# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 11:00:53*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708645.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_SRR1708645 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708645.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 11:00:52 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1708645.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,508,376 |
| Mapped reads | 3,385,028 / 96.48% |
| Unmapped reads | 123,348 / 3.52% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 107 / 0% |
| Read min/max/mean length | 30 / 50 / 50 |
| Duplicated reads (estimated) | 13,184 / 0.38% |
| Duplication rate | 0.38% |
| Clipped reads | 44,091 / 1.26% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 52,186,603 / 30.91% |
| Number/percentage of C's | 32,063,363 / 18.99% |
| Number/percentage of T's | 52,180,121 / 30.91% |
| Number/percentage of G's | 32,395,010 / 19.19% |
| Number/percentage of N's | 4,544 / 0% |
| GC Percentage | 38.18% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0545 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2402 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.65 |

## 2.5. Mismatches and indels

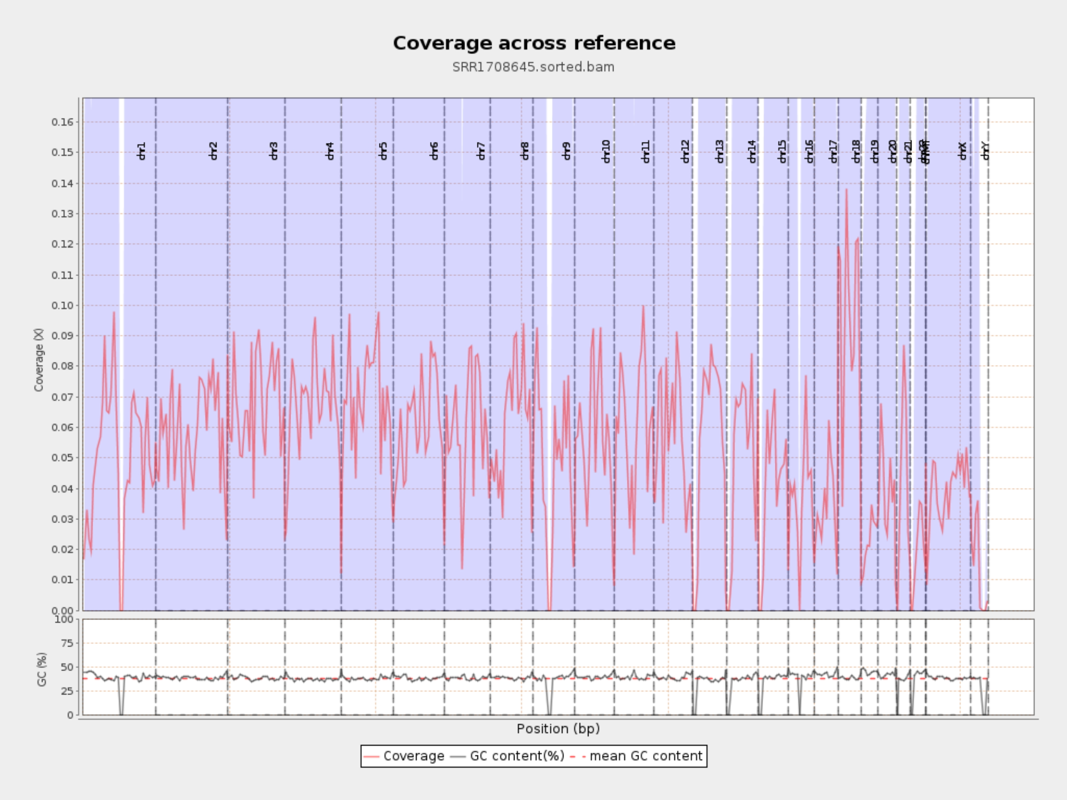
| | |
|---|---|
| General error rate | 0.17% |
| Mismatches | 272,851 |
| Insertions | 11,556 |
| Mapped reads with at least one insertion | 0.34% |
| Deletions | 9,780 |
| Mapped reads with at least one deletion | 0.29% |
| Homopolymer indels | 49.12% |

## 2.6. Chromosome stats

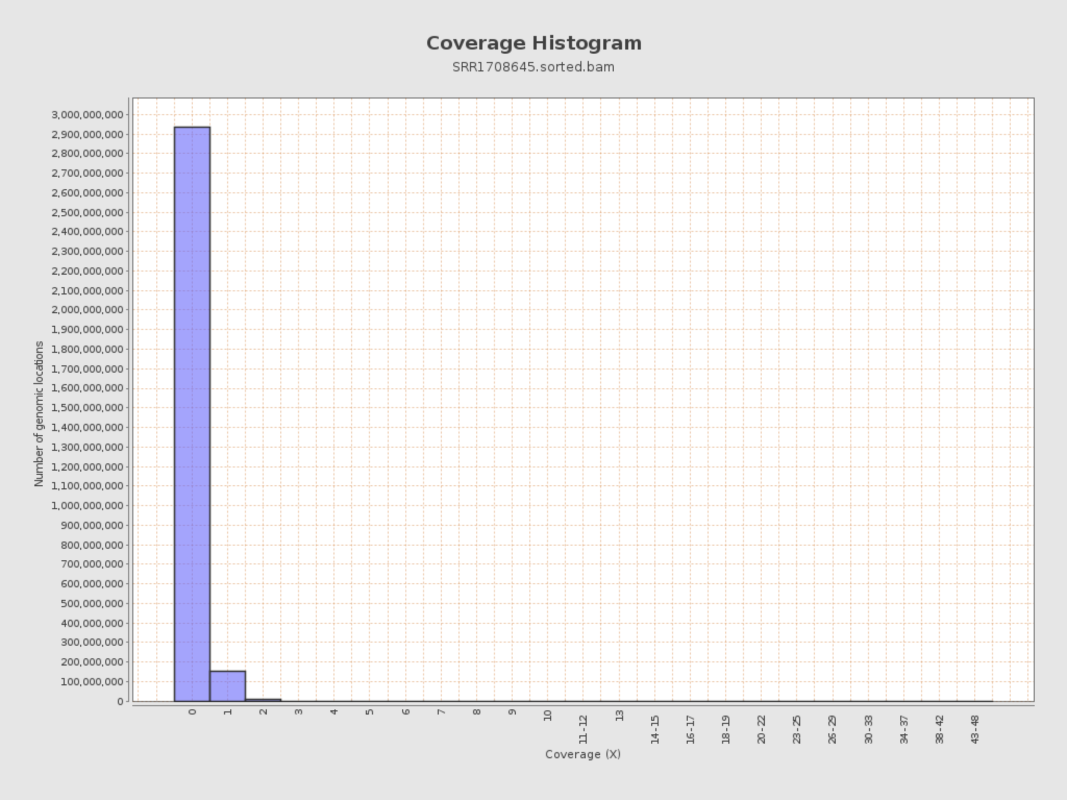
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 12485714 | 0.0501 | 0.2306 |
| chr2 | 243199373 | 14205812 | 0.0584 | 0.2479 |
| chr3 | 198022430 | 13522120 | 0.0683 | 0.2677 |
| chr4 | 191154276 | 12983426 | 0.0679 | 0.2665 |
| chr5 | 180915260 | 12390930 | 0.0685 | 0.2681 |
| chr6 | 171115067 | 10643837 | 0.0622 | 0.2553 |
| chr7 | 159138663 | 9344717 | 0.0587 | 0.2491 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 9123595 | 0.0623 | 0.2558 |
| chr9 | 141213431 | 6883392 | 0.0487 | 0.2272 |
| chr10 | 135534747 | 7871610 | 0.0581 | 0.2471 |
| chr11 | 135006516 | 8205968 | 0.0608 | 0.2548 |
| chr12 | 133851895 | 7521139 | 0.0562 | 0.2432 |
| chr13 | 115169878 | 6605314 | 0.0574 | 0.2458 |
| chr14 | 107349540 | 5377235 | 0.0501 | 0.2305 |
| chr15 | 102531392 | 4222567 | 0.0412 | 0.2092 |
| chr16 | 90354753 | 3310519 | 0.0366 | 0.1963 |
| chr17 | 81195210 | 2824844 | 0.0348 | 0.1917 |
| chr18 | 78077248 | 7576353 | 0.097 | 0.3212 |
| chr19 | 59128983 | 1350592 | 0.0228 | 0.1542 |
| chr20 | 63025520 | 2569152 | 0.0408 | 0.2065 |
| chr21 | 48129895 | 1949312 | 0.0405 | 0.2082 |
| chr22 | 51304566 | 996033 | 0.0194 | 0.1431 |
| chrMT | 16571 | 800 | 0.0483 | 0.2166 |
| chrX | 155270560 | 6096133 | 0.0393 | 0.2021 |
| chrY | 59373566 | 785184 | 0.0132 | 0.1182 |

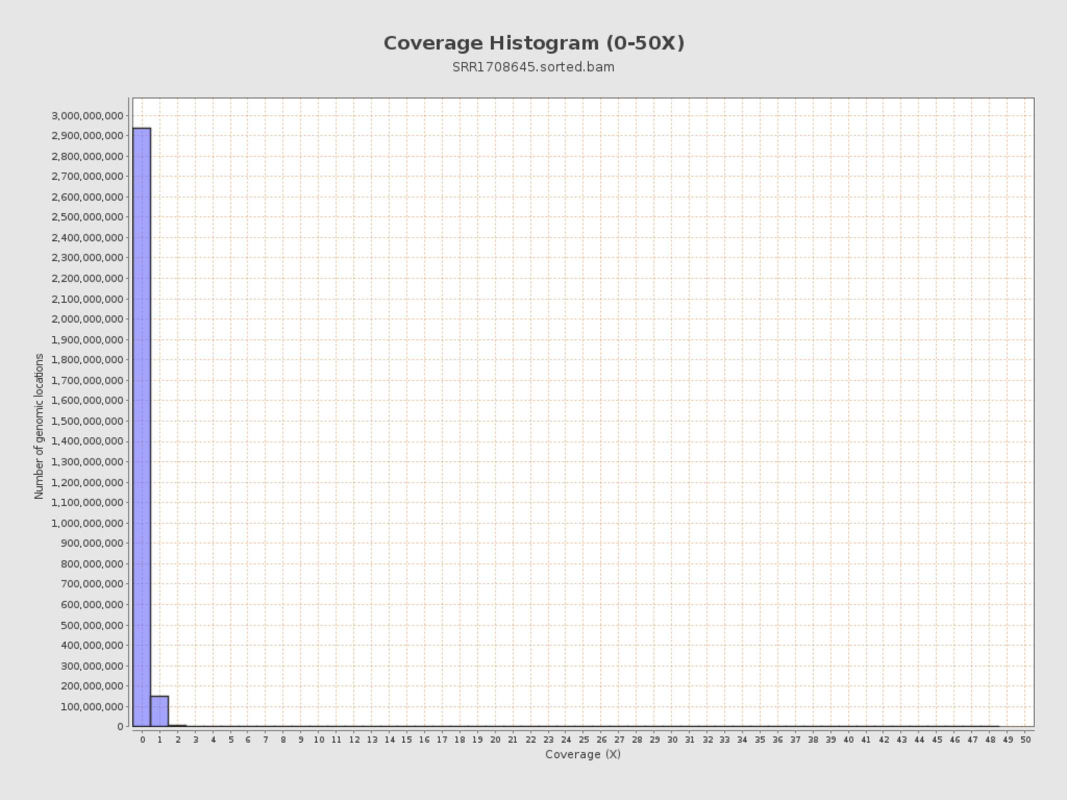
# 3. Results : Coverage across reference



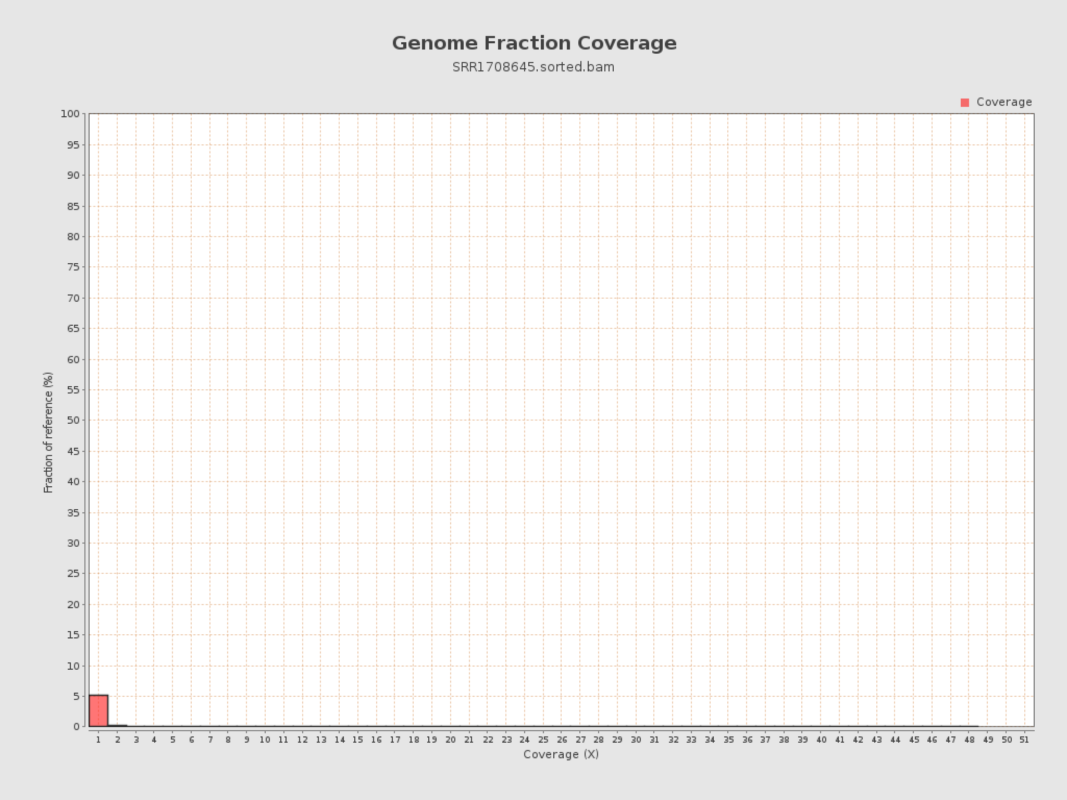
# 4. Results : Coverage Histogram



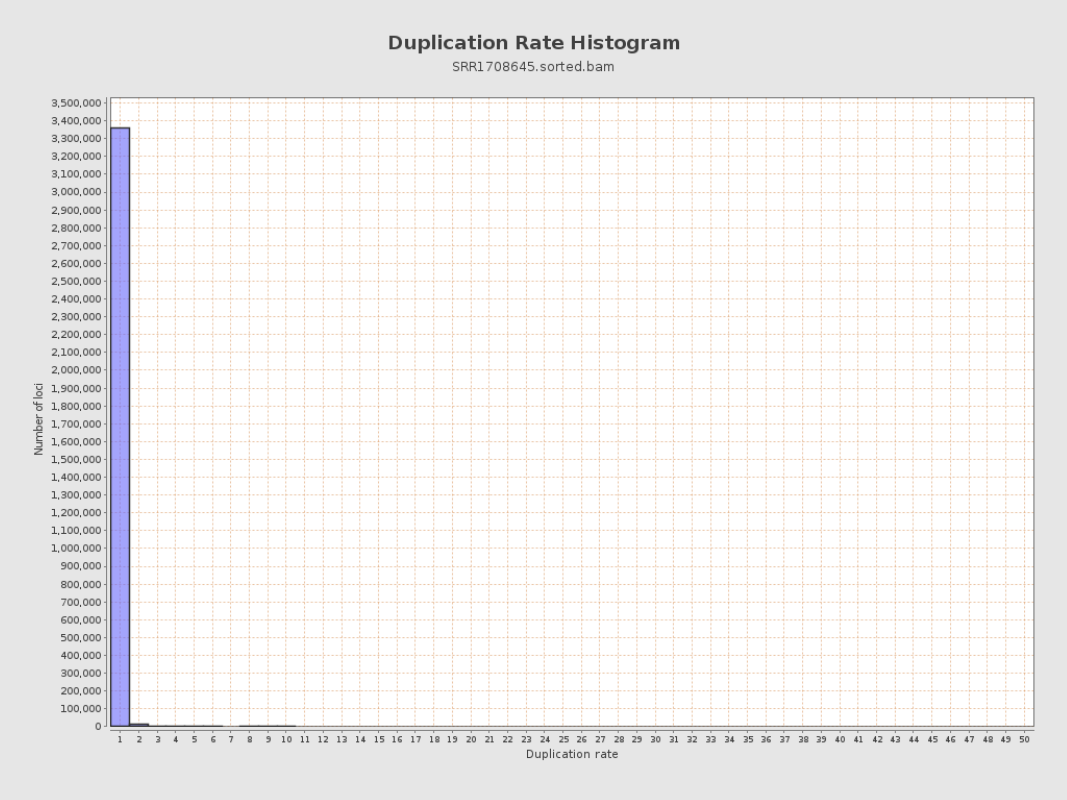
# 5. Results : Coverage Histogram (0-50X)



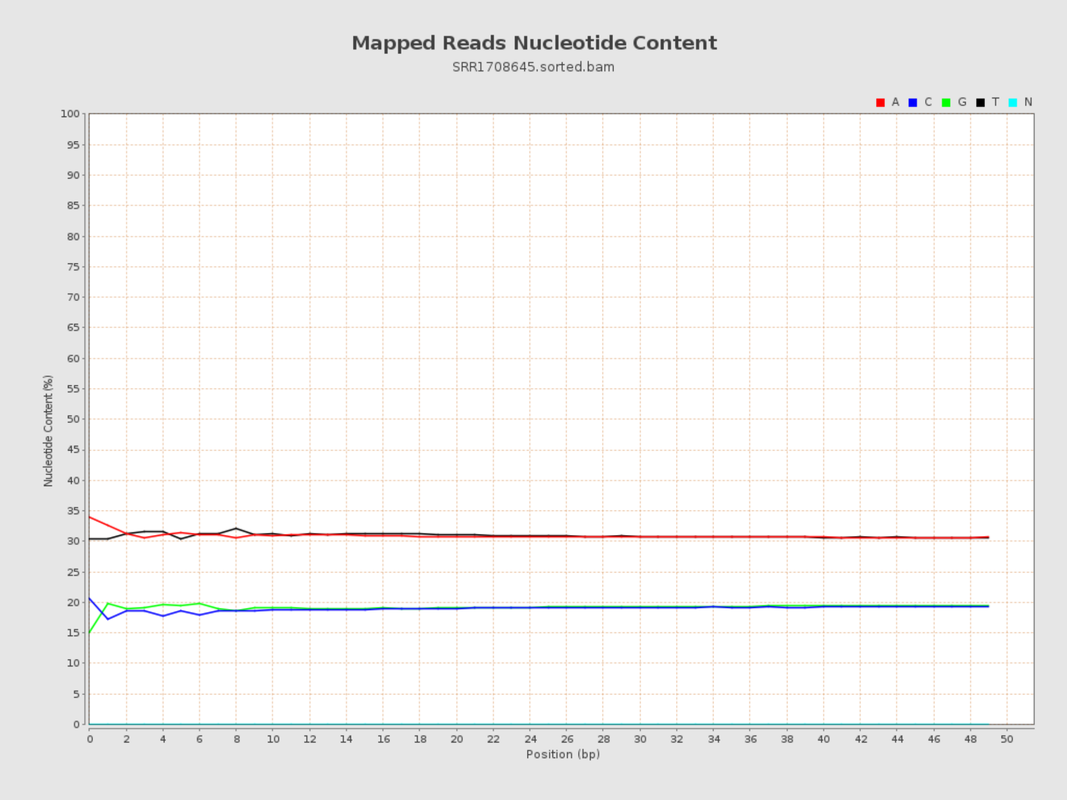
# 6. Results : Genome Fraction Coverage



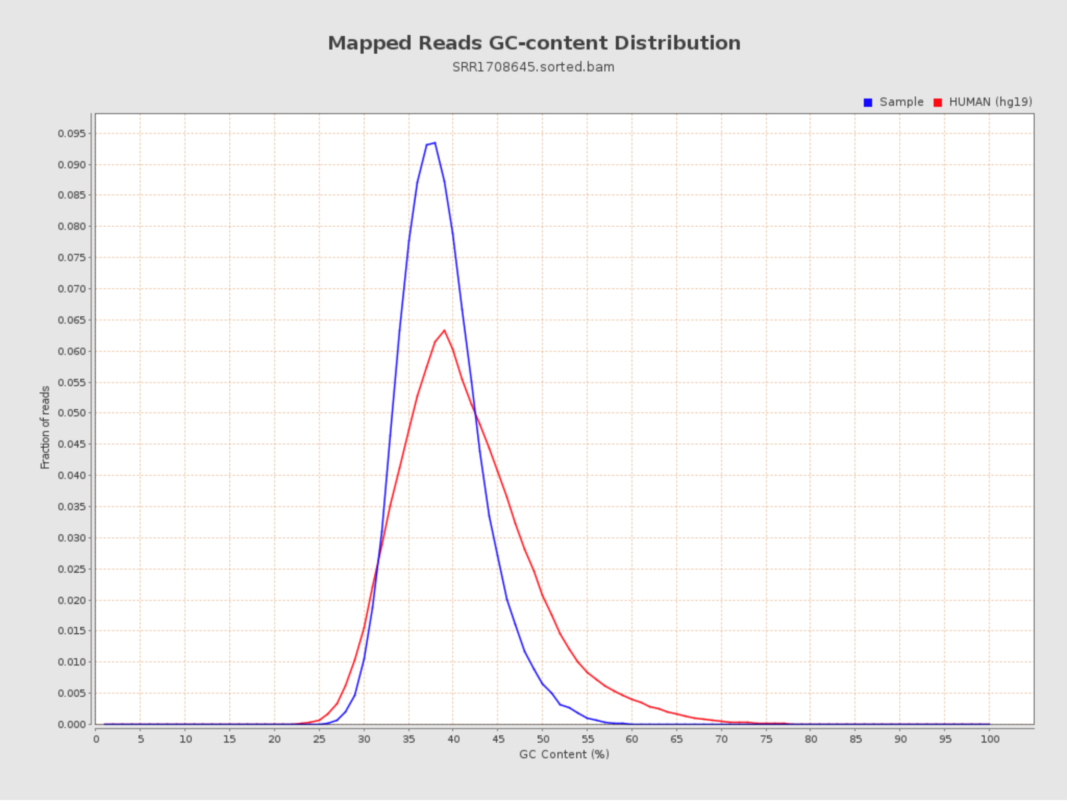
# 7. Results : Duplication Rate Histogram



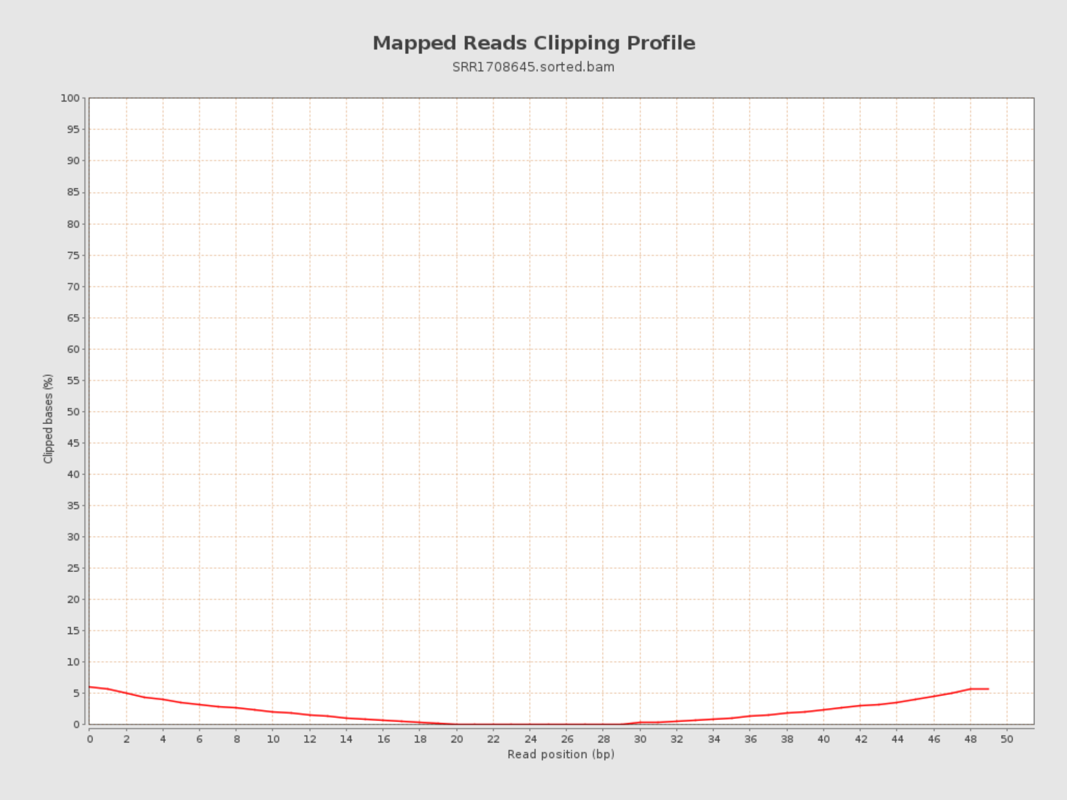
# 8. Results : Mapped Reads Nucleotide Content



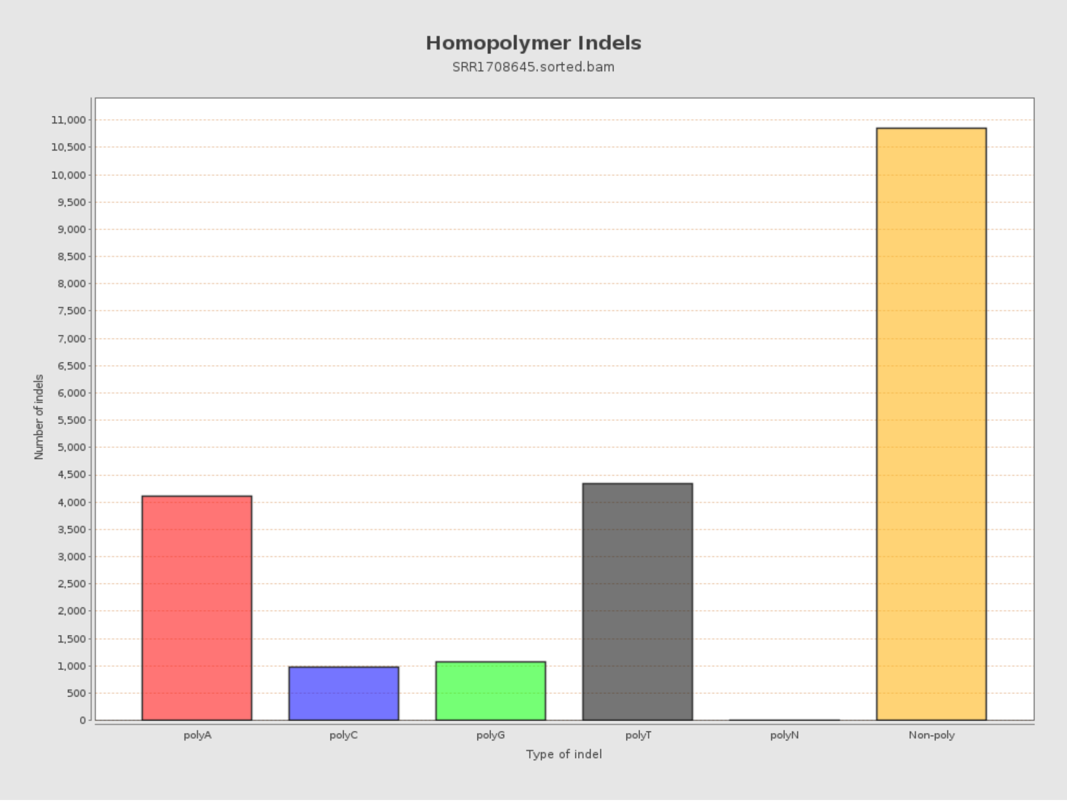
# 9. Results : Mapped Reads GC-content Distribution



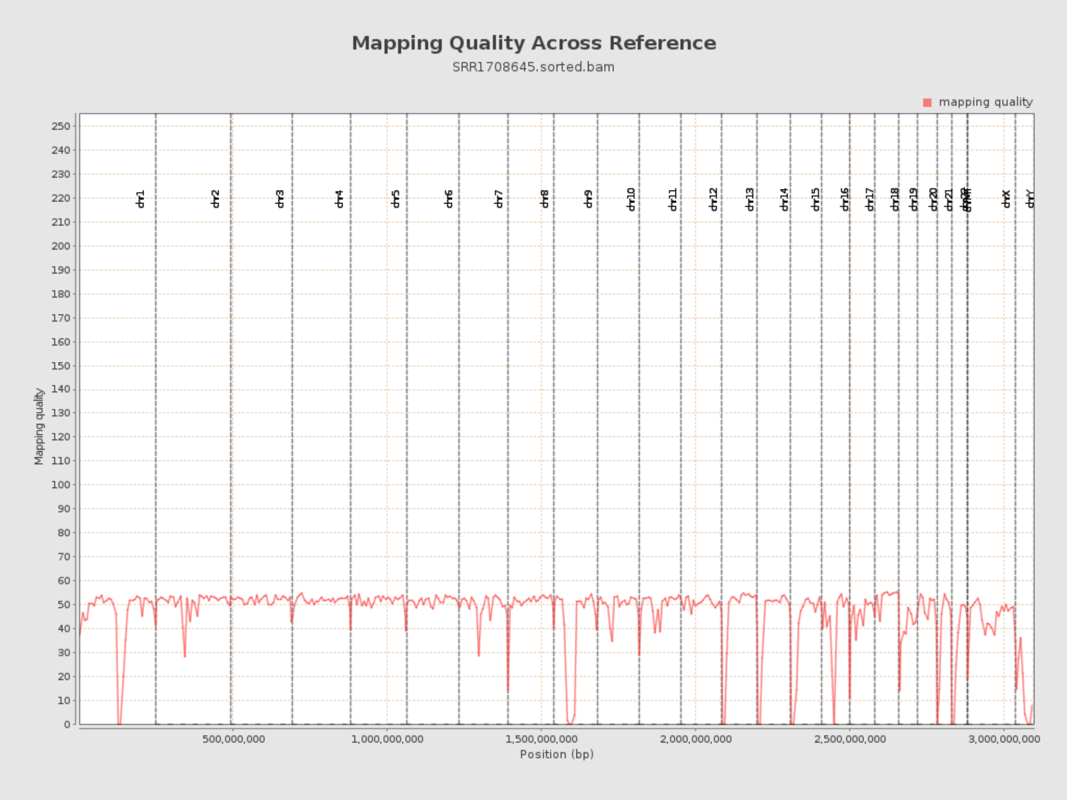
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram