# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 12:54:32*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525005.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_SRR10525005 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525005.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 12:54:25 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10525005.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,237,512 |
| Mapped reads | 1,128,372 / 91.18% |
| Unmapped reads | 109,140 / 8.82% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 4,272 / 0.35% |
| Read min/max/mean length | 30 / 76 / 76.12 |
| Duplicated reads (estimated) | 31,445 / 2.54% |
| Duplication rate | 2.02% |
| Clipped reads | 1,131,690 / 91.45% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 16,197,181 / 24.99% |
| Number/percentage of C's | 12,622,186 / 19.47% |
| Number/percentage of T's | 20,349,236 / 31.4% |
| Number/percentage of G's | 15,647,414 / 24.14% |
| Number/percentage of N's | 695 / 0% |
| GC Percentage | 43.61% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0209 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2069 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.23 |

## 2.5. Mismatches and indels

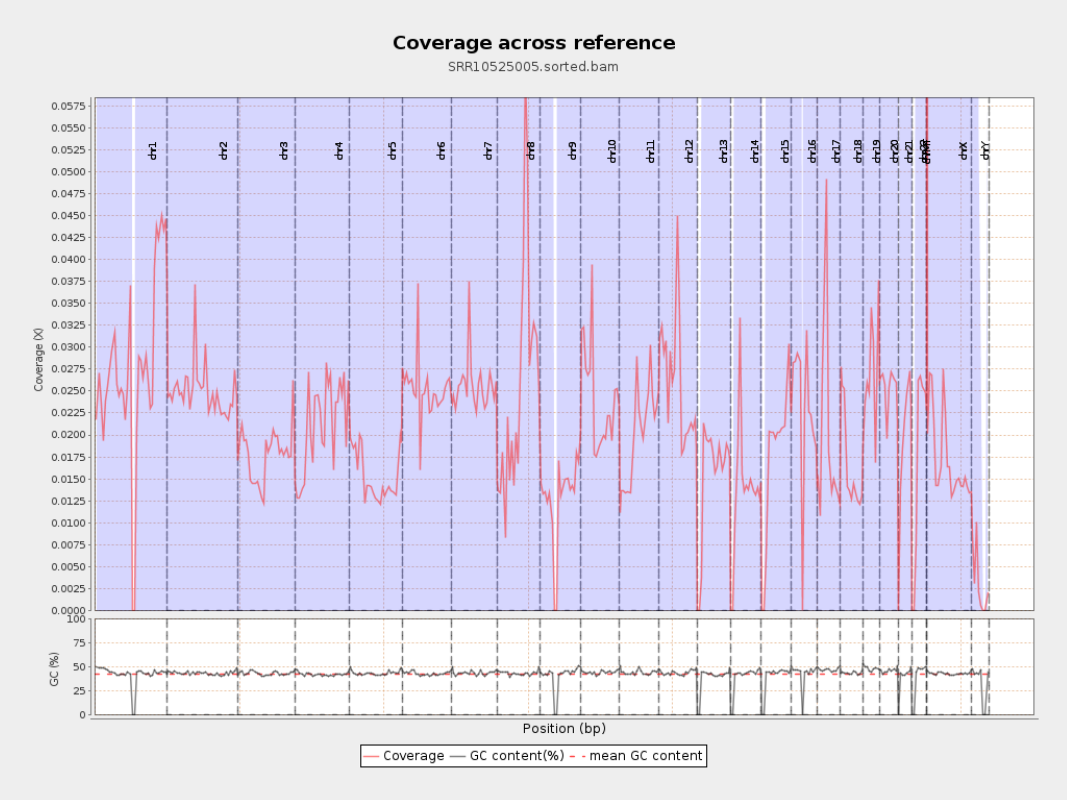
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 326,027 |
| Insertions | 3,468 |
| Mapped reads with at least one insertion | 0.31% |
| Deletions | 12,606 |
| Mapped reads with at least one deletion | 1.11% |
| Homopolymer indels | 44.63% |

## 2.6. Chromosome stats

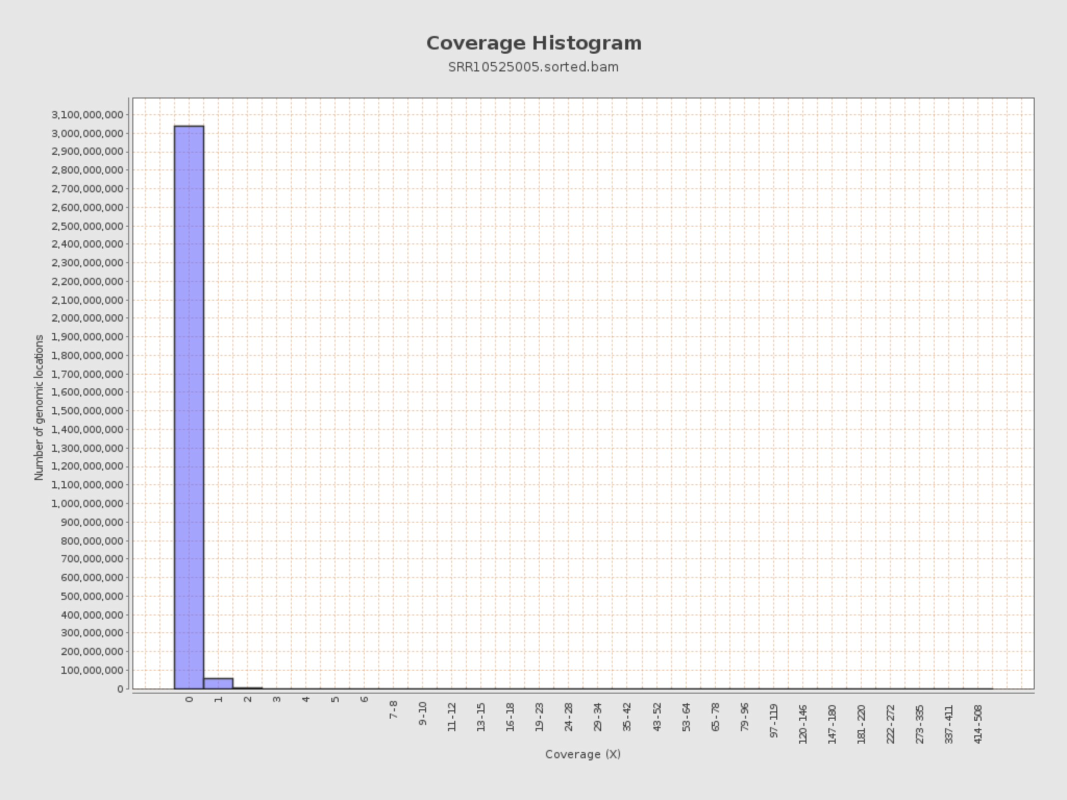
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 6863911 | 0.0275 | 0.3737 |
| chr2 | 243199373 | 6075781 | 0.025 | 0.2436 |
| chr3 | 198022430 | 3533212 | 0.0178 | 0.1432 |
| chr4 | 191154276 | 4056529 | 0.0212 | 0.1644 |
| chr5 | 180915260 | 2762730 | 0.0153 | 0.1336 |
| chr6 | 171115067 | 4308588 | 0.0252 | 0.2171 |
| chr7 | 159138663 | 4085220 | 0.0257 | 0.2626 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3795234 | 0.0259 | 0.2055 |
| chr9 | 141213431 | 1798955 | 0.0127 | 0.1586 |
| chr10 | 135534747 | 3278293 | 0.0242 | 0.2074 |
| chr11 | 135006516 | 2730284 | 0.0202 | 0.1852 |
| chr12 | 133851895 | 3495244 | 0.0261 | 0.1721 |
| chr13 | 115169878 | 1757163 | 0.0153 | 0.1318 |
| chr14 | 107349540 | 1464101 | 0.0136 | 0.1275 |
| chr15 | 102531392 | 1818021 | 0.0177 | 0.1455 |
| chr16 | 90354753 | 2076151 | 0.023 | 0.1666 |
| chr17 | 81195210 | 1698492 | 0.0209 | 0.1918 |
| chr18 | 78077248 | 1273839 | 0.0163 | 0.235 |
| chr19 | 59128983 | 1613912 | 0.0273 | 0.2437 |
| chr20 | 63025520 | 1592162 | 0.0253 | 0.1698 |
| chr21 | 48129895 | 940570 | 0.0195 | 0.1527 |
| chr22 | 51304566 | 905264 | 0.0176 | 0.1403 |
| chrMT | 16571 | 19495 | 1.1765 | 1.344 |
| chrX | 155270560 | 2712017 | 0.0175 | 0.159 |
| chrY | 59373566 | 182314 | 0.0031 | 0.0846 |

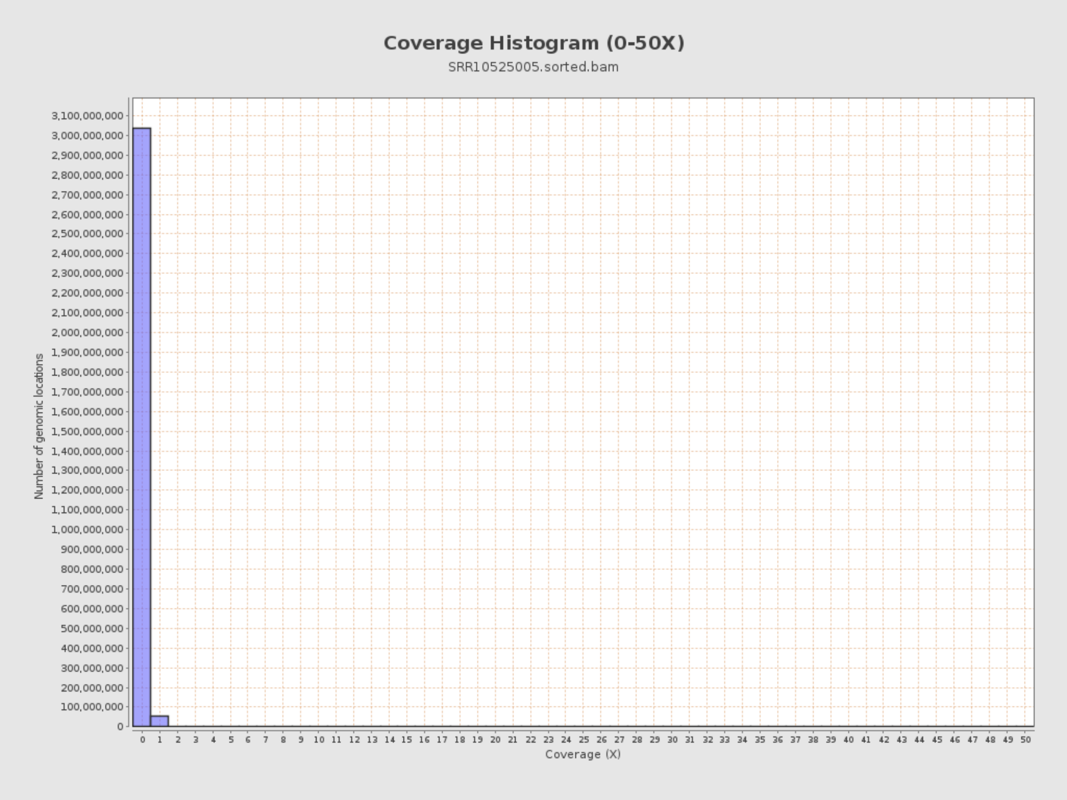
# 3. Results : Coverage across reference



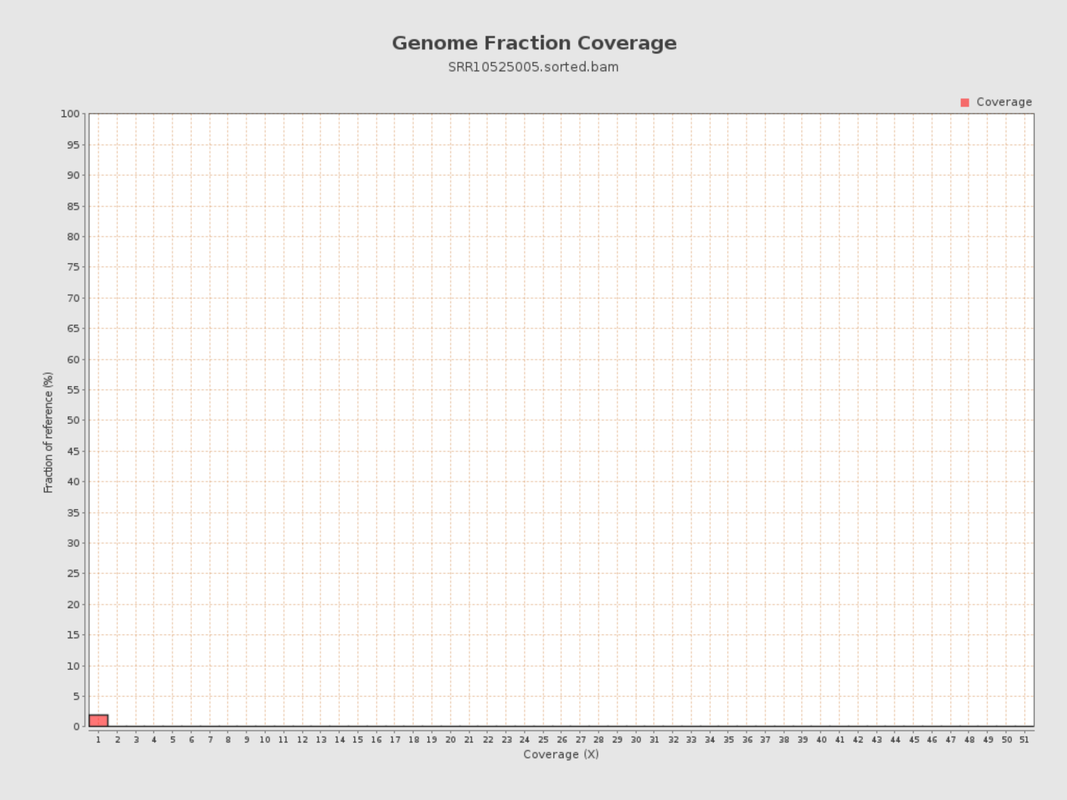
# 4. Results : Coverage Histogram



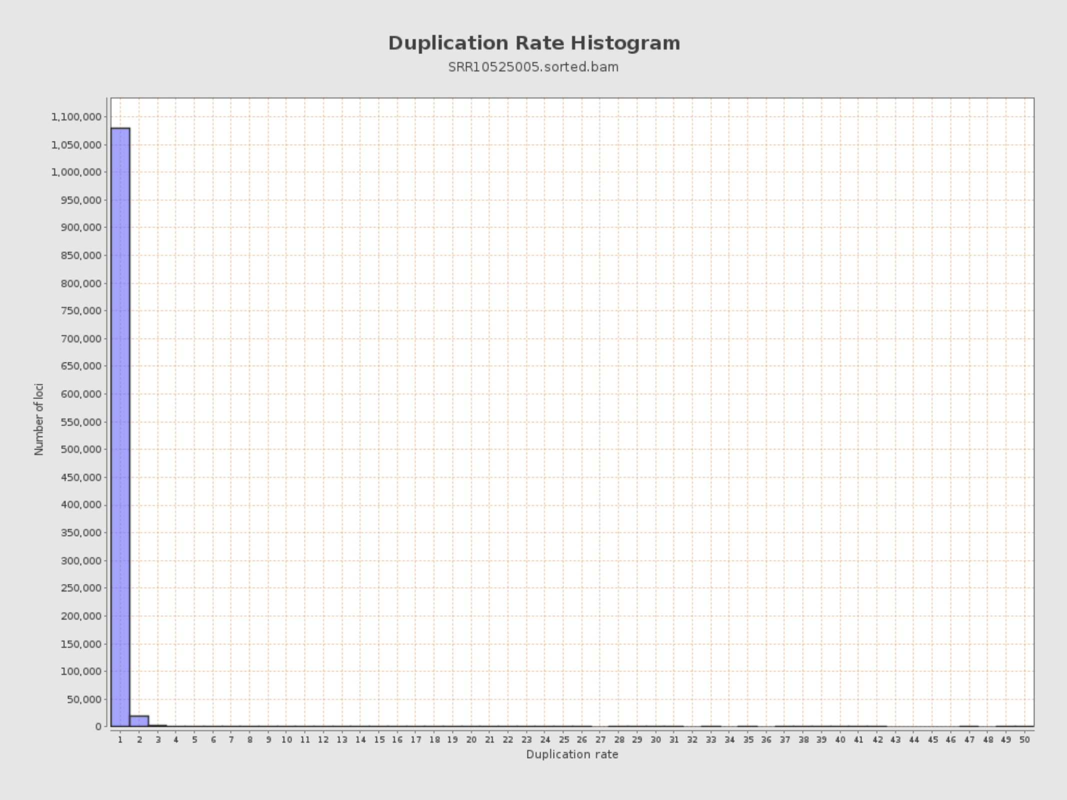
# 5. Results : Coverage Histogram (0-50X)



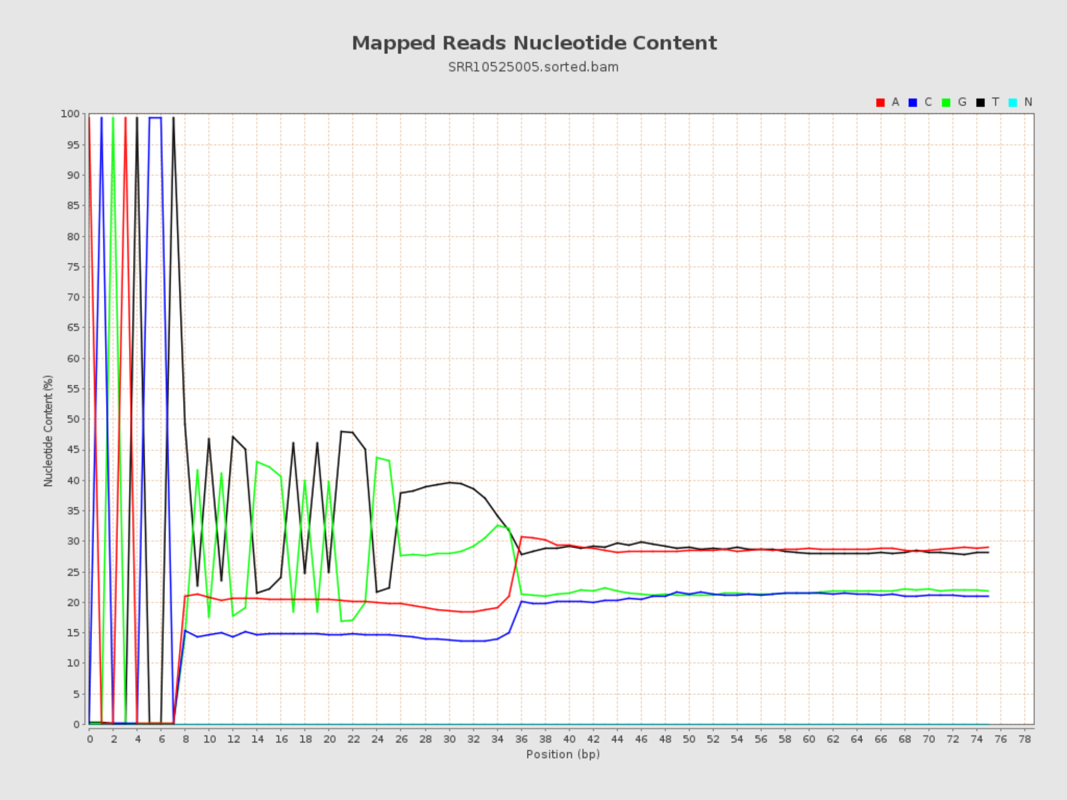
# 6. Results : Genome Fraction Coverage



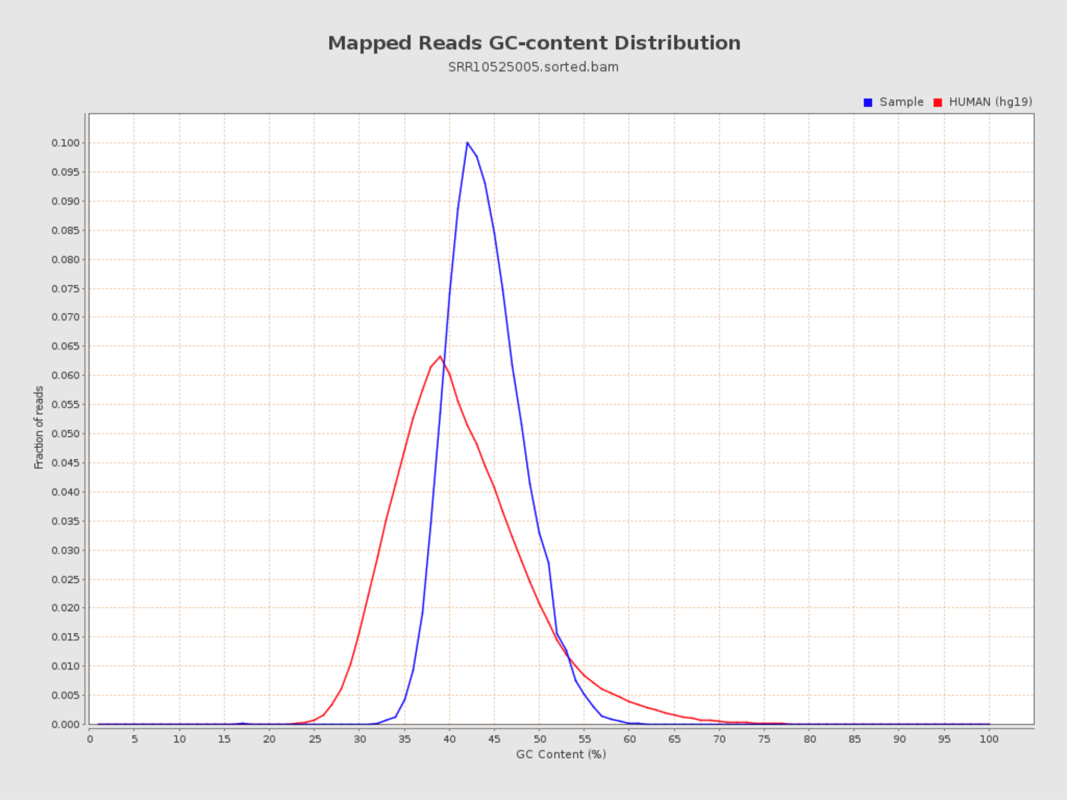
# 7. Results : Duplication Rate Histogram



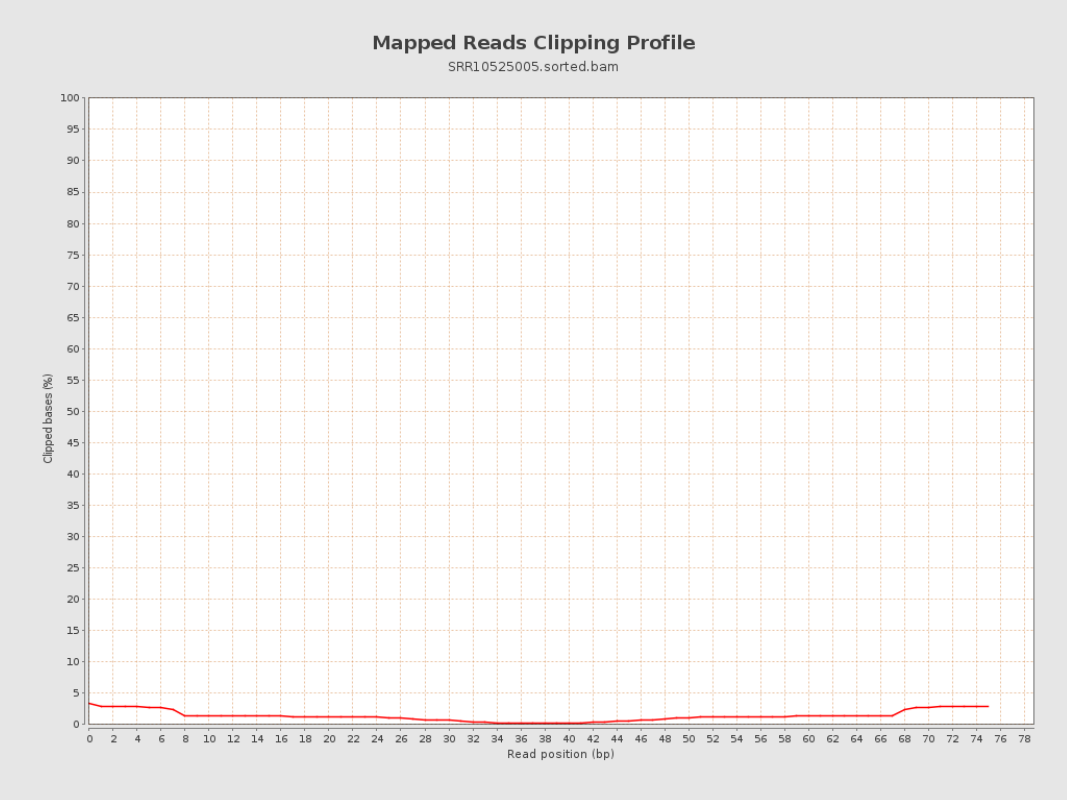
# 8. Results : Mapped Reads Nucleotide Content



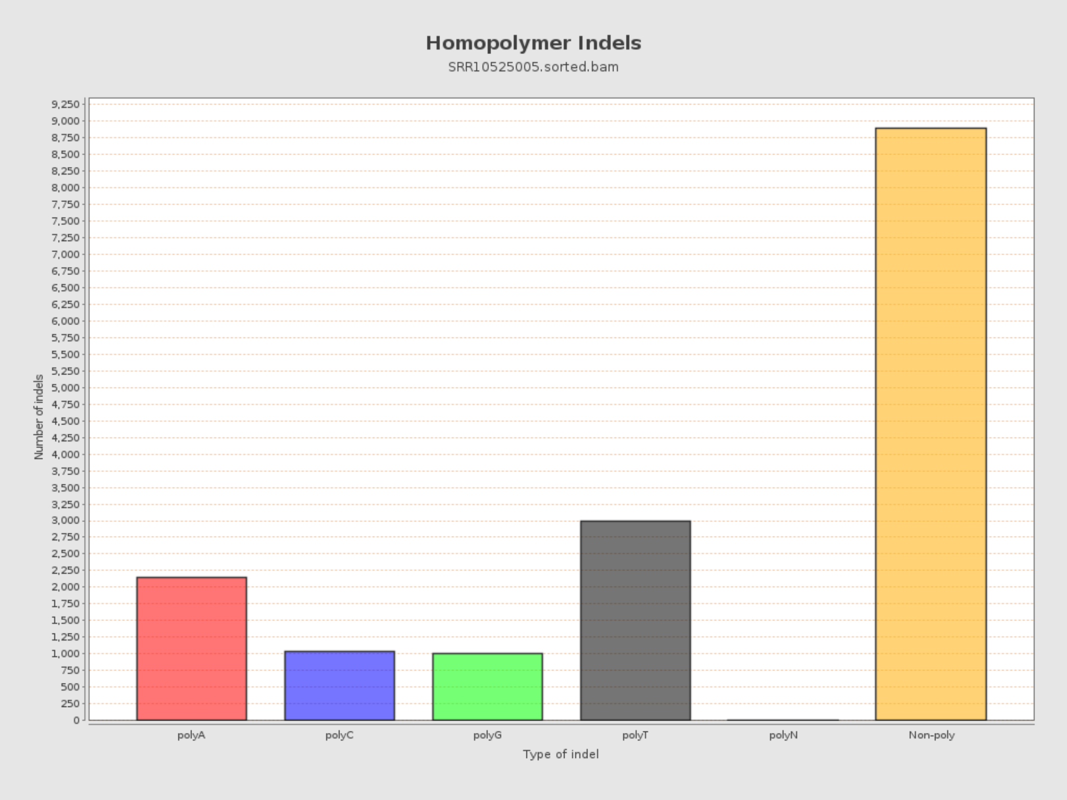
# 9. Results : Mapped Reads GC-content Distribution



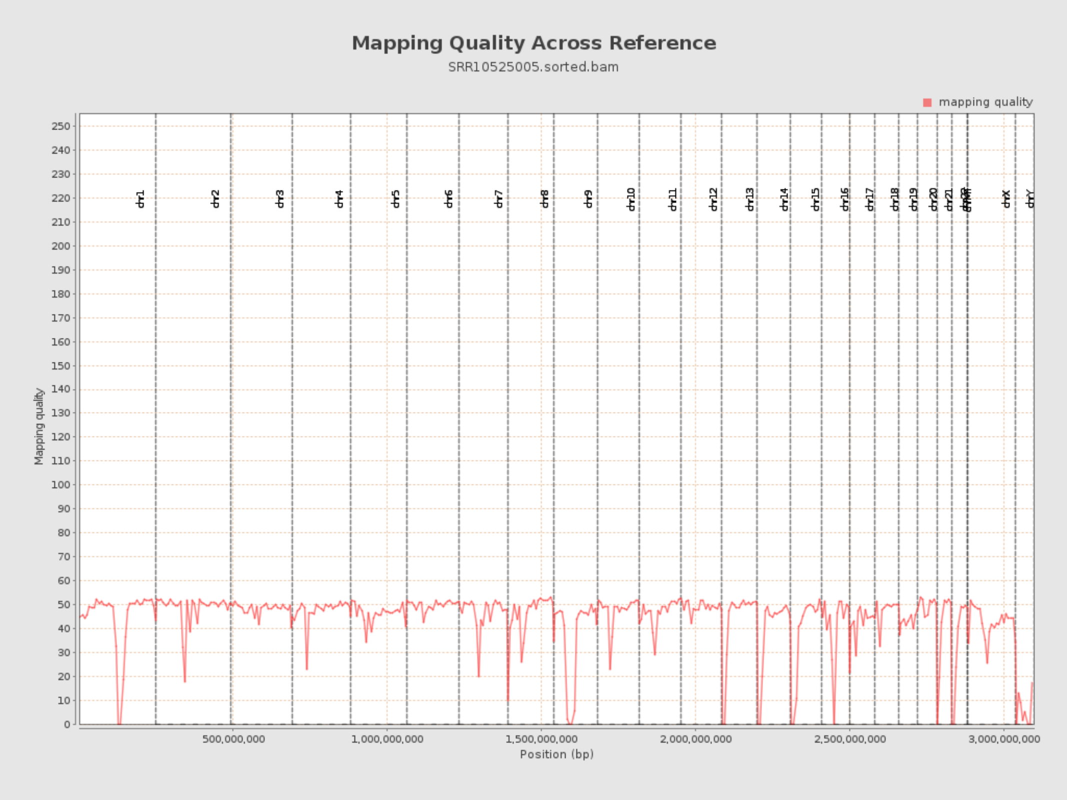
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram