# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/27 05:45:14*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094152.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_ERR2094152 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094152_1.fastq.gz ERR2094152_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Aug 27 05:45:13 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | ERR2094152.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 47,854 |
| Mapped reads | 5,293 / 11.06% |
| Unmapped reads | 42,561 / 88.94% |
| Mapped paired reads | 5,293 / 11.06% |
| Mapped reads, first in pair | 2,492 / 5.21% |
| Mapped reads,  second in pair | 2,801 / 5.85% |
| Mapped reads, both in pair | 4,802 / 10.03% |
| Mapped reads, singletons | 491 / 1.03% |
| Secondary alignments | 0 |
| Supplementary alignments | 65 / 0.14% |
| Read min/max/mean length | 30 / 151 / 72.59 |
| Duplicated reads (estimated) | 4,756 / 9.94% |
| Duplication rate | 28.07% |
| Clipped reads | 1,647 / 3.44% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 180,826 / 25.74% |
| Number/percentage of C's | 134,295 / 19.12% |
| Number/percentage of T's | 196,789 / 28.02% |
| Number/percentage of G's | 190,468 / 27.12% |
| Number/percentage of N's | 25 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 46.24% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0002 |
| Standard Deviation | 0.4689 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 6.98 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 87,474.09 |
| Standard Deviation | 2,547,003 |
| P25/Median/P75 | 177 / 233 / 237 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 2.39% |
| Mismatches | 16,152 |
| Insertions | 129 |
| Mapped reads with at least one insertion | 2% |
| Deletions | 856 |
| Mapped reads with at least one deletion | 14.94% |
| Homopolymer indels | 31.88% |

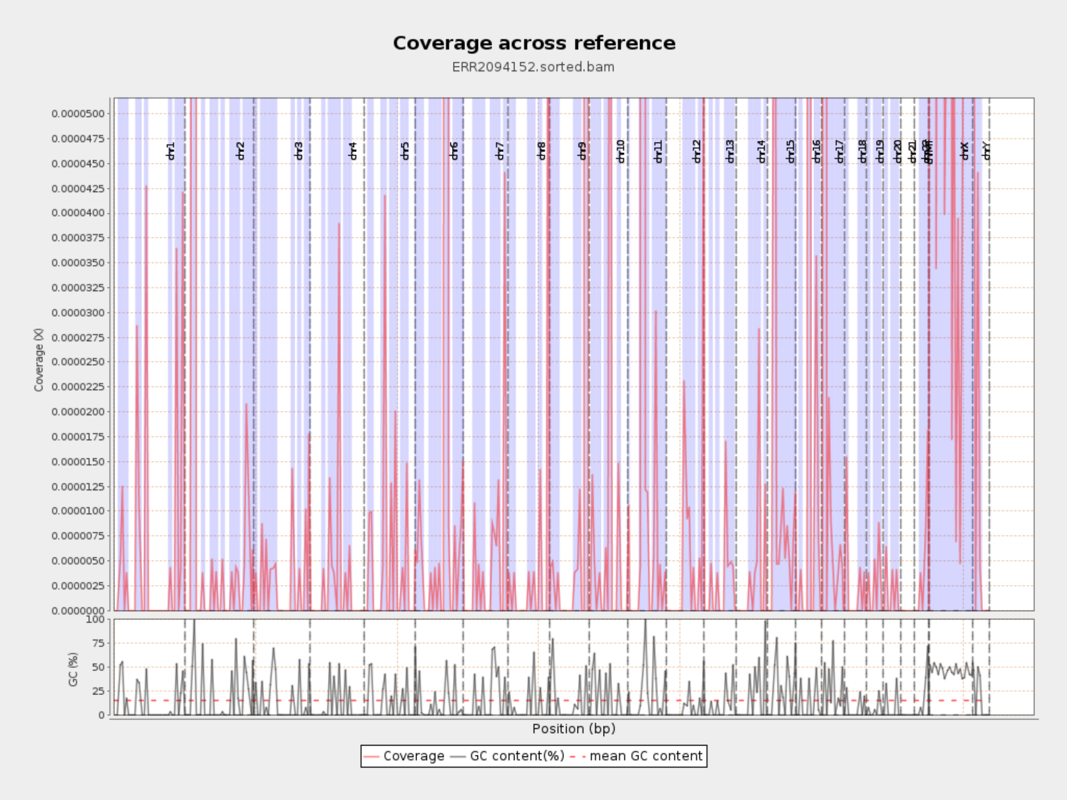
## 2.7. Chromosome stats

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

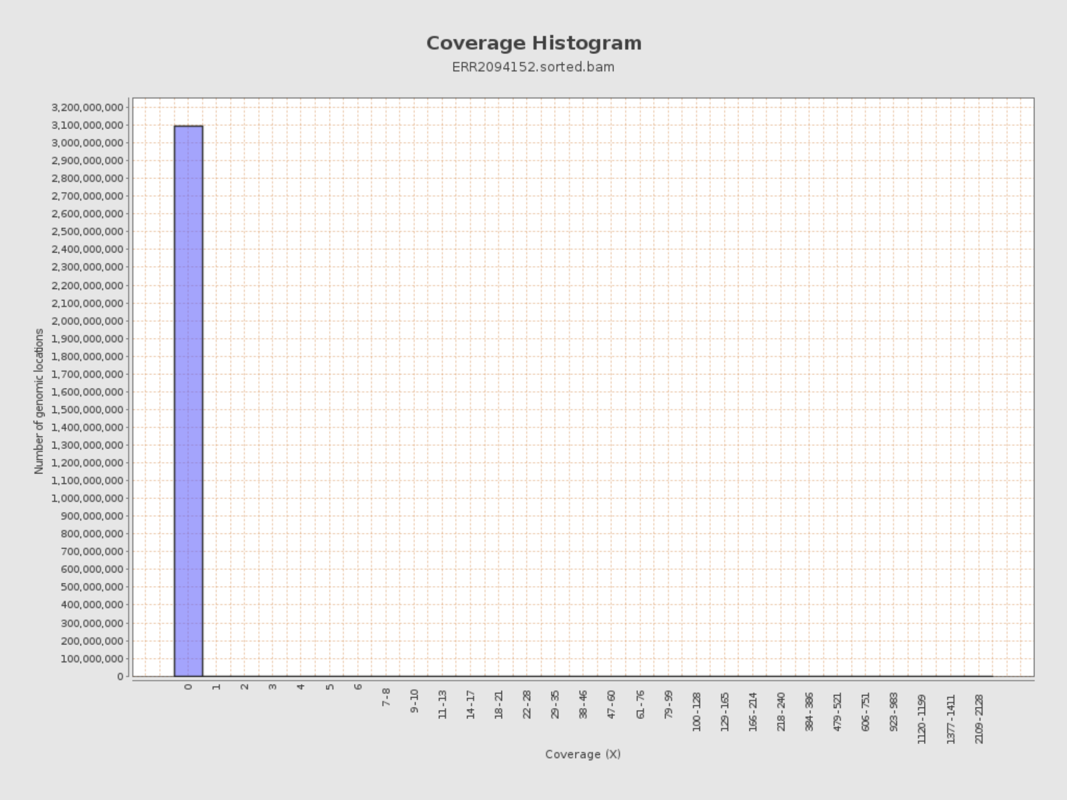
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 1472 | 0 | 0.0031 |
| chr2 | 243199373 | 39354 | 0.0002 | 0.1564 |
| chr3 | 198022430 | 508 | 0 | 0.0016 |
| chr4 | 191154276 | 585 | 0 | 0.002 |
| chr5 | 180915260 | 915 | 0 | 0.0039 |
| chr6 | 171115067 | 8377 | 0 | 0.048 |
| chr7 | 159138663 | 774 | 0 | 0.0027 |
| chr8 | 146364022 | 841 | 0 | 0.004 |
| chr9 | 141213431 | 30138 | 0.0002 | 0.1995 |
| chr10 | 135534747 | 1171 | 0 | 0.0049 |
| chr11 | 135006516 | 13347 | 0.0001 | 0.0864 |
| chr12 | 133851895 | 586 | 0 | 0.0024 |
| chr13 | 115169878 | 307 | 0 | 0.0017 |
| chr14 | 107349540 | 418 | 0 | 0.0033 |
| chr15 | 102531392 | 1260 | 0 | 0.0063 |
| chr16 | 90354753 | 2888 | 0 | 0.0193 |
| chr17 | 81195210 | 19299 | 0.0002 | 0.1712 |
| chr18 | 78077248 | 185 | 0 | 0.0018 |
| chr19 | 59128983 | 139 | 0 | 0.0015 |
| chr20 | 63025520 | 114 | 0 | 0.0013 |
| chr21 | 48129895 | 0 | 0 | 0 |
| chr22 | 51304566 | 235 | 0 | 0.0021 |
| chrMT | 16571 | 390970 | 23.5936 | 178.158 |
| chrX | 155270560 | 190583 | 0.0012 | 0.9151 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 785 | 0 | 0.0056 |

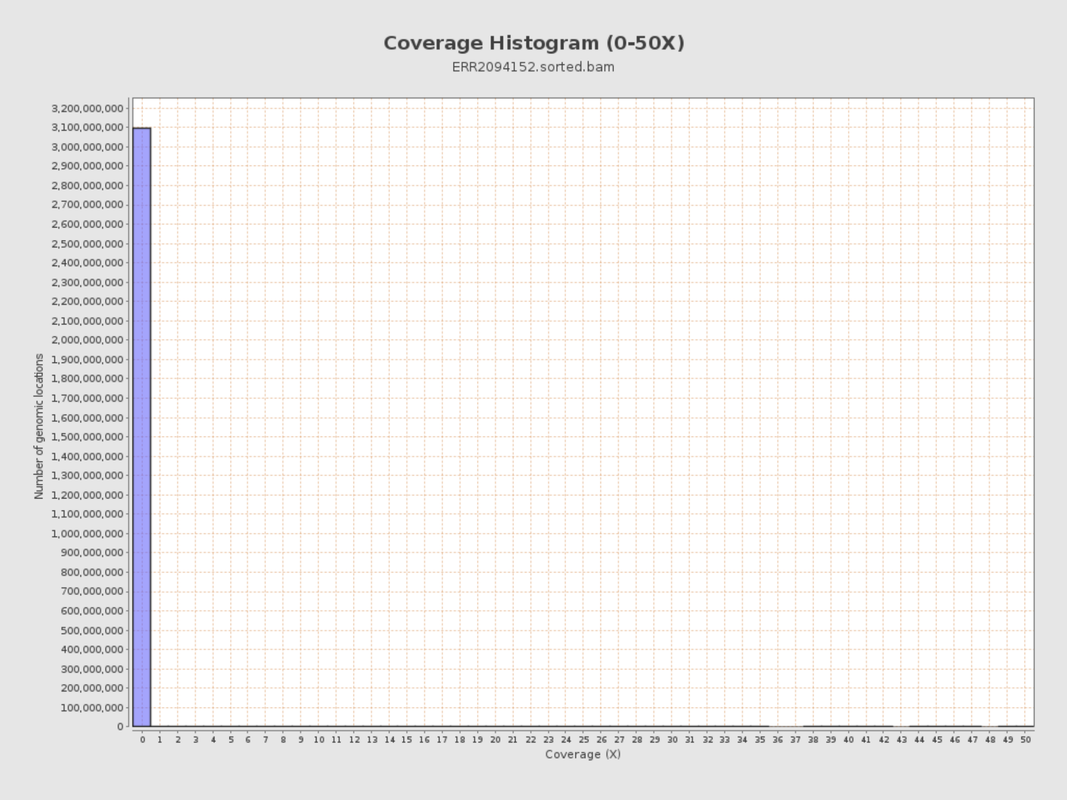
# 3. Results : Coverage across reference



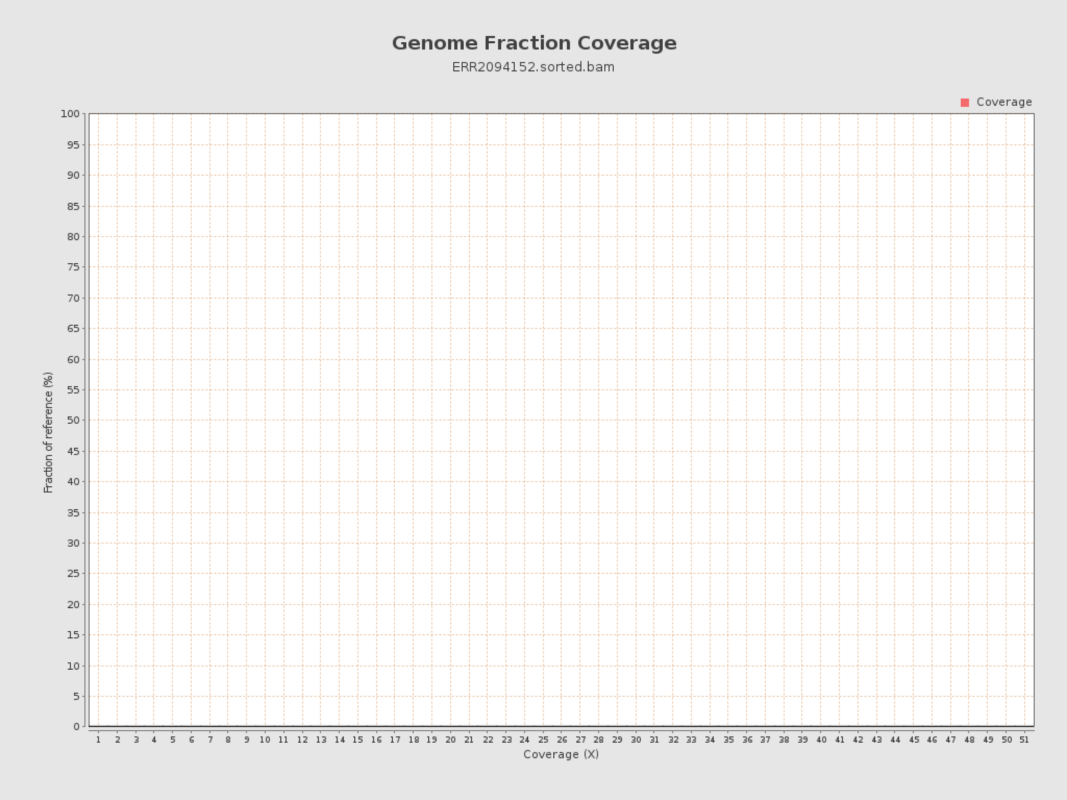
# 4. Results : Coverage Histogram



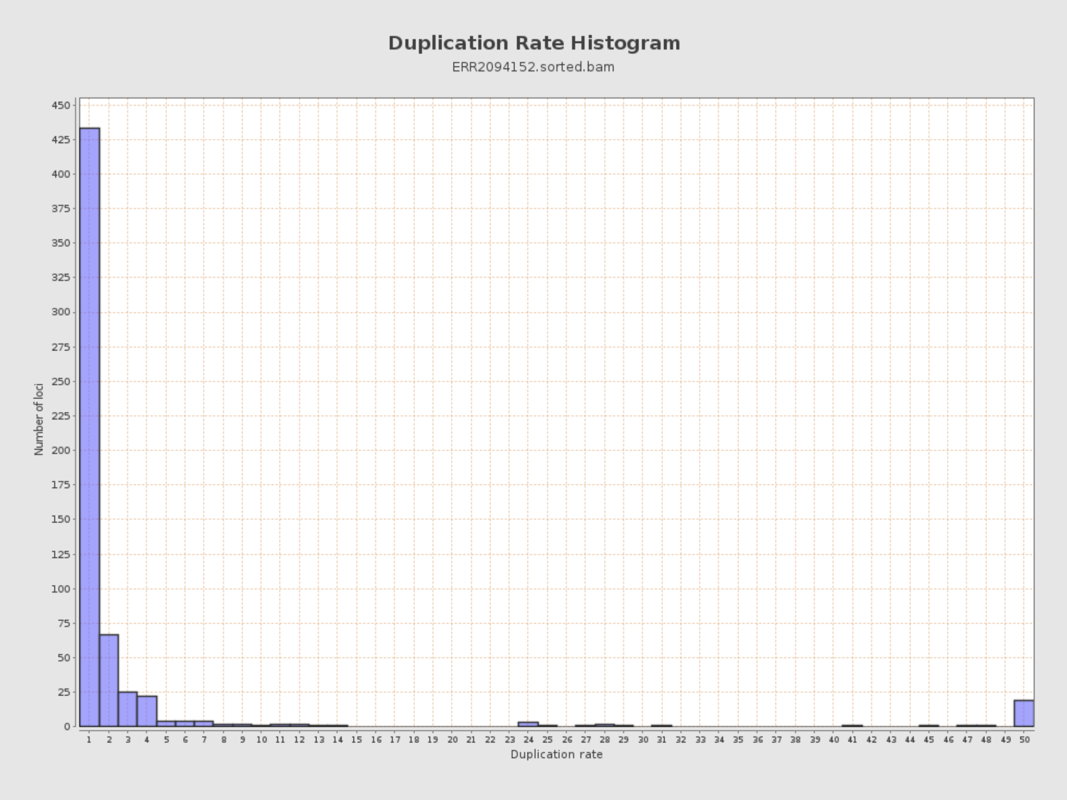
# 5. Results : Coverage Histogram (0-50X)



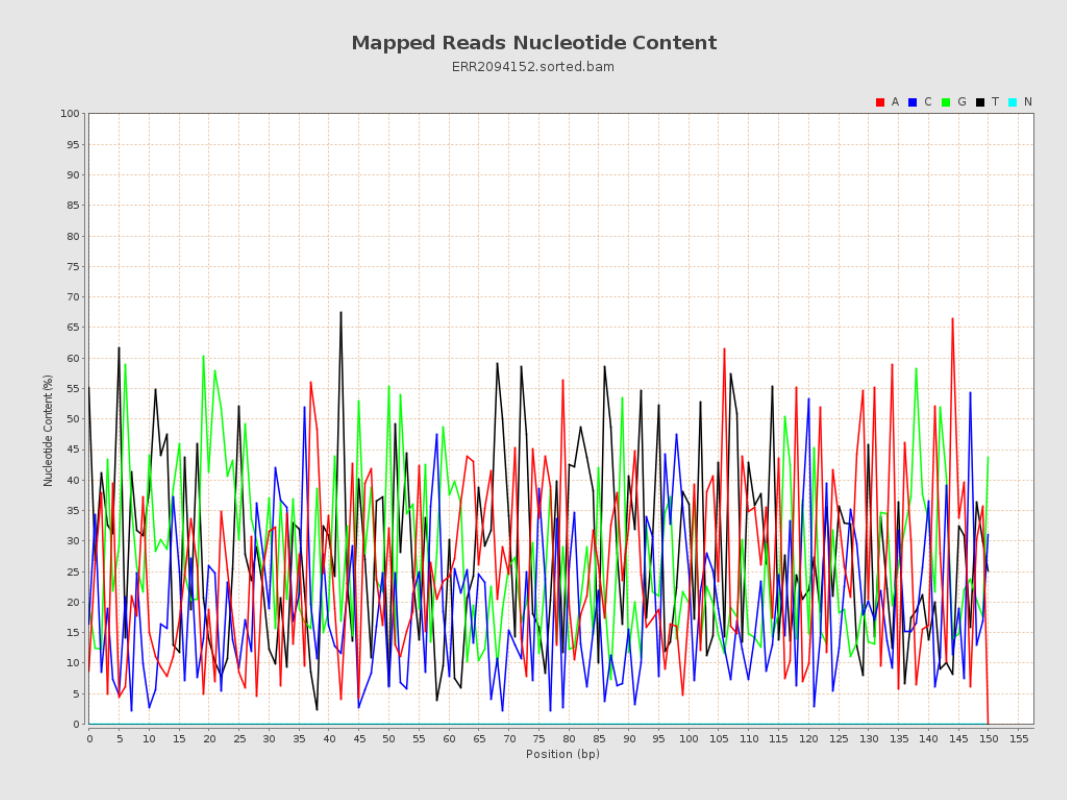
# 6. Results : Genome Fraction Coverage



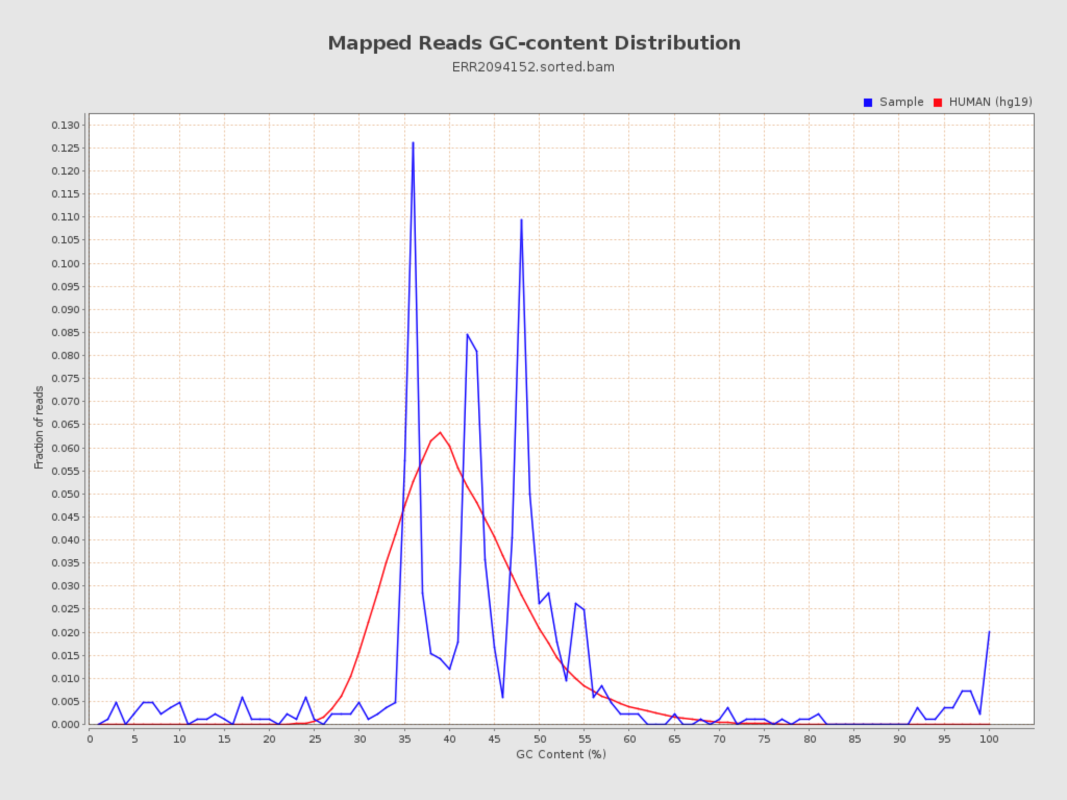
# 7. Results : Duplication Rate Histogram



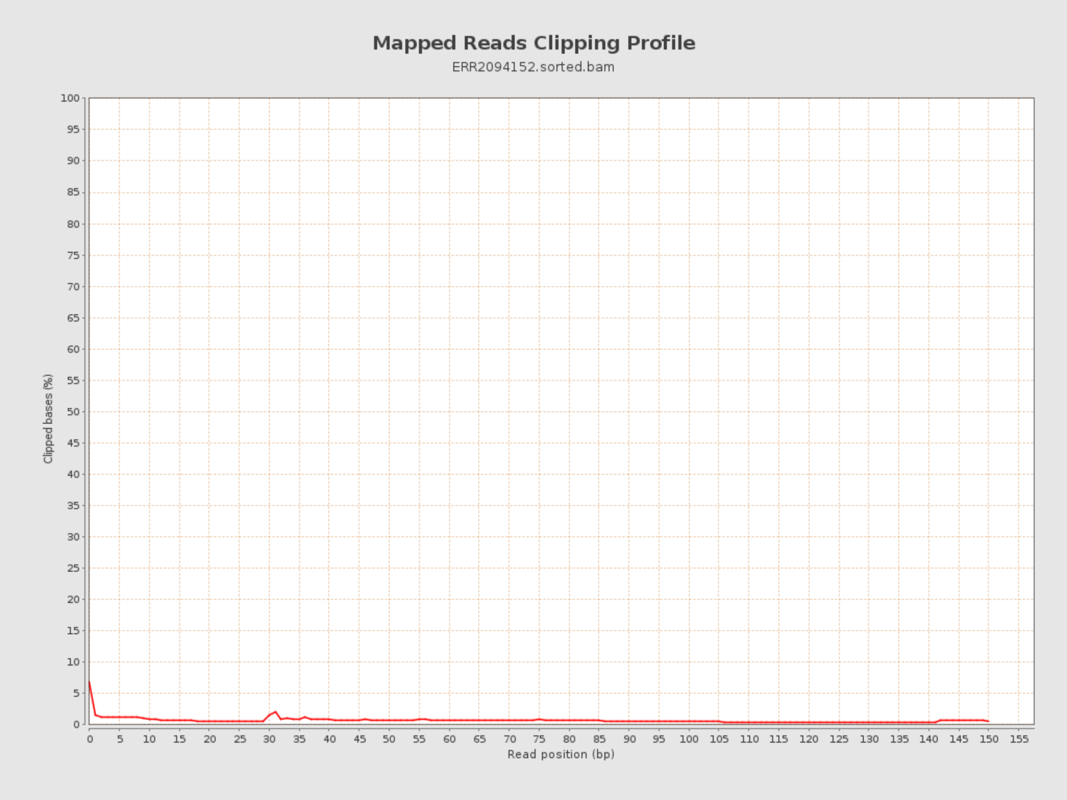
# 8. Results : Mapped Reads Nucleotide Content



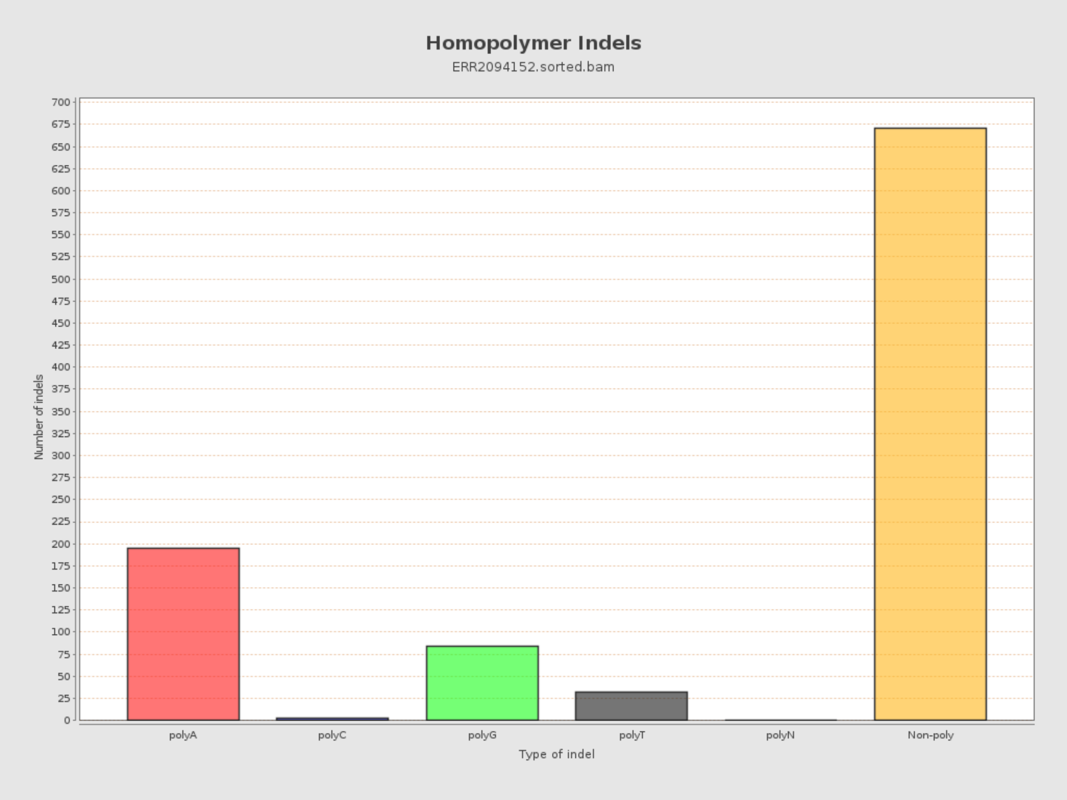
# 9. Results : Mapped Reads GC-content Distribution



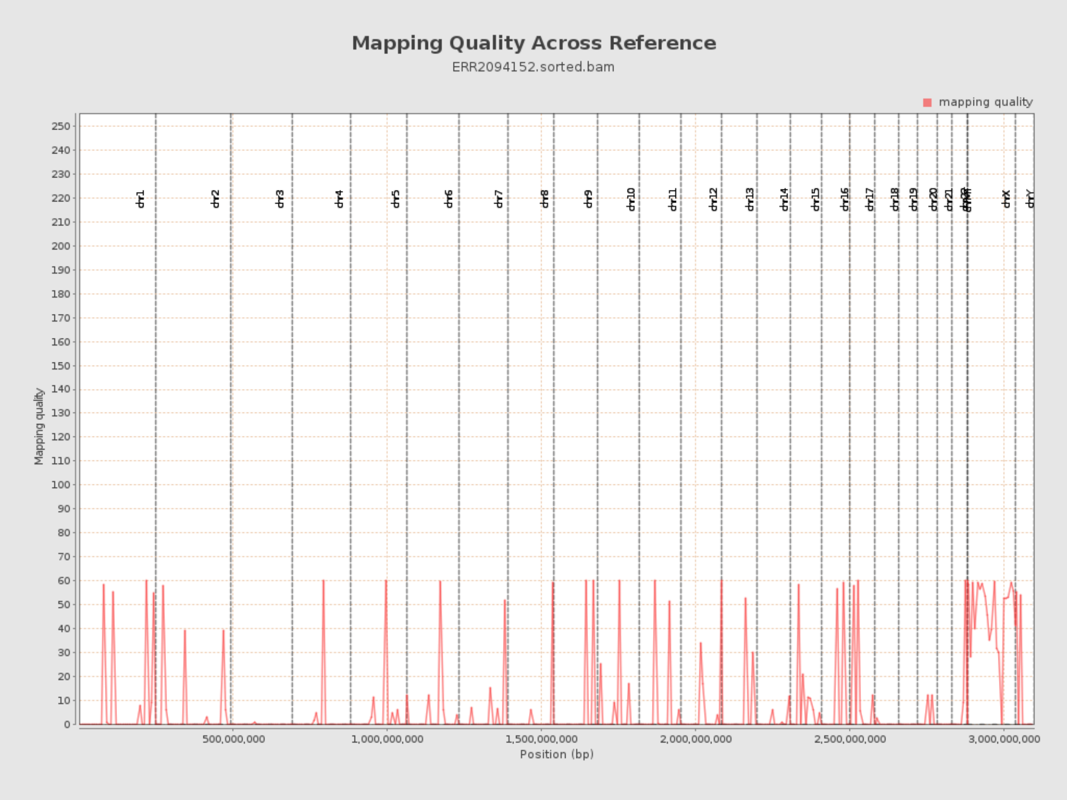
# 10. Results : Mapped Reads Clipping Profile



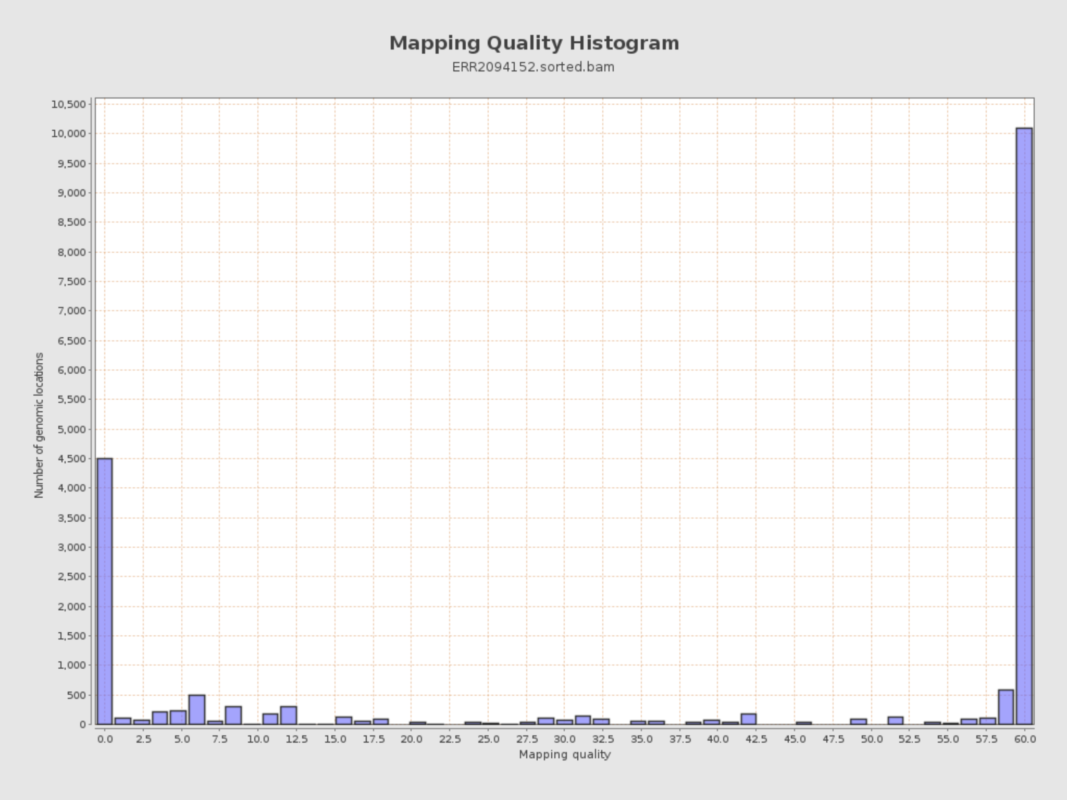
# 11. Results : Homopolymer Indels



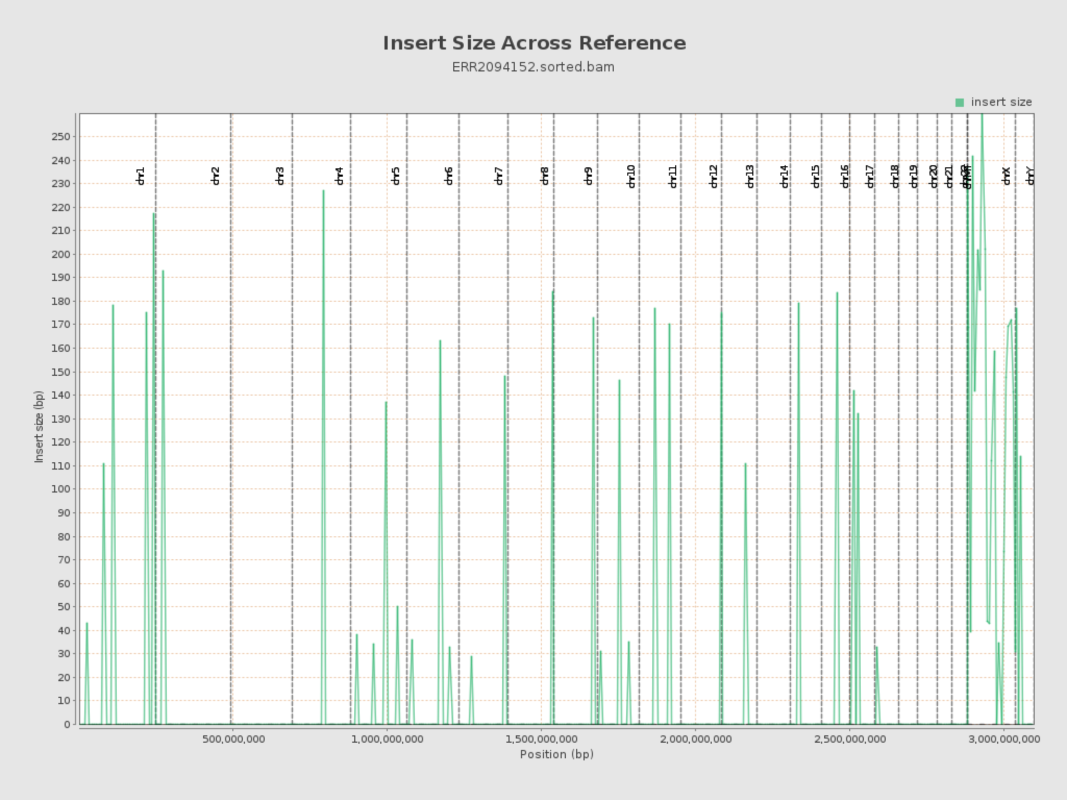
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram