# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 06:43:35*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1708596.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_SRR1708596 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1708596.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 06:43:33 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1708596.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,830,962 |
| Mapped reads | 3,746,984 / 97.81% |
| Unmapped reads | 83,978 / 2.19% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 114 / 0% |
| Read min/max/mean length | 30 / 50 / 50 |
| Duplicated reads (estimated) | 36,172 / 0.94% |
| Duplication rate | 0.97% |
| Clipped reads | 52,148 / 1.36% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 57,974,758 / 31.03% |
| Number/percentage of C's | 35,313,074 / 18.9% |
| Number/percentage of T's | 57,727,282 / 30.89% |
| Number/percentage of G's | 35,831,439 / 19.18% |
| Number/percentage of N's | 6,627 / 0% |
| GC Percentage | 38.08% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0604 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2549 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.72 |

## 2.5. Mismatches and indels

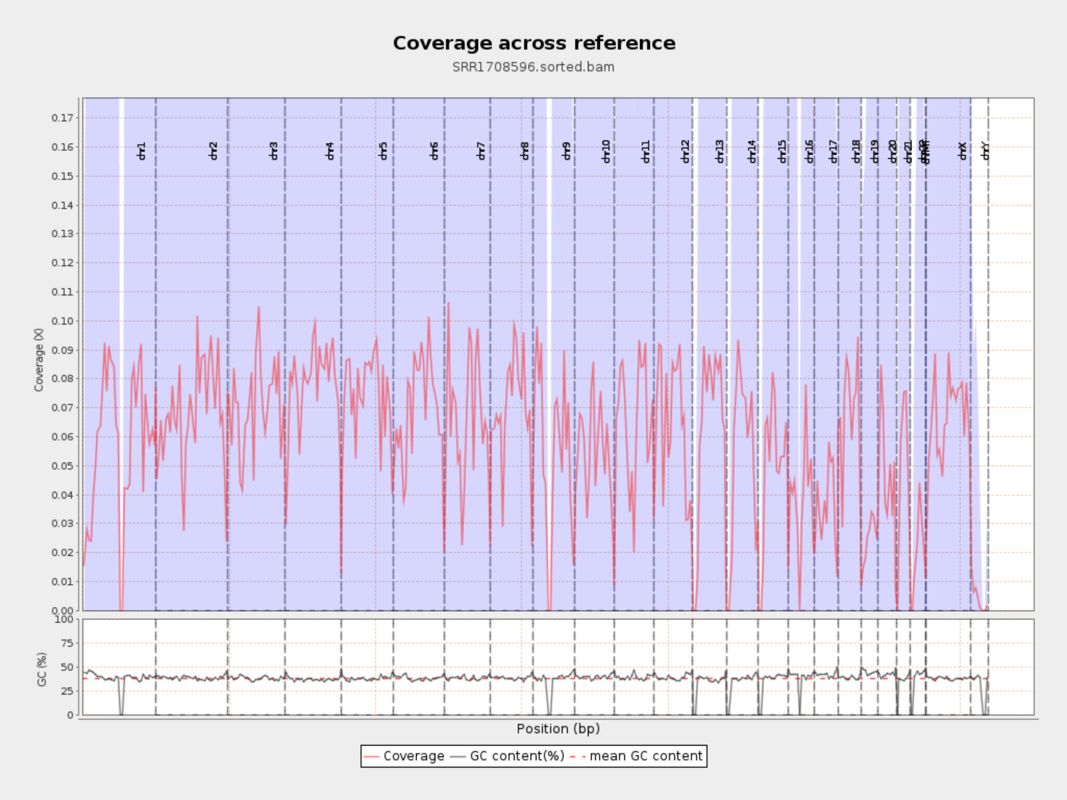
| | |
|---|---|
| General error rate | 0.15% |
| Mismatches | 272,774 |
| Insertions | 11,884 |
| Mapped reads with at least one insertion | 0.32% |
| Deletions | 9,593 |
| Mapped reads with at least one deletion | 0.26% |
| Homopolymer indels | 48.16% |

## 2.6. Chromosome stats

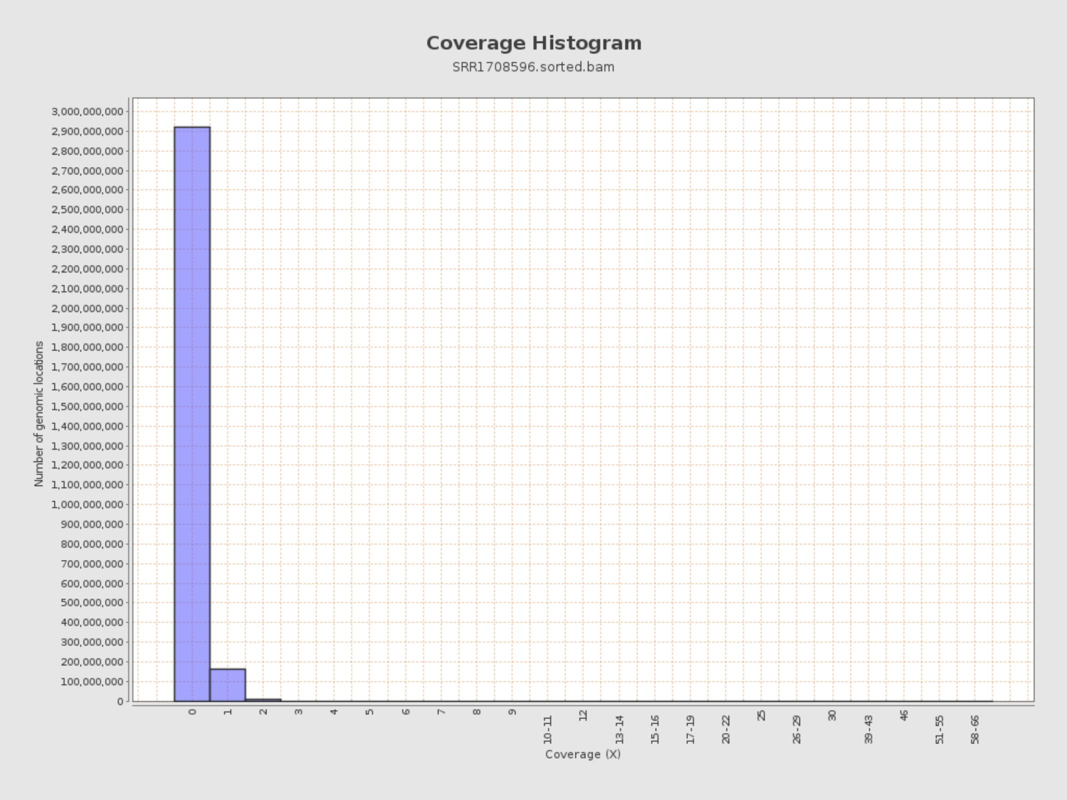
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 14332287 | 0.0575 | 0.2504 |
| chr2 | 243199373 | 16473950 | 0.0677 | 0.2689 |
| chr3 | 198022430 | 14060486 | 0.071 | 0.2753 |
| chr4 | 191154276 | 14936498 | 0.0781 | 0.2889 |
| chr5 | 180915260 | 13289760 | 0.0735 | 0.28 |
| chr6 | 171115067 | 12047486 | 0.0704 | 0.2742 |
| chr7 | 159138663 | 10437169 | 0.0656 | 0.2655 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 10227449 | 0.0699 | 0.2733 |
| chr9 | 141213431 | 7877489 | 0.0558 | 0.2456 |
| chr10 | 135534747 | 7556290 | 0.0558 | 0.2436 |
| chr11 | 135006516 | 8775545 | 0.065 | 0.265 |
| chr12 | 133851895 | 8578204 | 0.0641 | 0.2623 |
| chr13 | 115169878 | 7222146 | 0.0627 | 0.2595 |
| chr14 | 107349540 | 5840572 | 0.0544 | 0.2418 |
| chr15 | 102531392 | 4988473 | 0.0487 | 0.2295 |
| chr16 | 90354753 | 3413312 | 0.0378 | 0.2011 |
| chr17 | 81195210 | 2996304 | 0.0369 | 0.1988 |
| chr18 | 78077248 | 5398988 | 0.0691 | 0.272 |
| chr19 | 59128983 | 1468788 | 0.0248 | 0.1618 |
| chr20 | 63025520 | 3073771 | 0.0488 | 0.2297 |
| chr21 | 48129895 | 2239632 | 0.0465 | 0.2247 |
| chr22 | 51304566 | 1065009 | 0.0208 | 0.1494 |
| chrMT | 16571 | 350 | 0.0211 | 0.1438 |
| chrX | 155270560 | 10331015 | 0.0665 | 0.2667 |
| chrY | 59373566 | 238453 | 0.004 | 0.0659 |

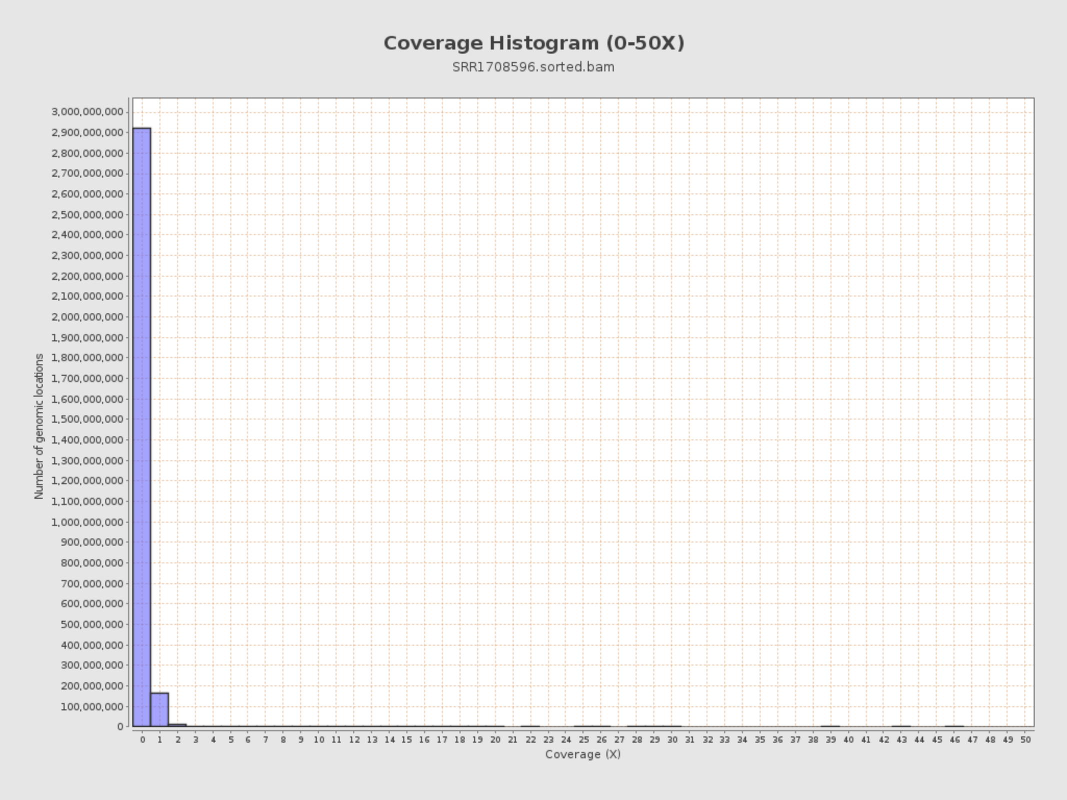
# 3. Results : Coverage across reference



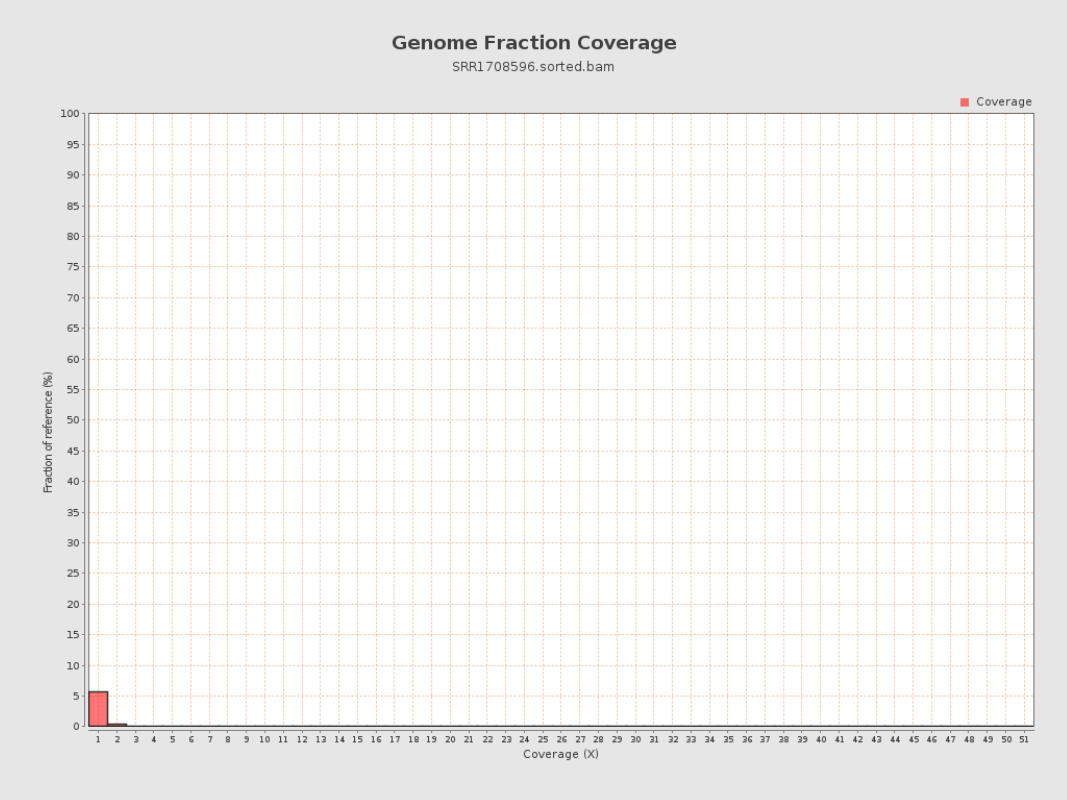
# 4. Results : Coverage Histogram



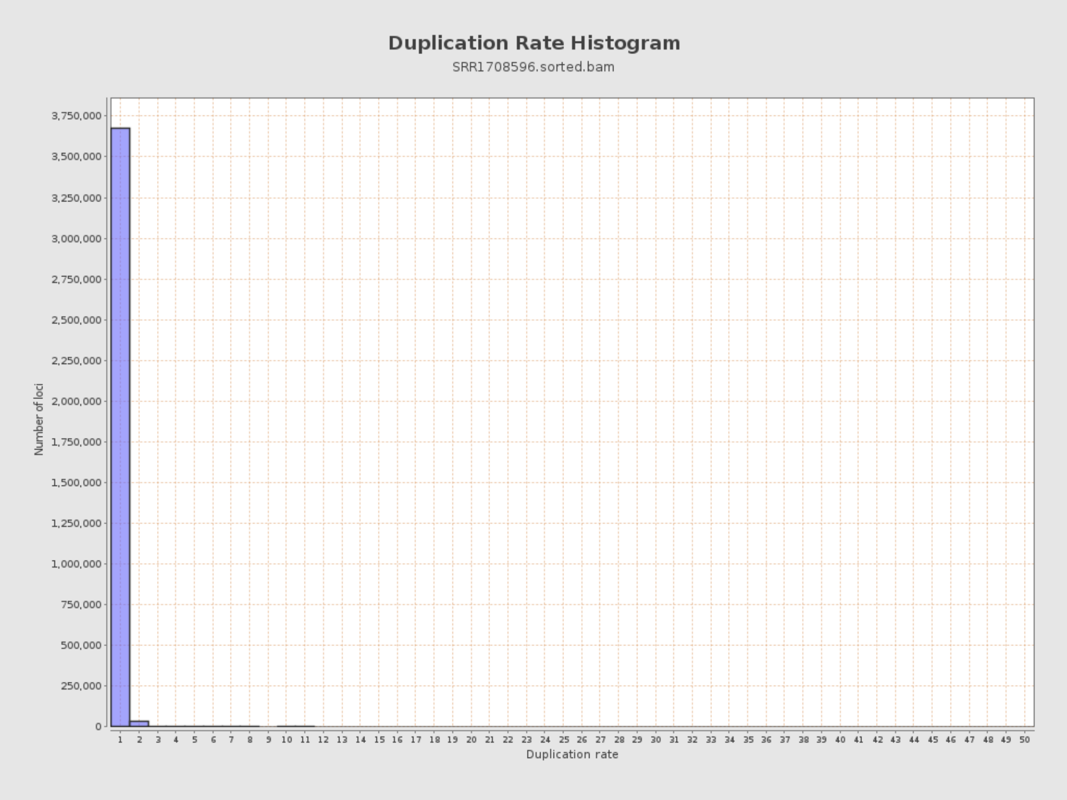
# 5. Results : Coverage Histogram (0-50X)



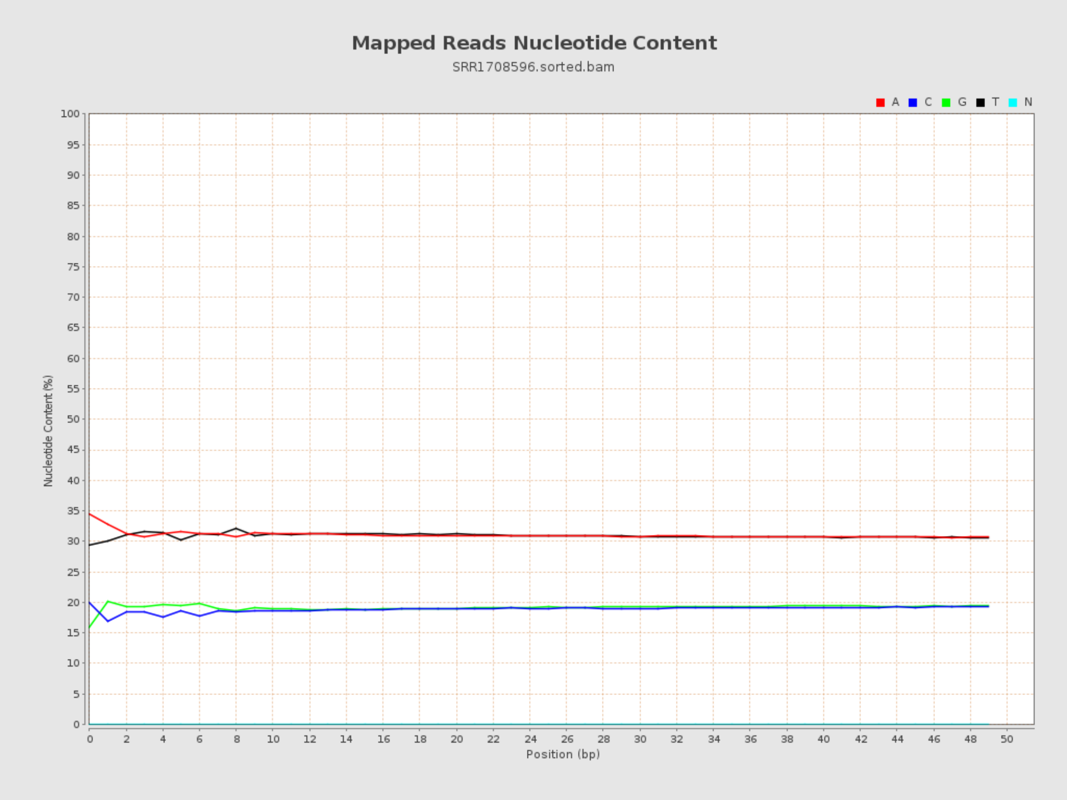
# 6. Results : Genome Fraction Coverage



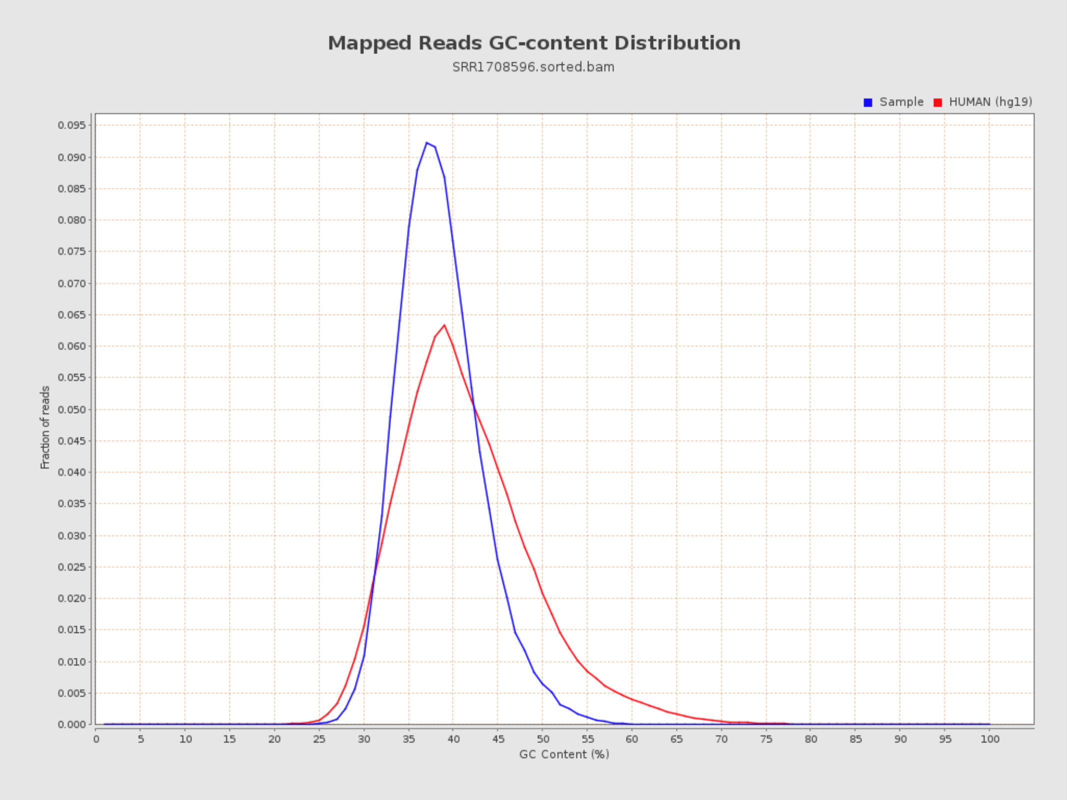
# 7. Results : Duplication Rate Histogram



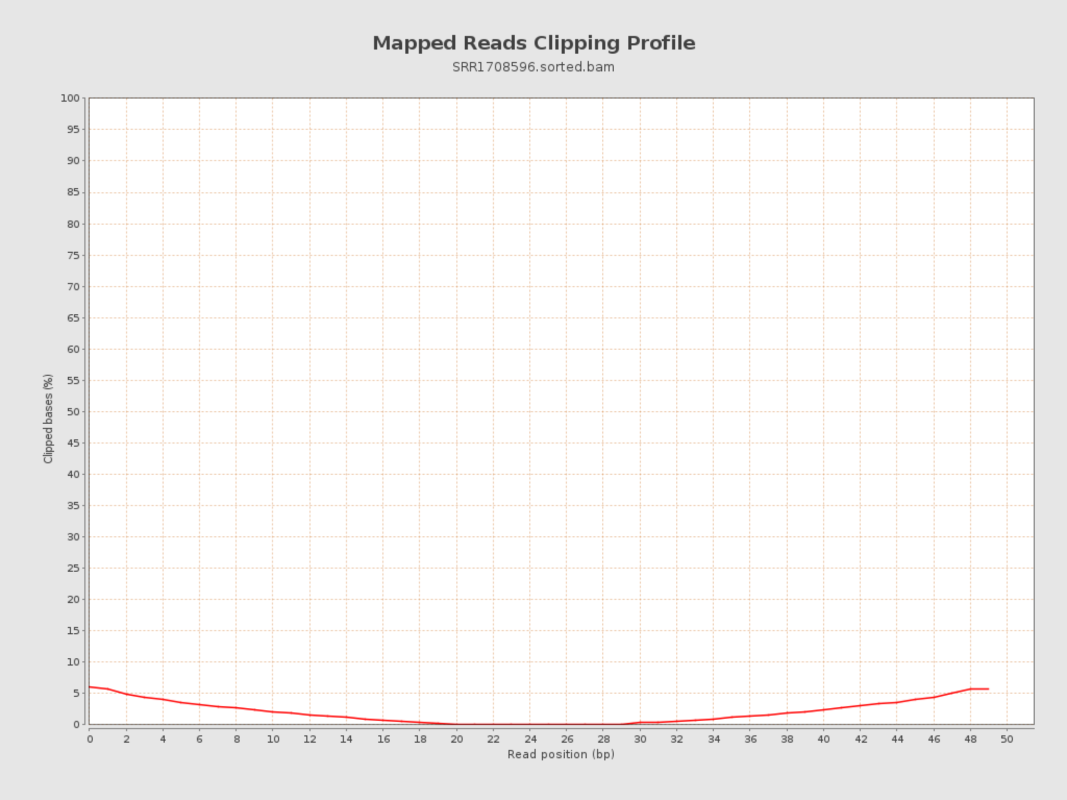
# 8. Results : Mapped Reads Nucleotide Content



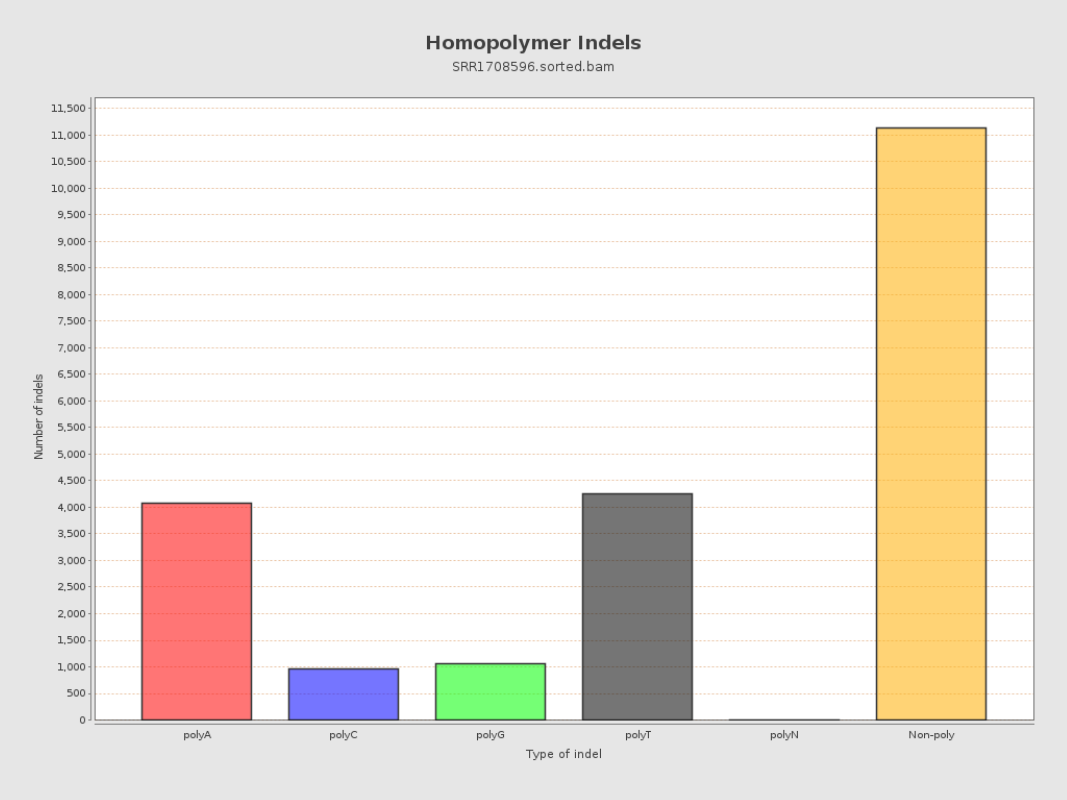
# 9. Results : Mapped Reads GC-content Distribution



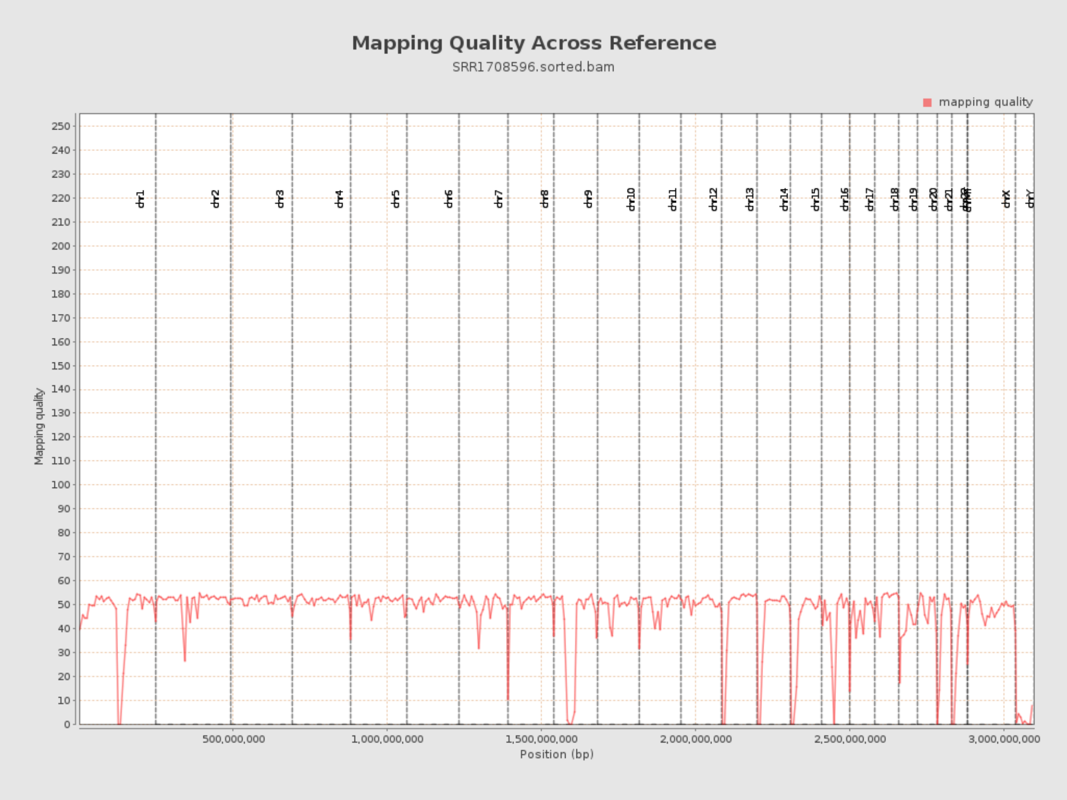
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram