# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 13:12:26*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716434.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_SRR9716434 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716434.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 13:12:25 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716434.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,653,457 |
| Mapped reads | 2,316,974 / 87.32% |
| Unmapped reads | 336,483 / 12.68% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 8,600 / 0.32% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 78,717 / 2.97% |
| Duplication rate | 2.37% |
| Clipped reads | 2,323,339 / 87.56% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 33,552,610 / 25.56% |
| Number/percentage of C's | 27,607,326 / 21.03% |
| Number/percentage of T's | 39,022,507 / 29.73% |
| Number/percentage of G's | 31,078,773 / 23.68% |
| Number/percentage of N's | 1,952 / 0% |
| GC Percentage | 44.71% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0424 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3687 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 42.25 |

## 2.5. Mismatches and indels

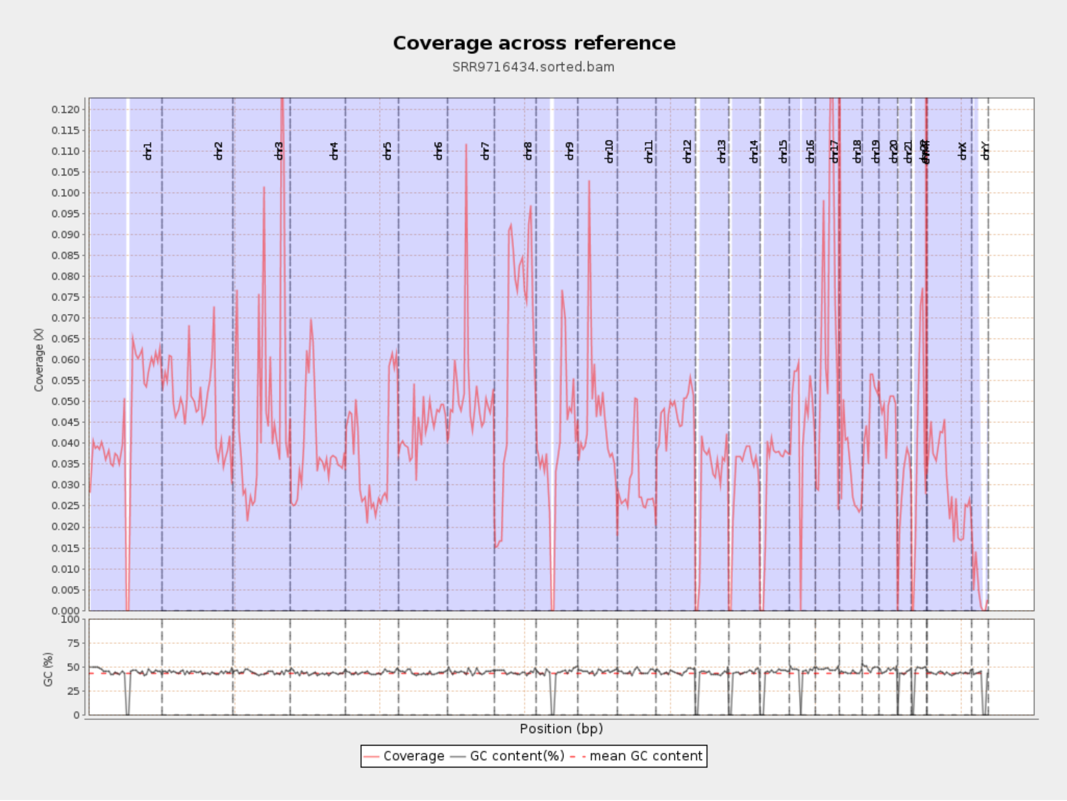
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 669,434 |
| Insertions | 7,858 |
| Mapped reads with at least one insertion | 0.34% |
| Deletions | 24,226 |
| Mapped reads with at least one deletion | 1.04% |
| Homopolymer indels | 42.81% |

## 2.6. Chromosome stats

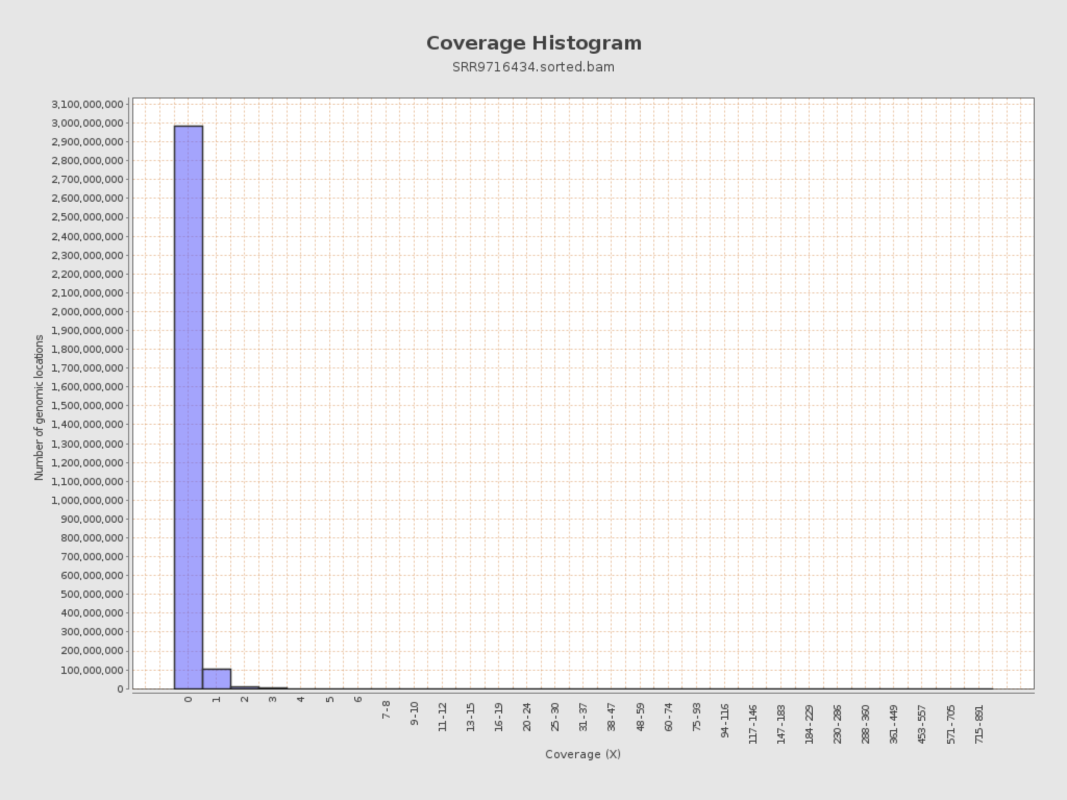
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 11101771 | 0.0445 | 0.4095 |
| chr2 | 243199373 | 12009281 | 0.0494 | 0.4622 |
| chr3 | 198022430 | 9823337 | 0.0496 | 0.2798 |
| chr4 | 191154276 | 7422981 | 0.0388 | 0.2324 |
| chr5 | 180915260 | 6731063 | 0.0372 | 0.2155 |
| chr6 | 171115067 | 7478227 | 0.0437 | 0.2659 |
| chr7 | 159138663 | 8356210 | 0.0525 | 0.9333 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 9221121 | 0.063 | 0.3406 |
| chr9 | 141213431 | 5481121 | 0.0388 | 0.2623 |
| chr10 | 135534747 | 6297395 | 0.0465 | 0.4597 |
| chr11 | 135006516 | 3979216 | 0.0295 | 0.2471 |
| chr12 | 133851895 | 6307567 | 0.0471 | 0.261 |
| chr13 | 115169878 | 3501559 | 0.0304 | 0.1941 |
| chr14 | 107349540 | 3327732 | 0.031 | 0.2078 |
| chr15 | 102531392 | 3194236 | 0.0312 | 0.2059 |
| chr16 | 90354753 | 4164366 | 0.0461 | 0.2565 |
| chr17 | 81195210 | 5687199 | 0.07 | 0.3177 |
| chr18 | 78077248 | 3015824 | 0.0386 | 0.3984 |
| chr19 | 59128983 | 2819019 | 0.0477 | 0.4284 |
| chr20 | 63025520 | 2973893 | 0.0472 | 0.2523 |
| chr21 | 48129895 | 1369756 | 0.0285 | 0.2002 |
| chr22 | 51304566 | 1945100 | 0.0379 | 0.2224 |
| chrMT | 16571 | 65846 | 3.9736 | 3.3451 |
| chrX | 155270560 | 4739522 | 0.0305 | 0.236 |
| chrY | 59373566 | 287590 | 0.0048 | 0.1102 |

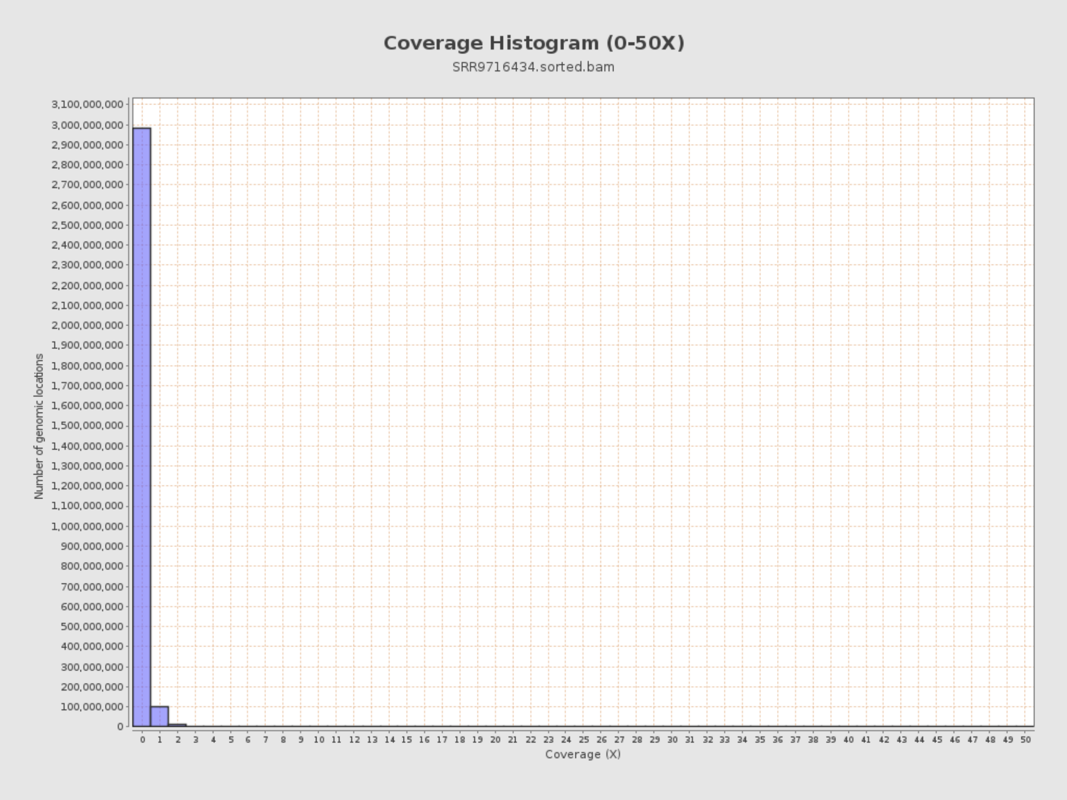
# 3. Results : Coverage across reference



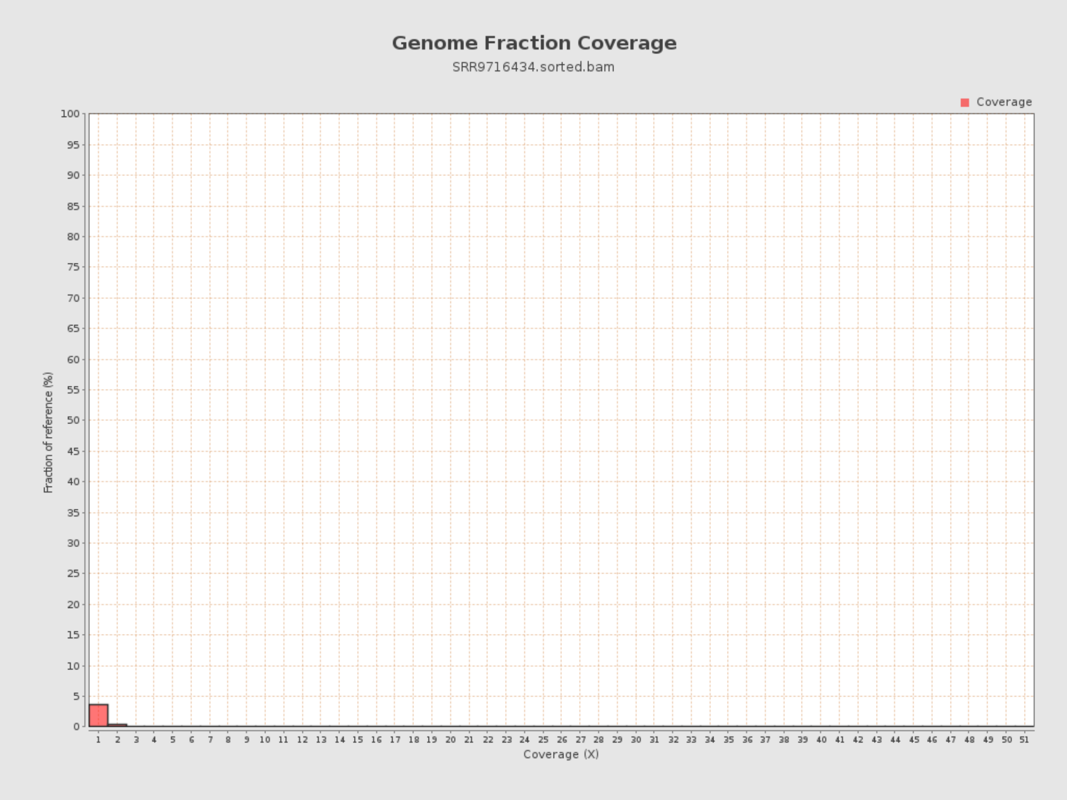
# 4. Results : Coverage Histogram



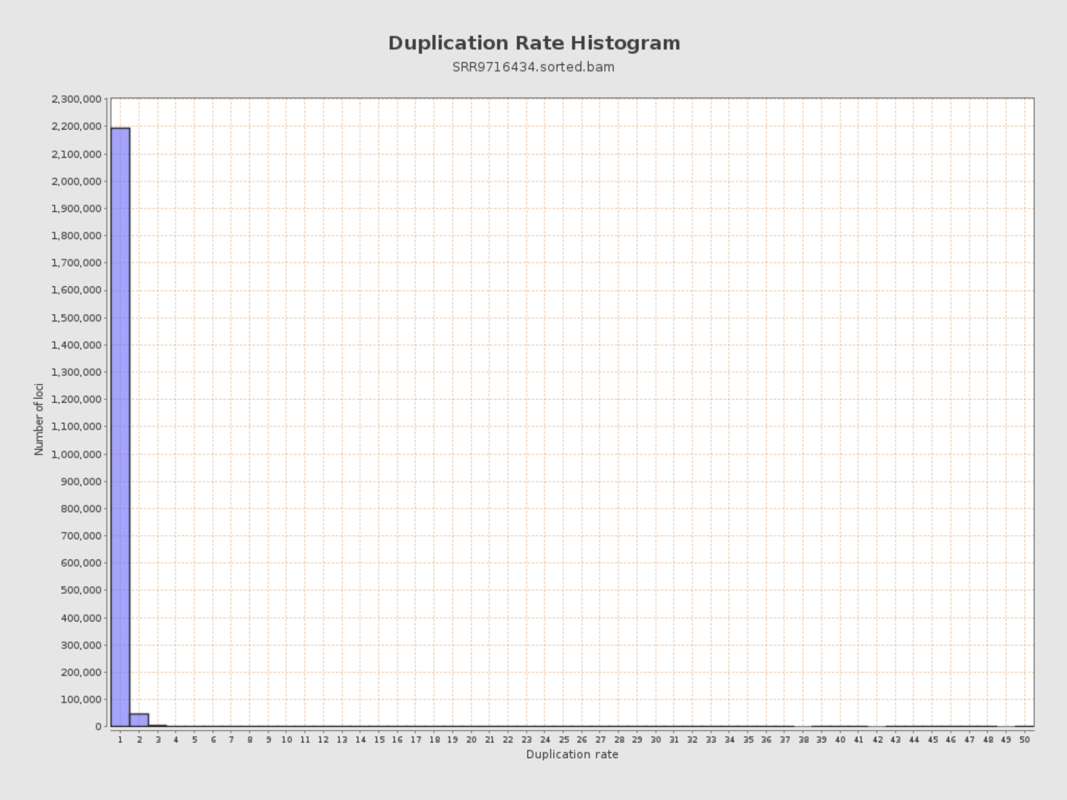
# 5. Results : Coverage Histogram (0-50X)



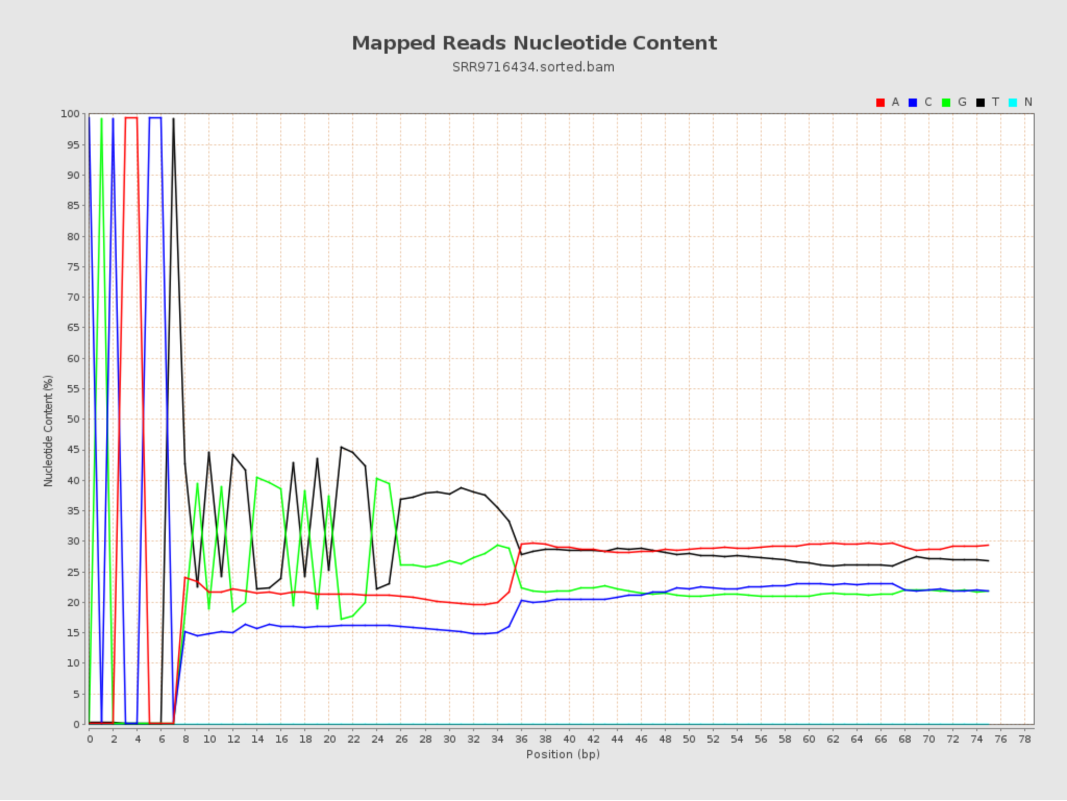
# 6. Results : Genome Fraction Coverage



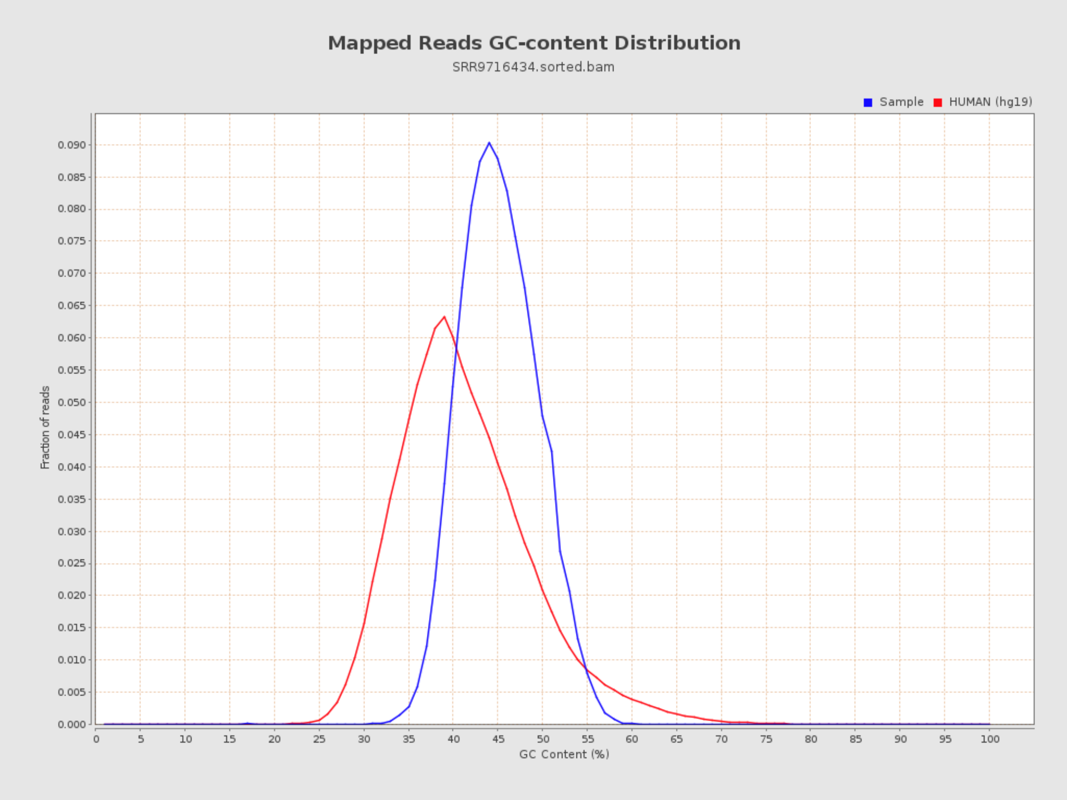
# 7. Results : Duplication Rate Histogram



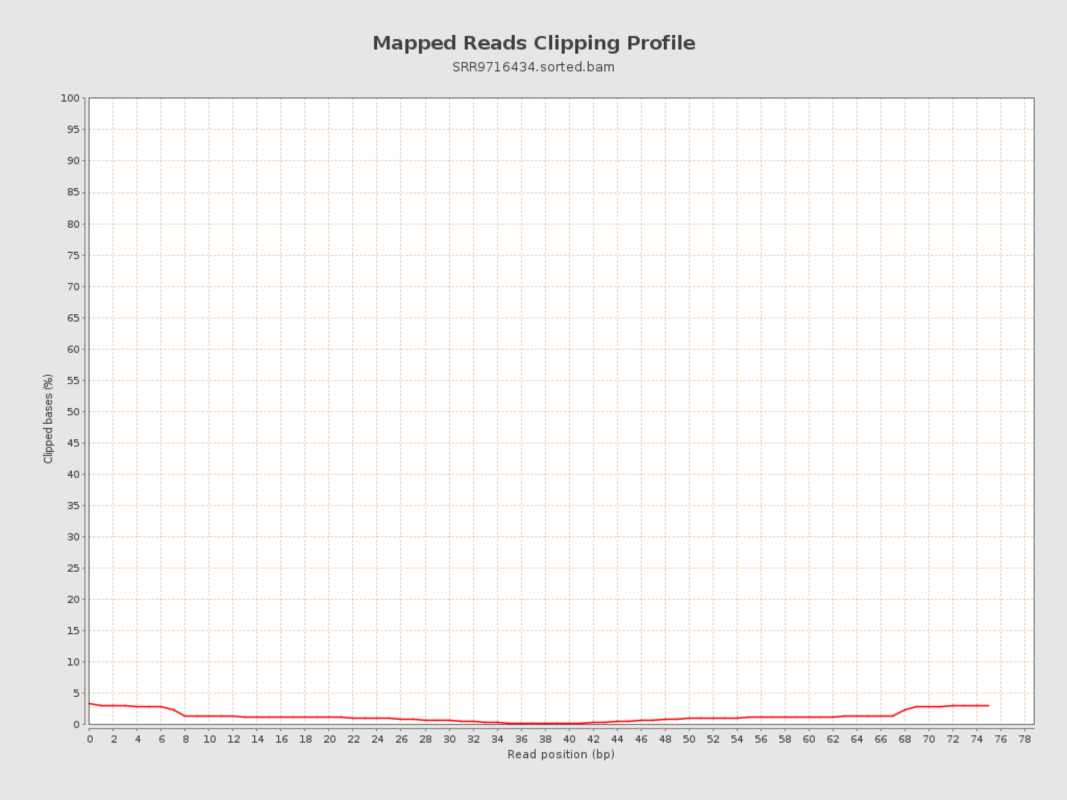
# 8. Results : Mapped Reads Nucleotide Content



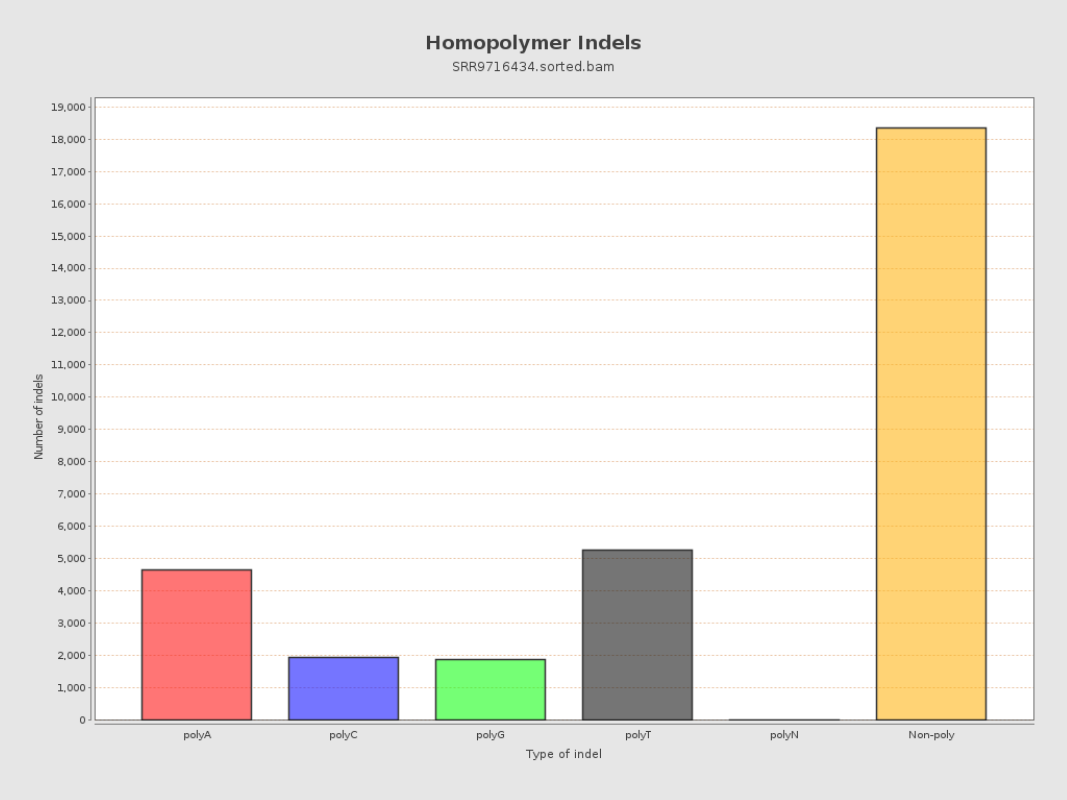
# 9. Results : Mapped Reads GC-content Distribution



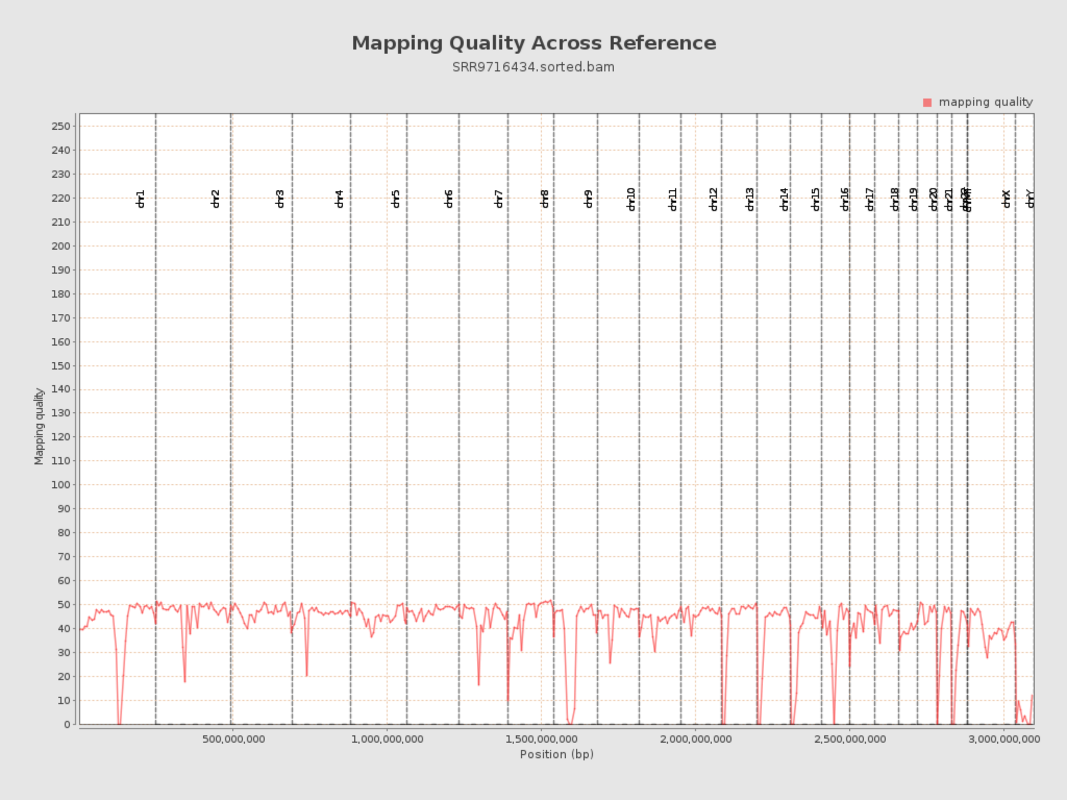
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram