# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 03:49:11*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524426.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_SRR10524426 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524426.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 03:49:10 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524426.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,723,030 |
| Mapped reads | 2,507,446 / 92.08% |
| Unmapped reads | 215,584 / 7.92% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 10,751 / 0.39% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 164,636 / 6.05% |
| Duplication rate | 4.86% |
| Clipped reads | 2,508,133 / 92.11% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 34,268,637 / 23.35% |
| Number/percentage of C's | 29,375,722 / 20.02% |
| Number/percentage of T's | 47,889,255 / 32.63% |
| Number/percentage of G's | 35,216,685 / 24% |
| Number/percentage of N's | 14,946 / 0.01% |
| GC Percentage | 44.01% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0474 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4463 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.53 |

## 2.5. Mismatches and indels

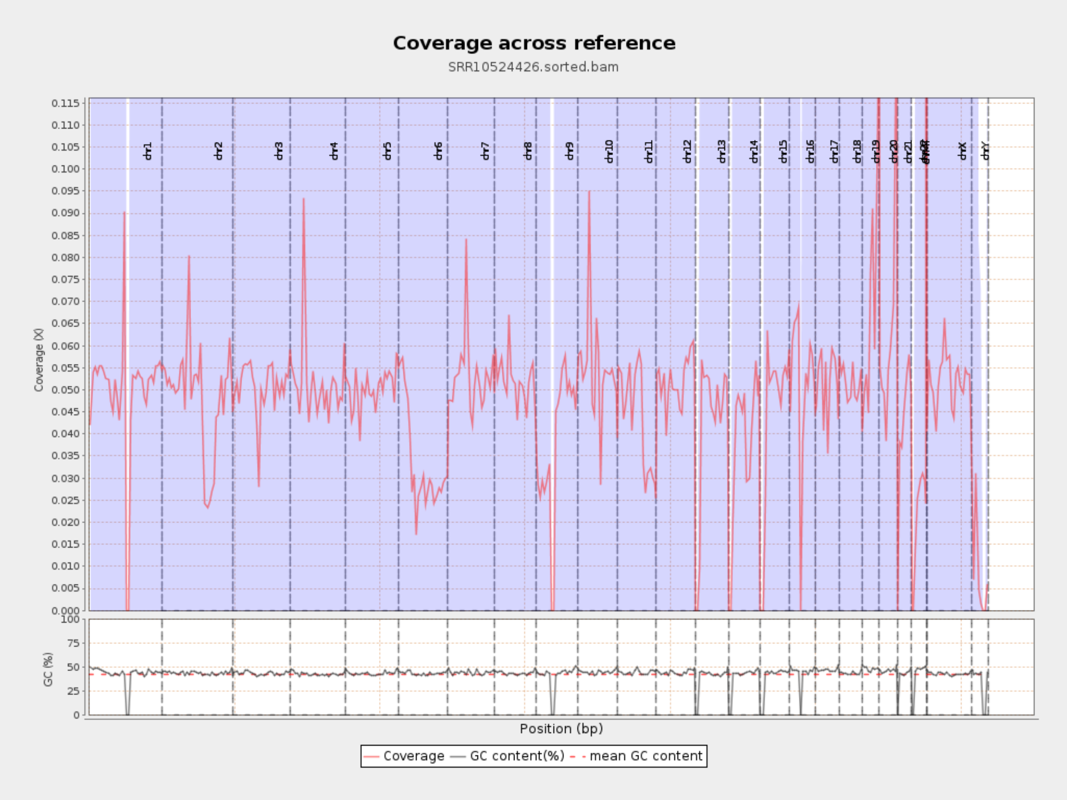
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 733,929 |
| Insertions | 11,291 |
| Mapped reads with at least one insertion | 0.45% |
| Deletions | 26,106 |
| Mapped reads with at least one deletion | 1.03% |
| Homopolymer indels | 41.06% |

## 2.6. Chromosome stats

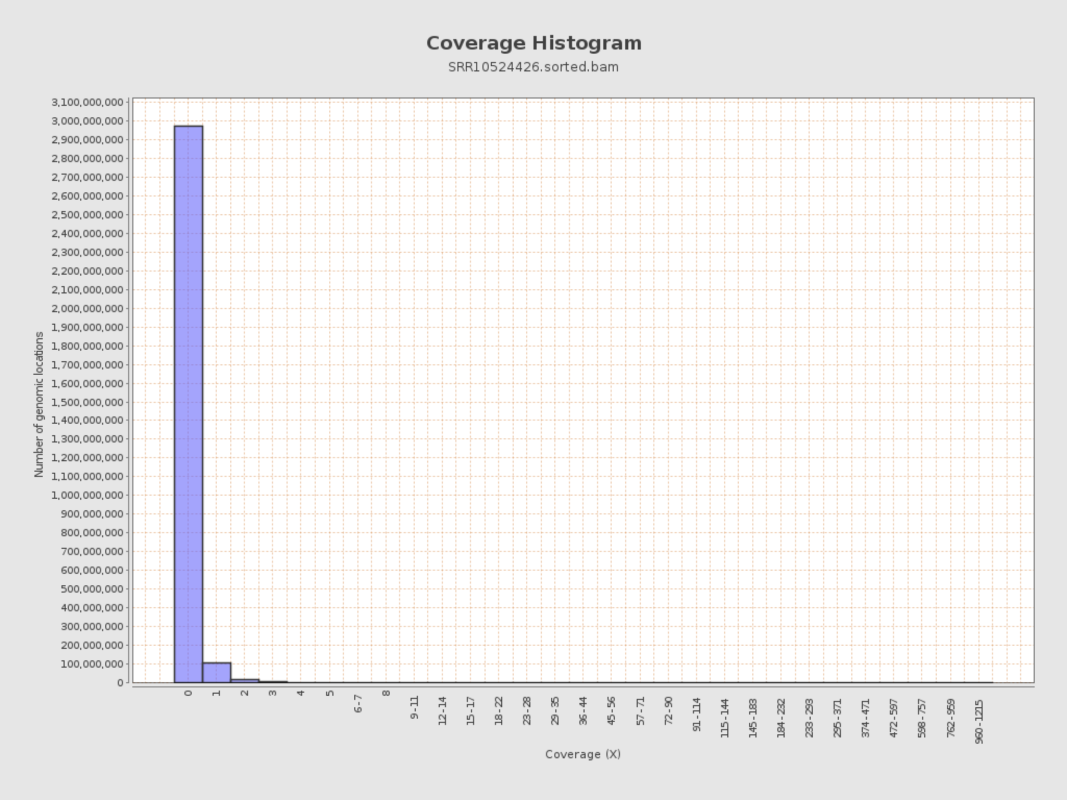
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 12344654 | 0.0495 | 0.955 |
| chr2 | 243199373 | 11815084 | 0.0486 | 0.5735 |
| chr3 | 198022430 | 10009761 | 0.0505 | 0.2657 |
| chr4 | 191154276 | 9820123 | 0.0514 | 0.3383 |
| chr5 | 180915260 | 9081853 | 0.0502 | 0.2618 |
| chr6 | 171115067 | 5704344 | 0.0333 | 0.2361 |
| chr7 | 159138663 | 8458112 | 0.0531 | 0.5824 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7669359 | 0.0524 | 0.3495 |
| chr9 | 141213431 | 5284550 | 0.0374 | 0.2918 |
| chr10 | 135534747 | 7456785 | 0.055 | 0.4629 |
| chr11 | 135006516 | 5957818 | 0.0441 | 0.3267 |
| chr12 | 133851895 | 6960924 | 0.052 | 0.2771 |
| chr13 | 115169878 | 4769538 | 0.0414 | 0.2389 |
| chr14 | 107349540 | 4018305 | 0.0374 | 0.2377 |
| chr15 | 102531392 | 4488823 | 0.0438 | 0.2467 |
| chr16 | 90354753 | 4681178 | 0.0518 | 0.2892 |
| chr17 | 81195210 | 4138975 | 0.051 | 0.2974 |
| chr18 | 78077248 | 4029901 | 0.0516 | 0.5475 |
| chr19 | 59128983 | 4295910 | 0.0727 | 0.657 |
| chr20 | 63025520 | 4110475 | 0.0652 | 0.3233 |
| chr21 | 48129895 | 2036872 | 0.0423 | 0.3224 |
| chr22 | 51304566 | 1052509 | 0.0205 | 0.1702 |
| chrMT | 16571 | 19730 | 1.1906 | 1.395 |
| chrX | 155270560 | 8101512 | 0.0522 | 0.3005 |
| chrY | 59373566 | 500056 | 0.0084 | 0.2557 |

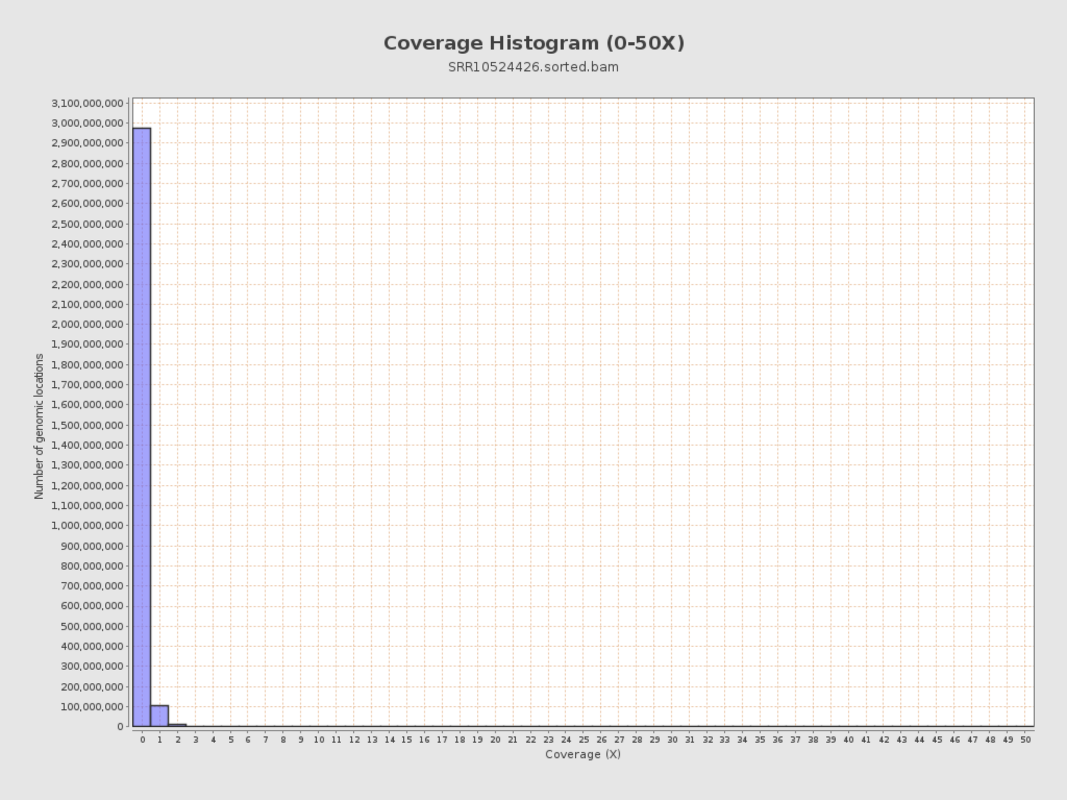
# 3. Results : Coverage across reference



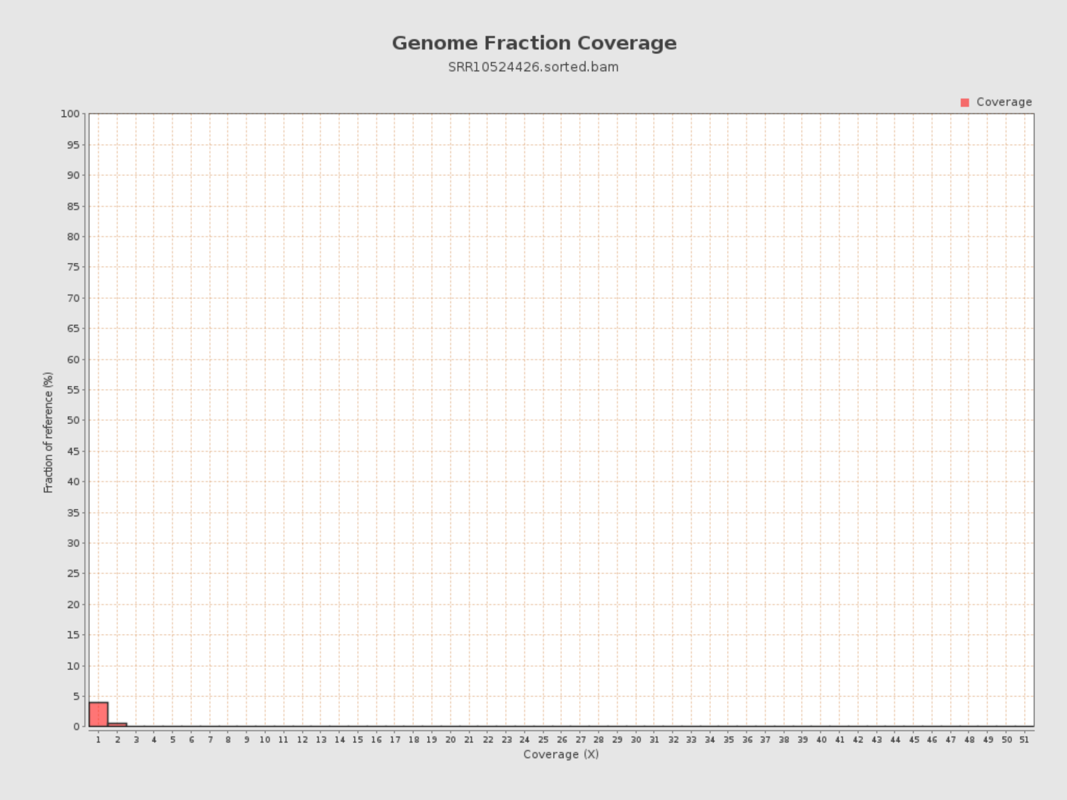
# 4. Results : Coverage Histogram



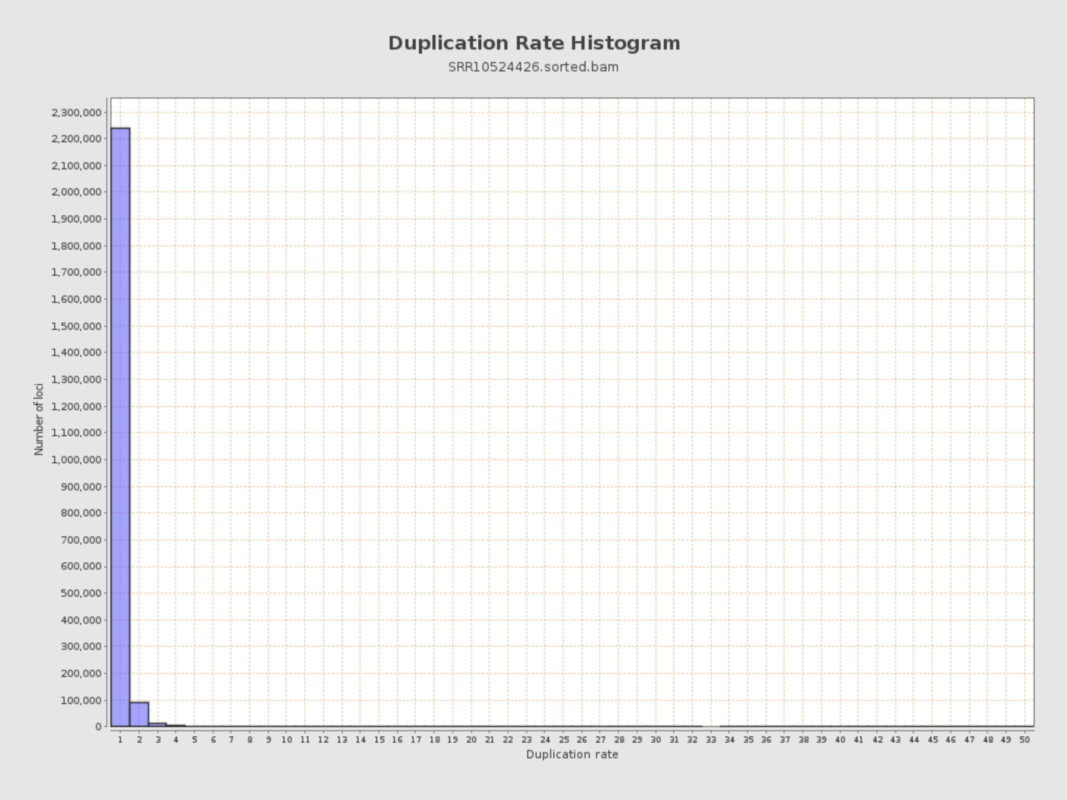
# 5. Results : Coverage Histogram (0-50X)



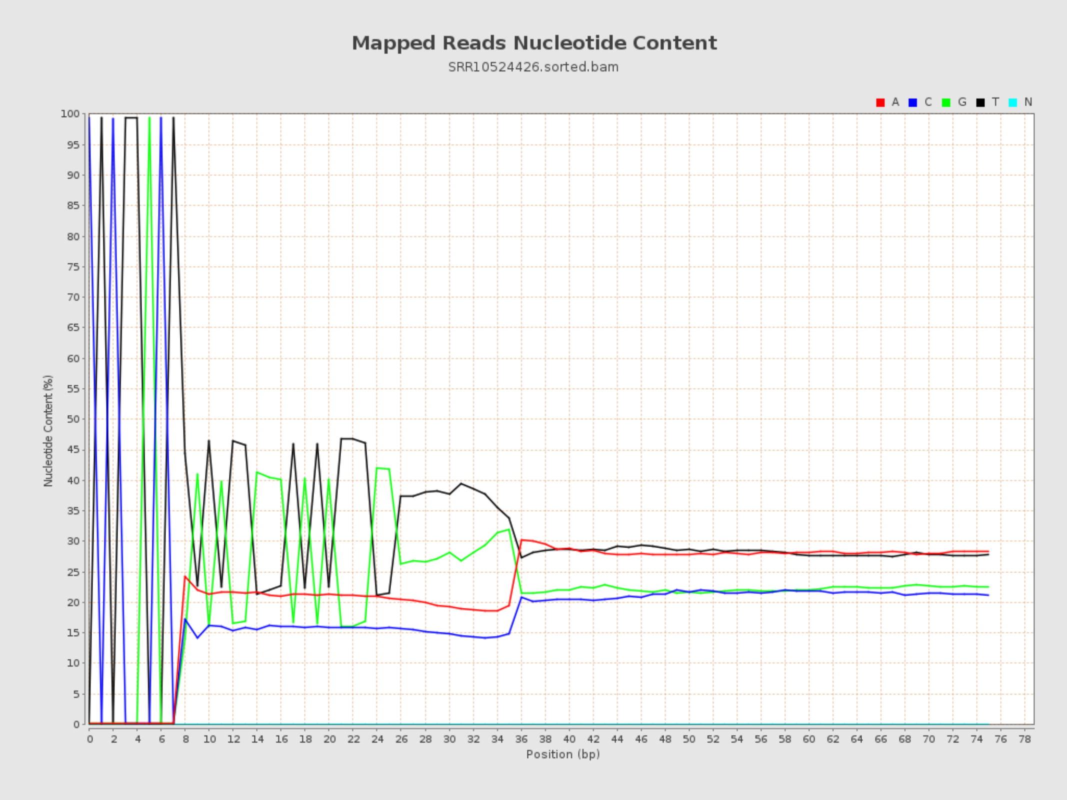
# 6. Results : Genome Fraction Coverage



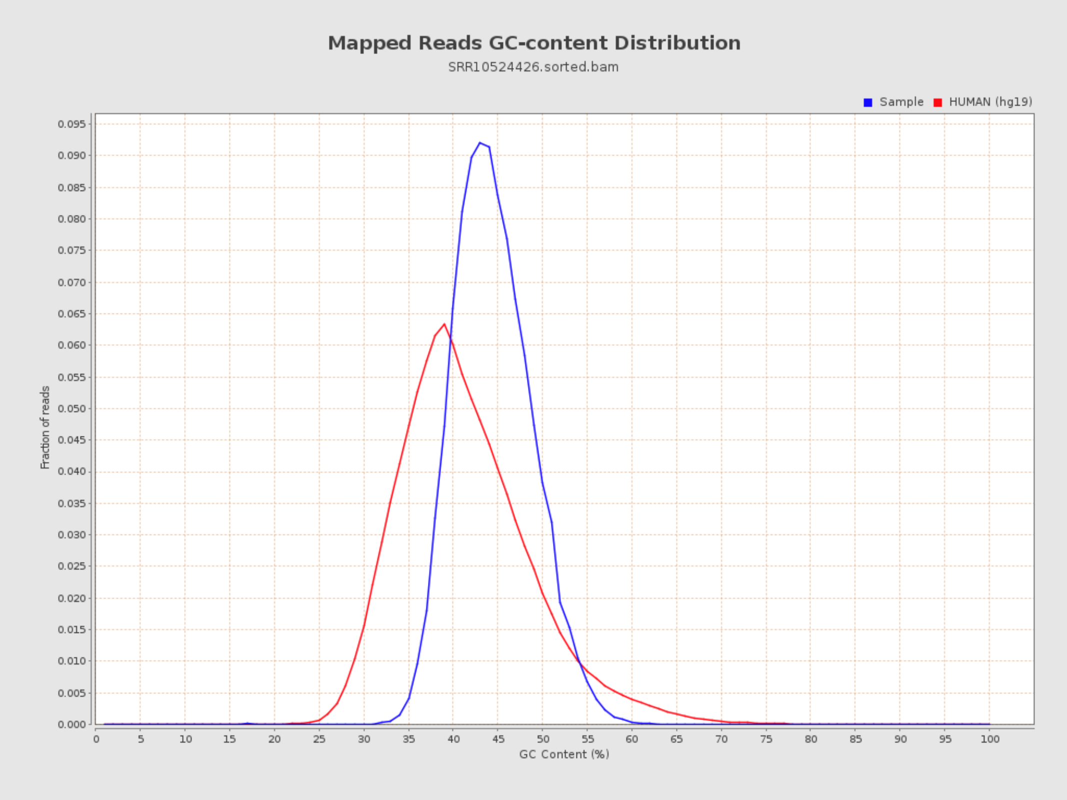
# 7. Results : Duplication Rate Histogram



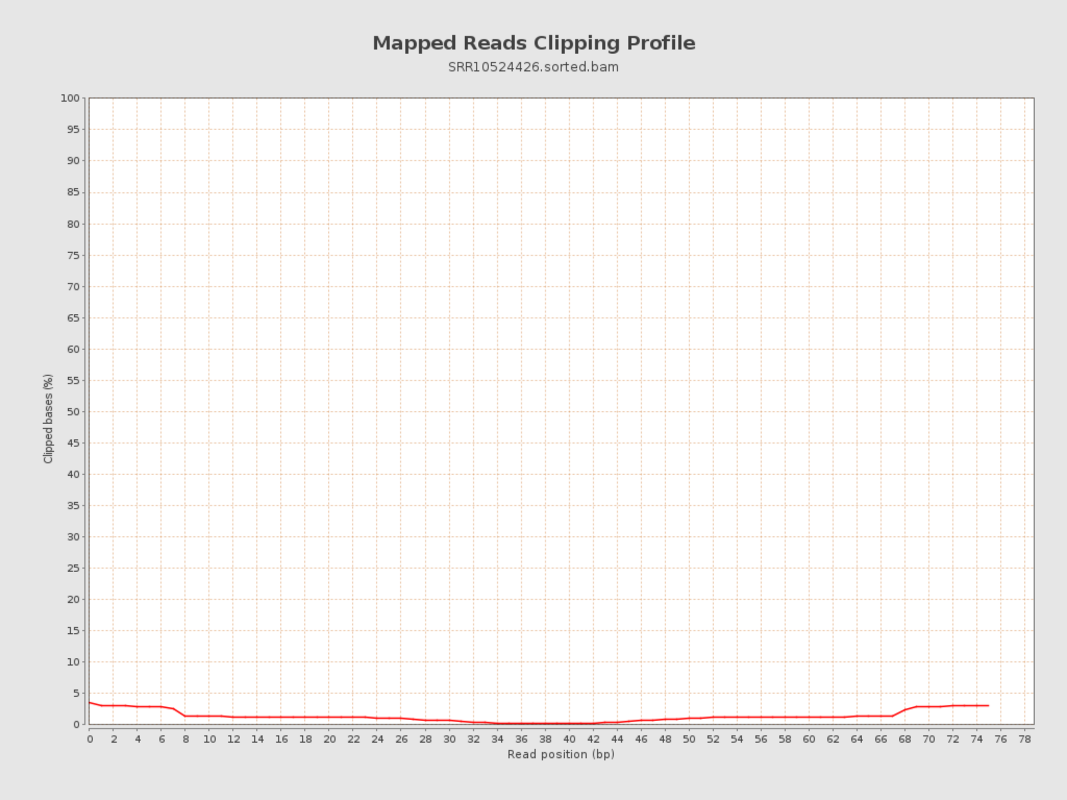
# 8. Results : Mapped Reads Nucleotide Content



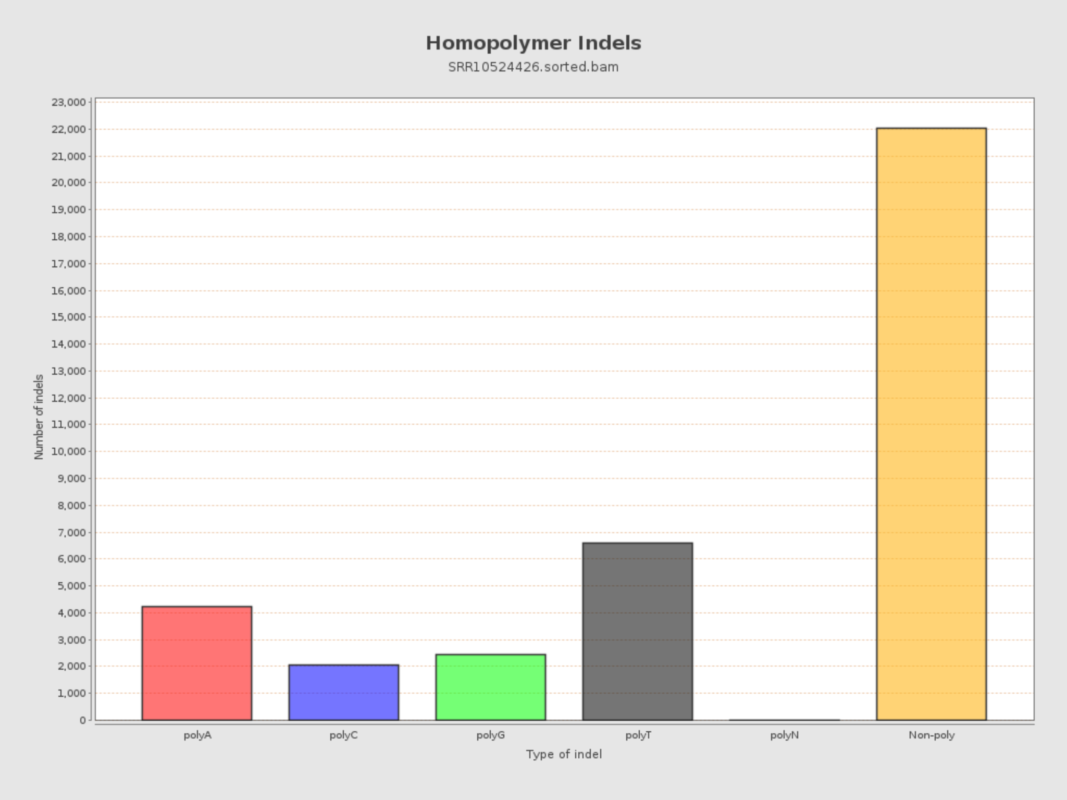
# 9. Results : Mapped Reads GC-content Distribution



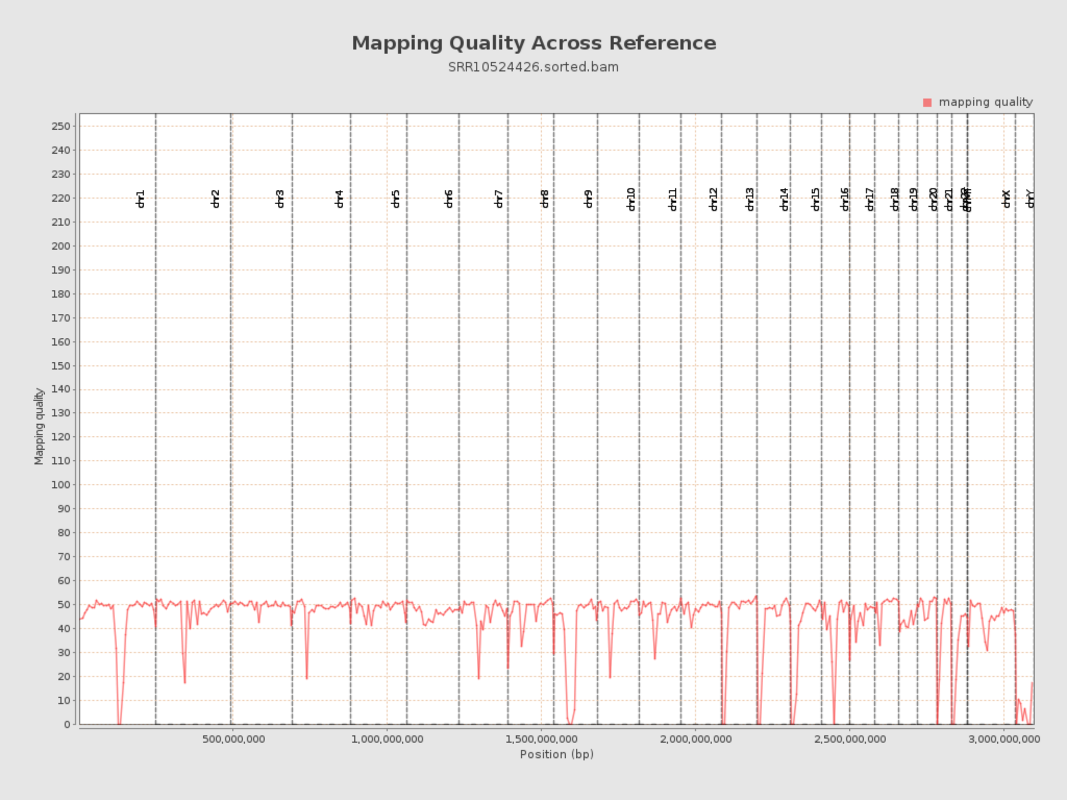
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram