# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 13:28:26*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524629.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_SRR10524629 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524629.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 13:28:25 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524629.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 727,545 |
| Mapped reads | 669,984 / 92.09% |
| Unmapped reads | 57,561 / 7.91% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 1,316 / 0.18% |
| Read min/max/mean length | 30 / 76 / 76.06 |
| Duplicated reads (estimated) | 17,498 / 2.41% |
| Duplication rate | 2.09% |
| Clipped reads | 669,616 / 92.04% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 9,778,883 / 25.27% |
| Number/percentage of C's | 7,088,669 / 18.32% |
| Number/percentage of T's | 12,546,165 / 32.42% |
| Number/percentage of G's | 9,285,609 / 23.99% |
| Number/percentage of N's | 288 / 0% |
| GC Percentage | 42.31% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0125 |
| | |

| | |
|---|---|
| Standard Deviation | 0.136 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.09 |

## 2.5. Mismatches and indels

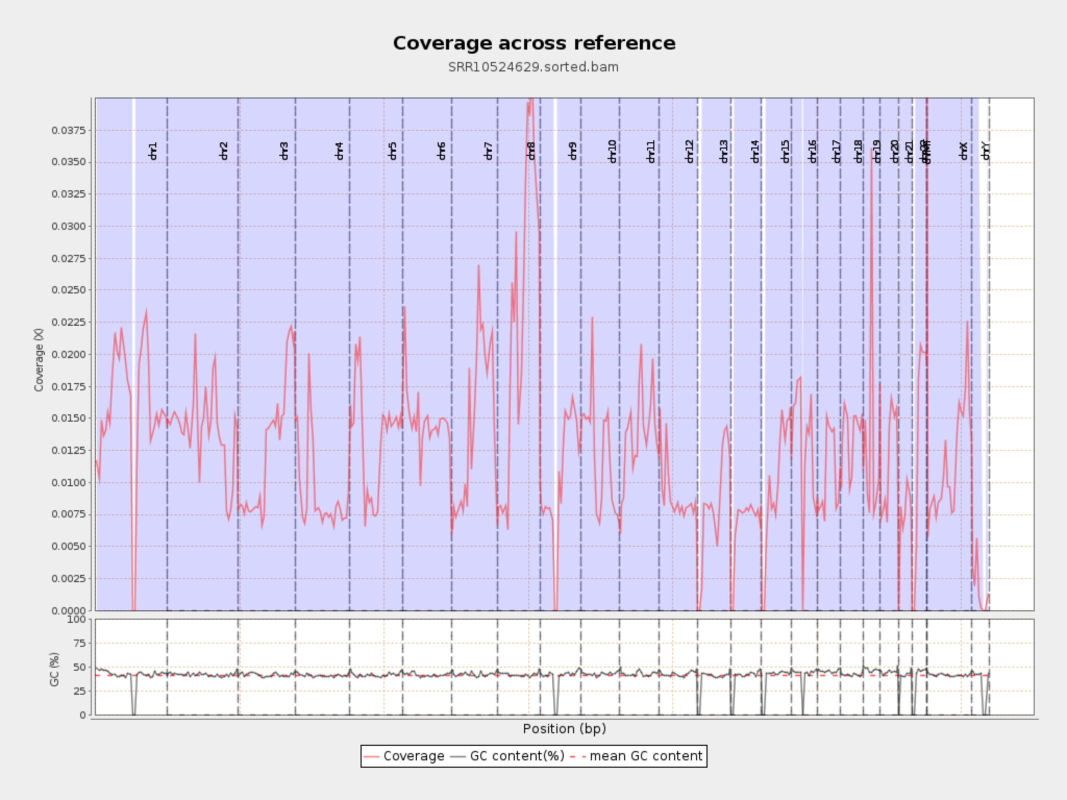
| | |
|---|---|
| General error rate | 0.49% |
| Mismatches | 184,304 |
| Insertions | 2,512 |
| Mapped reads with at least one insertion | 0.37% |
| Deletions | 7,061 |
| Mapped reads with at least one deletion | 1.05% |
| Homopolymer indels | 42.28% |

## 2.6. Chromosome stats

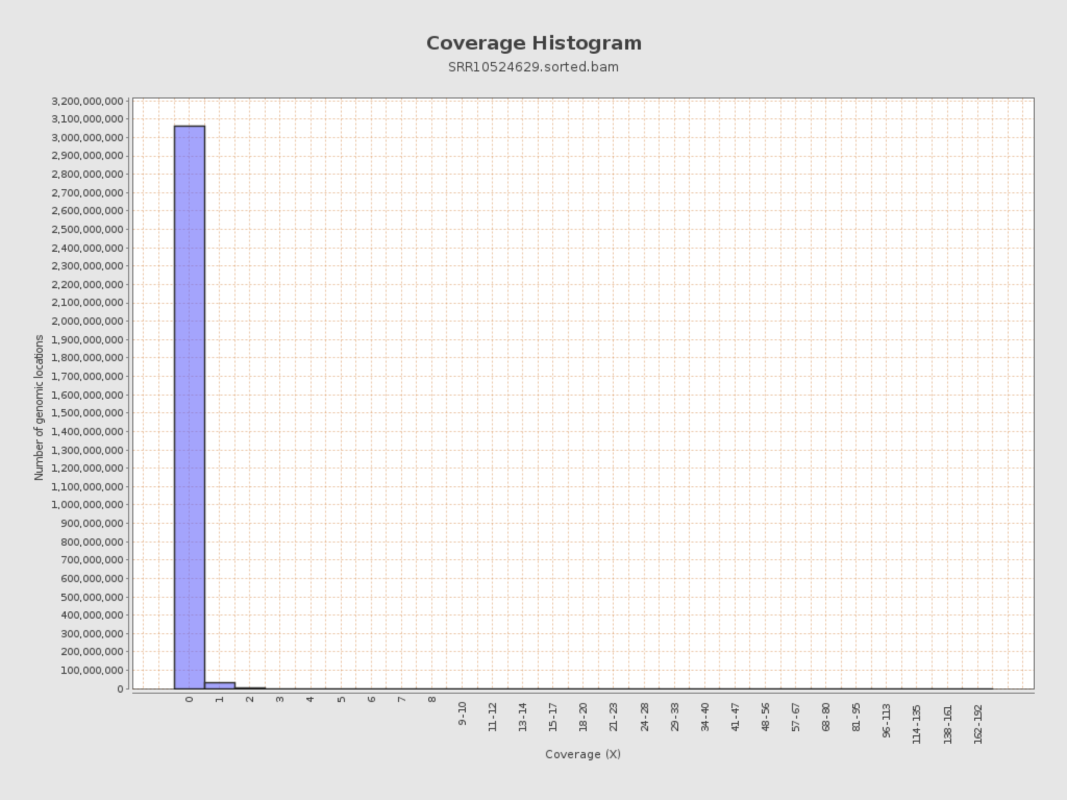
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 3934942 | 0.0158 | 0.1801 |
| chr2 | 243199373 | 3434698 | 0.0141 | 0.1569 |
| chr3 | 198022430 | 2481724 | 0.0125 | 0.1184 |
| chr4 | 191154276 | 1774514 | 0.0093 | 0.1094 |
| chr5 | 180915260 | 2423548 | 0.0134 | 0.1219 |
| chr6 | 171115067 | 2530929 | 0.0148 | 0.1324 |
| chr7 | 159138663 | 2336803 | 0.0147 | 0.1668 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3408729 | 0.0233 | 0.1871 |
| chr9 | 141213431 | 1447325 | 0.0102 | 0.124 |
| chr10 | 135534747 | 1673741 | 0.0123 | 0.1393 |
| chr11 | 135006516 | 1881482 | 0.0139 | 0.1407 |
| chr12 | 133851895 | 1211275 | 0.009 | 0.1039 |
| chr13 | 115169878 | 923707 | 0.008 | 0.0954 |
| chr14 | 107349540 | 709769 | 0.0066 | 0.0875 |
| chr15 | 102531392 | 983235 | 0.0096 | 0.1083 |
| chr16 | 90354753 | 1153434 | 0.0128 | 0.1218 |
| chr17 | 81195210 | 859903 | 0.0106 | 0.11 |
| chr18 | 78077248 | 1066225 | 0.0137 | 0.1855 |
| chr19 | 59128983 | 795374 | 0.0135 | 0.1536 |
| chr20 | 63025520 | 736682 | 0.0117 | 0.1155 |
| chr21 | 48129895 | 354261 | 0.0074 | 0.093 |
| chr22 | 51304566 | 688995 | 0.0134 | 0.1219 |
| chrMT | 16571 | 827 | 0.0499 | 0.2348 |
| chrX | 155270560 | 1802814 | 0.0116 | 0.1207 |
| chrY | 59373566 | 96655 | 0.0016 | 0.0555 |

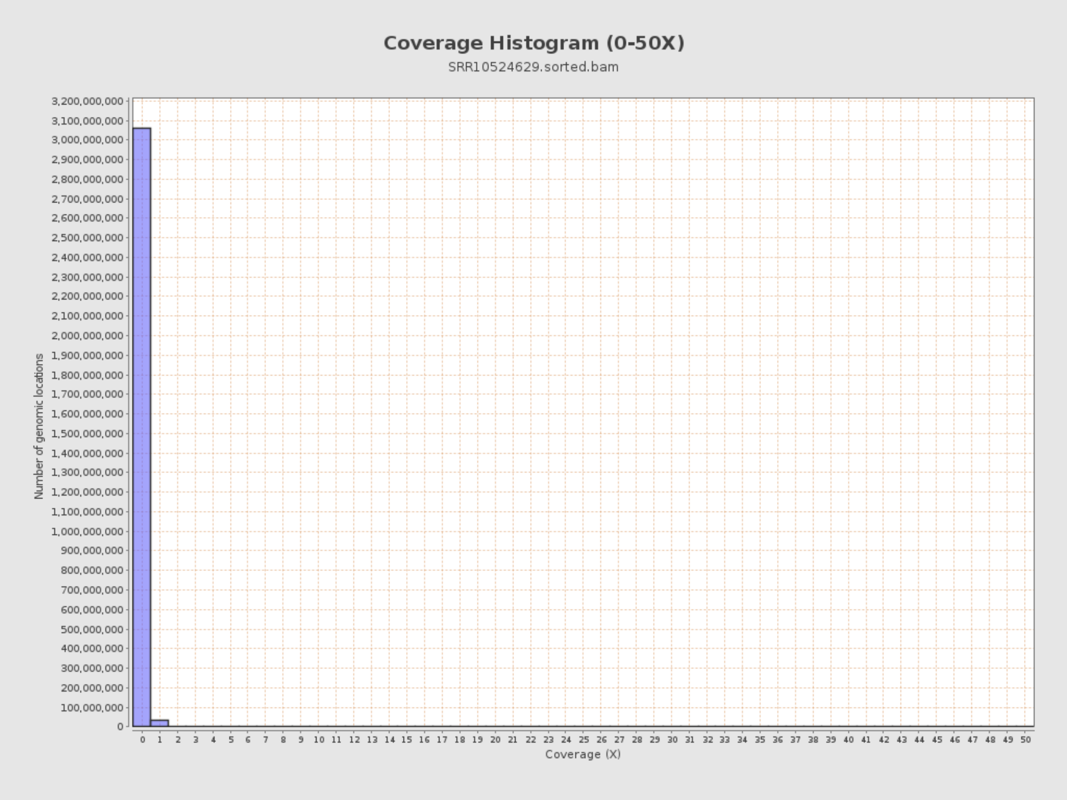
# 3. Results : Coverage across reference



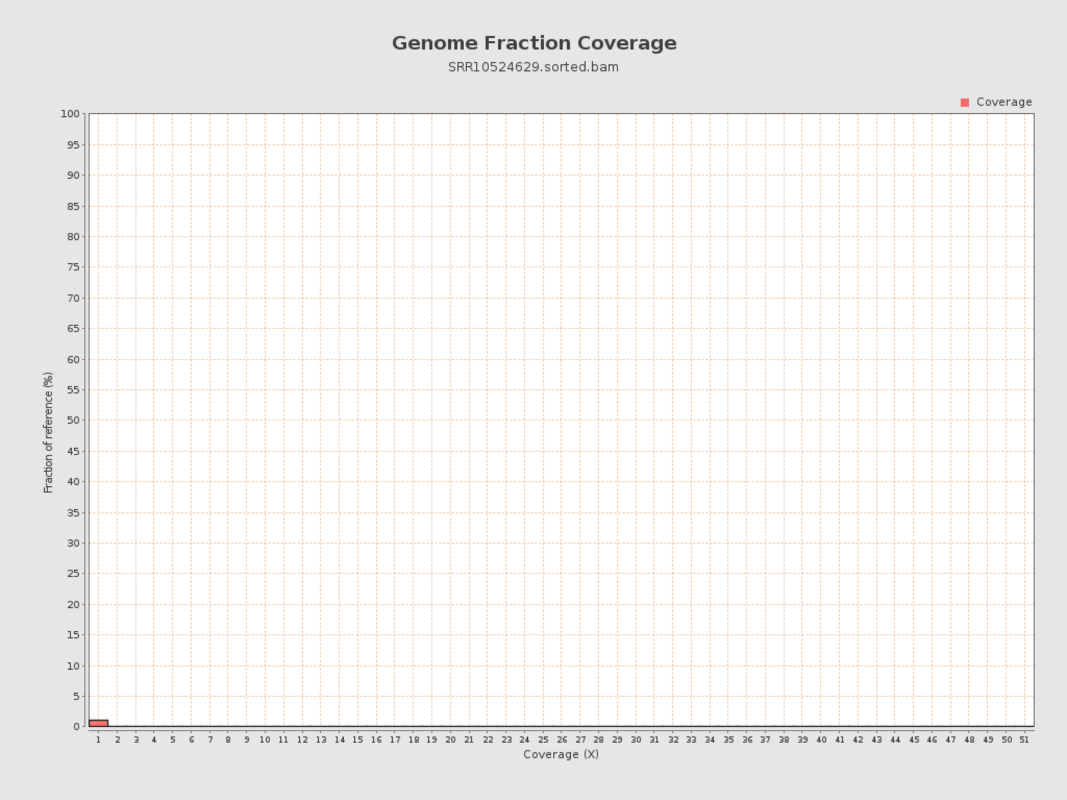
# 4. Results : Coverage Histogram



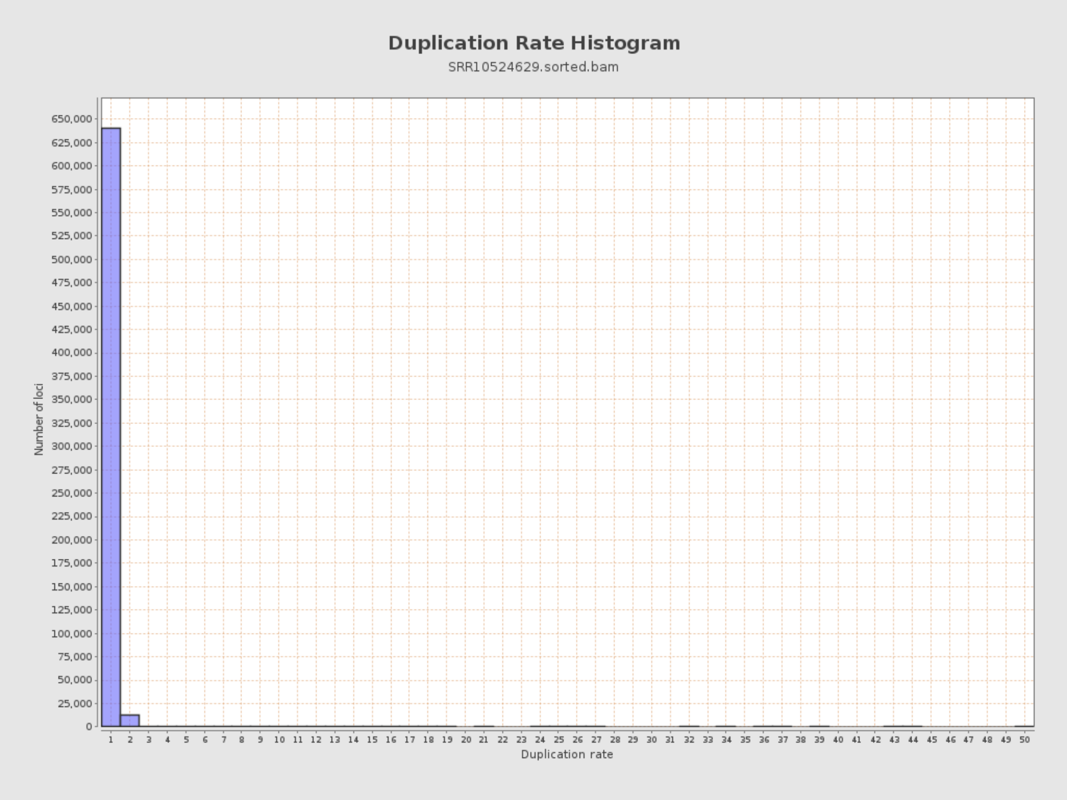
# 5. Results : Coverage Histogram (0-50X)



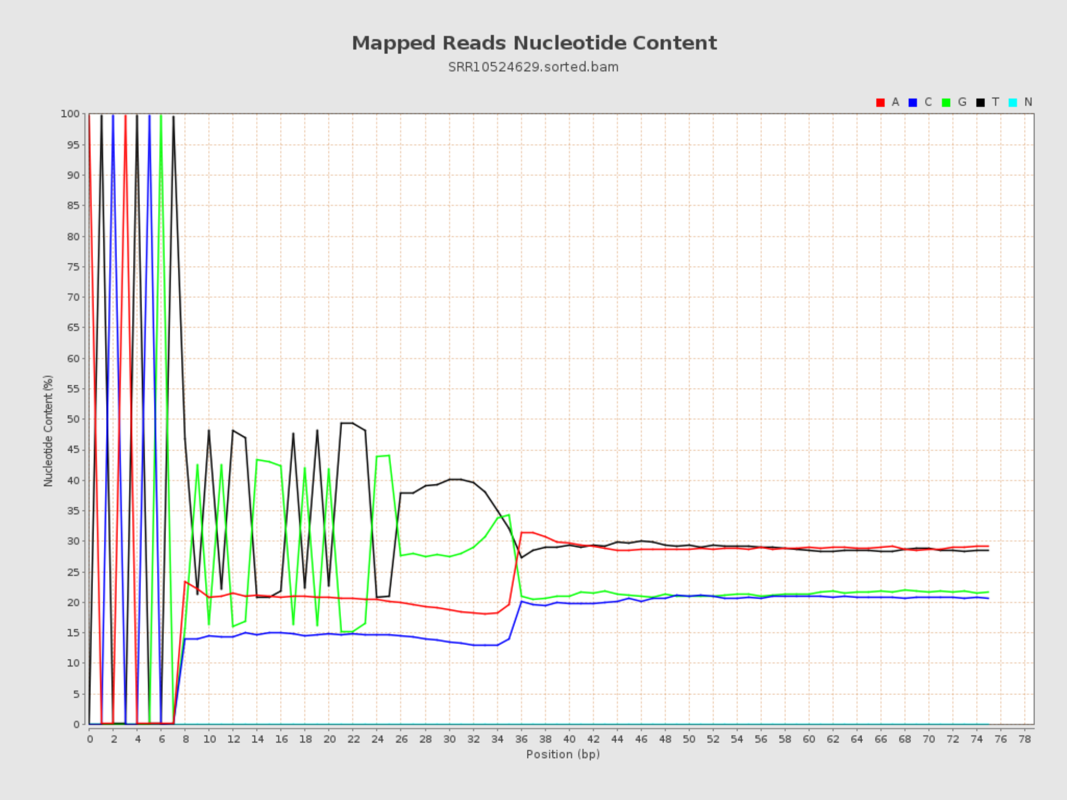
# 6. Results : Genome Fraction Coverage



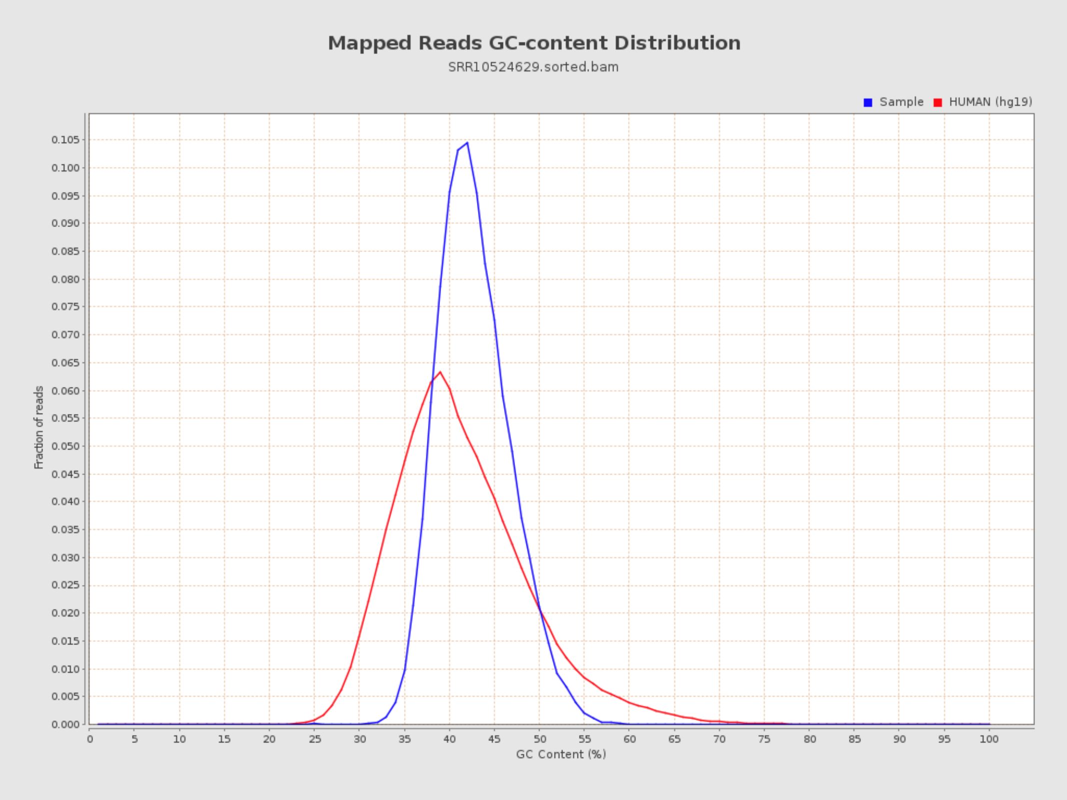
# 7. Results : Duplication Rate Histogram



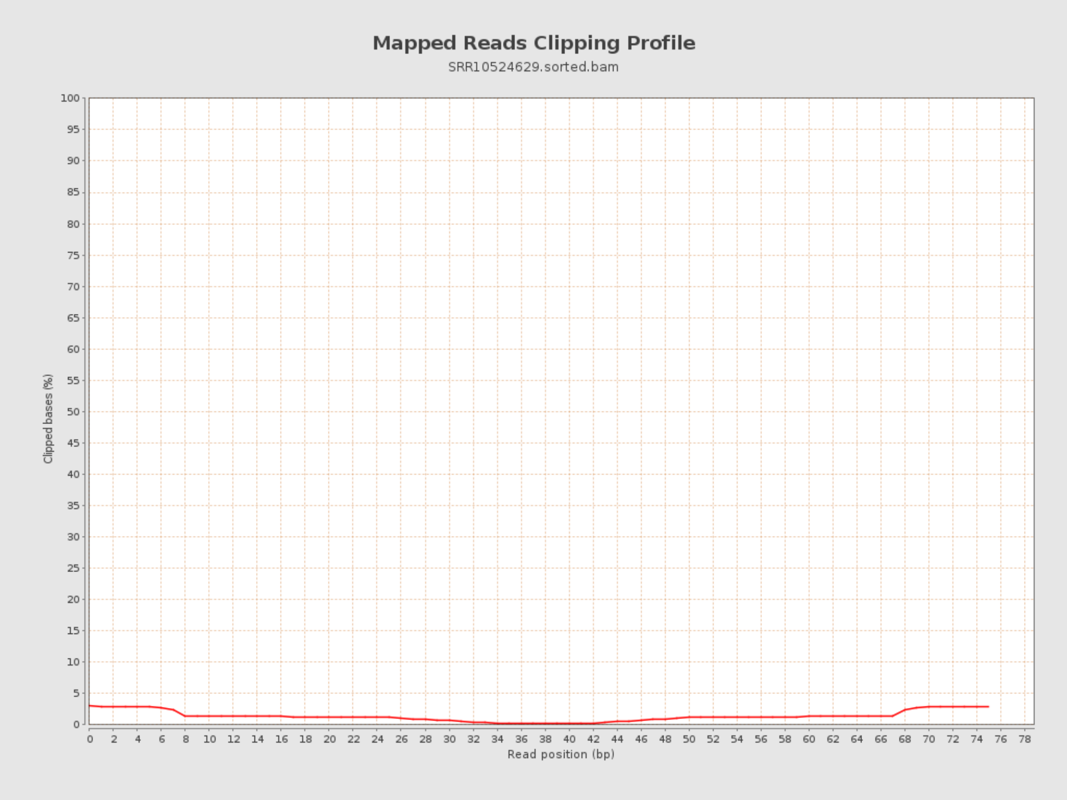
# 8. Results : Mapped Reads Nucleotide Content



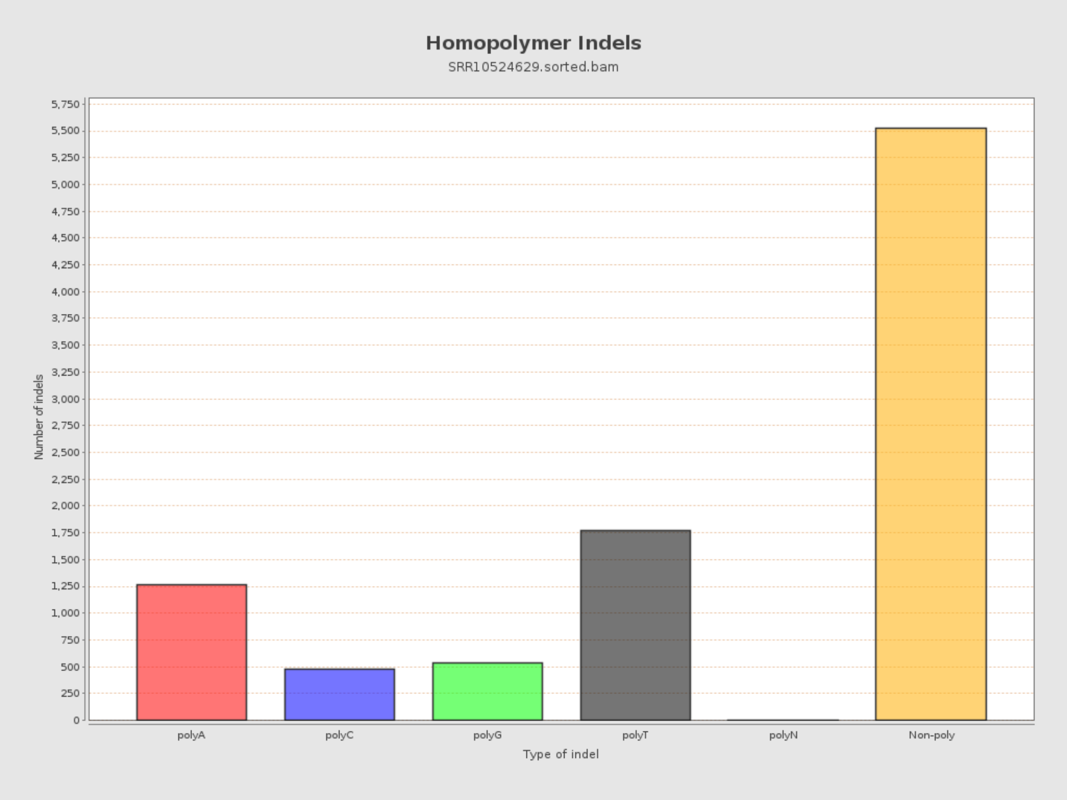
# 9. Results : Mapped Reads GC-content Distribution



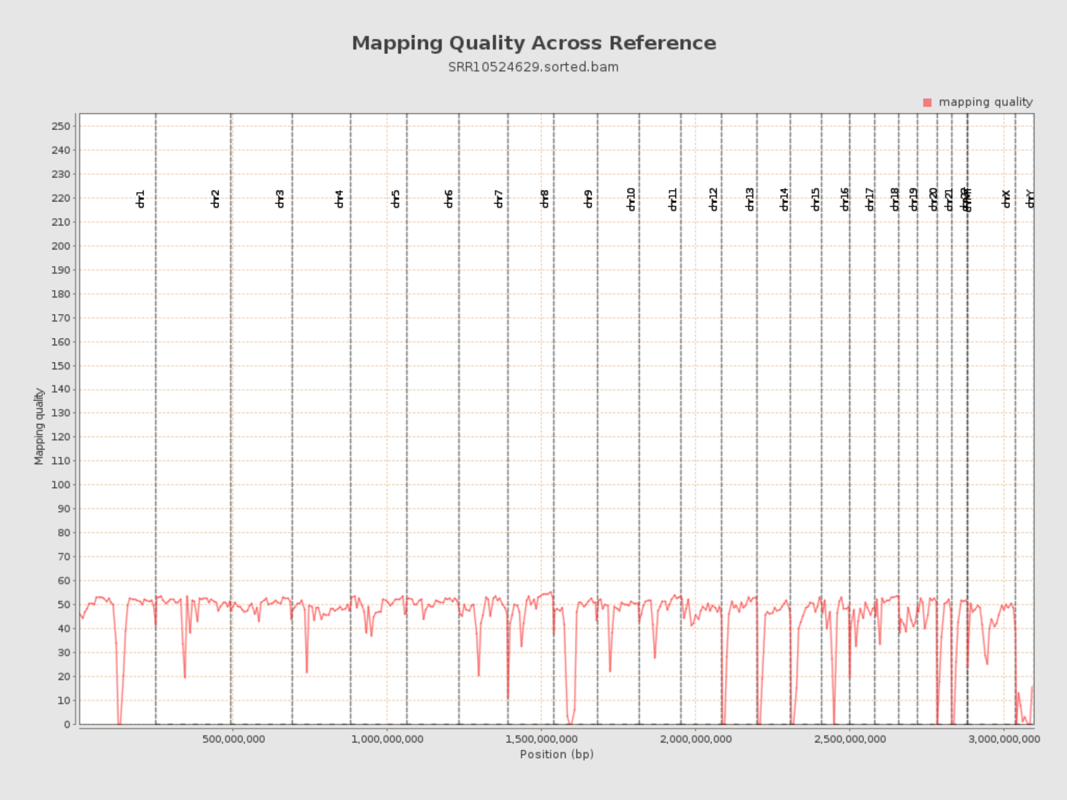
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram