# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/25 10:19:30*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472563.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_SRR3472563 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472563_1.fastq.gz SRR3472563_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Aug 25 10:19:24 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3472563.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 7,824,126 |
| Mapped reads | 7,675,216 / 98.1% |
| Unmapped reads | 148,910 / 1.9% |
| Mapped paired reads | 7,675,216 / 98.1% |
| Mapped reads, first in pair | 3,849,318 / 49.2% |
| Mapped reads, second in pair | 3,825,898 / 48.9% |
| Mapped reads, both in pair | 7,607,970 / 97.24% |
| Mapped reads, singletons | 67,246 / 0.86% |
| Secondary alignments | 0 |
| Supplementary alignments | 32,663 / 0.42% |
| Read min/max/mean length | 30 / 100 / 100.17 |
| Duplicated reads (estimated) | 6,312,076 / 80.67% |
| Duplication rate | 33.64% |
| Clipped reads | 739,900 / 9.46% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 212,213,996 / 28.24% |
| Number/percentage of C's | 164,767,419 / 21.93% |
| Number/percentage of T's | 208,084,775 / 27.69% |
| Number/percentage of G's | 166,224,091 / 22.12% |
| Number/percentage of N's | 115,679 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 44.05% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.2427 |
| Standard Deviation | 55.0653 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 50.1 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 35,420.54 |
| Standard Deviation | 1,882,795.51 |
| P25/Median/P75 | 170 / 244 / 334 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.62% |
| Mismatches | 4,582,061 |
| Insertions | 45,867 |
| Mapped reads with at least one insertion | 0.59% |
| Deletions | 30,687 |
| Mapped reads with at least one deletion | 0.4% |
| Homopolymer indels | 44.45% |

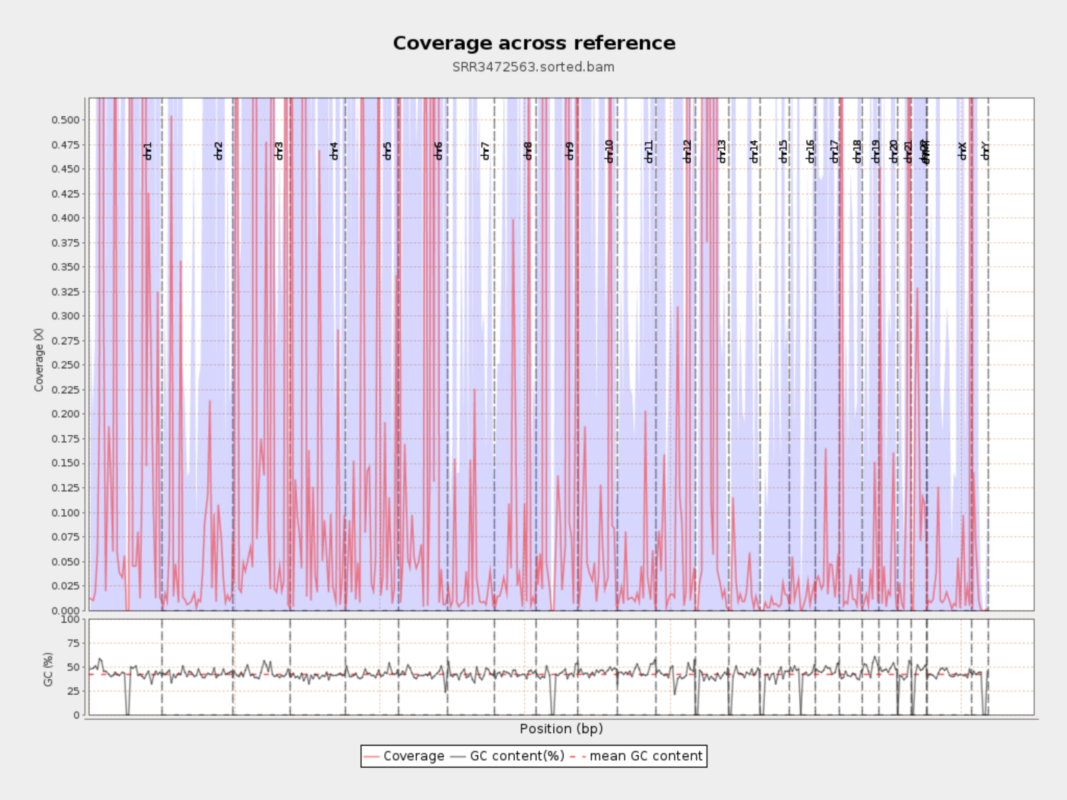
## 2.7. Chromosome stats

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

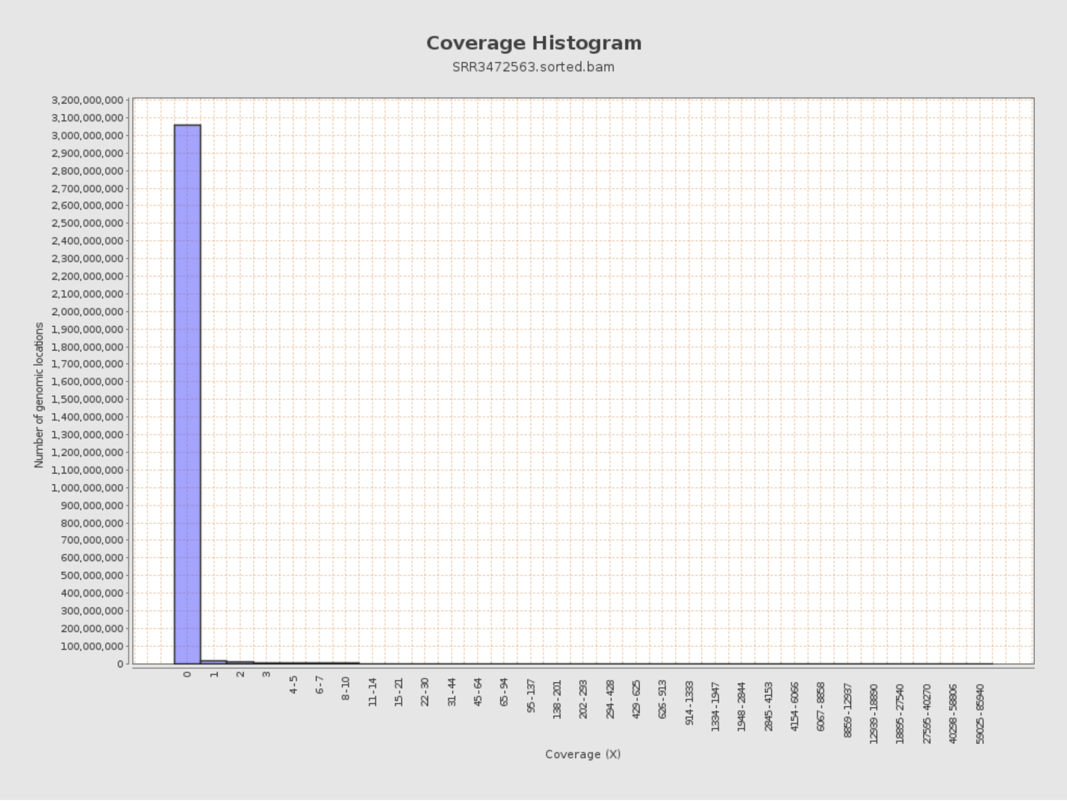
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 222864686 | 0.8941 | 161.2153 |
| chr2 | 243199373 | 15183669 | 0.0624 | 10.4392 |
| chr3 | 198022430 | 66193957 | 0.3343 | 34.1282 |
| chr4 | 191154276 | 33621392 | 0.1759 | 27.7273 |
| chr5 | 180915260 | 23572933 | 0.1303 | 12.73 |
| chr6 | 171115067 | 65708041 | 0.384 | 36.8852 |
| chr7 | 159138663 | 5963176 | 0.0375 | 6.0999 |
| chr8 | 146364022 | 13014500 | 0.0889 | 9.0936 |
| chr9 | 141213431 | 53315544 | 0.3776 | 58.1931 |
| chr10 | 135534747 | 13044893 | 0.0962 | 8.4959 |
| chr11 | 135006516 | 4423337 | 0.0328 | 2.5646 |
| chr12 | 133851895 | 19182267 | 0.1433 | 14.8239 |
| chr13 | 115169878 | 147705618 | 1.2825 | 109.6929 |
| chr14 | 107349540 | 2364044 | 0.022 | 1.3473 |
| chr15 | 102531392 | 872159 | 0.0085 | 0.3711 |
| chr16 | 90354753 | 1717391 | 0.019 | 0.4405 |
| chr17 | 81195210 | 3707483 | 0.0457 | 5.0097 |
| chr18 | 78077248 | 7087809 | 0.0908 | 25.3382 |
| chr19 | 59128983 | 1929856 | 0.0326 | 2.3947 |
| chr20 | 63025520 | 4637463 | 0.0736 | 2.349 |
| chr21 | 48129895 | 7394058 | 0.1536 | 18.7247 |
| chr22 | 51304566 | 6769990 | 0.132 | 5.461 |
| chrMT | 16571 | 860 | 0.0519 | 0.2482 |
| chrX | 155270560 | 29483266 | 0.1899 | 39.9903 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1715317 | 0.0289 | 1.7163 |

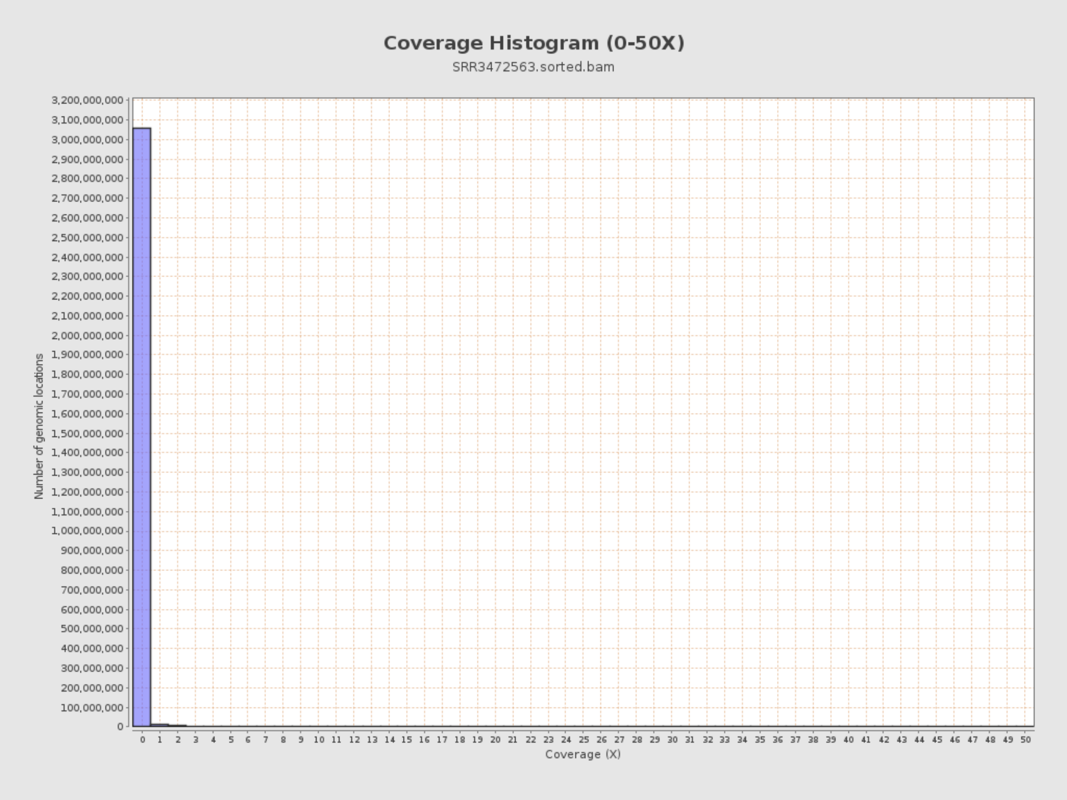
# 3. Results : Coverage across reference



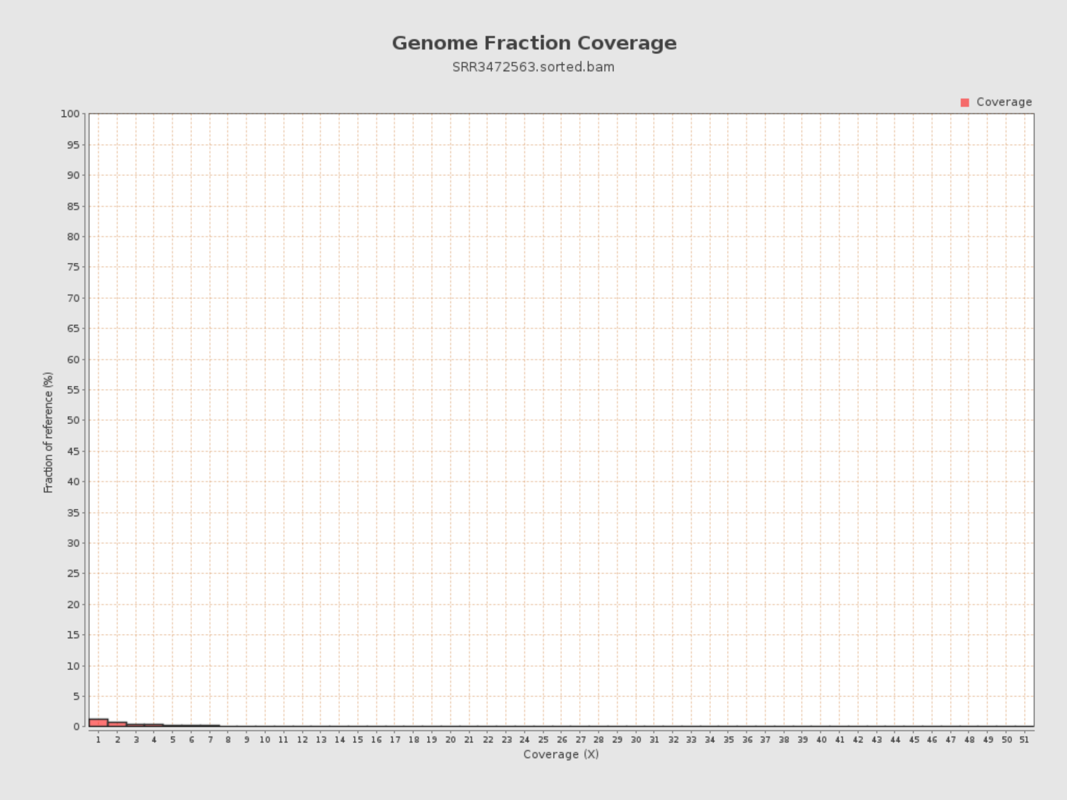
# 4. Results : Coverage Histogram



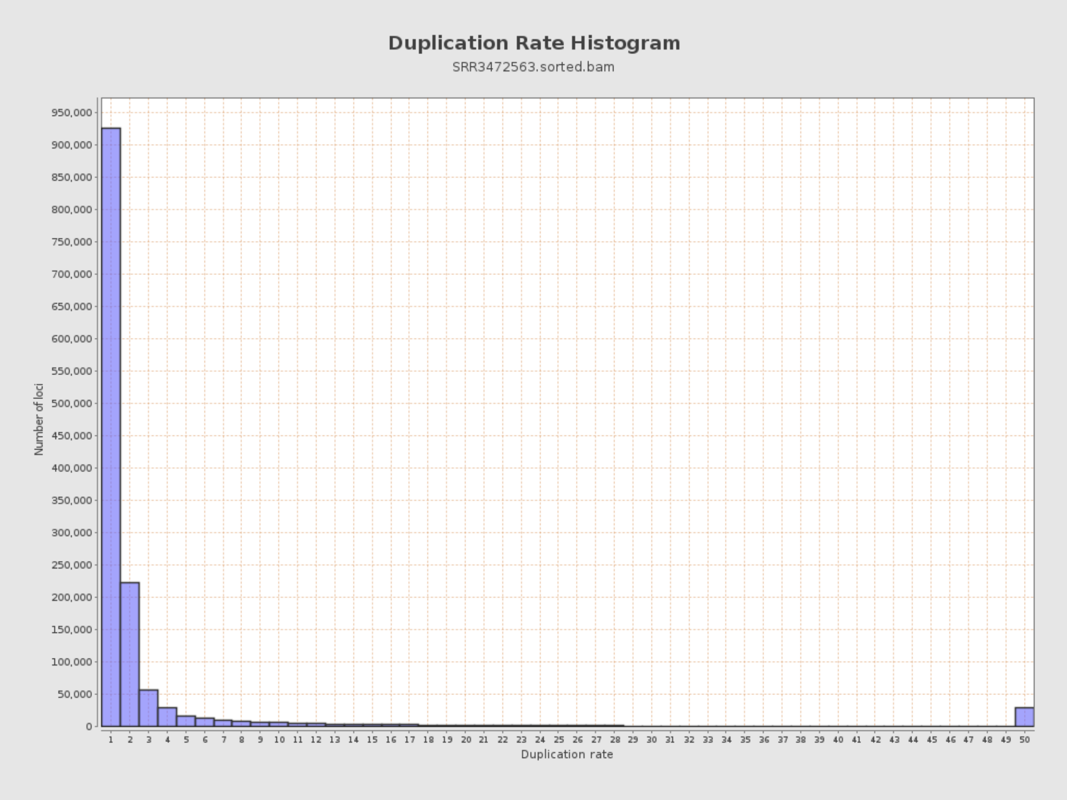
# 5. Results : Coverage Histogram (0-50X)



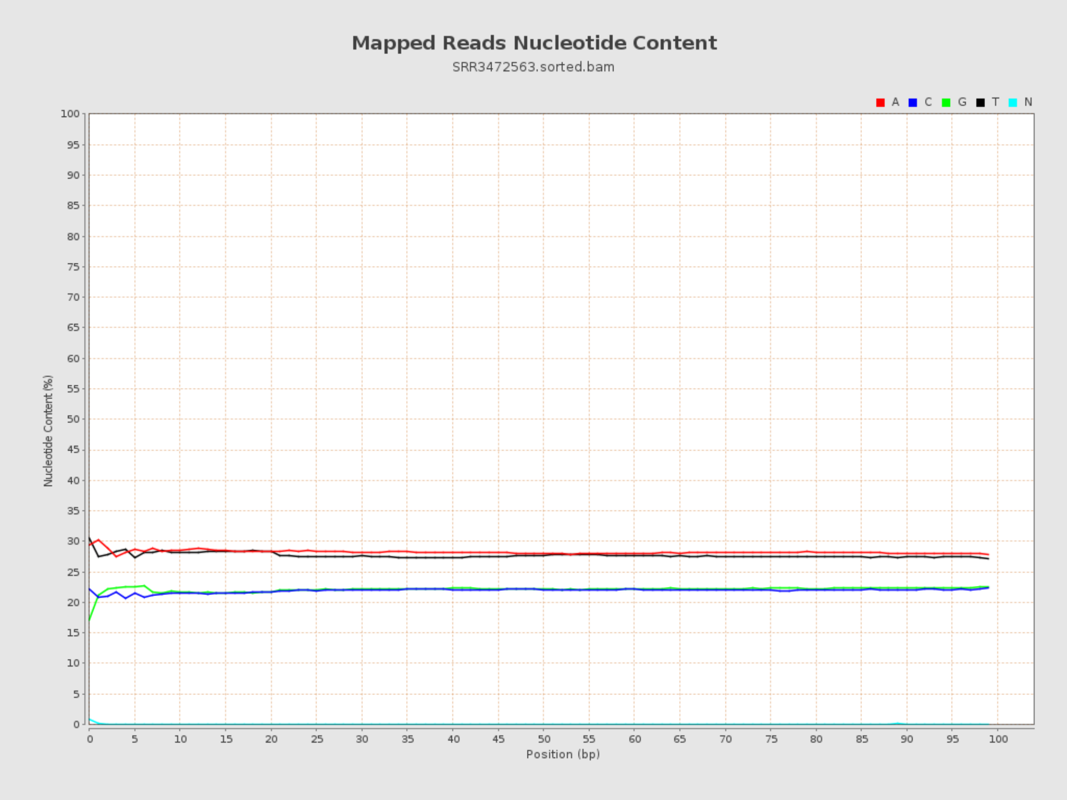
# 6. Results : Genome Fraction Coverage



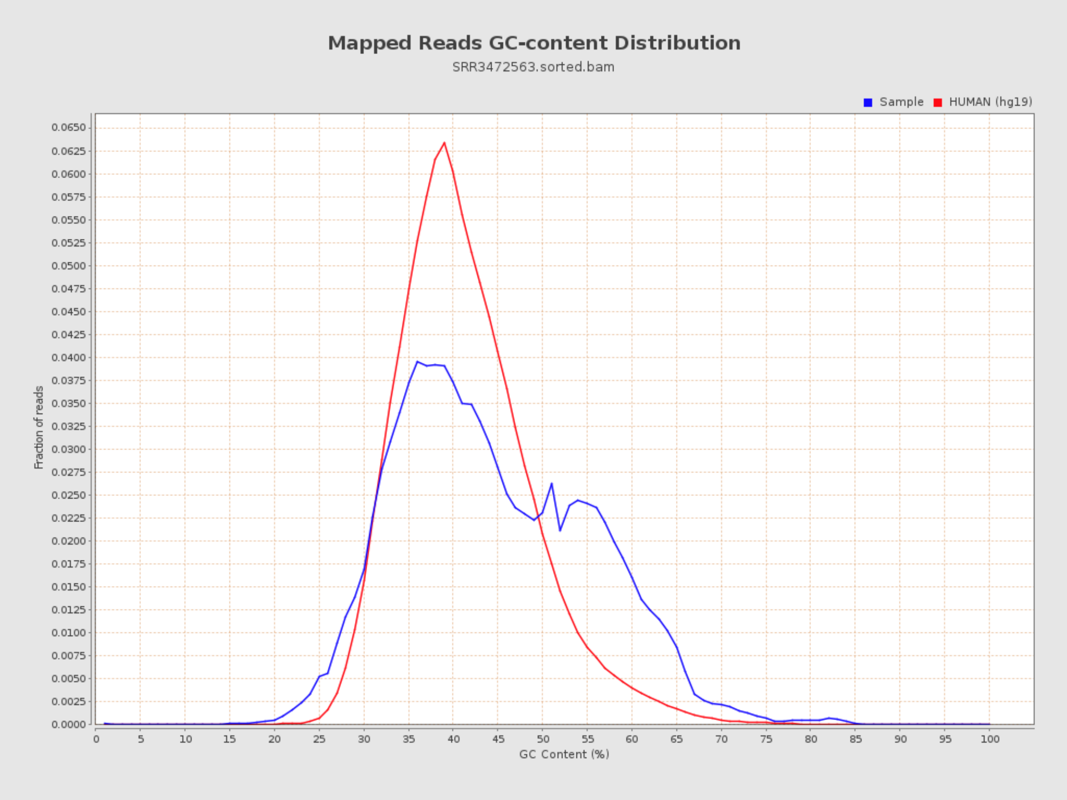
# 7. Results : Duplication Rate Histogram



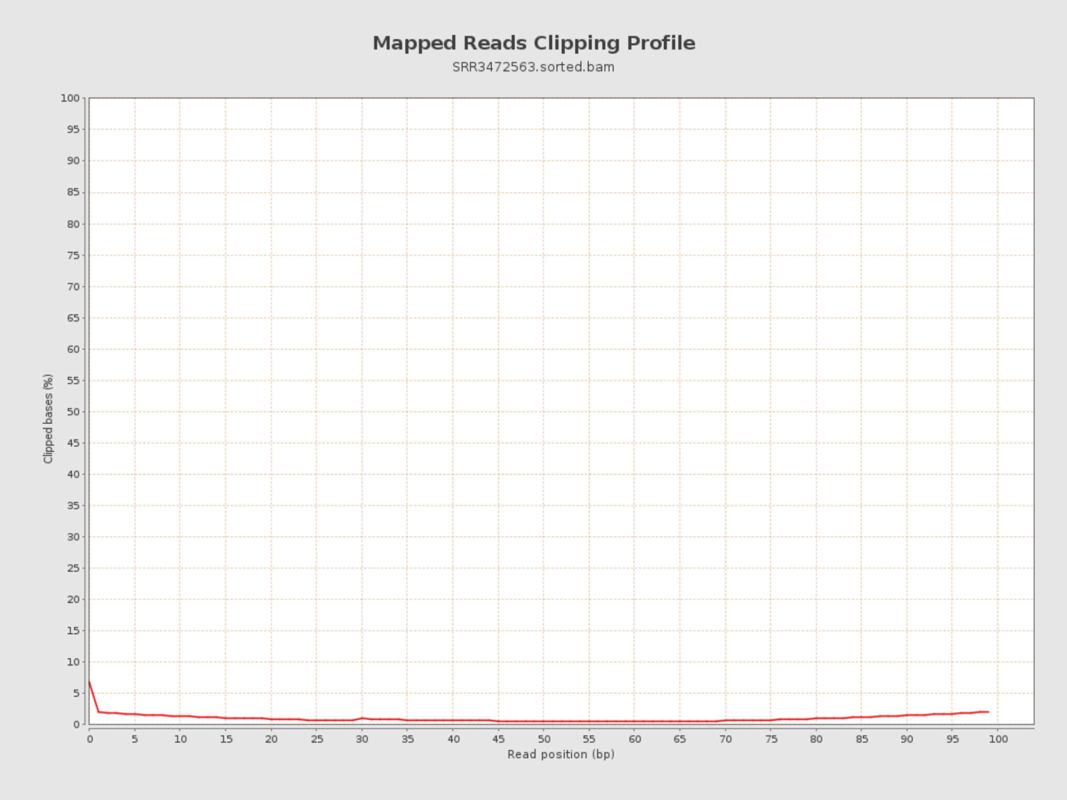
# 8. Results : Mapped Reads Nucleotide Content



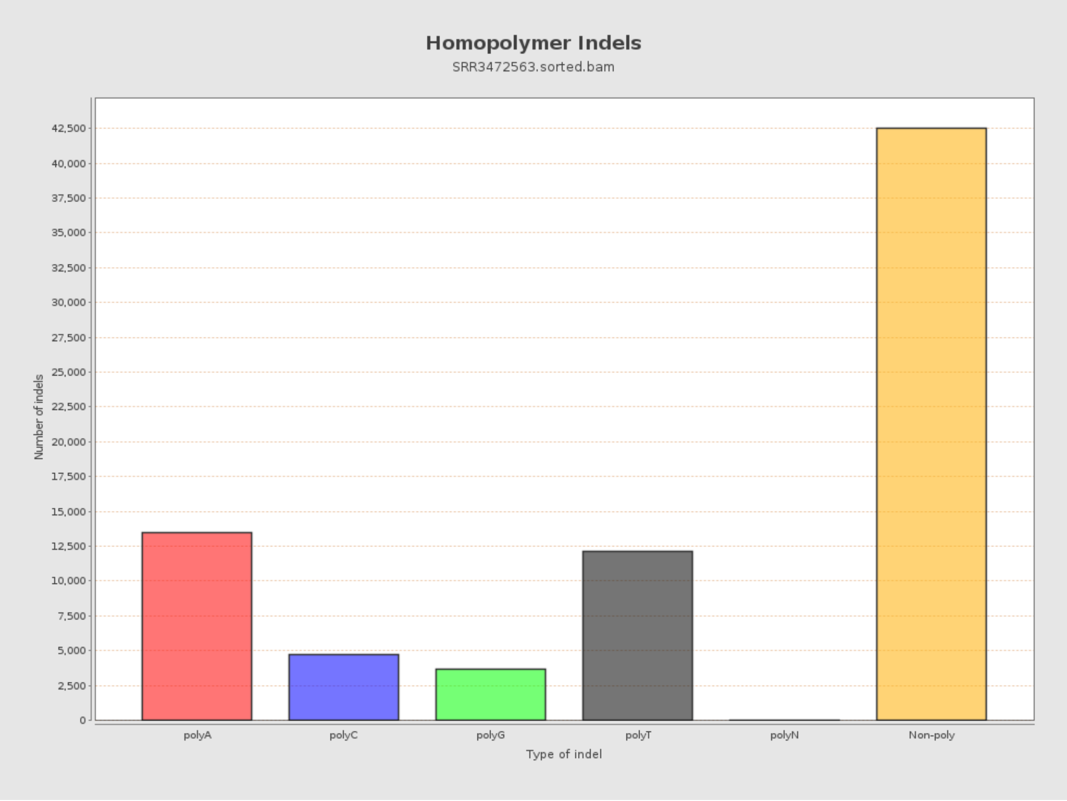
# 9. Results : Mapped Reads GC-content Distribution



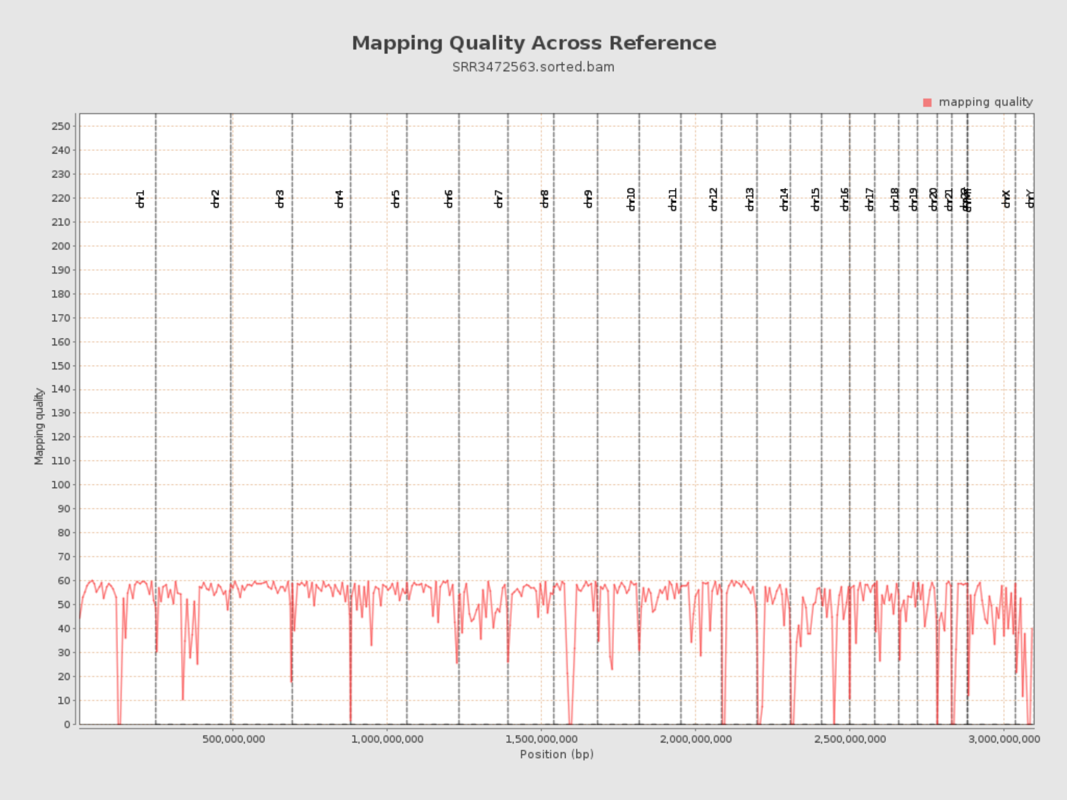
# 10. Results : Mapped Reads Clipping Profile



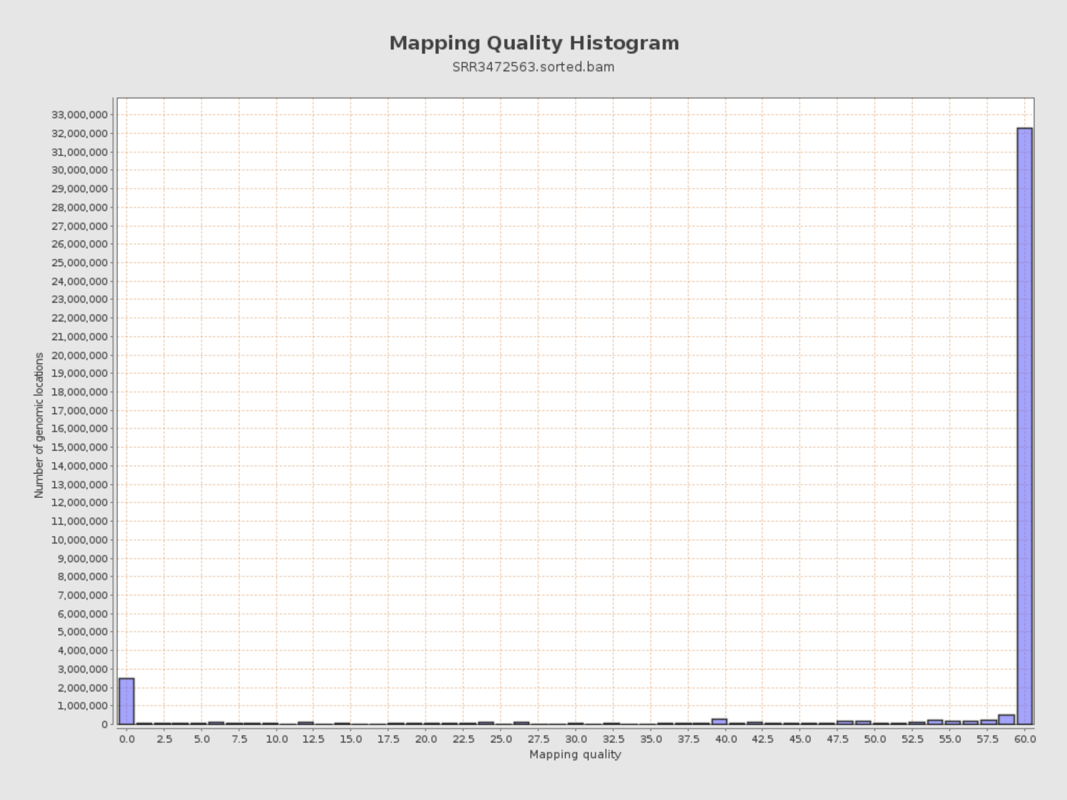
# 11. Results : Homopolymer Indels



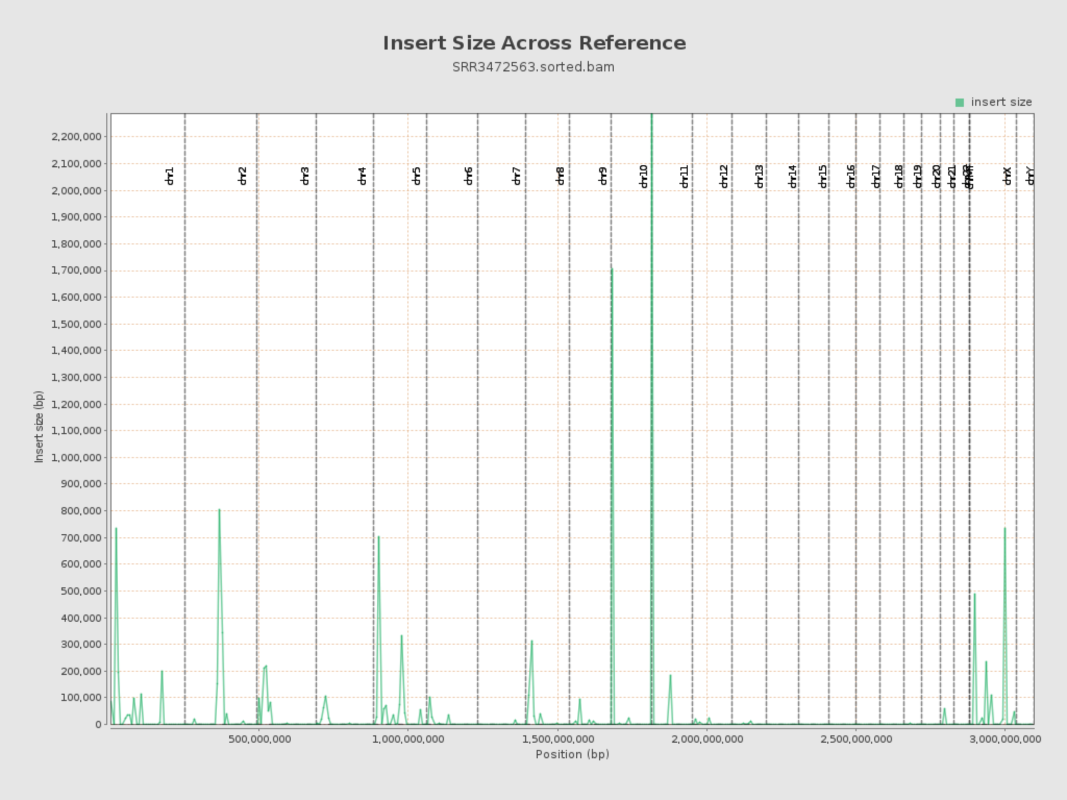
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram