# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/02 20:48:37*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714131.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_ERR9714131 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714131.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Oct 02 20:48:36 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | ERR9714131.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 655,936 |
| Mapped reads | 509,238 / 77.64% |
| Unmapped reads | 146,698 / 22.36% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 77,591 / 11.83% |
| Read min/max/mean length | 30 / 151 / 134.88 |
| Duplicated reads (estimated) | 575,902 / 87.8% |
| Duplication rate | 34.68% |
| Clipped reads | 572,359 / 87.26% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 11,283,779 / 19.59% |
| Number/percentage of C's | 10,533,751 / 18.29% |
| Number/percentage of T's | 11,872,599 / 20.61% |
| Number/percentage of G's | 23,916,108 / 41.52% |
| Number/percentage of N's | 351 / 0% |
| GC Percentage | 59.8% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0188 |
| | |

| | |
|---|---|
| Standard Deviation | 62.35 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 23.66 |

## 2.5. Mismatches and indels

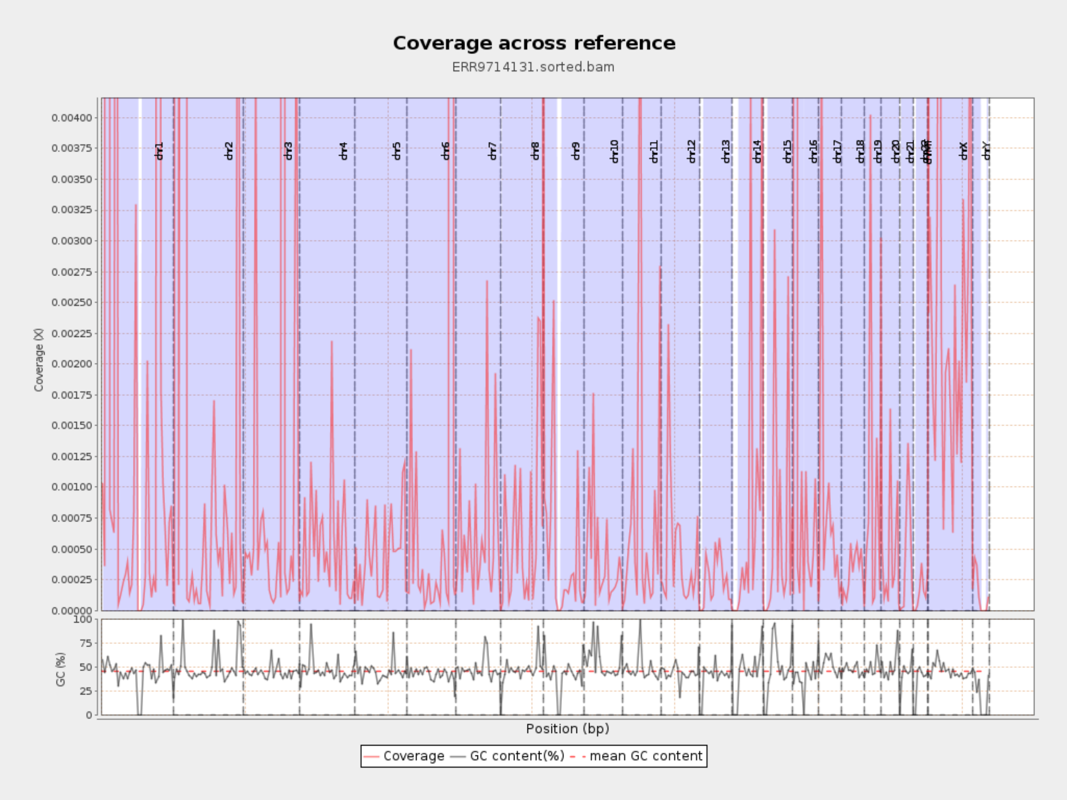
| | |
|---|---|
| General error rate | 2.99% |
| Mismatches | 1,655,204 |
| Insertions | 44,615 |
| Mapped reads with at least one insertion | 8.53% |
| Deletions | 65,553 |
| Mapped reads with at least one deletion | 12.34% |
| Homopolymer indels | 62.49% |

## 2.6. Chromosome stats

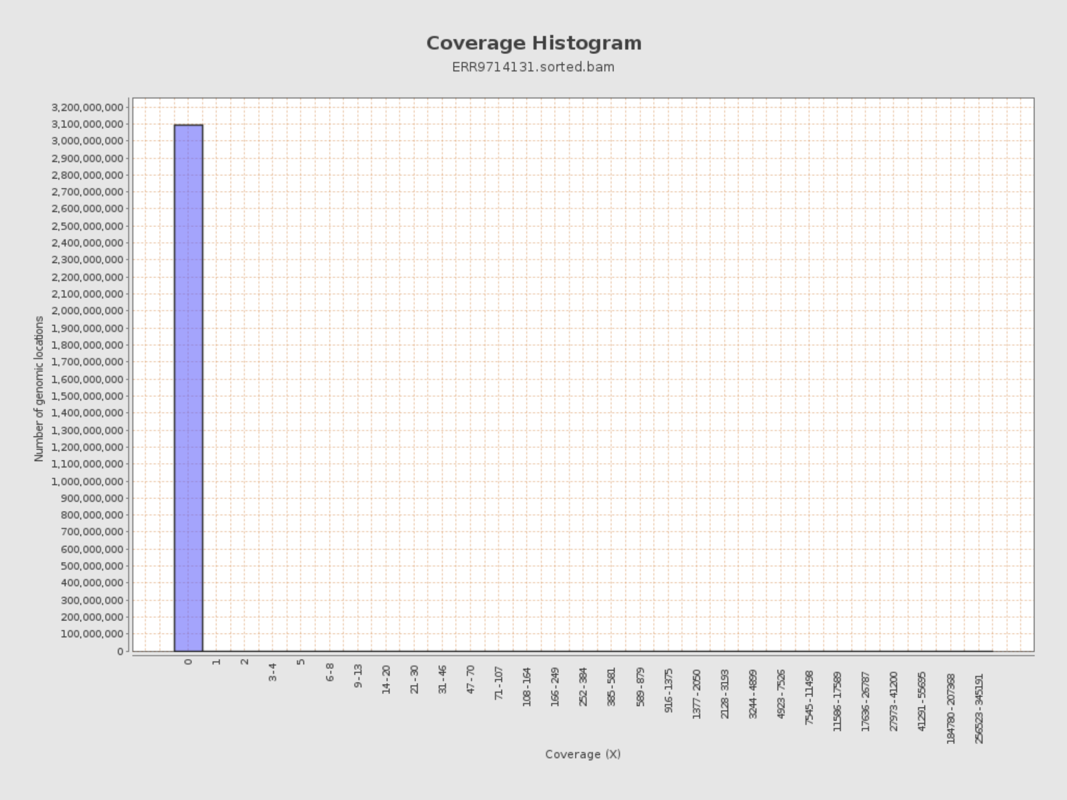
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 39354701 | 0.1579 | 215.5286 |
| chr2 | 243199373 | 7769395 | 0.0319 | 24.9447 |
| chr3 | 198022430 | 1426601 | 0.0072 | 7.1242 |
| chr4 | 191154276 | 100166 | 0.0005 | 0.2329 |
| chr5 | 180915260 | 89362 | 0.0005 | 0.106 |
| chr6 | 171115067 | 7482507 | 0.0437 | 41.4503 |
| chr7 | 159138663 | 102048 | 0.0006 | 0.2847 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 101078 | 0.0007 | 0.2669 |
| chr9 | 141213431 | 69513 | 0.0005 | 0.1232 |
| chr10 | 135534747 | 56621 | 0.0004 | 0.2248 |
| chr11 | 135006516 | 115341 | 0.0009 | 0.6899 |
| chr12 | 133851895 | 64985 | 0.0005 | 0.1845 |
| chr13 | 115169878 | 27992 | 0.0002 | 0.0476 |
| chr14 | 107349540 | 101809 | 0.0009 | 0.6163 |
| chr15 | 102531392 | 67145 | 0.0007 | 0.3835 |
| chr16 | 90354753 | 639347 | 0.0071 | 2.7457 |
| chr17 | 81195210 | 71567 | 0.0009 | 0.1622 |
| chr18 | 78077248 | 25766 | 0.0003 | 0.061 |
| chr19 | 59128983 | 60065 | 0.001 | 0.1867 |
| chr20 | 63025520 | 30480 | 0.0005 | 0.1726 |
| chr21 | 48129895 | 23202 | 0.0005 | 0.2283 |
| chr22 | 51304566 | 7323 | 0.0001 | 0.0259 |
| chrMT | 16571 | 20232 | 1.2209 | 10.4183 |
| chrX | 155270560 | 395506 | 0.0025 | 0.3594 |
| chrY | 59373566 | 8869 | 0.0001 | 0.0355 |

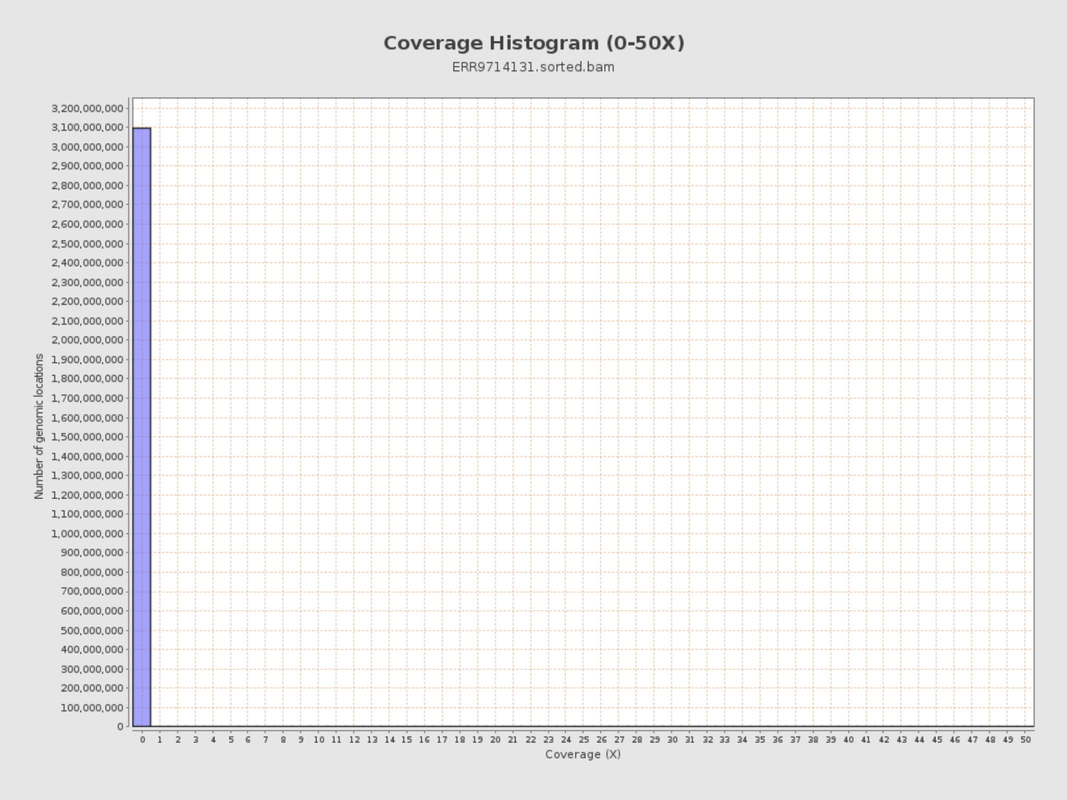
# 3. Results : Coverage across reference



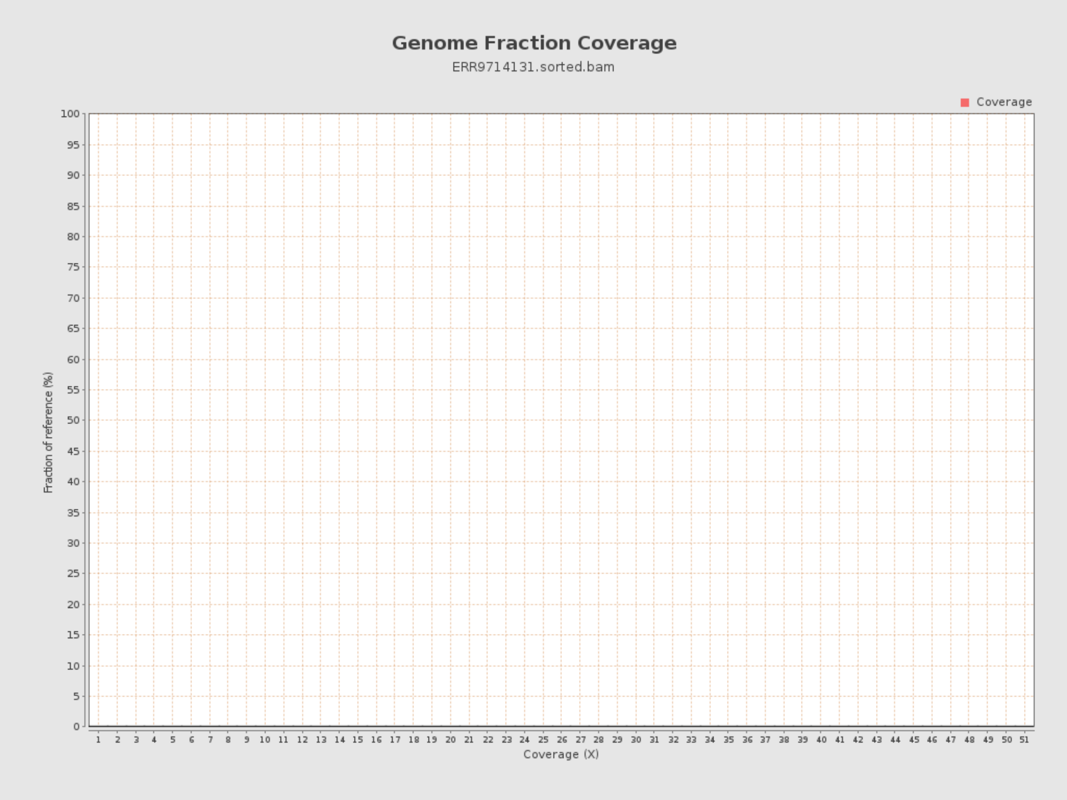
# 4. Results : Coverage Histogram



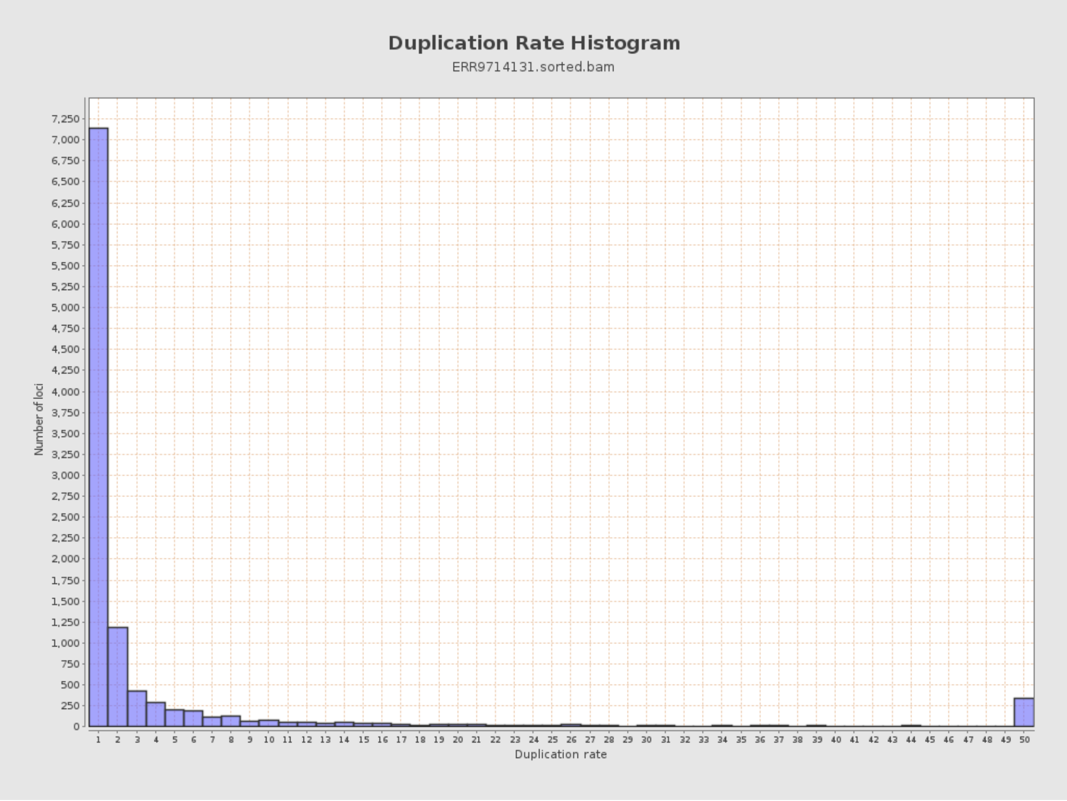
# 5. Results : Coverage Histogram (0-50X)



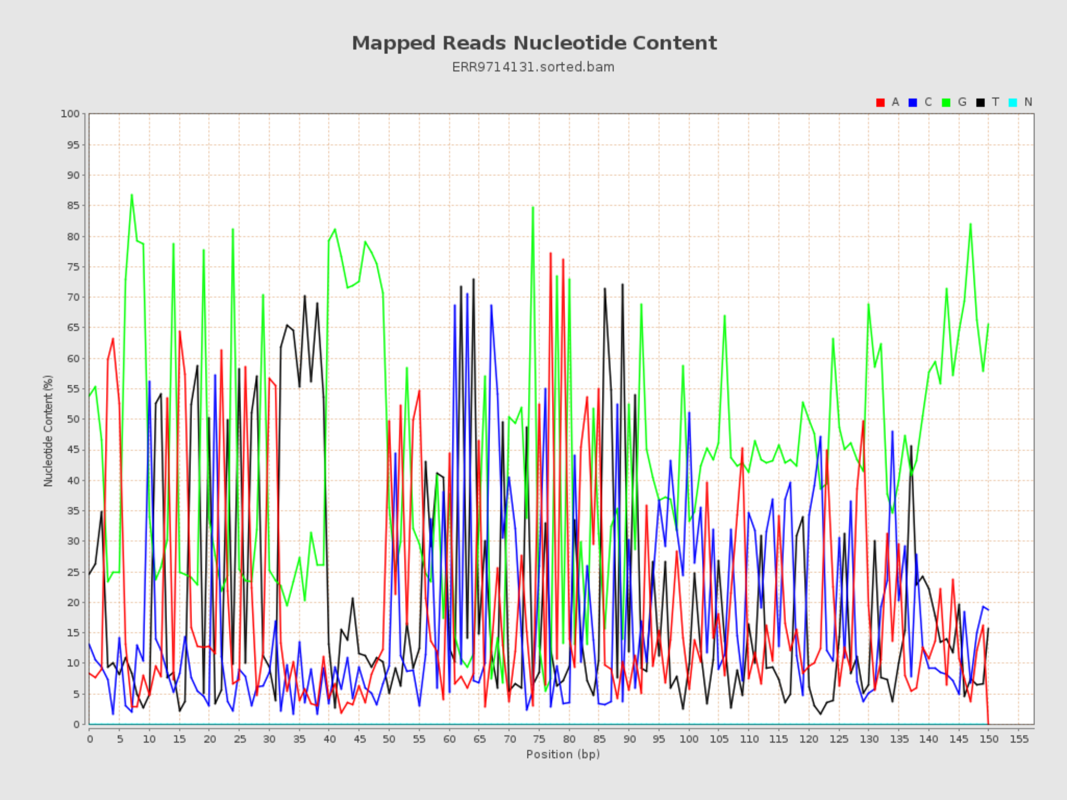
# 6. Results : Genome Fraction Coverage



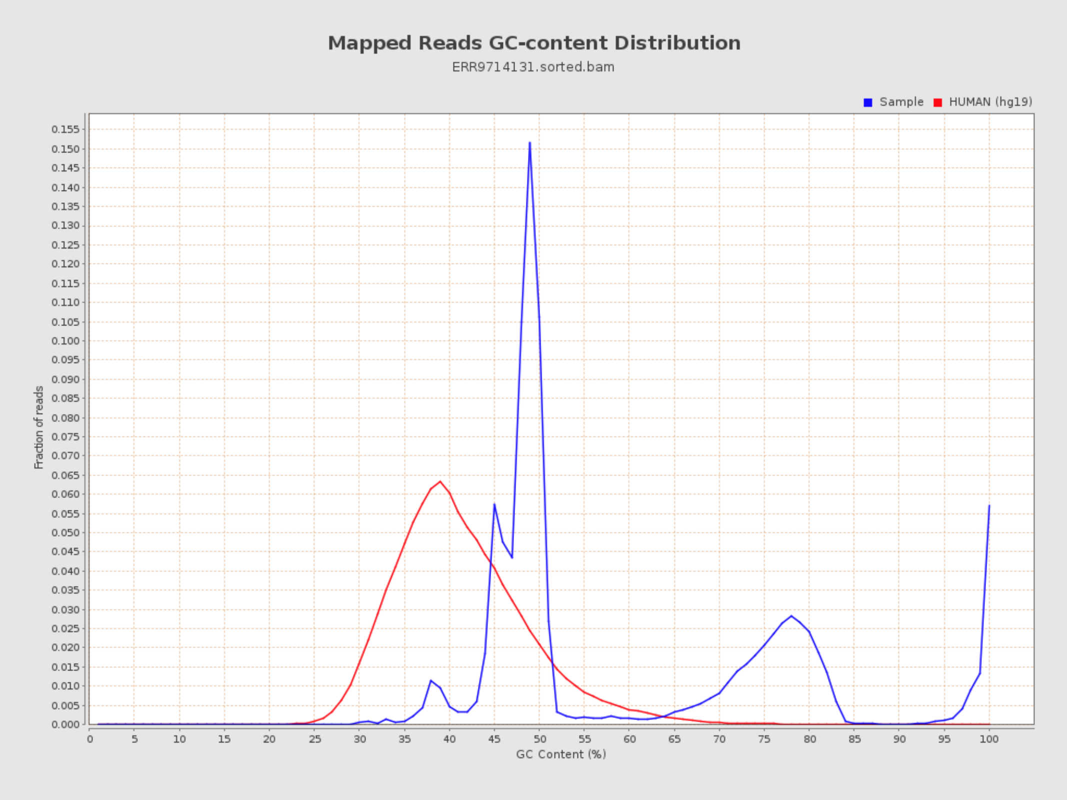
# 7. Results : Duplication Rate Histogram



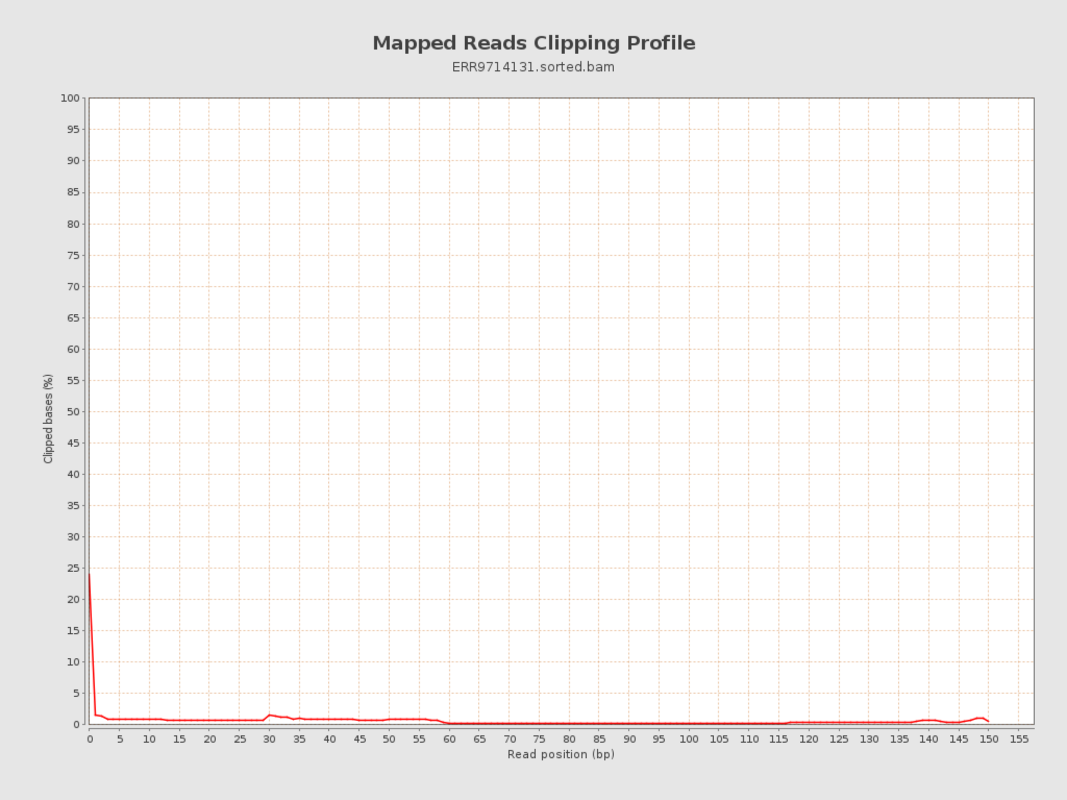
# 8. Results : Mapped Reads Nucleotide Content



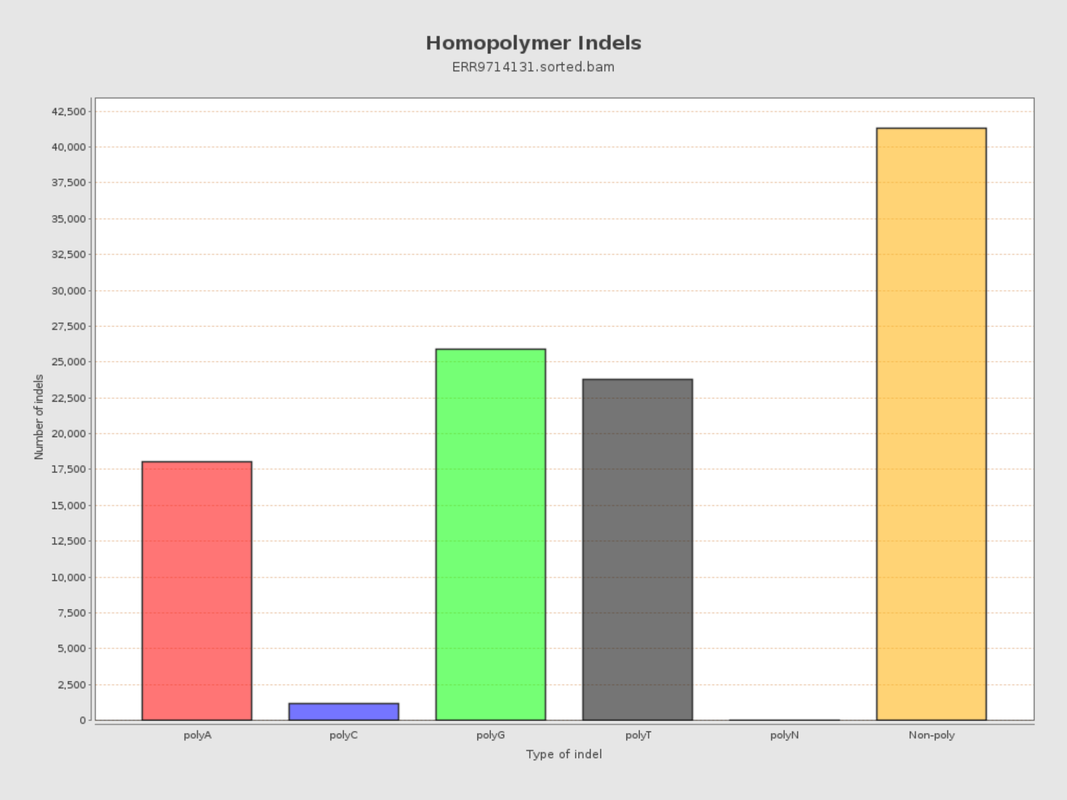
# 9. Results : Mapped Reads GC-content Distribution



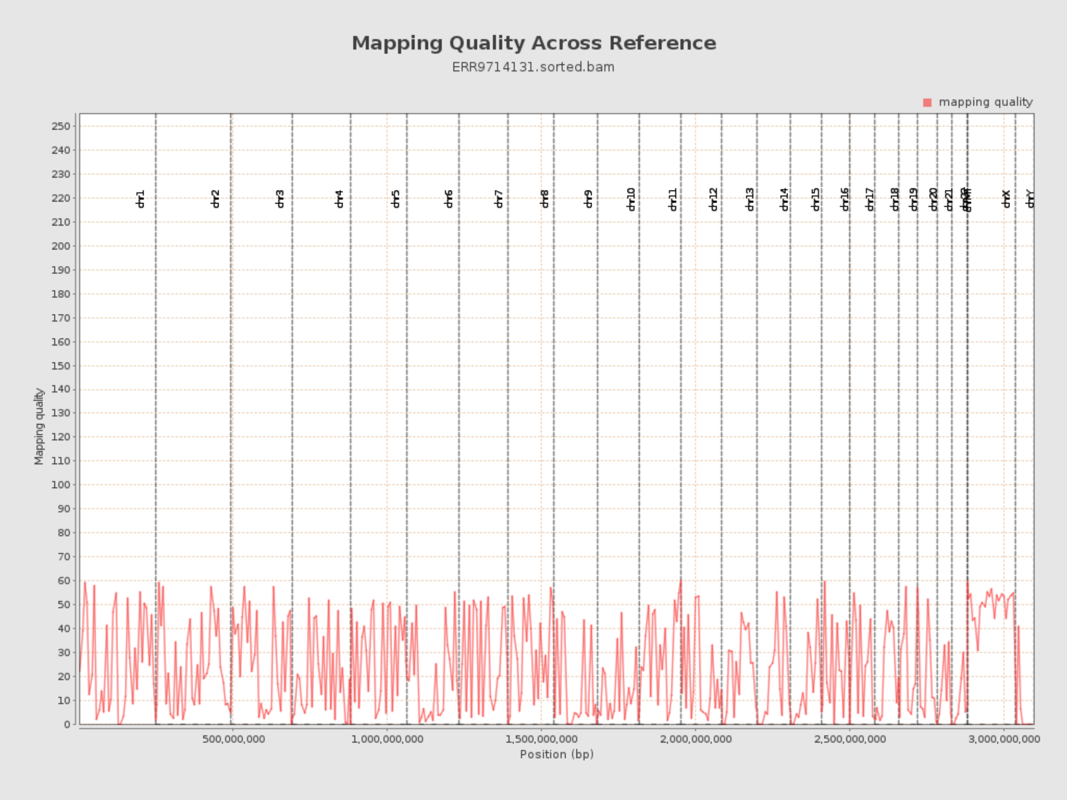
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram