# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/30 13:08:23*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472773.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_SRR3472773 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472773_1.fastq.gz SRR3472773_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 30 13:08:21 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3472773.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 13,755,740 |
| Mapped reads | 13,621,457 / 99.02% |
| Unmapped reads | 134,283 / 0.98% |
| Mapped paired reads | 13,621,457 / 99.02% |
| Mapped reads, first in pair | 6,835,691 / 49.69% |
| Mapped reads, second in pair | 6,785,766 / 49.33% |
| Mapped reads, both in pair | 13,542,040 / 98.45% |
| Mapped reads, singletons | 79,417 / 0.58% |
| Secondary alignments | 0 |
| Supplementary alignments | 46,617 / 0.34% |
| Read min/max/mean length | 30 / 100 / 100.14 |
| Duplicated reads (estimated) | 8,283,890 / 60.22% |
| Duplication rate | 46.62% |
| Clipped reads | 994,114 / 7.23% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 369,868,687 / 27.53% |
| Number/percentage of C's | 304,156,449 / 22.64% |
| Number/percentage of T's | 367,097,816 / 27.32% |
| Number/percentage of G's | 302,117,001 / 22.49% |
| Number/percentage of N's | 256,170 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 45.13% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.434 |
| Standard Deviation | 14.6503 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 55.21 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 21,164.48 |
| Standard Deviation | 1,421,673.74 |
| P25/Median/P75 | 184 / 257 / 342 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.66% |
| Mismatches | 8,654,155 |
| Insertions | 73,868 |
| Mapped reads with at least one insertion | 0.54% |
| Deletions | 74,722 |
| Mapped reads with at least one deletion | 0.54% |
| Homopolymer indels | 46.74% |

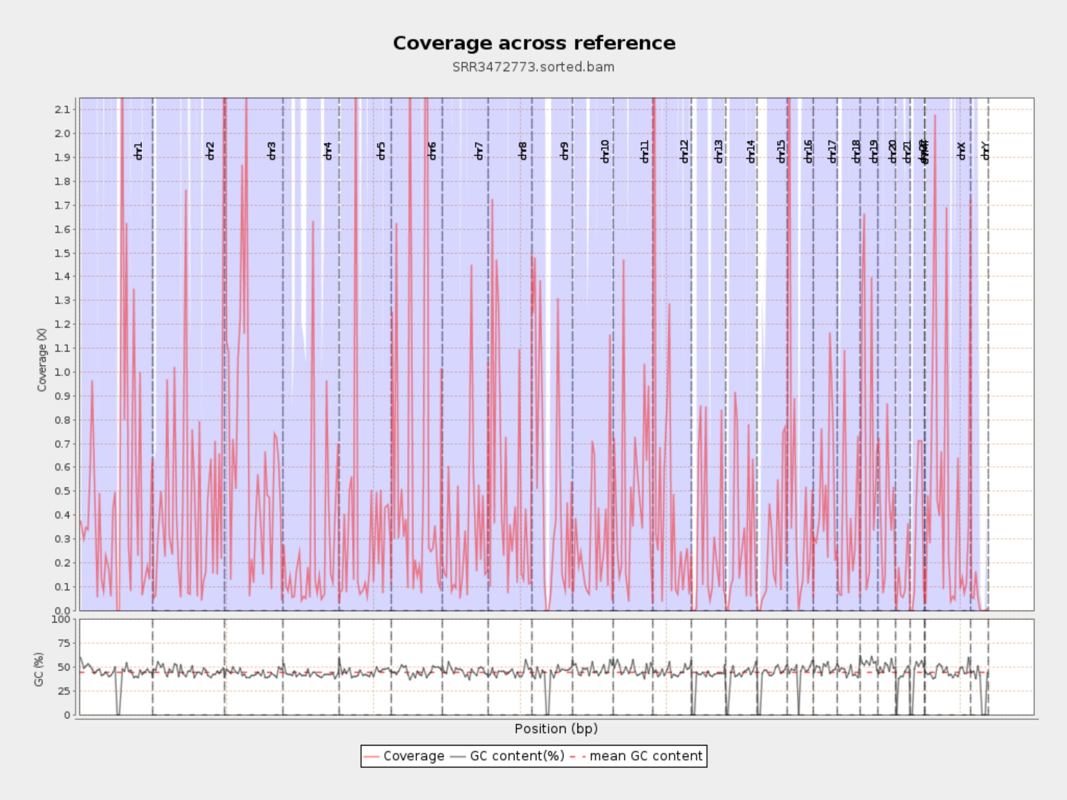
## 2.7. Chromosome stats

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

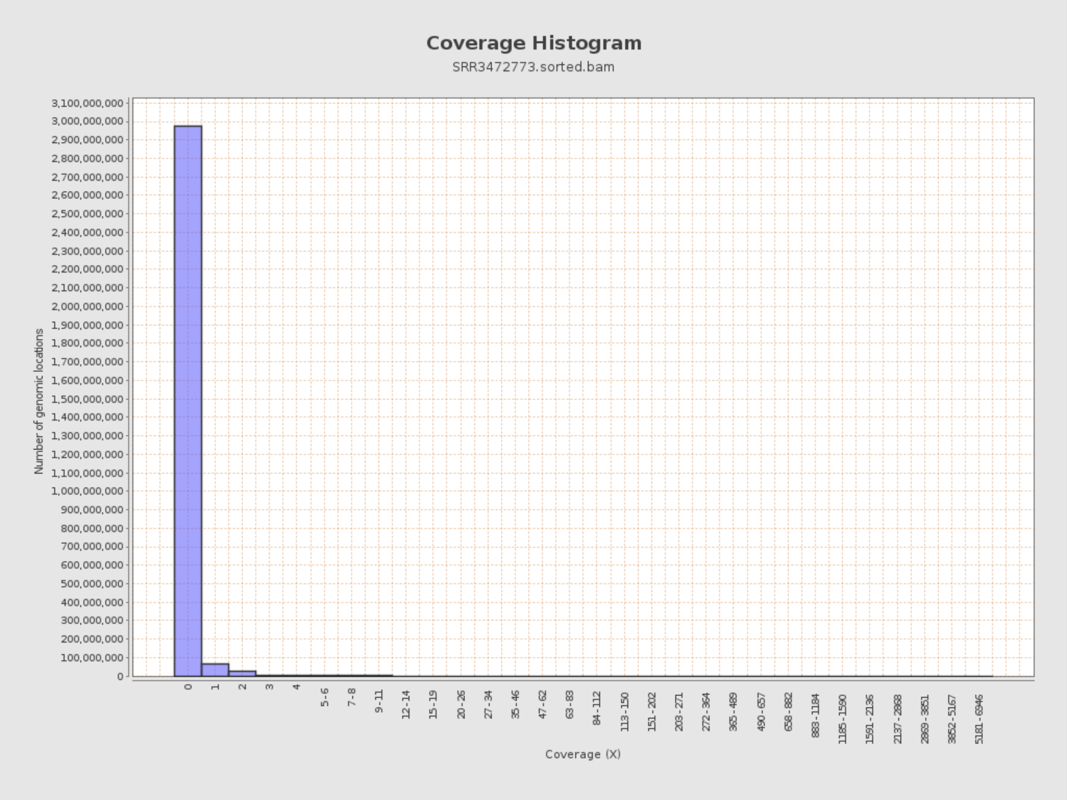
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 117730338 | 0.4723 | 14.61 |
| chr2 | 243199373 | 105518523 | 0.4339 | 15.3271 |
| chr3 | 198022430 | 143770390 | 0.726 | 15.7128 |
| chr4 | 191154276 | 48482153 | 0.2536 | 10.8887 |
| chr5 | 180915260 | 62482725 | 0.3454 | 10.164 |
| chr6 | 171115067 | 104303287 | 0.6096 | 22.7055 |
| chr7 | 159138663 | 52258061 | 0.3284 | 9.2953 |
| chr8 | 146364022 | 74227690 | 0.5071 | 17.994 |
| chr9 | 141213431 | 75628087 | 0.5356 | 14.7264 |
| chr10 | 135534747 | 40876648 | 0.3016 | 13.8982 |
| chr11 | 135006516 | 68686002 | 0.5088 | 16.0982 |
| chr12 | 133851895 | 72350409 | 0.5405 | 17.0967 |
| chr13 | 115169878 | 33182397 | 0.2881 | 12.0152 |
| chr14 | 107349540 | 33252737 | 0.3098 | 14.581 |
| chr15 | 102531392 | 26986755 | 0.2632 | 8.9175 |
| chr16 | 90354753 | 46396263 | 0.5135 | 14.2967 |
| chr17 | 81195210 | 39441615 | 0.4858 | 10.3755 |
| chr18 | 78077248 | 26941358 | 0.3451 | 14.5229 |
| chr19 | 59128983 | 44275484 | 0.7488 | 23.0554 |
| chr20 | 63025520 | 26630908 | 0.4225 | 14.5587 |
| chr21 | 48129895 | 6663041 | 0.1384 | 6.5122 |
| chr22 | 51304566 | 16045846 | 0.3128 | 9.5195 |
| chrMT | 16571 | 2952 | 0.1781 | 0.6009 |
| chrX | 155270560 | 75091278 | 0.4836 | 16.1606 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 2455450 | 0.0414 | 1.8517 |

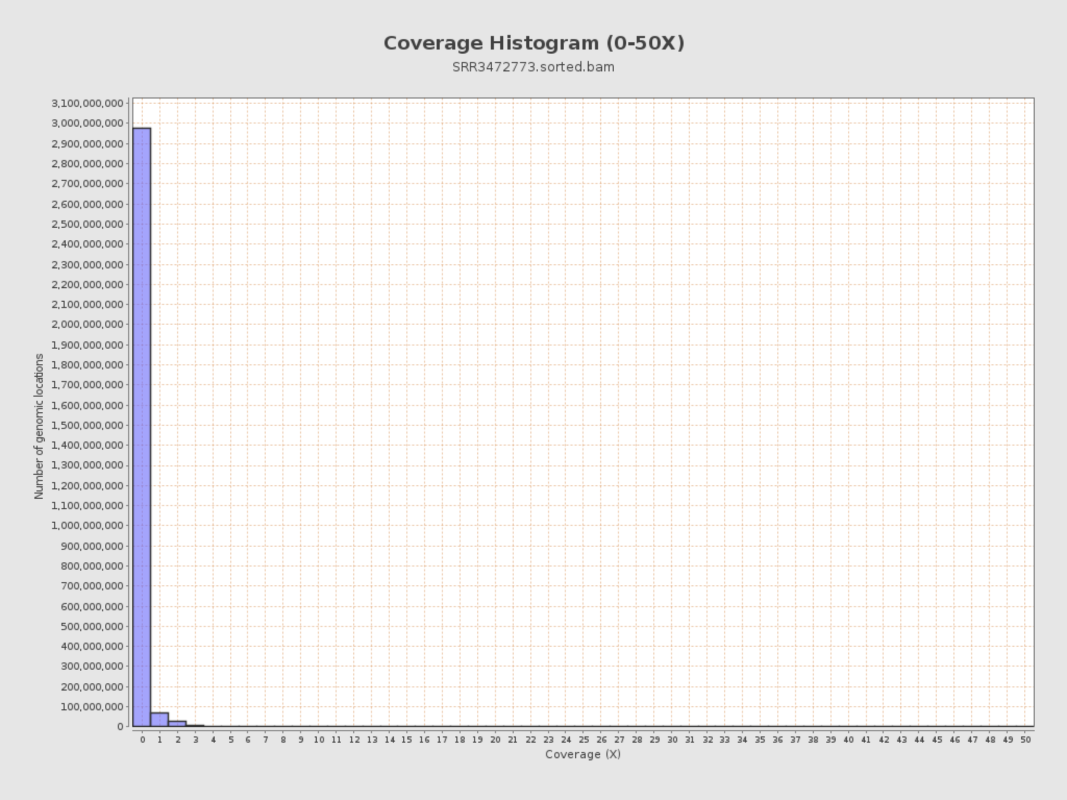
# 3. Results : Coverage across reference



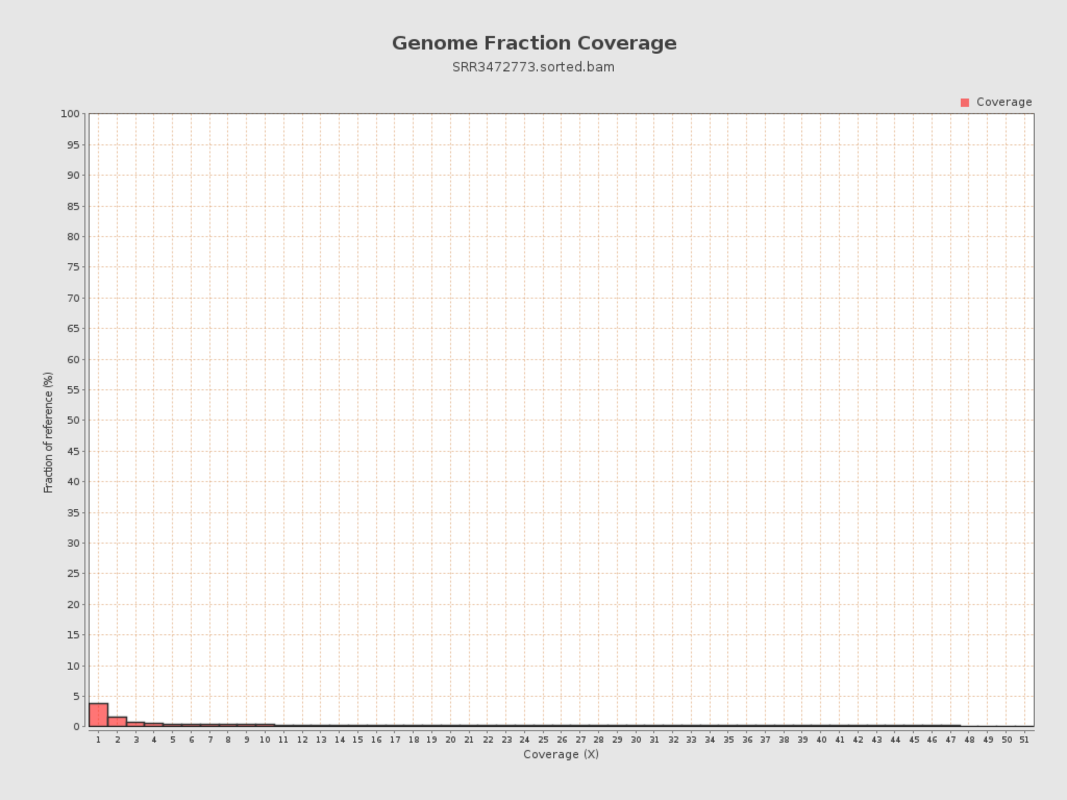
# 4. Results : Coverage Histogram



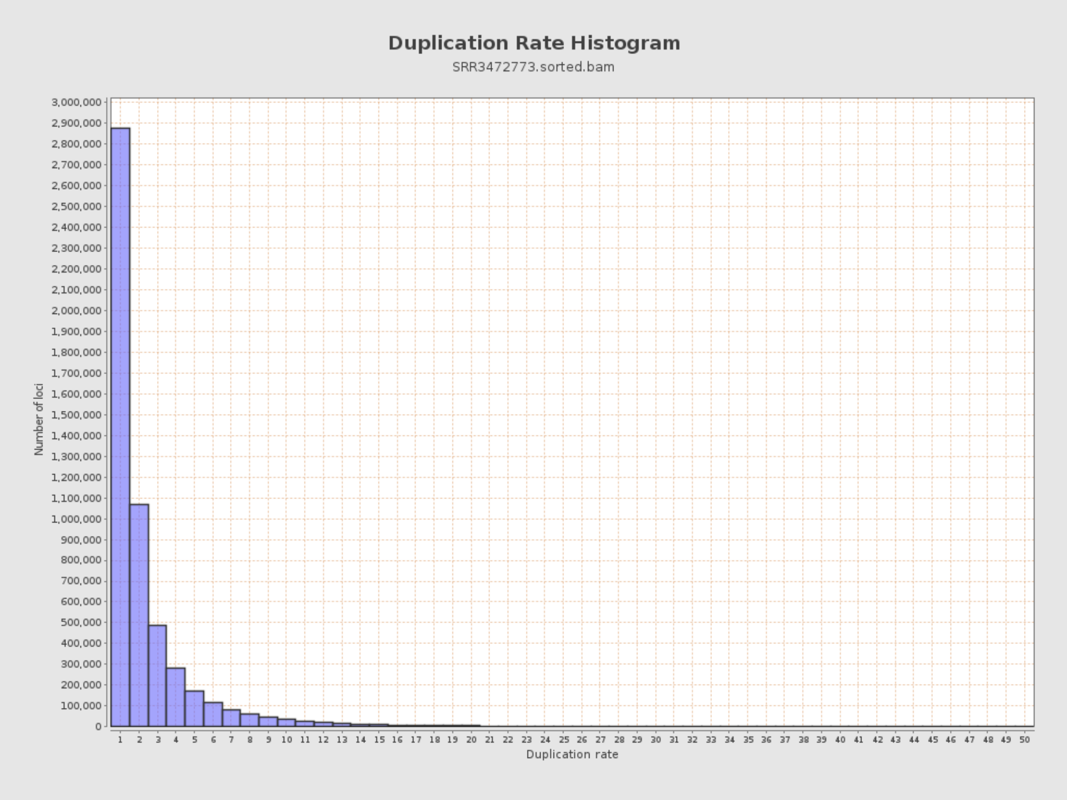
# 5. Results : Coverage Histogram (0-50X)



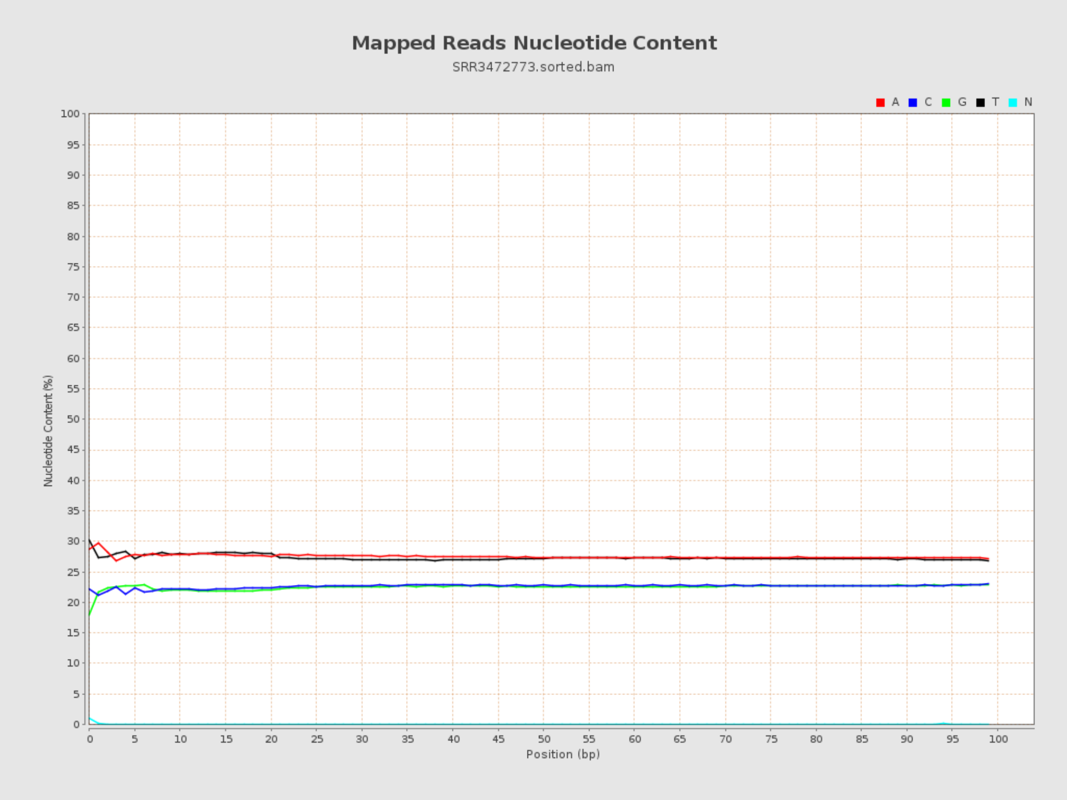
# 6. Results : Genome Fraction Coverage



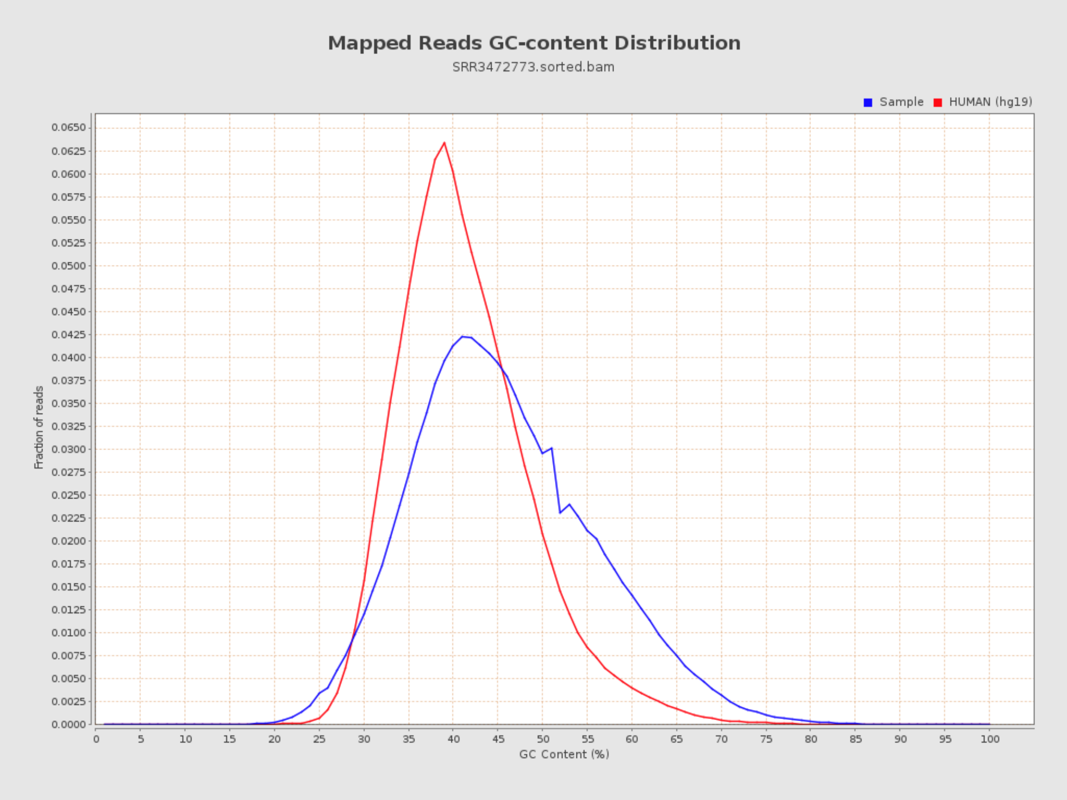
# 7. Results : Duplication Rate Histogram



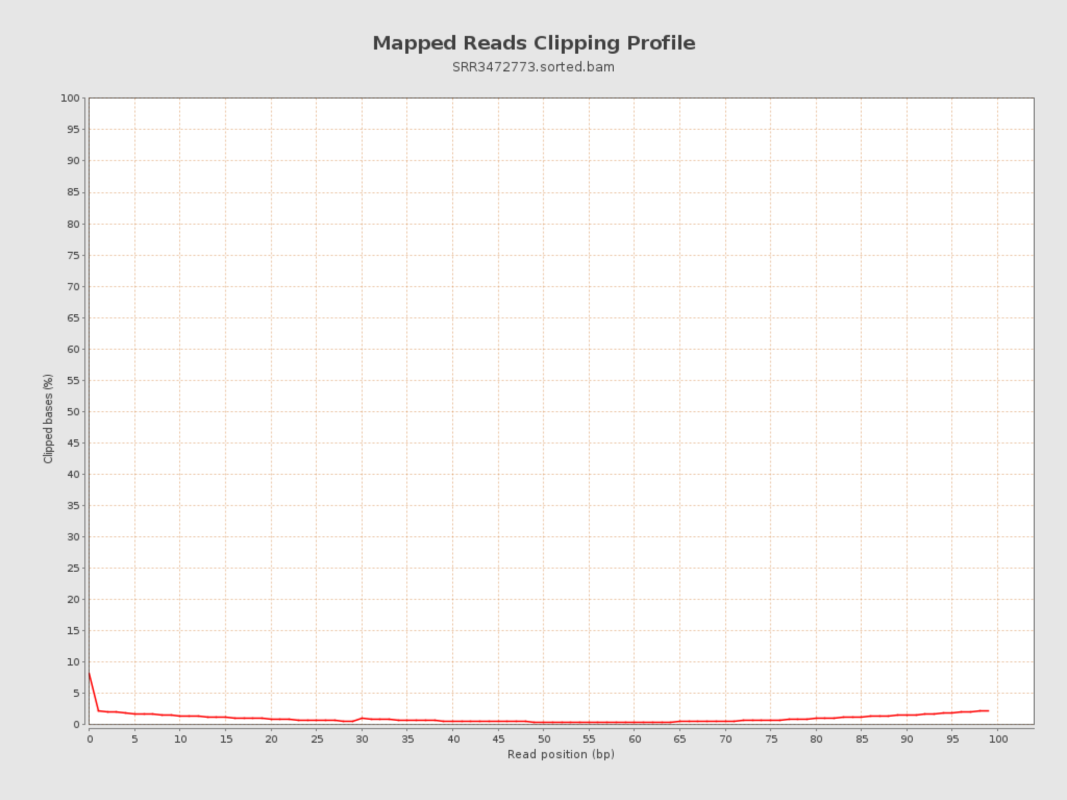
# 8. Results : Mapped Reads Nucleotide Content



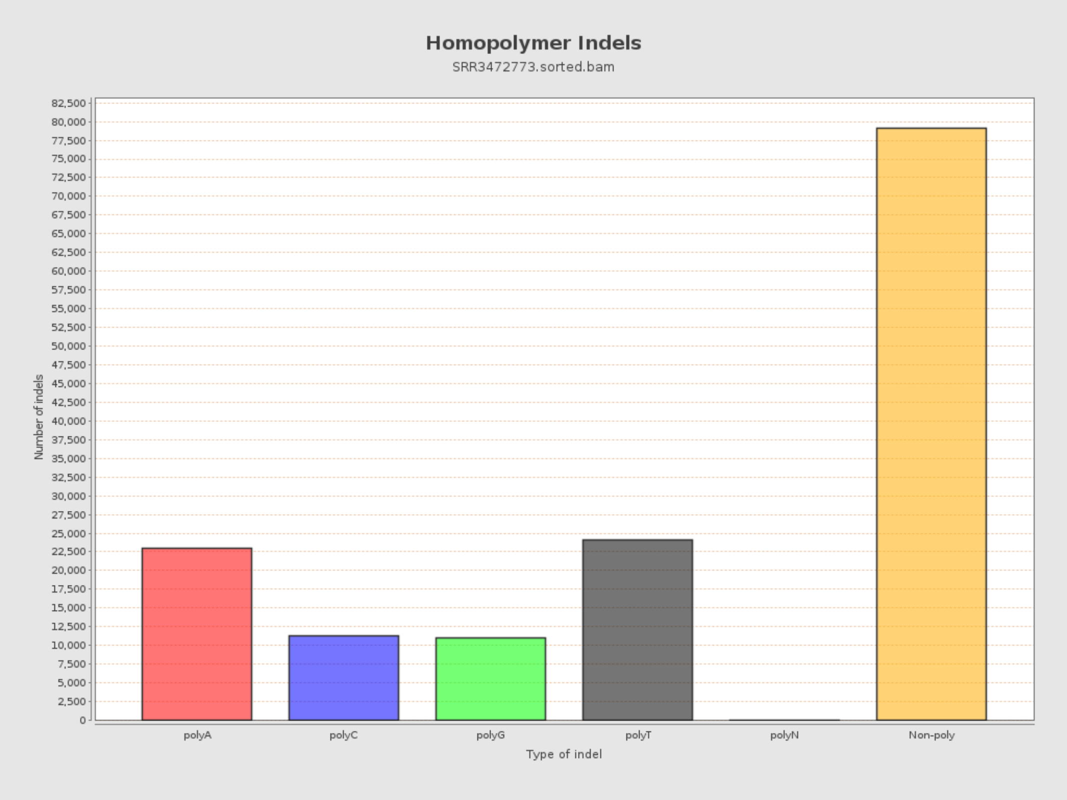
# 9. Results : Mapped Reads GC-content Distribution



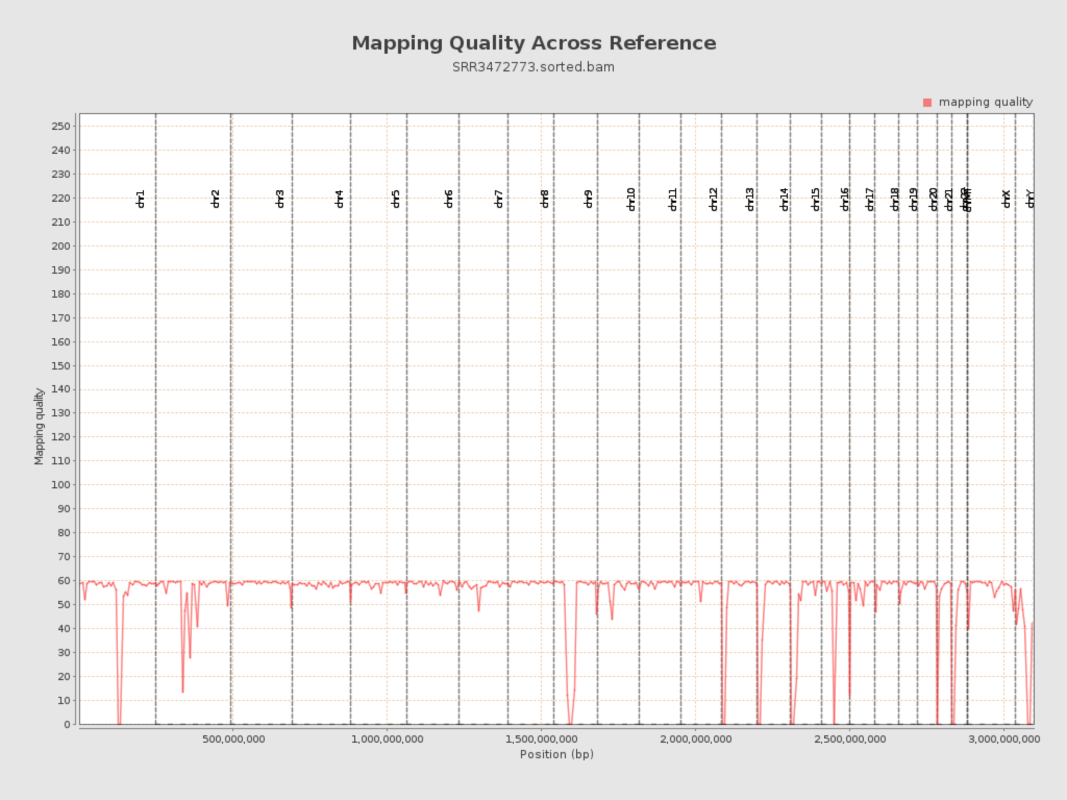
# 10. Results : Mapped Reads Clipping Profile



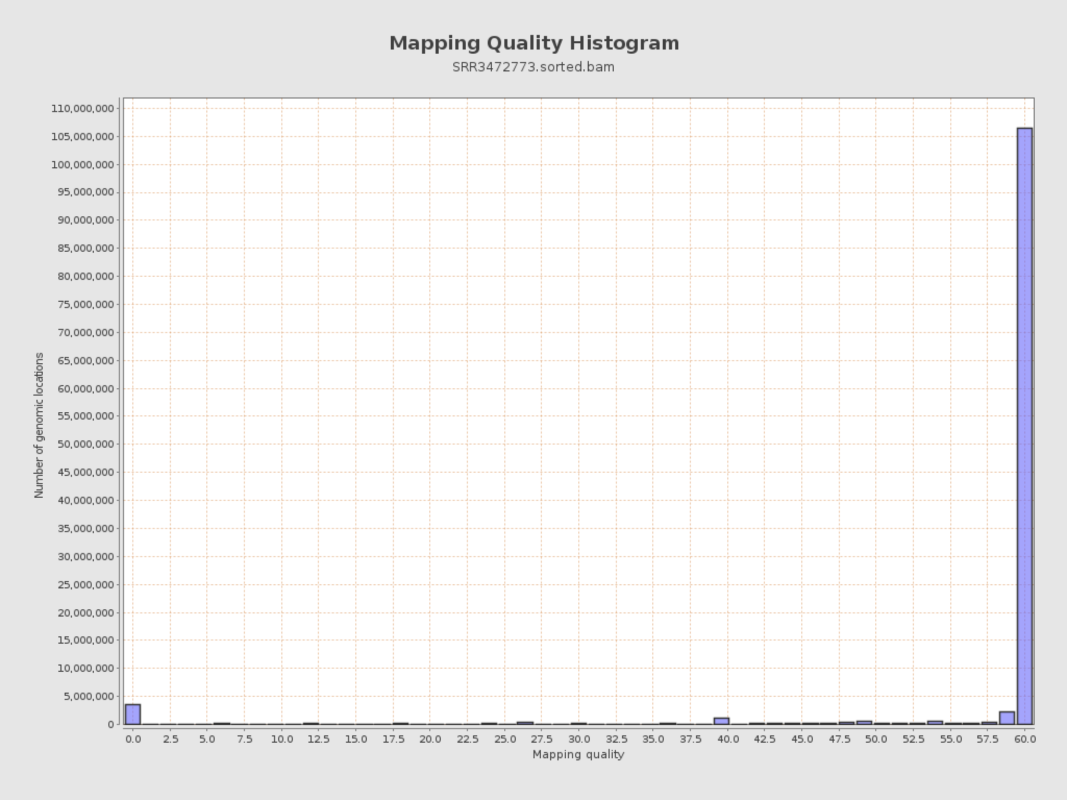
# 11. Results : Homopolymer Indels



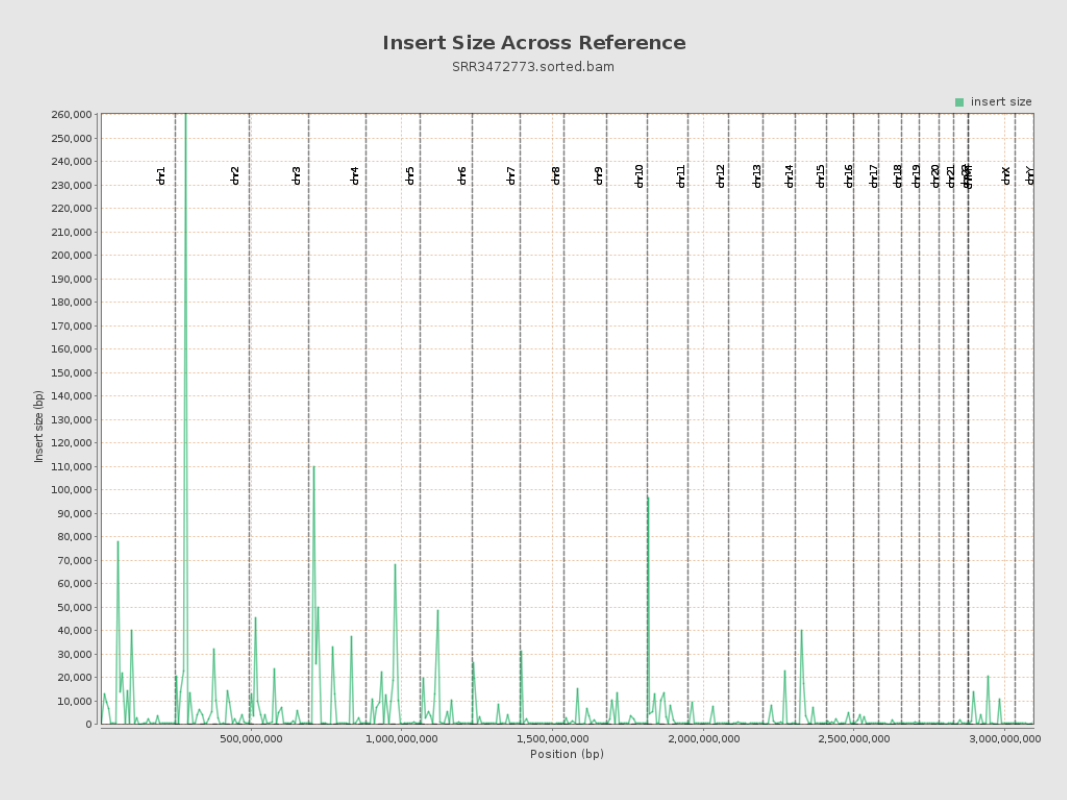
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram