# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/27 22:43:13*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524322.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_SRR10524322 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524322.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Aug 27 22:43:11 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524322.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 961,166 |
| Mapped reads | 882,900 / 91.86% |
| Unmapped reads | 78,266 / 8.14% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,295 / 0.34% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 27,766 / 2.89% |
| Duplication rate | 2.38% |
| Clipped reads | 884,452 / 92.02% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 12,802,173 / 24.96% |
| Number/percentage of C's | 8,978,708 / 17.51% |
| Number/percentage of T's | 16,268,106 / 31.72% |
| Number/percentage of G's | 13,234,948 / 25.81% |
| Number/percentage of N's | 1,175 / 0% |
| GC Percentage | 43.31% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0166 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1858 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.54 |

## 2.5. Mismatches and indels

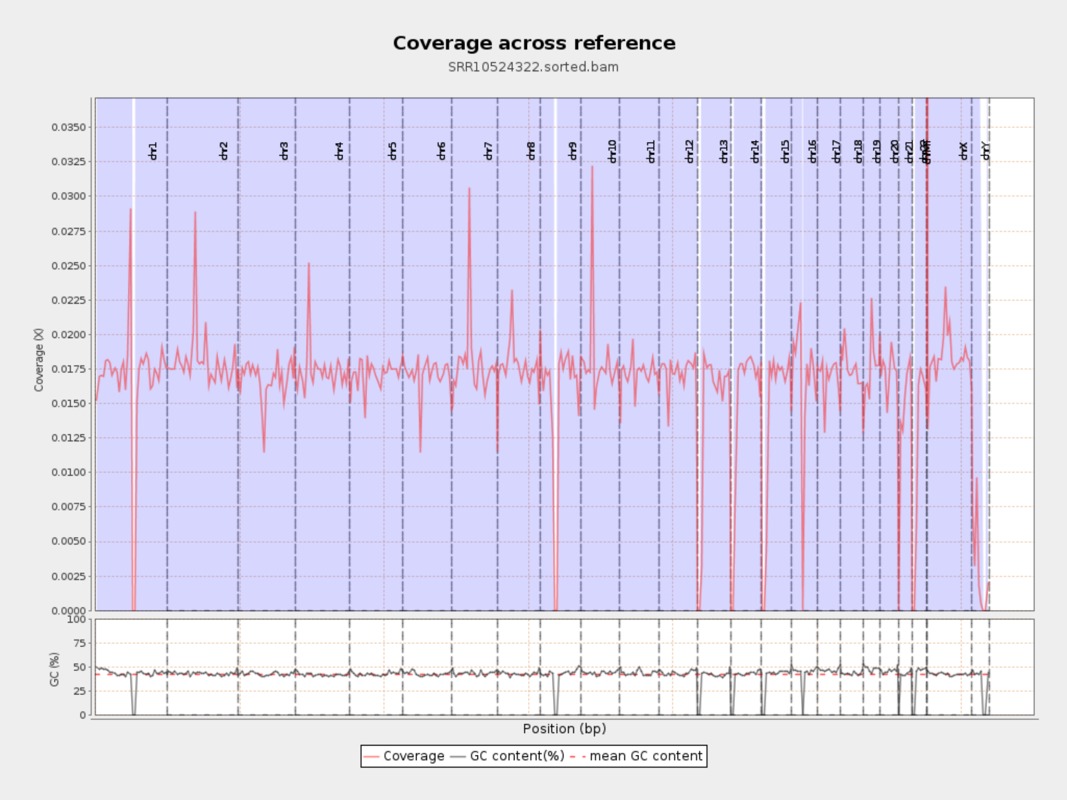
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 262,225 |
| Insertions | 3,558 |
| Mapped reads with at least one insertion | 0.4% |
| Deletions | 10,584 |
| Mapped reads with at least one deletion | 1.19% |
| Homopolymer indels | 43.32% |

## 2.6. Chromosome stats

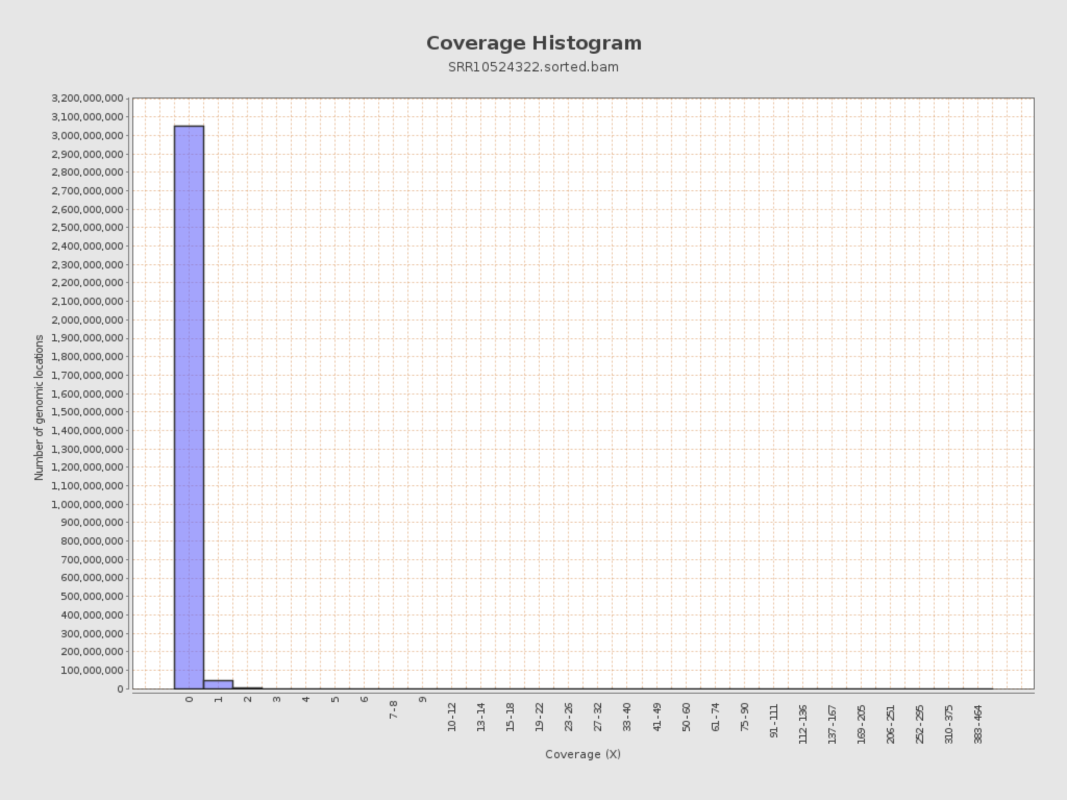
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 4142133 | 0.0166 | 0.3113 |
| chr2 | 243199373 | 4399910 | 0.0181 | 0.2458 |
| chr3 | 198022430 | 3318160 | 0.0168 | 0.1369 |
| chr4 | 191154276 | 3333128 | 0.0174 | 0.1462 |
| chr5 | 180915260 | 3113102 | 0.0172 | 0.1387 |
| chr6 | 171115067 | 2929447 | 0.0171 | 0.145 |
| chr7 | 159138663 | 2868472 | 0.018 | 0.2455 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2610658 | 0.0178 | 0.1976 |
| chr9 | 141213431 | 2146893 | 0.0152 | 0.1549 |
| chr10 | 135534747 | 2454503 | 0.0181 | 0.1831 |
| chr11 | 135006516 | 2327817 | 0.0172 | 0.1582 |
| chr12 | 133851895 | 2311049 | 0.0173 | 0.1396 |
| chr13 | 115169878 | 1634275 | 0.0142 | 0.1265 |
| chr14 | 107349540 | 1568331 | 0.0146 | 0.1297 |
| chr15 | 102531392 | 1436850 | 0.014 | 0.1248 |
| chr16 | 90354753 | 1475265 | 0.0163 | 0.1435 |
| chr17 | 81195210 | 1367430 | 0.0168 | 0.1417 |
| chr18 | 78077248 | 1375789 | 0.0176 | 0.2462 |
| chr19 | 59128983 | 1045042 | 0.0177 | 0.2358 |
| chr20 | 63025520 | 1081774 | 0.0172 | 0.1402 |
| chr21 | 48129895 | 679987 | 0.0141 | 0.1318 |
| chr22 | 51304566 | 592201 | 0.0115 | 0.1137 |
| chrMT | 16571 | 61642 | 3.7199 | 2.6526 |
| chrX | 155270560 | 2859141 | 0.0184 | 0.1515 |
| chrY | 59373566 | 169019 | 0.0028 | 0.0893 |

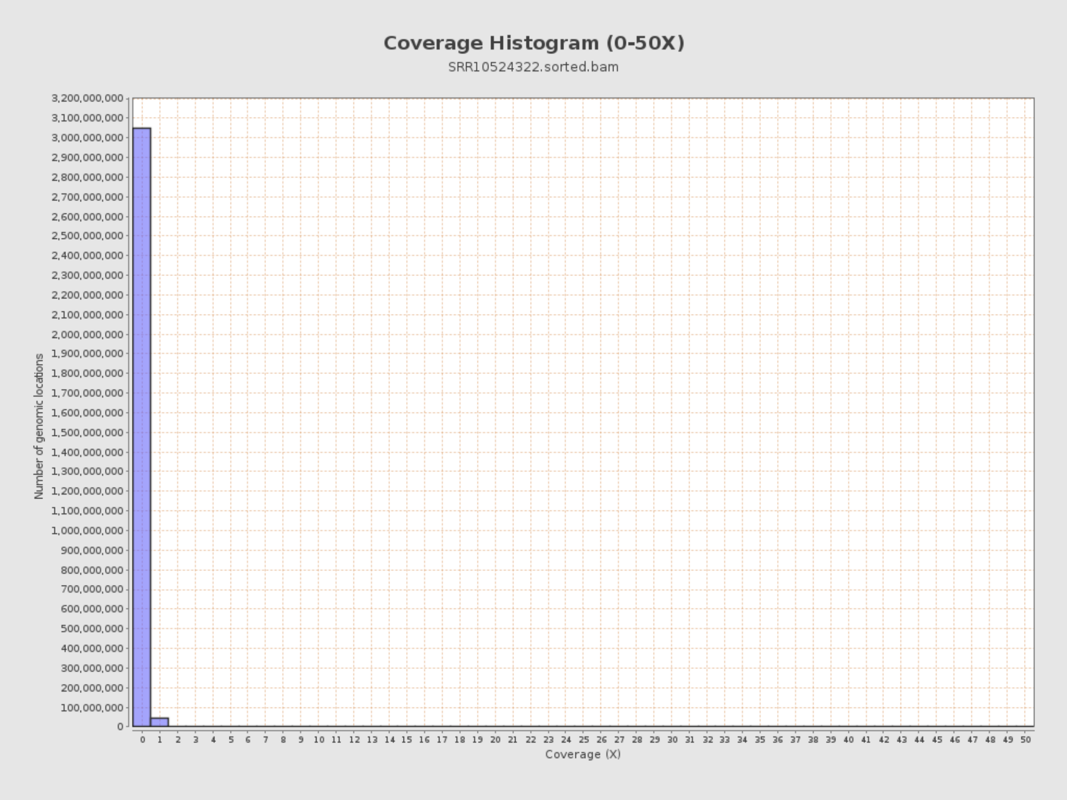
# 3. Results : Coverage across reference



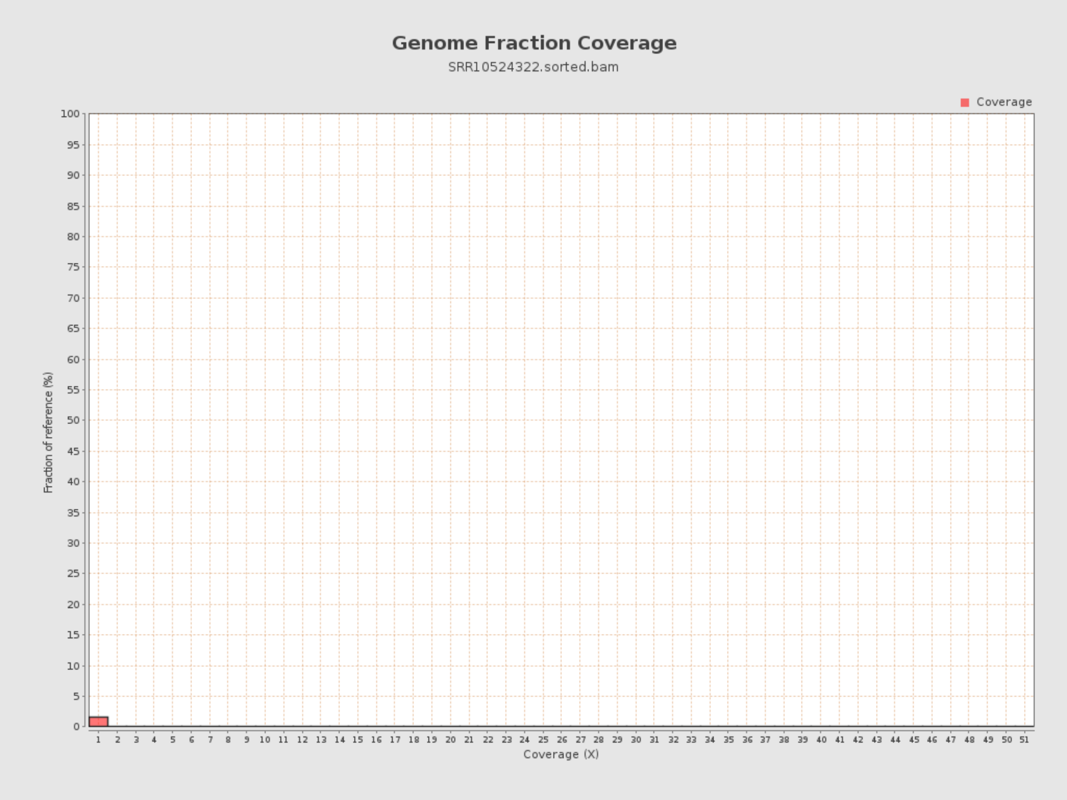
# 4. Results : Coverage Histogram



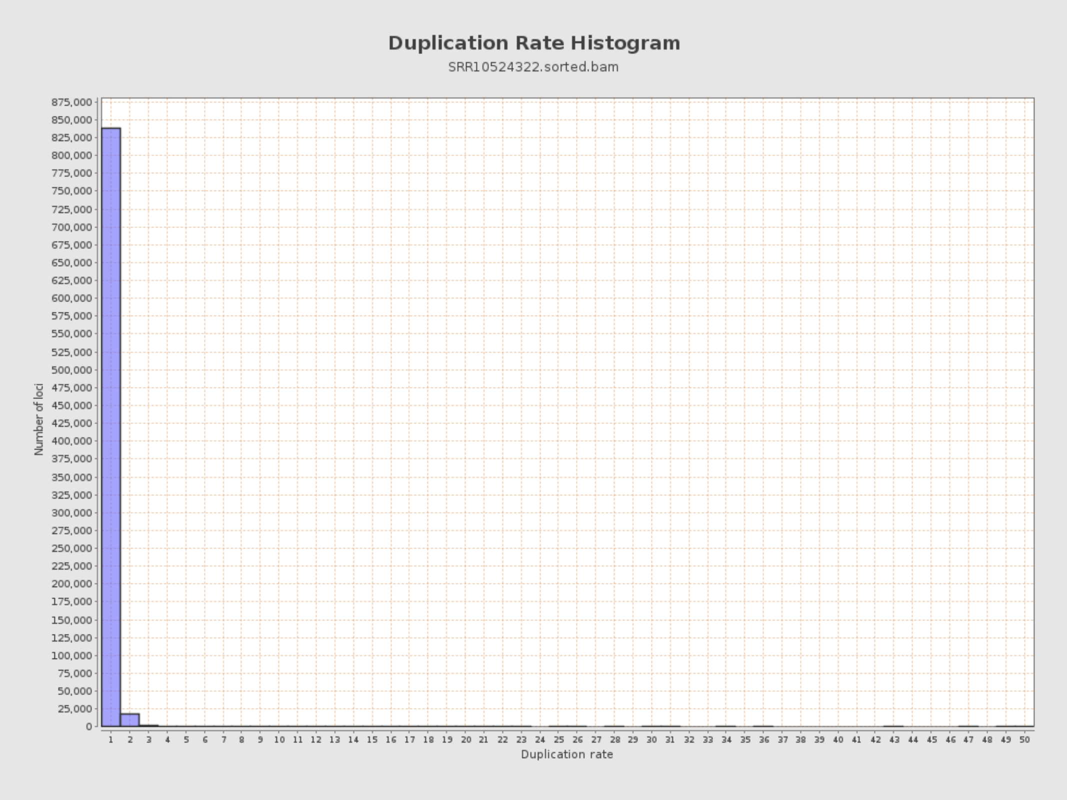
# 5. Results : Coverage Histogram (0-50X)



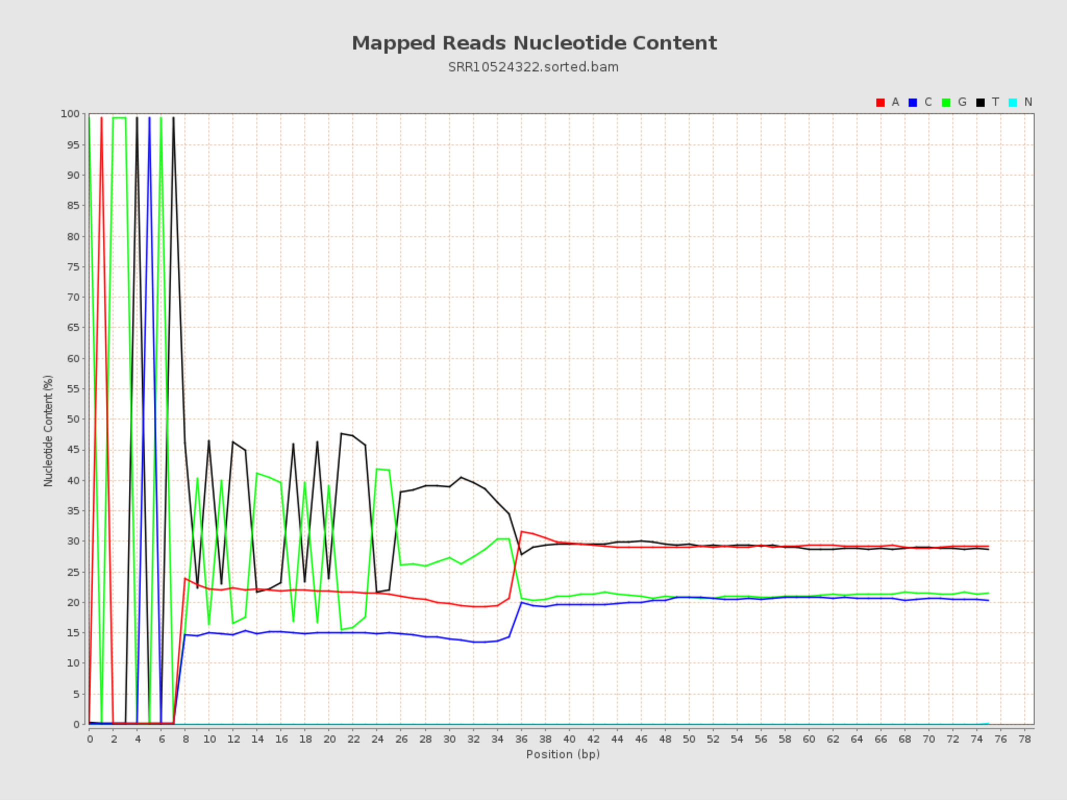
# 6. Results : Genome Fraction Coverage



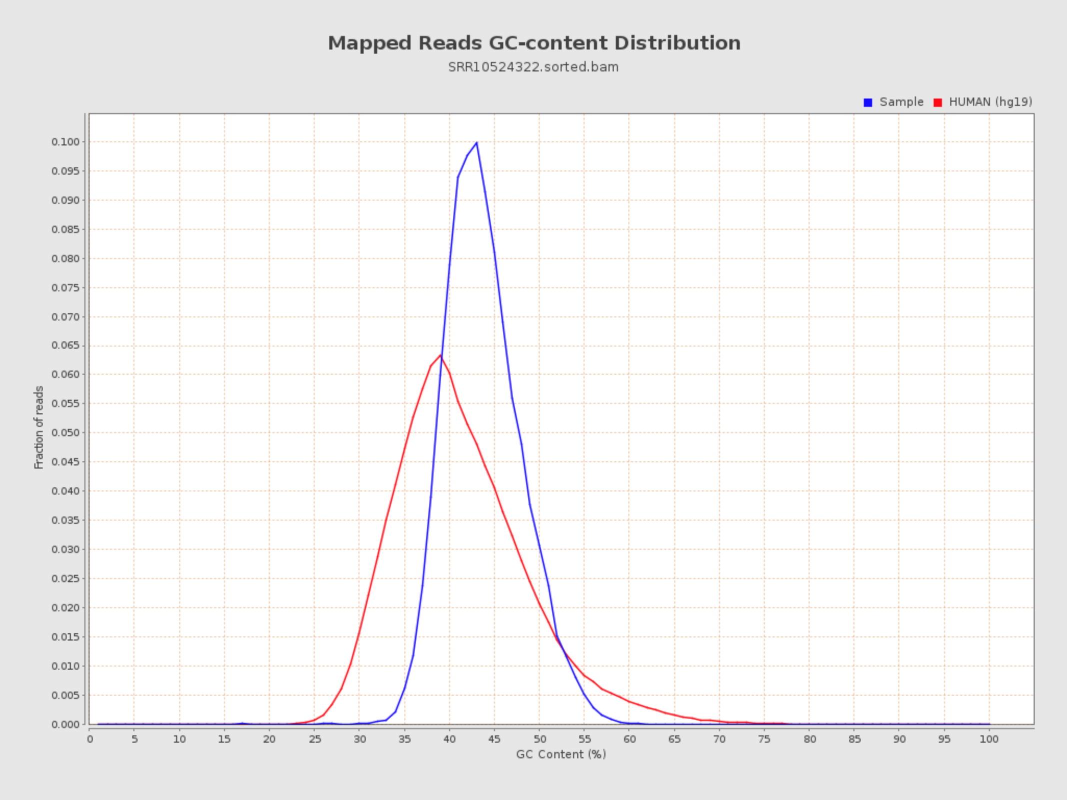
# 7. Results : Duplication Rate Histogram



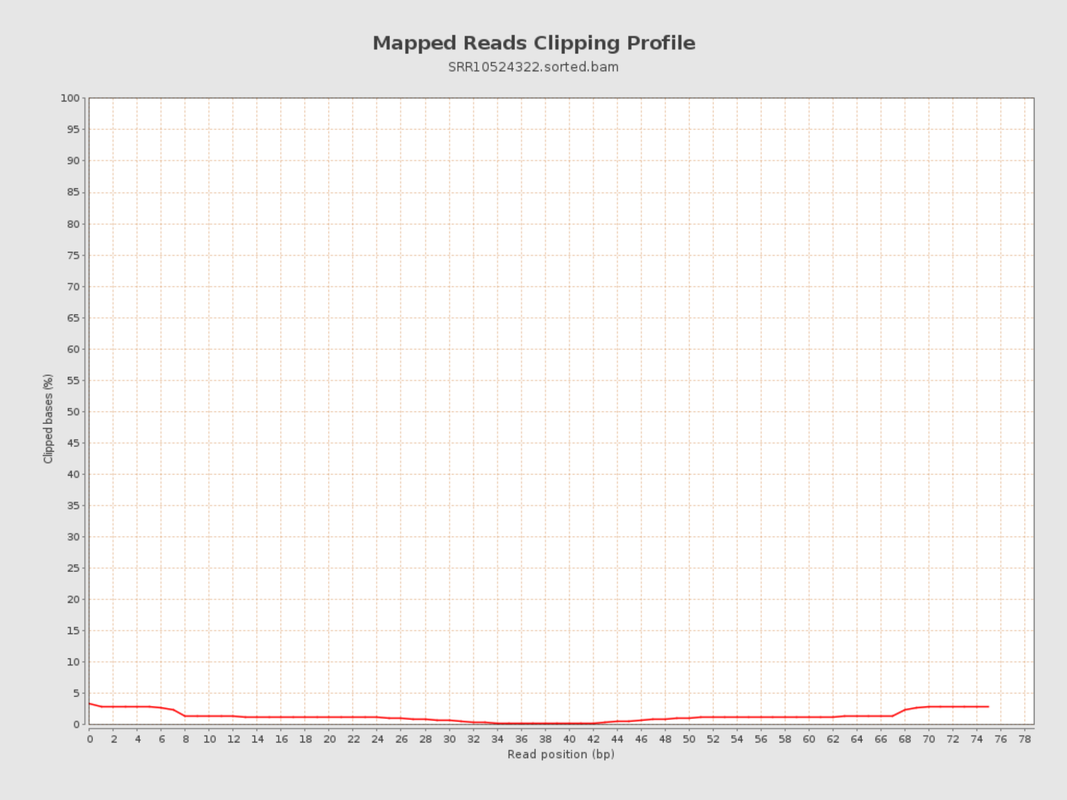
# 8. Results : Mapped Reads Nucleotide Content



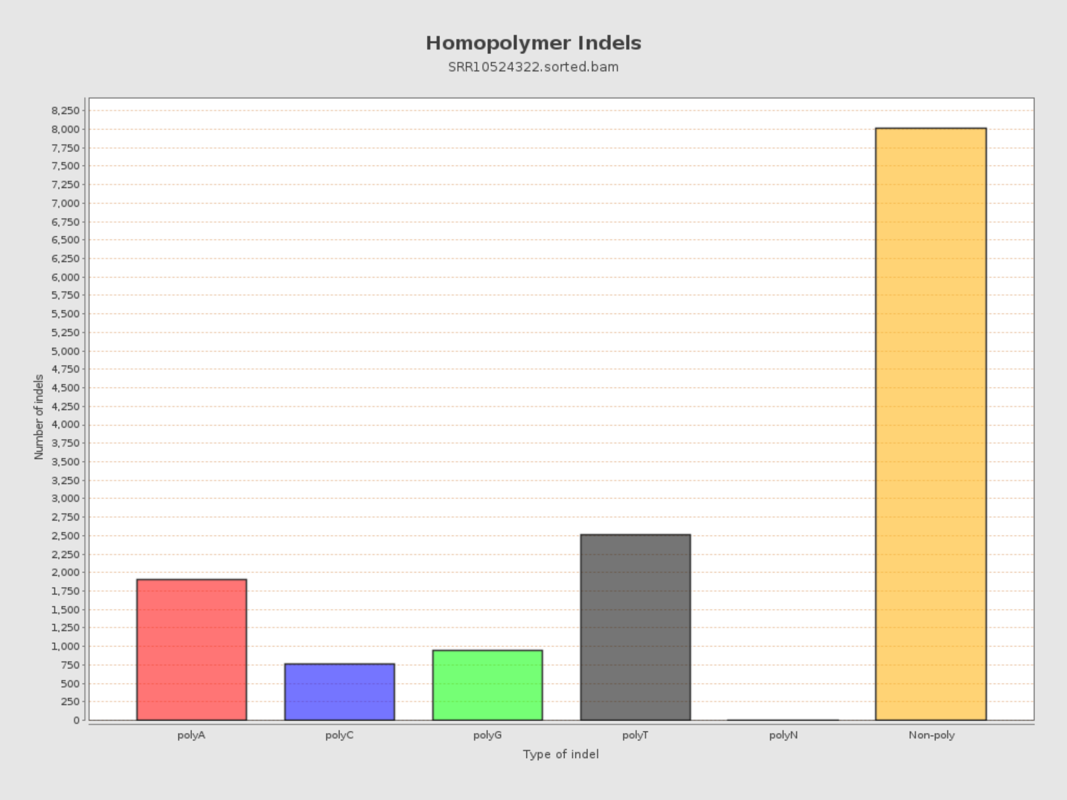
# 9. Results : Mapped Reads GC-content Distribution



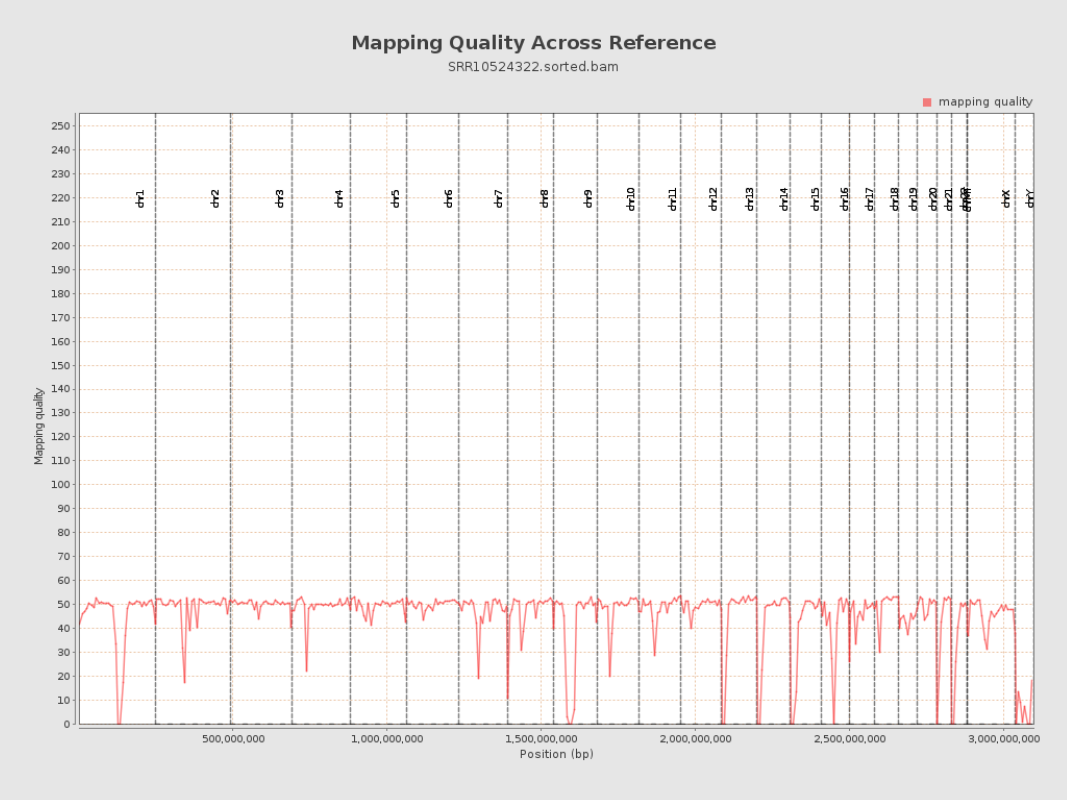
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram