# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 14:18:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716839.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_SRR9716839 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716839.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 14:18:49 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716839.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,607,929 |
| Mapped reads | 2,359,210 / 90.46% |
| Unmapped reads | 248,719 / 9.54% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 14,217 / 0.55% |
| Read min/max/mean length | 30 / 76 / 76.18 |
| Duplicated reads (estimated) | 125,304 / 4.8% |
| Duplication rate | 4.15% |
| Clipped reads | 2,367,646 / 90.79% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 34,269,632 / 25.16% |
| Number/percentage of C's | 25,221,928 / 18.52% |
| Number/percentage of T's | 43,807,330 / 32.17% |
| Number/percentage of G's | 32,884,368 / 24.15% |
| Number/percentage of N's | 988 / 0% |
| GC Percentage | 42.67% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.044 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3588 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.51 |

## 2.5. Mismatches and indels

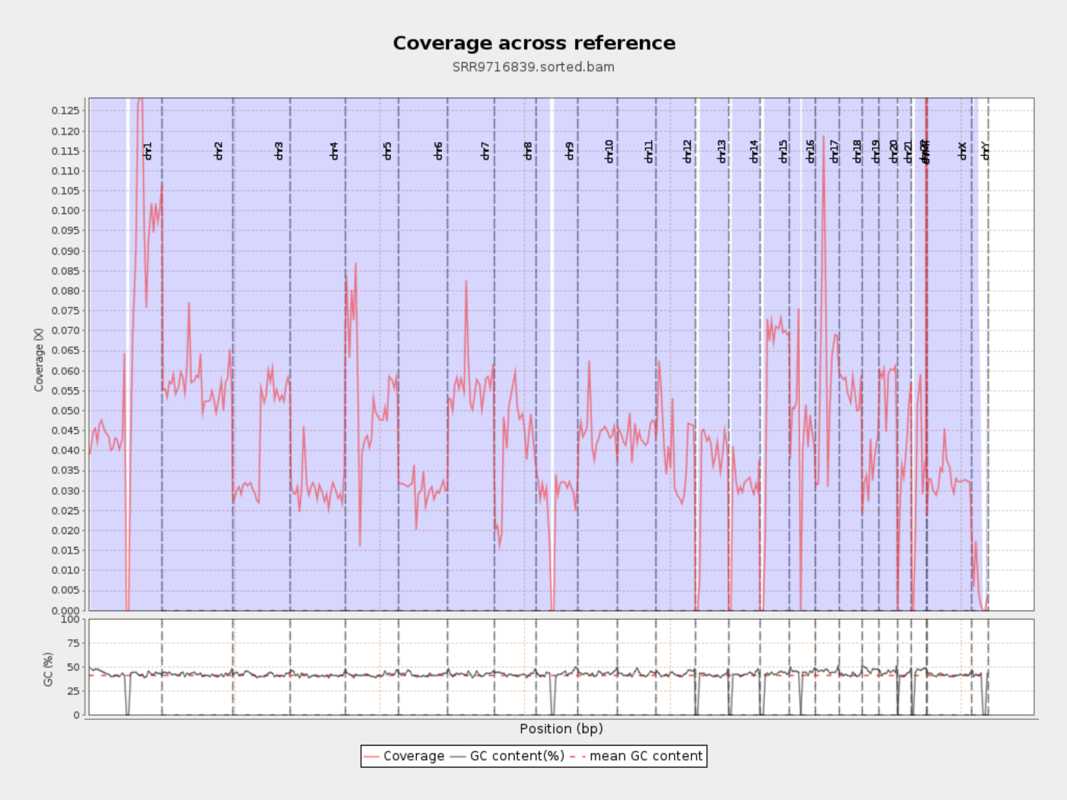
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 677,230 |
| Insertions | 9,565 |
| Mapped reads with at least one insertion | 0.4% |
| Deletions | 23,340 |
| Mapped reads with at least one deletion | 0.98% |
| Homopolymer indels | 42.21% |

## 2.6. Chromosome stats

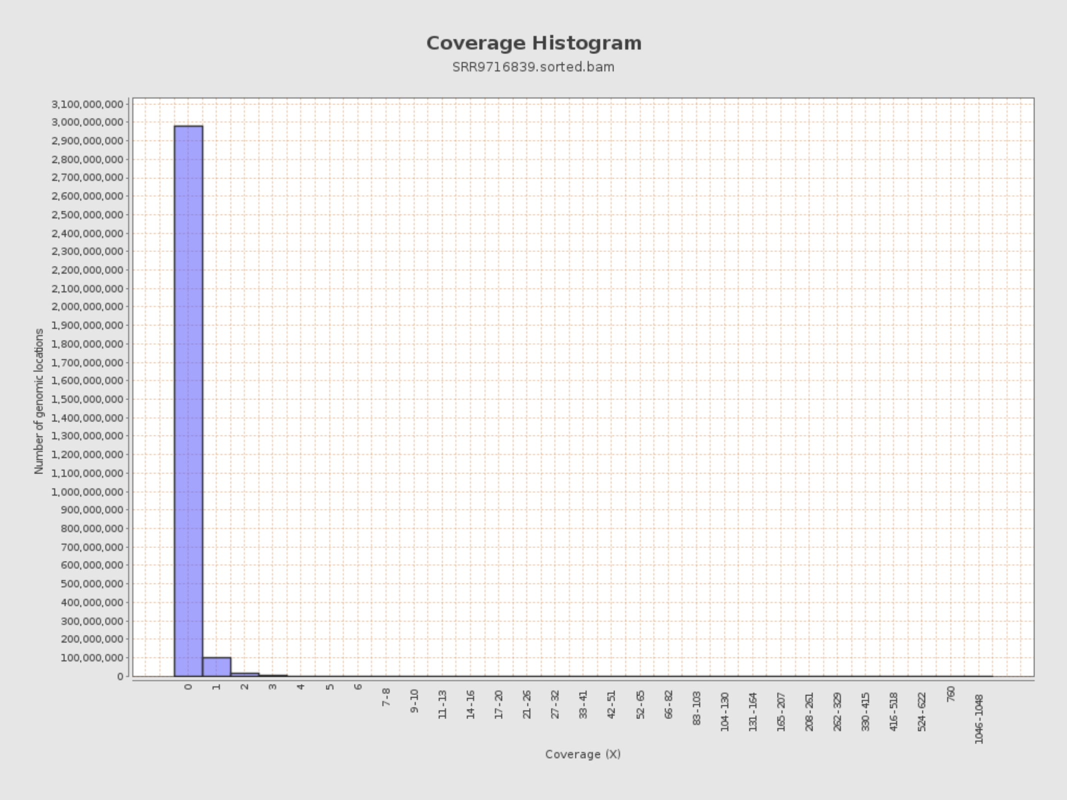
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 16123532 | 0.0647 | 0.5755 |
| chr2 | 243199373 | 13779273 | 0.0567 | 0.5339 |
| chr3 | 198022430 | 8541067 | 0.0431 | 0.2404 |
| chr4 | 191154276 | 5789718 | 0.0303 | 0.2315 |
| chr5 | 180915260 | 9802869 | 0.0542 | 0.2696 |
| chr6 | 171115067 | 5192830 | 0.0303 | 0.2303 |
| chr7 | 159138663 | 9056533 | 0.0569 | 0.5683 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6118180 | 0.0418 | 0.317 |
| chr9 | 141213431 | 3745715 | 0.0265 | 0.2696 |
| chr10 | 135534747 | 6065121 | 0.0447 | 0.3117 |
| chr11 | 135006516 | 5917818 | 0.0438 | 0.3484 |
| chr12 | 133851895 | 5380122 | 0.0402 | 0.2341 |
| chr13 | 115169878 | 3962308 | 0.0344 | 0.2135 |
| chr14 | 107349540 | 3001383 | 0.028 | 0.2048 |
| chr15 | 102531392 | 5791723 | 0.0565 | 0.2775 |
| chr16 | 90354753 | 4038335 | 0.0447 | 0.2618 |
| chr17 | 81195210 | 5083287 | 0.0626 | 0.3199 |
| chr18 | 78077248 | 4326217 | 0.0554 | 0.59 |
| chr19 | 59128983 | 2116012 | 0.0358 | 0.4066 |
| chr20 | 63025520 | 3618938 | 0.0574 | 0.2827 |
| chr21 | 48129895 | 1744652 | 0.0362 | 0.2336 |
| chr22 | 51304566 | 1578160 | 0.0308 | 0.201 |
| chrMT | 16571 | 25927 | 1.5646 | 1.5472 |
| chrX | 155270560 | 5107632 | 0.0329 | 0.241 |
| chrY | 59373566 | 313299 | 0.0053 | 0.1358 |

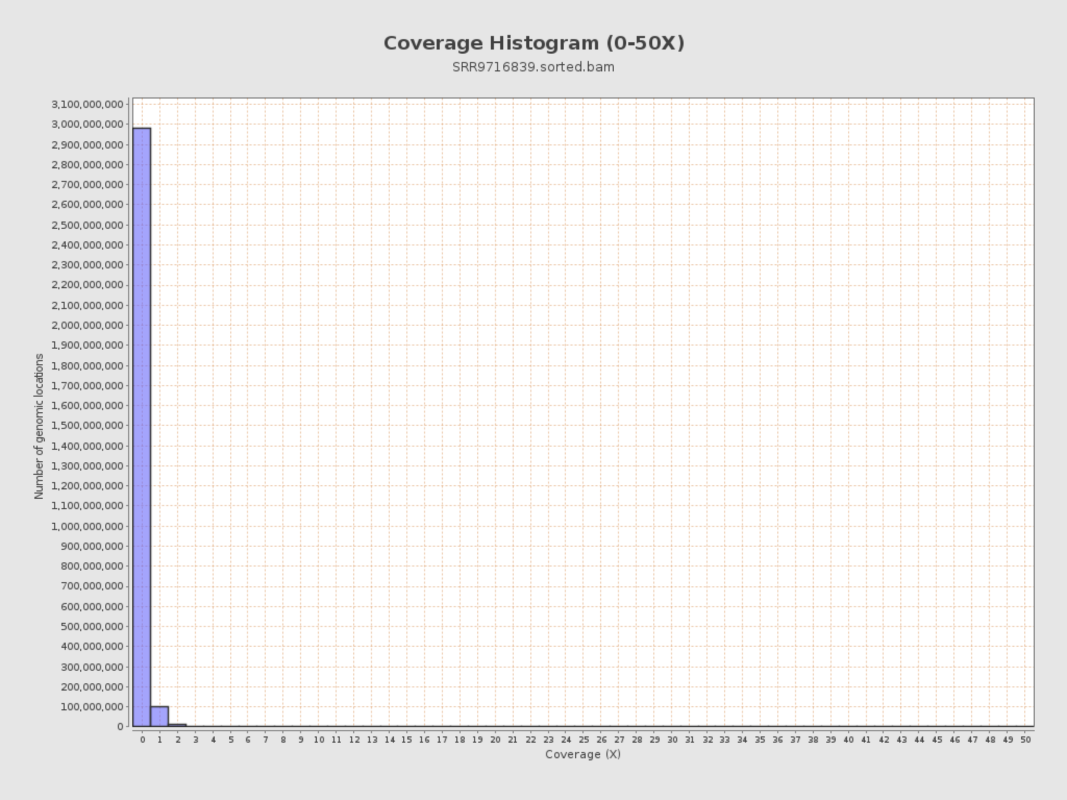
# 3. Results : Coverage across reference



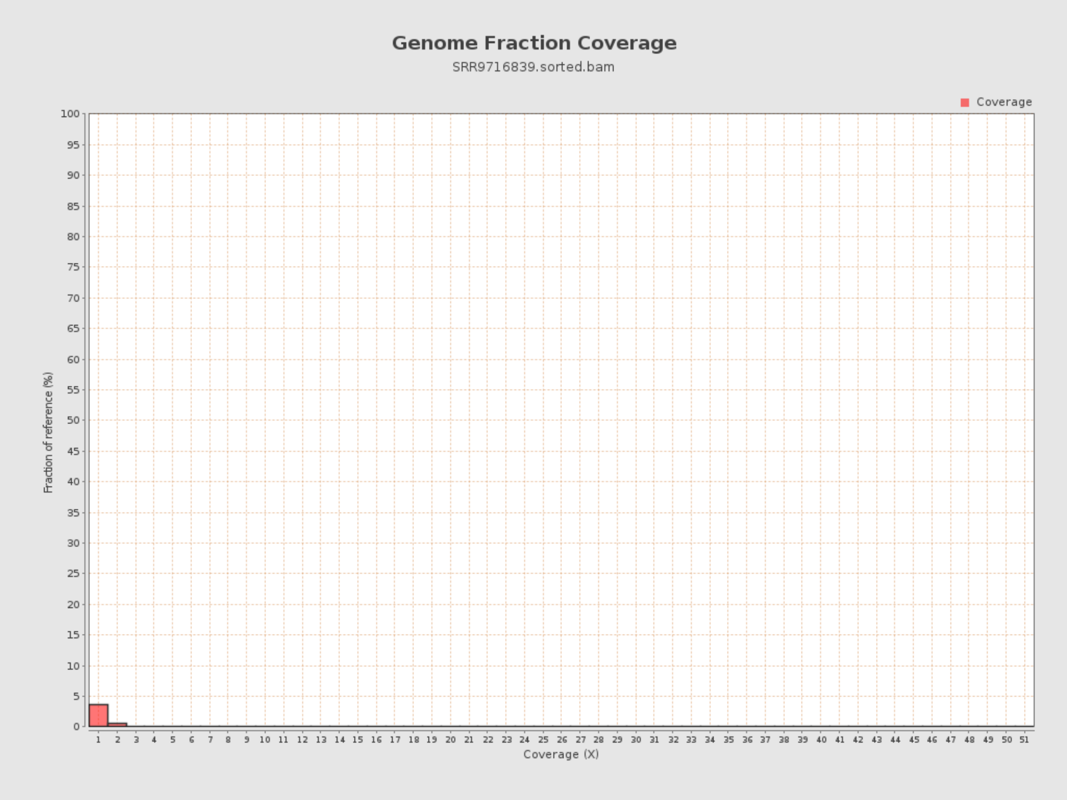
# 4. Results : Coverage Histogram



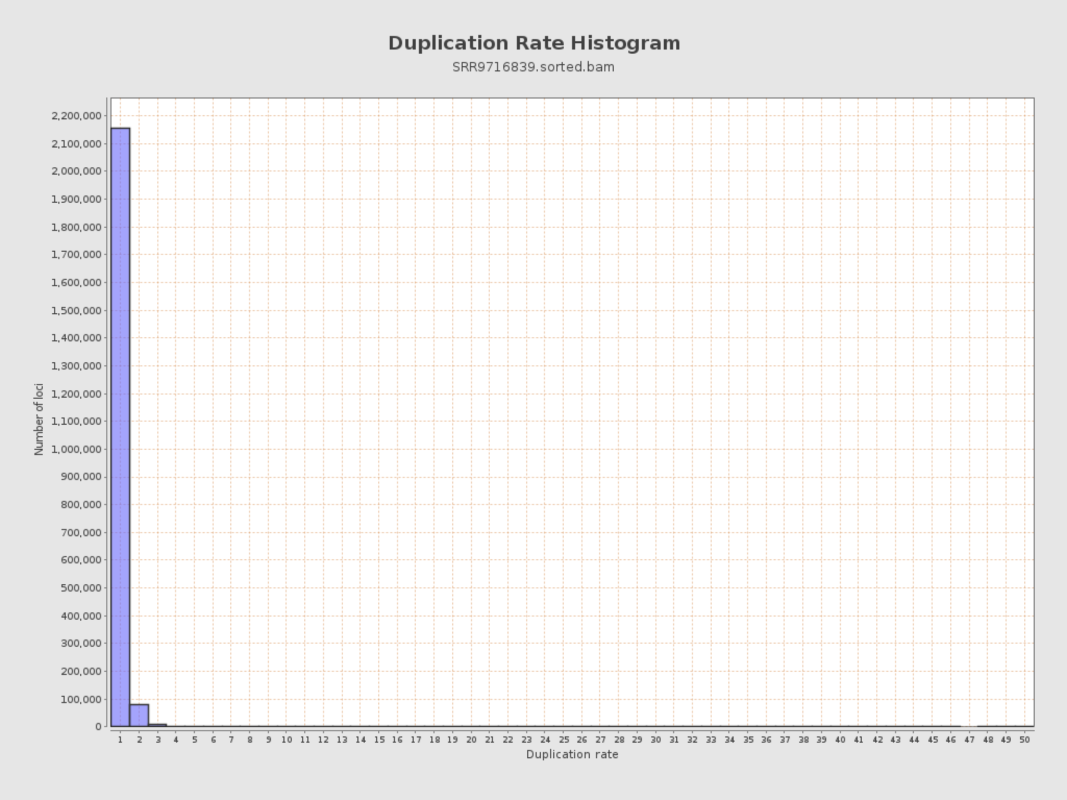
# 5. Results : Coverage Histogram (0-50X)



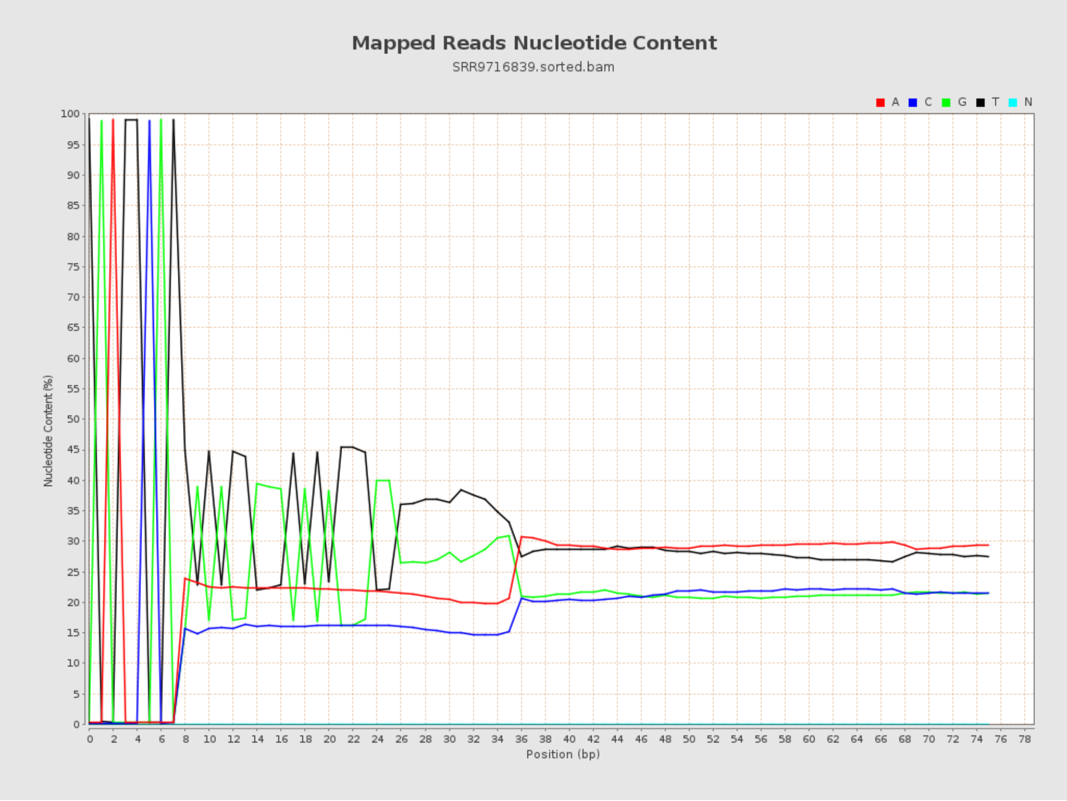
# 6. Results : Genome Fraction Coverage



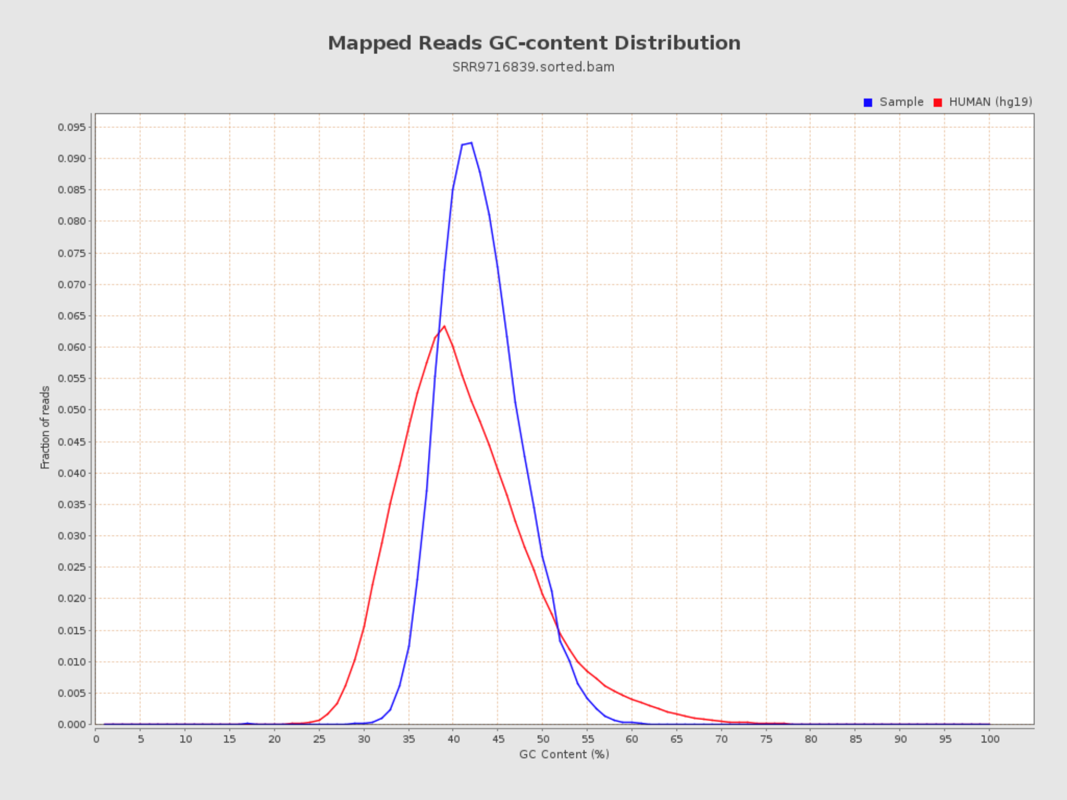
# 7. Results : Duplication Rate Histogram



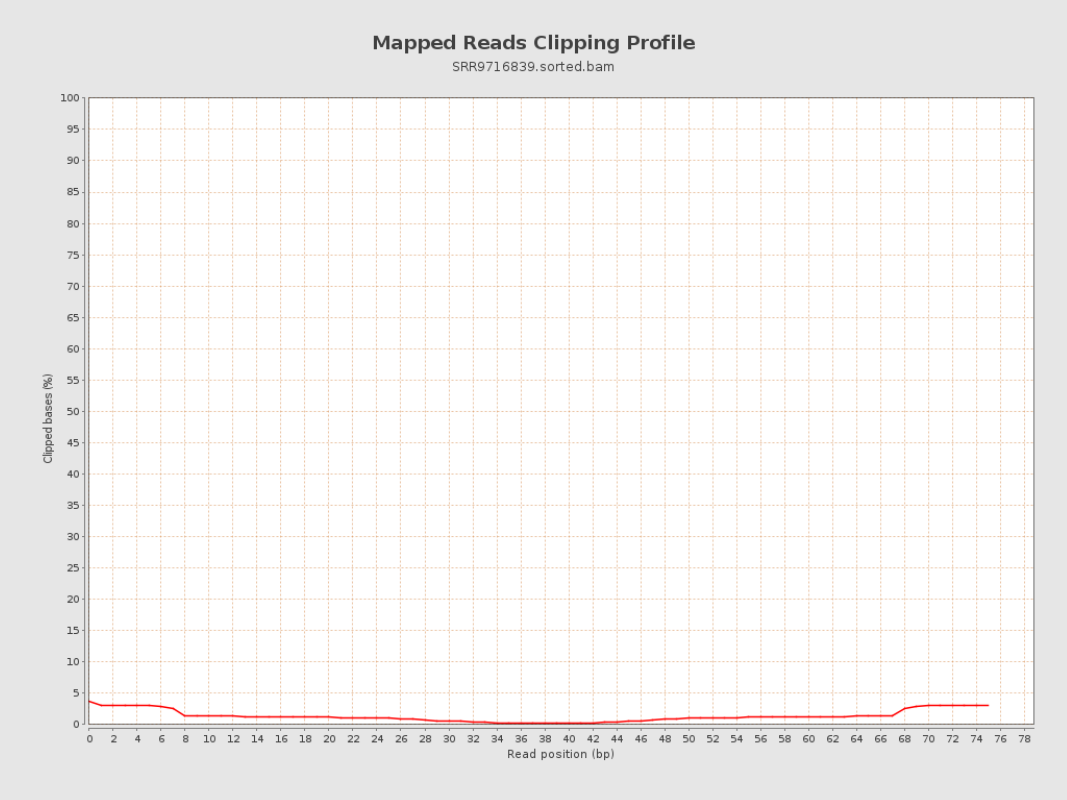
# 8. Results : Mapped Reads Nucleotide Content



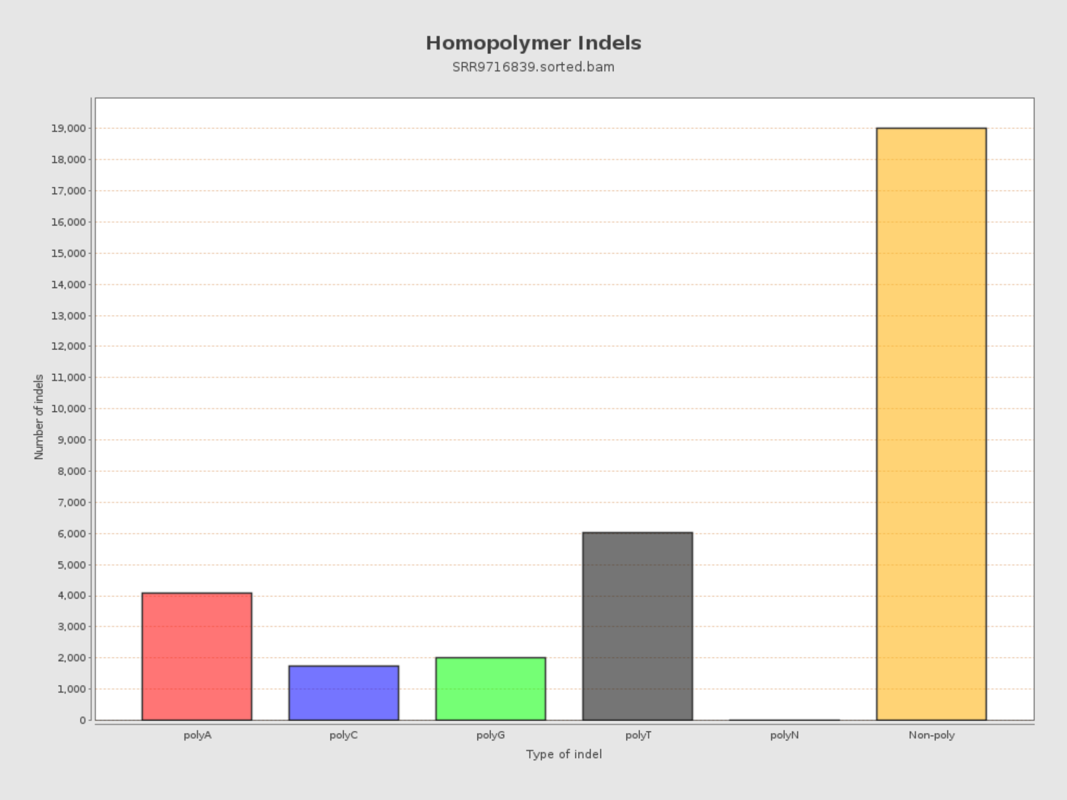
# 9. Results : Mapped Reads GC-content Distribution



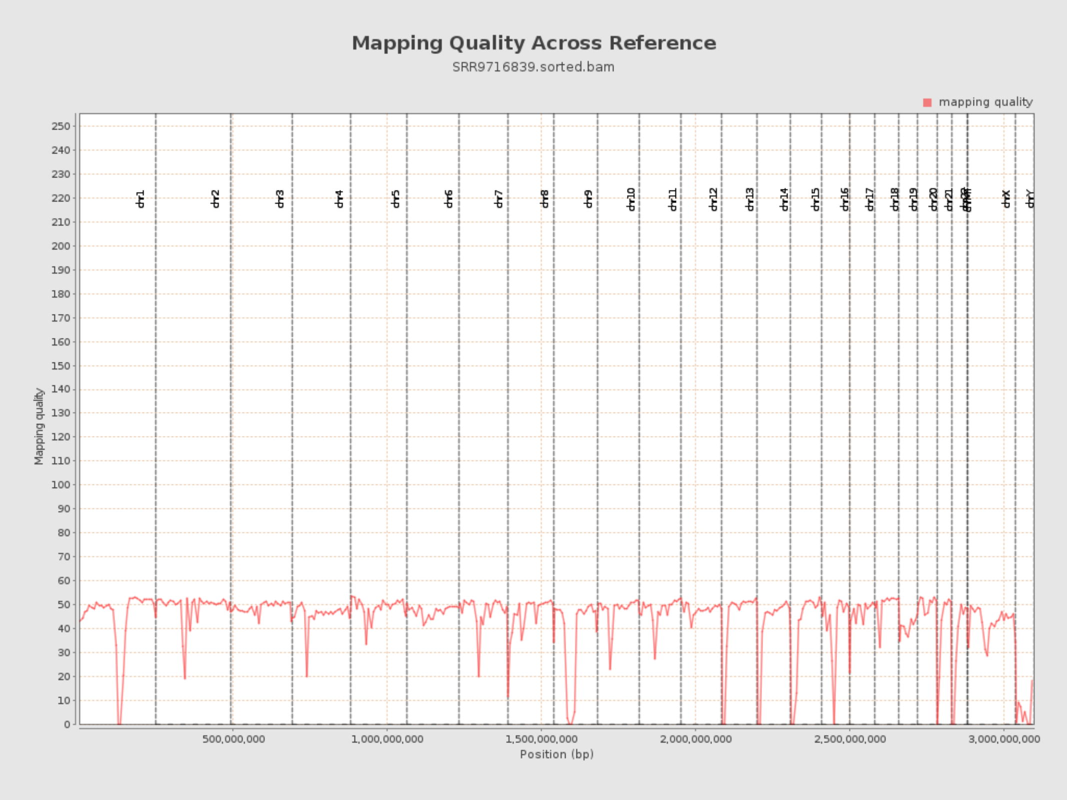
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram