# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 11:41:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524584.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_SRR10524584 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524584.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 11:41:49 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524584.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,408,316 |
| Mapped reads | 1,290,176 / 91.61% |
| Unmapped reads | 118,140 / 8.39% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 5,079 / 0.36% |
| Read min/max/mean length | 30 / 76 / 76.12 |
| Duplicated reads (estimated) | 44,397 / 3.15% |
| Duplication rate | 2.52% |
| Clipped reads | 1,293,665 / 91.86% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 18,454,932 / 24.64% |
| Number/percentage of C's | 14,723,825 / 19.66% |
| Number/percentage of T's | 23,299,093 / 31.11% |
| Number/percentage of G's | 18,411,627 / 24.58% |
| Number/percentage of N's | 1,152 / 0% |
| GC Percentage | 44.25% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0242 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2388 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.57 |

## 2.5. Mismatches and indels

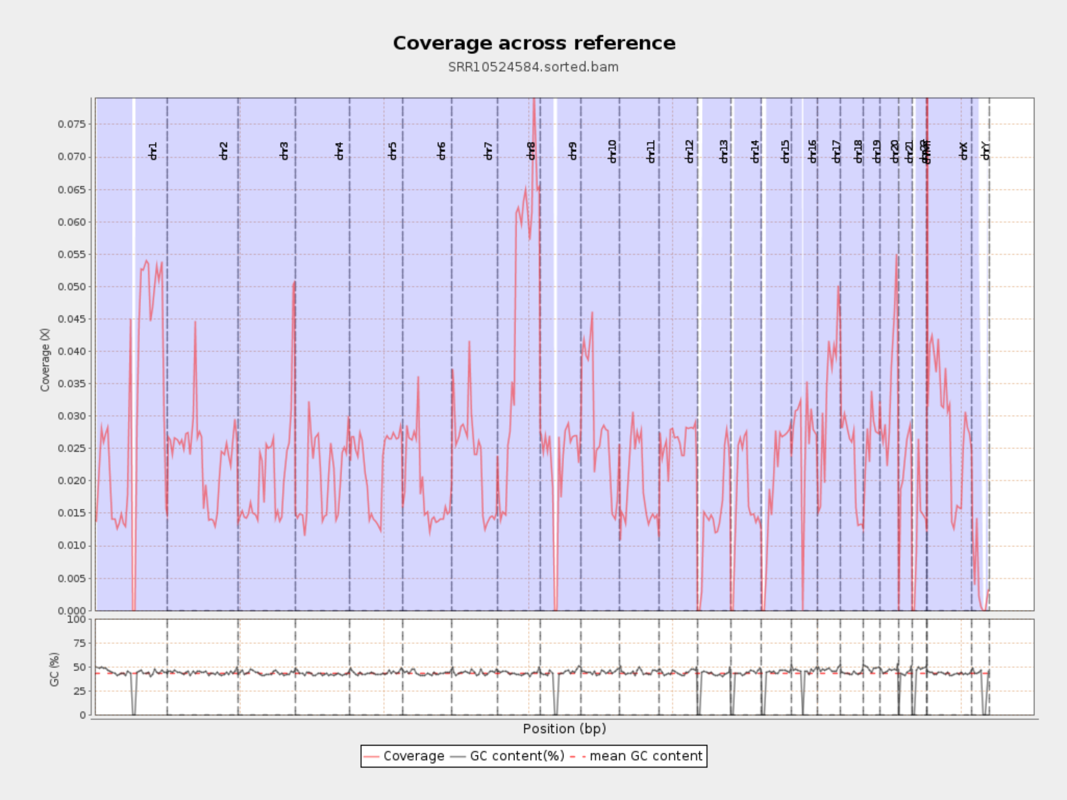
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 379,157 |
| Insertions | 4,178 |
| Mapped reads with at least one insertion | 0.32% |
| Deletions | 14,198 |
| Mapped reads with at least one deletion | 1.09% |
| Homopolymer indels | 44.75% |

## 2.6. Chromosome stats

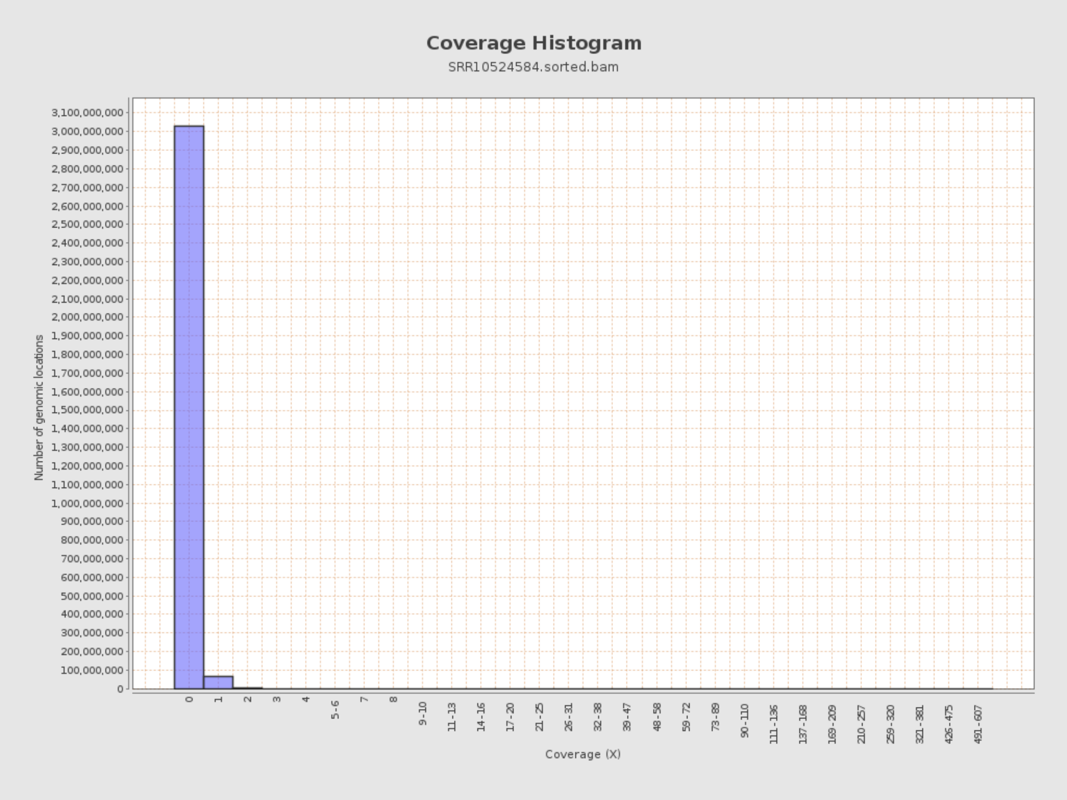
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 7428398 | 0.0298 | 0.4467 |
| chr2 | 243199373 | 5838185 | 0.024 | 0.2678 |
| chr3 | 198022430 | 4077401 | 0.0206 | 0.1562 |
| chr4 | 191154276 | 3890027 | 0.0204 | 0.1706 |
| chr5 | 180915260 | 4084293 | 0.0226 | 0.1626 |
| chr6 | 171115067 | 3252599 | 0.019 | 0.1908 |
| chr7 | 159138663 | 3800508 | 0.0239 | 0.2805 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6799955 | 0.0465 | 0.2715 |
| chr9 | 141213431 | 3176229 | 0.0225 | 0.2073 |
| chr10 | 135534747 | 3948029 | 0.0291 | 0.2477 |
| chr11 | 135006516 | 2600802 | 0.0193 | 0.213 |
| chr12 | 133851895 | 3512832 | 0.0262 | 0.1749 |
| chr13 | 115169878 | 1659551 | 0.0144 | 0.1301 |
| chr14 | 107349540 | 1789436 | 0.0167 | 0.1422 |
| chr15 | 102531392 | 1993480 | 0.0194 | 0.1516 |
| chr16 | 90354753 | 2377455 | 0.0263 | 0.186 |
| chr17 | 81195210 | 2701511 | 0.0333 | 0.2043 |
| chr18 | 78077248 | 1783031 | 0.0228 | 0.3501 |
| chr19 | 59128983 | 1579652 | 0.0267 | 0.3021 |
| chr20 | 63025520 | 2182335 | 0.0346 | 0.2024 |
| chr21 | 48129895 | 1037322 | 0.0216 | 0.1684 |
| chr22 | 51304566 | 641574 | 0.0125 | 0.1208 |
| chrMT | 16571 | 6017 | 0.3631 | 0.6518 |
| chrX | 155270560 | 4503238 | 0.029 | 0.2012 |
| chrY | 59373566 | 250556 | 0.0042 | 0.1246 |

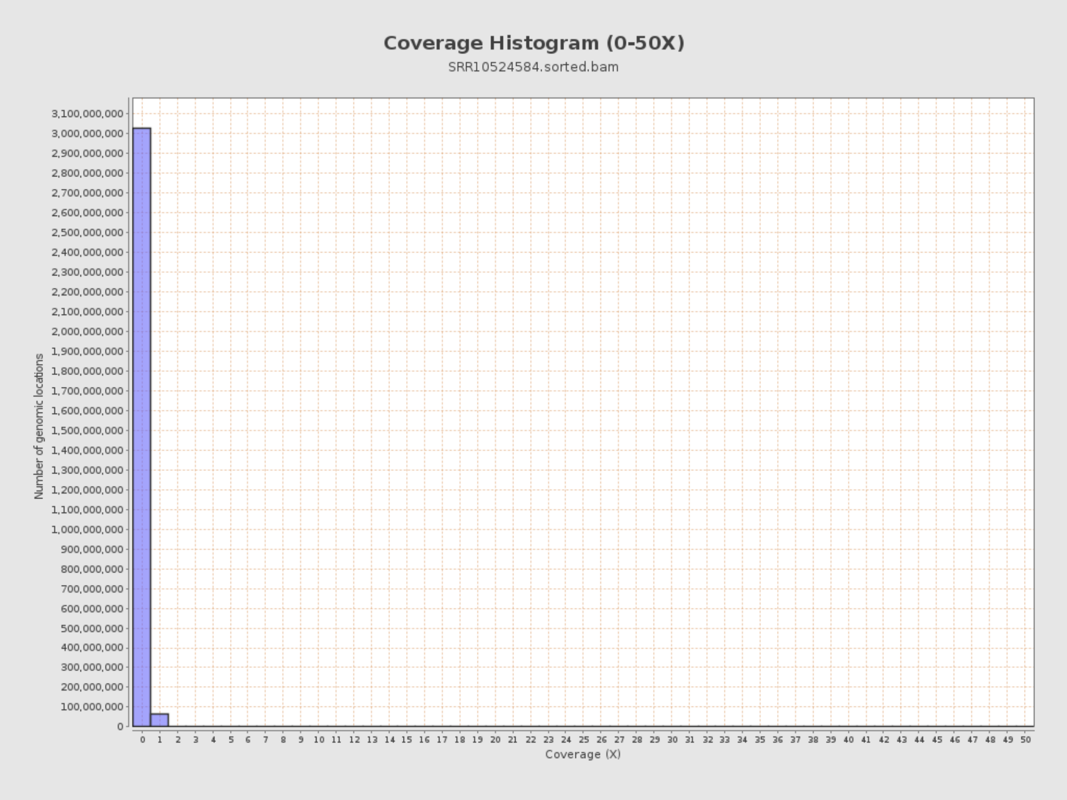
# 3. Results : Coverage across reference



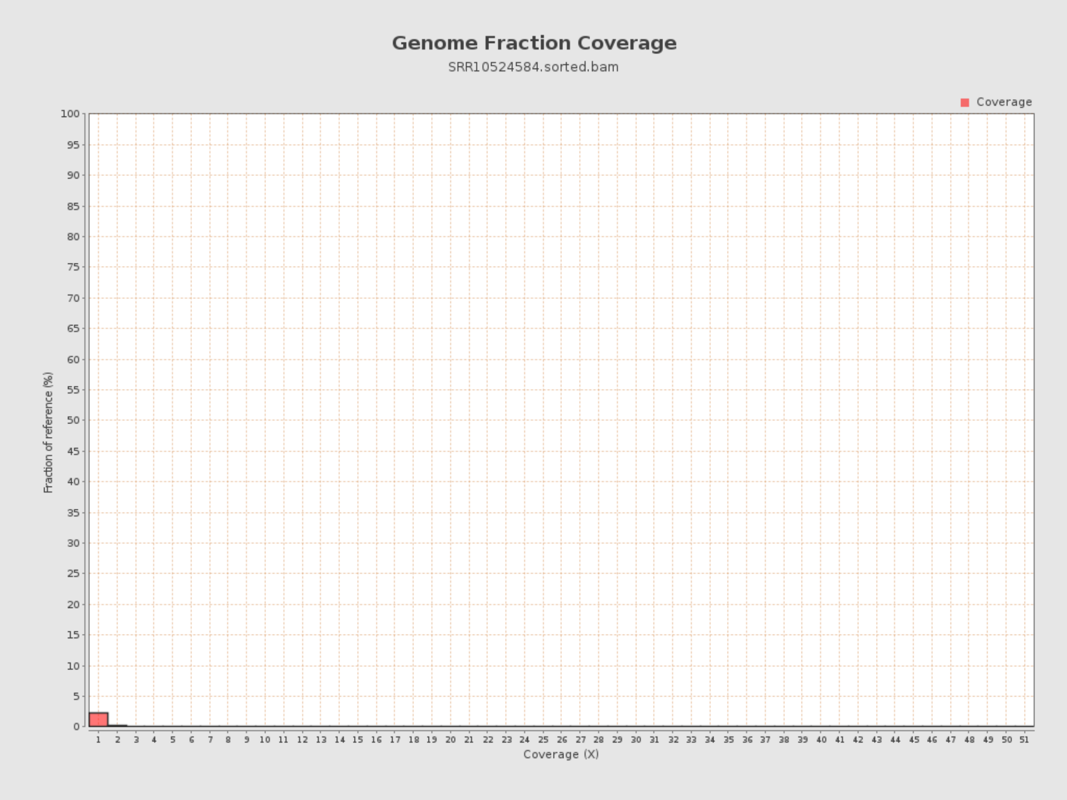
# 4. Results : Coverage Histogram



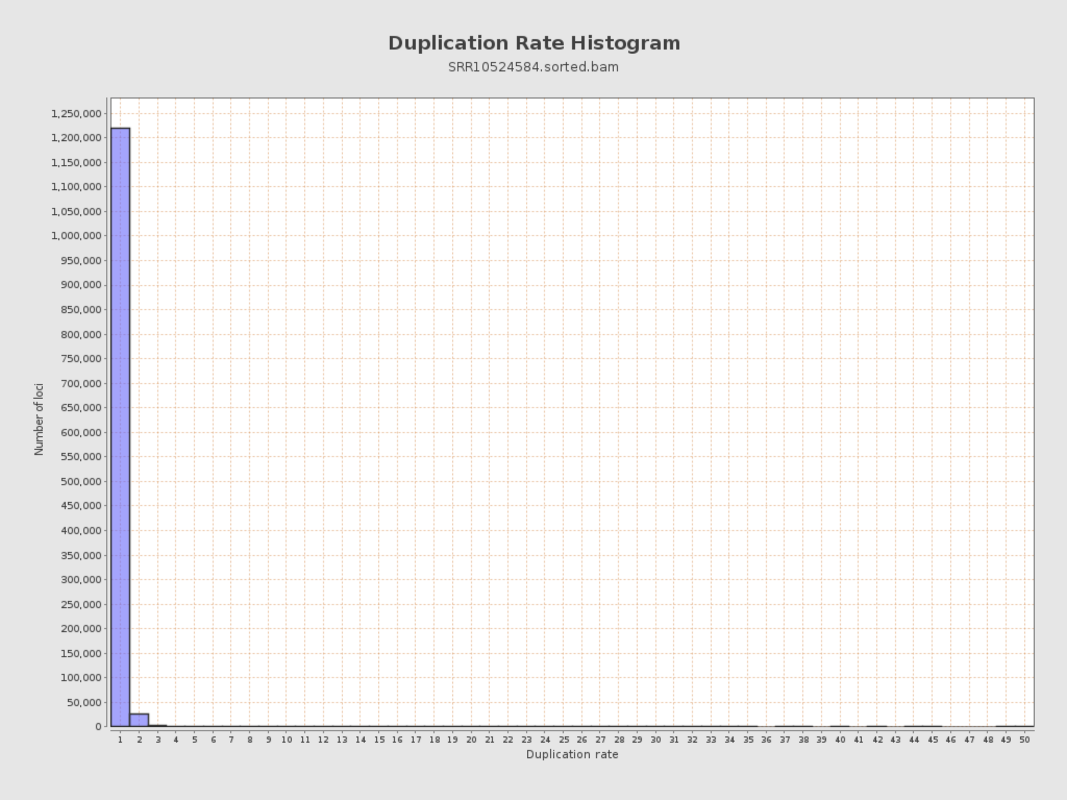
# 5. Results : Coverage Histogram (0-50X)



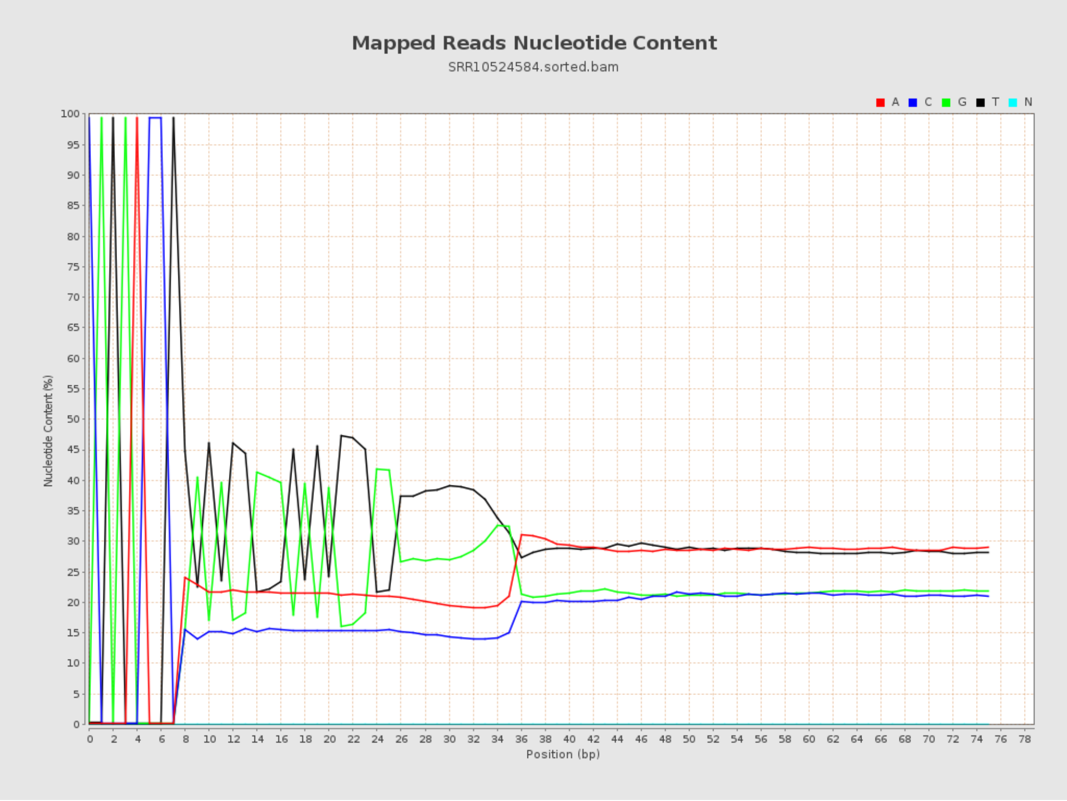
# 6. Results : Genome Fraction Coverage



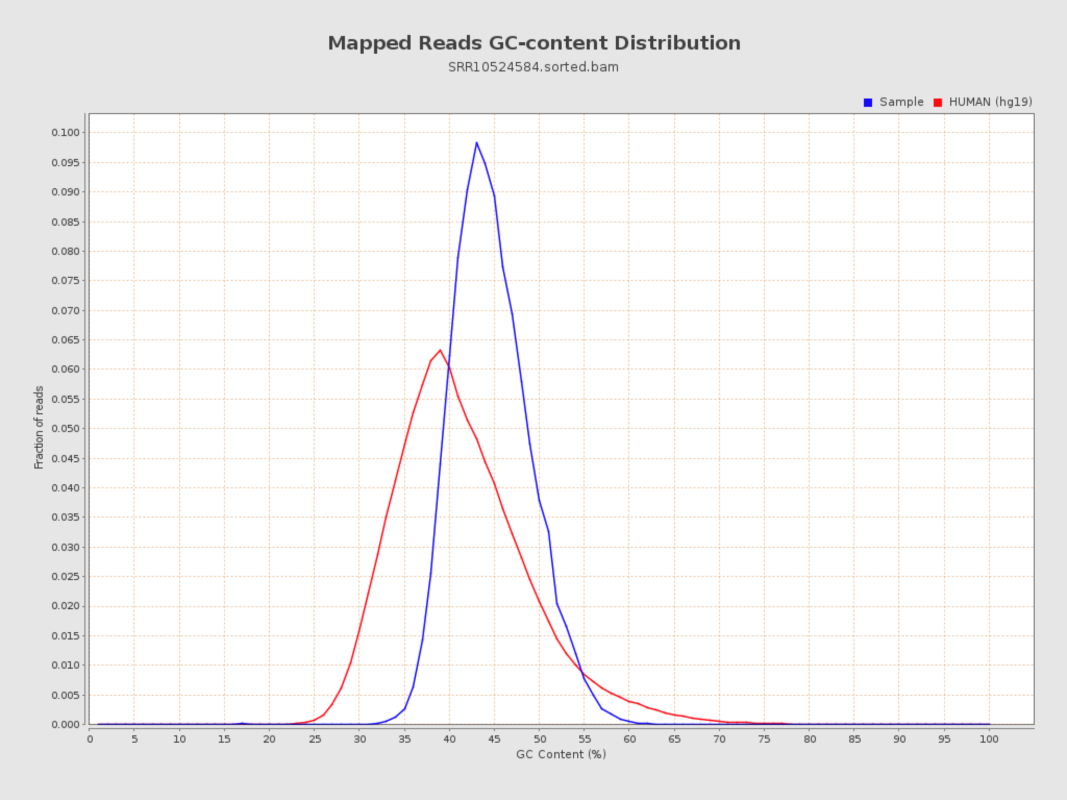
# 7. Results : Duplication Rate Histogram



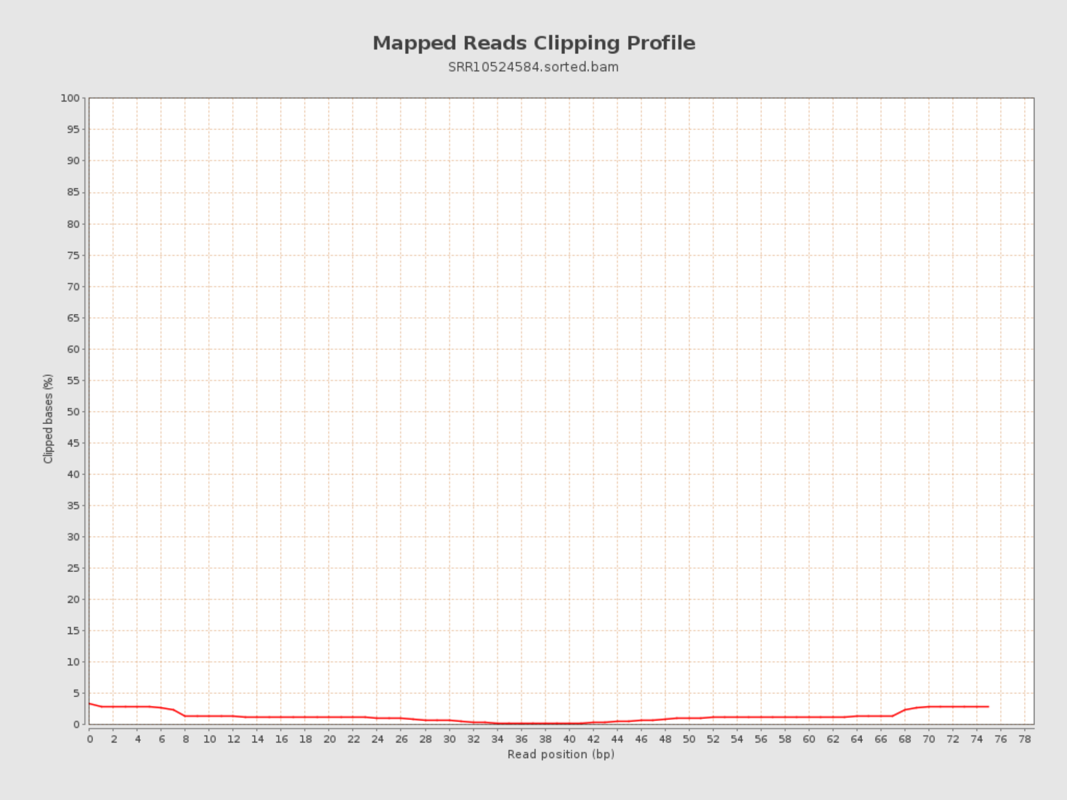
# 8. Results : Mapped Reads Nucleotide Content



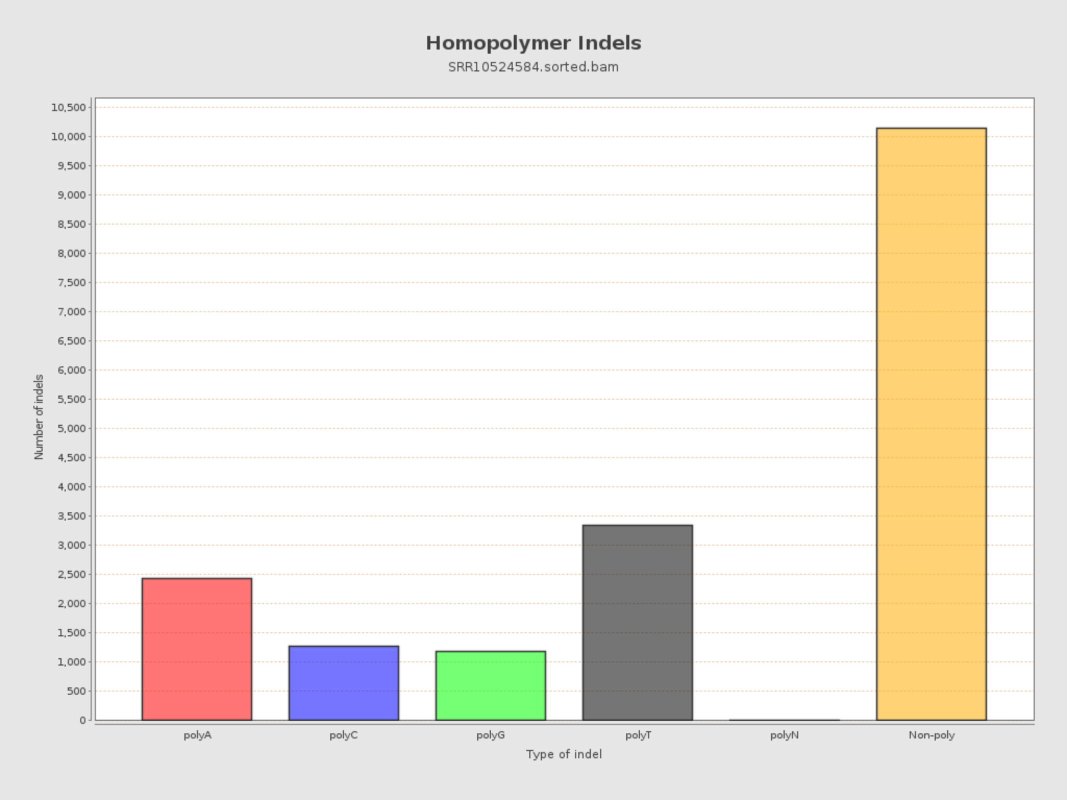
# 9. Results : Mapped Reads GC-content Distribution



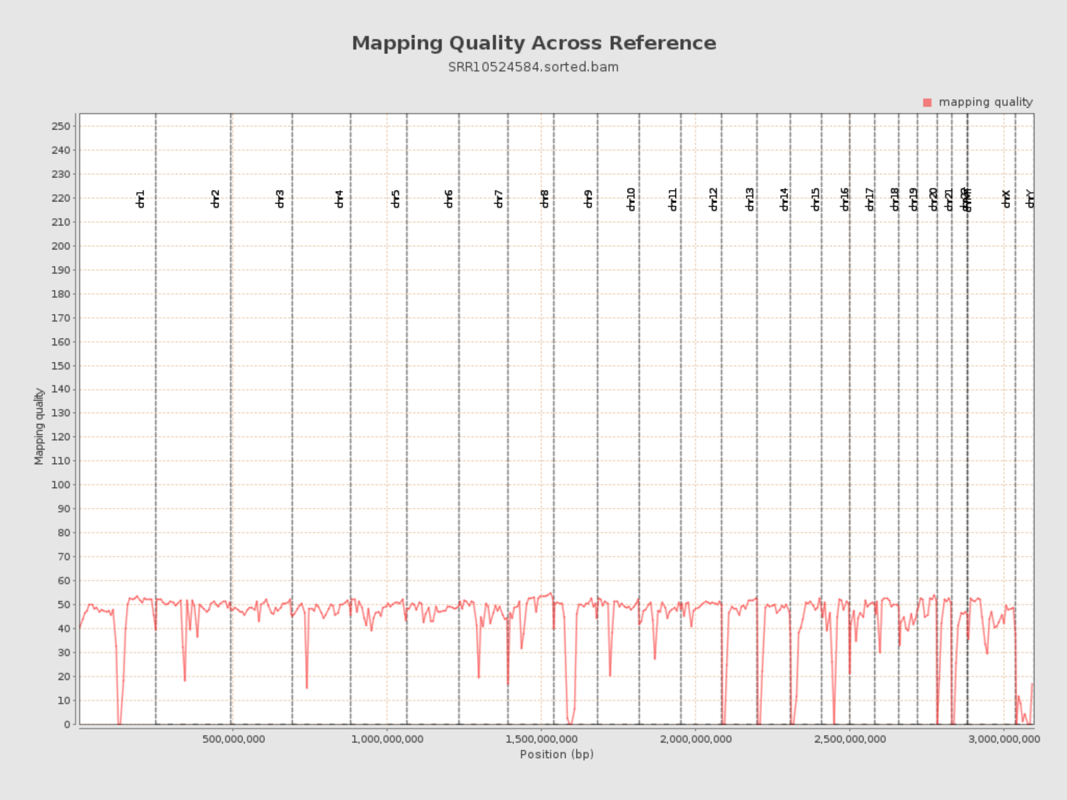
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram