# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/03/24 10:45:15*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1781808.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_SRR1781808 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1781808_1.fastq.gz SRR1781808_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Mar 24 10:45:14 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1781808.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 149,018,470 |
| Mapped reads | 146,320,497 / 98.19% |
| Unmapped reads | 2,697,973 / 1.81% |
| Mapped paired reads | 146,320,497 / 98.19% |
| Mapped reads, first in pair | 73,632,300 / 49.41% |
| Mapped reads, second in pair | 72,688,197 / 48.78% |
| Mapped reads, both in pair | 144,865,298 / 97.21% |
| Mapped reads, singletons | 1,455,199 / 0.98% |
| Secondary alignments | 0 |
| Supplementary alignments | 531,691 / 0.36% |
| Read min/max/mean length | 30 / 100 / 99.98 |
| Duplicated reads (estimated) | 8,307,952 / 5.58% |
| Duplication rate | 5.44% |
| Clipped reads | 5,942,465 / 3.99% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 4,281,766,645 / 29.47% |
| Number/percentage of C's | 2,968,317,869 / 20.43% |
| Number/percentage of T's | 4,270,556,476 / 29.39% |
| Number/percentage of G's | 3,009,564,158 / 20.71% |
| Number/percentage of N's | 1,379,018 / 0.01% |
| | |

| | |
|---|---|
| GC Percentage | 41.14% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 4.6951 |
| Standard Deviation | 5.6797 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 54.01 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 38,434.06 |
| Standard Deviation | 1,909,236.57 |
| P25/Median/P75 | 166 / 202 / 248 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.45% |
| Mismatches | 63,213,505 |
| Insertions | 1,325,569 |
| Mapped reads with at least one insertion | 0.89% |
| Deletions | 1,336,266 |
| Mapped reads with at least one deletion | 0.9% |
| Homopolymer indels | 46.16% |

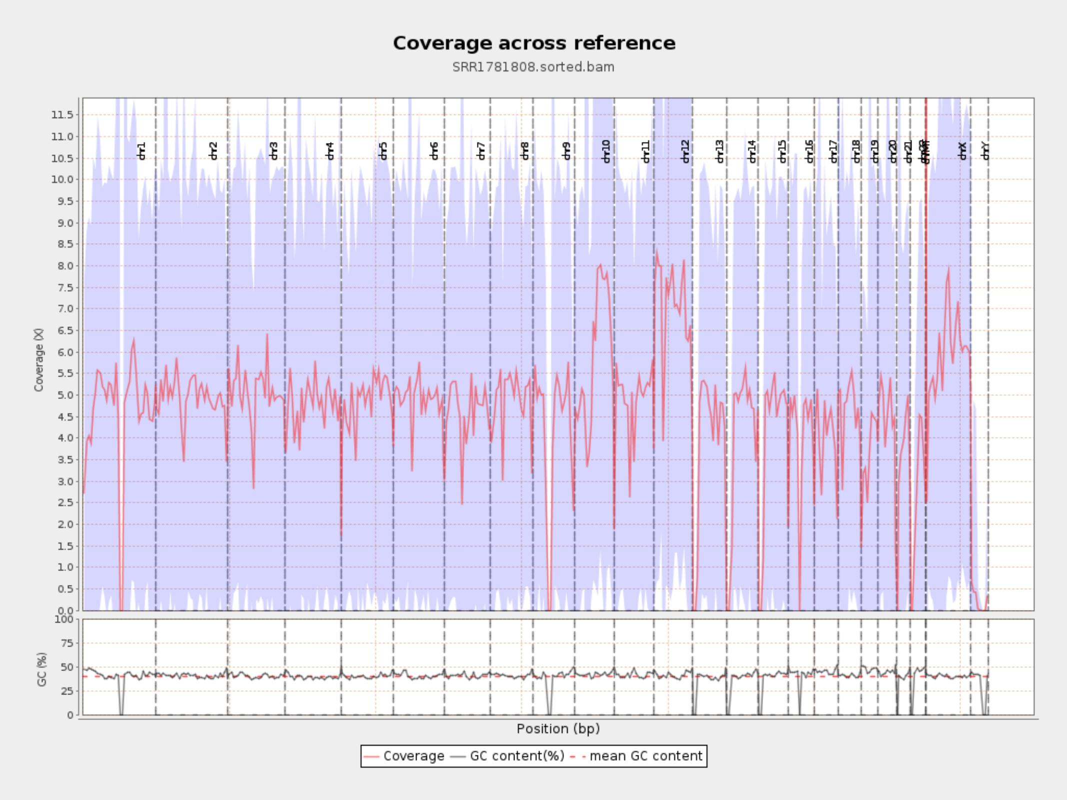
## 2.7. Chromosome stats

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

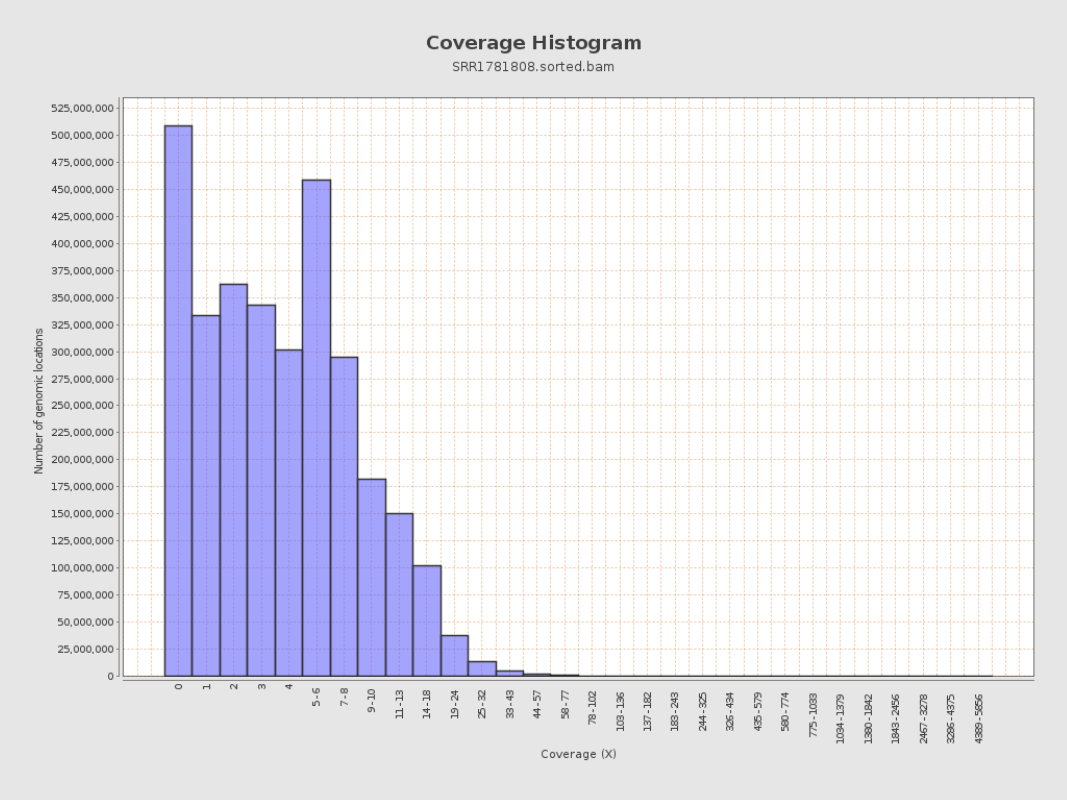
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 1145278246 | 4.5949 | 8.116 |
| chr2 | 243199373 | 1199964127 | 4.9341 | 5.4299 |
| chr3 | 198022430 | 999838080 | 5.0491 | 4.6551 |
| chr4 | 191154276 | 921394052 | 4.8202 | 5.2776 |
| chr5 | 180915260 | 880775353 | 4.8684 | 4.4396 |
| chr6 | 171115067 | 842674131 | 4.9246 | 5.0927 |
| chr7 | 159138663 | 732548568 | 4.6032 | 5.1652 |
| chr8 | 146364022 | 715271168 | 4.8869 | 4.644 |
| chr9 | 141213431 | 591715140 | 4.1902 | 5.7136 |
| chr10 | 135534747 | 803918883 | 5.9315 | 8.495 |
| chr11 | 135006516 | 657288660 | 4.8686 | 4.8127 |
| chr12 | 133851895 | 955782386 | 7.1406 | 6.3577 |
| chr13 | 115169878 | 450310133 | 3.91 | 4.2618 |
| chr14 | 107349540 | 430543955 | 4.0107 | 4.4999 |
| chr15 | 102531392 | 408059931 | 3.9799 | 4.5562 |
| chr16 | 90354753 | 355227322 | 3.9315 | 4.6533 |
| chr17 | 81195210 | 331255749 | 4.0797 | 5.125 |
| chr18 | 78077248 | 365298902 | 4.6787 | 5.7221 |
| chr19 | 59128983 | 214703964 | 3.6311 | 5.7486 |
| chr20 | 63025520 | 286624677 | 4.5478 | 5.324 |
| chr21 | 48129895 | 169945974 | 3.531 | 6.9772 |
| chr22 | 51304566 | 137721494 | 2.6844 | 4.0142 |
| chrMT | 16571 | 620882 | 37.468 | 11.0371 |
| chrX | 155270560 | 924709872 | 5.9555 | 5.5918 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 13127277 | 0.2211 | 2.4522 |

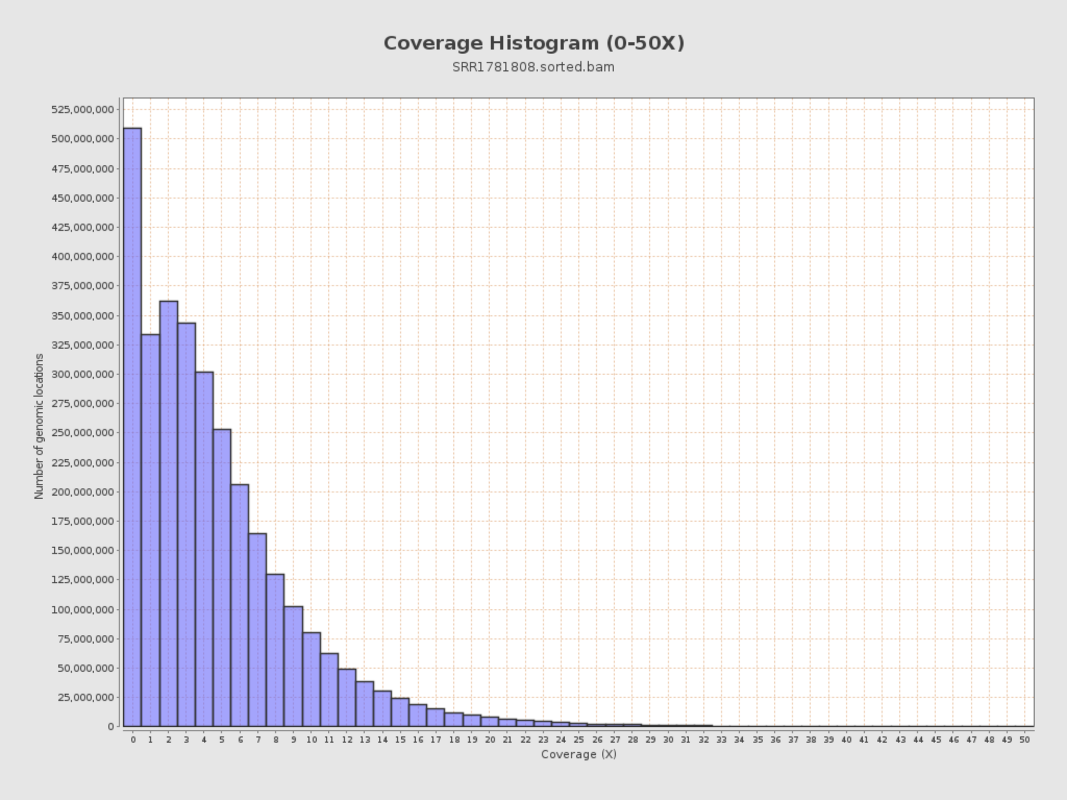
# 3. Results : Coverage across reference



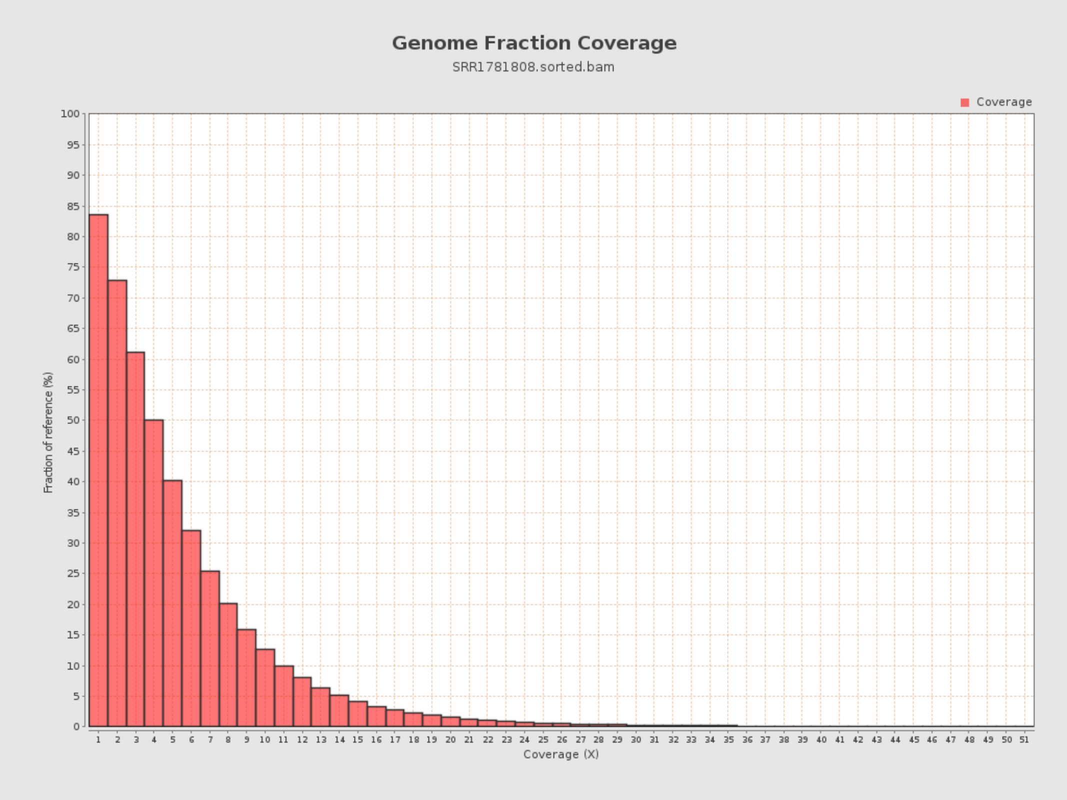
# 4. Results : Coverage Histogram



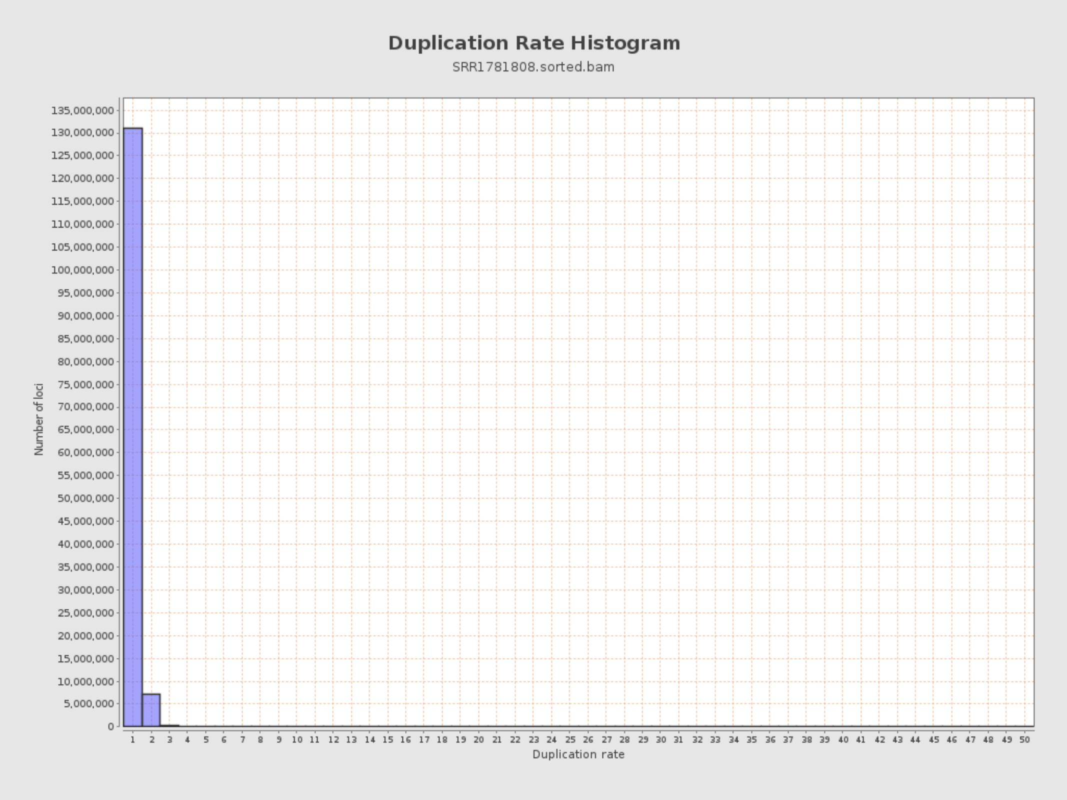
# 5. Results : Coverage Histogram (0-50X)



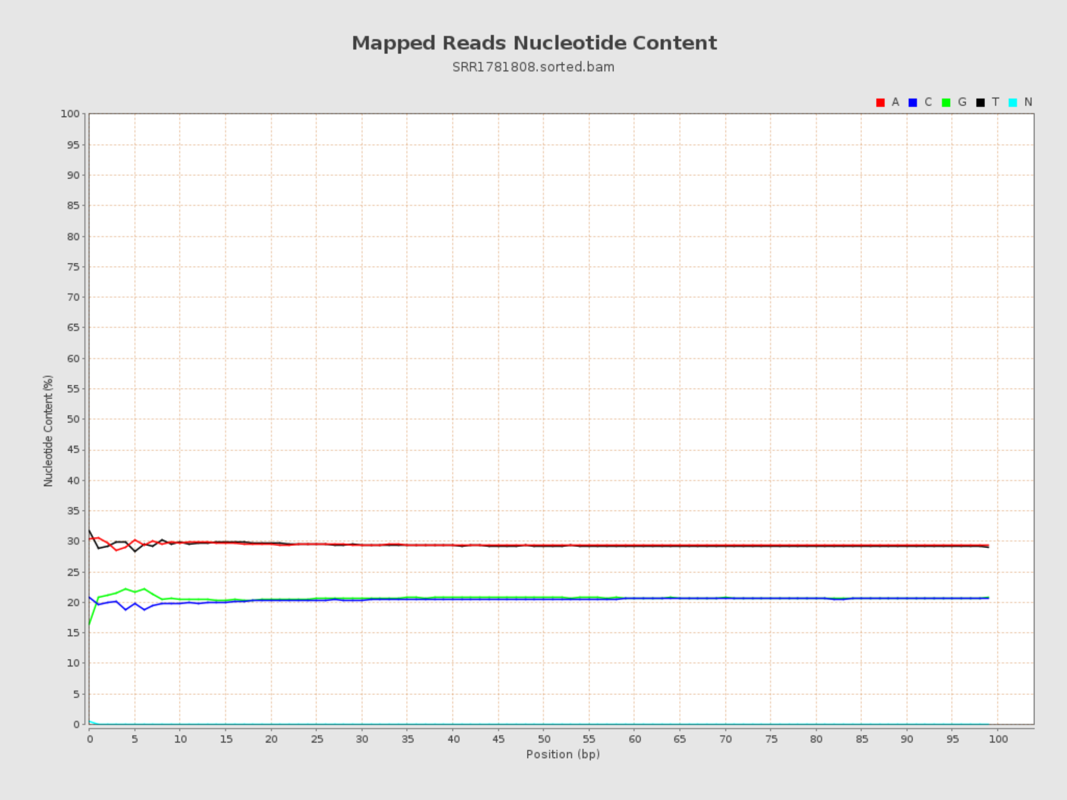
# 6. Results : Genome Fraction Coverage



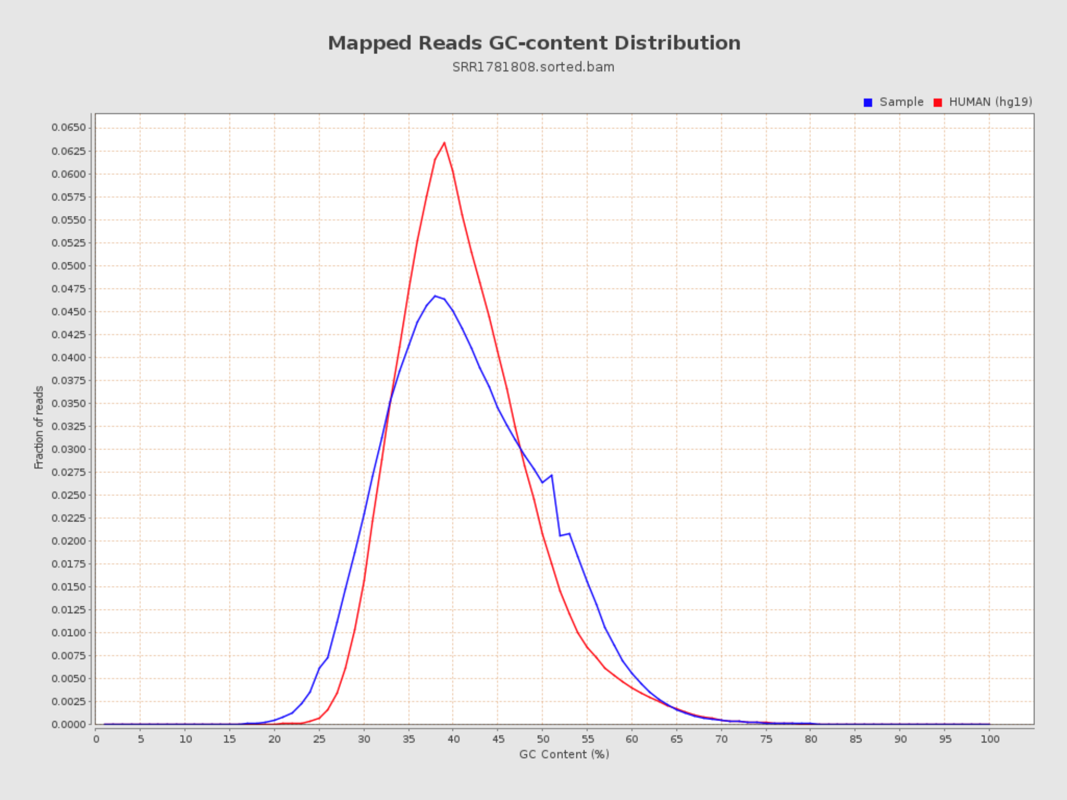
# 7. Results : Duplication Rate Histogram



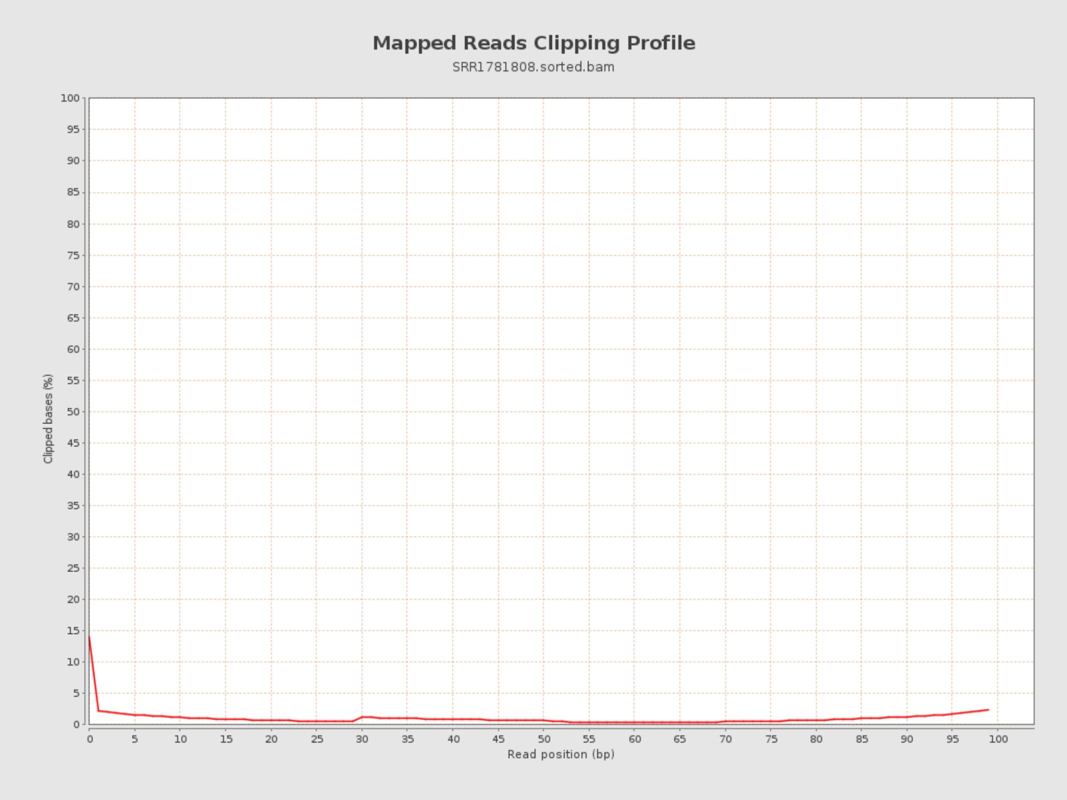
# 8. Results : Mapped Reads Nucleotide Content



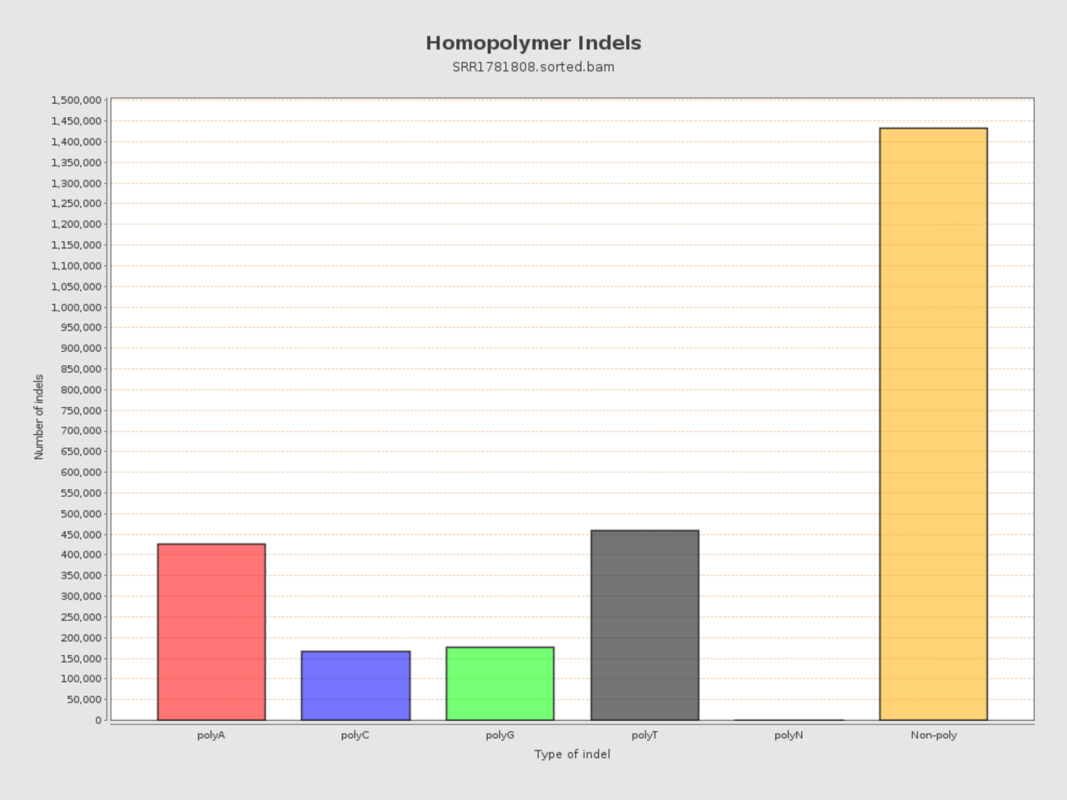
# 9. Results : Mapped Reads GC-content Distribution



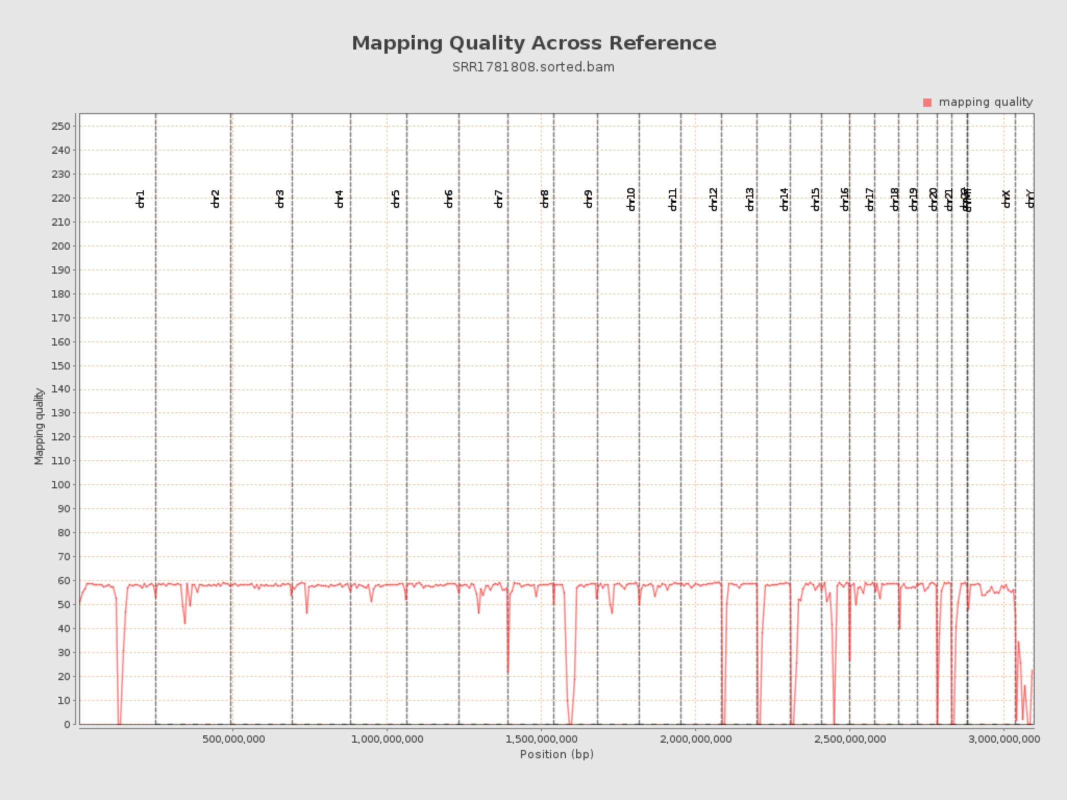
# 10. Results : Mapped Reads Clipping Profile



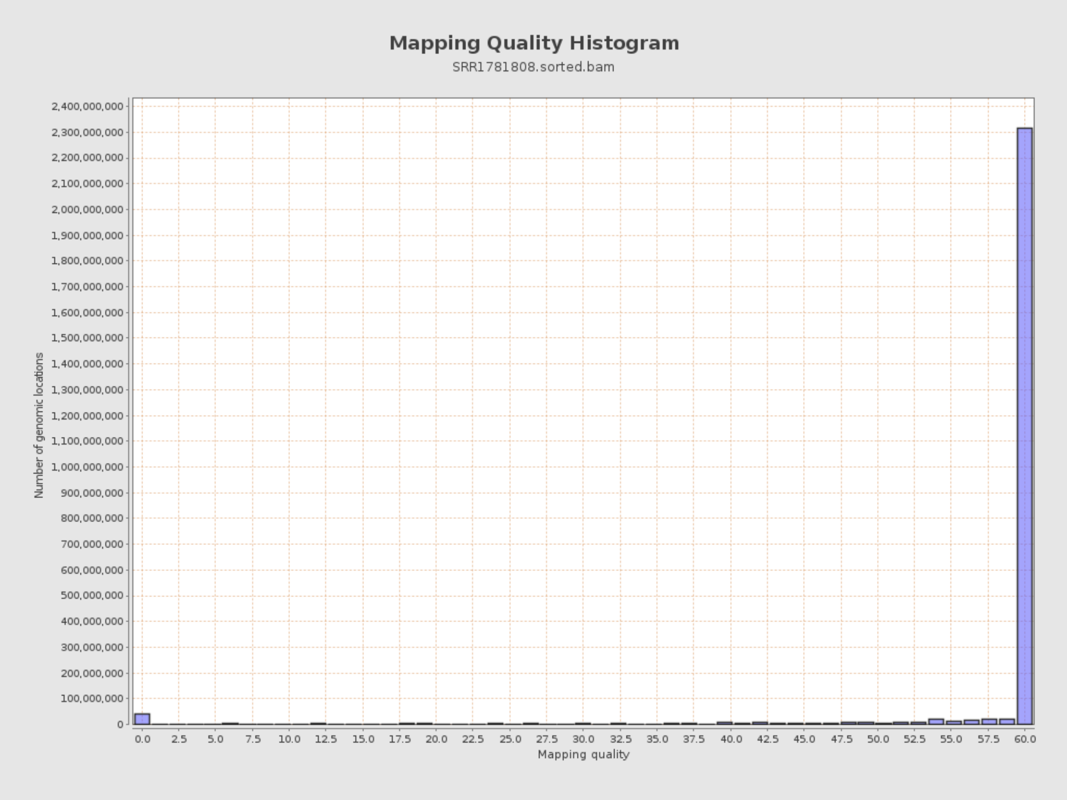
# 11. Results : Homopolymer Indels



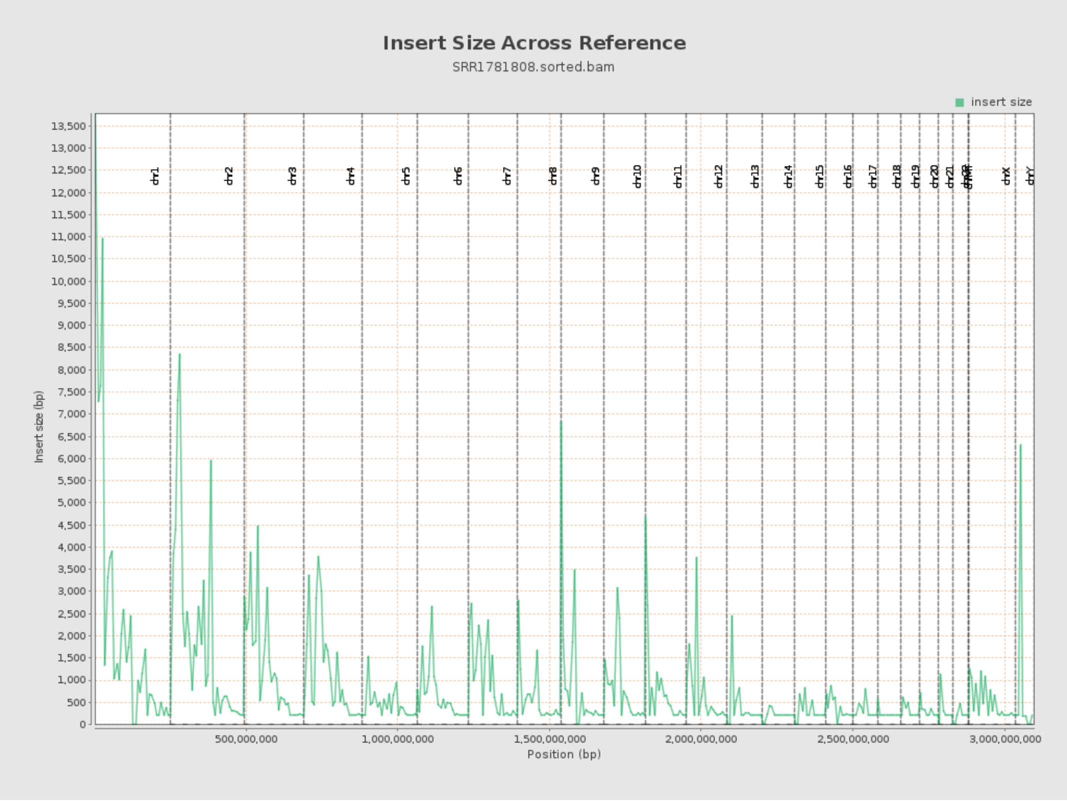
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram