# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/29 15:56:53*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472709.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_SRR3472709 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472709_1.fastq.gz SRR3472709_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 29 15:56:52 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3472709.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 18,596,144 |
| Mapped reads | 18,396,220 / 98.92% |
| Unmapped reads | 199,924 / 1.08% |
| Mapped paired reads | 18,396,220 / 98.92% |
| Mapped reads, first in pair | 9,234,842 / 49.66% |
| Mapped reads, second in pair | 9,161,378 / 49.26% |
| Mapped reads, both in pair | 18,280,986 / 98.31% |
| Mapped reads, singletons | 115,234 / 0.62% |
| Secondary alignments | 0 |
| Supplementary alignments | 64,561 / 0.35% |
| Read min/max/mean length | 30 / 100 / 100.14 |
| Duplicated reads (estimated) | 11,916,811 / 64.08% |
| Duplication rate | 47.96% |
| Clipped reads | 1,525,654 / 8.2% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 491,526,470 / 27.14% |
| Number/percentage of C's | 416,172,252 / 22.98% |
| Number/percentage of T's | 488,383,044 / 26.97% |
| Number/percentage of G's | 414,477,510 / 22.89% |
| Number/percentage of N's | 353,249 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 45.87% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.5851 |
| Standard Deviation | 19.7486 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 55.22 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 25,118.64 |
| Standard Deviation | 1,595,847.62 |
| P25/Median/P75 | 167 / 231 / 309 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.62% |
| Mismatches | 11,106,014 |
| Insertions | 101,438 |
| Mapped reads with at least one insertion | 0.55% |
| Deletions | 96,834 |
| Mapped reads with at least one deletion | 0.52% |
| Homopolymer indels | 45.39% |

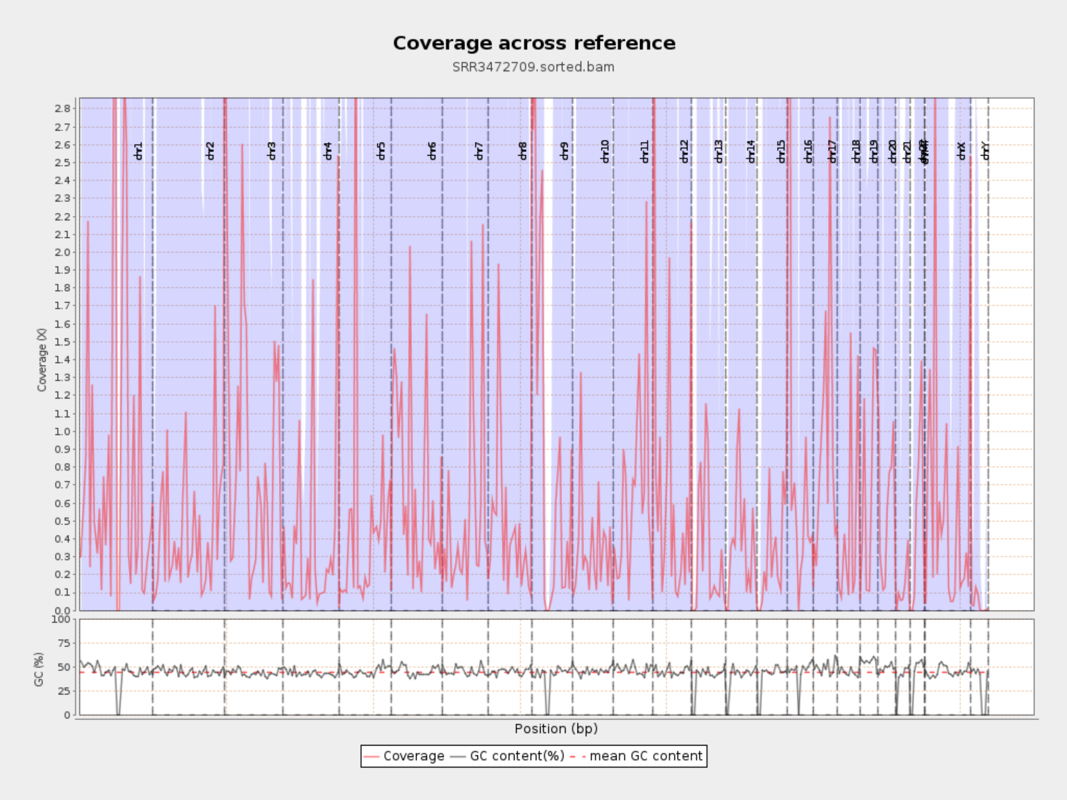
## 2.7. Chromosome stats

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

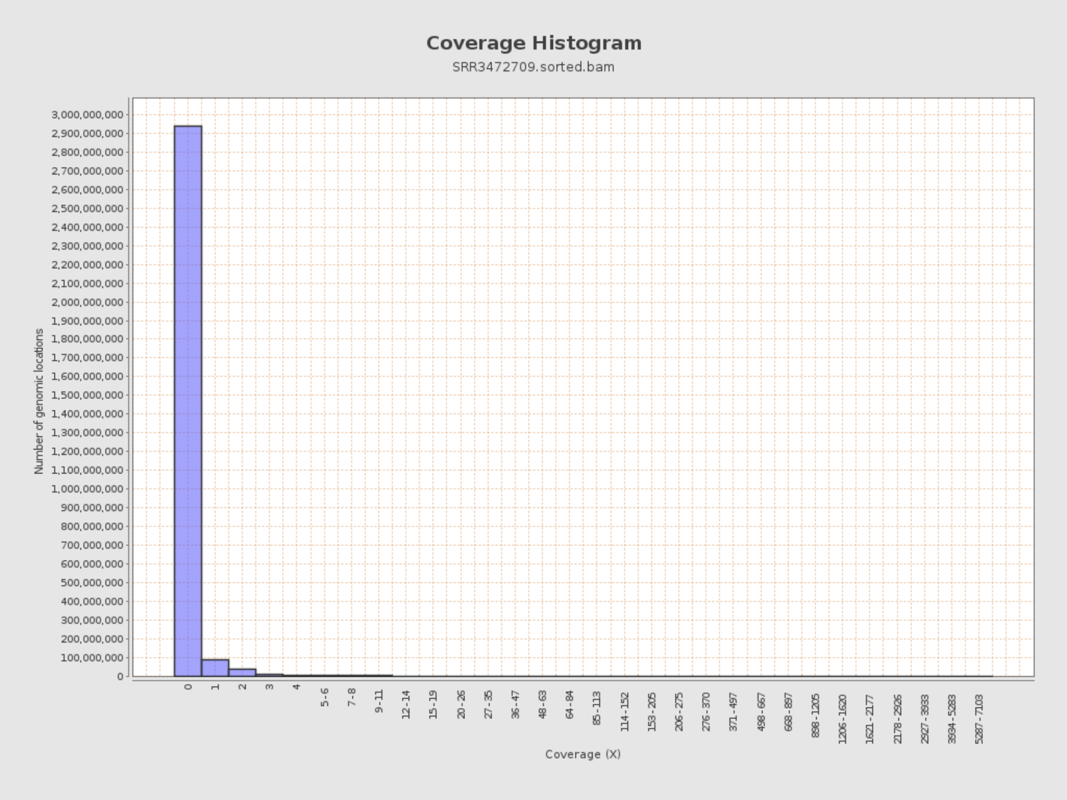
|  |  | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 224284352 | 0.8998 | 30.2367 |
| chr2 | 243199373 | 105595875 | 0.4342 | 17.7786 |
| chr3 | 198022430 | 178595936 | 0.9019 | 19.7877 |
| chr4 | 191154276 | 73444600 | 0.3842 | 18.5905 |
| chr5 | 180915260 | 88761222 | 0.4906 | 16.8261 |
| chr6 | 171115067 | 117709804 | 0.6879 | 19.7962 |
| chr7 | 159138663 | 84660138 | 0.532 | 20.0805 |
| chr8 | 146364022 | 65386971 | 0.4467 | 15.6206 |
| chr9 | 141213431 | 126238078 | 0.894 | 25.3576 |
| chr10 | 135534747 | 47280974 | 0.3488 | 15.8839 |
| chr11 | 135006516 | 89171087 | 0.6605 | 20.4419 |
| chr12 | 133851895 | 99653487 | 0.7445 | 23.91 |
| chr13 | 115169878 | 37110802 | 0.3222 | 13.1992 |
| chr14 | 107349540 | 40595950 | 0.3782 | 12.6457 |
| chr15 | 102531392 | 31242336 | 0.3047 | 10.0948 |
| chr16 | 90354753 | 84478153 | 0.935 | 26.4997 |
| chr17 | 81195210 | 77998983 | 0.9606 | 23.1162 |
| chr18 | 78077248 | 36714329 | 0.4702 | 18.0491 |
| chr19 | 59128983 | 44847986 | 0.7585 | 18.6562 |
| chr20 | 63025520 | 35737929 | 0.567 | 14.8597 |
| chr21 | 48129895 | 6135714 | 0.1275 | 4.141 |
| chr22 | 51304566 | 25020070 | 0.4877 | 14.4408 |
| chrMT | 16571 | 6651 | 0.4014 | 1.3106 |
| chrX | 155270560 | 88228112 | 0.5682 | 19.1009 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 2251655 | 0.0379 | 1.3898 |

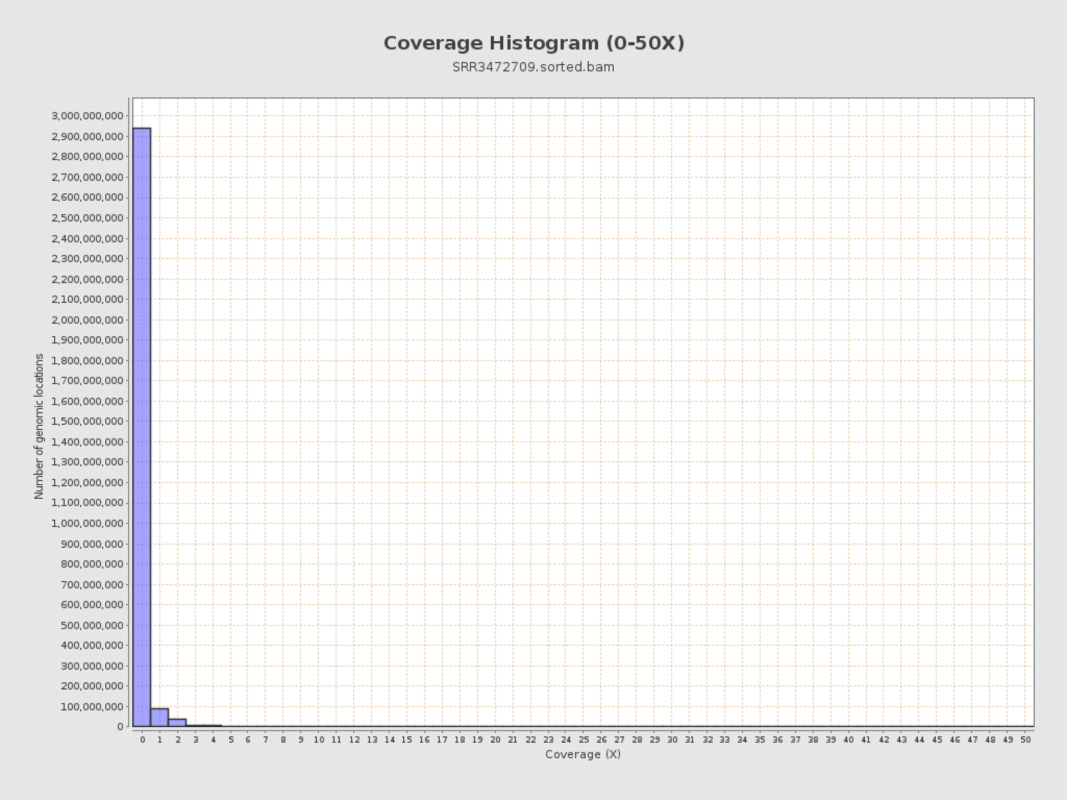
# 3. Results : Coverage across reference



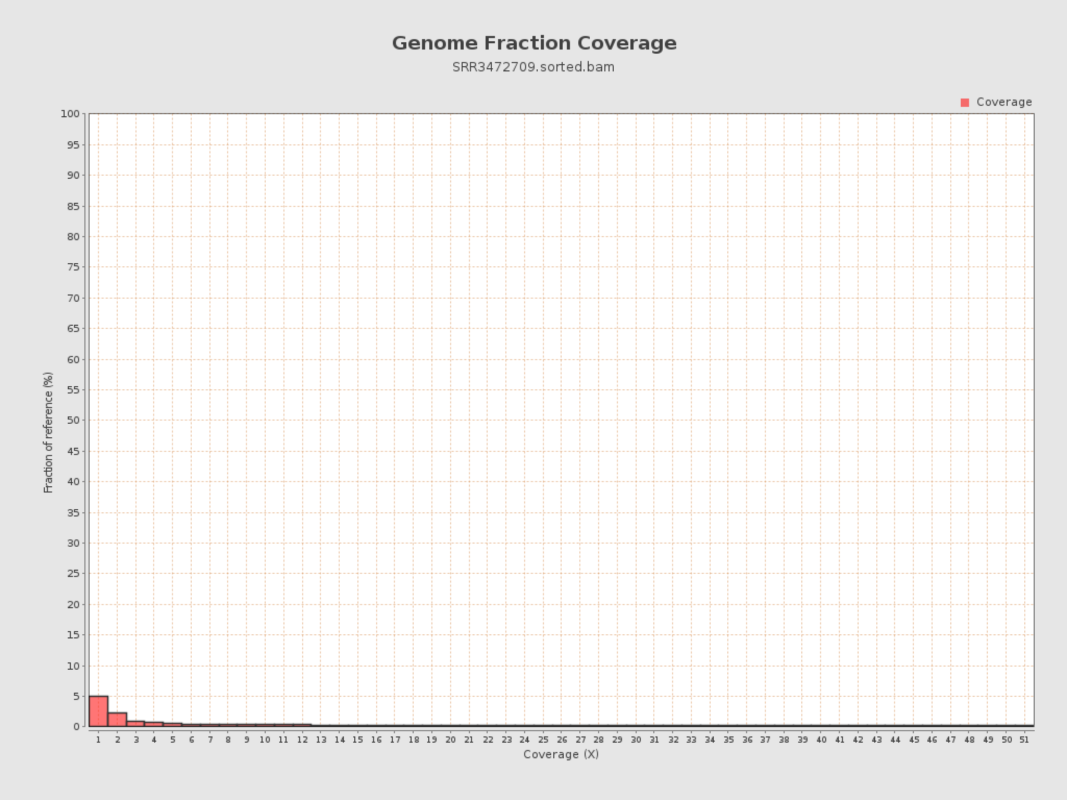
# 4. Results : Coverage Histogram



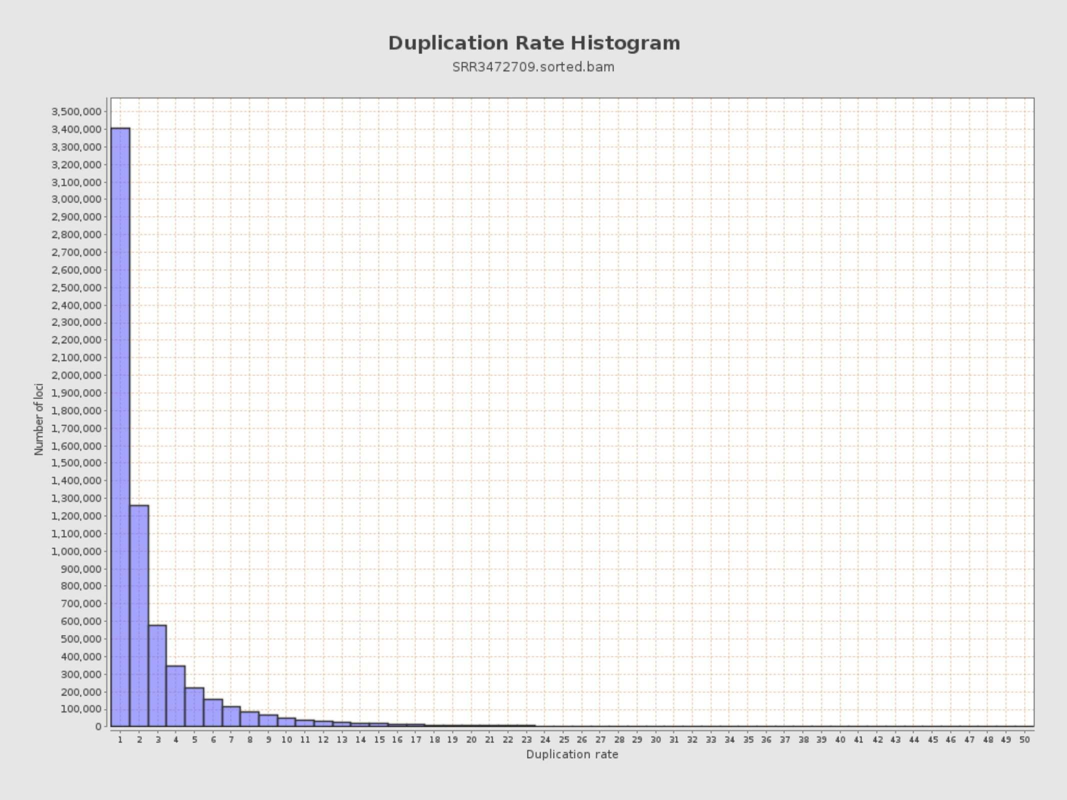
# 5. Results : Coverage Histogram (0-50X)



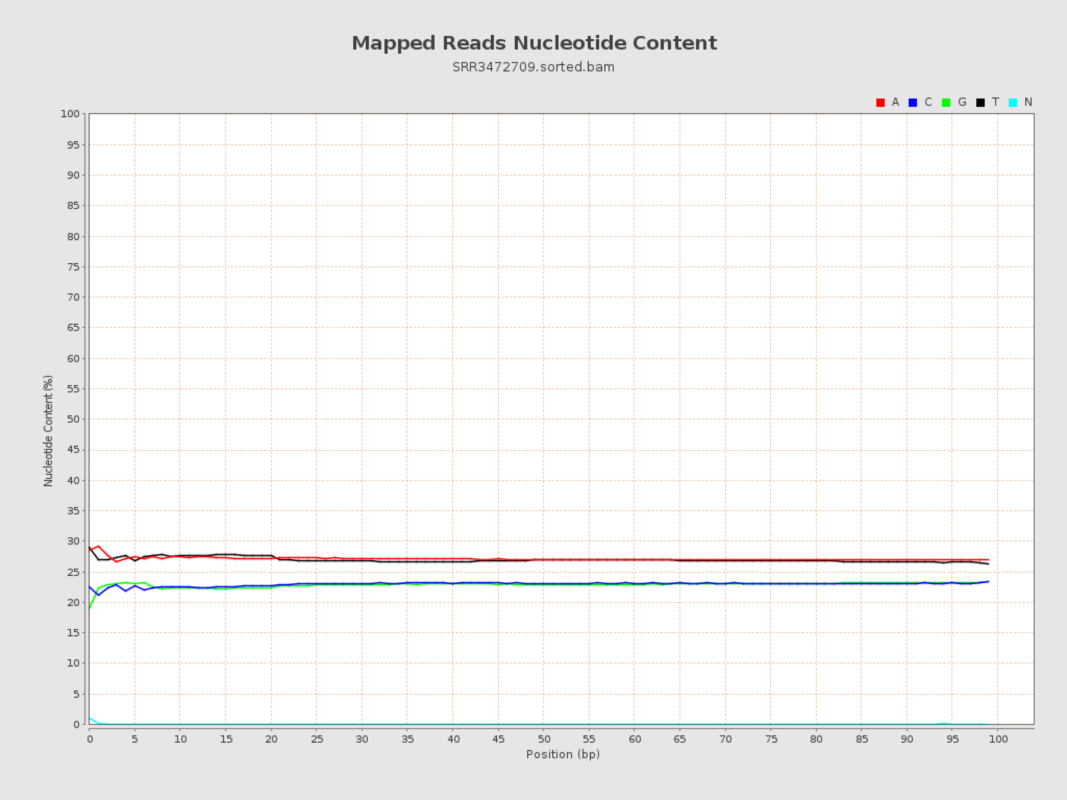
# 6. Results : Genome Fraction Coverage



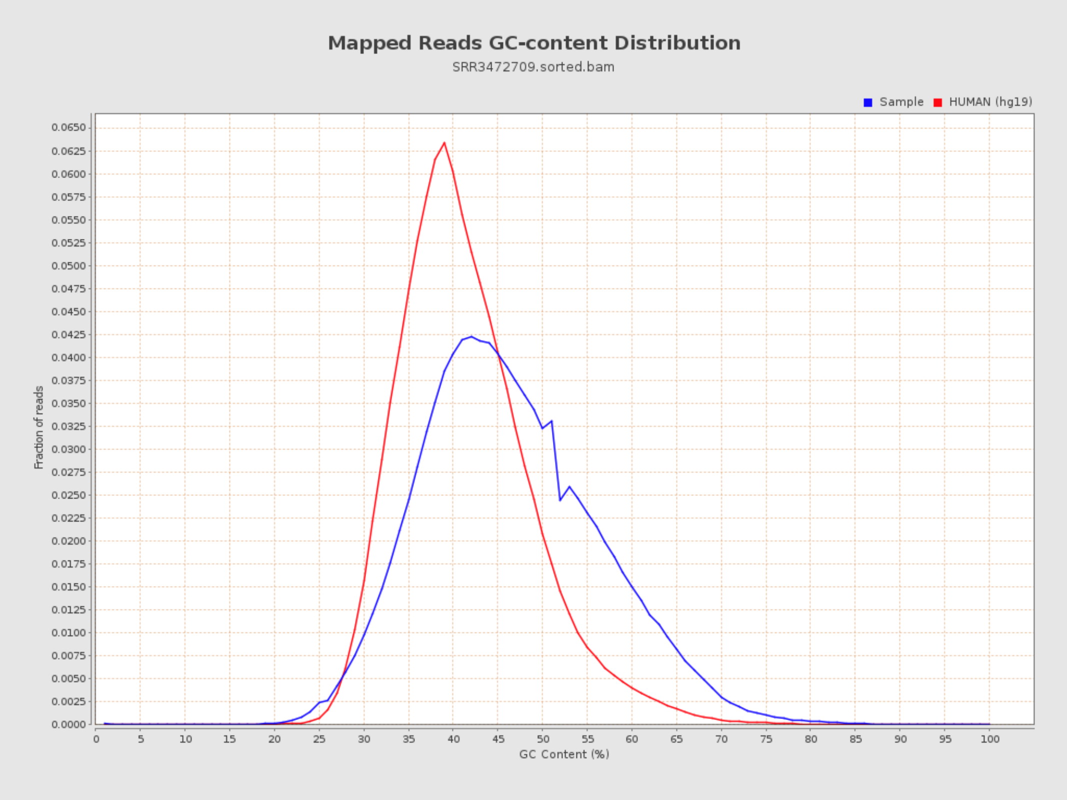
# 7. Results : Duplication Rate Histogram



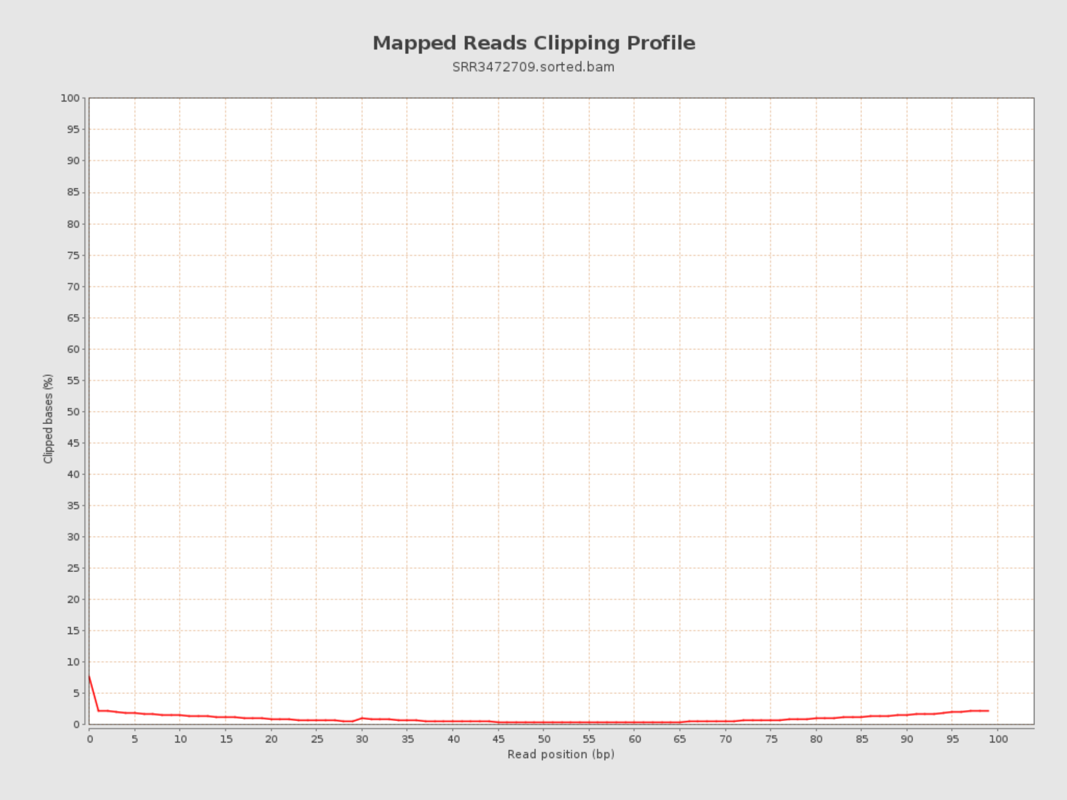
# 8. Results : Mapped Reads Nucleotide Content



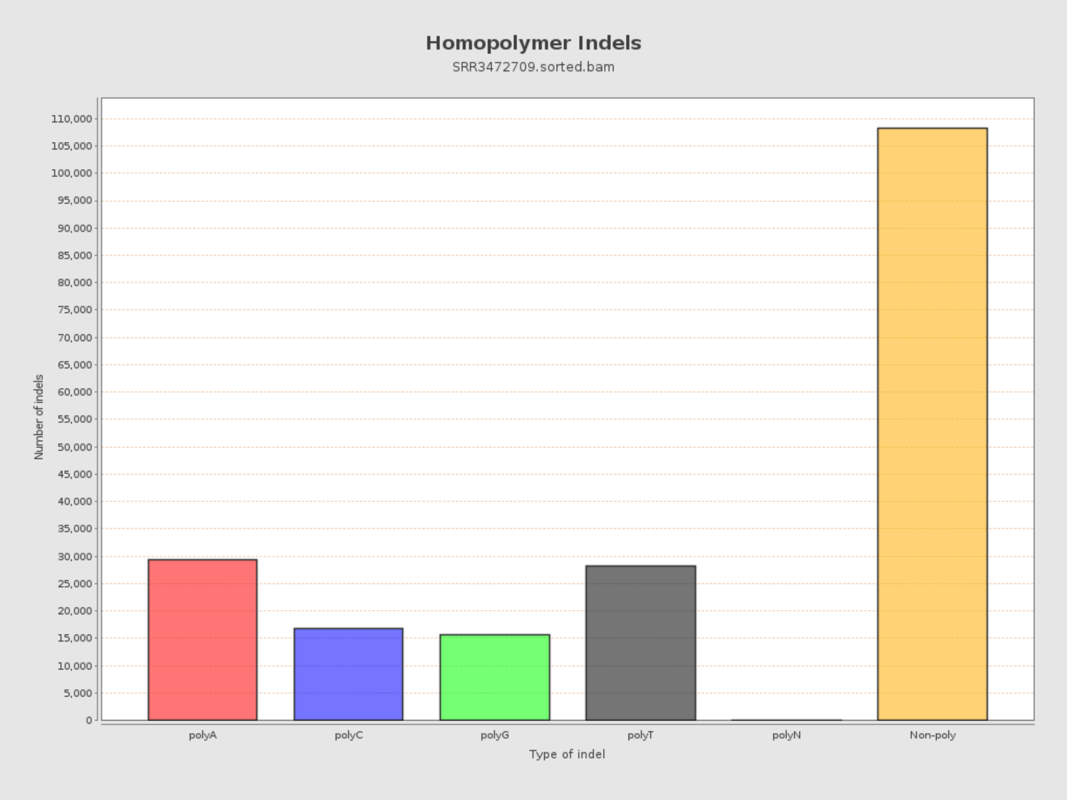
# 9. Results : Mapped Reads GC-content Distribution



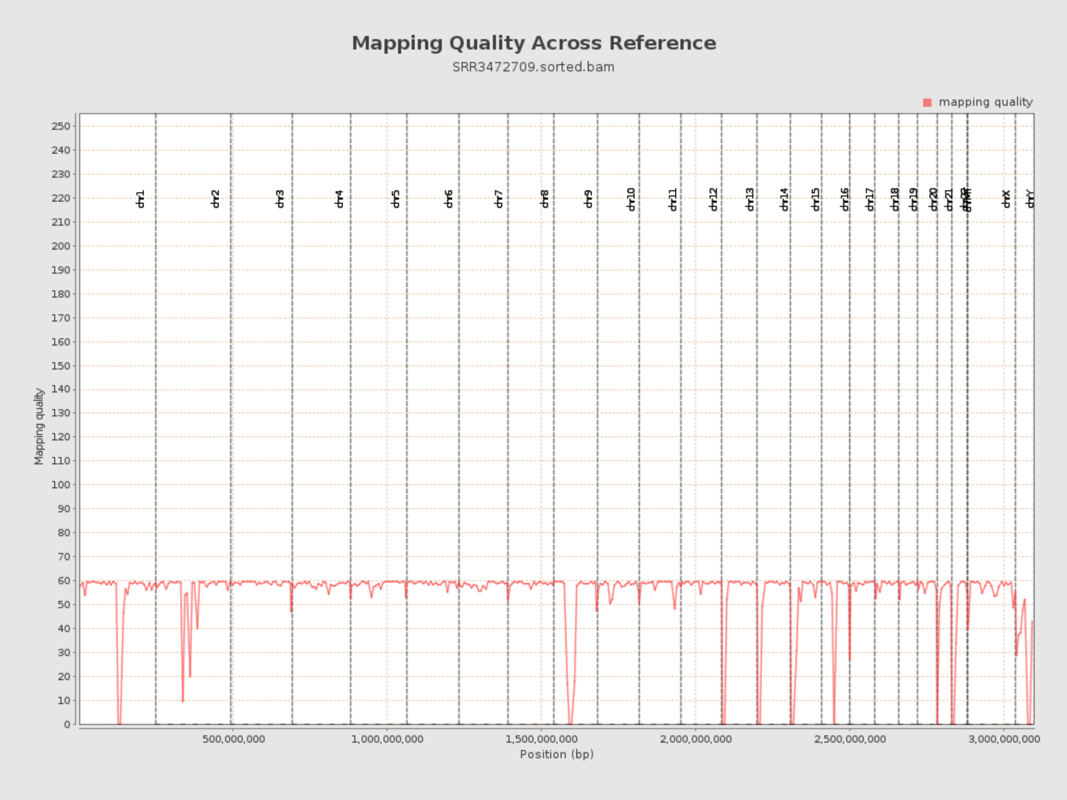
# 10. Results : Mapped Reads Clipping Profile



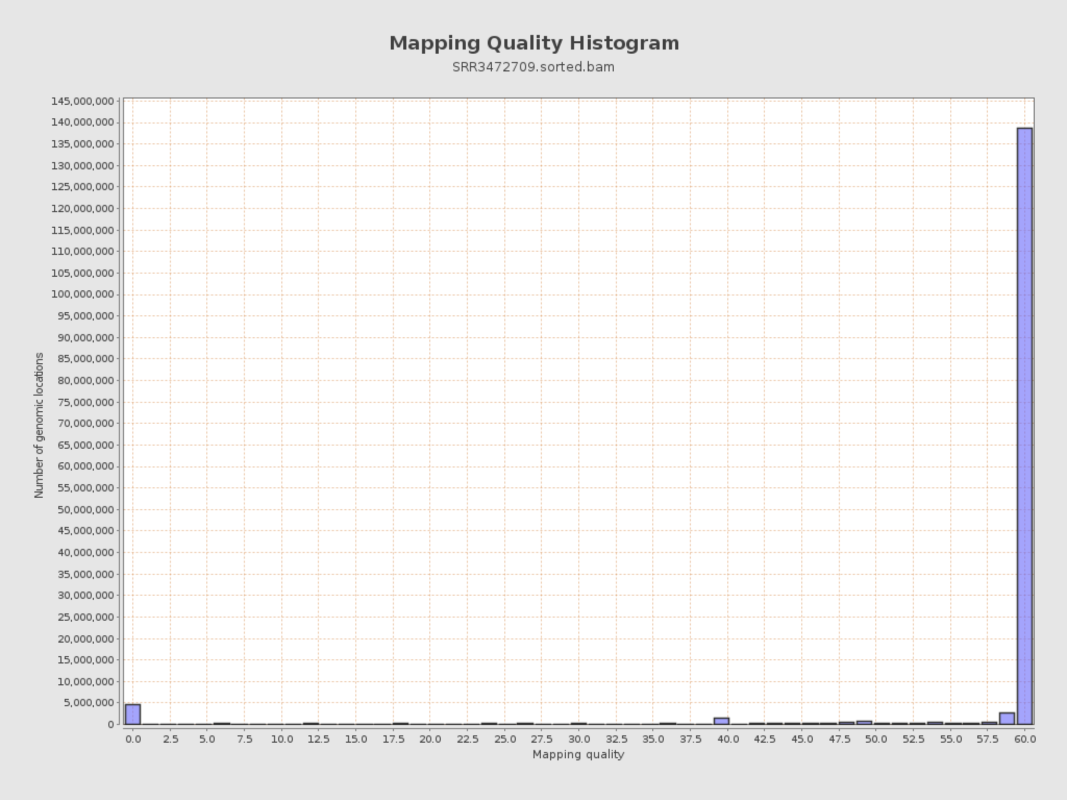
# 11. Results : Homopolymer Indels



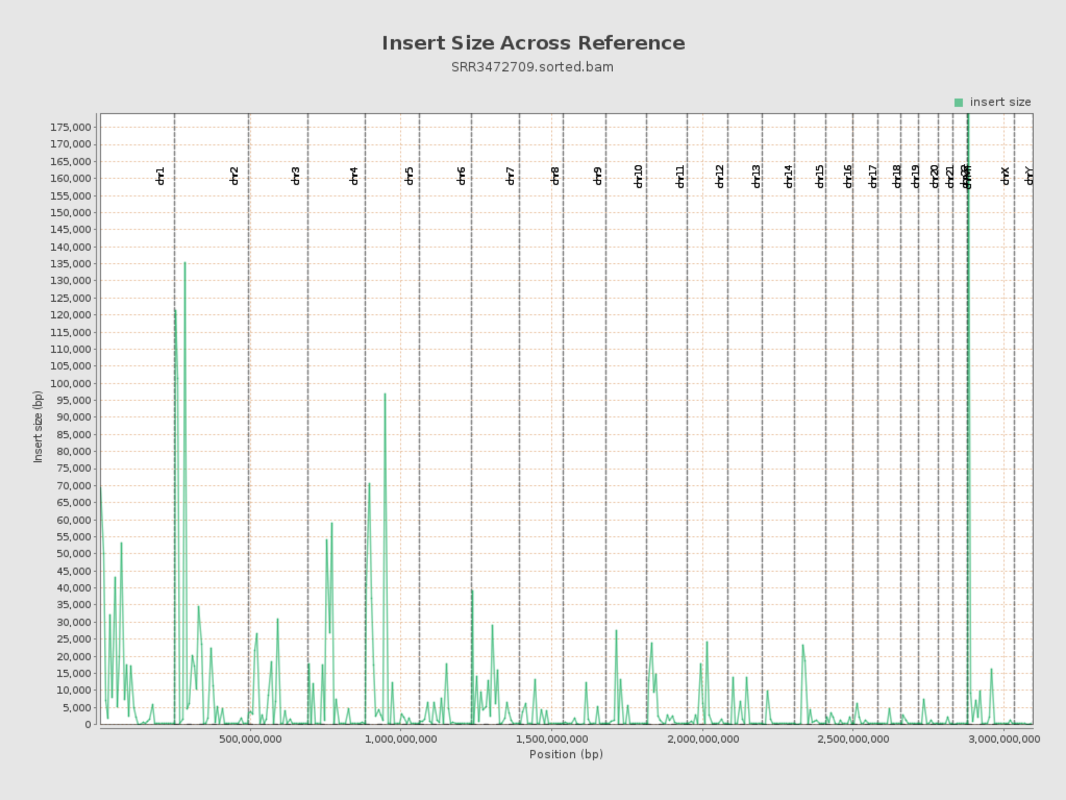
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram