# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/30 18:14:41*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472791.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_SRR3472791 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472791_1.fastq.gz SRR3472791_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 30 18:14:40 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3472791.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 10,039,032 |
| Mapped reads | 9,949,434 / 99.11% |
| Unmapped reads | 89,598 / 0.89% |
| Mapped paired reads | 9,949,434 / 99.11% |
| Mapped reads, first in pair | 4,989,864 / 49.7% |
| Mapped reads, second in pair | 4,959,570 / 49.4% |
| Mapped reads, both in pair | 9,897,024 / 98.59% |
| Mapped reads, singletons | 52,410 / 0.52% |
| Secondary alignments | 0 |
| Supplementary alignments | 35,207 / 0.35% |
| Read min/max/mean length | 30 / 100 / 100.14 |
| Duplicated reads (estimated) | 5,664,669 / 56.43% |
| Duplication rate | 45.15% |
| Clipped reads | 915,923 / 9.12% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 270,214,895 / 27.65% |
| Number/percentage of C's | 219,811,889 / 22.5% |
| Number/percentage of T's | 268,033,734 / 27.43% |
| Number/percentage of G's | 218,862,609 / 22.4% |
| Number/percentage of N's | 190,926 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 44.89% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.3157 |
| Standard Deviation | 11.4094 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 55.12 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 22,120.02 |
| Standard Deviation | 1,479,438.63 |
| P25/Median/P75 | 163 / 232 / 316 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.61% |
| Mismatches | 5,824,312 |
| Insertions | 58,612 |
| Mapped reads with at least one insertion | 0.58% |
| Deletions | 53,005 |
| Mapped reads with at least one deletion | 0.53% |
| Homopolymer indels | 44.21% |

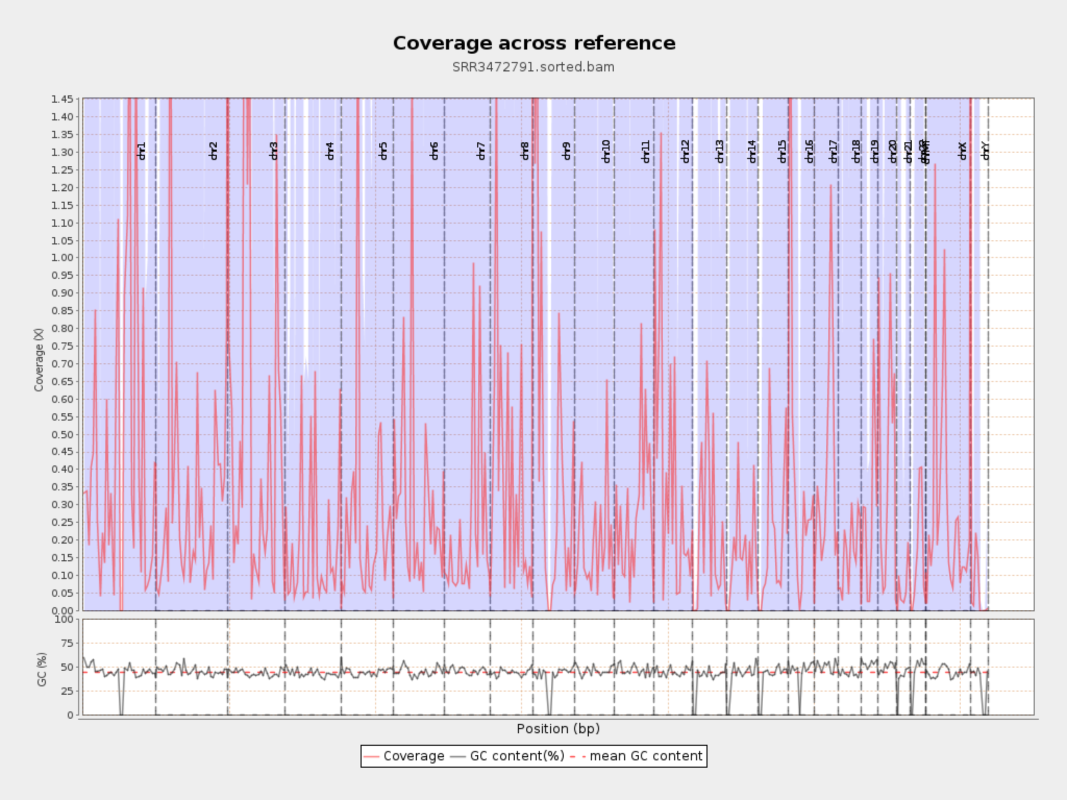
## 2.7. Chromosome stats

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

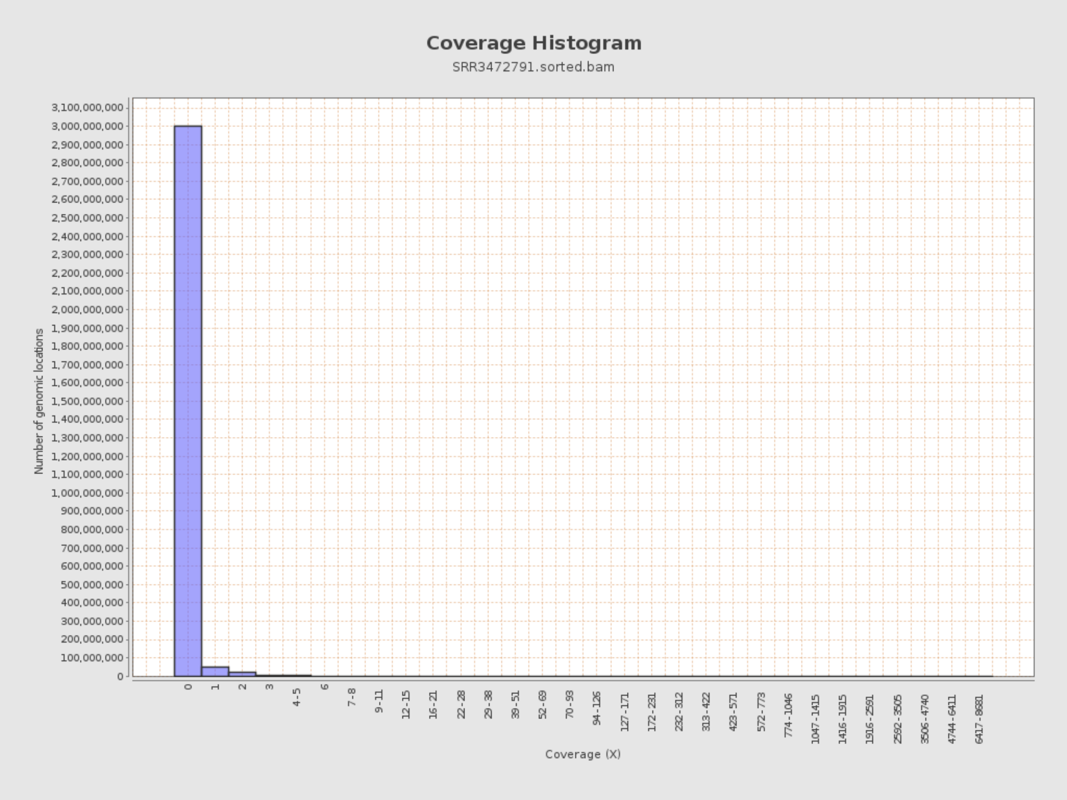
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 112261346 | 0.4504 | 13.8771 |
| chr2 | 243199373 | 80364560 | 0.3304 | 19.4757 |
| chr3 | 198022430 | 111884109 | 0.565 | 13.5063 |
| chr4 | 191154276 | 36378620 | 0.1903 | 7.403 |
| chr5 | 180915260 | 49192515 | 0.2719 | 10.0204 |
| chr6 | 171115067 | 54498944 | 0.3185 | 8.6404 |
| chr7 | 159138663 | 36551536 | 0.2297 | 9.3049 |
| chr8 | 146364022 | 54940755 | 0.3754 | 12.9466 |
| chr9 | 141213431 | 64324330 | 0.4555 | 12.9327 |
| chr10 | 135534747 | 26817145 | 0.1979 | 6.811 |
| chr11 | 135006516 | 38410732 | 0.2845 | 9.7665 |
| chr12 | 133851895 | 53642124 | 0.4008 | 12.2656 |
| chr13 | 115169878 | 25291167 | 0.2196 | 8.3876 |
| chr14 | 107349540 | 17853381 | 0.1663 | 5.5554 |
| chr15 | 102531392 | 21053834 | 0.2053 | 8.1652 |
| chr16 | 90354753 | 37228848 | 0.412 | 13.3855 |
| chr17 | 81195210 | 34773186 | 0.4283 | 10.3702 |
| chr18 | 78077248 | 12813497 | 0.1641 | 6.2003 |
| chr19 | 59128983 | 15757539 | 0.2665 | 8.2593 |
| chr20 | 63025520 | 26905932 | 0.4269 | 14.1897 |
| chr21 | 48129895 | 3463629 | 0.072 | 3.7707 |
| chr22 | 51304566 | 8509984 | 0.1659 | 5.2105 |
| chrMT | 16571 | 1779 | 0.1074 | 0.3894 |
| chrX | 155270560 | 51172356 | 0.3296 | 10.9232 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 3156619 | 0.0532 | 2.6586 |

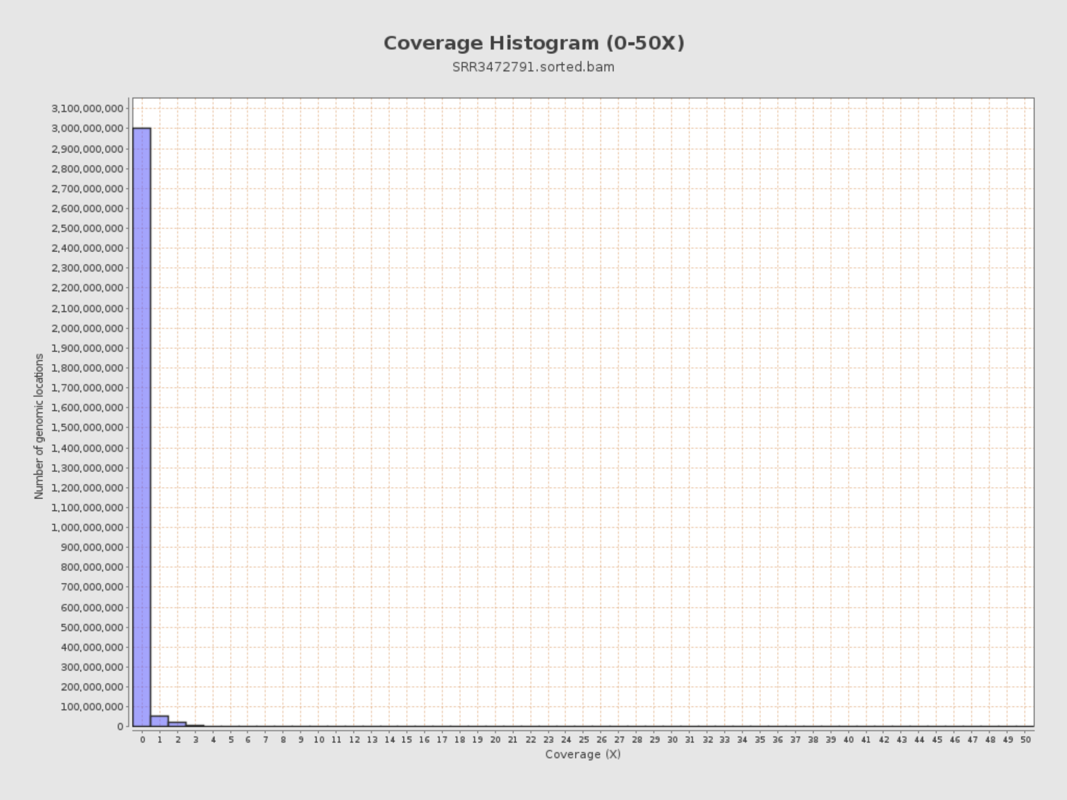
# 3. Results : Coverage across reference



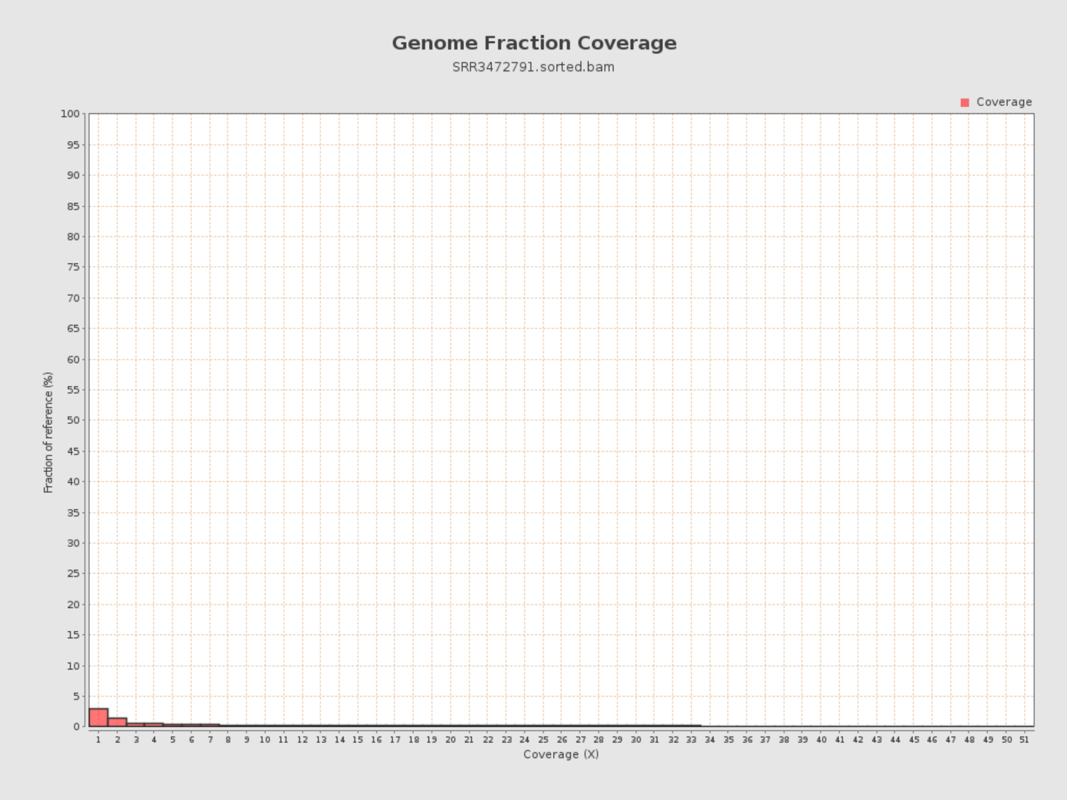
# 4. Results : Coverage Histogram



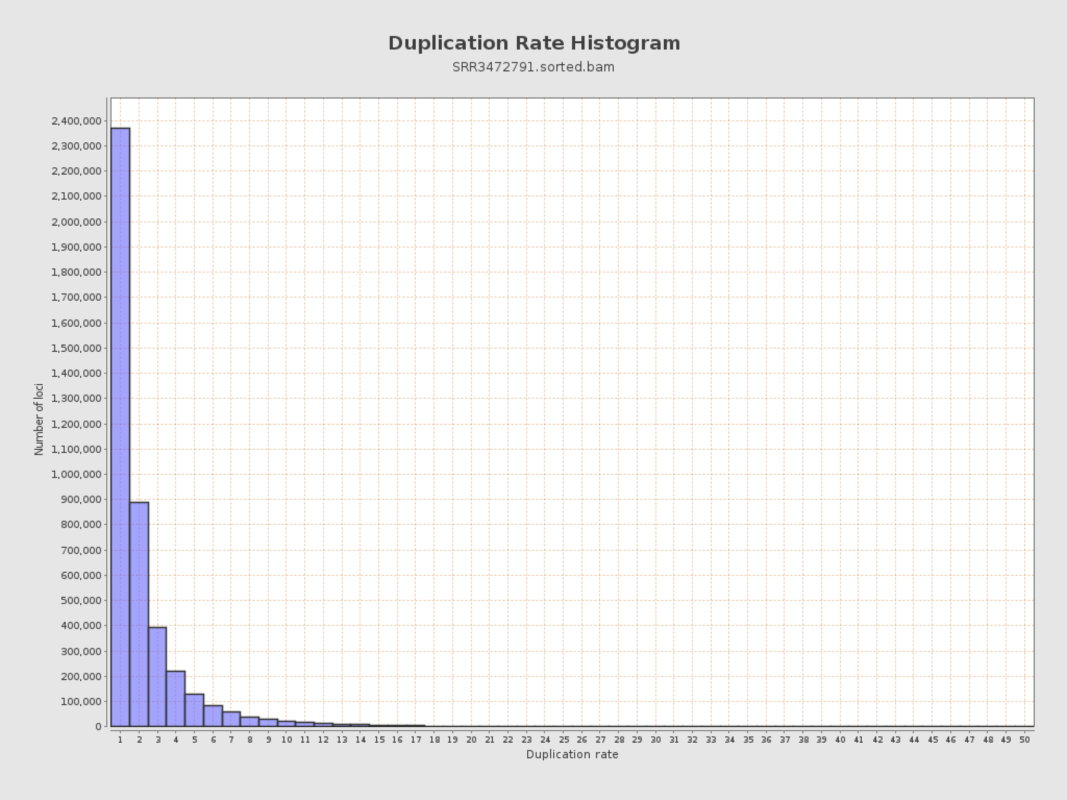
# 5. Results : Coverage Histogram (0-50X)



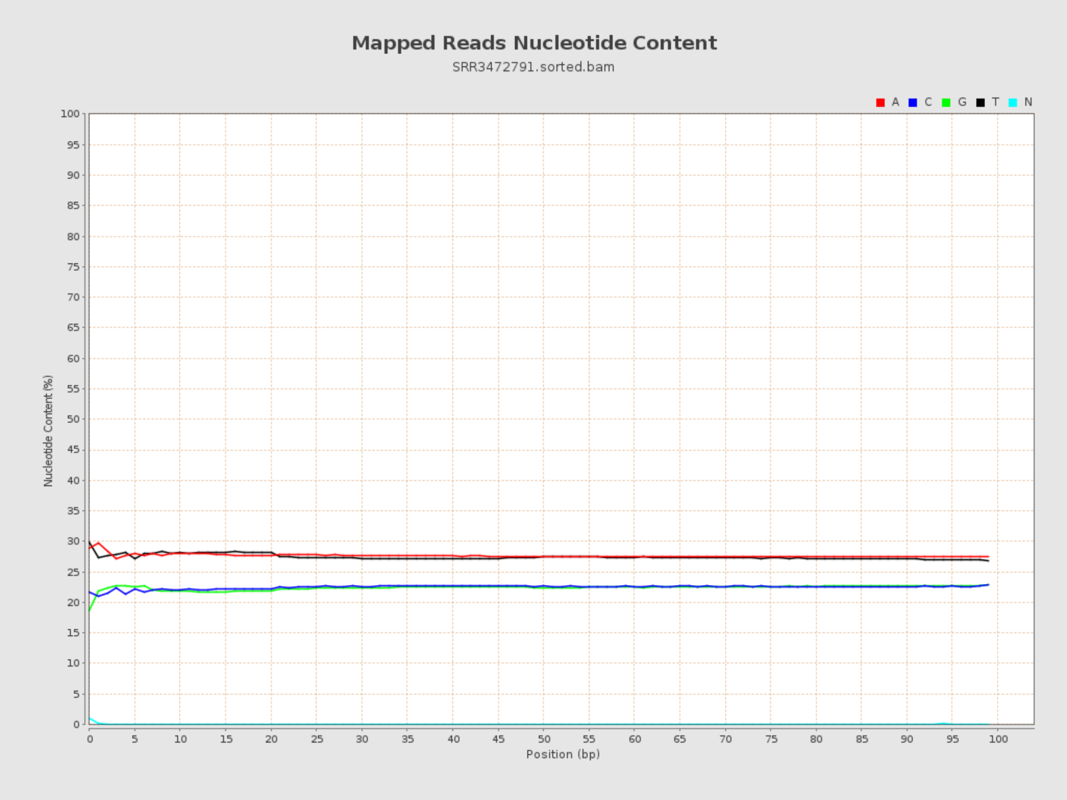
# 6. Results : Genome Fraction Coverage



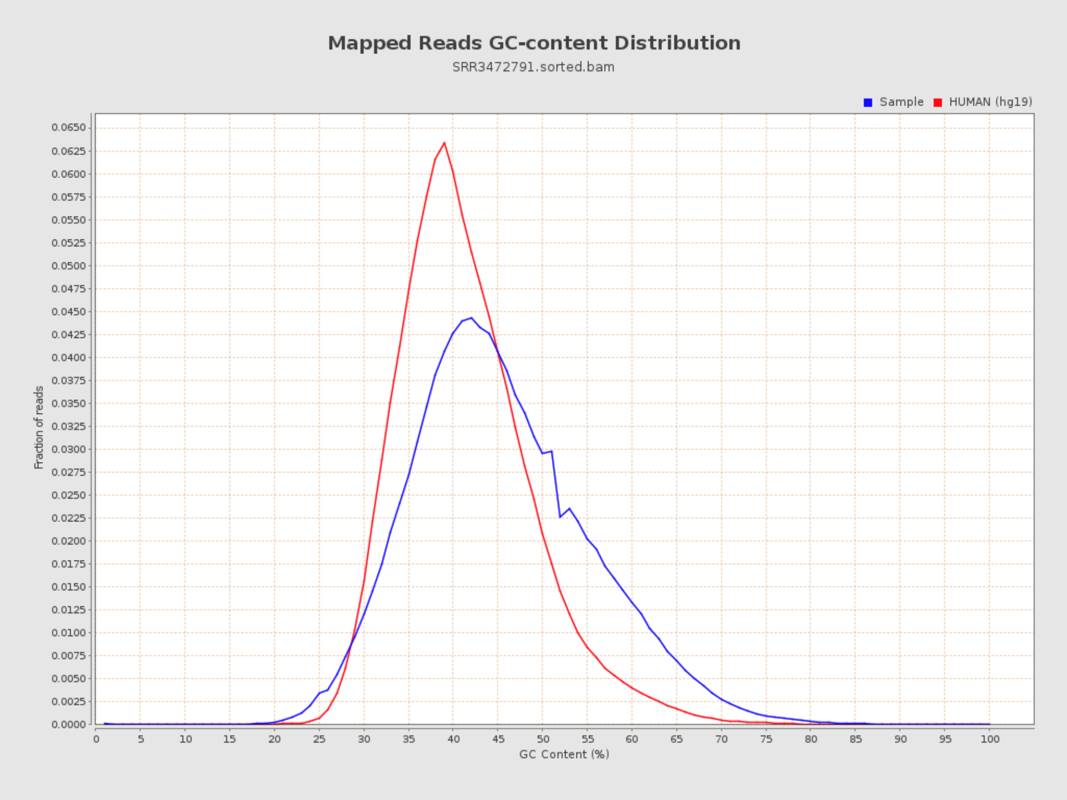
# 7. Results : Duplication Rate Histogram



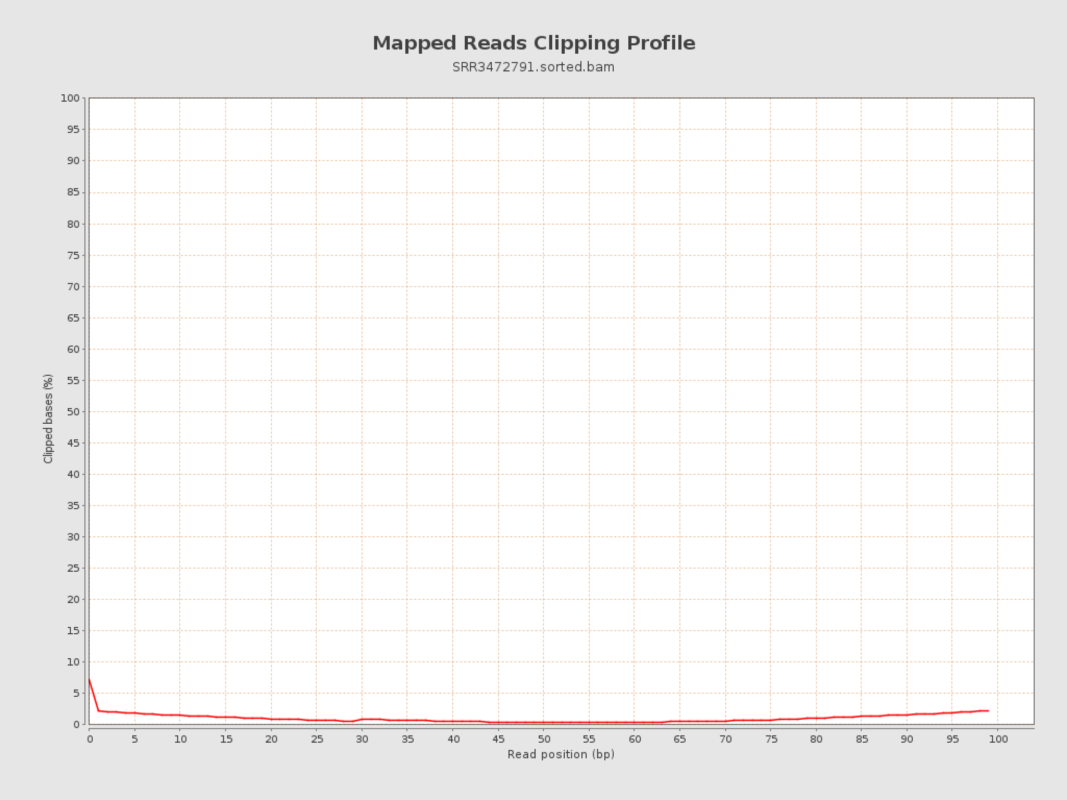
# 8. Results : Mapped Reads Nucleotide Content



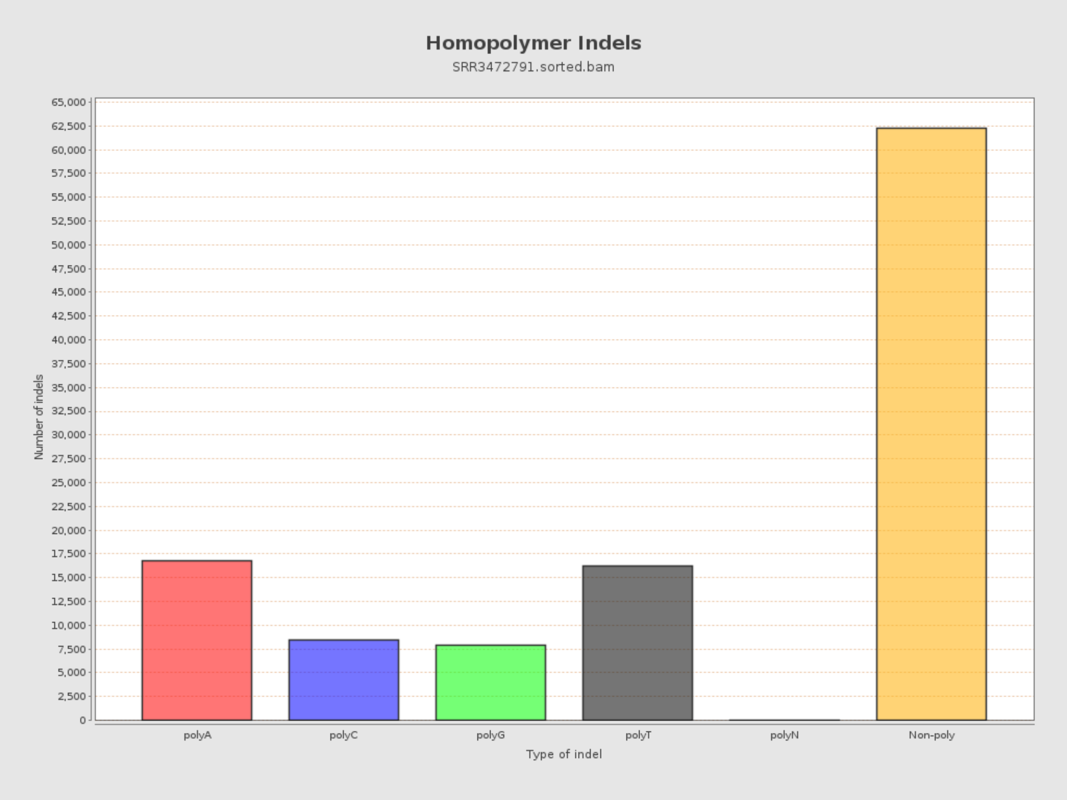
# 9. Results : Mapped Reads GC-content Distribution



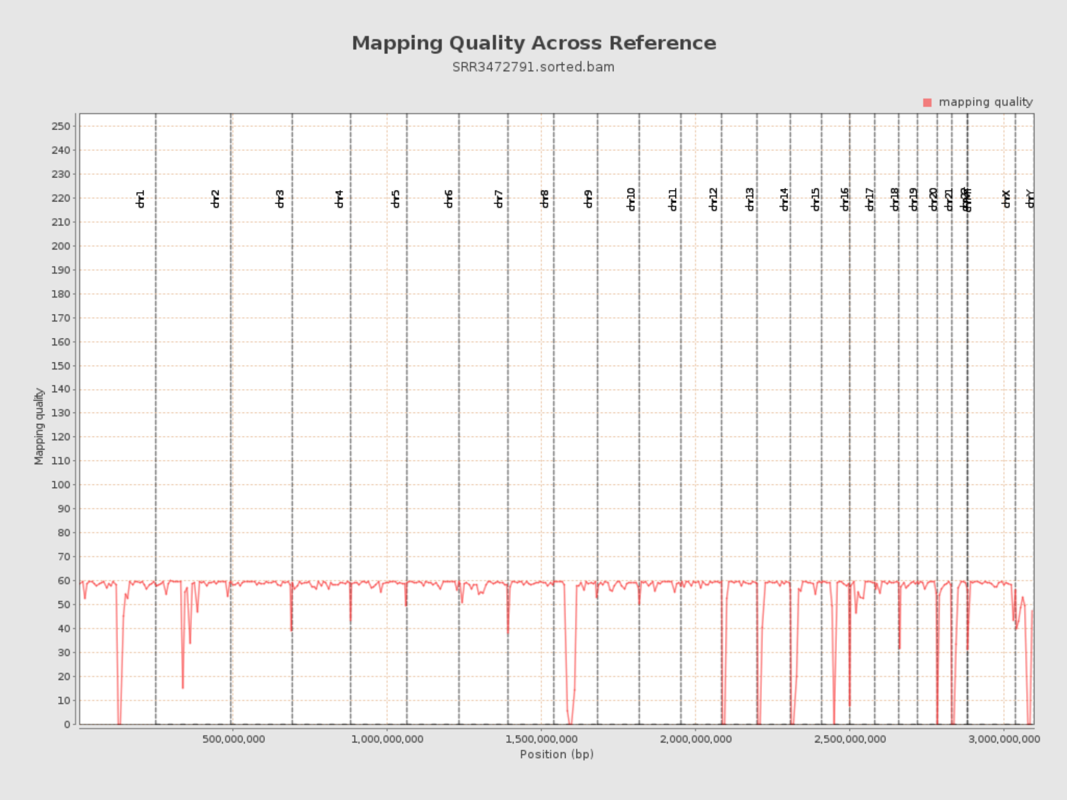
# 10. Results : Mapped Reads Clipping Profile



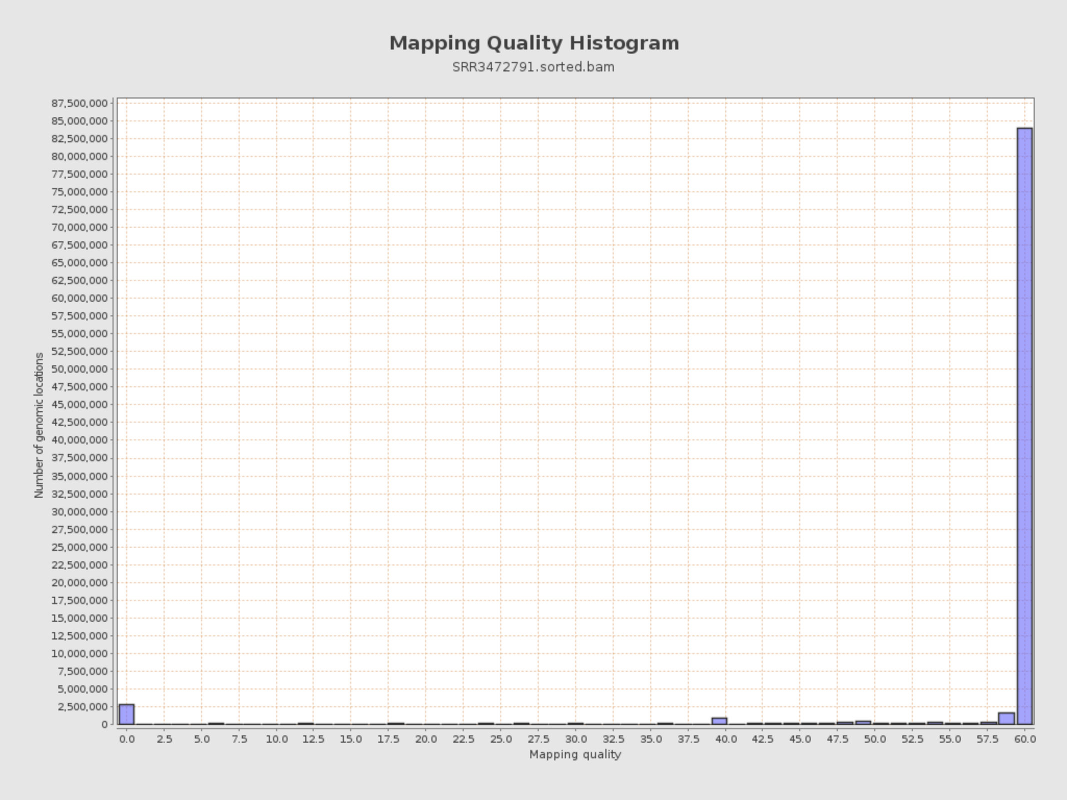
# 11. Results : Homopolymer Indels



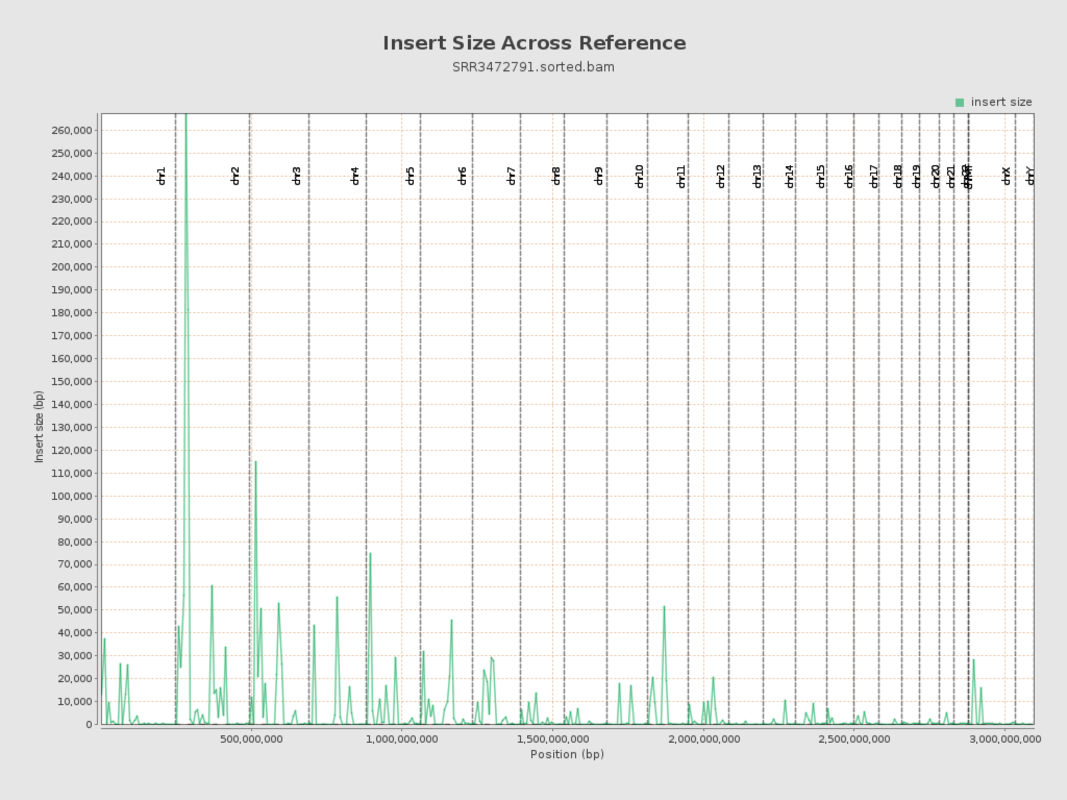
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram