# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/15 09:24:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068089.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_SRR6068089 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068089.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 15 09:24:49 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6068089.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,373,237 |
| Mapped reads | 4,115,675 / 94.11% |
| Unmapped reads | 257,562 / 5.89% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 26,000 / 0.59% |
| Read min/max/mean length | 30 / 76 / 76.2 |
| Duplicated reads (estimated) | 614,429 / 14.05% |
| Duplication rate | 12.63% |
| Clipped reads | 2,139,420 / 48.92% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 70,629,833 / 26.61% |
| Number/percentage of C's | 46,898,428 / 17.67% |
| Number/percentage of T's | 87,417,827 / 32.93% |
| Number/percentage of G's | 60,453,355 / 22.78% |
| Number/percentage of N's | 30,159 / 0.01% |
| GC Percentage | 40.44% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0858 |
| | |

| | |
|---|---|
| Standard Deviation | 0.923 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.25 |

## 2.5. Mismatches and indels

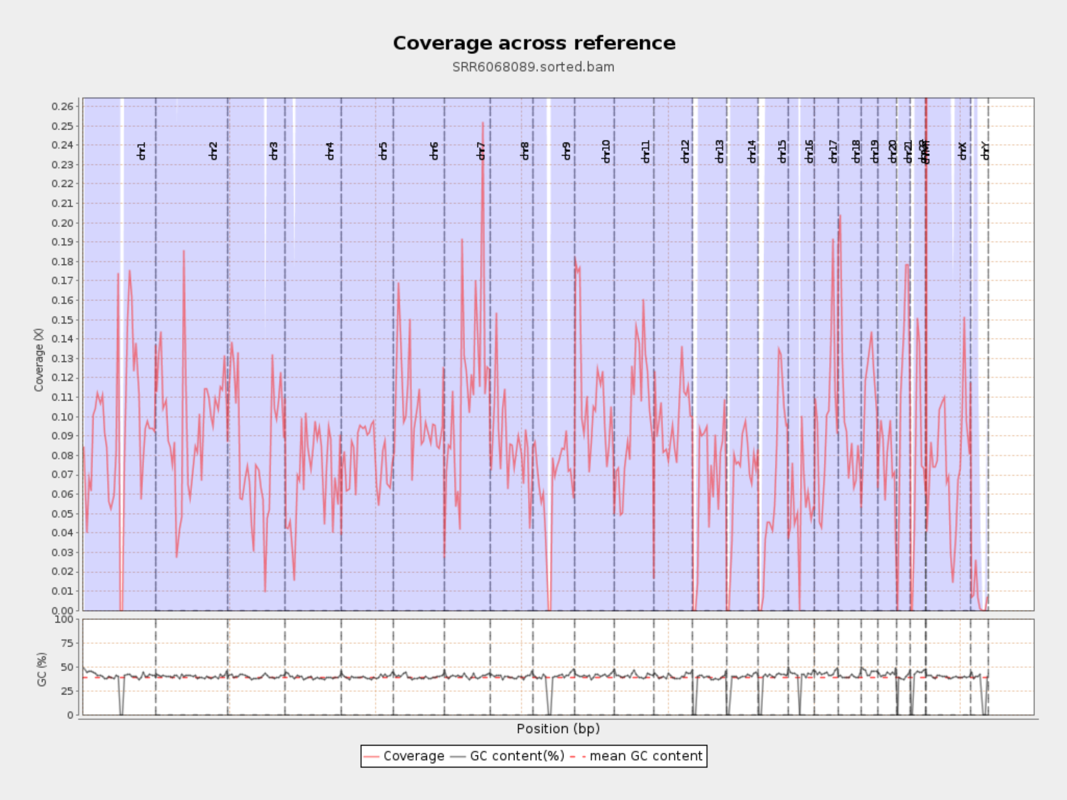
| | |
|---|---|
| General error rate | 0.54% |
| Mismatches | 1,388,663 |
| Insertions | 17,154 |
| Mapped reads with at least one insertion | 0.41% |
| Deletions | 59,003 |
| Mapped reads with at least one deletion | 1.42% |
| Homopolymer indels | 45.81% |

## 2.6. Chromosome stats

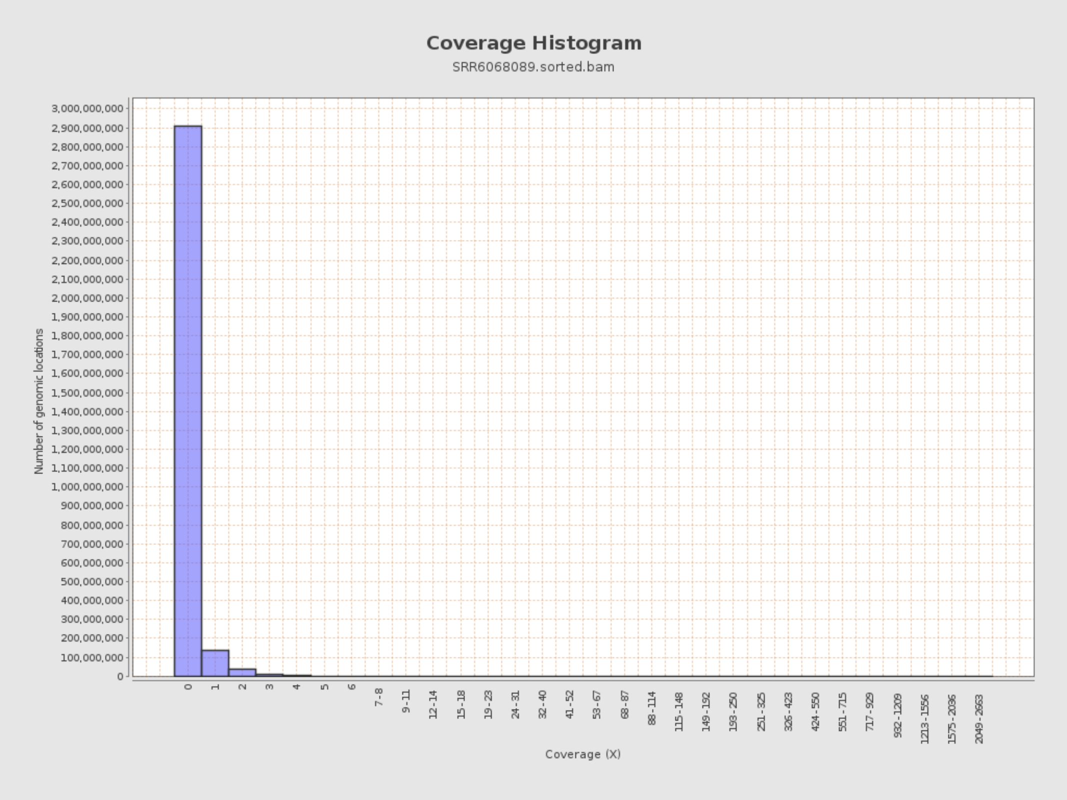
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 22930827 | 0.092 | 2.0487 |
| chr2 | 243199373 | 23508563 | 0.0967 | 1.3622 |
| chr3 | 198022430 | 16285317 | 0.0822 | 0.3883 |
| chr4 | 191154276 | 13347717 | 0.0698 | 0.3757 |
| chr5 | 180915260 | 14325448 | 0.0792 | 0.3821 |
| chr6 | 171115067 | 17718132 | 0.1035 | 0.6035 |
| chr7 | 159138663 | 18156945 | 0.1141 | 1.4179 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 12553099 | 0.0858 | 0.9734 |
| chr9 | 141213431 | 9003181 | 0.0638 | 0.5967 |
| chr10 | 135534747 | 15088789 | 0.1113 | 0.6119 |
| chr11 | 135006516 | 13461623 | 0.0997 | 0.6826 |
| chr12 | 133851895 | 13312724 | 0.0995 | 0.4465 |
| chr13 | 115169878 | 7763766 | 0.0674 | 0.4027 |
| chr14 | 107349540 | 7100346 | 0.0661 | 0.3785 |
| chr15 | 102531392 | 6328418 | 0.0617 | 0.3711 |
| chr16 | 90354753 | 4829939 | 0.0535 | 0.3504 |
| chr17 | 81195210 | 8187440 | 0.1008 | 0.4732 |
| chr18 | 78077248 | 7921837 | 0.1015 | 1.1404 |
| chr19 | 59128983 | 6705980 | 0.1134 | 1.2628 |
| chr20 | 63025520 | 4944423 | 0.0785 | 0.3886 |
| chr21 | 48129895 | 5544307 | 0.1152 | 0.4724 |
| chr22 | 51304566 | 3801656 | 0.0741 | 0.3623 |
| chrMT | 16571 | 266445 | 16.079 | 10.0665 |
| chrX | 155270560 | 12033013 | 0.0775 | 0.4725 |
| chrY | 59373566 | 411984 | 0.0069 | 0.2311 |

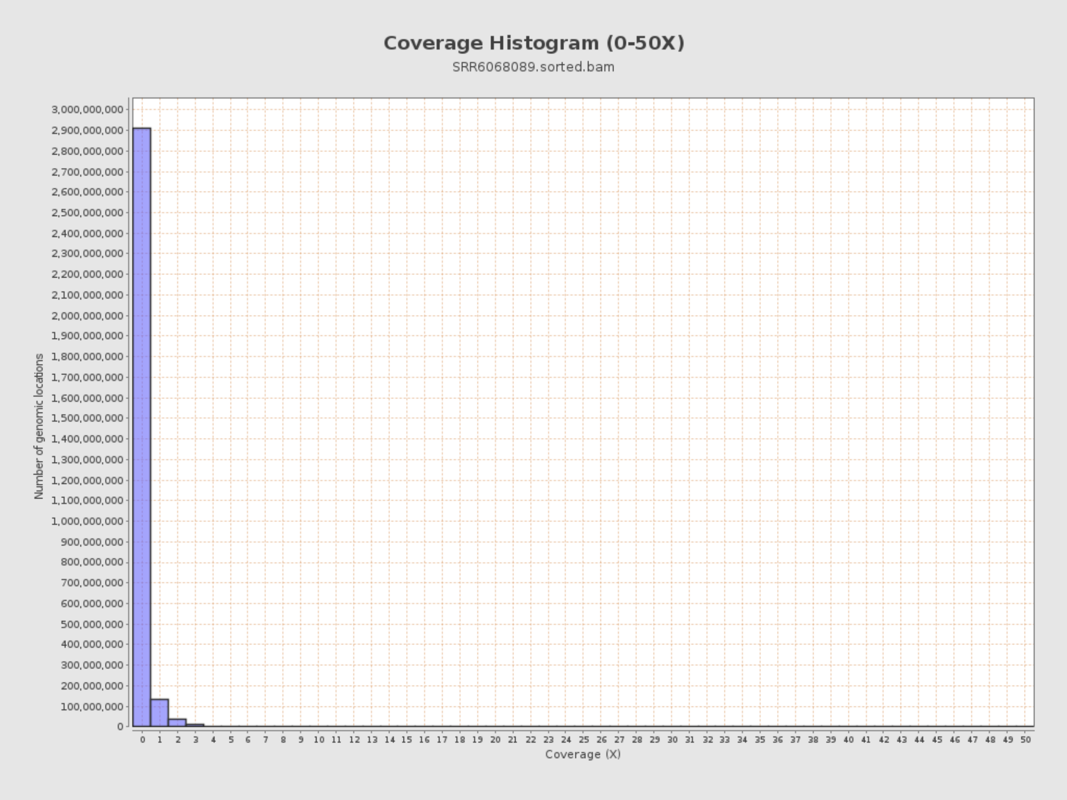
# 3. Results : Coverage across reference



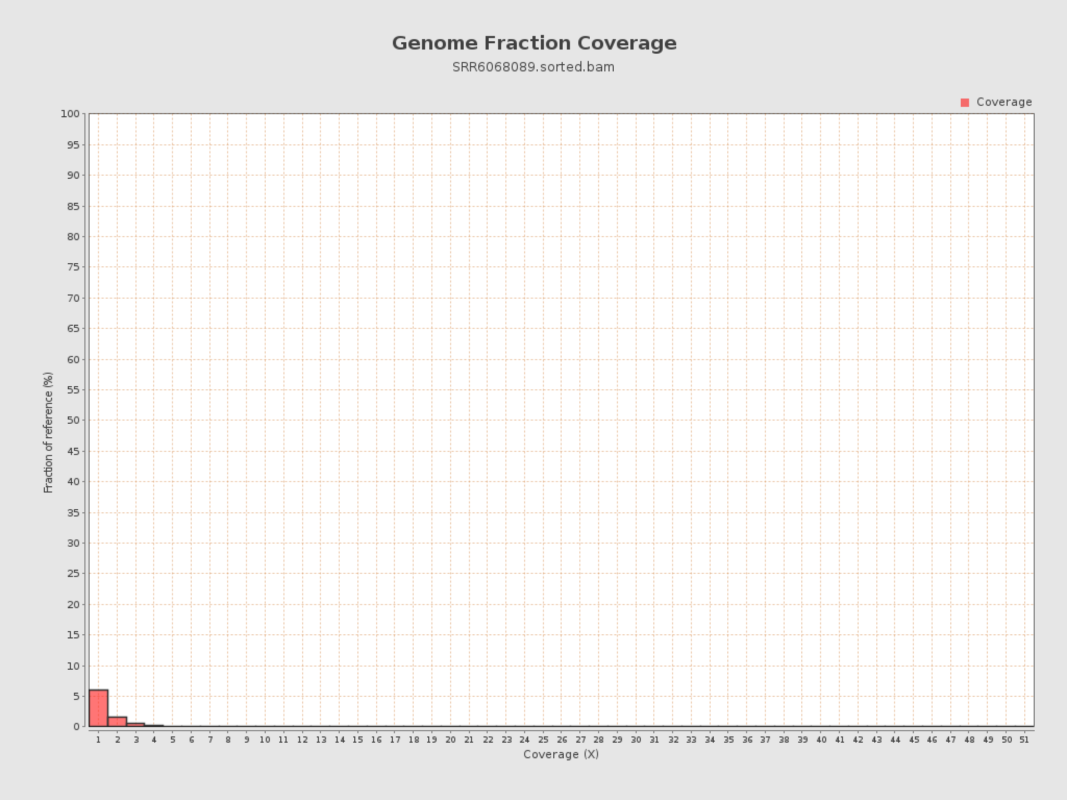
# 4. Results : Coverage Histogram



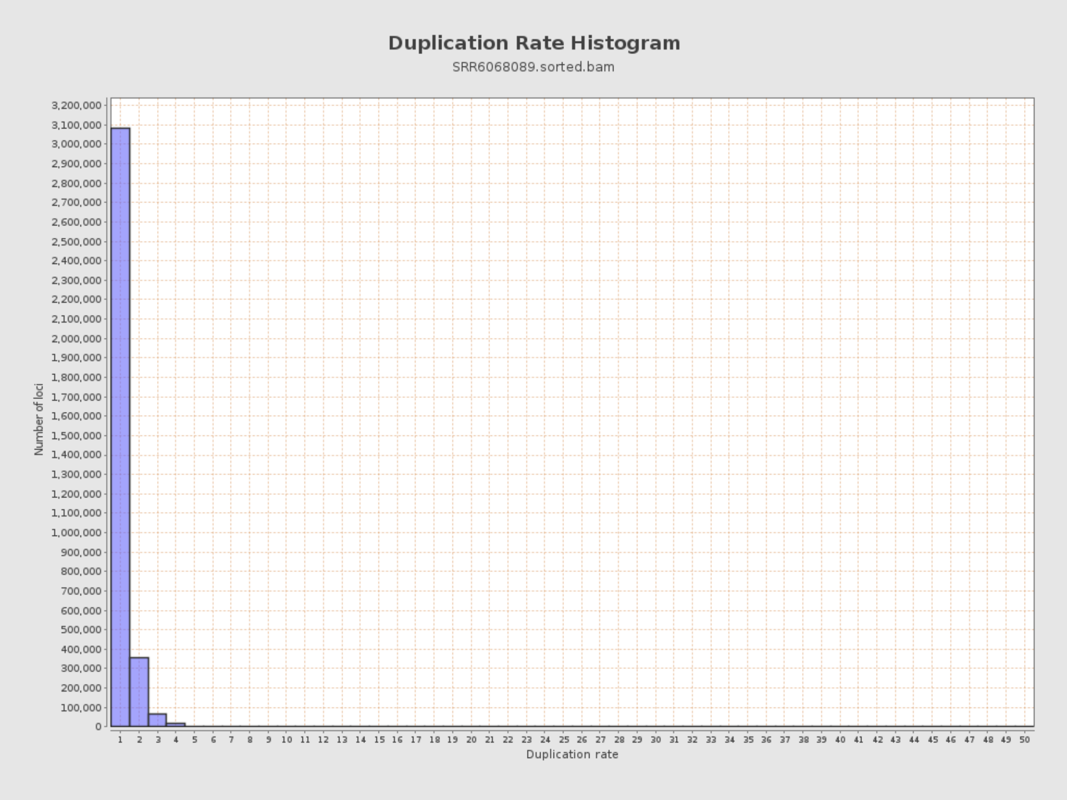
# 5. Results : Coverage Histogram (0-50X)



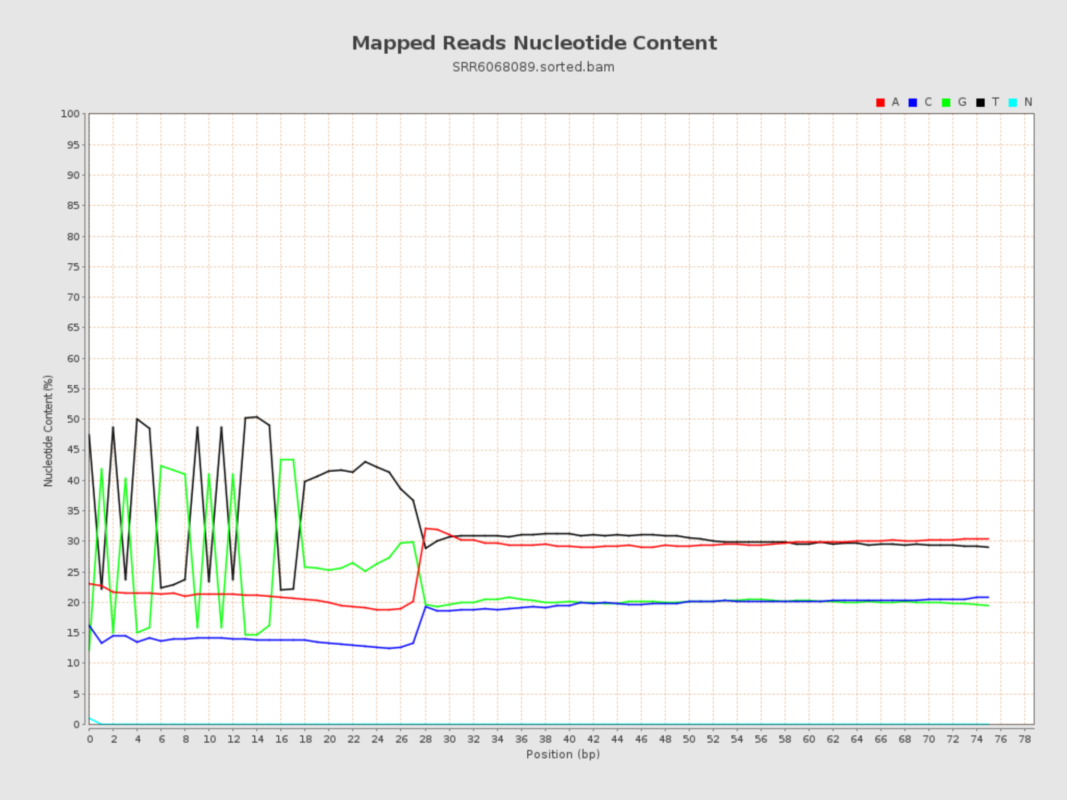
# 6. Results : Genome Fraction Coverage



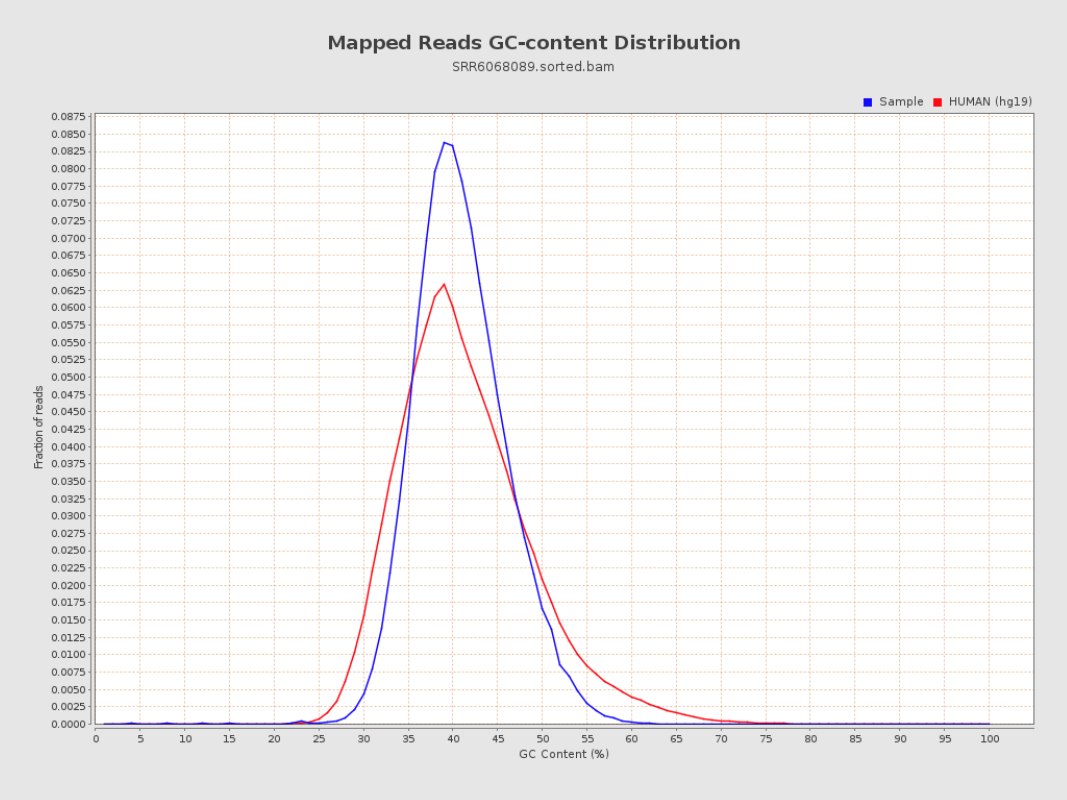
# 7. Results : Duplication Rate Histogram



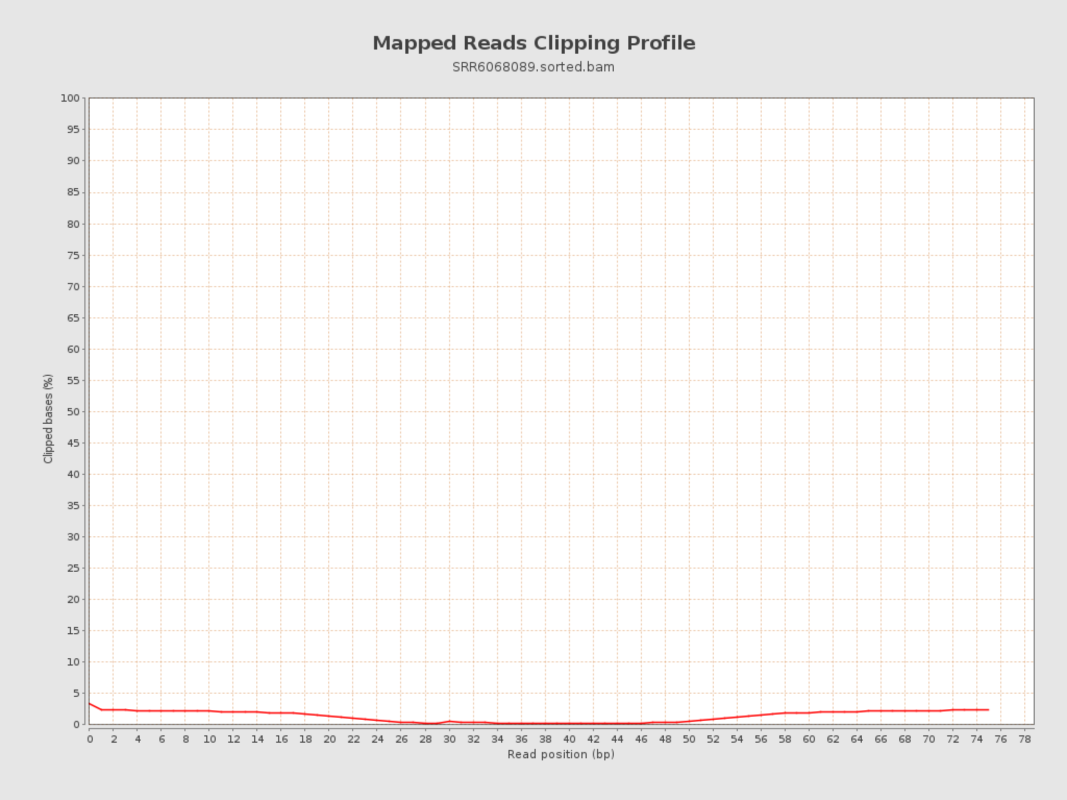
# 8. Results : Mapped Reads Nucleotide Content



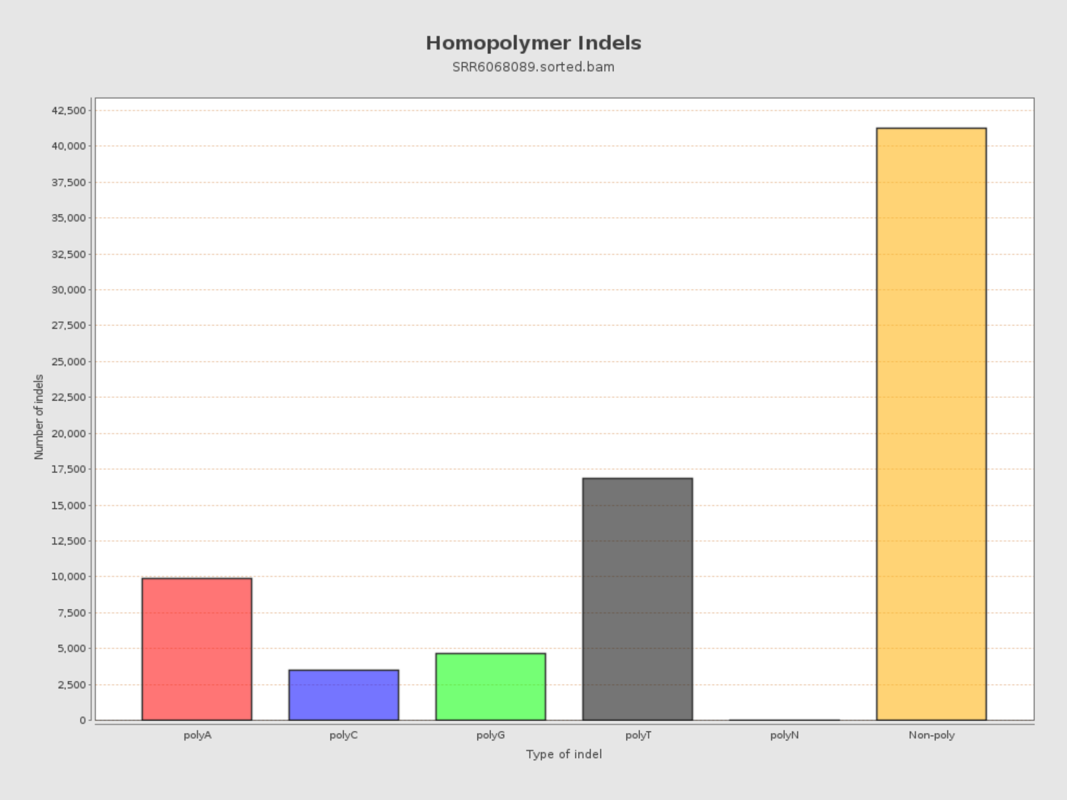
# 9. Results : Mapped Reads GC-content Distribution



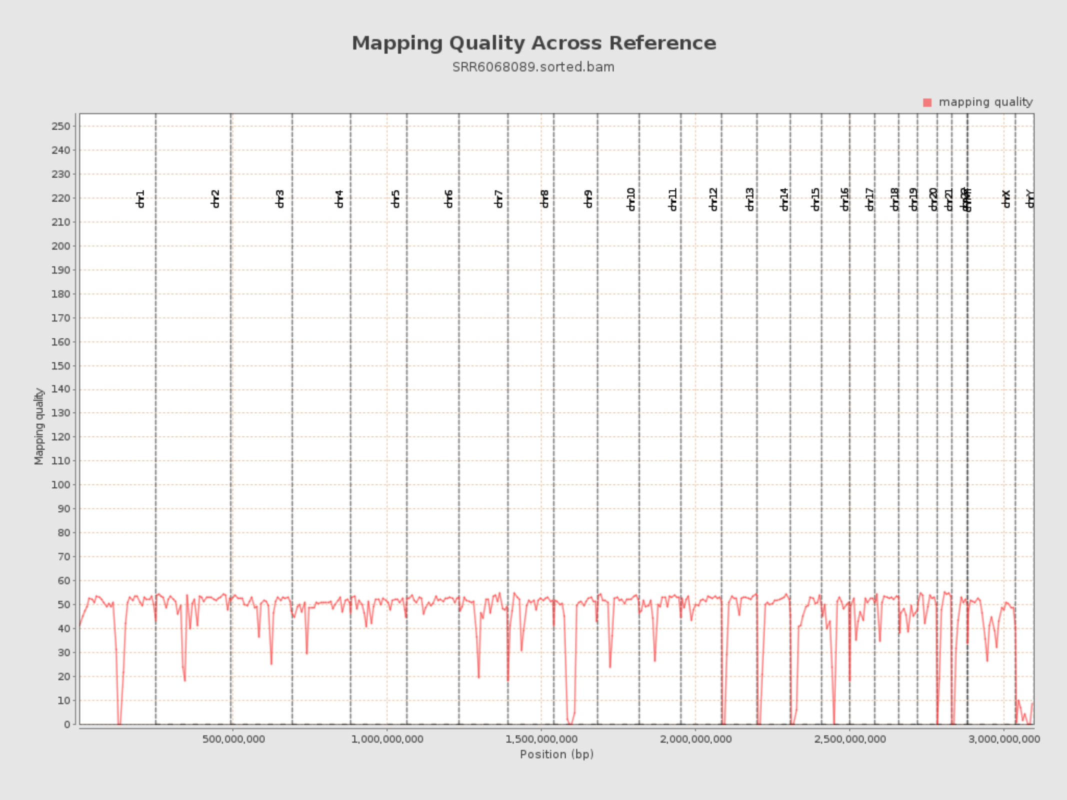
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram