# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 23:23:44*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716995.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_SRR9716995 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716995.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 23:23:44 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716995.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,384,206 |
| Mapped reads | 1,218,409 / 88.02% |
| Unmapped reads | 165,797 / 11.98% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 4,836 / 0.35% |
| Read min/max/mean length | 30 / 76 / 76.12 |
| Duplicated reads (estimated) | 34,475 / 2.49% |
| Duplication rate | 2.09% |
| Clipped reads | 1,218,832 / 88.05% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 16,581,156 / 23.76% |
| Number/percentage of C's | 13,954,620 / 20% |
| Number/percentage of T's | 22,660,576 / 32.47% |
| Number/percentage of G's | 16,586,800 / 23.77% |
| Number/percentage of N's | 477 / 0% |
| GC Percentage | 43.77% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0225 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2033 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.87 |

## 2.5. Mismatches and indels

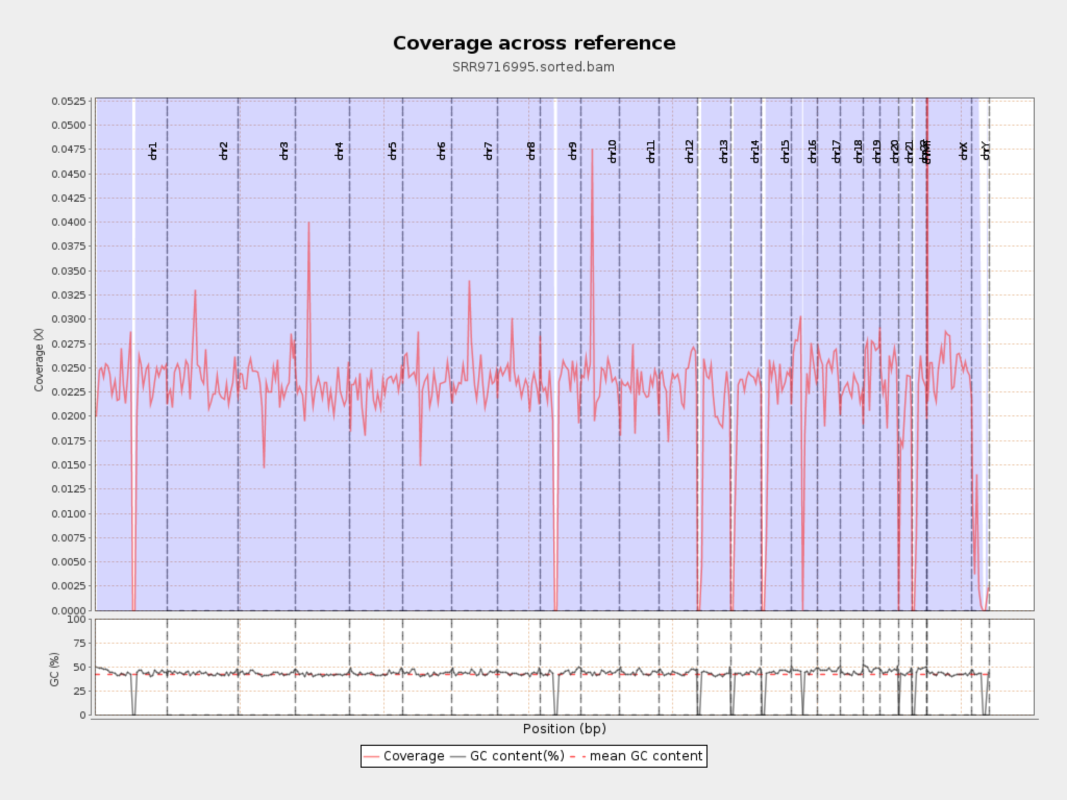
| | |
|---|---|
| General error rate | 0.55% |
| Mismatches | 370,103 |
| Insertions | 5,529 |
| Mapped reads with at least one insertion | 0.45% |
| Deletions | 13,742 |
| Mapped reads with at least one deletion | 1.12% |
| Homopolymer indels | 38.69% |

## 2.6. Chromosome stats

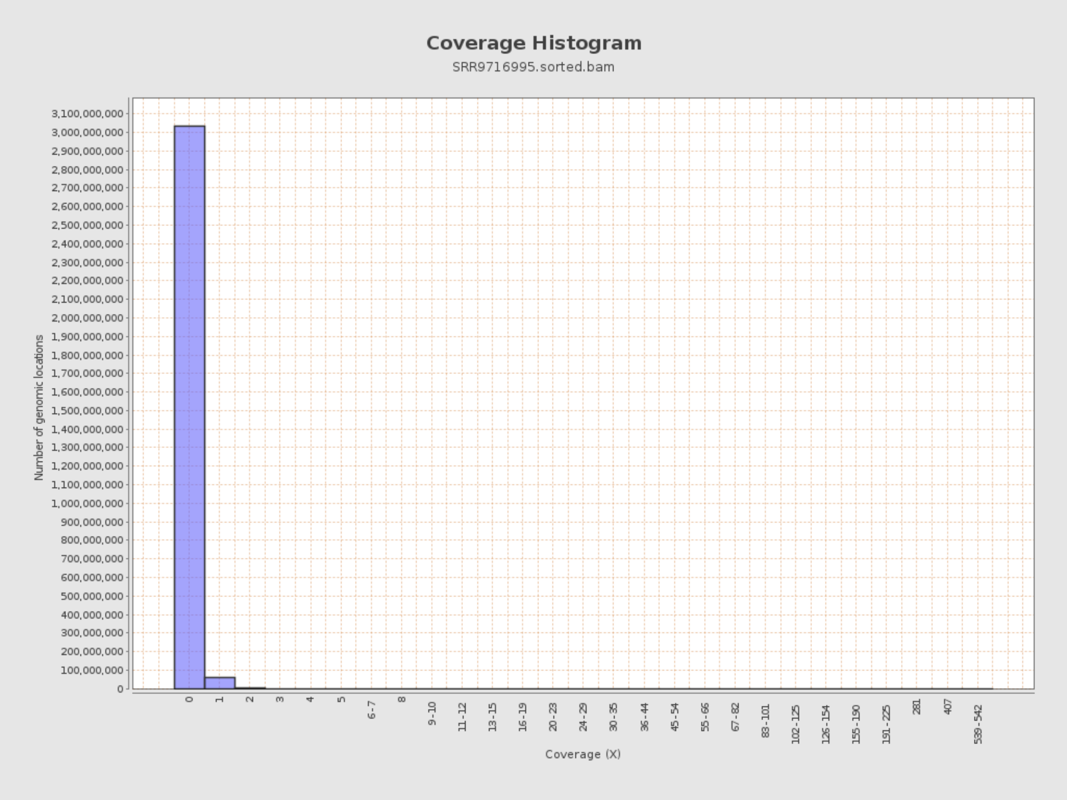
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5598531 | 0.0225 | 0.2477 |
| chr2 | 243199373 | 5804234 | 0.0239 | 0.2913 |
| chr3 | 198022430 | 4667067 | 0.0236 | 0.1662 |
| chr4 | 191154276 | 4455423 | 0.0233 | 0.1824 |
| chr5 | 180915260 | 4132607 | 0.0228 | 0.163 |
| chr6 | 171115067 | 4032733 | 0.0236 | 0.1898 |
| chr7 | 159138663 | 3844178 | 0.0242 | 0.2418 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3497810 | 0.0239 | 0.2125 |
| chr9 | 141213431 | 2952349 | 0.0209 | 0.1759 |
| chr10 | 135534747 | 3402212 | 0.0251 | 0.2505 |
| chr11 | 135006516 | 3128452 | 0.0232 | 0.1867 |
| chr12 | 133851895 | 3178013 | 0.0237 | 0.1676 |
| chr13 | 115169878 | 2156180 | 0.0187 | 0.147 |
| chr14 | 107349540 | 2132840 | 0.0199 | 0.1591 |
| chr15 | 102531392 | 1993170 | 0.0194 | 0.1533 |
| chr16 | 90354753 | 2080900 | 0.023 | 0.1742 |
| chr17 | 81195210 | 2013349 | 0.0248 | 0.1763 |
| chr18 | 78077248 | 1782300 | 0.0228 | 0.2673 |
| chr19 | 59128983 | 1543040 | 0.0261 | 0.2327 |
| chr20 | 63025520 | 1499553 | 0.0238 | 0.1711 |
| chr21 | 48129895 | 906129 | 0.0188 | 0.1639 |
| chr22 | 51304566 | 847530 | 0.0165 | 0.1388 |
| chrMT | 16571 | 17633 | 1.0641 | 1.2735 |
| chrX | 155270560 | 3904747 | 0.0251 | 0.1815 |
| chrY | 59373566 | 234668 | 0.004 | 0.1291 |

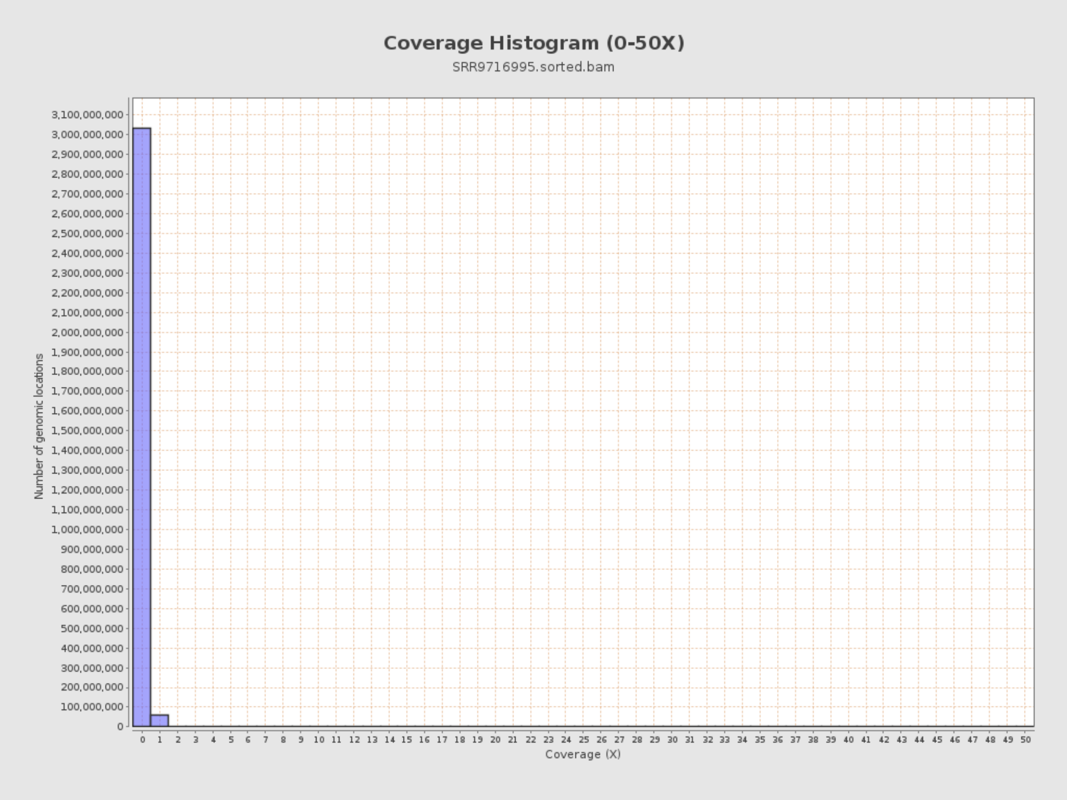
# 3. Results : Coverage across reference



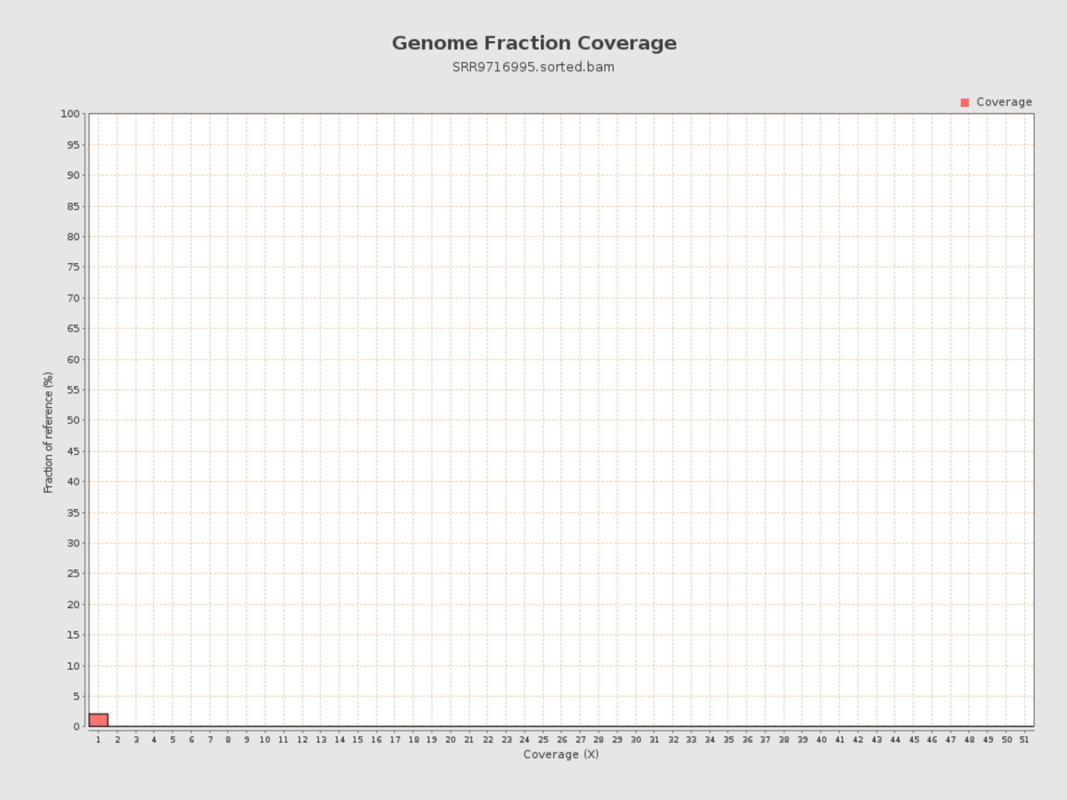
# 4. Results : Coverage Histogram



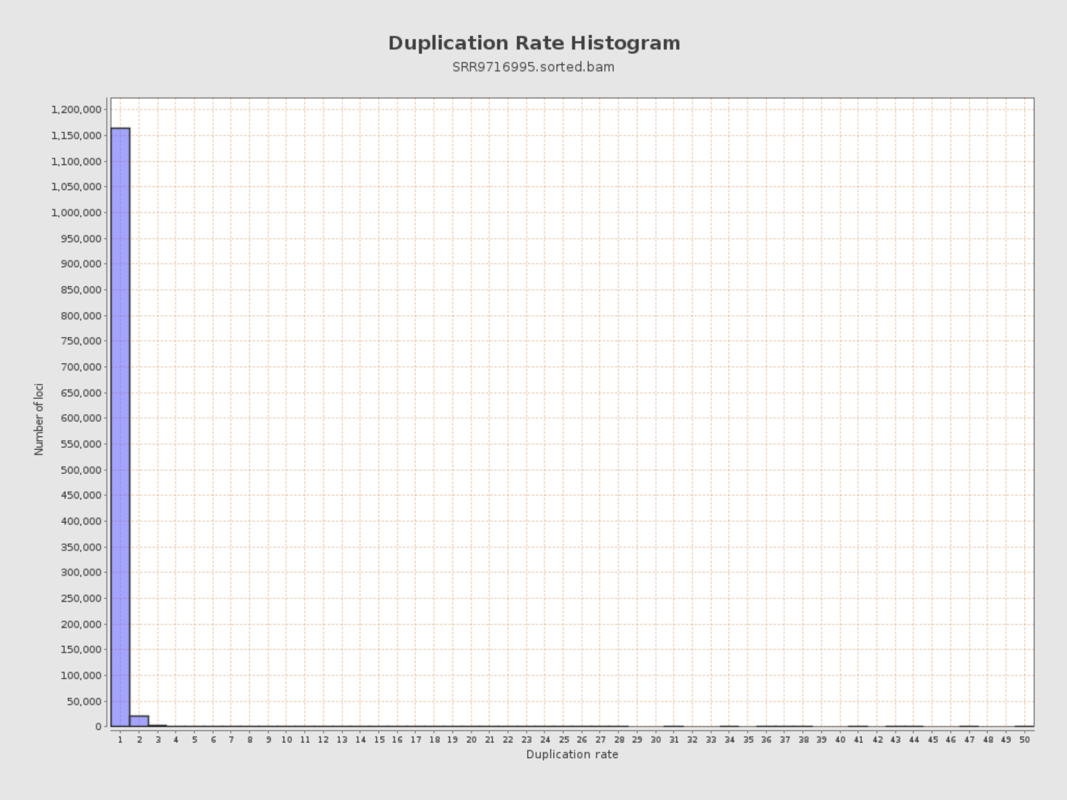
# 5. Results : Coverage Histogram (0-50X)



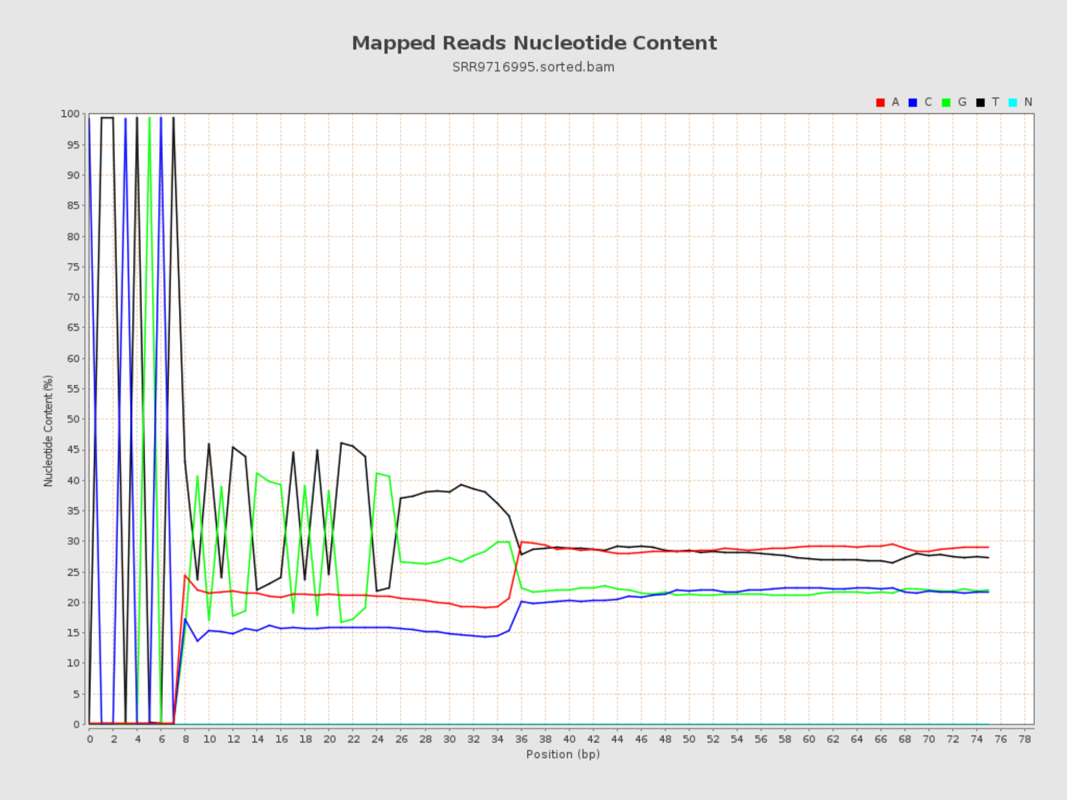
# 6. Results : Genome Fraction Coverage



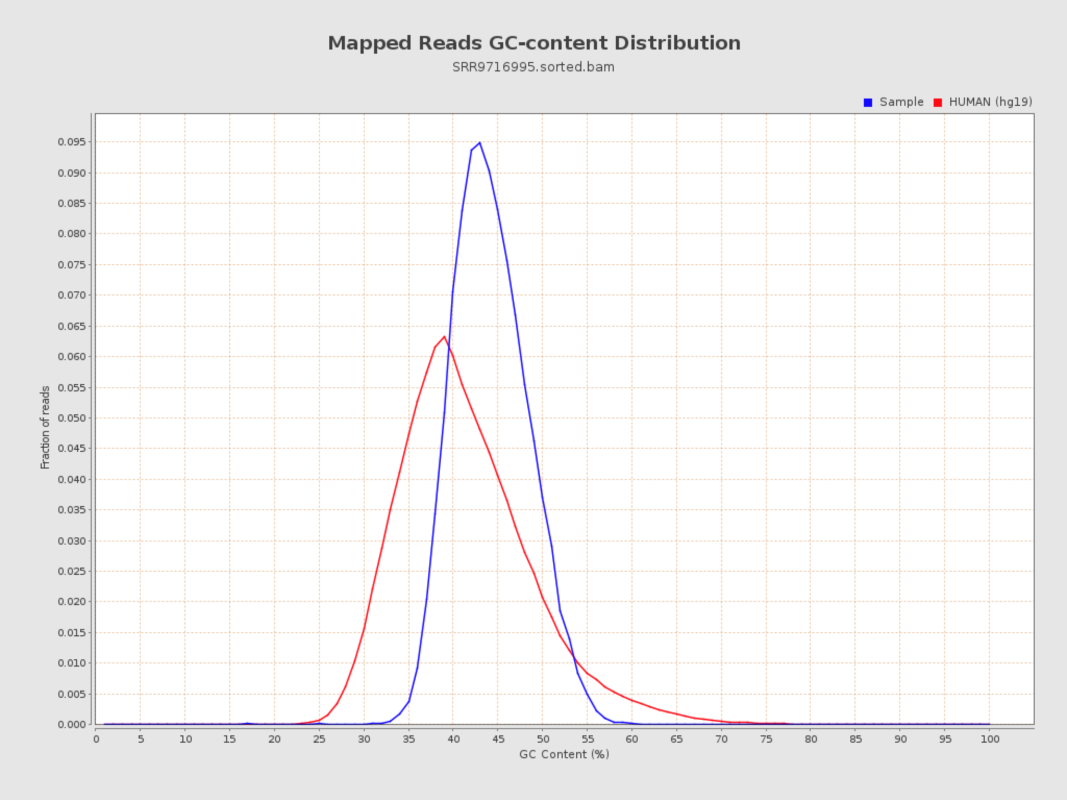
# 7. Results : Duplication Rate Histogram



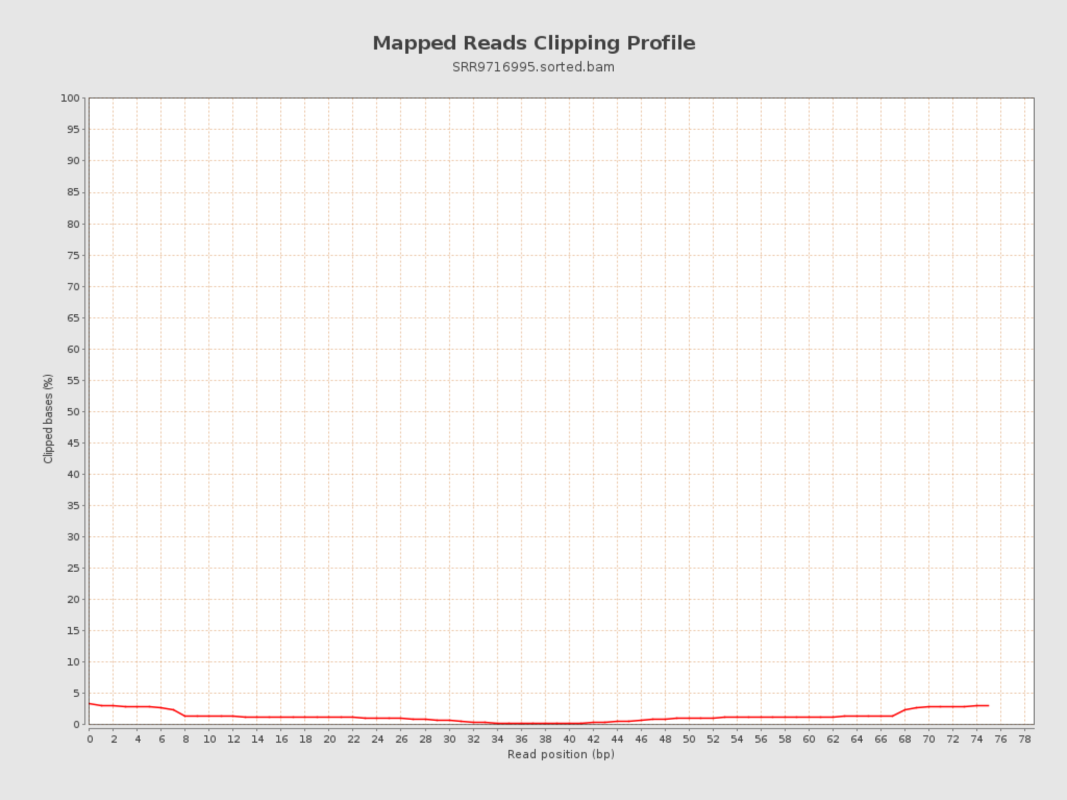
# 8. Results : Mapped Reads Nucleotide Content



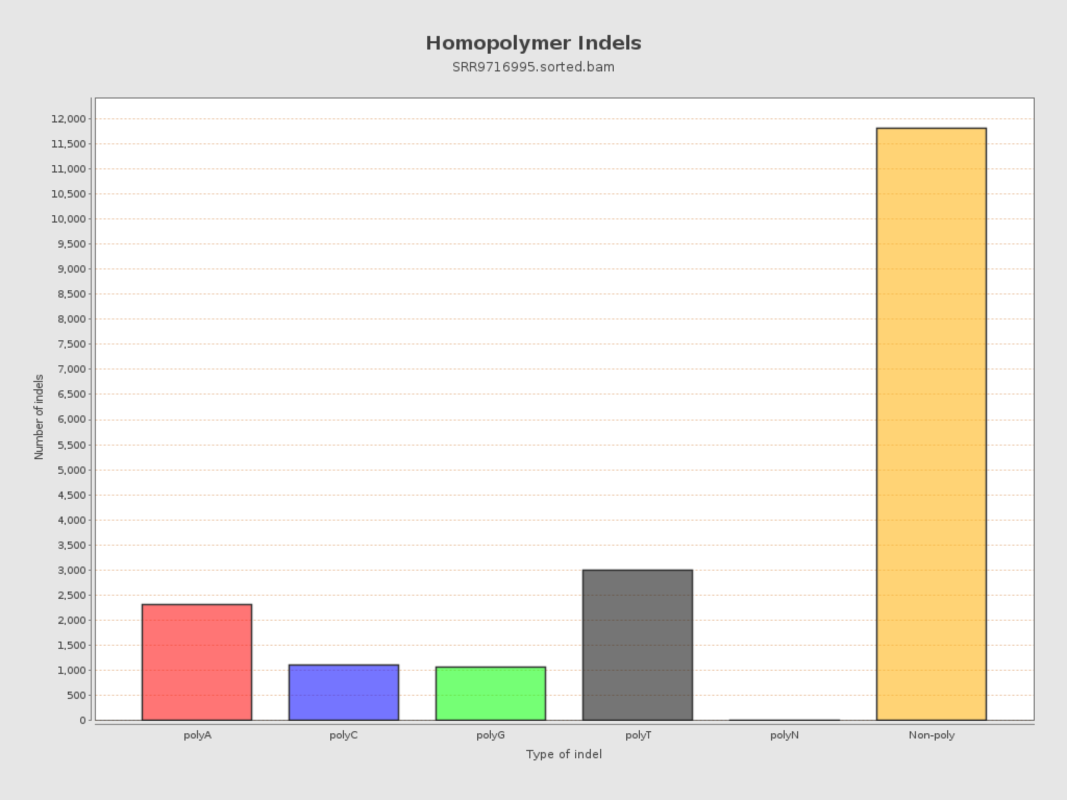
# 9. Results : Mapped Reads GC-content Distribution



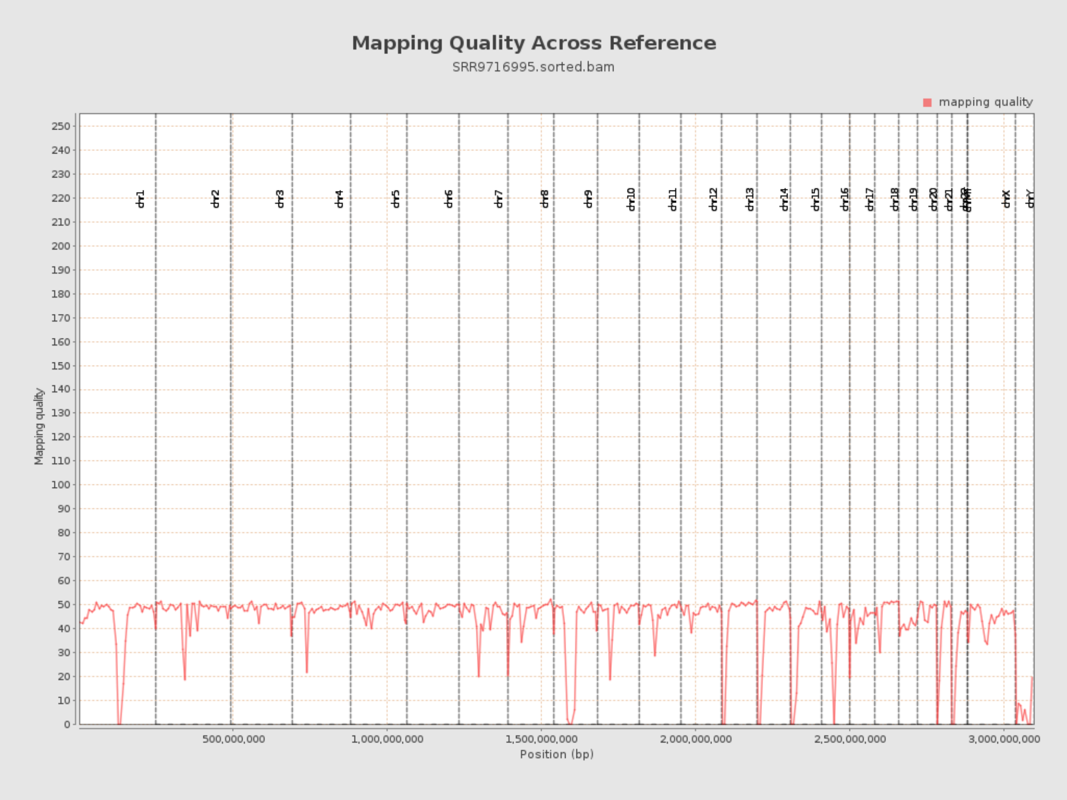
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram