# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/28 16:28:59*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472630.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_SRR3472630 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472630_1.fastq.gz SRR3472630_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 28 16:28:59 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3472630.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 17,145,816 |
| Mapped reads | 17,037,177 / 99.37% |
| Unmapped reads | 108,639 / 0.63% |
| Mapped paired reads | 17,037,177 / 99.37% |
| Mapped reads, first in pair | 8,541,473 / 49.82% |
| Mapped reads, second in pair | 8,495,704 / 49.55% |
| Mapped reads, both in pair | 16,960,140 / 98.92% |
| Mapped reads, singletons | 77,037 / 0.45% |
| Secondary alignments | 0 |
| Supplementary alignments | 86,315 / 0.5% |
| Read min/max/mean length | 30 / 101 / 99.85 |
| Duplicated reads (estimated) | 11,622,506 / 67.79% |
| Duplication rate | 49.64% |
| Clipped reads | 1,147,432 / 6.69% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 448,026,693 / 26.68% |
| Number/percentage of C's | 393,721,975 / 23.44% |
| Number/percentage of T's | 447,616,013 / 26.65% |
| Number/percentage of G's | 389,757,028 / 23.21% |
| Number/percentage of N's | 311,174 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 46.65% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.5426 |
| Standard Deviation | 22.2383 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 54.98 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 22,190.18 |
| Standard Deviation | 1,503,689.44 |
| P25/Median/P75 | 164 / 224 / 297 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.62% |
| Mismatches | 10,165,426 |
| Insertions | 99,944 |
| Mapped reads with at least one insertion | 0.58% |
| Deletions | 93,650 |
| Mapped reads with at least one deletion | 0.54% |
| Homopolymer indels | 45.48% |

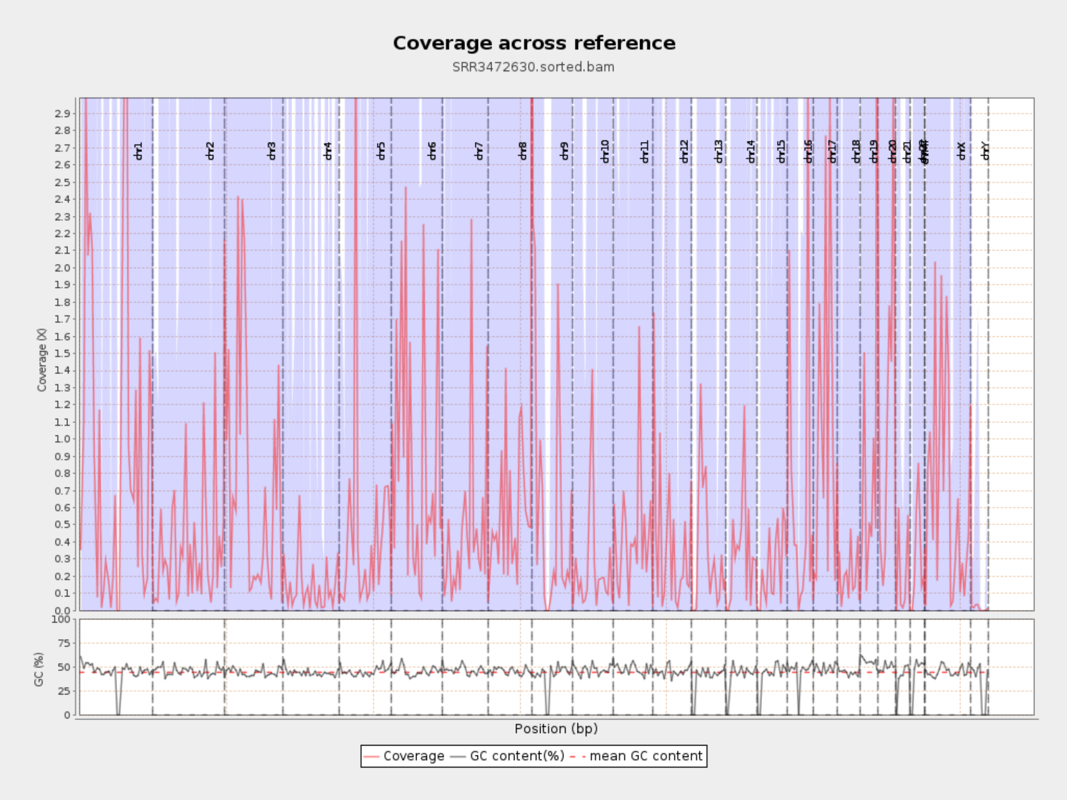
## 2.7. Chromosome stats

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

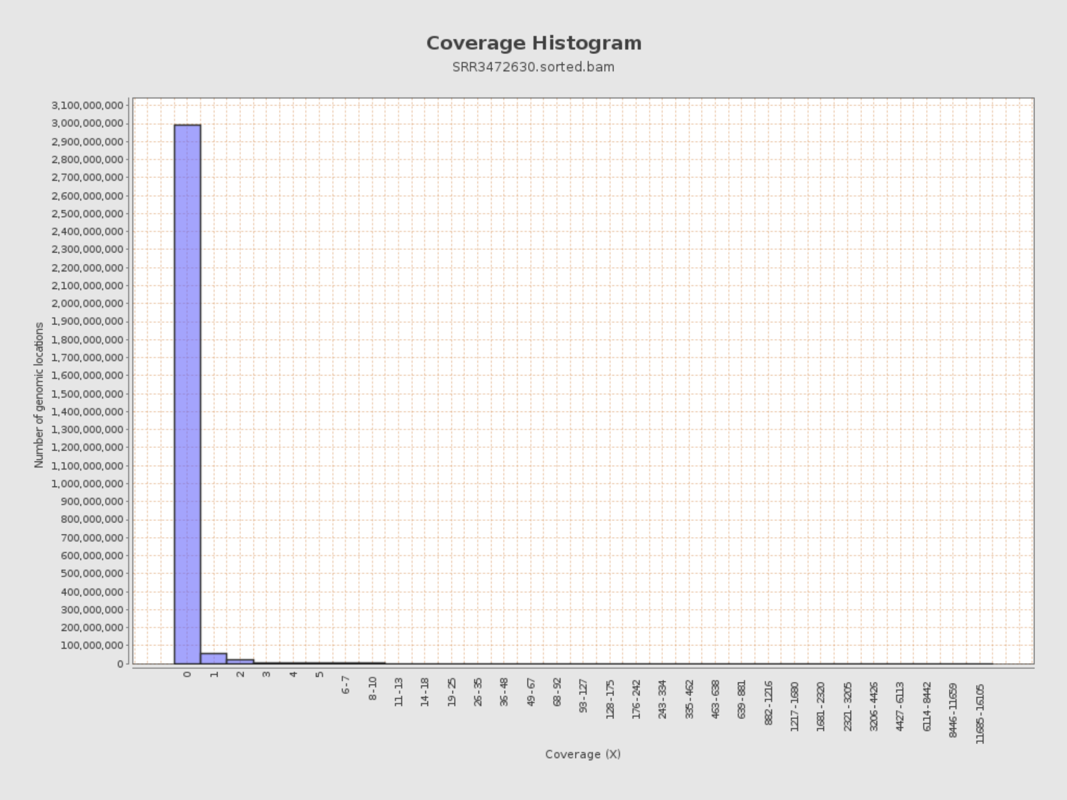
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 252506076 | 1.0131 | 30.7795 |
| chr2 | 243199373 | 88227663 | 0.3628 | 15.8877 |
| chr3 | 198022430 | 157727914 | 0.7965 | 24.2897 |
| chr4 | 191154276 | 26652973 | 0.1394 | 5.6617 |
| chr5 | 180915260 | 82277637 | 0.4548 | 21.2542 |
| chr6 | 171115067 | 151730106 | 0.8867 | 31.7197 |
| chr7 | 159138663 | 75439867 | 0.4741 | 16.8749 |
| chr8 | 146364022 | 84551819 | 0.5777 | 19.5347 |
| chr9 | 141213431 | 94642735 | 0.6702 | 35.4506 |
| chr10 | 135534747 | 33806356 | 0.2494 | 20.3405 |
| chr11 | 135006516 | 59608072 | 0.4415 | 17.5301 |
| chr12 | 133851895 | 52175909 | 0.3898 | 15.7464 |
| chr13 | 115169878 | 39595543 | 0.3438 | 13.3844 |
| chr14 | 107349540 | 35642529 | 0.332 | 16.1178 |
| chr15 | 102531392 | 25526439 | 0.249 | 9.8891 |
| chr16 | 90354753 | 63969971 | 0.708 | 23.7688 |
| chr17 | 81195210 | 88844802 | 1.0942 | 41.3019 |
| chr18 | 78077248 | 16531210 | 0.2117 | 8.6172 |
| chr19 | 59128983 | 43353175 | 0.7332 | 24.0419 |
| chr20 | 63025520 | 72600565 | 1.1519 | 31.3744 |
| chr21 | 48129895 | 10284959 | 0.2137 | 12.2841 |
| chr22 | 51304566 | 15000253 | 0.2924 | 9.6052 |
| chrMT | 16571 | 5987 | 0.3613 | 0.9418 |
| chrX | 155270560 | 108106189 | 0.6962 | 23.3669 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 857333 | 0.0144 | 0.7807 |

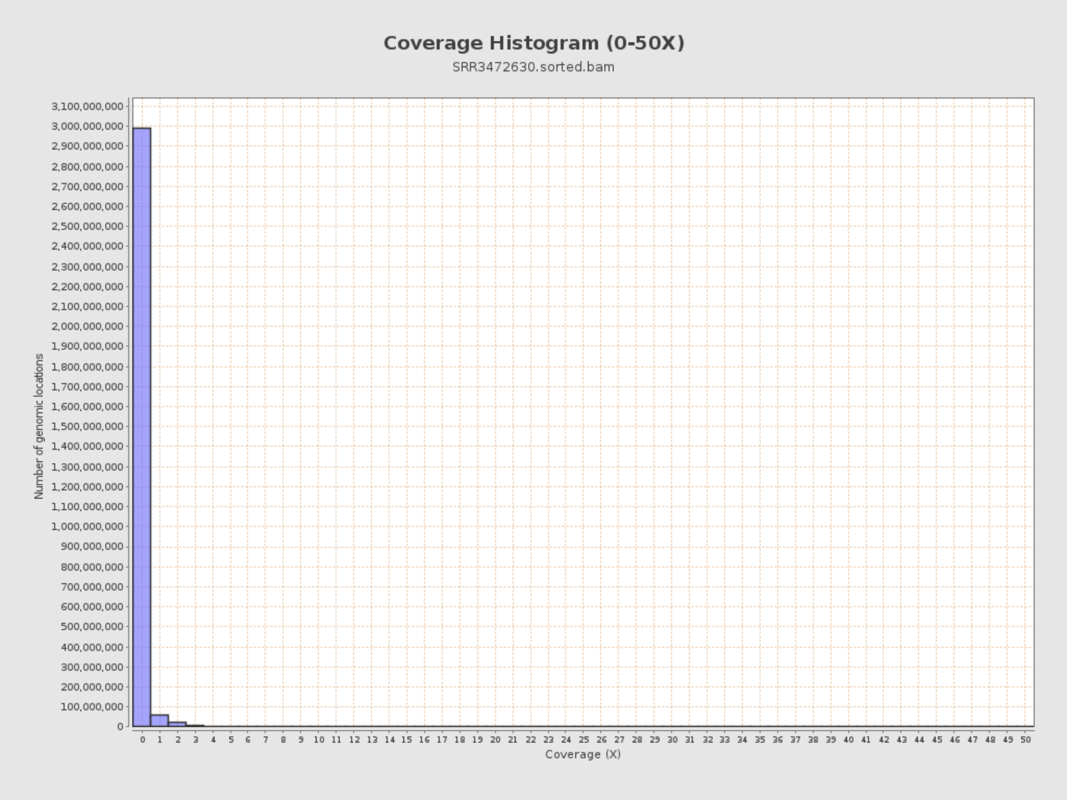
# 3. Results : Coverage across reference



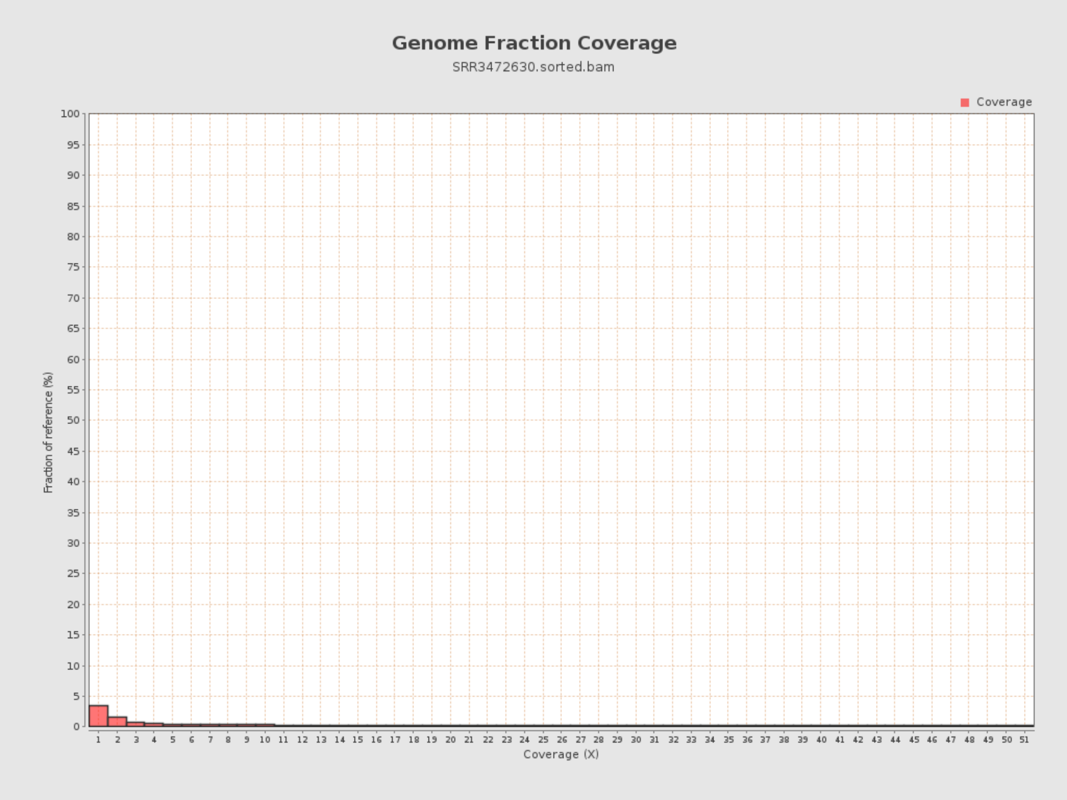
# 4. Results : Coverage Histogram



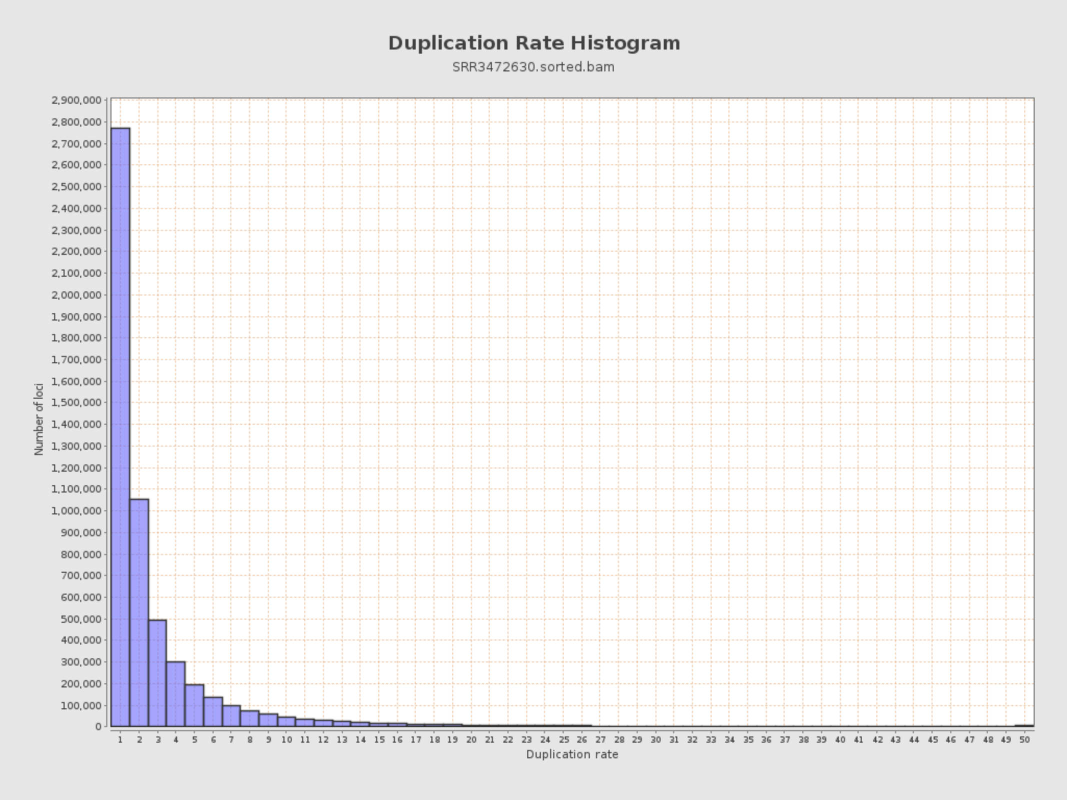
# 5. Results : Coverage Histogram (0-50X)



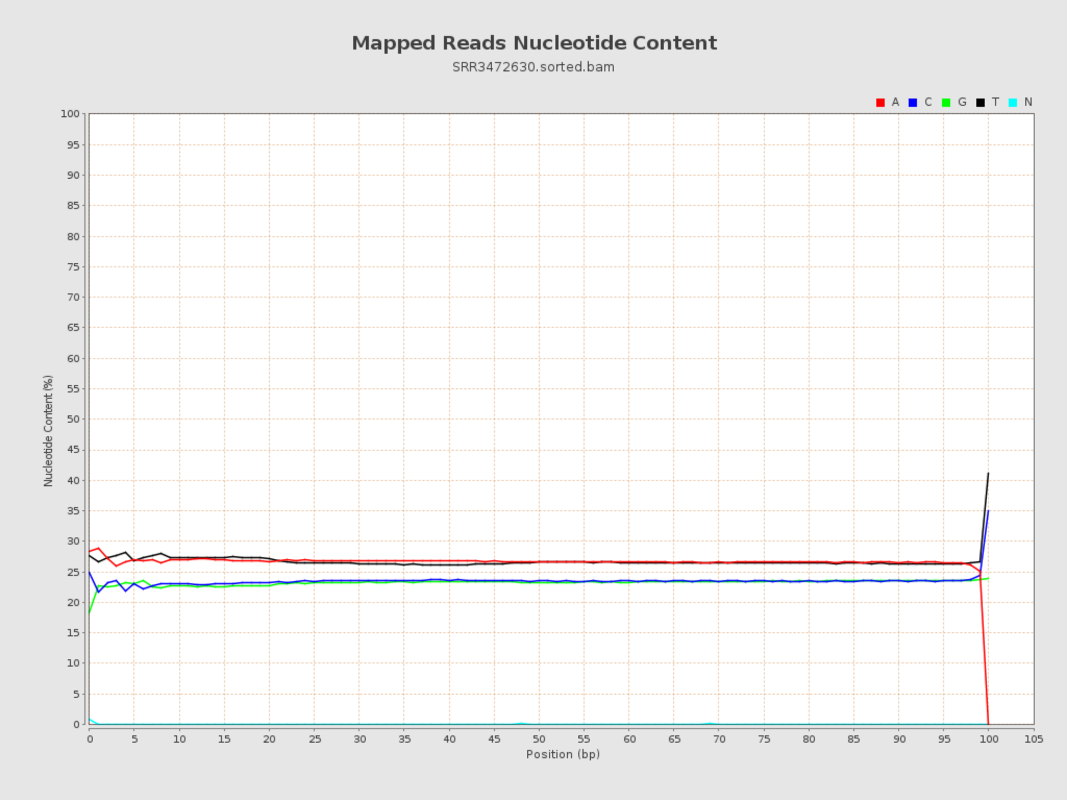
# 6. Results : Genome Fraction Coverage



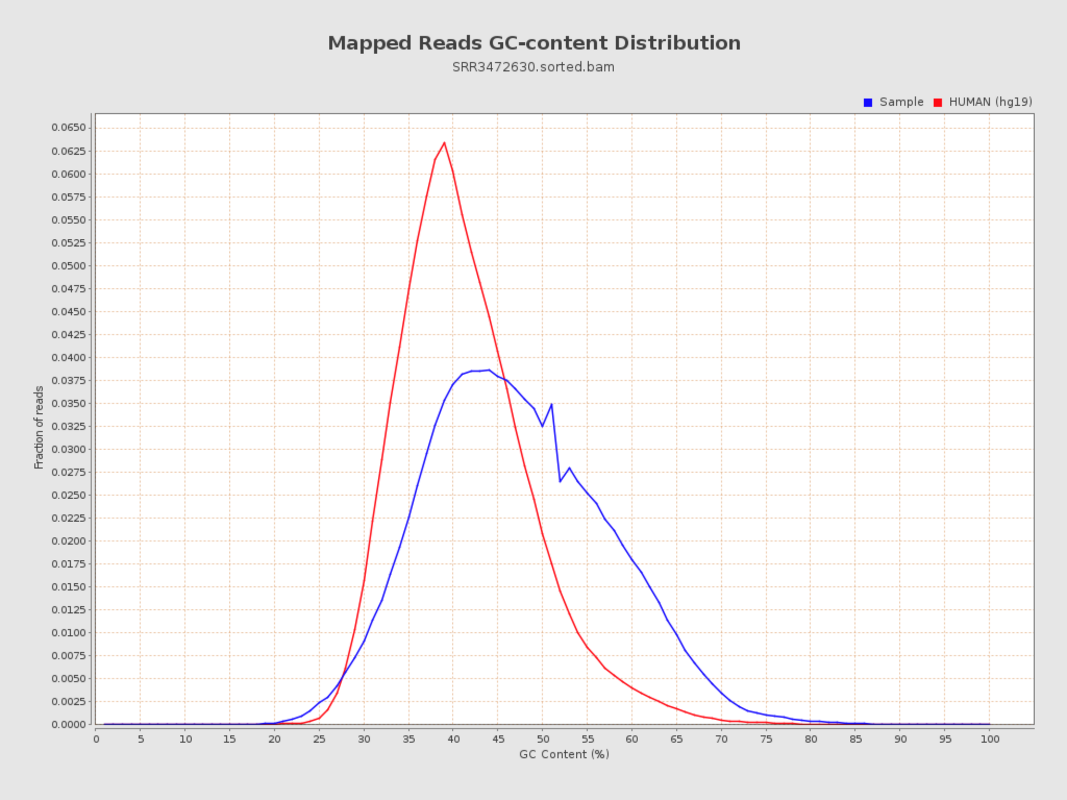
# 7. Results : Duplication Rate Histogram



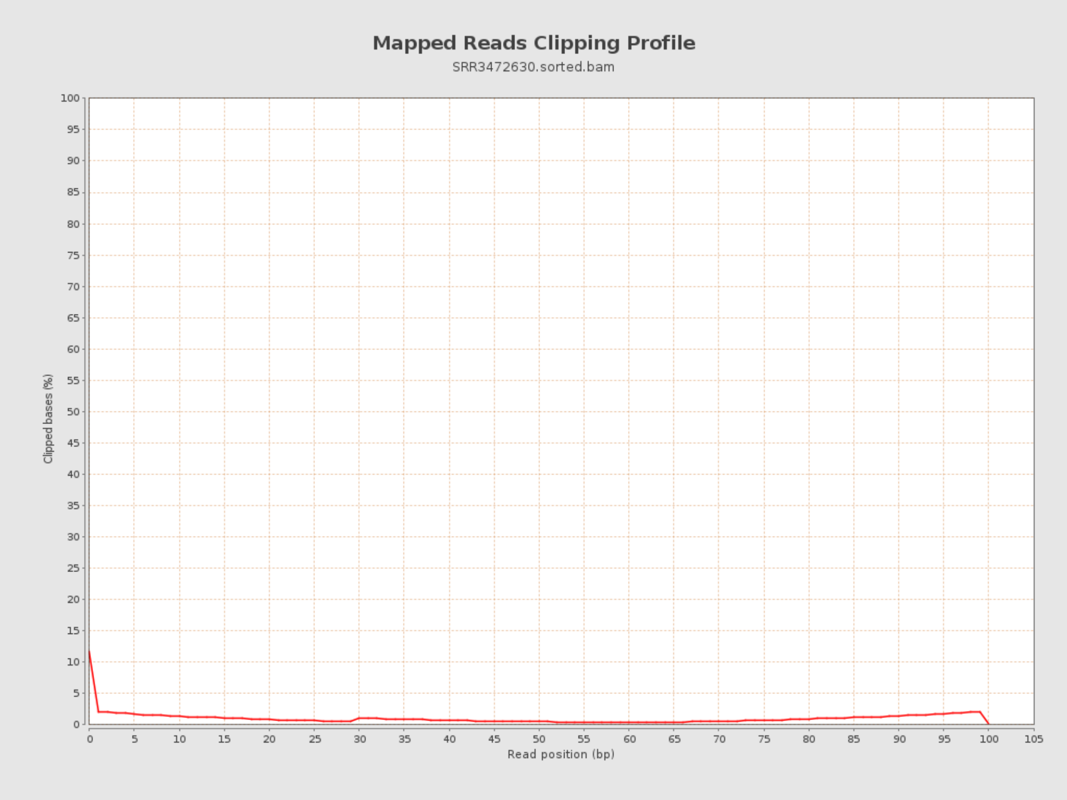
# 8. Results : Mapped Reads Nucleotide Content



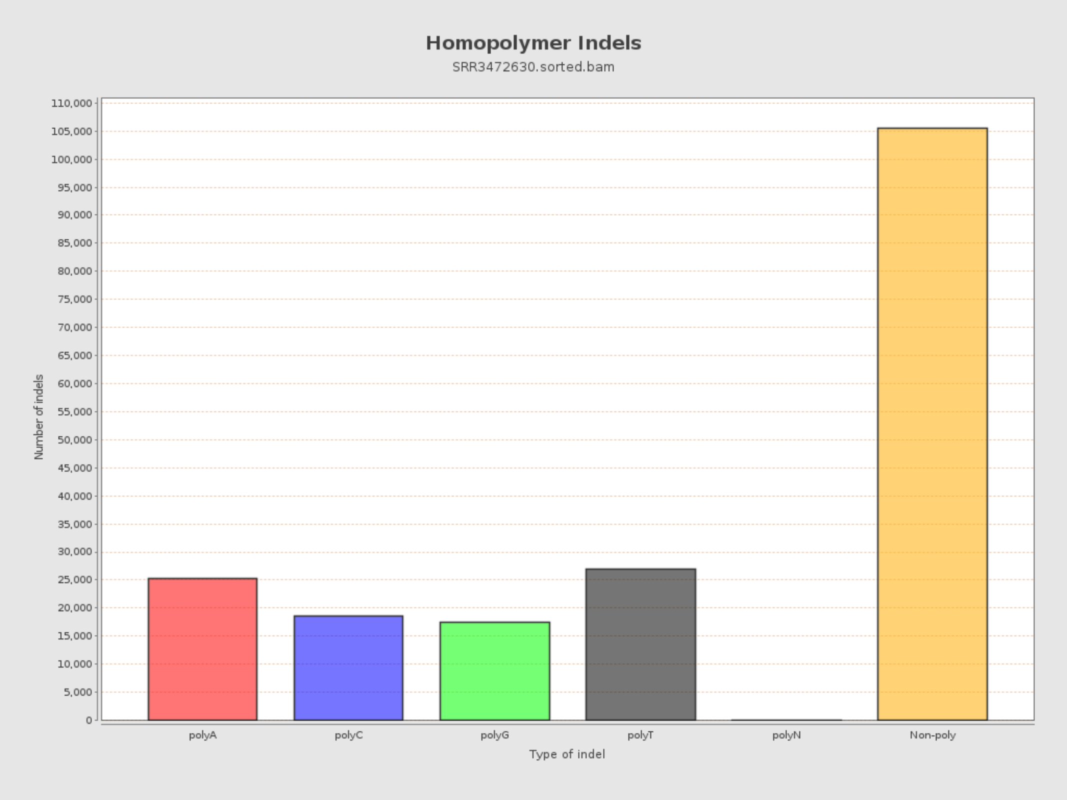
# 9. Results : Mapped Reads GC-content Distribution



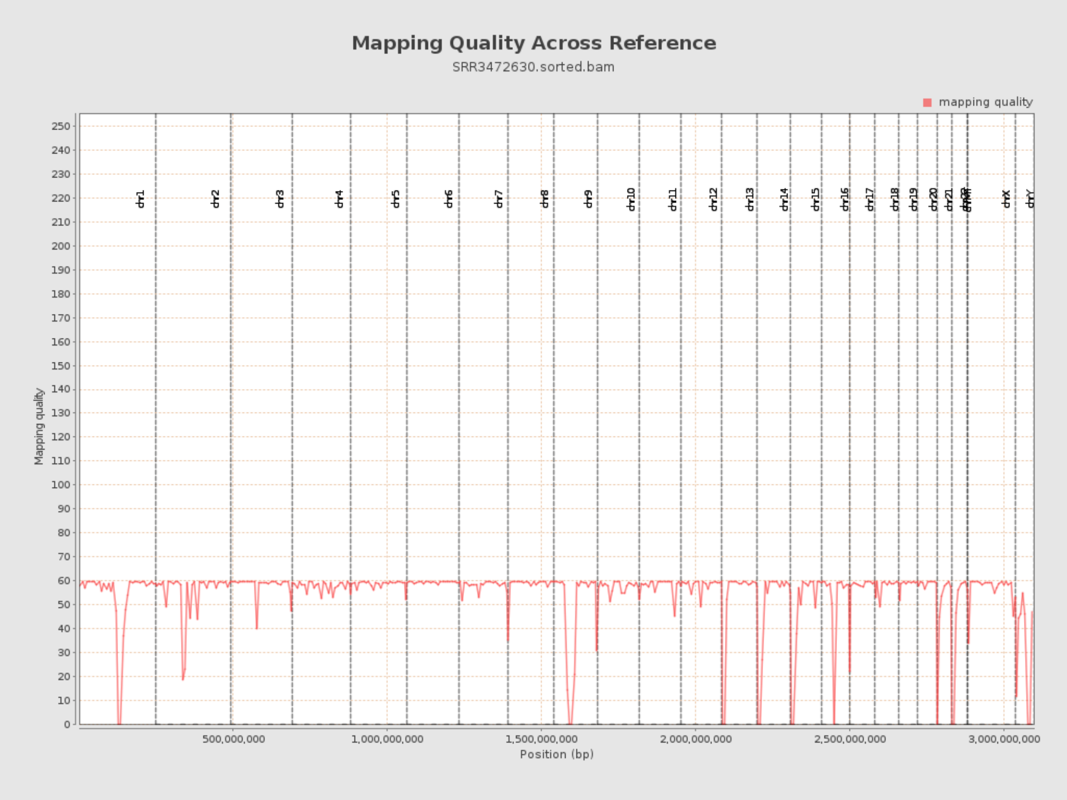
# 10. Results : Mapped Reads Clipping Profile



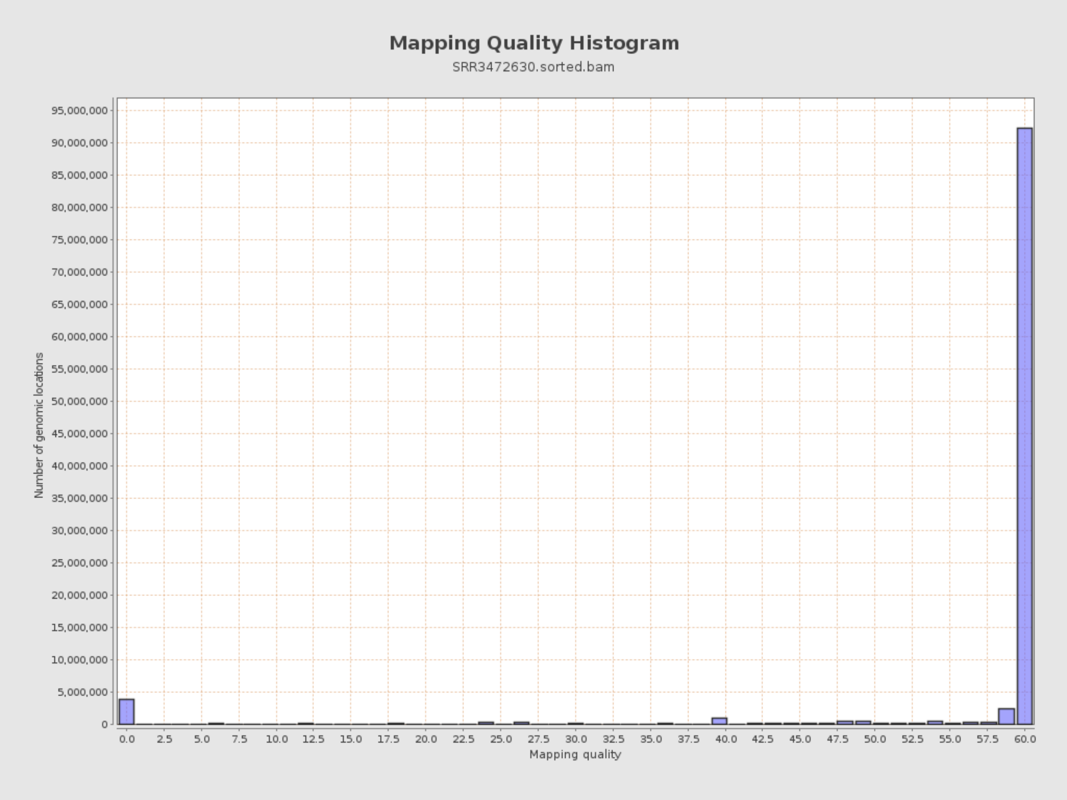
# 11. Results : Homopolymer Indels



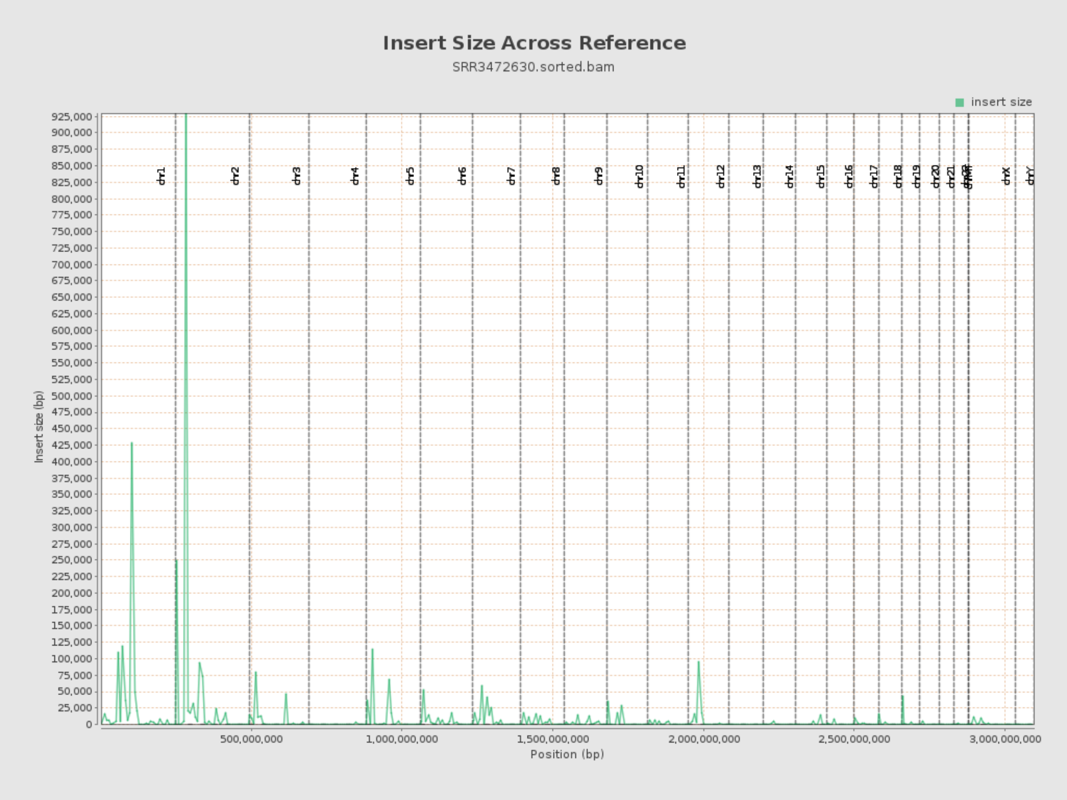
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram