# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 11:08:15*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524968.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_SRR10524968 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524968.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 11:08:14 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524968.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,930,510 |
| Mapped reads | 1,787,231 / 92.58% |
| Unmapped reads | 143,279 / 7.42% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 4,825 / 0.25% |
| Read min/max/mean length | 30 / 76 / 76.08 |
| Duplicated reads (estimated) | 59,387 / 3.08% |
| Duplication rate | 2.33% |
| Clipped reads | 1,786,346 / 92.53% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 25,688,533 / 24.49% |
| Number/percentage of C's | 20,398,677 / 19.44% |
| Number/percentage of T's | 34,044,023 / 32.45% |
| Number/percentage of G's | 24,774,031 / 23.62% |
| Number/percentage of N's | 1,355 / 0% |
| GC Percentage | 43.06% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0339 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3058 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.76 |

## 2.5. Mismatches and indels

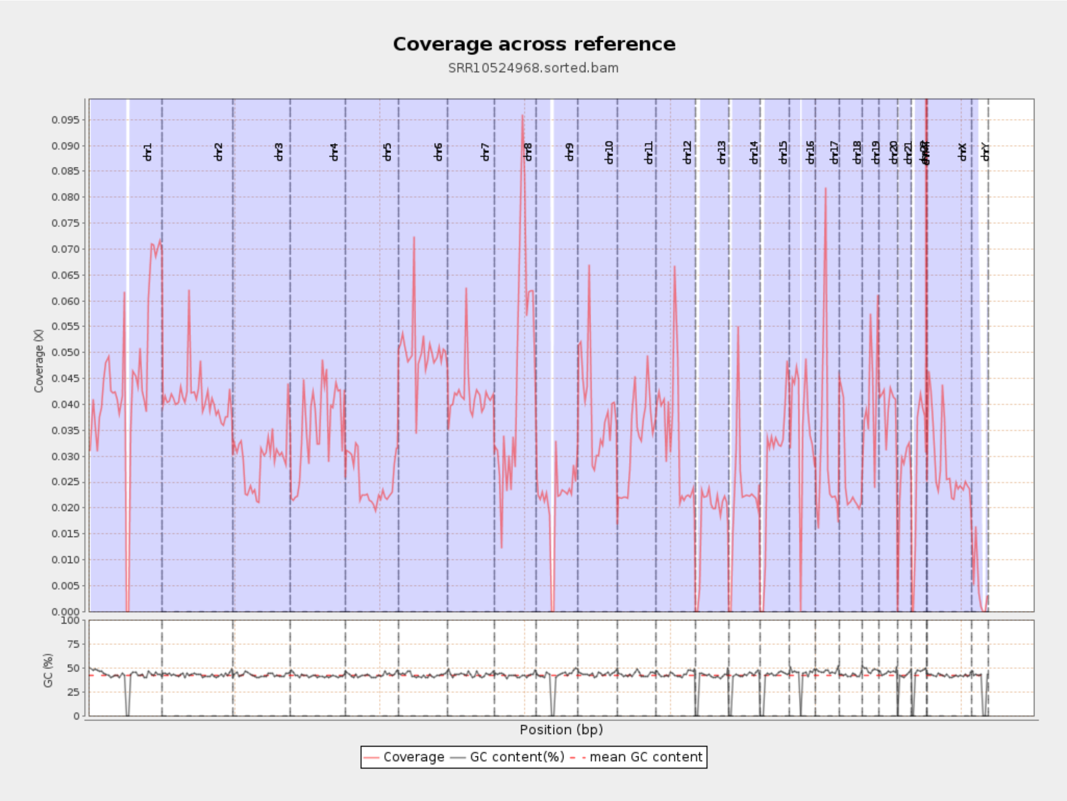
| | |
|---|---|
| General error rate | 0.5% |
| Mismatches | 515,096 |
| Insertions | 7,024 |
| Mapped reads with at least one insertion | 0.39% |
| Deletions | 20,585 |
| Mapped reads with at least one deletion | 1.14% |
| Homopolymer indels | 44.2% |

## 2.6. Chromosome stats

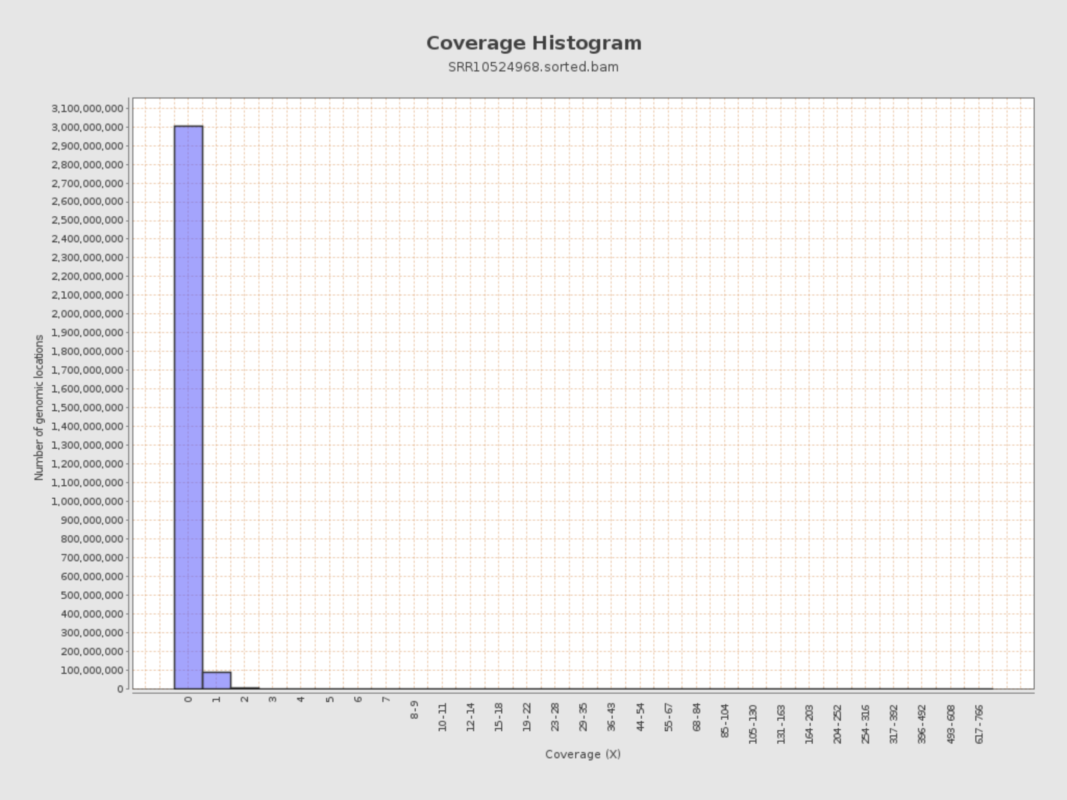
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 11126894 | 0.0446 | 0.5853 |
| chr2 | 243199373 | 10032762 | 0.0413 | 0.3582 |
| chr3 | 198022430 | 5810386 | 0.0293 | 0.1865 |
| chr4 | 191154276 | 6810271 | 0.0356 | 0.2256 |
| chr5 | 180915260 | 4530293 | 0.025 | 0.1756 |
| chr6 | 171115067 | 8585834 | 0.0502 | 0.3516 |
| chr7 | 159138663 | 6682579 | 0.042 | 0.4062 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6632140 | 0.0453 | 0.3149 |
| chr9 | 141213431 | 2971227 | 0.021 | 0.2394 |
| chr10 | 135534747 | 5306064 | 0.0391 | 0.3003 |
| chr11 | 135006516 | 4393767 | 0.0325 | 0.2667 |
| chr12 | 133851895 | 4463671 | 0.0333 | 0.202 |
| chr13 | 115169878 | 2061013 | 0.0179 | 0.1474 |
| chr14 | 107349540 | 2383139 | 0.0222 | 0.169 |
| chr15 | 102531392 | 2900407 | 0.0283 | 0.1953 |
| chr16 | 90354753 | 3254918 | 0.036 | 0.216 |
| chr17 | 81195210 | 2597189 | 0.032 | 0.257 |
| chr18 | 78077248 | 2078444 | 0.0266 | 0.3839 |
| chr19 | 59128983 | 2491464 | 0.0421 | 0.3692 |
| chr20 | 63025520 | 2496819 | 0.0396 | 0.2182 |
| chr21 | 48129895 | 1240460 | 0.0258 | 0.1834 |
| chr22 | 51304566 | 1371310 | 0.0267 | 0.1763 |
| chrMT | 16571 | 9649 | 0.5823 | 0.9307 |
| chrX | 155270560 | 4426114 | 0.0285 | 0.2173 |
| chrY | 59373566 | 284882 | 0.0048 | 0.1221 |

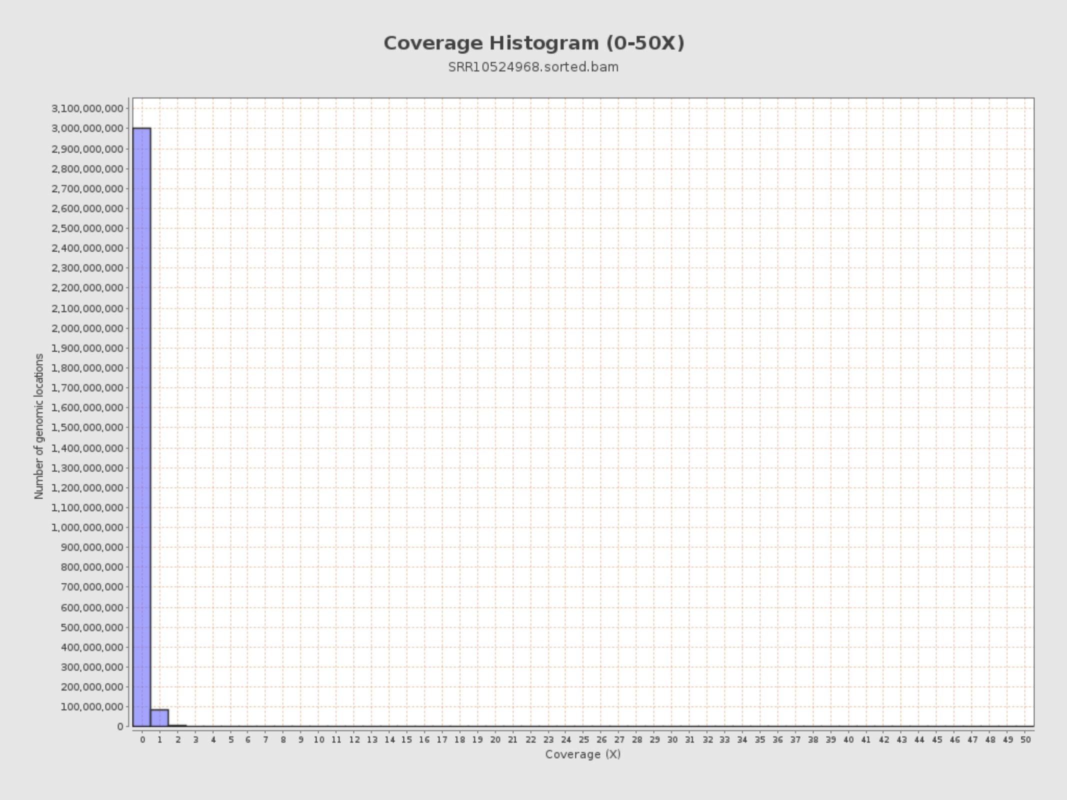
# 3. Results : Coverage across reference



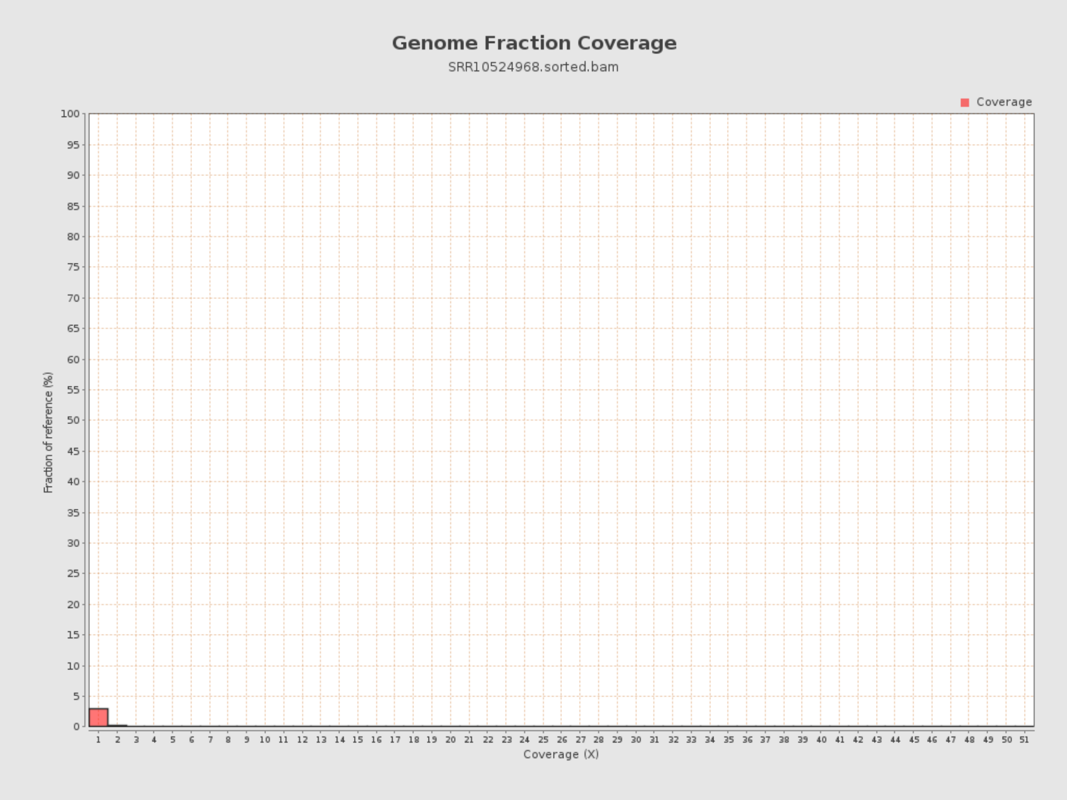
# 4. Results : Coverage Histogram



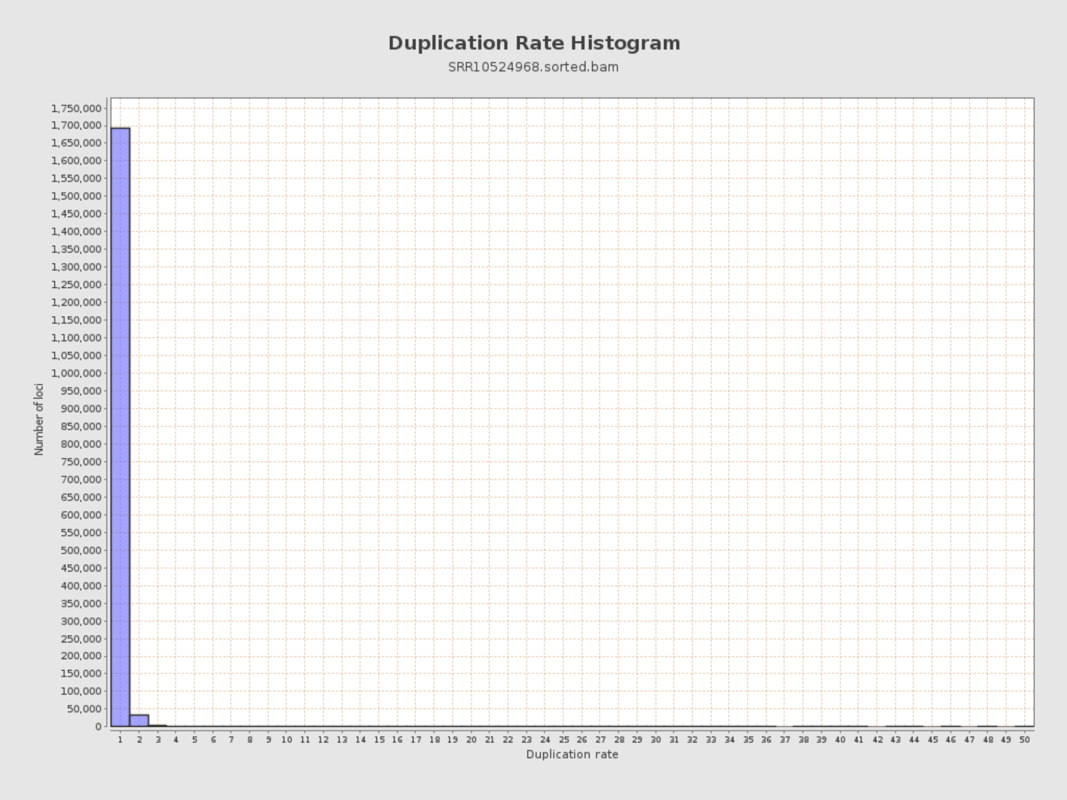
# 5. Results : Coverage Histogram (0-50X)



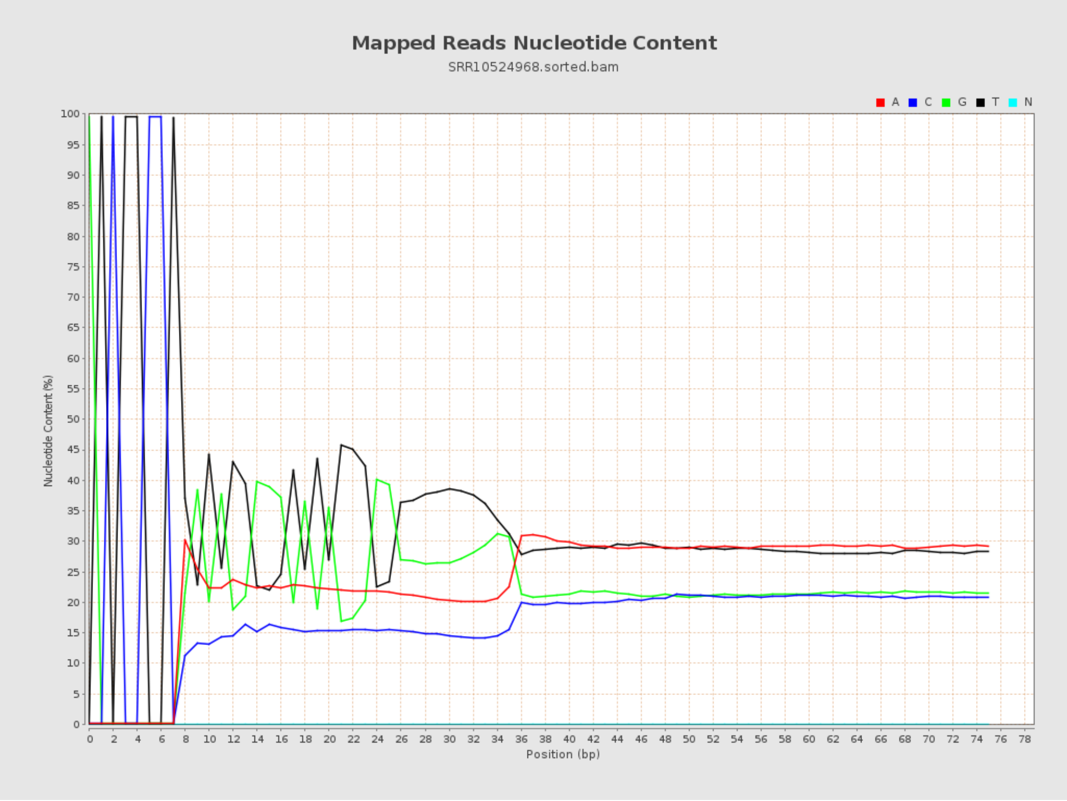
# 6. Results : Genome Fraction Coverage



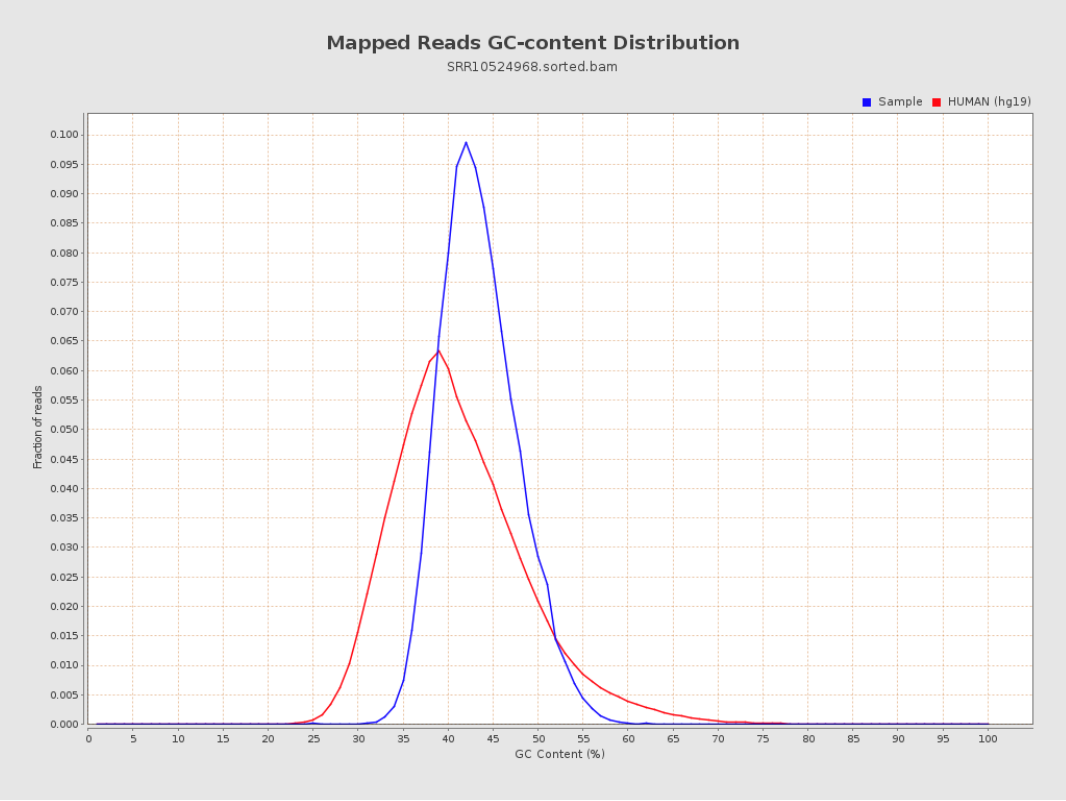
# 7. Results : Duplication Rate Histogram



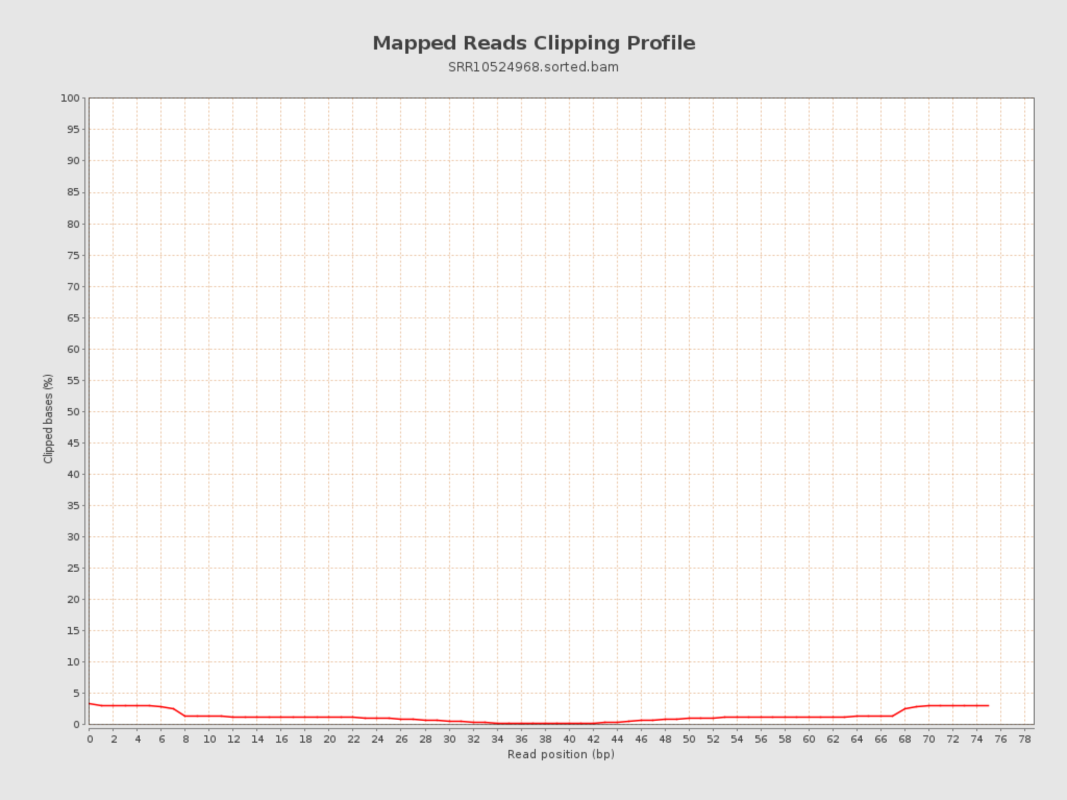
# 8. Results : Mapped Reads Nucleotide Content



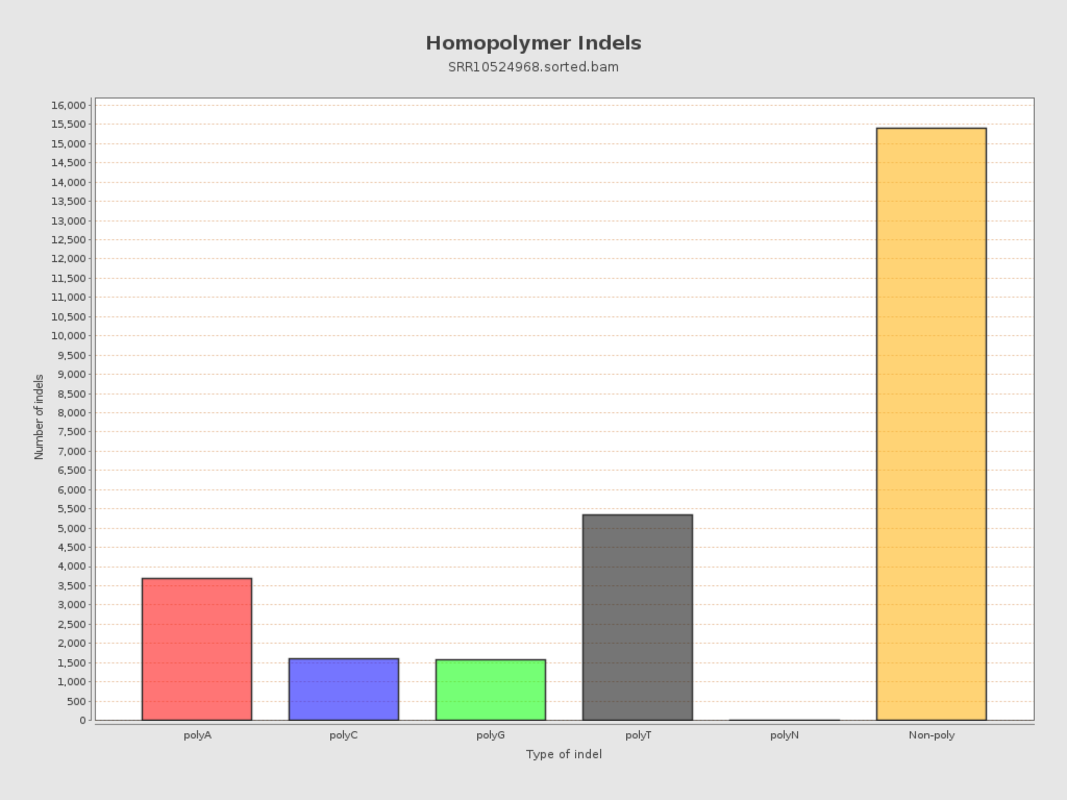
# 9. Results : Mapped Reads GC-content Distribution



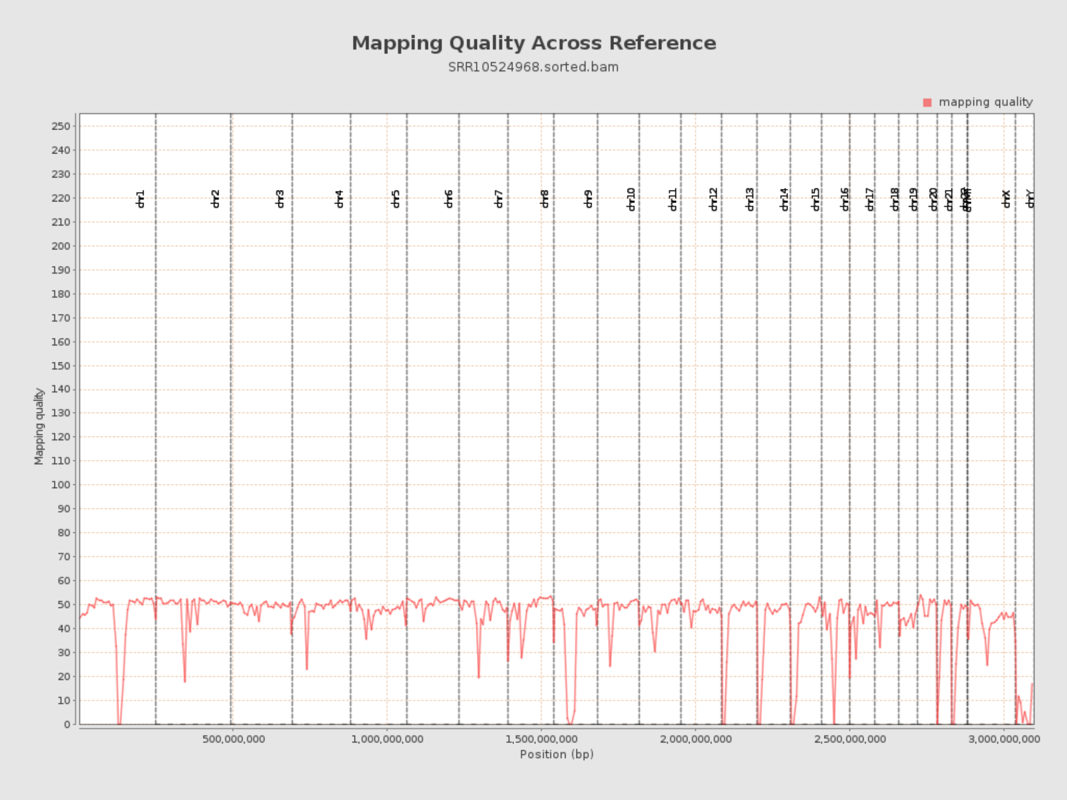
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram