# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/27 01:17:12*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR2094105.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_ERR2094105 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2094105_1.fastq.gz ERR2094105_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Aug 27 01:17:11 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | ERR2094105.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 402,328 |
| Mapped reads | 383,560 / 95.34% |
| Unmapped reads | 18,768 / 4.66% |
| Mapped paired reads | 383,560 / 95.34% |
| Mapped reads, first in pair | 192,563 / 47.86% |
| Mapped reads, second in pair | 190,997 / 47.47% |
| Mapped reads, both in pair | 380,946 / 94.69% |
| Mapped reads, singletons | 2,614 / 0.65% |
| Secondary alignments | 0 |
| Supplementary alignments | 13,058 / 3.25% |
| Read min/max/mean length | 30 / 151 / 144.24 |
| Duplicated reads (estimated) | 380,365 / 94.54% |
| Duplication rate | 47.02% |
| Clipped reads | 167,973 / 41.75% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 14,483,413 / 28.37% |
| Number/percentage of C's | 11,004,891 / 21.56% |
| Number/percentage of T's | 14,313,727 / 28.04% |
| Number/percentage of G's | 11,243,974 / 22.03% |
| Number/percentage of N's | 690 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 43.59% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0167 |
| Standard Deviation | 11.1783 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 31.88 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 200,864.23 |
| Standard Deviation | 4,357,942.19 |
| P25/Median/P75 | 154 / 194 / 236 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 3.43% |
| Mismatches | 1,496,309 |
| Insertions | 60,953 |
| Mapped reads with at least one insertion | 15.68% |
| Deletions | 116,859 |
| Mapped reads with at least one deletion | 28.02% |
| Homopolymer indels | 28.78% |

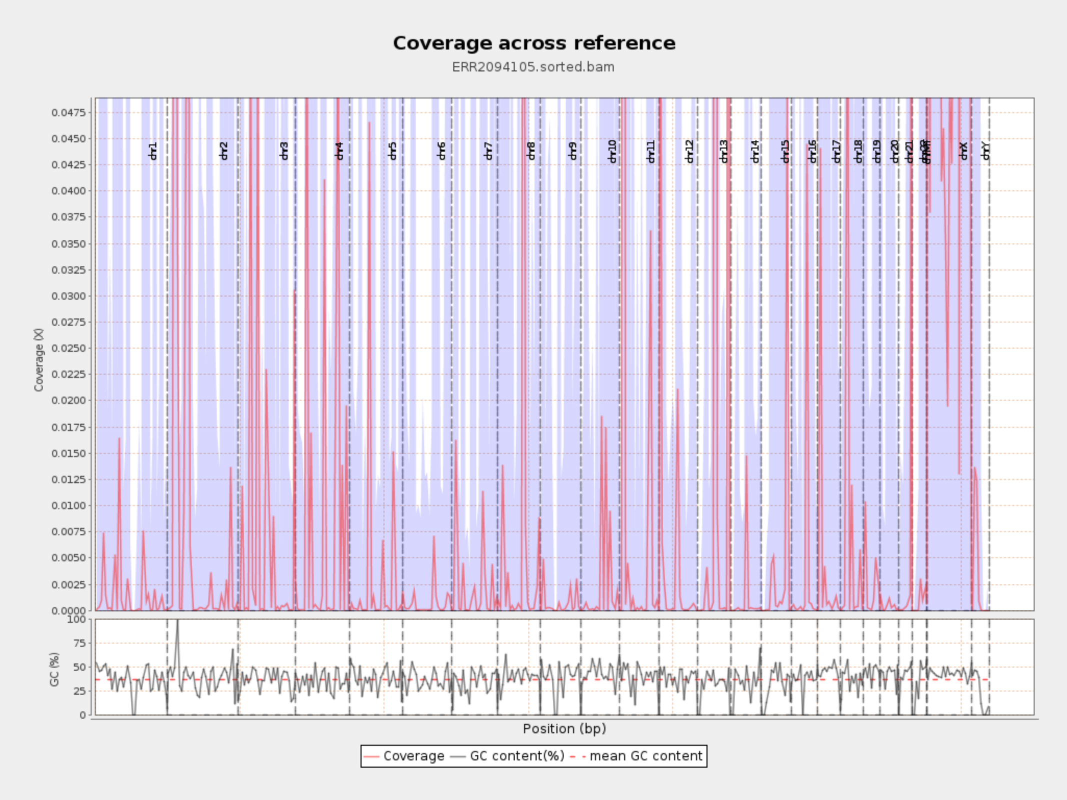
## 2.7. Chromosome stats

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

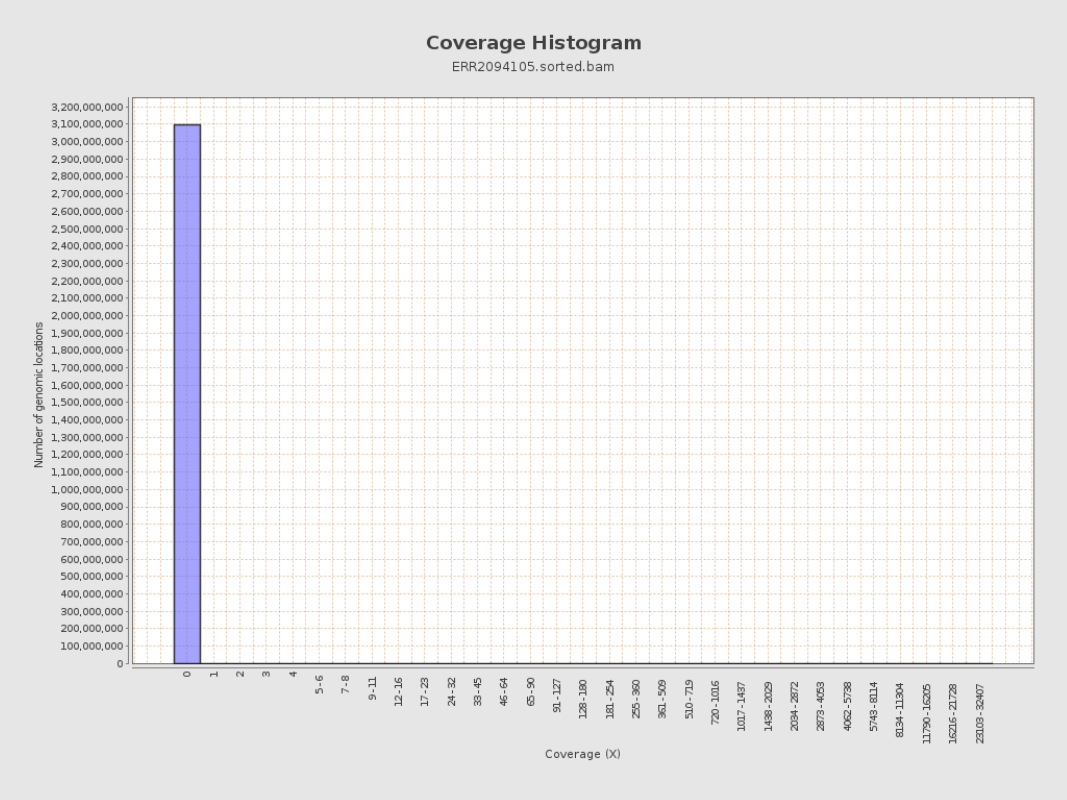
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 394998 | 0.0016 | 0.865 |
| chr2 | 243199373 | 2758033 | 0.0113 | 4.9182 |
| chr3 | 198022430 | 1426014 | 0.0072 | 3.5134 |
| chr4 | 191154276 | 1919942 | 0.01 | 4.2222 |
| chr5 | 180915260 | 575182 | 0.0032 | 1.9908 |
| chr6 | 171115067 | 136079 | 0.0008 | 0.4281 |
| chr7 | 159138663 | 357289 | 0.0022 | 1.0234 |
| chr8 | 146364022 | 1157948 | 0.0079 | 3.9678 |
| chr9 | 141213431 | 108184 | 0.0008 | 0.2767 |
| chr10 | 135534747 | 390935 | 0.0029 | 1.3067 |
| chr11 | 135006516 | 2758155 | 0.0204 | 13.2834 |
| chr12 | 133851895 | 842767 | 0.0063 | 4.0234 |
| chr13 | 115169878 | 3896182 | 0.0338 | 20.5708 |
| chr14 | 107349540 | 128761 | 0.0012 | 0.8316 |
| chr15 | 102531392 | 491007 | 0.0048 | 2.7842 |
| chr16 | 90354753 | 371379 | 0.0041 | 2.9099 |
| chr17 | 81195210 | 407897 | 0.005 | 3.1375 |
| chr18 | 78077248 | 653802 | 0.0084 | 5.0158 |
| chr19 | 59128983 | 150941 | 0.0026 | 0.8358 |
| chr20 | 63025520 | 27590 | 0.0004 | 0.1066 |
| chr21 | 48129895 | 338274 | 0.007 | 3.6146 |
| chr22 | 51304566 | 50410 | 0.001 | 0.2584 |
| chrMT | 16571 | 13784845 | 831.8656 | 3,585.3747 |
| chrX | 155270560 | 18435938 | 0.1187 | 20.7829 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 209906 | 0.0035 | 1.348 |

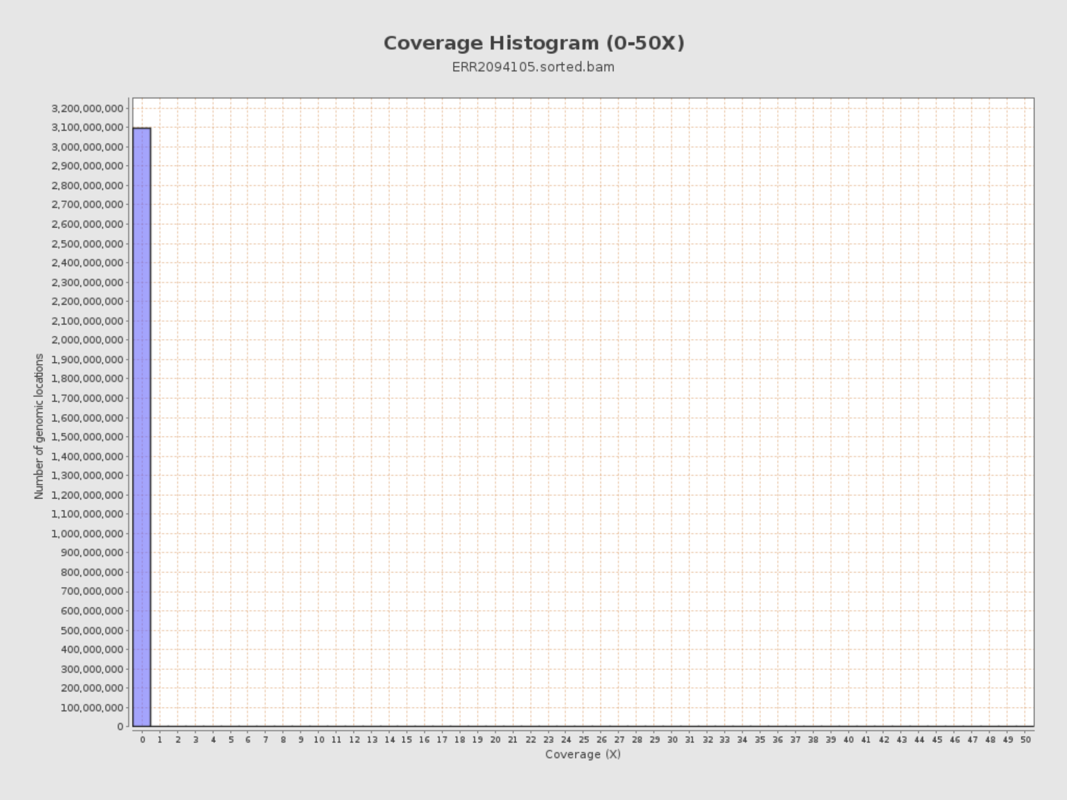
# 3. Results : Coverage across reference



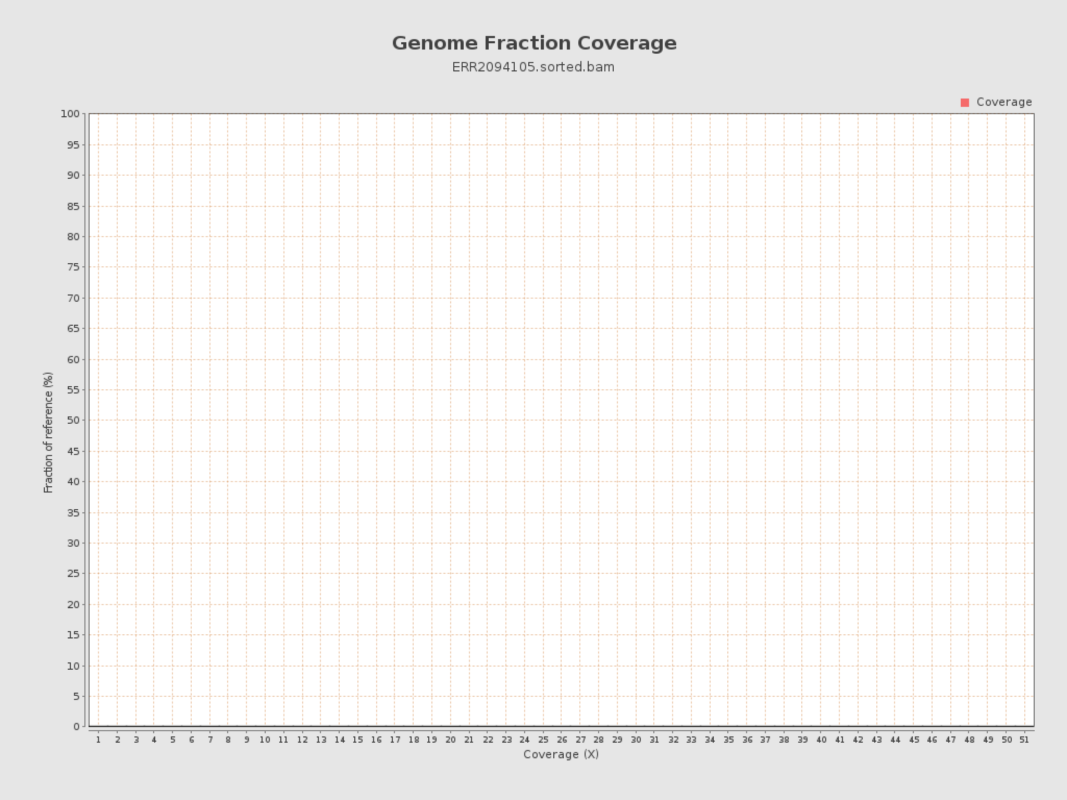
# 4. Results : Coverage Histogram



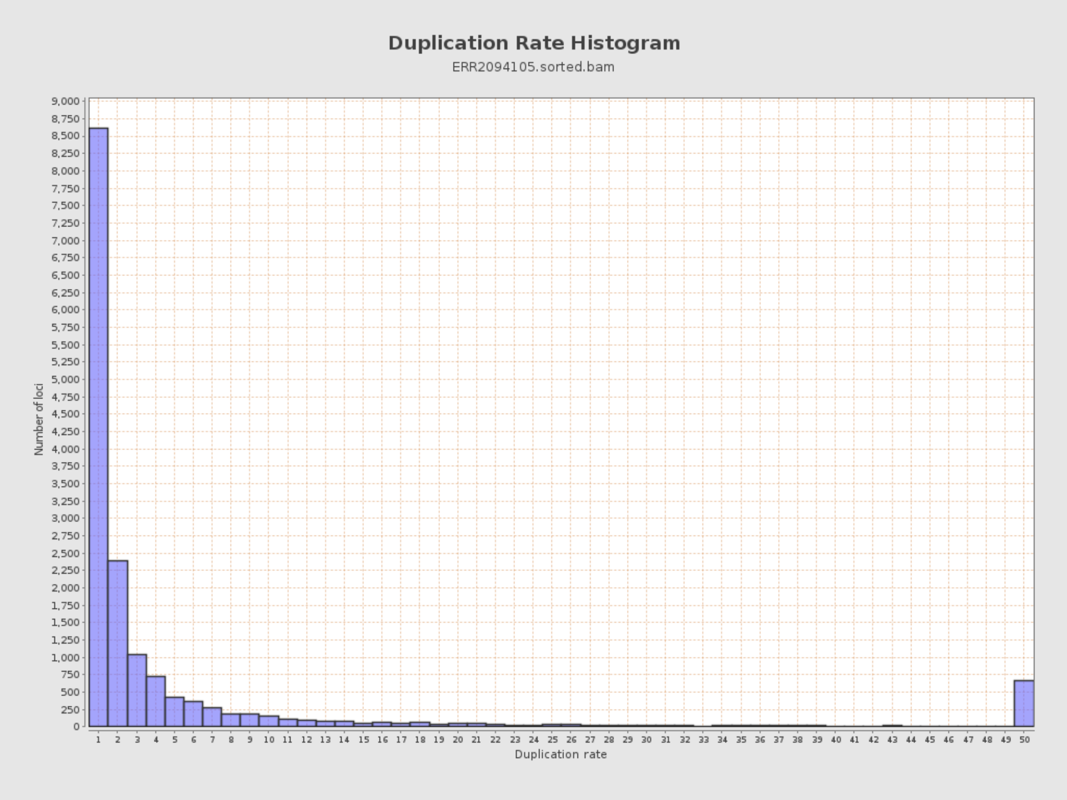
# 5. Results : Coverage Histogram (0-50X)



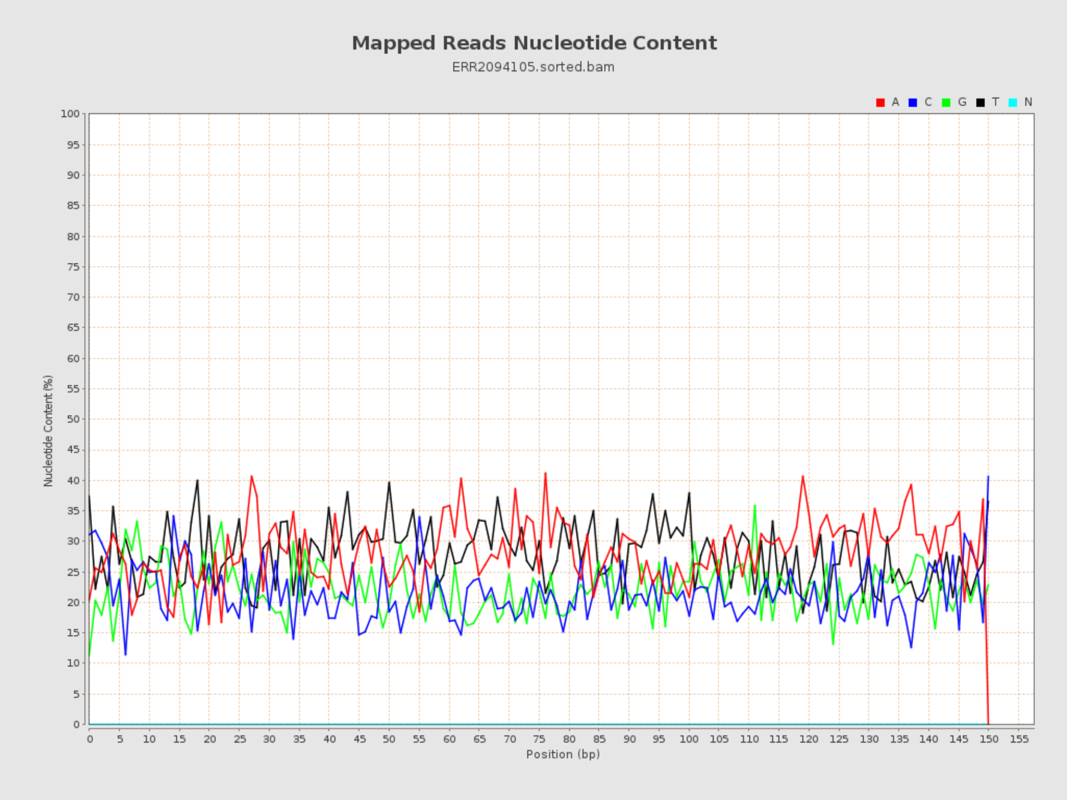
# 6. Results : Genome Fraction Coverage



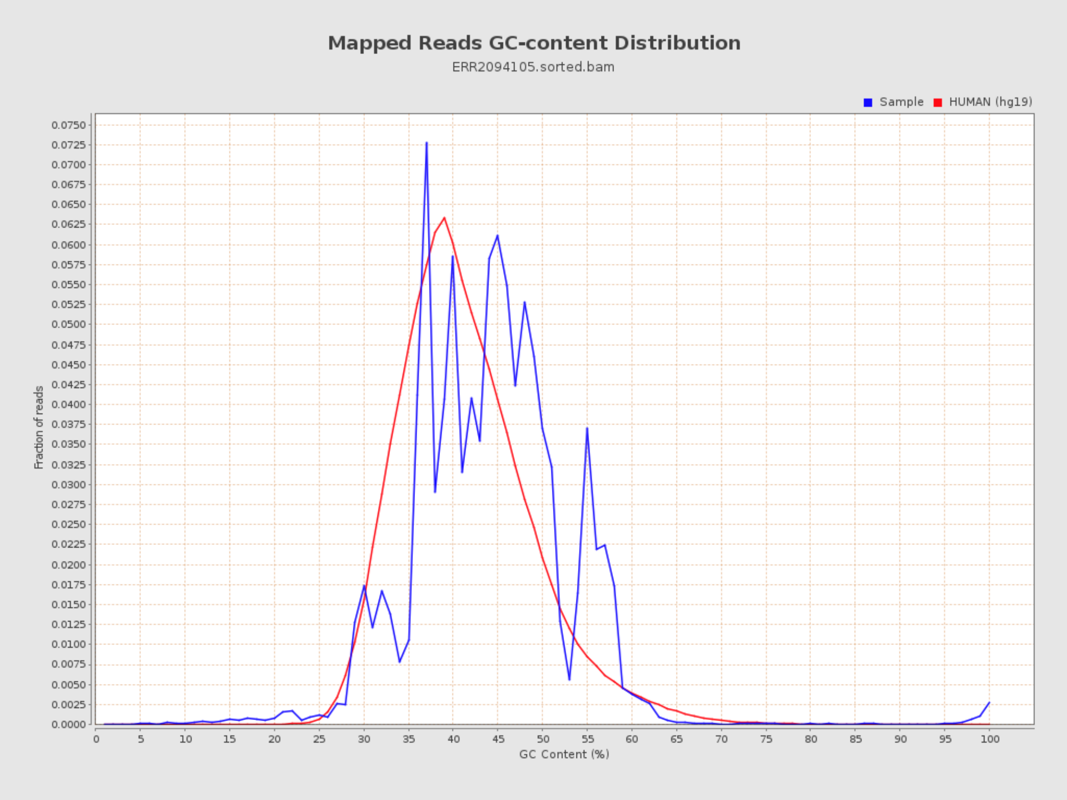
# 7. Results : Duplication Rate Histogram



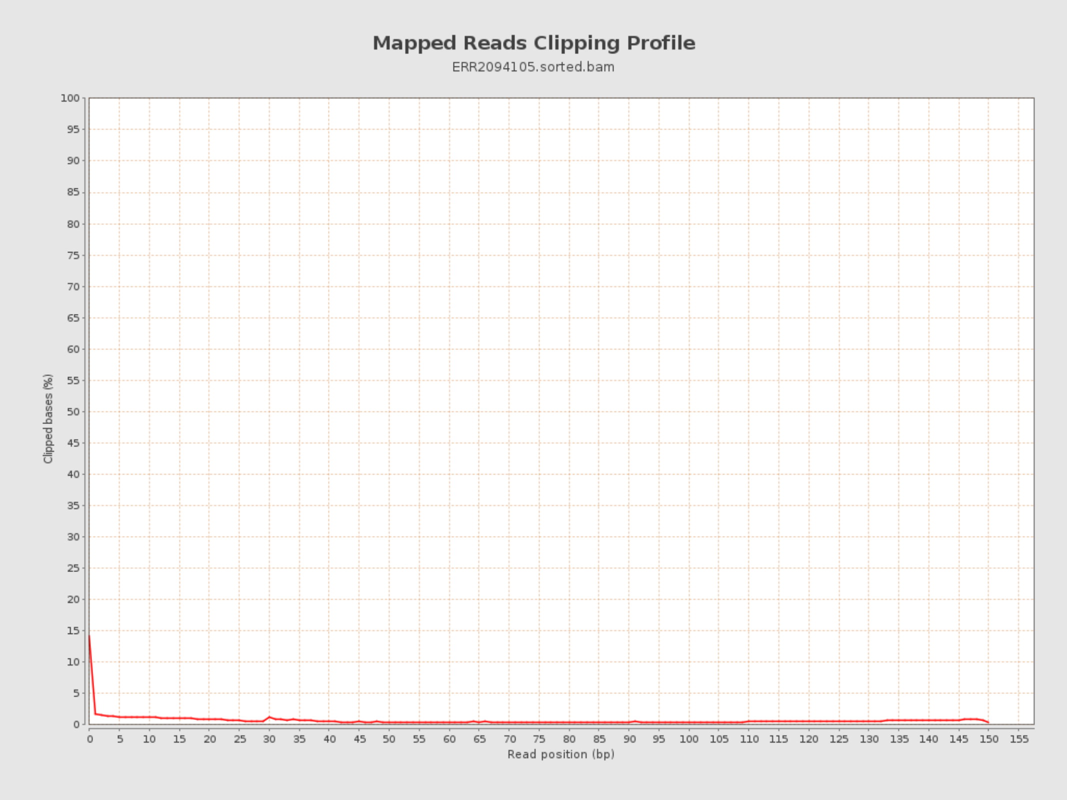
# 8. Results : Mapped Reads Nucleotide Content



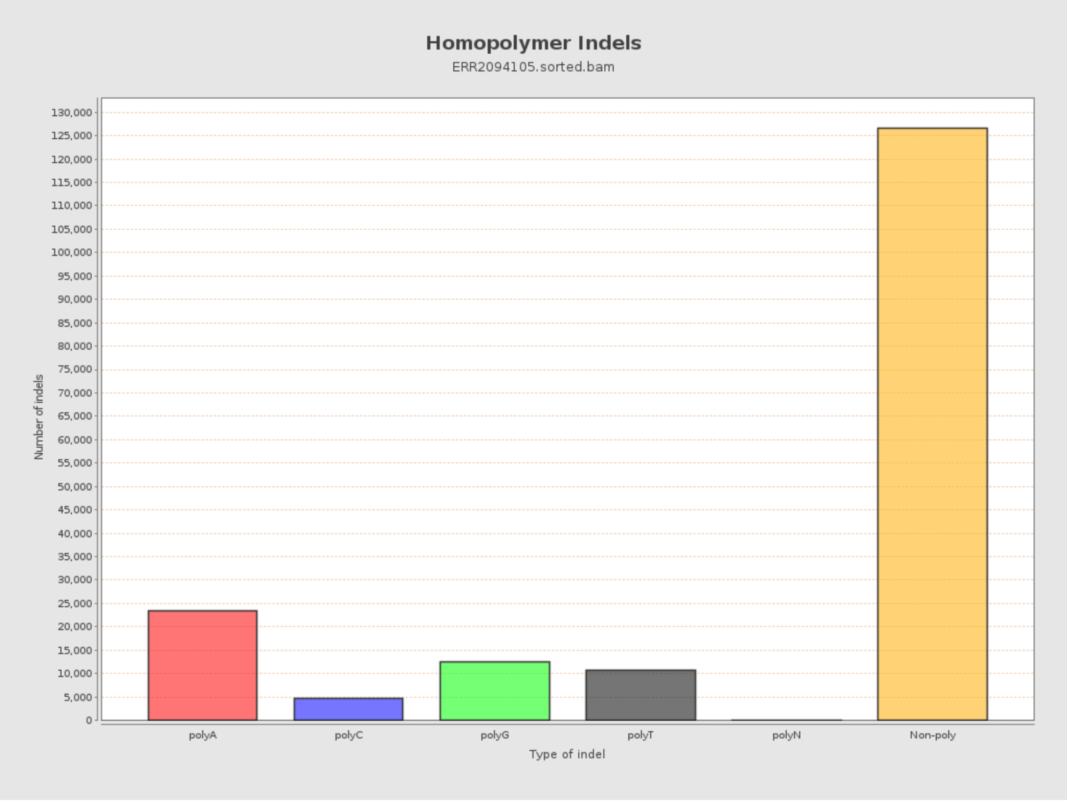
# 9. Results : Mapped Reads GC-content Distribution



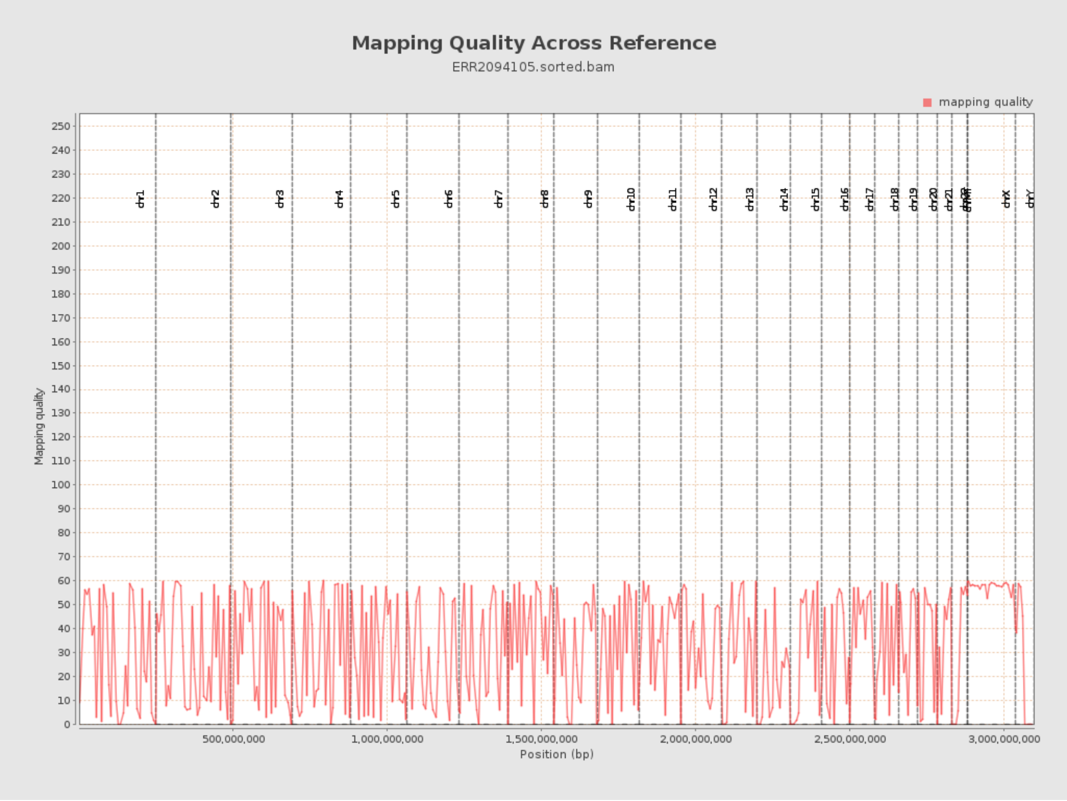
# 10. Results : Mapped Reads Clipping Profile



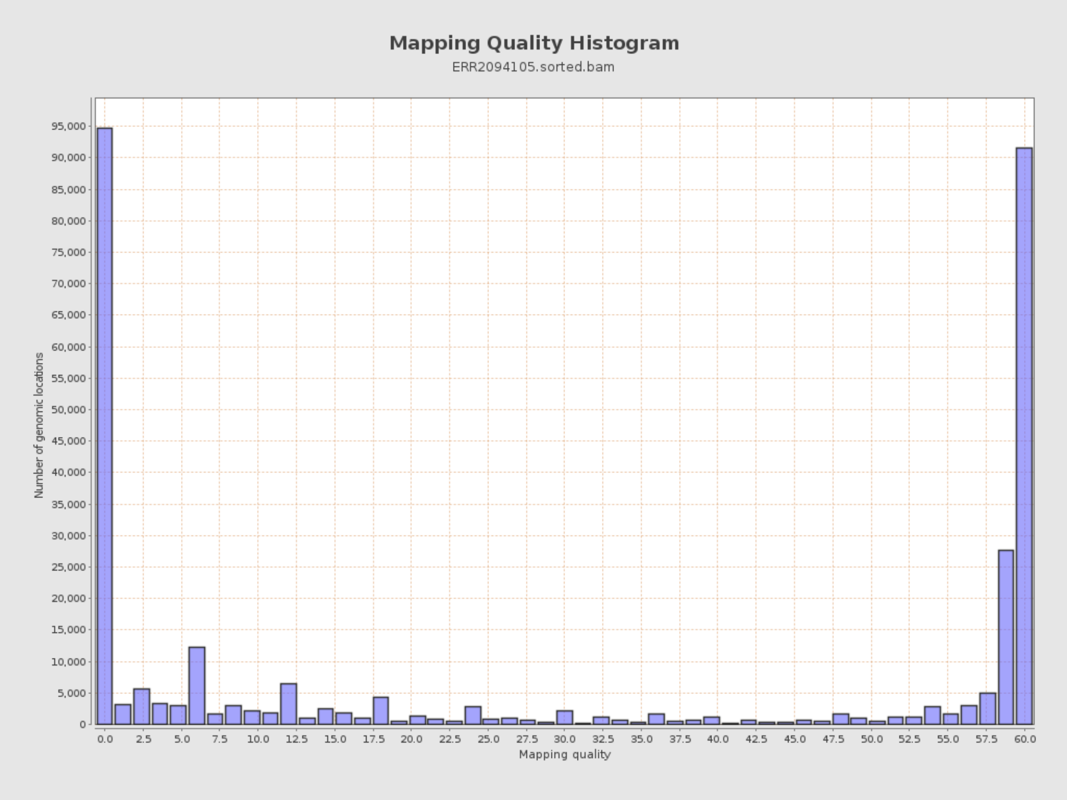
# 11. Results : Homopolymer Indels



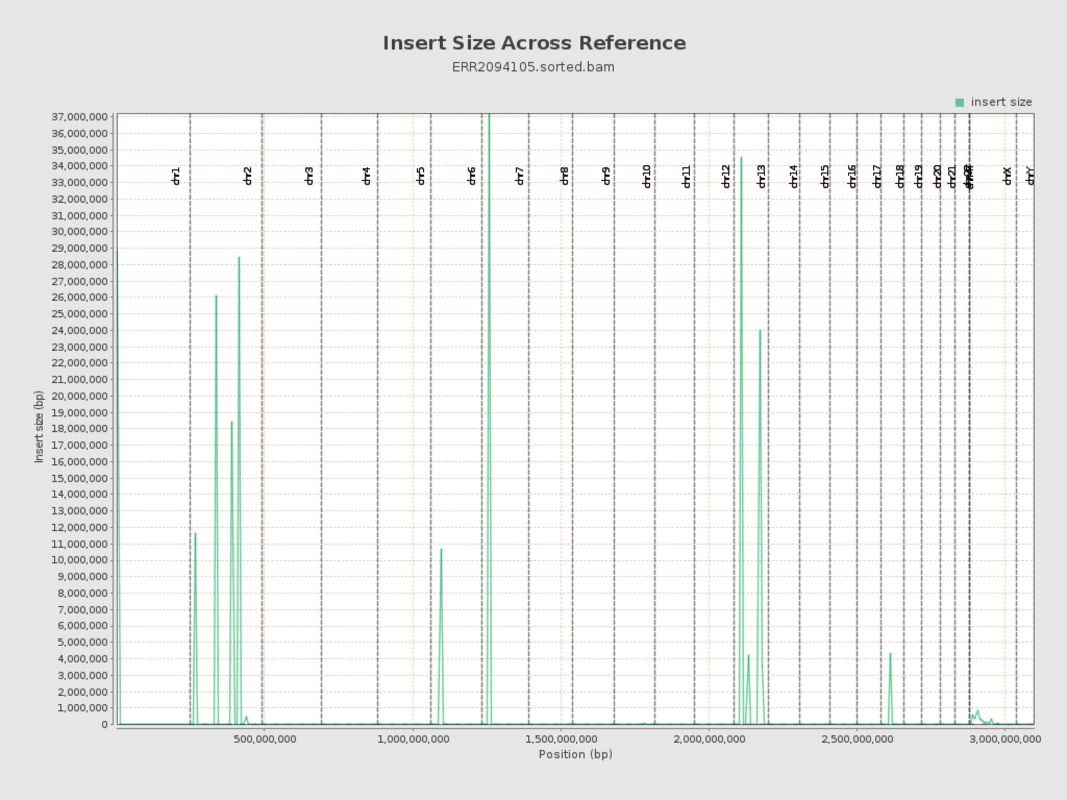
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram