# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 16:53:55*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525083.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_SRR10525083 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525083.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 16:53:54 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10525083.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 453,013 |
| Mapped reads | 388,715 / 85.81% |
| Unmapped reads | 64,298 / 14.19% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 1,485 / 0.33% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 10,547 / 2.33% |
| Duplication rate | 2.31% |
| Clipped reads | 389,035 / 85.88% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 5,980,018 / 26.03% |
| Number/percentage of C's | 4,349,340 / 18.93% |
| Number/percentage of T's | 6,959,122 / 30.29% |
| Number/percentage of G's | 5,683,351 / 24.74% |
| Number/percentage of N's | 2,692 / 0.01% |
| GC Percentage | 43.67% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0074 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1017 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.25 |

## 2.5. Mismatches and indels

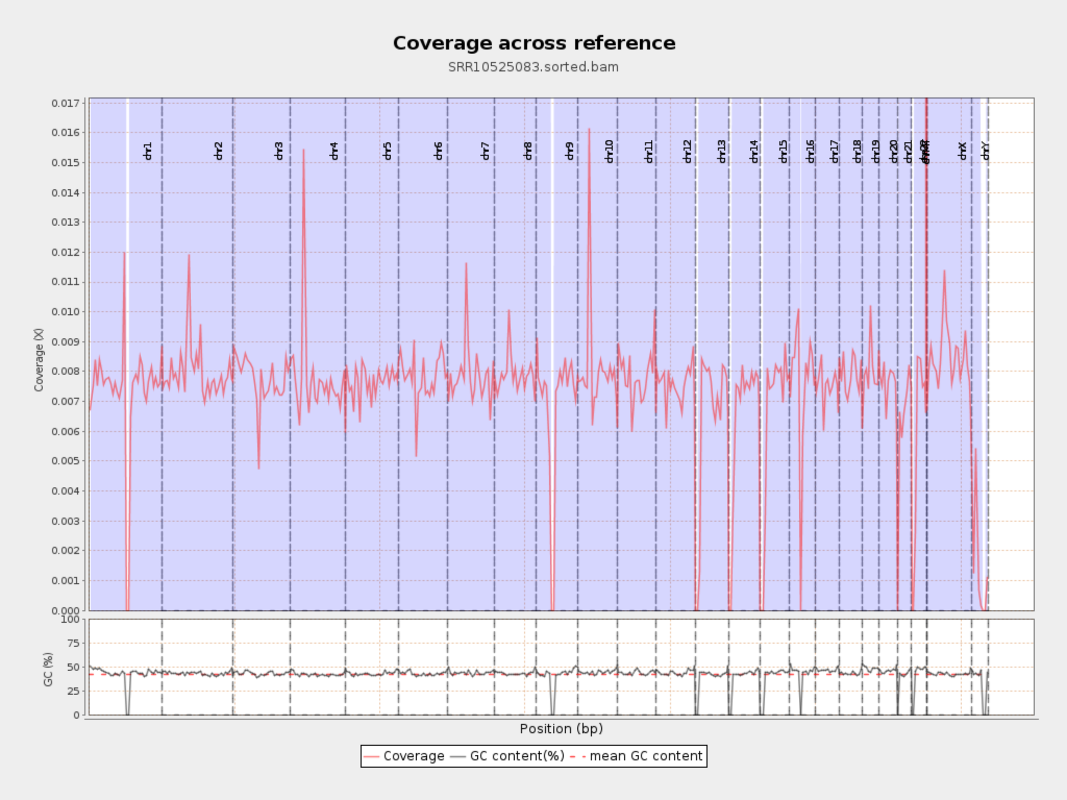
| | |
|---|---|
| General error rate | 0.49% |
| Mismatches | 107,924 |
| Insertions | 1,775 |
| Mapped reads with at least one insertion | 0.45% |
| Deletions | 4,490 |
| Mapped reads with at least one deletion | 1.15% |
| Homopolymer indels | 42.15% |

## 2.6. Chromosome stats

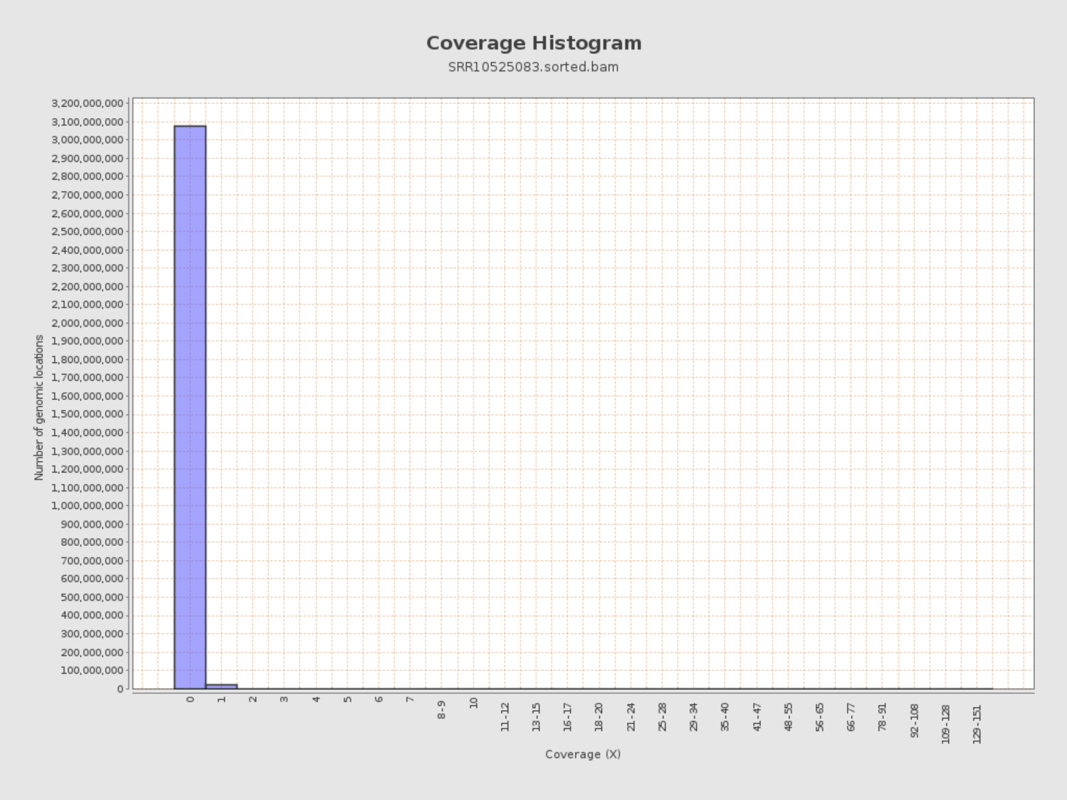
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 1819563 | 0.0073 | 0.1398 |
| chr2 | 243199373 | 1950457 | 0.008 | 0.1142 |
| chr3 | 198022430 | 1532690 | 0.0077 | 0.0916 |
| chr4 | 191154276 | 1485521 | 0.0078 | 0.0985 |
| chr5 | 180915260 | 1384486 | 0.0077 | 0.091 |
| chr6 | 171115067 | 1343232 | 0.0078 | 0.0943 |
| chr7 | 159138663 | 1255004 | 0.0079 | 0.1119 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1156812 | 0.0079 | 0.1038 |
| chr9 | 141213431 | 948409 | 0.0067 | 0.0905 |
| chr10 | 135534747 | 1103389 | 0.0081 | 0.1135 |
| chr11 | 135006516 | 1060722 | 0.0079 | 0.0958 |
| chr12 | 133851895 | 1015128 | 0.0076 | 0.0911 |
| chr13 | 115169878 | 729448 | 0.0063 | 0.083 |
| chr14 | 107349540 | 683657 | 0.0064 | 0.084 |
| chr15 | 102531392 | 656214 | 0.0064 | 0.0835 |
| chr16 | 90354753 | 684938 | 0.0076 | 0.0937 |
| chr17 | 81195210 | 607457 | 0.0075 | 0.0912 |
| chr18 | 78077248 | 617883 | 0.0079 | 0.1164 |
| chr19 | 59128983 | 476636 | 0.0081 | 0.1236 |
| chr20 | 63025520 | 478996 | 0.0076 | 0.0914 |
| chr21 | 48129895 | 305073 | 0.0063 | 0.0902 |
| chr22 | 51304566 | 281364 | 0.0055 | 0.077 |
| chrMT | 16571 | 2487 | 0.1501 | 0.3842 |
| chrX | 155270560 | 1318919 | 0.0085 | 0.0984 |
| chrY | 59373566 | 83385 | 0.0014 | 0.0594 |

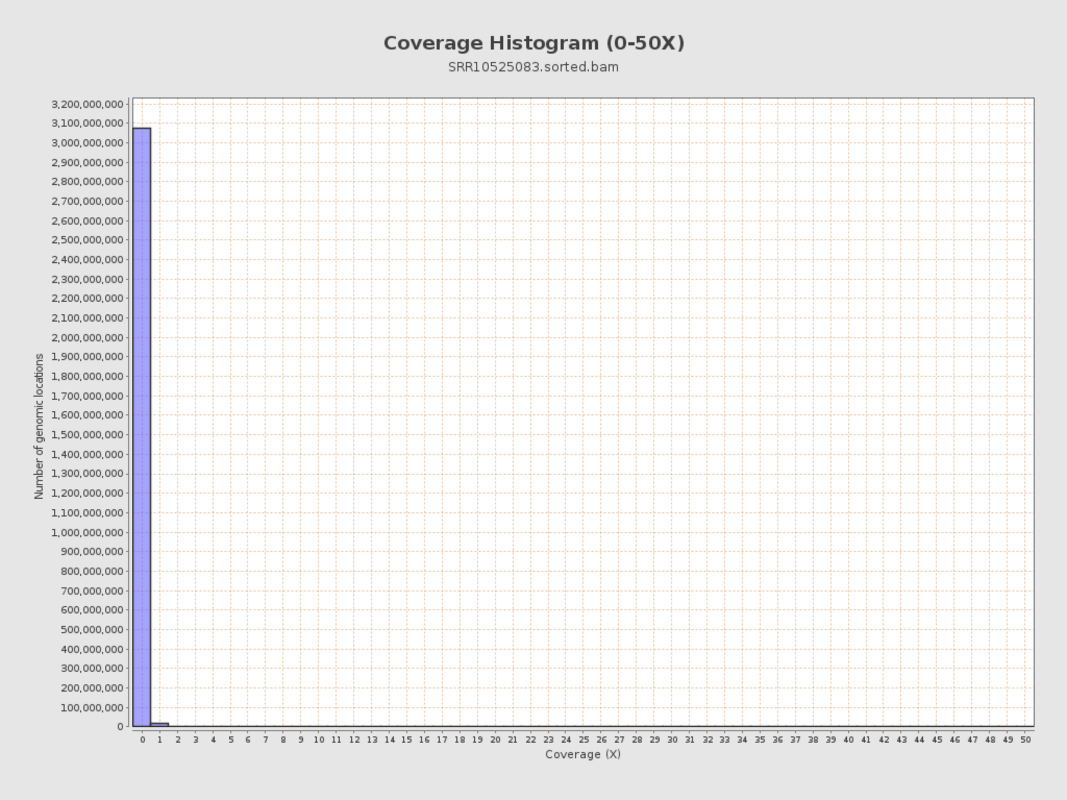
# 3. Results : Coverage across reference



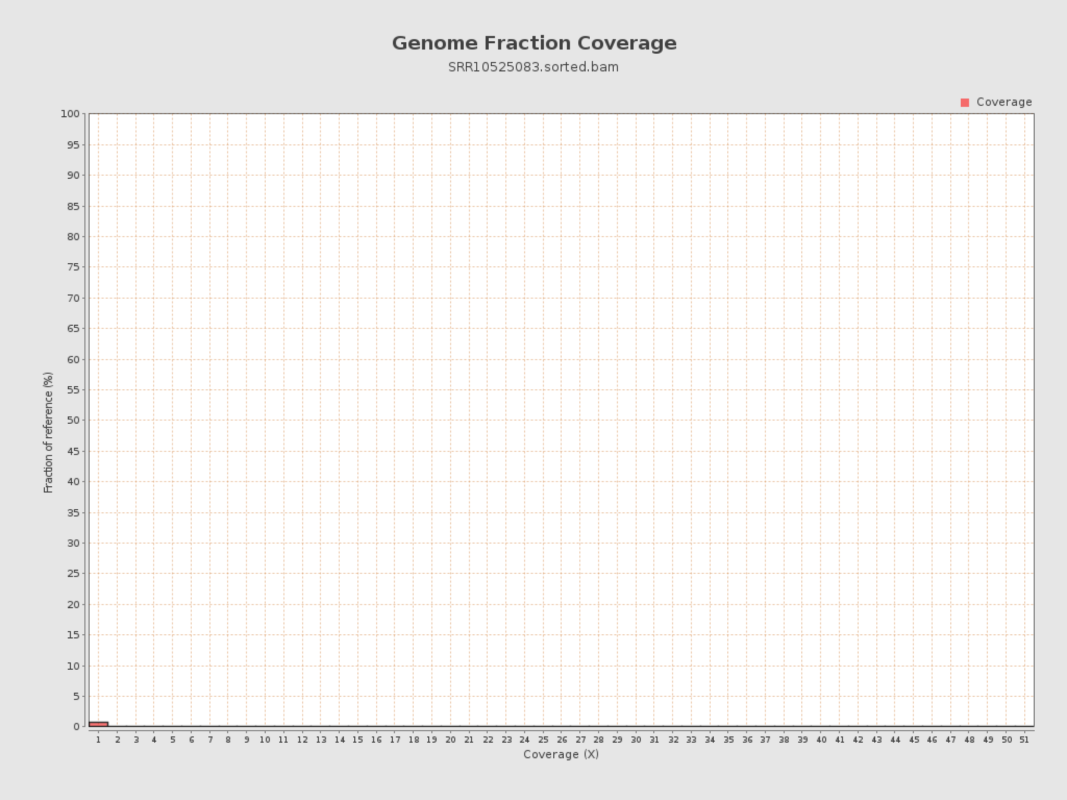
# 4. Results : Coverage Histogram



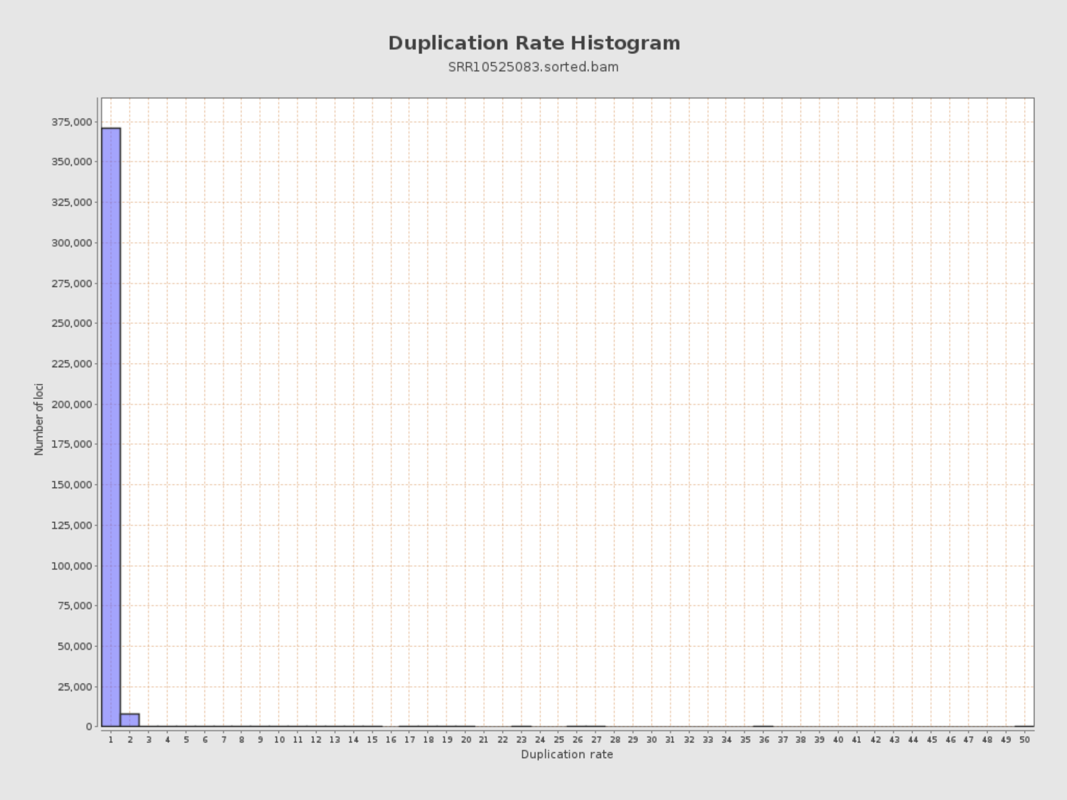
# 5. Results : Coverage Histogram (0-50X)



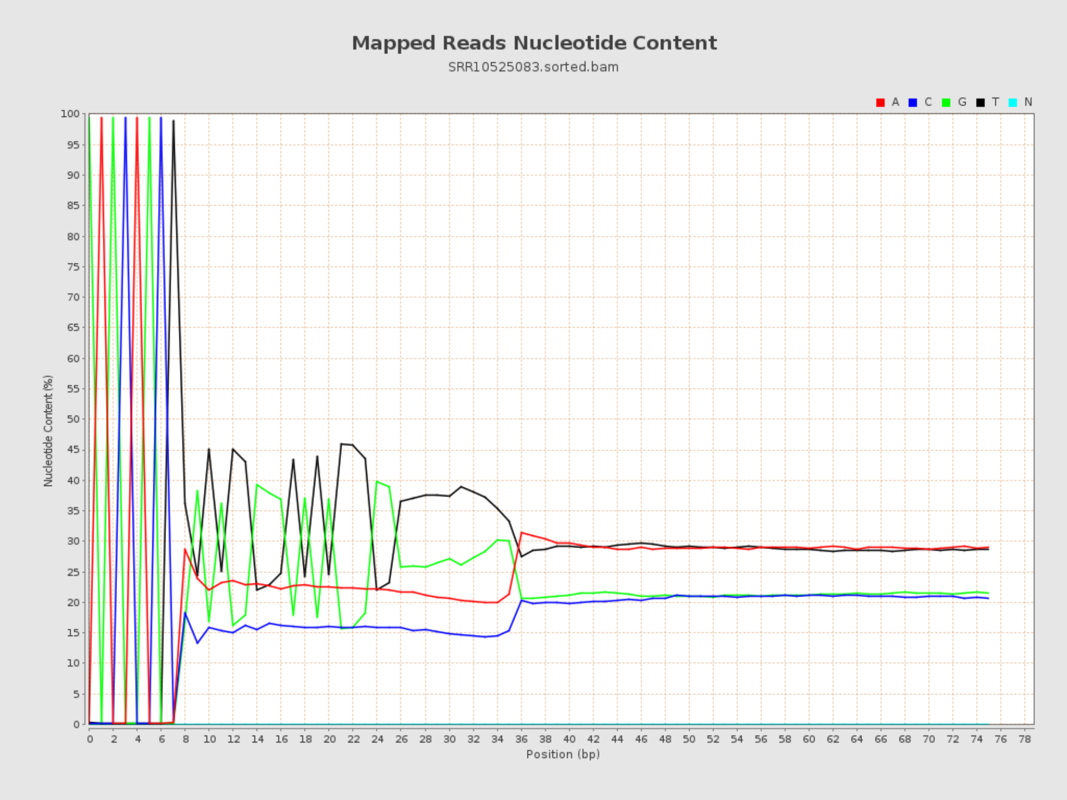
# 6. Results : Genome Fraction Coverage



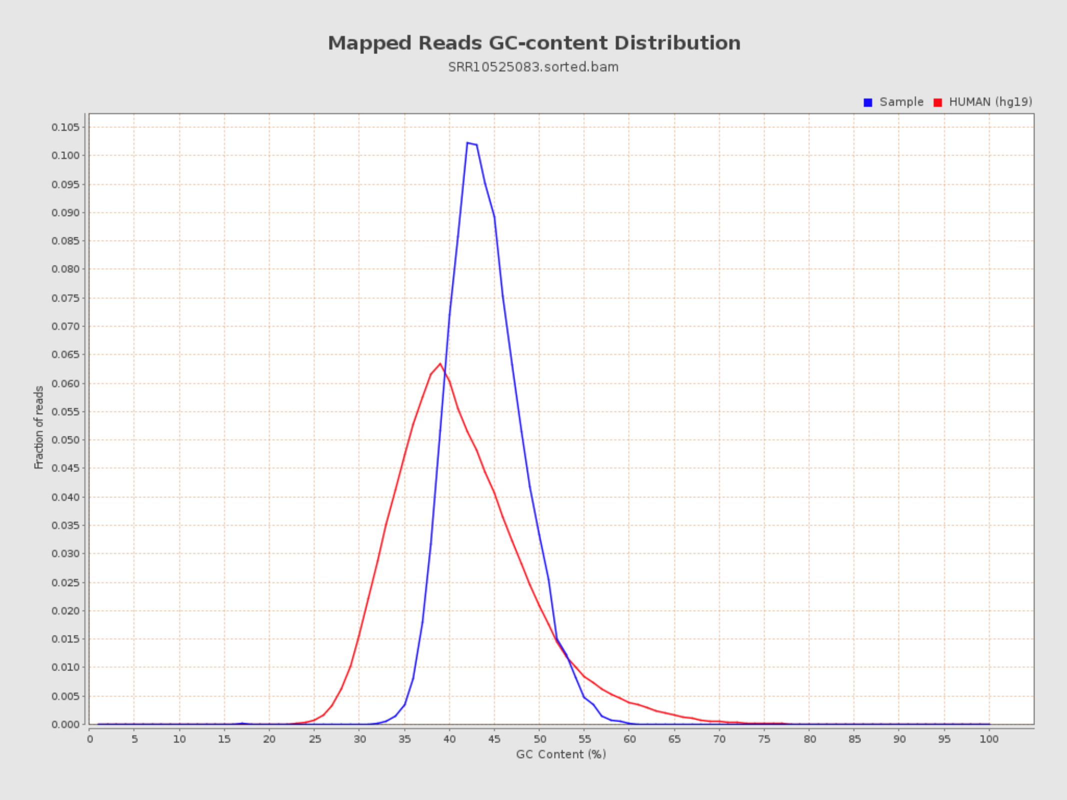
# 7. Results : Duplication Rate Histogram



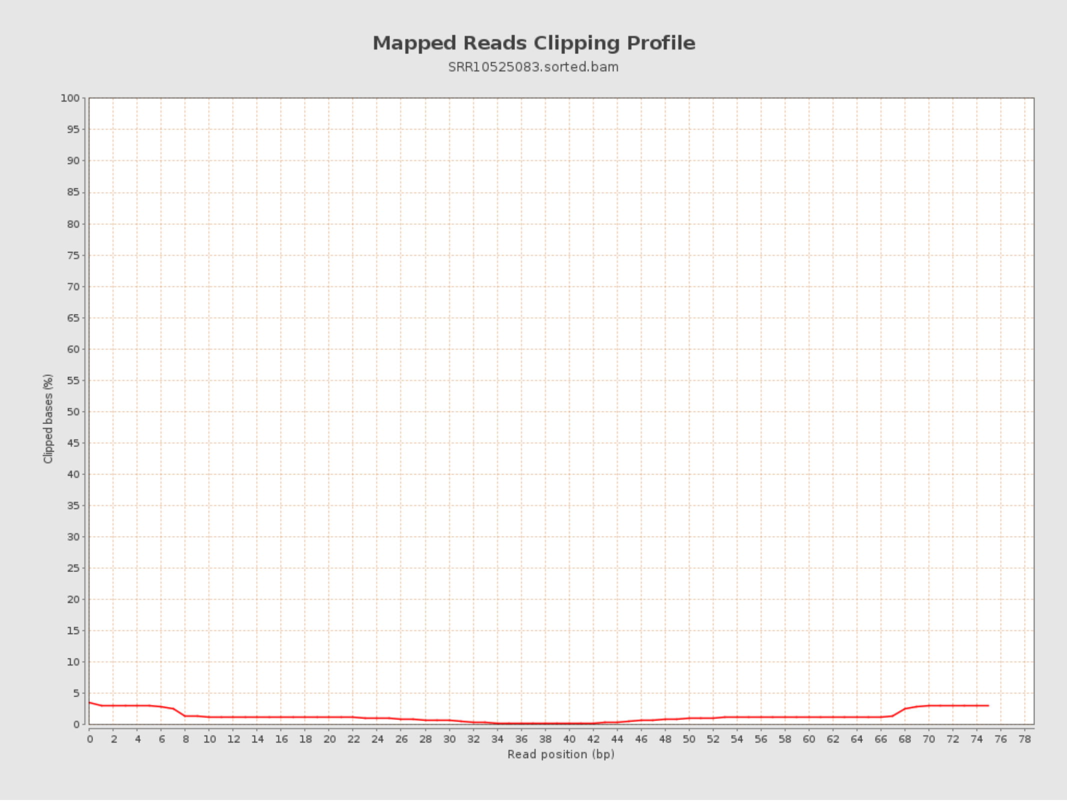
# 8. Results : Mapped Reads Nucleotide Content



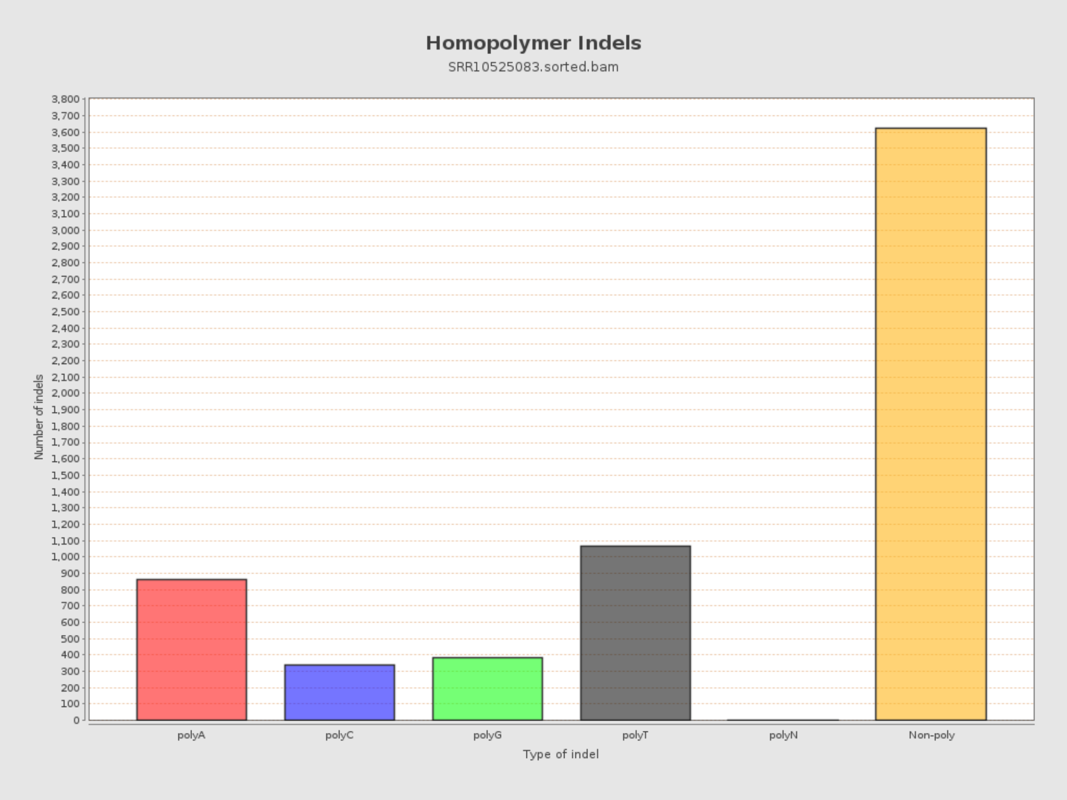
# 9. Results : Mapped Reads GC-content Distribution



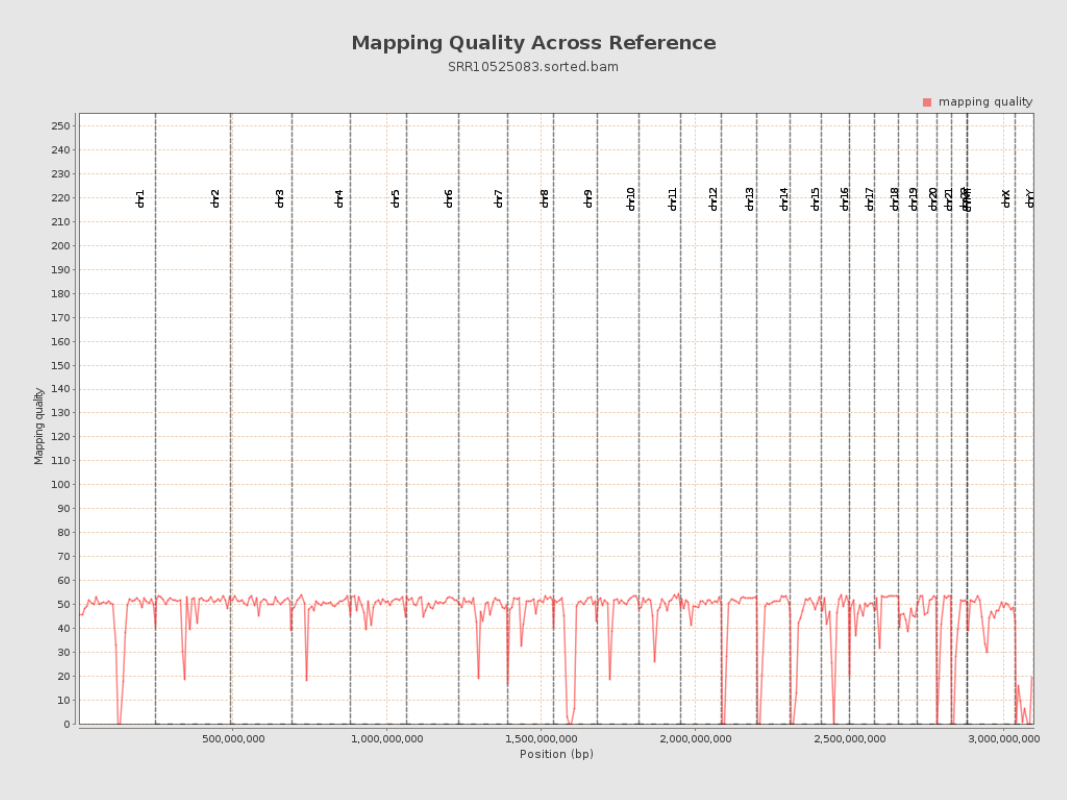
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram