# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/05 07:53:11*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124832.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_SRR3124832 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124832_1.fastq.gz SRR3124832_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Dec 05 07:53:10 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3124832.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 29,321,452 |
| Mapped reads | 28,828,195 / 98.32% |
| Unmapped reads | 493,257 / 1.68% |
| Mapped paired reads | 28,828,195 / 98.32% |
| Mapped reads, first in pair | 14,458,239 / 49.31% |
| Mapped reads, second in pair | 14,369,956 / 49.01% |
| Mapped reads, both in pair | 28,644,596 / 97.69% |
| Mapped reads, singletons | 183,599 / 0.63% |
| Secondary alignments | 0 |
| Supplementary alignments | 304,584 / 1.04% |
| Read min/max/mean length | 30 / 101 / 101.41 |
| Duplicated reads (estimated) | 6,832,772 / 23.3% |
| Duplication rate | 14.33% |
| Clipped reads | 15,405,443 / 52.54% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 698,862,937 / 28.33% |
| Number/percentage of C's | 455,856,323 / 18.48% |
| Number/percentage of T's | 743,757,605 / 30.15% |
| Number/percentage of G's | 568,300,995 / 23.04% |
| Number/percentage of N's | 22,165 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 41.52% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.7974 |
| Standard Deviation | 8.5978 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 52.12 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 108,939.39 |
| Standard Deviation | 3,127,452.45 |
| P25/Median/P75 | 132 / 179 / 253 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.86% |
| Mismatches | 20,367,578 |
| Insertions | 405,107 |
| Mapped reads with at least one insertion | 1.35% |
| Deletions | 909,401 |
| Mapped reads with at least one deletion | 3.08% |
| Homopolymer indels | 45.42% |

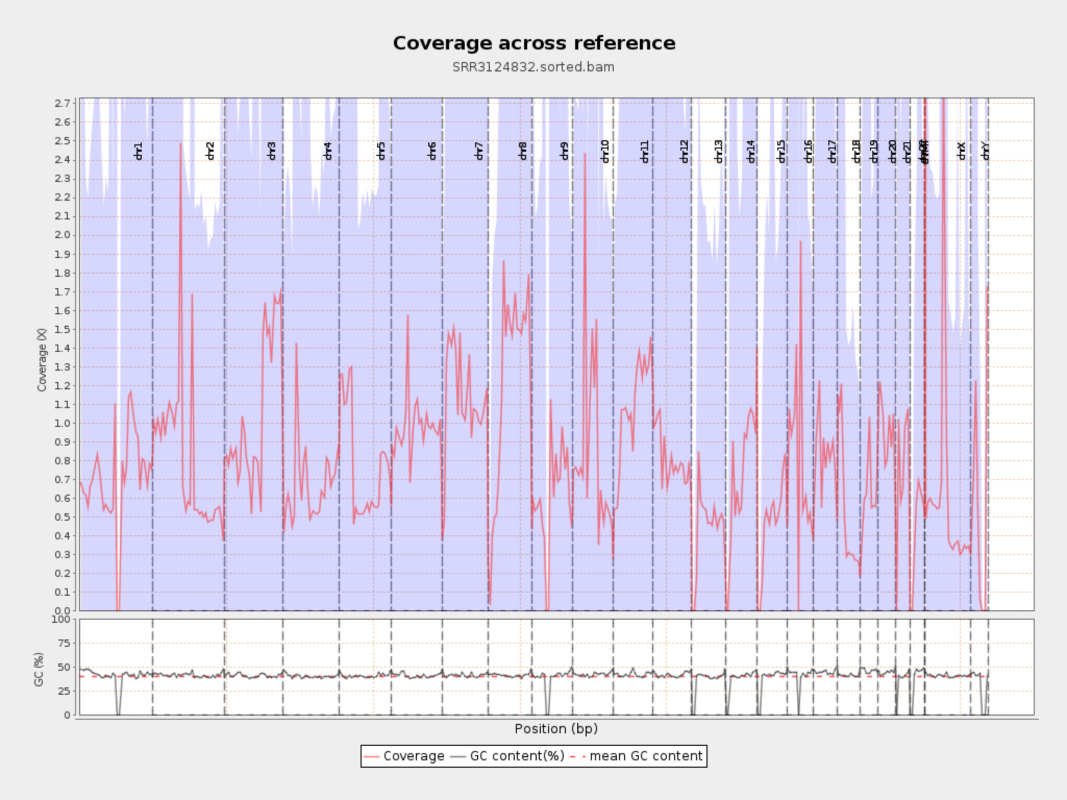
## 2.7. Chromosome stats

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

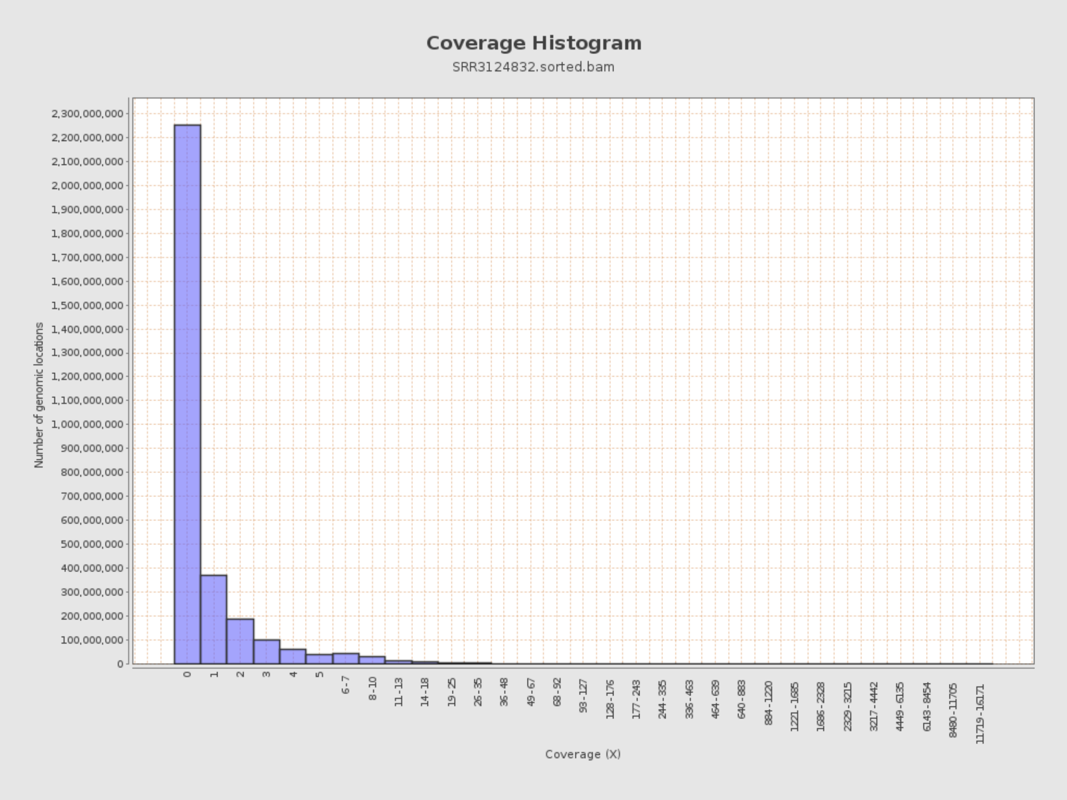
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 175442607 | 0.7039 | 8.7124 |
| chr2 | 243199373 | 197477913 | 0.812 | 17.246 |
| chr3 | 198022430 | 210633973 | 1.0637 | 2.5112 |
| chr4 | 191154276 | 126730648 | 0.663 | 5.3815 |
| chr5 | 180915260 | 139176425 | 0.7693 | 2.5677 |
| chr6 | 171115067 | 168802640 | 0.9865 | 7.0909 |
| chr7 | 159138663 | 180444889 | 1.1339 | 9.5706 |
| chr8 | 146364022 | 179805105 | 1.2285 | 4.7998 |
| chr9 | 141213431 | 83723072 | 0.5929 | 10.4086 |
| chr10 | 135534747 | 118024993 | 0.8708 | 14.969 |
| chr11 | 135006516 | 143984545 | 1.0665 | 6.4417 |
| chr12 | 133851895 | 108199010 | 0.8083 | 2.1526 |
| chr13 | 115169878 | 51292046 | 0.4454 | 1.5118 |
| chr14 | 107349540 | 74553182 | 0.6945 | 2.8489 |
| chr15 | 102531392 | 47495911 | 0.4632 | 1.6736 |
| chr16 | 90354753 | 71873430 | 0.7955 | 12.7412 |
| chr17 | 81195210 | 66121312 | 0.8143 | 7.1633 |
| chr18 | 78077248 | 39960033 | 0.5118 | 11.0735 |
| chr19 | 59128983 | 35301865 | 0.597 | 5.7438 |
| chr20 | 63025520 | 60753254 | 0.9639 | 3.3221 |
| chr21 | 48129895 | 36626938 | 0.761 | 4.0307 |
| chr22 | 51304566 | 22216496 | 0.433 | 2.1712 |
| chrMT | 16571 | 3658812 | 220.7961 | 130.5348 |
| chrX | 155270560 | 90700600 | 0.5841 | 4.006 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 35465659 | 0.5973 | 15.3285 |

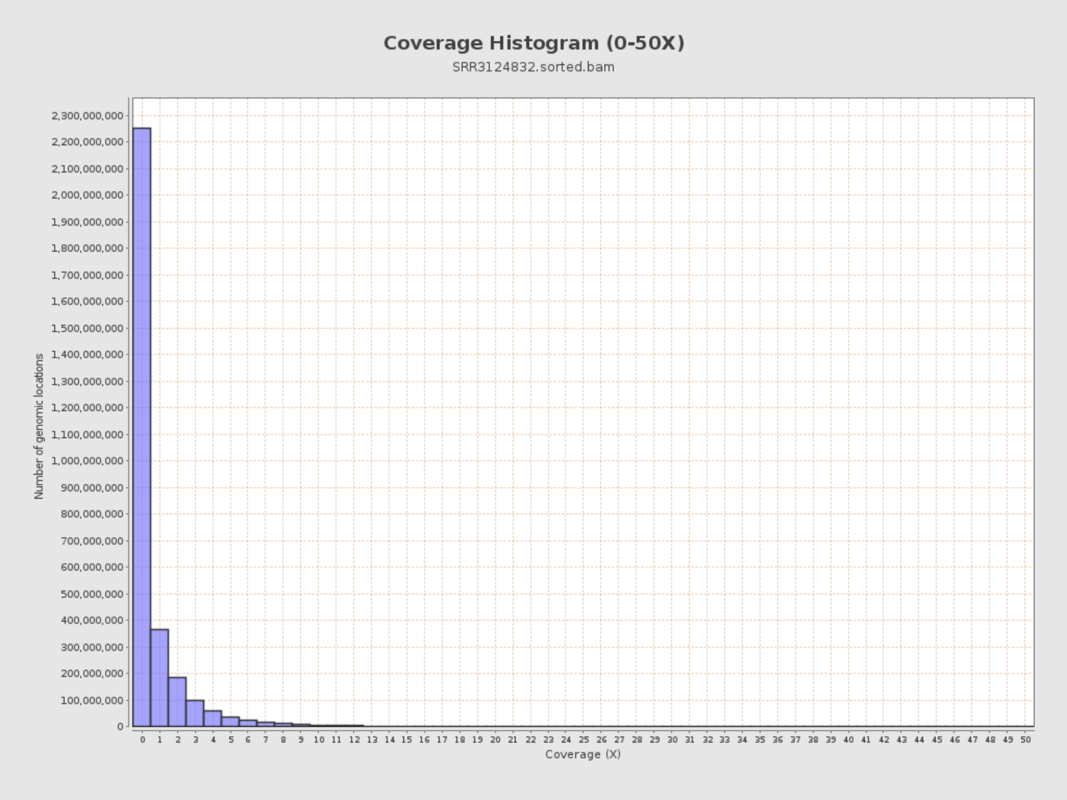
# 3. Results : Coverage across reference



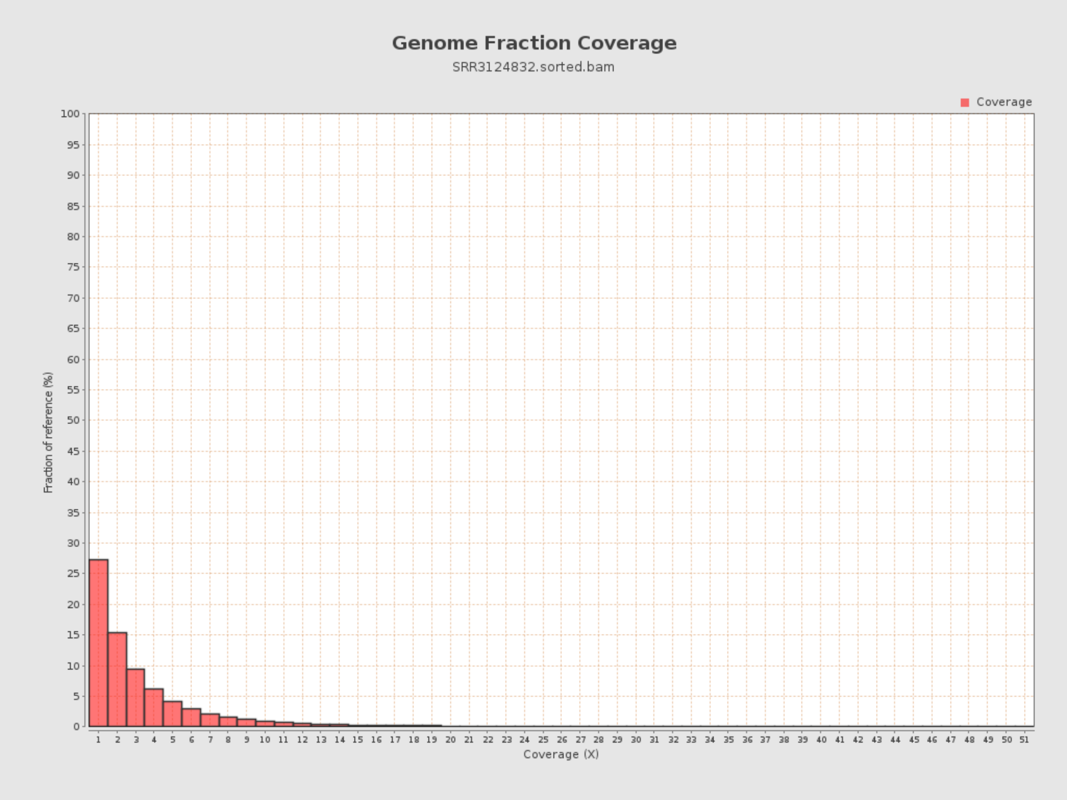
# 4. Results : Coverage Histogram



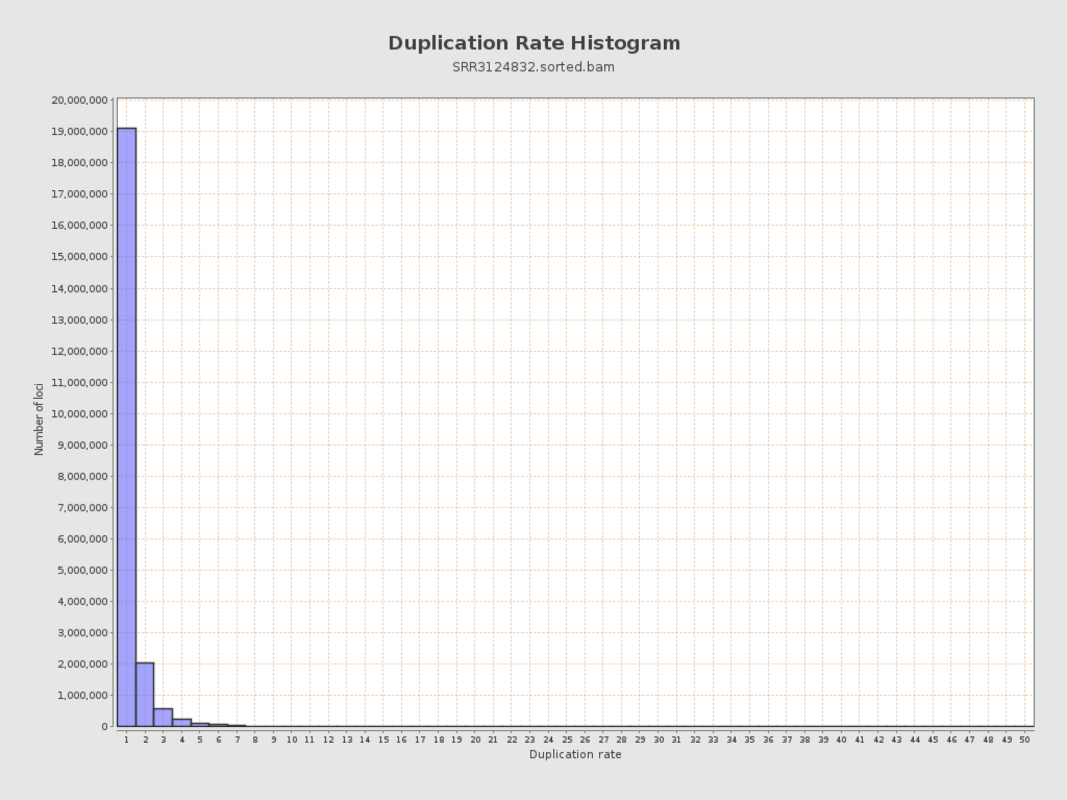
# 5. Results : Coverage Histogram (0-50X)



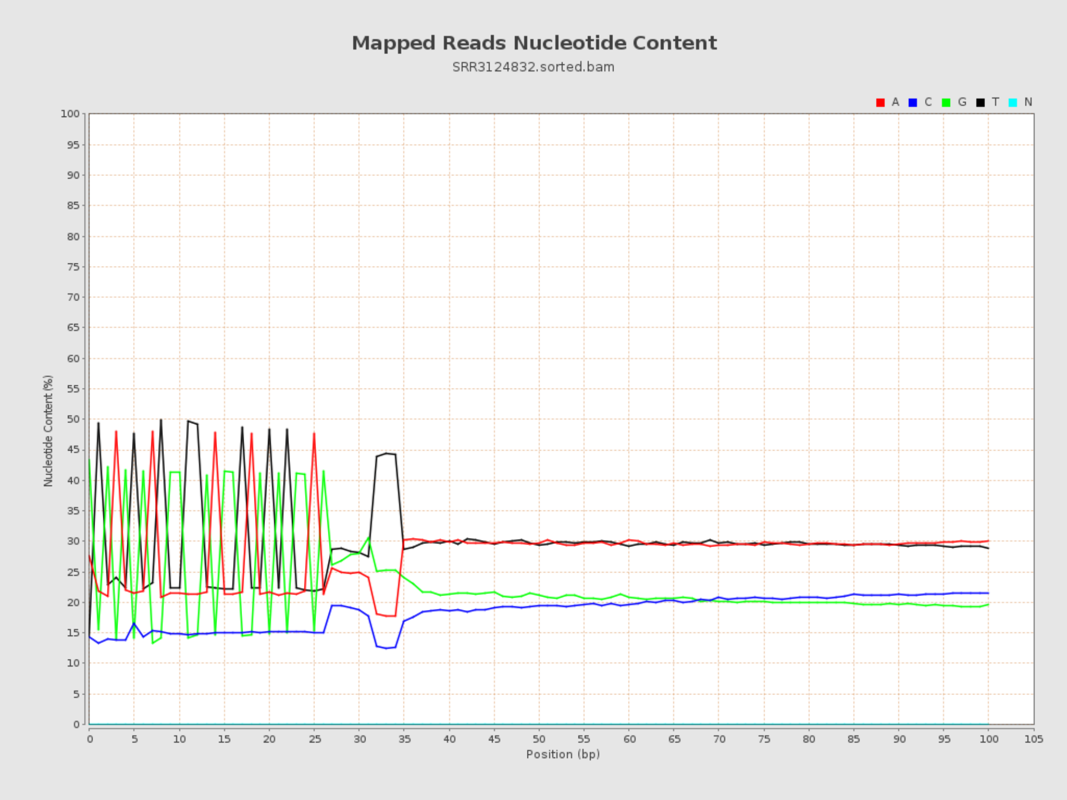
# 6. Results : Genome Fraction Coverage



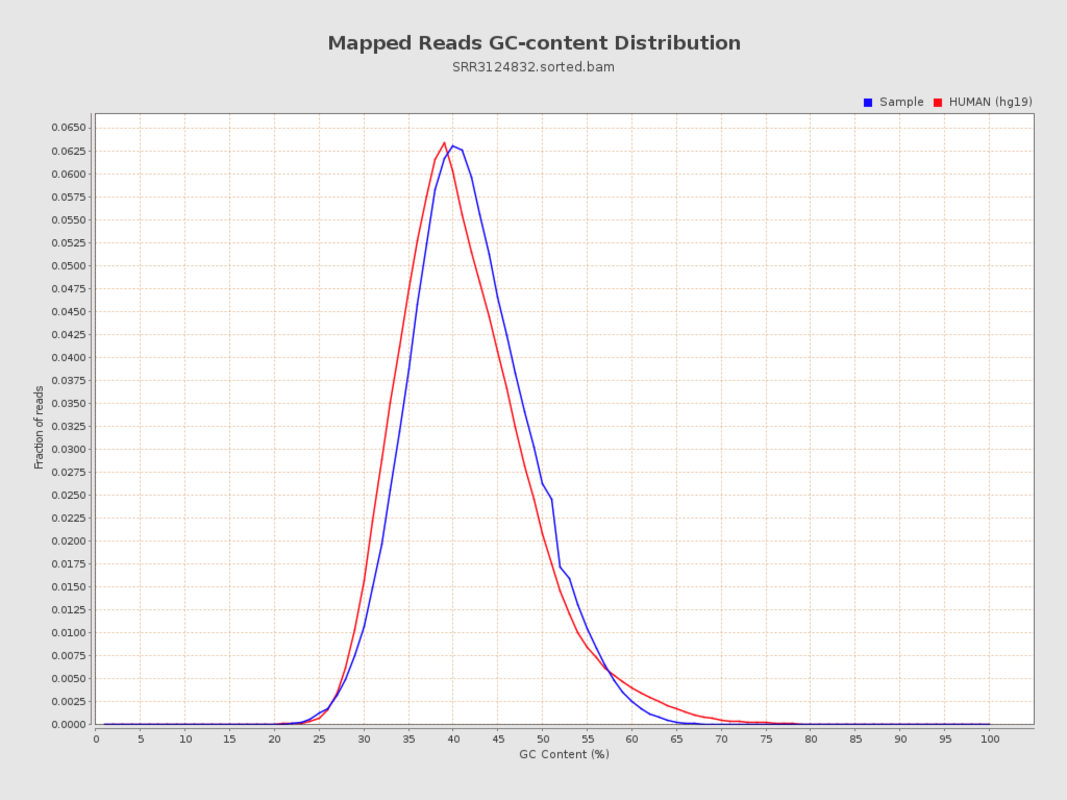
# 7. Results : Duplication Rate Histogram



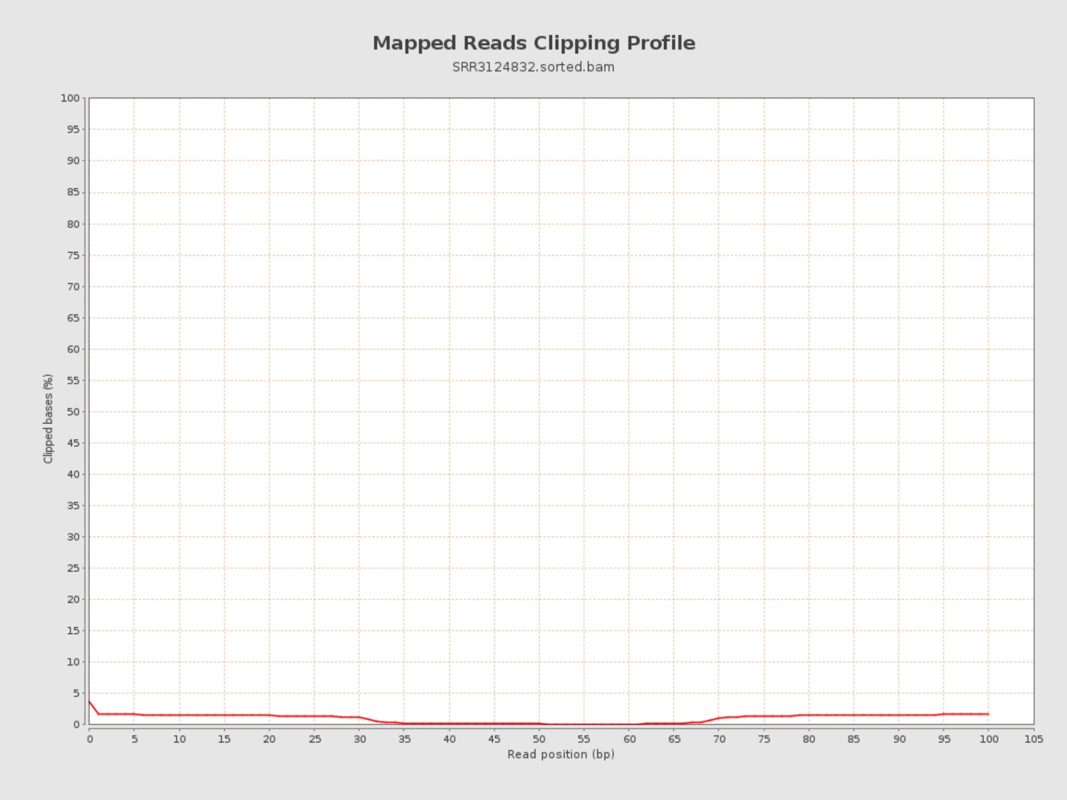
# 8. Results : Mapped Reads Nucleotide Content



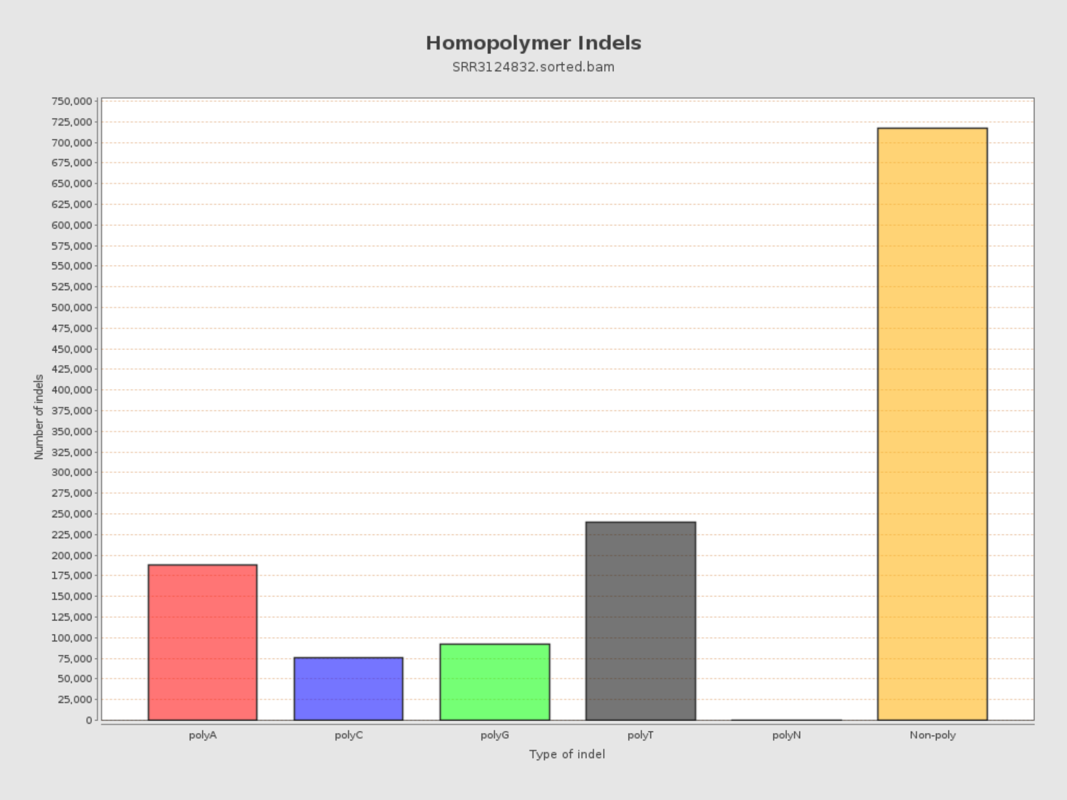
# 9. Results : Mapped Reads GC-content Distribution



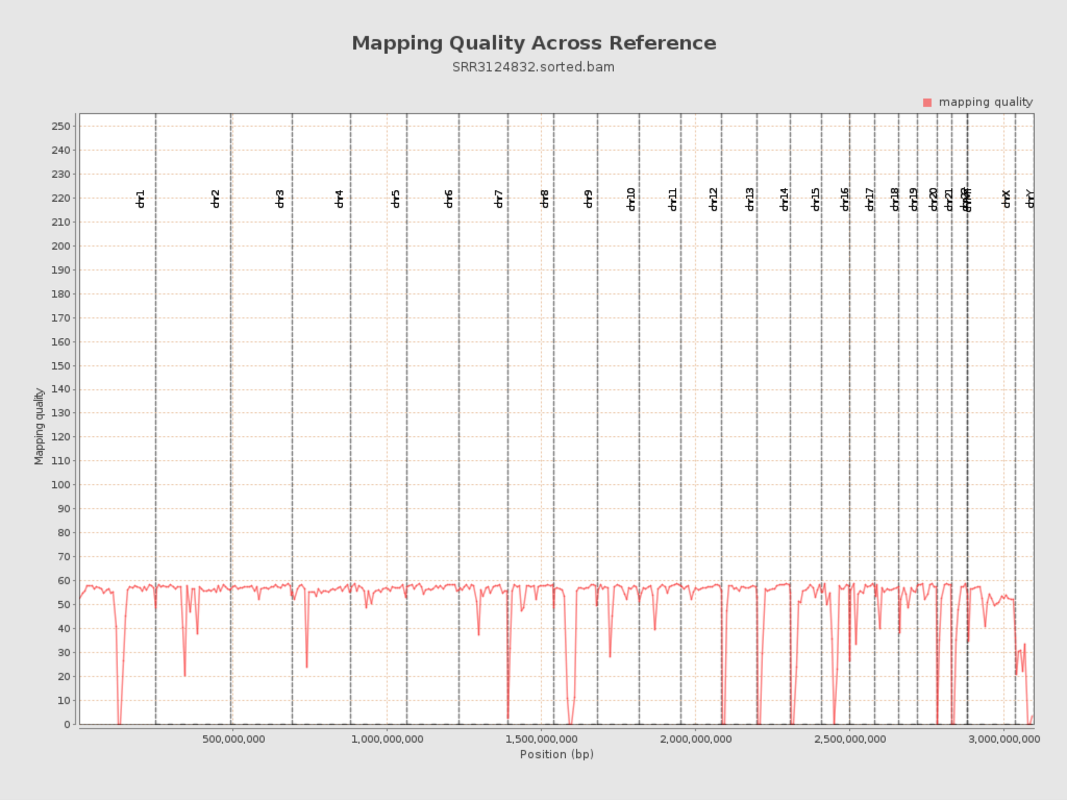
# 10. Results : Mapped Reads Clipping Profile



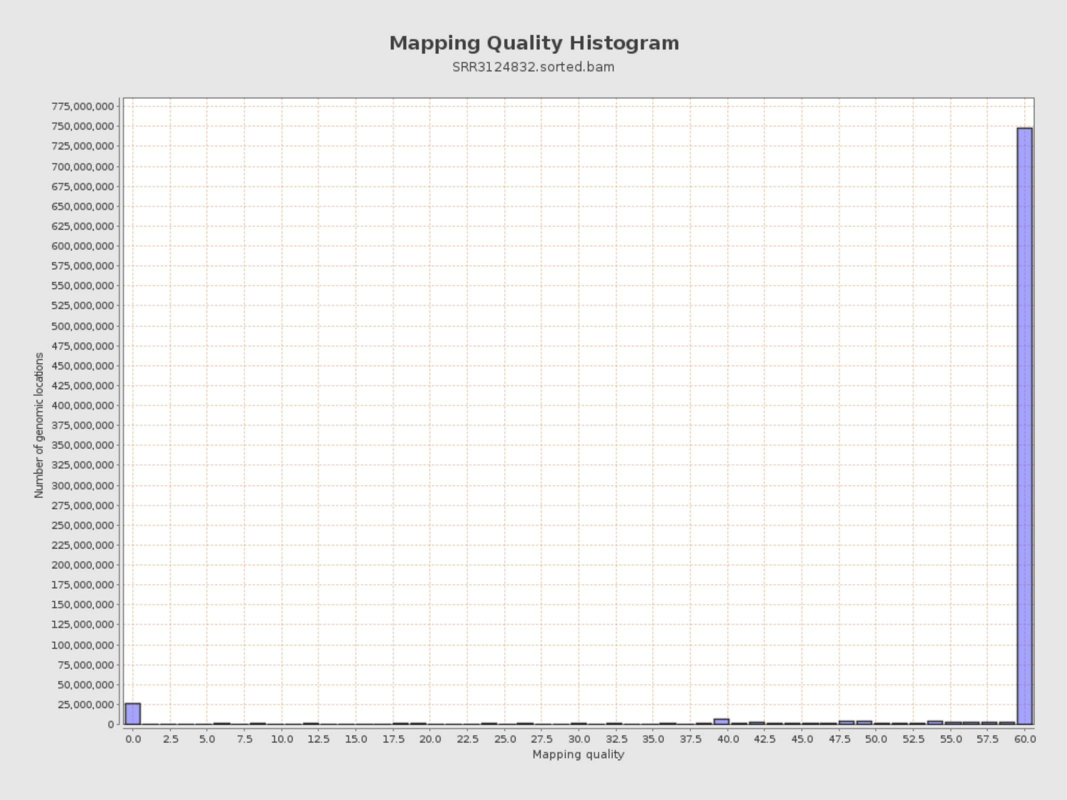
# 11. Results : Homopolymer Indels



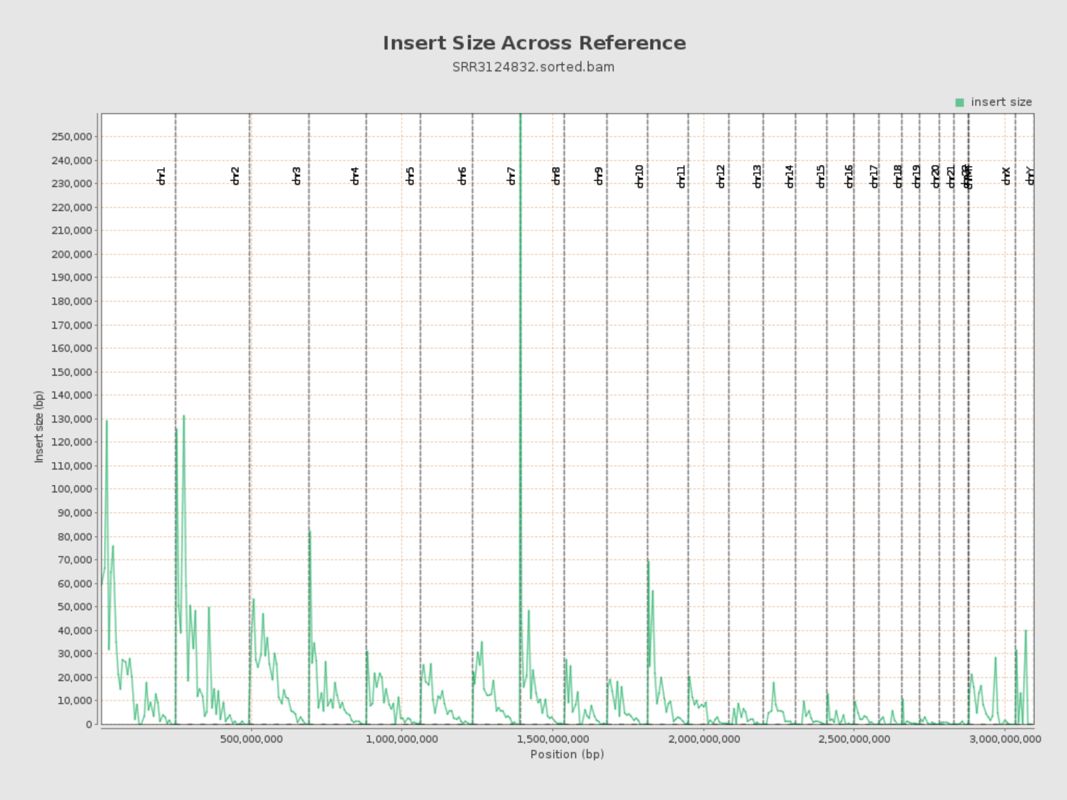
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram