# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/29 16:34:53*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472711.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_SRR3472711 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472711_1.fastq.gz SRR3472711_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 29 16:34:52 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3472711.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 18,216,496 |
| Mapped reads | 18,004,163 / 98.83% |
| Unmapped reads | 212,333 / 1.17% |
| Mapped paired reads | 18,004,163 / 98.83% |
| Mapped reads, first in pair | 9,046,844 / 49.66% |
| Mapped reads, second in pair | 8,957,319 / 49.17% |
| Mapped reads, both in pair | 17,876,174 / 98.13% |
| Mapped reads, singletons | 127,989 / 0.7% |
| Secondary alignments | 0 |
| Supplementary alignments | 55,098 / 0.3% |
| Read min/max/mean length | 30 / 100 / 100.12 |
| Duplicated reads (estimated) | 11,294,909 / 62% |
| Duplication rate | 47.77% |
| Clipped reads | 1,482,487 / 8.14% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 478,365,793 / 26.99% |
| Number/percentage of C's | 409,812,865 / 23.12% |
| Number/percentage of T's | 475,610,800 / 26.84% |
| Number/percentage of G's | 408,187,187 / 23.03% |
| Number/percentage of N's | 338,172 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 46.15% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.5726 |
| Standard Deviation | 17.2356 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 55.13 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 28,883.88 |
| Standard Deviation | 1,742,294.79 |
| P25/Median/P75 | 166 / 232 / 312 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.61% |
| Mismatches | 10,563,641 |
| Insertions | 96,362 |
| Mapped reads with at least one insertion | 0.53% |
| Deletions | 96,262 |
| Mapped reads with at least one deletion | 0.53% |
| Homopolymer indels | 45.36% |

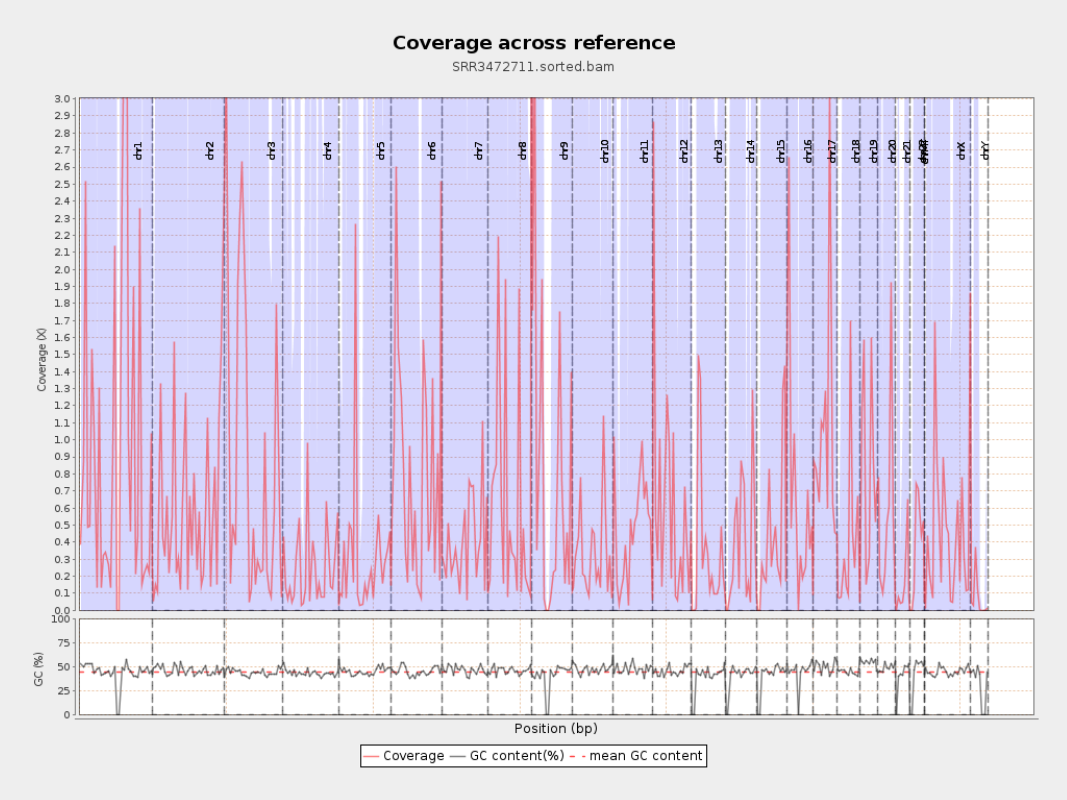
## 2.7. Chromosome stats

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

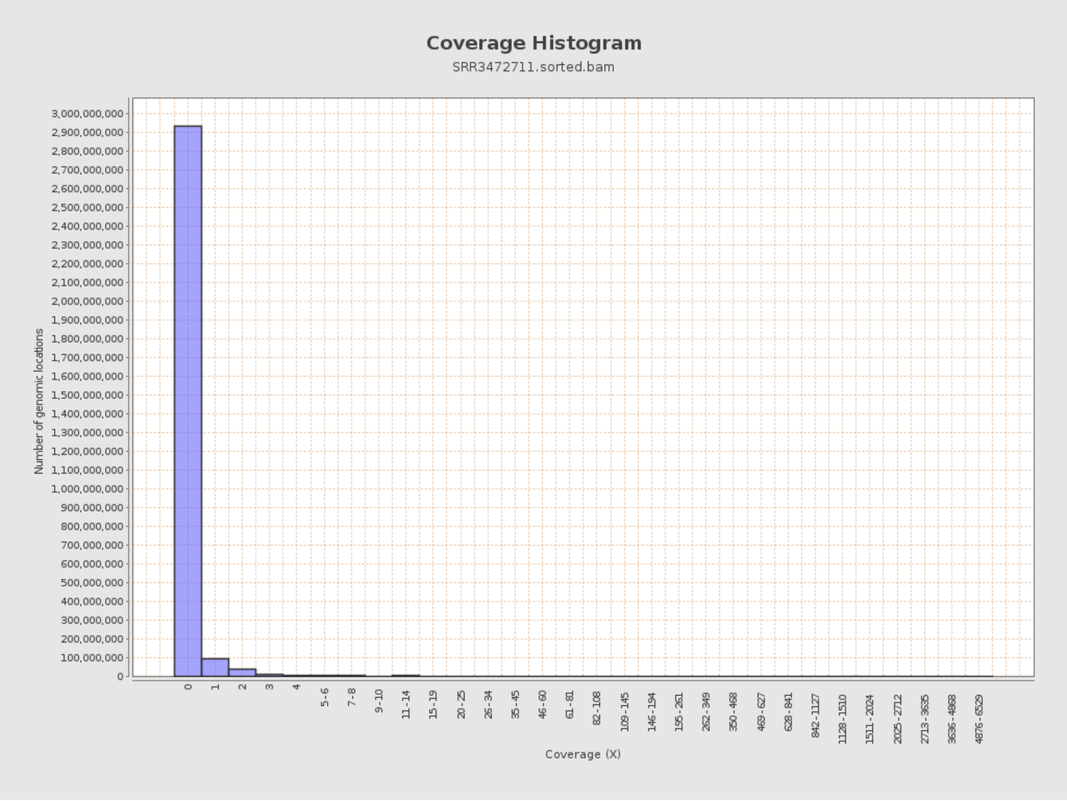
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 248622275 | 0.9975 | 28.031 |
| chr2 | 243199373 | 142202437 | 0.5847 | 16.5934 |
| chr3 | 198022430 | 187330079 | 0.946 | 21.5323 |
| chr4 | 191154276 | 47266011 | 0.2473 | 8.3505 |
| chr5 | 180915260 | 57970189 | 0.3204 | 9.5998 |
| chr6 | 171115067 | 135552507 | 0.7922 | 21.0341 |
| chr7 | 159138663 | 64879724 | 0.4077 | 10.8061 |
| chr8 | 146364022 | 90074098 | 0.6154 | 18.2095 |
| chr9 | 141213431 | 119035892 | 0.843 | 22.5704 |
| chr10 | 135534747 | 45727805 | 0.3374 | 10.8201 |
| chr11 | 135006516 | 63582411 | 0.471 | 14.9471 |
| chr12 | 133851895 | 82155930 | 0.6138 | 15.7424 |
| chr13 | 115169878 | 40537300 | 0.352 | 11.8325 |
| chr14 | 107349540 | 39494595 | 0.3679 | 12.0945 |
| chr15 | 102531392 | 45059503 | 0.4395 | 14.1556 |
| chr16 | 90354753 | 61604157 | 0.6818 | 15.8126 |
| chr17 | 81195210 | 83103658 | 1.0235 | 21.2907 |
| chr18 | 78077248 | 31058273 | 0.3978 | 16.9923 |
| chr19 | 59128983 | 49714526 | 0.8408 | 21.4847 |
| chr20 | 63025520 | 36390043 | 0.5774 | 25.0168 |
| chr21 | 48129895 | 7854214 | 0.1632 | 10.1277 |
| chr22 | 51304566 | 19671359 | 0.3834 | 9.428 |
| chrMT | 16571 | 2849 | 0.1719 | 0.6005 |
| chrX | 155270560 | 69247272 | 0.446 | 13.7756 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 4422747 | 0.0745 | 3.7321 |

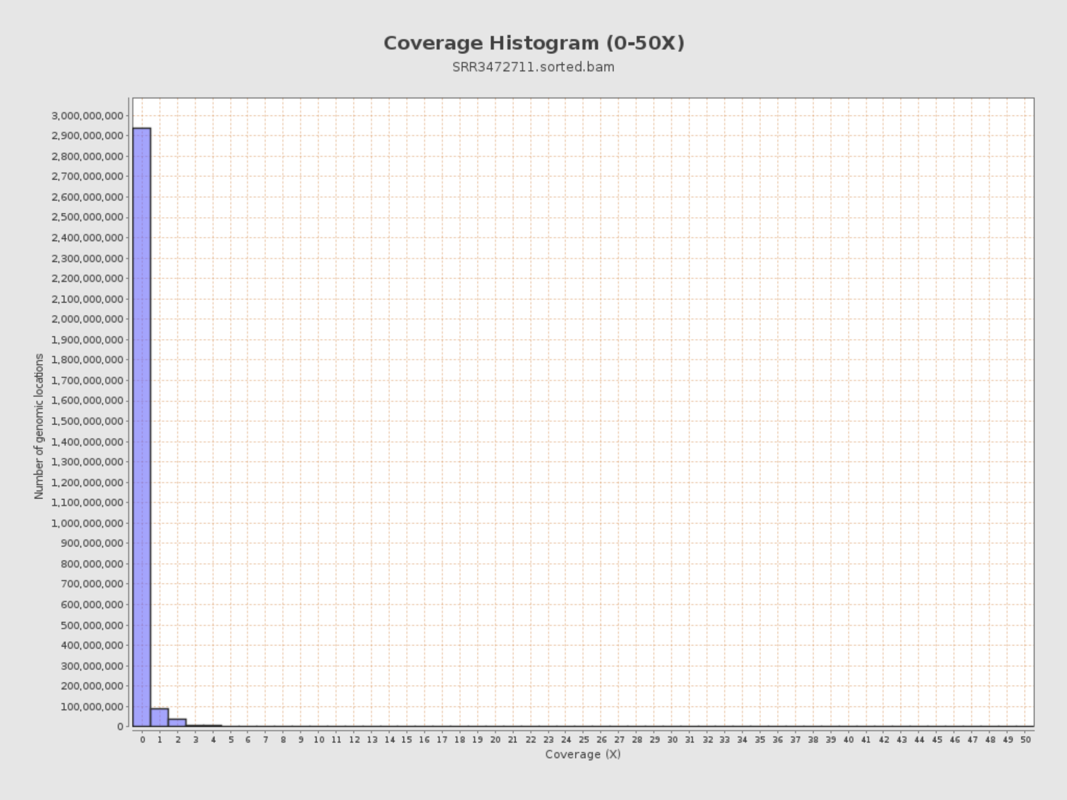
# 3. Results : Coverage across reference



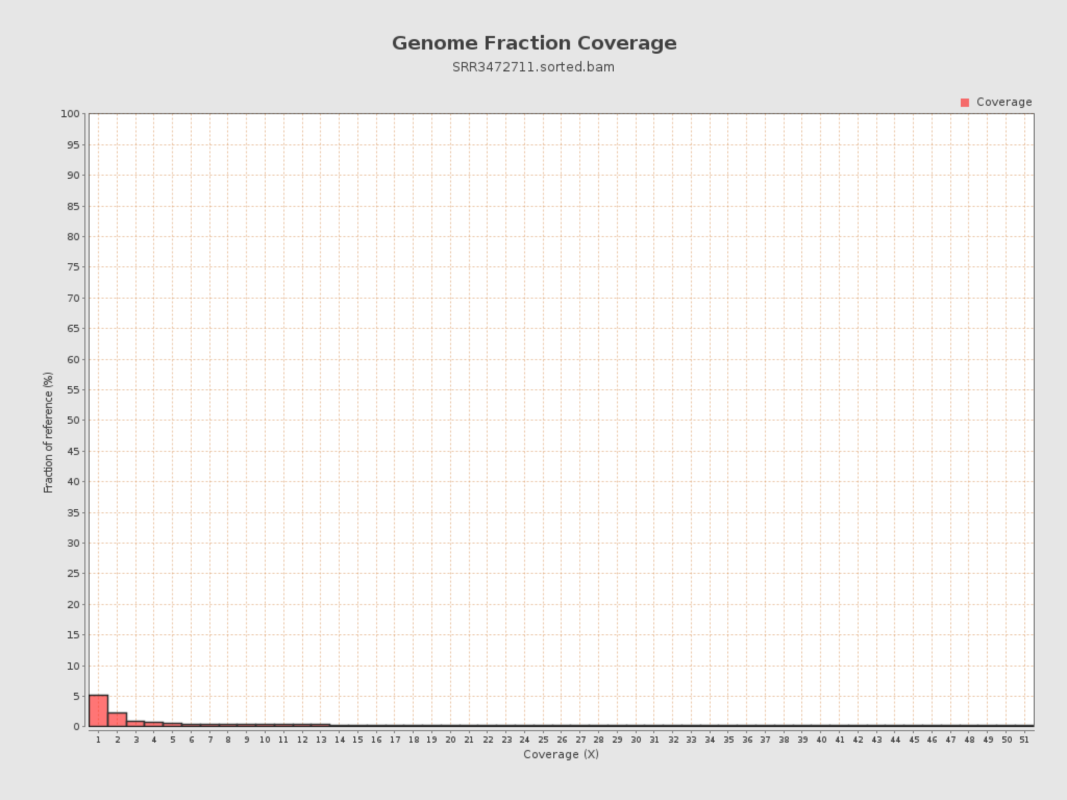
# 4. Results : Coverage Histogram



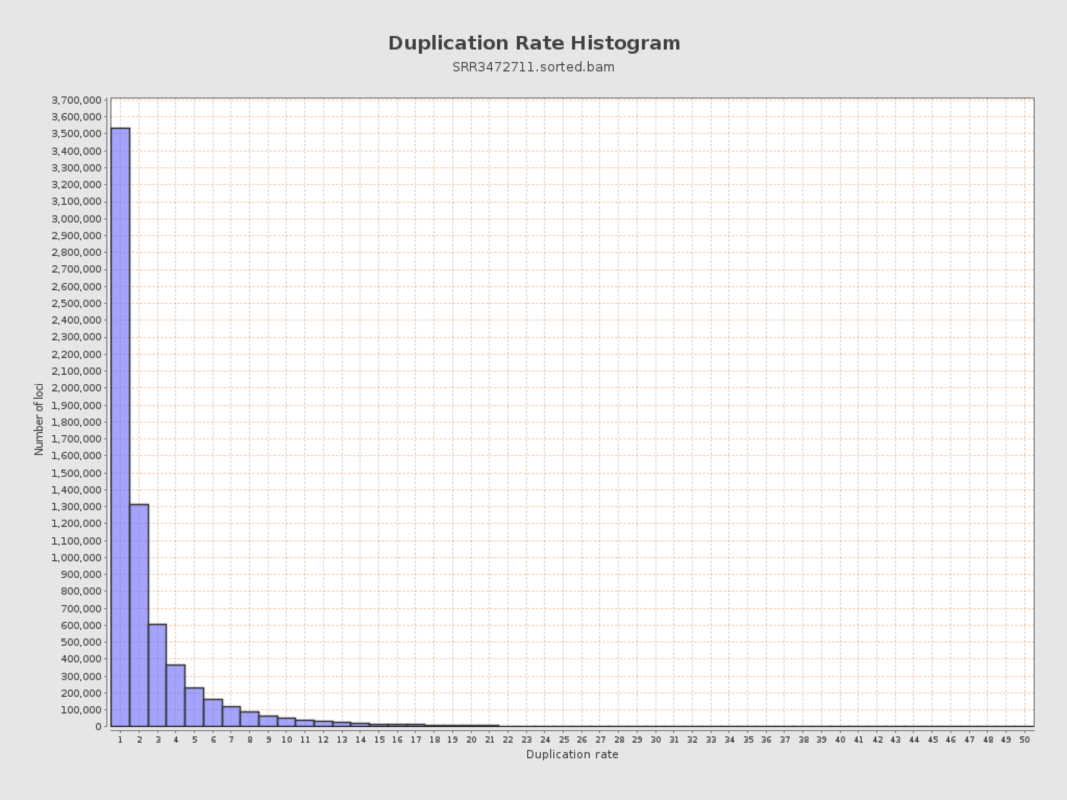
# 5. Results : Coverage Histogram (0-50X)



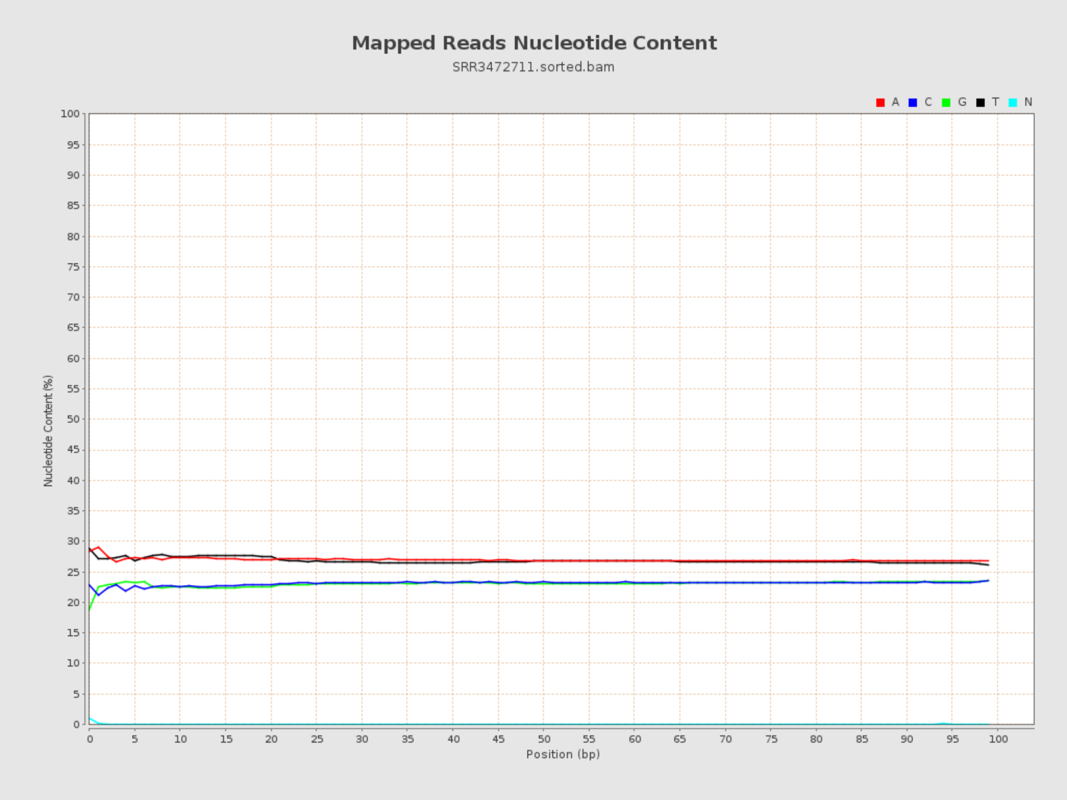
# 6. Results : Genome Fraction Coverage



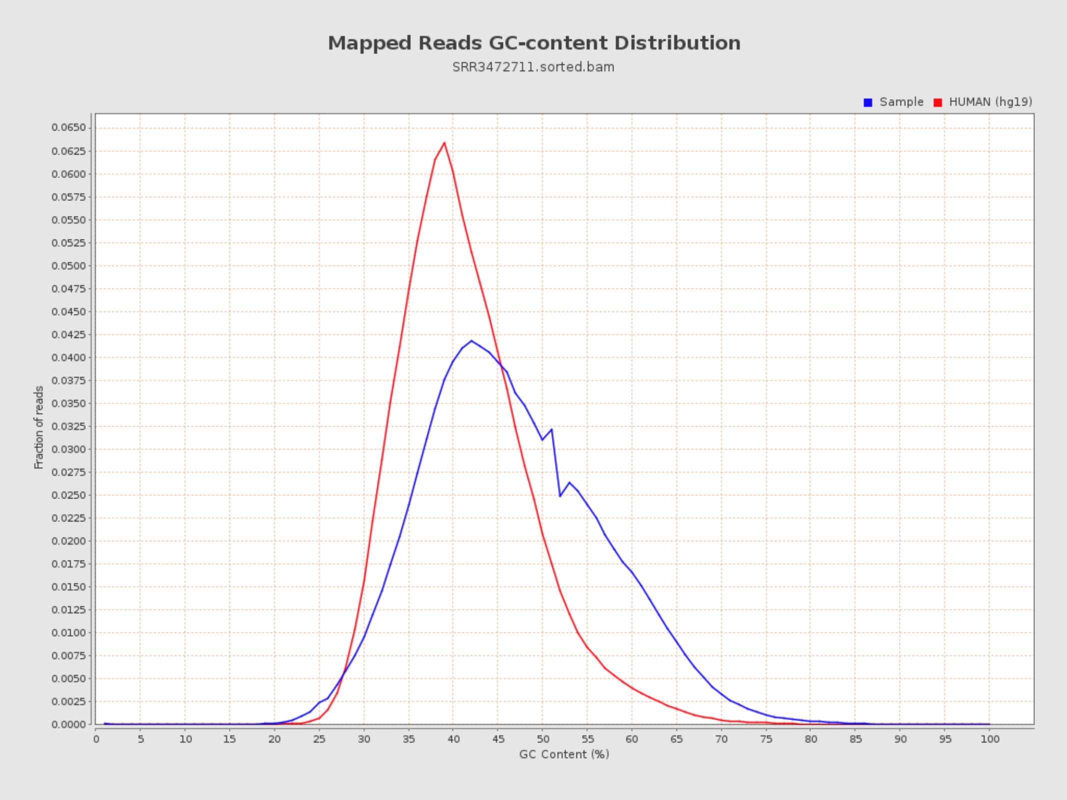
# 7. Results : Duplication Rate Histogram



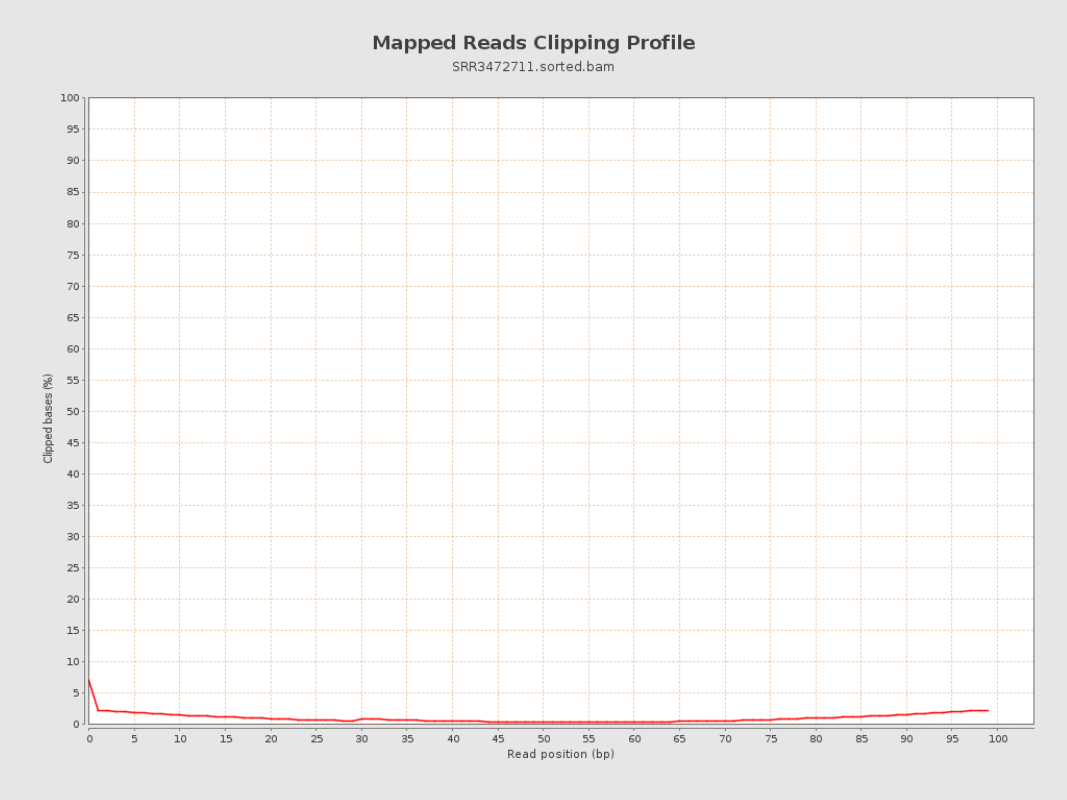
# 8. Results : Mapped Reads Nucleotide Content



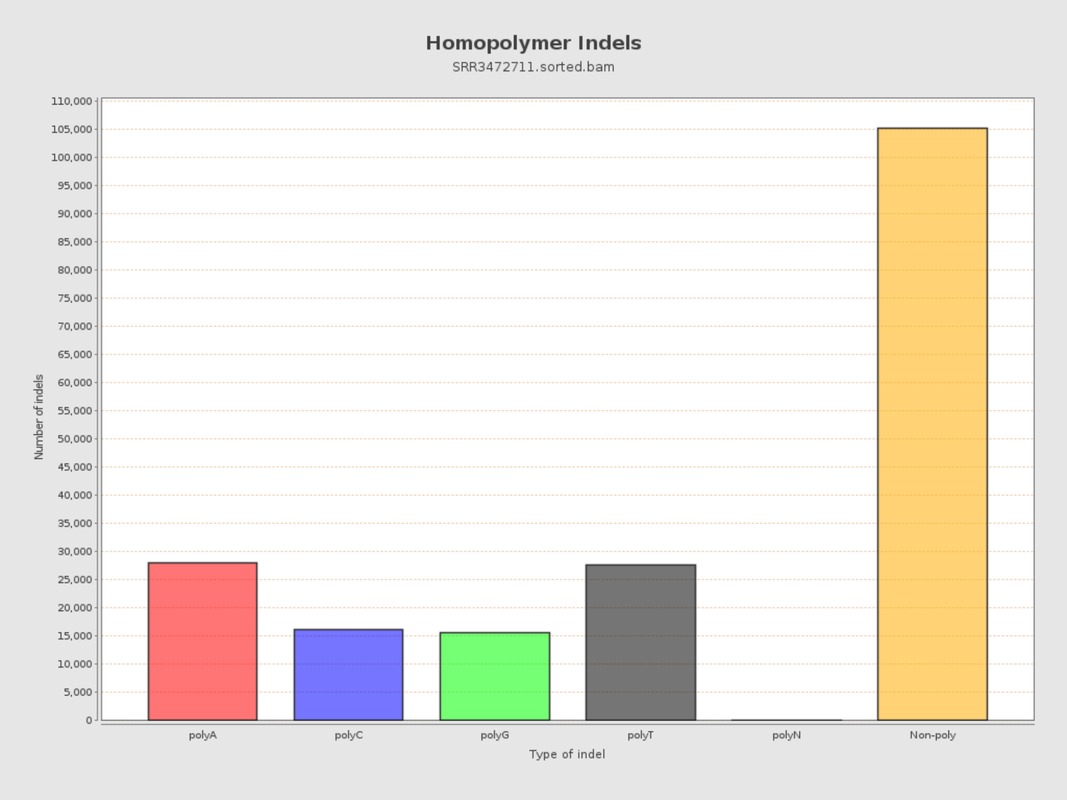
# 9. Results : Mapped Reads GC-content Distribution



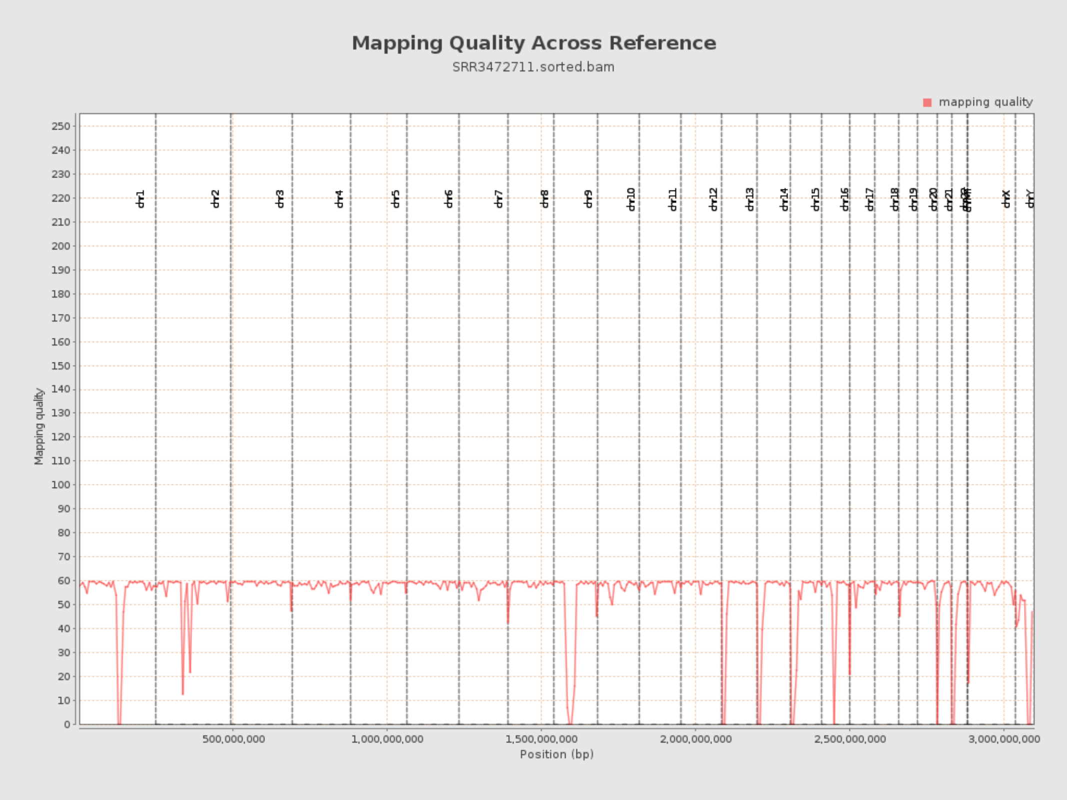
# 10. Results : Mapped Reads Clipping Profile



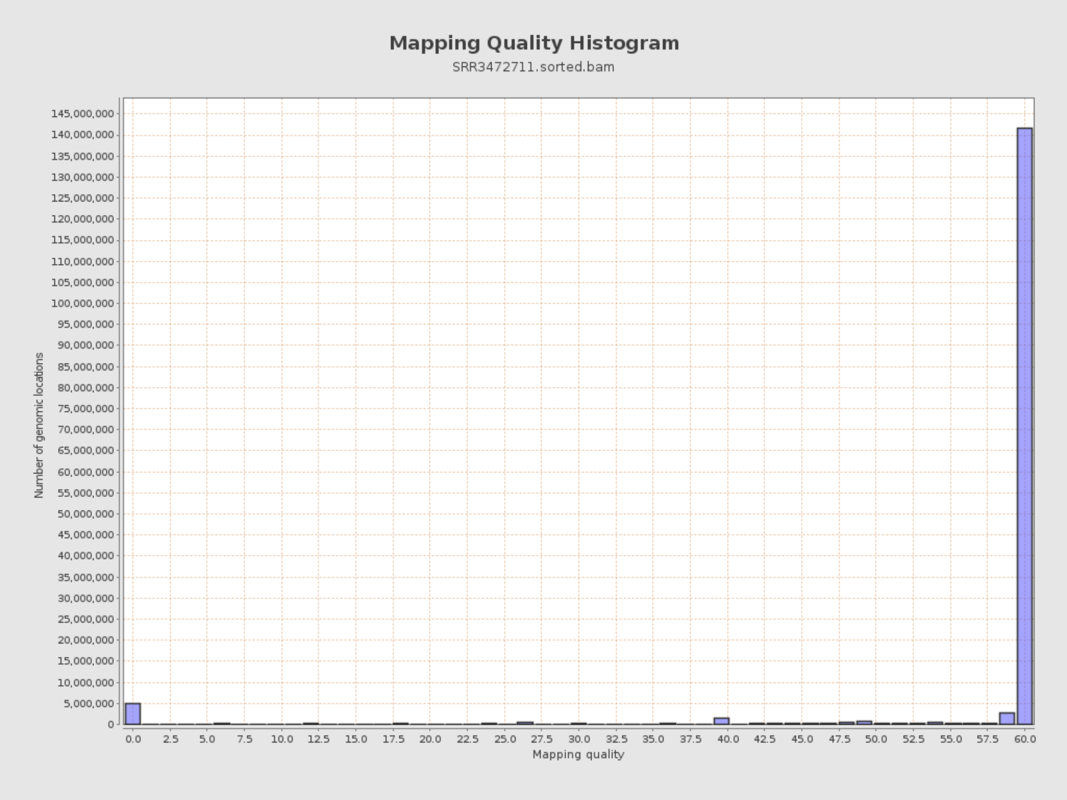
# 11. Results : Homopolymer Indels



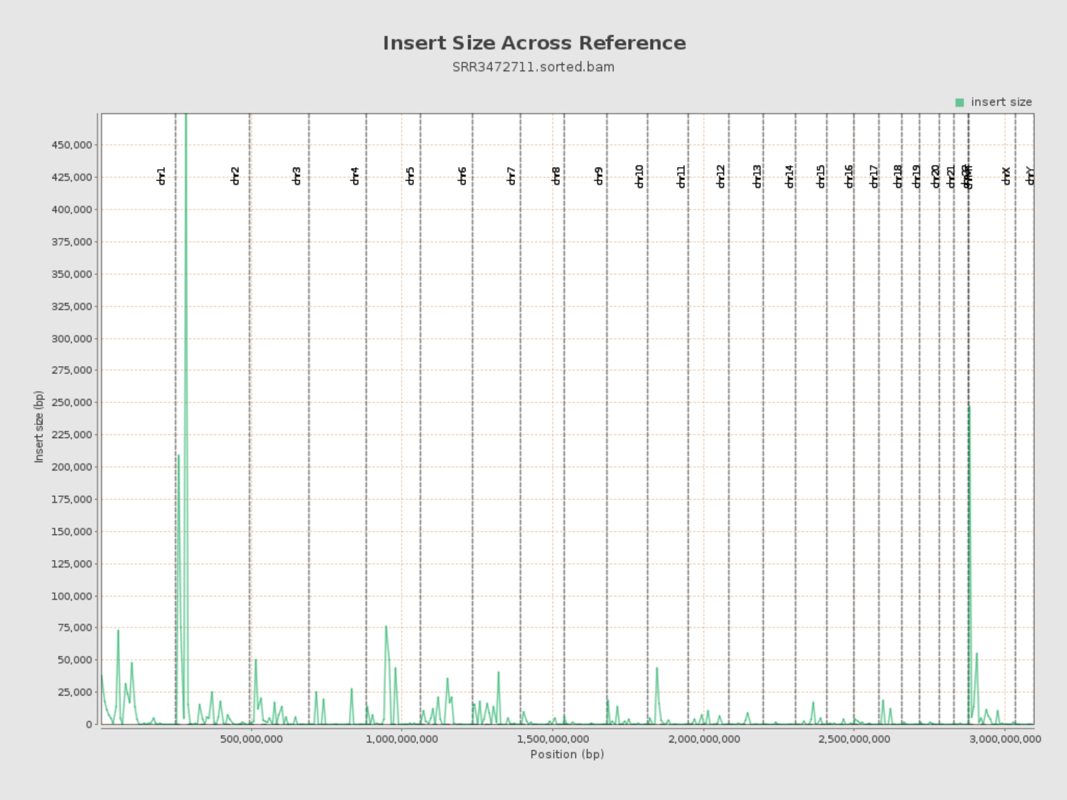
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram