# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 00:11:03*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085055.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_SRR3085055 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085055.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Aug 26 00:11:02 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3085055.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,948,947 |
| Mapped reads | 1,576,950 / 80.91% |
| Unmapped reads | 371,997 / 19.09% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 7,069 / 0.36% |
| Read min/max/mean length | 30 / 76 / 76.12 |
| Duplicated reads (estimated) | 42,509 / 2.18% |
| Duplication rate | 2.13% |
| Clipped reads | 1,094,891 / 56.18% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 27,821,971 / 29.29% |
| Number/percentage of C's | 18,849,931 / 19.85% |
| Number/percentage of T's | 27,182,899 / 28.62% |
| Number/percentage of G's | 21,125,004 / 22.24% |
| Number/percentage of N's | 2,026 / 0% |
| GC Percentage | 42.09% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0307 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2529 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.39 |

## 2.5. Mismatches and indels

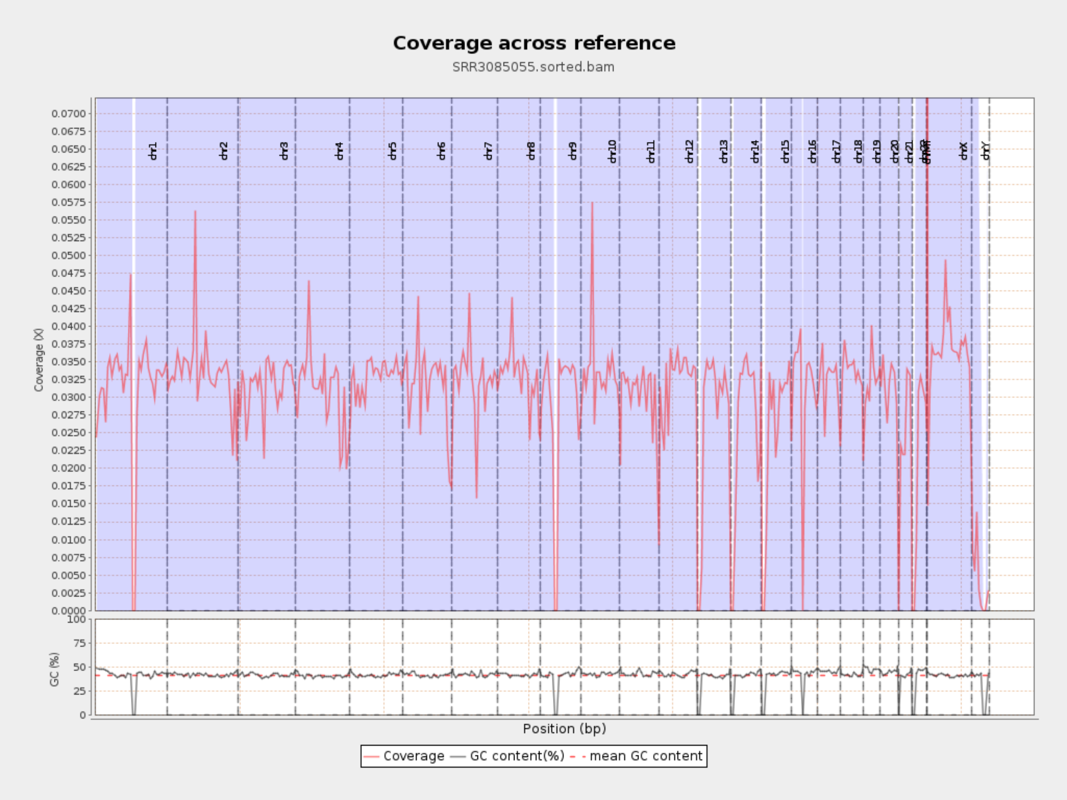
| | |
|---|---|
| General error rate | 0.9% |
| Mismatches | 840,038 |
| Insertions | 7,477 |
| Mapped reads with at least one insertion | 0.47% |
| Deletions | 19,387 |
| Mapped reads with at least one deletion | 1.22% |
| Homopolymer indels | 44.61% |

## 2.6. Chromosome stats

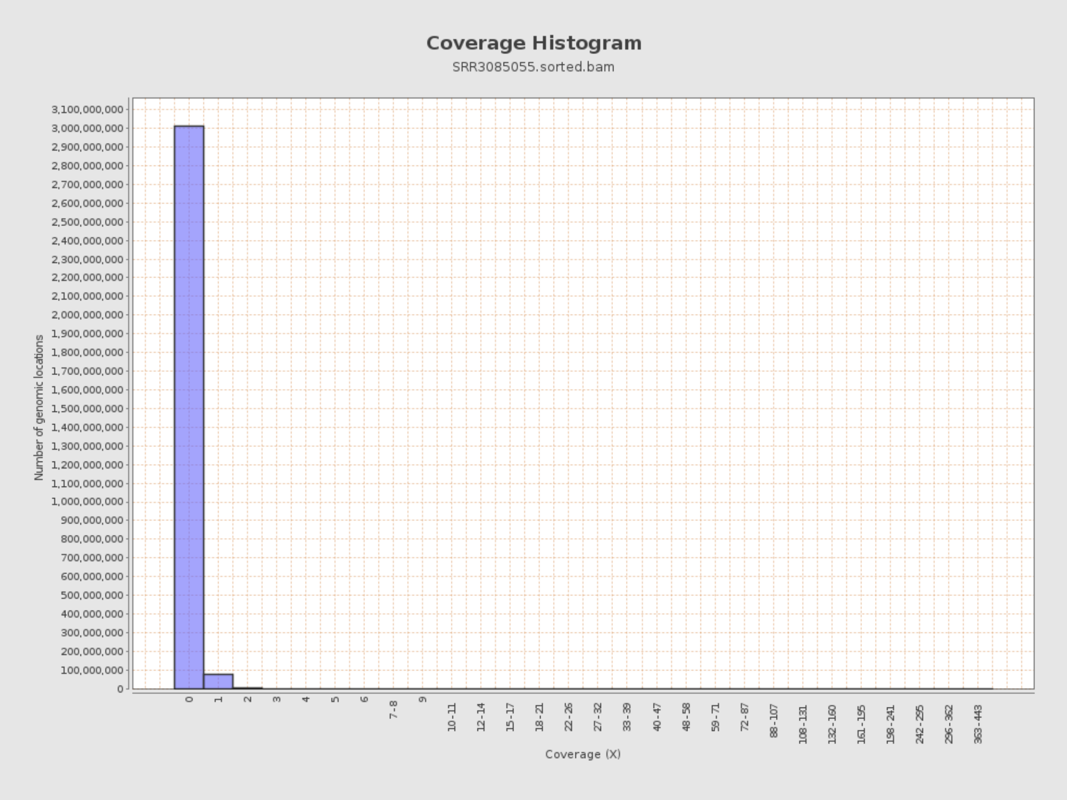
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 7788769 | 0.0312 | 0.3926 |
| chr2 | 243199373 | 8161704 | 0.0336 | 0.2856 |
| chr3 | 198022430 | 6247345 | 0.0315 | 0.1916 |
| chr4 | 191154276 | 5912919 | 0.0309 | 0.202 |
| chr5 | 180915260 | 5989267 | 0.0331 | 0.1957 |
| chr6 | 171115067 | 5457224 | 0.0319 | 0.2346 |
| chr7 | 159138663 | 5171085 | 0.0325 | 0.2552 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4866707 | 0.0333 | 0.3036 |
| chr9 | 141213431 | 4037958 | 0.0286 | 0.2419 |
| chr10 | 135534747 | 4583318 | 0.0338 | 0.2885 |
| chr11 | 135006516 | 4134785 | 0.0306 | 0.2386 |
| chr12 | 133851895 | 4348666 | 0.0325 | 0.1963 |
| chr13 | 115169878 | 3071533 | 0.0267 | 0.175 |
| chr14 | 107349540 | 2713803 | 0.0253 | 0.1864 |
| chr15 | 102531392 | 2520514 | 0.0246 | 0.1682 |
| chr16 | 90354753 | 2758334 | 0.0305 | 0.2013 |
| chr17 | 81195210 | 2604189 | 0.0321 | 0.2147 |
| chr18 | 78077248 | 2639857 | 0.0338 | 0.4399 |
| chr19 | 59128983 | 1907381 | 0.0323 | 0.3055 |
| chr20 | 63025520 | 1961111 | 0.0311 | 0.1952 |
| chr21 | 48129895 | 1143372 | 0.0238 | 0.1796 |
| chr22 | 51304566 | 1087910 | 0.0212 | 0.1564 |
| chrMT | 16571 | 7906 | 0.4771 | 0.8198 |
| chrX | 155270560 | 5653611 | 0.0364 | 0.2282 |
| chrY | 59373566 | 243534 | 0.0041 | 0.1003 |

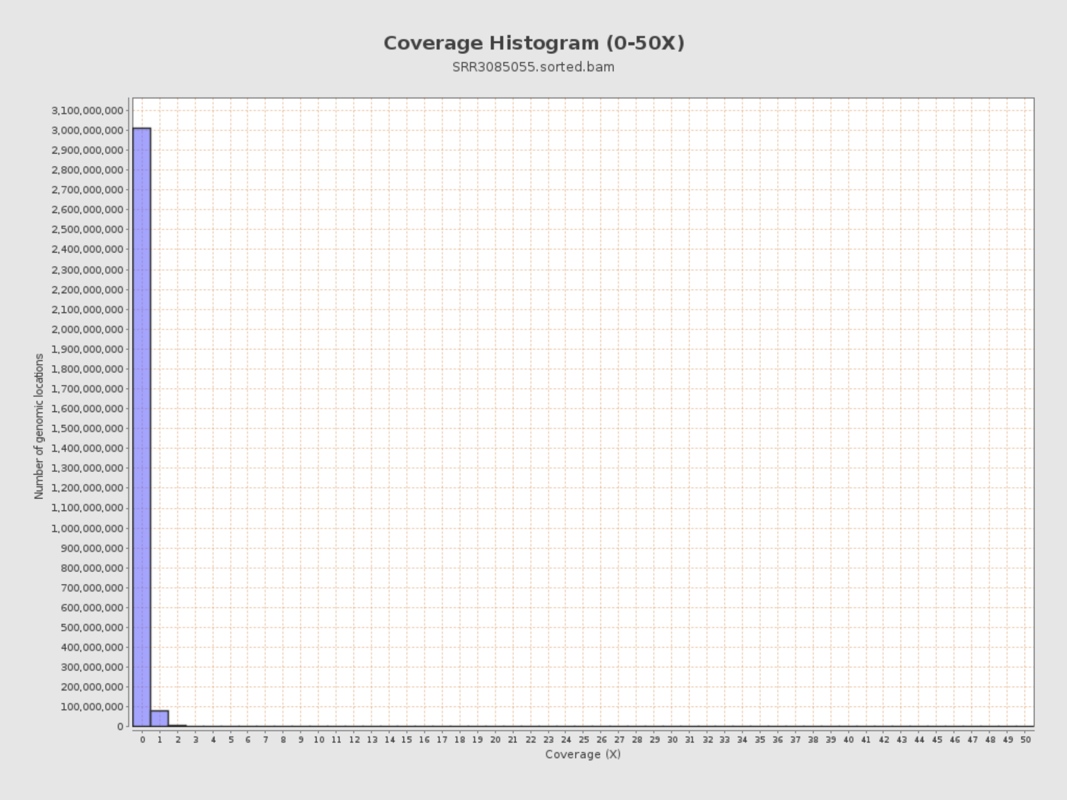
# 3. Results : Coverage across reference



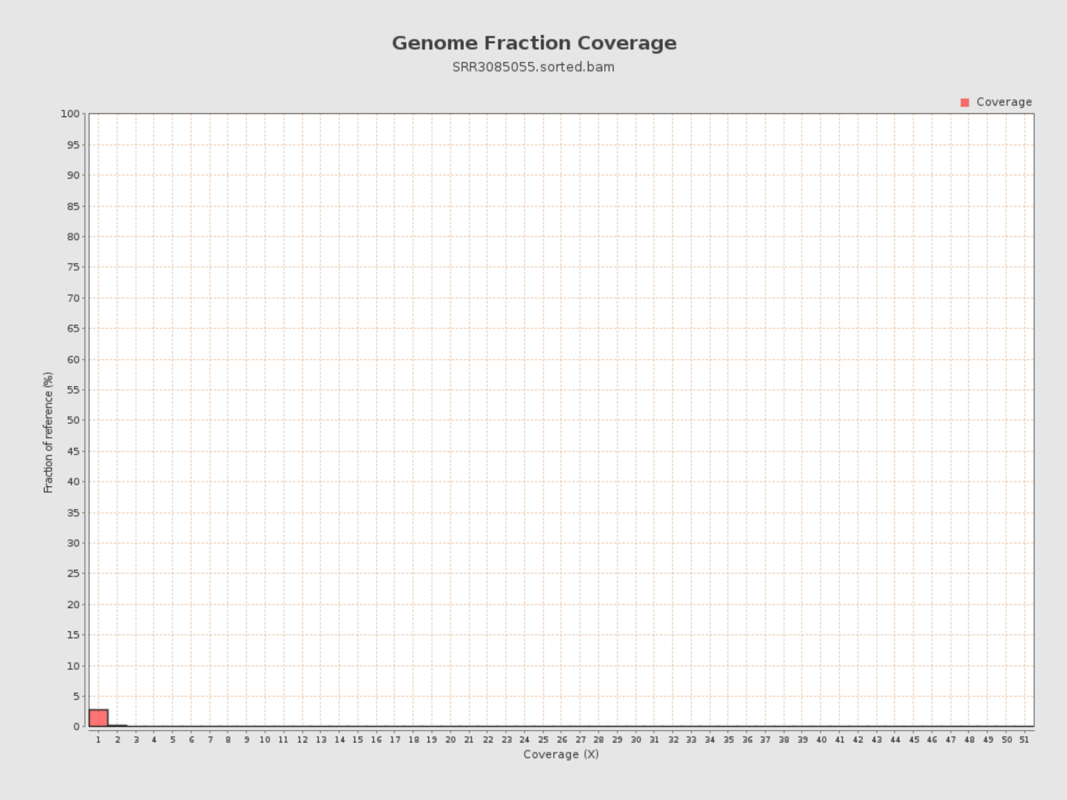
# 4. Results : Coverage Histogram



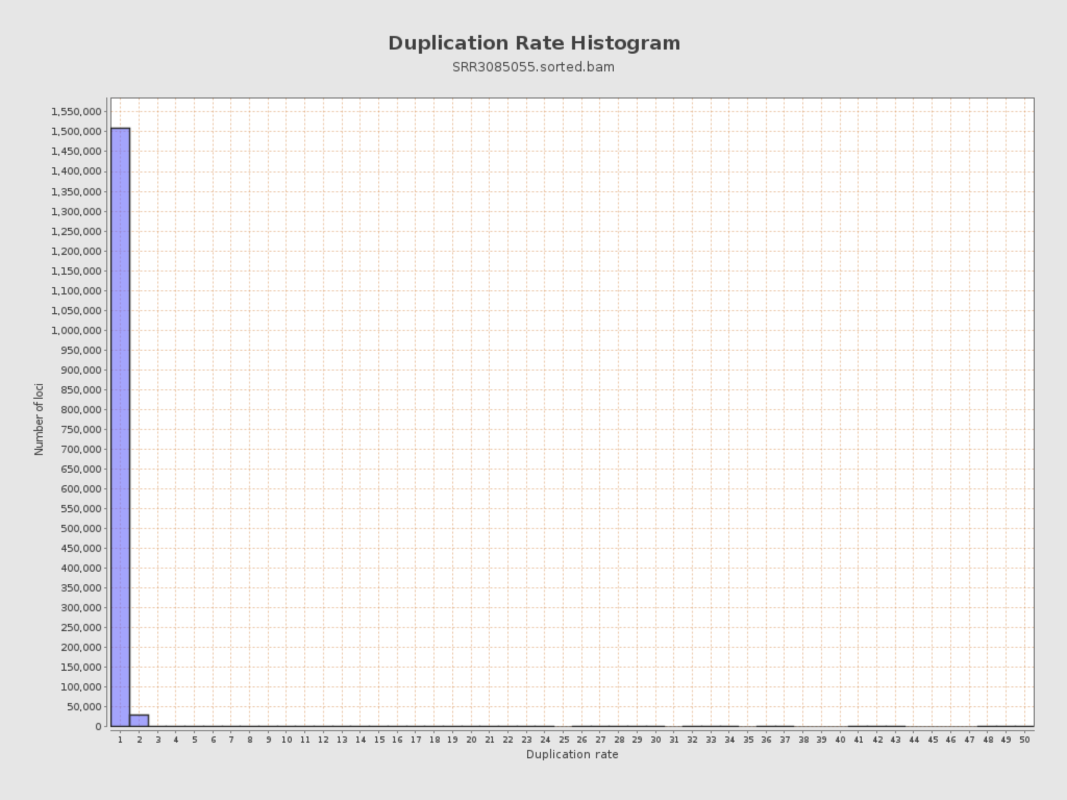
# 5. Results : Coverage Histogram (0-50X)



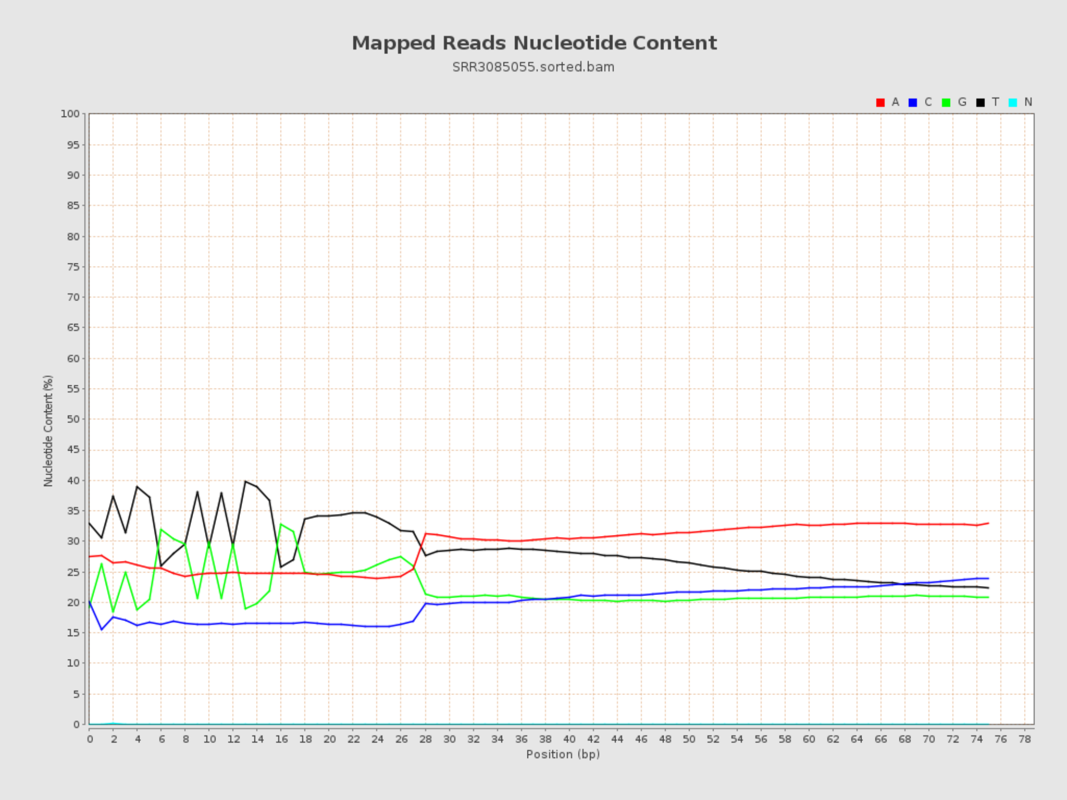
# 6. Results : Genome Fraction Coverage



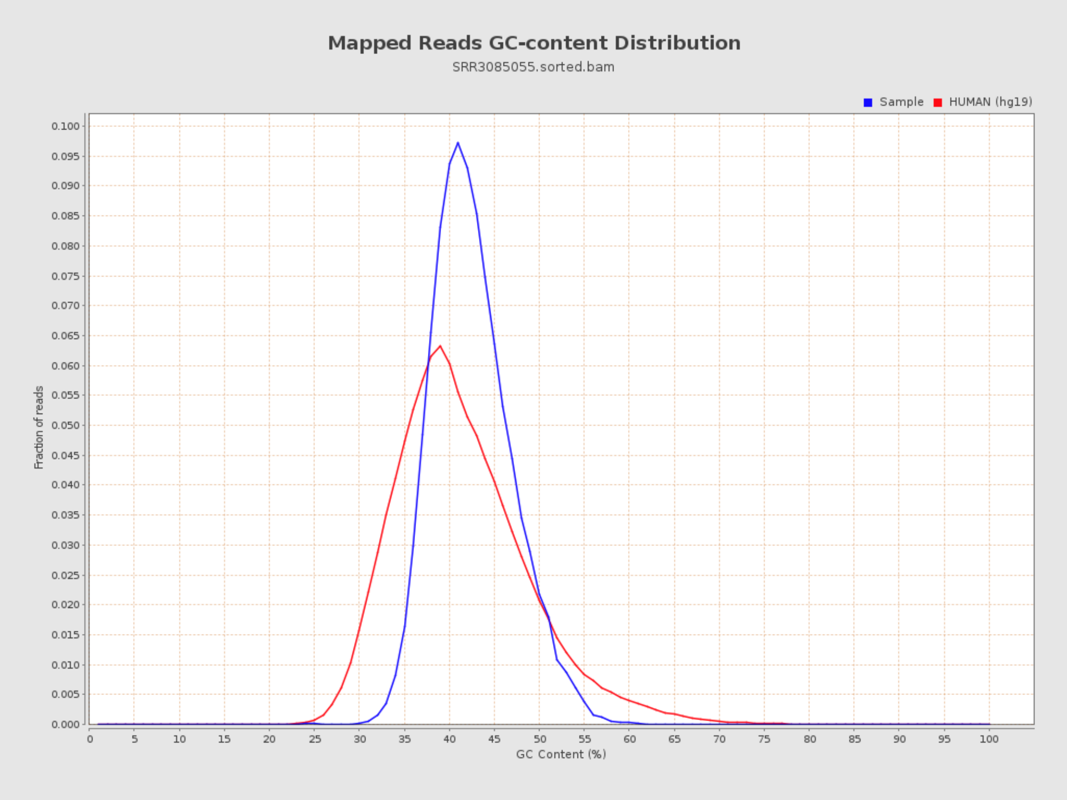
# 7. Results : Duplication Rate Histogram



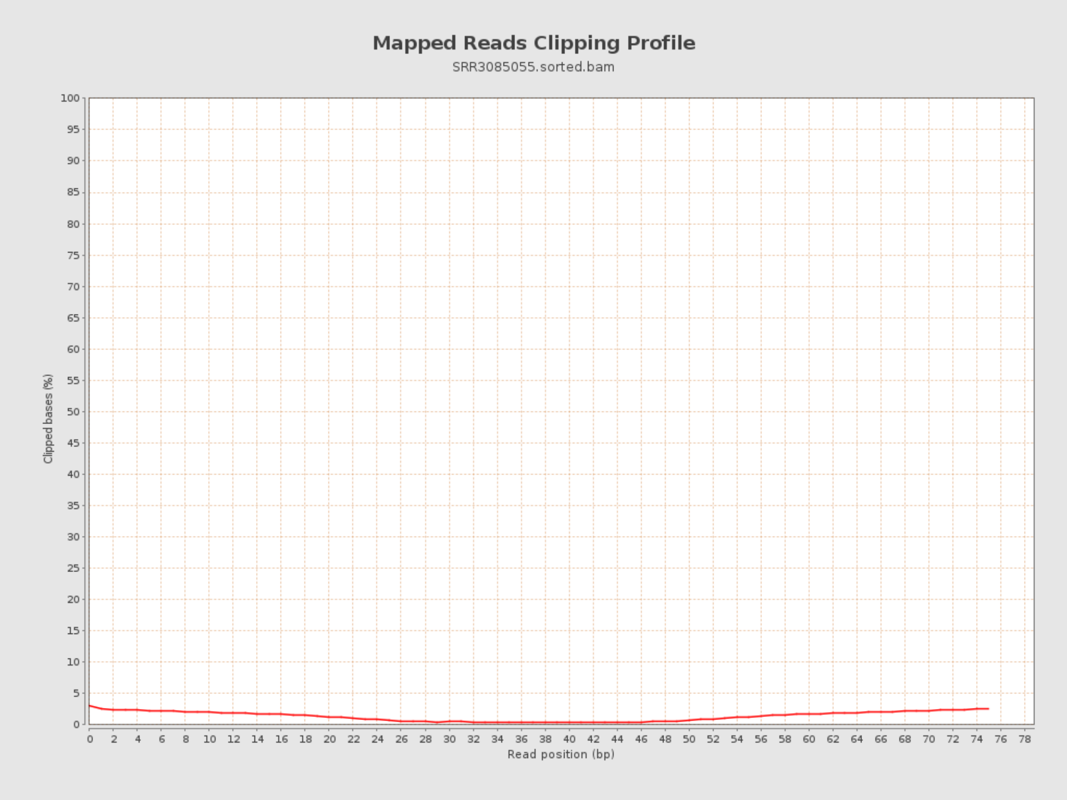
# 8. Results : Mapped Reads Nucleotide Content



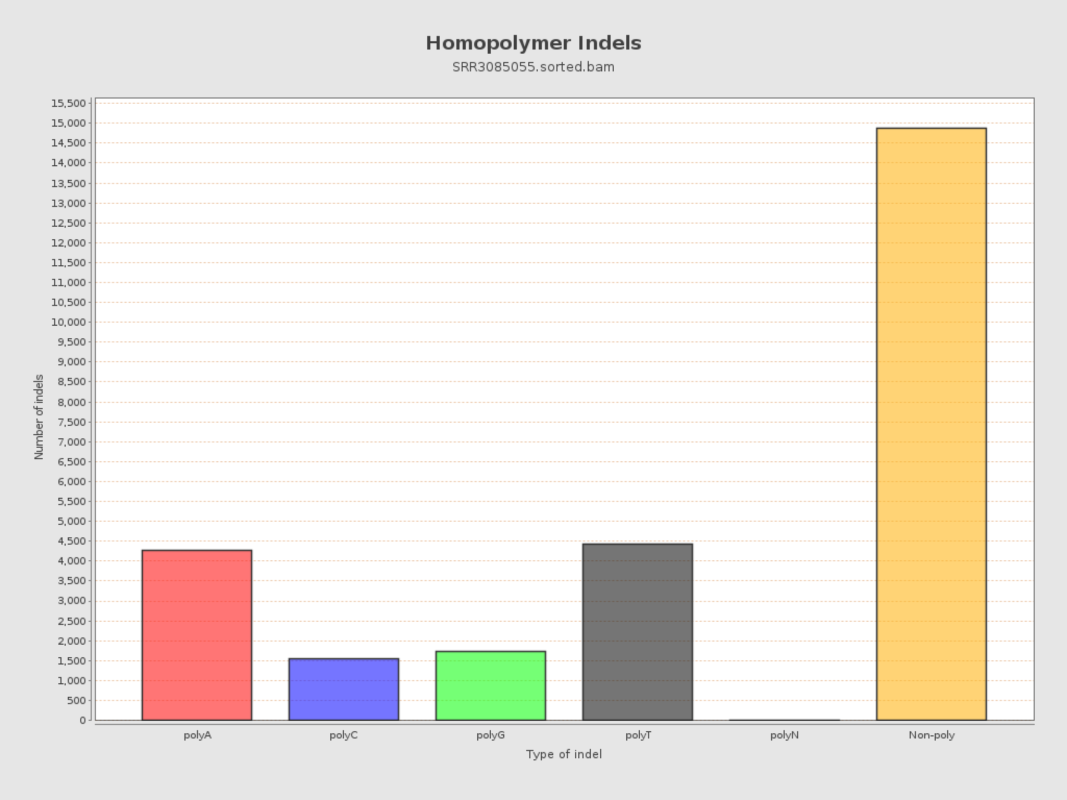
# 9. Results : Mapped Reads GC-content Distribution



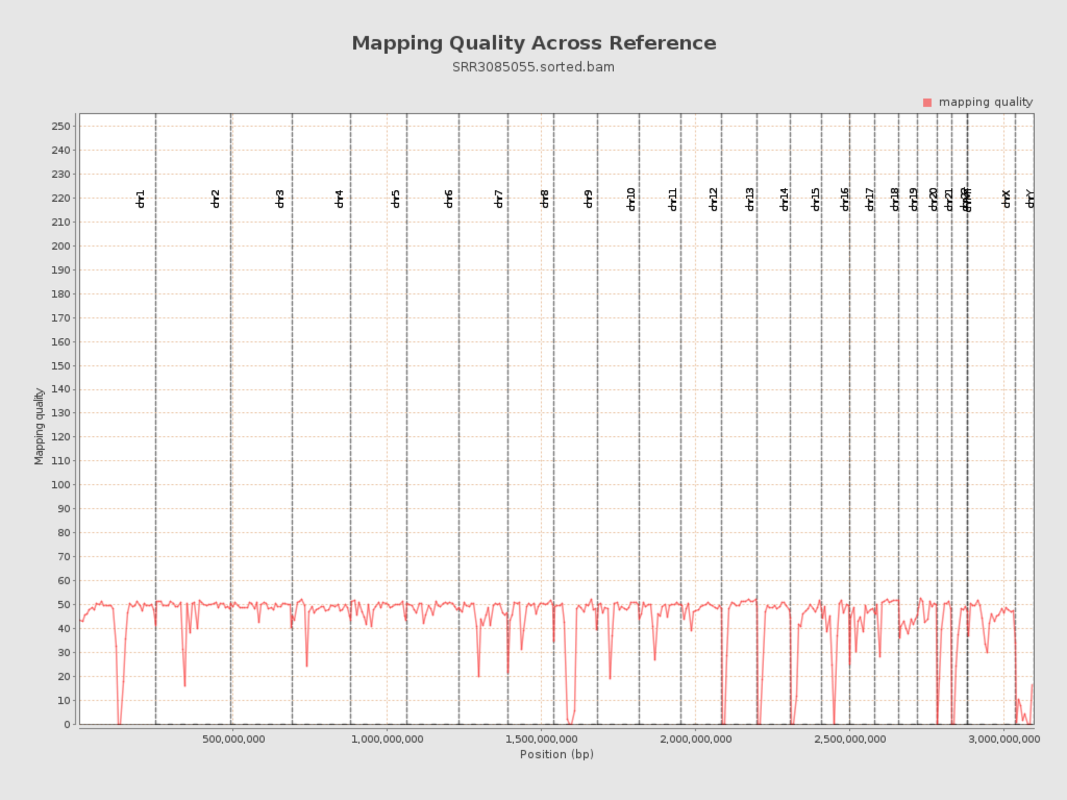
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram