# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/27 20:58:40*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524283.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_SRR10524283 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524283.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Aug 27 20:58:39 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524283.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,396,093 |
| Mapped reads | 1,285,565 / 92.08% |
| Unmapped reads | 110,528 / 7.92% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 4,246 / 0.3% |
| Read min/max/mean length | 30 / 76 / 76.1 |
| Duplicated reads (estimated) | 49,219 / 3.53% |
| Duplication rate | 2.75% |
| Clipped reads | 1,286,316 / 92.14% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 19,349,999 / 25.65% |
| Number/percentage of C's | 13,017,863 / 17.26% |
| Number/percentage of T's | 25,241,519 / 33.46% |
| Number/percentage of G's | 17,811,511 / 23.61% |
| Number/percentage of N's | 10,521 / 0.01% |
| GC Percentage | 40.87% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0244 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2728 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.72 |

## 2.5. Mismatches and indels

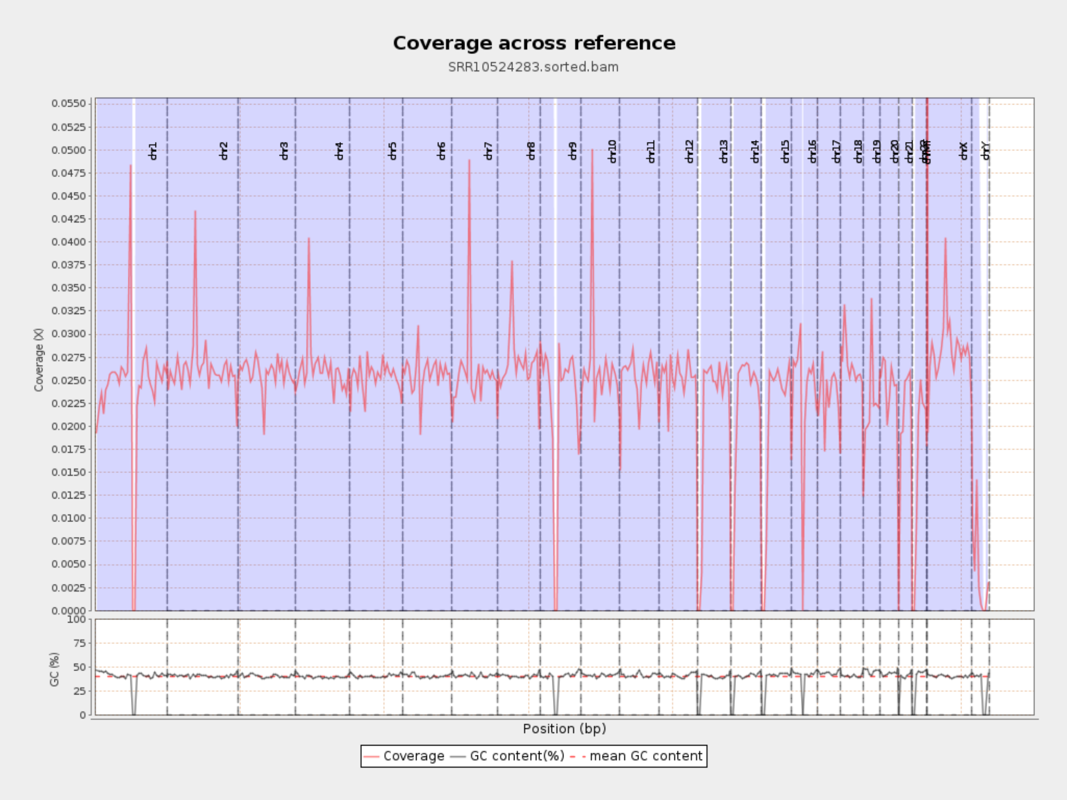
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 371,447 |
| Insertions | 5,188 |
| Mapped reads with at least one insertion | 0.4% |
| Deletions | 14,421 |
| Mapped reads with at least one deletion | 1.11% |
| Homopolymer indels | 44.21% |

## 2.6. Chromosome stats

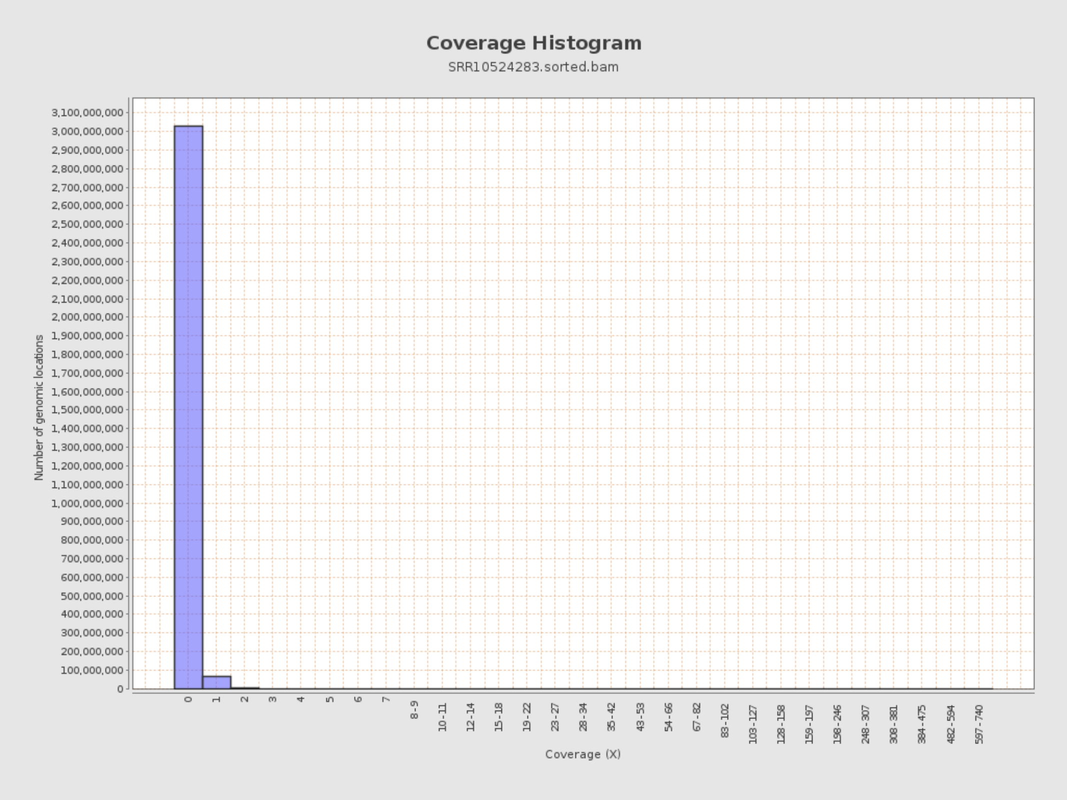
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5984114 | 0.024 | 0.5601 |
| chr2 | 243199373 | 6430458 | 0.0264 | 0.2722 |
| chr3 | 198022430 | 5106583 | 0.0258 | 0.1731 |
| chr4 | 191154276 | 5025128 | 0.0263 | 0.1938 |
| chr5 | 180915260 | 4619012 | 0.0255 | 0.1728 |
| chr6 | 171115067 | 4397958 | 0.0257 | 0.1866 |
| chr7 | 159138663 | 4164777 | 0.0262 | 0.3784 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3946088 | 0.027 | 0.2809 |
| chr9 | 141213431 | 3168258 | 0.0224 | 0.2346 |
| chr10 | 135534747 | 3582661 | 0.0264 | 0.2524 |
| chr11 | 135006516 | 3447121 | 0.0255 | 0.2267 |
| chr12 | 133851895 | 3389873 | 0.0253 | 0.1764 |
| chr13 | 115169878 | 2430991 | 0.0211 | 0.1557 |
| chr14 | 107349540 | 2287263 | 0.0213 | 0.1645 |
| chr15 | 102531392 | 2082218 | 0.0203 | 0.1526 |
| chr16 | 90354753 | 2086780 | 0.0231 | 0.178 |
| chr17 | 81195210 | 1896703 | 0.0234 | 0.1805 |
| chr18 | 78077248 | 2089259 | 0.0268 | 0.4422 |
| chr19 | 59128983 | 1333039 | 0.0225 | 0.3507 |
| chr20 | 63025520 | 1530900 | 0.0243 | 0.1717 |
| chr21 | 48129895 | 989566 | 0.0206 | 0.1729 |
| chr22 | 51304566 | 806250 | 0.0157 | 0.1341 |
| chrMT | 16571 | 11347 | 0.6848 | 0.9405 |
| chrX | 155270560 | 4411107 | 0.0284 | 0.2082 |
| chrY | 59373566 | 236908 | 0.004 | 0.1152 |

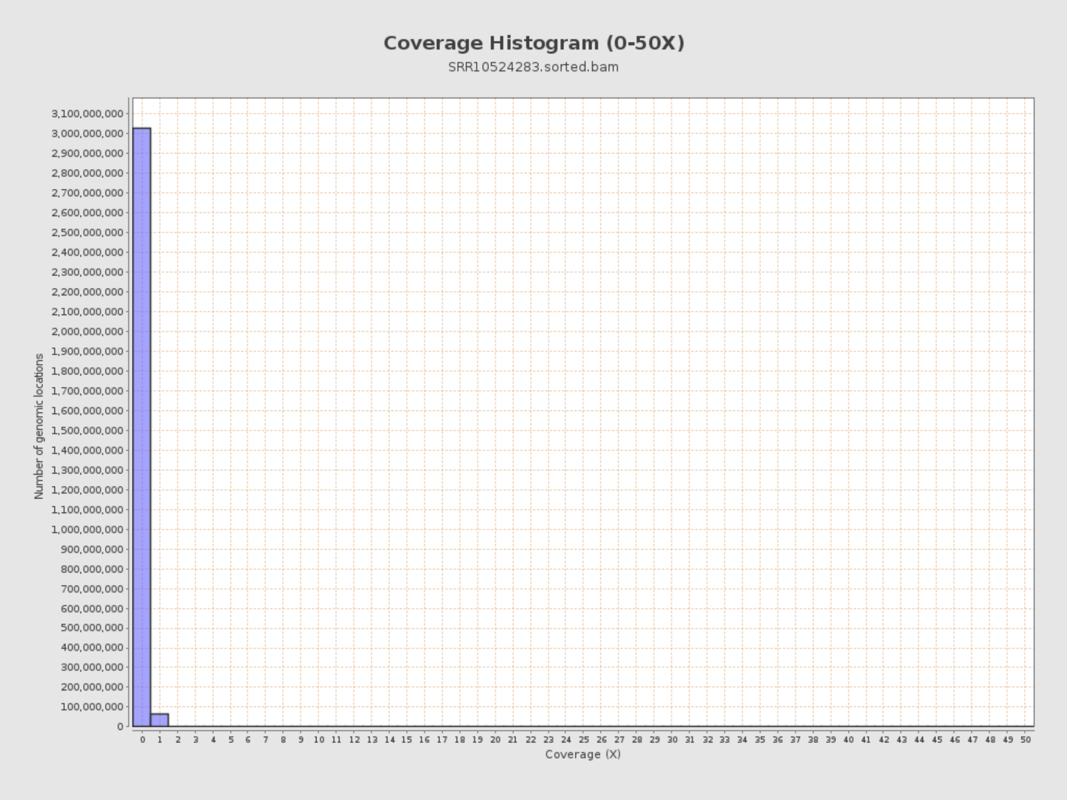
# 3. Results : Coverage across reference



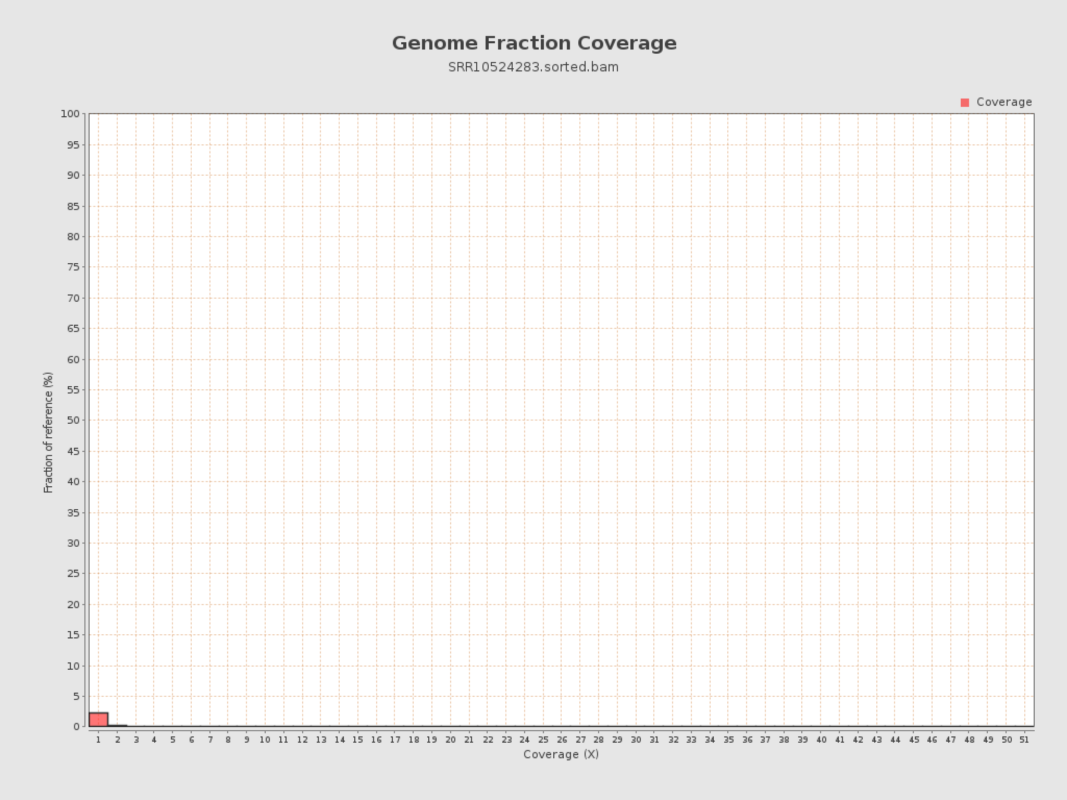
# 4. Results : Coverage Histogram



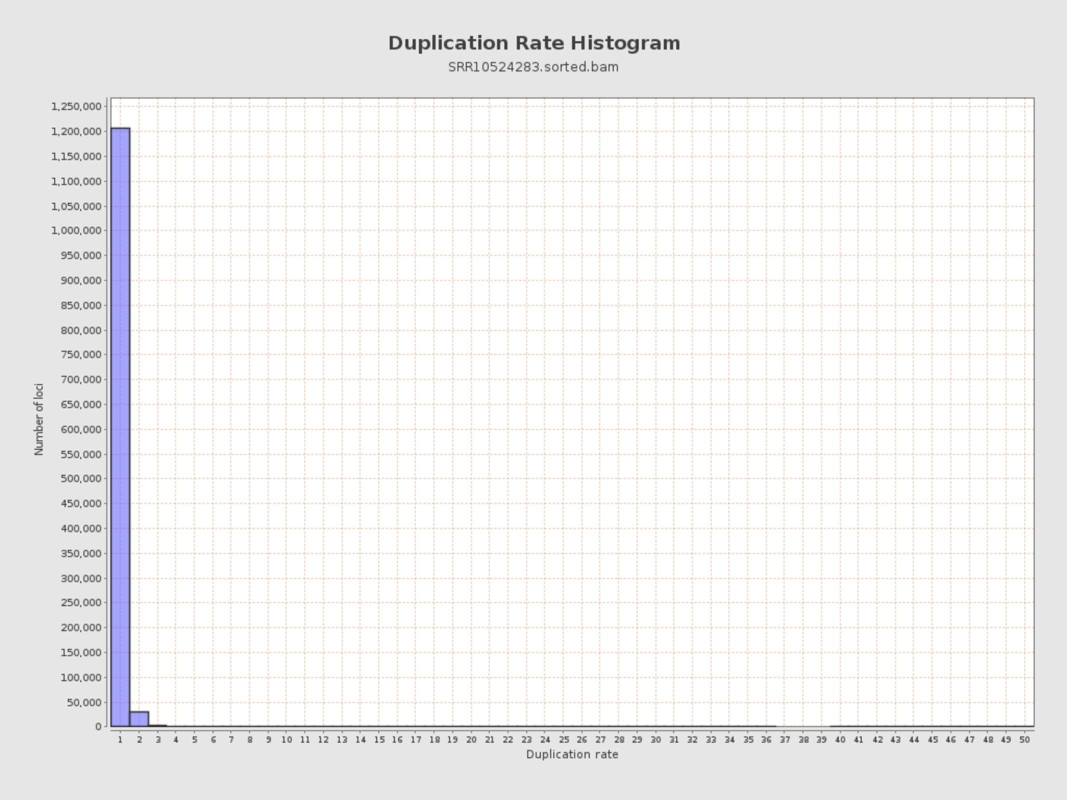
# 5. Results : Coverage Histogram (0-50X)



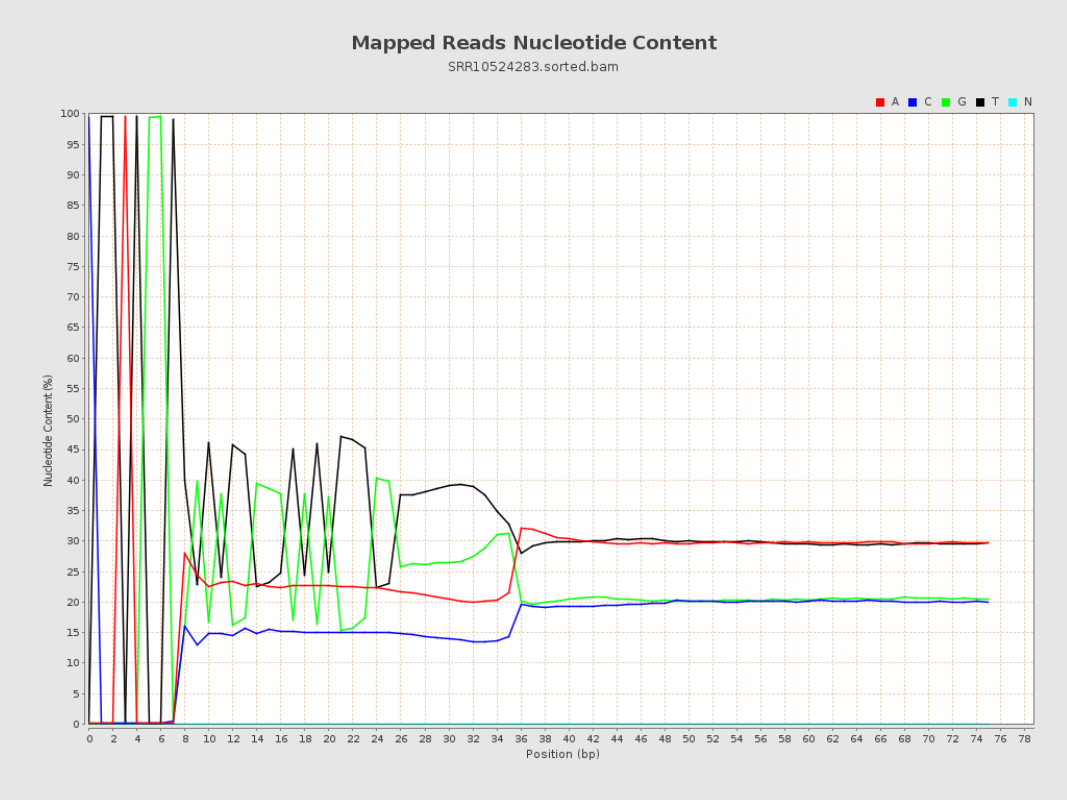
# 6. Results : Genome Fraction Coverage



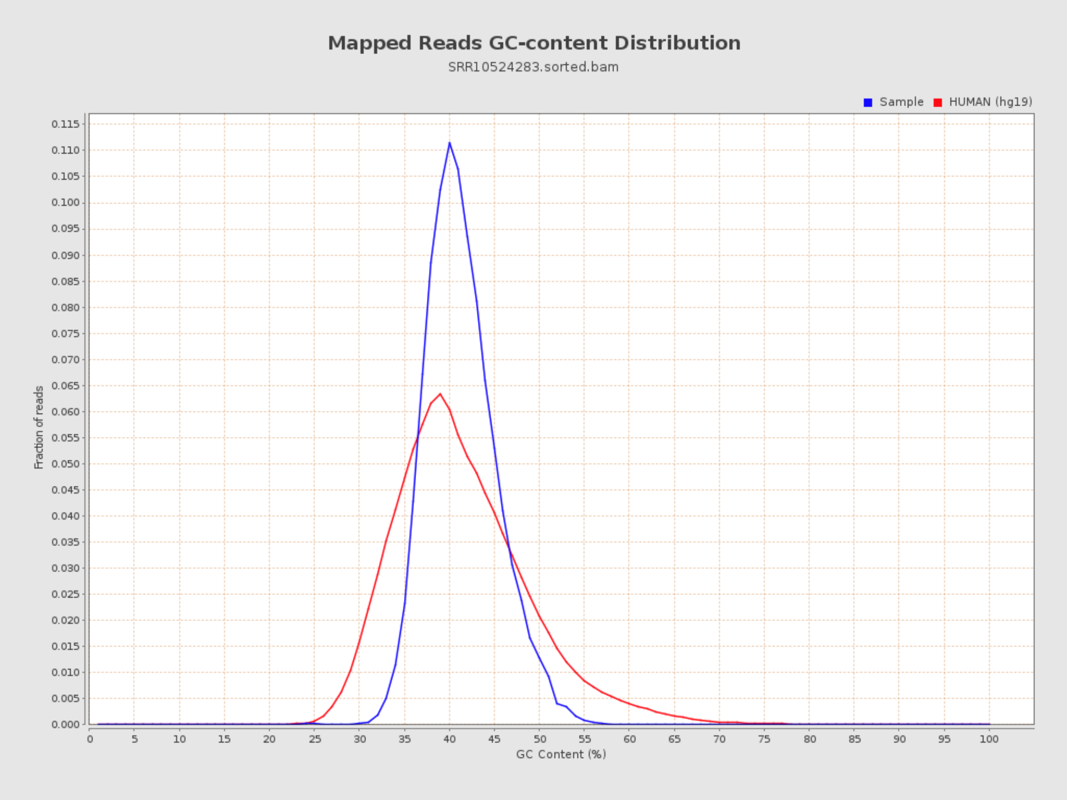
# 7. Results : Duplication Rate Histogram



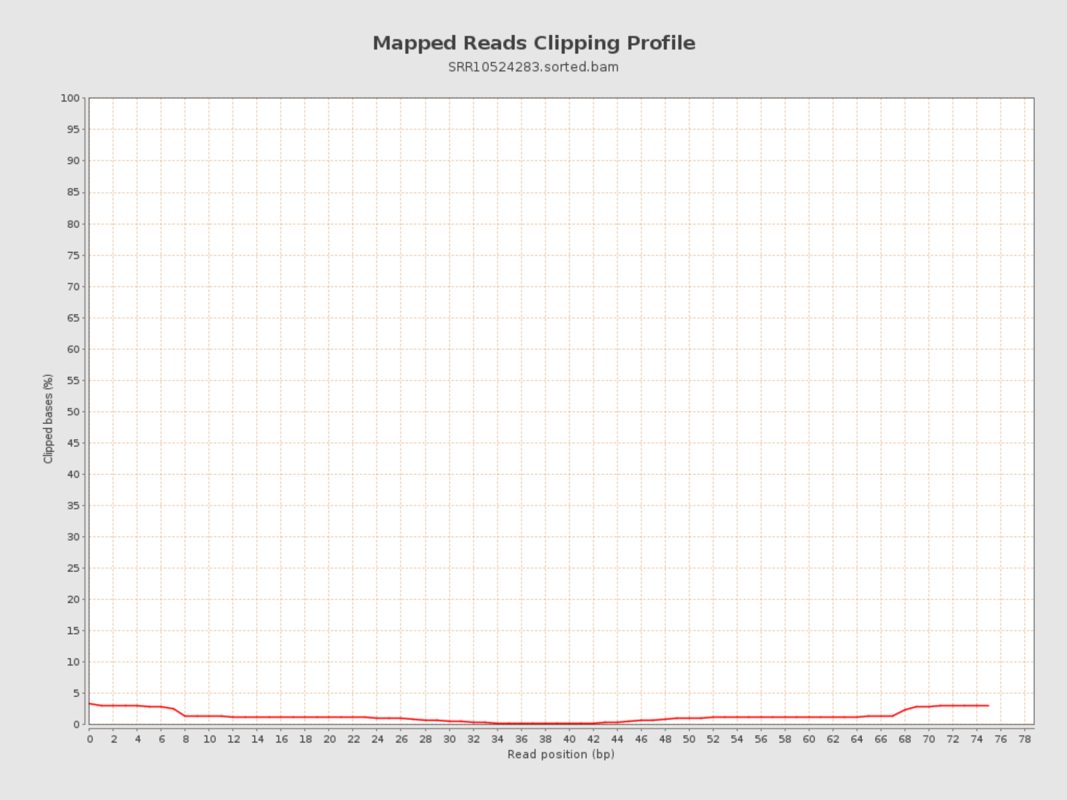
# 8. Results : Mapped Reads Nucleotide Content



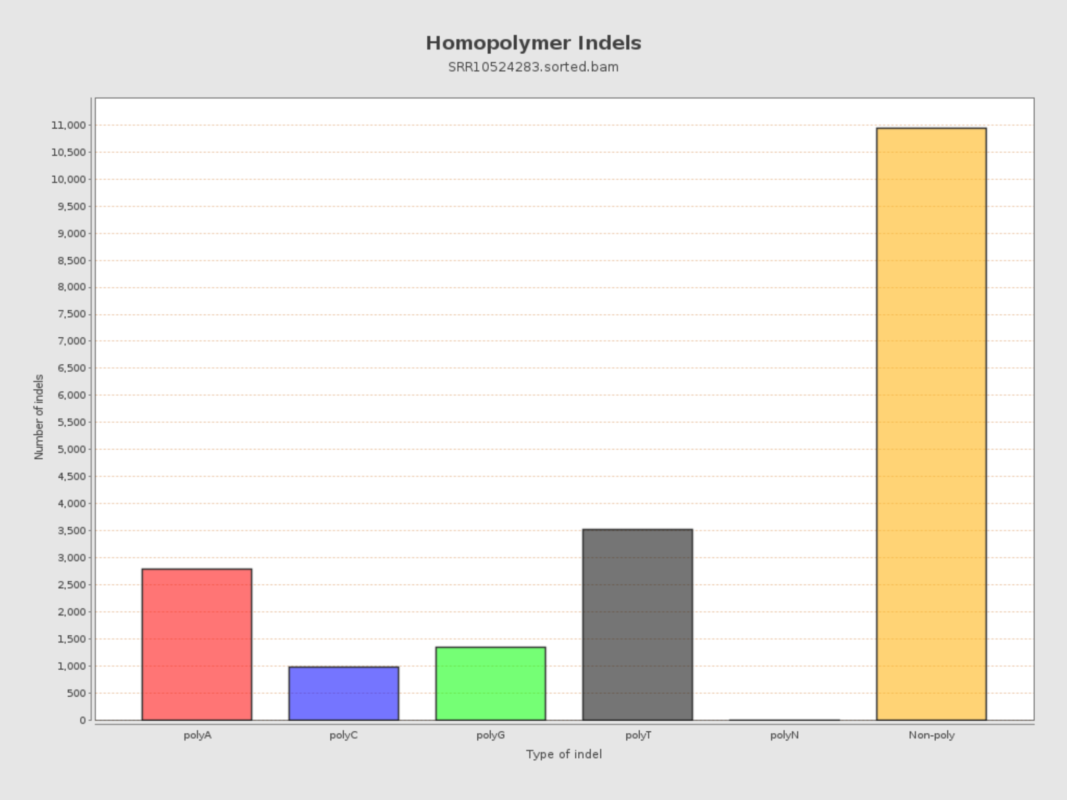
# 9. Results : Mapped Reads GC-content Distribution



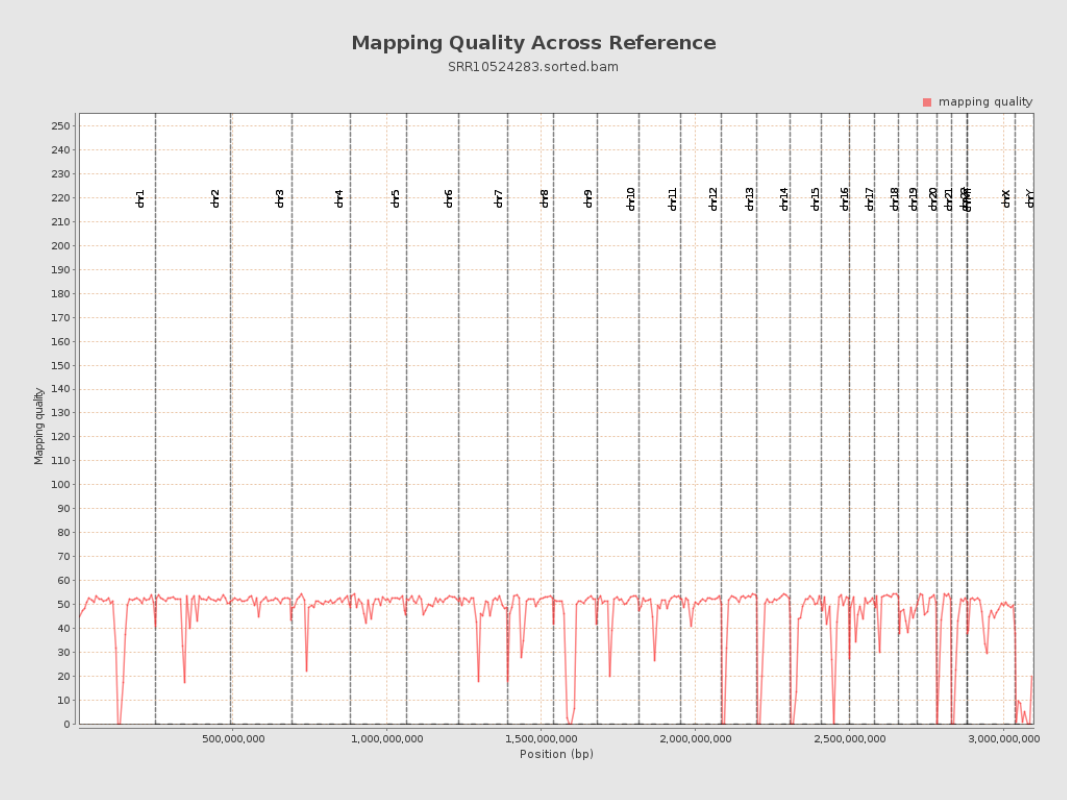
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram