# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/02 17:27:17*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716504.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_SRR9716504 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716504.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 02 17:27:16 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716504.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,828,423 |
| Mapped reads | 2,491,659 / 88.09% |
| Unmapped reads | 336,764 / 11.91% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 9,984 / 0.35% |
| Read min/max/mean length | 30 / 76 / 76.12 |
| Duplicated reads (estimated) | 115,272 / 4.08% |
| Duplication rate | 3.45% |
| Clipped reads | 2,494,444 / 88.19% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 34,919,451 / 24.57% |
| Number/percentage of C's | 28,190,497 / 19.84% |
| Number/percentage of T's | 46,320,458 / 32.59% |
| Number/percentage of G's | 32,679,205 / 23% |
| Number/percentage of N's | 1,034 / 0% |
| GC Percentage | 42.83% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0459 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3611 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.89 |

## 2.5. Mismatches and indels

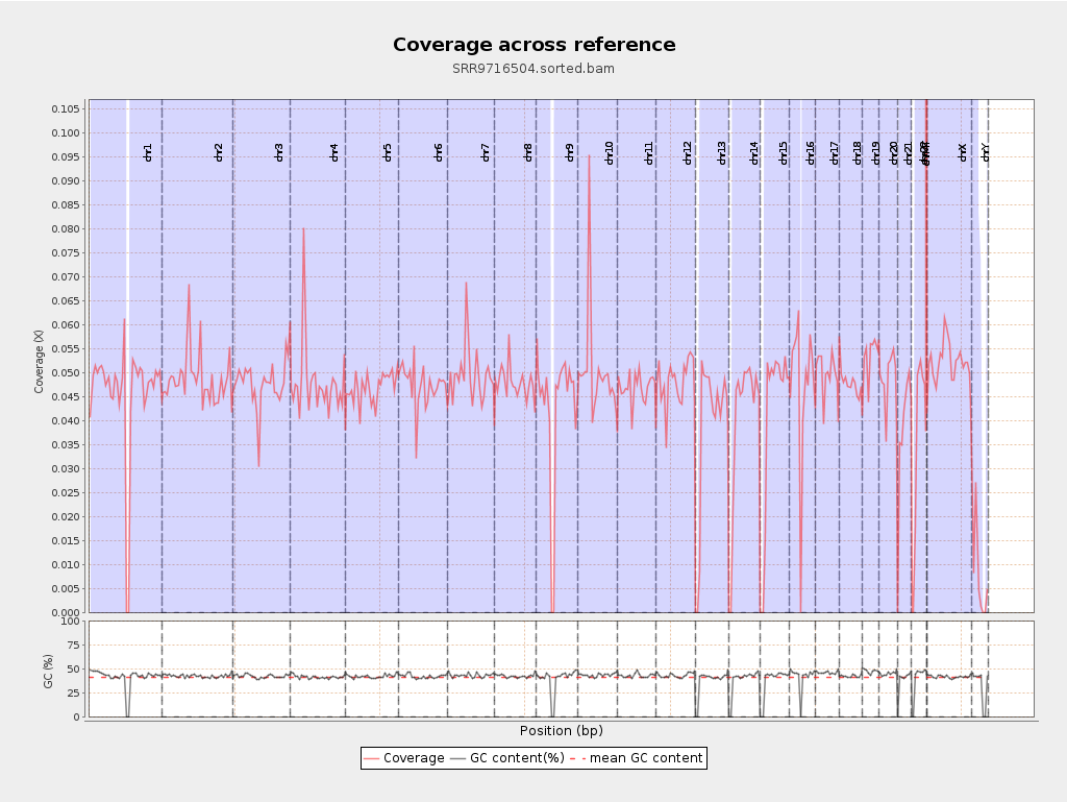
| | |
|---|---|
| General error rate | 0.54% |
| Mismatches | 755,259 |
| Insertions | 9,424 |
| Mapped reads with at least one insertion | 0.38% |
| Deletions | 27,180 |
| Mapped reads with at least one deletion | 1.08% |
| Homopolymer indels | 41.41% |

## 2.6. Chromosome stats

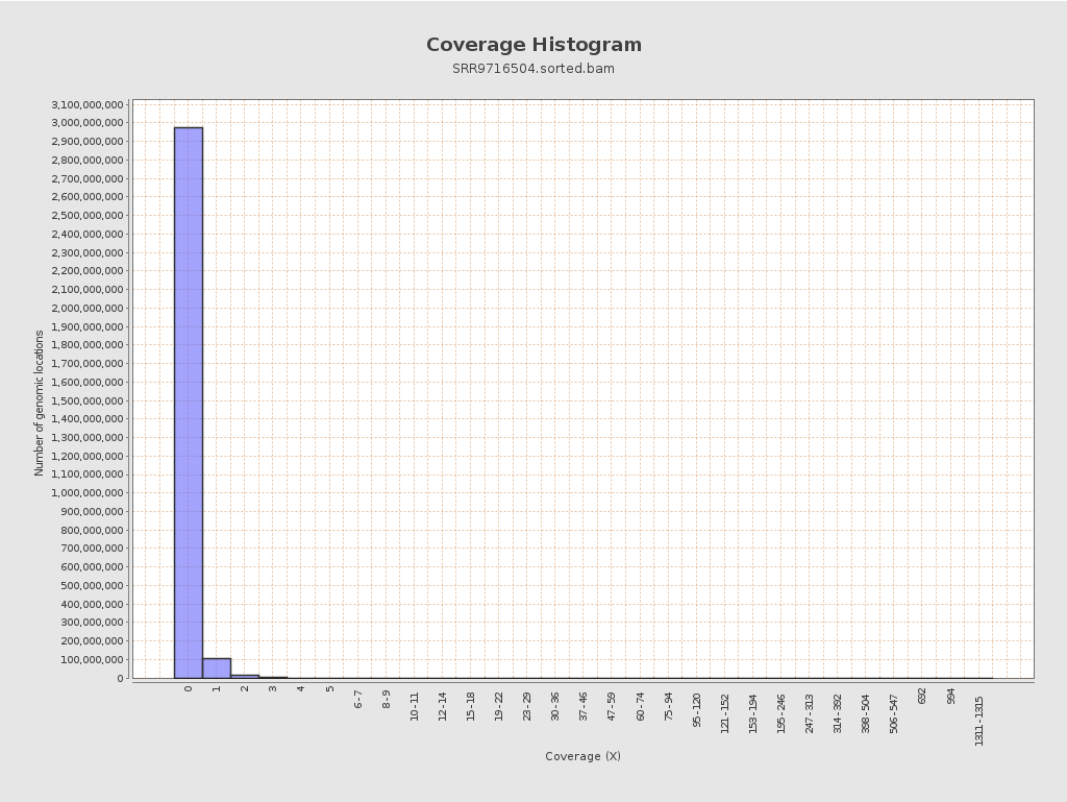
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 11367276 | 0.0456 | 0.4803 |
| chr2 | 243199373 | 11856848 | 0.0488 | 0.616 |
| chr3 | 198022430 | 9430997 | 0.0476 | 0.2561 |
| chr4 | 191154276 | 9099983 | 0.0476 | 0.2959 |
| chr5 | 180915260 | 8483003 | 0.0469 | 0.25 |
| chr6 | 171115067 | 8110927 | 0.0474 | 0.3014 |
| chr7 | 159138663 | 7890765 | 0.0496 | 0.4342 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7002812 | 0.0478 | 0.3585 |
| chr9 | 141213431 | 5919863 | 0.0419 | 0.2952 |
| chr10 | 135534747 | 6789693 | 0.0501 | 0.4493 |
| chr11 | 135006516 | 6317814 | 0.0468 | 0.3137 |
| chr12 | 133851895 | 6451036 | 0.0482 | 0.2578 |
| chr13 | 115169878 | 4431106 | 0.0385 | 0.2257 |
| chr14 | 107349540 | 4275869 | 0.0398 | 0.2425 |
| chr15 | 102531392 | 4172336 | 0.0407 | 0.2374 |
| chr16 | 90354753 | 4305867 | 0.0477 | 0.2844 |
| chr17 | 81195210 | 4010508 | 0.0494 | 0.2707 |
| chr18 | 78077248 | 3739599 | 0.0479 | 0.449 |
| chr19 | 59128983 | 3147452 | 0.0532 | 0.4281 |
| chr20 | 63025520 | 3051172 | 0.0484 | 0.2696 |
| chr21 | 48129895 | 1843507 | 0.0383 | 0.2606 |
| chr22 | 51304566 | 1749148 | 0.0341 | 0.2151 |
| chrMT | 16571 | 154722 | 9.3369 | 6.0391 |
| chrX | 155270560 | 8084661 | 0.0521 | 0.2931 |
| chrY | 59373566 | 467076 | 0.0079 | 0.2289 |

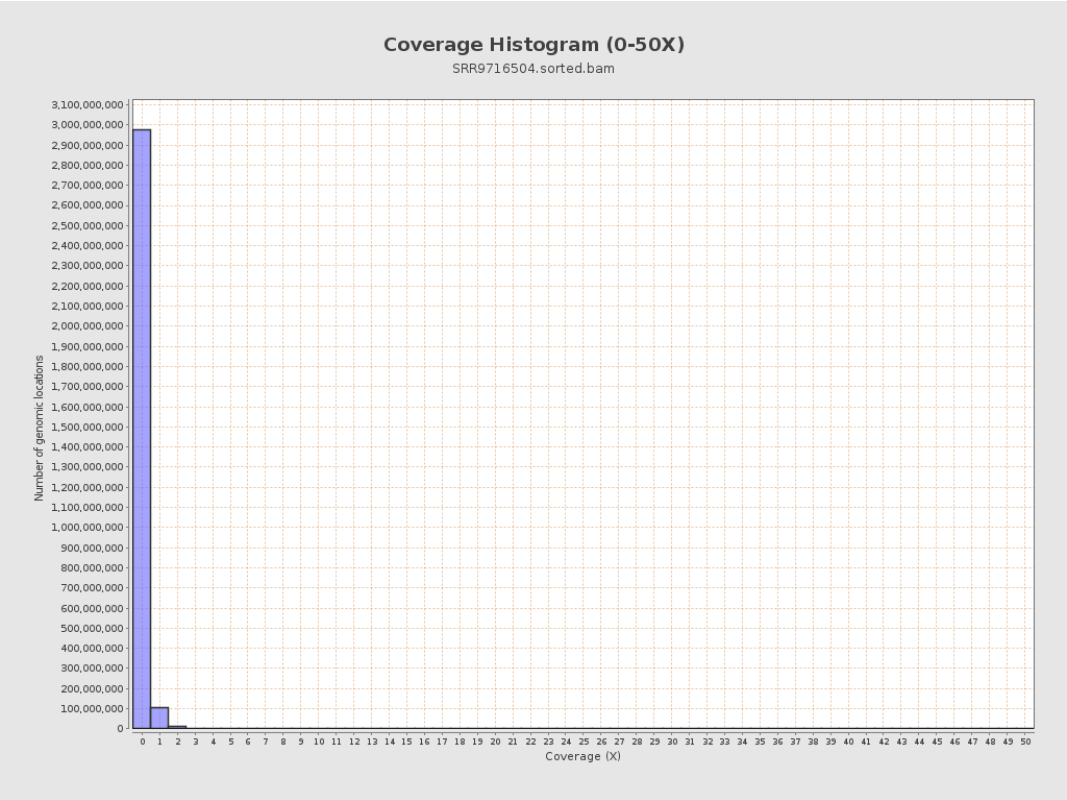
# 3. Results : Coverage across reference



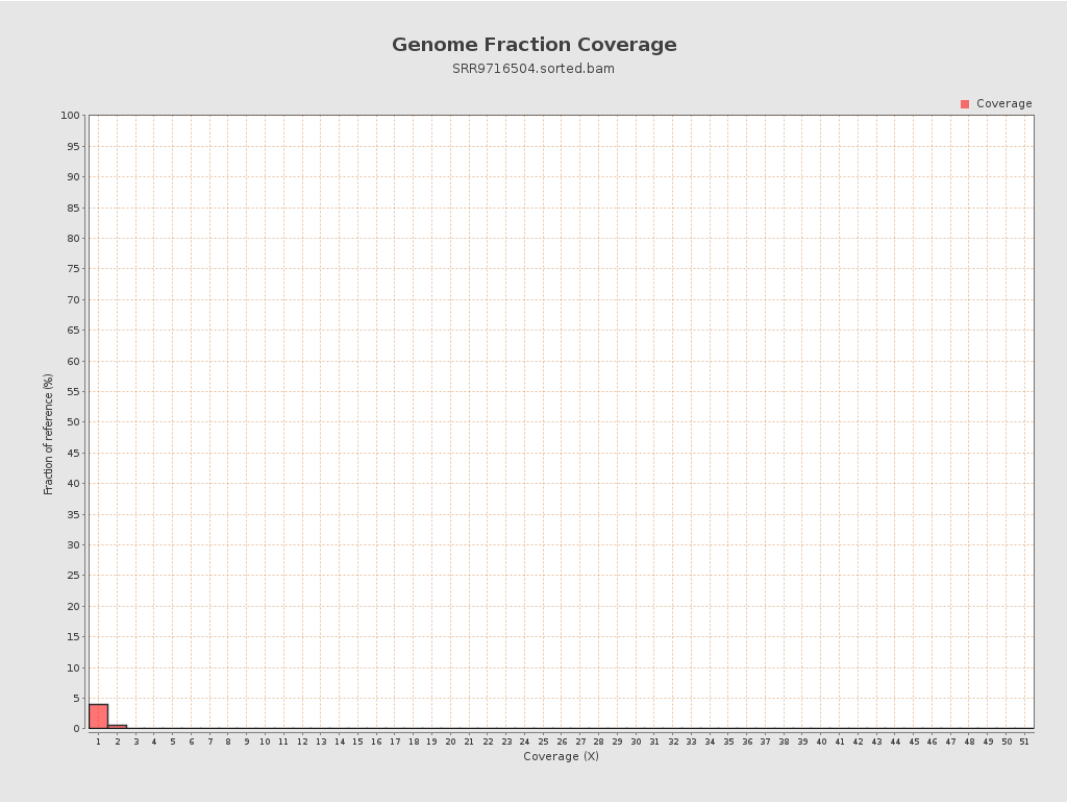
# 4. Results : Coverage Histogram



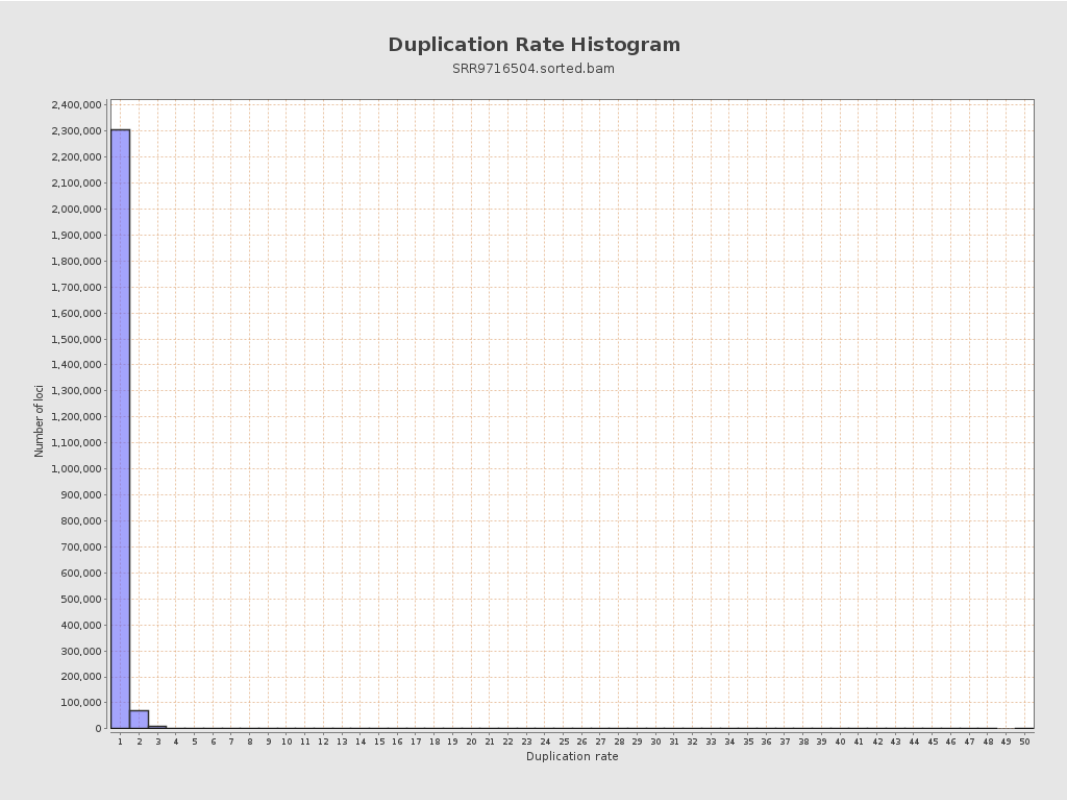
# 5. Results : Coverage Histogram (0-50X)



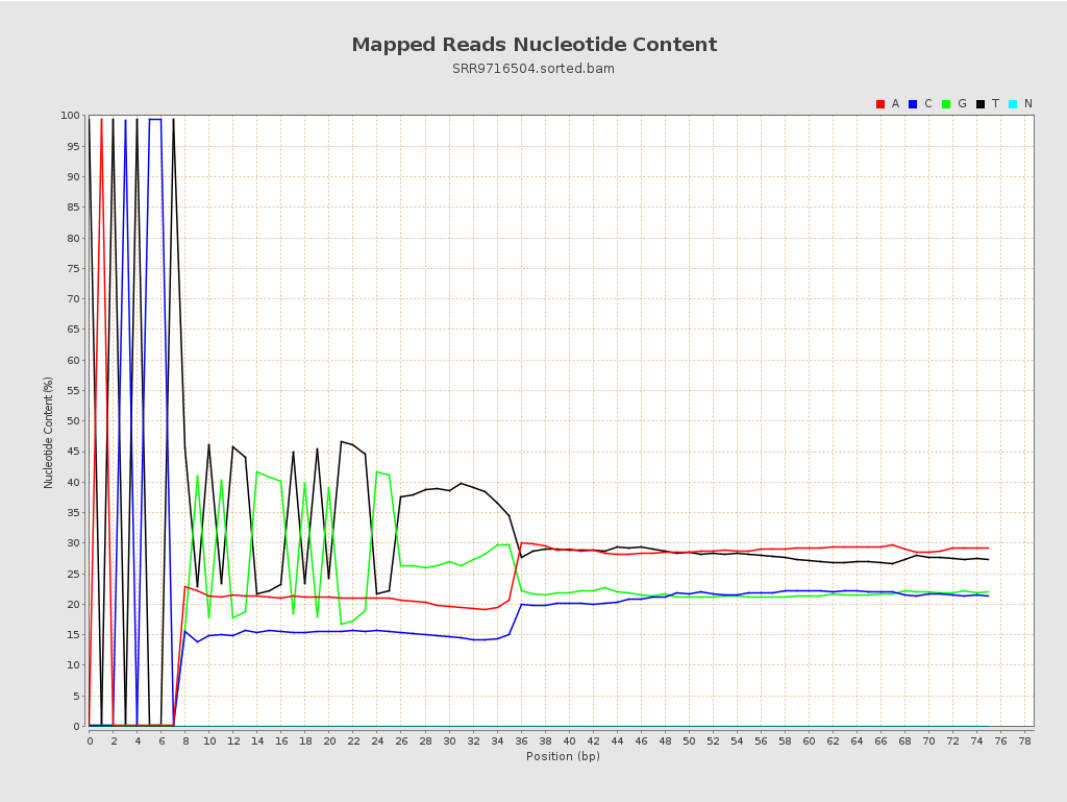
# 6. Results : Genome Fraction Coverage



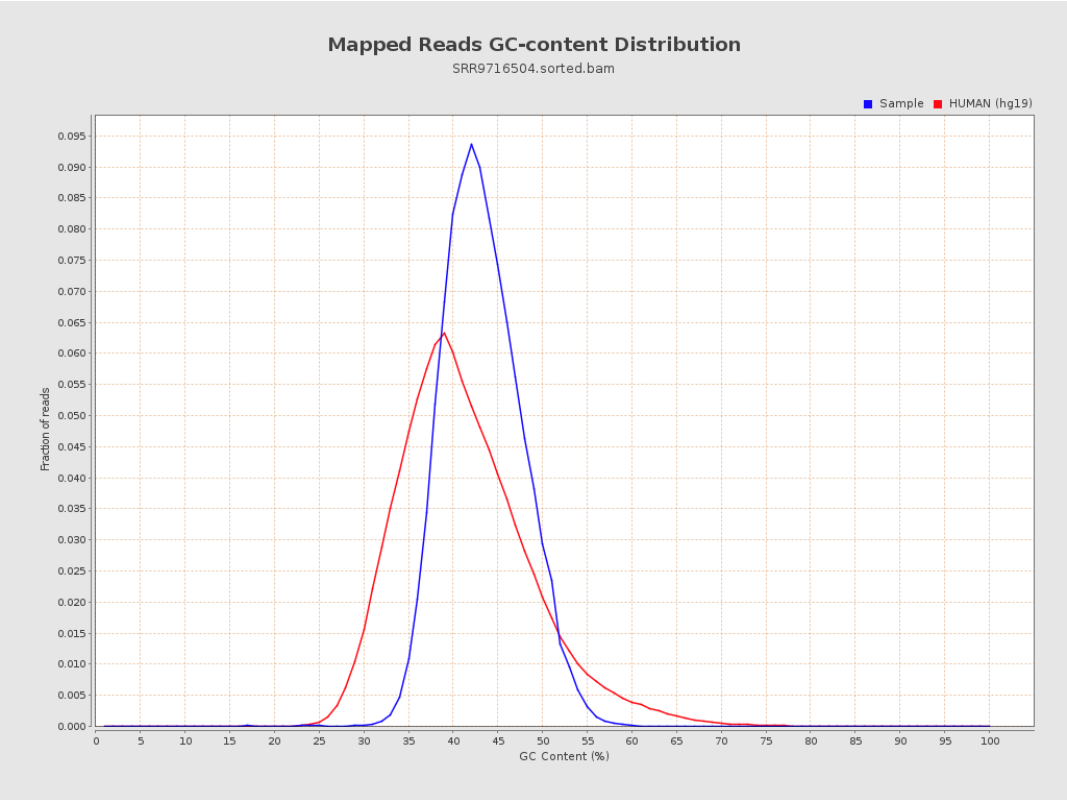
# 7. Results : Duplication Rate Histogram



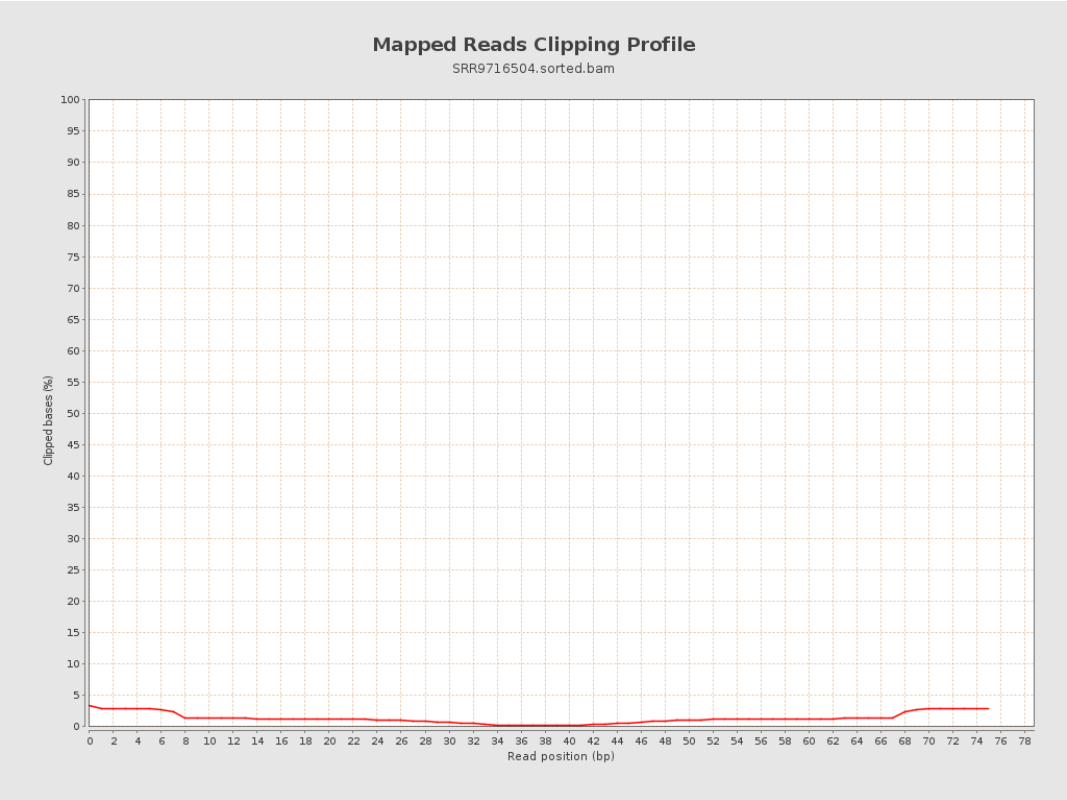
# 8. Results : Mapped Reads Nucleotide Content



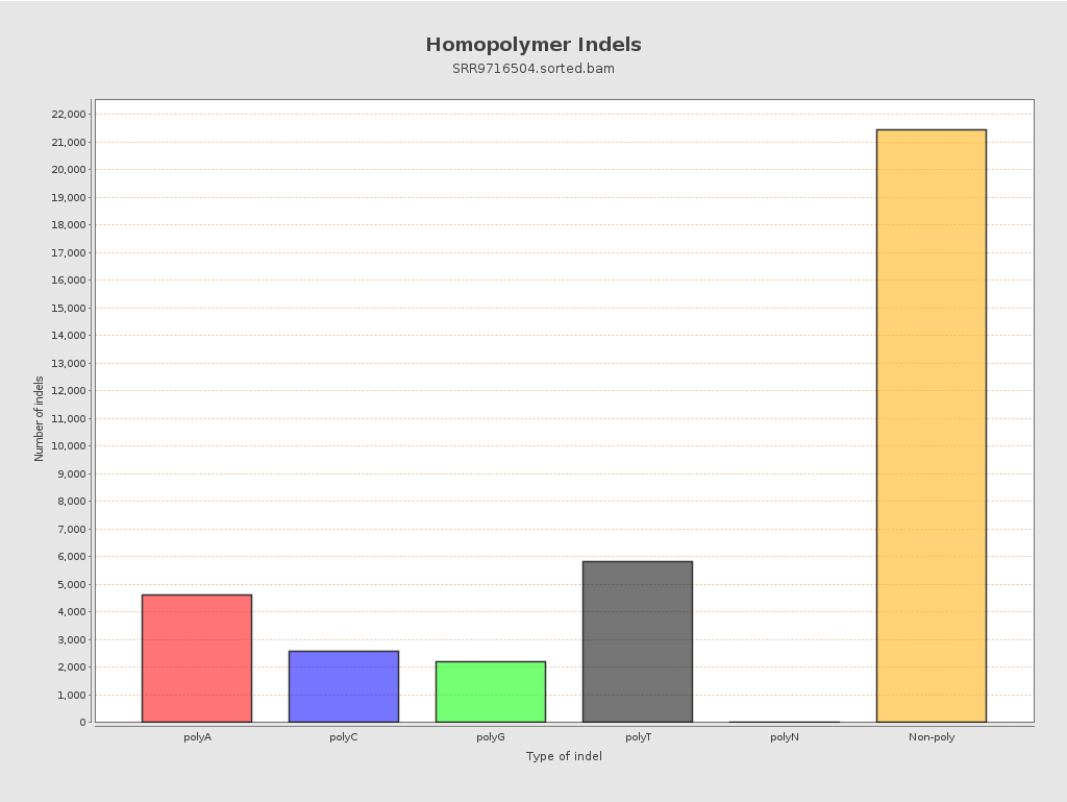
# 9. Results : Mapped Reads GC-content Distribution



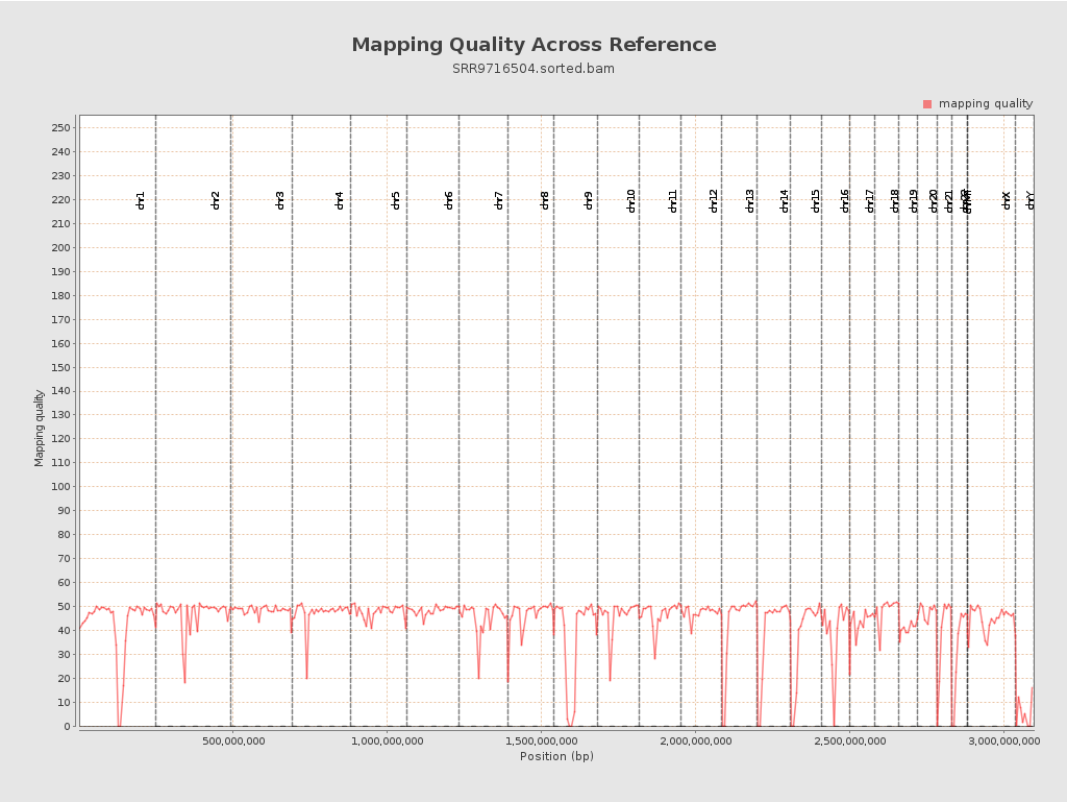
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram