# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/22 13:40:00*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080671.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_SRR3080671 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080671.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 22 13:39:58 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3080671.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,474,474 |
| Mapped reads | 1,326,278 / 89.95% |
| Unmapped reads | 148,196 / 10.05% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 11,705 / 0.79% |
| Read min/max/mean length | 30 / 76 / 76.28 |
| Duplicated reads (estimated) | 52,611 / 3.57% |
| Duplication rate | 3.45% |
| Clipped reads | 638,181 / 43.28% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 23,251,041 / 26.66% |
| Number/percentage of C's | 16,193,300 / 18.56% |
| Number/percentage of T's | 27,514,008 / 31.54% |
| Number/percentage of G's | 20,264,130 / 23.23% |
| Number/percentage of N's | 4,020 / 0% |
| GC Percentage | 41.8% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0282 |
| | |

| | |
|---|---|
| Standard Deviation | 0.234 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.22 |

## 2.5. Mismatches and indels

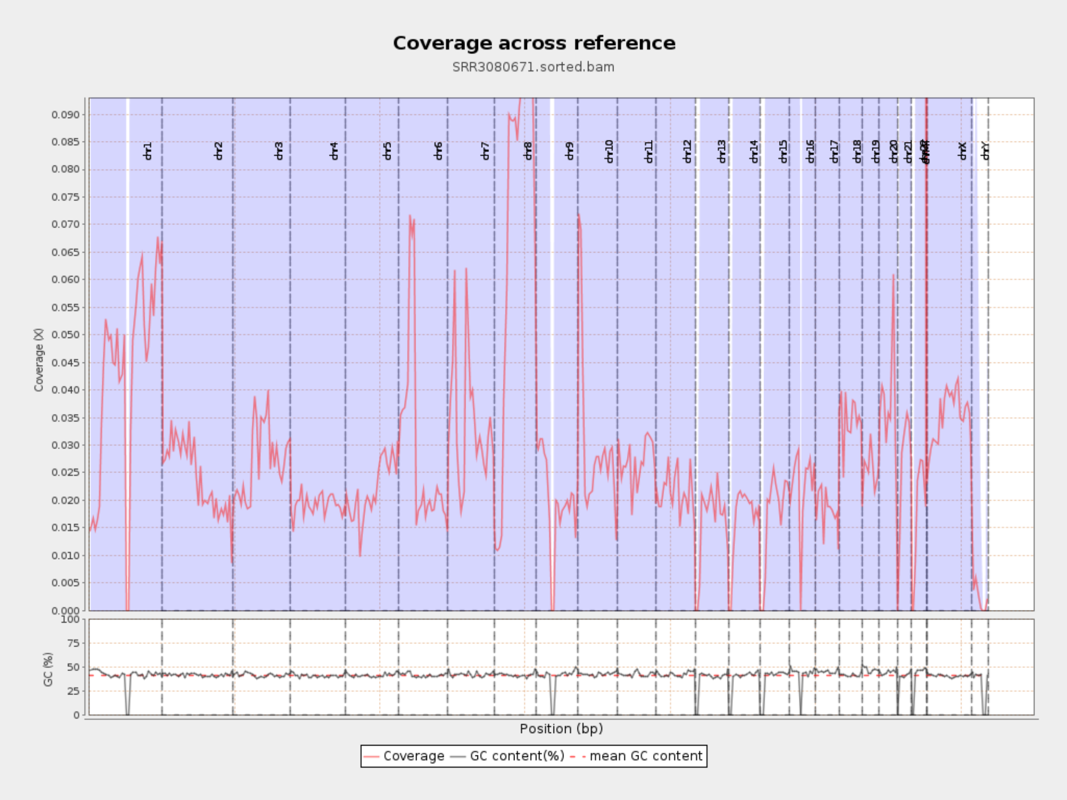
| | |
|---|---|
| General error rate | 0.7% |
| Mismatches | 596,535 |
| Insertions | 6,306 |
| Mapped reads with at least one insertion | 0.47% |
| Deletions | 20,092 |
| Mapped reads with at least one deletion | 1.5% |
| Homopolymer indels | 48.58% |

## 2.6. Chromosome stats

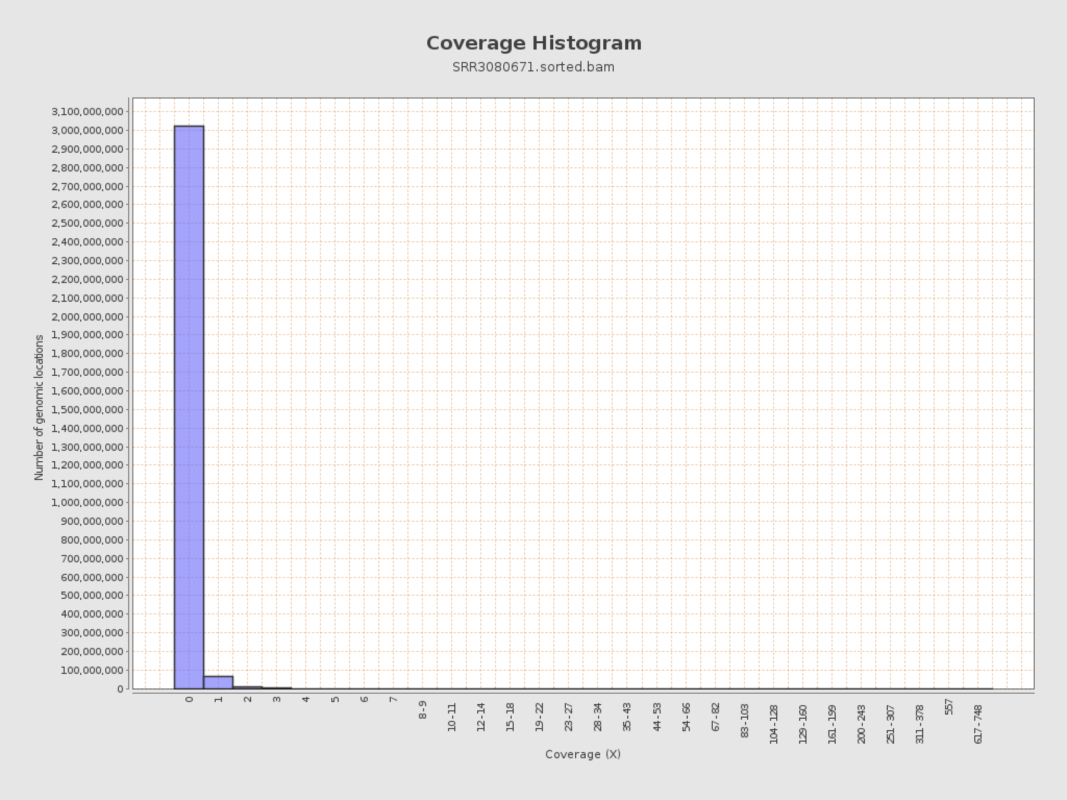
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 10644777 | 0.0427 | 0.2621 |
| chr2 | 243199373 | 5913114 | 0.0243 | 0.3609 |
| chr3 | 198022430 | 5388046 | 0.0272 | 0.1859 |
| chr4 | 191154276 | 3663639 | 0.0192 | 0.1594 |
| chr5 | 180915260 | 3957030 | 0.0219 | 0.1662 |
| chr6 | 171115067 | 5054367 | 0.0295 | 0.2274 |
| chr7 | 159138663 | 5542986 | 0.0348 | 0.4227 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 10455650 | 0.0714 | 0.3265 |
| chr9 | 141213431 | 2756683 | 0.0195 | 0.1719 |
| chr10 | 135534747 | 4148869 | 0.0306 | 0.2058 |
| chr11 | 135006516 | 3629581 | 0.0269 | 0.1933 |
| chr12 | 133851895 | 2854161 | 0.0213 | 0.1653 |
| chr13 | 115169878 | 1838516 | 0.016 | 0.1428 |
| chr14 | 107349540 | 1748343 | 0.0163 | 0.1436 |
| chr15 | 102531392 | 1760498 | 0.0172 | 0.1568 |
| chr16 | 90354753 | 2052879 | 0.0227 | 0.1716 |
| chr17 | 81195210 | 1477693 | 0.0182 | 0.1539 |
| chr18 | 78077248 | 2718474 | 0.0348 | 0.2425 |
| chr19 | 59128983 | 1531299 | 0.0259 | 0.1981 |
| chr20 | 63025520 | 2360375 | 0.0375 | 0.2216 |
| chr21 | 48129895 | 1243168 | 0.0258 | 0.1815 |
| chr22 | 51304566 | 876914 | 0.0171 | 0.1461 |
| chrMT | 16571 | 15663 | 0.9452 | 1.1726 |
| chrX | 155270560 | 5456117 | 0.0351 | 0.2192 |
| chrY | 59373566 | 169969 | 0.0029 | 0.0606 |

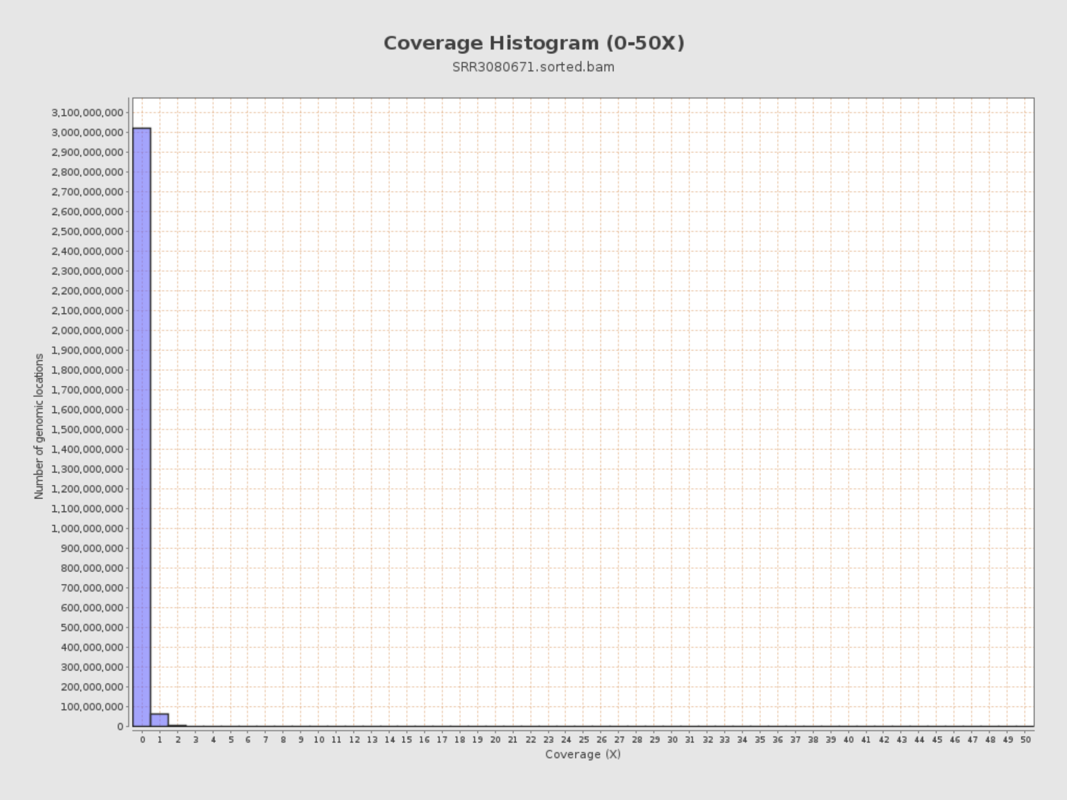
# 3. Results : Coverage across reference



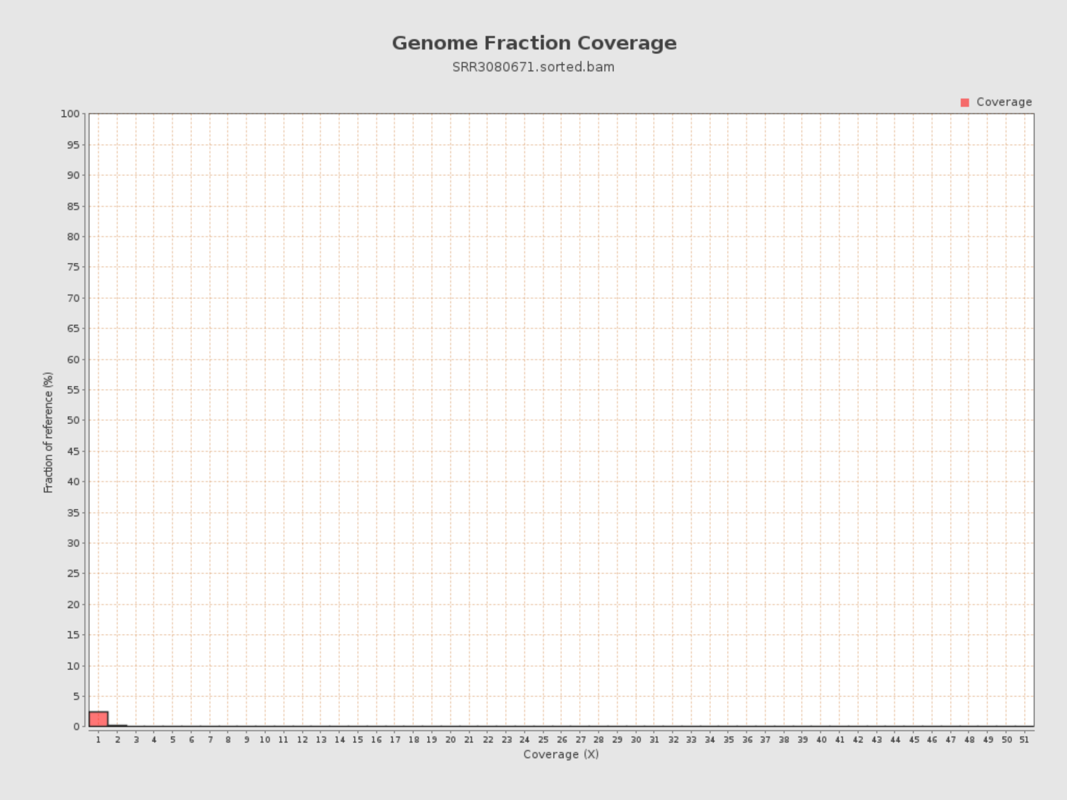
# 4. Results : Coverage Histogram



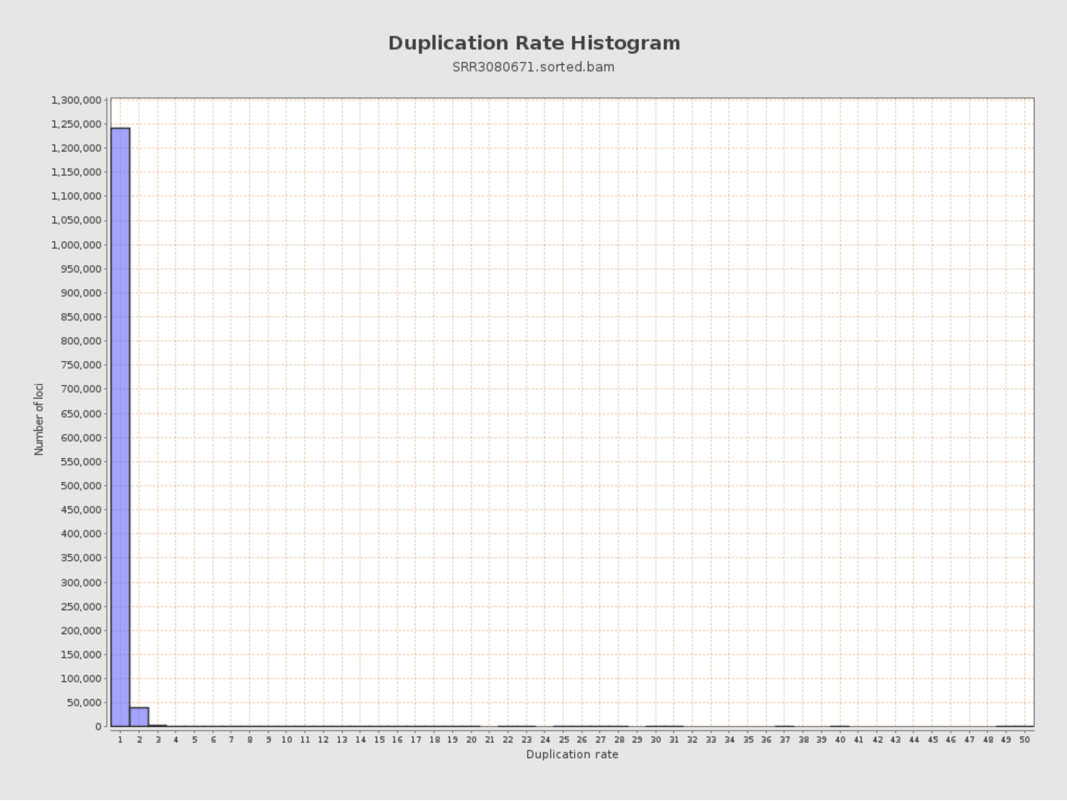
# 5. Results : Coverage Histogram (0-50X)



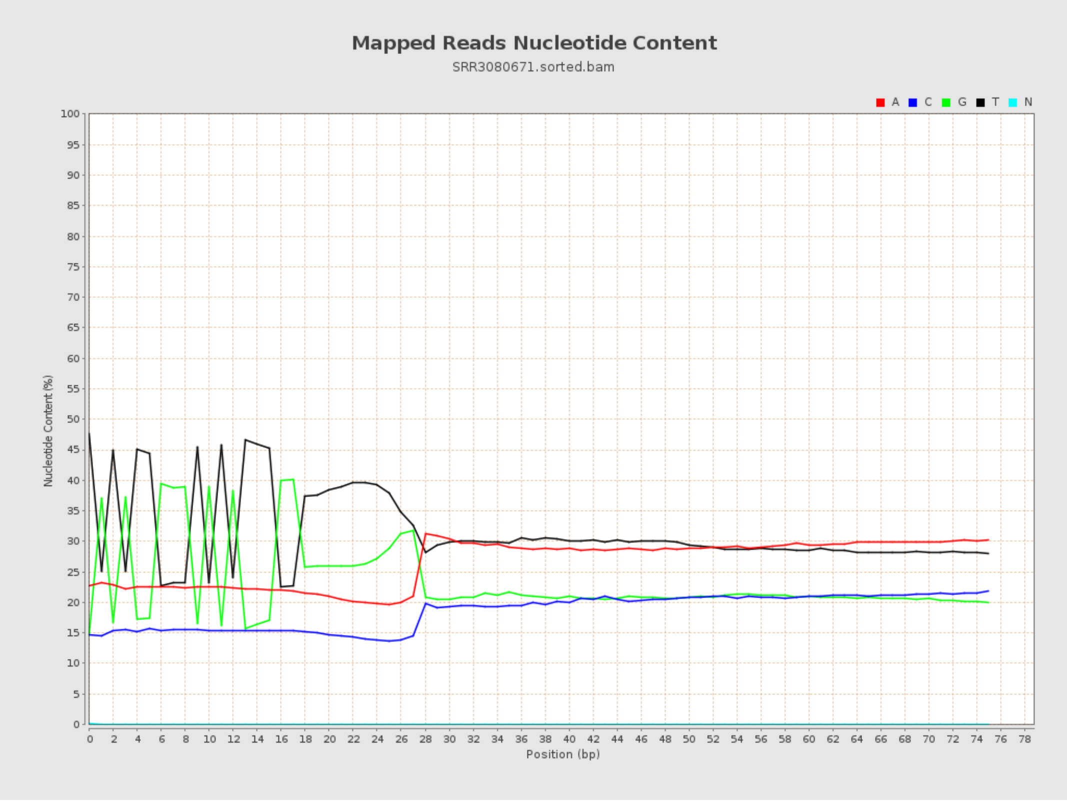
# 6. Results : Genome Fraction Coverage



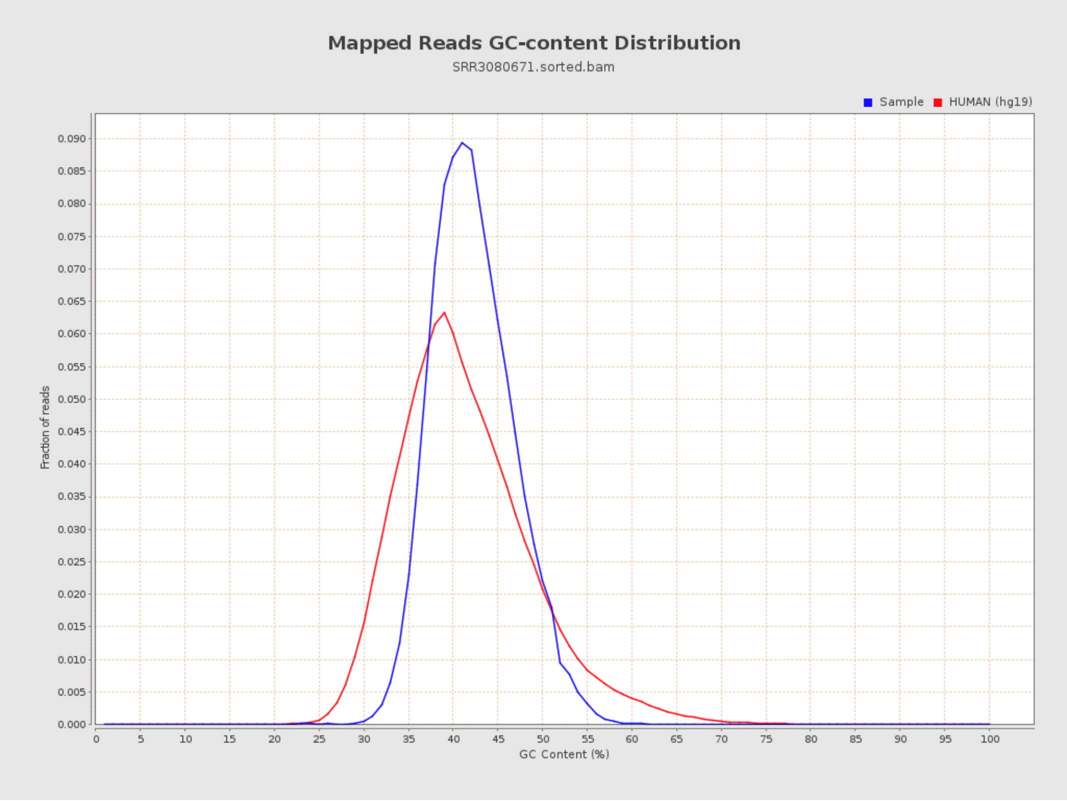
# 7. Results : Duplication Rate Histogram



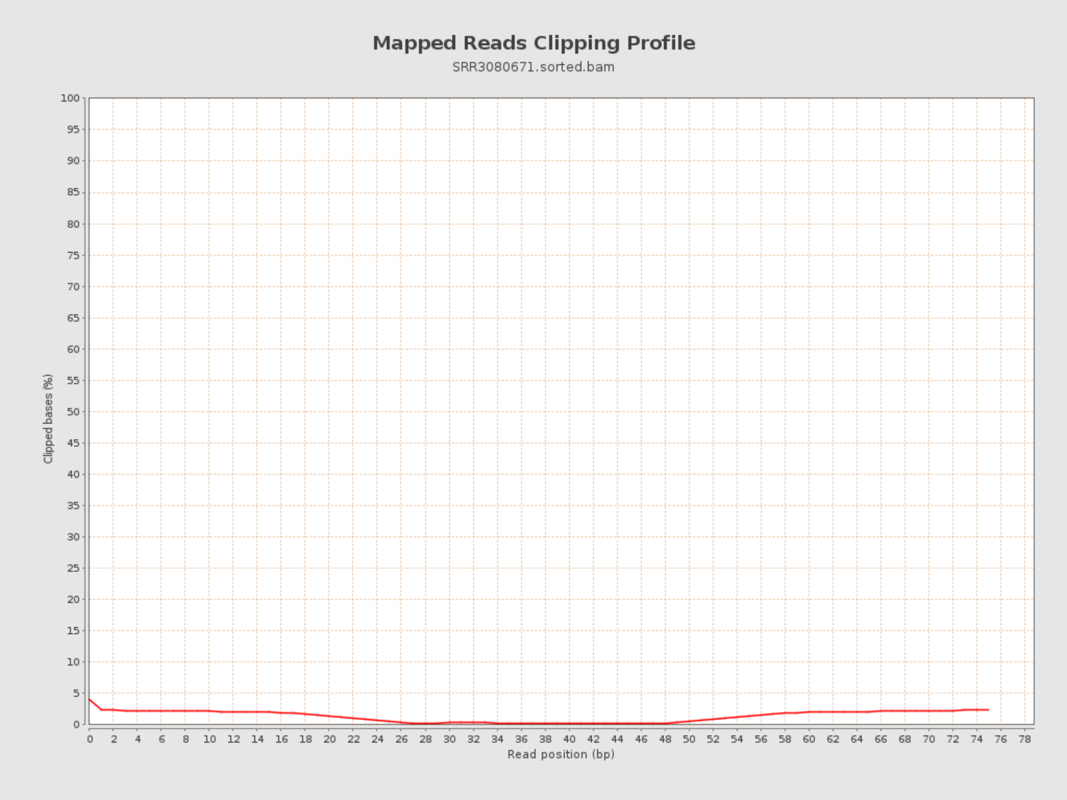
# 8. Results : Mapped Reads Nucleotide Content



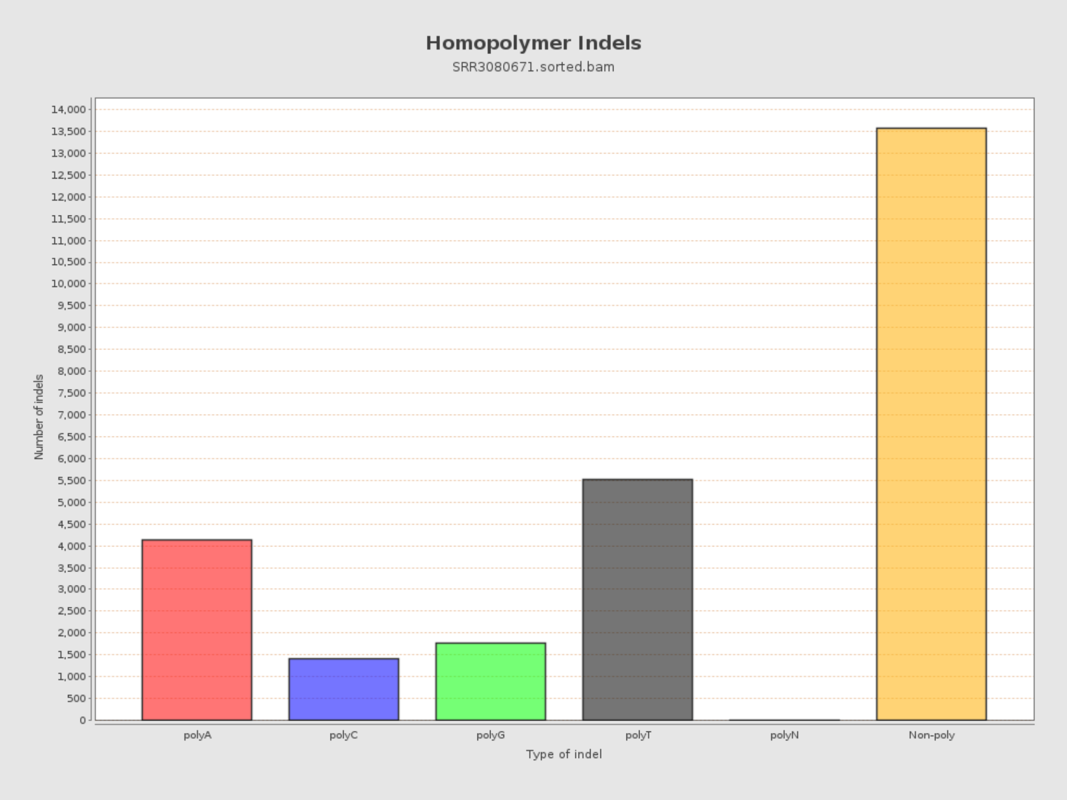
# 9. Results : Mapped Reads GC-content Distribution



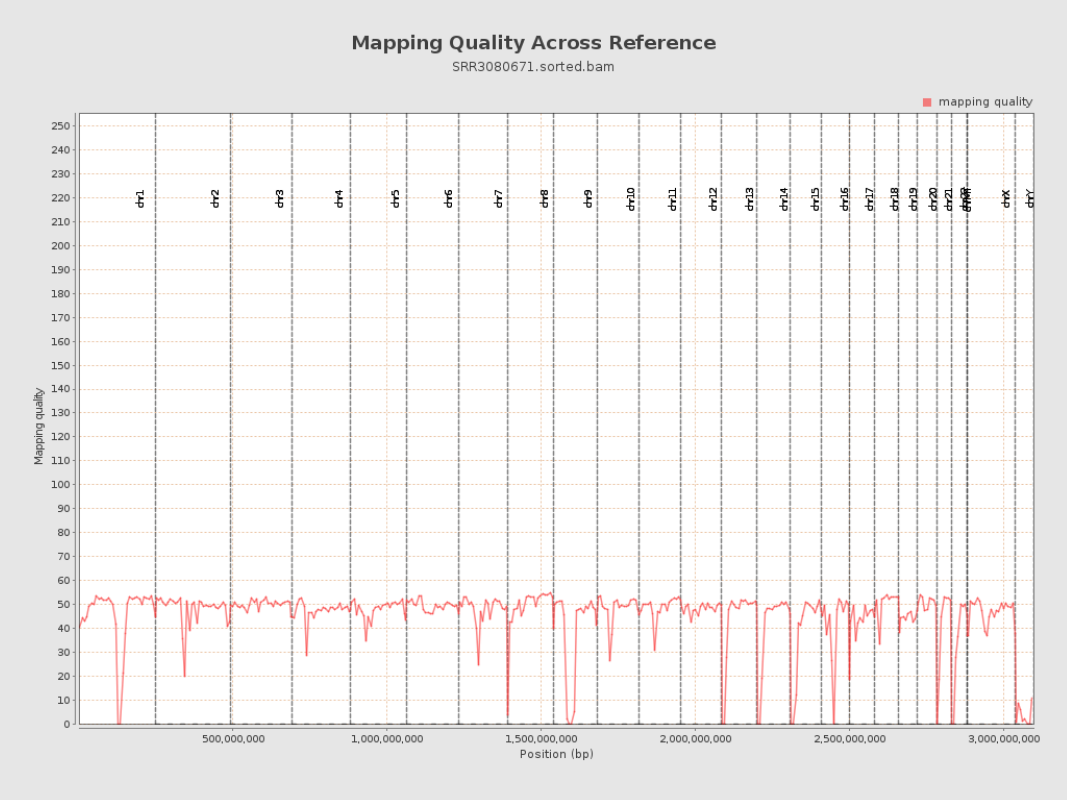
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram