# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 14:08:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080978.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_SRR3080978 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080978.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 14:08:49 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3080978.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,827,360 |
| Mapped reads | 4,086,883 / 84.66% |
| Unmapped reads | 740,477 / 15.34% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 38,847 / 0.8% |
| Read min/max/mean length | 30 / 76 / 76.28 |
| Duplicated reads (estimated) | 302,566 / 6.27% |
| Duplication rate | 5.96% |
| Clipped reads | 1,769,846 / 36.66% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 76,624,888 / 28% |
| Number/percentage of C's | 47,857,636 / 17.49% |
| Number/percentage of T's | 89,608,935 / 32.74% |
| Number/percentage of G's | 59,054,608 / 21.58% |
| Number/percentage of N's | 542,280 / 0.2% |
| GC Percentage | 39.06% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0884 |
| | |

| | |
|---|---|
| Standard Deviation | 0.6386 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.03 |

## 2.5. Mismatches and indels

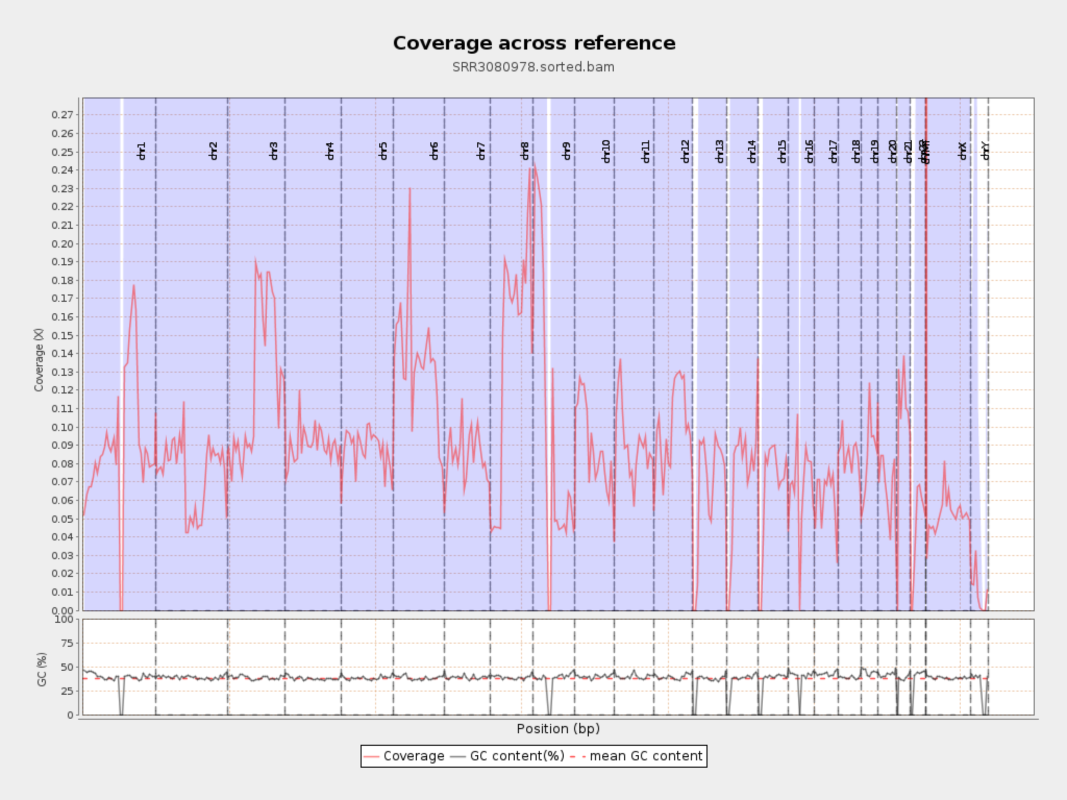
| | |
|---|---|
| General error rate | 1.01% |
| Mismatches | 2,729,663 |
| Insertions | 21,742 |
| Mapped reads with at least one insertion | 0.53% |
| Deletions | 59,617 |
| Mapped reads with at least one deletion | 1.44% |
| Homopolymer indels | 49.57% |

## 2.6. Chromosome stats

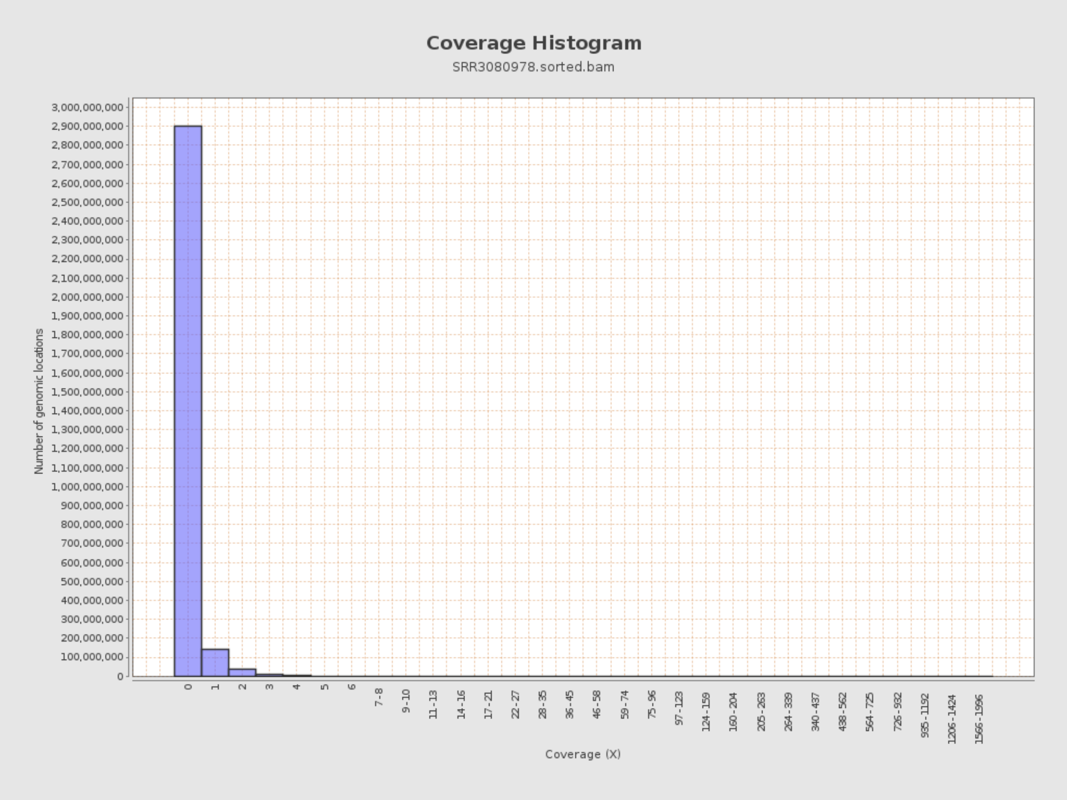
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 22489463 | 0.0902 | 0.926 |
| chr2 | 243199373 | 18183388 | 0.0748 | 0.5596 |
| chr3 | 198022430 | 24438370 | 0.1234 | 0.4698 |
| chr4 | 191154276 | 17292089 | 0.0905 | 0.4182 |
| chr5 | 180915260 | 15906671 | 0.0879 | 0.394 |
| chr6 | 171115067 | 23355061 | 0.1365 | 0.7224 |
| chr7 | 159138663 | 13507696 | 0.0849 | 0.6398 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 21049999 | 0.1438 | 1.3005 |
| chr9 | 141213431 | 14154043 | 0.1002 | 0.7545 |
| chr10 | 135534747 | 12260083 | 0.0905 | 0.5169 |
| chr11 | 135006516 | 12203858 | 0.0904 | 0.5129 |
| chr12 | 133851895 | 13492199 | 0.1008 | 0.4331 |
| chr13 | 115169878 | 7660662 | 0.0665 | 0.3381 |
| chr14 | 107349540 | 7656965 | 0.0713 | 0.4174 |
| chr15 | 102531392 | 6722751 | 0.0656 | 0.335 |
| chr16 | 90354753 | 5976997 | 0.0662 | 0.416 |
| chr17 | 81195210 | 5081243 | 0.0626 | 0.3449 |
| chr18 | 78077248 | 6670363 | 0.0854 | 1.3283 |
| chr19 | 59128983 | 5089061 | 0.0861 | 0.7062 |
| chr20 | 63025520 | 4350614 | 0.069 | 0.3665 |
| chr21 | 48129895 | 5070014 | 0.1053 | 0.5053 |
| chr22 | 51304566 | 2254950 | 0.044 | 0.2684 |
| chrMT | 16571 | 263982 | 15.9304 | 7.8588 |
| chrX | 155270560 | 8062357 | 0.0519 | 0.339 |
| chrY | 59373566 | 594160 | 0.01 | 0.2007 |

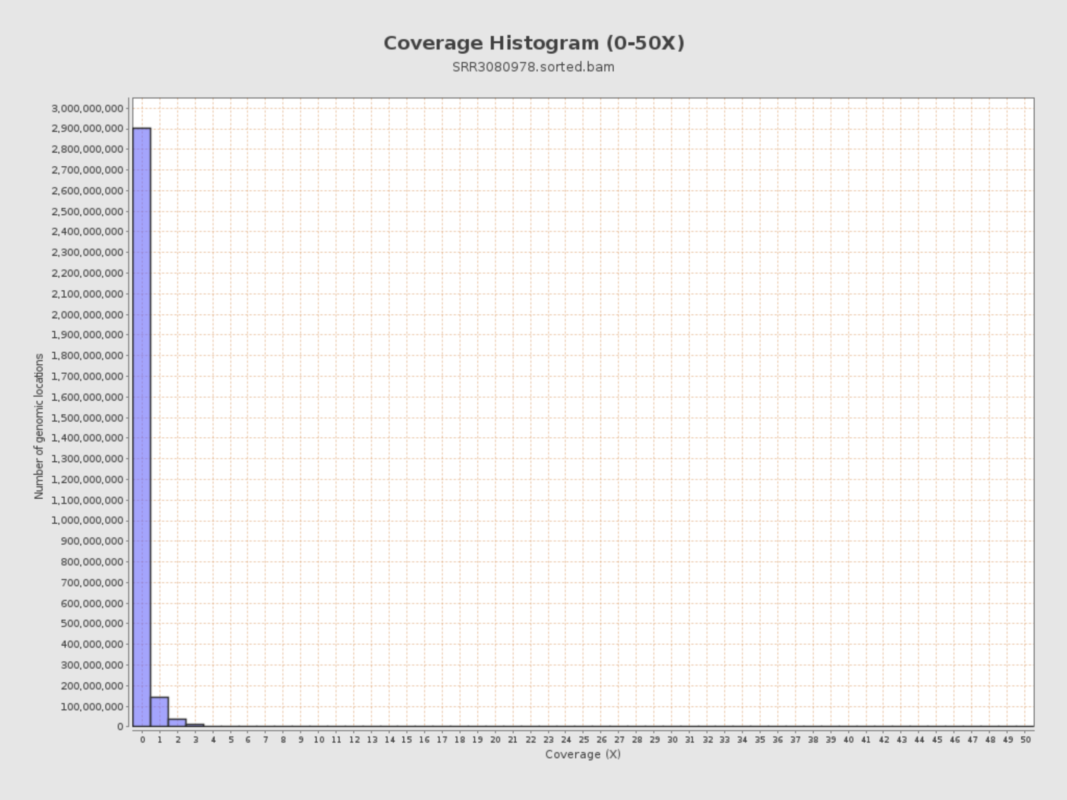
# 3. Results : Coverage across reference



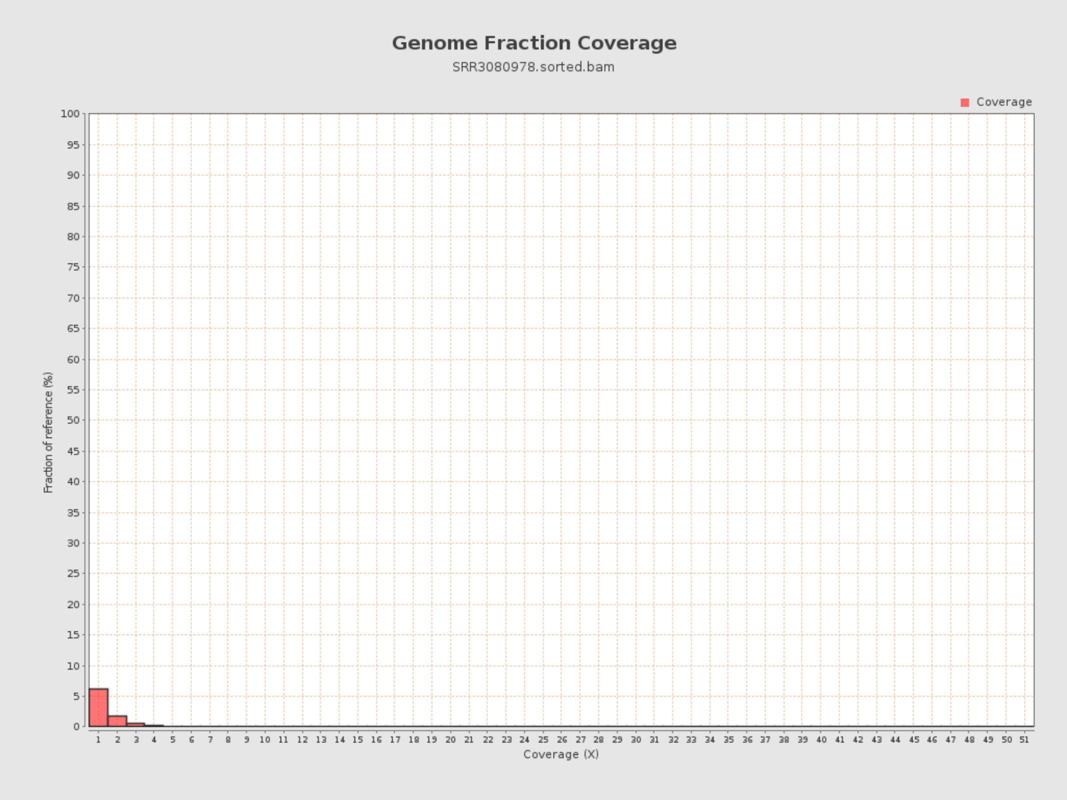
# 4. Results : Coverage Histogram



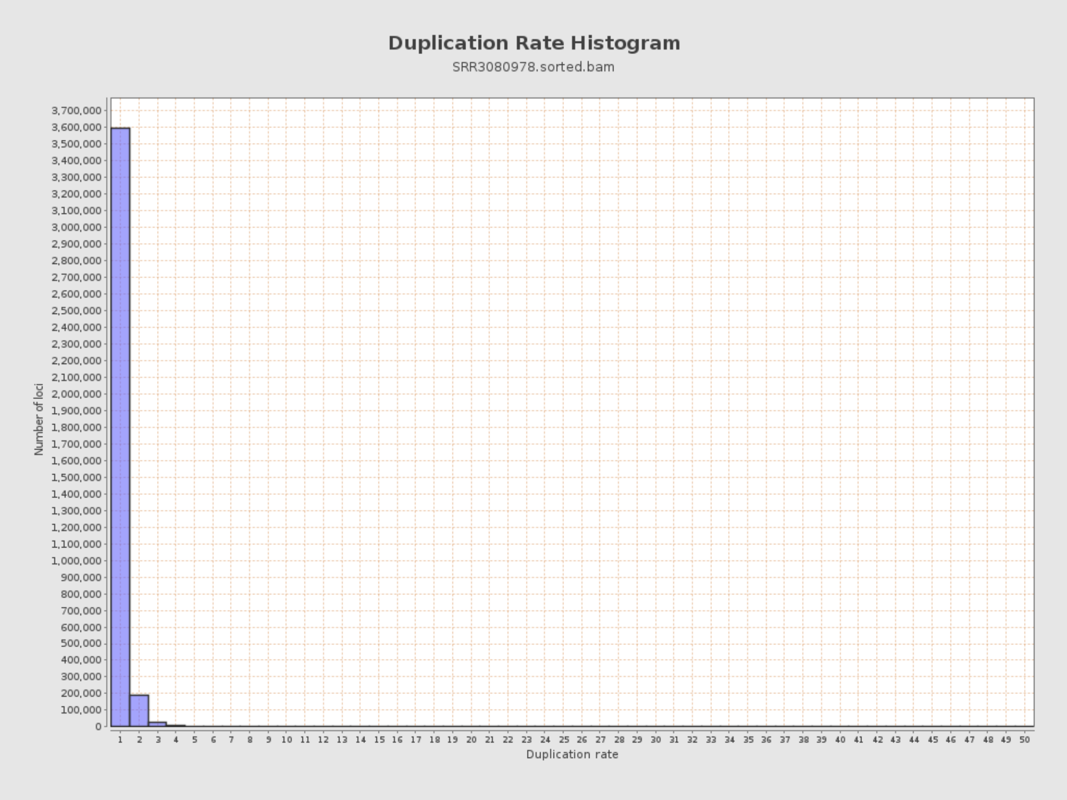
# 5. Results : Coverage Histogram (0-50X)



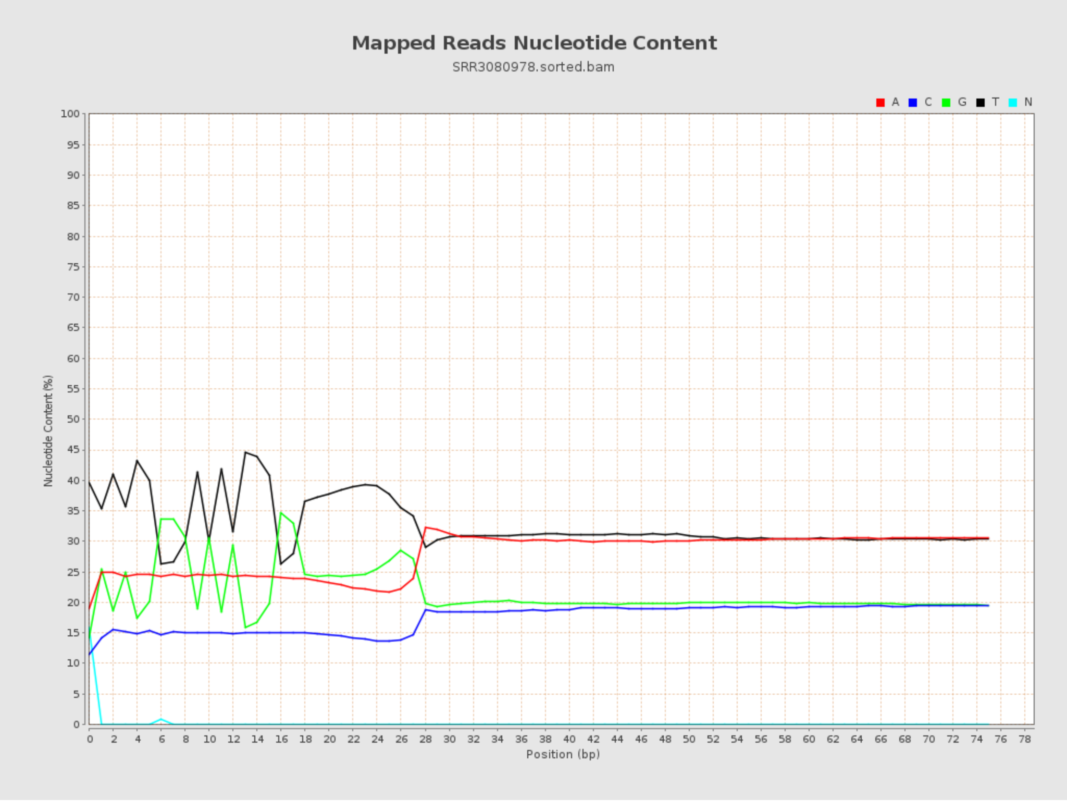
# 6. Results : Genome Fraction Coverage



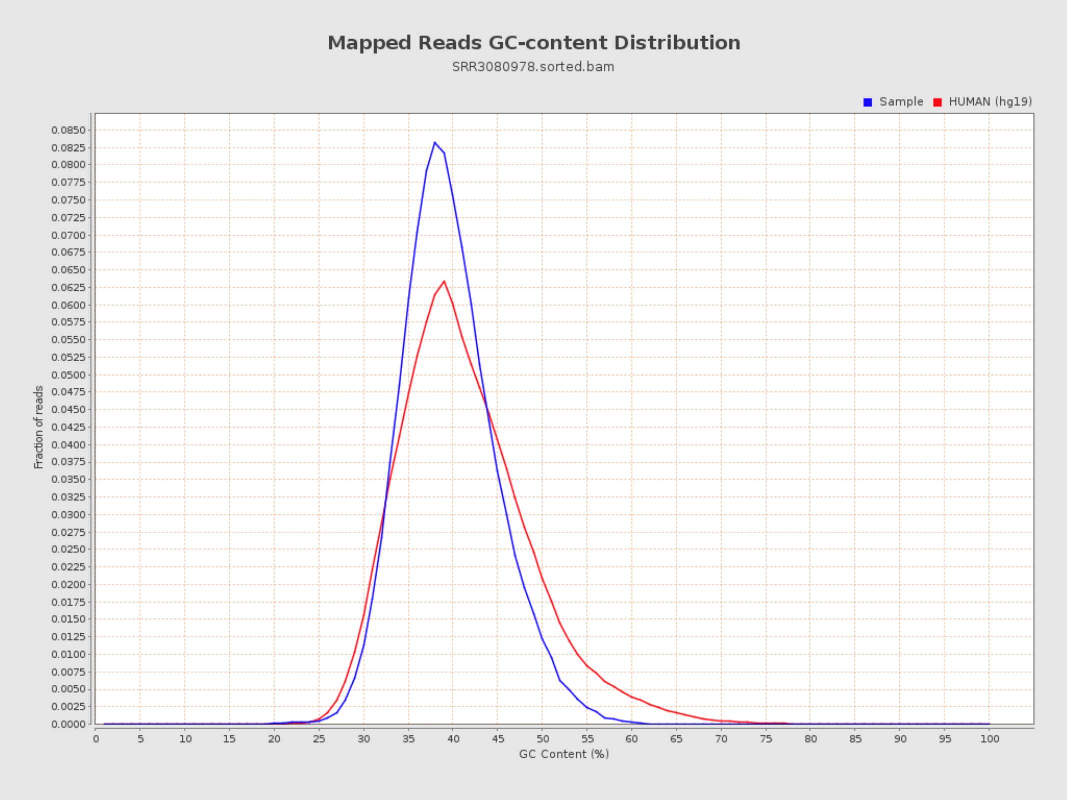
# 7. Results : Duplication Rate Histogram



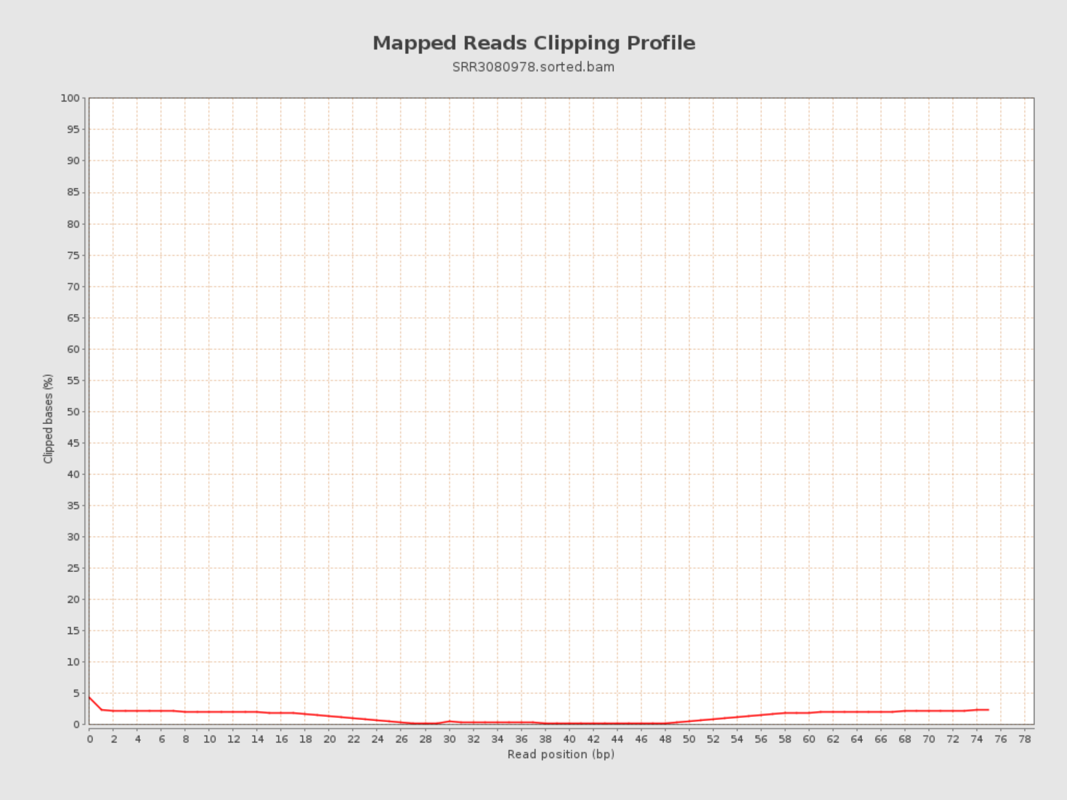
# 8. Results : Mapped Reads Nucleotide Content



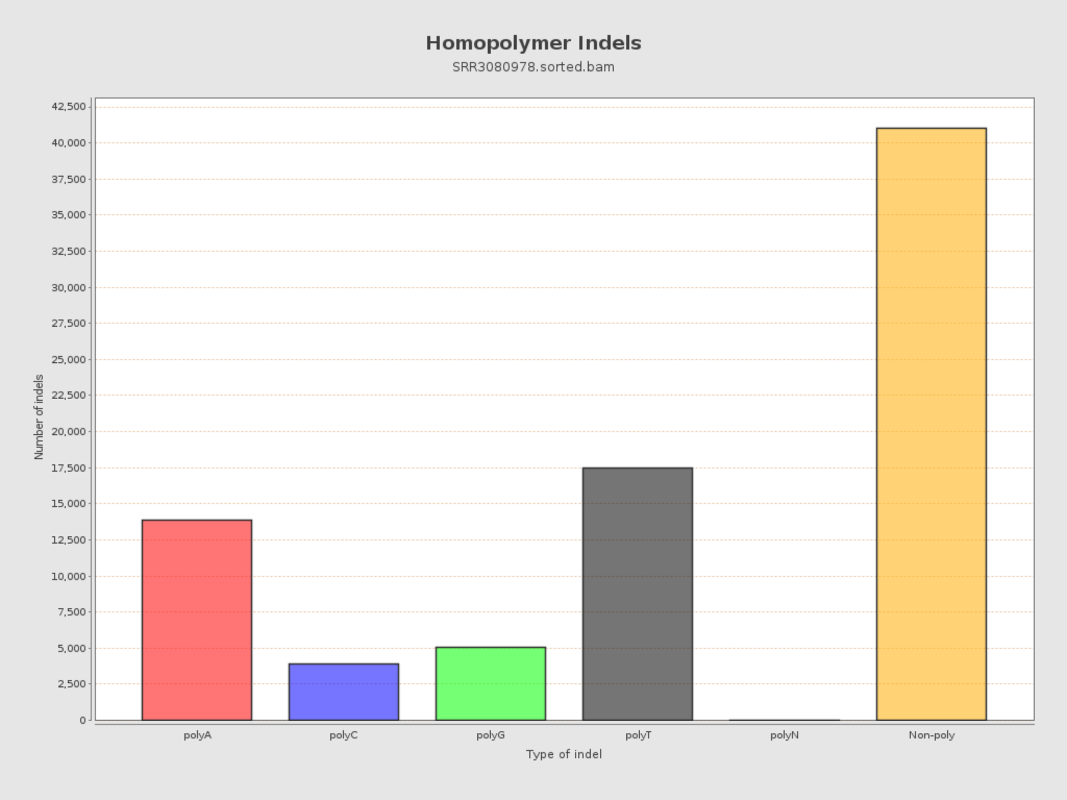
# 9. Results : Mapped Reads GC-content Distribution



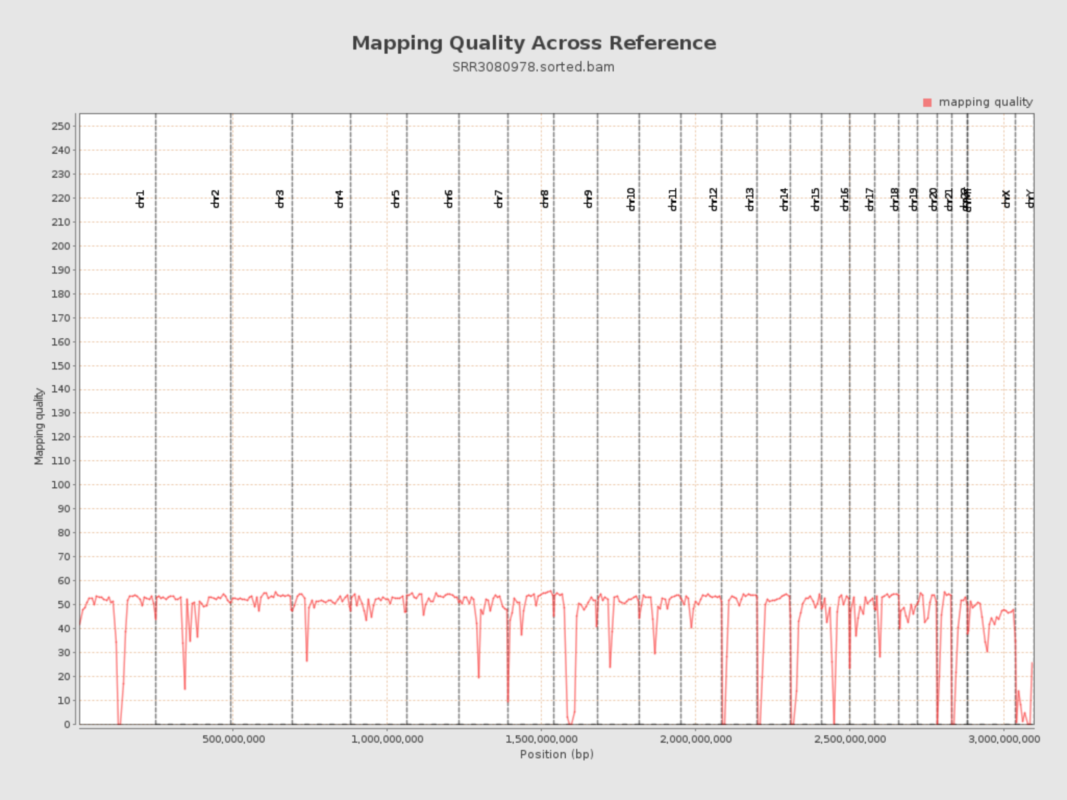
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram