# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 00:23:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708564.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_SRR1708564 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708564.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 00:23:48 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1708564.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,085,212 |
| Mapped reads | 3,348,071 / 81.96% |
| Unmapped reads | 737,141 / 18.04% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 103 / 0% |
| Read min/max/mean length | 30 / 50 / 50 |
| Duplicated reads (estimated) | 16,939 / 0.41% |
| Duplication rate | 0.5% |
| Clipped reads | 47,021 / 1.15% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 51,732,660 / 30.99% |
| Number/percentage of C's | 31,693,586 / 18.99% |
| Number/percentage of T's | 51,547,364 / 30.88% |
| Number/percentage of G's | 31,957,761 / 19.14% |
| Number/percentage of N's | 5,528 / 0% |
| GC Percentage | 38.13% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0539 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2429 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.81 |

## 2.5. Mismatches and indels

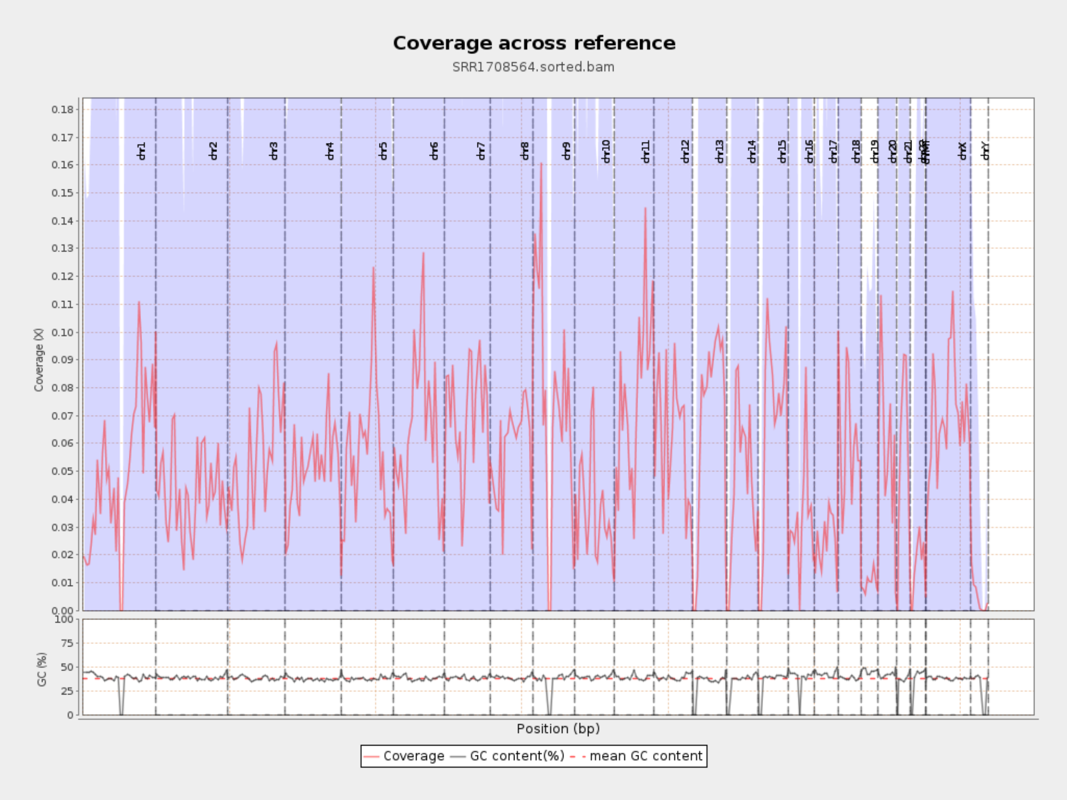
| | |
|---|---|
| General error rate | 0.17% |
| Mismatches | 270,154 |
| Insertions | 11,286 |
| Mapped reads with at least one insertion | 0.34% |
| Deletions | 9,191 |
| Mapped reads with at least one deletion | 0.27% |
| Homopolymer indels | 47.57% |

## 2.6. Chromosome stats

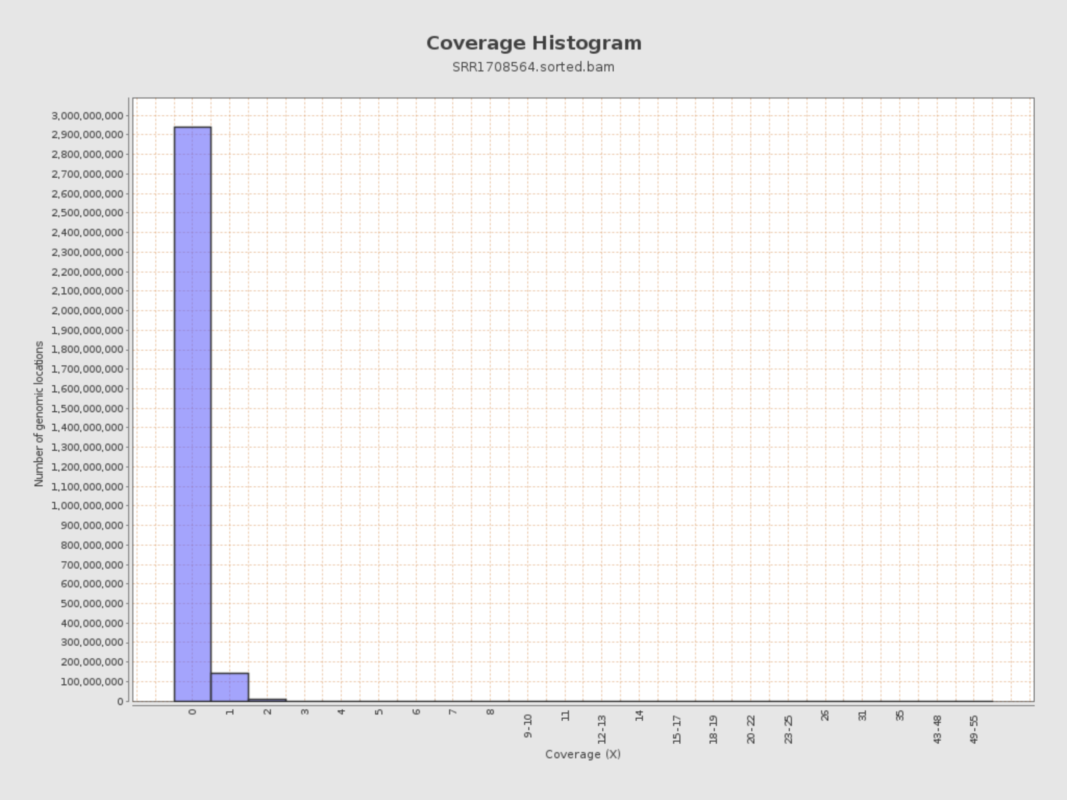
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 12393996 | 0.0497 | 0.2341 |
| chr2 | 243199373 | 10214487 | 0.042 | 0.2128 |
| chr3 | 198022430 | 10698753 | 0.054 | 0.2415 |
| chr4 | 191154276 | 9849753 | 0.0515 | 0.2358 |
| chr5 | 180915260 | 9909442 | 0.0548 | 0.2433 |
| chr6 | 171115067 | 11237461 | 0.0657 | 0.2675 |
| chr7 | 159138663 | 11050098 | 0.0694 | 0.2747 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 8496960 | 0.0581 | 0.2501 |
| chr9 | 141213431 | 10739197 | 0.076 | 0.2907 |
| chr10 | 135534747 | 5058089 | 0.0373 | 0.2002 |
| chr11 | 135006516 | 10207546 | 0.0756 | 0.2885 |
| chr12 | 133851895 | 8209282 | 0.0613 | 0.258 |
| chr13 | 115169878 | 8077093 | 0.0701 | 0.2764 |
| chr14 | 107349540 | 5017210 | 0.0467 | 0.2266 |
| chr15 | 102531392 | 6891054 | 0.0672 | 0.2733 |
| chr16 | 90354753 | 2963283 | 0.0328 | 0.1879 |
| chr17 | 81195210 | 2054568 | 0.0253 | 0.164 |
| chr18 | 78077248 | 4767219 | 0.0611 | 0.2566 |
| chr19 | 59128983 | 592811 | 0.01 | 0.1022 |
| chr20 | 63025520 | 3901639 | 0.0619 | 0.2611 |
| chr21 | 48129895 | 2648152 | 0.055 | 0.2474 |
| chr22 | 51304566 | 857249 | 0.0167 | 0.1335 |
| chrMT | 16571 | 150 | 0.0091 | 0.0947 |
| chrX | 155270560 | 10832565 | 0.0698 | 0.2761 |
| chrY | 59373566 | 284468 | 0.0048 | 0.0729 |

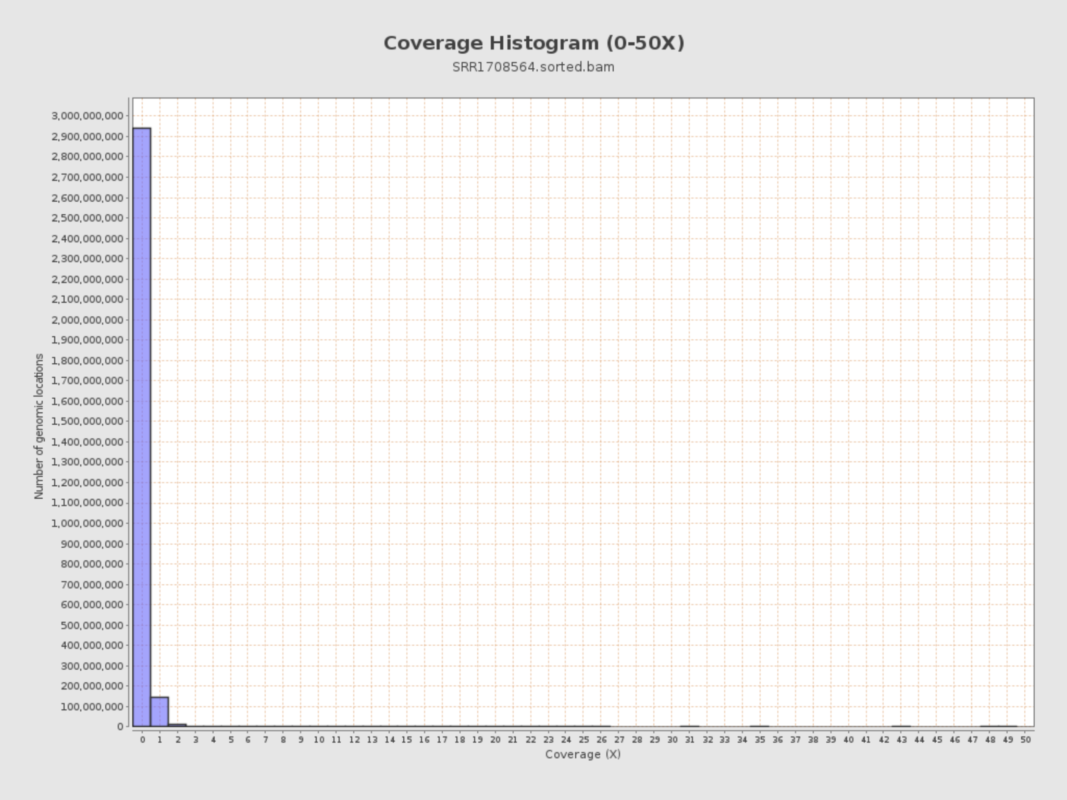
# 3. Results : Coverage across reference



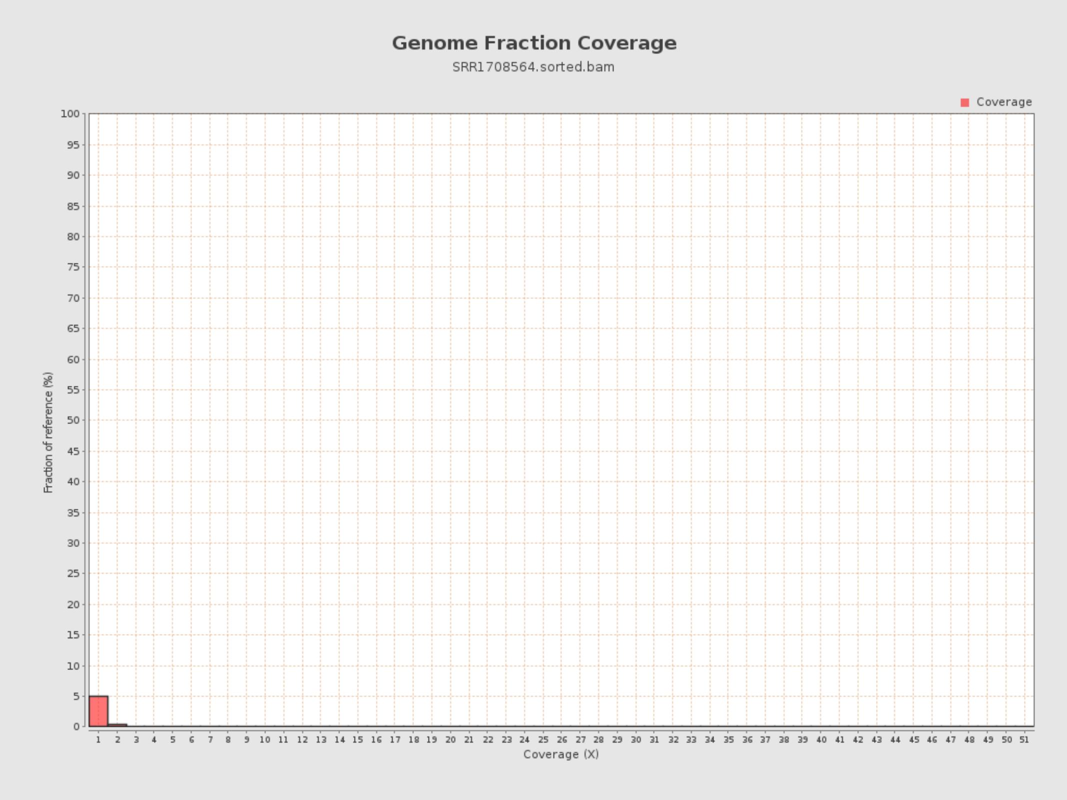
# 4. Results : Coverage Histogram



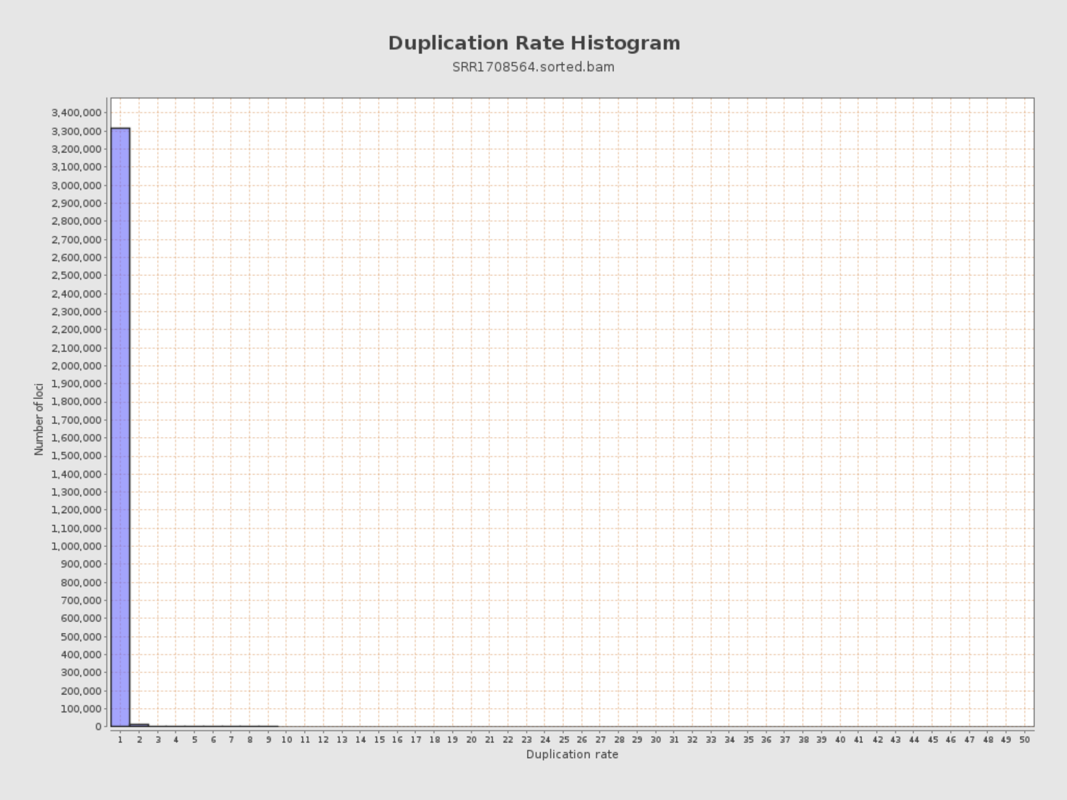
# 5. Results : Coverage Histogram (0-50X)



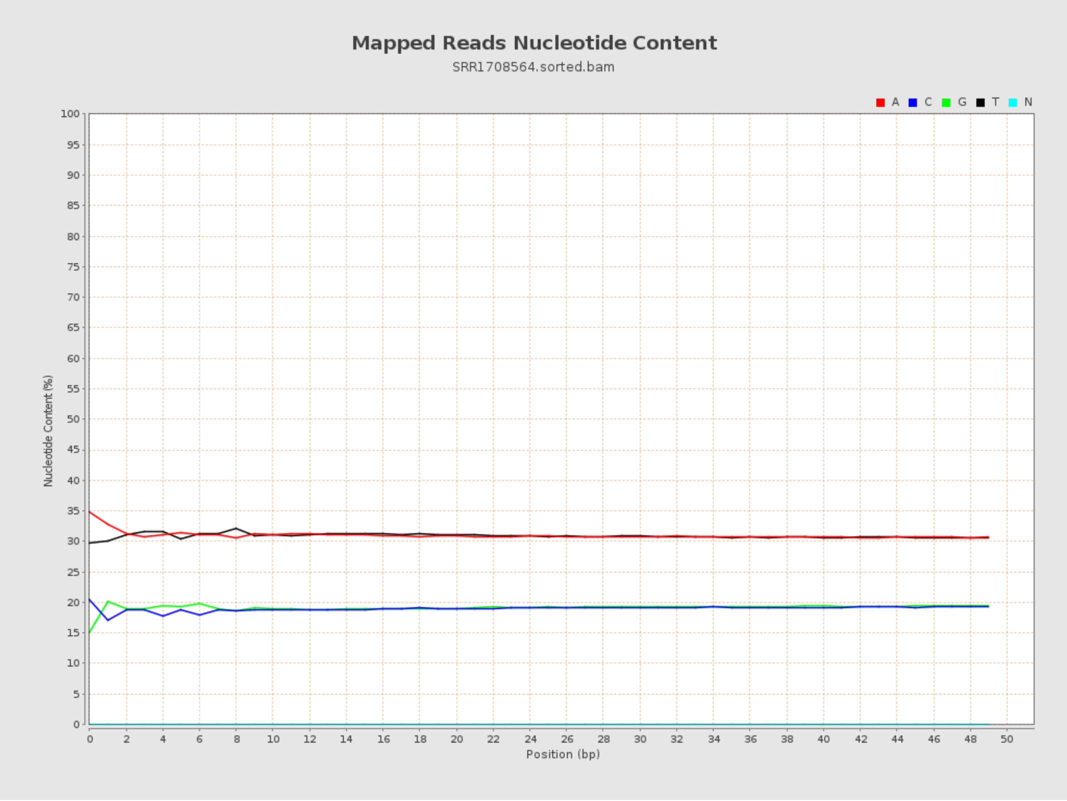
# 6. Results : Genome Fraction Coverage



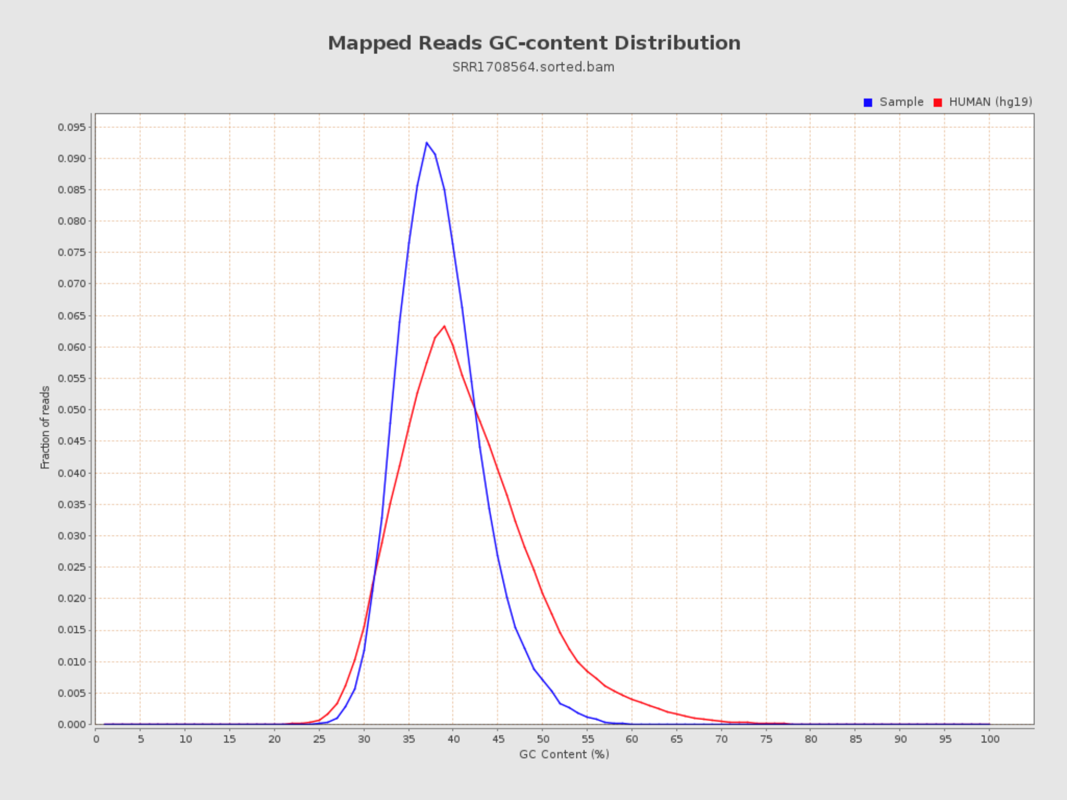
# 7. Results : Duplication Rate Histogram



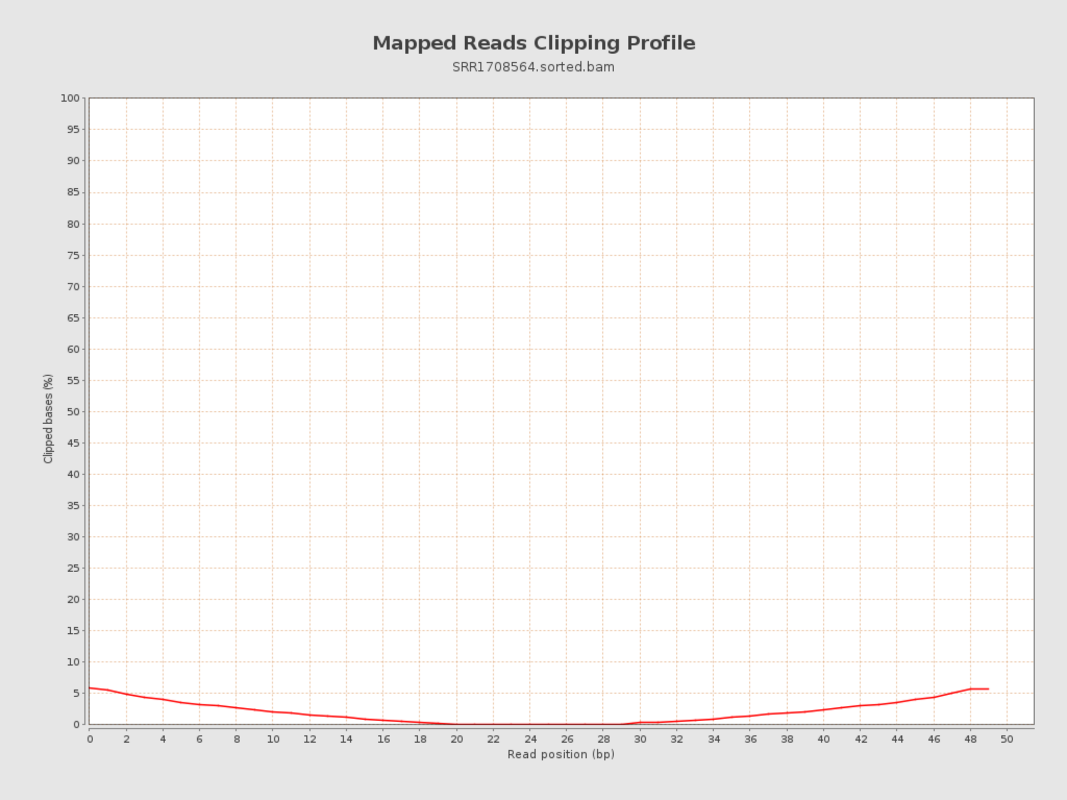
# 8. Results : Mapped Reads Nucleotide Content



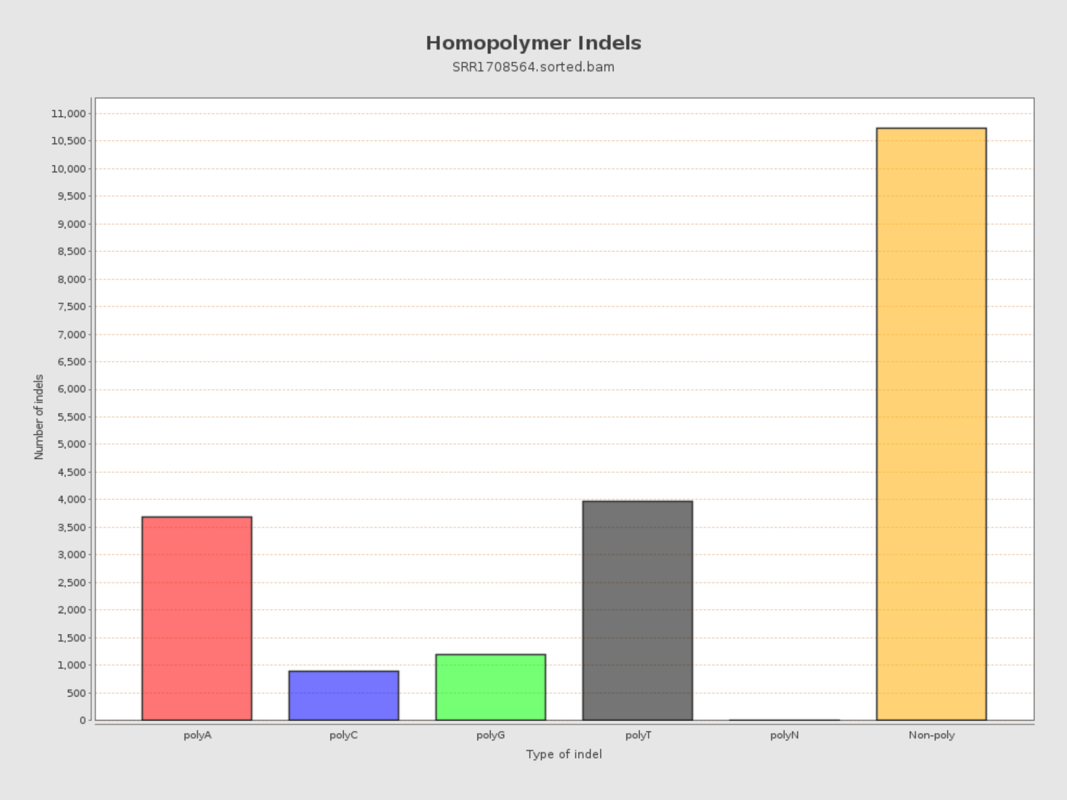
# 9. Results : Mapped Reads GC-content Distribution



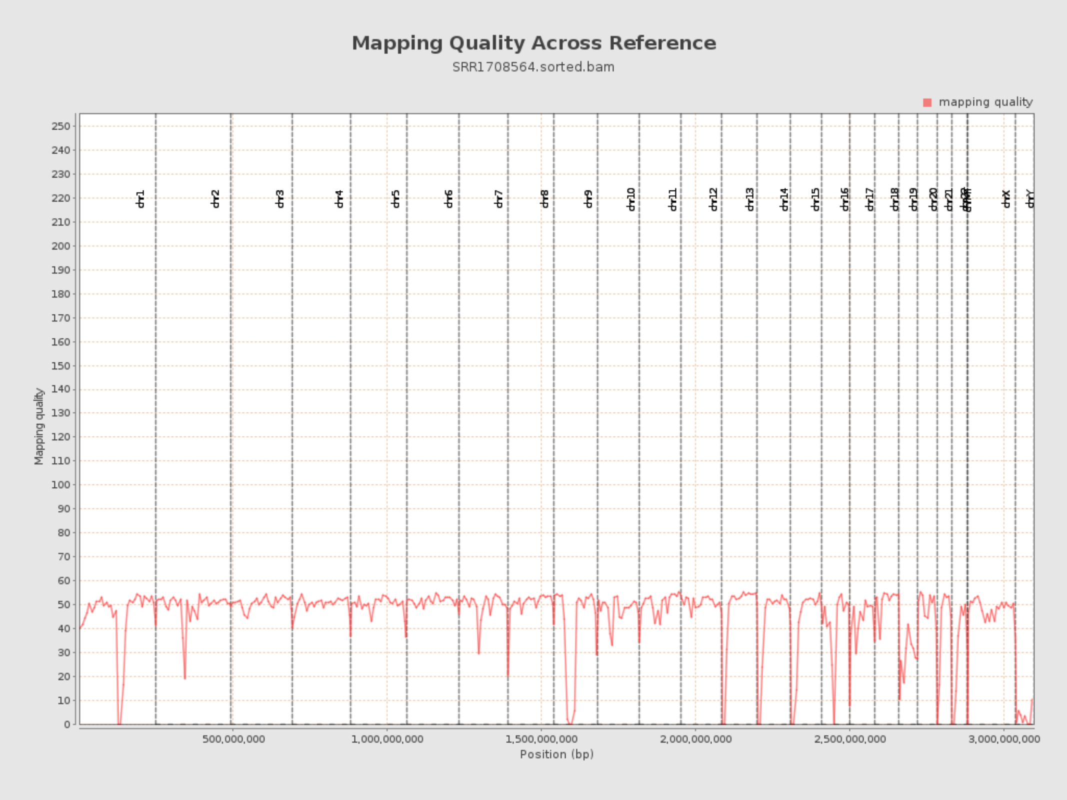
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram