# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 09:56:43*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472420.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_SRR3472420 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472420_1.fastq.gz SRR3472420_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 09:56:42 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3472420.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 33,776,426 |
| Mapped reads | 33,419,478 / 98.94% |
| Unmapped reads | 356,948 / 1.06% |
| Mapped paired reads | 33,419,478 / 98.94% |
| Mapped reads, first in pair | 16,812,746 / 49.78% |
| Mapped reads,  second in pair | 16,606,732 / 49.17% |
| Mapped reads, both in pair | 33,166,630 / 98.19% |
| Mapped reads, singletons | 252,848 / 0.75% |
| Secondary alignments | 0 |
| Supplementary alignments | 50,334 / 0.15% |
| Read min/max/mean length | 30 / 100 / 99.38 |
| Duplicated reads (estimated) | 21,397,781 / 63.35% |
| Duplication rate | 52.95% |
| Clipped reads | 1,807,098 / 5.35% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 919,876,504 / 28.01% |
| Number/percentage of C's | 722,658,891 / 22% |
| Number/percentage of T's | 924,871,630 / 28.16% |
| Number/percentage of G's | 716,650,055 / 21.82% |
| Number/percentage of N's | 449,561 / 0.01% |
| | |

| | |
|---|---|
| GC Percentage | 43.82% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 1.0611 |
| Standard Deviation | 20.1436 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 54.87 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 34,679.89 |
| Standard Deviation | 1,872,161.03 |
| P25/Median/P75 | 160 / 224 / 305 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.5% |
| Mismatches | 15,964,862 |
| Insertions | 159,047 |
| Mapped reads with at least one insertion | 0.47% |
| Deletions | 195,999 |
| Mapped reads with at least one deletion | 0.58% |
| Homopolymer indels | 45.6% |

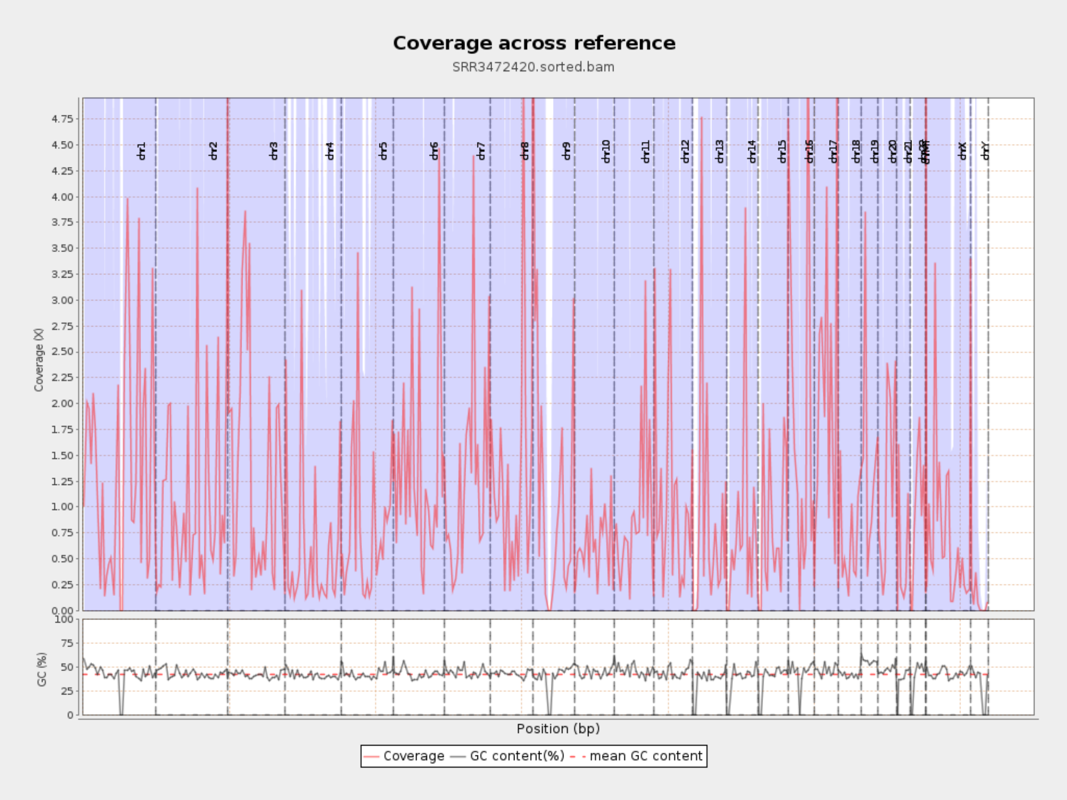
## 2.7. Chromosome stats

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

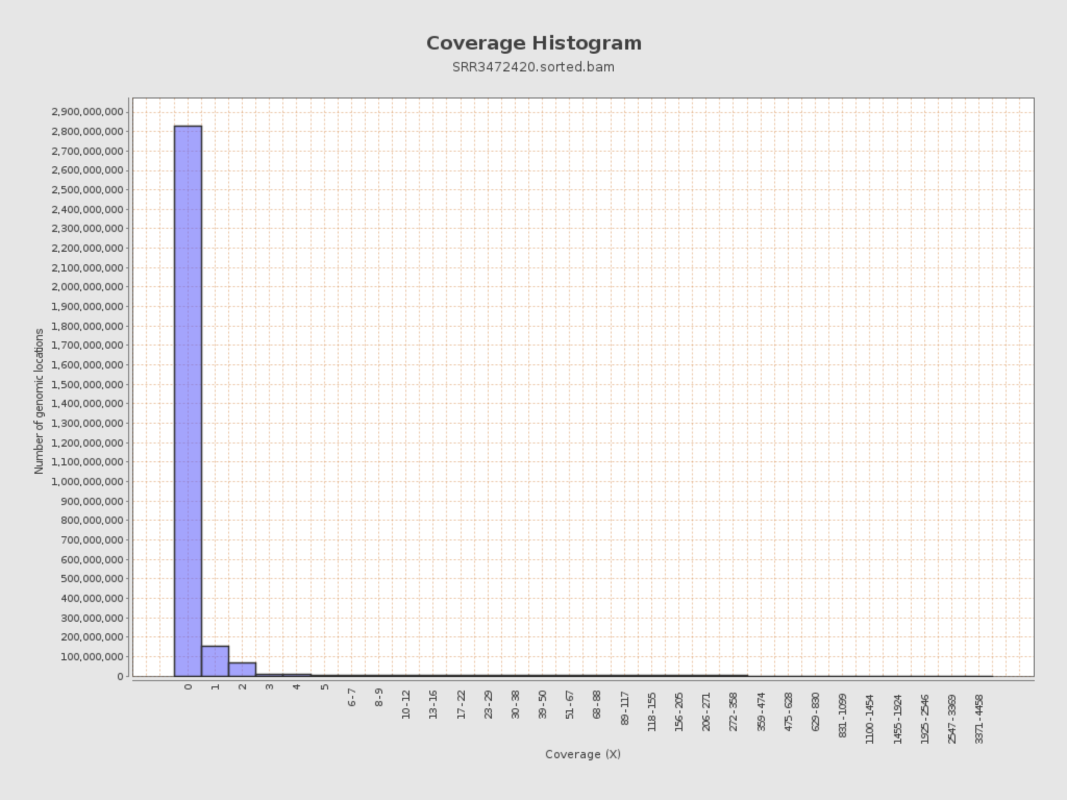
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 339432260 | 1.3618 | 23.0171 |
| chr2 | 243199373 | 247767003 | 1.0188 | 20.9313 |
| chr3 | 198022430 | 281041345 | 1.4192 | 21.7019 |
| chr4 | 191154276 | 115657307 | 0.605 | 14.9453 |
| chr5 | 180915260 | 150653914 | 0.8327 | 17.072 |
| chr6 | 171115067 | 232888322 | 1.361 | 21.3812 |
| chr7 | 159138663 | 209806741 | 1.3184 | 25.5649 |
| chr8 | 146364022 | 181607232 | 1.2408 | 21.2794 |
| chr9 | 141213431 | 150202621 | 1.0637 | 17.5323 |
| chr10 | 135534747 | 88934299 | 0.6562 | 14.3204 |
| chr11 | 135006516 | 125501971 | 0.9296 | 19.03 |
| chr12 | 133851895 | 147965113 | 1.1054 | 17.6908 |
| chr13 | 115169878 | 98568886 | 0.8559 | 21.9201 |
| chr14 | 107349540 | 84035691 | 0.7828 | 15.949 |
| chr15 | 102531392 | 80835982 | 0.7884 | 18.2843 |
| chr16 | 90354753 | 165906012 | 1.8362 | 31.5577 |
| chr17 | 81195210 | 170143122 | 2.0955 | 31.1565 |
| chr18 | 78077248 | 51247662 | 0.6564 | 13.1714 |
| chr19 | 59128983 | 84879324 | 1.4355 | 18.9784 |
| chr20 | 63025520 | 77505394 | 1.2297 | 22.7035 |
| chr21 | 48129895 | 27541276 | 0.5722 | 21.5304 |
| chr22 | 51304566 | 50887172 | 0.9919 | 20.19 |
| chrMT | 16571 | 126378 | 7.6265 | 3.9015 |
| chrX | 155270560 | 116169930 | 0.7482 | 11.6934 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 5668450 | 0.0955 | 2.6237 |

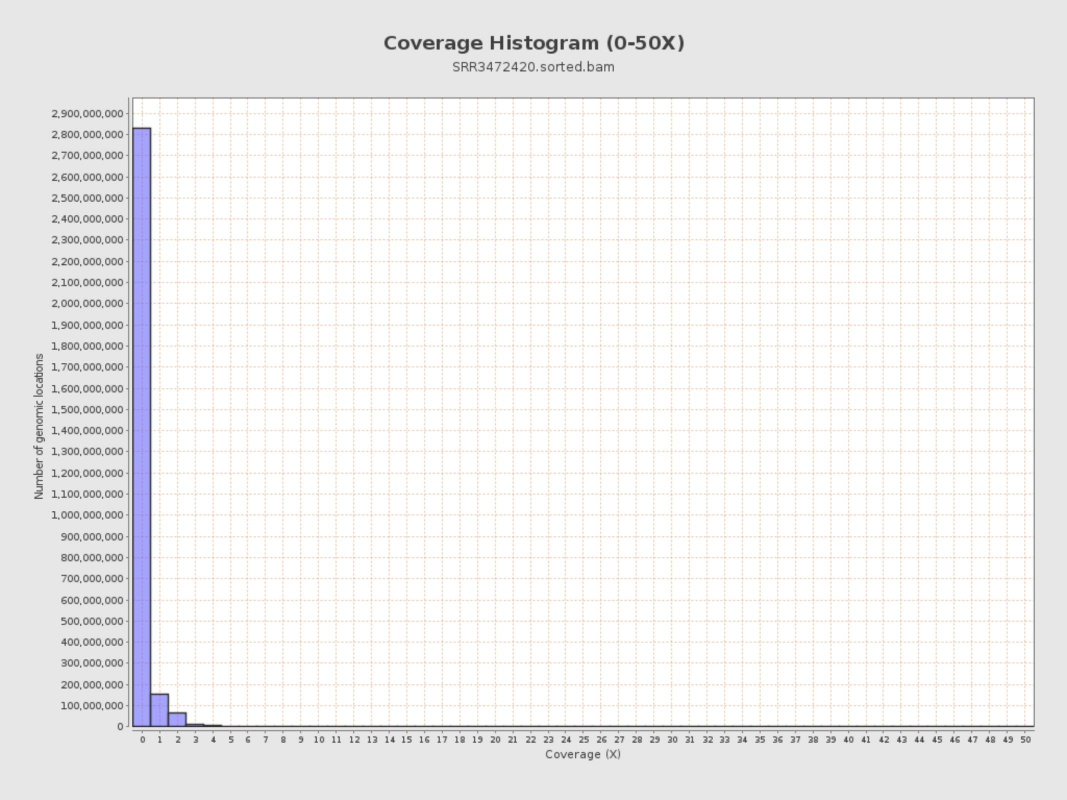
# 3. Results : Coverage across reference



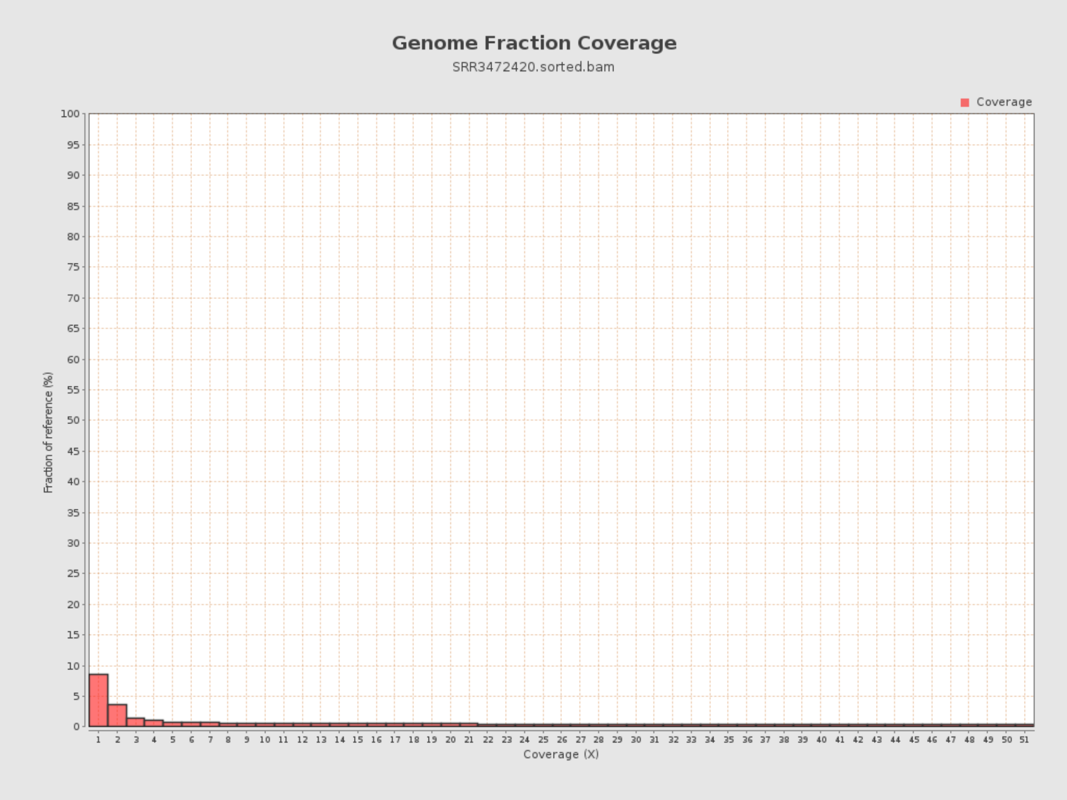
# 4. Results : Coverage Histogram



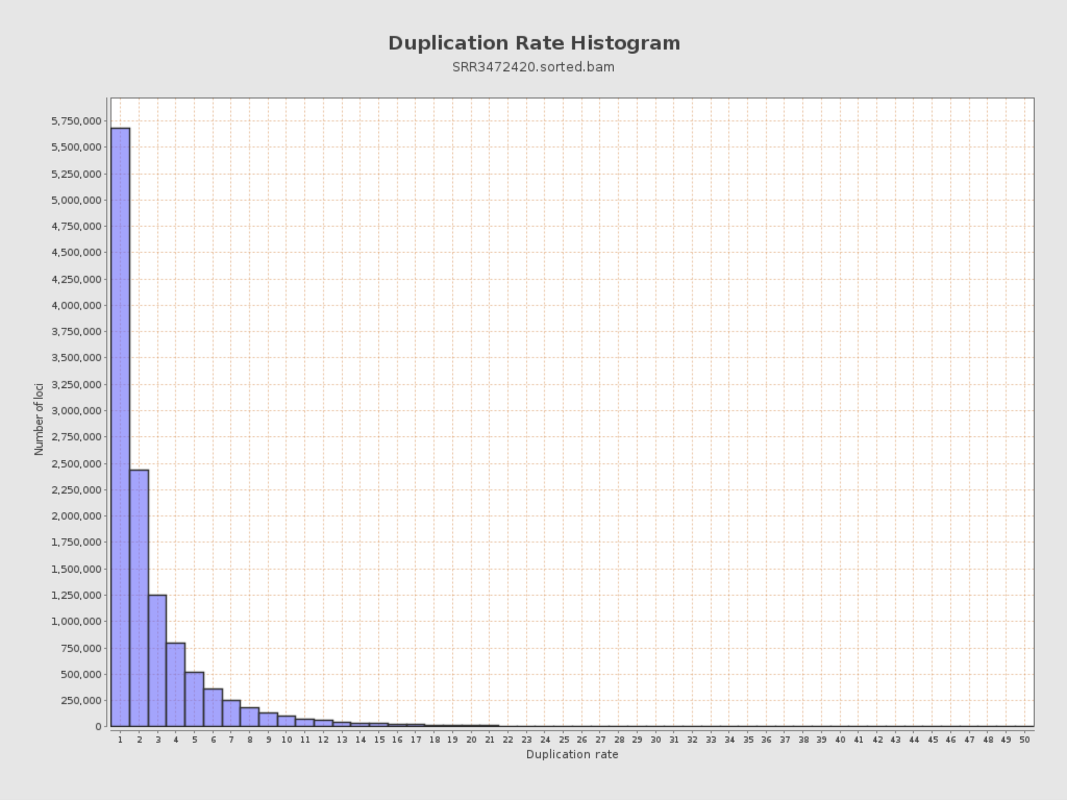
# 5. Results : Coverage Histogram (0-50X)



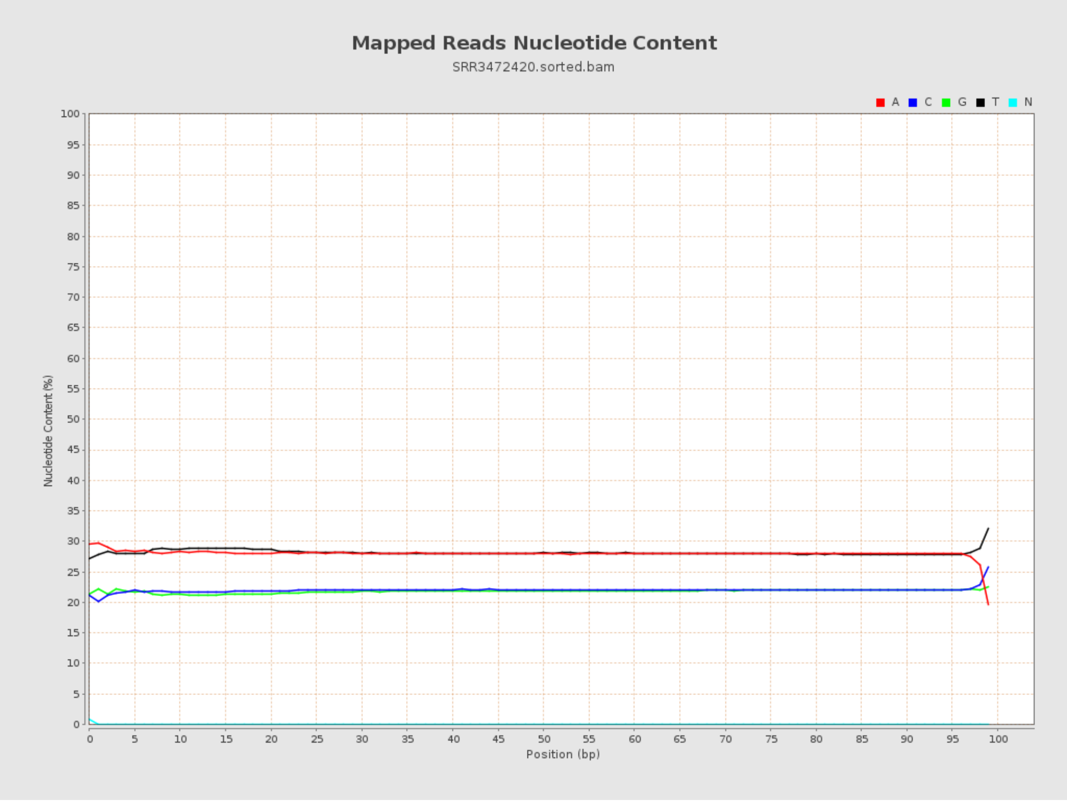
# 6. Results : Genome Fraction Coverage



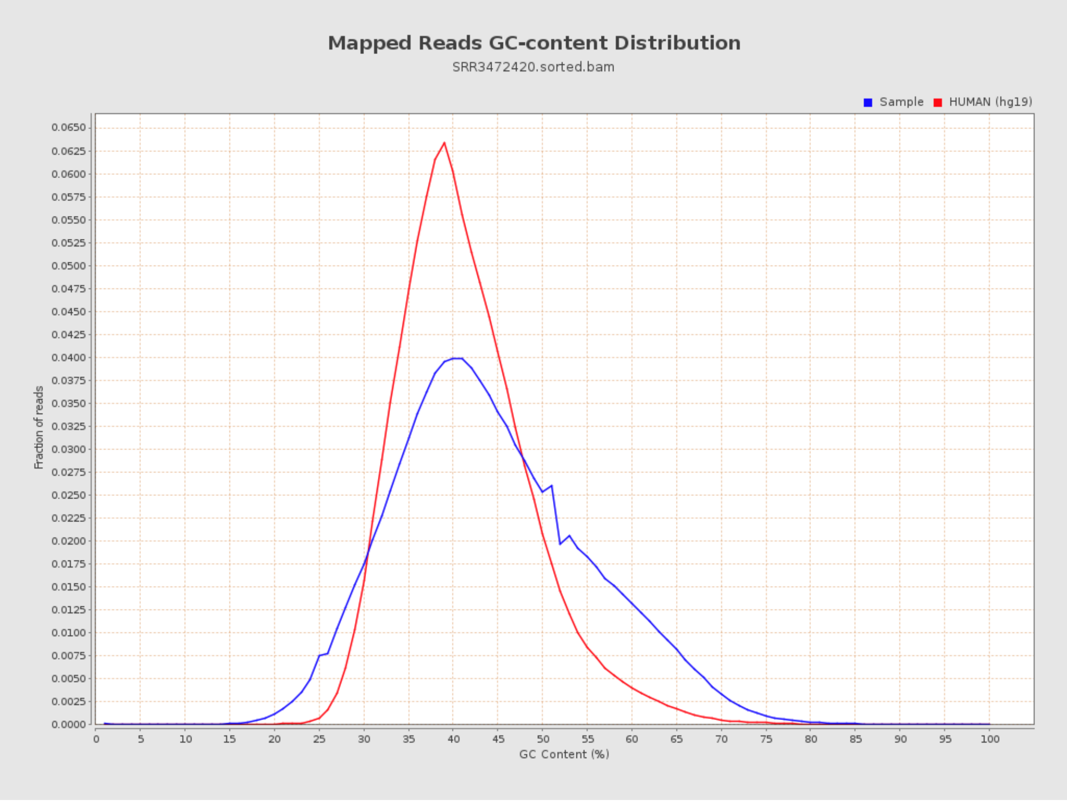
# 7. Results : Duplication Rate Histogram



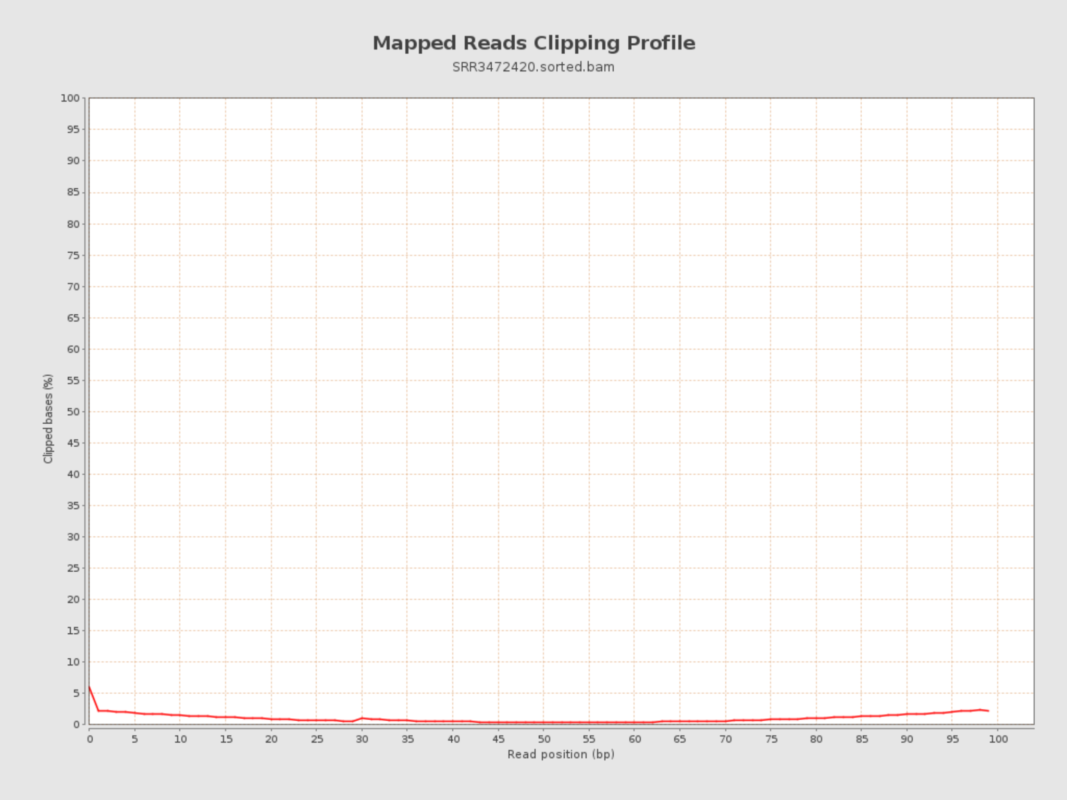
# 8. Results : Mapped Reads Nucleotide Content



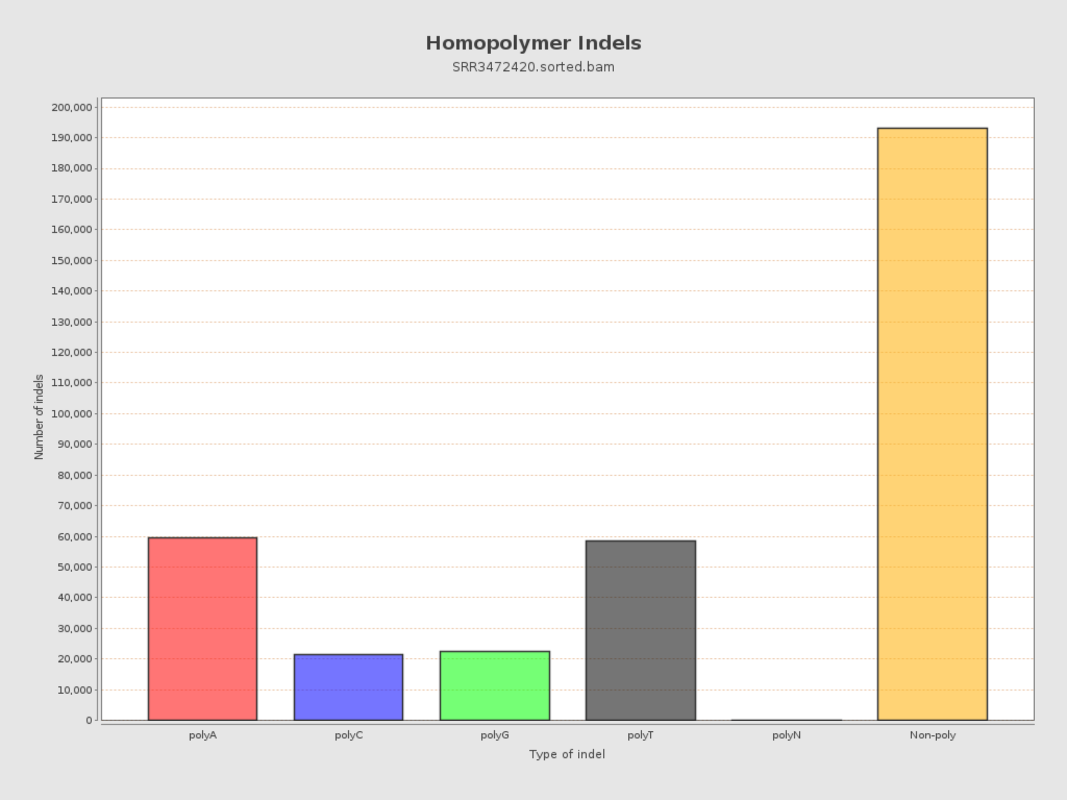
# 9. Results : Mapped Reads GC-content Distribution



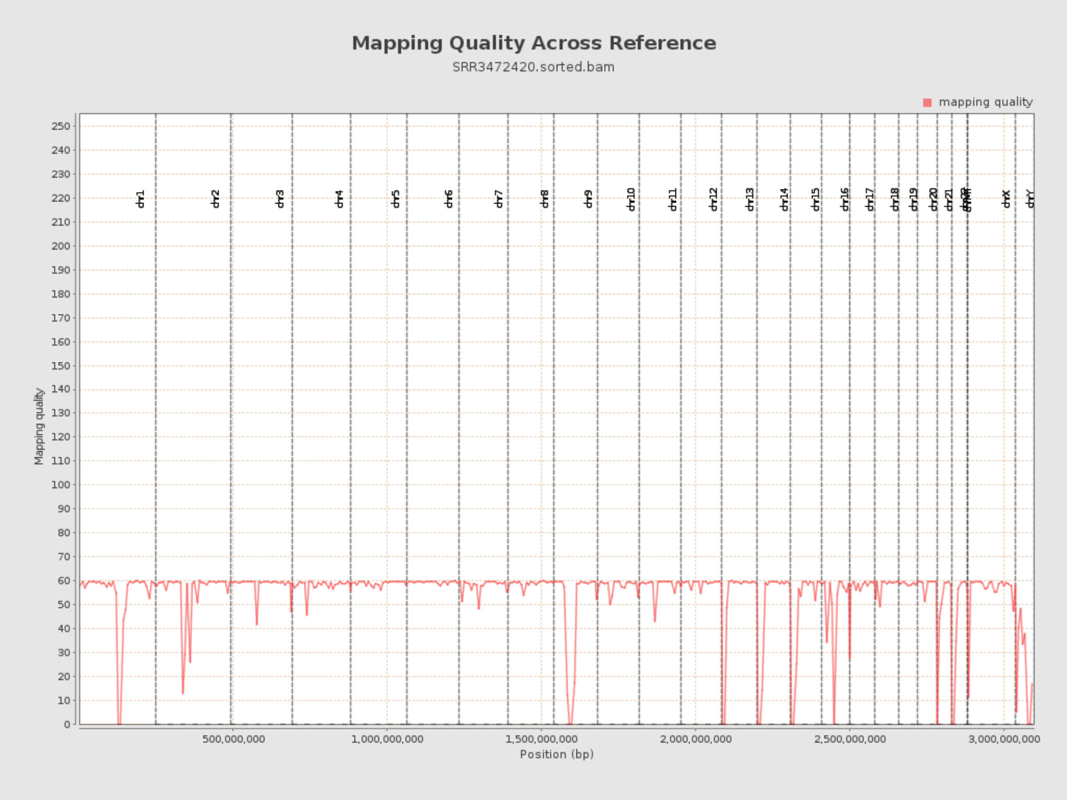
# 10. Results : Mapped Reads Clipping Profile



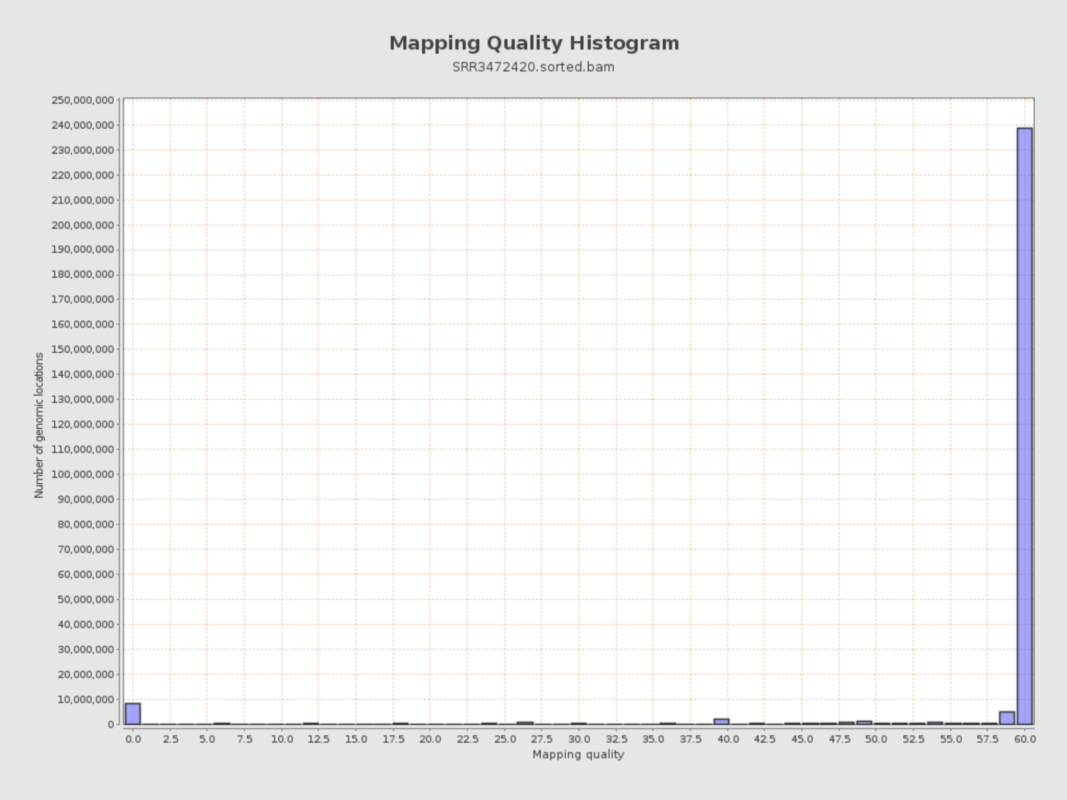
# 11. Results : Homopolymer Indels



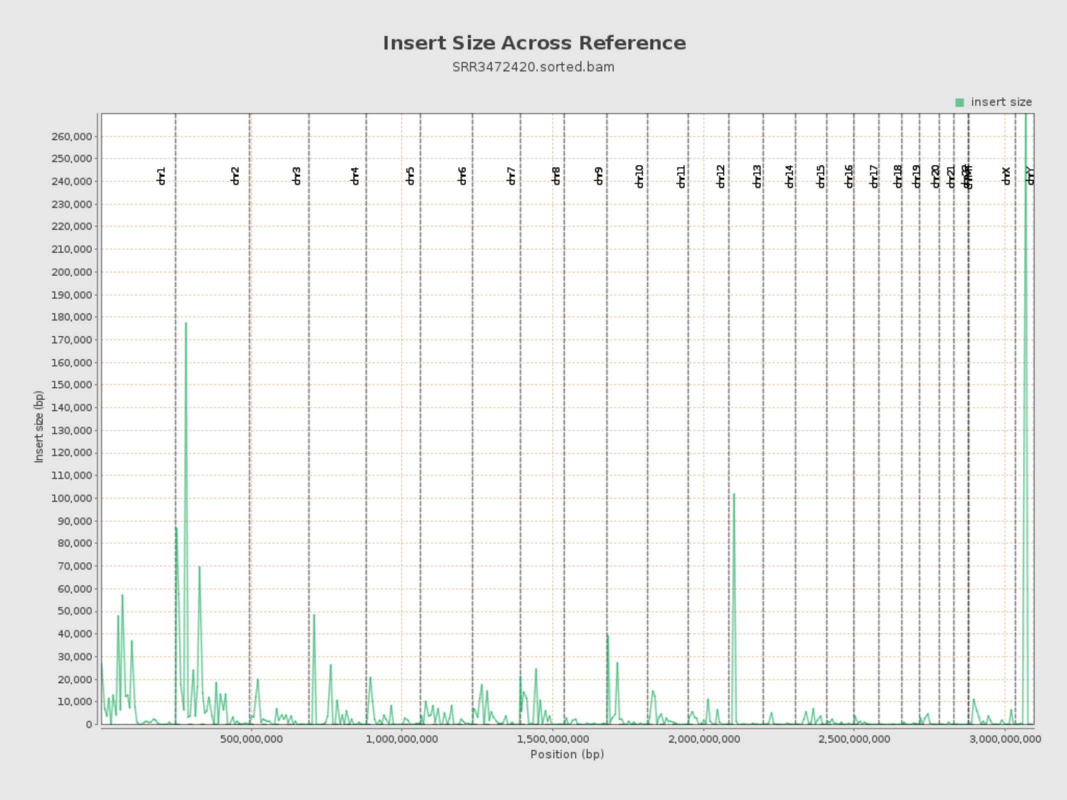
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram