# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 17:20:05*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524705.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_SRR10524705 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524705.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 17:20:05 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524705.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 576,461 |
| Mapped reads | 536,904 / 93.14% |
| Unmapped reads | 39,557 / 6.86% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 2,198 / 0.38% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 10,102 / 1.75% |
| Duplication rate | 1.38% |
| Clipped reads | 537,326 / 93.21% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 8,635,239 / 26.69% |
| Number/percentage of C's | 6,200,921 / 19.16% |
| Number/percentage of T's | 9,698,146 / 29.97% |
| Number/percentage of G's | 7,819,076 / 24.16% |
| Number/percentage of N's | 4,491 / 0.01% |
| GC Percentage | 43.33% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0105 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1282 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.31 |

## 2.5. Mismatches and indels

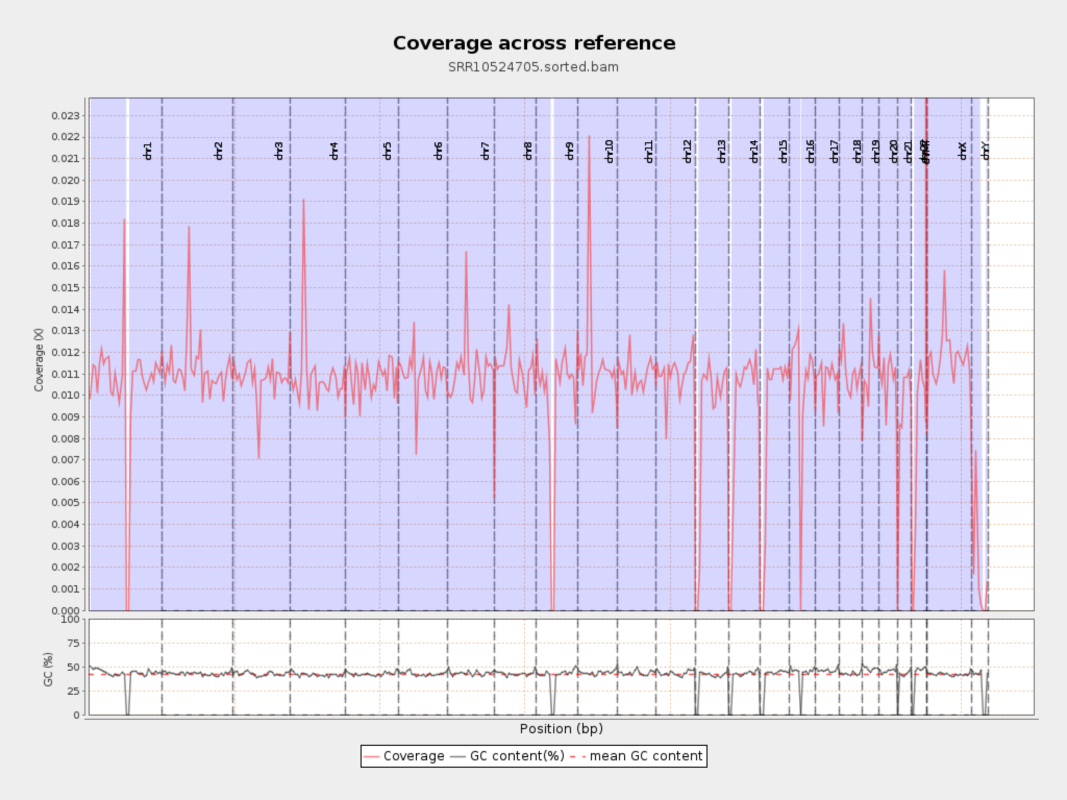
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 158,028 |
| Insertions | 2,643 |
| Mapped reads with at least one insertion | 0.49% |
| Deletions | 6,277 |
| Mapped reads with at least one deletion | 1.16% |
| Homopolymer indels | 41.64% |

## 2.6. Chromosome stats

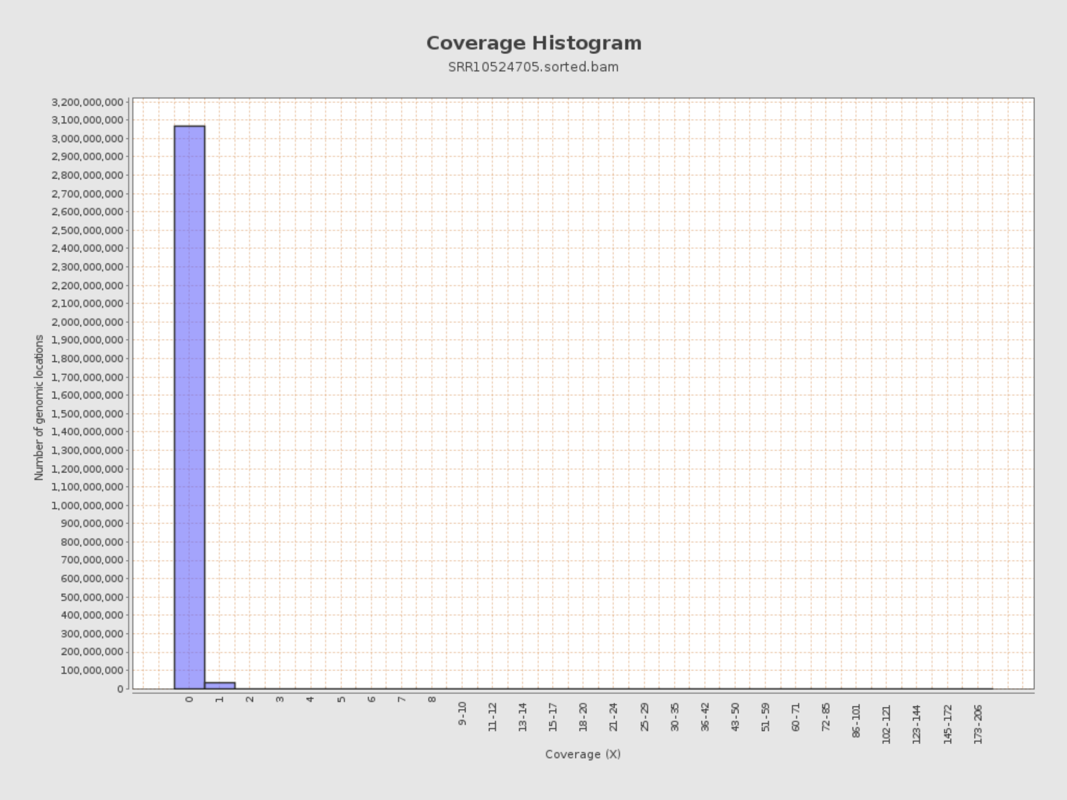
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 2605657 | 0.0105 | 0.19 |
| chr2 | 243199373 | 2745061 | 0.0113 | 0.1458 |
| chr3 | 198022430 | 2125040 | 0.0107 | 0.1068 |
| chr4 | 191154276 | 2083291 | 0.0109 | 0.1145 |
| chr5 | 180915260 | 1956205 | 0.0108 | 0.1074 |
| chr6 | 171115067 | 1875419 | 0.011 | 0.1129 |
| chr7 | 159138663 | 1774693 | 0.0112 | 0.1465 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1635279 | 0.0112 | 0.1458 |
| chr9 | 141213431 | 1347235 | 0.0095 | 0.1145 |
| chr10 | 135534747 | 1574998 | 0.0116 | 0.1401 |
| chr11 | 135006516 | 1480109 | 0.011 | 0.1206 |
| chr12 | 133851895 | 1468902 | 0.011 | 0.1085 |
| chr13 | 115169878 | 1018324 | 0.0088 | 0.0973 |
| chr14 | 107349540 | 976603 | 0.0091 | 0.1007 |
| chr15 | 102531392 | 914383 | 0.0089 | 0.0973 |
| chr16 | 90354753 | 945394 | 0.0105 | 0.1093 |
| chr17 | 81195210 | 874769 | 0.0108 | 0.1099 |
| chr18 | 78077248 | 872171 | 0.0112 | 0.1748 |
| chr19 | 59128983 | 666318 | 0.0113 | 0.1539 |
| chr20 | 63025520 | 680664 | 0.0108 | 0.1087 |
| chr21 | 48129895 | 434721 | 0.009 | 0.1038 |
| chr22 | 51304566 | 376512 | 0.0073 | 0.0884 |
| chrMT | 16571 | 3793 | 0.2289 | 0.5068 |
| chrX | 155270560 | 1821164 | 0.0117 | 0.1162 |
| chrY | 59373566 | 111266 | 0.0019 | 0.0767 |

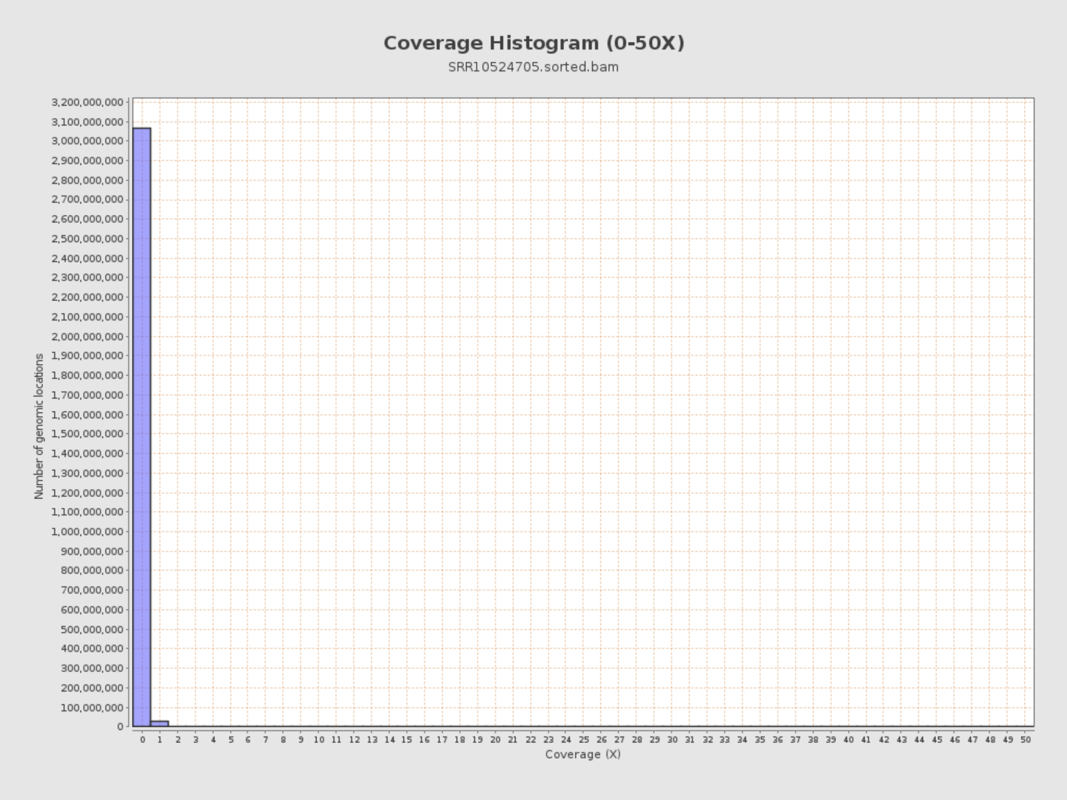
# 3. Results : Coverage across reference



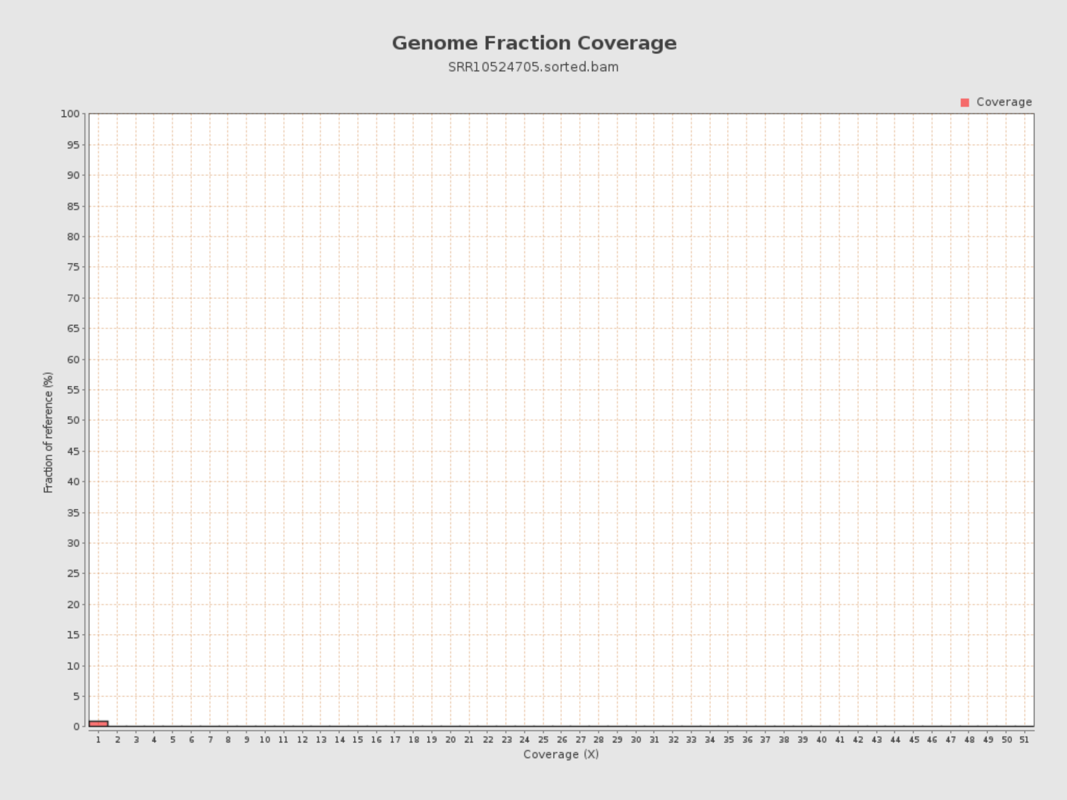
# 4. Results : Coverage Histogram



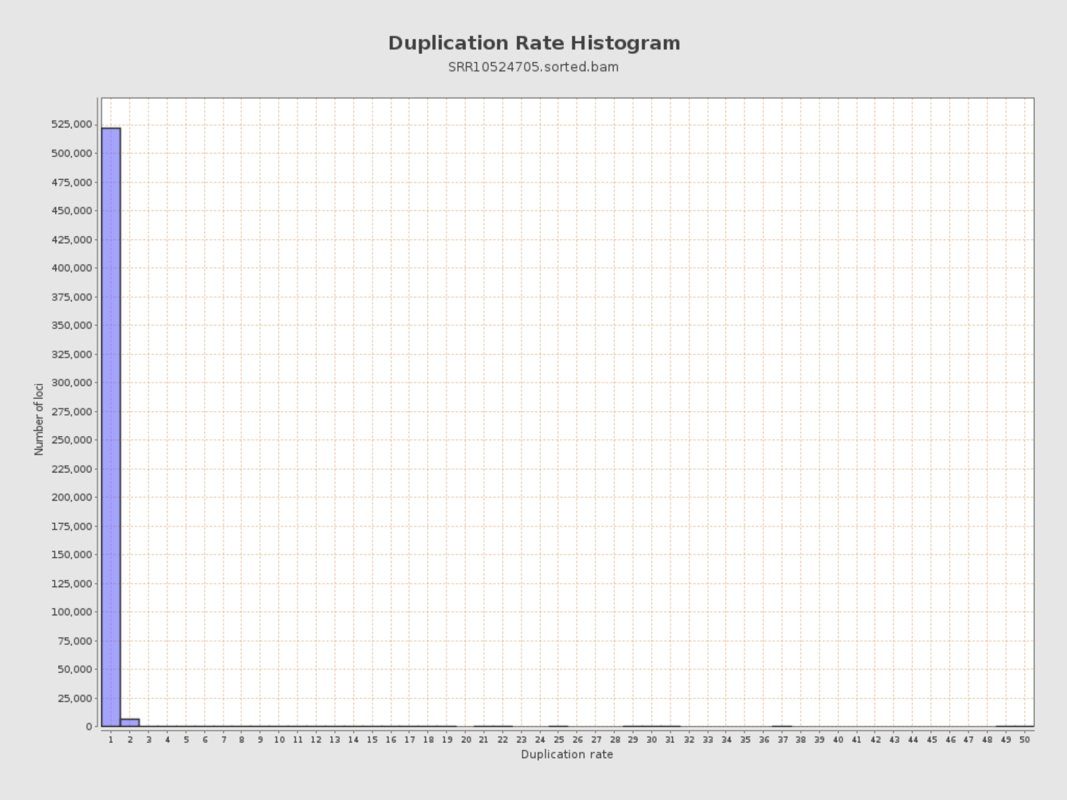
# 5. Results : Coverage Histogram (0-50X)



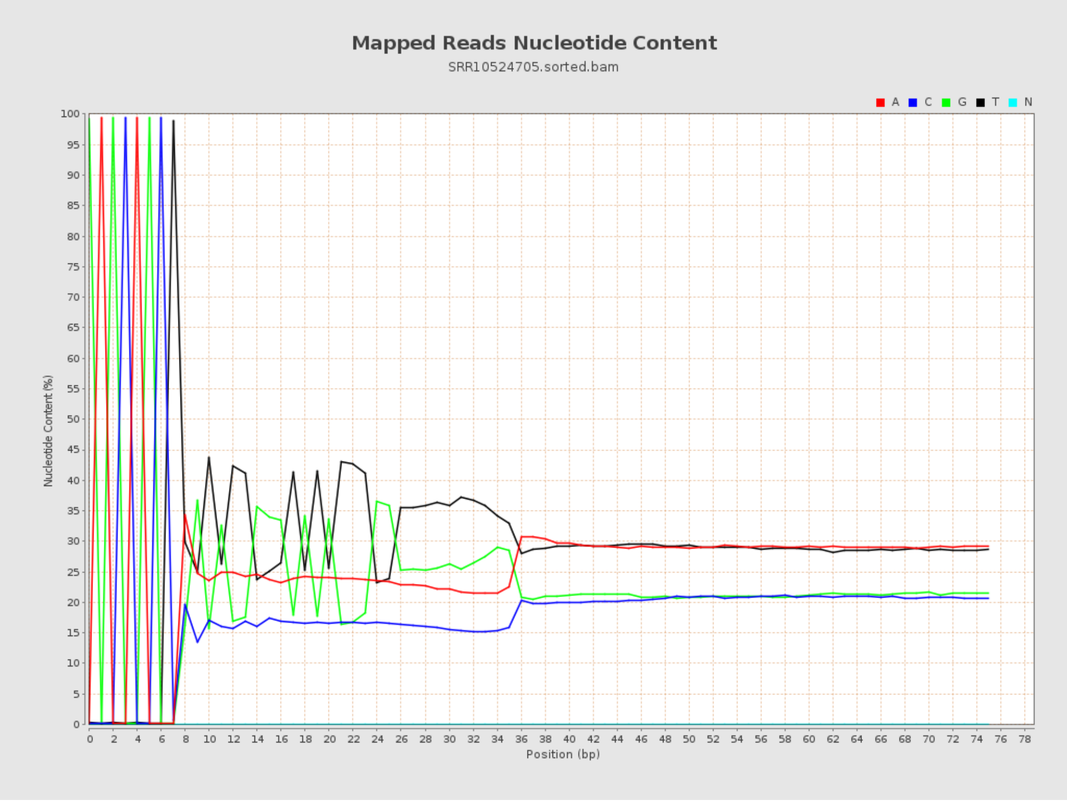
# 6. Results : Genome Fraction Coverage



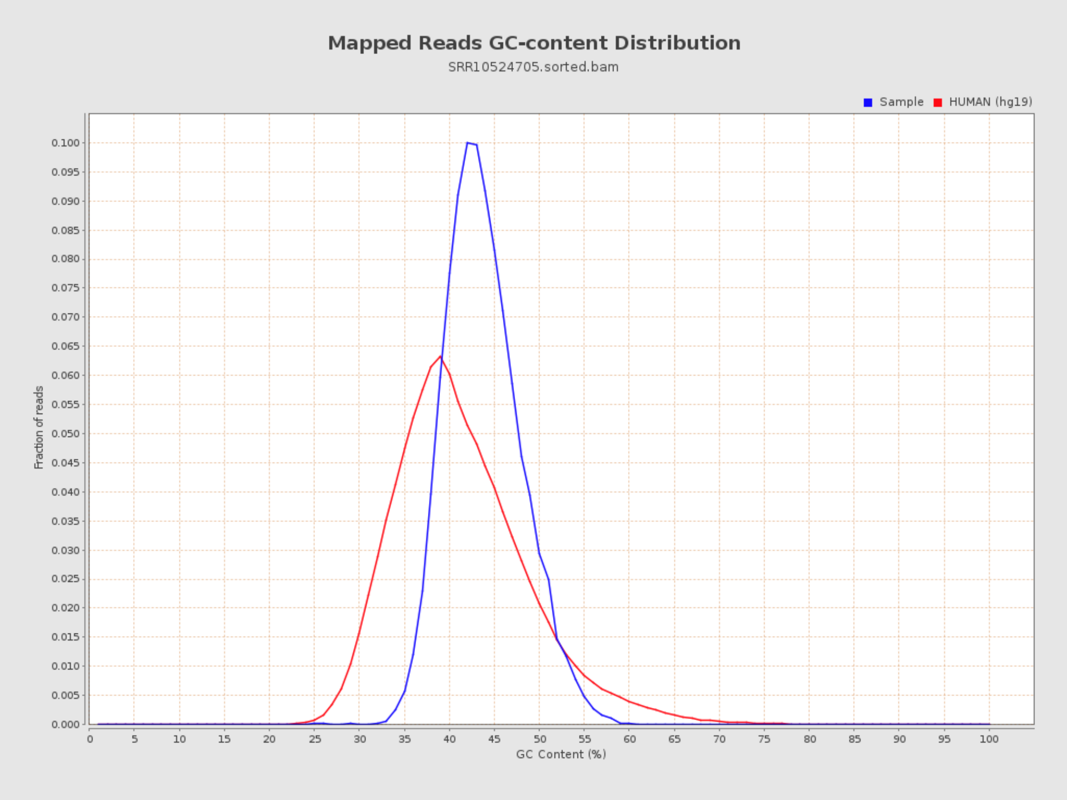
# 7. Results : Duplication Rate Histogram



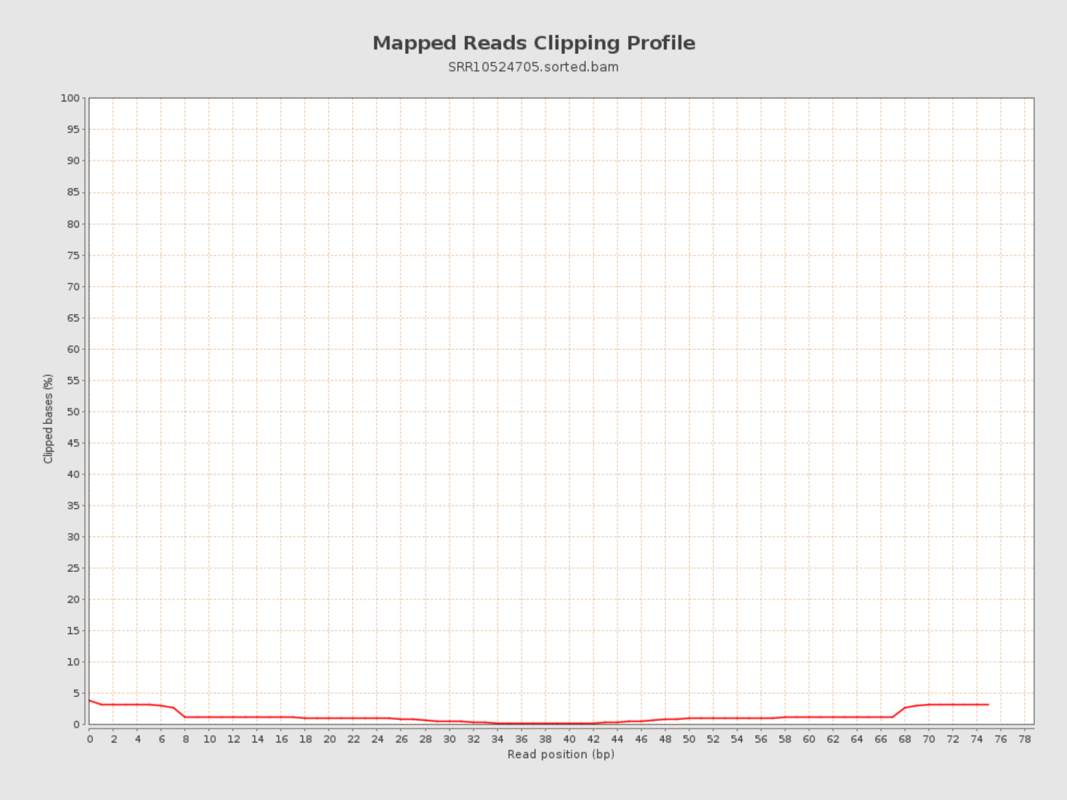
# 8. Results : Mapped Reads Nucleotide Content



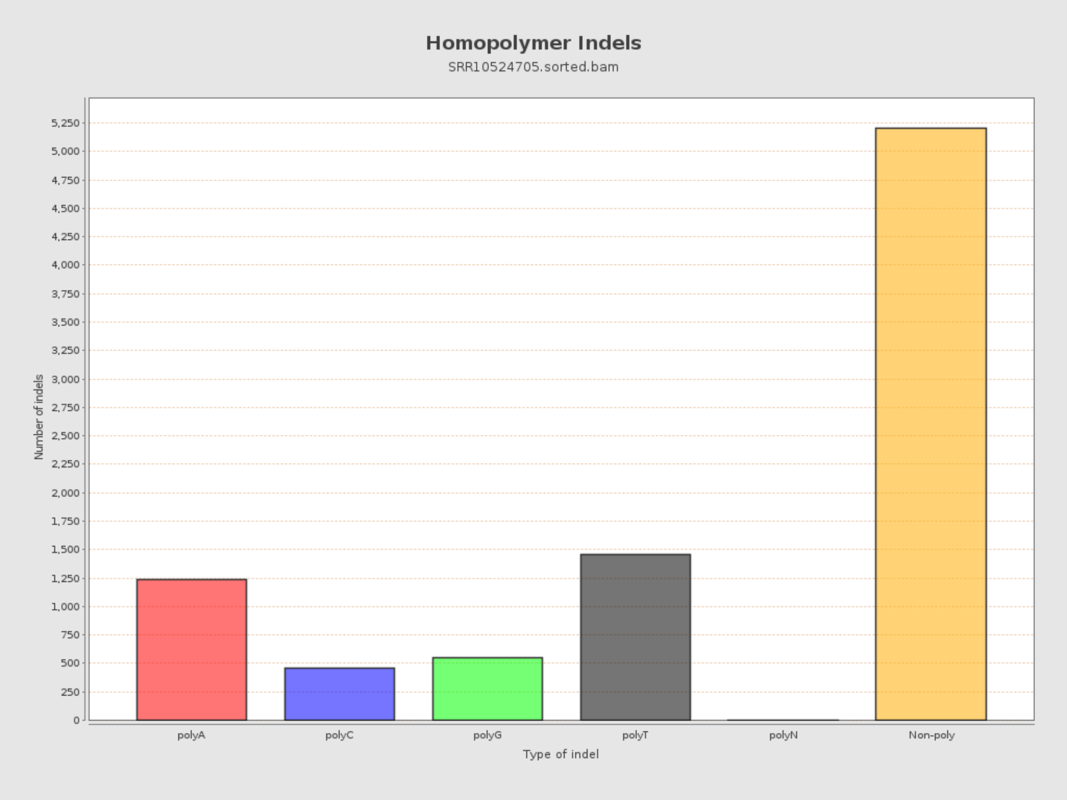
# 9. Results : Mapped Reads GC-content Distribution



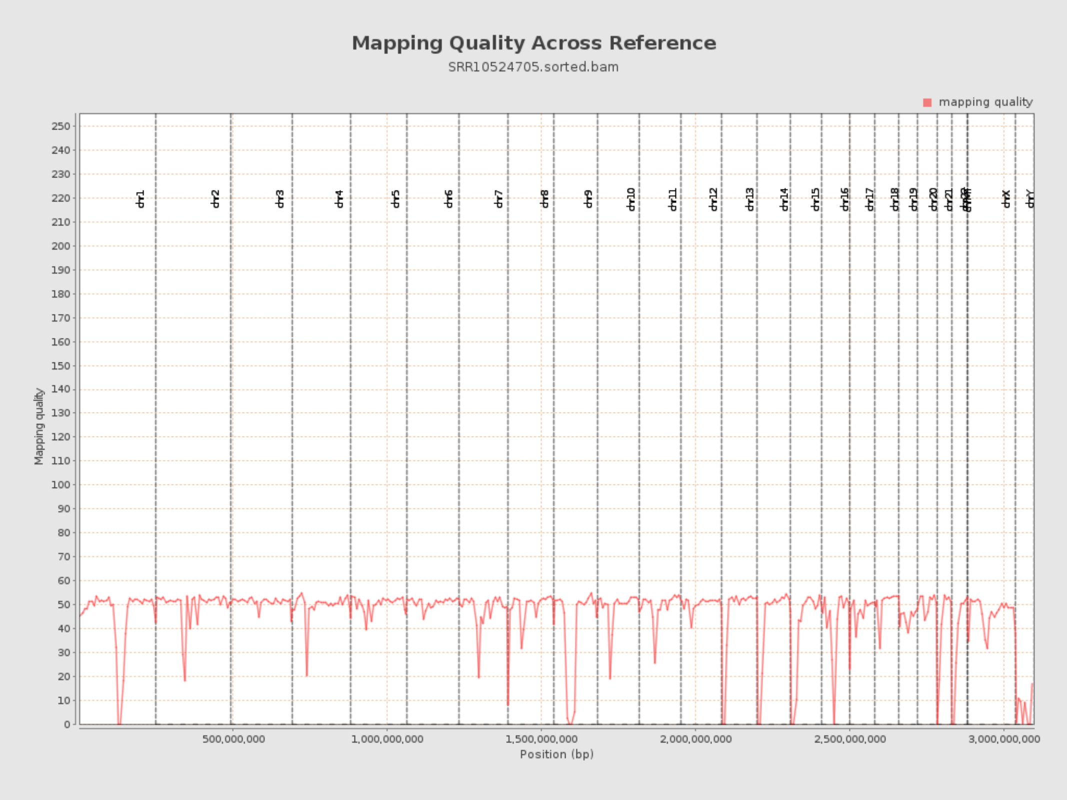
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram