# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 00:40:20*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085090.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_SRR3085090 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085090.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Aug 26 00:40:19 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3085090.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,015,716 |
| Mapped reads | 2,616,995 / 86.78% |
| Unmapped reads | 398,721 / 13.22% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 21,610 / 0.72% |
| Read min/max/mean length | 30 / 76 / 76.25 |
| Duplicated reads (estimated) | 114,453 / 3.8% |
| Duplication rate | 3.51% |
| Clipped reads | 1,895,565 / 62.86% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 47,094,839 / 30.04% |
| Number/percentage of C's | 30,865,620 / 19.69% |
| Number/percentage of T's | 46,104,760 / 29.41% |
| Number/percentage of G's | 32,701,018 / 20.86% |
| Number/percentage of N's | 3,397 / 0% |
| GC Percentage | 40.55% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0507 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4154 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.6 |

## 2.5. Mismatches and indels

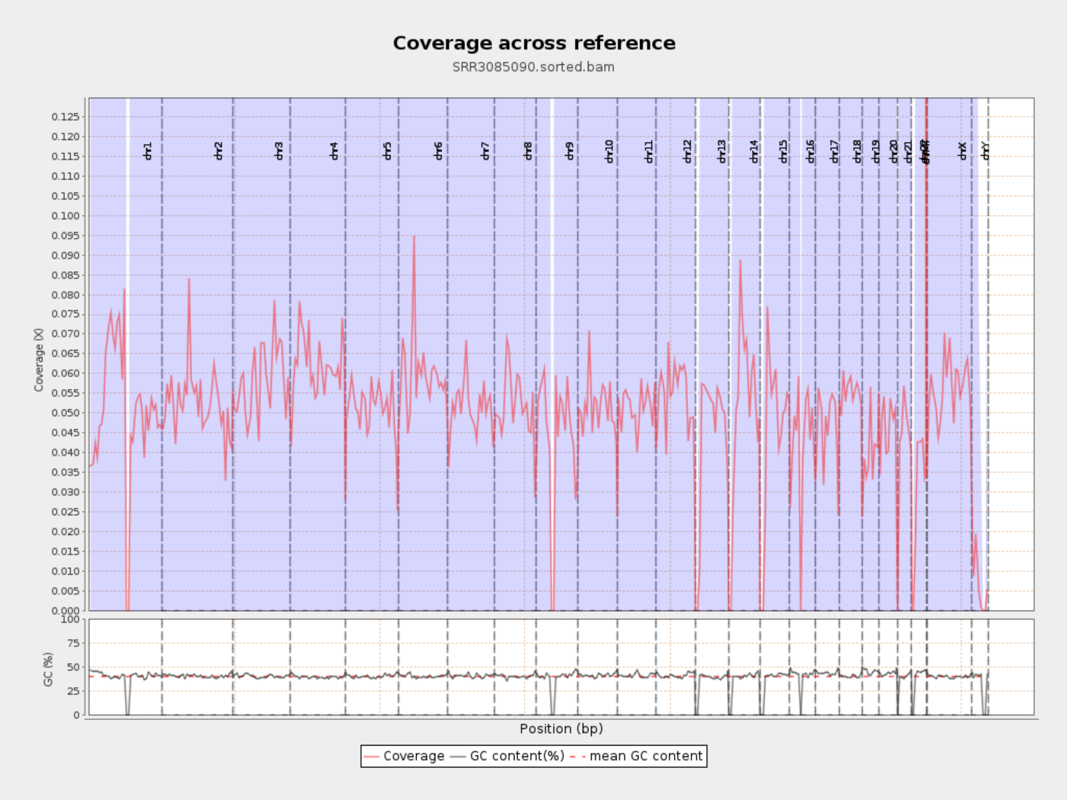
| | |
|---|---|
| General error rate | 0.84% |
| Mismatches | 1,297,677 |
| Insertions | 11,384 |
| Mapped reads with at least one insertion | 0.43% |
| Deletions | 31,042 |
| Mapped reads with at least one deletion | 1.17% |
| Homopolymer indels | 46.07% |

## 2.6. Chromosome stats

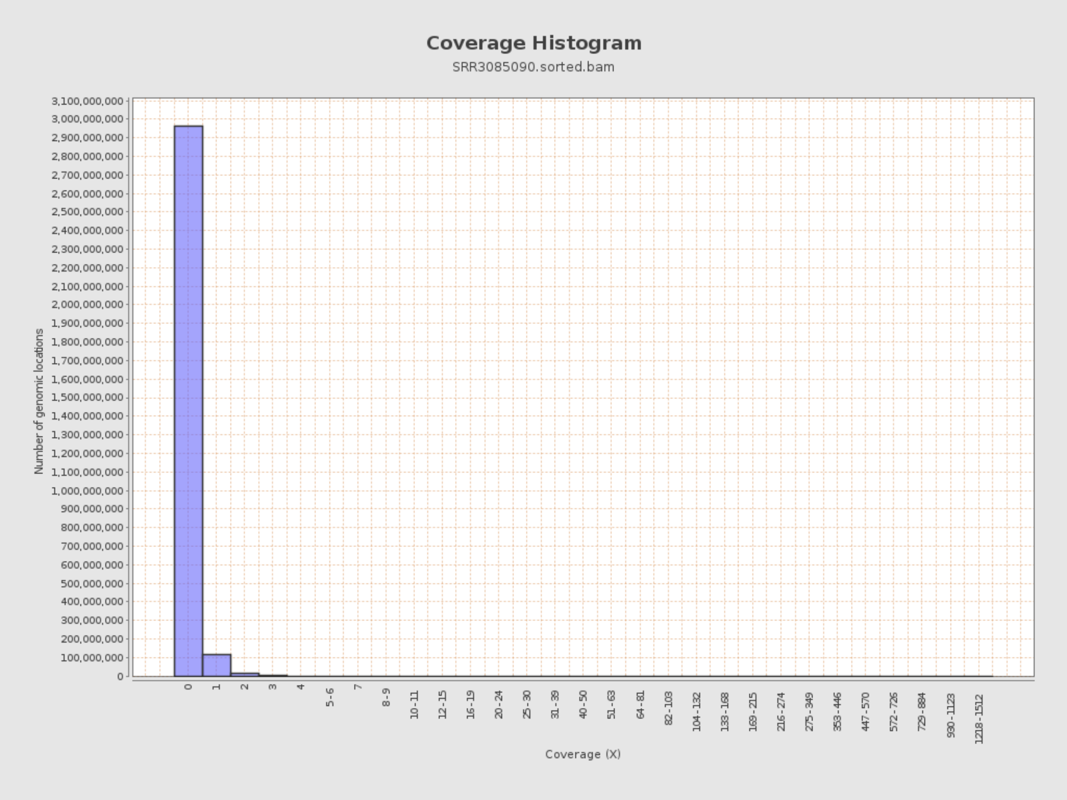
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 12626391 | 0.0507 | 0.6857 |
| chr2 | 243199373 | 12849291 | 0.0528 | 0.3729 |
| chr3 | 198022430 | 11510268 | 0.0581 | 0.2764 |
| chr4 | 191154276 | 11887791 | 0.0622 | 0.2928 |
| chr5 | 180915260 | 9290729 | 0.0514 | 0.2615 |
| chr6 | 171115067 | 10235264 | 0.0598 | 0.4062 |
| chr7 | 159138663 | 8206303 | 0.0516 | 0.3583 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7580860 | 0.0518 | 0.8839 |
| chr9 | 141213431 | 6255179 | 0.0443 | 0.3459 |
| chr10 | 135534747 | 7007332 | 0.0517 | 0.3633 |
| chr11 | 135006516 | 6900093 | 0.0511 | 0.3418 |
| chr12 | 133851895 | 7333183 | 0.0548 | 0.2757 |
| chr13 | 115169878 | 4993124 | 0.0434 | 0.2381 |
| chr14 | 107349540 | 5442658 | 0.0507 | 0.2743 |
| chr15 | 102531392 | 4643954 | 0.0453 | 0.2442 |
| chr16 | 90354753 | 3825381 | 0.0423 | 0.2535 |
| chr17 | 81195210 | 3736165 | 0.046 | 0.2746 |
| chr18 | 78077248 | 4325898 | 0.0554 | 0.6827 |
| chr19 | 59128983 | 2362295 | 0.04 | 0.4647 |
| chr20 | 63025520 | 2877906 | 0.0457 | 0.2542 |
| chr21 | 48129895 | 2041350 | 0.0424 | 0.2484 |
| chr22 | 51304566 | 1453155 | 0.0283 | 0.19 |
| chrMT | 16571 | 355808 | 21.4717 | 11.7536 |
| chrX | 155270560 | 8698007 | 0.056 | 0.2996 |
| chrY | 59373566 | 380080 | 0.0064 | 0.1169 |

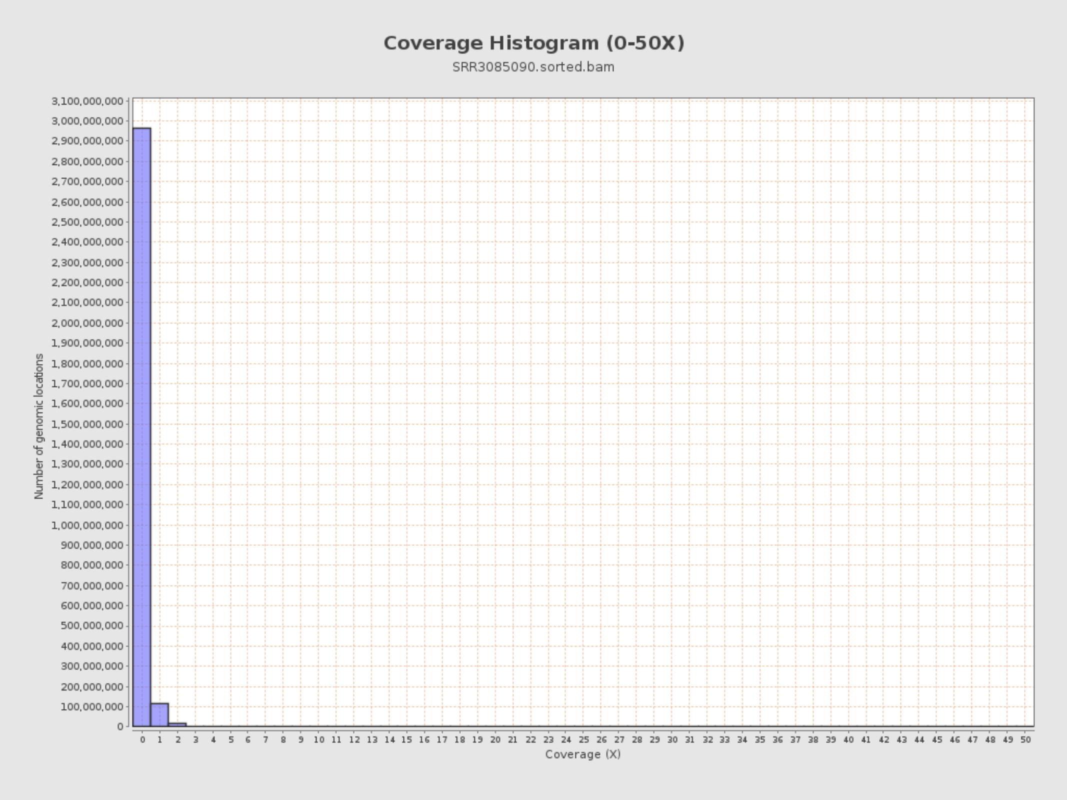
# 3. Results : Coverage across reference



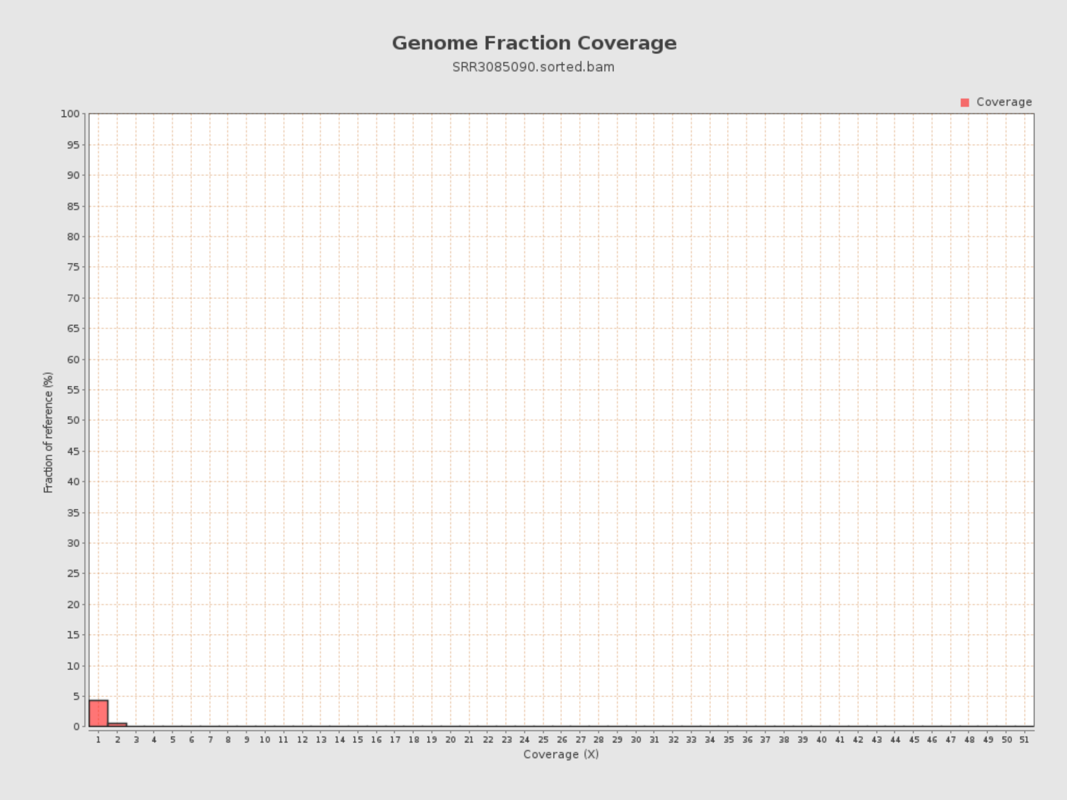
# 4. Results : Coverage Histogram



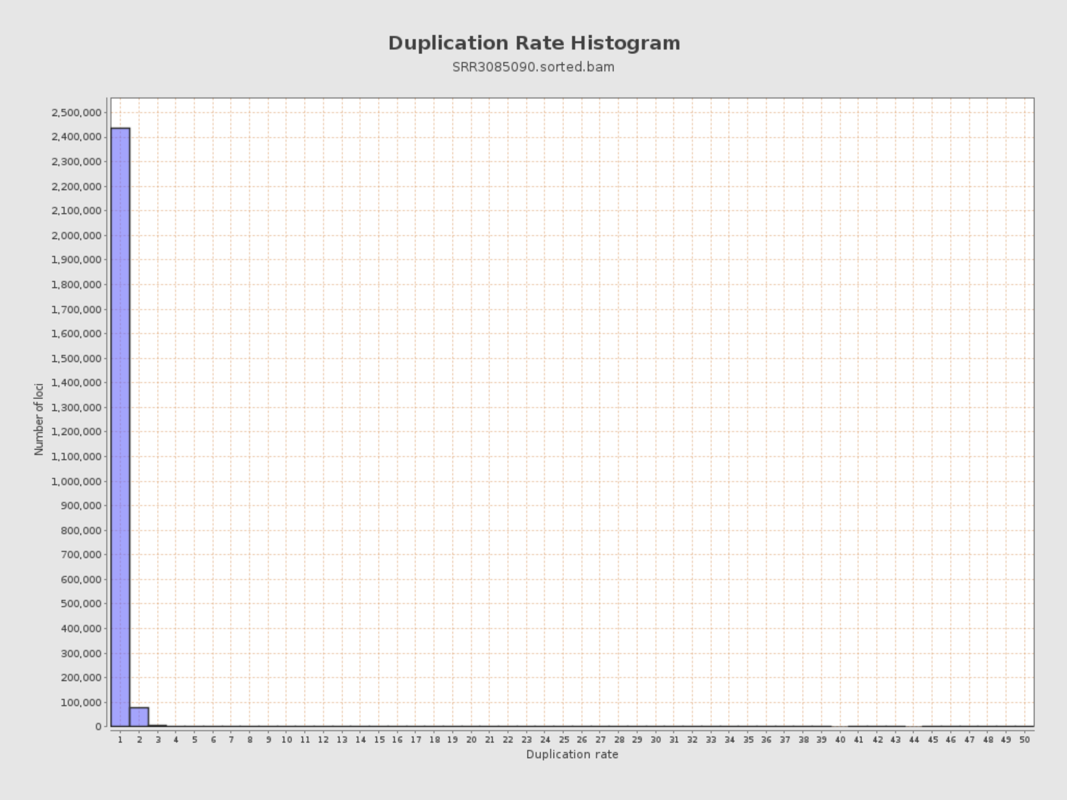
# 5. Results : Coverage Histogram (0-50X)



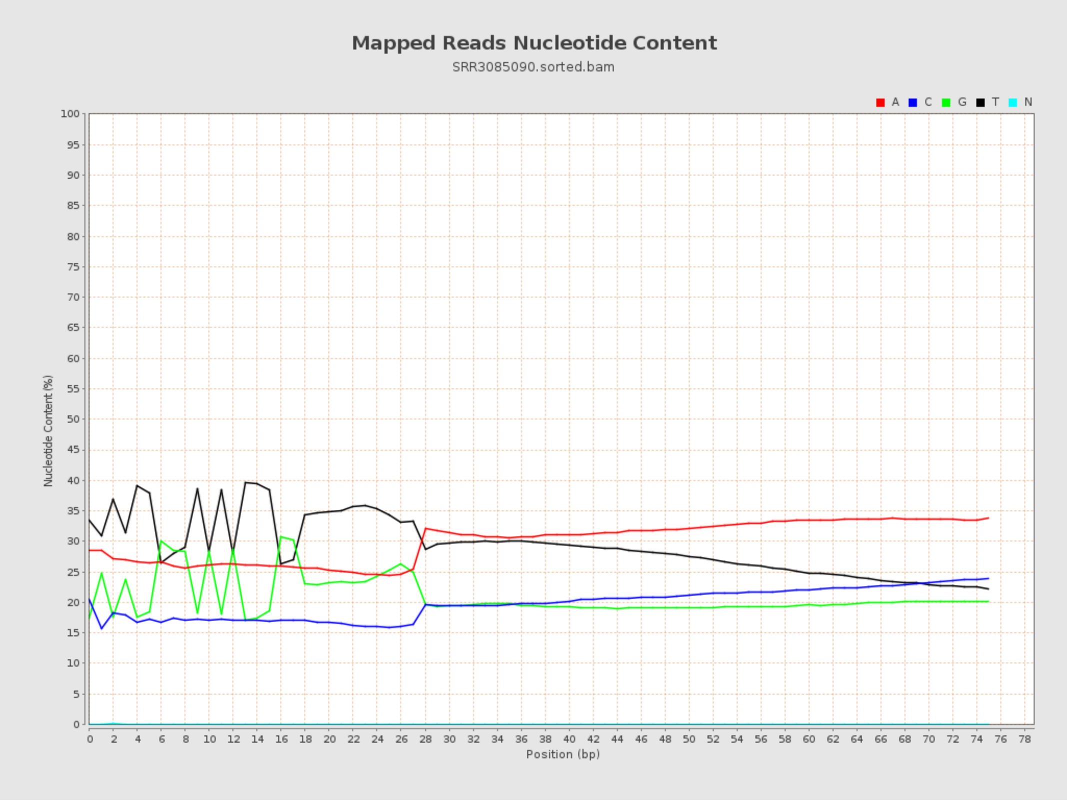
# 6. Results : Genome Fraction Coverage



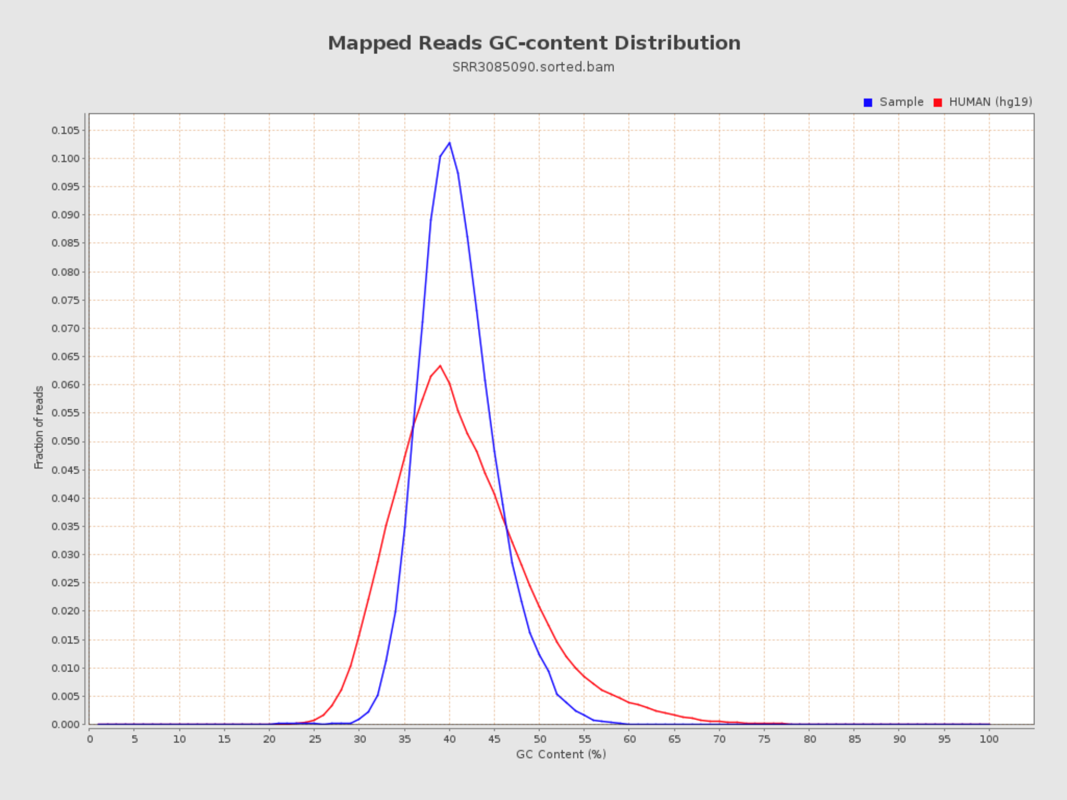
# 7. Results : Duplication Rate Histogram



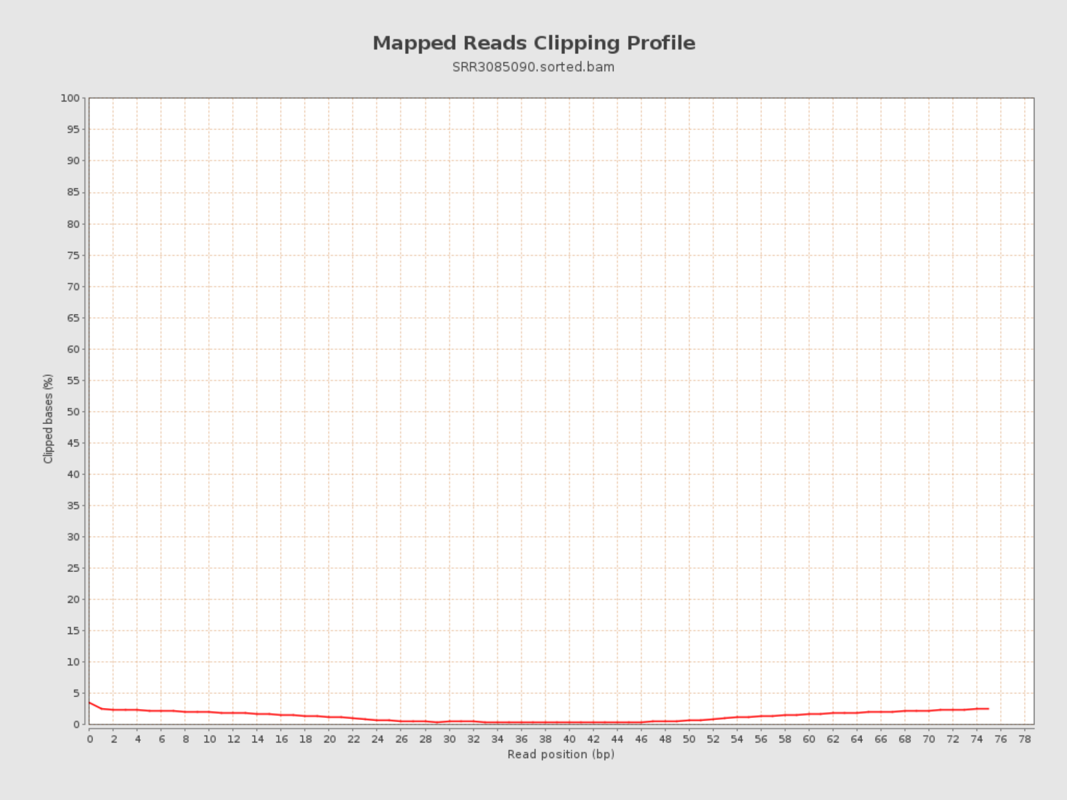
# 8. Results : Mapped Reads Nucleotide Content



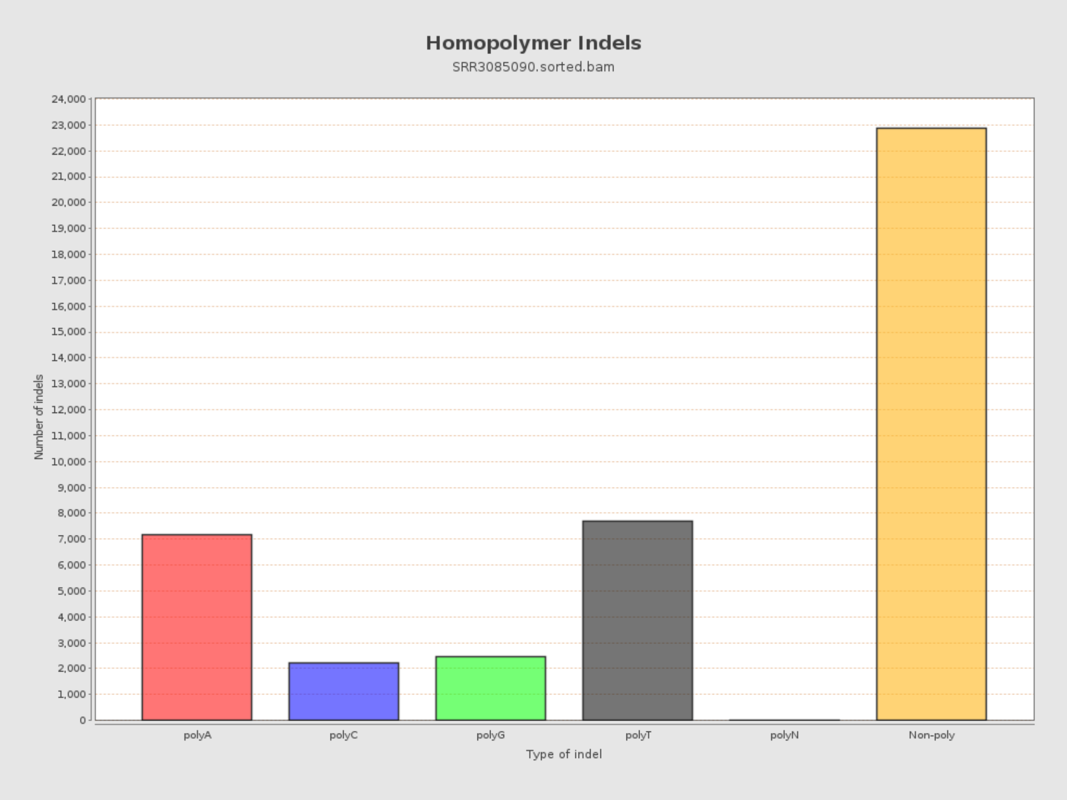
# 9. Results : Mapped Reads GC-content Distribution



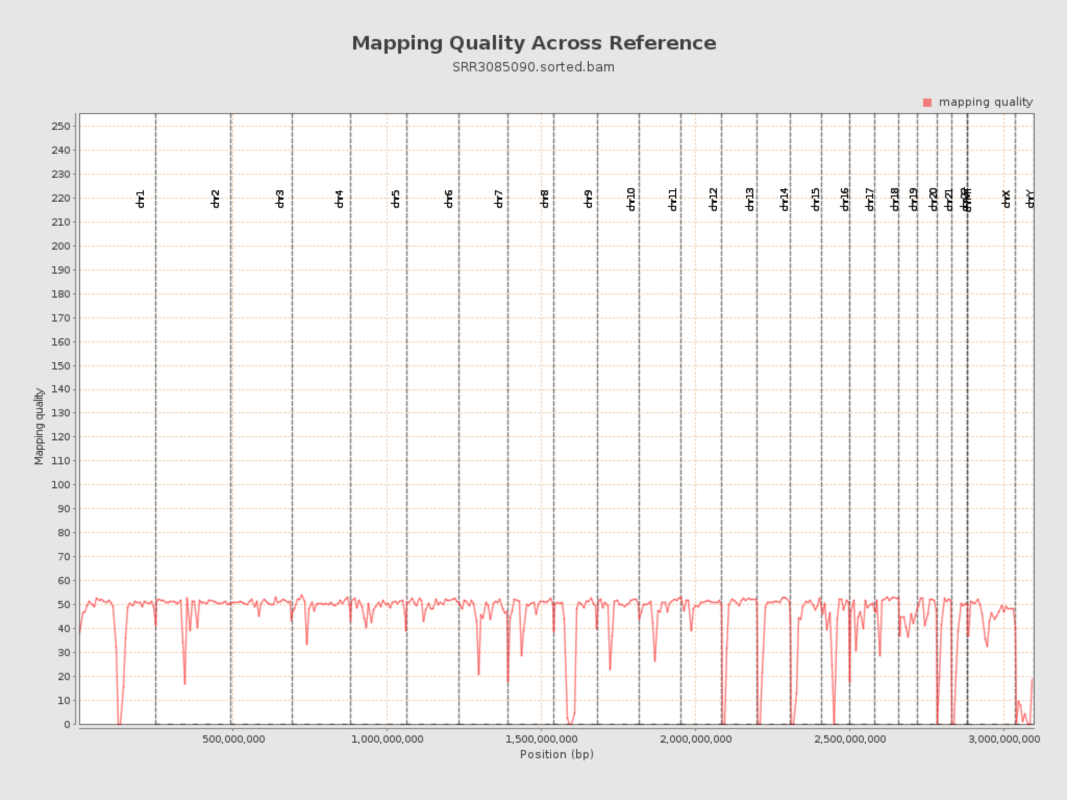
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram