# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/28 21:01:11*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472647.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_SRR3472647 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472647_1.fastq.gz SRR3472647_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 28 21:01:10 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3472647.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 8,341,912 |
| Mapped reads | 8,256,938 / 98.98% |
| Unmapped reads | 84,974 / 1.02% |
| Mapped paired reads | 8,256,938 / 98.98% |
| Mapped reads, first in pair | 4,137,062 / 49.59% |
| Mapped reads, second in pair | 4,119,876 / 49.39% |
| Mapped reads, both in pair | 8,203,568 / 98.34% |
| Mapped reads, singletons | 53,370 / 0.64% |
| Secondary alignments | 0 |
| Supplementary alignments | 41,809 / 0.5% |
| Read min/max/mean length | 30 / 101 / 99.55 |
| Duplicated reads (estimated) | 5,172,308 / 62% |
| Duplication rate | 41.82% |
| Clipped reads | 531,363 / 6.37% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 221,312,803 / 27.27% |
| Number/percentage of C's | 185,812,065 / 22.9% |
| Number/percentage of T's | 221,158,439 / 27.25% |
| Number/percentage of G's | 183,119,128 / 22.57% |
| Number/percentage of N's | 104,040 / 0.01% |
| | |

| | |
|---|---|
| GC Percentage | 45.46% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.2622 |
| Standard Deviation | 13.9802 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 54.71 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 22,651 |
| Standard Deviation | 1,464,466.1 |
| P25/Median/P75 | 158 / 219 / 291 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.84% |
| Mismatches | 6,732,617 |
| Insertions | 48,756 |
| Mapped reads with at least one insertion | 0.59% |
| Deletions | 45,165 |
| Mapped reads with at least one deletion | 0.54% |
| Homopolymer indels | 48.03% |

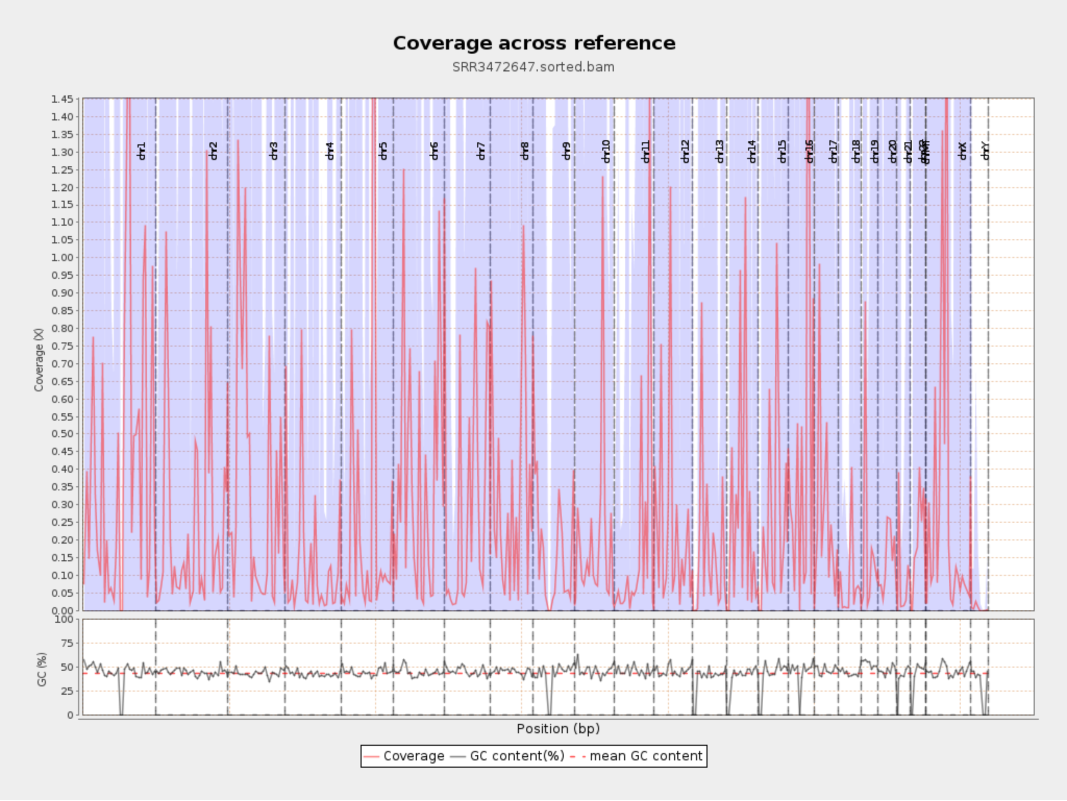
## 2.7. Chromosome stats

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

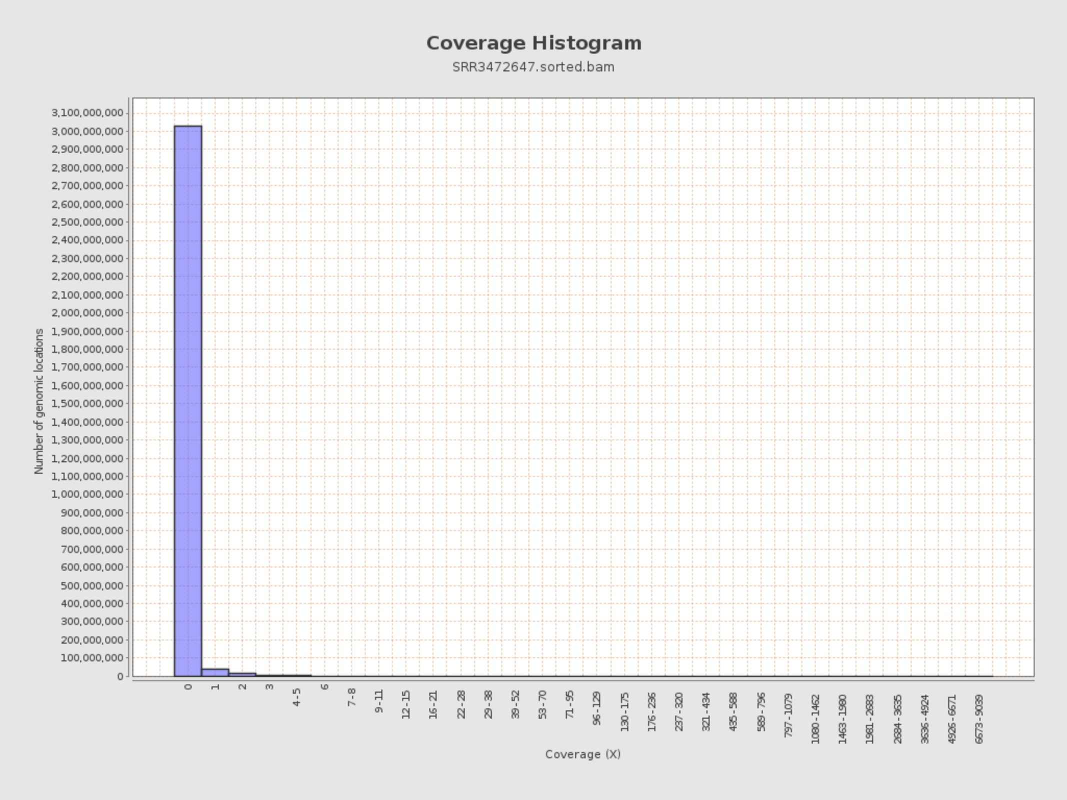
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 103763142 | 0.4163 | 14.0426 |
| chr2 | 243199373 | 60439248 | 0.2485 | 15.1087 |
| chr3 | 198022430 | 68422940 | 0.3455 | 13.6534 |
| chr4 | 191154276 | 26833465 | 0.1404 | 6.4451 |
| chr5 | 180915260 | 47067868 | 0.2602 | 21.518 |
| chr6 | 171115067 | 63479059 | 0.371 | 14.3891 |
| chr7 | 159138663 | 51754874 | 0.3252 | 15.8185 |
| chr8 | 146364022 | 49309969 | 0.3369 | 16.0462 |
| chr9 | 141213431 | 22088397 | 0.1564 | 4.9983 |
| chr10 | 135534747 | 28223811 | 0.2082 | 16.8871 |
| chr11 | 135006516 | 24409167 | 0.1808 | 14.1194 |
| chr12 | 133851895 | 33260882 | 0.2485 | 9.4896 |
| chr13 | 115169878 | 19963140 | 0.1733 | 8.2948 |
| chr14 | 107349540 | 29958450 | 0.2791 | 11.8773 |
| chr15 | 102531392 | 27260047 | 0.2659 | 17.3585 |
| chr16 | 90354753 | 42099412 | 0.4659 | 19.5701 |
| chr17 | 81195210 | 22702756 | 0.2796 | 18.4853 |
| chr18 | 78077248 | 5764935 | 0.0738 | 5.9776 |
| chr19 | 59128983 | 11030714 | 0.1866 | 7.67 |
| chr20 | 63025520 | 9075439 | 0.144 | 5.3489 |
| chr21 | 48129895 | 4875669 | 0.1013 | 6.266 |
| chr22 | 51304566 | 10372485 | 0.2022 | 8.6588 |
| chrMT | 16571 | 5295 | 0.3195 | 0.7662 |
| chrX | 155270560 | 49050927 | 0.3159 | 17.494 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 402899 | 0.0068 | 0.2515 |

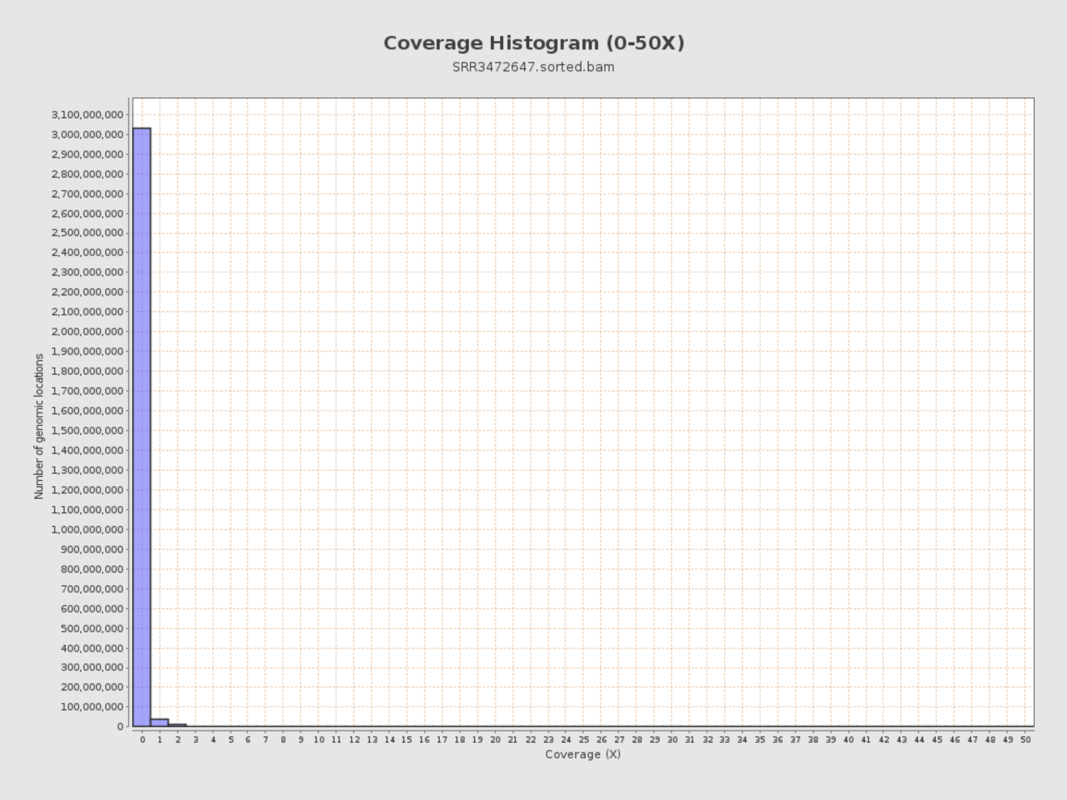
# 3. Results : Coverage across reference



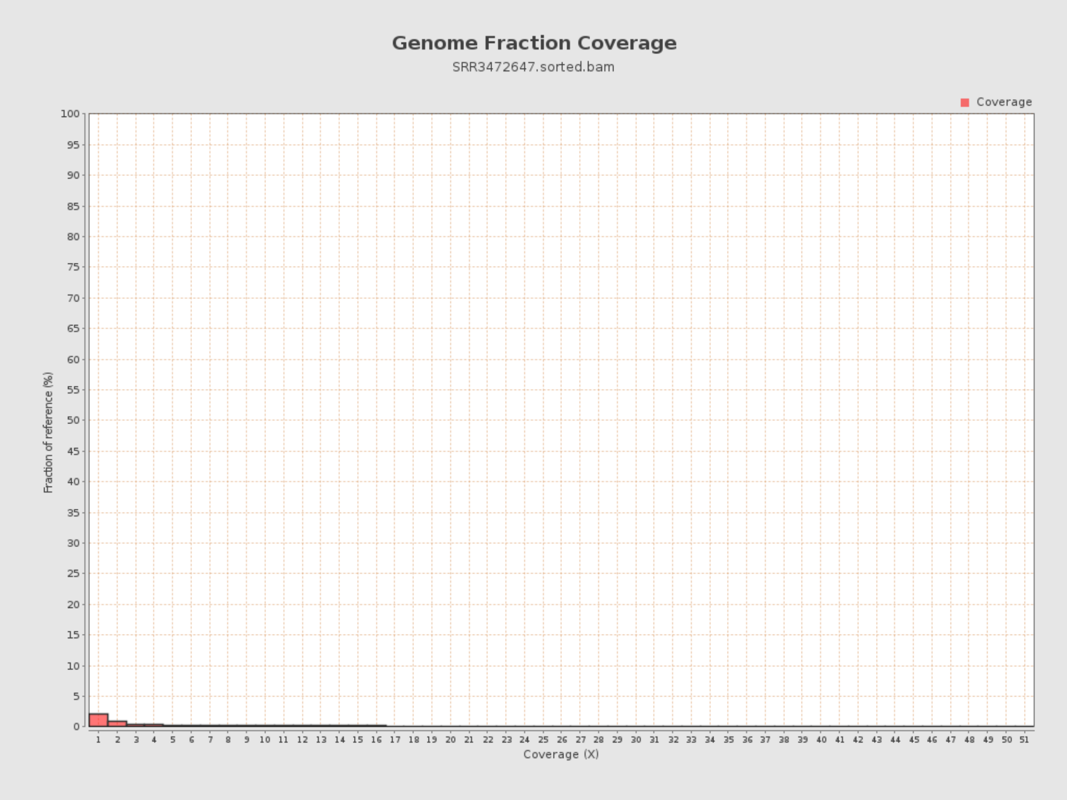
# 4. Results : Coverage Histogram



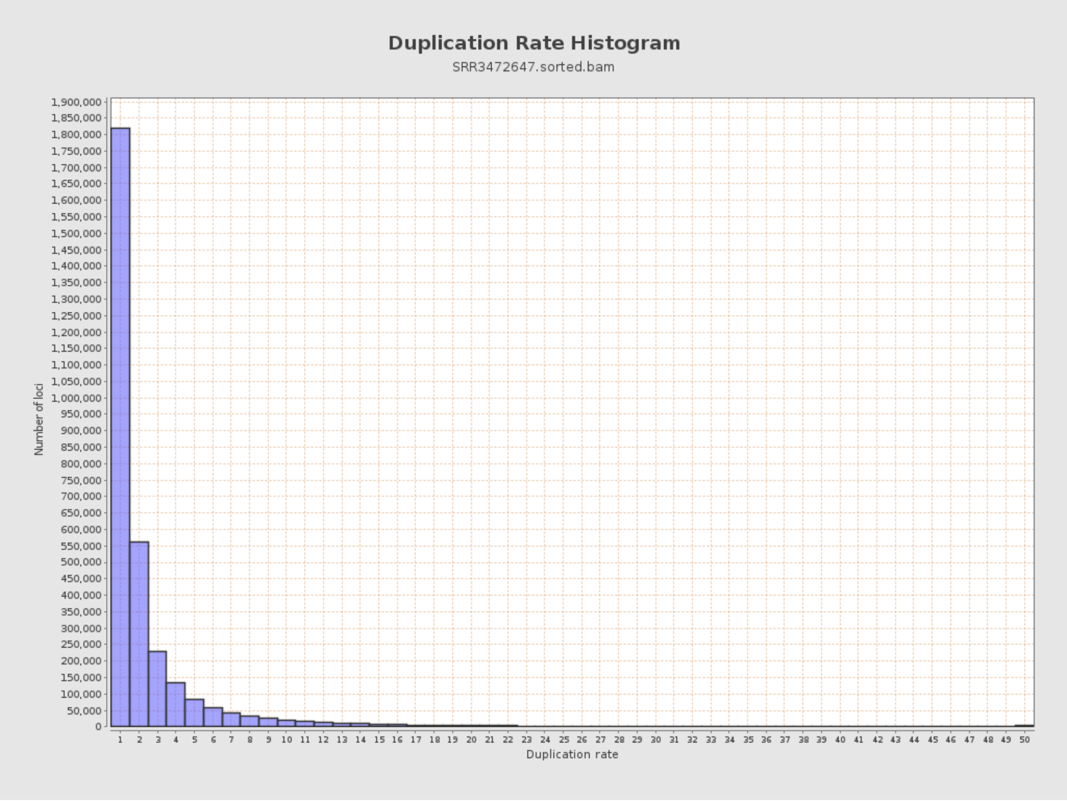
# 5. Results : Coverage Histogram (0-50X)



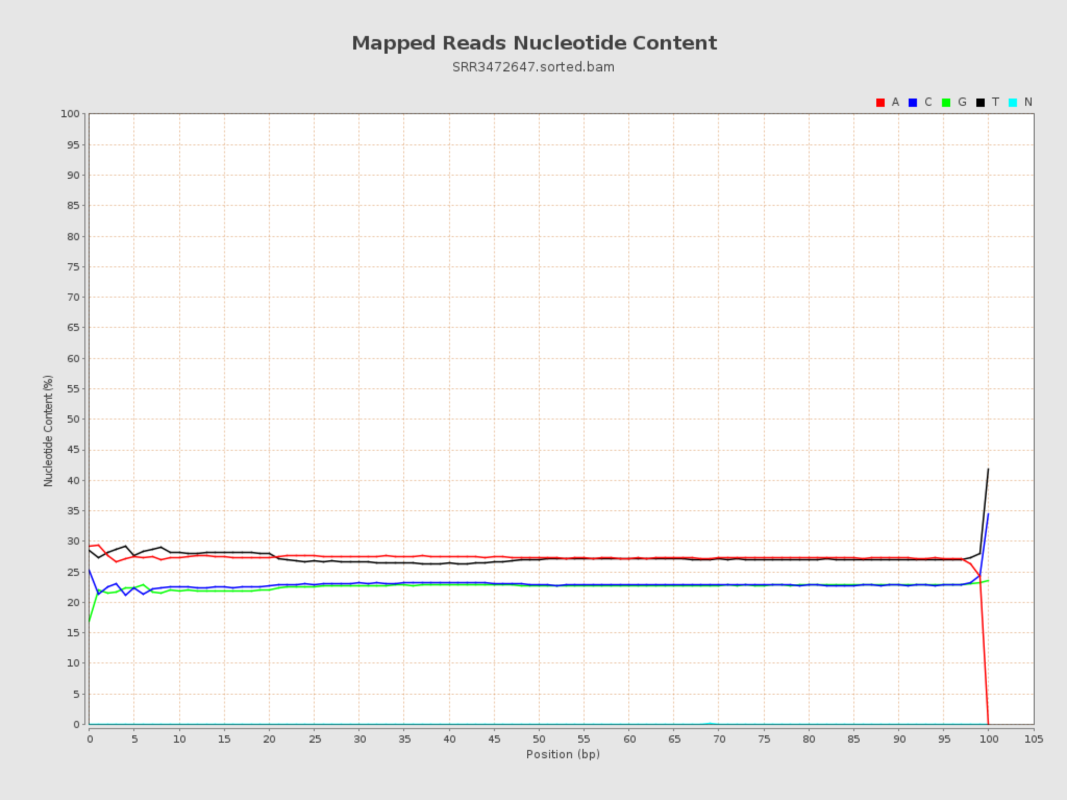
# 6. Results : Genome Fraction Coverage



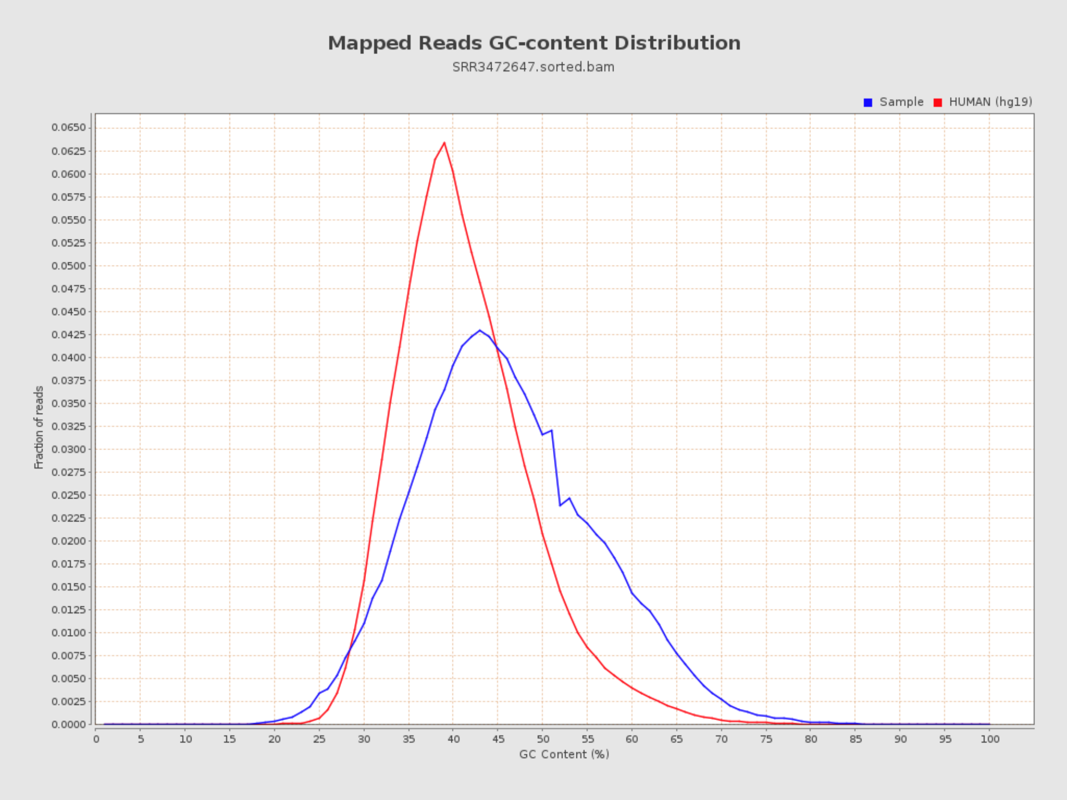
# 7. Results : Duplication Rate Histogram



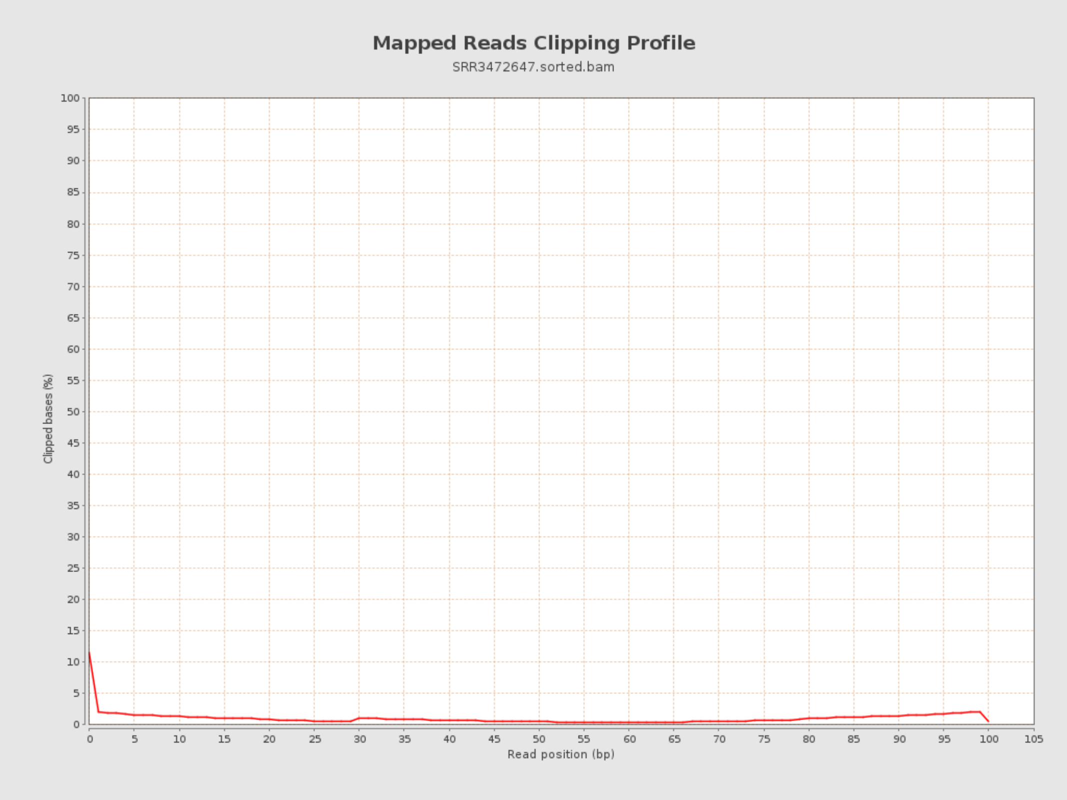
# 8. Results : Mapped Reads Nucleotide Content



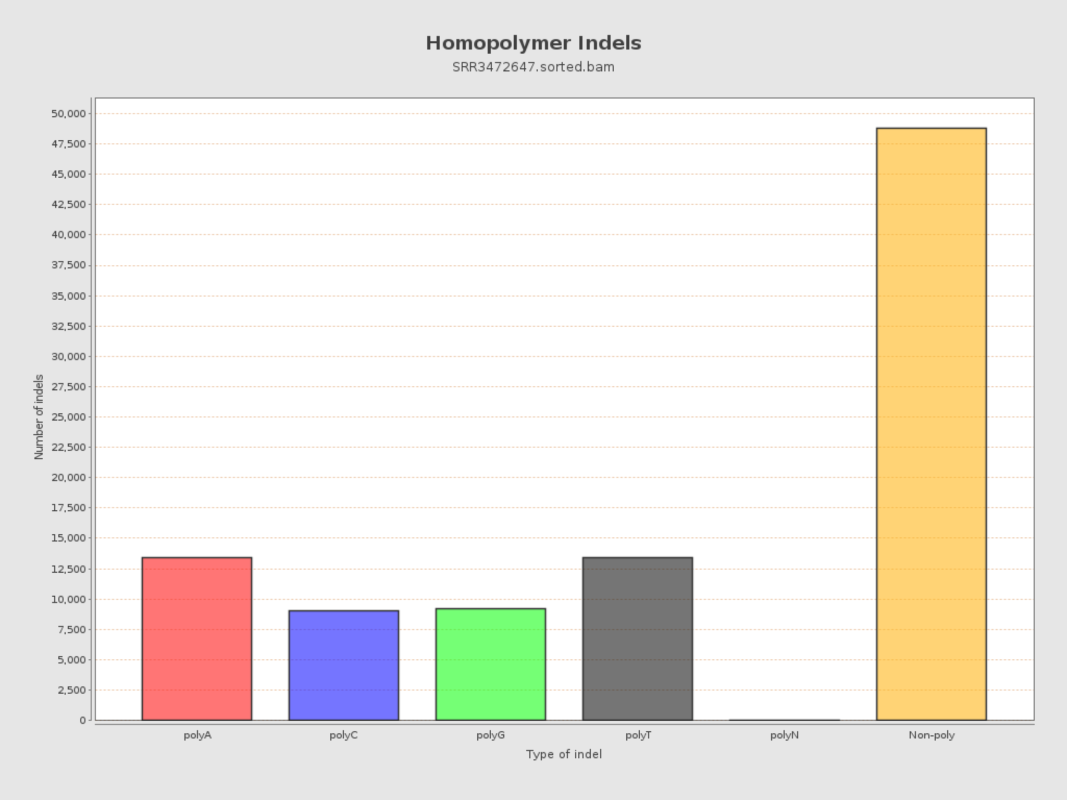
# 9. Results : Mapped Reads GC-content Distribution



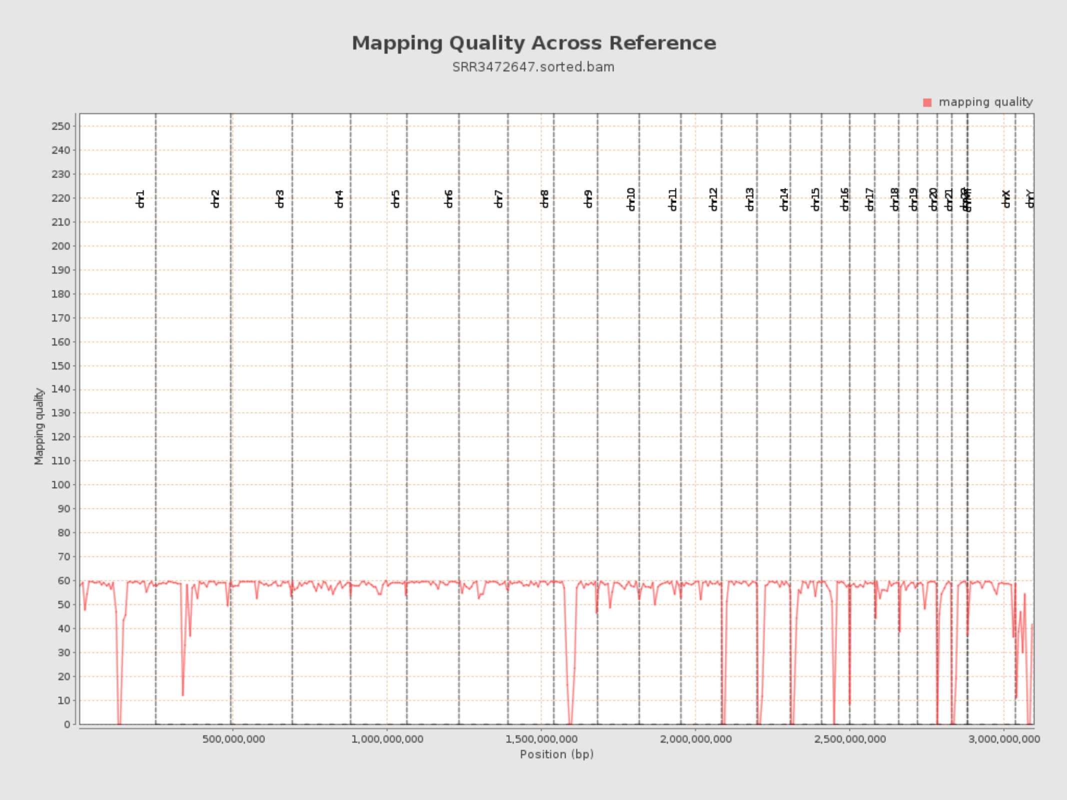
# 10. Results : Mapped Reads Clipping Profile



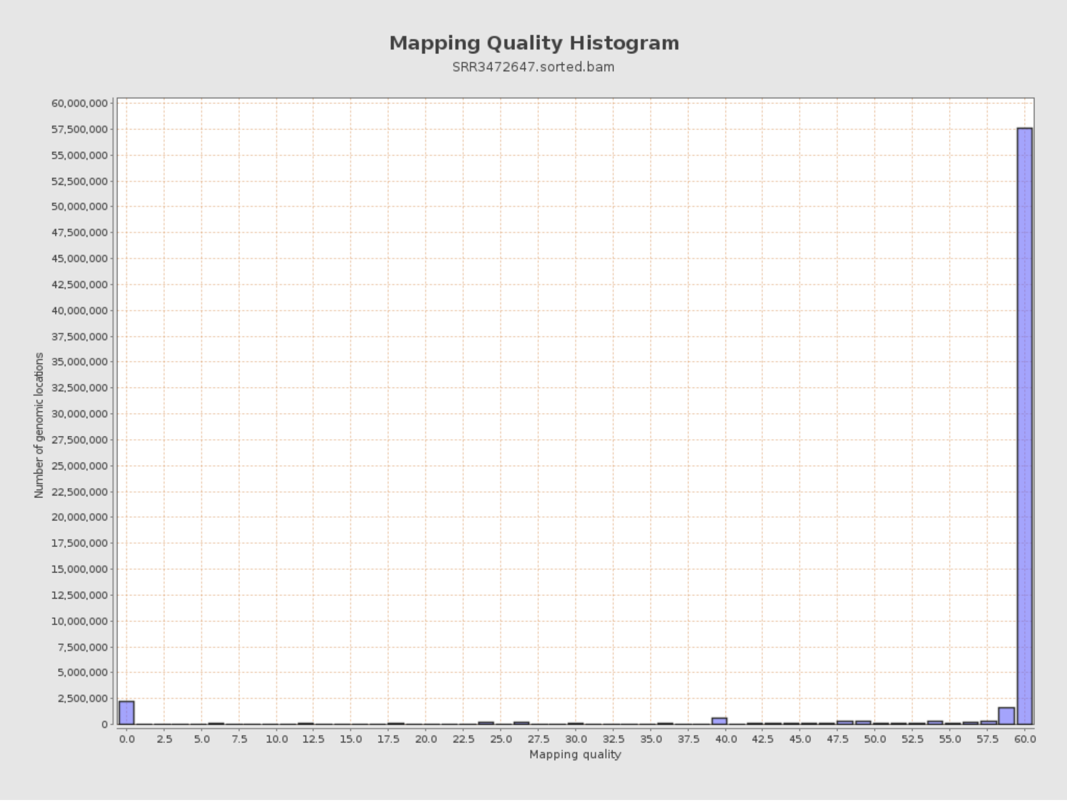
# 11. Results : Homopolymer Indels



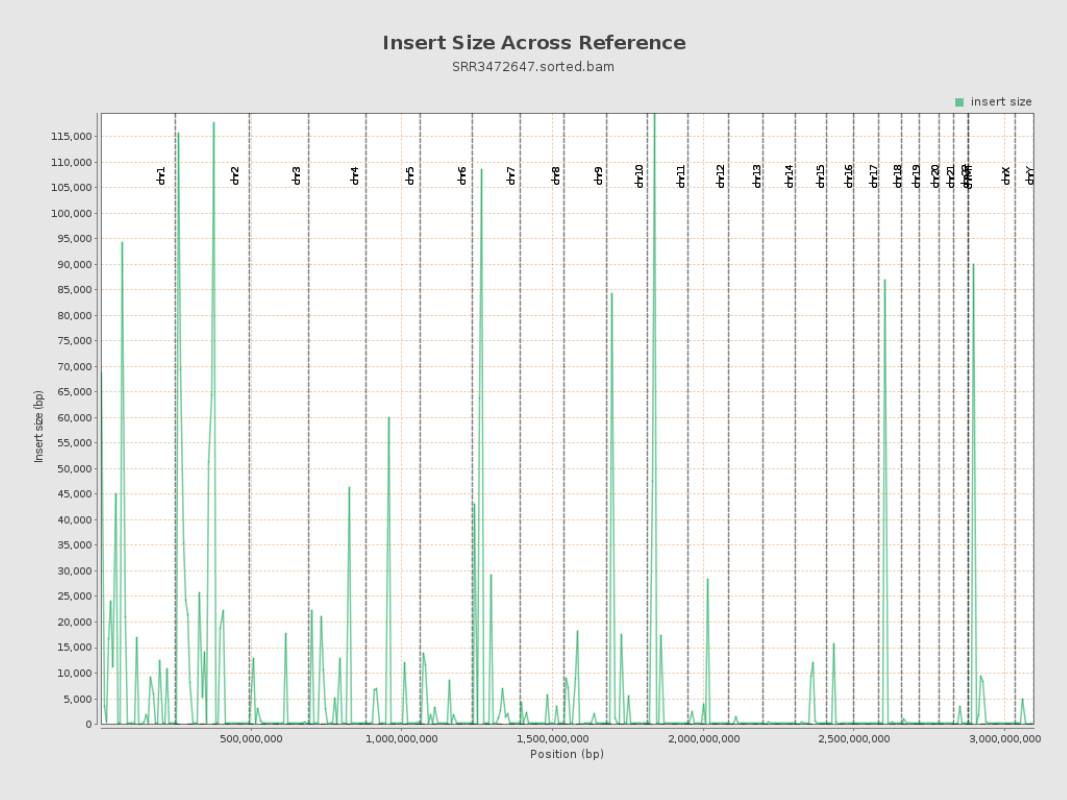
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram