# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 22:43:35*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082979.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_SRR3082979 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082979.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Aug 24 22:43:33 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3082979.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,555,530 |
| Mapped reads | 2,849,468 / 80.14% |
| Unmapped reads | 706,062 / 19.86% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 18,726 / 0.53% |
| Read min/max/mean length | 30 / 76 / 76.18 |
| Duplicated reads (estimated) | 105,198 / 2.96% |
| Duplication rate | 2.96% |
| Clipped reads | 1,071,097 / 30.12% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 56,739,207 / 28.95% |
| Number/percentage of C's | 36,202,348 / 18.47% |
| Number/percentage of T's | 62,700,871 / 32% |
| Number/percentage of G's | 40,301,298 / 20.57% |
| Number/percentage of N's | 19,813 / 0.01% |
| GC Percentage | 39.04% |

## 2.3. Coverage

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

| | |
|---|---|
| Standard Deviation | 0.4394 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.14 |

## 2.5. Mismatches and indels

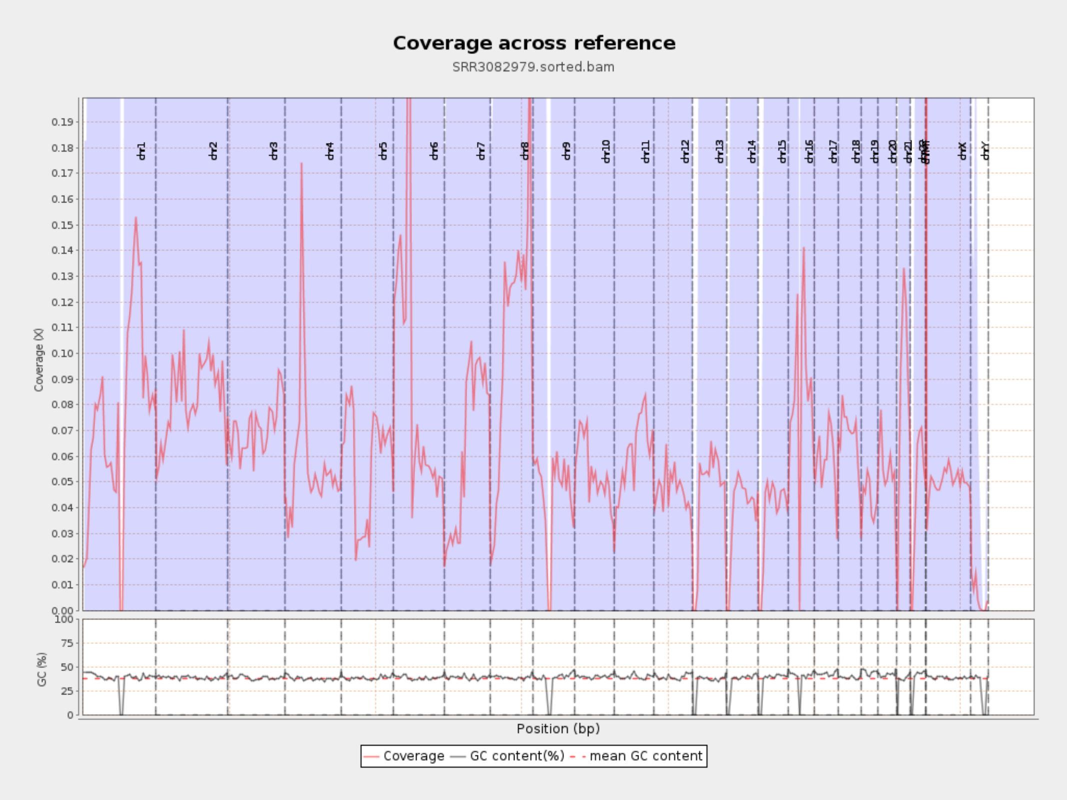
| | |
|---|---|
| General error rate | 0.94% |
| Mismatches | 1,818,118 |
| Insertions | 16,588 |
| Mapped reads with at least one insertion | 0.58% |
| Deletions | 43,530 |
| Mapped reads with at least one deletion | 1.51% |
| Homopolymer indels | 48.07% |

## 2.6. Chromosome stats

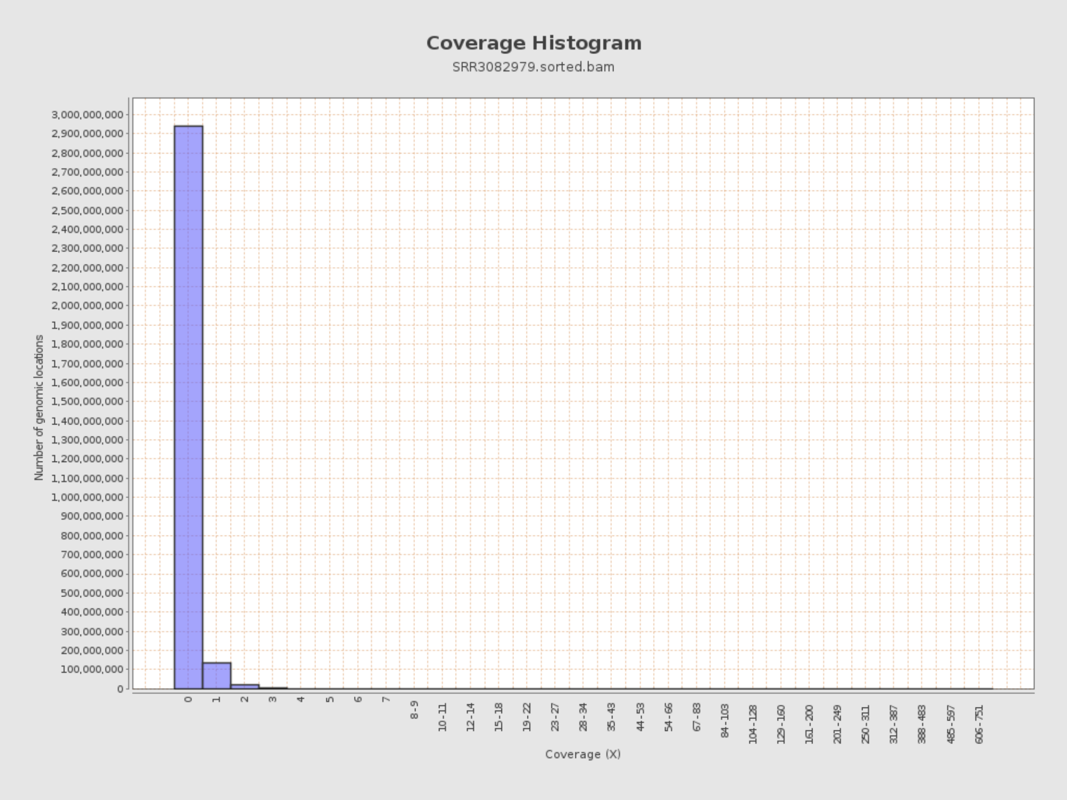
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 18976049 | 0.0761 | 0.6962 |
| chr2 | 243199373 | 20237003 | 0.0832 | 0.5359 |
| chr3 | 198022430 | 14033825 | 0.0709 | 0.3139 |
| chr4 | 191154276 | 11277007 | 0.059 | 0.2979 |
| chr5 | 180915260 | 10433453 | 0.0577 | 0.2851 |
| chr6 | 171115067 | 15130519 | 0.0884 | 0.493 |
| chr7 | 159138663 | 10199141 | 0.0641 | 0.3872 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 15989735 | 0.1092 | 0.6208 |
| chr9 | 141213431 | 6394270 | 0.0453 | 0.3904 |
| chr10 | 135534747 | 7386915 | 0.0545 | 0.3659 |
| chr11 | 135006516 | 8249928 | 0.0611 | 0.3793 |
| chr12 | 133851895 | 6255283 | 0.0467 | 0.2617 |
| chr13 | 115169878 | 5214375 | 0.0453 | 0.2508 |
| chr14 | 107349540 | 4167526 | 0.0388 | 0.2879 |
| chr15 | 102531392 | 3725690 | 0.0363 | 0.2233 |
| chr16 | 90354753 | 7504722 | 0.0831 | 0.3943 |
| chr17 | 81195210 | 4815382 | 0.0593 | 0.3349 |
| chr18 | 78077248 | 5368148 | 0.0688 | 0.9669 |
| chr19 | 59128983 | 2601471 | 0.044 | 0.5204 |
| chr20 | 63025520 | 3523077 | 0.0559 | 0.3038 |
| chr21 | 48129895 | 4024662 | 0.0836 | 0.3543 |
| chr22 | 51304566 | 2309184 | 0.045 | 0.2489 |
| chrMT | 16571 | 134352 | 8.1077 | 6.1588 |
| chrX | 155270560 | 7774704 | 0.0501 | 0.2982 |
| chrY | 59373566 | 311701 | 0.0052 | 0.1098 |

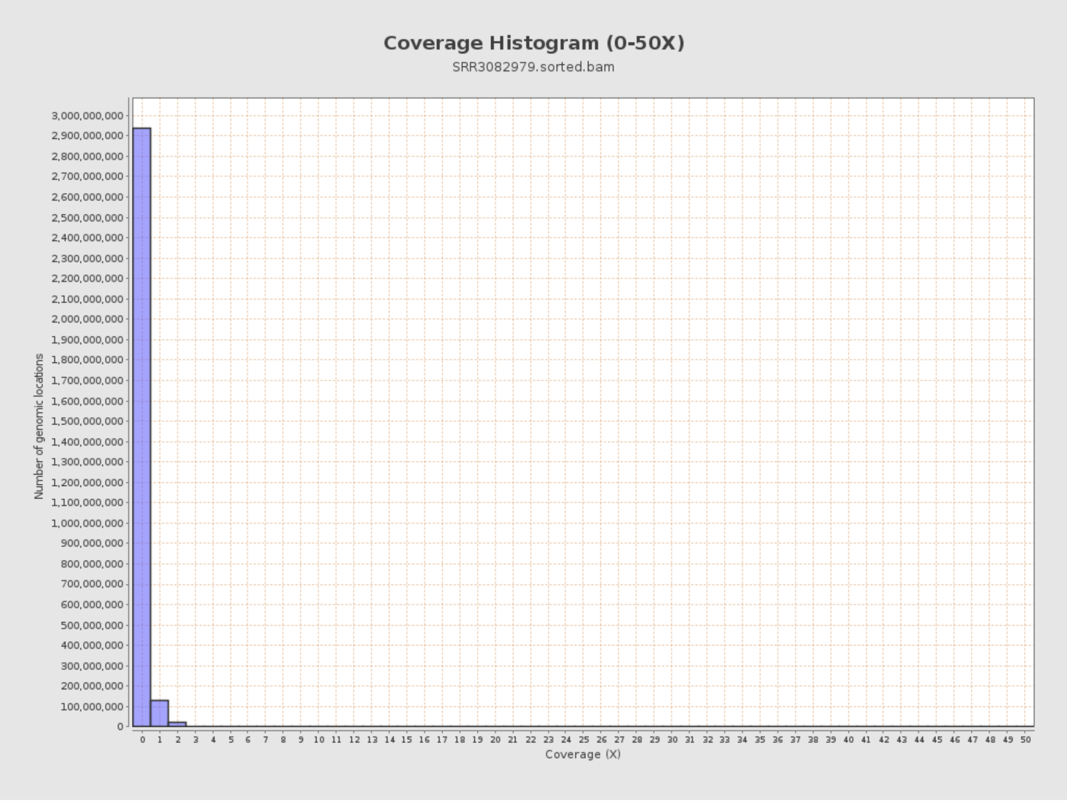
# 3. Results : Coverage across reference



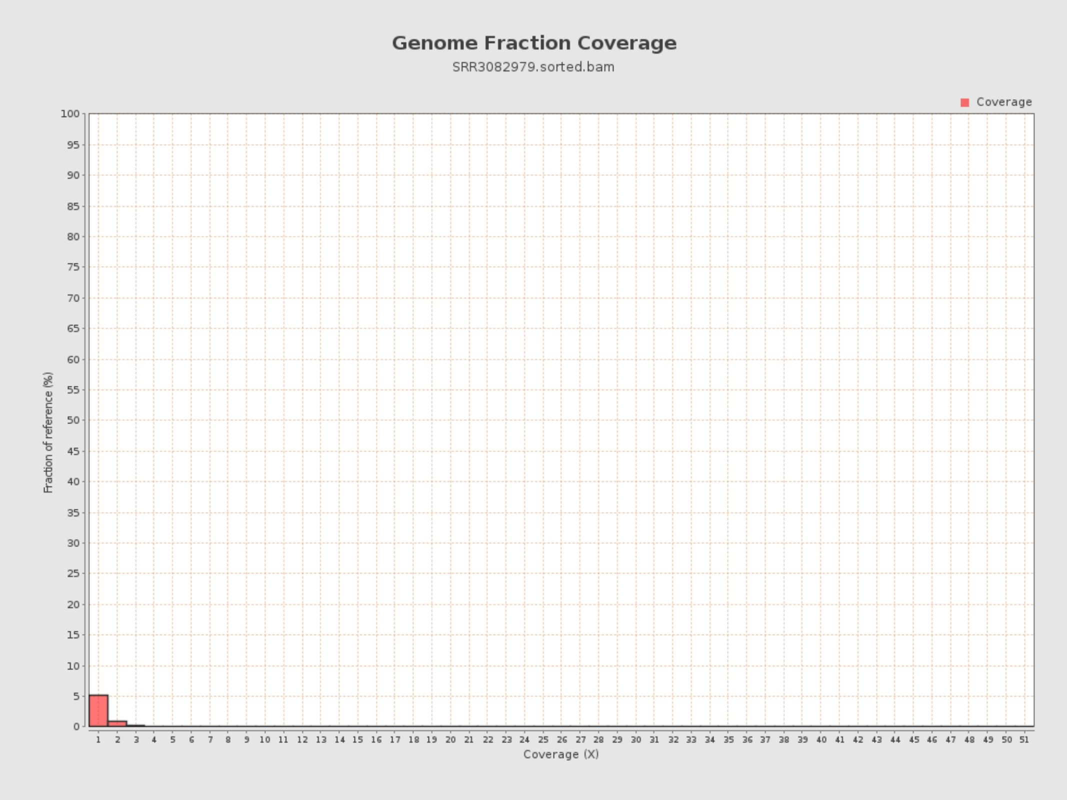
# 4. Results : Coverage Histogram



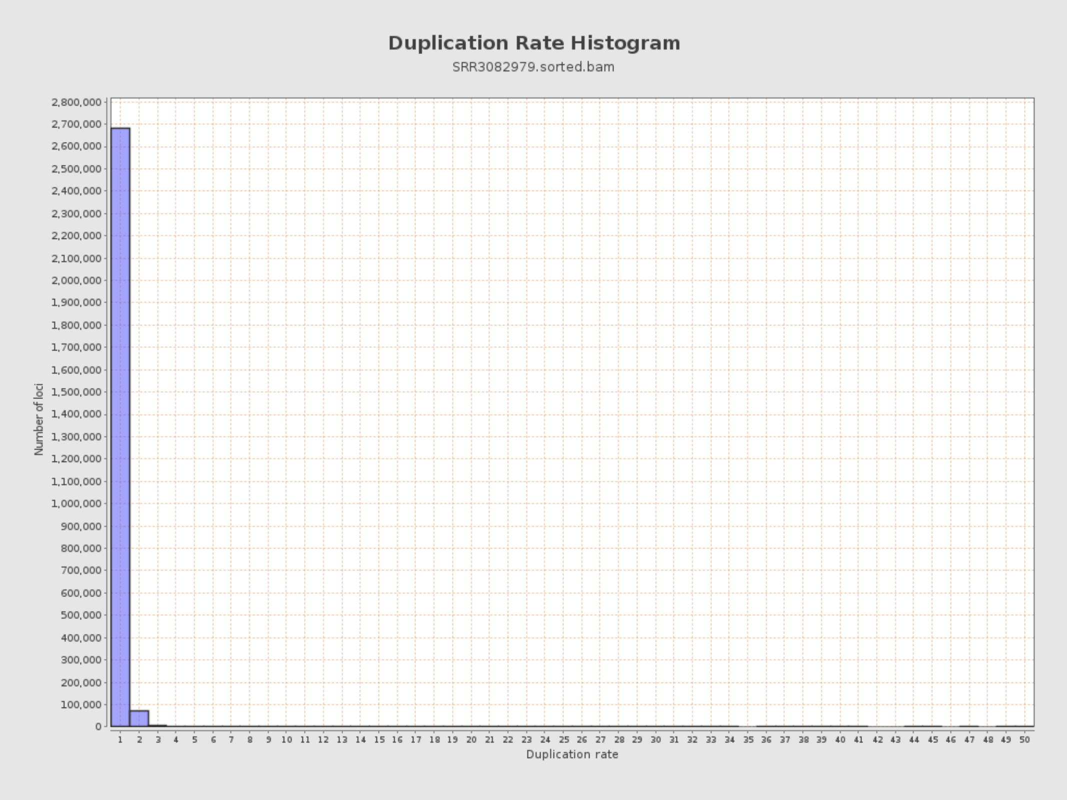
# 5. Results : Coverage Histogram (0-50X)



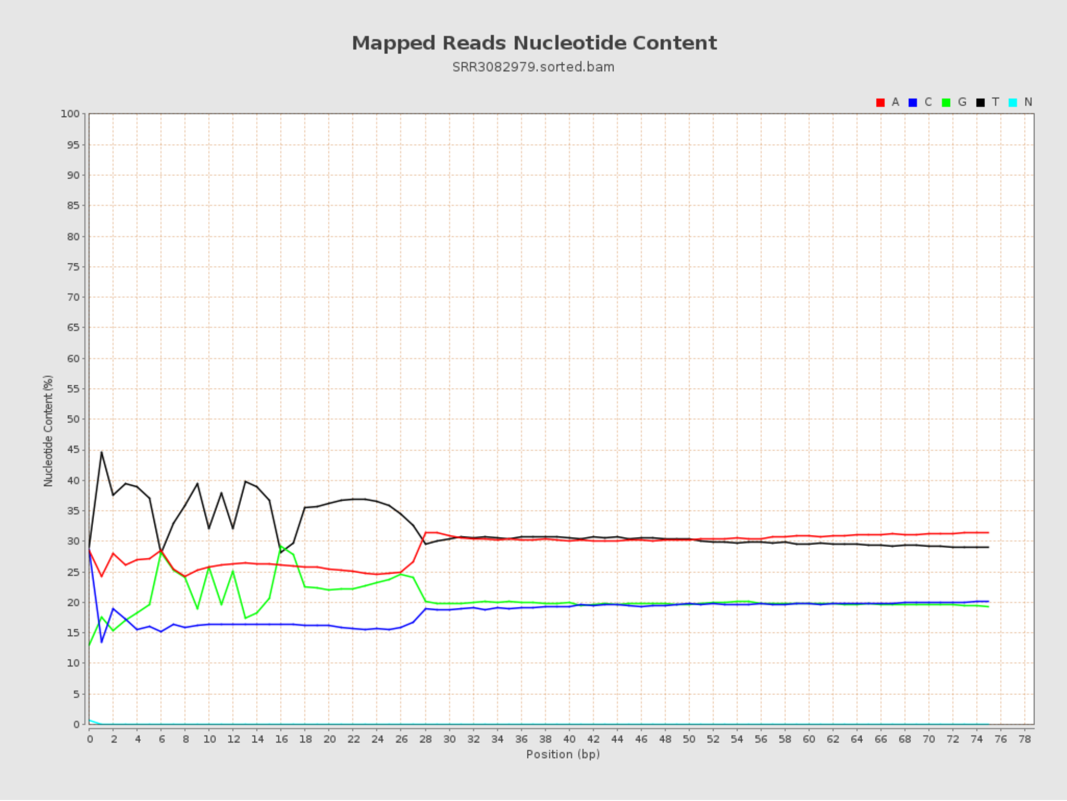
# 6. Results : Genome Fraction Coverage



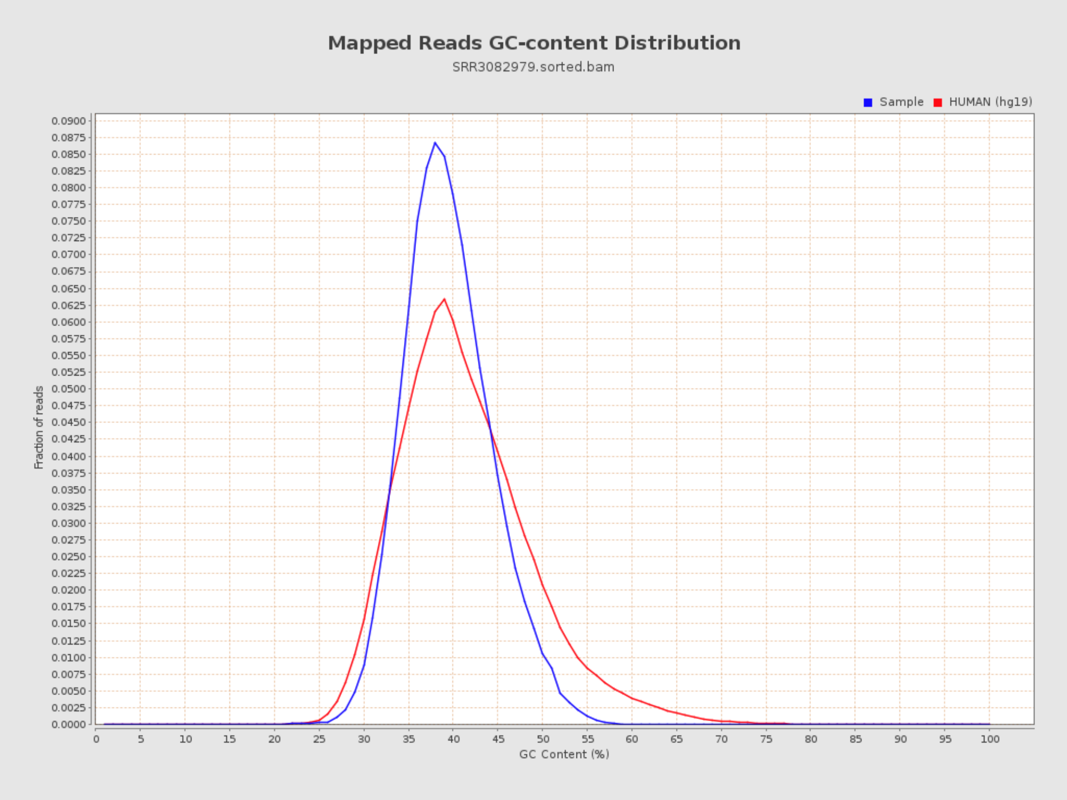
# 7. Results : Duplication Rate Histogram



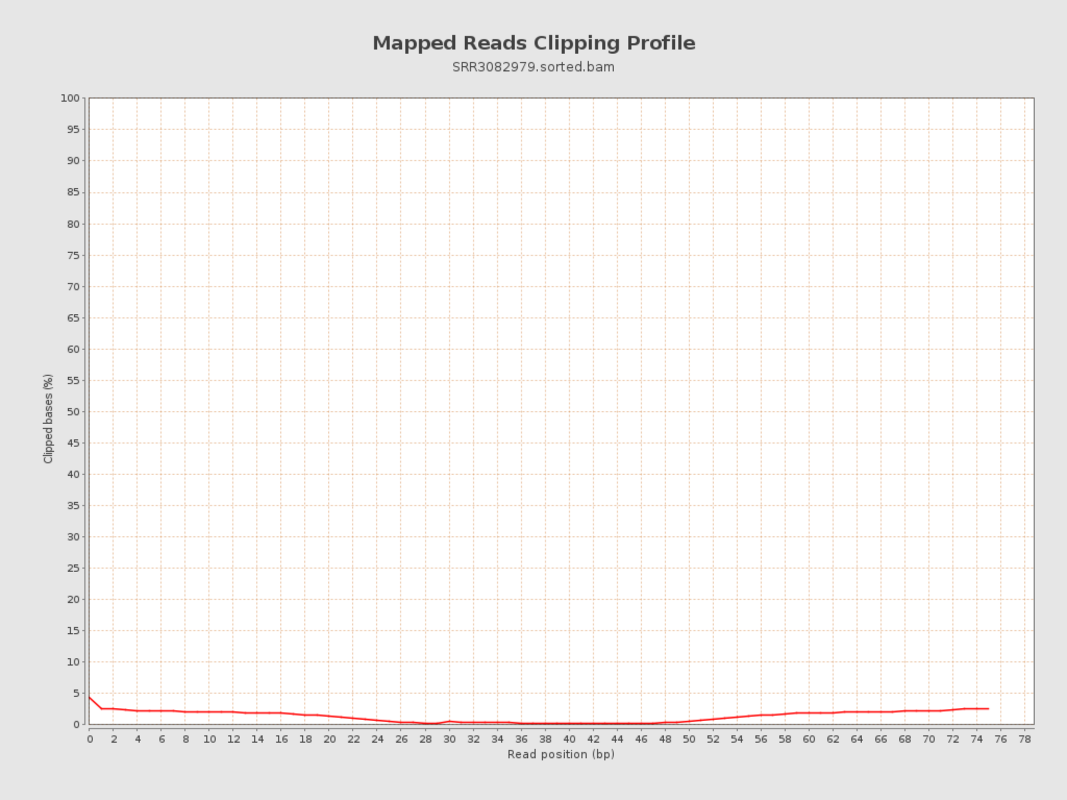
# 8. Results : Mapped Reads Nucleotide Content



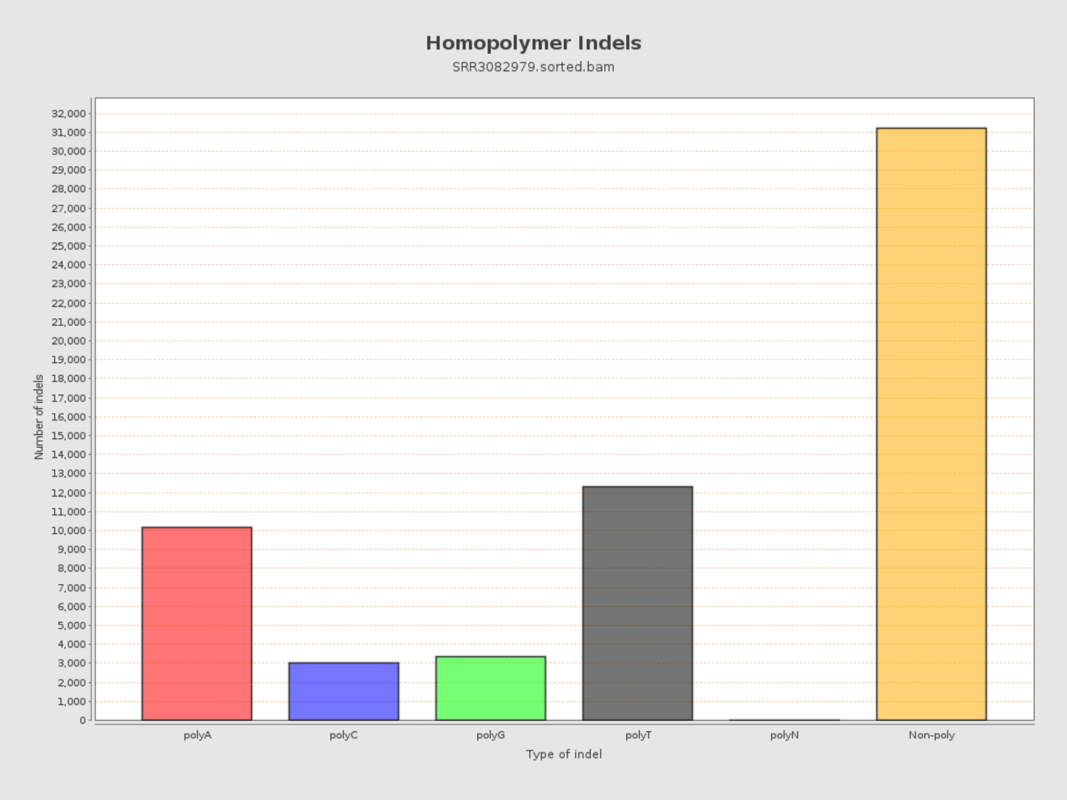
# 9. Results : Mapped Reads GC-content Distribution



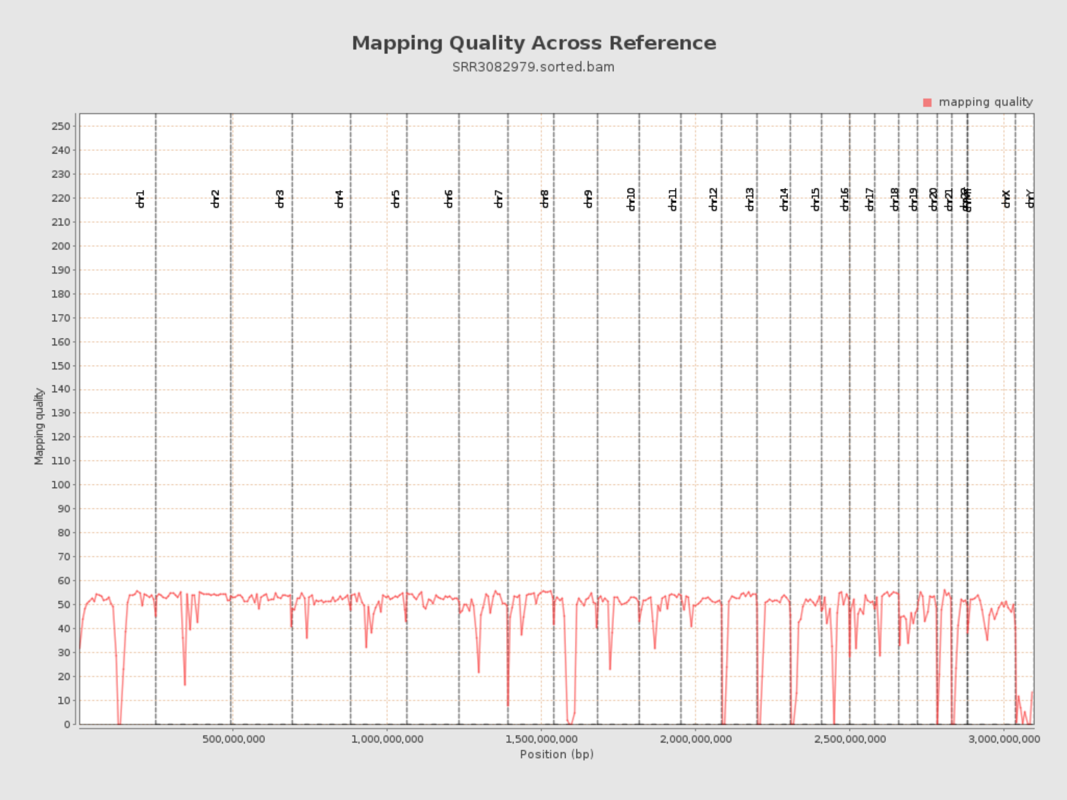
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram