# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/28 16:50:17*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472631.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_SRR3472631 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472631_1.fastq.gz SRR3472631_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 28 16:50:16 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3472631.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 17,559,254 |
| Mapped reads | 17,400,065 / 99.09% |
| Unmapped reads | 159,189 / 0.91% |
| Mapped paired reads | 17,400,065 / 99.09% |
| Mapped reads, first in pair | 8,721,067 / 49.67% |
| Mapped reads, second in pair | 8,678,998 / 49.43% |
| Mapped reads, both in pair | 17,300,688 / 98.53% |
| Mapped reads, singletons | 99,377 / 0.57% |
| Secondary alignments | 0 |
| Supplementary alignments | 80,443 / 0.46% |
| Read min/max/mean length | 30 / 101 / 99.65 |
| Duplicated reads (estimated) | 12,046,056 / 68.6% |
| Duplication rate | 50.35% |
| Clipped reads | 1,275,855 / 7.27% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 446,689,331 / 26.15% |
| Number/percentage of C's | 410,352,238 / 24.02% |
| Number/percentage of T's | 446,612,099 / 26.14% |
| Number/percentage of G's | 404,517,012 / 23.68% |
| Number/percentage of N's | 317,760 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 47.7% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.552 |
| Standard Deviation | 22.2472 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 54.77 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 20,519.07 |
| Standard Deviation | 1,410,958.91 |
| P25/Median/P75 | 154 / 213 / 282 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.63% |
| Mismatches | 10,603,571 |
| Insertions | 103,602 |
| Mapped reads with at least one insertion | 0.59% |
| Deletions | 87,539 |
| Mapped reads with at least one deletion | 0.5% |
| Homopolymer indels | 47.43% |

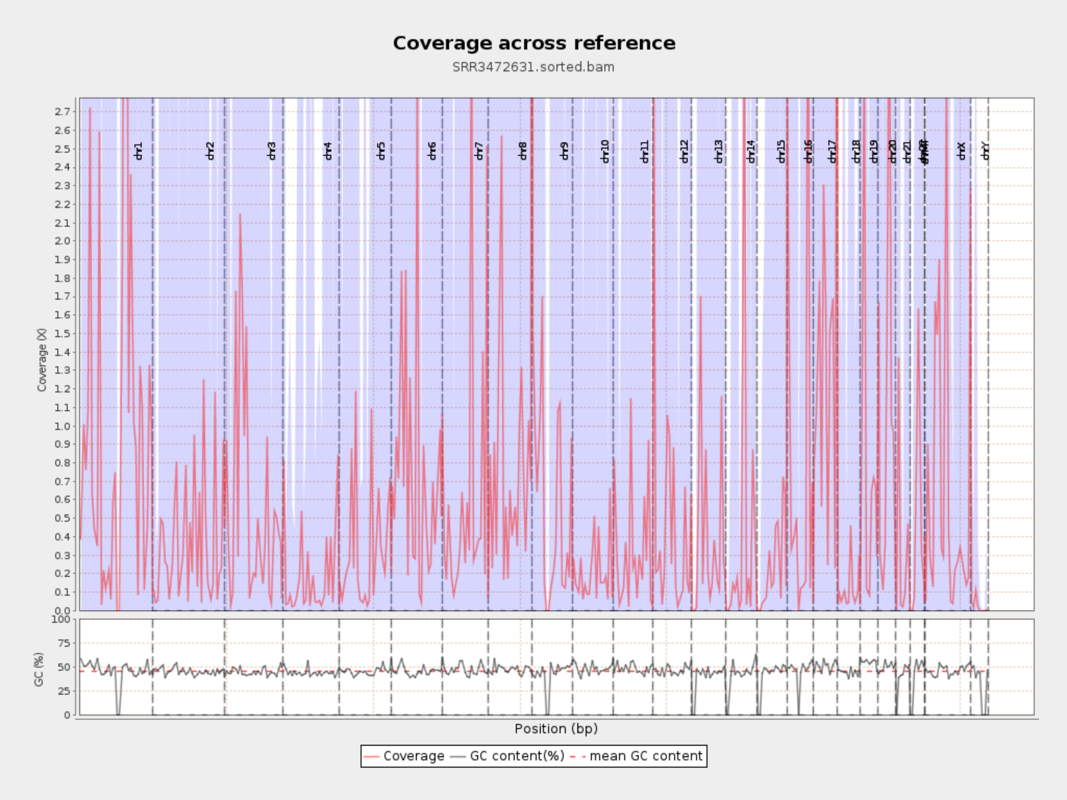
## 2.7. Chromosome stats

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

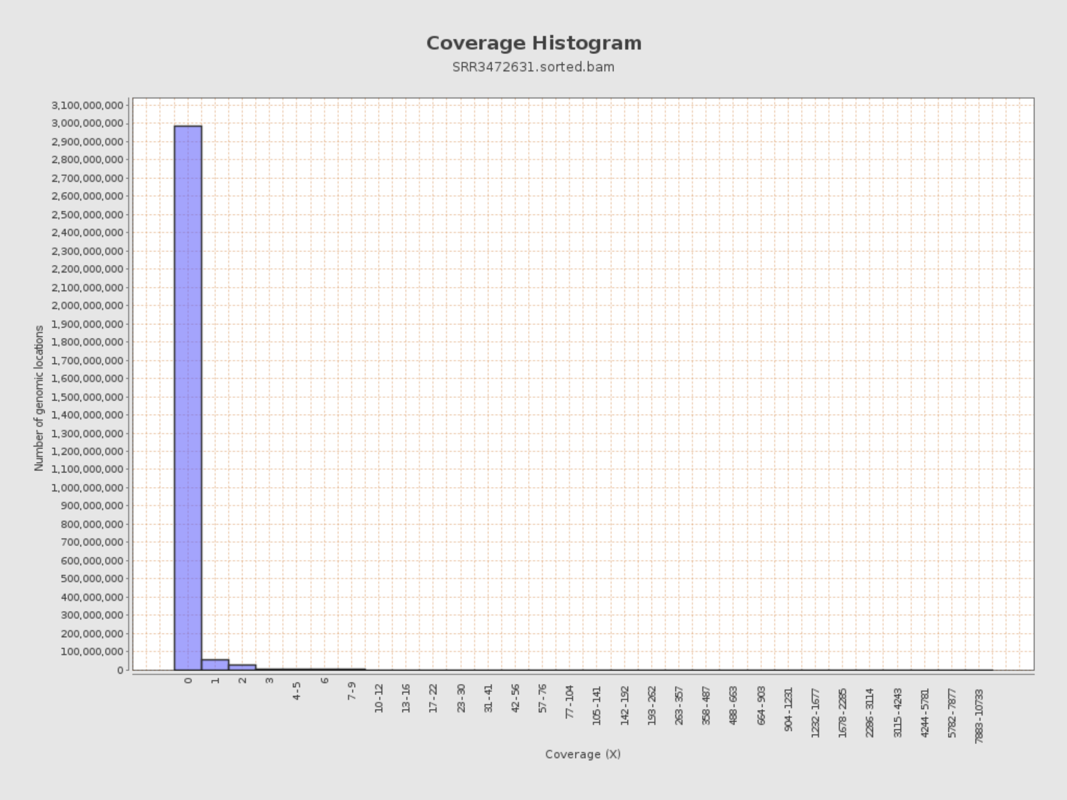
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 262319148 | 1.0524 | 37.9959 |
| chr2 | 243199373 | 89162577 | 0.3666 | 14.9239 |
| chr3 | 198022430 | 113922190 | 0.5753 | 19.2566 |
| chr4 | 191154276 | 35667533 | 0.1866 | 11.3752 |
| chr5 | 180915260 | 61369841 | 0.3392 | 13.8849 |
| chr6 | 171115067 | 130563975 | 0.763 | 25.0036 |
| chr7 | 159138663 | 102719354 | 0.6455 | 24.8846 |
| chr8 | 146364022 | 108673675 | 0.7425 | 25.1426 |
| chr9 | 141213431 | 92615208 | 0.6559 | 18.5136 |
| chr10 | 135534747 | 29084626 | 0.2146 | 10.2677 |
| chr11 | 135006516 | 44784022 | 0.3317 | 17.2403 |
| chr12 | 133851895 | 64413812 | 0.4812 | 15.2179 |
| chr13 | 115169878 | 46232667 | 0.4014 | 15.1435 |
| chr14 | 107349540 | 39873597 | 0.3714 | 27.7345 |
| chr15 | 102531392 | 24647075 | 0.2404 | 9.9464 |
| chr16 | 90354753 | 76566753 | 0.8474 | 33.0056 |
| chr17 | 81195210 | 111968133 | 1.379 | 34.1455 |
| chr18 | 78077248 | 9551026 | 0.1223 | 6.0293 |
| chr19 | 59128983 | 51191423 | 0.8658 | 22.0945 |
| chr20 | 63025520 | 72480153 | 1.15 | 30.2893 |
| chr21 | 48129895 | 16452652 | 0.3418 | 27.7461 |
| chr22 | 51304566 | 23089000 | 0.45 | 21.395 |
| chrMT | 16571 | 6744 | 0.407 | 0.751 |
| chrX | 155270560 | 99934455 | 0.6436 | 24.1521 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1409574 | 0.0237 | 1.397 |

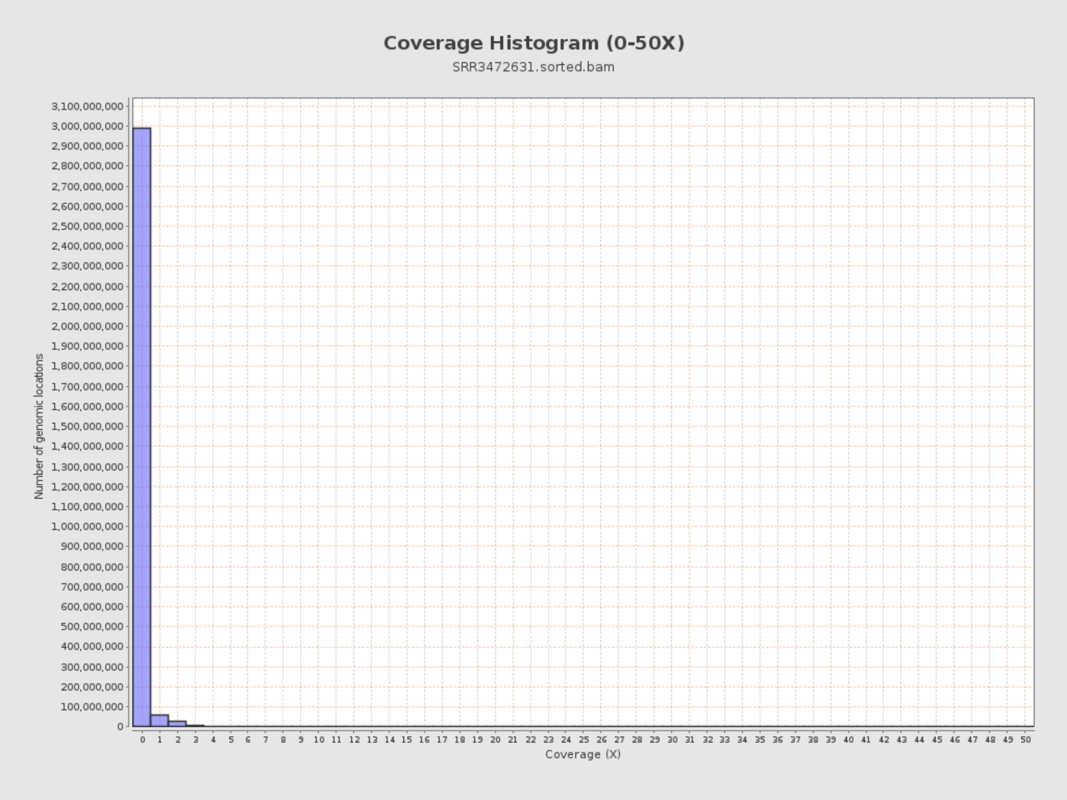
# 3. Results : Coverage across reference



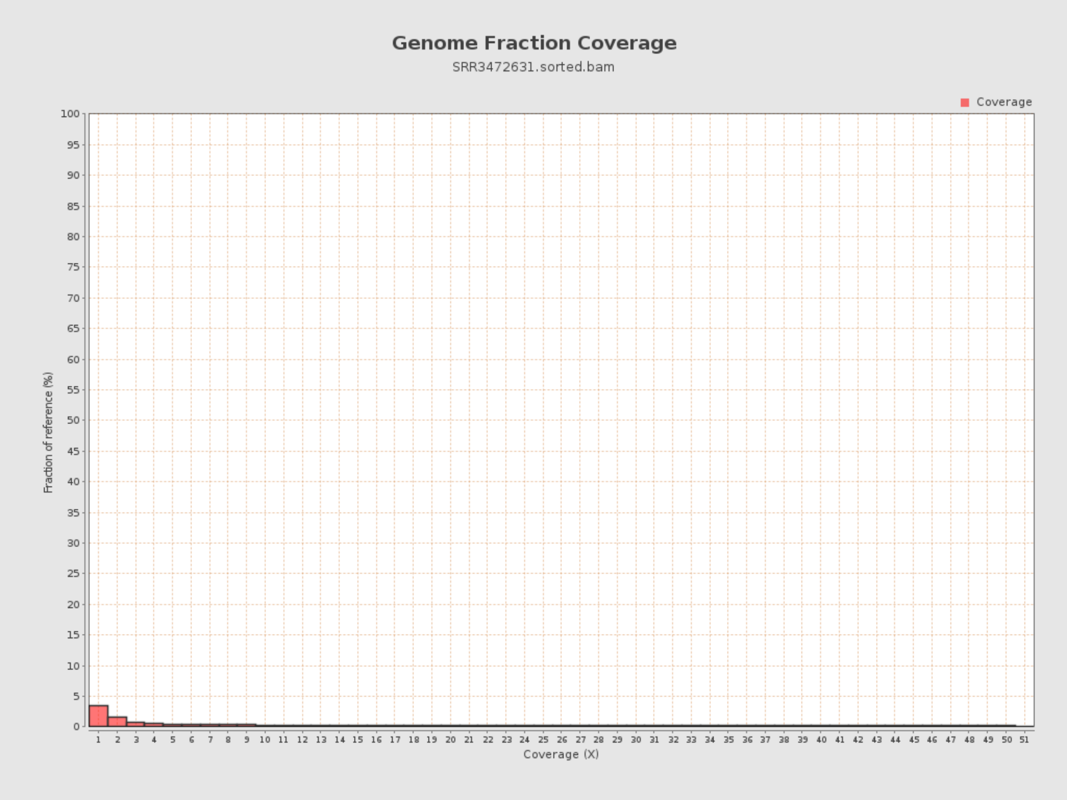
# 4. Results : Coverage Histogram



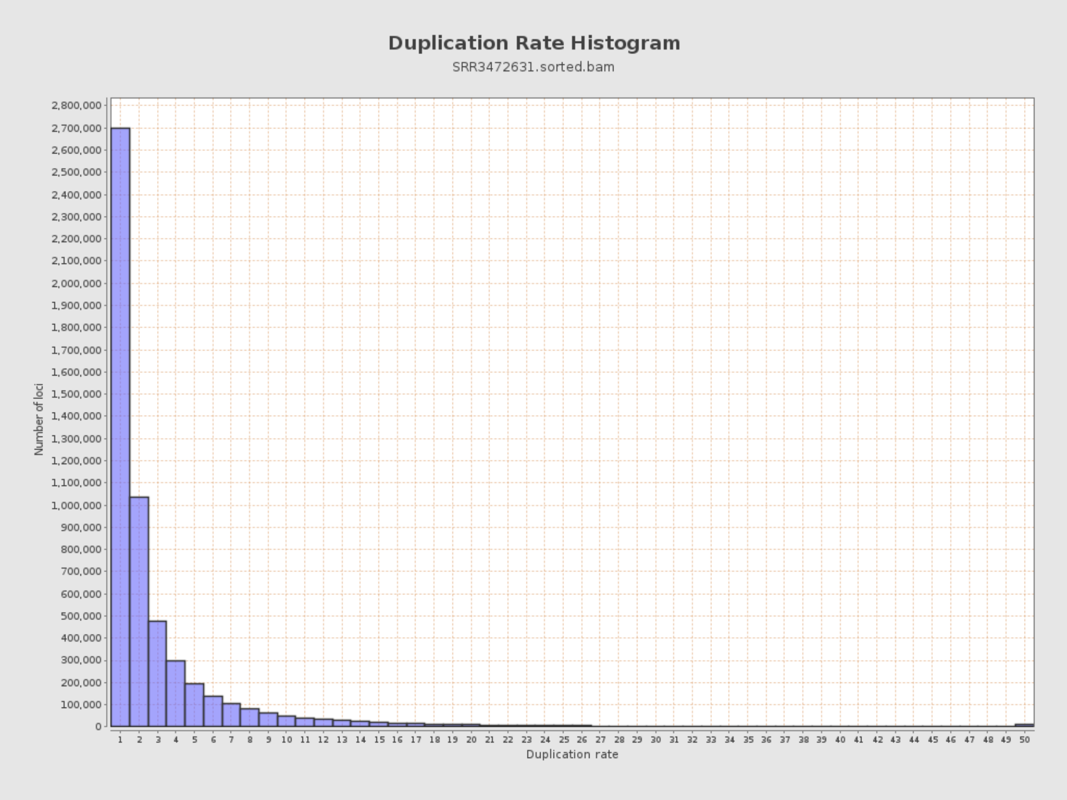
# 5. Results : Coverage Histogram (0-50X)



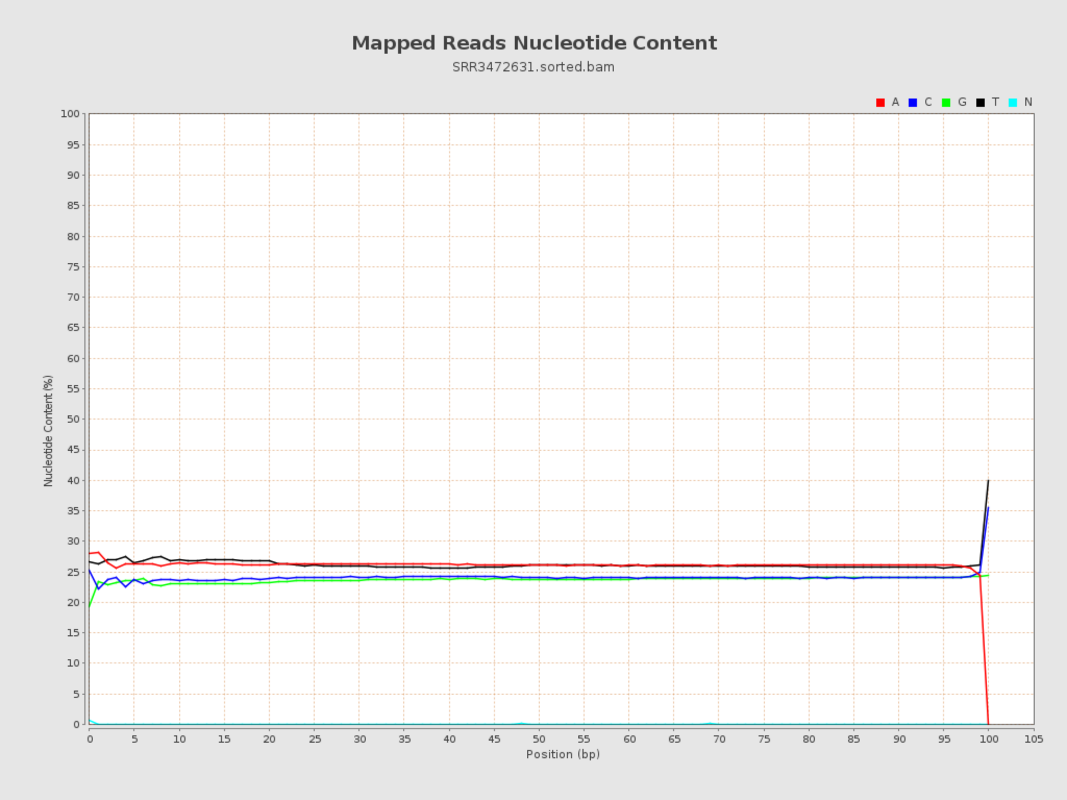
# 6. Results : Genome Fraction Coverage



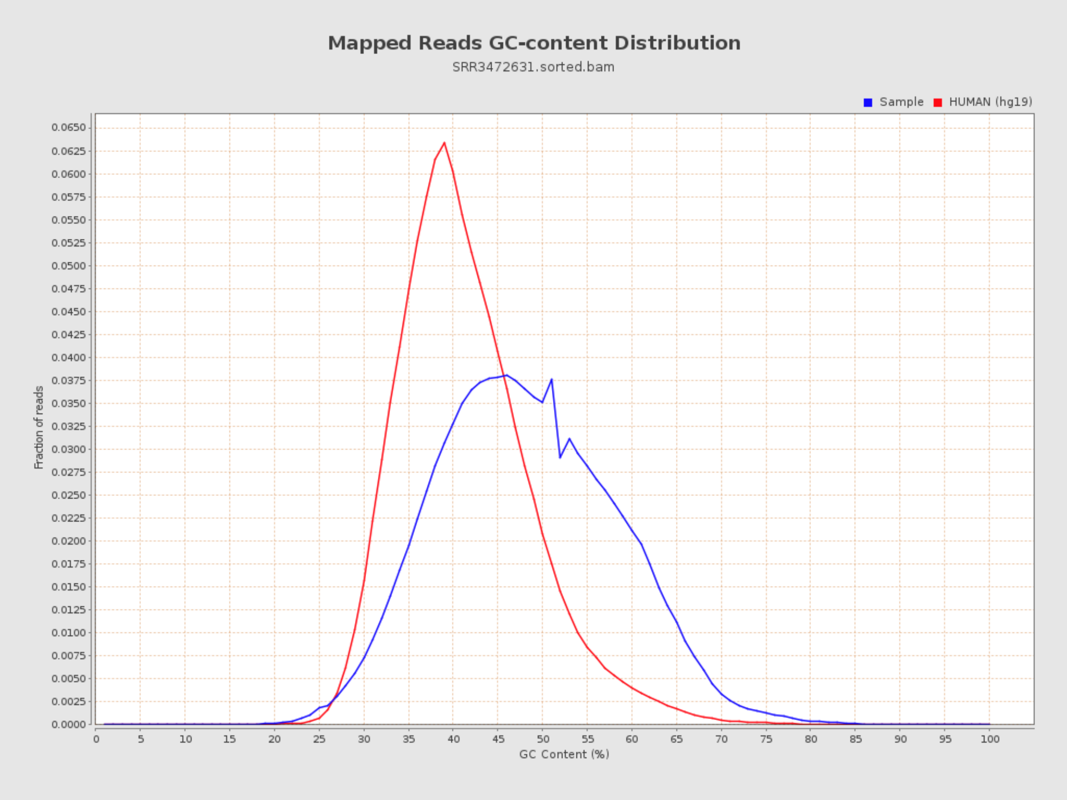
# 7. Results : Duplication Rate Histogram



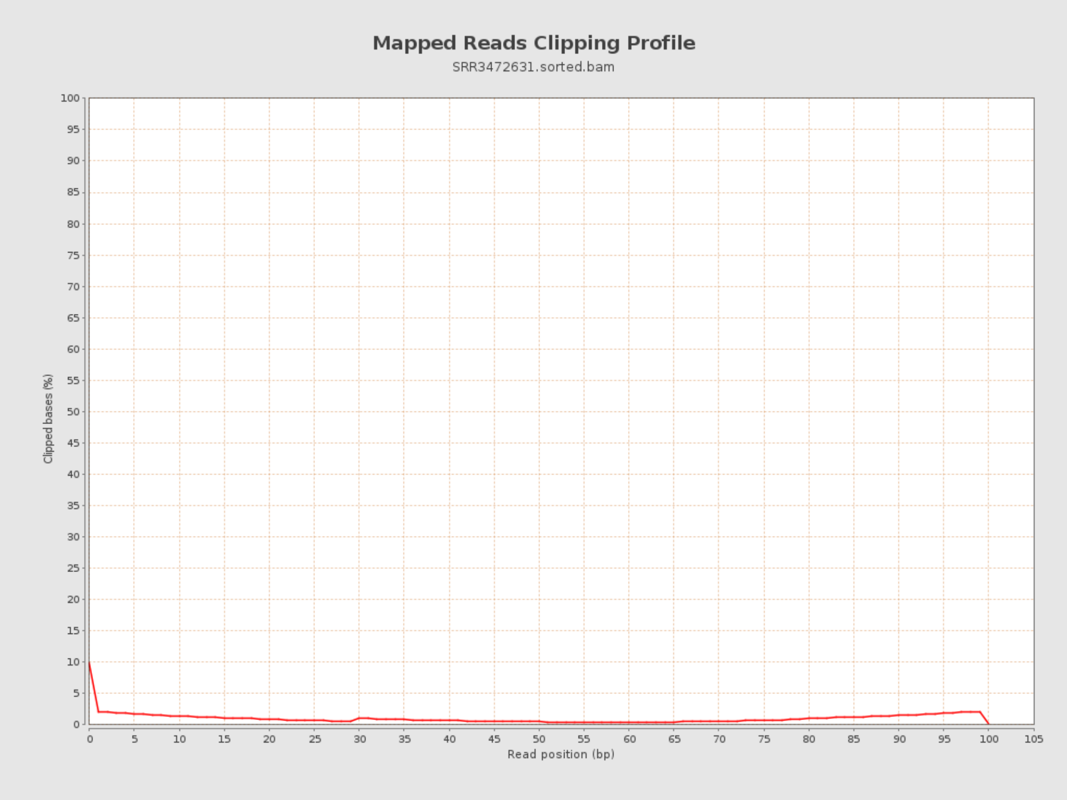
# 8. Results : Mapped Reads Nucleotide Content



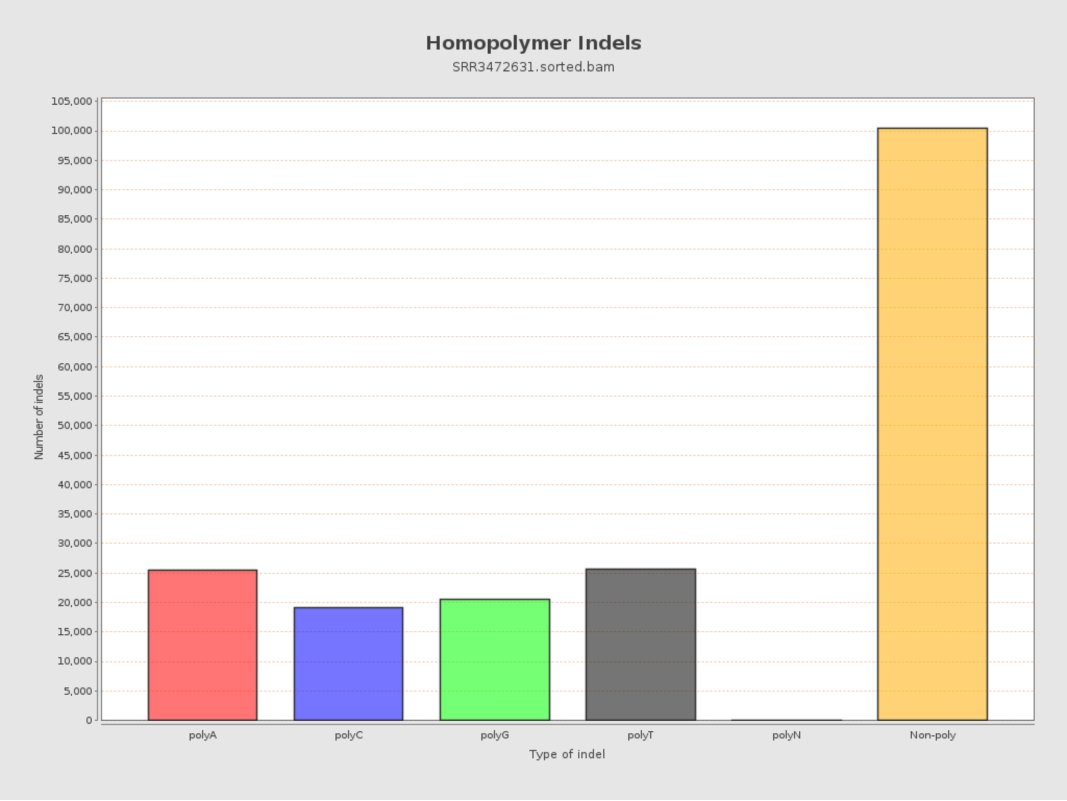
# 9. Results : Mapped Reads GC-content Distribution



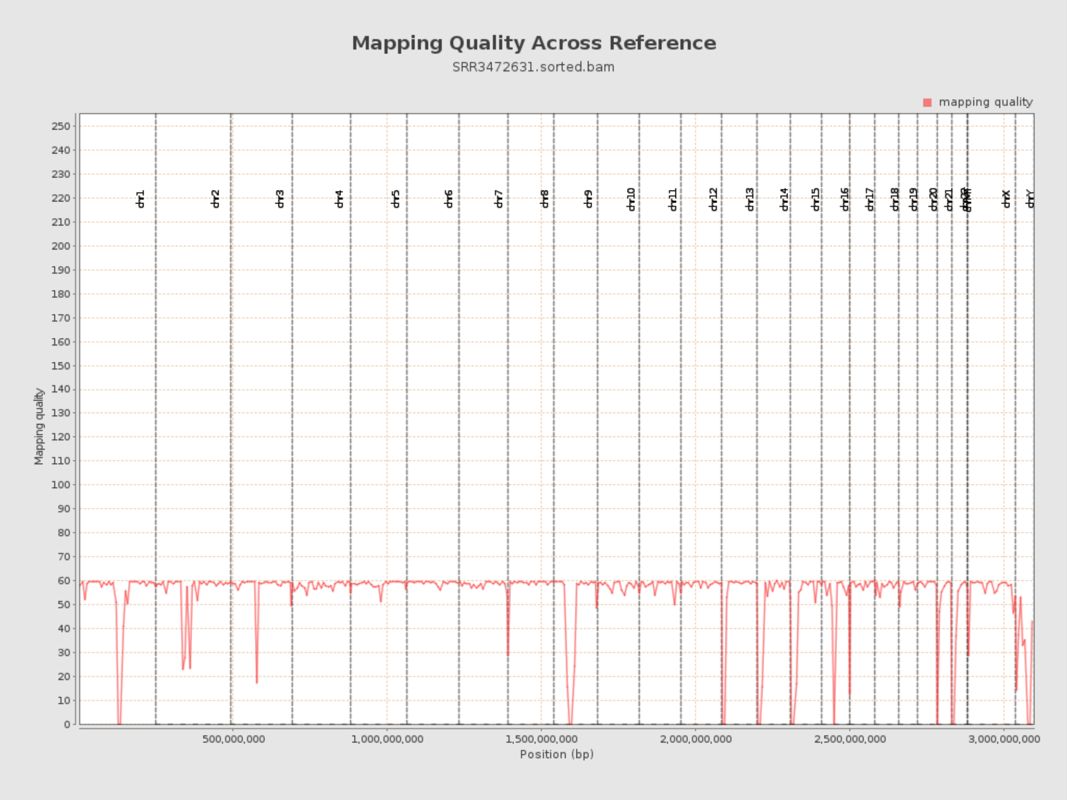
# 10. Results : Mapped Reads Clipping Profile



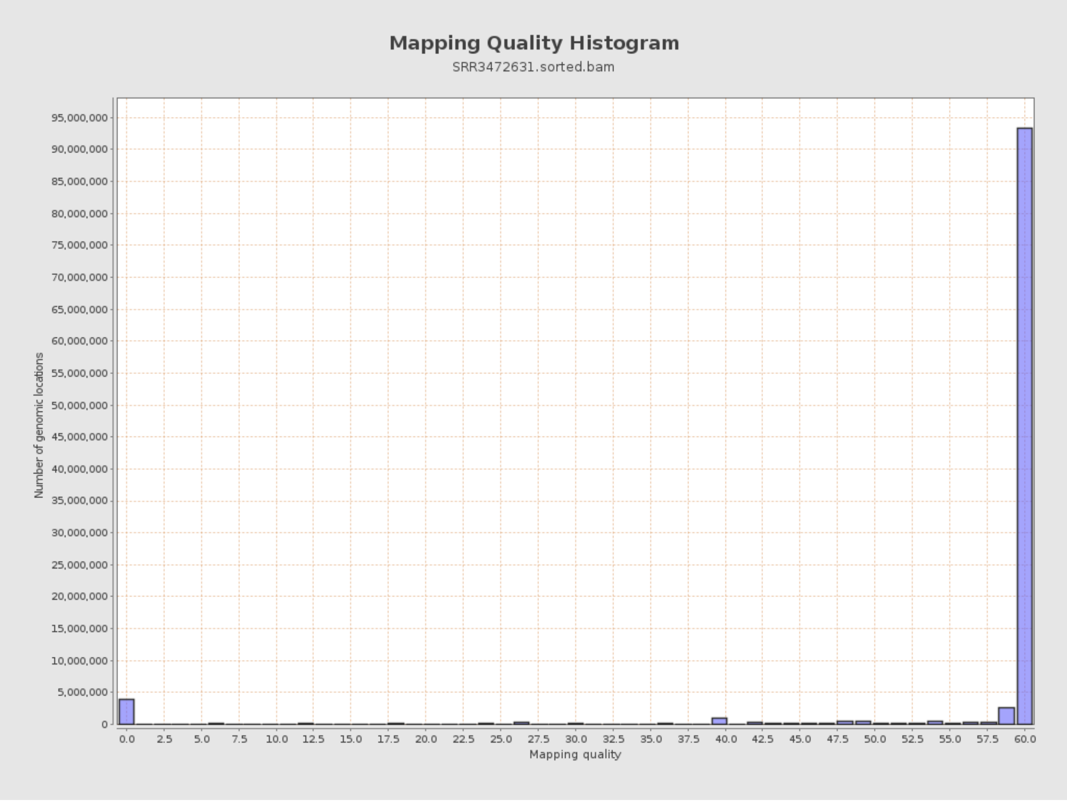
# 11. Results : Homopolymer Indels



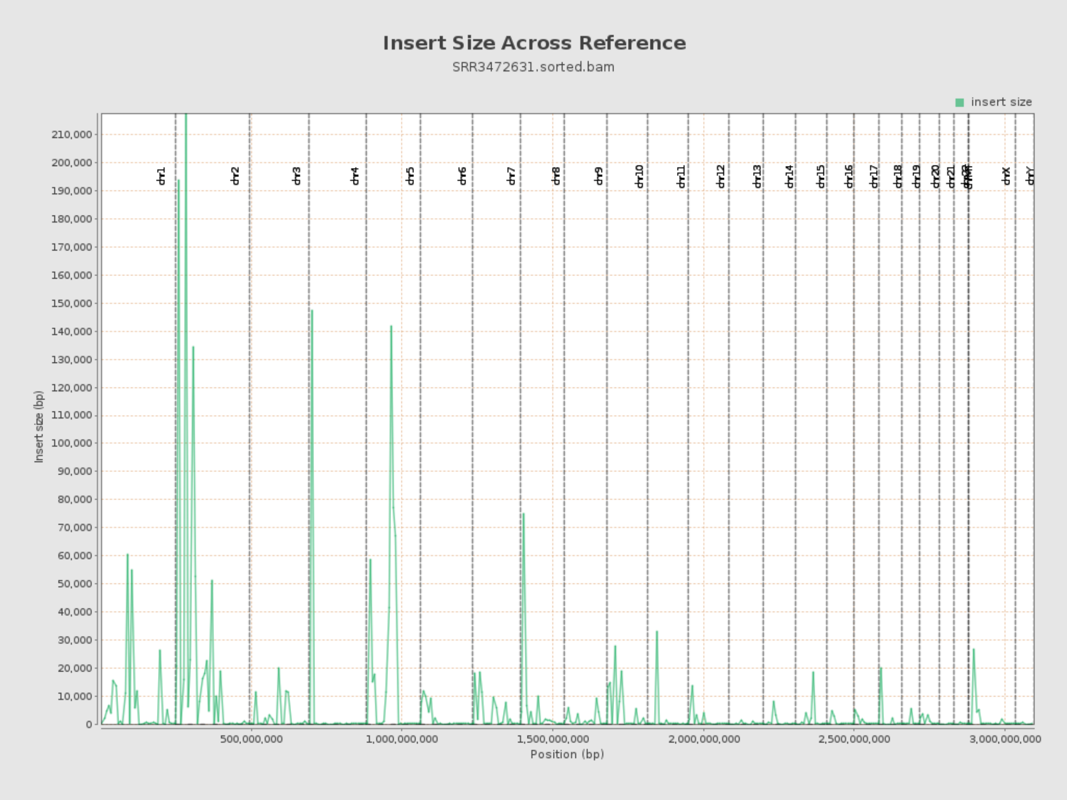
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram