# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 15:07:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716854.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_SRR9716854 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716854.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 15:07:48 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716854.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,473,470 |
| Mapped reads | 2,320,489 / 93.82% |
| Unmapped reads | 152,981 / 6.18% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 47,696 / 1.93% |
| Read min/max/mean length | 30 / 101 / 101.7 |
| Duplicated reads (estimated) | 145,212 / 5.87% |
| Duplication rate | 4.82% |
| Clipped reads | 2,363,161 / 95.54% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 43,285,748 / 24.02% |
| Number/percentage of C's | 35,603,594 / 19.76% |
| Number/percentage of T's | 55,229,337 / 30.65% |
| Number/percentage of G's | 46,095,694 / 25.58% |
| Number/percentage of N's | 6,338 / 0% |
| GC Percentage | 45.33% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0582 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4625 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.6 |

## 2.5. Mismatches and indels

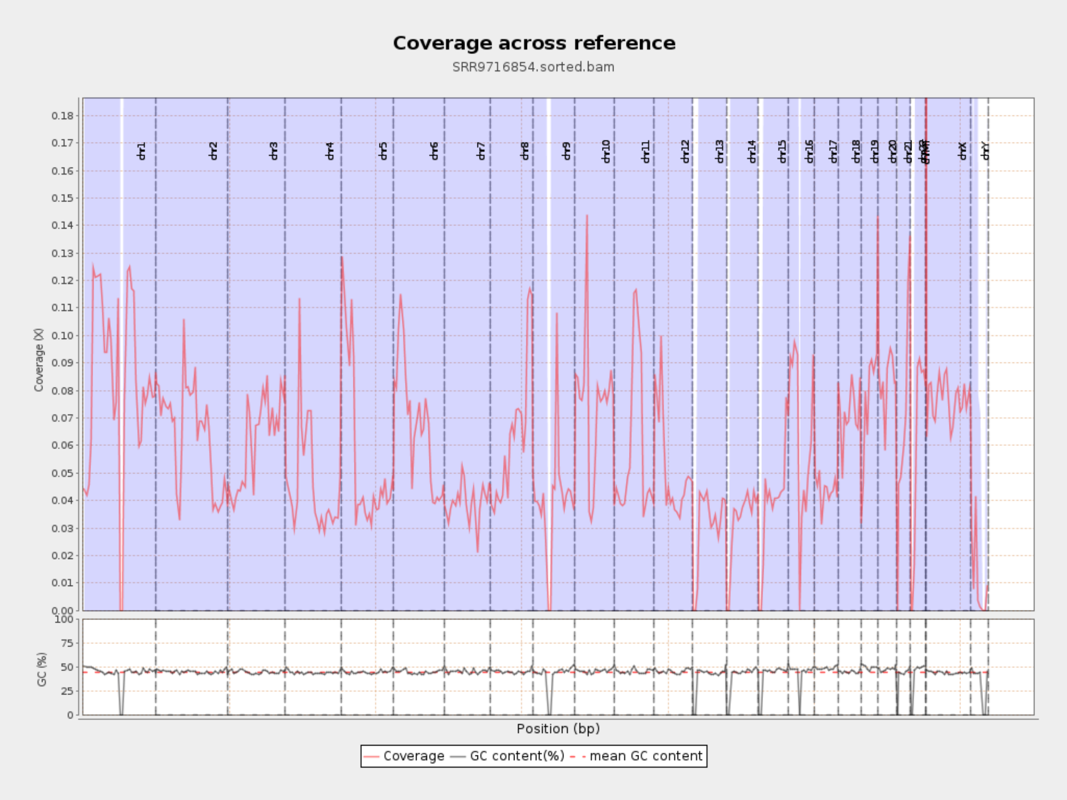
| | |
|---|---|
| General error rate | 0.68% |
| Mismatches | 1,186,509 |
| Insertions | 16,196 |
| Mapped reads with at least one insertion | 0.69% |
| Deletions | 34,144 |
| Mapped reads with at least one deletion | 1.44% |
| Homopolymer indels | 37.91% |

## 2.6. Chromosome stats

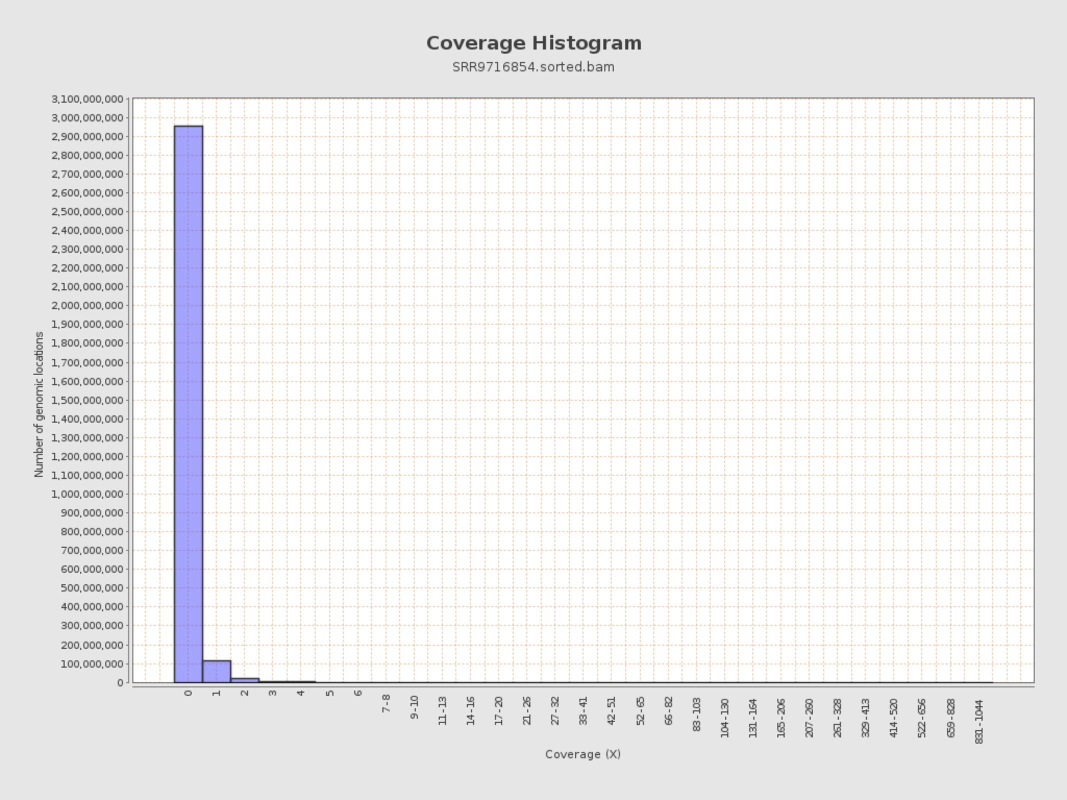
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 20918699 | 0.0839 | 0.9534 |
| chr2 | 243199373 | 15709045 | 0.0646 | 0.4858 |
| chr3 | 198022430 | 12176937 | 0.0615 | 0.3078 |
| chr4 | 191154276 | 8770541 | 0.0459 | 0.4234 |
| chr5 | 180915260 | 10257847 | 0.0567 | 0.2954 |
| chr6 | 171115067 | 11504028 | 0.0672 | 0.3388 |
| chr7 | 159138663 | 6229377 | 0.0391 | 0.3389 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 9345874 | 0.0639 | 0.4107 |
| chr9 | 141213431 | 5642819 | 0.04 | 0.3233 |
| chr10 | 135534747 | 10135850 | 0.0748 | 0.6883 |
| chr11 | 135006516 | 7976564 | 0.0591 | 0.381 |
| chr12 | 133851895 | 7038549 | 0.0526 | 0.2821 |
| chr13 | 115169878 | 3553238 | 0.0309 | 0.2114 |
| chr14 | 107349540 | 3474821 | 0.0324 | 0.2461 |
| chr15 | 102531392 | 3878811 | 0.0378 | 0.2358 |
| chr16 | 90354753 | 5710645 | 0.0632 | 0.3423 |
| chr17 | 81195210 | 3576826 | 0.0441 | 0.3037 |
| chr18 | 78077248 | 5559954 | 0.0712 | 0.5109 |
| chr19 | 59128983 | 4651153 | 0.0787 | 0.6799 |
| chr20 | 63025520 | 5228869 | 0.083 | 0.387 |
| chr21 | 48129895 | 3347055 | 0.0695 | 0.4232 |
| chr22 | 51304566 | 3036379 | 0.0592 | 0.3237 |
| chrMT | 16571 | 13003 | 0.7847 | 1.1399 |
| chrX | 155270560 | 11917704 | 0.0768 | 0.3631 |
| chrY | 59373566 | 638295 | 0.0108 | 0.4053 |

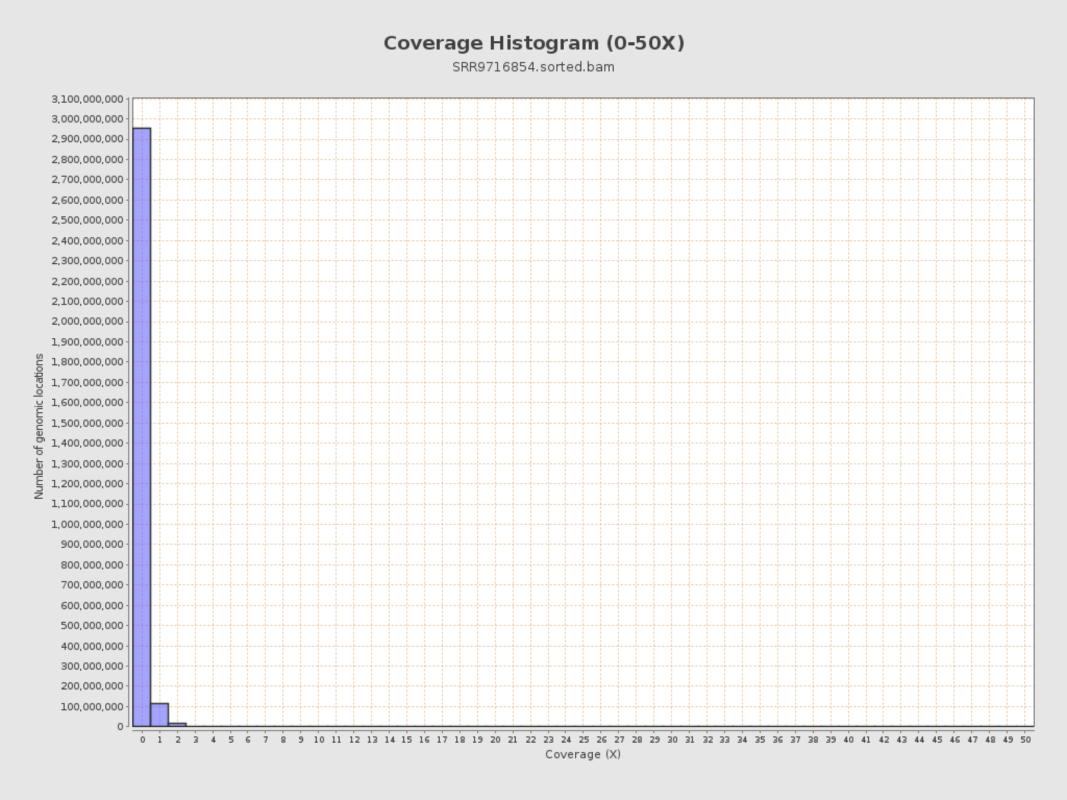
# 3. Results : Coverage across reference



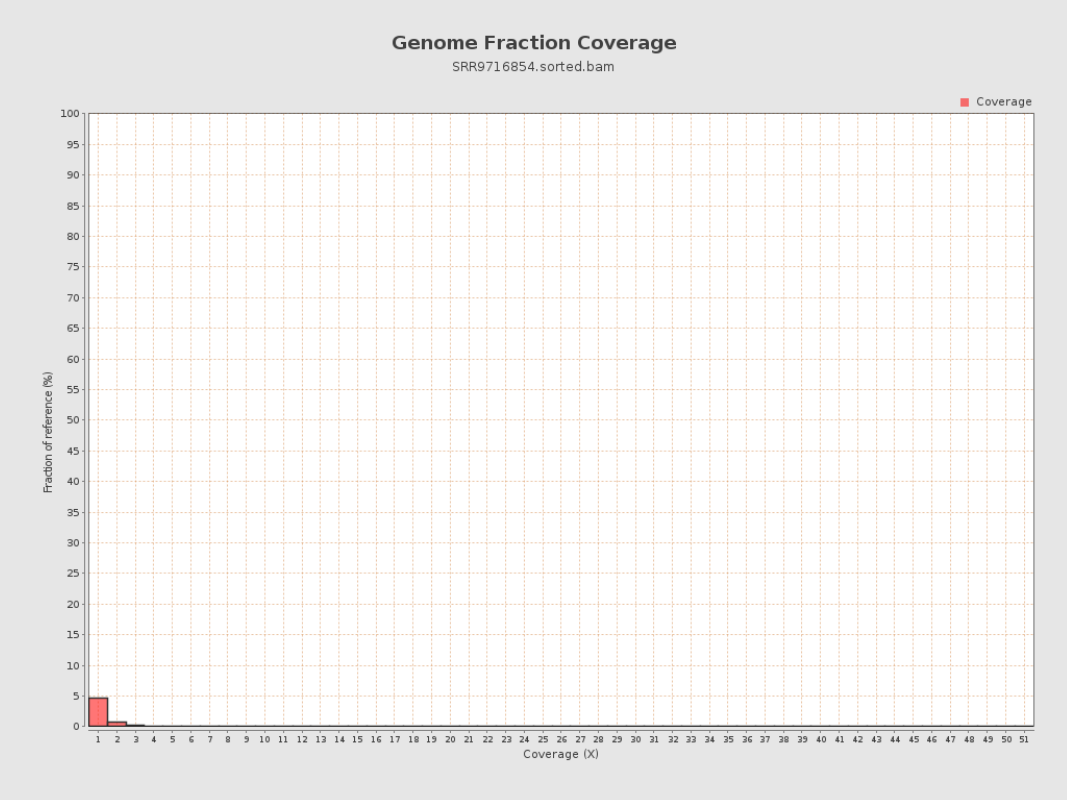
# 4. Results : Coverage Histogram



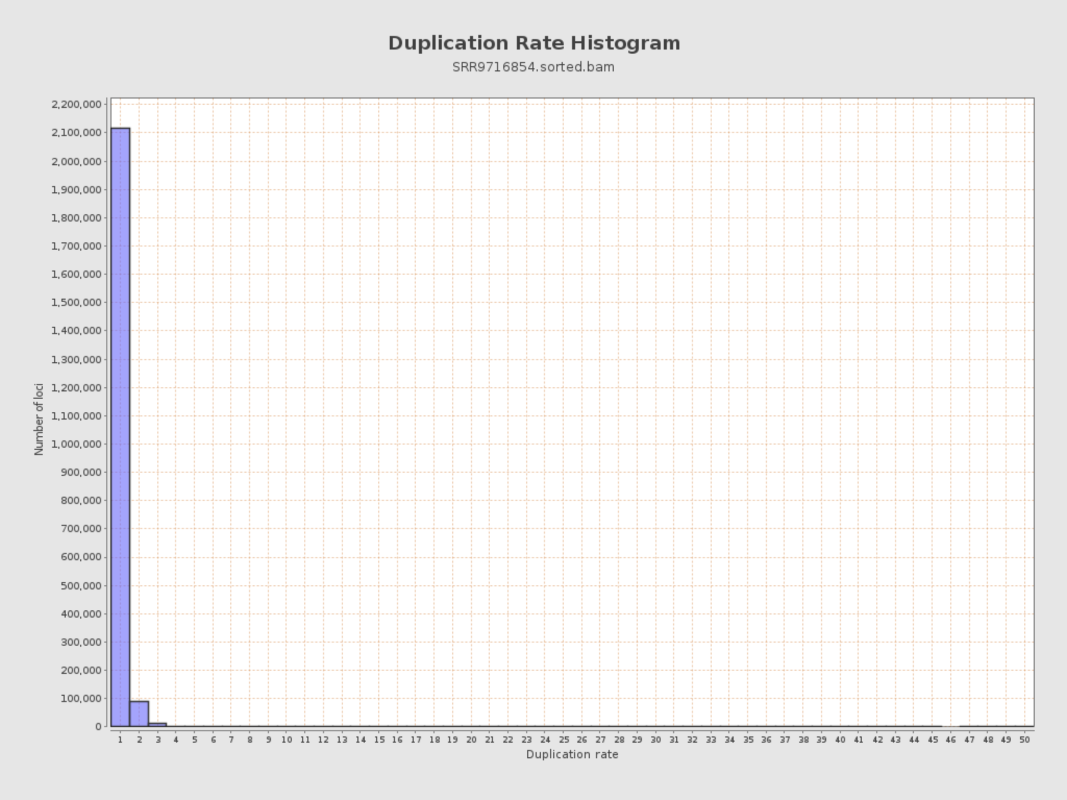
# 5. Results : Coverage Histogram (0-50X)



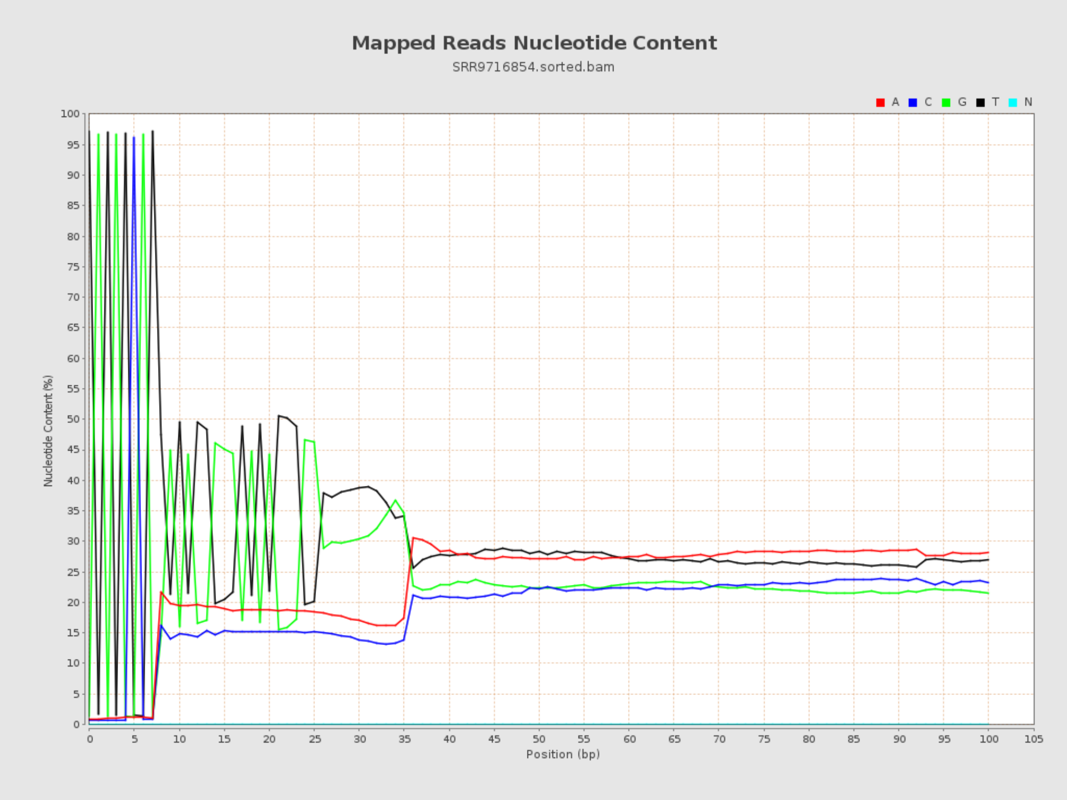
# 6. Results : Genome Fraction Coverage



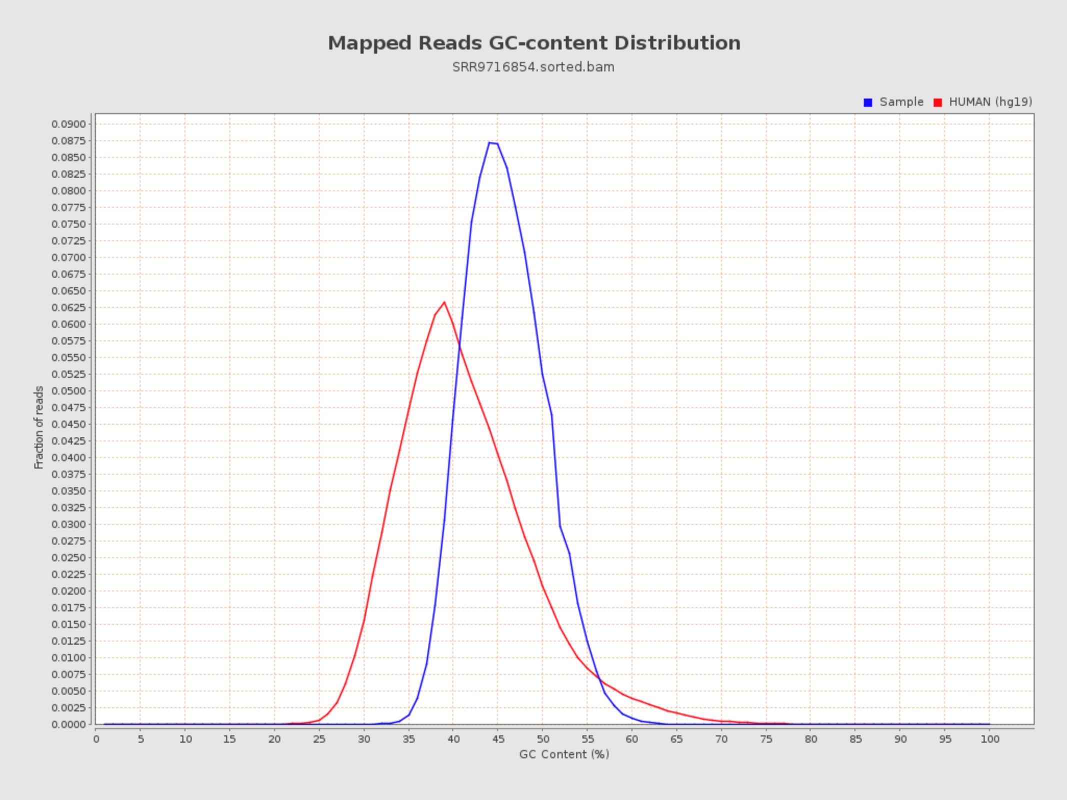
# 7. Results : Duplication Rate Histogram



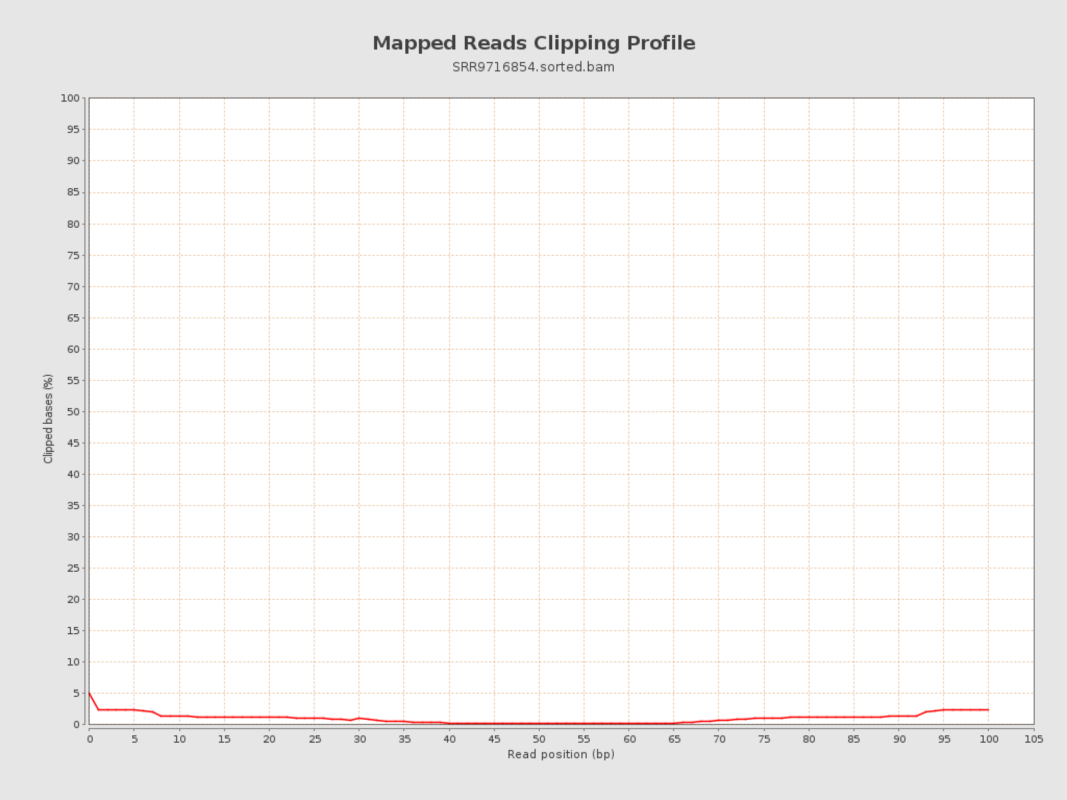
# 8. Results : Mapped Reads Nucleotide Content



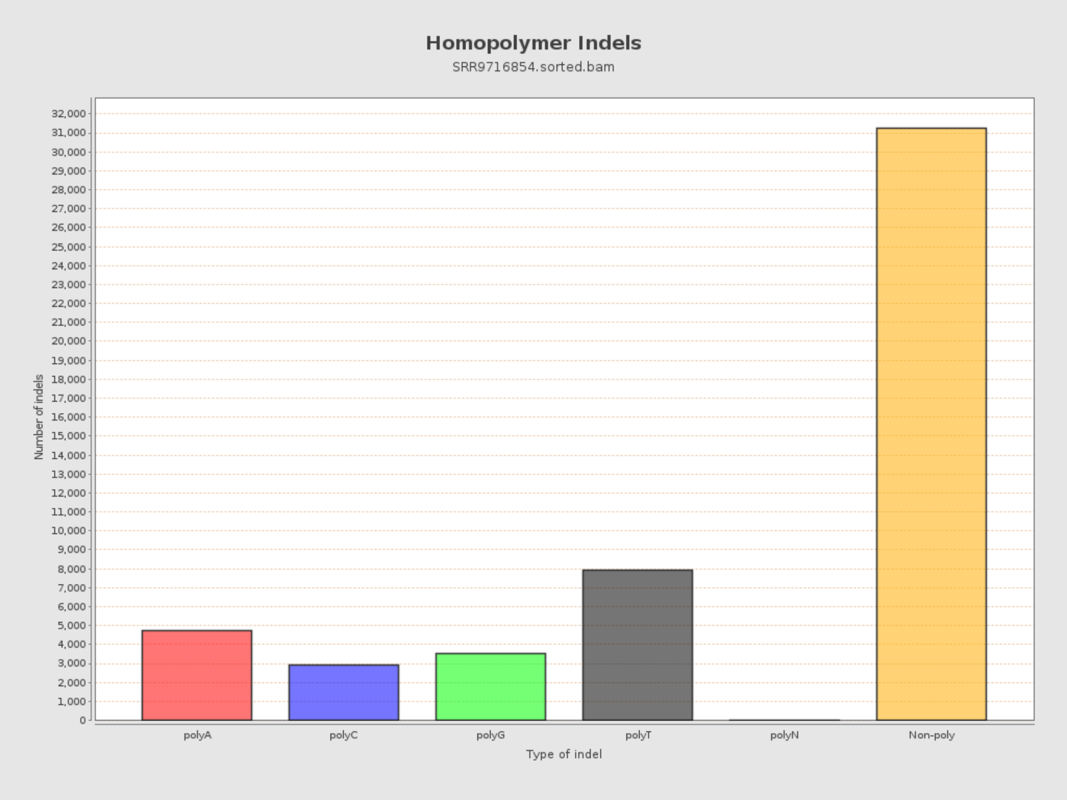
# 9. Results : Mapped Reads GC-content Distribution



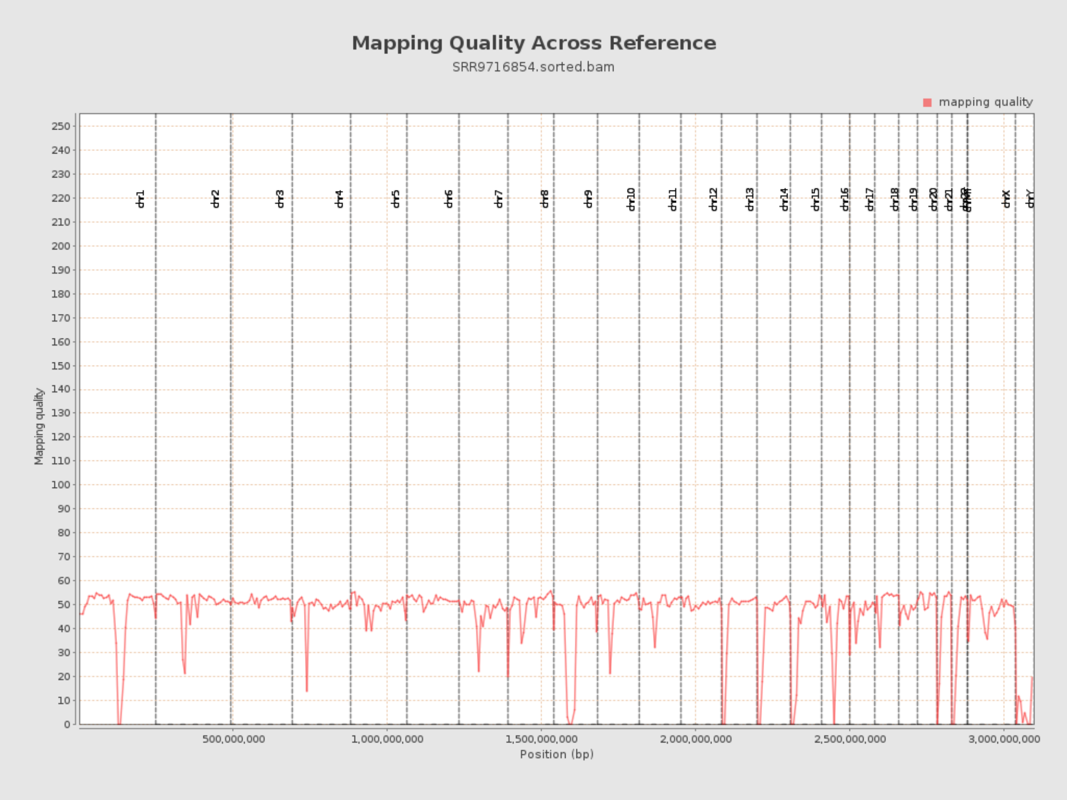
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram