# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 18:23:00*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716911.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_SRR9716911 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716911.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 18:22:59 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716911.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,392,420 |
| Mapped reads | 954,729 / 68.57% |
| Unmapped reads | 437,691 / 31.43% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,749 / 0.27% |
| Read min/max/mean length | 30 / 76 / 76.09 |
| Duplicated reads (estimated) | 19,618 / 1.41% |
| Duplication rate | 1.44% |
| Clipped reads | 956,568 / 68.7% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 12,842,843 / 24.13% |
| Number/percentage of C's | 11,052,933 / 20.76% |
| Number/percentage of T's | 15,783,472 / 29.65% |
| Number/percentage of G's | 13,553,531 / 25.46% |
| Number/percentage of N's | 1,473 / 0% |
| GC Percentage | 46.22% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0172 |
| | |

| | |
|---|---|
| Standard Deviation | 0.167 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 39.26 |

## 2.5. Mismatches and indels

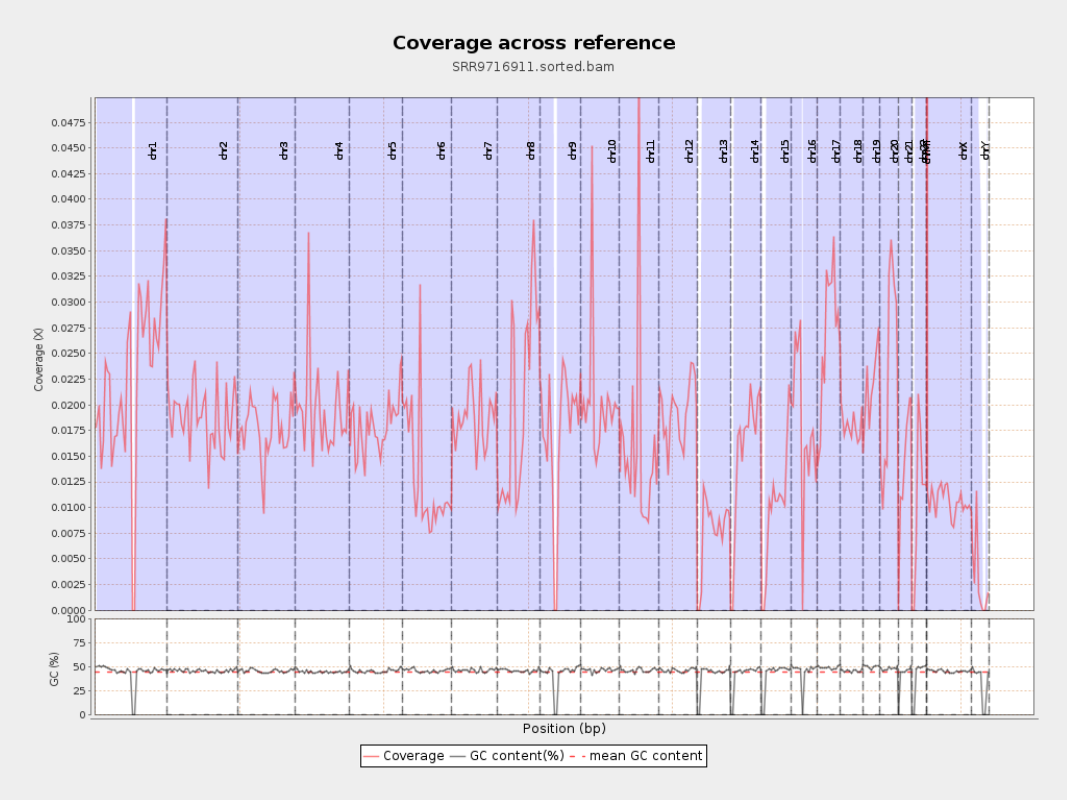
| | |
|---|---|
| General error rate | 0.55% |
| Mismatches | 283,406 |
| Insertions | 4,109 |
| Mapped reads with at least one insertion | 0.43% |
| Deletions | 8,589 |
| Mapped reads with at least one deletion | 0.89% |
| Homopolymer indels | 33.31% |

## 2.6. Chromosome stats

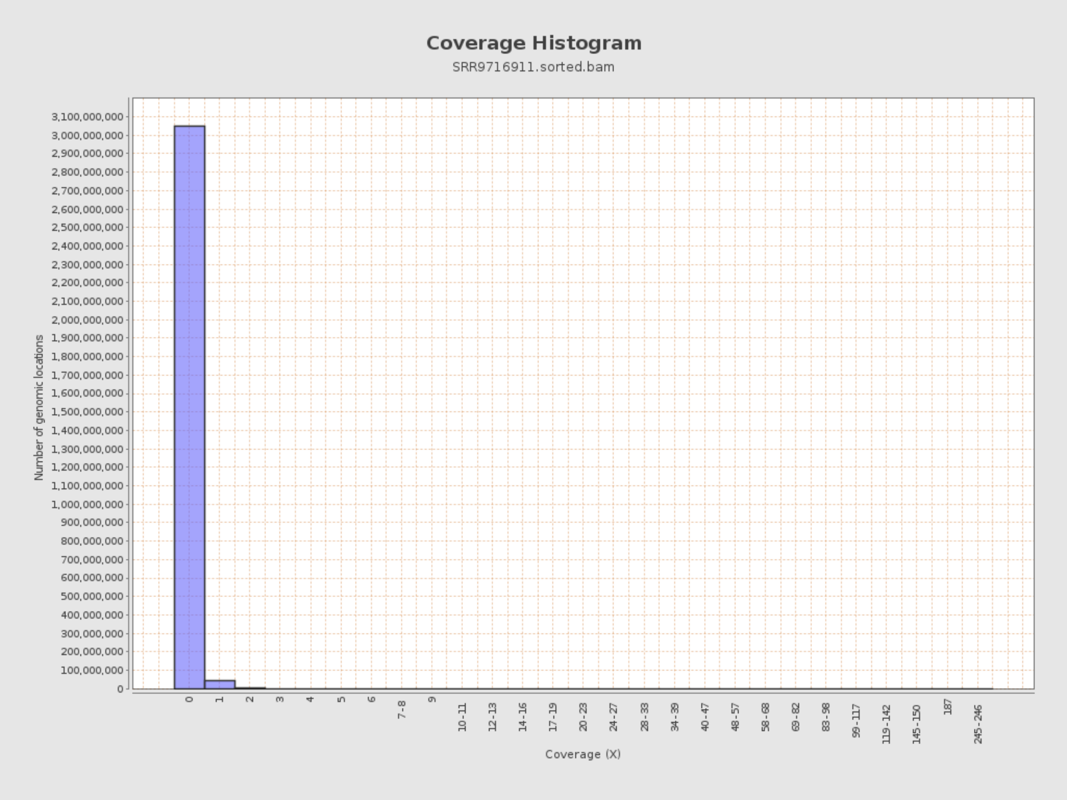
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5590390 | 0.0224 | 0.1993 |
| chr2 | 243199373 | 4589604 | 0.0189 | 0.2013 |
| chr3 | 198022430 | 3497704 | 0.0177 | 0.1477 |
| chr4 | 191154276 | 3731866 | 0.0195 | 0.1722 |
| chr5 | 180915260 | 3250723 | 0.018 | 0.1448 |
| chr6 | 171115067 | 2204116 | 0.0129 | 0.1254 |
| chr7 | 159138663 | 2997193 | 0.0188 | 0.1814 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2930284 | 0.02 | 0.1607 |
| chr9 | 141213431 | 2407418 | 0.017 | 0.1551 |
| chr10 | 135534747 | 2754218 | 0.0203 | 0.2742 |
| chr11 | 135006516 | 2145375 | 0.0159 | 0.1623 |
| chr12 | 133851895 | 2578784 | 0.0193 | 0.1513 |
| chr13 | 115169878 | 873692 | 0.0076 | 0.0955 |
| chr14 | 107349540 | 1641301 | 0.0153 | 0.138 |
| chr15 | 102531392 | 1049595 | 0.0102 | 0.1112 |
| chr16 | 90354753 | 1589914 | 0.0176 | 0.1565 |
| chr17 | 81195210 | 2166549 | 0.0267 | 0.1855 |
| chr18 | 78077248 | 1399149 | 0.0179 | 0.1862 |
| chr19 | 59128983 | 1299048 | 0.022 | 0.1936 |
| chr20 | 63025520 | 1462936 | 0.0232 | 0.1725 |
| chr21 | 48129895 | 685132 | 0.0142 | 0.1517 |
| chr22 | 51304566 | 564977 | 0.011 | 0.1155 |
| chrMT | 16571 | 21643 | 1.3061 | 1.507 |
| chrX | 155270560 | 1643383 | 0.0106 | 0.1177 |
| chrY | 59373566 | 174057 | 0.0029 | 0.1054 |

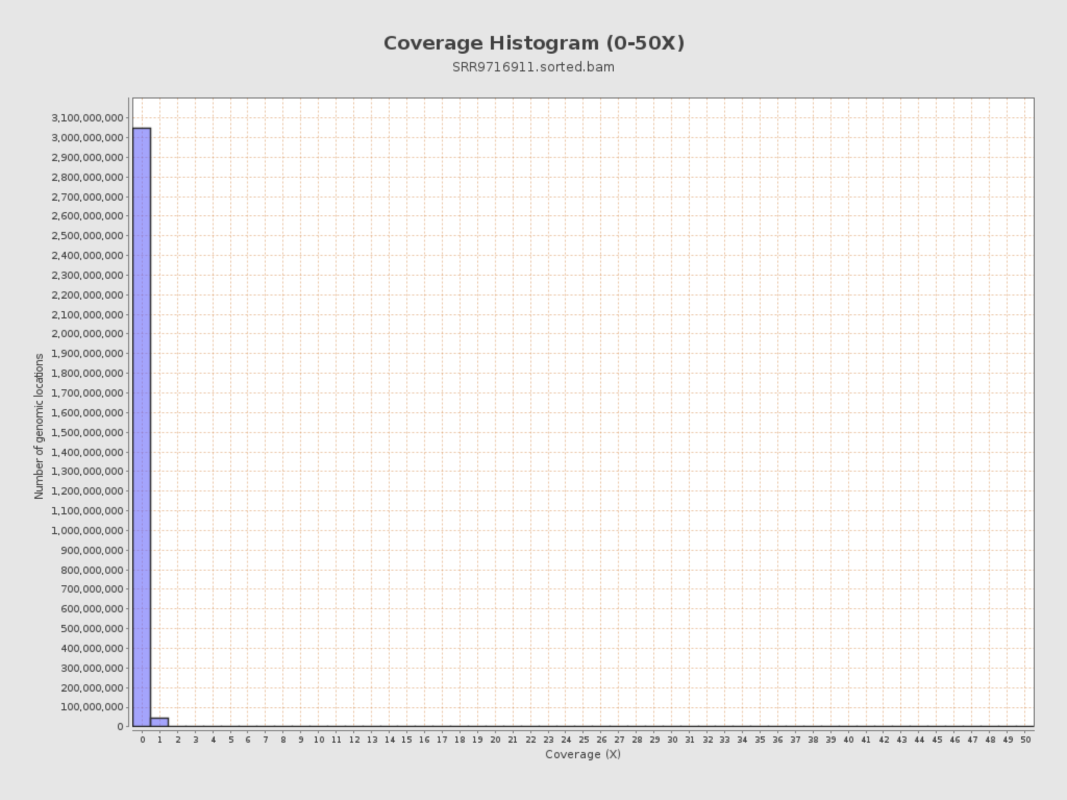
# 3. Results : Coverage across reference



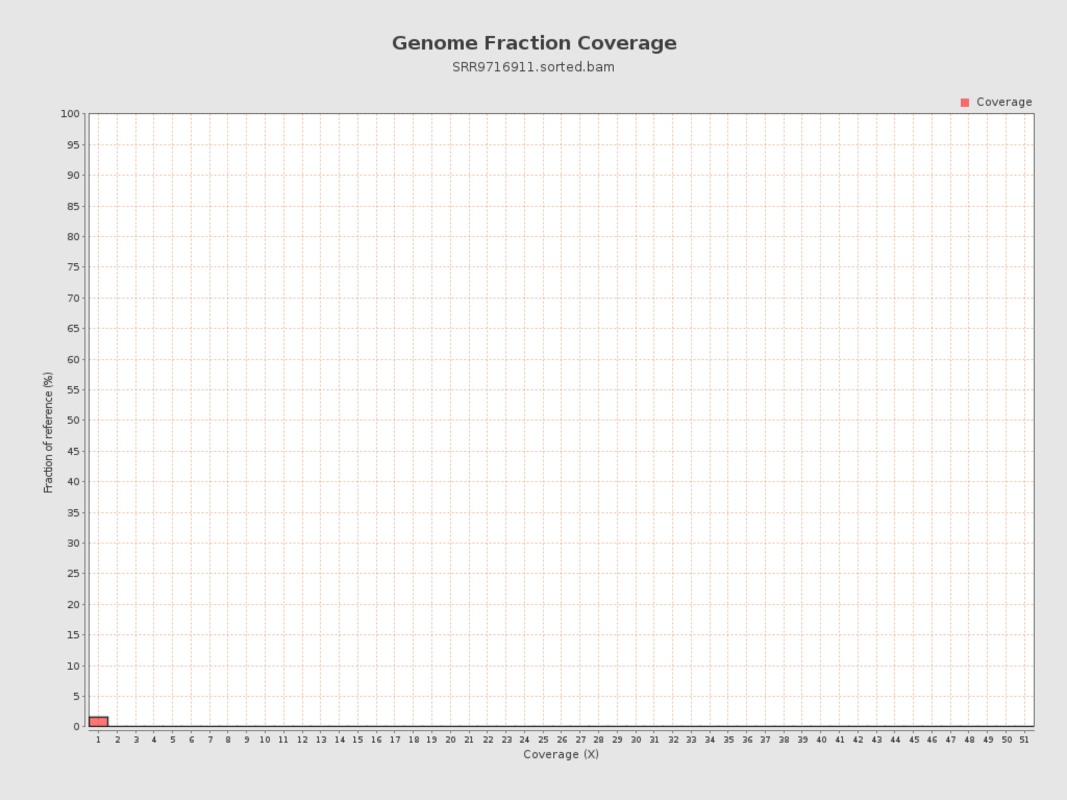
# 4. Results : Coverage Histogram



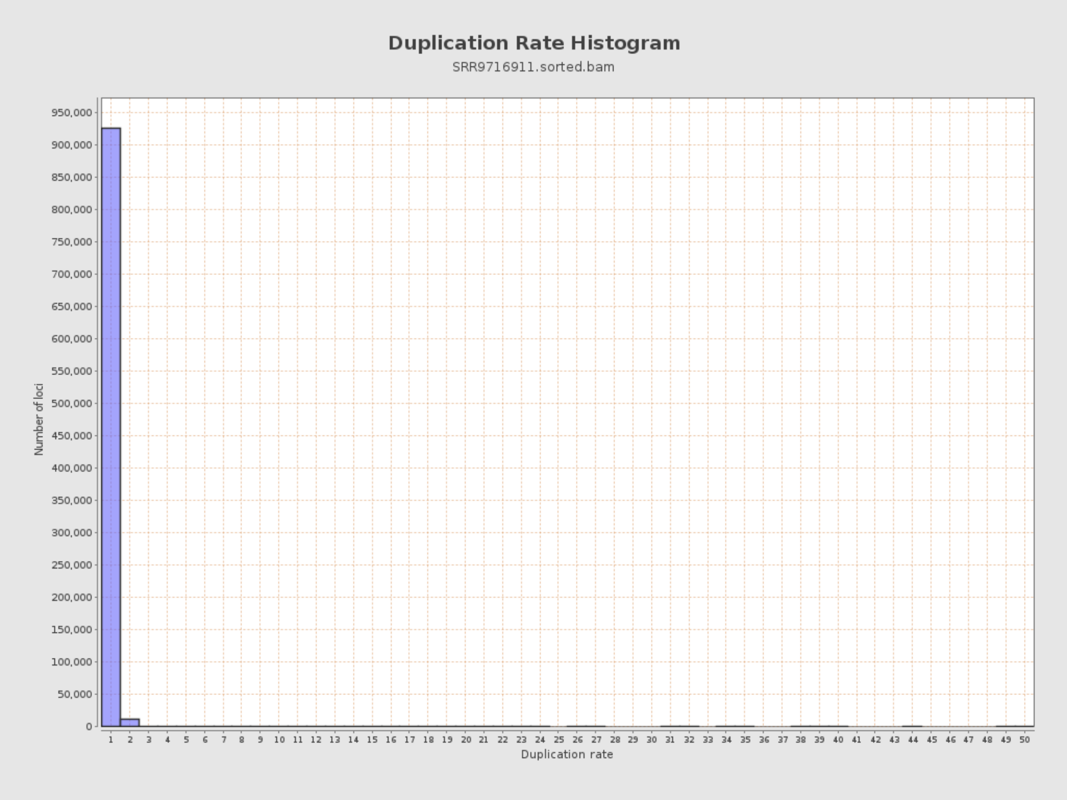
# 5. Results : Coverage Histogram (0-50X)



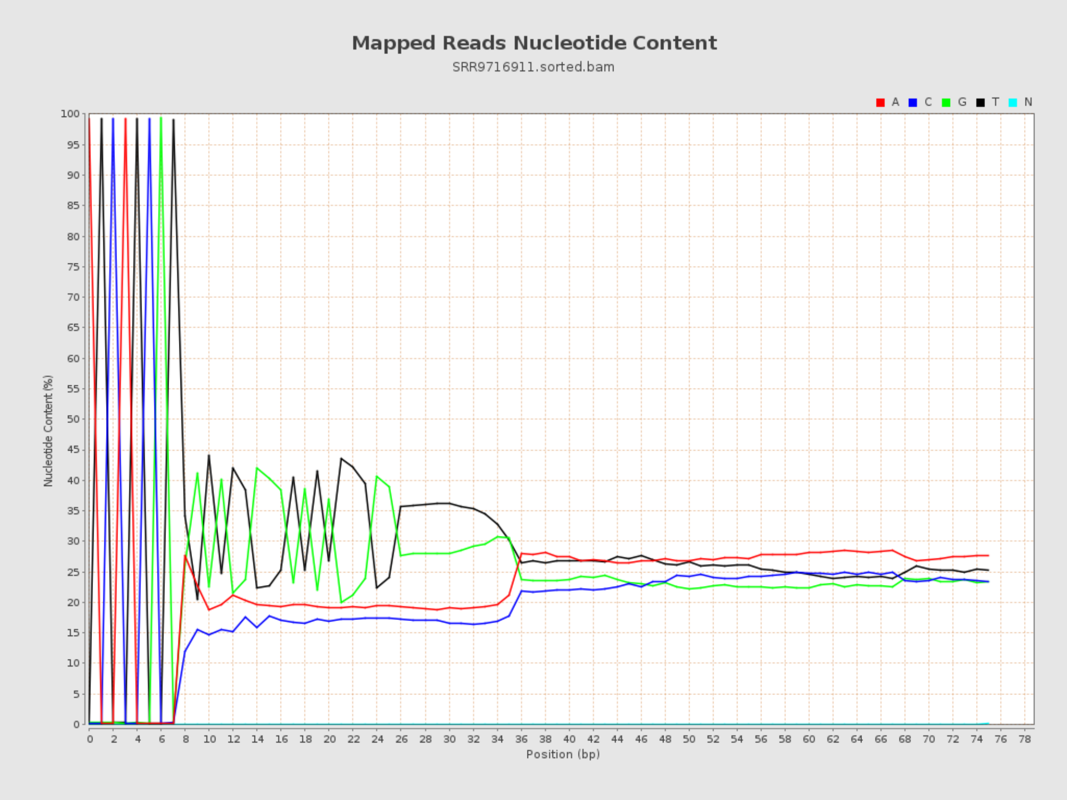
# 6. Results : Genome Fraction Coverage



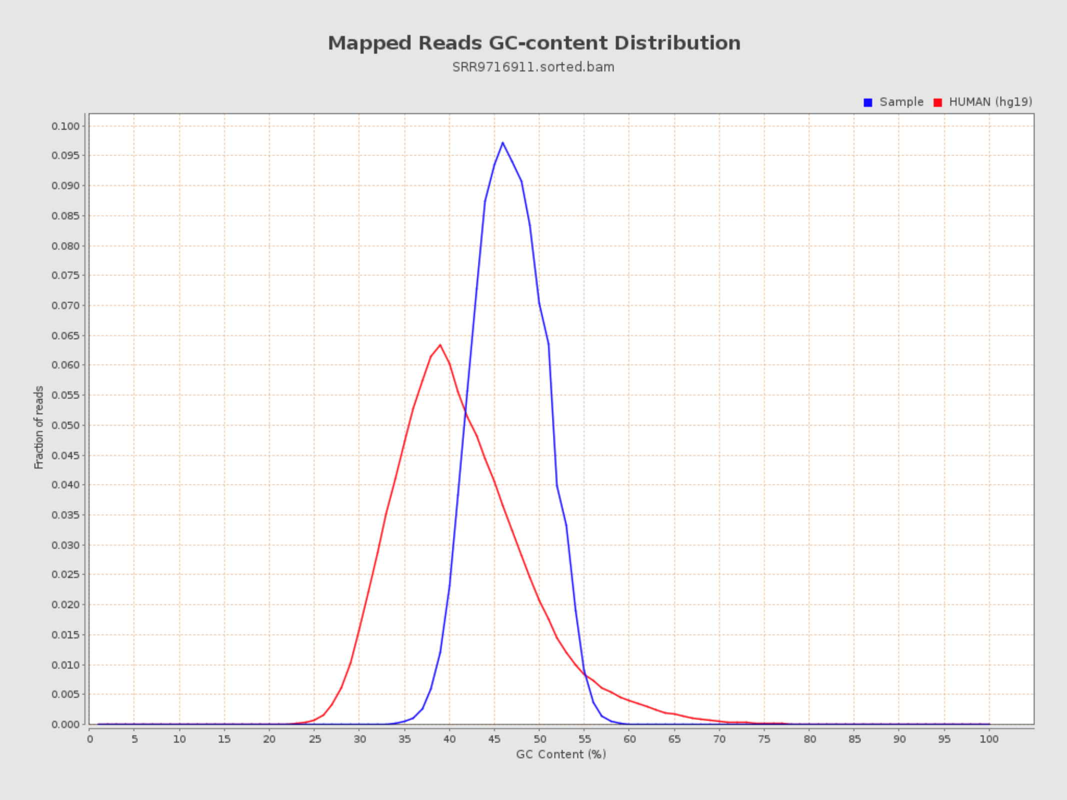
# 7. Results : Duplication Rate Histogram



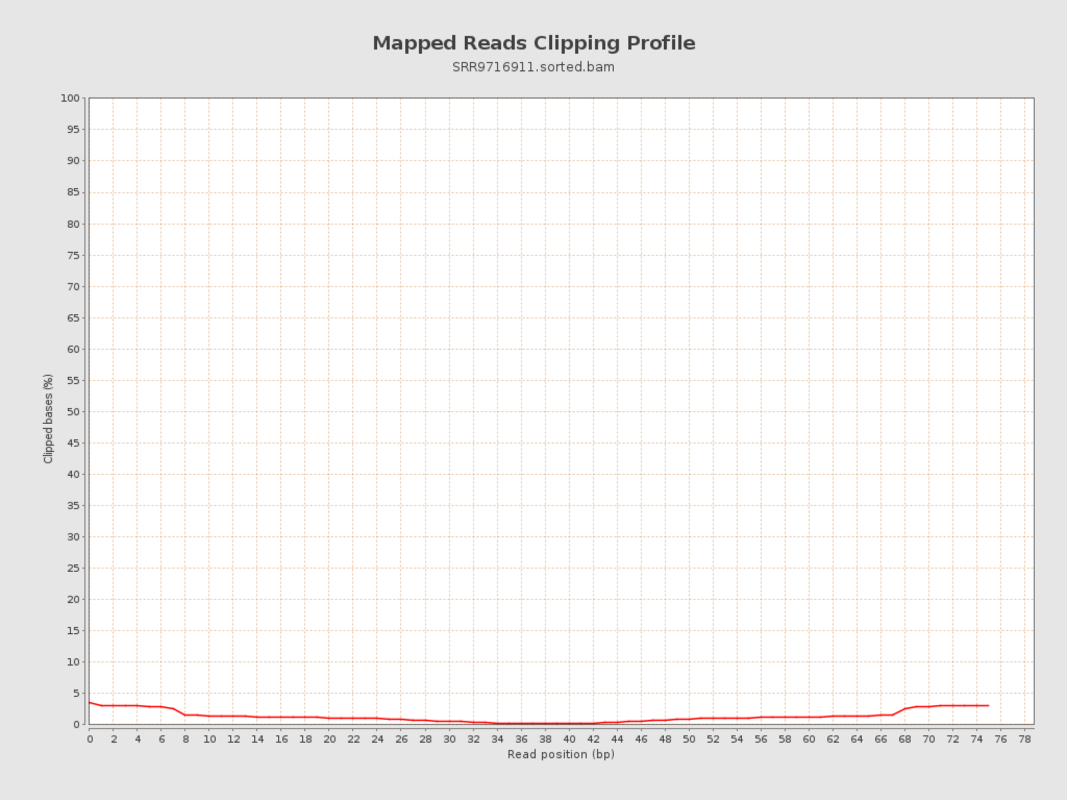
# 8. Results : Mapped Reads Nucleotide Content



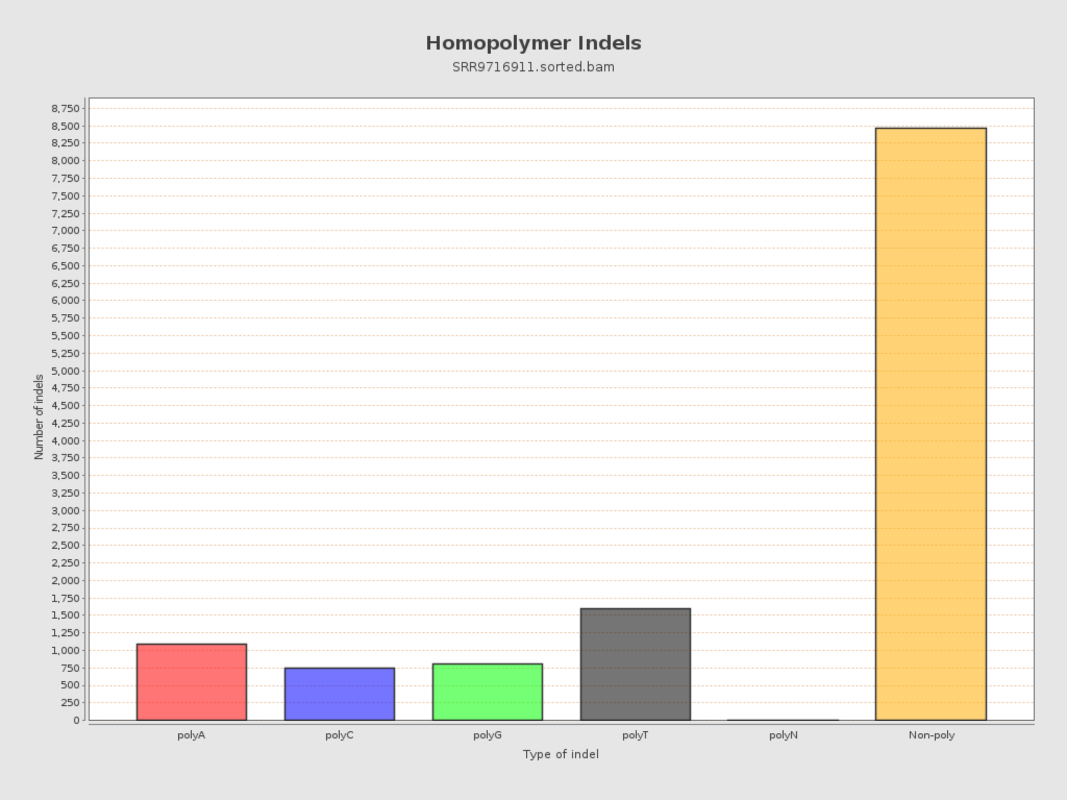
# 9. Results : Mapped Reads GC-content Distribution



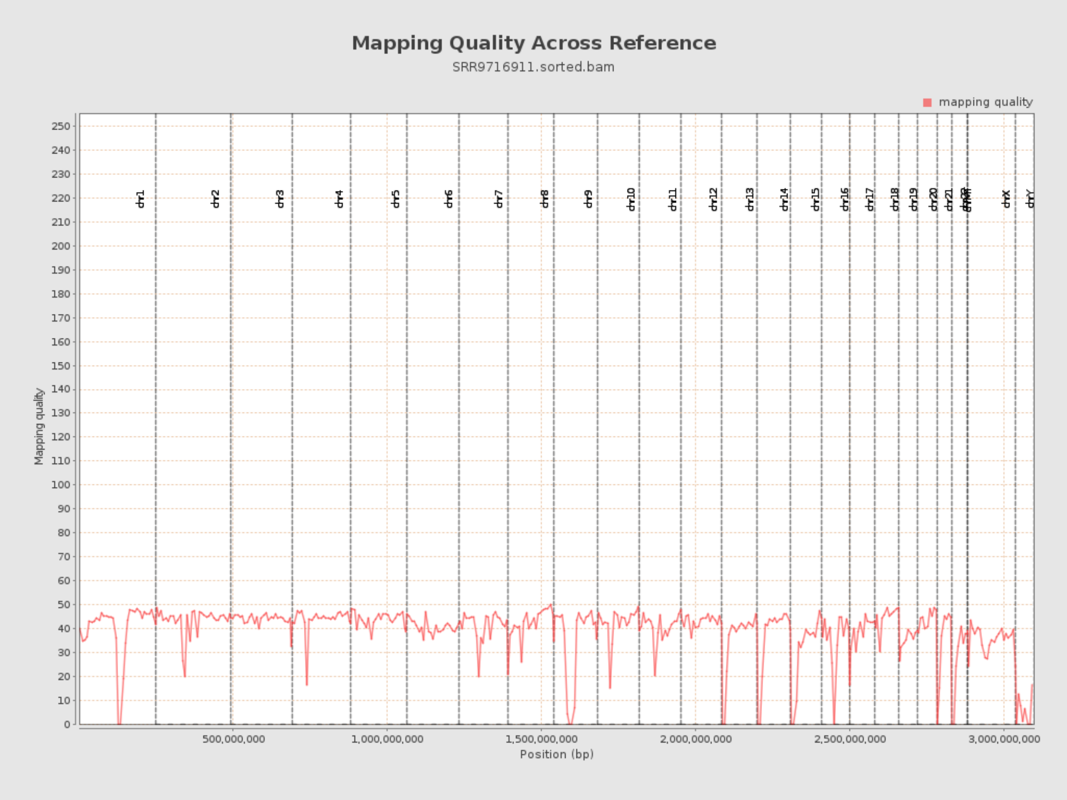
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram