# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/09 19:19:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR617493.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_SRR617493 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617493_1.fastq.gz SRR617493_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Oct 09 19:19:49 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR617493.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 32,000,000 |
| Mapped reads | 30,488,491 / 95.28% |
| Unmapped reads | 1,511,509 / 4.72% |
| Mapped paired reads | 30,488,491 / 95.28% |
| Mapped reads, first in pair | 15,376,185 / 48.05% |
| Mapped reads, second in pair | 15,112,306 / 47.23% |
| Mapped reads, both in pair | 29,941,990 / 93.57% |
| Mapped reads, singletons | 546,501 / 1.71% |
| Secondary alignments | 0 |
| Supplementary alignments | 158,747 / 0.5% |
| Read min/max/mean length | 30 / 100 / 100.2 |
| Duplicated reads (estimated) | 6,272,564 / 19.6% |
| Duplication rate | 9.93% |
| Clipped reads | 5,994,100 / 18.73% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 875,567,341 / 29.51% |
| Number/percentage of C's | 599,357,861 / 20.2% |
| Number/percentage of T's | 875,250,237 / 29.5% |
| Number/percentage of G's | 613,658,919 / 20.68% |
| Number/percentage of N's | 3,049,169 / 0.1% |
| | |

| | |
|---|---|
| GC Percentage | 40.89% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.959 |
| Standard Deviation | 9.6736 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 52.7 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 39,444.66 |
| Standard Deviation | 1,865,041.38 |
| P25/Median/P75 | 173 / 218 / 289 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 1.19% |
| Mismatches | 34,346,854 |
| Insertions | 445,024 |
| Mapped reads with at least one insertion | 1.43% |
| Deletions | 1,036,164 |
| Mapped reads with at least one deletion | 3.33% |
| Homopolymer indels | 47.46% |

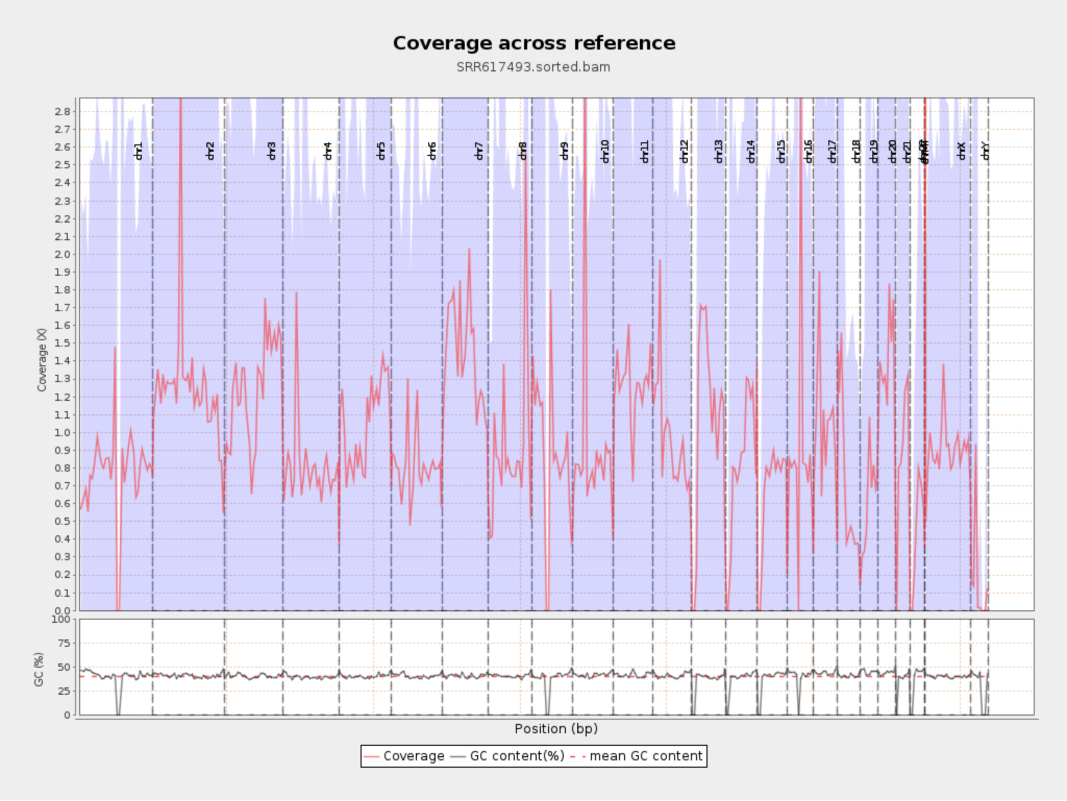
## 2.7. Chromosome stats

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

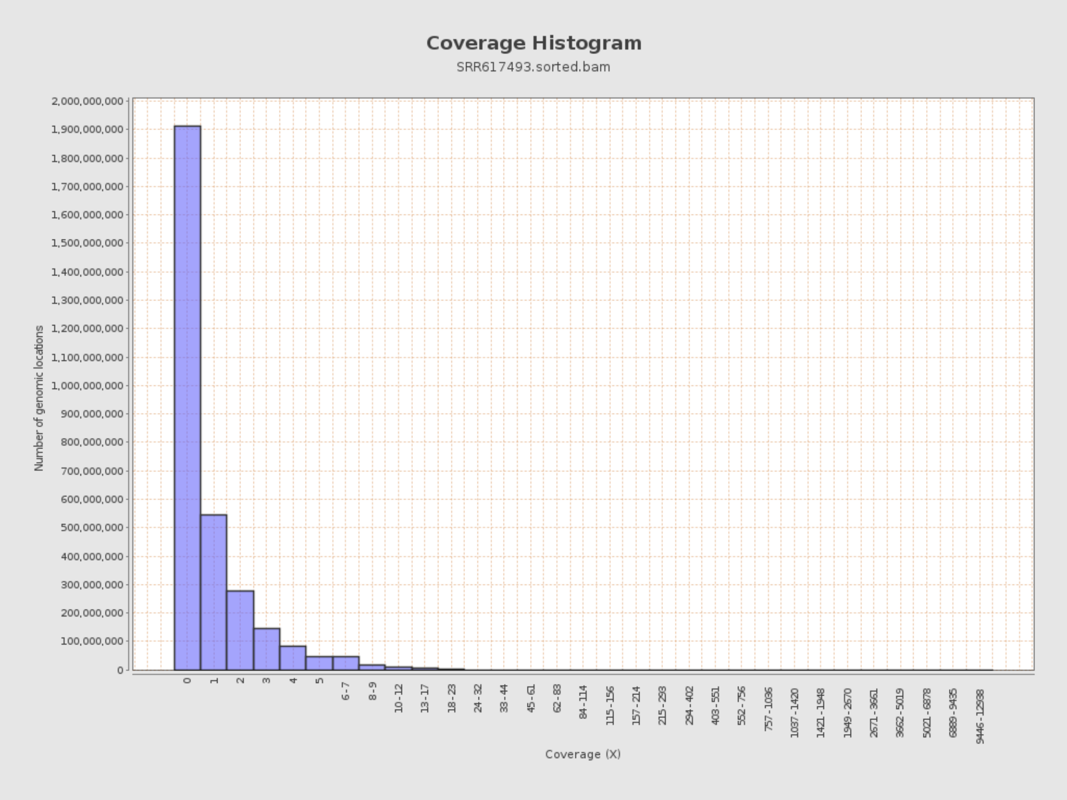
|  |  | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 191510921 | 0.7683 | 9.3561 |
| chr2 | 243199373 | 307007082 | 1.2624 | 11.4539 |
| chr3 | 198022430 | 245222586 | 1.2384 | 2.2523 |
| chr4 | 191154276 | 153344543 | 0.8022 | 6.1352 |
| chr5 | 180915260 | 189790476 | 1.0491 | 2.0918 |
| chr6 | 171115067 | 139857499 | 0.8173 | 5.4245 |
| chr7 | 159138663 | 229104144 | 1.4397 | 13.1856 |
| chr8 | 146364022 | 131796793 | 0.9005 | 3.8633 |
| chr9 | 141213431 | 122781768 | 0.8695 | 18.161 |
| chr10 | 135534747 | 126099886 | 0.9304 | 18.6158 |
| chr11 | 135006516 | 167483870 | 1.2406 | 12.717 |
| chr12 | 133851895 | 129597891 | 0.9682 | 1.9963 |
| chr13 | 115169878 | 125858464 | 1.0928 | 2.1254 |
| chr14 | 107349540 | 86462110 | 0.8054 | 2.238 |
| chr15 | 102531392 | 67063961 | 0.6541 | 1.4978 |
| chr16 | 90354753 | 80004331 | 0.8854 | 14.7727 |
| chr17 | 81195210 | 82797991 | 1.0197 | 13.5733 |
| chr18 | 78077248 | 53087741 | 0.6799 | 16.9381 |
| chr19 | 59128983 | 35612817 | 0.6023 | 5.9025 |
| chr20 | 63025520 | 87575568 | 1.3895 | 2.7981 |
| chr21 | 48129895 | 42512620 | 0.8833 | 3.7558 |
| chr22 | 51304566 | 22210567 | 0.4329 | 1.2609 |
| chrMT | 16571 | 2063310 | 124.5133 | 90.9957 |
| chrX | 155270560 | 139516719 | 0.8985 | 4.1883 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 10289991 | 0.1733 | 13.7239 |

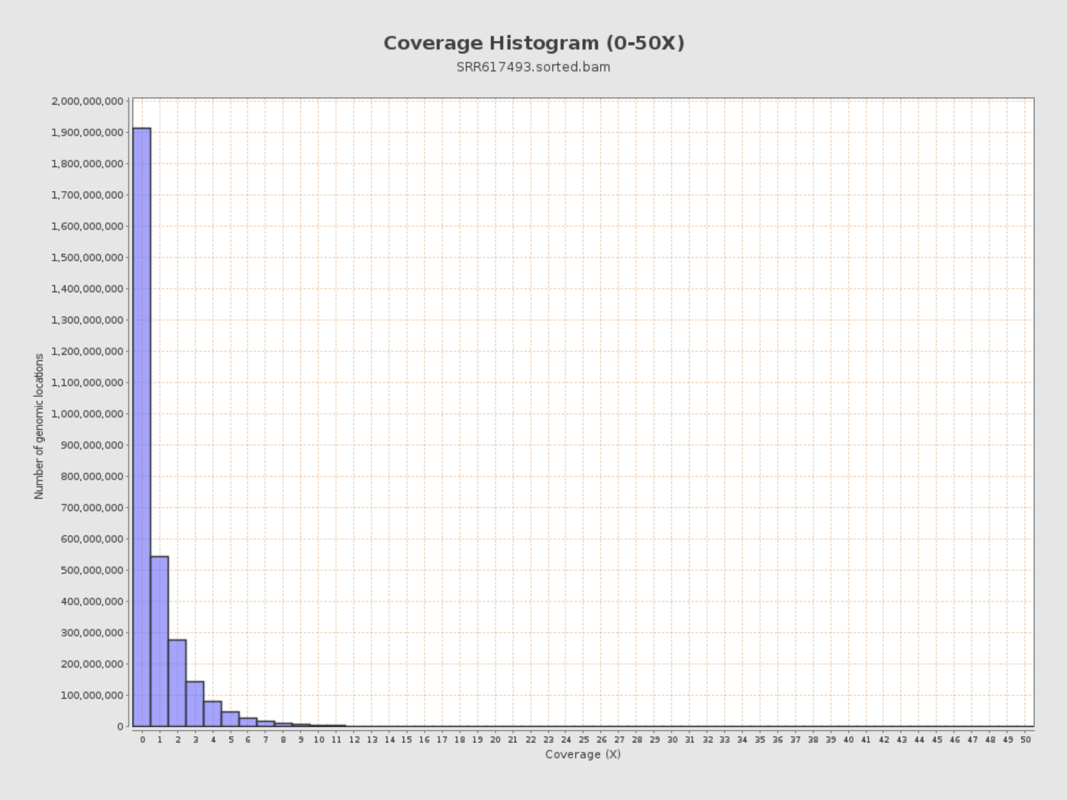
# 3. Results : Coverage across reference



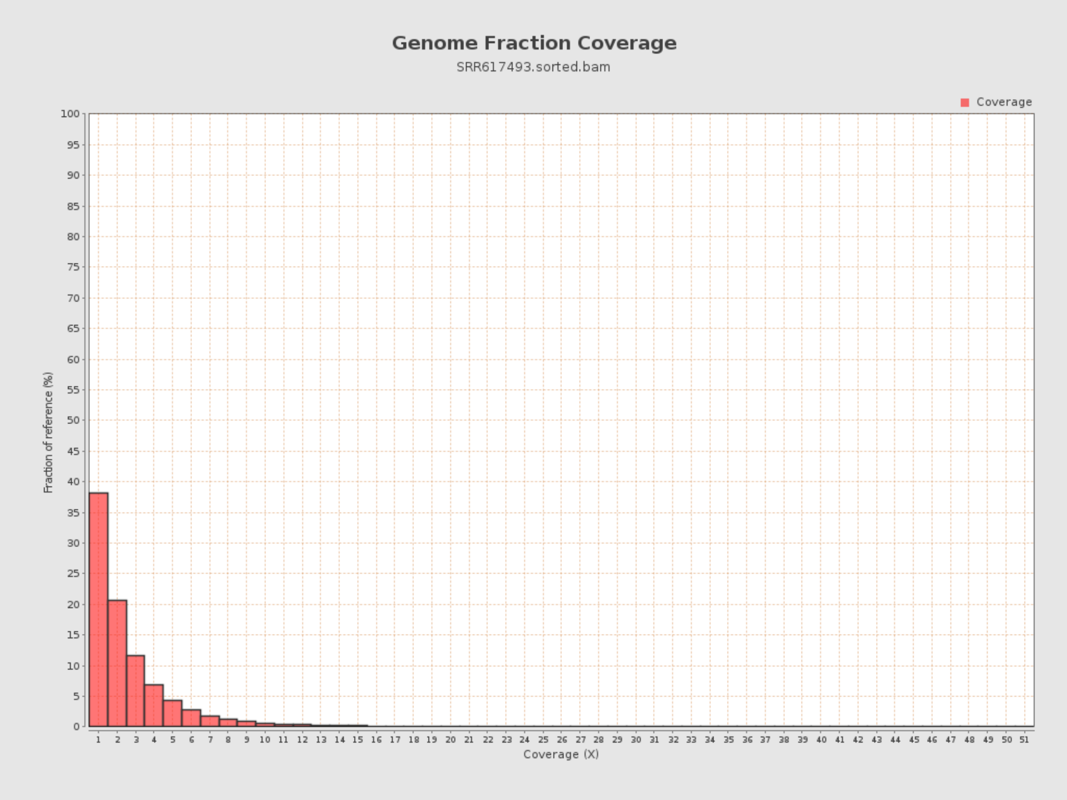
# 4. Results : Coverage Histogram



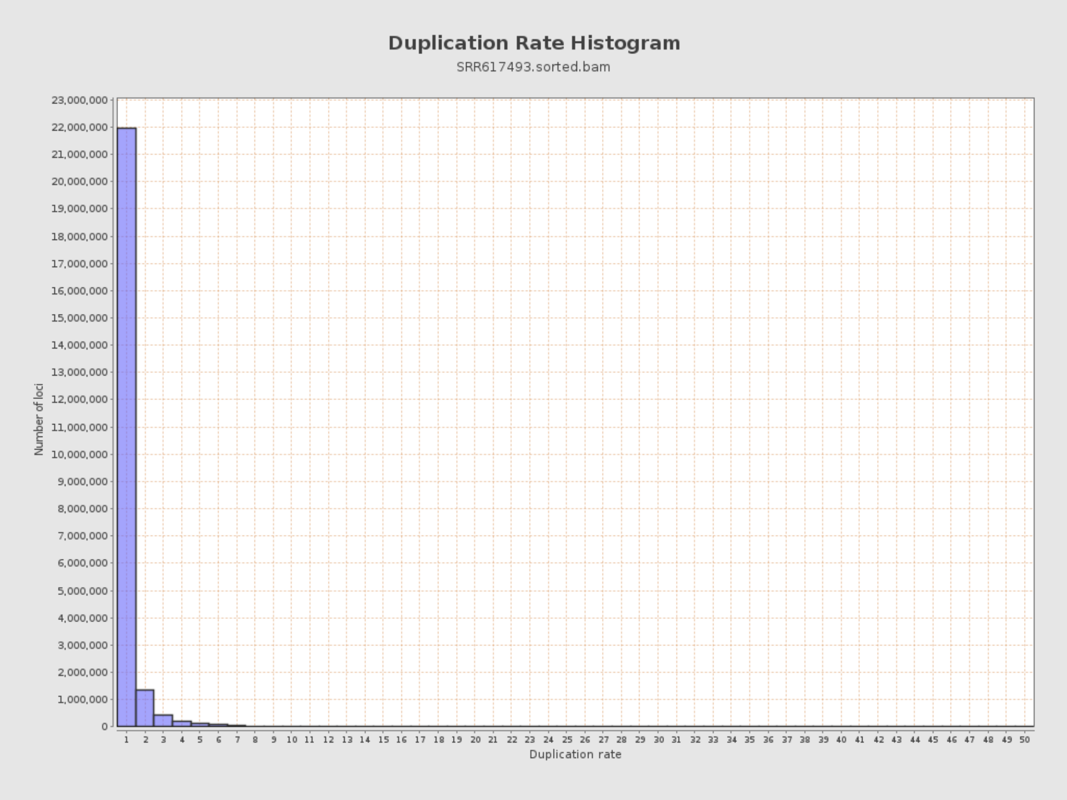
# 5. Results : Coverage Histogram (0-50X)



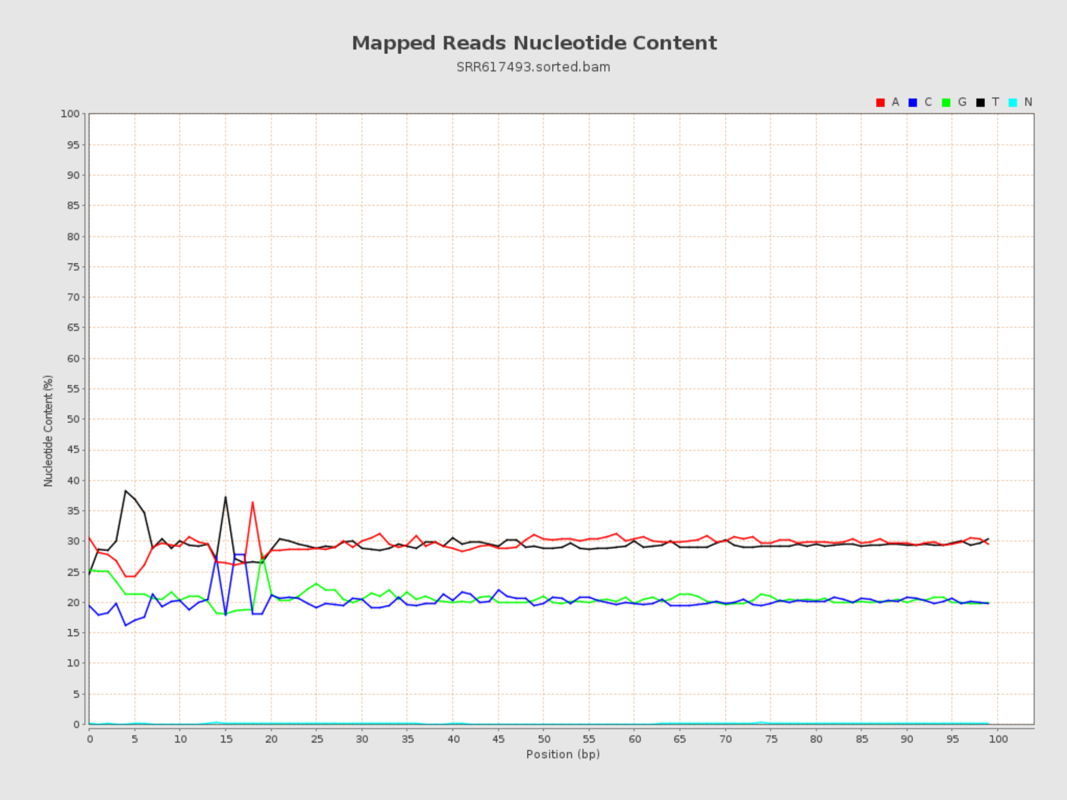
# 6. Results : Genome Fraction Coverage



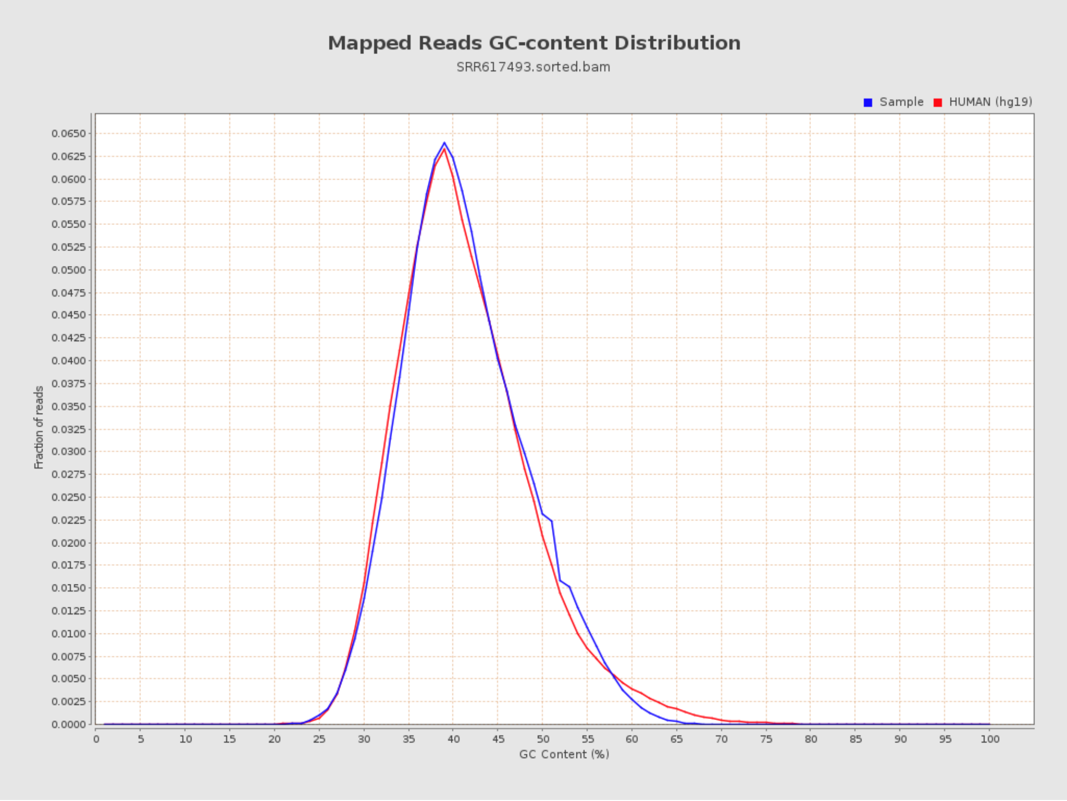
# 7. Results : Duplication Rate Histogram



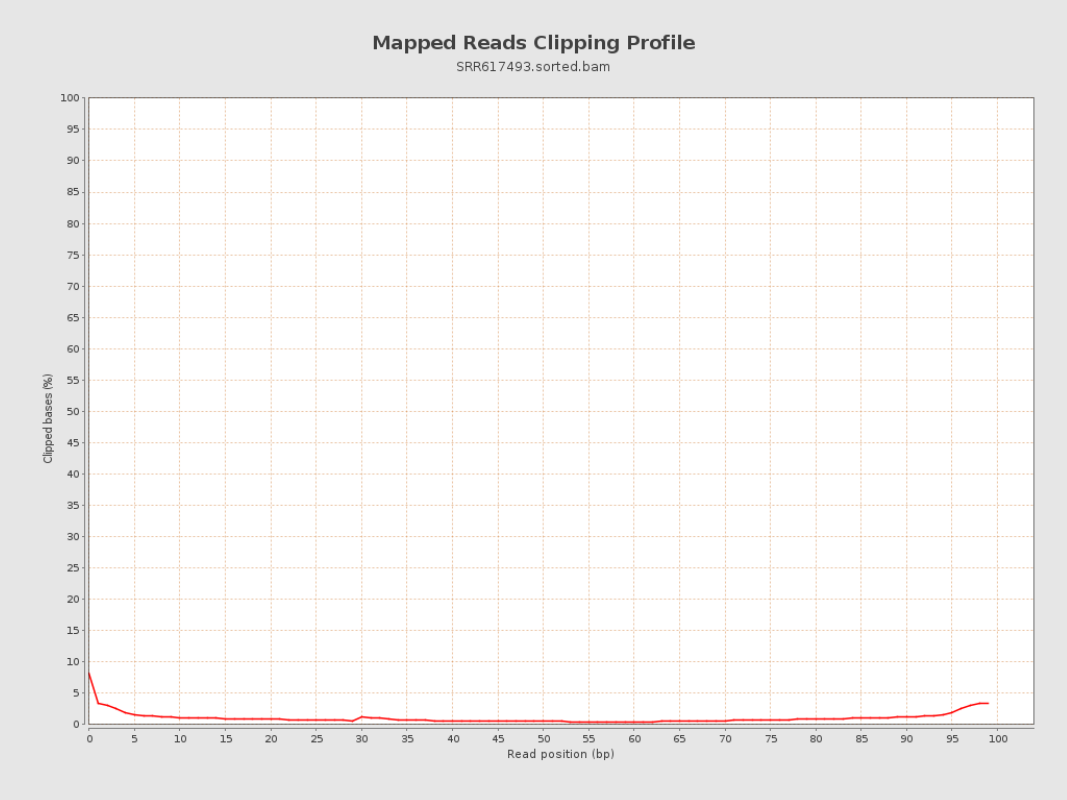
# 8. Results : Mapped Reads Nucleotide Content



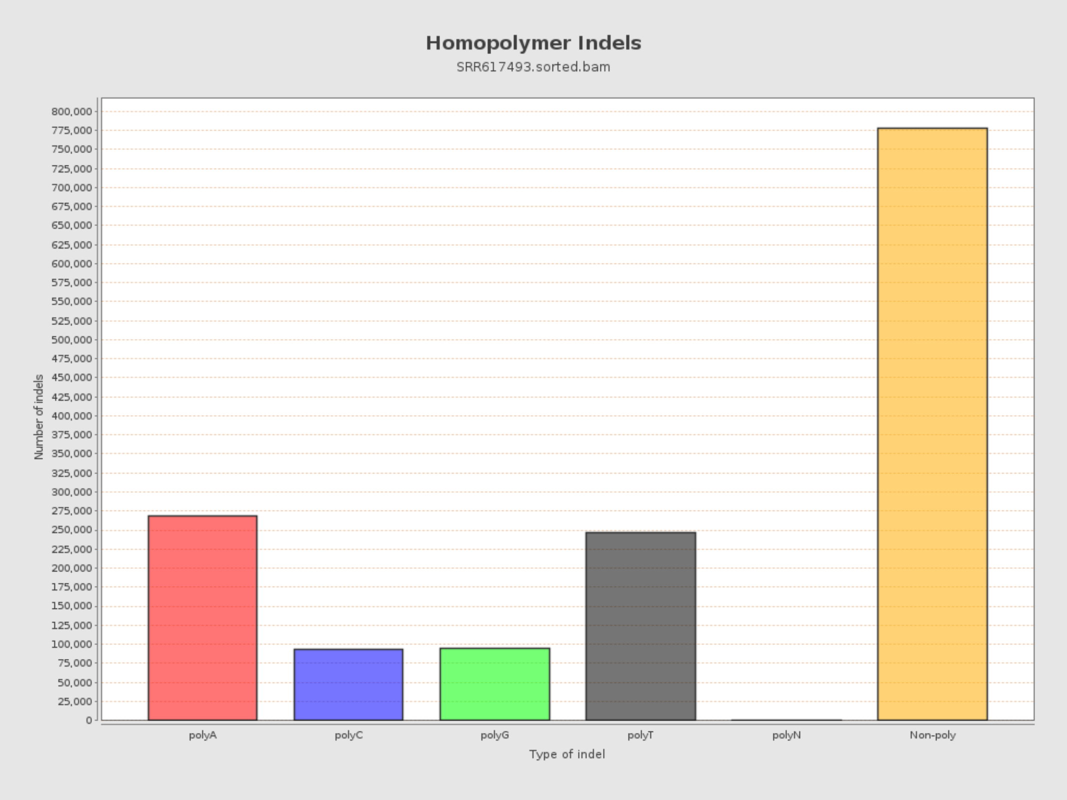
# 9. Results : Mapped Reads GC-content Distribution



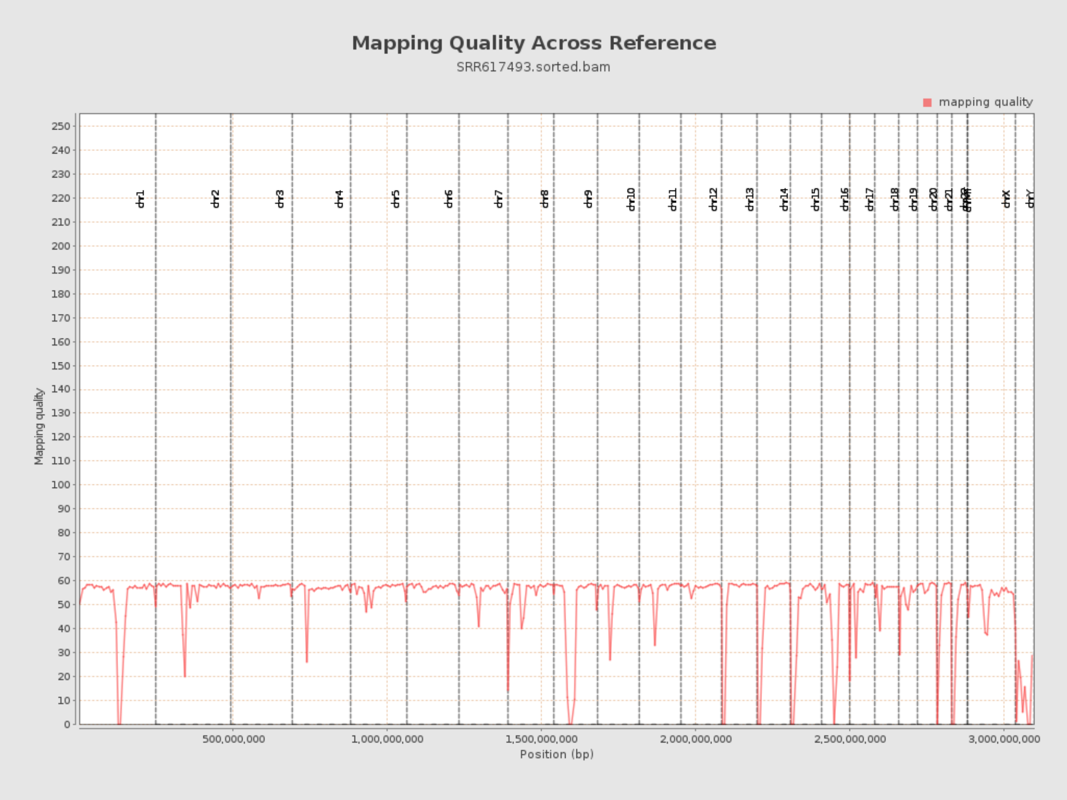
# 10. Results : Mapped Reads Clipping Profile



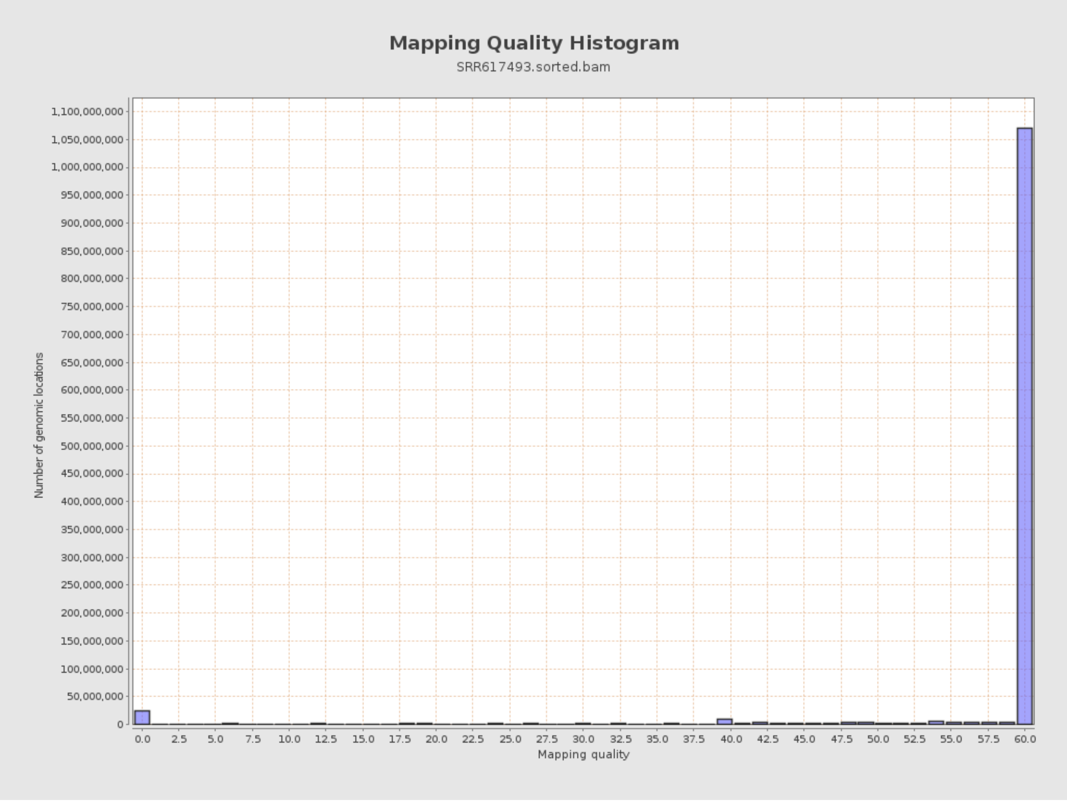
# 11. Results : Homopolymer Indels



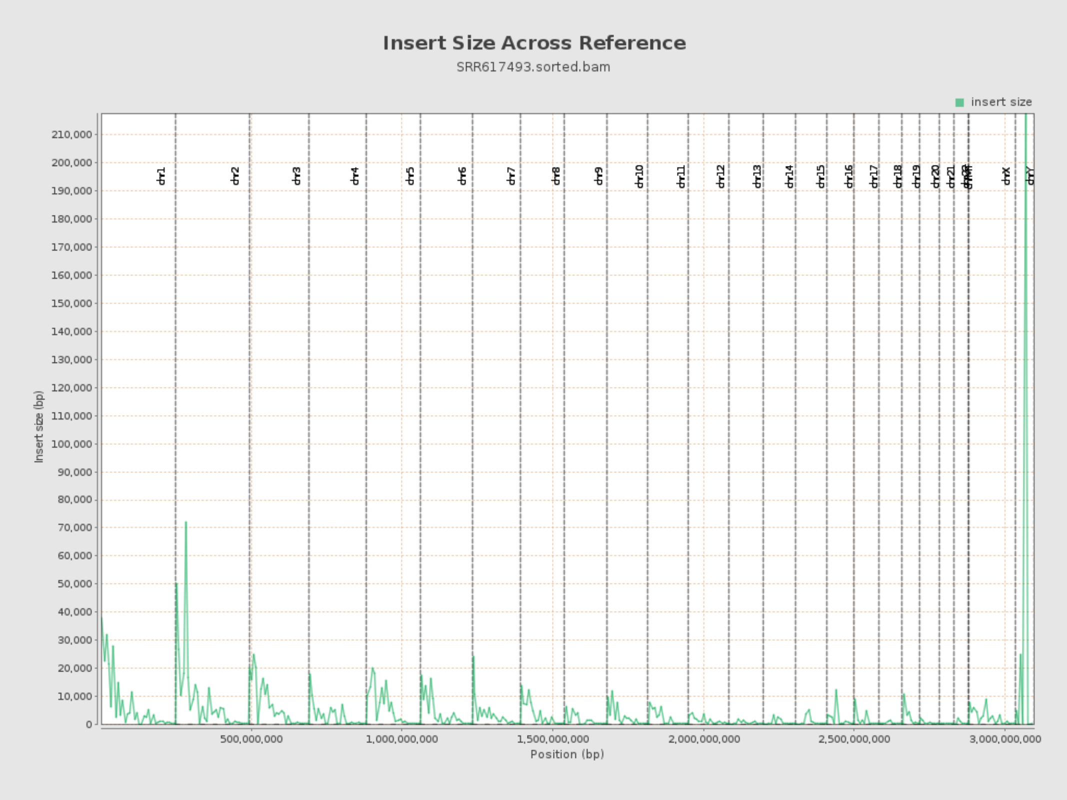
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



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# 15. Results : Insert Size Histogram