# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 07:01:45*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708598.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_SRR1708598 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708598.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 07:01:44 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1708598.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 5,258,436 |
| Mapped reads | 5,042,790 / 95.9% |
| Unmapped reads | 215,646 / 4.1% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 122 / 0% |
| Read min/max/mean length | 30 / 50 / 50 |
| Duplicated reads (estimated) | 48,955 / 0.93% |
| Duplication rate | 0.97% |
| Clipped reads | 63,946 / 1.22% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 77,889,947 / 30.97% |
| Number/percentage of C's | 47,803,060 / 19% |
| Number/percentage of T's | 77,386,561 / 30.77% |
| Number/percentage of G's | 48,443,905 / 19.26% |
| Number/percentage of N's | 6,681 / 0% |
| GC Percentage | 38.26% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0813 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2972 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.75 |

## 2.5. Mismatches and indels

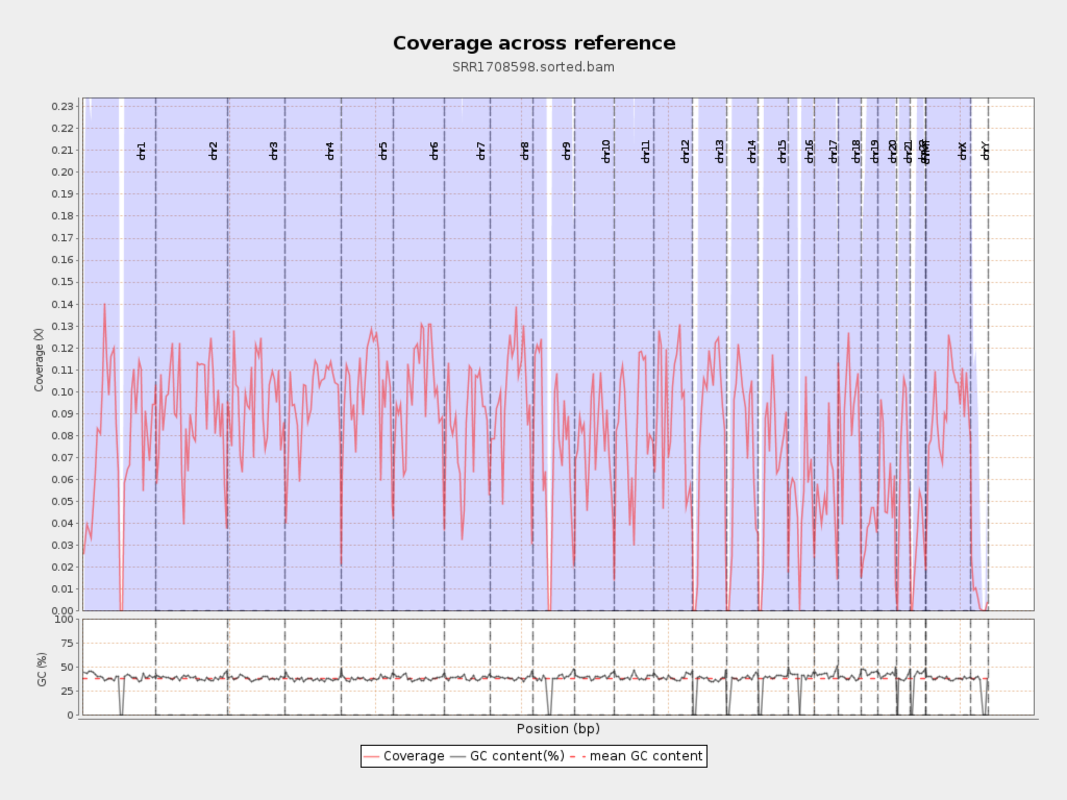
| | |
|---|---|
| General error rate | 0.15% |
| Mismatches | 357,188 |
| Insertions | 15,745 |
| Mapped reads with at least one insertion | 0.31% |
| Deletions | 12,583 |
| Mapped reads with at least one deletion | 0.25% |
| Homopolymer indels | 48.56% |

## 2.6. Chromosome stats

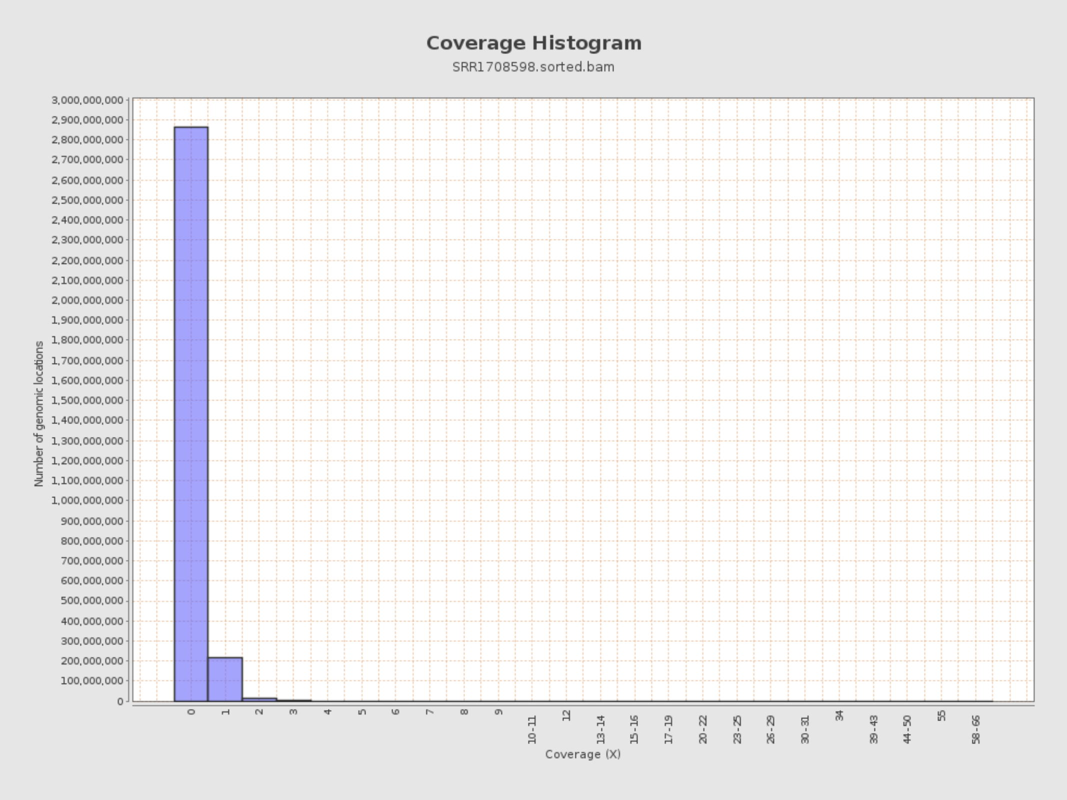
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 19133330 | 0.0768 | 0.2906 |
| chr2 | 243199373 | 22070184 | 0.0907 | 0.3124 |
| chr3 | 198022430 | 18819157 | 0.095 | 0.3195 |
| chr4 | 191154276 | 18341214 | 0.0959 | 0.3204 |
| chr5 | 180915260 | 17934169 | 0.0991 | 0.3264 |
| chr6 | 171115067 | 17324900 | 0.1012 | 0.33 |
| chr7 | 159138663 | 13226655 | 0.0831 | 0.2999 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 14472361 | 0.0989 | 0.3263 |
| chr9 | 141213431 | 10478567 | 0.0742 | 0.2849 |
| chr10 | 135534747 | 10631749 | 0.0784 | 0.2903 |
| chr11 | 135006516 | 11310613 | 0.0838 | 0.3038 |
| chr12 | 133851895 | 11905305 | 0.0889 | 0.3105 |
| chr13 | 115169878 | 9722451 | 0.0844 | 0.303 |
| chr14 | 107349540 | 7958335 | 0.0741 | 0.2853 |
| chr15 | 102531392 | 6847507 | 0.0668 | 0.2704 |
| chr16 | 90354753 | 4608738 | 0.051 | 0.2346 |
| chr17 | 81195210 | 4287823 | 0.0528 | 0.2393 |
| chr18 | 78077248 | 7197310 | 0.0922 | 0.3145 |
| chr19 | 59128983 | 2136799 | 0.0361 | 0.1967 |
| chr20 | 63025520 | 3784953 | 0.0601 | 0.2555 |
| chr21 | 48129895 | 3079933 | 0.064 | 0.2656 |
| chr22 | 51304566 | 1507583 | 0.0294 | 0.1785 |
| chrMT | 16571 | 399 | 0.0241 | 0.1533 |
| chrX | 155270560 | 14411165 | 0.0928 | 0.3164 |
| chrY | 59373566 | 360320 | 0.0061 | 0.0821 |

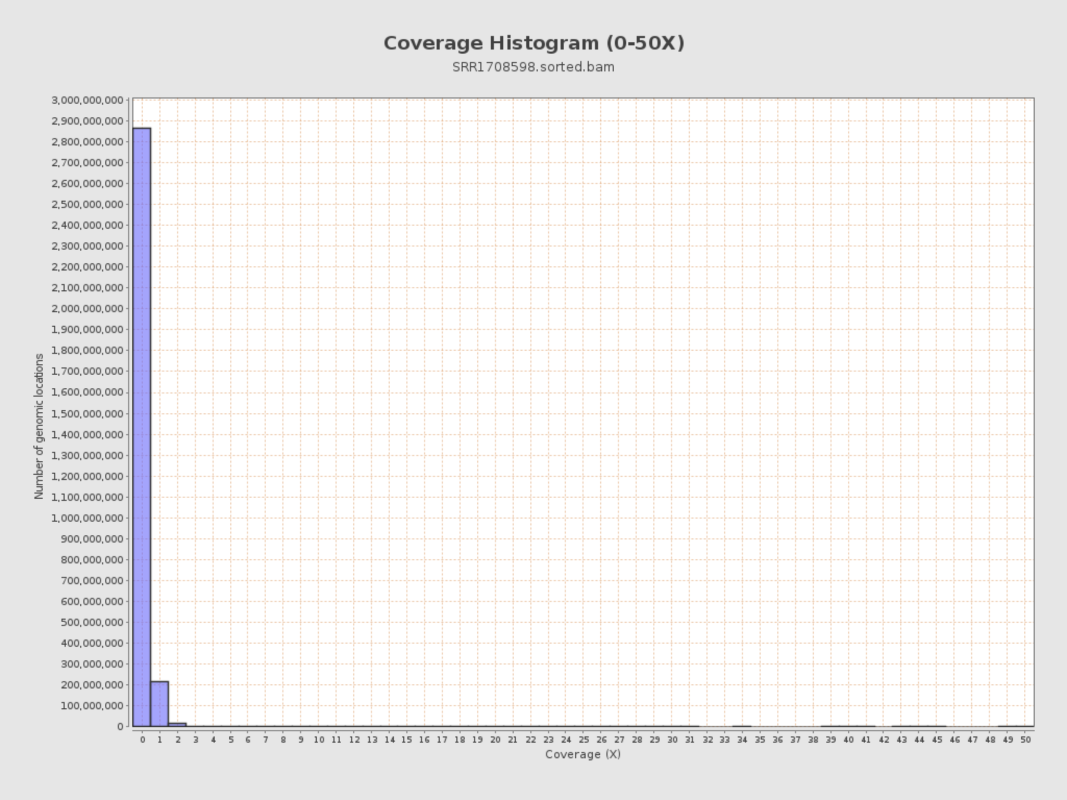
# 3. Results : Coverage across reference



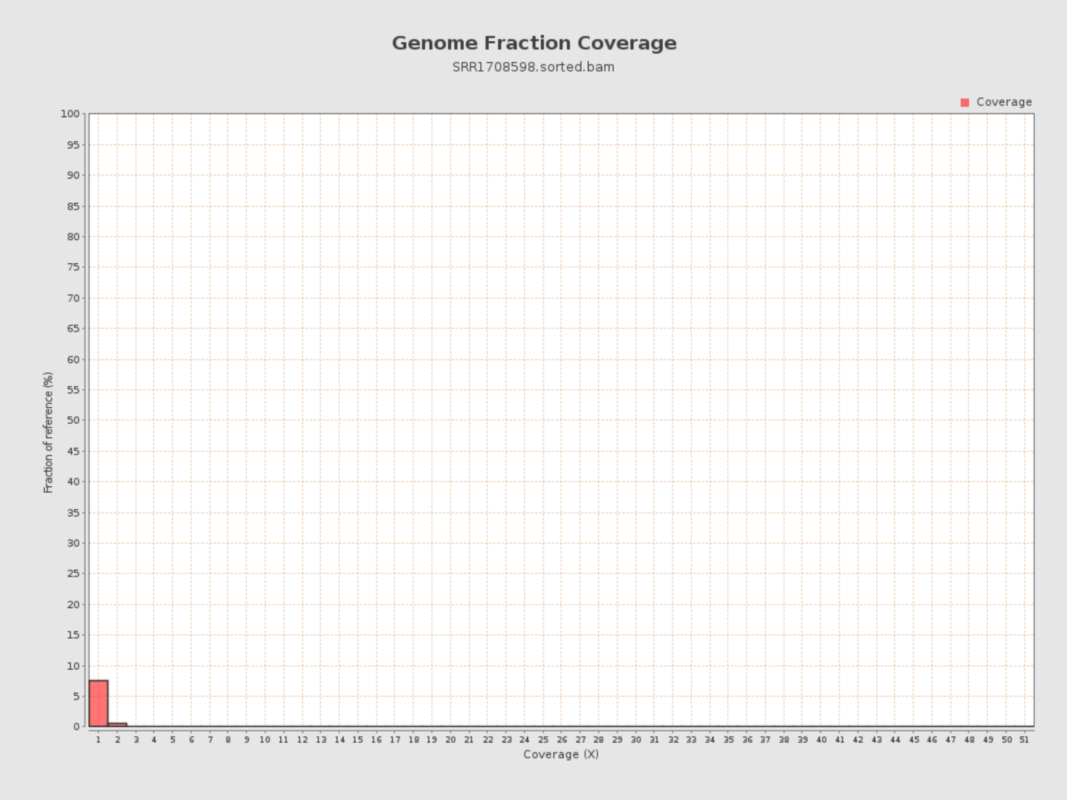
# 4. Results : Coverage Histogram



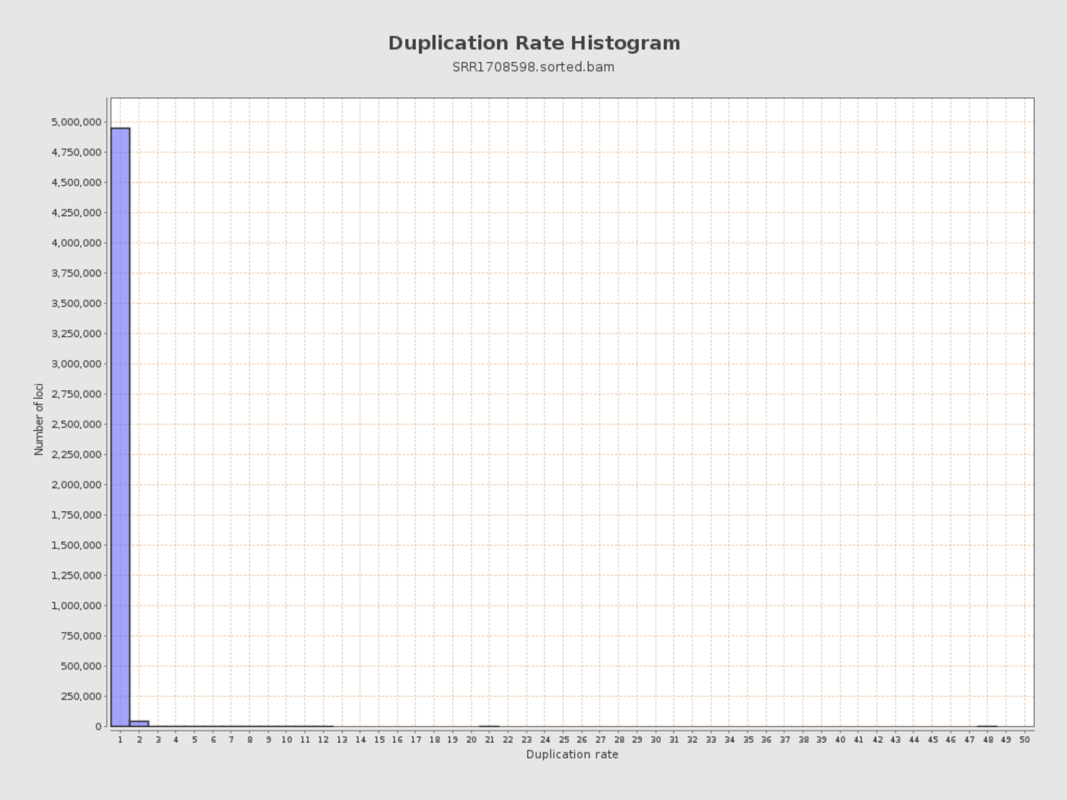
# 5. Results : Coverage Histogram (0-50X)



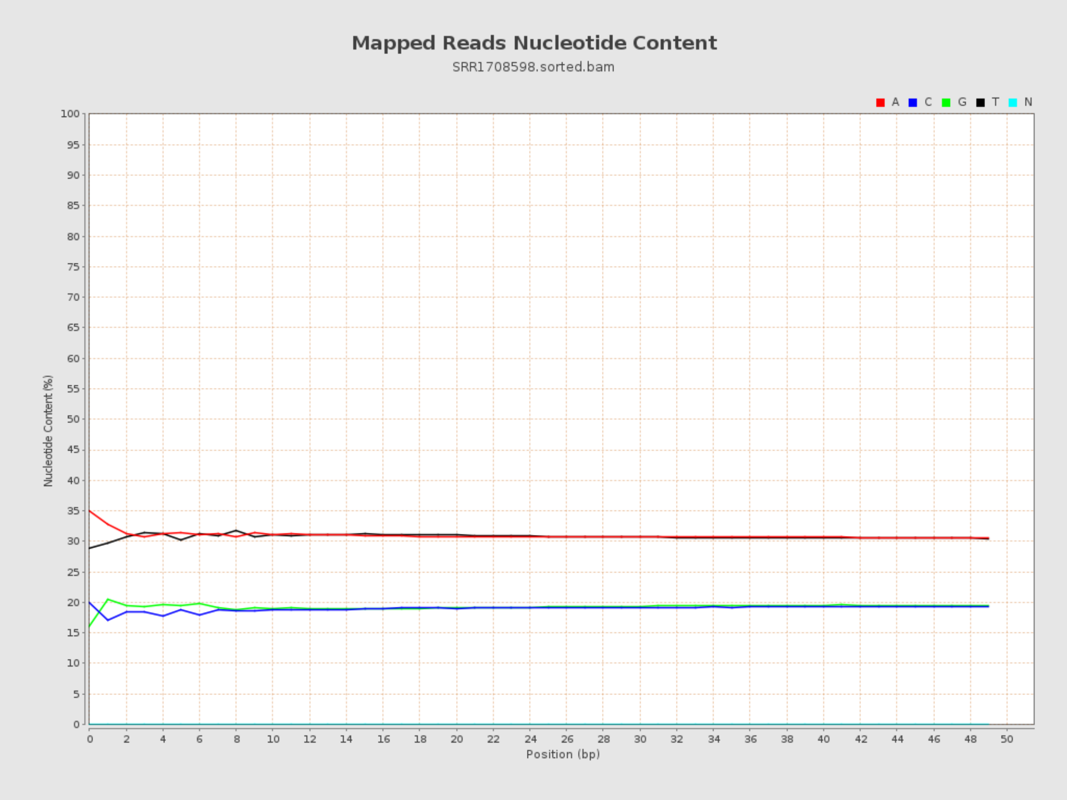
# 6. Results : Genome Fraction Coverage



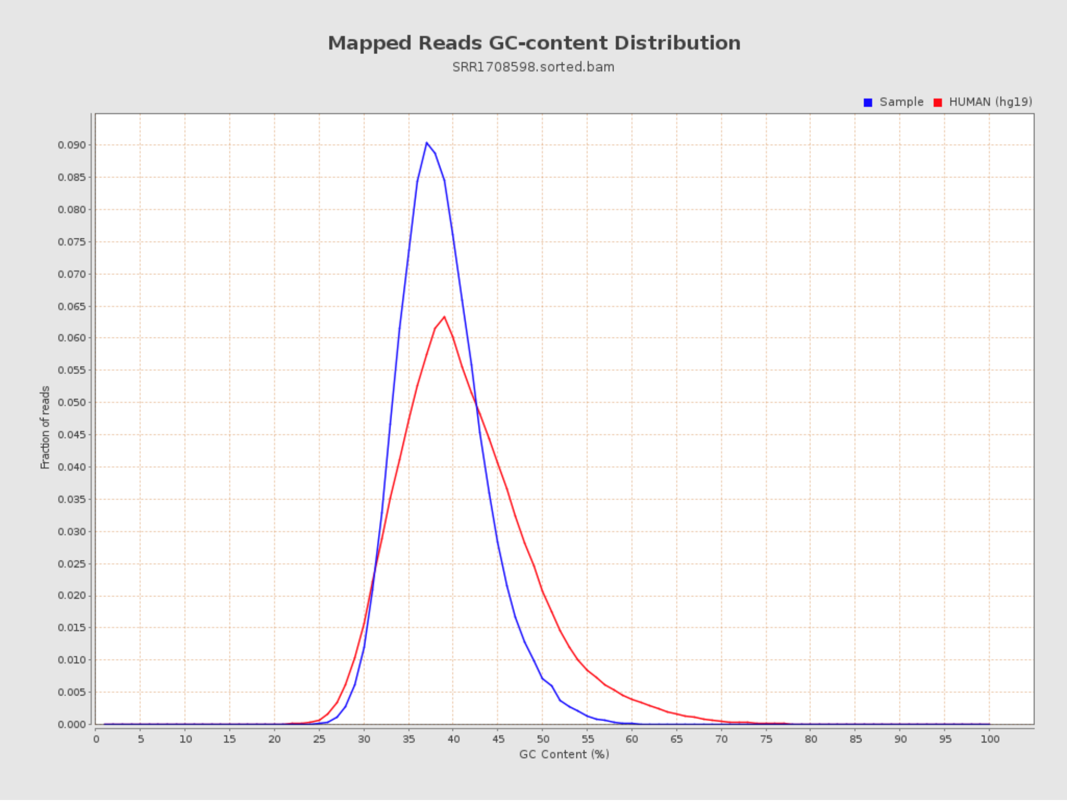
# 7. Results : Duplication Rate Histogram



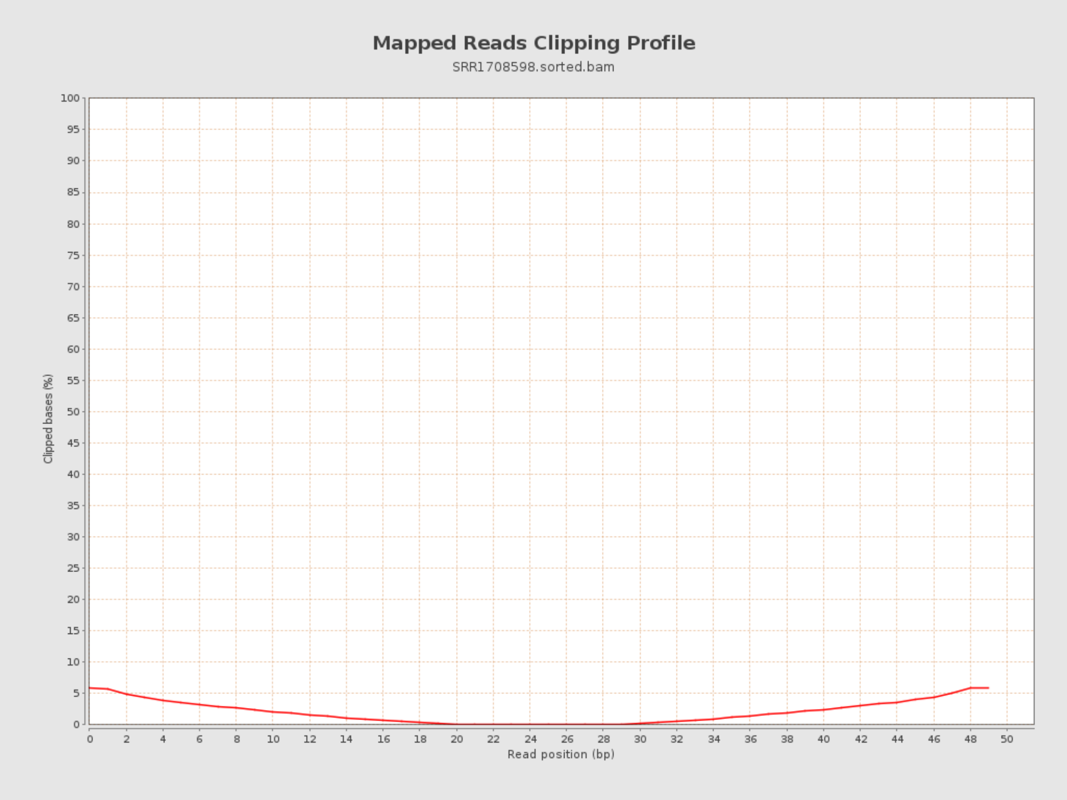
# 8. Results : Mapped Reads Nucleotide Content



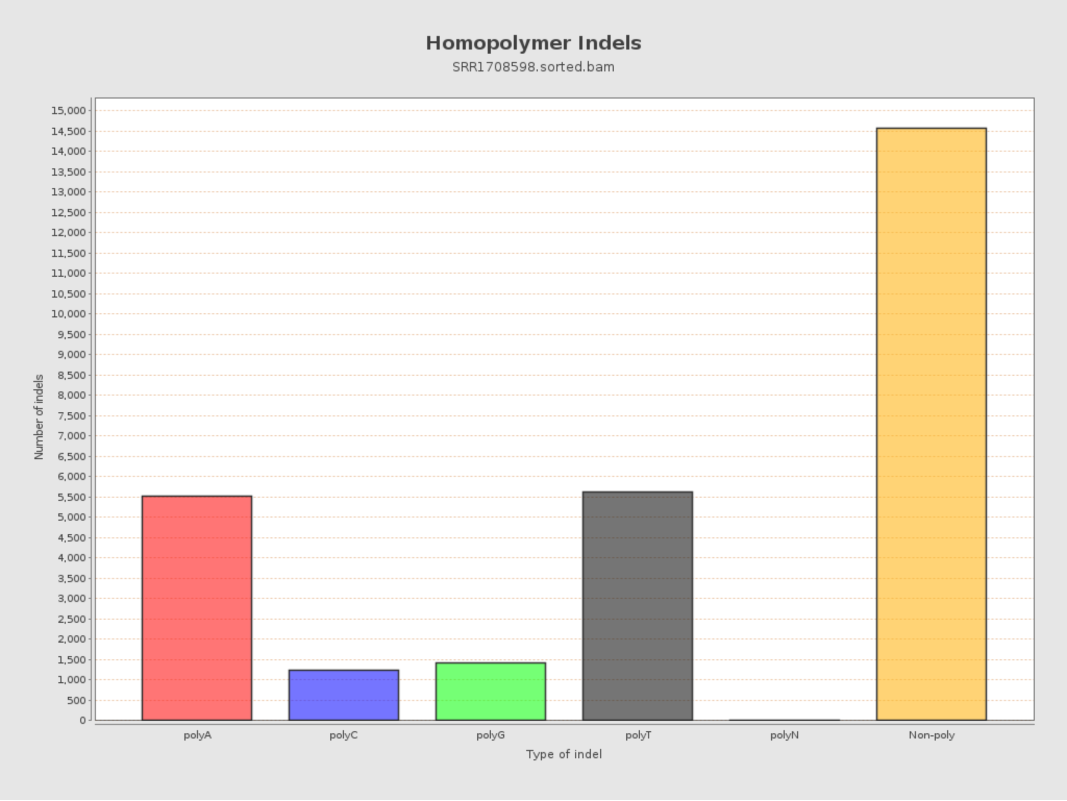
# 9. Results : Mapped Reads GC-content Distribution



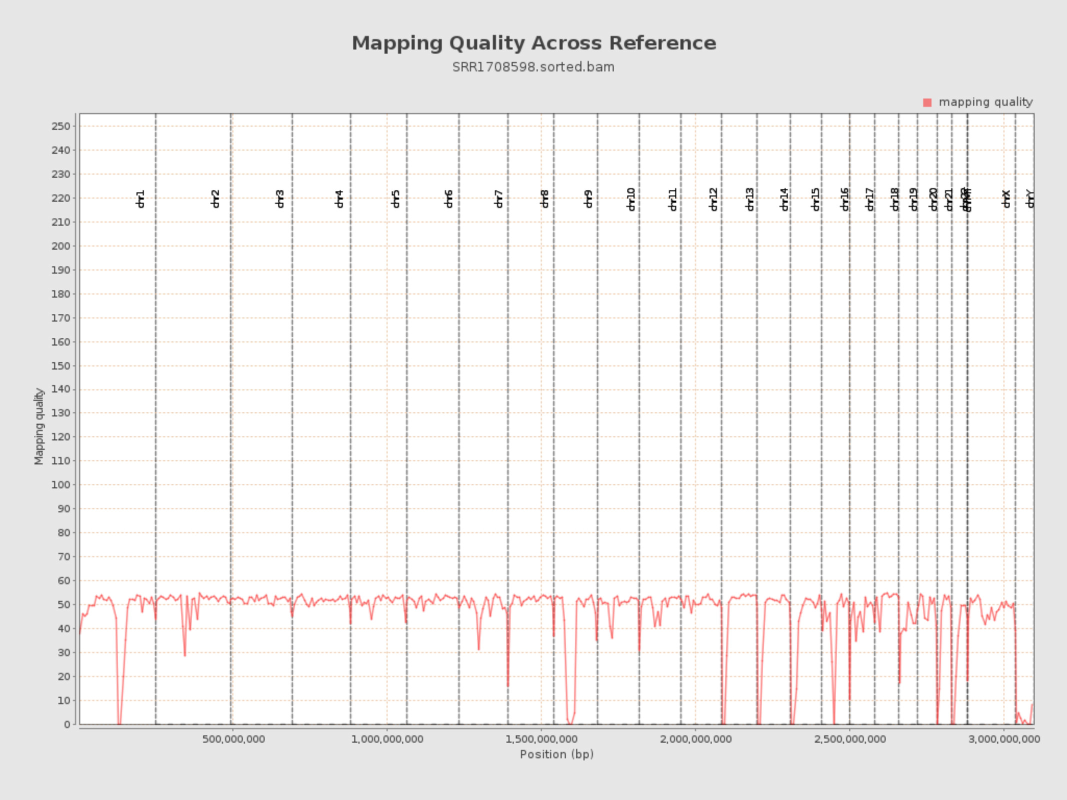
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram