# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/25 07:39:40*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR927067.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_SRR927067 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927067_1.fastq.gz SRR927067_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Apr 25 07:39:39 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR927067.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 28,984,800 |
| Mapped reads | 28,354,068 / 97.82% |
| Unmapped reads | 630,732 / 2.18% |
| Mapped paired reads | 28,354,068 / 97.82% |
| Mapped reads, first in pair | 14,227,667 / 49.09% |
| Mapped reads, second in pair | 14,126,401 / 48.74% |
| Mapped reads, both in pair | 28,053,616 / 96.79% |
| Mapped reads, singletons | 300,452 / 1.04% |
| Secondary alignments | 0 |
| Supplementary alignments | 519,020 / 1.79% |
| Read min/max/mean length | 30 / 101 / 101.74 |
| Duplicated reads (estimated) | 2,054,009 / 7.09% |
| Duplication rate | 5.62% |
| Clipped reads | 7,349,805 / 25.36% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 776,565,609 / 28.84% |
| Number/percentage of C's | 538,918,867 / 20.01% |
| Number/percentage of T's | 782,403,719 / 29.05% |
| Number/percentage of G's | 594,927,186 / 22.09% |
| Number/percentage of N's | 190,235 / 0.01% |
| | |

| | |
|---|---|
| GC Percentage | 42.1% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.8706 |
| Standard Deviation | 3.5599 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.36 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 185,072.05 |
| Standard Deviation | 4,216,335.66 |
| P25/Median/P75 | 147 / 188 / 251 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.98% |
| Mismatches | 25,557,301 |
| Insertions | 451,240 |
| Mapped reads with at least one insertion | 1.56% |
| Deletions | 1,418,114 |
| Mapped reads with at least one deletion | 4.87% |
| Homopolymer indels | 52.66% |

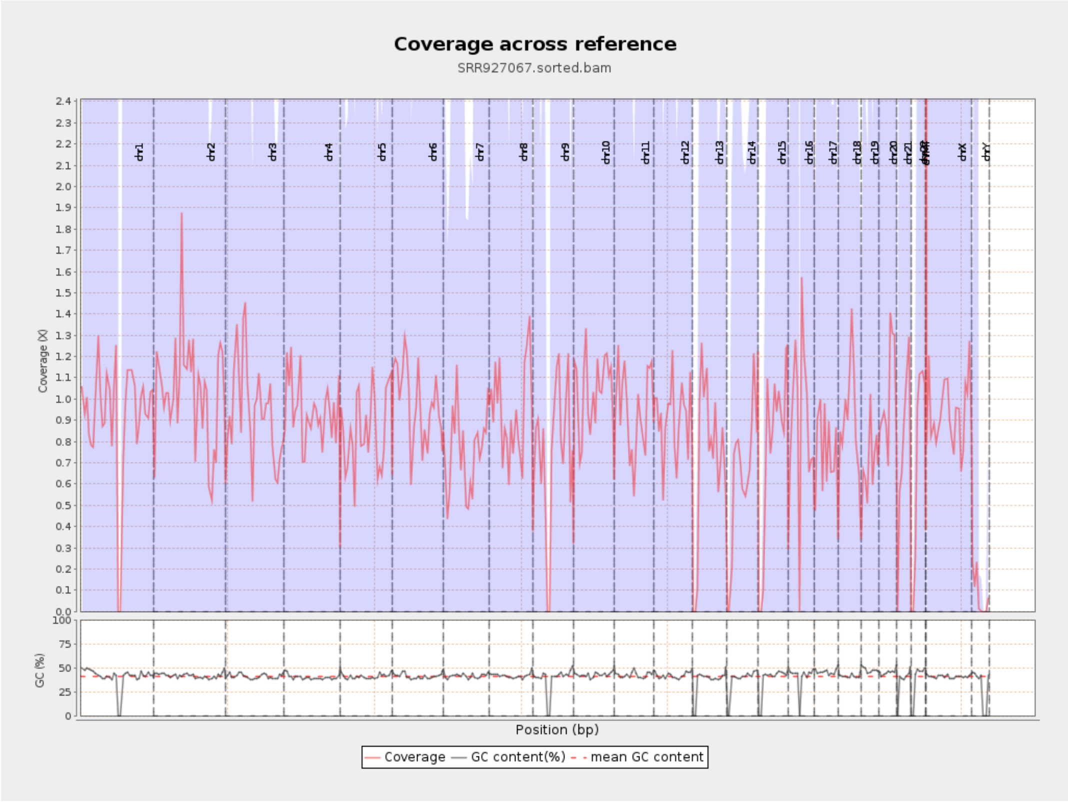
## 2.7. Chromosome stats

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

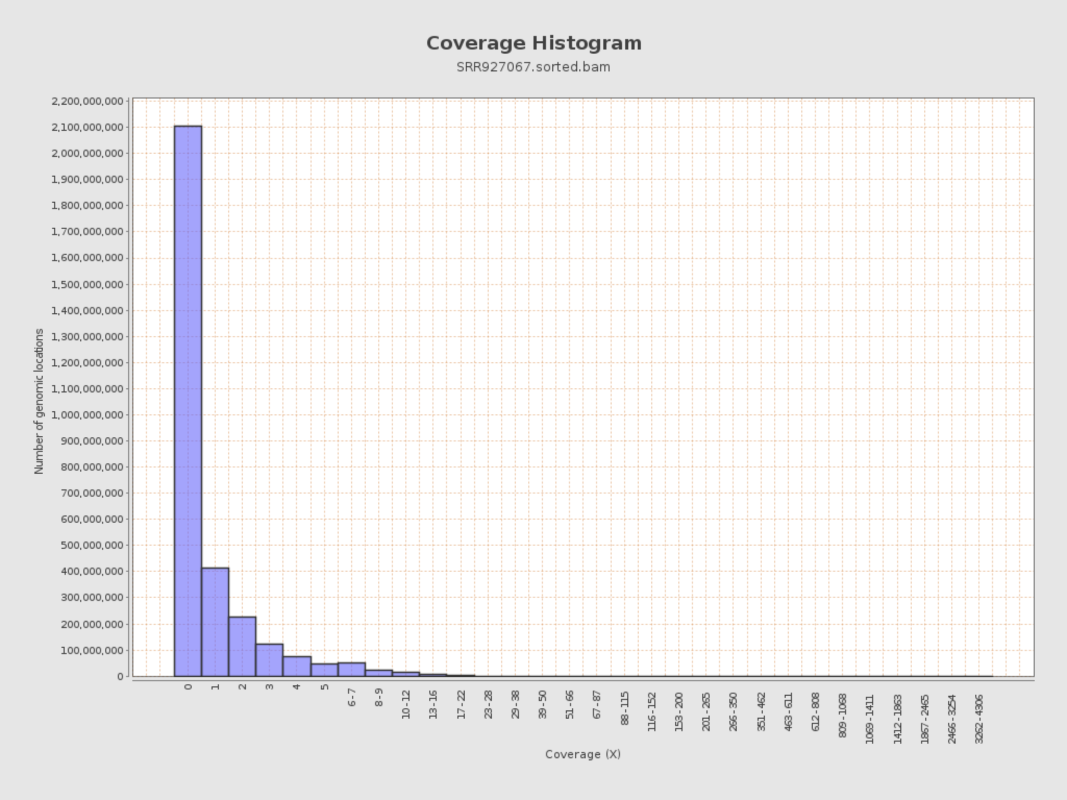
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 230021048 | 0.9229 | 4.9224 |
| chr2 | 243199373 | 253682368 | 1.0431 | 6.5371 |
| chr3 | 198022430 | 186085366 | 0.9397 | 1.9689 |
| chr4 | 191154276 | 180697256 | 0.9453 | 3.0273 |
| chr5 | 180915260 | 153687774 | 0.8495 | 1.8547 |
| chr6 | 171115067 | 168859270 | 0.9868 | 2.067 |
| chr7 | 159138663 | 119790718 | 0.7527 | 2.6753 |
| chr8 | 146364022 | 136913154 | 0.9354 | 2.1925 |
| chr9 | 141213431 | 105121899 | 0.7444 | 4.0246 |
| chr10 | 135534747 | 141436556 | 1.0435 | 4.4059 |
| chr11 | 135006516 | 126536114 | 0.9373 | 3.0497 |
| chr12 | 133851895 | 121203659 | 0.9055 | 2.0685 |
| chr13 | 115169878 | 83170078 | 0.7222 | 1.7438 |
| chr14 | 107349540 | 67619844 | 0.6299 | 1.6814 |
| chr15 | 102531392 | 76096169 | 0.7422 | 1.8162 |
| chr16 | 90354753 | 78667790 | 0.8707 | 5.2977 |
| chr17 | 81195210 | 60187403 | 0.7413 | 3.2659 |
| chr18 | 78077248 | 71843237 | 0.9202 | 4.3346 |
| chr19 | 59128983 | 41052019 | 0.6943 | 2.8814 |
| chr20 | 63025520 | 64658075 | 1.0259 | 2.3093 |
| chr21 | 48129895 | 38273485 | 0.7952 | 2.462 |
| chr22 | 51304566 | 35928700 | 0.7003 | 1.8545 |
| chrMT | 16571 | 4533720 | 273.5936 | 186.4632 |
| chrX | 155270560 | 144457691 | 0.9304 | 2.2335 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 4520099 | 0.0761 | 2.9633 |

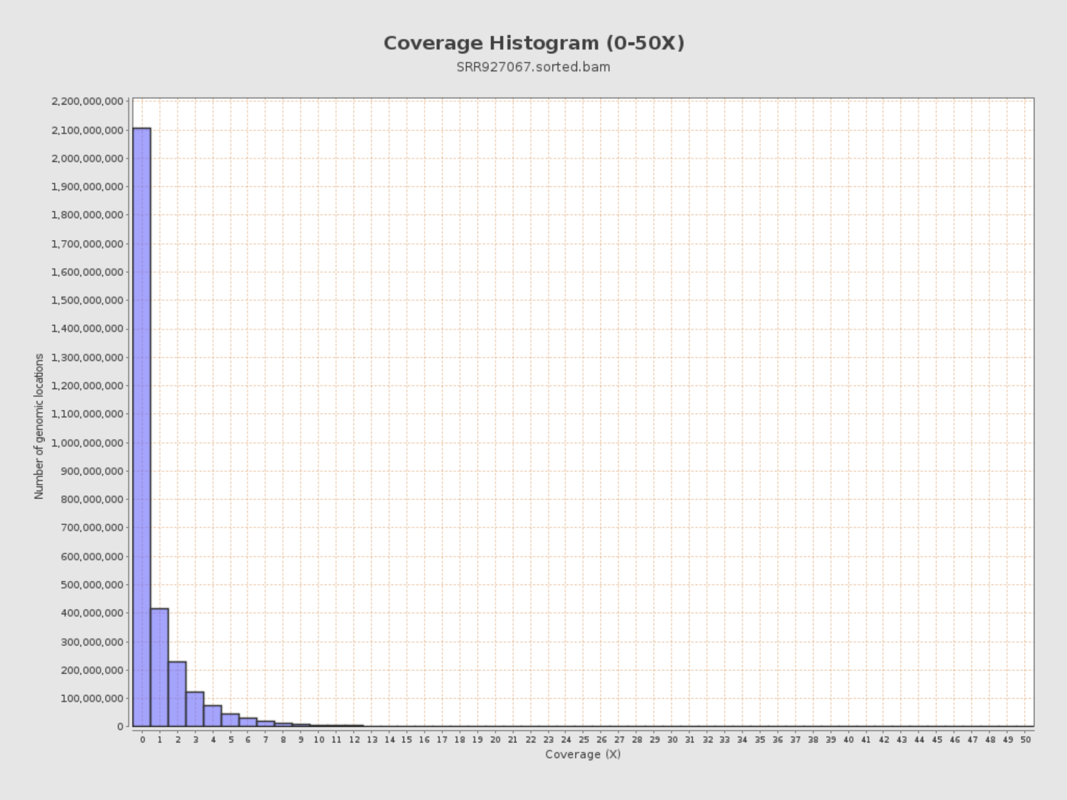
# 3. Results : Coverage across reference



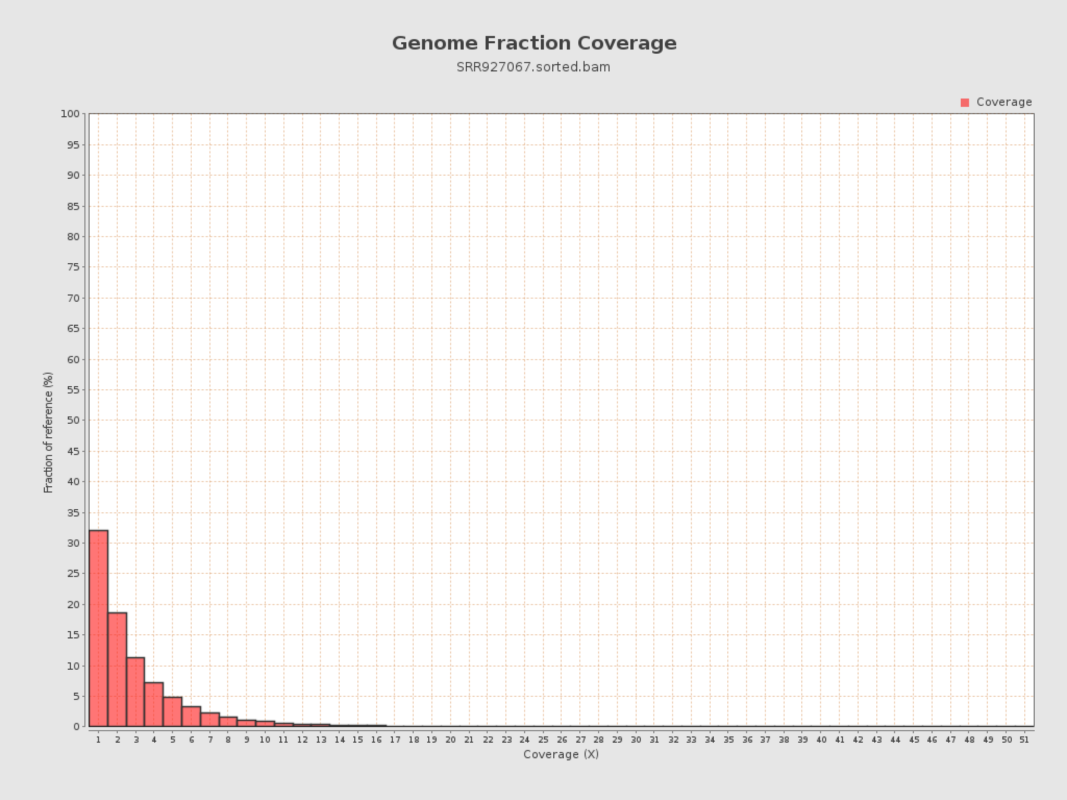
# 4. Results : Coverage Histogram



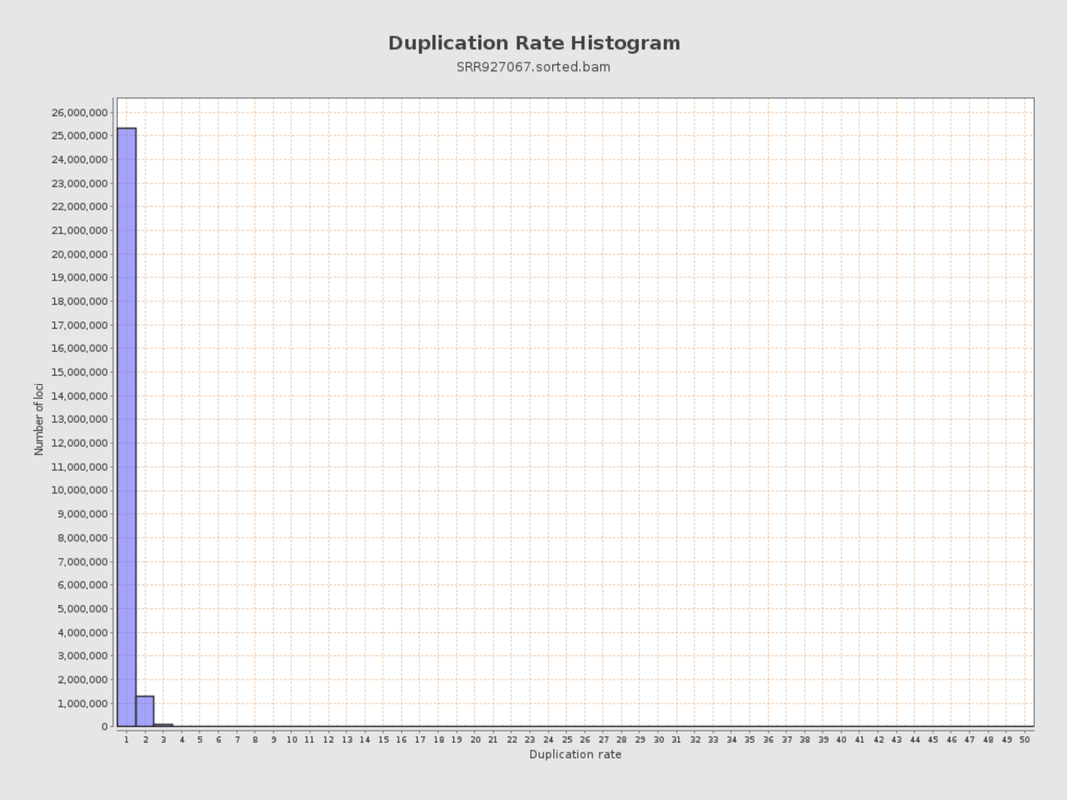
# 5. Results : Coverage Histogram (0-50X)



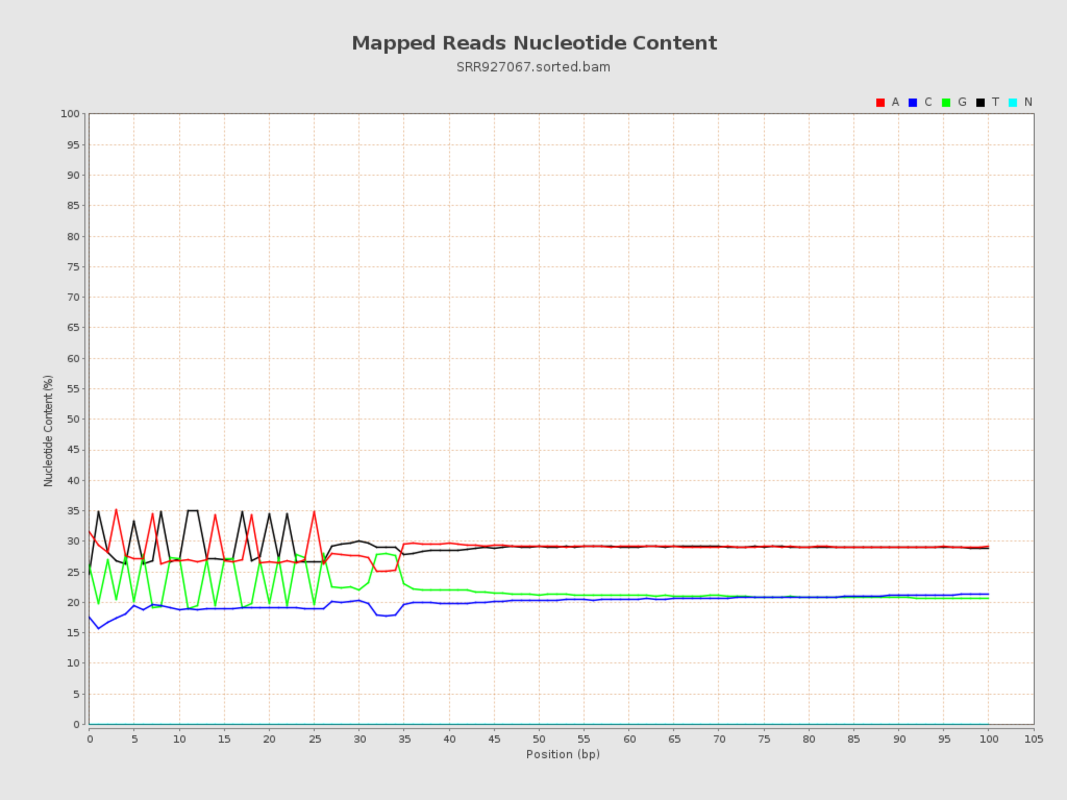
# 6. Results : Genome Fraction Coverage



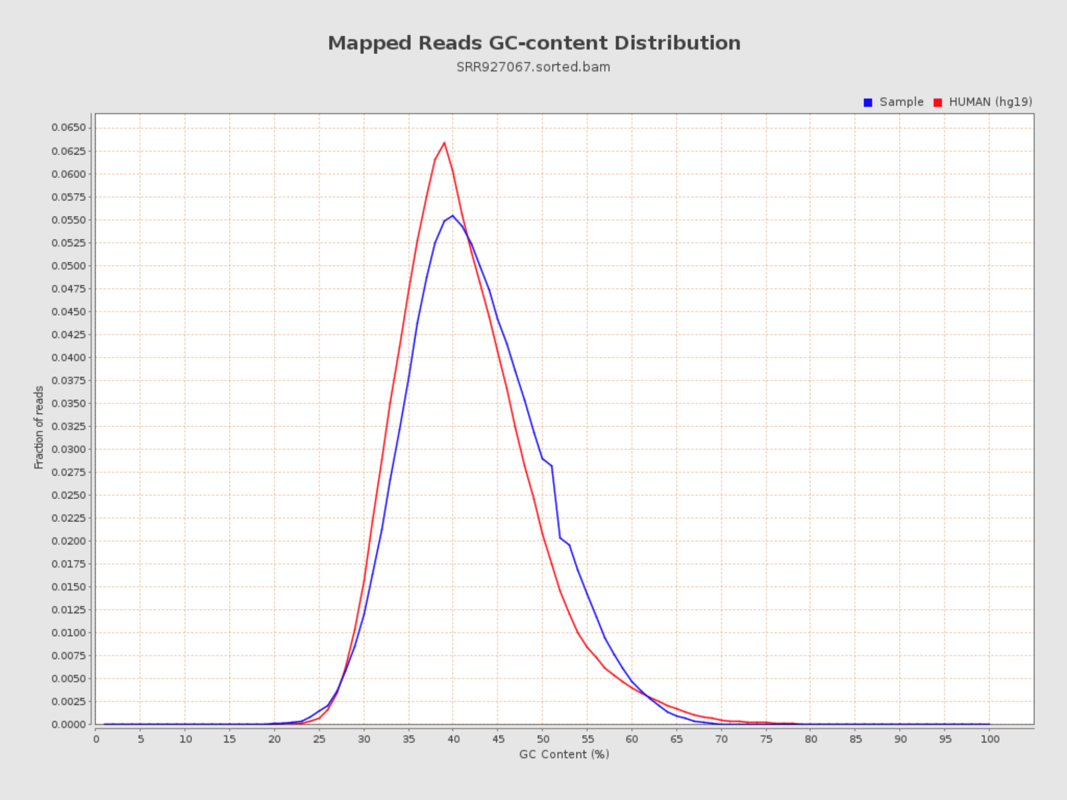
# 7. Results : Duplication Rate Histogram



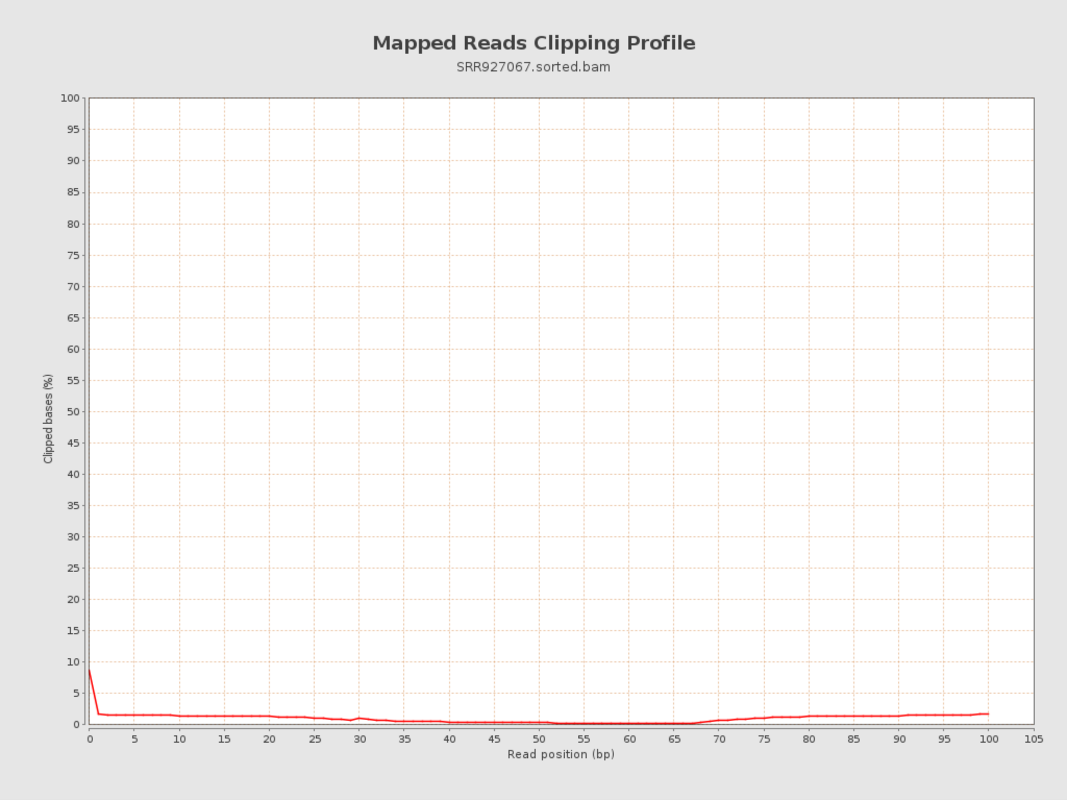
# 8. Results : Mapped Reads Nucleotide Content



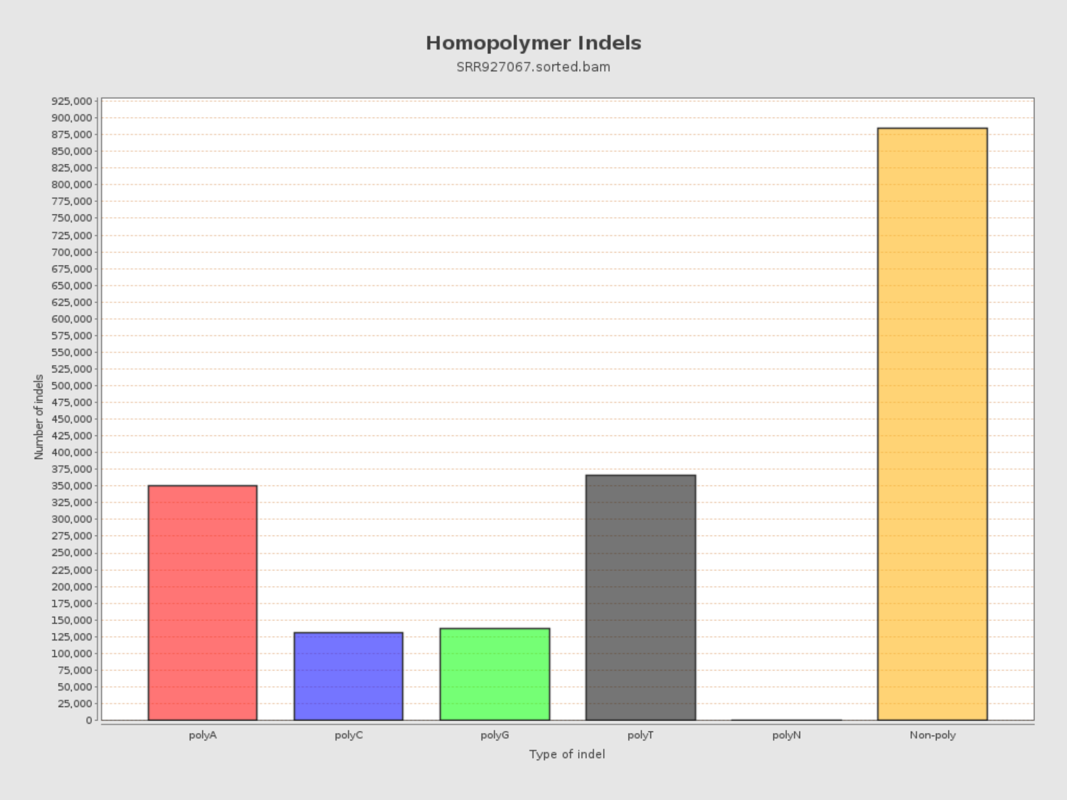
# 9. Results : Mapped Reads GC-content Distribution



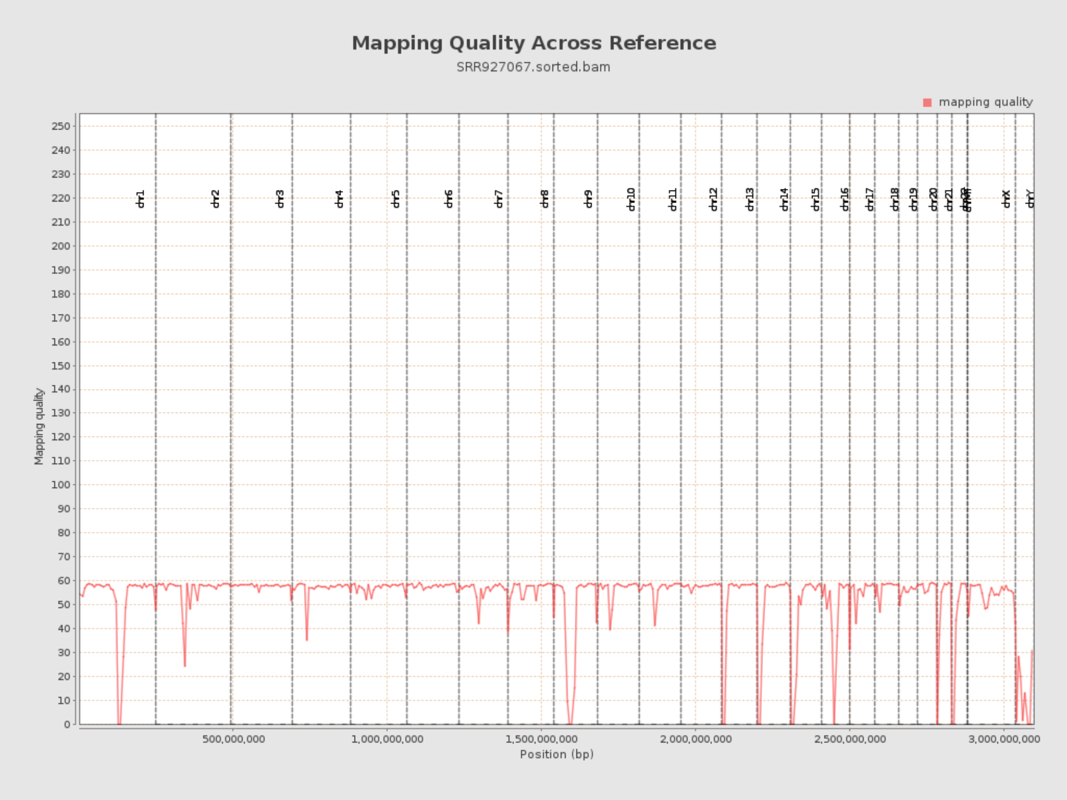
# 10. Results : Mapped Reads Clipping Profile



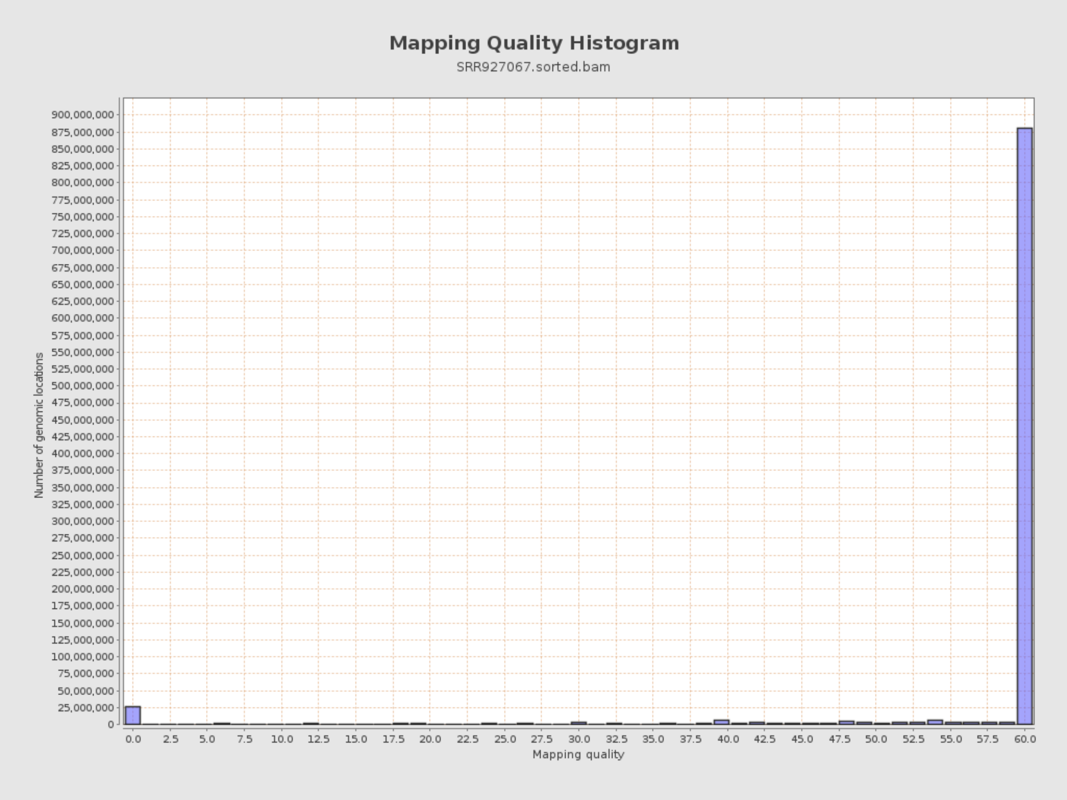
# 11. Results : Homopolymer Indels



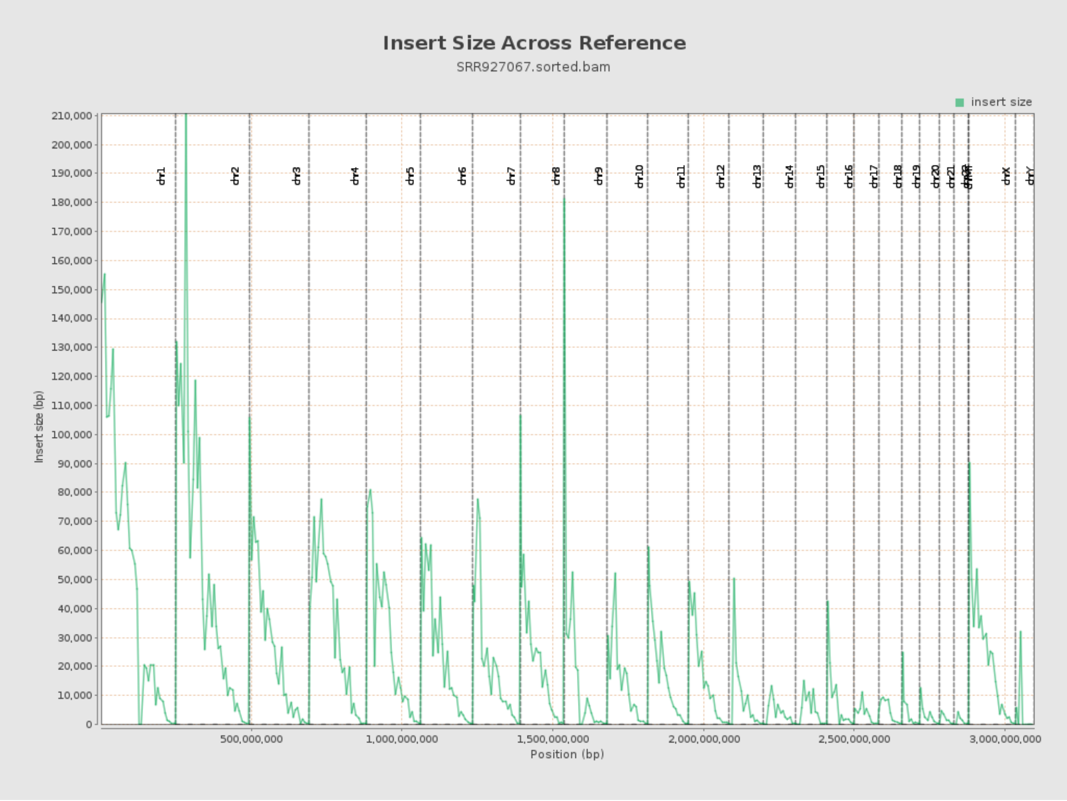
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram