# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/25 08:08:25*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR927068.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_SRR927068 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927068_1.fastq.gz SRR927068_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Apr 25 08:08:24 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR927068.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 22,695,710 |
| Mapped reads | 22,011,093 / 96.98% |
| Unmapped reads | 684,617 / 3.02% |
| Mapped paired reads | 22,011,093 / 96.98% |
| Mapped reads, first in pair | 11,051,881 / 48.7% |
| Mapped reads, second in pair | 10,959,212 / 48.29% |
| Mapped reads, both in pair | 21,604,908 / 95.19% |
| Mapped reads, singletons | 406,185 / 1.79% |
| Secondary alignments | 0 |
| Supplementary alignments | 572,322 / 2.52% |
| Read min/max/mean length | 30 / 101 / 102.05 |
| Duplicated reads (estimated) | 1,768,522 / 7.79% |
| Duplication rate | 6.32% |
| Clipped reads | 10,303,297 / 45.4% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 569,669,856 / 28.67% |
| Number/percentage of C's | 383,652,671 / 19.31% |
| Number/percentage of T's | 581,480,346 / 29.27% |
| Number/percentage of G's | 451,851,581 / 22.74% |
| Number/percentage of N's | 267,356 / 0.01% |
| | |

| | |
|---|---|
| GC Percentage | 42.05% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.6423 |
| Standard Deviation | 2.551 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 52.78 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 287,890.73 |
| Standard Deviation | 5,242,805.26 |
| P25/Median/P75 | 137 / 180 / 244 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 1.06% |
| Mismatches | 20,479,370 |
| Insertions | 330,306 |
| Mapped reads with at least one insertion | 1.47% |
| Deletions | 972,246 |
| Mapped reads with at least one deletion | 4.31% |
| Homopolymer indels | 51.55% |

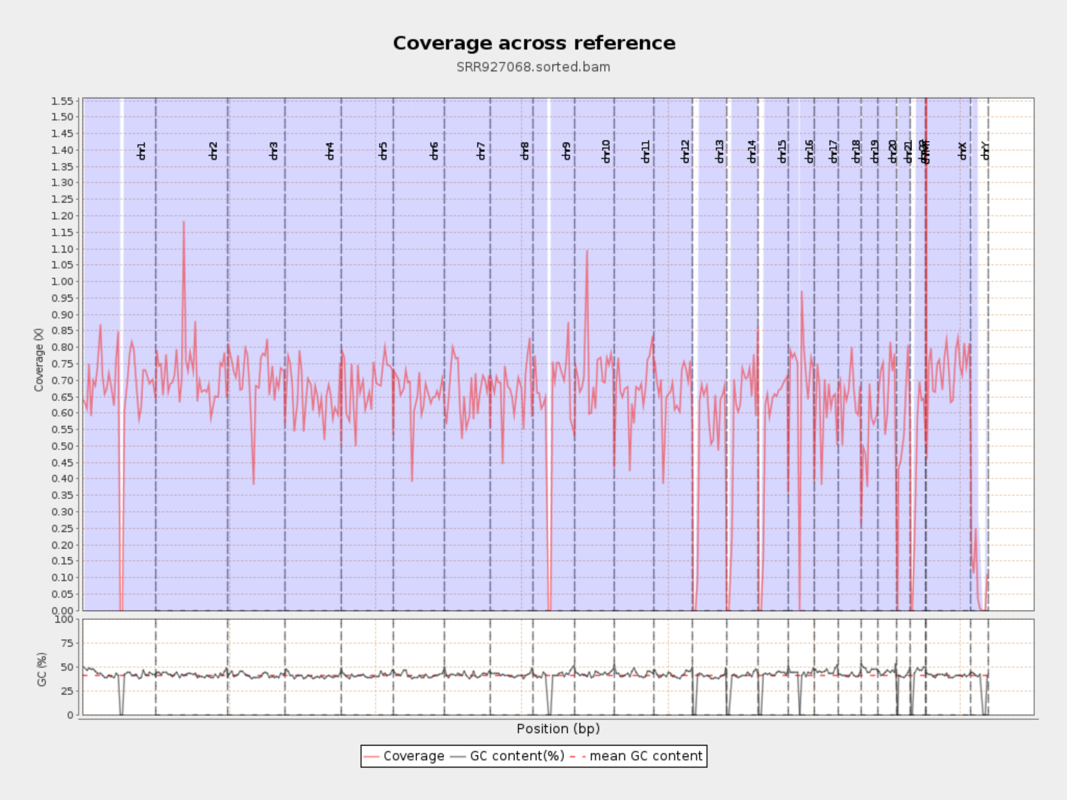
## 2.7. Chromosome stats

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

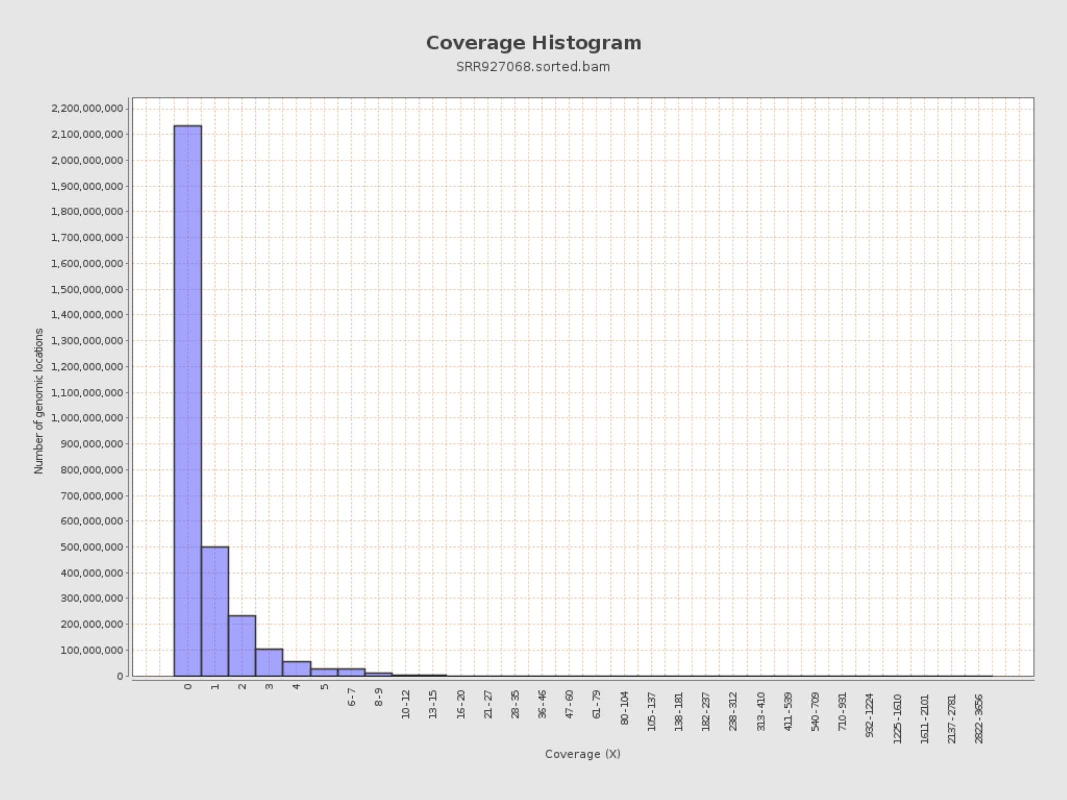
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 164404783 | 0.6596 | 3.8989 |
| chr2 | 243199373 | 175974887 | 0.7236 | 4.1842 |
| chr3 | 198022430 | 139773671 | 0.7058 | 1.4033 |
| chr4 | 191154276 | 125199253 | 0.655 | 2.1947 |
| chr5 | 180915260 | 123921539 | 0.685 | 1.3656 |
| chr6 | 171115067 | 112537874 | 0.6577 | 1.4179 |
| chr7 | 159138663 | 105399979 | 0.6623 | 2.0489 |
| chr8 | 146364022 | 98409813 | 0.6724 | 1.6309 |
| chr9 | 141213431 | 87222059 | 0.6177 | 2.7766 |
| chr10 | 135534747 | 98174094 | 0.7243 | 4.7233 |
| chr11 | 135006516 | 90381651 | 0.6695 | 1.9057 |
| chr12 | 133851895 | 89294652 | 0.6671 | 1.3614 |
| chr13 | 115169878 | 58764835 | 0.5102 | 1.164 |
| chr14 | 107349540 | 60386036 | 0.5625 | 1.3074 |
| chr15 | 102531392 | 54158587 | 0.5282 | 1.2179 |
| chr16 | 90354753 | 61737671 | 0.6833 | 3.4364 |
| chr17 | 81195210 | 50590519 | 0.6231 | 2.0591 |
| chr18 | 78077248 | 51095244 | 0.6544 | 2.919 |
| chr19 | 59128983 | 31398124 | 0.531 | 2.2194 |
| chr20 | 63025520 | 43619048 | 0.6921 | 1.4872 |
| chr21 | 48129895 | 25290555 | 0.5255 | 1.7403 |
| chr22 | 51304566 | 22319301 | 0.435 | 1.1932 |
| chrMT | 16571 | 126484 | 7.6329 | 4.1995 |
| chrX | 155270560 | 113349418 | 0.73 | 1.6428 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 4822612 | 0.0812 | 2.9823 |

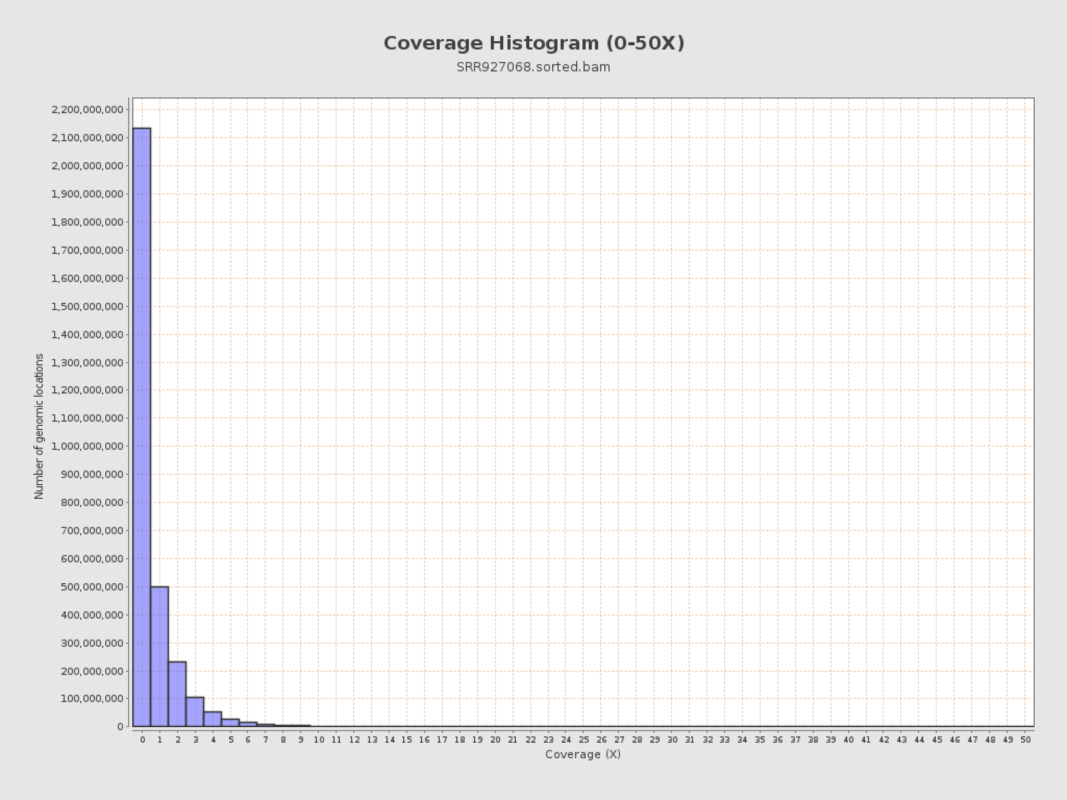
# 3. Results : Coverage across reference



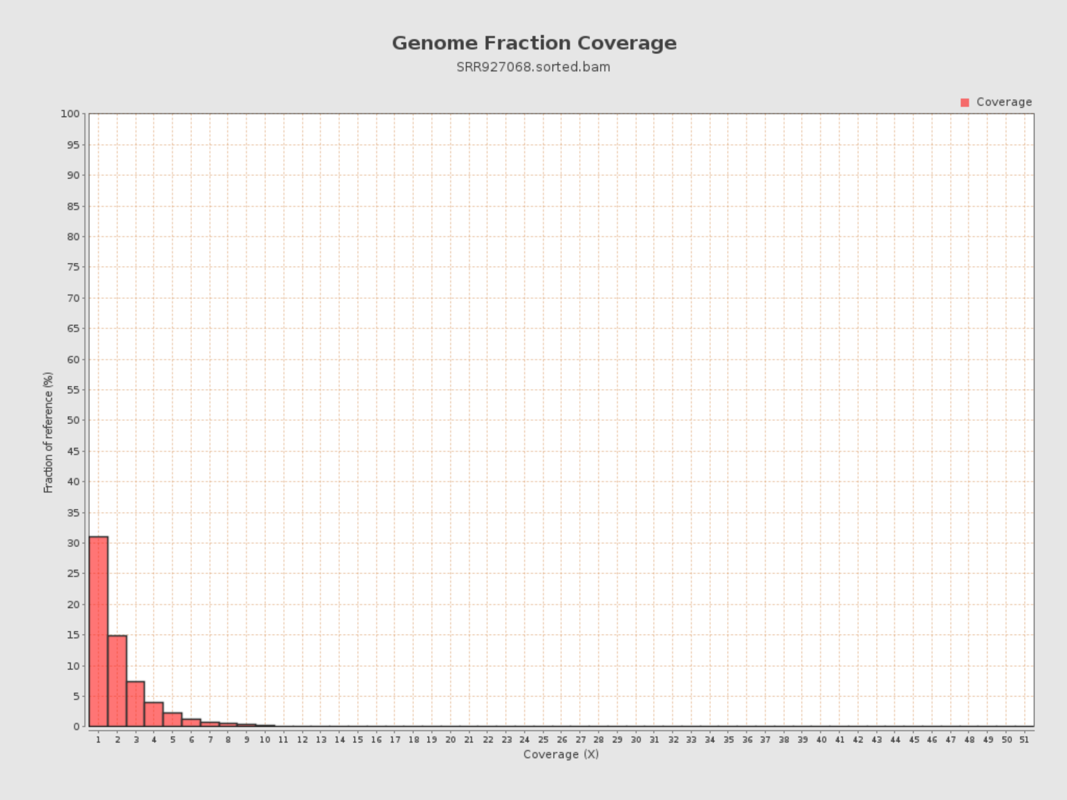
# 4. Results : Coverage Histogram



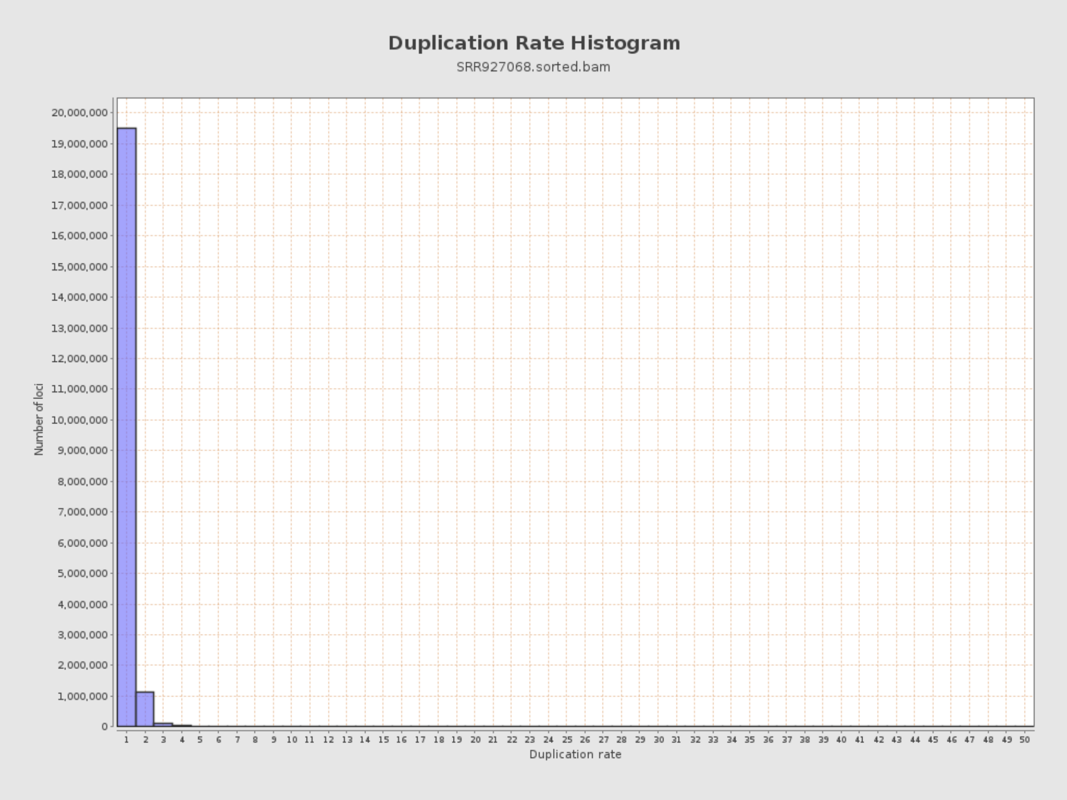
# 5. Results : Coverage Histogram (0-50X)



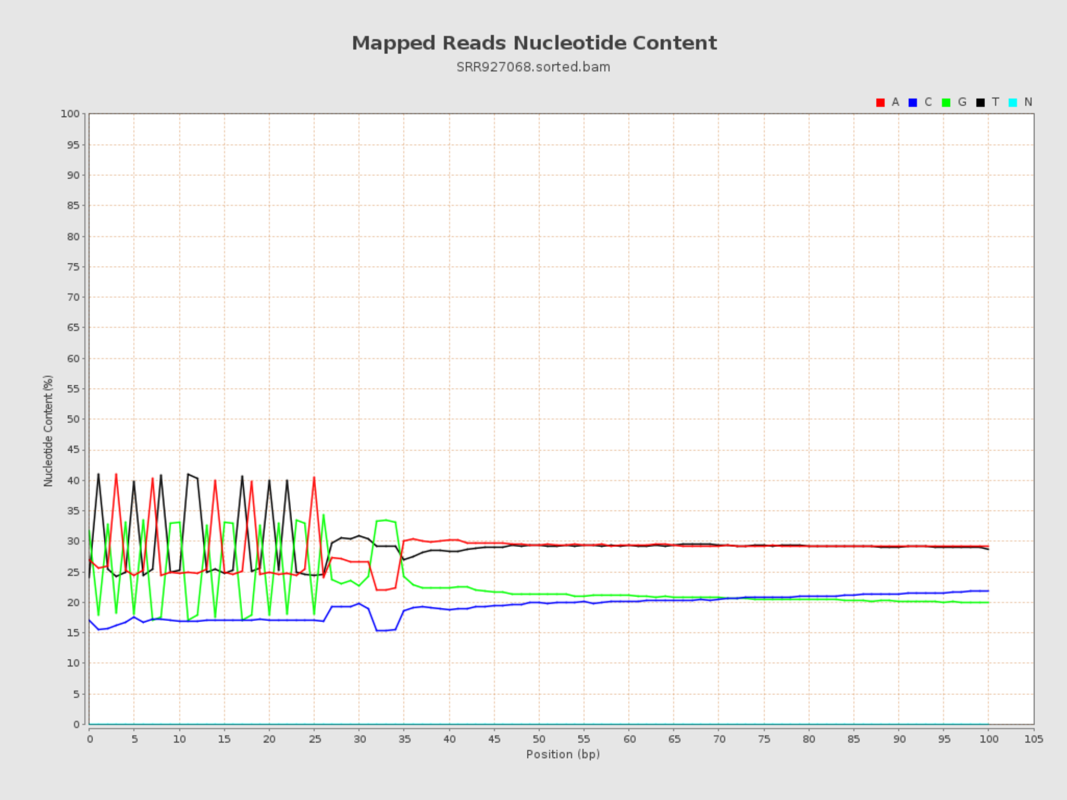
# 6. Results : Genome Fraction Coverage



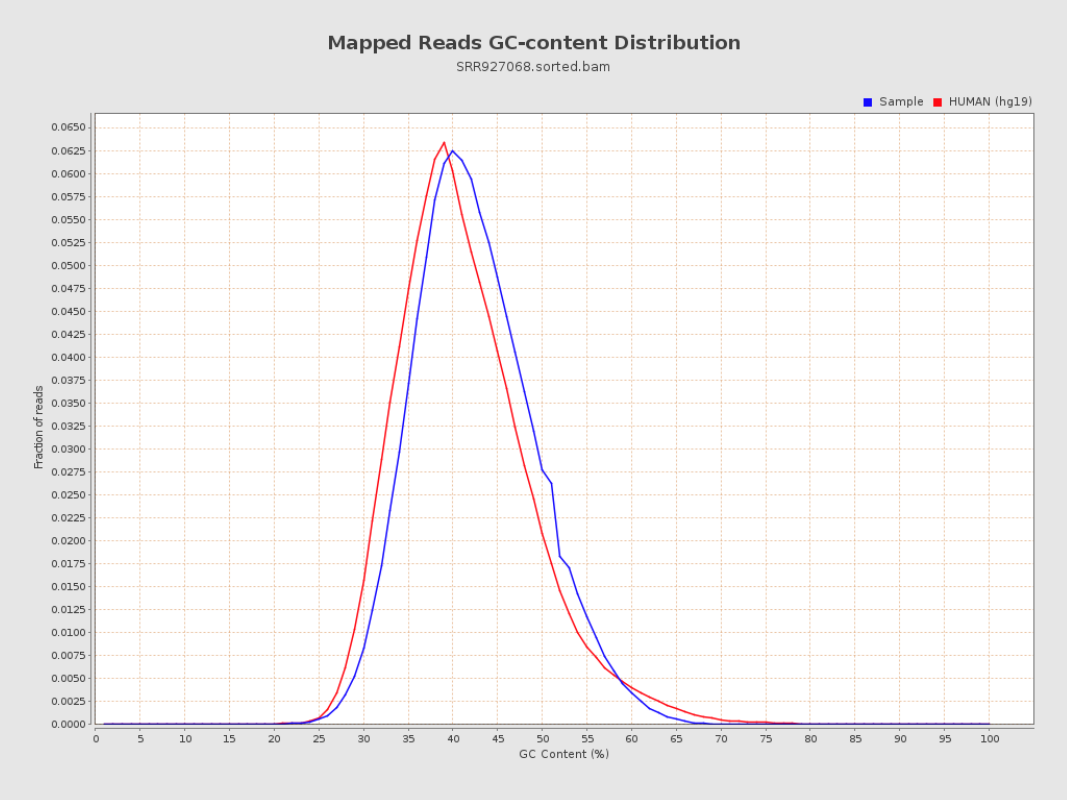
# 7. Results : Duplication Rate Histogram



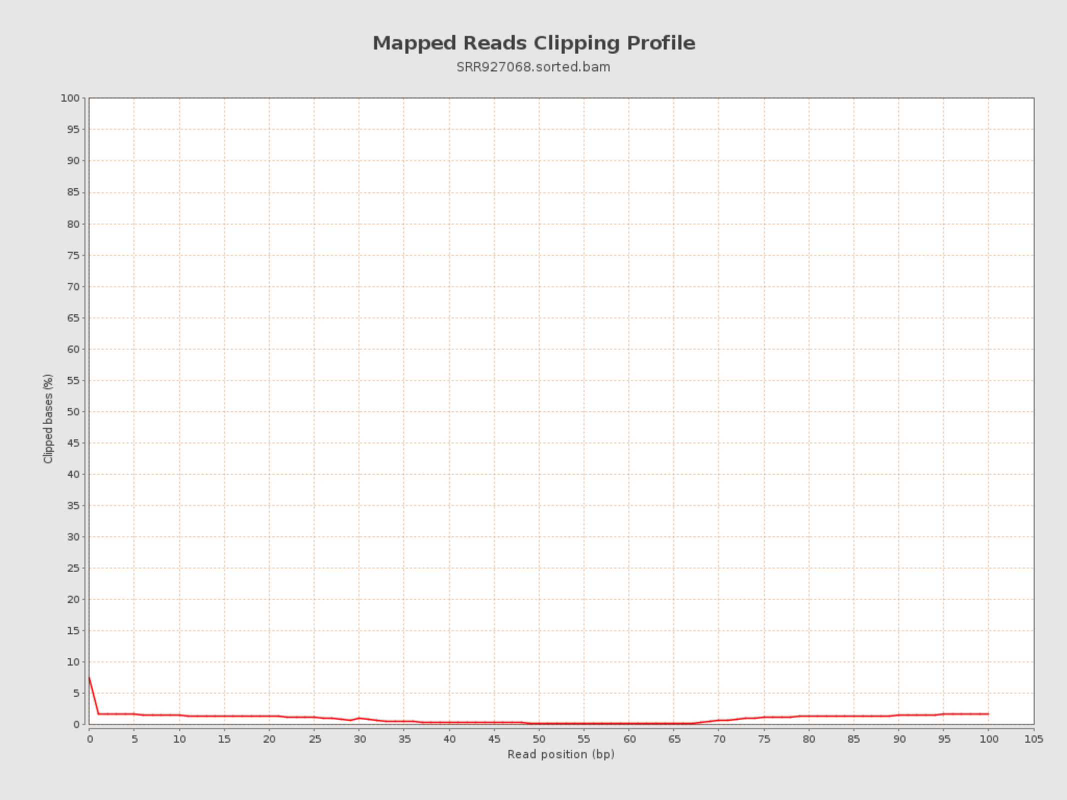
# 8. Results : Mapped Reads Nucleotide Content



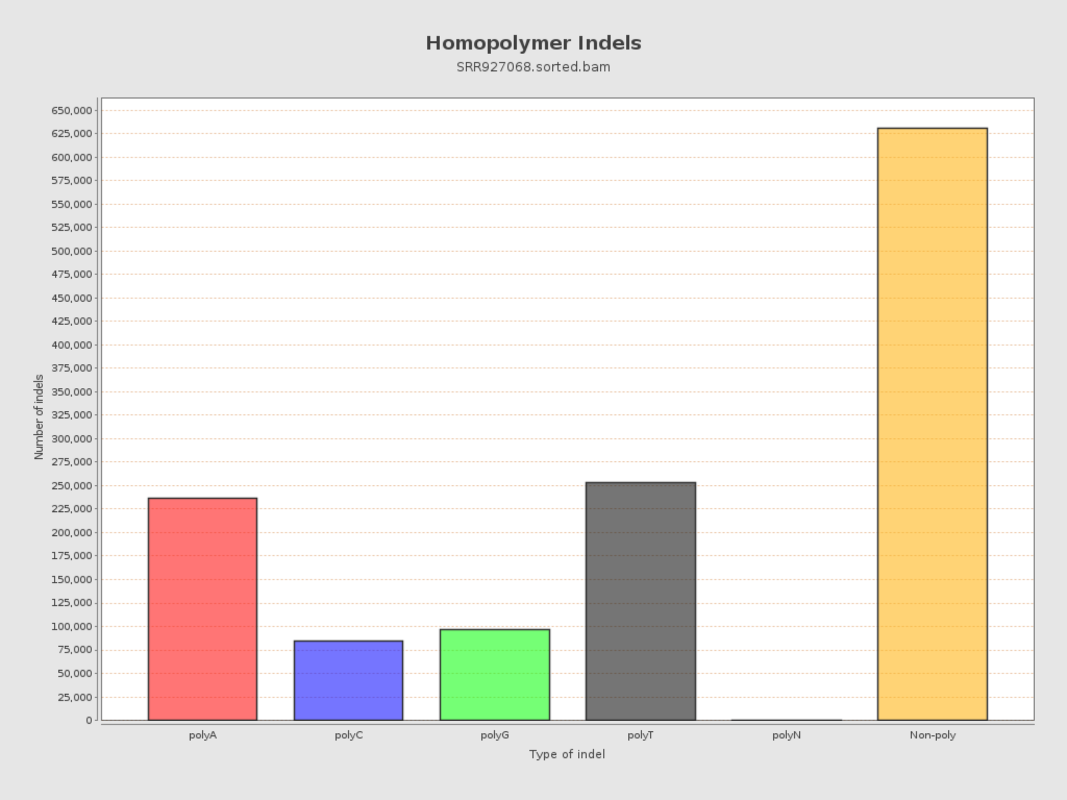
# 9. Results : Mapped Reads GC-content Distribution



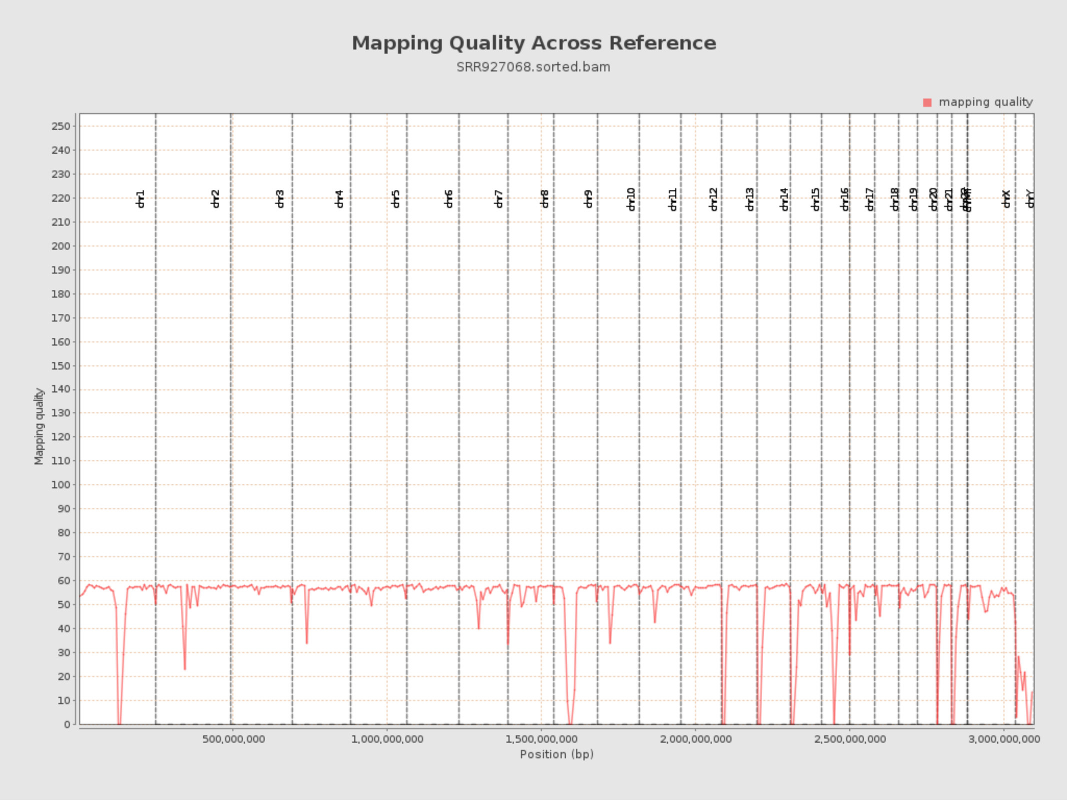
# 10. Results : Mapped Reads Clipping Profile



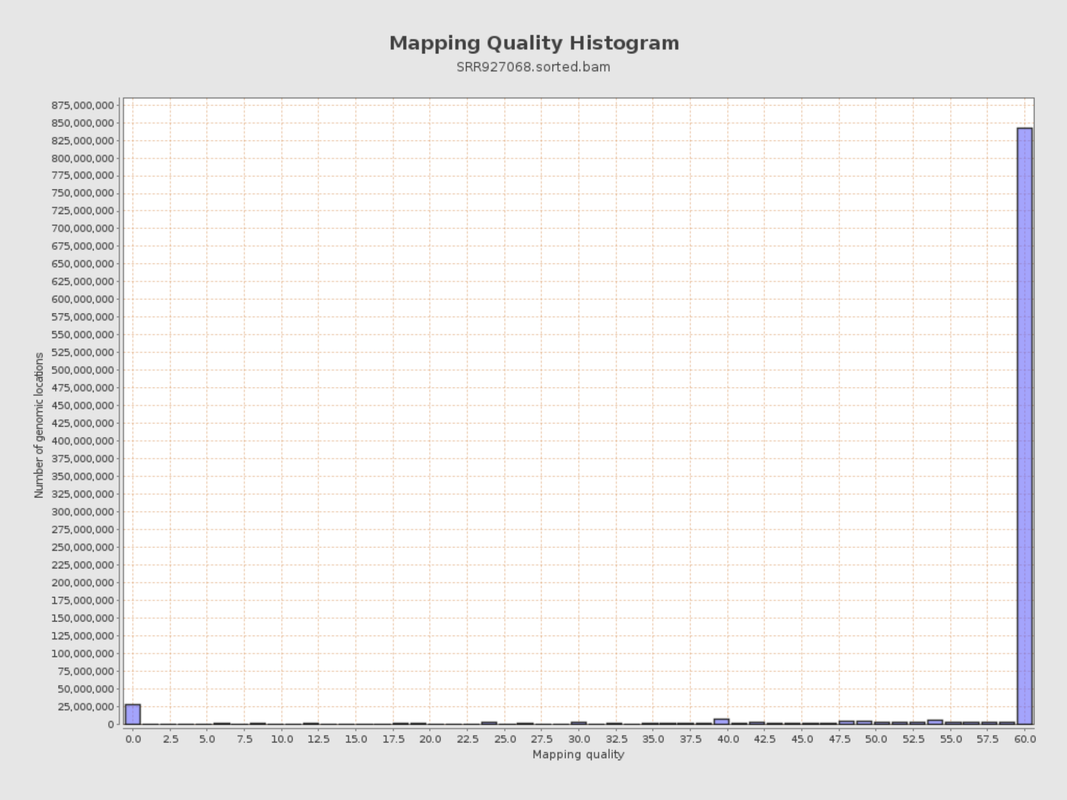
# 11. Results : Homopolymer Indels



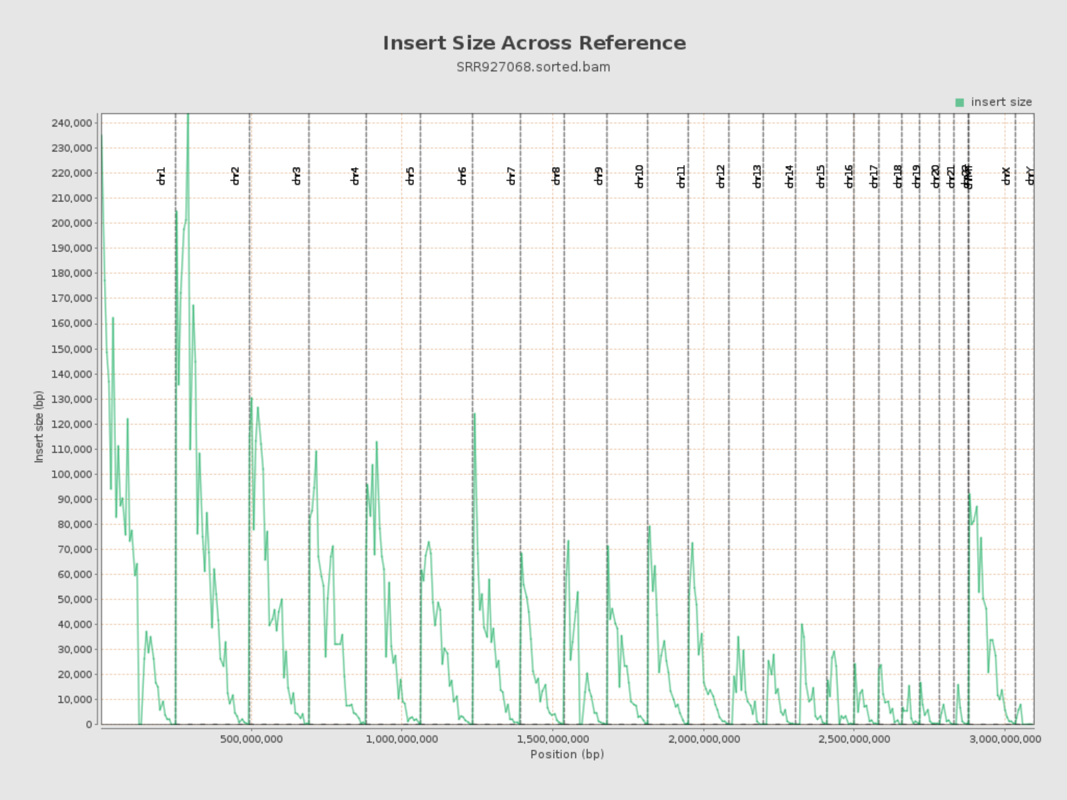
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram