# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/29 04:55:35*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472675.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_SRR3472675 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472675_1.fastq.gz SRR3472675_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 29 04:55:34 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3472675.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 17,029,742 |
| Mapped reads | 16,888,744 / 99.17% |
| Unmapped reads | 140,998 / 0.83% |
| Mapped paired reads | 16,888,744 / 99.17% |
| Mapped reads, first in pair | 8,468,040 / 49.73% |
| Mapped reads, second in pair | 8,420,704 / 49.45% |
| Mapped reads, both in pair | 16,800,696 / 98.66% |
| Mapped reads, singletons | 88,048 / 0.52% |
| Secondary alignments | 0 |
| Supplementary alignments | 99,753 / 0.59% |
| Read min/max/mean length | 30 / 101 / 99.73 |
| Duplicated reads (estimated) | 11,736,916 / 68.92% |
| Duplication rate | 49.15% |
| Clipped reads | 1,262,287 / 7.41% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 439,555,600 / 26.48% |
| Number/percentage of C's | 392,251,478 / 23.63% |
| Number/percentage of T's | 439,896,219 / 26.5% |
| Number/percentage of G's | 388,018,026 / 23.37% |
| Number/percentage of N's | 312,607 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 47% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.5363 |
| Standard Deviation | 24.6795 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 54.84 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 24,875.96 |
| Standard Deviation | 1,611,554 |
| P25/Median/P75 | 155 / 211 / 279 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.61% |
| Mismatches | 9,969,484 |
| Insertions | 99,951 |
| Mapped reads with at least one insertion | 0.58% |
| Deletions | 86,569 |
| Mapped reads with at least one deletion | 0.5% |
| Homopolymer indels | 45.93% |

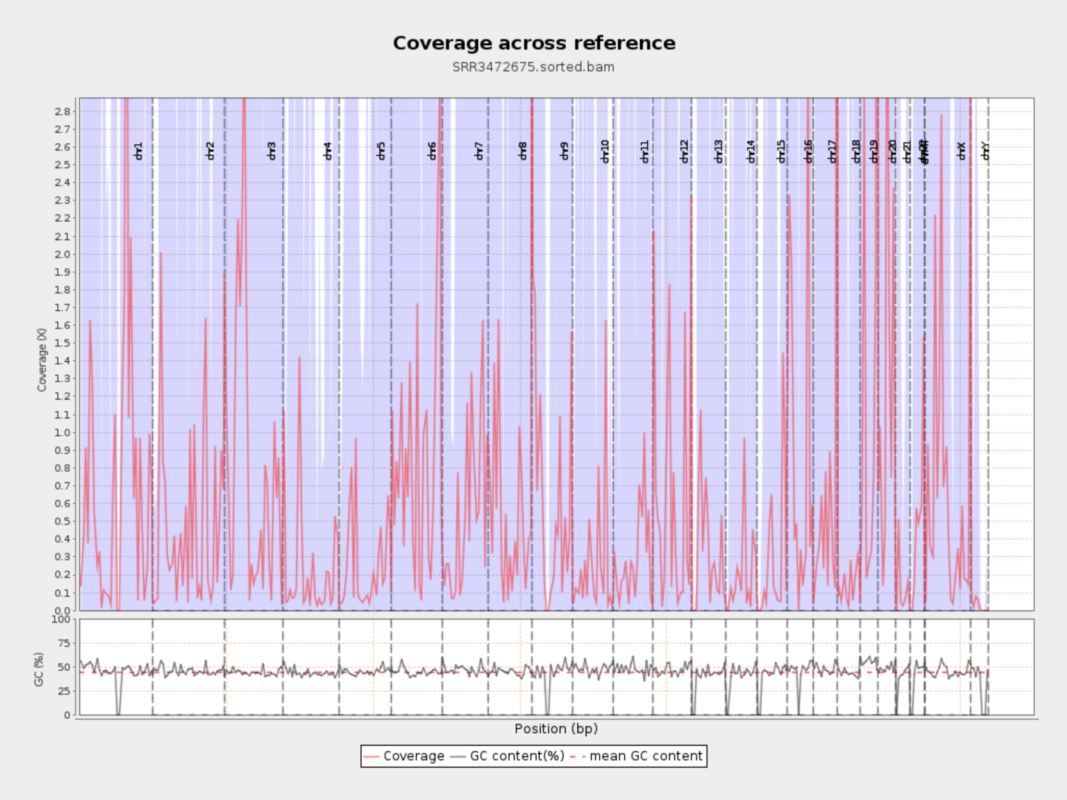
## 2.7. Chromosome stats

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

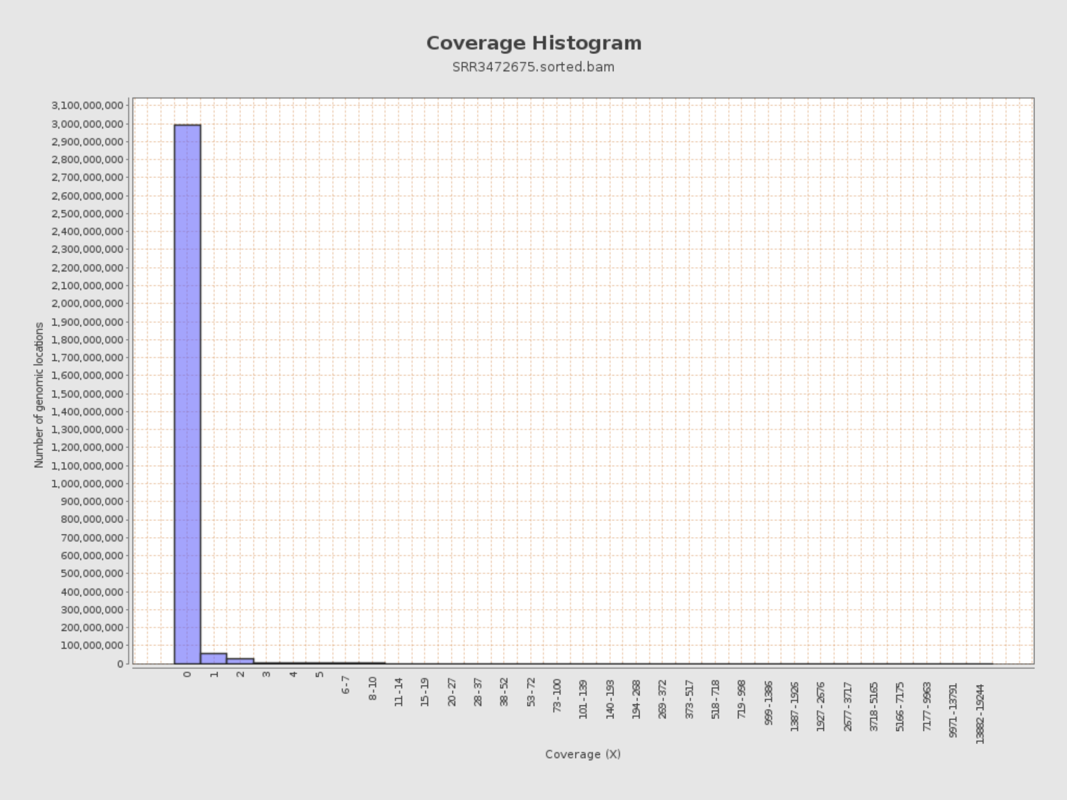
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 188075397 | 0.7546 | 30.0742 |
| chr2 | 243199373 | 116138945 | 0.4775 | 24.2001 |
| chr3 | 198022430 | 168407229 | 0.8504 | 28.8262 |
| chr4 | 191154276 | 43758140 | 0.2289 | 12.8648 |
| chr5 | 180915260 | 45649081 | 0.2523 | 10.3256 |
| chr6 | 171115067 | 152609740 | 0.8919 | 41.831 |
| chr7 | 159138663 | 89281592 | 0.561 | 20.2241 |
| chr8 | 146364022 | 74517524 | 0.5091 | 19.1162 |
| chr9 | 141213431 | 92943210 | 0.6582 | 18.2038 |
| chr10 | 135534747 | 36281025 | 0.2677 | 22.7944 |
| chr11 | 135006516 | 40312117 | 0.2986 | 14.9605 |
| chr12 | 133851895 | 86953772 | 0.6496 | 27.3786 |
| chr13 | 115169878 | 37430532 | 0.325 | 12.3192 |
| chr14 | 107349540 | 21234289 | 0.1978 | 8.2852 |
| chr15 | 102531392 | 31304417 | 0.3053 | 24.4013 |
| chr16 | 90354753 | 84619288 | 0.9365 | 30.9449 |
| chr17 | 81195210 | 51094997 | 0.6293 | 23.0154 |
| chr18 | 78077248 | 11643205 | 0.1491 | 7.1449 |
| chr19 | 59128983 | 67449620 | 1.1407 | 42.0363 |
| chr20 | 63025520 | 83770654 | 1.3292 | 50.0744 |
| chr21 | 48129895 | 6546033 | 0.136 | 9.9811 |
| chr22 | 51304566 | 25913779 | 0.5051 | 20.485 |
| chrMT | 16571 | 8655 | 0.5223 | 0.8886 |
| chrX | 155270560 | 102592880 | 0.6607 | 28.6822 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1706173 | 0.0287 | 1.7558 |

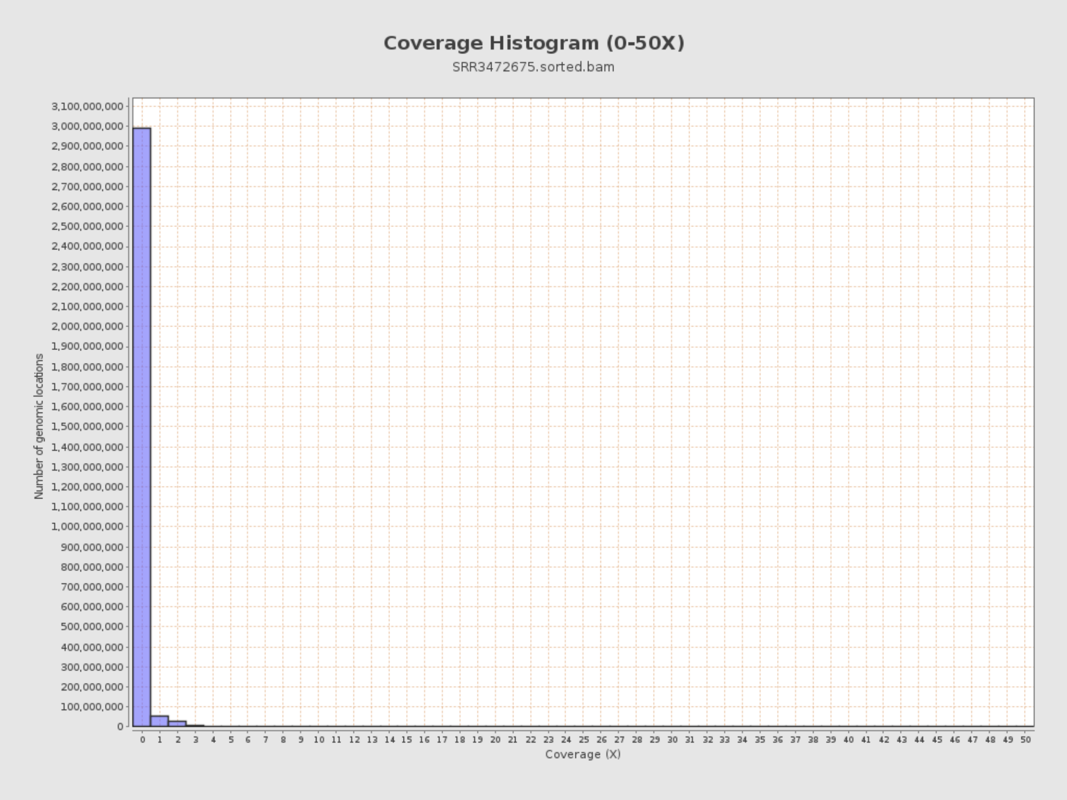
# 3. Results : Coverage across reference



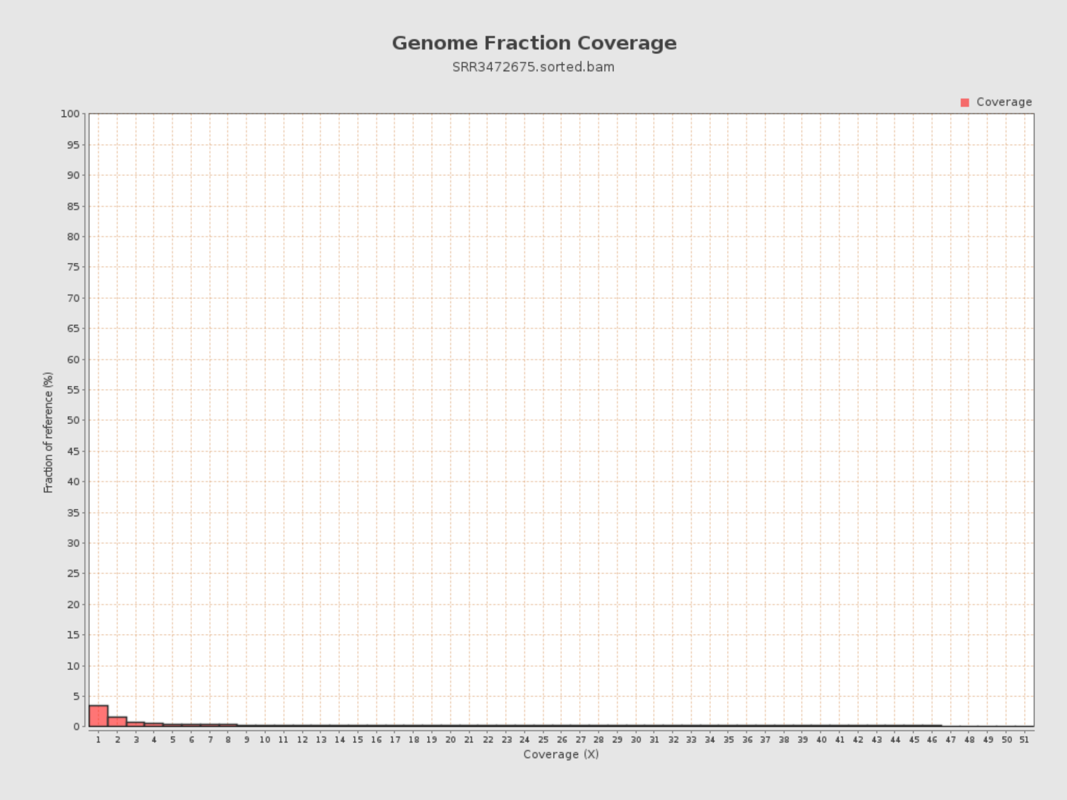
# 4. Results : Coverage Histogram



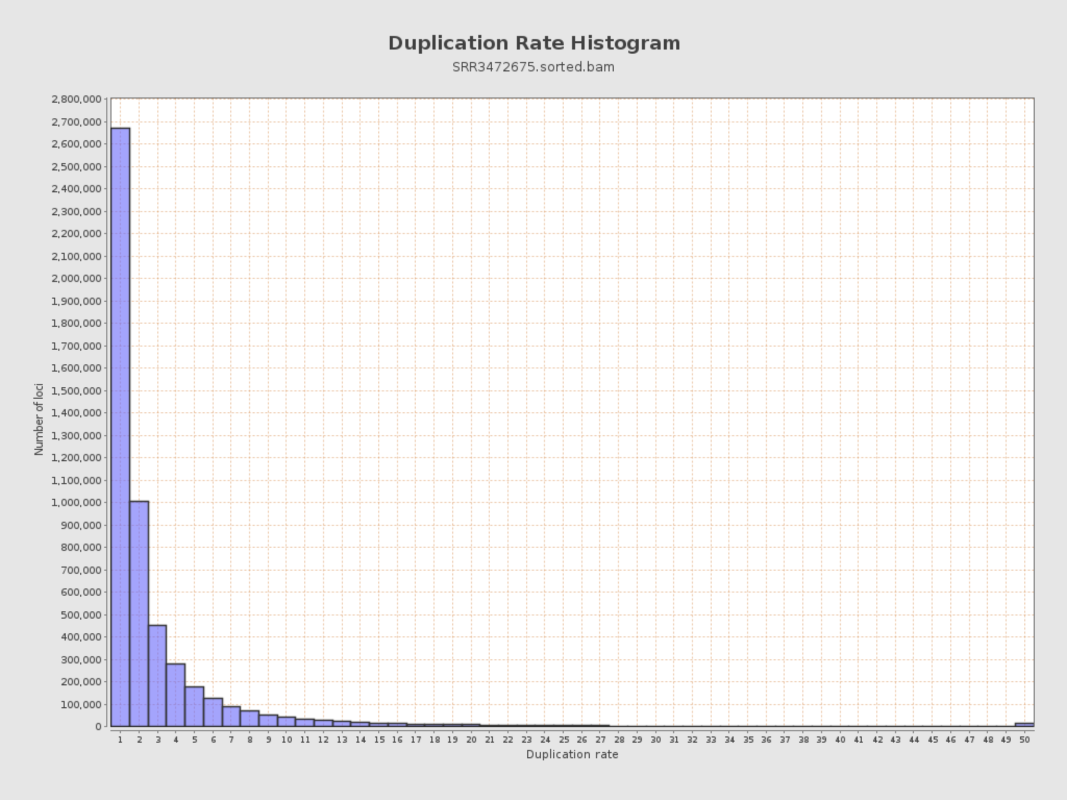
# 5. Results : Coverage Histogram (0-50X)



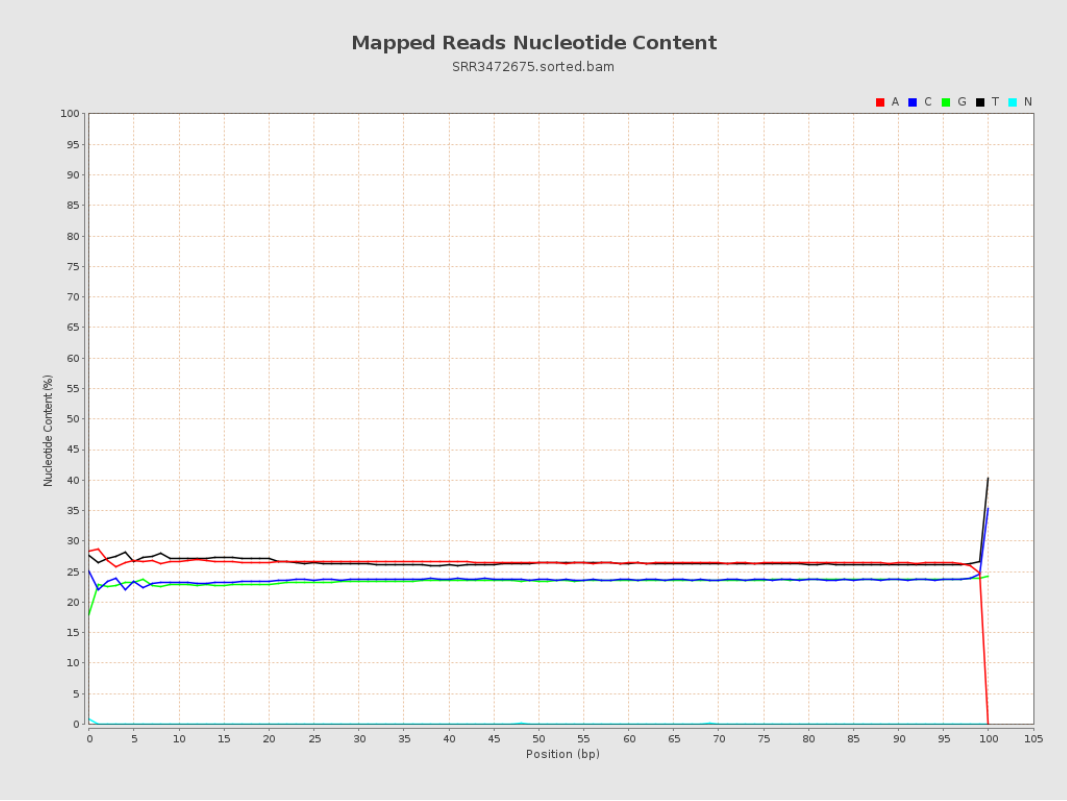
# 6. Results : Genome Fraction Coverage



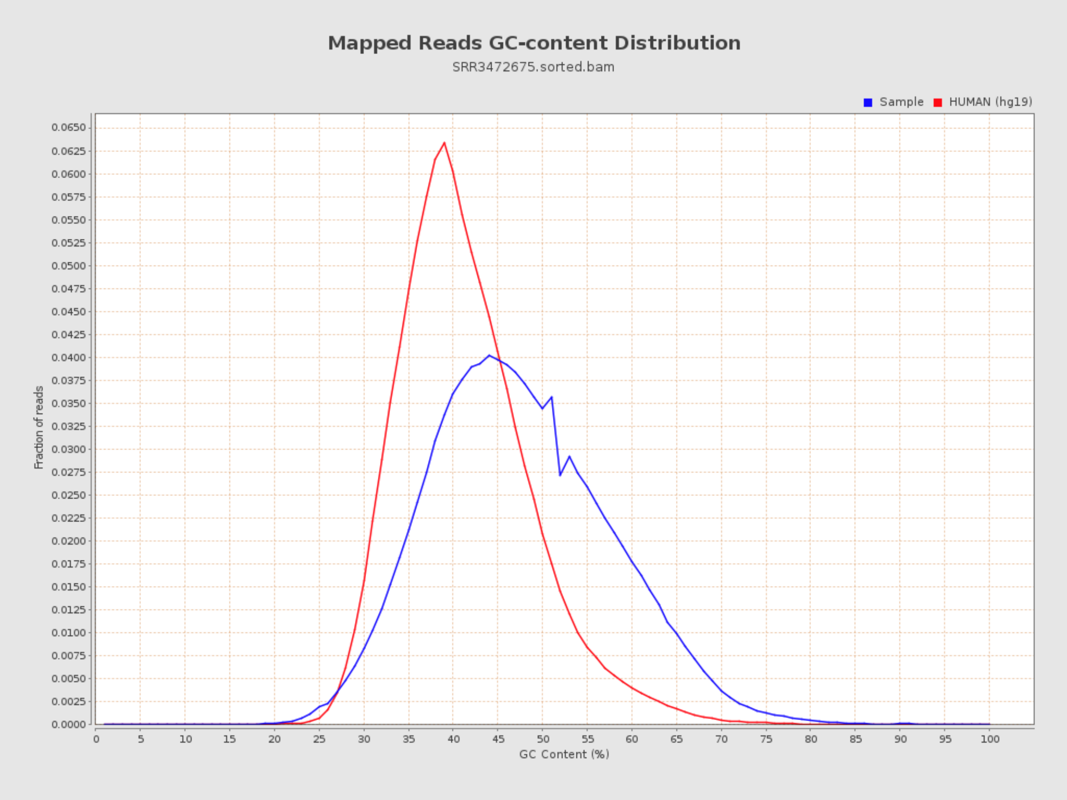
# 7. Results : Duplication Rate Histogram



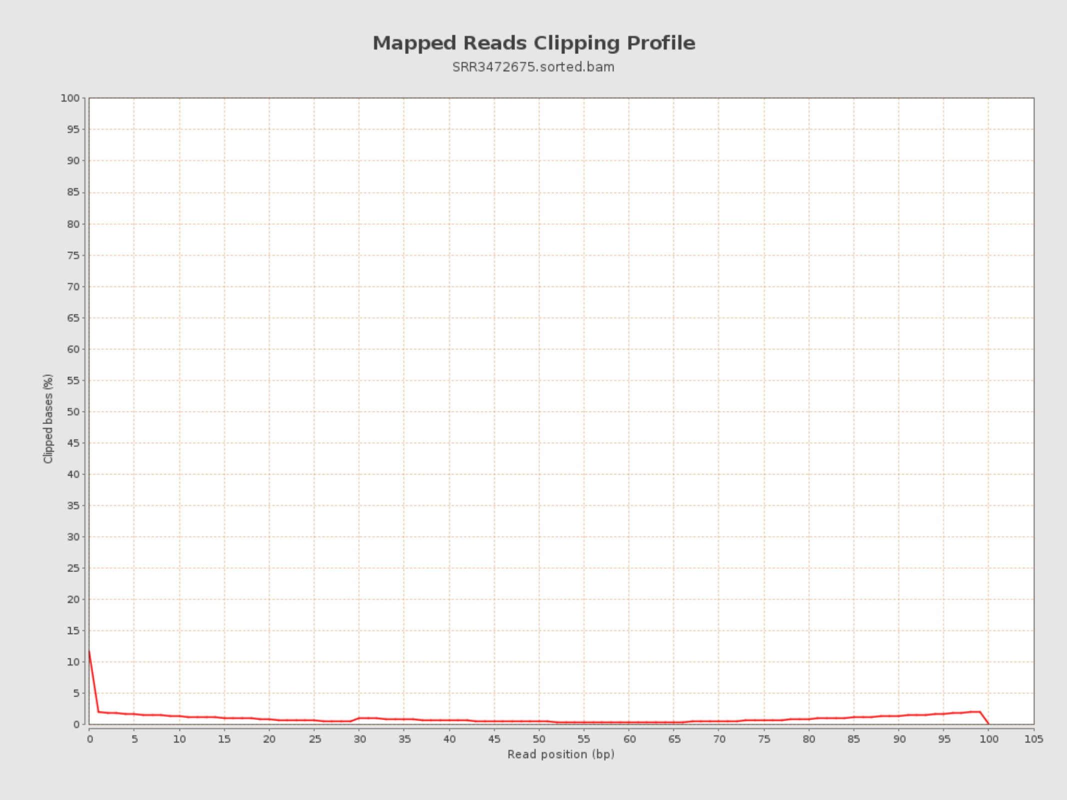
# 8. Results : Mapped Reads Nucleotide Content



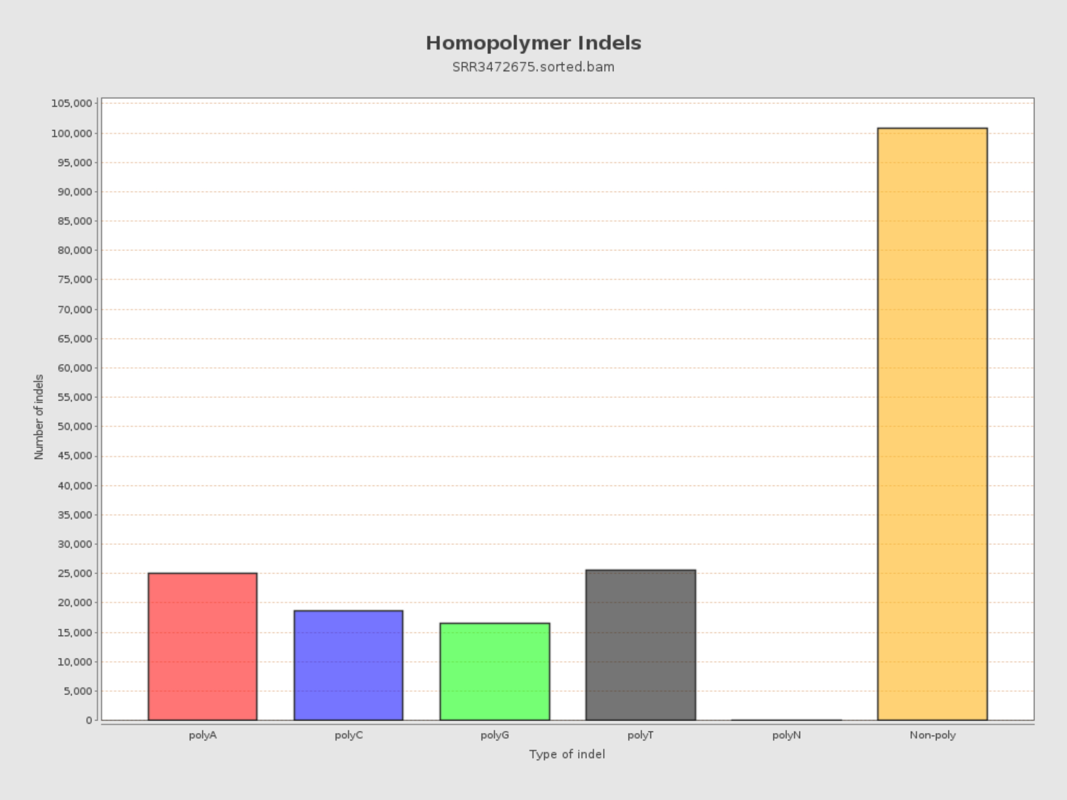
# 9. Results : Mapped Reads GC-content Distribution



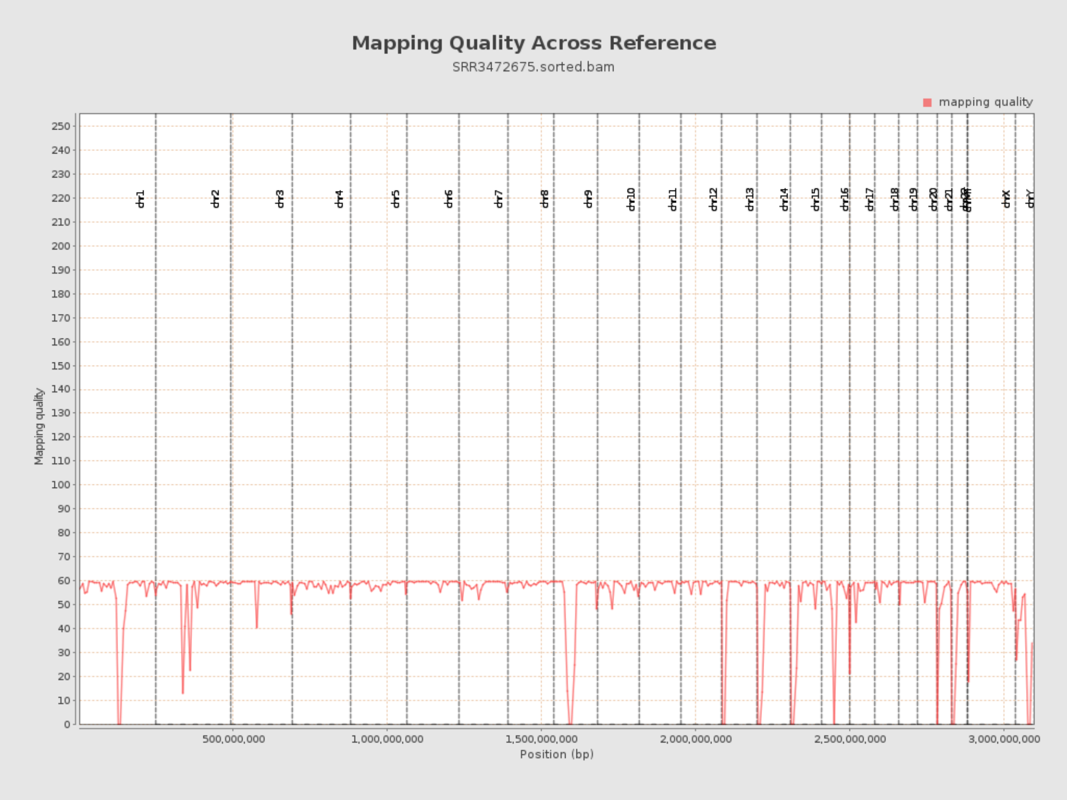
# 10. Results : Mapped Reads Clipping Profile



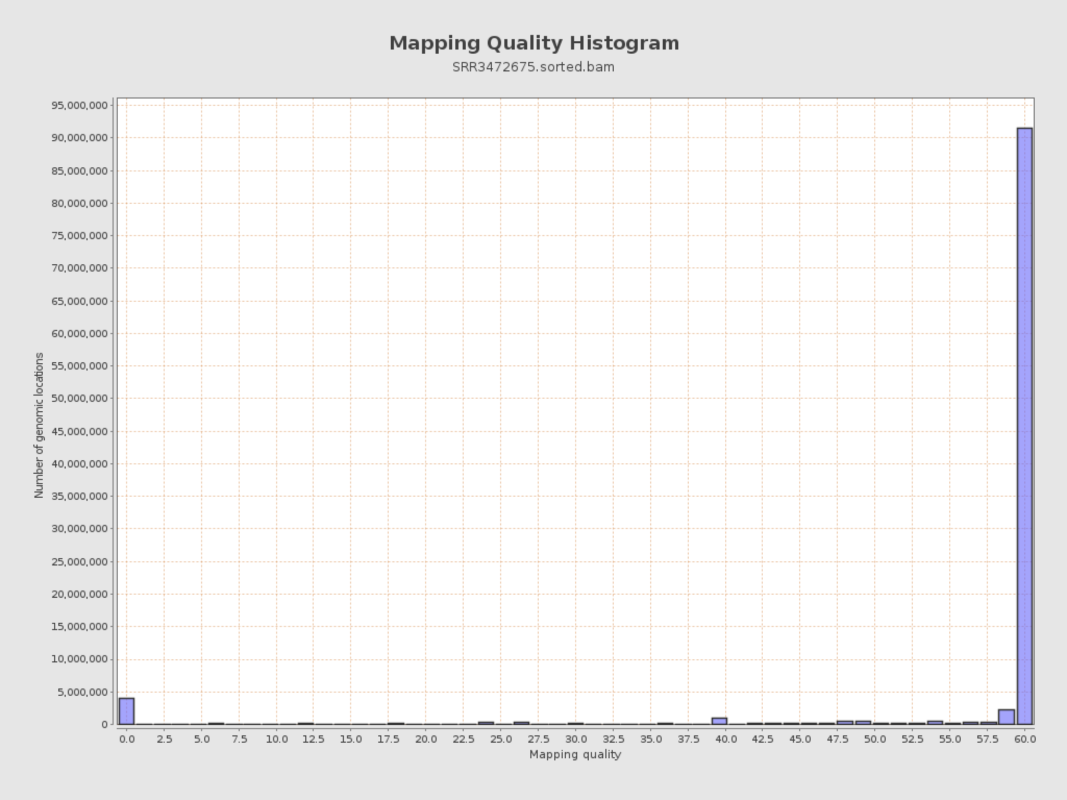
# 11. Results : Homopolymer Indels



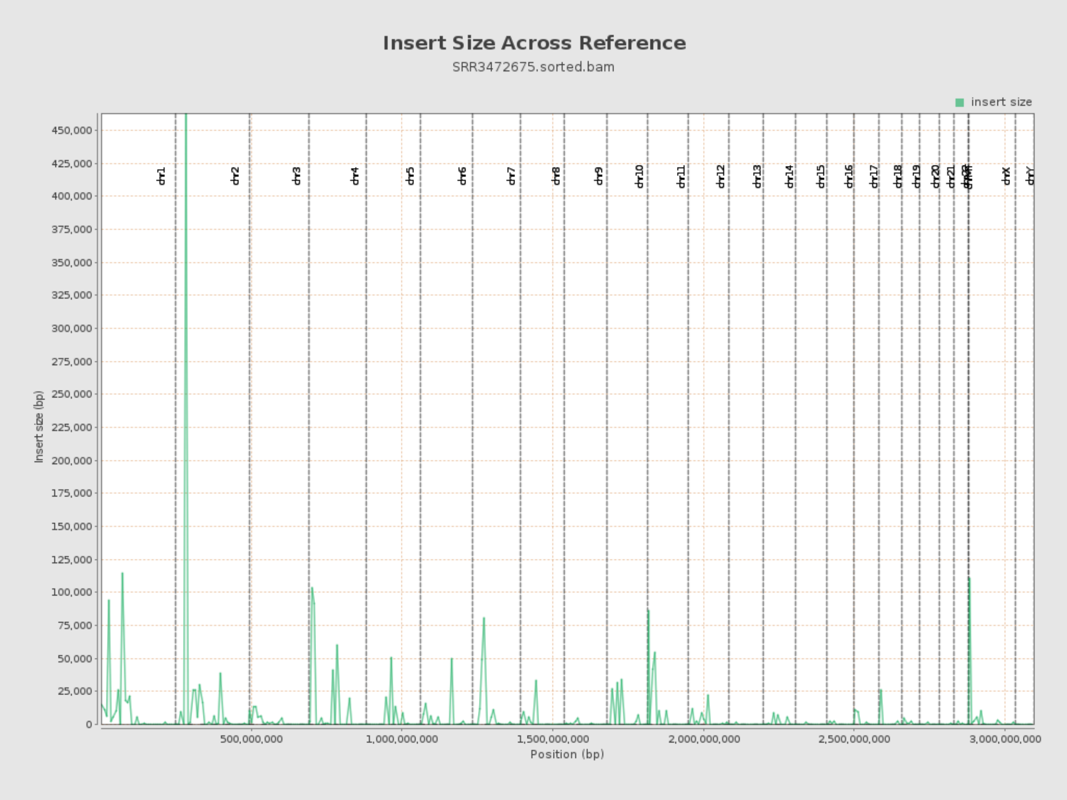
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram