# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 10:24:58*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081925.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_SRR3081925 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081925.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Aug 24 10:24:57 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3081925.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,838,242 |
| Mapped reads | 2,607,072 / 91.86% |
| Unmapped reads | 231,170 / 8.14% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 17,336 / 0.61% |
| Read min/max/mean length | 30 / 76 / 76.21 |
| Duplicated reads (estimated) | 135,012 / 4.76% |
| Duplication rate | 3.64% |
| Clipped reads | 1,045,031 / 36.82% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 49,298,954 / 27.96% |
| Number/percentage of C's | 32,695,005 / 18.54% |
| Number/percentage of T's | 55,300,132 / 31.36% |
| Number/percentage of G's | 39,021,795 / 22.13% |
| Number/percentage of N's | 22,293 / 0.01% |
| GC Percentage | 40.67% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.057 |
| | |

| | |
|---|---|
| Standard Deviation | 0.6117 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.99 |

## 2.5. Mismatches and indels

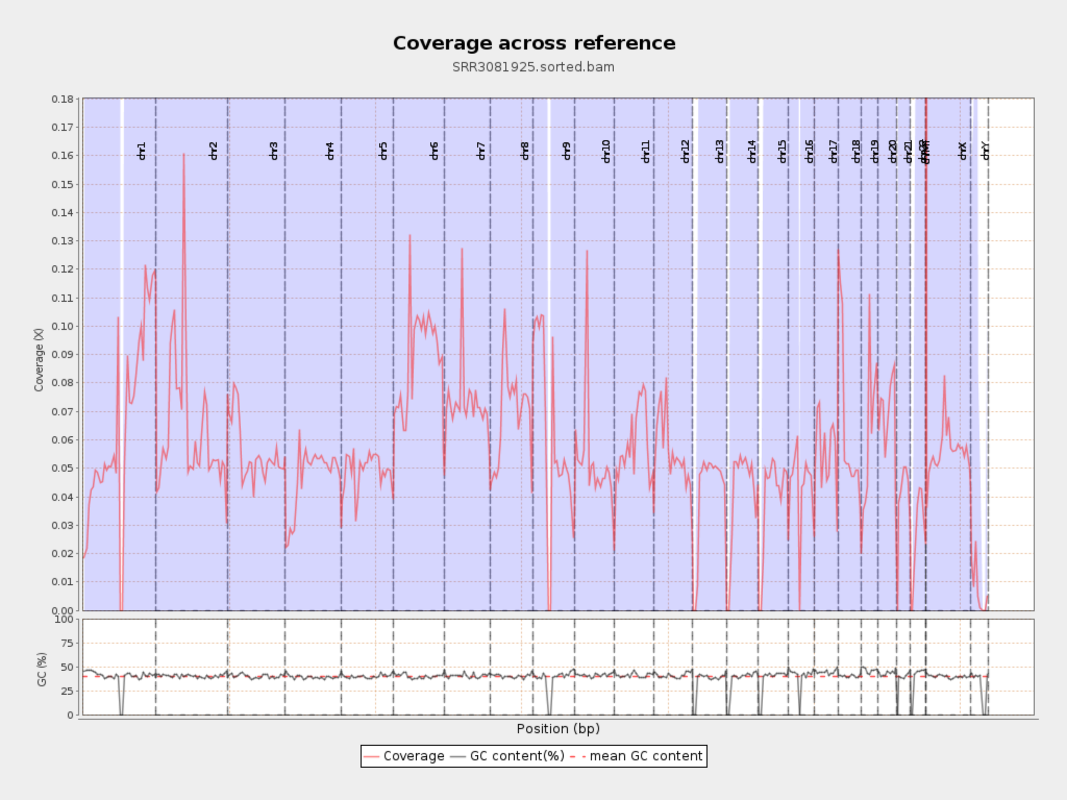
| | |
|---|---|
| General error rate | 0.78% |
| Mismatches | 1,354,141 |
| Insertions | 12,965 |
| Mapped reads with at least one insertion | 0.49% |
| Deletions | 35,289 |
| Mapped reads with at least one deletion | 1.34% |
| Homopolymer indels | 47.33% |

## 2.6. Chromosome stats

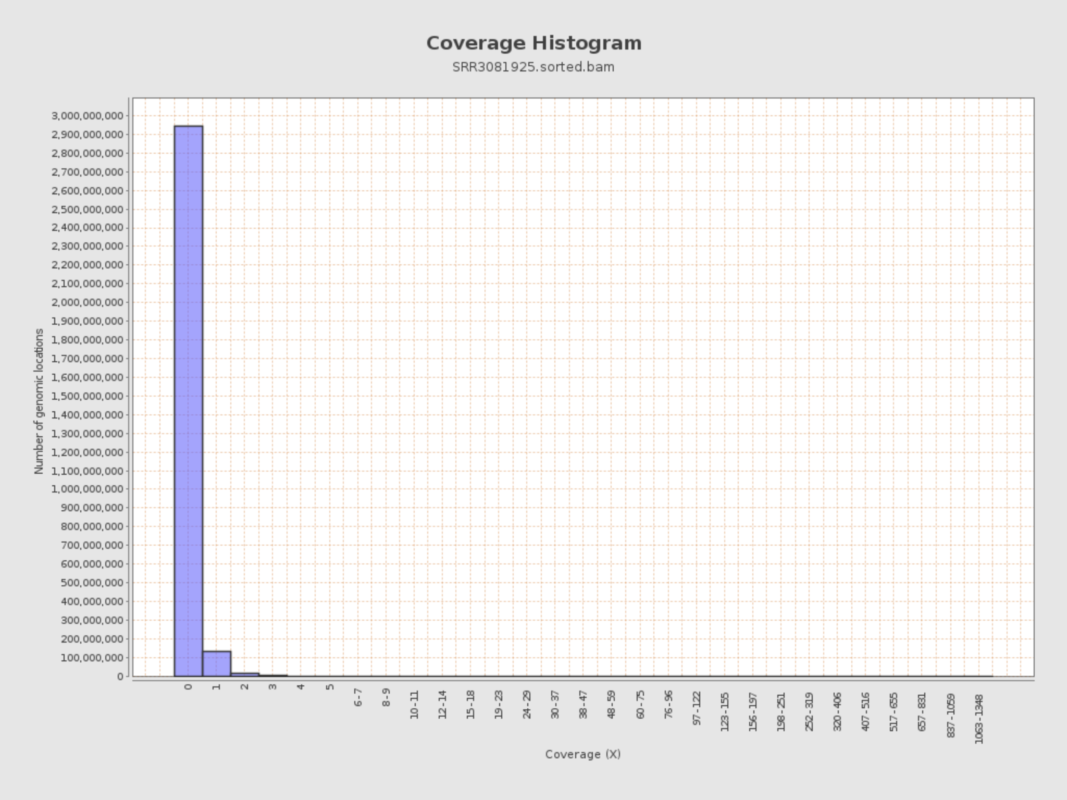
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 16201941 | 0.065 | 1.1918 |
| chr2 | 243199373 | 15718792 | 0.0646 | 0.8497 |
| chr3 | 198022430 | 11053616 | 0.0558 | 0.2673 |
| chr4 | 191154276 | 8984777 | 0.047 | 0.2916 |
| chr5 | 180915260 | 8836027 | 0.0488 | 0.2539 |
| chr6 | 171115067 | 15309707 | 0.0895 | 0.5094 |
| chr7 | 159138663 | 11626605 | 0.0731 | 0.894 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 10139296 | 0.0693 | 0.7673 |
| chr9 | 141213431 | 8608262 | 0.061 | 0.6199 |
| chr10 | 135534747 | 7194643 | 0.0531 | 0.6121 |
| chr11 | 135006516 | 7903840 | 0.0585 | 0.4176 |
| chr12 | 133851895 | 7477845 | 0.0559 | 0.2837 |
| chr13 | 115169878 | 4700844 | 0.0408 | 0.2242 |
| chr14 | 107349540 | 4433120 | 0.0413 | 0.276 |
| chr15 | 102531392 | 3946845 | 0.0385 | 0.2256 |
| chr16 | 90354753 | 3829145 | 0.0424 | 0.2972 |
| chr17 | 81195210 | 4622236 | 0.0569 | 0.3313 |
| chr18 | 78077248 | 5058469 | 0.0648 | 0.9842 |
| chr19 | 59128983 | 3721497 | 0.0629 | 0.8451 |
| chr20 | 63025520 | 4456087 | 0.0707 | 0.3197 |
| chr21 | 48129895 | 1902820 | 0.0395 | 0.2832 |
| chr22 | 51304566 | 1372736 | 0.0268 | 0.1813 |
| chrMT | 16571 | 129693 | 7.8265 | 4.9389 |
| chrX | 155270560 | 8742788 | 0.0563 | 0.3494 |
| chrY | 59373566 | 430120 | 0.0072 | 0.2059 |

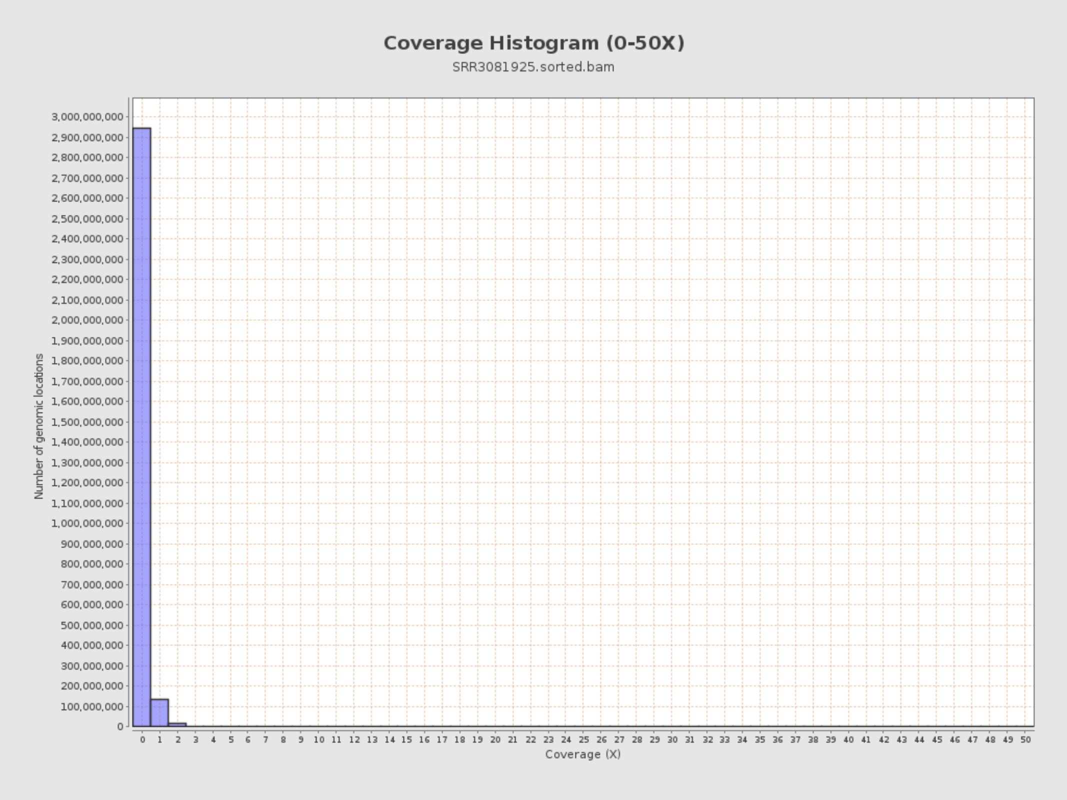
# 3. Results : Coverage across reference



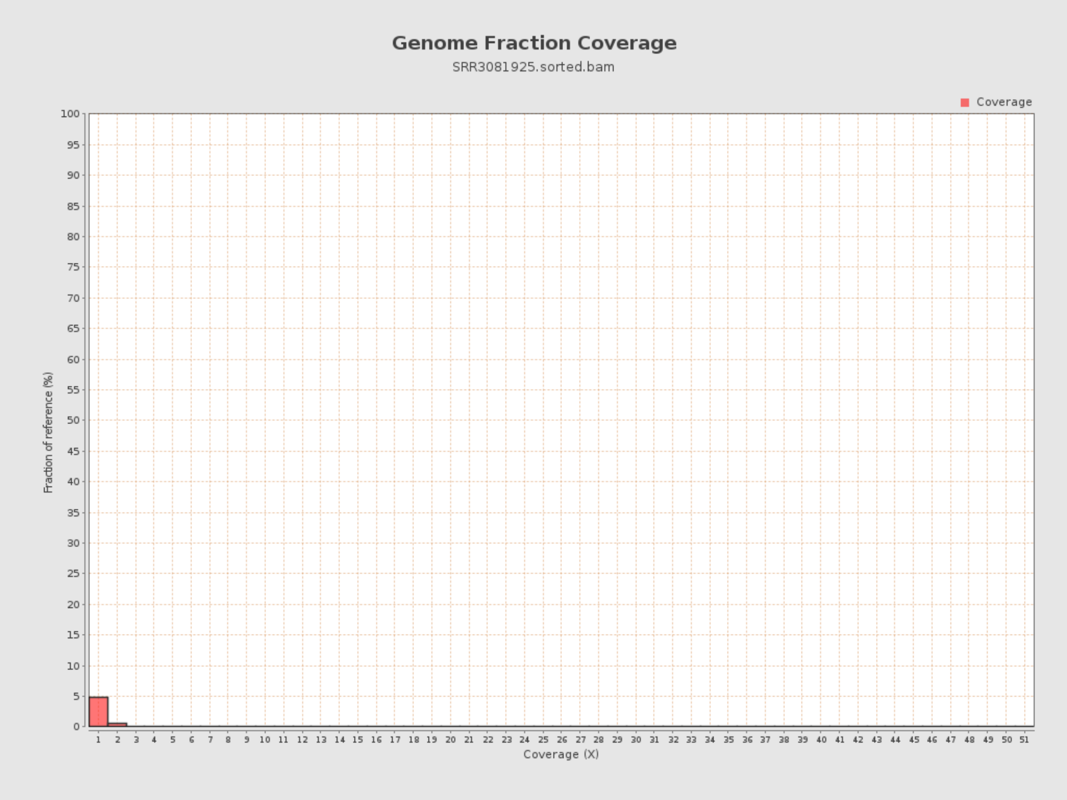
# 4. Results : Coverage Histogram



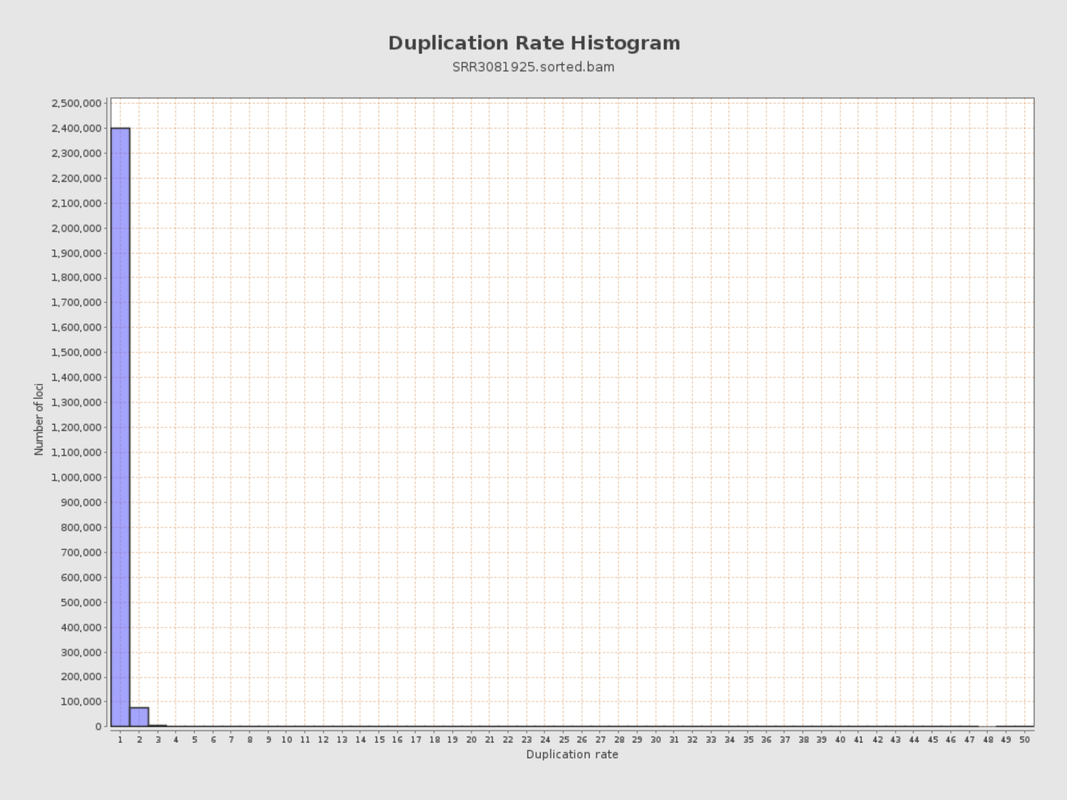
# 5. Results : Coverage Histogram (0-50X)



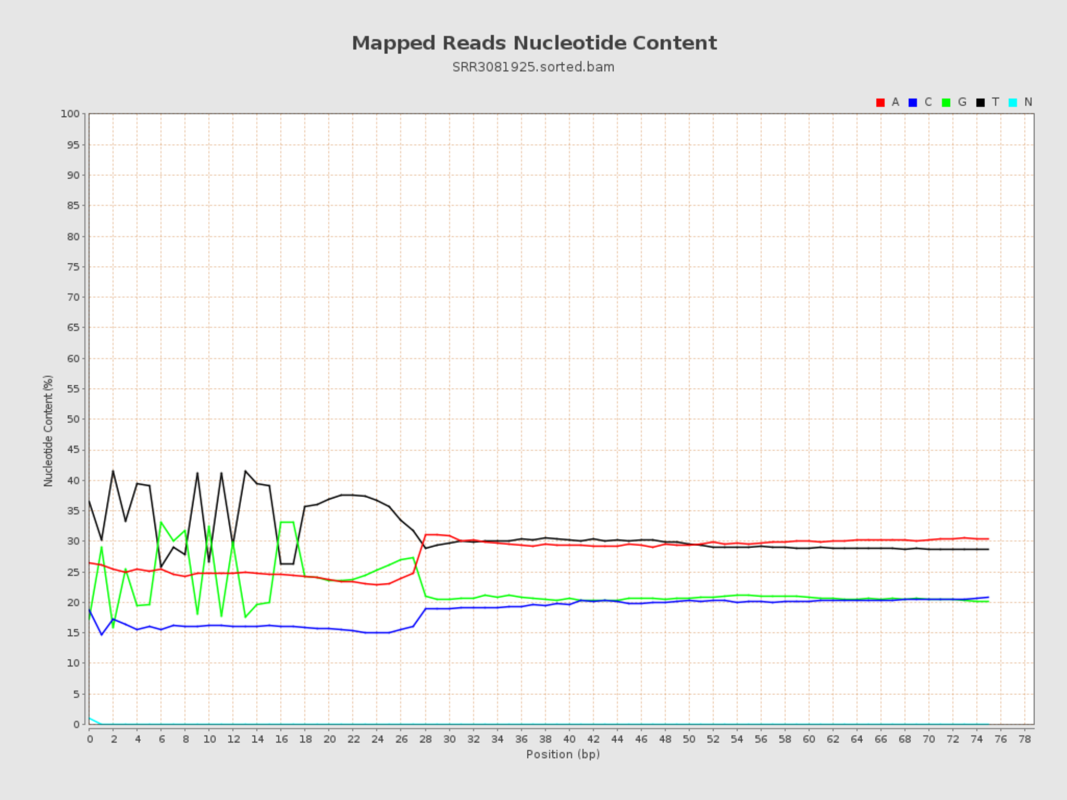
# 6. Results : Genome Fraction Coverage



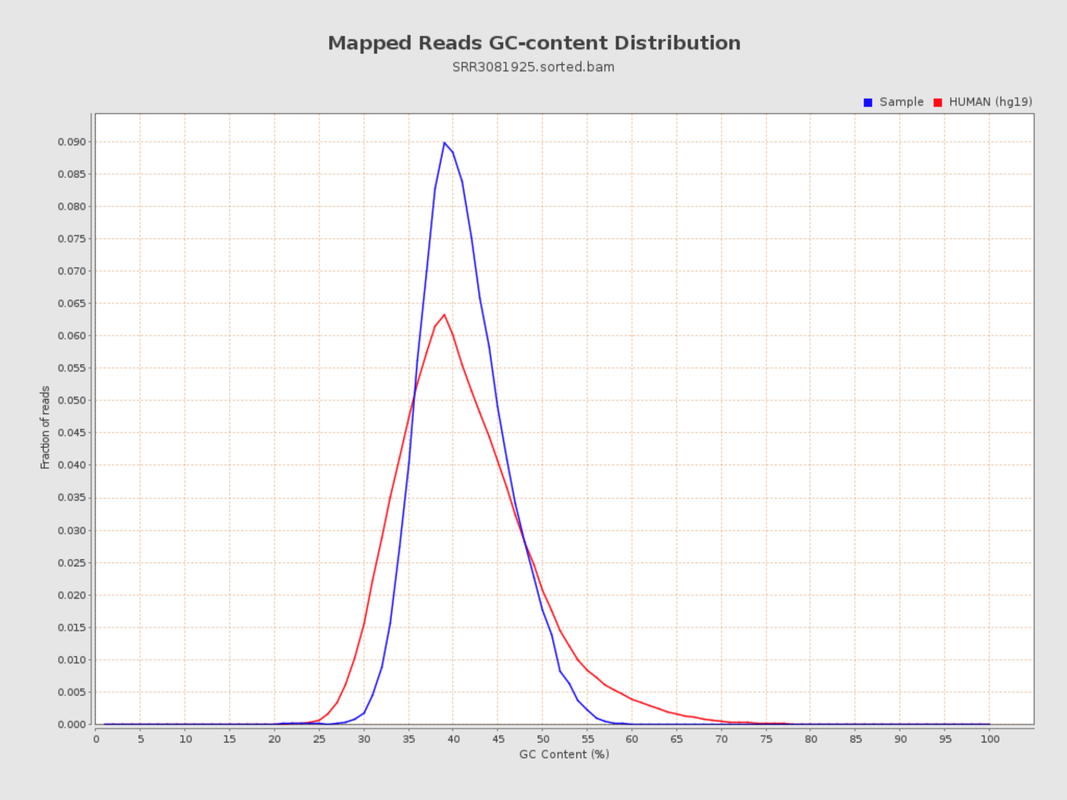
# 7. Results : Duplication Rate Histogram



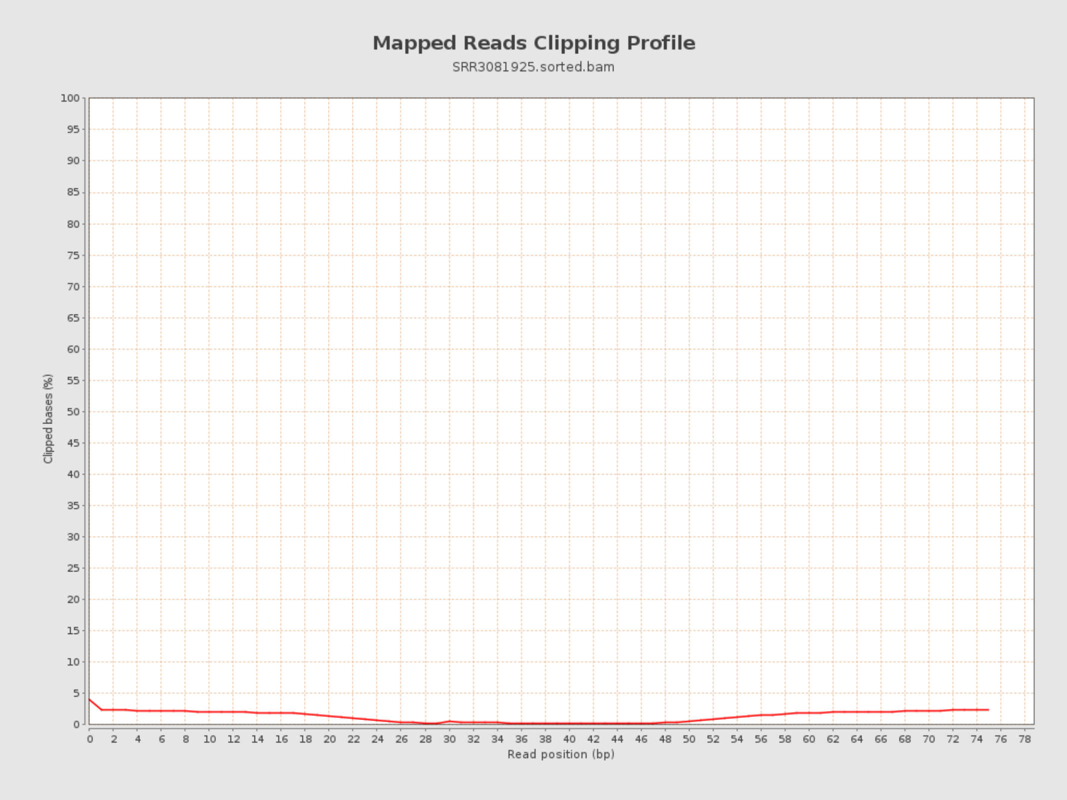
# 8. Results : Mapped Reads Nucleotide Content



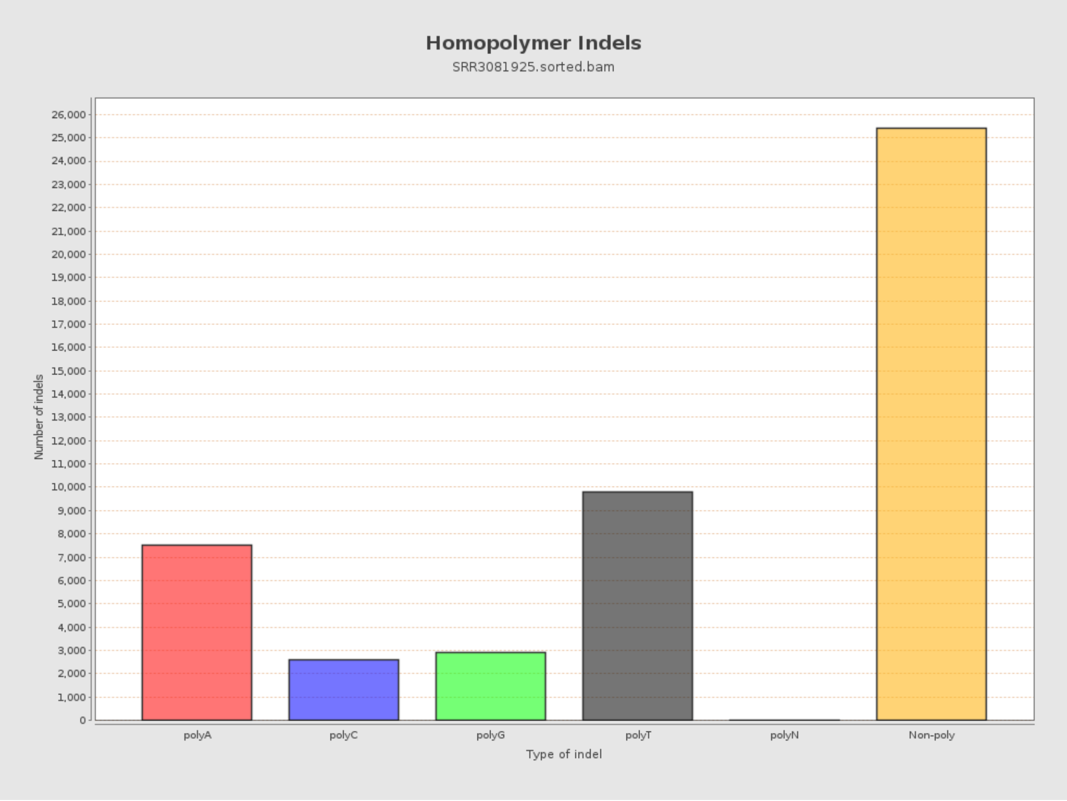
# 9. Results : Mapped Reads GC-content Distribution



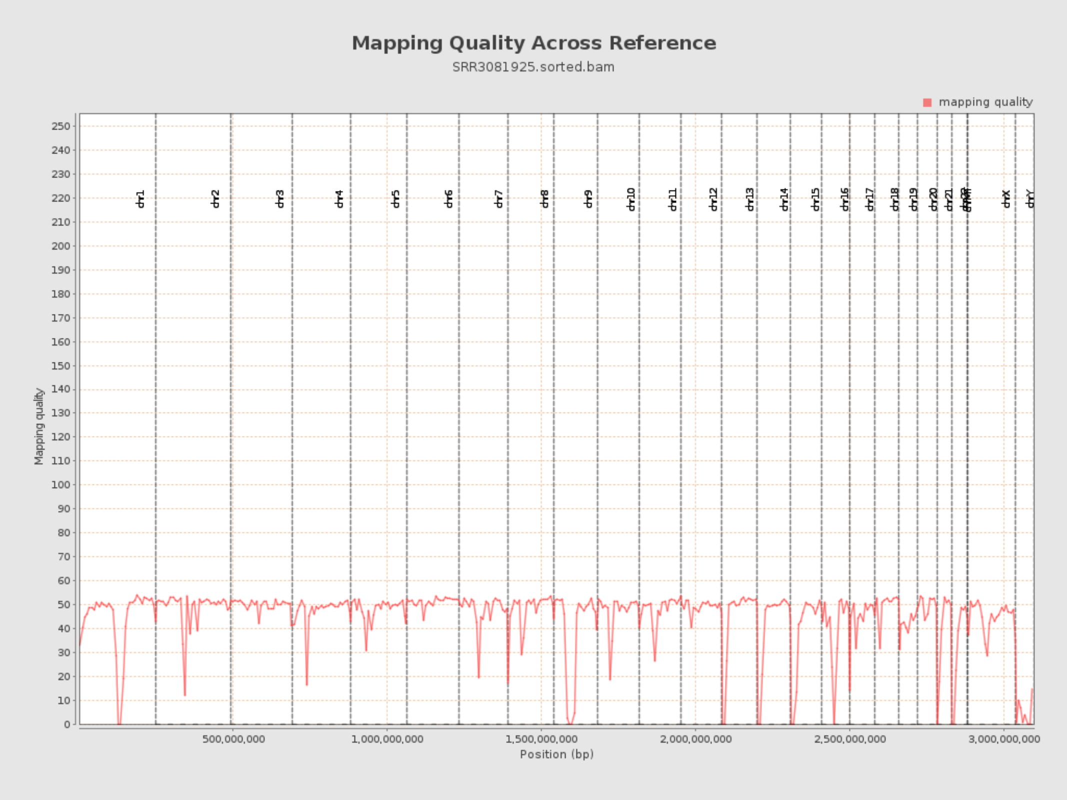
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram