# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/15 04:04:24*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063589.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_SRR6063589 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063589.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 15 04:04:24 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6063589.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,362,631 |
| Mapped reads | 3,080,236 / 91.6% |
| Unmapped reads | 282,395 / 8.4% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 22,605 / 0.67% |
| Read min/max/mean length | 30 / 76 / 76.23 |
| Duplicated reads (estimated) | 209,288 / 6.22% |
| Duplication rate | 5.62% |
| Clipped reads | 1,306,581 / 38.86% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 56,506,179 / 27.32% |
| Number/percentage of C's | 38,879,849 / 18.8% |
| Number/percentage of T's | 64,653,553 / 31.26% |
| Number/percentage of G's | 46,570,773 / 22.52% |
| Number/percentage of N's | 227,906 / 0.11% |
| GC Percentage | 41.31% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0668 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4806 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.3 |

## 2.5. Mismatches and indels

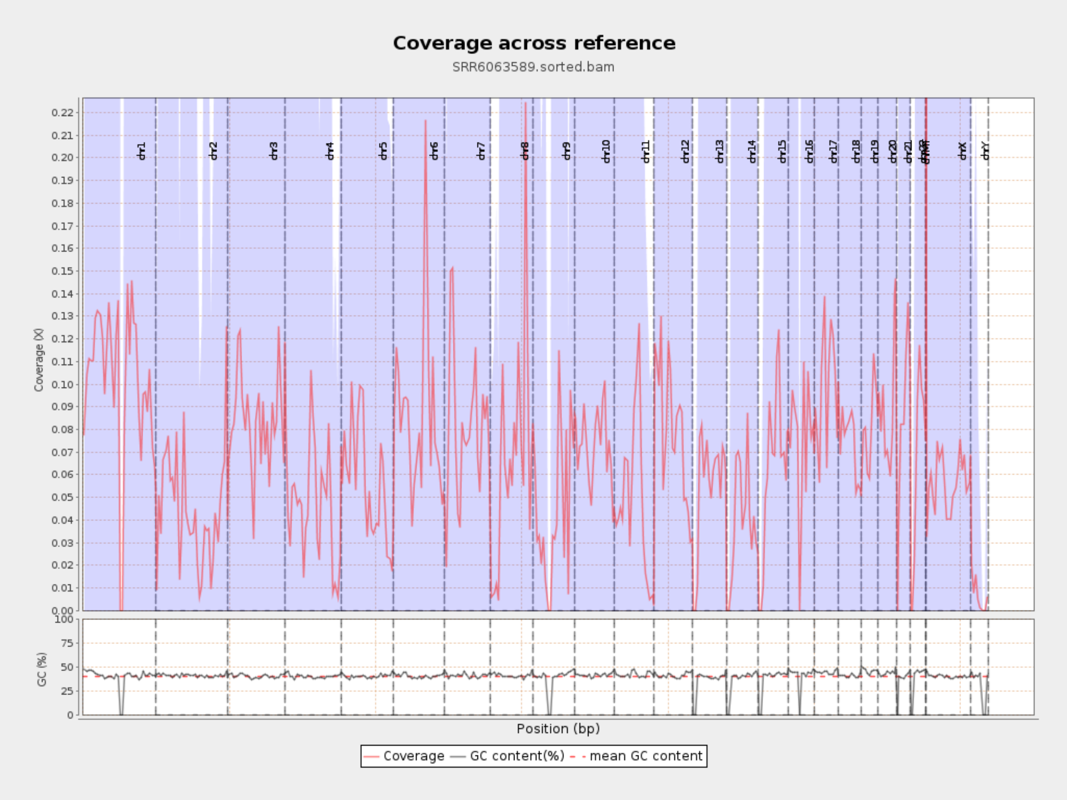
| | |
|---|---|
| General error rate | 0.79% |
| Mismatches | 1,611,543 |
| Insertions | 13,939 |
| Mapped reads with at least one insertion | 0.45% |
| Deletions | 49,690 |
| Mapped reads with at least one deletion | 1.6% |
| Homopolymer indels | 47.5% |

## 2.6. Chromosome stats

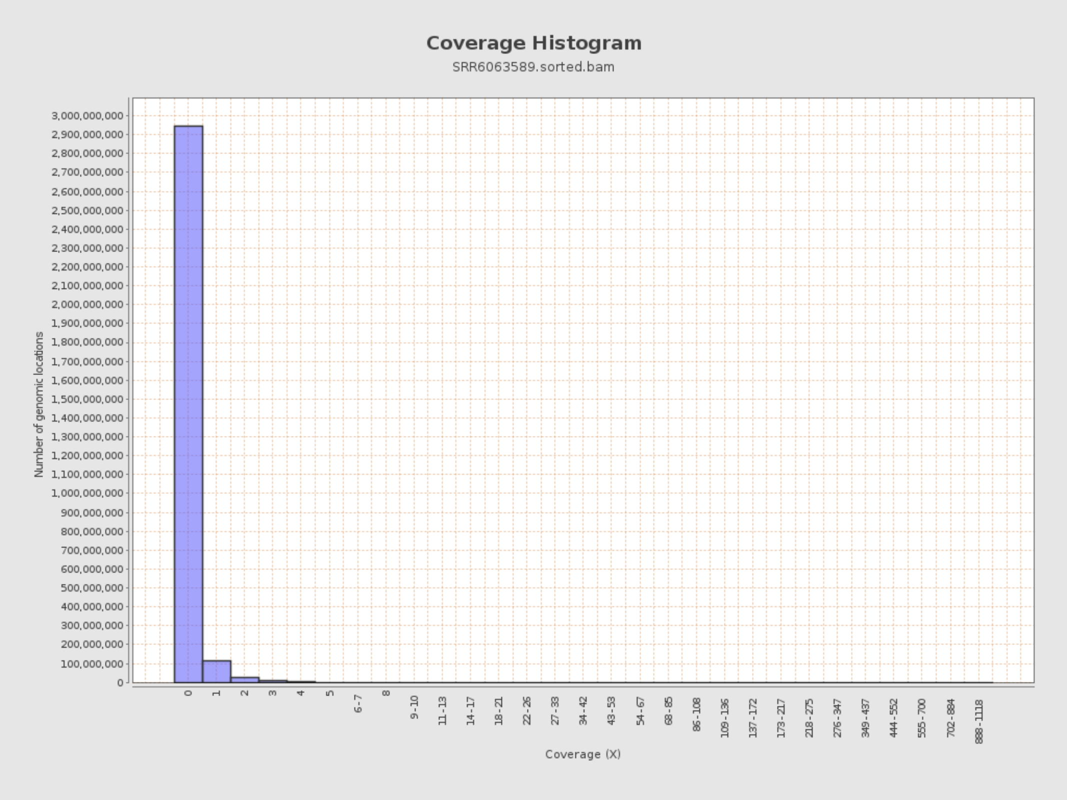
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 25291850 | 0.1015 | 0.932 |
| chr2 | 243199373 | 10732742 | 0.0441 | 0.5762 |
| chr3 | 198022430 | 16541018 | 0.0835 | 0.3733 |
| chr4 | 191154276 | 8871751 | 0.0464 | 0.2882 |
| chr5 | 180915260 | 10242578 | 0.0566 | 0.315 |
| chr6 | 171115067 | 14778627 | 0.0864 | 0.4123 |
| chr7 | 159138663 | 12761817 | 0.0802 | 0.5235 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 9898461 | 0.0676 | 0.6004 |
| chr9 | 141213431 | 6030118 | 0.0427 | 0.3425 |
| chr10 | 135534747 | 9899331 | 0.073 | 0.4095 |
| chr11 | 135006516 | 6590991 | 0.0488 | 0.3287 |
| chr12 | 133851895 | 10818461 | 0.0808 | 0.3707 |
| chr13 | 115169878 | 6311354 | 0.0548 | 0.3071 |
| chr14 | 107349540 | 4359384 | 0.0406 | 0.2687 |
| chr15 | 102531392 | 6277112 | 0.0612 | 0.3257 |
| chr16 | 90354753 | 6717266 | 0.0743 | 0.3662 |
| chr17 | 81195210 | 7996999 | 0.0985 | 0.4315 |
| chr18 | 78077248 | 5874561 | 0.0752 | 0.6948 |
| chr19 | 59128983 | 4748452 | 0.0803 | 0.6164 |
| chr20 | 63025520 | 5621327 | 0.0892 | 0.4044 |
| chr21 | 48129895 | 4020867 | 0.0835 | 0.3809 |
| chr22 | 51304566 | 3420761 | 0.0667 | 0.3343 |
| chrMT | 16571 | 13758 | 0.8302 | 1.1375 |
| chrX | 155270560 | 8724369 | 0.0562 | 0.326 |
| chrY | 59373566 | 381799 | 0.0064 | 0.1163 |

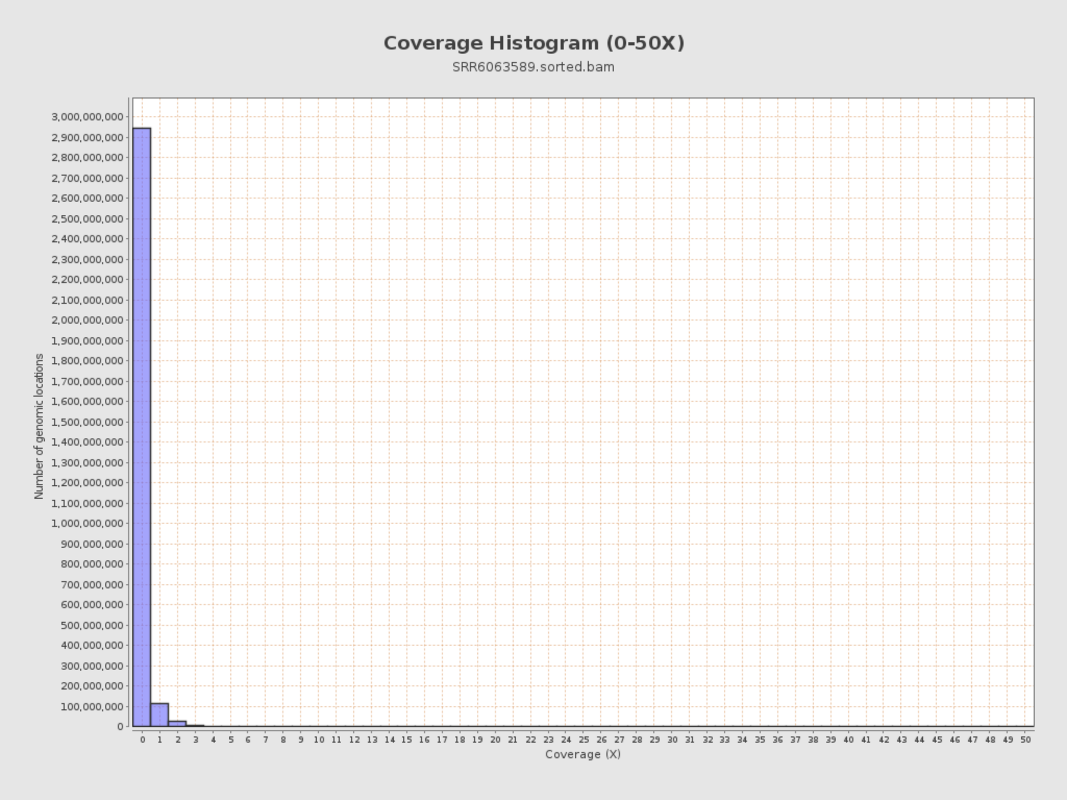
# 3. Results : Coverage across reference



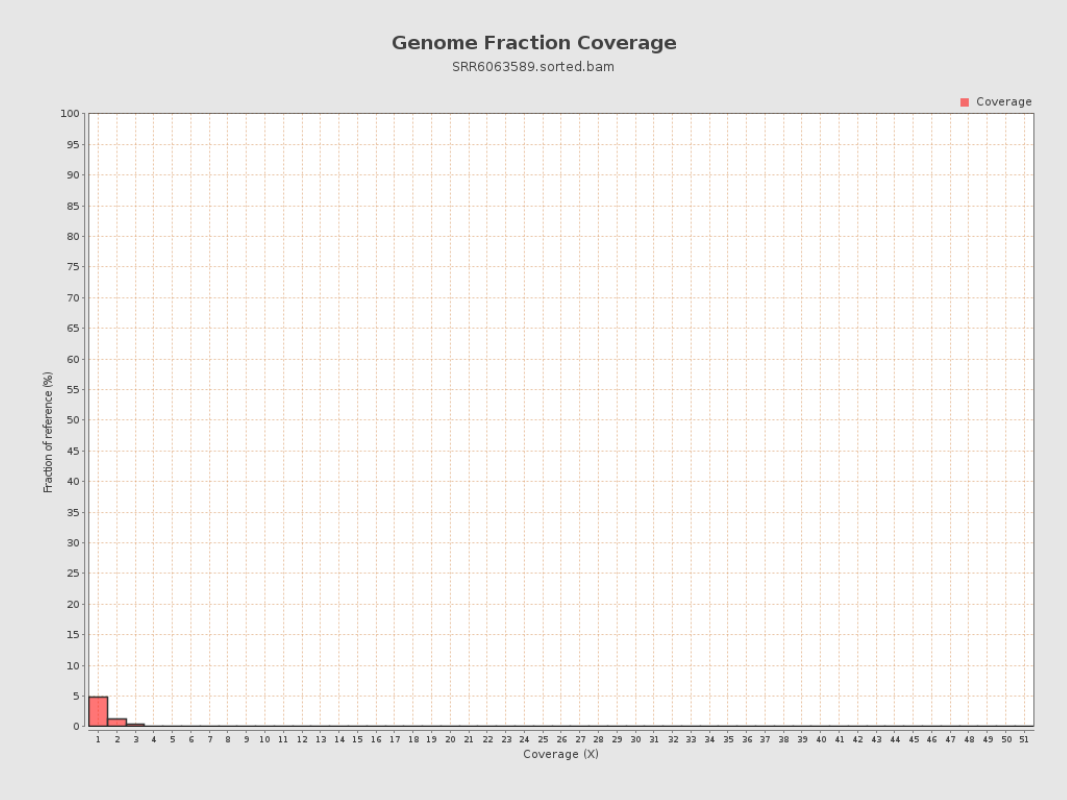
# 4. Results : Coverage Histogram



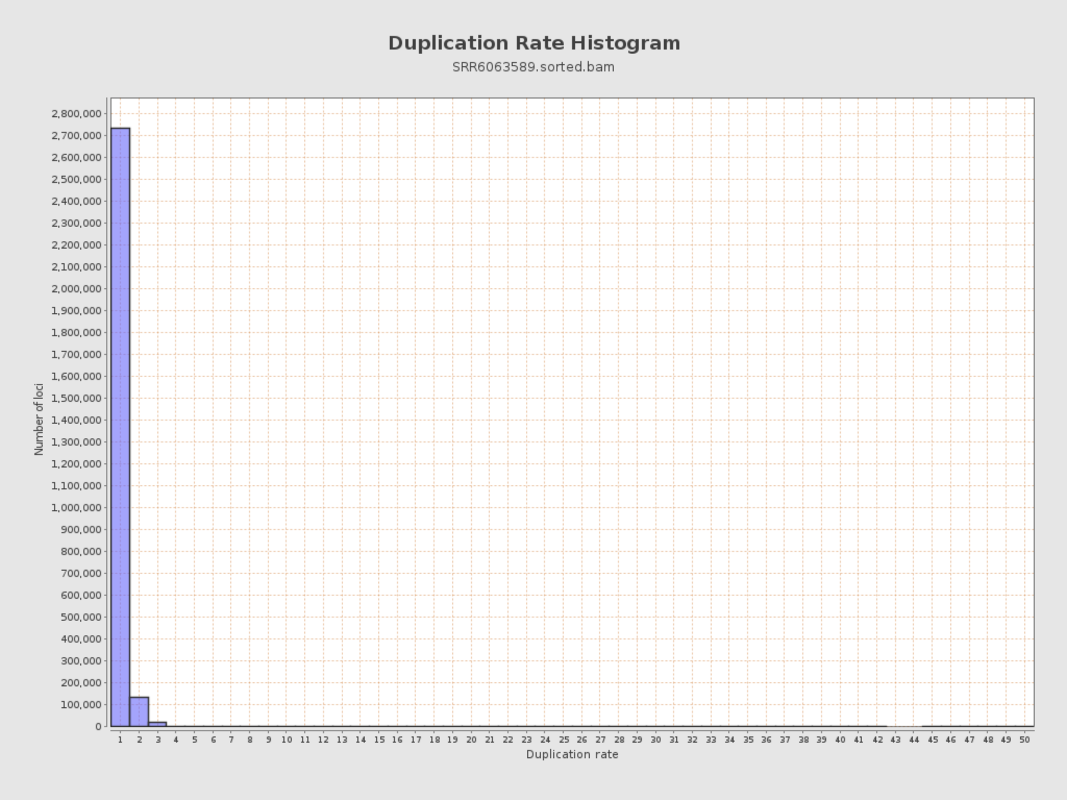
# 5. Results : Coverage Histogram (0-50X)



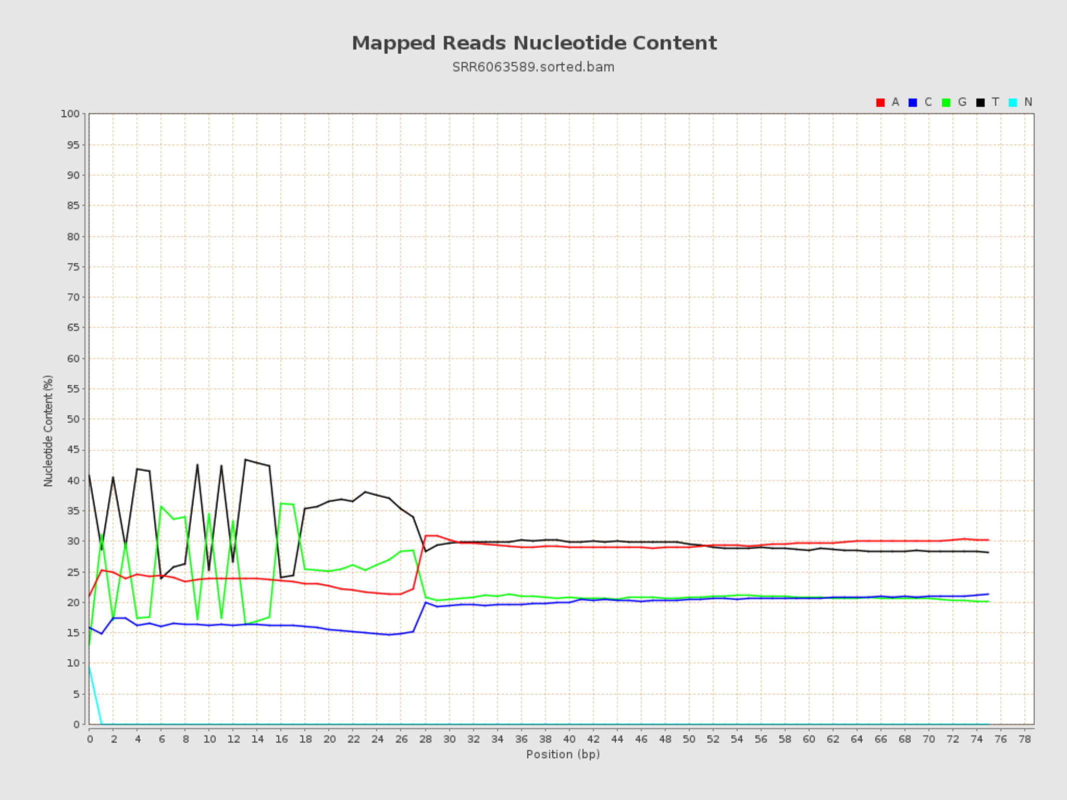
# 6. Results : Genome Fraction Coverage



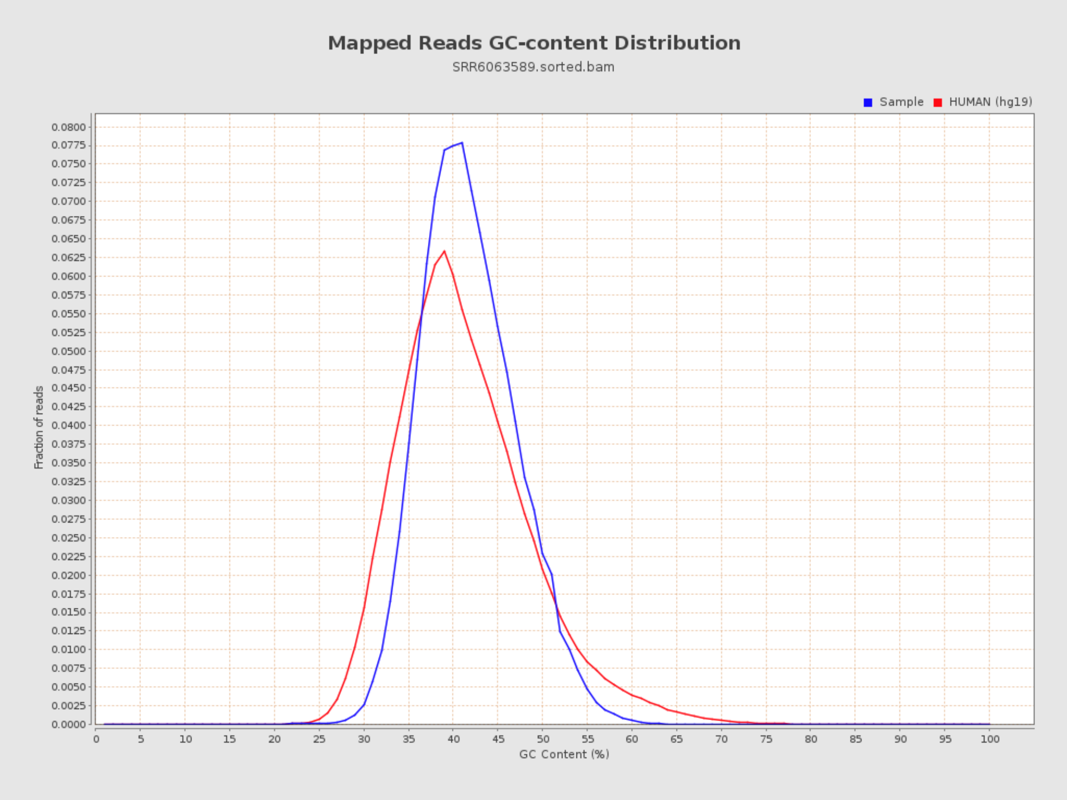
# 7. Results : Duplication Rate Histogram



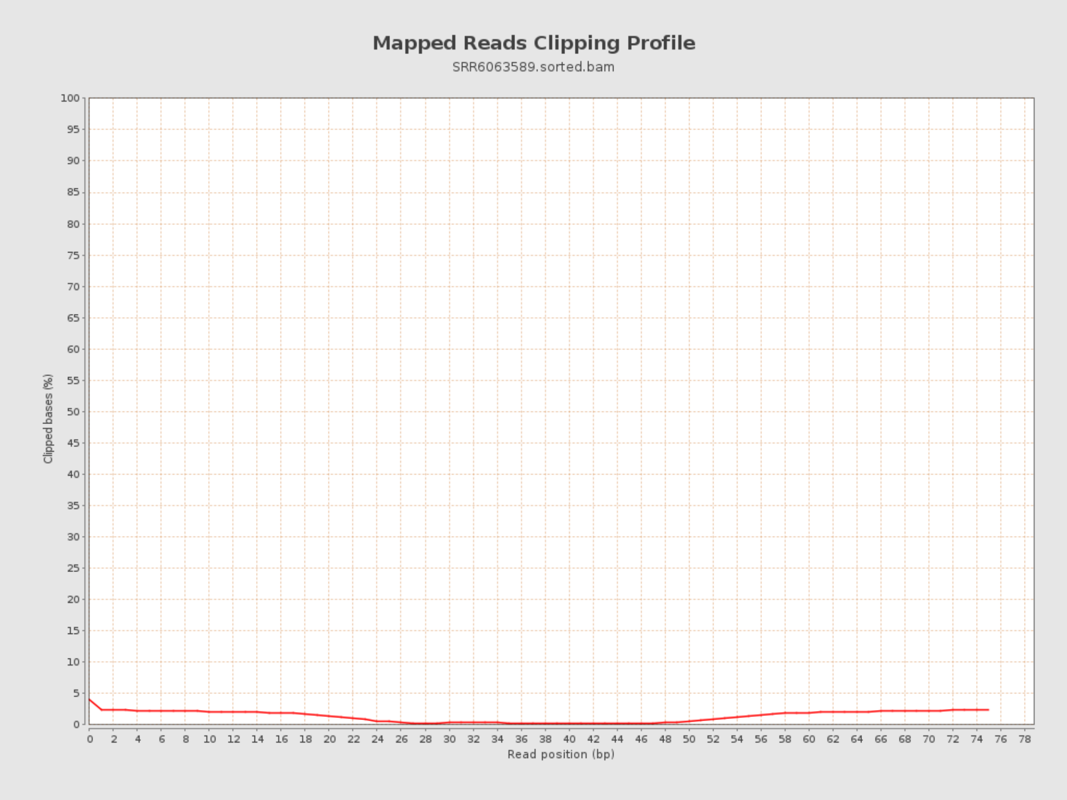
# 8. Results : Mapped Reads Nucleotide Content



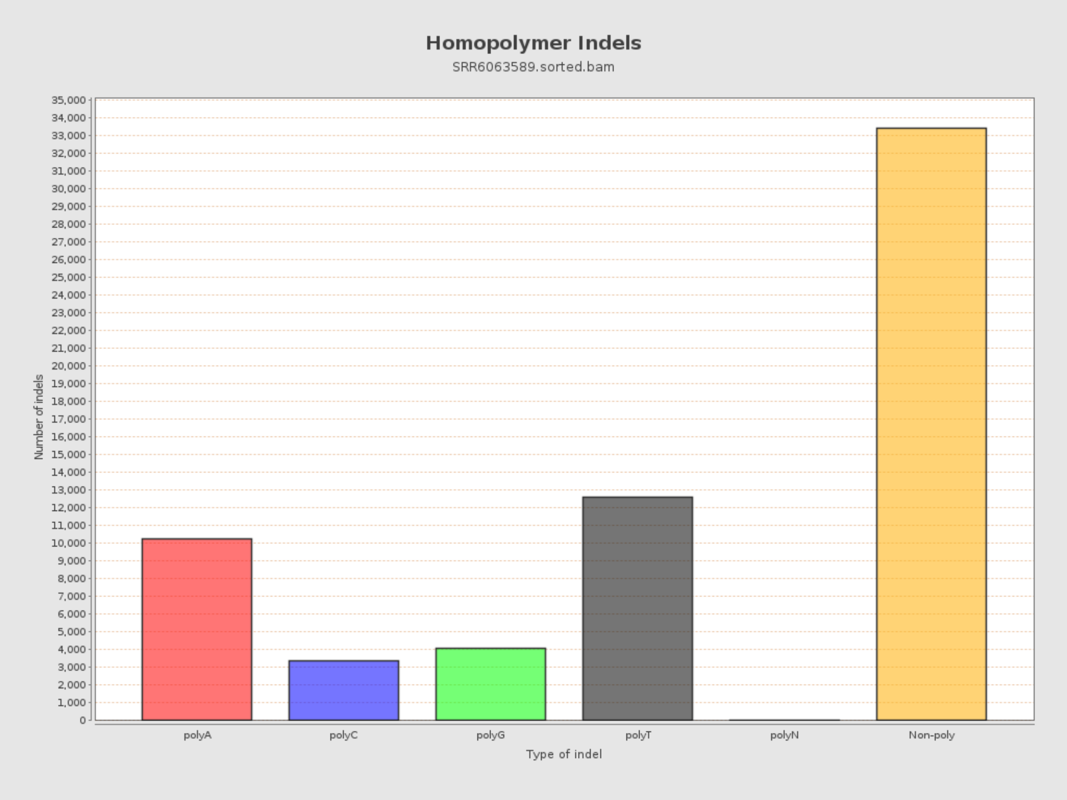
# 9. Results : Mapped Reads GC-content Distribution



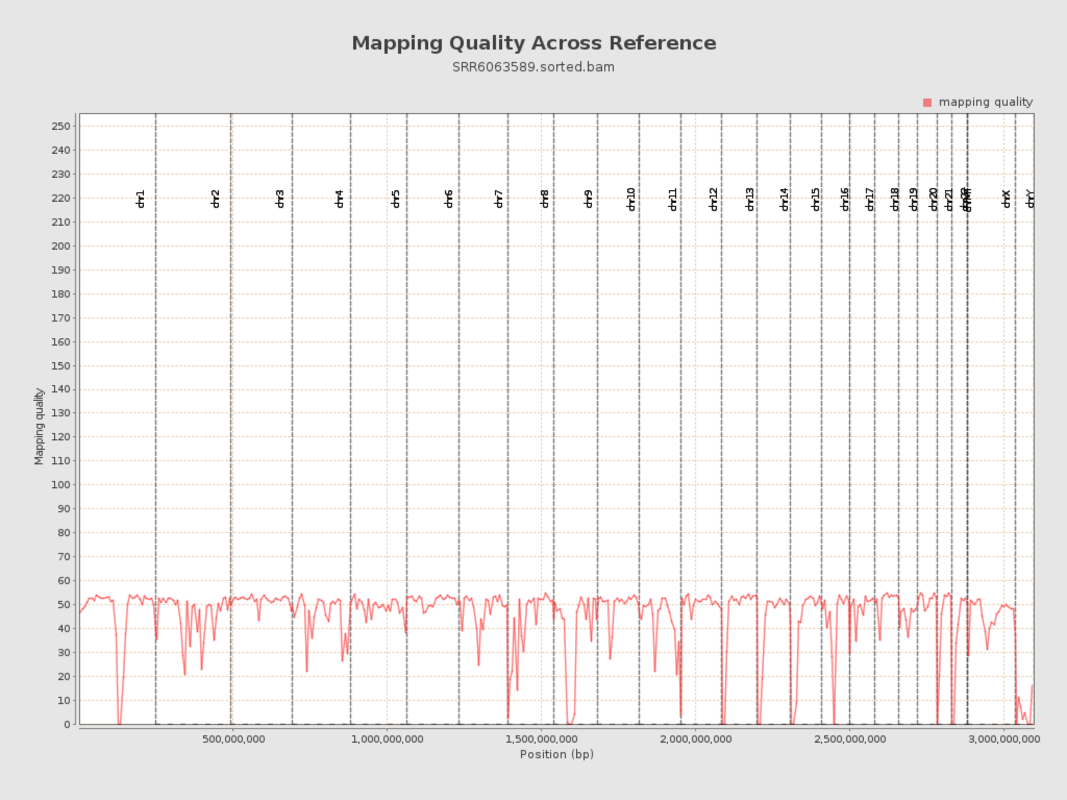
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram