# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 01:56:57*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524397.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_SRR10524397 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524397.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 01:56:56 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524397.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 540,299 |
| Mapped reads | 492,989 / 91.24% |
| Unmapped reads | 47,310 / 8.76% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 1,813 / 0.34% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 9,123 / 1.69% |
| Duplication rate | 1.35% |
| Clipped reads | 492,924 / 91.23% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 7,637,626 / 26.66% |
| Number/percentage of C's | 5,023,080 / 17.53% |
| Number/percentage of T's | 9,001,771 / 31.42% |
| Number/percentage of G's | 6,983,397 / 24.38% |
| Number/percentage of N's | 3,588 / 0.01% |
| GC Percentage | 41.91% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0093 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1209 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.69 |

## 2.5. Mismatches and indels

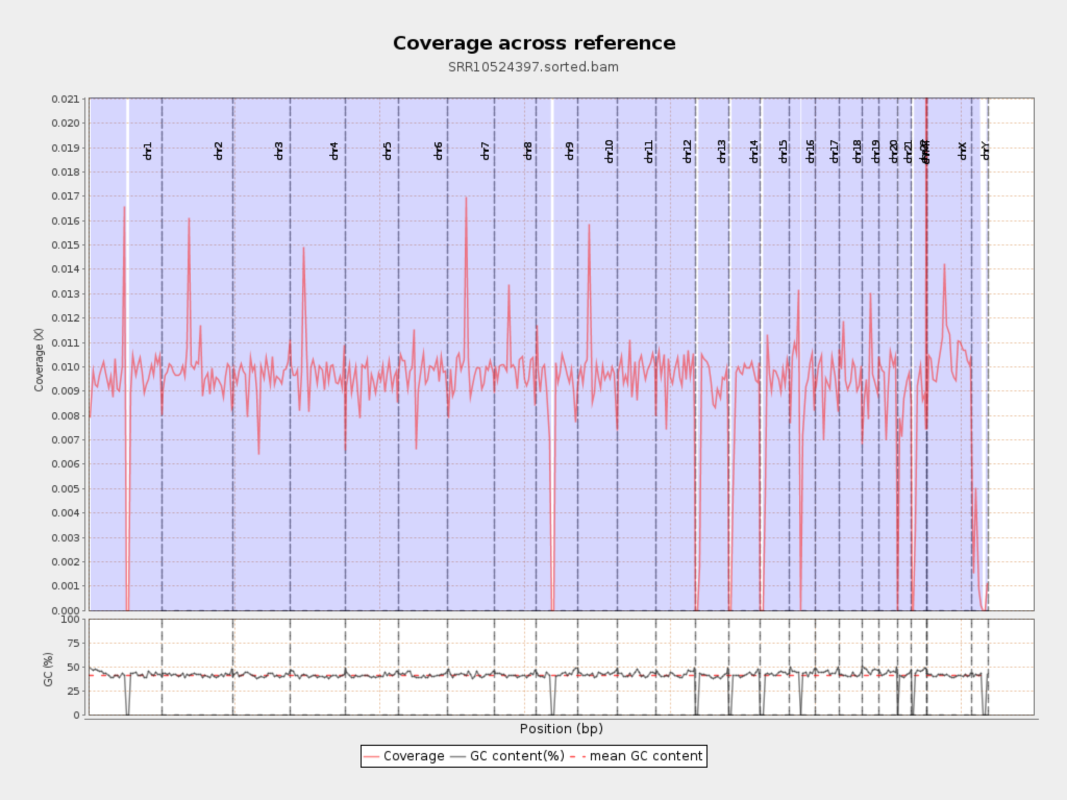
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 141,326 |
| Insertions | 2,361 |
| Mapped reads with at least one insertion | 0.48% |
| Deletions | 5,153 |
| Mapped reads with at least one deletion | 1.04% |
| Homopolymer indels | 43.73% |

## 2.6. Chromosome stats

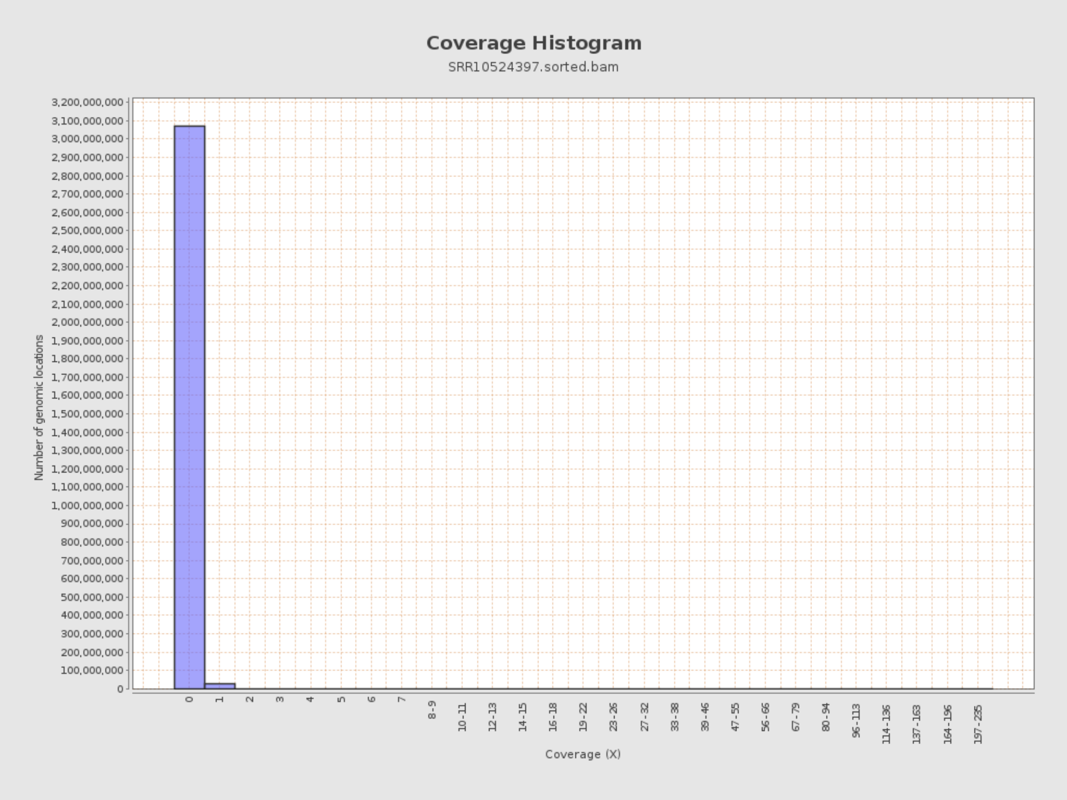
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 2305178 | 0.0092 | 0.1897 |
| chr2 | 243199373 | 2416485 | 0.0099 | 0.1354 |
| chr3 | 198022430 | 1896875 | 0.0096 | 0.1005 |
| chr4 | 191154276 | 1889258 | 0.0099 | 0.1059 |
| chr5 | 180915260 | 1712717 | 0.0095 | 0.1002 |
| chr6 | 171115067 | 1675979 | 0.0098 | 0.1066 |
| chr7 | 159138663 | 1597382 | 0.01 | 0.1518 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1465830 | 0.01 | 0.118 |
| chr9 | 141213431 | 1186312 | 0.0084 | 0.1092 |
| chr10 | 135534747 | 1346275 | 0.0099 | 0.1164 |
| chr11 | 135006516 | 1326026 | 0.0098 | 0.1175 |
| chr12 | 133851895 | 1312926 | 0.0098 | 0.1029 |
| chr13 | 115169878 | 912403 | 0.0079 | 0.0914 |
| chr14 | 107349540 | 883696 | 0.0082 | 0.0957 |
| chr15 | 102531392 | 821025 | 0.008 | 0.0921 |
| chr16 | 90354753 | 814316 | 0.009 | 0.0995 |
| chr17 | 81195210 | 753597 | 0.0093 | 0.102 |
| chr18 | 78077248 | 769554 | 0.0099 | 0.1697 |
| chr19 | 59128983 | 559831 | 0.0095 | 0.1403 |
| chr20 | 63025520 | 596298 | 0.0095 | 0.1017 |
| chr21 | 48129895 | 374587 | 0.0078 | 0.0946 |
| chr22 | 51304566 | 325058 | 0.0063 | 0.0817 |
| chrMT | 16571 | 1200 | 0.0724 | 0.2871 |
| chrX | 155270560 | 1628663 | 0.0105 | 0.1103 |
| chrY | 59373566 | 85937 | 0.0014 | 0.0501 |

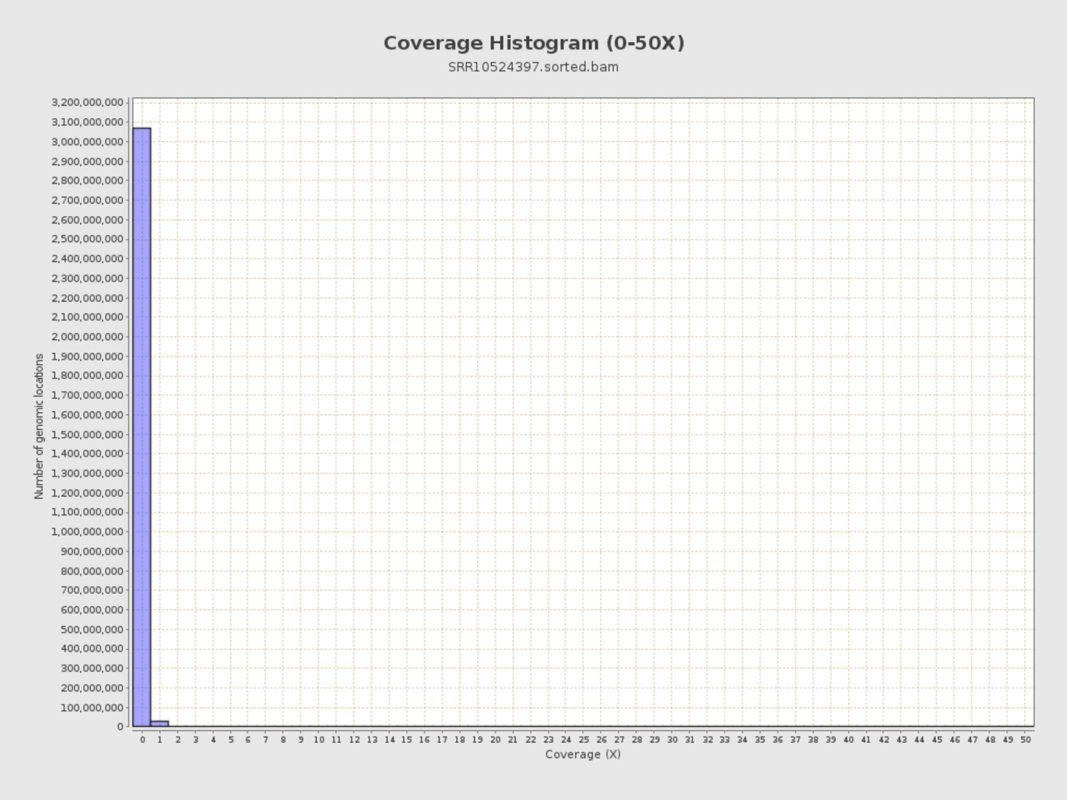
# 3. Results : Coverage across reference



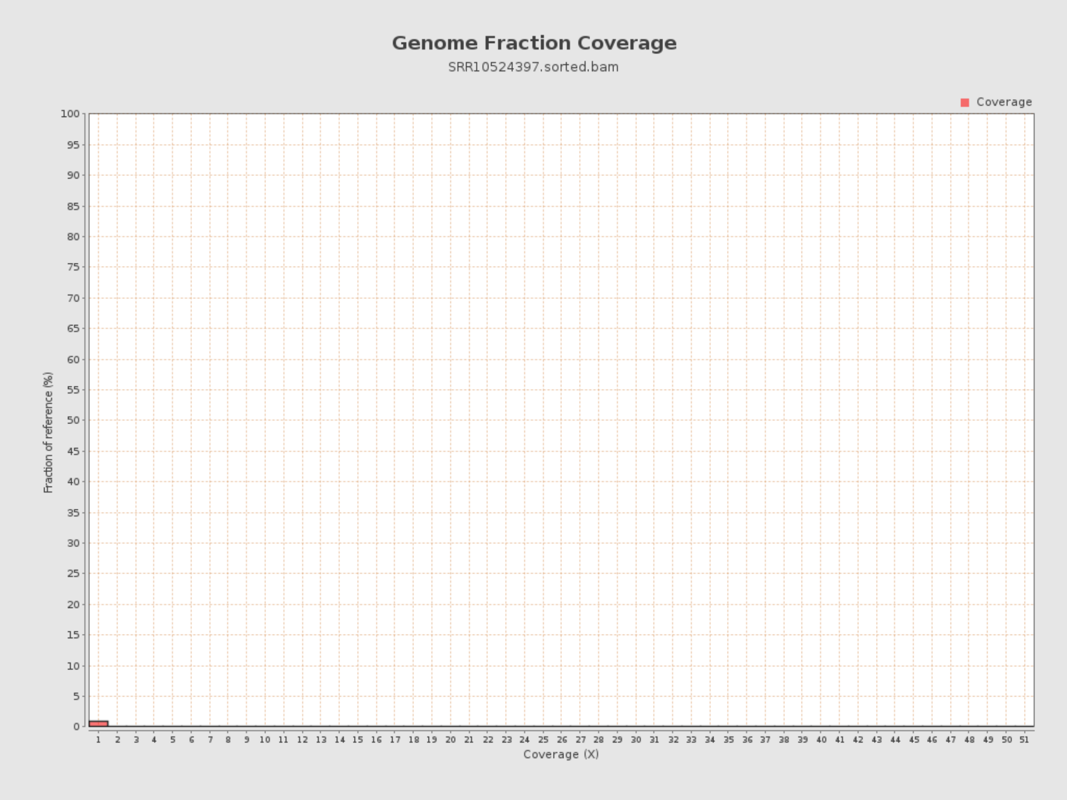
# 4. Results : Coverage Histogram



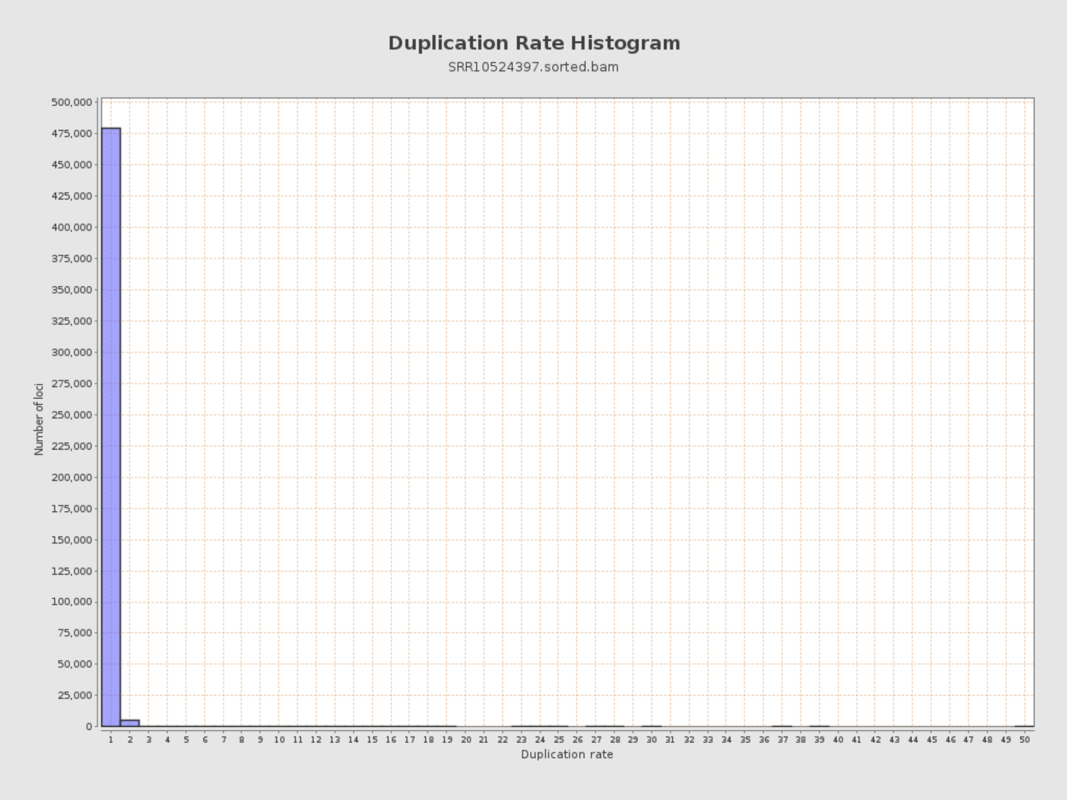
# 5. Results : Coverage Histogram (0-50X)



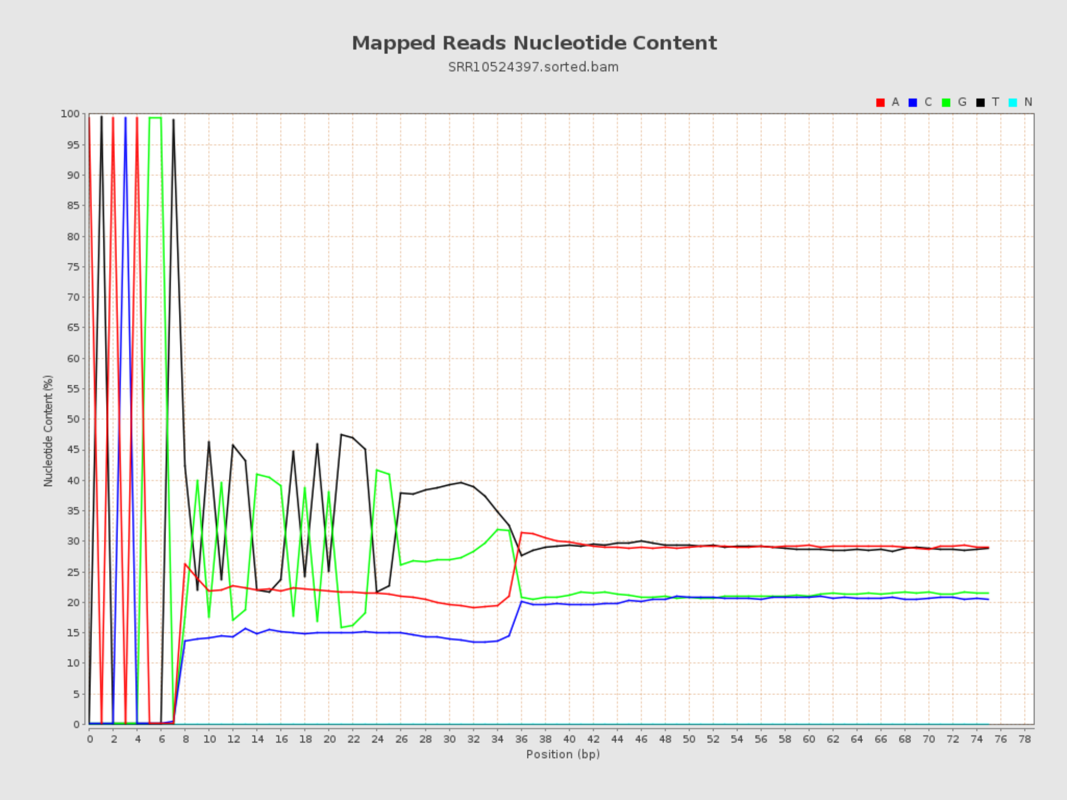
# 6. Results : Genome Fraction Coverage



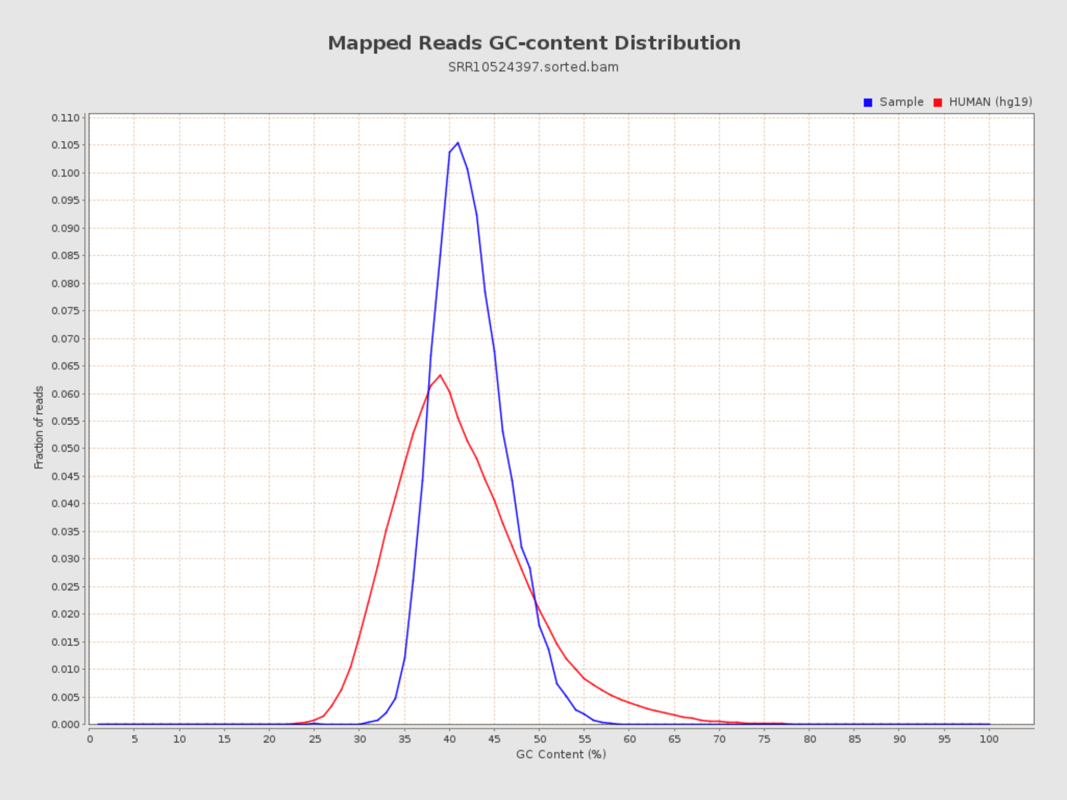
# 7. Results : Duplication Rate Histogram



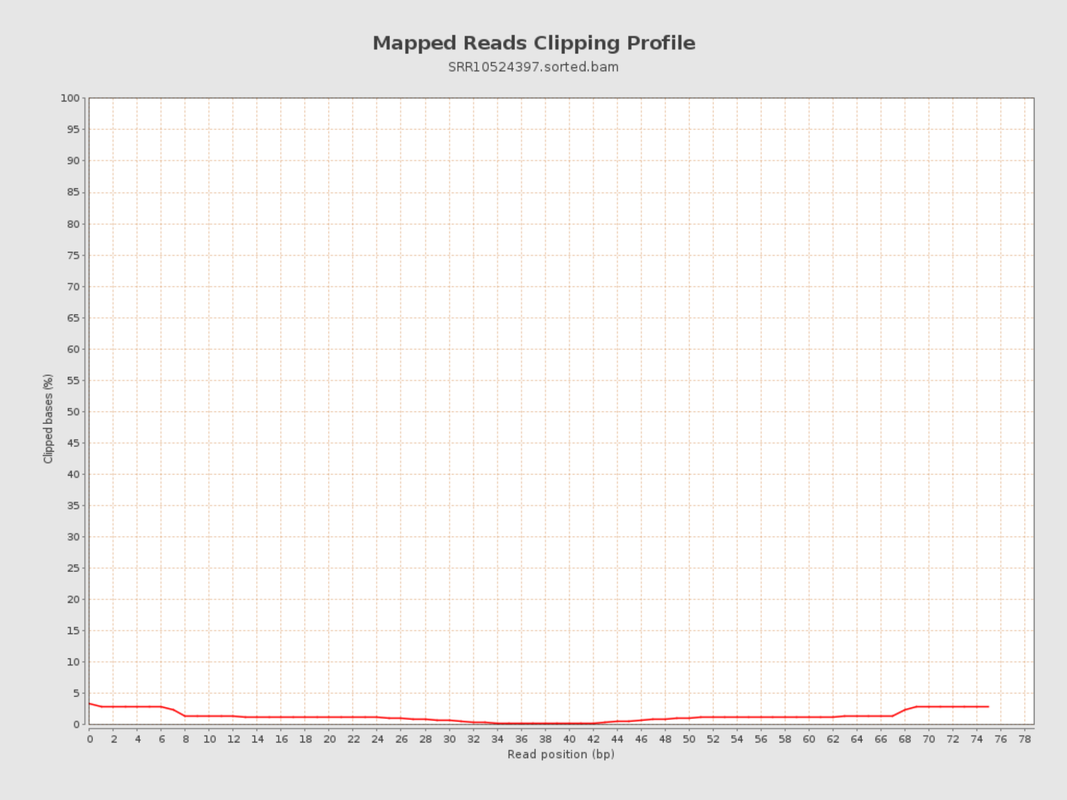
# 8. Results : Mapped Reads Nucleotide Content



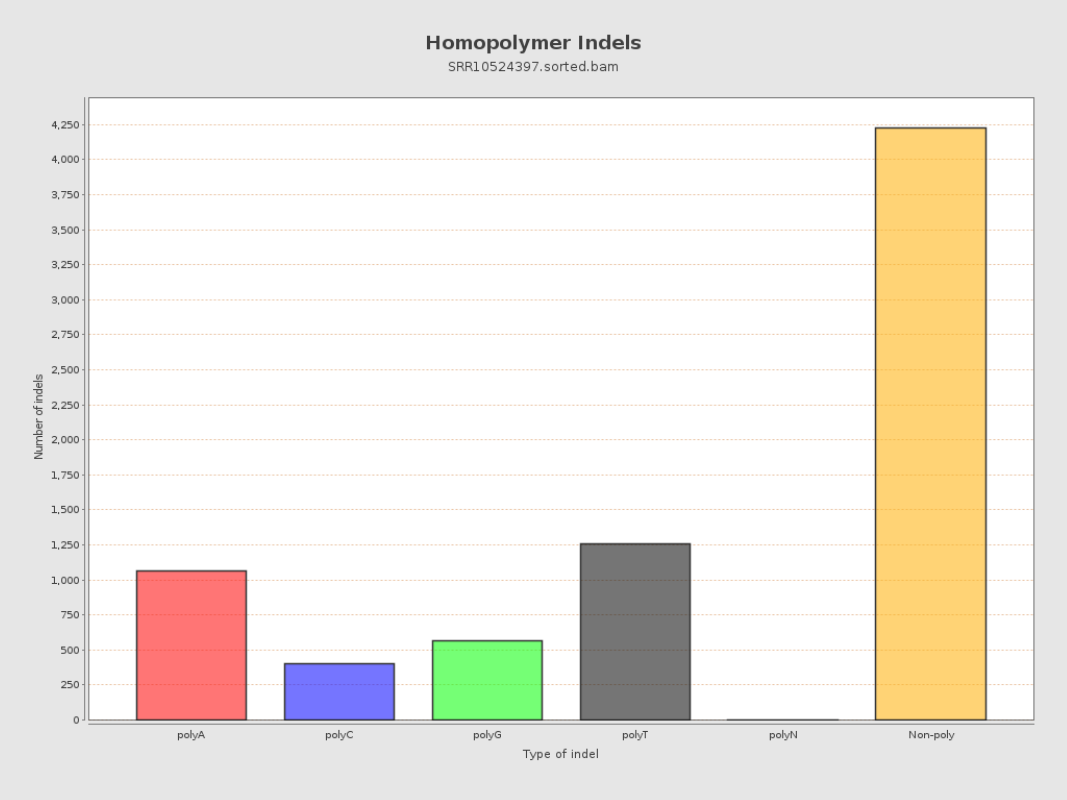
# 9. Results : Mapped Reads GC-content Distribution



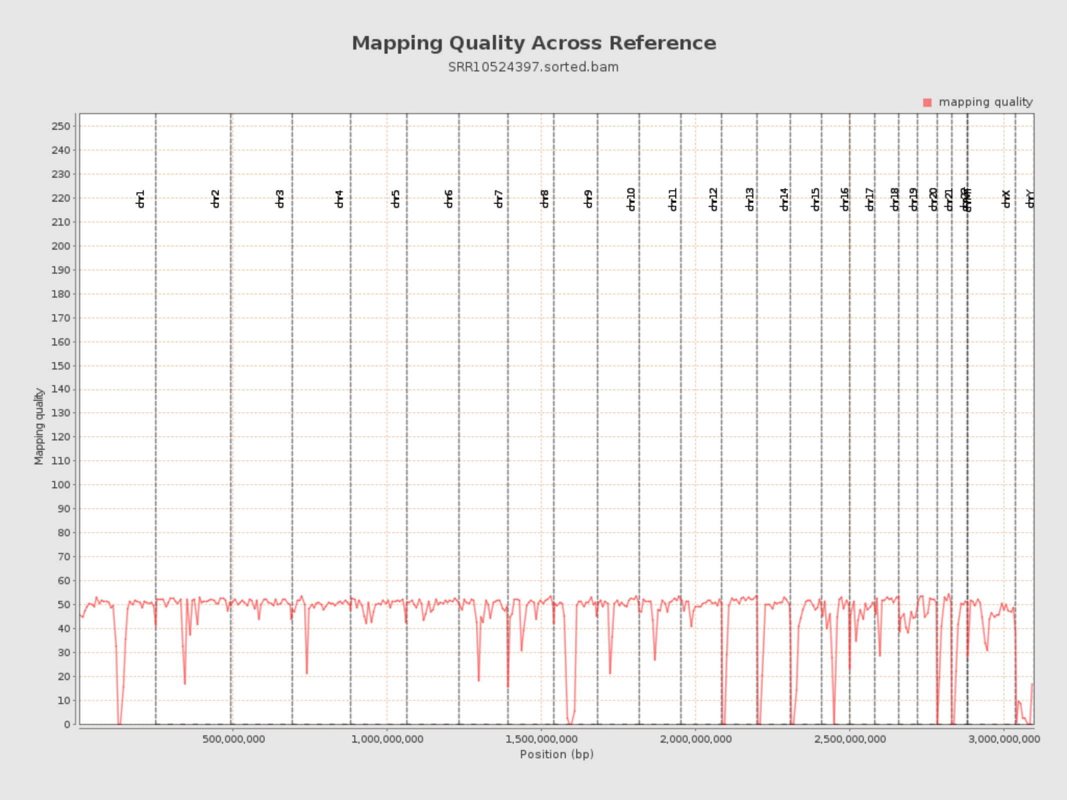
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram