# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/28 06:24:58*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472598.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_SRR3472598 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472598_1.fastq.gz SRR3472598_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 28 06:24:57 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3472598.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 8,254,052 |
| Mapped reads | 6,777,787 / 82.11% |
| Unmapped reads | 1,476,265 / 17.89% |
| Mapped paired reads | 6,777,787 / 82.11% |
| Mapped reads, first in pair | 3,431,350 / 41.57% |
| Mapped reads, second in pair | 3,346,437 / 40.54% |
| Mapped reads, both in pair | 6,598,148 / 79.94% |
| Mapped reads, singletons | 179,639 / 2.18% |
| Secondary alignments | 0 |
| Supplementary alignments | 124,548 / 1.51% |
| Read min/max/mean length | 30 / 100 / 100.57 |
| Duplicated reads (estimated) | 1,527,801 / 18.51% |
| Duplication rate | 17.92% |
| Clipped reads | 4,775,860 / 57.86% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 147,617,301 / 26.6% |
| Number/percentage of C's | 107,360,489 / 19.35% |
| Number/percentage of T's | 169,080,147 / 30.47% |
| Number/percentage of G's | 130,452,435 / 23.51% |
| Number/percentage of N's | 354,964 / 0.06% |
| | |

| | |
|---|---|
| GC Percentage | 42.86% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1793 |
| Standard Deviation | 3.6039 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 51.7 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 72,702.65 |
| Standard Deviation | 2,578,802.74 |
| P25/Median/P75 | 92 / 130 / 179 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 1.15% |
| Mismatches | 6,315,022 |
| Insertions | 45,122 |
| Mapped reads with at least one insertion | 0.66% |
| Deletions | 141,645 |
| Mapped reads with at least one deletion | 2.04% |
| Homopolymer indels | 43.3% |

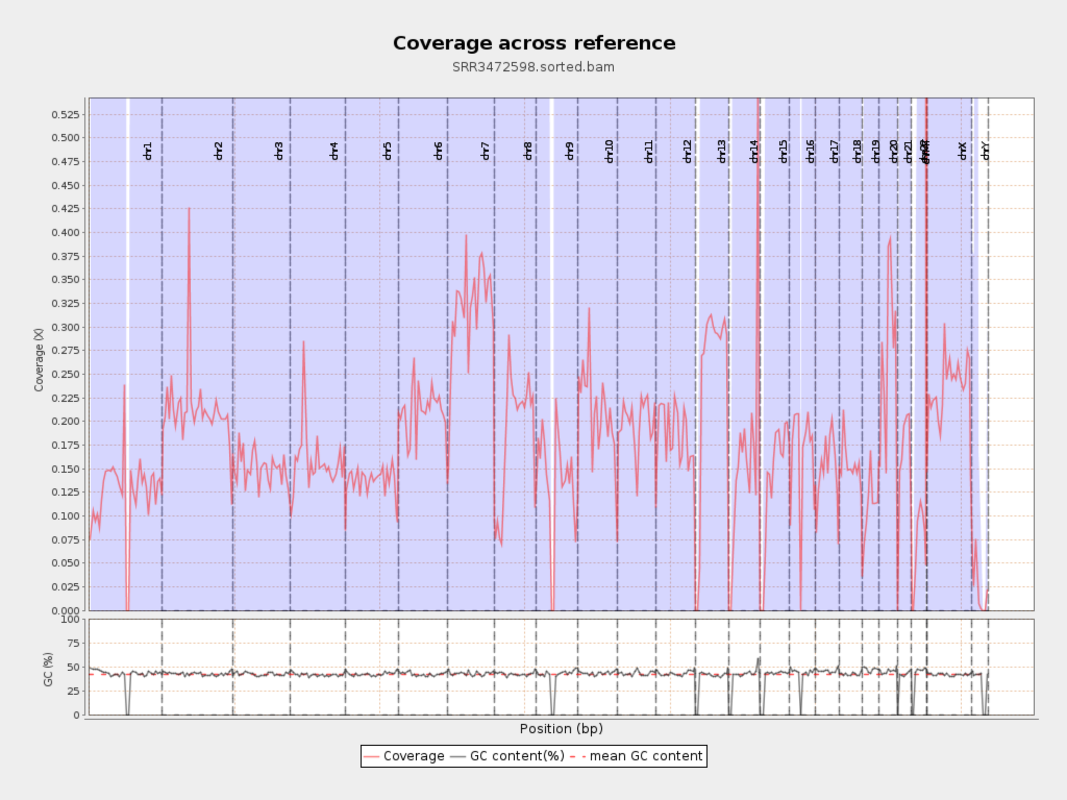
## 2.7. Chromosome stats

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

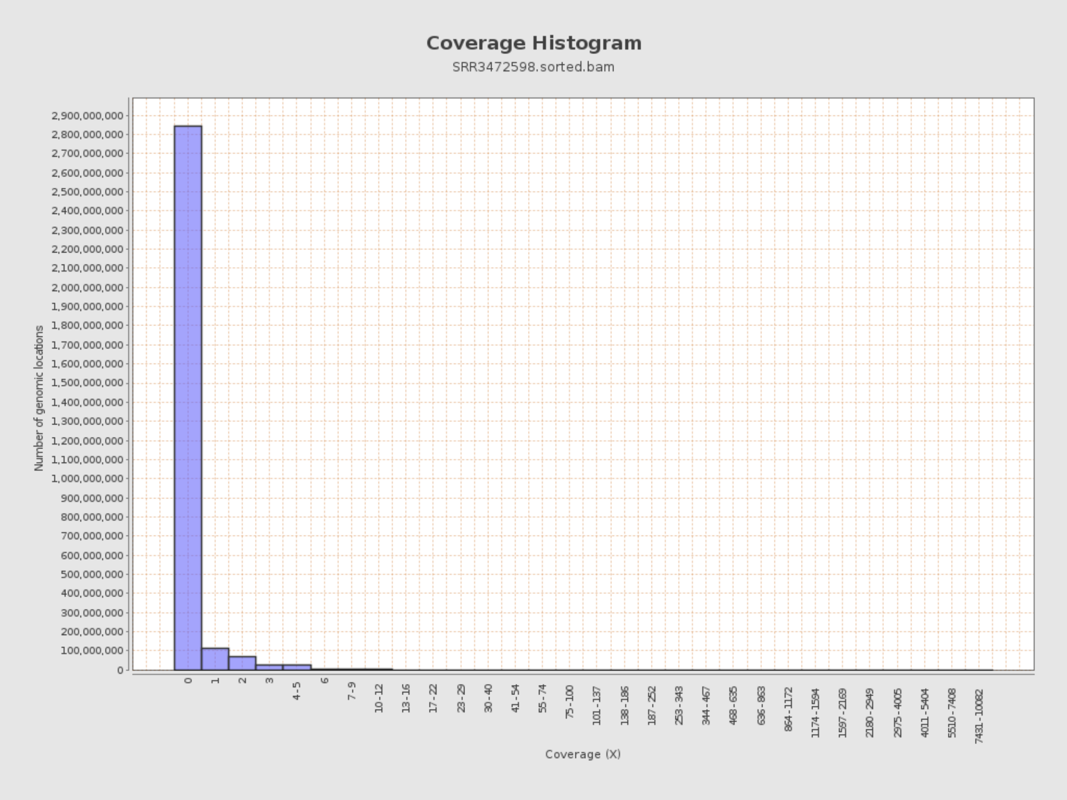
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 30937604 | 0.1241 | 2.0049 |
| chr2 | 243199373 | 52105171 | 0.2142 | 2.0472 |
| chr3 | 198022430 | 29887049 | 0.1509 | 0.7046 |
| chr4 | 191154276 | 30189164 | 0.1579 | 1.0041 |
| chr5 | 180915260 | 24888361 | 0.1376 | 0.6772 |
| chr6 | 171115067 | 36188118 | 0.2115 | 1.5528 |
| chr7 | 159138663 | 51322122 | 0.3225 | 3.0398 |
| chr8 | 146364022 | 27451656 | 0.1876 | 1.913 |
| chr9 | 141213431 | 19446152 | 0.1377 | 1.6101 |
| chr10 | 135534747 | 29039724 | 0.2143 | 1.6094 |
| chr11 | 135006516 | 26536990 | 0.1966 | 1.5643 |
| chr12 | 133851895 | 24796806 | 0.1853 | 0.8019 |
| chr13 | 115169878 | 28034020 | 0.2434 | 0.9144 |
| chr14 | 107349540 | 17681652 | 0.1647 | 17.2901 |
| chr15 | 102531392 | 13957749 | 0.1361 | 0.6753 |
| chr16 | 90354753 | 14792861 | 0.1637 | 0.8863 |
| chr17 | 81195210 | 12042512 | 0.1483 | 1.1341 |
| chr18 | 78077248 | 12197190 | 0.1562 | 2.3508 |
| chr19 | 59128983 | 6604153 | 0.1117 | 1.3951 |
| chr20 | 63025520 | 17103986 | 0.2714 | 3.9201 |
| chr21 | 48129895 | 7592528 | 0.1578 | 0.8023 |
| chr22 | 51304566 | 3494762 | 0.0681 | 0.476 |
| chrMT | 16571 | 949839 | 57.3194 | 25.0434 |
| chrX | 155270560 | 36607403 | 0.2358 | 1.0837 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1279288 | 0.0215 | 0.7582 |

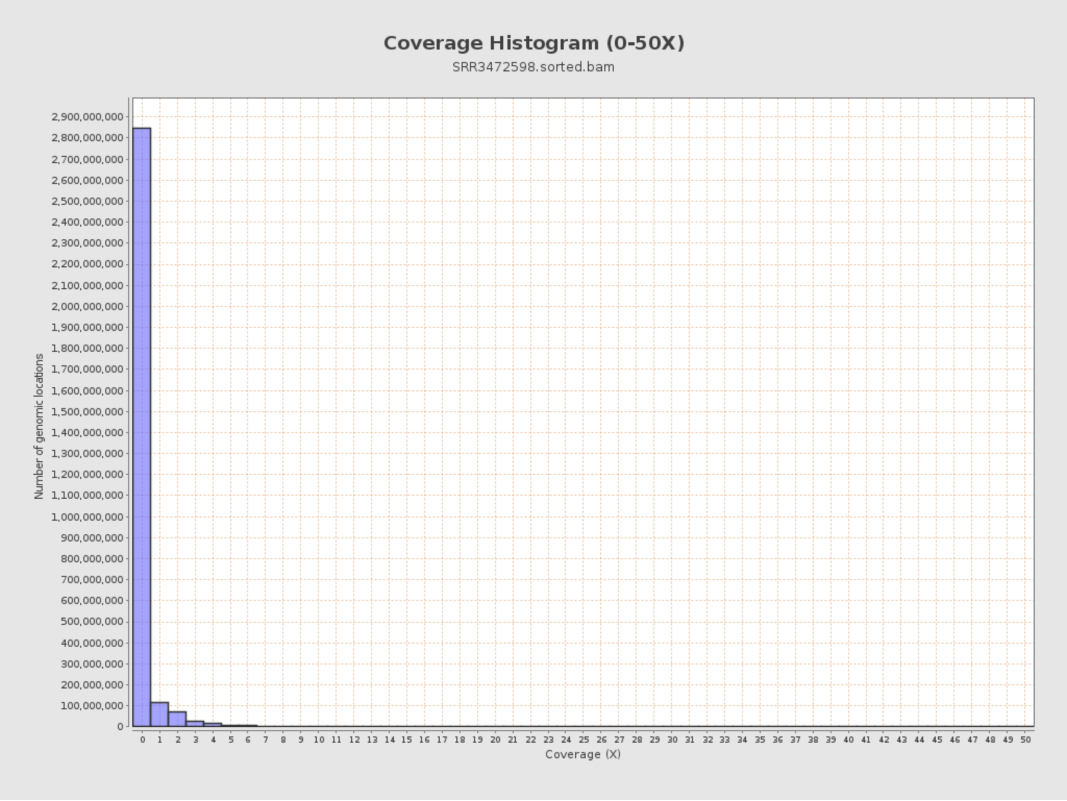
# 3. Results : Coverage across reference



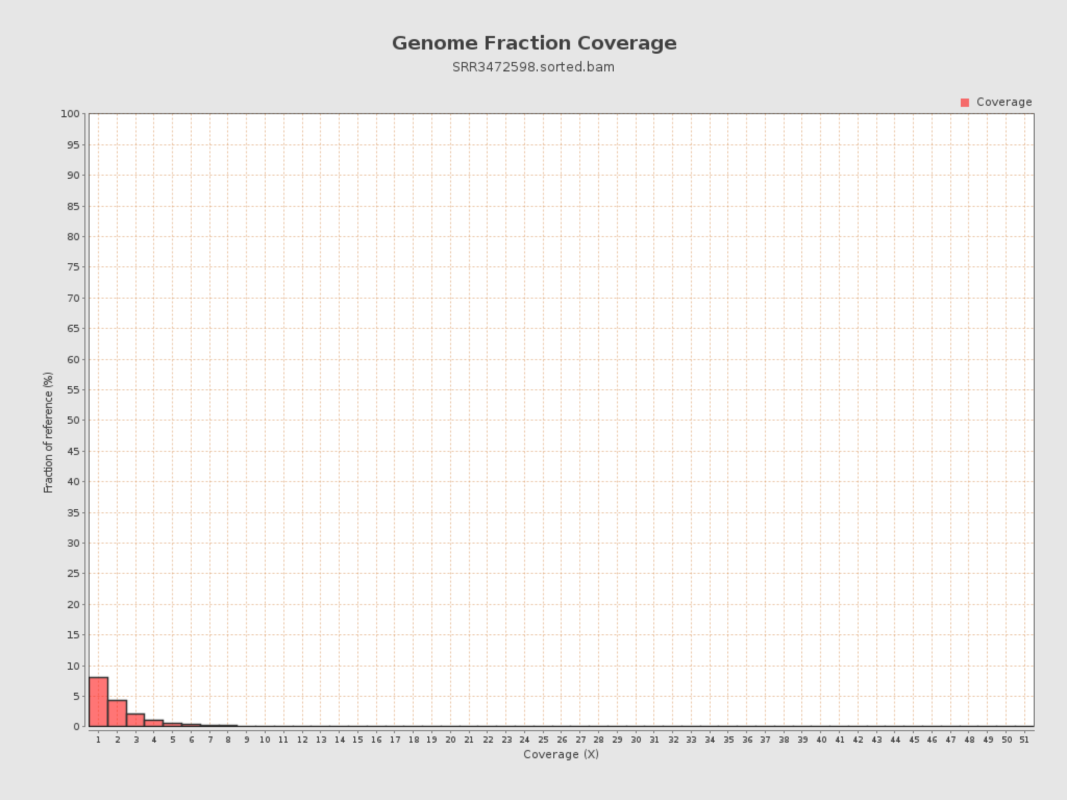
# 4. Results : Coverage Histogram



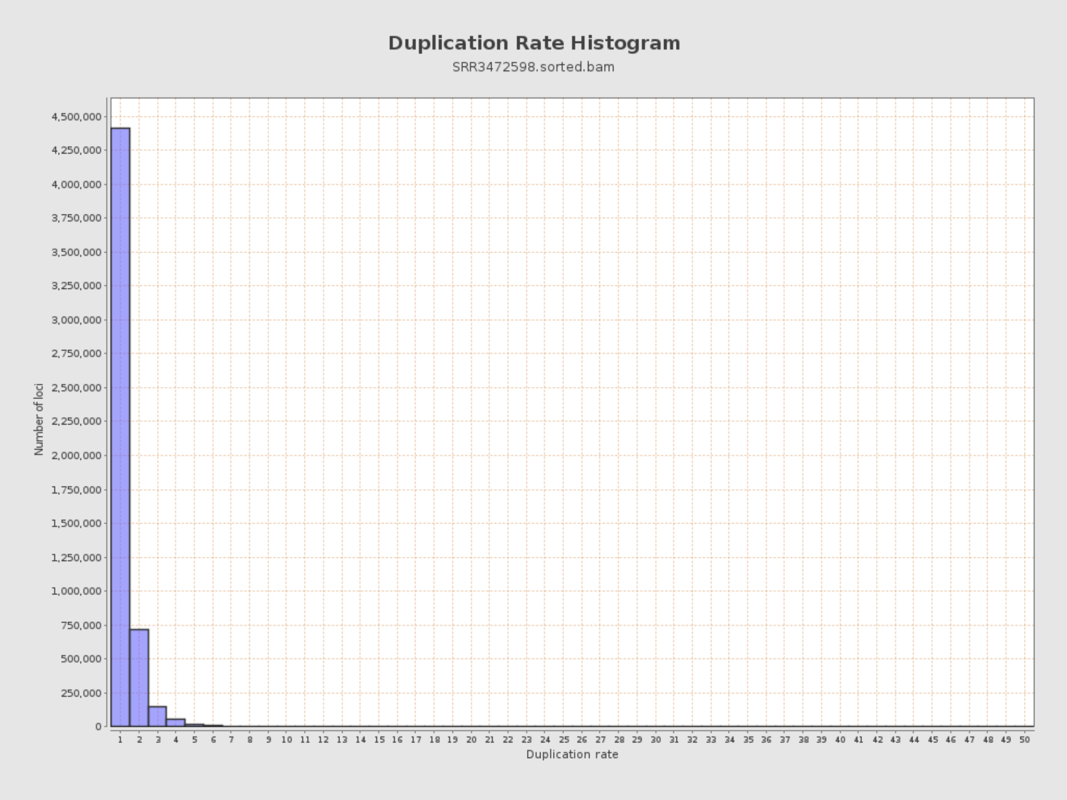
# 5. Results : Coverage Histogram (0-50X)



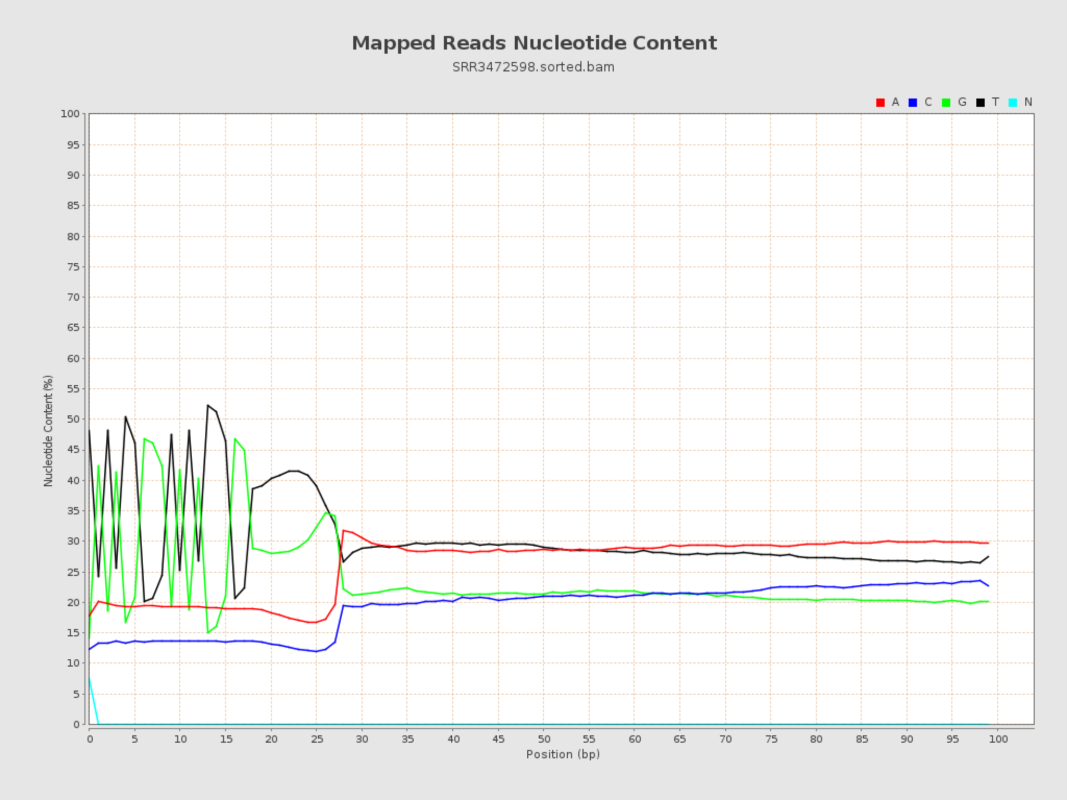
# 6. Results : Genome Fraction Coverage



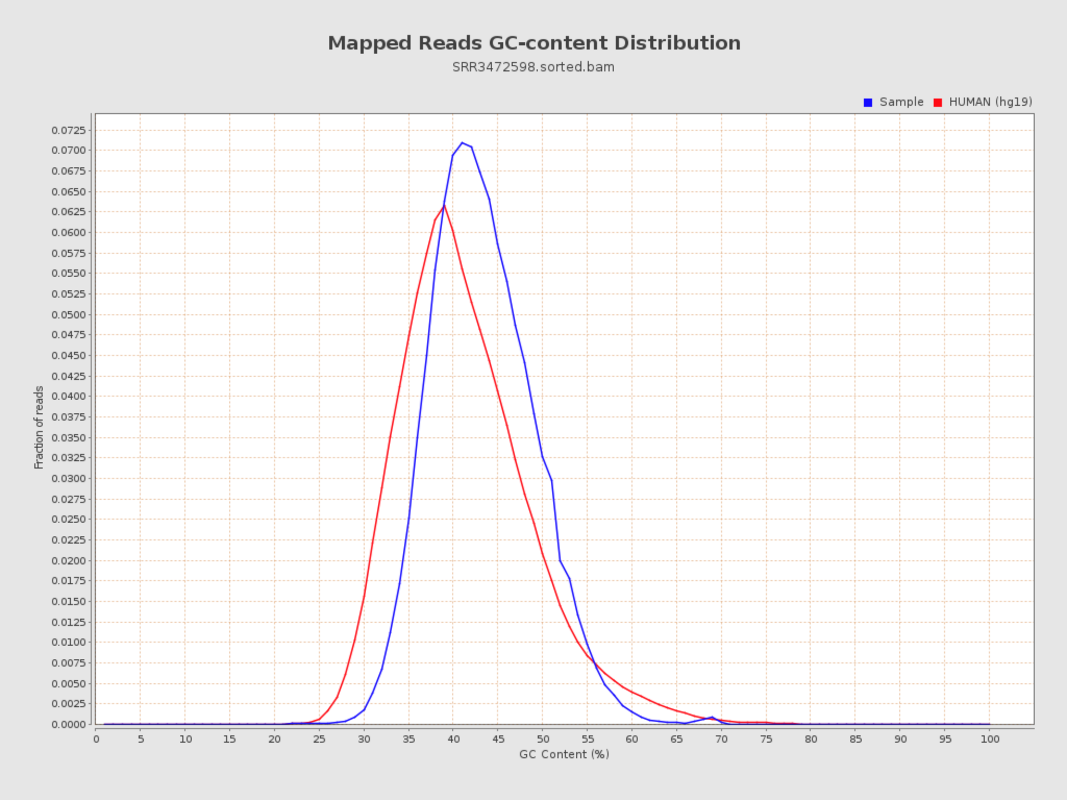
# 7. Results : Duplication Rate Histogram



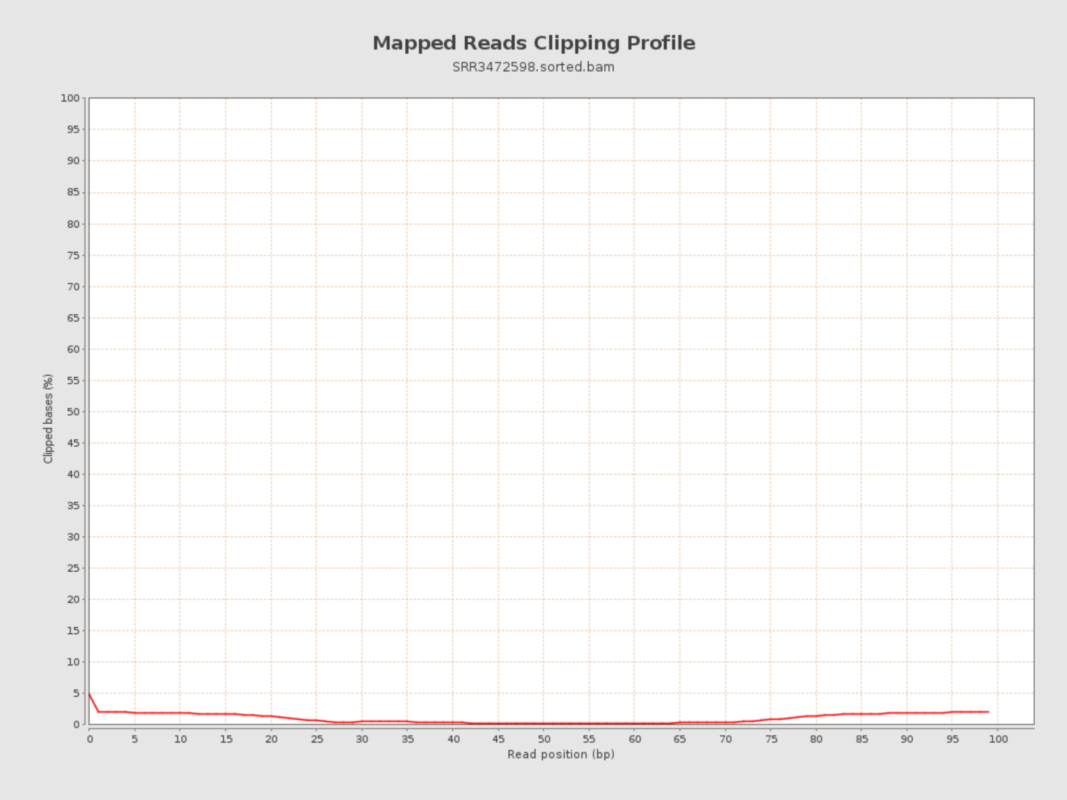
# 8. Results : Mapped Reads Nucleotide Content



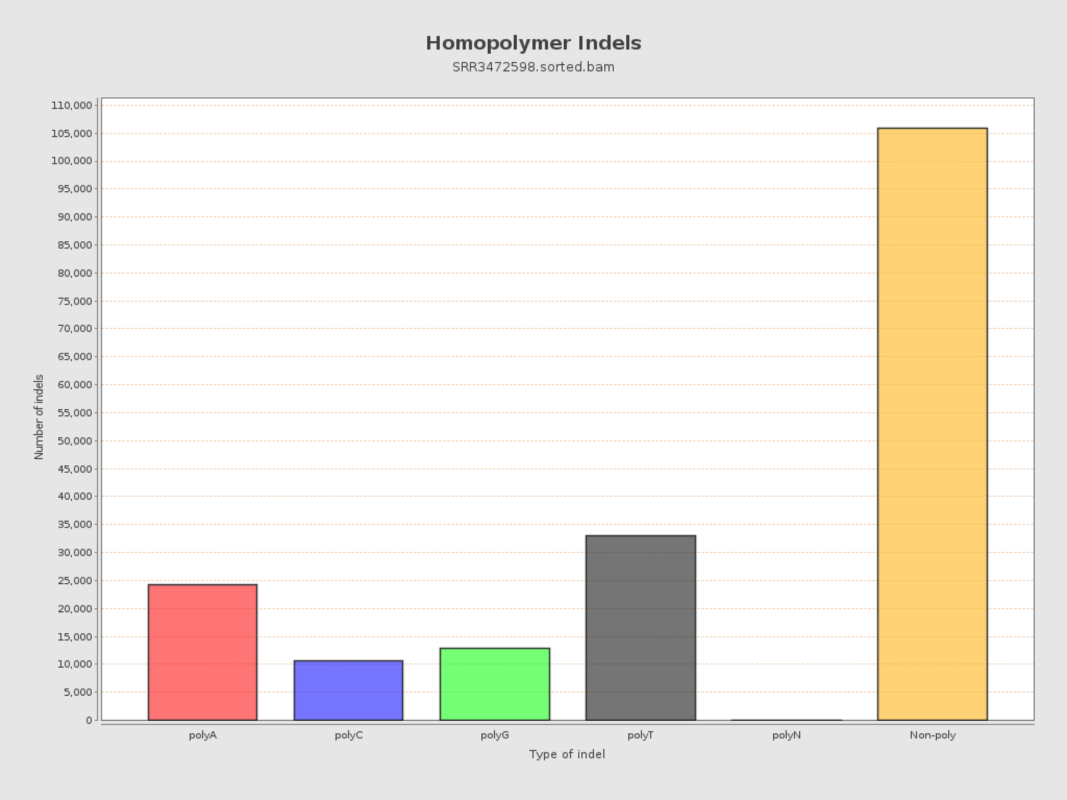
# 9. Results : Mapped Reads GC-content Distribution



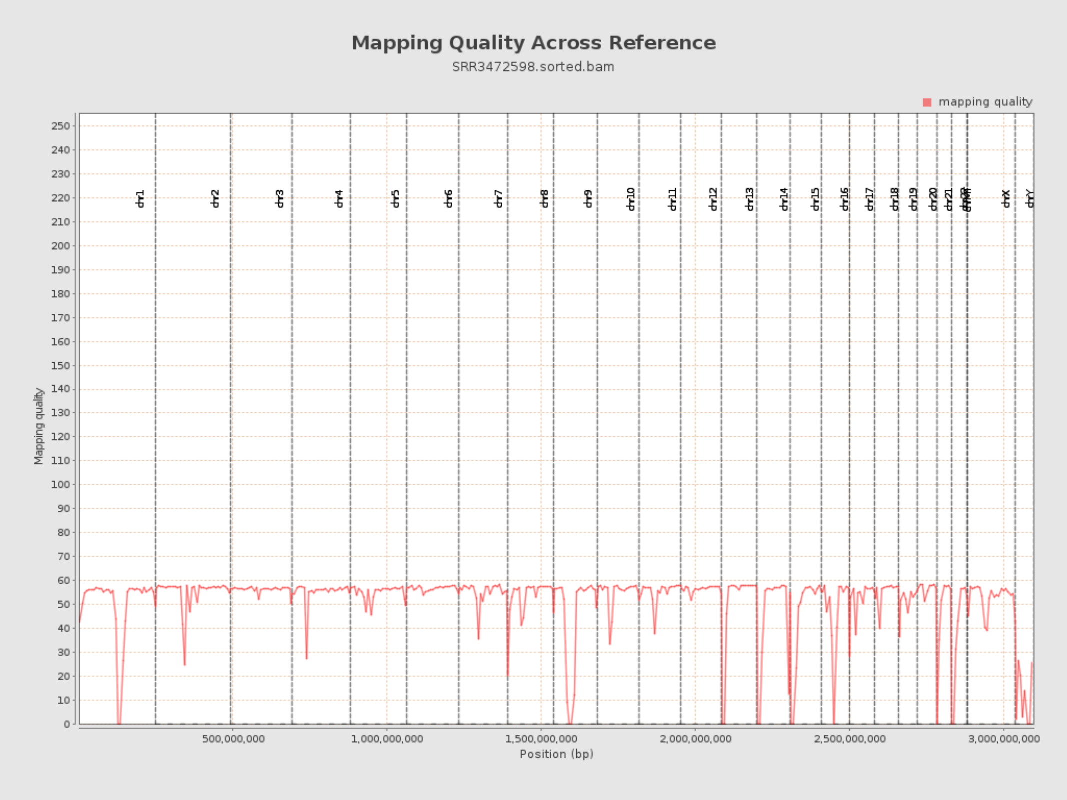
# 10. Results : Mapped Reads Clipping Profile



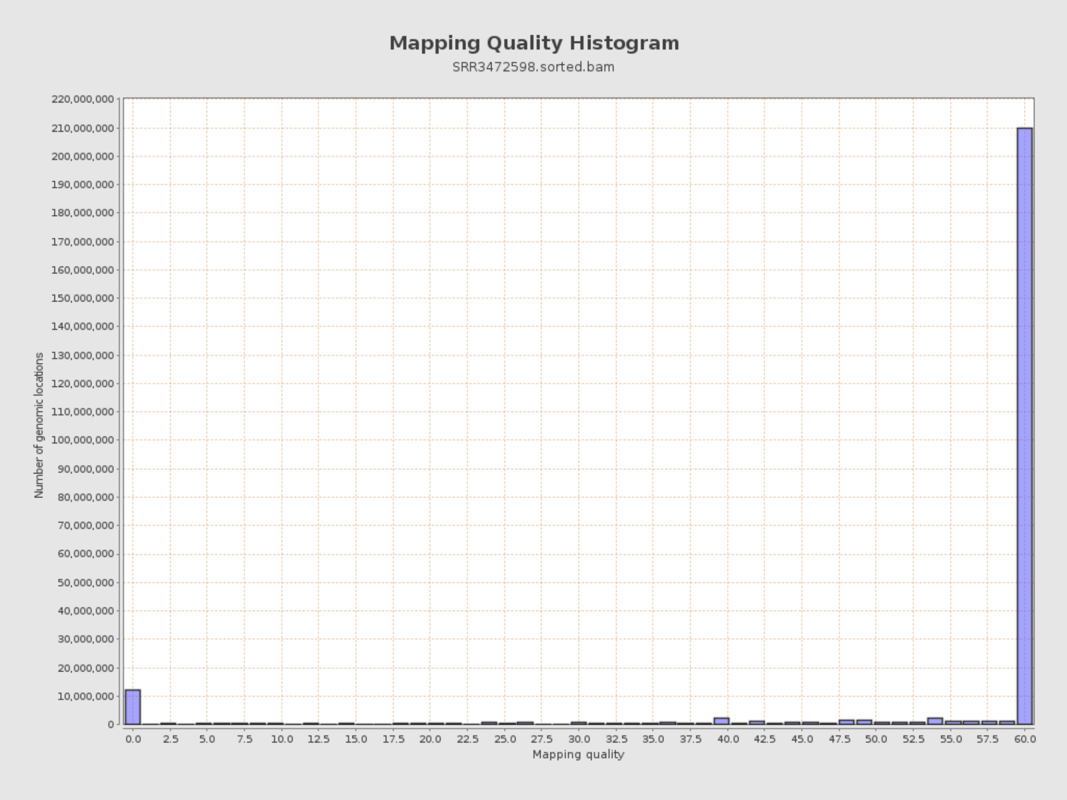
# 11. Results : Homopolymer Indels



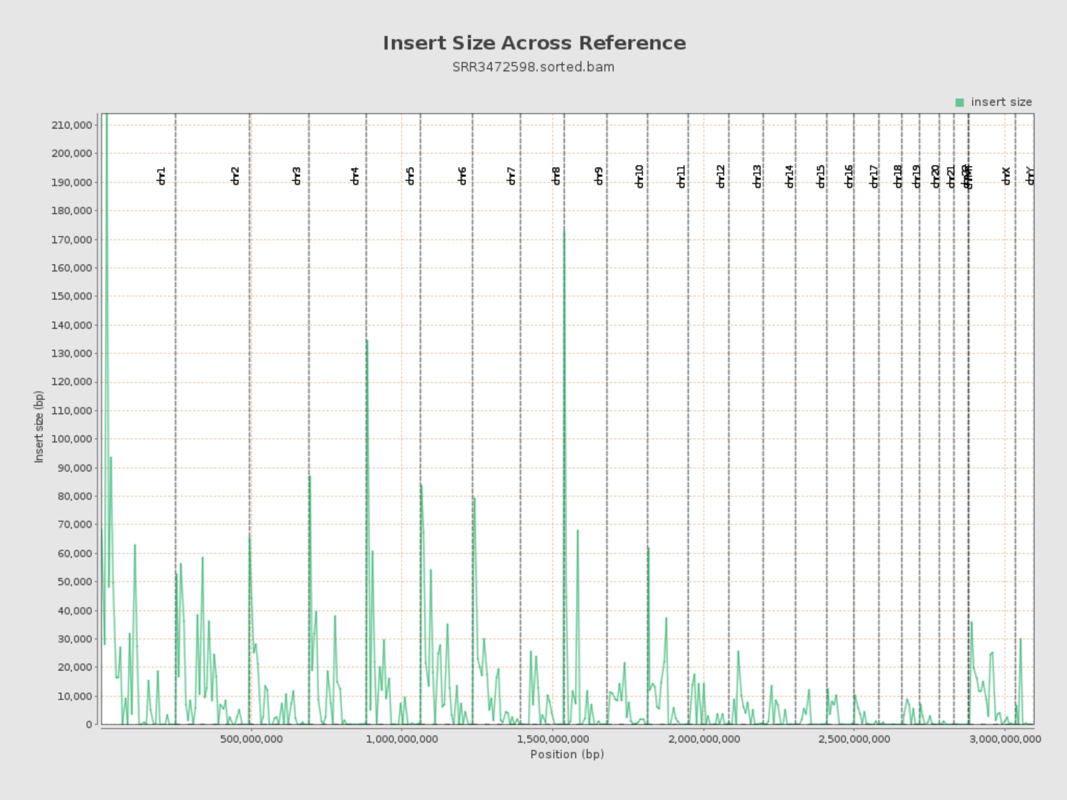
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram