# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/07 06:02:07*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR617361.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_SRR617361 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617361_1.fastq.gz SRR617361_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Oct 07 06:02:05 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR617361.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 32,000,000 |
| Mapped reads | 30,050,362 / 93.91% |
| Unmapped reads | 1,949,638 / 6.09% |
| Mapped paired reads | 30,050,362 / 93.91% |
| Mapped reads, first in pair | 15,104,903 / 47.2% |
| Mapped reads, second in pair | 14,945,459 / 46.7% |
| Mapped reads, both in pair | 29,499,524 / 92.19% |
| Mapped reads, singletons | 550,838 / 1.72% |
| Secondary alignments | 0 |
| Supplementary alignments | 66,889 / 0.21% |
| Read min/max/mean length | 30 / 100 / 100.08 |
| Duplicated reads (estimated) | 1,547,853 / 4.84% |
| Duplication rate | 1.48% |
| Clipped reads | 2,421,715 / 7.57% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 893,878,406 / 30.3% |
| Number/percentage of C's | 586,062,594 / 19.86% |
| Number/percentage of T's | 881,078,767 / 29.86% |
| Number/percentage of G's | 588,568,373 / 19.95% |
| Number/percentage of N's | 964,291 / 0.03% |
| | |

| | |
|---|---|
| GC Percentage | 39.81% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.9534 |
| Standard Deviation | 9.7227 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.46 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 52,369.77 |
| Standard Deviation | 2,183,127.4 |
| P25/Median/P75 | 170 / 210 / 271 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 1.18% |
| Mismatches | 33,929,338 |
| Insertions | 294,854 |
| Mapped reads with at least one insertion | 0.95% |
| Deletions | 358,472 |
| Mapped reads with at least one deletion | 1.16% |
| Homopolymer indels | 41.19% |

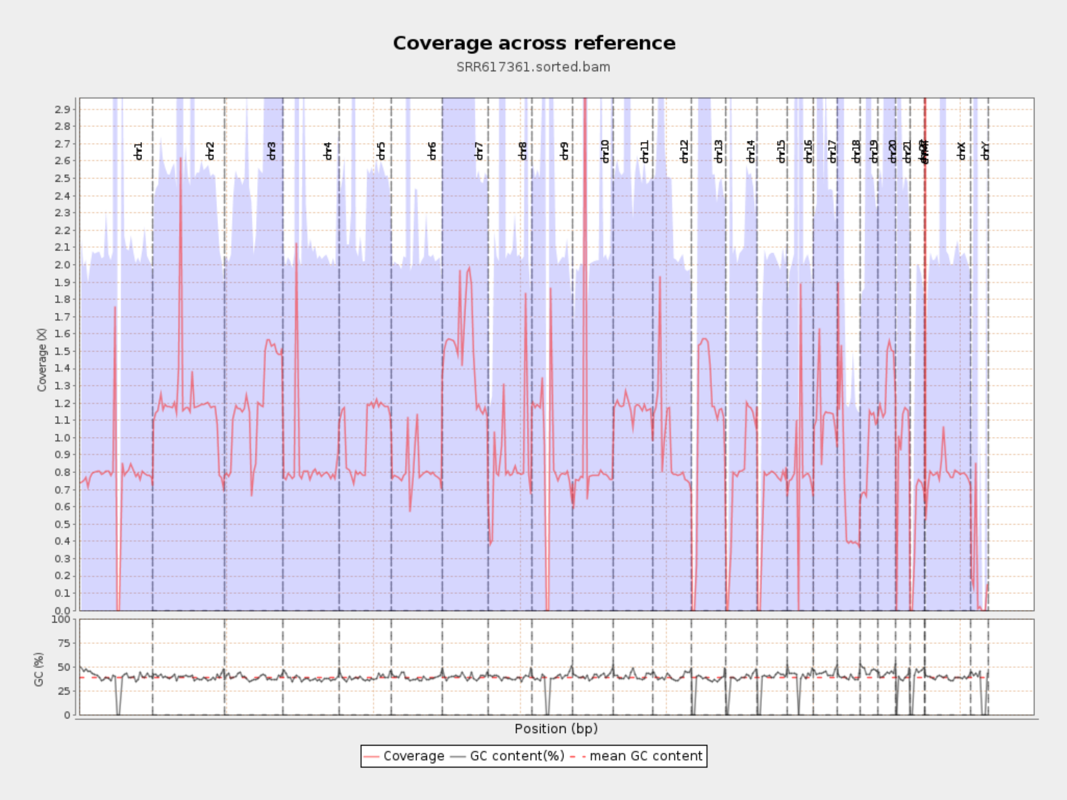
## 2.7. Chromosome stats

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

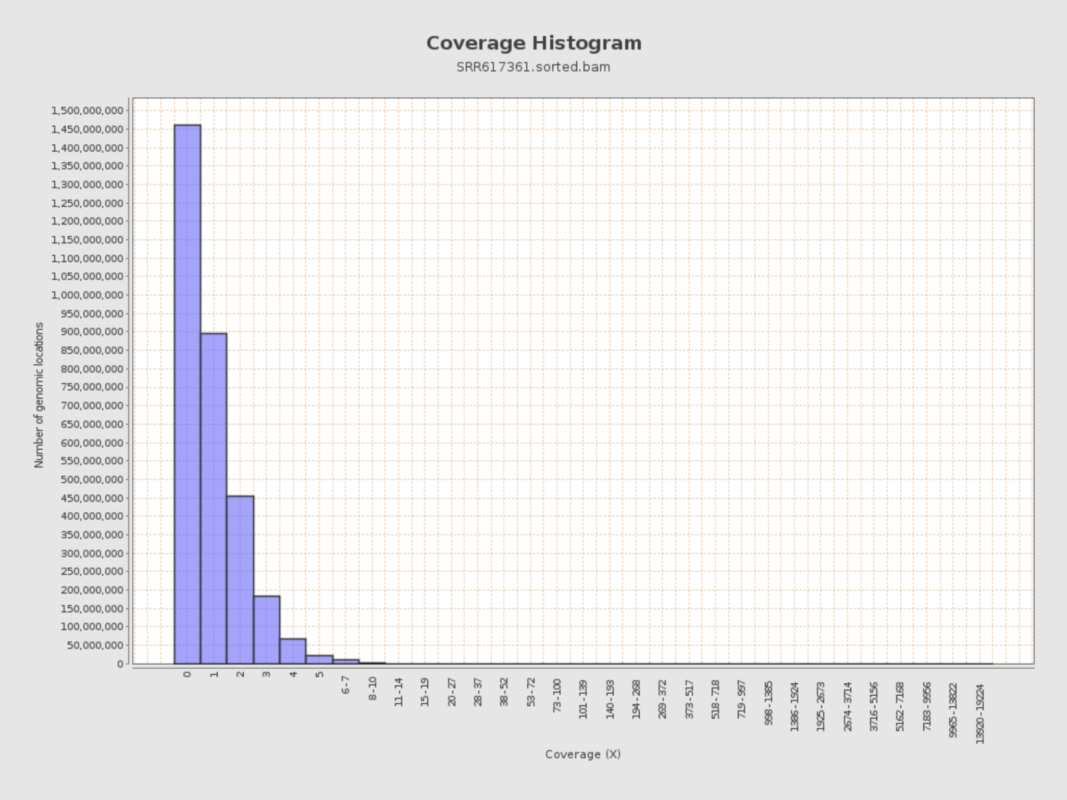
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 191940426 | 0.7701 | 19.6399 |
| chr2 | 243199373 | 291434965 | 1.1983 | 8.745 |
| chr3 | 198022430 | 235199676 | 1.1877 | 1.4594 |
| chr4 | 191154276 | 161442567 | 0.8446 | 9.2467 |
| chr5 | 180915260 | 185587334 | 1.0258 | 1.4608 |
| chr6 | 171115067 | 138539049 | 0.8096 | 3.6517 |
| chr7 | 159138663 | 239551170 | 1.5053 | 10.9585 |
| chr8 | 146364022 | 124387311 | 0.8498 | 7.5159 |
| chr9 | 141213431 | 124480654 | 0.8815 | 14.792 |
| chr10 | 135534747 | 124273511 | 0.9169 | 20.2007 |
| chr11 | 135006516 | 158240361 | 1.1721 | 5.5701 |
| chr12 | 133851895 | 130060854 | 0.9717 | 1.3583 |
| chr13 | 115169878 | 128563866 | 1.1163 | 1.2908 |
| chr14 | 107349540 | 85526473 | 0.7967 | 1.3625 |
| chr15 | 102531392 | 66589705 | 0.6495 | 0.9761 |
| chr16 | 90354753 | 74059734 | 0.8197 | 7.8723 |
| chr17 | 81195210 | 91746065 | 1.1299 | 7.1168 |
| chr18 | 78077248 | 53287564 | 0.6825 | 15.2005 |
| chr19 | 59128983 | 54693226 | 0.925 | 9.6608 |
| chr20 | 63025520 | 84159868 | 1.3353 | 2.4304 |
| chr21 | 48129895 | 46922170 | 0.9749 | 3.1957 |
| chr22 | 51304566 | 25998818 | 0.5068 | 0.9063 |
| chrMT | 16571 | 1969573 | 118.8566 | 20.5296 |
| chrX | 155270560 | 122771953 | 0.7907 | 3.019 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 9984608 | 0.1682 | 8.1482 |

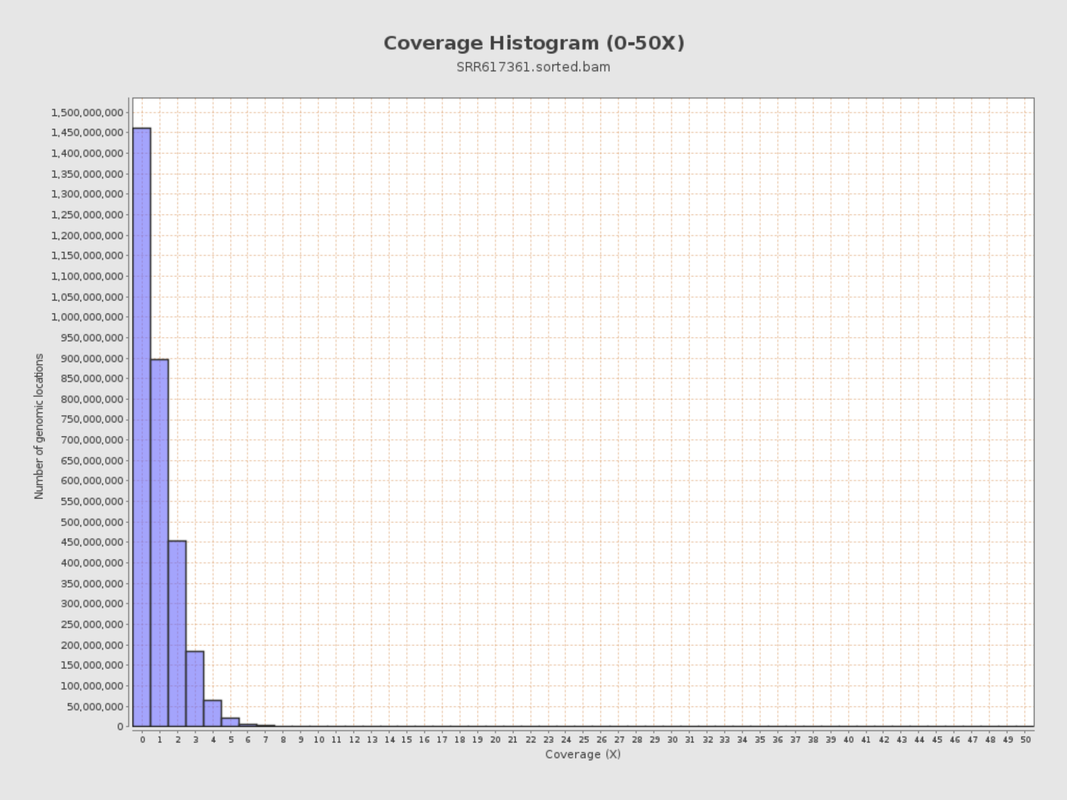
# 3. Results : Coverage across reference



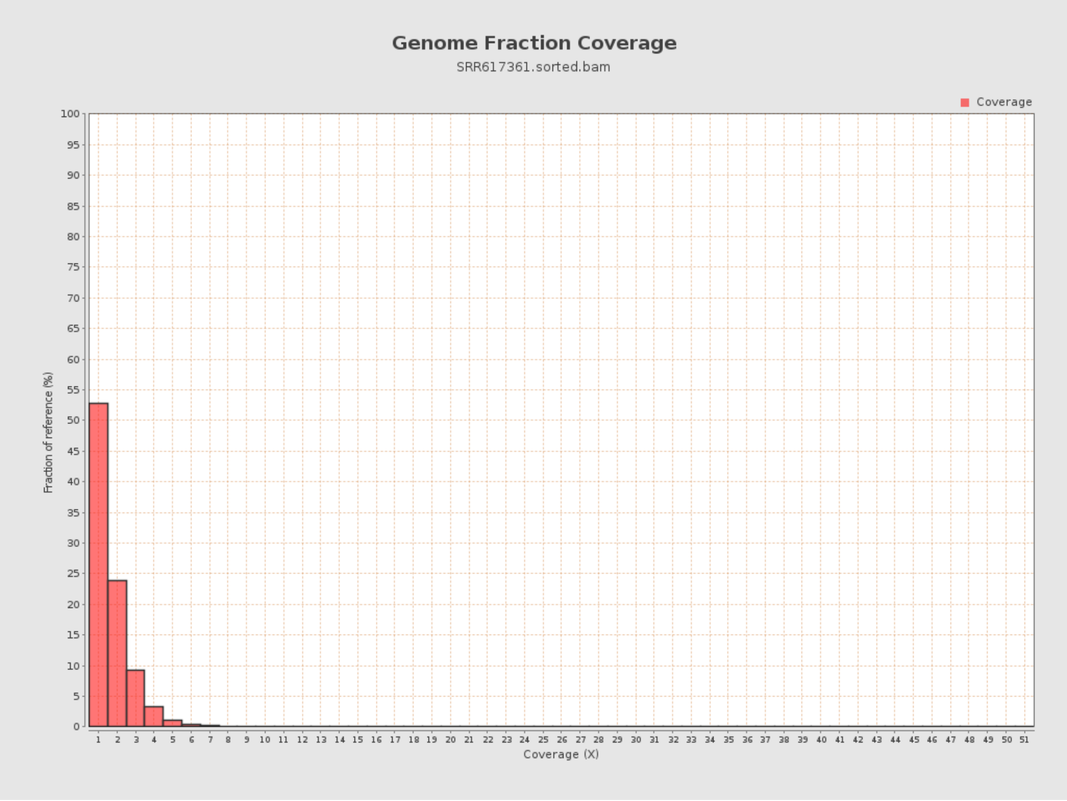
# 4. Results : Coverage Histogram



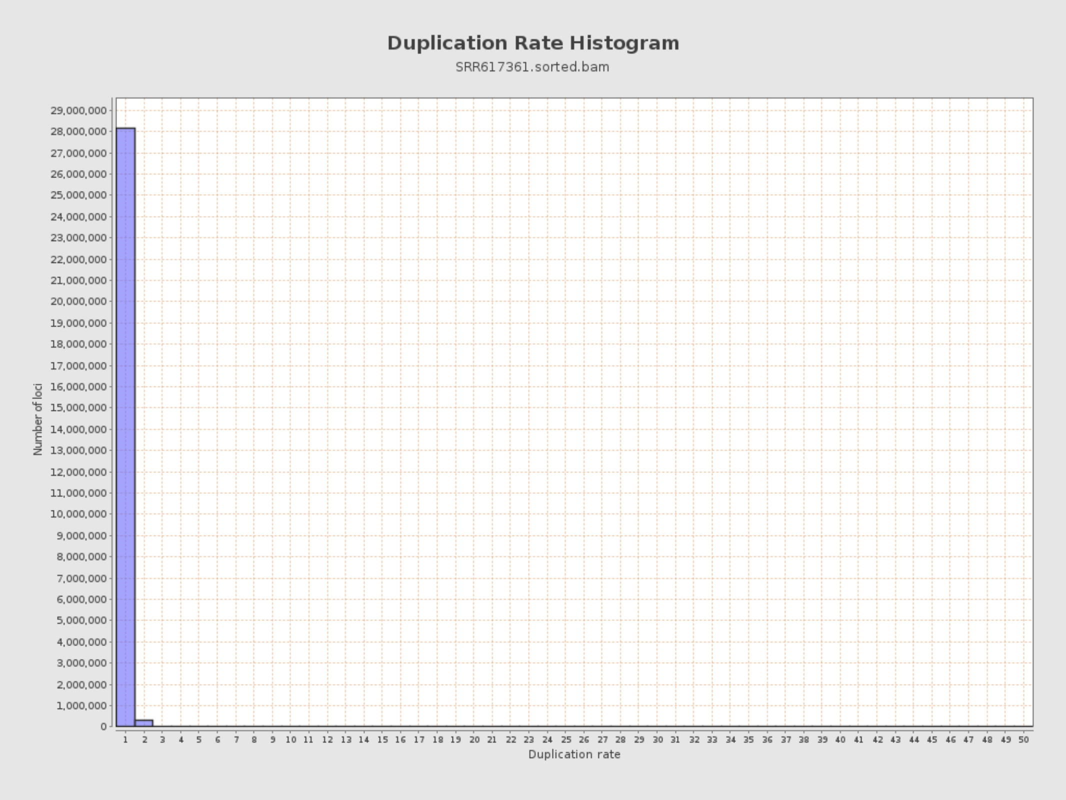
# 5. Results : Coverage Histogram (0-50X)



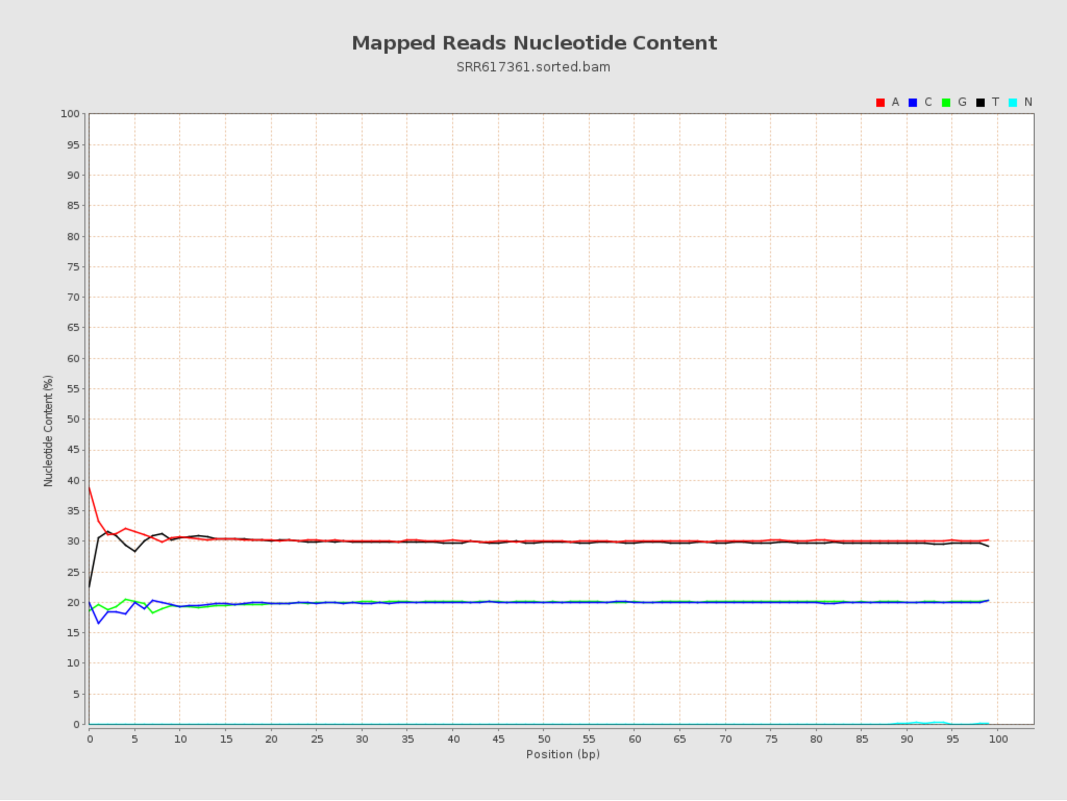
# 6. Results : Genome Fraction Coverage



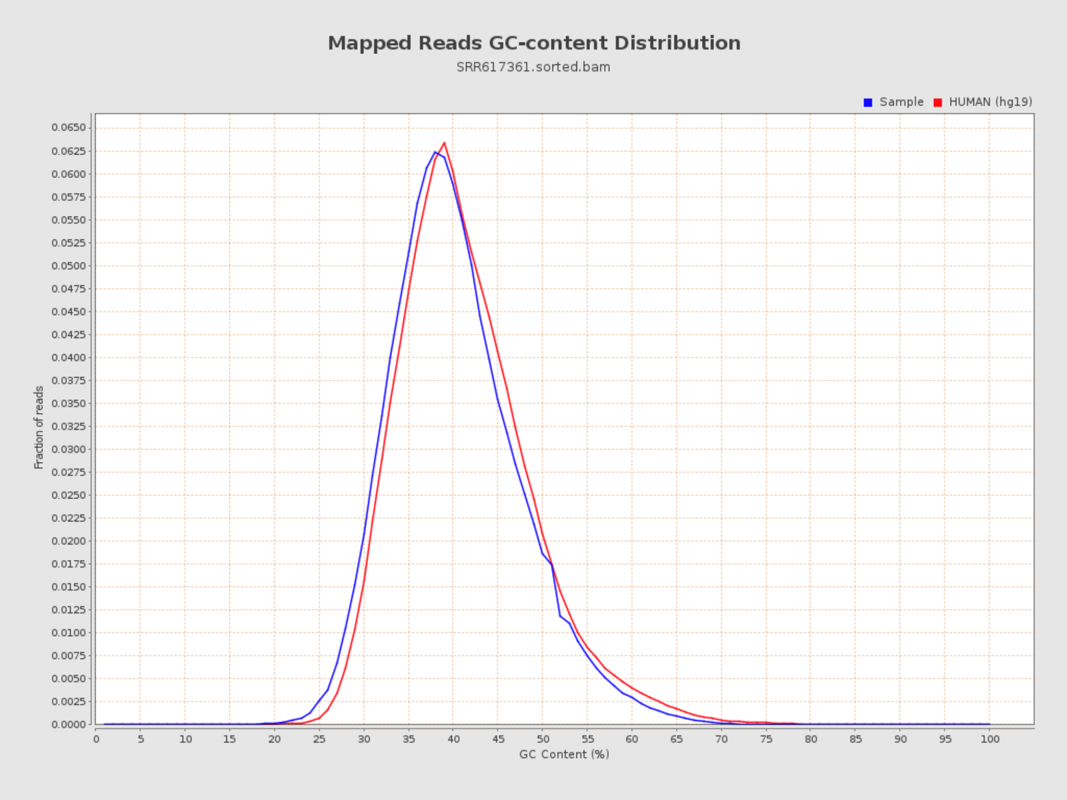
# 7. Results : Duplication Rate Histogram



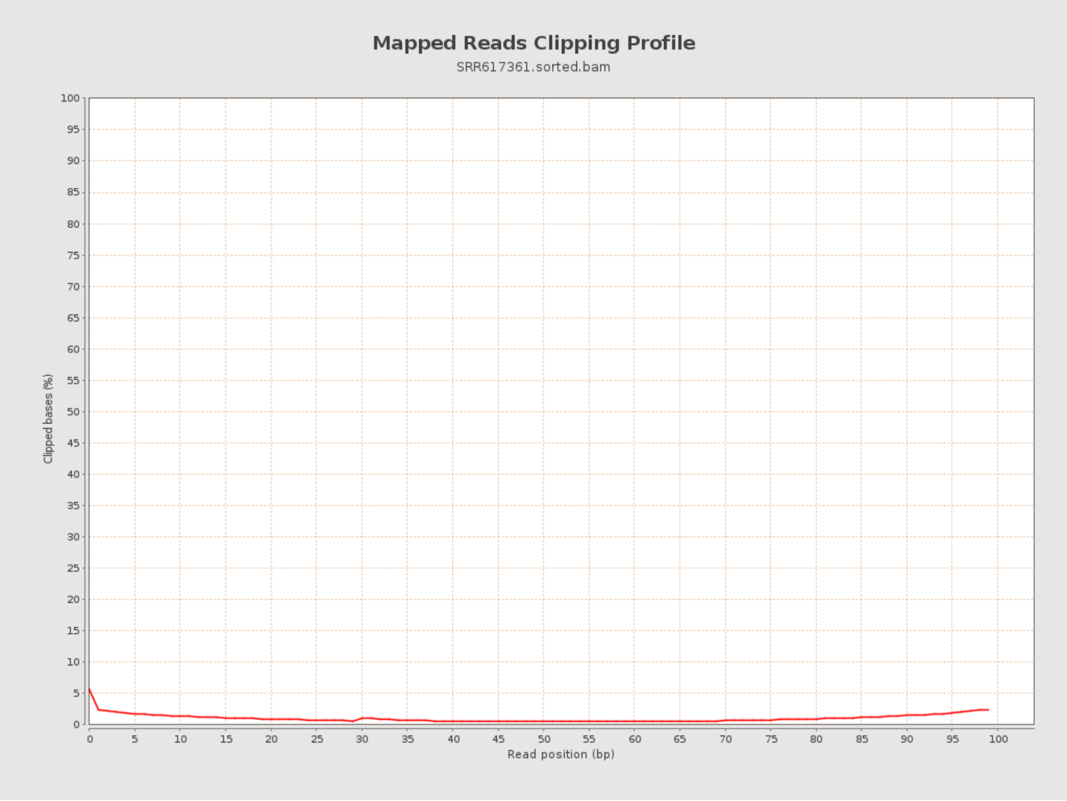
# 8. Results : Mapped Reads Nucleotide Content



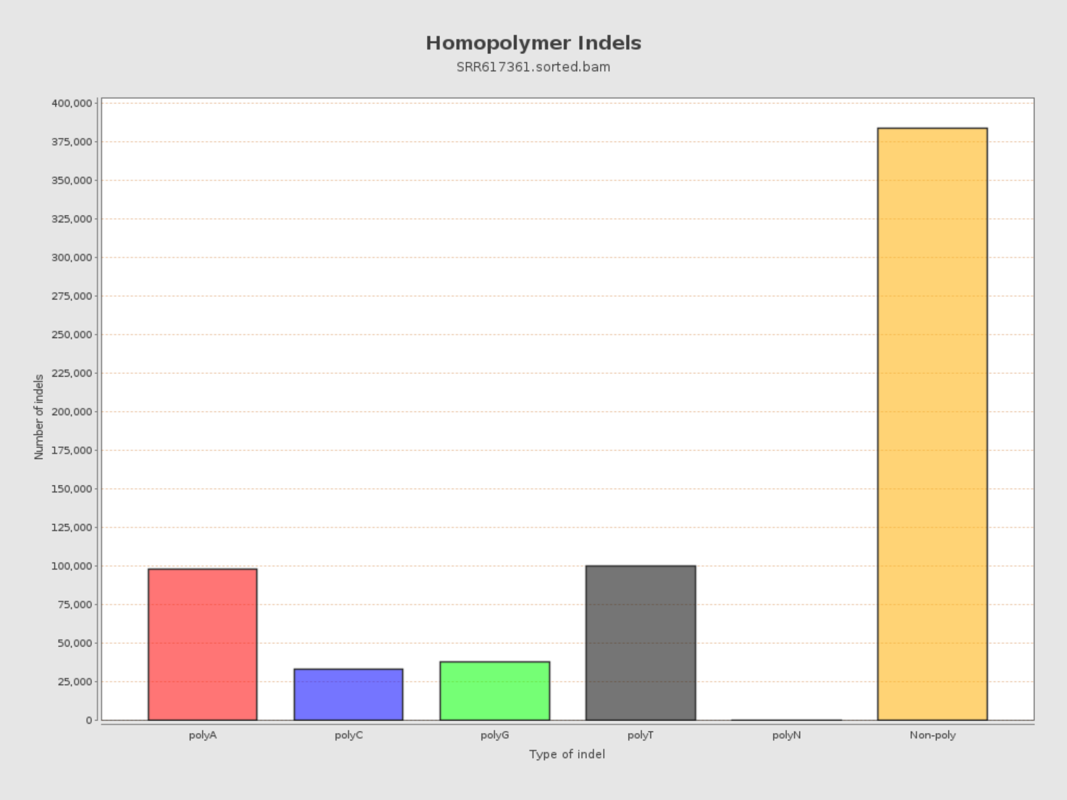
# 9. Results : Mapped Reads GC-content Distribution



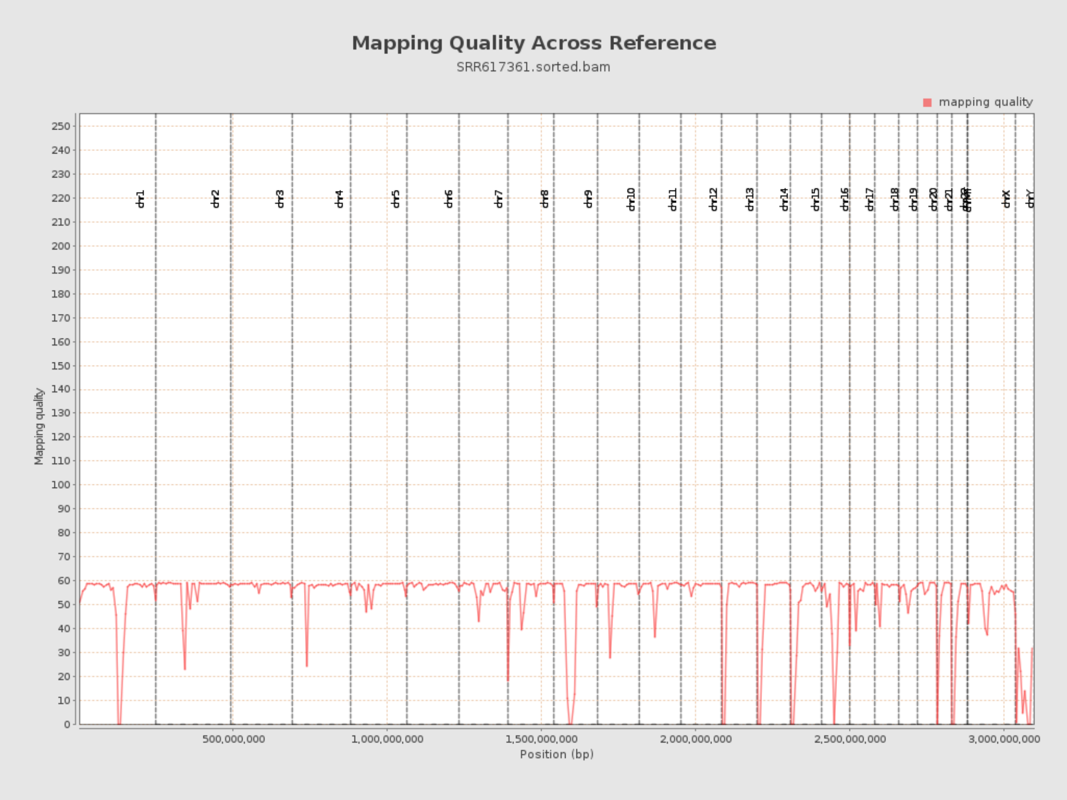
# 10. Results : Mapped Reads Clipping Profile



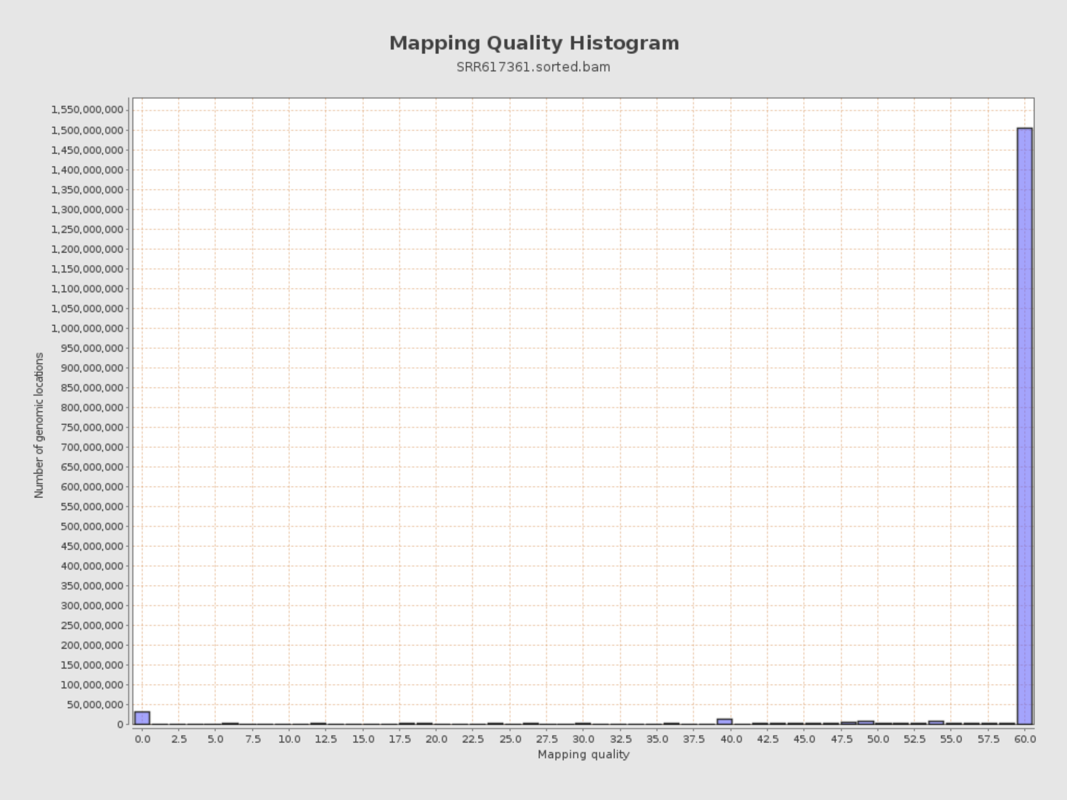
# 11. Results : Homopolymer Indels



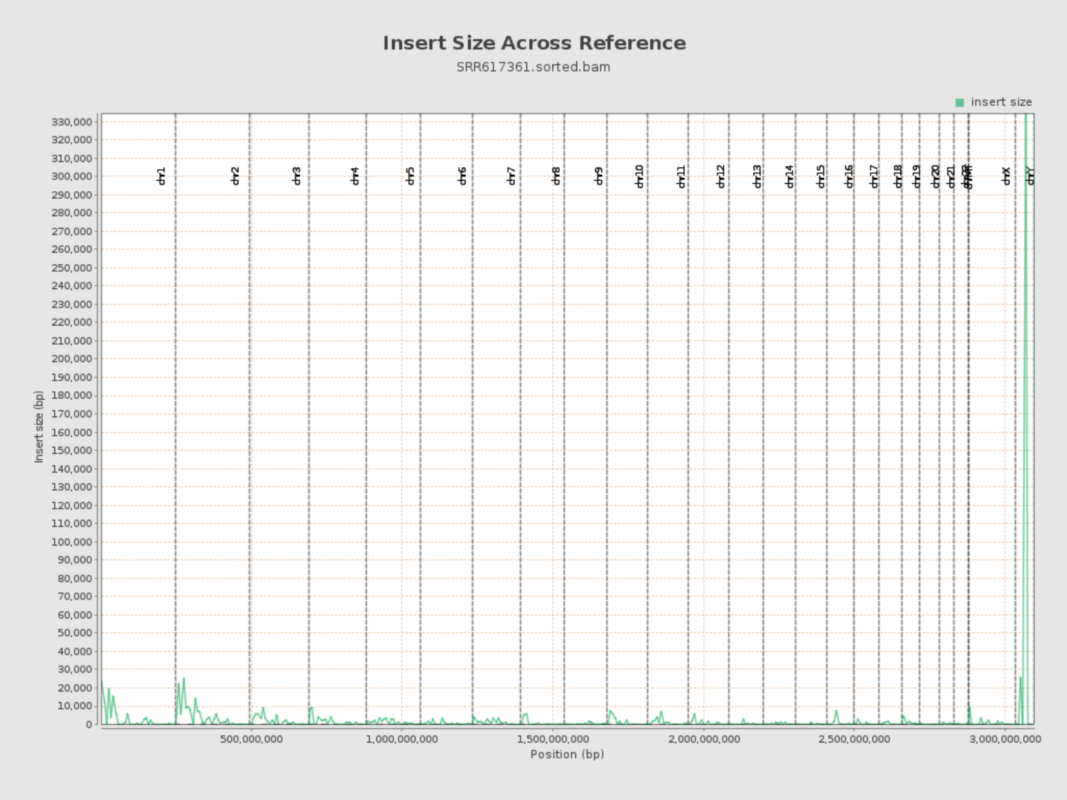
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram