# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/24 08:23:17*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR927022.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_SRR927022 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927022_1.fastq.gz SRR927022_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Apr 24 08:23:16 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR927022.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 8,853,220 |
| Mapped reads | 8,678,980 / 98.03% |
| Unmapped reads | 174,240 / 1.97% |
| Mapped paired reads | 8,678,980 / 98.03% |
| Mapped reads, first in pair | 4,349,169 / 49.13% |
| Mapped reads, second in pair | 4,329,811 / 48.91% |
| Mapped reads, both in pair | 8,569,154 / 96.79% |
| Mapped reads, singletons | 109,826 / 1.24% |
| Secondary alignments | 0 |
| Supplementary alignments | 263,846 / 2.98% |
| Read min/max/mean length | 30 / 101 / 102.25 |
| Duplicated reads (estimated) | 432,834 / 4.89% |
| Duplication rate | 3.87% |
| Clipped reads | 3,501,341 / 39.55% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 227,922,227 / 28.61% |
| Number/percentage of C's | 155,547,617 / 19.53% |
| Number/percentage of T's | 232,402,007 / 29.17% |
| Number/percentage of G's | 180,602,223 / 22.67% |
| Number/percentage of N's | 152,772 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 42.2% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.2575 |
| Standard Deviation | 1.3615 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 52.29 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 355,254.16 |
| Standard Deviation | 5,867,915.6 |
| P25/Median/P75 | 144 / 187 / 250 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.98% |
| Mismatches | 7,599,882 |
| Insertions | 140,359 |
| Mapped reads with at least one insertion | 1.59% |
| Deletions | 415,679 |
| Mapped reads with at least one deletion | 4.67% |
| Homopolymer indels | 51.74% |

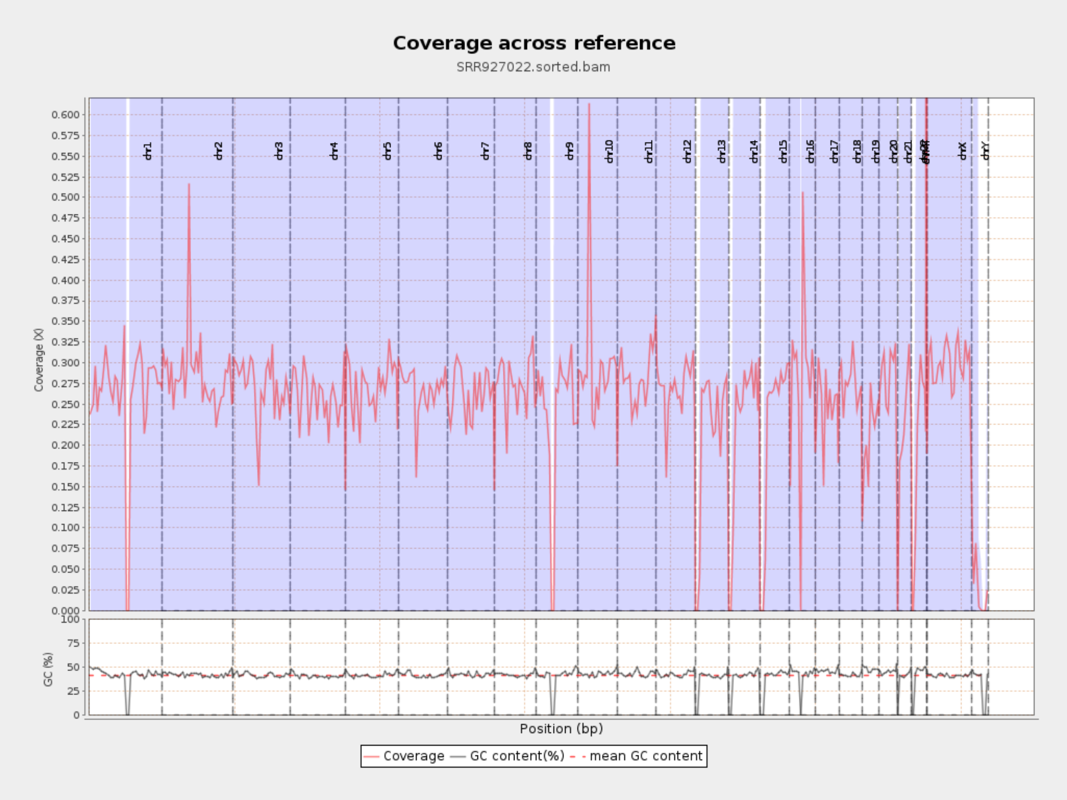
## 2.7. Chromosome stats

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

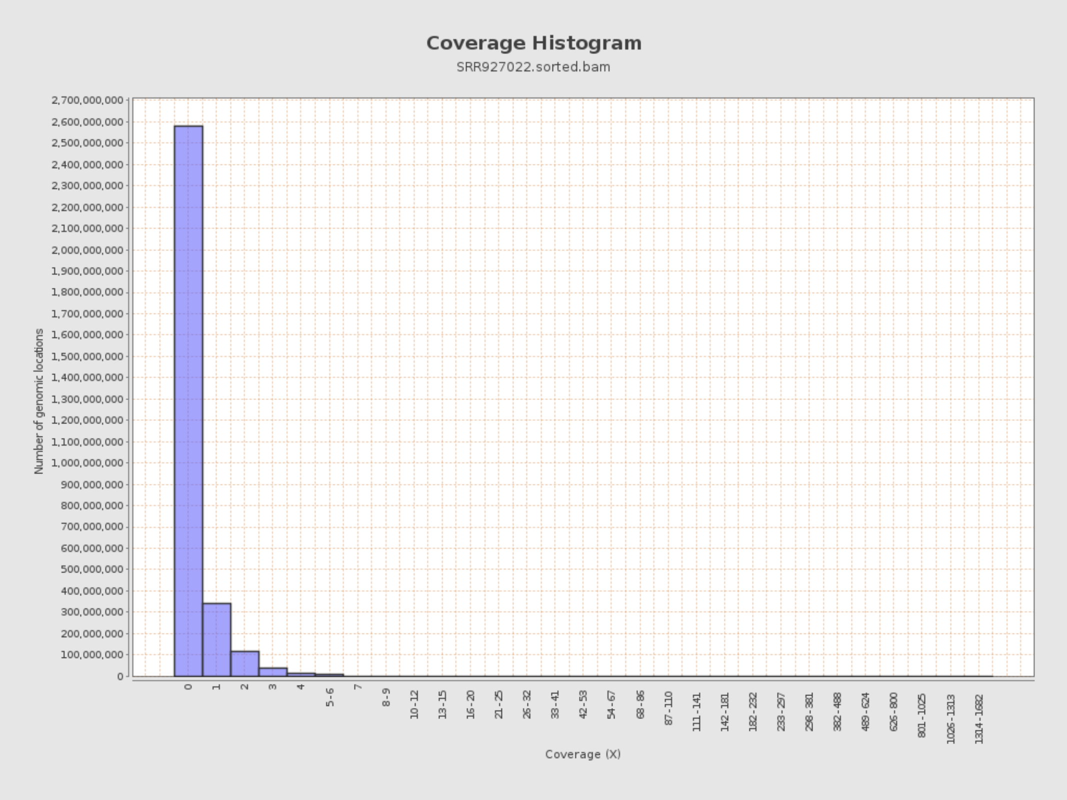
|  |  | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 64897790 | 0.2604 | 1.9092 |
| chr2 | 243199373 | 69747531 | 0.2868 | 1.7868 |
| chr3 | 198022430 | 53533983 | 0.2703 | 0.7248 |
| chr4 | 191154276 | 49404762 | 0.2585 | 0.9603 |
| chr5 | 180915260 | 48938601 | 0.2705 | 0.6994 |
| chr6 | 171115067 | 45900858 | 0.2682 | 0.7859 |
| chr7 | 159138663 | 41915390 | 0.2634 | 0.9635 |
| chr8 | 146364022 | 40433475 | 0.2763 | 0.8194 |
| chr9 | 141213431 | 33347743 | 0.2362 | 1.5204 |
| chr10 | 135534747 | 40334958 | 0.2976 | 3.3896 |
| chr11 | 135006516 | 37729400 | 0.2795 | 1.514 |
| chr12 | 133851895 | 36040485 | 0.2693 | 0.7069 |
| chr13 | 115169878 | 24062695 | 0.2089 | 0.6115 |
| chr14 | 107349540 | 23875655 | 0.2224 | 0.6519 |
| chr15 | 102531392 | 22551832 | 0.22 | 0.6423 |
| chr16 | 90354753 | 25246974 | 0.2794 | 1.9424 |
| chr17 | 81195210 | 19918407 | 0.2453 | 0.7952 |
| chr18 | 78077248 | 21571531 | 0.2763 | 1.6574 |
| chr19 | 59128983 | 12585041 | 0.2128 | 1.202 |
| chr20 | 63025520 | 17862663 | 0.2834 | 0.7513 |
| chr21 | 48129895 | 10380143 | 0.2157 | 0.8308 |
| chr22 | 51304566 | 9441743 | 0.184 | 0.6078 |
| chrMT | 16571 | 75508 | 4.5566 | 4.3959 |
| chrX | 155270560 | 45973252 | 0.2961 | 0.8643 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1469726 | 0.0248 | 0.8206 |

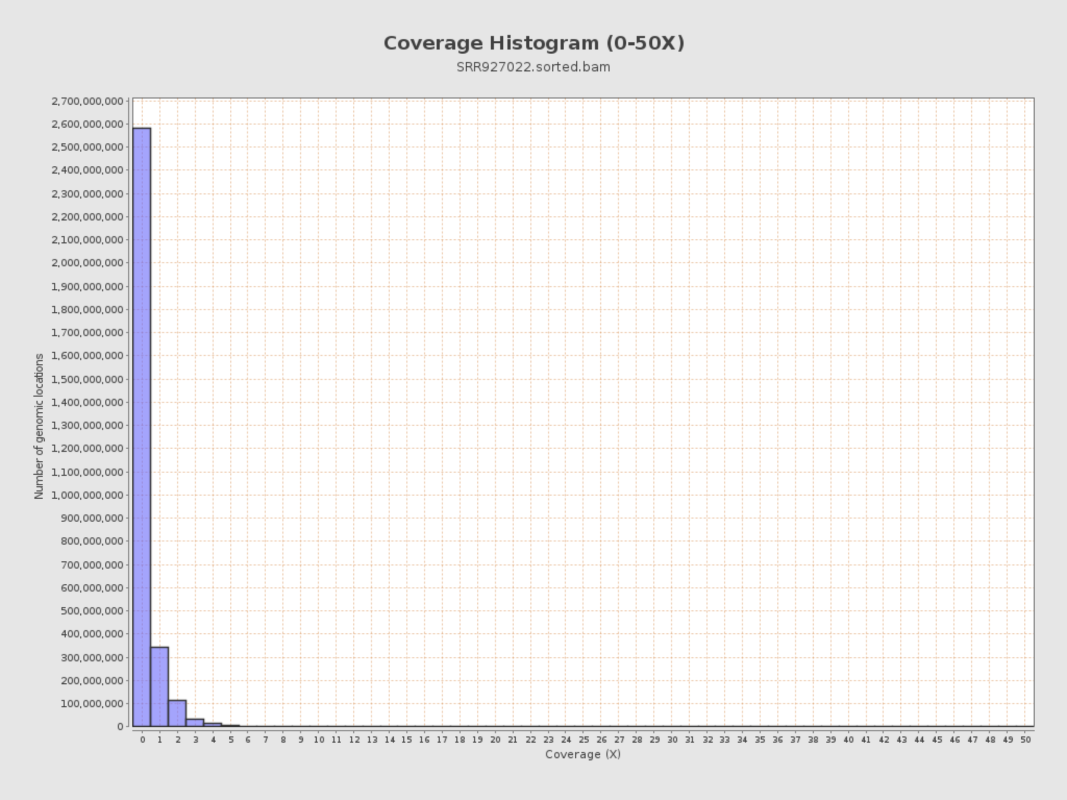
# 3. Results : Coverage across reference



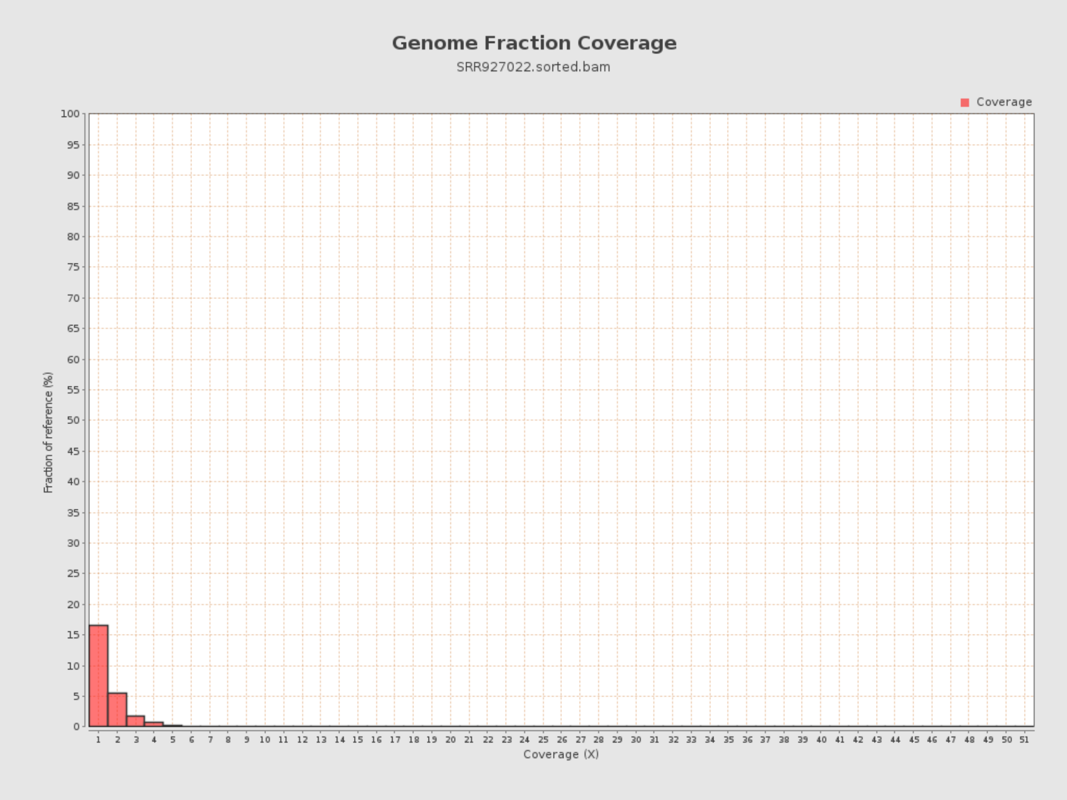
# 4. Results : Coverage Histogram



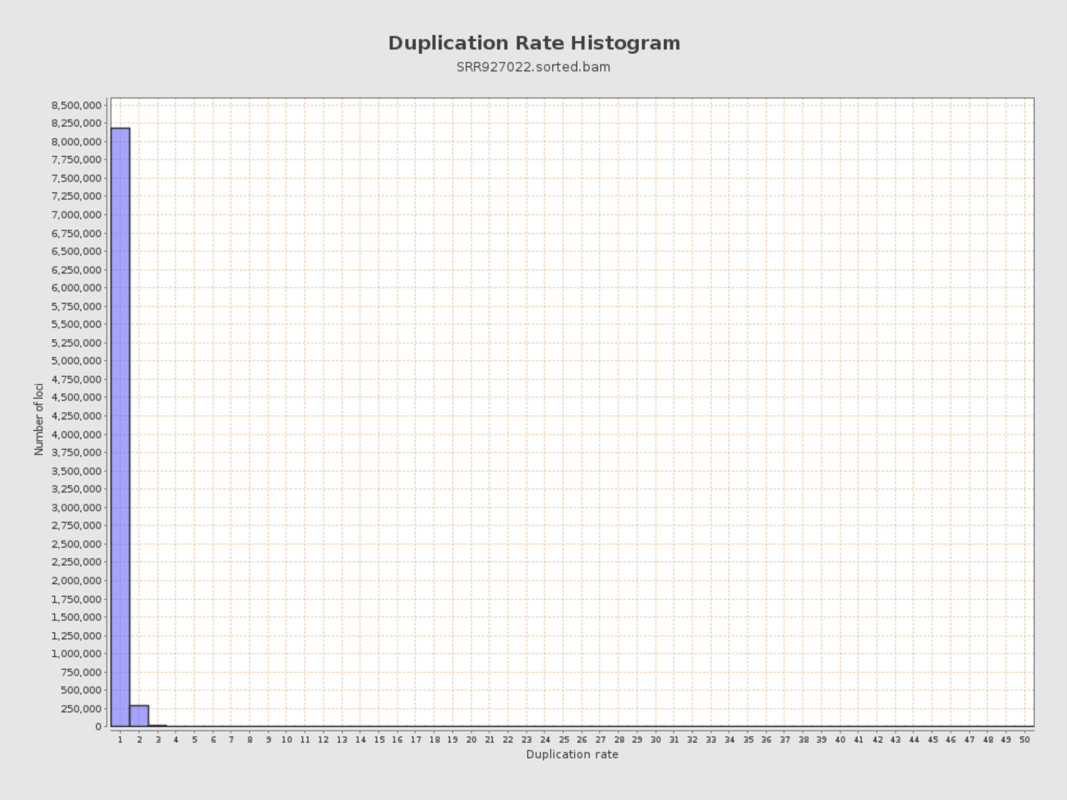
# 5. Results : Coverage Histogram (0-50X)



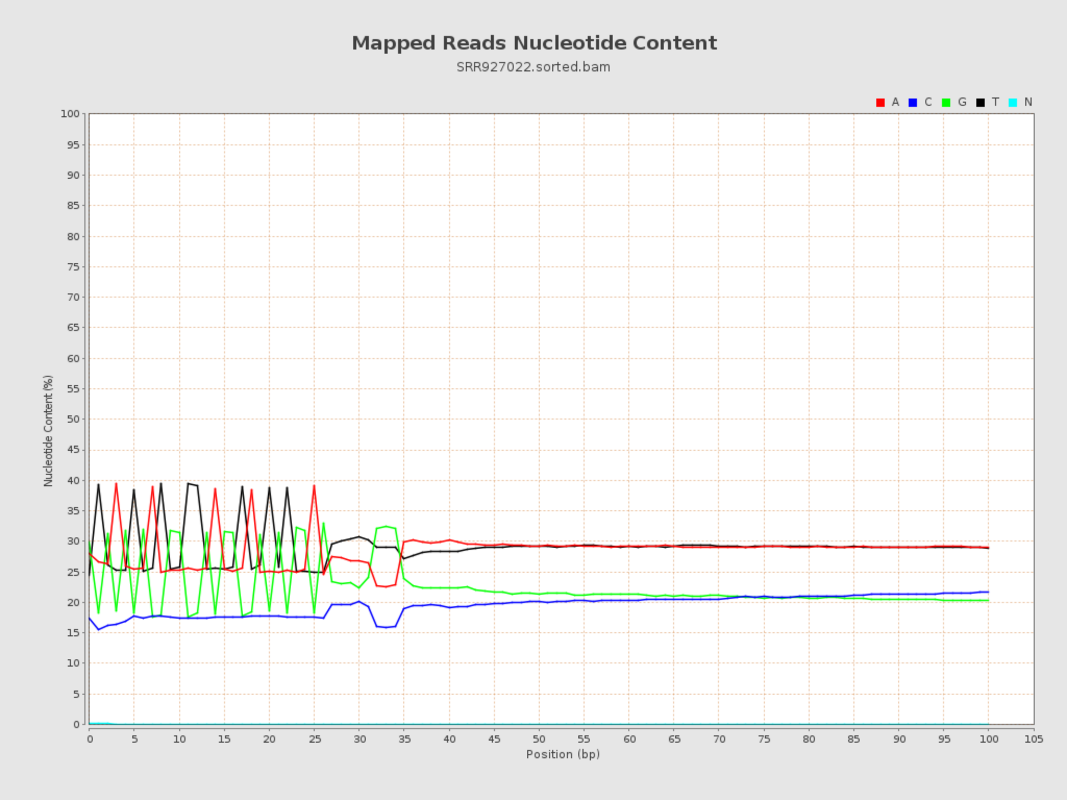
# 6. Results : Genome Fraction Coverage



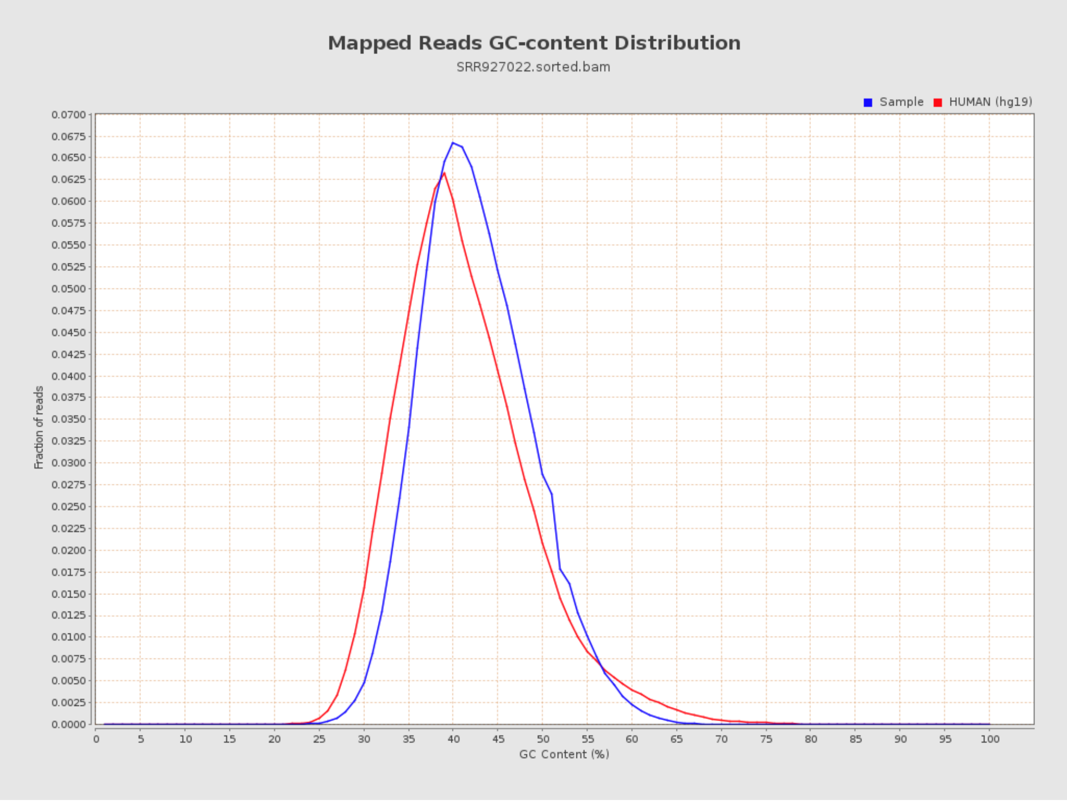
# 7. Results : Duplication Rate Histogram



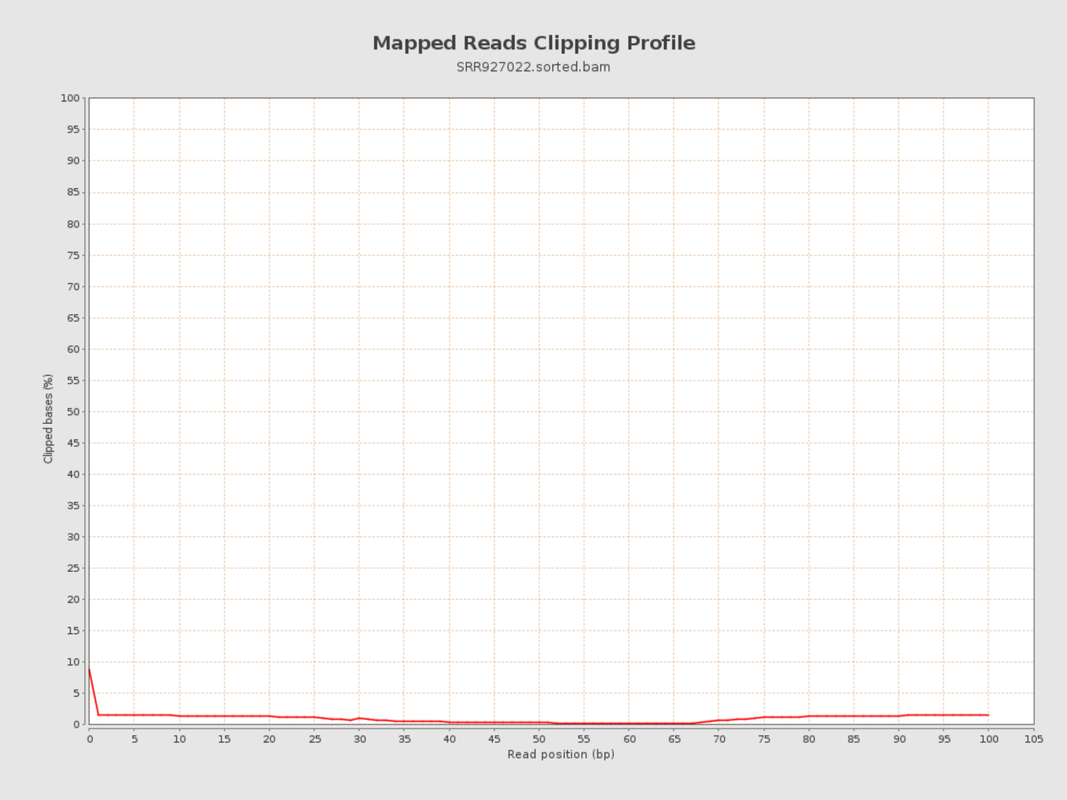
# 8. Results : Mapped Reads Nucleotide Content



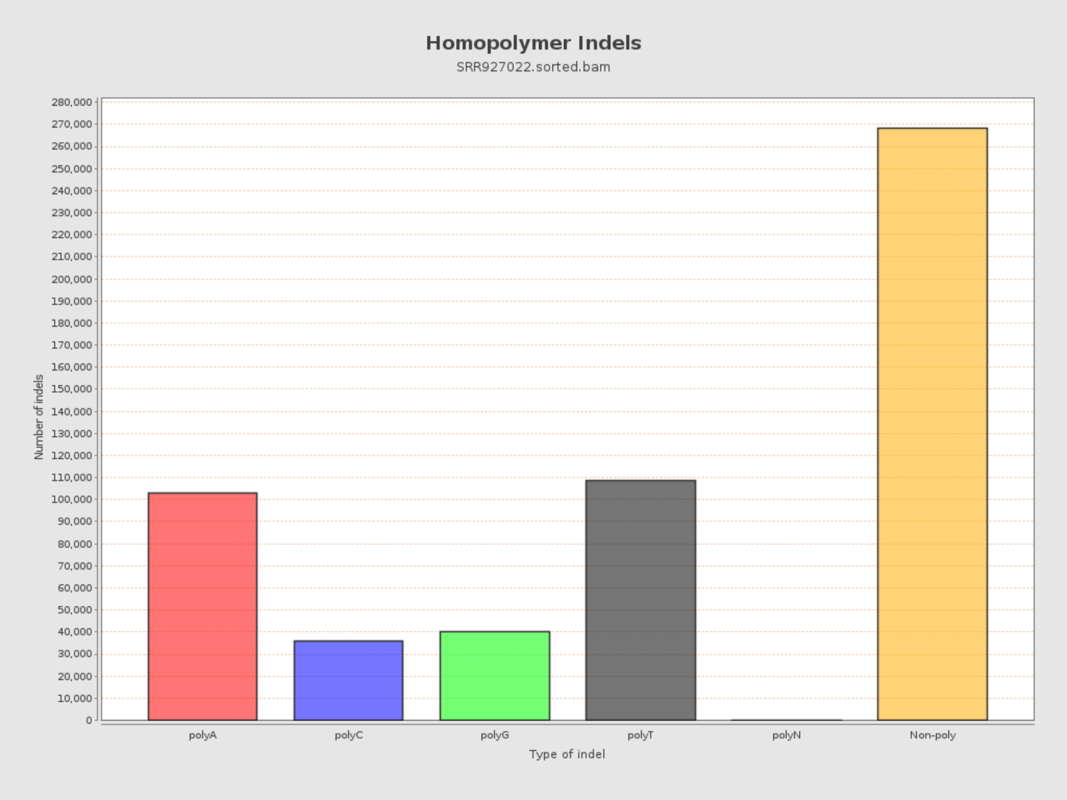
# 9. Results : Mapped Reads GC-content Distribution



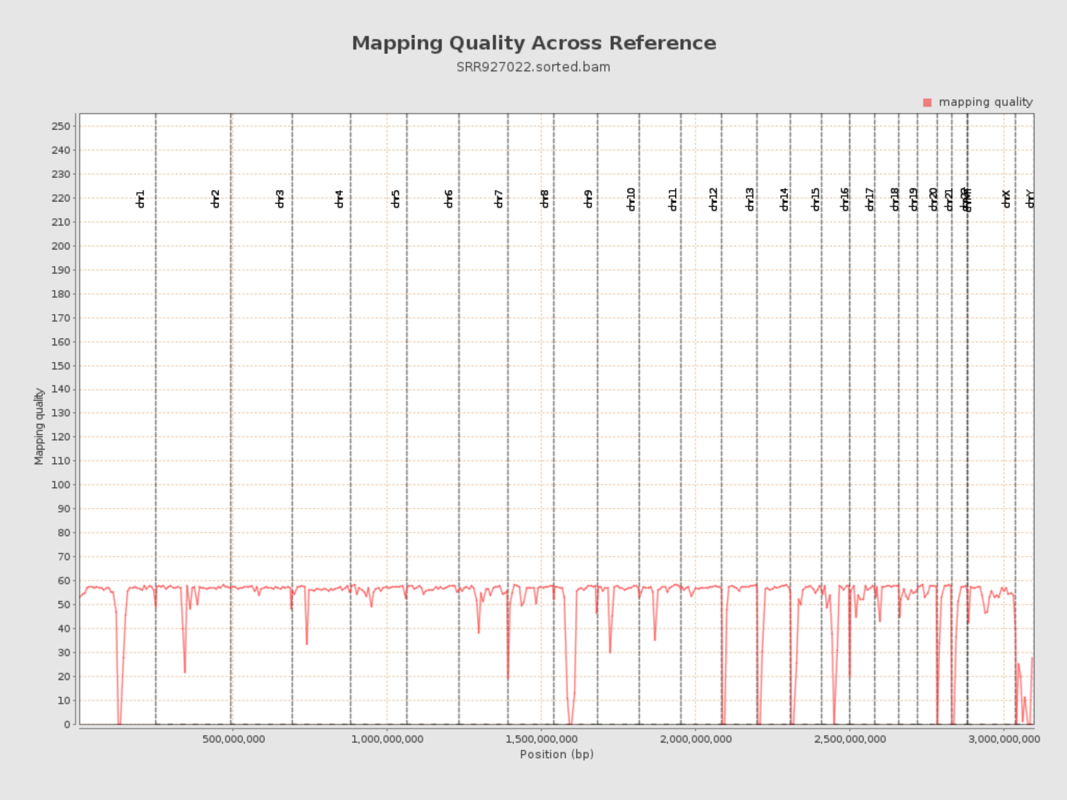
# 10. Results : Mapped Reads Clipping Profile



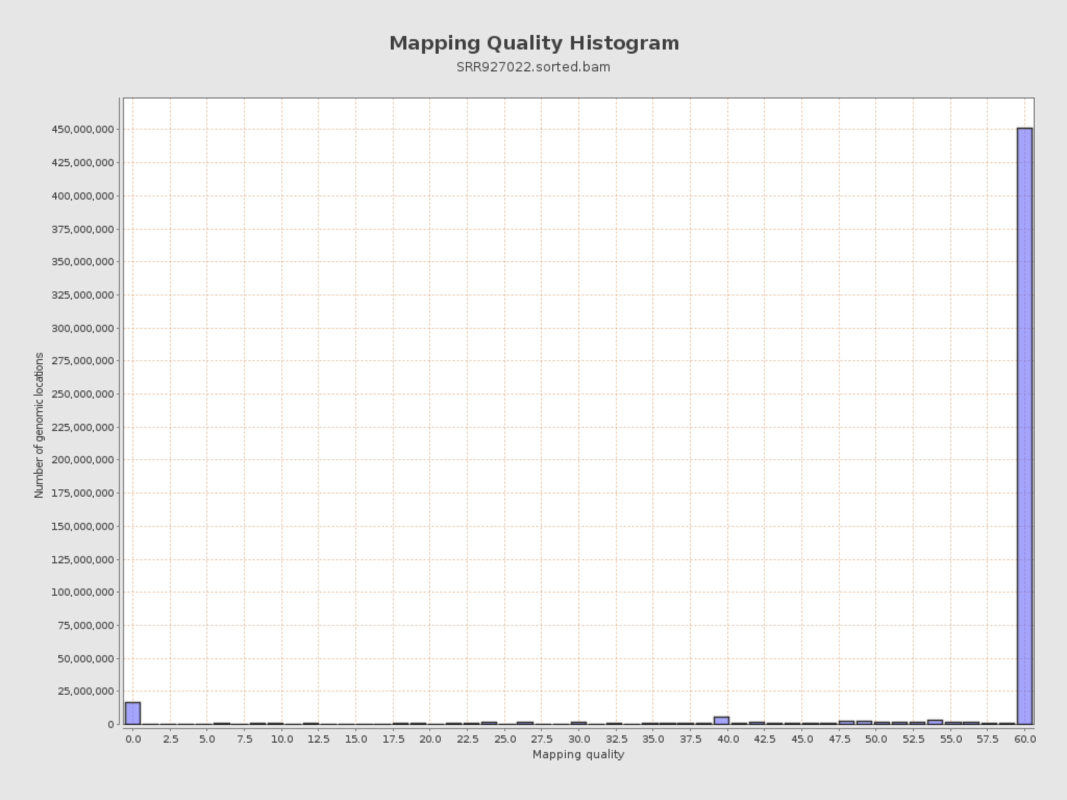
# 11. Results : Homopolymer Indels



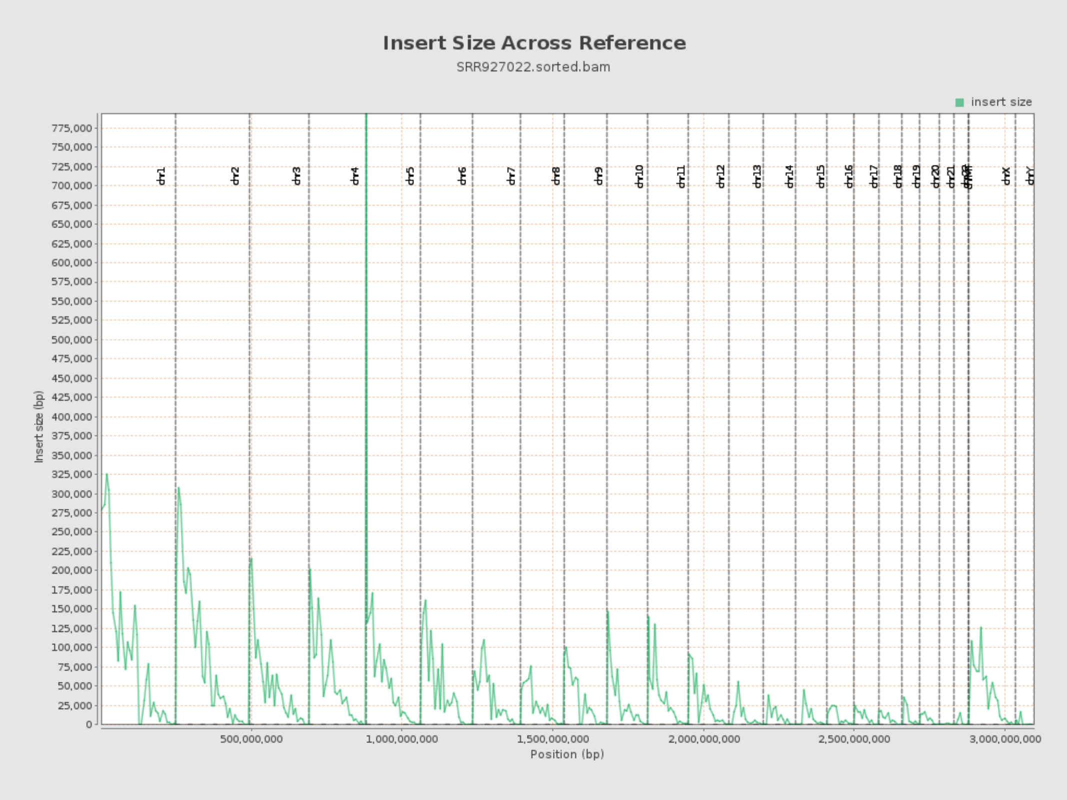
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram