# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 09:27:49*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081912.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_SRR3081912 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081912.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Aug 24 09:27:48 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3081912.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,918,975 |
| Mapped reads | 2,715,797 / 93.04% |
| Unmapped reads | 203,178 / 6.96% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 20,500 / 0.7% |
| Read min/max/mean length | 30 / 76 / 76.24 |
| Duplicated reads (estimated) | 100,963 / 3.46% |
| Duplication rate | 2.87% |
| Clipped reads | 1,015,109 / 34.78% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 52,753,398 / 28.39% |
| Number/percentage of C's | 34,713,253 / 18.68% |
| Number/percentage of T's | 58,293,813 / 31.37% |
| Number/percentage of G's | 40,085,481 / 21.57% |
| Number/percentage of N's | 2,270 / 0% |
| GC Percentage | 40.25% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0601 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4462 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.81 |

## 2.5. Mismatches and indels

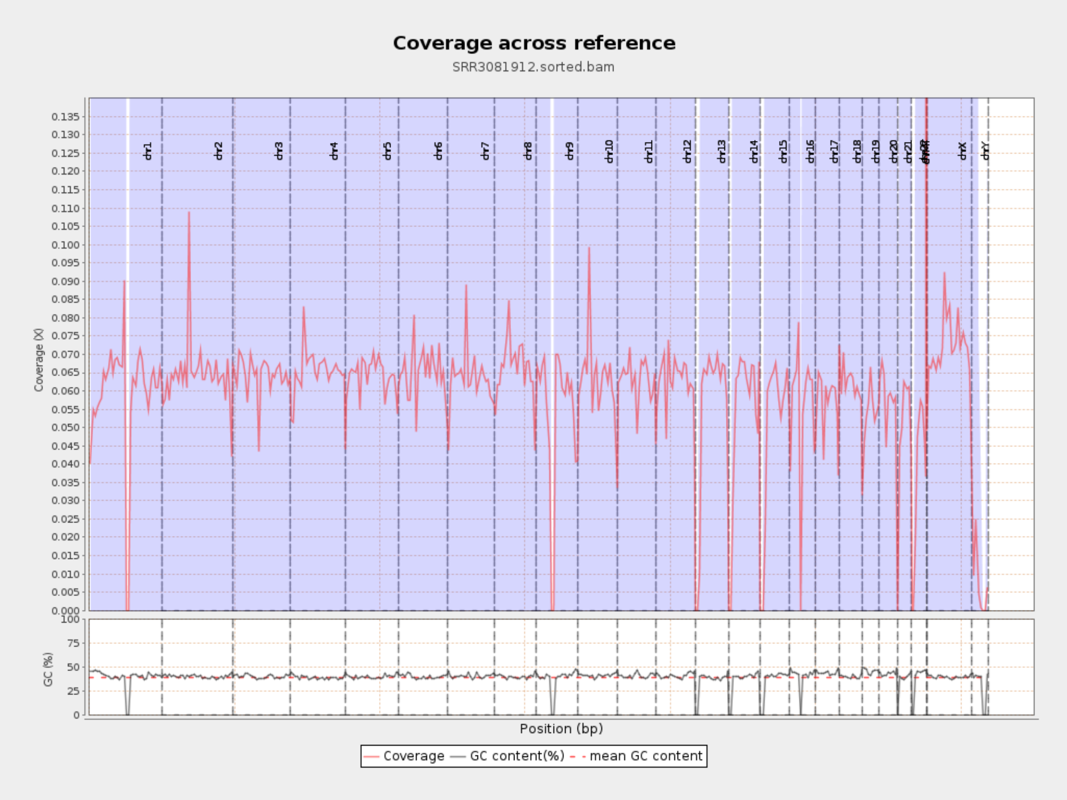
| | |
|---|---|
| General error rate | 0.86% |
| Mismatches | 1,571,089 |
| Insertions | 14,721 |
| Mapped reads with at least one insertion | 0.54% |
| Deletions | 41,433 |
| Mapped reads with at least one deletion | 1.51% |
| Homopolymer indels | 48.35% |

## 2.6. Chromosome stats

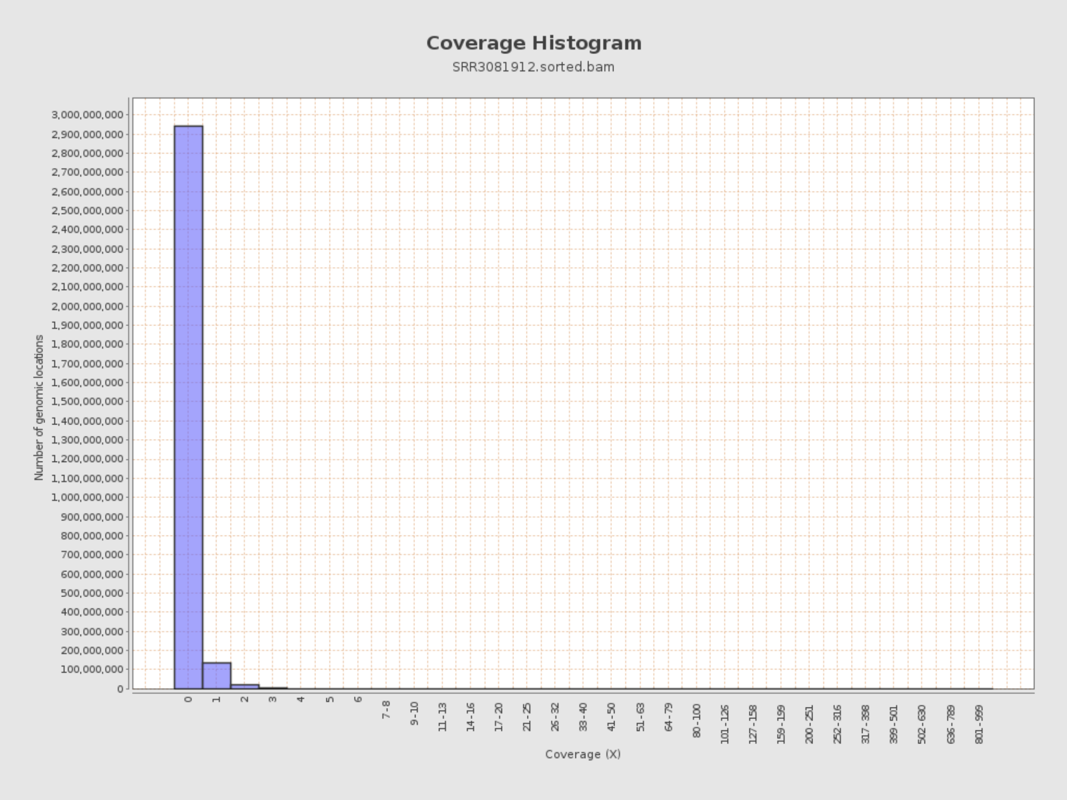
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 14754277 | 0.0592 | 0.733 |
| chr2 | 243199373 | 15771434 | 0.0648 | 0.5343 |
| chr3 | 198022430 | 12766691 | 0.0645 | 0.2916 |
| chr4 | 191154276 | 12519320 | 0.0655 | 0.3176 |
| chr5 | 180915260 | 11629452 | 0.0643 | 0.2903 |
| chr6 | 171115067 | 11157567 | 0.0652 | 0.3435 |
| chr7 | 159138663 | 10216169 | 0.0642 | 0.5399 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 9674526 | 0.0661 | 0.6904 |
| chr9 | 141213431 | 7644709 | 0.0541 | 0.4328 |
| chr10 | 135534747 | 8663993 | 0.0639 | 0.469 |
| chr11 | 135006516 | 8477175 | 0.0628 | 0.3865 |
| chr12 | 133851895 | 8440336 | 0.0631 | 0.2908 |
| chr13 | 115169878 | 6232512 | 0.0541 | 0.2645 |
| chr14 | 107349540 | 5657327 | 0.0527 | 0.2817 |
| chr15 | 102531392 | 5094791 | 0.0497 | 0.2646 |
| chr16 | 90354753 | 5010992 | 0.0555 | 0.3091 |
| chr17 | 81195210 | 4592604 | 0.0566 | 0.2998 |
| chr18 | 78077248 | 4880147 | 0.0625 | 0.7641 |
| chr19 | 59128983 | 3201960 | 0.0542 | 0.579 |
| chr20 | 63025520 | 3630070 | 0.0576 | 0.285 |
| chr21 | 48129895 | 2369449 | 0.0492 | 0.2807 |
| chr22 | 51304566 | 1814039 | 0.0354 | 0.2111 |
| chrMT | 16571 | 86768 | 5.2361 | 3.5717 |
| chrX | 155270560 | 11149730 | 0.0718 | 0.3427 |
| chrY | 59373566 | 480548 | 0.0081 | 0.179 |

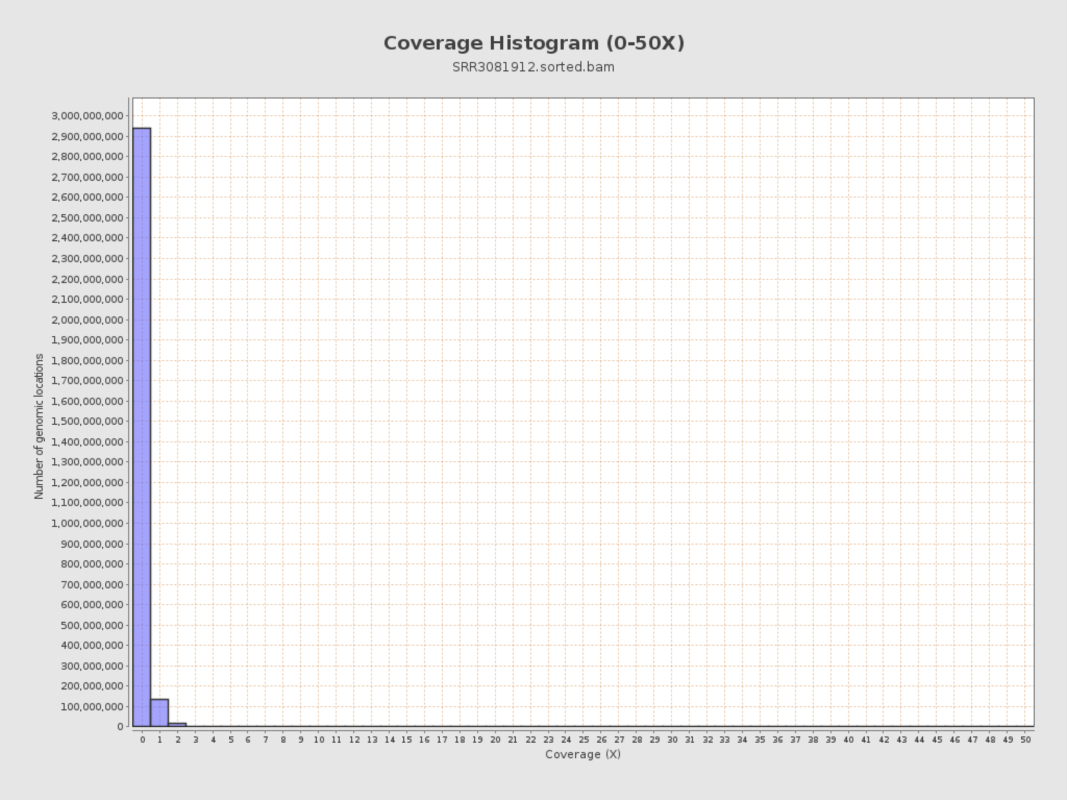
# 3. Results : Coverage across reference



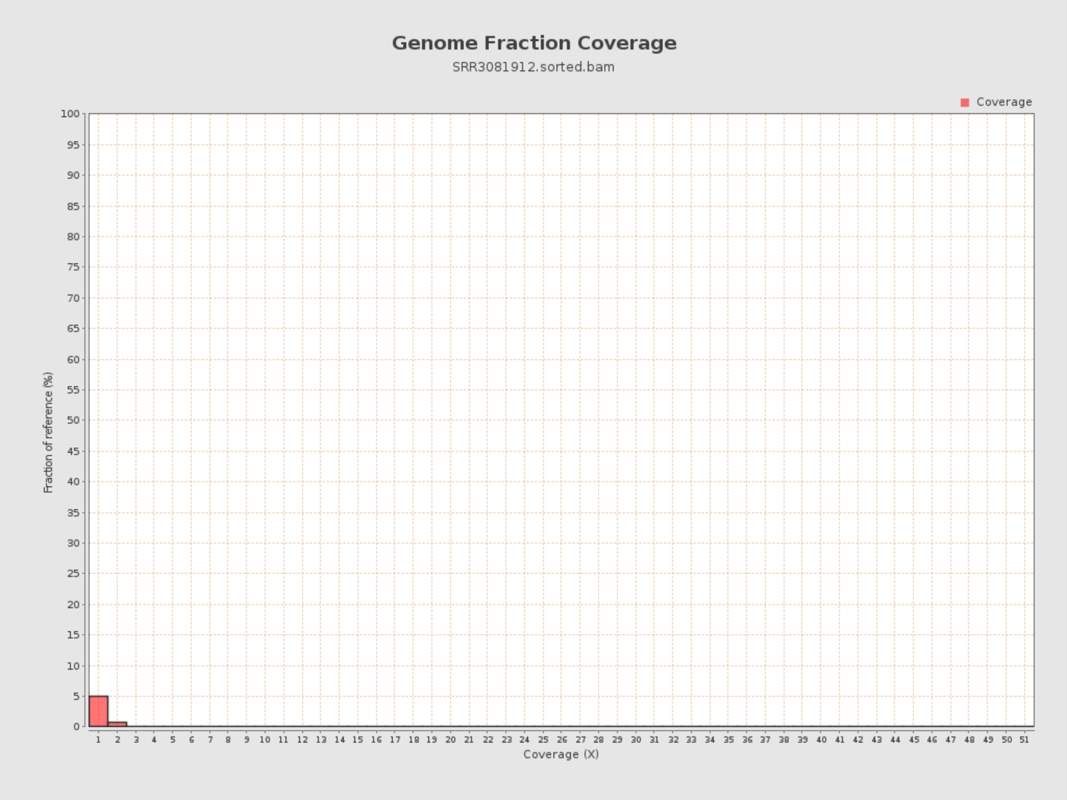
# 4. Results : Coverage Histogram



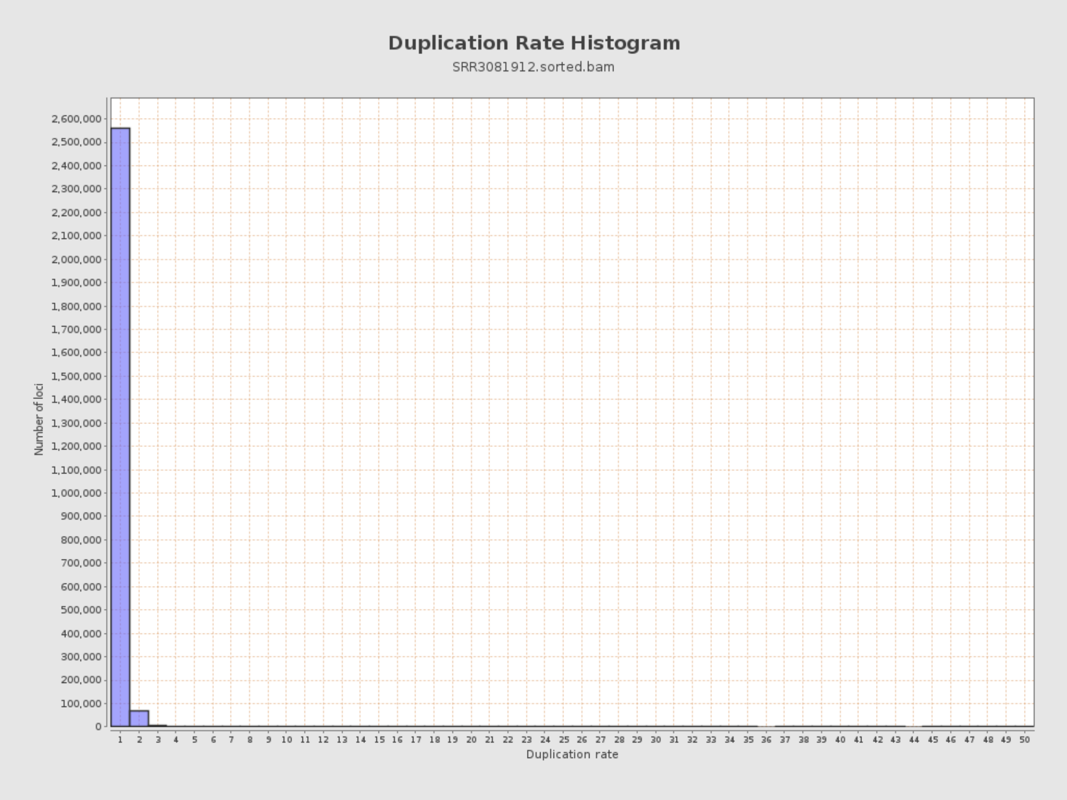
# 5. Results : Coverage Histogram (0-50X)



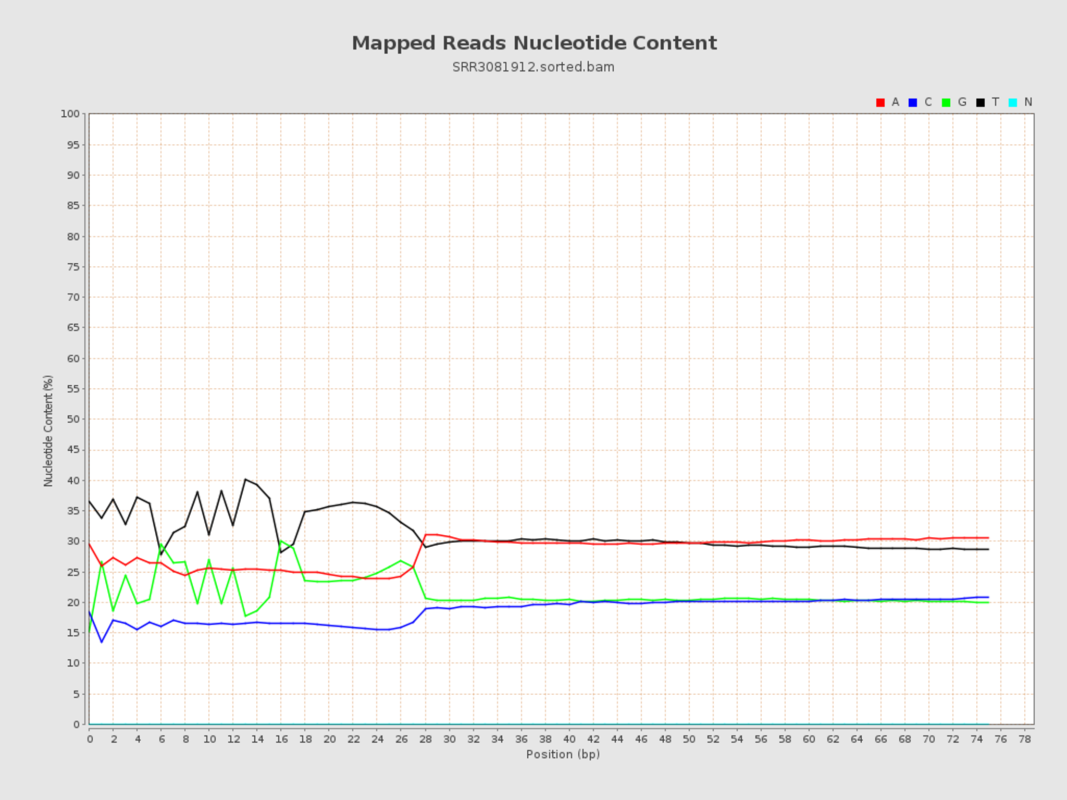
# 6. Results : Genome Fraction Coverage



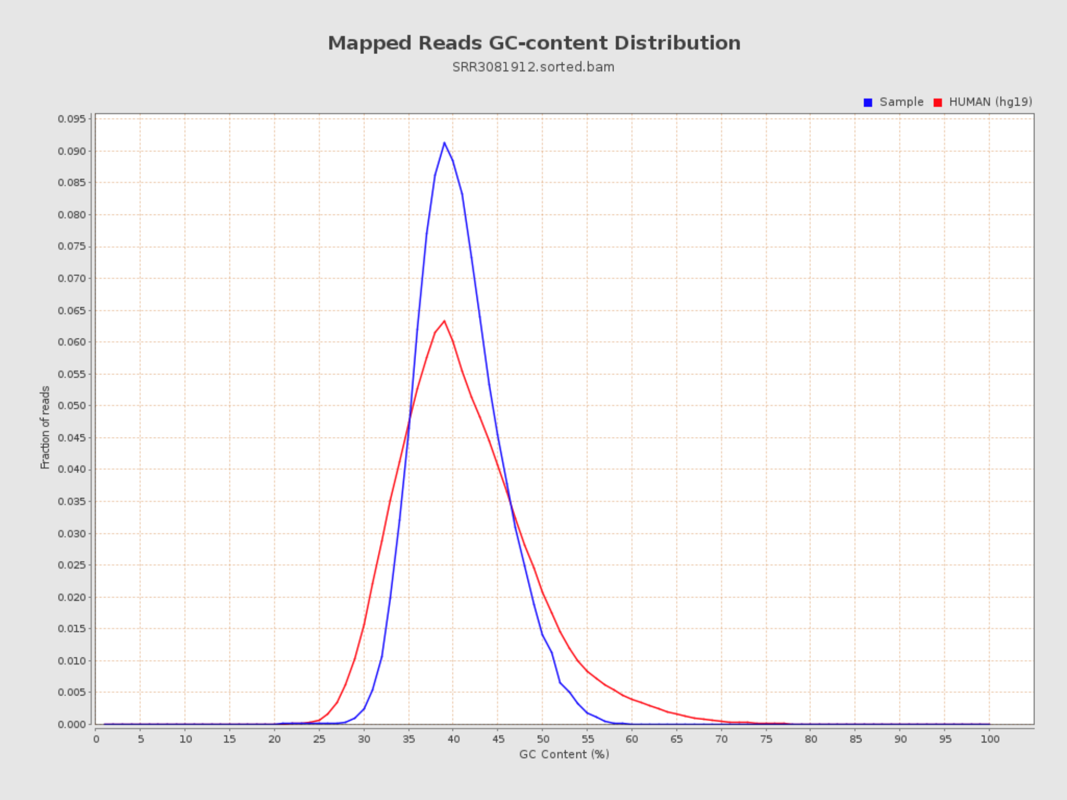
# 7. Results : Duplication Rate Histogram



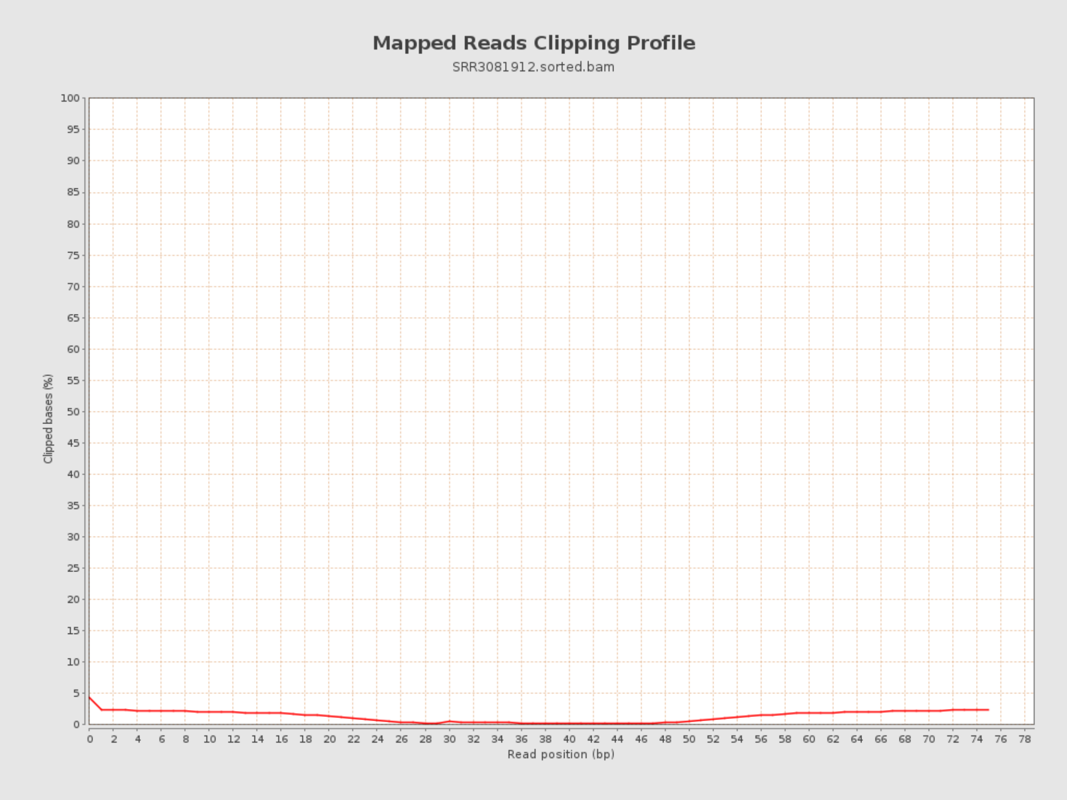
# 8. Results : Mapped Reads Nucleotide Content



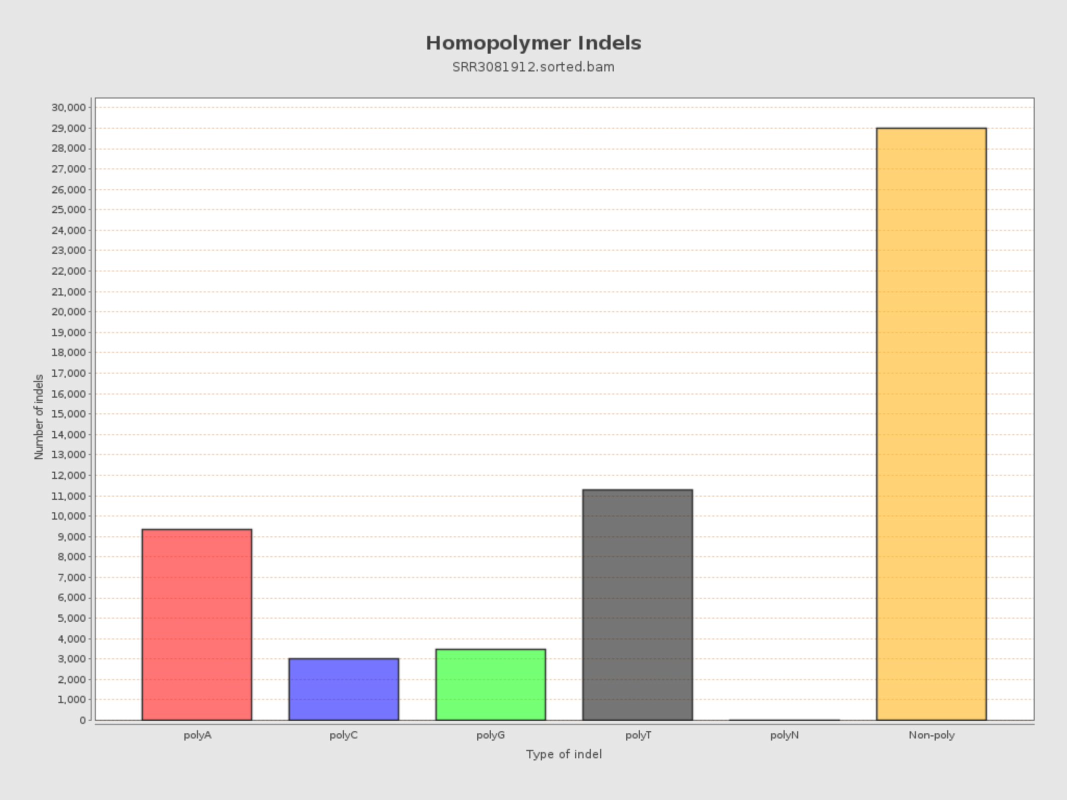
# 9. Results : Mapped Reads GC-content Distribution



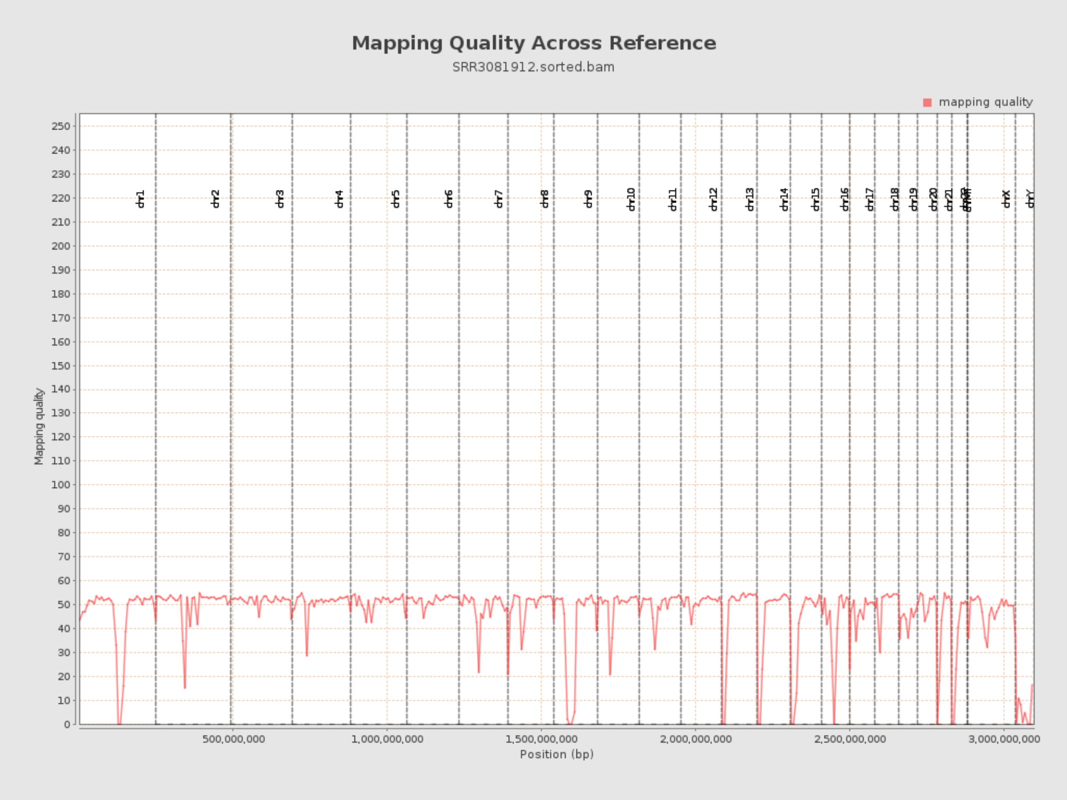
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram