# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/04 05:07:30*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9717084.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_SRR9717084 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9717084.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Sep 04 05:07:29 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9717084.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,856,124 |
| Mapped reads | 1,718,100 / 92.56% |
| Unmapped reads | 138,024 / 7.44% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 27,789 / 1.5% |
| Read min/max/mean length | 30 / 101 / 101.55 |
| Duplicated reads (estimated) | 78,448 / 4.23% |
| Duplication rate | 2.92% |
| Clipped reads | 1,742,073 / 93.86% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 32,723,151 / 24.26% |
| Number/percentage of C's | 27,181,005 / 20.15% |
| Number/percentage of T's | 42,493,118 / 31.5% |
| Number/percentage of G's | 32,476,848 / 24.08% |
| Number/percentage of N's | 7,514 / 0.01% |
| GC Percentage | 44.23% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0436 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4763 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.08 |

## 2.5. Mismatches and indels

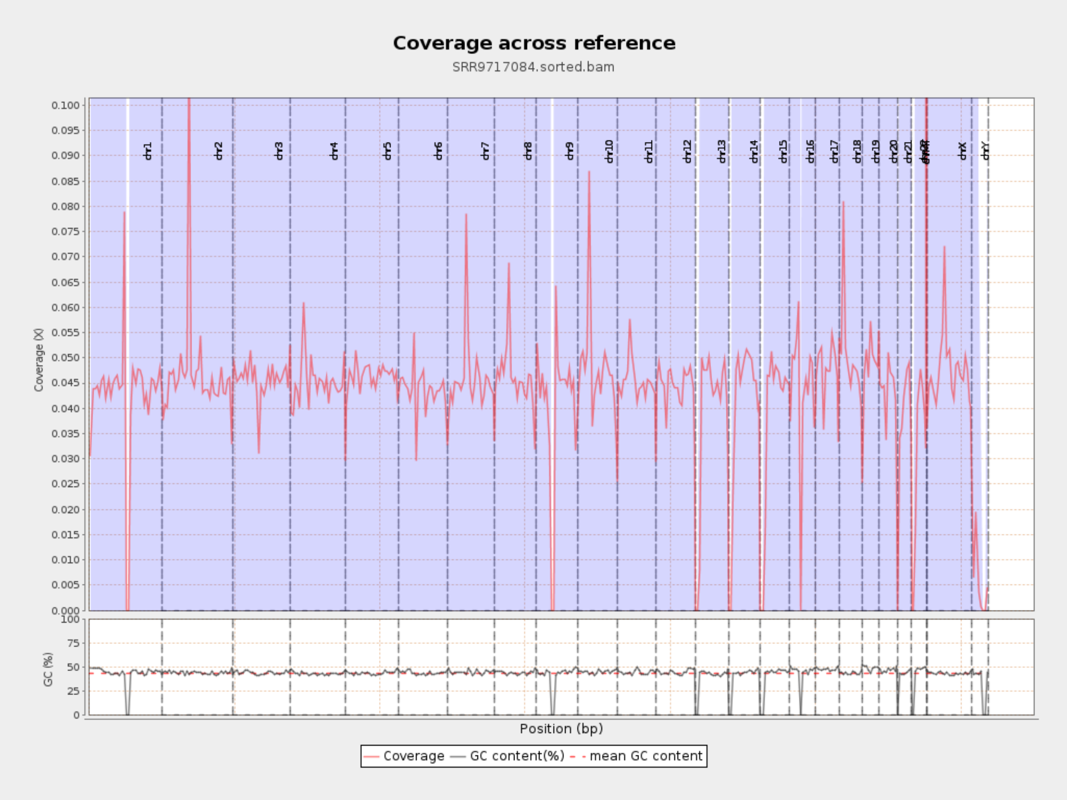
| | |
|---|---|
| General error rate | 0.84% |
| Mismatches | 1,109,462 |
| Insertions | 12,547 |
| Mapped reads with at least one insertion | 0.72% |
| Deletions | 33,794 |
| Mapped reads with at least one deletion | 1.94% |
| Homopolymer indels | 43.38% |

## 2.6. Chromosome stats

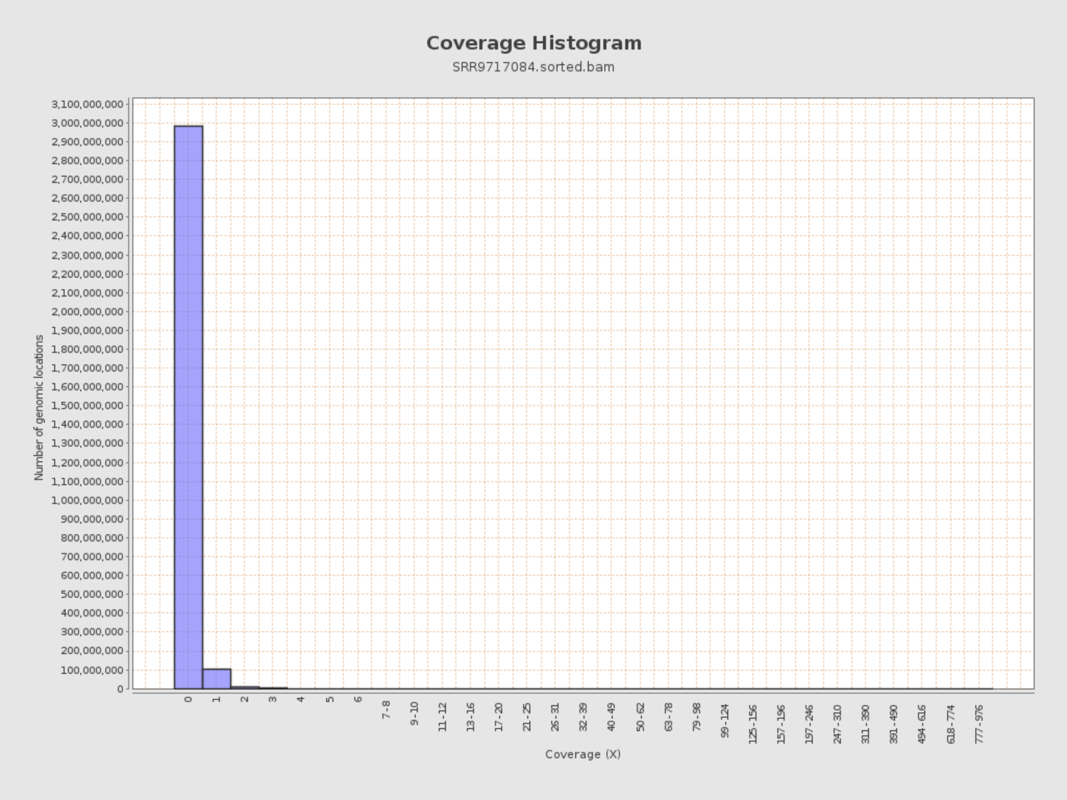
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 10565991 | 0.0424 | 0.7733 |
| chr2 | 243199373 | 11459266 | 0.0471 | 0.7111 |
| chr3 | 198022430 | 9055875 | 0.0457 | 0.2447 |
| chr4 | 191154276 | 8637776 | 0.0452 | 0.2695 |
| chr5 | 180915260 | 8414765 | 0.0465 | 0.2526 |
| chr6 | 171115067 | 7448868 | 0.0435 | 0.2971 |
| chr7 | 159138663 | 7369343 | 0.0463 | 0.569 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6762292 | 0.0462 | 0.6404 |
| chr9 | 141213431 | 5660749 | 0.0401 | 0.5243 |
| chr10 | 135534747 | 6525100 | 0.0481 | 0.4471 |
| chr11 | 135006516 | 6086314 | 0.0451 | 0.4541 |
| chr12 | 133851895 | 5982943 | 0.0447 | 0.2473 |
| chr13 | 115169878 | 4405847 | 0.0383 | 0.2202 |
| chr14 | 107349540 | 4272690 | 0.0398 | 0.3137 |
| chr15 | 102531392 | 3847439 | 0.0375 | 0.2266 |
| chr16 | 90354753 | 3914847 | 0.0433 | 0.2813 |
| chr17 | 81195210 | 3832876 | 0.0472 | 0.2824 |
| chr18 | 78077248 | 3994436 | 0.0512 | 1.0011 |
| chr19 | 59128983 | 2899925 | 0.049 | 0.5957 |
| chr20 | 63025520 | 2726445 | 0.0433 | 0.2525 |
| chr21 | 48129895 | 1789827 | 0.0372 | 0.2442 |
| chr22 | 51304566 | 1509240 | 0.0294 | 0.1948 |
| chrMT | 16571 | 34869 | 2.1042 | 2.1448 |
| chrX | 155270560 | 7388418 | 0.0476 | 0.3536 |
| chrY | 59373566 | 354223 | 0.006 | 0.1657 |

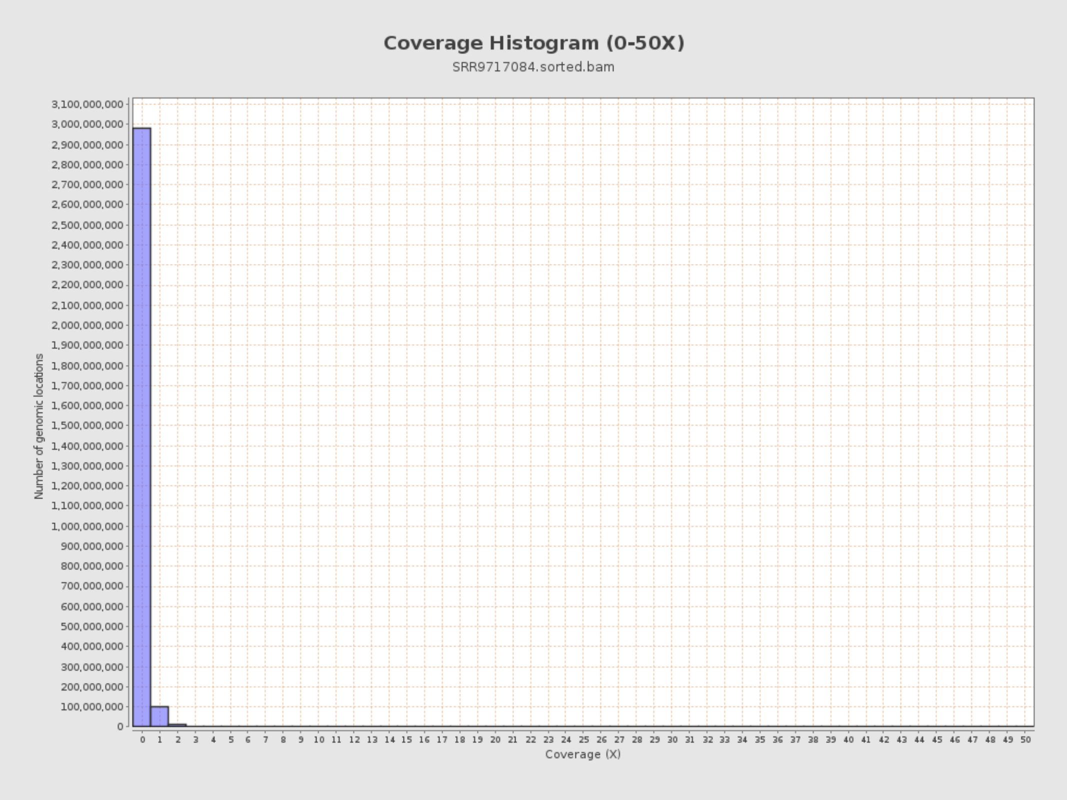
# 3. Results : Coverage across reference



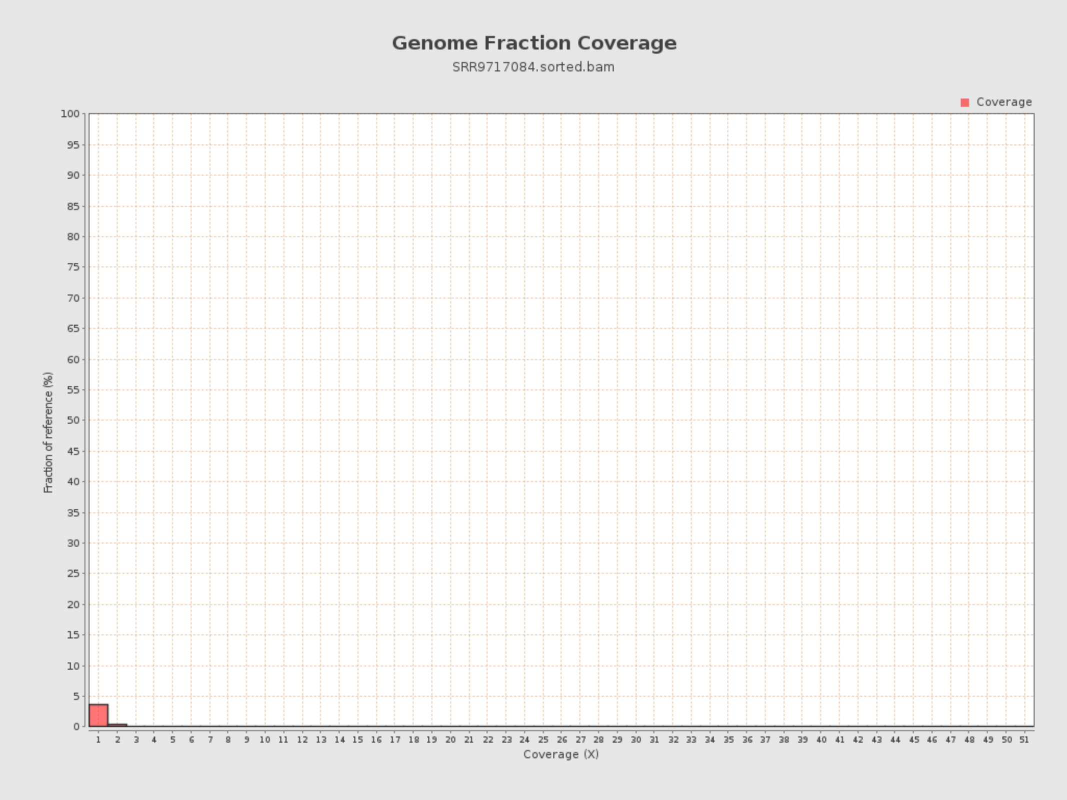
# 4. Results : Coverage Histogram



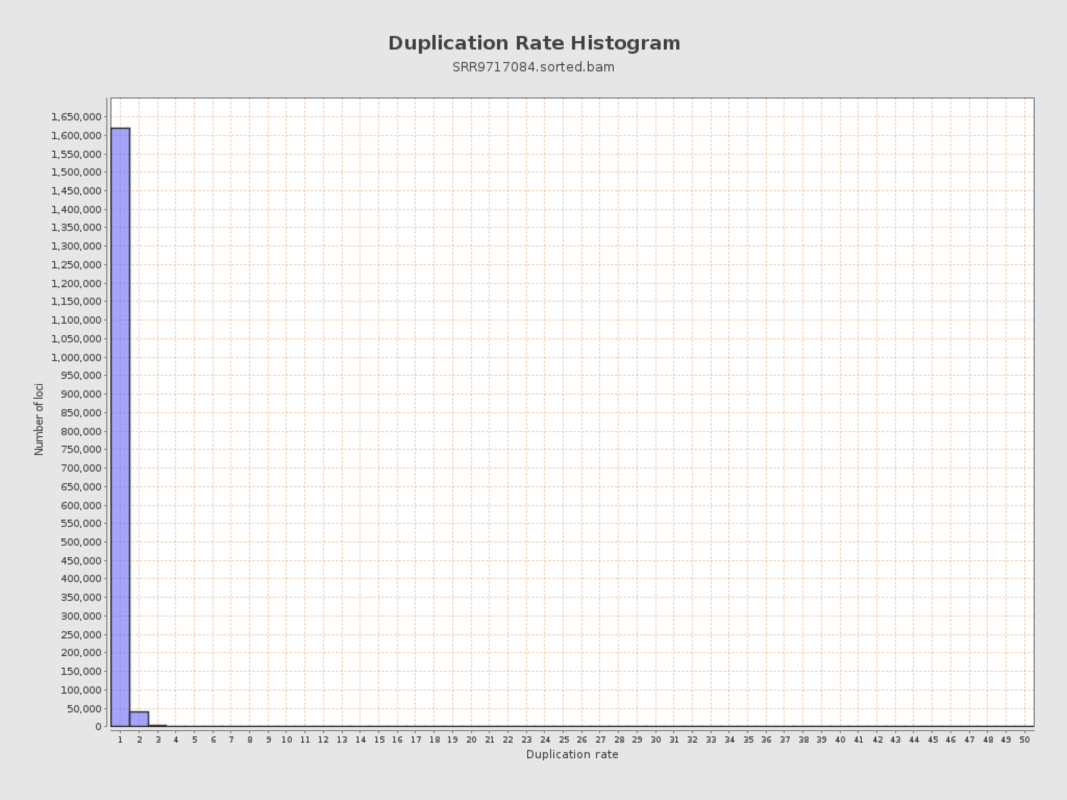
# 5. Results : Coverage Histogram (0-50X)



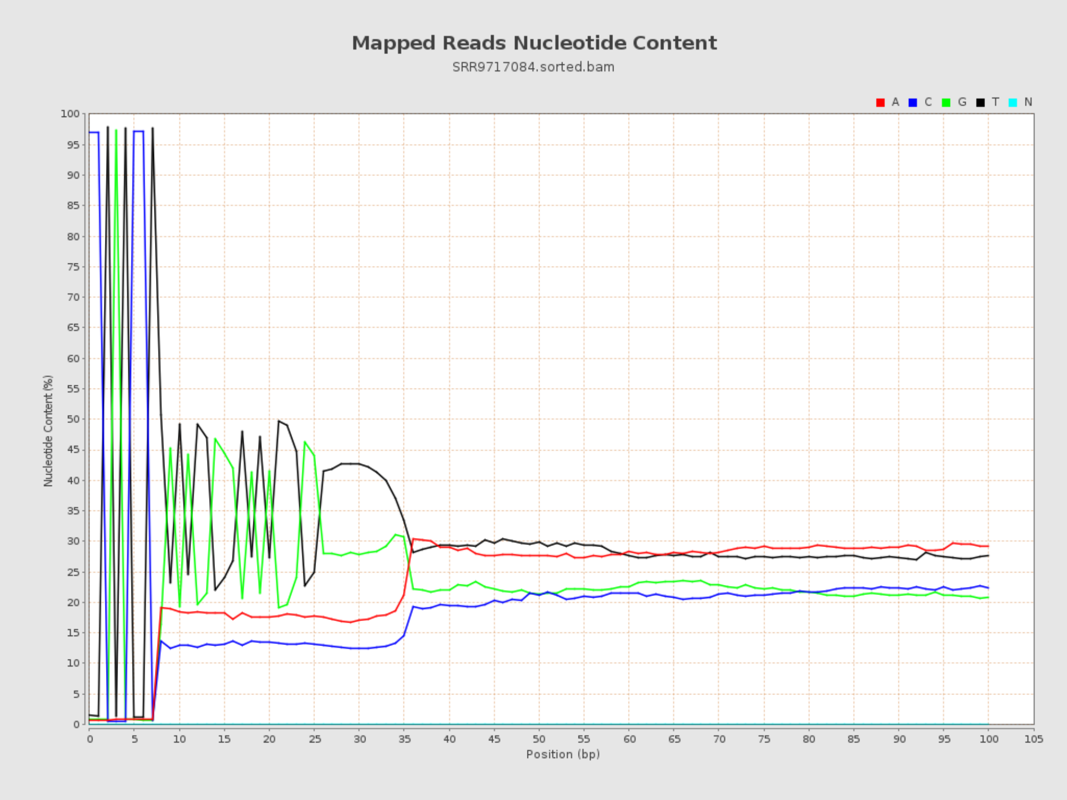
# 6. Results : Genome Fraction Coverage



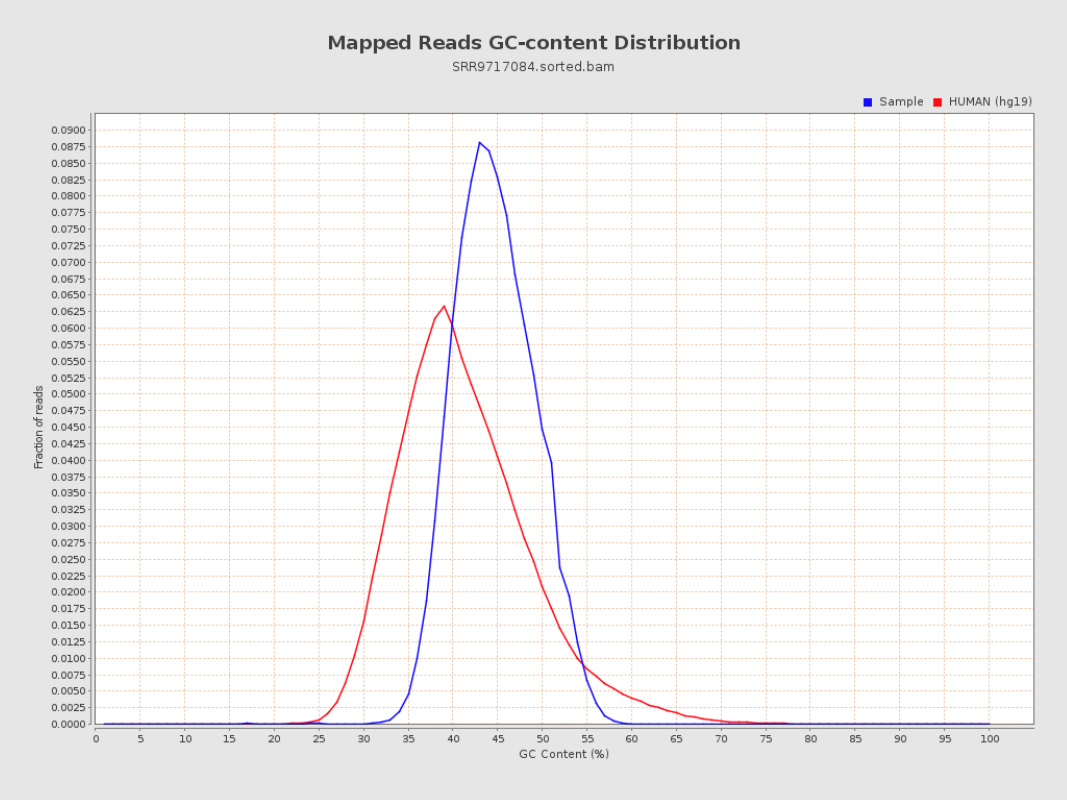
# 7. Results : Duplication Rate Histogram



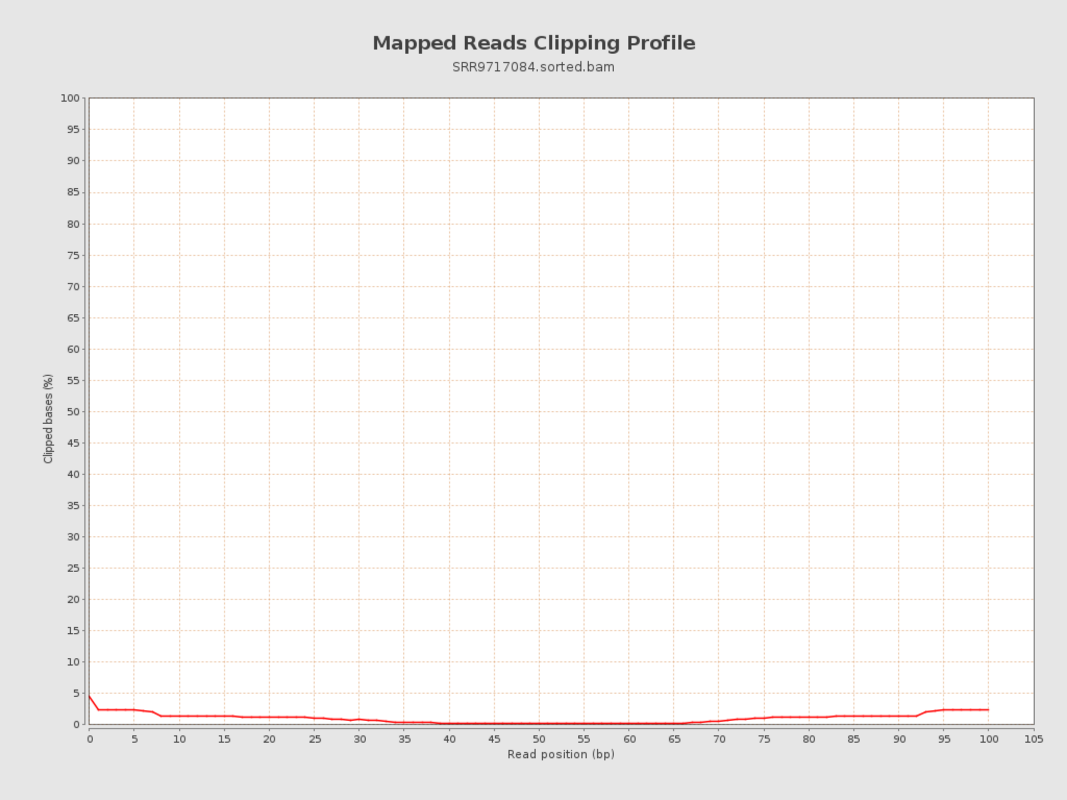
# 8. Results : Mapped Reads Nucleotide Content



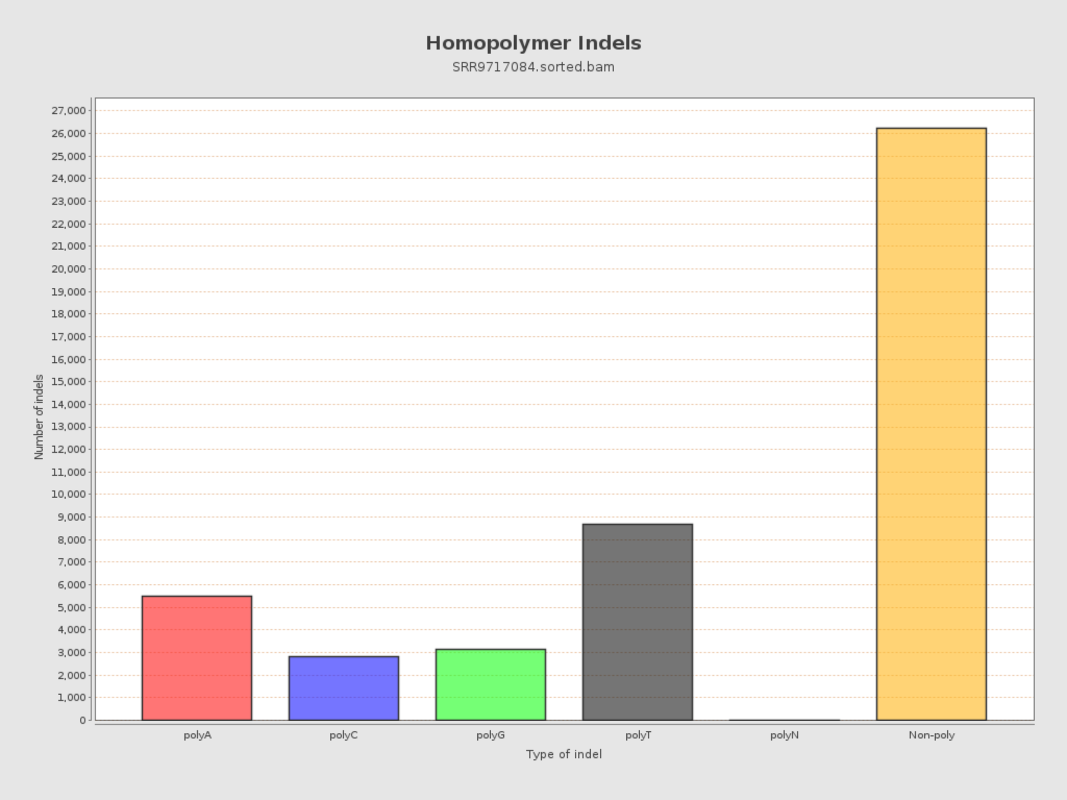
# 9. Results : Mapped Reads GC-content Distribution



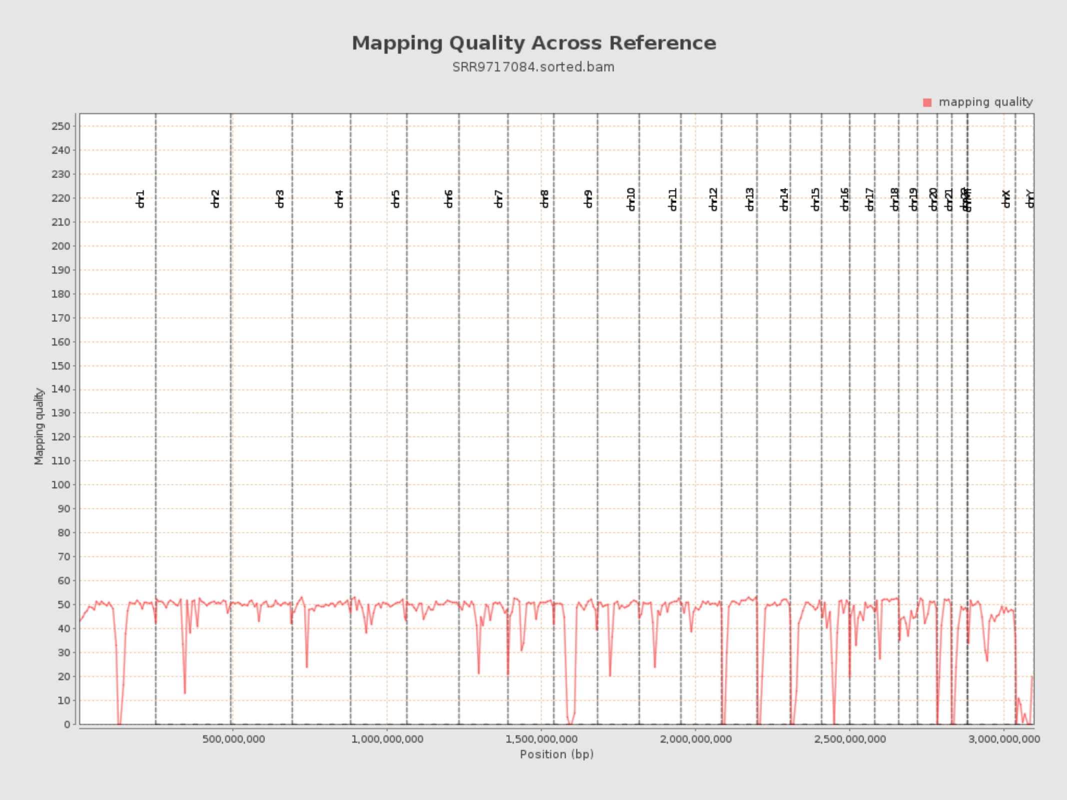
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram