# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 08:27:15*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524939.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_SRR10524939 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524939.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 08:27:12 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524939.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 985,230 |
| Mapped reads | 905,134 / 91.87% |
| Unmapped reads | 80,096 / 8.13% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,965 / 0.4% |
| Read min/max/mean length | 30 / 76 / 76.14 |
| Duplicated reads (estimated) | 34,559 / 3.51% |
| Duplication rate | 2.99% |
| Clipped reads | 906,598 / 92.02% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 13,849,749 / 26.26% |
| Number/percentage of C's | 9,448,770 / 17.92% |
| Number/percentage of T's | 16,517,999 / 31.32% |
| Number/percentage of G's | 12,917,892 / 24.5% |
| Number/percentage of N's | 407 / 0% |
| GC Percentage | 42.41% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.017 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1841 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.86 |

## 2.5. Mismatches and indels

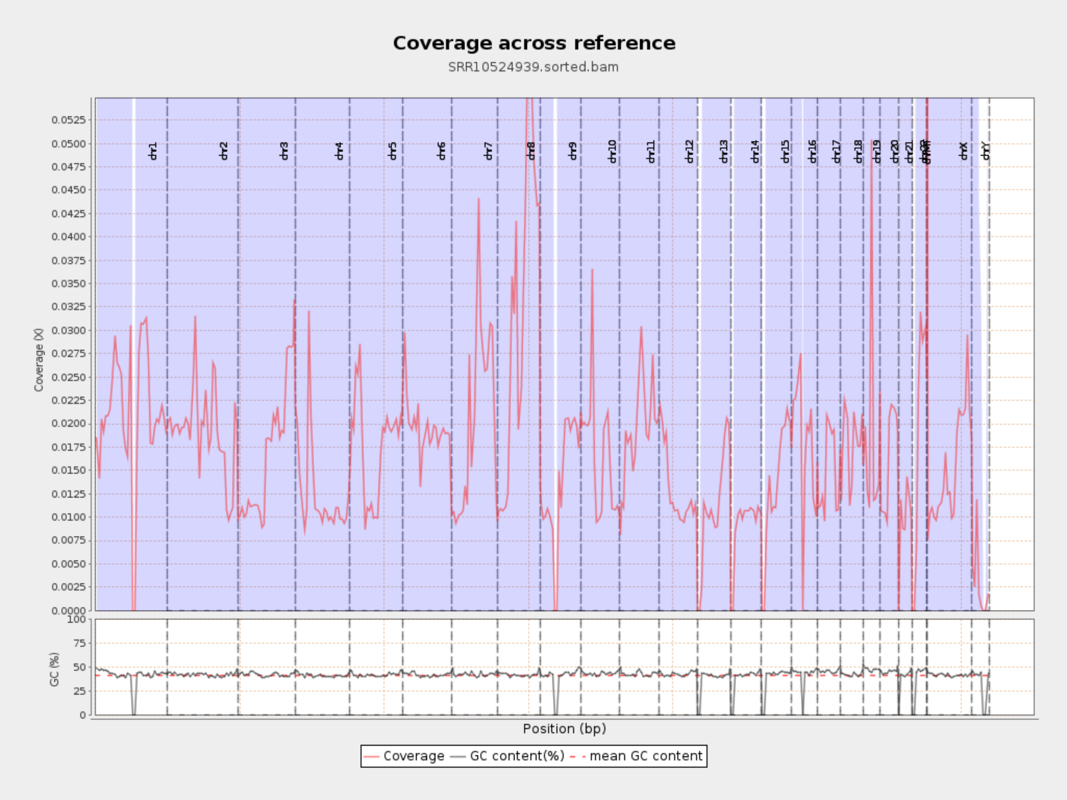
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 268,929 |
| Insertions | 3,699 |
| Mapped reads with at least one insertion | 0.41% |
| Deletions | 10,086 |
| Mapped reads with at least one deletion | 1.11% |
| Homopolymer indels | 41.94% |

## 2.6. Chromosome stats

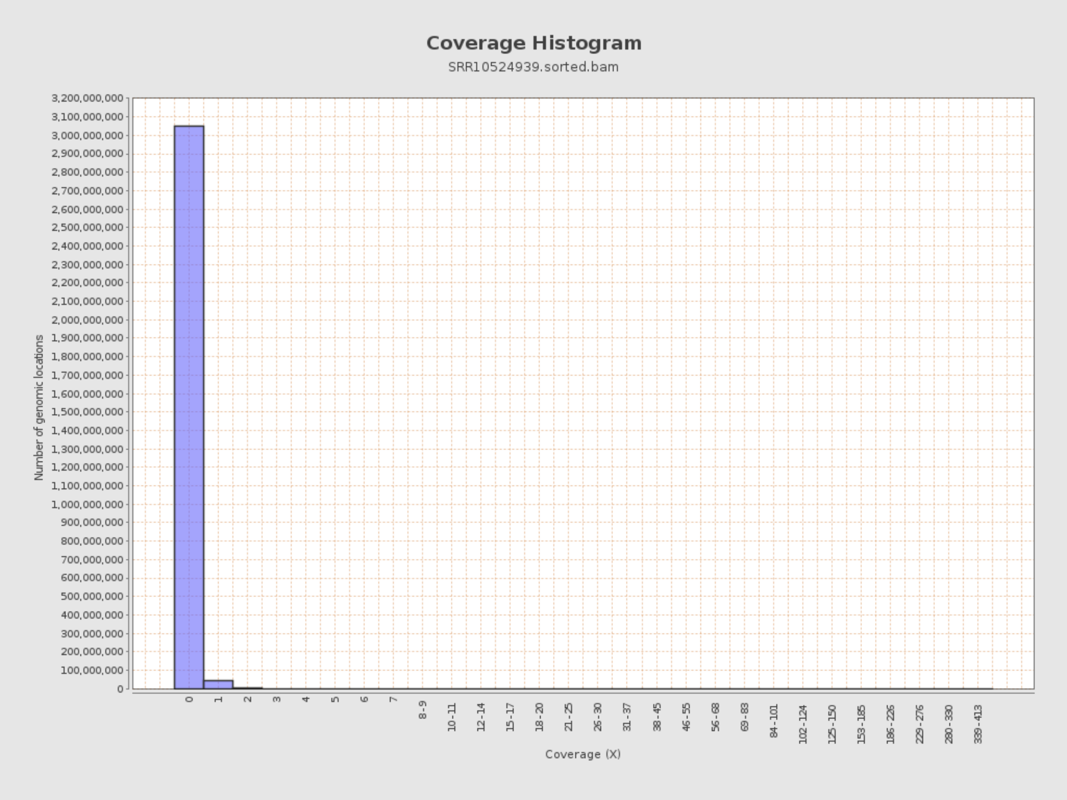
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5243950 | 0.021 | 0.3206 |
| chr2 | 243199373 | 4676171 | 0.0192 | 0.2197 |
| chr3 | 198022430 | 3292789 | 0.0166 | 0.1398 |
| chr4 | 191154276 | 2432625 | 0.0127 | 0.1426 |
| chr5 | 180915260 | 3197624 | 0.0177 | 0.1427 |
| chr6 | 171115067 | 3351889 | 0.0196 | 0.1563 |
| chr7 | 159138663 | 3291283 | 0.0207 | 0.2128 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4750461 | 0.0325 | 0.2449 |
| chr9 | 141213431 | 1901922 | 0.0135 | 0.1487 |
| chr10 | 135534747 | 2293079 | 0.0169 | 0.1981 |
| chr11 | 135006516 | 2668355 | 0.0198 | 0.1689 |
| chr12 | 133851895 | 1733533 | 0.013 | 0.1246 |
| chr13 | 115169878 | 1274323 | 0.0111 | 0.1134 |
| chr14 | 107349540 | 972919 | 0.0091 | 0.1049 |
| chr15 | 102531392 | 1360961 | 0.0133 | 0.1251 |
| chr16 | 90354753 | 1598545 | 0.0177 | 0.1493 |
| chr17 | 81195210 | 1190840 | 0.0147 | 0.1345 |
| chr18 | 78077248 | 1383859 | 0.0177 | 0.2207 |
| chr19 | 59128983 | 1111540 | 0.0188 | 0.2198 |
| chr20 | 63025520 | 1017676 | 0.0161 | 0.1402 |
| chr21 | 48129895 | 475811 | 0.0099 | 0.1287 |
| chr22 | 51304566 | 990229 | 0.0193 | 0.1504 |
| chrMT | 16571 | 5508 | 0.3324 | 0.6733 |
| chrX | 155270560 | 2367136 | 0.0152 | 0.1409 |
| chrY | 59373566 | 168882 | 0.0028 | 0.1172 |

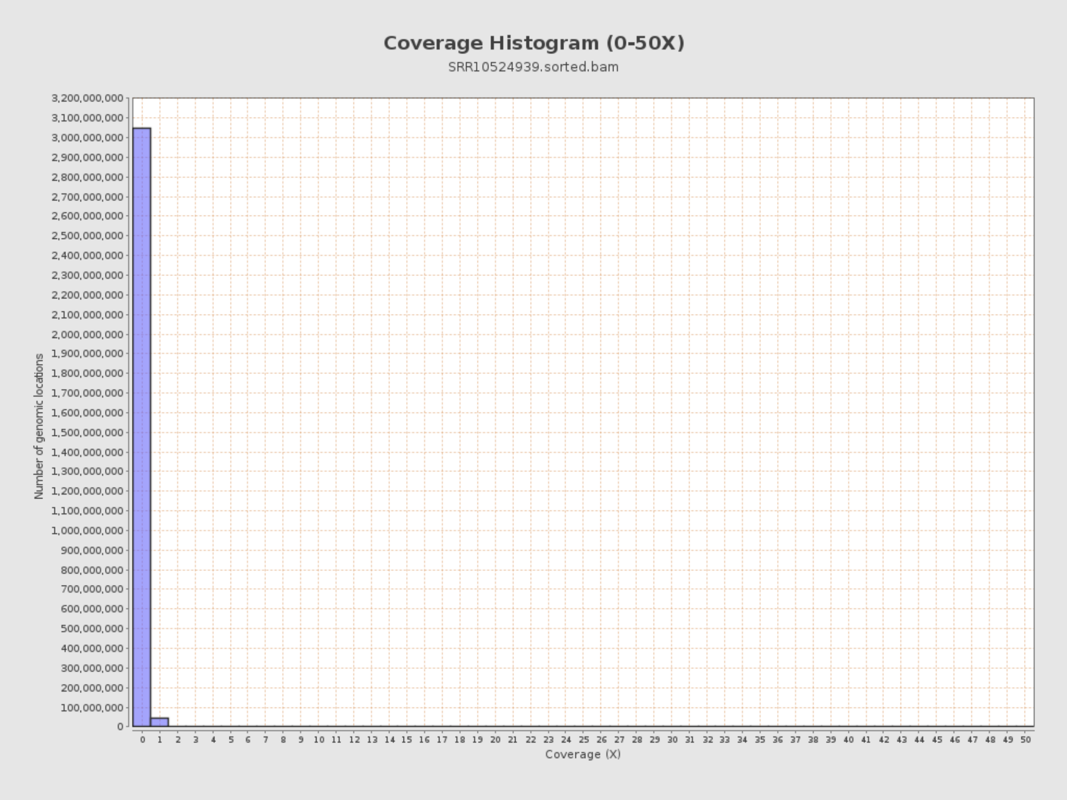
# 3. Results : Coverage across reference



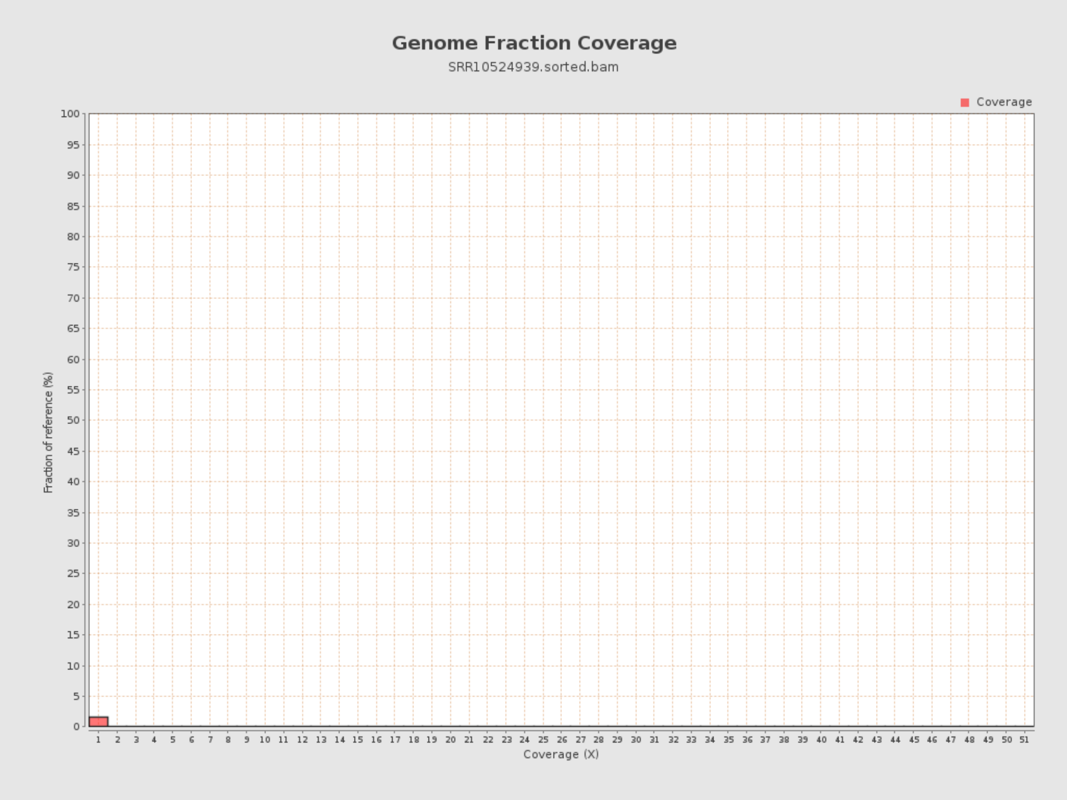
# 4. Results : Coverage Histogram



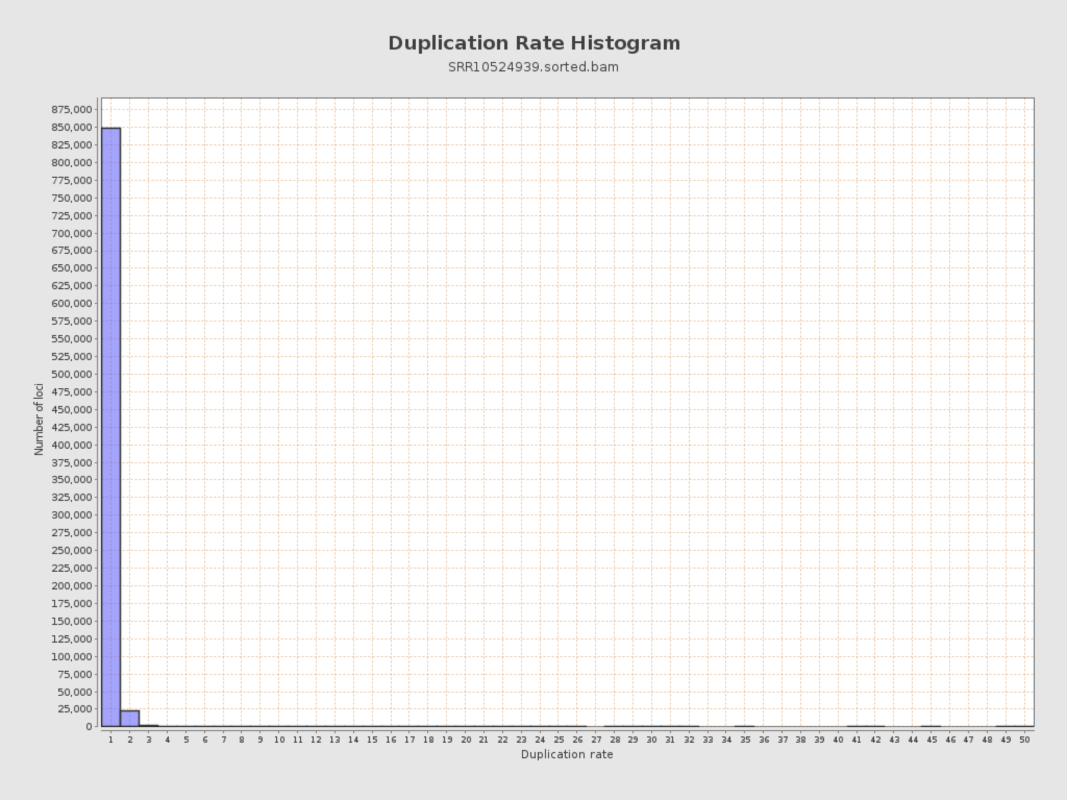
# 5. Results : Coverage Histogram (0-50X)



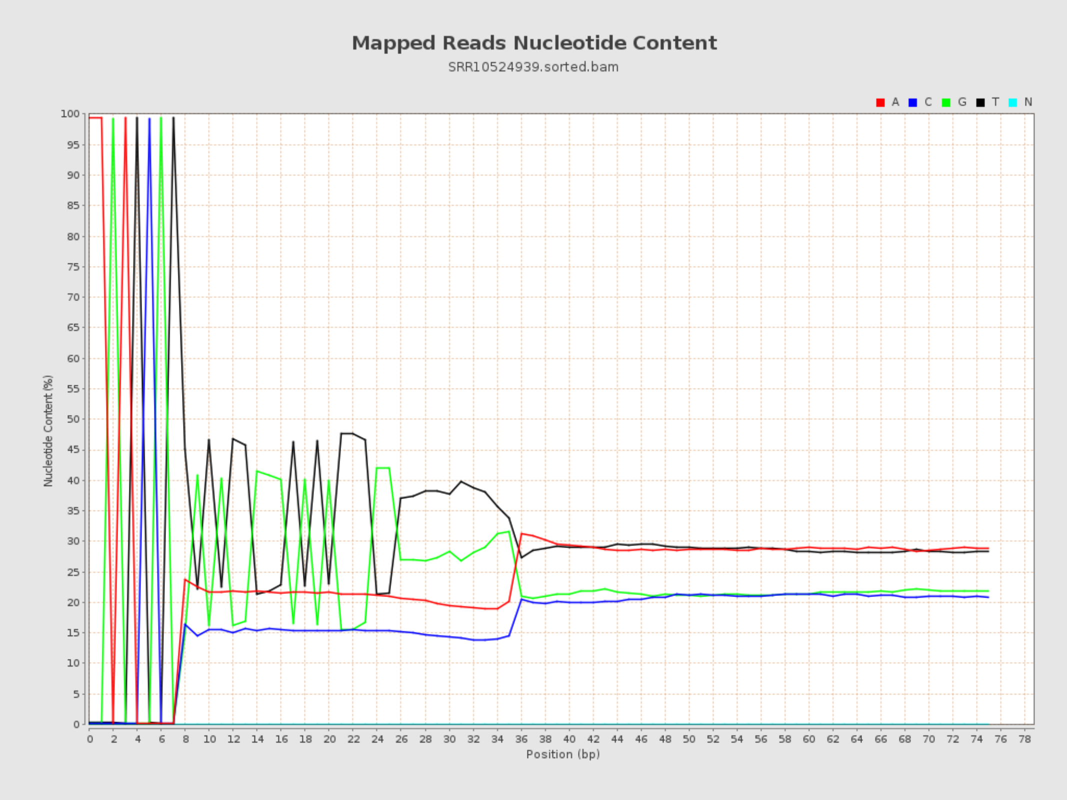
# 6. Results : Genome Fraction Coverage



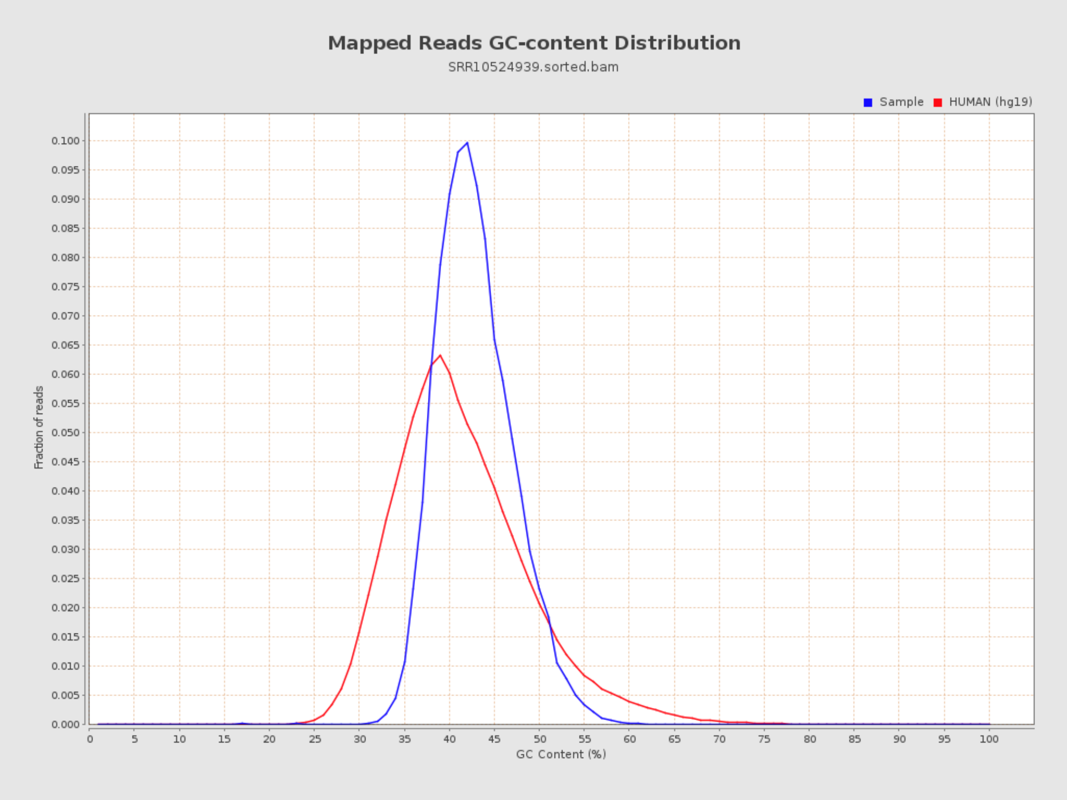
# 7. Results : Duplication Rate Histogram



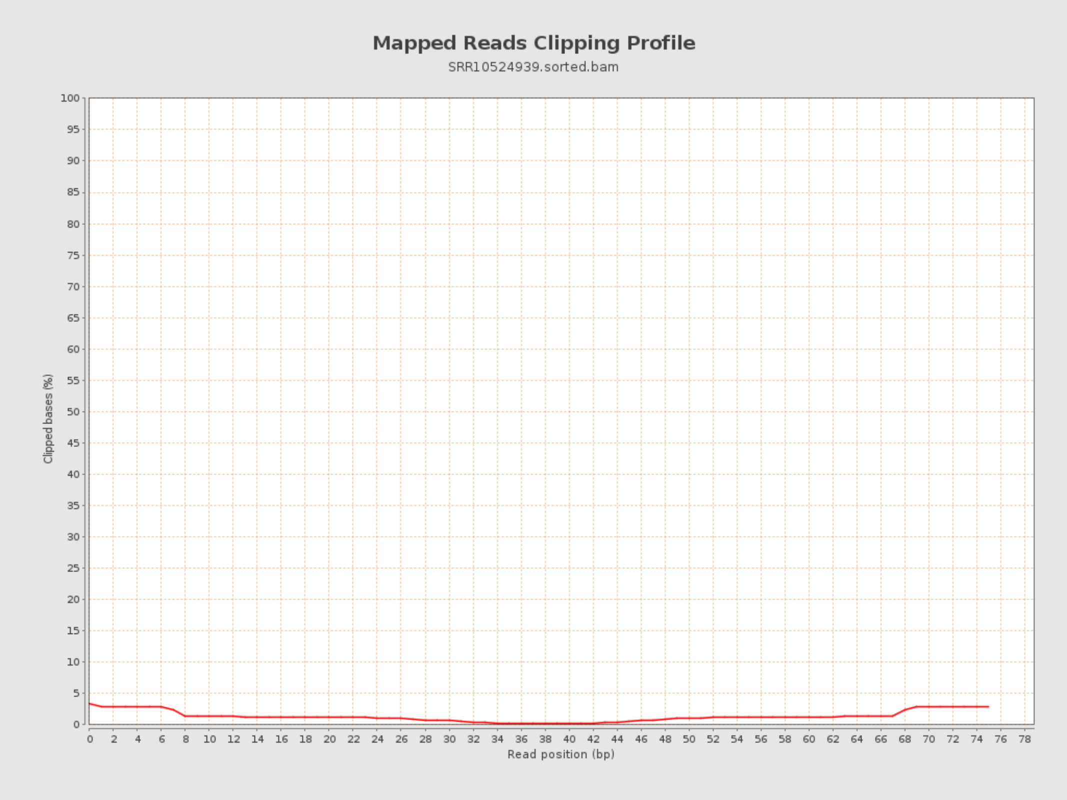
# 8. Results : Mapped Reads Nucleotide Content



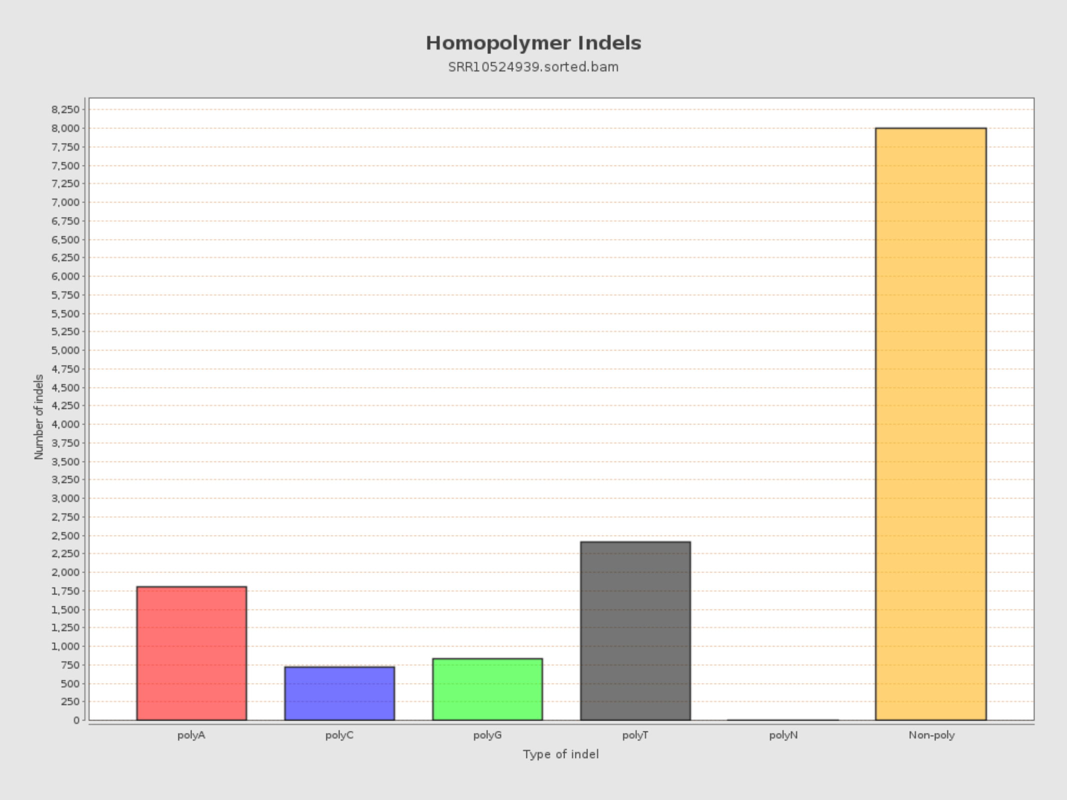
# 9. Results : Mapped Reads GC-content Distribution



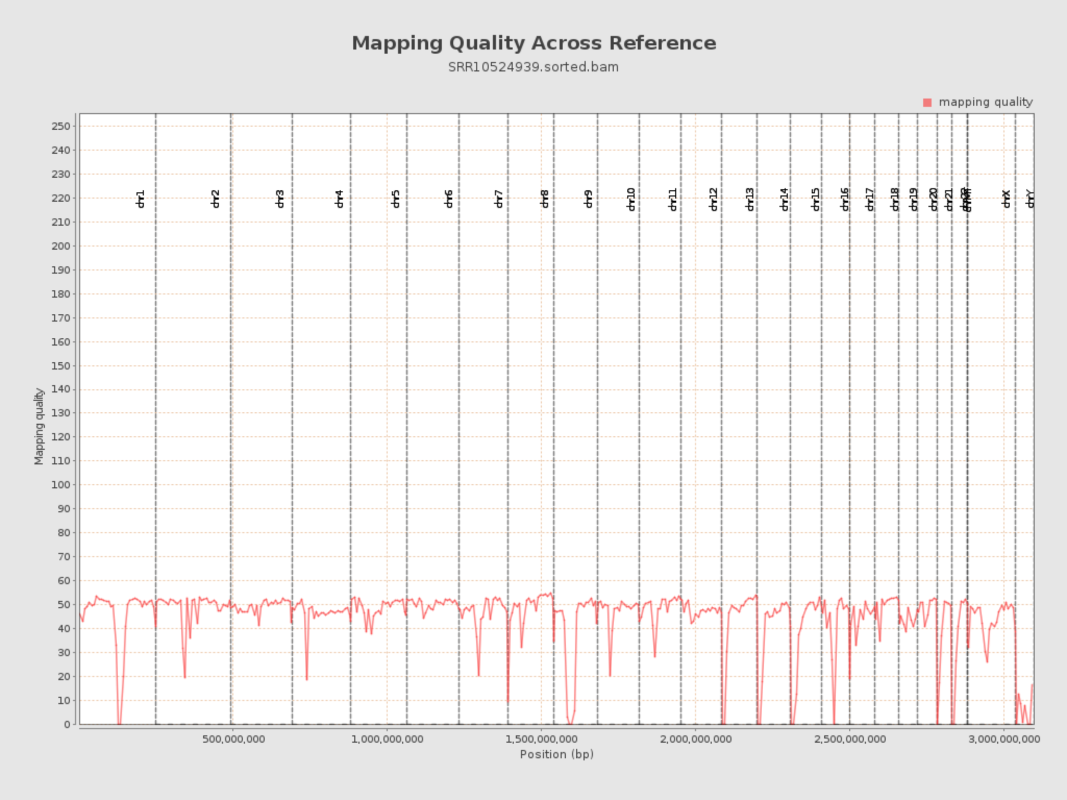
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram