# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/01 18:45:32*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524452.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_SRR10524452 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524452.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 01 18:45:32 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524452.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,659,200 |
| Mapped reads | 3,365,712 / 91.98% |
| Unmapped reads | 293,488 / 8.02% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 7,462 / 0.2% |
| Read min/max/mean length | 30 / 76 / 76.07 |
| Duplicated reads (estimated) | 254,656 / 6.96% |
| Duplication rate | 5.65% |
| Clipped reads | 3,363,418 / 91.92% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 48,867,903 / 24.94% |
| Number/percentage of C's | 33,007,822 / 16.84% |
| Number/percentage of T's | 62,882,620 / 32.09% |
| Number/percentage of G's | 51,196,970 / 26.13% |
| Number/percentage of N's | 3,595 / 0% |
| GC Percentage | 42.97% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0633 |
| | |

| | |
|---|---|
| Standard Deviation | 0.5311 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.46 |

## 2.5. Mismatches and indels

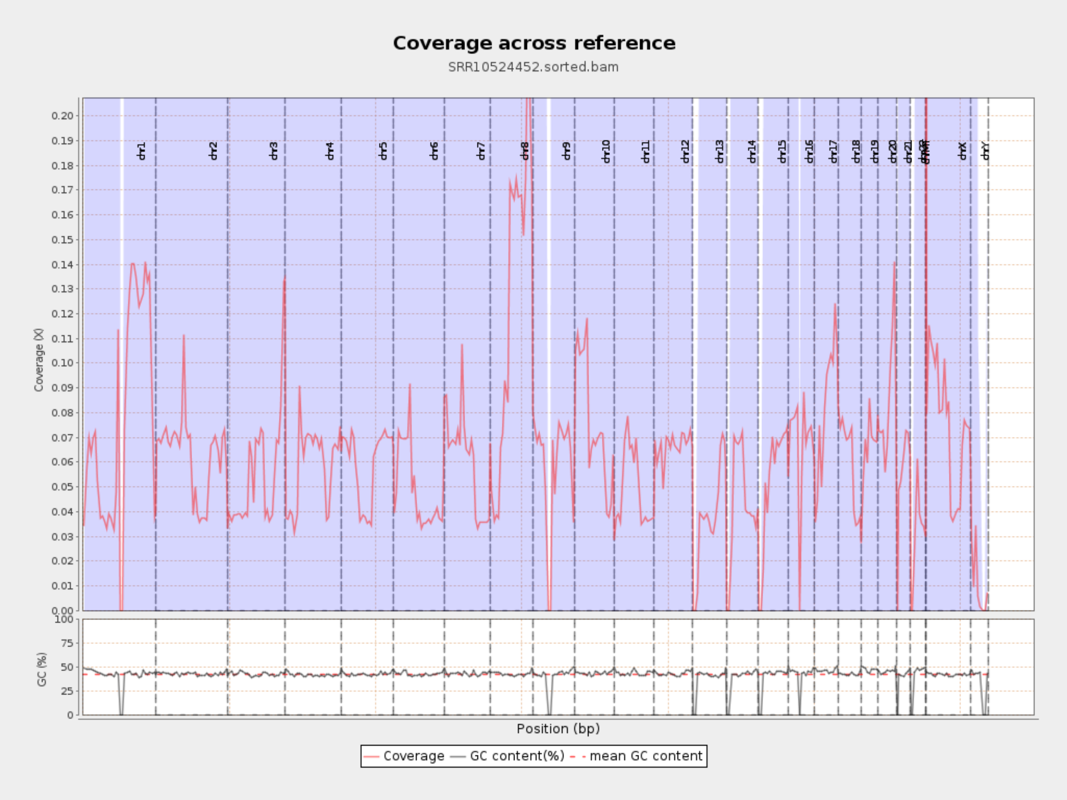
| | |
|---|---|
| General error rate | 0.48% |
| Mismatches | 914,575 |
| Insertions | 12,732 |
| Mapped reads with at least one insertion | 0.38% |
| Deletions | 36,537 |
| Mapped reads with at least one deletion | 1.08% |
| Homopolymer indels | 43.92% |

## 2.6. Chromosome stats

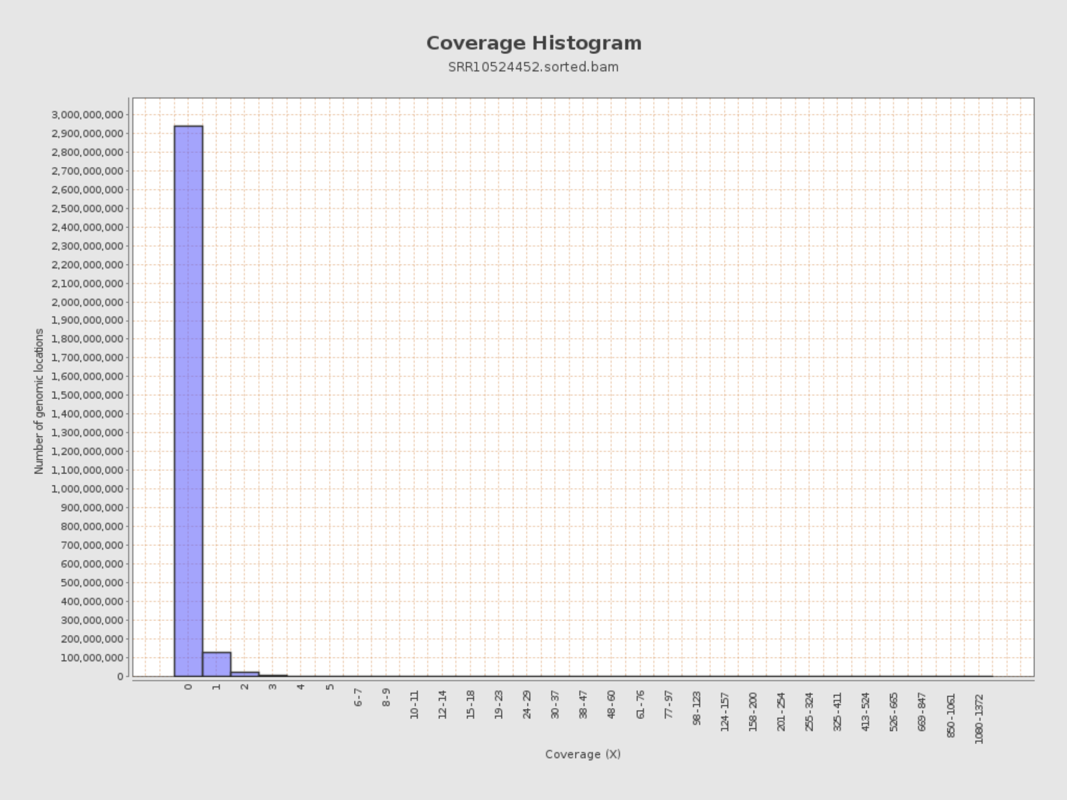
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 19193461 | 0.077 | 1.0636 |
| chr2 | 243199373 | 15396550 | 0.0633 | 0.5934 |
| chr3 | 198022430 | 10870595 | 0.0549 | 0.2878 |
| chr4 | 191154276 | 11188449 | 0.0585 | 0.3613 |
| chr5 | 180915260 | 10740615 | 0.0594 | 0.301 |
| chr6 | 171115067 | 8397388 | 0.0491 | 0.3914 |
| chr7 | 159138663 | 9611218 | 0.0604 | 0.7129 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 18696282 | 0.1277 | 0.5579 |
| chr9 | 141213431 | 8216517 | 0.0582 | 0.4462 |
| chr10 | 135534747 | 10242865 | 0.0756 | 0.5394 |
| chr11 | 135006516 | 6623501 | 0.0491 | 0.4954 |
| chr12 | 133851895 | 8938617 | 0.0668 | 0.3177 |
| chr13 | 115169878 | 4380894 | 0.038 | 0.2407 |
| chr14 | 107349540 | 4733305 | 0.0441 | 0.2666 |
| chr15 | 102531392 | 5180717 | 0.0505 | 0.2977 |
| chr16 | 90354753 | 5989530 | 0.0663 | 0.3572 |
| chr17 | 81195210 | 6704632 | 0.0826 | 0.379 |
| chr18 | 78077248 | 4712107 | 0.0604 | 0.848 |
| chr19 | 59128983 | 3925873 | 0.0664 | 0.7293 |
| chr20 | 63025520 | 5538269 | 0.0879 | 0.3667 |
| chr21 | 48129895 | 2705683 | 0.0562 | 0.3202 |
| chr22 | 51304566 | 1545341 | 0.0301 | 0.2111 |
| chrMT | 16571 | 38995 | 2.3532 | 2.4802 |
| chrX | 155270560 | 11847393 | 0.0763 | 0.4073 |
| chrY | 59373566 | 602238 | 0.0101 | 0.2569 |

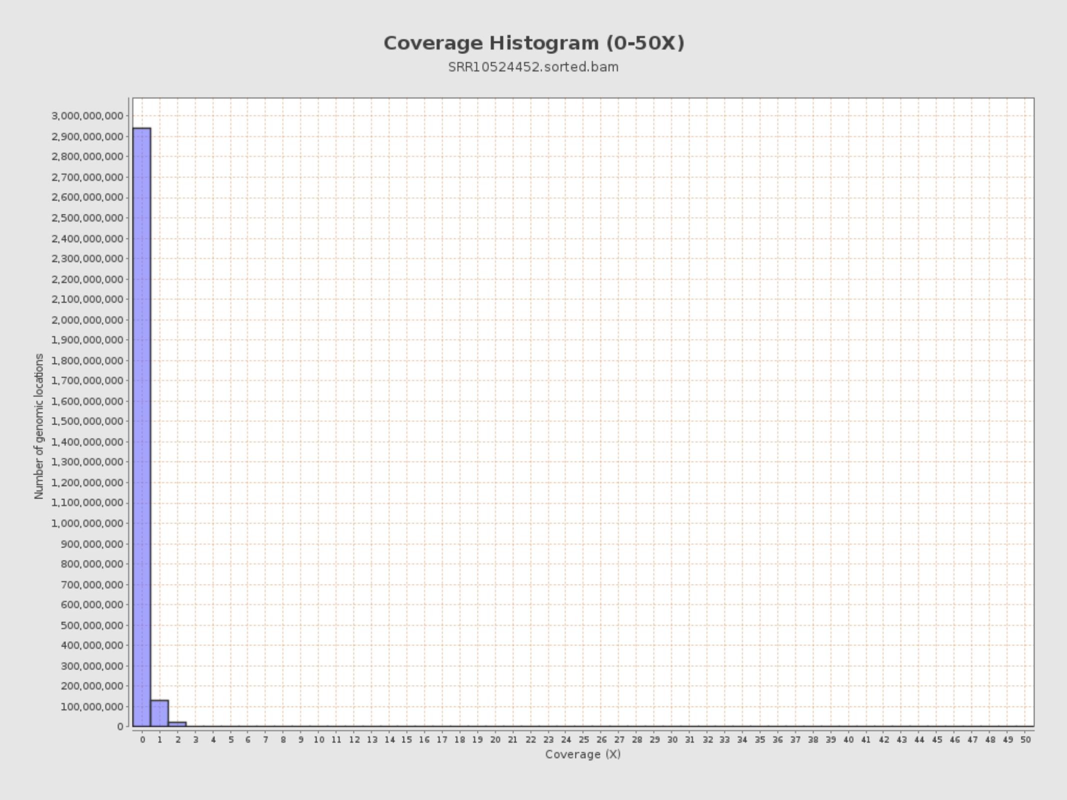
# 3. Results : Coverage across reference



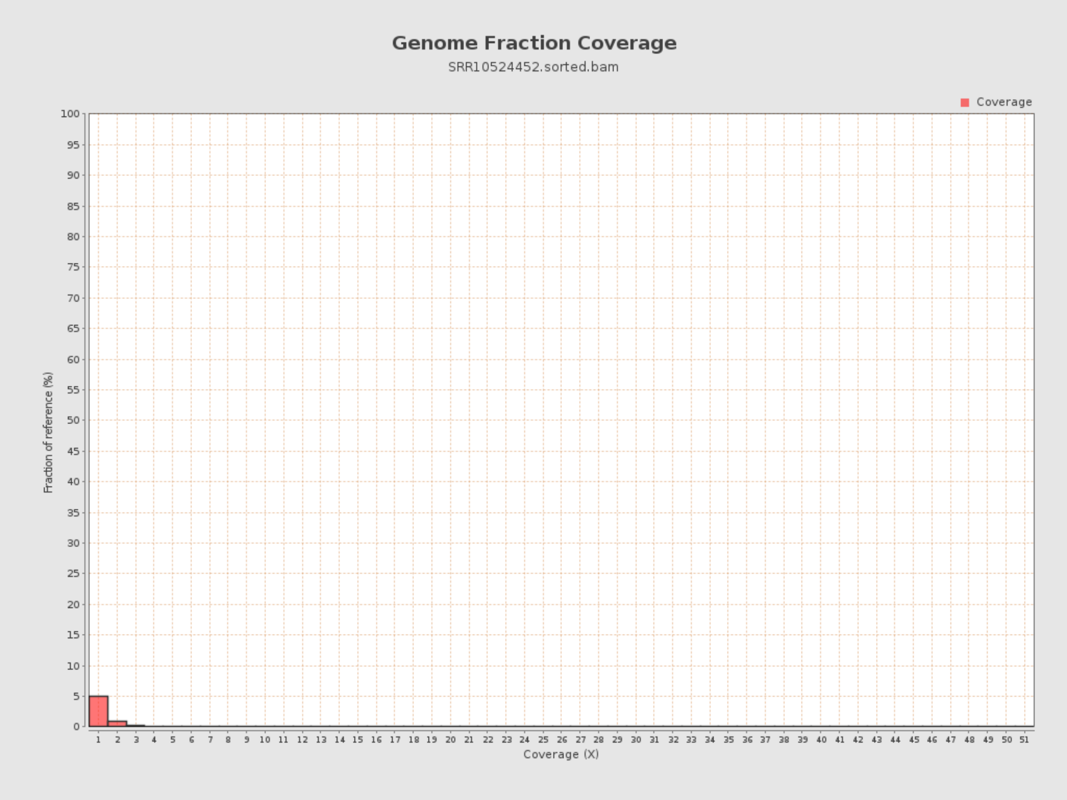
# 4. Results : Coverage Histogram



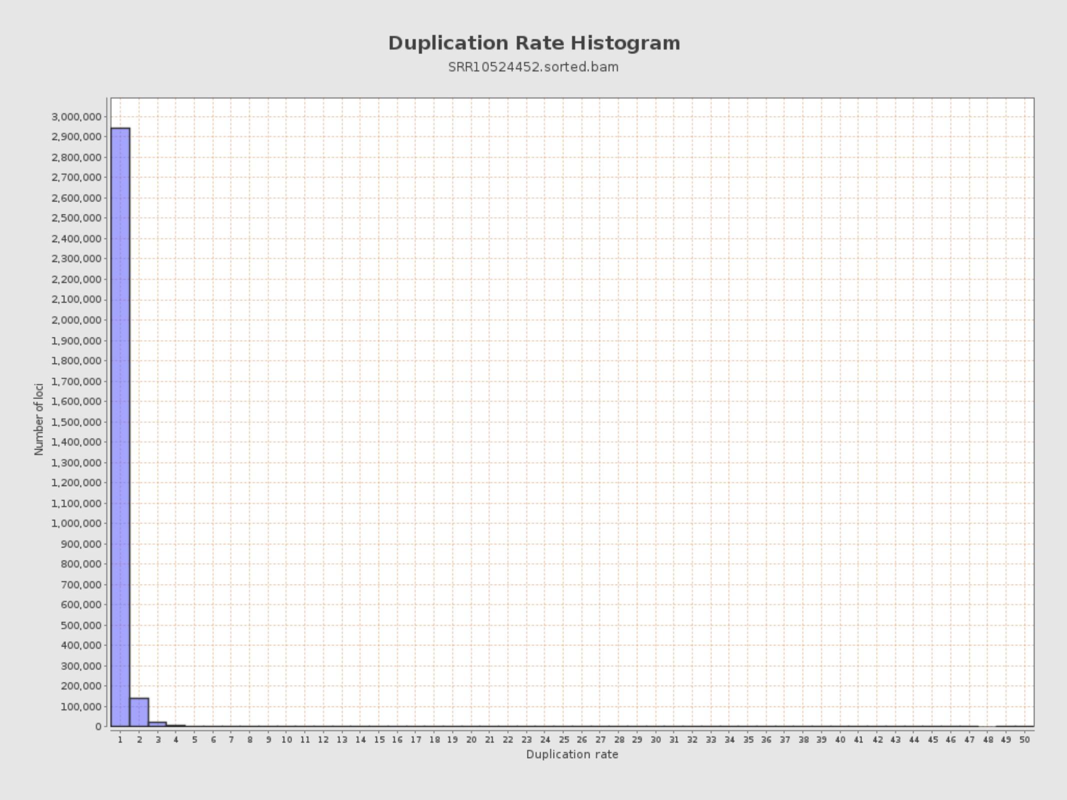
# 5. Results : Coverage Histogram (0-50X)



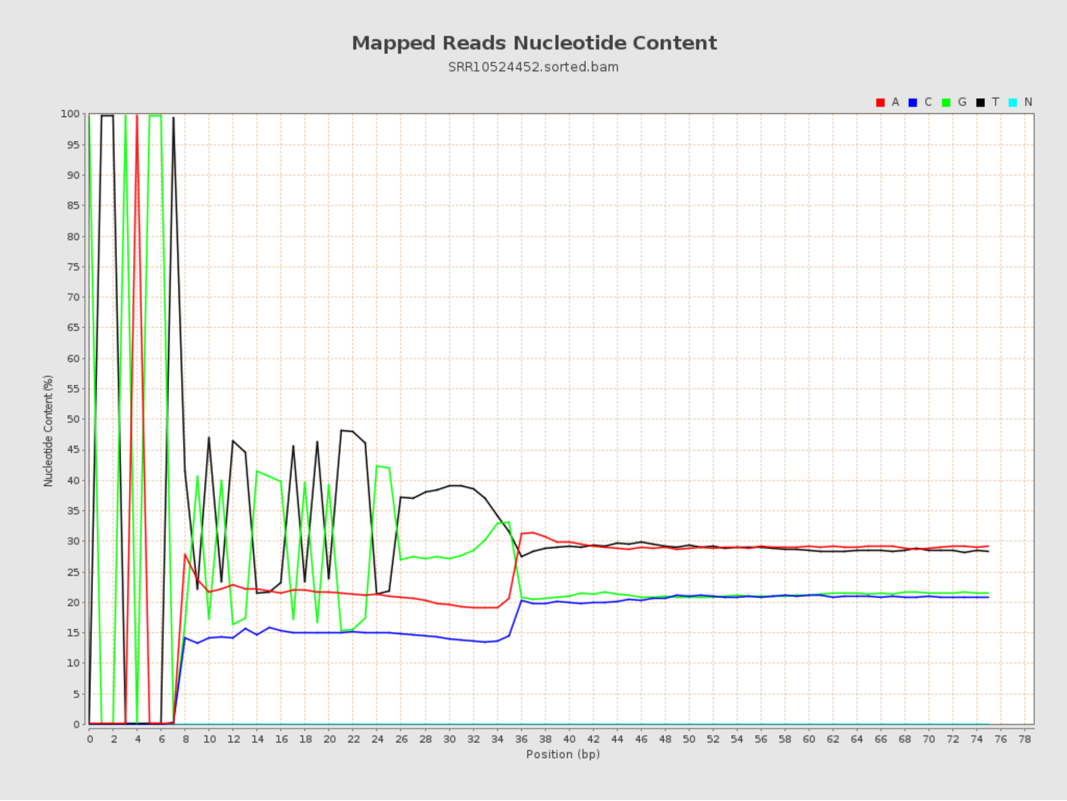
# 6. Results : Genome Fraction Coverage



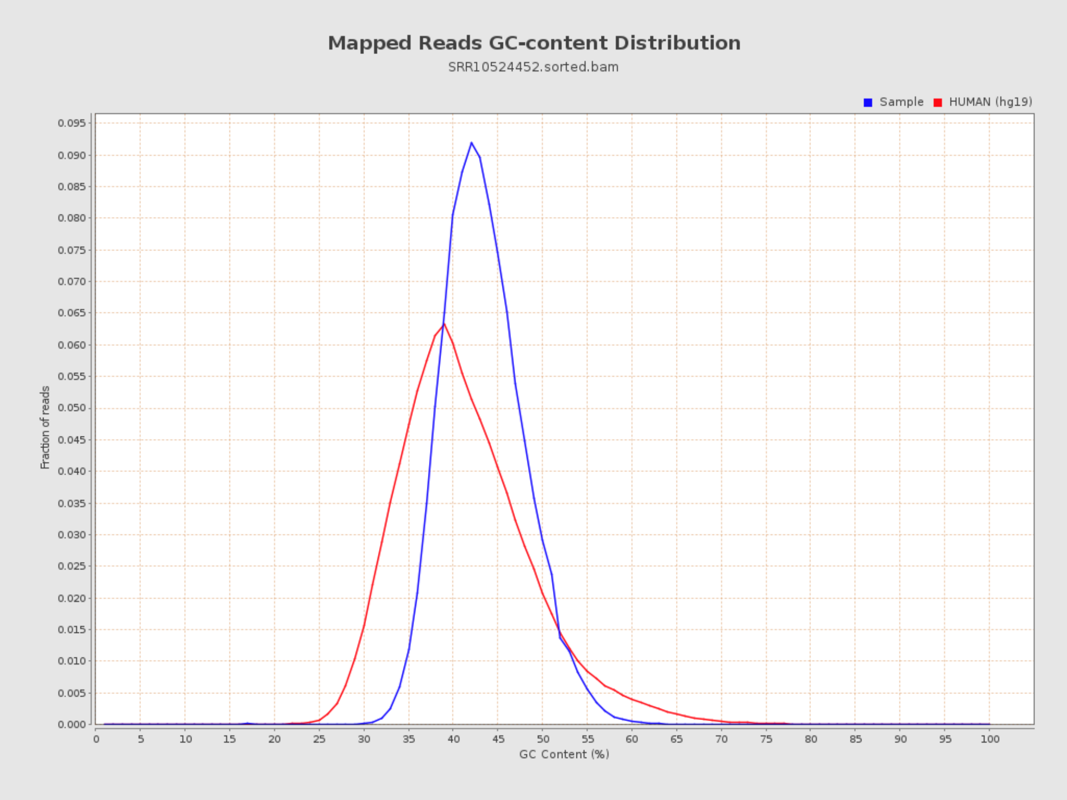
# 7. Results : Duplication Rate Histogram



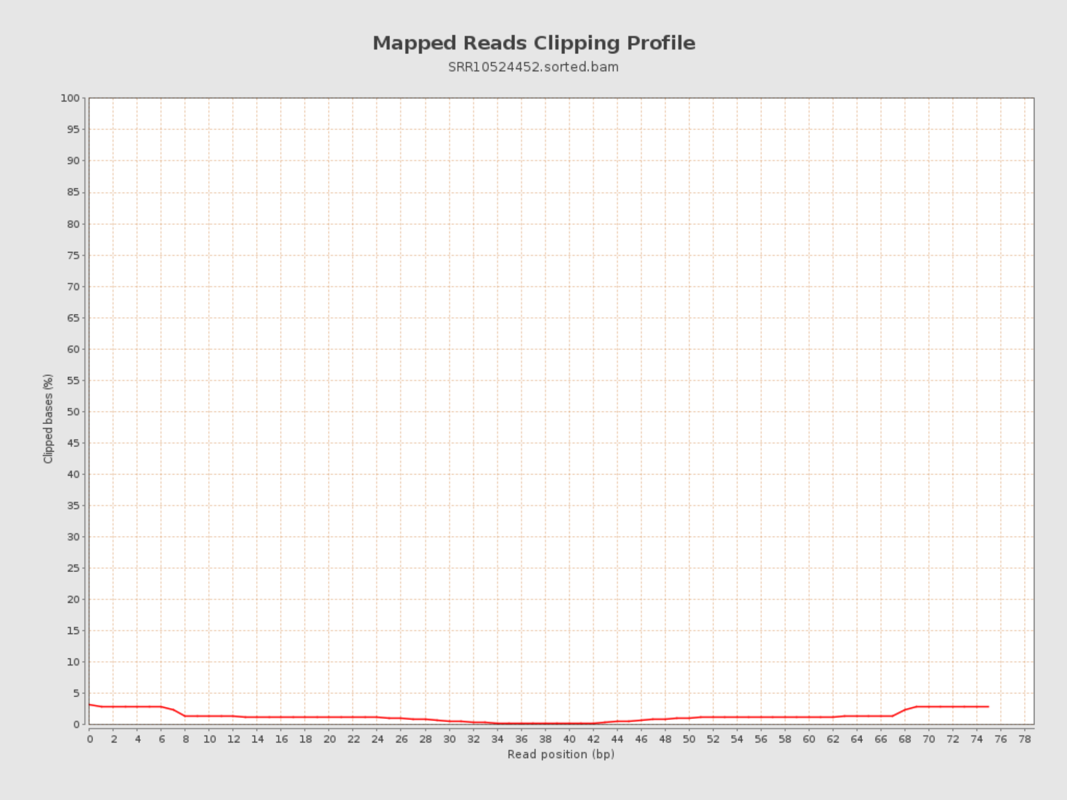
# 8. Results : Mapped Reads Nucleotide Content



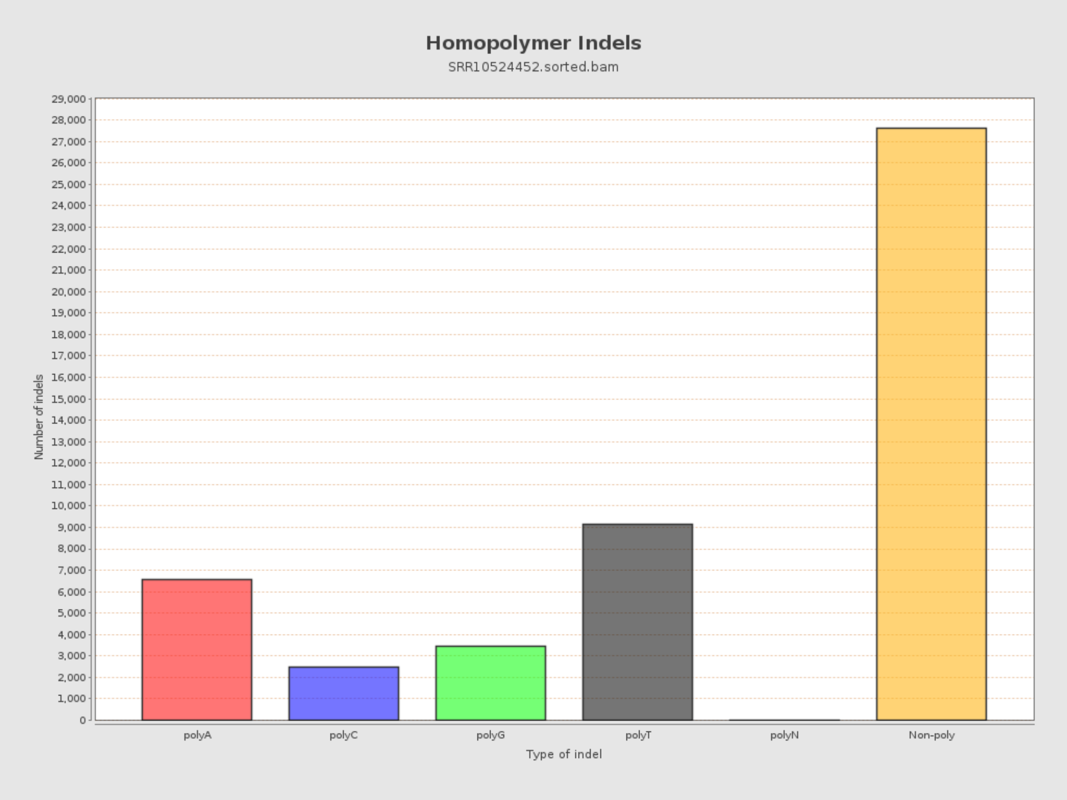
# 9. Results : Mapped Reads GC-content Distribution



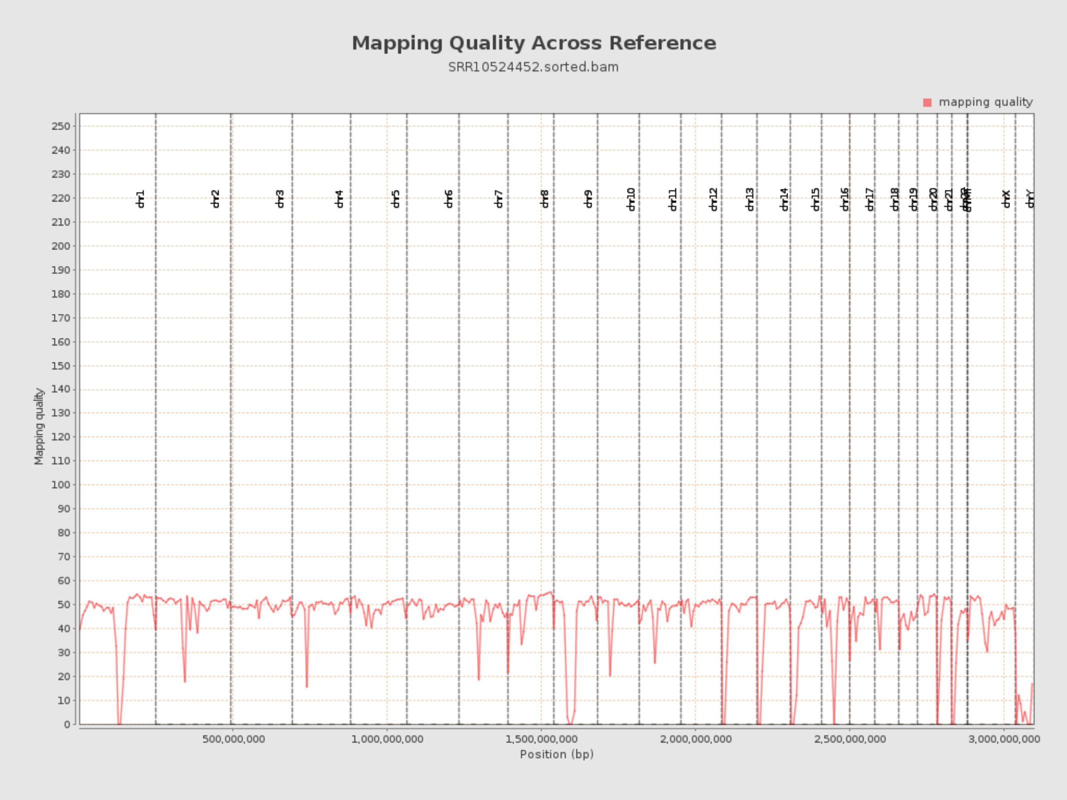
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram