# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/14 17:42:43*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013243.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_SRR6013243 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013243.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 14 17:42:43 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6013243.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,744,028 |
| Mapped reads | 1,536,185 / 88.08% |
| Unmapped reads | 207,843 / 11.92% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 18,342 / 1.05% |
| Read min/max/mean length | 30 / 76 / 76.37 |
| Duplicated reads (estimated) | 107,954 / 6.19% |
| Duplication rate | 5.81% |
| Clipped reads | 812,224 / 46.57% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 28,196,486 / 28.31% |
| Number/percentage of C's | 17,688,067 / 17.76% |
| Number/percentage of T's | 32,460,493 / 32.59% |
| Number/percentage of G's | 21,227,741 / 21.31% |
| Number/percentage of N's | 21,012 / 0.02% |
| GC Percentage | 39.07% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0322 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3317 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.98 |

## 2.5. Mismatches and indels

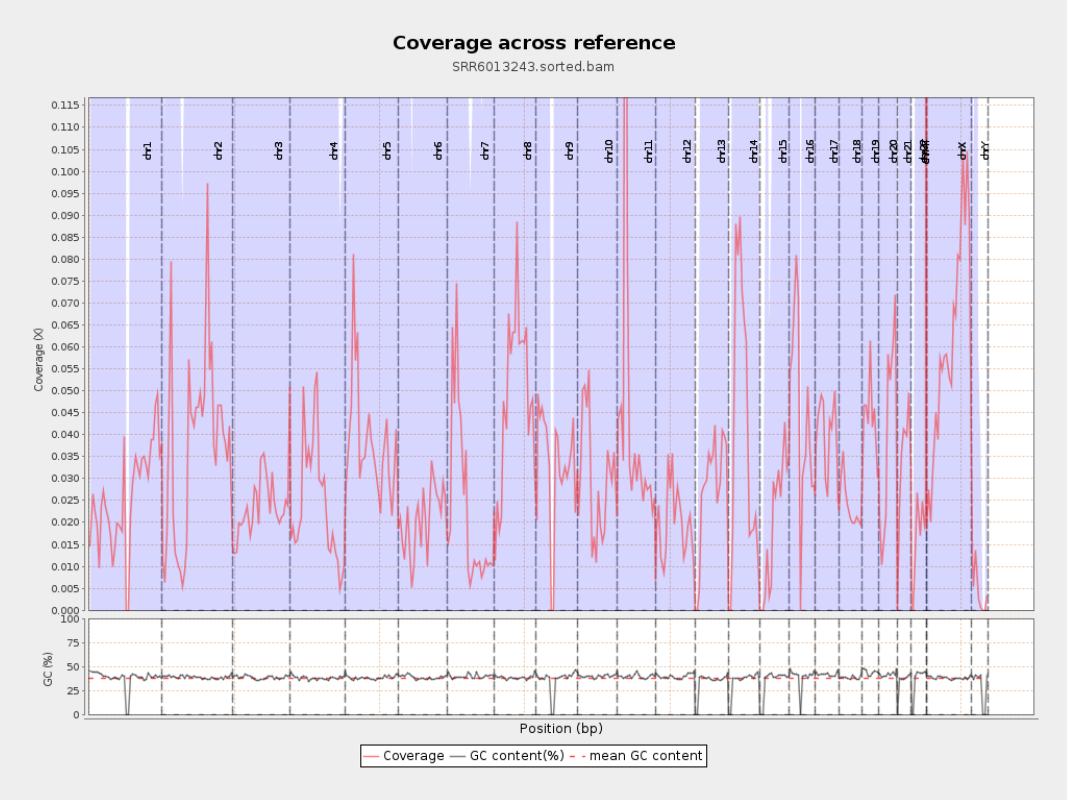
| | |
|---|---|
| General error rate | 0.94% |
| Mismatches | 918,106 |
| Insertions | 7,672 |
| Mapped reads with at least one insertion | 0.5% |
| Deletions | 42,844 |
| Mapped reads with at least one deletion | 2.74% |
| Homopolymer indels | 43.85% |

## 2.6. Chromosome stats

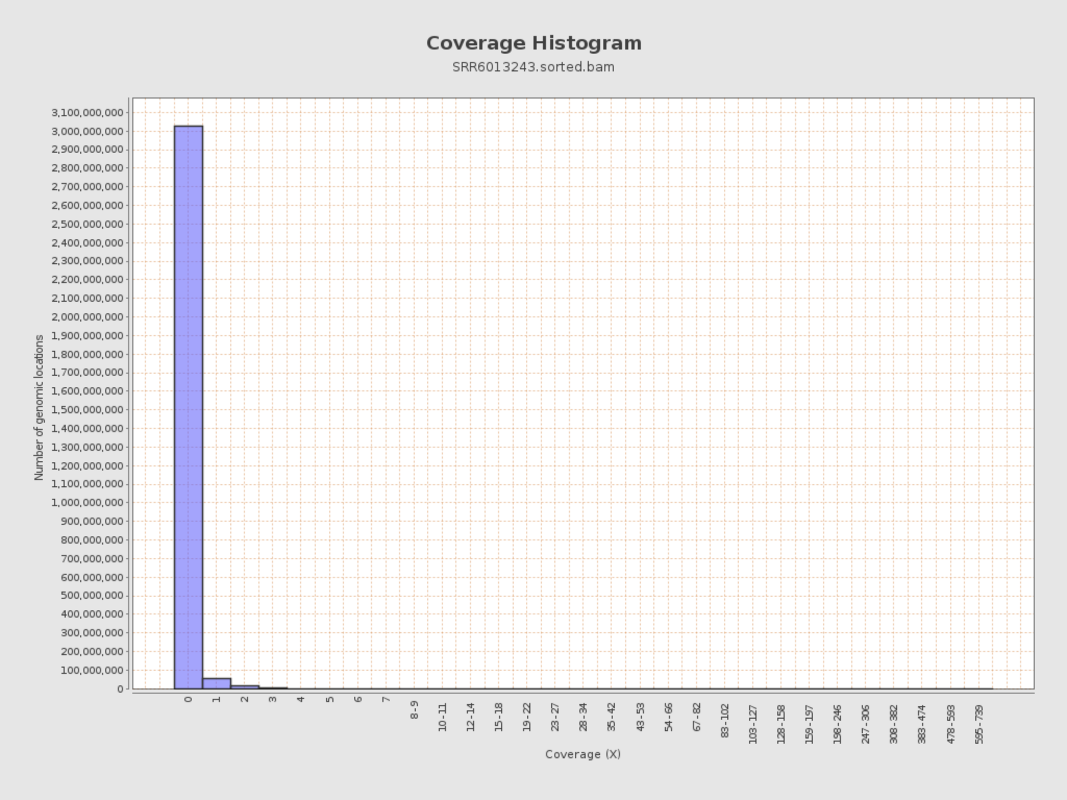
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 6379069 | 0.0256 | 0.575 |
| chr2 | 243199373 | 9020326 | 0.0371 | 0.3839 |
| chr3 | 198022430 | 4664559 | 0.0236 | 0.2015 |
| chr4 | 191154276 | 4635830 | 0.0243 | 0.2386 |
| chr5 | 180915260 | 7035735 | 0.0389 | 0.2624 |
| chr6 | 171115067 | 3528387 | 0.0206 | 0.1999 |
| chr7 | 159138663 | 3735260 | 0.0235 | 0.3029 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7084838 | 0.0484 | 0.5138 |
| chr9 | 141213431 | 4665169 | 0.033 | 0.2916 |
| chr10 | 135534747 | 4060132 | 0.03 | 0.326 |
| chr11 | 135006516 | 6158201 | 0.0456 | 0.3239 |
| chr12 | 133851895 | 2716344 | 0.0203 | 0.1885 |
| chr13 | 115169878 | 3197904 | 0.0278 | 0.2218 |
| chr14 | 107349540 | 4379544 | 0.0408 | 0.2834 |
| chr15 | 102531392 | 2014971 | 0.0197 | 0.1835 |
| chr16 | 90354753 | 4077279 | 0.0451 | 0.2884 |
| chr17 | 81195210 | 3234517 | 0.0398 | 0.2864 |
| chr18 | 78077248 | 1884834 | 0.0241 | 0.3839 |
| chr19 | 59128983 | 2585580 | 0.0437 | 0.4786 |
| chr20 | 63025520 | 2507708 | 0.0398 | 0.2653 |
| chr21 | 48129895 | 1630924 | 0.0339 | 0.2595 |
| chr22 | 51304566 | 818937 | 0.016 | 0.161 |
| chrMT | 16571 | 8605 | 0.5193 | 0.9749 |
| chrX | 155270560 | 9383431 | 0.0604 | 0.3399 |
| chrY | 59373566 | 260240 | 0.0044 | 0.1401 |

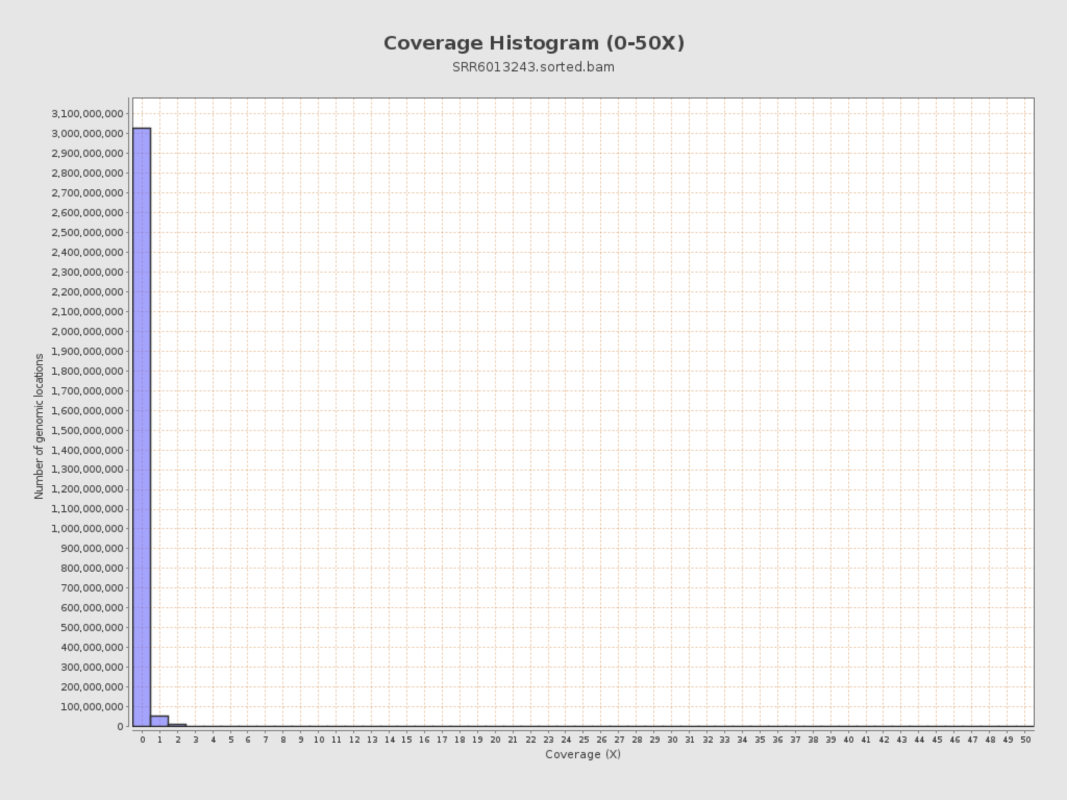
# 3. Results : Coverage across reference



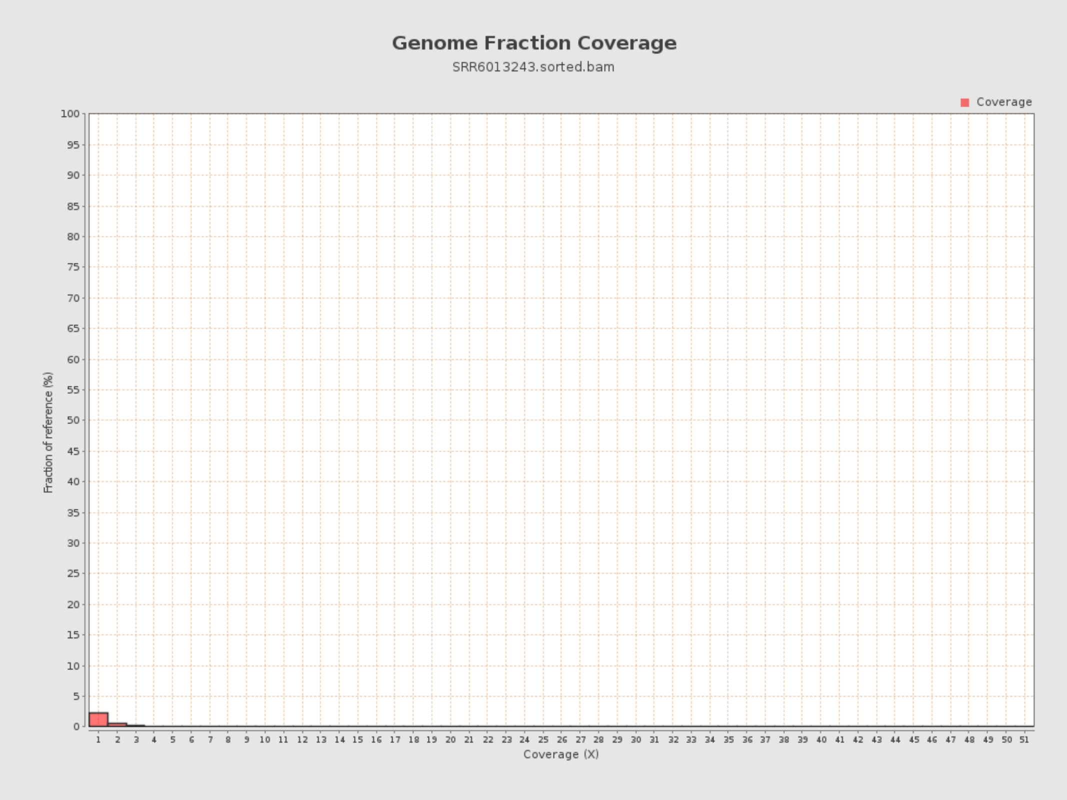
# 4. Results : Coverage Histogram



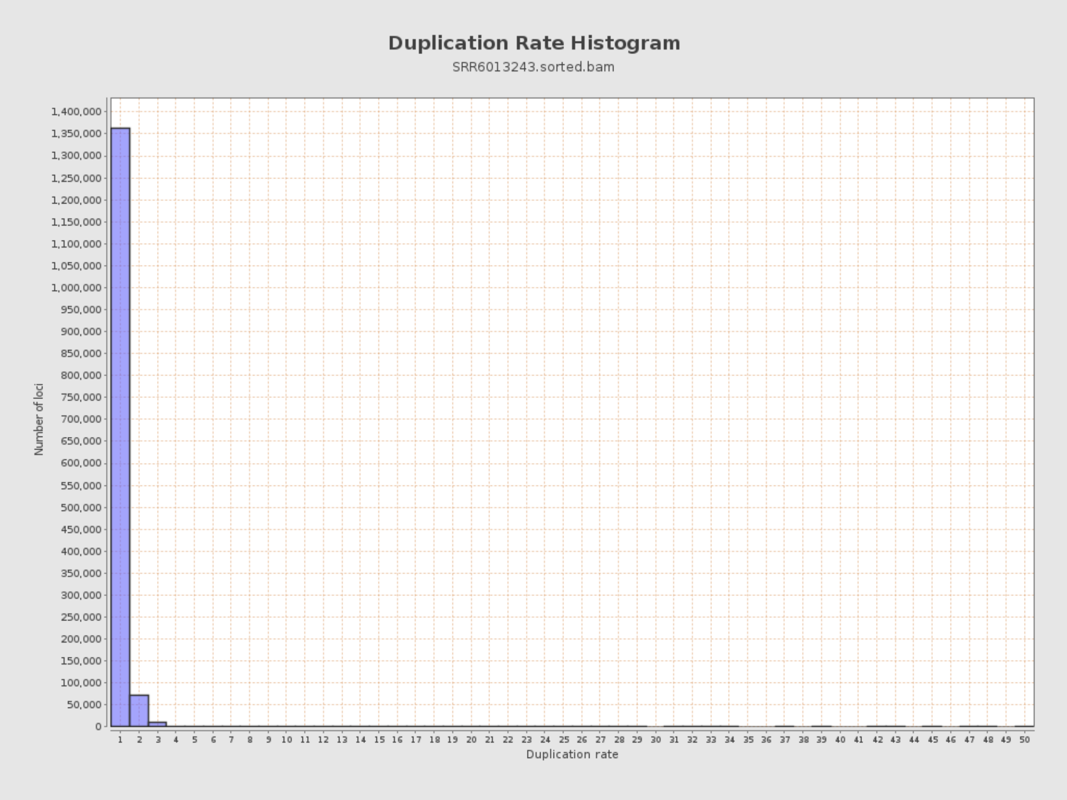
# 5. Results : Coverage Histogram (0-50X)



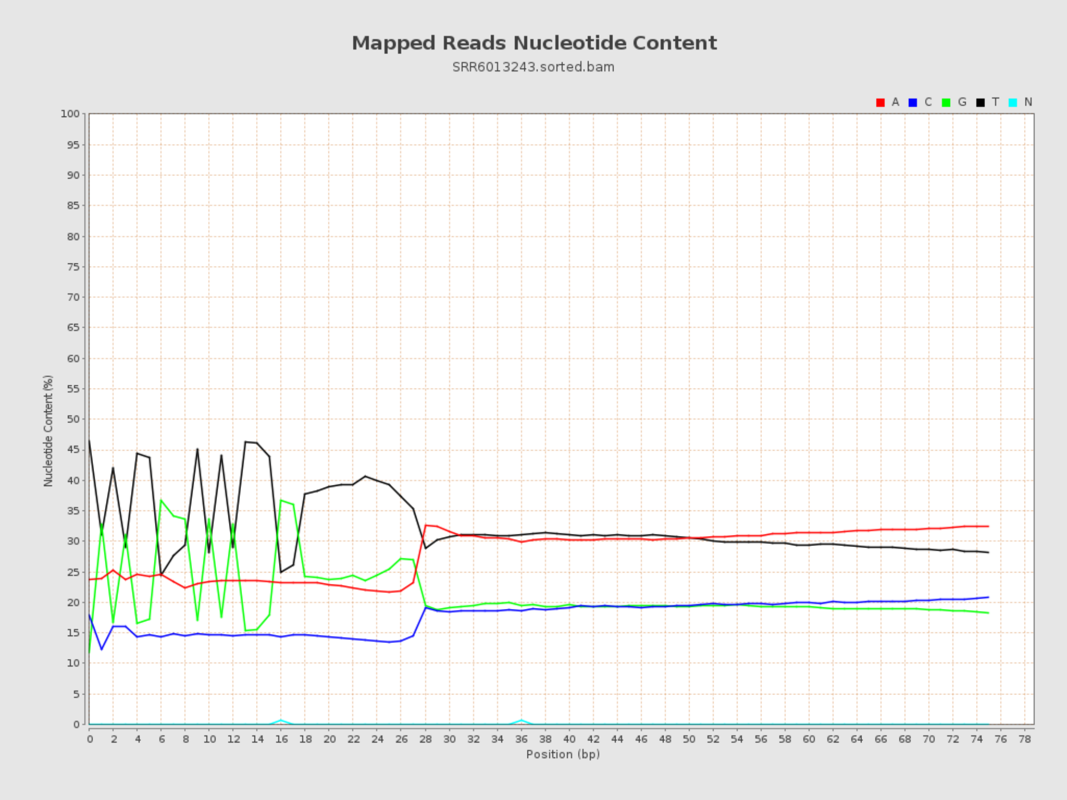
# 6. Results : Genome Fraction Coverage



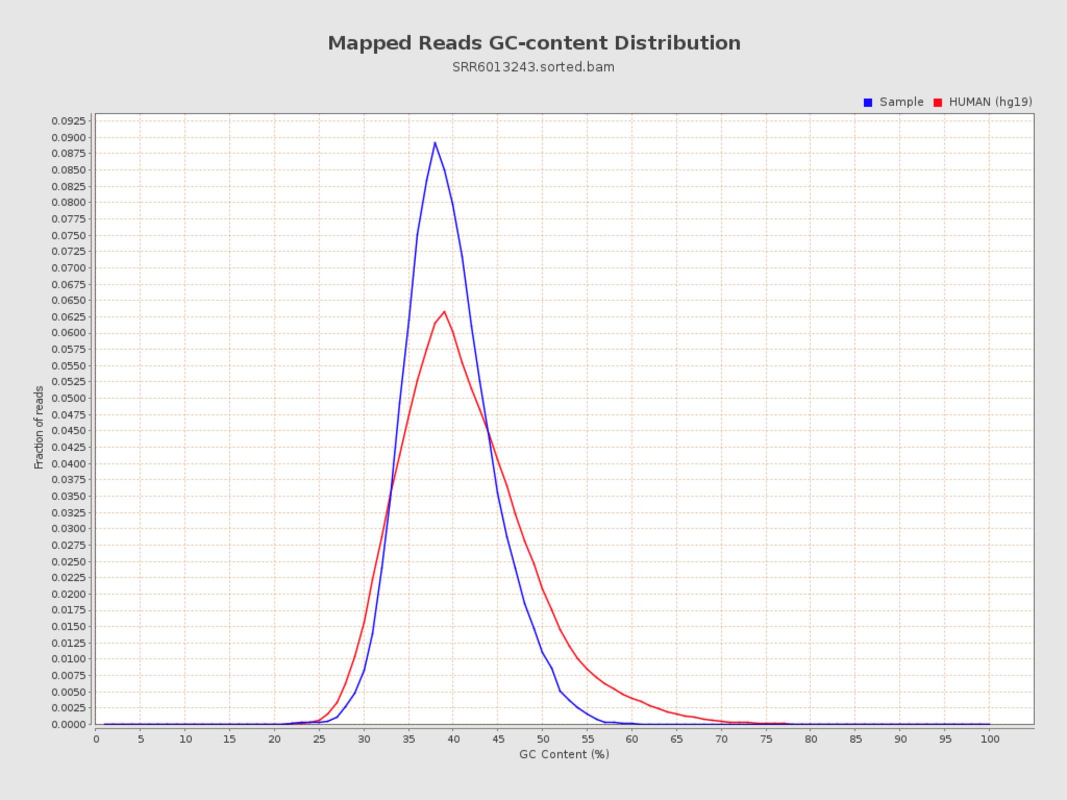
# 7. Results : Duplication Rate Histogram



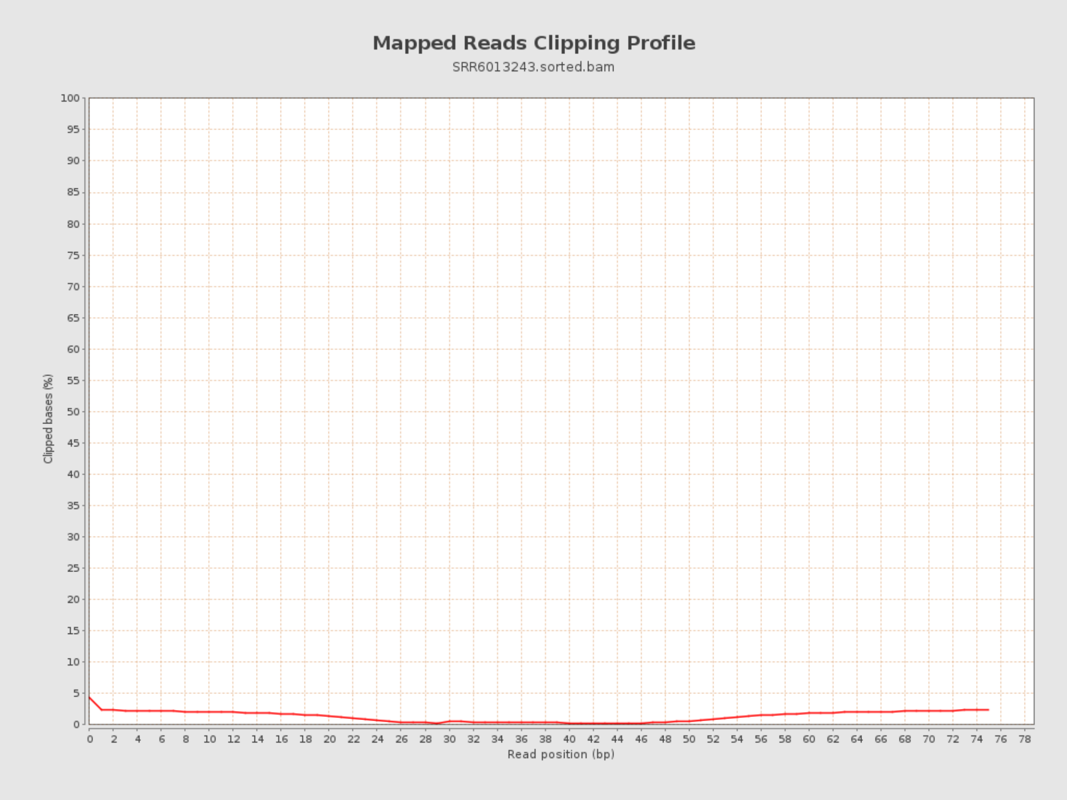
# 8. Results : Mapped Reads Nucleotide Content



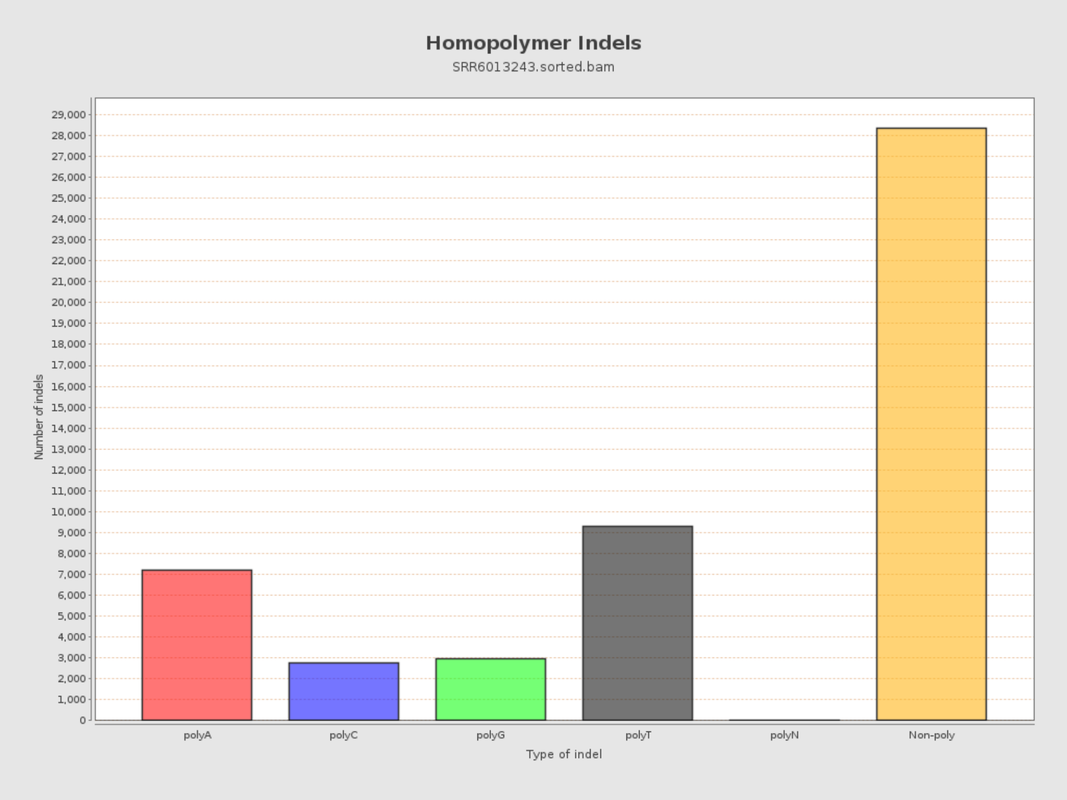
# 9. Results : Mapped Reads GC-content Distribution



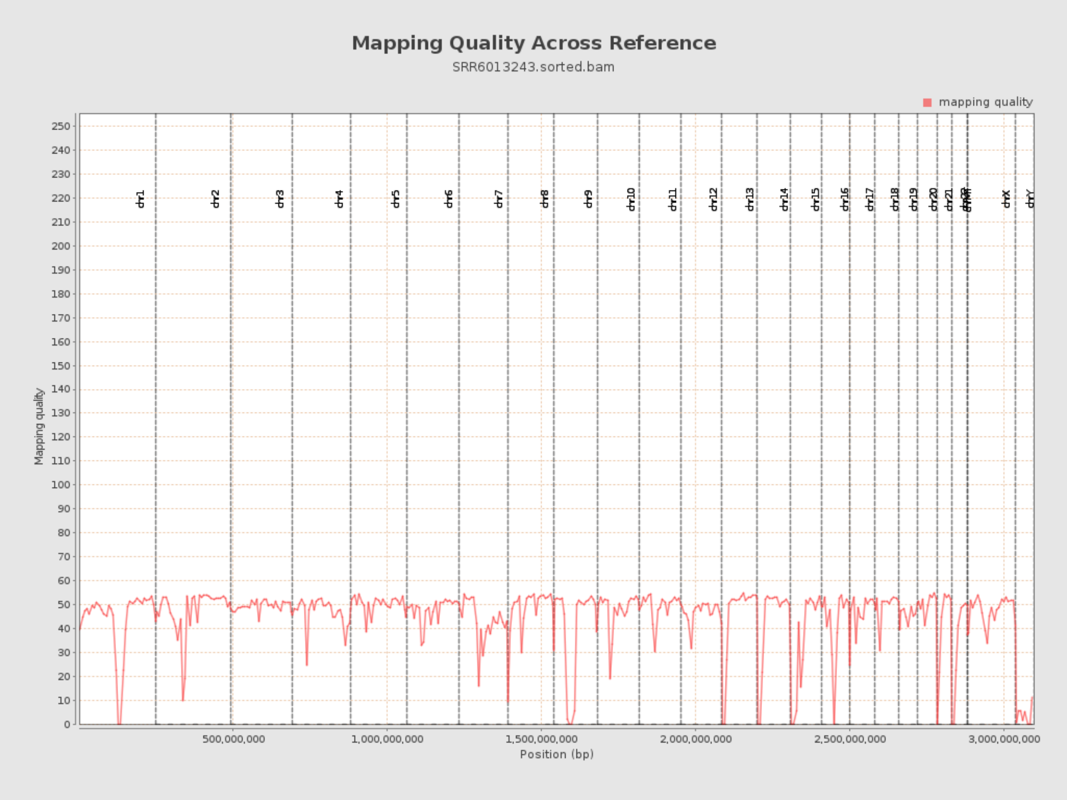
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram