# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/27 22:52:04*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524325.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_SRR10524325 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524325.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Aug 27 22:52:03 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524325.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,177,562 |
| Mapped reads | 1,078,375 / 91.58% |
| Unmapped reads | 99,187 / 8.42% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 4,652 / 0.4% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 25,088 / 2.13% |
| Duplication rate | 1.59% |
| Clipped reads | 1,080,596 / 91.77% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 15,291,820 / 24.42% |
| Number/percentage of C's | 12,948,202 / 20.67% |
| Number/percentage of T's | 18,945,099 / 30.25% |
| Number/percentage of G's | 15,435,708 / 24.65% |
| Number/percentage of N's | 8,546 / 0.01% |
| GC Percentage | 45.32% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0202 |
| | |

|  |  |
|---|---|
| Standard Deviation | 0.2063 |

## 2.4. Mapping Quality

|  |  |
|---|---|
| Mean Mapping Quality | 43.52 |

## 2.5. Mismatches and indels

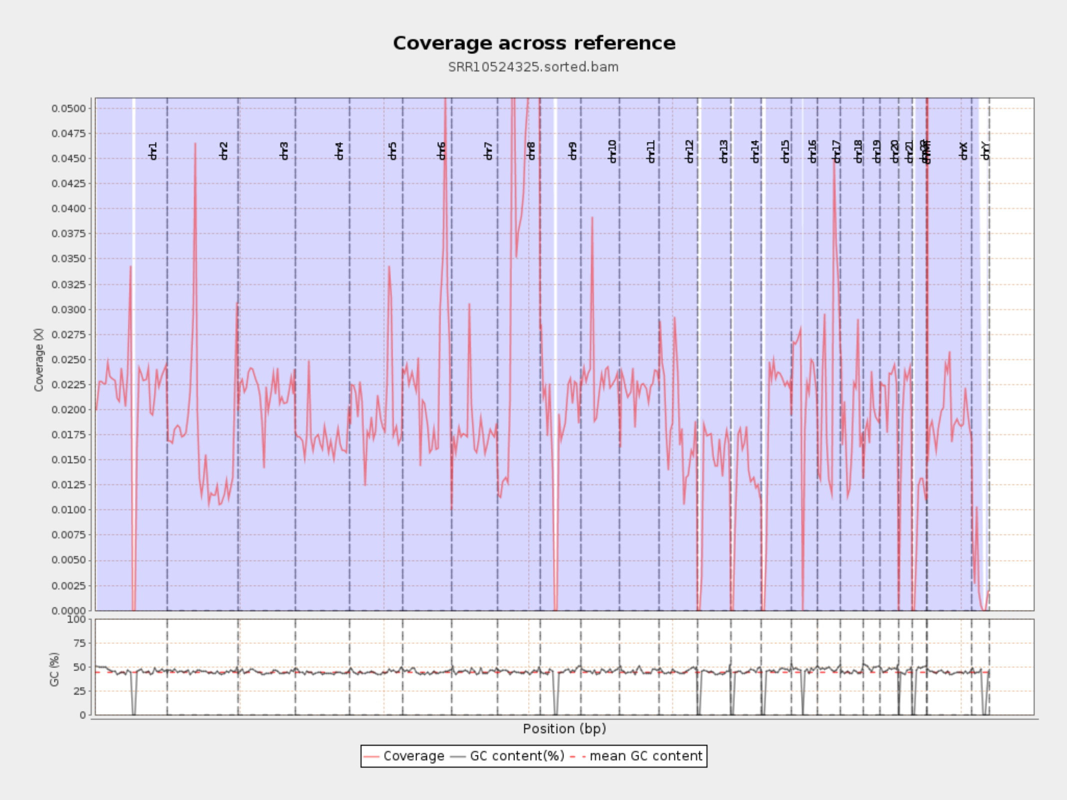
|  |  |
|---|---|
| General error rate | 0.51% |
| Mismatches | 314,045 |
| Insertions | 4,156 |
| Mapped reads with at least one insertion | 0.38% |
| Deletions | 9,848 |
| Mapped reads with at least one deletion | 0.91% |
| Homopolymer indels | 41.67% |

## 2.6. Chromosome stats

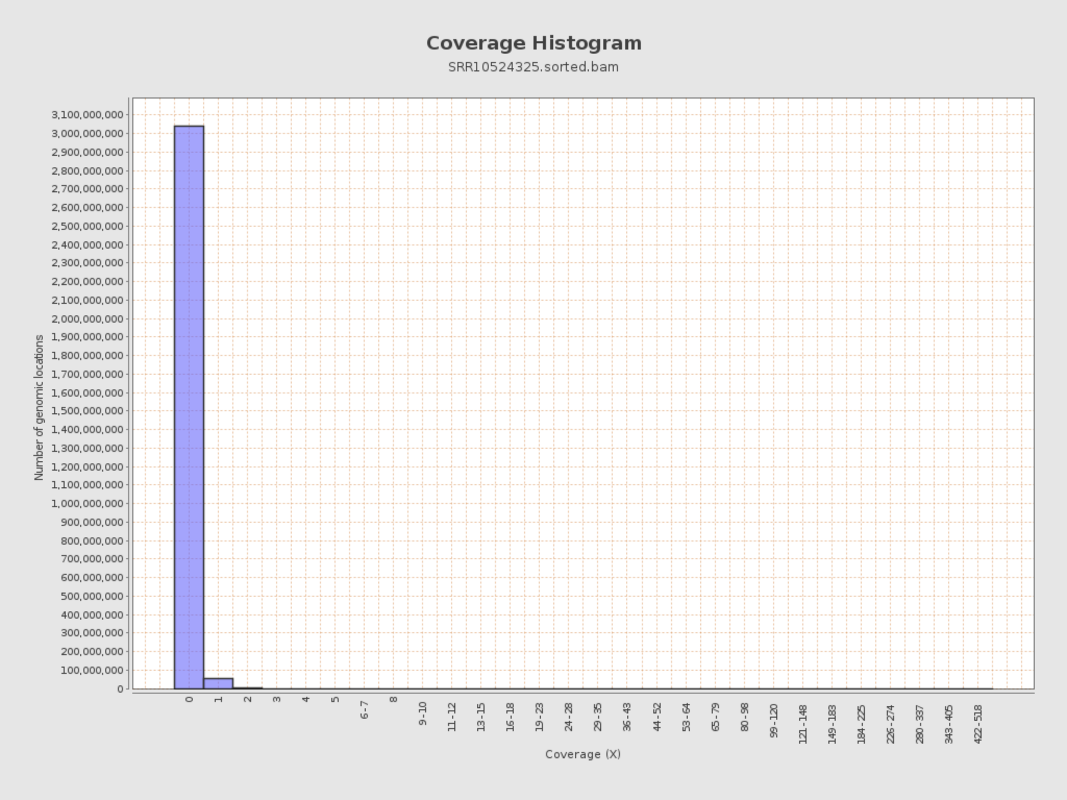
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5327833 | 0.0214 | 0.3656 |
| chr2 | 243199373 | 4068781 | 0.0167 | 0.2538 |
| chr3 | 198022430 | 4314652 | 0.0218 | 0.1562 |
| chr4 | 191154276 | 3281900 | 0.0172 | 0.1469 |
| chr5 | 180915260 | 3654196 | 0.0202 | 0.1506 |
| chr6 | 171115067 | 4010567 | 0.0234 | 0.1702 |
| chr7 | 159138663 | 2861490 | 0.018 | 0.2443 |
|  |  |  |  |  |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6508857 | 0.0445 | 0.2637 |
| chr9 | 141213431 | 2596550 | 0.0184 | 0.1685 |
| chr10 | 135534747 | 3183730 | 0.0235 | 0.2118 |
| chr11 | 135006516 | 2996555 | 0.0222 | 0.1817 |
| chr12 | 133851895 | 2505840 | 0.0187 | 0.1465 |
| chr13 | 115169878 | 1570903 | 0.0136 | 0.1232 |
| chr14 | 107349540 | 1335231 | 0.0124 | 0.1218 |
| chr15 | 102531392 | 1922397 | 0.0187 | 0.1464 |
| chr16 | 90354753 | 1977669 | 0.0219 | 0.1632 |
| chr17 | 81195210 | 1934192 | 0.0238 | 0.172 |
| chr18 | 78077248 | 1464506 | 0.0188 | 0.267 |
| chr19 | 59128983 | 1129055 | 0.0191 | 0.2504 |
| chr20 | 63025520 | 1392188 | 0.0221 | 0.1594 |
| chr21 | 48129895 | 901919 | 0.0187 | 0.1518 |
| chr22 | 51304566 | 450841 | 0.0088 | 0.099 |
| chrMT | 16571 | 71073 | 4.289 | 3.1047 |
| chrX | 155270560 | 3013650 | 0.0194 | 0.1564 |
| chrY | 59373566 | 170619 | 0.0029 | 0.0883 |

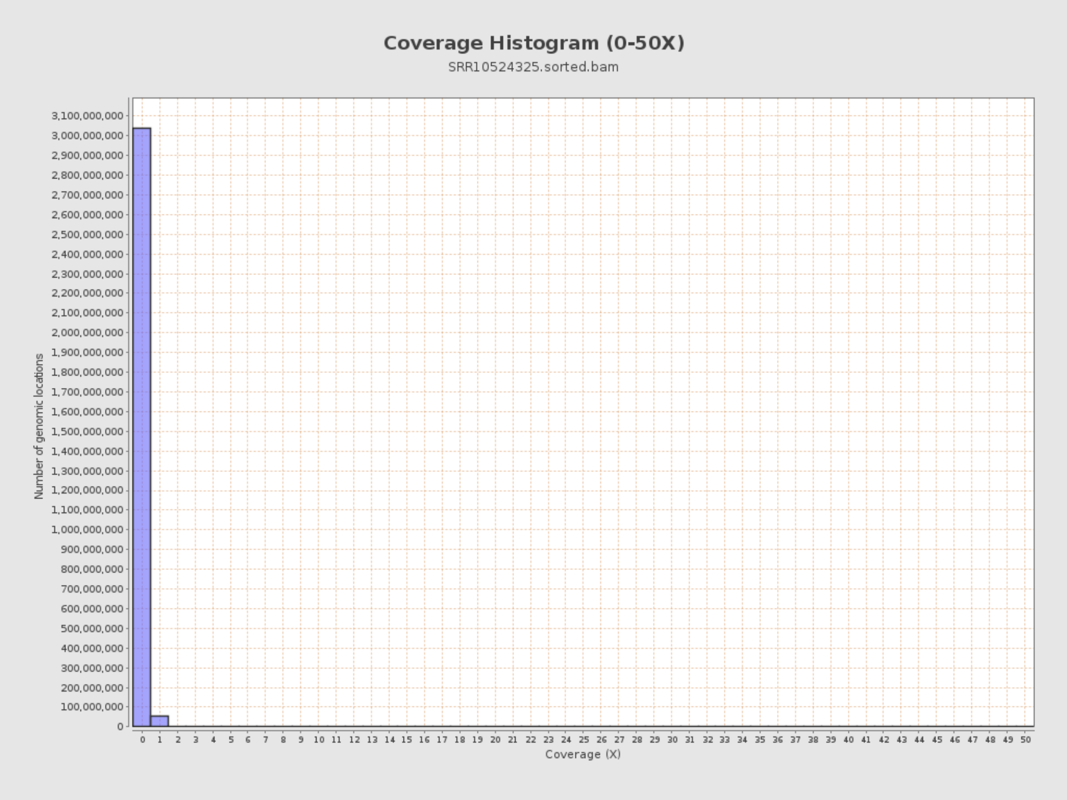
# 3. Results : Coverage across reference



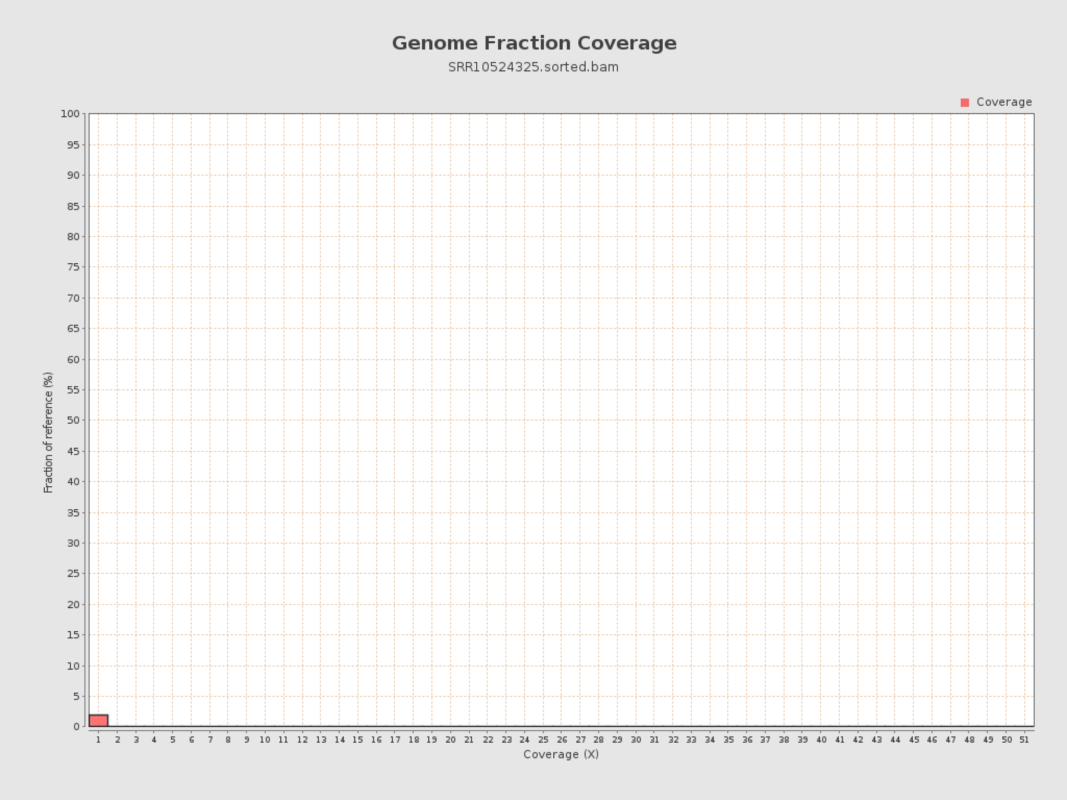
# 4. Results : Coverage Histogram



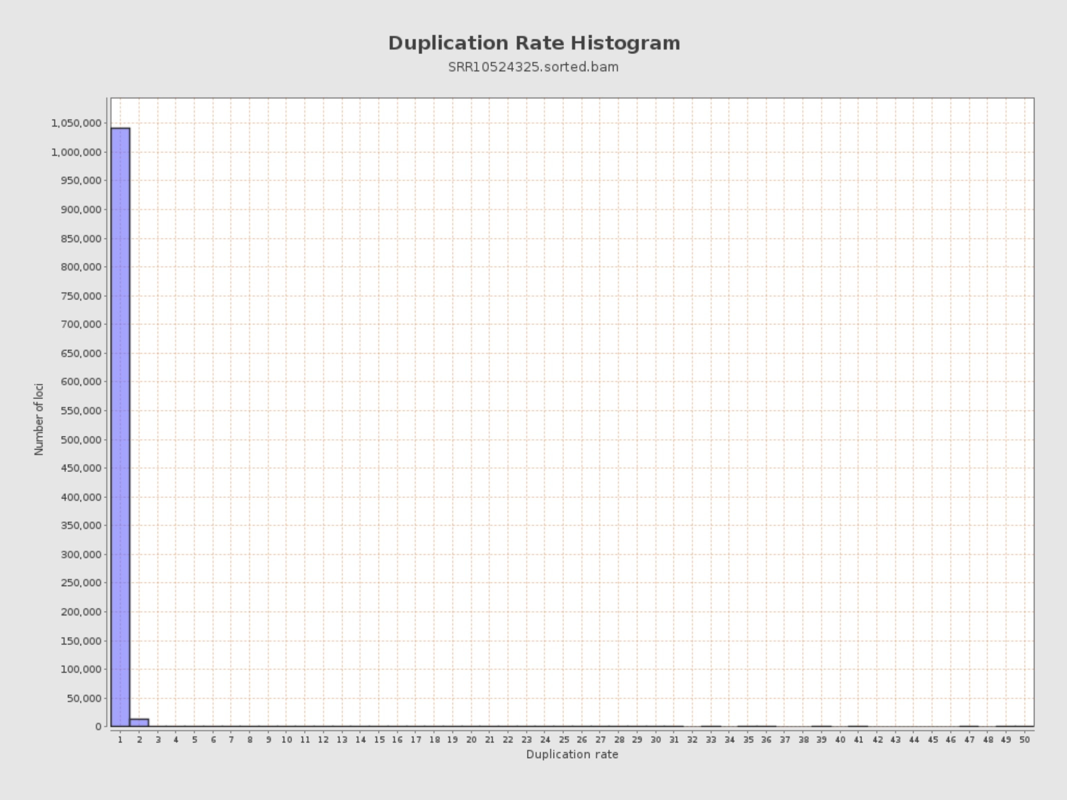
# 5. Results : Coverage Histogram (0-50X)



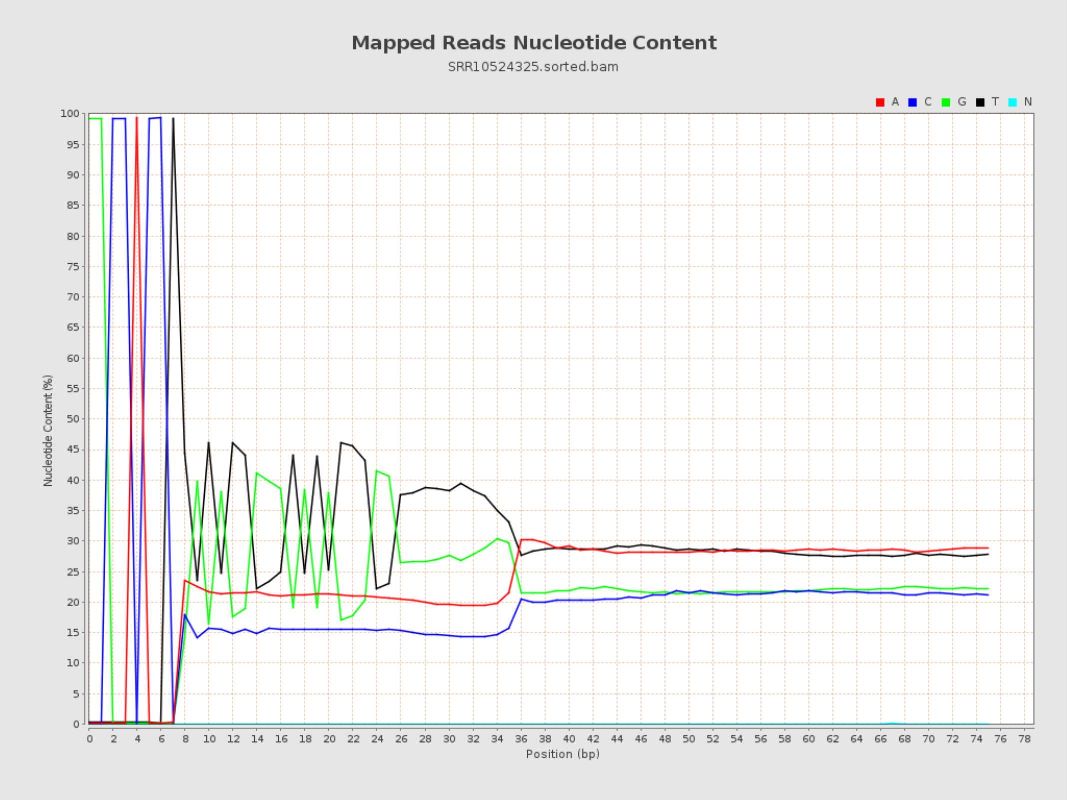
# 6. Results : Genome Fraction Coverage



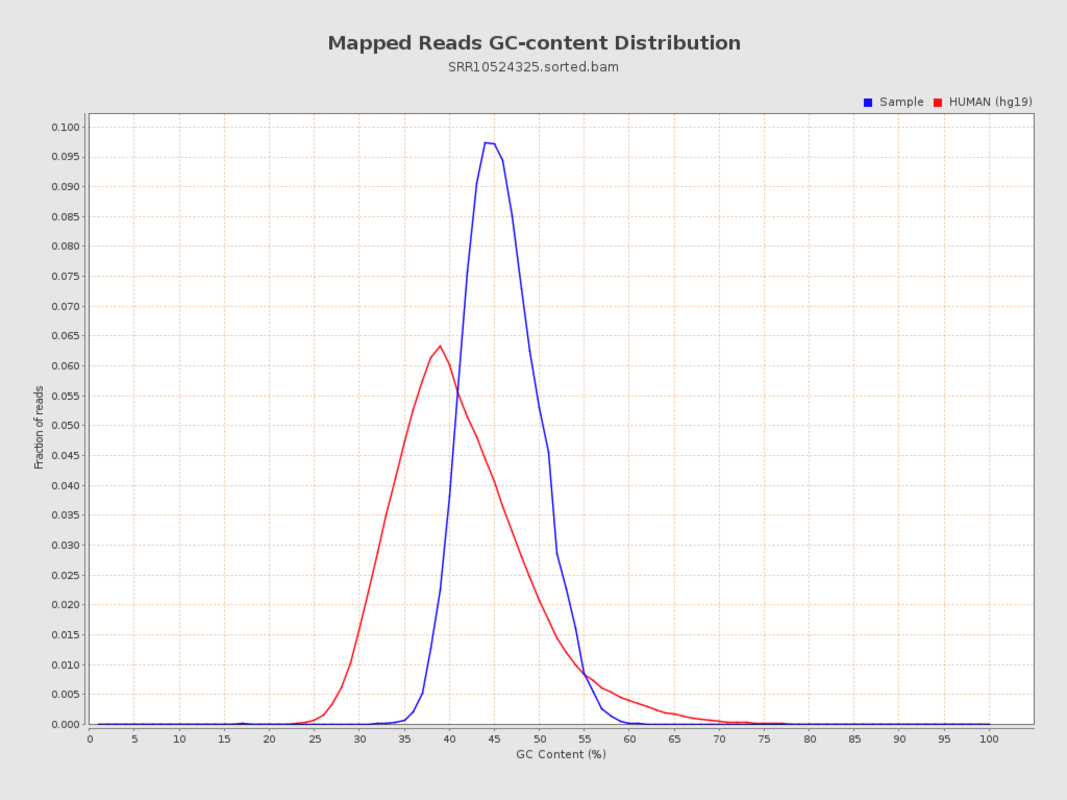
# 7. Results : Duplication Rate Histogram



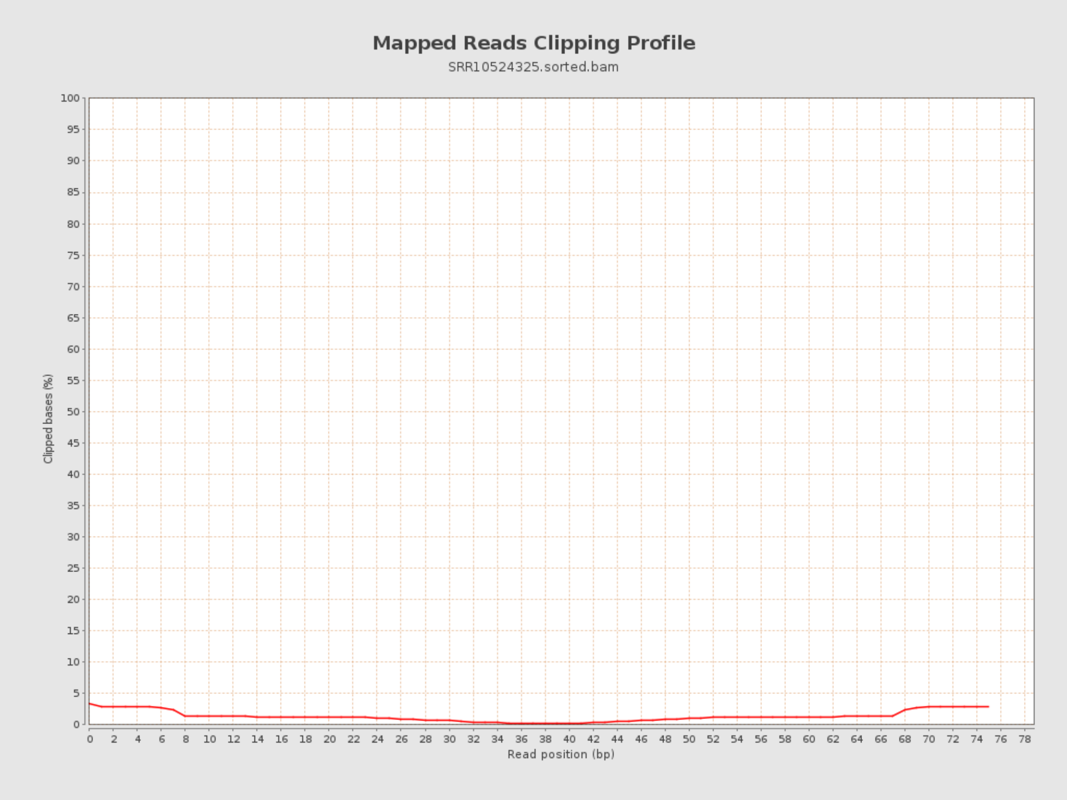
# 8. Results : Mapped Reads Nucleotide Content



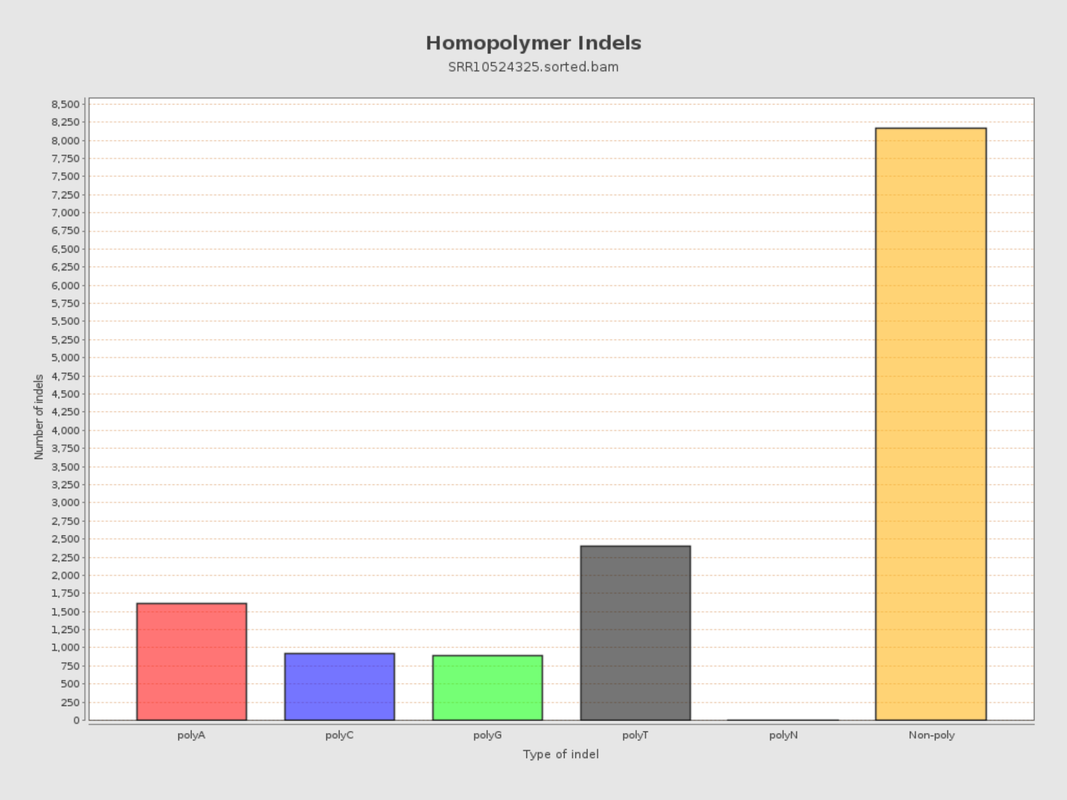
# 9. Results : Mapped Reads GC-content Distribution



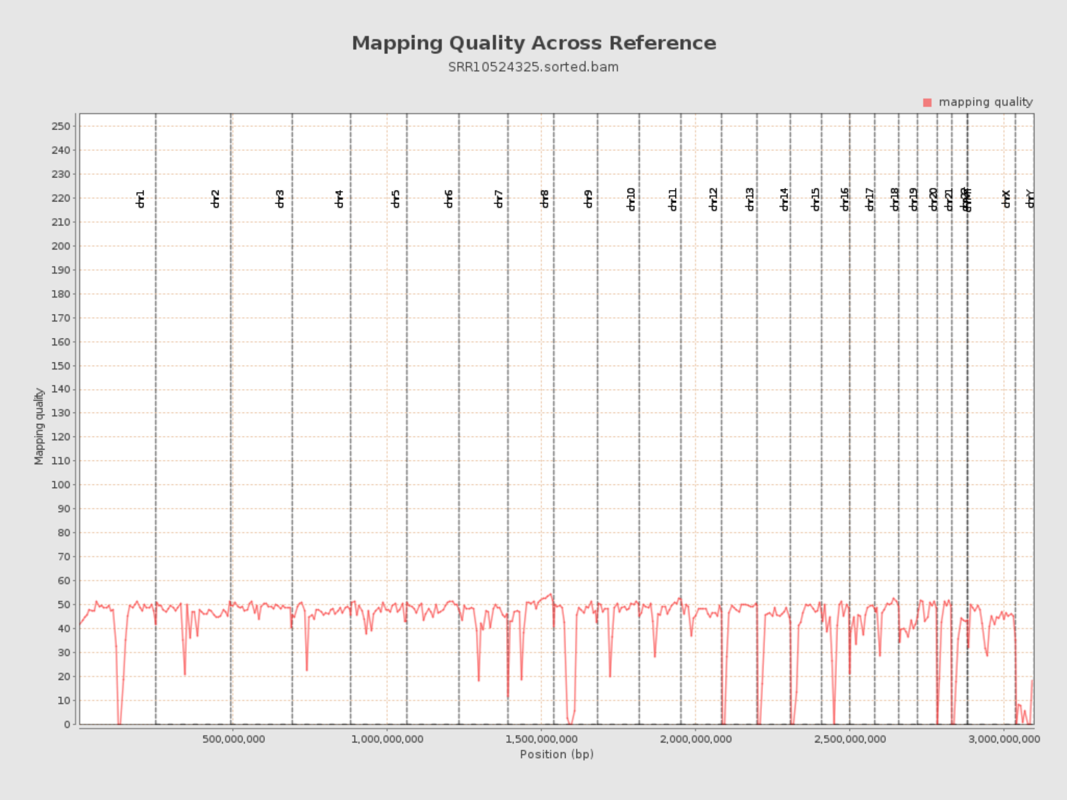
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram