# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/07 21:55:22*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779094.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_SRR1779094 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779094_1.fastq.gz SRR1779094_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Oct 07 21:55:20 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1779094.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,460,120 |
| Mapped reads | 3,350,657 / 96.84% |
| Unmapped reads | 109,463 / 3.16% |
| Mapped paired reads | 3,350,657 / 96.84% |
| Mapped reads, first in pair | 1,686,299 / 48.74% |
| Mapped reads,  second in pair | 1,664,358 / 48.1% |
| Mapped reads, both in pair | 3,315,642 / 95.82% |
| Mapped reads, singletons | 35,015 / 1.01% |
| Secondary alignments | 0 |
| Supplementary alignments | 20,085 / 0.58% |
| Read min/max/mean length | 30 / 101 / 101.23 |
| Duplicated reads (estimated) | 42,675 / 1.23% |
| Duplication rate | 1.18% |
| Clipped reads | 210,925 / 6.1% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 102,652,550 / 30.68% |
| Number/percentage of C's | 64,328,706 / 19.22% |
| Number/percentage of T's | 102,319,933 / 30.58% |
| Number/percentage of G's | 65,173,062 / 19.48% |
| Number/percentage of N's | 137,327 / 0.04% |
| | |

| | |
|---|---|
| GC Percentage | 38.7% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1081 |
| Standard Deviation | 0.4626 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.31 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 63,568.53 |
| Standard Deviation | 2,433,895.02 |
| P25/Median/P75 | 159 / 211 / 286 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.42% |
| Mismatches | 1,364,023 |
| Insertions | 28,486 |
| Mapped reads with at least one insertion | 0.84% |
| Deletions | 34,343 |
| Mapped reads with at least one deletion | 1.01% |
| Homopolymer indels | 46.74% |

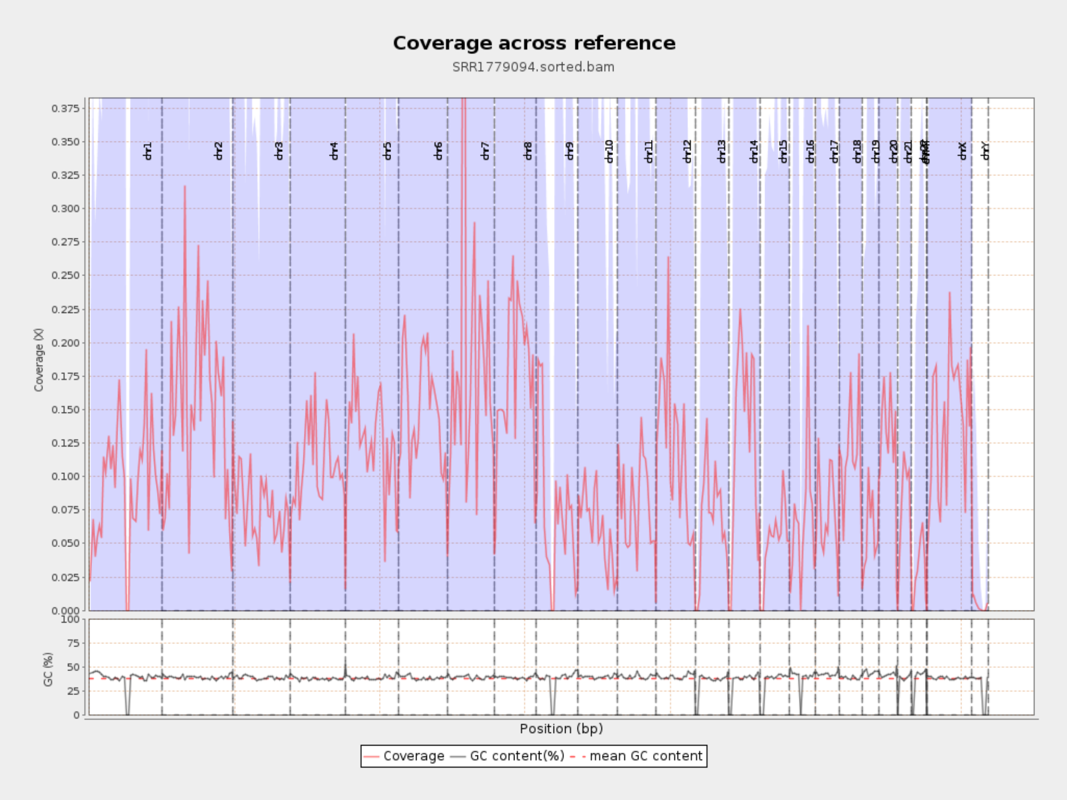
## 2.7. Chromosome stats

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

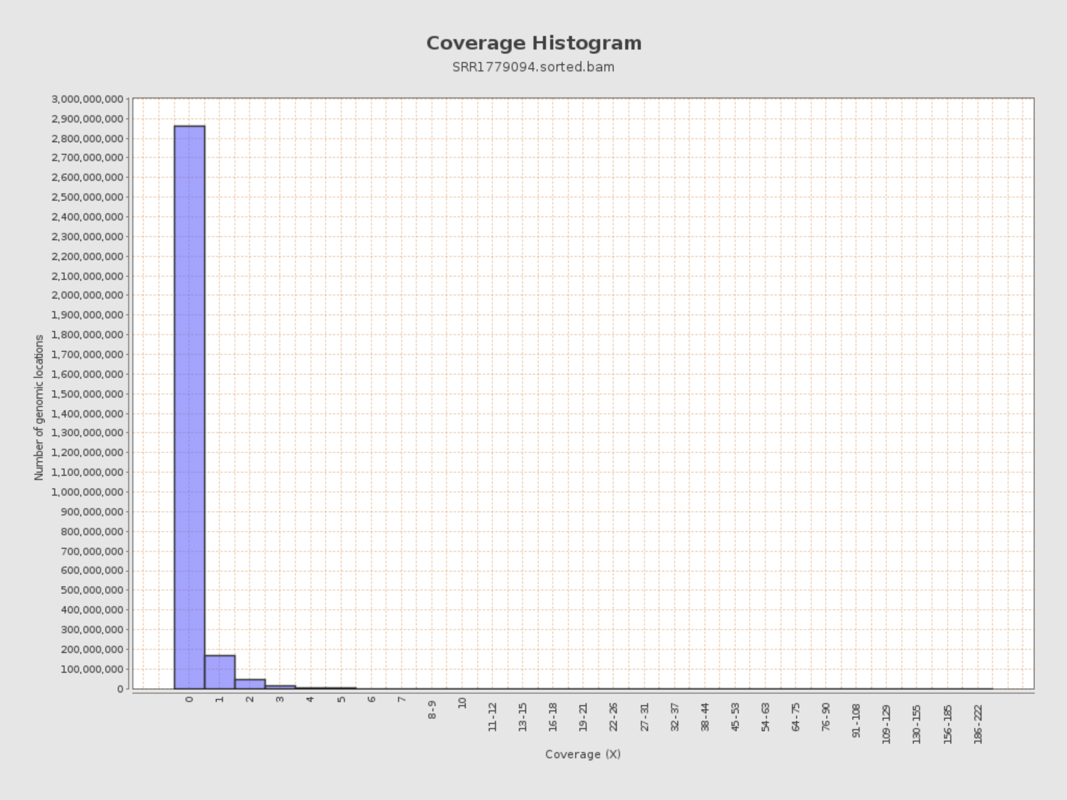
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 23405039 | 0.0939 | 0.4421 |
| chr2 | 243199373 | 37097467 | 0.1525 | 0.5356 |
| chr3 | 198022430 | 15100147 | 0.0763 | 0.3536 |
| chr4 | 191154276 | 21145530 | 0.1106 | 0.4352 |
| chr5 | 180915260 | 22793170 | 0.126 | 0.4575 |
| chr6 | 171115067 | 25456898 | 0.1488 | 0.5044 |
| chr7 | 159138663 | 30595407 | 0.1923 | 0.79 |
| chr8 | 146364022 | 25868776 | 0.1767 | 0.5586 |
| chr9 | 141213431 | 10679832 | 0.0756 | 0.3835 |
| chr10 | 135534747 | 8517552 | 0.0628 | 0.458 |
| chr11 | 135006516 | 10717759 | 0.0794 | 0.3735 |
| chr12 | 133851895 | 16060534 | 0.12 | 0.4628 |
| chr13 | 115169878 | 7645670 | 0.0664 | 0.3335 |
| chr14 | 107349540 | 13985221 | 0.1303 | 0.4852 |
| chr15 | 102531392 | 5405213 | 0.0527 | 0.2994 |
| chr16 | 90354753 | 6260458 | 0.0693 | 0.3348 |
| chr17 | 81195210 | 5686298 | 0.07 | 0.3457 |
| chr18 | 78077248 | 9219955 | 0.1181 | 0.4406 |
| chr19 | 59128983 | 3575683 | 0.0605 | 0.3503 |
| chr20 | 63025520 | 8452800 | 0.1341 | 0.5049 |
| chr21 | 48129895 | 3651821 | 0.0759 | 0.3563 |
| chr22 | 51304566 | 1649287 | 0.0321 | 0.2197 |
| chrMT | 16571 | 0 | 0 | 0 |
| chrX | 155270560 | 21467511 | 0.1383 | 0.5056 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 249902 | 0.0042 | 0.0924 |

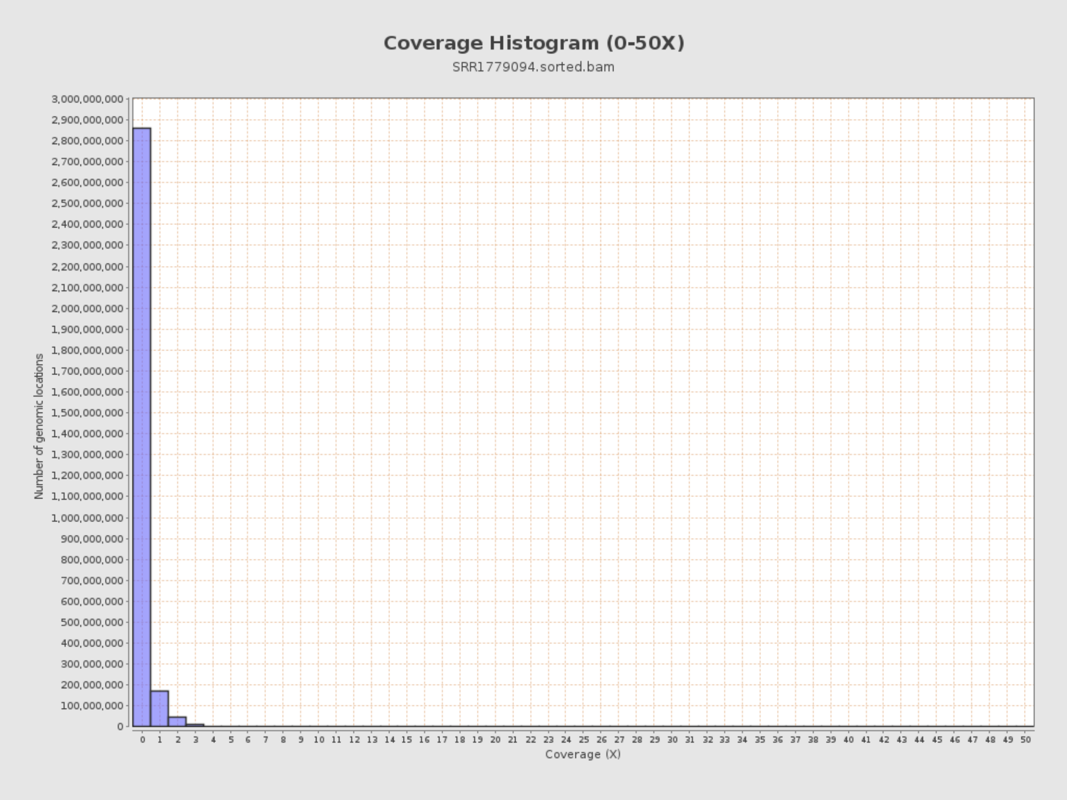
# 3. Results : Coverage across reference



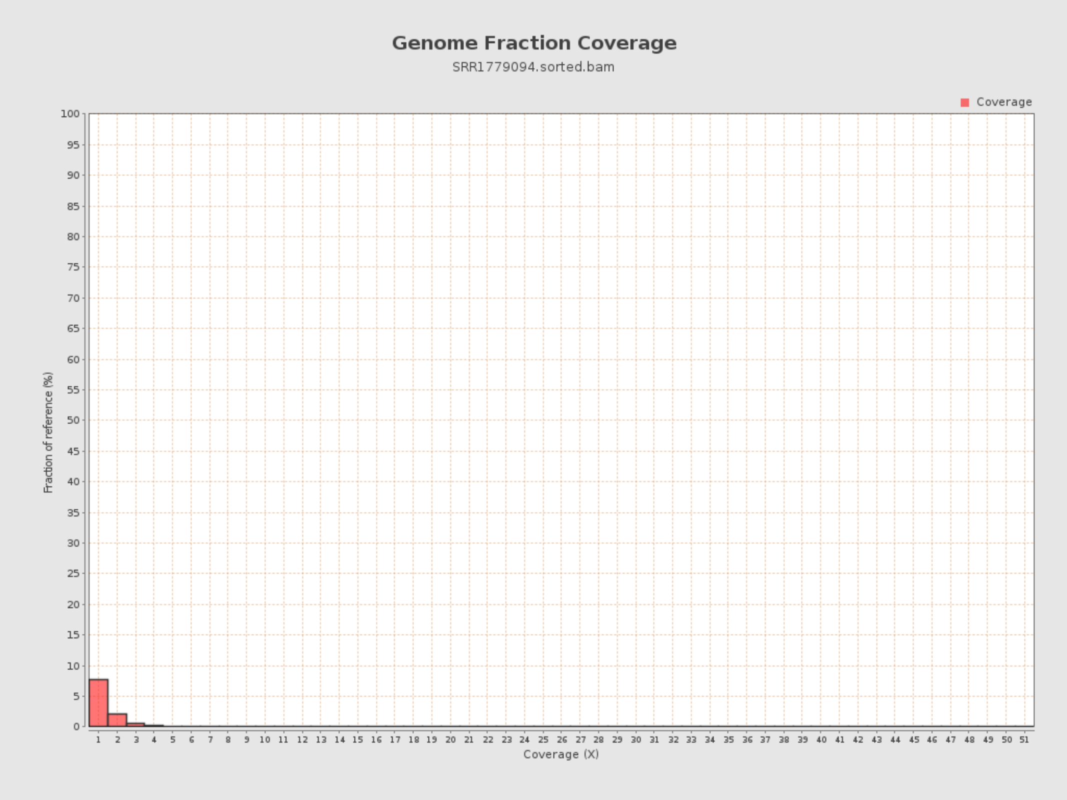
# 4. Results : Coverage Histogram



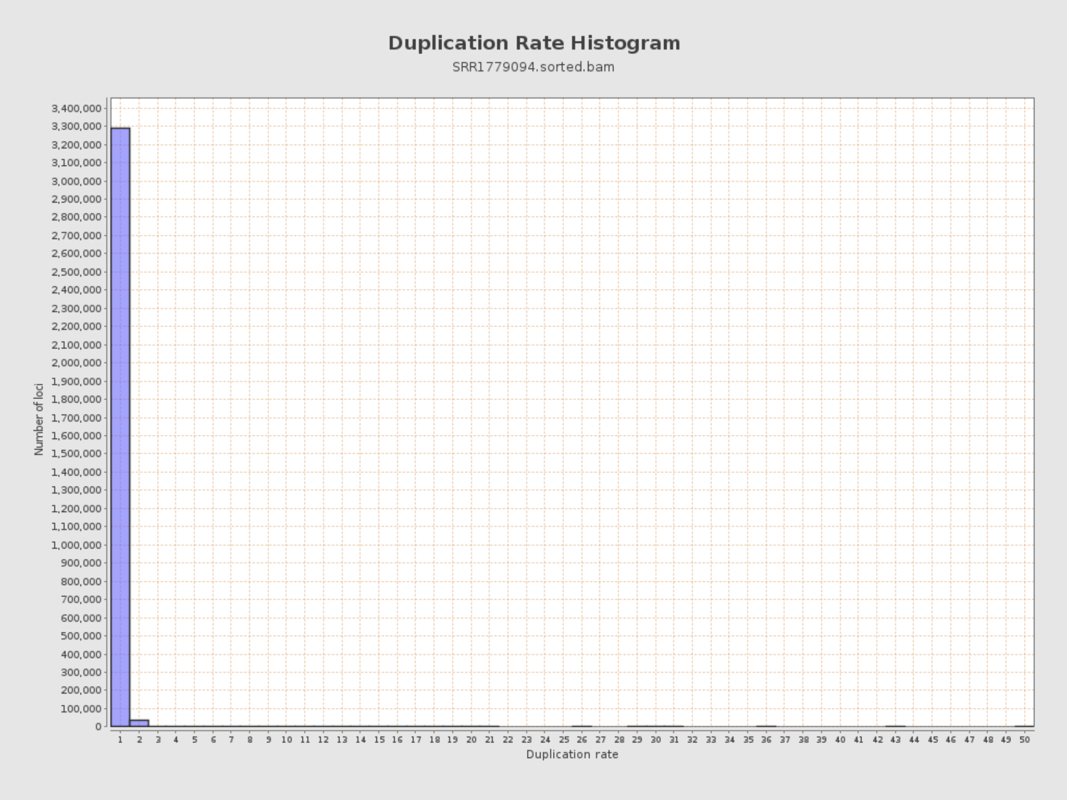
# 5. Results : Coverage Histogram (0-50X)



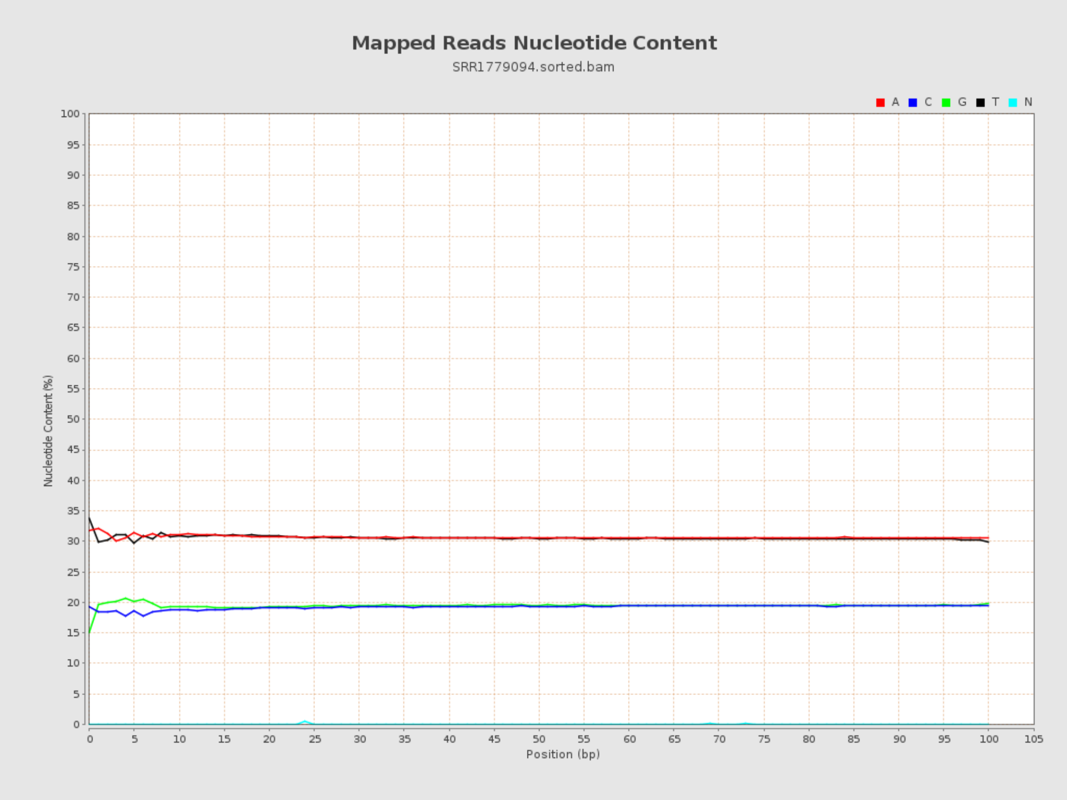
# 6. Results : Genome Fraction Coverage



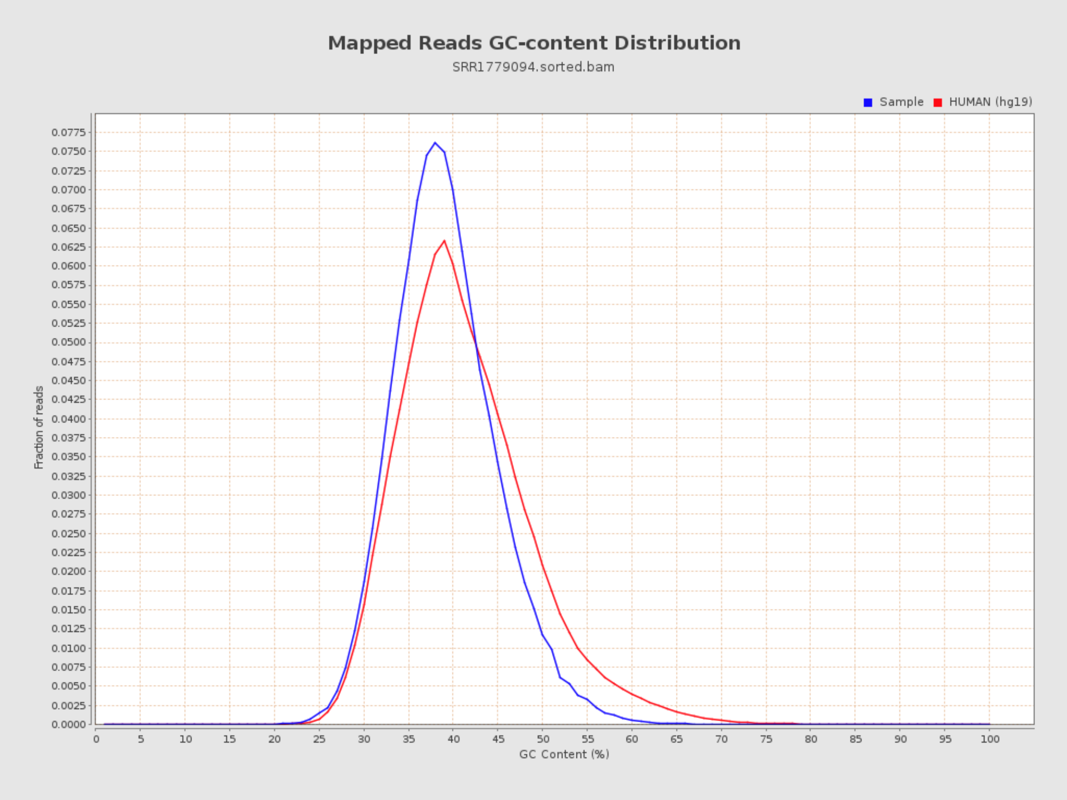
# 7. Results : Duplication Rate Histogram



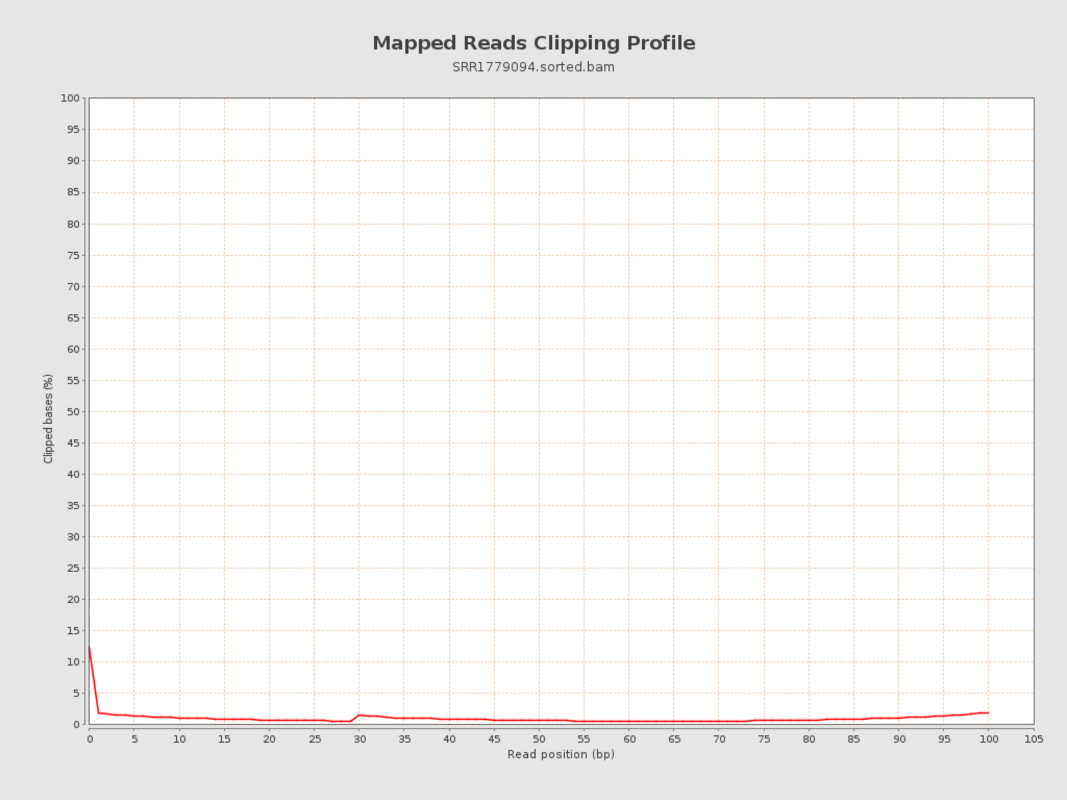
# 8. Results : Mapped Reads Nucleotide Content



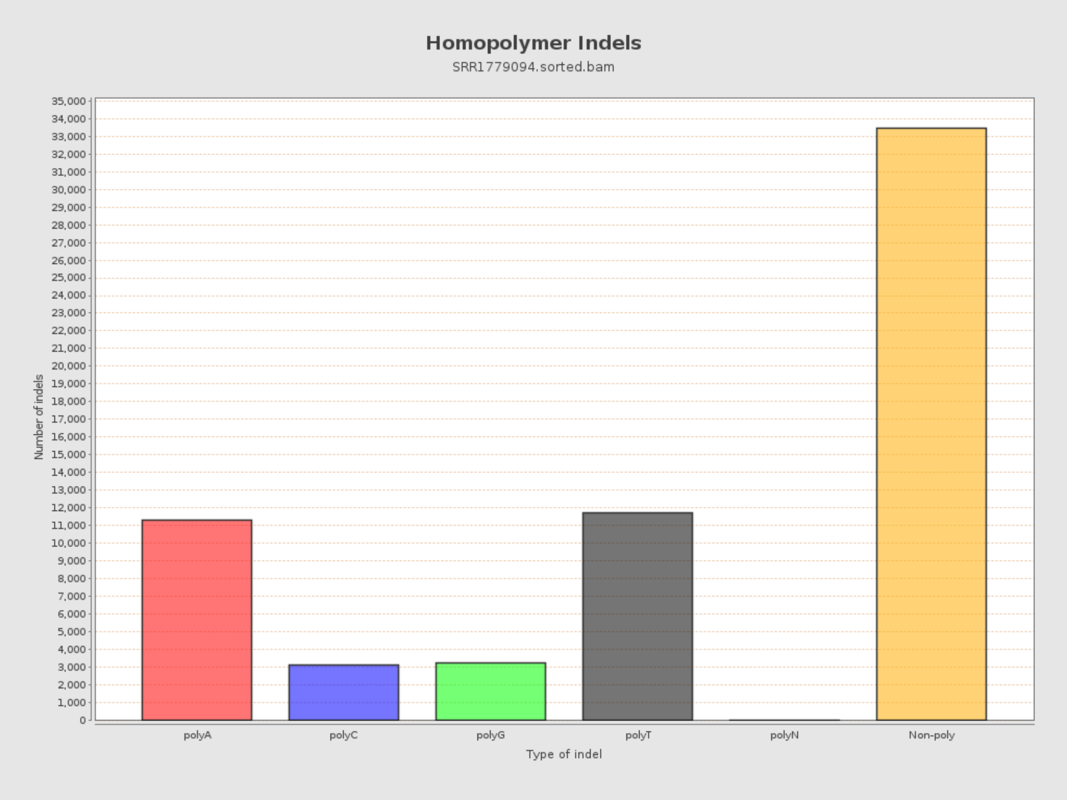
# 9. Results : Mapped Reads GC-content Distribution



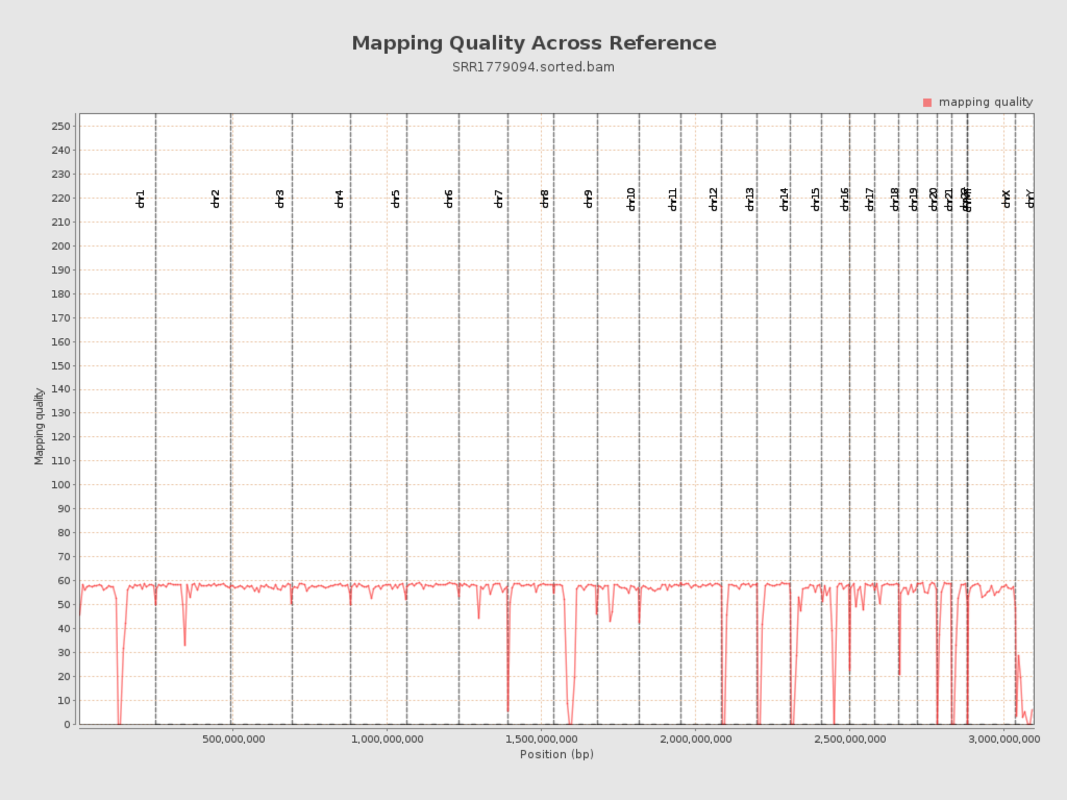
# 10. Results : Mapped Reads Clipping Profile



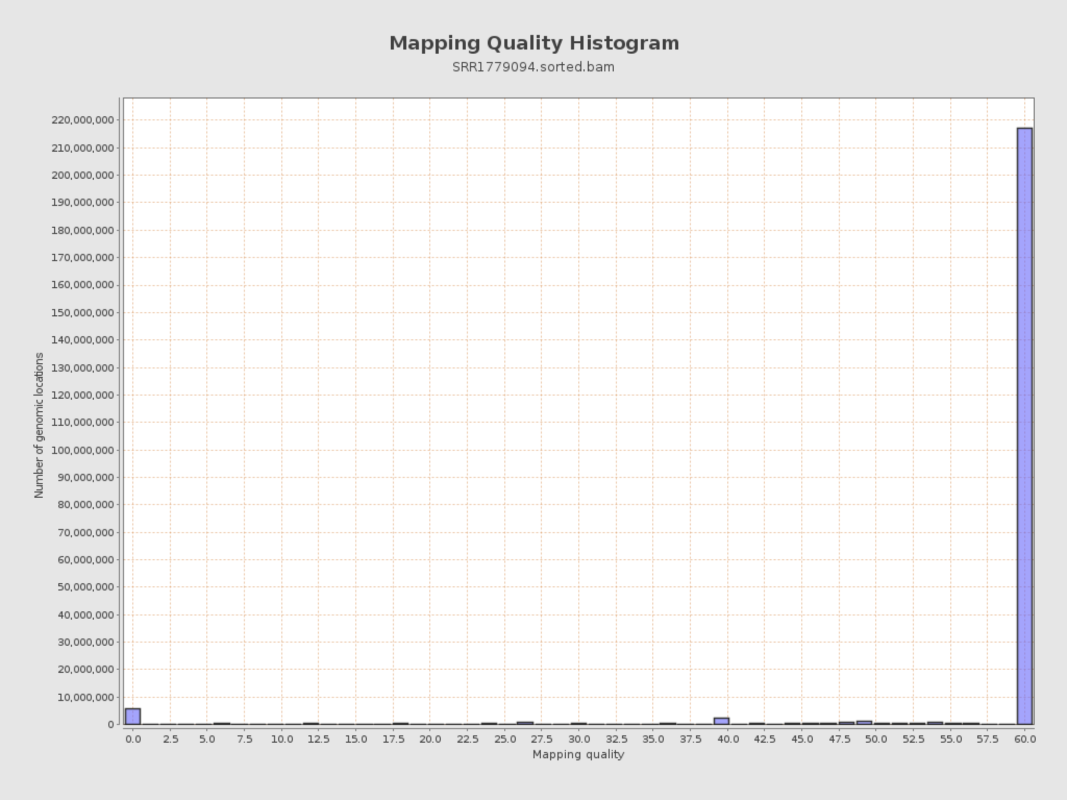
# 11. Results : Homopolymer Indels



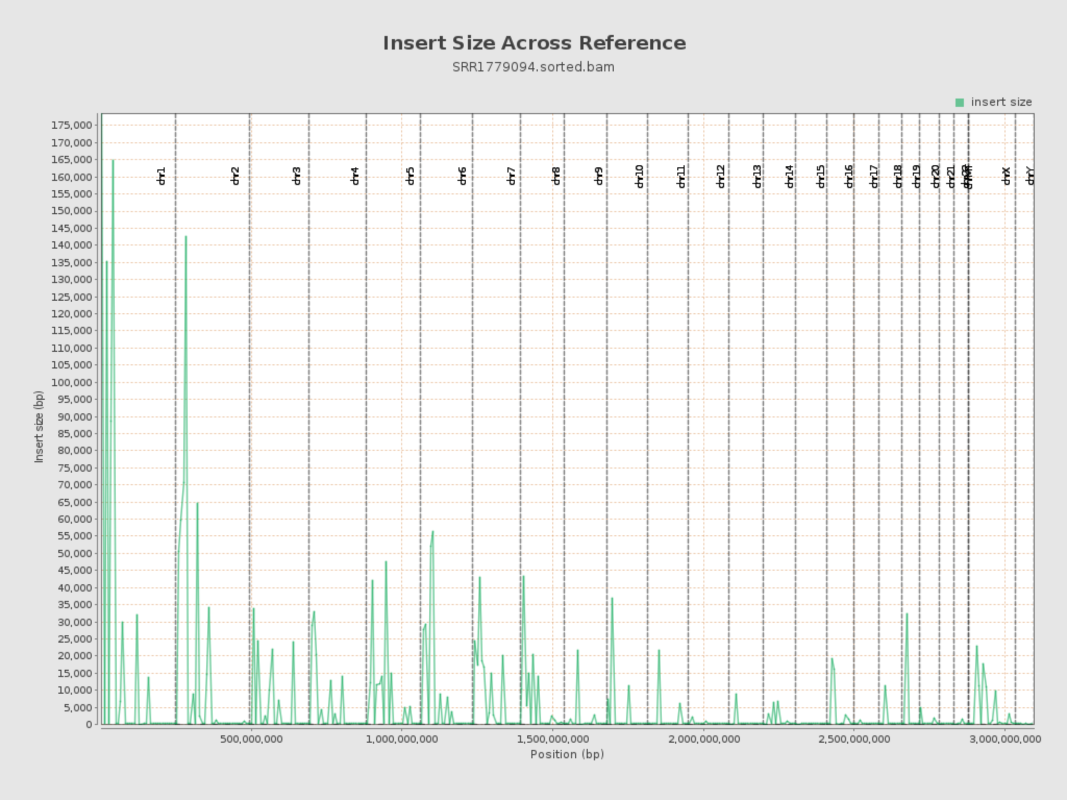
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram