# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 00:02:33*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3085052.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_SRR3085052 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3085052.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Aug 26 00:02:32 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3085052.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,164,433 |
| Mapped reads | 2,892,673 / 91.41% |
| Unmapped reads | 271,760 / 8.59% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 41,603 / 1.31% |
| Read min/max/mean length | 30 / 76 / 76.46 |
| Duplicated reads (estimated) | 121,406 / 3.84% |
| Duplication rate | 3.36% |
| Clipped reads | 1,113,495 / 35.19% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 60,555,440 / 30.28% |
| Number/percentage of C's | 41,016,175 / 20.51% |
| Number/percentage of T's | 58,984,635 / 29.49% |
| Number/percentage of G's | 39,405,730 / 19.7% |
| Number/percentage of N's | 22,615 / 0.01% |
| GC Percentage | 40.21% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0646 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4809 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.73 |

## 2.5. Mismatches and indels

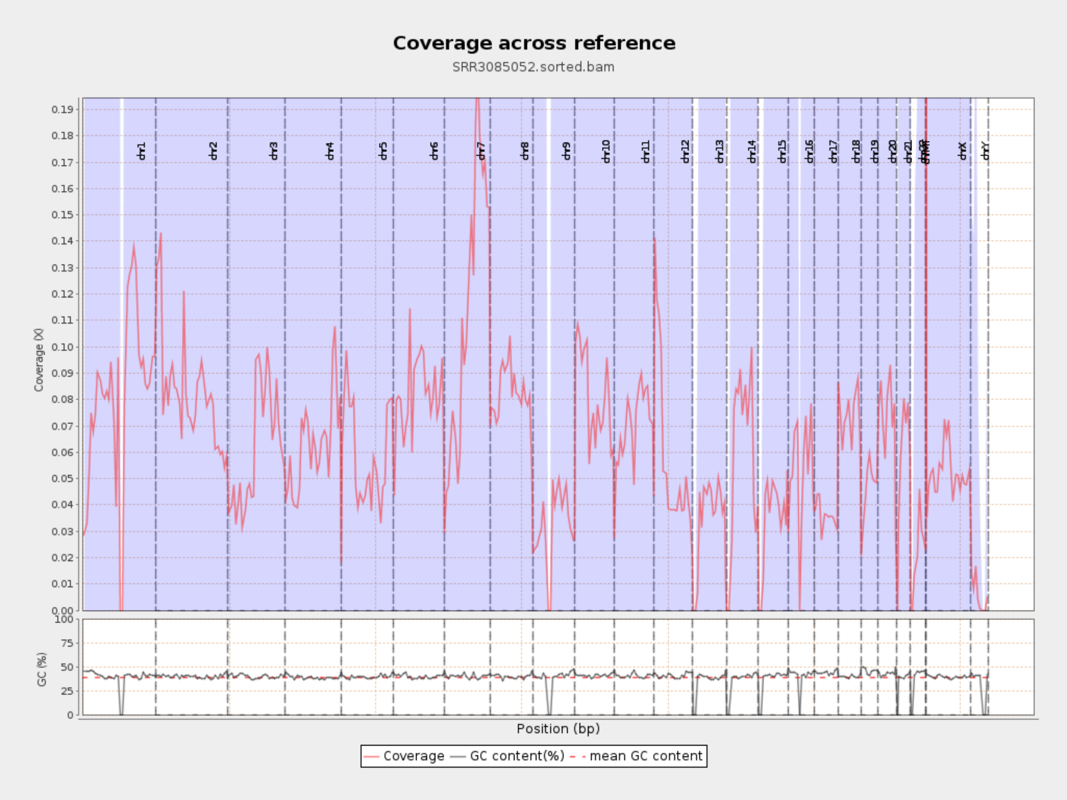
| | |
|---|---|
| General error rate | 0.91% |
| Mismatches | 1,795,236 |
| Insertions | 13,740 |
| Mapped reads with at least one insertion | 0.47% |
| Deletions | 41,622 |
| Mapped reads with at least one deletion | 1.43% |
| Homopolymer indels | 47.51% |

## 2.6. Chromosome stats

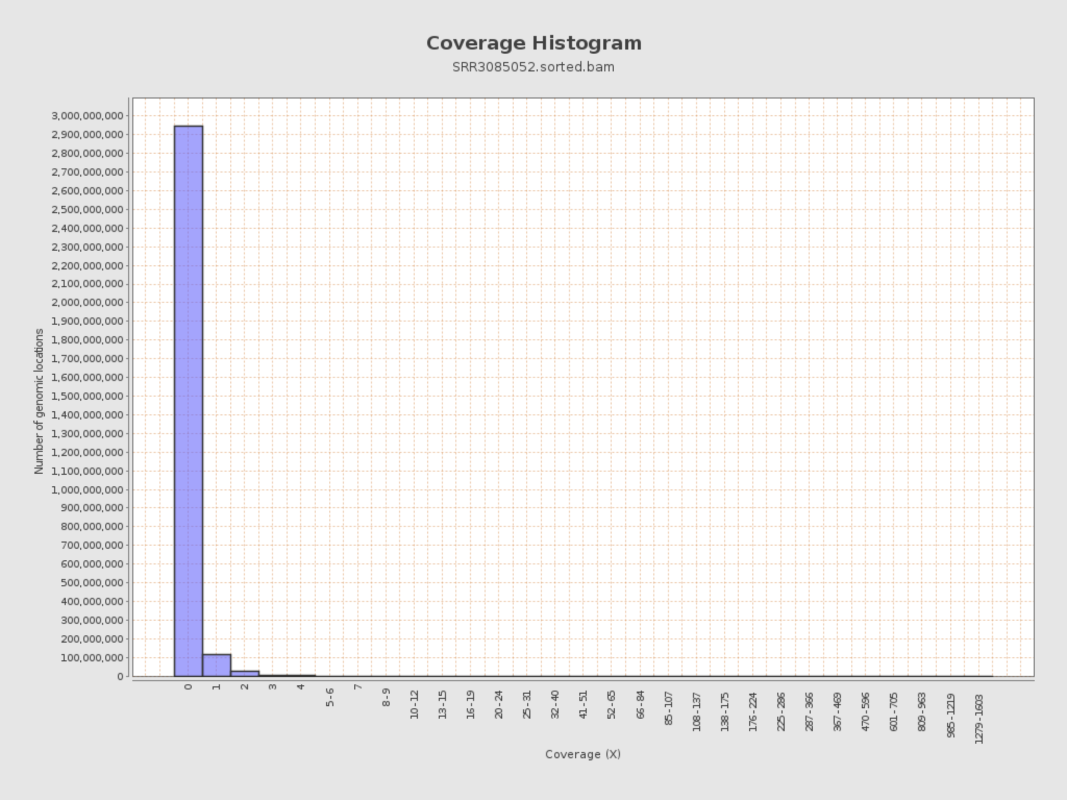
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 20265389 | 0.0813 | 0.5845 |
| chr2 | 243199373 | 20246560 | 0.0833 | 0.583 |
| chr3 | 198022430 | 12141838 | 0.0613 | 0.3188 |
| chr4 | 191154276 | 12036858 | 0.063 | 0.3275 |
| chr5 | 180915260 | 10626855 | 0.0587 | 0.3119 |
| chr6 | 171115067 | 14139974 | 0.0826 | 0.5253 |
| chr7 | 159138663 | 18119719 | 0.1139 | 0.577 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 12074883 | 0.0825 | 1.0493 |
| chr9 | 141213431 | 4588681 | 0.0325 | 0.3575 |
| chr10 | 135534747 | 11080444 | 0.0818 | 0.53 |
| chr11 | 135006516 | 9520222 | 0.0705 | 0.5567 |
| chr12 | 133851895 | 7848572 | 0.0586 | 0.3166 |
| chr13 | 115169878 | 4017371 | 0.0349 | 0.2373 |
| chr14 | 107349540 | 6580965 | 0.0613 | 0.3332 |
| chr15 | 102531392 | 3465161 | 0.0338 | 0.2622 |
| chr16 | 90354753 | 4665781 | 0.0516 | 0.3014 |
| chr17 | 81195210 | 2943089 | 0.0362 | 0.3006 |
| chr18 | 78077248 | 5820687 | 0.0746 | 0.6152 |
| chr19 | 59128983 | 2808832 | 0.0475 | 0.4611 |
| chr20 | 63025520 | 4686212 | 0.0744 | 0.3533 |
| chr21 | 48129895 | 2798134 | 0.0581 | 0.3175 |
| chr22 | 51304566 | 1111414 | 0.0217 | 0.183 |
| chrMT | 16571 | 16503 | 0.9959 | 1.3452 |
| chrX | 155270560 | 8104889 | 0.0522 | 0.3343 |
| chrY | 59373566 | 347235 | 0.0058 | 0.1177 |

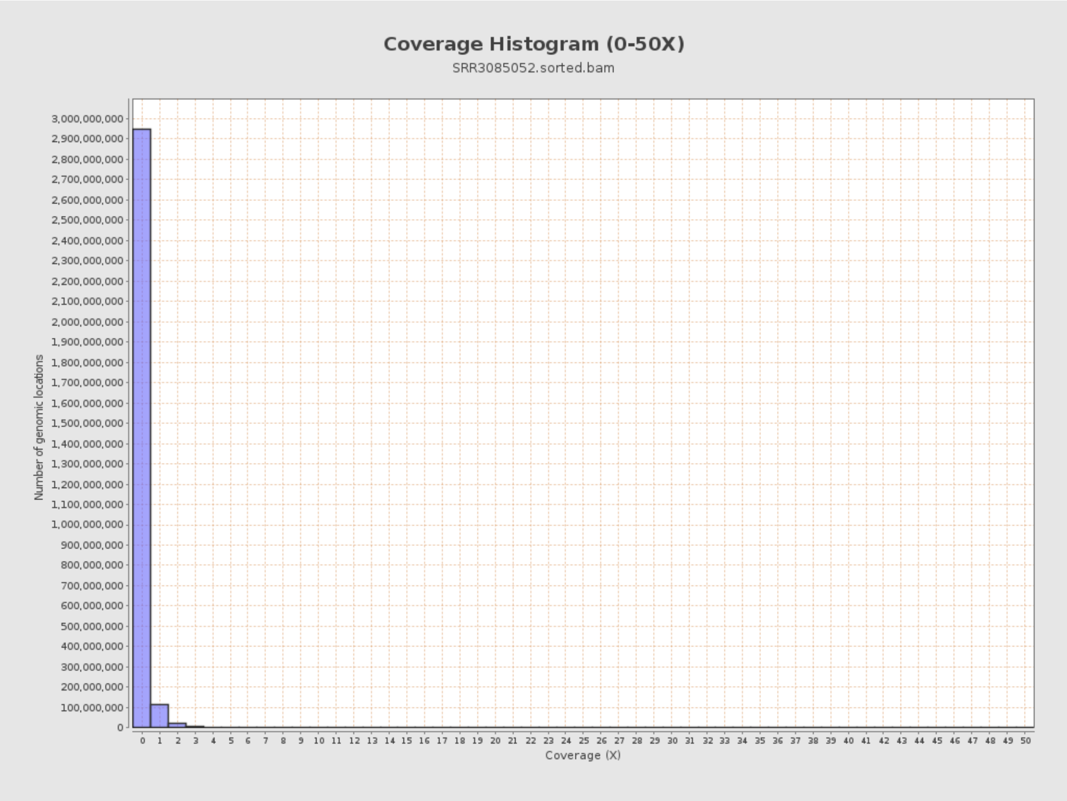
# 3. Results : Coverage across reference



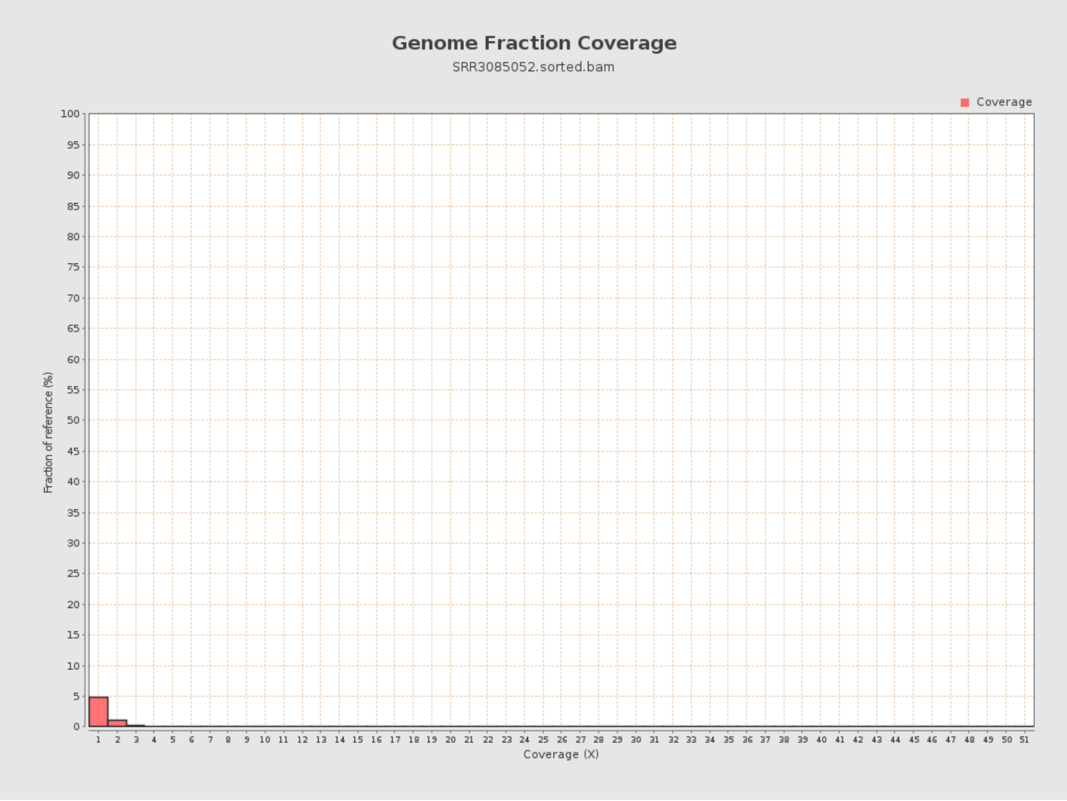
# 4. Results : Coverage Histogram



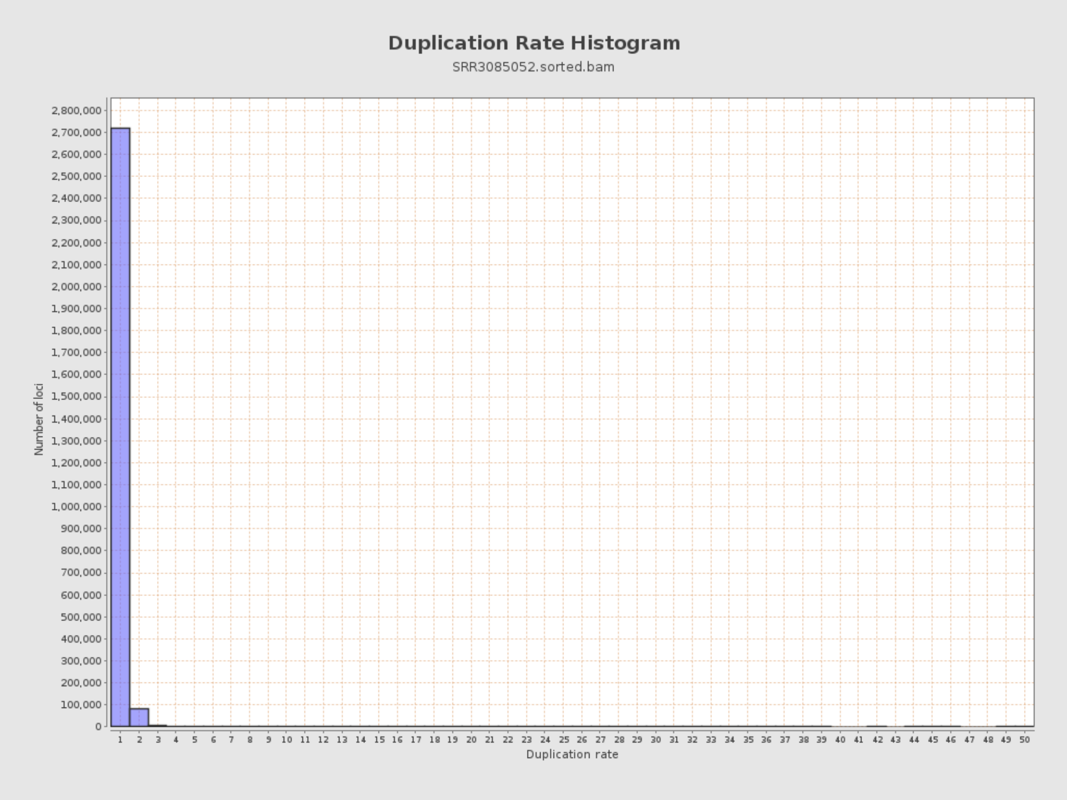
# 5. Results : Coverage Histogram (0-50X)



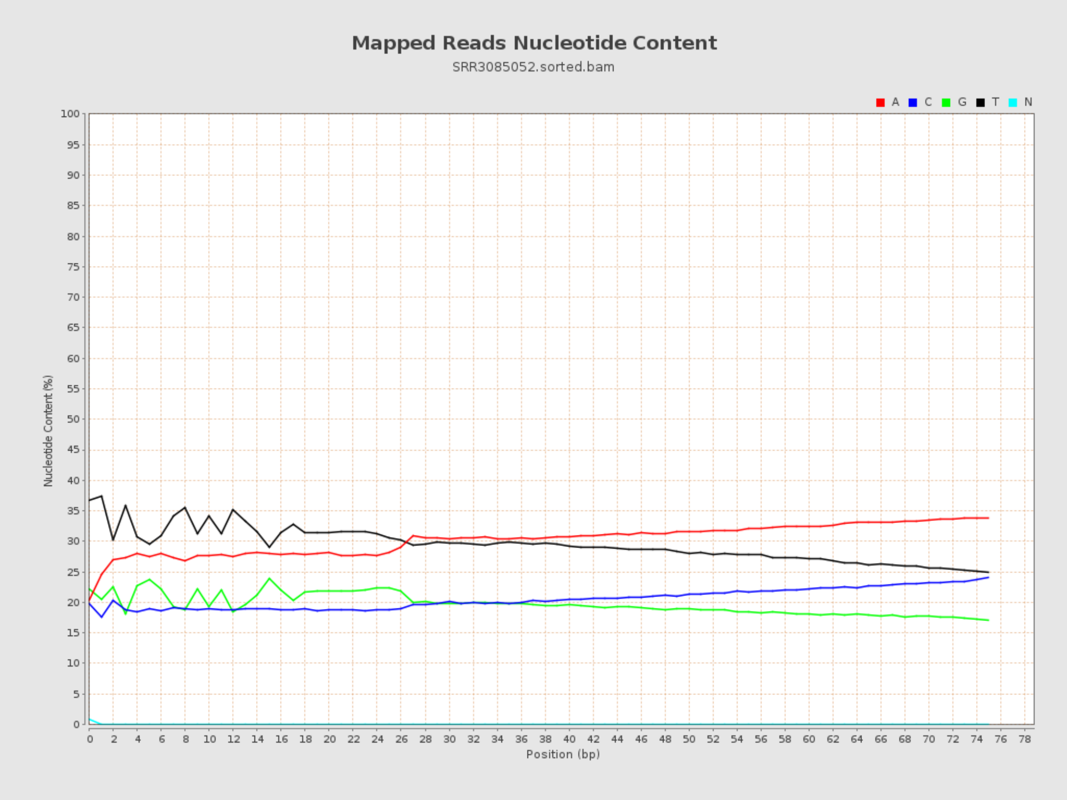
# 6. Results : Genome Fraction Coverage



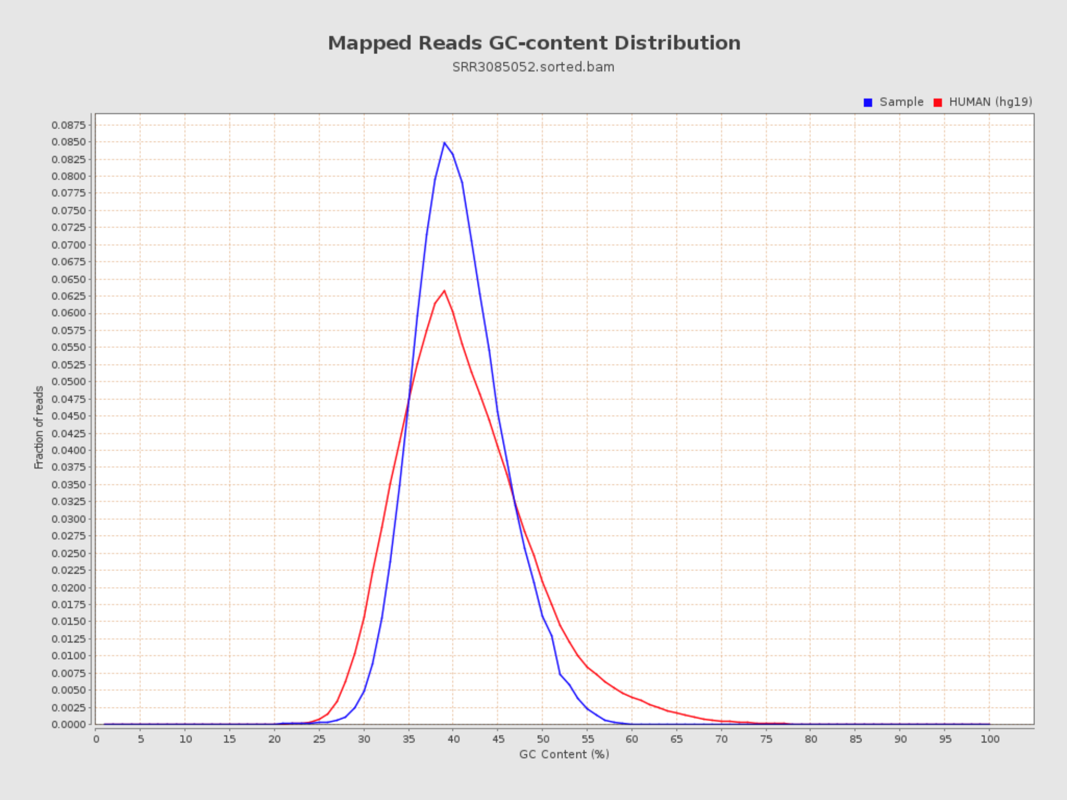
# 7. Results : Duplication Rate Histogram



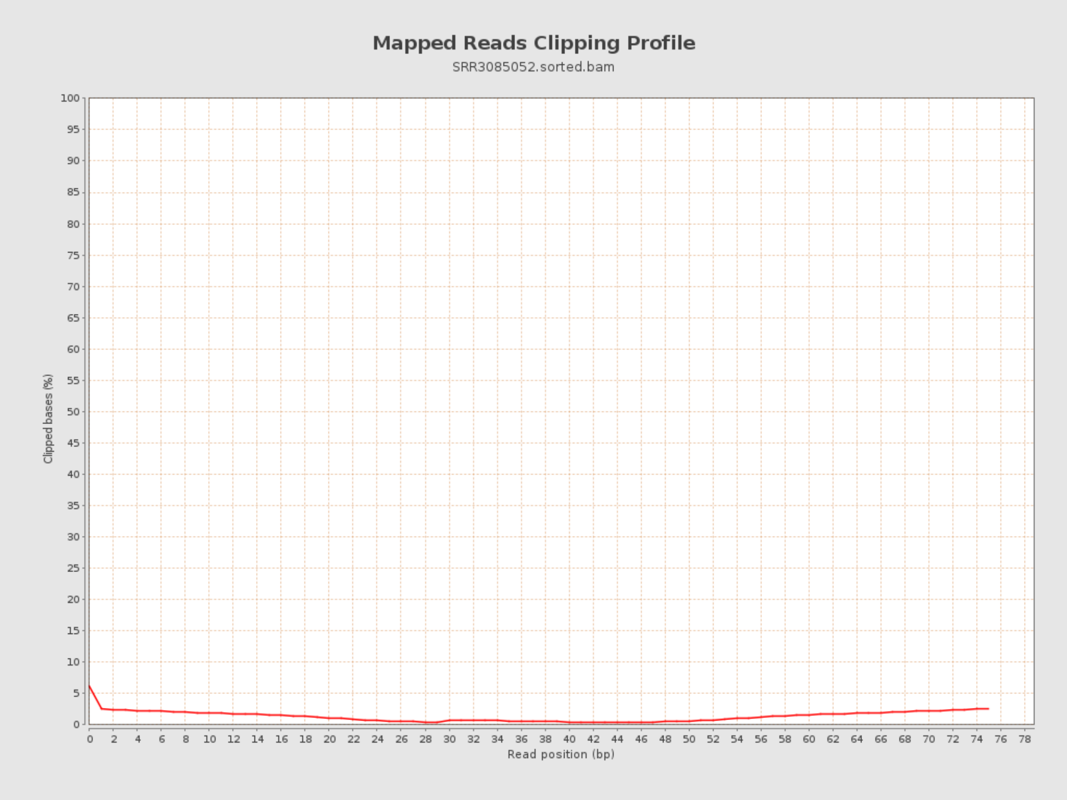
# 8. Results : Mapped Reads Nucleotide Content



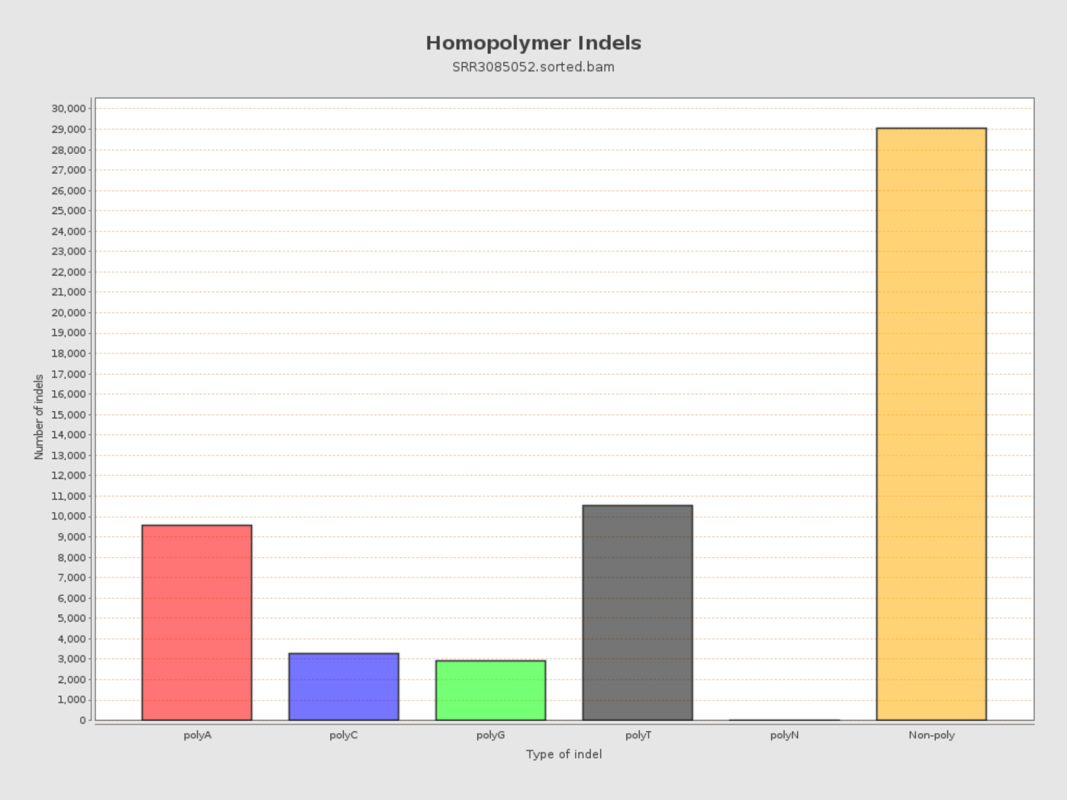
# 9. Results : Mapped Reads GC-content Distribution



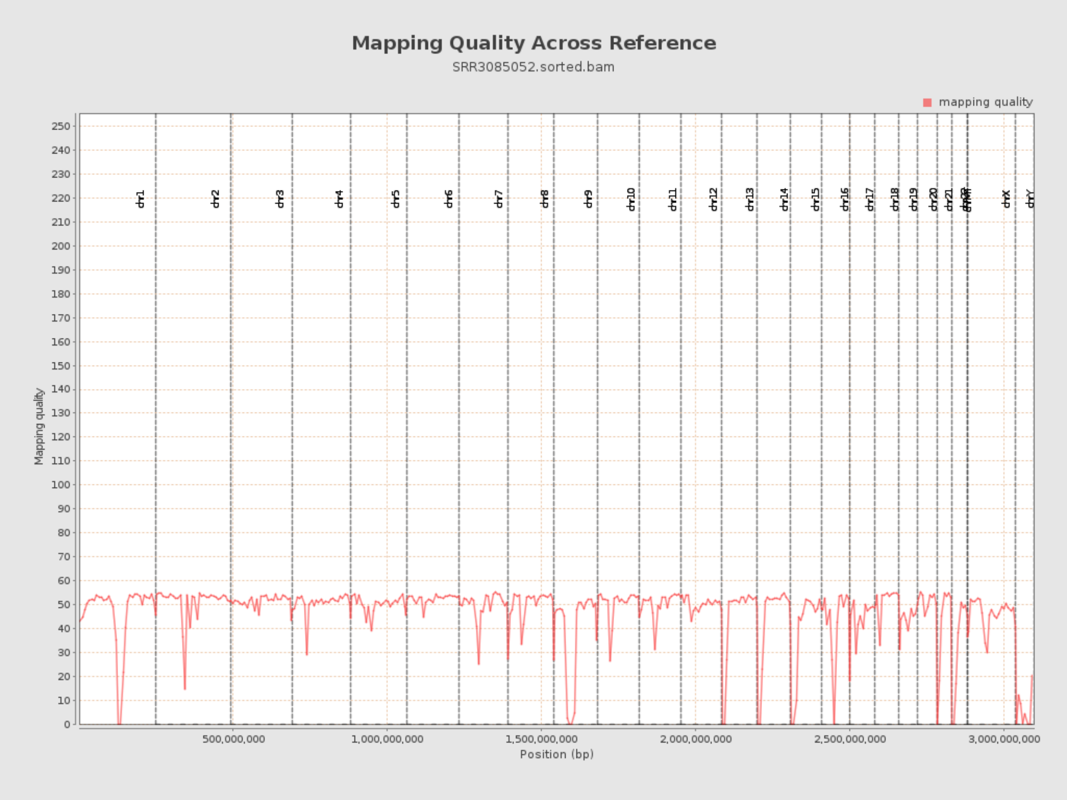
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram