# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 06:55:21*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR975202.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_SRR975202 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975202_1.fastq.gz SRR975202_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 06:55:13 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR975202.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 51,961,912 |
| Mapped reads | 51,829,191 / 99.74% |
| Unmapped reads | 132,721 / 0.26% |
| Mapped paired reads | 51,829,191 / 99.74% |
| Mapped reads, first in pair | 25,910,878 / 49.87% |
| Mapped reads, second in pair | 25,918,313 / 49.88% |
| Mapped reads, both in pair | 51,747,190 / 99.59% |
| Mapped reads, singletons | 82,001 / 0.16% |
| Secondary alignments | 0 |
| Supplementary alignments | 115,719 / 0.22% |
| Read min/max/mean length | 30 / 101 / 101.09 |
| Duplicated reads (estimated) | 34,923,264 / 67.21% |
| Duplication rate | 47.2% |
| Clipped reads | 30,542,075 / 58.78% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 1,324,892,902 / 27.04% |
| Number/percentage of C's | 1,082,980,533 / 22.1% |
| Number/percentage of T's | 1,347,597,163 / 27.5% |
| Number/percentage of G's | 1,143,994,389 / 23.35% |
| Number/percentage of N's | 248,460 / 0.01% |
| | |

| | |
|---|---|
| GC Percentage | 45.45% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 1.5833 |
| Standard Deviation | 28.1355 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 55.79 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 159,737.31 |
| Standard Deviation | 3,942,628.02 |
| P25/Median/P75 | 190 / 234 / 284 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.62% |
| Mismatches | 29,576,419 |
| Insertions | 573,495 |
| Mapped reads with at least one insertion | 1.09% |
| Deletions | 1,158,442 |
| Mapped reads with at least one deletion | 2.2% |
| Homopolymer indels | 44.75% |

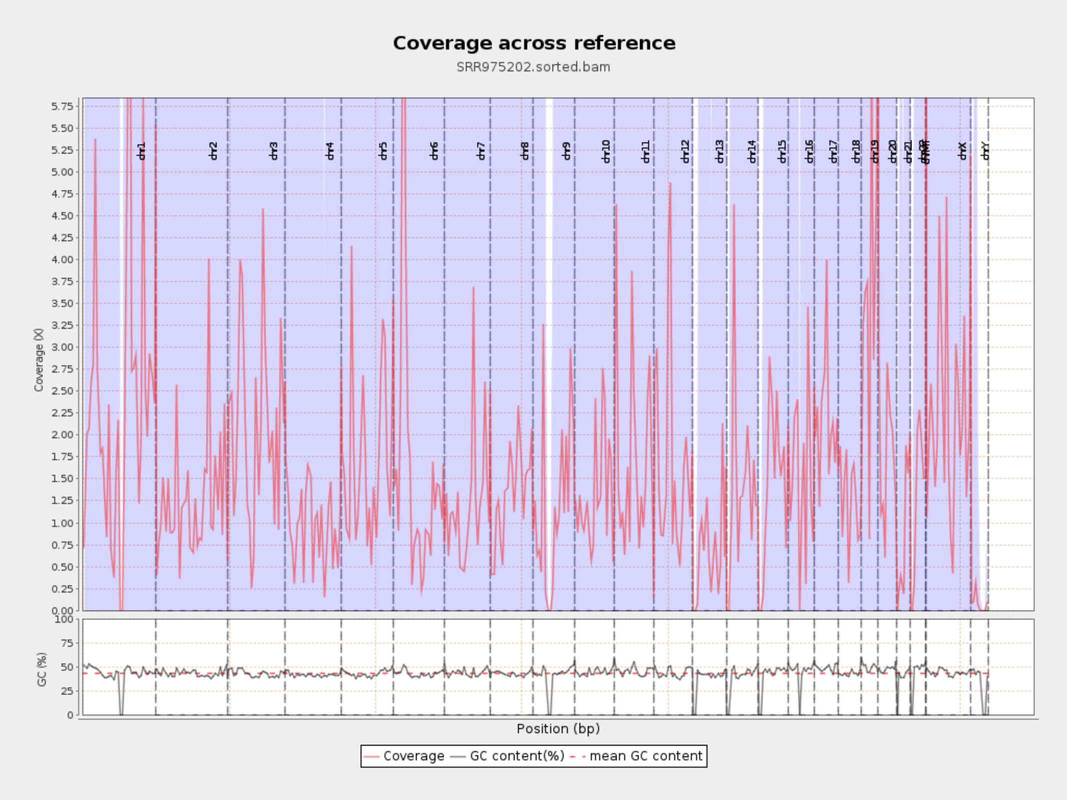
## 2.7. Chromosome stats

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

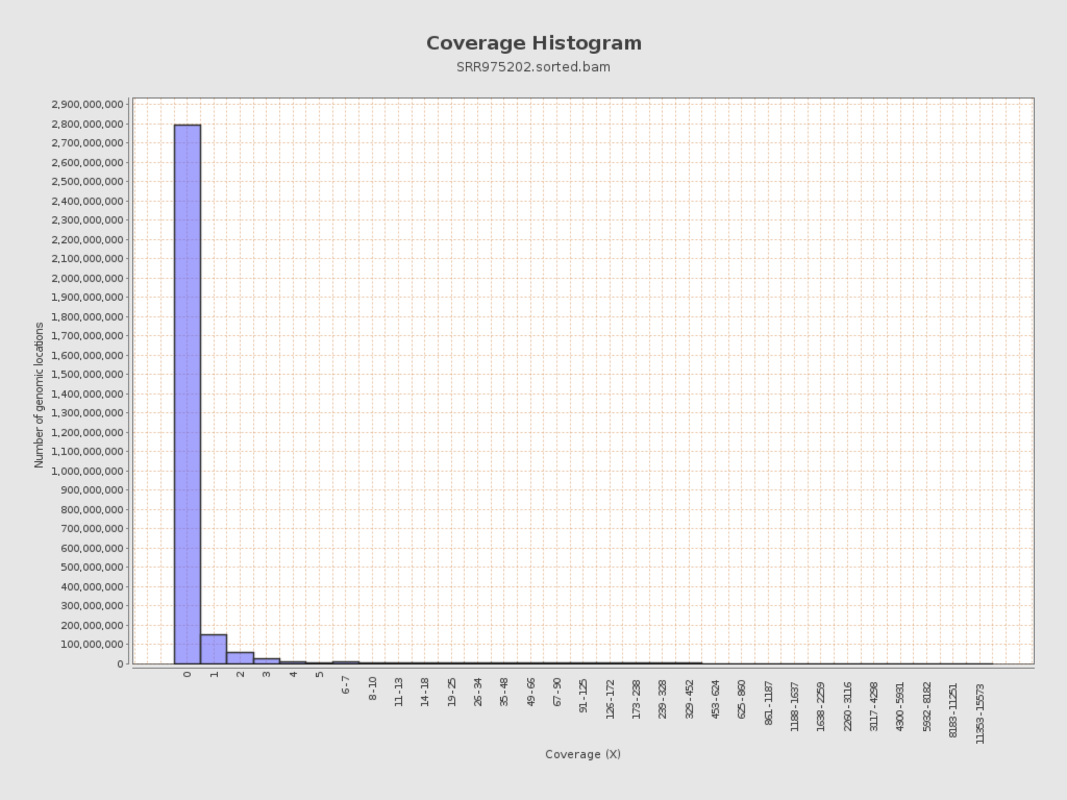
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 610566933 | 2.4496 | 36.5186 |
| chr2 | 243199373 | 309181077 | 1.2713 | 21.6215 |
| chr3 | 198022430 | 412050611 | 2.0808 | 32.9049 |
| chr4 | 191154276 | 182877025 | 0.9567 | 18.8453 |
| chr5 | 180915260 | 318026656 | 1.7579 | 29.7586 |
| chr6 | 171115067 | 280365286 | 1.6385 | 30.6439 |
| chr7 | 159138663 | 193288202 | 1.2146 | 23.2672 |
| chr8 | 146364022 | 196257121 | 1.3409 | 23.7754 |
| chr9 | 141213431 | 165916866 | 1.1749 | 24.5128 |
| chr10 | 135534747 | 182503083 | 1.3465 | 22.2043 |
| chr11 | 135006516 | 235020182 | 1.7408 | 29.2032 |
| chr12 | 133851895 | 234897720 | 1.7549 | 28.1864 |
| chr13 | 115169878 | 77970228 | 0.677 | 16.0369 |
| chr14 | 107349540 | 154439022 | 1.4387 | 24.1349 |
| chr15 | 102531392 | 140041124 | 1.3658 | 24.718 |
| chr16 | 90354753 | 134634619 | 1.4901 | 24.4057 |
| chr17 | 81195210 | 178538117 | 2.1989 | 33.6112 |
| chr18 | 78077248 | 100206926 | 1.2834 | 23.6803 |
| chr19 | 59128983 | 223377378 | 3.7778 | 57.6317 |
| chr20 | 63025520 | 110800830 | 1.758 | 28.8985 |
| chr21 | 48129895 | 42668919 | 0.8865 | 20.5419 |
| chr22 | 51304566 | 65650491 | 1.2796 | 23.9576 |
| chrMT | 16571 | 596569 | 36.0008 | 42.3205 |
| chrX | 155270560 | 346717136 | 2.233 | 37.1359 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 4916736 | 0.0828 | 4.2977 |

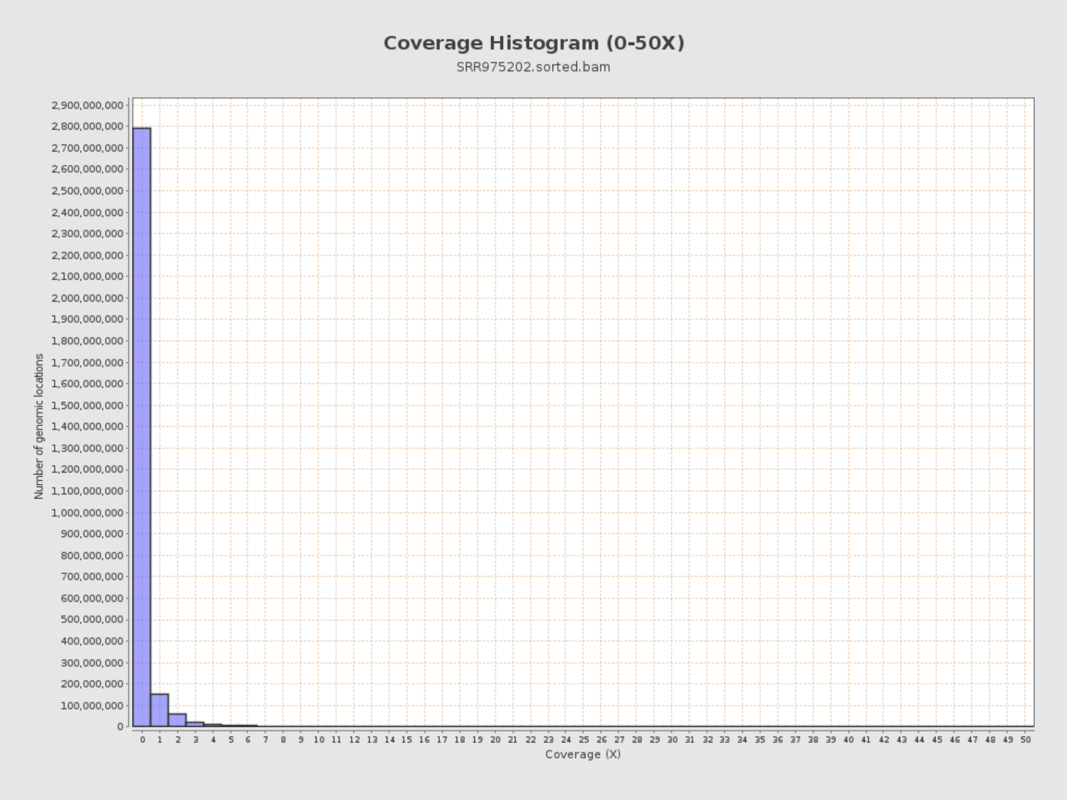
# 3. Results : Coverage across reference



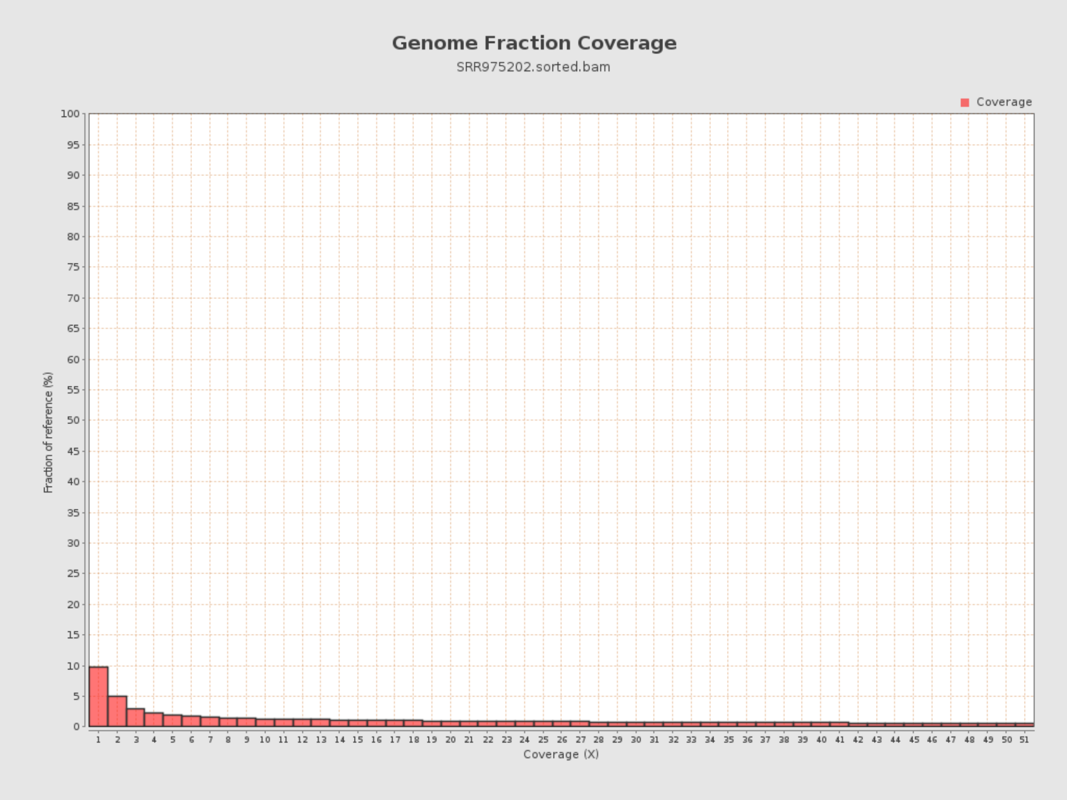
# 4. Results : Coverage Histogram



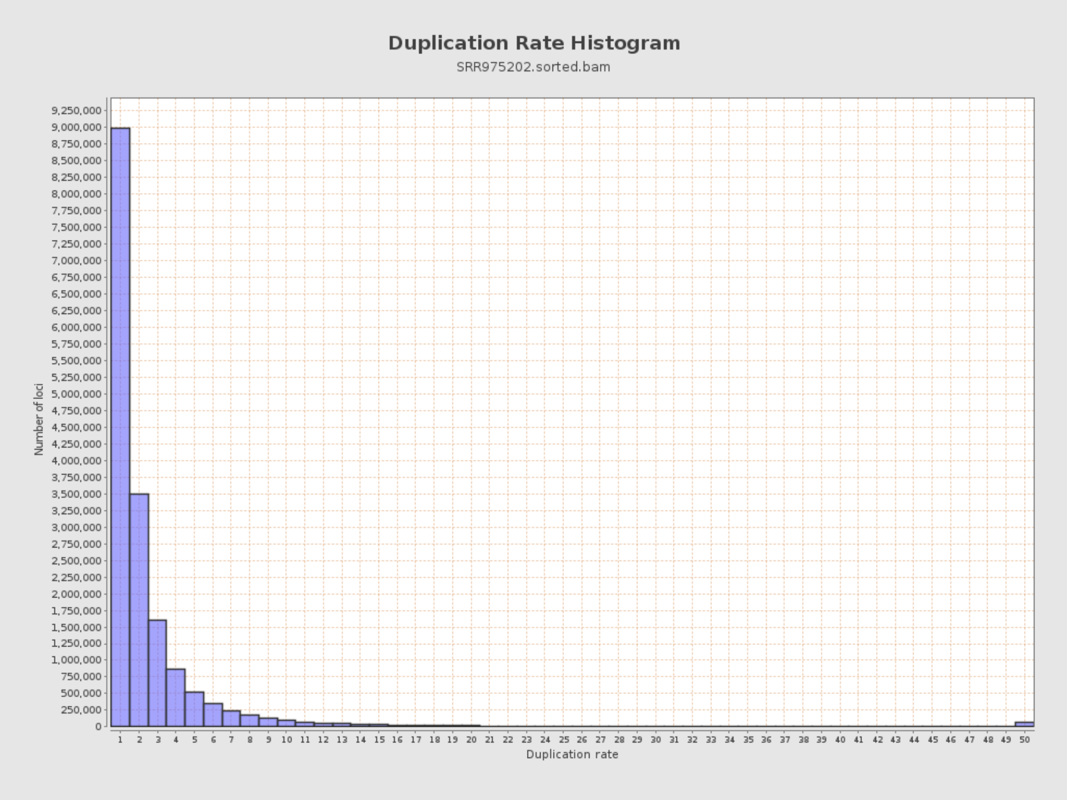
# 5. Results : Coverage Histogram (0-50X)



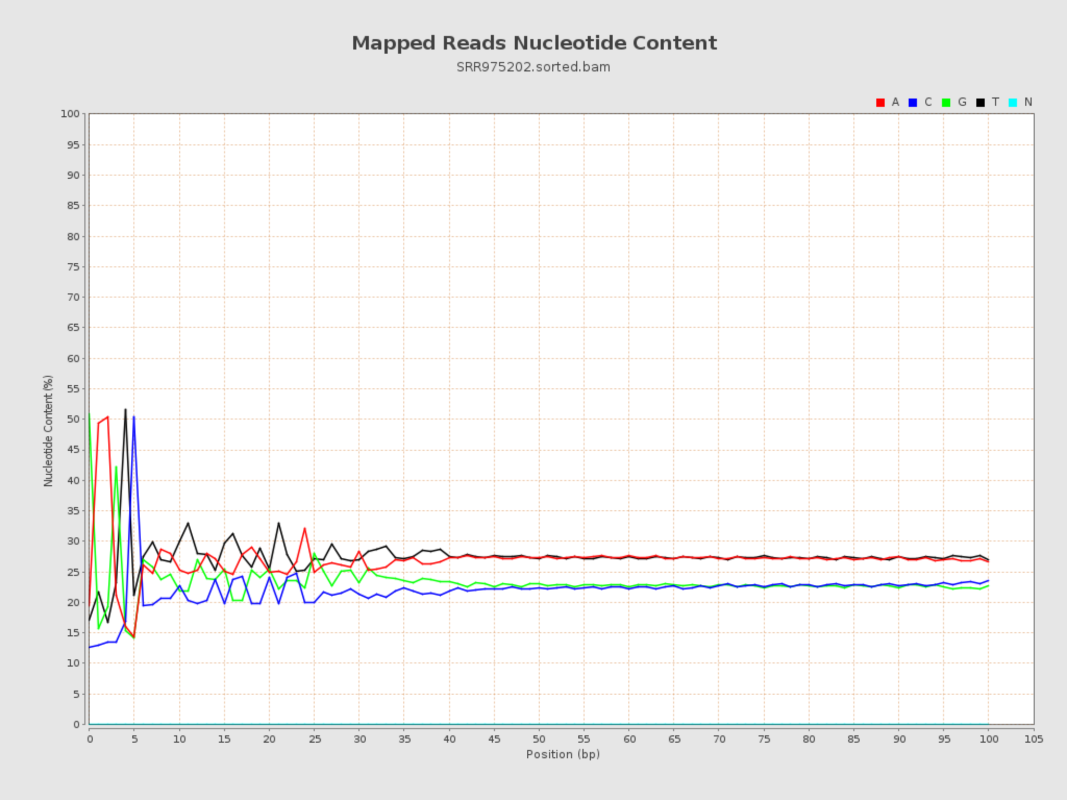
# 6. Results : Genome Fraction Coverage



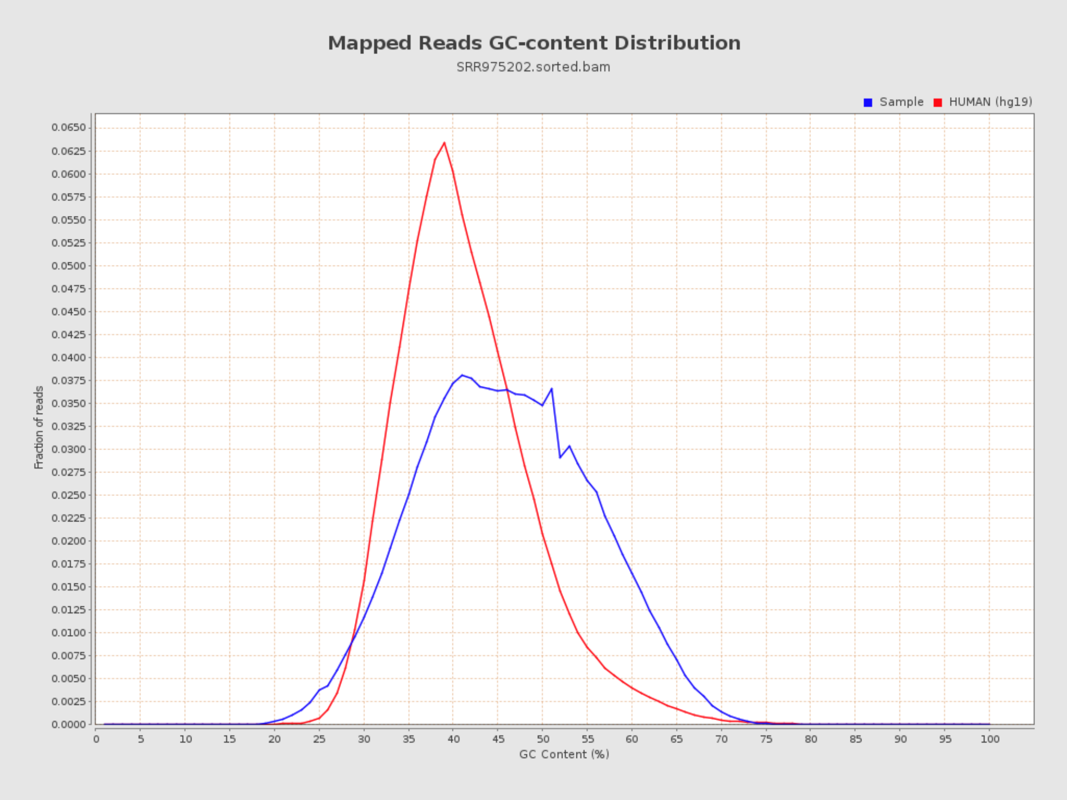
# 7. Results : Duplication Rate Histogram



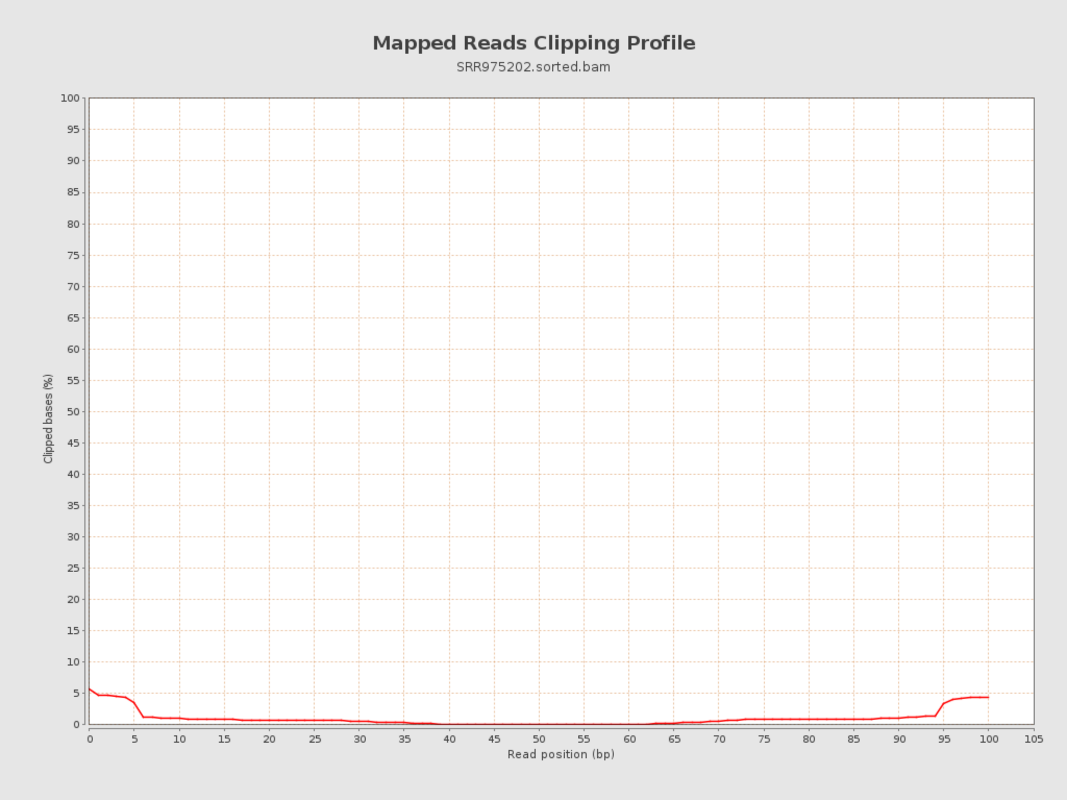
# 8. Results : Mapped Reads Nucleotide Content



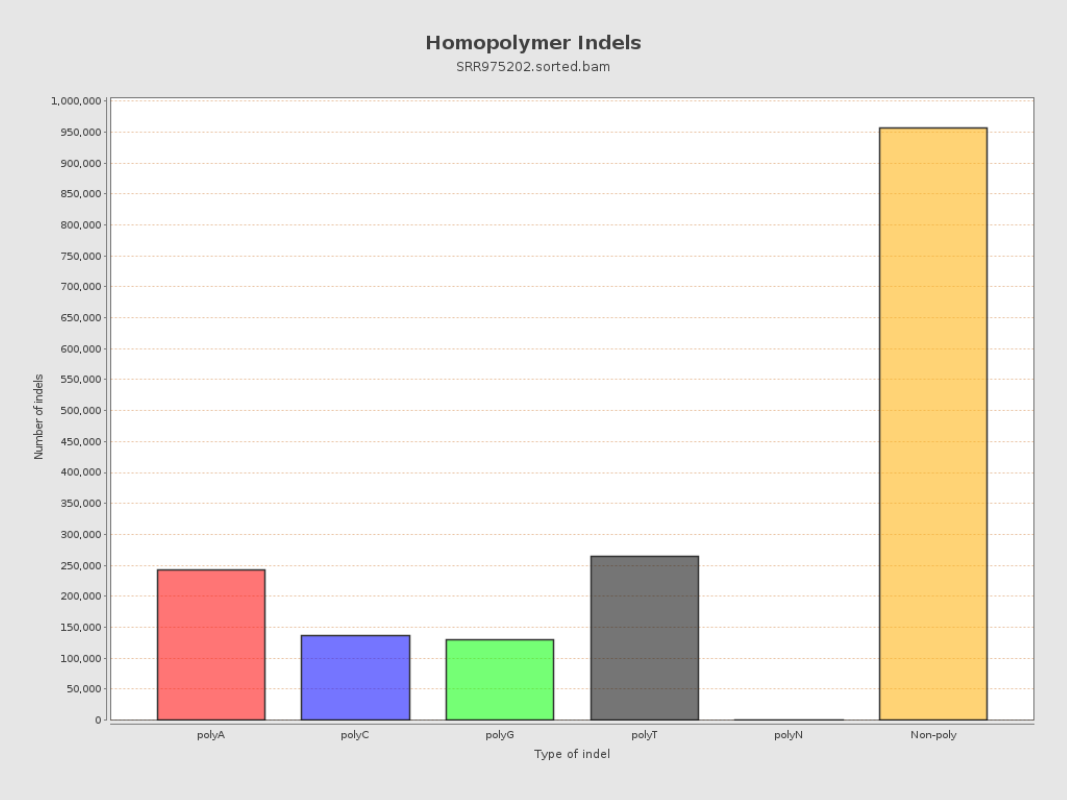
# 9. Results : Mapped Reads GC-content Distribution



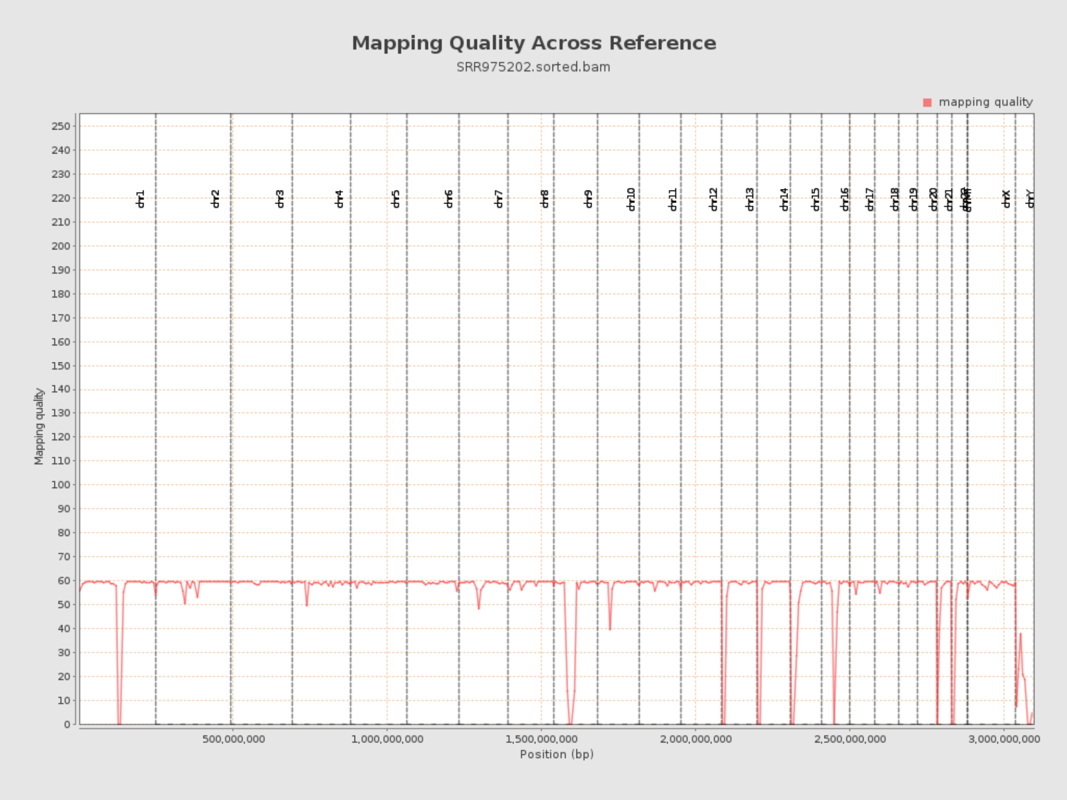
# 10. Results : Mapped Reads Clipping Profile



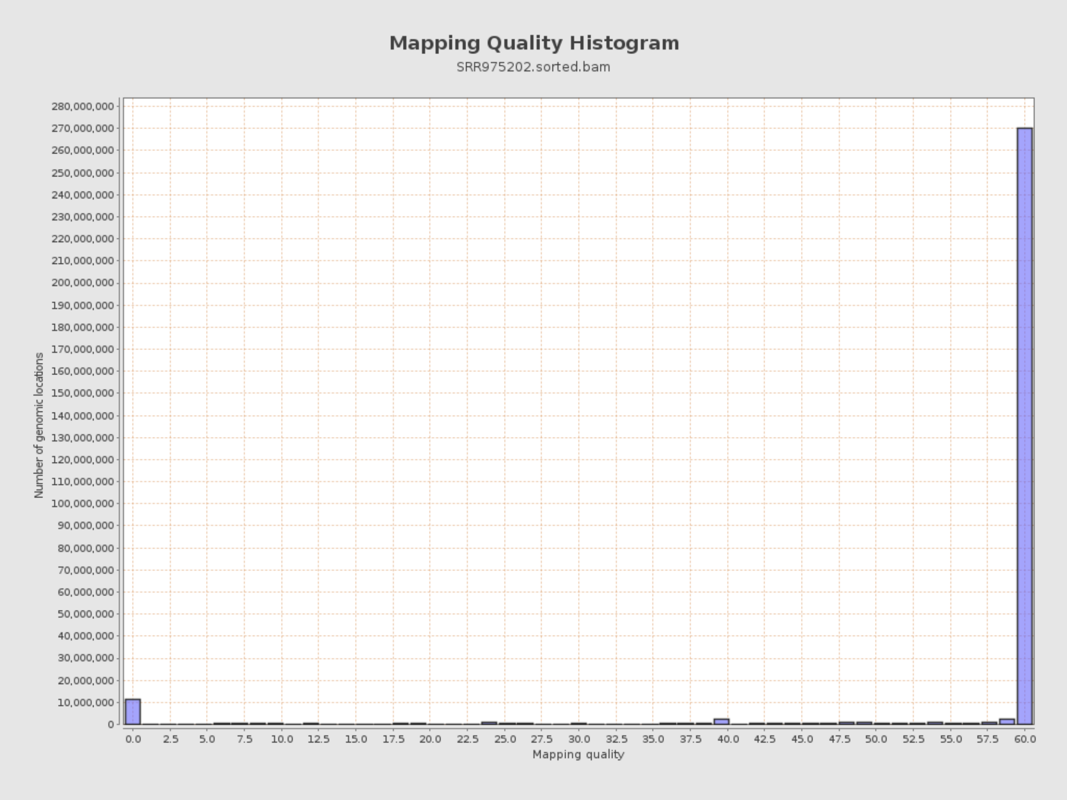
# 11. Results : Homopolymer Indels



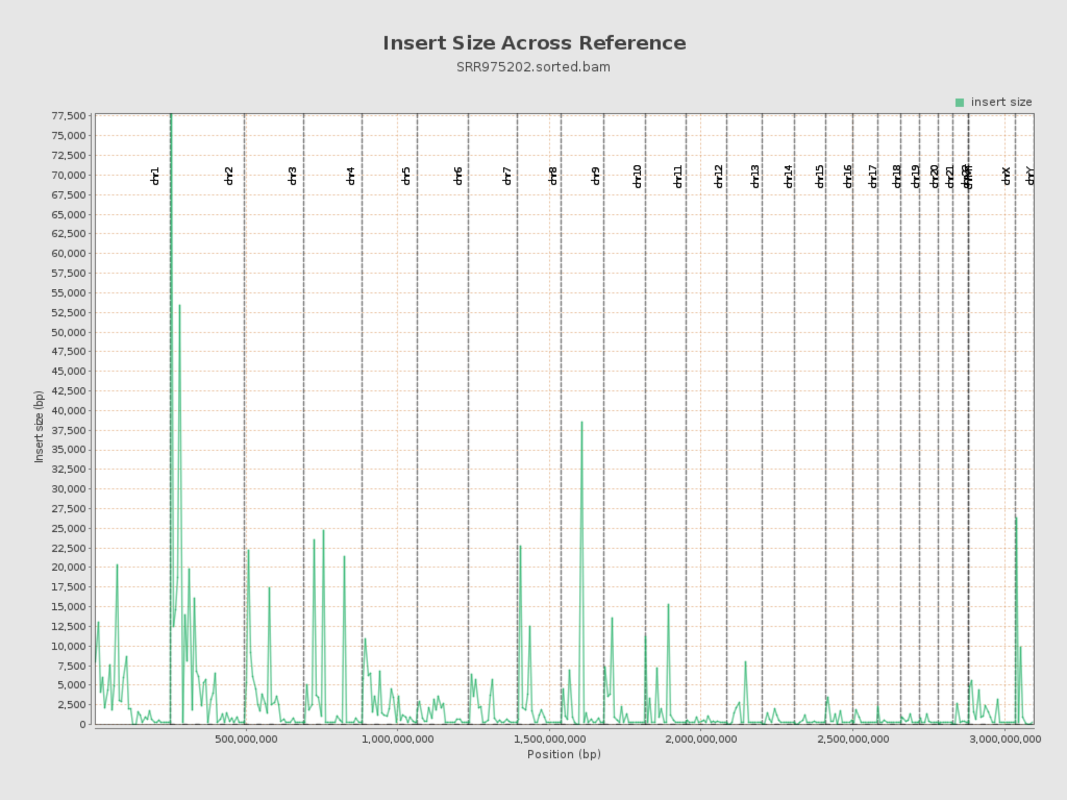
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram