# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/24 09:35:20*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR927025.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_SRR927025 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927025_1.fastq.gz SRR927025_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Apr 24 09:35:19 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR927025.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 27,383,484 |
| Mapped reads | 26,998,342 / 98.59% |
| Unmapped reads | 385,142 / 1.41% |
| Mapped paired reads | 26,998,342 / 98.59% |
| Mapped reads, first in pair | 13,534,154 / 49.42% |
| Mapped reads, second in pair | 13,464,188 / 49.17% |
| Mapped reads, both in pair | 26,766,526 / 97.75% |
| Mapped reads, singletons | 231,816 / 0.85% |
| Secondary alignments | 0 |
| Supplementary alignments | 242,591 / 0.89% |
| Read min/max/mean length | 30 / 101 / 101.37 |
| Duplicated reads (estimated) | 1,780,223 / 6.5% |
| Duplication rate | 4.9% |
| Clipped reads | 6,780,928 / 24.76% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 735,383,790 / 28.83% |
| Number/percentage of C's | 504,695,247 / 19.79% |
| Number/percentage of T's | 744,996,251 / 29.21% |
| Number/percentage of G's | 564,995,824 / 22.15% |
| Number/percentage of N's | 555,454 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 41.94% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.8245 |
| Standard Deviation | 3.9923 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.52 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 95,524.73 |
| Standard Deviation | 3,012,659.91 |
| P25/Median/P75 | 159 / 205 / 272 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.95% |
| Mismatches | 23,478,649 |
| Insertions | 413,110 |
| Mapped reads with at least one insertion | 1.51% |
| Deletions | 1,351,479 |
| Mapped reads with at least one deletion | 4.87% |
| Homopolymer indels | 53.1% |

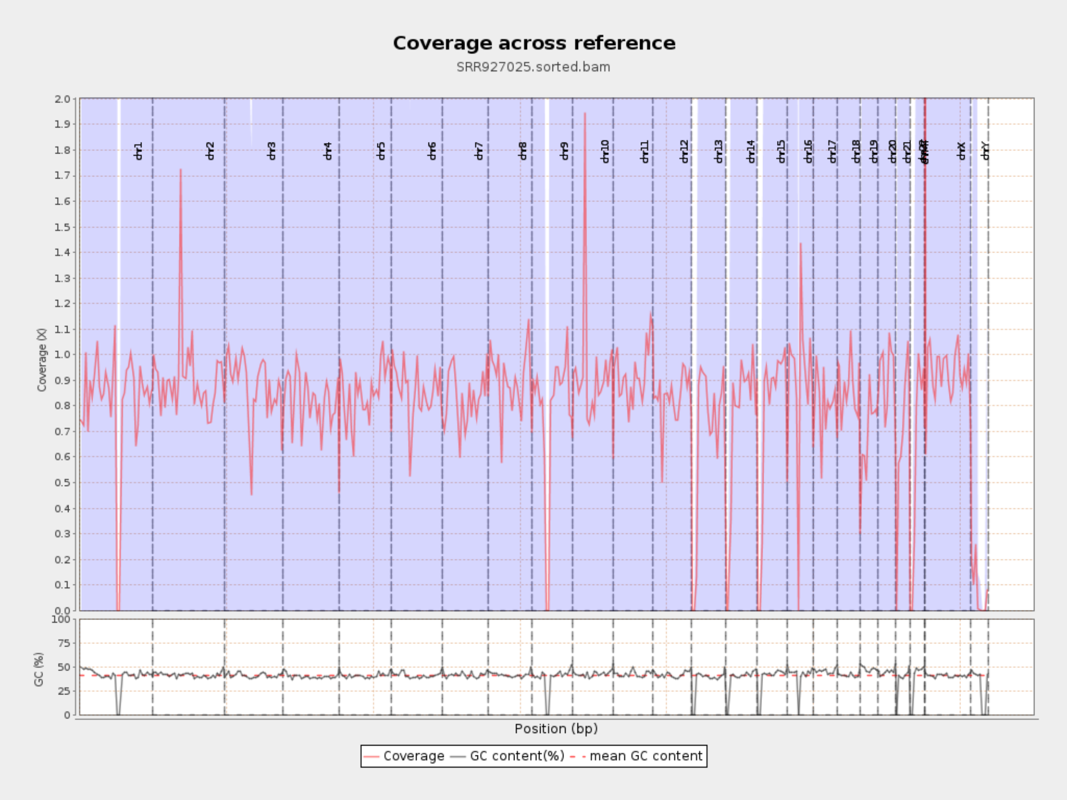
## 2.7. Chromosome stats

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

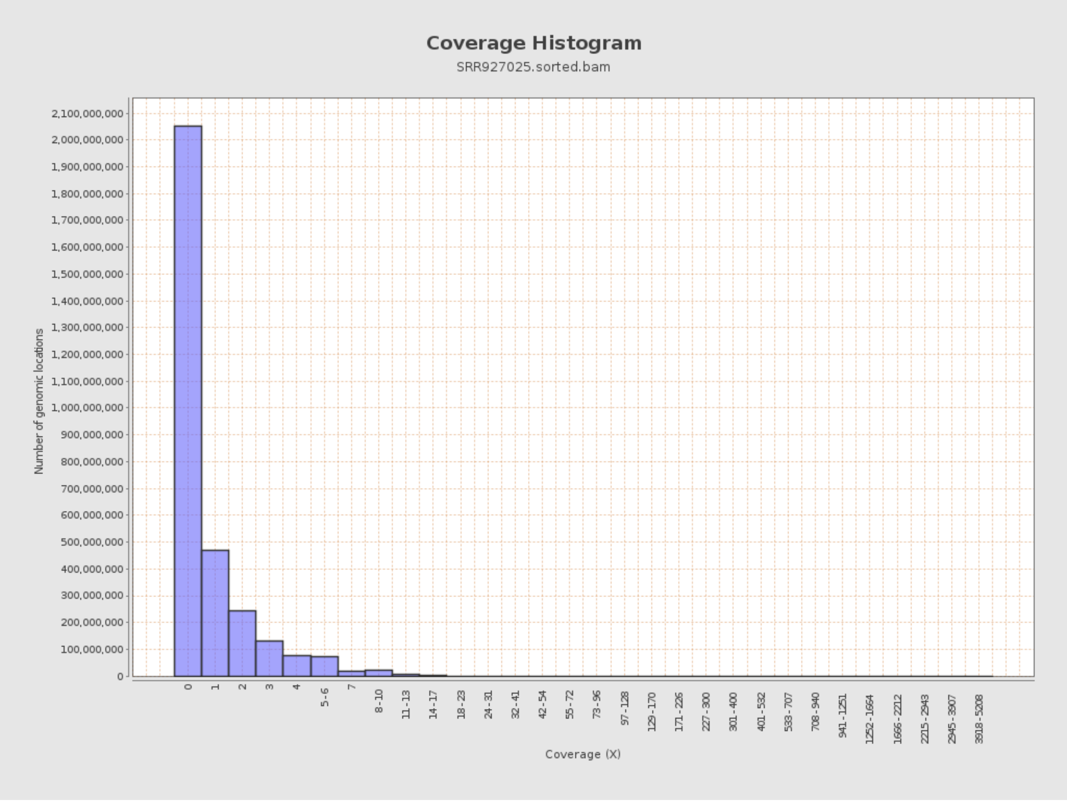
| | | **bases** | **coverage** | **deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 203518445 | 0.8165 | 5.7934 |
| chr2 | 243199373 | 221408611 | 0.9104 | 5.8556 |
| chr3 | 198022430 | 174167201 | 0.8795 | 1.7695 |
| chr4 | 191154276 | 157521853 | 0.8241 | 2.5818 |
| chr5 | 180915260 | 154126451 | 0.8519 | 1.669 |
| chr6 | 171115067 | 147289397 | 0.8608 | 1.7592 |
| chr7 | 159138663 | 131733749 | 0.8278 | 2.5954 |
| chr8 | 146364022 | 132198155 | 0.9032 | 2.0585 |
| chr9 | 141213431 | 108448809 | 0.768 | 3.9669 |
| chr10 | 135534747 | 127414339 | 0.9401 | 10.7587 |
| chr11 | 135006516 | 123300473 | 0.9133 | 4.1356 |
| chr12 | 133851895 | 111280236 | 0.8314 | 1.6691 |
| chr13 | 115169878 | 78987247 | 0.6858 | 1.4993 |
| chr14 | 107349540 | 78070829 | 0.7273 | 1.6059 |
| chr15 | 102531392 | 76550510 | 0.7466 | 1.6342 |
| chr16 | 90354753 | 80224381 | 0.8879 | 5.1125 |
| chr17 | 81195210 | 65089887 | 0.8016 | 2.1369 |
| chr18 | 78077248 | 68466611 | 0.8769 | 4.2391 |
| chr19 | 59128983 | 40956303 | 0.6927 | 3.4967 |
| chr20 | 63025520 | 58146065 | 0.9226 | 1.9147 |
| chr21 | 48129895 | 33701095 | 0.7002 | 2.4151 |
| chr22 | 51304566 | 31489409 | 0.6138 | 1.5594 |
| chrMT | 16571 | 136431 | 8.2331 | 6.9125 |
| chrX | 155270560 | 143822184 | 0.9263 | 2.1784 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 4497375 | 0.0757 | 2.3601 |

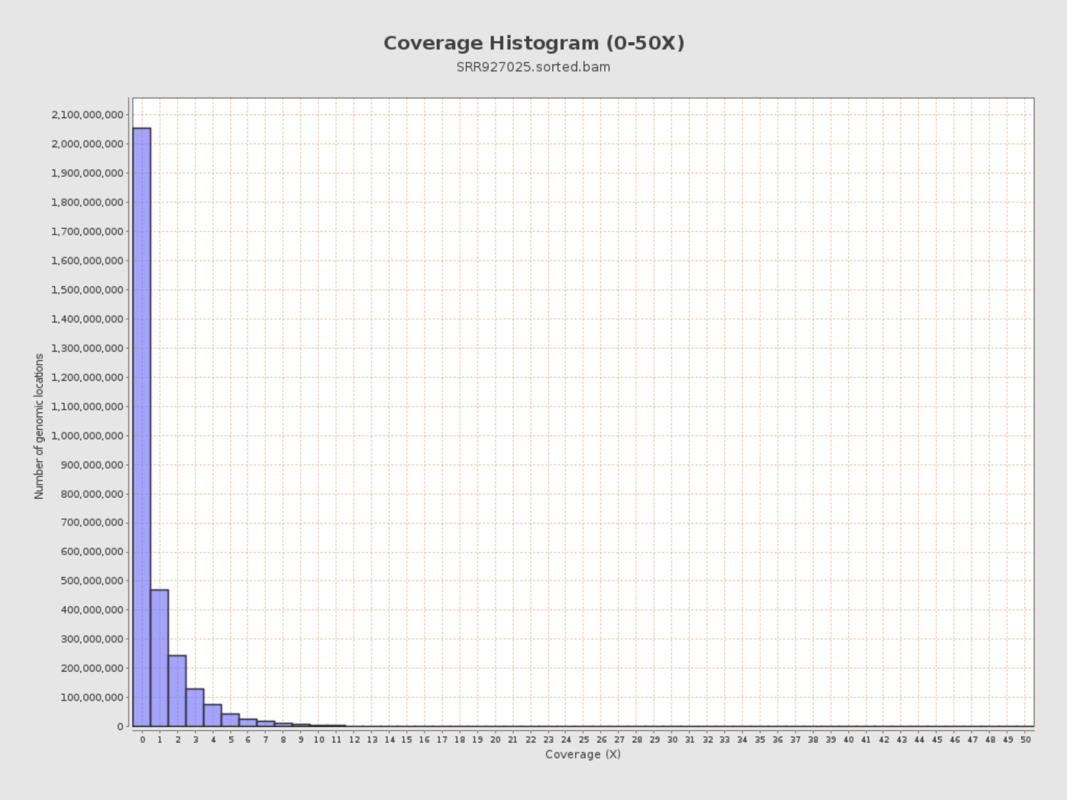
# 3. Results : Coverage across reference



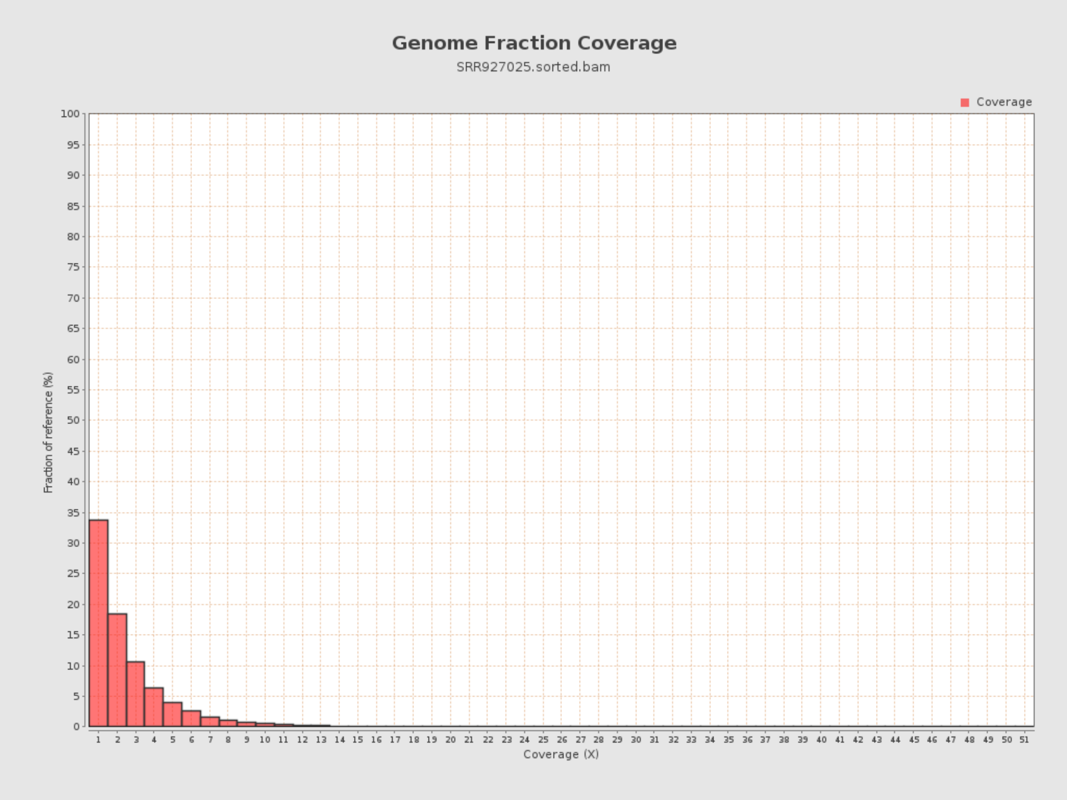
# 4. Results : Coverage Histogram



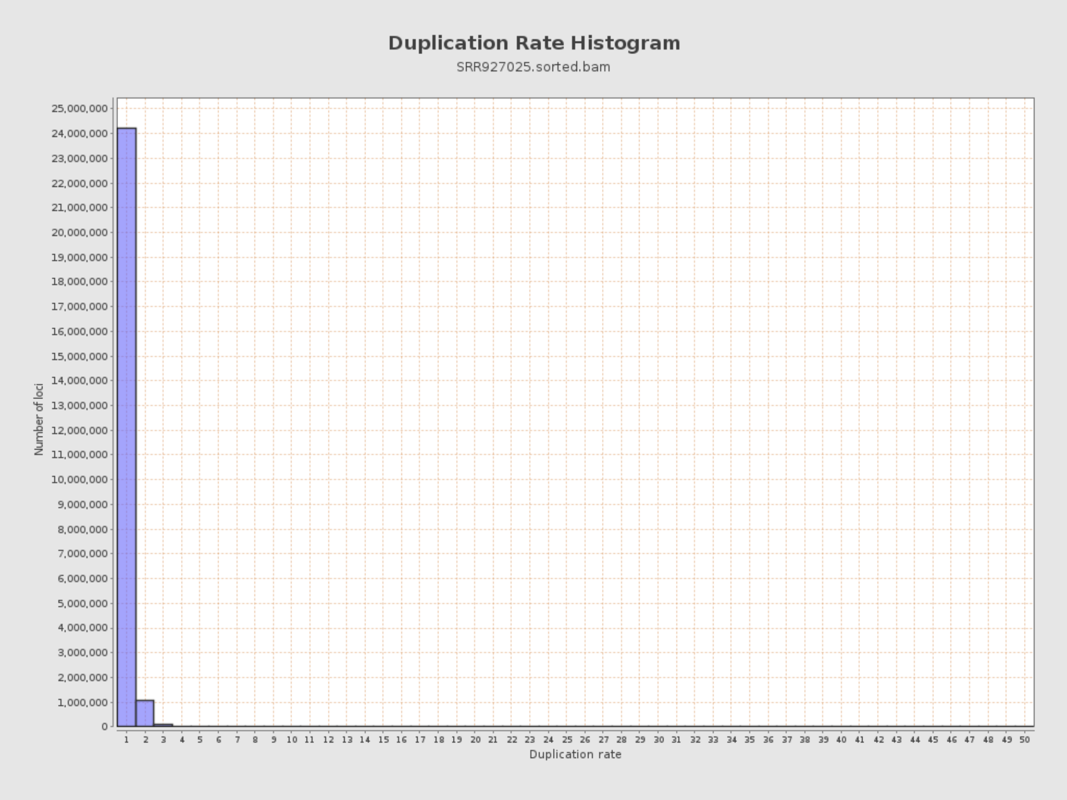
# 5. Results : Coverage Histogram (0-50X)



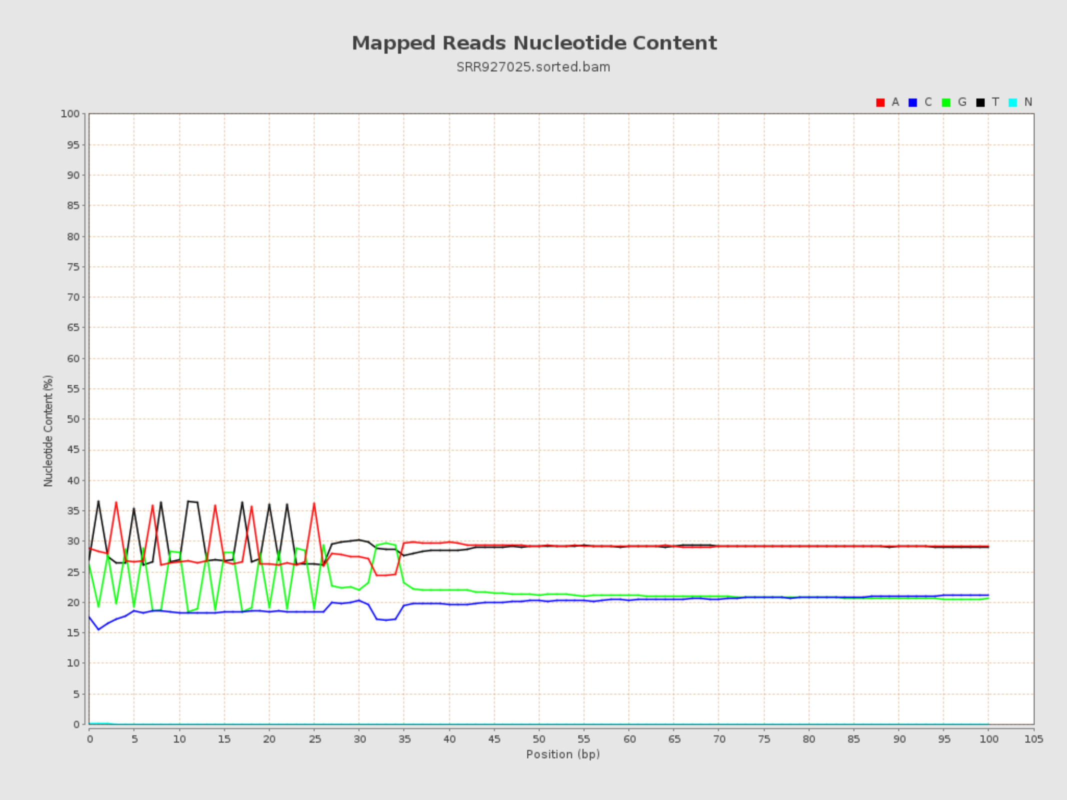
# 6. Results : Genome Fraction Coverage



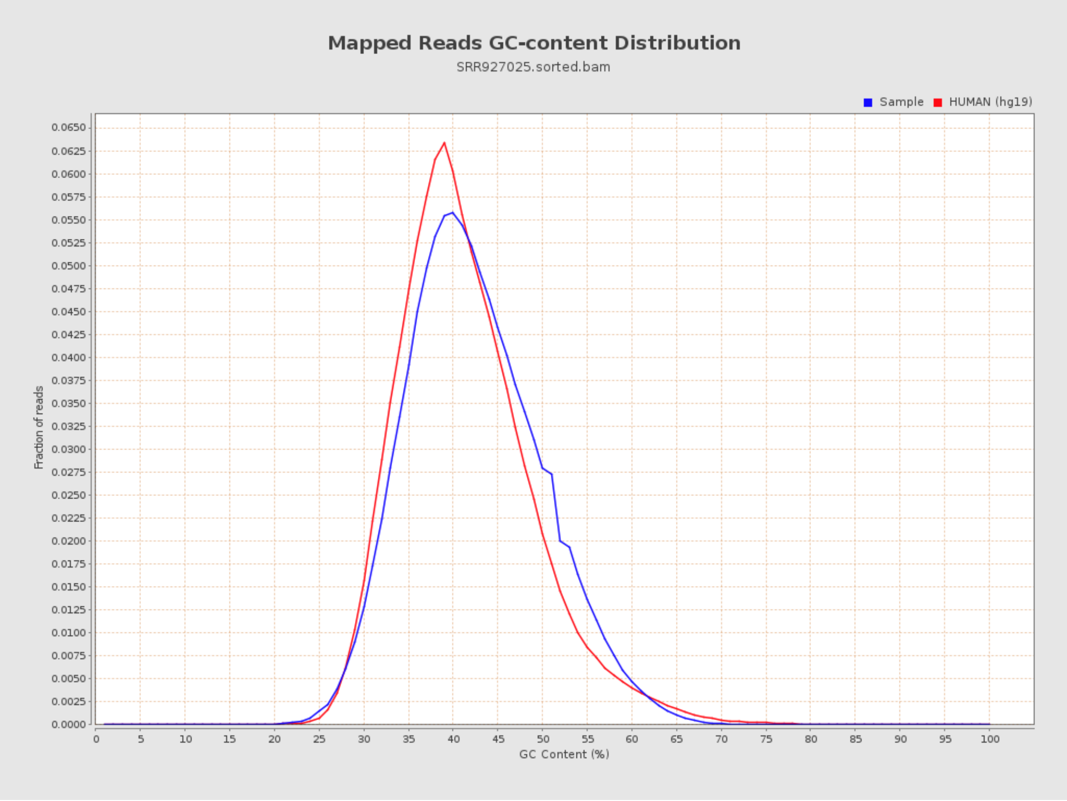
# 7. Results : Duplication Rate Histogram



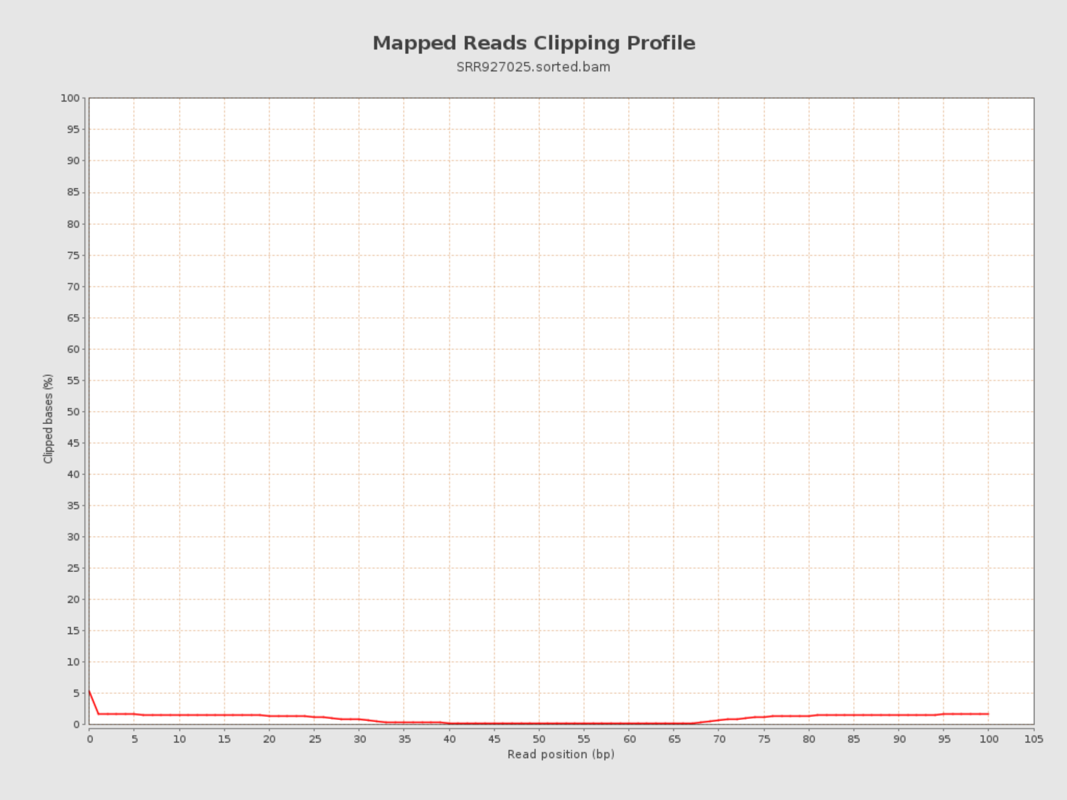
# 8. Results : Mapped Reads Nucleotide Content



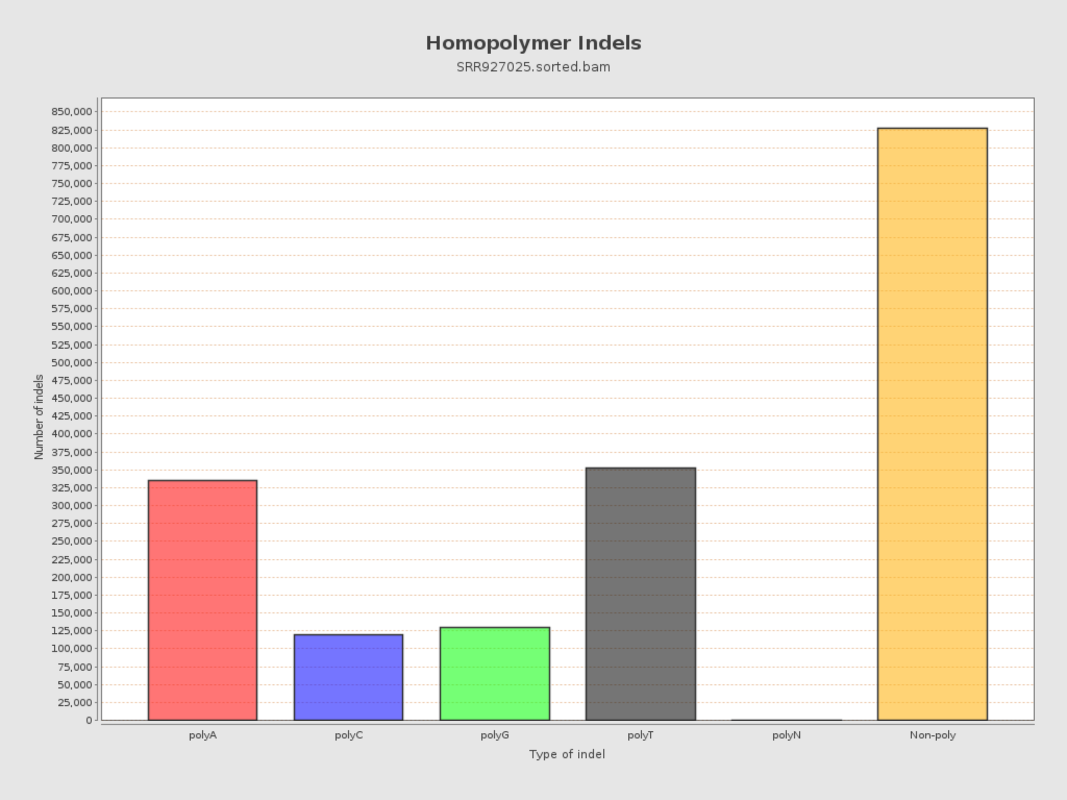
# 9. Results : Mapped Reads GC-content Distribution



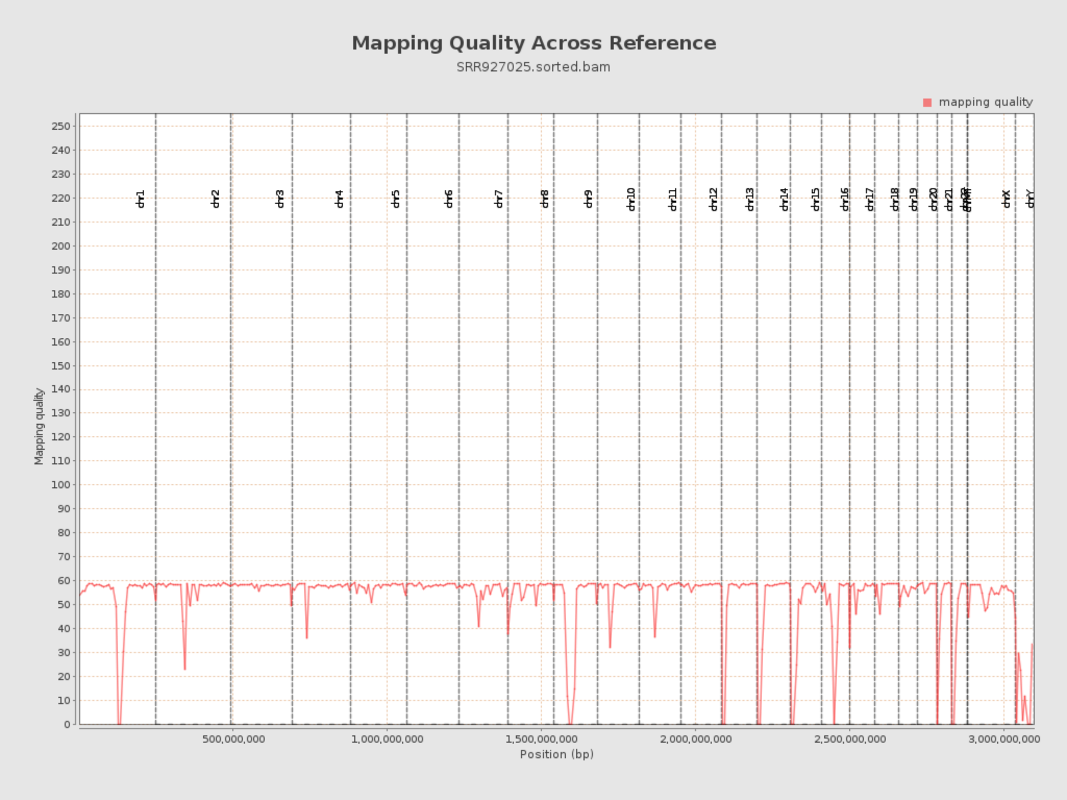
# 10. Results : Mapped Reads Clipping Profile



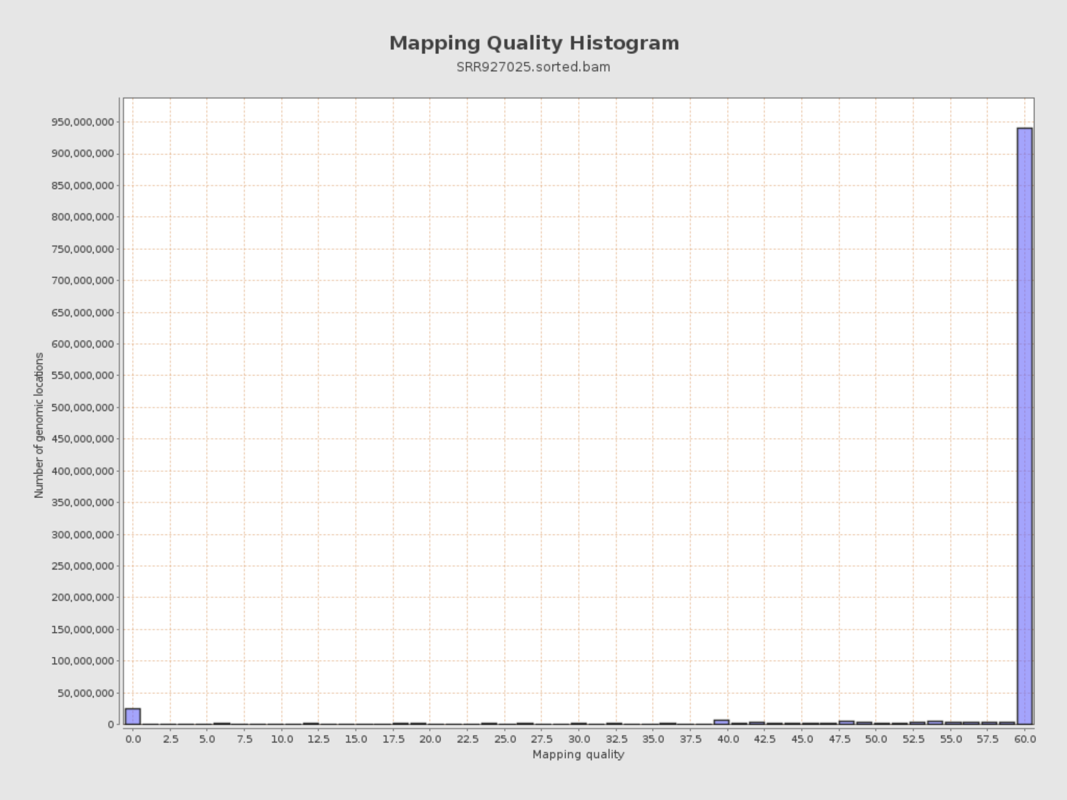
# 11. Results : Homopolymer Indels



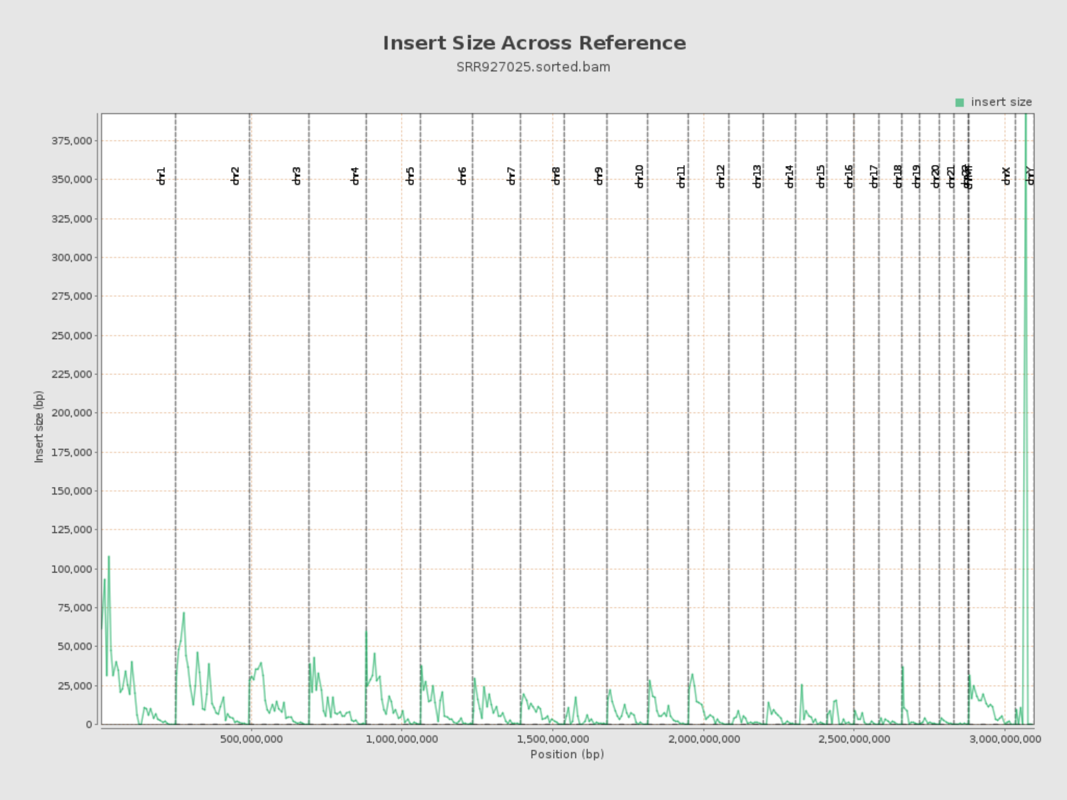
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram