# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/02 21:14:44*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714140.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_ERR9714140 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714140.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Oct 02 21:14:43 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | ERR9714140.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 690,544 |
| Mapped reads | 565,057 / 81.83% |
| Unmapped reads | 125,487 / 18.17% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 20,367 / 2.95% |
| Read min/max/mean length | 30 / 151 / 133.25 |
| Duplicated reads (estimated) | 471,315 / 68.25% |
| Duplication rate | 43.77% |
| Clipped reads | 539,628 / 78.15% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 19,515,641 / 27.57% |
| Number/percentage of C's | 15,421,907 / 21.79% |
| Number/percentage of T's | 18,466,281 / 26.09% |
| Number/percentage of G's | 17,375,463 / 24.55% |
| Number/percentage of N's | 526 / 0% |
| GC Percentage | 46.34% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0233 |
| | |

| | |
|---|---|
| Standard Deviation | 2.663 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 52.58 |

## 2.5. Mismatches and indels

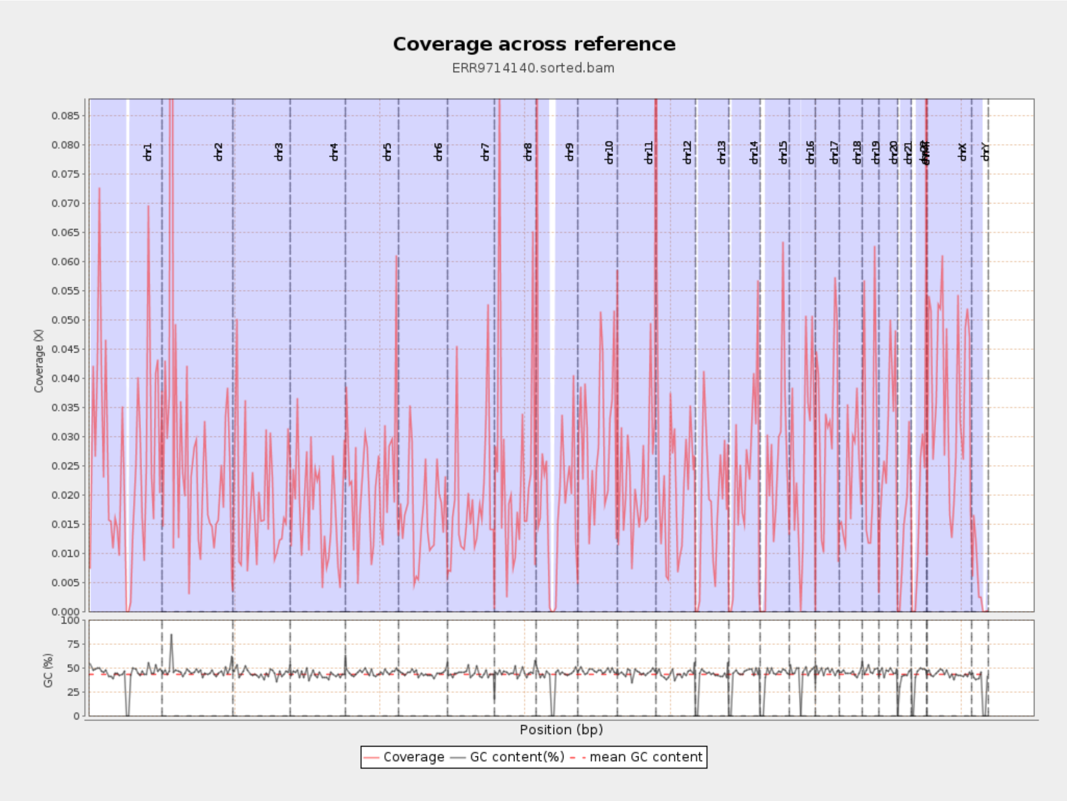
| | |
|---|---|
| General error rate | 4.22% |
| Mismatches | 2,739,979 |
| Insertions | 79,838 |
| Mapped reads with at least one insertion | 13.72% |
| Deletions | 239,082 |
| Mapped reads with at least one deletion | 40.36% |
| Homopolymer indels | 28.43% |

## 2.6. Chromosome stats

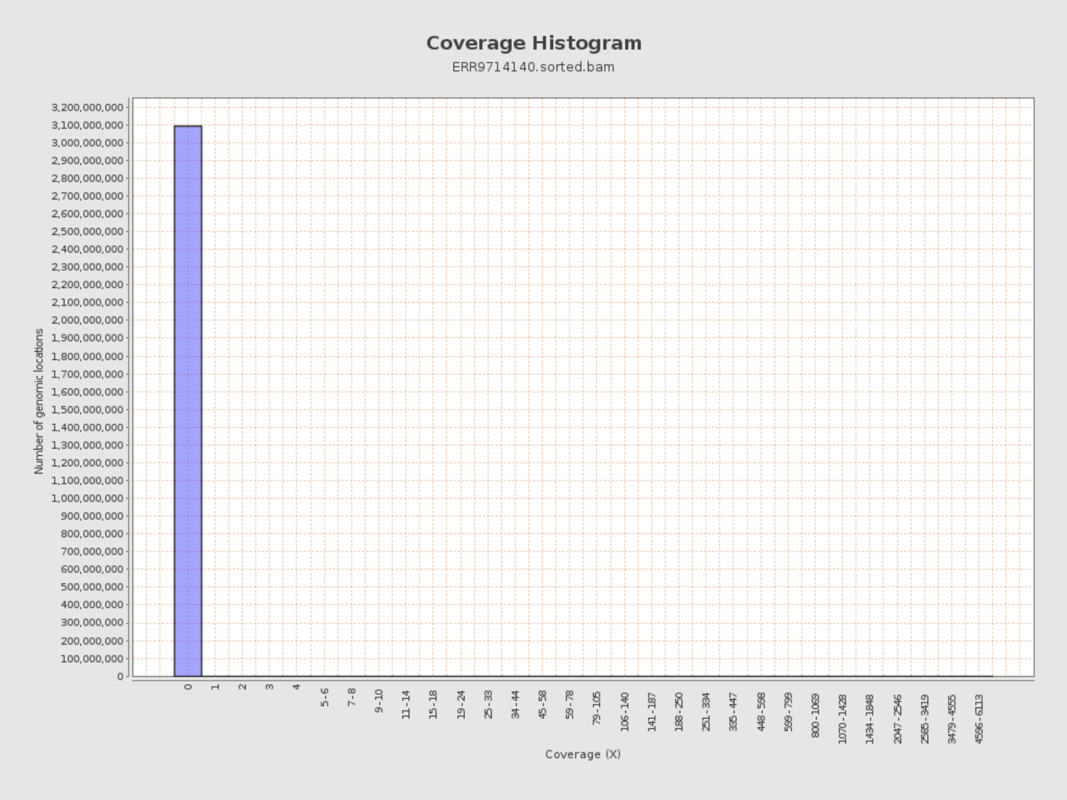
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 6336344 | 0.0254 | 2.5851 |
| chr2 | 243199373 | 7131492 | 0.0293 | 5.2651 |
| chr3 | 198022430 | 3702902 | 0.0187 | 1.8027 |
| chr4 | 191154276 | 3371232 | 0.0176 | 1.8694 |
| chr5 | 180915260 | 4095993 | 0.0226 | 2.15 |
| chr6 | 171115067 | 2830293 | 0.0165 | 1.4722 |
| chr7 | 159138663 | 3015354 | 0.0189 | 1.9677 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3535064 | 0.0242 | 2.8518 |
| chr9 | 141213431 | 2556953 | 0.0181 | 1.9759 |
| chr10 | 135534747 | 4069412 | 0.03 | 2.542 |
| chr11 | 135006516 | 3255075 | 0.0241 | 2.3419 |
| chr12 | 133851895 | 2983132 | 0.0223 | 2.1272 |
| chr13 | 115169878 | 2019953 | 0.0175 | 2.0222 |
| chr14 | 107349540 | 2463493 | 0.0229 | 2.3157 |
| chr15 | 102531392 | 2299897 | 0.0224 | 2.1502 |
| chr16 | 90354753 | 2430845 | 0.0269 | 2.8024 |
| chr17 | 81195210 | 2651723 | 0.0327 | 3.1152 |
| chr18 | 78077248 | 1802579 | 0.0231 | 2.149 |
| chr19 | 59128983 | 1601499 | 0.0271 | 2.6404 |
| chr20 | 63025520 | 1949198 | 0.0309 | 2.5043 |
| chr21 | 48129895 | 659123 | 0.0137 | 1.5497 |
| chr22 | 51304566 | 803068 | 0.0157 | 1.5725 |
| chrMT | 16571 | 462675 | 27.9208 | 257.8215 |
| chrX | 155270560 | 5850888 | 0.0377 | 2.3671 |
| chrY | 59373566 | 293750 | 0.0049 | 0.7601 |

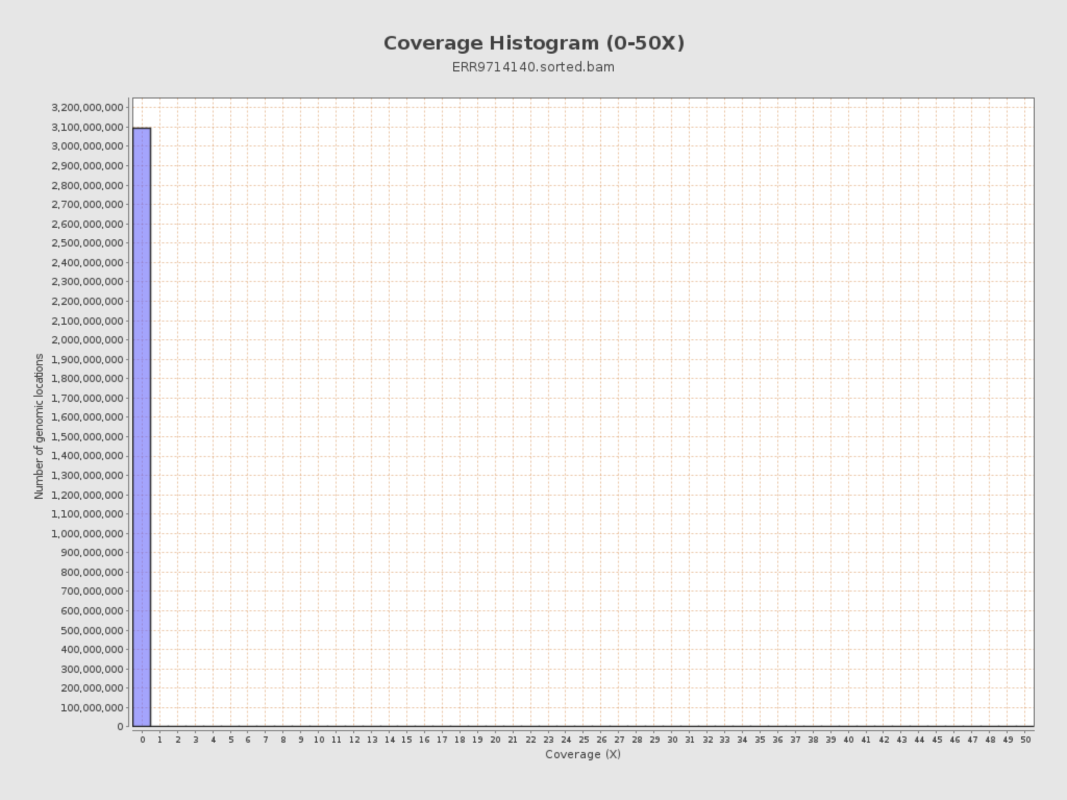
# 3. Results : Coverage across reference



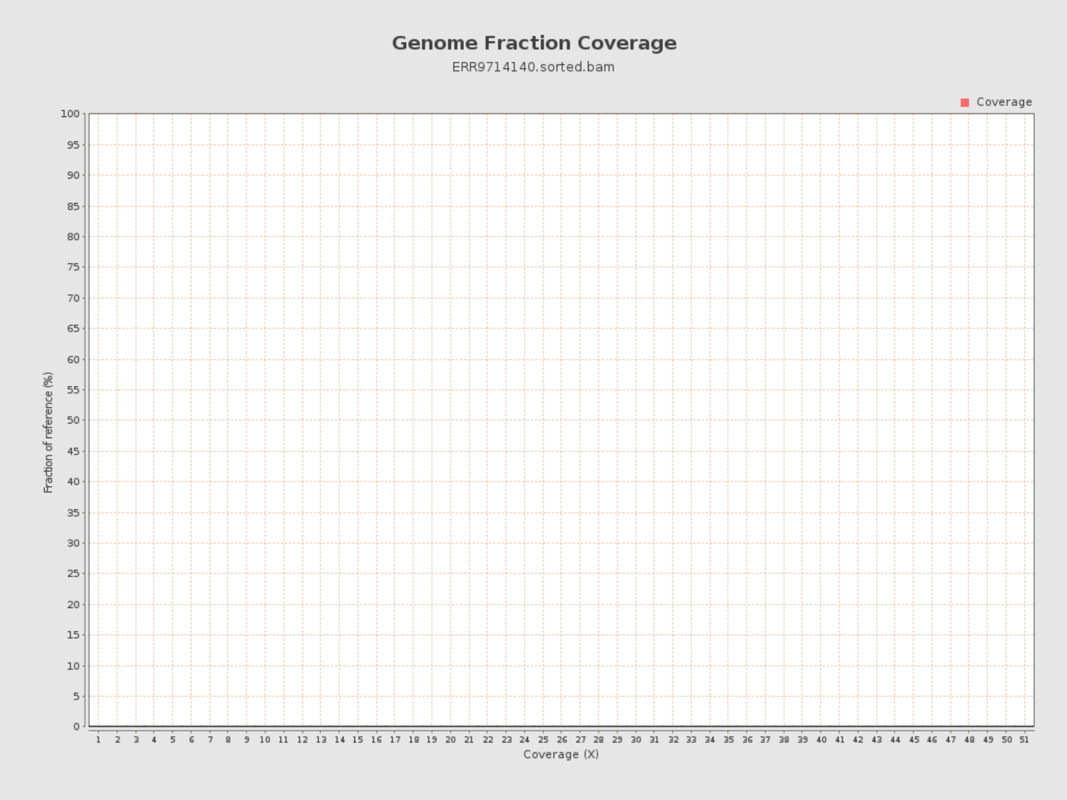
# 4. Results : Coverage Histogram



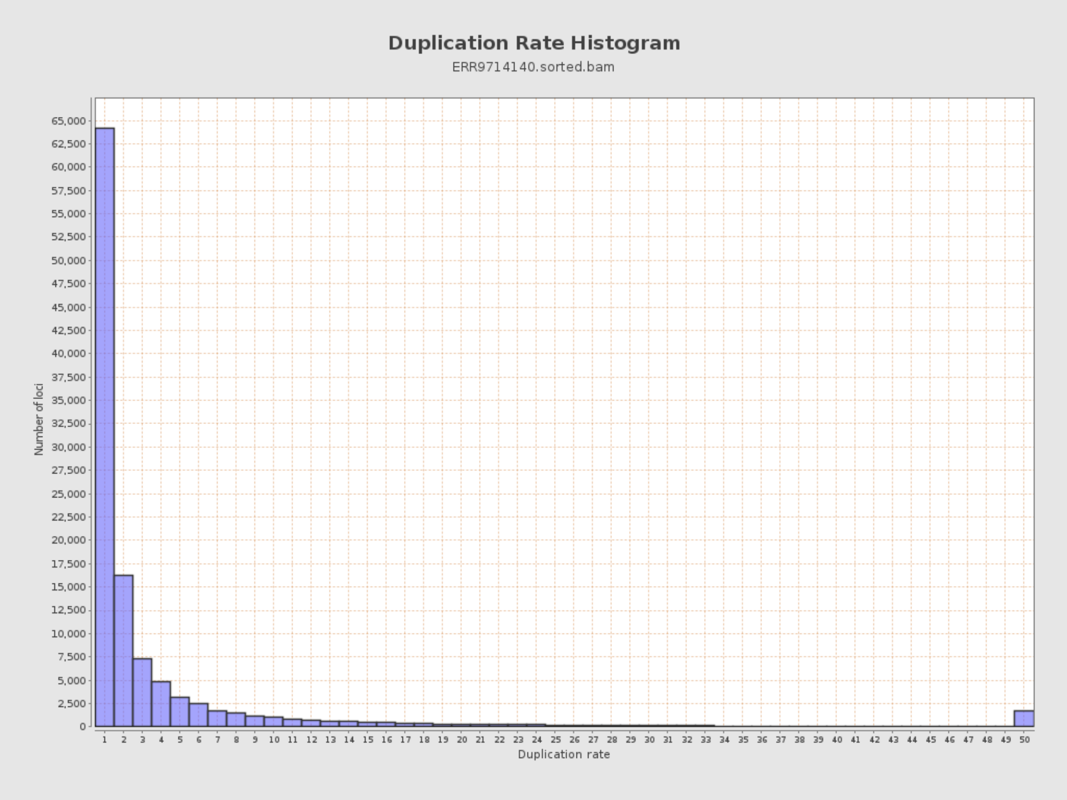
# 5. Results : Coverage Histogram (0-50X)



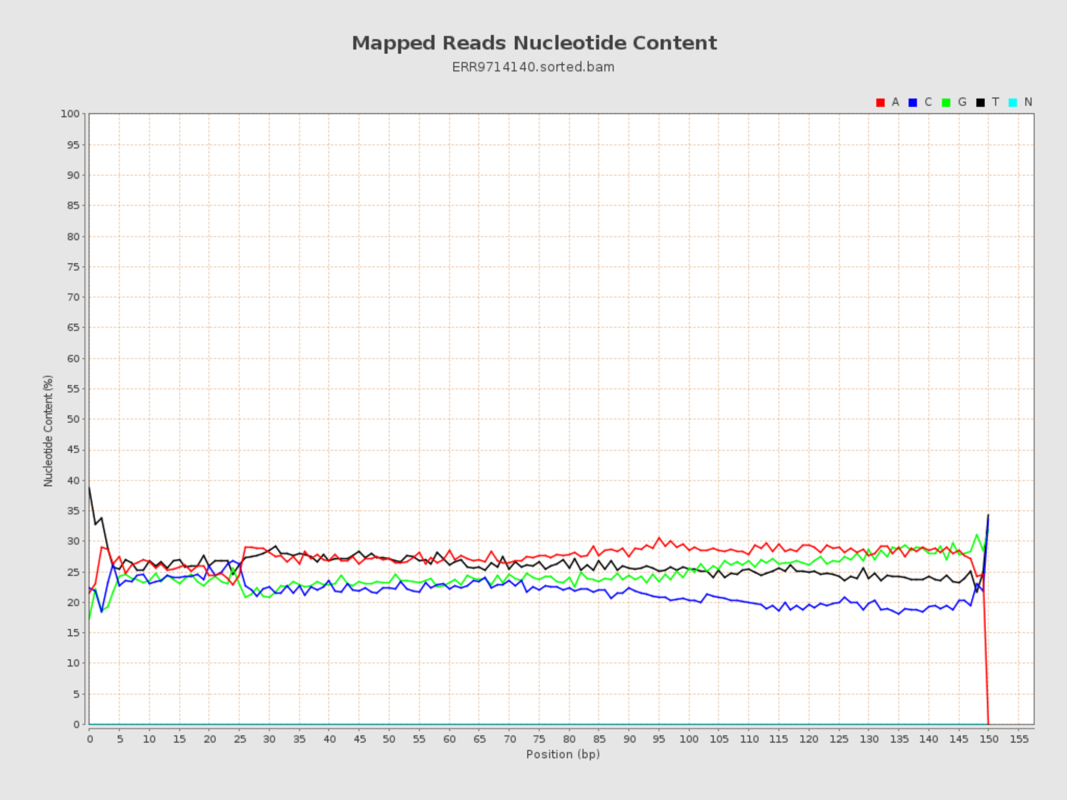
# 6. Results : Genome Fraction Coverage



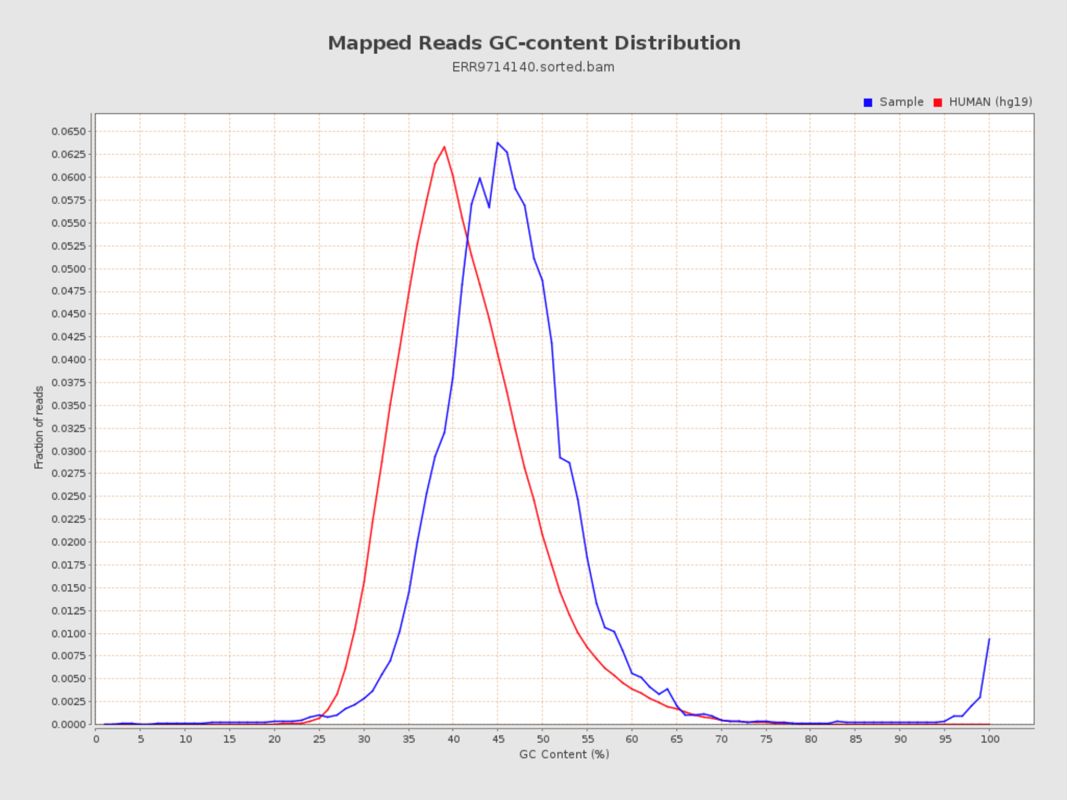
# 7. Results : Duplication Rate Histogram



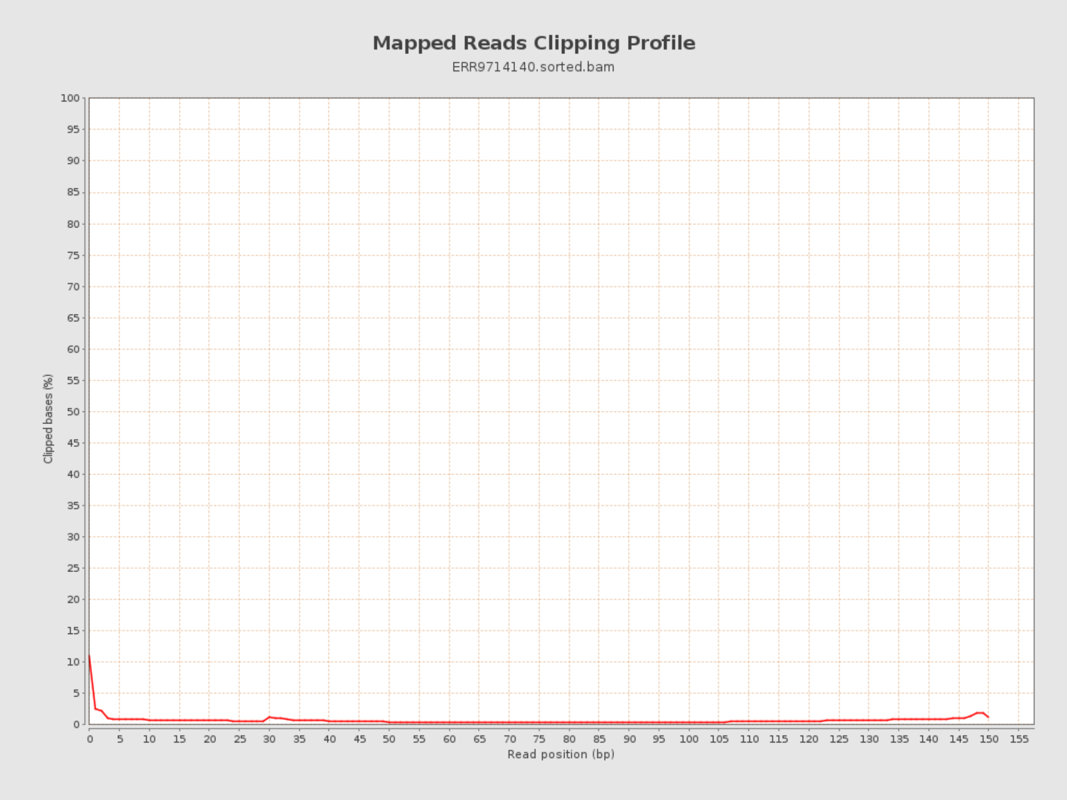
# 8. Results : Mapped Reads Nucleotide Content



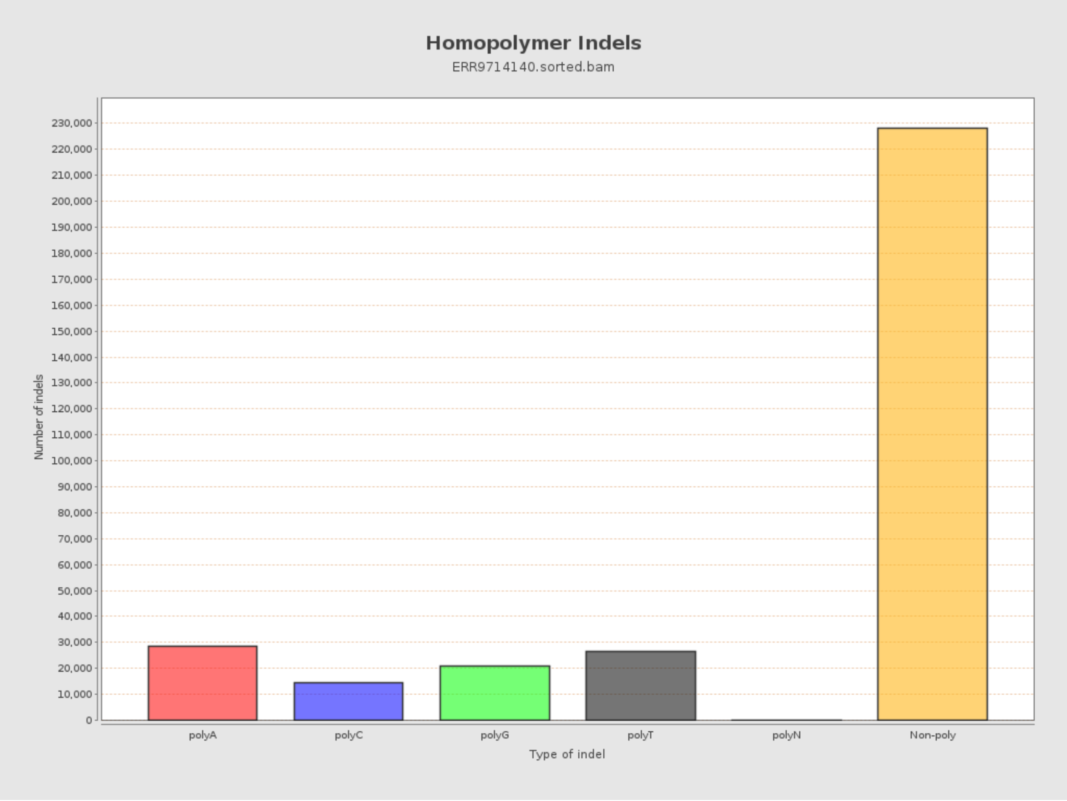
# 9. Results : Mapped Reads GC-content Distribution



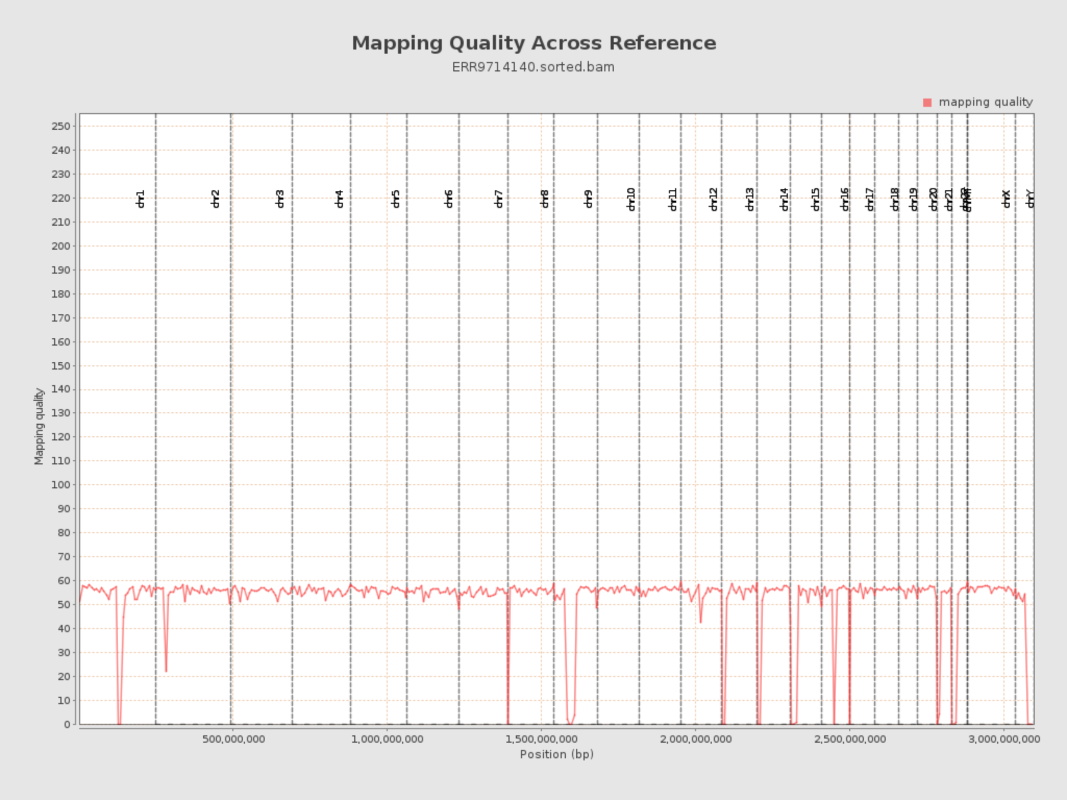
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram