# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/07 18:17:29*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779090.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_SRR1779090 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779090_1.fastq.gz SRR1779090_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Oct 07 18:17:28 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1779090.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 20,940,504 |
| Mapped reads | 20,277,243 / 96.83% |
| Unmapped reads | 663,261 / 3.17% |
| Mapped paired reads | 20,277,243 / 96.83% |
| Mapped reads, first in pair | 10,250,842 / 48.95% |
| Mapped reads, second in pair | 10,026,401 / 47.88% |
| Mapped reads, both in pair | 19,982,522 / 95.43% |
| Mapped reads, singletons | 294,721 / 1.41% |
| Secondary alignments | 0 |
| Supplementary alignments | 116,918 / 0.56% |
| Read min/max/mean length | 30 / 101 / 101.22 |
| Duplicated reads (estimated) | 445,548 / 2.13% |
| Duplication rate | 1.9% |
| Clipped reads | 1,216,815 / 5.81% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 616,512,933 / 30.45% |
| Number/percentage of C's | 393,265,687 / 19.42% |
| Number/percentage of T's | 615,196,267 / 30.38% |
| Number/percentage of G's | 399,278,625 / 19.72% |
| Number/percentage of N's | 678,132 / 0.03% |
| | |

| | |
|---|---|
| GC Percentage | 39.14% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.6543 |
| Standard Deviation | 1.6825 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.63 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 71,130.9 |
| Standard Deviation | 2,554,078.87 |
| P25/Median/P75 | 202 / 265 / 338 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 10,093,419 |
| Insertions | 184,623 |
| Mapped reads with at least one insertion | 0.9% |
| Deletions | 224,562 |
| Mapped reads with at least one deletion | 1.09% |
| Homopolymer indels | 47.08% |

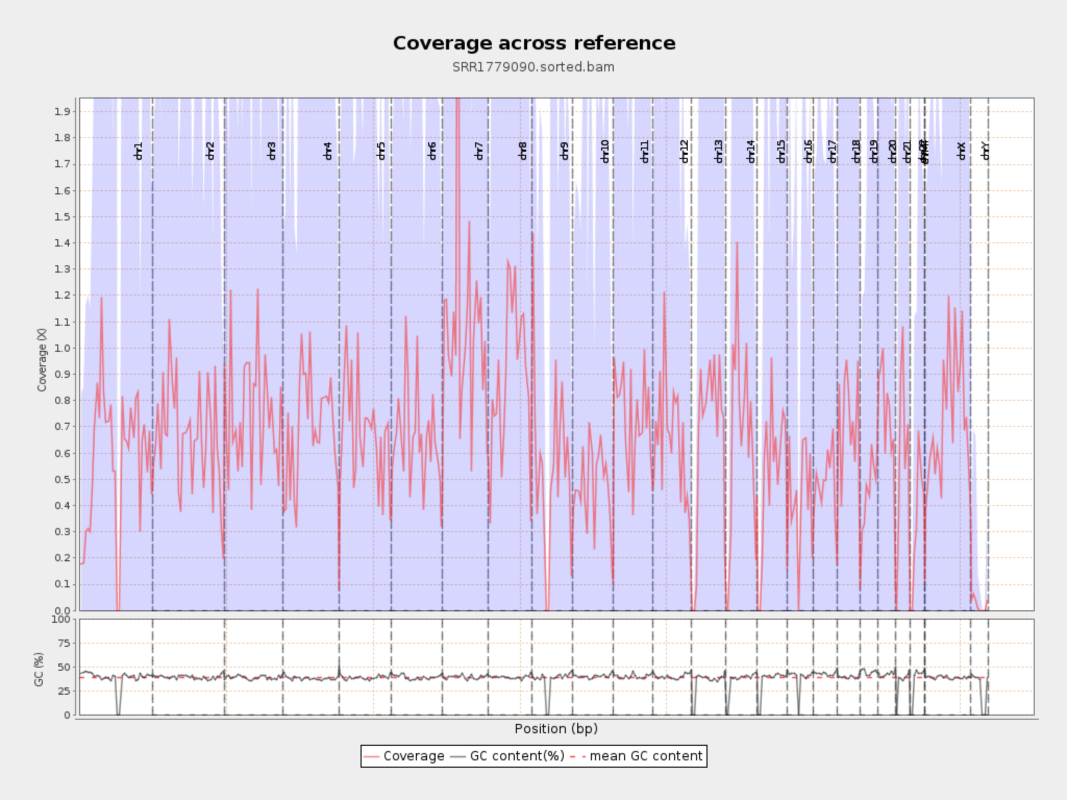
## 2.7. Chromosome stats

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

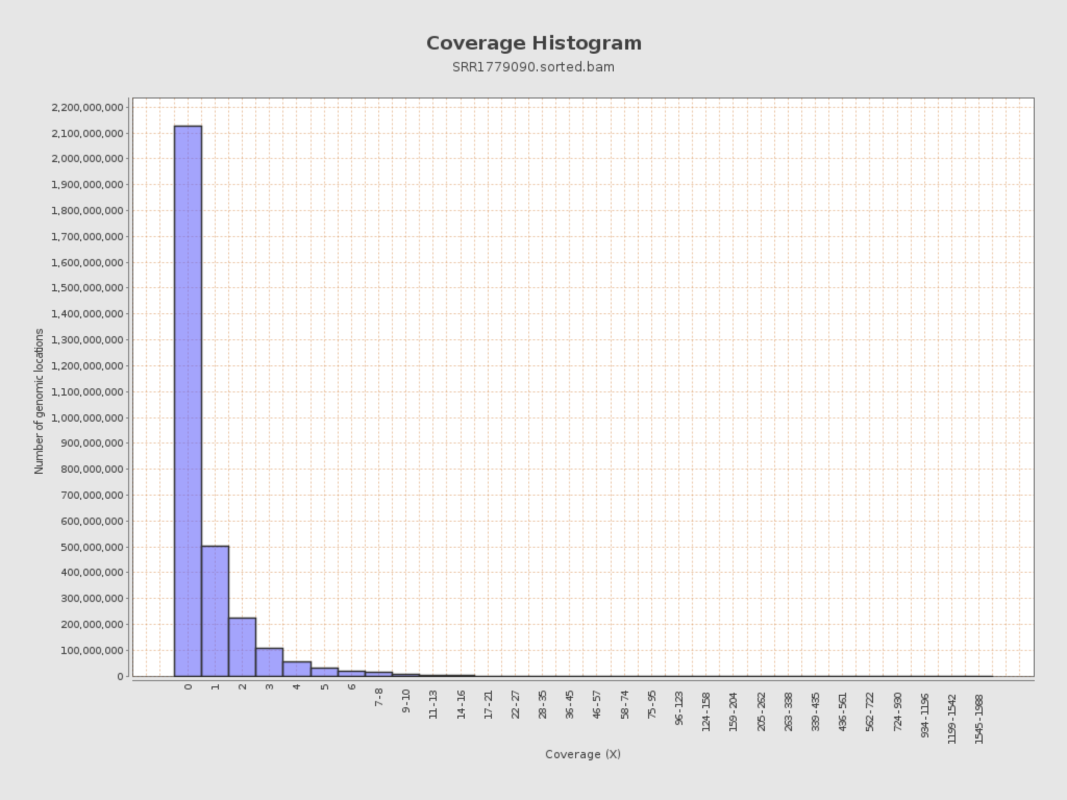
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 143571875 | 0.576 | 2.4164 |
| chr2 | 243199373 | 161148126 | 0.6626 | 1.5066 |
| chr3 | 198022430 | 147945831 | 0.7471 | 1.4614 |
| chr4 | 191154276 | 133772057 | 0.6998 | 1.4465 |
| chr5 | 180915260 | 121071872 | 0.6692 | 1.3718 |
| chr6 | 171115067 | 114487225 | 0.6691 | 1.4132 |
| chr7 | 159138663 | 174552420 | 1.0969 | 2.8058 |
| chr8 | 146364022 | 131863436 | 0.9009 | 1.5919 |
| chr9 | 141213431 | 76566253 | 0.5422 | 1.3743 |
| chr10 | 135534747 | 64852869 | 0.4785 | 2.546 |
| chr11 | 135006516 | 98906093 | 0.7326 | 1.441 |
| chr12 | 133851895 | 86034004 | 0.6428 | 1.4065 |
| chr13 | 115169878 | 77669829 | 0.6744 | 1.3983 |
| chr14 | 107349540 | 70408927 | 0.6559 | 1.3637 |
| chr15 | 102531392 | 53592433 | 0.5227 | 1.2634 |
| chr16 | 90354753 | 37294094 | 0.4128 | 1.0966 |
| chr17 | 81195210 | 39085042 | 0.4814 | 1.215 |
| chr18 | 78077248 | 57236765 | 0.7331 | 1.4696 |
| chr19 | 59128983 | 26539098 | 0.4488 | 1.7761 |
| chr20 | 63025520 | 46918932 | 0.7444 | 1.5878 |
| chr21 | 48129895 | 29142359 | 0.6055 | 1.3697 |
| chr22 | 51304566 | 17310473 | 0.3374 | 0.9385 |
| chrMT | 16571 | 1855 | 0.1119 | 0.4517 |
| chrX | 155270560 | 114111799 | 0.7349 | 1.5427 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1348966 | 0.0227 | 0.36 |

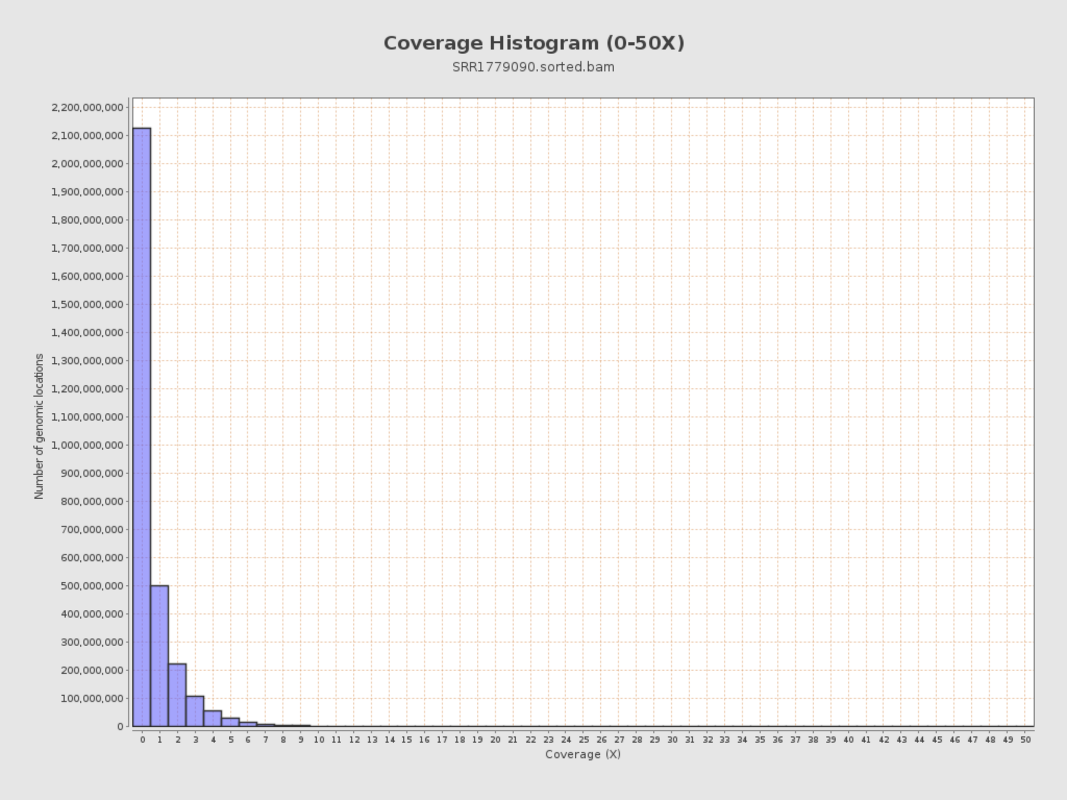
# 3. Results : Coverage across reference



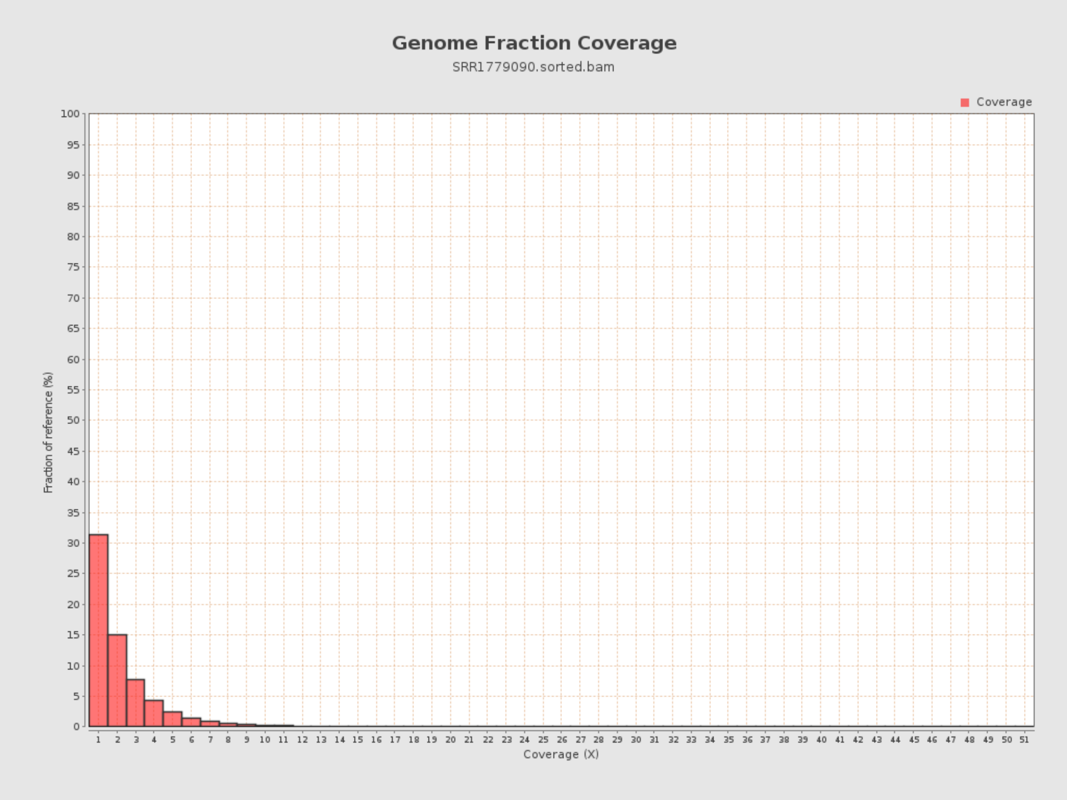
# 4. Results : Coverage Histogram



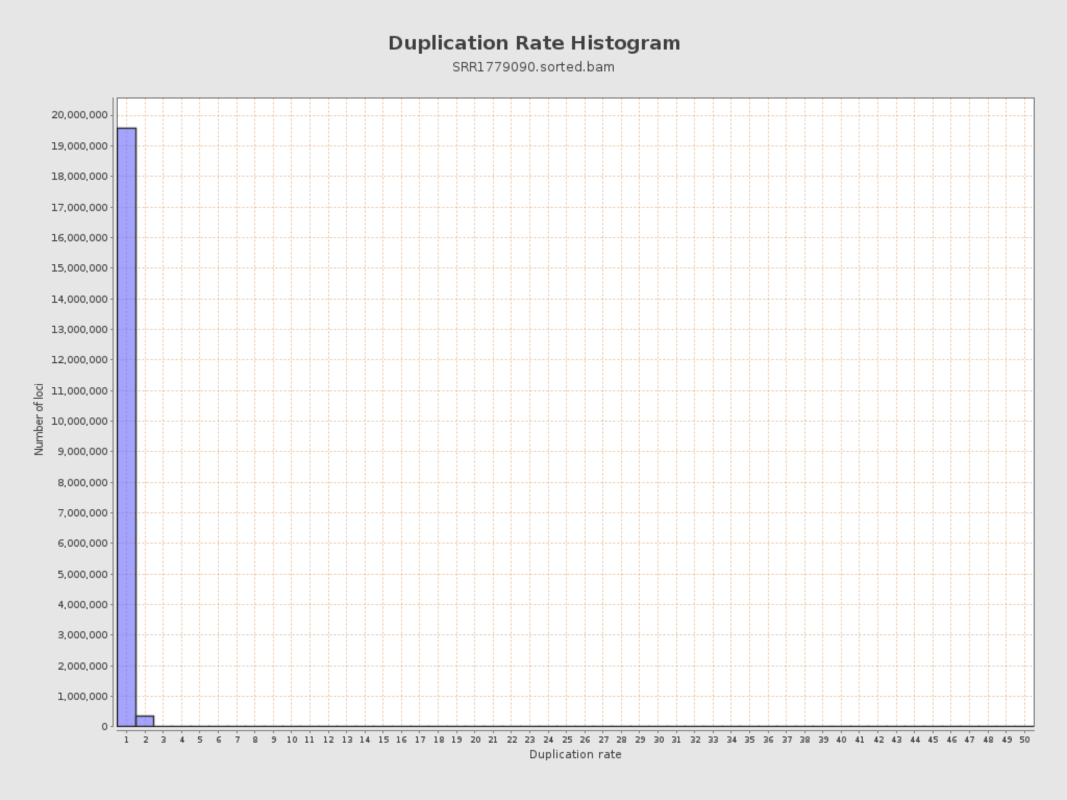
# 5. Results : Coverage Histogram (0-50X)



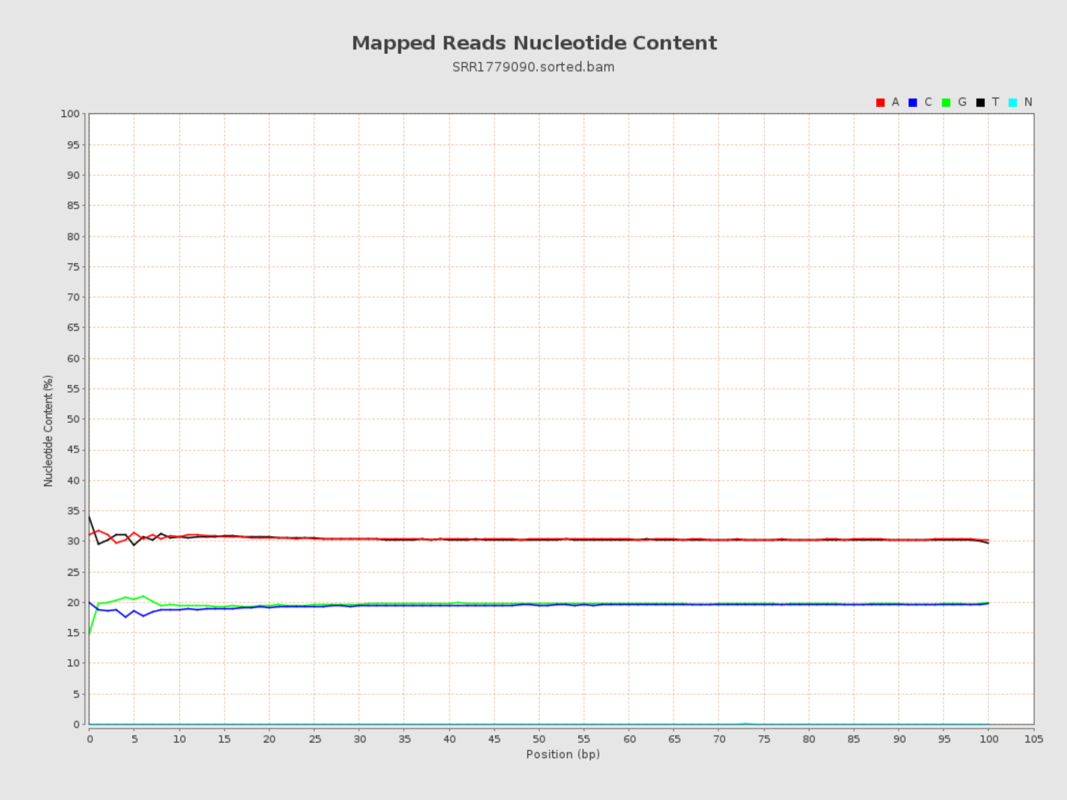
# 6. Results : Genome Fraction Coverage



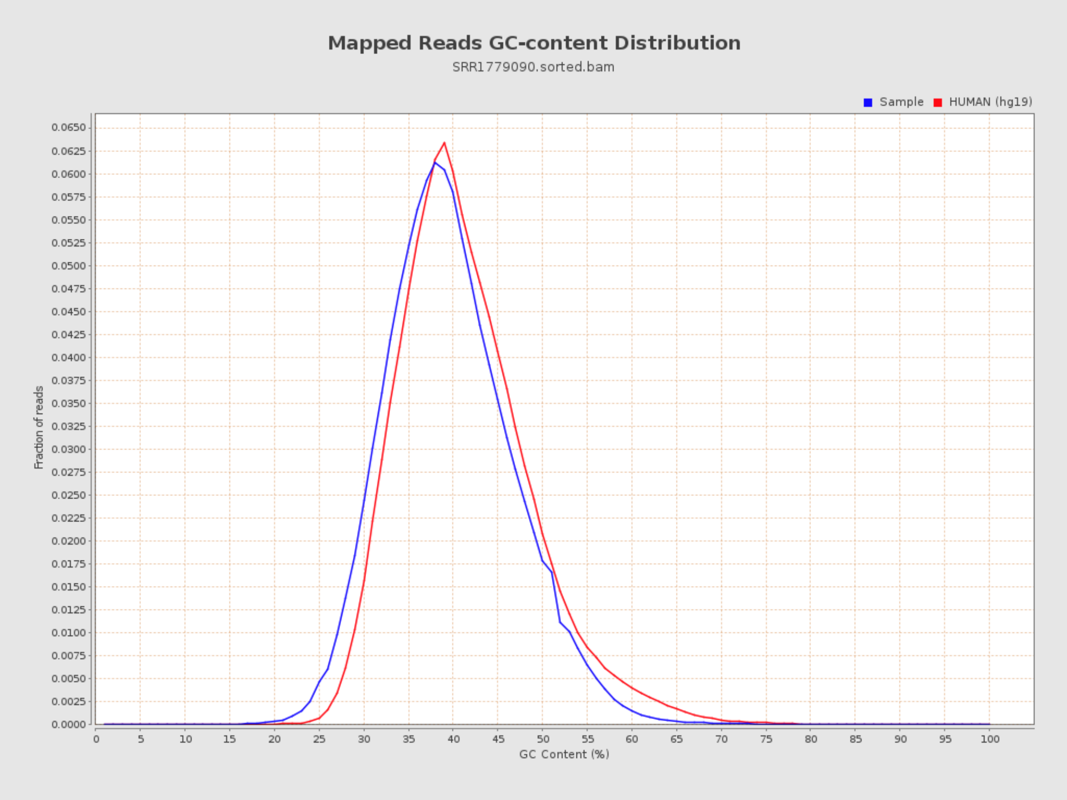
# 7. Results : Duplication Rate Histogram



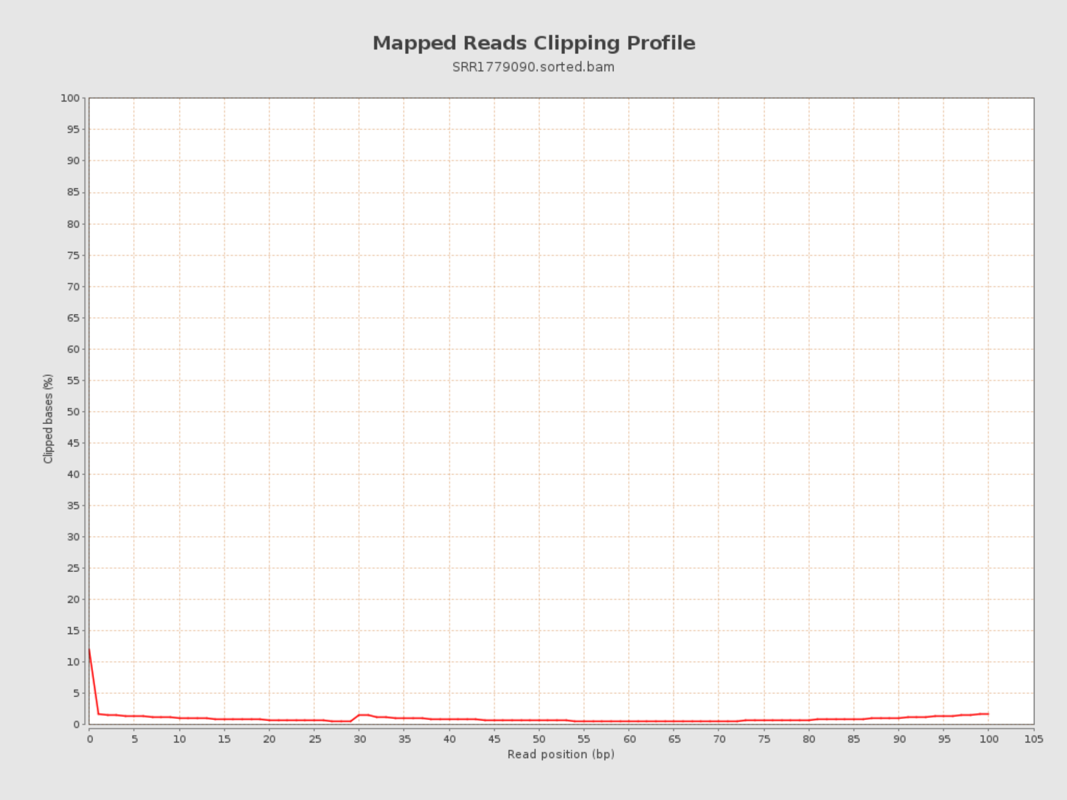
# 8. Results : Mapped Reads Nucleotide Content



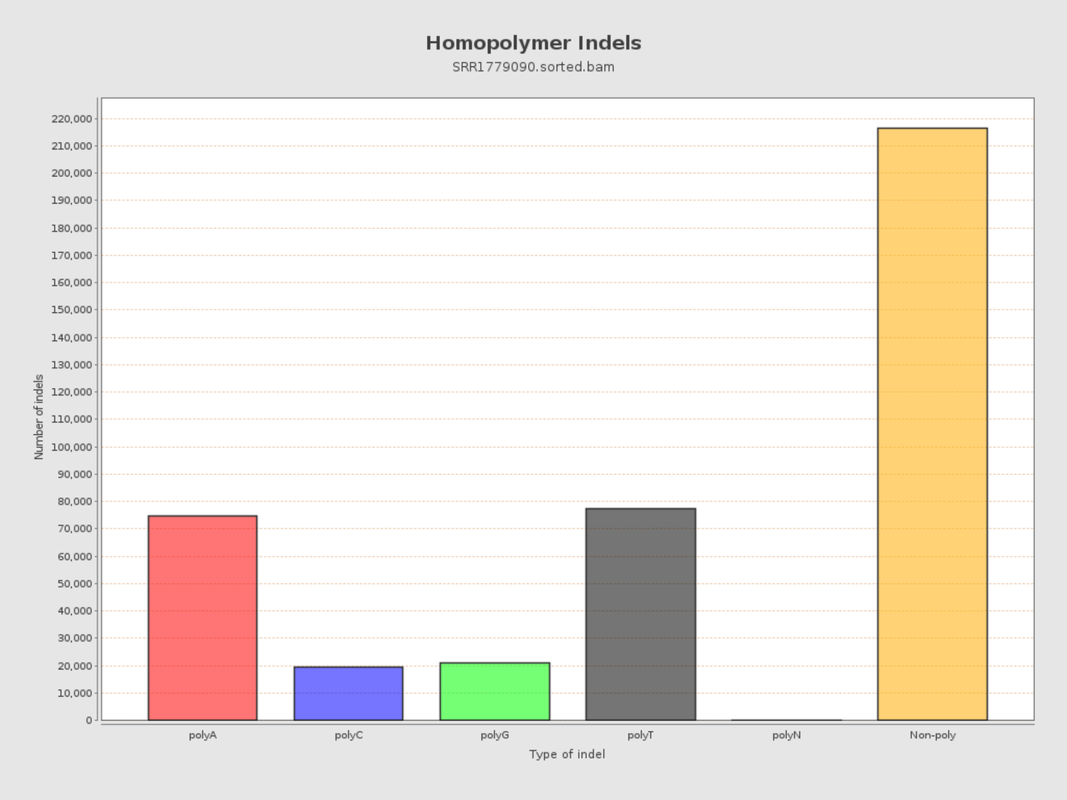
# 9. Results : Mapped Reads GC-content Distribution



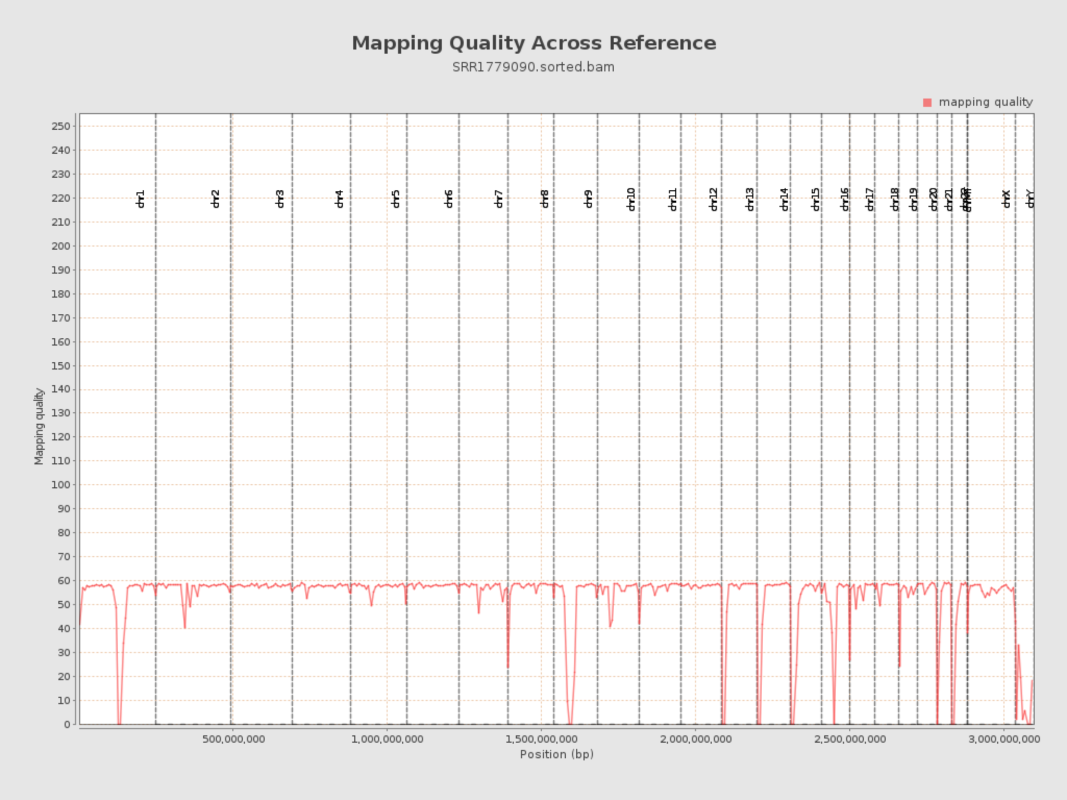
# 10. Results : Mapped Reads Clipping Profile



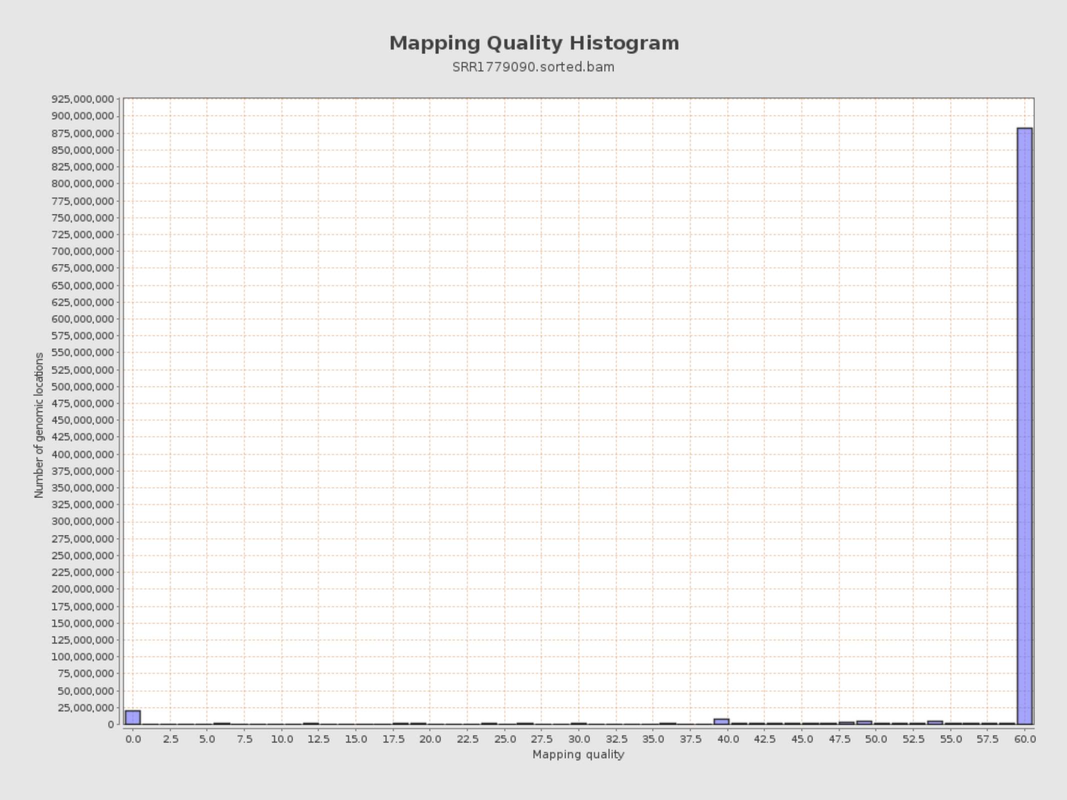
# 11. Results : Homopolymer Indels



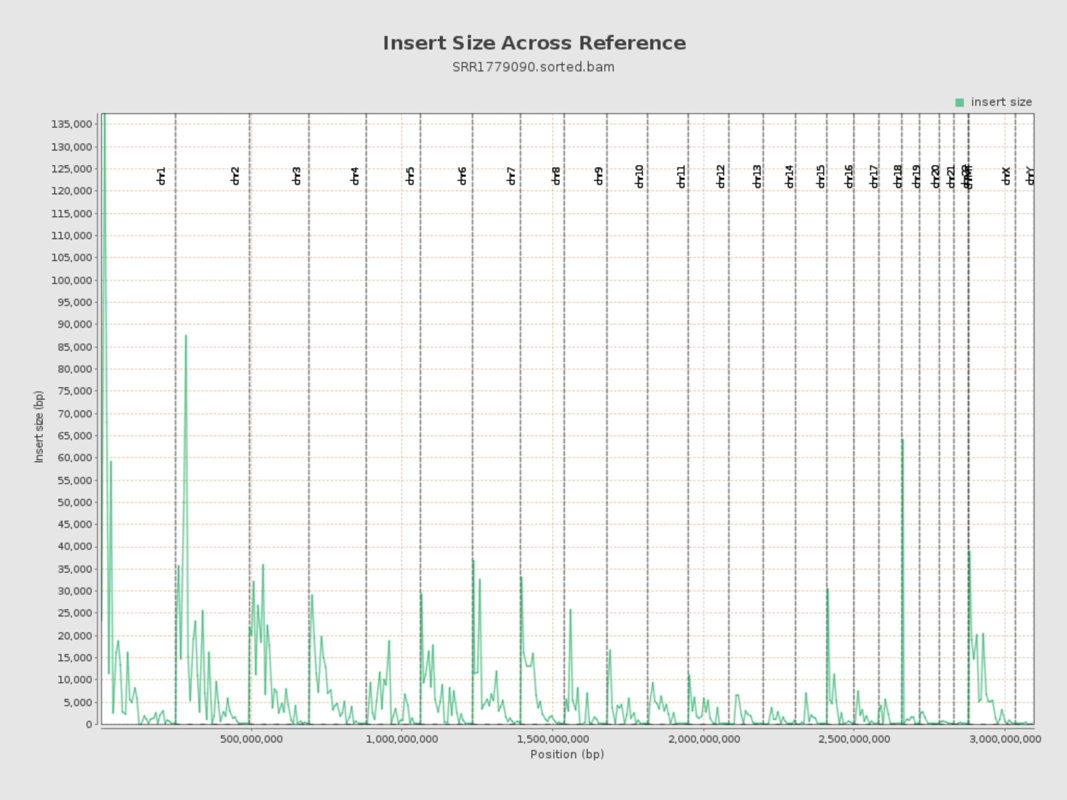
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram