# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 21:22:04*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524807.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_SRR10524807 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524807.fastq.gz` |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 21:22:04 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524807.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,695,450 |
| Mapped reads | 1,555,807 / 91.76% |
| Unmapped reads | 139,643 / 8.24% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 6,484 / 0.38% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 62,677 / 3.7% |
| Duplication rate | 3.08% |
| Clipped reads | 1,557,312 / 91.85% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 20,699,156 / 23.2% |
| Number/percentage of C's | 18,099,792 / 20.29% |
| Number/percentage of T's | 28,829,429 / 32.31% |
| Number/percentage of G's | 21,582,710 / 24.19% |
| Number/percentage of N's | 10,872 / 0.01% |
| GC Percentage | 44.48% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0288 |
| | |

| | |
|---|---|
| Standard Deviation | 0.25 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.54 |

## 2.5. Mismatches and indels

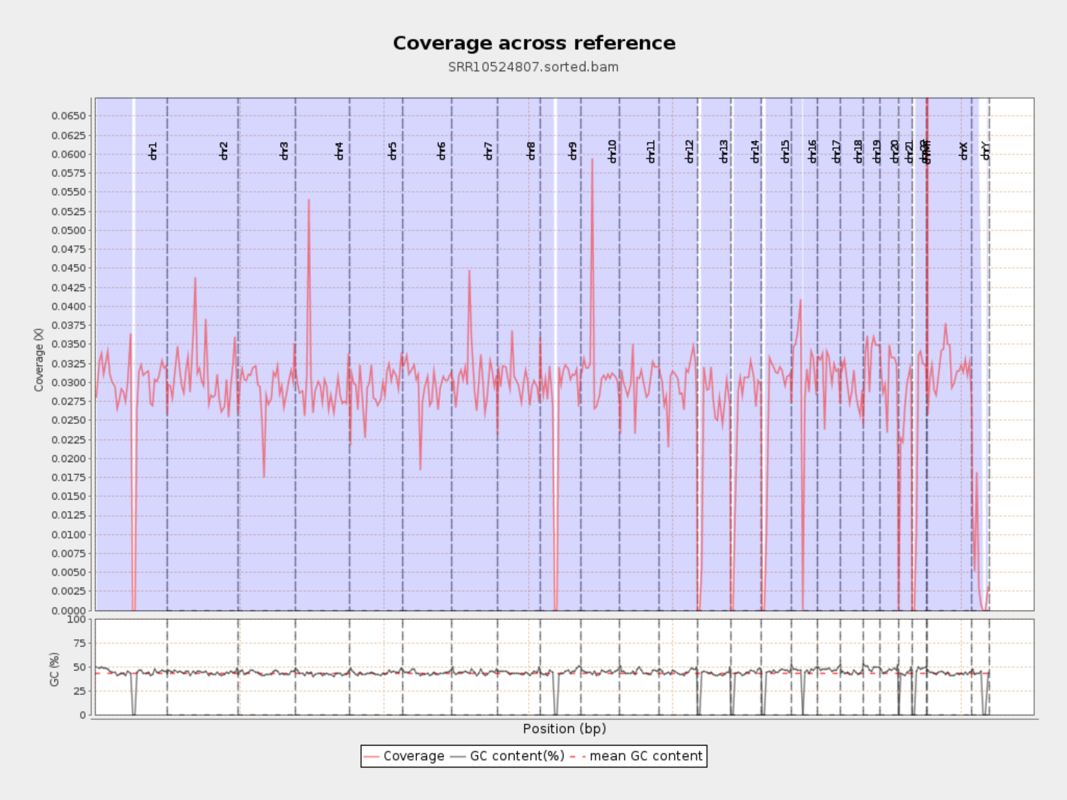
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 450,370 |
| Insertions | 6,418 |
| Mapped reads with at least one insertion | 0.41% |
| Deletions | 17,839 |
| Mapped reads with at least one deletion | 1.14% |
| Homopolymer indels | 41.44% |

## 2.6. Chromosome stats

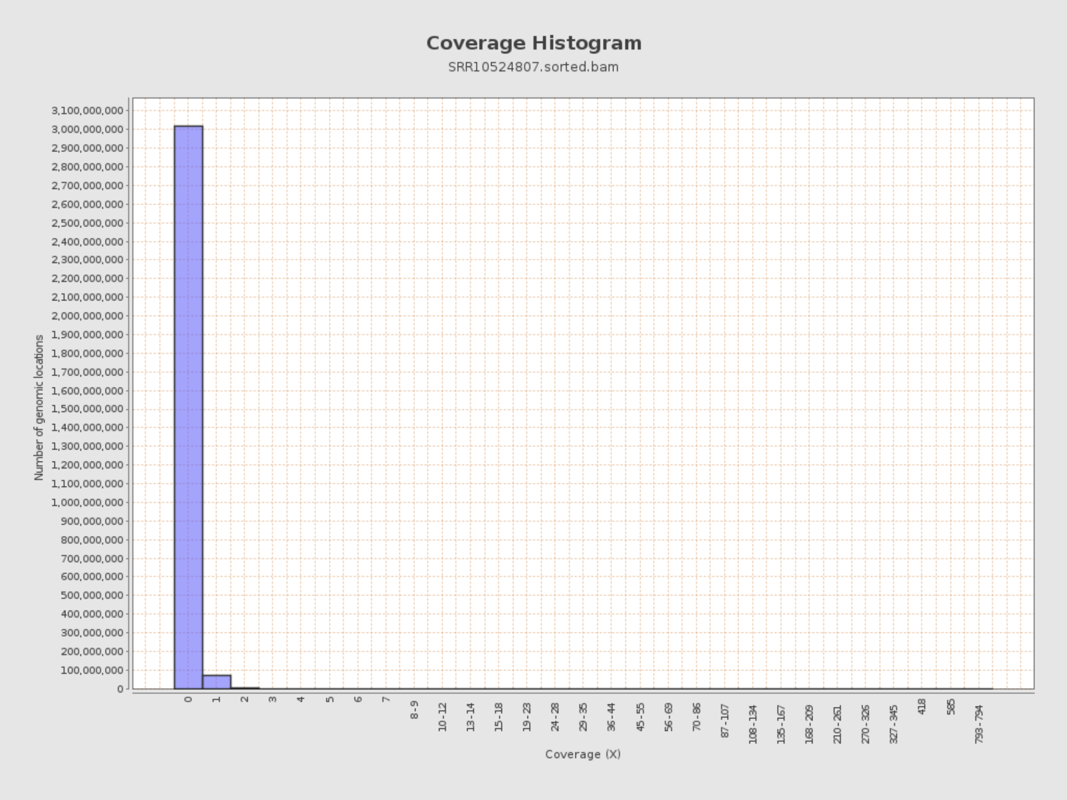
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 7125835 | 0.0286 | 0.3218 |
| chr2 | 243199373 | 7487009 | 0.0308 | 0.3976 |
| chr3 | 198022430 | 5810713 | 0.0293 | 0.1926 |
| chr4 | 191154276 | 5702937 | 0.0298 | 0.2192 |
| chr5 | 180915260 | 5349976 | 0.0296 | 0.1896 |
| chr6 | 171115067 | 5085523 | 0.0297 | 0.205 |
| chr7 | 159138663 | 4924291 | 0.0309 | 0.3025 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4435216 | 0.0303 | 0.2338 |
| chr9 | 141213431 | 3821811 | 0.0271 | 0.2197 |
| chr10 | 135534747 | 4344035 | 0.0321 | 0.2989 |
| chr11 | 135006516 | 4063609 | 0.0301 | 0.2262 |
| chr12 | 133851895 | 4003077 | 0.0299 | 0.1926 |
| chr13 | 115169878 | 2718121 | 0.0236 | 0.1689 |
| chr14 | 107349540 | 2685283 | 0.025 | 0.1794 |
| chr15 | 102531392 | 2603201 | 0.0254 | 0.1776 |
| chr16 | 90354753 | 2708870 | 0.03 | 0.213 |
| chr17 | 81195210 | 2554043 | 0.0315 | 0.2045 |
| chr18 | 78077248 | 2292452 | 0.0294 | 0.3523 |
| chr19 | 59128983 | 1995307 | 0.0337 | 0.2748 |
| chr20 | 63025520 | 1926695 | 0.0306 | 0.2014 |
| chr21 | 48129895 | 1180165 | 0.0245 | 0.1907 |
| chr22 | 51304566 | 1160645 | 0.0226 | 0.168 |
| chrMT | 16571 | 42073 | 2.539 | 2.2931 |
| chrX | 155270560 | 4930657 | 0.0318 | 0.2103 |
| chrY | 59373566 | 298863 | 0.005 | 0.1422 |

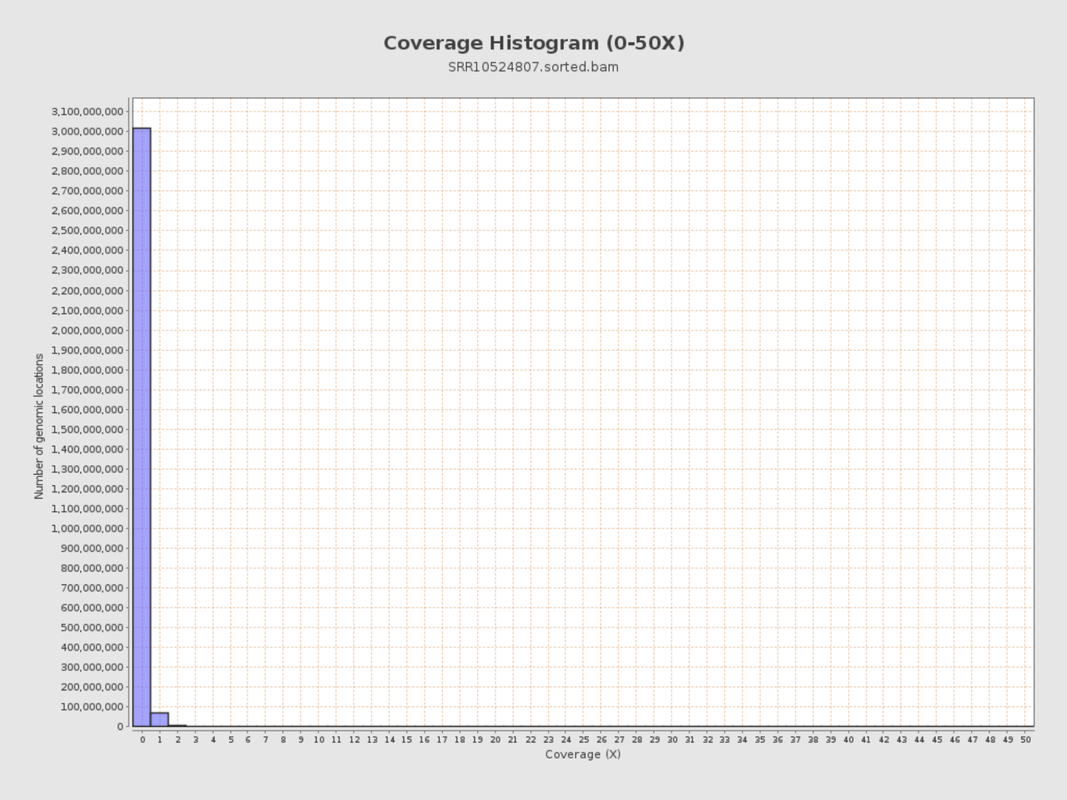
# 3. Results : Coverage across reference



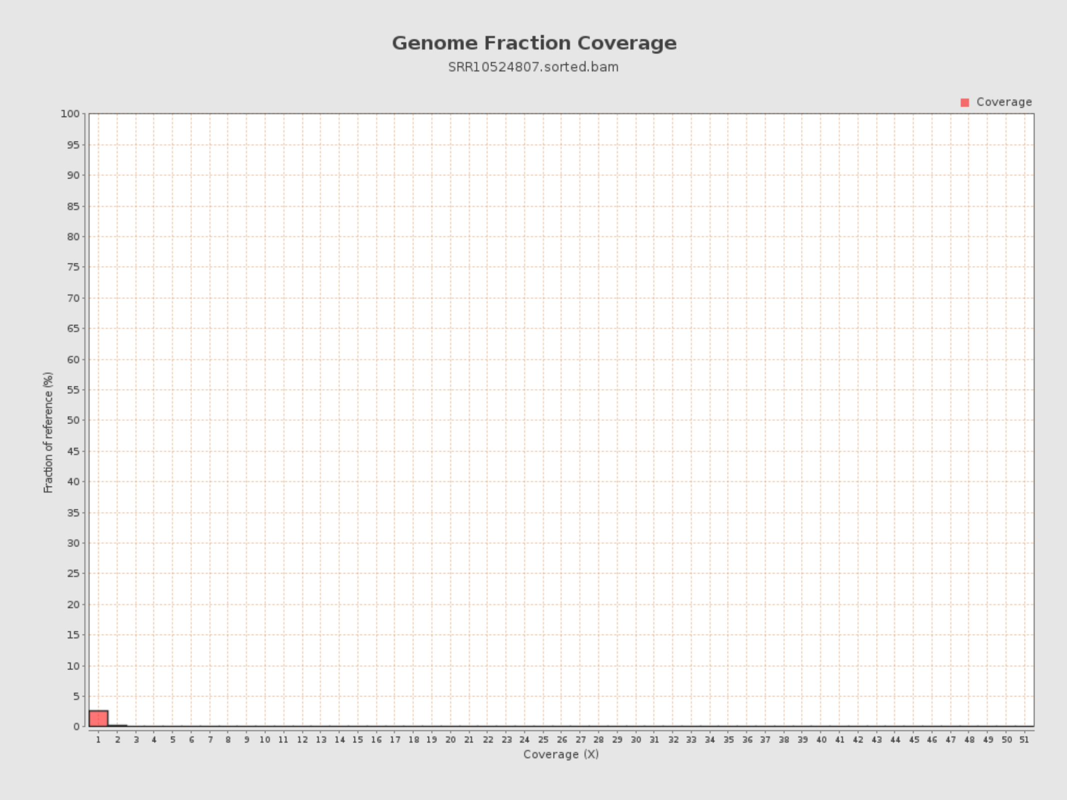
# 4. Results : Coverage Histogram



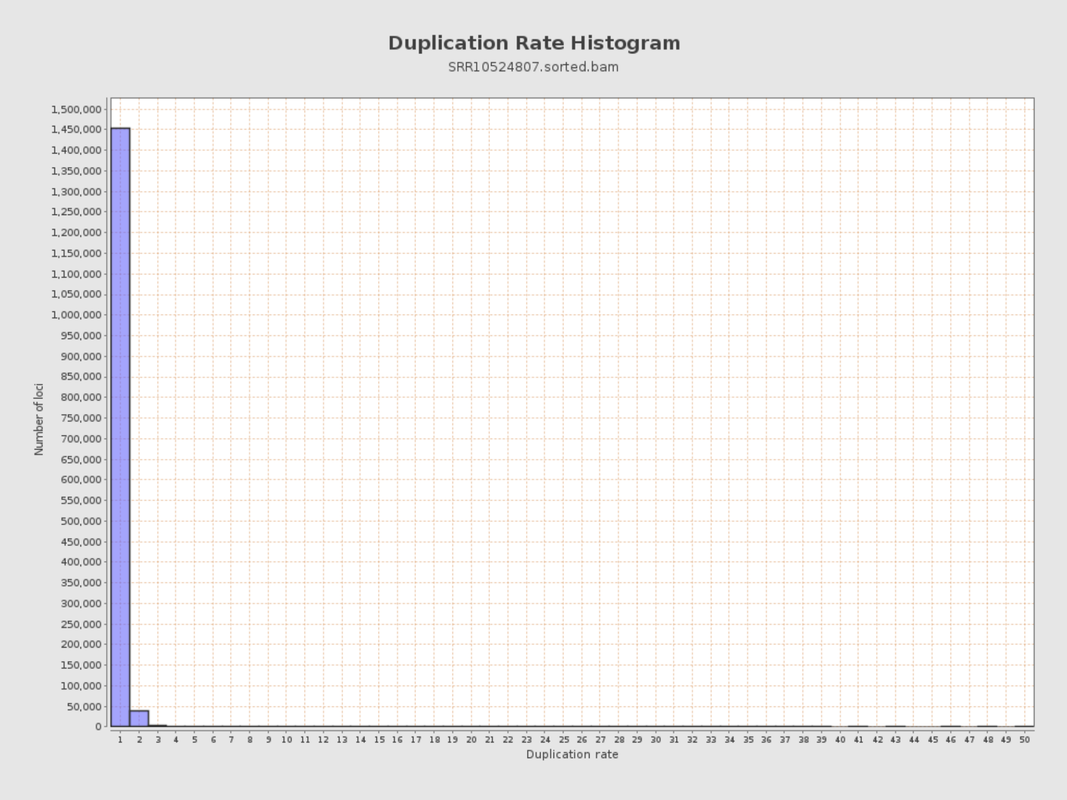
# 5. Results : Coverage Histogram (0-50X)



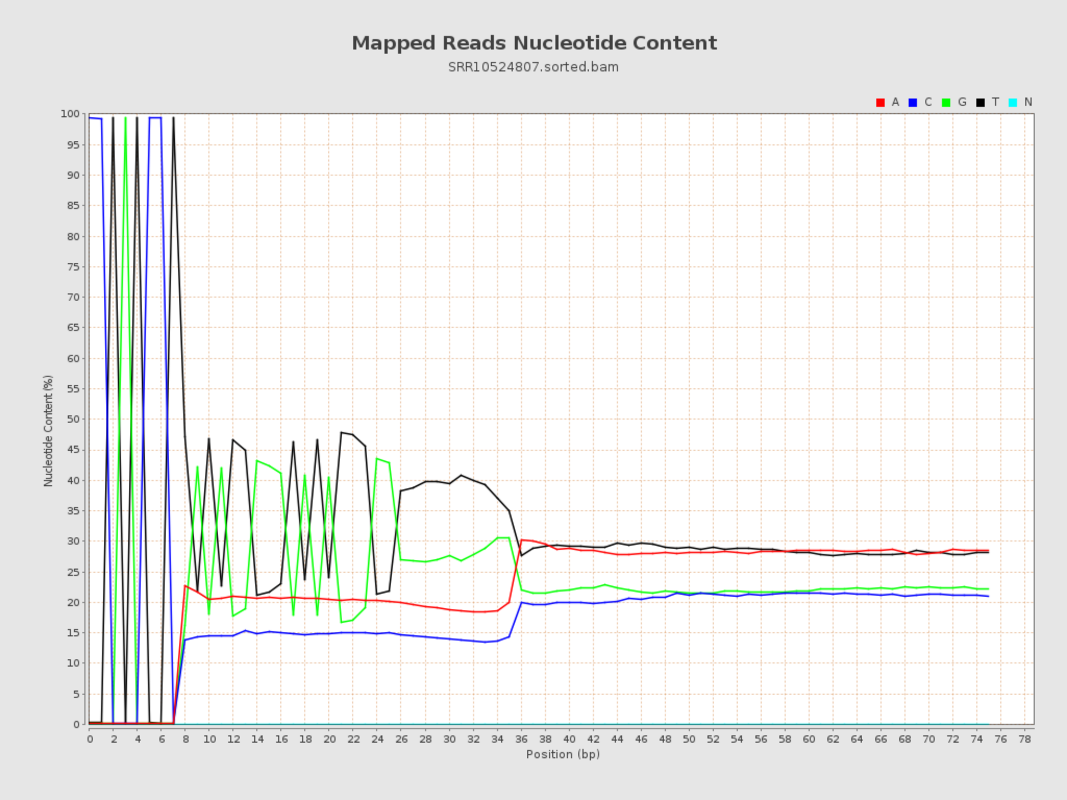
# 6. Results : Genome Fraction Coverage



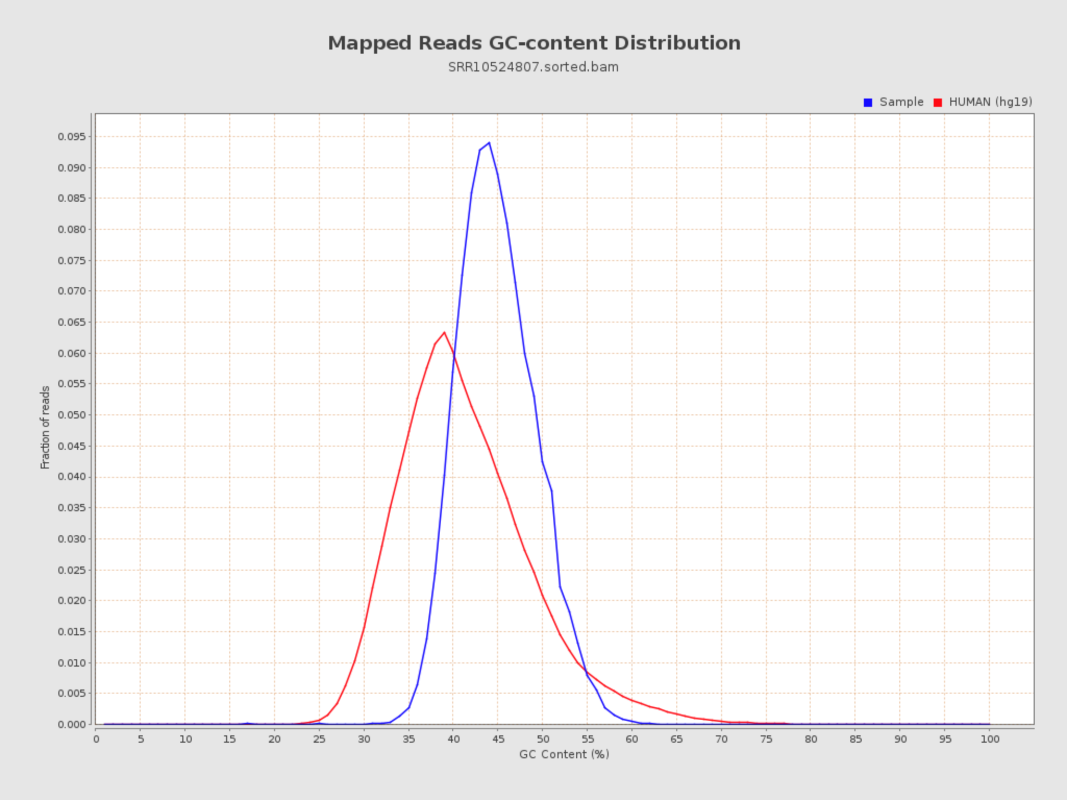
# 7. Results : Duplication Rate Histogram



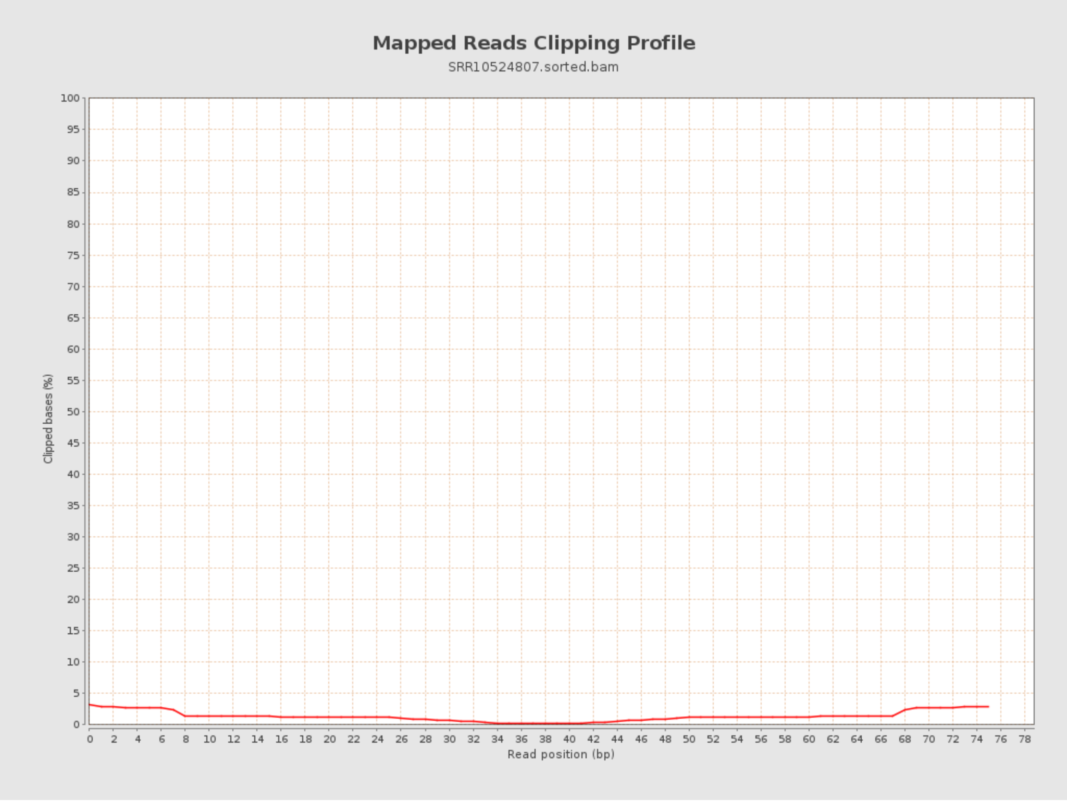
# 8. Results : Mapped Reads Nucleotide Content



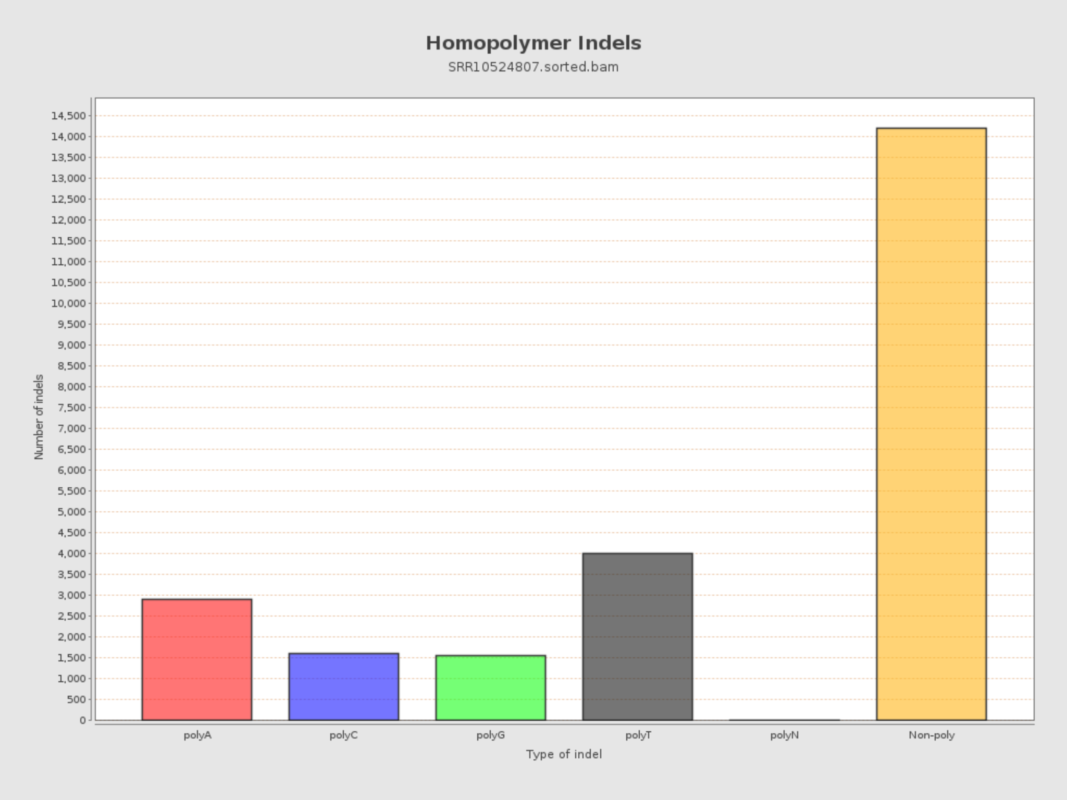
# 9. Results : Mapped Reads GC-content Distribution



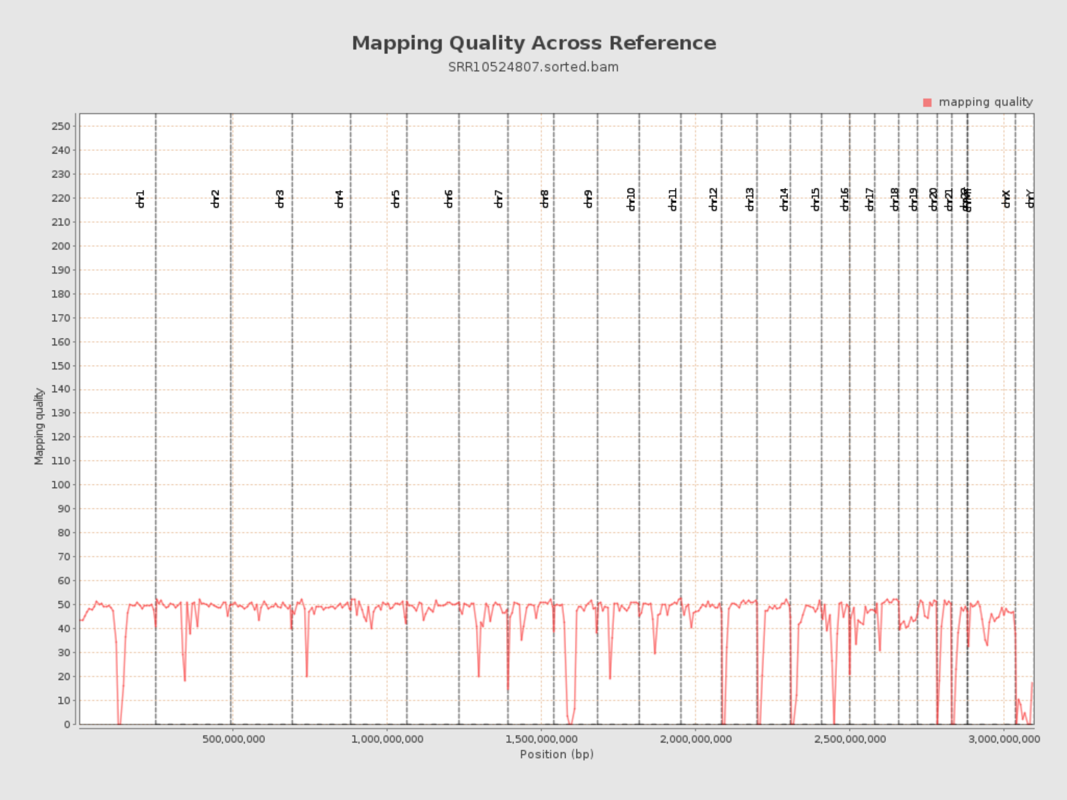
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram