# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2025/01/09 10:52:52*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR961011.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_SRR961011 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR961011_1.fastq.gz SRR961011_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Jan 09 10:52:51 CST 2025 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR961011.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 385,800,550 |
| Mapped reads | 366,065,892 / 94.88% |
| Unmapped reads | 19,734,658 / 5.12% |
| Mapped paired reads | 366,065,892 / 94.88% |
| Mapped reads, first in pair | 188,759,704 / 48.93% |
| Mapped reads,  second in pair | 177,306,188 / 45.96% |
| Mapped reads, both in pair | 353,505,484 / 91.63% |
| Mapped reads, singletons | 12,560,408 / 3.26% |
| Secondary alignments | 0 |
| Supplementary alignments | 5,941,743 / 1.54% |
| Read min/max/mean length | 30 / 100 / 100.64 |
| Duplicated reads (estimated) | 57,834,830 / 14.99% |
| Duplication rate | 10.92% |
| Clipped reads | 50,158,290 / 13% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 10,402,571,013 / 29.07% |
| Number/percentage of C's | 7,374,863,386 / 20.61% |
| Number/percentage of T's | 10,355,248,419 / 28.94% |
| Number/percentage of G's | 7,451,406,022 / 20.82% |
| Number/percentage of N's | 203,292,432 / 0.57% |
| | |

| | |
|---|---|
| GC Percentage | 41.43% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 11.5637 |
| Standard Deviation | 140.3108 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.11 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 85,434.37 |
| Standard Deviation | 2,817,553.92 |
| P25/Median/P75 | 127 / 142 / 155 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 1.64% |
| Mismatches | 576,494,259 |
| Insertions | 3,594,593 |
| Mapped reads with at least one insertion | 0.95% |
| Deletions | 4,196,489 |
| Mapped reads with at least one deletion | 1.11% |
| Homopolymer indels | 39.97% |

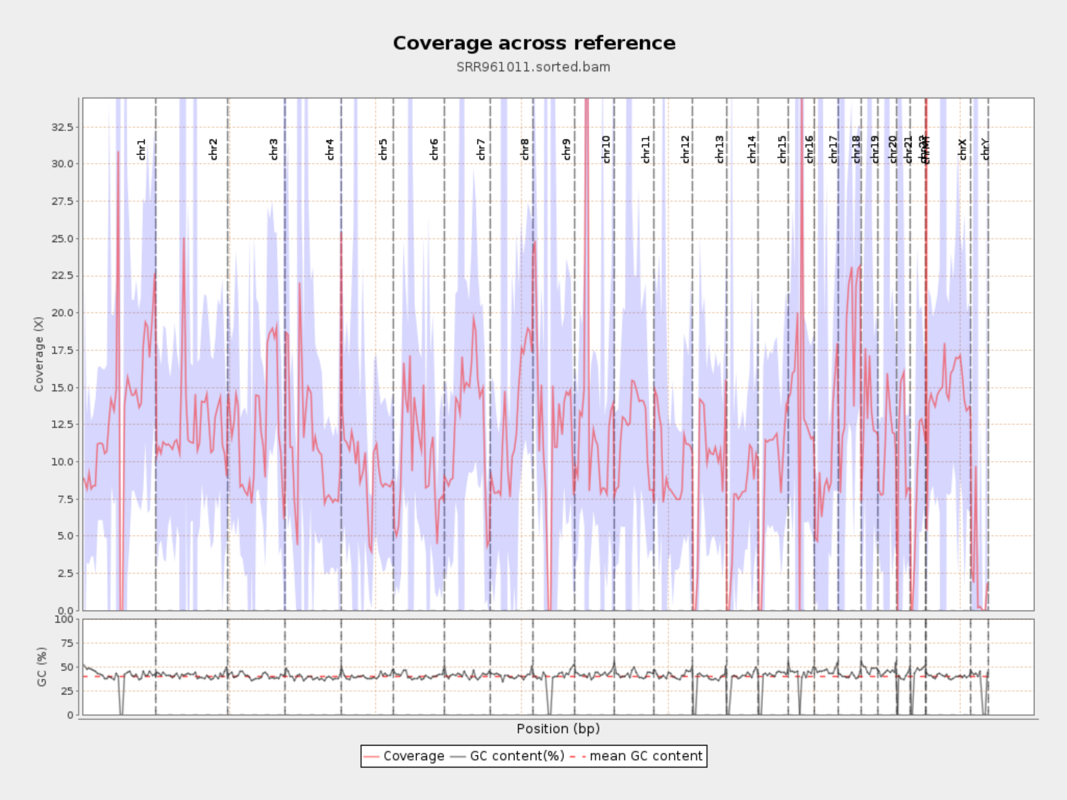
## 2.7. Chromosome stats

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

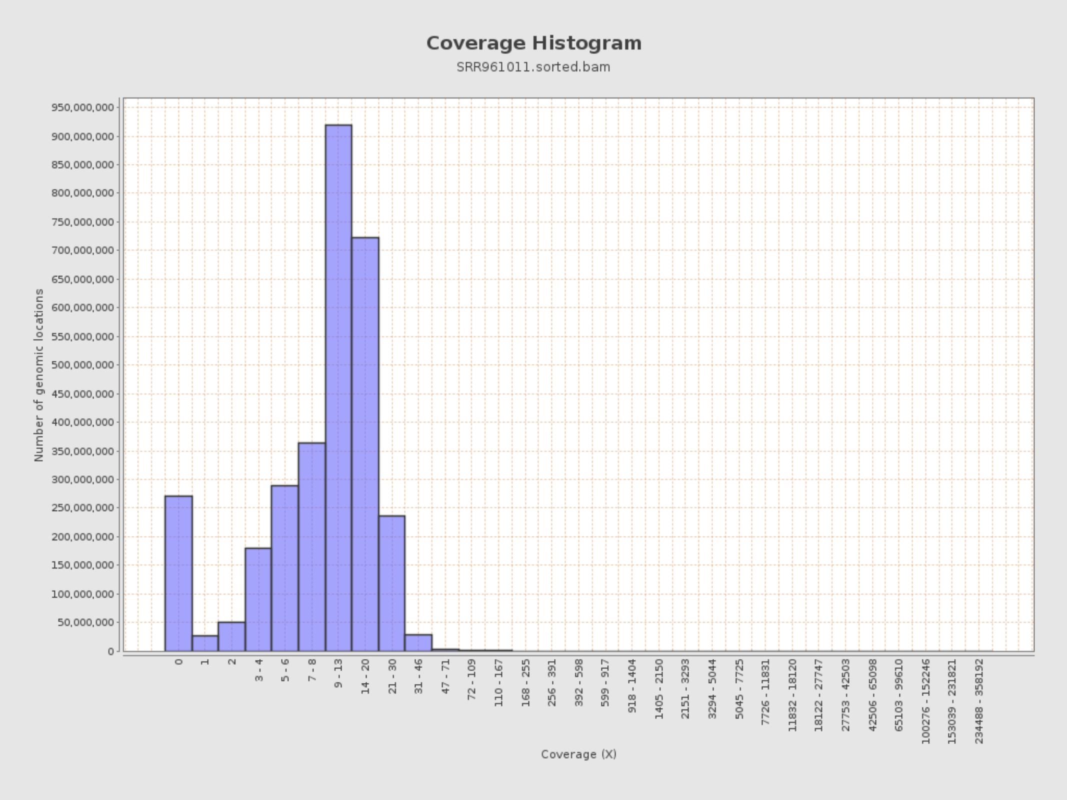
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 3311940591 | 13.2876 | 360.7475 |
| chr2 | 243199373 | 3022941526 | 12.4299 | 82.0967 |
| chr3 | 198022430 | 2426329040 | 12.2528 | 30.8667 |
| chr4 | 191154276 | 2140957518 | 11.2002 | 91.3254 |
| chr5 | 180915260 | 1722816272 | 9.5228 | 13.8622 |
| chr6 | 171115067 | 1759396695 | 10.282 | 44.0961 |
| chr7 | 159138663 | 2023026727 | 12.7124 | 90.2745 |
| chr8 | 146364022 | 1840160880 | 12.5725 | 117.0986 |
| chr9 | 141213431 | 1701586935 | 12.0498 | 105.6297 |
| chr10 | 135534747 | 1772219754 | 13.0758 | 307.8377 |
| chr11 | 135006516 | 1624777397 | 12.0348 | 59.0099 |
| chr12 | 133851895 | 1345151428 | 10.0496 | 11.7969 |
| chr13 | 115169878 | 1096599531 | 9.5216 | 6.9957 |
| chr14 | 107349540 | 787677985 | 7.3375 | 11.3908 |
| chr15 | 102531392 | 945915518 | 9.2256 | 7.1151 |
| chr16 | 90354753 | 1332443014 | 14.7468 | 148.3641 |
| chr17 | 81195210 | 763153469 | 9.399 | 35.3361 |
| chr18 | 78077248 | 1361426340 | 17.4369 | 133.7356 |
| chr19 | 59128983 | 790570054 | 13.3703 | 174.9147 |
| chr20 | 63025520 | 698140693 | 11.0771 | 33.7718 |
| chr21 | 48129895 | 500447156 | 10.3978 | 51.5339 |
| chr22 | 51304566 | 412777346 | 8.0456 | 9.2809 |
| chrMT | 16571 | 8090534 | 488.2345 | 89.3365 |
| chrX | 155270560 | 2288342739 | 14.7378 | 45.7619 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 120678404 | 2.0325 | 103.4122 |

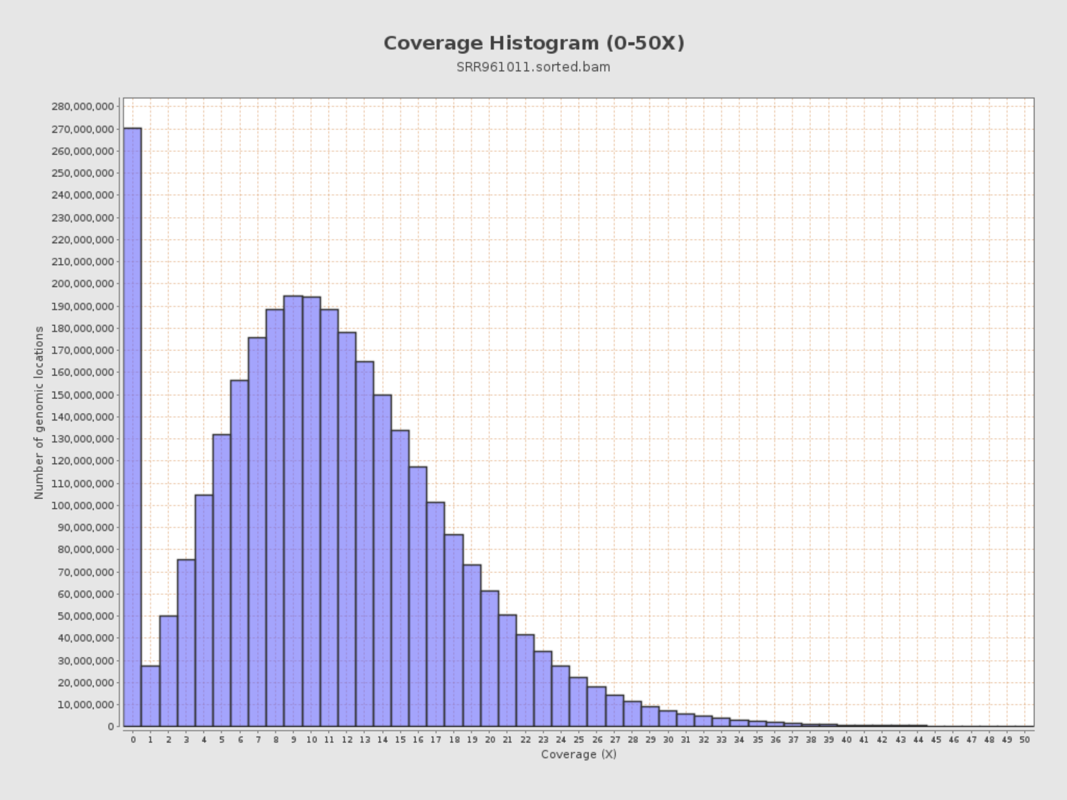
# 3. Results : Coverage across reference



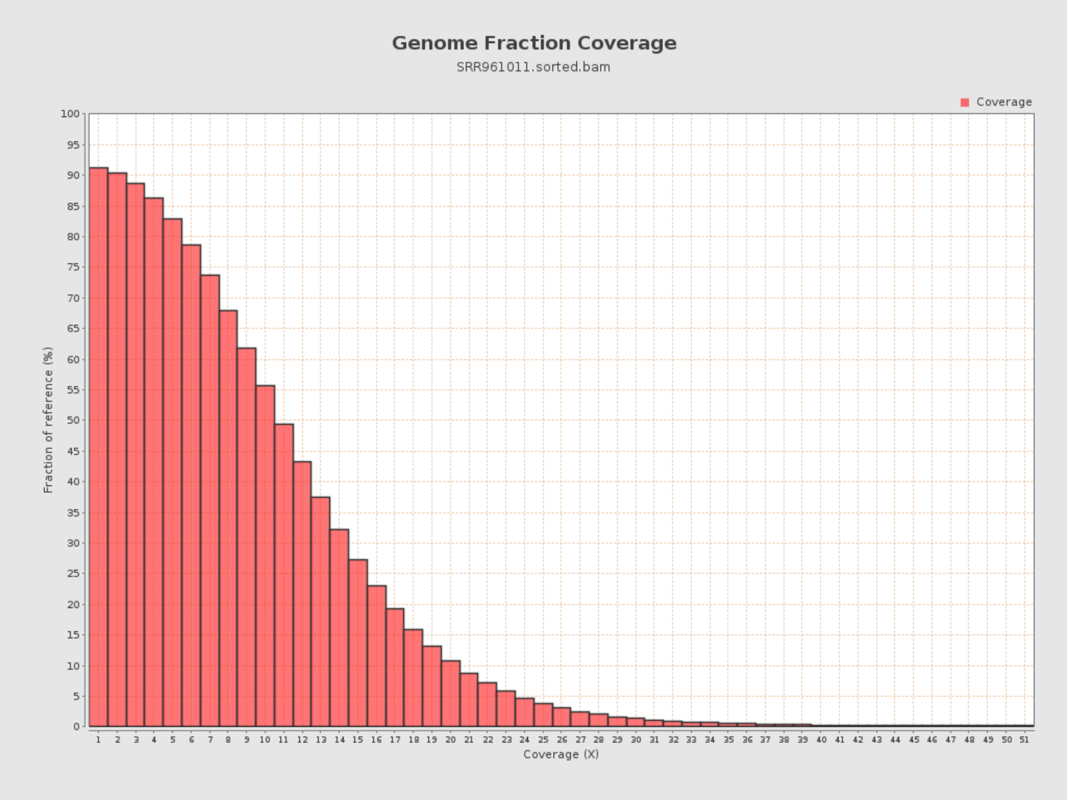
# 4. Results : Coverage Histogram



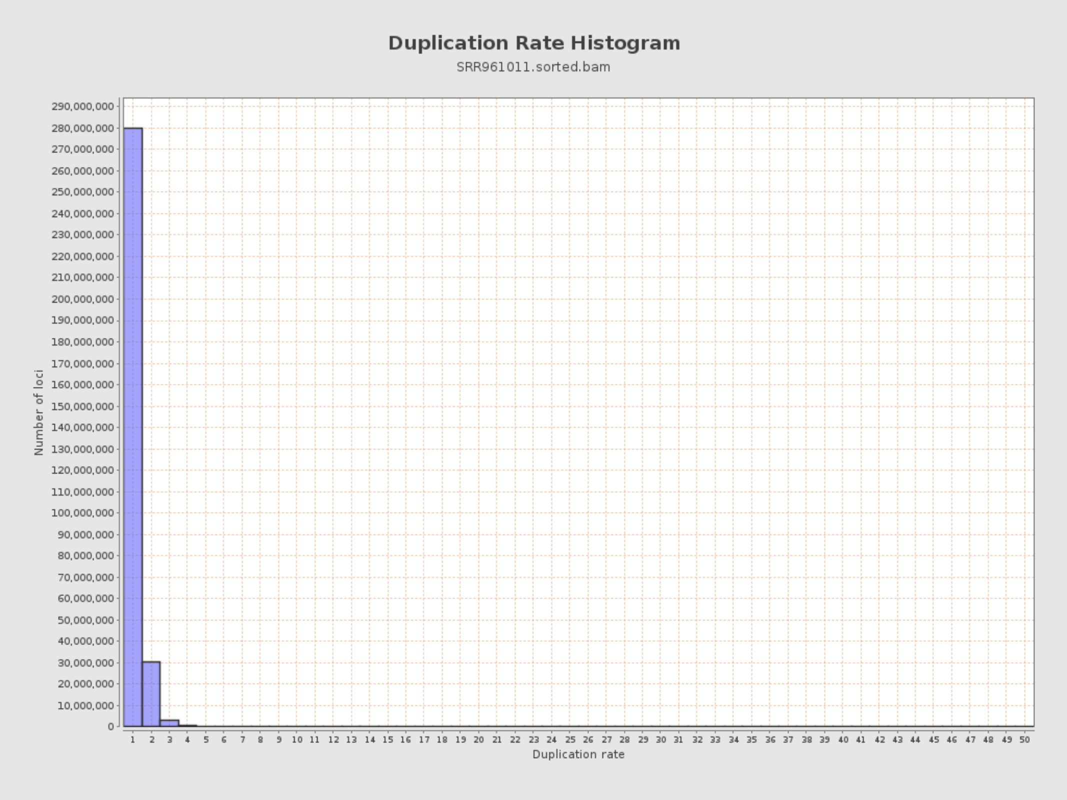
# 5. Results : Coverage Histogram (0-50X)



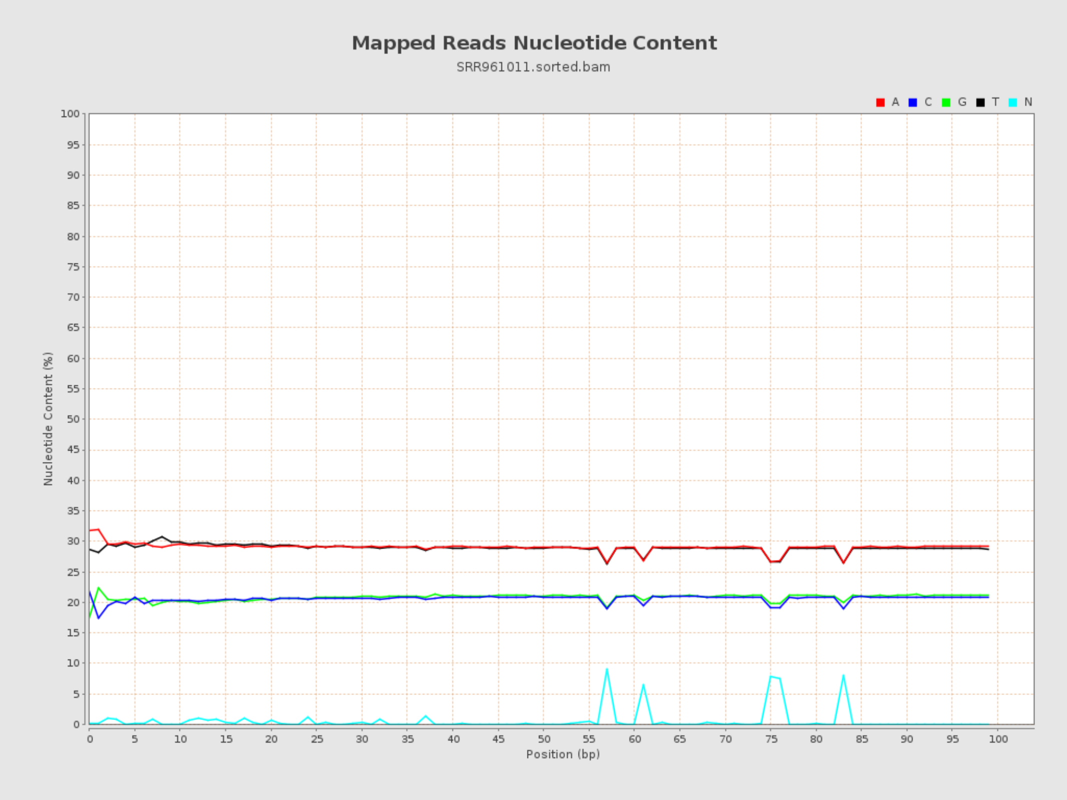
# 6. Results : Genome Fraction Coverage



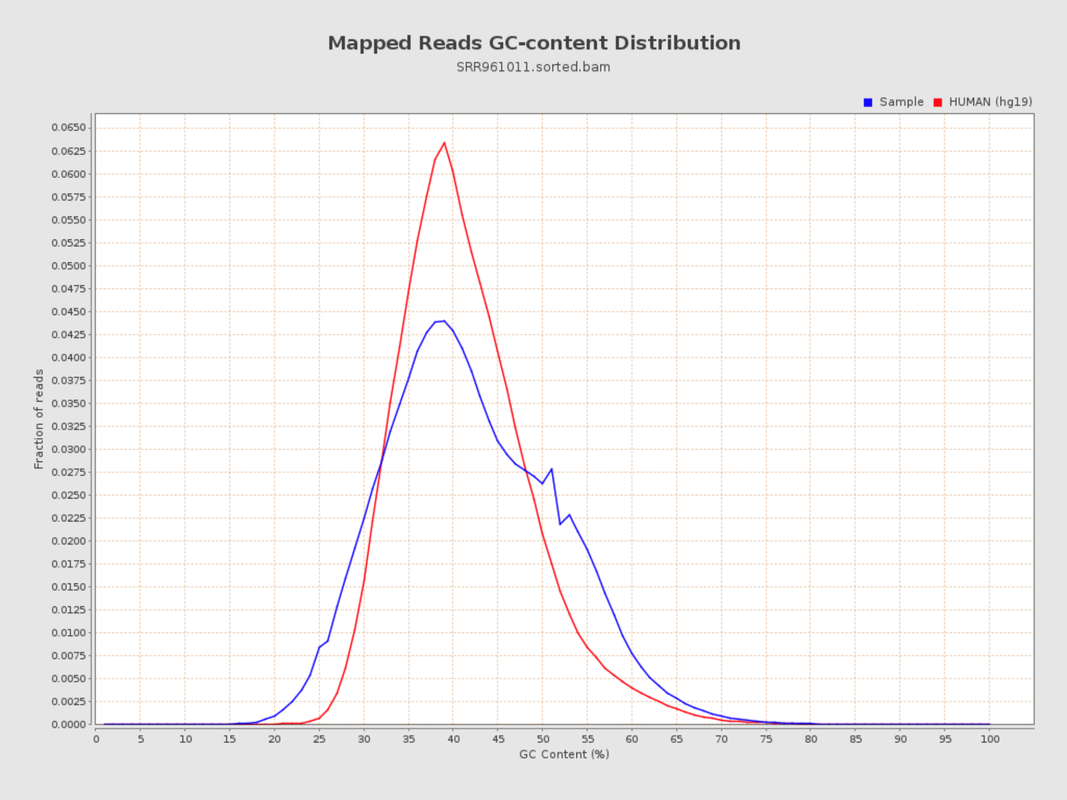
# 7. Results : Duplication Rate Histogram



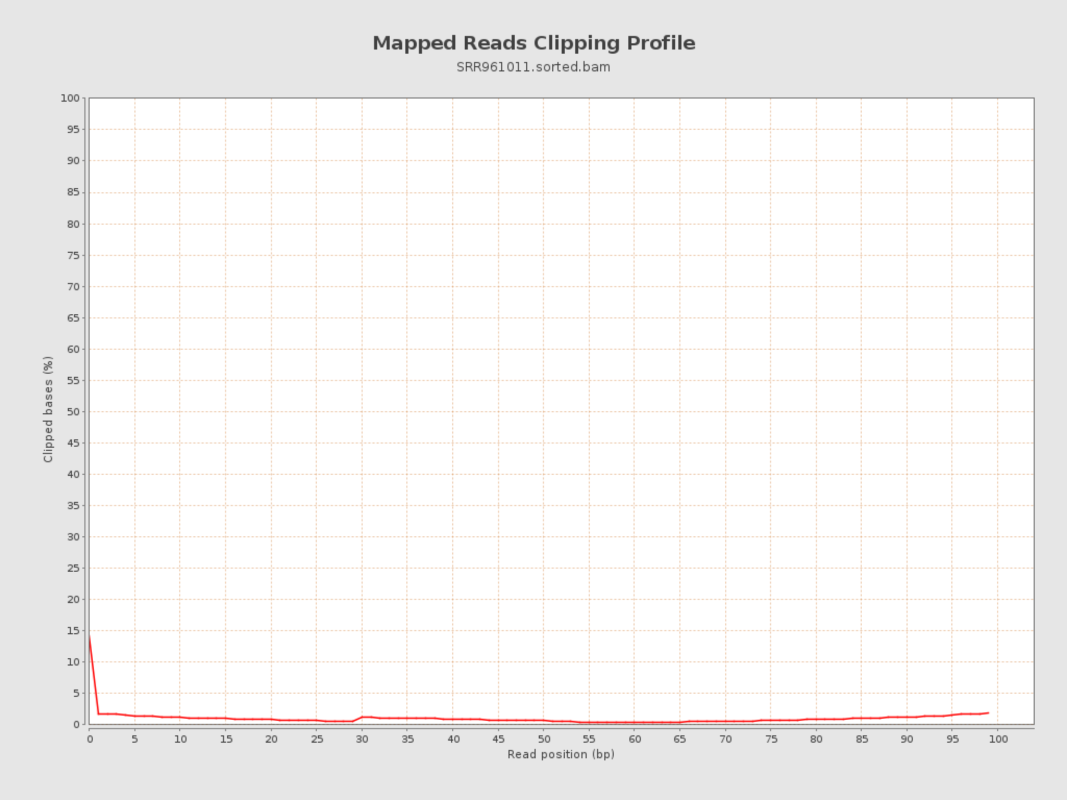
# 8. Results : Mapped Reads Nucleotide Content



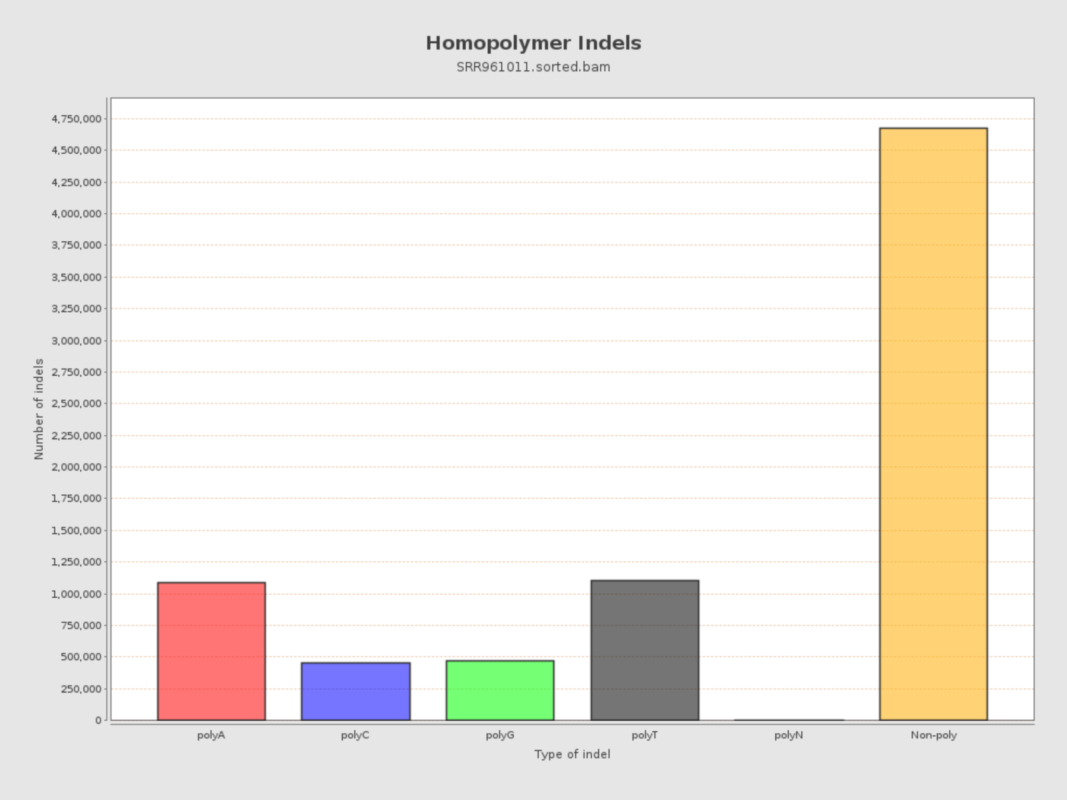
# 9. Results : Mapped Reads GC-content Distribution



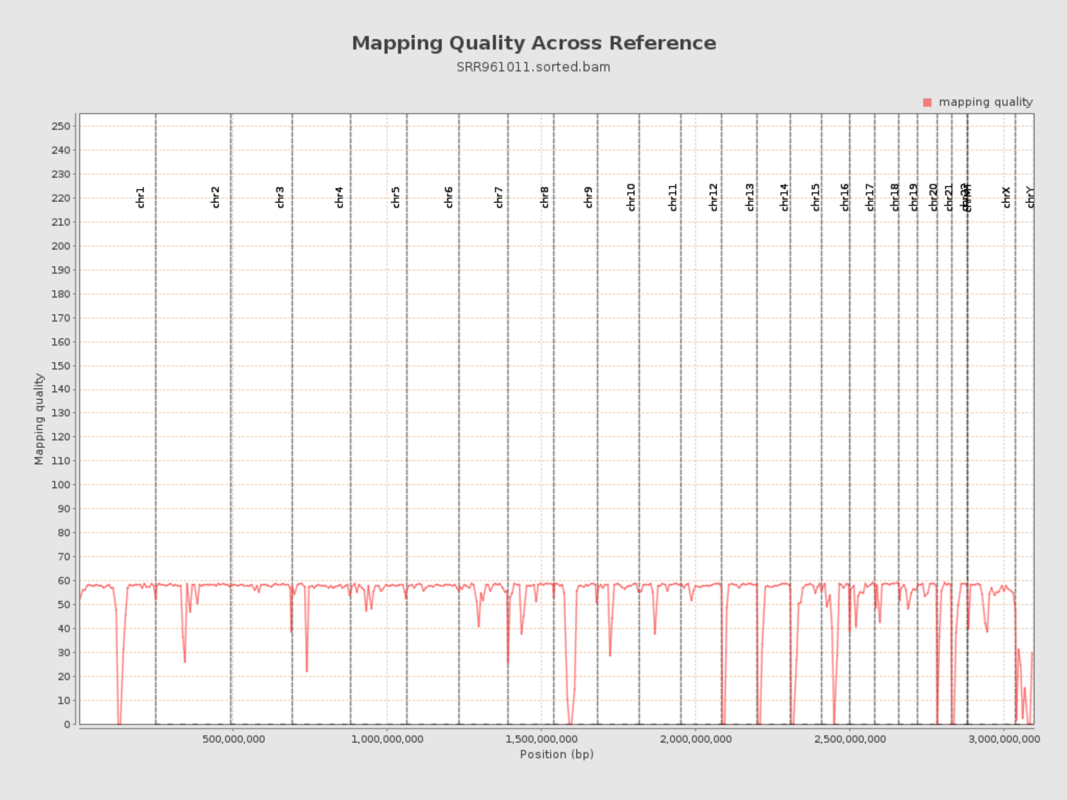
# 10. Results : Mapped Reads Clipping Profile



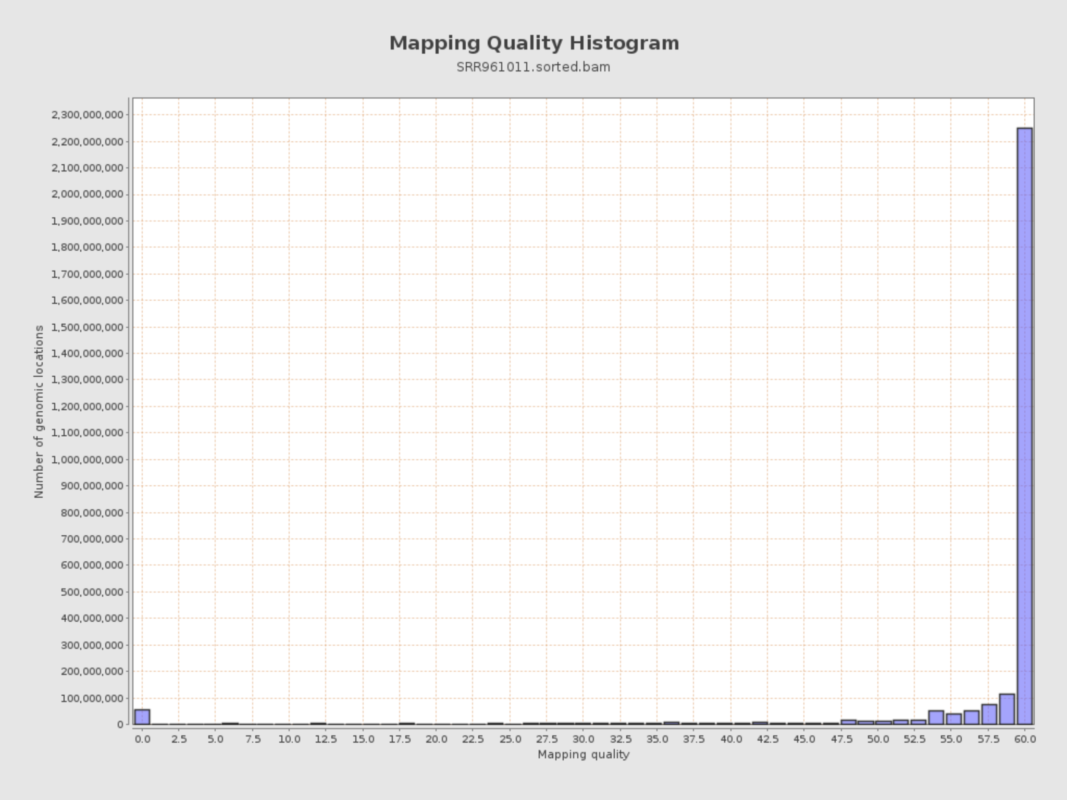
# 11. Results : Homopolymer Indels



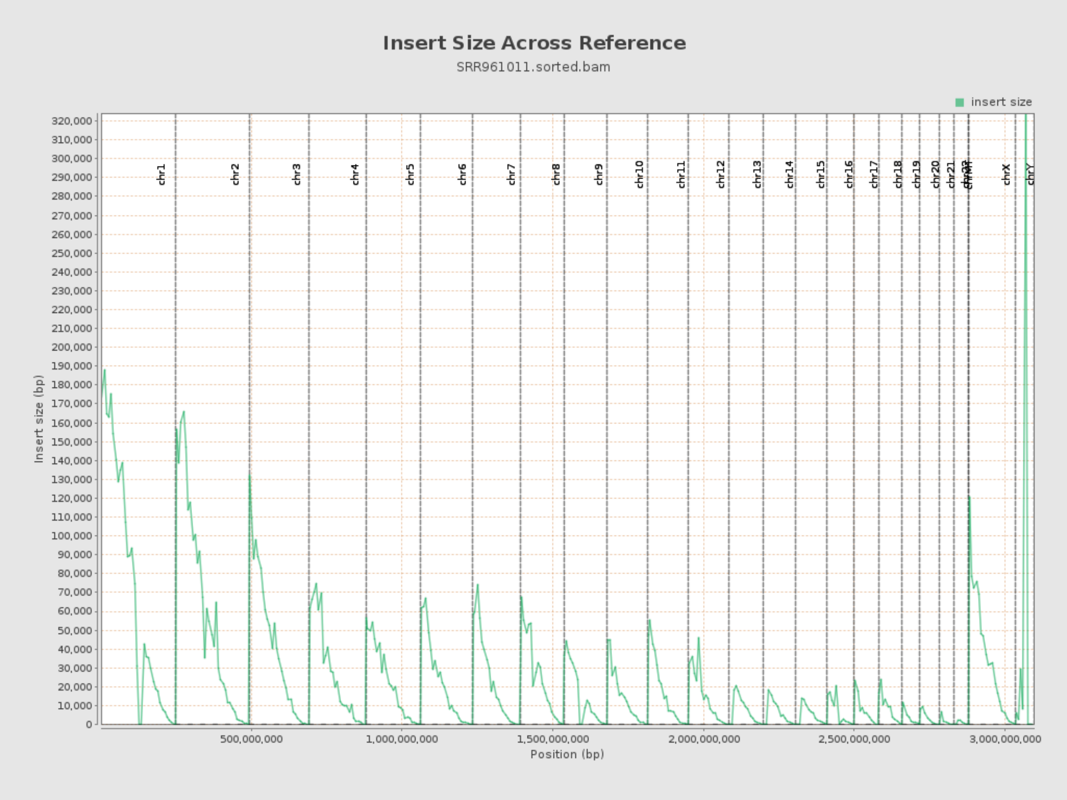
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram