# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/02 23:50:55*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR9714192.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_ERR9714192 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR9714192.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Oct 02 23:50:54 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | ERR9714192.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,480 |
| Mapped reads | 1,521 / 33.95% |
| Unmapped reads | 2,959 / 66.05% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 76 / 1.7% |
| Read min/max/mean length | 30 / 151 / 94.33 |
| Duplicated reads (estimated) | 739 / 16.5% |
| Duplication rate | 34.97% |
| Clipped reads | 1,314 / 29.33% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 42,660 / 24.52% |
| Number/percentage of C's | 35,214 / 20.24% |
| Number/percentage of T's | 39,789 / 22.87% |
| Number/percentage of G's | 56,298 / 32.36% |
| Number/percentage of N's | 4 / 0% |
| GC Percentage | 52.6% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0001 |
| | |

| | |
|---|---|
| Standard Deviation | 0.0328 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 19.69 |

## 2.5. Mismatches and indels

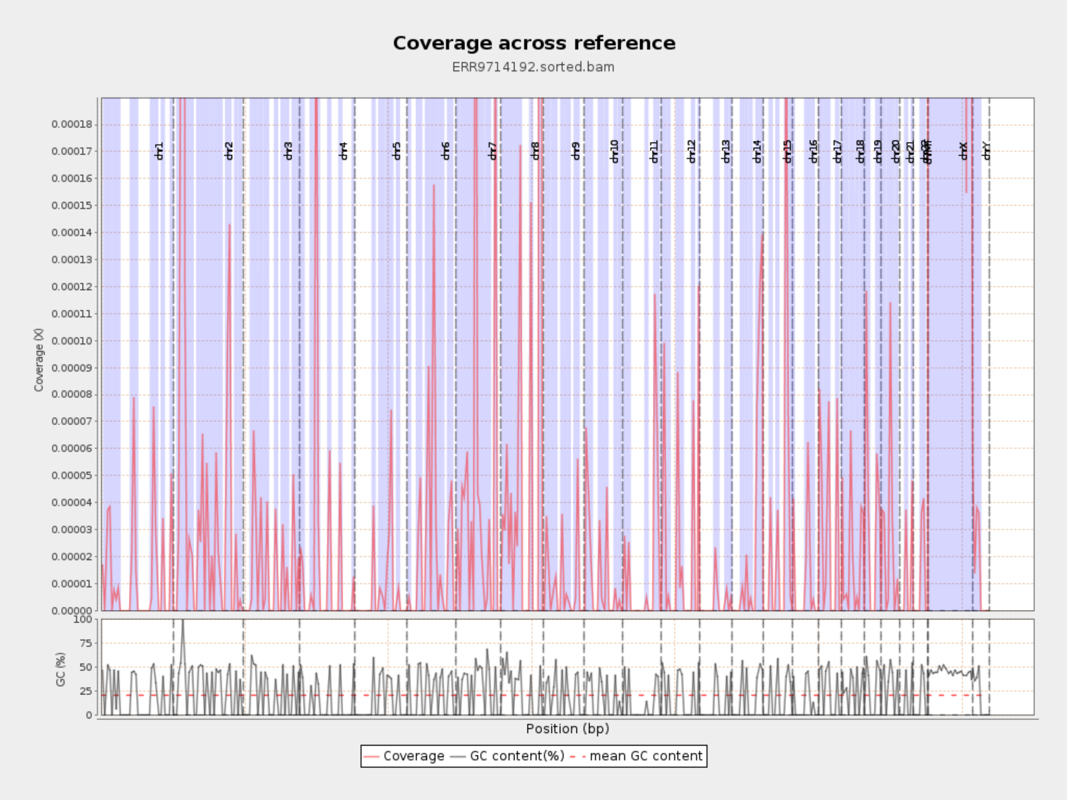
| | |
|---|---|
| General error rate | 3.87% |
| Mismatches | 6,477 |
| Insertions | 90 |
| Mapped reads with at least one insertion | 5.13% |
| Deletions | 488 |
| Mapped reads with at least one deletion | 31.1% |
| Homopolymer indels | 26.82% |

## 2.6. Chromosome stats

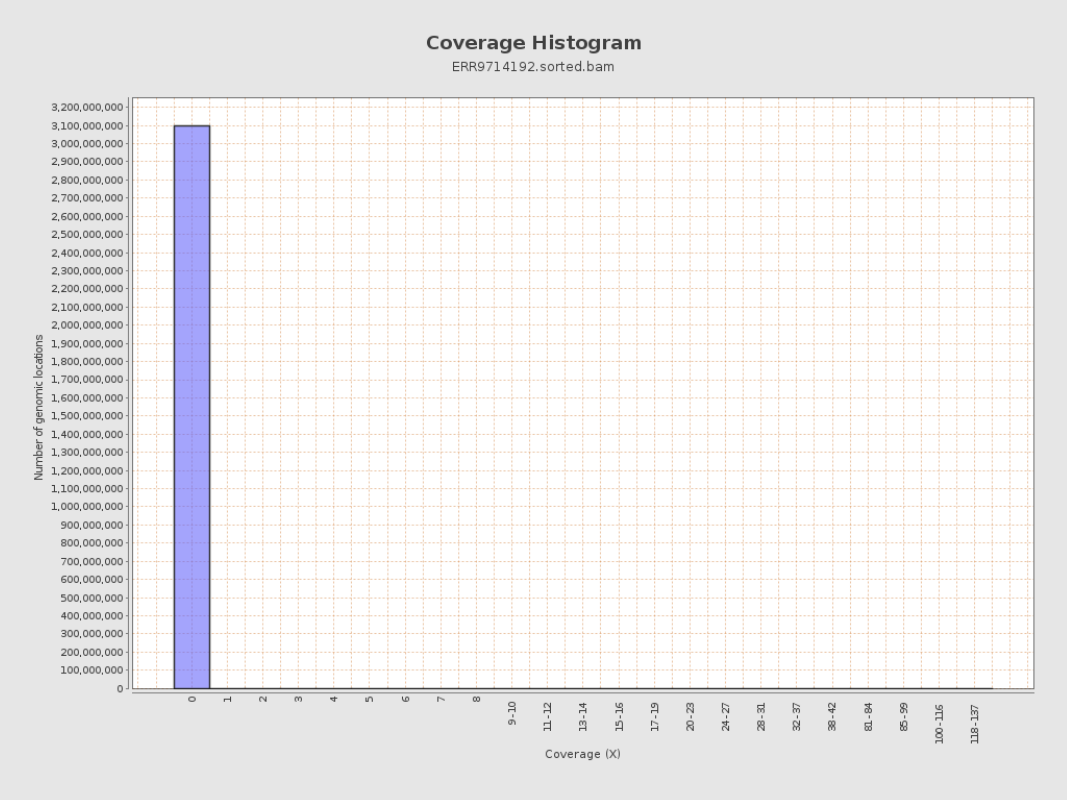
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3270 | 0 | 0.006 |
| chr2 | 243199373 | 28827 | 0.0001 | 0.0913 |
| chr3 | 198022430 | 2735 | 0 | 0.005 |
| chr4 | 191154276 | 3669 | 0 | 0.0082 |
| chr5 | 180915260 | 1402 | 0 | 0.0044 |
| chr6 | 171115067 | 3923 | 0 | 0.0094 |
| chr7 | 159138663 | 7082 | 0 | 0.0198 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 11021 | 0.0001 | 0.0429 |
| chr9 | 141213431 | 1392 | 0 | 0.0048 |
| chr10 | 135534747 | 1680 | 0 | 0.0055 |
| chr11 | 135006516 | 1731 | 0 | 0.0061 |
| chr12 | 133851895 | 2780 | 0 | 0.0095 |
| chr13 | 115169878 | 342 | 0 | 0.002 |
| chr14 | 107349540 | 2873 | 0 | 0.0095 |
| chr15 | 102531392 | 3088 | 0 | 0.0144 |
| chr16 | 90354753 | 854 | 0 | 0.0047 |
| chr17 | 81195210 | 2309 | 0 | 0.0085 |
| chr18 | 78077248 | 1431 | 0 | 0.007 |
| chr19 | 59128983 | 1933 | 0 | 0.011 |
| chr20 | 63025520 | 1750 | 0 | 0.0077 |
| chr21 | 48129895 | 527 | 0 | 0.0041 |
| chr22 | 51304566 | 602 | 0 | 0.0046 |
| chrMT | 16571 | 453 | 0.0273 | 0.204 |
| chrX | 155270560 | 91117 | 0.0006 | 0.0733 |
| chrY | 59373566 | 983 | 0 | 0.0057 |

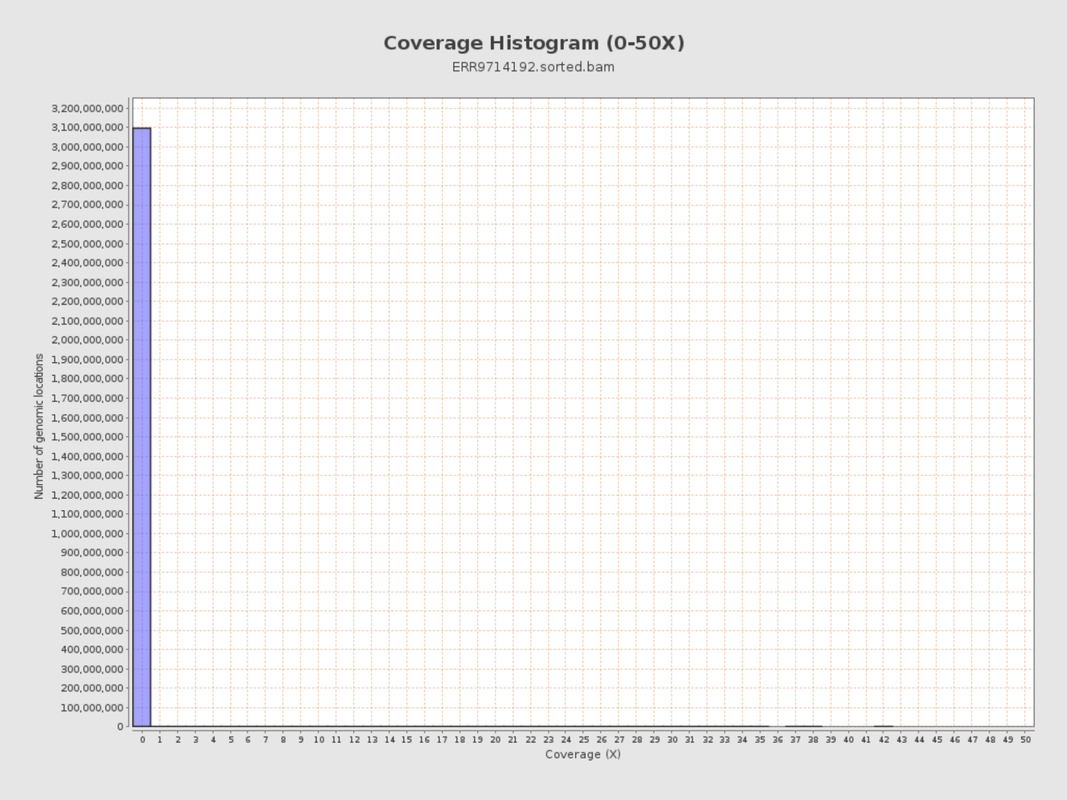
# 3. Results : Coverage across reference



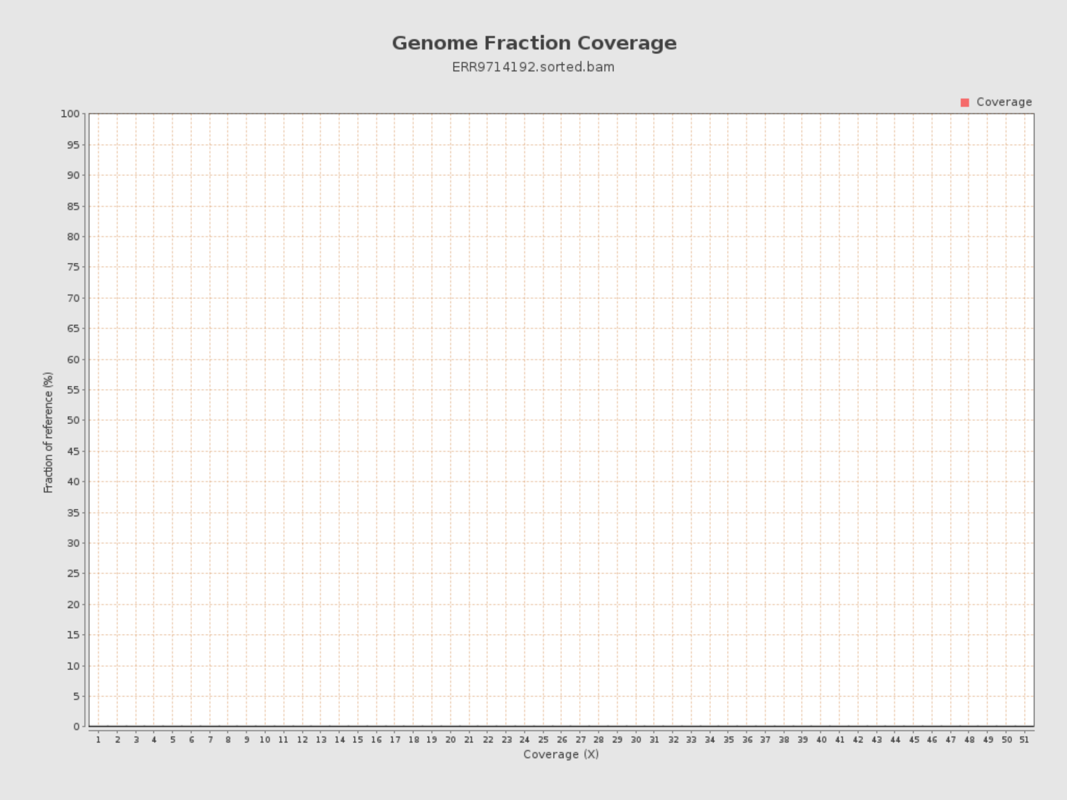
# 4. Results : Coverage Histogram



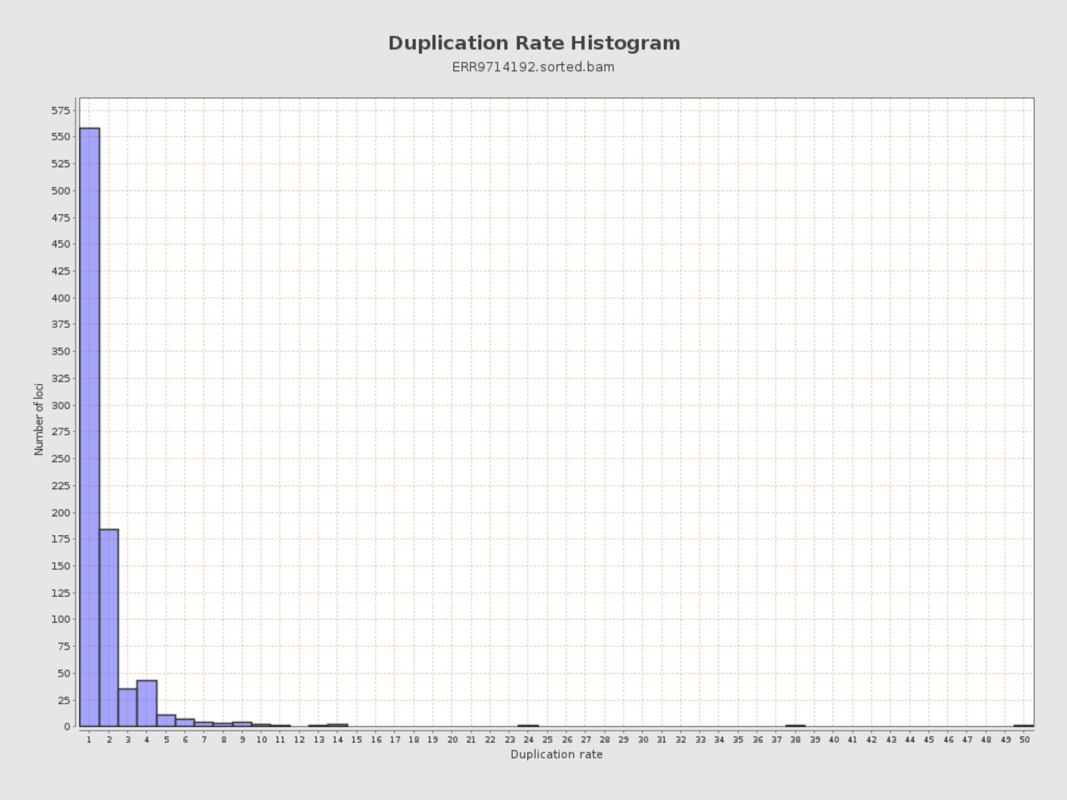
# 5. Results : Coverage Histogram (0-50X)



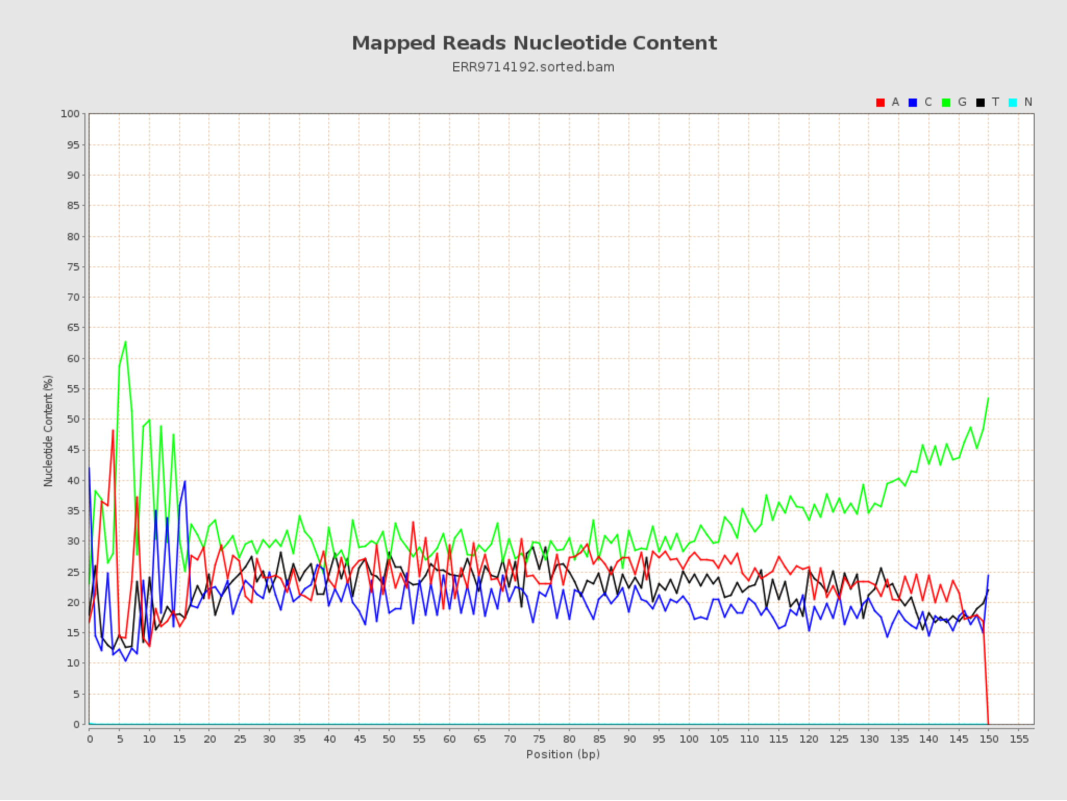
# 6. Results : Genome Fraction Coverage



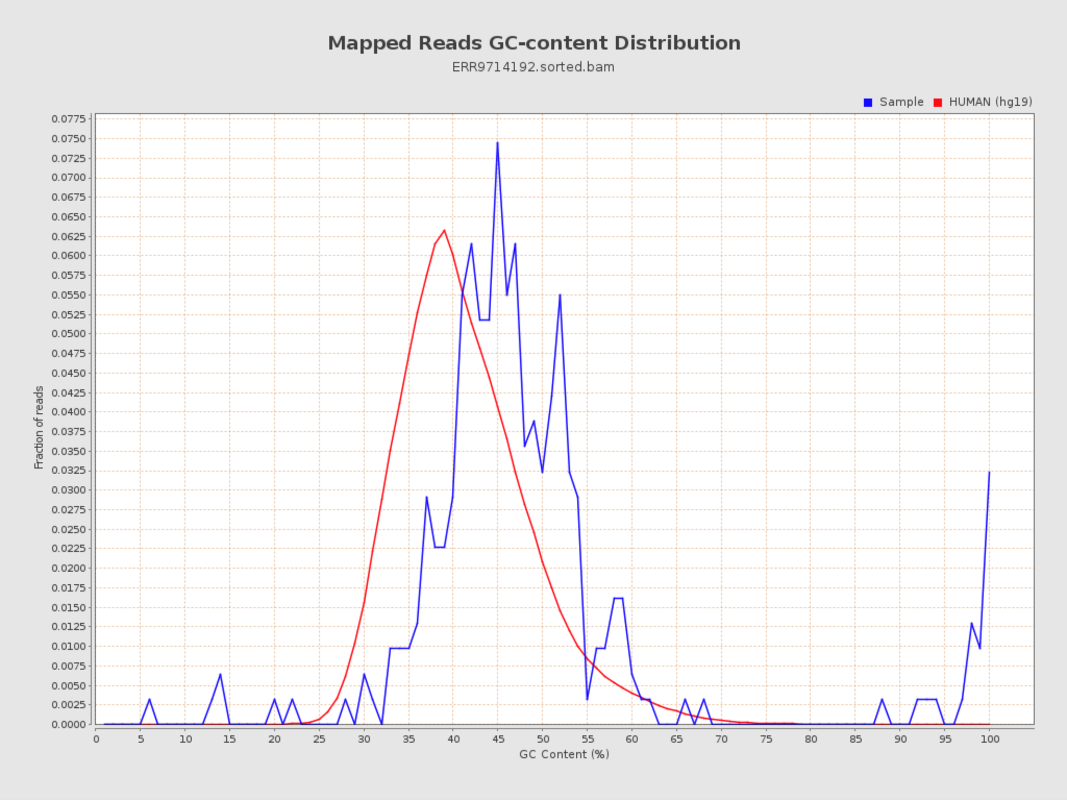
# 7. Results : Duplication Rate Histogram



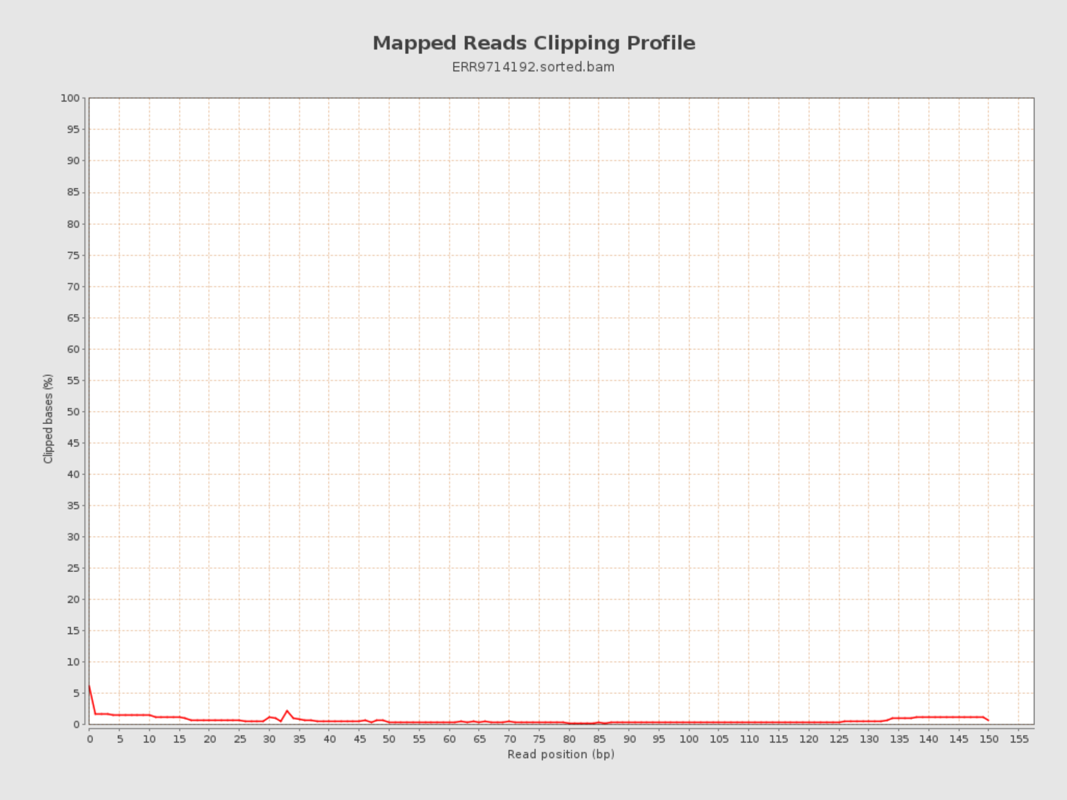
# 8. Results : Mapped Reads Nucleotide Content



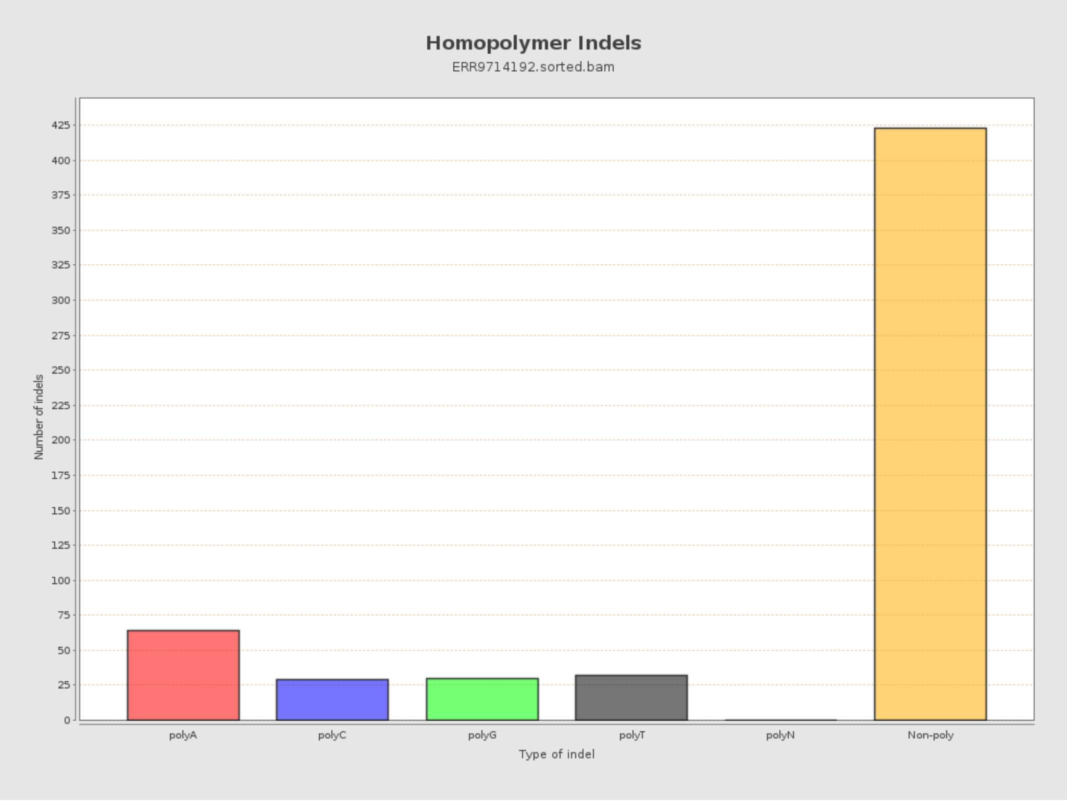
# 9. Results : Mapped Reads GC-content Distribution



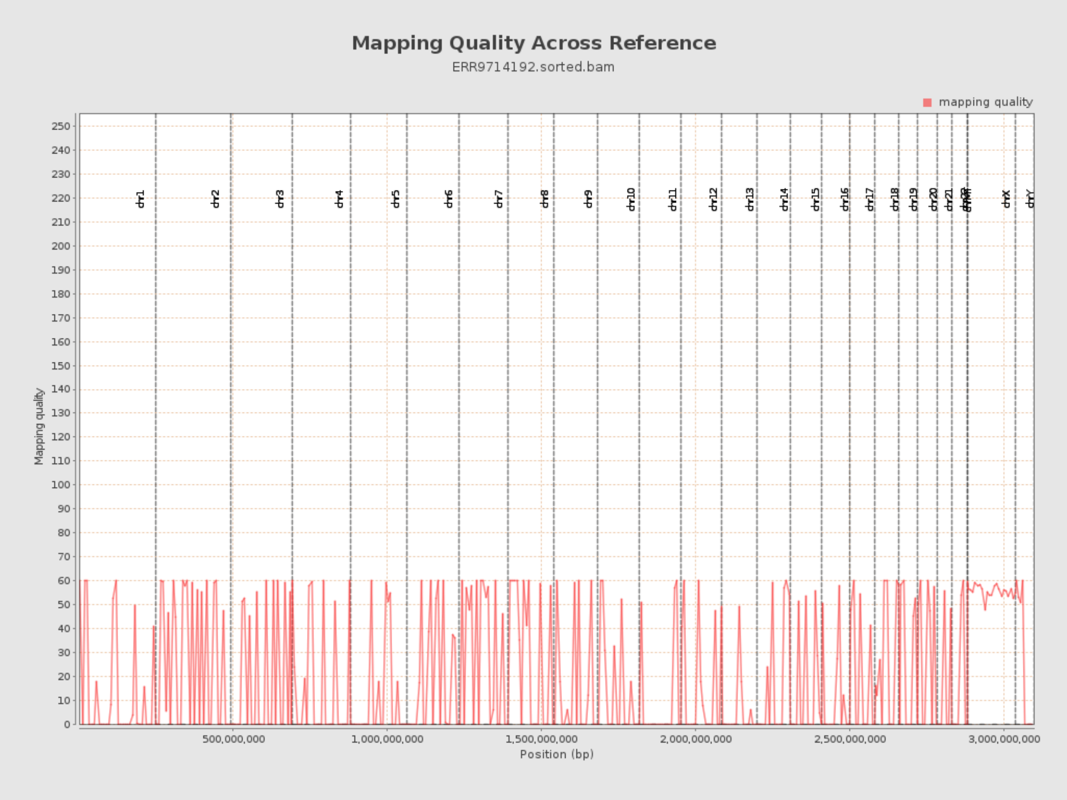
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram