# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/10 03:20:09*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124904.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_SRR3124904 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124904_1.fastq.gz SRR3124904_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Dec 10 03:20:09 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3124904.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,696,056 |
| Mapped reads | 4,596,948 / 97.89% |
| Unmapped reads | 99,108 / 2.11% |
| Mapped paired reads | 4,596,948 / 97.89% |
| Mapped reads, first in pair | 2,302,202 / 49.02% |
| Mapped reads,  second in pair | 2,294,746 / 48.87% |
| Mapped reads, both in pair | 4,581,484 / 97.56% |
| Mapped reads, singletons | 15,464 / 0.33% |
| Secondary alignments | 0 |
| Supplementary alignments | 18,011 / 0.38% |
| Read min/max/mean length | 30 / 101 / 101.15 |
| Duplicated reads (estimated) | 399,751 / 8.51% |
| Duplication rate | 6.55% |
| Clipped reads | 2,219,280 / 47.26% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 111,558,789 / 28.02% |
| Number/percentage of C's | 74,659,139 / 18.75% |
| Number/percentage of T's | 117,503,147 / 29.51% |
| Number/percentage of G's | 94,441,973 / 23.72% |
| Number/percentage of N's | 4,890 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 42.47% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1287 |
| Standard Deviation | 1.0027 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 52.88 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 28,598.85 |
| Standard Deviation | 1,573,007.32 |
| P25/Median/P75 | 143 / 192 / 266 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.74% |
| Mismatches | 2,835,080 |
| Insertions | 53,174 |
| Mapped reads with at least one insertion | 1.12% |
| Deletions | 131,042 |
| Mapped reads with at least one deletion | 2.79% |
| Homopolymer indels | 47.24% |

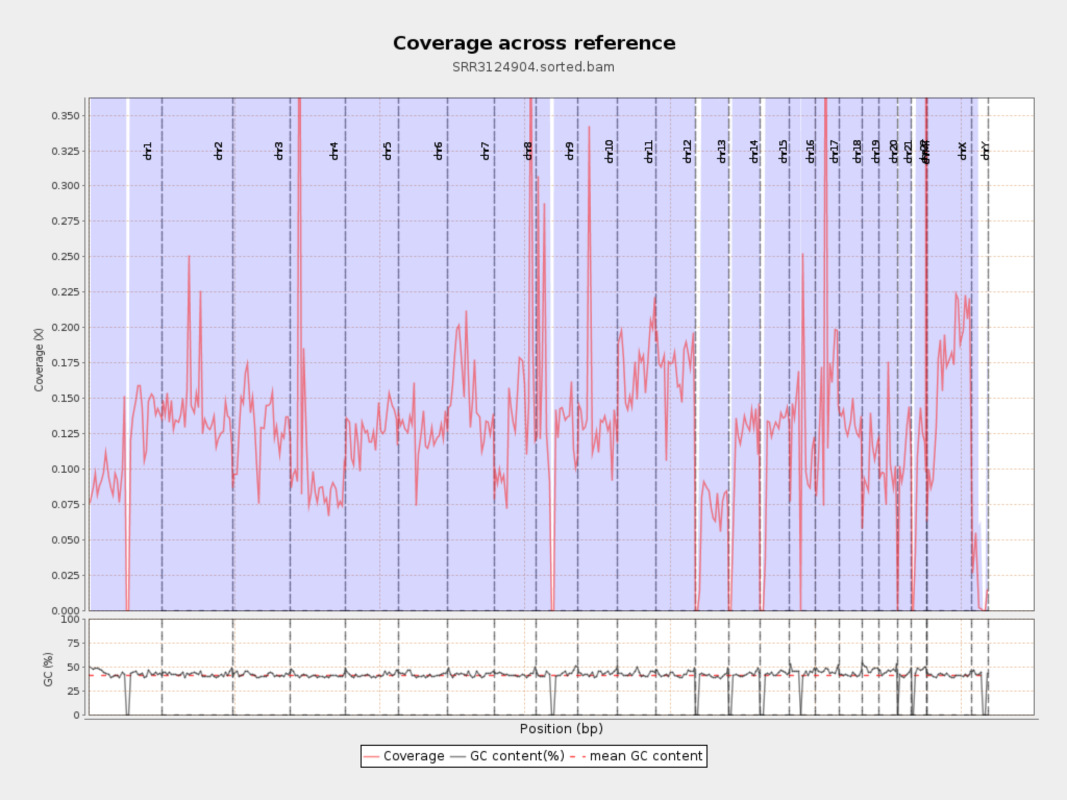
## 2.7. Chromosome stats

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

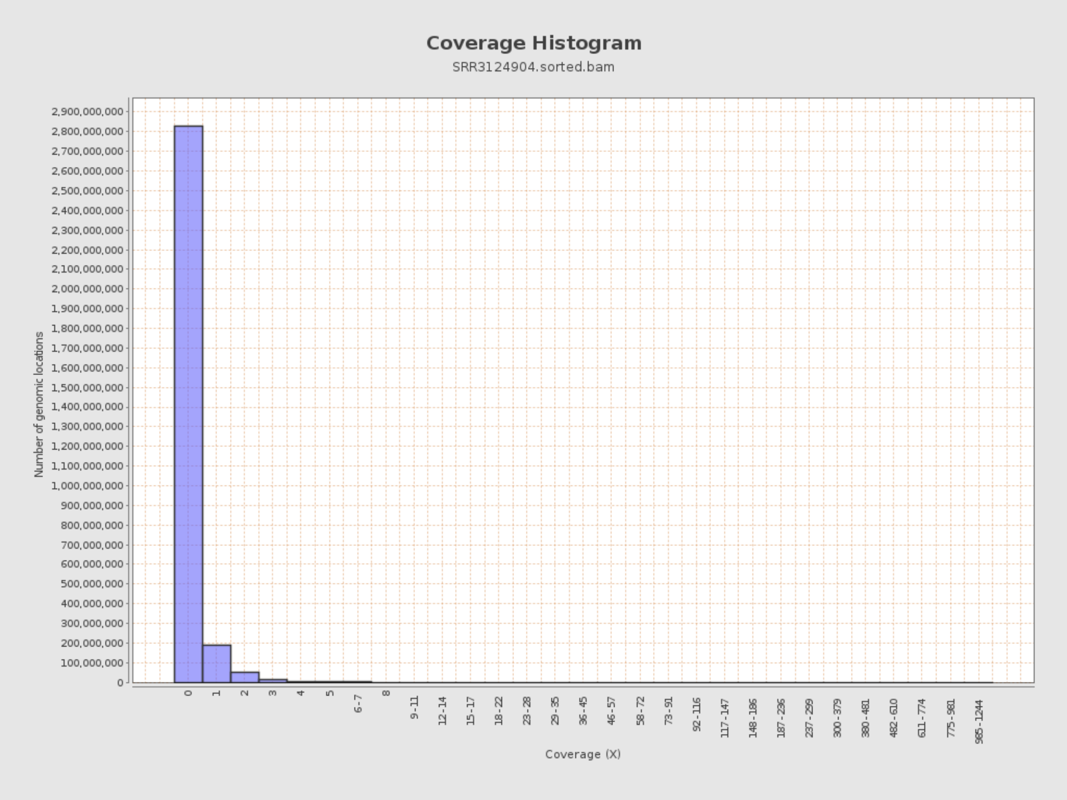
| | | **bases** | **coverage** | **deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 27048779 | 0.1085 | 1.0275 |
| chr2 | 243199373 | 34761259 | 0.1429 | 1.2989 |
| chr3 | 198022430 | 25909856 | 0.1308 | 0.4779 |
| chr4 | 191154276 | 20566540 | 0.1076 | 0.9406 |
| chr5 | 180915260 | 23071474 | 0.1275 | 0.4832 |
| chr6 | 171115067 | 21600417 | 0.1262 | 0.6374 |
| chr7 | 159138663 | 24547796 | 0.1543 | 1.5977 |
| chr8 | 146364022 | 21315458 | 0.1456 | 0.7733 |
| chr9 | 141213431 | 19123056 | 0.1354 | 1.1492 |
| chr10 | 135534747 | 18987061 | 0.1401 | 1.8957 |
| chr11 | 135006516 | 23411070 | 0.1734 | 0.9359 |
| chr12 | 133851895 | 22948682 | 0.1714 | 0.561 |
| chr13 | 115169878 | 7420803 | 0.0644 | 0.3269 |
| chr14 | 107349540 | 11577178 | 0.1078 | 0.4856 |
| chr15 | 102531392 | 11002351 | 0.1073 | 0.4361 |
| chr16 | 90354753 | 10993071 | 0.1217 | 1.4319 |
| chr17 | 81195210 | 14291089 | 0.176 | 1.671 |
| chr18 | 78077248 | 10410458 | 0.1333 | 1.2373 |
| chr19 | 59128983 | 6219156 | 0.1052 | 0.6656 |
| chr20 | 63025520 | 6455618 | 0.1024 | 0.4712 |
| chr21 | 48129895 | 4935252 | 0.1025 | 0.5374 |
| chr22 | 51304566 | 4349726 | 0.0848 | 0.4082 |
| chrMT | 16571 | 49886 | 3.0104 | 2.7576 |
| chrX | 155270560 | 26423005 | 0.1702 | 0.6806 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 971180 | 0.0164 | 0.9927 |

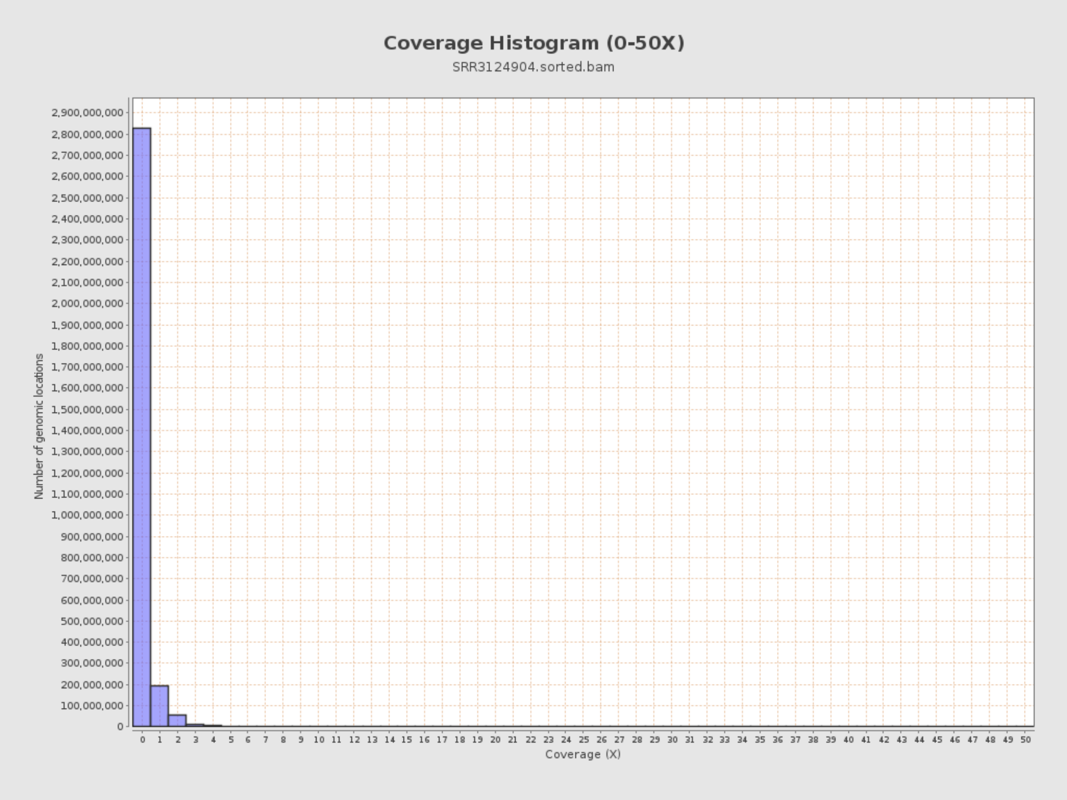
# 3. Results : Coverage across reference



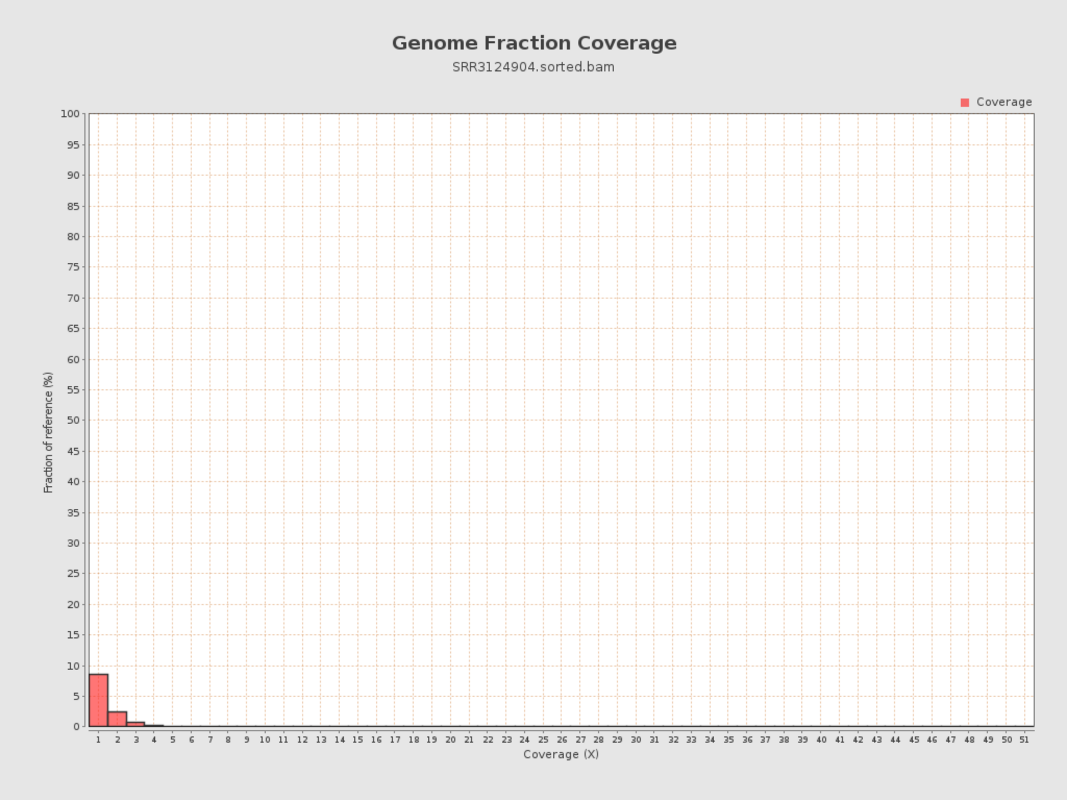
# 4. Results : Coverage Histogram



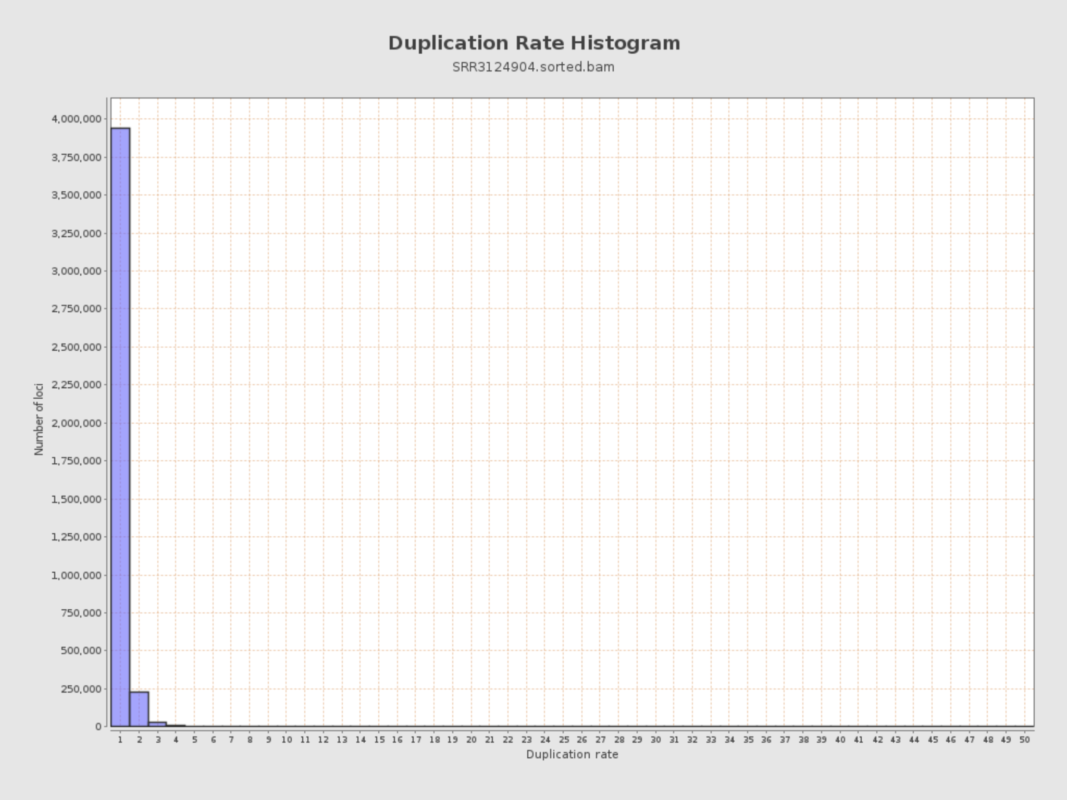
# 5. Results : Coverage Histogram (0-50X)



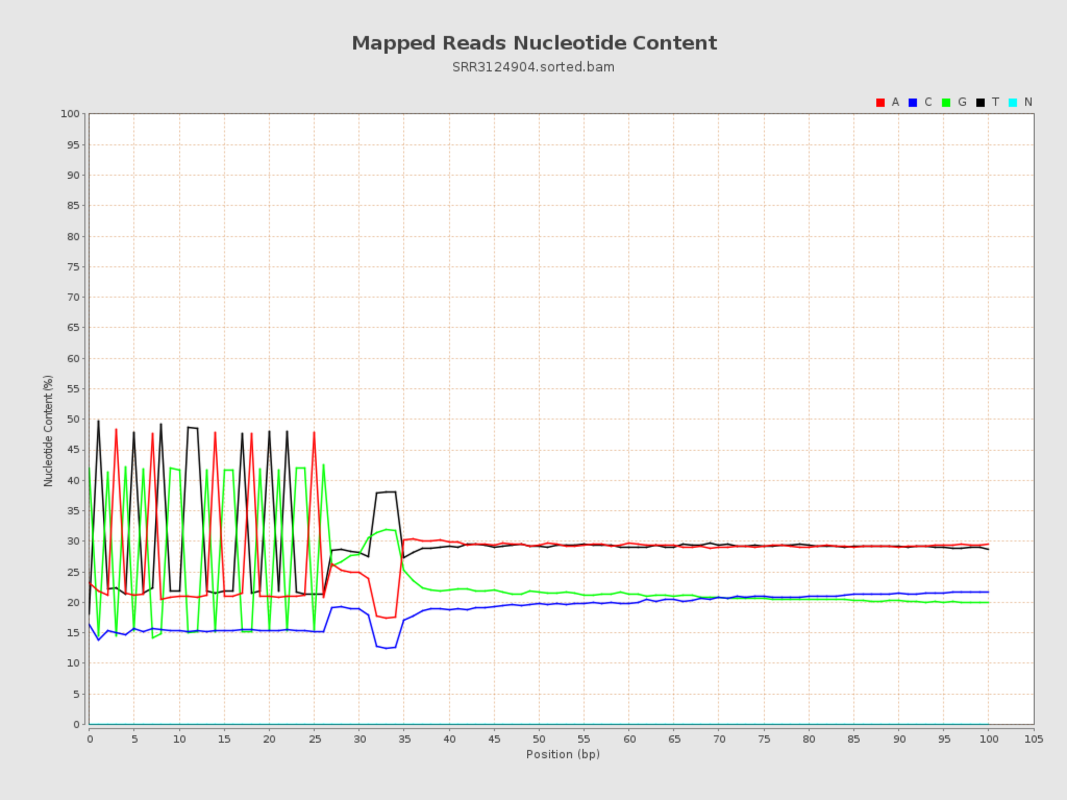
# 6. Results : Genome Fraction Coverage



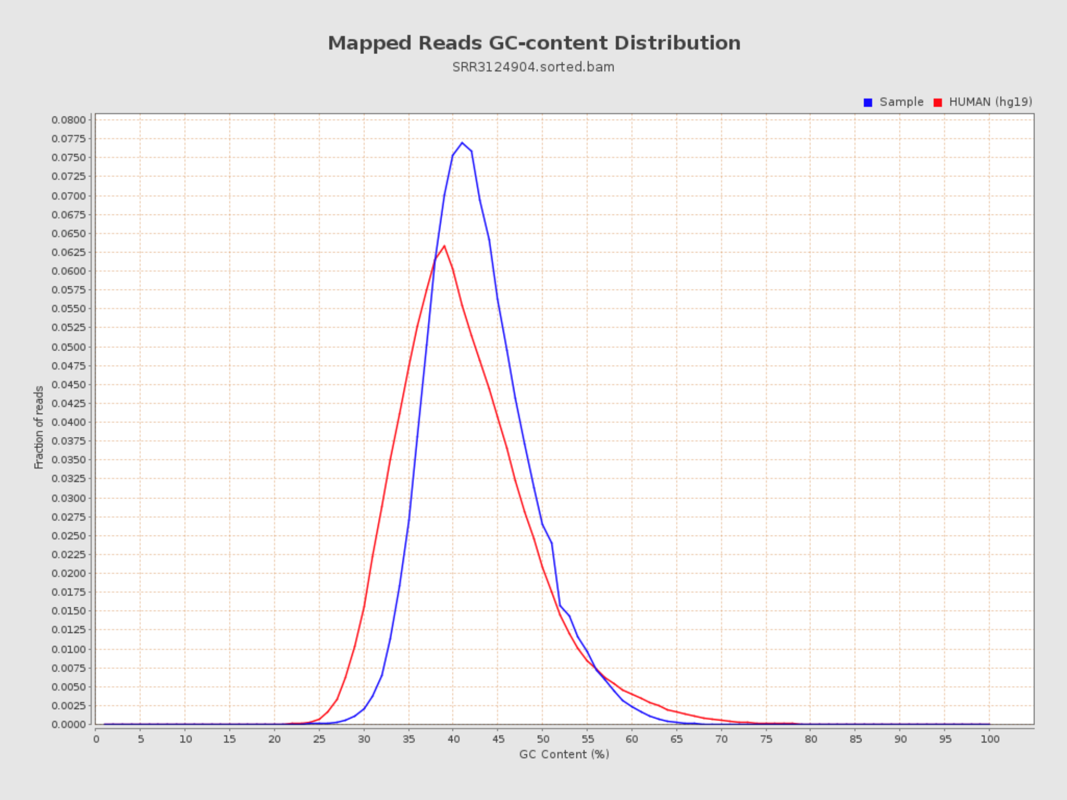
# 7. Results : Duplication Rate Histogram



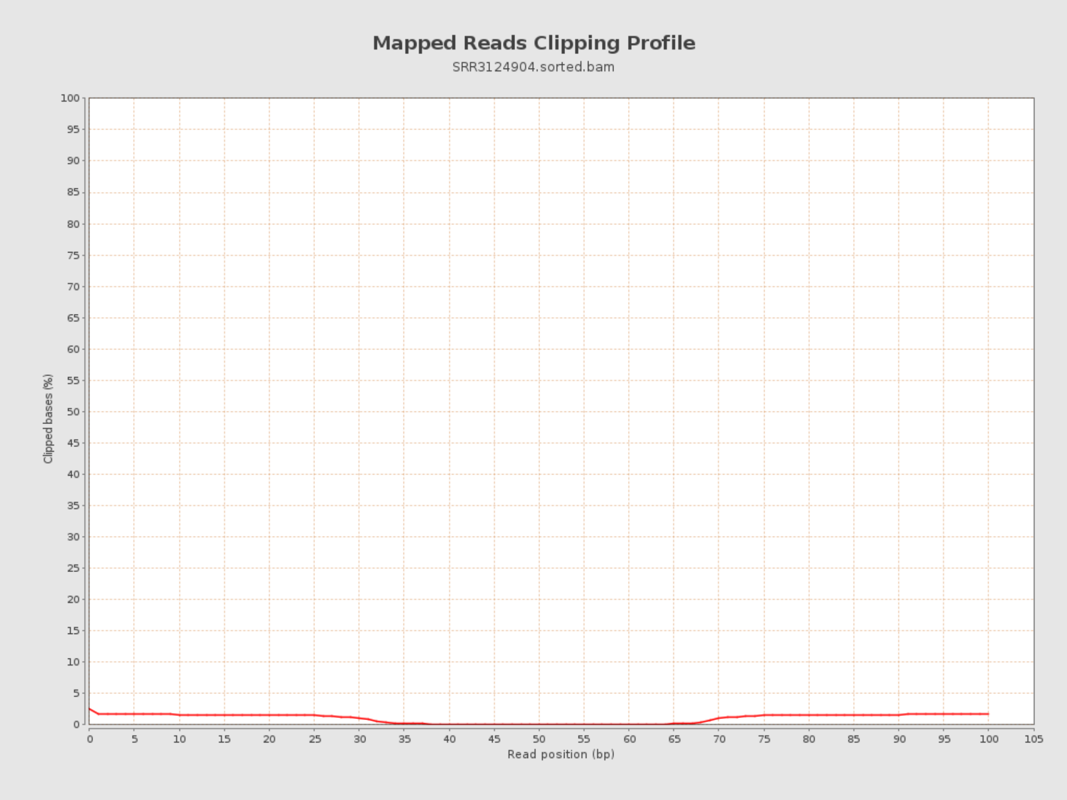
# 8. Results : Mapped Reads Nucleotide Content



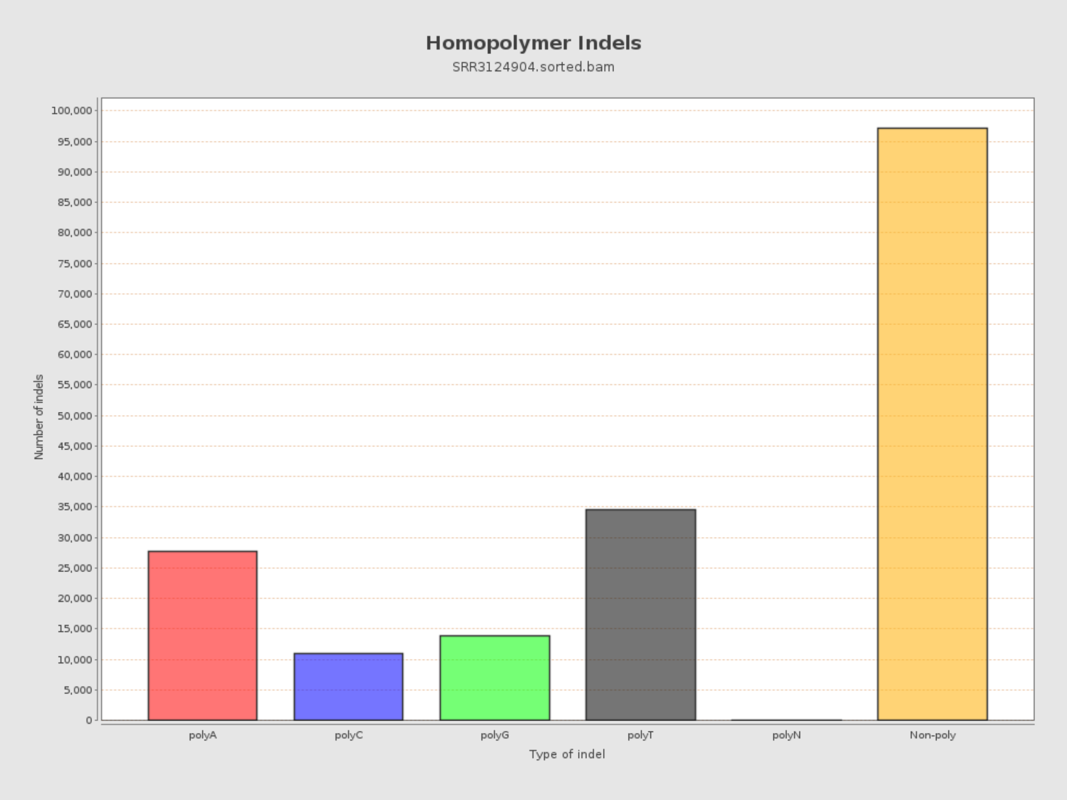
# 9. Results : Mapped Reads GC-content Distribution



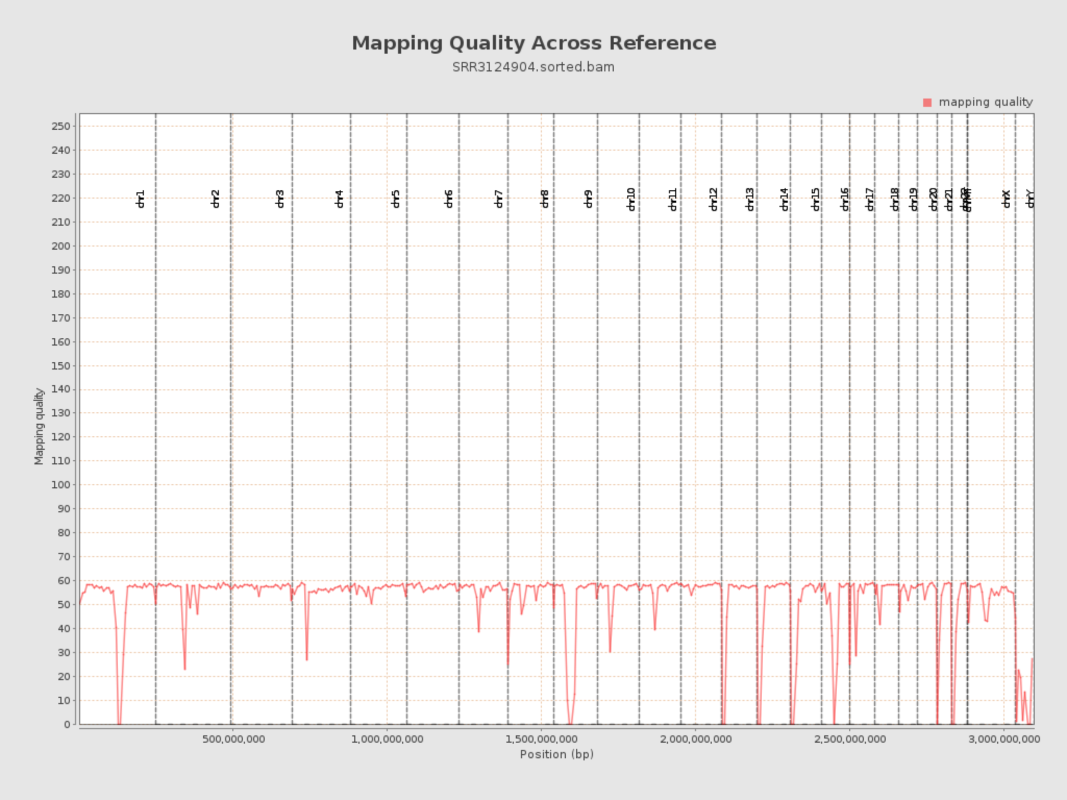
# 10. Results : Mapped Reads Clipping Profile



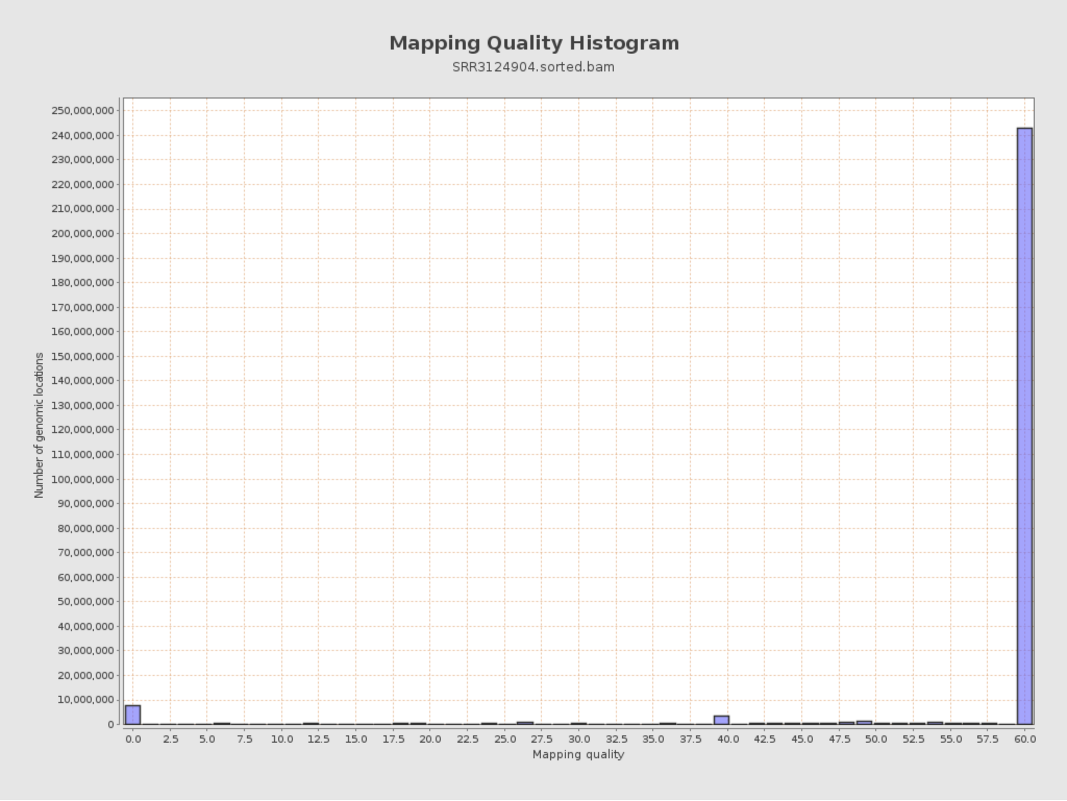
# 11. Results : Homopolymer Indels



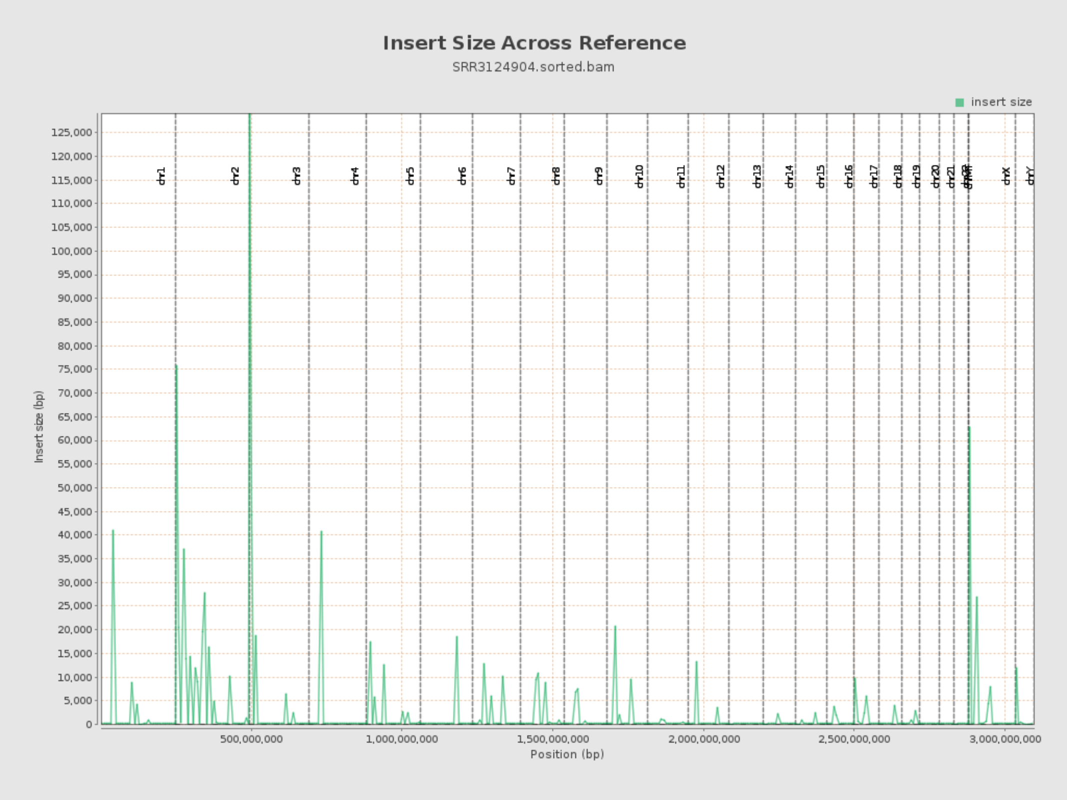
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram