# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/09 00:36:47*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR617411.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_SRR617411 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617411_1.fastq.gz SRR617411_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Oct 09 00:36:46 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR617411.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 32,000,000 |
| Mapped reads | 30,372,911 / 94.92% |
| Unmapped reads | 1,627,089 / 5.08% |
| Mapped paired reads | 30,372,911 / 94.92% |
| Mapped reads, first in pair | 15,259,270 / 47.69% |
| Mapped reads, second in pair | 15,113,641 / 47.23% |
| Mapped reads, both in pair | 29,958,060 / 93.62% |
| Mapped reads, singletons | 414,851 / 1.3% |
| Secondary alignments | 0 |
| Supplementary alignments | 464,111 / 1.45% |
| Read min/max/mean length | 30 / 100 / 100.6 |
| Duplicated reads (estimated) | 1,405,960 / 4.39% |
| Duplication rate | 4.21% |
| Clipped reads | 3,091,258 / 9.66% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 892,707,192 / 29.8% |
| Number/percentage of C's | 602,618,398 / 20.12% |
| Number/percentage of T's | 884,185,455 / 29.51% |
| Number/percentage of G's | 615,012,124 / 20.53% |
| Number/percentage of N's | 1,294,474 / 0.04% |
| | |

| | |
|---|---|
| GC Percentage | 40.64% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.9679 |
| Standard Deviation | 2.9569 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.96 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 48,046.56 |
| Standard Deviation | 2,071,765.45 |
| P25/Median/P75 | 172 / 212 / 276 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 1.02% |
| Mismatches | 29,954,098 |
| Insertions | 242,790 |
| Mapped reads with at least one insertion | 0.79% |
| Deletions | 289,954 |
| Mapped reads with at least one deletion | 0.93% |
| Homopolymer indels | 44.91% |

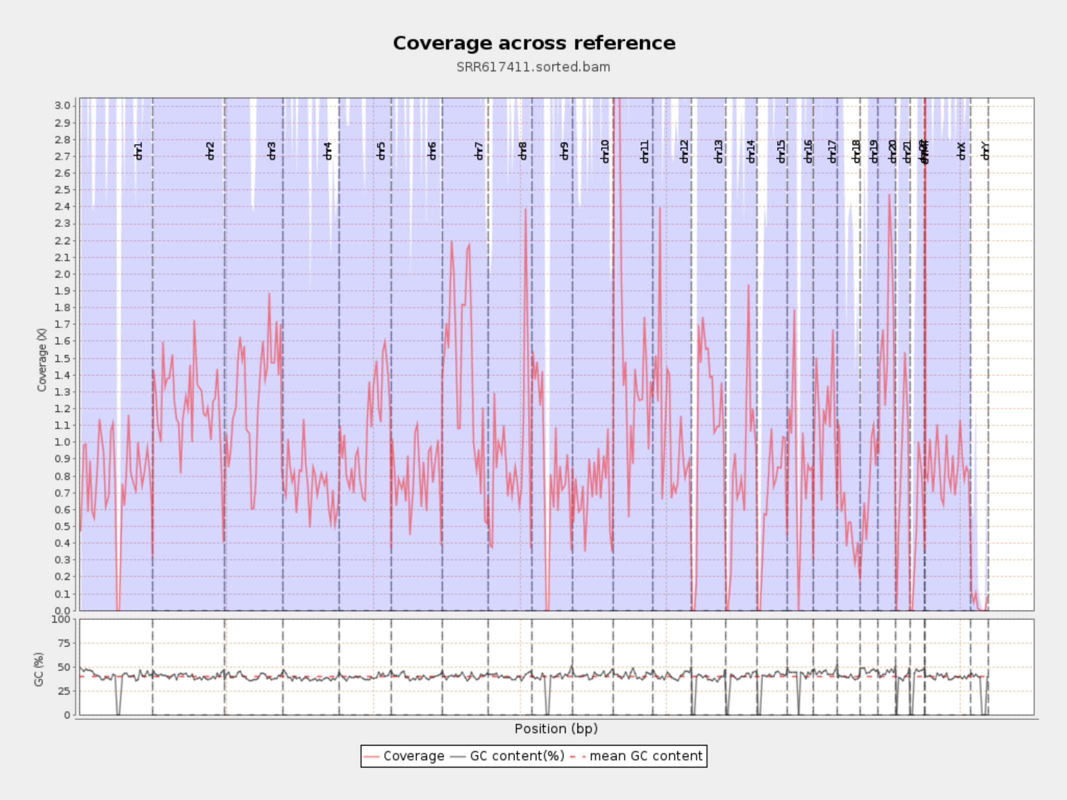
## 2.7. Chromosome stats

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

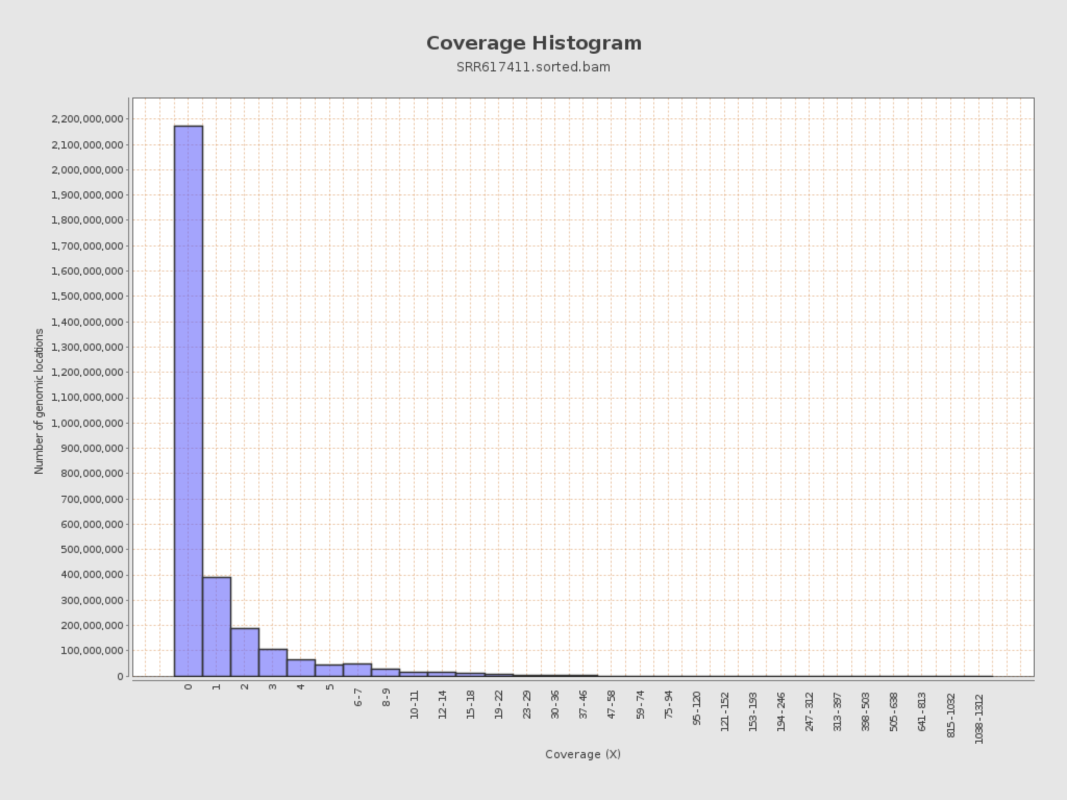
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 192777122 | 0.7734 | 2.7648 |
| chr2 | 243199373 | 298778496 | 1.2285 | 3.1004 |
| chr3 | 198022430 | 252818038 | 1.2767 | 3.4488 |
| chr4 | 191154276 | 143882674 | 0.7527 | 2.3016 |
| chr5 | 180915260 | 191323429 | 1.0575 | 2.8973 |
| chr6 | 171115067 | 137285273 | 0.8023 | 2.627 |
| chr7 | 159138663 | 224288972 | 1.4094 | 3.2673 |
| chr8 | 146364022 | 132648391 | 0.9063 | 3.3026 |
| chr9 | 141213431 | 119678347 | 0.8475 | 2.6429 |
| chr10 | 135534747 | 95916724 | 0.7077 | 2.4339 |
| chr11 | 135006516 | 222623730 | 1.649 | 3.89 |
| chr12 | 133851895 | 142884447 | 1.0675 | 2.814 |
| chr13 | 115169878 | 129767199 | 1.1267 | 2.8014 |
| chr14 | 107349540 | 87098781 | 0.8114 | 2.9202 |
| chr15 | 102531392 | 68842649 | 0.6714 | 2.3752 |
| chr16 | 90354753 | 75785578 | 0.8388 | 3.3778 |
| chr17 | 81195210 | 92679863 | 1.1414 | 3.7199 |
| chr18 | 78077248 | 42948961 | 0.5501 | 2.0272 |
| chr19 | 59128983 | 42830966 | 0.7244 | 2.3698 |
| chr20 | 63025520 | 102302839 | 1.6232 | 4.8042 |
| chr21 | 48129895 | 40997149 | 0.8518 | 2.5584 |
| chr22 | 51304566 | 24320645 | 0.474 | 2.1275 |
| chrMT | 16571 | 191288 | 11.5435 | 5.1383 |
| chrX | 155270560 | 131411549 | 0.8463 | 2.593 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 2386654 | 0.0402 | 0.5834 |

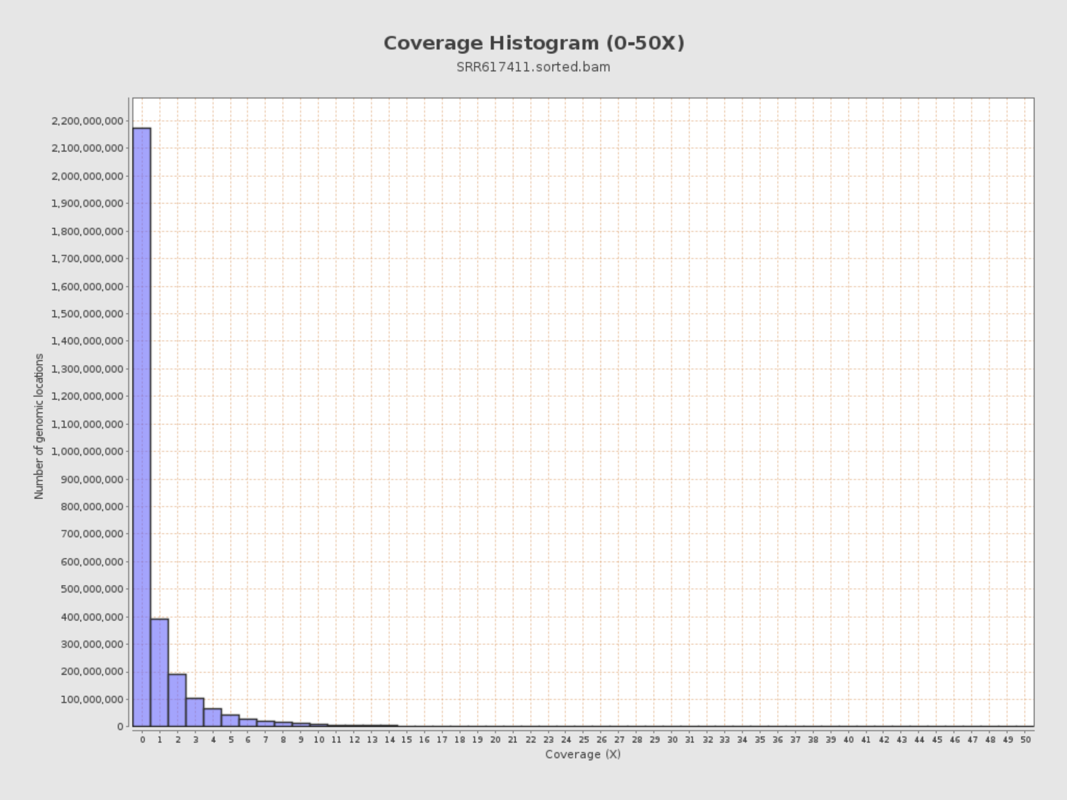
# 3. Results : Coverage across reference



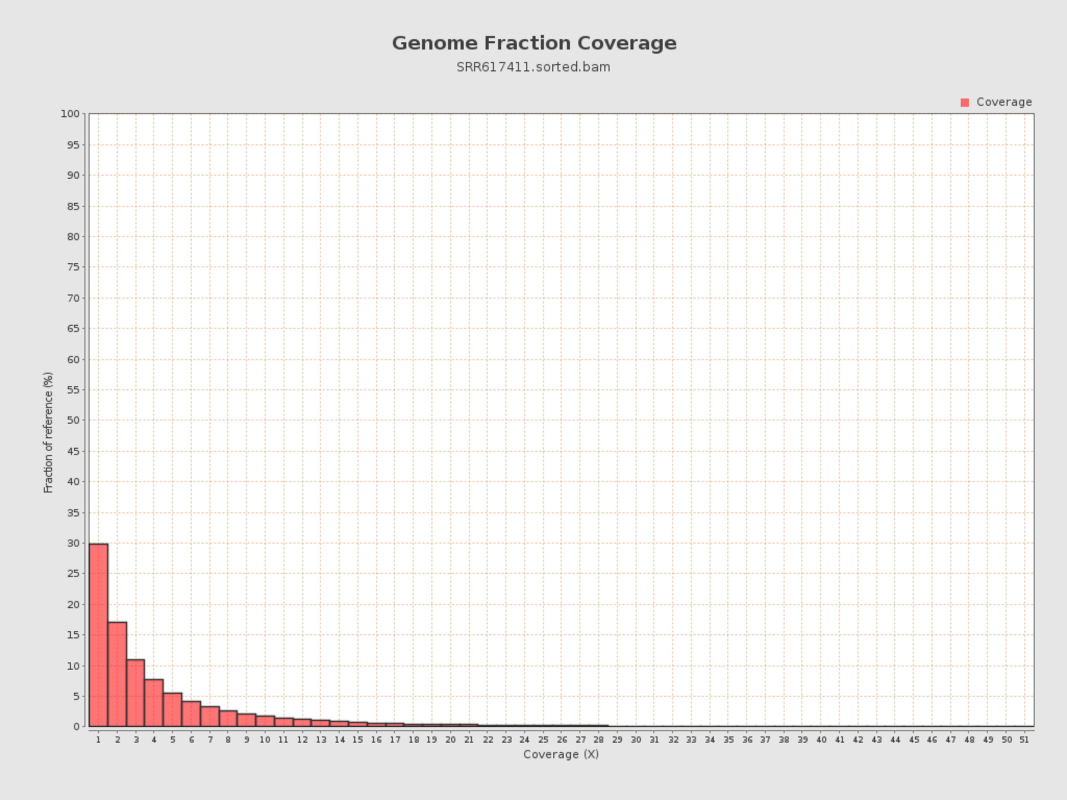
# 4. Results : Coverage Histogram



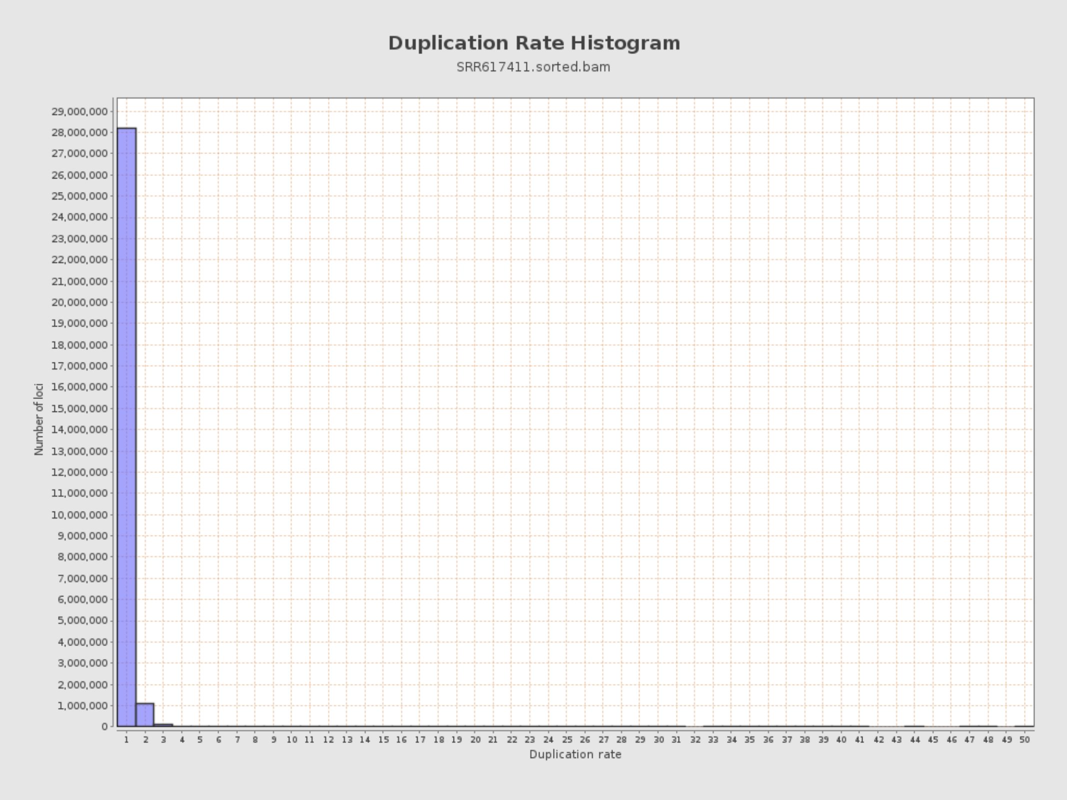
# 5. Results : Coverage Histogram (0-50X)



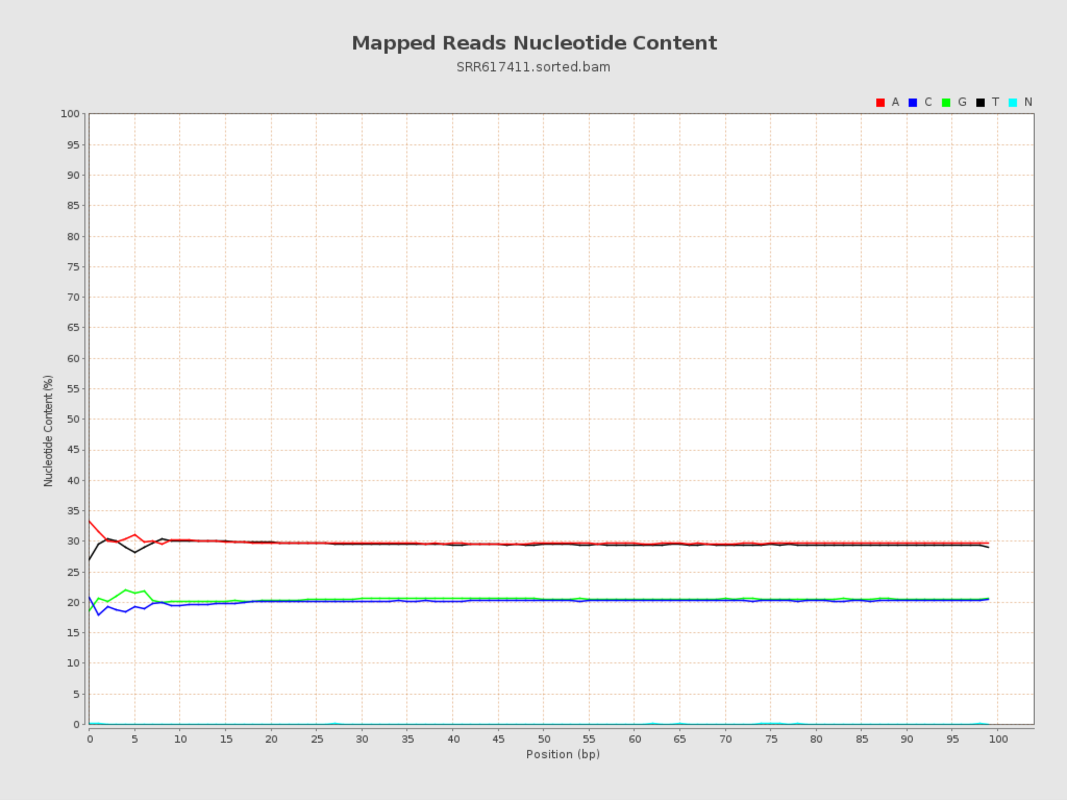
# 6. Results : Genome Fraction Coverage



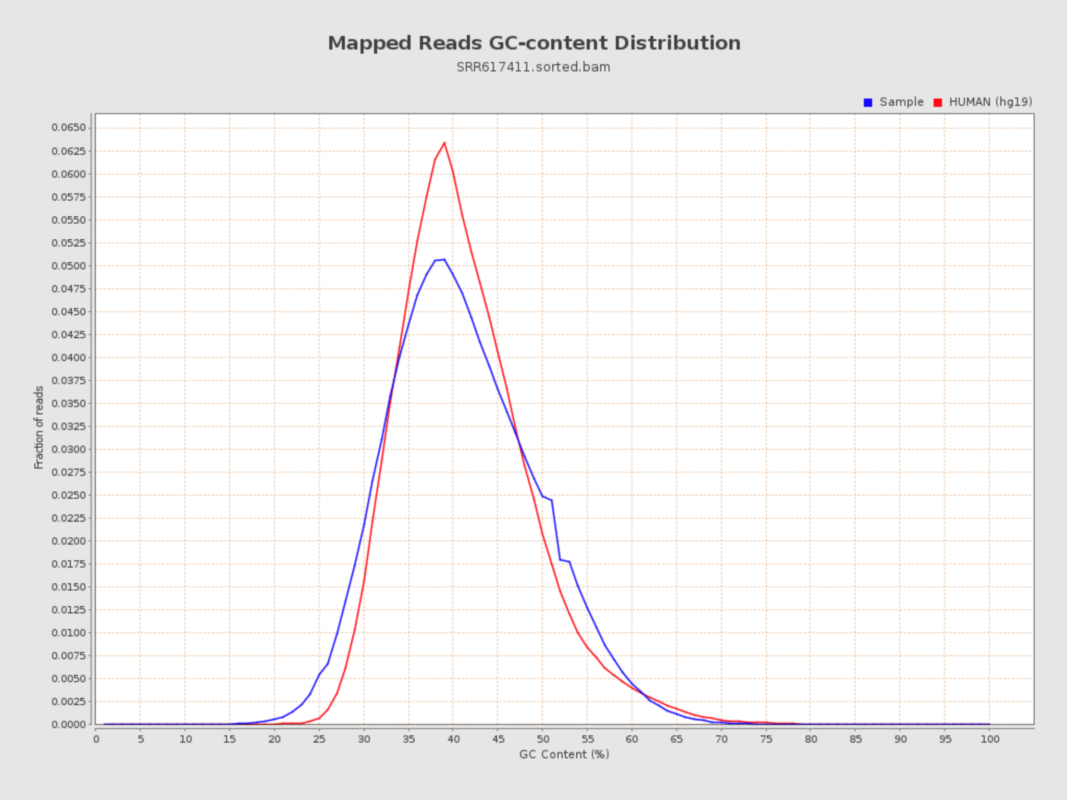
# 7. Results : Duplication Rate Histogram



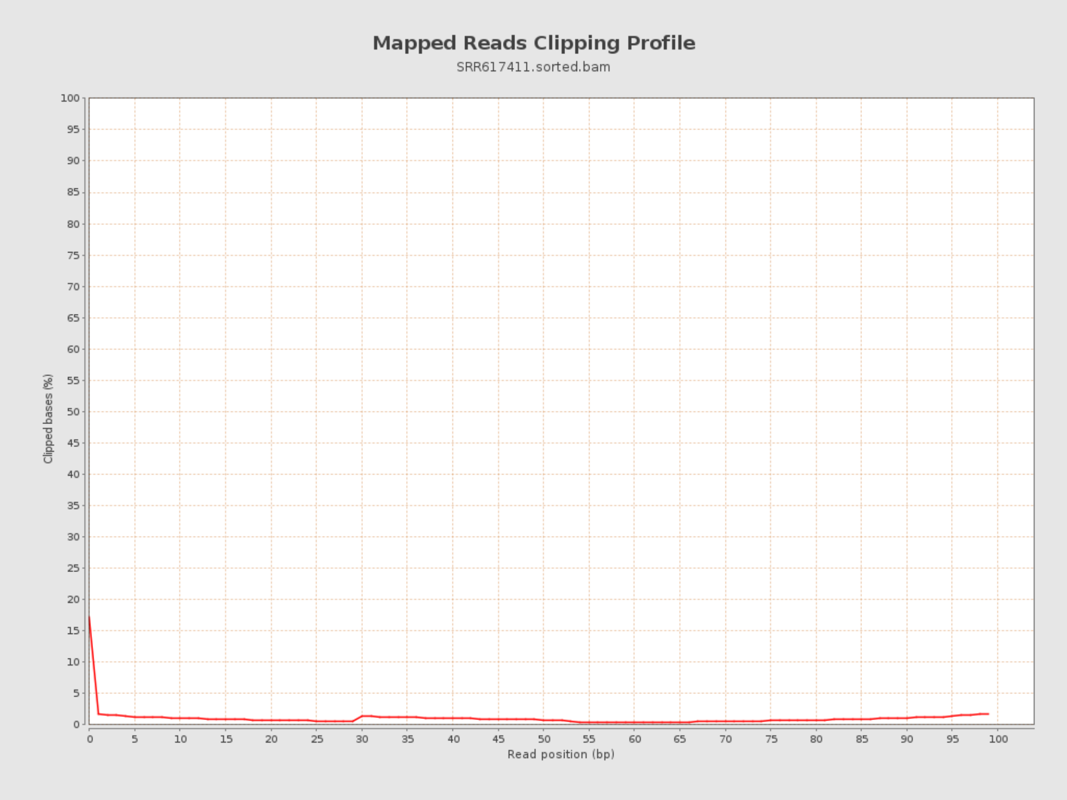
# 8. Results : Mapped Reads Nucleotide Content



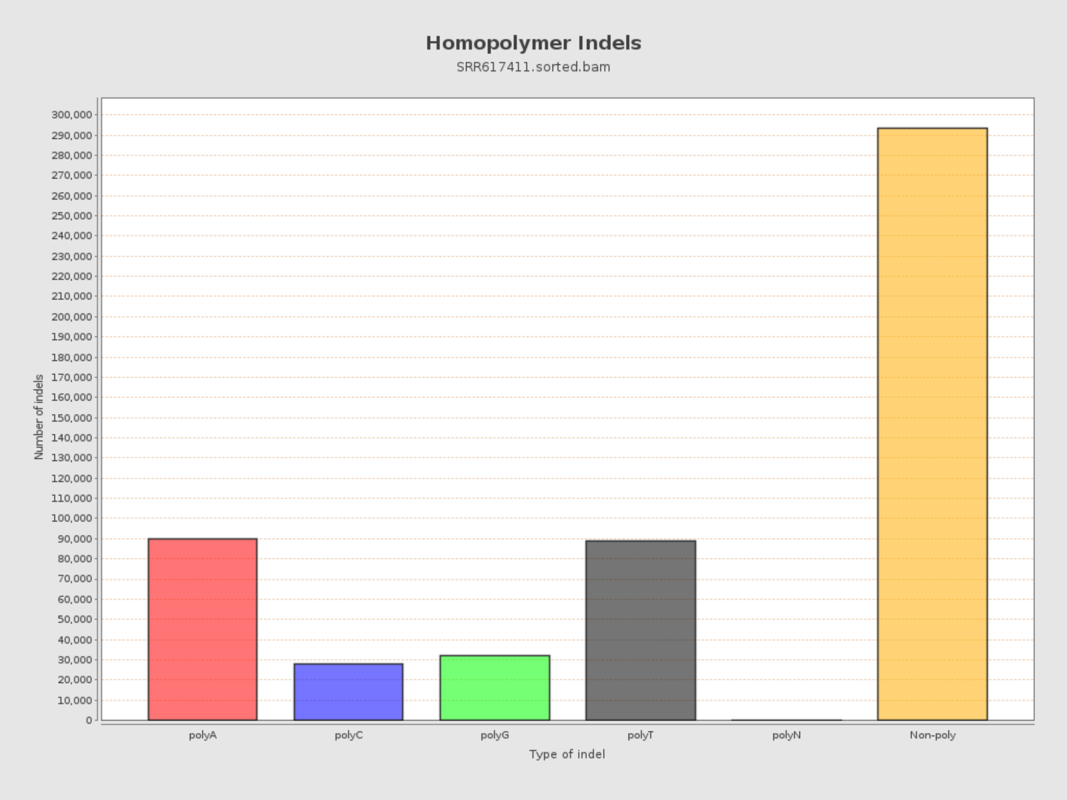
# 9. Results : Mapped Reads GC-content Distribution



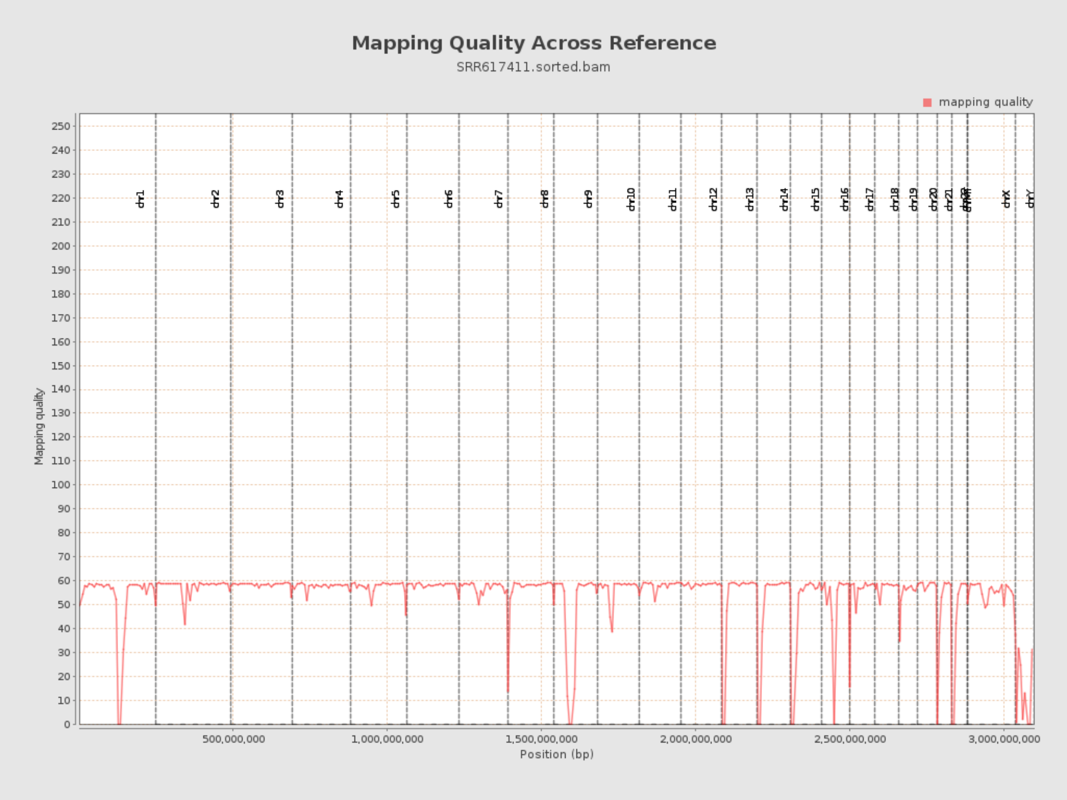
# 10. Results : Mapped Reads Clipping Profile



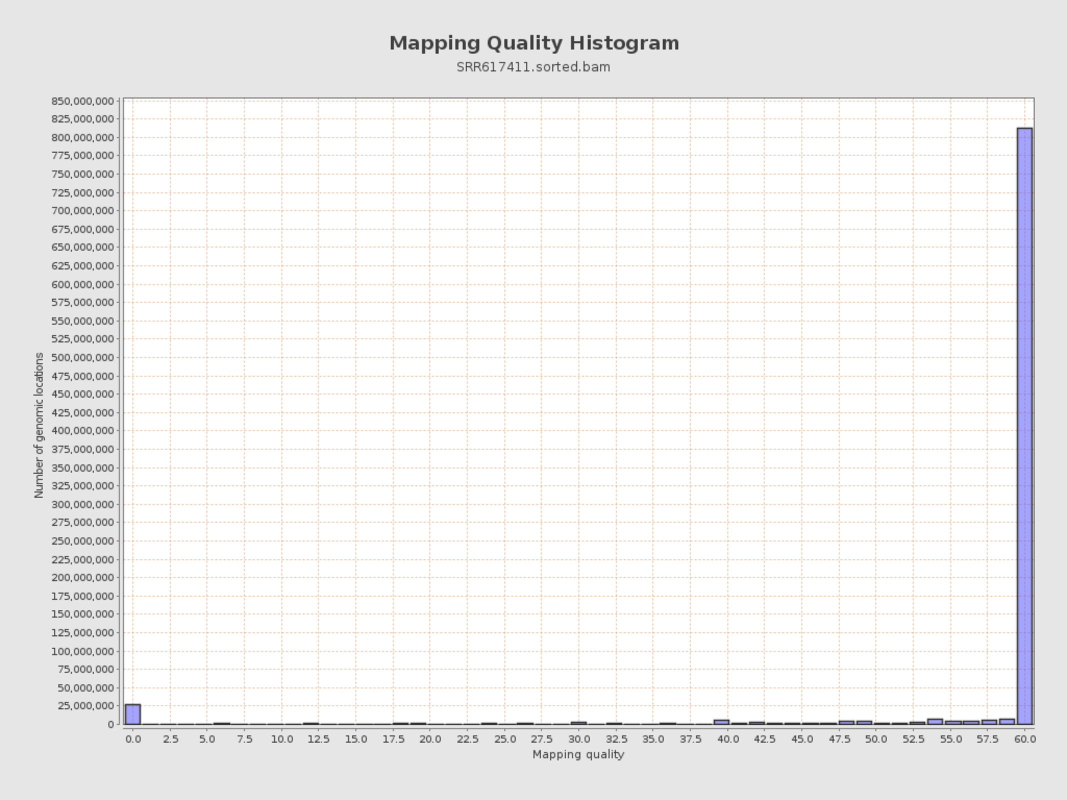
# 11. Results : Homopolymer Indels



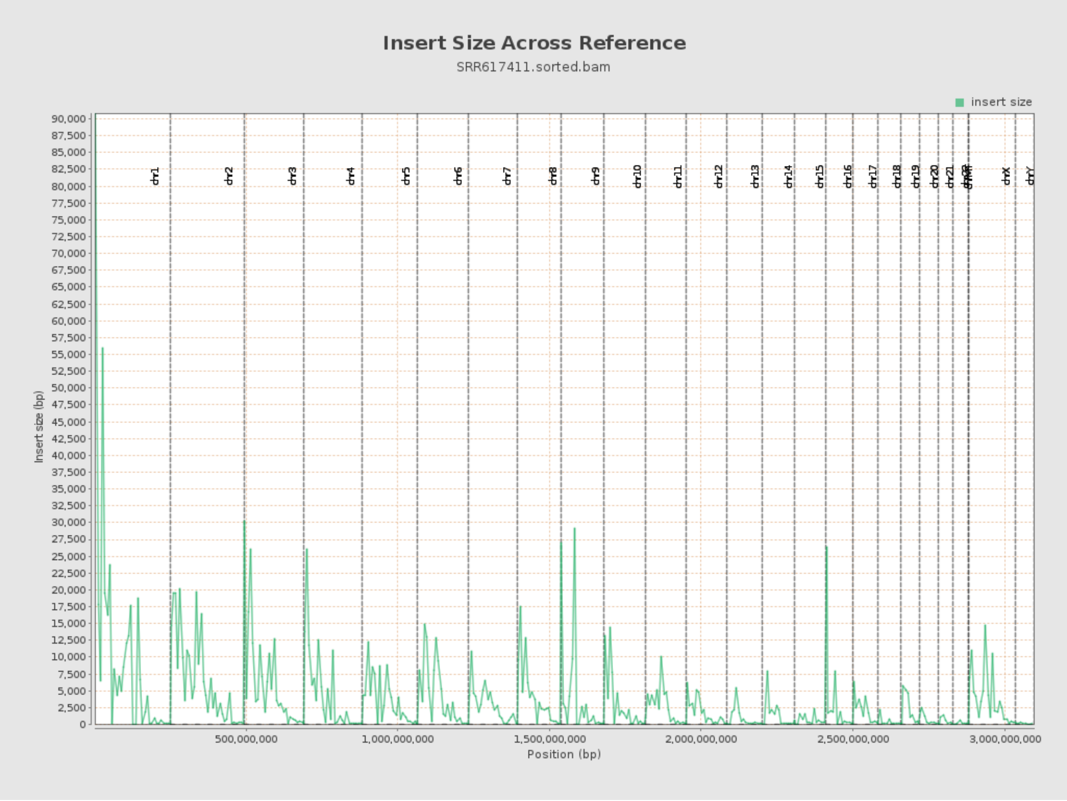
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram