# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/29 10:29:12*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472692.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_SRR3472692 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472692_1.fastq.gz SRR3472692_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 29 10:29:11 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3472692.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 19,588,334 |
| Mapped reads | 19,452,259 / 99.31% |
| Unmapped reads | 136,075 / 0.69% |
| Mapped paired reads | 19,452,259 / 99.31% |
| Mapped reads, first in pair | 9,751,651 / 49.78% |
| Mapped reads, second in pair | 9,700,608 / 49.52% |
| Mapped reads, both in pair | 19,360,686 / 98.84% |
| Mapped reads, singletons | 91,573 / 0.47% |
| Secondary alignments | 0 |
| Supplementary alignments | 121,863 / 0.62% |
| Read min/max/mean length | 30 / 101 / 99.92 |
| Duplicated reads (estimated) | 14,471,921 / 73.88% |
| Duplication rate | 50.38% |
| Clipped reads | 1,432,876 / 7.31% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 509,486,435 / 26.58% |
| Number/percentage of C's | 452,056,537 / 23.59% |
| Number/percentage of T's | 509,381,406 / 26.58% |
| Number/percentage of G's | 445,179,120 / 23.23% |
| Number/percentage of N's | 373,122 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 46.82% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.6192 |
| Standard Deviation | 32.124 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 54.96 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 19,659.7 |
| Standard Deviation | 1,341,009.58 |
| P25/Median/P75 | 158 / 216 / 290 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.6% |
| Mismatches | 11,194,101 |
| Insertions | 133,182 |
| Mapped reads with at least one insertion | 0.68% |
| Deletions | 97,397 |
| Mapped reads with at least one deletion | 0.49% |
| Homopolymer indels | 44.16% |

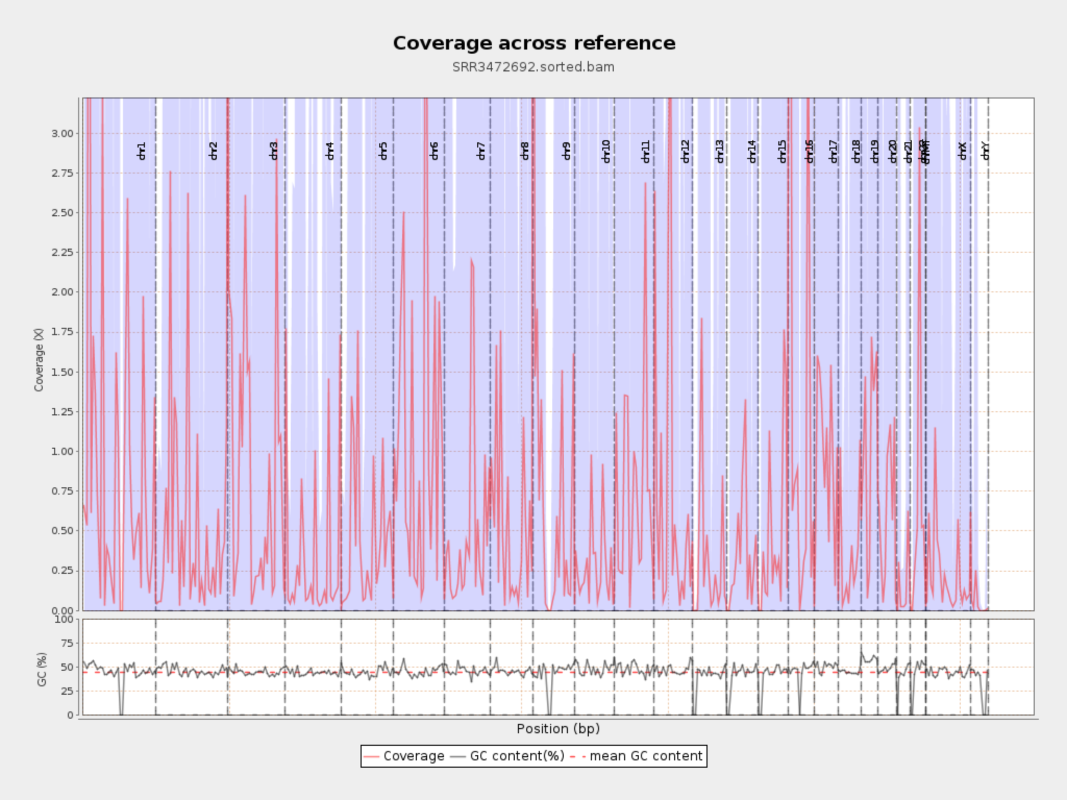
## 2.7. Chromosome stats

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

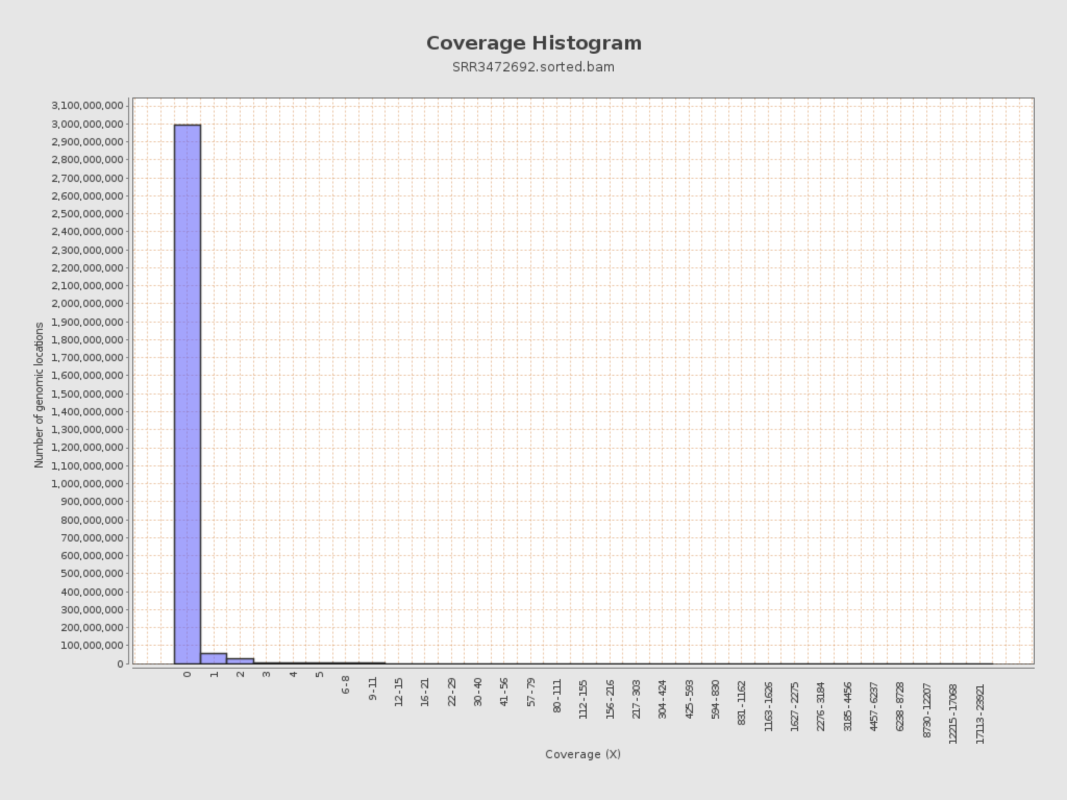
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 240839329 | 0.9663 | 45.4041 |
| chr2 | 243199373 | 125835858 | 0.5174 | 27.3623 |
| chr3 | 198022430 | 176662527 | 0.8921 | 37.1267 |
| chr4 | 191154276 | 65549497 | 0.3429 | 25.6889 |
| chr5 | 180915260 | 82366885 | 0.4553 | 20.3942 |
| chr6 | 171115067 | 187207916 | 1.094 | 54.5016 |
| chr7 | 159138663 | 81030759 | 0.5092 | 23.8983 |
| chr8 | 146364022 | 77477655 | 0.5293 | 28.1709 |
| chr9 | 141213431 | 91389798 | 0.6472 | 26.8285 |
| chr10 | 135534747 | 41273661 | 0.3045 | 21.3497 |
| chr11 | 135006516 | 103670428 | 0.7679 | 35.3411 |
| chr12 | 133851895 | 107399736 | 0.8024 | 35.5872 |
| chr13 | 115169878 | 38169058 | 0.3314 | 15.5637 |
| chr14 | 107349540 | 38387362 | 0.3576 | 17.3835 |
| chr15 | 102531392 | 47356555 | 0.4619 | 23.2968 |
| chr16 | 90354753 | 121506517 | 1.3448 | 57.7238 |
| chr17 | 81195210 | 79403023 | 0.9779 | 34.3058 |
| chr18 | 78077248 | 25247054 | 0.3234 | 17.453 |
| chr19 | 59128983 | 60910348 | 1.0301 | 36.9405 |
| chr20 | 63025520 | 39300839 | 0.6236 | 23.8614 |
| chr21 | 48129895 | 8196784 | 0.1703 | 11.6024 |
| chr22 | 51304566 | 37572809 | 0.7323 | 49.5981 |
| chrMT | 16571 | 5490 | 0.3313 | 0.7177 |
| chrX | 155270560 | 37294872 | 0.2402 | 11.5481 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 2653888 | 0.0447 | 3.7244 |

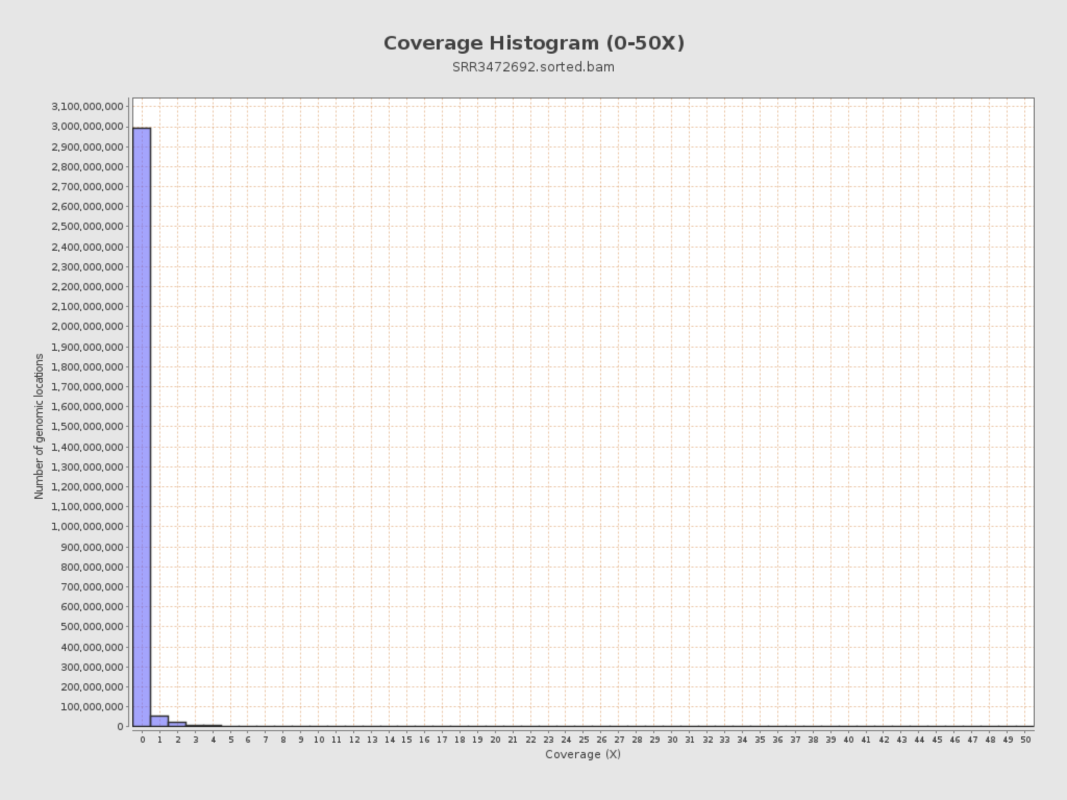
# 3. Results : Coverage across reference



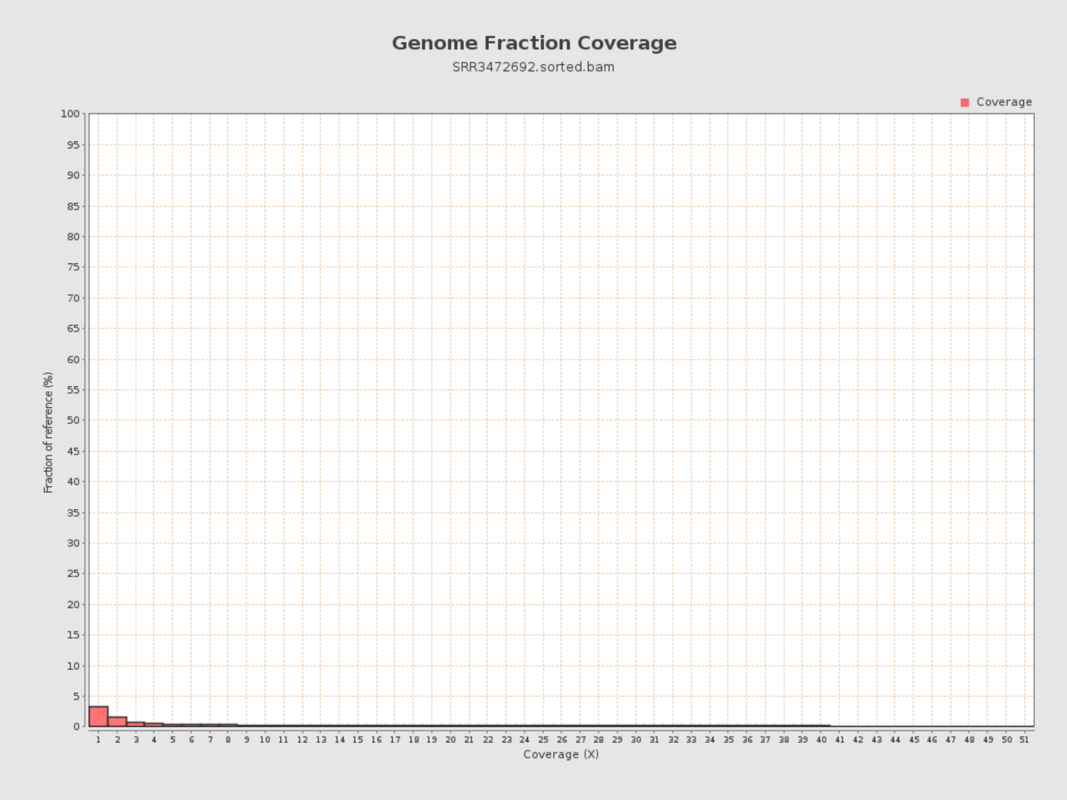
# 4. Results : Coverage Histogram



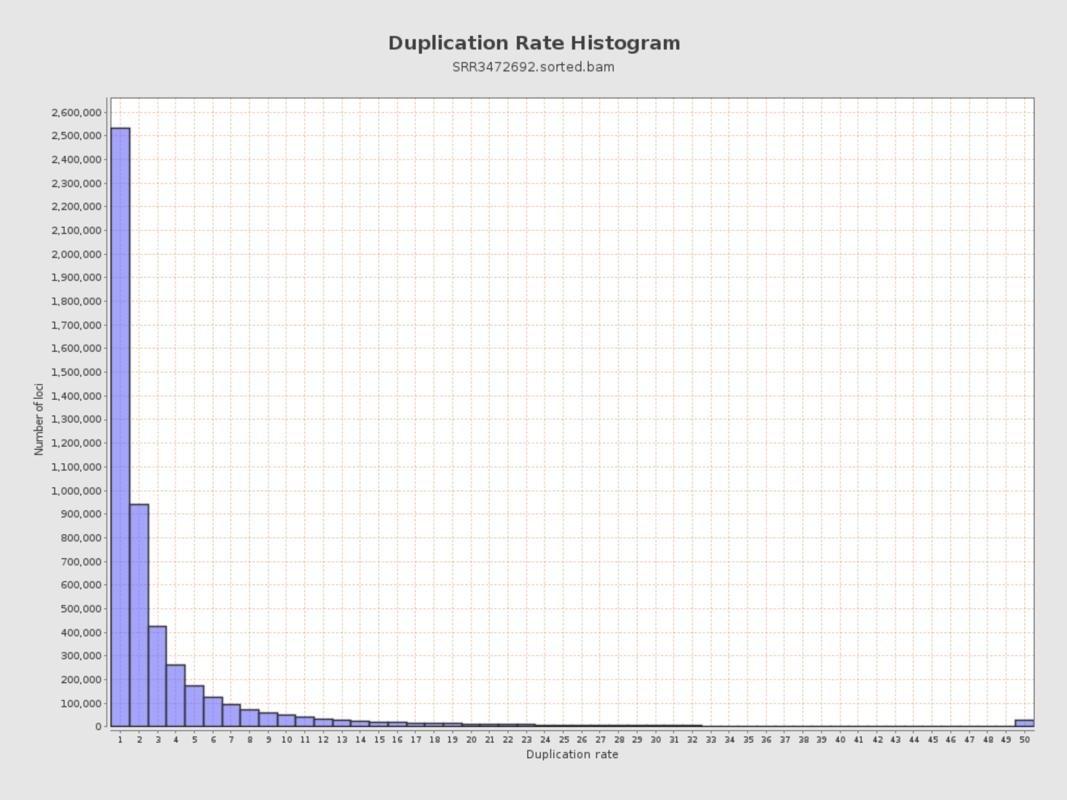
# 5. Results : Coverage Histogram (0-50X)



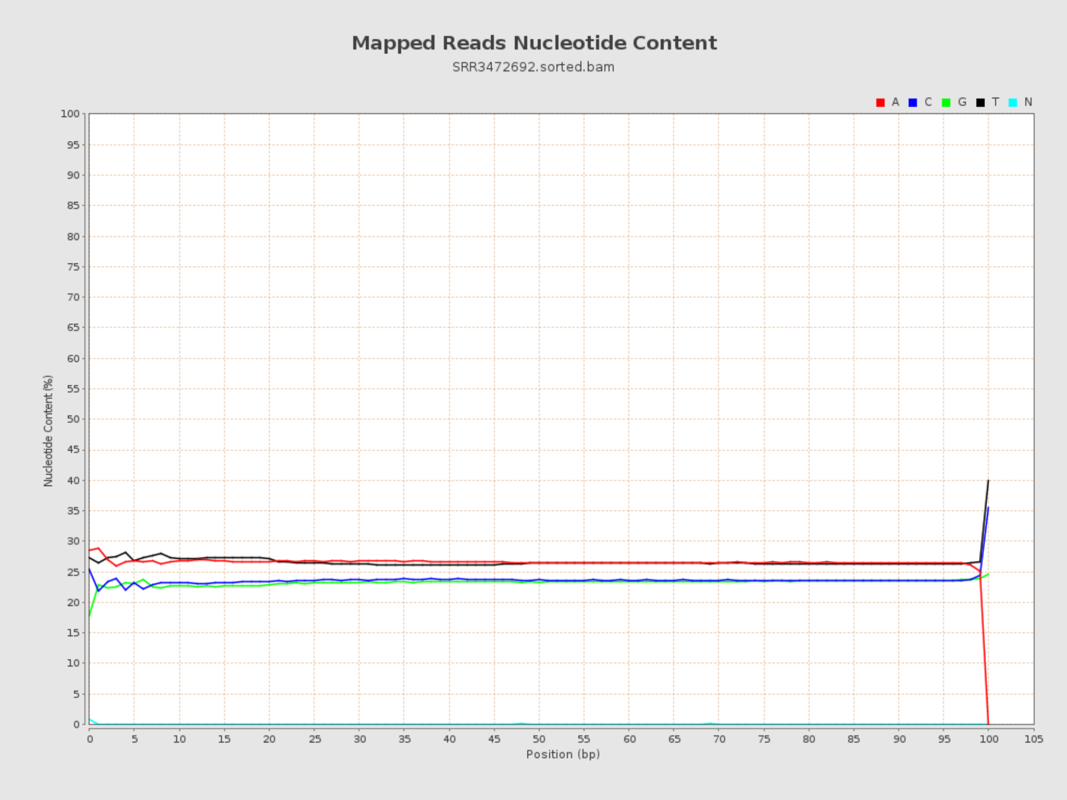
# 6. Results : Genome Fraction Coverage



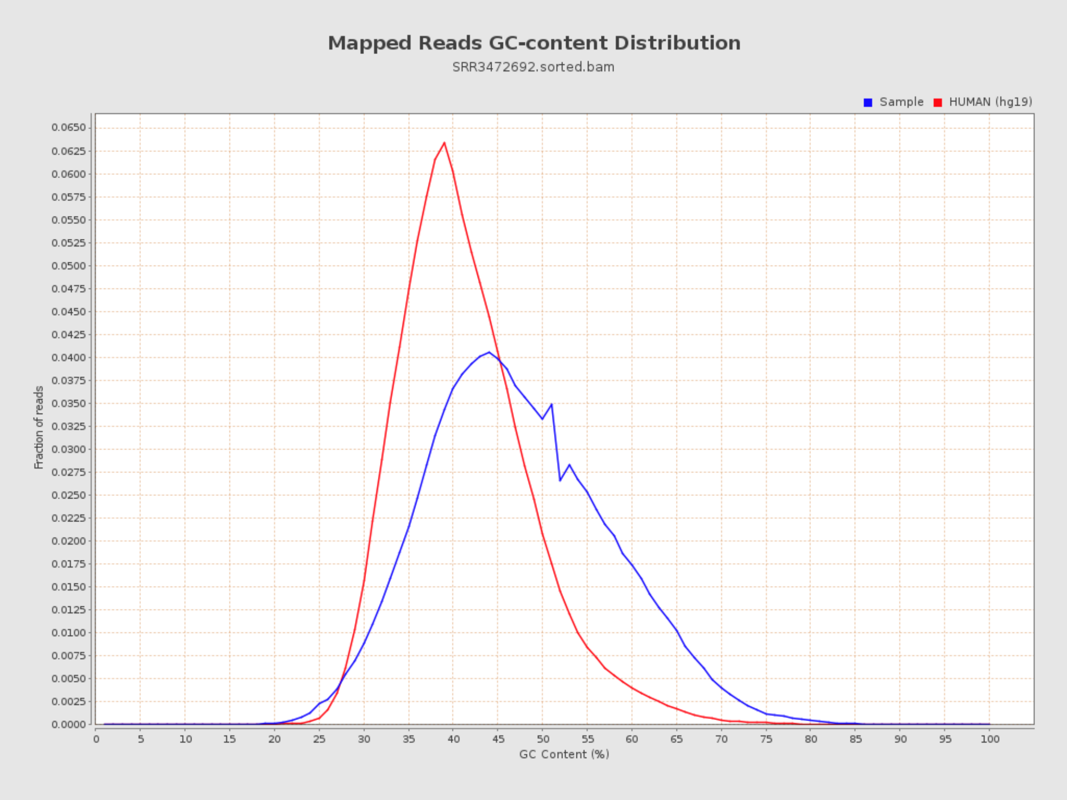
# 7. Results : Duplication Rate Histogram



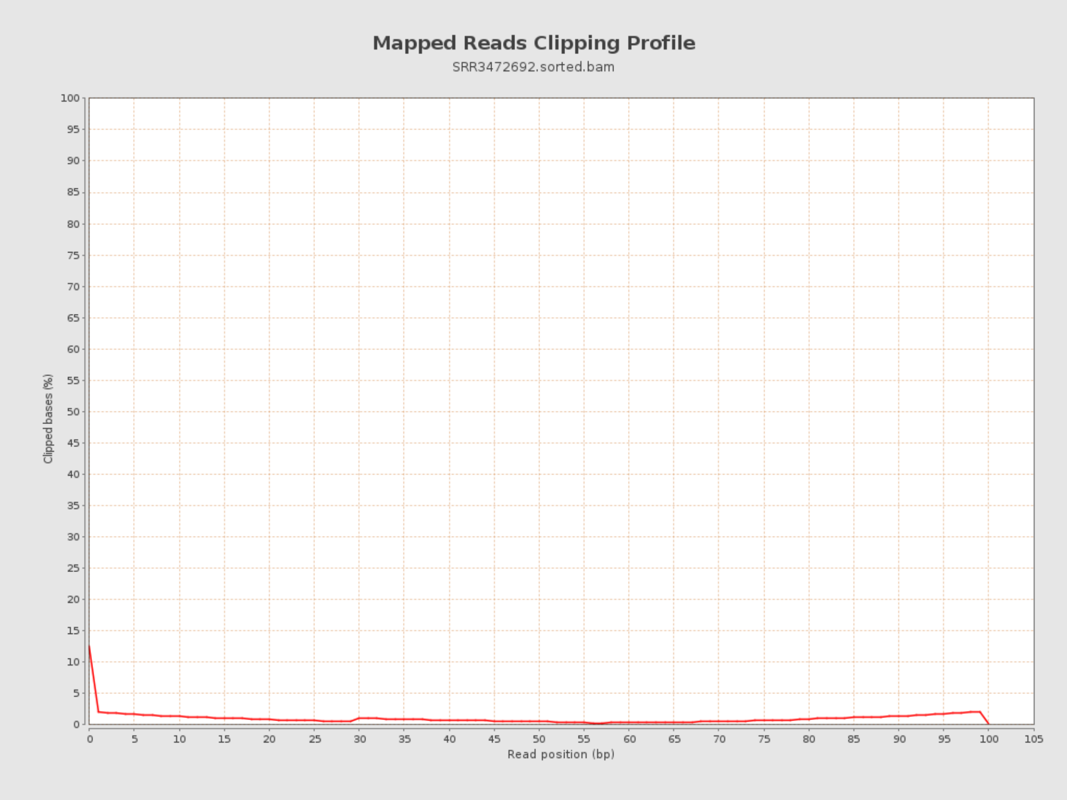
# 8. Results : Mapped Reads Nucleotide Content



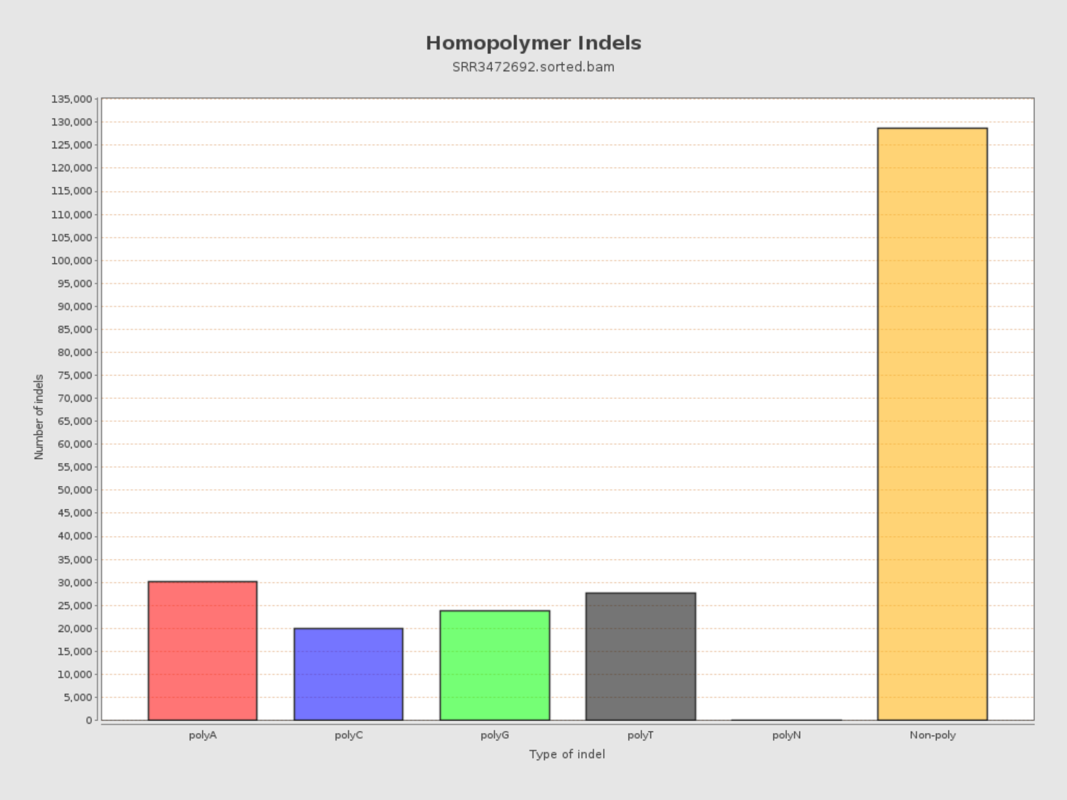
# 9. Results : Mapped Reads GC-content Distribution



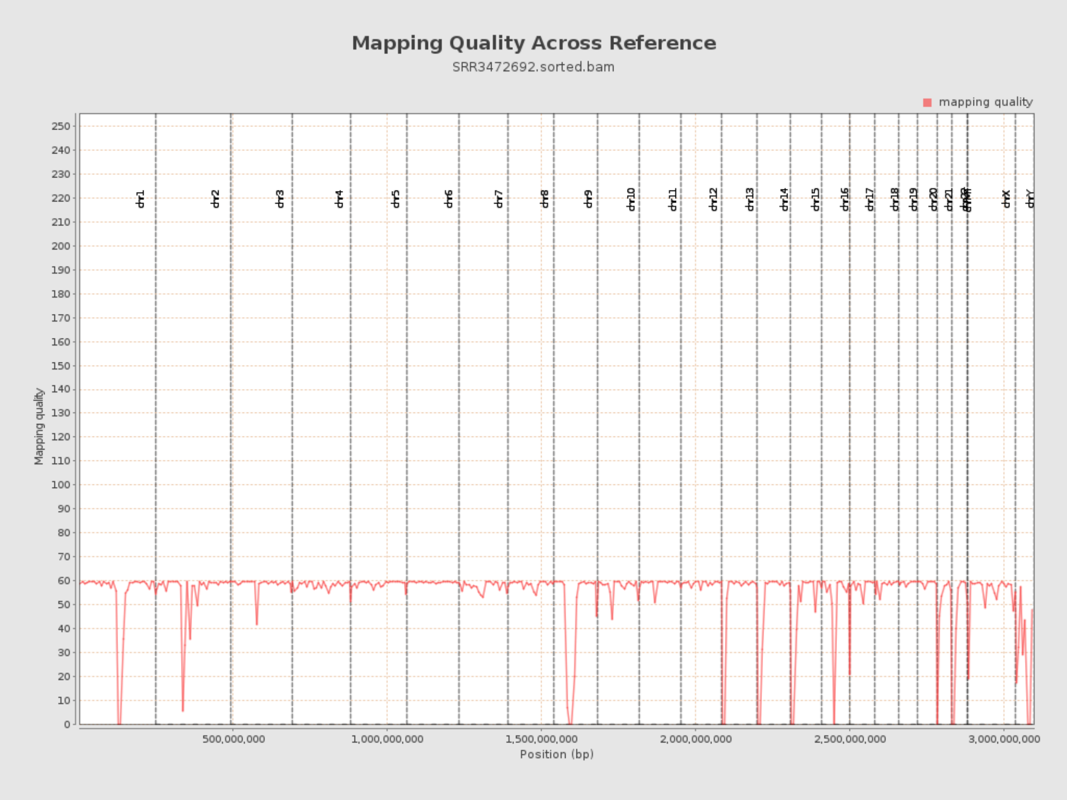
# 10. Results : Mapped Reads Clipping Profile



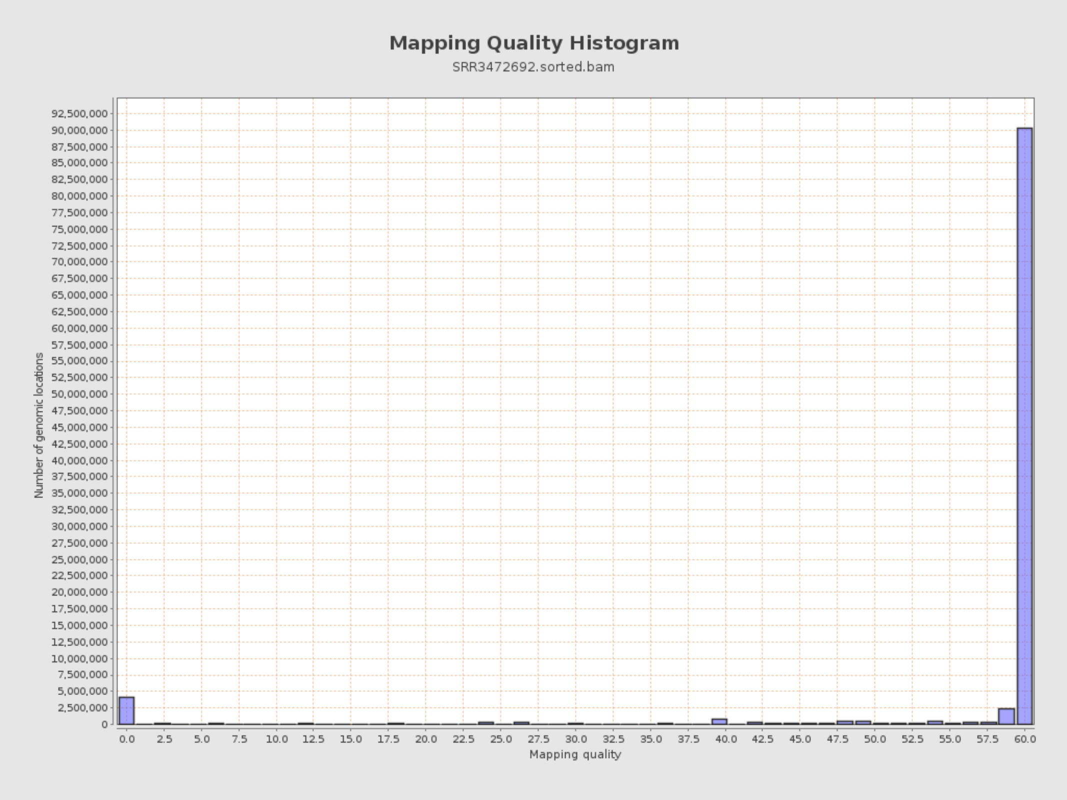
# 11. Results : Homopolymer Indels



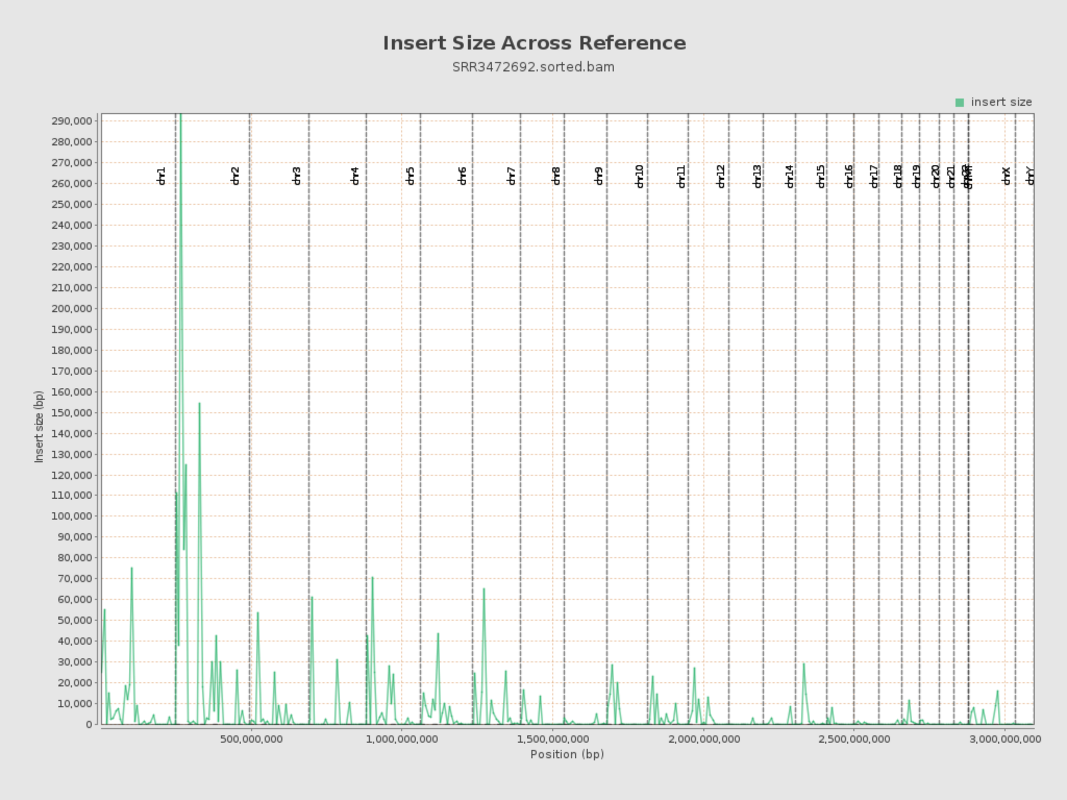
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram