# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 07:36:20*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524515.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_SRR10524515 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524515.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 07:36:05 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524515.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,124,212 |
| Mapped reads | 1,032,537 / 91.85% |
| Unmapped reads | 91,675 / 8.15% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 4,082 / 0.36% |
| Read min/max/mean length | 30 / 76 / 76.12 |
| Duplicated reads (estimated) | 55,176 / 4.91% |
| Duplication rate | 4.24% |
| Clipped reads | 1,032,635 / 91.85% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 14,980,202 / 24.81% |
| Number/percentage of C's | 11,404,193 / 18.89% |
| Number/percentage of T's | 19,373,772 / 32.08% |
| Number/percentage of G's | 14,624,393 / 24.22% |
| Number/percentage of N's | 896 / 0% |
| GC Percentage | 43.11% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0195 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2114 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.02 |

## 2.5. Mismatches and indels

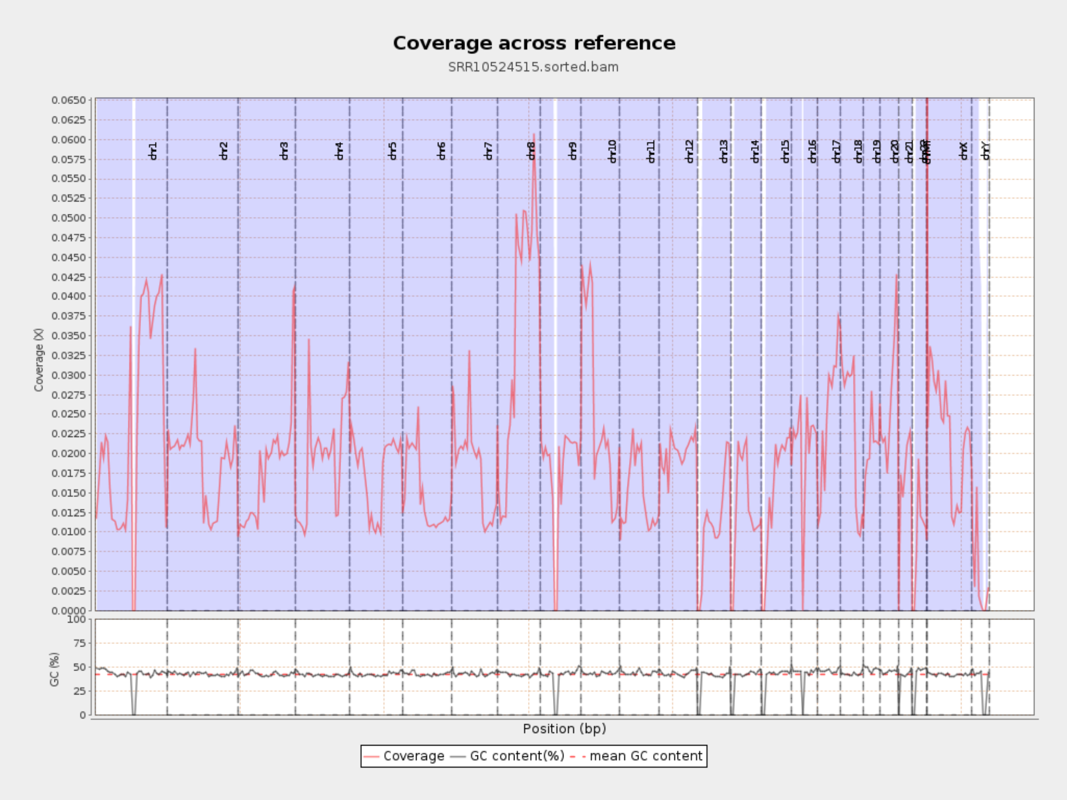
| | |
|---|---|
| General error rate | 0.53% |
| Mismatches | 309,021 |
| Insertions | 4,891 |
| Mapped reads with at least one insertion | 0.47% |
| Deletions | 11,219 |
| Mapped reads with at least one deletion | 1.08% |
| Homopolymer indels | 40.38% |

## 2.6. Chromosome stats

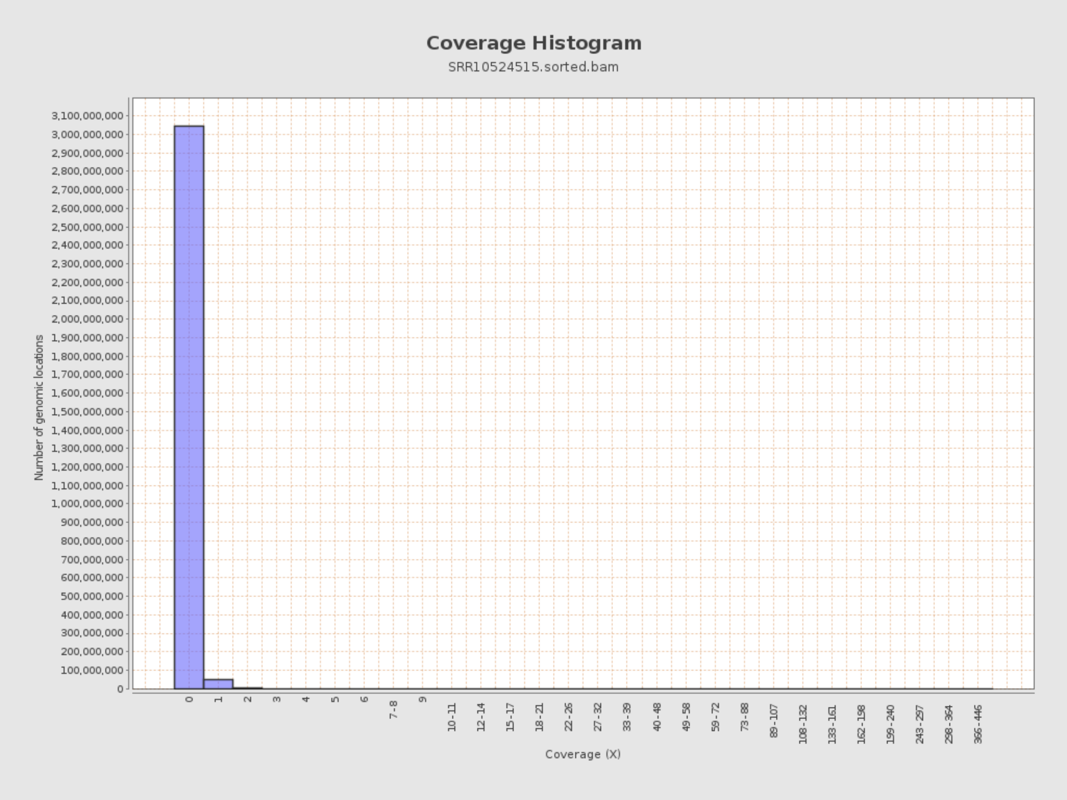
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5763149 | 0.0231 | 0.3666 |
| chr2 | 243199373 | 4685753 | 0.0193 | 0.2583 |
| chr3 | 198022430 | 3538504 | 0.0179 | 0.1494 |
| chr4 | 191154276 | 3714236 | 0.0194 | 0.1804 |
| chr5 | 180915260 | 3217520 | 0.0178 | 0.1499 |
| chr6 | 171115067 | 2509117 | 0.0147 | 0.1564 |
| chr7 | 159138663 | 2947159 | 0.0185 | 0.2339 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 5285736 | 0.0361 | 0.2489 |
| chr9 | 141213431 | 2508542 | 0.0178 | 0.1739 |
| chr10 | 135534747 | 3548733 | 0.0262 | 0.2478 |
| chr11 | 135006516 | 2000495 | 0.0148 | 0.1717 |
| chr12 | 133851895 | 2715829 | 0.0203 | 0.1601 |
| chr13 | 115169878 | 1291225 | 0.0112 | 0.1175 |
| chr14 | 107349540 | 1397278 | 0.013 | 0.1283 |
| chr15 | 102531392 | 1550435 | 0.0151 | 0.1366 |
| chr16 | 90354753 | 1852558 | 0.0205 | 0.1684 |
| chr17 | 81195210 | 2036054 | 0.0251 | 0.1849 |
| chr18 | 78077248 | 1839295 | 0.0236 | 0.285 |
| chr19 | 59128983 | 1229944 | 0.0208 | 0.2747 |
| chr20 | 63025520 | 1708664 | 0.0271 | 0.1872 |
| chr21 | 48129895 | 820729 | 0.0171 | 0.1639 |
| chr22 | 51304566 | 483863 | 0.0094 | 0.1073 |
| chrMT | 16571 | 2717 | 0.164 | 0.4058 |
| chrX | 155270560 | 3518916 | 0.0227 | 0.1786 |
| chrY | 59373566 | 235953 | 0.004 | 0.1511 |

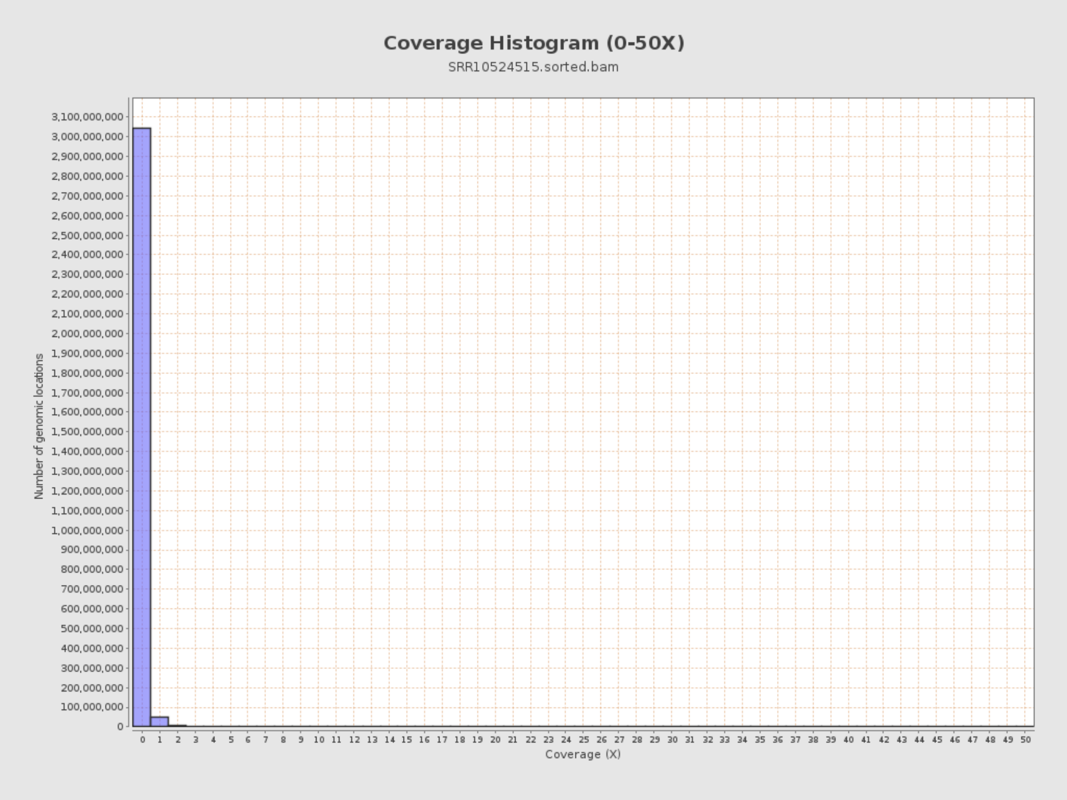
# 3. Results : Coverage across reference



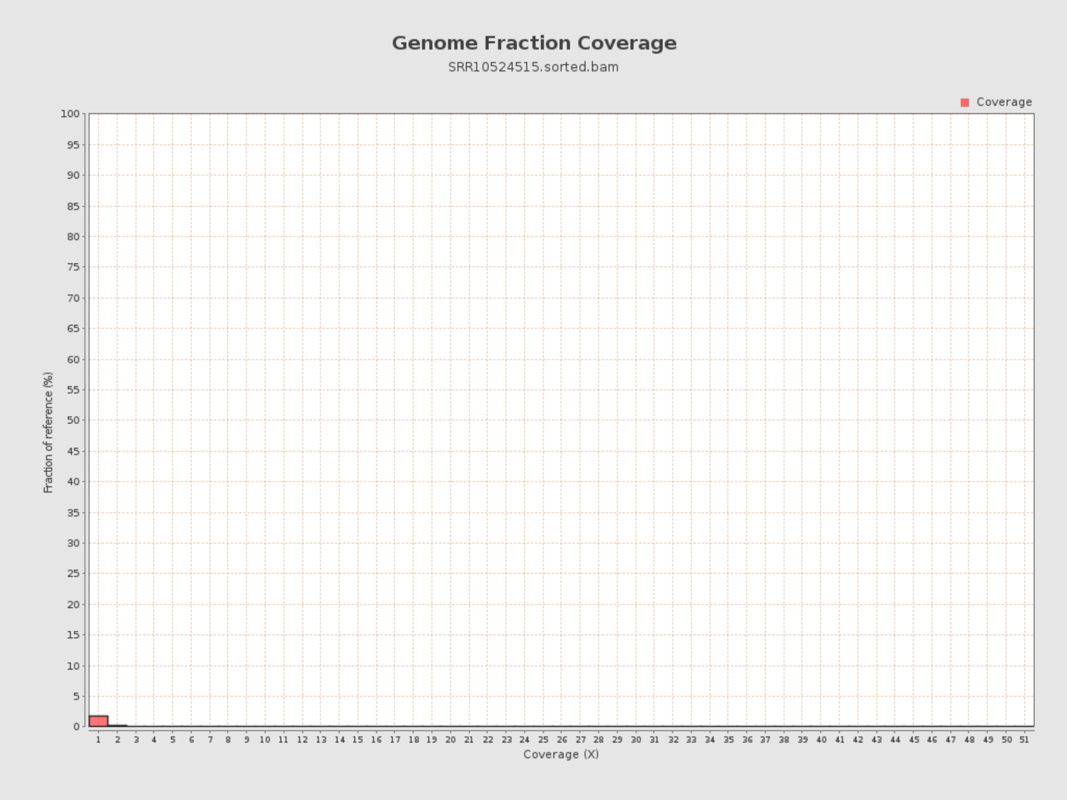
# 4. Results : Coverage Histogram



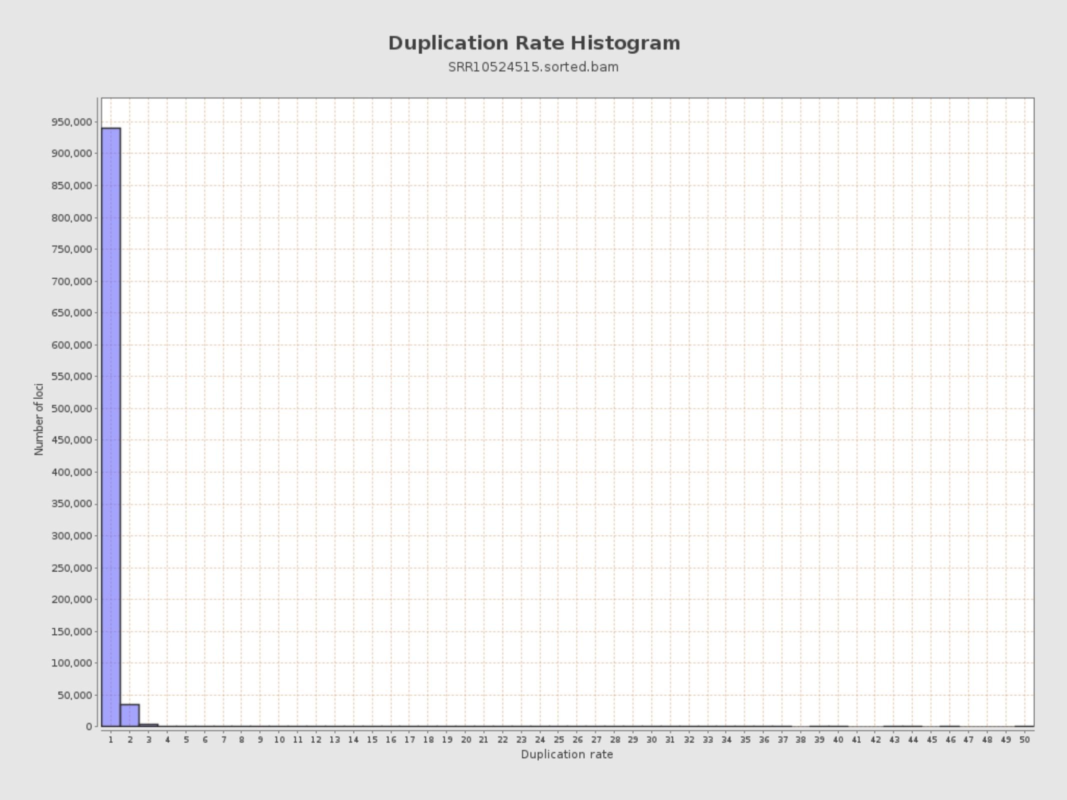
# 5. Results : Coverage Histogram (0-50X)



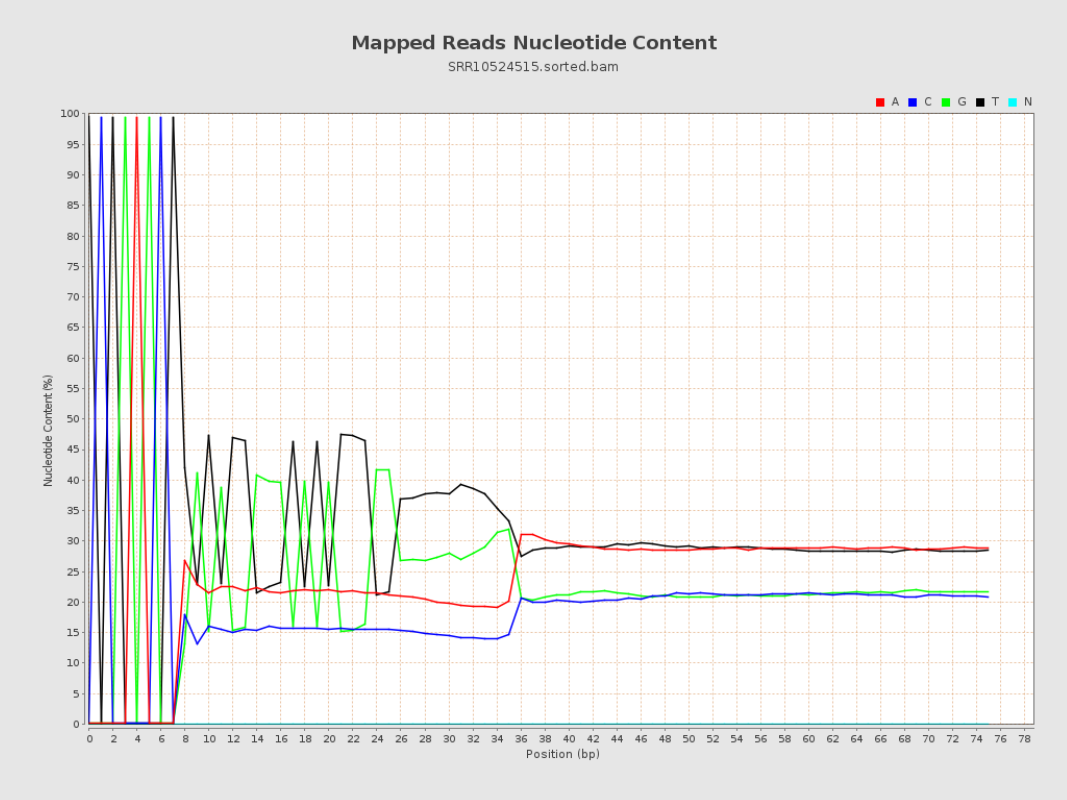
# 6. Results : Genome Fraction Coverage



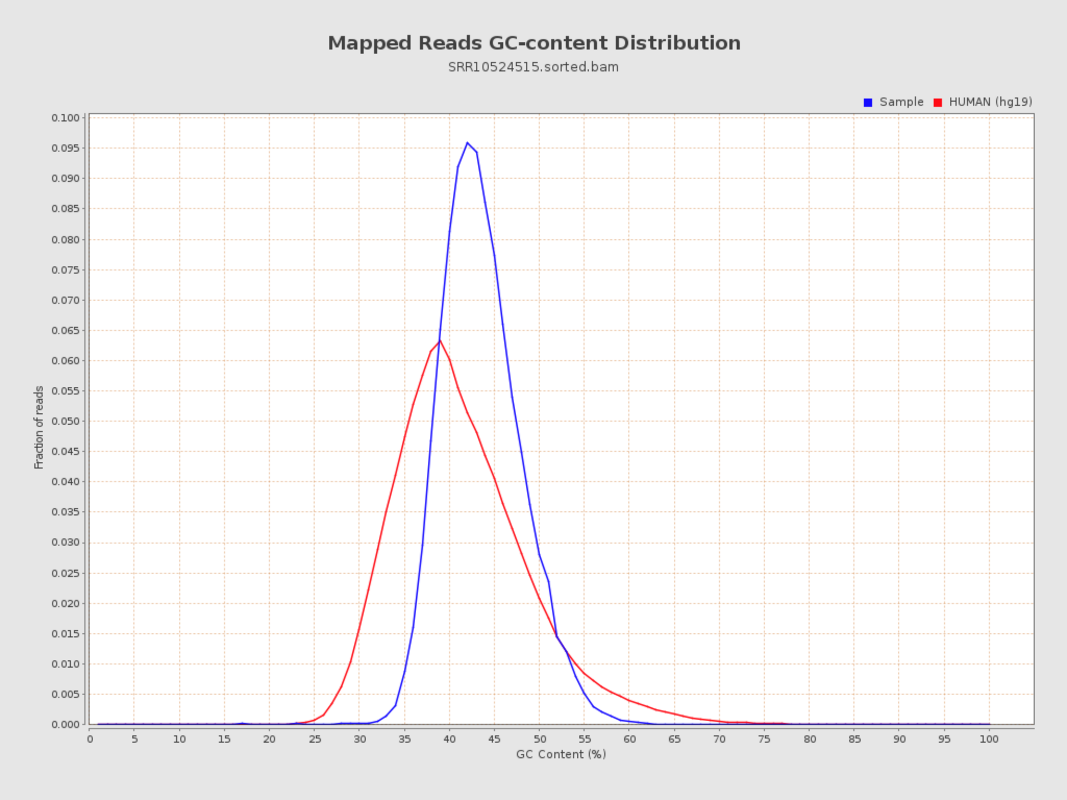
# 7. Results : Duplication Rate Histogram



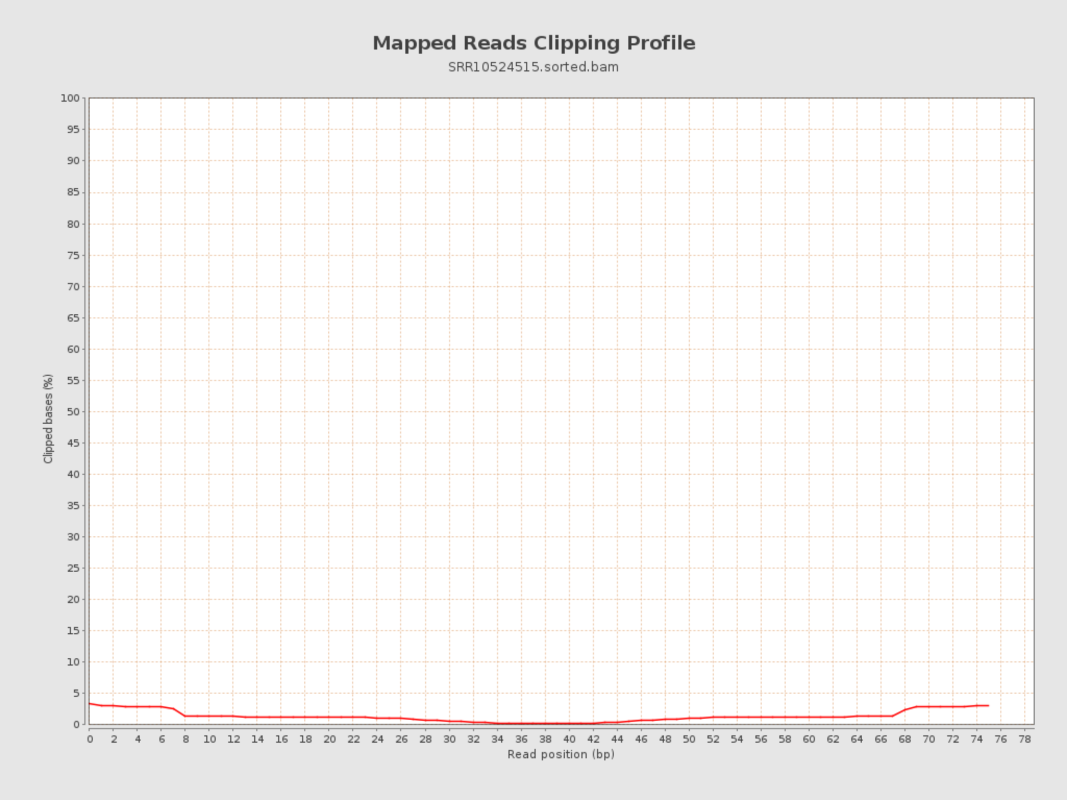
# 8. Results : Mapped Reads Nucleotide Content



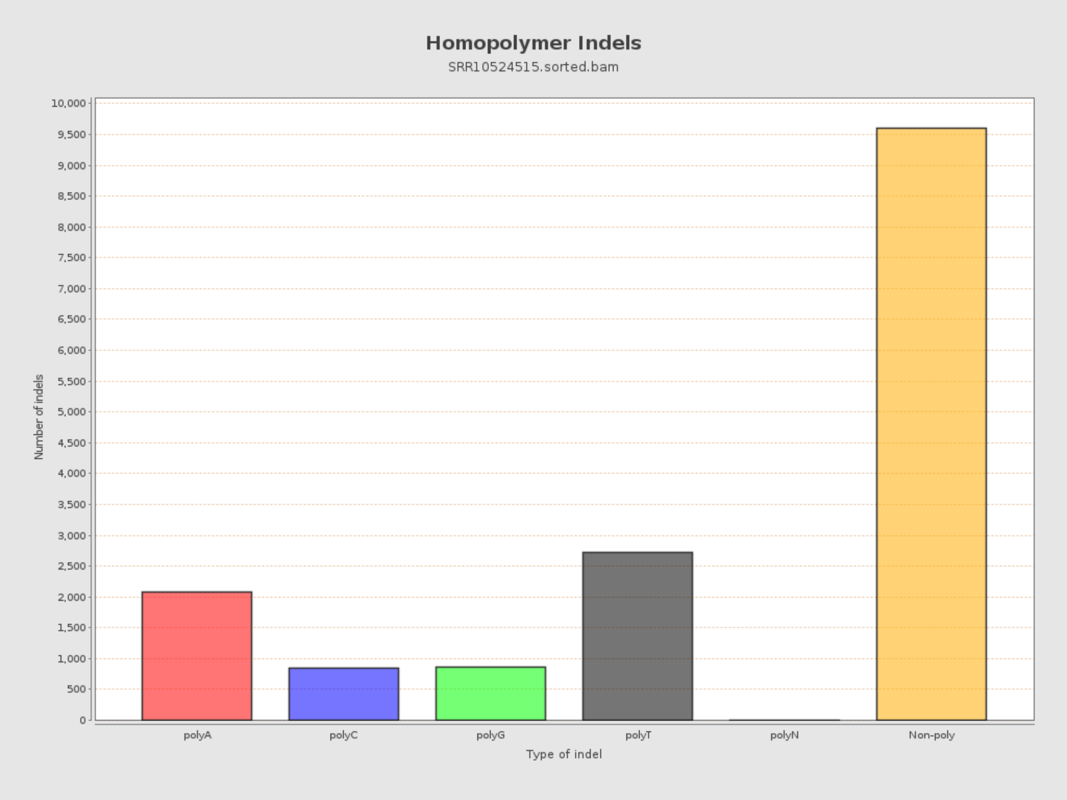
# 9. Results : Mapped Reads GC-content Distribution



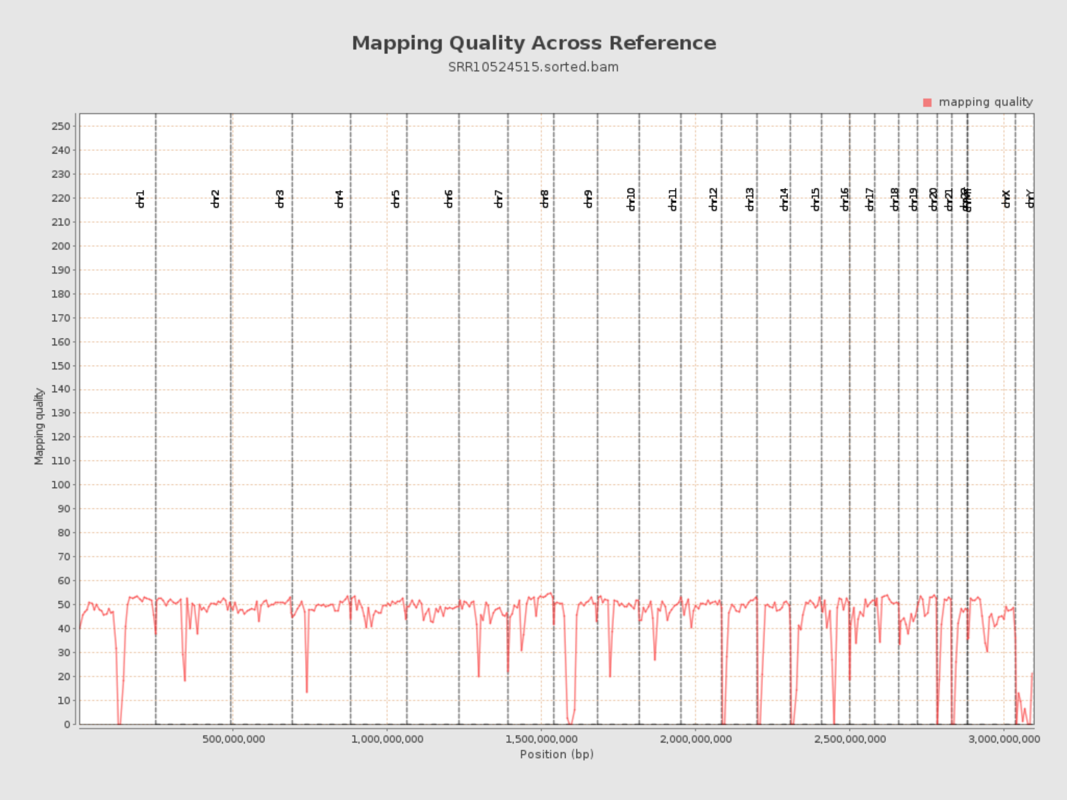
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram