# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/28 15:50:31*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472628.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_SRR3472628 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472628_1.fastq.gz SRR3472628_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 28 15:50:31 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3472628.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 13,808,828 |
| Mapped reads | 13,692,460 / 99.16% |
| Unmapped reads | 116,368 / 0.84% |
| Mapped paired reads | 13,692,460 / 99.16% |
| Mapped reads, first in pair | 6,859,307 / 49.67% |
| Mapped reads, second in pair | 6,833,153 / 49.48% |
| Mapped reads, both in pair | 13,619,472 / 98.63% |
| Mapped reads, singletons | 72,988 / 0.53% |
| Secondary alignments | 0 |
| Supplementary alignments | 65,255 / 0.47% |
| Read min/max/mean length | 30 / 101 / 99.71 |
| Duplicated reads (estimated) | 8,971,645 / 64.97% |
| Duplication rate | 49.41% |
| Clipped reads | 1,003,649 / 7.27% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 356,013,161 / 26.46% |
| Number/percentage of C's | 318,377,115 / 23.66% |
| Number/percentage of T's | 356,220,561 / 26.48% |
| Number/percentage of G's | 314,589,568 / 23.38% |
| Number/percentage of N's | 246,785 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 47.05% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.4347 |
| Standard Deviation | 16.9038 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 54.72 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 20,557.62 |
| Standard Deviation | 1,448,036.14 |
| P25/Median/P75 | 152 / 208 / 276 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.62% |
| Mismatches | 8,170,395 |
| Insertions | 76,164 |
| Mapped reads with at least one insertion | 0.55% |
| Deletions | 73,573 |
| Mapped reads with at least one deletion | 0.53% |
| Homopolymer indels | 48.51% |

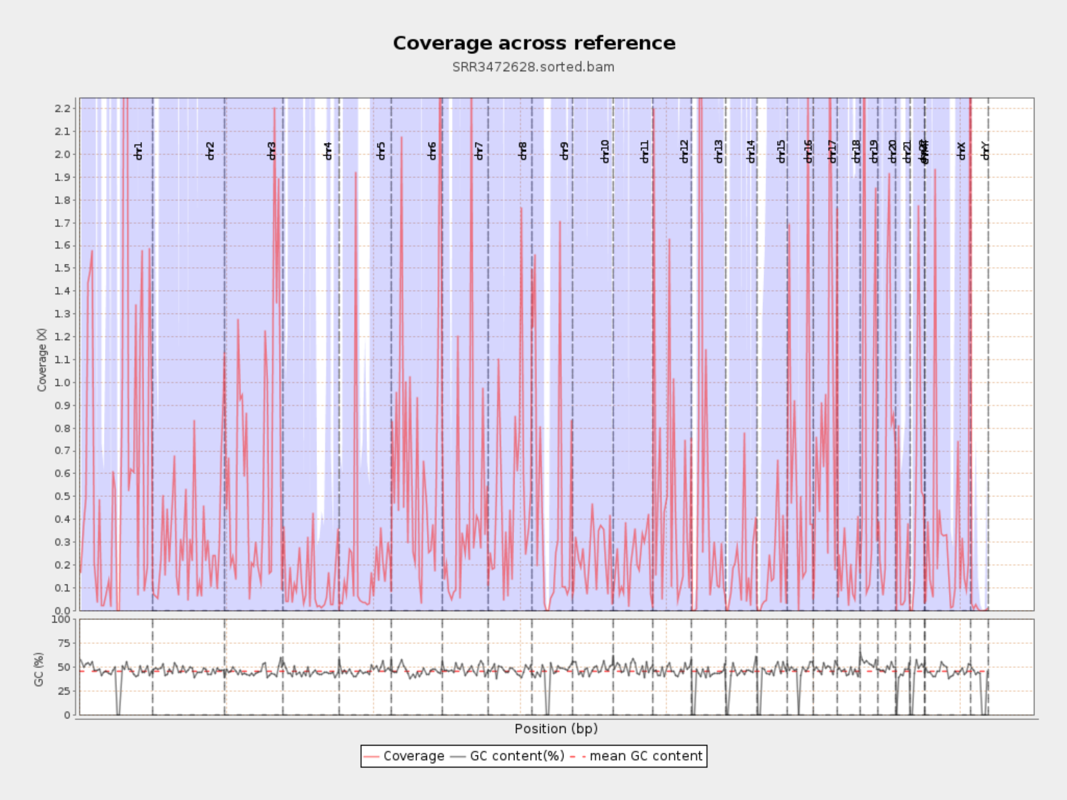
## 2.7. Chromosome stats

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

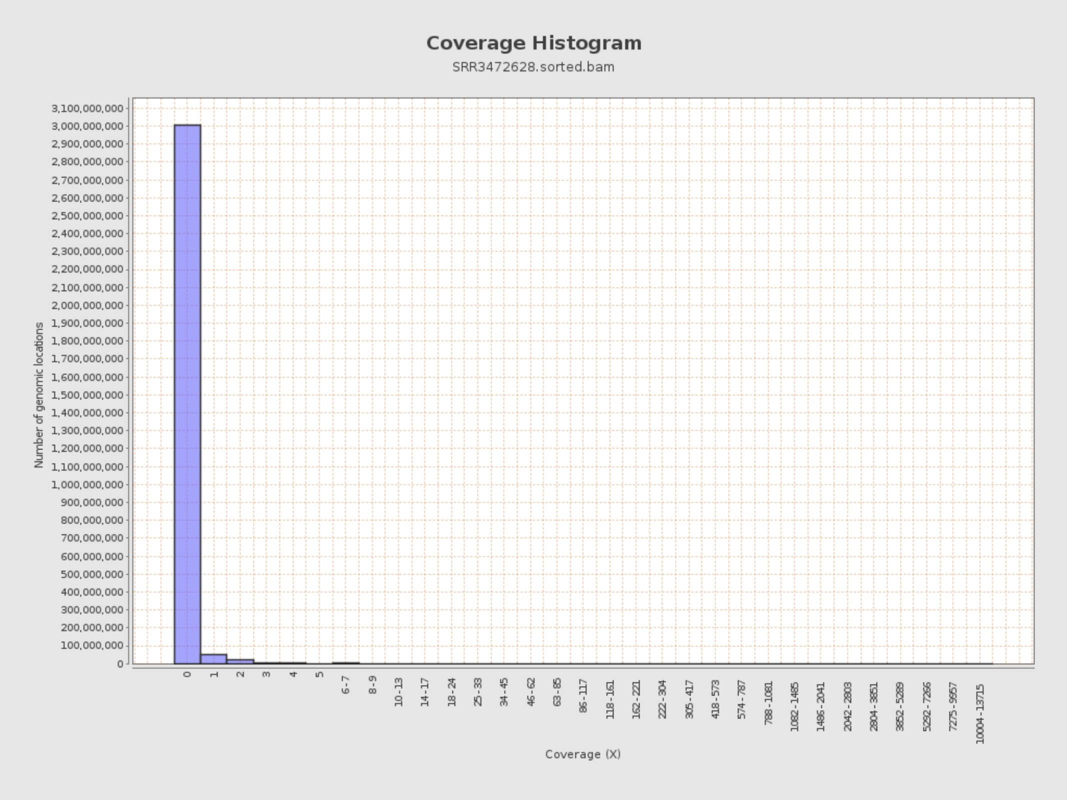
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 187869849 | 0.7537 | 22.5643 |
| chr2 | 243199373 | 70134891 | 0.2884 | 9.8814 |
| chr3 | 198022430 | 130401111 | 0.6585 | 21.0764 |
| chr4 | 191154276 | 22736930 | 0.1189 | 6.3293 |
| chr5 | 180915260 | 37839423 | 0.2092 | 11.3428 |
| chr6 | 171115067 | 119760153 | 0.6999 | 26.1233 |
| chr7 | 159138663 | 70671534 | 0.4441 | 16.6687 |
| chr8 | 146364022 | 73071502 | 0.4992 | 16.9597 |
| chr9 | 141213431 | 62250162 | 0.4408 | 16.5604 |
| chr10 | 135534747 | 32237217 | 0.2379 | 8.8366 |
| chr11 | 135006516 | 29169218 | 0.2161 | 8.2252 |
| chr12 | 133851895 | 72592004 | 0.5423 | 16.0507 |
| chr13 | 115169878 | 62278399 | 0.5408 | 24.6434 |
| chr14 | 107349540 | 20394325 | 0.19 | 7.9522 |
| chr15 | 102531392 | 17702446 | 0.1727 | 9.2505 |
| chr16 | 90354753 | 59775955 | 0.6616 | 18.6763 |
| chr17 | 81195210 | 67918506 | 0.8365 | 24.5416 |
| chr18 | 78077248 | 14103800 | 0.1806 | 6.4462 |
| chr19 | 59128983 | 52825197 | 0.8934 | 32.9745 |
| chr20 | 63025520 | 47683648 | 0.7566 | 20.4597 |
| chr21 | 48129895 | 10316492 | 0.2143 | 14.3883 |
| chr22 | 51304566 | 27746670 | 0.5408 | 22.1417 |
| chrMT | 16571 | 3357 | 0.2026 | 0.5794 |
| chrX | 155270560 | 55593642 | 0.358 | 12.396 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 543300 | 0.0092 | 0.4302 |

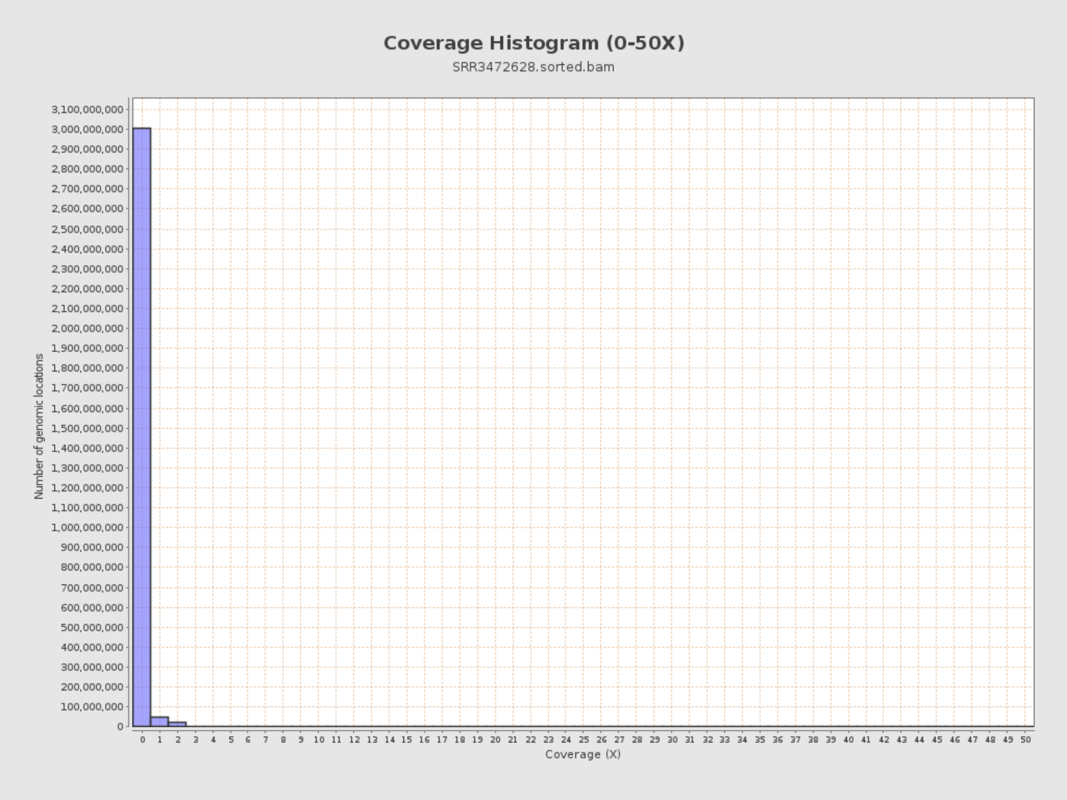
# 3. Results : Coverage across reference



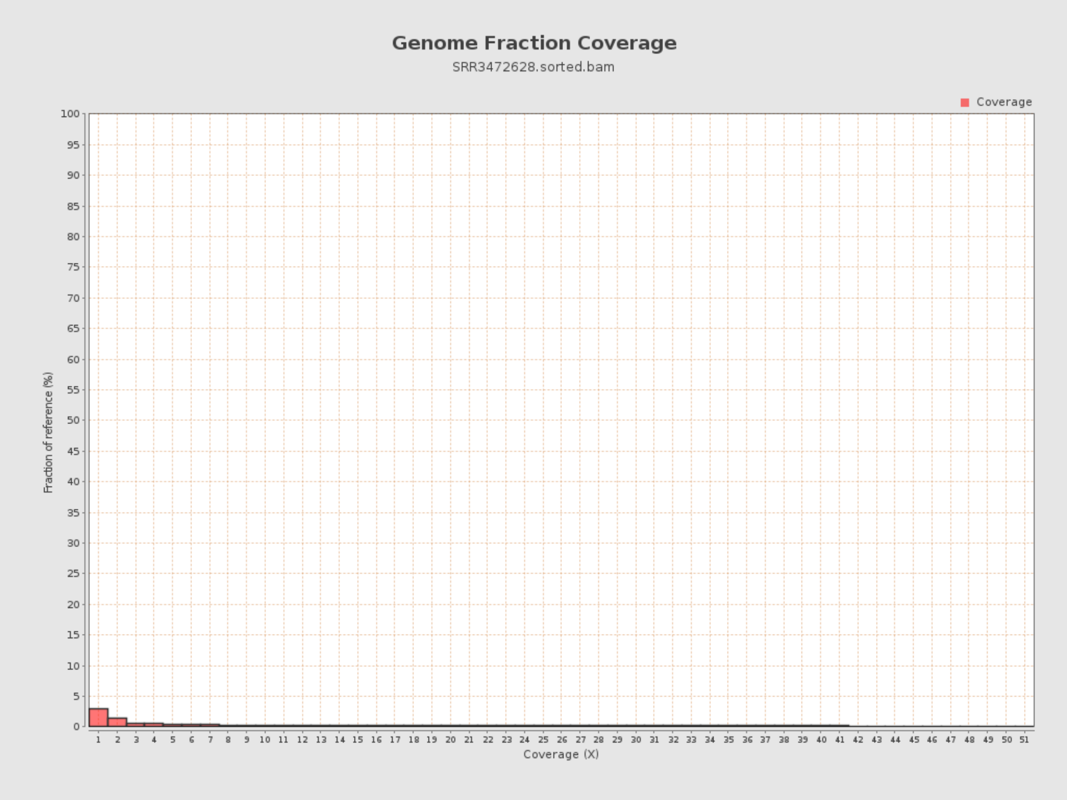
# 4. Results : Coverage Histogram



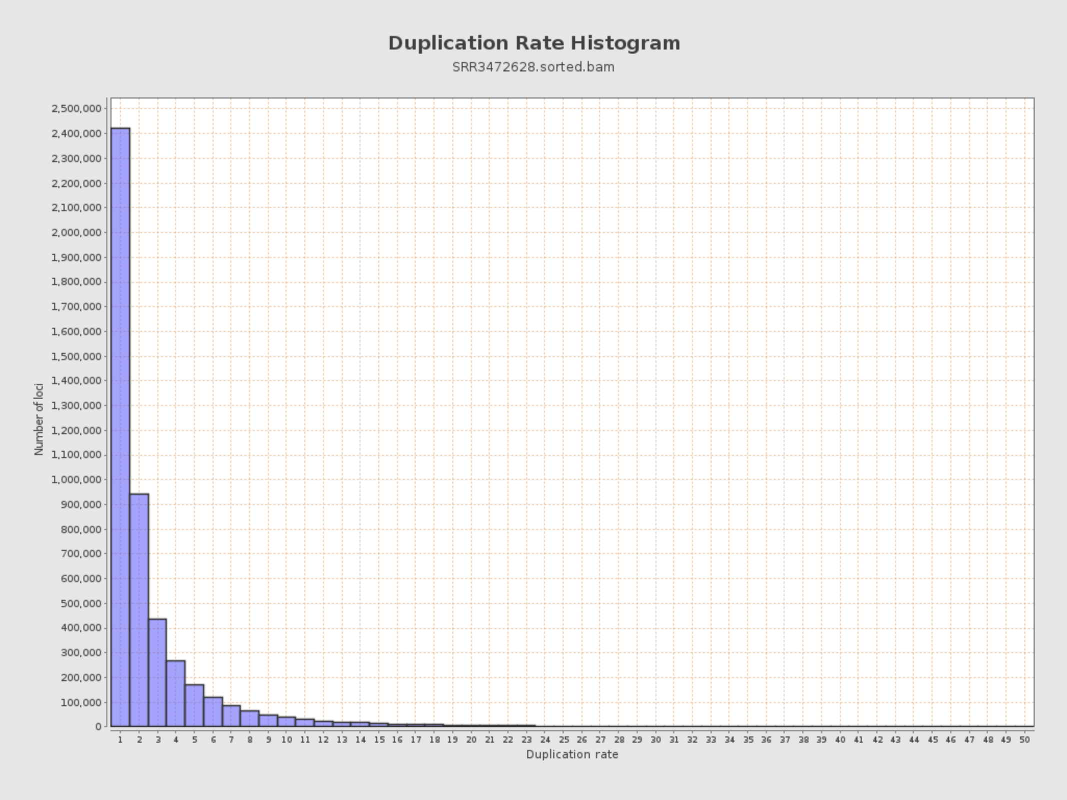
# 5. Results : Coverage Histogram (0-50X)



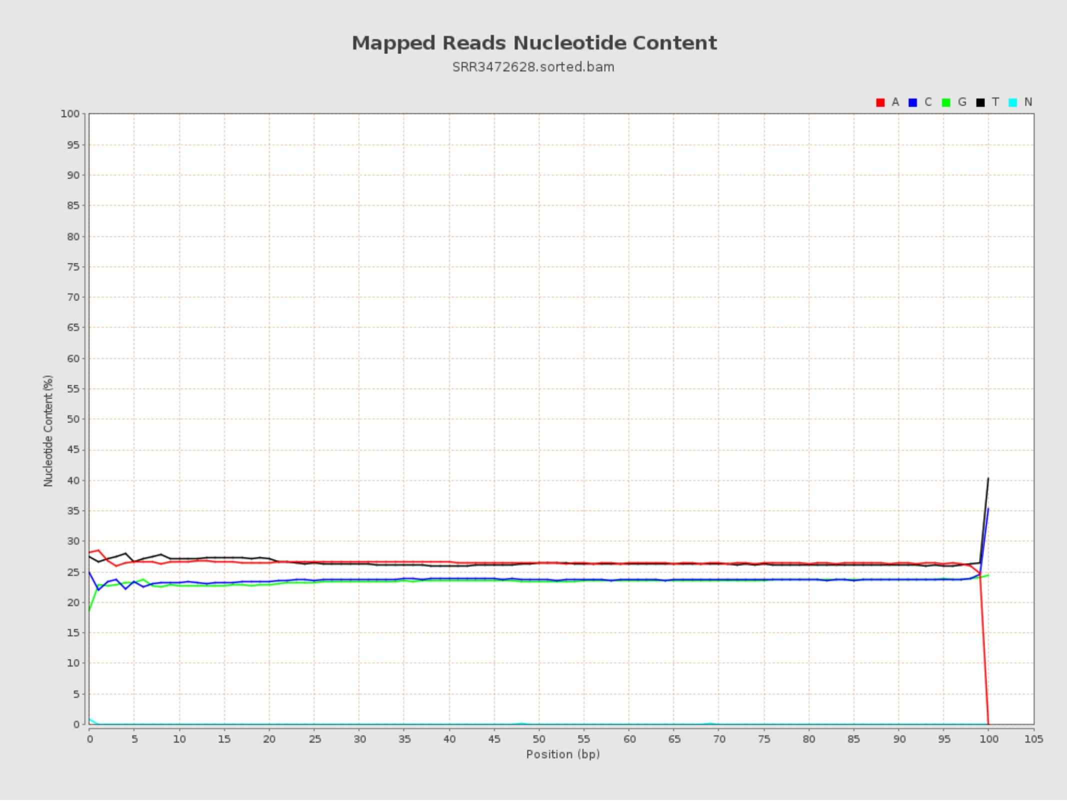
# 6. Results : Genome Fraction Coverage



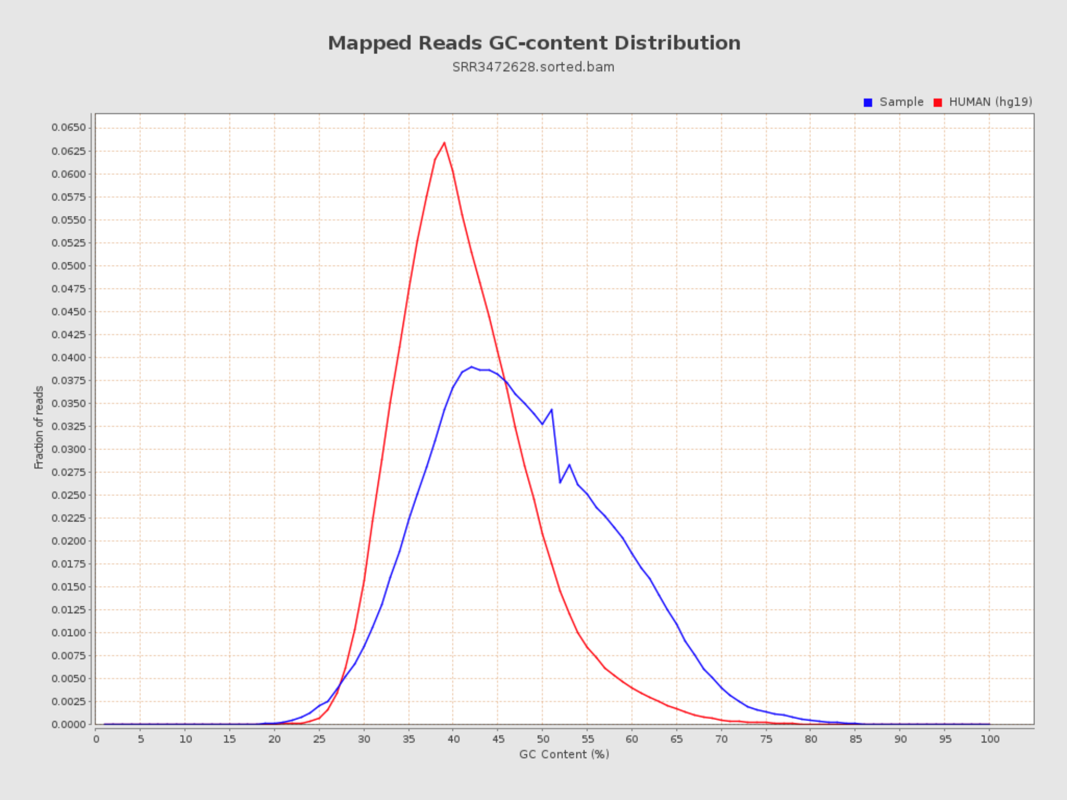
# 7. Results : Duplication Rate Histogram



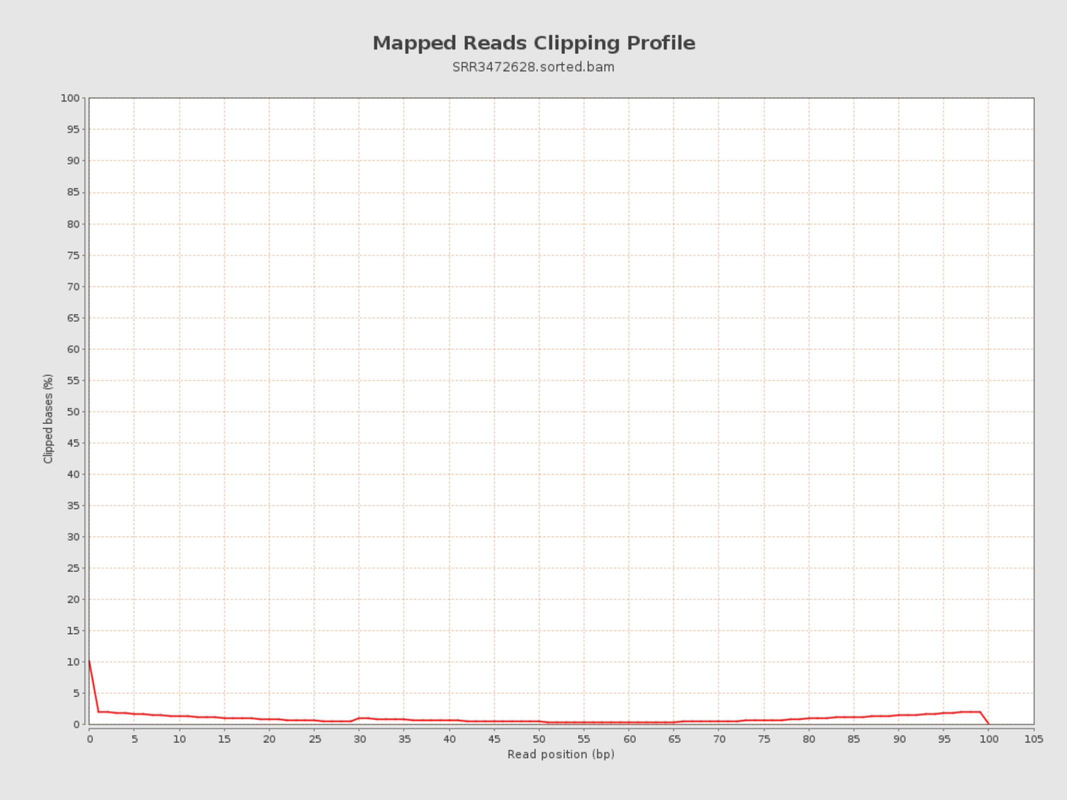
# 8. Results : Mapped Reads Nucleotide Content



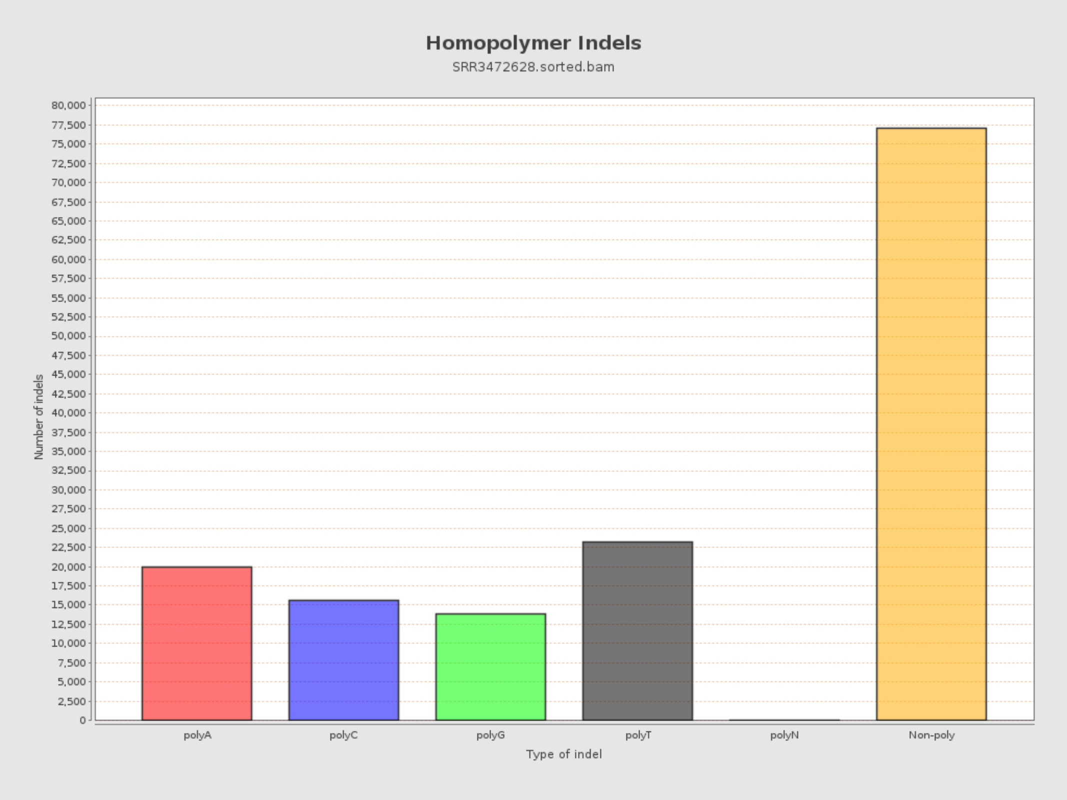
# 9. Results : Mapped Reads GC-content Distribution



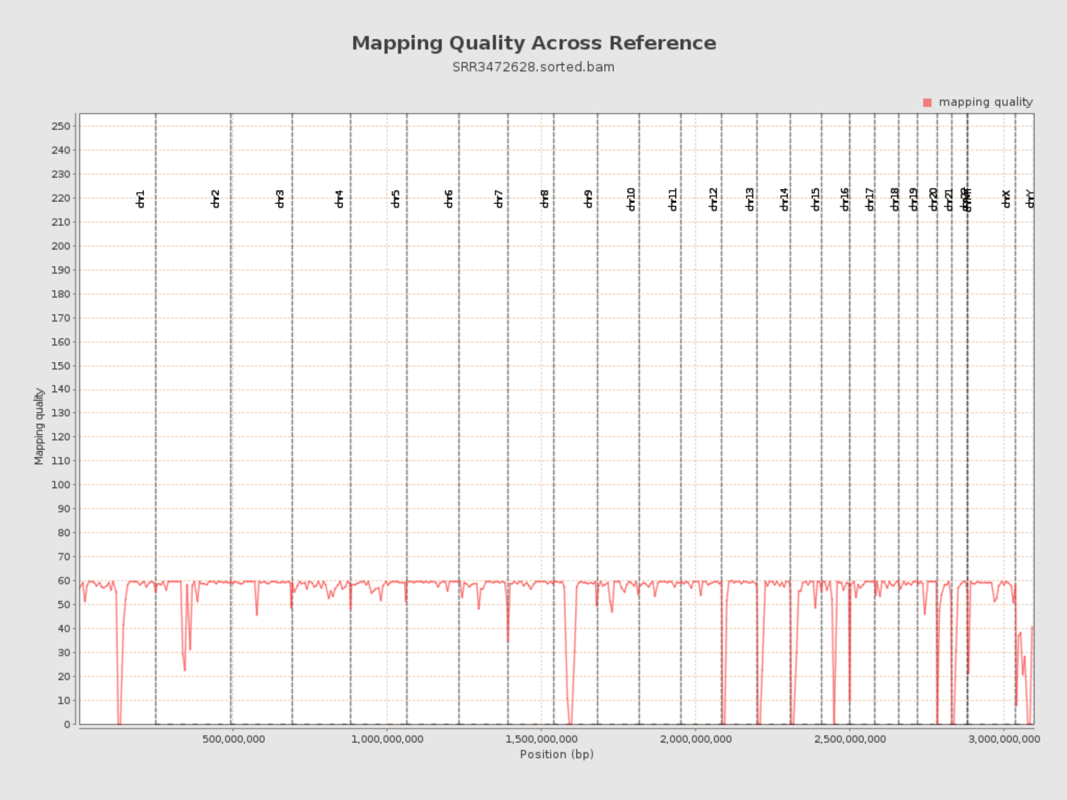
# 10. Results : Mapped Reads Clipping Profile



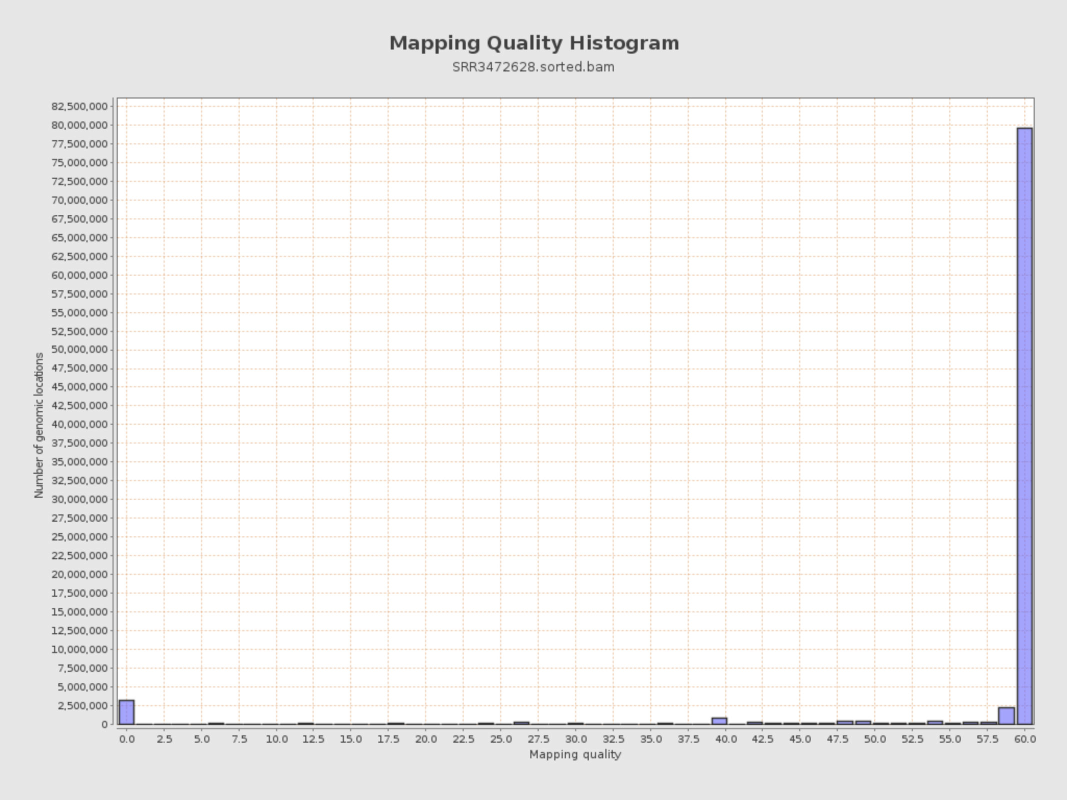
# 11. Results : Homopolymer Indels



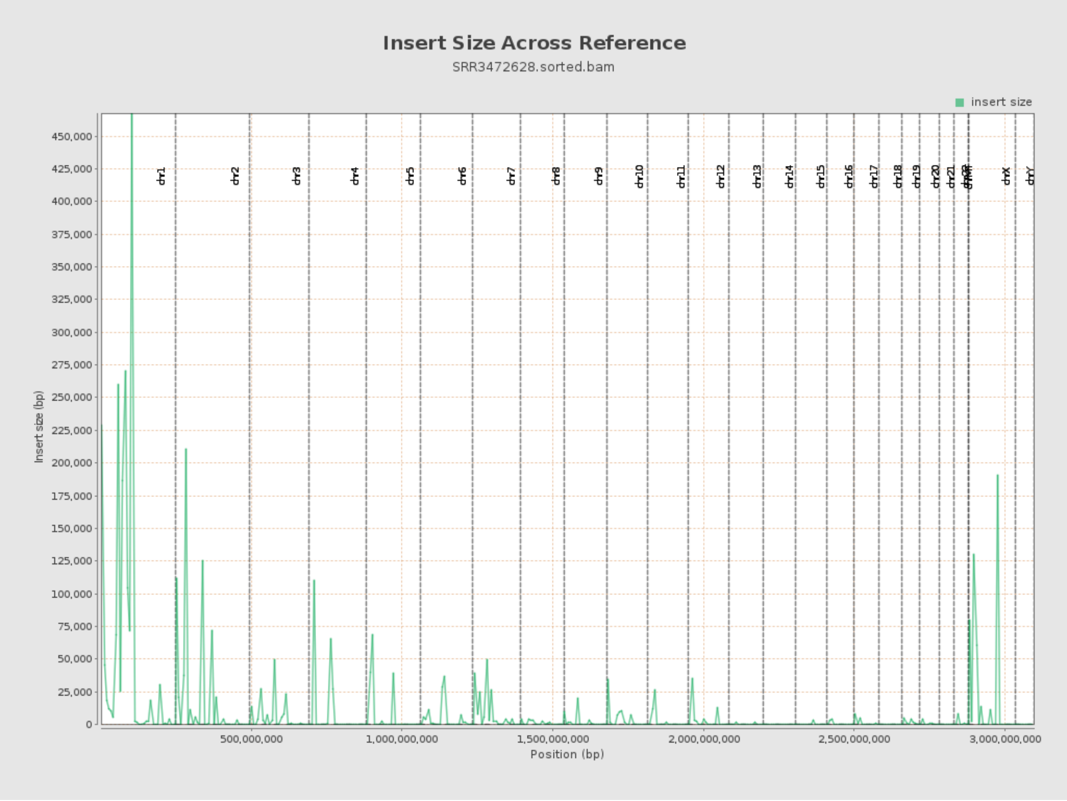
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram