# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/23 10:03:06*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR926972.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_SRR926972 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926972_1.fastq.gz SRR926972_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Apr 23 10:03:05 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR926972.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 28,758,952 |
| Mapped reads | 28,279,308 / 98.33% |
| Unmapped reads | 479,644 / 1.67% |
| Mapped paired reads | 28,279,308 / 98.33% |
| Mapped reads, first in pair | 14,196,840 / 49.36% |
| Mapped reads,  second in pair | 14,082,468 / 48.97% |
| Mapped reads, both in pair | 28,039,358 / 97.5% |
| Mapped reads, singletons | 239,950 / 0.83% |
| Secondary alignments | 0 |
| Supplementary alignments | 525,131 / 1.83% |
| Read min/max/mean length | 30 / 101 / 101.75 |
| Duplicated reads (estimated) | 2,306,165 / 8.02% |
| Duplication rate | 6.38% |
| Clipped reads | 8,820,795 / 30.67% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 743,646,467 / 28.12% |
| Number/percentage of C's | 541,321,045 / 20.47% |
| Number/percentage of T's | 753,119,914 / 28.48% |
| Number/percentage of G's | 605,980,641 / 22.92% |
| Number/percentage of N's | 190,858 / 0.01% |
| | |

| | |
|---|---|
| GC Percentage | 43.39% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.8548 |
| Standard Deviation | 3.3043 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.18 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 170,755.05 |
| Standard Deviation | 4,087,626.31 |
| P25/Median/P75 | 133 / 169 / 223 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.97% |
| Mismatches | 24,851,147 |
| Insertions | 439,811 |
| Mapped reads with at least one insertion | 1.53% |
| Deletions | 1,385,361 |
| Mapped reads with at least one deletion | 4.77% |
| Homopolymer indels | 52.2% |

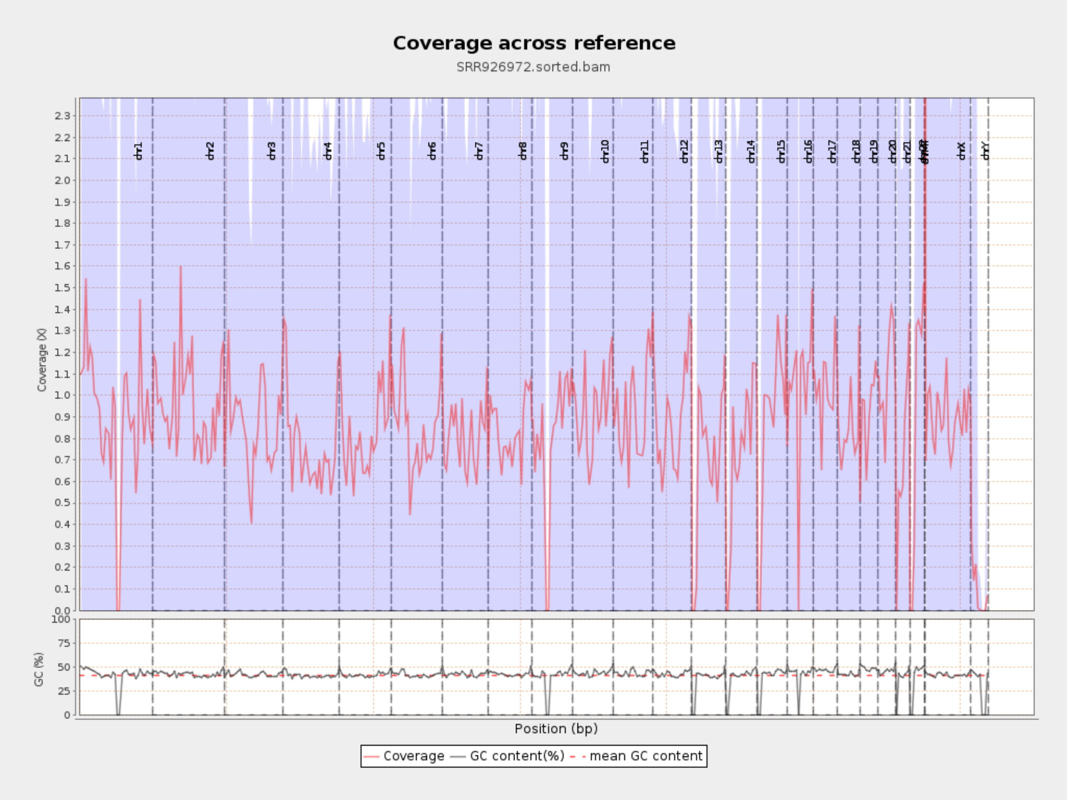
## 2.7. Chromosome stats

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

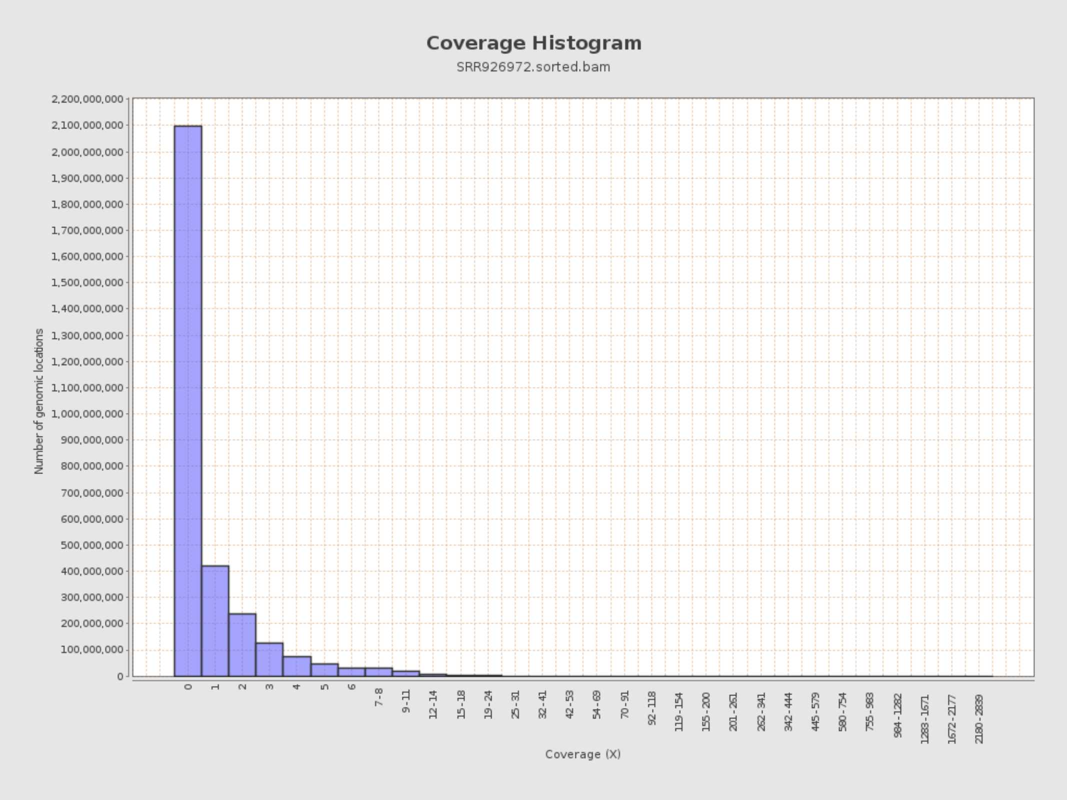
| | | **bases** | **coverage** | **deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 223400496 | 0.8963 | 3.8639 |
| chr2 | 243199373 | 233385538 | 0.9596 | 5.173 |
| chr3 | 198022430 | 170157700 | 0.8593 | 1.8331 |
| chr4 | 191154276 | 144010854 | 0.7534 | 2.5887 |
| chr5 | 180915260 | 151104281 | 0.8352 | 1.7913 |
| chr6 | 171115067 | 145429735 | 0.8499 | 2.2227 |
| chr7 | 159138663 | 129577250 | 0.8142 | 2.576 |
| chr8 | 146364022 | 123284528 | 0.8423 | 2.1059 |
| chr9 | 141213431 | 111811331 | 0.7918 | 3.7874 |
| chr10 | 135534747 | 126463057 | 0.9331 | 4.6751 |
| chr11 | 135006516 | 123675716 | 0.9161 | 3.8571 |
| chr12 | 133851895 | 119528611 | 0.893 | 2.0825 |
| chr13 | 115169878 | 78434767 | 0.681 | 1.6418 |
| chr14 | 107349540 | 76529163 | 0.7129 | 1.7545 |
| chr15 | 102531392 | 87753352 | 0.8559 | 1.996 |
| chr16 | 90354753 | 93352747 | 1.0332 | 4.1824 |
| chr17 | 81195210 | 84612918 | 1.0421 | 2.5946 |
| chr18 | 78077248 | 65928869 | 0.8444 | 3.9664 |
| chr19 | 59128983 | 55940901 | 0.9461 | 2.7968 |
| chr20 | 63025520 | 69434323 | 1.1017 | 2.3354 |
| chr21 | 48129895 | 35437020 | 0.7363 | 3.5411 |
| chr22 | 51304566 | 47546015 | 0.9267 | 2.3047 |
| chrMT | 16571 | 6274377 | 378.636 | 281.9791 |
| chrX | 155270560 | 138204184 | 0.8901 | 2.2078 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 4990639 | 0.0841 | 2.3678 |

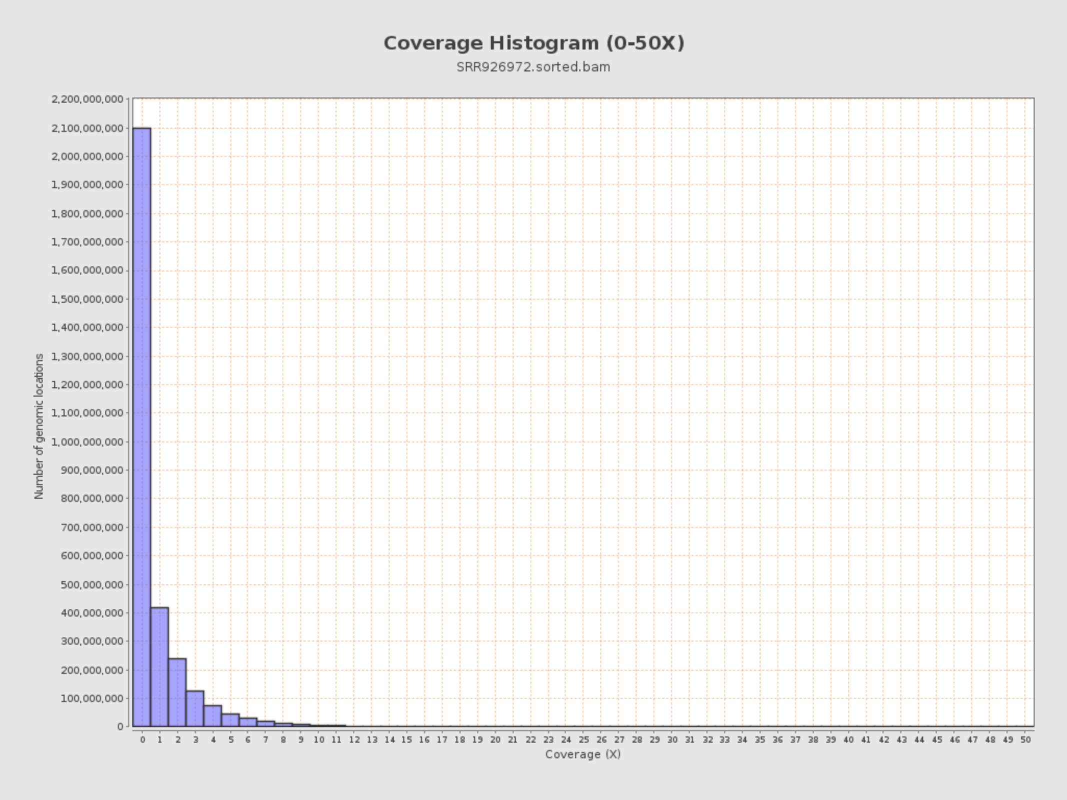
# 3. Results : Coverage across reference



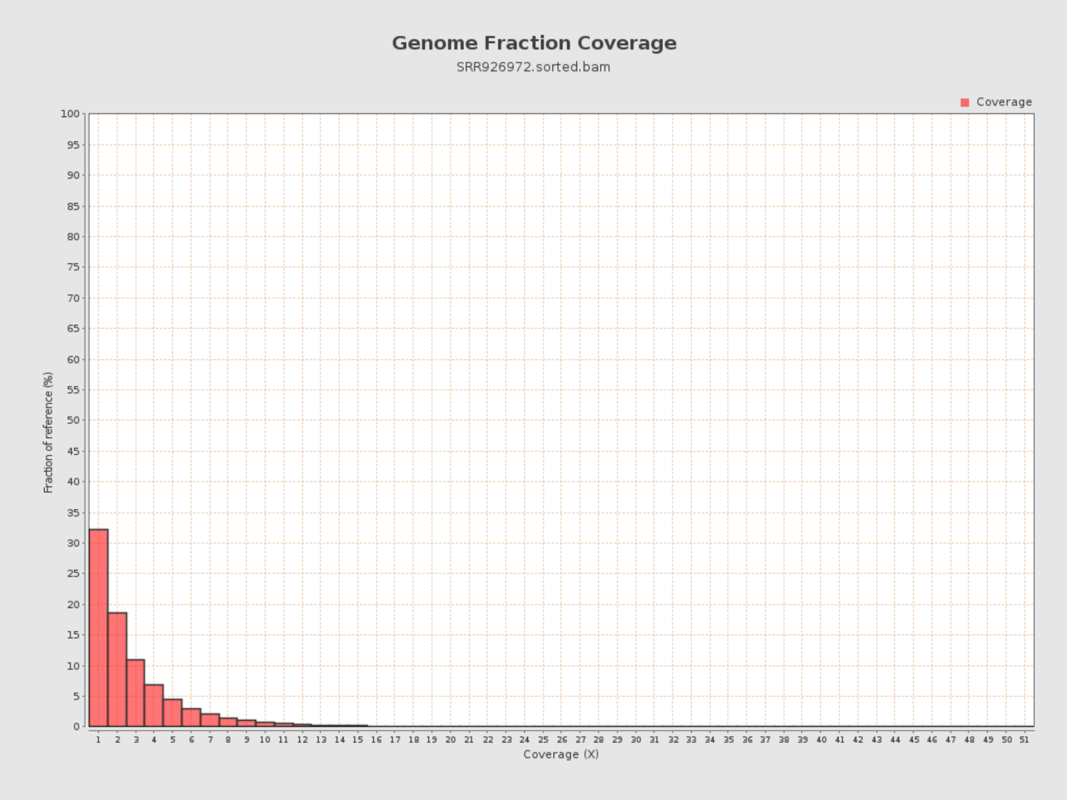
# 4. Results : Coverage Histogram



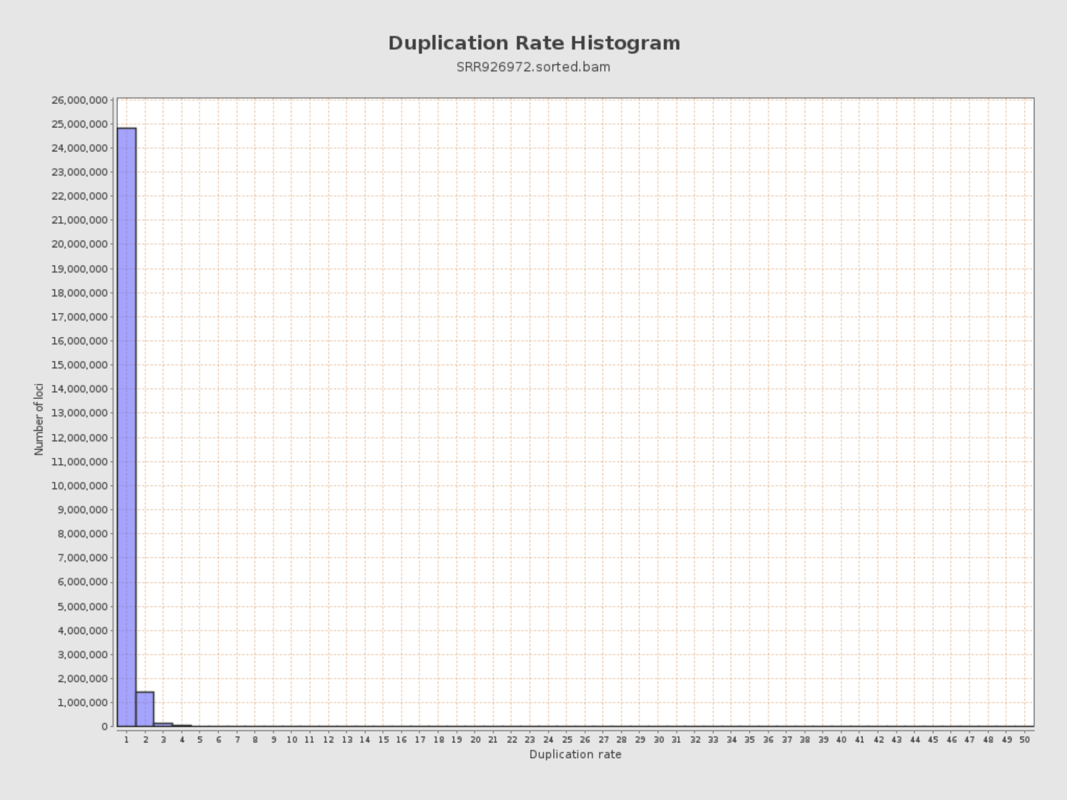
# 5. Results : Coverage Histogram (0-50X)



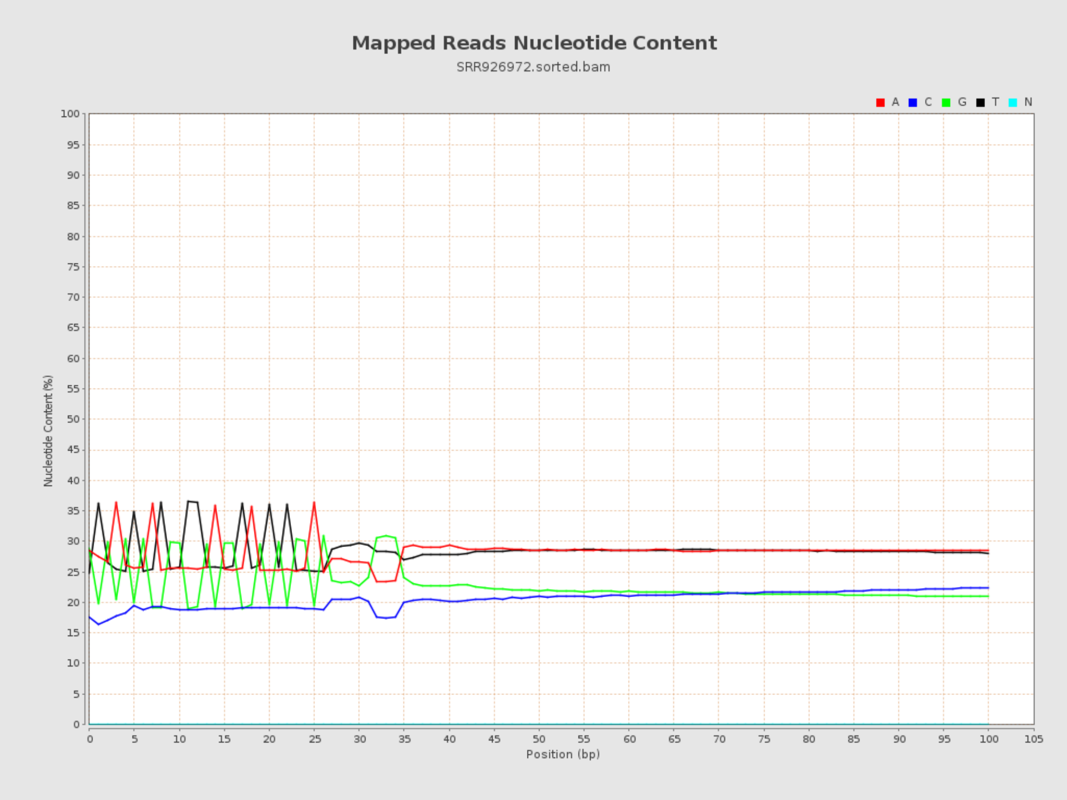
# 6. Results : Genome Fraction Coverage



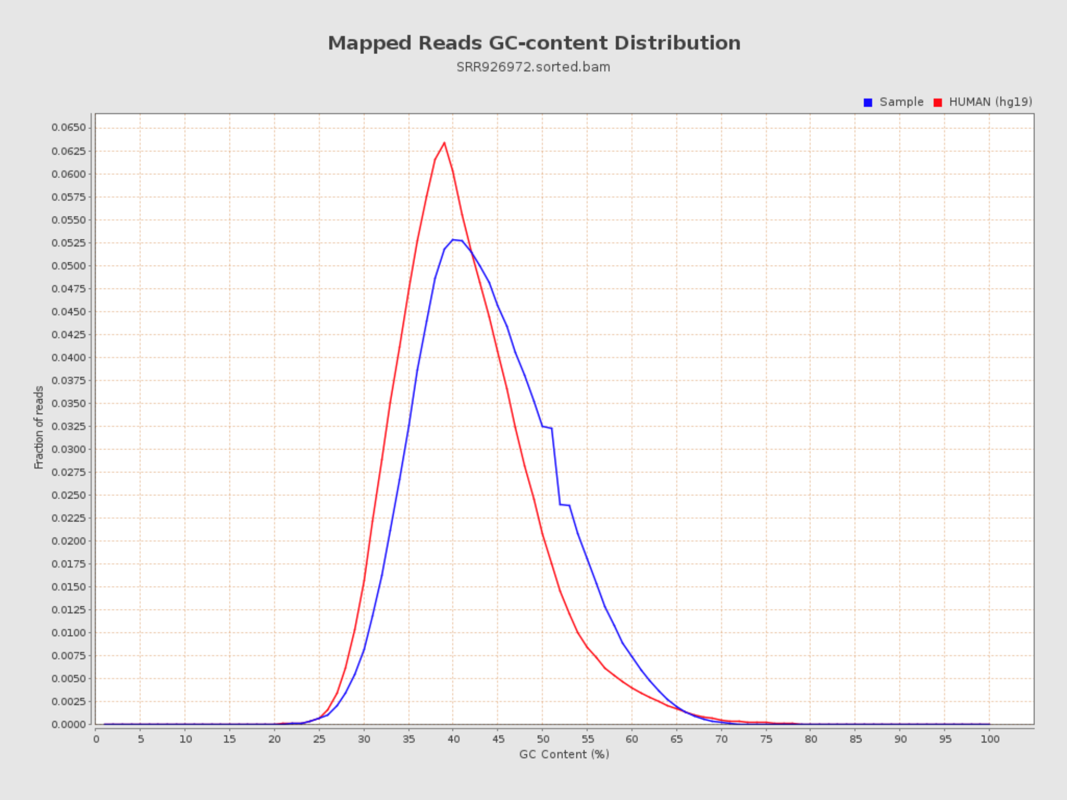
# 7. Results : Duplication Rate Histogram



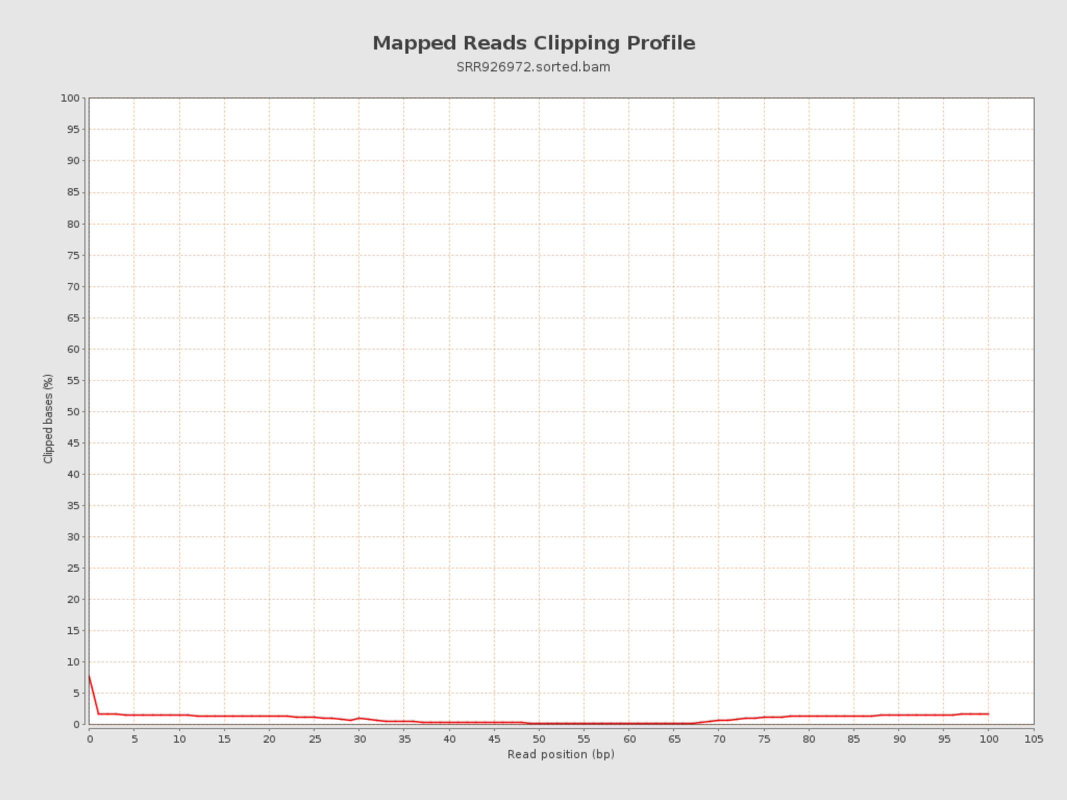
# 8. Results : Mapped Reads Nucleotide Content



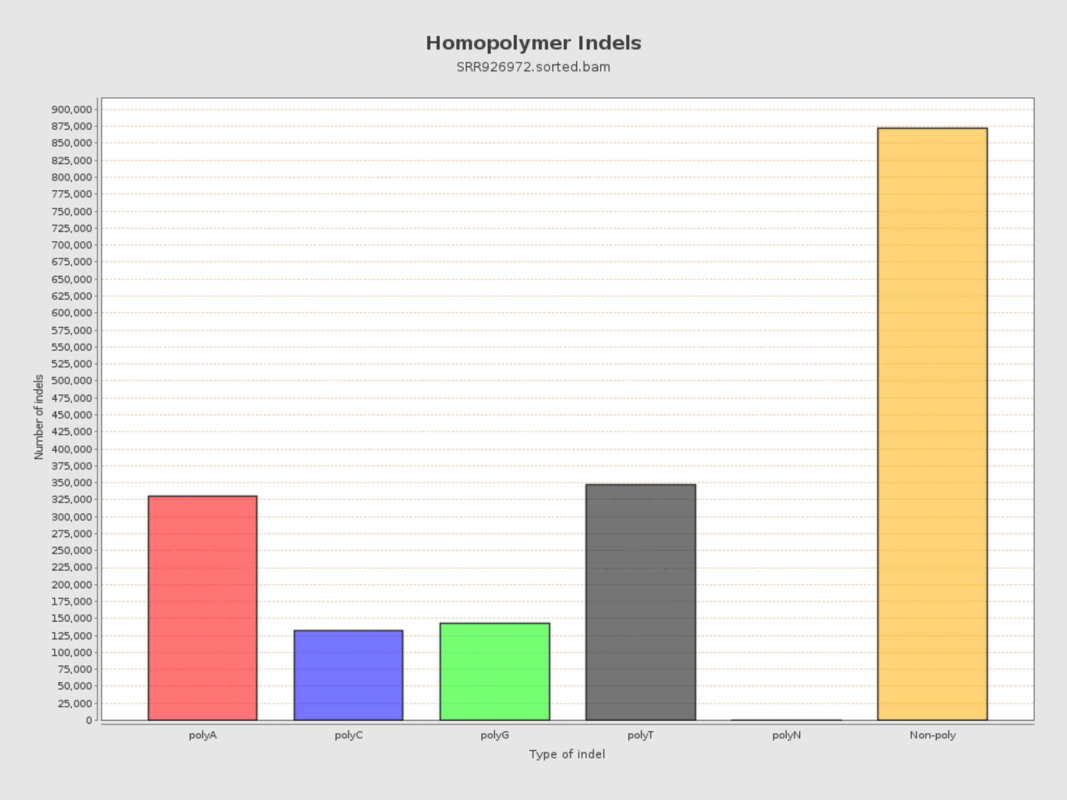
# 9. Results : Mapped Reads GC-content Distribution



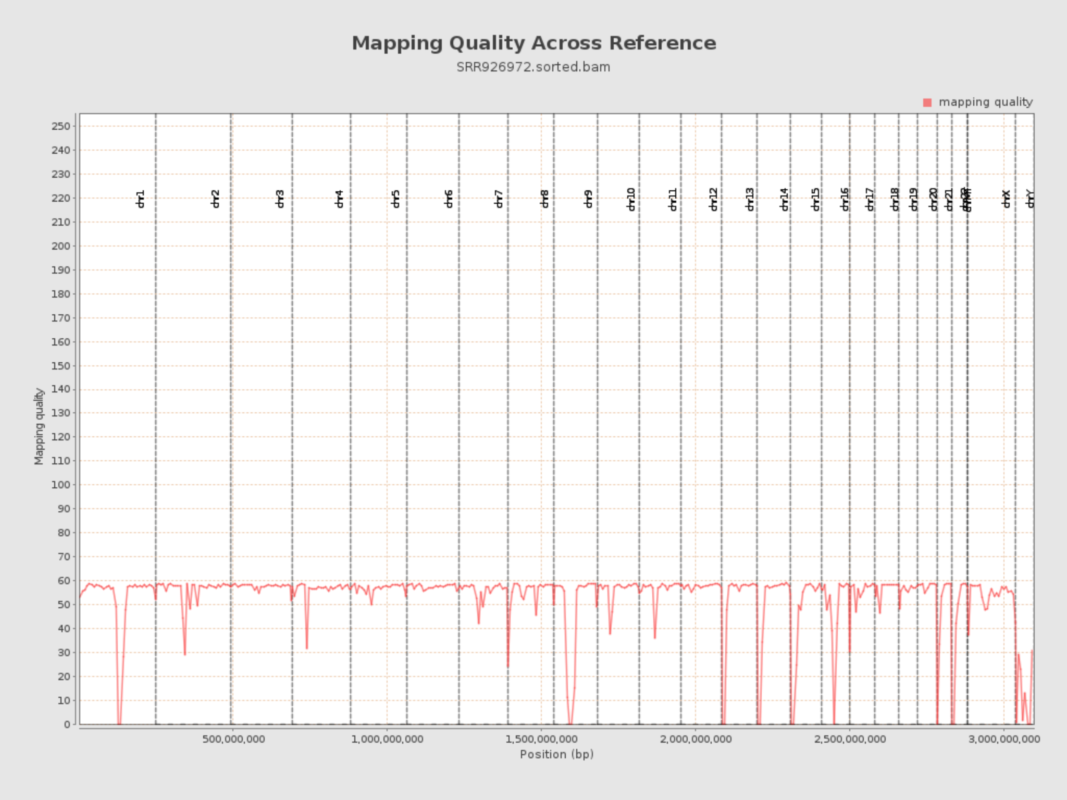
# 10. Results : Mapped Reads Clipping Profile



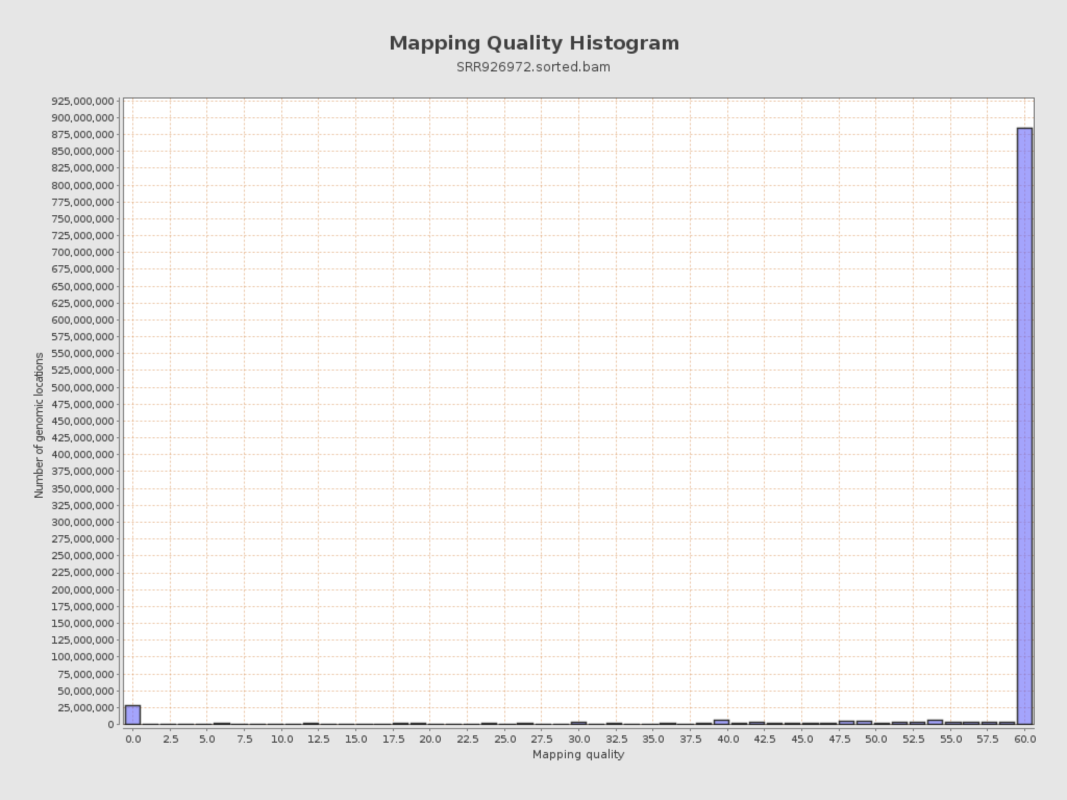
# 11. Results : Homopolymer Indels



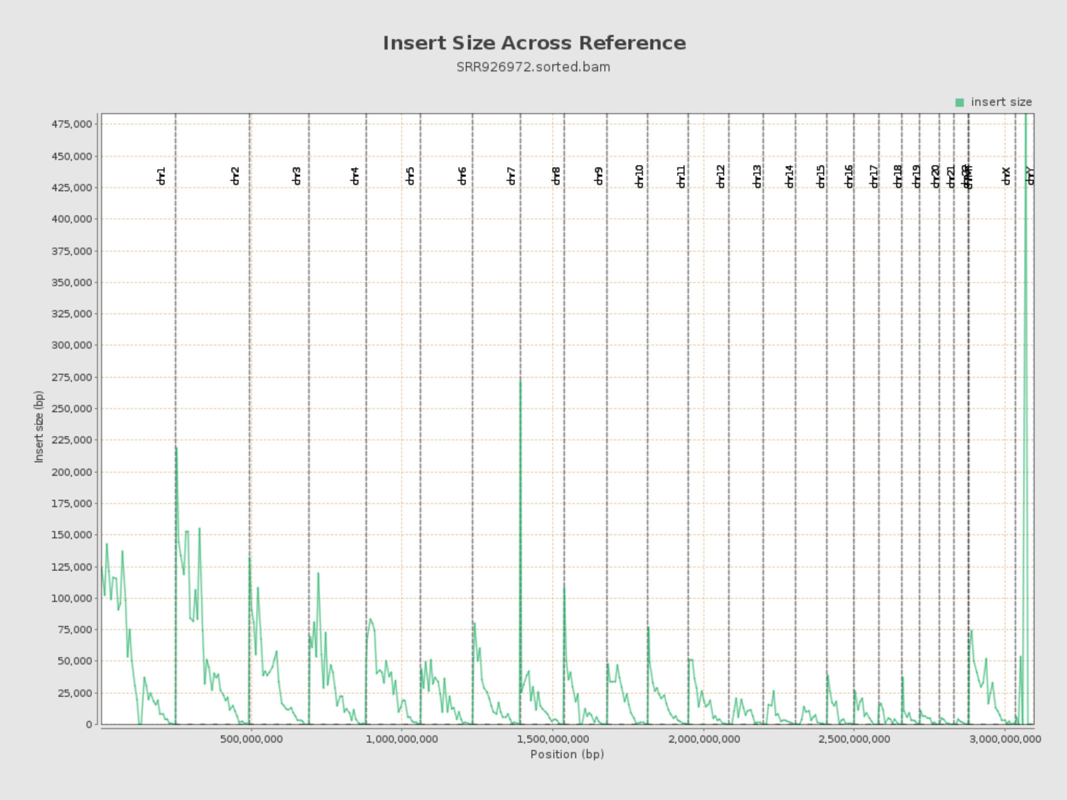
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram