# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/07 13:34:16*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779081.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_SRR1779081 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779081_1.fastq.gz SRR1779081_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Oct 07 13:34:15 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1779081.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 22,903,382 |
| Mapped reads | 22,097,234 / 96.48% |
| Unmapped reads | 806,148 / 3.52% |
| Mapped paired reads | 22,097,234 / 96.48% |
| Mapped reads, first in pair | 11,131,788 / 48.6% |
| Mapped reads, second in pair | 10,965,446 / 47.88% |
| Mapped reads, both in pair | 21,844,234 / 95.38% |
| Mapped reads, singletons | 253,000 / 1.1% |
| Secondary alignments | 0 |
| Supplementary alignments | 122,323 / 0.53% |
| Read min/max/mean length | 30 / 101 / 101.21 |
| Duplicated reads (estimated) | 812,303 / 3.55% |
| Duplication rate | 3.28% |
| Clipped reads | 1,682,780 / 7.35% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 674,058,430 / 30.6% |
| Number/percentage of C's | 425,310,037 / 19.31% |
| Number/percentage of T's | 670,922,800 / 30.45% |
| Number/percentage of G's | 432,067,569 / 19.61% |
| Number/percentage of N's | 743,145 / 0.03% |
| | |

| | |
|---|---|
| GC Percentage | 38.92% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.7118 |
| Standard Deviation | 2.1966 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.48 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 62,064.67 |
| Standard Deviation | 2,388,414.14 |
| P25/Median/P75 | 150 / 207 / 286 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.48% |
| Mismatches | 10,205,022 |
| Insertions | 189,156 |
| Mapped reads with at least one insertion | 0.84% |
| Deletions | 230,738 |
| Mapped reads with at least one deletion | 1.02% |
| Homopolymer indels | 46.47% |

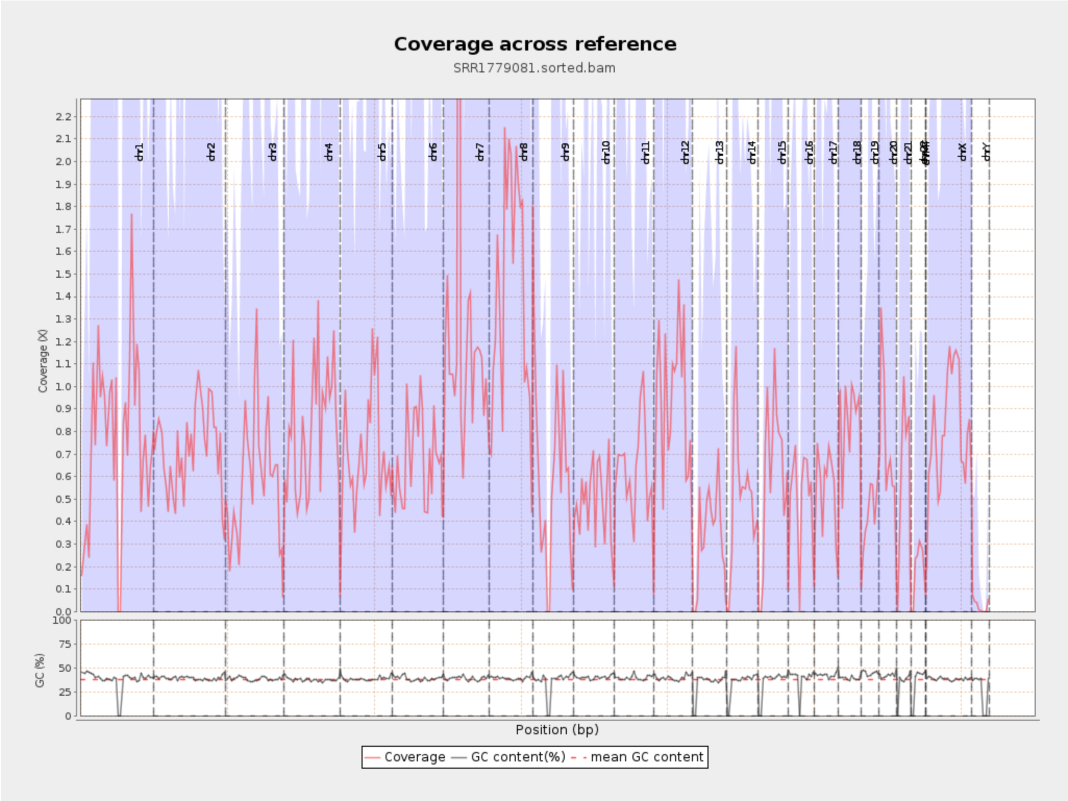
## 2.7. Chromosome stats

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

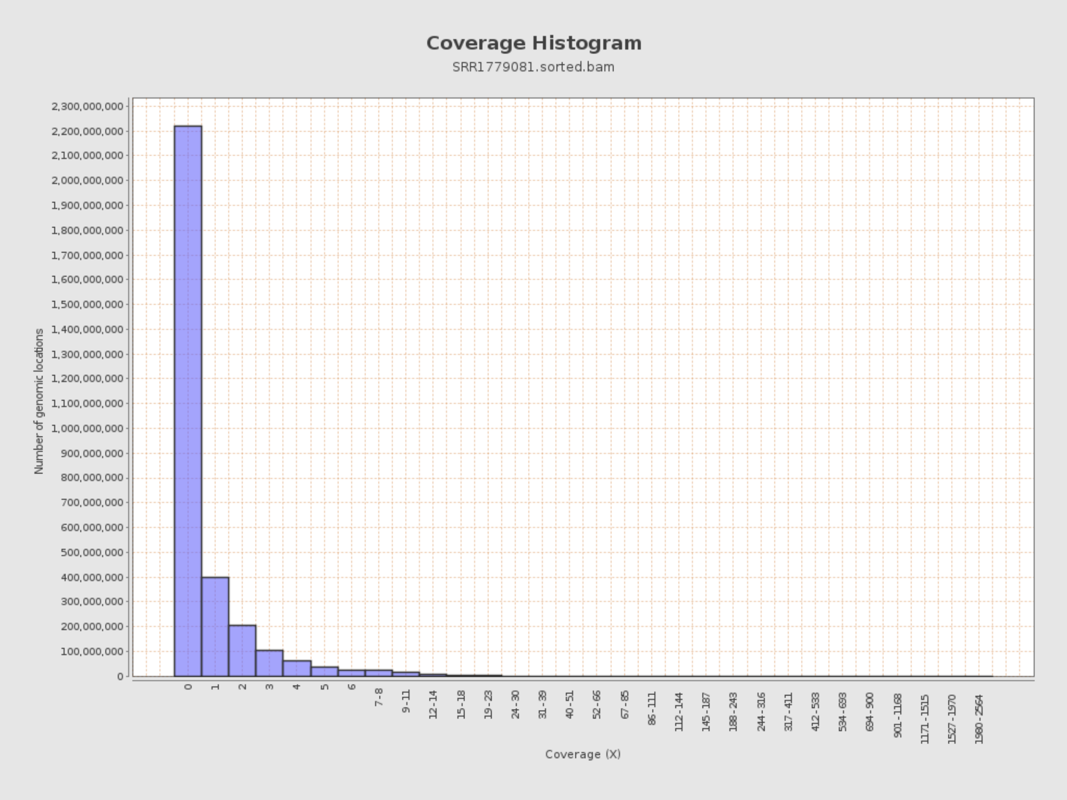
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 191029195 | 0.7664 | 3.25 |
| chr2 | 243199373 | 175654932 | 0.7223 | 1.8138 |
| chr3 | 198022430 | 117325804 | 0.5925 | 1.5273 |
| chr4 | 191154276 | 156659904 | 0.8195 | 1.901 |
| chr5 | 180915260 | 126327283 | 0.6983 | 1.6362 |
| chr6 | 171115067 | 117339625 | 0.6857 | 1.6315 |
| chr7 | 159138663 | 198367998 | 1.2465 | 4.1678 |
| chr8 | 146364022 | 212844227 | 1.4542 | 2.5052 |
| chr9 | 141213431 | 82164592 | 0.5818 | 1.6765 |
| chr10 | 135534747 | 67440796 | 0.4976 | 3.6844 |
| chr11 | 135006516 | 84159350 | 0.6234 | 1.537 |
| chr12 | 133851895 | 125300492 | 0.9361 | 1.9518 |
| chr13 | 115169878 | 39192981 | 0.3403 | 1.0676 |
| chr14 | 107349540 | 55271323 | 0.5149 | 1.4479 |
| chr15 | 102531392 | 61616180 | 0.6009 | 1.6105 |
| chr16 | 90354753 | 43390430 | 0.4802 | 1.2896 |
| chr17 | 81195210 | 43786448 | 0.5393 | 1.5407 |
| chr18 | 78077248 | 68015882 | 0.8711 | 1.9759 |
| chr19 | 59128983 | 25265255 | 0.4273 | 2.0938 |
| chr20 | 63025520 | 46077318 | 0.7311 | 1.6759 |
| chr21 | 48129895 | 30096030 | 0.6253 | 1.5092 |
| chr22 | 51304566 | 9494230 | 0.1851 | 0.7249 |
| chrMT | 16571 | 3174 | 0.1915 | 0.5452 |
| chrX | 155270560 | 125208187 | 0.8064 | 1.9398 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1582358 | 0.0267 | 0.3747 |

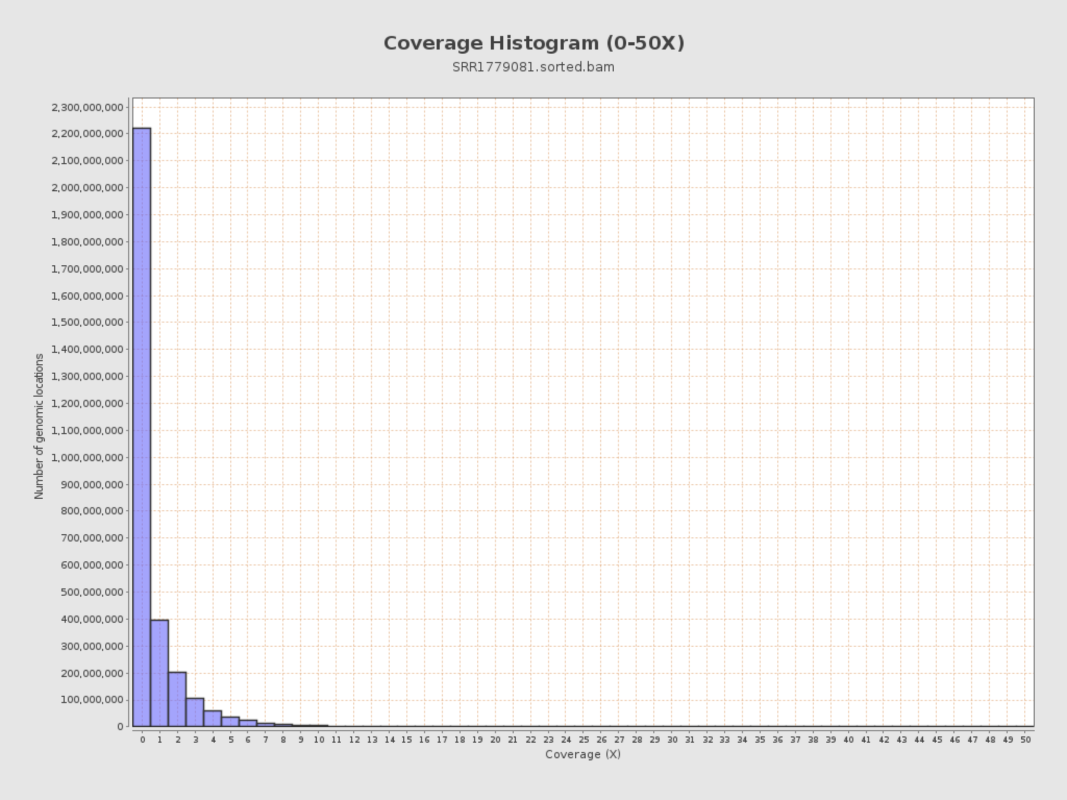
# 3. Results : Coverage across reference



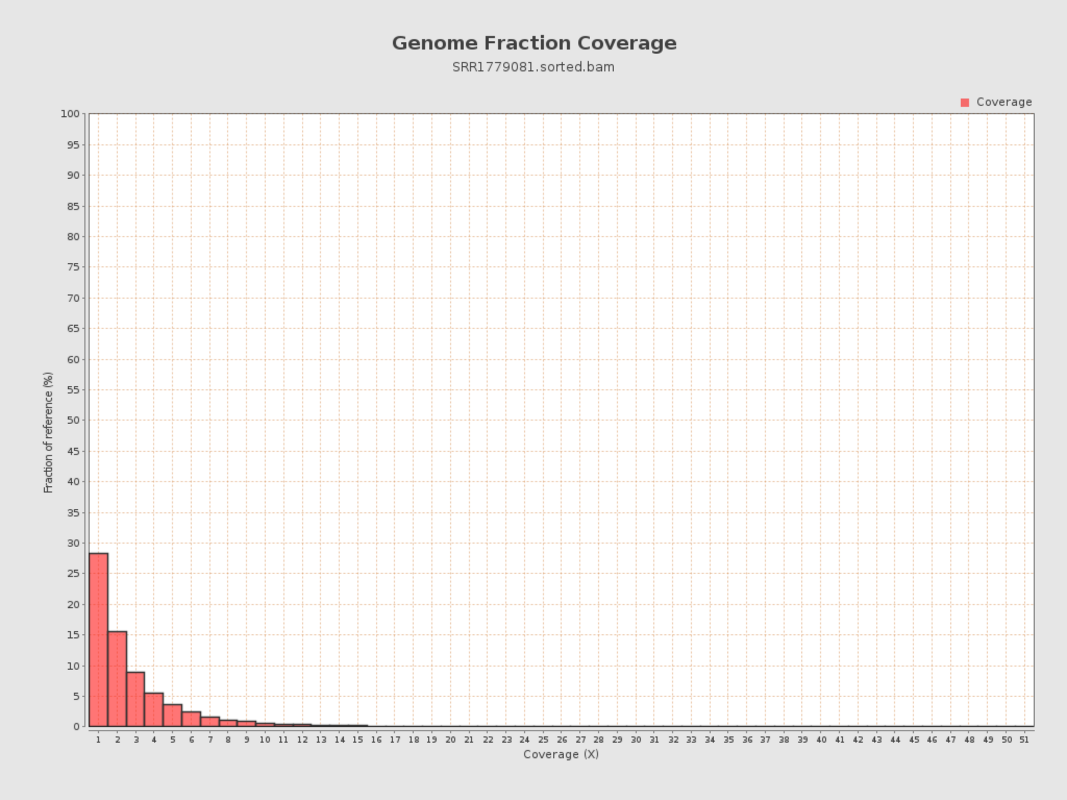
# 4. Results : Coverage Histogram



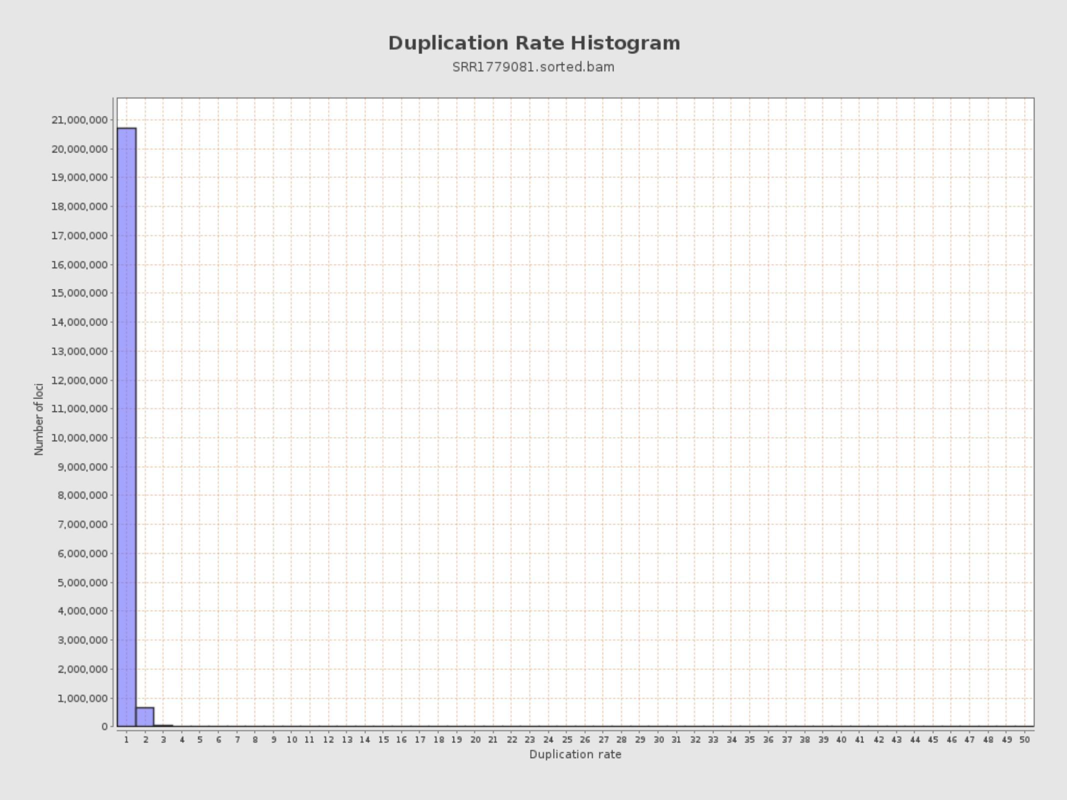
# 5. Results : Coverage Histogram (0-50X)



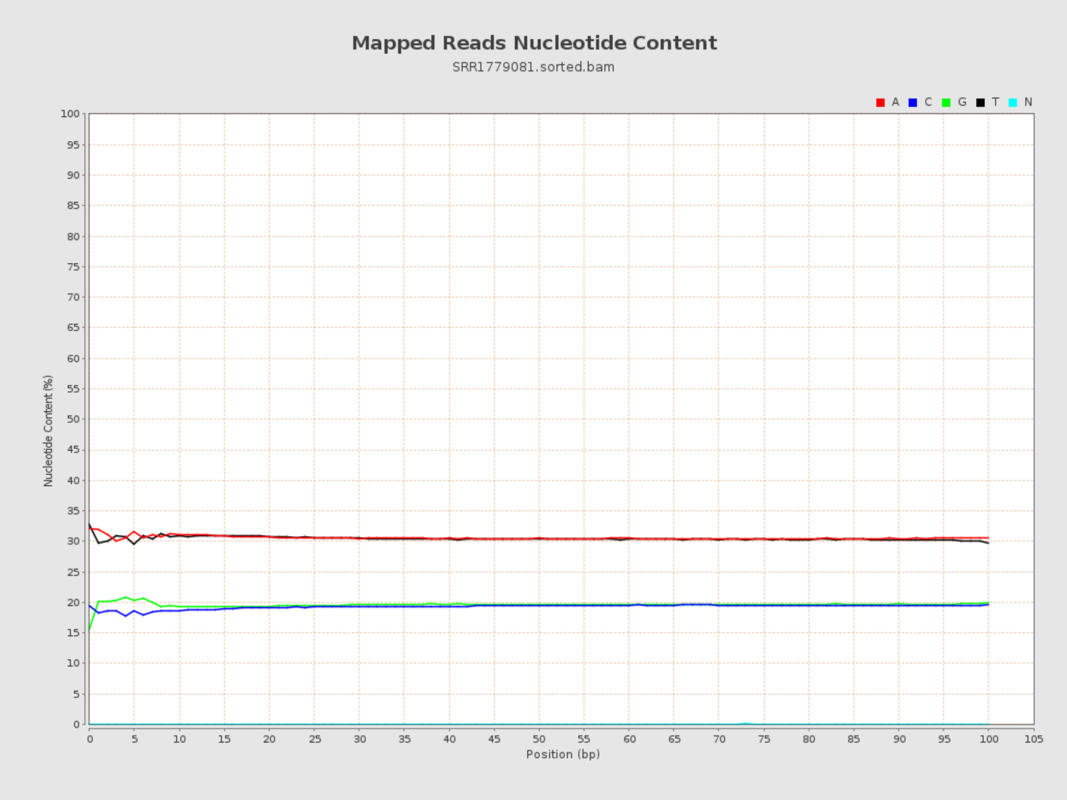
# 6. Results : Genome Fraction Coverage



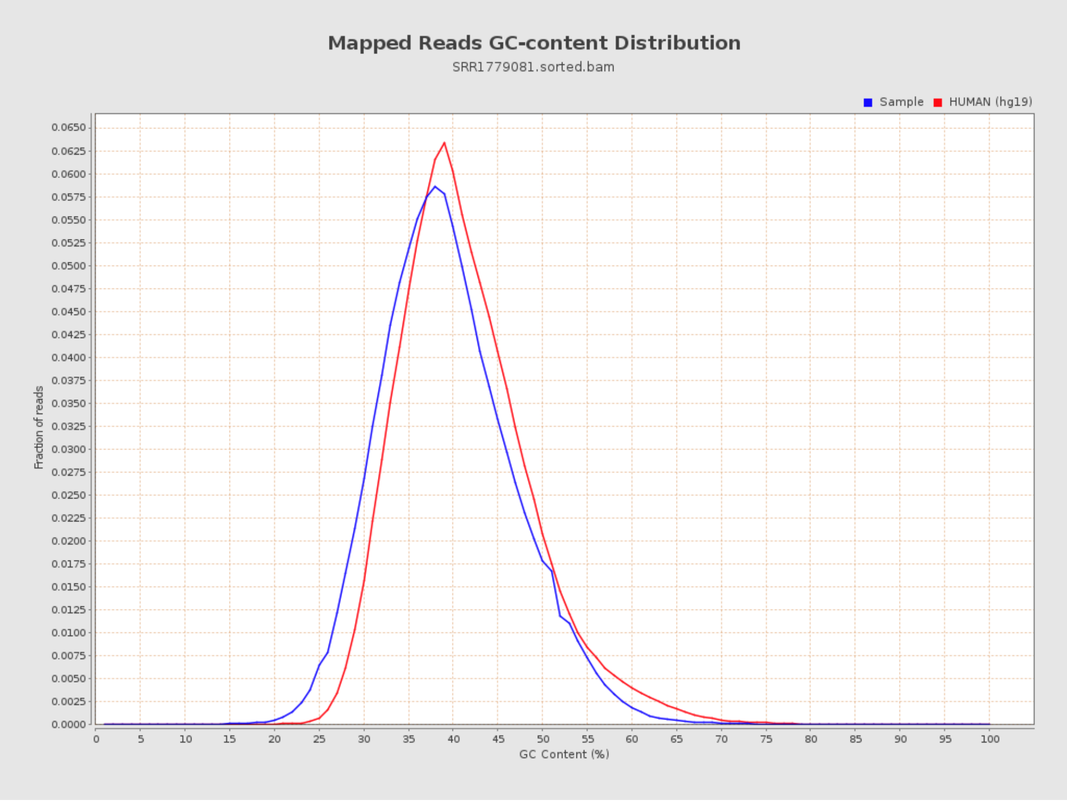
# 7. Results : Duplication Rate Histogram



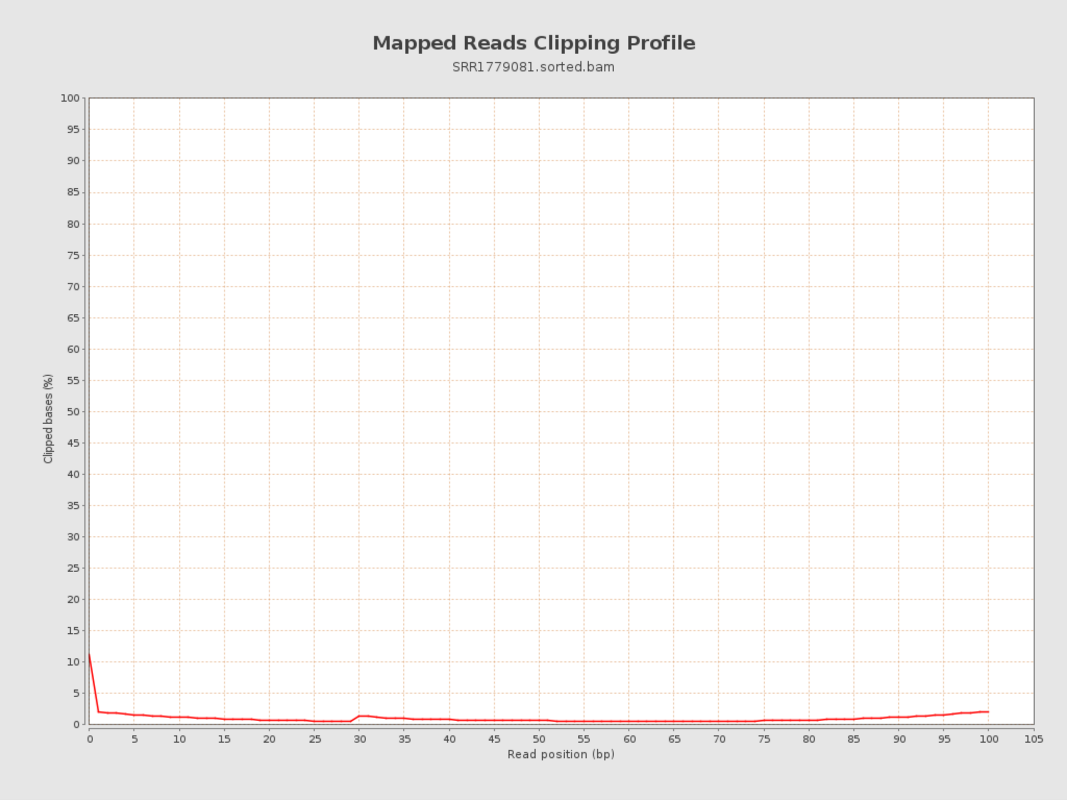
# 8. Results : Mapped Reads Nucleotide Content



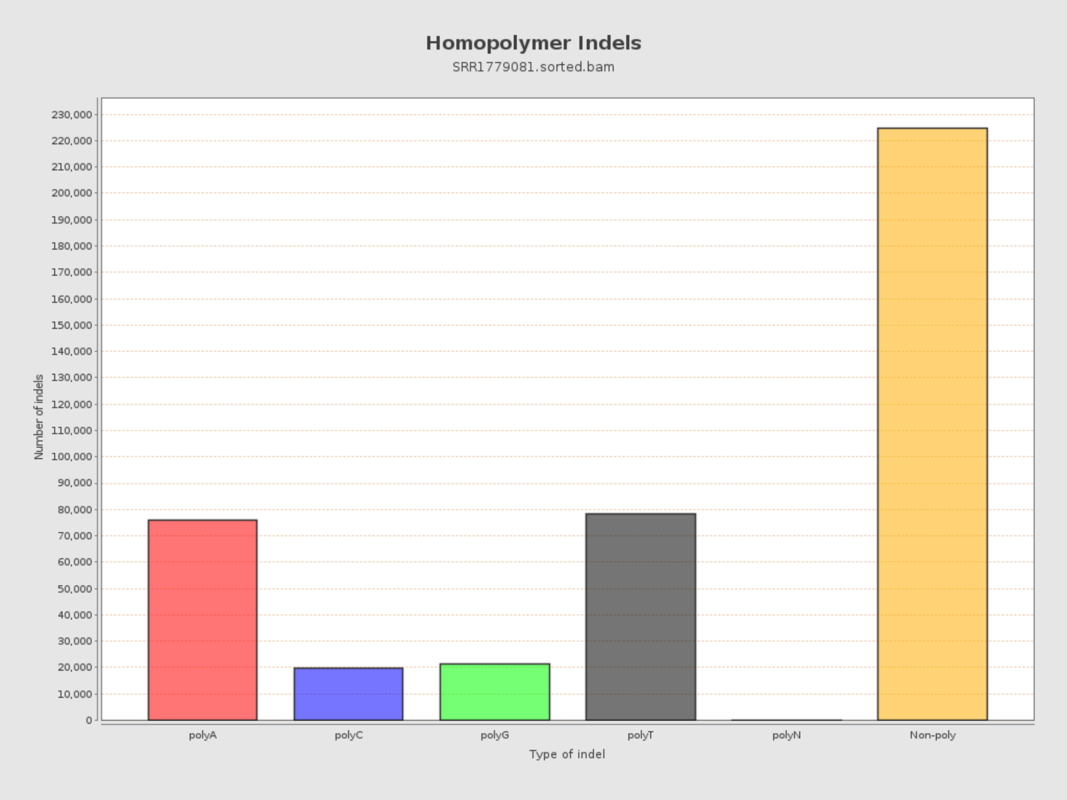
# 9. Results : Mapped Reads GC-content Distribution



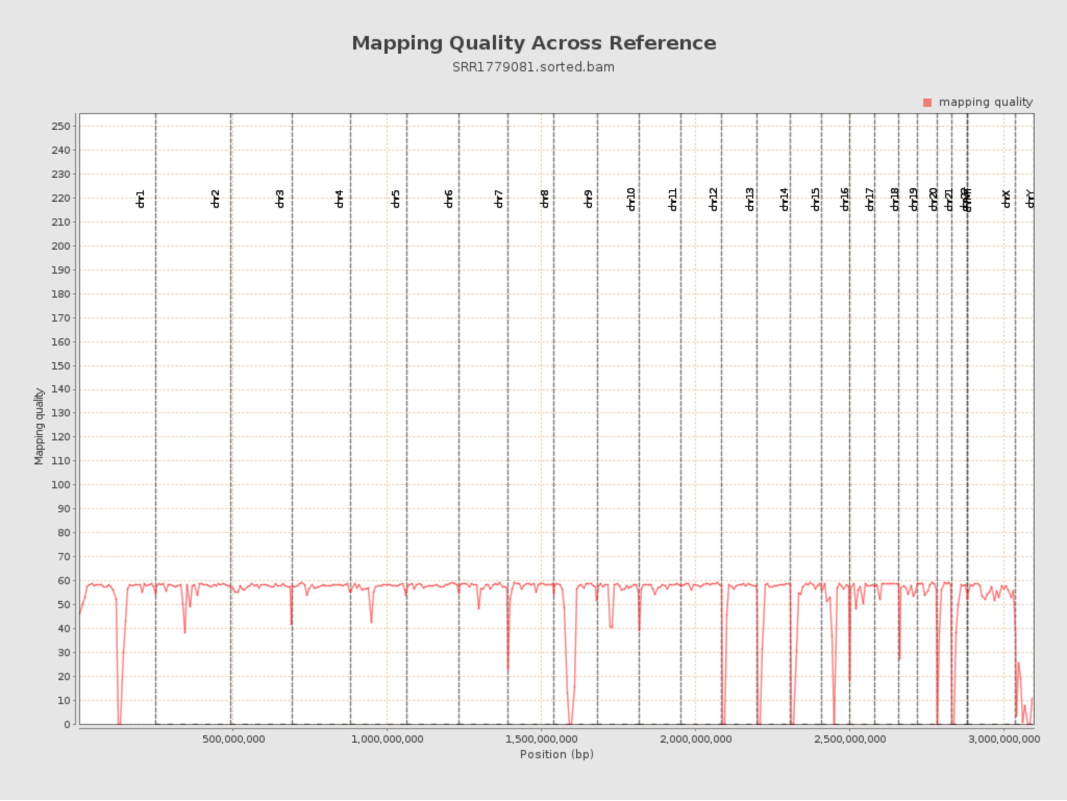
# 10. Results : Mapped Reads Clipping Profile



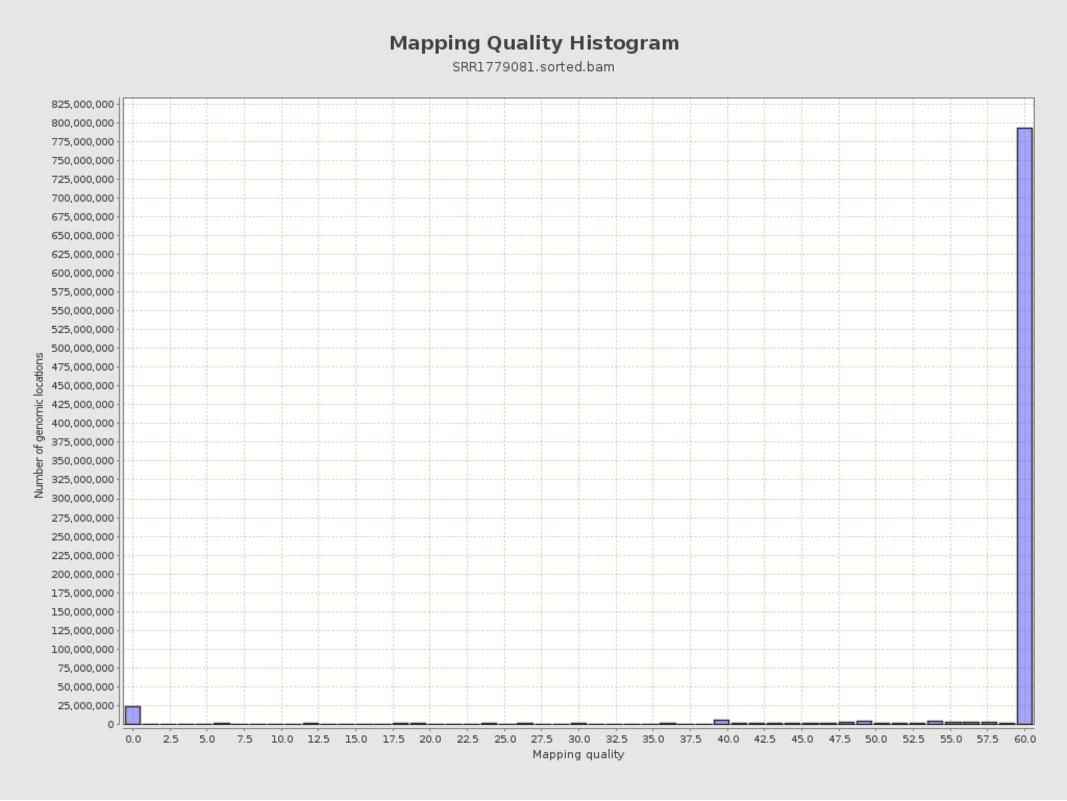
# 11. Results : Homopolymer Indels



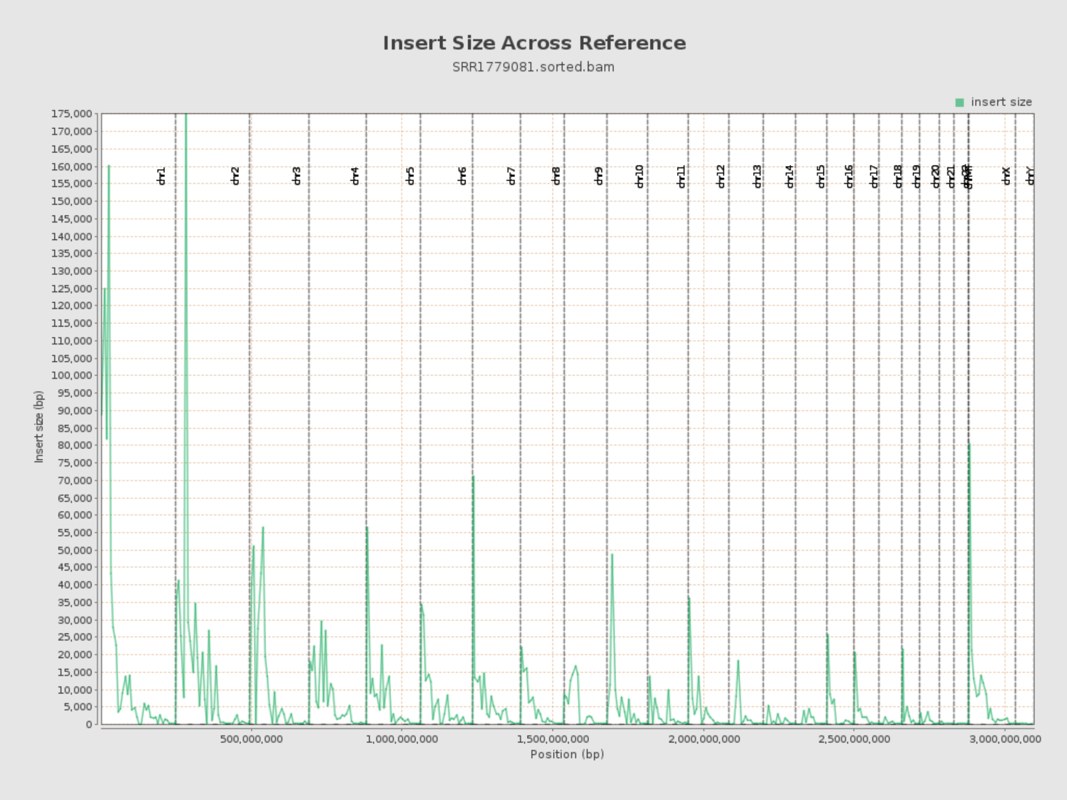
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram