# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/30 16:30:49*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472783.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_SRR3472783 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472783_1.fastq.gz SRR3472783_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 30 16:30:48 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3472783.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 16,482,296 |
| Mapped reads | 16,324,594 / 99.04% |
| Unmapped reads | 157,702 / 0.96% |
| Mapped paired reads | 16,324,594 / 99.04% |
| Mapped reads, first in pair | 8,187,966 / 49.68% |
| Mapped reads,  second in pair | 8,136,628 / 49.37% |
| Mapped reads, both in pair | 16,235,414 / 98.5% |
| Mapped reads, singletons | 89,180 / 0.54% |
| Secondary alignments | 0 |
| Supplementary alignments | 73,378 / 0.45% |
| Read min/max/mean length | 30 / 100 / 100.18 |
| Duplicated reads (estimated) | 10,355,406 / 62.83% |
| Duplication rate | 46.53% |
| Clipped reads | 1,399,055 / 8.49% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 445,354,649 / 27.71% |
| Number/percentage of C's | 360,081,405 / 22.41% |
| Number/percentage of T's | 443,070,459 / 27.57% |
| Number/percentage of G's | 358,276,837 / 22.29% |
| Number/percentage of N's | 311,146 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 44.7% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.5192 |
| Standard Deviation | 18.3031 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 55.09 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 32,004.03 |
| Standard Deviation | 1,741,523.83 |
| P25/Median/P75 | 166 / 232 / 315 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.61% |
| Mismatches | 9,559,217 |
| Insertions | 98,335 |
| Mapped reads with at least one insertion | 0.6% |
| Deletions | 90,507 |
| Mapped reads with at least one deletion | 0.55% |
| Homopolymer indels | 44.1% |

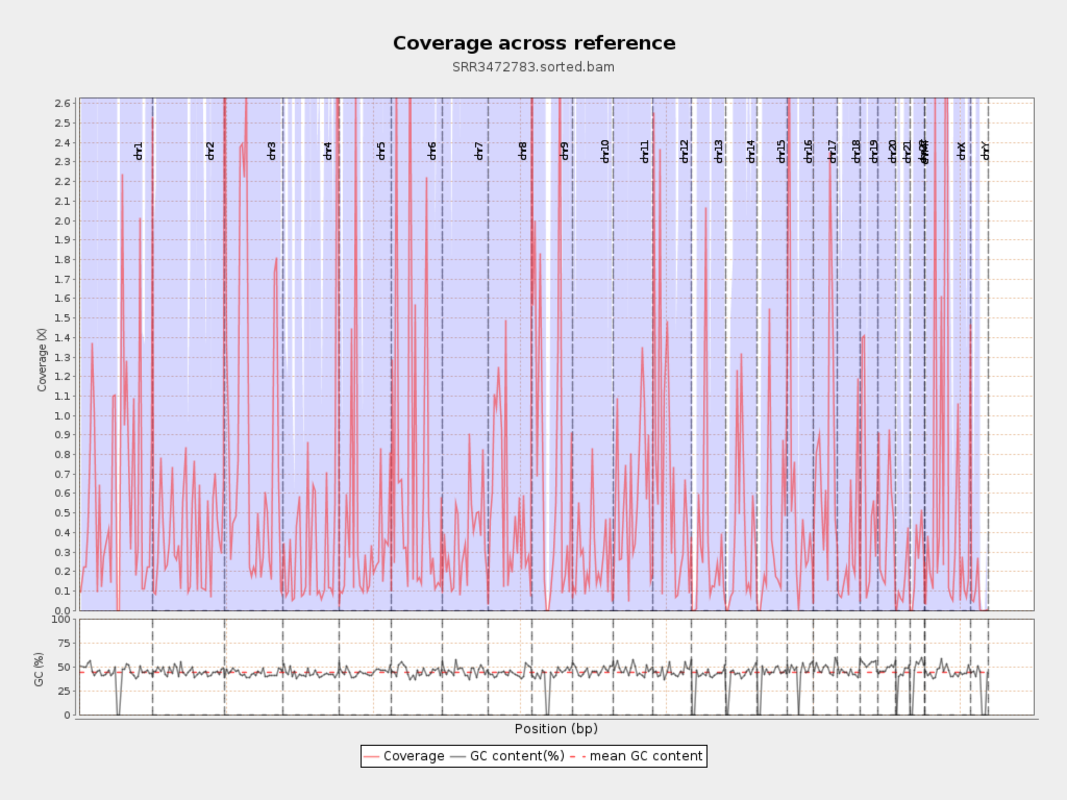
## 2.7. Chromosome stats

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

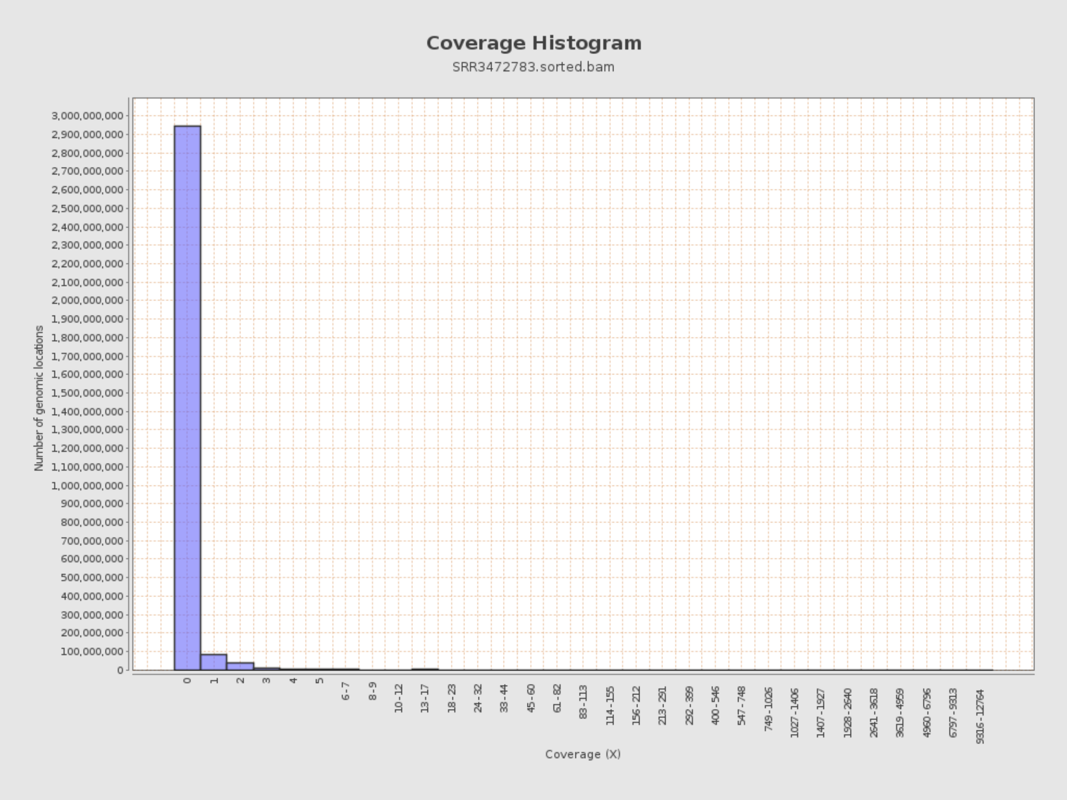
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 152105418 | 0.6103 | 17.5399 |
| chr2 | 243199373 | 90014267 | 0.3701 | 11.9697 |
| chr3 | 198022430 | 176712074 | 0.8924 | 23.1312 |
| chr4 | 191154276 | 76960700 | 0.4026 | 17.0832 |
| chr5 | 180915260 | 77170719 | 0.4266 | 15.3387 |
| chr6 | 171115067 | 123515191 | 0.7218 | 28.8902 |
| chr7 | 159138663 | 58125201 | 0.3652 | 12.9219 |
| chr8 | 146364022 | 80106902 | 0.5473 | 16.1367 |
| chr9 | 141213431 | 113090856 | 0.8009 | 23.0504 |
| chr10 | 135534747 | 37299698 | 0.2752 | 12.3074 |
| chr11 | 135006516 | 77737235 | 0.5758 | 18.5571 |
| chr12 | 133851895 | 98464000 | 0.7356 | 24.6011 |
| chr13 | 115169878 | 37458850 | 0.3252 | 14.5635 |
| chr14 | 107349540 | 41773662 | 0.3891 | 14.7488 |
| chr15 | 102531392 | 36690130 | 0.3578 | 10.7291 |
| chr16 | 90354753 | 54803346 | 0.6065 | 16.0065 |
| chr17 | 81195210 | 63730181 | 0.7849 | 21.0006 |
| chr18 | 78077248 | 24395843 | 0.3125 | 11.5144 |
| chr19 | 59128983 | 34952070 | 0.5911 | 14.0839 |
| chr20 | 63025520 | 28747713 | 0.4561 | 14.4279 |
| chr21 | 48129895 | 6873244 | 0.1428 | 5.0045 |
| chr22 | 51304566 | 12630207 | 0.2462 | 7.4606 |
| chrMT | 16571 | 4177 | 0.2521 | 0.6821 |
| chrX | 155270560 | 100284601 | 0.6459 | 29.153 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 3681958 | 0.062 | 3.6517 |

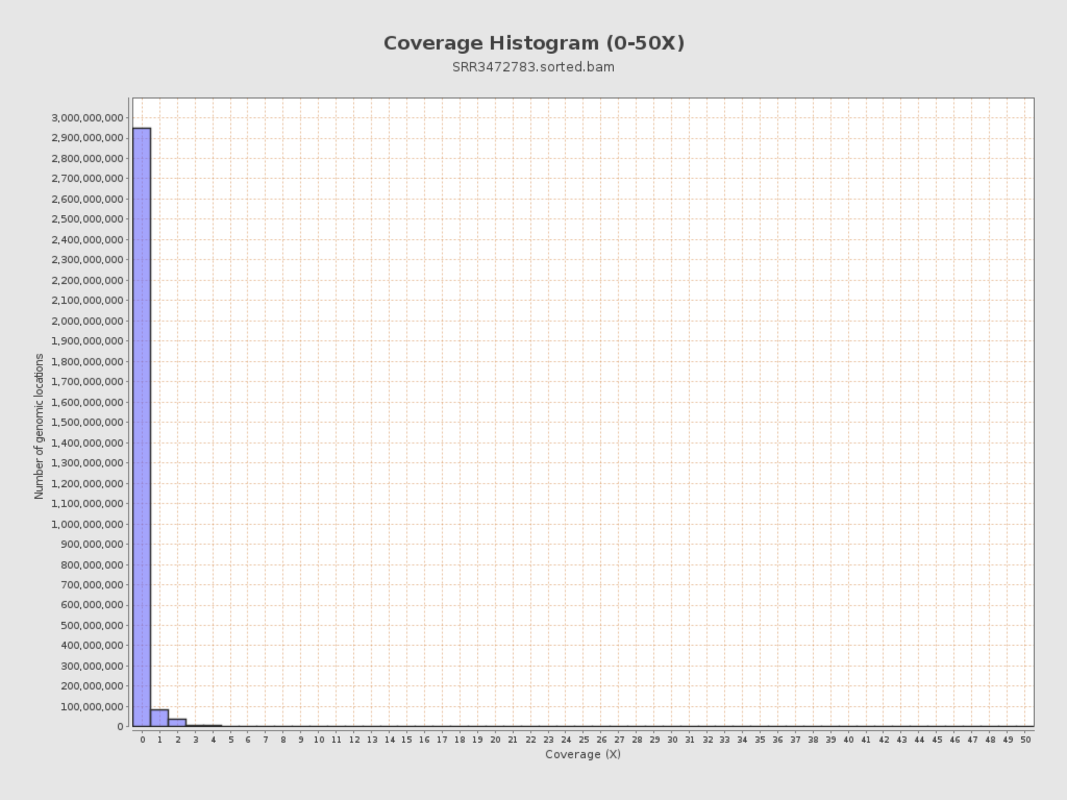
# 3. Results : Coverage across reference



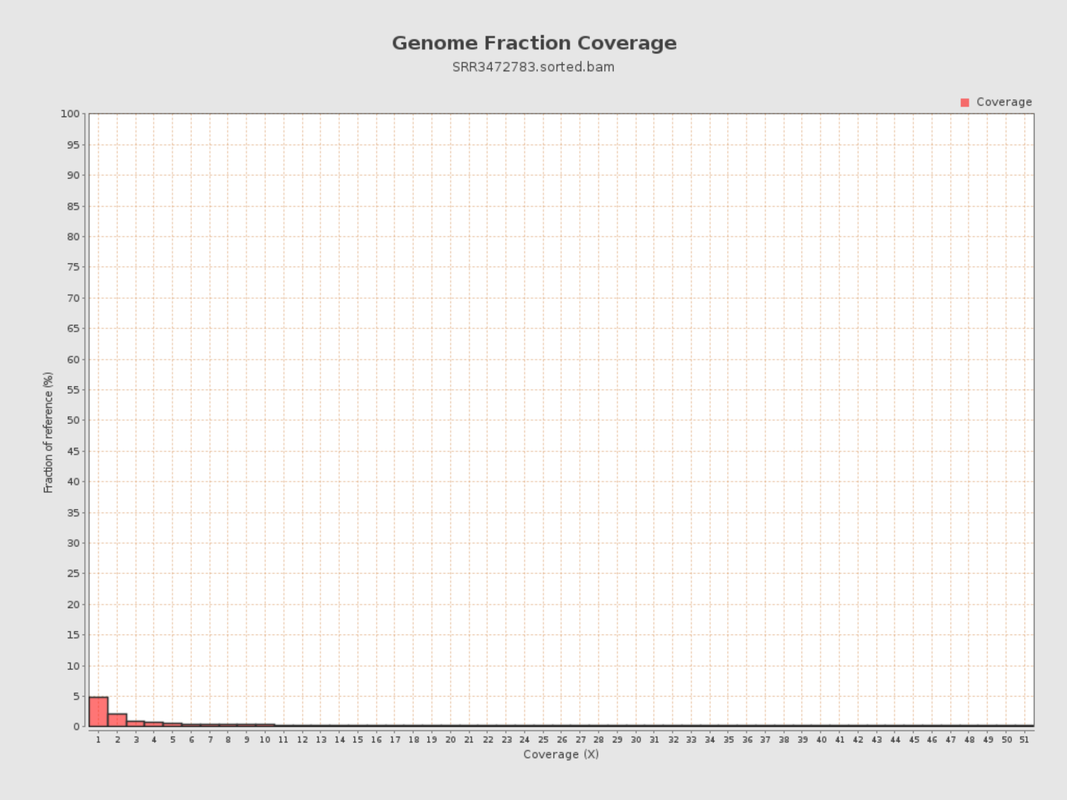
# 4. Results : Coverage Histogram



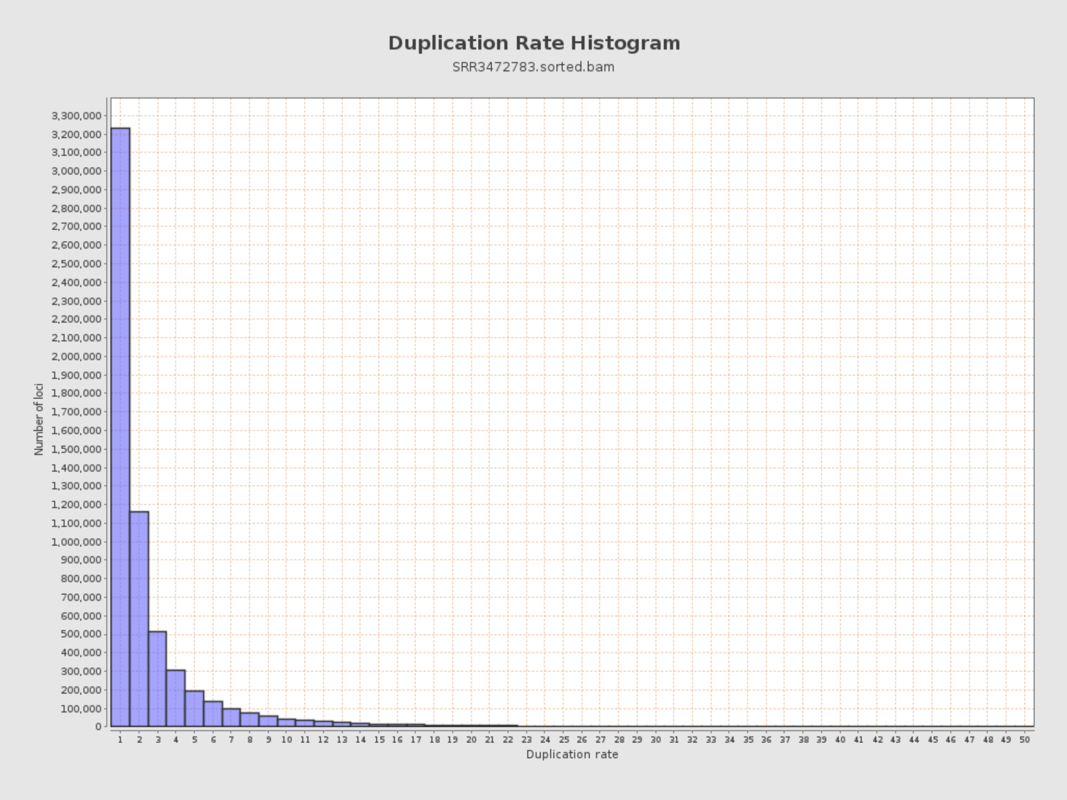
# 5. Results : Coverage Histogram (0-50X)



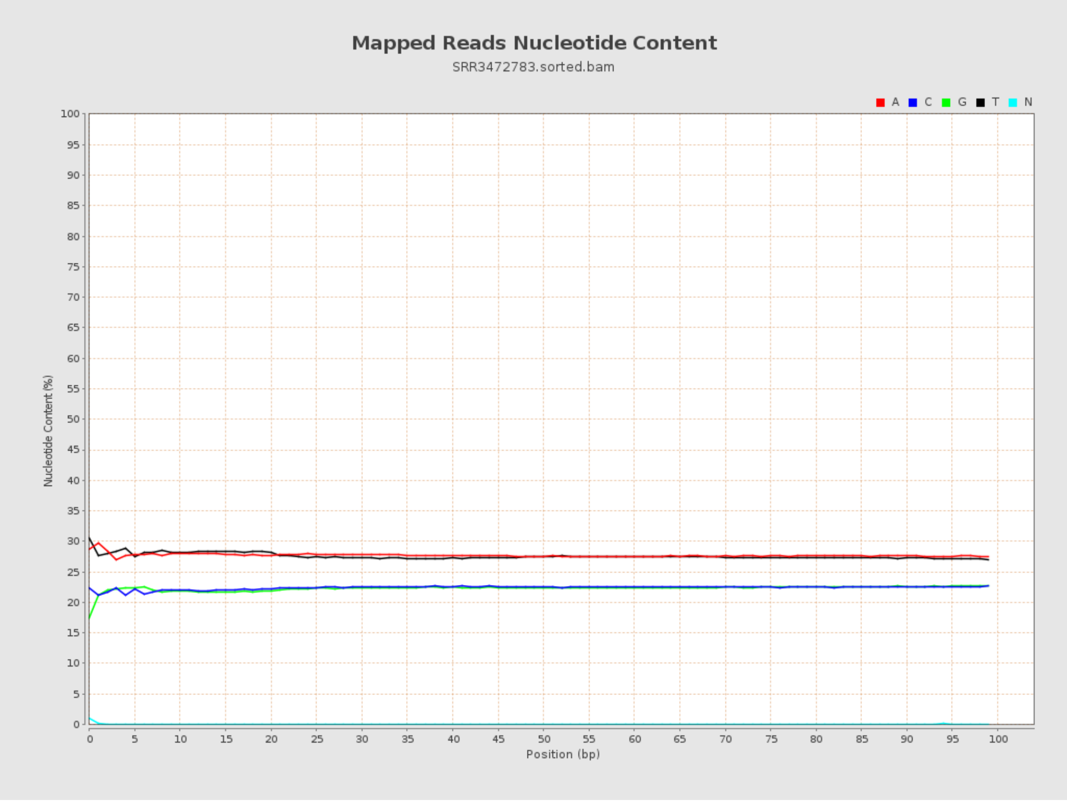
# 6. Results : Genome Fraction Coverage



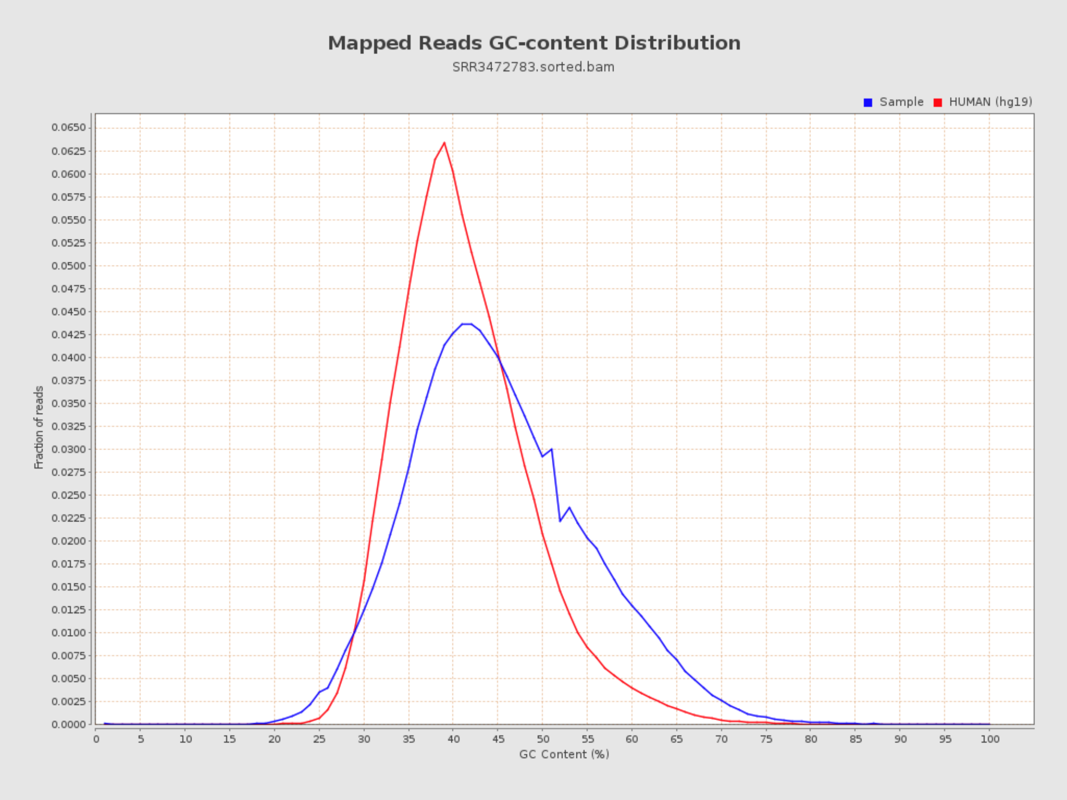
# 7. Results : Duplication Rate Histogram



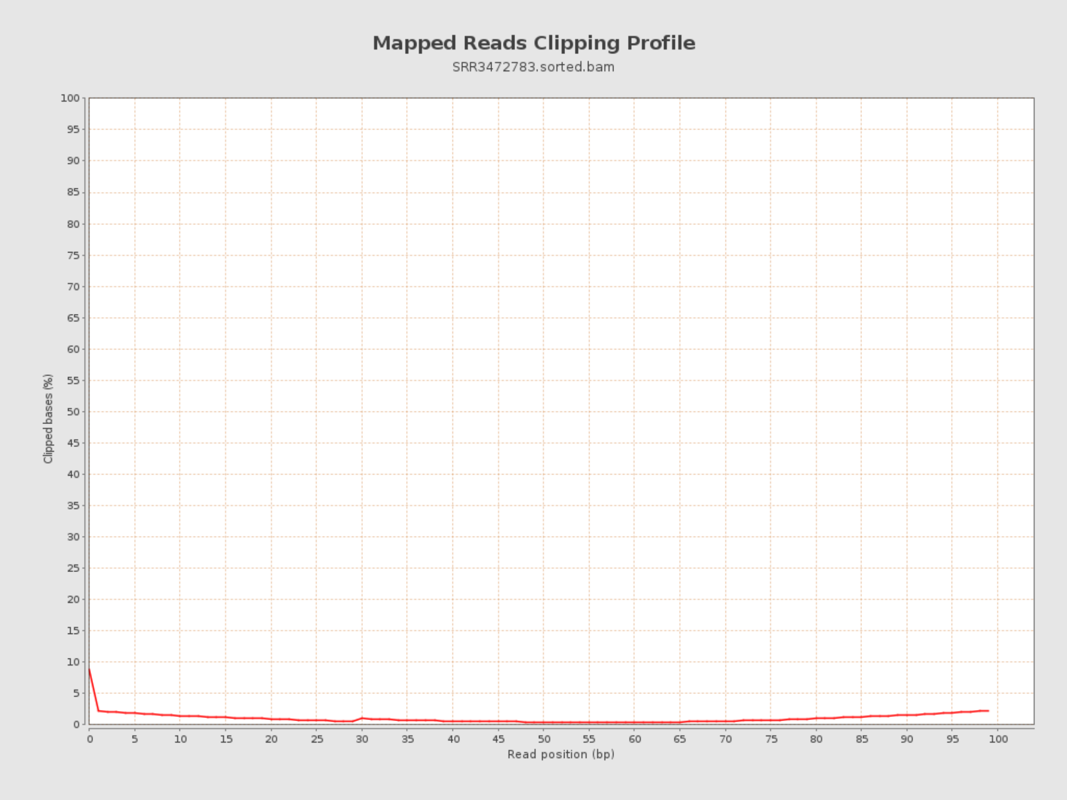
# 8. Results : Mapped Reads Nucleotide Content



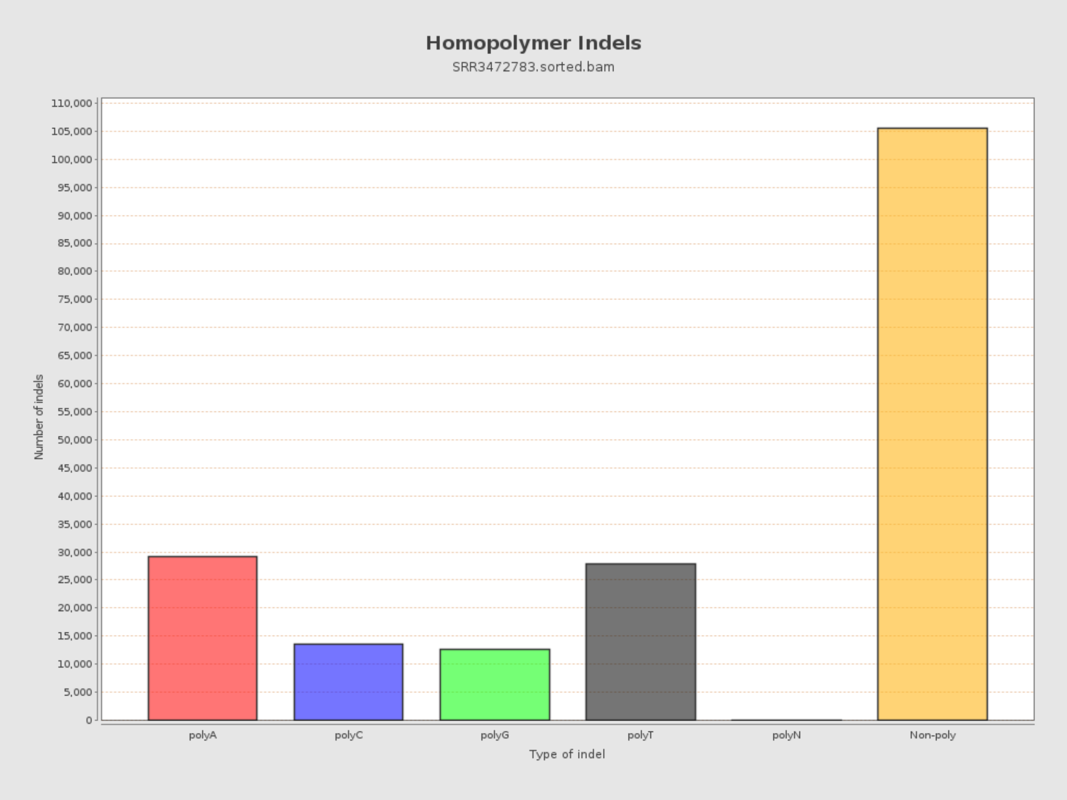
# 9. Results : Mapped Reads GC-content Distribution



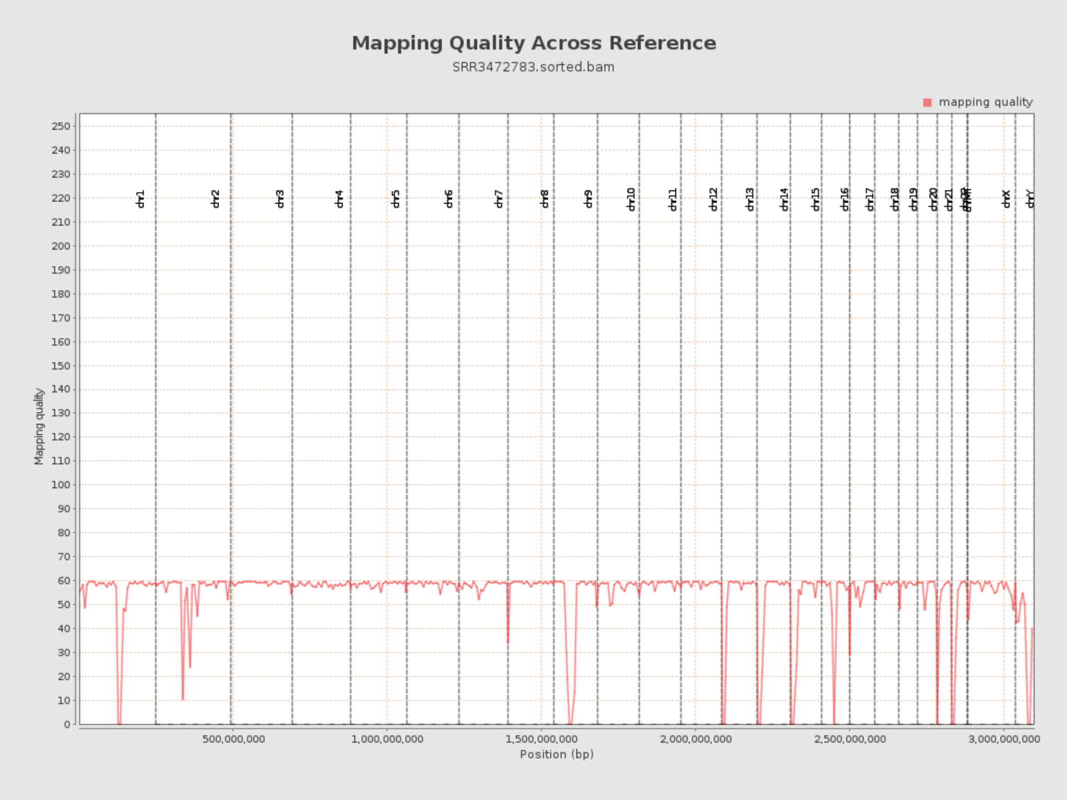
# 10. Results : Mapped Reads Clipping Profile



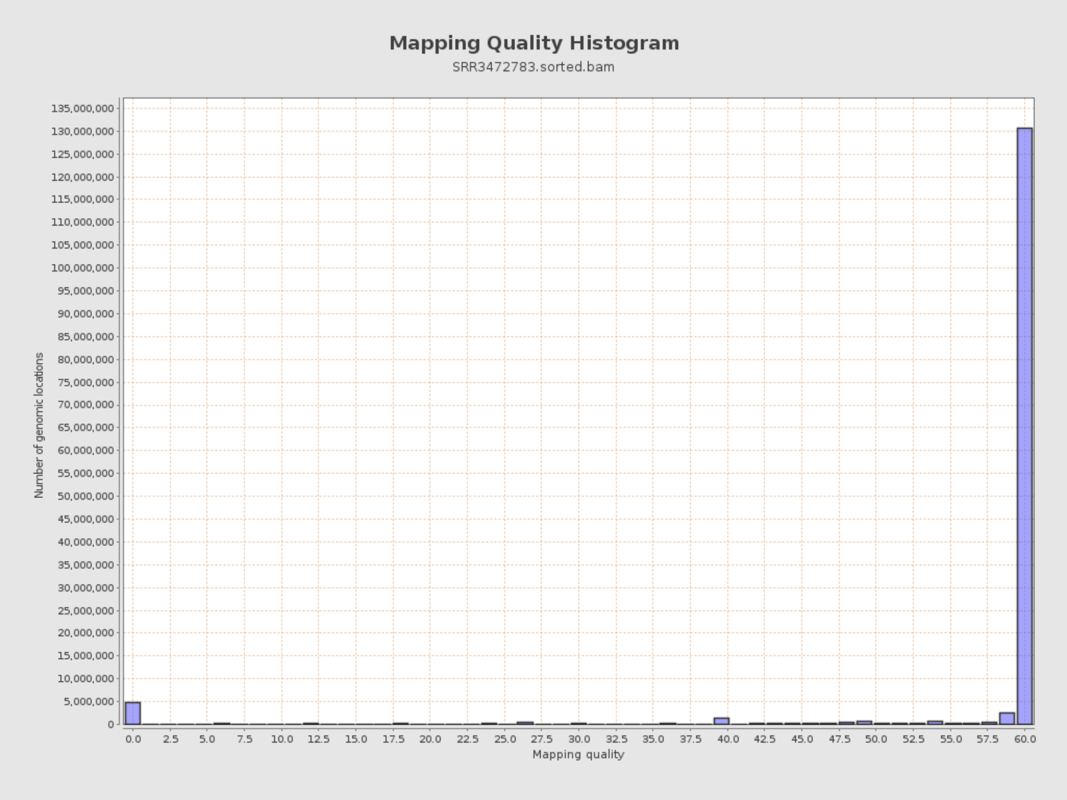
# 11. Results : Homopolymer Indels



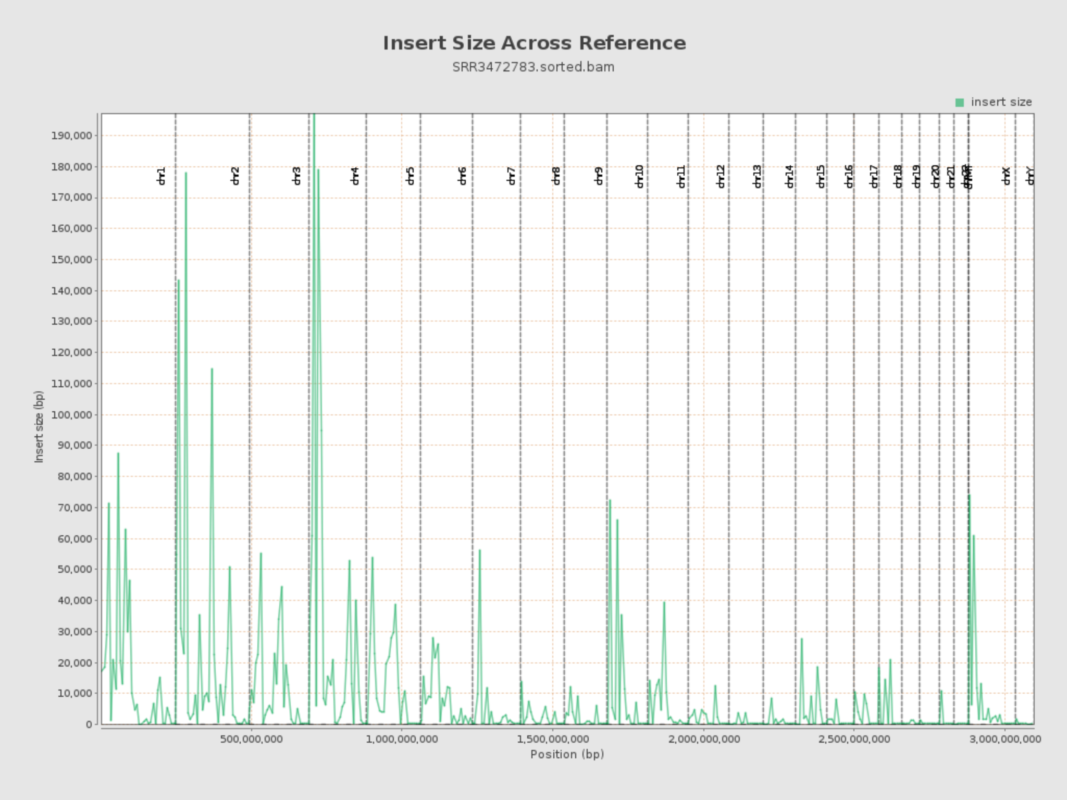
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram