# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/22 21:29:45*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR926931.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_SRR926931 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926931_1.fastq.gz SRR926931_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Apr 22 21:29:44 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR926931.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 12,063,998 |
| Mapped reads | 11,783,296 / 97.67% |
| Unmapped reads | 280,702 / 2.33% |
| Mapped paired reads | 11,783,296 / 97.67% |
| Mapped reads, first in pair | 5,908,348 / 48.98% |
| Mapped reads,  second in pair | 5,874,948 / 48.7% |
| Mapped reads, both in pair | 11,690,880 / 96.91% |
| Mapped reads, singletons | 92,416 / 0.77% |
| Secondary alignments | 0 |
| Supplementary alignments | 78,415 / 0.65% |
| Read min/max/mean length | 30 / 101 / 101.27 |
| Duplicated reads (estimated) | 530,114 / 4.39% |
| Duplication rate | 3.43% |
| Clipped reads | 2,884,943 / 23.91% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 320,166,783 / 28.75% |
| Number/percentage of C's | 221,488,372 / 19.89% |
| Number/percentage of T's | 323,616,413 / 29.06% |
| Number/percentage of G's | 247,927,426 / 22.27% |
| Number/percentage of N's | 243,792 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 42.16% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.36 |
| Standard Deviation | 1.7152 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.61 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 68,488.43 |
| Standard Deviation | 2,547,968.68 |
| P25/Median/P75 | 151 / 194 / 257 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.97% |
| Mismatches | 10,433,125 |
| Insertions | 181,862 |
| Mapped reads with at least one insertion | 1.52% |
| Deletions | 611,698 |
| Mapped reads with at least one deletion | 5.05% |
| Homopolymer indels | 53.08% |

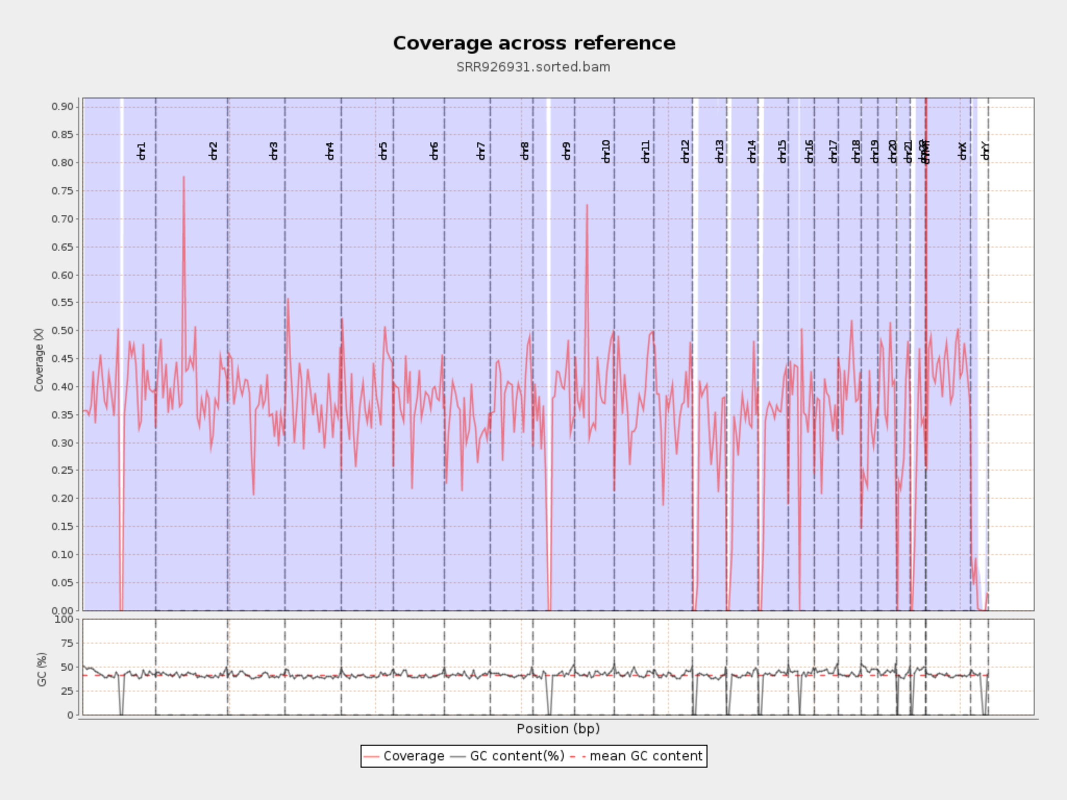
## 2.7. Chromosome stats

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

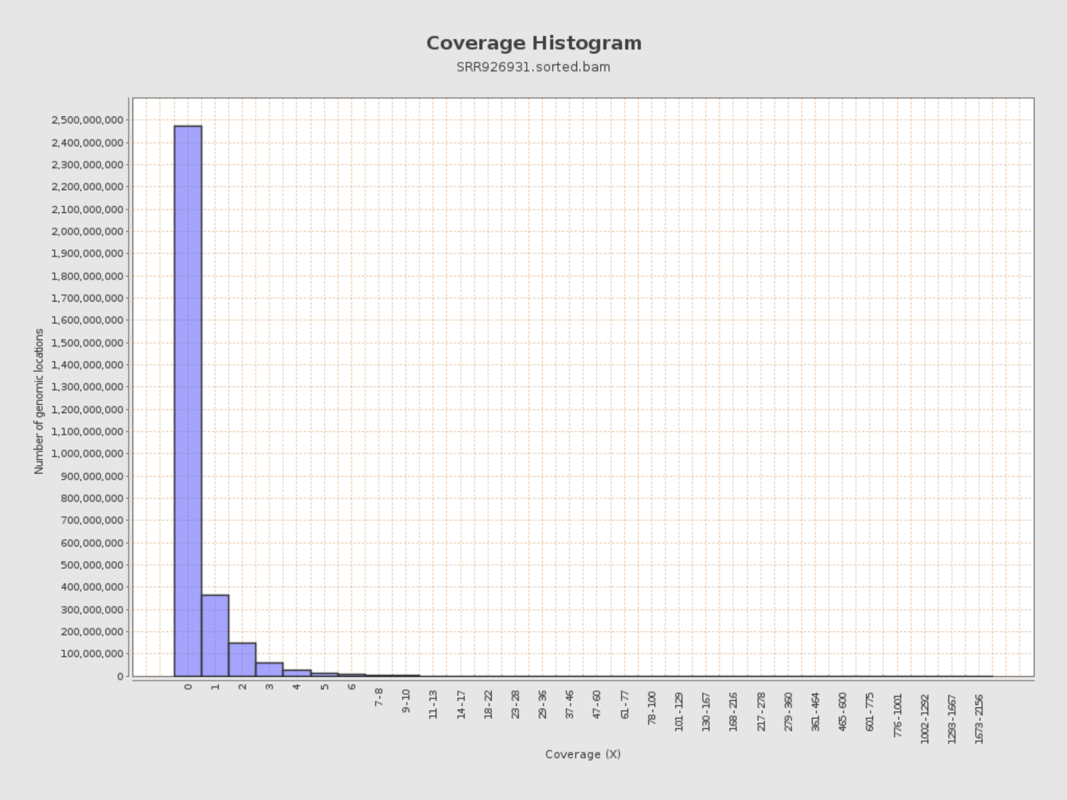
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 93758253 | 0.3762 | 2.5138 |
| chr2 | 243199373 | 99711462 | 0.41 | 2.6429 |
| chr3 | 198022430 | 72850825 | 0.3679 | 0.9138 |
| chr4 | 191154276 | 72564753 | 0.3796 | 1.6158 |
| chr5 | 180915260 | 69769769 | 0.3856 | 0.9332 |
| chr6 | 171115067 | 65073947 | 0.3803 | 1.5024 |
| chr7 | 159138663 | 52766919 | 0.3316 | 1.0216 |
| chr8 | 146364022 | 57559309 | 0.3933 | 1.1089 |
| chr9 | 141213431 | 47275207 | 0.3348 | 1.9614 |
| chr10 | 135534747 | 55382194 | 0.4086 | 3.611 |
| chr11 | 135006516 | 52029084 | 0.3854 | 1.3697 |
| chr12 | 133851895 | 49224310 | 0.3678 | 0.9405 |
| chr13 | 115169878 | 32576271 | 0.2829 | 0.7904 |
| chr14 | 107349540 | 31128341 | 0.29 | 0.8342 |
| chr15 | 102531392 | 30511302 | 0.2976 | 0.8339 |
| chr16 | 90354753 | 32078293 | 0.355 | 1.7468 |
| chr17 | 81195210 | 28428433 | 0.3501 | 1.1417 |
| chr18 | 78077248 | 32090150 | 0.411 | 2.1459 |
| chr19 | 59128983 | 17456610 | 0.2952 | 1.4965 |
| chr20 | 63025520 | 25924502 | 0.4113 | 1.0711 |
| chr21 | 48129895 | 14364266 | 0.2984 | 1.1925 |
| chr22 | 51304566 | 12631564 | 0.2462 | 0.7981 |
| chrMT | 16571 | 796993 | 48.0956 | 35.6903 |
| chrX | 155270560 | 66506486 | 0.4283 | 1.0993 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1848747 | 0.0311 | 1.1104 |

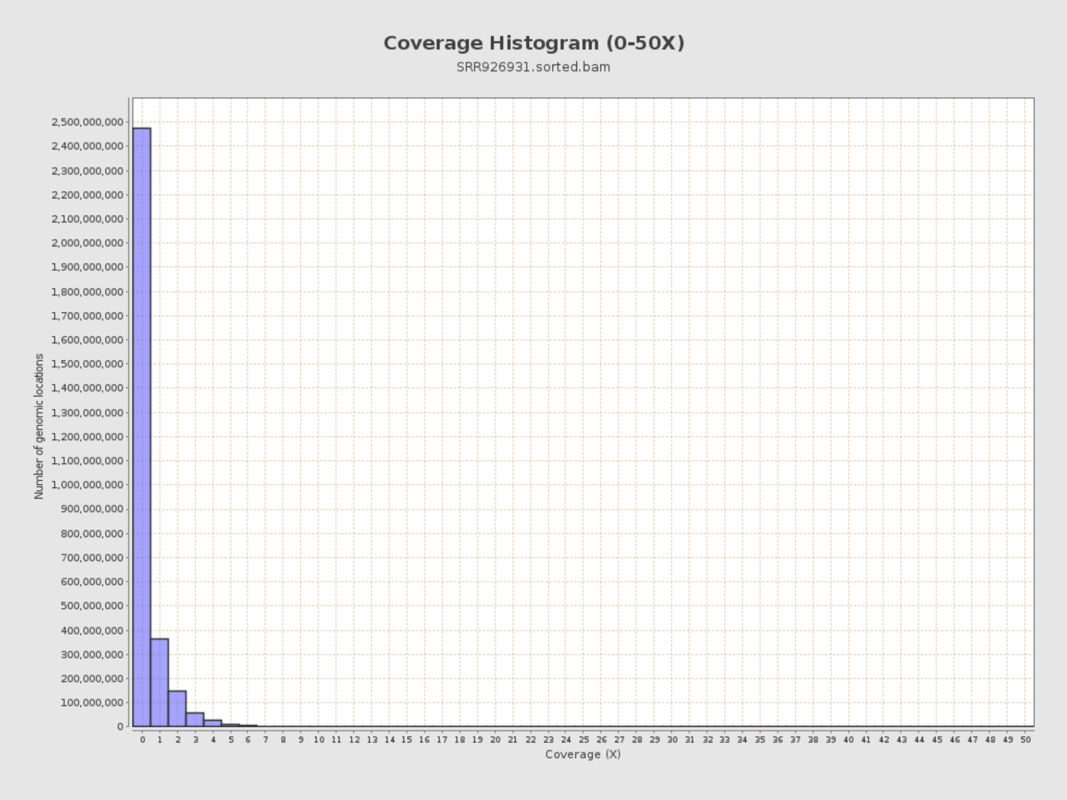
# 3. Results : Coverage across reference



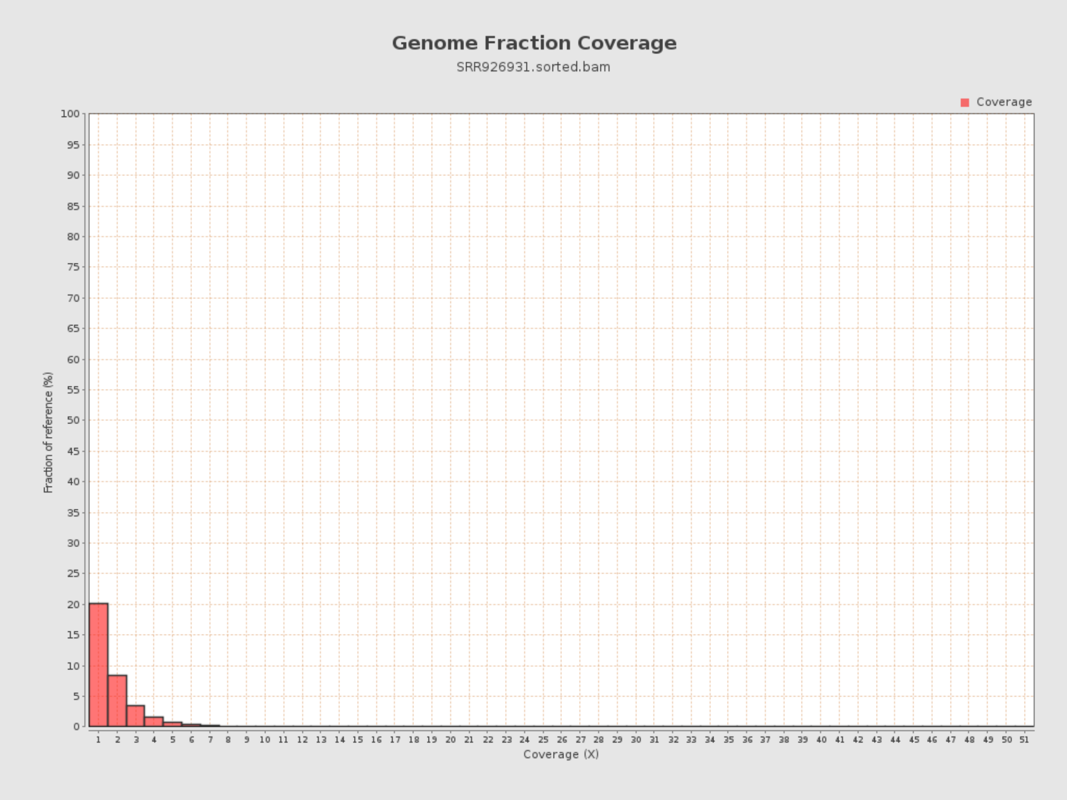
# 4. Results : Coverage Histogram



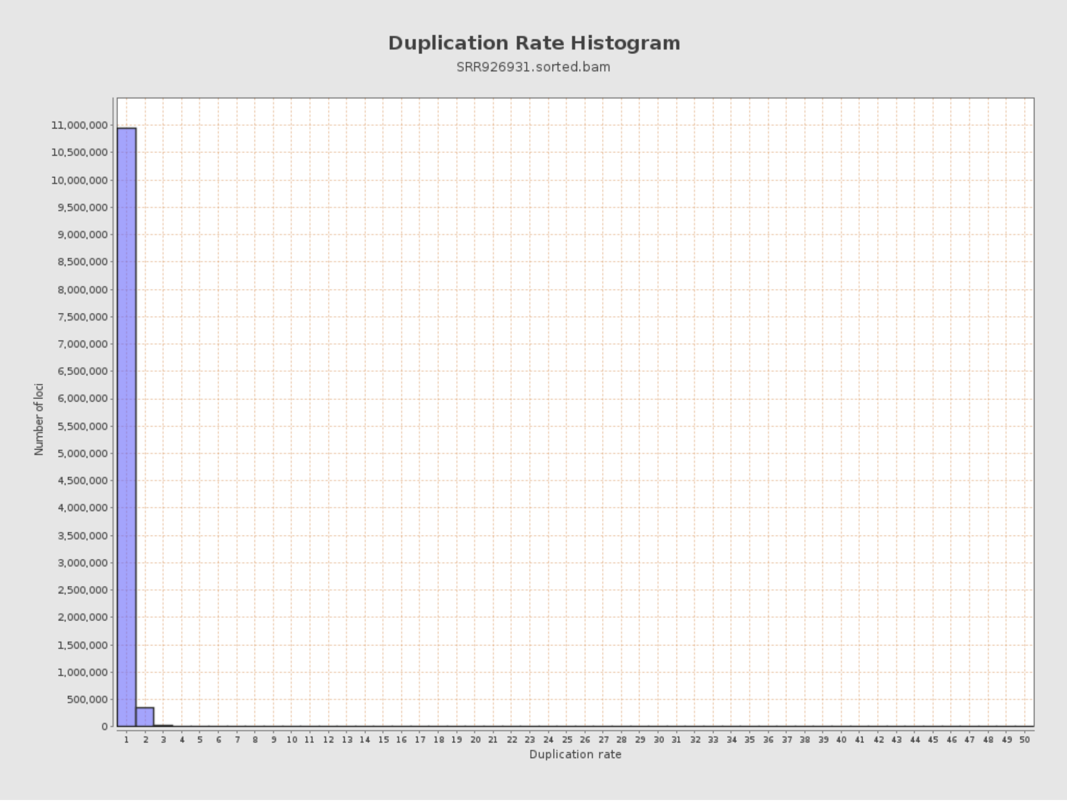
# 5. Results : Coverage Histogram (0-50X)



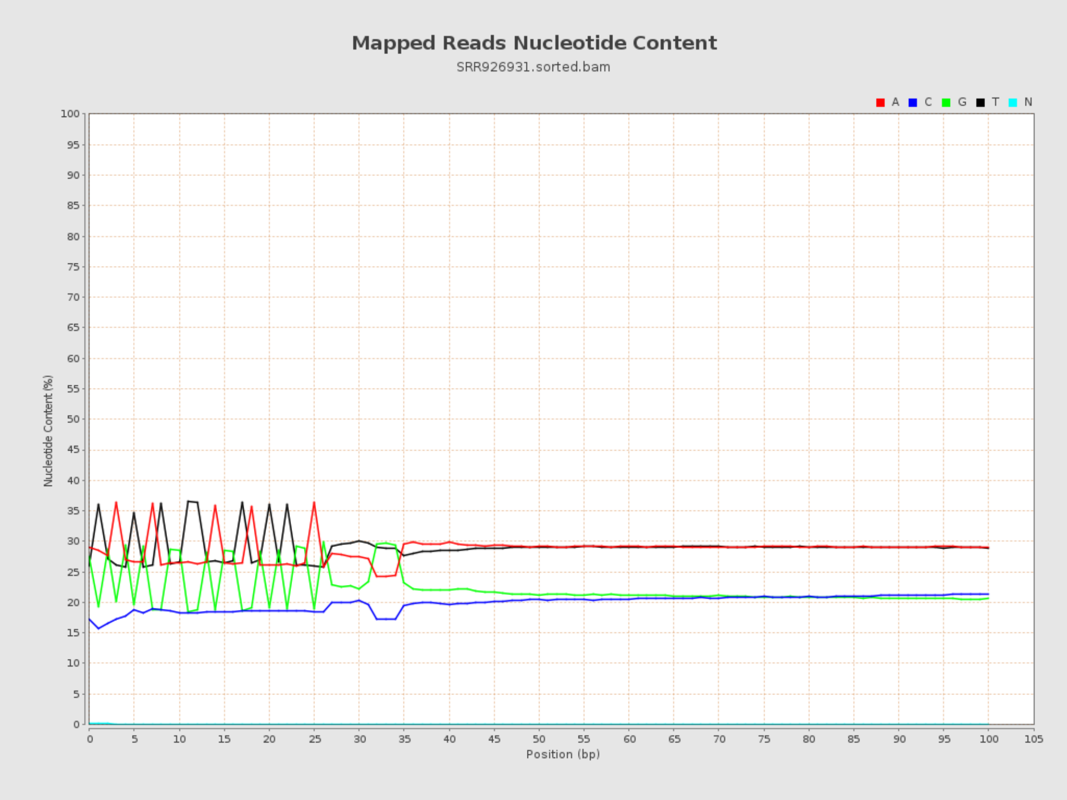
# 6. Results : Genome Fraction Coverage



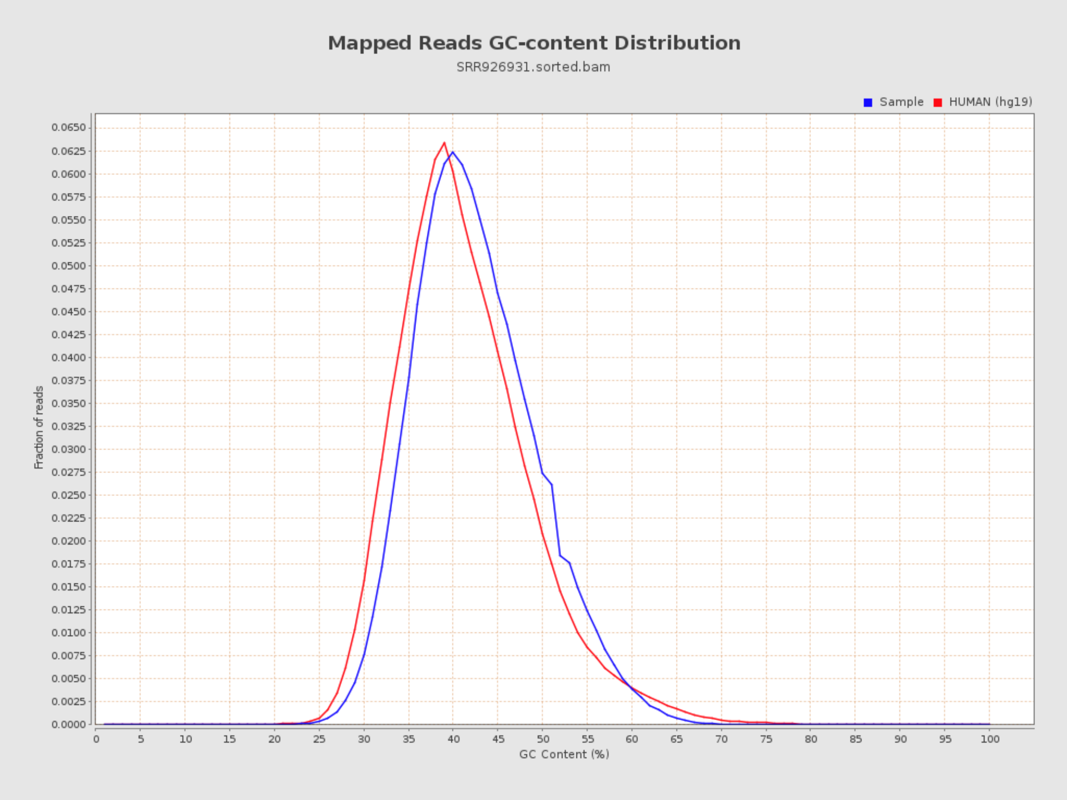
# 7. Results : Duplication Rate Histogram



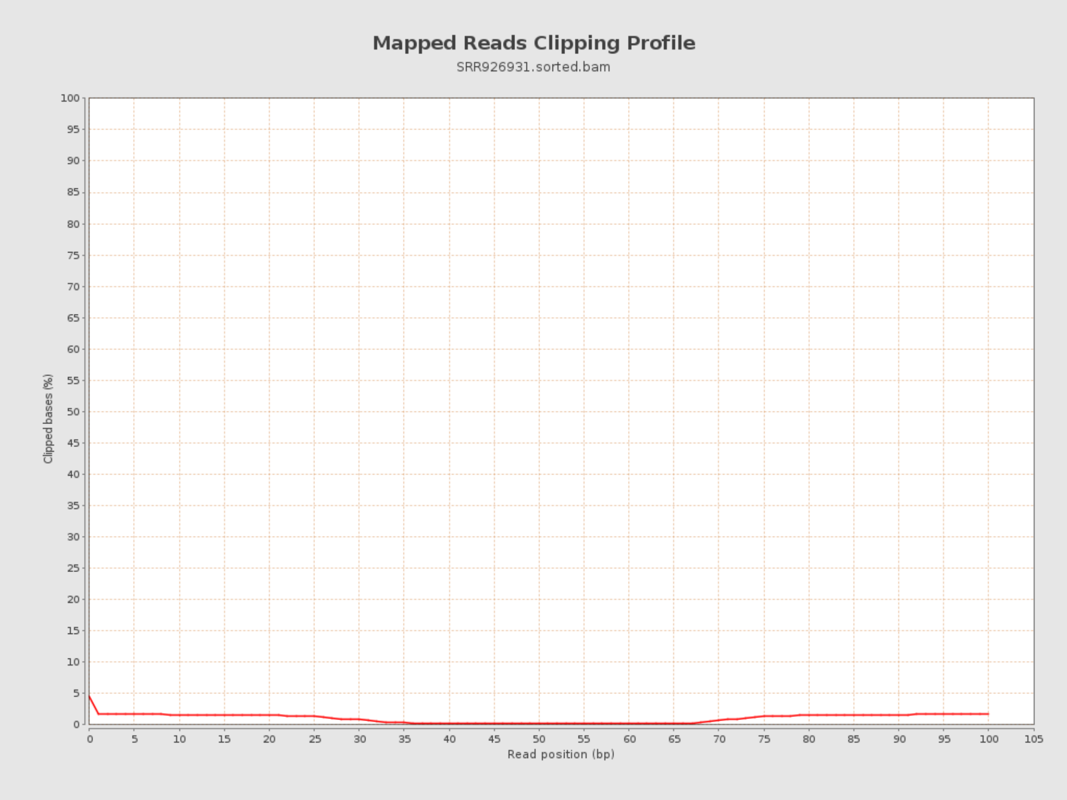
# 8. Results : Mapped Reads Nucleotide Content



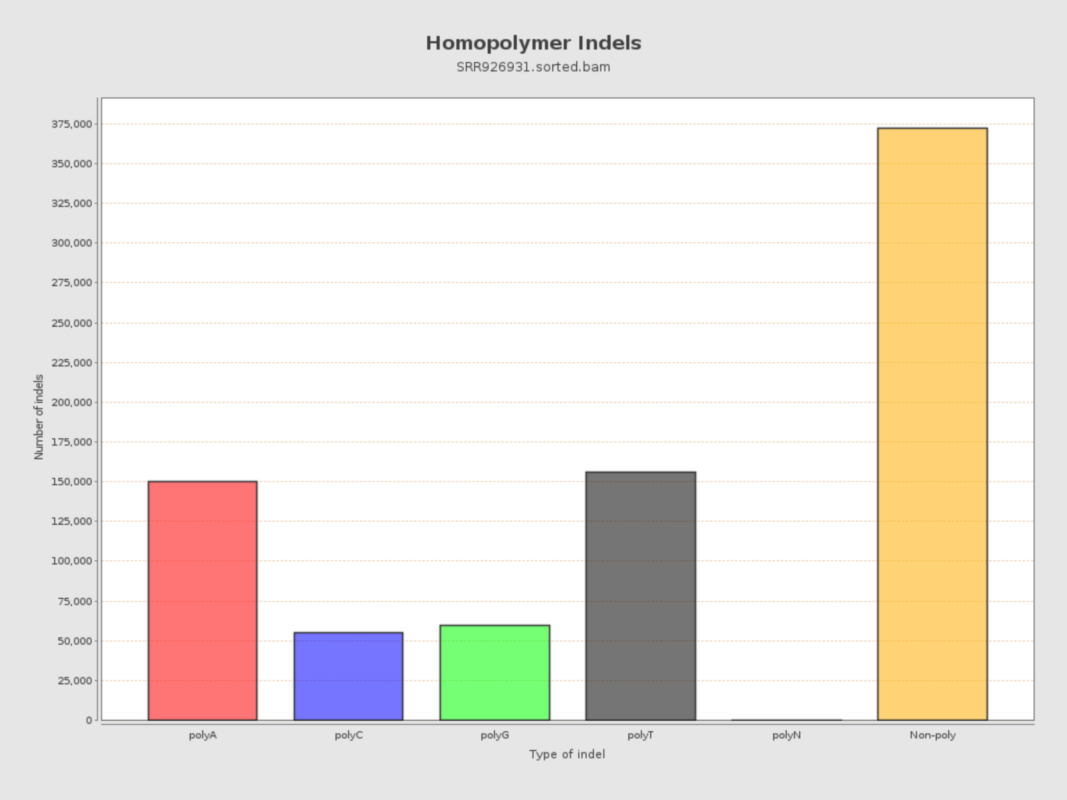
# 9. Results : Mapped Reads GC-content Distribution



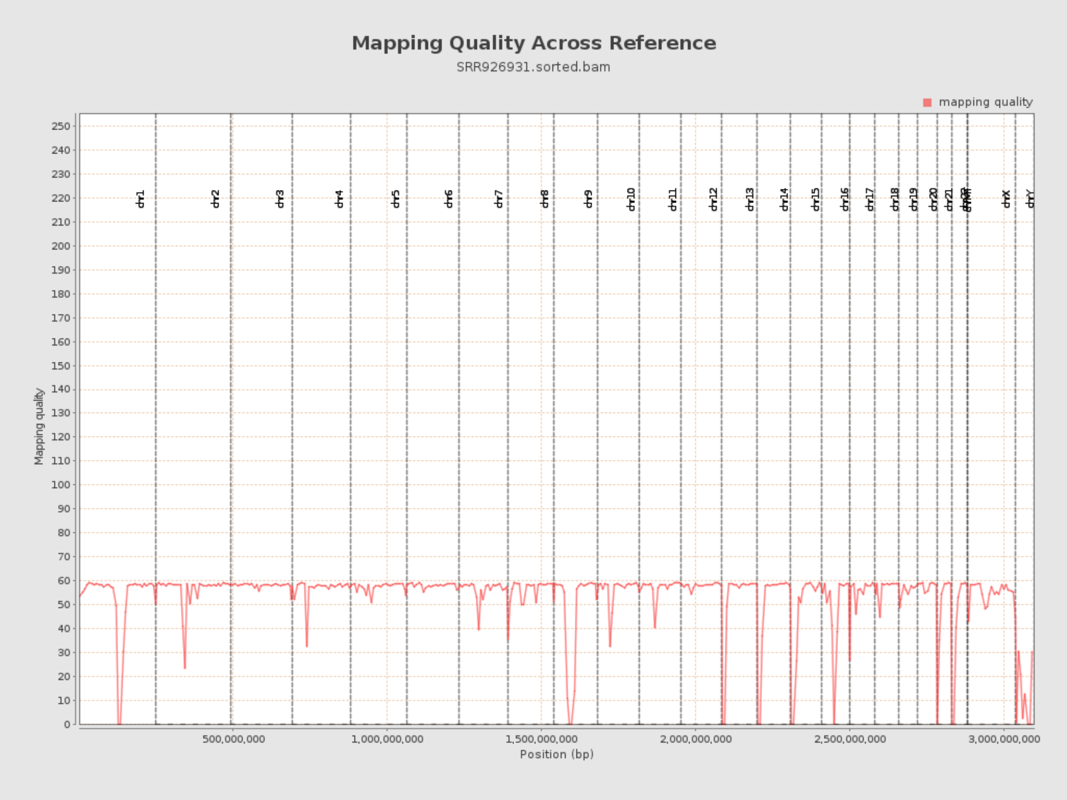
# 10. Results : Mapped Reads Clipping Profile



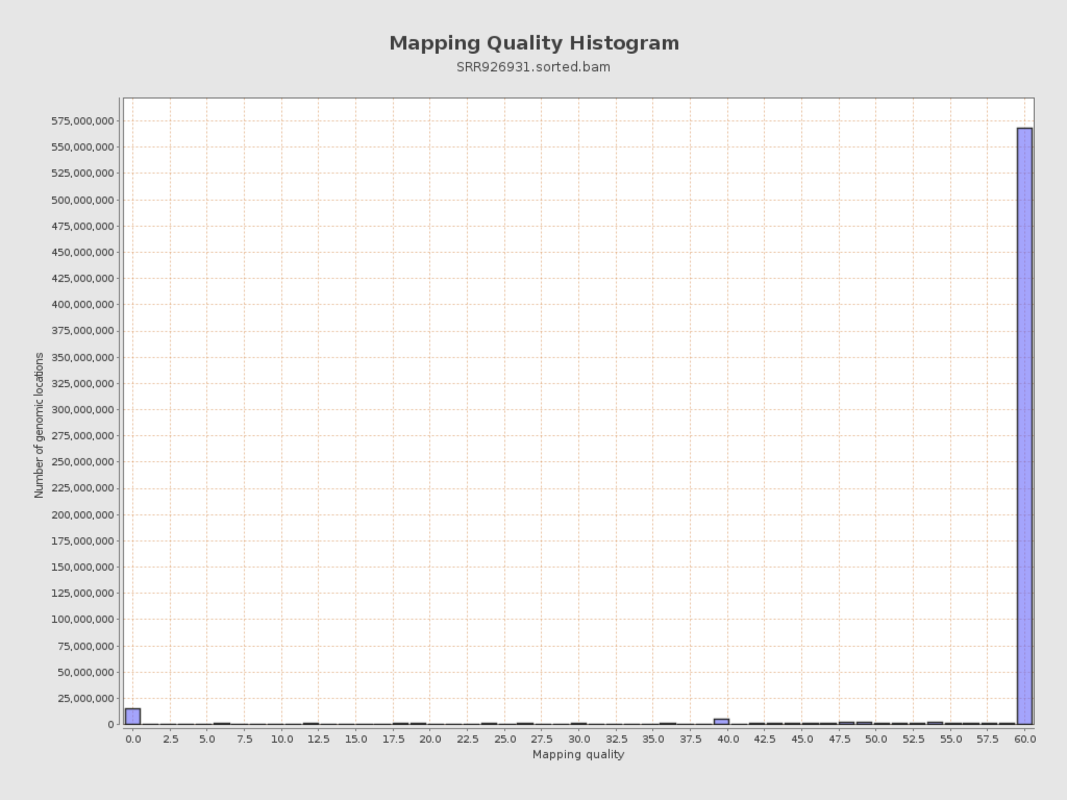
# 11. Results : Homopolymer Indels



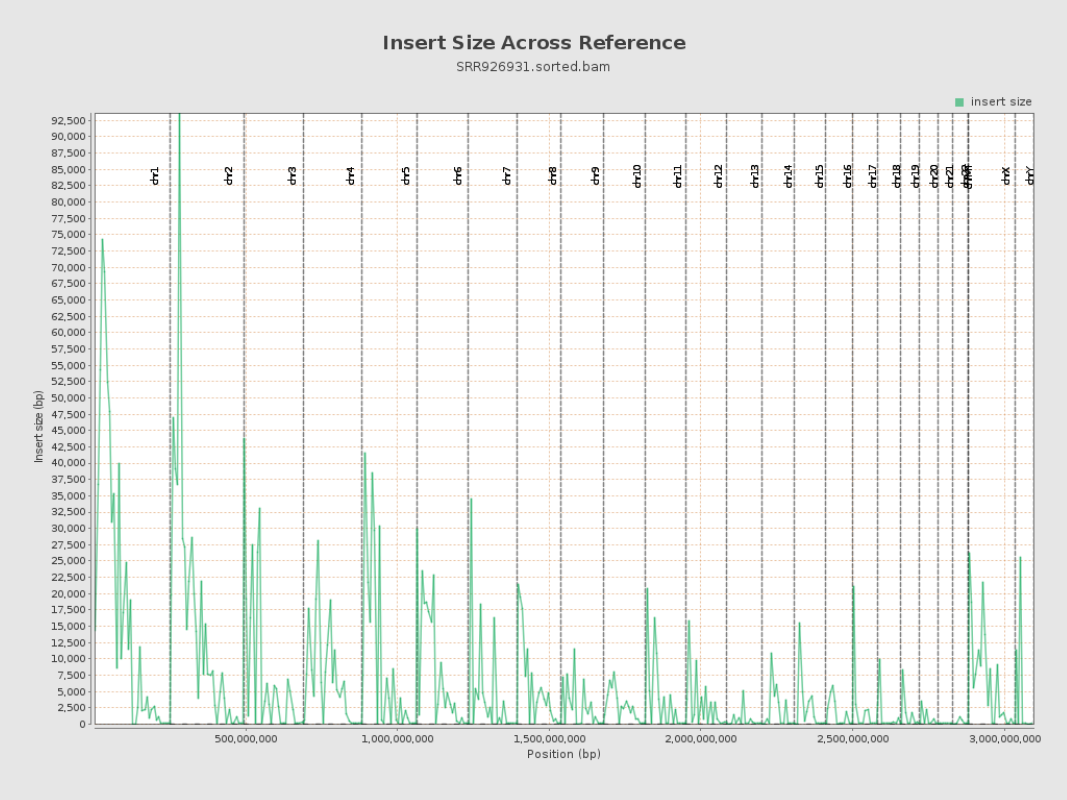
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram