# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/30 03:11:41*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR975233.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_SRR975233 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975233_1.fastq.gz SRR975233_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 30 03:11:16 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR975233.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,560,316 |
| Mapped reads | 4,528,313 / 99.3% |
| Unmapped reads | 32,003 / 0.7% |
| Mapped paired reads | 4,528,313 / 99.3% |
| Mapped reads, first in pair | 2,263,524 / 49.64% |
| Mapped reads, second in pair | 2,264,789 / 49.66% |
| Mapped reads, both in pair | 4,517,586 / 99.06% |
| Mapped reads, singletons | 10,727 / 0.24% |
| Secondary alignments | 0 |
| Supplementary alignments | 34,893 / 0.77% |
| Read min/max/mean length | 30 / 101 / 101.31 |
| Duplicated reads (estimated) | 181,872 / 3.99% |
| Duplication rate | 2.71% |
| Clipped reads | 2,663,054 / 58.4% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 122,954,410 / 28.96% |
| Number/percentage of C's | 87,729,393 / 20.66% |
| Number/percentage of T's | 122,553,270 / 28.86% |
| Number/percentage of G's | 91,385,534 / 21.52% |
| Number/percentage of N's | 6,275 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 42.18% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1372 |
| Standard Deviation | 0.9497 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.07 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 125,570.82 |
| Standard Deviation | 3,453,516.8 |
| P25/Median/P75 | 140 / 174 / 221 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.75% |
| Mismatches | 3,065,492 |
| Insertions | 71,637 |
| Mapped reads with at least one insertion | 1.55% |
| Deletions | 140,419 |
| Mapped reads with at least one deletion | 3.04% |
| Homopolymer indels | 46.13% |

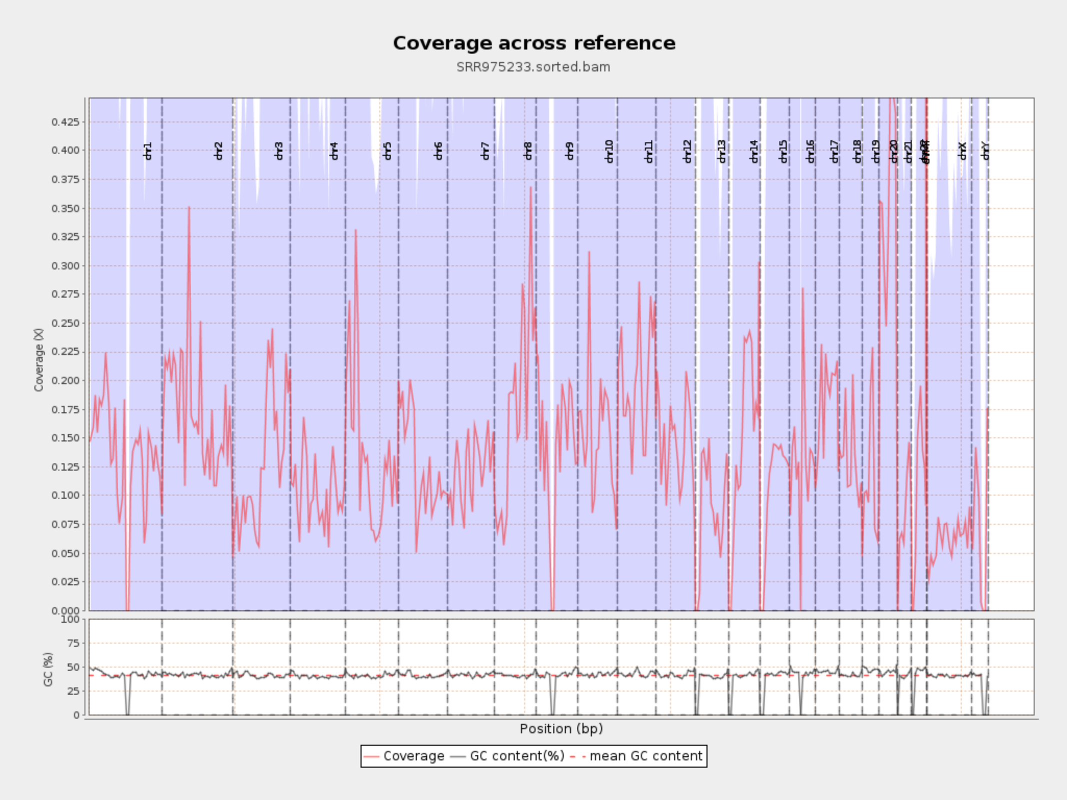
## 2.7. Chromosome stats

| **Name** | **Length** | **Mapped** | **Mean** | **Standard** |
|---|---|---|---|---|

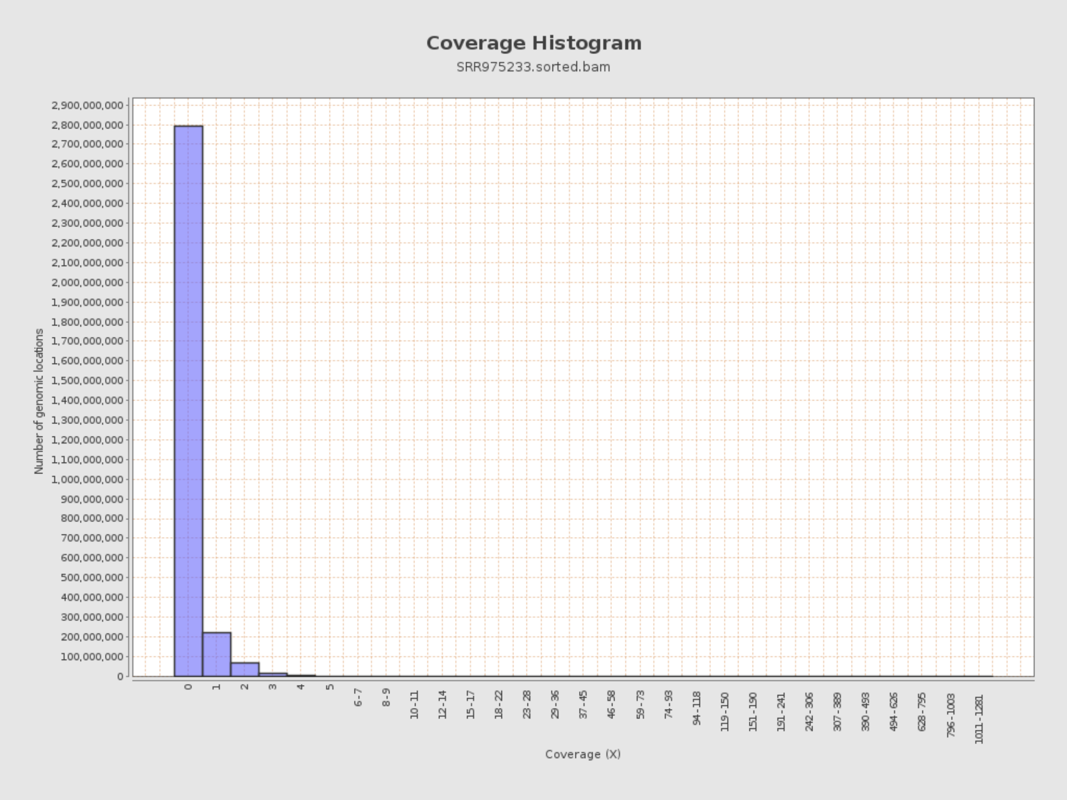
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 33174054 | 0.1331 | 1.3585 |
| chr2 | 243199373 | 42502417 | 0.1748 | 1.3855 |
| chr3 | 198022430 | 25170768 | 0.1271 | 0.4521 |
| chr4 | 191154276 | 19370868 | 0.1013 | 0.7209 |
| chr5 | 180915260 | 24587904 | 0.1359 | 0.4747 |
| chr6 | 171115067 | 21757828 | 0.1272 | 0.5663 |
| chr7 | 159138663 | 19665932 | 0.1236 | 0.8514 |
| chr8 | 146364022 | 25749324 | 0.1759 | 0.6268 |
| chr9 | 141213431 | 19622885 | 0.139 | 1.3362 |
| chr10 | 135534747 | 20698337 | 0.1527 | 1.7021 |
| chr11 | 135006516 | 26908336 | 0.1993 | 0.828 |
| chr12 | 133851895 | 19697659 | 0.1472 | 0.4795 |
| chr13 | 115169878 | 9839747 | 0.0854 | 0.3576 |
| chr14 | 107349540 | 15788968 | 0.1471 | 0.5047 |
| chr15 | 102531392 | 10851517 | 0.1058 | 0.4016 |
| chr16 | 90354753 | 11671025 | 0.1292 | 1.201 |
| chr17 | 81195210 | 14815611 | 0.1825 | 1.5943 |
| chr18 | 78077248 | 10471735 | 0.1341 | 1.1648 |
| chr19 | 59128983 | 6935800 | 0.1173 | 0.6998 |
| chr20 | 63025520 | 22560219 | 0.358 | 0.82 |
| chr21 | 48129895 | 3992587 | 0.083 | 0.4255 |
| chr22 | 51304566 | 5204917 | 0.1015 | 0.4112 |
| chrMT | 16571 | 99812 | 6.0233 | 3.9502 |
| chrX | 155270560 | 9584134 | 0.0617 | 0.3779 |

|  |  |  |  |  |
|---|---|---|---|---|
| chrY | 59373566 | 4146474 | 0.0698 | 1.0792 |

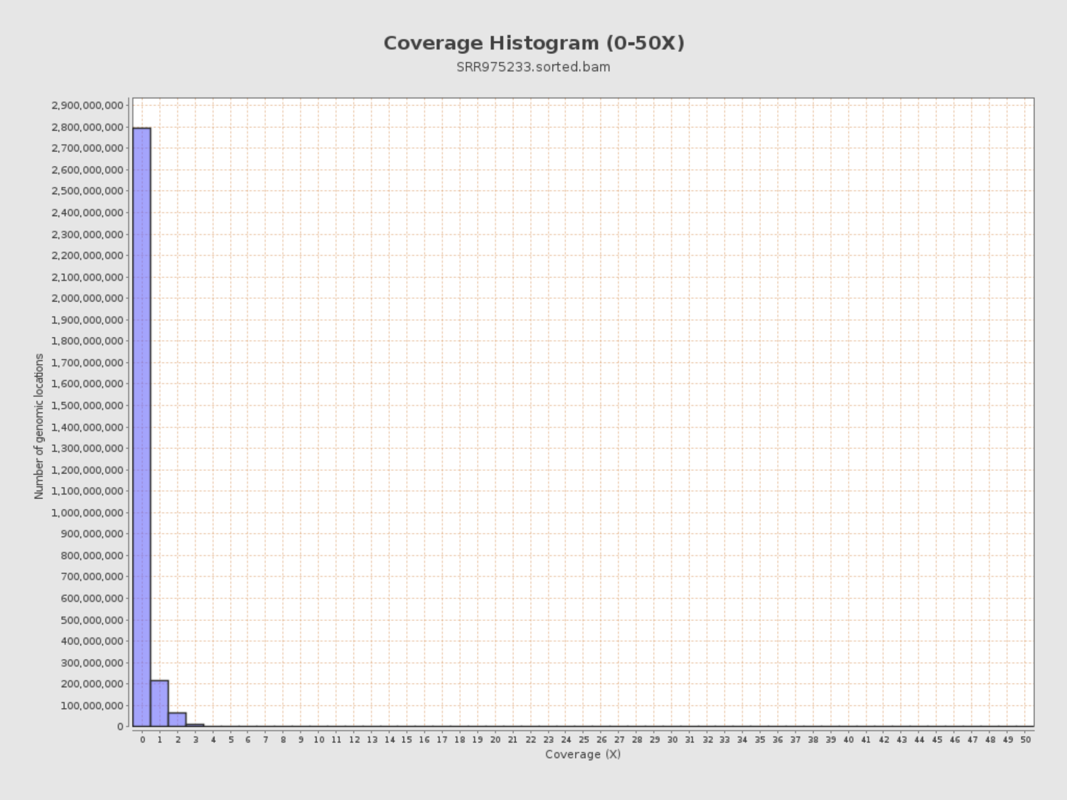
# 3. Results : Coverage across reference



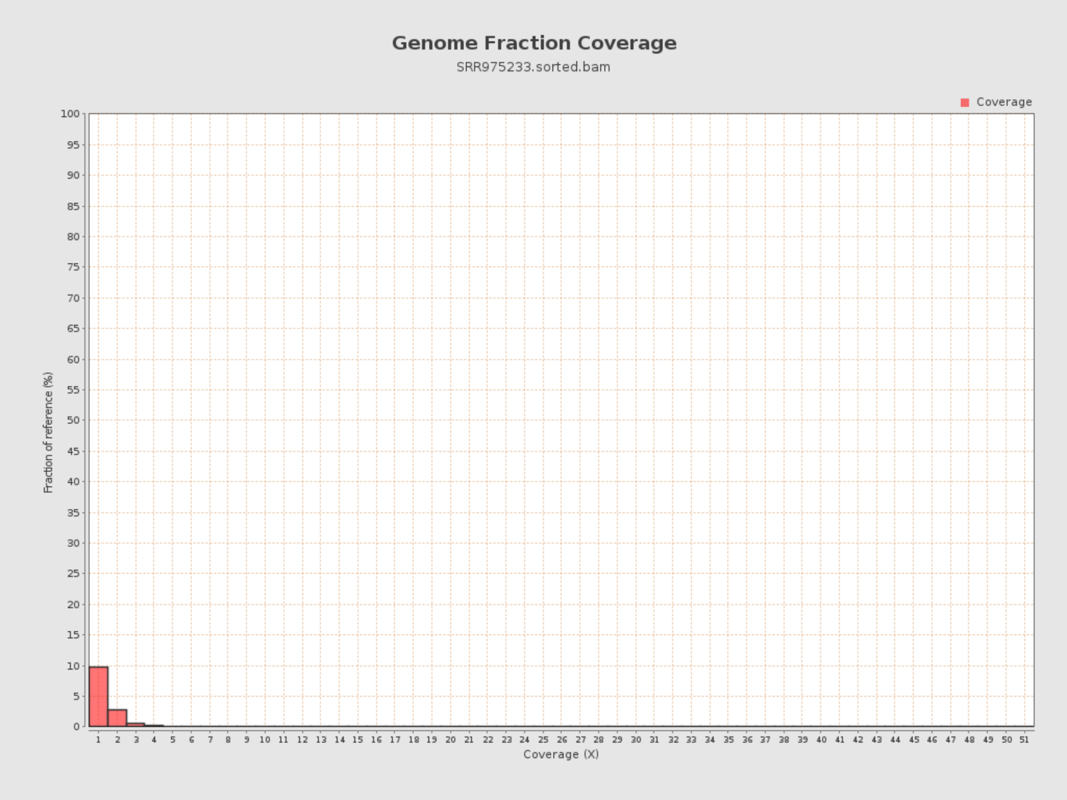
# 4. Results : Coverage Histogram



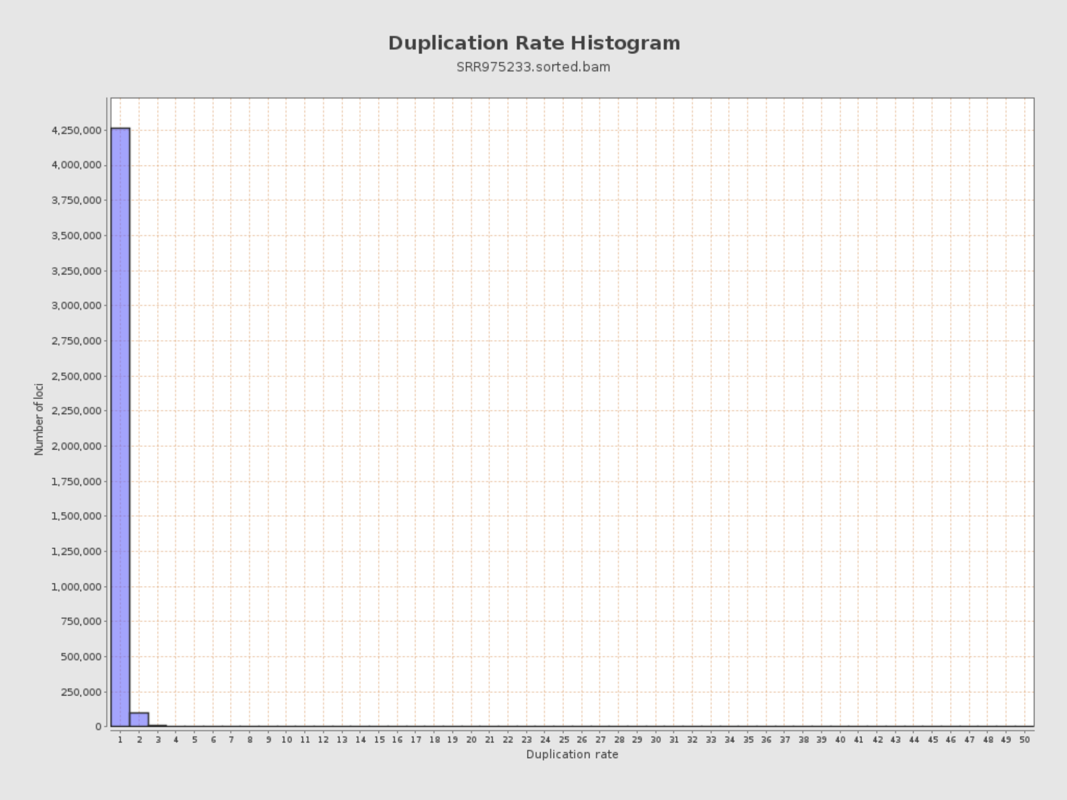
# 5. Results : Coverage Histogram (0-50X)



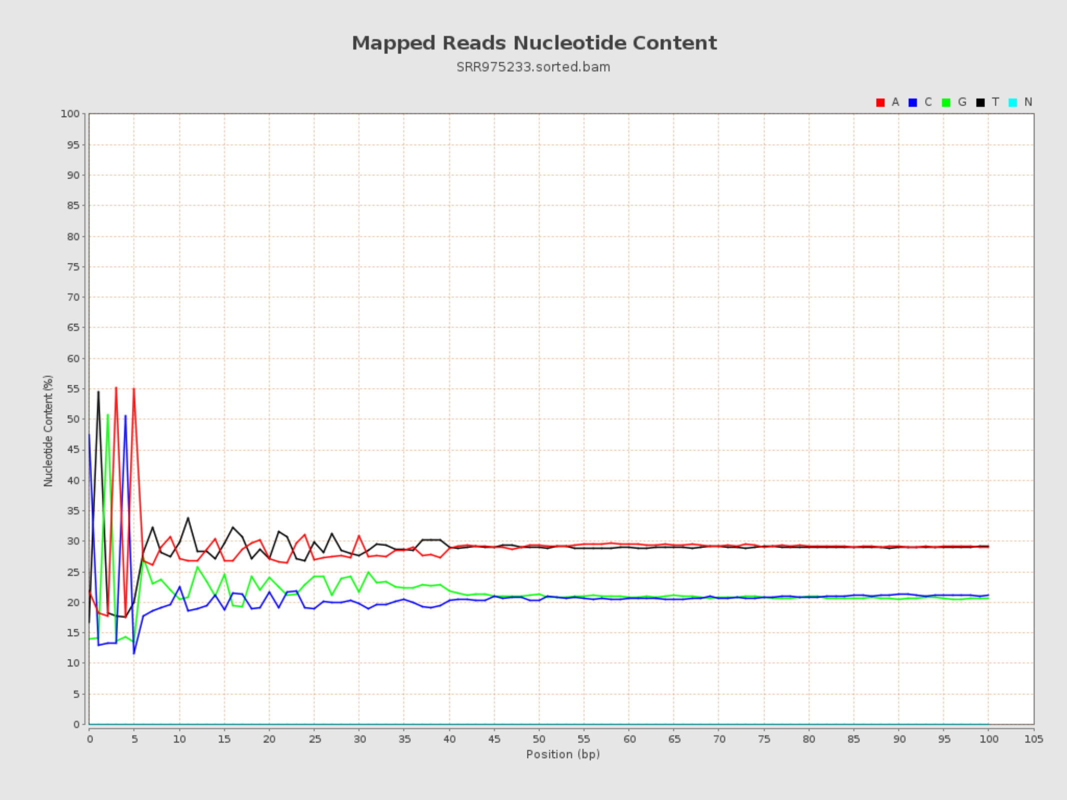
# 6. Results : Genome Fraction Coverage



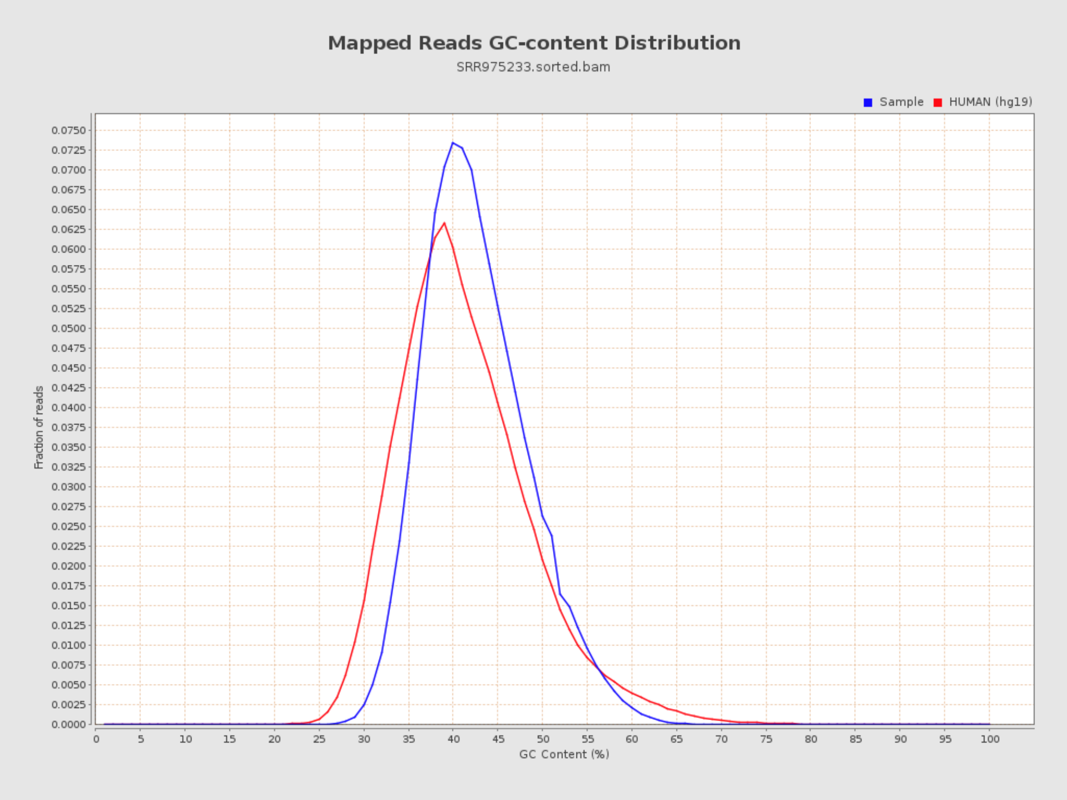
# 7. Results : Duplication Rate Histogram



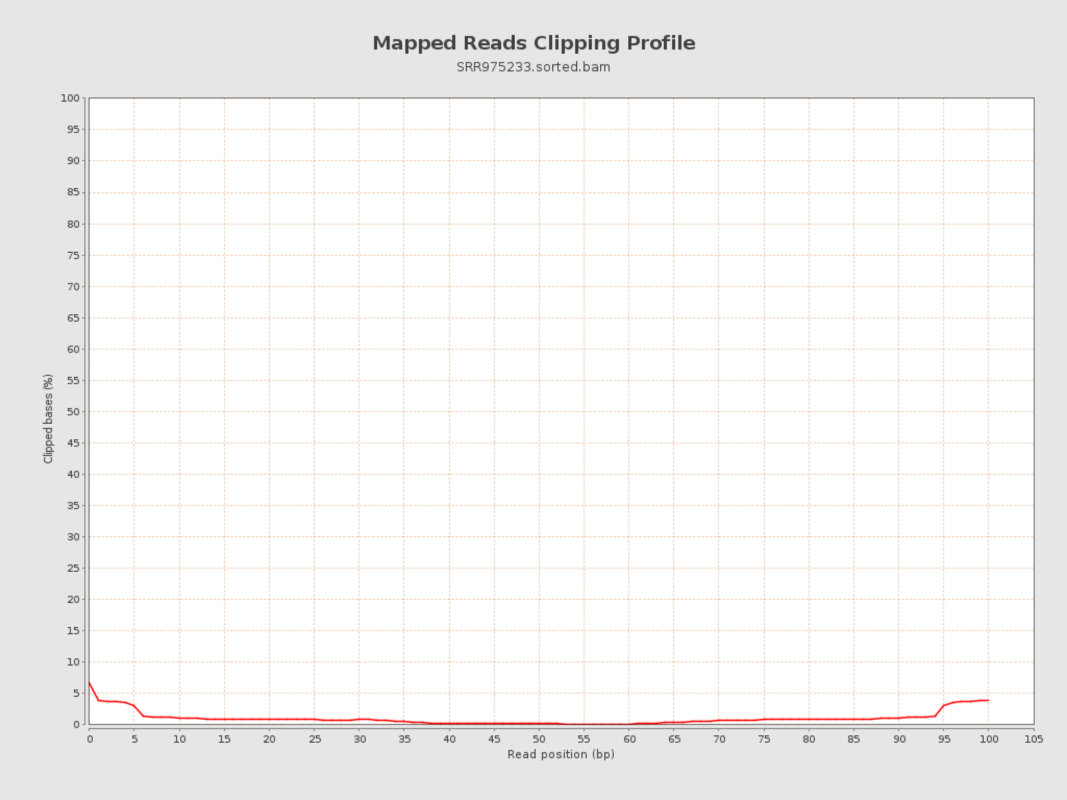
# 8. Results : Mapped Reads Nucleotide Content



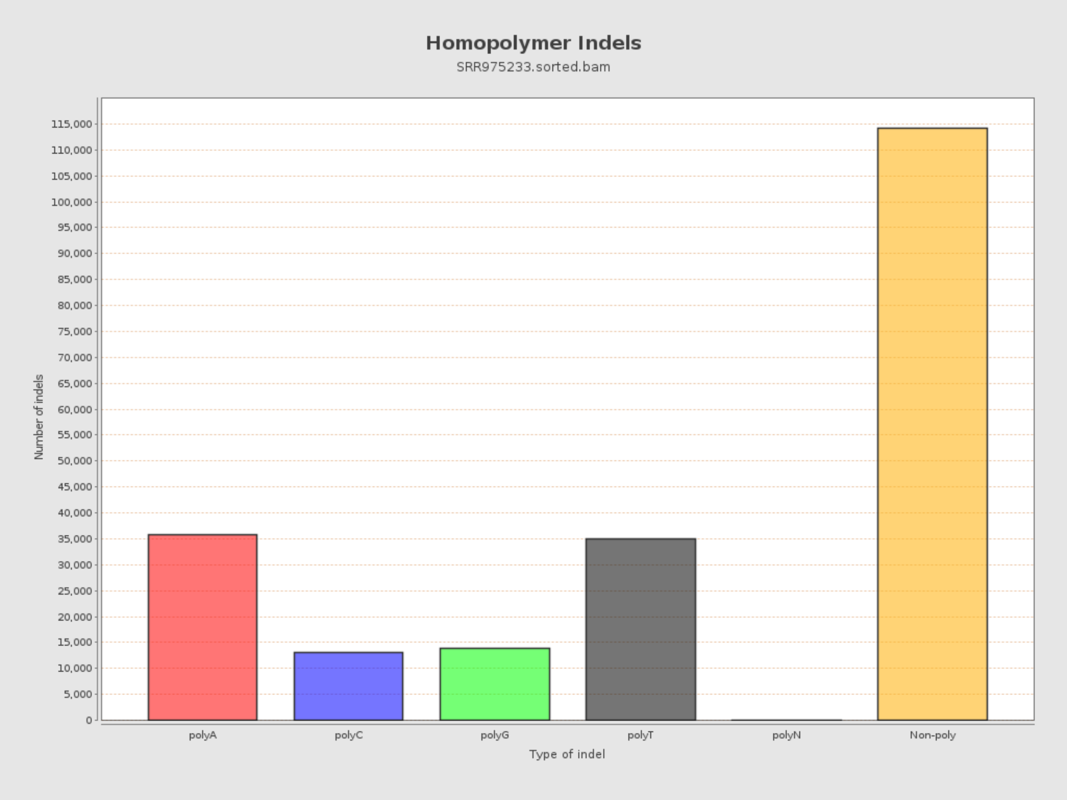
# 9. Results : Mapped Reads GC-content Distribution



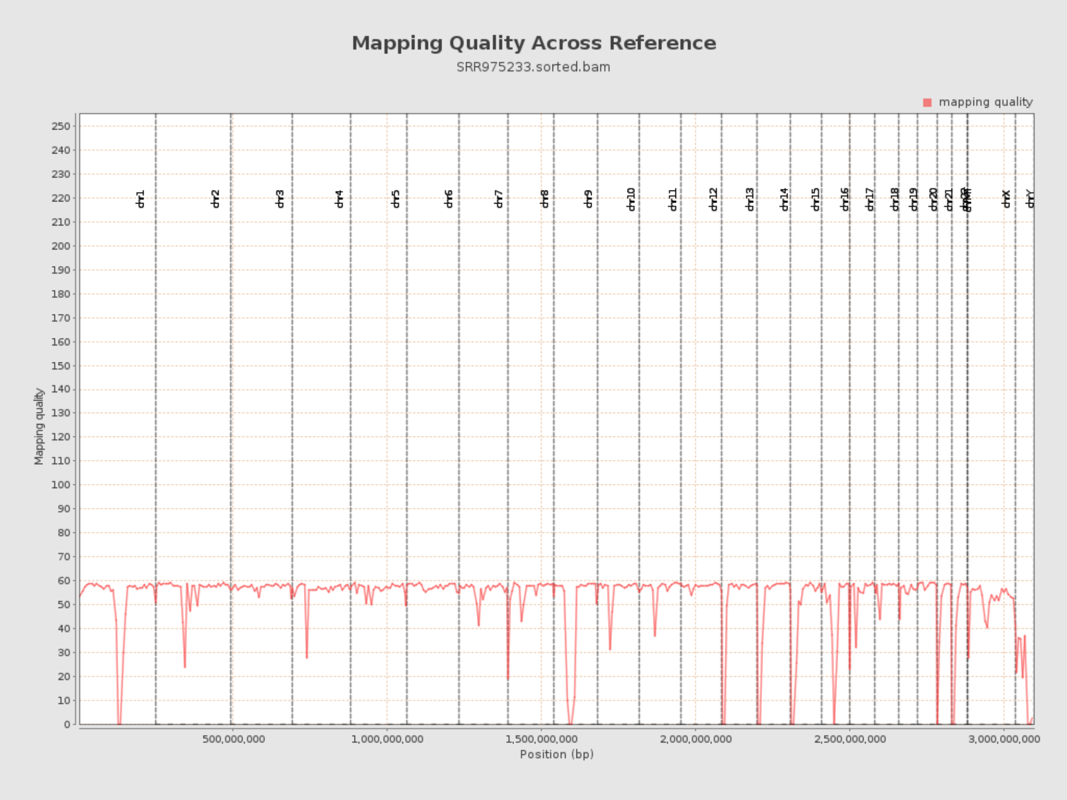
# 10. Results : Mapped Reads Clipping Profile



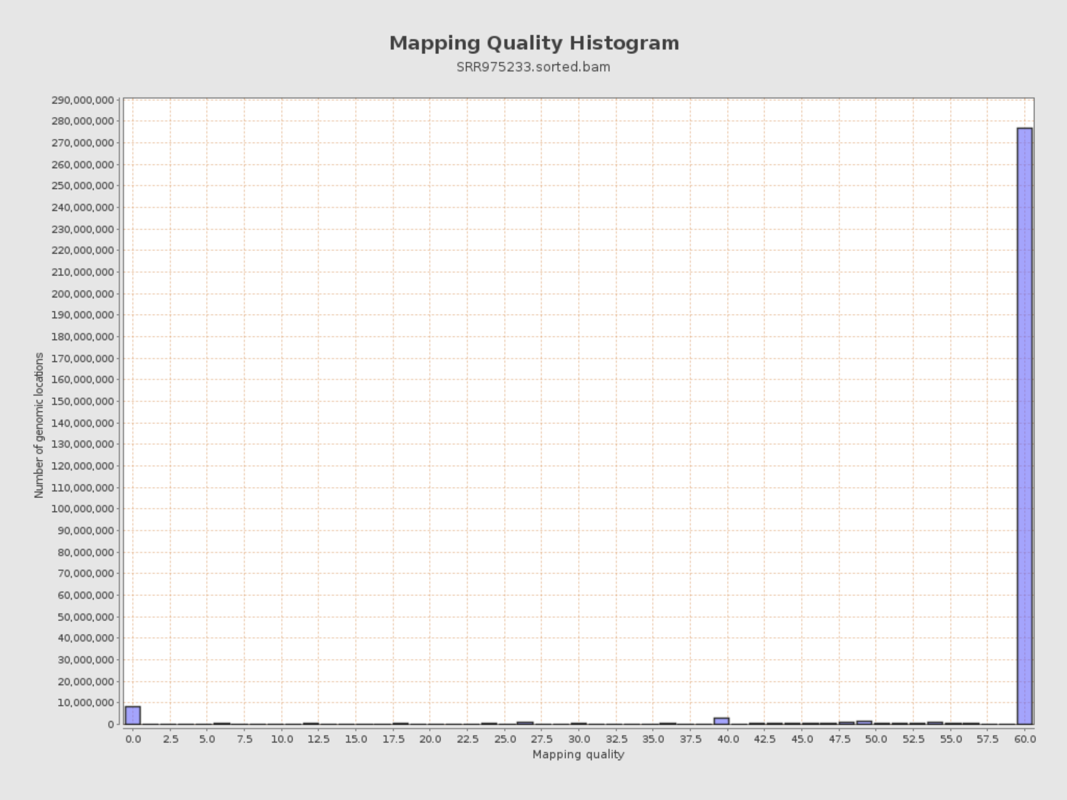
# 11. Results : Homopolymer Indels



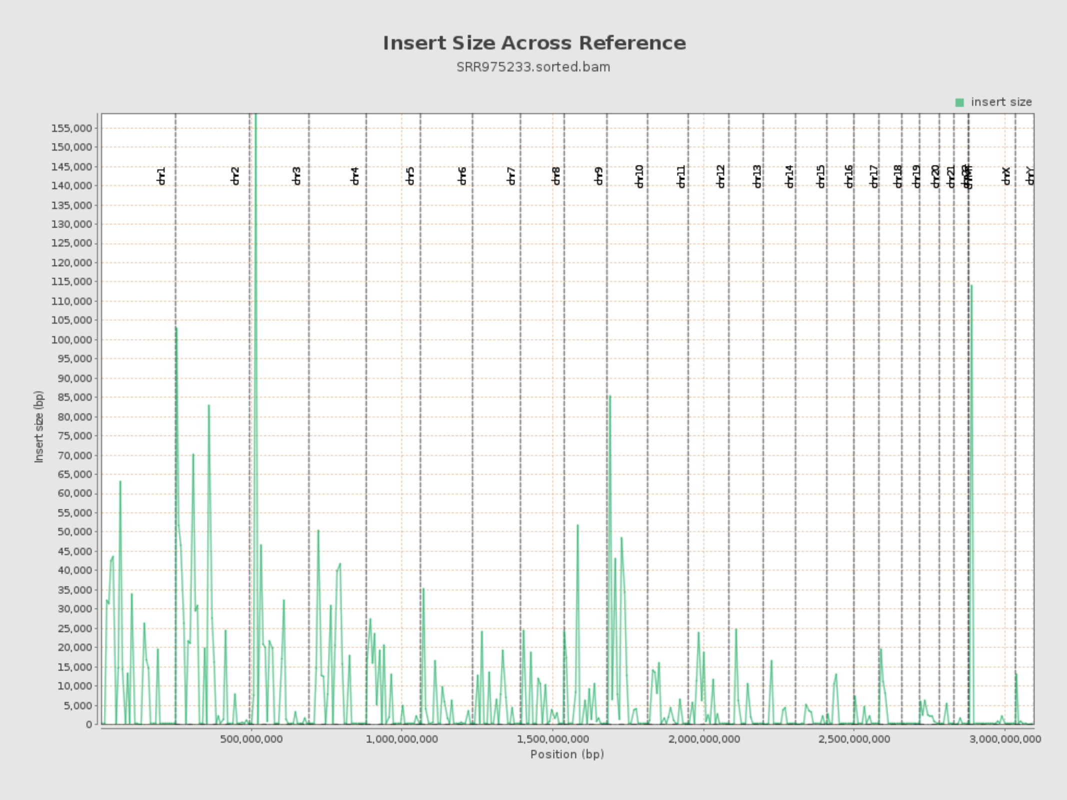
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram