# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/02 23:23:14*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714181.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_ERR9714181 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714181.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Oct 02 23:23:14 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | ERR9714181.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,940,634 |
| Mapped reads | 1,849,974 / 95.33% |
| Unmapped reads | 90,660 / 4.67% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 84,917 / 4.38% |
| Read min/max/mean length | 30 / 151 / 146.68 |
| Duplicated reads (estimated) | 1,756,071 / 90.49% |
| Duplication rate | 43.6% |
| Clipped reads | 1,772,907 / 91.36% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 72,384,255 / 30.6% |
| Number/percentage of C's | 46,357,304 / 19.6% |
| Number/percentage of T's | 67,695,862 / 28.62% |
| Number/percentage of G's | 50,124,814 / 21.19% |
| Number/percentage of N's | 1,673 / 0% |
| GC Percentage | 40.78% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0779 |
| | |

| | |
|---|---|
| Standard Deviation | 13.8432 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 50.53 |

## 2.5. Mismatches and indels

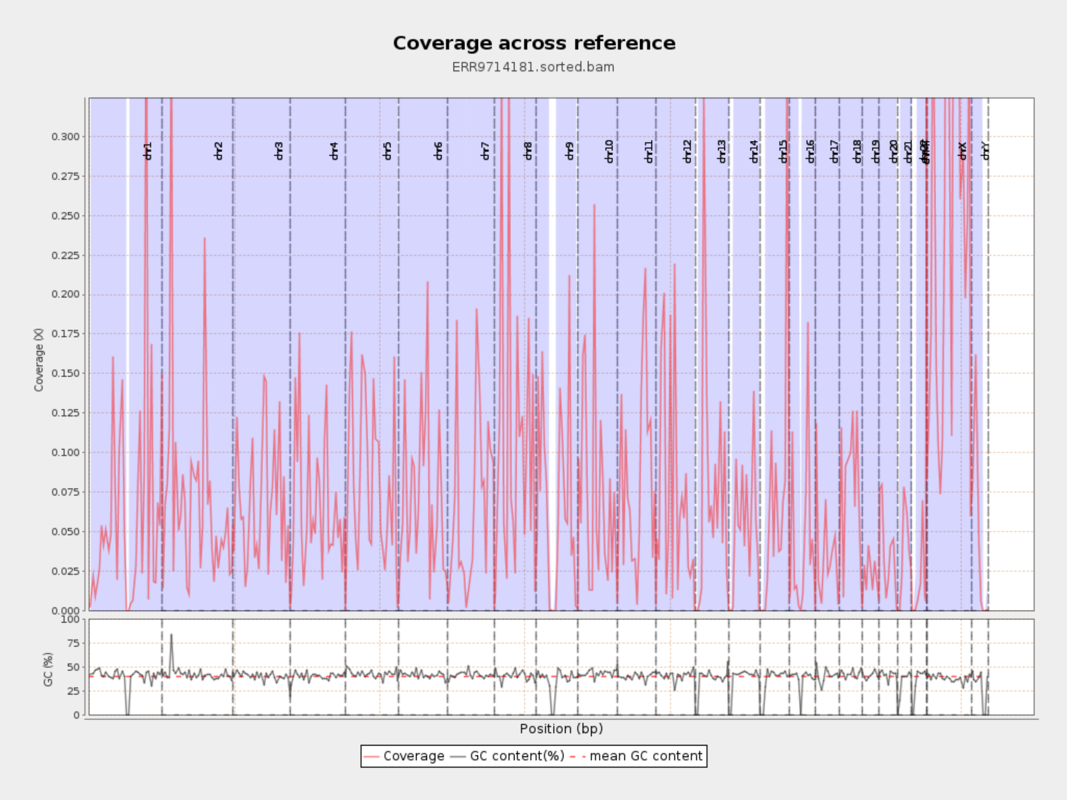
| | |
|---|---|
| General error rate | 4.08% |
| Mismatches | 8,832,911 |
| Insertions | 268,512 |
| Mapped reads with at least one insertion | 14.09% |
| Deletions | 755,280 |
| Mapped reads with at least one deletion | 38.78% |
| Homopolymer indels | 24.97% |

## 2.6. Chromosome stats

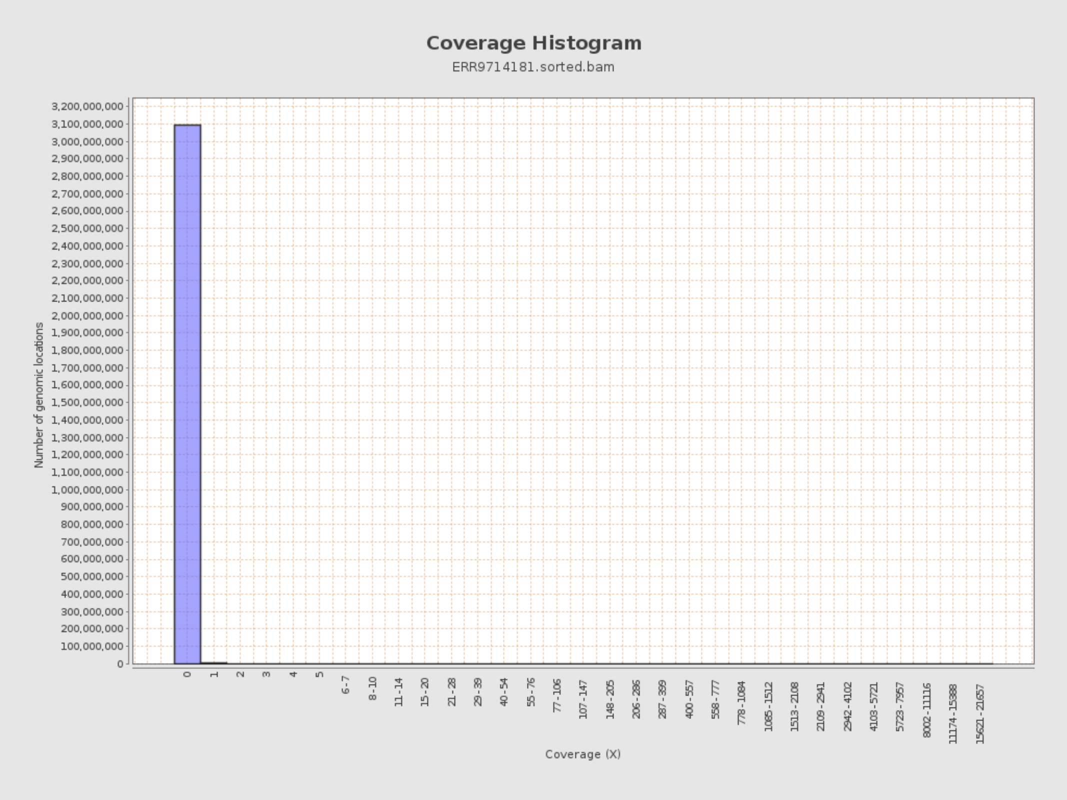
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 15666342 | 0.0629 | 16.4612 |
| chr2 | 243199373 | 17560966 | 0.0722 | 11.401 |
| chr3 | 198022430 | 13417849 | 0.0678 | 8.6523 |
| chr4 | 191154276 | 13015944 | 0.0681 | 9.8081 |
| chr5 | 180915260 | 14887174 | 0.0823 | 11.9907 |
| chr6 | 171115067 | 12377737 | 0.0723 | 10.1662 |
| chr7 | 159138663 | 10722365 | 0.0674 | 9.977 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 16207116 | 0.1107 | 19.6875 |
| chr9 | 141213431 | 10010666 | 0.0709 | 14.799 |
| chr10 | 135534747 | 10637724 | 0.0785 | 12.6779 |
| chr11 | 135006516 | 11313368 | 0.0838 | 12.0014 |
| chr12 | 133851895 | 9924454 | 0.0741 | 14.4518 |
| chr13 | 115169878 | 8560474 | 0.0743 | 13.8096 |
| chr14 | 107349540 | 5767626 | 0.0537 | 6.8262 |
| chr15 | 102531392 | 7145067 | 0.0697 | 13.8707 |
| chr16 | 90354753 | 4007705 | 0.0444 | 7.436 |
| chr17 | 81195210 | 3055123 | 0.0376 | 8.713 |
| chr18 | 78077248 | 6287829 | 0.0805 | 9.9149 |
| chr19 | 59128983 | 1332761 | 0.0225 | 3.5235 |
| chr20 | 63025520 | 2276492 | 0.0361 | 4.9249 |
| chr21 | 48129895 | 1661611 | 0.0345 | 5.1474 |
| chr22 | 51304566 | 802225 | 0.0156 | 2.4698 |
| chrMT | 16571 | 11615 | 0.7009 | 6.1346 |
| chrX | 155270560 | 41589933 | 0.2679 | 33.1638 |
| chrY | 59373566 | 2873256 | 0.0484 | 8.545 |

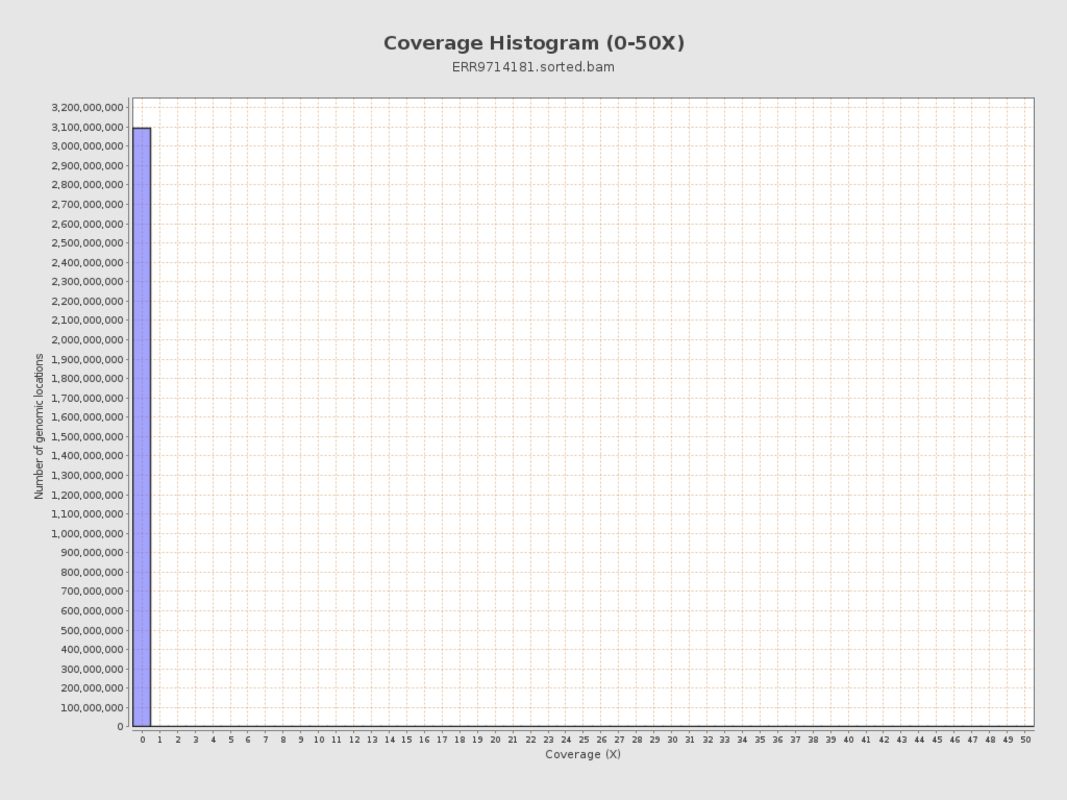
# 3. Results : Coverage across reference



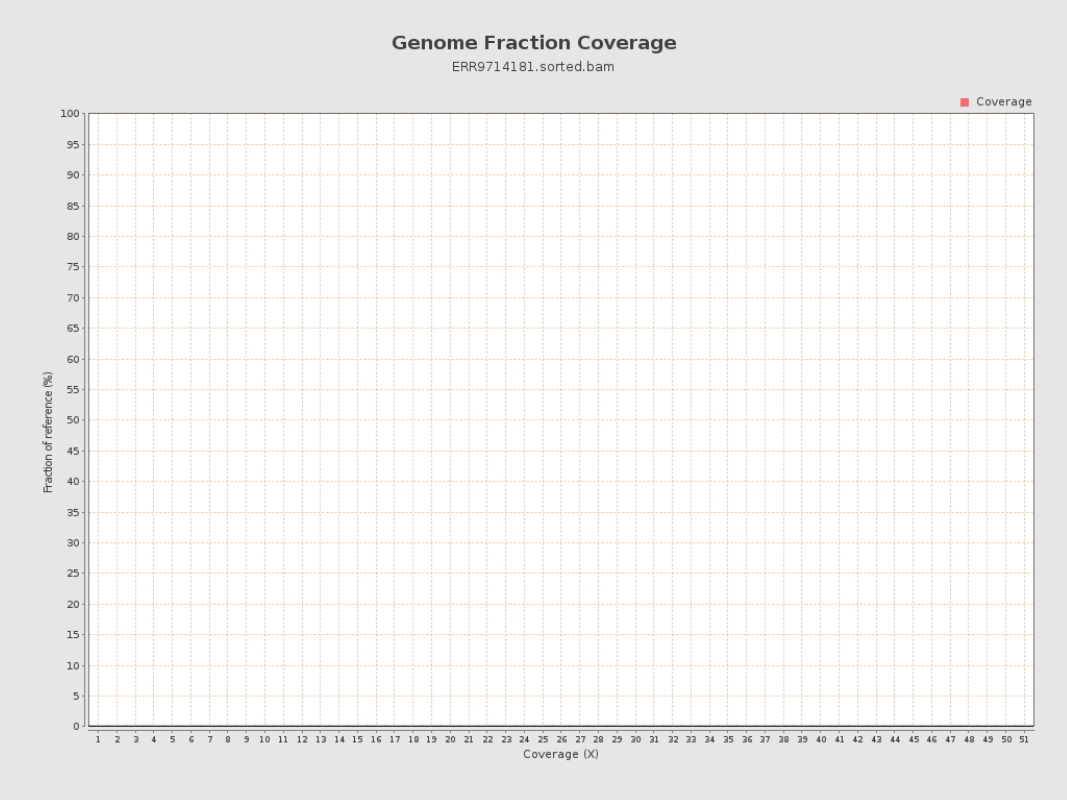
# 4. Results : Coverage Histogram



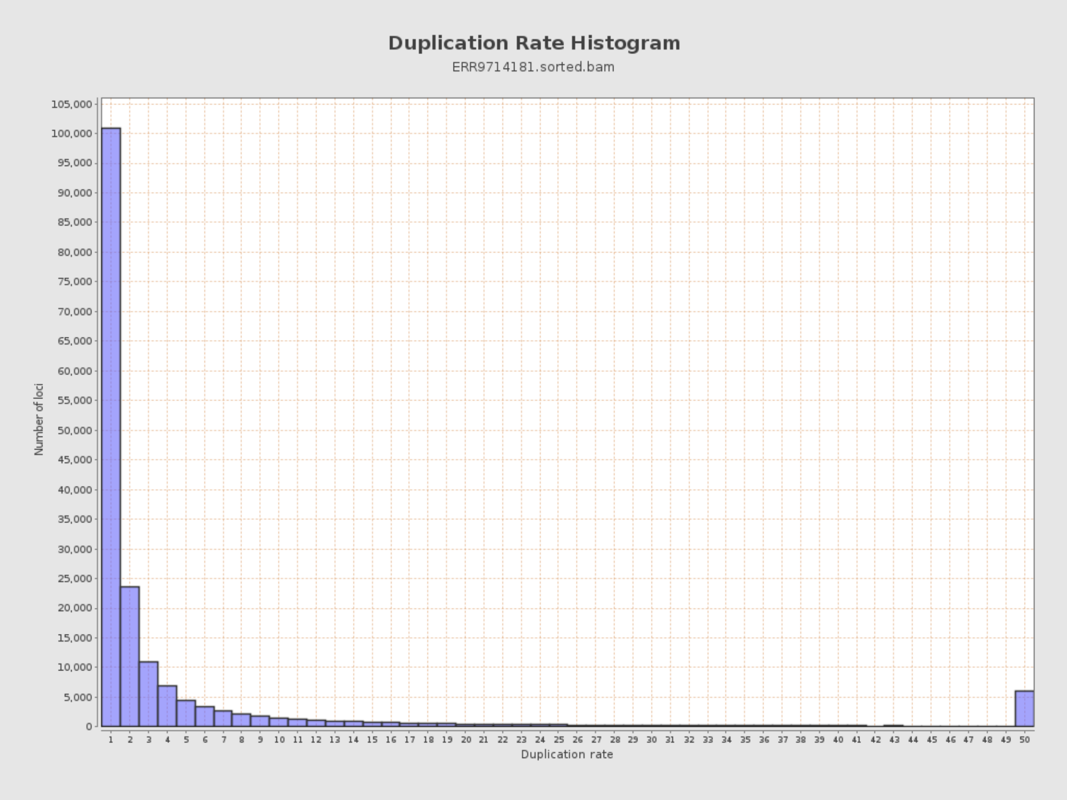
# 5. Results : Coverage Histogram (0-50X)



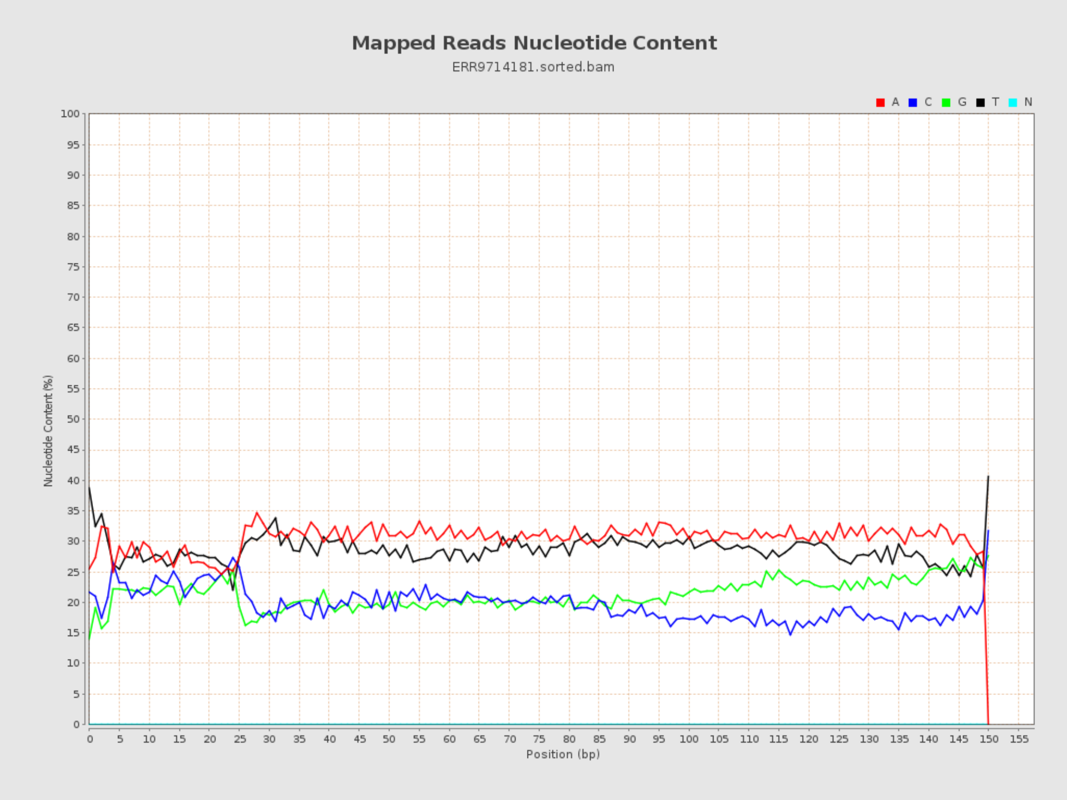
# 6. Results : Genome Fraction Coverage



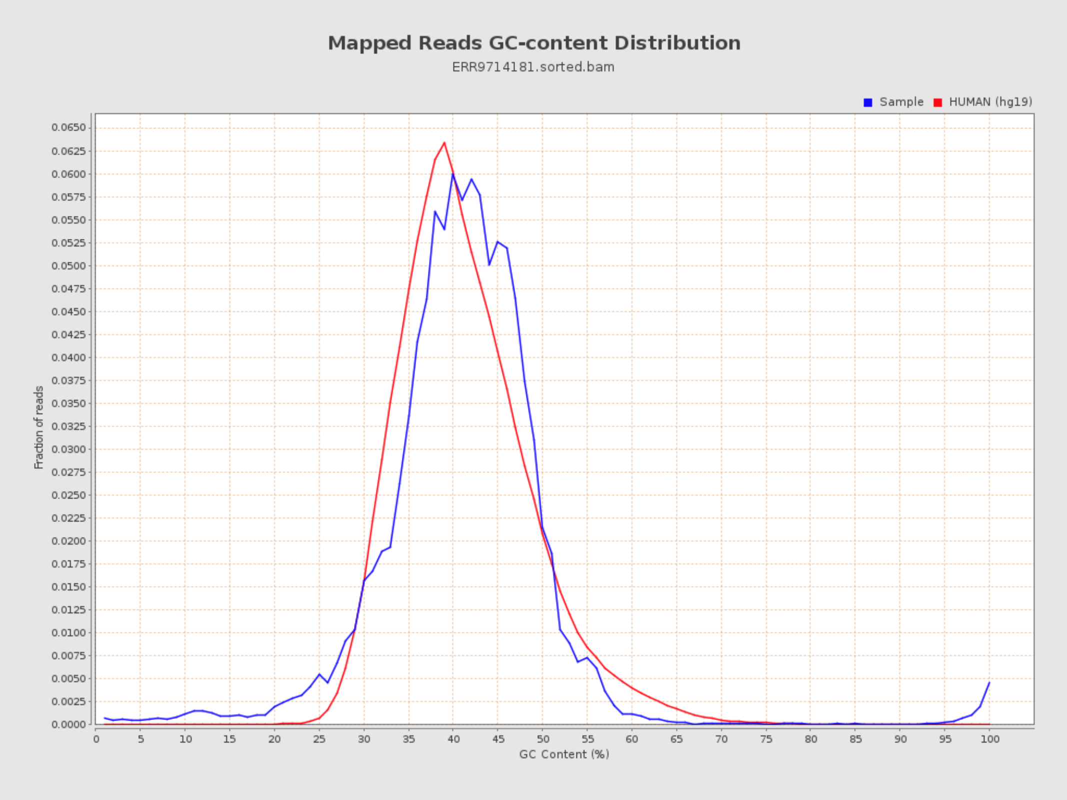
# 7. Results : Duplication Rate Histogram



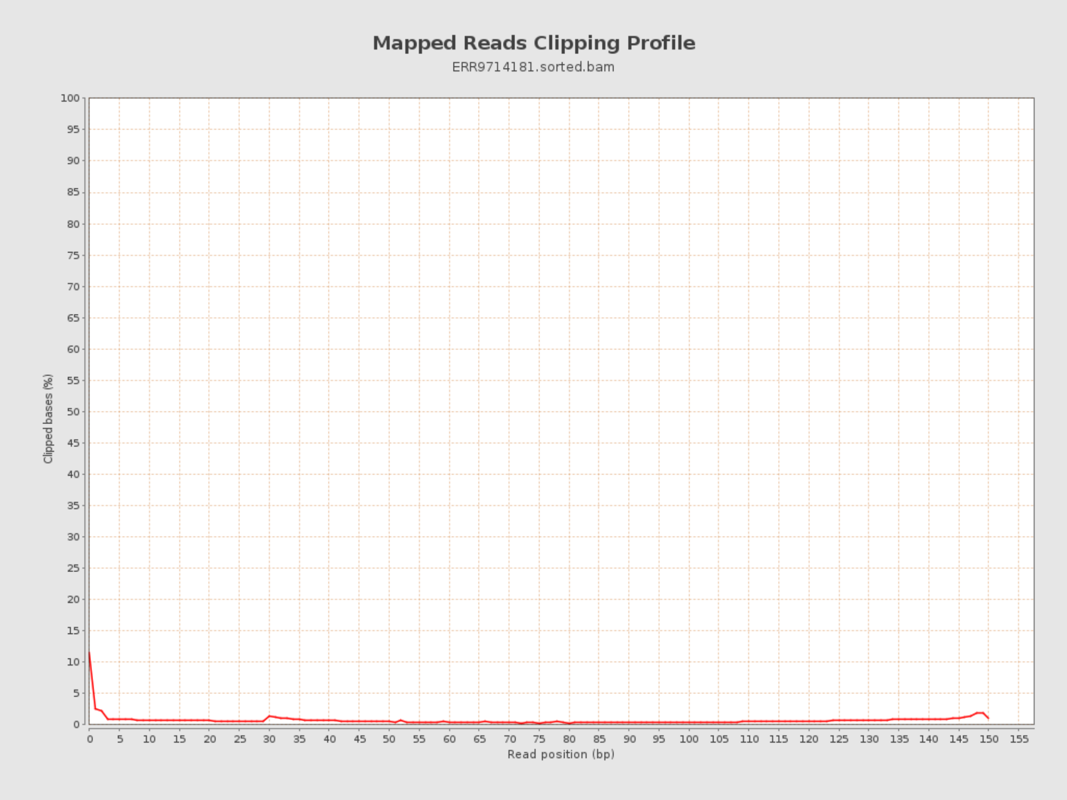
# 8. Results : Mapped Reads Nucleotide Content



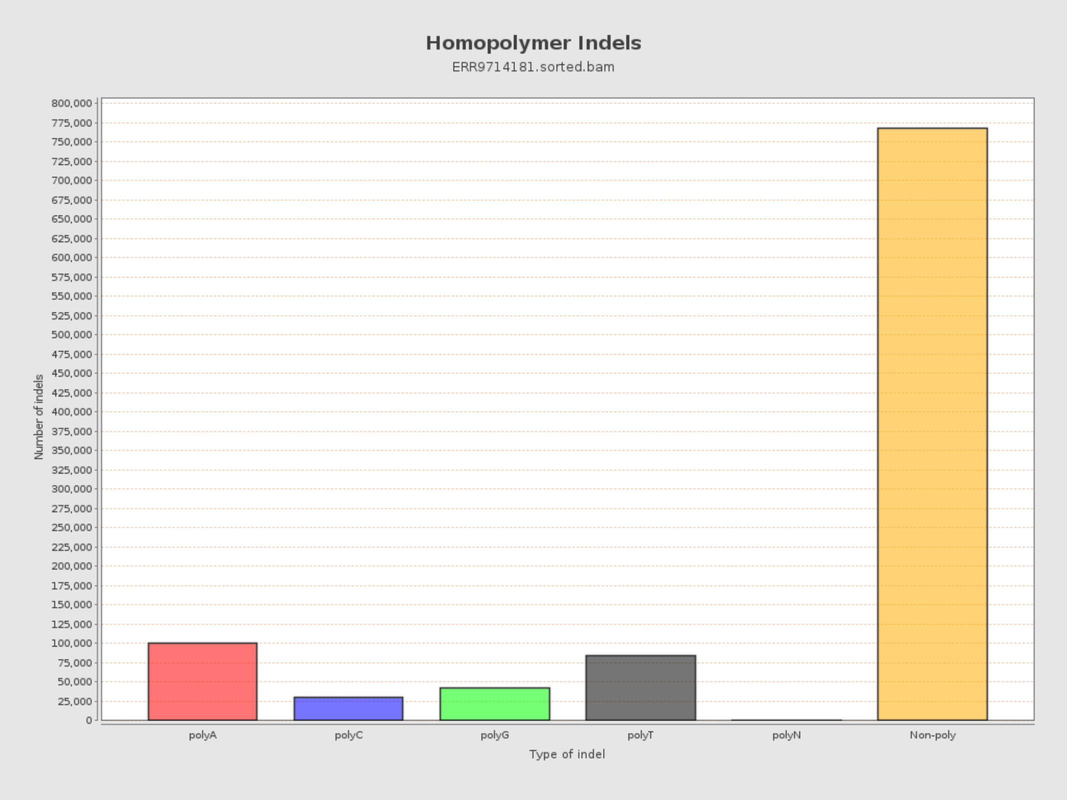
# 9. Results : Mapped Reads GC-content Distribution



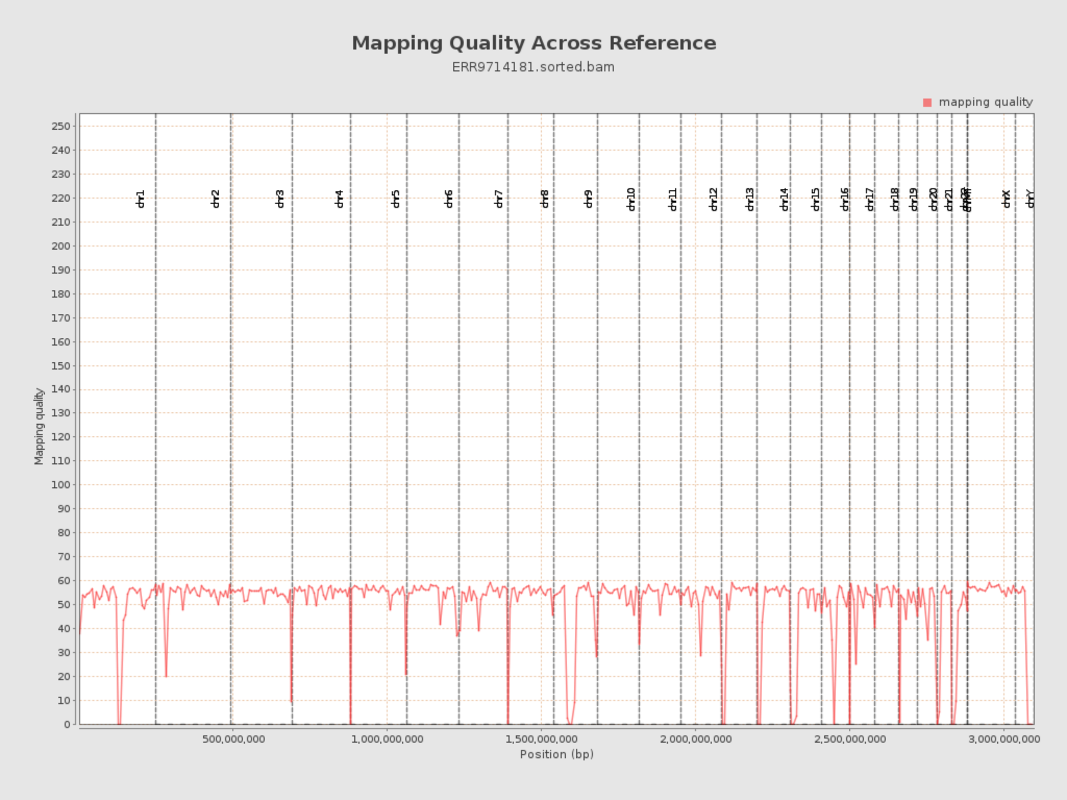
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram