# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 23:37:30*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524863.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_SRR10524863 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524863.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 23:37:29 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524863.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,973,949 |
| Mapped reads | 1,808,668 / 91.63% |
| Unmapped reads | 165,281 / 8.37% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 8,732 / 0.44% |
| Read min/max/mean length | 30 / 76 / 76.15 |
| Duplicated reads (estimated) | 58,838 / 2.98% |
| Duplication rate | 2.18% |
| Clipped reads | 1,812,255 / 91.81% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 26,564,501 / 25.32% |
| Number/percentage of C's | 18,182,855 / 17.33% |
| Number/percentage of T's | 34,968,233 / 33.33% |
| Number/percentage of G's | 25,171,294 / 24% |
| Number/percentage of N's | 13,787 / 0.01% |
| GC Percentage | 41.33% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0339 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3302 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.76 |

## 2.5. Mismatches and indels

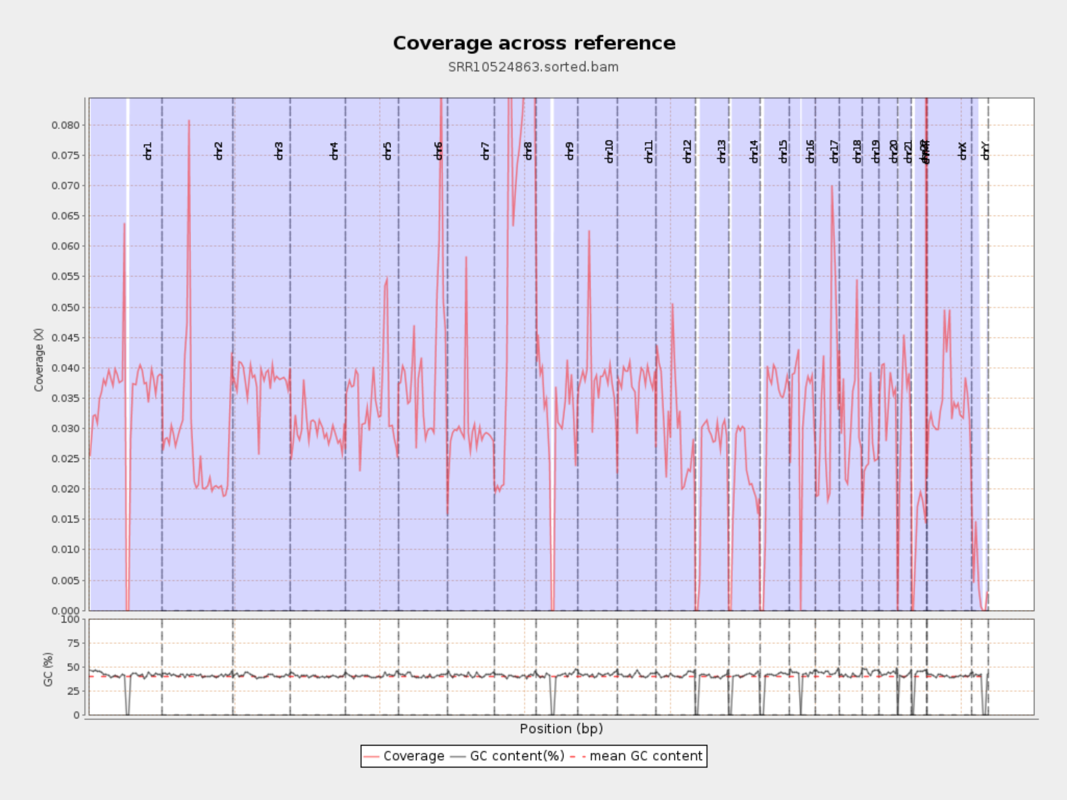
| | |
|---|---|
| General error rate | 0.5% |
| Mismatches | 508,662 |
| Insertions | 7,576 |
| Mapped reads with at least one insertion | 0.42% |
| Deletions | 19,624 |
| Mapped reads with at least one deletion | 1.08% |
| Homopolymer indels | 43.5% |

## 2.6. Chromosome stats

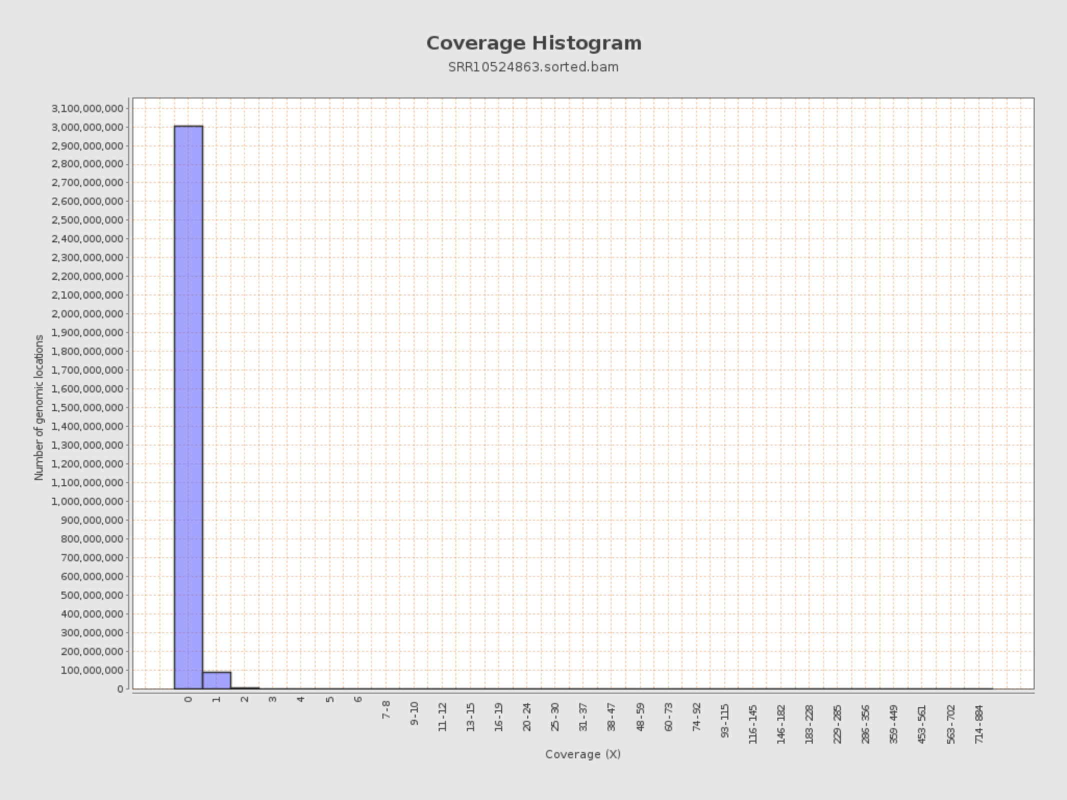
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 8753737 | 0.0351 | 0.6489 |
| chr2 | 243199373 | 6760660 | 0.0278 | 0.3507 |
| chr3 | 198022430 | 7515598 | 0.038 | 0.2106 |
| chr4 | 191154276 | 5656824 | 0.0296 | 0.1992 |
| chr5 | 180915260 | 6361555 | 0.0352 | 0.2043 |
| chr6 | 171115067 | 6887004 | 0.0402 | 0.2416 |
| chr7 | 159138663 | 4803459 | 0.0302 | 0.4678 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 11260527 | 0.0769 | 0.434 |
| chr9 | 141213431 | 4339295 | 0.0307 | 0.2697 |
| chr10 | 135534747 | 5240951 | 0.0387 | 0.3089 |
| chr11 | 135006516 | 5073555 | 0.0376 | 0.288 |
| chr12 | 133851895 | 4121793 | 0.0308 | 0.1954 |
| chr13 | 115169878 | 2818459 | 0.0245 | 0.1703 |
| chr14 | 107349540 | 2215900 | 0.0206 | 0.1704 |
| chr15 | 102531392 | 3121059 | 0.0304 | 0.1906 |
| chr16 | 90354753 | 3024088 | 0.0335 | 0.2142 |
| chr17 | 81195210 | 2832526 | 0.0349 | 0.2333 |
| chr18 | 78077248 | 2577006 | 0.033 | 0.5162 |
| chr19 | 59128983 | 1552776 | 0.0263 | 0.4537 |
| chr20 | 63025520 | 2241464 | 0.0356 | 0.2066 |
| chr21 | 48129895 | 1512589 | 0.0314 | 0.2031 |
| chr22 | 51304566 | 640136 | 0.0125 | 0.1187 |
| chrMT | 16571 | 15614 | 0.9422 | 1.072 |
| chrX | 155270560 | 5341585 | 0.0344 | 0.2363 |
| chrY | 59373566 | 263207 | 0.0044 | 0.1078 |

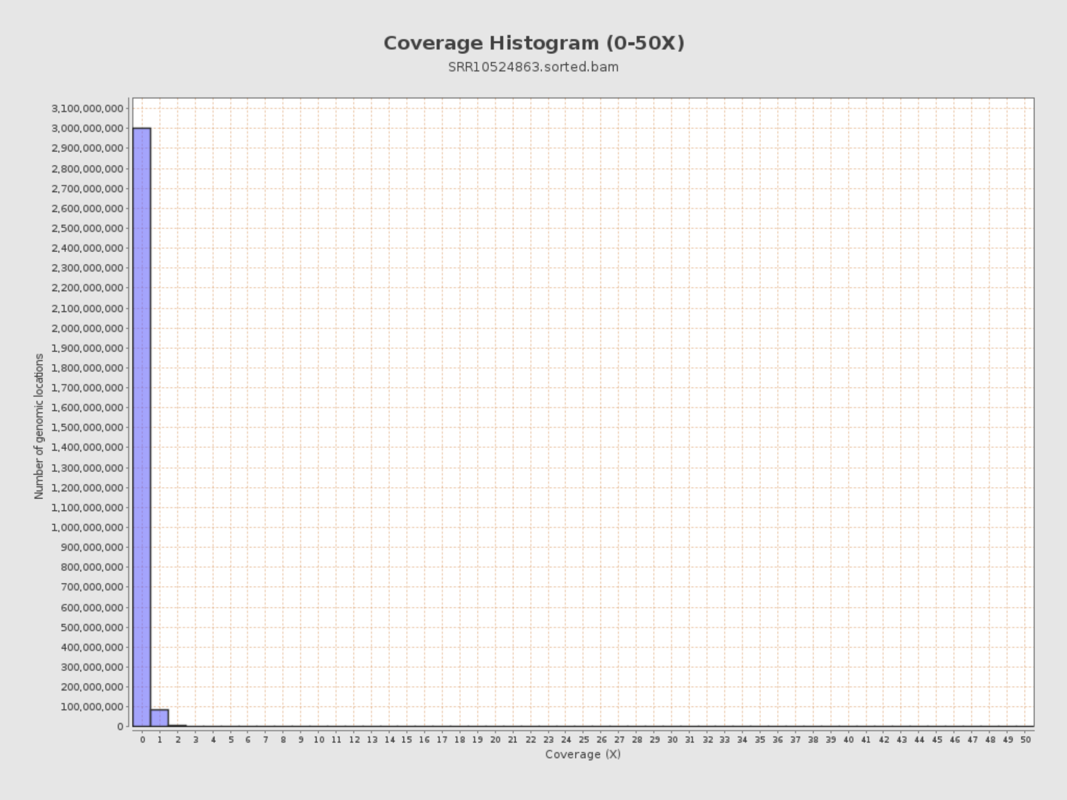
# 3. Results : Coverage across reference



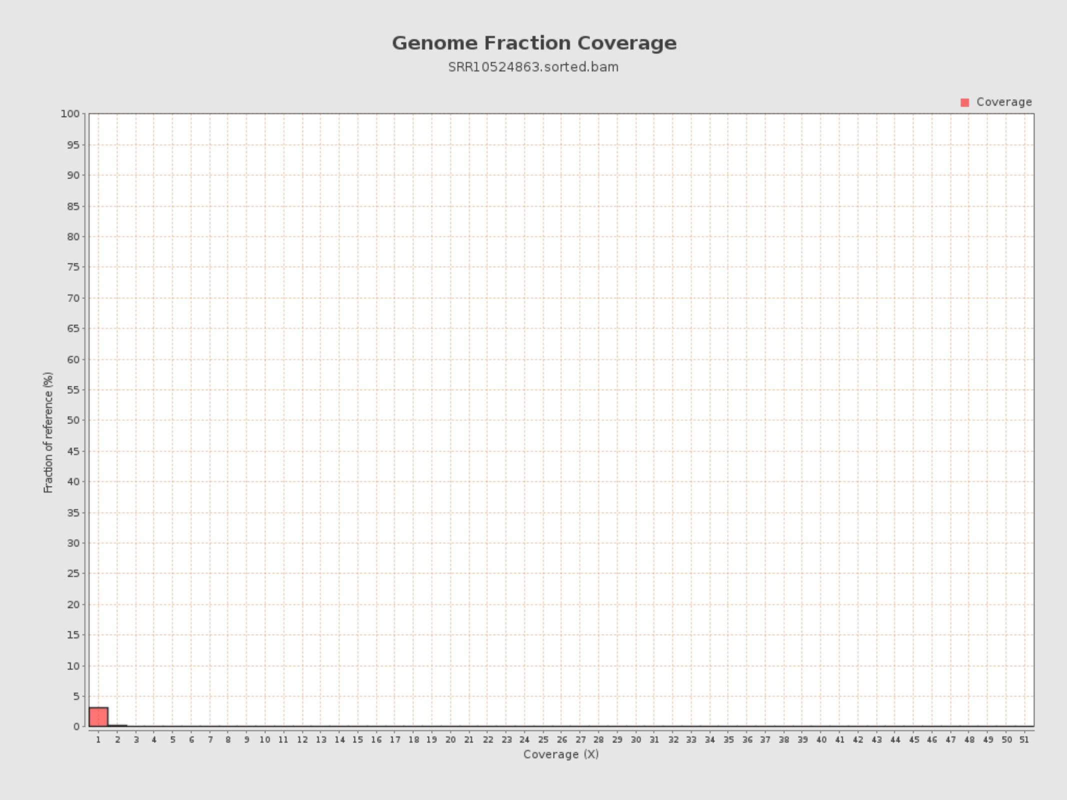
# 4. Results : Coverage Histogram



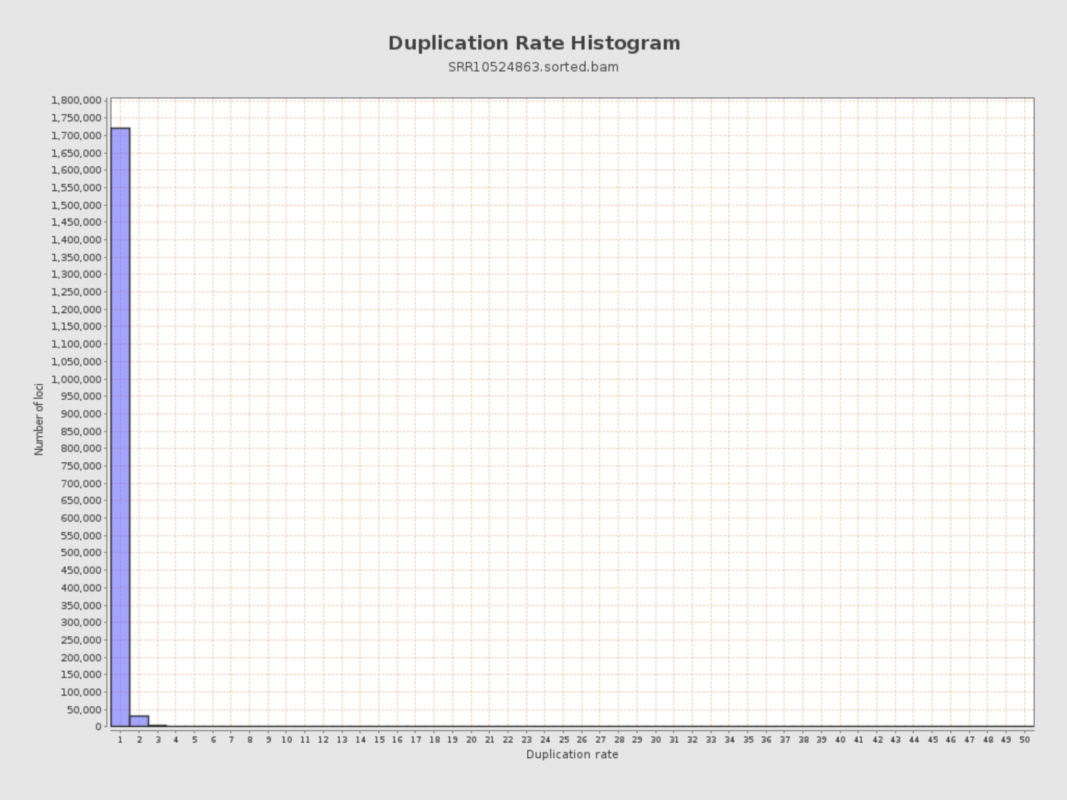
# 5. Results : Coverage Histogram (0-50X)



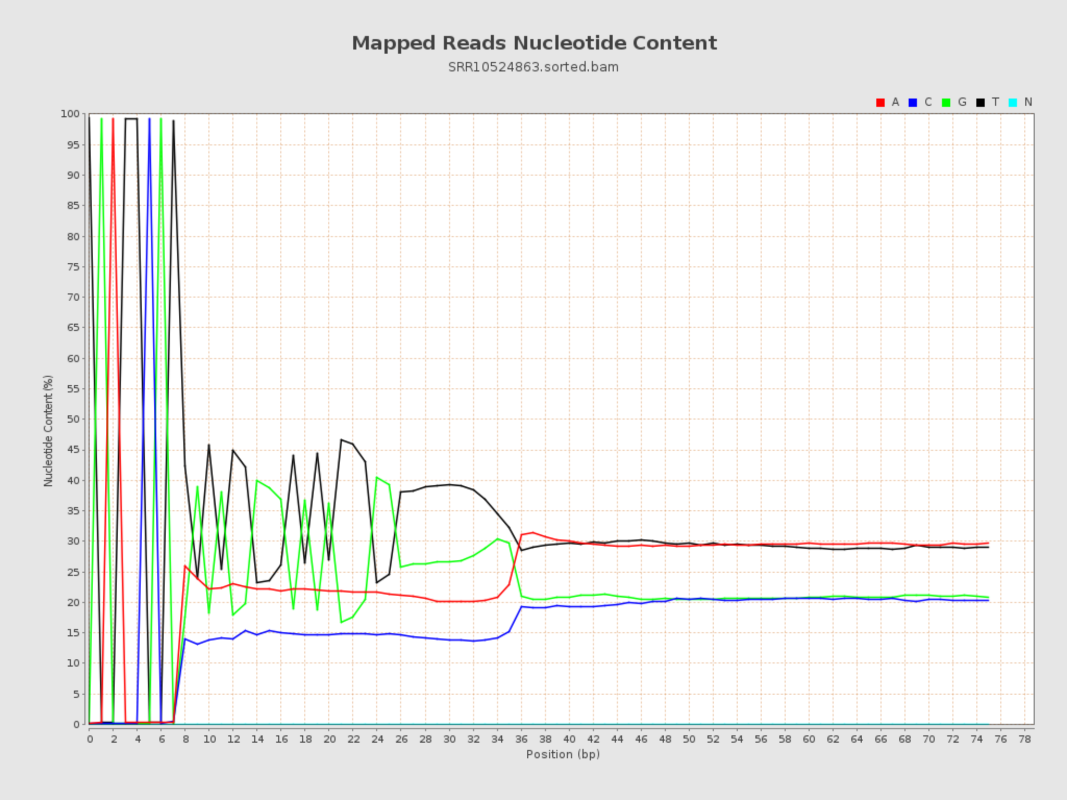
# 6. Results : Genome Fraction Coverage



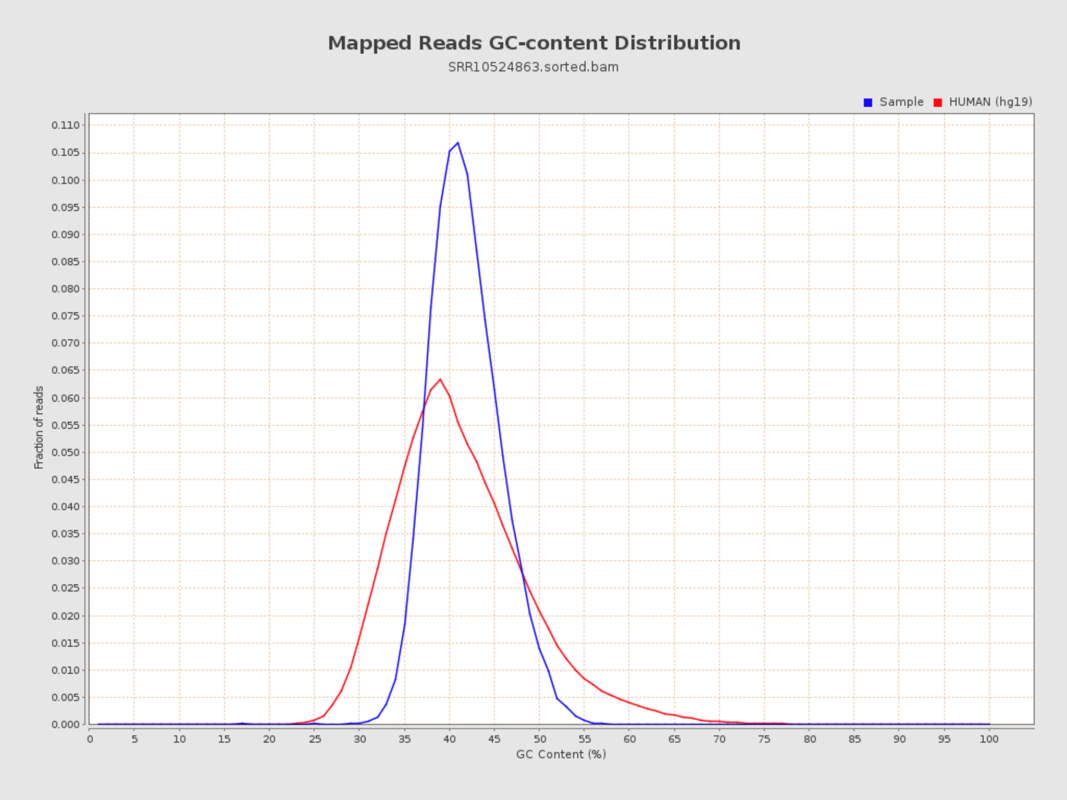
# 7. Results : Duplication Rate Histogram



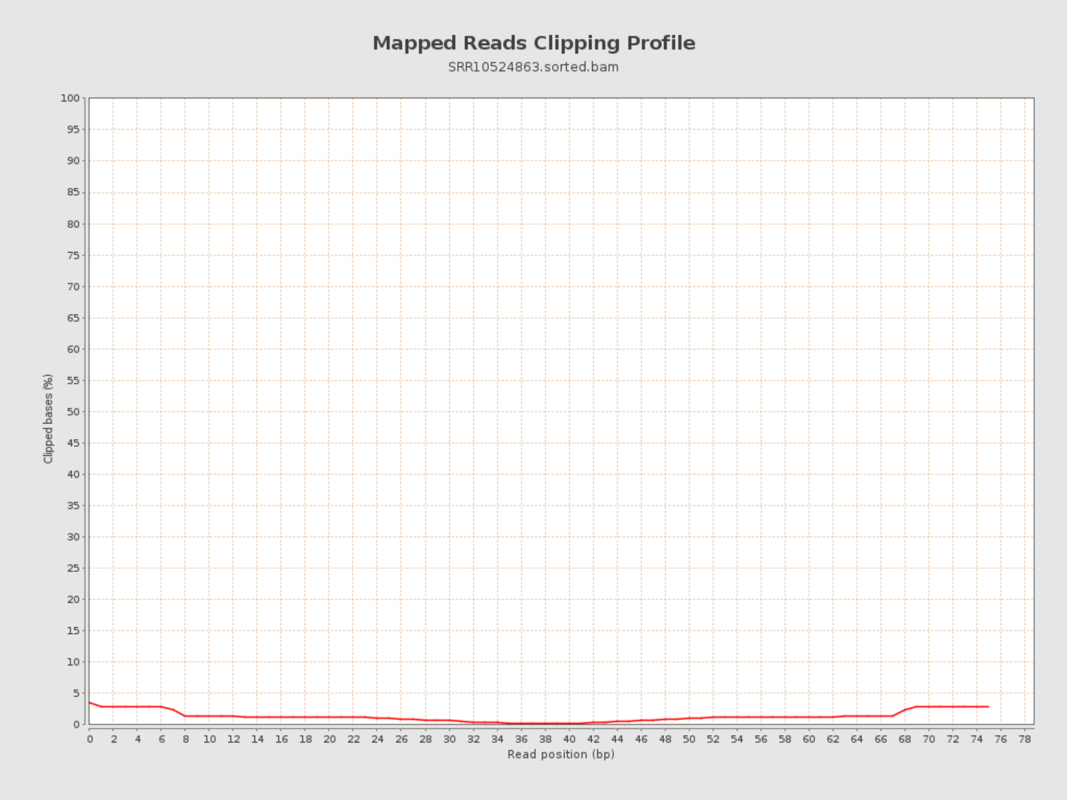
# 8. Results : Mapped Reads Nucleotide Content



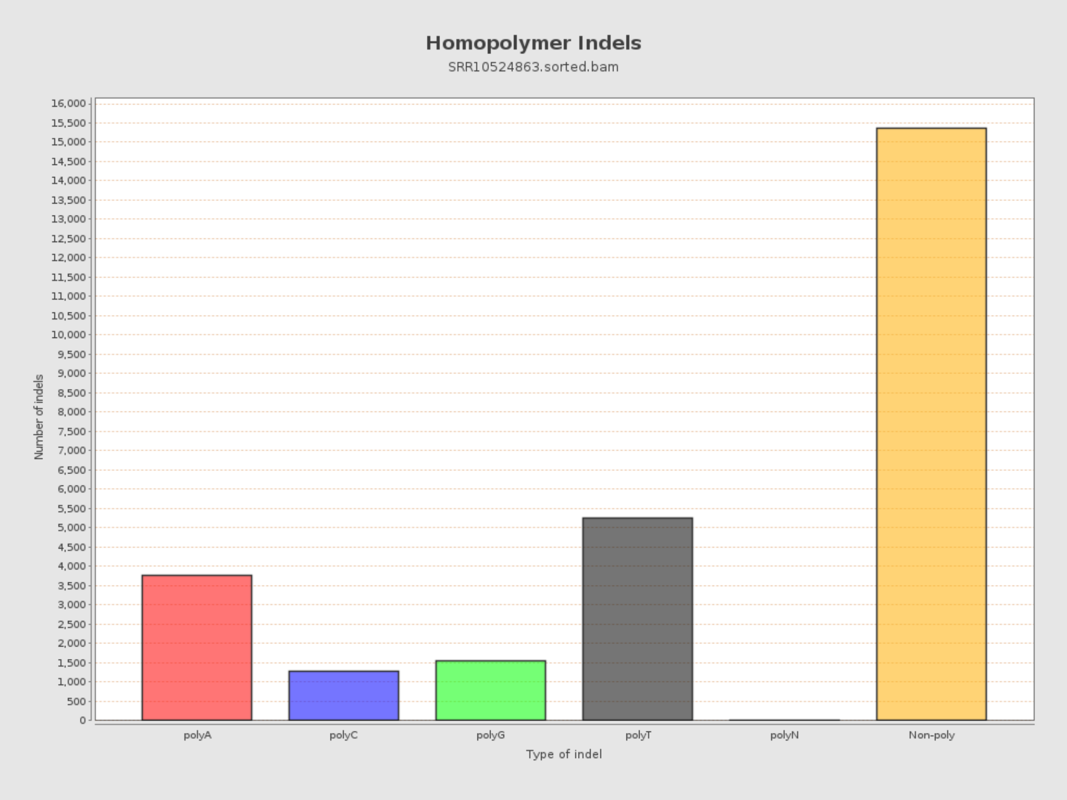
# 9. Results : Mapped Reads GC-content Distribution



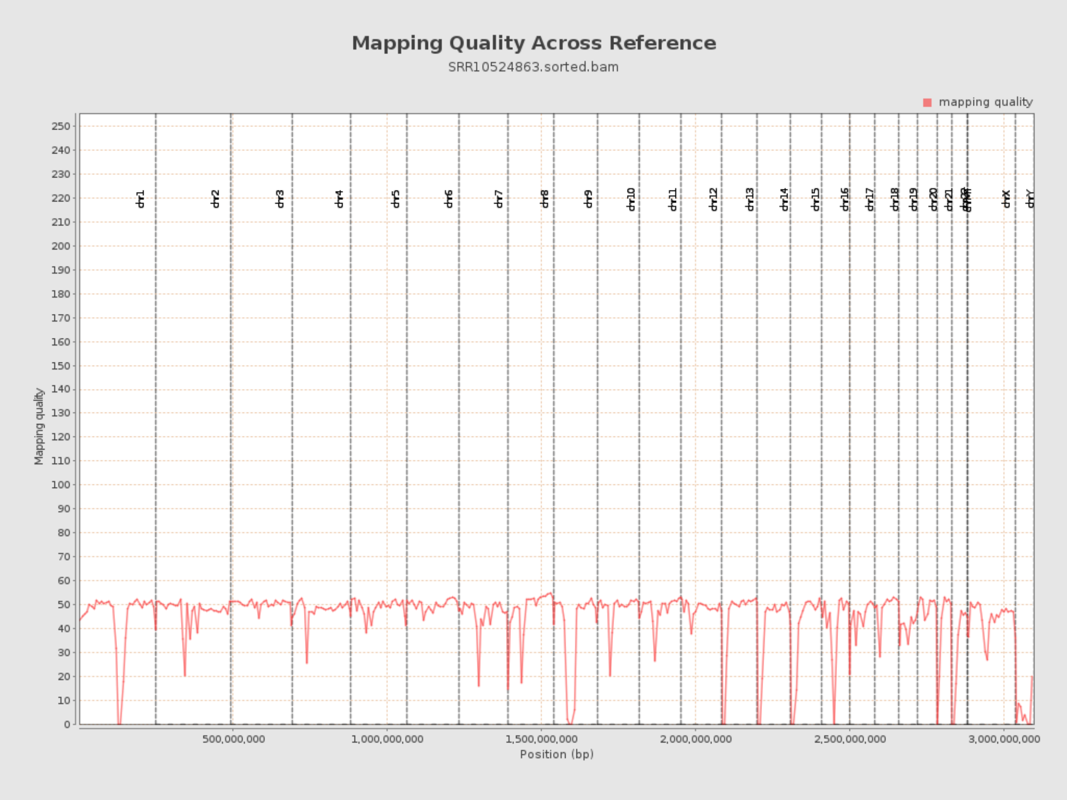
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram