# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 00:18:04*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524356.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_SRR10524356 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524356.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 00:18:03 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524356.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 448,686 |
| Mapped reads | 413,546 / 92.17% |
| Unmapped reads | 35,140 / 7.83% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 1,993 / 0.44% |
| Read min/max/mean length | 30 / 76 / 76.15 |
| Duplicated reads (estimated) | 9,166 / 2.04% |
| Duplication rate | 1.67% |
| Clipped reads | 414,310 / 92.34% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 5,989,075 / 24.67% |
| Number/percentage of C's | 4,426,162 / 18.23% |
| Number/percentage of T's | 7,929,727 / 32.67% |
| Number/percentage of G's | 5,926,985 / 24.42% |
| Number/percentage of N's | 3,660 / 0.02% |
| GC Percentage | 42.65% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0078 |
| | |

| | |
|---|---|
| Standard Deviation | 0.11 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.18 |

## 2.5. Mismatches and indels

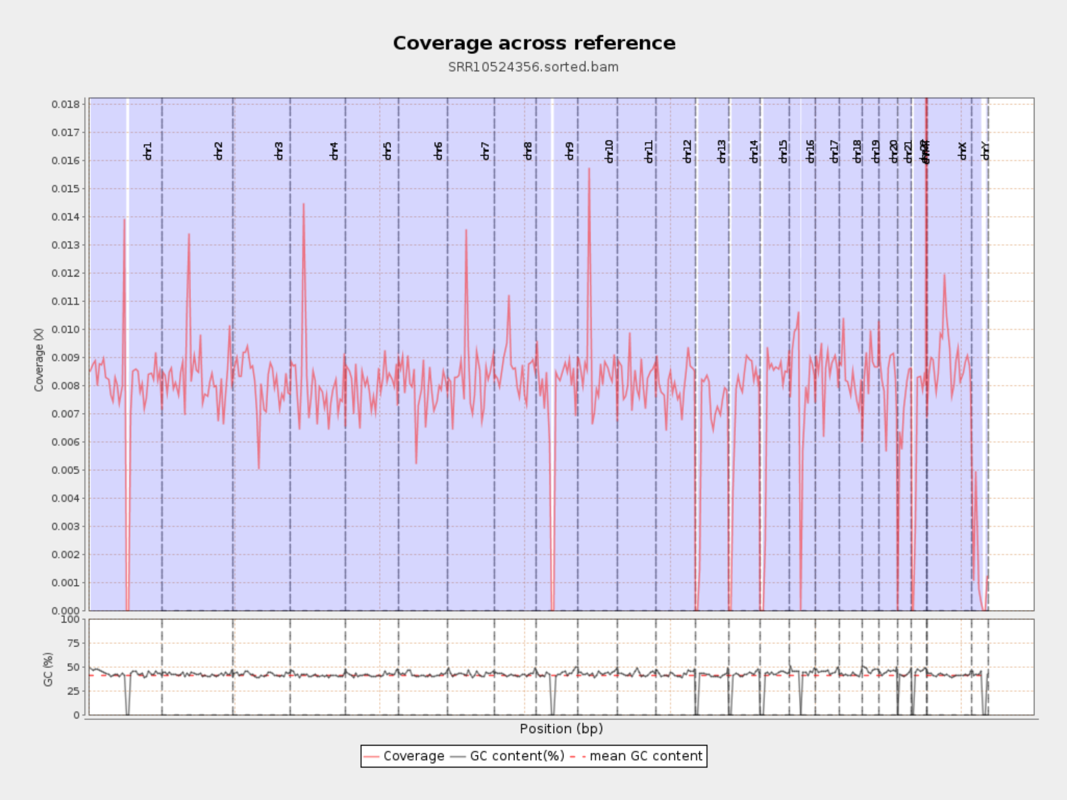
| | |
|---|---|
| General error rate | 0.53% |
| Mismatches | 123,846 |
| Insertions | 1,955 |
| Mapped reads with at least one insertion | 0.47% |
| Deletions | 4,211 |
| Mapped reads with at least one deletion | 1.01% |
| Homopolymer indels | 42.65% |

## 2.6. Chromosome stats

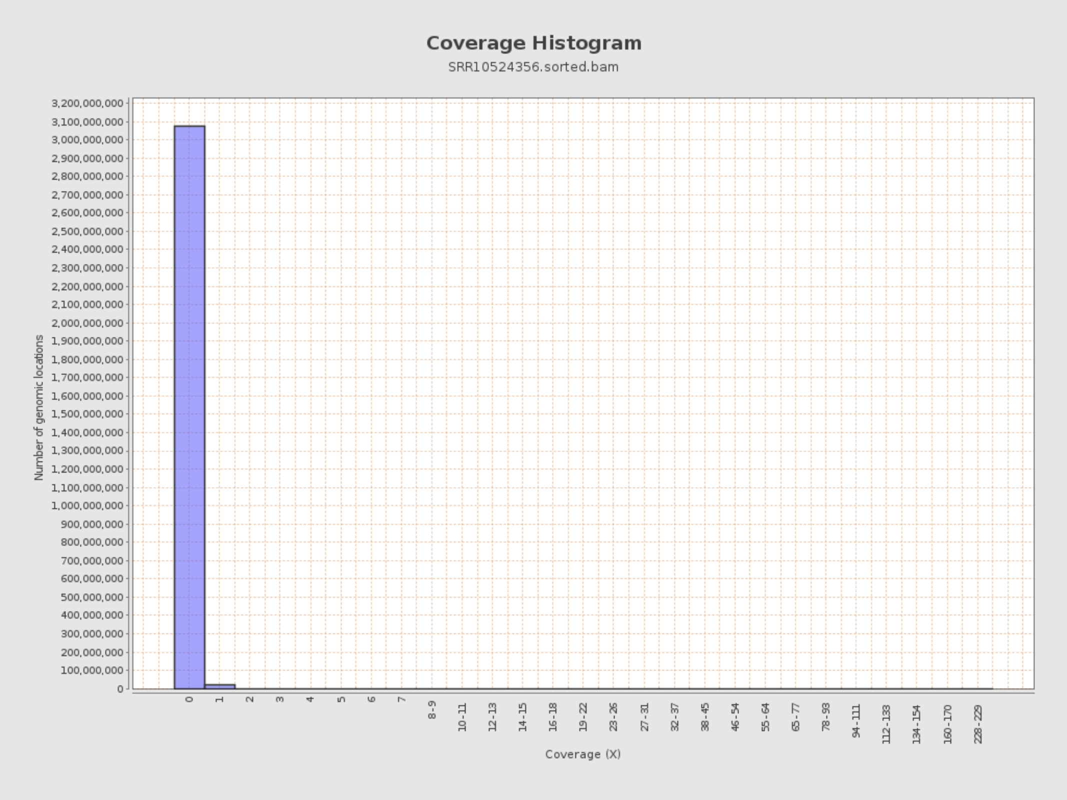
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 1963064 | 0.0079 | 0.1617 |
| chr2 | 243199373 | 2047433 | 0.0084 | 0.1358 |
| chr3 | 198022430 | 1604551 | 0.0081 | 0.0934 |
| chr4 | 191154276 | 1533799 | 0.008 | 0.098 |
| chr5 | 180915260 | 1453823 | 0.008 | 0.0929 |
| chr6 | 171115067 | 1358254 | 0.0079 | 0.0952 |
| chr7 | 159138663 | 1329494 | 0.0084 | 0.1247 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1256450 | 0.0086 | 0.1066 |
| chr9 | 141213431 | 1018301 | 0.0072 | 0.0987 |
| chr10 | 135534747 | 1174921 | 0.0087 | 0.1148 |
| chr11 | 135006516 | 1107069 | 0.0082 | 0.1035 |
| chr12 | 133851895 | 1076426 | 0.008 | 0.0939 |
| chr13 | 115169878 | 726327 | 0.0063 | 0.0822 |
| chr14 | 107349540 | 754859 | 0.007 | 0.088 |
| chr15 | 102531392 | 715390 | 0.007 | 0.0863 |
| chr16 | 90354753 | 713486 | 0.0079 | 0.094 |
| chr17 | 81195210 | 695429 | 0.0086 | 0.0979 |
| chr18 | 78077248 | 645324 | 0.0083 | 0.1568 |
| chr19 | 59128983 | 513274 | 0.0087 | 0.1268 |
| chr20 | 63025520 | 512485 | 0.0081 | 0.0945 |
| chr21 | 48129895 | 321716 | 0.0067 | 0.0894 |
| chr22 | 51304566 | 294329 | 0.0057 | 0.0786 |
| chrMT | 16571 | 2138 | 0.129 | 0.3693 |
| chrX | 155270560 | 1382572 | 0.0089 | 0.1021 |
| chrY | 59373566 | 81312 | 0.0014 | 0.0533 |

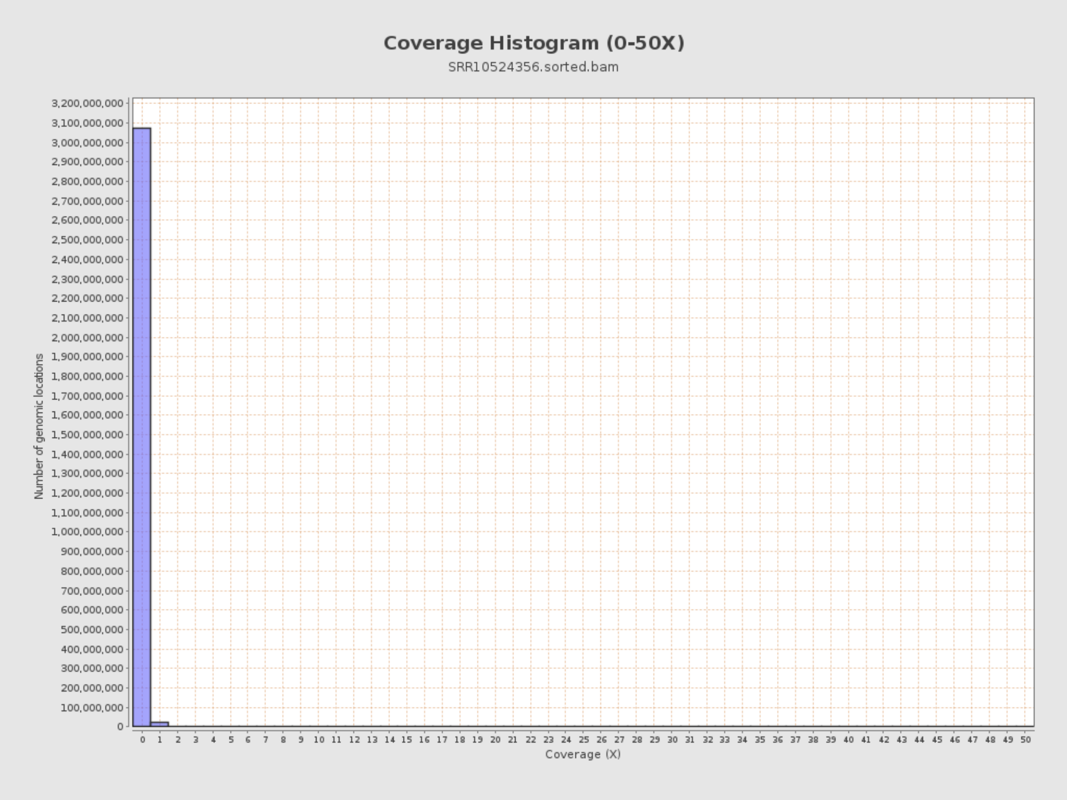
# 3. Results : Coverage across reference



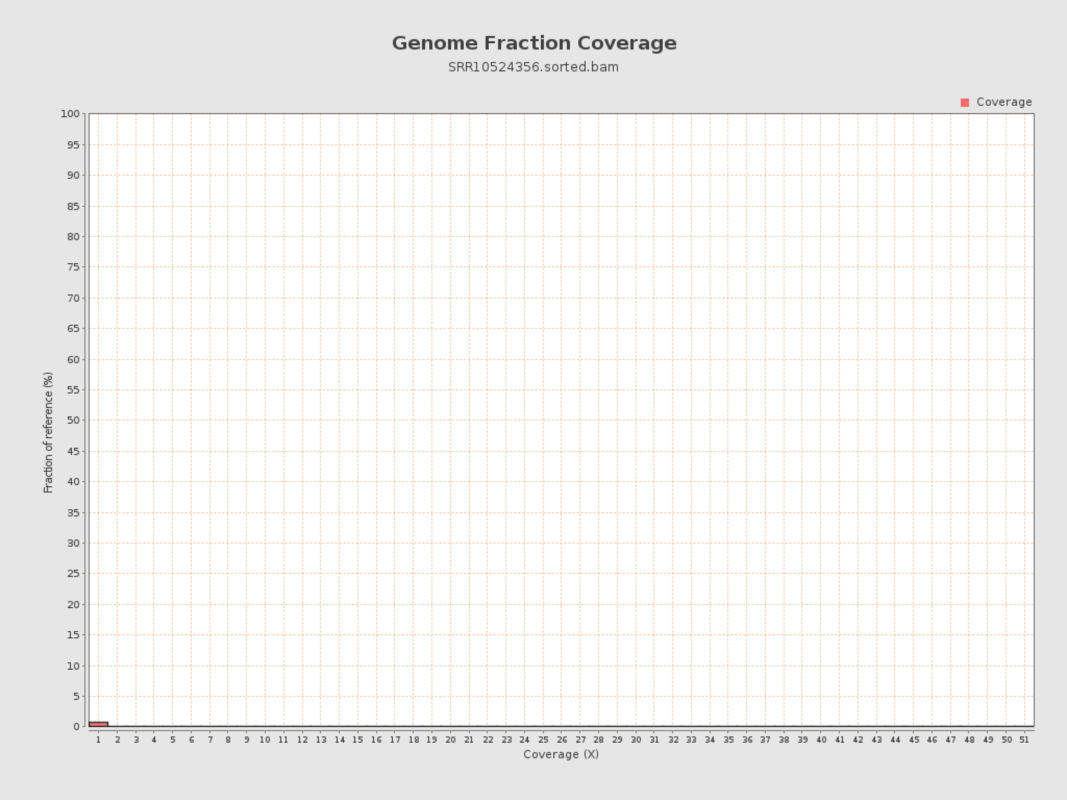
# 4. Results : Coverage Histogram



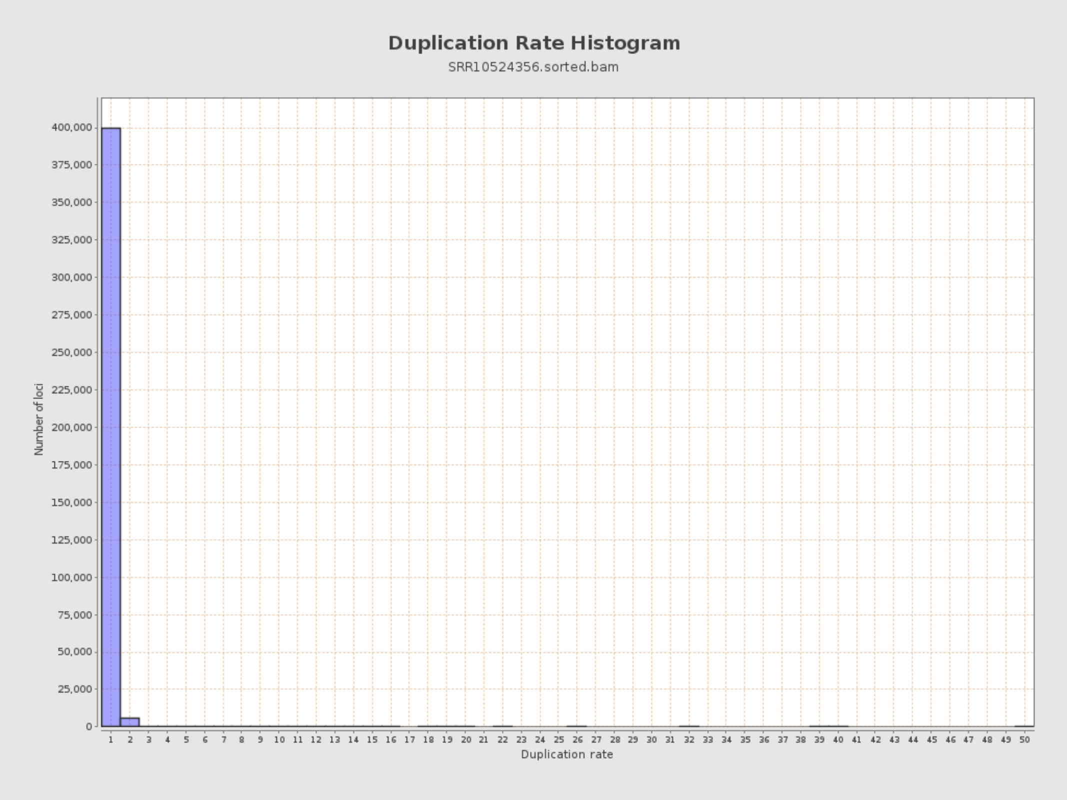
# 5. Results : Coverage Histogram (0-50X)



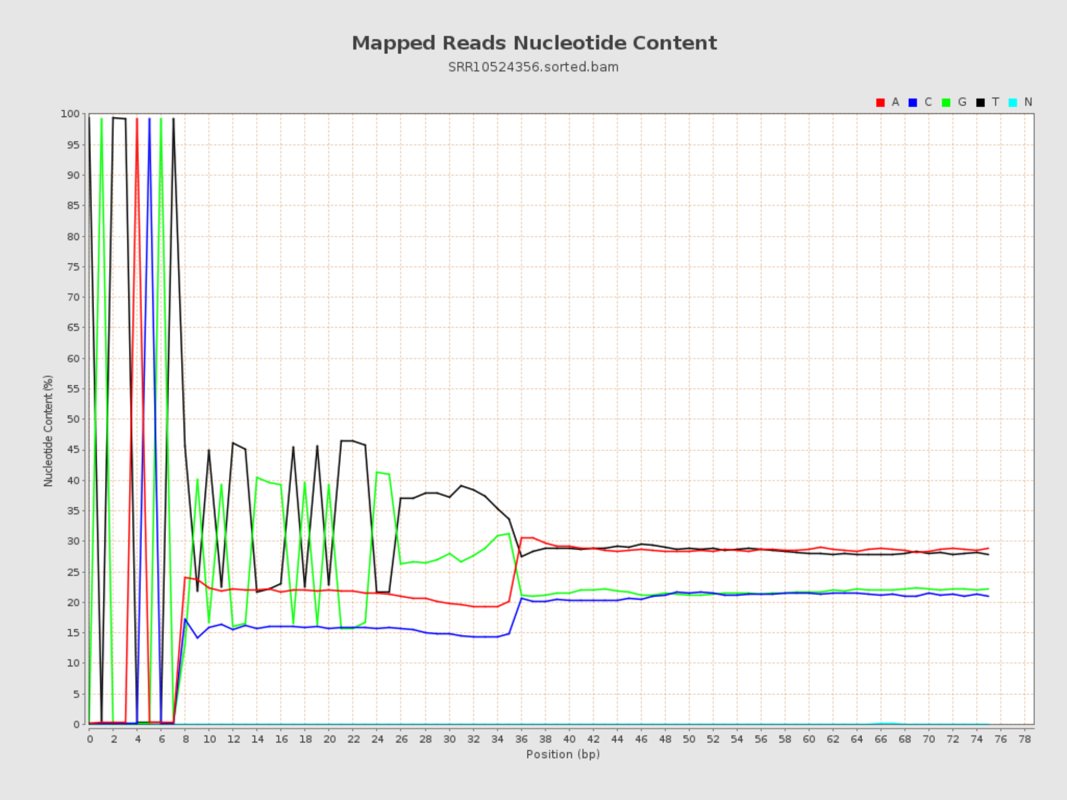
# 6. Results : Genome Fraction Coverage



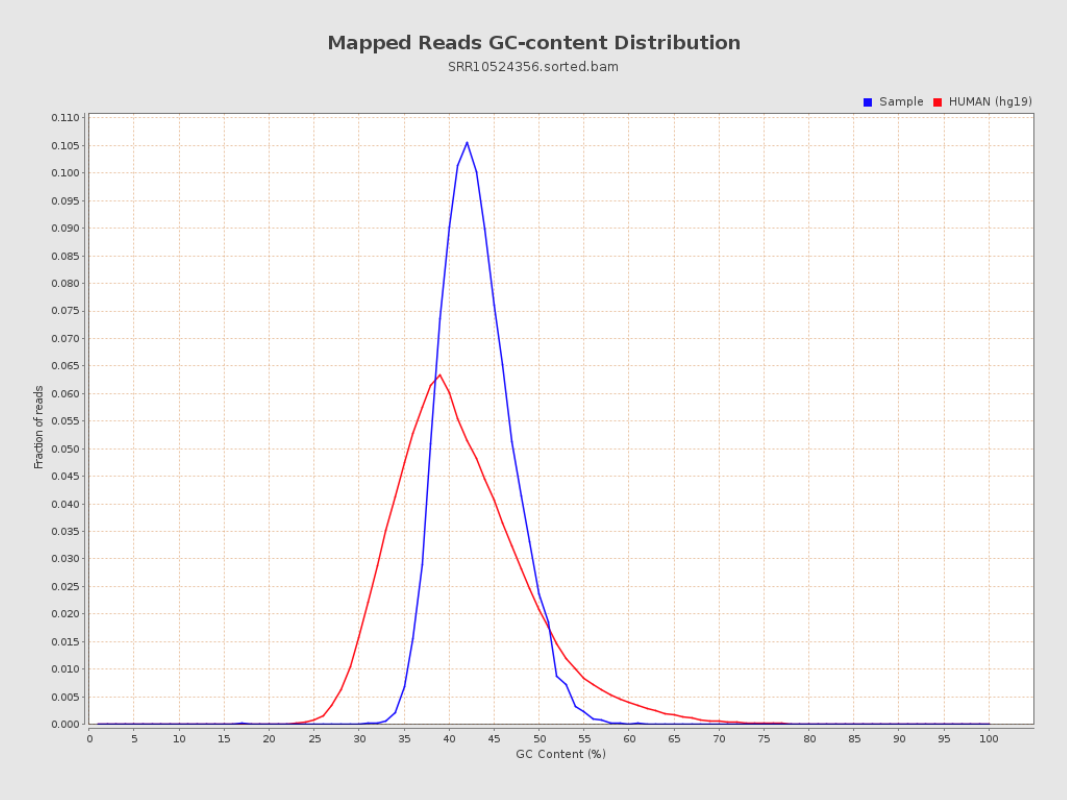
# 7. Results : Duplication Rate Histogram



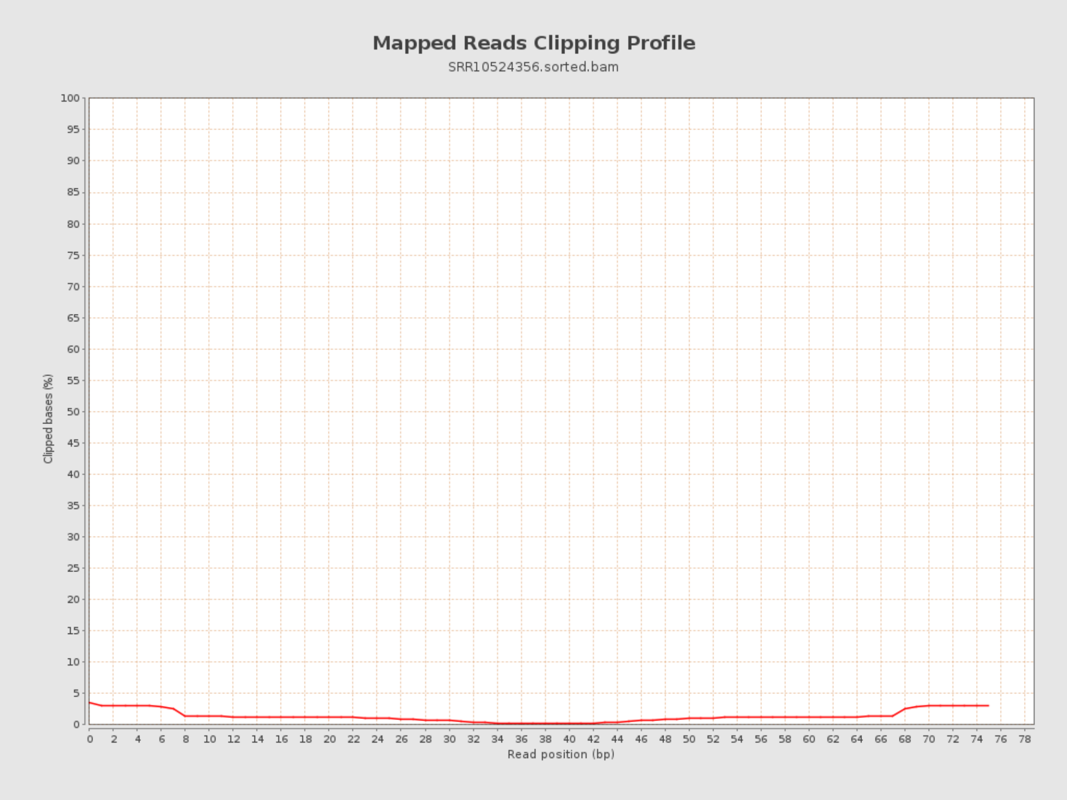
# 8. Results : Mapped Reads Nucleotide Content



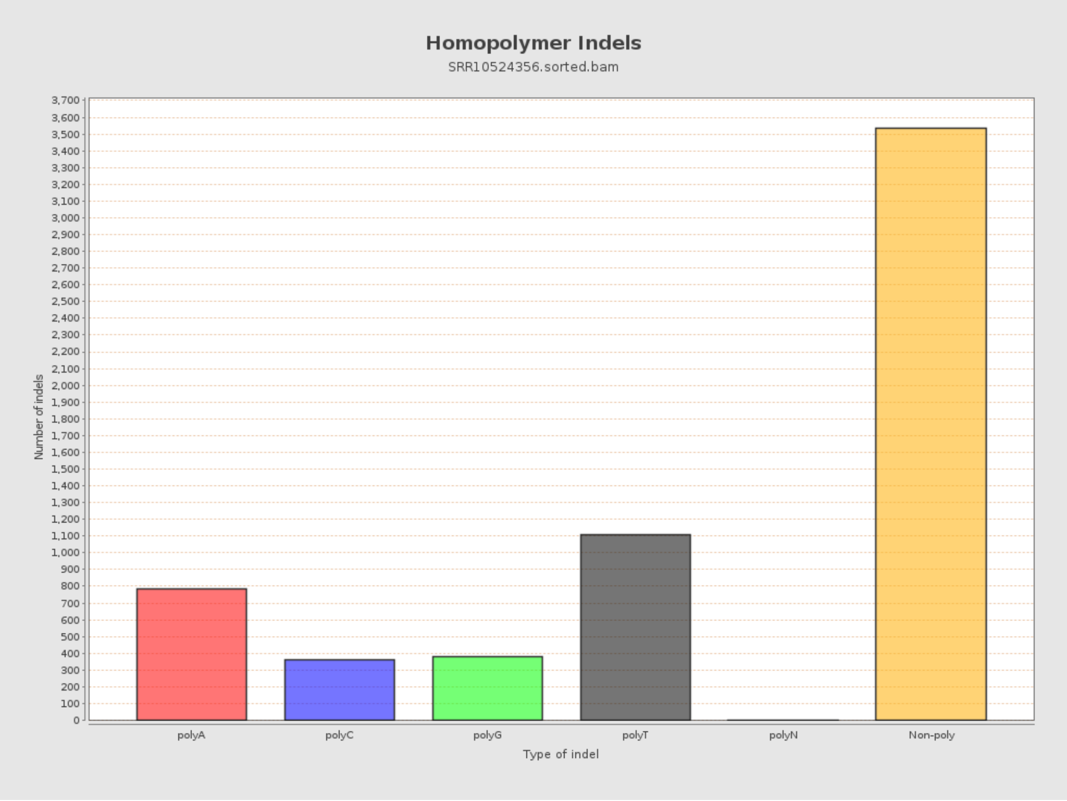
# 9. Results : Mapped Reads GC-content Distribution



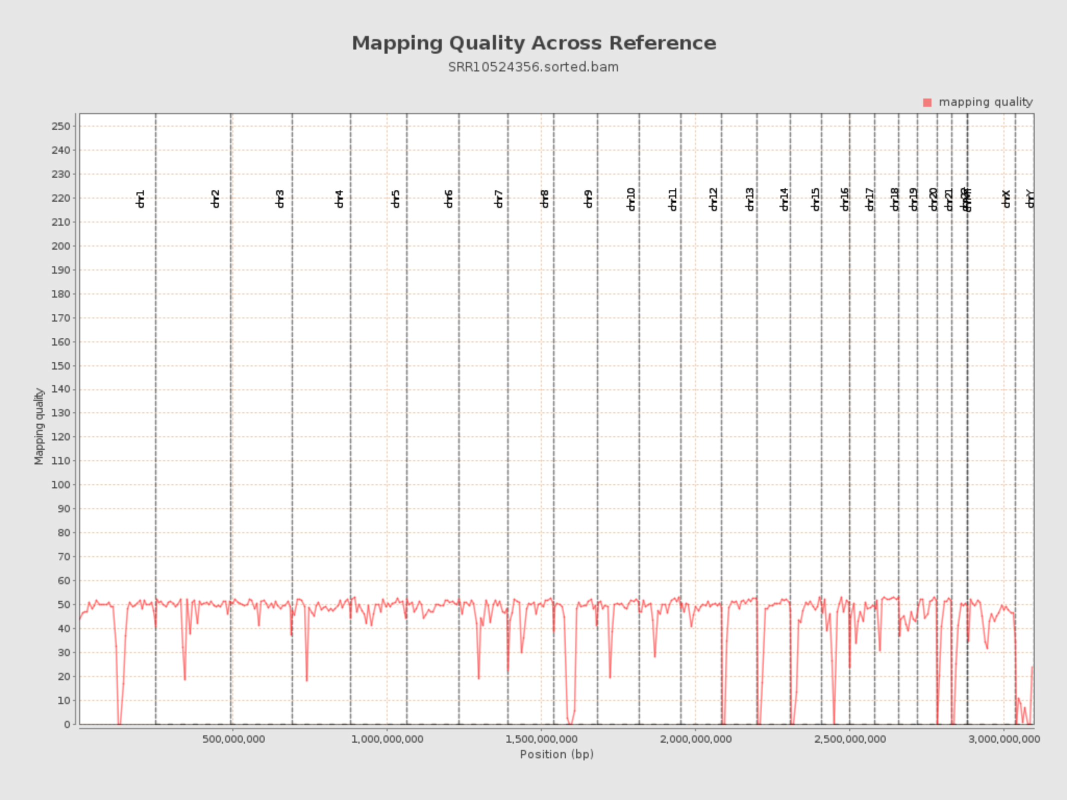
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram