# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 04:30:04*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524440.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_SRR10524440 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524440.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 04:30:03 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524440.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 694,195 |
| Mapped reads | 636,708 / 91.72% |
| Unmapped reads | 57,487 / 8.28% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 2,747 / 0.4% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 19,777 / 2.85% |
| Duplication rate | 2.34% |
| Clipped reads | 638,767 / 92.02% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 8,973,381 / 24.15% |
| Number/percentage of C's | 6,927,234 / 18.64% |
| Number/percentage of T's | 11,424,437 / 30.75% |
| Number/percentage of G's | 9,826,896 / 26.45% |
| Number/percentage of N's | 3,774 / 0.01% |
| GC Percentage | 45.09% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.012 |
| | |

| | |
|---|---|
| Standard Deviation | 0.1519 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.9 |

## 2.5. Mismatches and indels

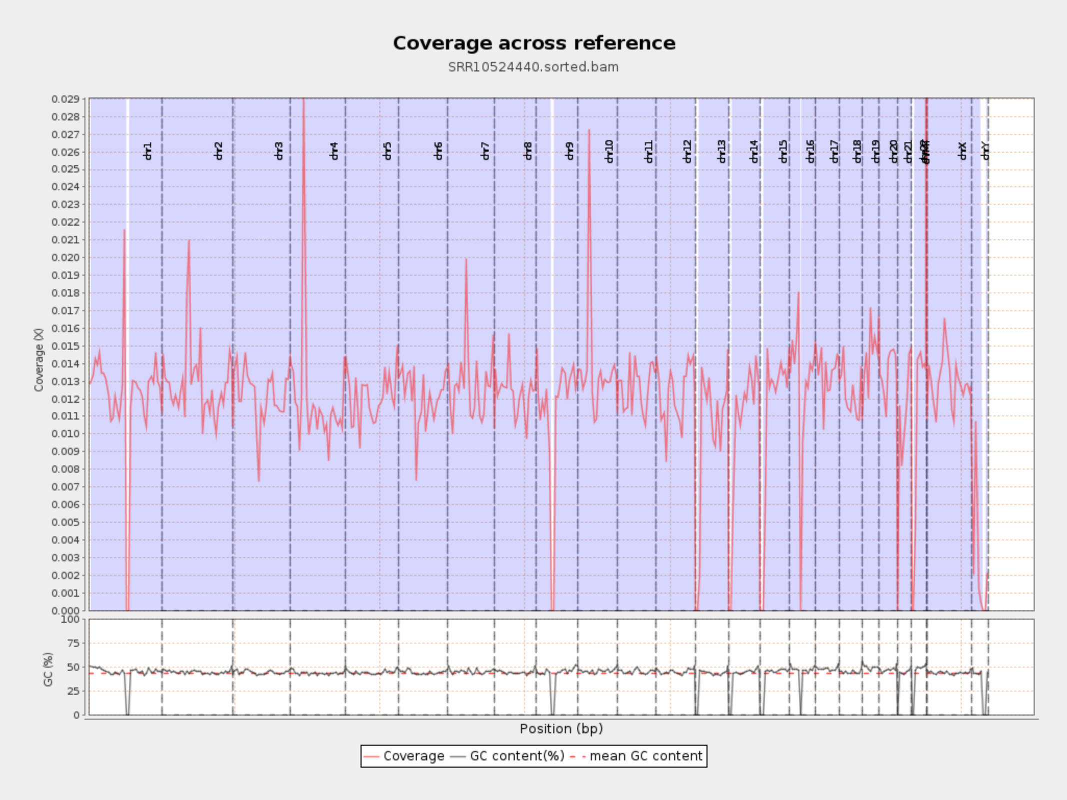
| | |
|---|---|
| General error rate | 0.53% |
| Mismatches | 191,265 |
| Insertions | 2,324 |
| Mapped reads with at least one insertion | 0.36% |
| Deletions | 6,315 |
| Mapped reads with at least one deletion | 0.98% |
| Homopolymer indels | 42.01% |

## 2.6. Chromosome stats

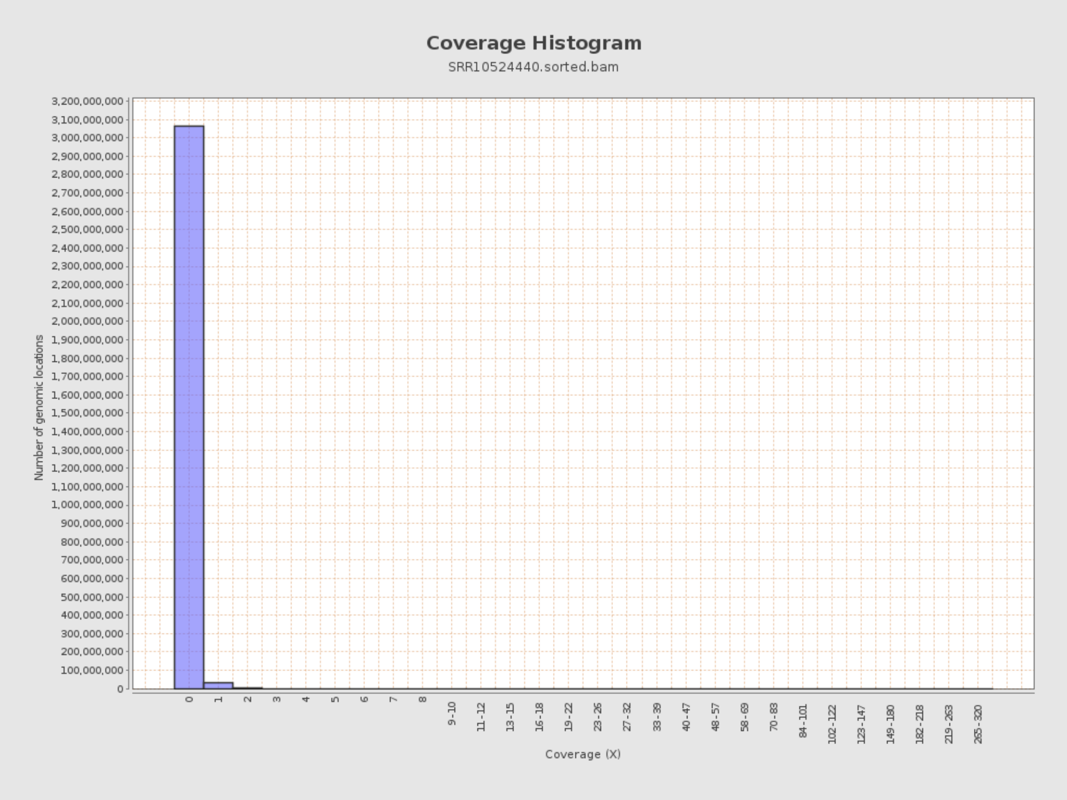
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3016917 | 0.0121 | 0.2575 |
| chr2 | 243199373 | 3147264 | 0.0129 | 0.1825 |
| chr3 | 198022430 | 2415326 | 0.0122 | 0.1164 |
| chr4 | 191154276 | 2280368 | 0.0119 | 0.1387 |
| chr5 | 180915260 | 2183393 | 0.0121 | 0.1157 |
| chr6 | 171115067 | 2076387 | 0.0121 | 0.1211 |
| chr7 | 159138663 | 2037634 | 0.0128 | 0.1778 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1807581 | 0.0123 | 0.1323 |
| chr9 | 141213431 | 1550090 | 0.011 | 0.1255 |
| chr10 | 135534747 | 1858977 | 0.0137 | 0.177 |
| chr11 | 135006516 | 1697584 | 0.0126 | 0.1372 |
| chr12 | 133851895 | 1650468 | 0.0123 | 0.1177 |
| chr13 | 115169878 | 1120007 | 0.0097 | 0.104 |
| chr14 | 107349540 | 1109934 | 0.0103 | 0.1101 |
| chr15 | 102531392 | 1117622 | 0.0109 | 0.1098 |
| chr16 | 90354753 | 1152755 | 0.0128 | 0.123 |
| chr17 | 81195210 | 1092572 | 0.0135 | 0.1286 |
| chr18 | 78077248 | 960008 | 0.0123 | 0.1967 |
| chr19 | 59128983 | 853649 | 0.0144 | 0.1846 |
| chr20 | 63025520 | 849561 | 0.0135 | 0.1255 |
| chr21 | 48129895 | 506159 | 0.0105 | 0.129 |
| chr22 | 51304566 | 501076 | 0.0098 | 0.1049 |
| chrMT | 16571 | 6729 | 0.4061 | 0.7129 |
| chrX | 155270560 | 2014984 | 0.013 | 0.1257 |
| chrY | 59373566 | 158916 | 0.0027 | 0.1047 |

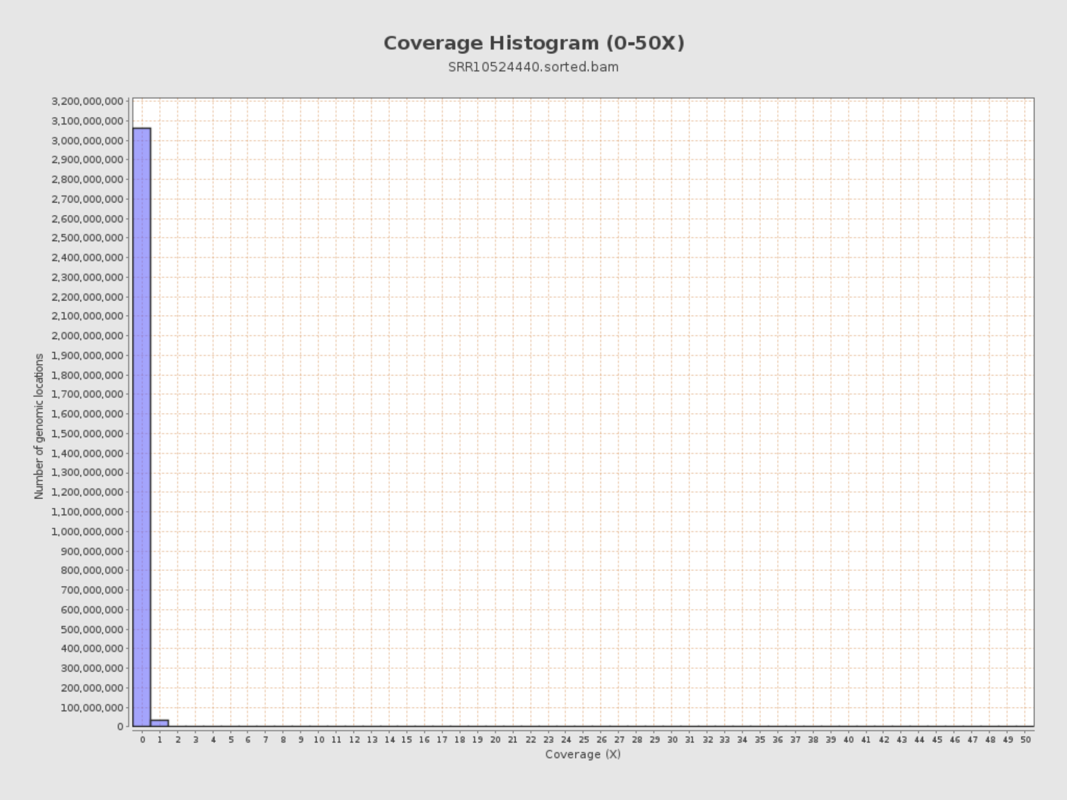
# 3. Results : Coverage across reference



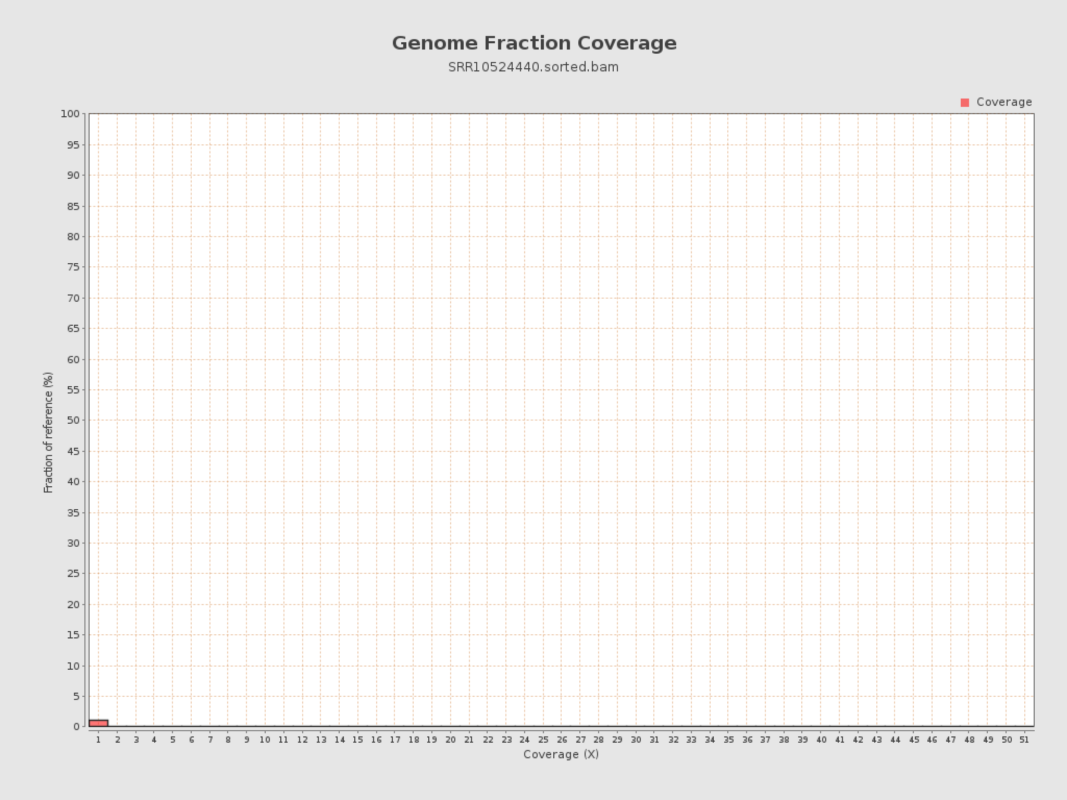
# 4. Results : Coverage Histogram



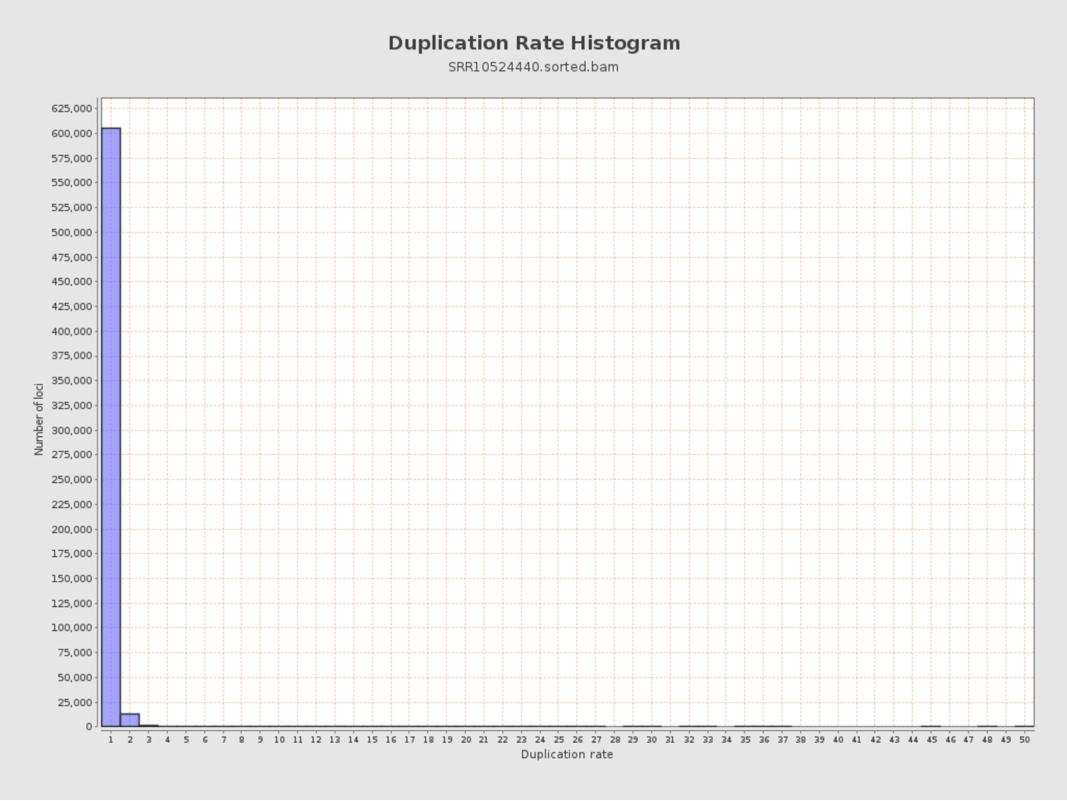
# 5. Results : Coverage Histogram (0-50X)



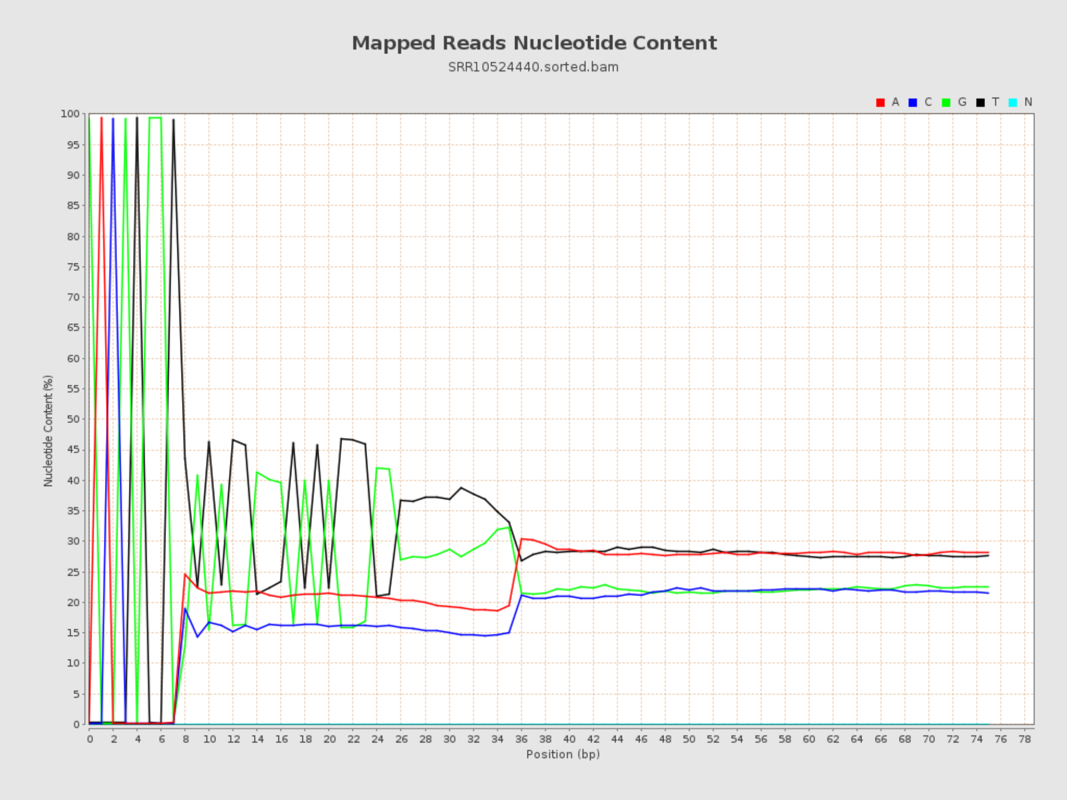
# 6. Results : Genome Fraction Coverage



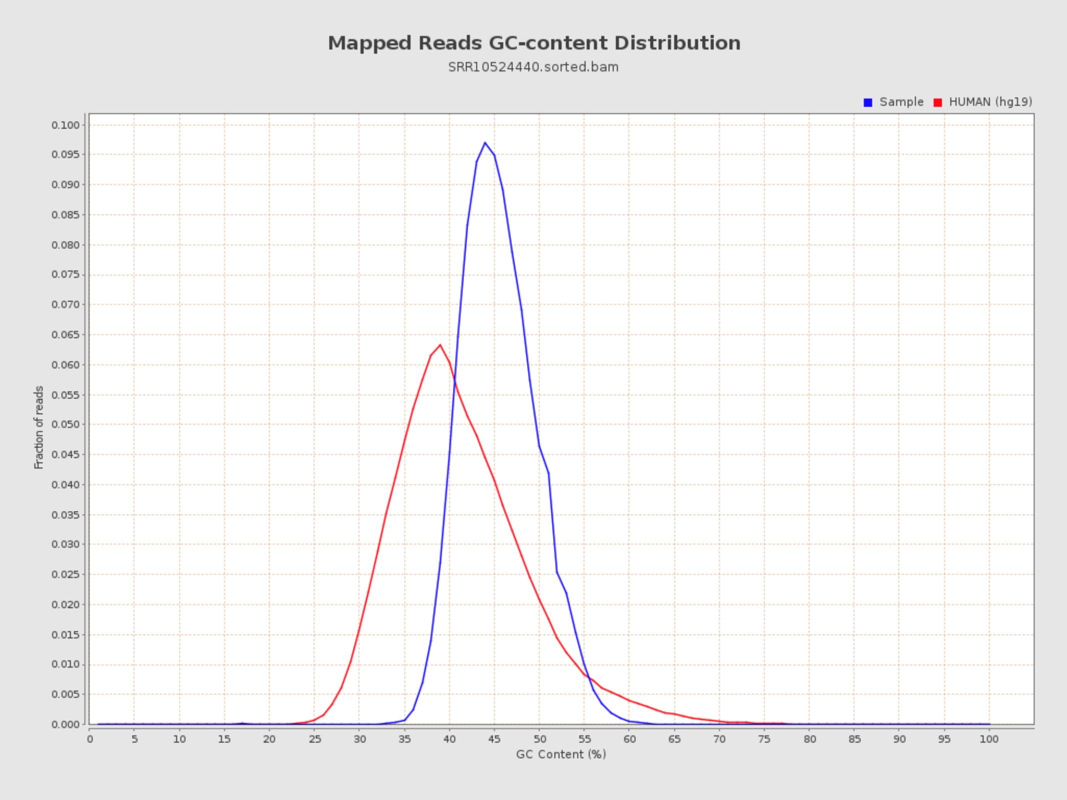
# 7. Results : Duplication Rate Histogram



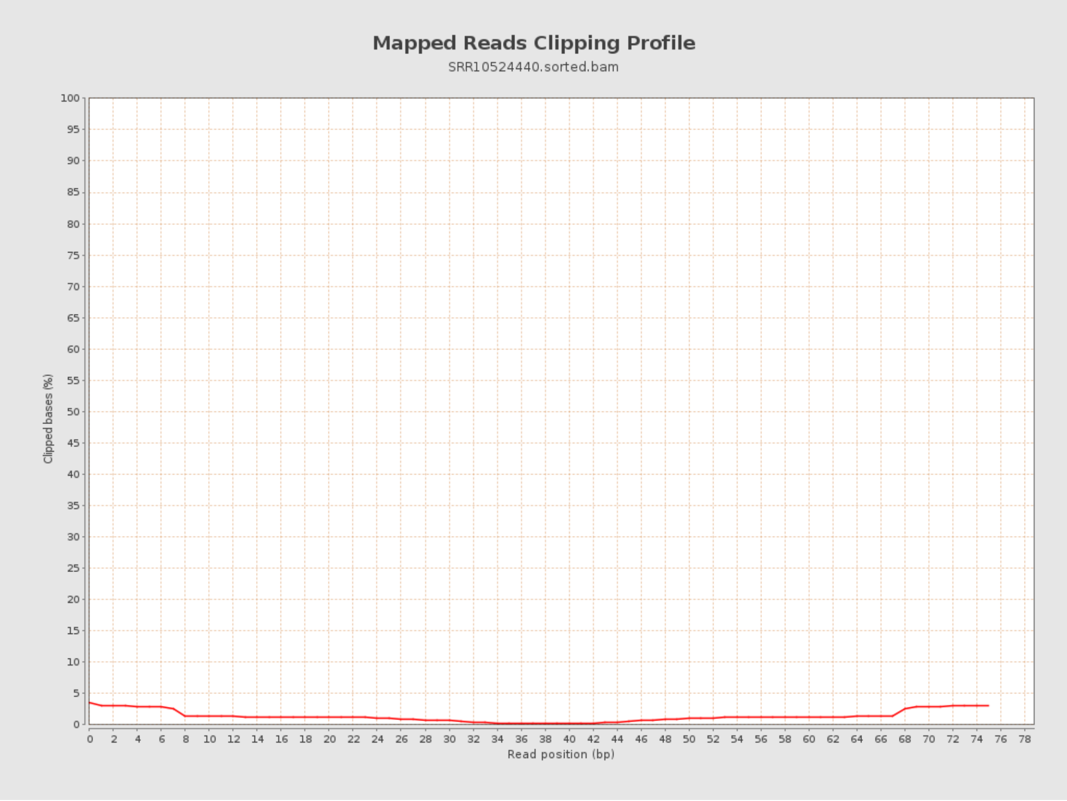
# 8. Results : Mapped Reads Nucleotide Content



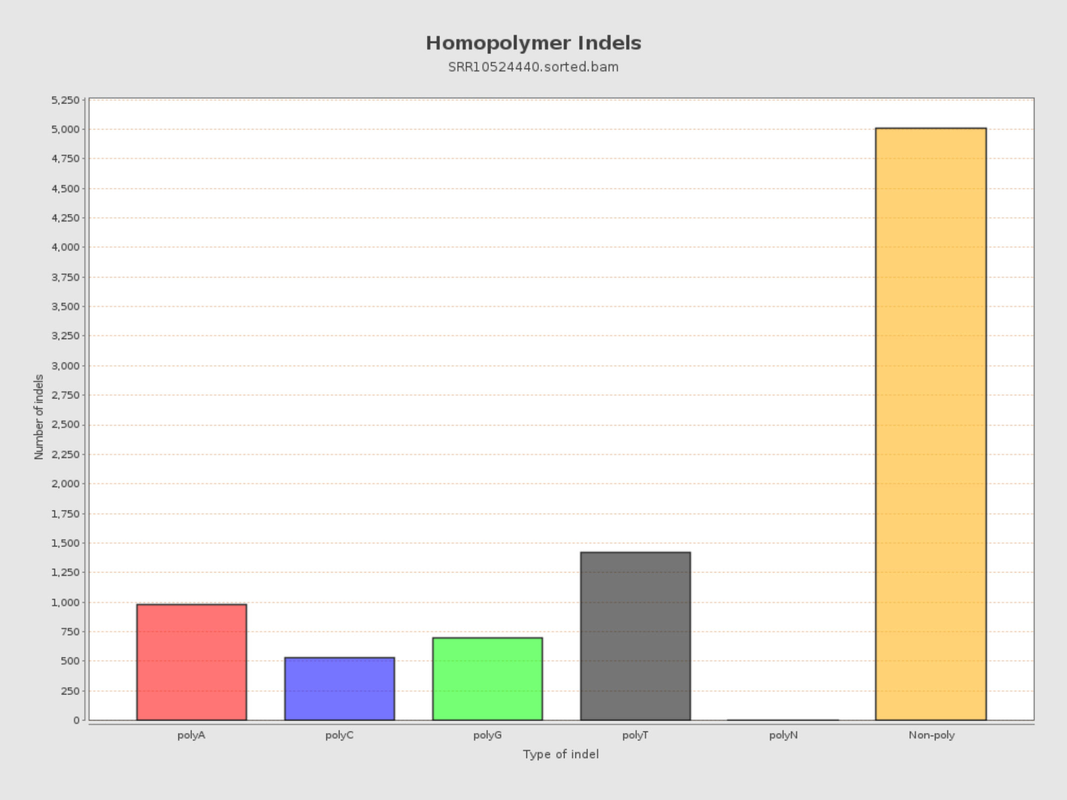
# 9. Results : Mapped Reads GC-content Distribution



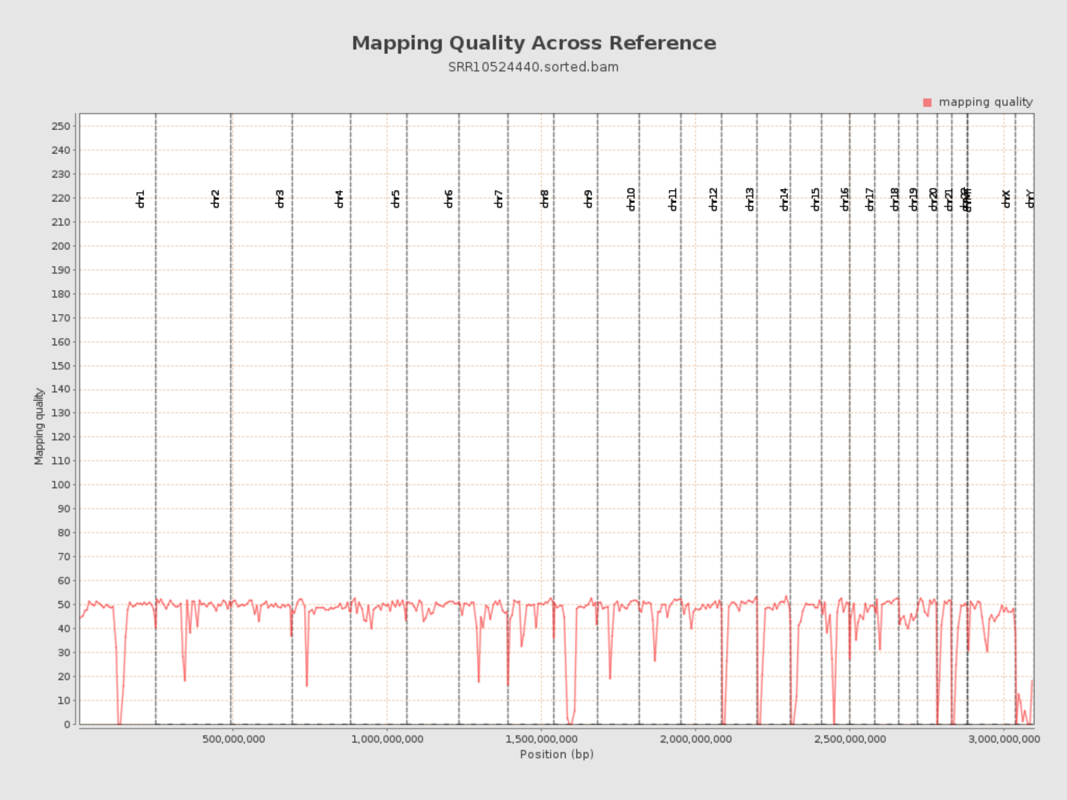
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram