# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/03 01:46:24*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714261.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_ERR9714261 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714261.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Oct 03 01:46:23 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | ERR9714261.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 438,034 |
| Mapped reads | 26,403 / 6.03% |
| Unmapped reads | 411,631 / 93.97% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 565 / 0.13% |
| Read min/max/mean length | 30 / 151 / 56.61 |
| Duplicated reads (estimated) | 23,773 / 5.43% |
| Duplication rate | 35.21% |
| Clipped reads | 21,331 / 4.87% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 318,397 / 13.69% |
| Number/percentage of C's | 204,722 / 8.81% |
| Number/percentage of T's | 268,299 / 11.54% |
| Number/percentage of G's | 1,533,552 / 65.96% |
| Number/percentage of N's | 77 / 0% |
| GC Percentage | 74.76% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0008 |
| | |

| | |
|---|---|
| Standard Deviation | 1.5564 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 21 |

## 2.5. Mismatches and indels

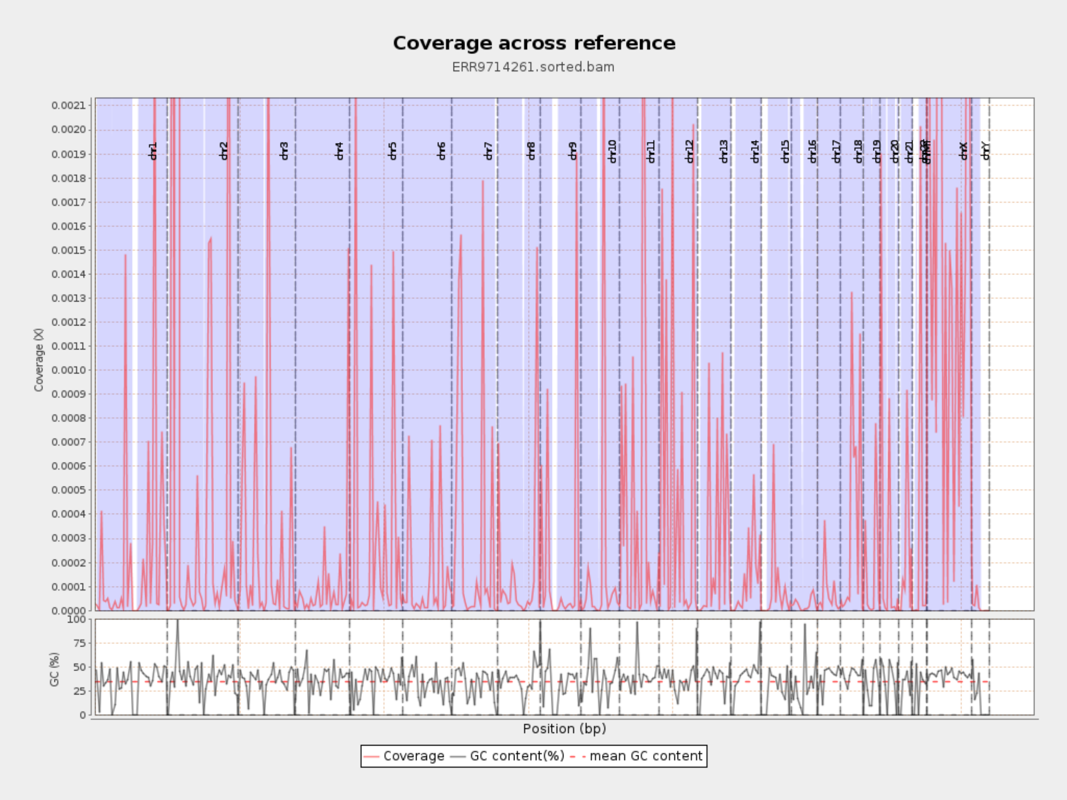
| | |
|---|---|
| General error rate | 3.5% |
| Mismatches | 69,083 |
| Insertions | 2,664 |
| Mapped reads with at least one insertion | 7.75% |
| Deletions | 4,014 |
| Mapped reads with at least one deletion | 14.79% |
| Homopolymer indels | 36.84% |

## 2.6. Chromosome stats

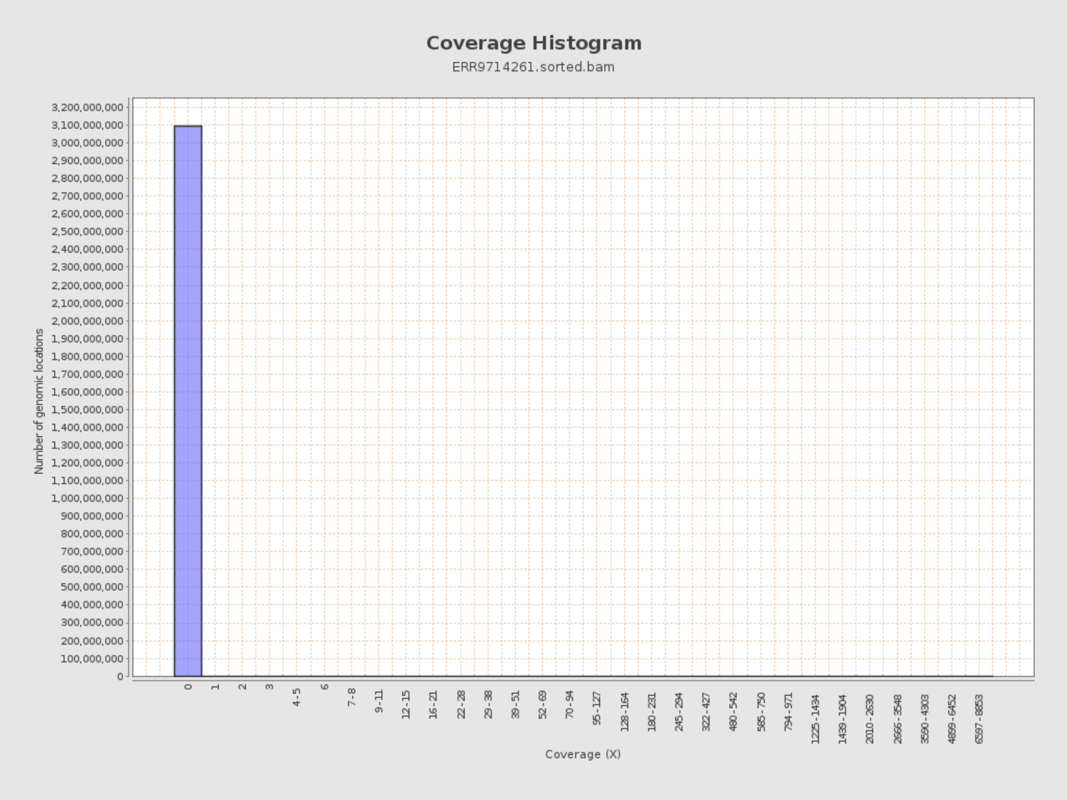
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 59623 | 0.0002 | 0.1233 |
| chr2 | 243199373 | 1447717 | 0.006 | 5.5344 |
| chr3 | 198022430 | 56303 | 0.0003 | 0.106 |
| chr4 | 191154276 | 22239 | 0.0001 | 0.0673 |
| chr5 | 180915260 | 56521 | 0.0003 | 0.1233 |
| chr6 | 171115067 | 23780 | 0.0001 | 0.0609 |
| chr7 | 159138663 | 50133 | 0.0003 | 0.2172 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 24233 | 0.0002 | 0.0752 |
| chr9 | 141213431 | 29248 | 0.0002 | 0.1129 |
| chr10 | 135534747 | 26458 | 0.0002 | 0.1354 |
| chr11 | 135006516 | 59045 | 0.0004 | 0.1466 |
| chr12 | 133851895 | 71901 | 0.0005 | 0.1811 |
| chr13 | 115169878 | 33741 | 0.0003 | 0.1093 |
| chr14 | 107349540 | 14317 | 0.0001 | 0.0668 |
| chr15 | 102531392 | 9197 | 0.0001 | 0.0433 |
| chr16 | 90354753 | 2525 | 0 | 0.0097 |
| chr17 | 81195210 | 6152 | 0.0001 | 0.0492 |
| chr18 | 78077248 | 31185 | 0.0004 | 0.1211 |
| chr19 | 59128983 | 9669 | 0.0002 | 0.0747 |
| chr20 | 63025520 | 18465 | 0.0003 | 0.1197 |
| chr21 | 48129895 | 10178 | 0.0002 | 0.0745 |
| chr22 | 51304566 | 16210 | 0.0003 | 0.1234 |
| chrMT | 16571 | 3107 | 0.1875 | 1.4269 |
| chrX | 155270560 | 266993 | 0.0017 | 0.3025 |
| chrY | 59373566 | 1196 | 0 | 0.0088 |

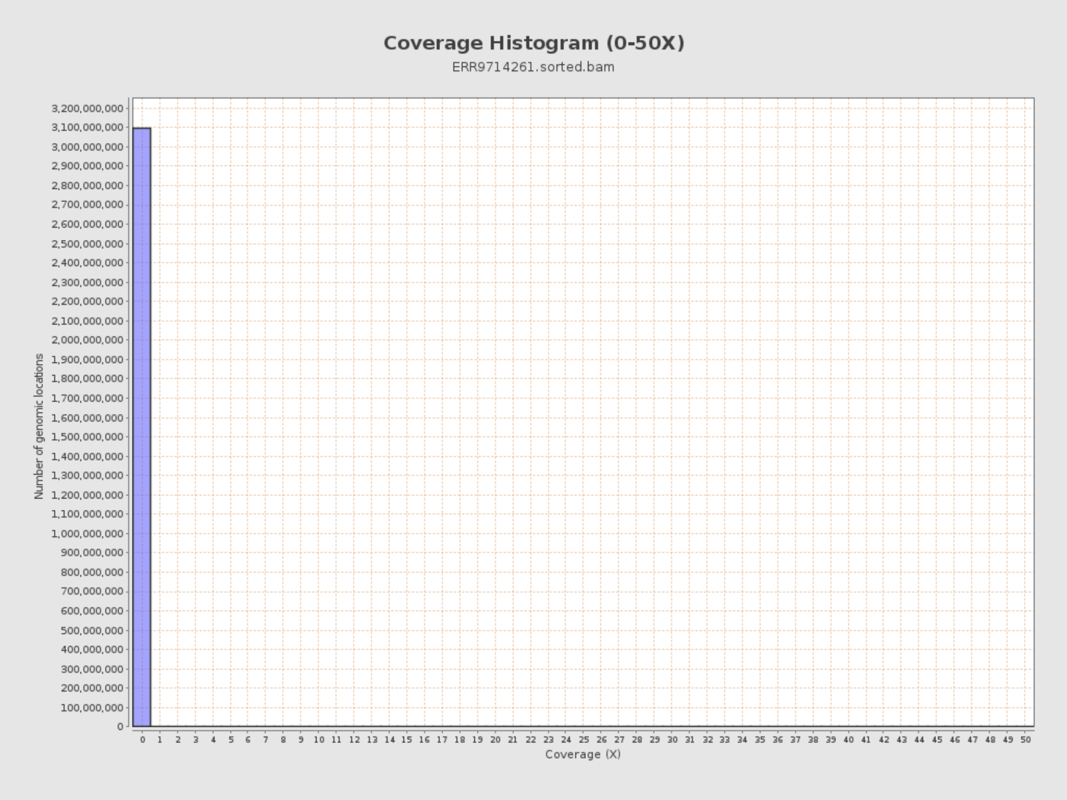
# 3. Results : Coverage across reference



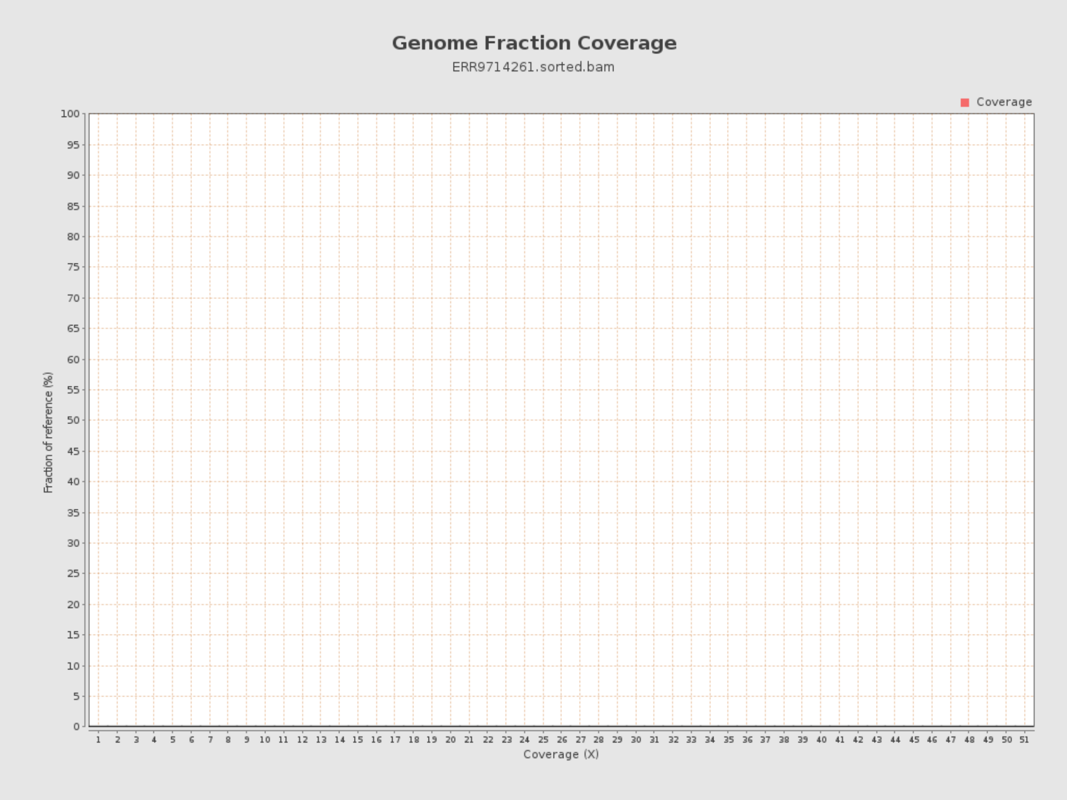
# 4. Results : Coverage Histogram



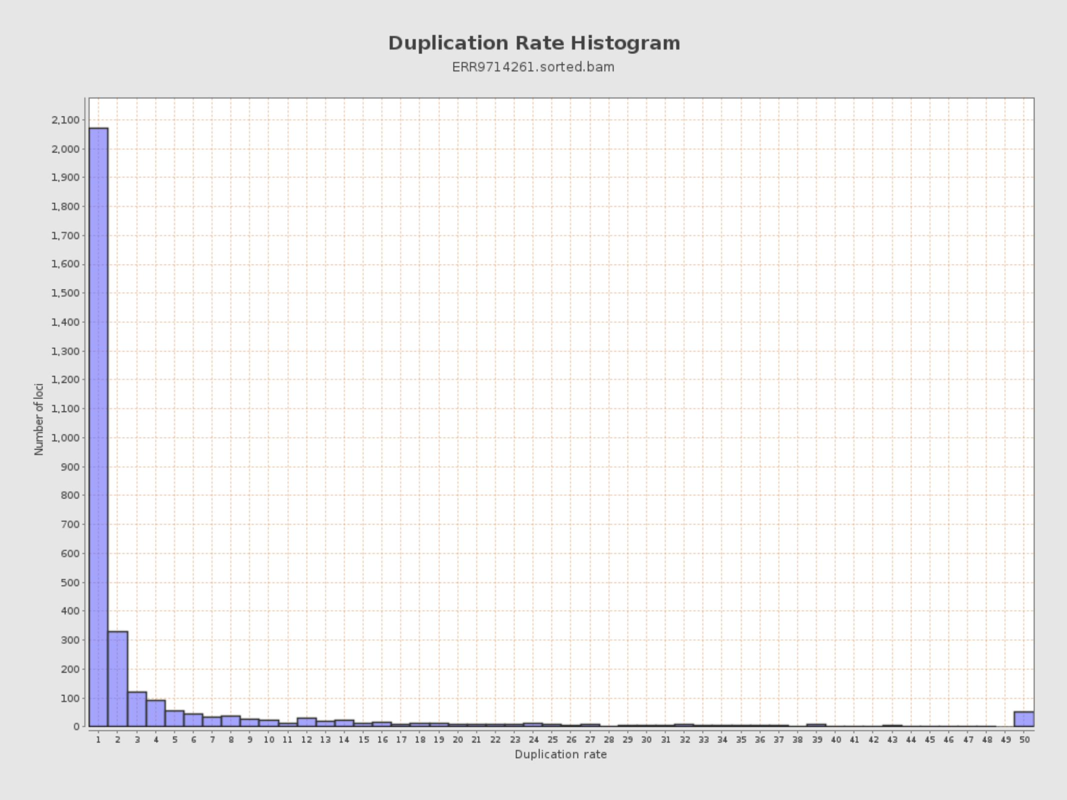
# 5. Results : Coverage Histogram (0-50X)



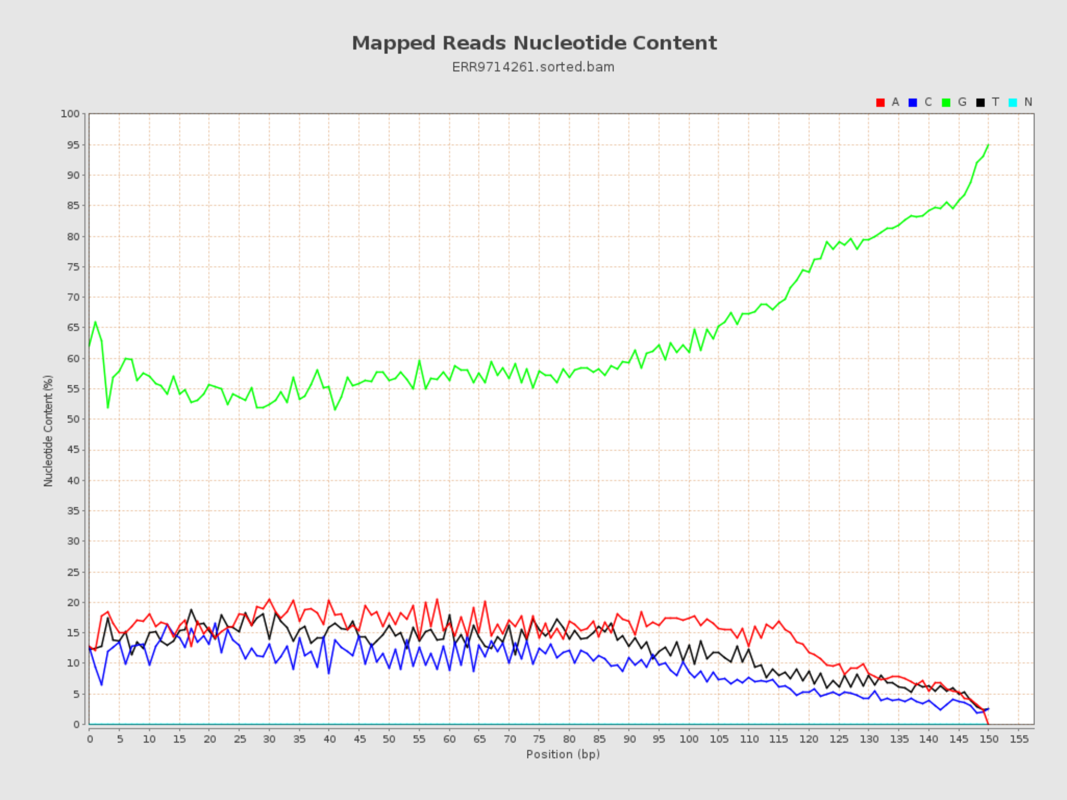
# 6. Results : Genome Fraction Coverage



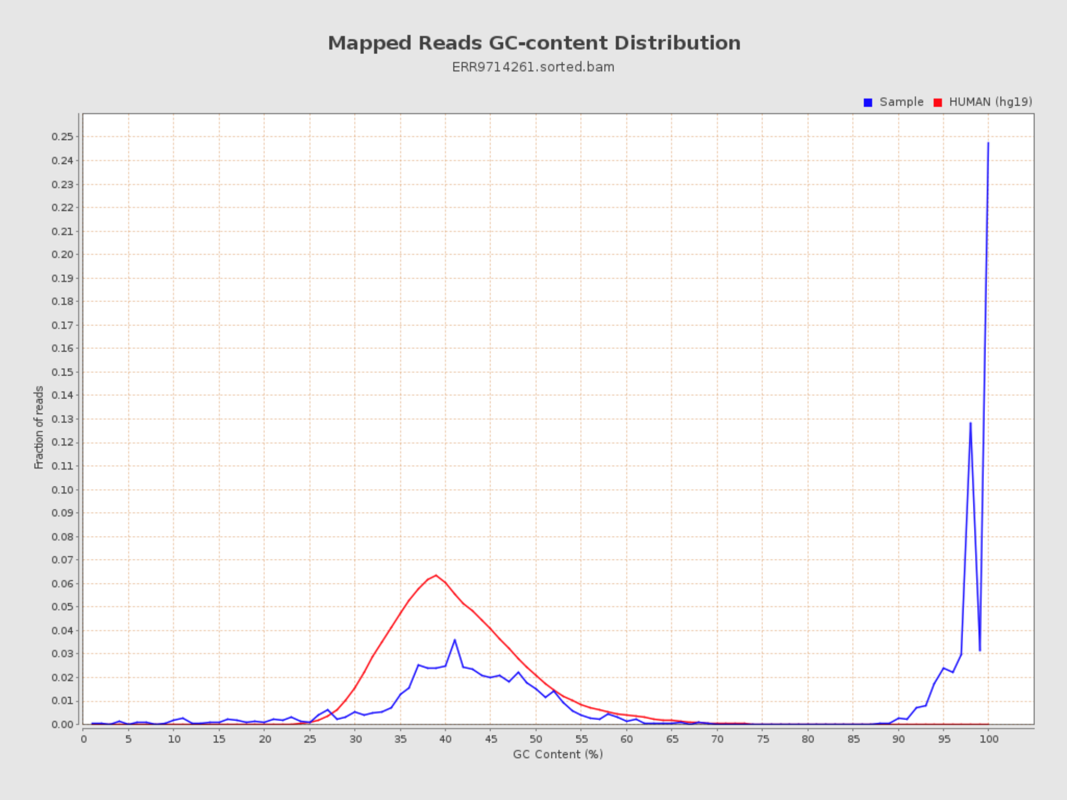
# 7. Results : Duplication Rate Histogram



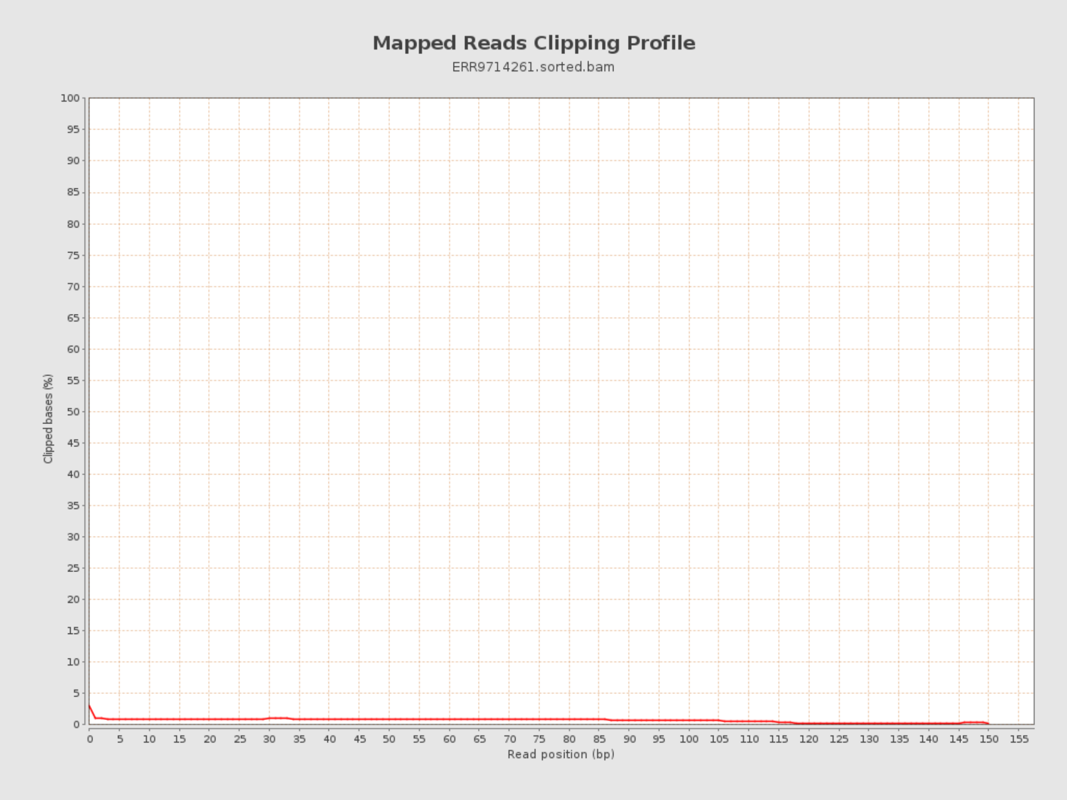
# 8. Results : Mapped Reads Nucleotide Content



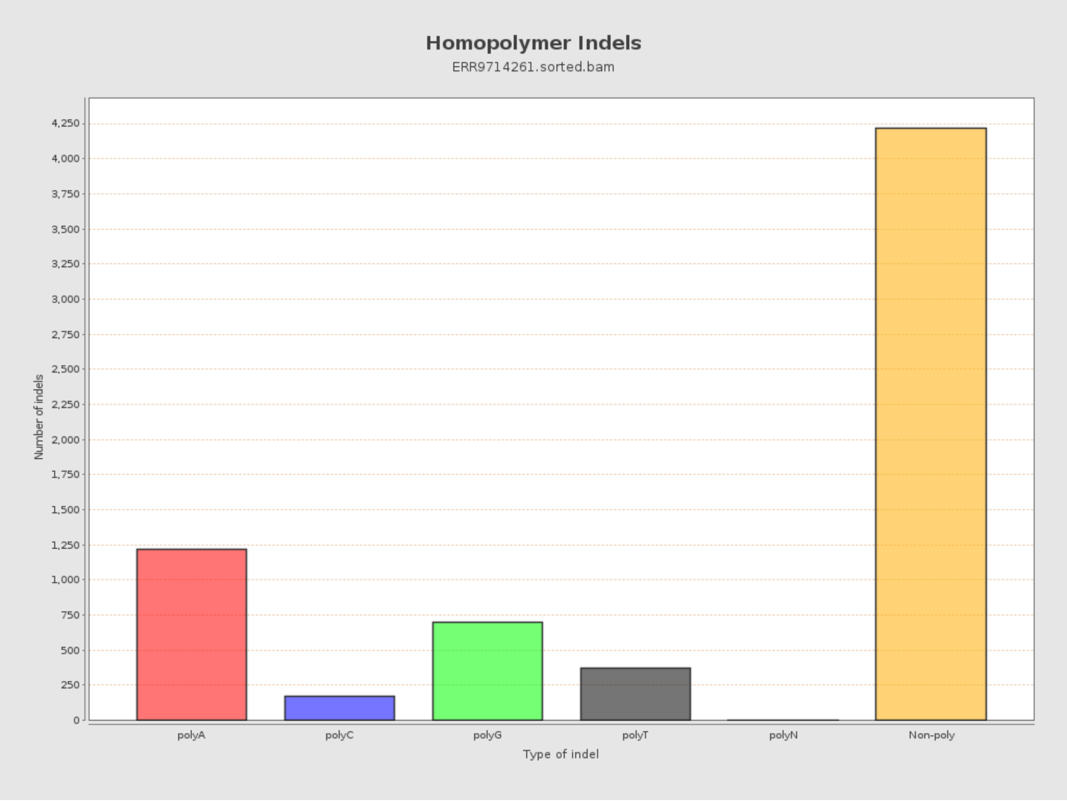
# 9. Results : Mapped Reads GC-content Distribution



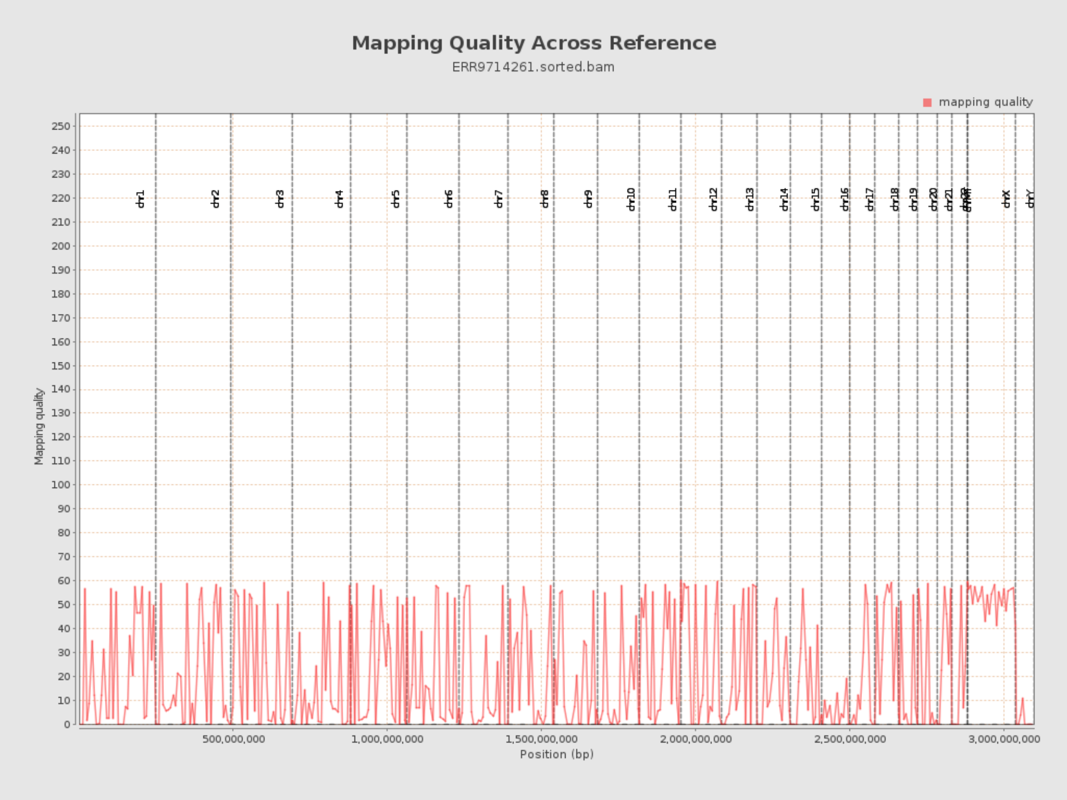
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram