# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 14:04:20*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716834.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_SRR9716834 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716834.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 14:04:19 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716834.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 933,617 |
| Mapped reads | 823,346 / 88.19% |
| Unmapped reads | 110,271 / 11.81% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 4,866 / 0.52% |
| Read min/max/mean length | 30 / 76 / 76.17 |
| Duplicated reads (estimated) | 28,305 / 3.03% |
| Duplication rate | 2.8% |
| Clipped reads | 825,638 / 88.43% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 11,928,676 / 24.99% |
| Number/percentage of C's | 9,476,503 / 19.85% |
| Number/percentage of T's | 15,464,988 / 32.4% |
| Number/percentage of G's | 10,863,378 / 22.76% |
| Number/percentage of N's | 329 / 0% |
| GC Percentage | 42.61% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0154 |
| | |

| | |
|---|---|
| Standard Deviation | 0.16 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.98 |

## 2.5. Mismatches and indels

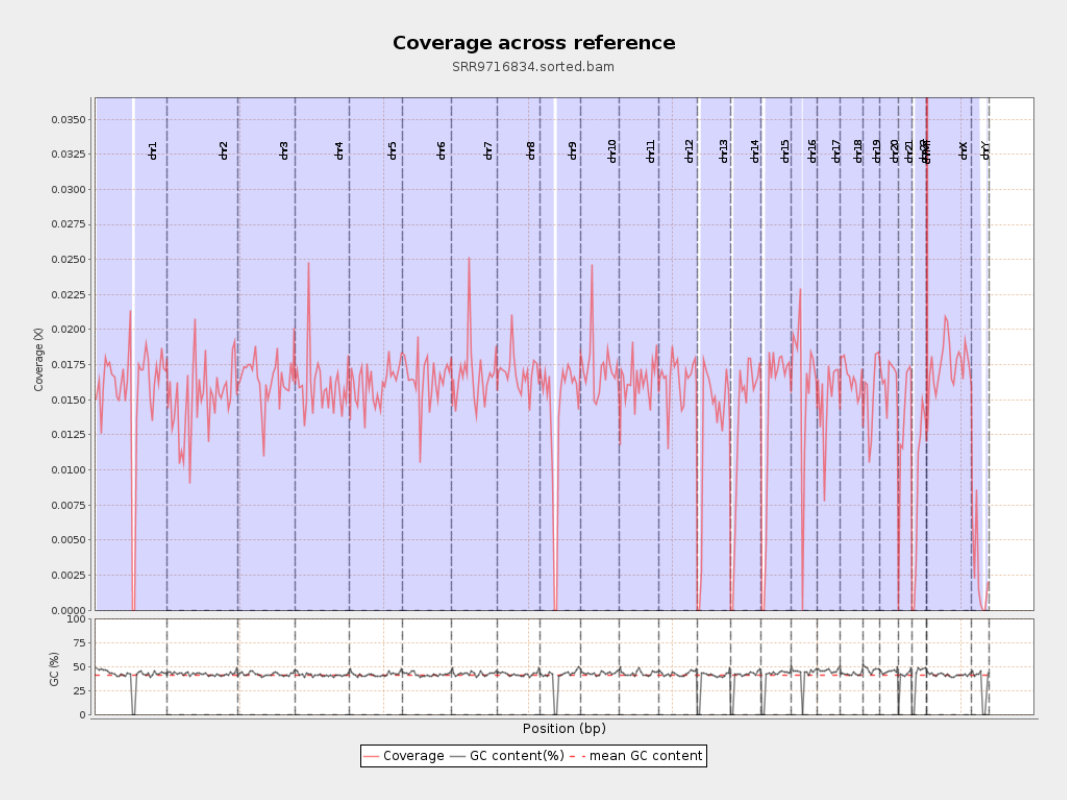
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 235,896 |
| Insertions | 3,145 |
| Mapped reads with at least one insertion | 0.38% |
| Deletions | 8,330 |
| Mapped reads with at least one deletion | 1% |
| Homopolymer indels | 42.32% |

## 2.6. Chromosome stats

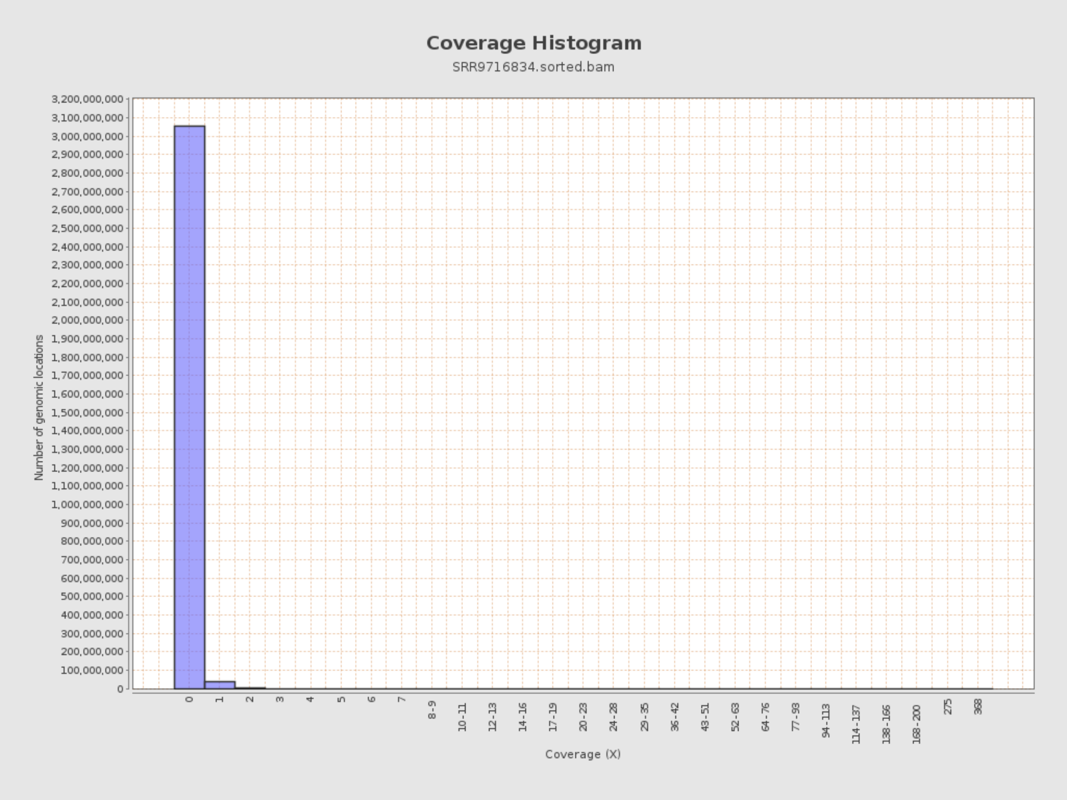
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3871185 | 0.0155 | 0.205 |
| chr2 | 243199373 | 3658799 | 0.015 | 0.2054 |
| chr3 | 198022430 | 3245986 | 0.0164 | 0.1383 |
| chr4 | 191154276 | 3069728 | 0.0161 | 0.1479 |
| chr5 | 180915260 | 2931055 | 0.0162 | 0.1371 |
| chr6 | 171115067 | 2821615 | 0.0165 | 0.1485 |
| chr7 | 159138663 | 2676421 | 0.0168 | 0.2054 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2483586 | 0.017 | 0.1756 |
| chr9 | 141213431 | 1984786 | 0.0141 | 0.1375 |
| chr10 | 135534747 | 2339337 | 0.0173 | 0.1695 |
| chr11 | 135006516 | 2213062 | 0.0164 | 0.1522 |
| chr12 | 133851895 | 2202261 | 0.0165 | 0.1386 |
| chr13 | 115169878 | 1486670 | 0.0129 | 0.1223 |
| chr14 | 107349540 | 1433760 | 0.0134 | 0.1269 |
| chr15 | 102531392 | 1438185 | 0.014 | 0.1295 |
| chr16 | 90354753 | 1449831 | 0.016 | 0.1406 |
| chr17 | 81195210 | 1221057 | 0.015 | 0.1363 |
| chr18 | 78077248 | 1298636 | 0.0166 | 0.2049 |
| chr19 | 59128983 | 903723 | 0.0153 | 0.1697 |
| chr20 | 63025520 | 1037037 | 0.0165 | 0.1402 |
| chr21 | 48129895 | 641579 | 0.0133 | 0.13 |
| chr22 | 51304566 | 455070 | 0.0089 | 0.1017 |
| chrMT | 16571 | 6431 | 0.3881 | 0.7083 |
| chrX | 155270560 | 2728125 | 0.0176 | 0.1485 |
| chrY | 59373566 | 149043 | 0.0025 | 0.0815 |

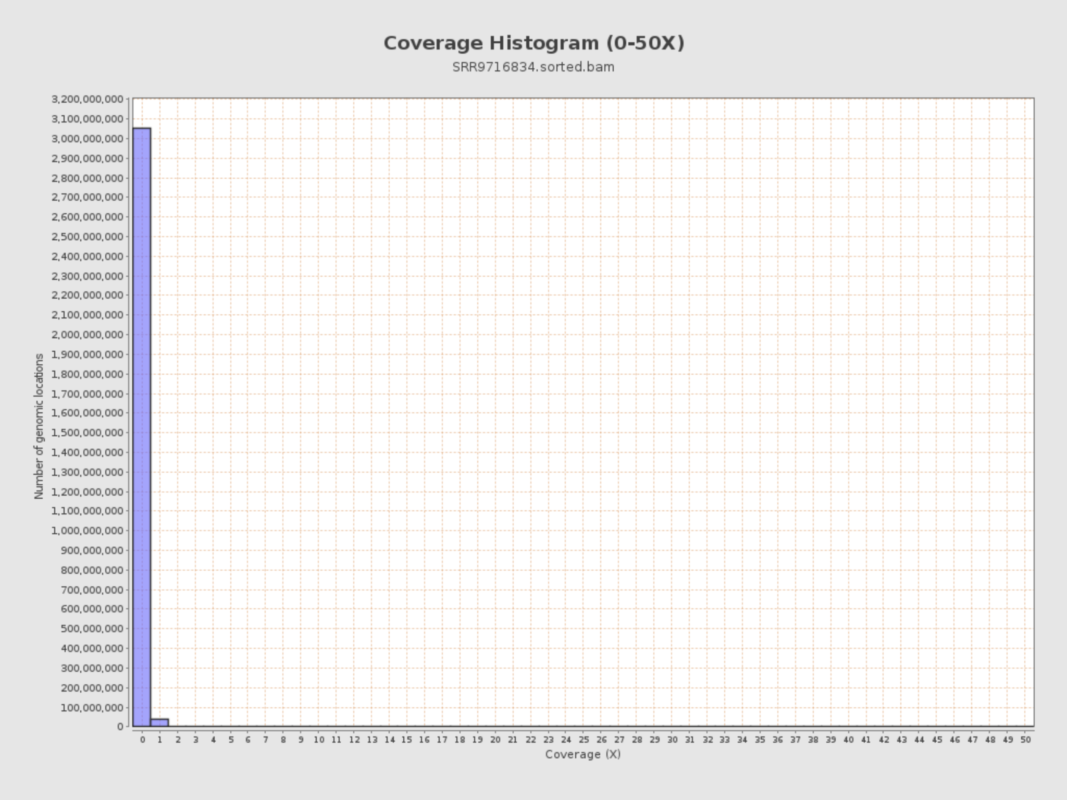
# 3. Results : Coverage across reference



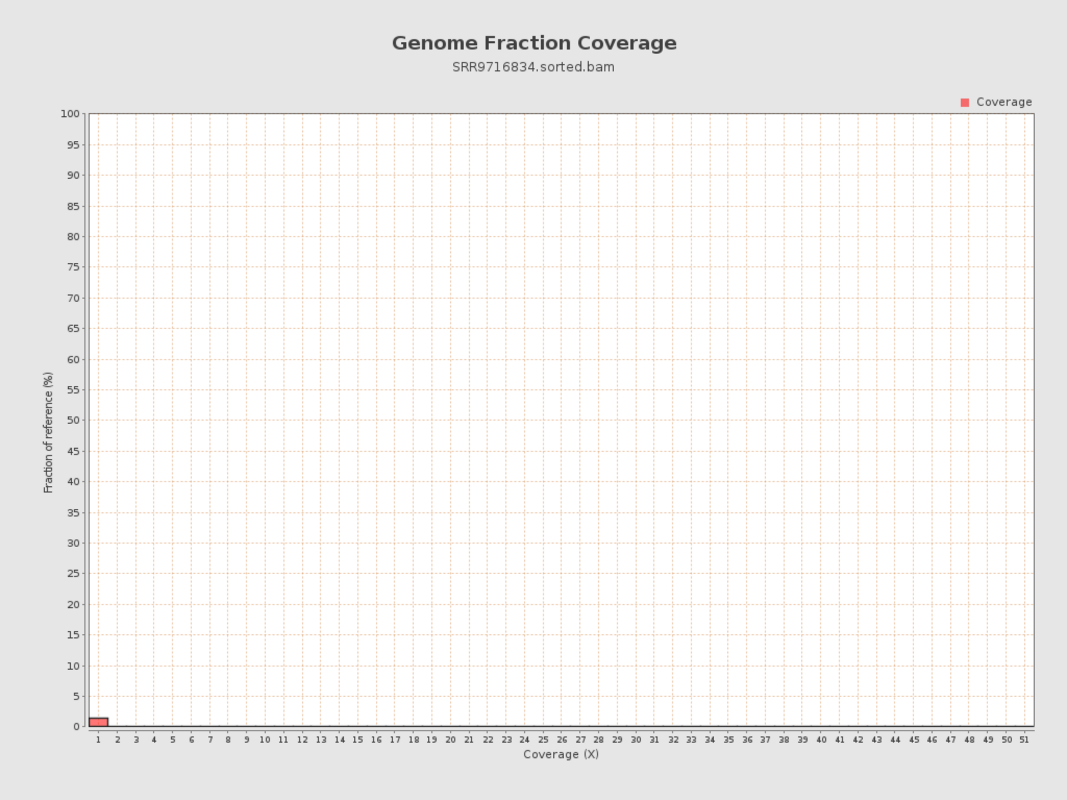
# 4. Results : Coverage Histogram



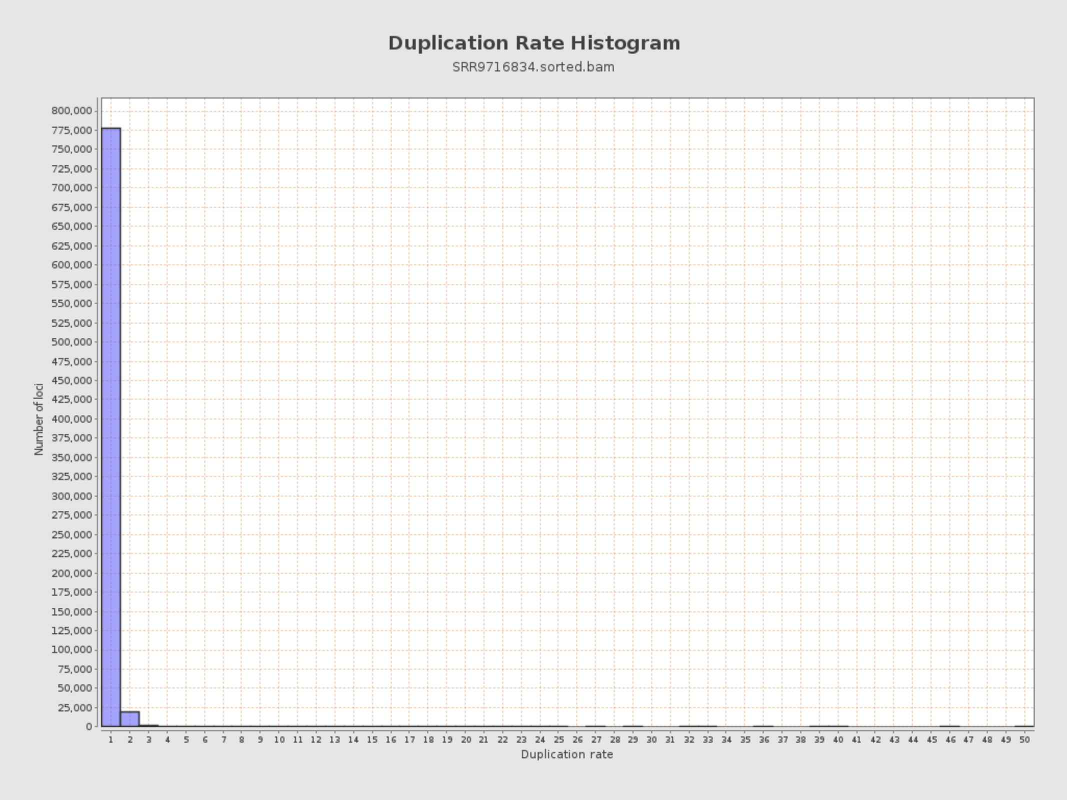
# 5. Results : Coverage Histogram (0-50X)



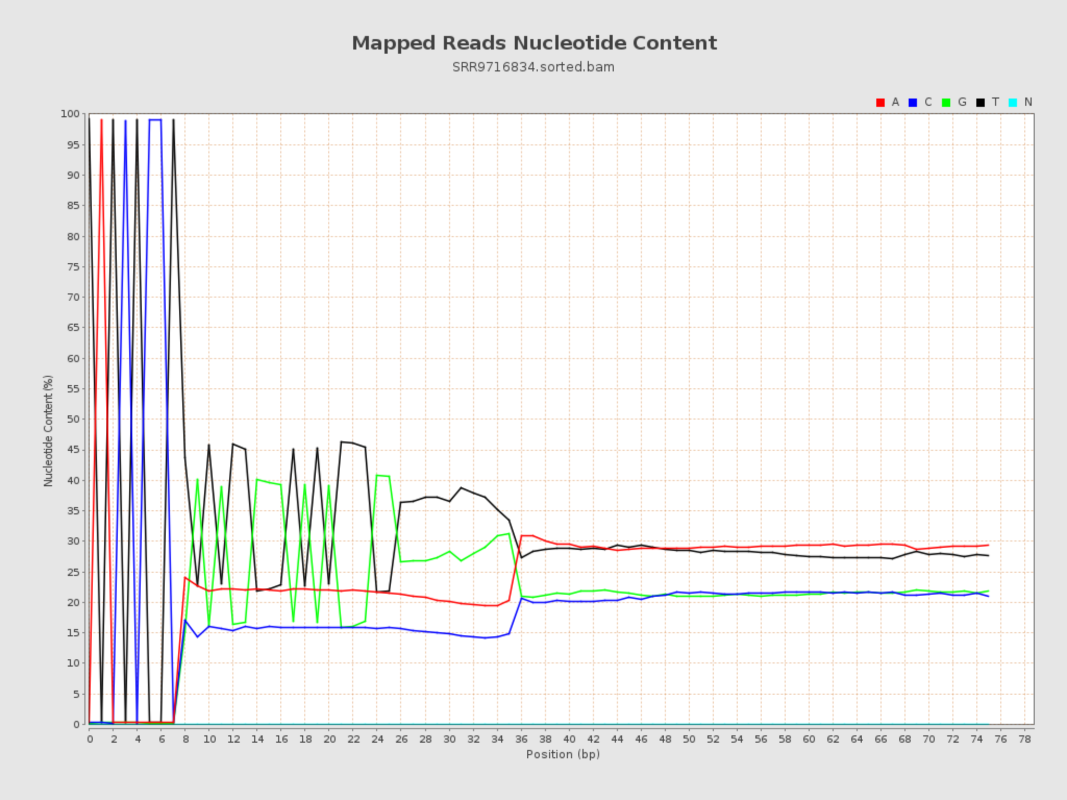
# 6. Results : Genome Fraction Coverage



# 7. Results : Duplication Rate Histogram



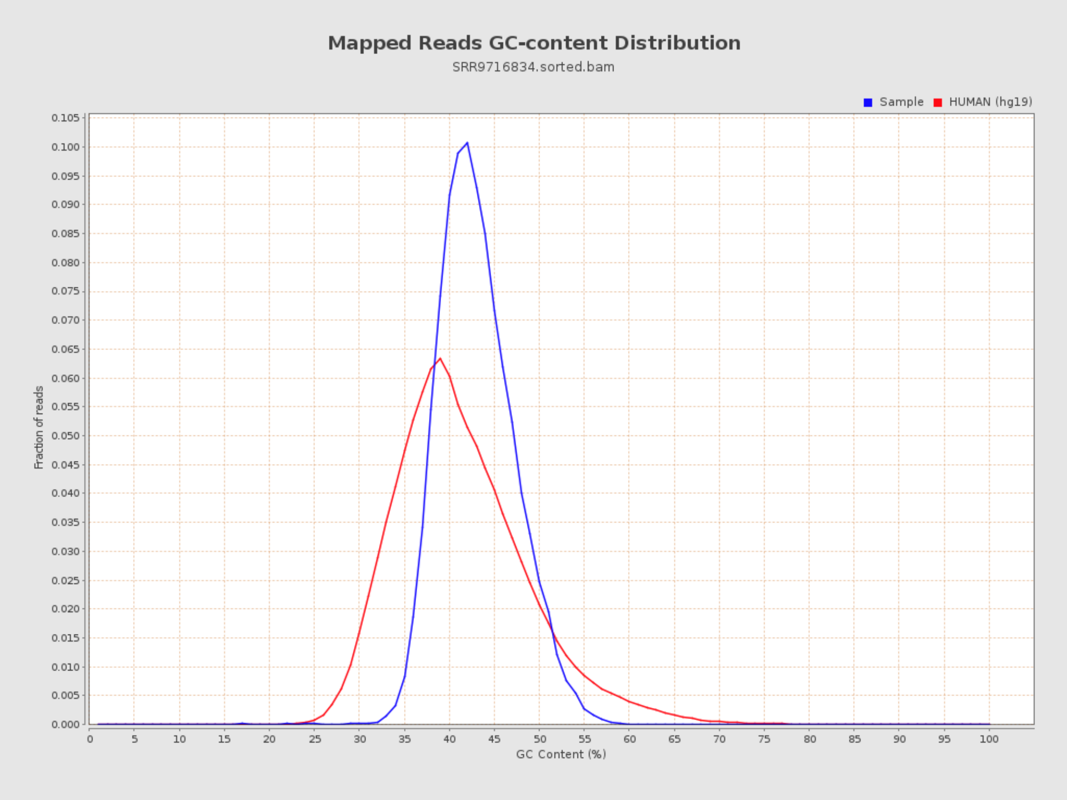
# 8. Results : Mapped Reads Nucleotide Content



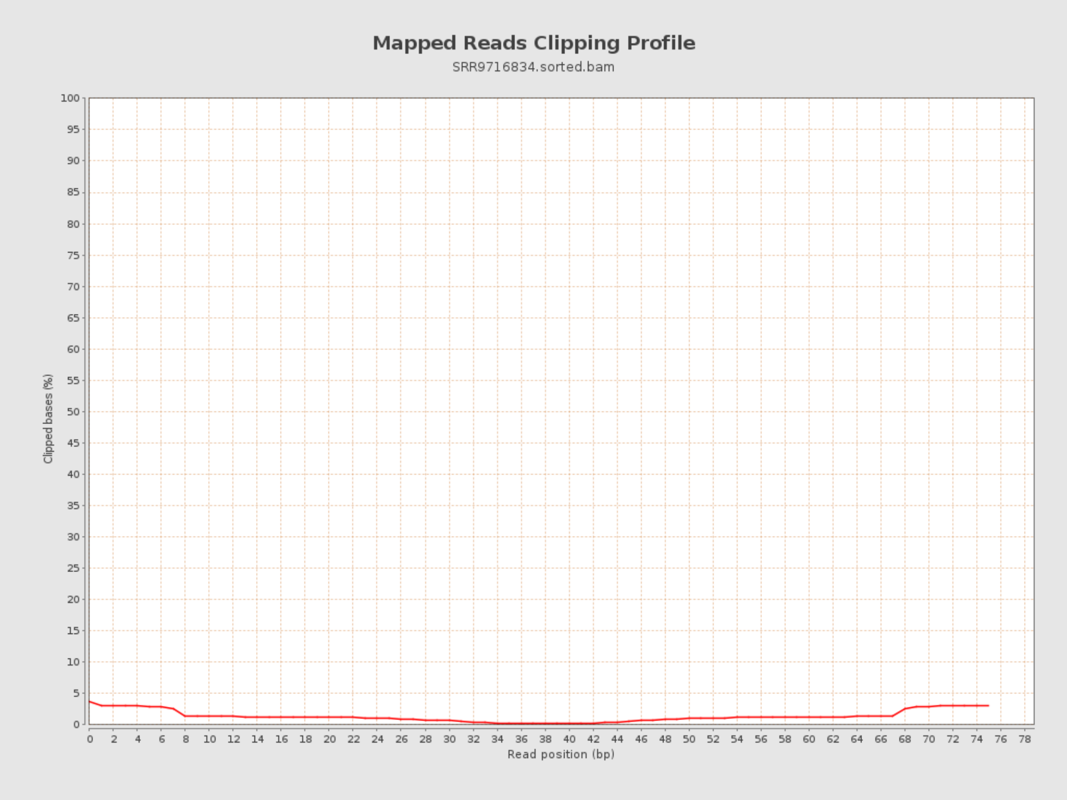
Mapped Reads Nucleotide Content

SRR9716834.sorted.bam

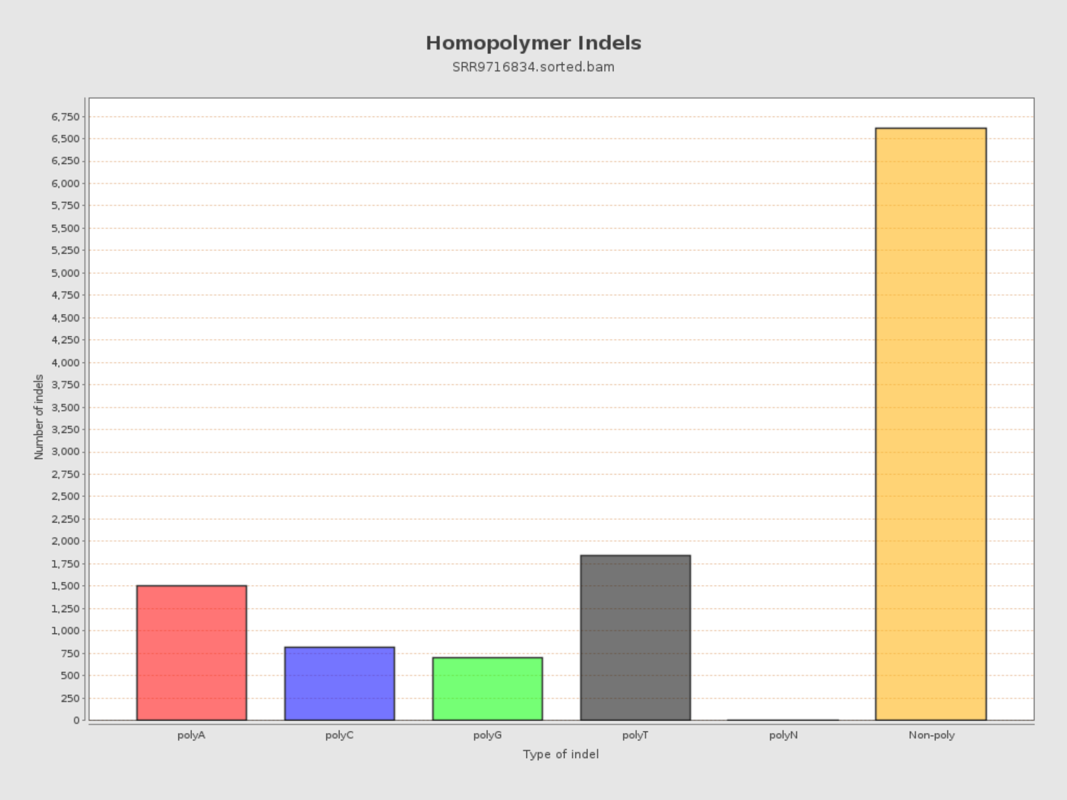
# 9. Results : Mapped Reads GC-content Distribution



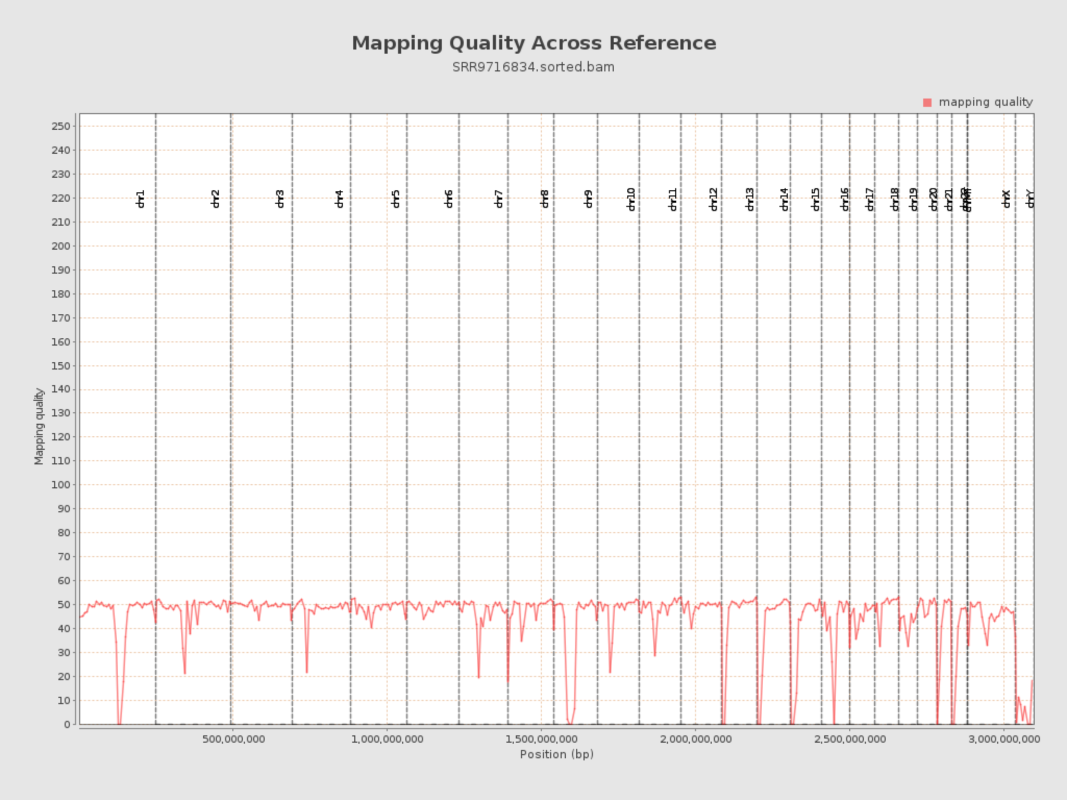
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram