# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 10:36:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716765.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_SRR9716765 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716765.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 10:36:47 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716765.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 746,973 |
| Mapped reads | 685,686 / 91.8% |
| Unmapped reads | 61,287 / 8.2% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 2,894 / 0.39% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 20,442 / 2.74% |
| Duplication rate | 2.23% |
| Clipped reads | 687,361 / 92.02% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 9,710,232 / 24.39% |
| Number/percentage of C's | 7,464,243 / 18.75% |
| Number/percentage of T's | 12,827,457 / 32.22% |
| Number/percentage of G's | 9,815,275 / 24.65% |
| Number/percentage of N's | 827 / 0% |
| GC Percentage | 43.4% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0129 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1511 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.84 |

## 2.5. Mismatches and indels

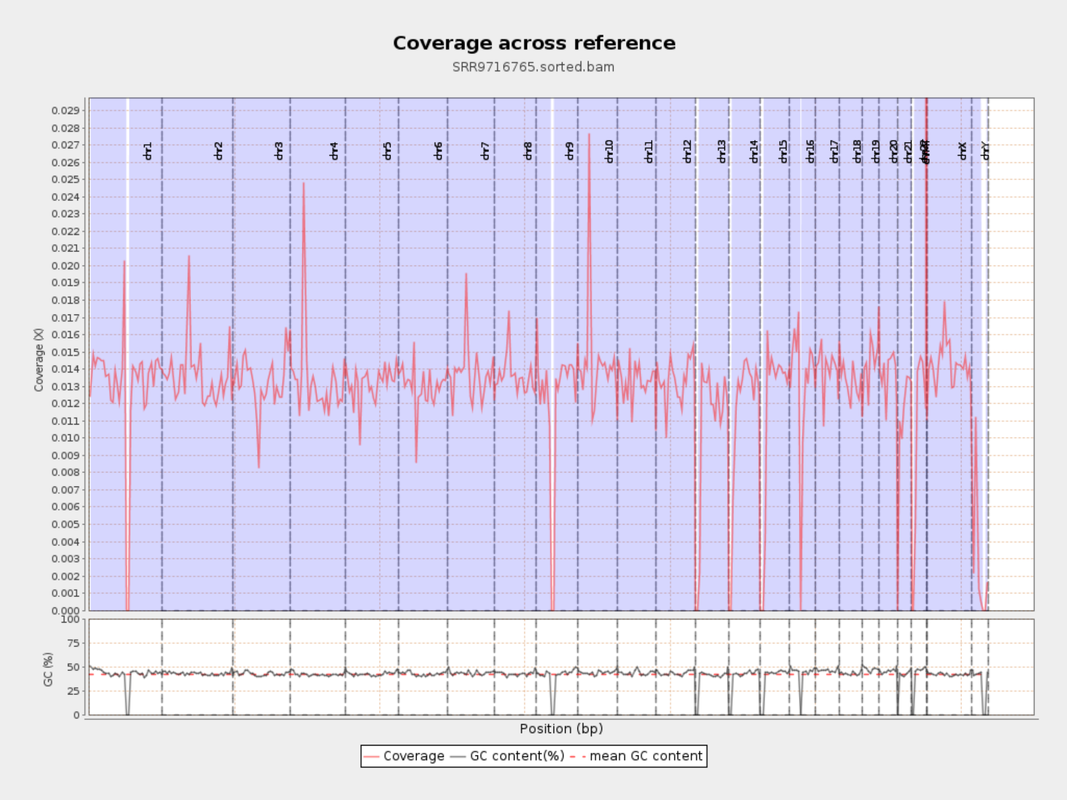
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 199,525 |
| Insertions | 2,866 |
| Mapped reads with at least one insertion | 0.42% |
| Deletions | 7,333 |
| Mapped reads with at least one deletion | 1.06% |
| Homopolymer indels | 41.73% |

## 2.6. Chromosome stats

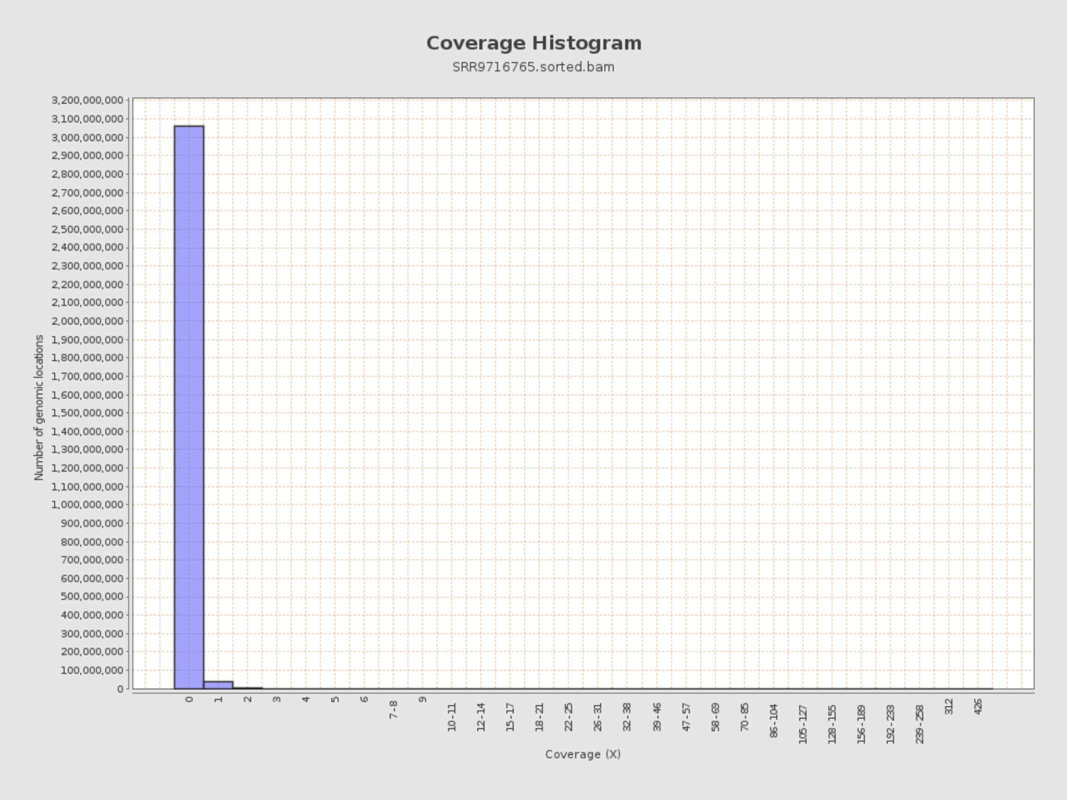
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3231595 | 0.013 | 0.2123 |
| chr2 | 243199373 | 3331112 | 0.0137 | 0.2153 |
| chr3 | 198022430 | 2625109 | 0.0133 | 0.1216 |
| chr4 | 191154276 | 2547646 | 0.0133 | 0.1372 |
| chr5 | 180915260 | 2383361 | 0.0132 | 0.121 |
| chr6 | 171115067 | 2225983 | 0.013 | 0.1272 |
| chr7 | 159138663 | 2188367 | 0.0138 | 0.1645 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1995246 | 0.0136 | 0.1728 |
| chr9 | 141213431 | 1674576 | 0.0119 | 0.1321 |
| chr10 | 135534747 | 1961112 | 0.0145 | 0.1671 |
| chr11 | 135006516 | 1796048 | 0.0133 | 0.1331 |
| chr12 | 133851895 | 1792722 | 0.0134 | 0.123 |
| chr13 | 115169878 | 1211706 | 0.0105 | 0.1085 |
| chr14 | 107349540 | 1203277 | 0.0112 | 0.1132 |
| chr15 | 102531392 | 1168315 | 0.0114 | 0.1122 |
| chr16 | 90354753 | 1186021 | 0.0131 | 0.1248 |
| chr17 | 81195210 | 1132488 | 0.0139 | 0.1284 |
| chr18 | 78077248 | 1042876 | 0.0134 | 0.1782 |
| chr19 | 59128983 | 852759 | 0.0144 | 0.1657 |
| chr20 | 63025520 | 867760 | 0.0138 | 0.1261 |
| chr21 | 48129895 | 529126 | 0.011 | 0.1294 |
| chr22 | 51304566 | 494050 | 0.0096 | 0.1038 |
| chrMT | 16571 | 12206 | 0.7366 | 0.9805 |
| chrX | 155270560 | 2216285 | 0.0143 | 0.1309 |
| chrY | 59373566 | 160033 | 0.0027 | 0.129 |

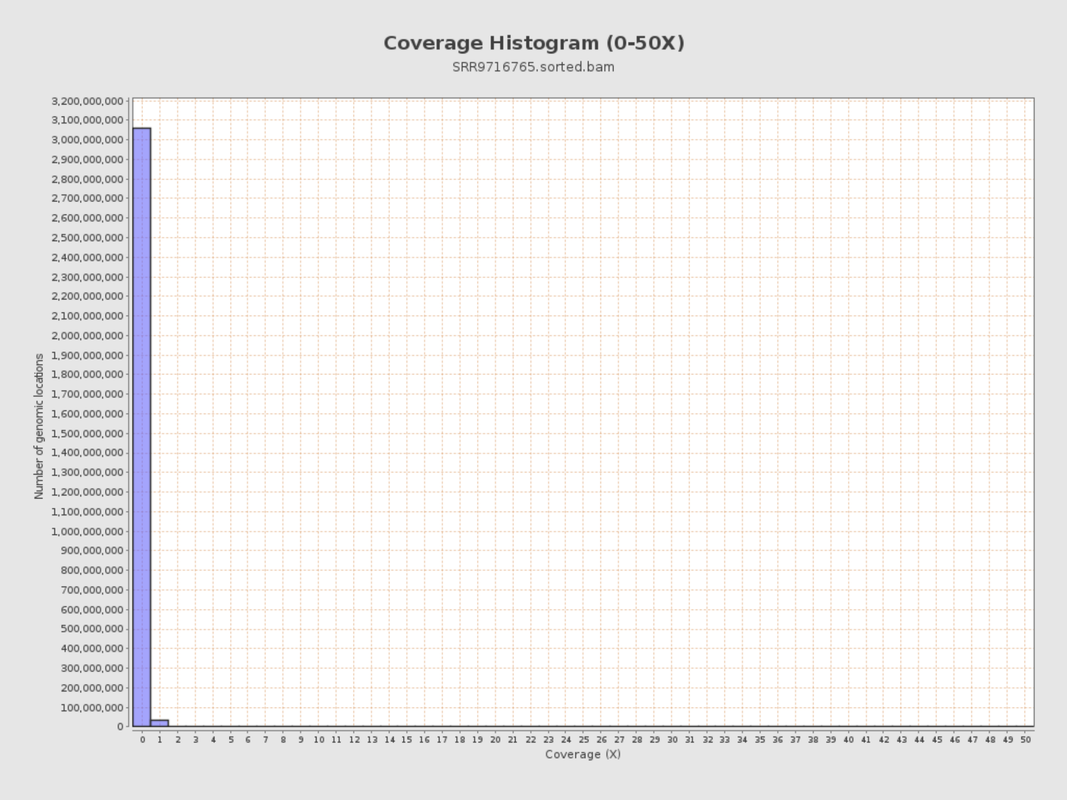
# 3. Results : Coverage across reference



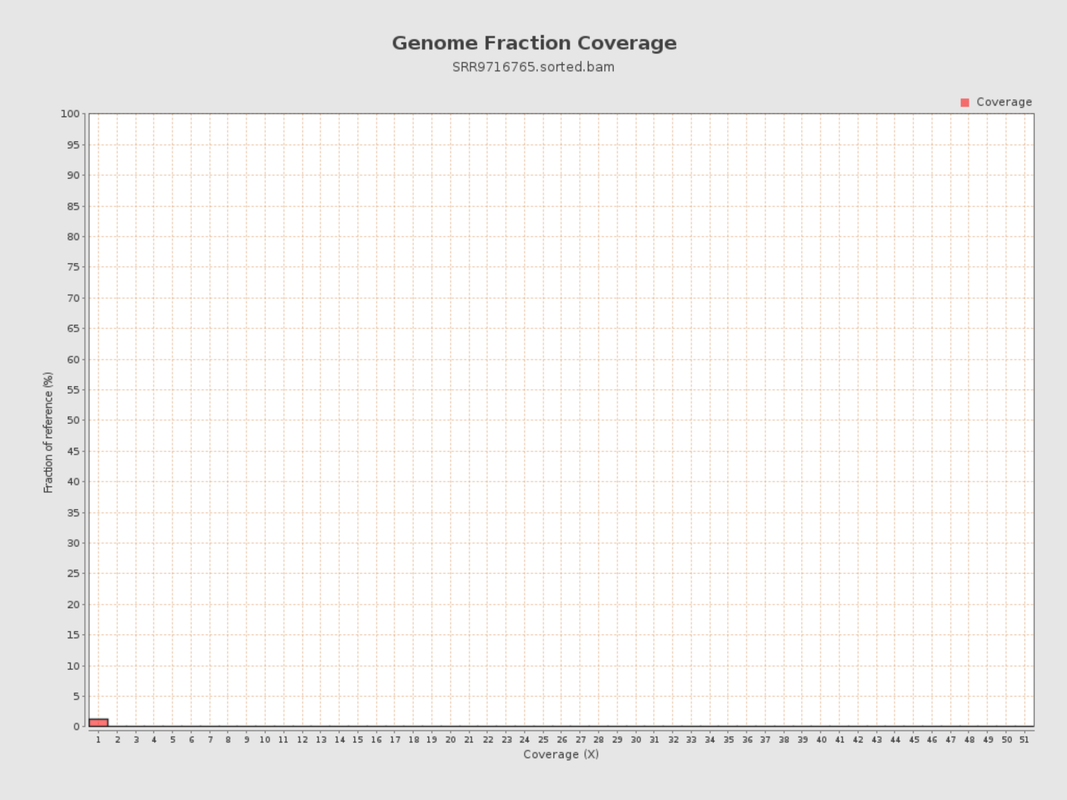
# 4. Results : Coverage Histogram



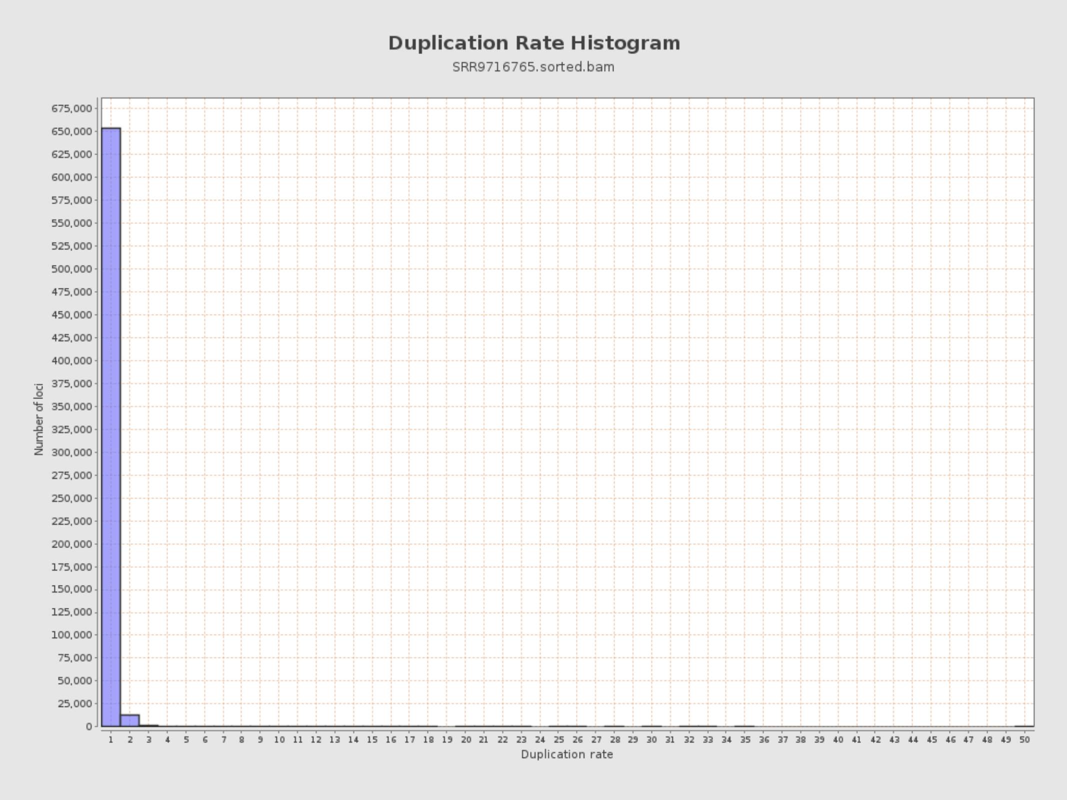
# 5. Results : Coverage Histogram (0-50X)



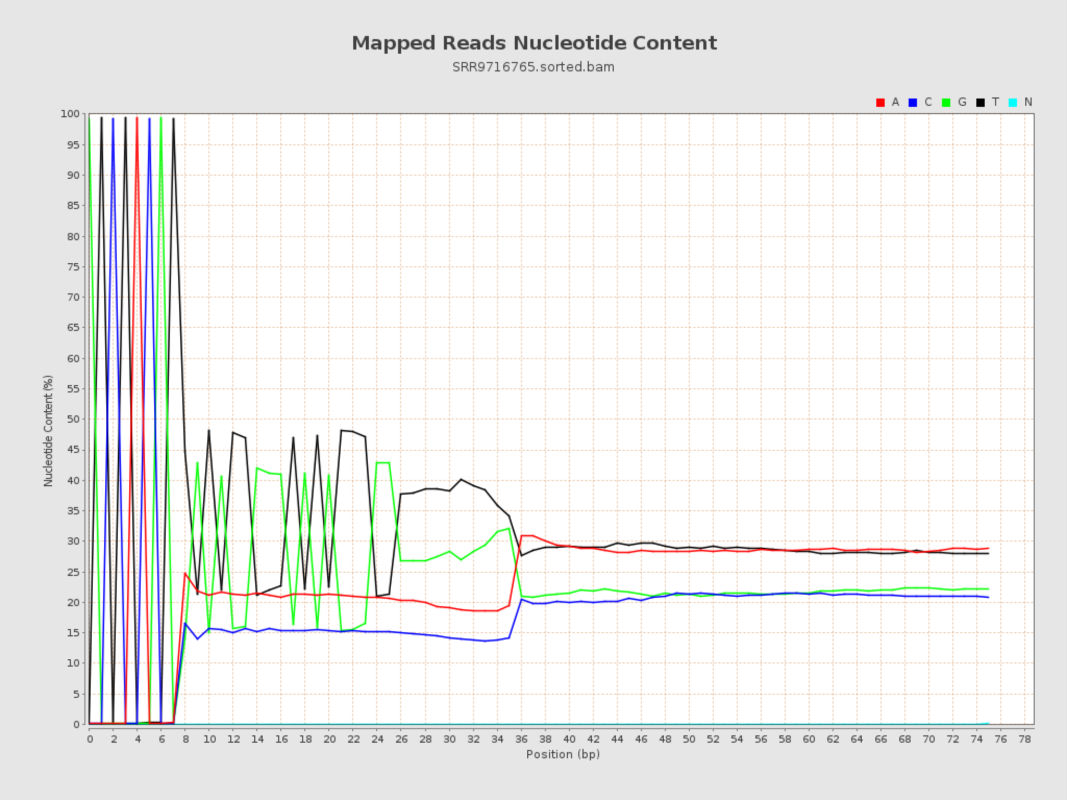
# 6. Results : Genome Fraction Coverage



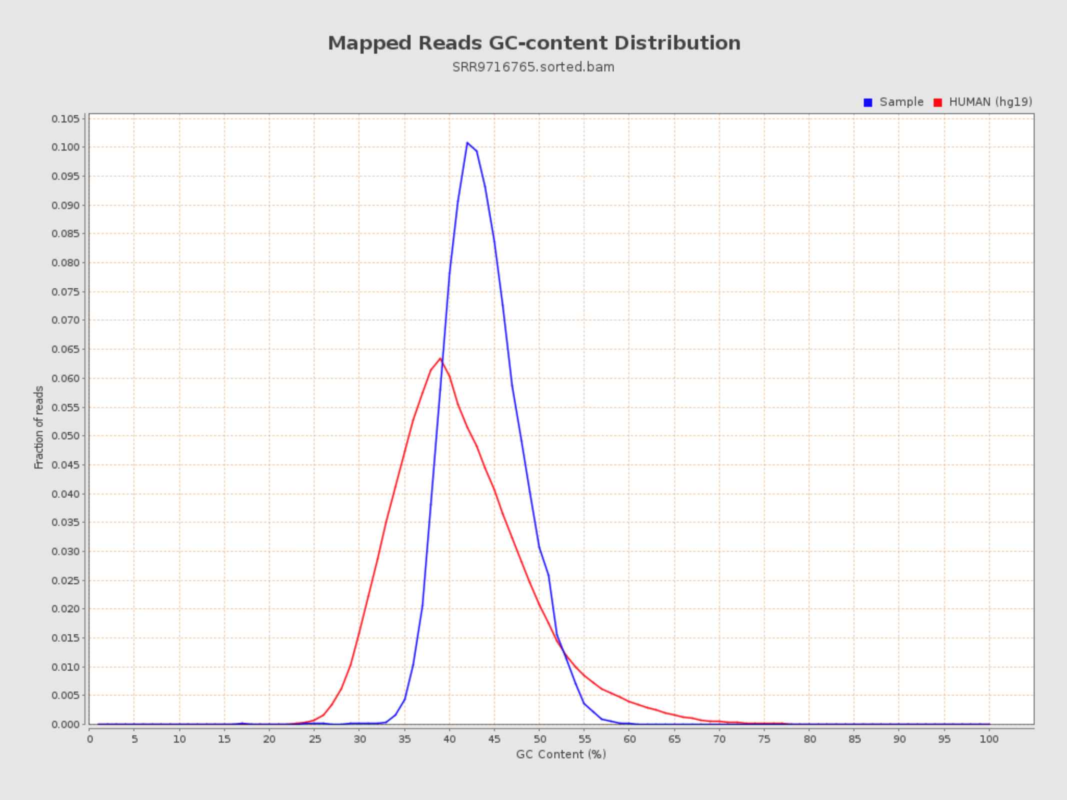
# 7. Results : Duplication Rate Histogram



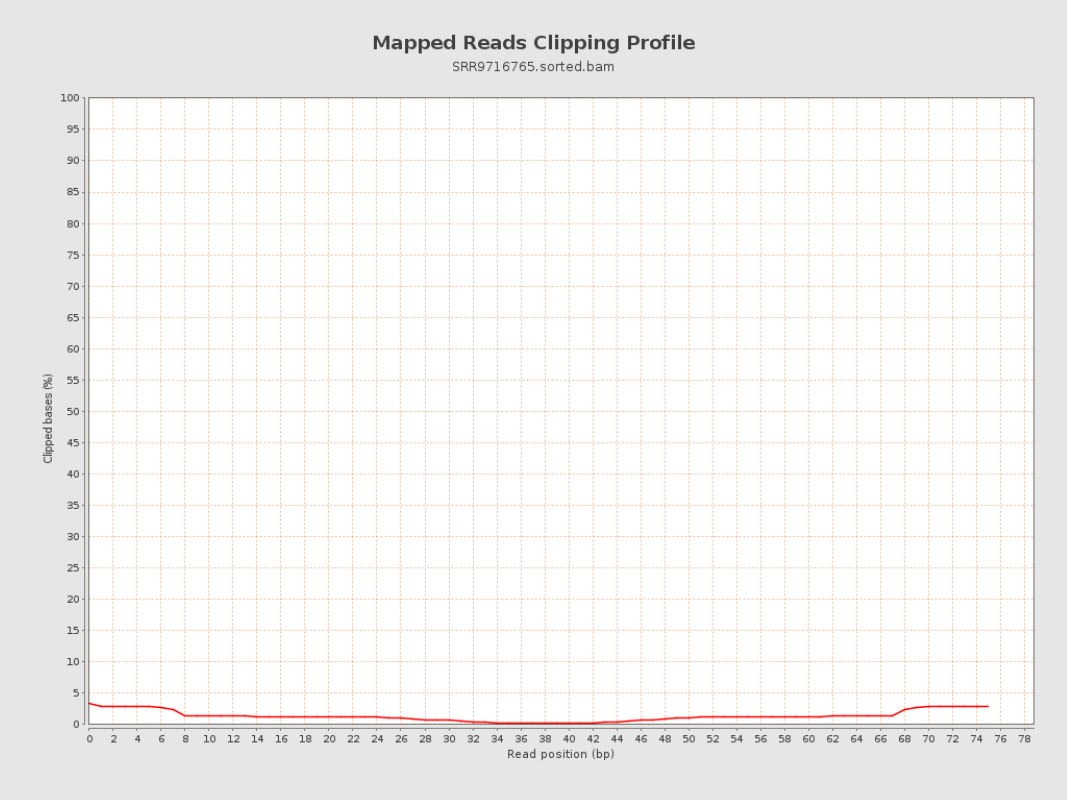
# 8. Results : Mapped Reads Nucleotide Content



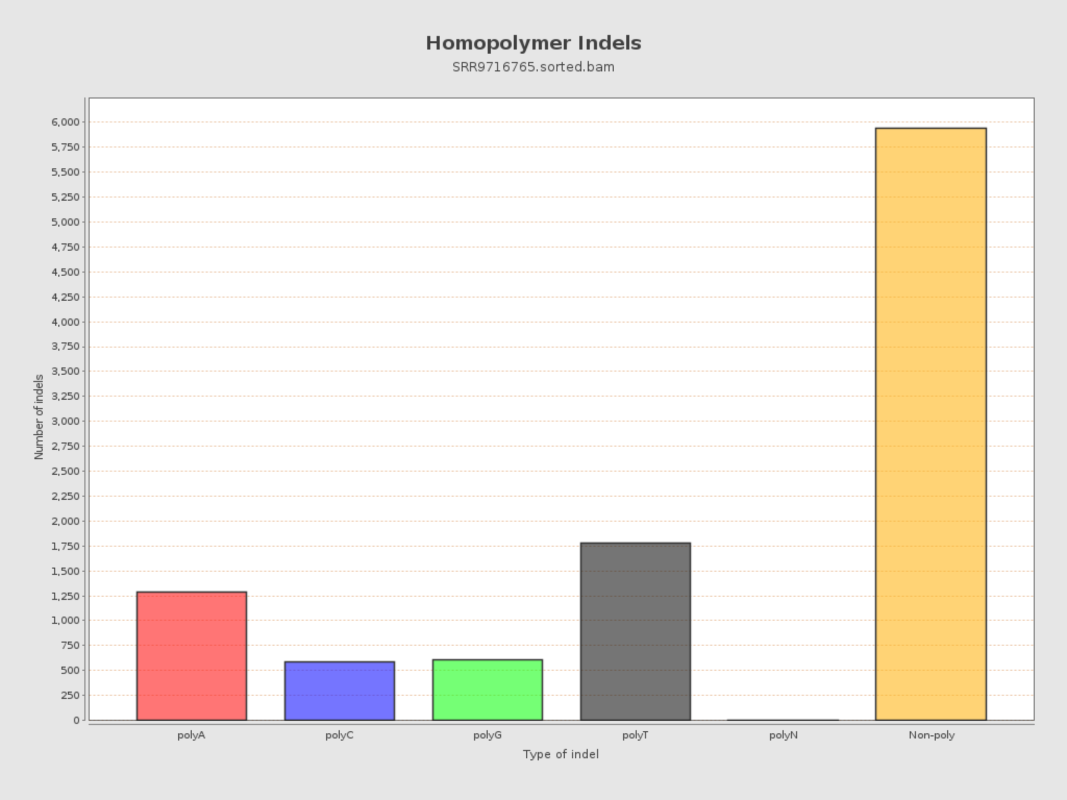
# 9. Results : Mapped Reads GC-content Distribution



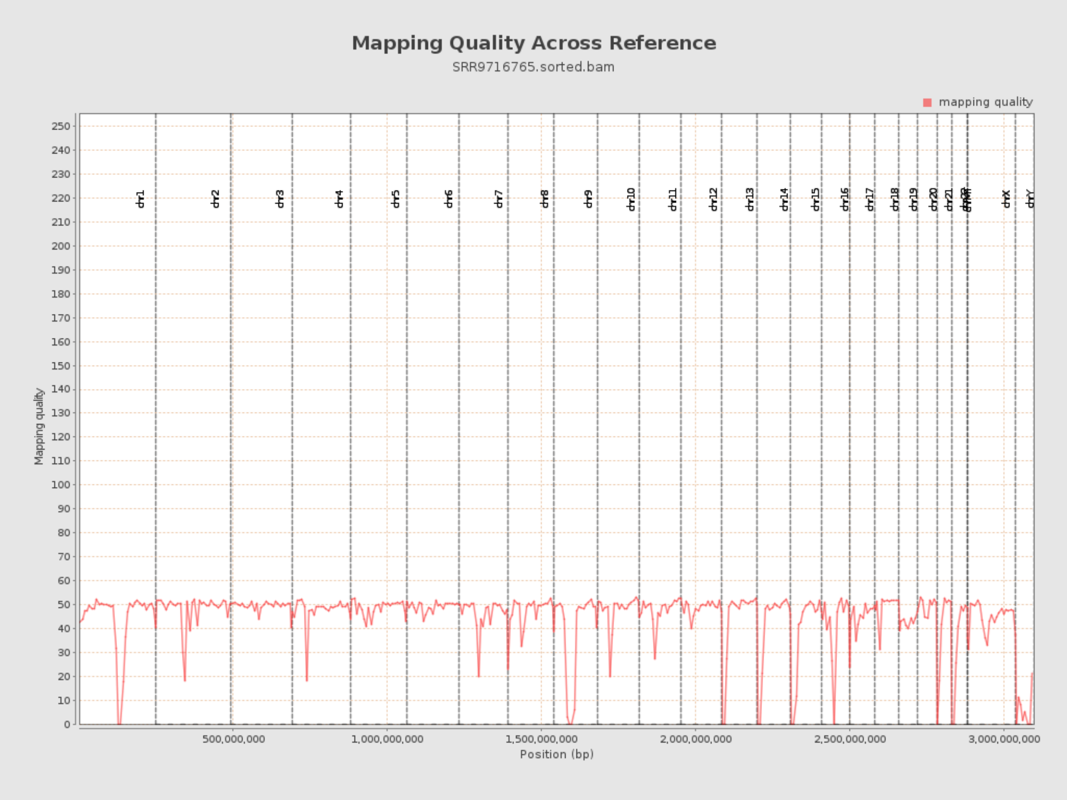
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram