# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/15 17:07:22*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068953.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_SRR6068953 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068953.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 15 17:07:21 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6068953.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,367,309 |
| Mapped reads | 1,942,363 / 82.05% |
| Unmapped reads | 424,946 / 17.95% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 8,168 / 0.35% |
| Read min/max/mean length | 30 / 76 / 76.12 |
| Duplicated reads (estimated) | 79,603 / 3.36% |
| Duplication rate | 3.04% |
| Clipped reads | 1,089,817 / 46.04% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 32,458,850 / 26.13% |
| Number/percentage of C's | 21,041,393 / 16.94% |
| Number/percentage of T's | 41,443,420 / 33.36% |
| Number/percentage of G's | 28,977,646 / 23.33% |
| Number/percentage of N's | 292,762 / 0.24% |
| GC Percentage | 40.27% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0401 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3644 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45 |

## 2.5. Mismatches and indels

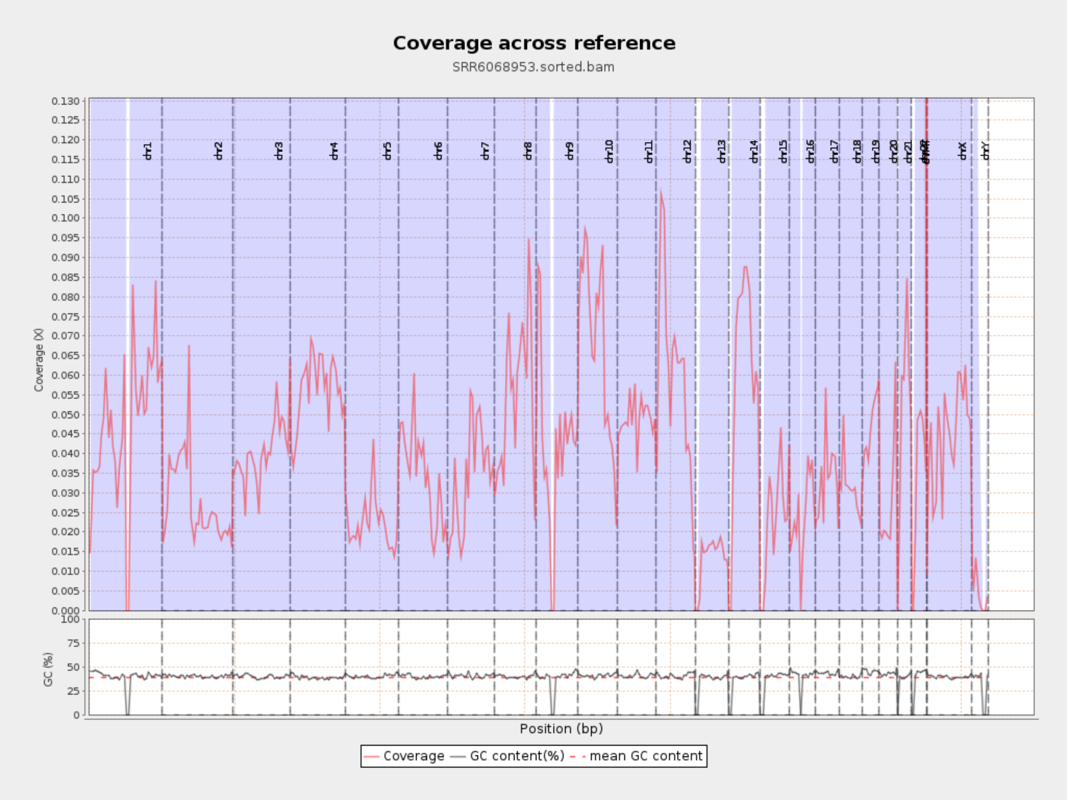
| | |
|---|---|
| General error rate | 0.94% |
| Mismatches | 1,152,403 |
| Insertions | 11,001 |
| Mapped reads with at least one insertion | 0.56% |
| Deletions | 35,239 |
| Mapped reads with at least one deletion | 1.8% |
| Homopolymer indels | 48.27% |

## 2.6. Chromosome stats

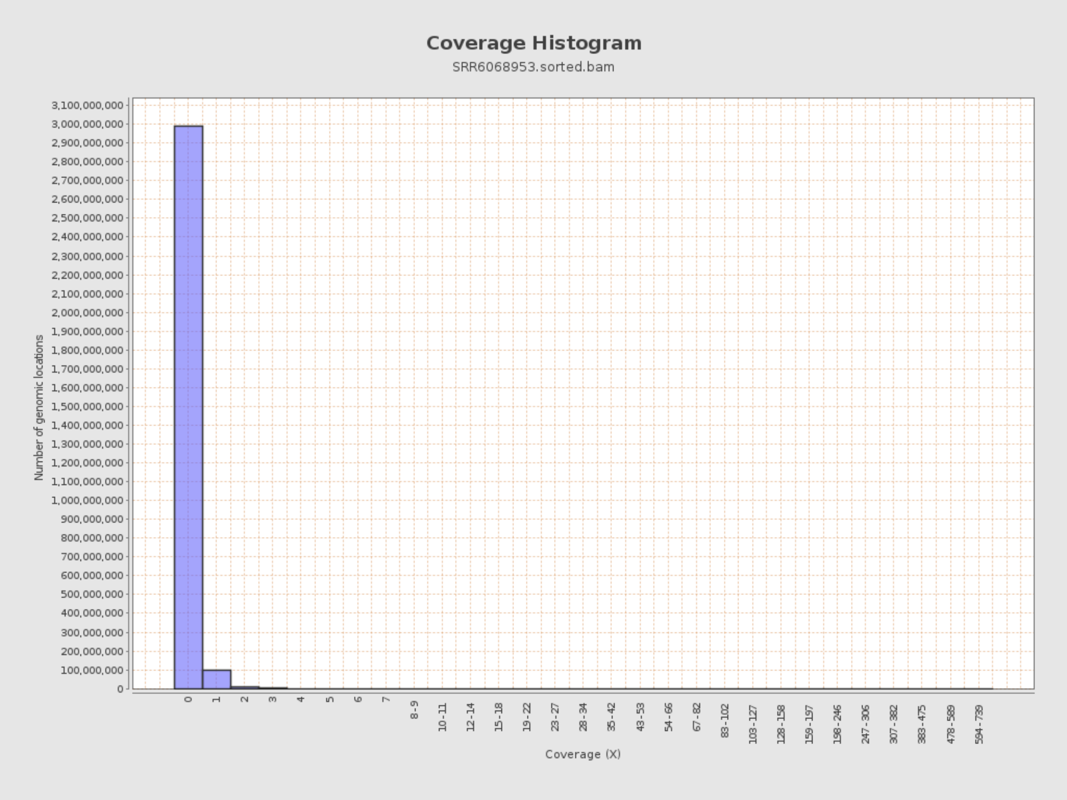
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 11740797 | 0.0471 | 0.6193 |
| chr2 | 243199373 | 6805638 | 0.028 | 0.373 |
| chr3 | 198022430 | 7908680 | 0.0399 | 0.225 |
| chr4 | 191154276 | 10747609 | 0.0562 | 0.2708 |
| chr5 | 180915260 | 4039773 | 0.0223 | 0.1706 |
| chr6 | 171115067 | 5925051 | 0.0346 | 0.2703 |
| chr7 | 159138663 | 5504359 | 0.0346 | 0.3284 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 8017147 | 0.0548 | 0.5032 |
| chr9 | 141213431 | 5915500 | 0.0419 | 0.4668 |
| chr10 | 135534747 | 9407636 | 0.0694 | 0.405 |
| chr11 | 135006516 | 6552714 | 0.0485 | 0.4112 |
| chr12 | 133851895 | 8002319 | 0.0598 | 0.2852 |
| chr13 | 115169878 | 1530129 | 0.0133 | 0.1287 |
| chr14 | 107349540 | 6531201 | 0.0608 | 0.305 |
| chr15 | 102531392 | 2357713 | 0.023 | 0.1686 |
| chr16 | 90354753 | 2187432 | 0.0242 | 0.2272 |
| chr17 | 81195210 | 2723215 | 0.0335 | 0.2377 |
| chr18 | 78077248 | 2458331 | 0.0315 | 0.753 |
| chr19 | 59128983 | 2757109 | 0.0466 | 0.3664 |
| chr20 | 63025520 | 1765364 | 0.028 | 0.2067 |
| chr21 | 48129895 | 2470330 | 0.0513 | 0.2681 |
| chr22 | 51304566 | 1698199 | 0.0331 | 0.2037 |
| chrMT | 16571 | 82120 | 4.9556 | 3.9099 |
| chrX | 155270560 | 6891685 | 0.0444 | 0.2834 |
| chrY | 59373566 | 250872 | 0.0042 | 0.1032 |

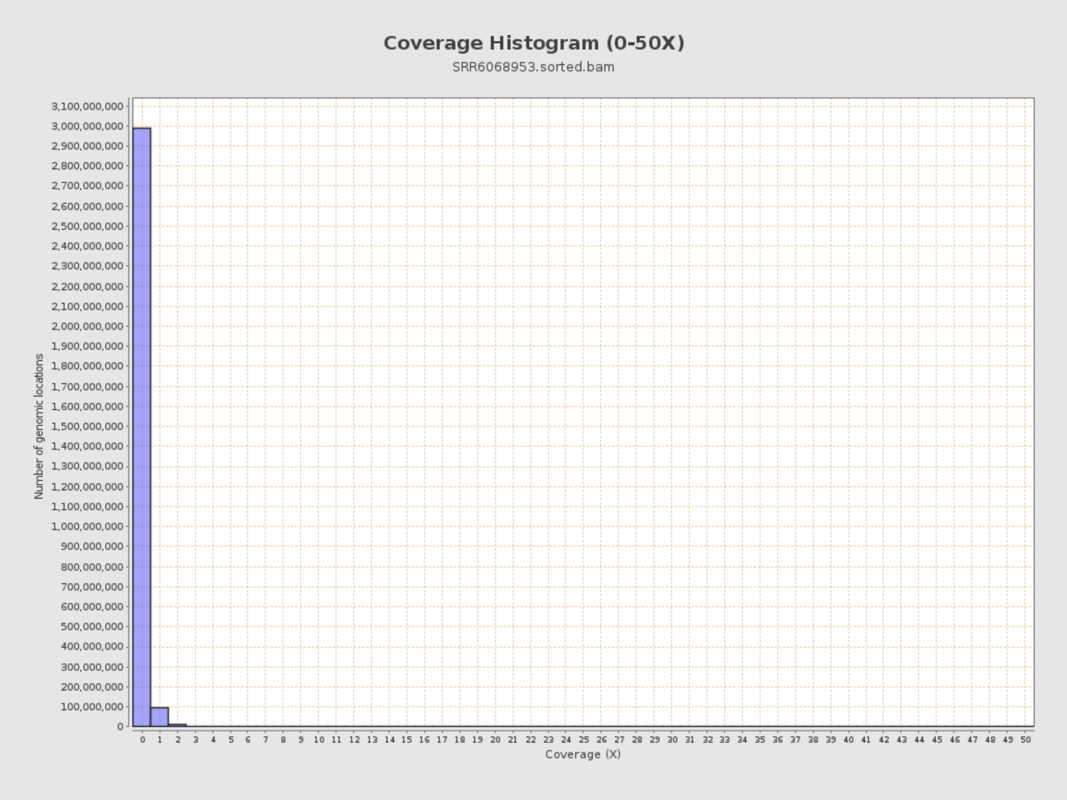
# 3. Results : Coverage across reference



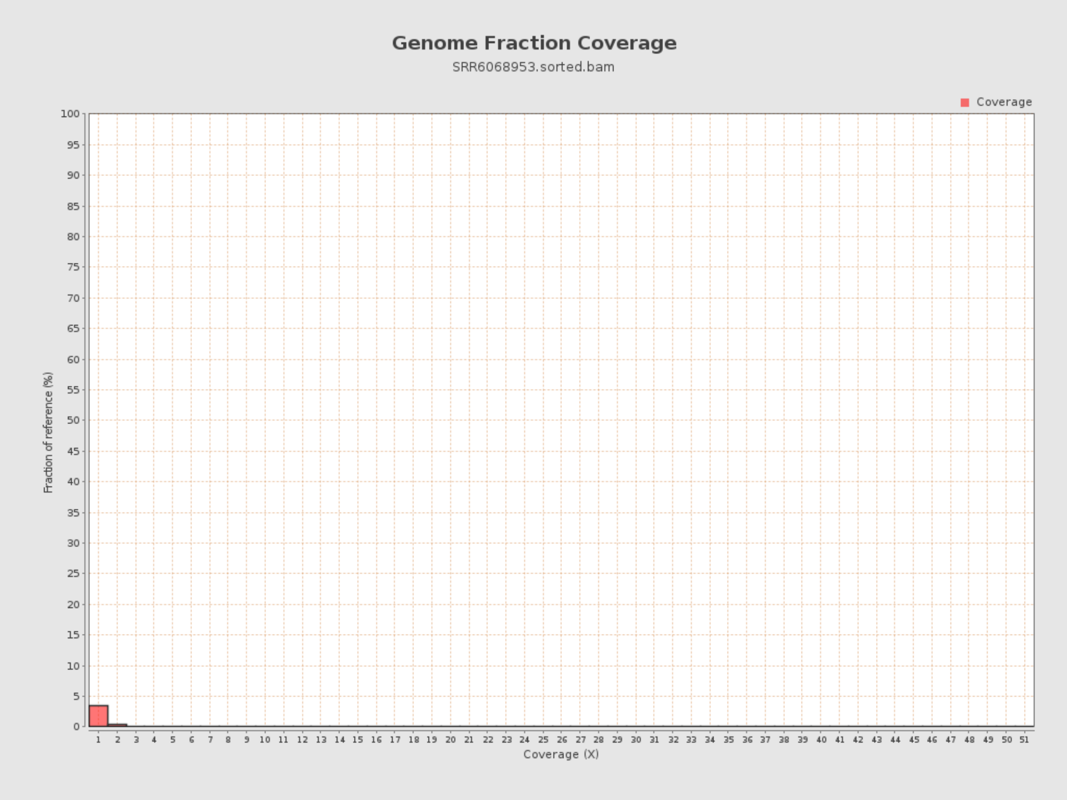
# 4. Results : Coverage Histogram



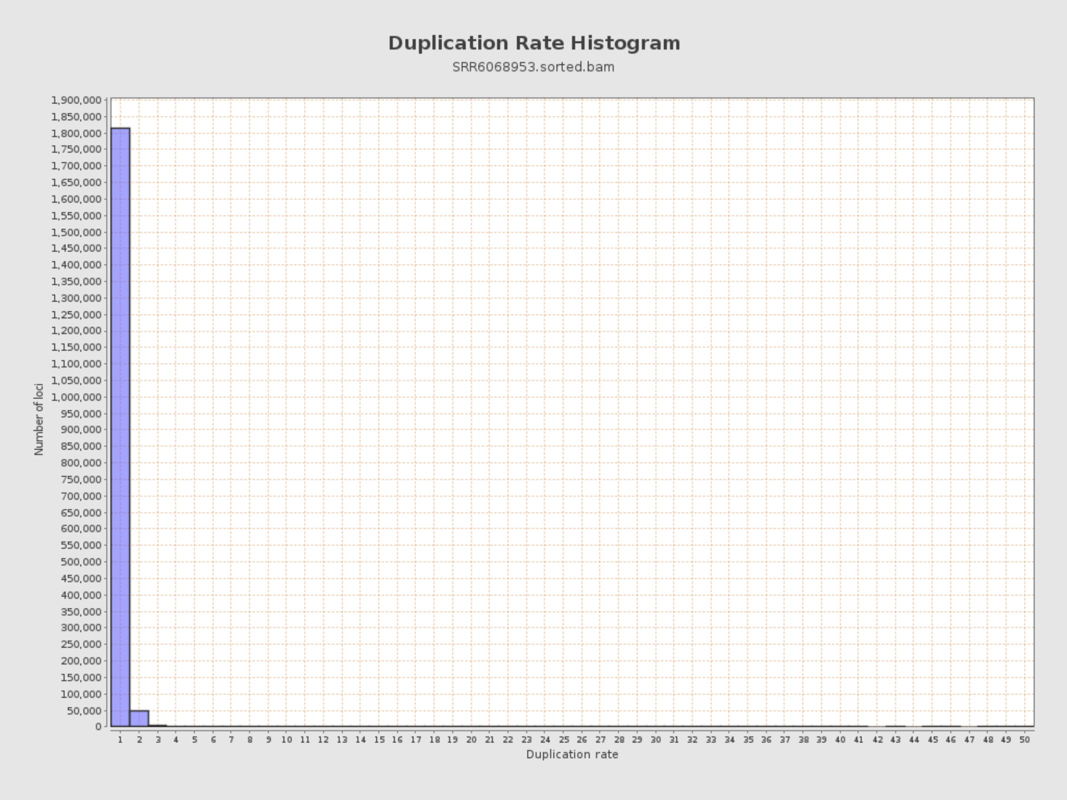
# 5. Results : Coverage Histogram (0-50X)



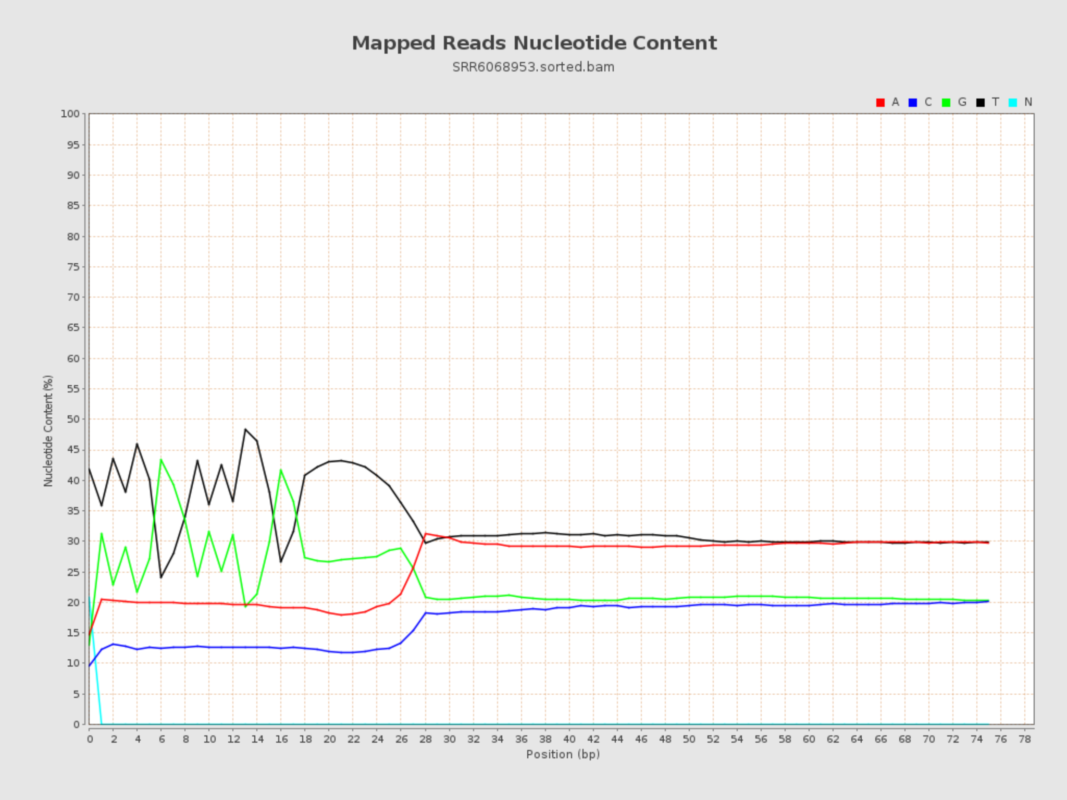
# 6. Results : Genome Fraction Coverage



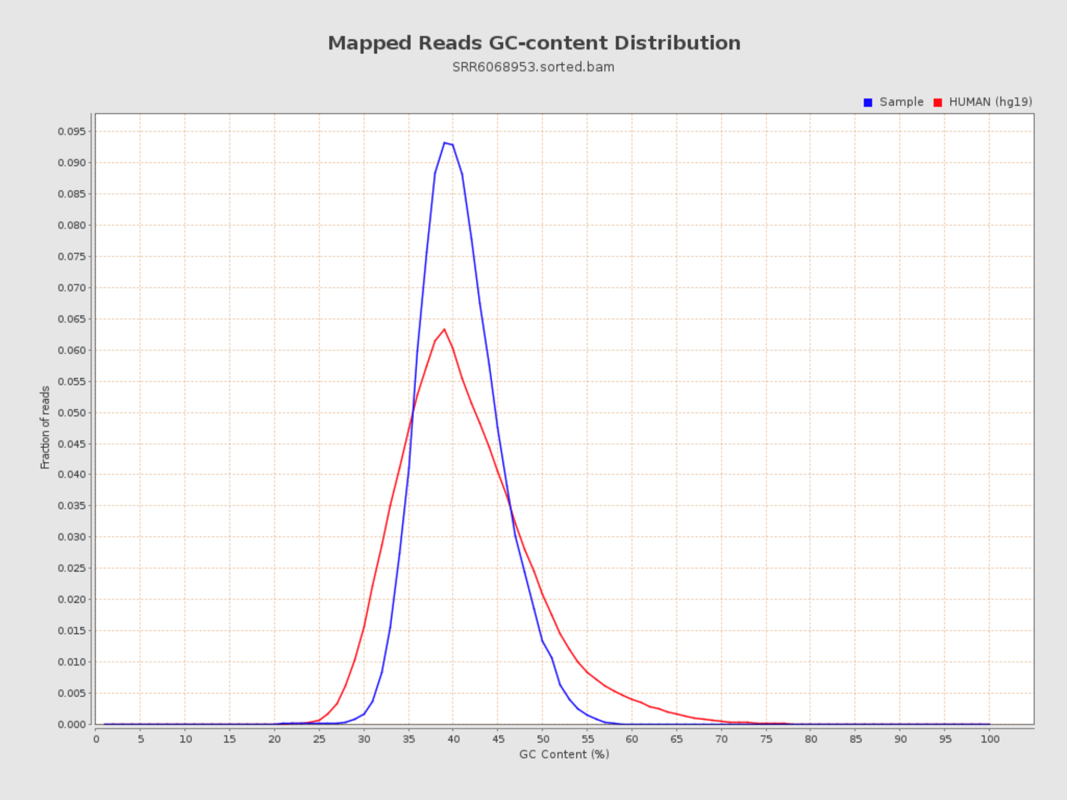
# 7. Results : Duplication Rate Histogram



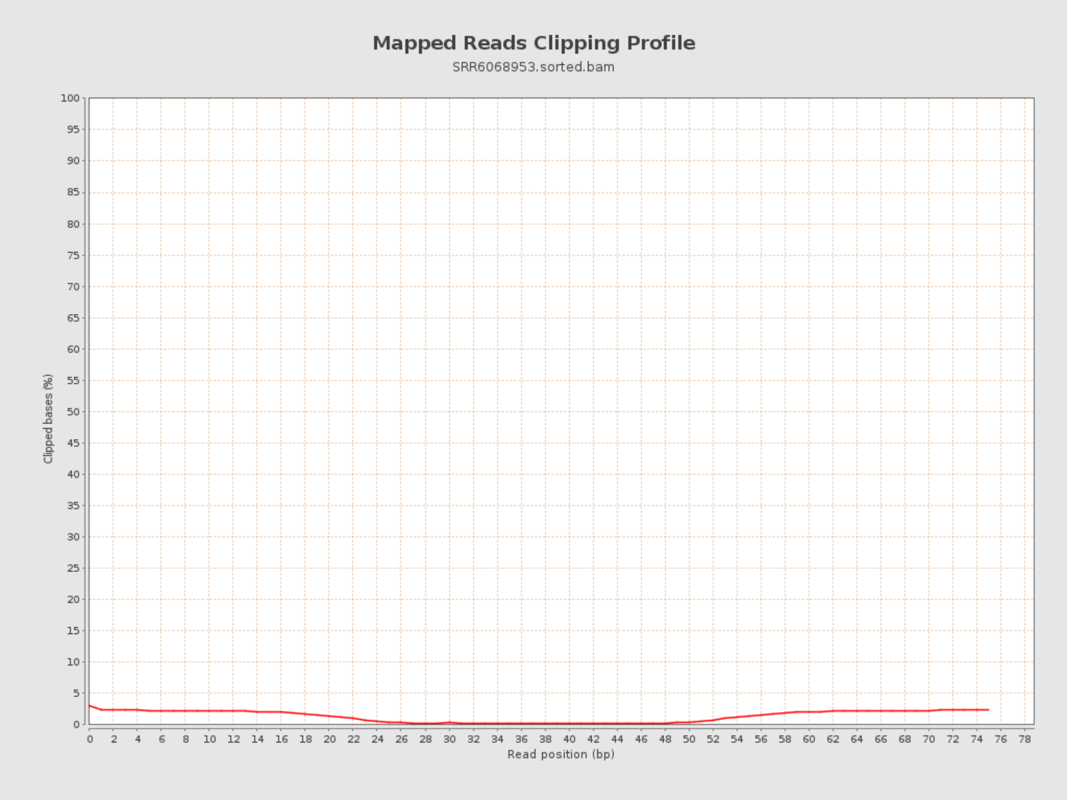
# 8. Results : Mapped Reads Nucleotide Content



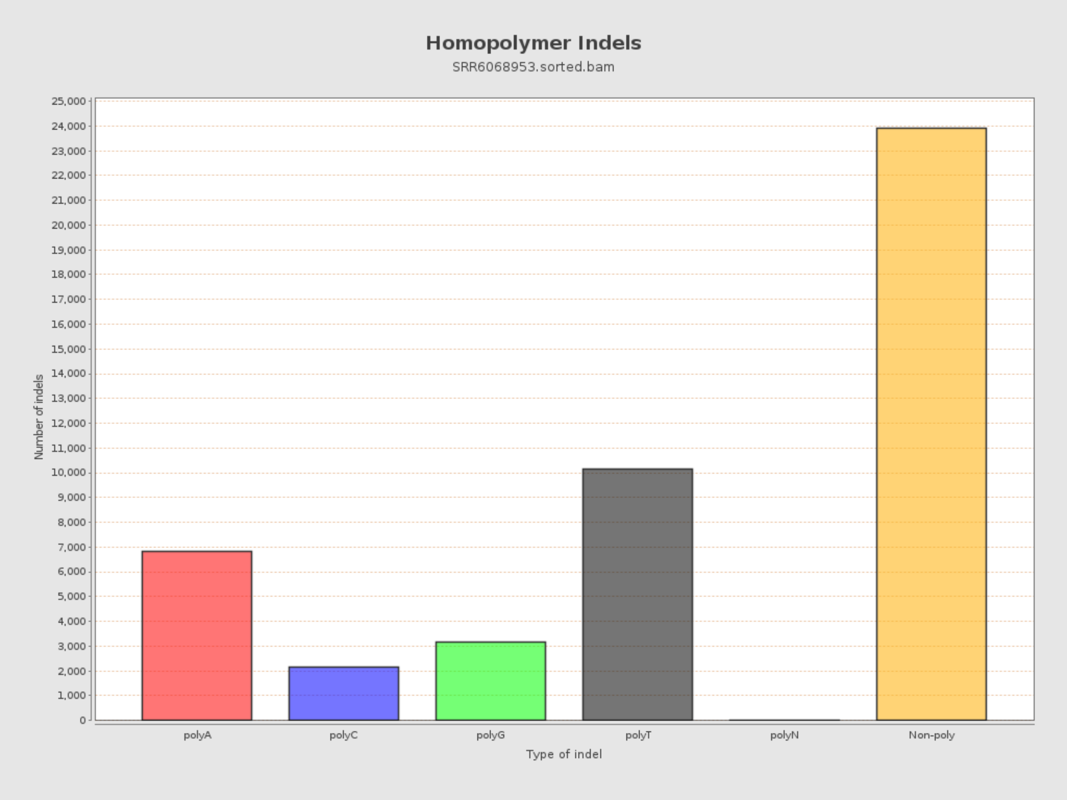
# 9. Results : Mapped Reads GC-content Distribution



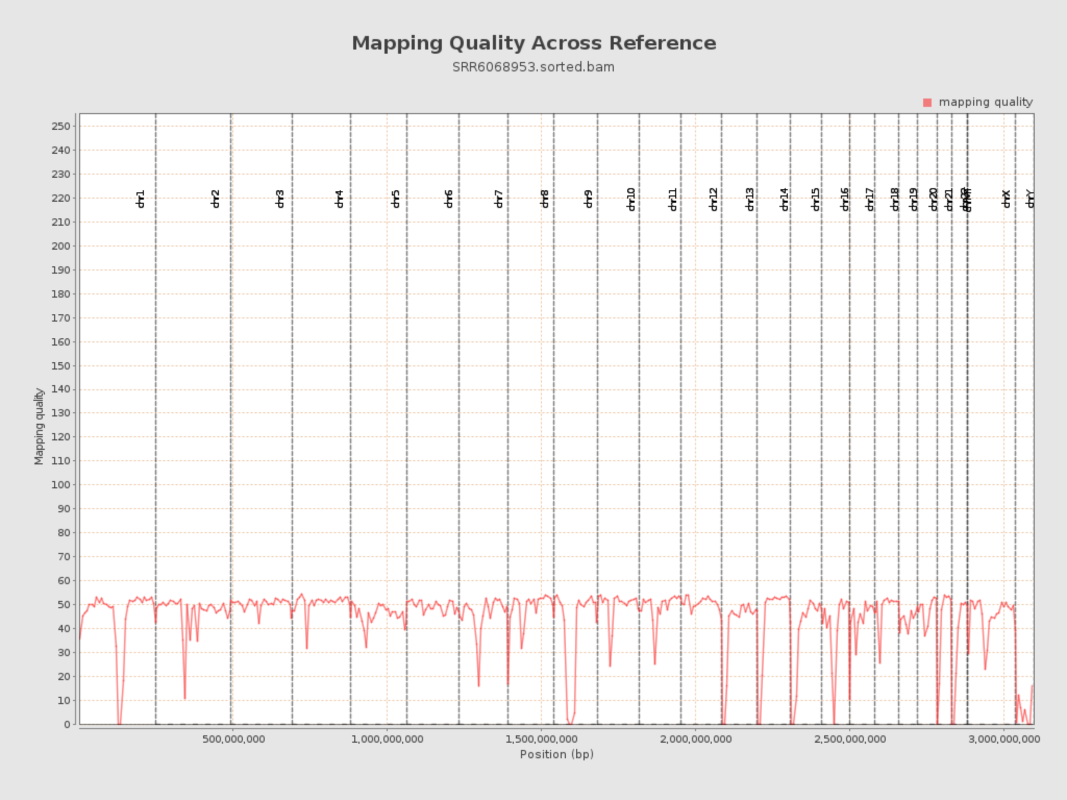
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram