# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 14:46:19*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR975213.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_SRR975213 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975213_1.fastq.gz SRR975213_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 14:46:19 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR975213.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,065,678 |
| Mapped reads | 3,033,203 / 98.94% |
| Unmapped reads | 32,475 / 1.06% |
| Mapped paired reads | 3,033,203 / 98.94% |
| Mapped reads, first in pair | 1,518,406 / 49.53% |
| Mapped reads,  second in pair | 1,514,797 / 49.41% |
| Mapped reads, both in pair | 3,024,450 / 98.66% |
| Mapped reads, singletons | 8,753 / 0.29% |
| Secondary alignments | 0 |
| Supplementary alignments | 178,074 / 5.81% |
| Read min/max/mean length | 30 / 151 / 154.06 |
| Duplicated reads (estimated) | 701,448 / 22.88% |
| Duplication rate | 23.14% |
| Clipped reads | 2,470,382 / 80.58% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 115,845,356 / 28.07% |
| Number/percentage of C's | 90,026,633 / 21.81% |
| Number/percentage of T's | 114,215,513 / 27.67% |
| Number/percentage of G's | 92,603,020 / 22.44% |
| Number/percentage of N's | 24,398 / 0.01% |
| | |

| | |
|---|---|
| GC Percentage | 44.25% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1334 |
| Standard Deviation | 2.6211 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 52.66 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 248,694.07 |
| Standard Deviation | 4,888,941.42 |
| P25/Median/P75 | 127 / 151 / 184 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 1.08% |
| Mismatches | 4,211,482 |
| Insertions | 90,783 |
| Mapped reads with at least one insertion | 2.82% |
| Deletions | 93,169 |
| Mapped reads with at least one deletion | 2.93% |
| Homopolymer indels | 40.27% |

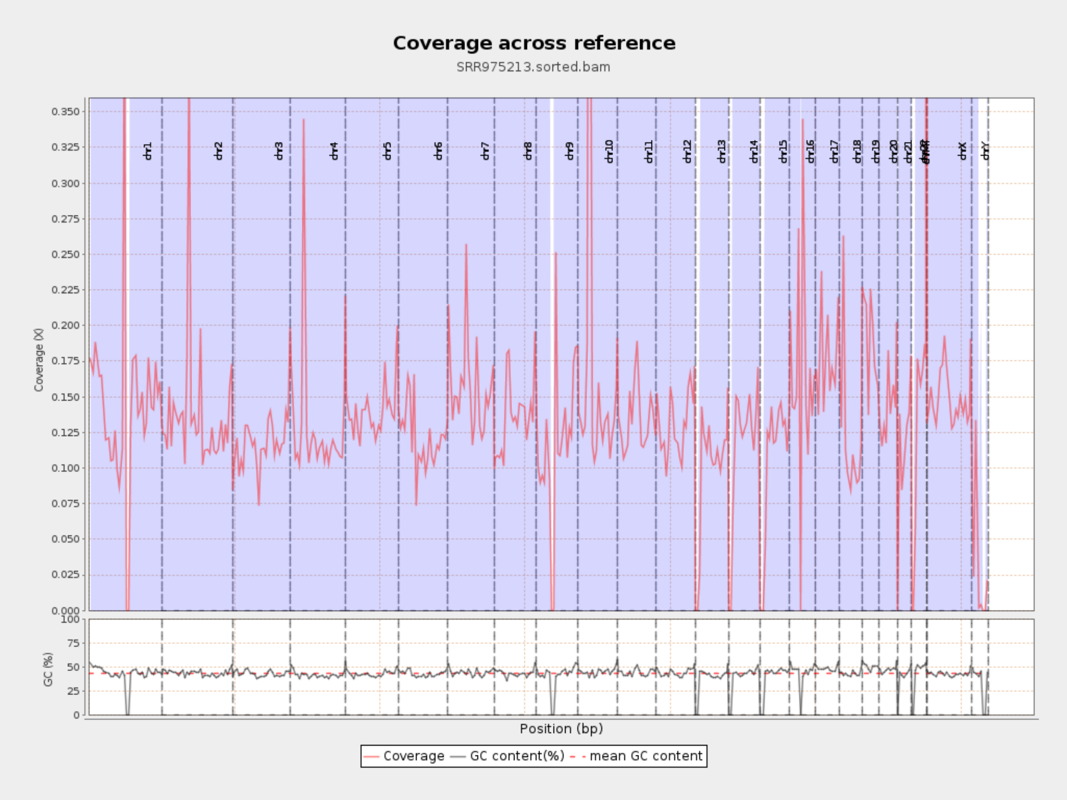
## 2.7. Chromosome stats

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

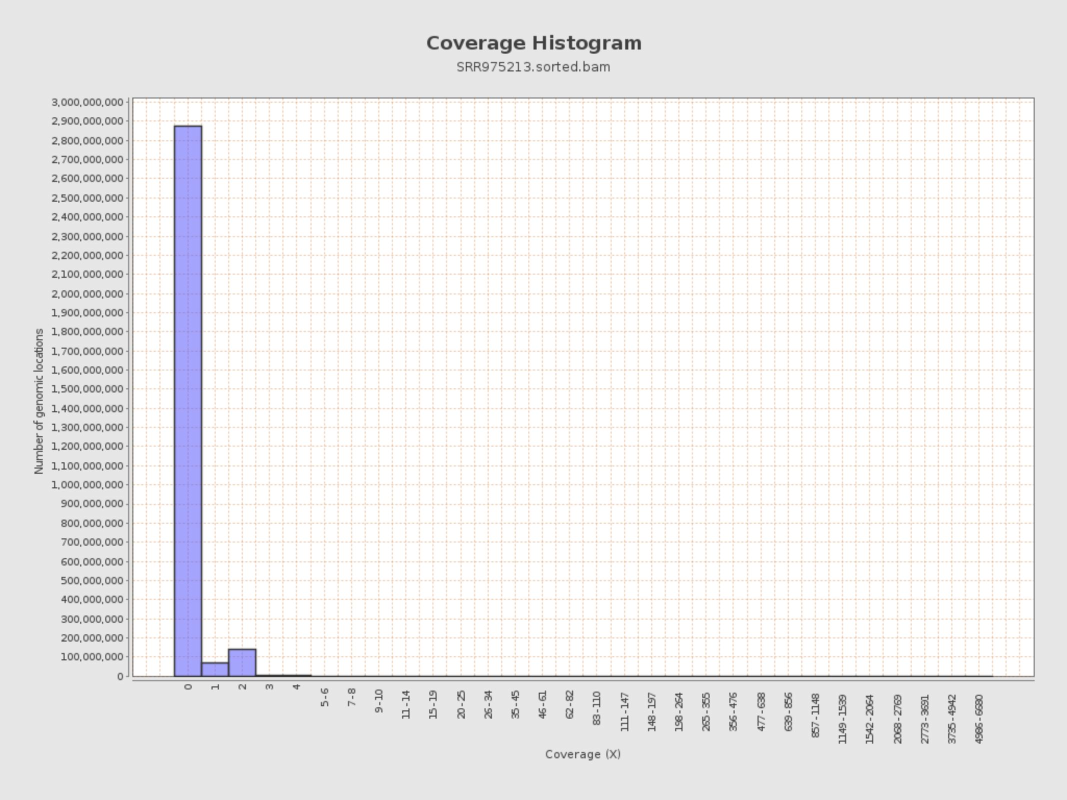
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 35989884 | 0.1444 | 6.6325 |
| chr2 | 243199373 | 33655962 | 0.1384 | 1.667 |
| chr3 | 198022430 | 23021816 | 0.1163 | 0.6014 |
| chr4 | 191154276 | 24221197 | 0.1267 | 1.5517 |
| chr5 | 180915260 | 25344206 | 0.1401 | 0.5347 |
| chr6 | 171115067 | 20732347 | 0.1212 | 0.7421 |
| chr7 | 159138663 | 24825379 | 0.156 | 1.8781 |
| chr8 | 146364022 | 19923736 | 0.1361 | 2.1558 |
| chr9 | 141213431 | 16184253 | 0.1146 | 2.7322 |
| chr10 | 135534747 | 22891136 | 0.1689 | 5.6771 |
| chr11 | 135006516 | 18292844 | 0.1355 | 0.9353 |
| chr12 | 133851895 | 17469815 | 0.1305 | 0.5061 |
| chr13 | 115169878 | 11212311 | 0.0974 | 0.4301 |
| chr14 | 107349540 | 12354855 | 0.1151 | 0.4969 |
| chr15 | 102531392 | 10726224 | 0.1046 | 0.4453 |
| chr16 | 90354753 | 14810562 | 0.1639 | 1.5915 |
| chr17 | 81195210 | 14390441 | 0.1772 | 1.1105 |
| chr18 | 78077248 | 9547548 | 0.1223 | 2.9058 |
| chr19 | 59128983 | 11241701 | 0.1901 | 3.3617 |
| chr20 | 63025520 | 9002152 | 0.1428 | 0.8035 |
| chr21 | 48129895 | 5475033 | 0.1138 | 0.9709 |
| chr22 | 51304566 | 6143102 | 0.1197 | 0.4829 |
| chrMT | 16571 | 713158 | 43.0365 | 13.4316 |
| chrX | 155270560 | 23023195 | 0.1483 | 0.7501 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1763787 | 0.0297 | 1.7768 |

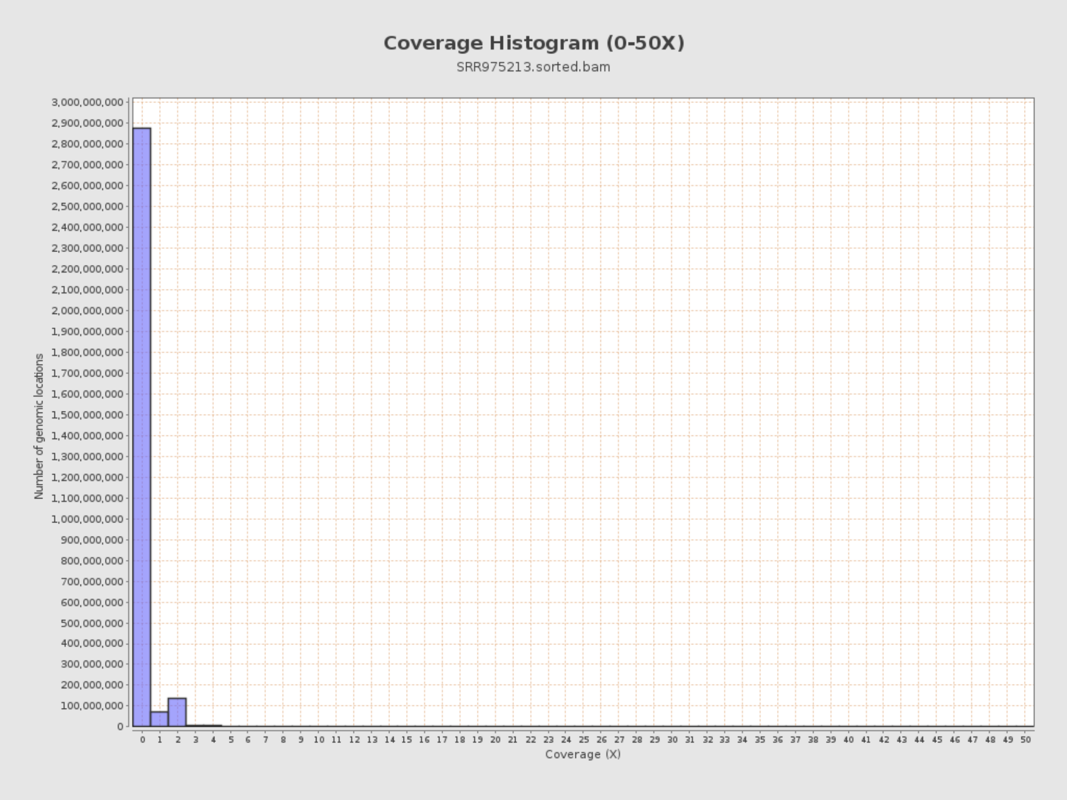
# 3. Results : Coverage across reference



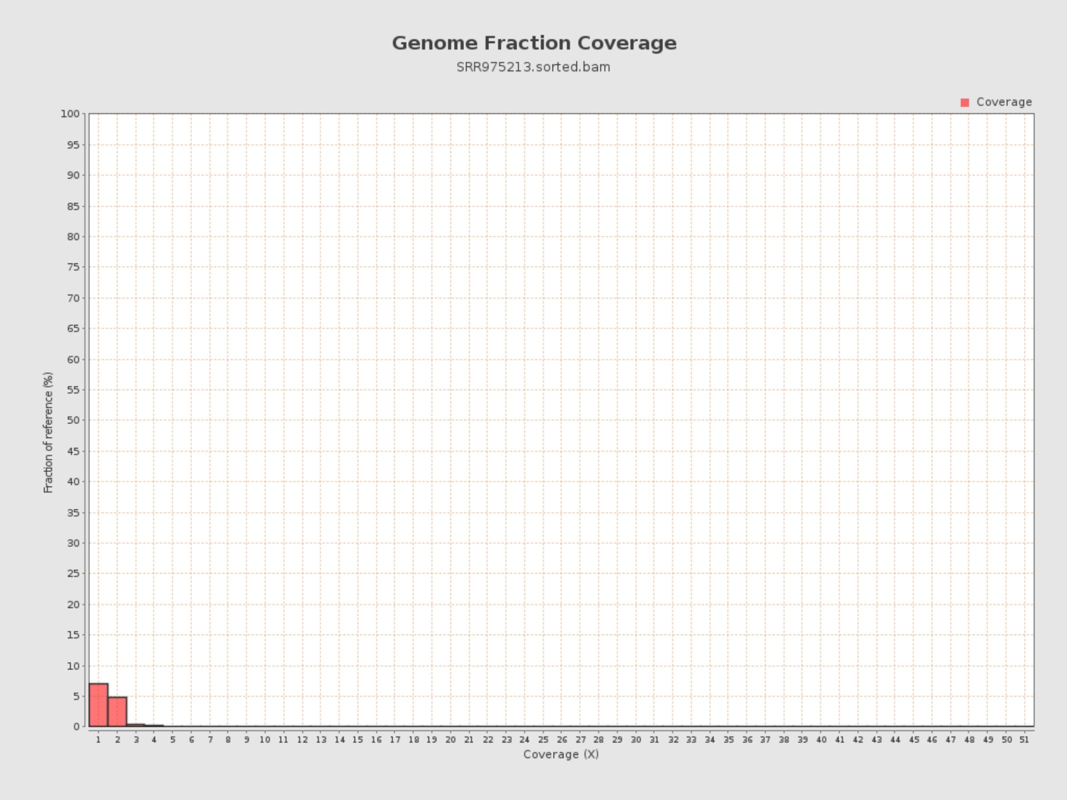
# 4. Results : Coverage Histogram



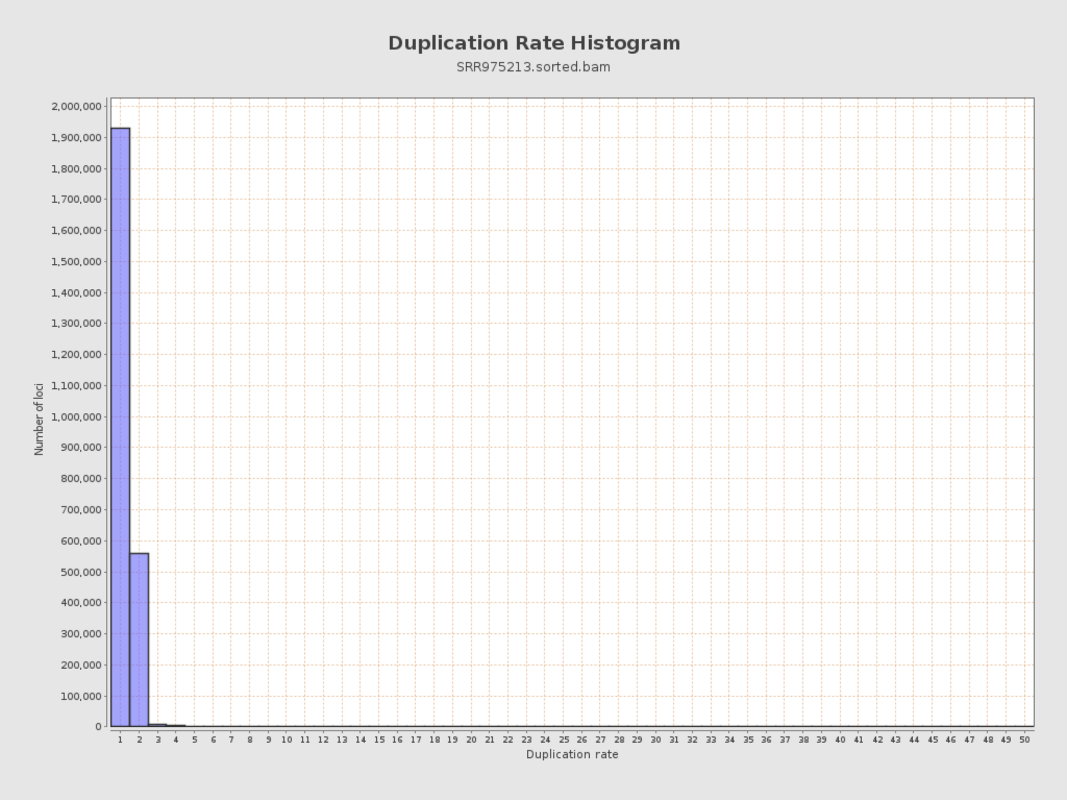
# 5. Results : Coverage Histogram (0-50X)



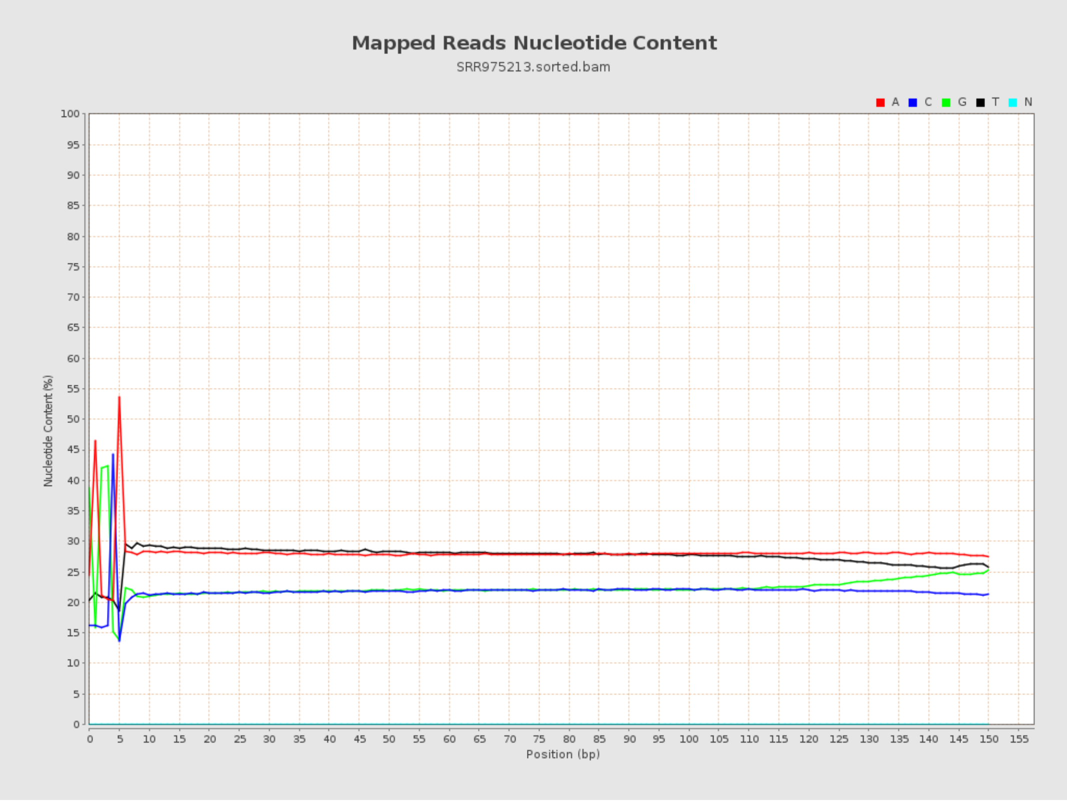
# 6. Results : Genome Fraction Coverage



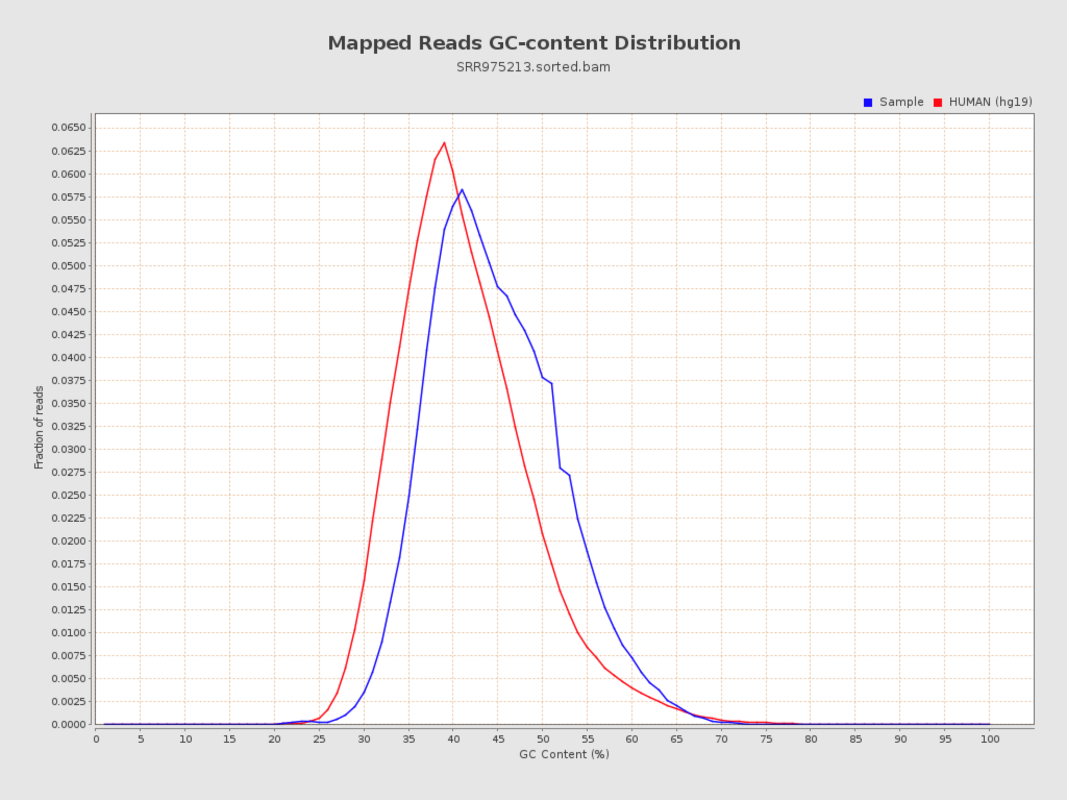
# 7. Results : Duplication Rate Histogram



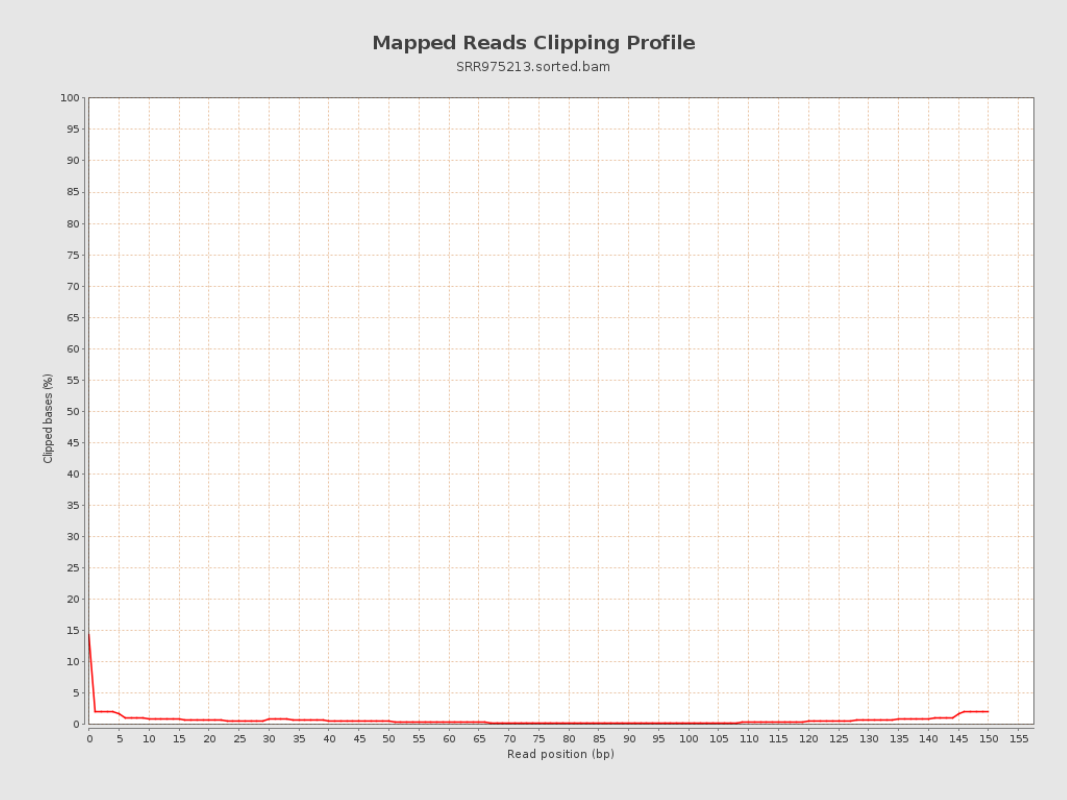
# 8. Results : Mapped Reads Nucleotide Content



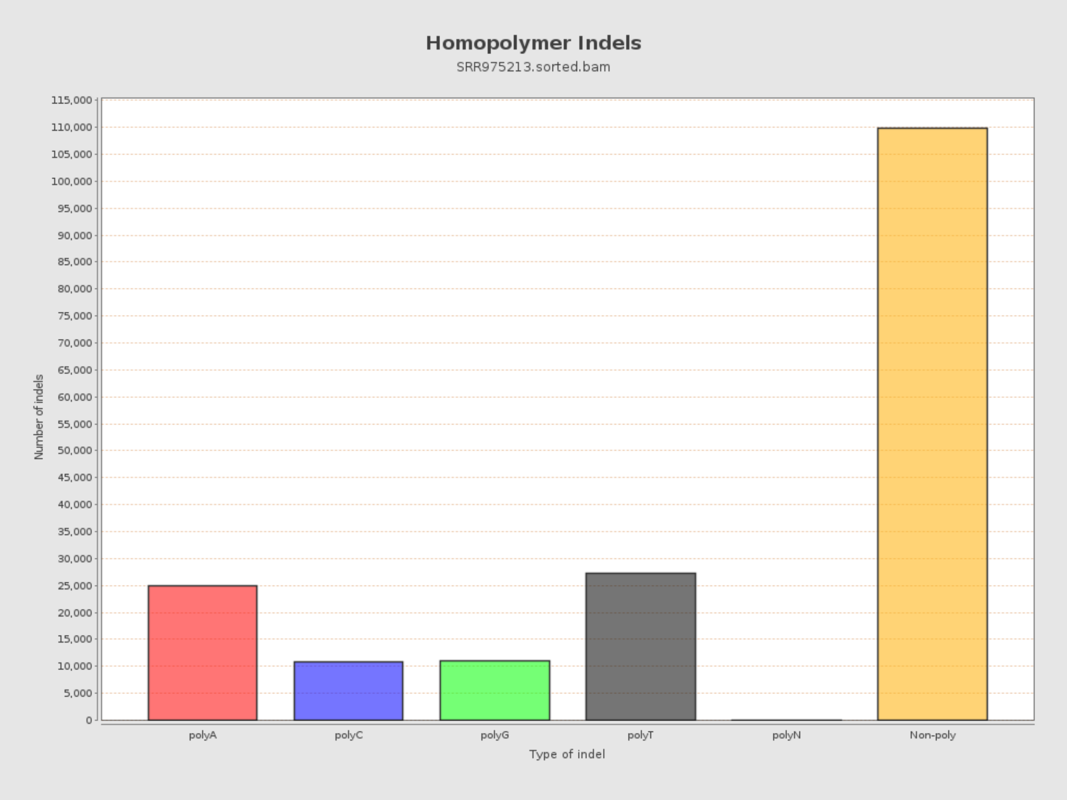
# 9. Results : Mapped Reads GC-content Distribution



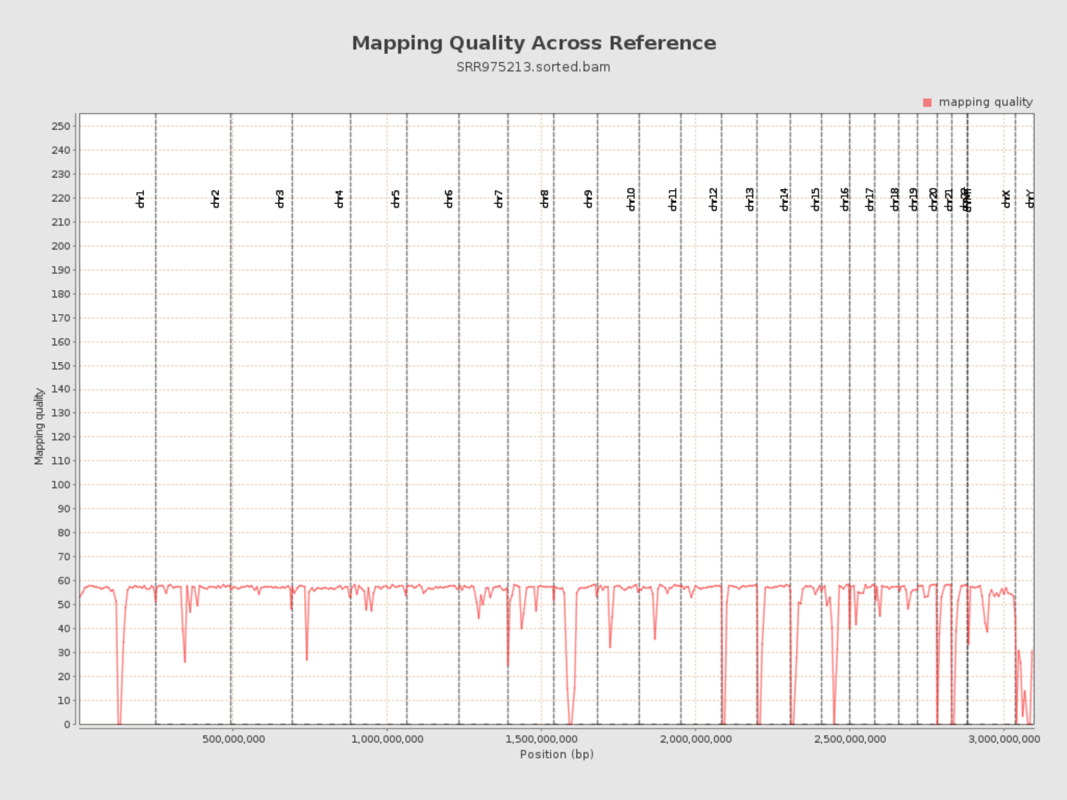
# 10. Results : Mapped Reads Clipping Profile



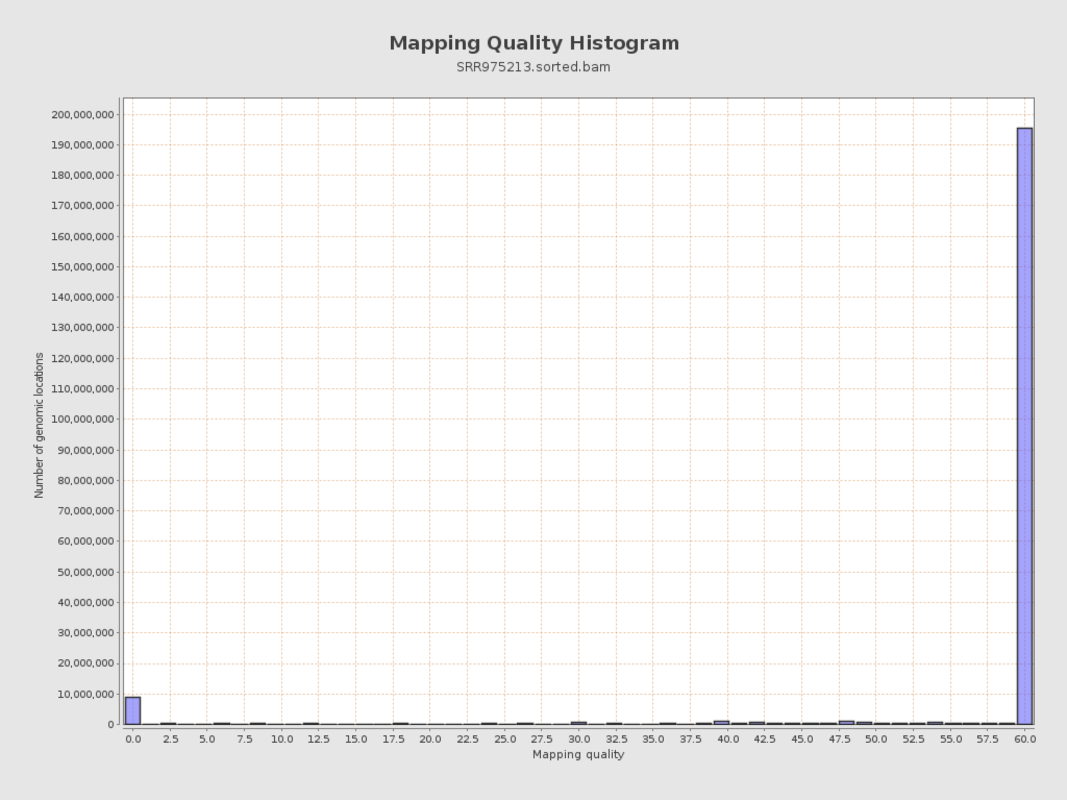
# 11. Results : Homopolymer Indels



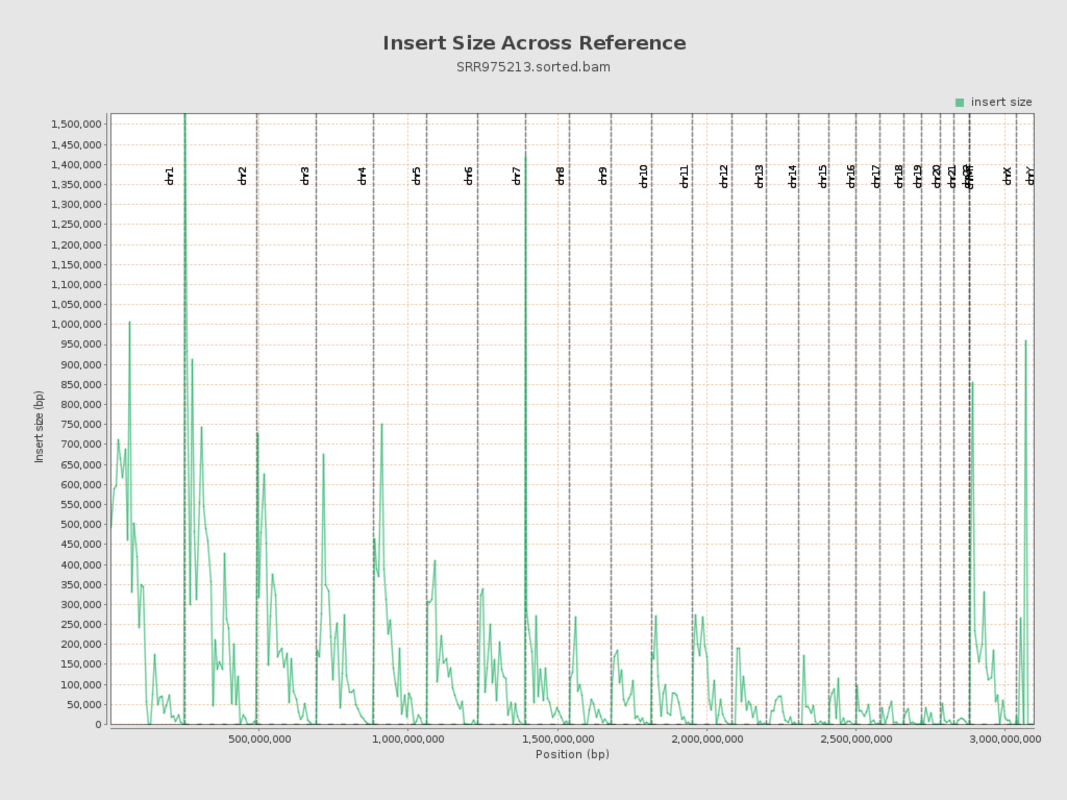
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram