# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 00:19:15*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085058.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_SRR3085058 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085058.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Aug 26 00:19:14 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3085058.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,403,947 |
| Mapped reads | 1,000,018 / 71.23% |
| Unmapped reads | 403,929 / 28.77% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 4,264 / 0.3% |
| Read min/max/mean length | 30 / 76 / 76.1 |
| Duplicated reads (estimated) | 20,700 / 1.47% |
| Duplication rate | 1.73% |
| Clipped reads | 544,776 / 38.8% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 18,952,529 / 29.93% |
| Number/percentage of C's | 11,591,566 / 18.31% |
| Number/percentage of T's | 18,747,373 / 29.61% |
| Number/percentage of G's | 14,022,320 / 22.15% |
| Number/percentage of N's | 1,271 / 0% |
| GC Percentage | 40.45% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0205 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1782 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.63 |

## 2.5. Mismatches and indels

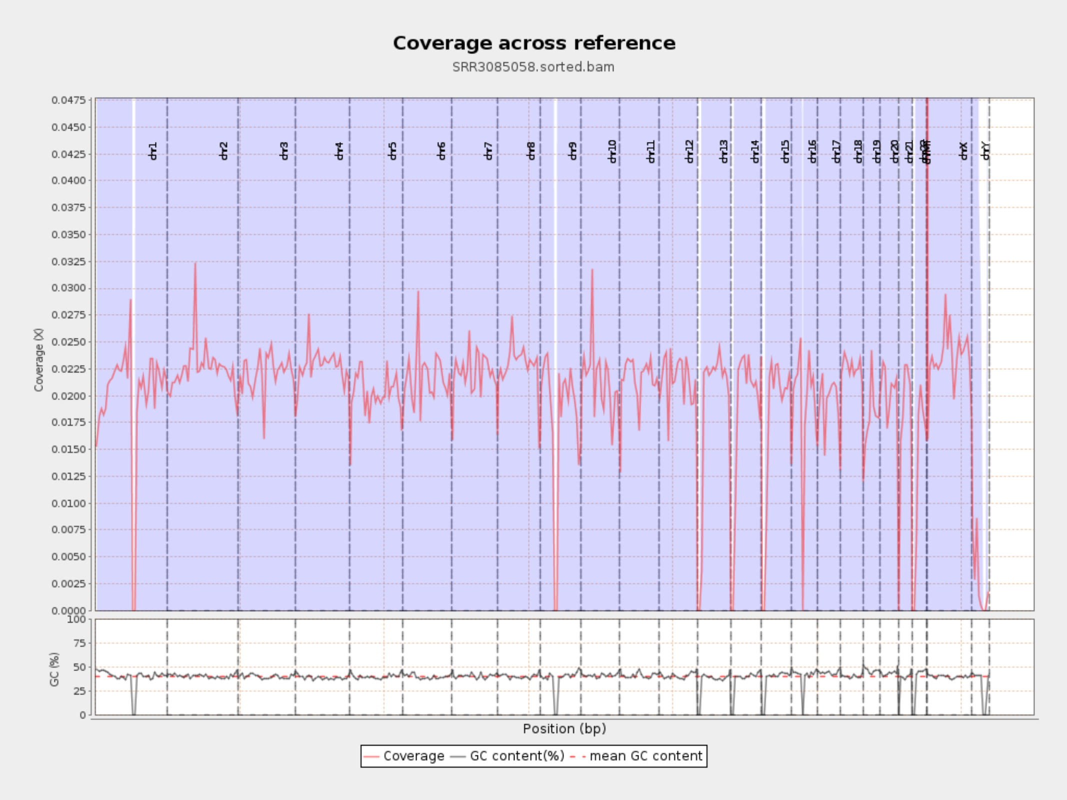
| | |
|---|---|
| General error rate | 0.96% |
| Mismatches | 599,483 |
| Insertions | 4,710 |
| Mapped reads with at least one insertion | 0.47% |
| Deletions | 13,966 |
| Mapped reads with at least one deletion | 1.38% |
| Homopolymer indels | 46.71% |

## 2.6. Chromosome stats

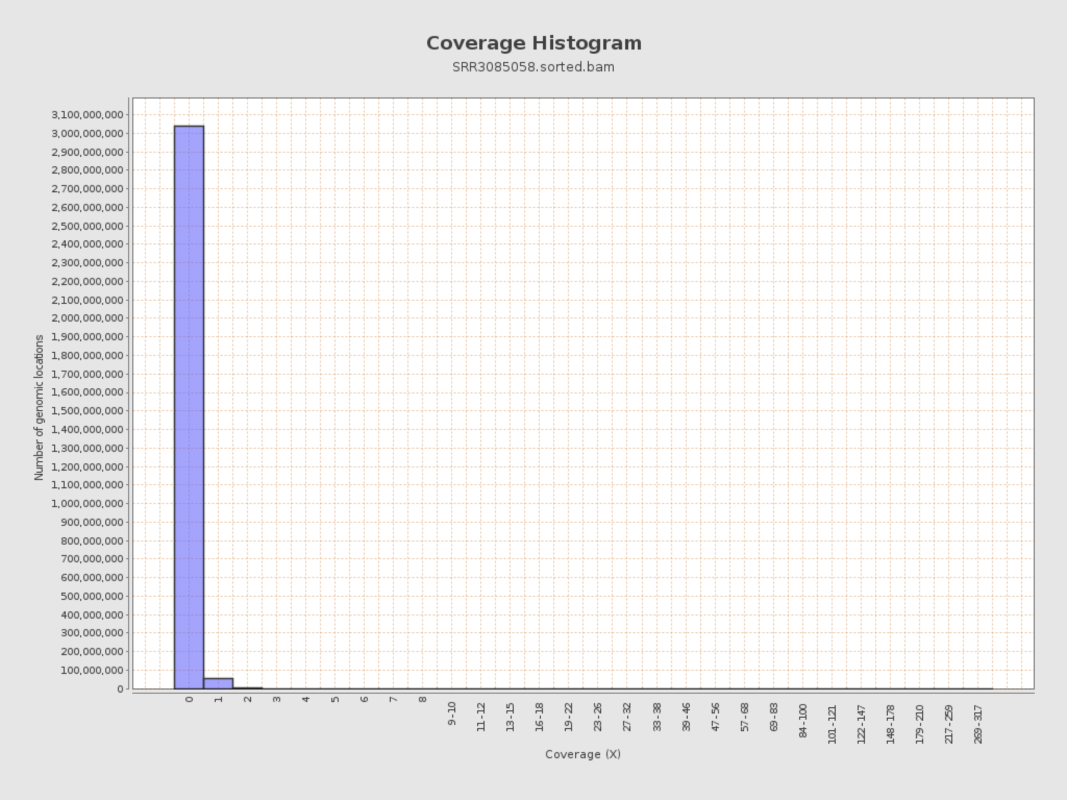
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 4981618 | 0.02 | 0.2351 |
| chr2 | 243199373 | 5492916 | 0.0226 | 0.1924 |
| chr3 | 198022430 | 4382624 | 0.0221 | 0.1563 |
| chr4 | 191154276 | 4340649 | 0.0227 | 0.1623 |
| chr5 | 180915260 | 3684807 | 0.0204 | 0.15 |
| chr6 | 171115067 | 3697893 | 0.0216 | 0.1693 |
| chr7 | 159138663 | 3537041 | 0.0222 | 0.1779 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3356825 | 0.0229 | 0.2486 |
| chr9 | 141213431 | 2547887 | 0.018 | 0.1649 |
| chr10 | 135534747 | 2909429 | 0.0215 | 0.1865 |
| chr11 | 135006516 | 2917621 | 0.0216 | 0.1802 |
| chr12 | 133851895 | 2875821 | 0.0215 | 0.1542 |
| chr13 | 115169878 | 2128014 | 0.0185 | 0.1424 |
| chr14 | 107349540 | 1938272 | 0.0181 | 0.1446 |
| chr15 | 102531392 | 1787374 | 0.0174 | 0.1389 |
| chr16 | 90354753 | 1699407 | 0.0188 | 0.1498 |
| chr17 | 81195210 | 1565486 | 0.0193 | 0.1535 |
| chr18 | 78077248 | 1768732 | 0.0227 | 0.2718 |
| chr19 | 59128983 | 1075416 | 0.0182 | 0.1937 |
| chr20 | 63025520 | 1282203 | 0.0203 | 0.1506 |
| chr21 | 48129895 | 860727 | 0.0179 | 0.147 |
| chr22 | 51304566 | 660753 | 0.0129 | 0.1192 |
| chrMT | 16571 | 9512 | 0.574 | 0.8711 |
| chrX | 155270560 | 3680367 | 0.0237 | 0.1698 |
| chrY | 59373566 | 155937 | 0.0026 | 0.0656 |

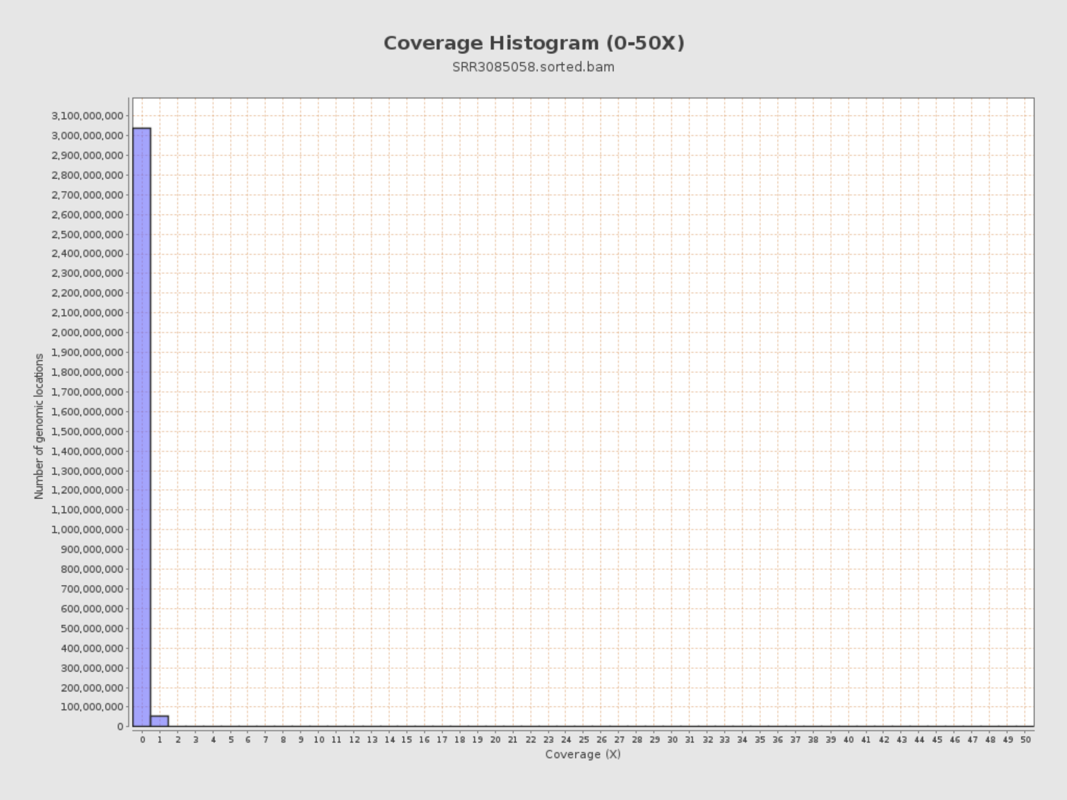
# 3. Results : Coverage across reference



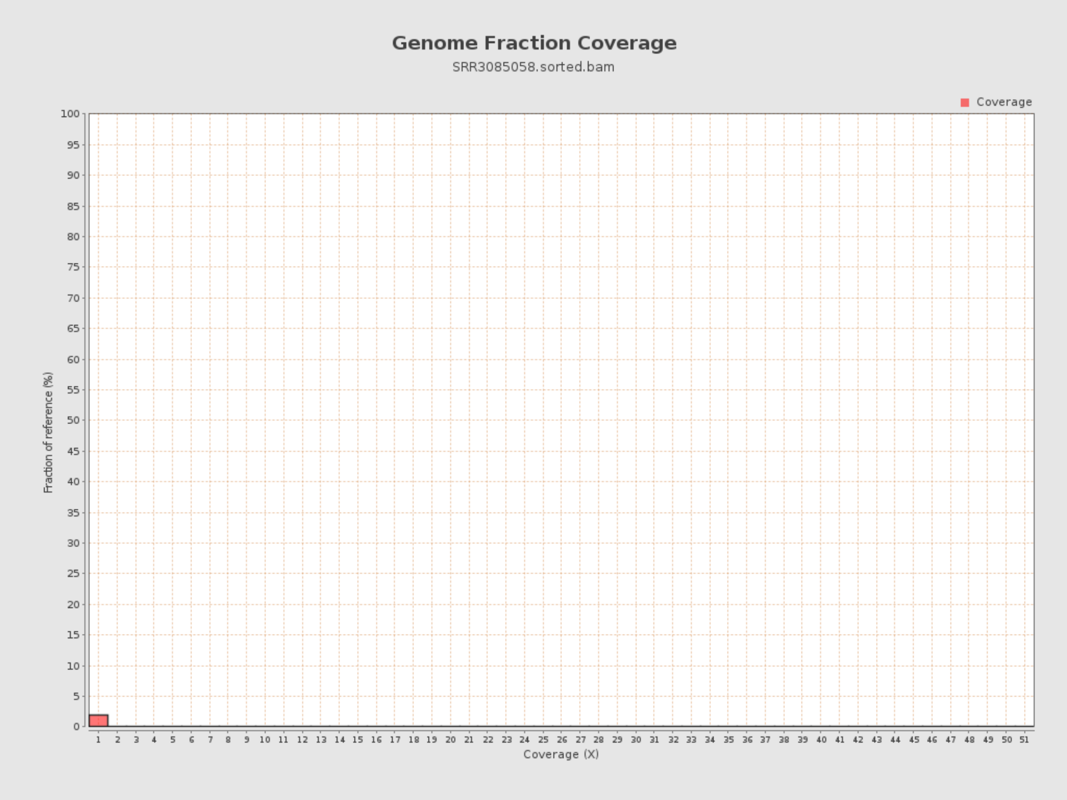
# 4. Results : Coverage Histogram



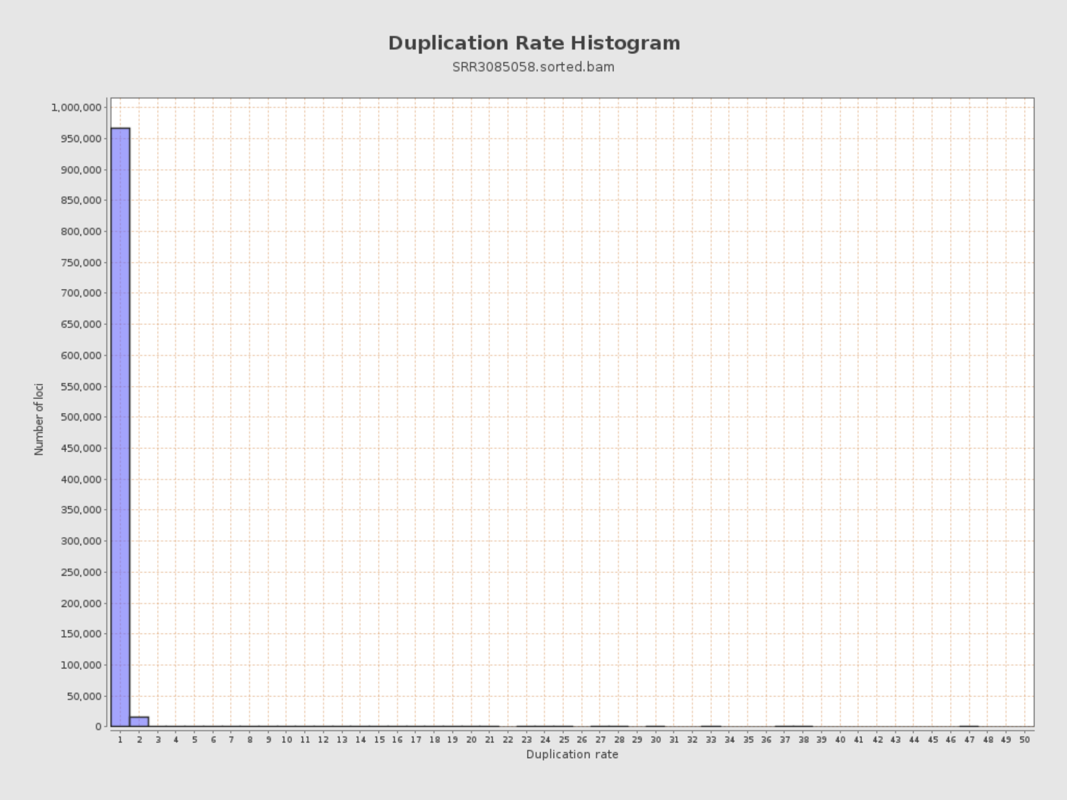
# 5. Results : Coverage Histogram (0-50X)



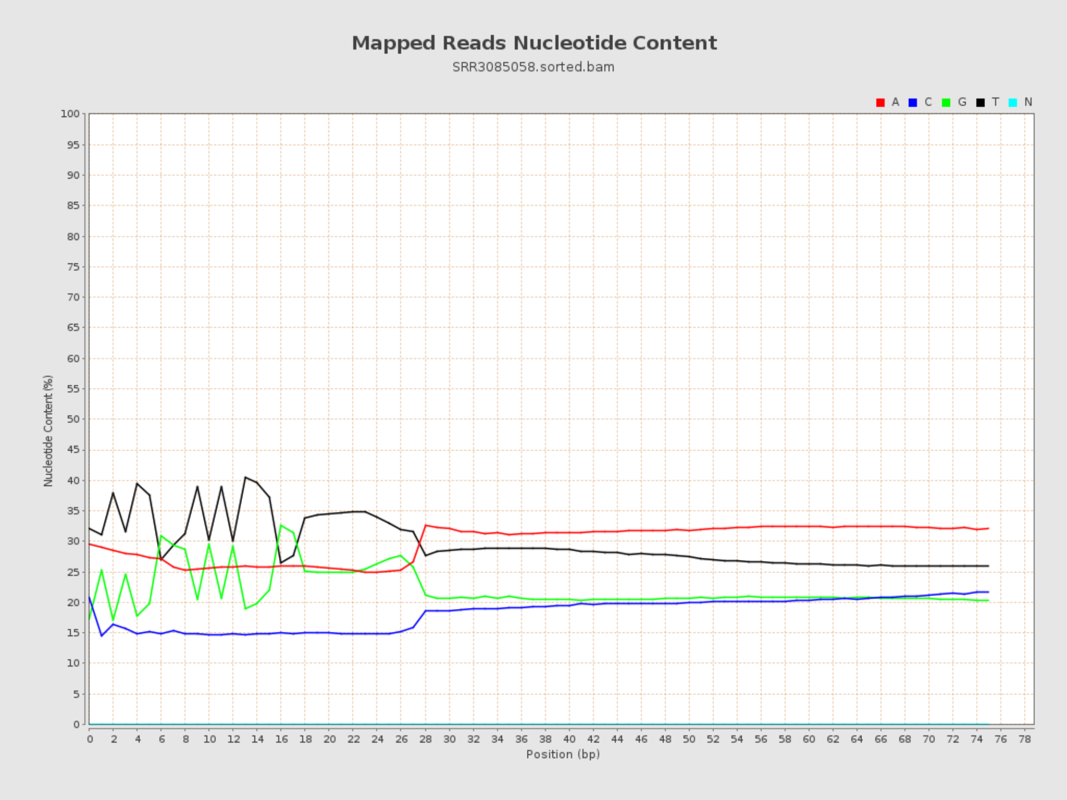
# 6. Results : Genome Fraction Coverage



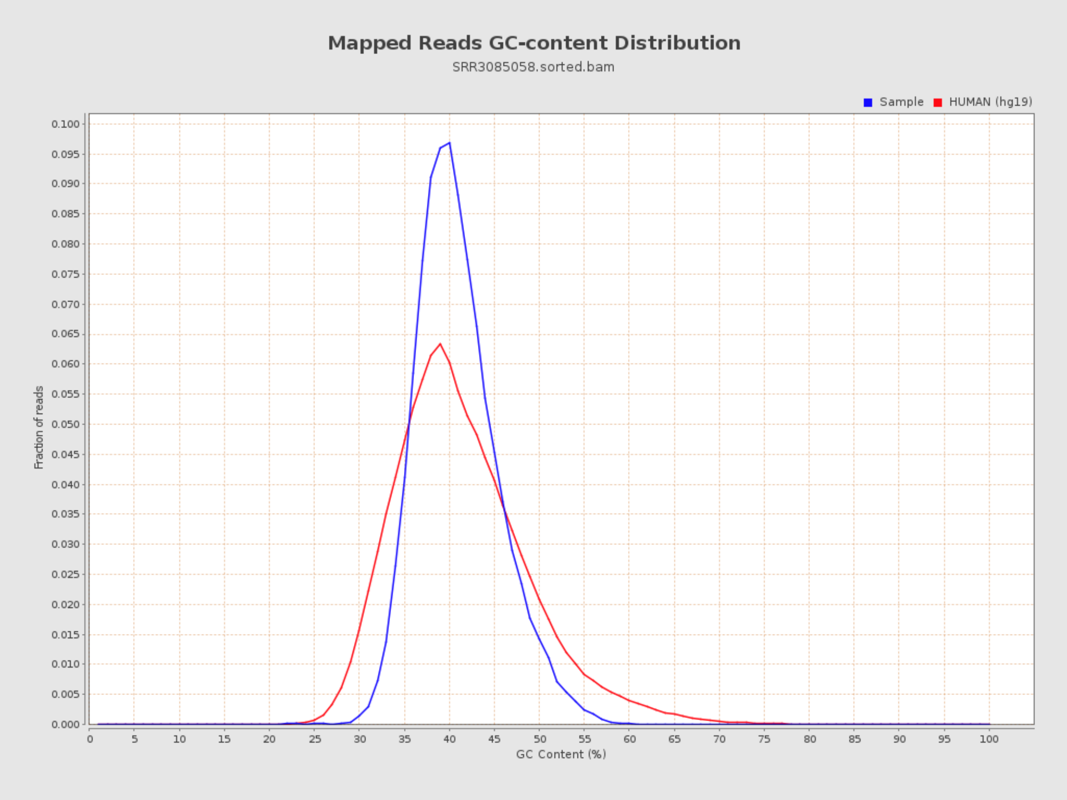
# 7. Results : Duplication Rate Histogram



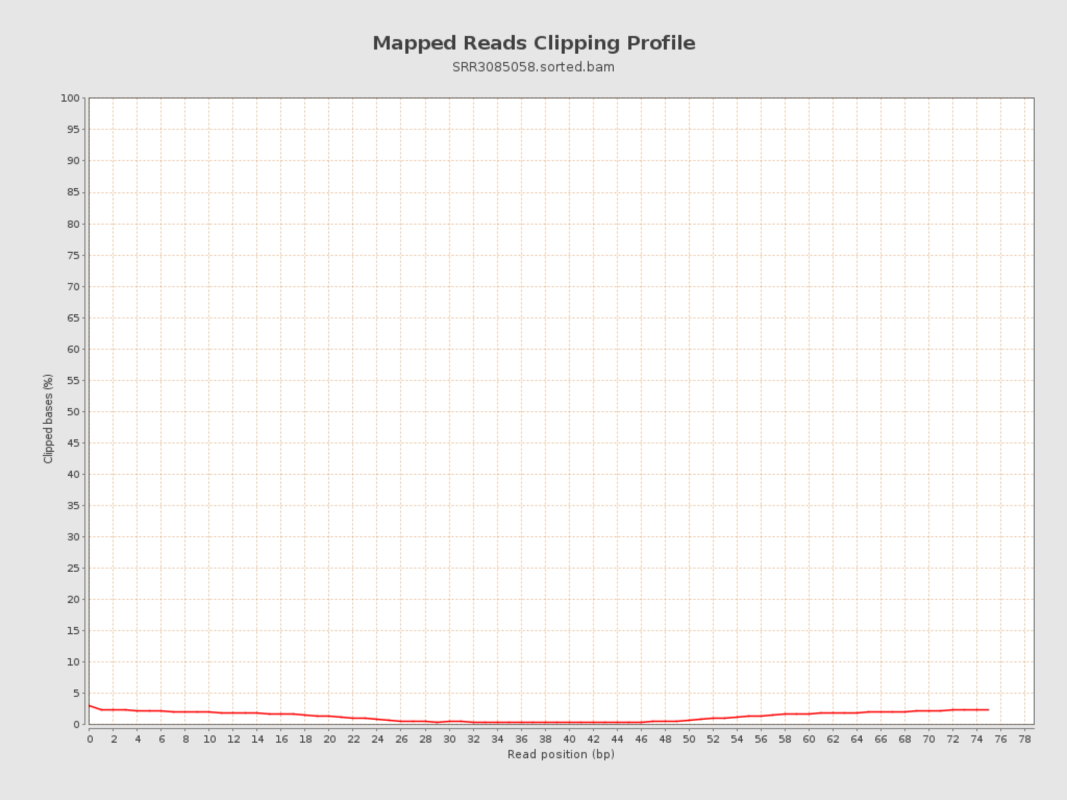
# 8. Results : Mapped Reads Nucleotide Content



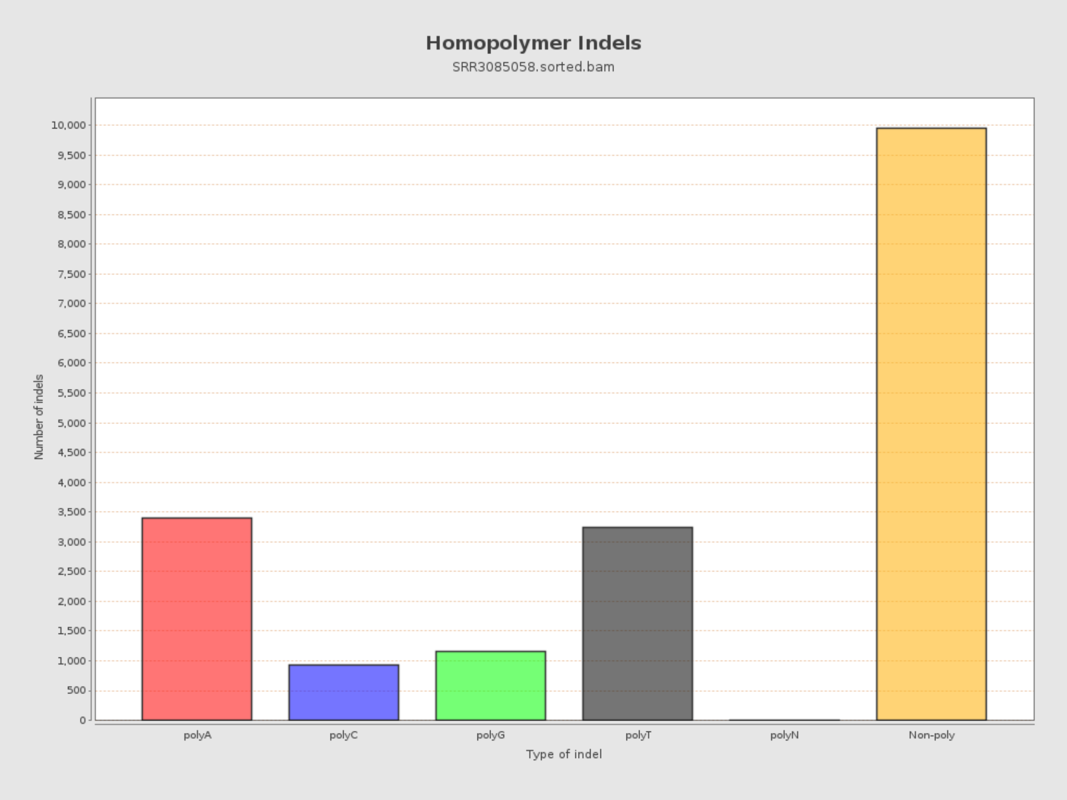
# 9. Results : Mapped Reads GC-content Distribution



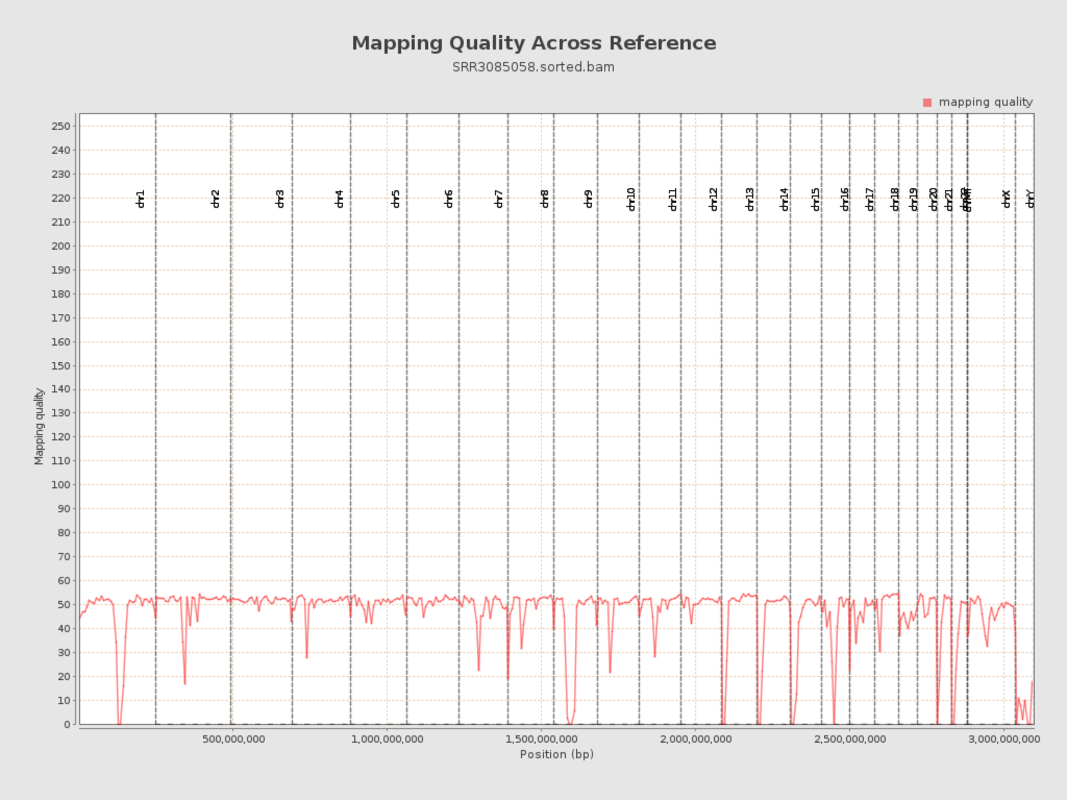
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram