# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/15 07:51:15*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068067.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_SRR6068067 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068067.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 15 07:51:14 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6068067.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,794,165 |
| Mapped reads | 1,332,373 / 74.26% |
| Unmapped reads | 461,792 / 25.74% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 12,630 / 0.7% |
| Read min/max/mean length | 30 / 76 / 76.24 |
| Duplicated reads (estimated) | 279,478 / 15.58% |
| Duplication rate | 16.48% |
| Clipped reads | 924,615 / 51.53% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 20,007,804 / 24.9% |
| Number/percentage of C's | 13,540,631 / 16.85% |
| Number/percentage of T's | 27,780,462 / 34.57% |
| Number/percentage of G's | 19,027,711 / 23.68% |
| Number/percentage of N's | 7,228 / 0.01% |
| GC Percentage | 40.53% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.026 |
| | |

| | |
|---|---|
| Standard Deviation | 0.5319 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.76 |

## 2.5. Mismatches and indels

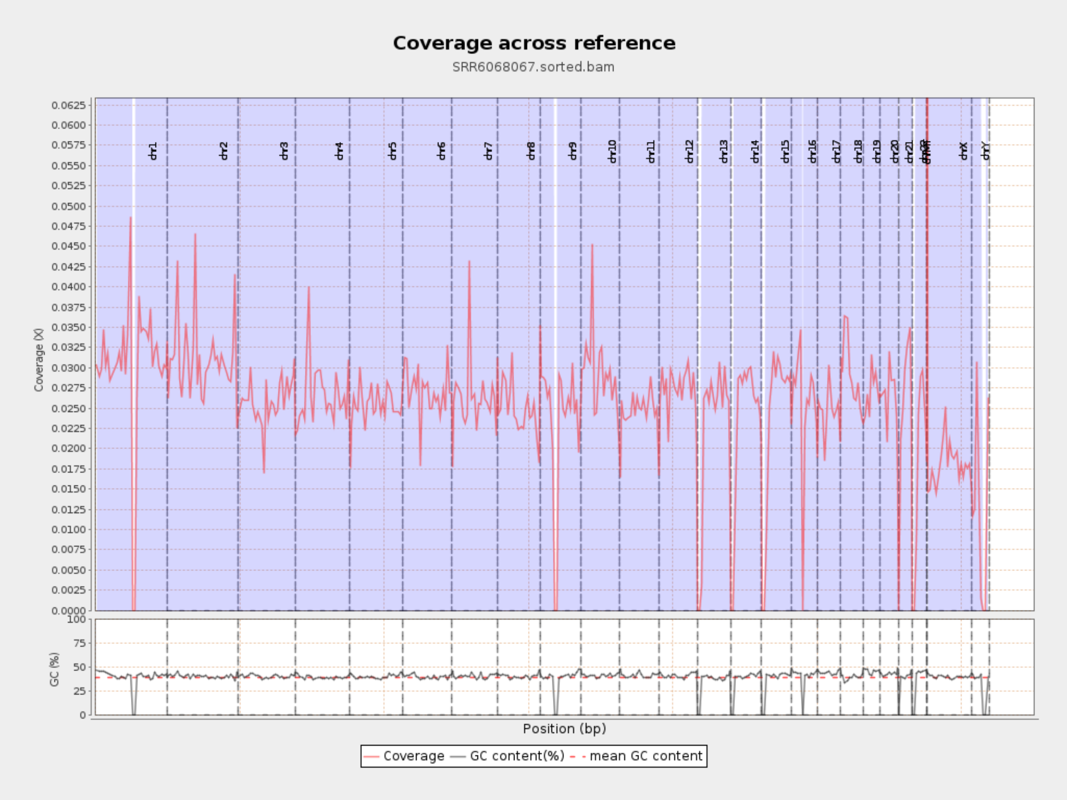
| | |
|---|---|
| General error rate | 0.71% |
| Mismatches | 561,345 |
| Insertions | 5,512 |
| Mapped reads with at least one insertion | 0.41% |
| Deletions | 20,924 |
| Mapped reads with at least one deletion | 1.56% |
| Homopolymer indels | 40.87% |

## 2.6. Chromosome stats

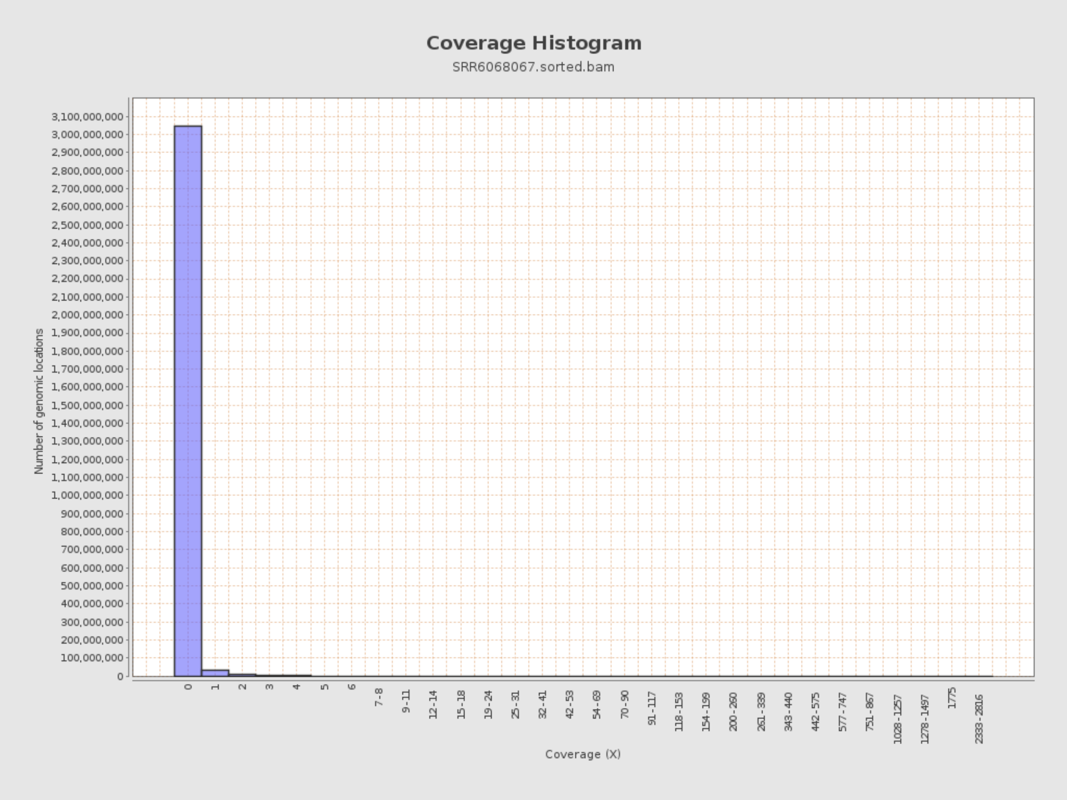
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 7538375 | 0.0302 | 0.5144 |
| chr2 | 243199373 | 7581785 | 0.0312 | 1.3348 |
| chr3 | 198022430 | 5104750 | 0.0258 | 0.2577 |
| chr4 | 191154276 | 5122371 | 0.0268 | 0.2622 |
| chr5 | 180915260 | 4637936 | 0.0256 | 0.2574 |
| chr6 | 171115067 | 4634884 | 0.0271 | 0.4993 |
| chr7 | 159138663 | 4177406 | 0.0263 | 0.3779 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3624630 | 0.0248 | 0.3691 |
| chr9 | 141213431 | 3297012 | 0.0233 | 0.2832 |
| chr10 | 135534747 | 3993364 | 0.0295 | 0.3146 |
| chr11 | 135006516 | 3373703 | 0.025 | 0.2723 |
| chr12 | 133851895 | 3687330 | 0.0275 | 0.2596 |
| chr13 | 115169878 | 2565131 | 0.0223 | 0.3266 |
| chr14 | 107349540 | 2483663 | 0.0231 | 0.2461 |
| chr15 | 102531392 | 2400421 | 0.0234 | 0.3 |
| chr16 | 90354753 | 2264140 | 0.0251 | 0.2633 |
| chr17 | 81195210 | 1994477 | 0.0246 | 0.2498 |
| chr18 | 78077248 | 2275651 | 0.0291 | 1.1421 |
| chr19 | 59128983 | 1592846 | 0.0269 | 0.394 |
| chr20 | 63025520 | 1658891 | 0.0263 | 0.2525 |
| chr21 | 48129895 | 1238896 | 0.0257 | 0.255 |
| chr22 | 51304566 | 920326 | 0.0179 | 0.205 |
| chrMT | 16571 | 700552 | 42.2758 | 23.5596 |
| chrX | 155270560 | 2801222 | 0.018 | 0.2129 |
| chrY | 59373566 | 728810 | 0.0123 | 0.2449 |

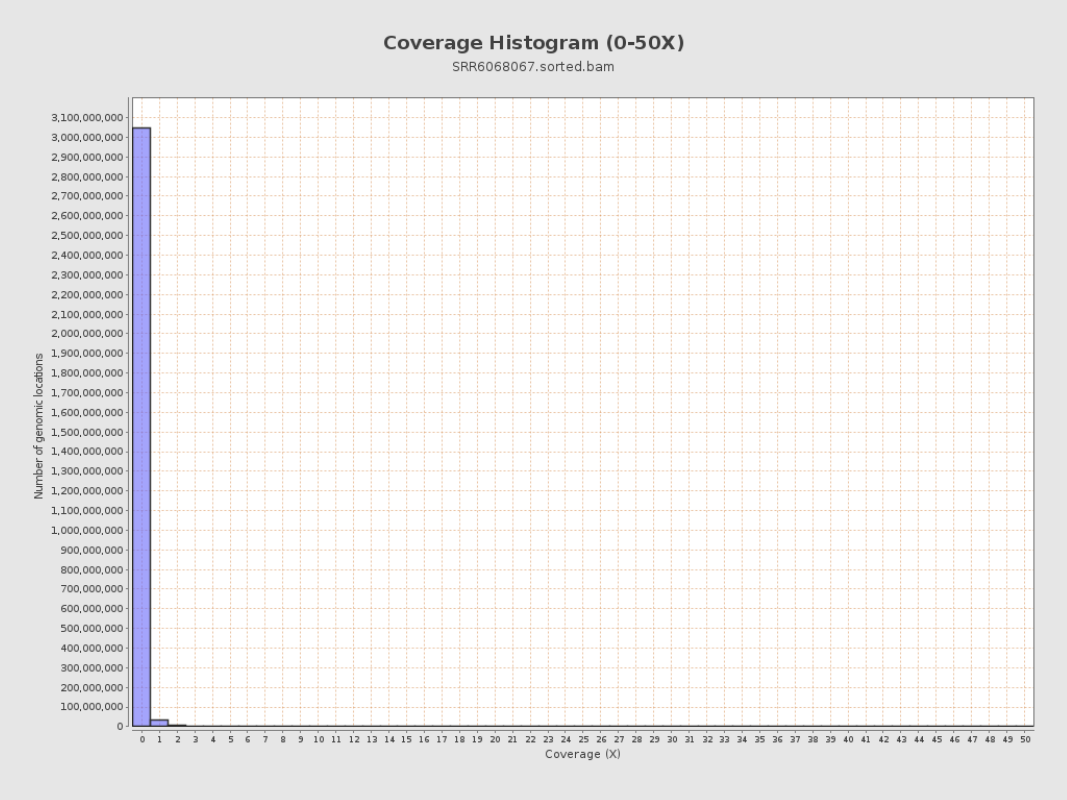
# 3. Results : Coverage across reference



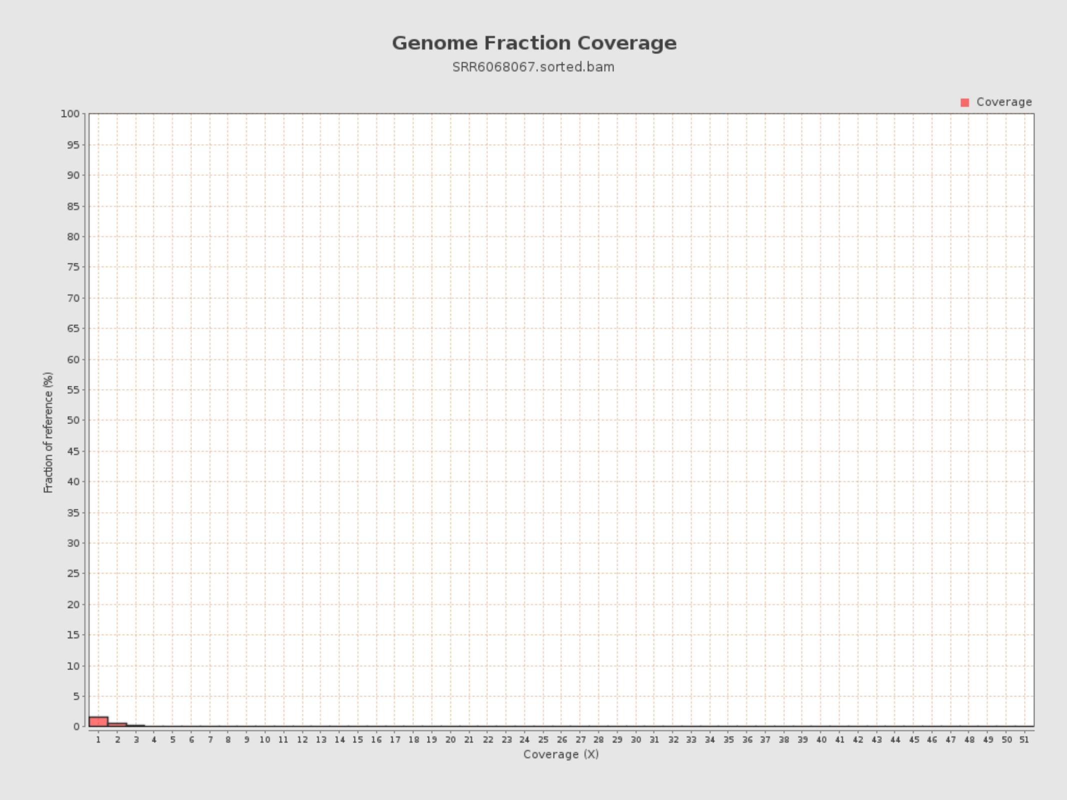
# 4. Results : Coverage Histogram



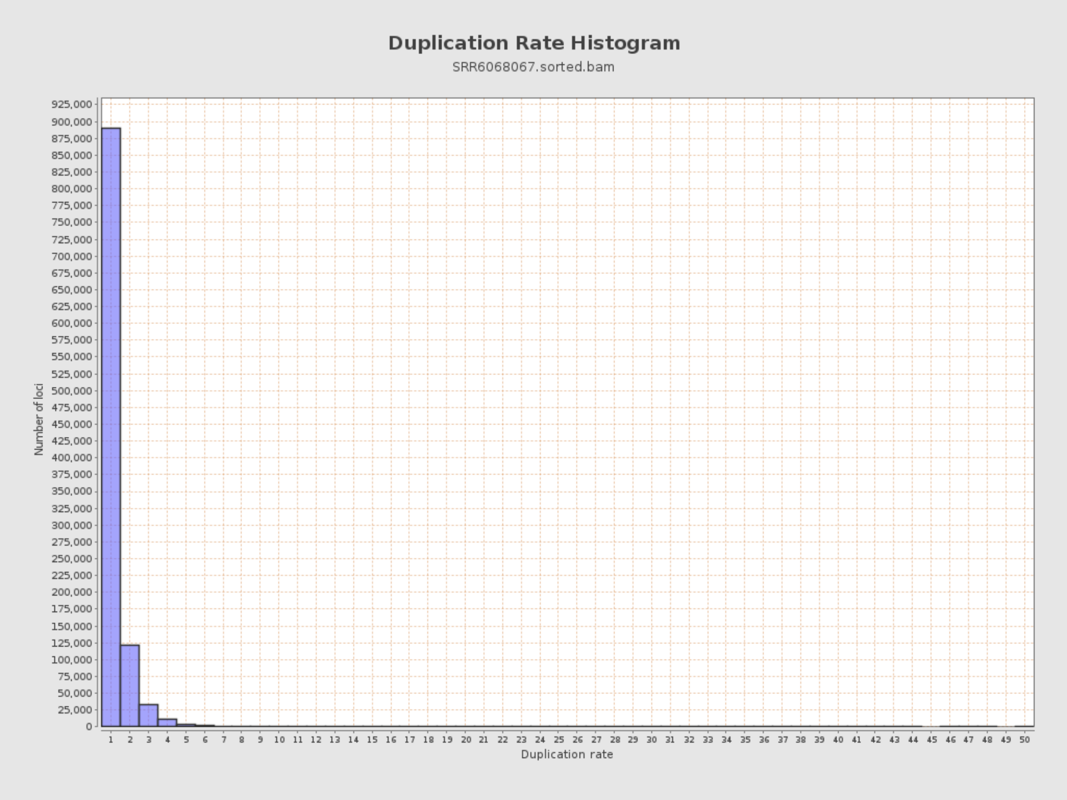
# 5. Results : Coverage Histogram (0-50X)



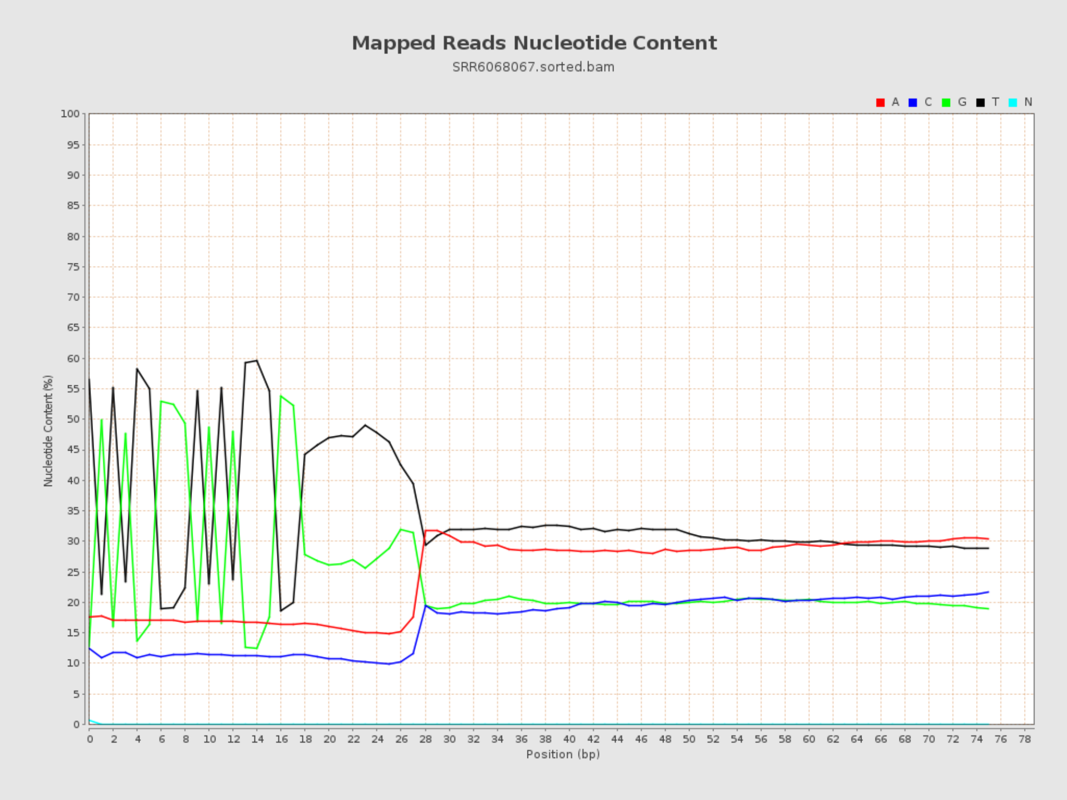
# 6. Results : Genome Fraction Coverage



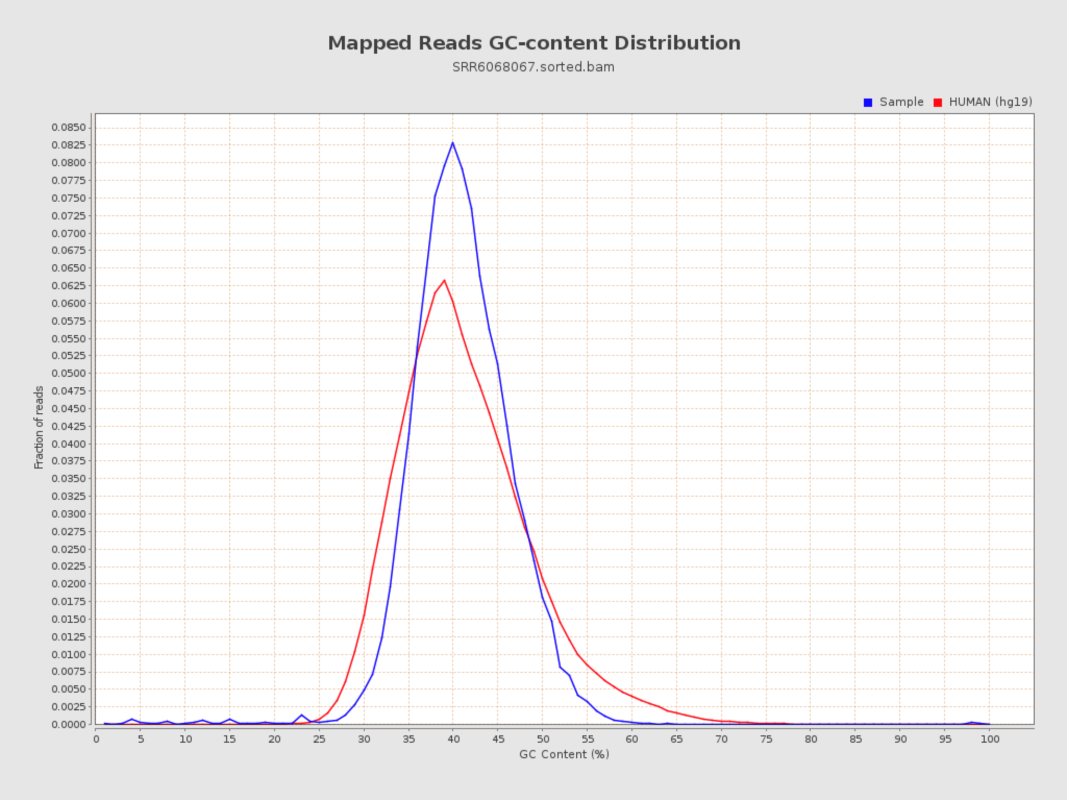
# 7. Results : Duplication Rate Histogram



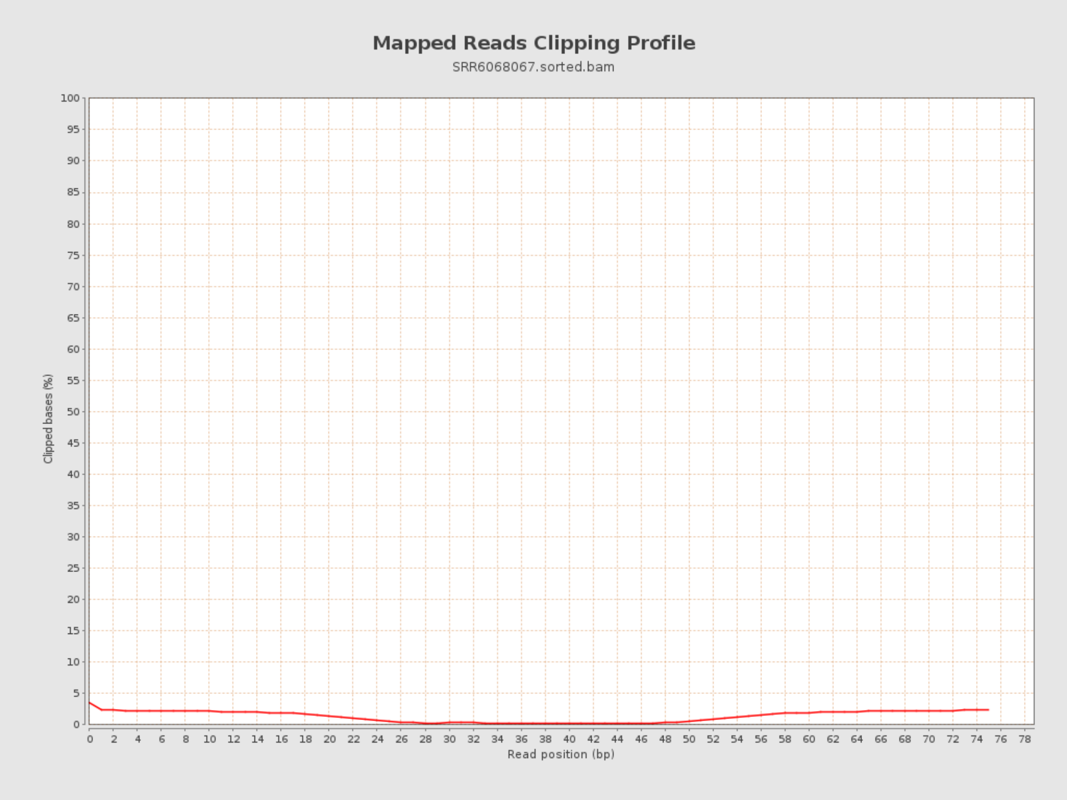
# 8. Results : Mapped Reads Nucleotide Content



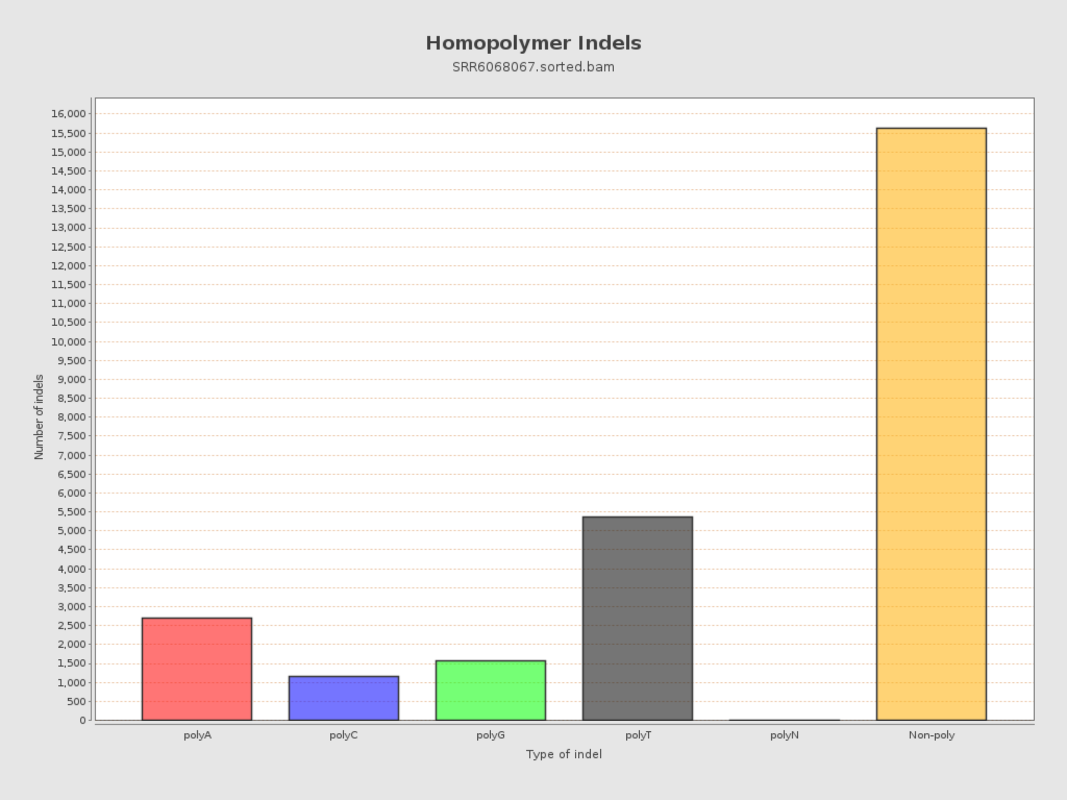
# 9. Results : Mapped Reads GC-content Distribution



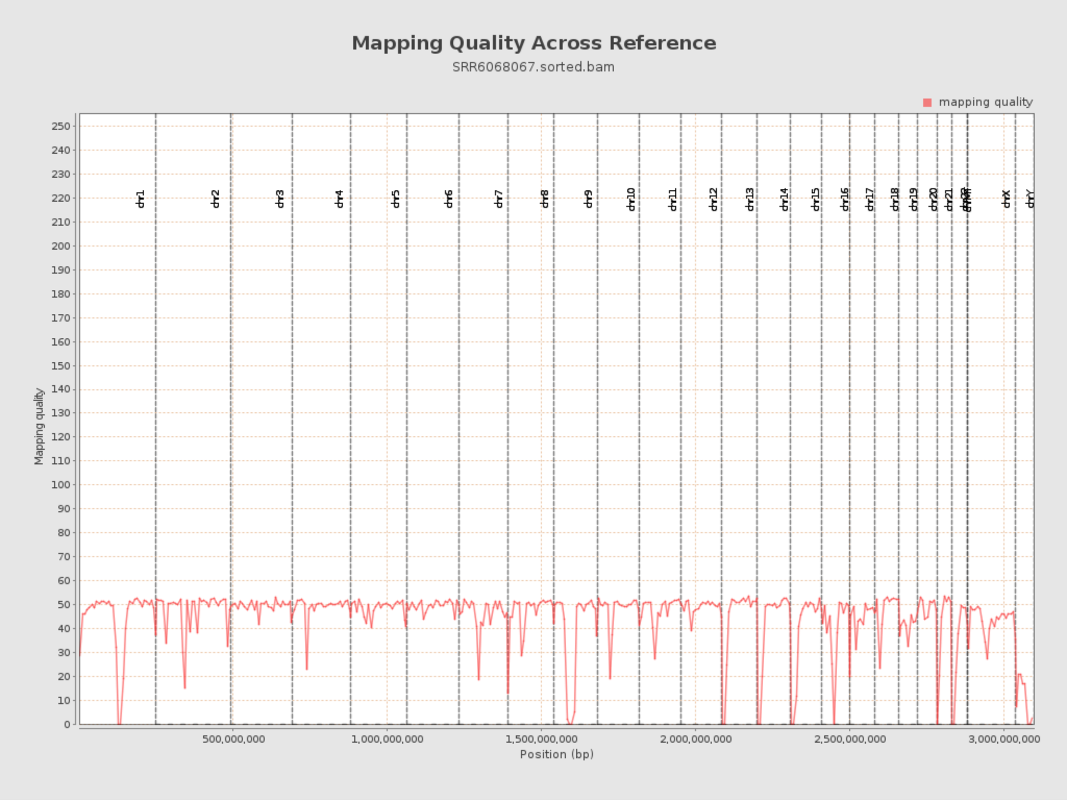
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram