# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 23:50:44*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716600.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_SRR9716600 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716600.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 23:50:43 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716600.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,011,433 |
| Mapped reads | 857,247 / 84.76% |
| Unmapped reads | 154,186 / 15.24% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 5,233 / 0.52% |
| Read min/max/mean length | 30 / 76 / 76.17 |
| Duplicated reads (estimated) | 19,706 / 1.95% |
| Duplication rate | 1.77% |
| Clipped reads | 860,496 / 85.08% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 12,978,495 / 25.98% |
| Number/percentage of C's | 9,408,217 / 18.83% |
| Number/percentage of T's | 15,158,317 / 30.34% |
| Number/percentage of G's | 12,414,559 / 24.85% |
| Number/percentage of N's | 640 / 0% |
| GC Percentage | 43.68% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0161 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1631 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.87 |

## 2.5. Mismatches and indels

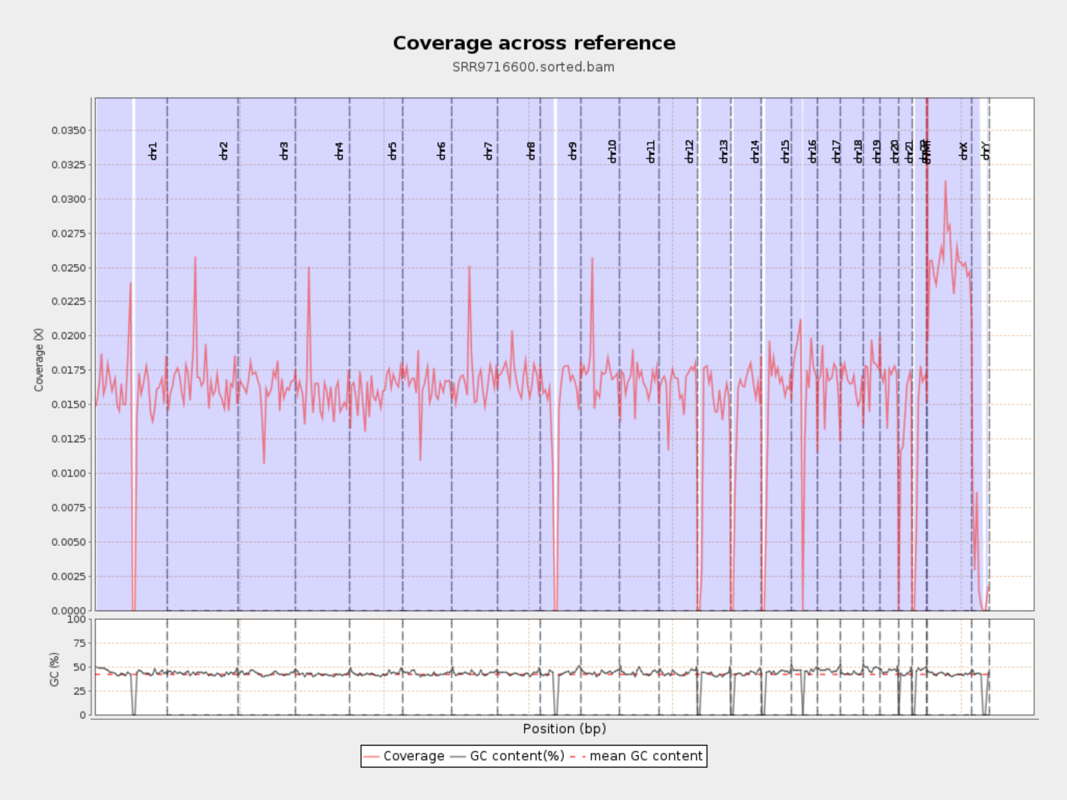
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 246,956 |
| Insertions | 3,395 |
| Mapped reads with at least one insertion | 0.39% |
| Deletions | 9,063 |
| Mapped reads with at least one deletion | 1.05% |
| Homopolymer indels | 40.02% |

## 2.6. Chromosome stats

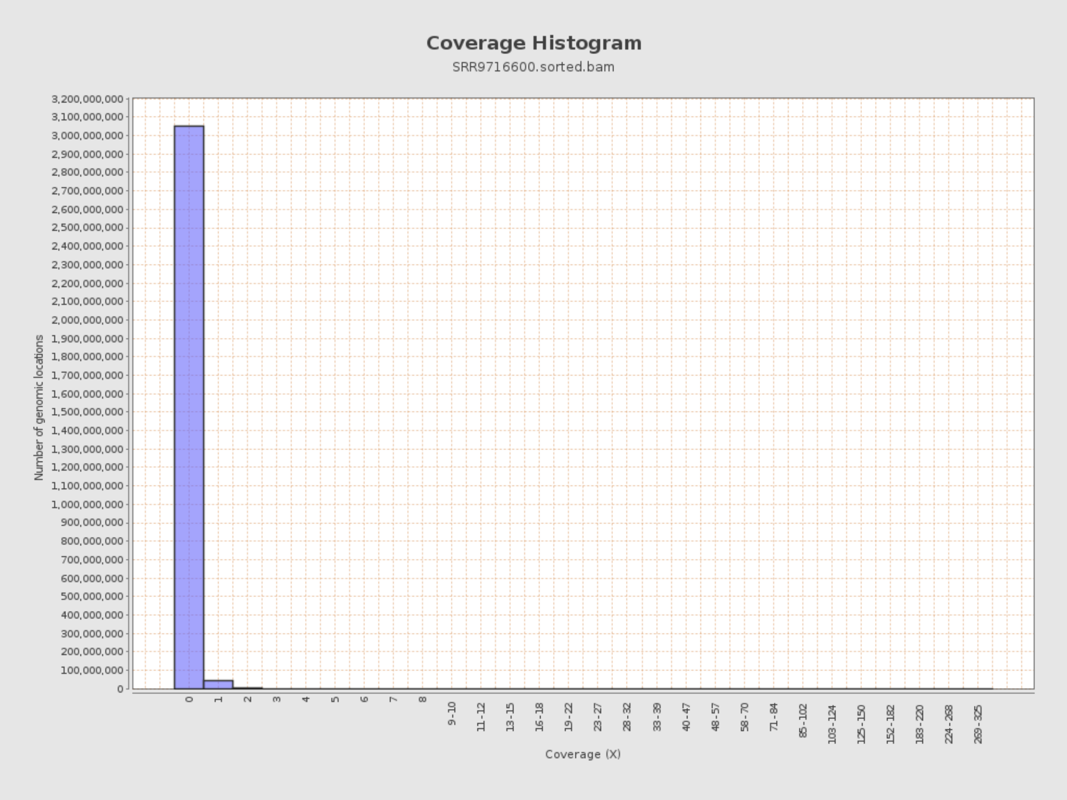
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3837111 | 0.0154 | 0.2386 |
| chr2 | 243199373 | 4078617 | 0.0168 | 0.1978 |
| chr3 | 198022430 | 3214030 | 0.0162 | 0.1339 |
| chr4 | 191154276 | 3062190 | 0.016 | 0.1429 |
| chr5 | 180915260 | 2909607 | 0.0161 | 0.1336 |
| chr6 | 171115067 | 2804900 | 0.0164 | 0.1404 |
| chr7 | 159138663 | 2696162 | 0.0169 | 0.1955 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2504259 | 0.0171 | 0.1695 |
| chr9 | 141213431 | 2027572 | 0.0144 | 0.1397 |
| chr10 | 135534747 | 2368894 | 0.0175 | 0.1687 |
| chr11 | 135006516 | 2262221 | 0.0168 | 0.1576 |
| chr12 | 133851895 | 2199506 | 0.0164 | 0.135 |
| chr13 | 115169878 | 1529377 | 0.0133 | 0.1215 |
| chr14 | 107349540 | 1495671 | 0.0139 | 0.1269 |
| chr15 | 102531392 | 1435402 | 0.014 | 0.126 |
| chr16 | 90354753 | 1465068 | 0.0162 | 0.1374 |
| chr17 | 81195210 | 1356412 | 0.0167 | 0.1426 |
| chr18 | 78077248 | 1293733 | 0.0166 | 0.2163 |
| chr19 | 59128983 | 1035349 | 0.0175 | 0.1893 |
| chr20 | 63025520 | 1053225 | 0.0167 | 0.1374 |
| chr21 | 48129895 | 634327 | 0.0132 | 0.1256 |
| chr22 | 51304566 | 594832 | 0.0116 | 0.1135 |
| chrMT | 16571 | 7415 | 0.4475 | 0.7188 |
| chrX | 155270560 | 3944293 | 0.0254 | 0.1736 |
| chrY | 59373566 | 164461 | 0.0028 | 0.0773 |

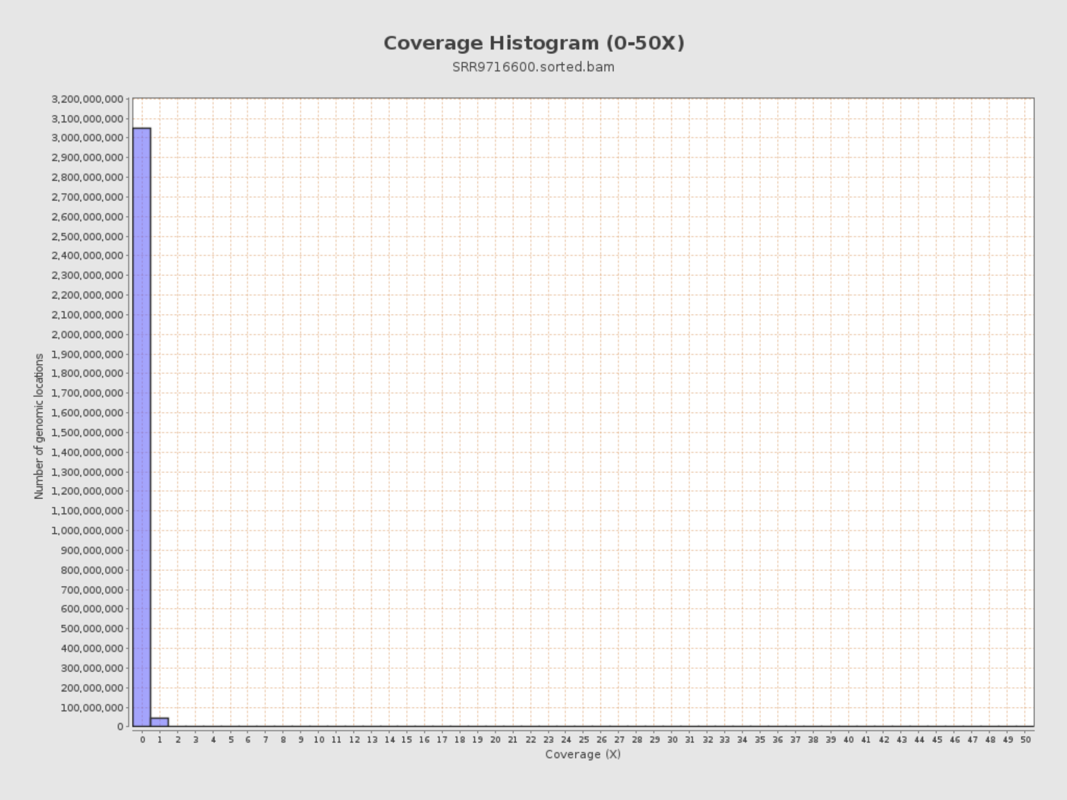
# 3. Results : Coverage across reference



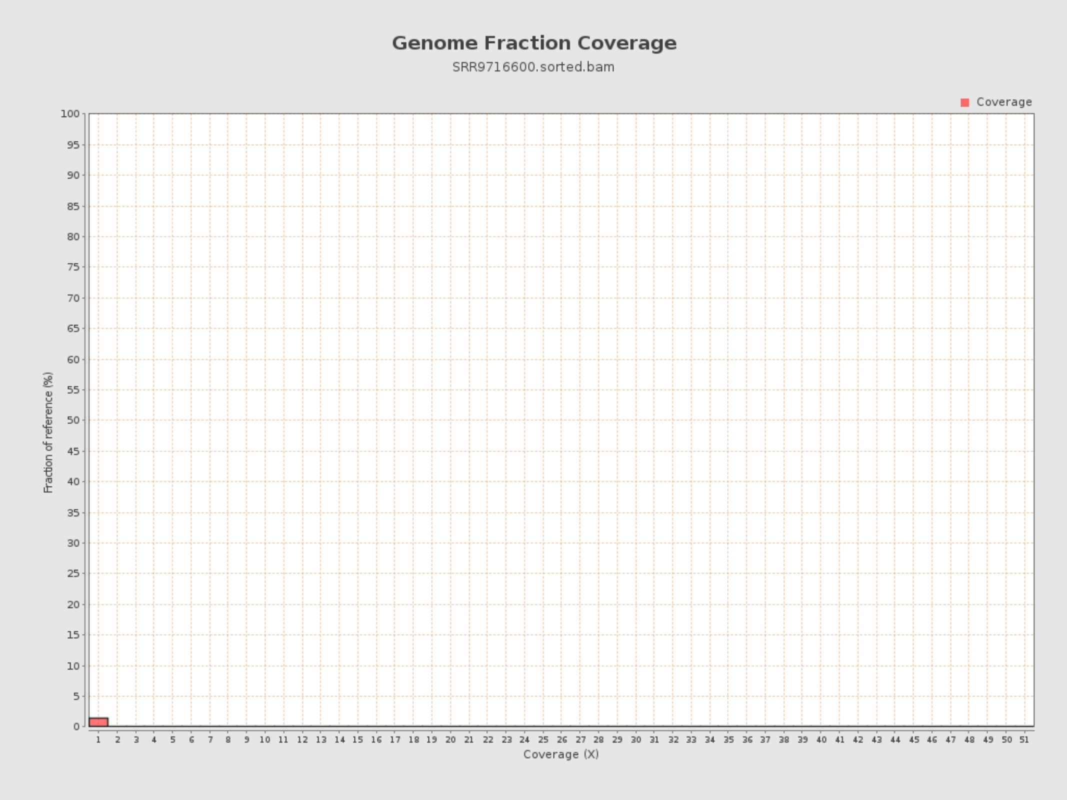
# 4. Results : Coverage Histogram



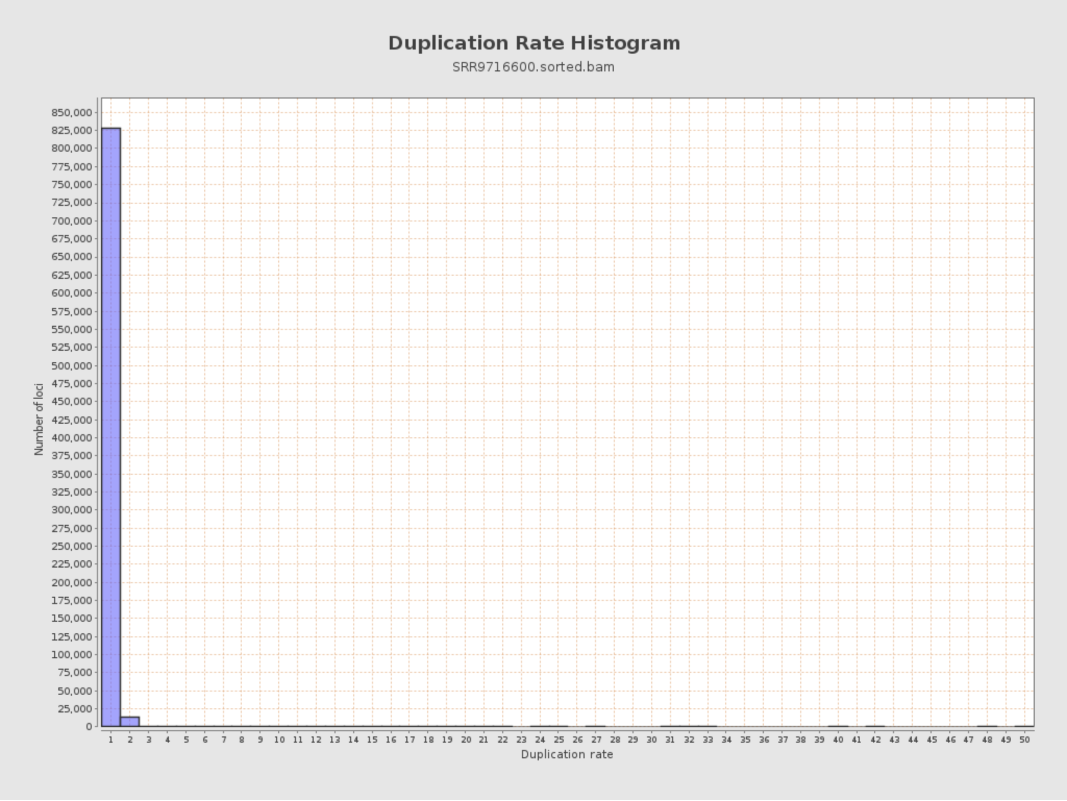
# 5. Results : Coverage Histogram (0-50X)



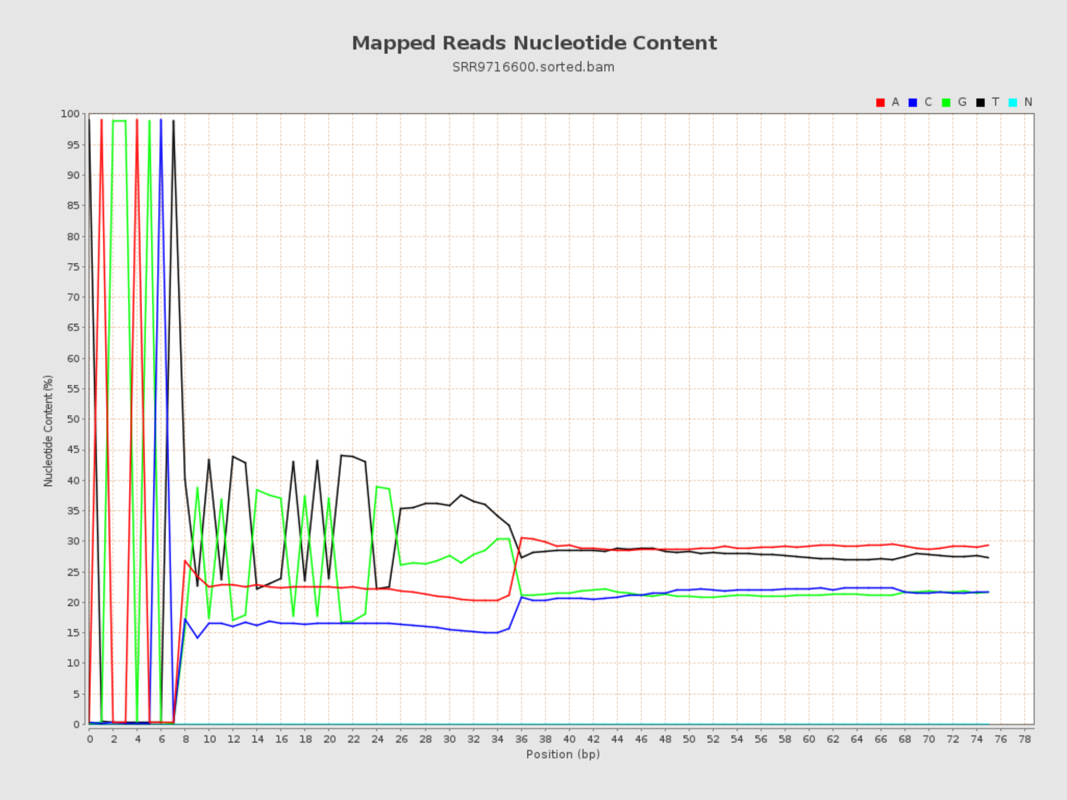
# 6. Results : Genome Fraction Coverage



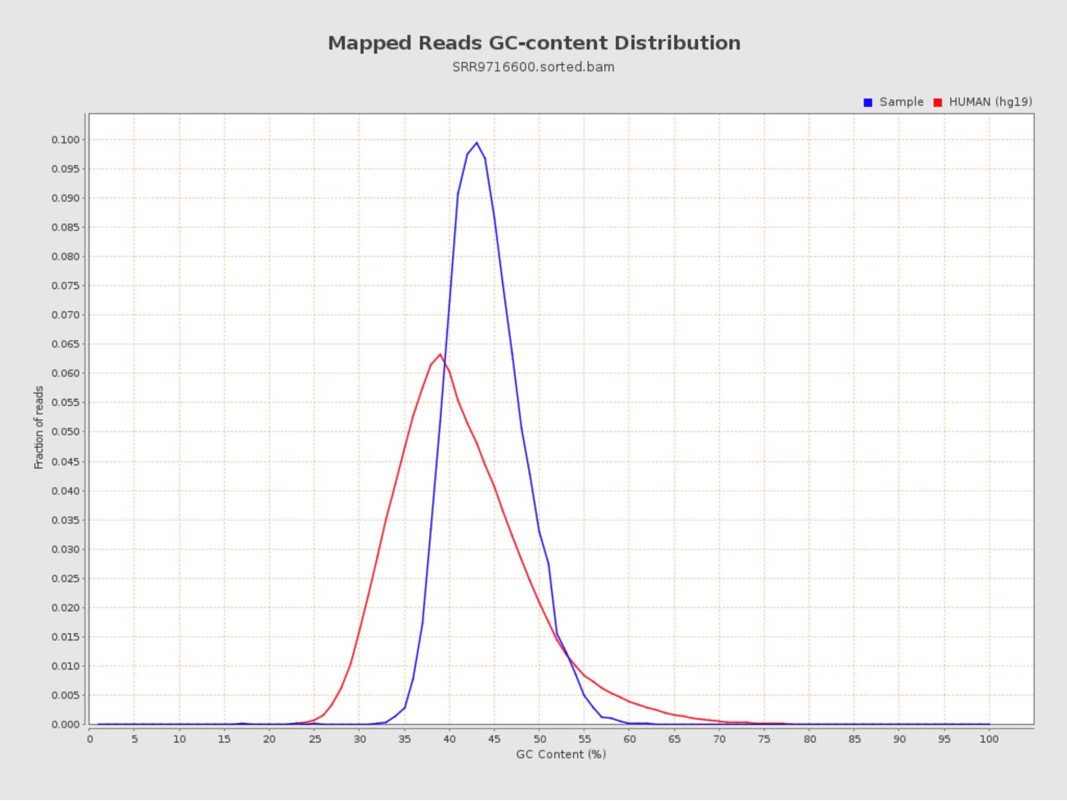
# 7. Results : Duplication Rate Histogram



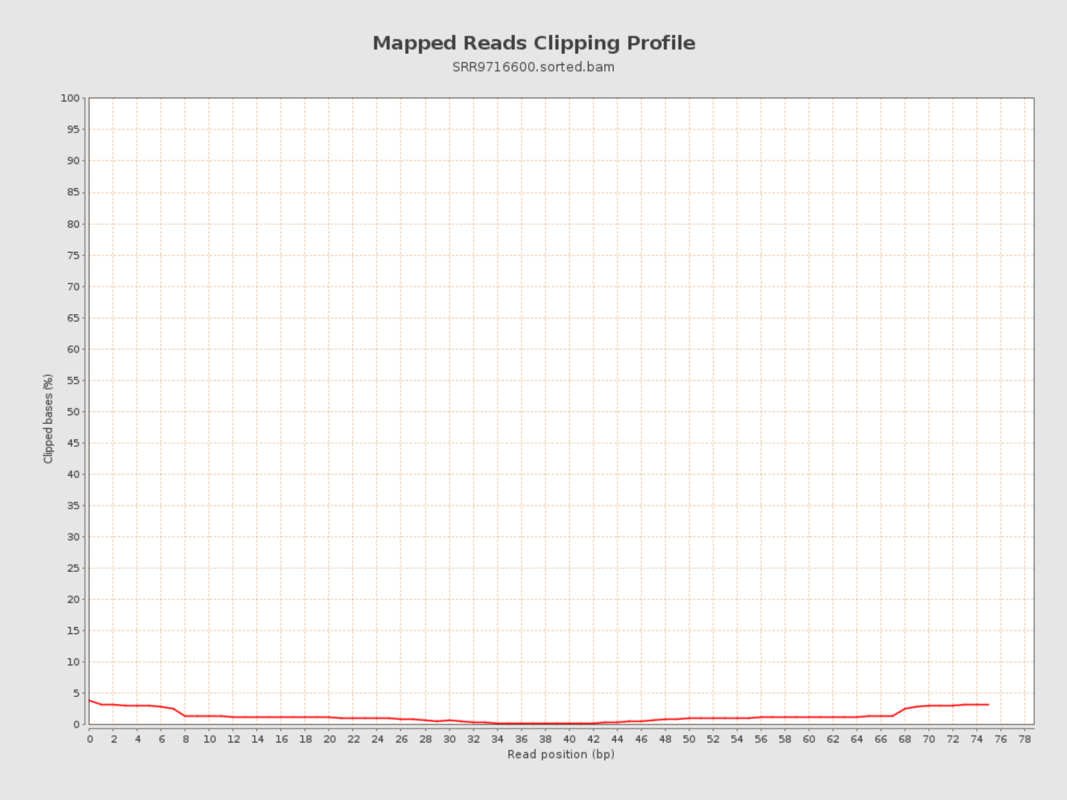
# 8. Results : Mapped Reads Nucleotide Content



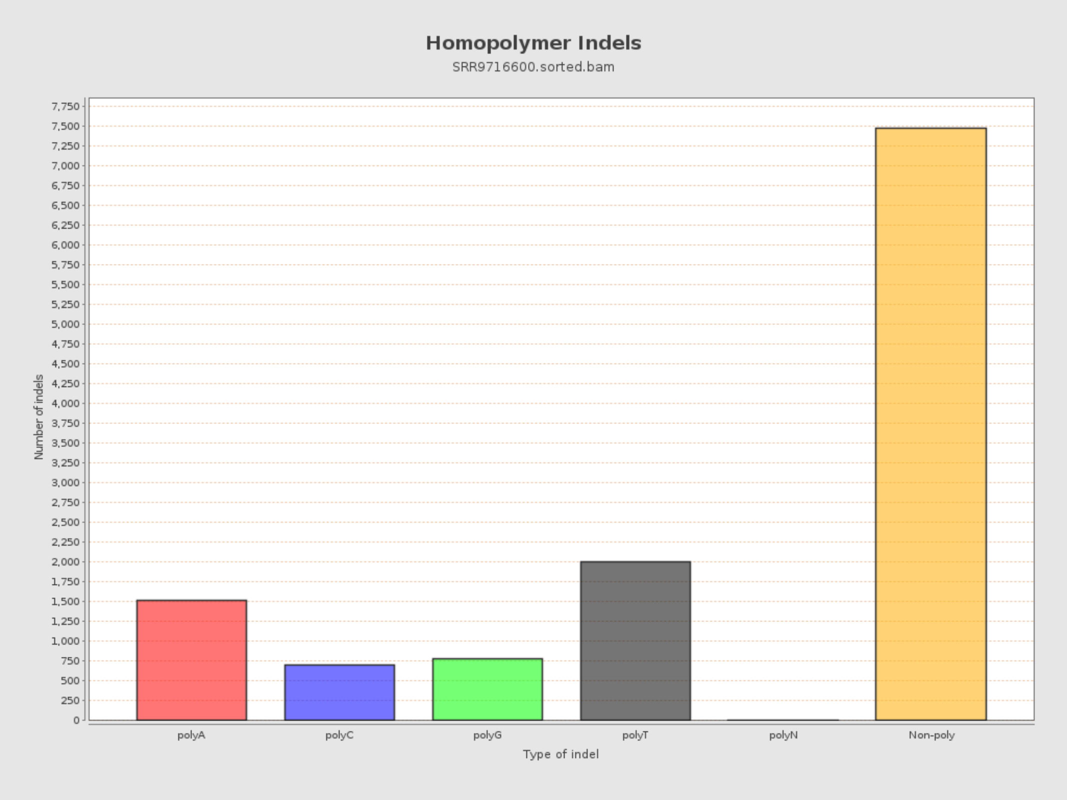
# 9. Results : Mapped Reads GC-content Distribution



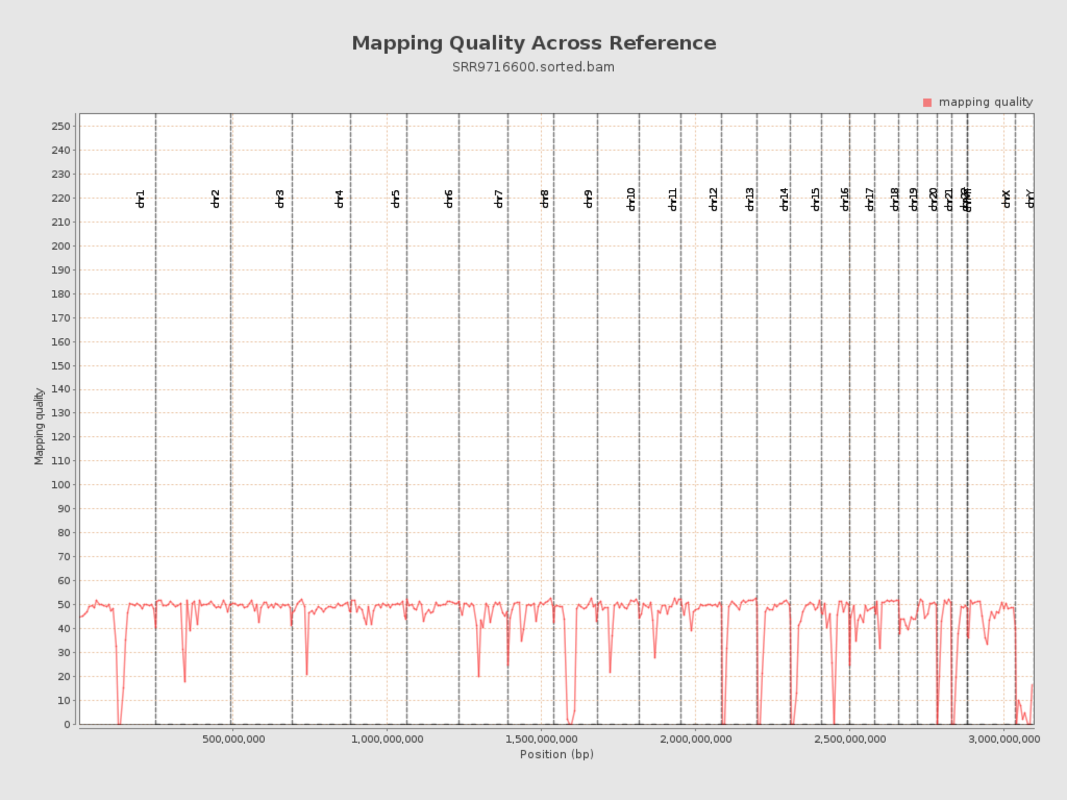
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram