# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/07 19:14:31*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779091.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_SRR1779091 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779091_1.fastq.gz SRR1779091_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Oct 07 19:14:30 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1779091.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 32,738,126 |
| Mapped reads | 31,380,333 / 95.85% |
| Unmapped reads | 1,357,793 / 4.15% |
| Mapped paired reads | 31,380,333 / 95.85% |
| Mapped reads, first in pair | 15,921,624 / 48.63% |
| Mapped reads, second in pair | 15,458,709 / 47.22% |
| Mapped reads, both in pair | 30,806,840 / 94.1% |
| Mapped reads, singletons | 573,493 / 1.75% |
| Secondary alignments | 0 |
| Supplementary alignments | 168,143 / 0.51% |
| Read min/max/mean length | 30 / 101 / 101.2 |
| Duplicated reads (estimated) | 1,419,080 / 4.33% |
| Duplication rate | 3.88% |
| Clipped reads | 1,801,524 / 5.5% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 958,139,116 / 30.57% |
| Number/percentage of C's | 605,238,336 / 19.31% |
| Number/percentage of T's | 954,499,481 / 30.45% |
| Number/percentage of G's | 615,427,011 / 19.63% |
| Number/percentage of N's | 1,042,740 / 0.03% |
| | |

| | |
|---|---|
| GC Percentage | 38.94% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 1.0127 |
| Standard Deviation | 3.1662 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.38 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 79,920.56 |
| Standard Deviation | 2,789,734.45 |
| P25/Median/P75 | 207 / 279 / 356 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.5% |
| Mismatches | 15,293,327 |
| Insertions | 273,279 |
| Mapped reads with at least one insertion | 0.86% |
| Deletions | 332,628 |
| Mapped reads with at least one deletion | 1.04% |
| Homopolymer indels | 47.31% |

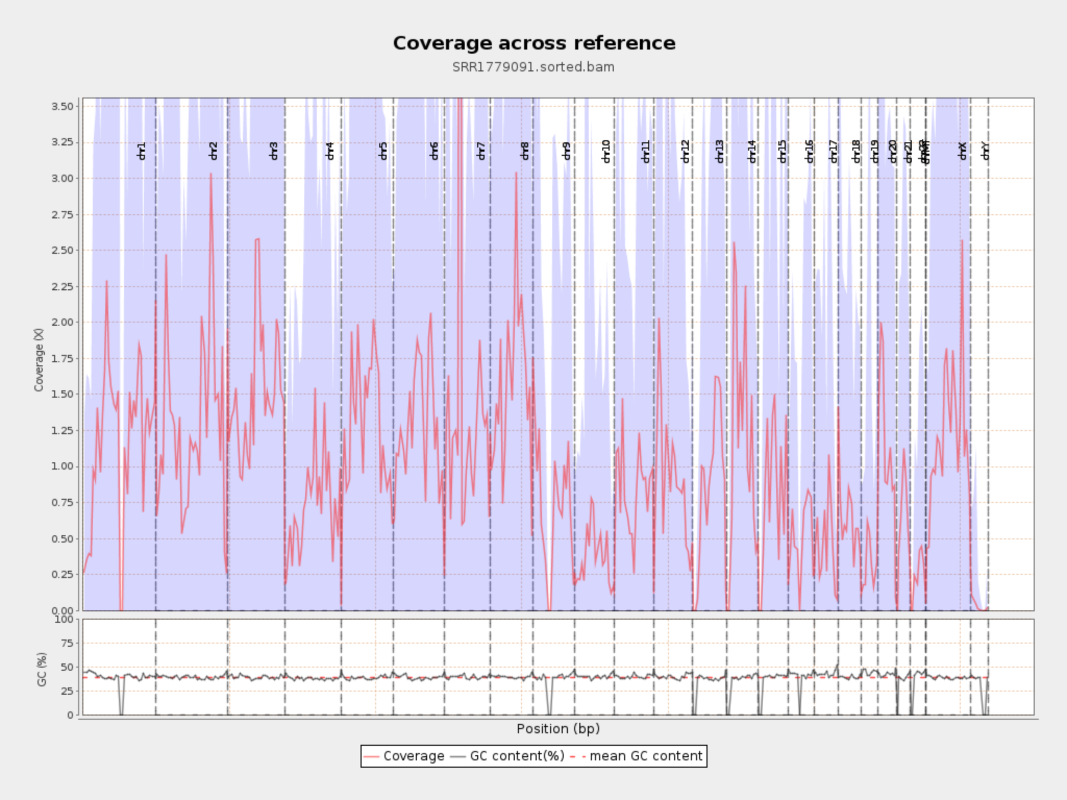
## 2.7. Chromosome stats

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

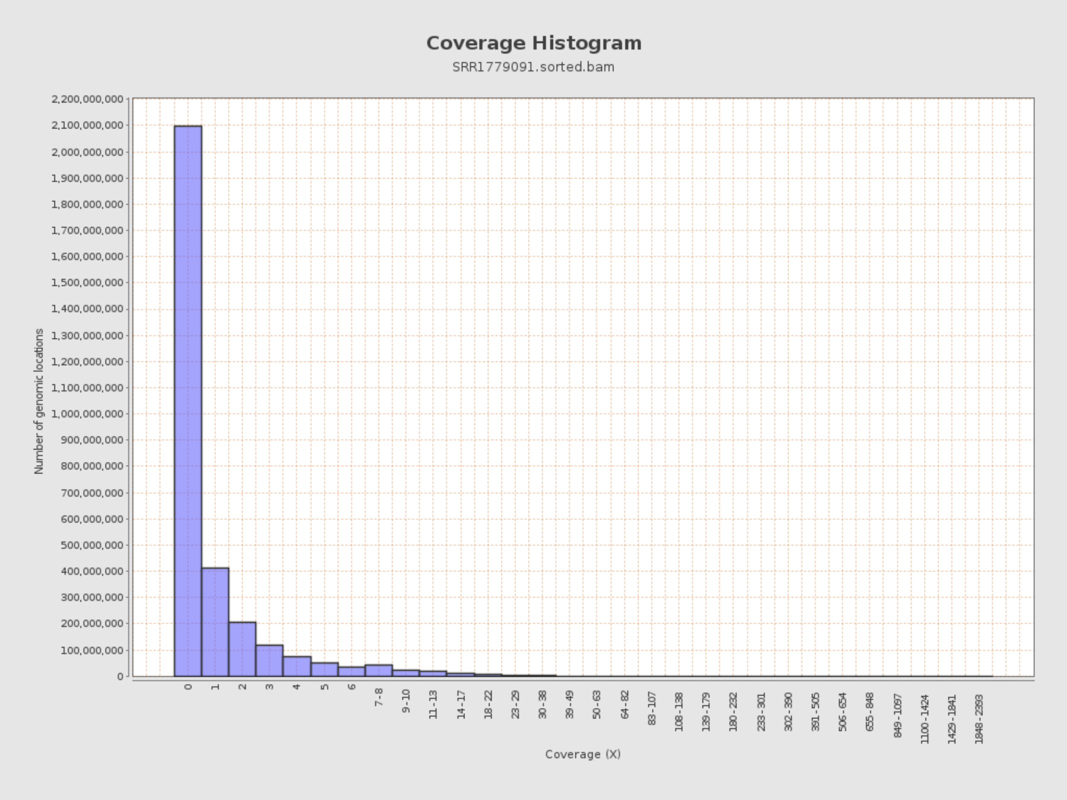
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 291412723 | 1.1692 | 3.5342 |
| chr2 | 243199373 | 314947885 | 1.295 | 3.0635 |
| chr3 | 198022430 | 297856172 | 1.5042 | 3.0606 |
| chr4 | 191154276 | 140216903 | 0.7335 | 2.0521 |
| chr5 | 180915260 | 234950277 | 1.2987 | 2.7872 |
| chr6 | 171115067 | 223906560 | 1.3085 | 2.8441 |
| chr7 | 159138663 | 243184531 | 1.5281 | 7.8335 |
| chr8 | 146364022 | 232341359 | 1.5874 | 2.9676 |
| chr9 | 141213431 | 99980369 | 0.708 | 2.0297 |
| chr10 | 135534747 | 51401398 | 0.3792 | 3.6634 |
| chr11 | 135006516 | 112568597 | 0.8338 | 2.0987 |
| chr12 | 133851895 | 123727447 | 0.9244 | 2.3925 |
| chr13 | 115169878 | 99369697 | 0.8628 | 2.2003 |
| chr14 | 107349540 | 126505935 | 1.1784 | 2.8186 |
| chr15 | 102531392 | 83396669 | 0.8134 | 2.3637 |
| chr16 | 90354753 | 44685057 | 0.4946 | 1.5767 |
| chr17 | 81195210 | 38625423 | 0.4757 | 1.7761 |
| chr18 | 78077248 | 49034513 | 0.628 | 1.9315 |
| chr19 | 59128983 | 19954102 | 0.3375 | 1.7221 |
| chr20 | 63025520 | 74348190 | 1.1797 | 2.4954 |
| chr21 | 48129895 | 29492053 | 0.6128 | 1.8246 |
| chr22 | 51304566 | 12708876 | 0.2477 | 1.0992 |
| chrMT | 16571 | 855 | 0.0516 | 0.2362 |
| chrX | 155270560 | 188689694 | 1.2152 | 2.9281 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1784030 | 0.03 | 0.517 |

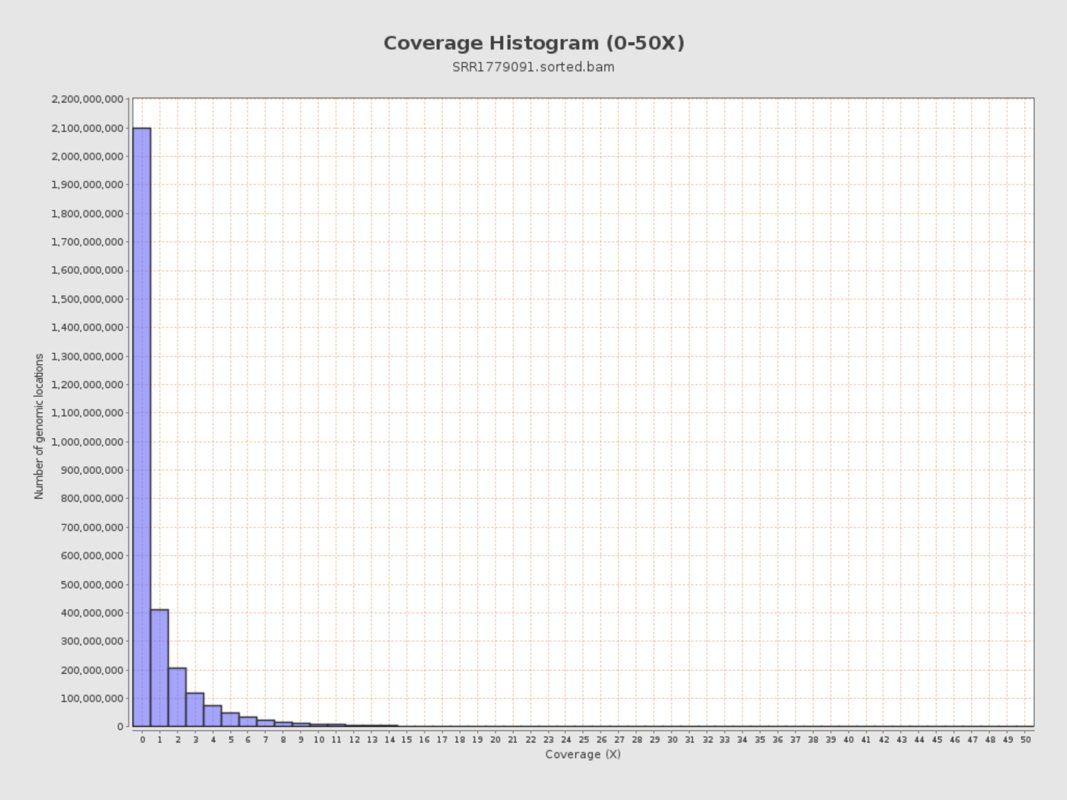
# 3. Results : Coverage across reference



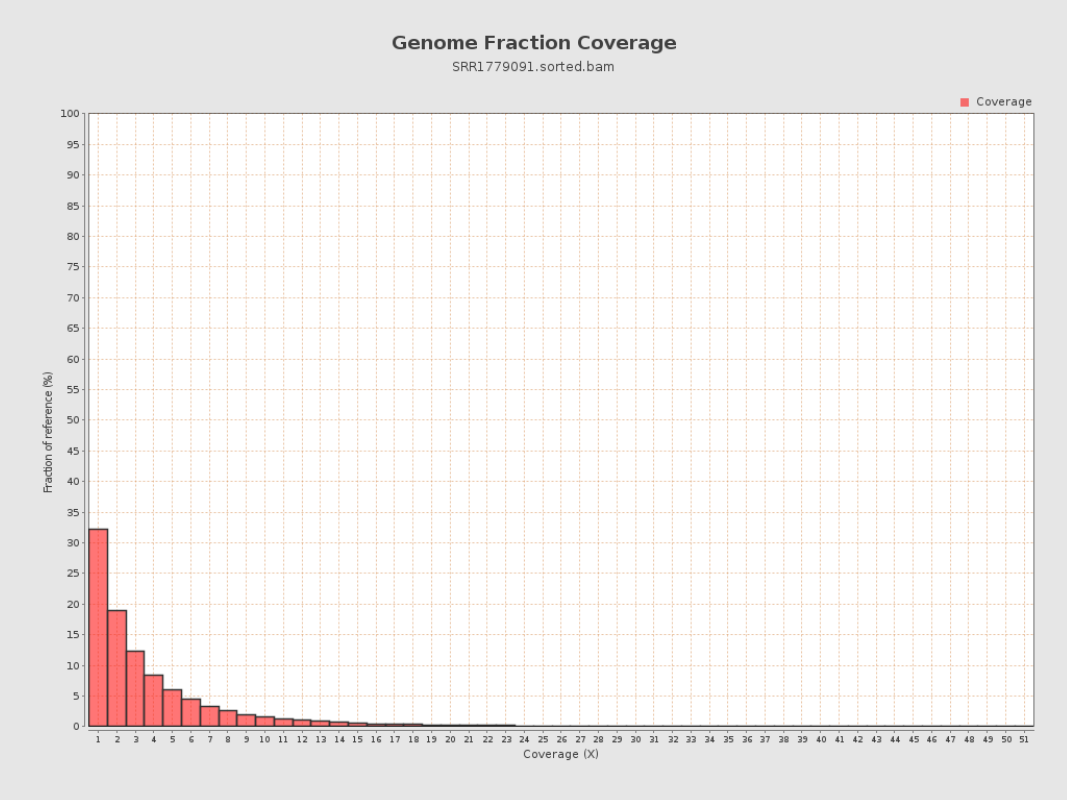
# 4. Results : Coverage Histogram



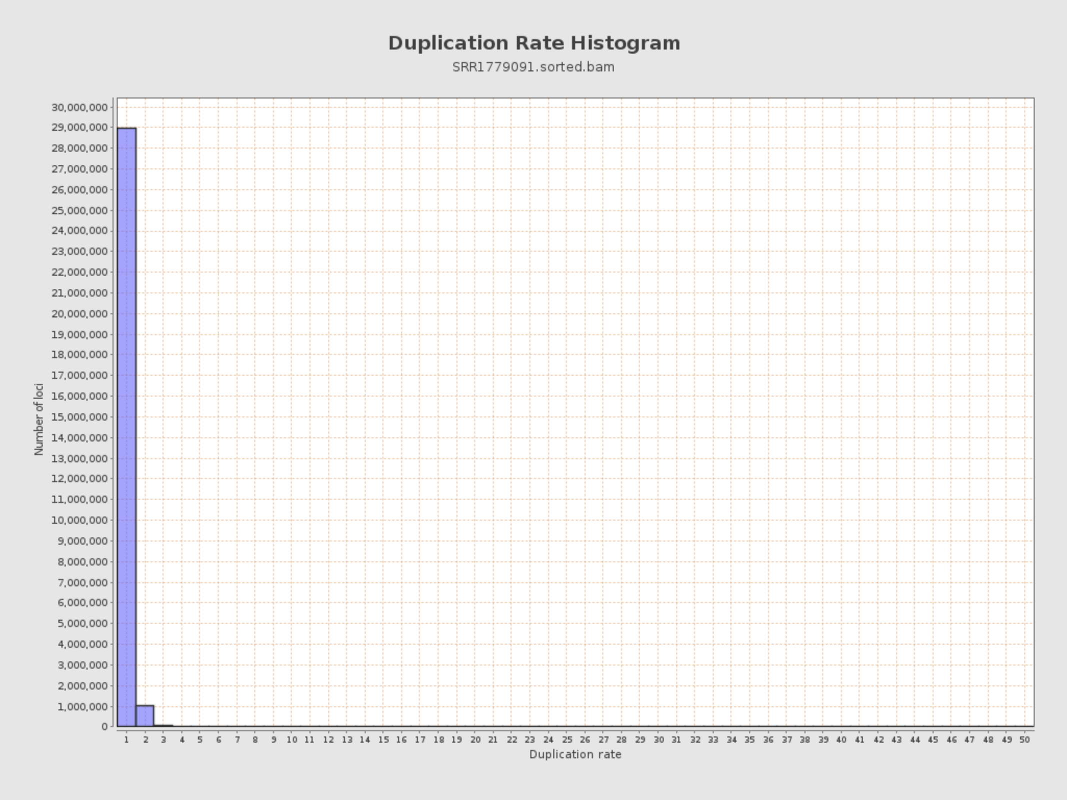
# 5. Results : Coverage Histogram (0-50X)



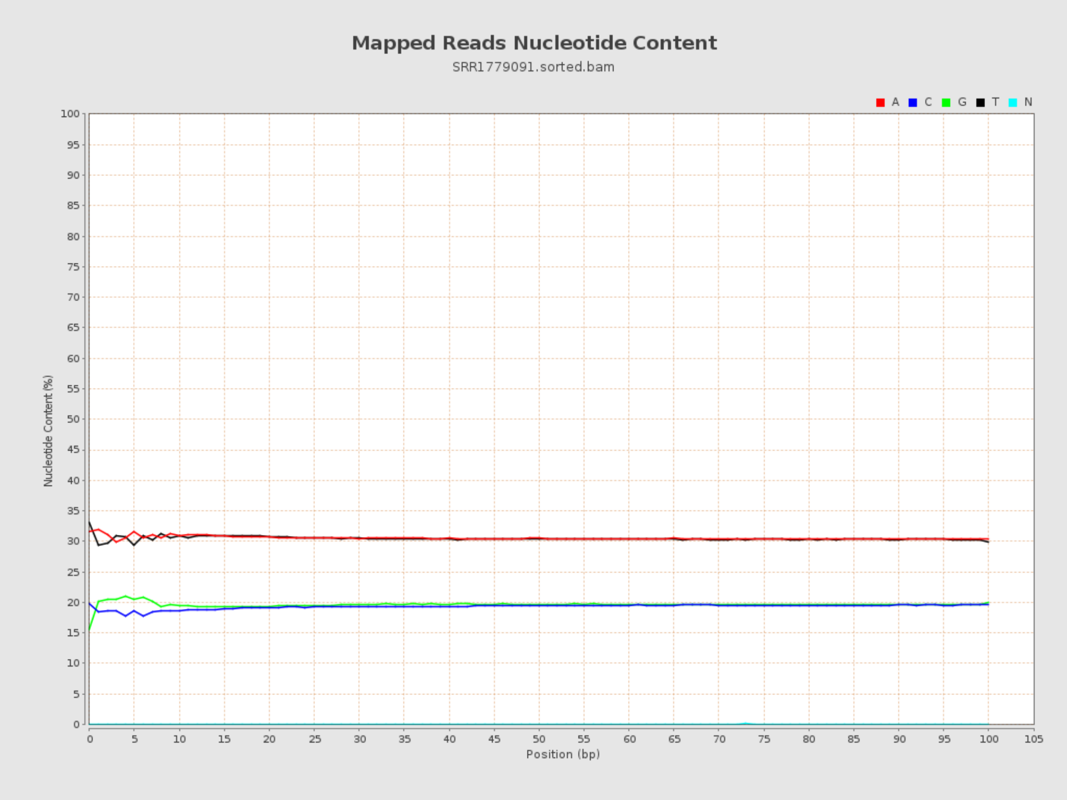
# 6. Results : Genome Fraction Coverage



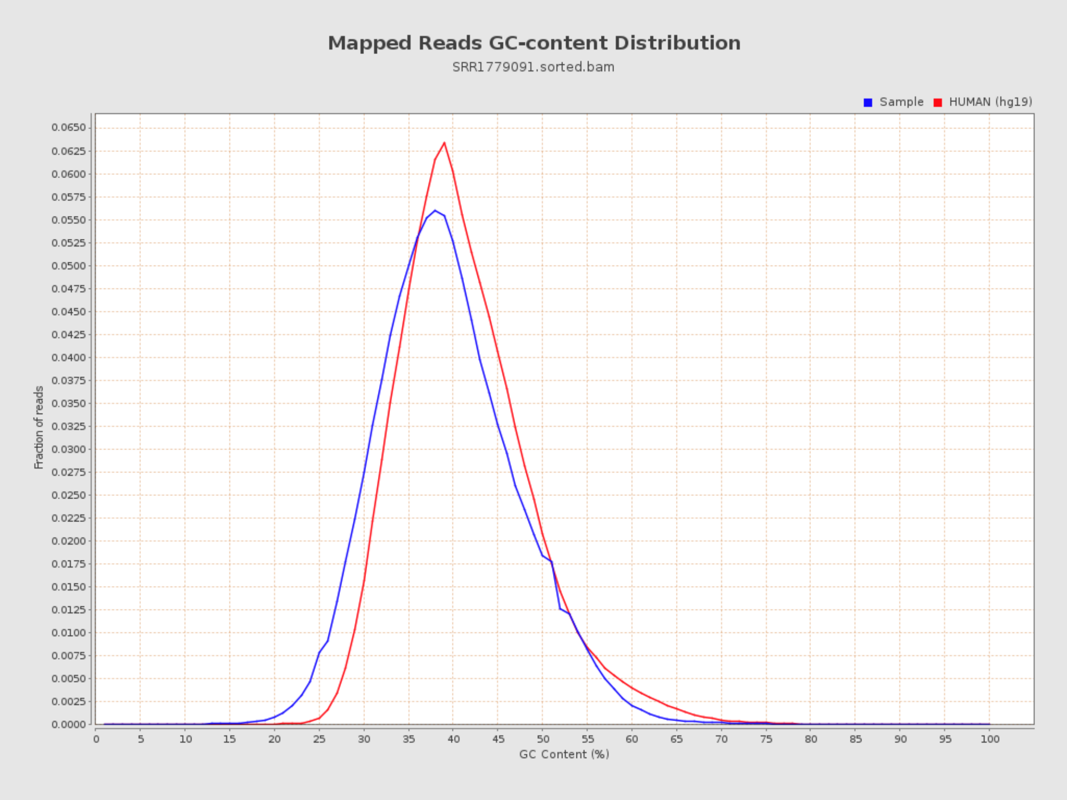
# 7. Results : Duplication Rate Histogram



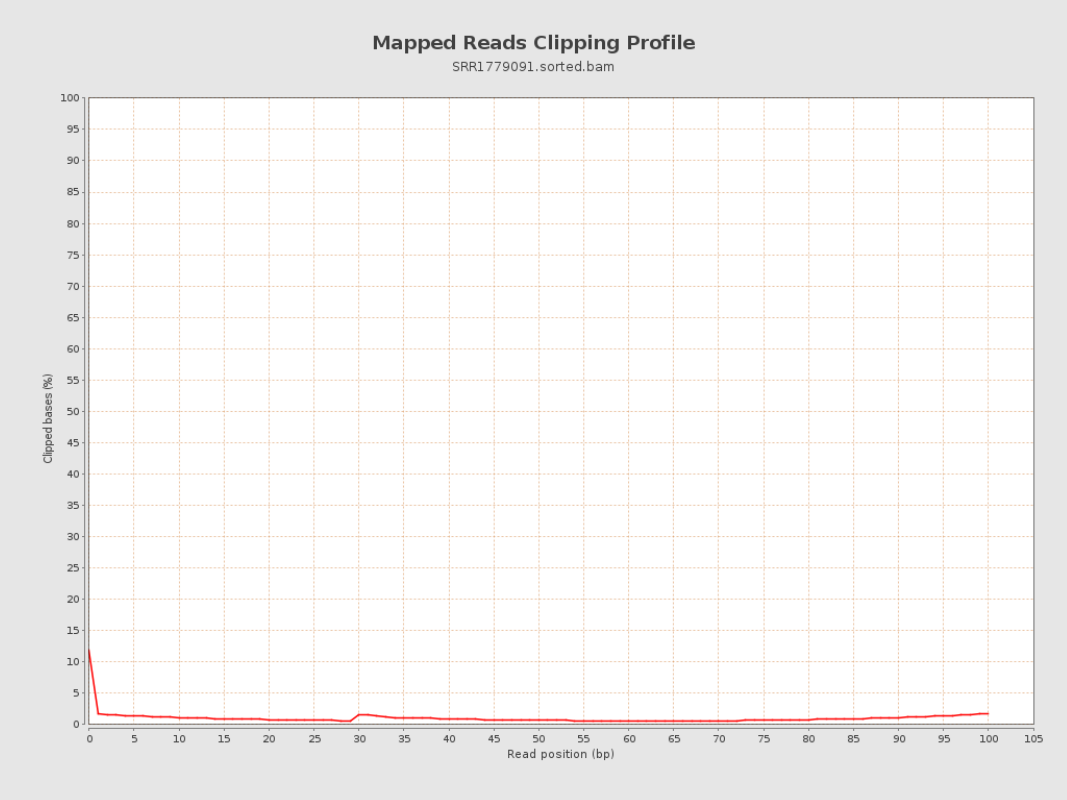
# 8. Results : Mapped Reads Nucleotide Content



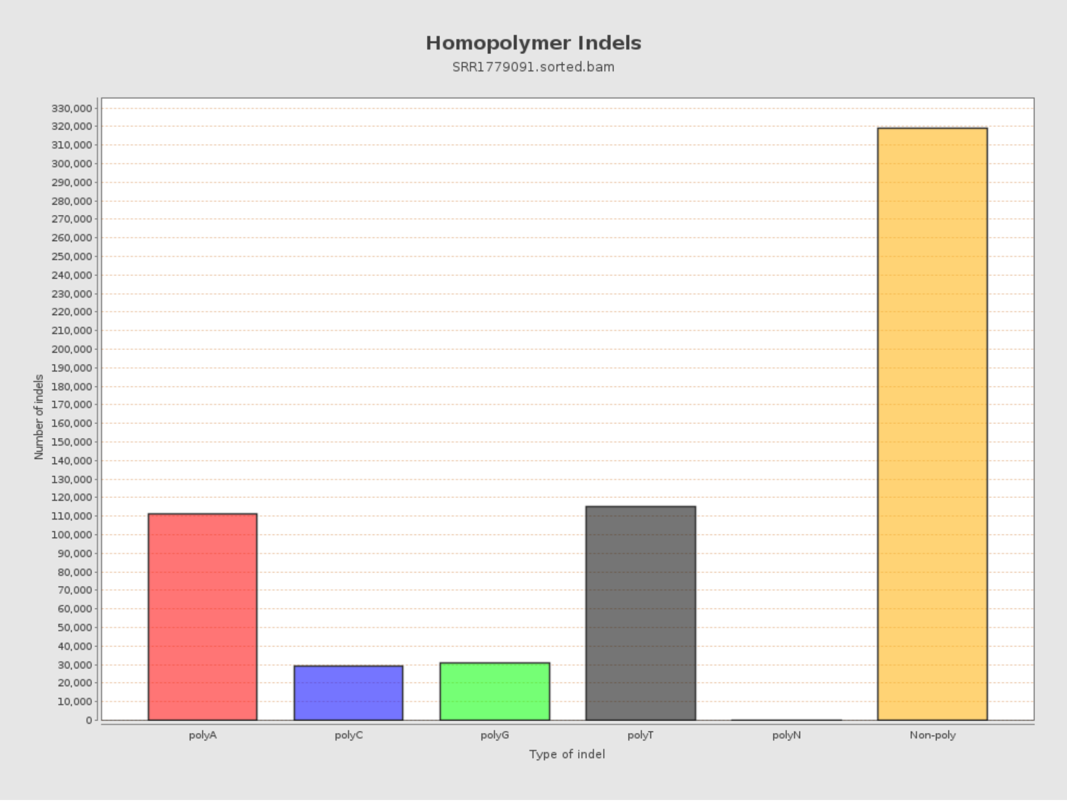
# 9. Results : Mapped Reads GC-content Distribution



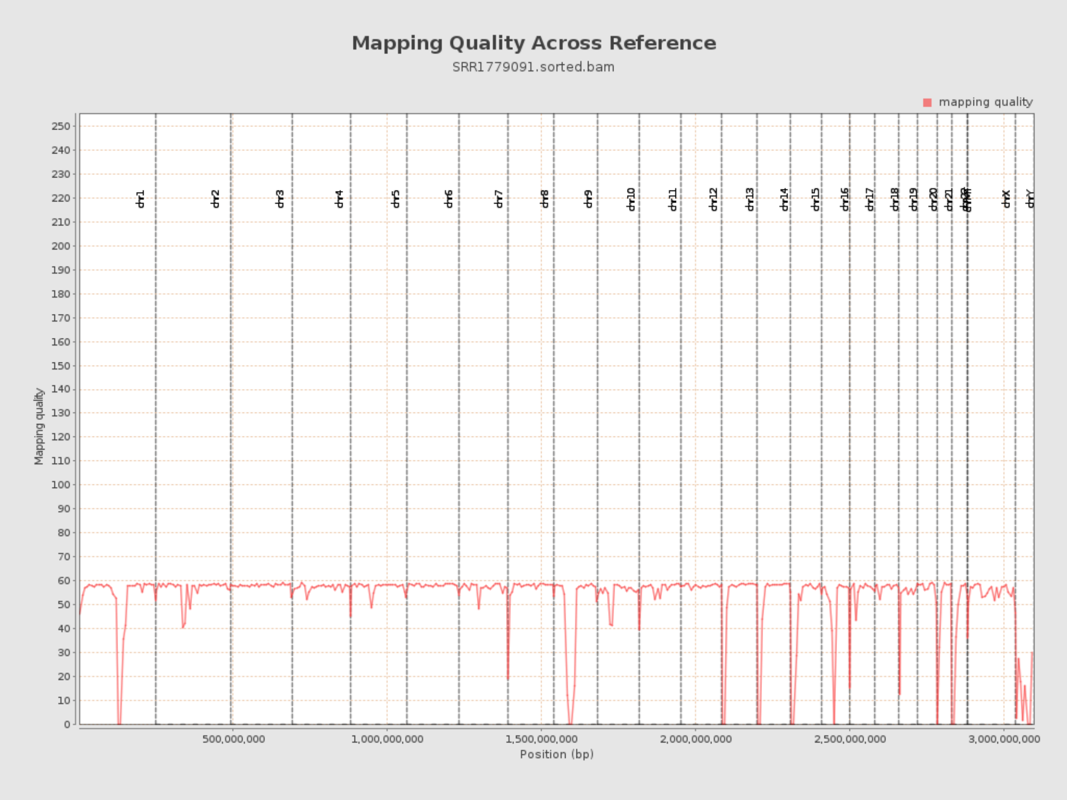
# 10. Results : Mapped Reads Clipping Profile



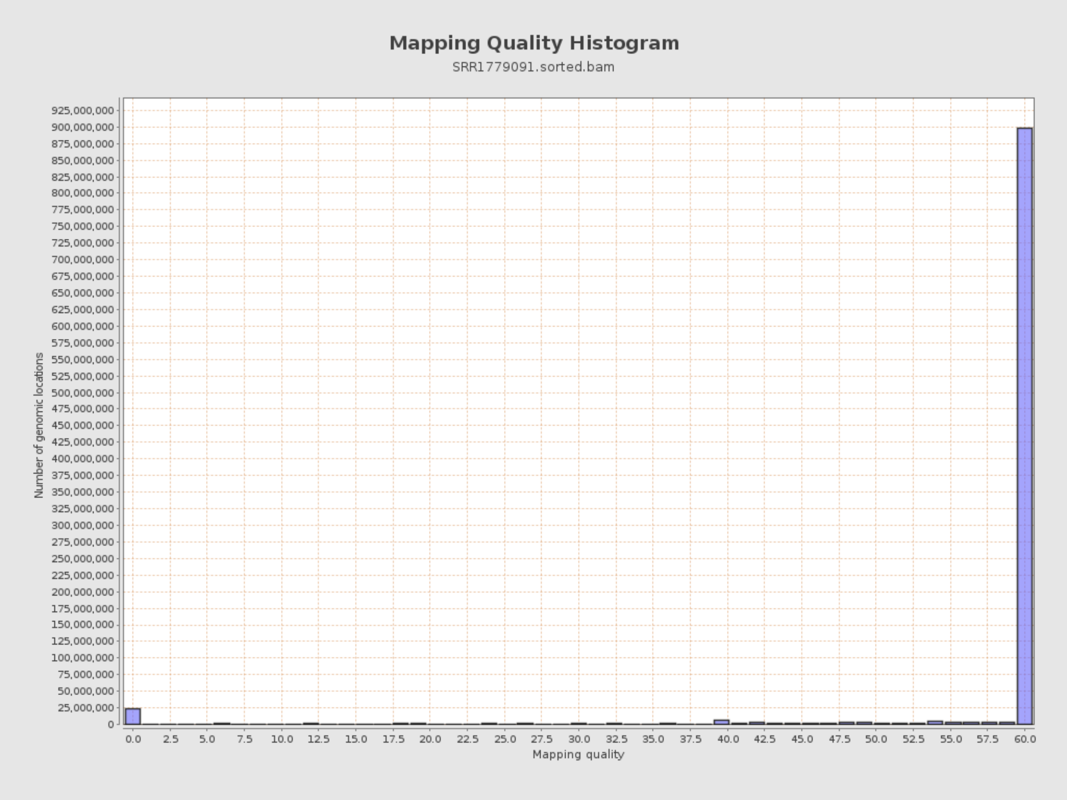
# 11. Results : Homopolymer Indels



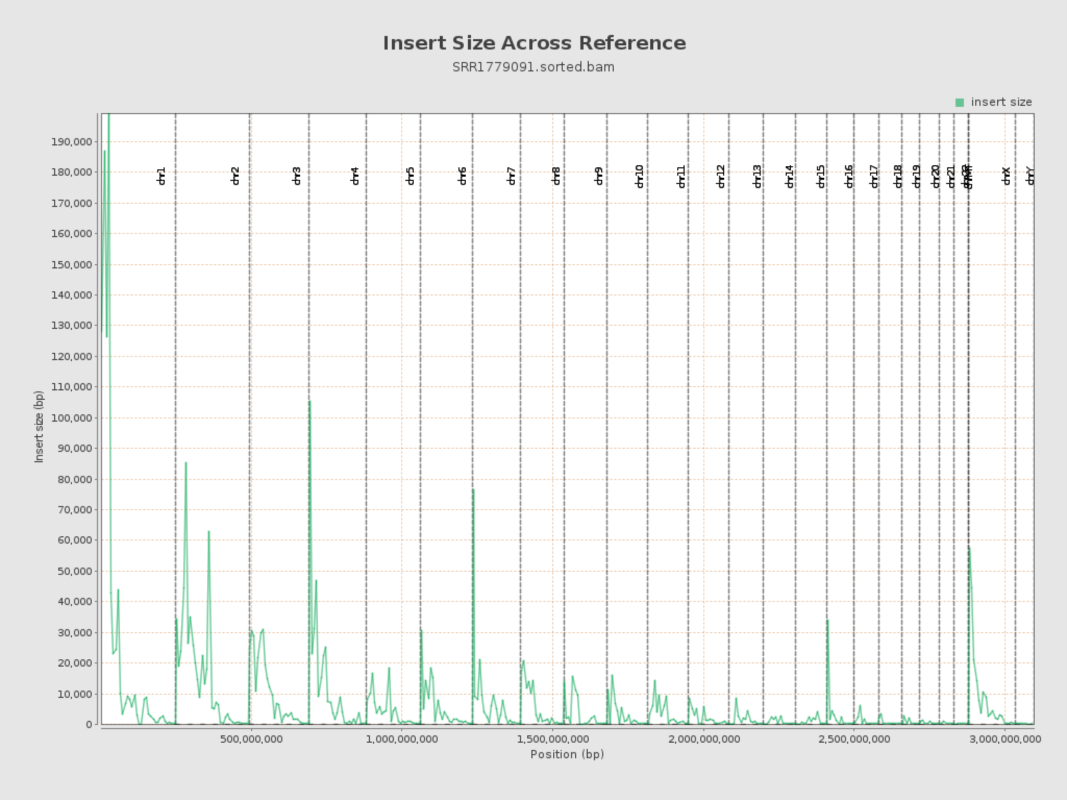
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram