# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 14:14:39*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080979.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_SRR3080979 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080979.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 14:14:38 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3080979.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,118,703 |
| Mapped reads | 3,453,350 / 83.85% |
| Unmapped reads | 665,353 / 16.15% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 24,105 / 0.59% |
| Read min/max/mean length | 30 / 76 / 76.2 |
| Duplicated reads (estimated) | 239,556 / 5.82% |
| Duplication rate | 5.59% |
| Clipped reads | 1,377,324 / 33.44% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 65,782,361 / 28.23% |
| Number/percentage of C's | 41,046,431 / 17.61% |
| Number/percentage of T's | 76,188,261 / 32.69% |
| Number/percentage of G's | 49,579,939 / 21.27% |
| Number/percentage of N's | 464,093 / 0.2% |
| GC Percentage | 38.89% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0753 |
| | |

| | |
|---|---|
| Standard Deviation | 0.5847 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.31 |

## 2.5. Mismatches and indels

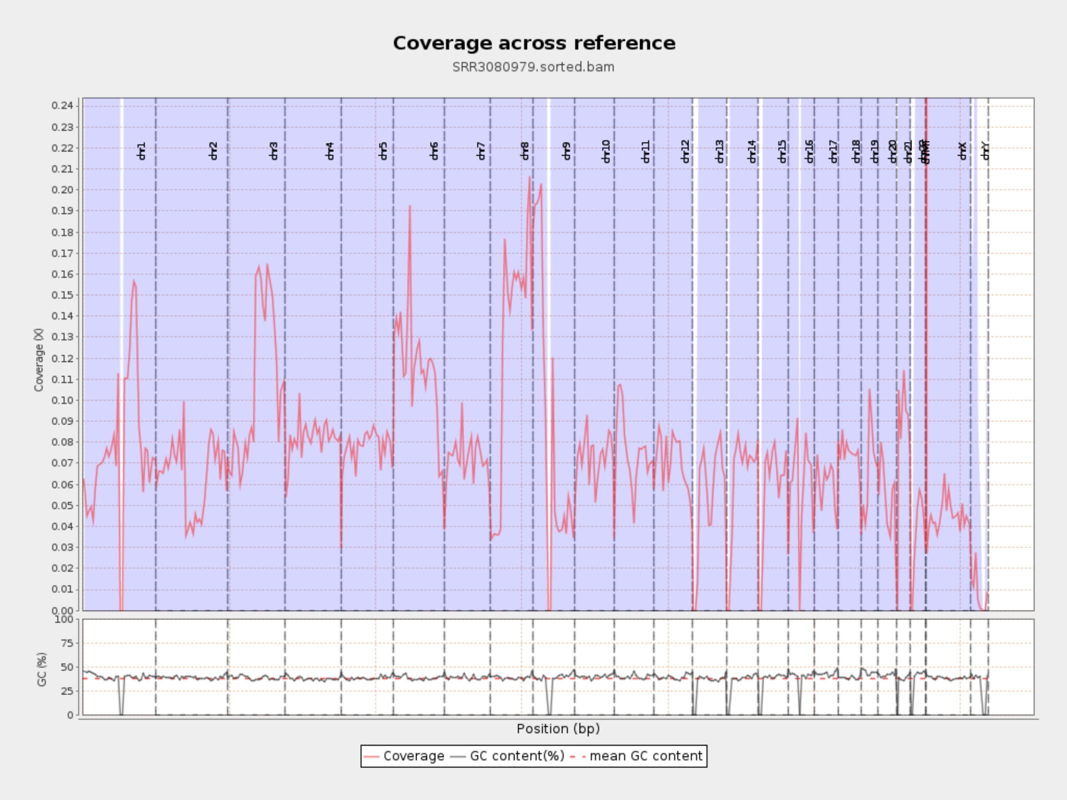
| | |
|---|---|
| General error rate | 0.99% |
| Mismatches | 2,264,848 |
| Insertions | 17,474 |
| Mapped reads with at least one insertion | 0.5% |
| Deletions | 46,762 |
| Mapped reads with at least one deletion | 1.34% |
| Homopolymer indels | 49.27% |

## 2.6. Chromosome stats

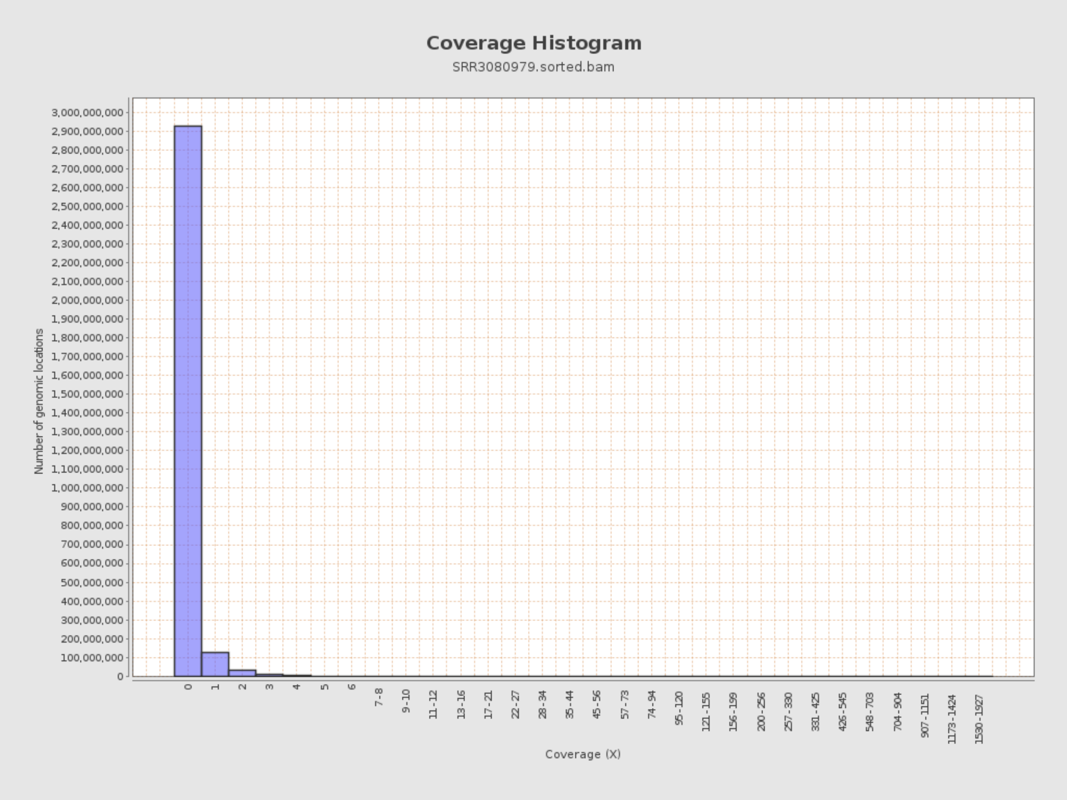
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 19152962 | 0.0768 | 0.8903 |
| chr2 | 243199373 | 15724274 | 0.0647 | 0.488 |
| chr3 | 198022430 | 21155376 | 0.1068 | 0.4315 |
| chr4 | 191154276 | 15689718 | 0.0821 | 0.3921 |
| chr5 | 180915260 | 14094719 | 0.0779 | 0.3699 |
| chr6 | 171115067 | 20034601 | 0.1171 | 0.6213 |
| chr7 | 159138663 | 11478063 | 0.0721 | 0.5424 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 18482023 | 0.1263 | 1.2517 |
| chr9 | 141213431 | 11947119 | 0.0846 | 0.7101 |
| chr10 | 135534747 | 9954358 | 0.0734 | 0.4766 |
| chr11 | 135006516 | 10204966 | 0.0756 | 0.4399 |
| chr12 | 133851895 | 9426401 | 0.0704 | 0.3717 |
| chr13 | 115169878 | 6246740 | 0.0542 | 0.303 |
| chr14 | 107349540 | 6658723 | 0.062 | 0.4019 |
| chr15 | 102531392 | 5835488 | 0.0569 | 0.3096 |
| chr16 | 90354753 | 5250460 | 0.0581 | 0.3768 |
| chr17 | 81195210 | 4906505 | 0.0604 | 0.327 |
| chr18 | 78077248 | 5869223 | 0.0752 | 1.1228 |
| chr19 | 59128983 | 3981835 | 0.0673 | 0.6633 |
| chr20 | 63025520 | 3515154 | 0.0558 | 0.3324 |
| chr21 | 48129895 | 4152988 | 0.0863 | 0.4466 |
| chr22 | 51304566 | 1833426 | 0.0357 | 0.2406 |
| chrMT | 16571 | 116221 | 7.0135 | 4.7825 |
| chrX | 155270560 | 6933611 | 0.0447 | 0.3145 |
| chrY | 59373566 | 498725 | 0.0084 | 0.1704 |

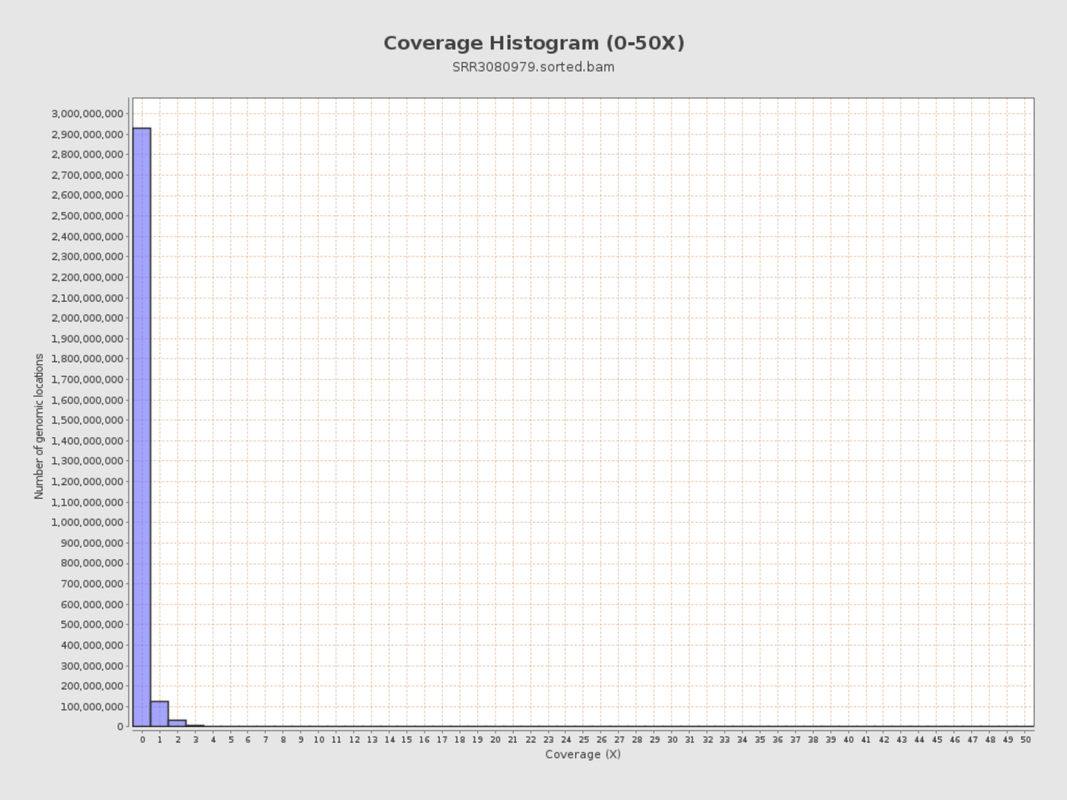
# 3. Results : Coverage across reference



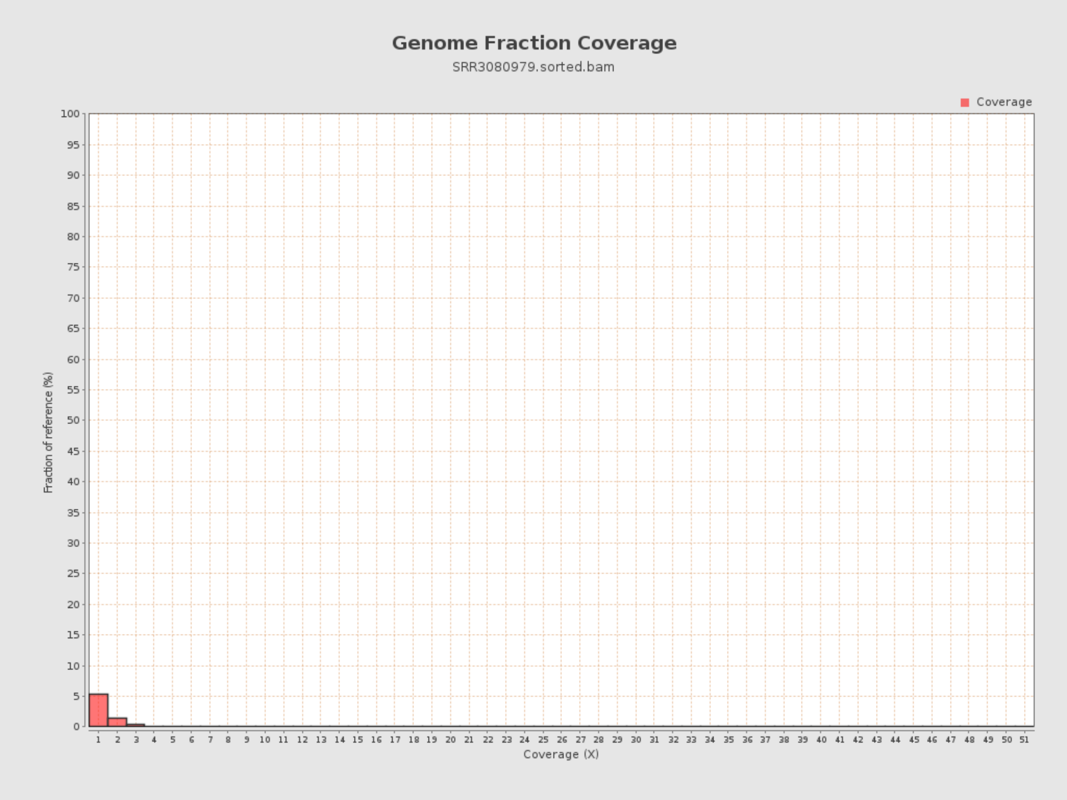
# 4. Results : Coverage Histogram



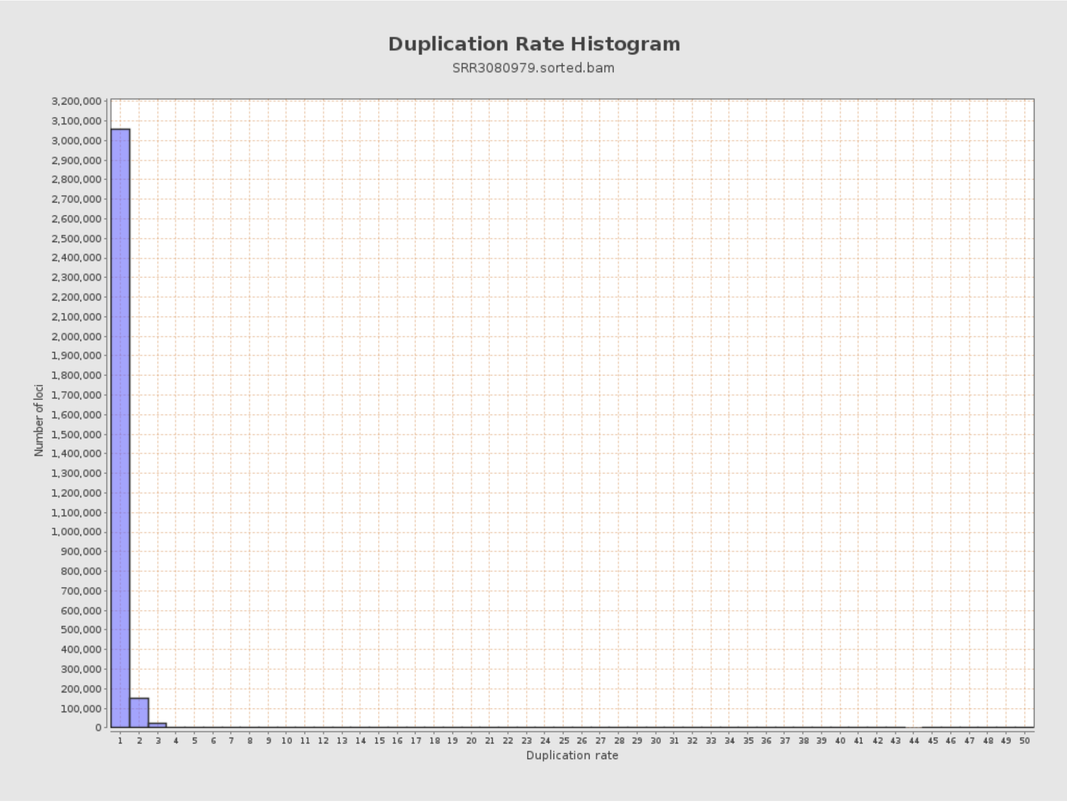
# 5. Results : Coverage Histogram (0-50X)



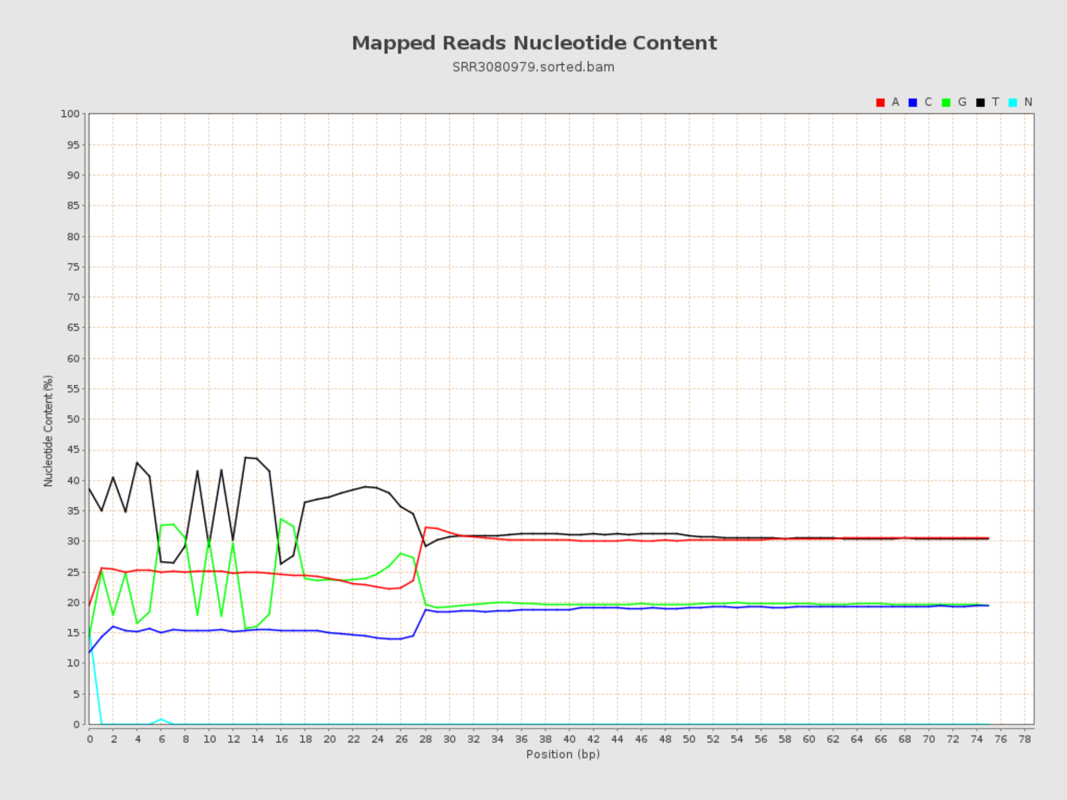
# 6. Results : Genome Fraction Coverage



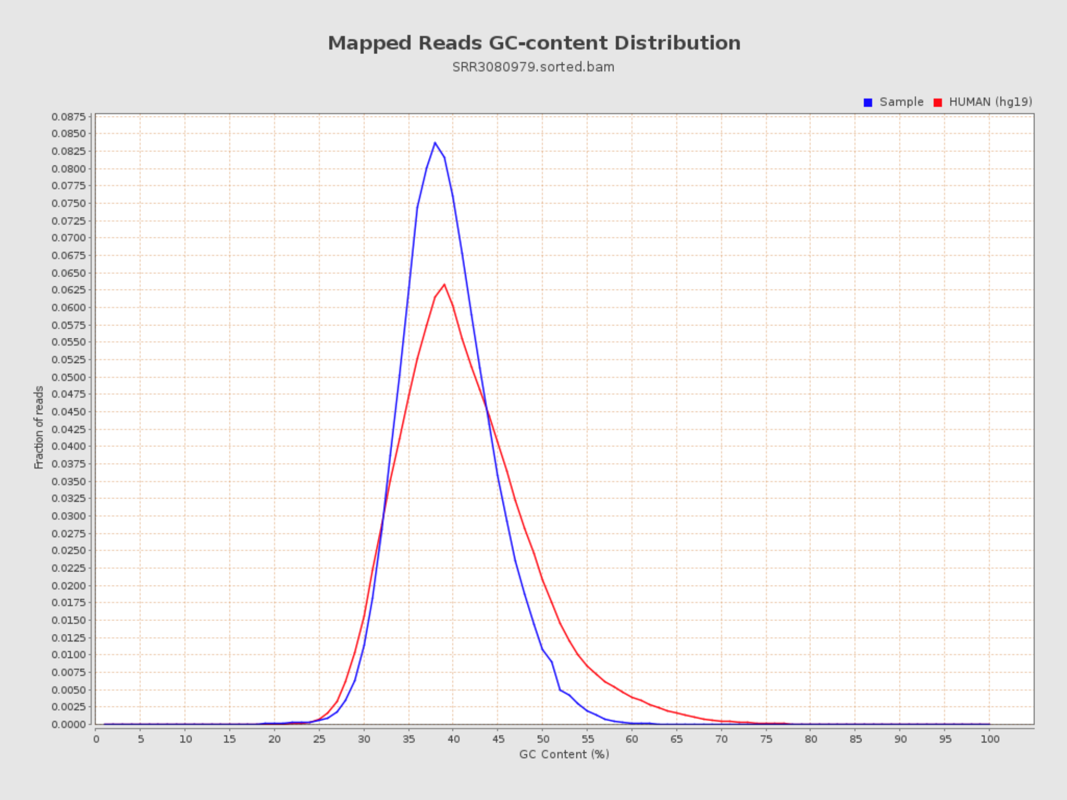
# 7. Results : Duplication Rate Histogram



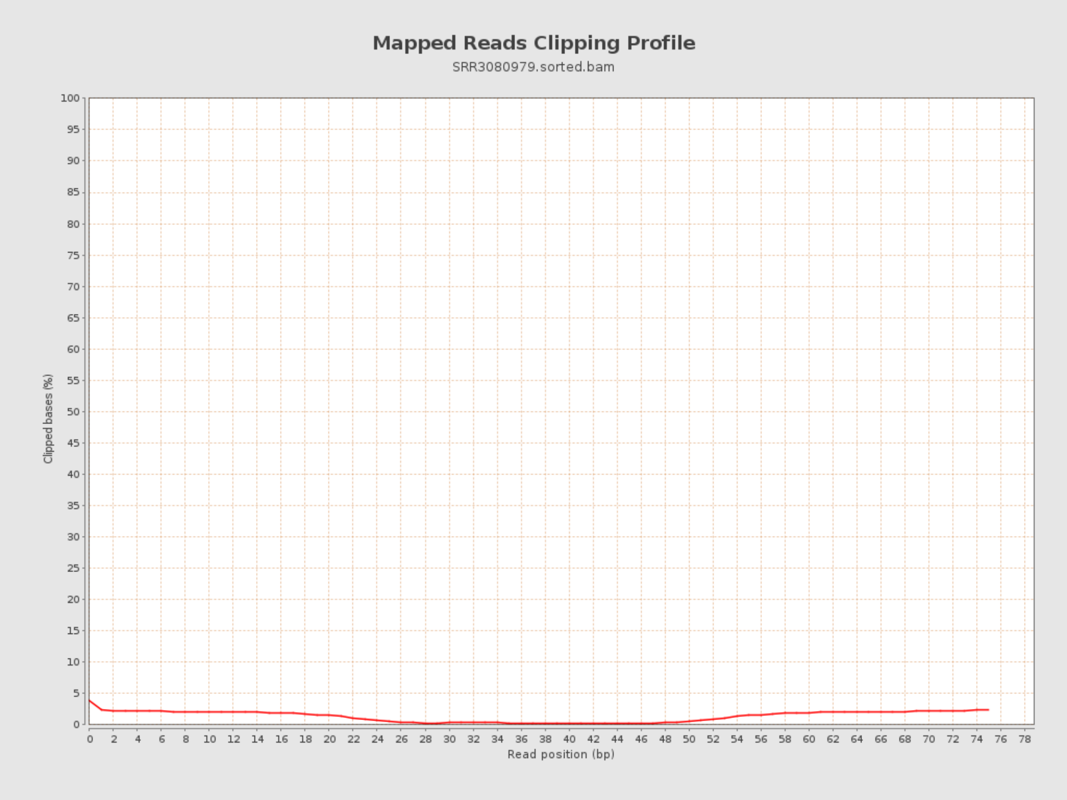
# 8. Results : Mapped Reads Nucleotide Content



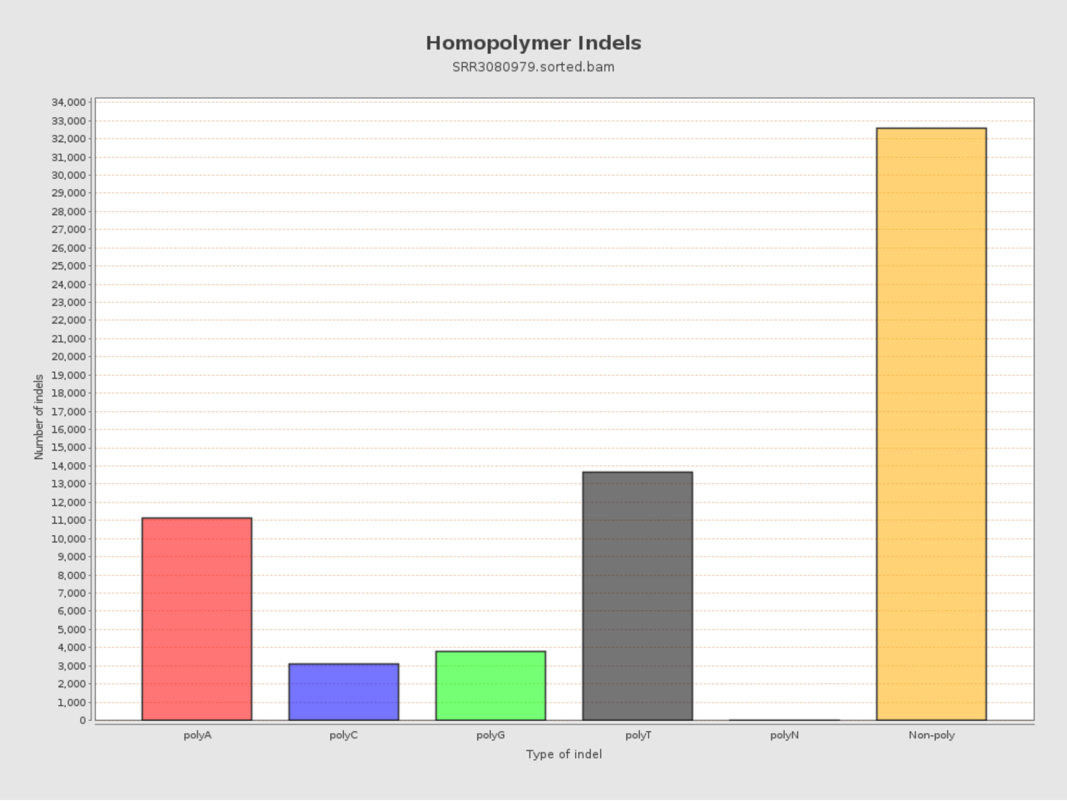
# 9. Results : Mapped Reads GC-content Distribution



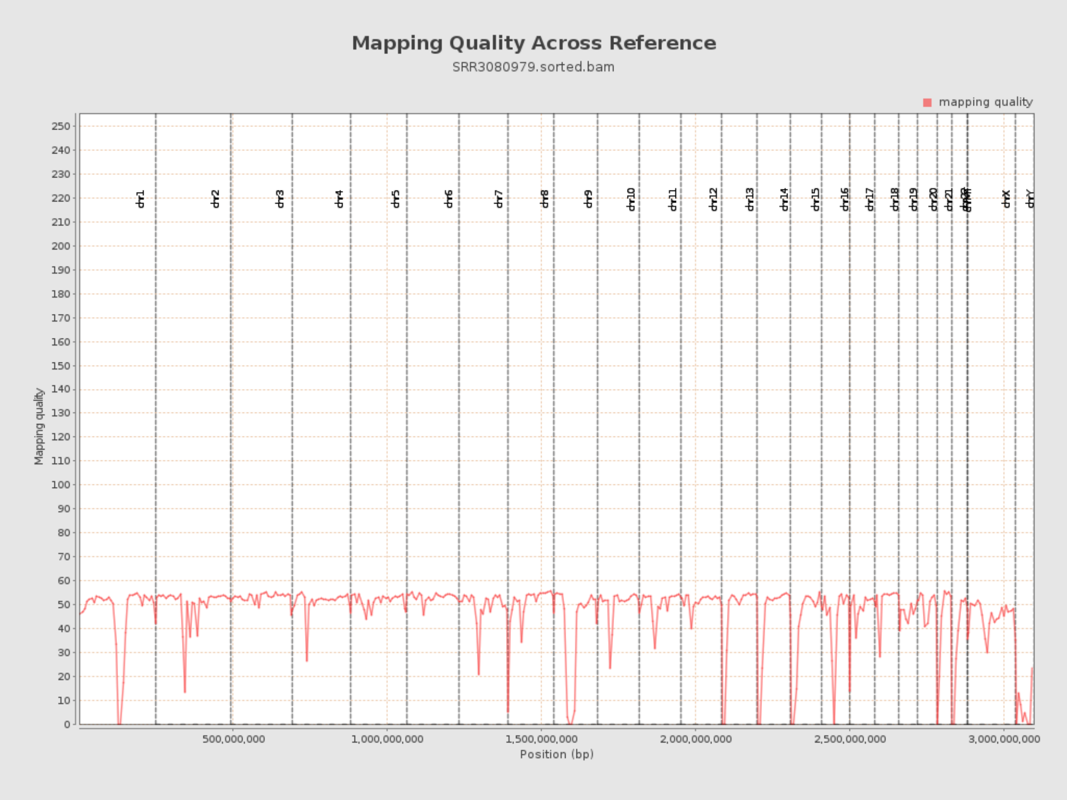
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram