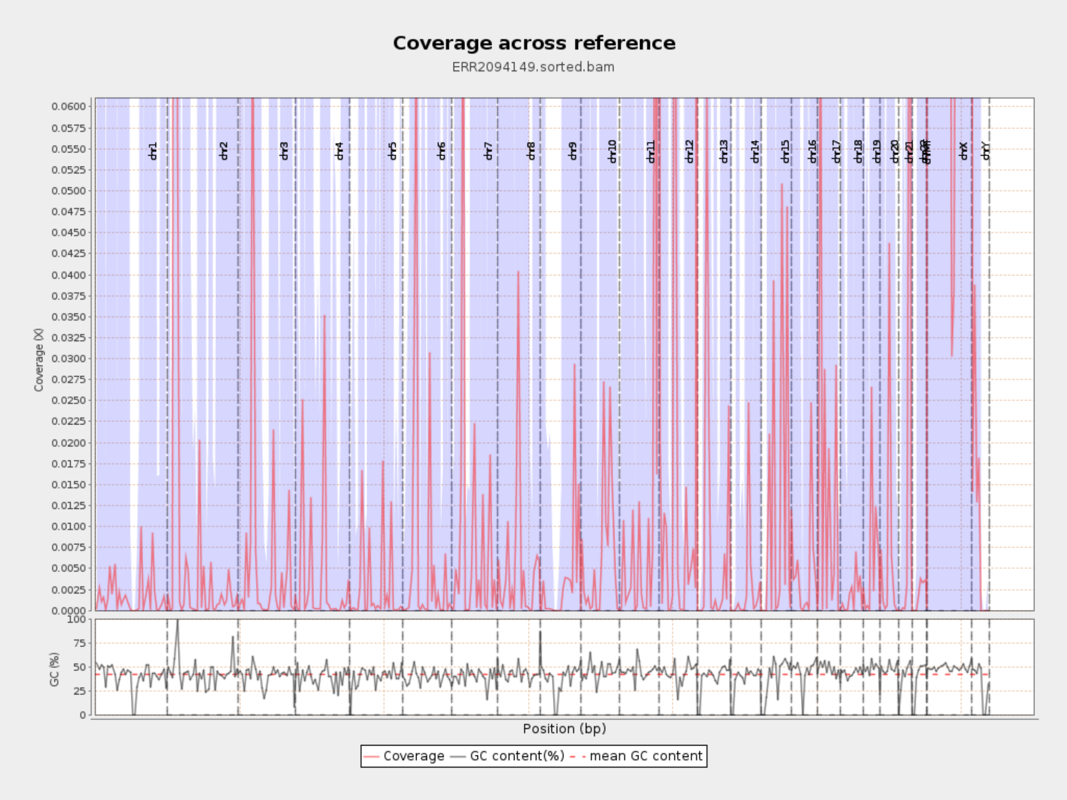
## 2.7. Chromosome stats

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

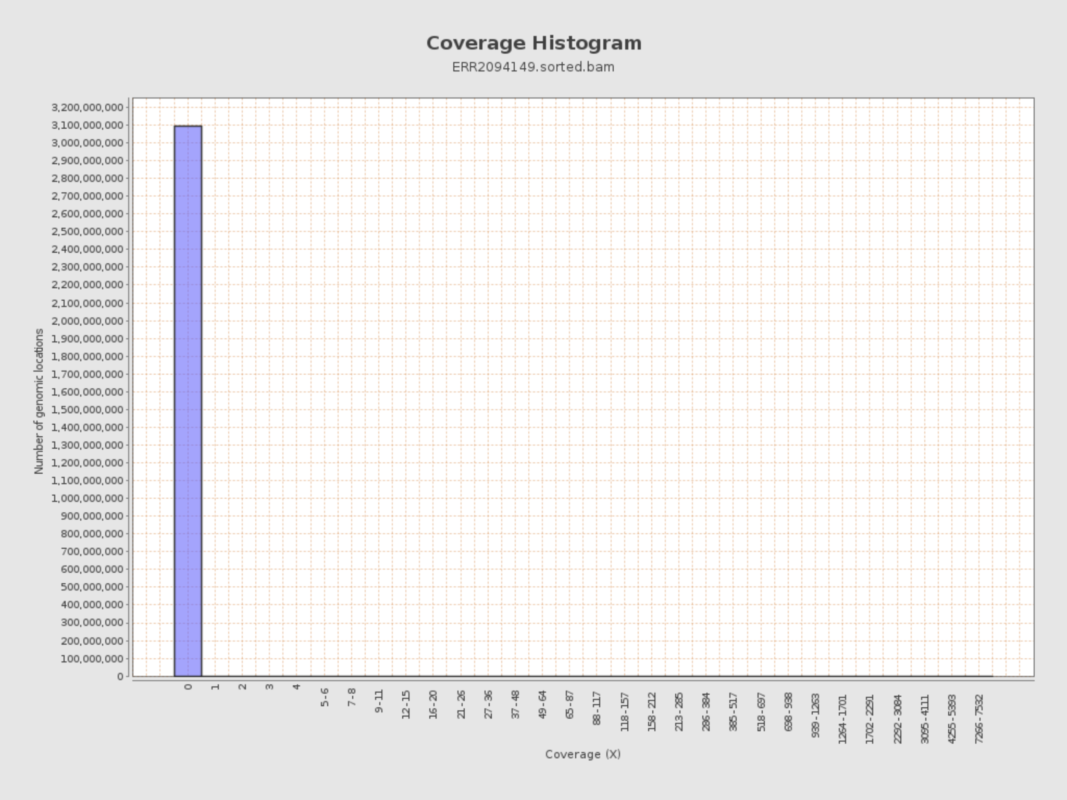
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 446179 | 0.0018 | 0.6354 |
| chr2 | 243199373 | 2783526 | 0.0114 | 4.9921 |
| chr3 | 198022430 | 1206859 | 0.0061 | 2.3961 |
| chr4 | 191154276 | 746931 | 0.0039 | 1.5685 |
| chr5 | 180915260 | 515503 | 0.0028 | 1.2598 |
| chr6 | 171115067 | 1204409 | 0.007 | 3.5478 |
| chr7 | 159138663 | 1368188 | 0.0086 | 3.5062 |
| chr8 | 146364022 | 782664 | 0.0053 | 1.995 |
| chr9 | 141213431 | 528984 | 0.0037 | 1.3958 |
| chr10 | 135534747 | 903512 | 0.0067 | 2.0564 |
| chr11 | 135006516 | 1577070 | 0.0117 | 3.4507 |
| chr12 | 133851895 | 1757211 | 0.0131 | 5.3809 |
| chr13 | 115169878 | 940727 | 0.0082 | 2.4189 |
| chr14 | 107349540 | 300218 | 0.0028 | 1.4204 |
| chr15 | 102531392 | 1304801 | 0.0127 | 3.3343 |
| chr16 | 90354753 | 448656 | 0.005 | 1.5083 |
| chr17 | 81195210 | 1280530 | 0.0158 | 4.2983 |
| chr18 | 78077248 | 152528 | 0.002 | 0.5527 |
| chr19 | 59128983 | 383170 | 0.0065 | 1.9473 |
| chr20 | 63025520 | 453494 | 0.0072 | 2.5545 |
| chr21 | 48129895 | 958059 | 0.0199 | 8.406 |
| chr22 | 51304566 | 96804 | 0.0019 | 0.3814 |
| chrMT | 16571 | 1188707 | 71.7342 | 422.9214 |
| chrX | 155270560 | 33751591 | 0.2174 | 16.3728 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 613804 | 0.0103 | 2.5523 |

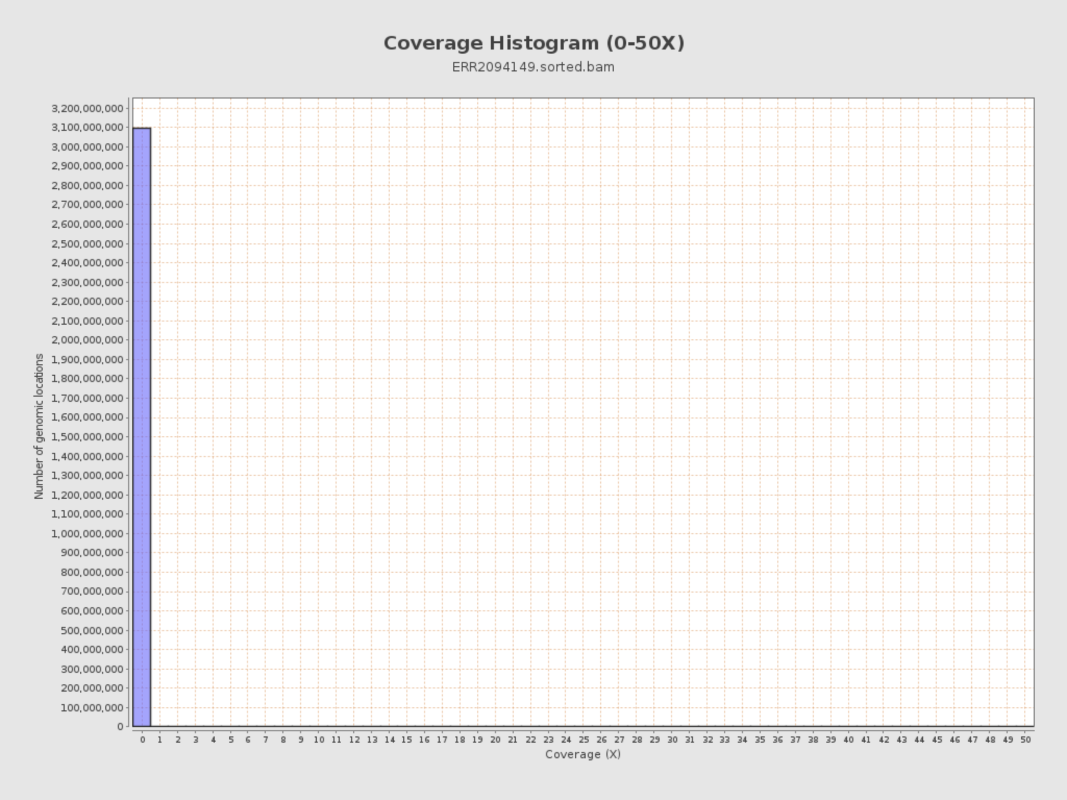
# 3. Results : Coverage across reference



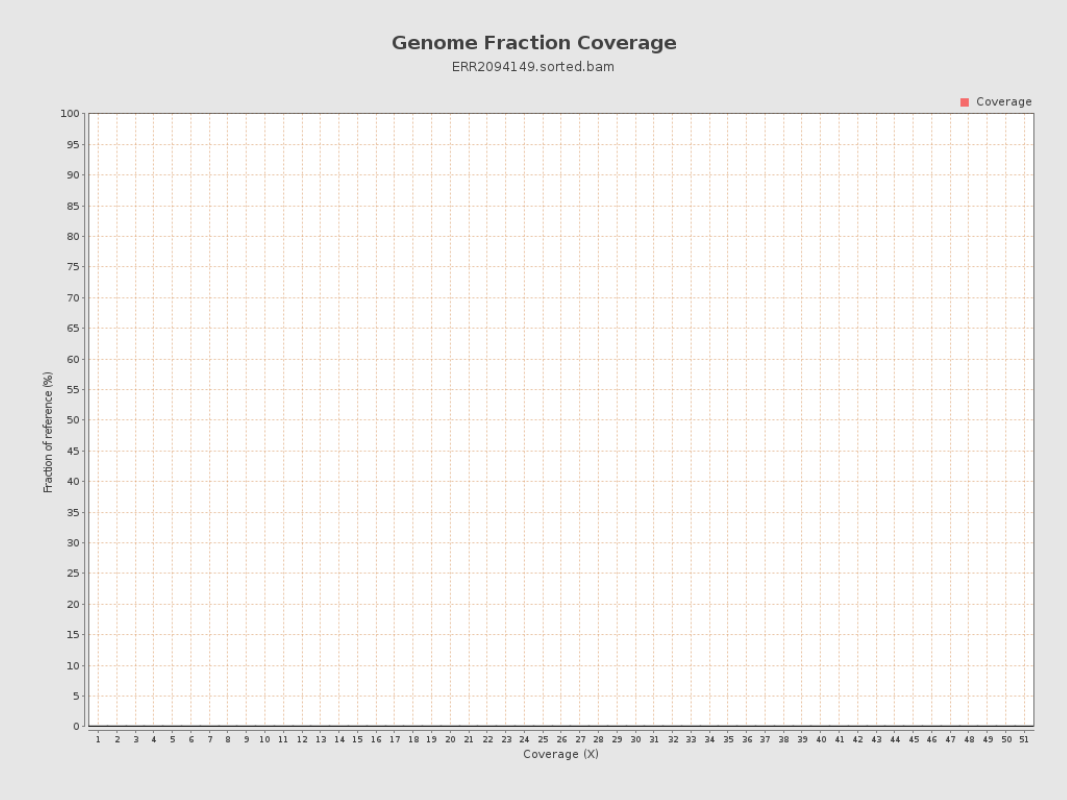
# 4. Results : Coverage Histogram



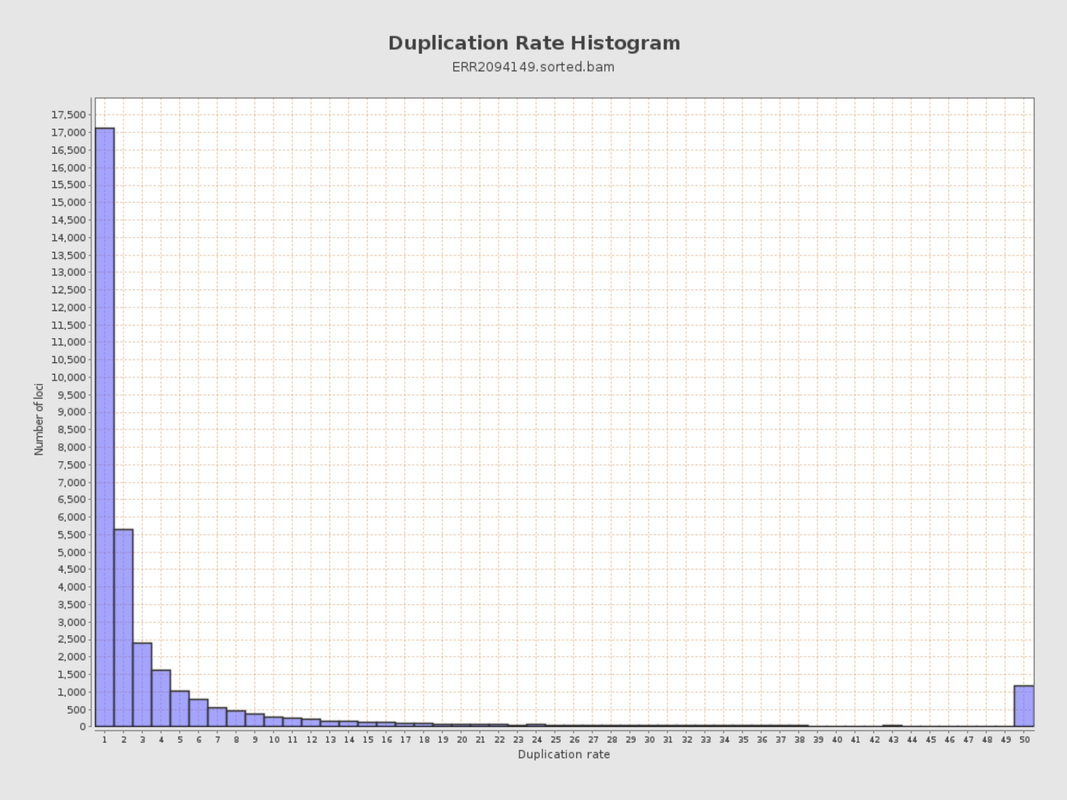
# 5. Results : Coverage Histogram (0-50X)



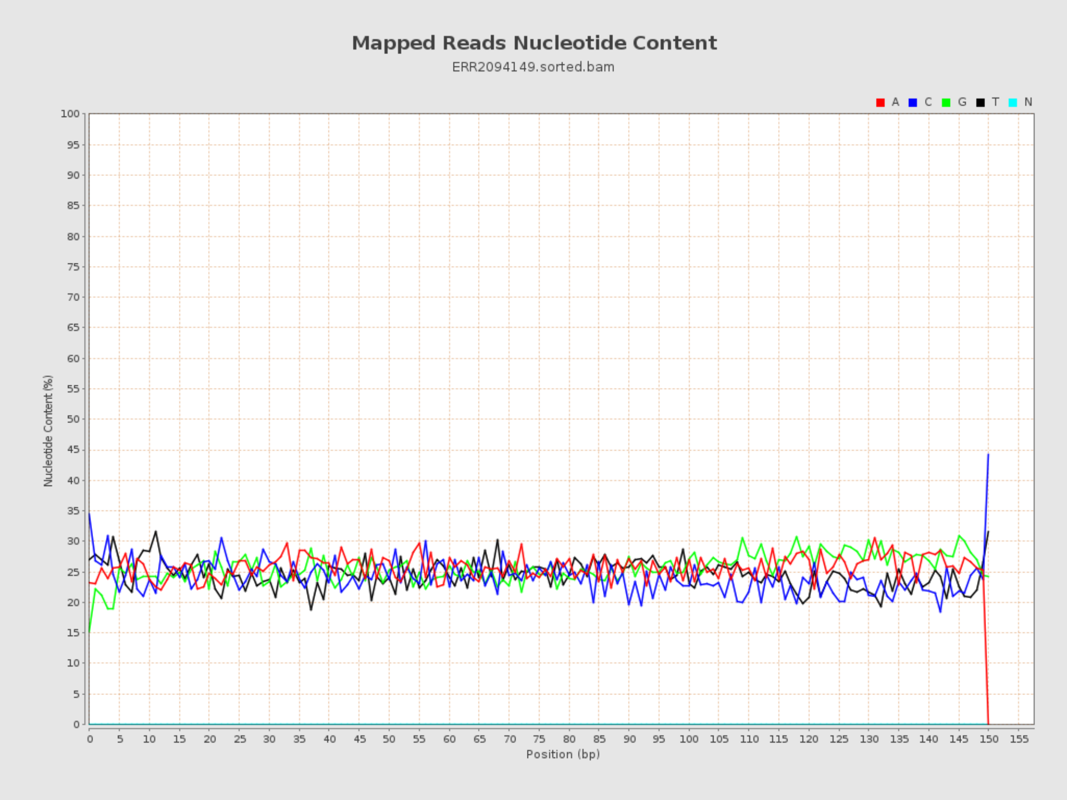
# 6. Results : Genome Fraction Coverage



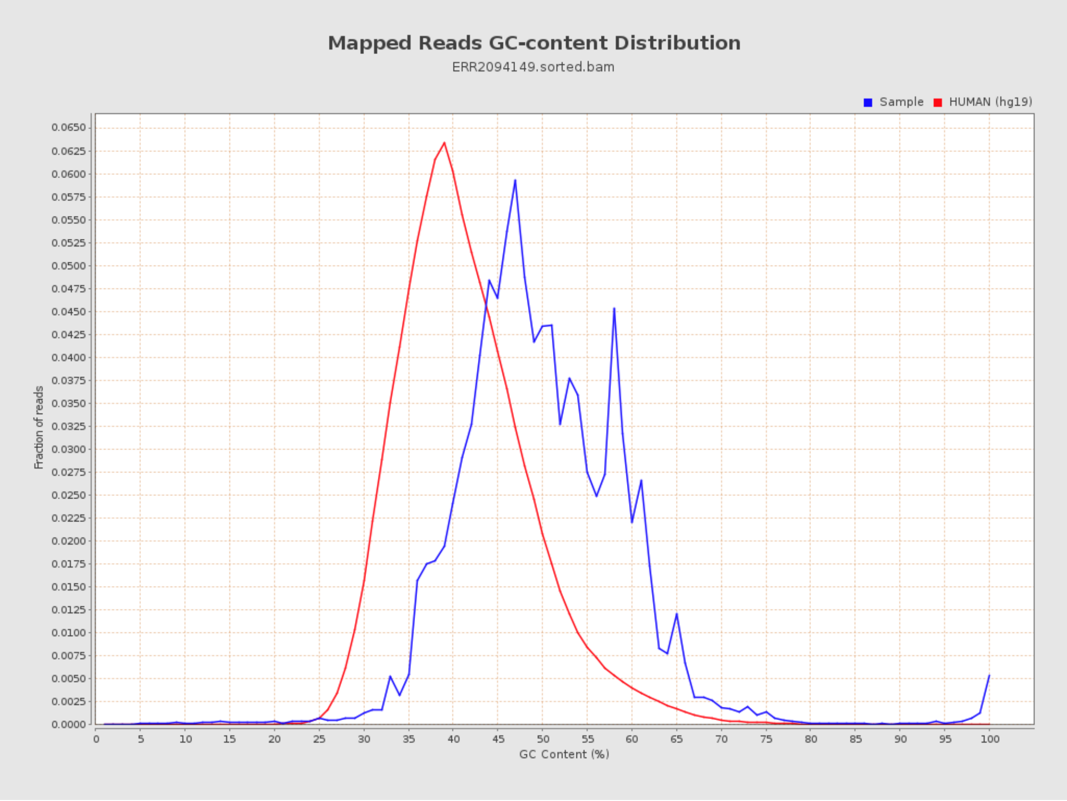
# 7. Results : Duplication Rate Histogram



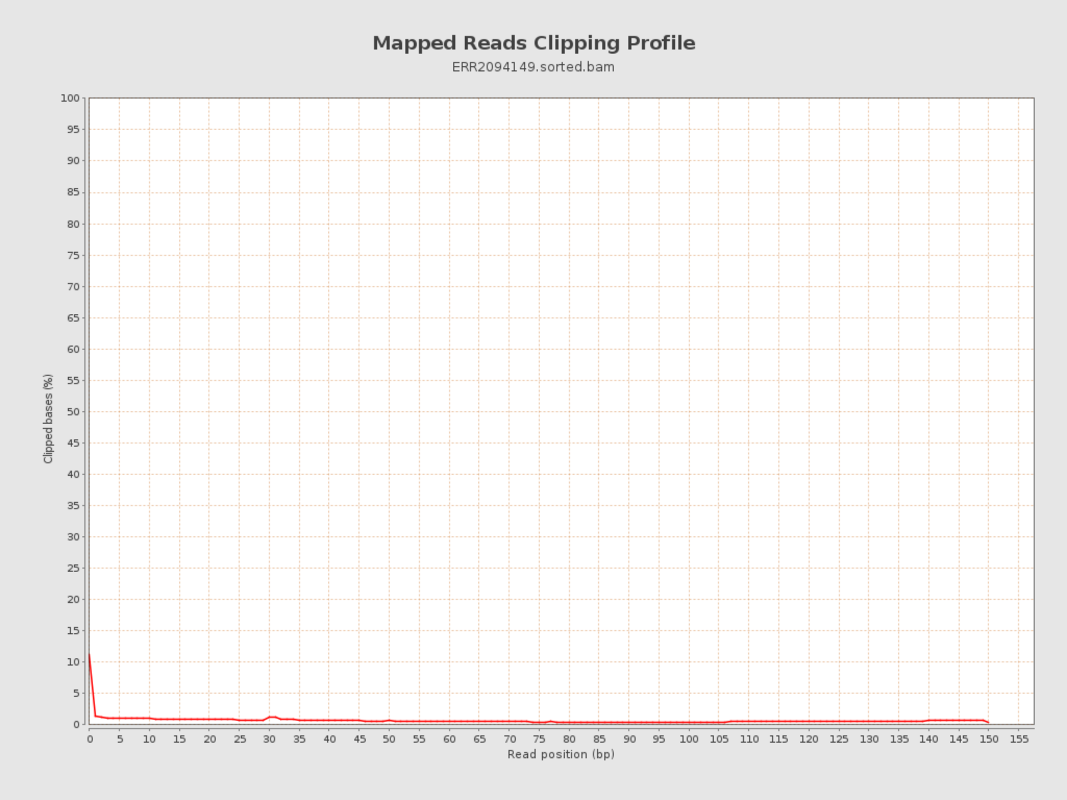
# 8. Results : Mapped Reads Nucleotide Content



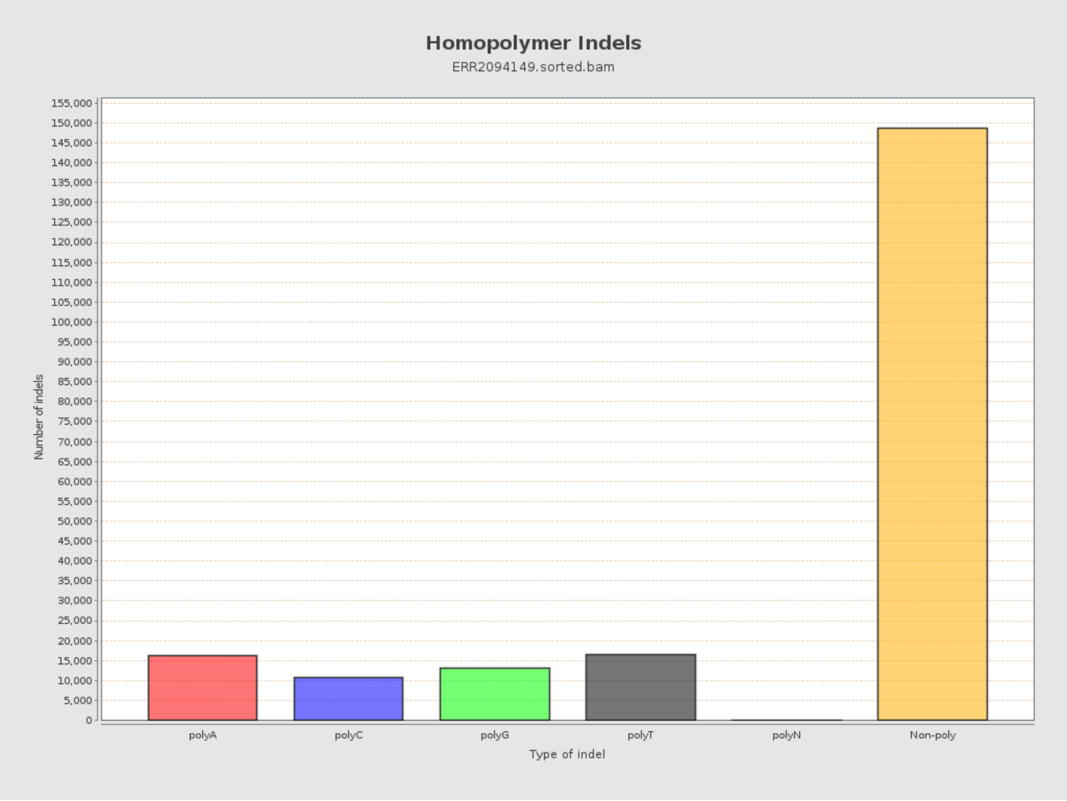
# 9. Results : Mapped Reads GC-content Distribution



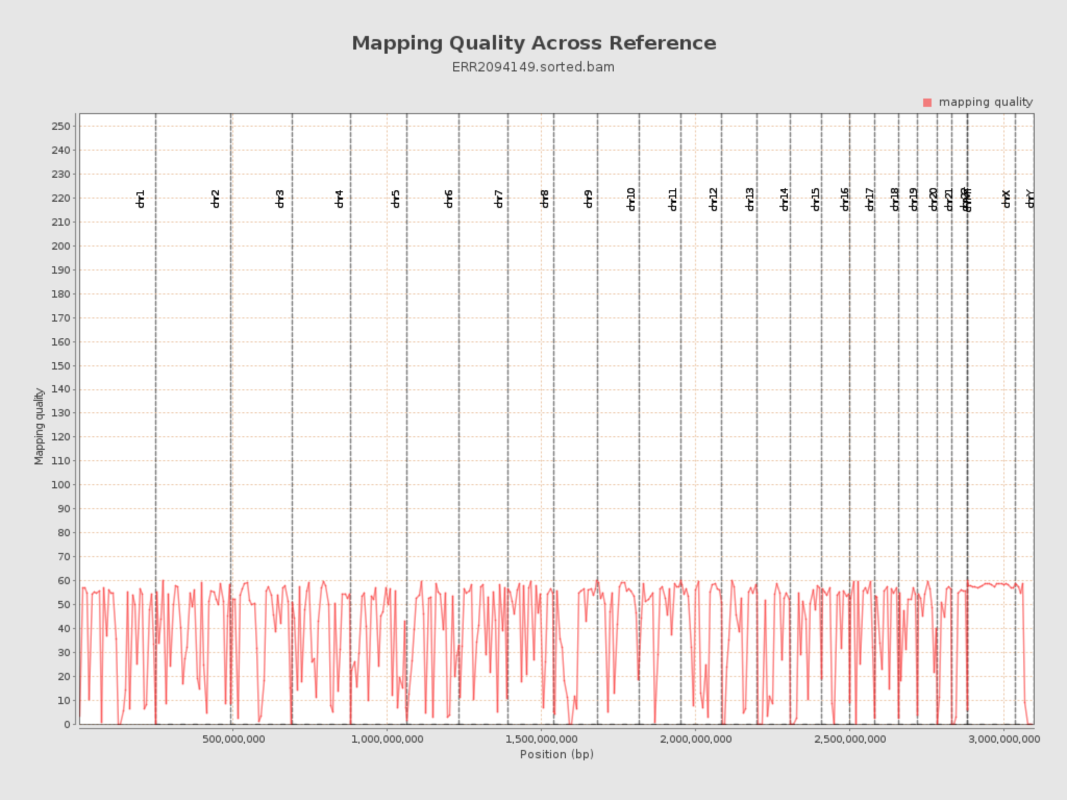
# 10. Results : Mapped Reads Clipping Profile



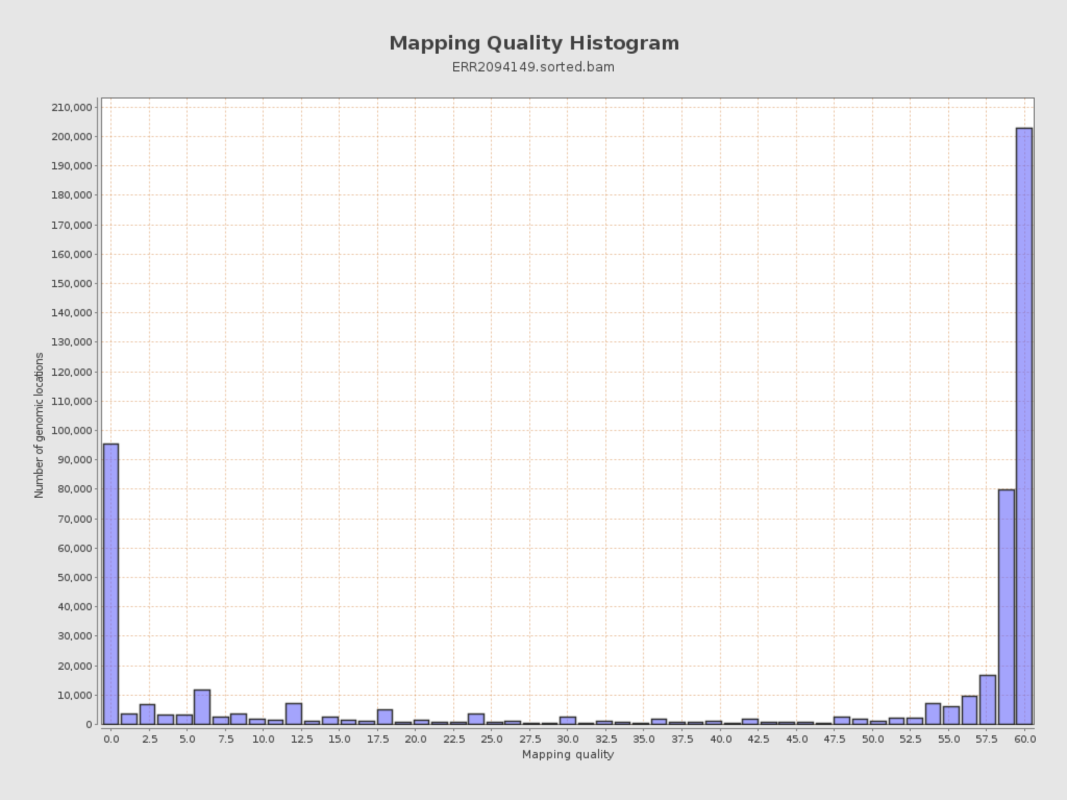
# 11. Results : Homopolymer Indels



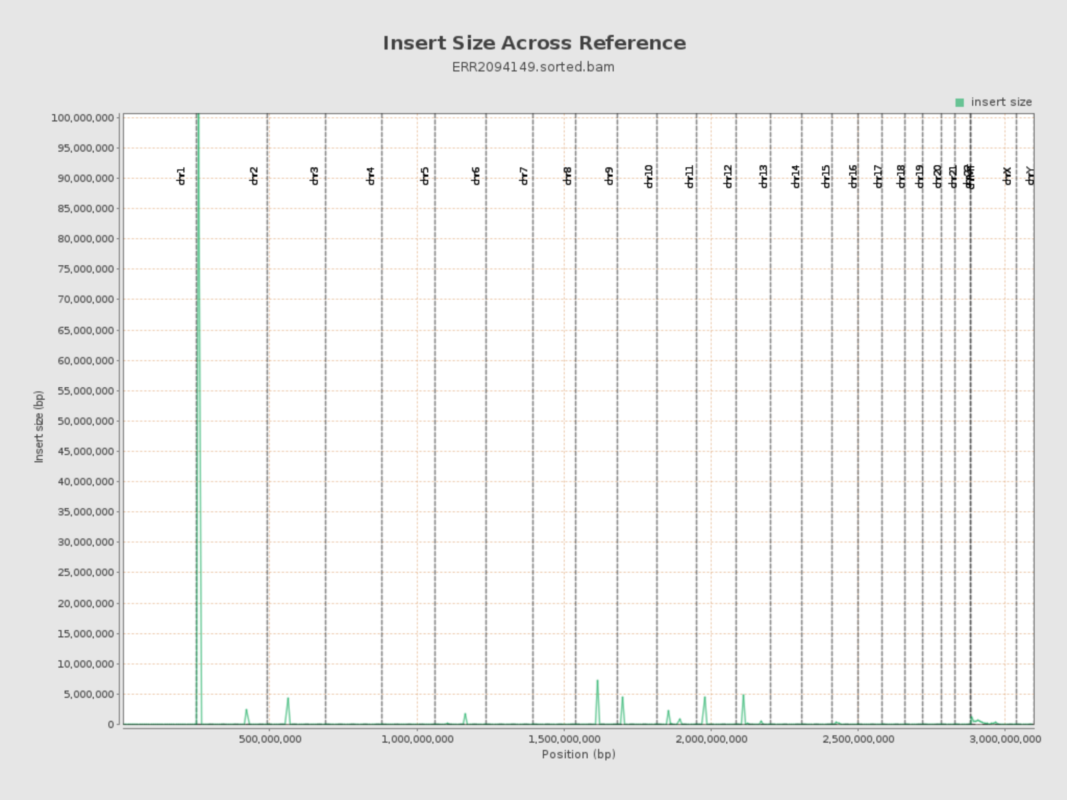
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram