# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/09 23:24:33*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124870.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_SRR3124870 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124870_1.fastq.gz SRR3124870_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Dec 09 23:24:32 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3124870.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,743,698 |
| Mapped reads | 4,674,419 / 98.54% |
| Unmapped reads | 69,279 / 1.46% |
| Mapped paired reads | 4,674,419 / 98.54% |
| Mapped reads, first in pair | 2,340,685 / 49.34% |
| Mapped reads,  second in pair | 2,333,734 / 49.2% |
| Mapped reads, both in pair | 4,660,580 / 98.25% |
| Mapped reads, singletons | 13,839 / 0.29% |
| Secondary alignments | 0 |
| Supplementary alignments | 14,317 / 0.3% |
| Read min/max/mean length | 30 / 101 / 101.12 |
| Duplicated reads (estimated) | 329,092 / 6.94% |
| Duplication rate | 5.23% |
| Clipped reads | 2,148,843 / 45.3% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 114,419,290 / 28.07% |
| Number/percentage of C's | 76,564,685 / 18.78% |
| Number/percentage of T's | 120,635,199 / 29.59% |
| Number/percentage of G's | 96,010,556 / 23.55% |
| Number/percentage of N's | 5,143 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 42.34% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1317 |
| Standard Deviation | 1.0573 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.12 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 23,422.86 |
| Standard Deviation | 1,399,981 |
| P25/Median/P75 | 150 / 196 / 267 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.71% |
| Mismatches | 2,806,411 |
| Insertions | 50,522 |
| Mapped reads with at least one insertion | 1.06% |
| Deletions | 122,800 |
| Mapped reads with at least one deletion | 2.58% |
| Homopolymer indels | 48.91% |

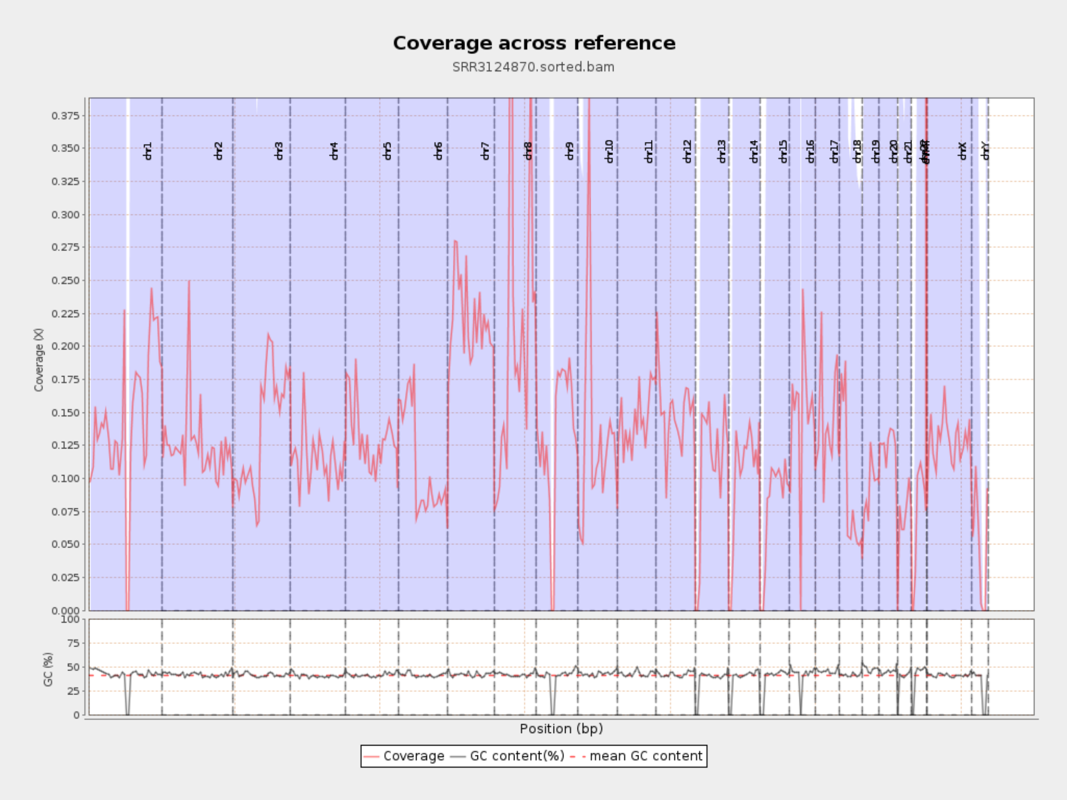
## 2.7. Chromosome stats

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

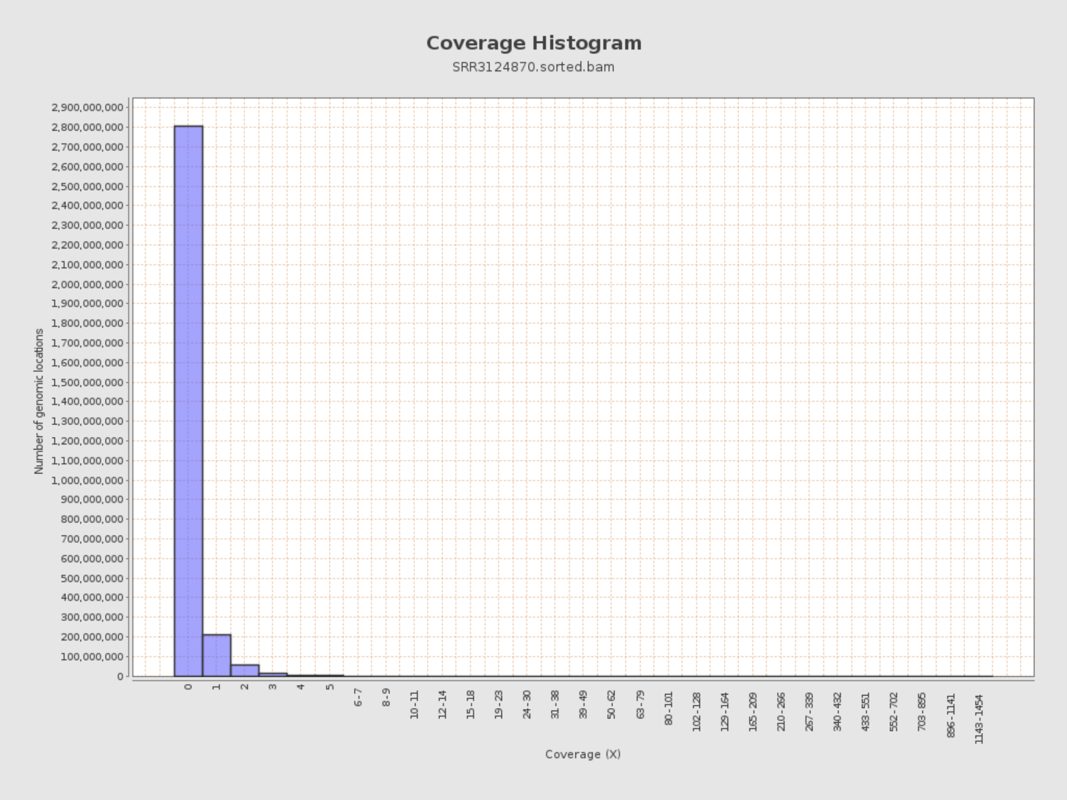
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 35985997 | 0.1444 | 1.4662 |
| chr2 | 243199373 | 30554285 | 0.1256 | 1.0157 |
| chr3 | 198022430 | 26952674 | 0.1361 | 0.4707 |
| chr4 | 191154276 | 21694849 | 0.1135 | 0.6756 |
| chr5 | 180915260 | 23835221 | 0.1317 | 0.4689 |
| chr6 | 171115067 | 18924394 | 0.1106 | 0.6797 |
| chr7 | 159138663 | 35303604 | 0.2218 | 1.8781 |
| chr8 | 146364022 | 31565811 | 0.2157 | 0.8245 |
| chr9 | 141213431 | 18595615 | 0.1317 | 1.2386 |
| chr10 | 135534747 | 17979026 | 0.1327 | 2.2373 |
| chr11 | 135006516 | 19336144 | 0.1432 | 0.8011 |
| chr12 | 133851895 | 20141948 | 0.1505 | 0.502 |
| chr13 | 115169878 | 12562537 | 0.1091 | 0.4187 |
| chr14 | 107349540 | 10702886 | 0.0997 | 0.4309 |
| chr15 | 102531392 | 8173319 | 0.0797 | 0.3608 |
| chr16 | 90354753 | 13386089 | 0.1482 | 1.1332 |
| chr17 | 81195210 | 11587739 | 0.1427 | 1.8676 |
| chr18 | 78077248 | 7444540 | 0.0953 | 1.2386 |
| chr19 | 59128983 | 5444556 | 0.0921 | 0.9008 |
| chr20 | 63025520 | 7871891 | 0.1249 | 0.4676 |
| chr21 | 48129895 | 3367928 | 0.07 | 0.4242 |
| chr22 | 51304566 | 3520085 | 0.0686 | 0.3371 |
| chrMT | 16571 | 134991 | 8.1462 | 6.0293 |
| chrX | 155270560 | 19950693 | 0.1285 | 0.5988 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 2817134 | 0.0474 | 0.7956 |

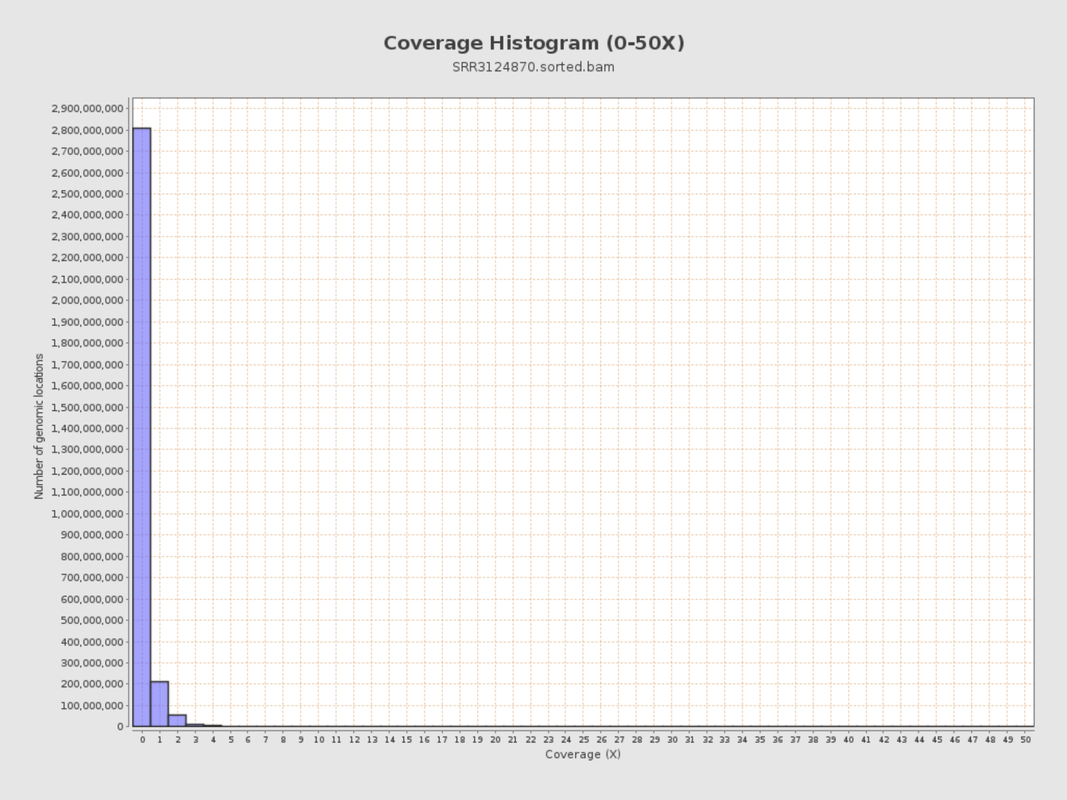
# 3. Results : Coverage across reference



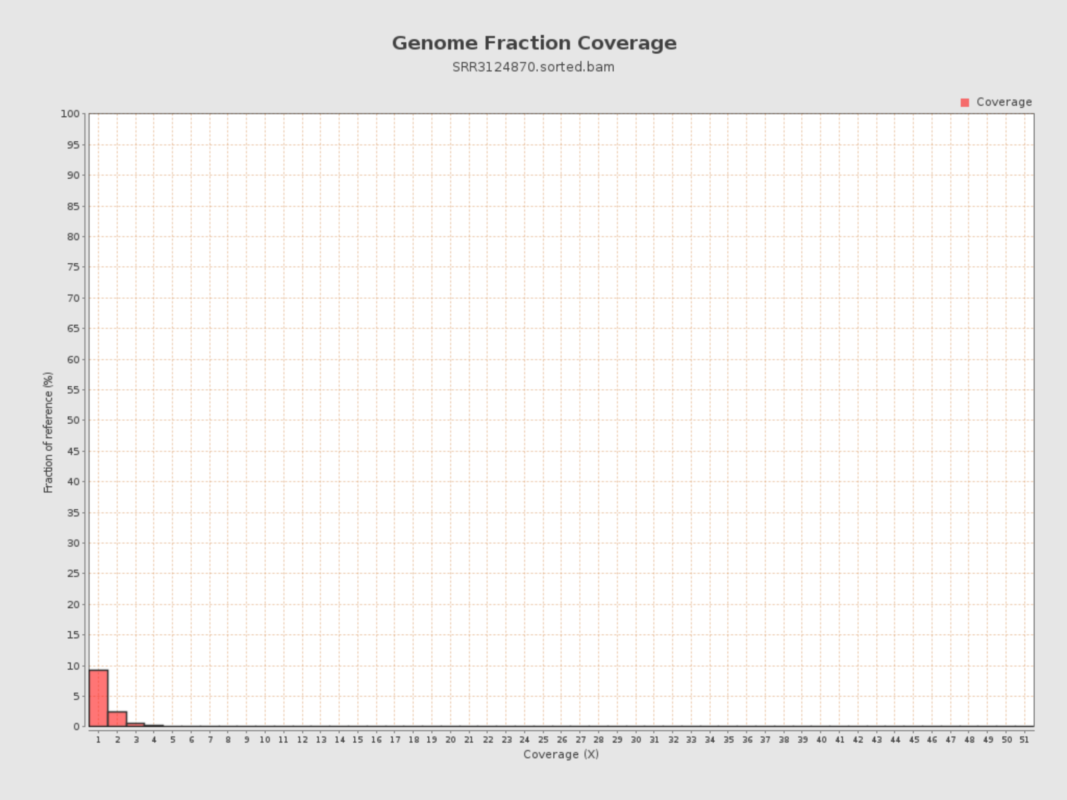
# 4. Results : Coverage Histogram



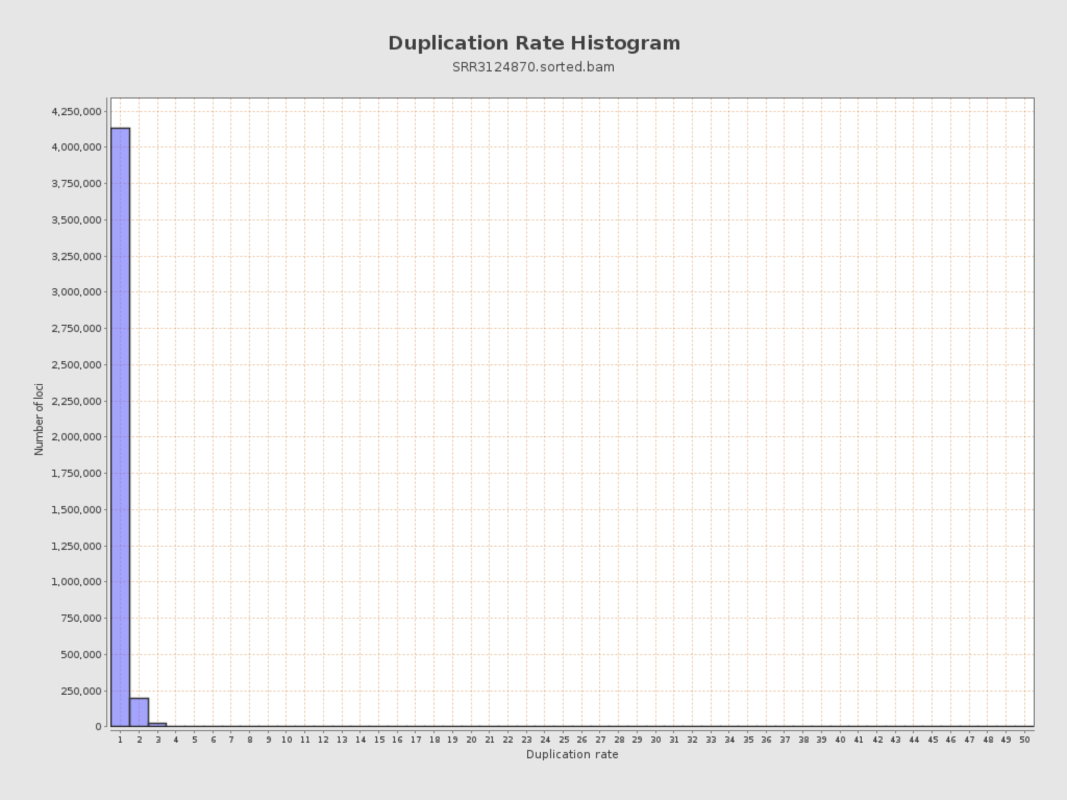
# 5. Results : Coverage Histogram (0-50X)



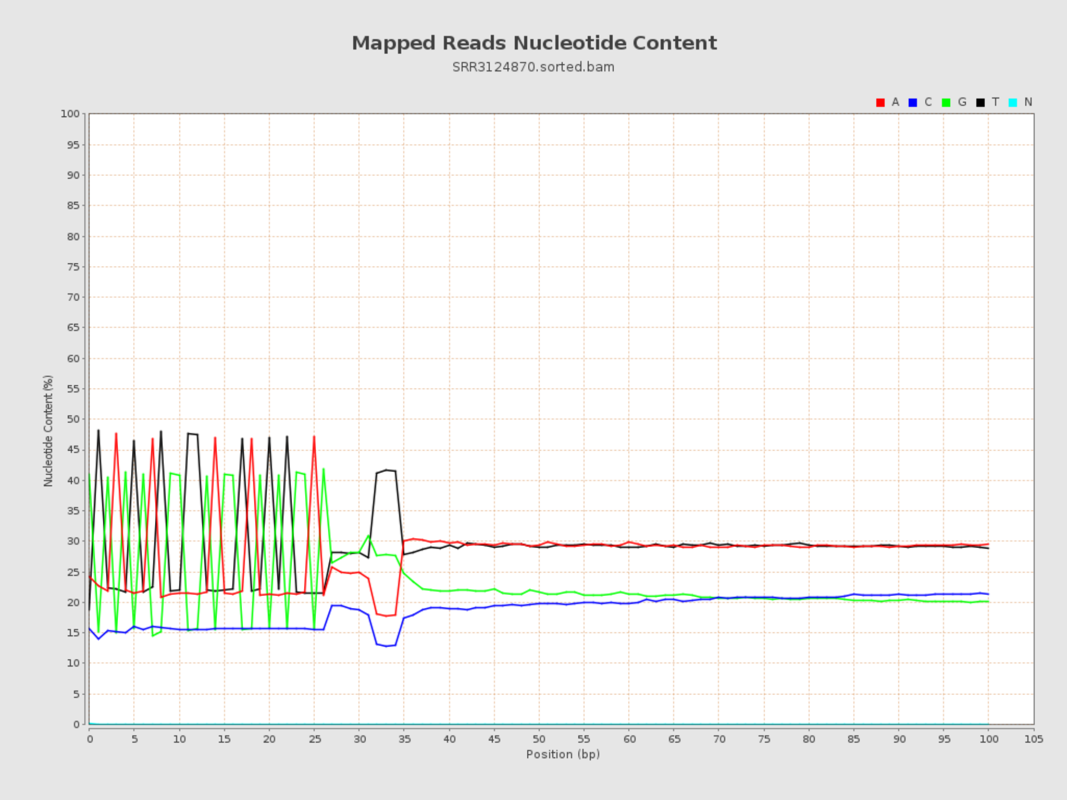
# 6. Results : Genome Fraction Coverage



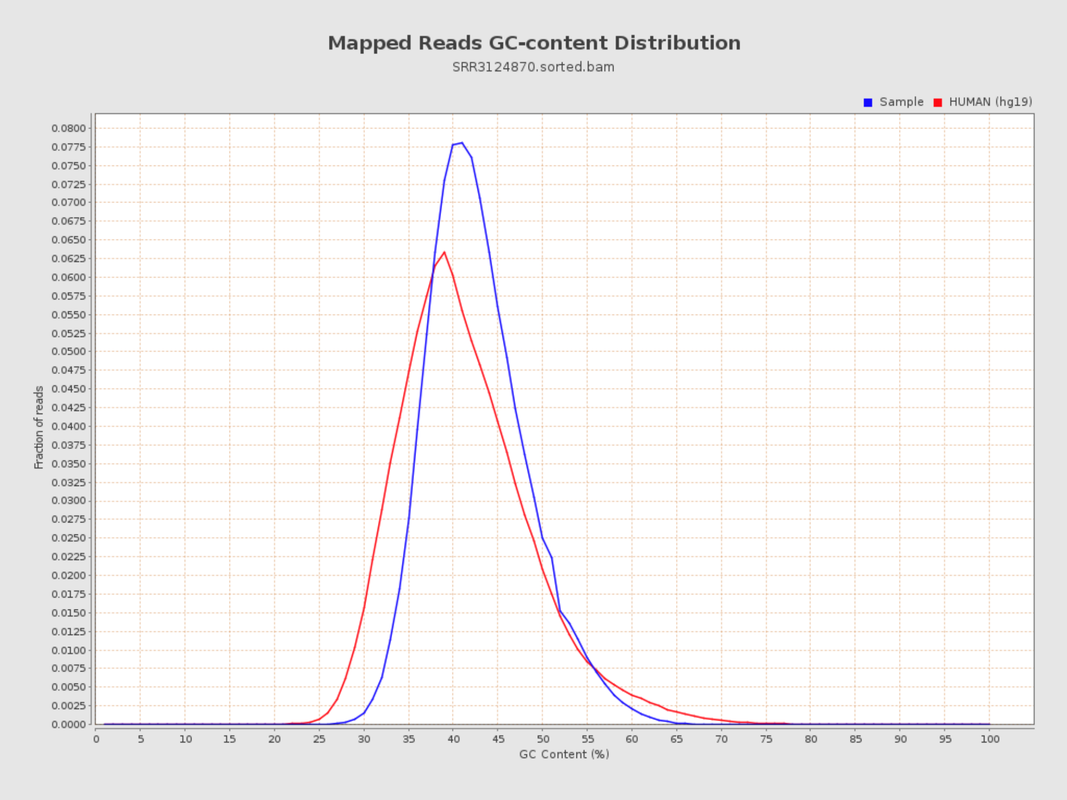
# 7. Results : Duplication Rate Histogram



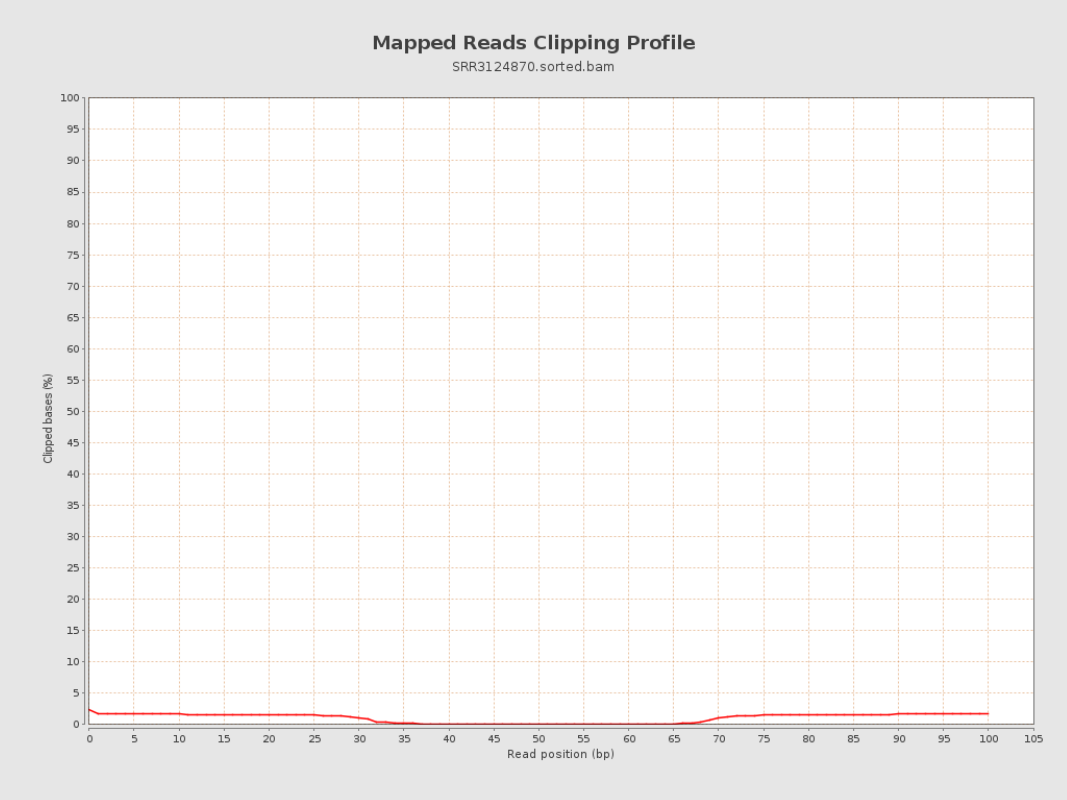
# 8. Results : Mapped Reads Nucleotide Content



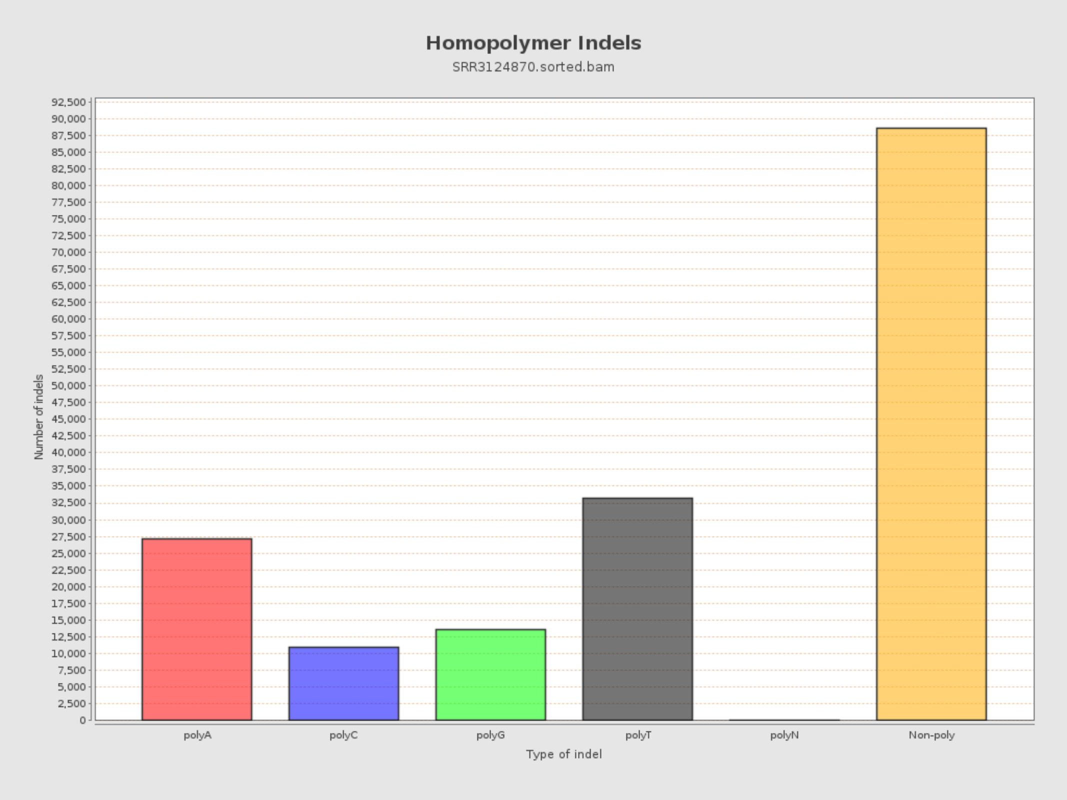
# 9. Results : Mapped Reads GC-content Distribution



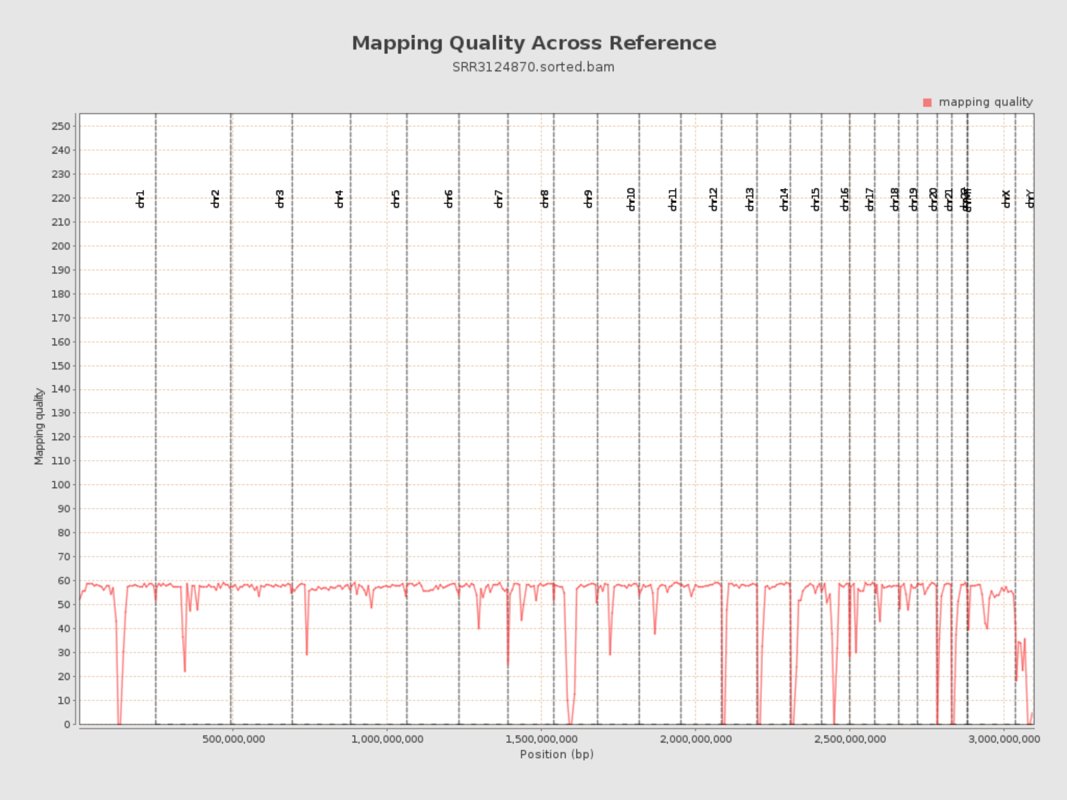
# 10. Results : Mapped Reads Clipping Profile



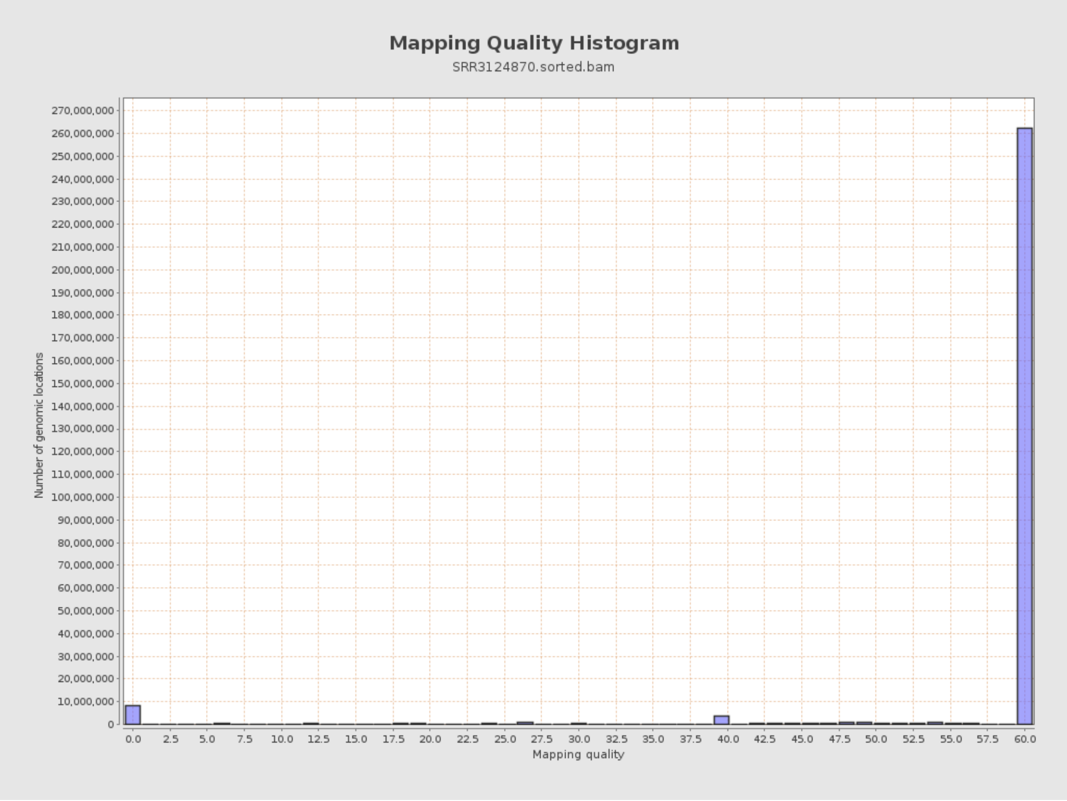
# 11. Results : Homopolymer Indels



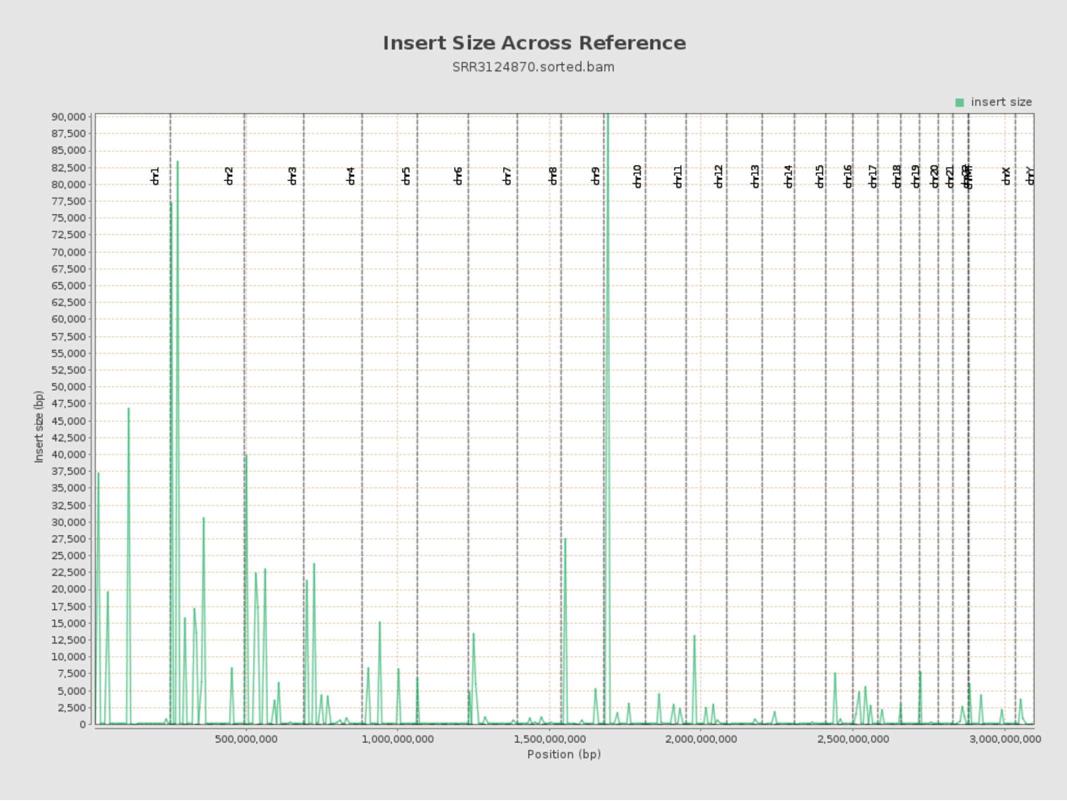
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram