# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 19:18:54*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716936.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_SRR9716936 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716936.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 19:18:54 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716936.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,023,554 |
| Mapped reads | 802,863 / 78.44% |
| Unmapped reads | 220,691 / 21.56% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 911 / 0.09% |
| Read min/max/mean length | 30 / 76 / 76.03 |
| Duplicated reads (estimated) | 52,420 / 5.12% |
| Duplication rate | 5.82% |
| Clipped reads | 802,553 / 78.41% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 9,260,242 / 21.45% |
| Number/percentage of C's | 7,439,041 / 17.24% |
| Number/percentage of T's | 13,754,487 / 31.87% |
| Number/percentage of G's | 12,707,528 / 29.44% |
| Number/percentage of N's | 699 / 0% |
| GC Percentage | 46.68% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0139 |
| | |

| | |
|---|---|
| Standard Deviation | 0.149 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.3 |

## 2.5. Mismatches and indels

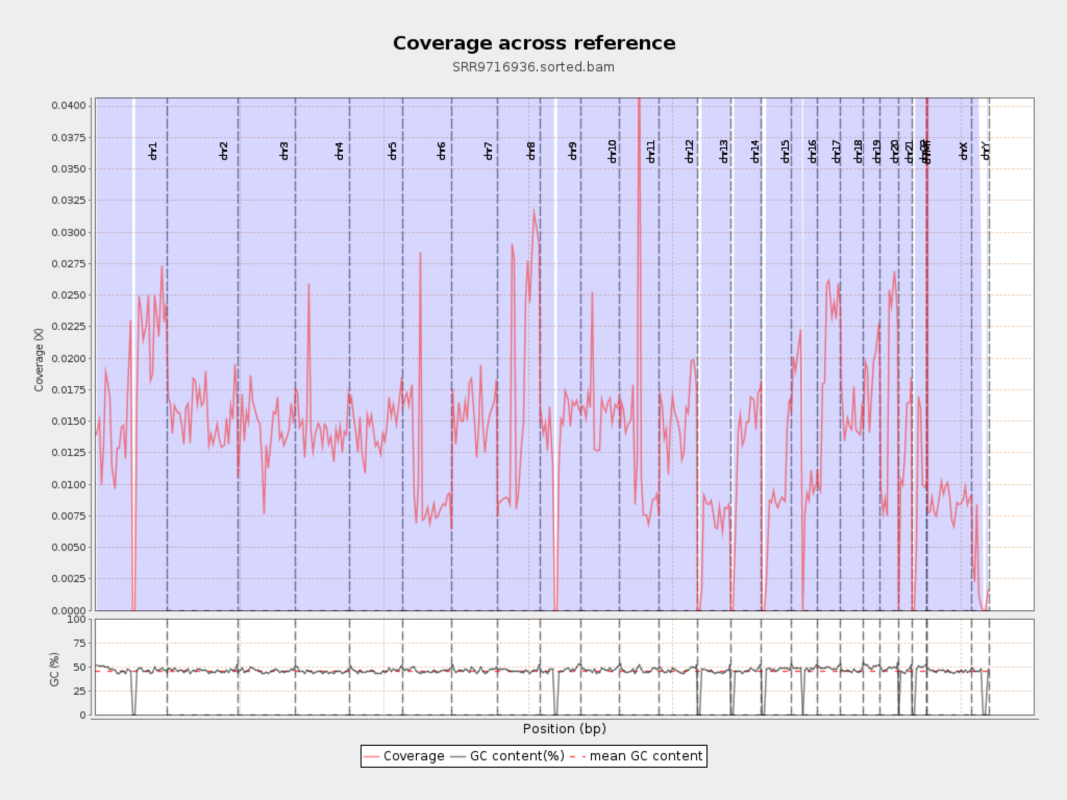
| | |
|---|---|
| General error rate | 0.67% |
| Mismatches | 283,805 |
| Insertions | 2,462 |
| Mapped reads with at least one insertion | 0.3% |
| Deletions | 6,591 |
| Mapped reads with at least one deletion | 0.82% |
| Homopolymer indels | 42.26% |

## 2.6. Chromosome stats

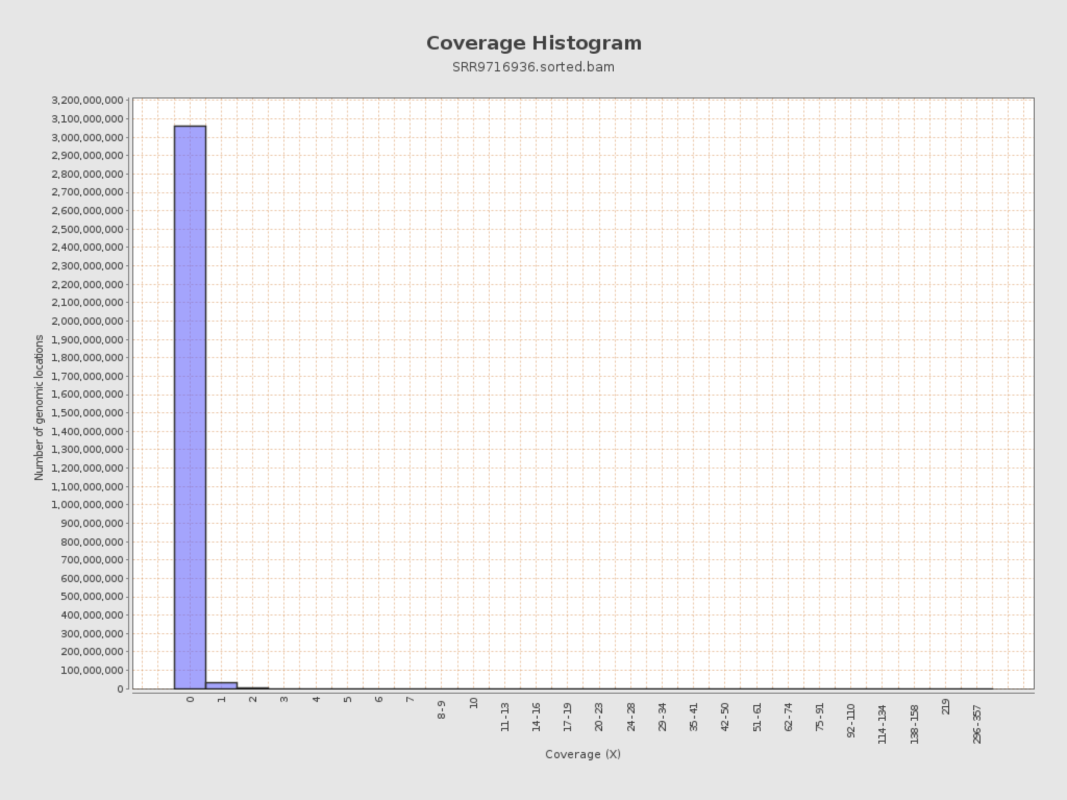
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 4290992 | 0.0172 | 0.1819 |
| chr2 | 243199373 | 3761546 | 0.0155 | 0.2041 |
| chr3 | 198022430 | 2859725 | 0.0144 | 0.1359 |
| chr4 | 191154276 | 2816318 | 0.0147 | 0.1448 |
| chr5 | 180915260 | 2649978 | 0.0146 | 0.1355 |
| chr6 | 171115067 | 1858676 | 0.0109 | 0.1283 |
| chr7 | 159138663 | 2497489 | 0.0157 | 0.1601 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2683448 | 0.0183 | 0.1567 |
| chr9 | 141213431 | 1888786 | 0.0134 | 0.1382 |
| chr10 | 135534747 | 2184611 | 0.0161 | 0.1678 |
| chr11 | 135006516 | 1847620 | 0.0137 | 0.1433 |
| chr12 | 133851895 | 2083941 | 0.0156 | 0.1411 |
| chr13 | 115169878 | 758435 | 0.0066 | 0.0908 |
| chr14 | 107349540 | 1368698 | 0.0127 | 0.1288 |
| chr15 | 102531392 | 846526 | 0.0083 | 0.1023 |
| chr16 | 90354753 | 1145707 | 0.0127 | 0.1334 |
| chr17 | 81195210 | 1678302 | 0.0207 | 0.1684 |
| chr18 | 78077248 | 1181871 | 0.0151 | 0.1585 |
| chr19 | 59128983 | 1111228 | 0.0188 | 0.179 |
| chr20 | 63025520 | 1096102 | 0.0174 | 0.1551 |
| chr21 | 48129895 | 600763 | 0.0125 | 0.1324 |
| chr22 | 51304566 | 466223 | 0.0091 | 0.1132 |
| chrMT | 16571 | 32465 | 1.9591 | 1.9563 |
| chrX | 155270560 | 1337087 | 0.0086 | 0.1079 |
| chrY | 59373566 | 126726 | 0.0021 | 0.0746 |

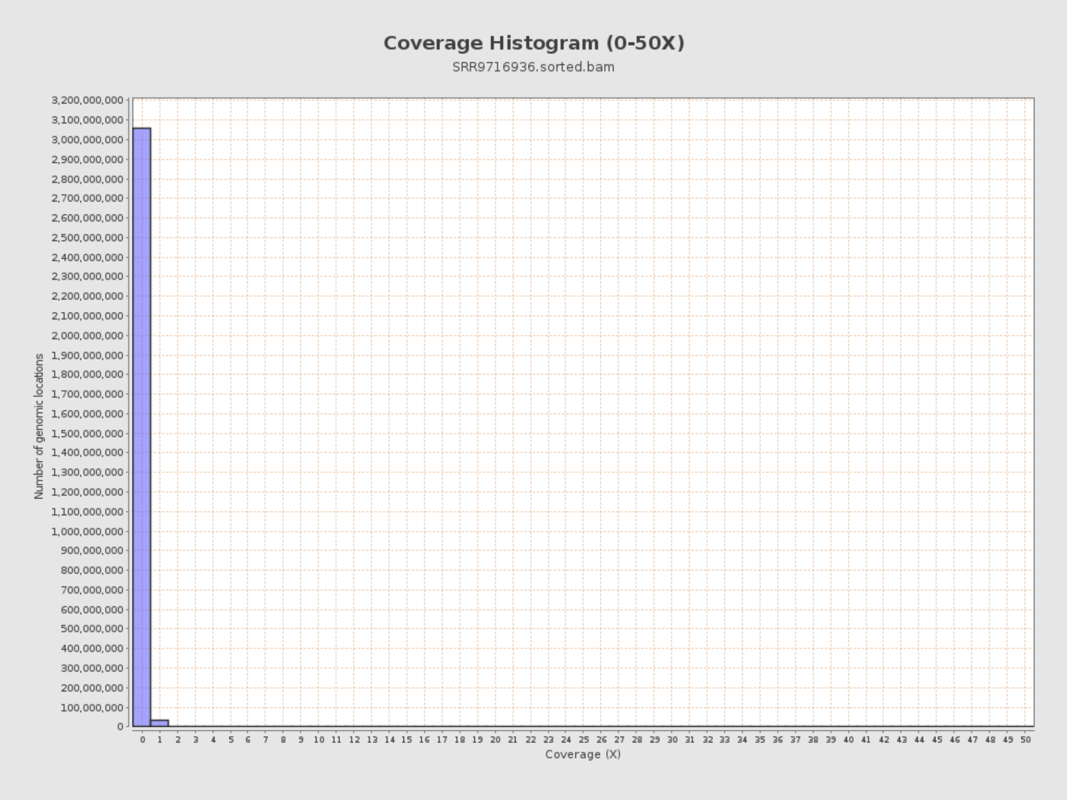
# 3. Results : Coverage across reference



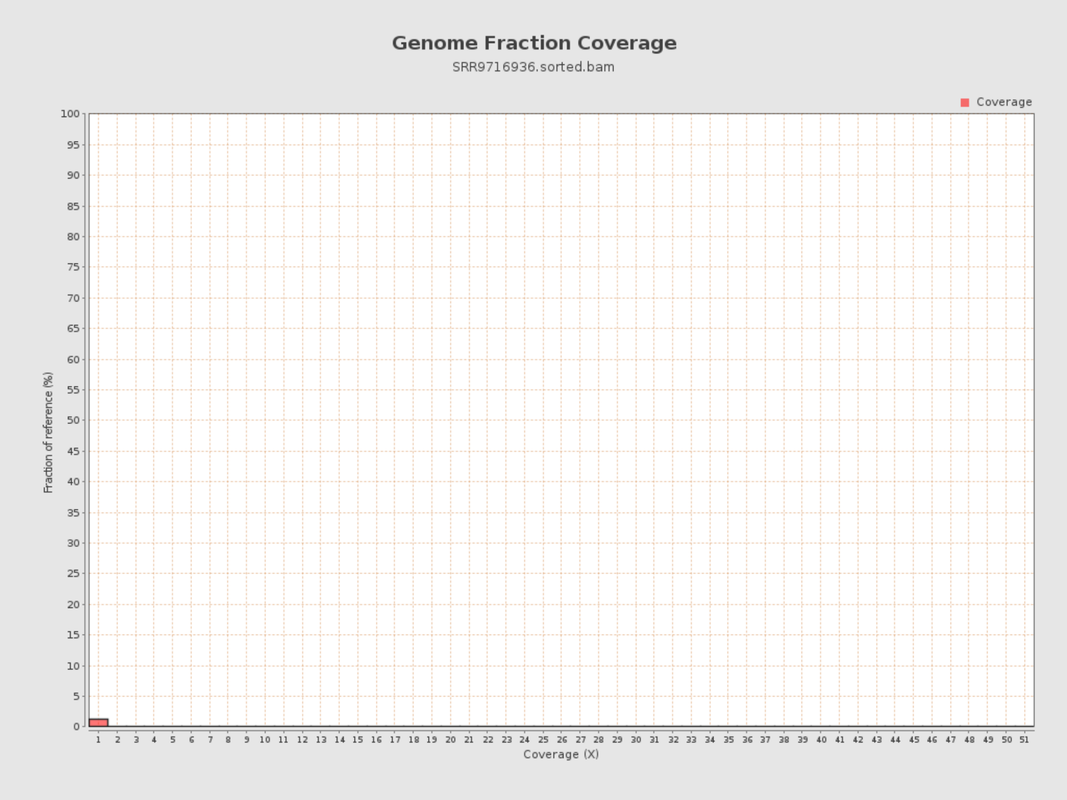
# 4. Results : Coverage Histogram



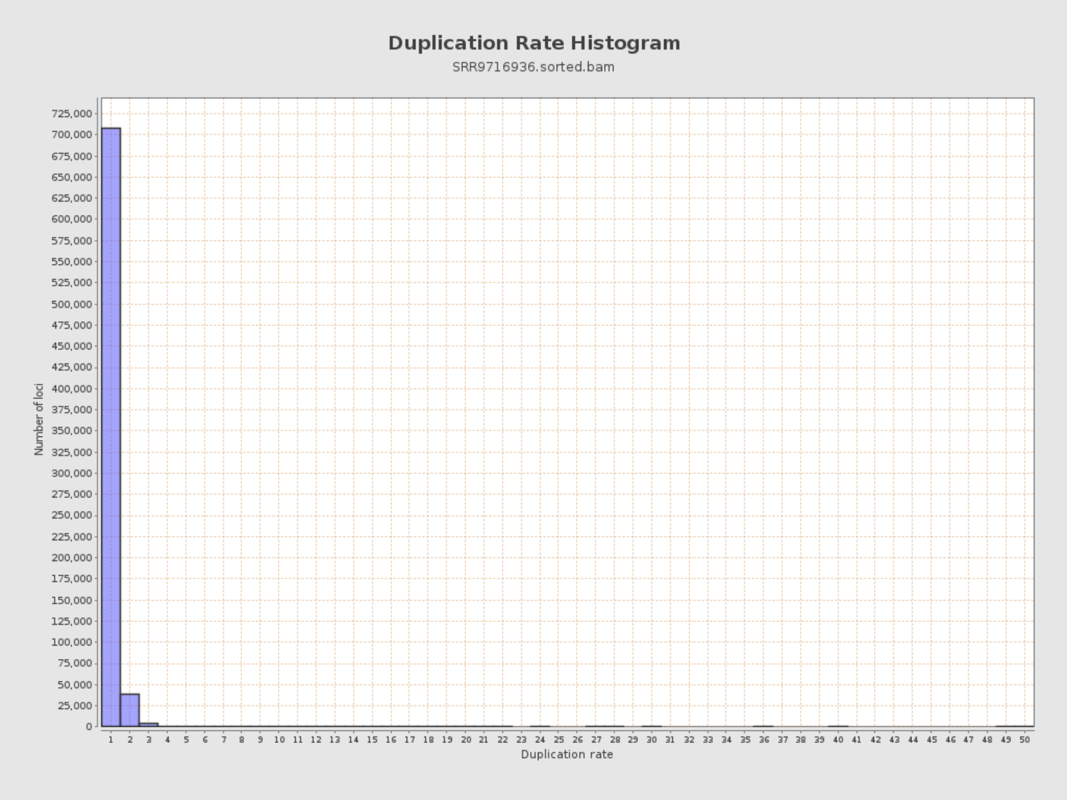
# 5. Results : Coverage Histogram (0-50X)



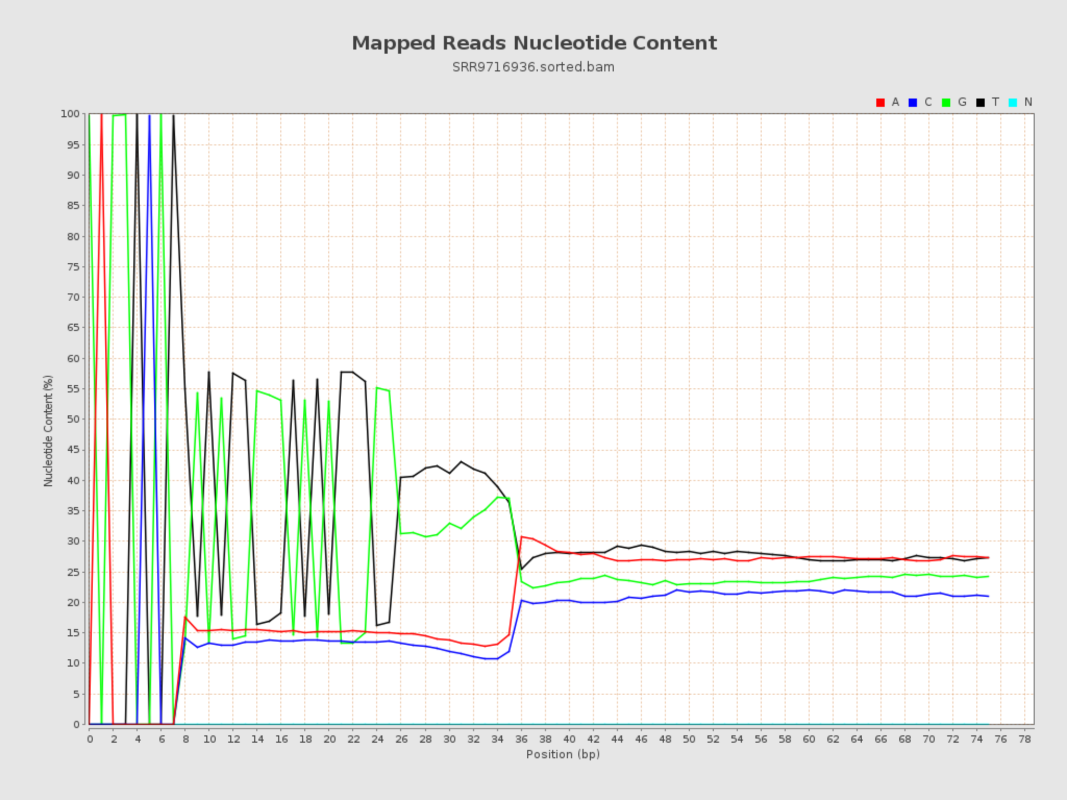
# 6. Results : Genome Fraction Coverage



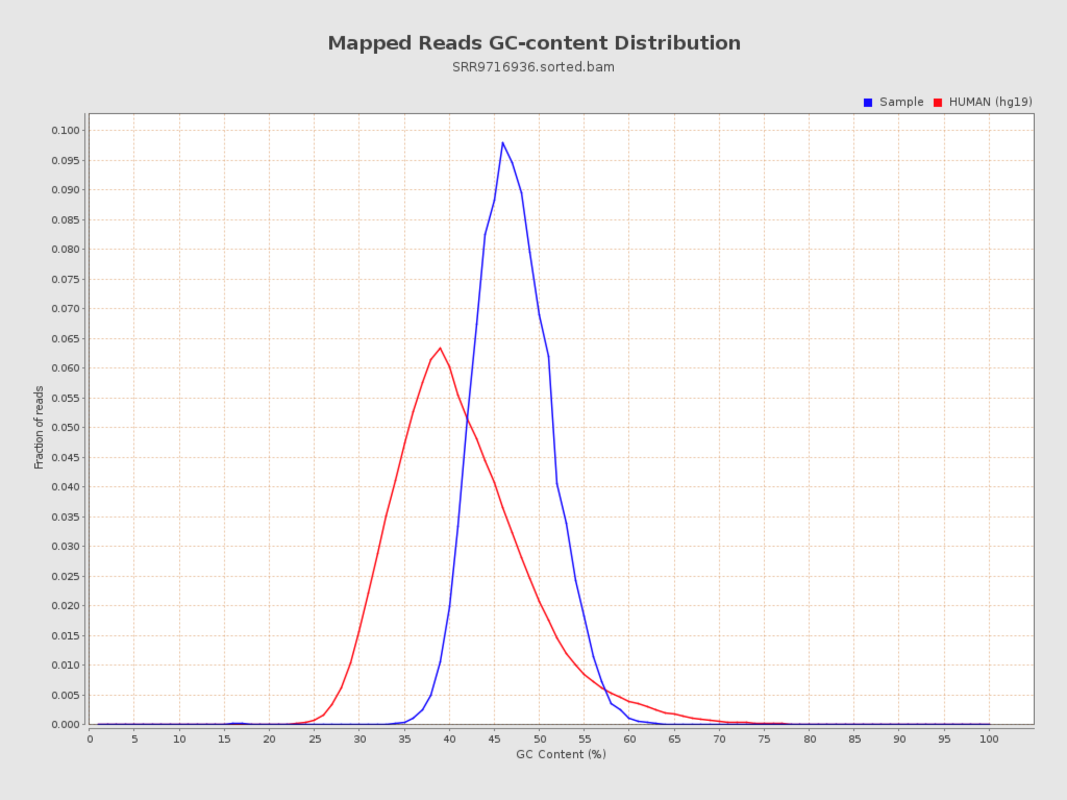
# 7. Results : Duplication Rate Histogram



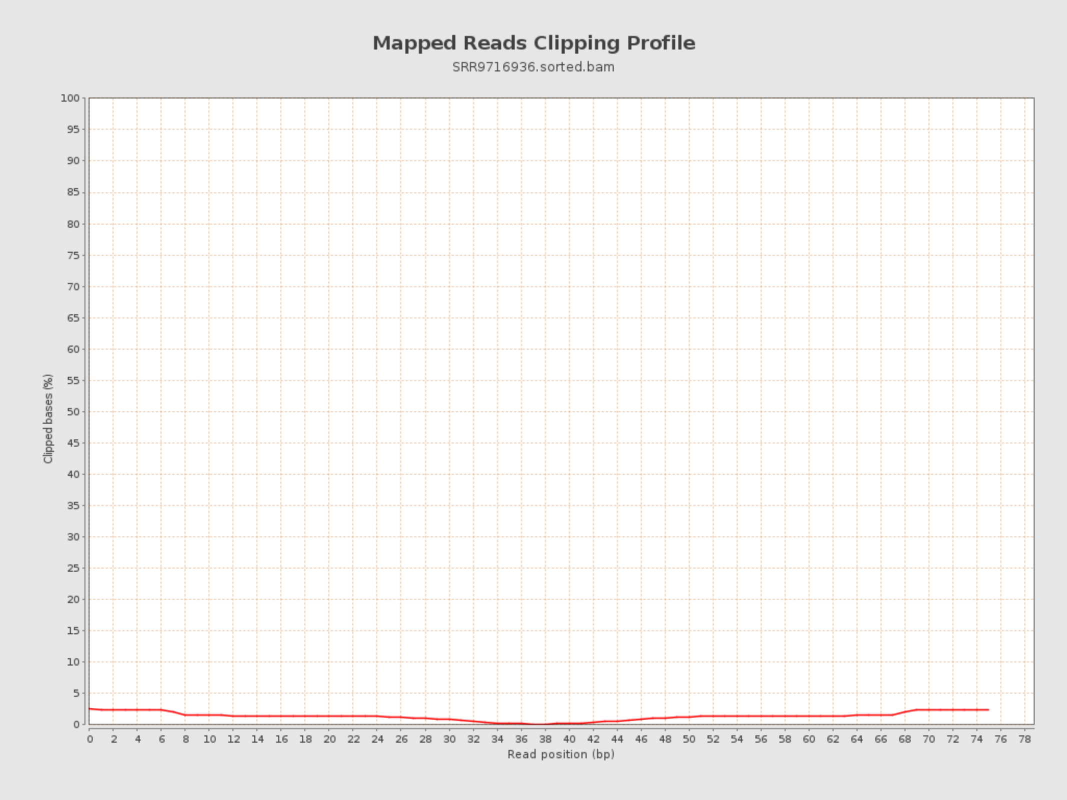
# 8. Results : Mapped Reads Nucleotide Content



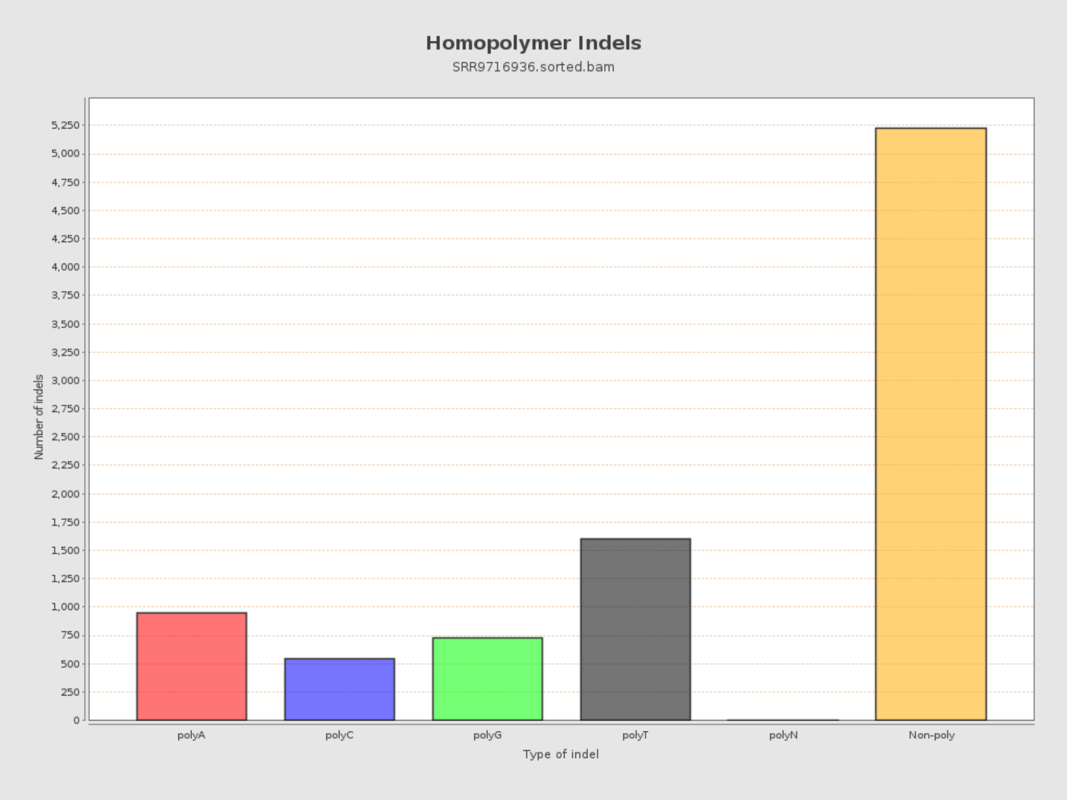
# 9. Results : Mapped Reads GC-content Distribution



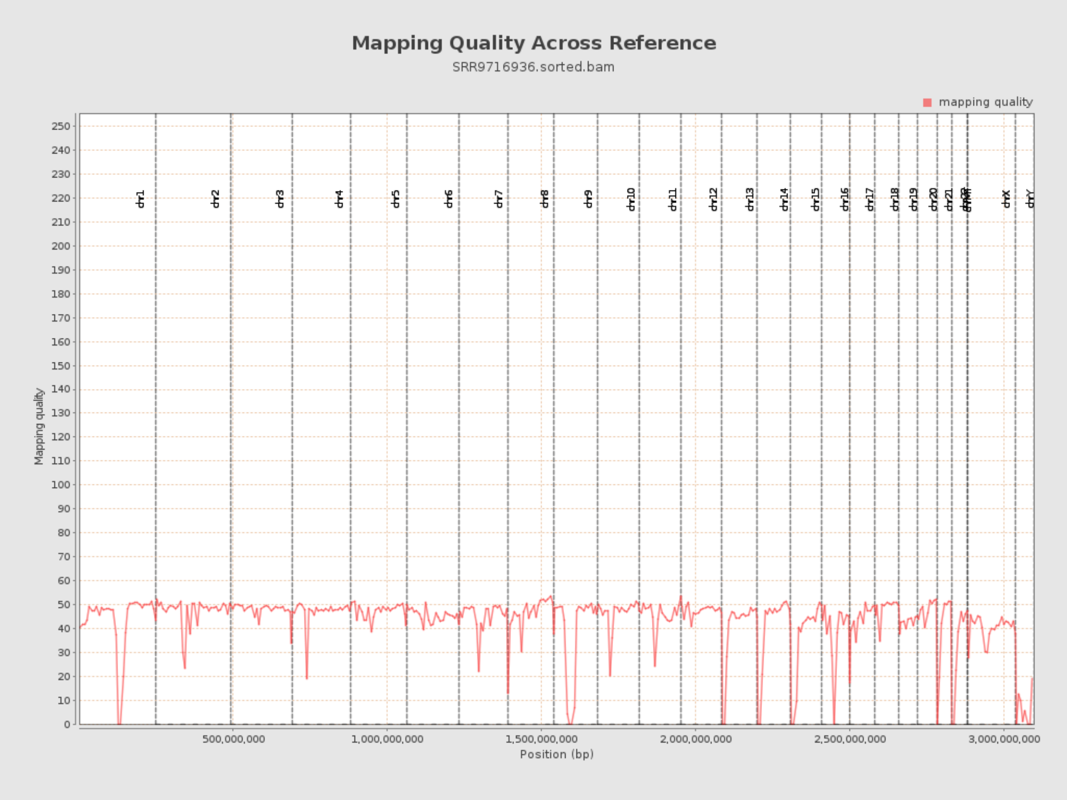
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram