# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 15:42:37*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR975215.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_SRR975215 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR975215_1.fastq.gz SRR975215_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 15:42:37 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR975215.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,320,184 |
| Mapped reads | 4,275,464 / 98.96% |
| Unmapped reads | 44,720 / 1.04% |
| Mapped paired reads | 4,275,464 / 98.96% |
| Mapped reads, first in pair | 2,145,220 / 49.66% |
| Mapped reads, second in pair | 2,130,244 / 49.31% |
| Mapped reads, both in pair | 4,257,764 / 98.56% |
| Mapped reads, singletons | 17,700 / 0.41% |
| Secondary alignments | 0 |
| Supplementary alignments | 58,060 / 1.34% |
| Read min/max/mean length | 30 / 151 / 151.68 |
| Duplicated reads (estimated) | 650,934 / 15.07% |
| Duplication rate | 12.9% |
| Clipped reads | 1,699,711 / 39.34% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 182,382,194 / 29.85% |
| Number/percentage of C's | 122,201,312 / 20% |
| Number/percentage of T's | 180,798,013 / 29.59% |
| Number/percentage of G's | 125,536,597 / 20.55% |
| Number/percentage of N's | 57,929 / 0.01% |
| | |

| | |
|---|---|
| GC Percentage | 40.55% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1975 |
| Standard Deviation | 2.5131 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.62 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 60,547.85 |
| Standard Deviation | 2,358,464.28 |
| P25/Median/P75 | 146 / 174 / 215 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.91% |
| Mismatches | 5,266,074 |
| Insertions | 112,413 |
| Mapped reads with at least one insertion | 2.48% |
| Deletions | 220,478 |
| Mapped reads with at least one deletion | 4.95% |
| Homopolymer indels | 47.42% |

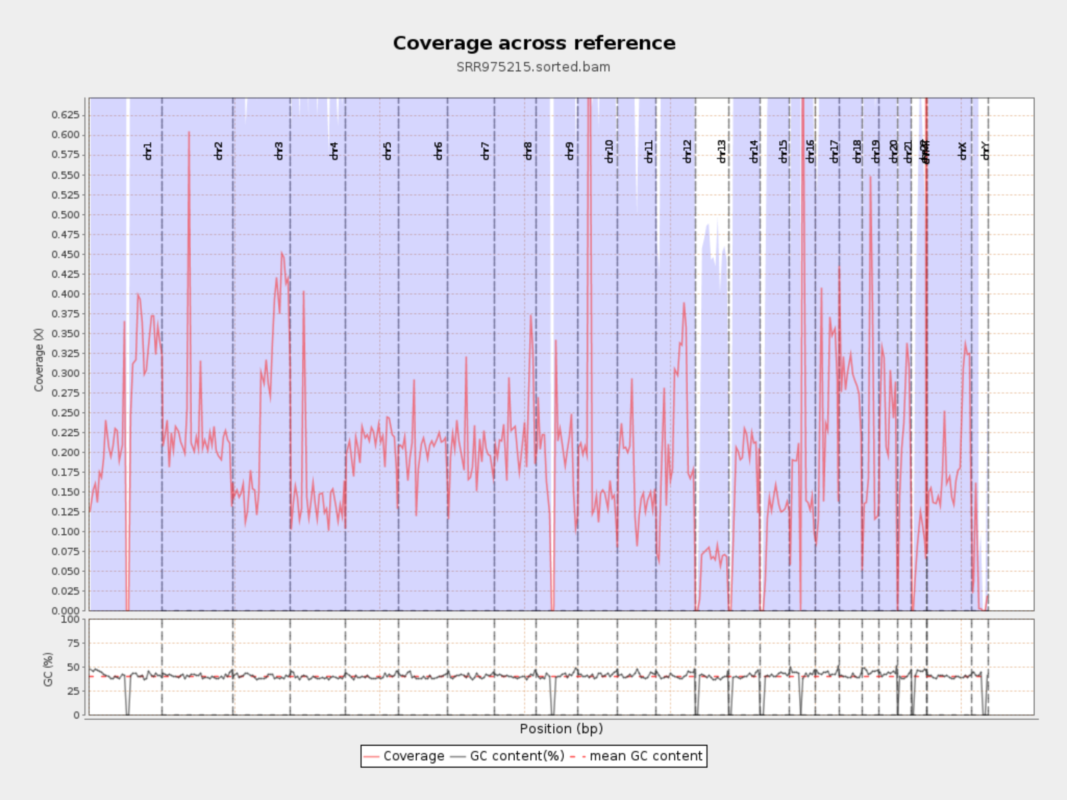
## 2.7. Chromosome stats

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

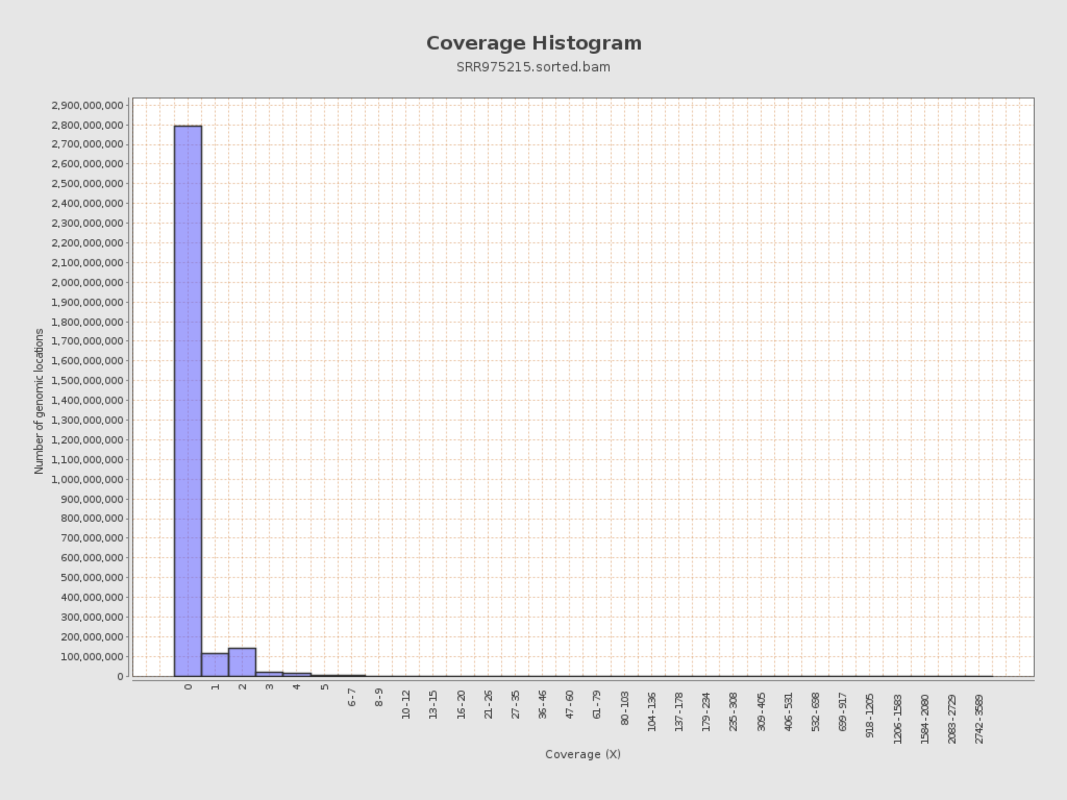
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 61719310 | 0.2476 | 2.7036 |
| chr2 | 243199373 | 55353065 | 0.2276 | 2.6882 |
| chr3 | 198022430 | 50884084 | 0.257 | 0.8323 |
| chr4 | 191154276 | 27606276 | 0.1444 | 1.7781 |
| chr5 | 180915260 | 38231786 | 0.2113 | 0.7006 |
| chr6 | 171115067 | 35155490 | 0.2054 | 1.1361 |
| chr7 | 159138663 | 31982021 | 0.201 | 2.7233 |
| chr8 | 146364022 | 33779233 | 0.2308 | 1.0398 |
| chr9 | 141213431 | 25883133 | 0.1833 | 3.4639 |
| chr10 | 135534747 | 27838735 | 0.2054 | 7.0212 |
| chr11 | 135006516 | 22291285 | 0.1651 | 2.4023 |
| chr12 | 133851895 | 29725630 | 0.2221 | 0.7283 |
| chr13 | 115169878 | 6728063 | 0.0584 | 0.347 |
| chr14 | 107349540 | 17870104 | 0.1665 | 0.6381 |
| chr15 | 102531392 | 11024176 | 0.1075 | 0.4837 |
| chr16 | 90354753 | 17370677 | 0.1922 | 4.0636 |
| chr17 | 81195210 | 20451075 | 0.2519 | 3.9279 |
| chr18 | 78077248 | 23076370 | 0.2956 | 3.0399 |
| chr19 | 59128983 | 12801083 | 0.2165 | 1.6737 |
| chr20 | 63025520 | 16354805 | 0.2595 | 1.0282 |
| chr21 | 48129895 | 10227782 | 0.2125 | 1.1189 |
| chr22 | 51304566 | 3587763 | 0.0699 | 0.4025 |
| chrMT | 16571 | 147169 | 8.8811 | 5.8977 |
| chrX | 155270560 | 29516265 | 0.1901 | 1.0333 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1811557 | 0.0305 | 2.3592 |

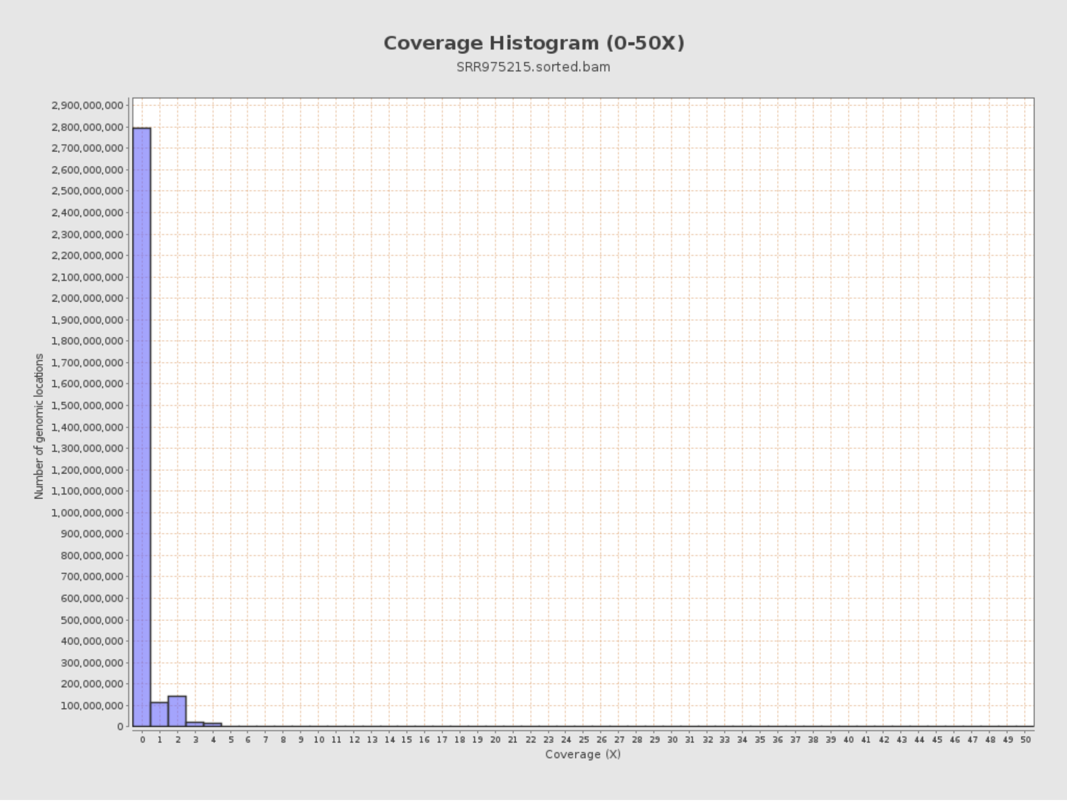
# 3. Results : Coverage across reference



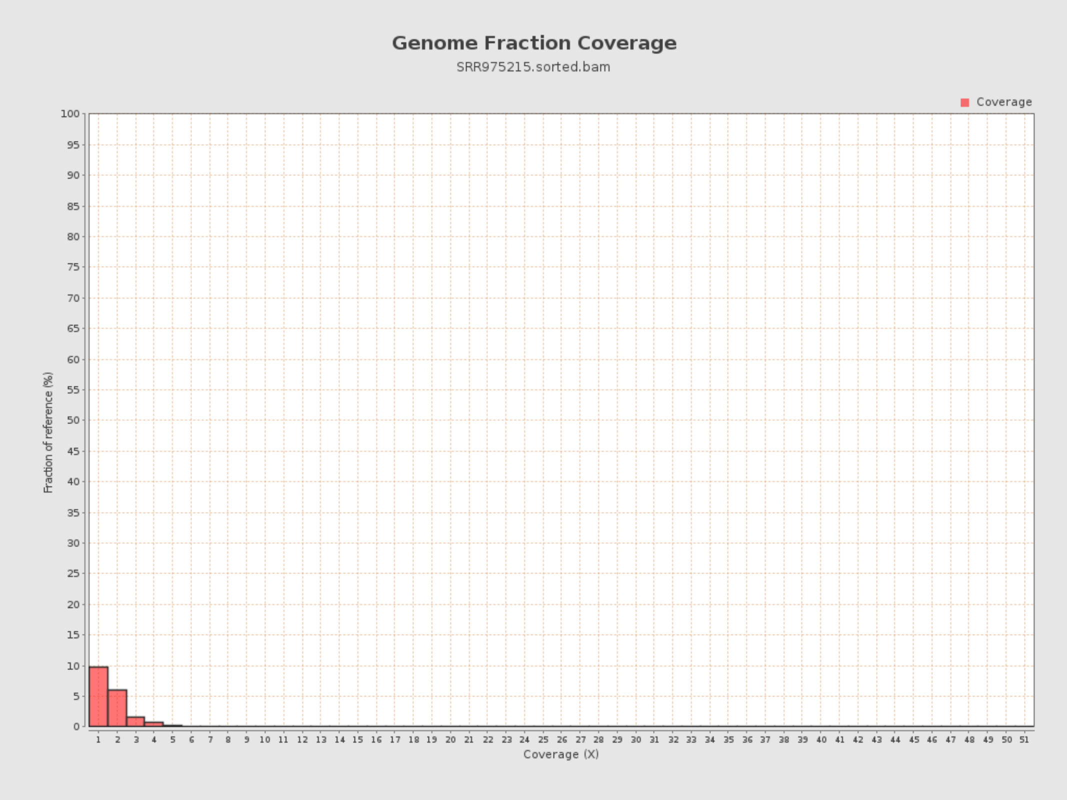
# 4. Results : Coverage Histogram



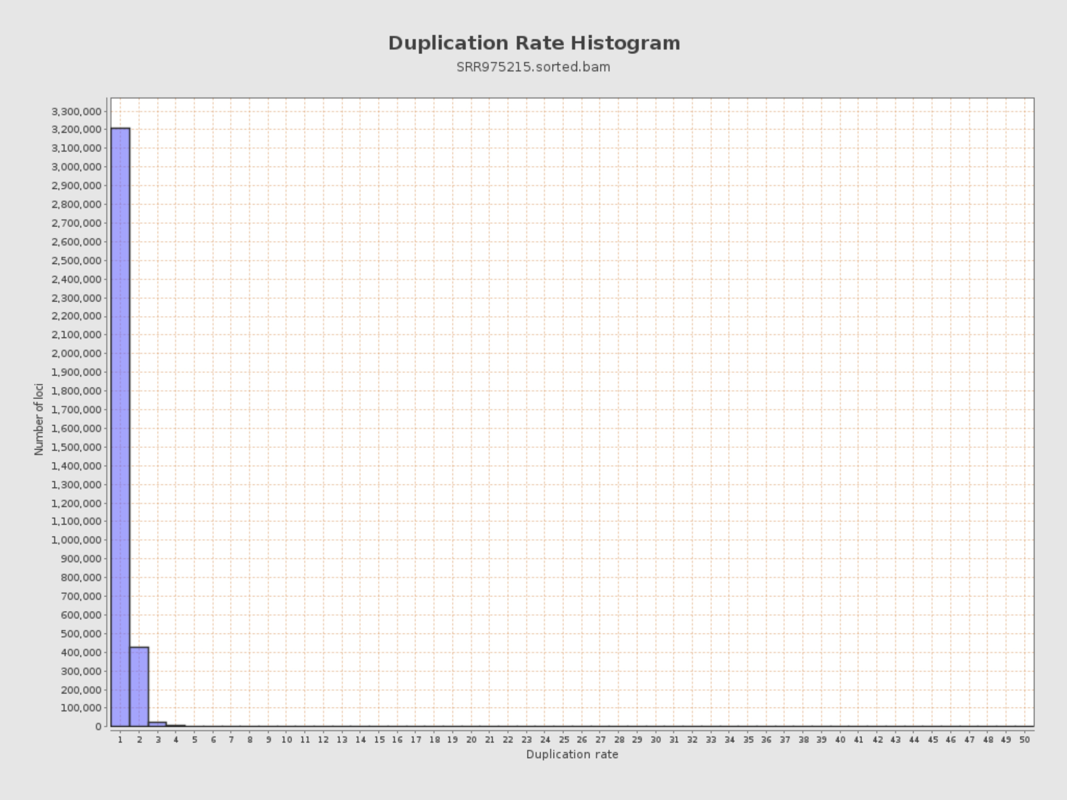
# 5. Results : Coverage Histogram (0-50X)



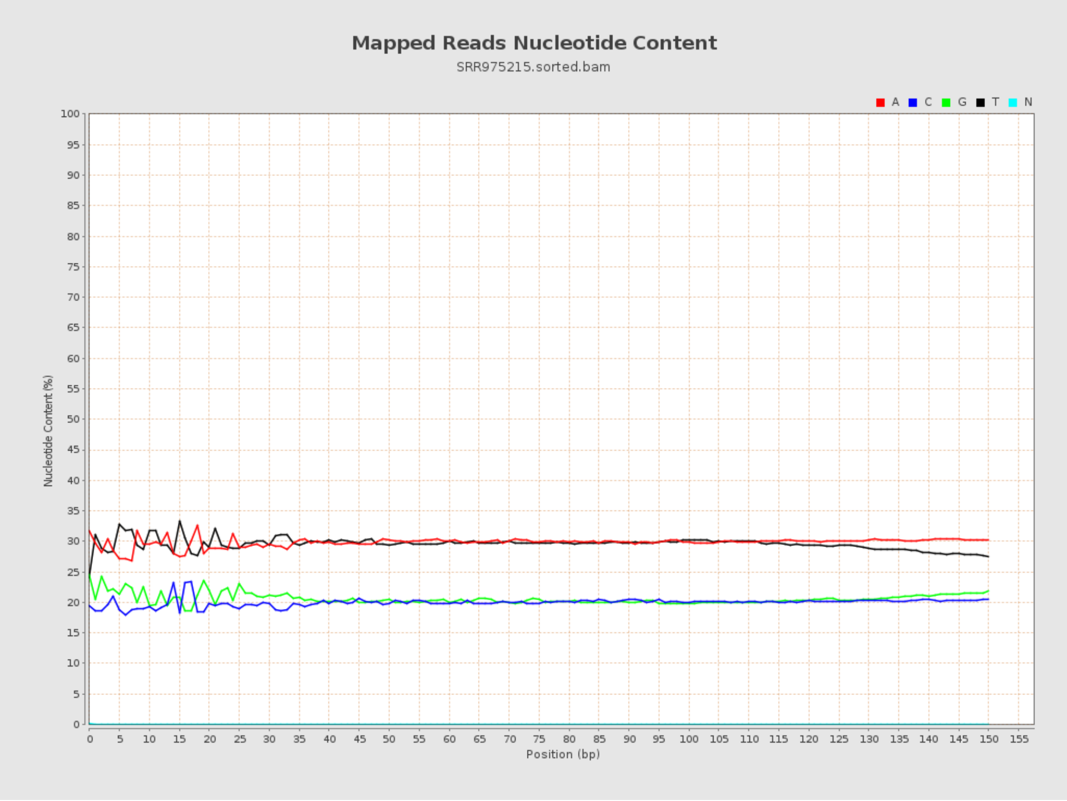
# 6. Results : Genome Fraction Coverage



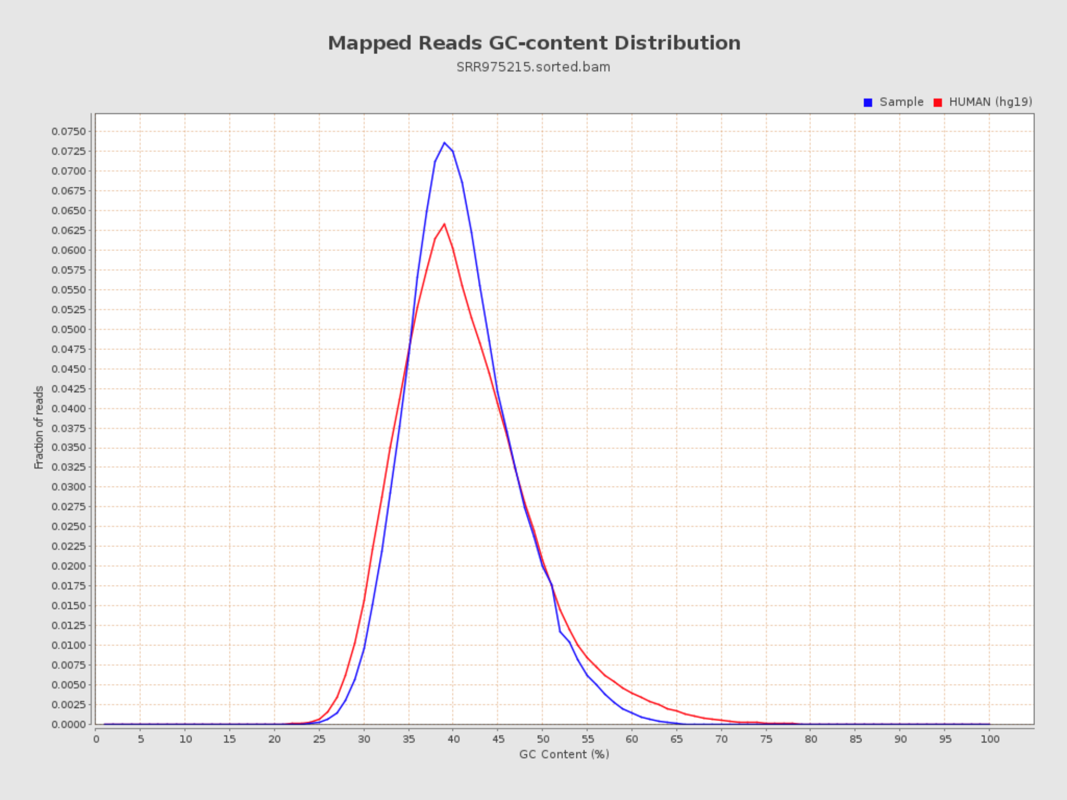
# 7. Results : Duplication Rate Histogram



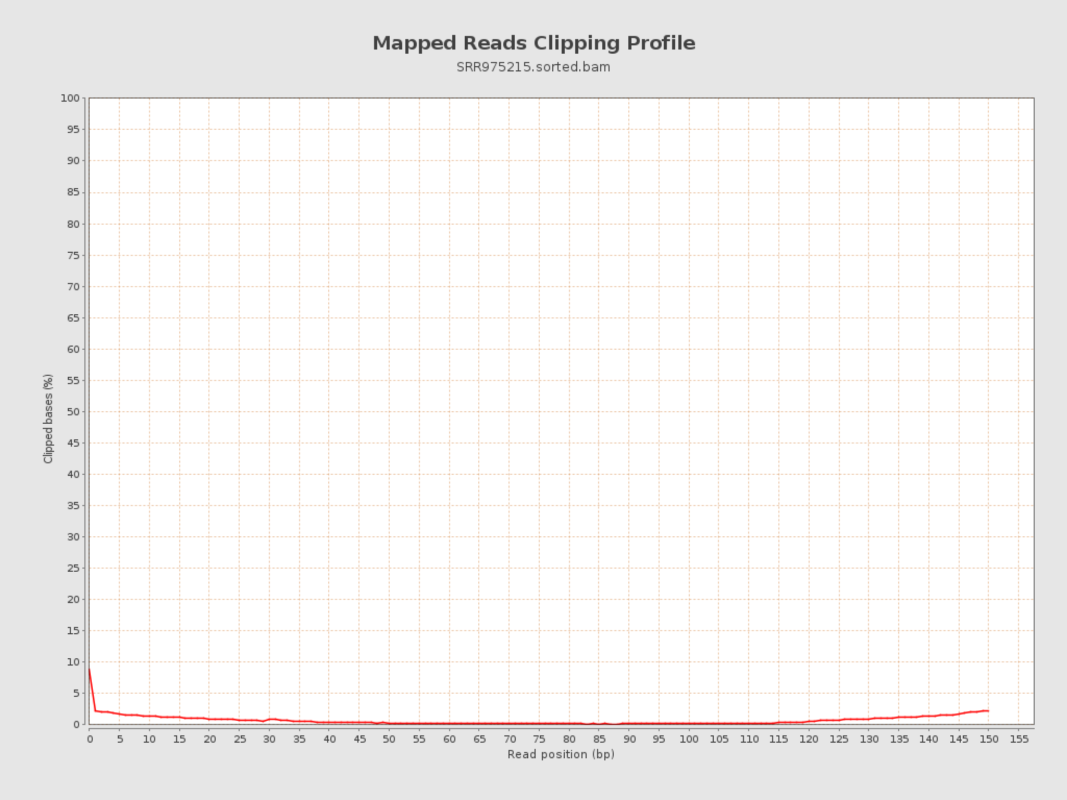
# 8. Results : Mapped Reads Nucleotide Content



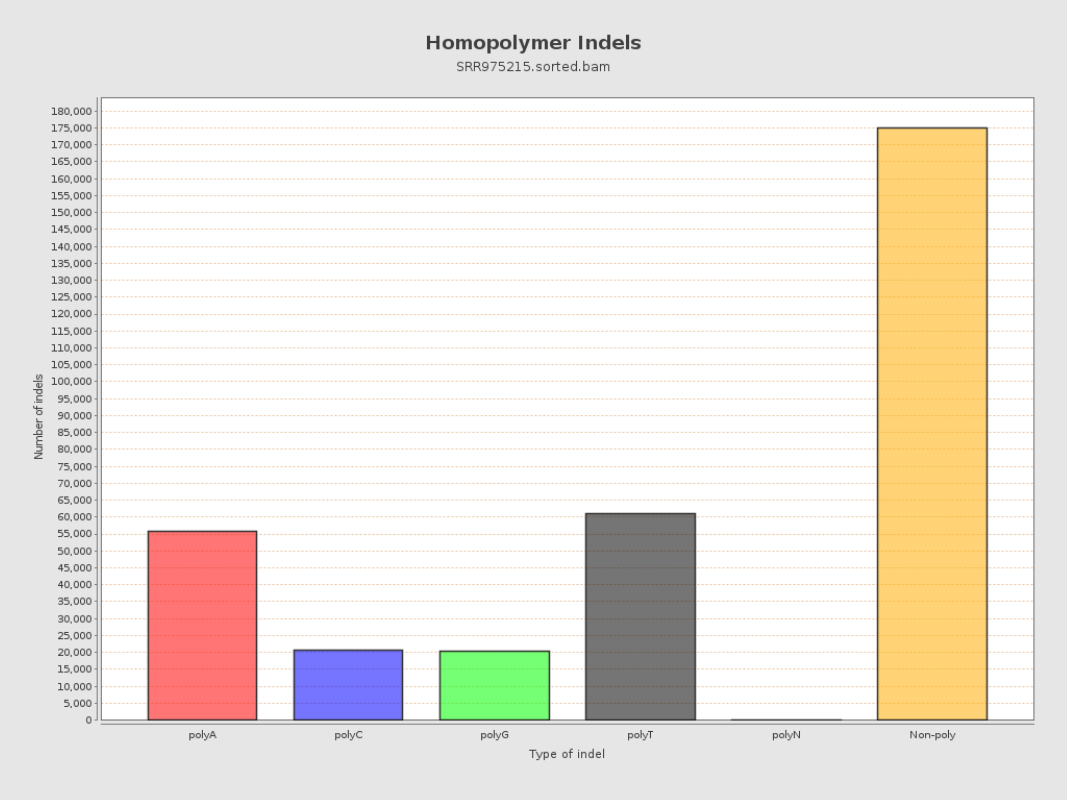
# 9. Results : Mapped Reads GC-content Distribution



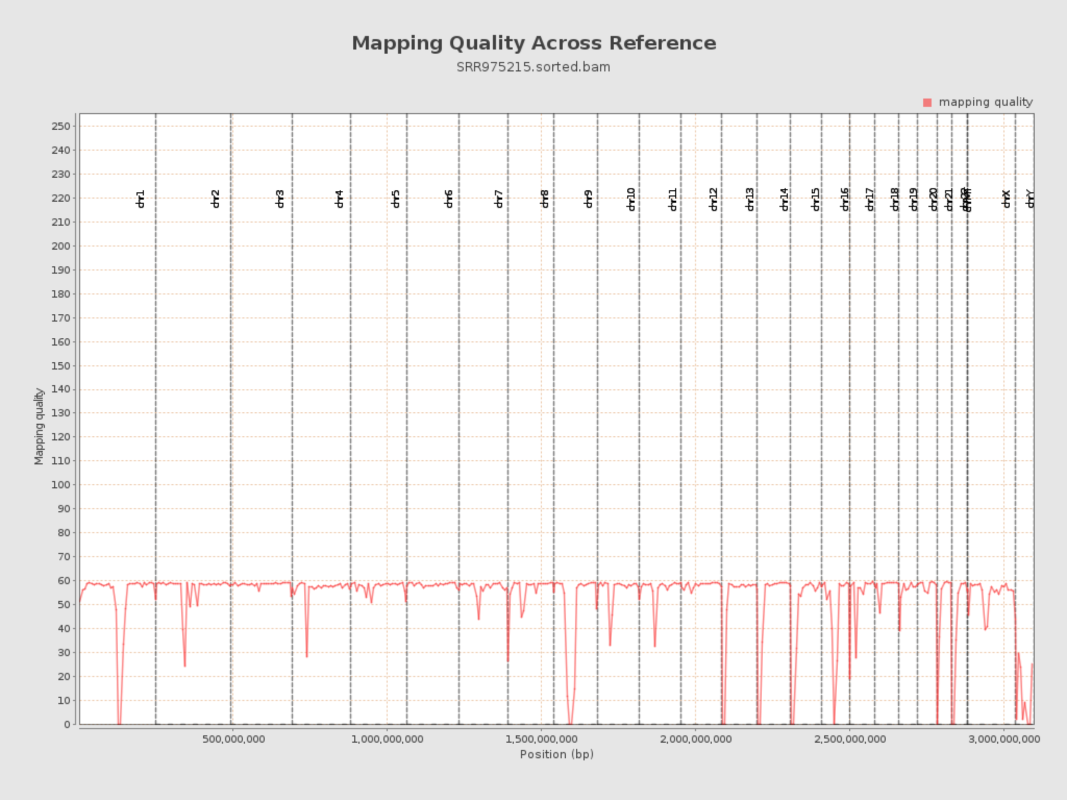
# 10. Results : Mapped Reads Clipping Profile



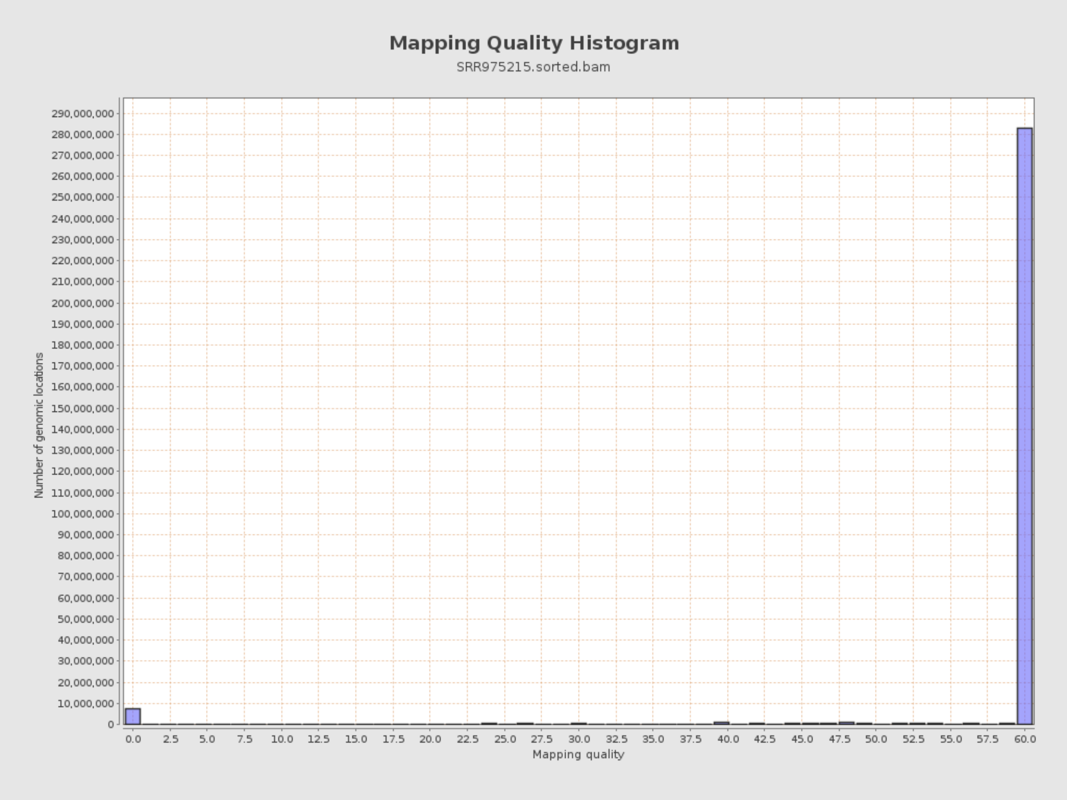
# 11. Results : Homopolymer Indels



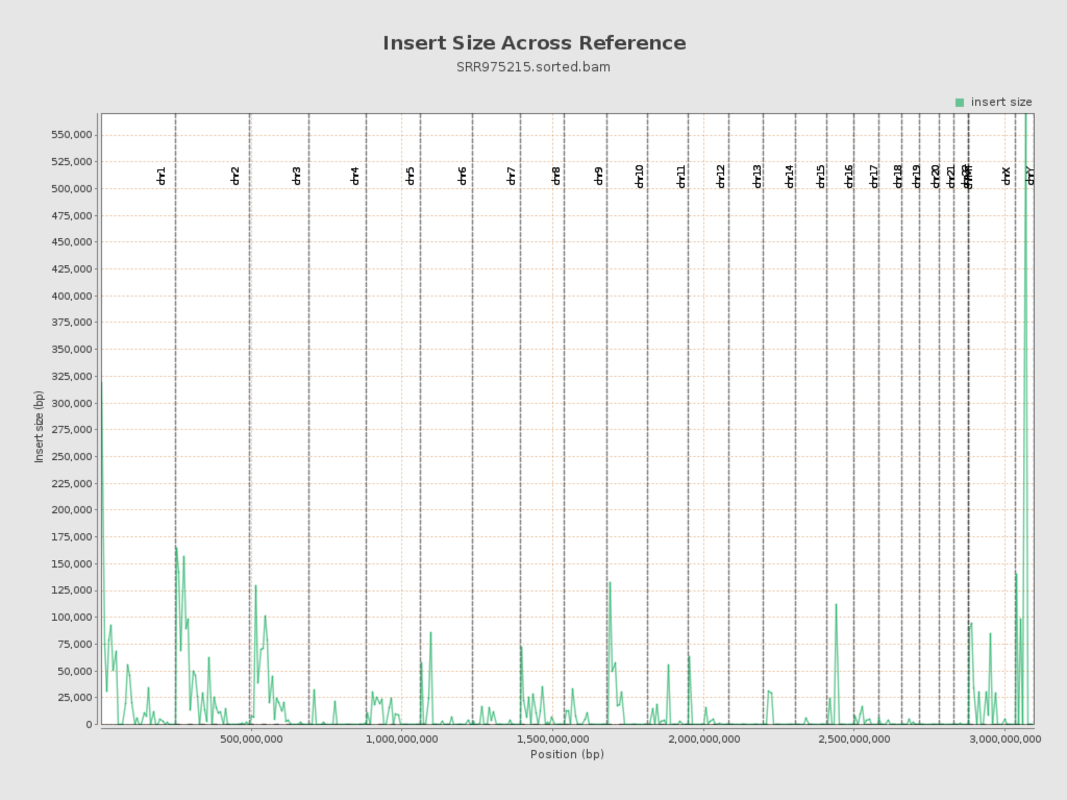
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram