# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/02 22:43:36*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714170.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_ERR9714170 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714170.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Oct 02 22:43:36 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | ERR9714170.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,050,514 |
| Mapped reads | 252,357 / 24.02% |
| Unmapped reads | 798,157 / 75.98% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 8,149 / 0.78% |
| Read min/max/mean length | 30 / 151 / 114.66 |
| Duplicated reads (estimated) | 214,477 / 20.42% |
| Duplication rate | 42.88% |
| Clipped reads | 237,941 / 22.65% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 8,480,231 / 26.44% |
| Number/percentage of C's | 7,147,760 / 22.29% |
| Number/percentage of T's | 8,014,547 / 24.99% |
| Number/percentage of G's | 8,428,447 / 26.28% |
| Number/percentage of N's | 216 / 0% |
| GC Percentage | 48.57% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0106 |
| | |

| | |
|---|---|
| Standard Deviation | 3.2243 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 50.75 |

## 2.5. Mismatches and indels

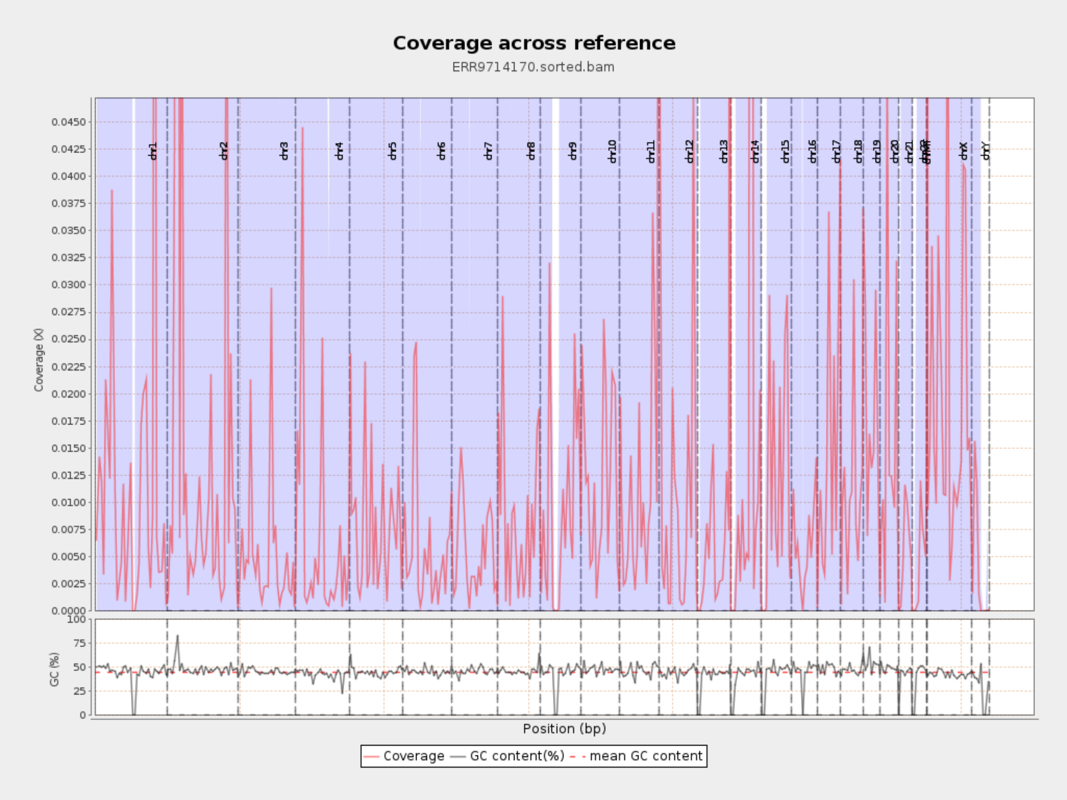
| | |
|---|---|
| General error rate | 4.43% |
| Mismatches | 1,330,378 |
| Insertions | 33,496 |
| Mapped reads with at least one insertion | 12.73% |
| Deletions | 114,319 |
| Mapped reads with at least one deletion | 42.89% |
| Homopolymer indels | 29.93% |

## 2.6. Chromosome stats

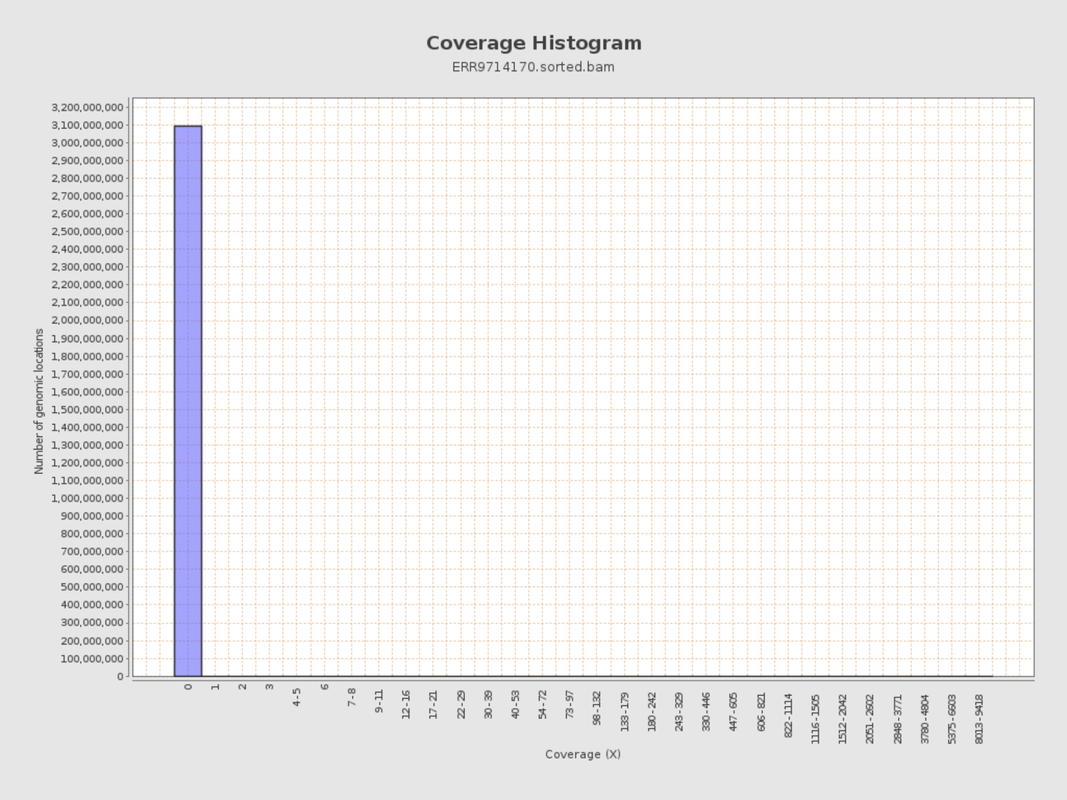
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 2965699 | 0.0119 | 3.1353 |
| chr2 | 243199373 | 4515658 | 0.0186 | 6.1663 |
| chr3 | 198022430 | 1021133 | 0.0052 | 0.888 |
| chr4 | 191154276 | 1182627 | 0.0062 | 1.6668 |
| chr5 | 180915260 | 1352489 | 0.0075 | 1.499 |
| chr6 | 171115067 | 1000391 | 0.0058 | 1.0656 |
| chr7 | 159138663 | 850683 | 0.0053 | 0.8694 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1243070 | 0.0085 | 1.54 |
| chr9 | 141213431 | 1251077 | 0.0089 | 1.7808 |
| chr10 | 135534747 | 1641706 | 0.0121 | 1.9522 |
| chr11 | 135006516 | 1470978 | 0.0109 | 2.0594 |
| chr12 | 133851895 | 1519115 | 0.0113 | 2.413 |
| chr13 | 115169878 | 927593 | 0.0081 | 2.8095 |
| chr14 | 107349540 | 2064191 | 0.0192 | 10.6456 |
| chr15 | 102531392 | 1202009 | 0.0117 | 2.1549 |
| chr16 | 90354753 | 552109 | 0.0061 | 0.8115 |
| chr17 | 81195210 | 1225572 | 0.0151 | 2.3825 |
| chr18 | 78077248 | 830465 | 0.0106 | 2.0957 |
| chr19 | 59128983 | 1010292 | 0.0171 | 1.9192 |
| chr20 | 63025520 | 1059620 | 0.0168 | 3.5017 |
| chr21 | 48129895 | 269759 | 0.0056 | 0.956 |
| chr22 | 51304566 | 244633 | 0.0048 | 0.6322 |
| chrMT | 16571 | 83403 | 5.0331 | 42.776 |
| chrX | 155270560 | 3089126 | 0.0199 | 2.3869 |
| chrY | 59373566 | 233346 | 0.0039 | 0.6982 |

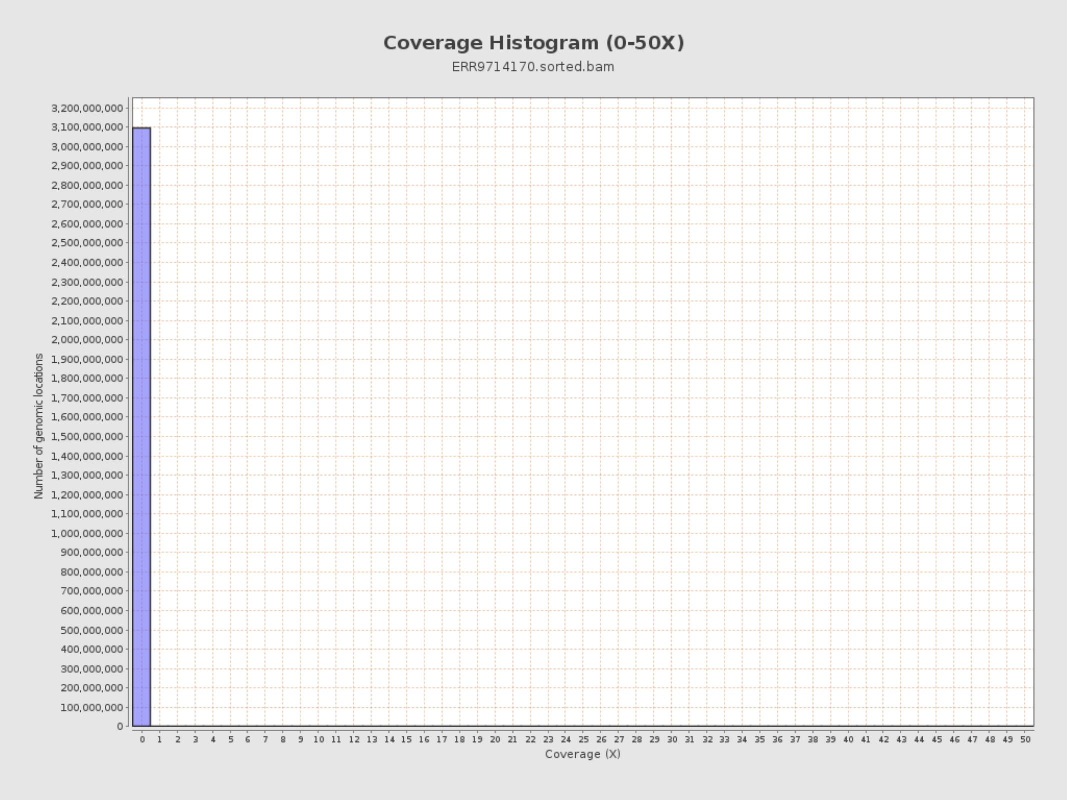
# 3. Results : Coverage across reference



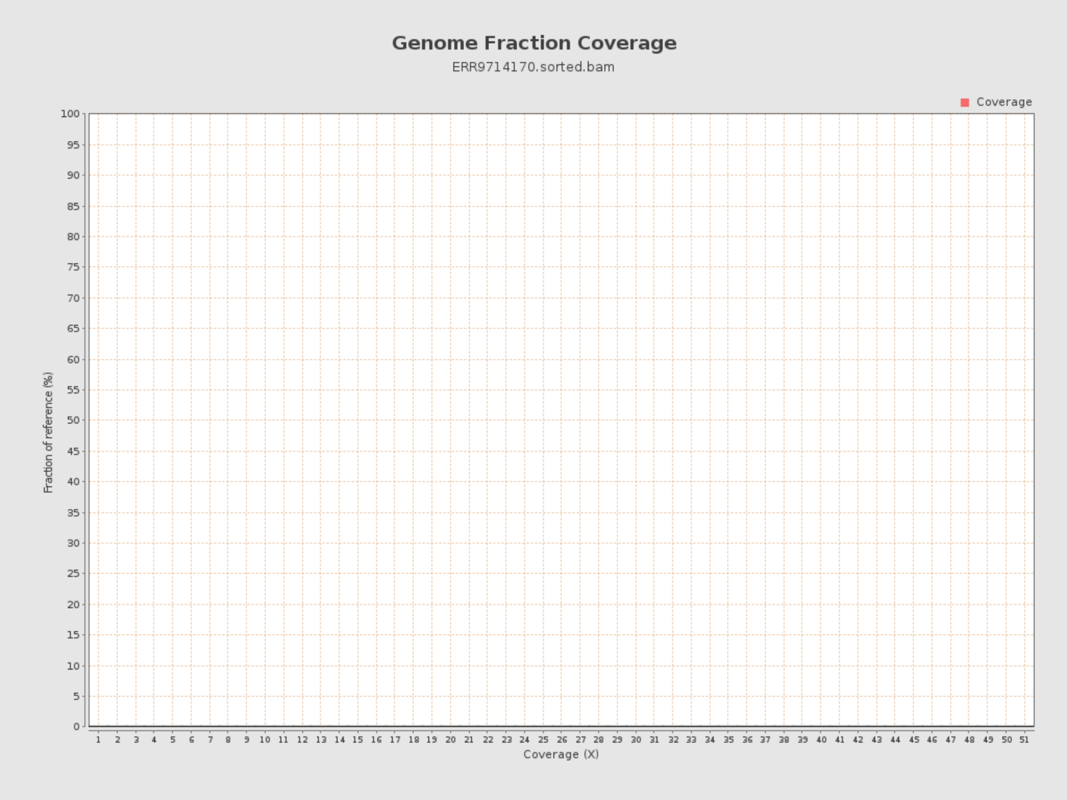
# 4. Results : Coverage Histogram



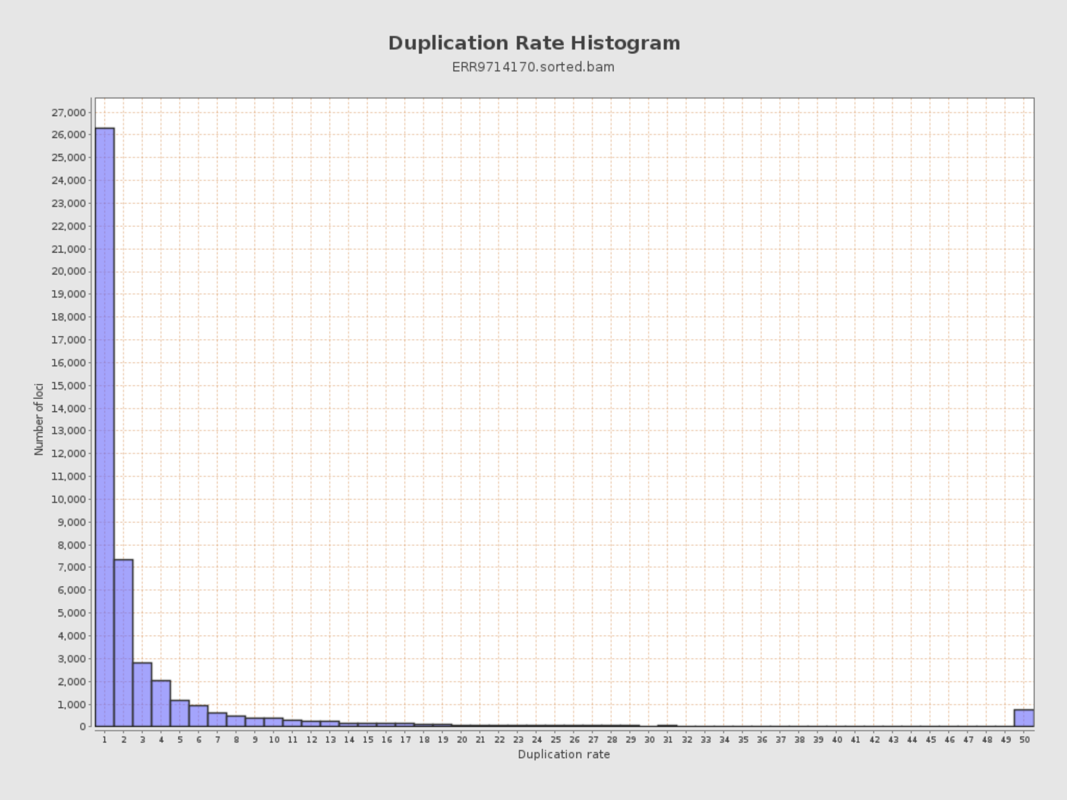
# 5. Results : Coverage Histogram (0-50X)



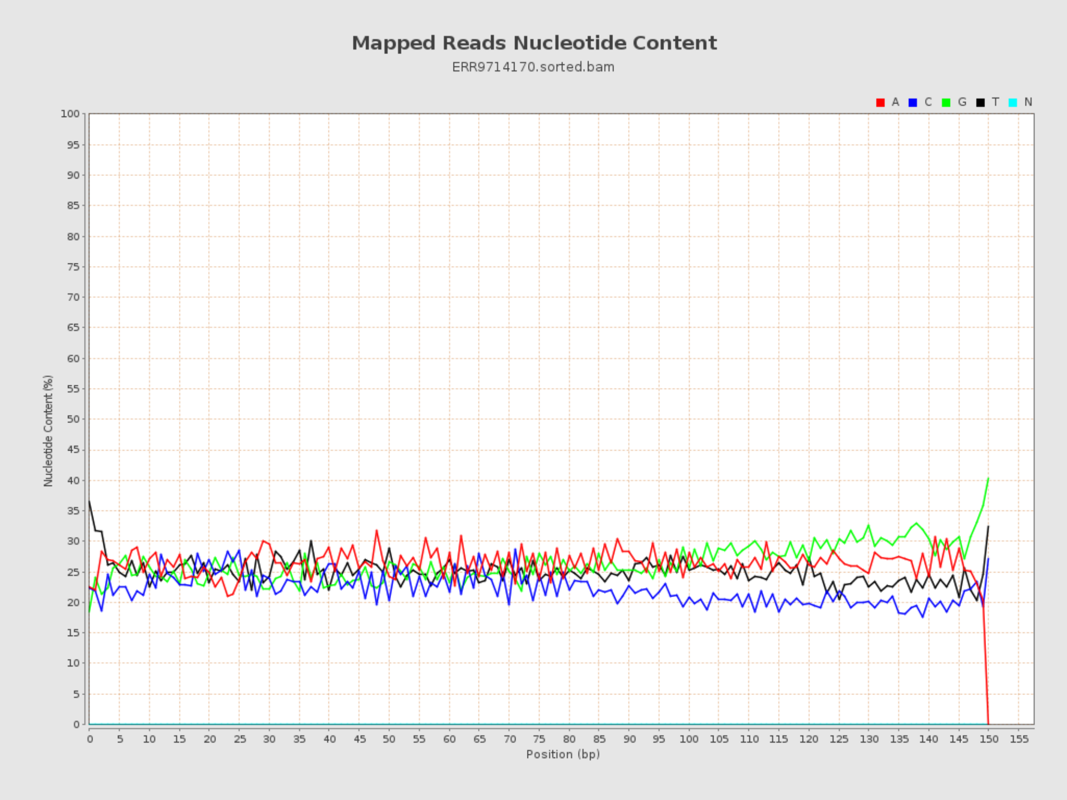
# 6. Results : Genome Fraction Coverage



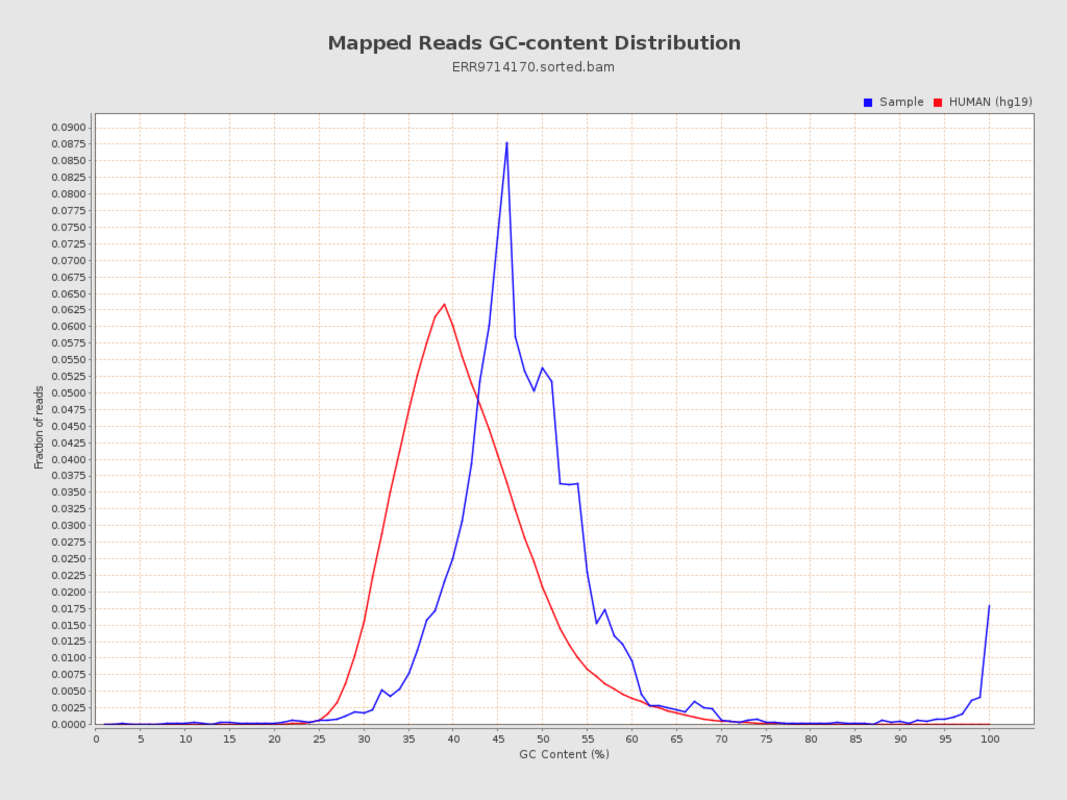
# 7. Results : Duplication Rate Histogram



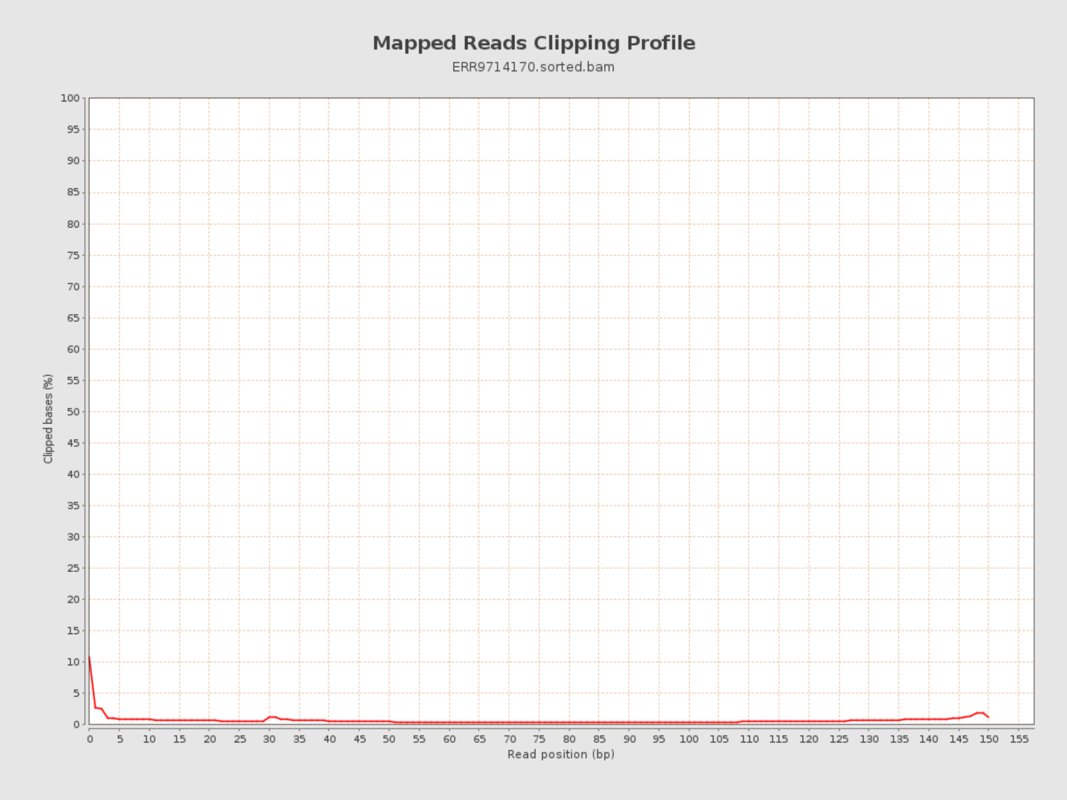
# 8. Results : Mapped Reads Nucleotide Content



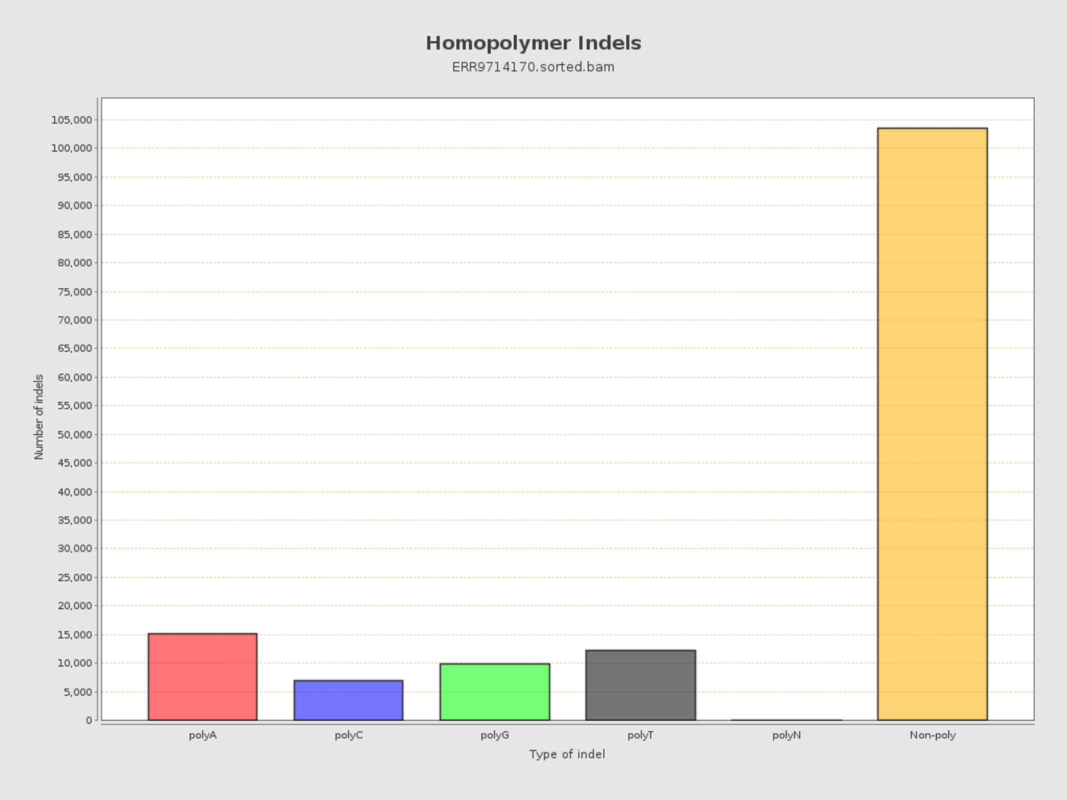
# 9. Results : Mapped Reads GC-content Distribution



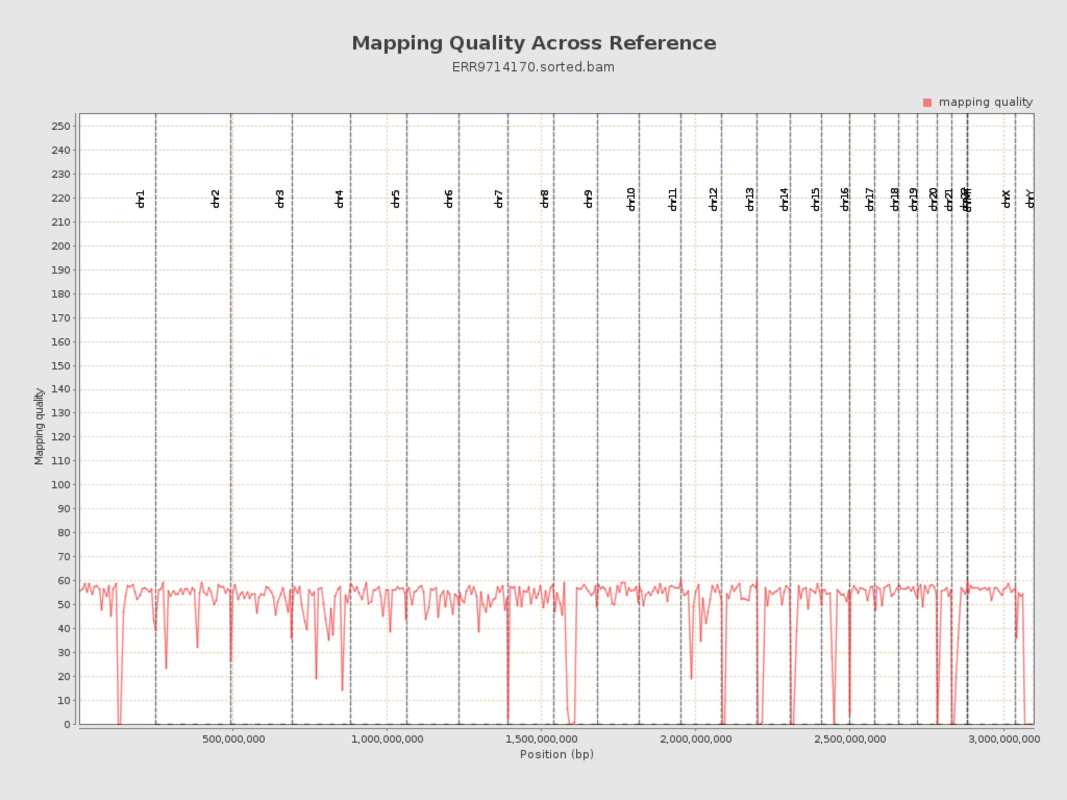
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram