# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 08:23:30*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080794.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_SRR3080794 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080794.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 08:23:29 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3080794.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,789,002 |
| Mapped reads | 1,555,350 / 86.94% |
| Unmapped reads | 233,652 / 13.06% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 19,267 / 1.08% |
| Read min/max/mean length | 30 / 76 / 76.37 |
| Duplicated reads (estimated) | 40,734 / 2.28% |
| Duplication rate | 1.63% |
| Clipped reads | 778,195 / 43.5% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 29,842,956 / 29.16% |
| Number/percentage of C's | 19,885,837 / 19.43% |
| Number/percentage of T's | 29,946,579 / 29.26% |
| Number/percentage of G's | 22,682,327 / 22.16% |
| Number/percentage of N's | 1,932 / 0% |
| GC Percentage | 41.59% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0331 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3707 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.57 |

## 2.5. Mismatches and indels

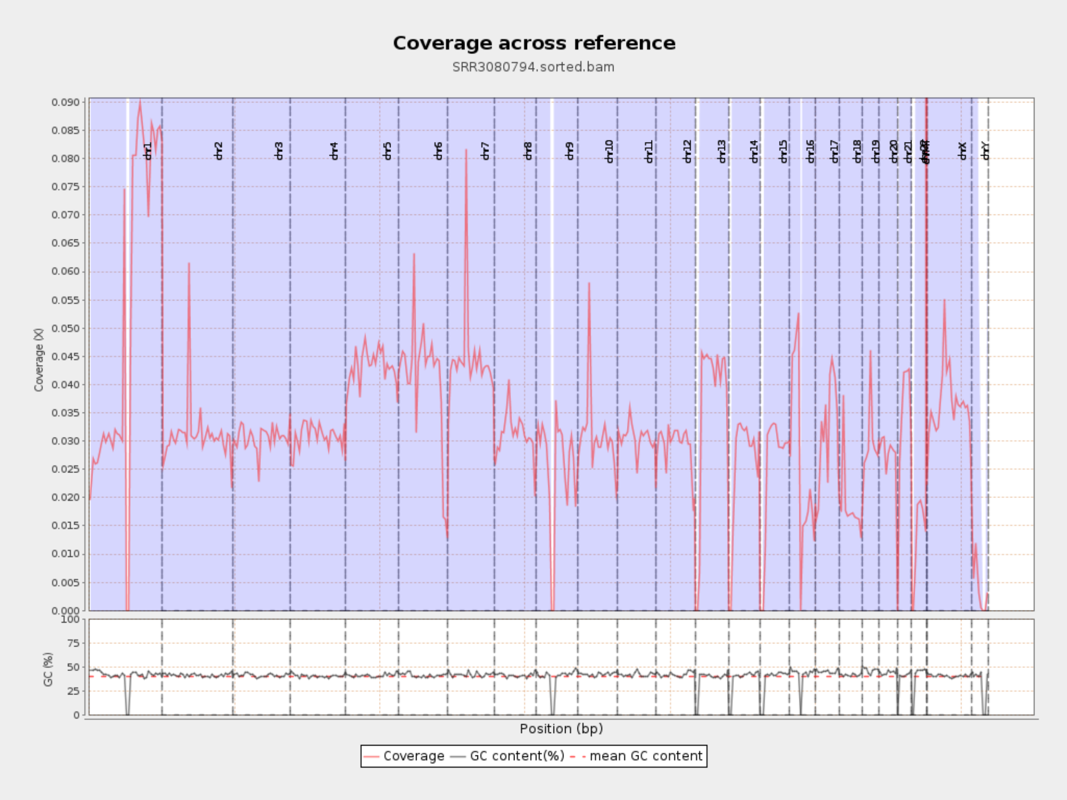
| | |
|---|---|
| General error rate | 0.79% |
| Mismatches | 797,903 |
| Insertions | 8,761 |
| Mapped reads with at least one insertion | 0.56% |
| Deletions | 21,153 |
| Mapped reads with at least one deletion | 1.35% |
| Homopolymer indels | 43.36% |

## 2.6. Chromosome stats

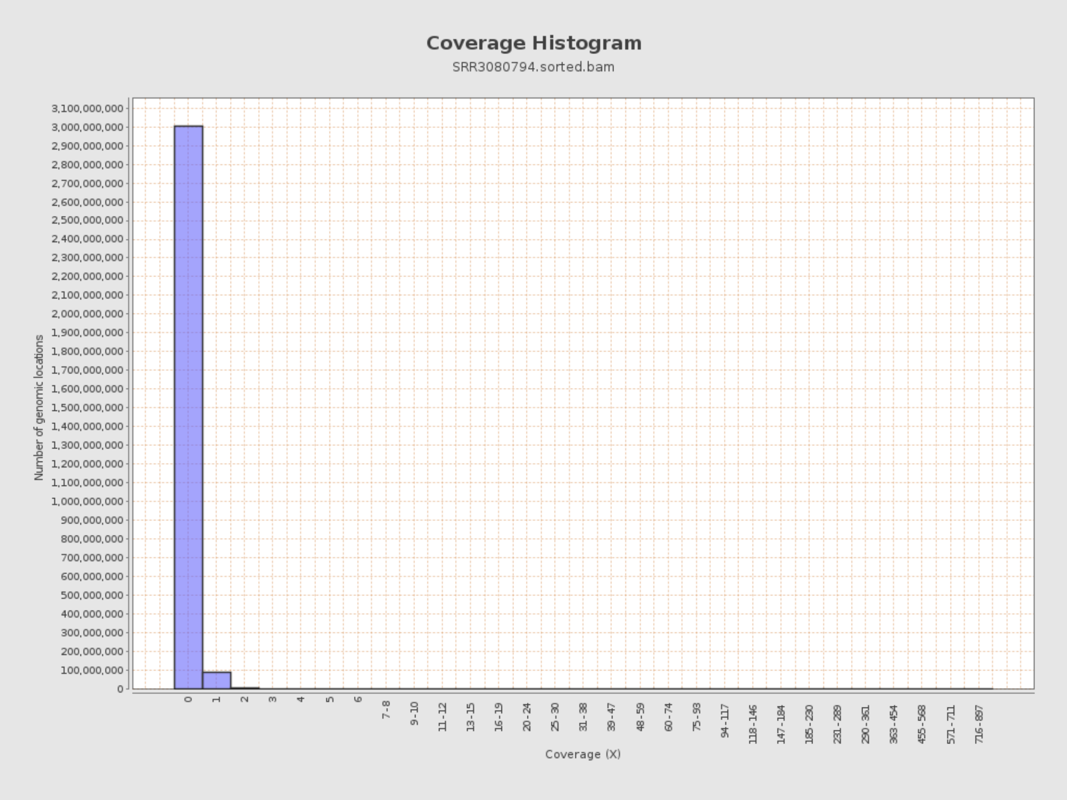
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 12799030 | 0.0514 | 0.8018 |
| chr2 | 243199373 | 7618934 | 0.0313 | 0.3497 |
| chr3 | 198022430 | 6037167 | 0.0305 | 0.1858 |
| chr4 | 191154276 | 5898536 | 0.0309 | 0.1924 |
| chr5 | 180915260 | 7816080 | 0.0432 | 0.2206 |
| chr6 | 171115067 | 7078517 | 0.0414 | 0.3131 |
| chr7 | 159138663 | 7153848 | 0.045 | 0.6082 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4551813 | 0.0311 | 0.3346 |
| chr9 | 141213431 | 3571258 | 0.0253 | 0.285 |
| chr10 | 135534747 | 4227357 | 0.0312 | 0.3284 |
| chr11 | 135006516 | 4121299 | 0.0305 | 0.2661 |
| chr12 | 133851895 | 3914753 | 0.0292 | 0.1837 |
| chr13 | 115169878 | 4147107 | 0.036 | 0.2003 |
| chr14 | 107349540 | 2711120 | 0.0253 | 0.1925 |
| chr15 | 102531392 | 2556431 | 0.0249 | 0.1756 |
| chr16 | 90354753 | 2407410 | 0.0266 | 0.2054 |
| chr17 | 81195210 | 2568790 | 0.0316 | 0.2077 |
| chr18 | 78077248 | 1474350 | 0.0189 | 0.5855 |
| chr19 | 59128983 | 1768549 | 0.0299 | 0.589 |
| chr20 | 63025520 | 1750303 | 0.0278 | 0.1867 |
| chr21 | 48129895 | 1607810 | 0.0334 | 0.2053 |
| chr22 | 51304566 | 644484 | 0.0126 | 0.1159 |
| chrMT | 16571 | 32444 | 1.9579 | 1.7788 |
| chrX | 155270560 | 5689825 | 0.0366 | 0.2338 |
| chrY | 59373566 | 246651 | 0.0042 | 0.0875 |

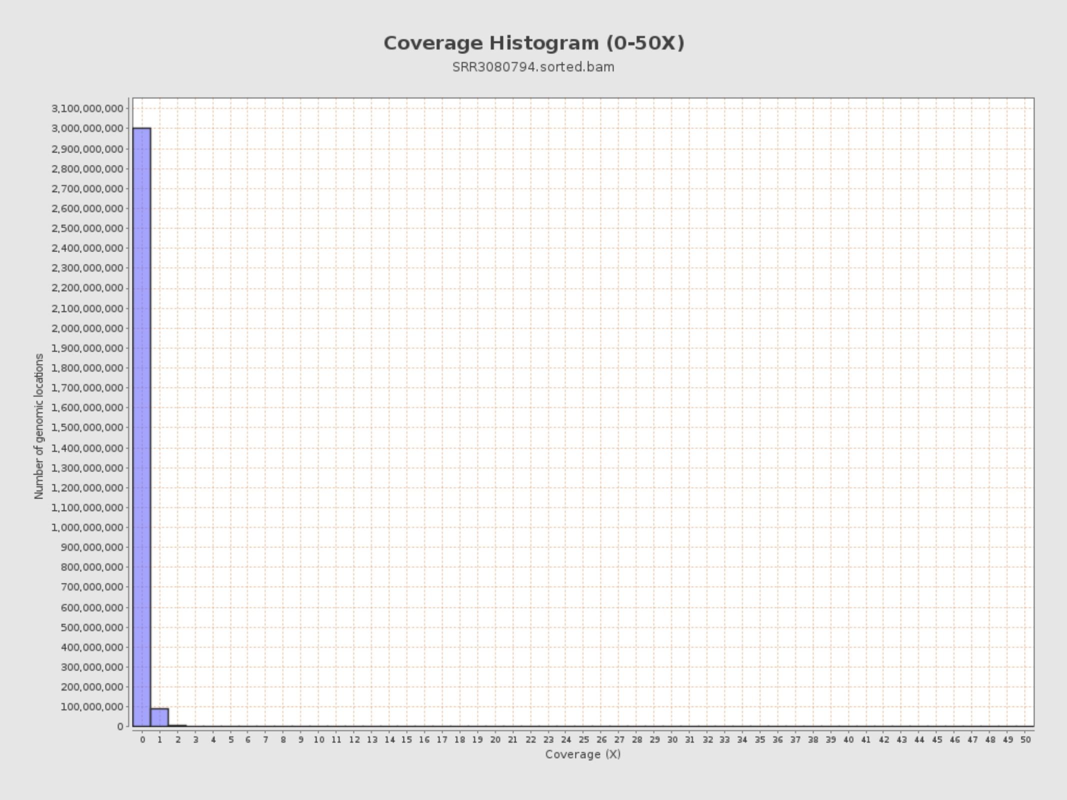
# 3. Results : Coverage across reference



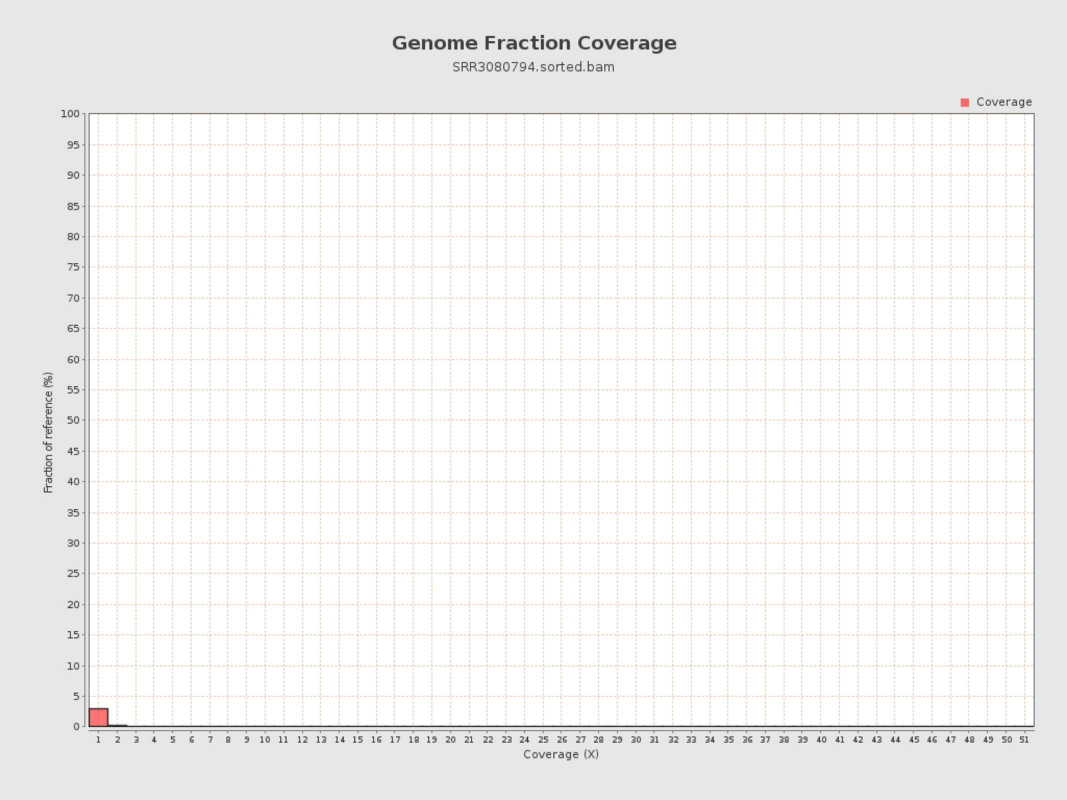
# 4. Results : Coverage Histogram



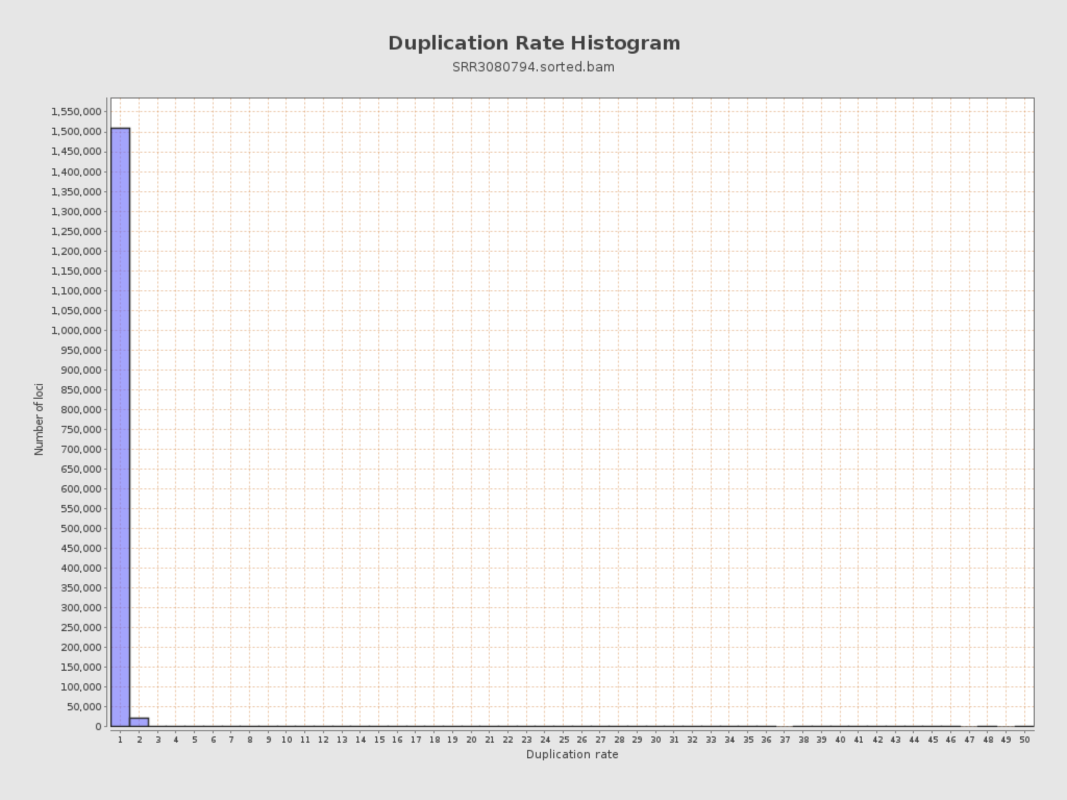
# 5. Results : Coverage Histogram (0-50X)



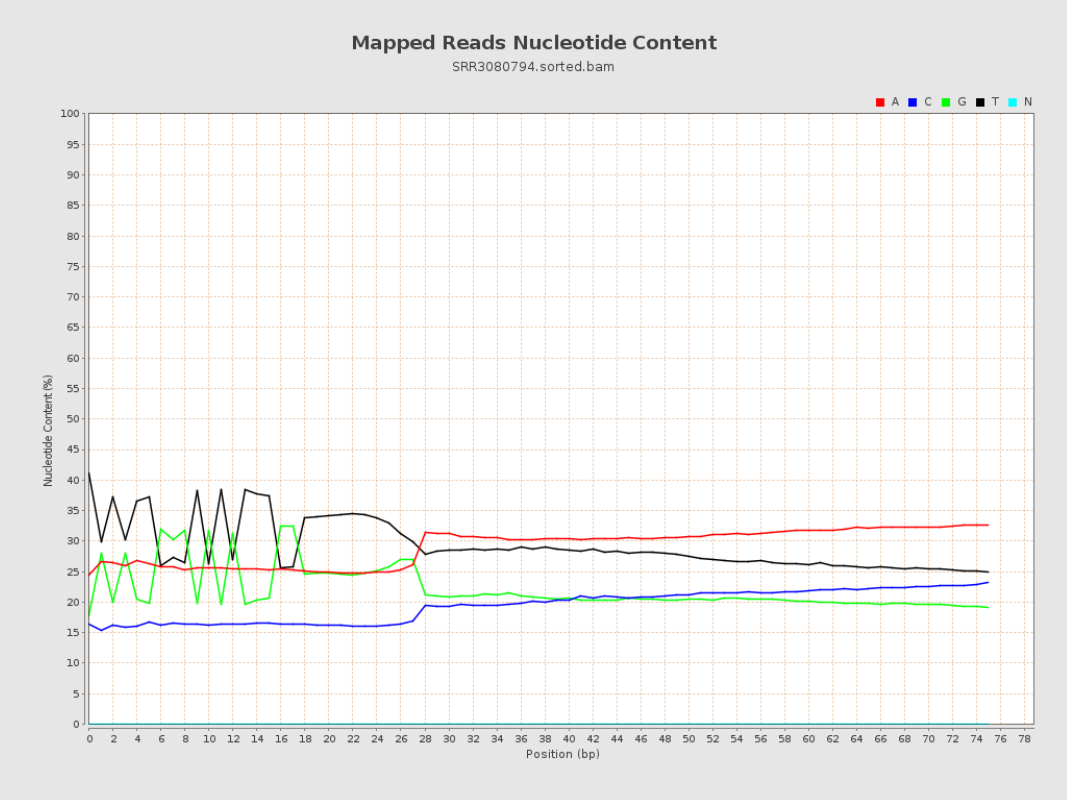
# 6. Results : Genome Fraction Coverage



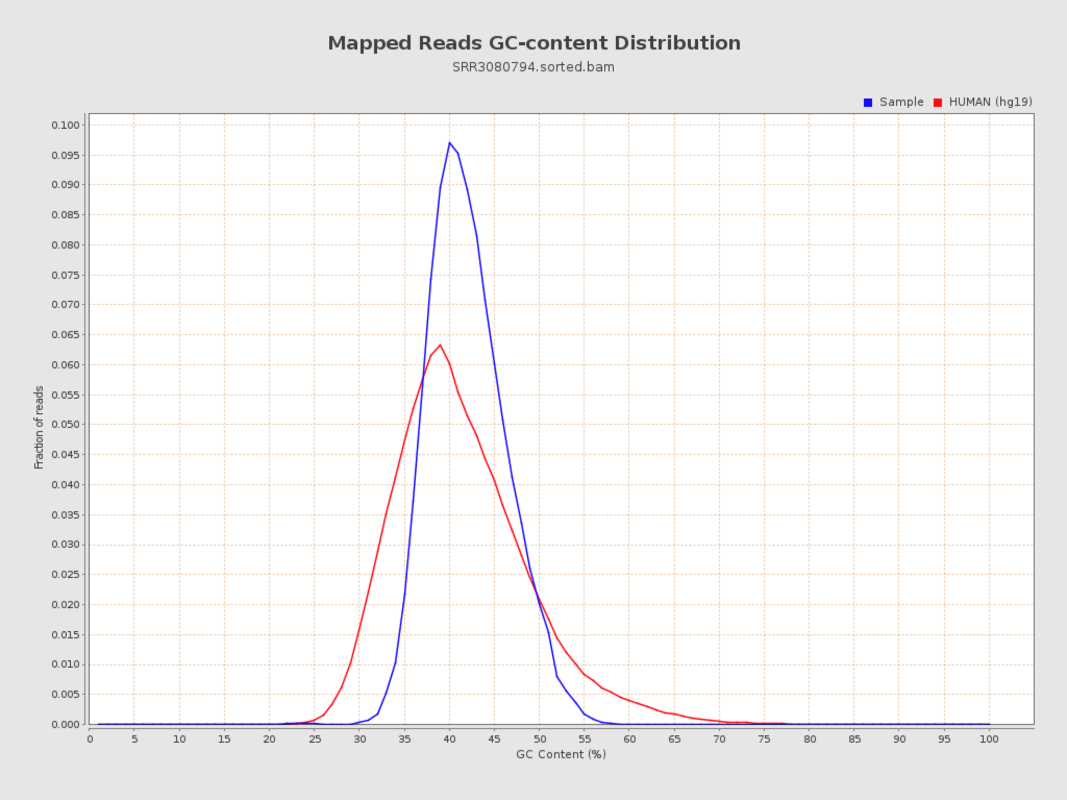
# 7. Results : Duplication Rate Histogram



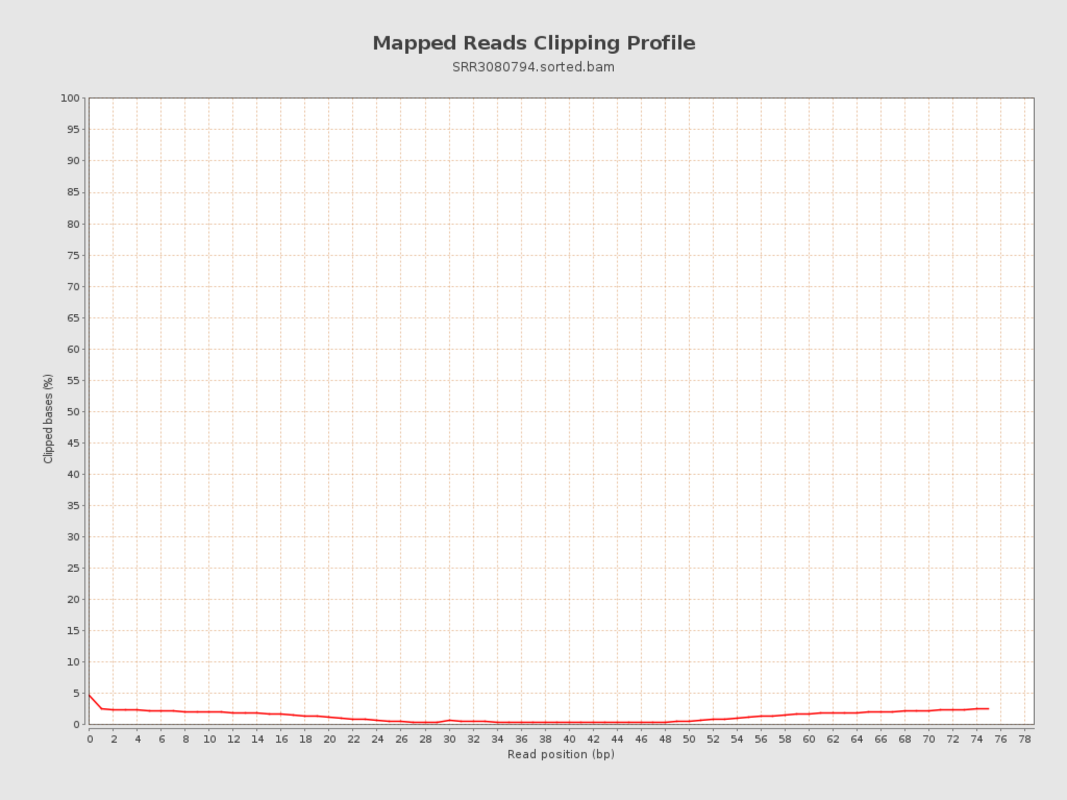
# 8. Results : Mapped Reads Nucleotide Content



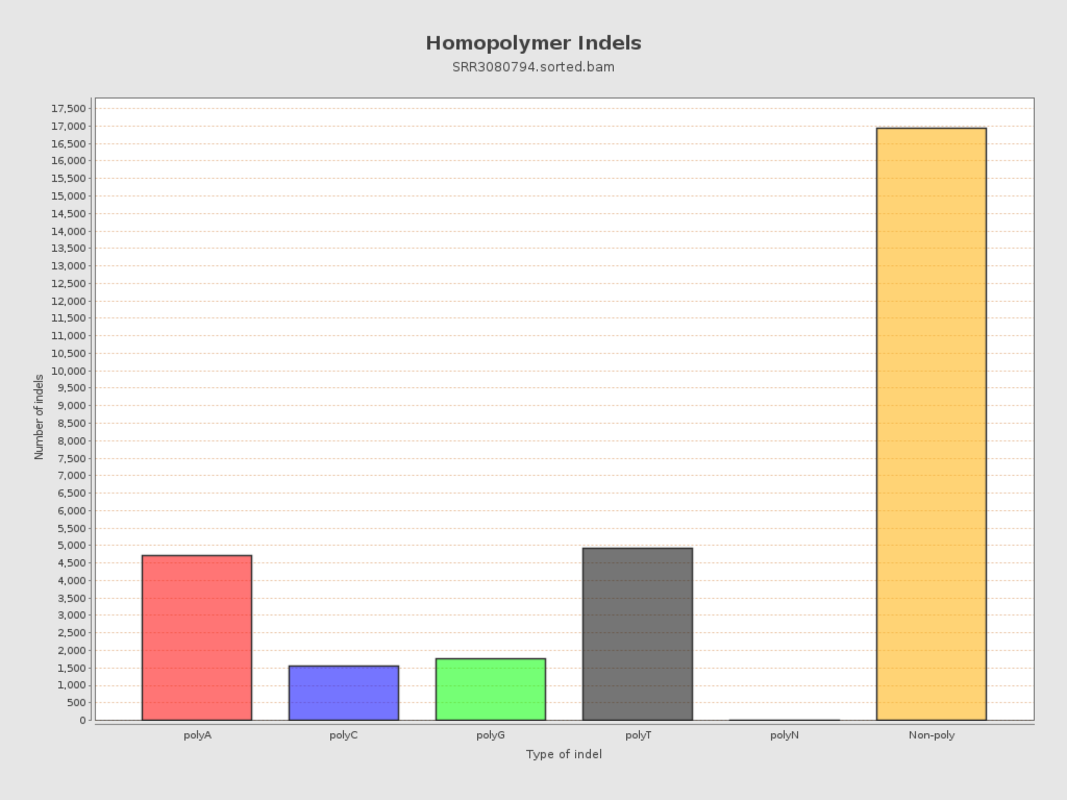
# 9. Results : Mapped Reads GC-content Distribution



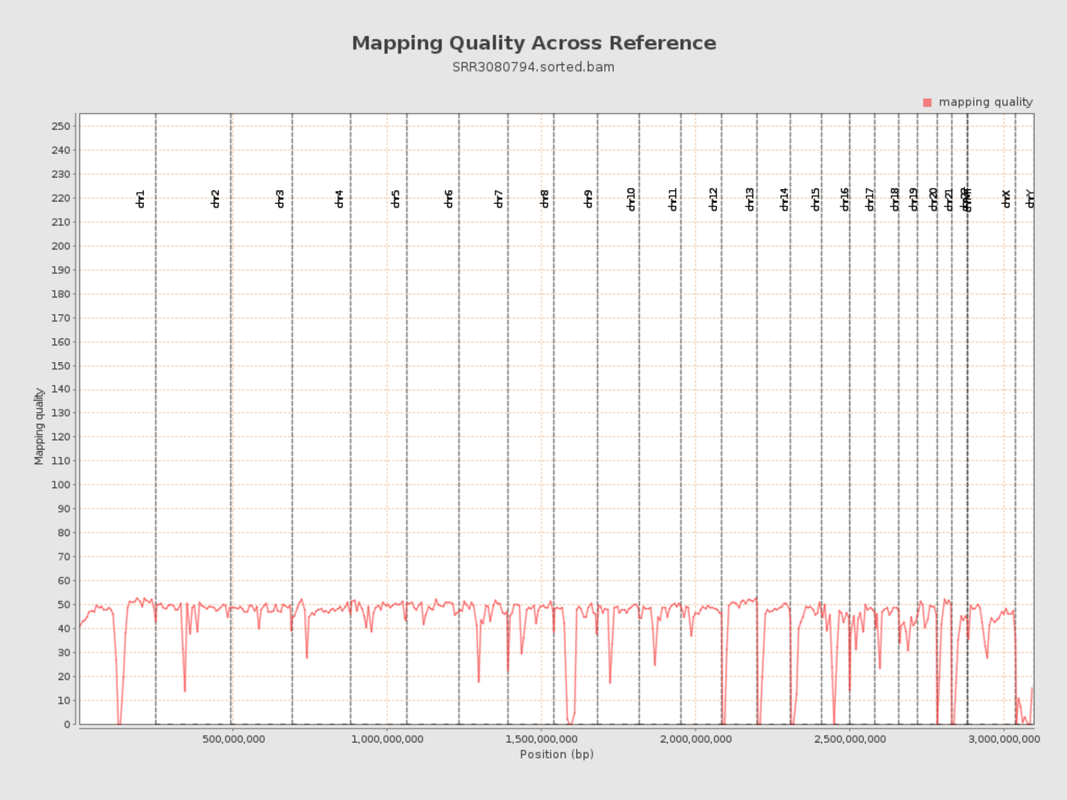
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram