# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/21 10:12:38*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR8438275.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_SRR8438275 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8438275_1.fastq.gz SRR8438275_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Dec 21 10:12:36 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR8438275.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,018,290,224 |
| Mapped reads | 1,014,020,573 / 99.58% |
| Unmapped reads | 4,269,651 / 0.42% |
| Mapped paired reads | 1,014,020,573 / 99.58% |
| Mapped reads, first in pair | 507,336,618 / 49.82% |
| Mapped reads, second in pair | 506,683,955 / 49.76% |
| Mapped reads, both in pair | 1,011,970,618 / 99.38% |
| Mapped reads, singletons | 2,049,955 / 0.2% |
| Secondary alignments | 0 |
| Supplementary alignments | 12,041,453 / 1.18% |
| Read min/max/mean length | 30 / 149 / 115.24 |
| Duplicated reads (estimated) | 419,315,114 / 41.18% |
| Duplication rate | 41.35% |
| Clipped reads | 234,520,649 / 23.03% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 33,813,235,207 / 30.38% |
| Number/percentage of C's | 22,048,259,577 / 19.81% |
| Number/percentage of T's | 33,007,992,930 / 29.65% |
| Number/percentage of G's | 22,443,239,153 / 20.16% |
| Number/percentage of N's | 294,544 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 39.97% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 35.966 |
| Standard Deviation | 460.0129 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.08 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 90,028.61 |
| Standard Deviation | 3,131,405.42 |
| P25/Median/P75 | 76 / 124 / 200 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.32% |
| Mismatches | 337,359,124 |
| Insertions | 15,410,032 |
| Mapped reads with at least one insertion | 1.5% |
| Deletions | 11,262,586 |
| Mapped reads with at least one deletion | 1.1% |
| Homopolymer indels | 47.36% |

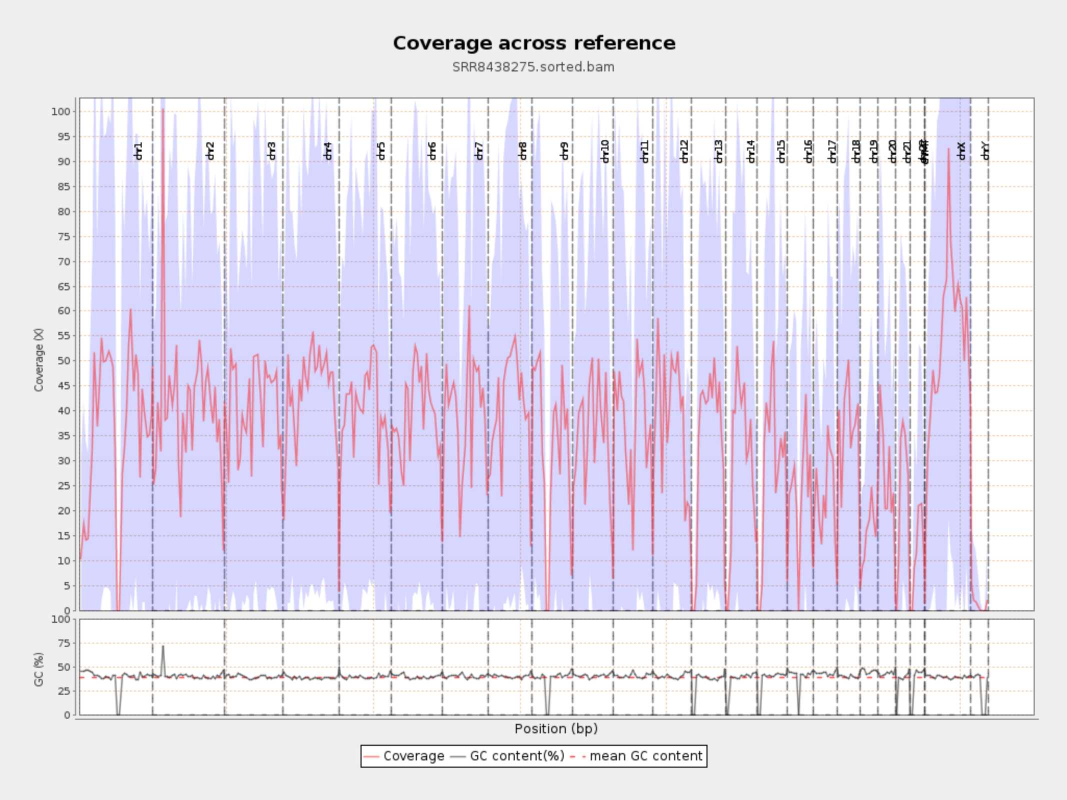
## 2.7. Chromosome stats

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

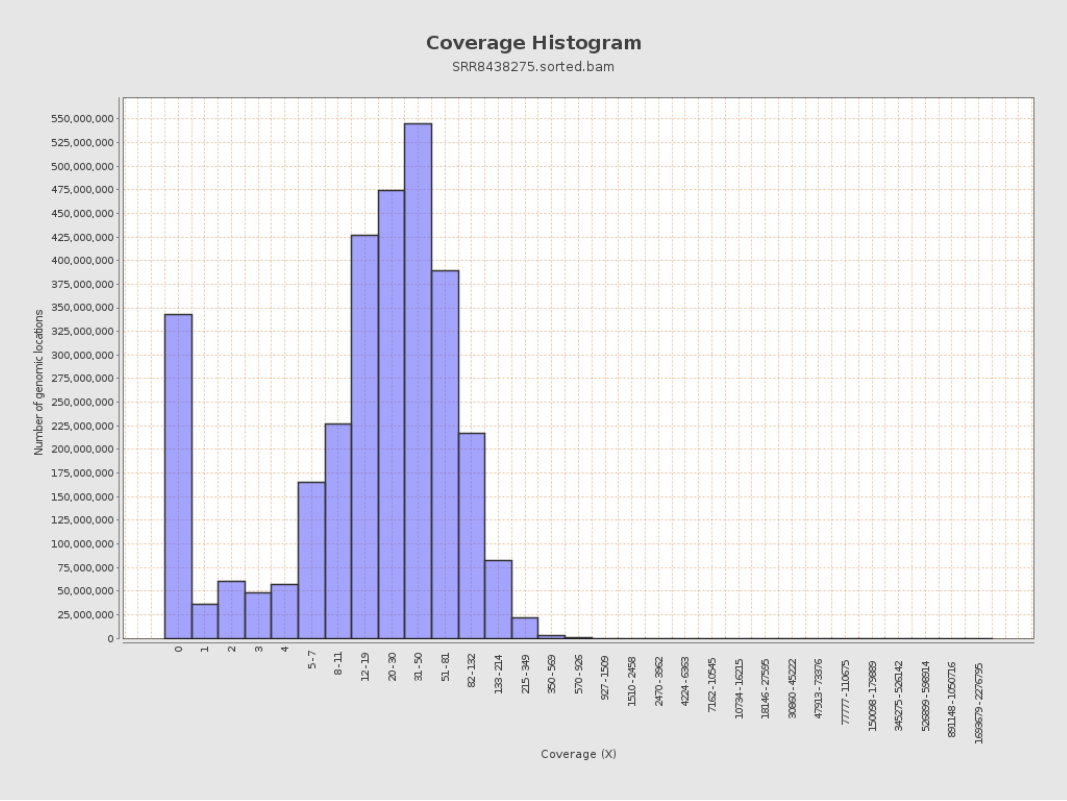
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 9062202331 | 36.3578 | 46.0175 |
| chr2 | 243199373 | 9959111834 | 40.9504 | 1,634.6294 |
| chr3 | 198022430 | 8175257972 | 41.2845 | 42.2357 |
| chr4 | 191154276 | 8431198075 | 44.1068 | 43.9912 |
| chr5 | 180915260 | 7137430261 | 39.4518 | 41.2996 |
| chr6 | 171115067 | 6800212387 | 39.7406 | 41.7058 |
| chr7 | 159138663 | 6244736141 | 39.2408 | 44.3316 |
| chr8 | 146364022 | 6043800683 | 41.2929 | 43.1102 |
| chr9 | 141213431 | 4522265307 | 32.0243 | 41.8991 |
| chr10 | 135534747 | 4830213711 | 35.6382 | 41.717 |
| chr11 | 135006516 | 5033208736 | 37.2812 | 43.0708 |
| chr12 | 133851895 | 5185460189 | 38.7403 | 44.2339 |
| chr13 | 115169878 | 3884162563 | 33.7255 | 39.7397 |
| chr14 | 107349540 | 3237724828 | 30.1606 | 39.6958 |
| chr15 | 102531392 | 2947849213 | 28.7507 | 40.3445 |
| chr16 | 90354753 | 2019803098 | 22.3541 | 31.1496 |
| chr17 | 81195210 | 1824180925 | 22.4666 | 31.034 |
| chr18 | 78077248 | 2943023352 | 37.6937 | 39.782 |
| chr19 | 59128983 | 914154824 | 15.4604 | 24.1521 |
| chr20 | 63025520 | 1714258142 | 27.1994 | 36.2973 |
| chr21 | 48129895 | 1174786448 | 24.4087 | 35.0411 |
| chr22 | 51304566 | 592986486 | 11.5582 | 23.8273 |
| chrMT | 16571 | 23522 | 1.4195 | 3.4725 |
| chrX | 155270560 | 8578900580 | 55.2513 | 58.0639 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 82682729 | 1.3926 | 8.3272 |

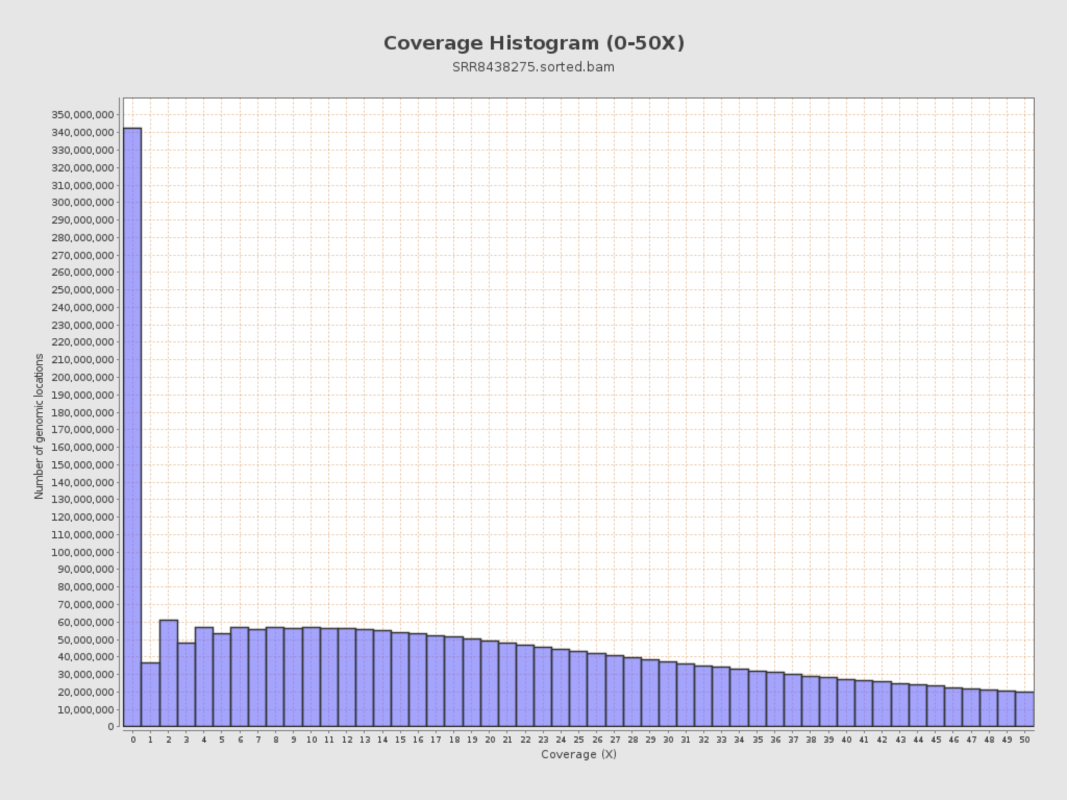
# 3. Results : Coverage across reference



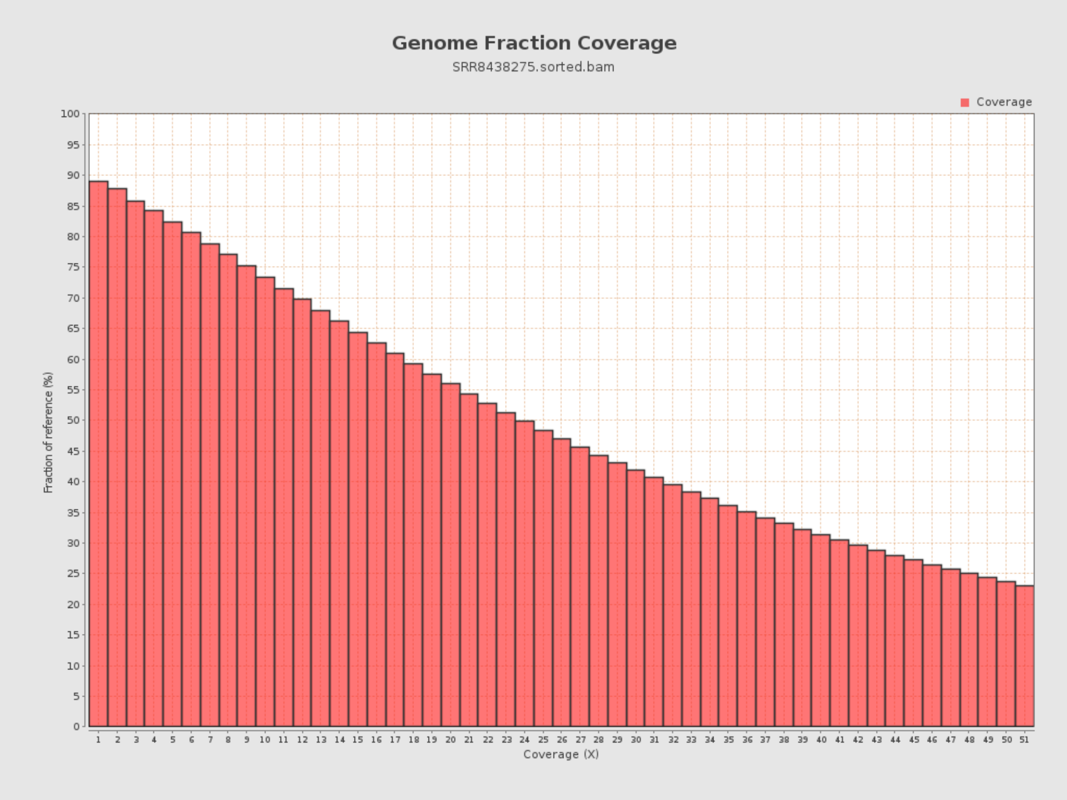
# 4. Results : Coverage Histogram



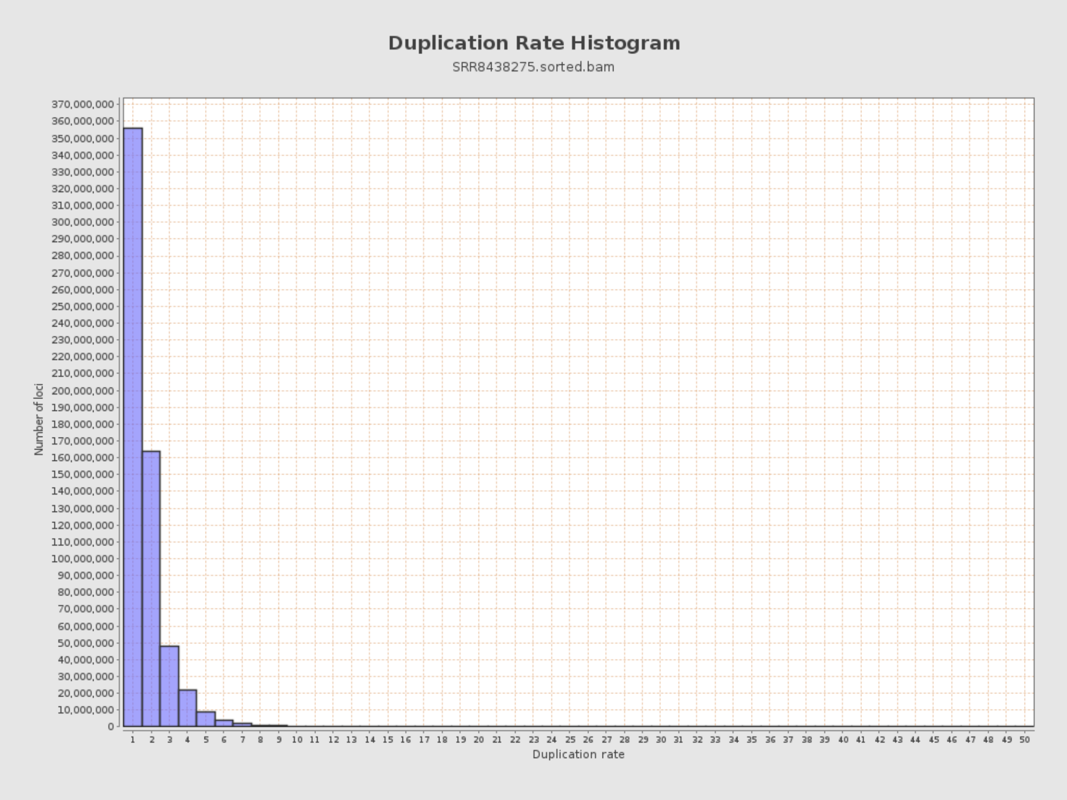
# 5. Results : Coverage Histogram (0-50X)



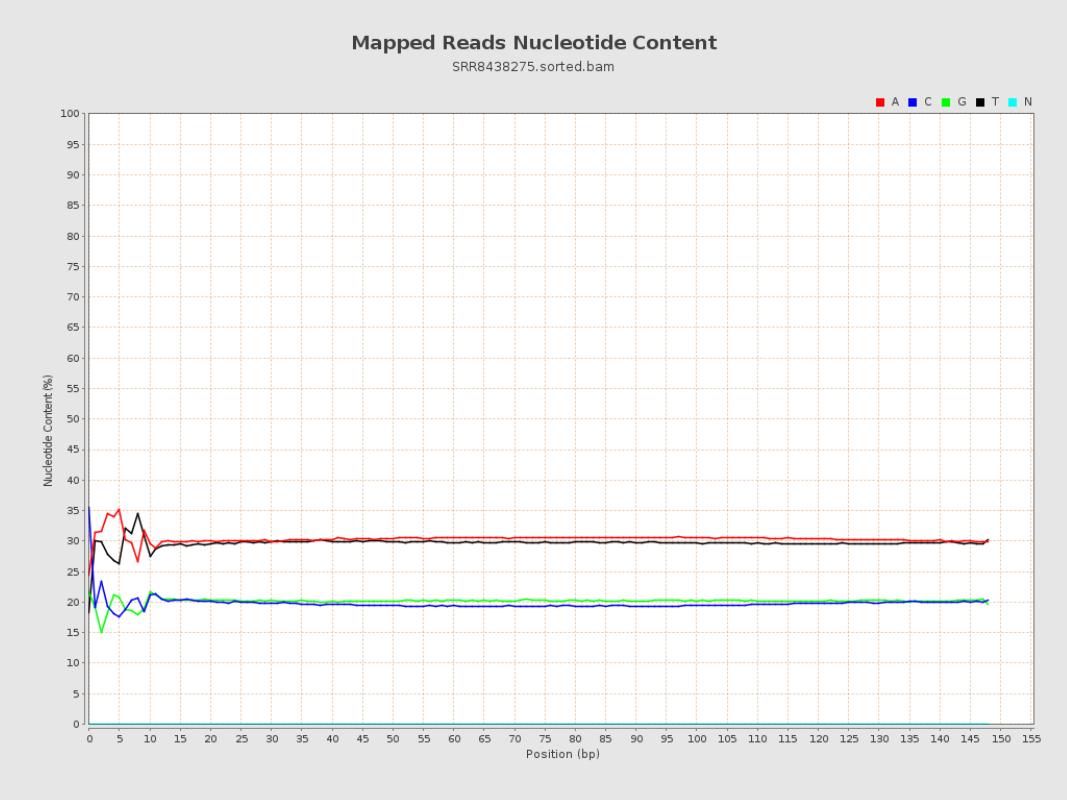
# 6. Results : Genome Fraction Coverage



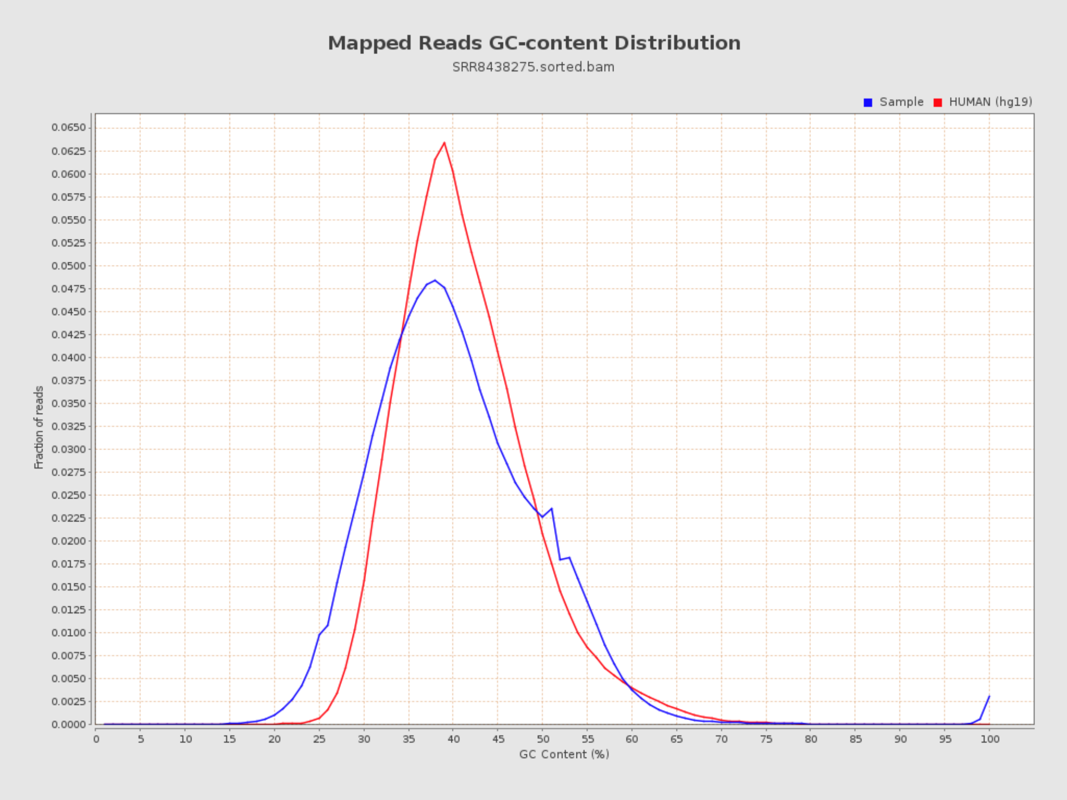
# 7. Results : Duplication Rate Histogram



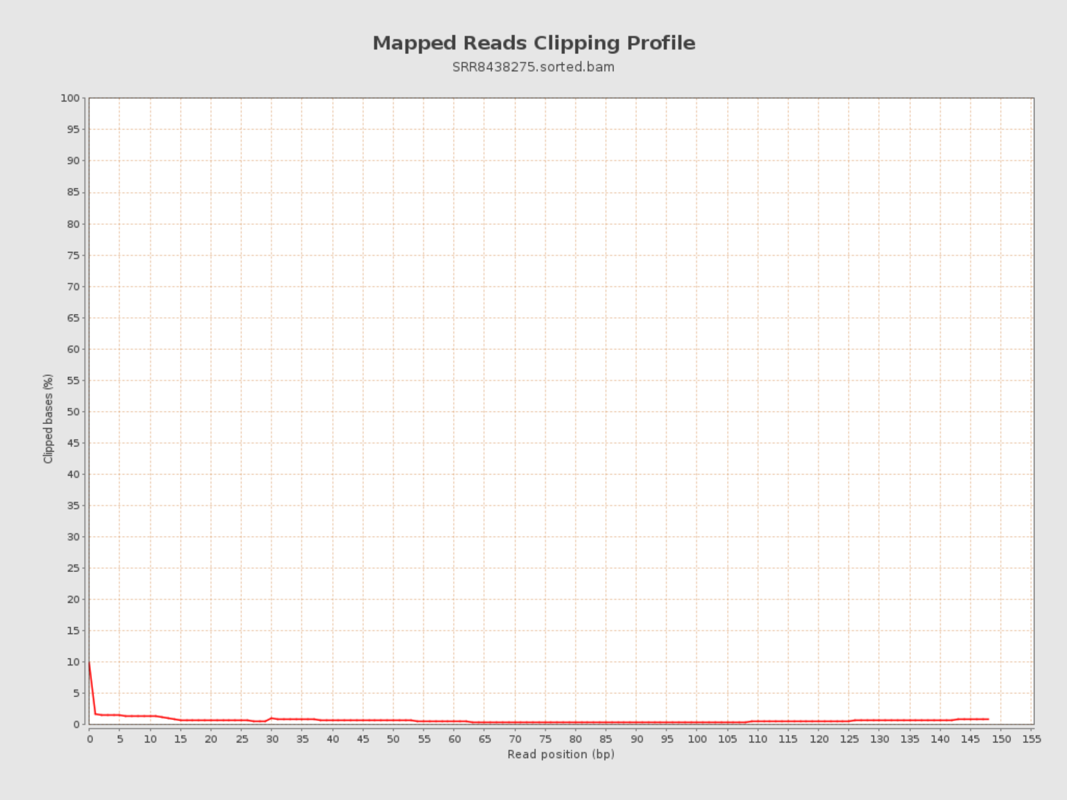
# 8. Results : Mapped Reads Nucleotide Content



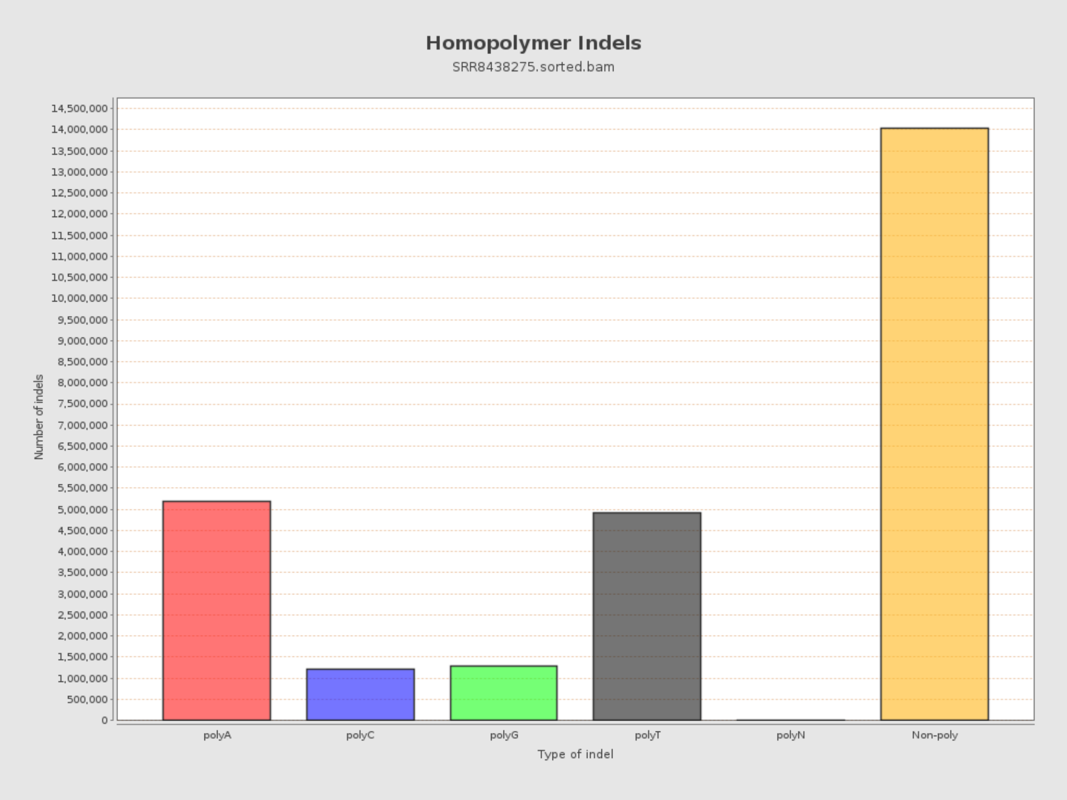
# 9. Results : Mapped Reads GC-content Distribution



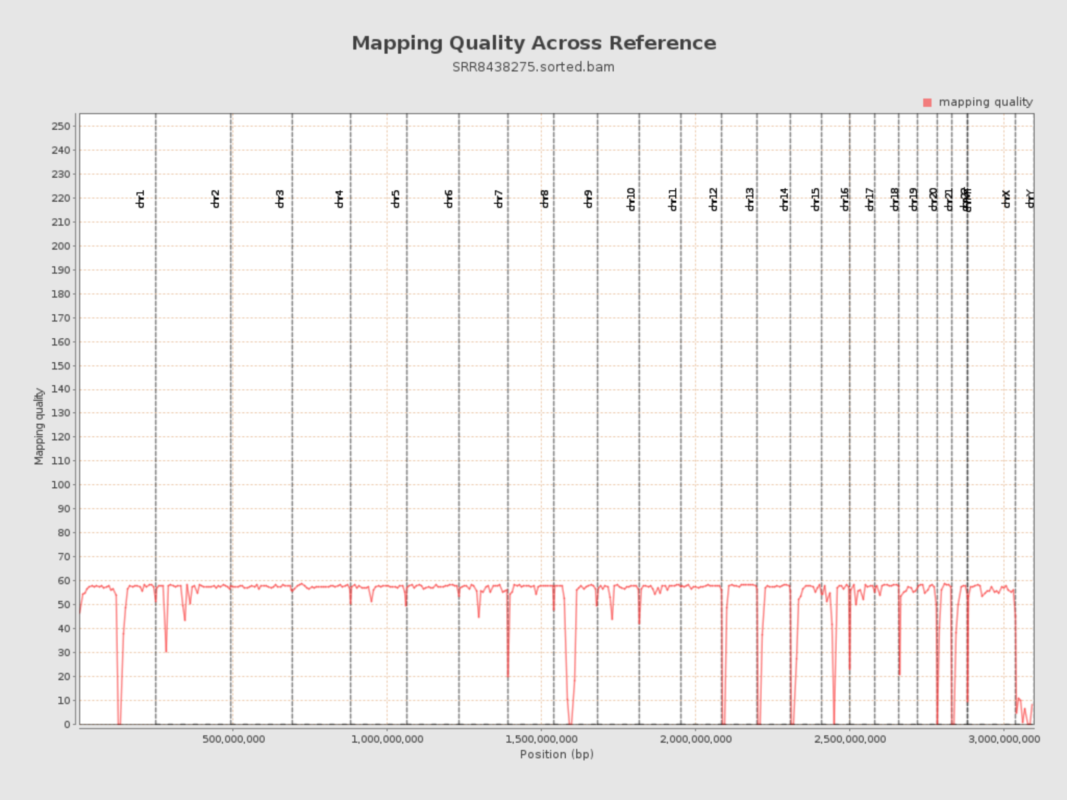
# 10. Results : Mapped Reads Clipping Profile



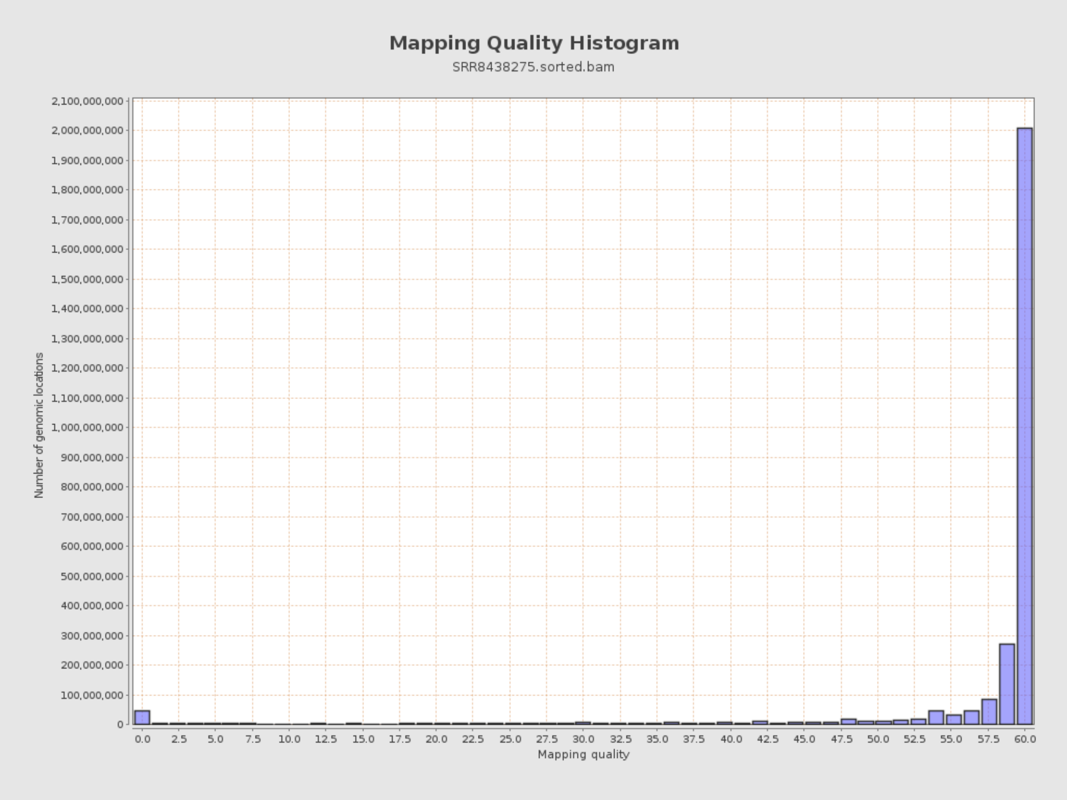
# 11. Results : Homopolymer Indels



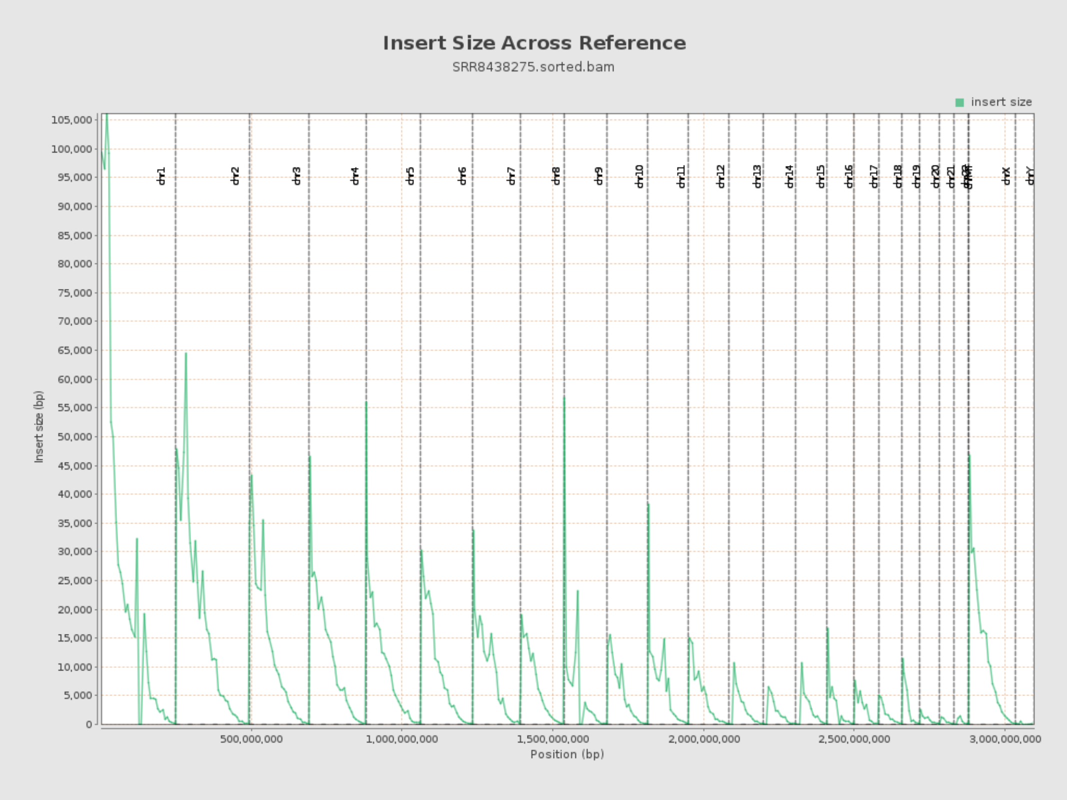
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram