# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/22 14:10:24*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080674.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_SRR3080674 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080674.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 22 14:10:22 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3080674.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 834,971 |
| Mapped reads | 763,037 / 91.38% |
| Unmapped reads | 71,934 / 8.62% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 6,220 / 0.74% |
| Read min/max/mean length | 30 / 76 / 76.26 |
| Duplicated reads (estimated) | 17,101 / 2.05% |
| Duplication rate | 2% |
| Clipped reads | 272,988 / 32.69% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 14,857,788 / 28.41% |
| Number/percentage of C's | 9,537,193 / 18.23% |
| Number/percentage of T's | 16,730,625 / 31.99% |
| Number/percentage of G's | 11,176,364 / 21.37% |
| Number/percentage of N's | 2,335 / 0% |
| GC Percentage | 39.6% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0169 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1545 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.92 |

## 2.5. Mismatches and indels

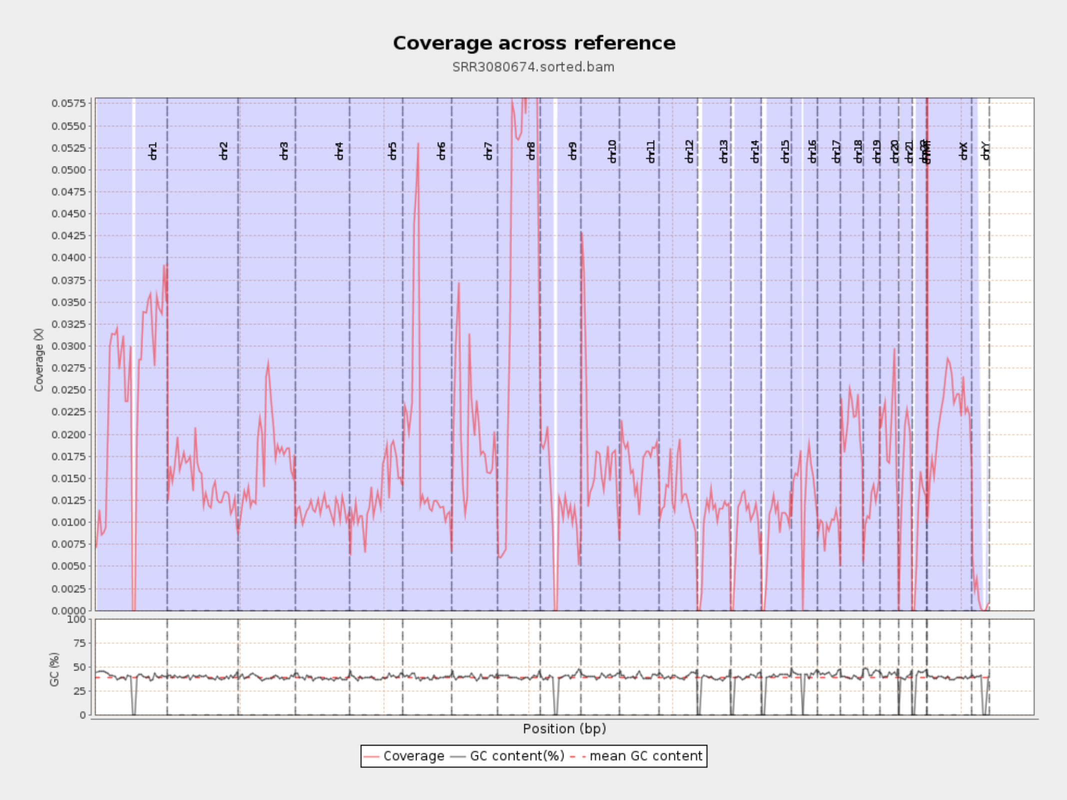
| | |
|---|---|
| General error rate | 0.72% |
| Mismatches | 369,563 |
| Insertions | 4,198 |
| Mapped reads with at least one insertion | 0.55% |
| Deletions | 12,295 |
| Mapped reads with at least one deletion | 1.6% |
| Homopolymer indels | 48.99% |

## 2.6. Chromosome stats

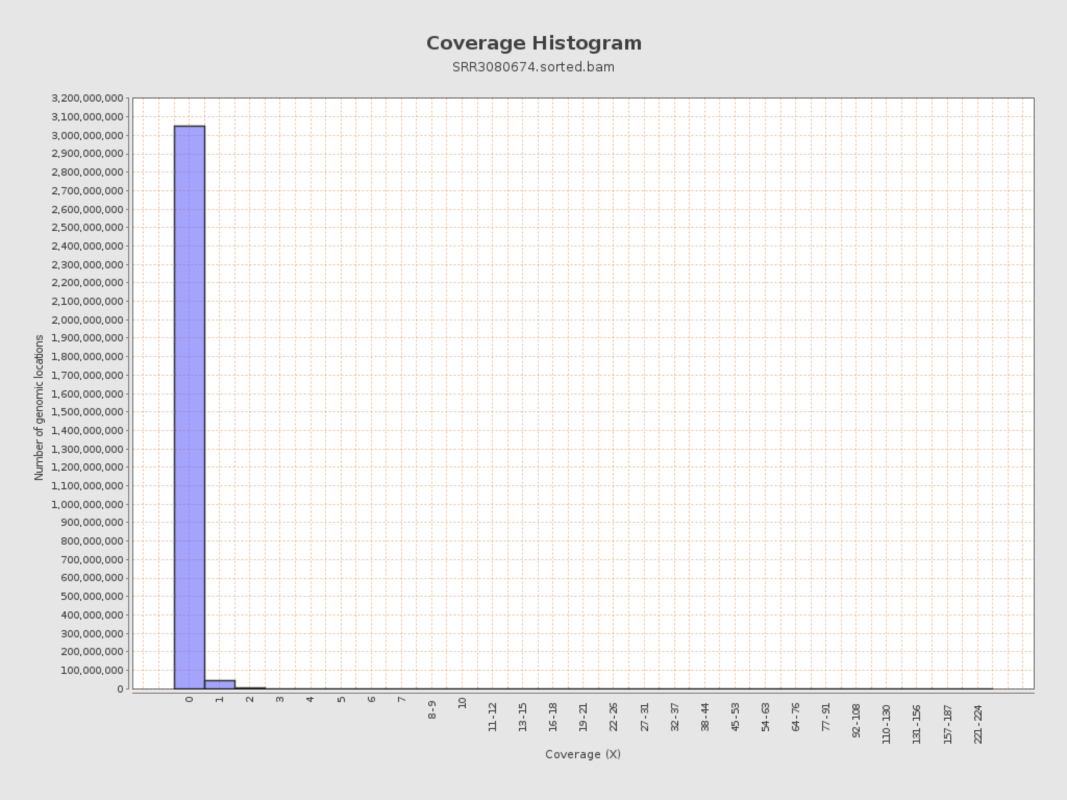
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 6319411 | 0.0254 | 0.1866 |
| chr2 | 243199373 | 3535932 | 0.0145 | 0.1664 |
| chr3 | 198022430 | 3394278 | 0.0171 | 0.1391 |
| chr4 | 191154276 | 2187727 | 0.0114 | 0.115 |
| chr5 | 180915260 | 2412995 | 0.0133 | 0.1227 |
| chr6 | 171115067 | 3193160 | 0.0187 | 0.1622 |
| chr7 | 159138663 | 3190521 | 0.02 | 0.2448 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6347777 | 0.0434 | 0.2466 |
| chr9 | 141213431 | 1661910 | 0.0118 | 0.1258 |
| chr10 | 135534747 | 2518602 | 0.0186 | 0.1486 |
| chr11 | 135006516 | 2281531 | 0.0169 | 0.143 |
| chr12 | 133851895 | 1723634 | 0.0129 | 0.121 |
| chr13 | 115169878 | 1123444 | 0.0098 | 0.1053 |
| chr14 | 107349540 | 1008985 | 0.0094 | 0.104 |
| chr15 | 102531392 | 918177 | 0.009 | 0.1022 |
| chr16 | 90354753 | 1253708 | 0.0139 | 0.1269 |
| chr17 | 81195210 | 765828 | 0.0094 | 0.105 |
| chr18 | 78077248 | 1696121 | 0.0217 | 0.1791 |
| chr19 | 59128983 | 727906 | 0.0123 | 0.1248 |
| chr20 | 63025520 | 1283720 | 0.0204 | 0.1531 |
| chr21 | 48129895 | 751446 | 0.0156 | 0.1341 |
| chr22 | 51304566 | 482752 | 0.0094 | 0.1032 |
| chrMT | 16571 | 5886 | 0.3552 | 0.683 |
| chrX | 155270560 | 3445723 | 0.0222 | 0.1616 |
| chrY | 59373566 | 93170 | 0.0016 | 0.044 |

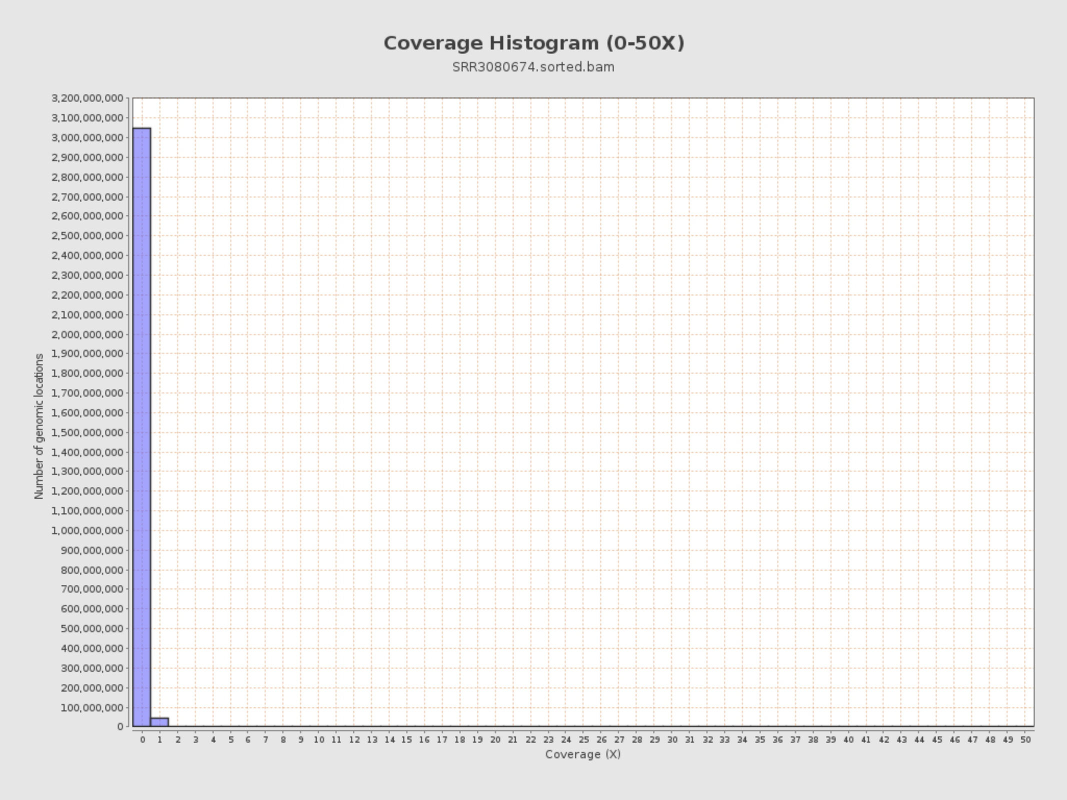
# 3. Results : Coverage across reference



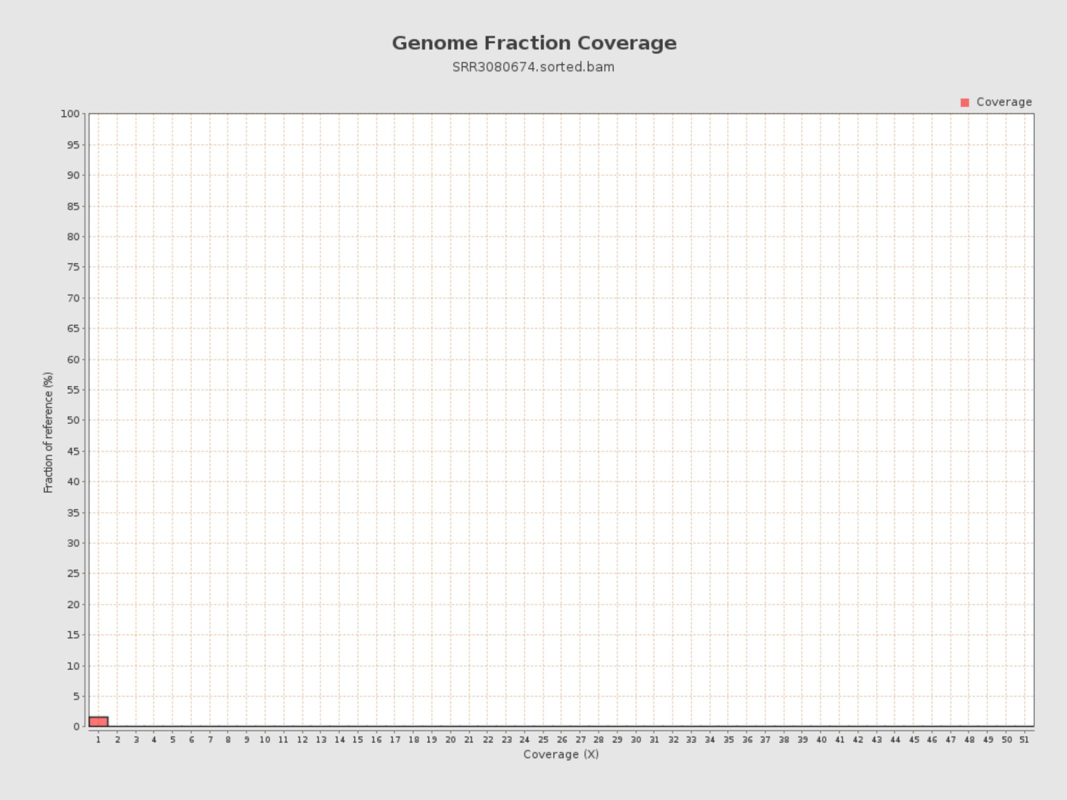
# 4. Results : Coverage Histogram



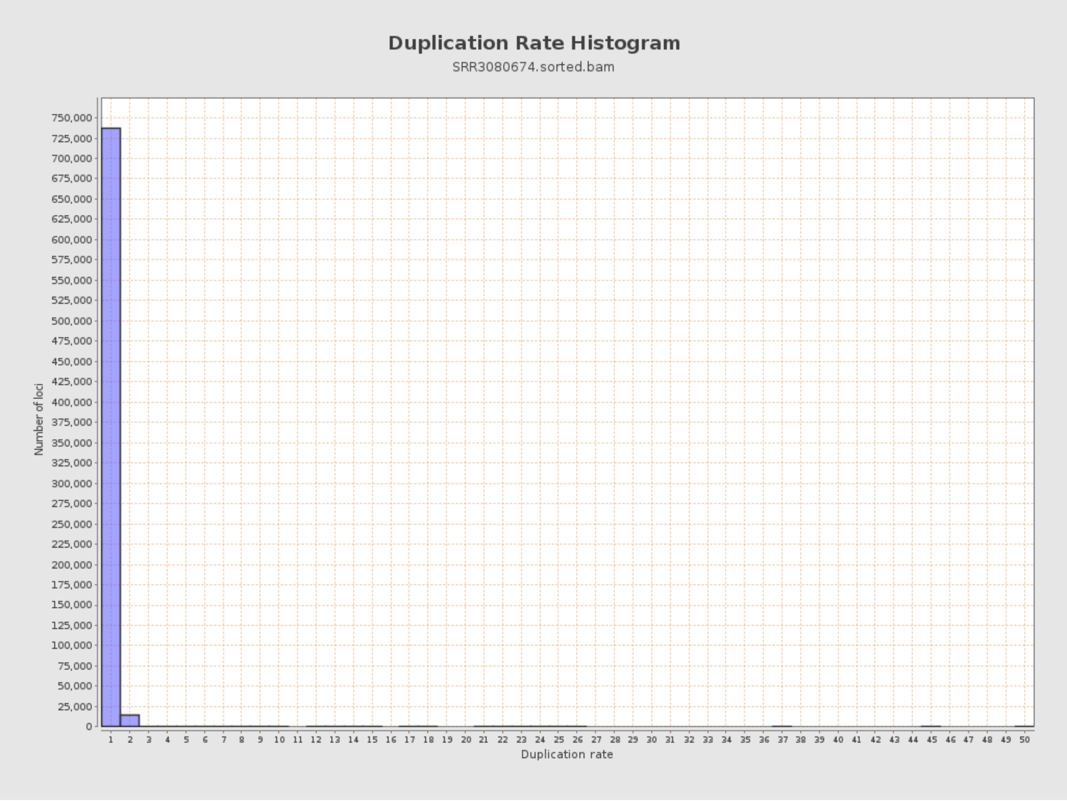
# 5. Results : Coverage Histogram (0-50X)



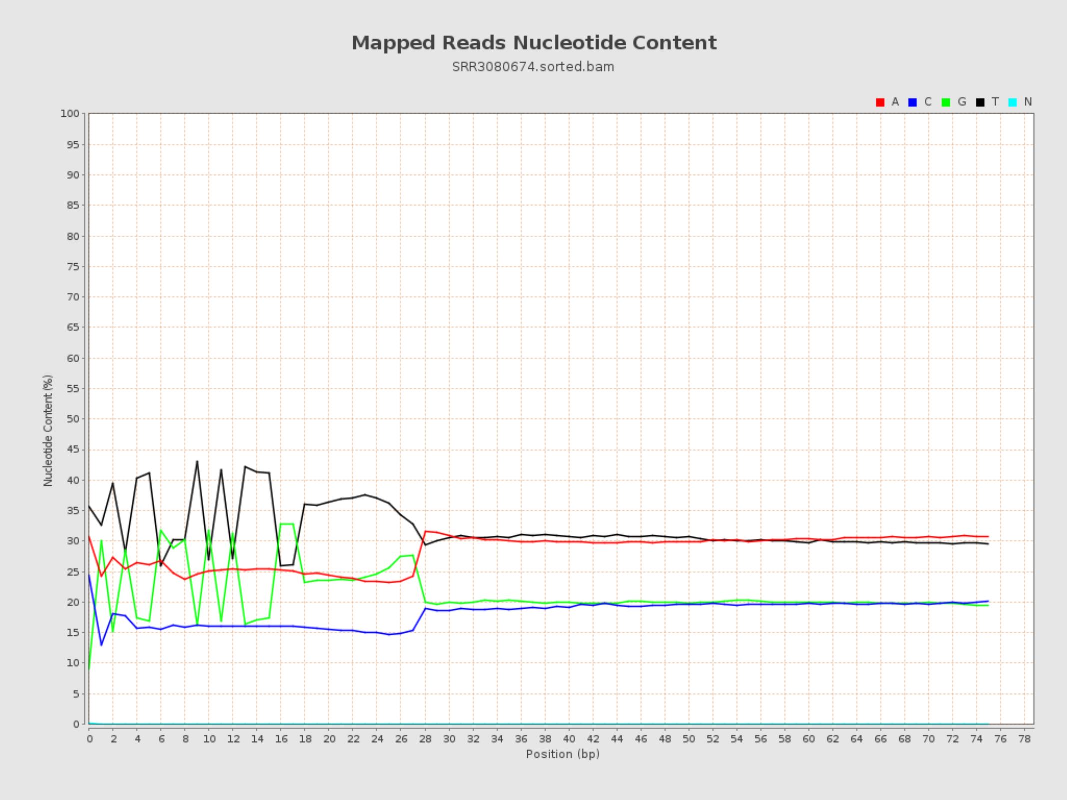
# 6. Results : Genome Fraction Coverage



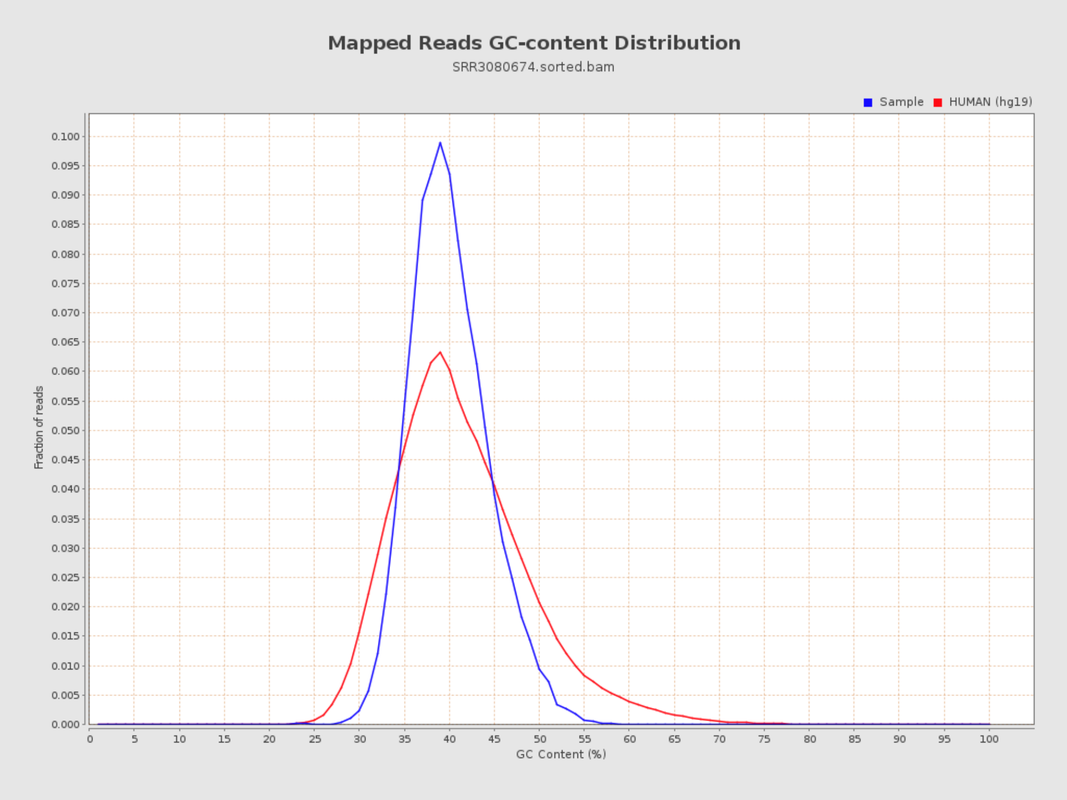
# 7. Results : Duplication Rate Histogram



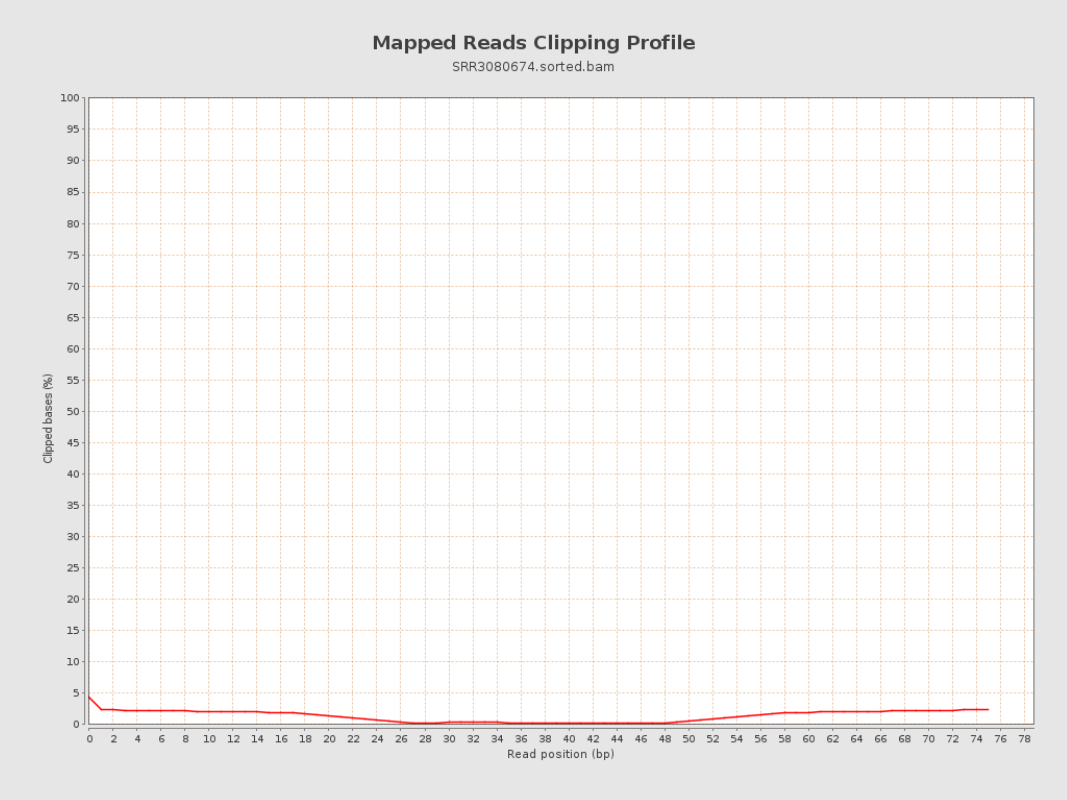
# 8. Results : Mapped Reads Nucleotide Content



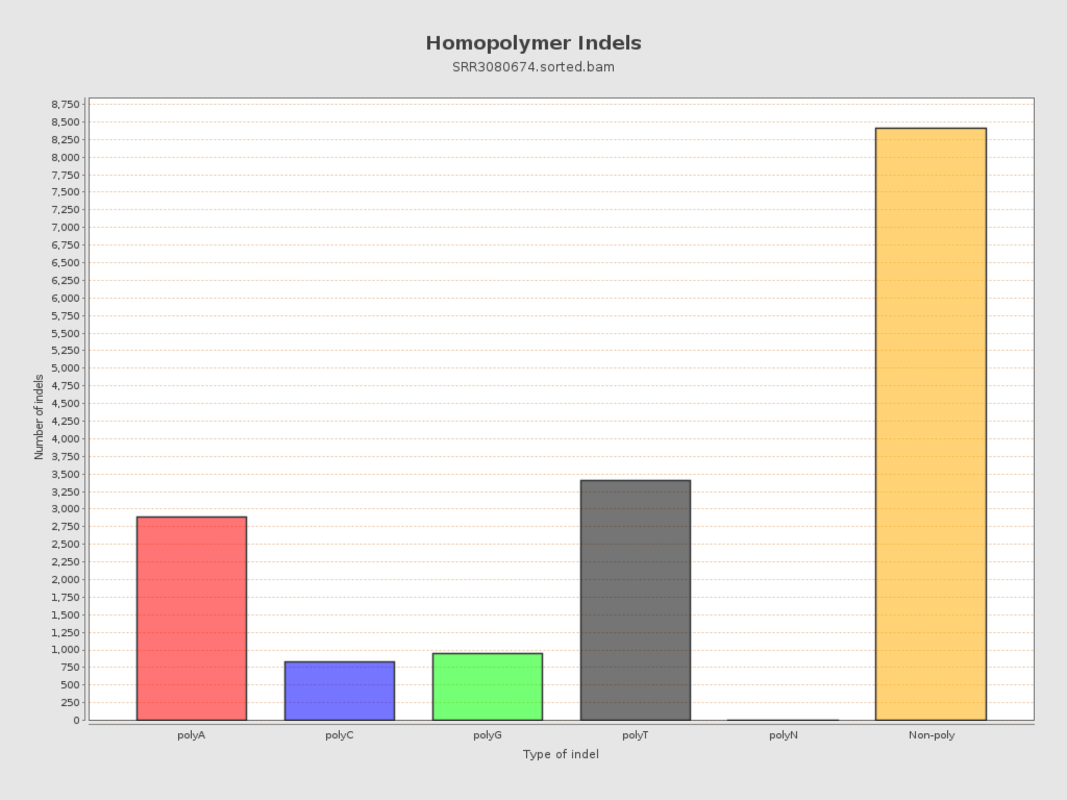
# 9. Results : Mapped Reads GC-content Distribution



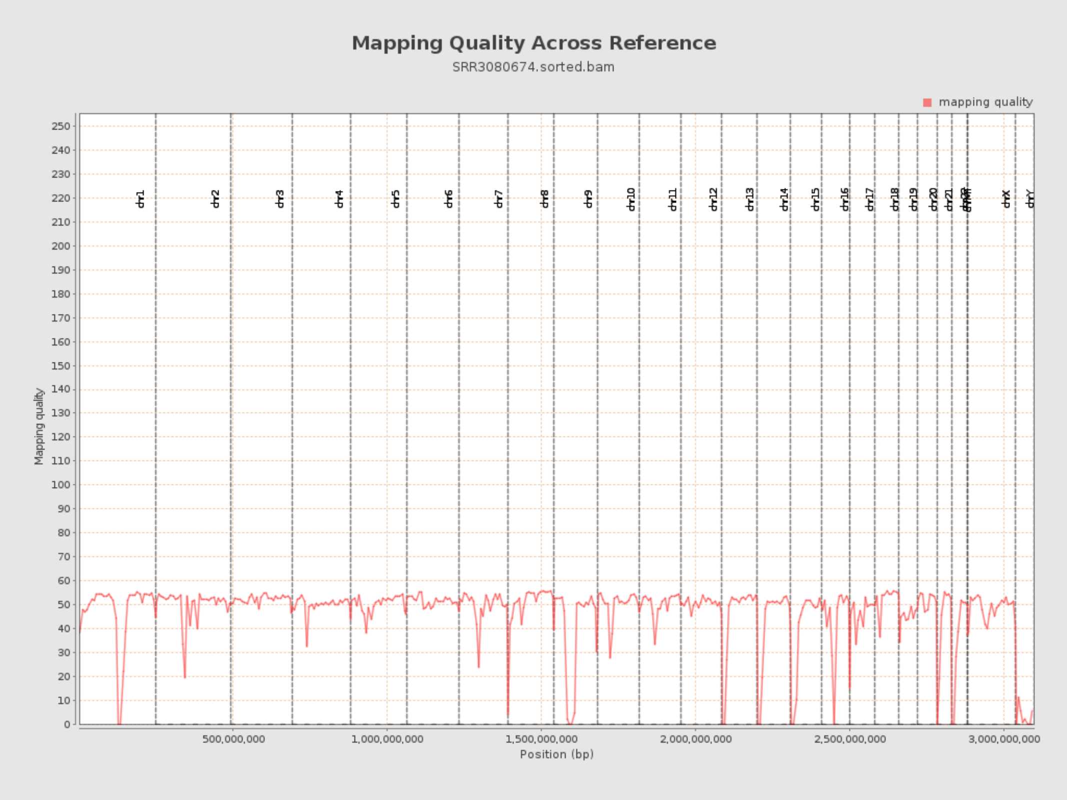
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram