# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 10:55:11*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524963.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_SRR10524963 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524963.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 10:55:09 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524963.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,417,198 |
| Mapped reads | 2,240,822 / 92.7% |
| Unmapped reads | 176,376 / 7.3% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 5,611 / 0.23% |
| Read min/max/mean length | 30 / 76 / 76.08 |
| Duplicated reads (estimated) | 86,705 / 3.59% |
| Duplication rate | 2.68% |
| Clipped reads | 2,240,422 / 92.69% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 32,916,983 / 25.11% |
| Number/percentage of C's | 23,237,867 / 17.73% |
| Number/percentage of T's | 42,845,365 / 32.68% |
| Number/percentage of G's | 32,098,078 / 24.48% |
| Number/percentage of N's | 1,392 / 0% |
| GC Percentage | 42.21% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0424 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3826 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.62 |

## 2.5. Mismatches and indels

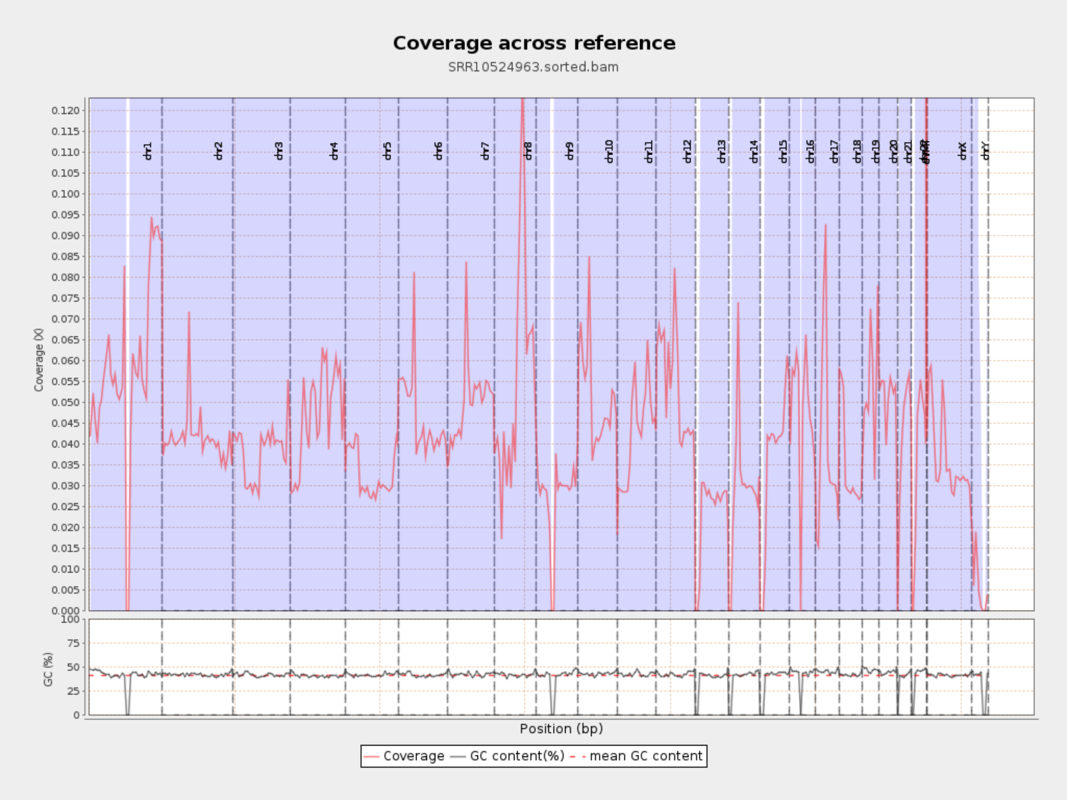
| | |
|---|---|
| General error rate | 0.5% |
| Mismatches | 642,284 |
| Insertions | 8,889 |
| Mapped reads with at least one insertion | 0.39% |
| Deletions | 25,455 |
| Mapped reads with at least one deletion | 1.13% |
| Homopolymer indels | 43.43% |

## 2.6. Chromosome stats

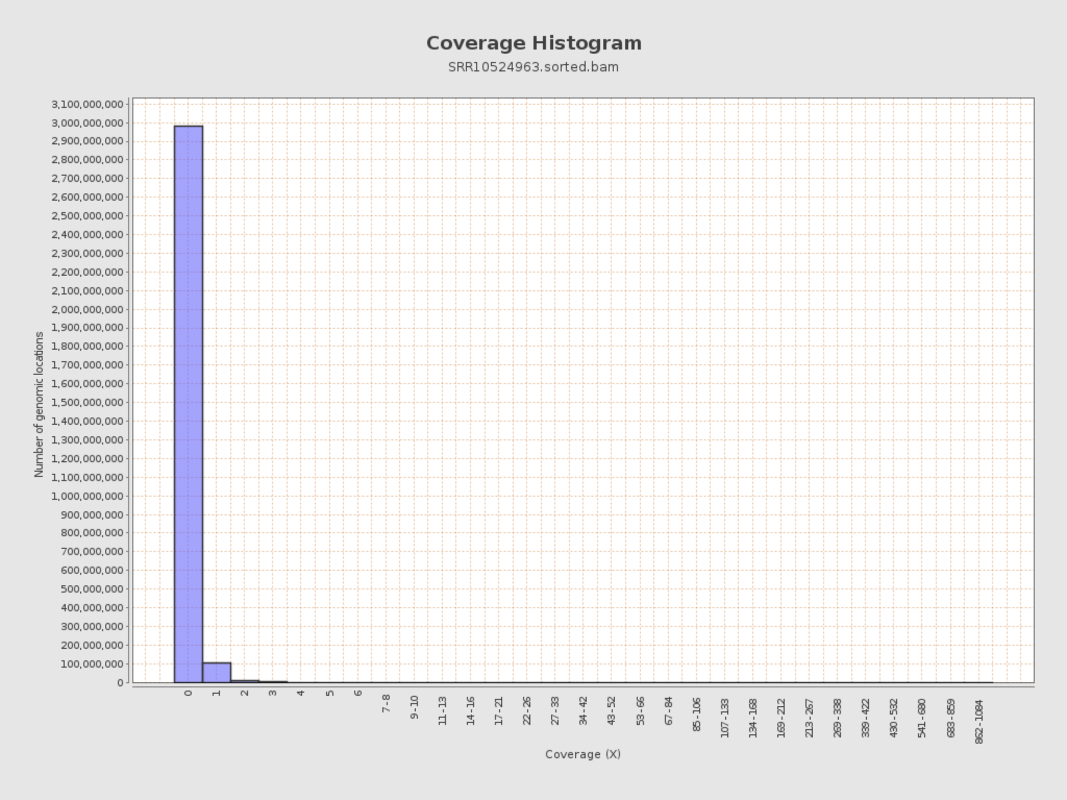
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 14427463 | 0.0579 | 0.7962 |
| chr2 | 243199373 | 10101708 | 0.0415 | 0.4144 |
| chr3 | 198022430 | 7554031 | 0.0381 | 0.2198 |
| chr4 | 191154276 | 9004762 | 0.0471 | 0.2609 |
| chr5 | 180915260 | 5948191 | 0.0329 | 0.2059 |
| chr6 | 171115067 | 7965057 | 0.0465 | 0.3794 |
| chr7 | 159138663 | 8034045 | 0.0505 | 0.5274 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 8191520 | 0.056 | 0.369 |
| chr9 | 141213431 | 3770926 | 0.0267 | 0.2821 |
| chr10 | 135534747 | 6943277 | 0.0512 | 0.3754 |
| chr11 | 135006516 | 5692444 | 0.0422 | 0.3314 |
| chr12 | 133851895 | 7214697 | 0.0539 | 0.2601 |
| chr13 | 115169878 | 2691789 | 0.0234 | 0.1703 |
| chr14 | 107349540 | 3124299 | 0.0291 | 0.1985 |
| chr15 | 102531392 | 3728847 | 0.0364 | 0.2281 |
| chr16 | 90354753 | 4285154 | 0.0474 | 0.2586 |
| chr17 | 81195210 | 3262688 | 0.0402 | 0.3252 |
| chr18 | 78077248 | 2738267 | 0.0351 | 0.4815 |
| chr19 | 59128983 | 3223122 | 0.0545 | 0.4379 |
| chr20 | 63025520 | 3224228 | 0.0512 | 0.2545 |
| chr21 | 48129895 | 1982035 | 0.0412 | 0.2388 |
| chr22 | 51304566 | 1752907 | 0.0342 | 0.2031 |
| chrMT | 16571 | 160728 | 9.6994 | 6.4146 |
| chrX | 155270560 | 5770362 | 0.0372 | 0.2591 |
| chrY | 59373566 | 350464 | 0.0059 | 0.1315 |

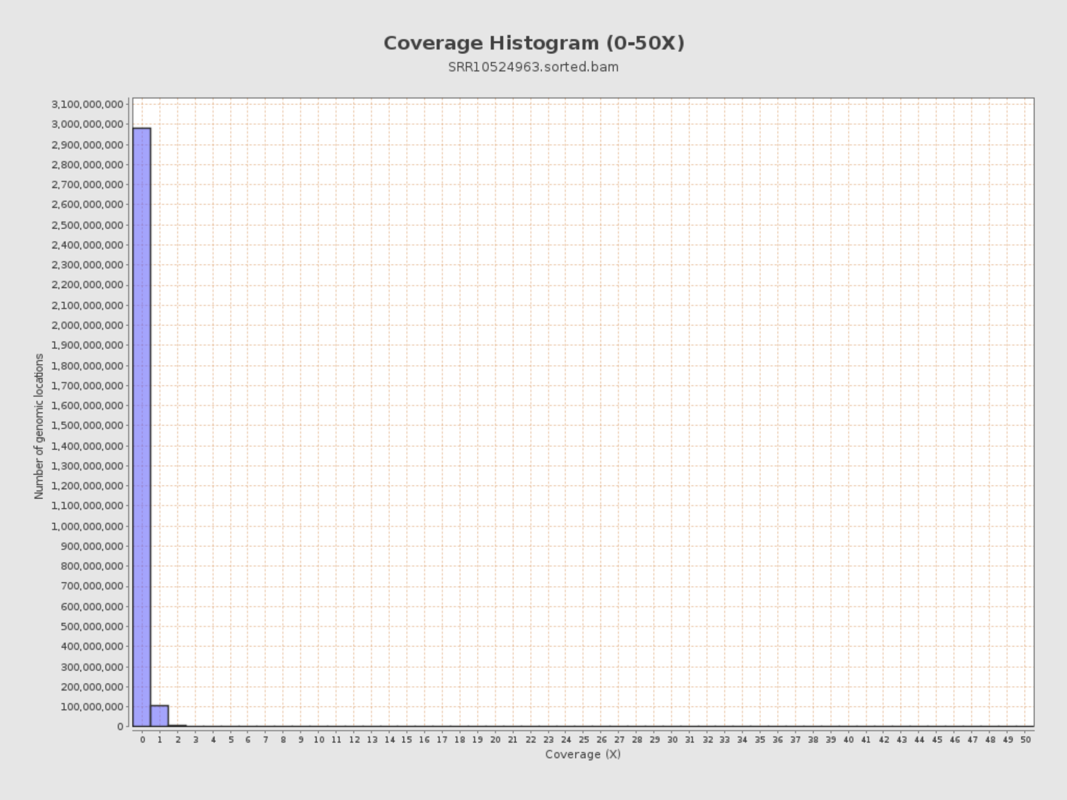
# 3. Results : Coverage across reference



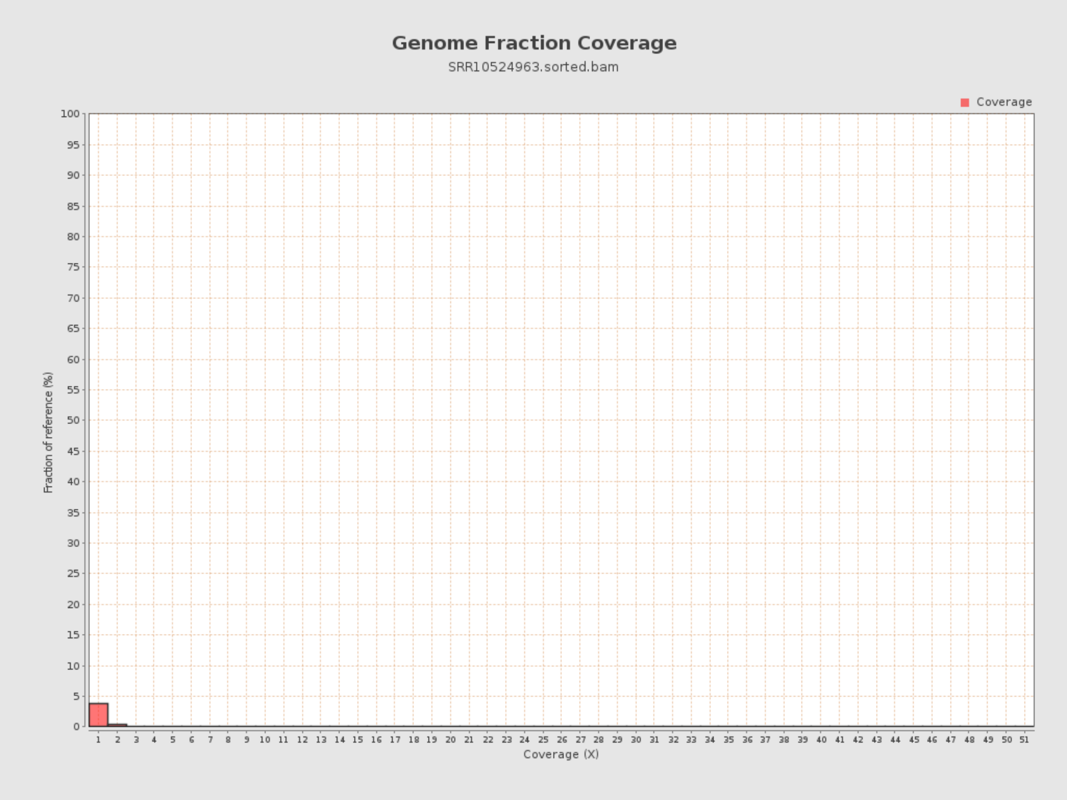
# 4. Results : Coverage Histogram



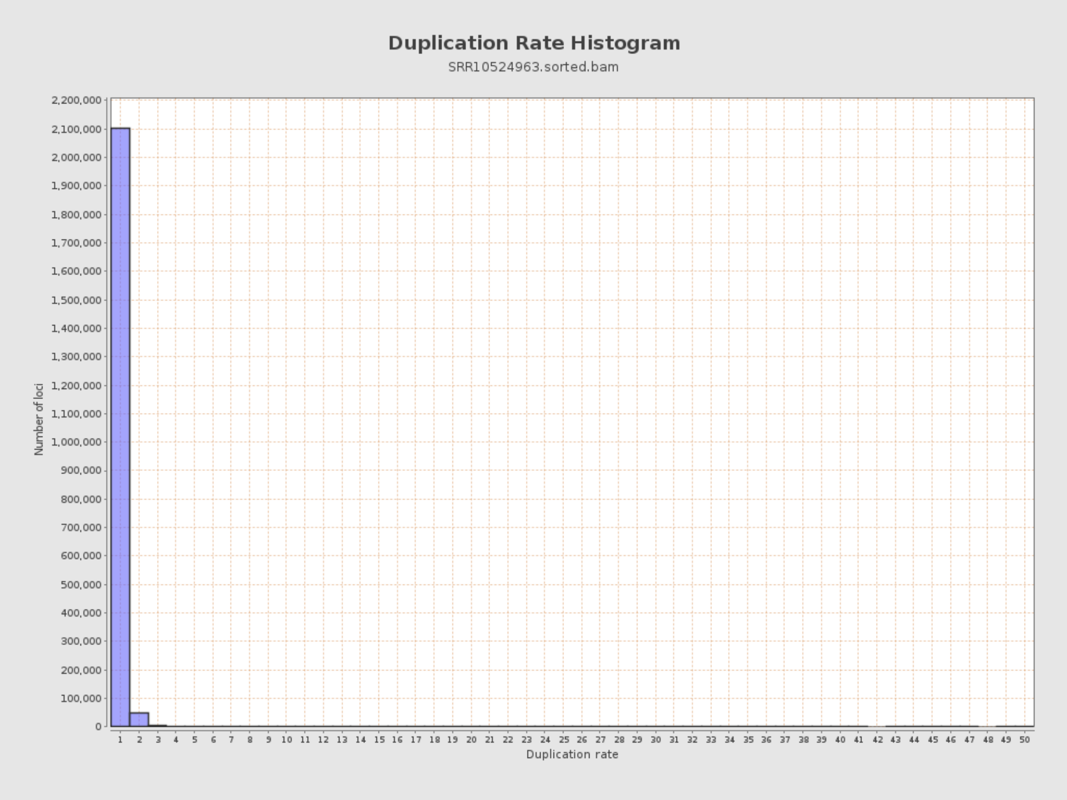
# 5. Results : Coverage Histogram (0-50X)



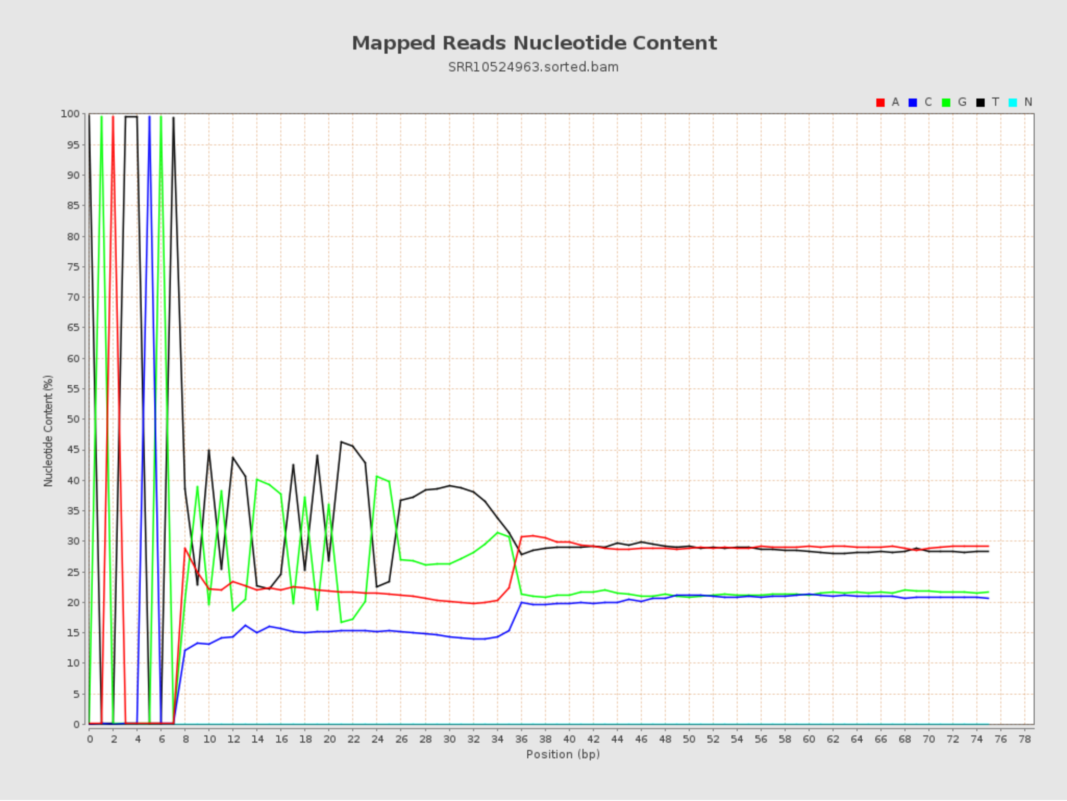
# 6. Results : Genome Fraction Coverage



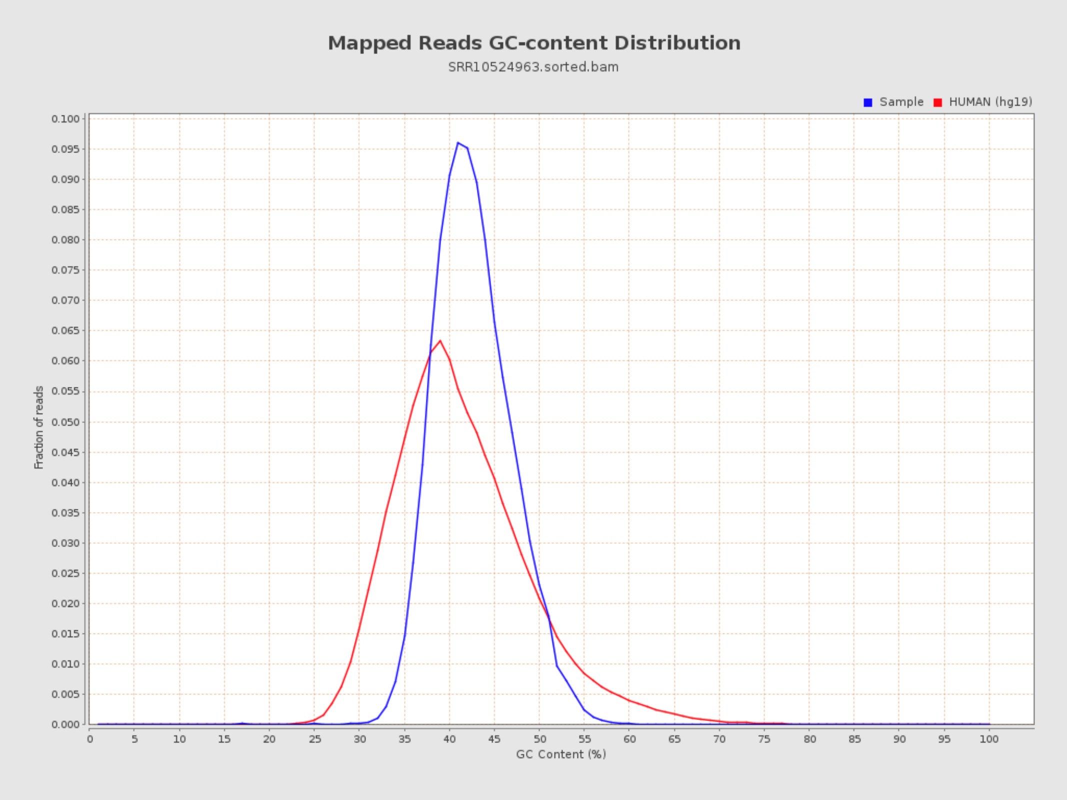
# 7. Results : Duplication Rate Histogram



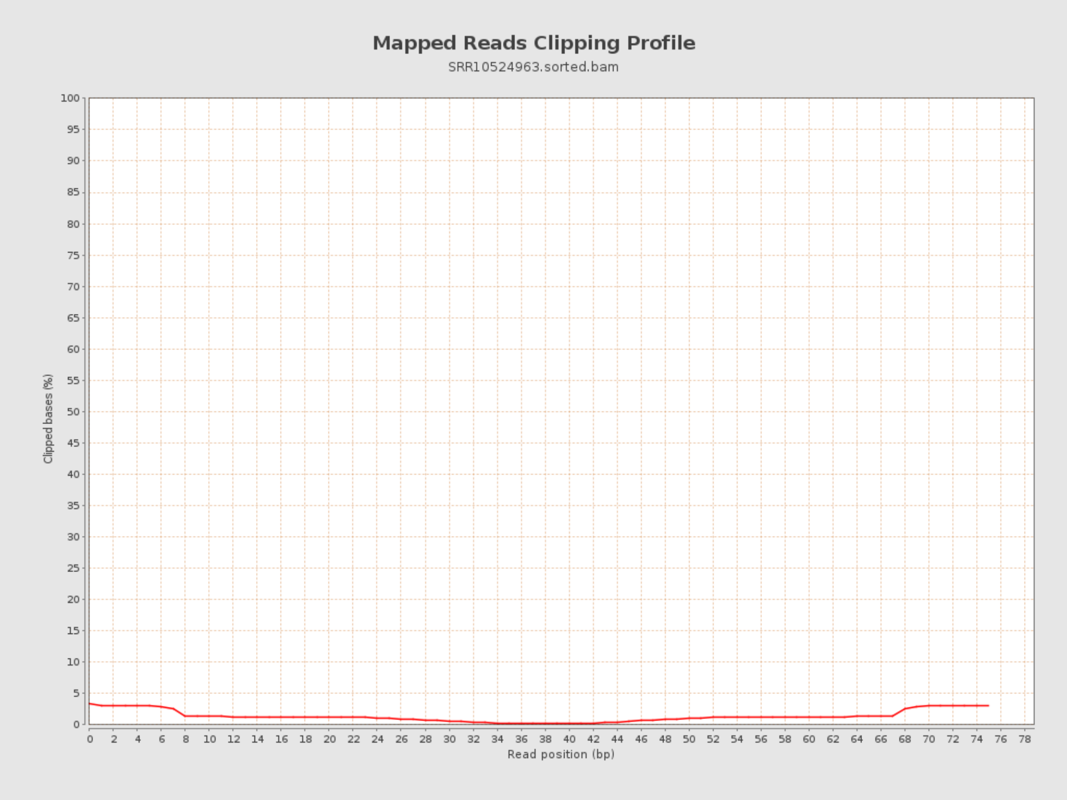
# 8. Results : Mapped Reads Nucleotide Content



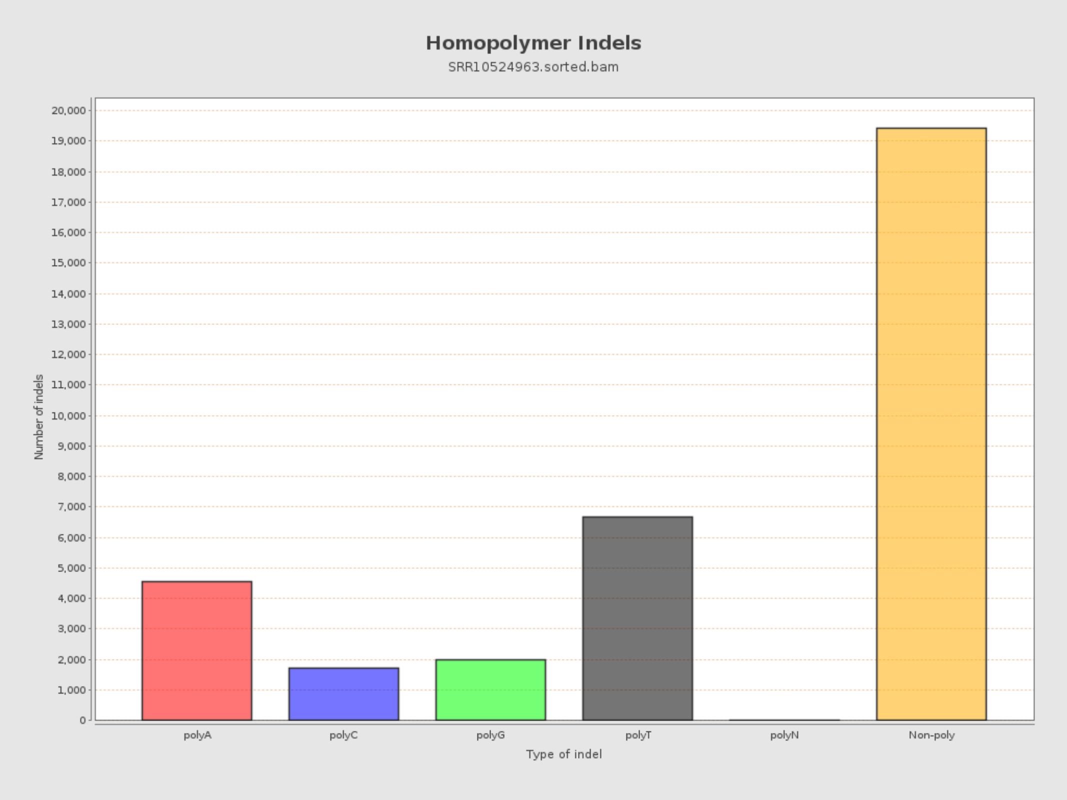
# 9. Results : Mapped Reads GC-content Distribution



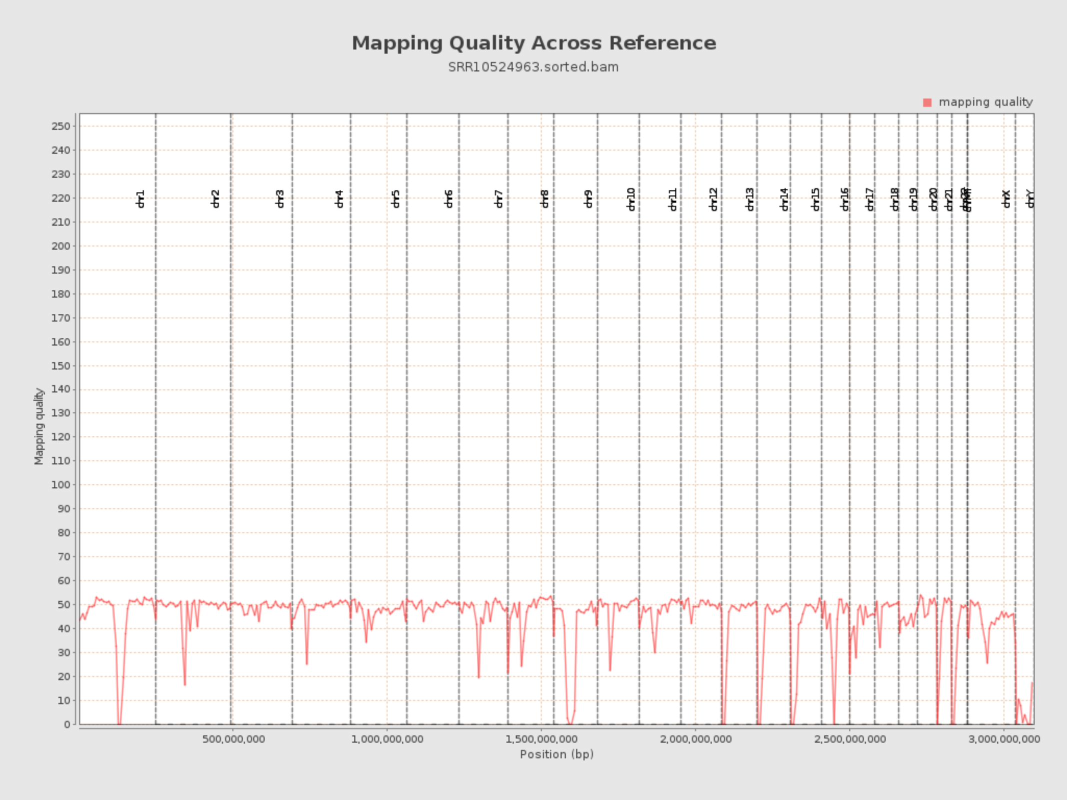
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram