# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 12:14:20*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080956.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_SRR3080956 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080956.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 12:14:18 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3080956.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,750,328 |
| Mapped reads | 4,361,206 / 91.81% |
| Unmapped reads | 389,122 / 8.19% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 66,609 / 1.4% |
| Read min/max/mean length | 30 / 76 / 76.5 |
| Duplicated reads (estimated) | 231,651 / 4.88% |
| Duplication rate | 4.14% |
| Clipped reads | 1,503,427 / 31.65% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 88,985,003 / 29.38% |
| Number/percentage of C's | 54,451,796 / 17.98% |
| Number/percentage of T's | 95,937,313 / 31.67% |
| Number/percentage of G's | 62,066,200 / 20.49% |
| Number/percentage of N's | 1,466,494 / 0.48% |
| GC Percentage | 38.47% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0979 |
| | |

| | |
|---|---|
| Standard Deviation | 0.6725 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.43 |

## 2.5. Mismatches and indels

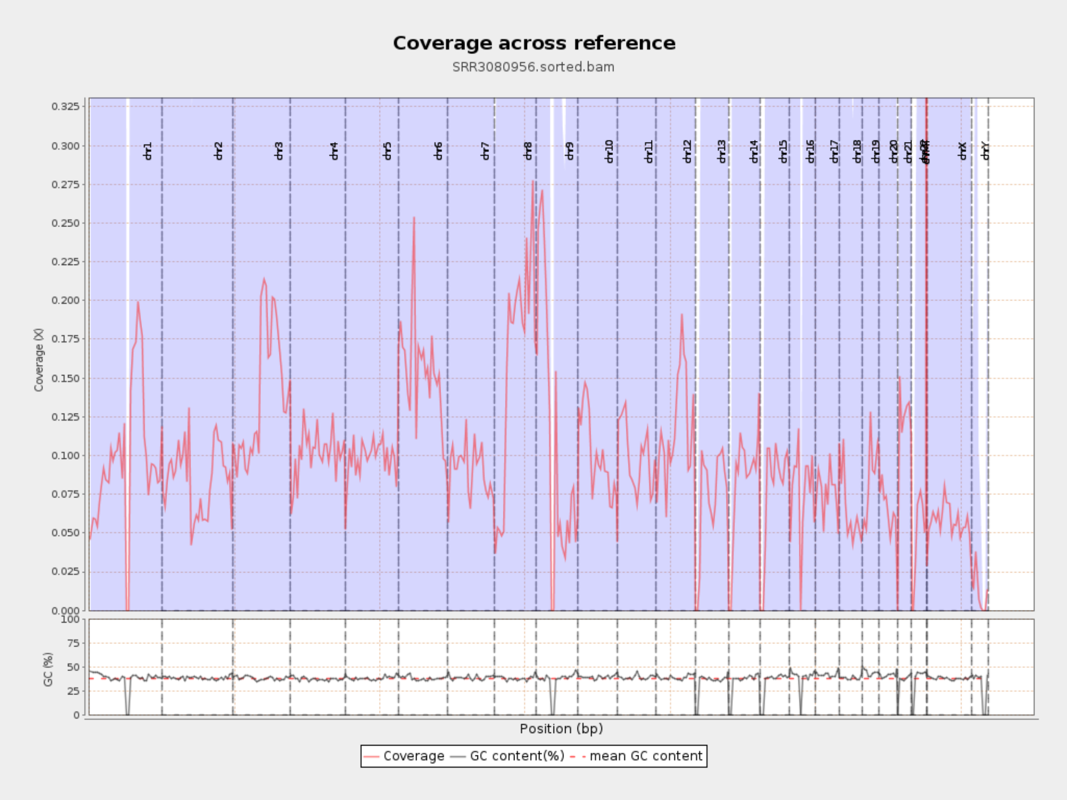
| | |
|---|---|
| General error rate | 1.18% |
| Mismatches | 3,521,219 |
| Insertions | 23,907 |
| Mapped reads with at least one insertion | 0.54% |
| Deletions | 68,534 |
| Mapped reads with at least one deletion | 1.55% |
| Homopolymer indels | 49.46% |

## 2.6. Chromosome stats

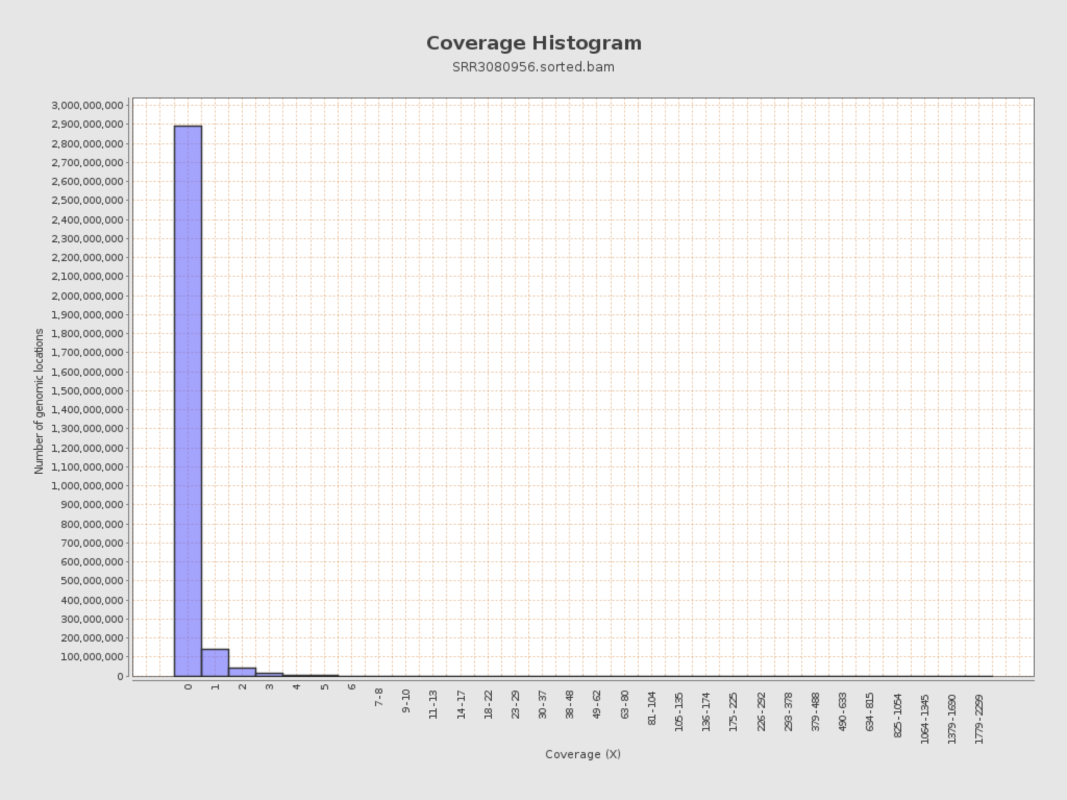
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 24489994 | 0.0983 | 0.8494 |
| chr2 | 243199373 | 20807544 | 0.0856 | 0.6123 |
| chr3 | 198022430 | 27577616 | 0.1393 | 0.5168 |
| chr4 | 191154276 | 19433066 | 0.1017 | 0.4717 |
| chr5 | 180915260 | 17847531 | 0.0987 | 0.4325 |
| chr6 | 171115067 | 26387848 | 0.1542 | 0.7435 |
| chr7 | 159138663 | 14528178 | 0.0913 | 0.6195 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 23662620 | 0.1617 | 1.5426 |
| chr9 | 141213431 | 15567822 | 0.1102 | 0.7865 |
| chr10 | 135534747 | 13802727 | 0.1018 | 0.5807 |
| chr11 | 135006516 | 13346768 | 0.0989 | 0.5085 |
| chr12 | 133851895 | 15833272 | 0.1183 | 0.497 |
| chr13 | 115169878 | 8145216 | 0.0707 | 0.3636 |
| chr14 | 107349540 | 8800587 | 0.082 | 0.5226 |
| chr15 | 102531392 | 7896765 | 0.077 | 0.3789 |
| chr16 | 90354753 | 6914605 | 0.0765 | 0.4783 |
| chr17 | 81195210 | 6149843 | 0.0757 | 0.3875 |
| chr18 | 78077248 | 5052315 | 0.0647 | 1.2434 |
| chr19 | 59128983 | 5043008 | 0.0853 | 0.6789 |
| chr20 | 63025520 | 4128109 | 0.0655 | 0.3752 |
| chr21 | 48129895 | 5649315 | 0.1174 | 0.5647 |
| chr22 | 51304566 | 2382289 | 0.0464 | 0.287 |
| chrMT | 16571 | 20264 | 1.2229 | 1.5918 |
| chrX | 155270560 | 8888673 | 0.0572 | 0.3605 |
| chrY | 59373566 | 664295 | 0.0112 | 0.2278 |

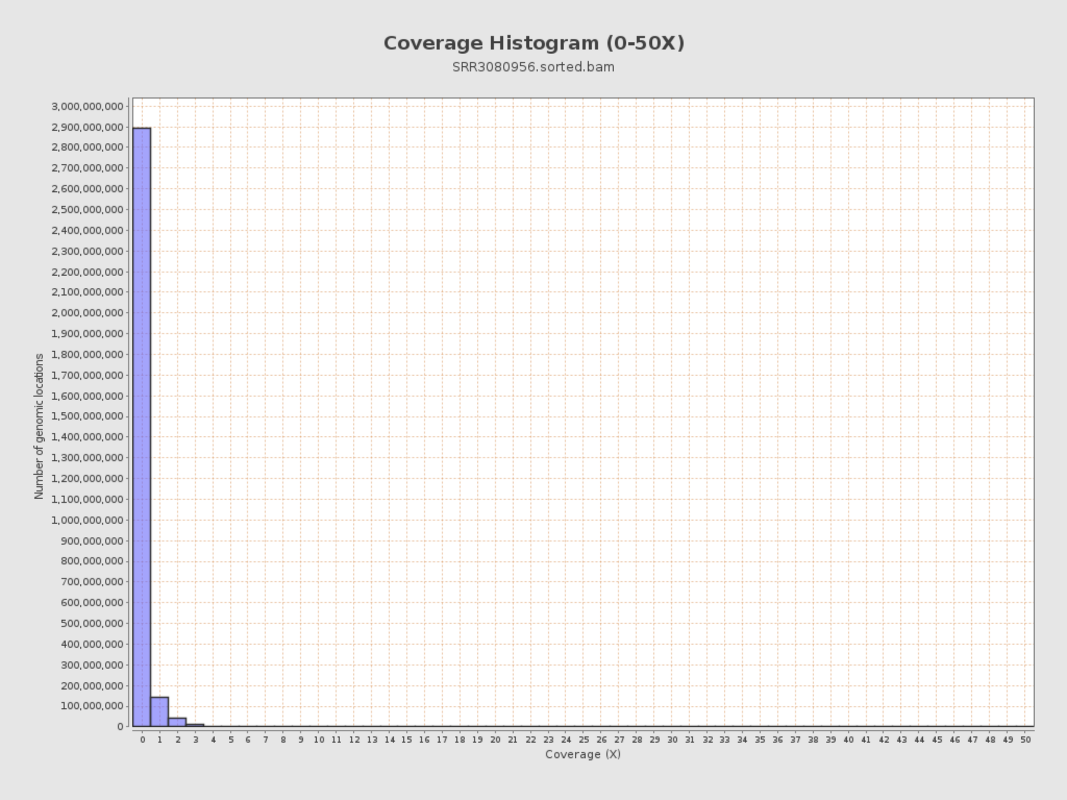
# 3. Results : Coverage across reference



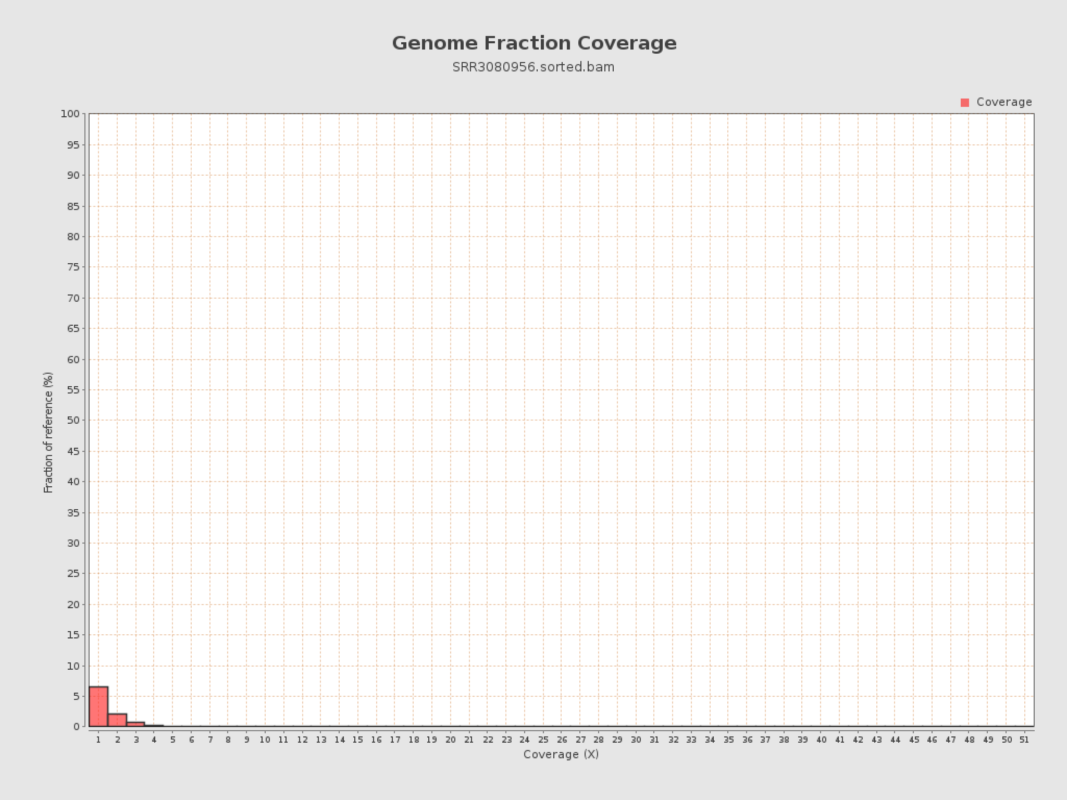
# 4. Results : Coverage Histogram



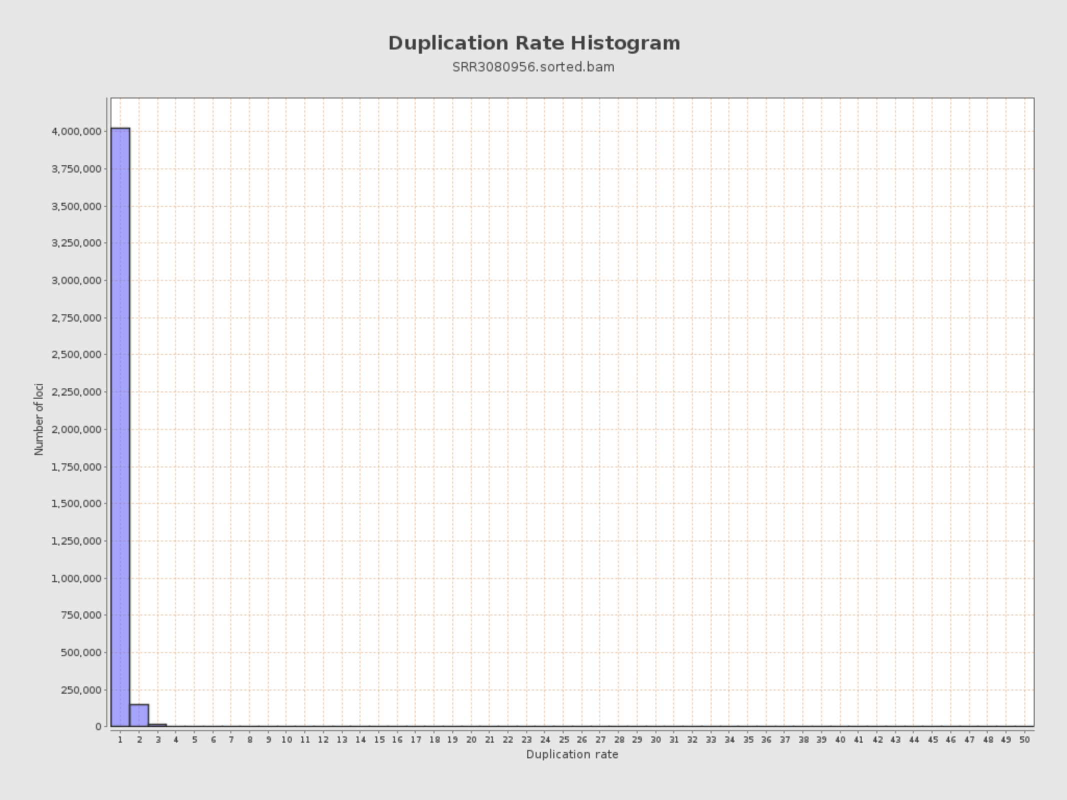
# 5. Results : Coverage Histogram (0-50X)



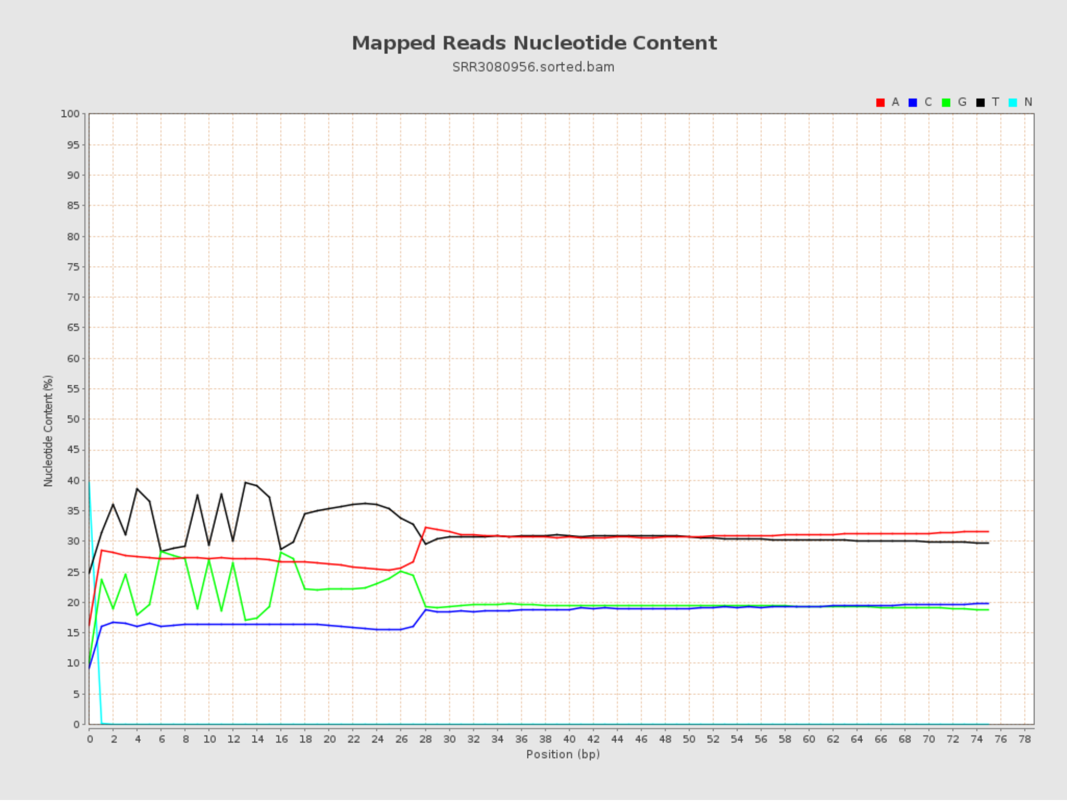
# 6. Results : Genome Fraction Coverage



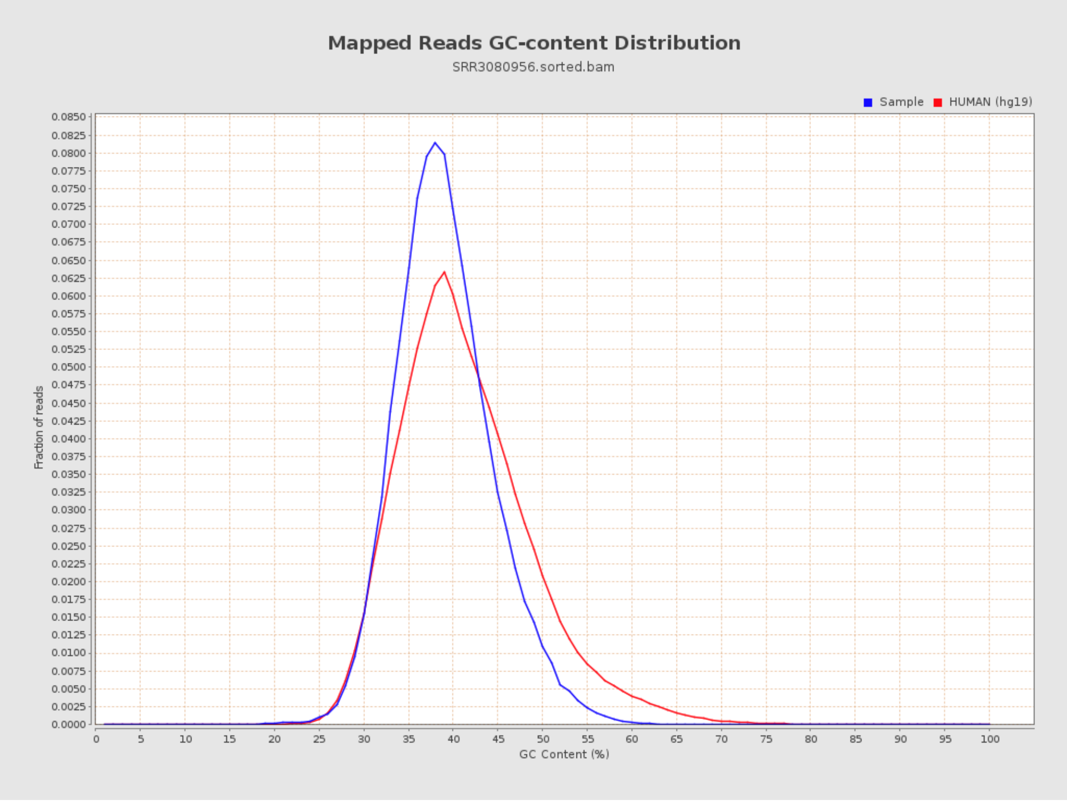
# 7. Results : Duplication Rate Histogram



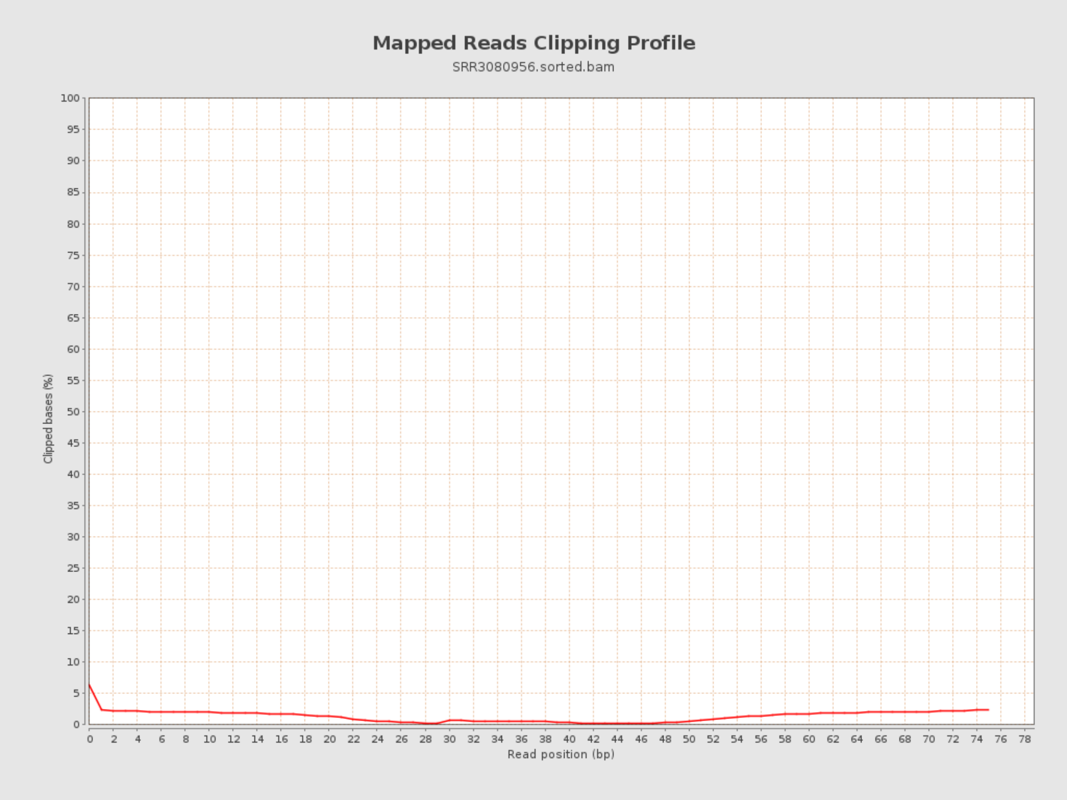
# 8. Results : Mapped Reads Nucleotide Content



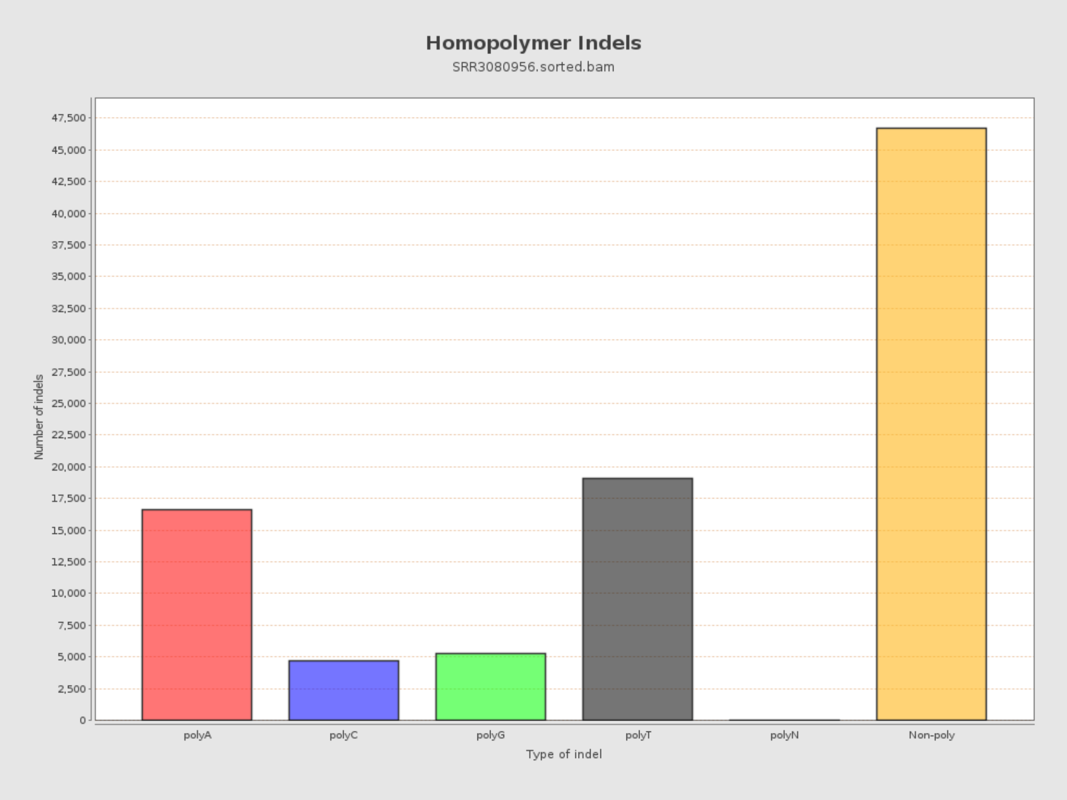
# 9. Results : Mapped Reads GC-content Distribution



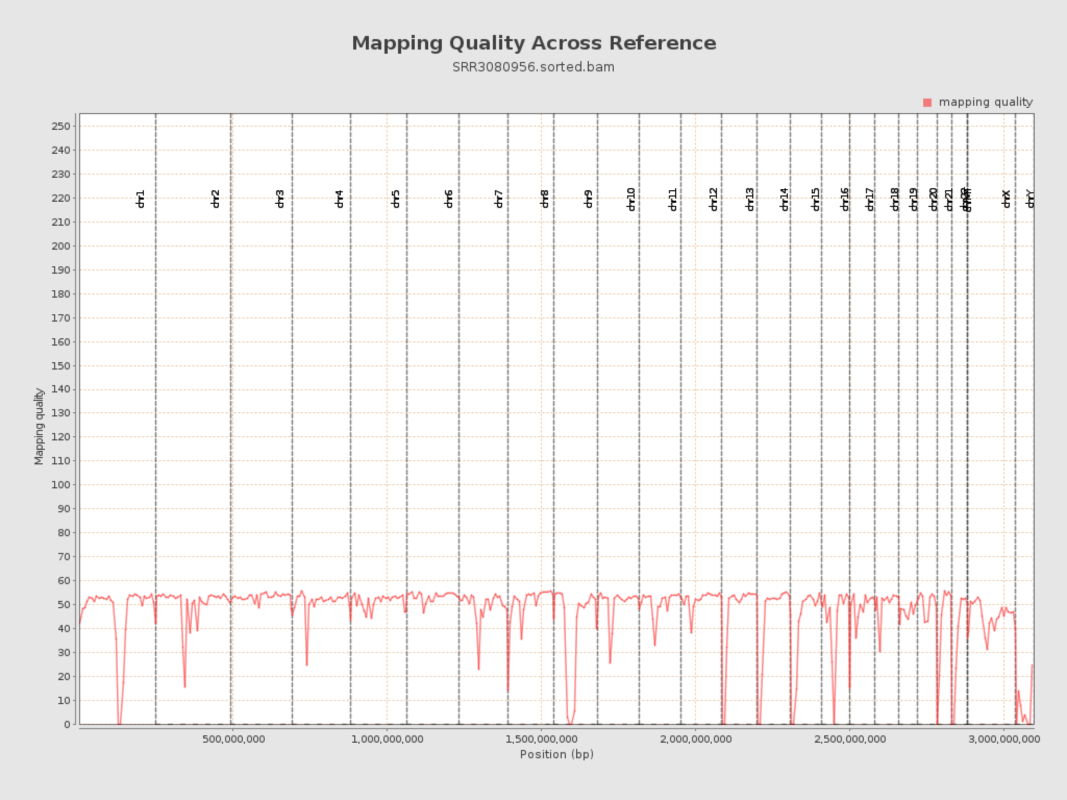
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram