# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 01:15:20*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524380.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_SRR10524380 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524380.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 01:15:20 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524380.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,319,201 |
| Mapped reads | 2,135,607 / 92.08% |
| Unmapped reads | 183,594 / 7.92% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 7,883 / 0.34% |
| Read min/max/mean length | 30 / 76 / 76.11 |
| Duplicated reads (estimated) | 89,102 / 3.84% |
| Duplication rate | 3% |
| Clipped reads | 2,140,525 / 92.3% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 31,873,586 / 25.29% |
| Number/percentage of C's | 23,792,244 / 18.88% |
| Number/percentage of T's | 37,762,700 / 29.97% |
| Number/percentage of G's | 32,569,292 / 25.85% |
| Number/percentage of N's | 15,487 / 0.01% |
| GC Percentage | 44.73% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0407 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3843 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.01 |

## 2.5. Mismatches and indels

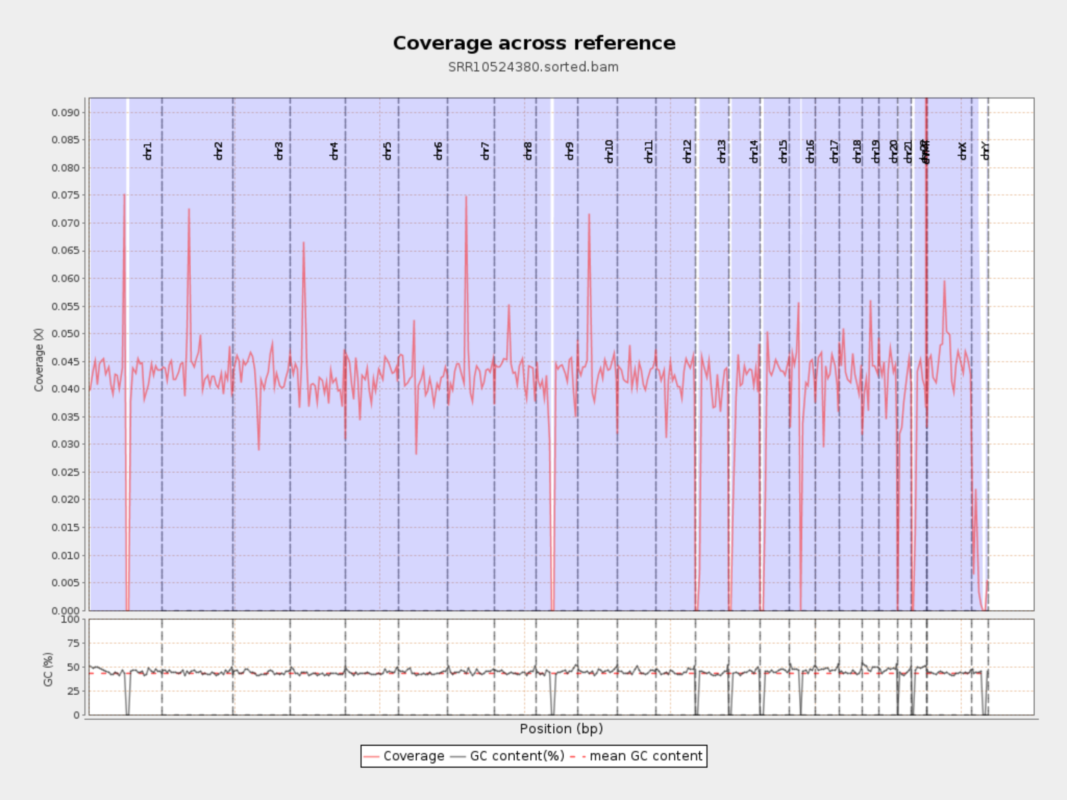
| | |
|---|---|
| General error rate | 0.5% |
| Mismatches | 619,850 |
| Insertions | 7,554 |
| Mapped reads with at least one insertion | 0.35% |
| Deletions | 21,952 |
| Mapped reads with at least one deletion | 1.02% |
| Homopolymer indels | 45.61% |

## 2.6. Chromosome stats

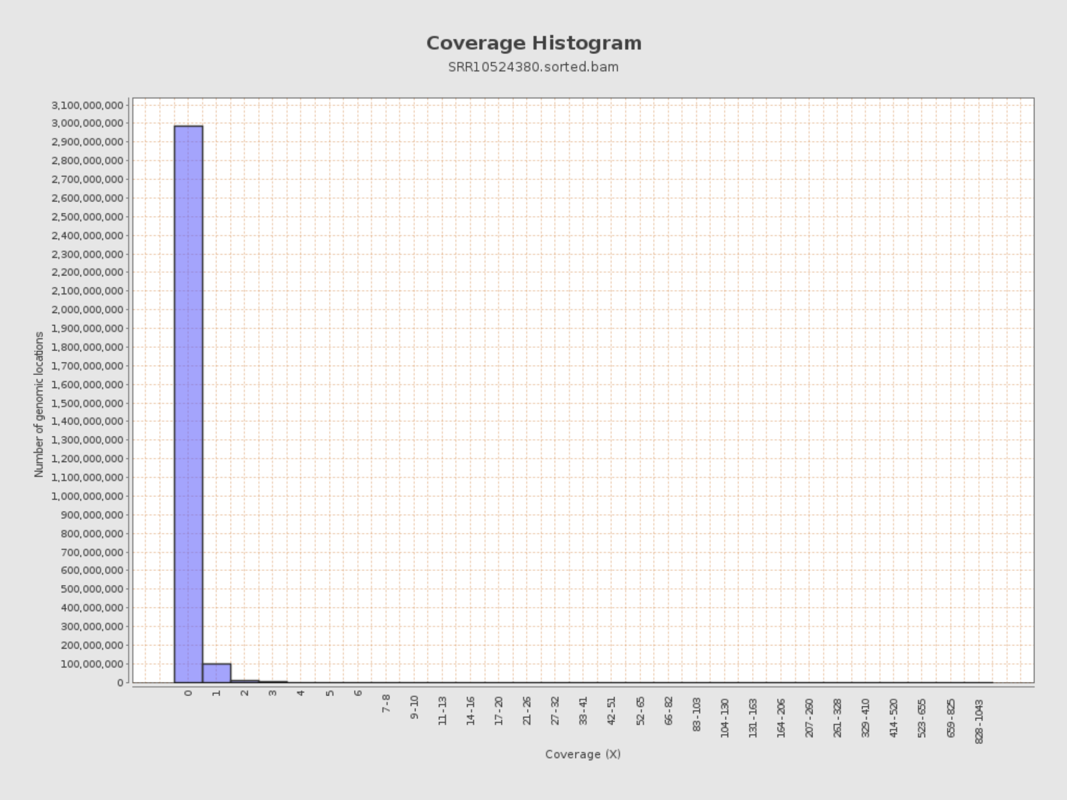
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 10216178 | 0.041 | 0.8179 |
| chr2 | 243199373 | 10737408 | 0.0442 | 0.4164 |
| chr3 | 198022430 | 8435120 | 0.0426 | 0.227 |
| chr4 | 191154276 | 8074531 | 0.0422 | 0.2609 |
| chr5 | 180915260 | 7639264 | 0.0422 | 0.2279 |
| chr6 | 171115067 | 7134754 | 0.0417 | 0.2641 |
| chr7 | 159138663 | 6991501 | 0.0439 | 0.5456 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6423852 | 0.0439 | 0.325 |
| chr9 | 141213431 | 5210318 | 0.0369 | 0.3012 |
| chr10 | 135534747 | 6052152 | 0.0447 | 0.3388 |
| chr11 | 135006516 | 5749757 | 0.0426 | 0.3432 |
| chr12 | 133851895 | 5633417 | 0.0421 | 0.2363 |
| chr13 | 115169878 | 3983671 | 0.0346 | 0.2058 |
| chr14 | 107349540 | 3786511 | 0.0353 | 0.2216 |
| chr15 | 102531392 | 3706289 | 0.0361 | 0.2101 |
| chr16 | 90354753 | 3588074 | 0.0397 | 0.2414 |
| chr17 | 81195210 | 3414918 | 0.0421 | 0.252 |
| chr18 | 78077248 | 3410090 | 0.0437 | 0.5772 |
| chr19 | 59128983 | 2549860 | 0.0431 | 0.5285 |
| chr20 | 63025520 | 2684275 | 0.0426 | 0.2353 |
| chr21 | 48129895 | 1678341 | 0.0349 | 0.2424 |
| chr22 | 51304566 | 1506693 | 0.0294 | 0.1905 |
| chrMT | 16571 | 14346 | 0.8657 | 1.0961 |
| chrX | 155270560 | 7042133 | 0.0454 | 0.2732 |
| chrY | 59373566 | 384610 | 0.0065 | 0.1693 |

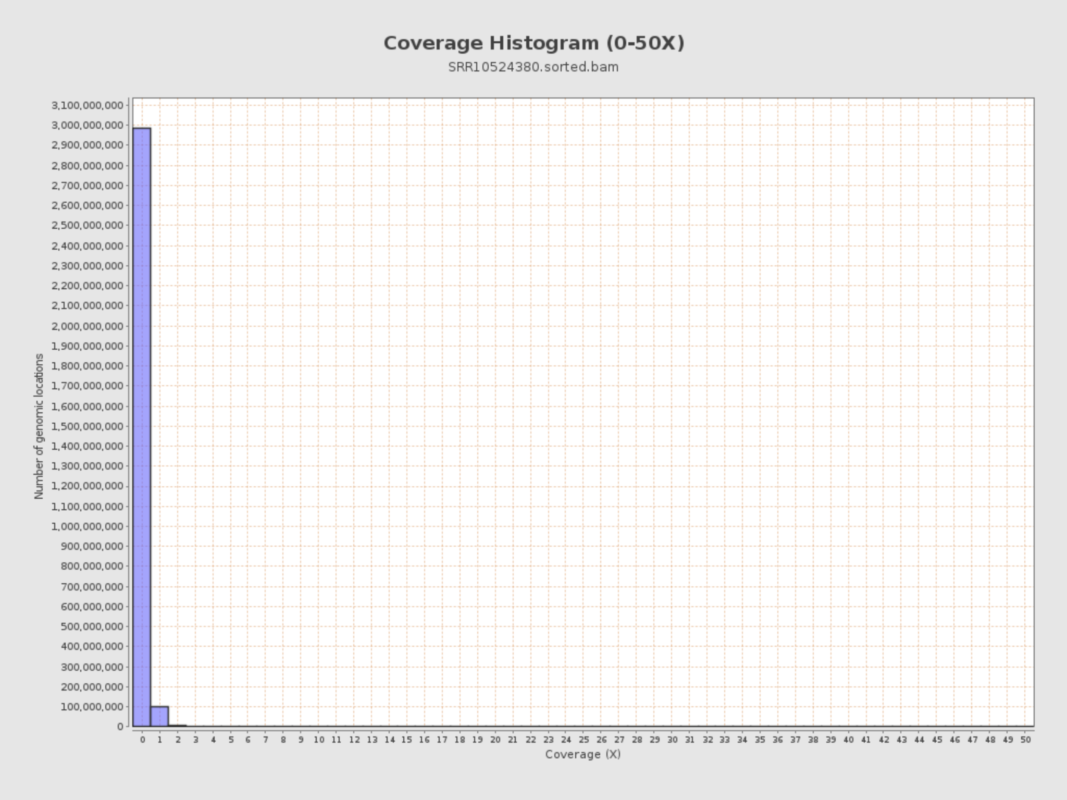
# 3. Results : Coverage across reference



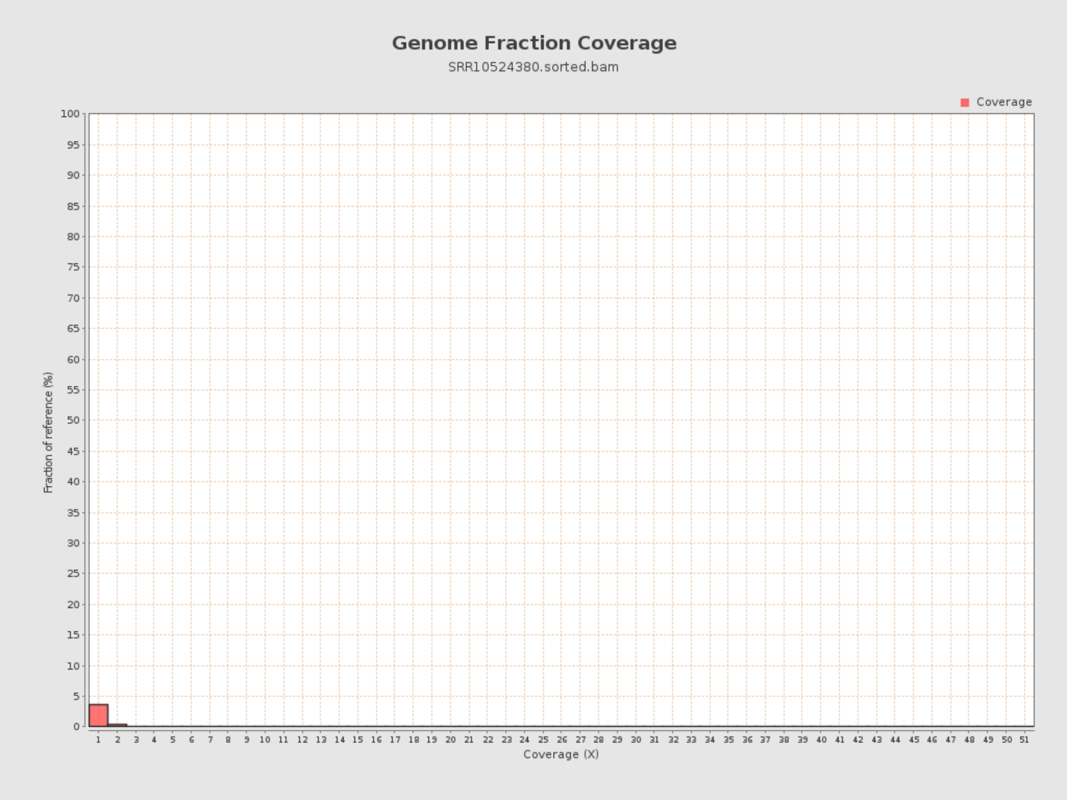
# 4. Results : Coverage Histogram



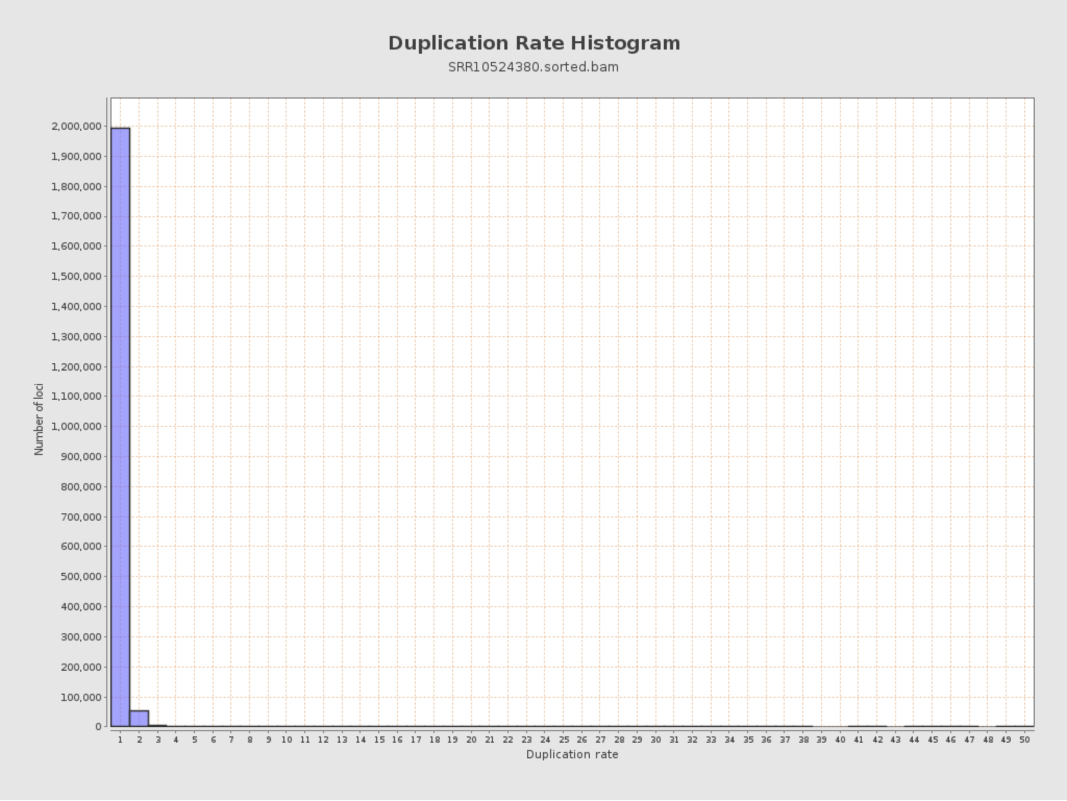
# 5. Results : Coverage Histogram (0-50X)



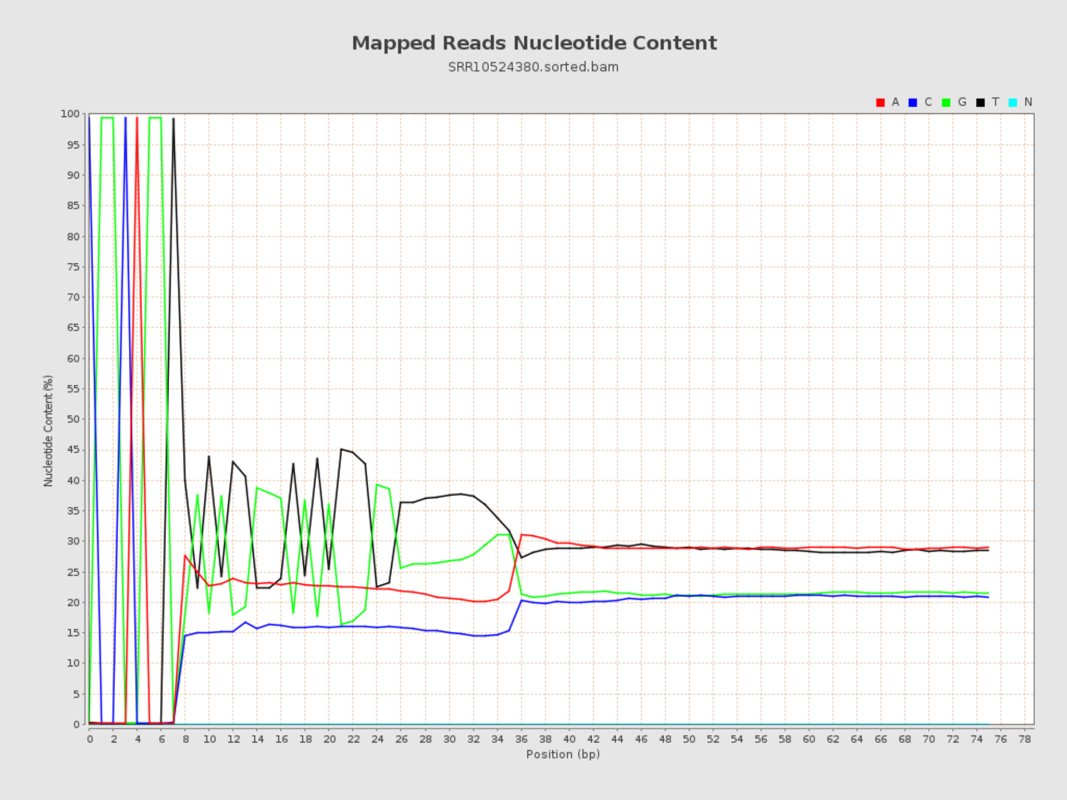
# 6. Results : Genome Fraction Coverage



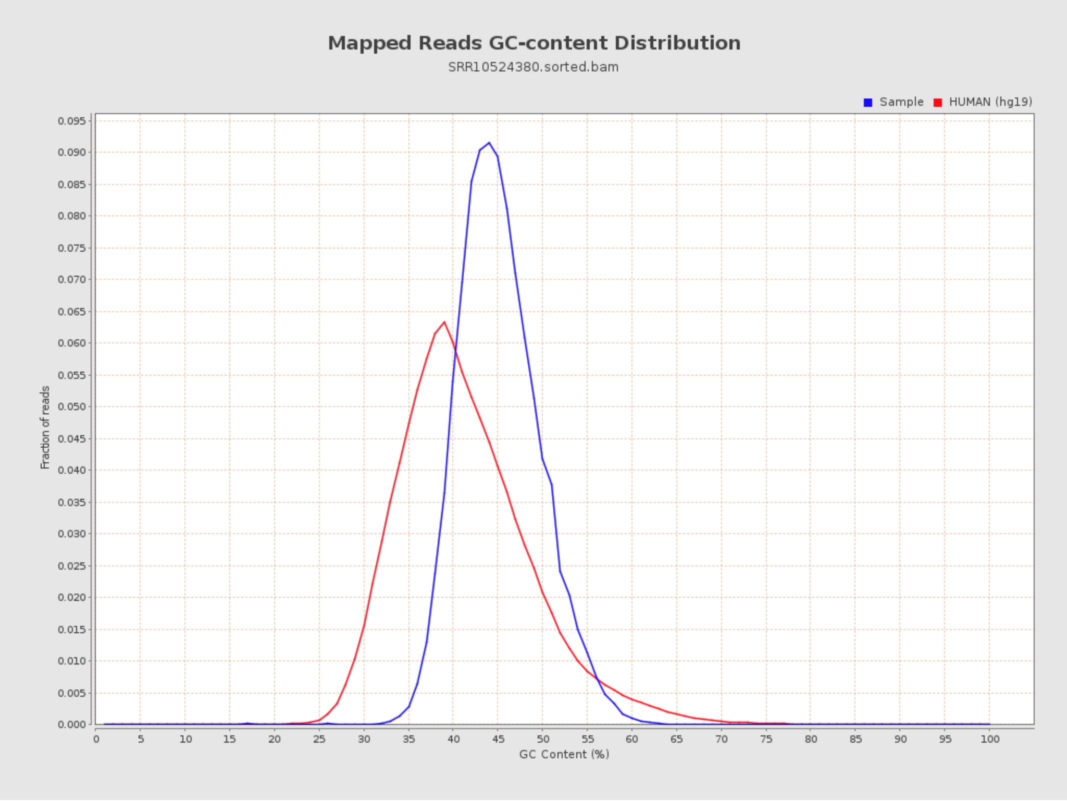
# 7. Results : Duplication Rate Histogram



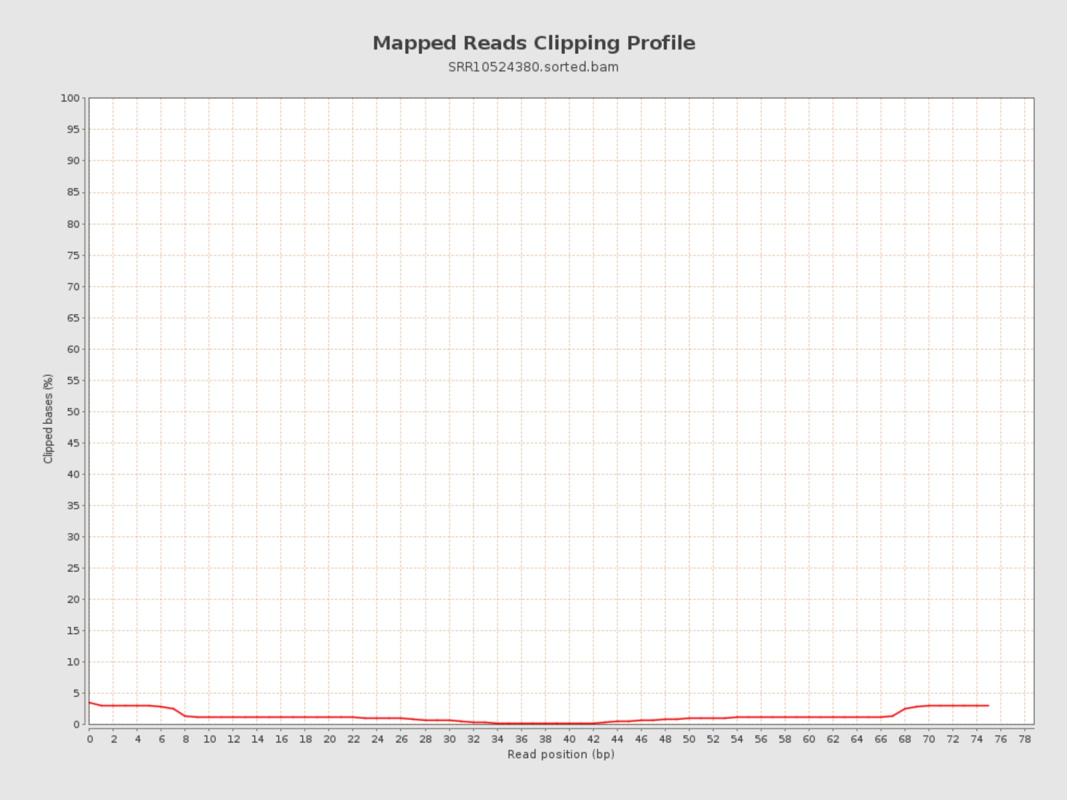
# 8. Results : Mapped Reads Nucleotide Content



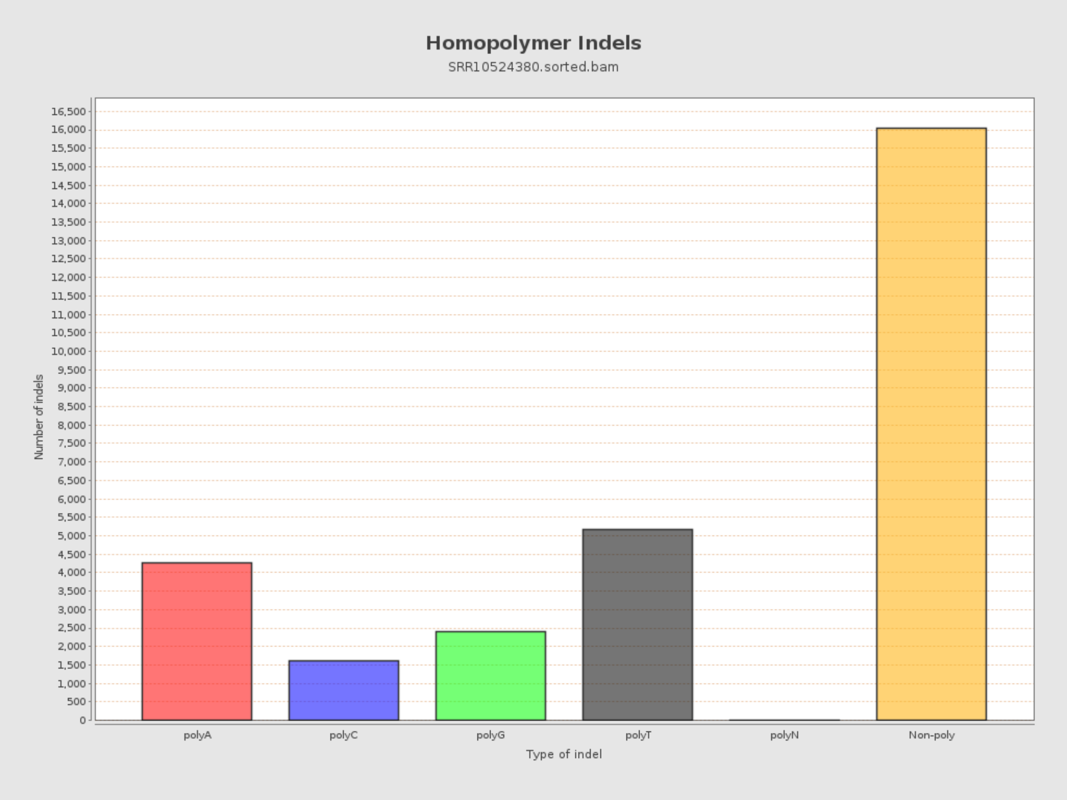
# 9. Results : Mapped Reads GC-content Distribution



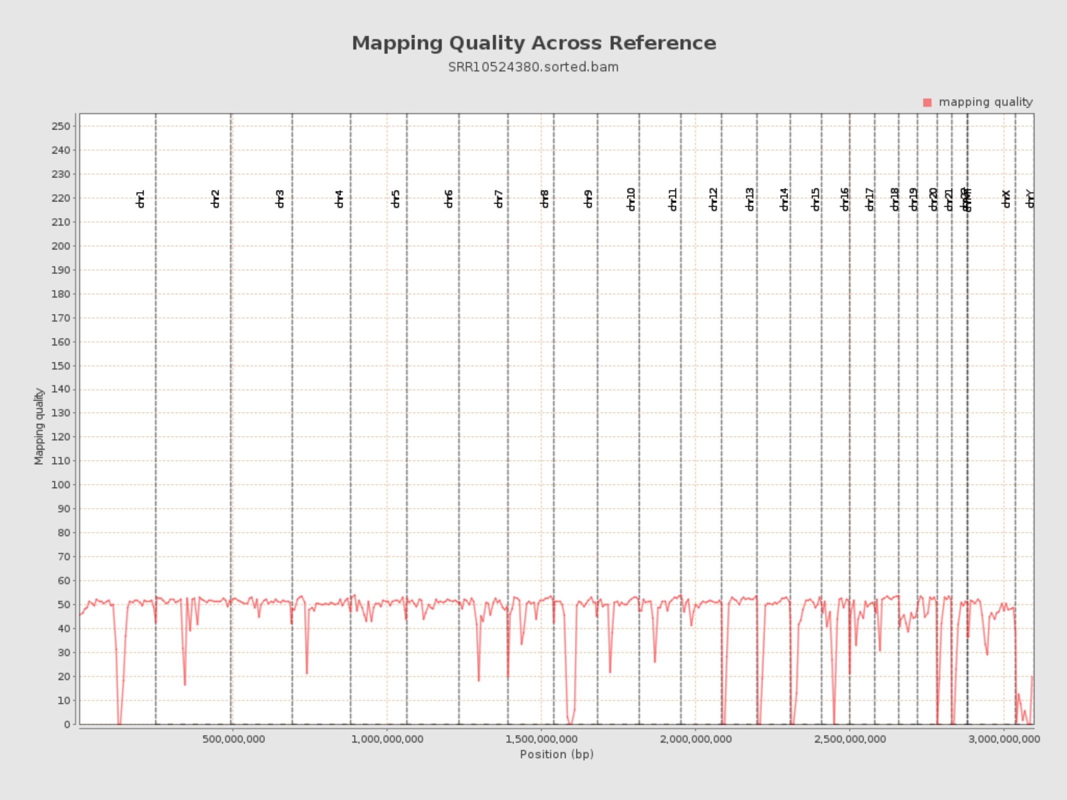
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram