# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/23 22:07:03*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR926998.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_SRR926998 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926998_1.fastq.gz SRR926998_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Apr 23 22:07:03 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR926998.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 11,262,984 |
| Mapped reads | 11,037,482 / 98% |
| Unmapped reads | 225,502 / 2% |
| Mapped paired reads | 11,037,482 / 98% |
| Mapped reads, first in pair | 5,527,341 / 49.08% |
| Mapped reads, second in pair | 5,510,141 / 48.92% |
| Mapped reads, both in pair | 10,906,532 / 96.84% |
| Mapped reads, singletons | 130,950 / 1.16% |
| Secondary alignments | 0 |
| Supplementary alignments | 175,954 / 1.56% |
| Read min/max/mean length | 30 / 101 / 101.65 |
| Duplicated reads (estimated) | 609,539 / 5.41% |
| Duplication rate | 4.86% |
| Clipped reads | 3,657,558 / 32.47% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 290,095,921 / 28.3% |
| Number/percentage of C's | 206,207,846 / 20.12% |
| Number/percentage of T's | 293,024,410 / 28.58% |
| Number/percentage of G's | 235,571,961 / 22.98% |
| Number/percentage of N's | 200,208 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 43.1% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.3314 |
| Standard Deviation | 1.0782 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.43 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 131,085.48 |
| Standard Deviation | 3,561,033.2 |
| P25/Median/P75 | 139 / 182 / 247 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.93% |
| Mismatches | 9,232,969 |
| Insertions | 159,099 |
| Mapped reads with at least one insertion | 1.42% |
| Deletions | 519,183 |
| Mapped reads with at least one deletion | 4.58% |
| Homopolymer indels | 52.63% |

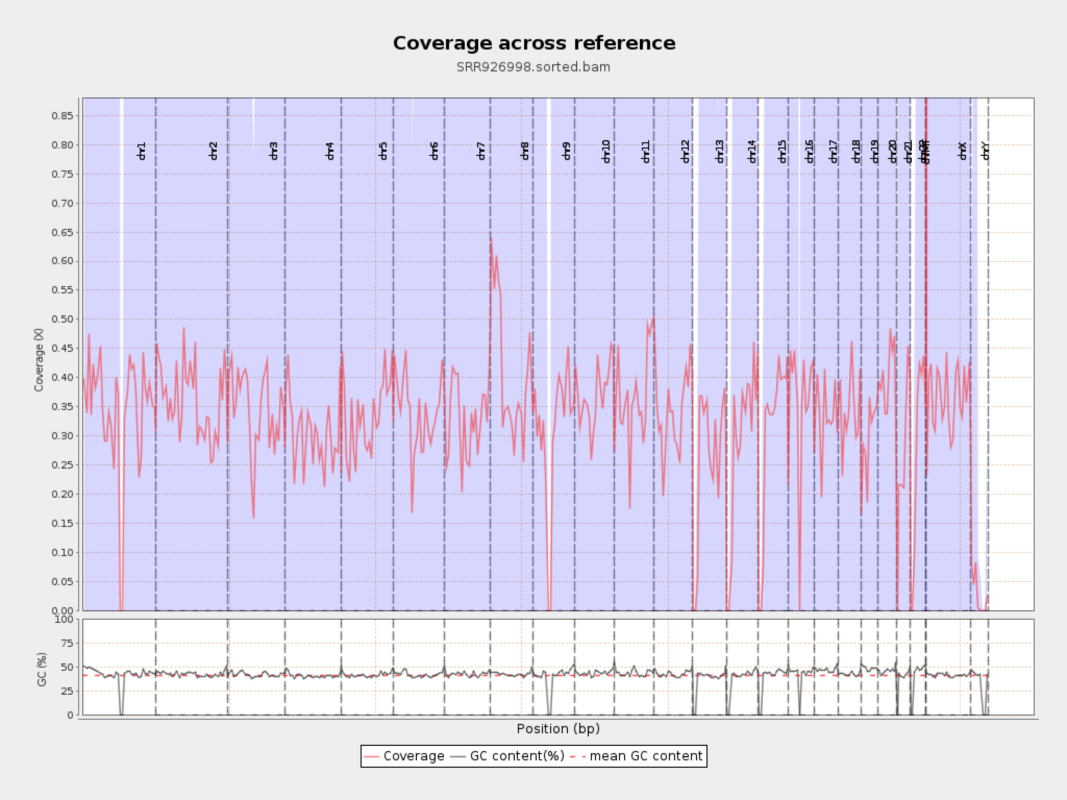
## 2.7. Chromosome stats

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

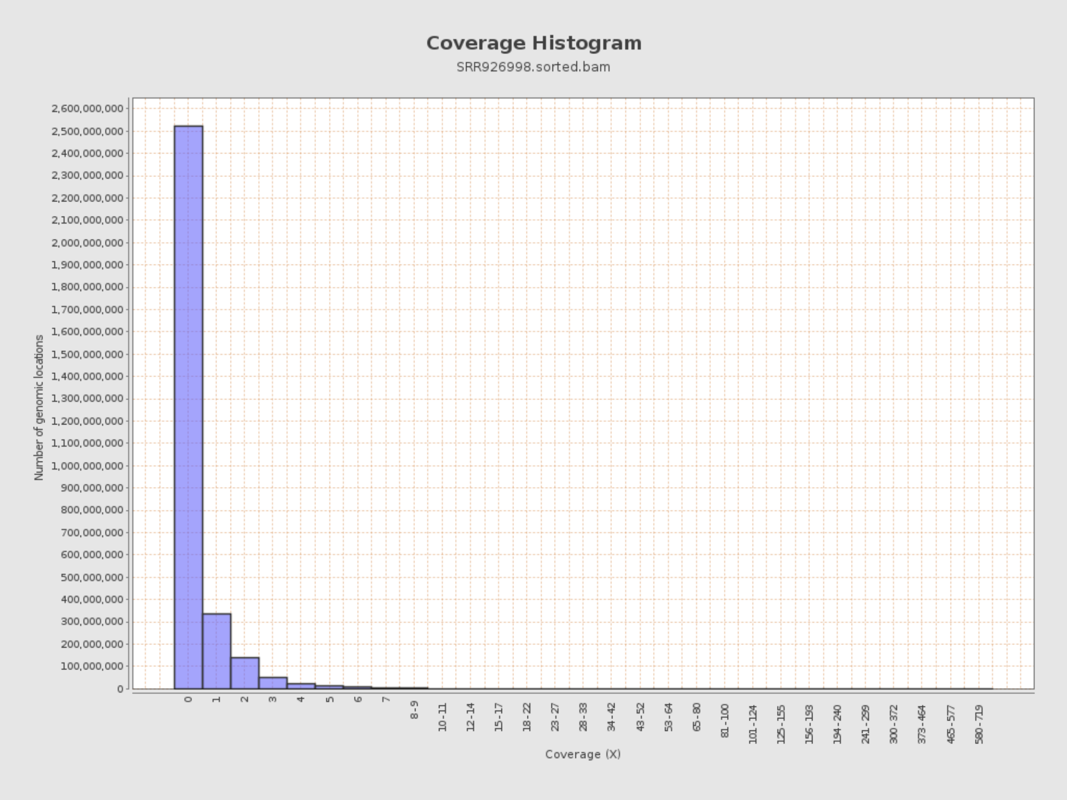
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 85192517 | 0.3418 | 1.2557 |
| chr2 | 243199373 | 87881585 | 0.3614 | 1.5499 |
| chr3 | 198022430 | 68207457 | 0.3444 | 0.8878 |
| chr4 | 191154276 | 58397110 | 0.3055 | 0.9759 |
| chr5 | 180915260 | 60866325 | 0.3364 | 0.8766 |
| chr6 | 171115067 | 58236949 | 0.3403 | 0.9656 |
| chr7 | 159138663 | 52082740 | 0.3273 | 0.9794 |
| chr8 | 146364022 | 59953432 | 0.4096 | 1.0566 |
| chr9 | 141213431 | 43331371 | 0.3069 | 1.1991 |
| chr10 | 135534747 | 49882412 | 0.368 | 1.2859 |
| chr11 | 135006516 | 49403933 | 0.3659 | 0.9896 |
| chr12 | 133851895 | 46148009 | 0.3448 | 0.9047 |
| chr13 | 115169878 | 29947865 | 0.26 | 0.7671 |
| chr14 | 107349540 | 30767530 | 0.2866 | 0.827 |
| chr15 | 102531392 | 30735207 | 0.2998 | 0.8548 |
| chr16 | 90354753 | 31918961 | 0.3533 | 1.2484 |
| chr17 | 81195210 | 27384762 | 0.3373 | 0.9955 |
| chr18 | 78077248 | 26790248 | 0.3431 | 1.2416 |
| chr19 | 59128983 | 17664879 | 0.2988 | 1.007 |
| chr20 | 63025520 | 25566233 | 0.4056 | 1.0329 |
| chr21 | 48129895 | 13128676 | 0.2728 | 1.2878 |
| chr22 | 51304566 | 14048495 | 0.2738 | 0.8539 |
| chrMT | 16571 | 179268 | 10.8182 | 11.0979 |
| chrX | 155270560 | 56501104 | 0.3639 | 0.9437 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1626706 | 0.0274 | 0.882 |

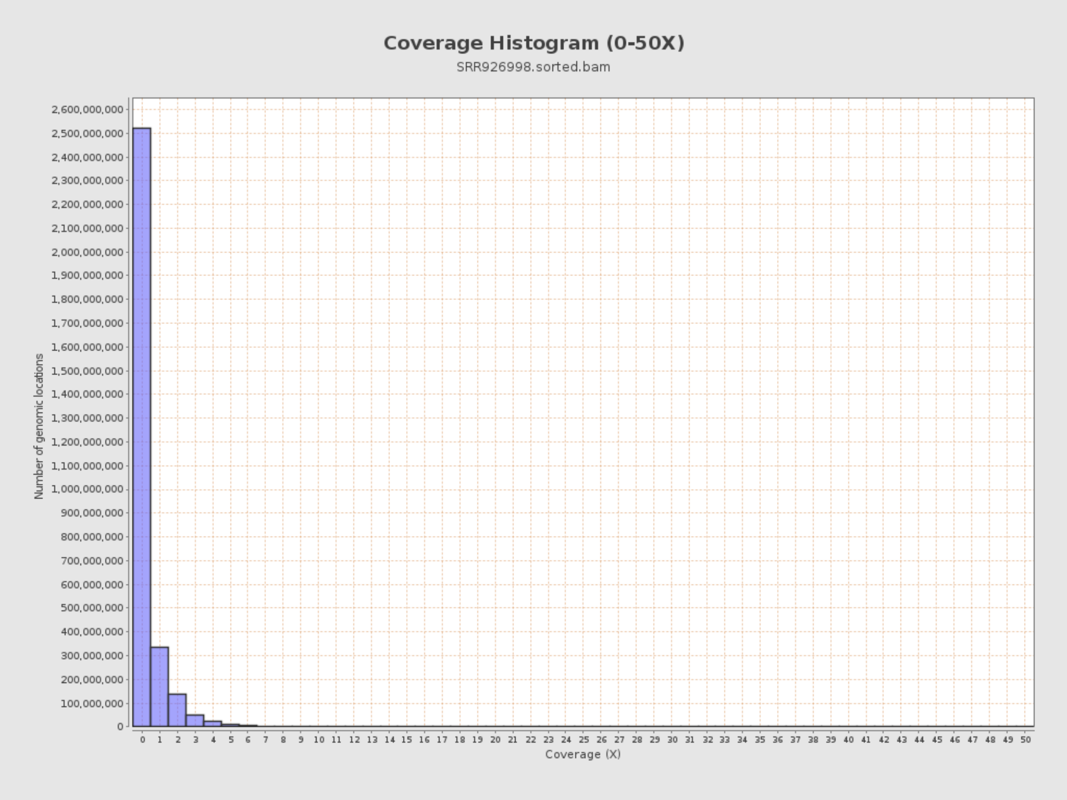
# 3. Results : Coverage across reference



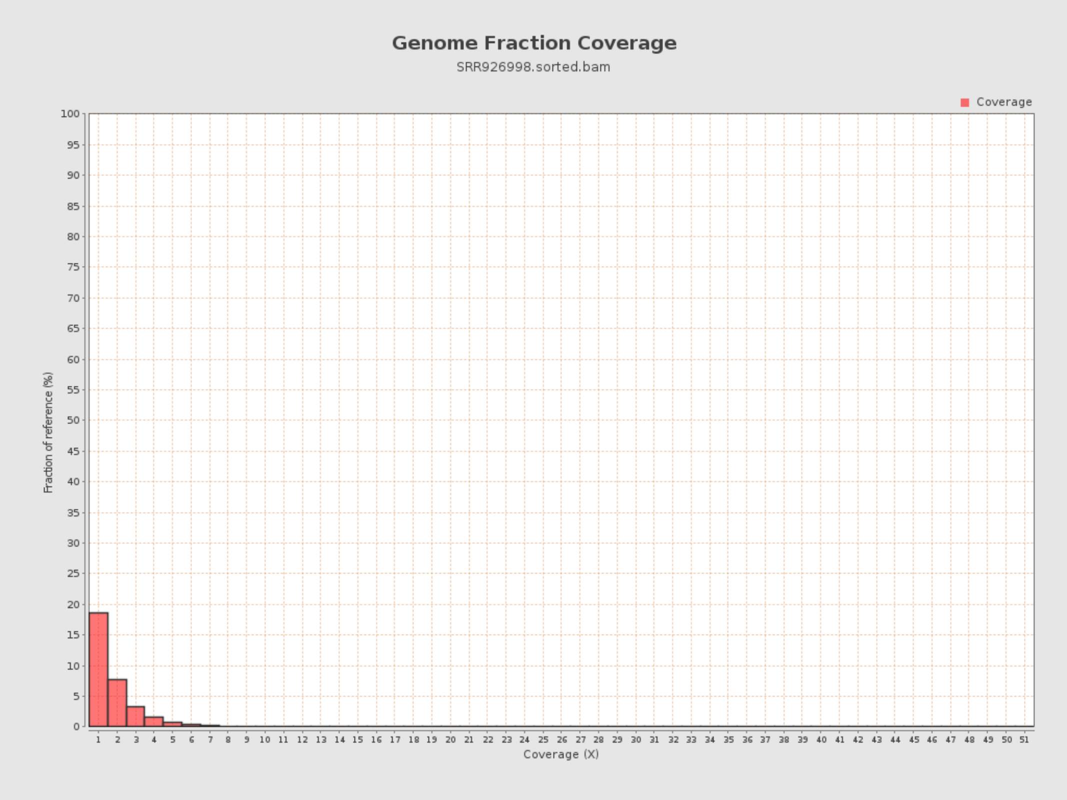
# 4. Results : Coverage Histogram



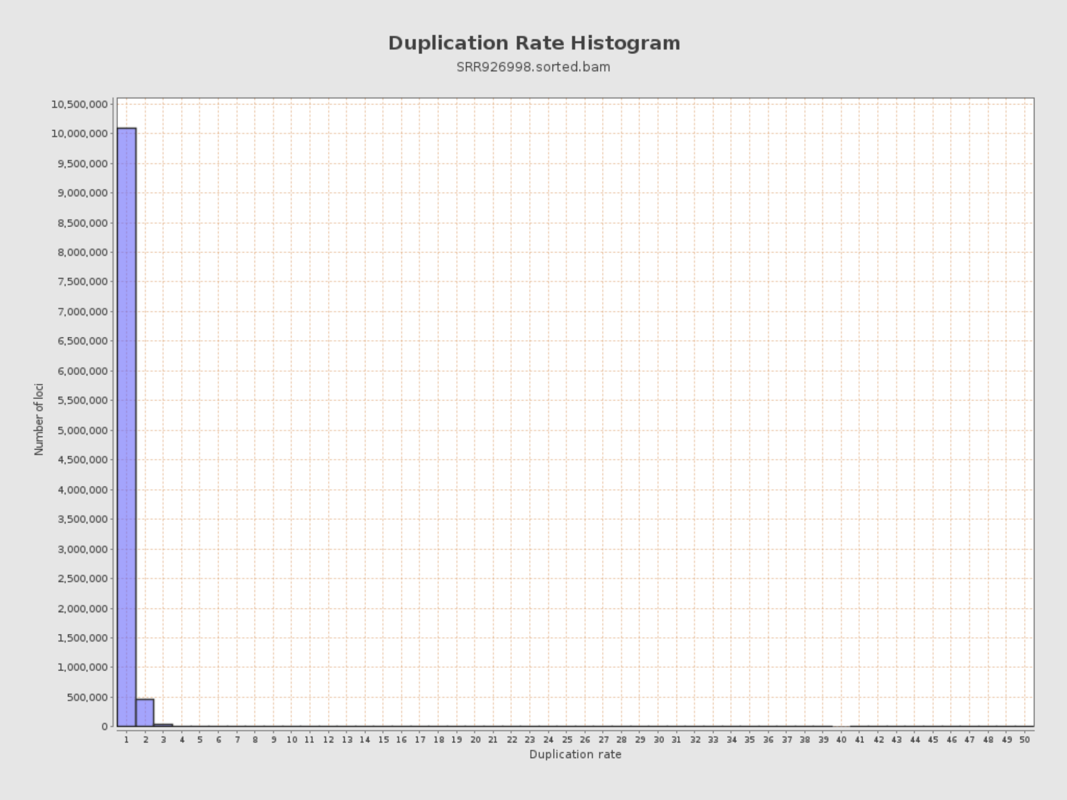
# 5. Results : Coverage Histogram (0-50X)



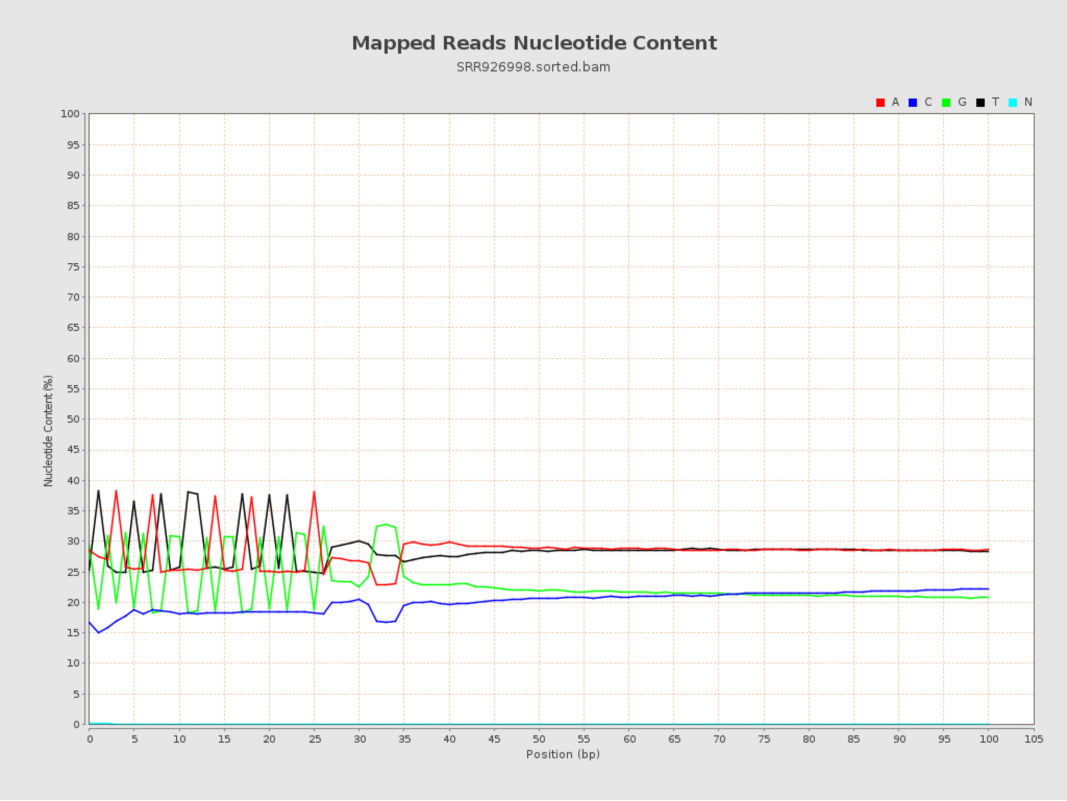
# 6. Results : Genome Fraction Coverage



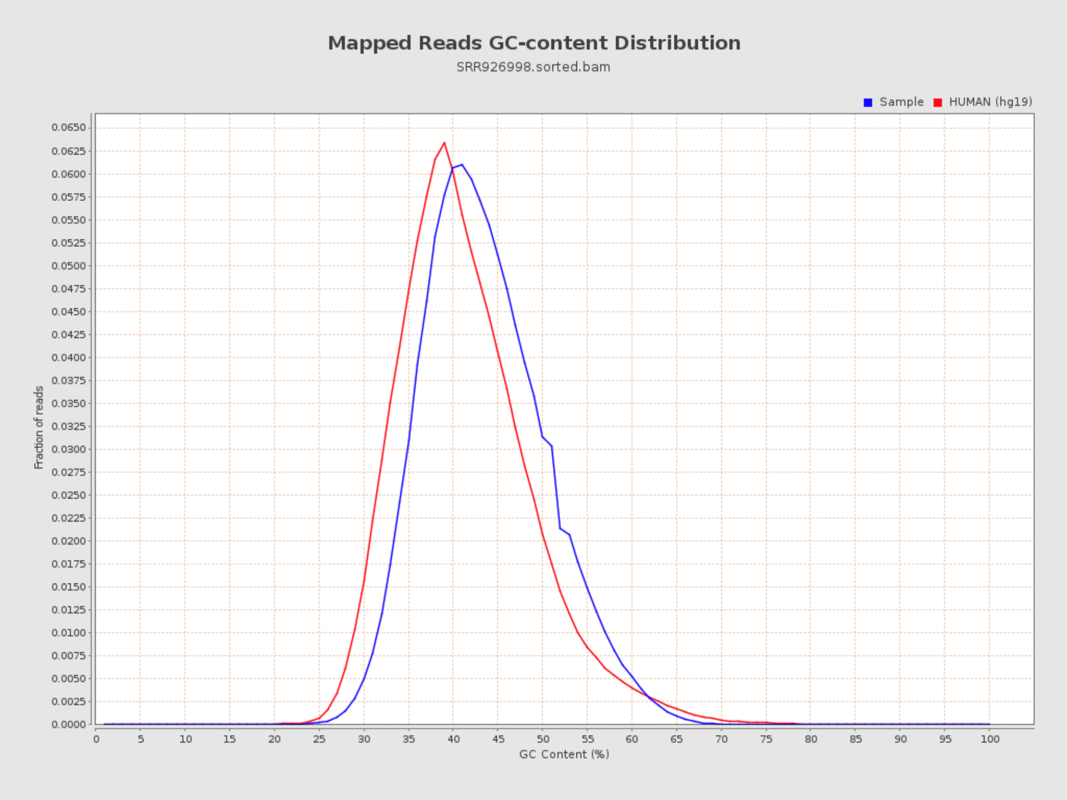
# 7. Results : Duplication Rate Histogram



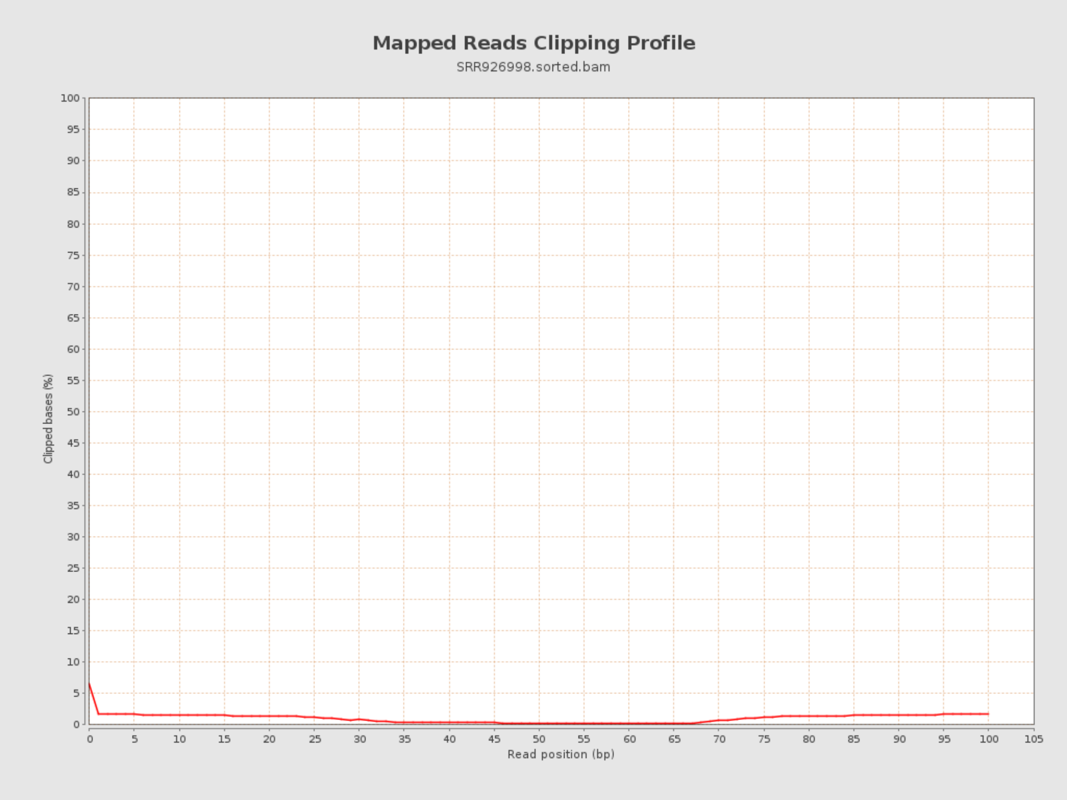
# 8. Results : Mapped Reads Nucleotide Content



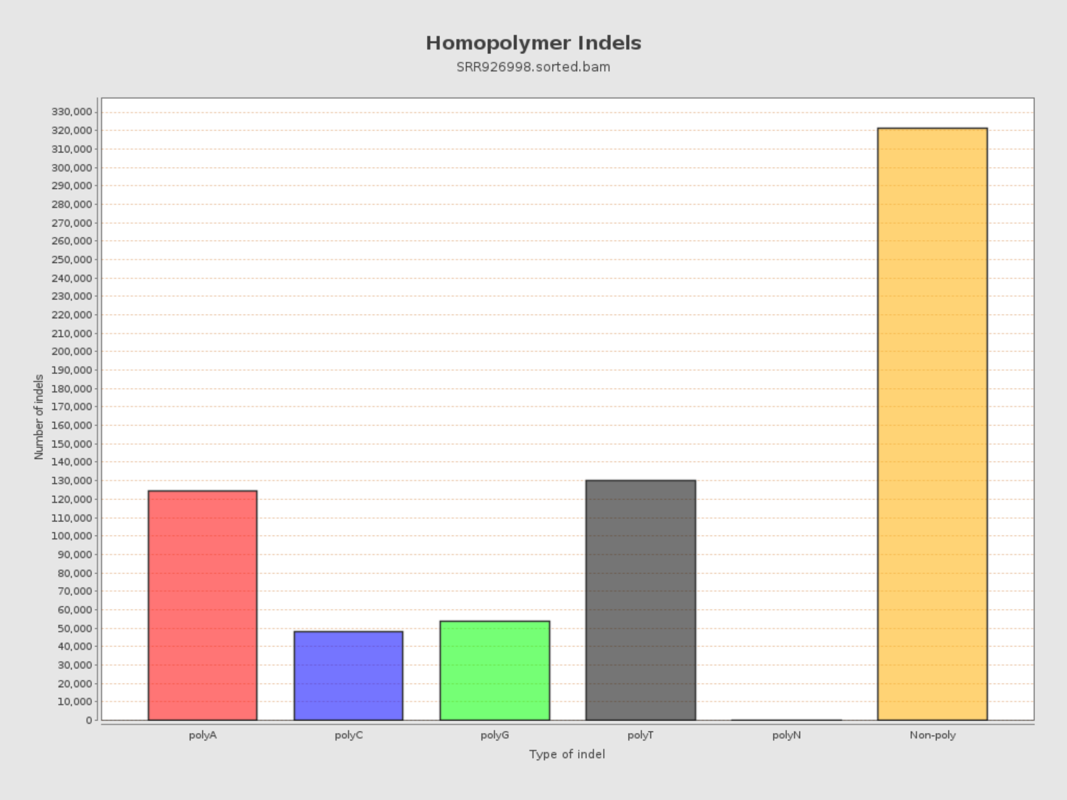
# 9. Results : Mapped Reads GC-content Distribution



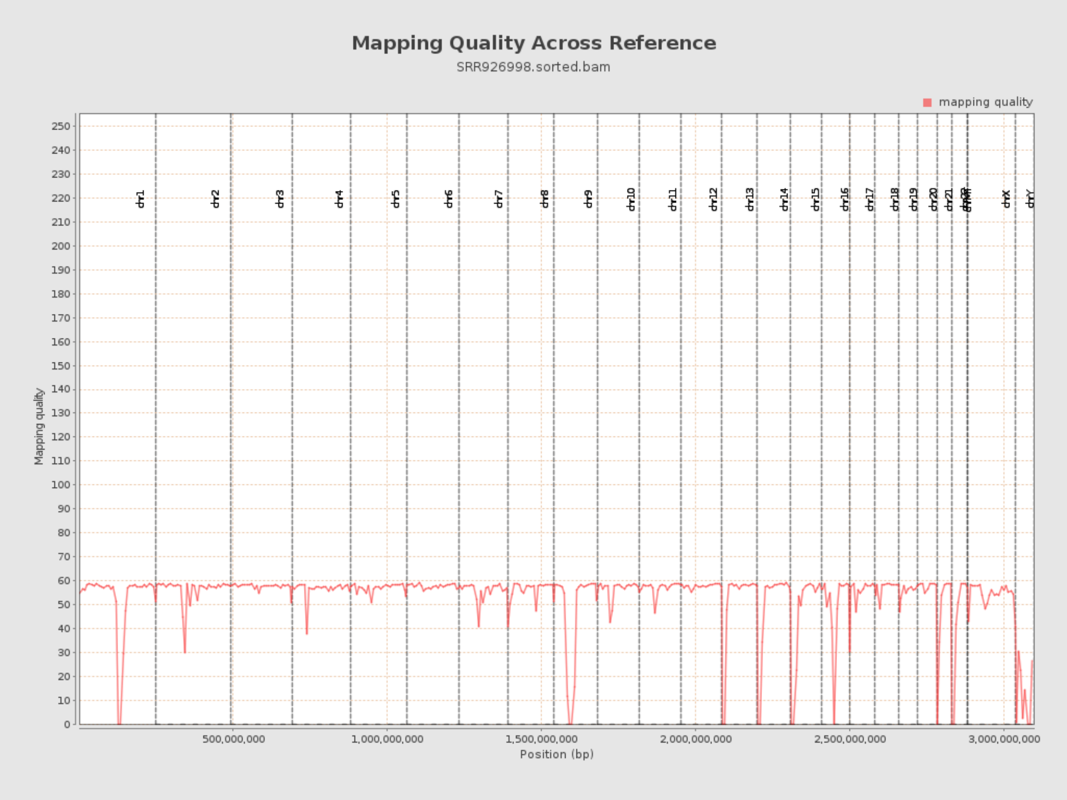
# 10. Results : Mapped Reads Clipping Profile



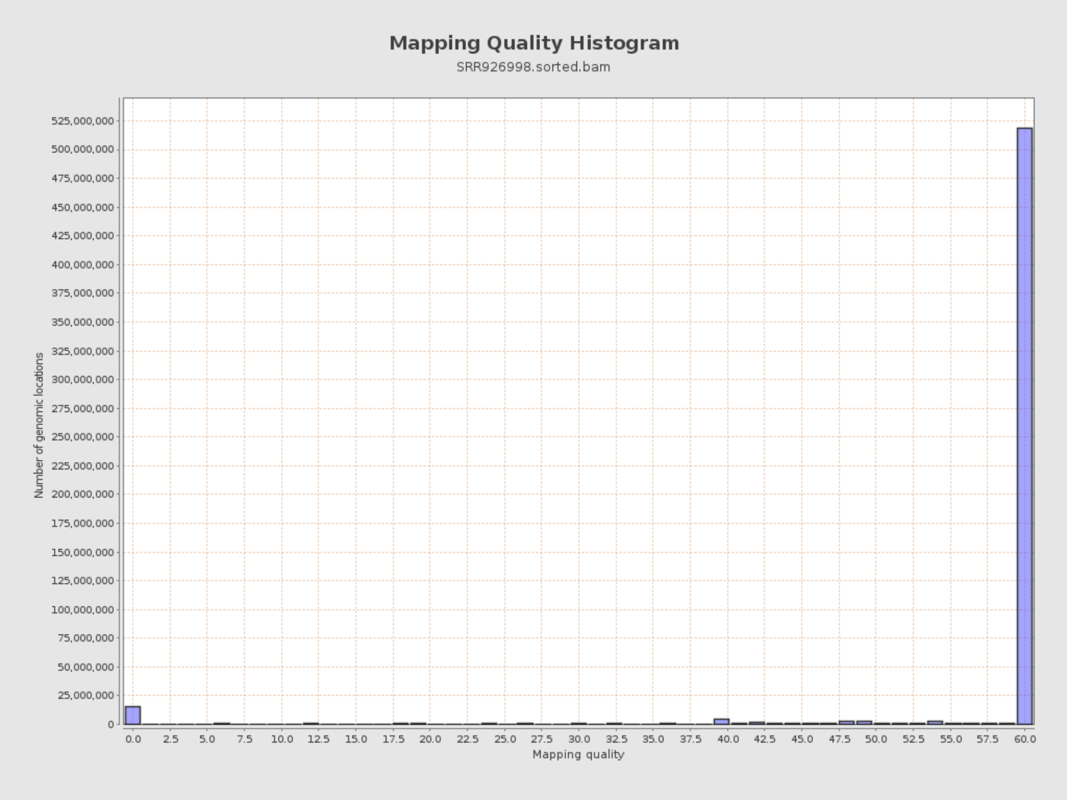
# 11. Results : Homopolymer Indels



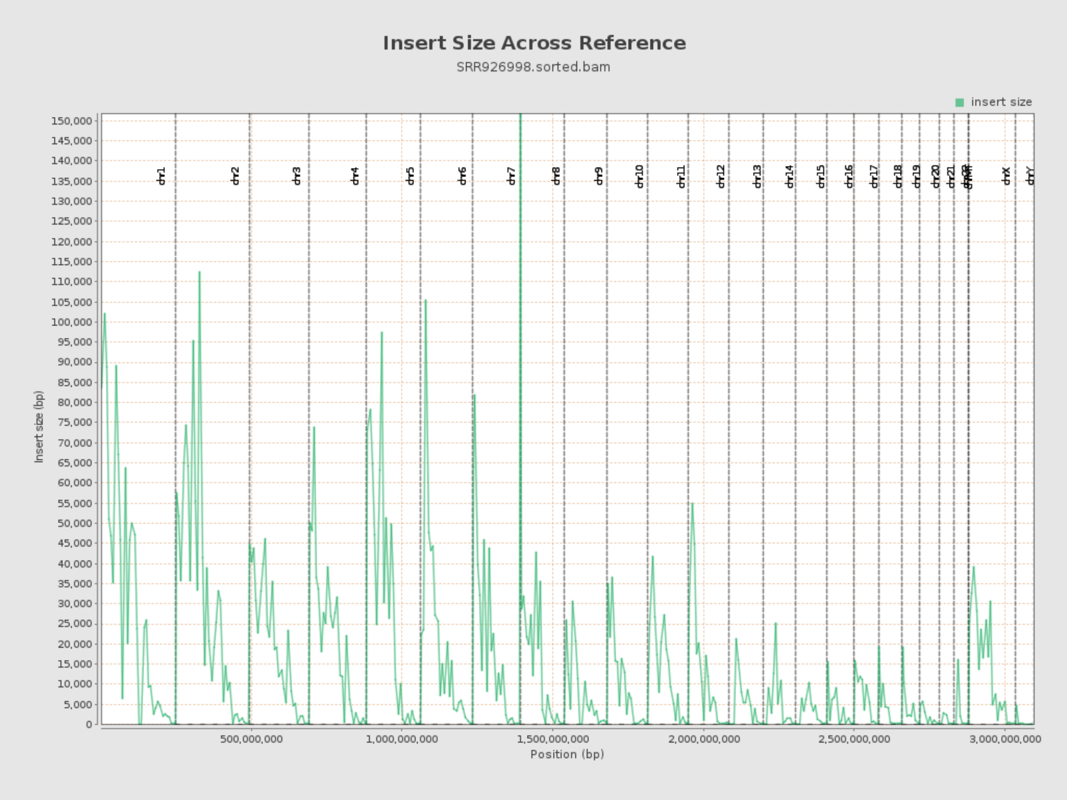
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram