# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/01 21:52:33*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716164.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_SRR9716164 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716164.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 01 21:52:33 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716164.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,050,577 |
| Mapped reads | 936,405 / 89.13% |
| Unmapped reads | 114,172 / 10.87% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 4,002 / 0.38% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 20,244 / 1.93% |
| Duplication rate | 1.68% |
| Clipped reads | 937,330 / 89.22% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 13,659,753 / 25.42% |
| Number/percentage of C's | 9,915,846 / 18.45% |
| Number/percentage of T's | 16,498,850 / 30.7% |
| Number/percentage of G's | 13,659,121 / 25.42% |
| Number/percentage of N's | 1,181 / 0% |
| GC Percentage | 43.87% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0174 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1637 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.65 |

## 2.5. Mismatches and indels

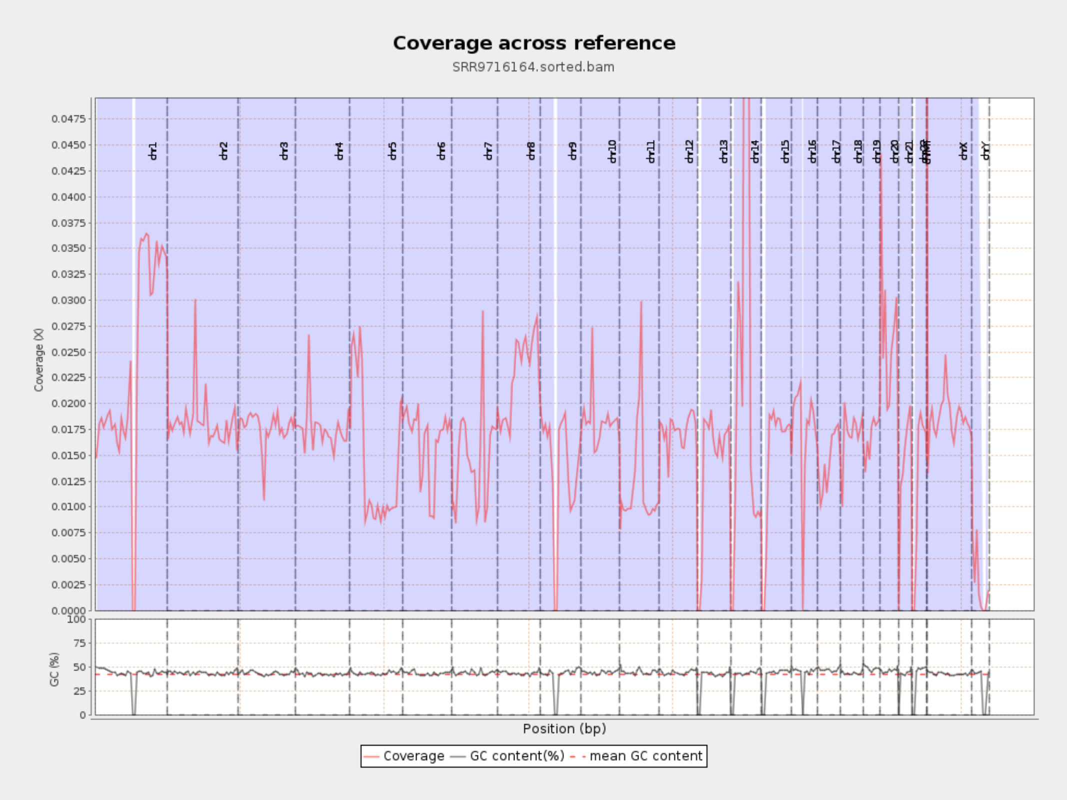
| | |
|---|---|
| General error rate | 0.49% |
| Mismatches | 255,616 |
| Insertions | 4,147 |
| Mapped reads with at least one insertion | 0.44% |
| Deletions | 8,358 |
| Mapped reads with at least one deletion | 0.89% |
| Homopolymer indels | 38.4% |

## 2.6. Chromosome stats

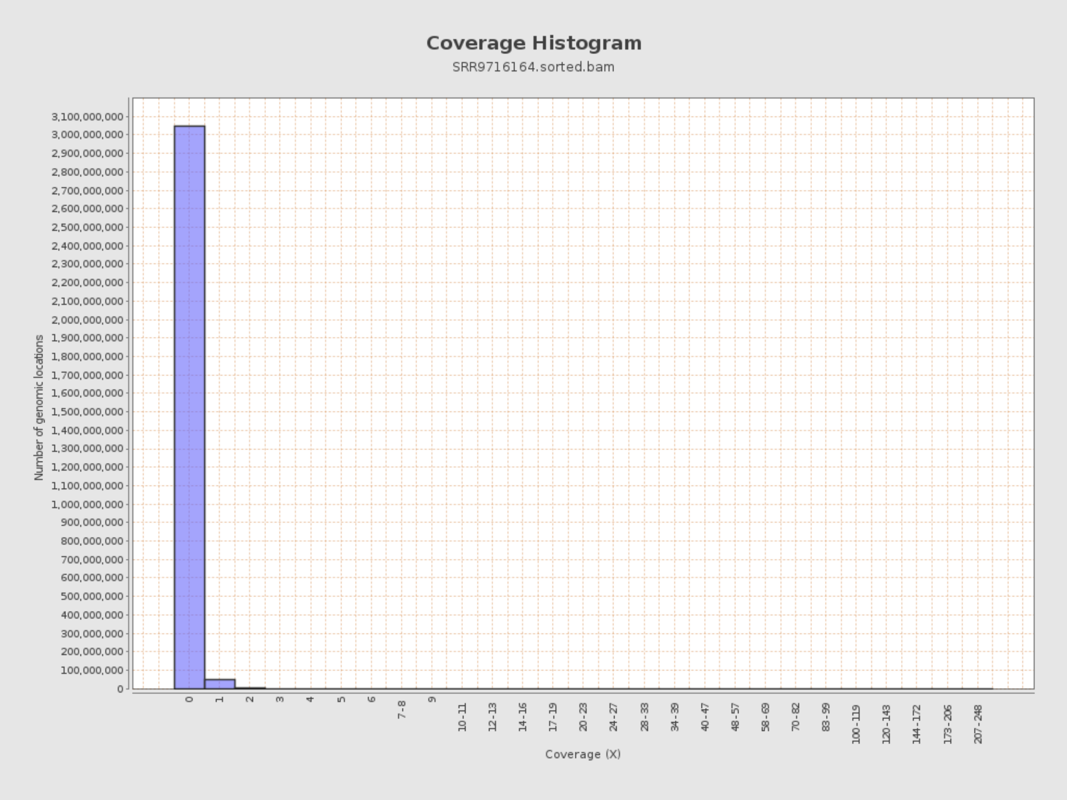
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5914856 | 0.0237 | 0.2351 |
| chr2 | 243199373 | 4428255 | 0.0182 | 0.1782 |
| chr3 | 198022430 | 3498643 | 0.0177 | 0.14 |
| chr4 | 191154276 | 3367406 | 0.0176 | 0.1456 |
| chr5 | 180915260 | 2618980 | 0.0145 | 0.1281 |
| chr6 | 171115067 | 2786271 | 0.0163 | 0.1413 |
| chr7 | 159138663 | 2360462 | 0.0148 | 0.1453 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3334647 | 0.0228 | 0.176 |
| chr9 | 141213431 | 1932431 | 0.0137 | 0.1546 |
| chr10 | 135534747 | 2488859 | 0.0184 | 0.1667 |
| chr11 | 135006516 | 1673096 | 0.0124 | 0.1474 |
| chr12 | 133851895 | 2332621 | 0.0174 | 0.14 |
| chr13 | 115169878 | 1630464 | 0.0142 | 0.125 |
| chr14 | 107349540 | 2787166 | 0.026 | 0.1782 |
| chr15 | 102531392 | 1502947 | 0.0147 | 0.1273 |
| chr16 | 90354753 | 1547830 | 0.0171 | 0.1471 |
| chr17 | 81195210 | 1171444 | 0.0144 | 0.1288 |
| chr18 | 78077248 | 1307124 | 0.0167 | 0.2977 |
| chr19 | 59128983 | 993369 | 0.0168 | 0.1728 |
| chr20 | 63025520 | 1693203 | 0.0269 | 0.1758 |
| chr21 | 48129895 | 689934 | 0.0143 | 0.1343 |
| chr22 | 51304566 | 633763 | 0.0124 | 0.1169 |
| chrMT | 16571 | 1179 | 0.0711 | 0.2754 |
| chrX | 155270560 | 2905086 | 0.0187 | 0.1567 |
| chrY | 59373566 | 148771 | 0.0025 | 0.0656 |

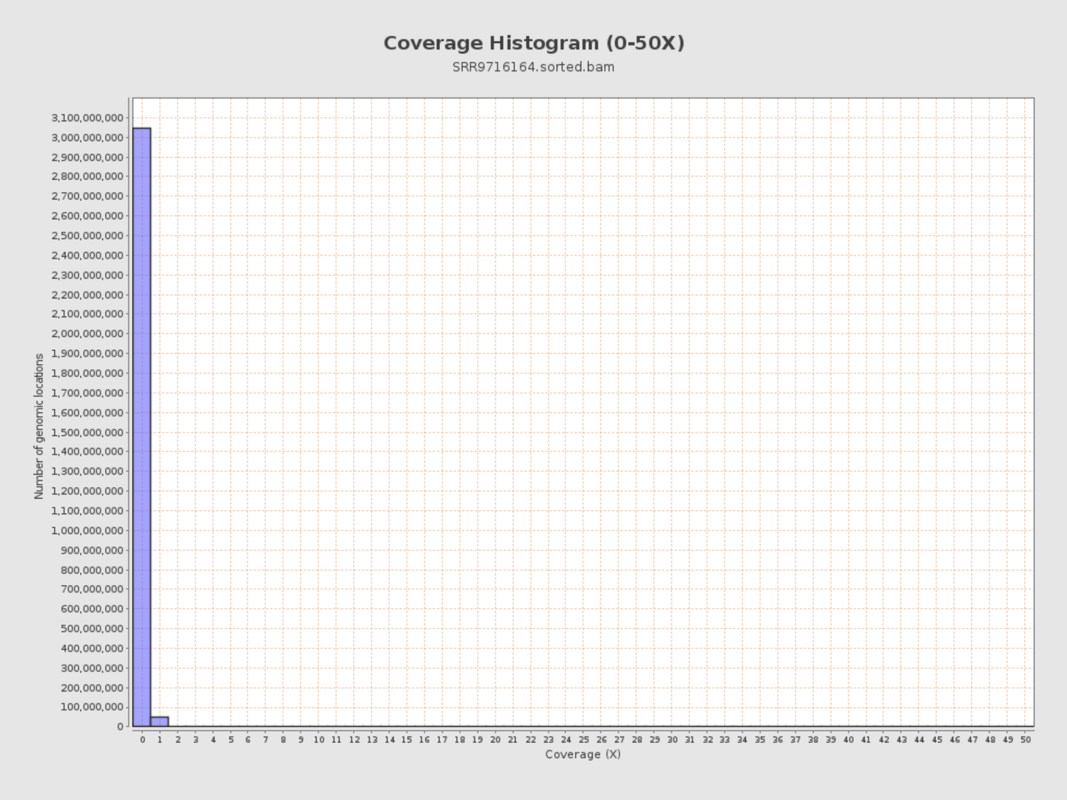
# 3. Results : Coverage across reference



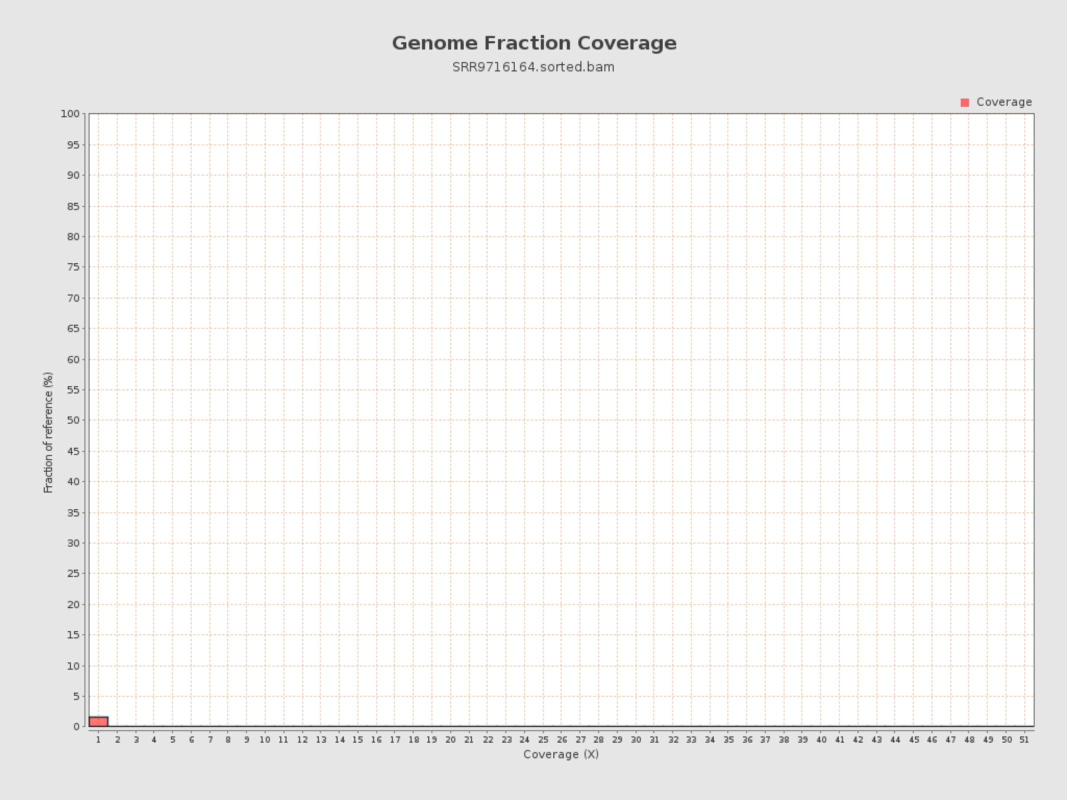
# 4. Results : Coverage Histogram



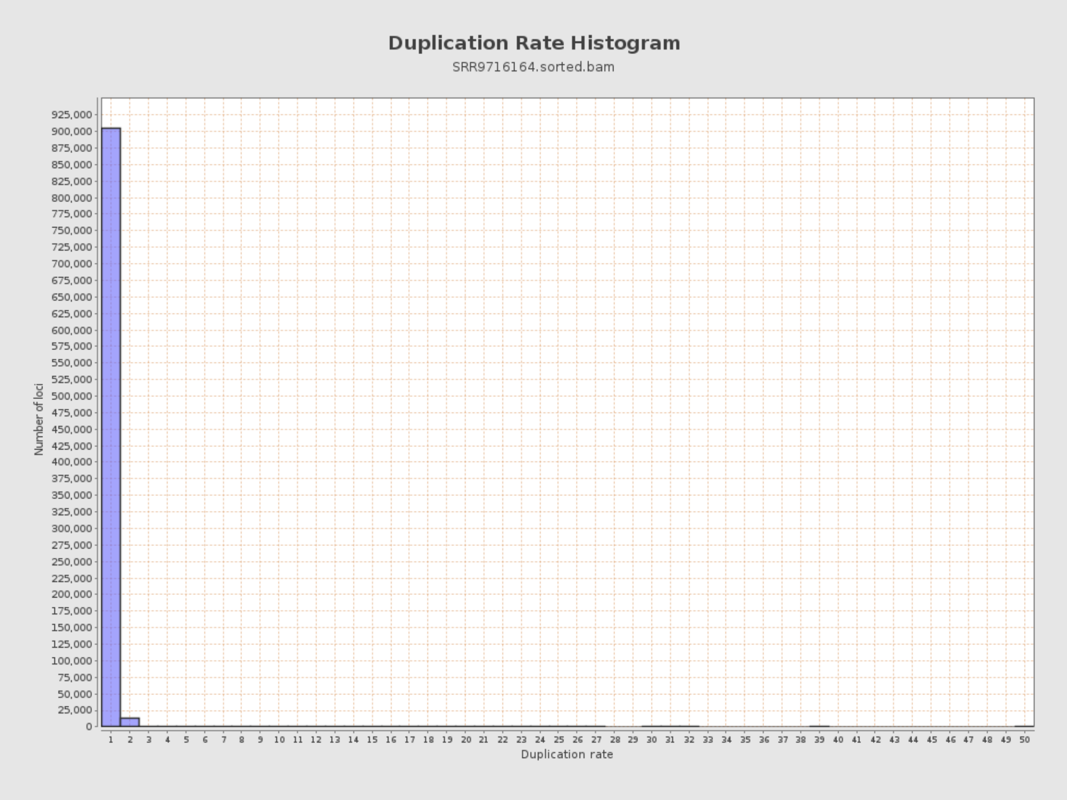
# 5. Results : Coverage Histogram (0-50X)



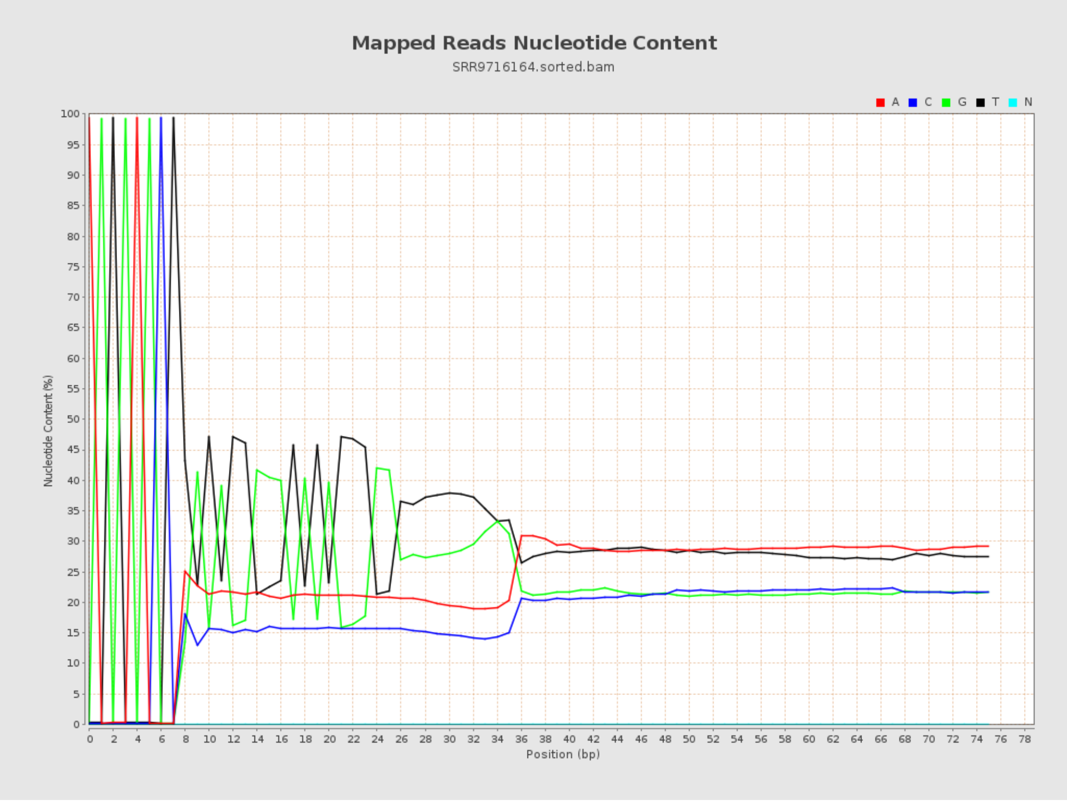
# 6. Results : Genome Fraction Coverage



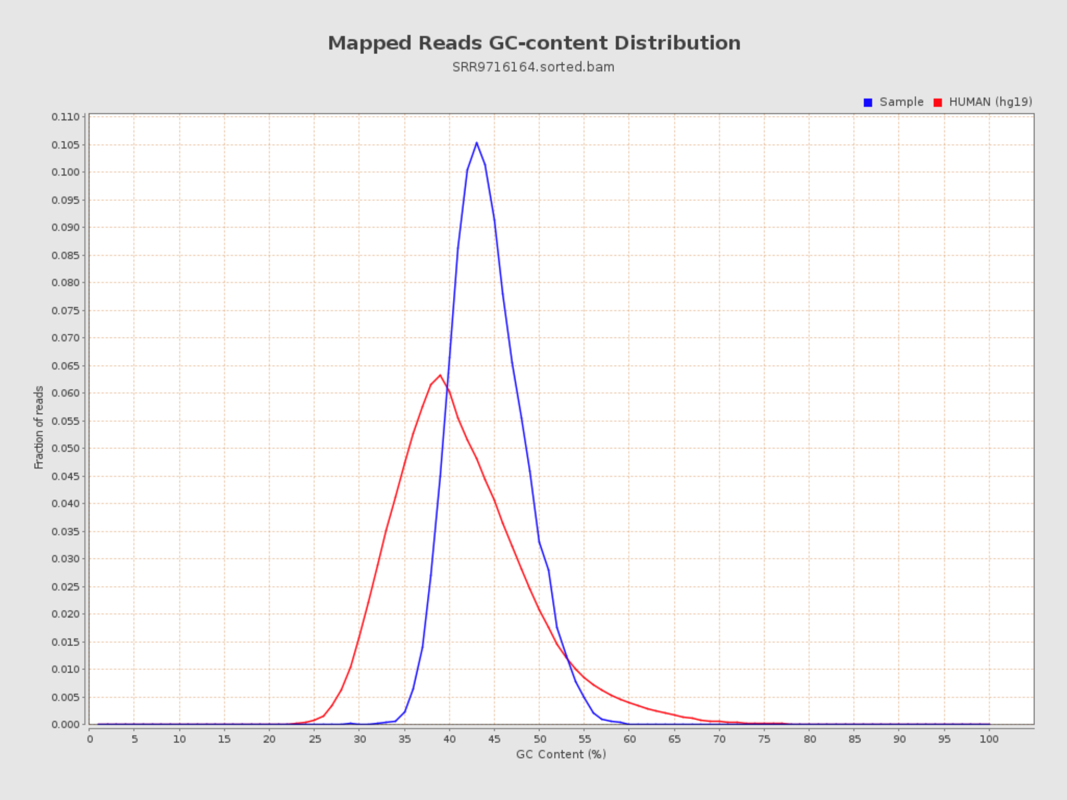
# 7. Results : Duplication Rate Histogram



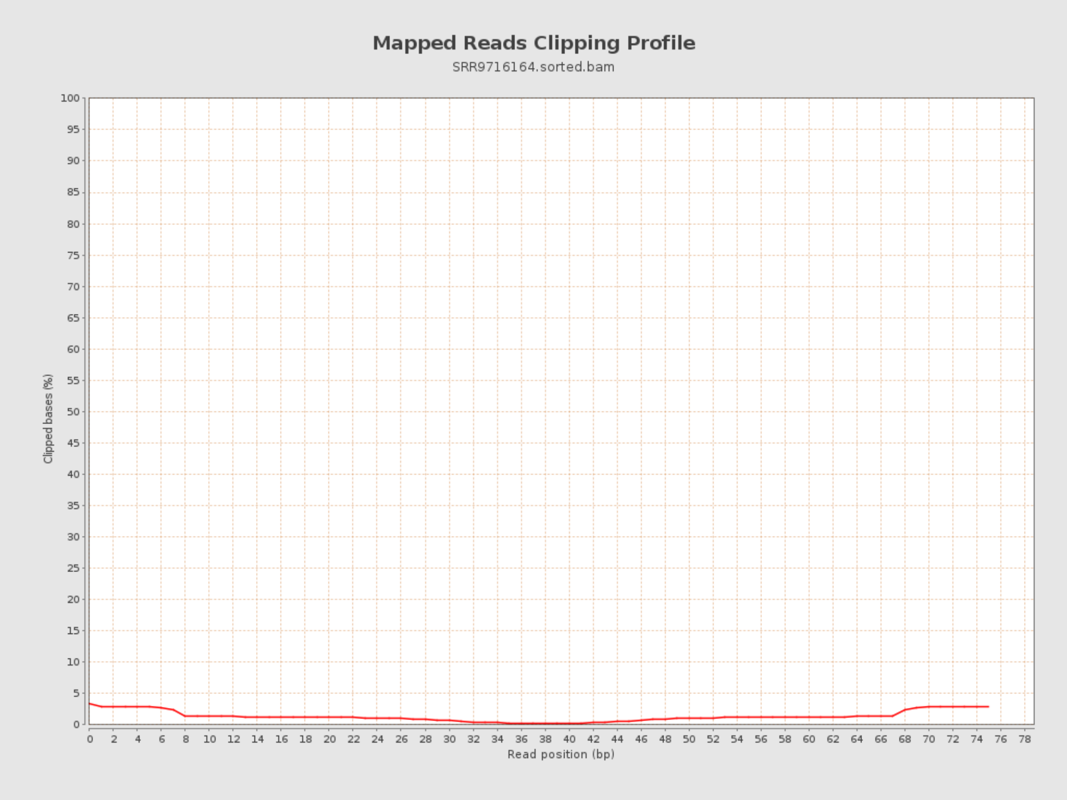
# 8. Results : Mapped Reads Nucleotide Content



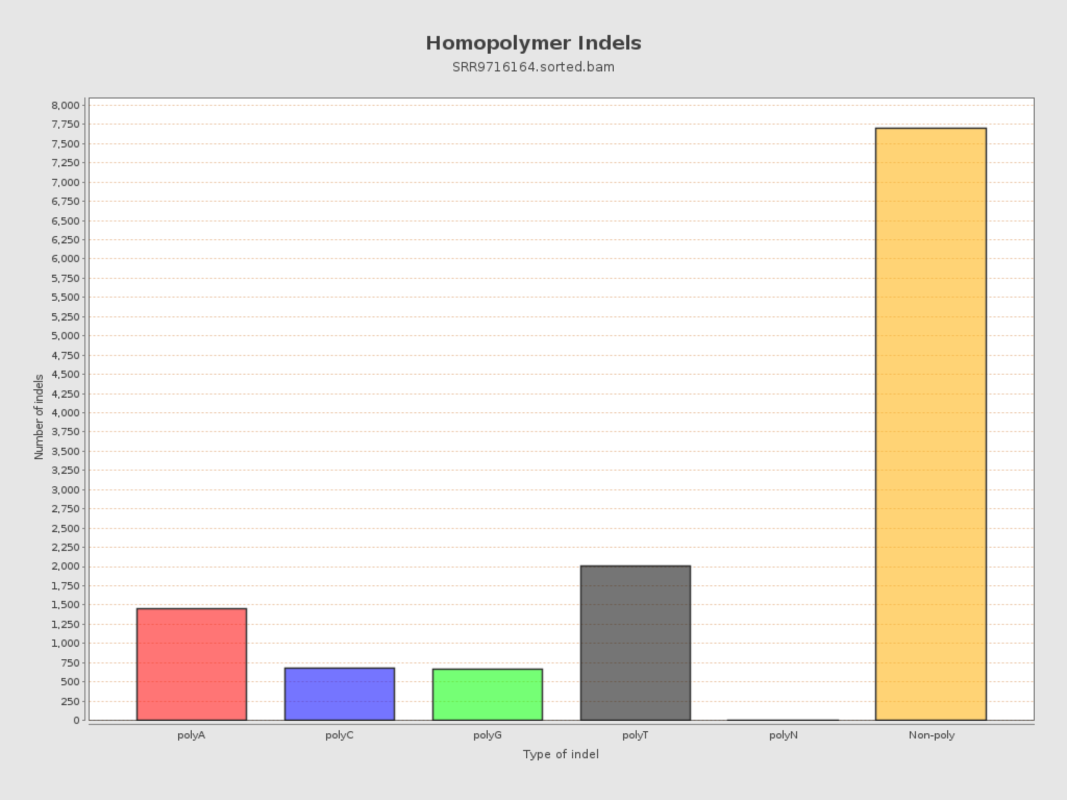
# 9. Results : Mapped Reads GC-content Distribution



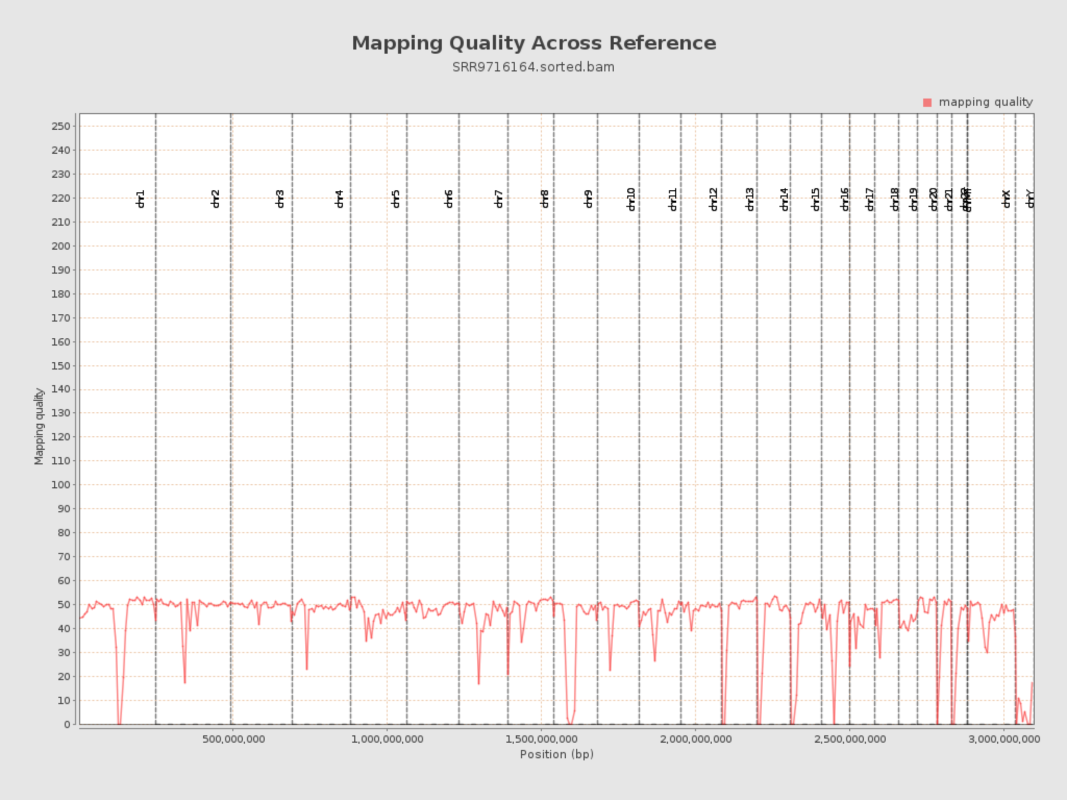
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram