# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/23 12:07:17*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR926977.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_SRR926977 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926977_1.fastq.gz SRR926977_2.fastq.gz` |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Apr 23 12:07:16 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR926977.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 21,767,278 |
| Mapped reads | 21,462,613 / 98.6% |
| Unmapped reads | 304,665 / 1.4% |
| Mapped paired reads | 21,462,613 / 98.6% |
| Mapped reads, first in pair | 10,777,624 / 49.51% |
| Mapped reads,  second in pair | 10,684,989 / 49.09% |
| Mapped reads, both in pair | 21,275,452 / 97.74% |
| Mapped reads, singletons | 187,161 / 0.86% |
| Secondary alignments | 0 |
| Supplementary alignments | 164,984 / 0.76% |
| Read min/max/mean length | 30 / 101 / 101.3 |
| Duplicated reads (estimated) | 1,229,226 / 5.65% |
| Duplication rate | 4.38% |
| Clipped reads | 4,415,592 / 20.29% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 583,898,893 / 28.44% |
| Number/percentage of C's | 420,369,305 / 20.48% |
| Number/percentage of T's | 590,811,481 / 28.78% |
| Number/percentage of G's | 457,721,782 / 22.3% |
| Number/percentage of N's | 167,084 / 0.01% |
| | |

| | |
|---|---|
| GC Percentage | 42.77% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.6637 |
| Standard Deviation | 2.772 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.65 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 73,335.15 |
| Standard Deviation | 2,654,840.25 |
| P25/Median/P75 | 145 / 180 / 232 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.97% |
| Mismatches | 19,386,141 |
| Insertions | 331,024 |
| Mapped reads with at least one insertion | 1.52% |
| Deletions | 1,099,617 |
| Mapped reads with at least one deletion | 4.99% |
| Homopolymer indels | 52.92% |

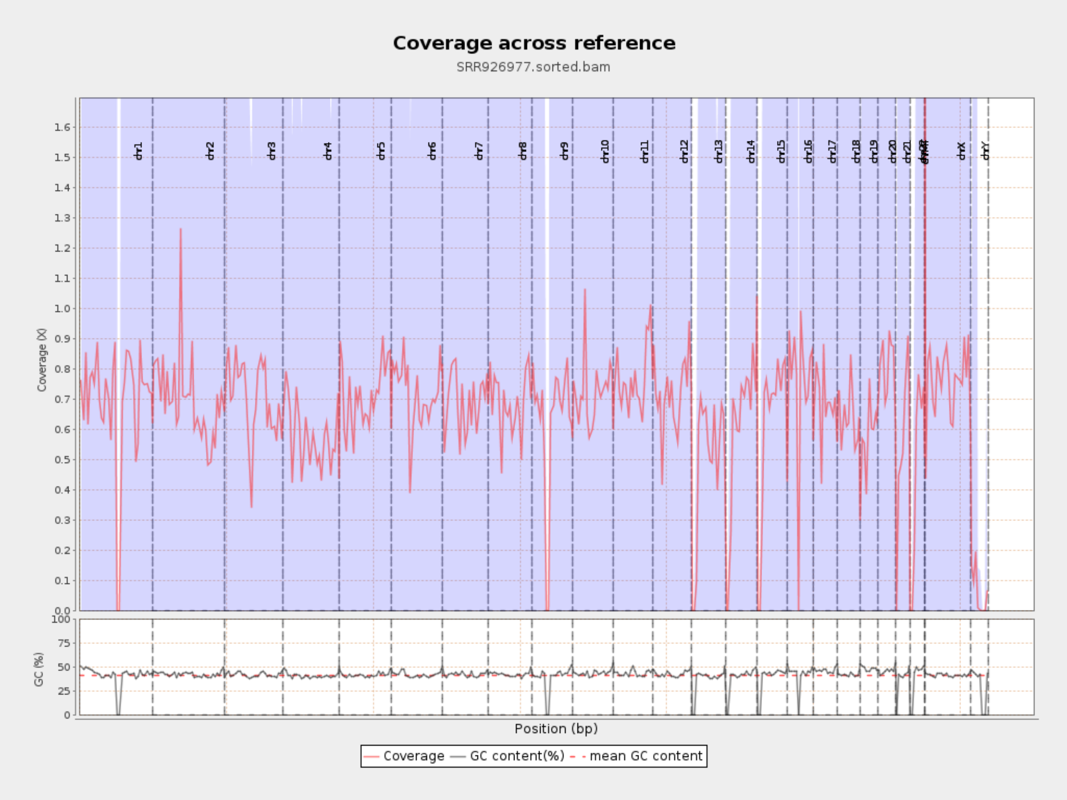
## 2.7. Chromosome stats

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

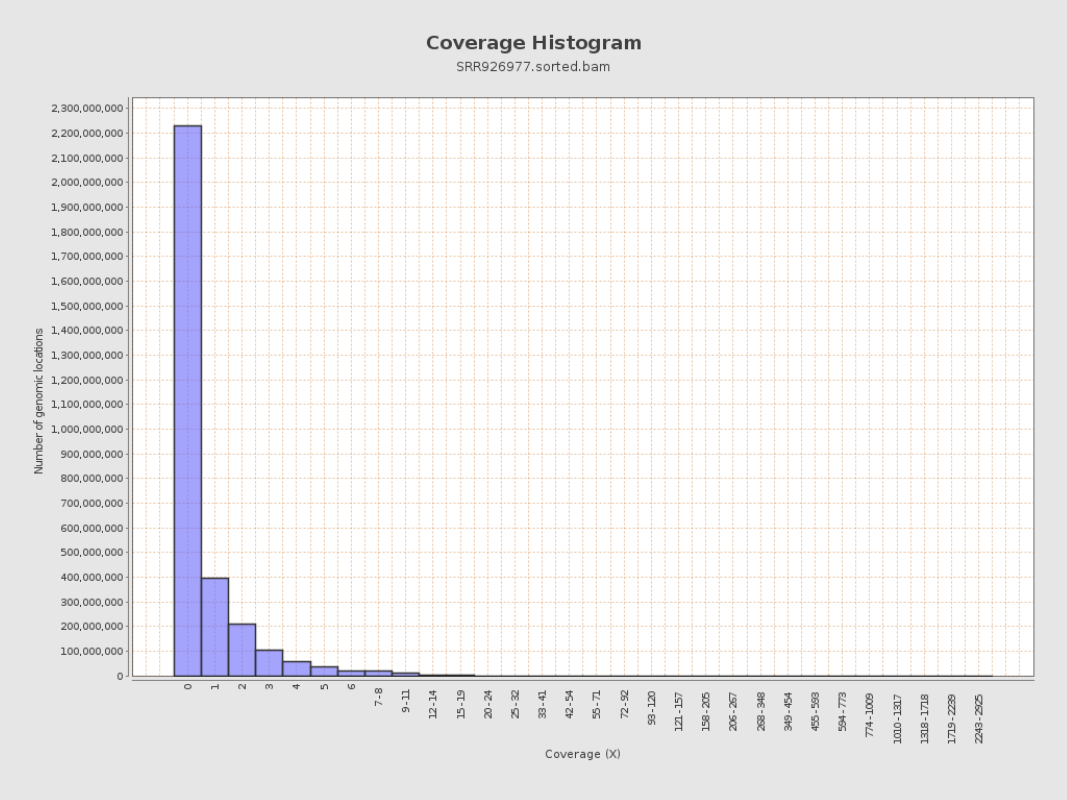
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 172211111 | 0.6909 | 3.5724 |
| chr2 | 243199373 | 170187828 | 0.6998 | 4.4892 |
| chr3 | 198022430 | 139143895 | 0.7027 | 1.5411 |
| chr4 | 191154276 | 110001065 | 0.5755 | 2.1891 |
| chr5 | 180915260 | 129214138 | 0.7142 | 1.5399 |
| chr6 | 171115067 | 122879815 | 0.7181 | 2.008 |
| chr7 | 159138663 | 109942706 | 0.6909 | 2.2658 |
| chr8 | 146364022 | 100294996 | 0.6852 | 1.7912 |
| chr9 | 141213431 | 87767781 | 0.6215 | 3.3882 |
| chr10 | 135534747 | 98526506 | 0.7269 | 4.5704 |
| chr11 | 135006516 | 103417853 | 0.766 | 3.8896 |
| chr12 | 133851895 | 95896131 | 0.7164 | 1.8065 |
| chr13 | 115169878 | 57142408 | 0.4962 | 1.3382 |
| chr14 | 107349540 | 63485420 | 0.5914 | 1.4751 |
| chr15 | 102531392 | 62666562 | 0.6112 | 1.543 |
| chr16 | 90354753 | 66661088 | 0.7378 | 3.543 |
| chr17 | 81195210 | 55563212 | 0.6843 | 2.1239 |
| chr18 | 78077248 | 50694364 | 0.6493 | 3.5678 |
| chr19 | 59128983 | 34077195 | 0.5763 | 2.2461 |
| chr20 | 63025520 | 50905538 | 0.8077 | 1.8154 |
| chr21 | 48129895 | 27489406 | 0.5712 | 2.3113 |
| chr22 | 51304566 | 24478362 | 0.4771 | 1.397 |
| chrMT | 16571 | 45872 | 2.7682 | 2.9561 |
| chrX | 155270560 | 118247443 | 0.7616 | 2.0945 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 3584329 | 0.0604 | 1.927 |

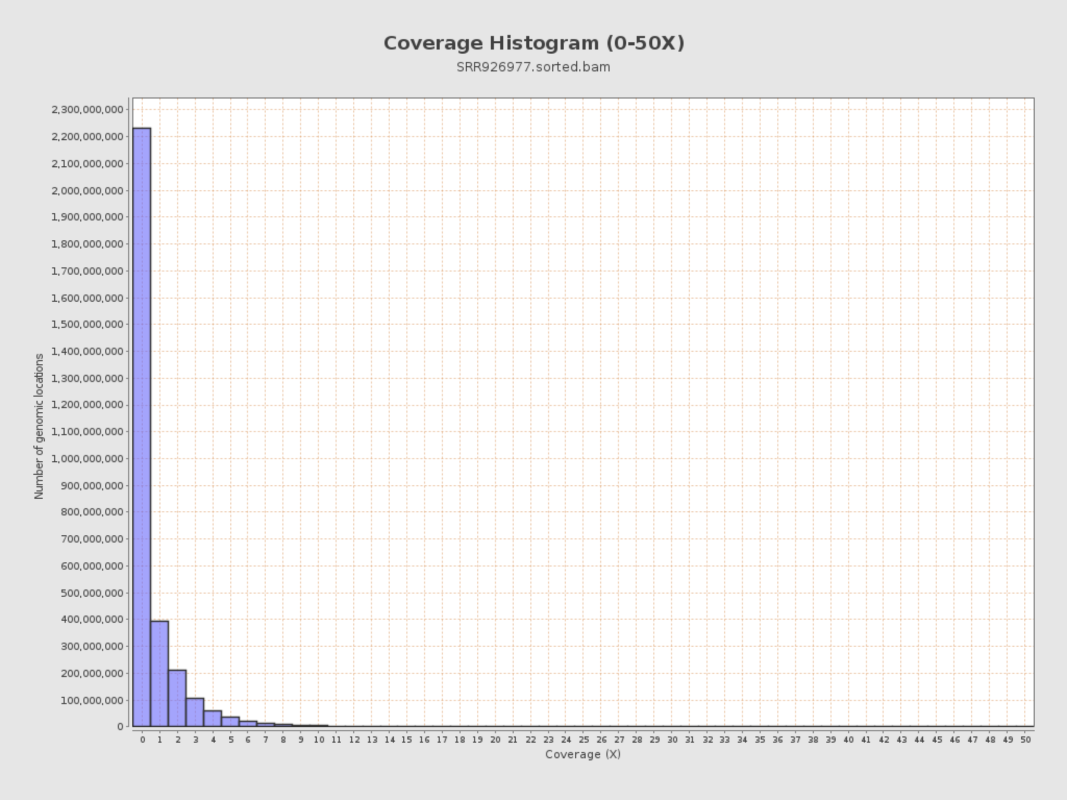
# 3. Results : Coverage across reference



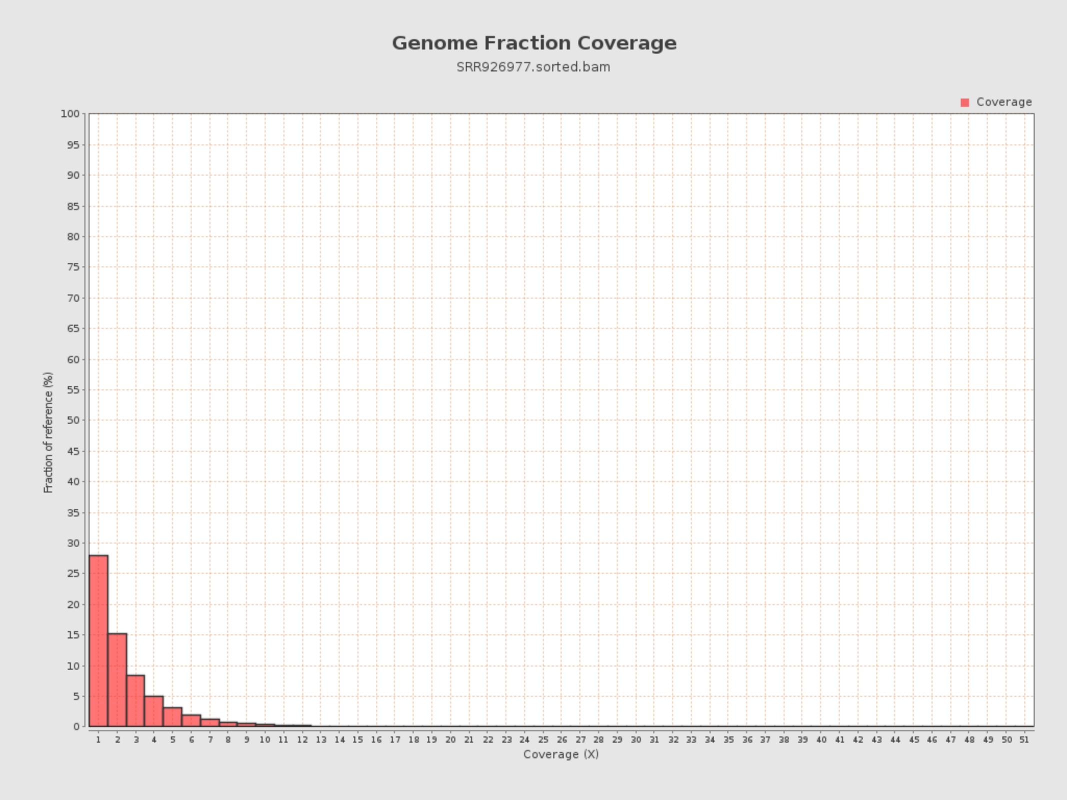
# 4. Results : Coverage Histogram



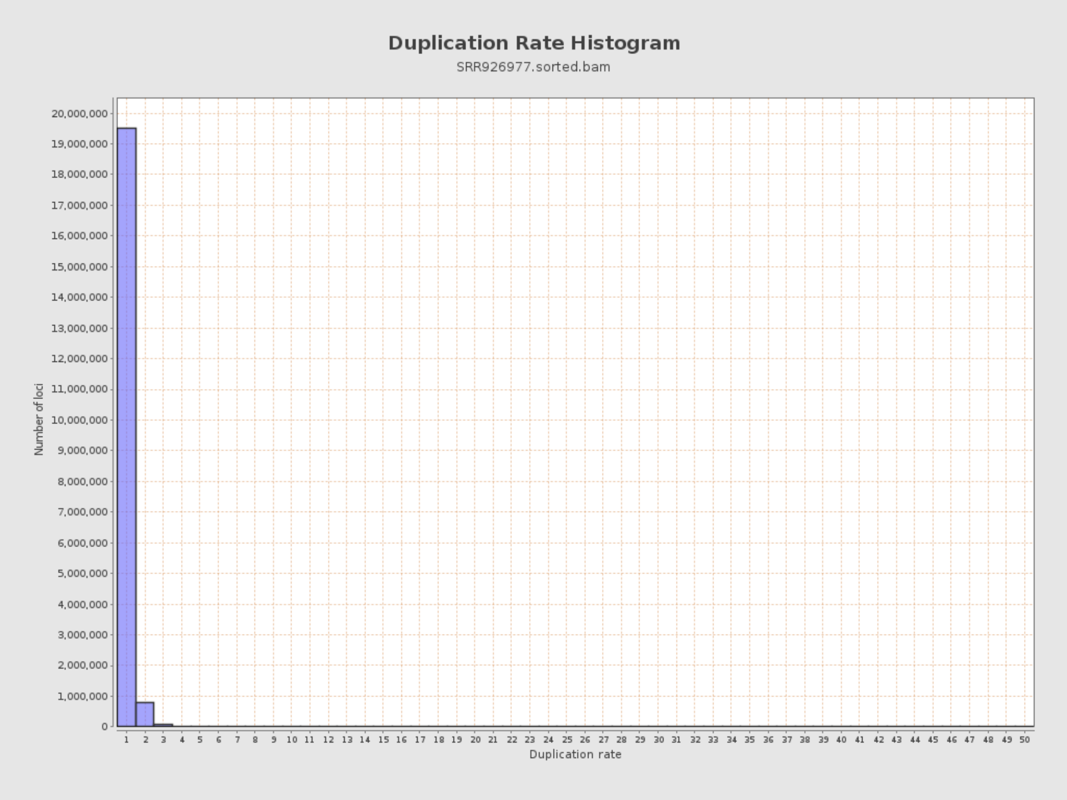
# 5. Results : Coverage Histogram (0-50X)



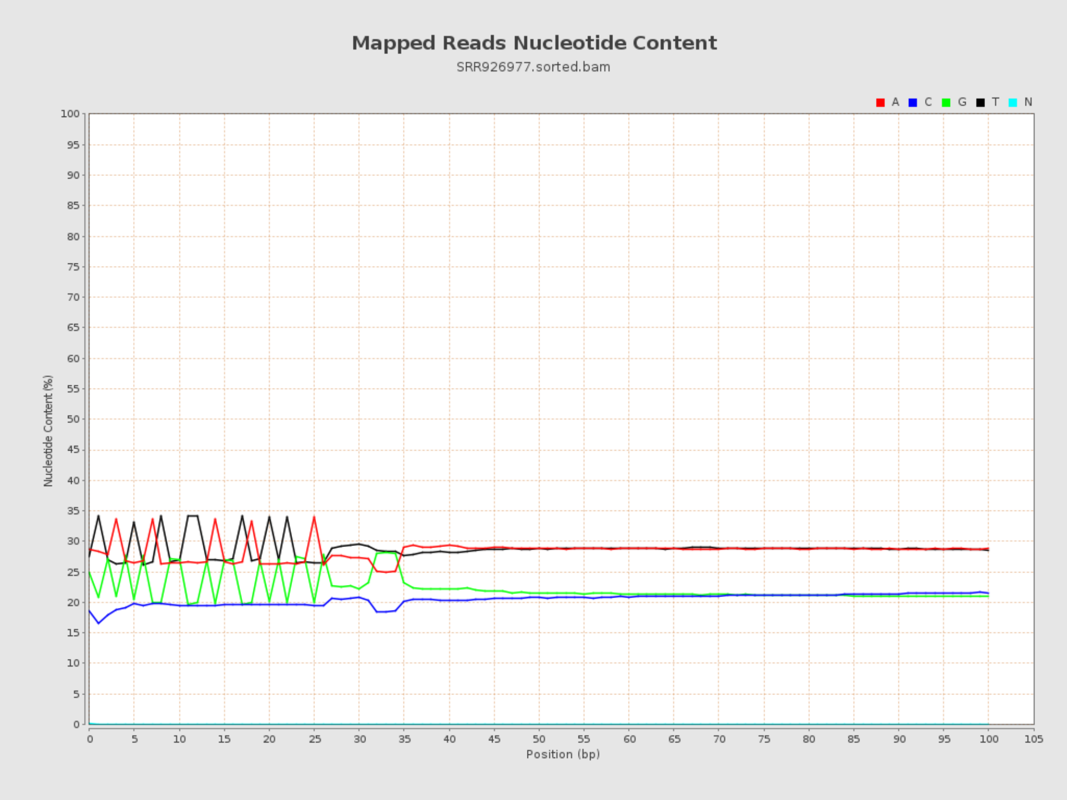
# 6. Results : Genome Fraction Coverage



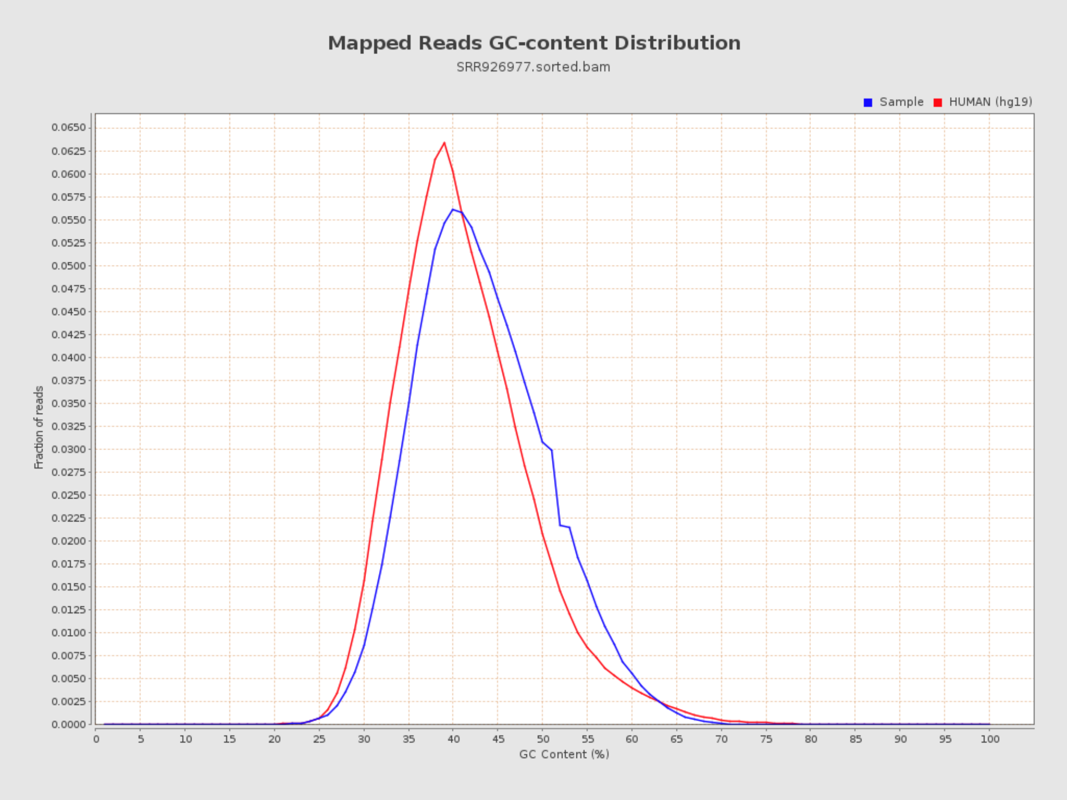
# 7. Results : Duplication Rate Histogram



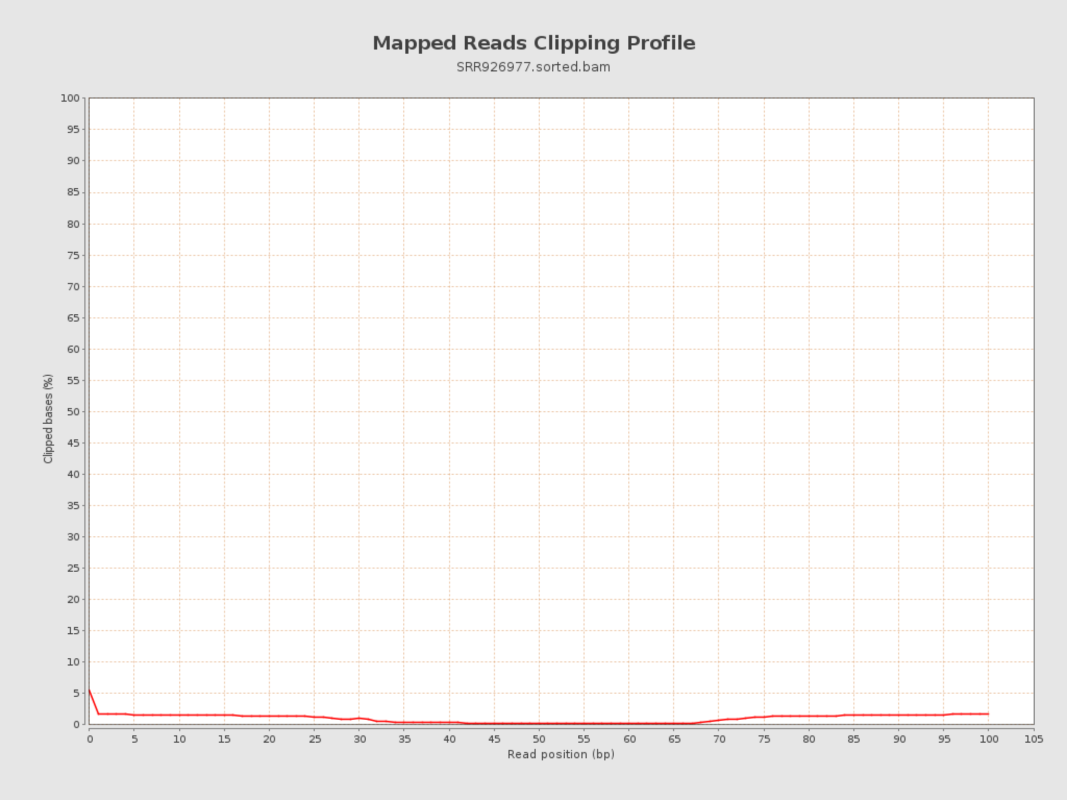
# 8. Results : Mapped Reads Nucleotide Content



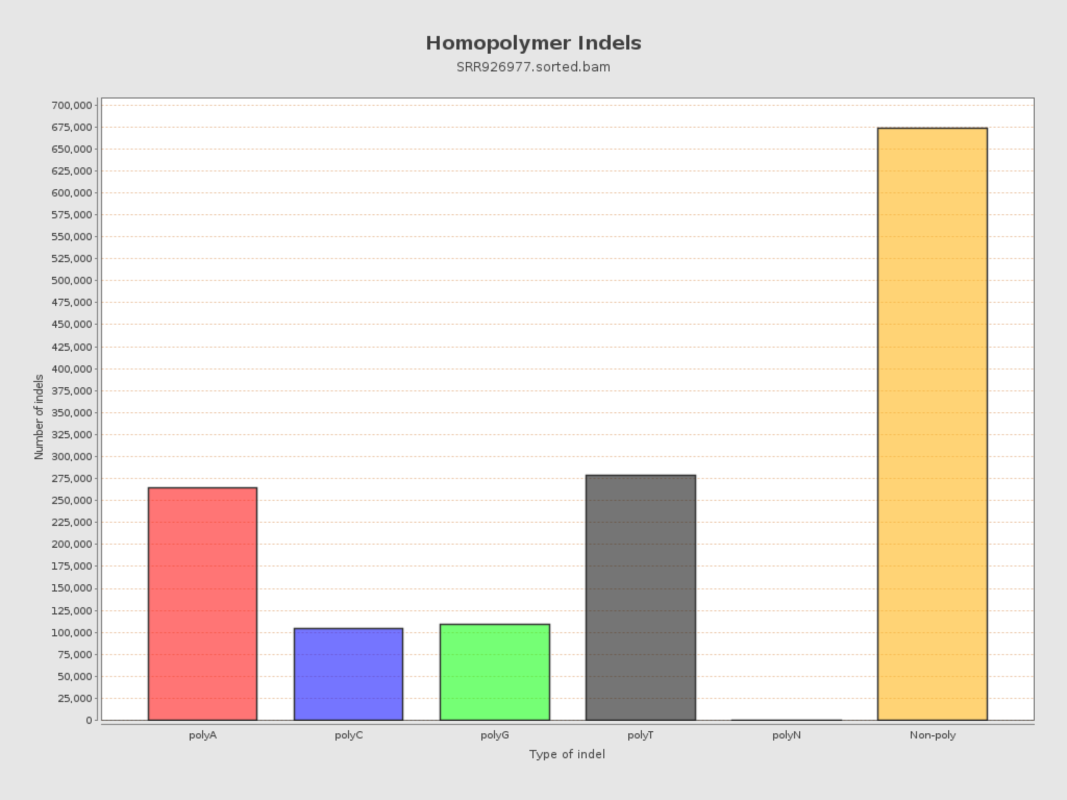
# 9. Results : Mapped Reads GC-content Distribution



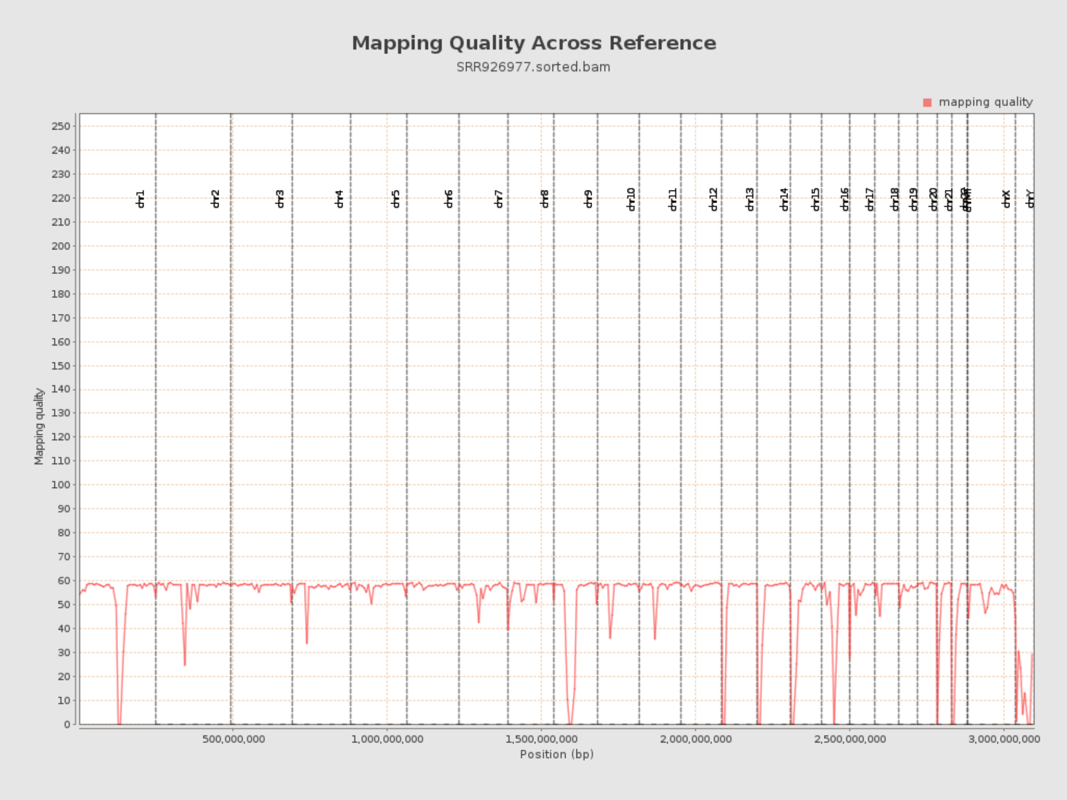
# 10. Results : Mapped Reads Clipping Profile



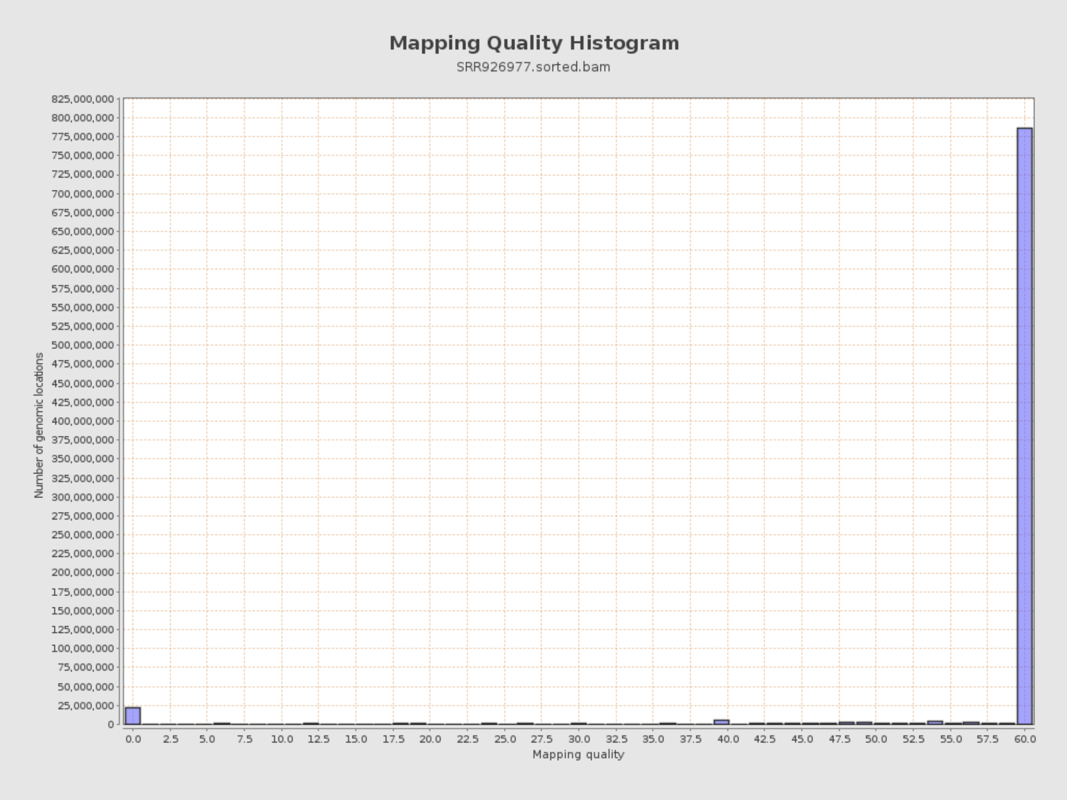
# 11. Results : Homopolymer Indels



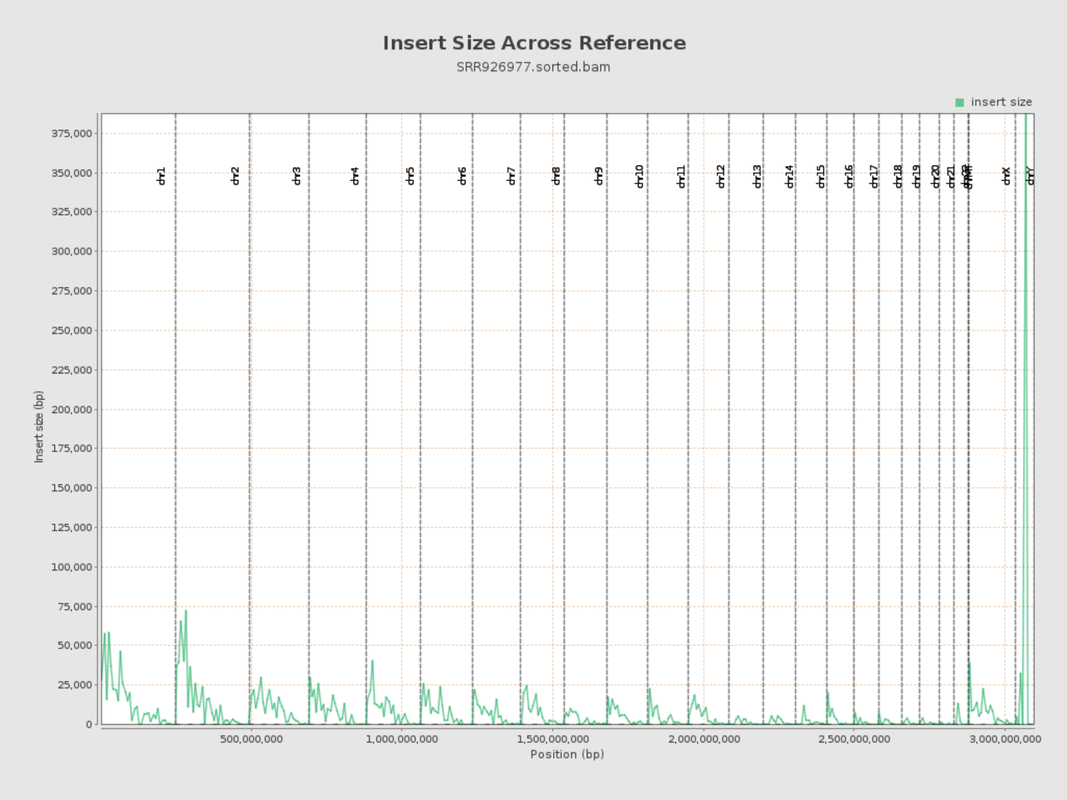
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram