# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 08:12:30*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716711.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_SRR9716711 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716711.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 08:12:29 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716711.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,254,528 |
| Mapped reads | 1,168,406 / 93.14% |
| Unmapped reads | 86,122 / 6.86% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 26,167 / 2.09% |
| Read min/max/mean length | 30 / 101 / 101.76 |
| Duplicated reads (estimated) | 41,460 / 3.3% |
| Duplication rate | 2.7% |
| Clipped reads | 1,191,579 / 94.98% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 23,842,686 / 26.32% |
| Number/percentage of C's | 18,018,566 / 19.89% |
| Number/percentage of T's | 26,721,522 / 29.49% |
| Number/percentage of G's | 22,010,572 / 24.3% |
| Number/percentage of N's | 3,491 / 0% |
| GC Percentage | 44.18% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0293 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2509 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.03 |

## 2.5. Mismatches and indels

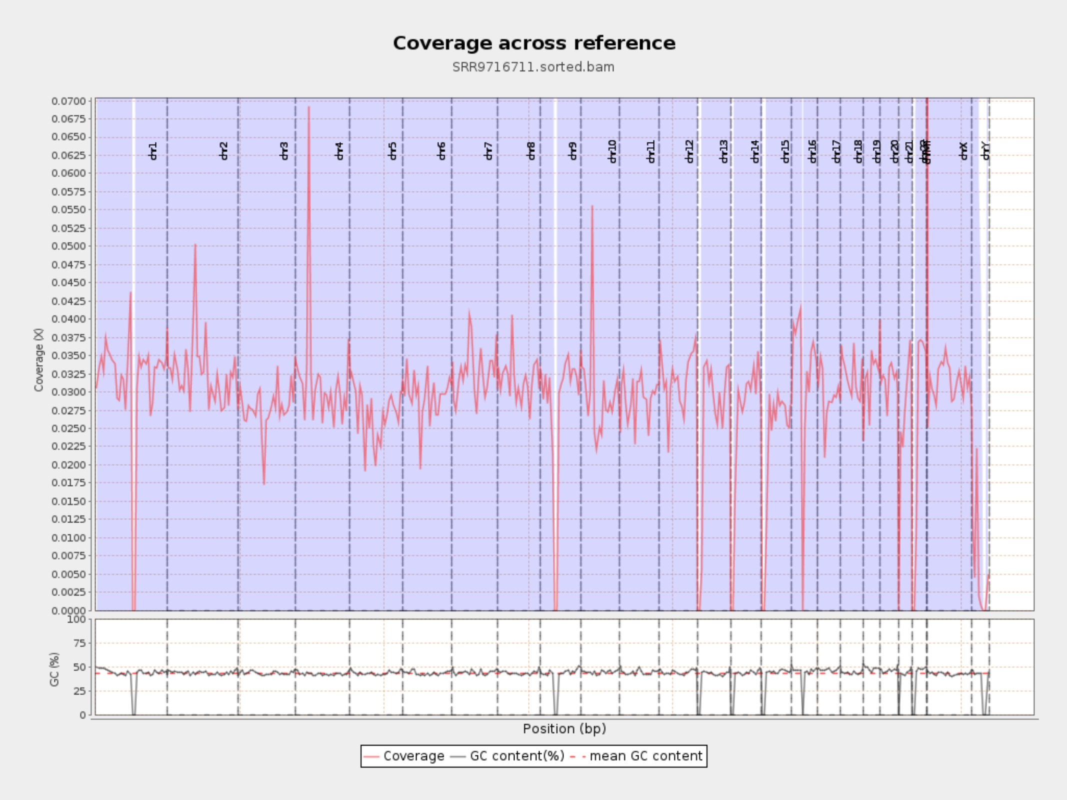
| | |
|---|---|
| General error rate | 0.69% |
| Mismatches | 603,221 |
| Insertions | 8,955 |
| Mapped reads with at least one insertion | 0.75% |
| Deletions | 18,285 |
| Mapped reads with at least one deletion | 1.54% |
| Homopolymer indels | 37.92% |

## 2.6. Chromosome stats

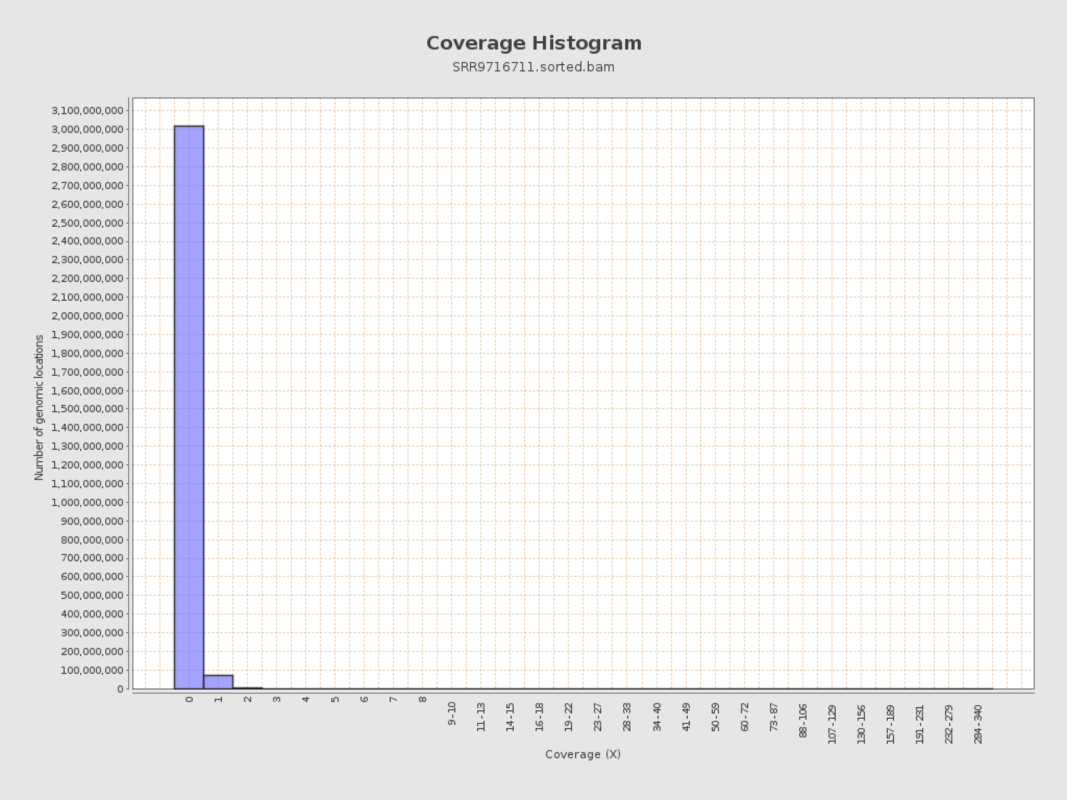
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 7770679 | 0.0312 | 0.362 |
| chr2 | 243199373 | 7940758 | 0.0327 | 0.2887 |
| chr3 | 198022430 | 5488508 | 0.0277 | 0.184 |
| chr4 | 191154276 | 6054540 | 0.0317 | 0.2702 |
| chr5 | 180915260 | 4877325 | 0.027 | 0.1812 |
| chr6 | 171115067 | 5035219 | 0.0294 | 0.1973 |
| chr7 | 159138663 | 5219141 | 0.0328 | 0.2986 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4636024 | 0.0317 | 0.2557 |
| chr9 | 141213431 | 3912327 | 0.0277 | 0.2372 |
| chr10 | 135534747 | 4045784 | 0.0299 | 0.3296 |
| chr11 | 135006516 | 3954128 | 0.0293 | 0.2383 |
| chr12 | 133851895 | 4252259 | 0.0318 | 0.1982 |
| chr13 | 115169878 | 2940818 | 0.0255 | 0.1774 |
| chr14 | 107349540 | 2770405 | 0.0258 | 0.1871 |
| chr15 | 102531392 | 2284204 | 0.0223 | 0.1653 |
| chr16 | 90354753 | 2884729 | 0.0319 | 0.2159 |
| chr17 | 81195210 | 2387637 | 0.0294 | 0.208 |
| chr18 | 78077248 | 2508126 | 0.0321 | 0.3598 |
| chr19 | 59128983 | 1907160 | 0.0323 | 0.2804 |
| chr20 | 63025520 | 1996805 | 0.0317 | 0.2083 |
| chr21 | 48129895 | 1272358 | 0.0264 | 0.2285 |
| chr22 | 51304566 | 1279864 | 0.0249 | 0.1803 |
| chrMT | 16571 | 5816 | 0.351 | 0.6535 |
| chrX | 155270560 | 4882082 | 0.0314 | 0.2105 |
| chrY | 59373566 | 328265 | 0.0055 | 0.2149 |

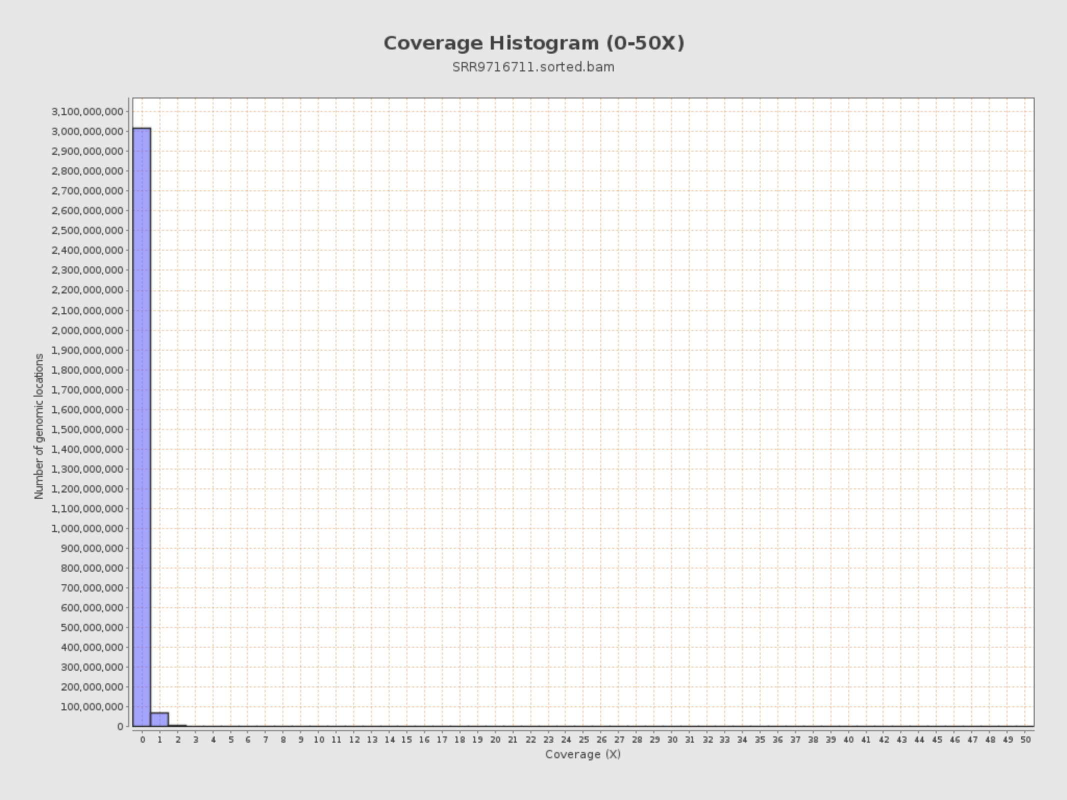
# 3. Results : Coverage across reference



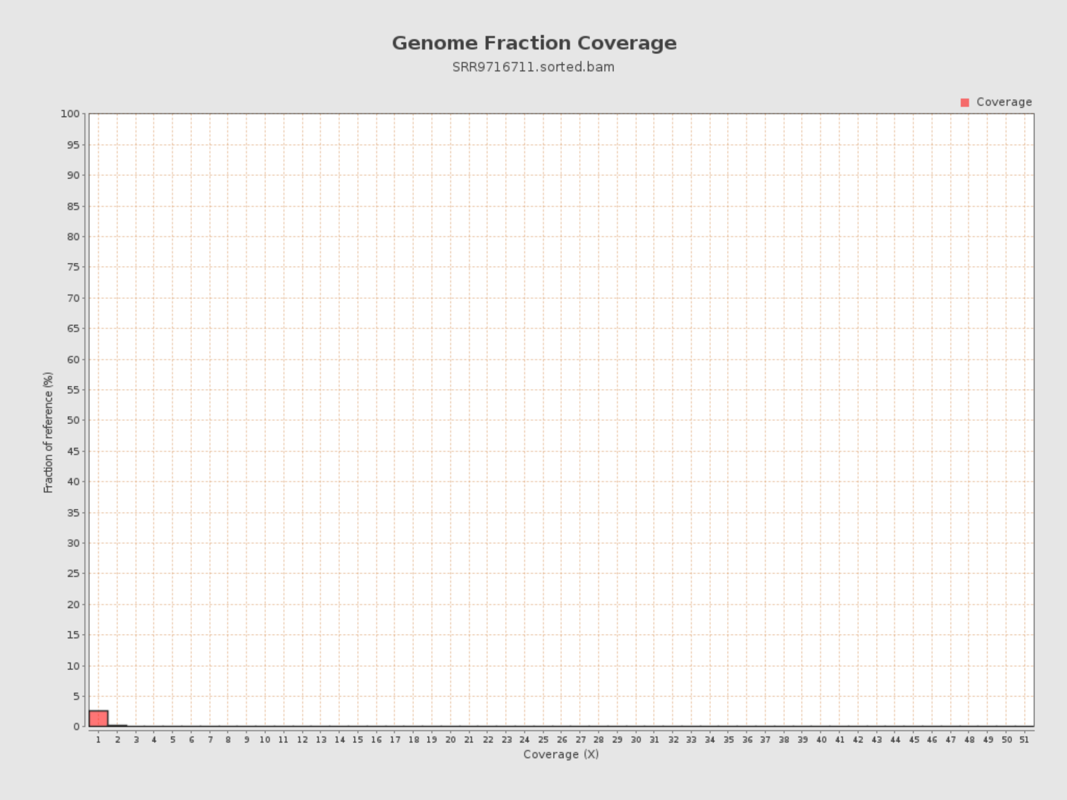
# 4. Results : Coverage Histogram



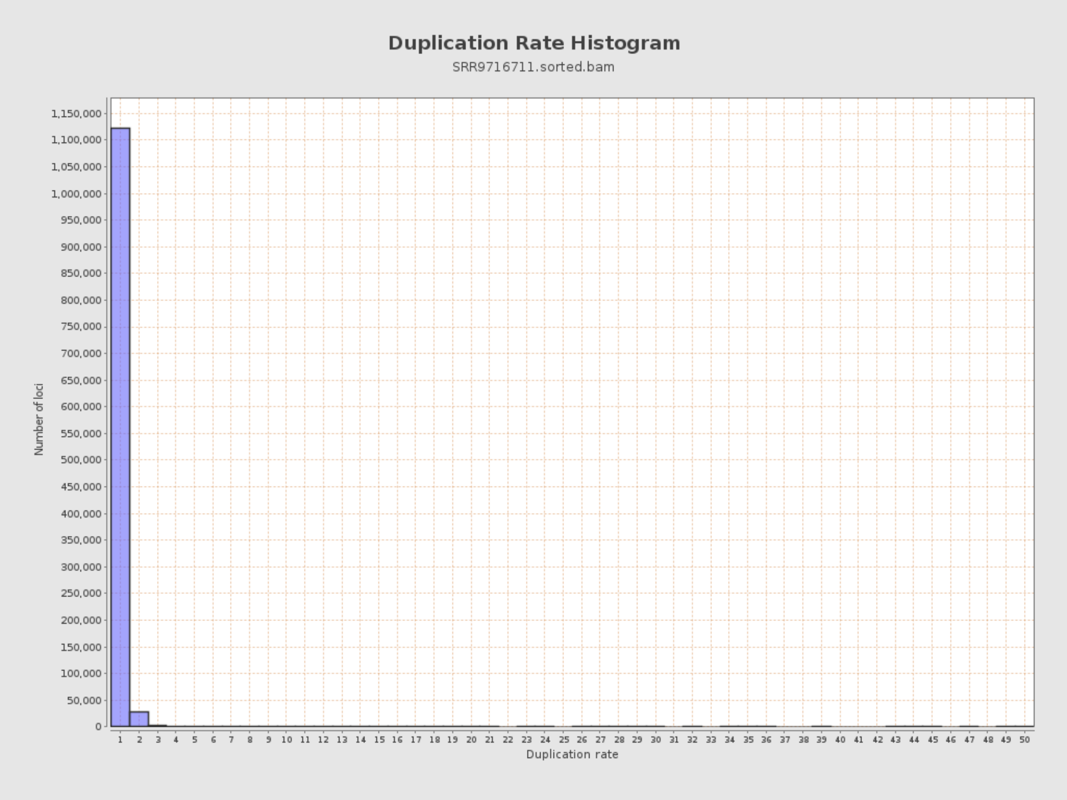
# 5. Results : Coverage Histogram (0-50X)



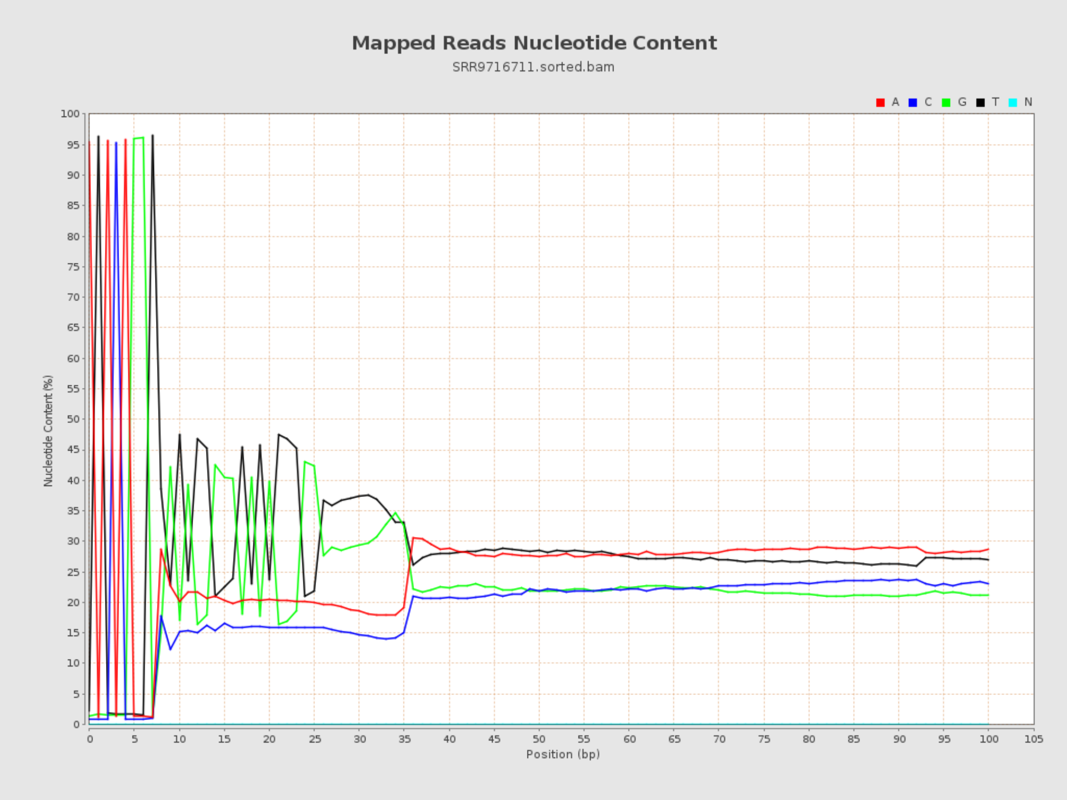
# 6. Results : Genome Fraction Coverage



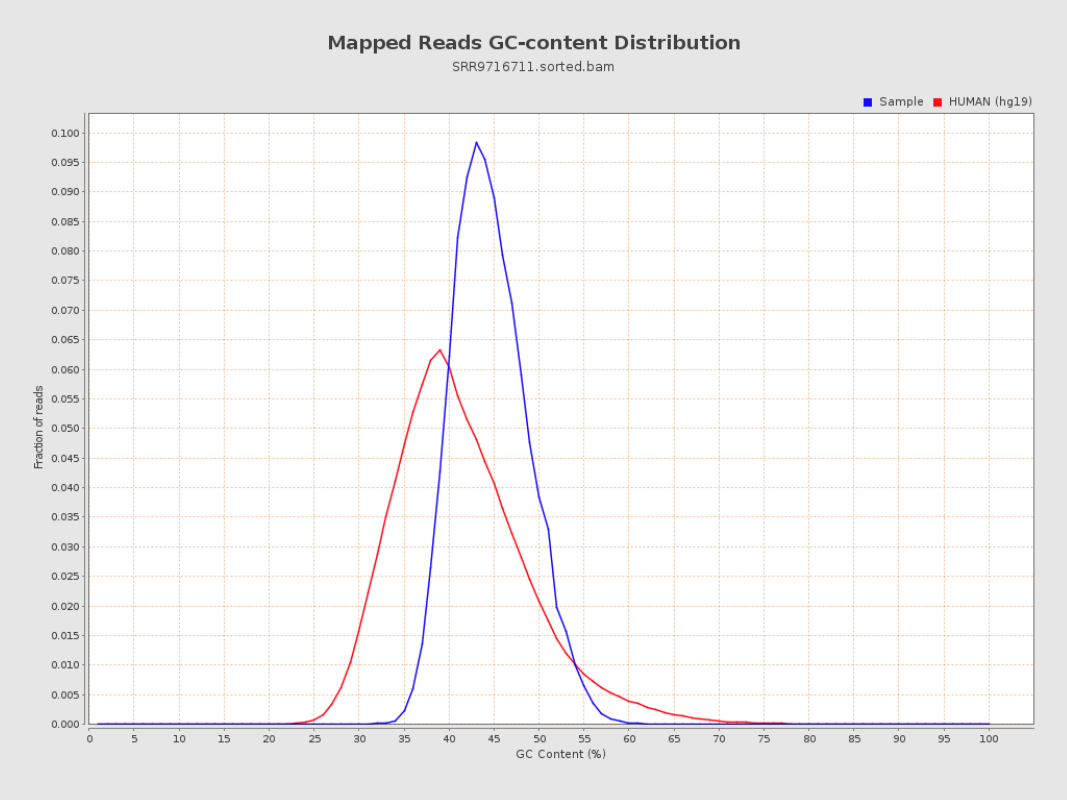
# 7. Results : Duplication Rate Histogram



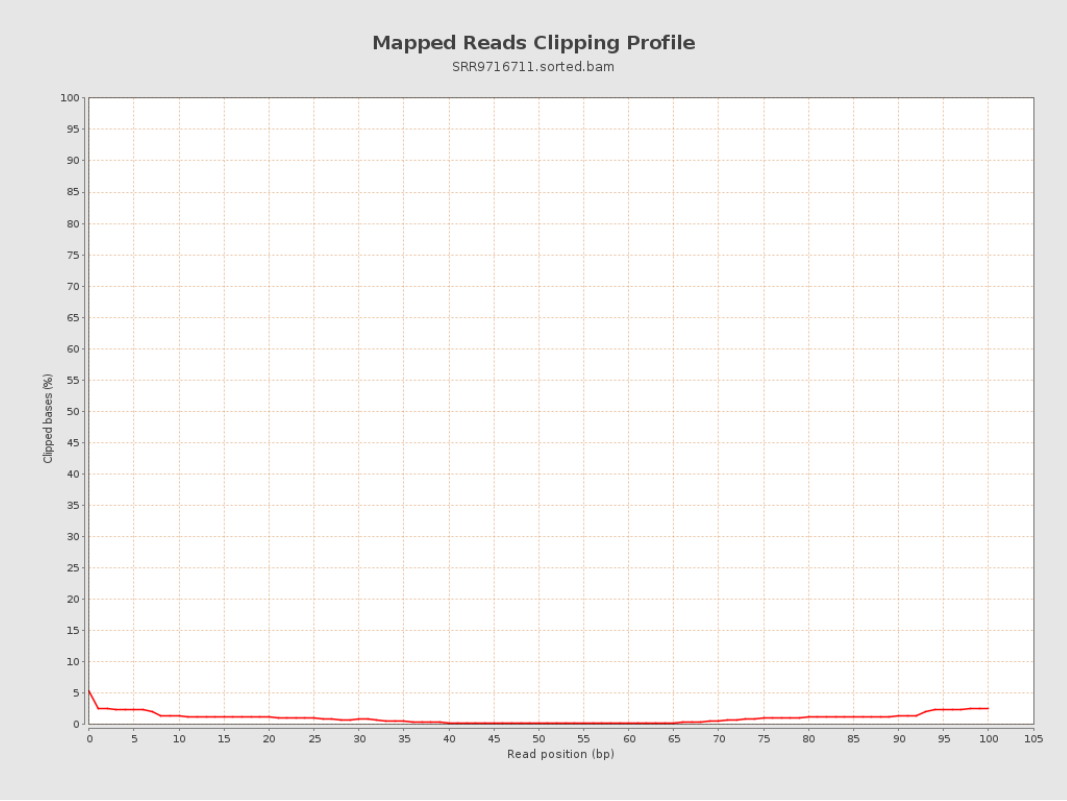
# 8. Results : Mapped Reads Nucleotide Content



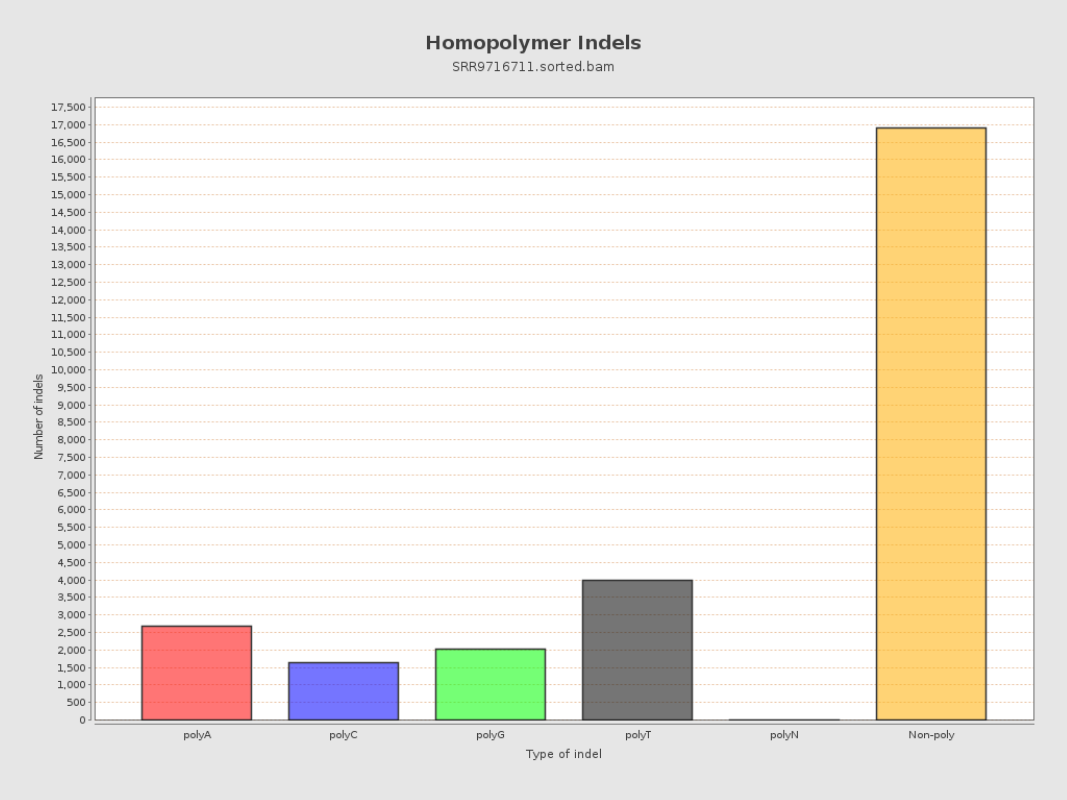
# 9. Results : Mapped Reads GC-content Distribution



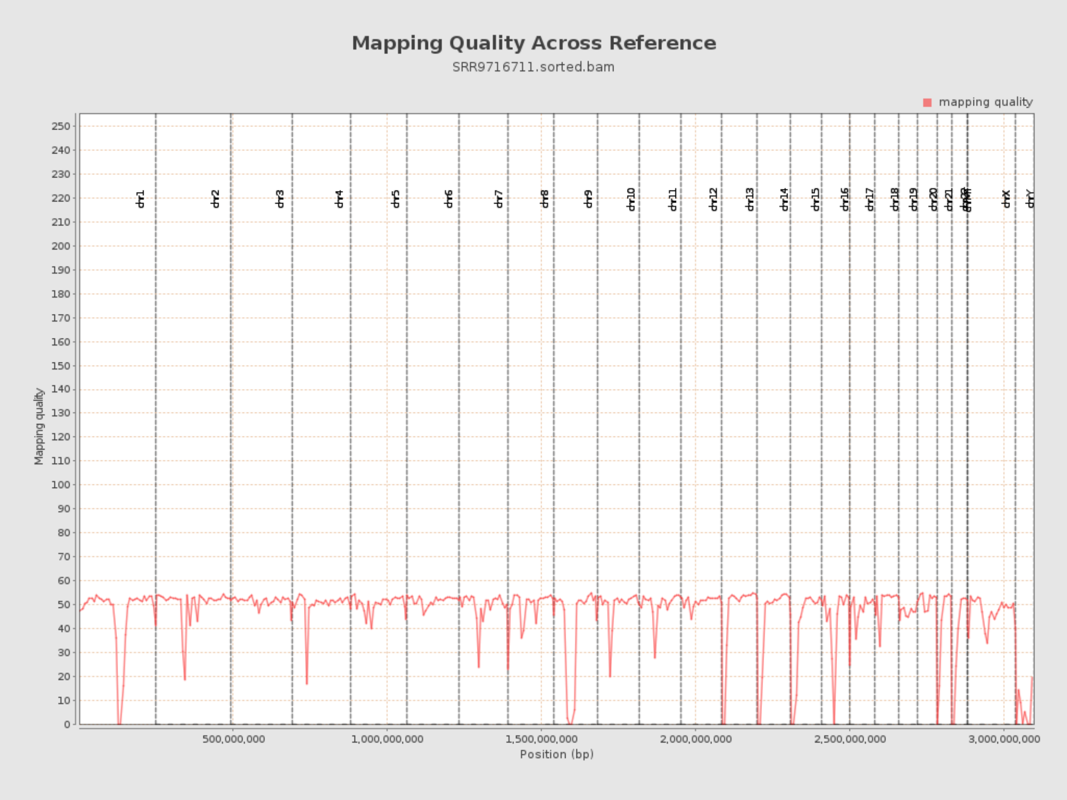
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram