# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 23:15:49*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716587.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_SRR9716587 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716587.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 23:15:48 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716587.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,020,164 |
| Mapped reads | 659,598 / 64.66% |
| Unmapped reads | 360,566 / 35.34% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,080 / 0.3% |
| Read min/max/mean length | 30 / 76 / 76.1 |
| Duplicated reads (estimated) | 13,963 / 1.37% |
| Duplication rate | 1.59% |
| Clipped reads | 661,583 / 64.85% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 9,580,759 / 25.52% |
| Number/percentage of C's | 7,110,784 / 18.94% |
| Number/percentage of T's | 11,952,352 / 31.83% |
| Number/percentage of G's | 8,903,056 / 23.71% |
| Number/percentage of N's | 491 / 0% |
| GC Percentage | 42.65% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0121 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1403 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.76 |

## 2.5. Mismatches and indels

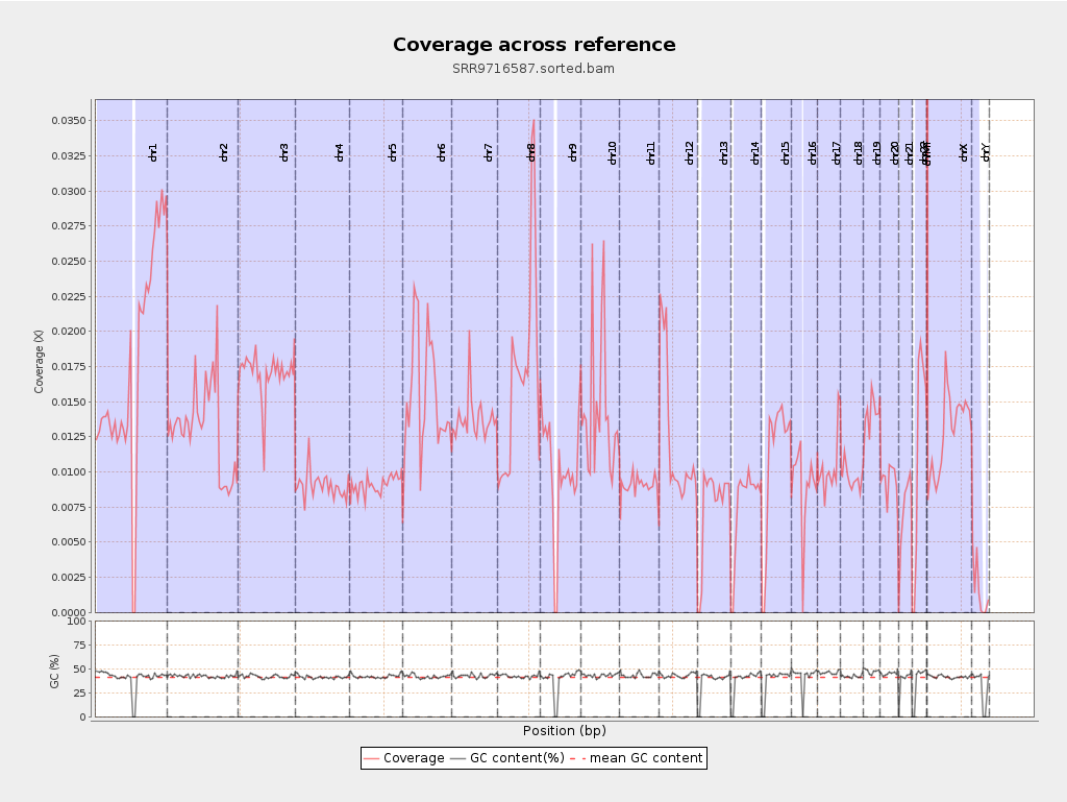
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 186,286 |
| Insertions | 2,329 |
| Mapped reads with at least one insertion | 0.35% |
| Deletions | 6,234 |
| Mapped reads with at least one deletion | 0.94% |
| Homopolymer indels | 41% |

## 2.6. Chromosome stats

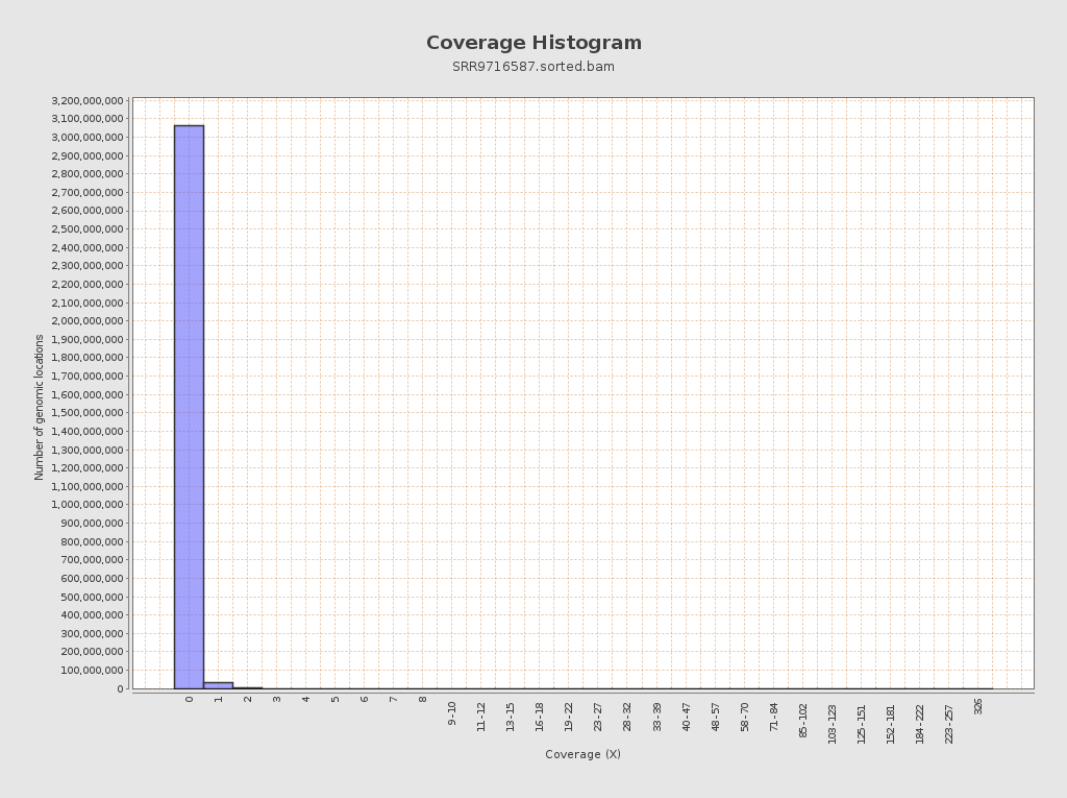
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 4389555 | 0.0176 | 0.2208 |
| chr2 | 243199373 | 3184745 | 0.0131 | 0.1778 |
| chr3 | 198022430 | 3359646 | 0.017 | 0.1365 |
| chr4 | 191154276 | 1726387 | 0.009 | 0.1013 |
| chr5 | 180915260 | 1649327 | 0.0091 | 0.1004 |
| chr6 | 171115067 | 2635672 | 0.0154 | 0.1487 |
| chr7 | 159138663 | 2202302 | 0.0138 | 0.1677 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2444552 | 0.0167 | 0.1421 |
| chr9 | 141213431 | 1396059 | 0.0099 | 0.12 |
| chr10 | 135534747 | 1948442 | 0.0144 | 0.1506 |
| chr11 | 135006516 | 1228159 | 0.0091 | 0.1129 |
| chr12 | 133851895 | 1654674 | 0.0124 | 0.1168 |
| chr13 | 115169878 | 858086 | 0.0075 | 0.0906 |
| chr14 | 107349540 | 817261 | 0.0076 | 0.0971 |
| chr15 | 102531392 | 1119030 | 0.0109 | 0.1103 |
| chr16 | 90354753 | 803793 | 0.0089 | 0.1025 |
| chr17 | 81195210 | 840558 | 0.0104 | 0.1083 |
| chr18 | 78077248 | 744002 | 0.0095 | 0.1692 |
| chr19 | 59128983 | 838395 | 0.0142 | 0.1681 |
| chr20 | 63025520 | 590893 | 0.0094 | 0.1012 |
| chr21 | 48129895 | 345830 | 0.0072 | 0.0918 |
| chr22 | 51304566 | 616002 | 0.012 | 0.1145 |
| chrMT | 16571 | 60838 | 3.6714 | 2.7514 |
| chrX | 155270560 | 2011567 | 0.013 | 0.1279 |
| chrY | 59373566 | 91460 | 0.0015 | 0.0469 |

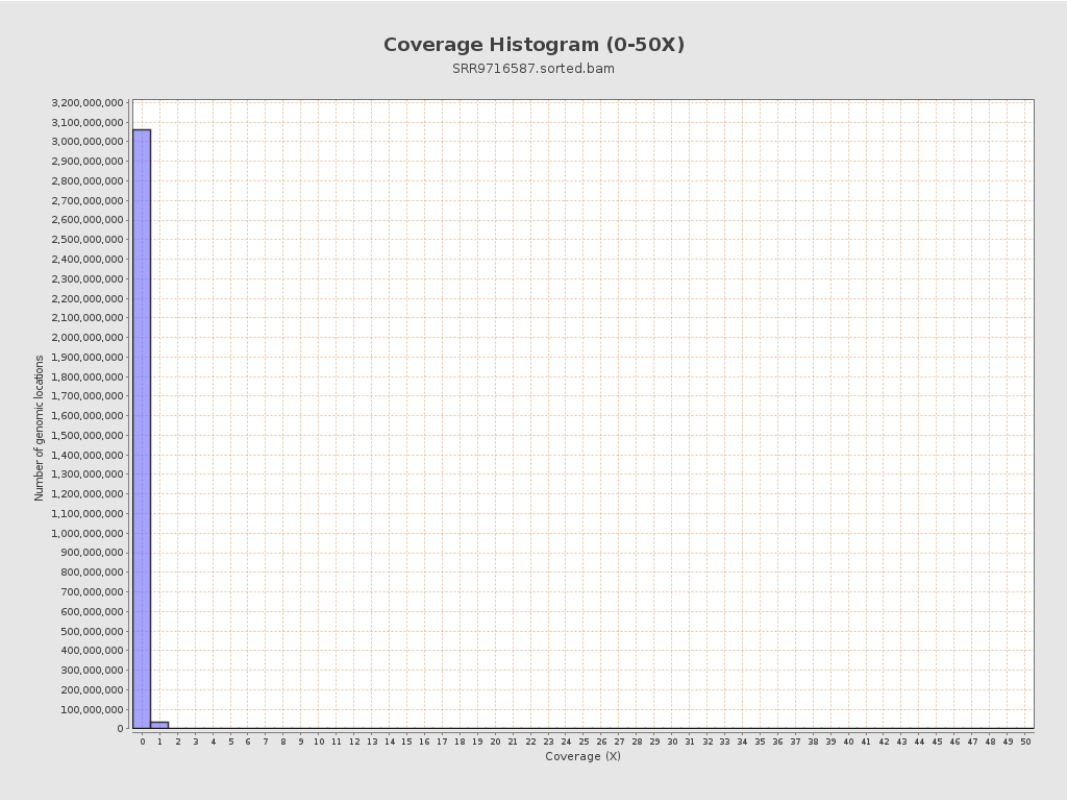
# 3. Results : Coverage across reference



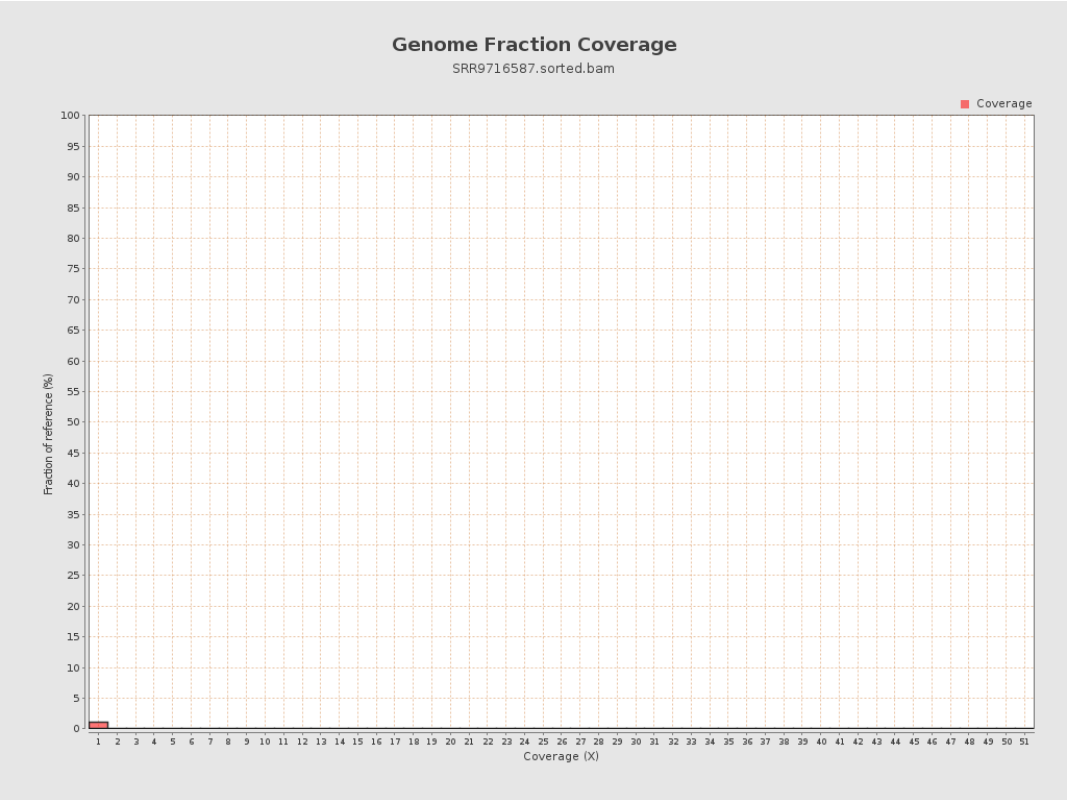
# 4. Results : Coverage Histogram



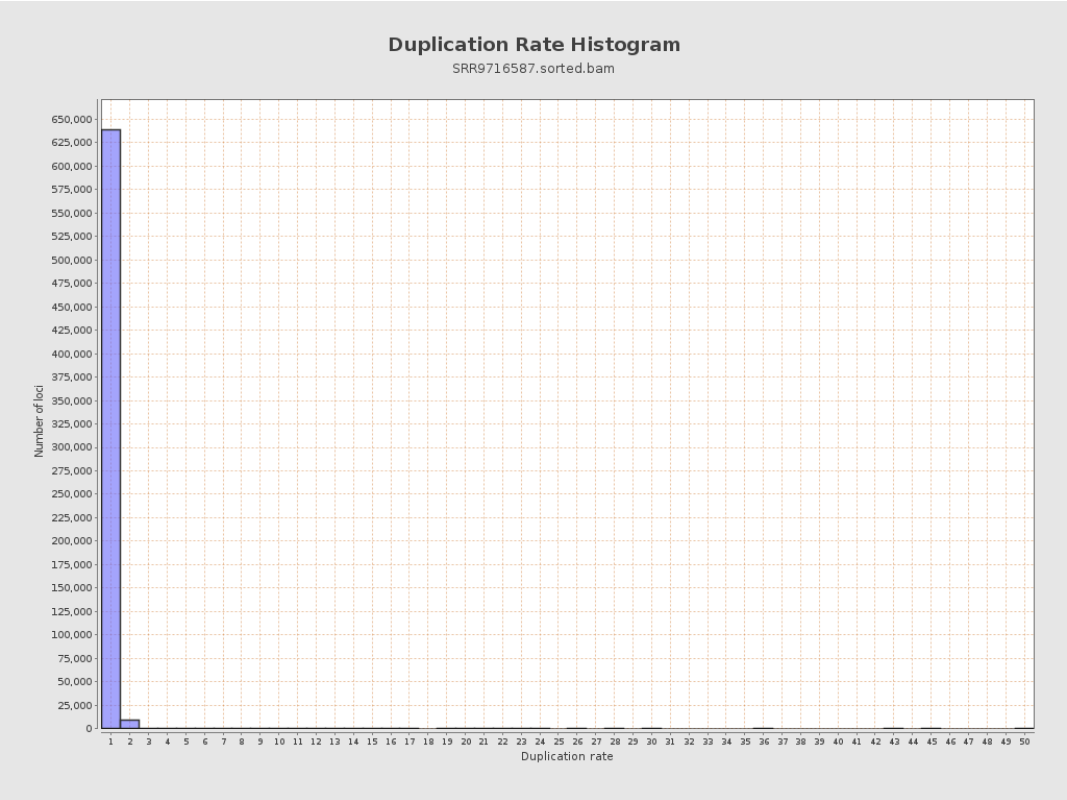
# 5. Results : Coverage Histogram (0-50X)



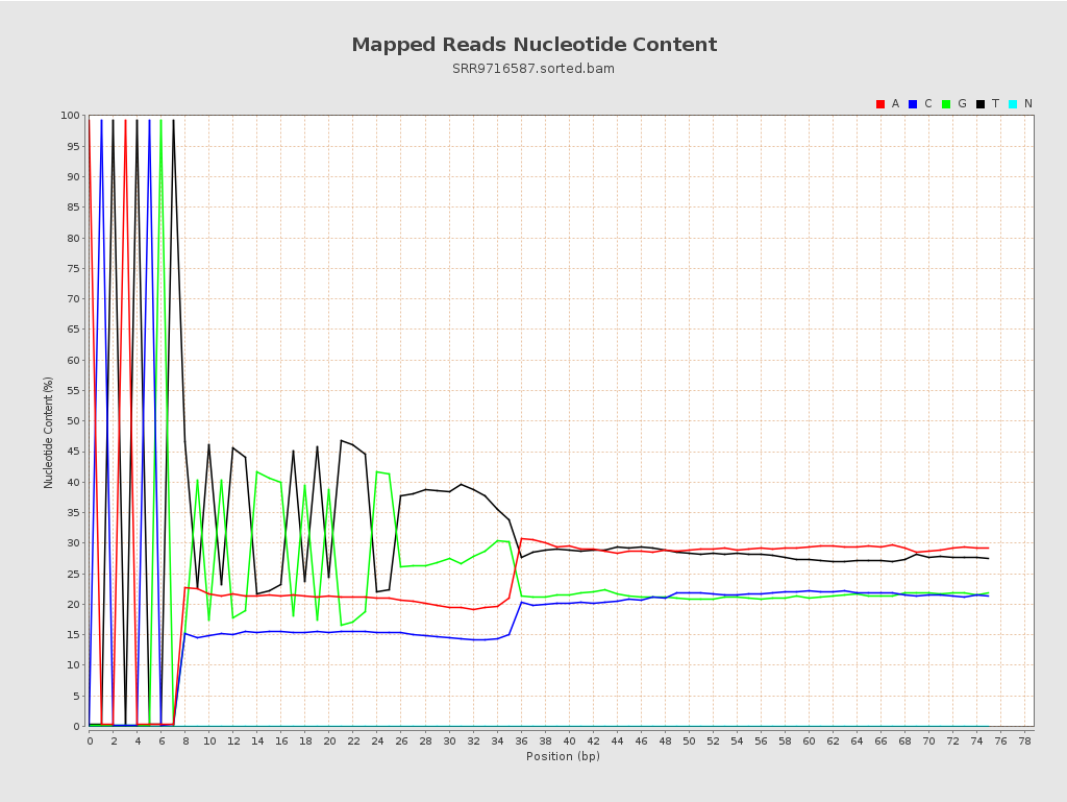
# 6. Results : Genome Fraction Coverage



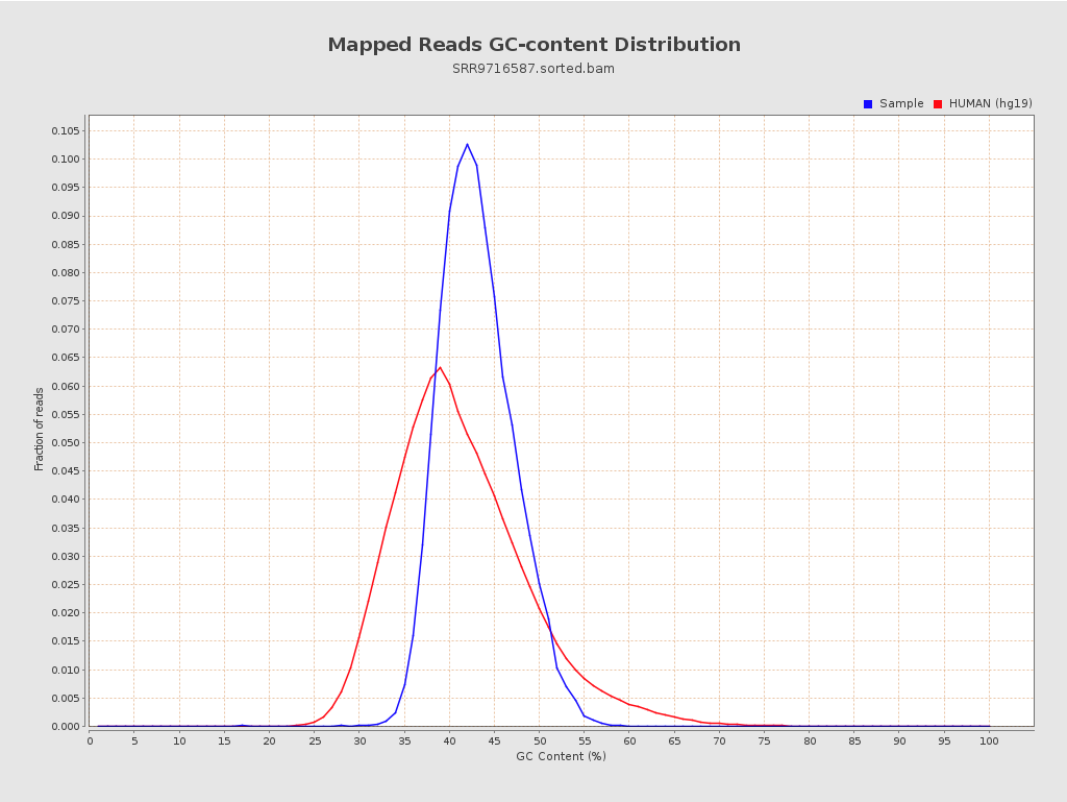
# 7. Results : Duplication Rate Histogram



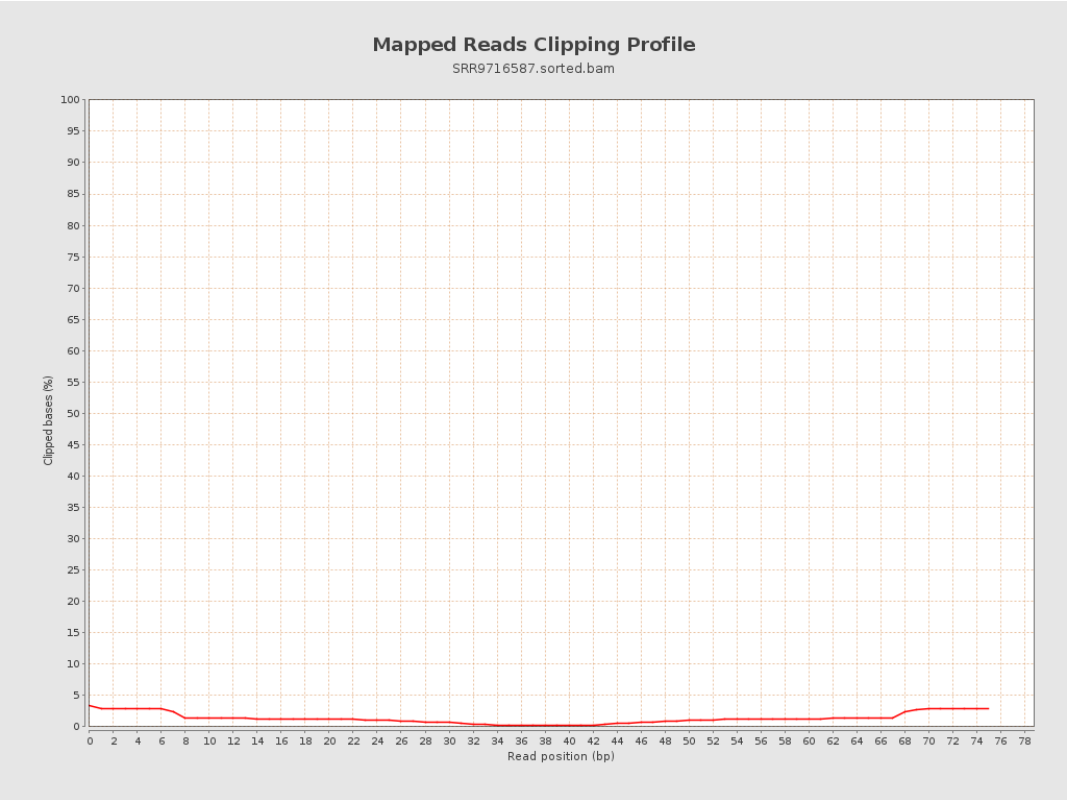
# 8. Results : Mapped Reads Nucleotide Content



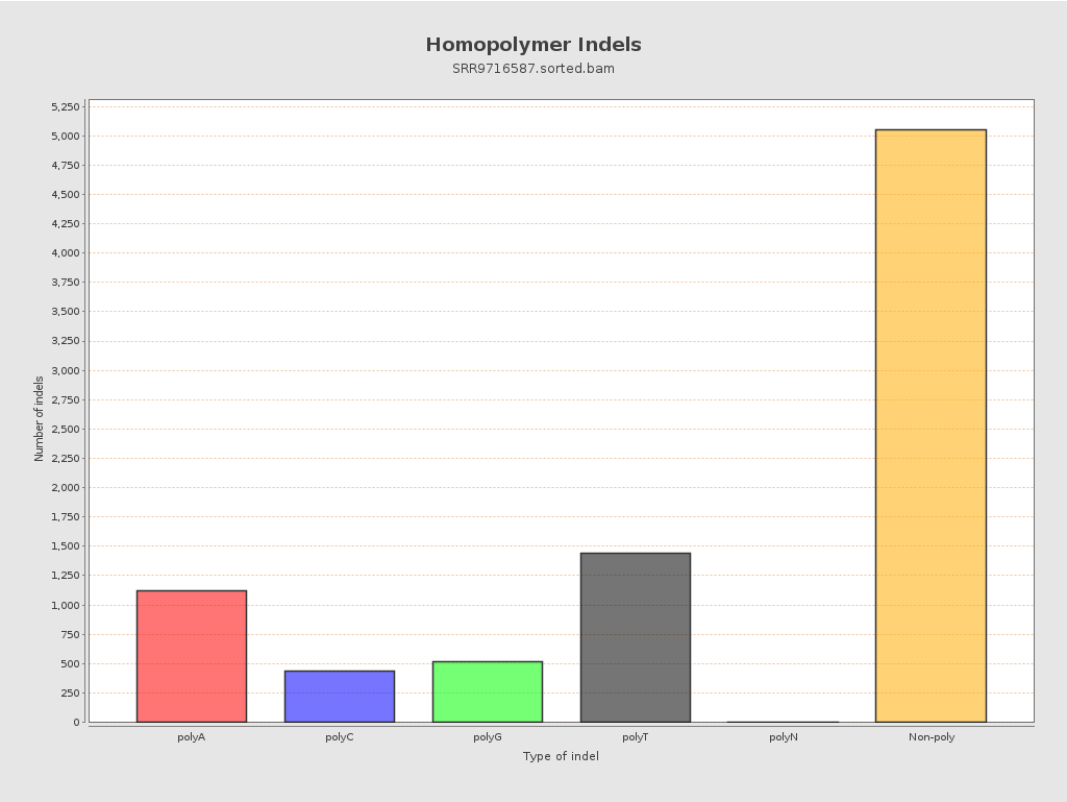
# 9. Results : Mapped Reads GC-content Distribution



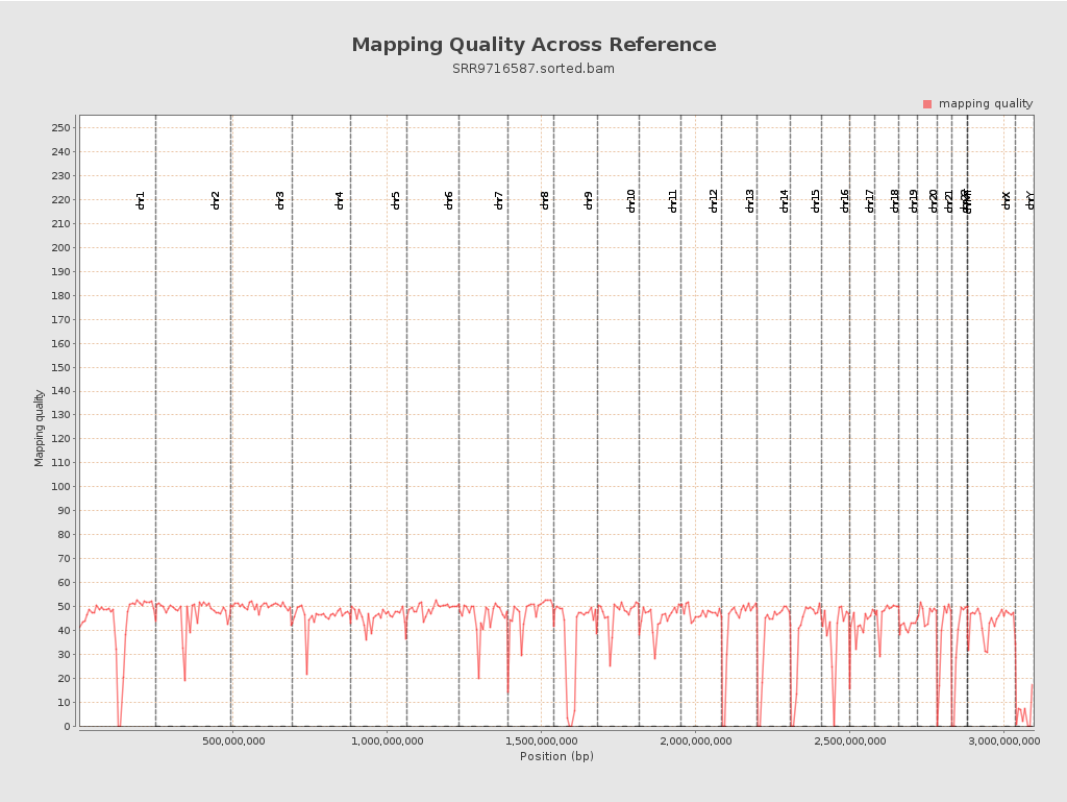
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram