# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 00:23:03*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524358.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_SRR10524358 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524358.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 00:23:02 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524358.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,773,716 |
| Mapped reads | 3,448,453 / 91.38% |
| Unmapped reads | 325,263 / 8.62% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 14,231 / 0.38% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 266,500 / 7.06% |
| Duplication rate | 5.64% |
| Clipped reads | 3,453,709 / 91.52% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 50,051,216 / 25.1% |
| Number/percentage of C's | 37,349,548 / 18.73% |
| Number/percentage of T's | 64,241,897 / 32.21% |
| Number/percentage of G's | 47,772,412 / 23.95% |
| Number/percentage of N's | 28,168 / 0.01% |
| GC Percentage | 42.68% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0644 |
| | |

| | |
|---|---|
| Standard Deviation | 0.5947 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.5 |

## 2.5. Mismatches and indels

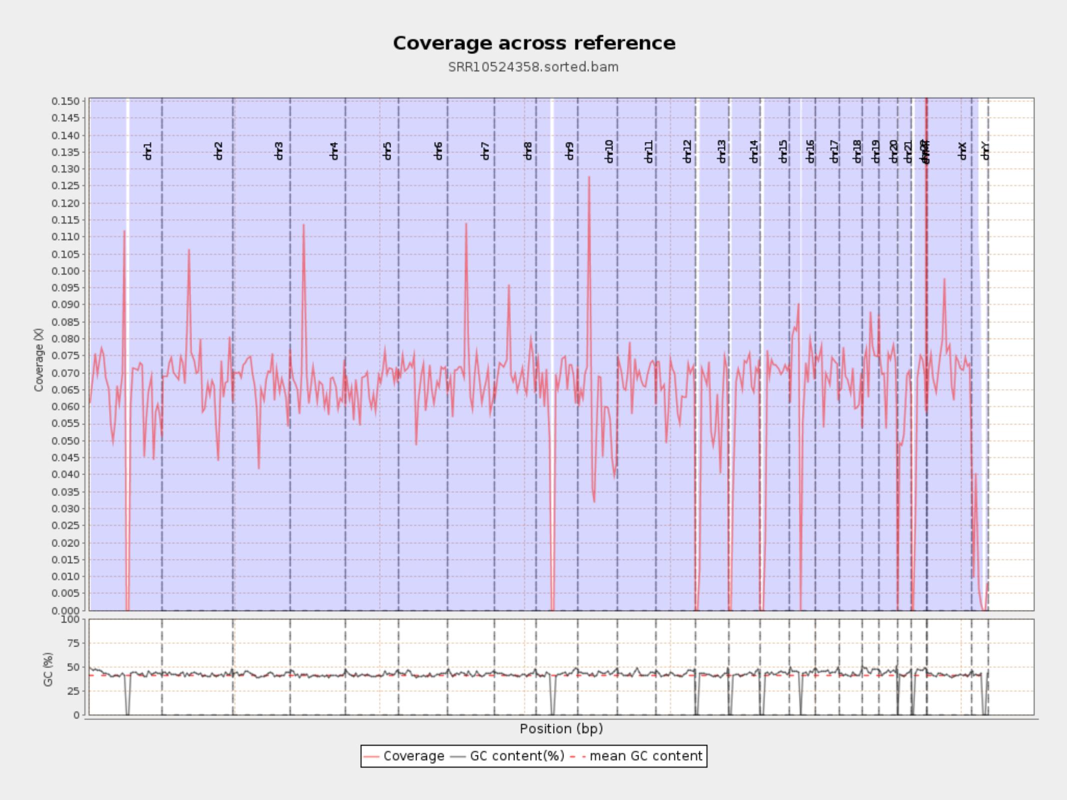
| | |
|---|---|
| General error rate | 0.53% |
| Mismatches | 1,036,523 |
| Insertions | 14,926 |
| Mapped reads with at least one insertion | 0.43% |
| Deletions | 34,955 |
| Mapped reads with at least one deletion | 1.01% |
| Homopolymer indels | 42.1% |

## 2.6. Chromosome stats

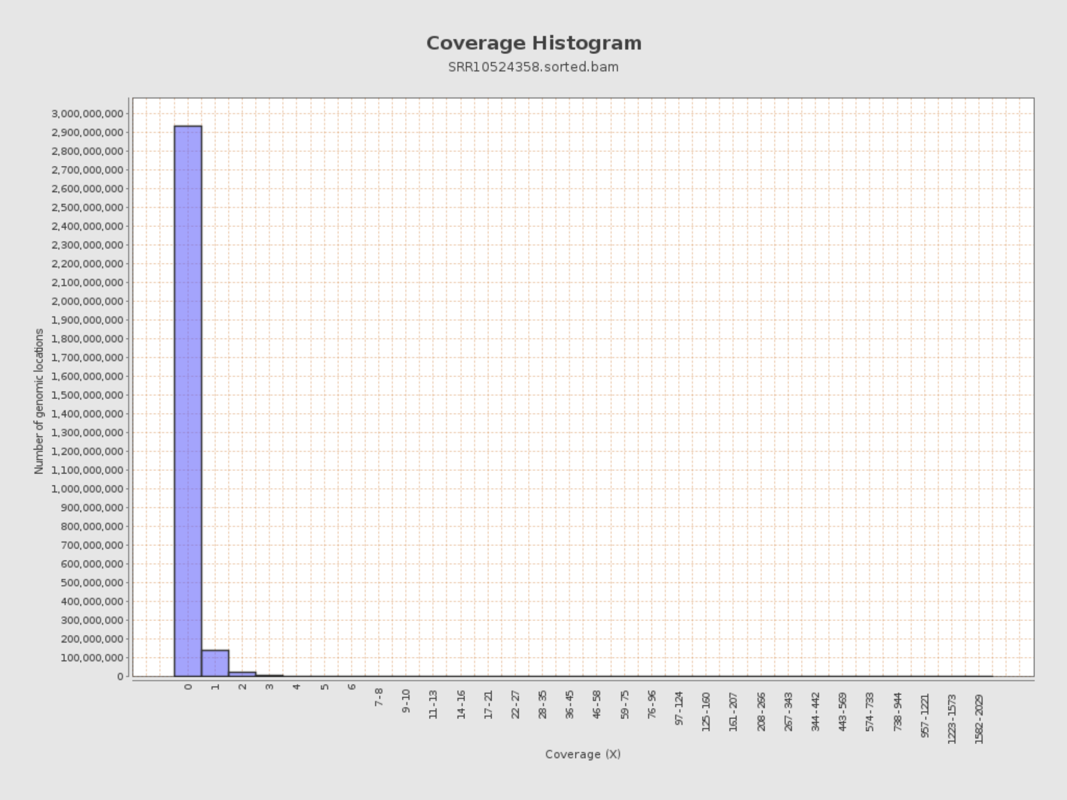
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 15411793 | 0.0618 | 1.2198 |
| chr2 | 243199373 | 16987609 | 0.0699 | 0.8937 |
| chr3 | 198022430 | 13231602 | 0.0668 | 0.3217 |
| chr4 | 191154276 | 12877451 | 0.0674 | 0.3925 |
| chr5 | 180915260 | 11997292 | 0.0663 | 0.3162 |
| chr6 | 171115067 | 11631272 | 0.068 | 0.3613 |
| chr7 | 159138663 | 11070172 | 0.0696 | 0.7276 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 10401801 | 0.0711 | 0.4688 |
| chr9 | 141213431 | 8505632 | 0.0602 | 0.465 |
| chr10 | 135534747 | 8059606 | 0.0595 | 0.5416 |
| chr11 | 135006516 | 9355995 | 0.0693 | 0.4817 |
| chr12 | 133851895 | 8788316 | 0.0657 | 0.3257 |
| chr13 | 115169878 | 5993957 | 0.052 | 0.277 |
| chr14 | 107349540 | 6274870 | 0.0585 | 0.3263 |
| chr15 | 102531392 | 5929916 | 0.0578 | 0.2965 |
| chr16 | 90354753 | 6175834 | 0.0684 | 0.3656 |
| chr17 | 81195210 | 5691323 | 0.0701 | 0.3622 |
| chr18 | 78077248 | 5174355 | 0.0663 | 0.959 |
| chr19 | 59128983 | 4431824 | 0.075 | 0.7836 |
| chr20 | 63025520 | 4435680 | 0.0704 | 0.3384 |
| chr21 | 48129895 | 2551314 | 0.053 | 0.3486 |
| chr22 | 51304566 | 2540379 | 0.0495 | 0.2747 |
| chrMT | 16571 | 43530 | 2.6269 | 2.4673 |
| chrX | 155270560 | 11276731 | 0.0726 | 0.3999 |
| chrY | 59373566 | 660339 | 0.0111 | 0.2876 |

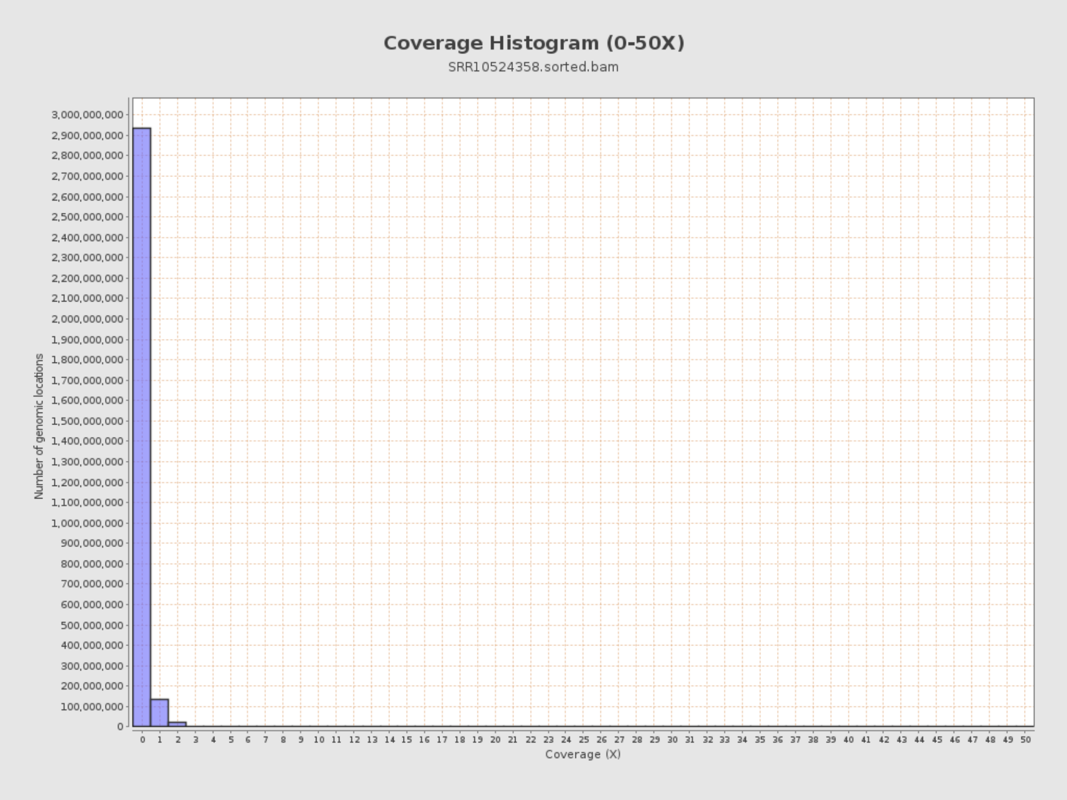
# 3. Results : Coverage across reference



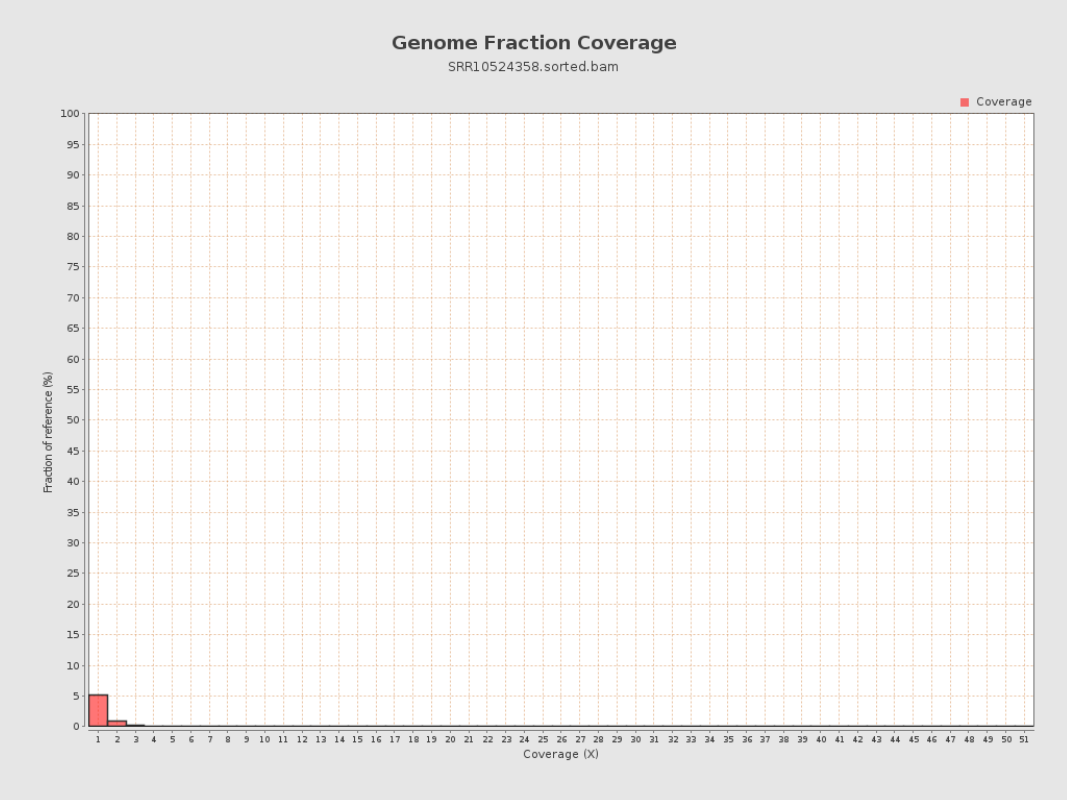
# 4. Results : Coverage Histogram



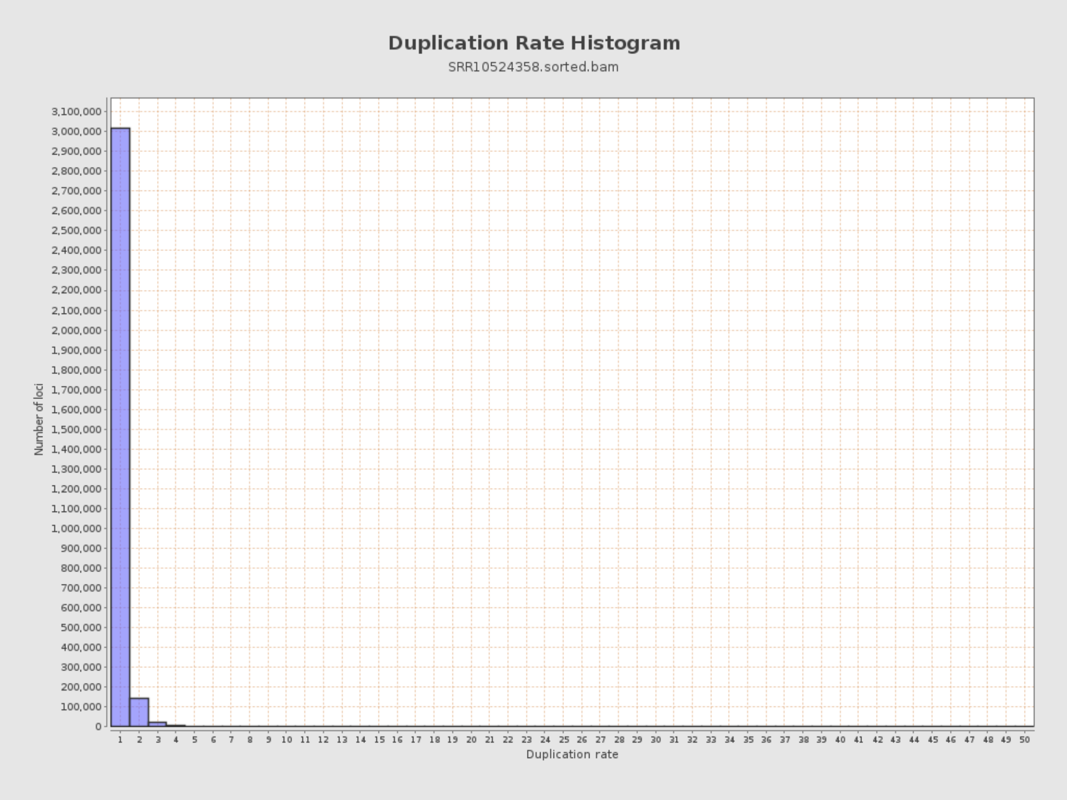
# 5. Results : Coverage Histogram (0-50X)



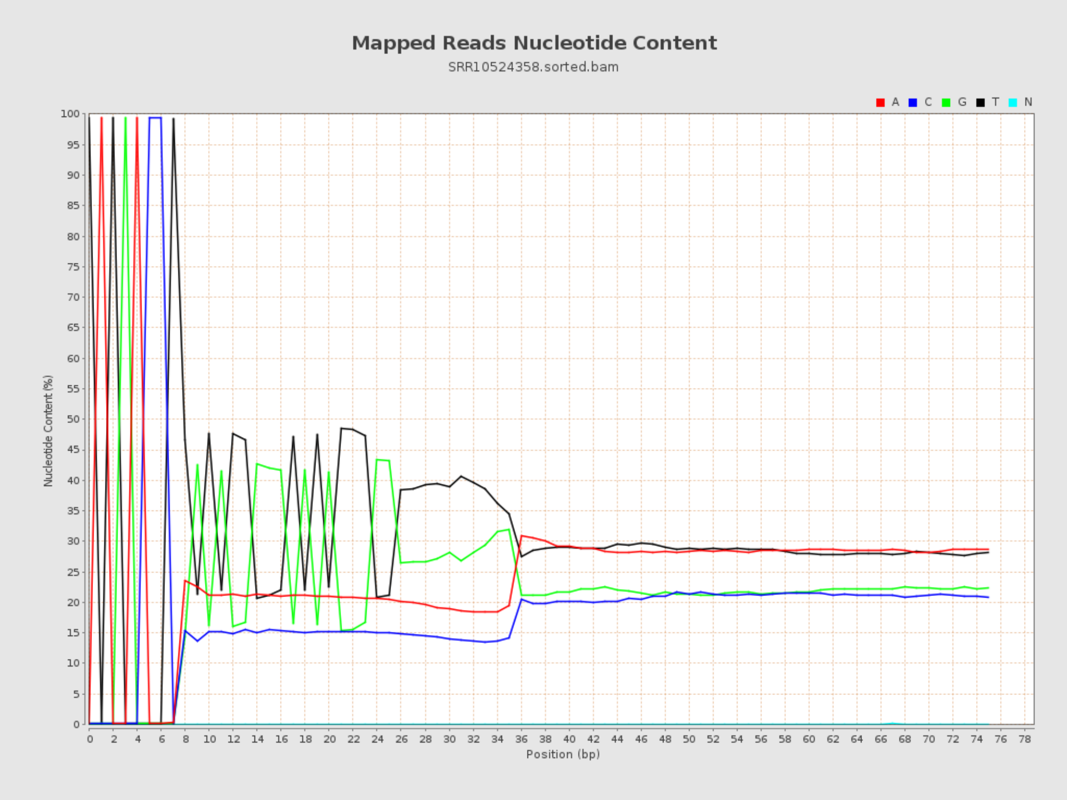
# 6. Results : Genome Fraction Coverage



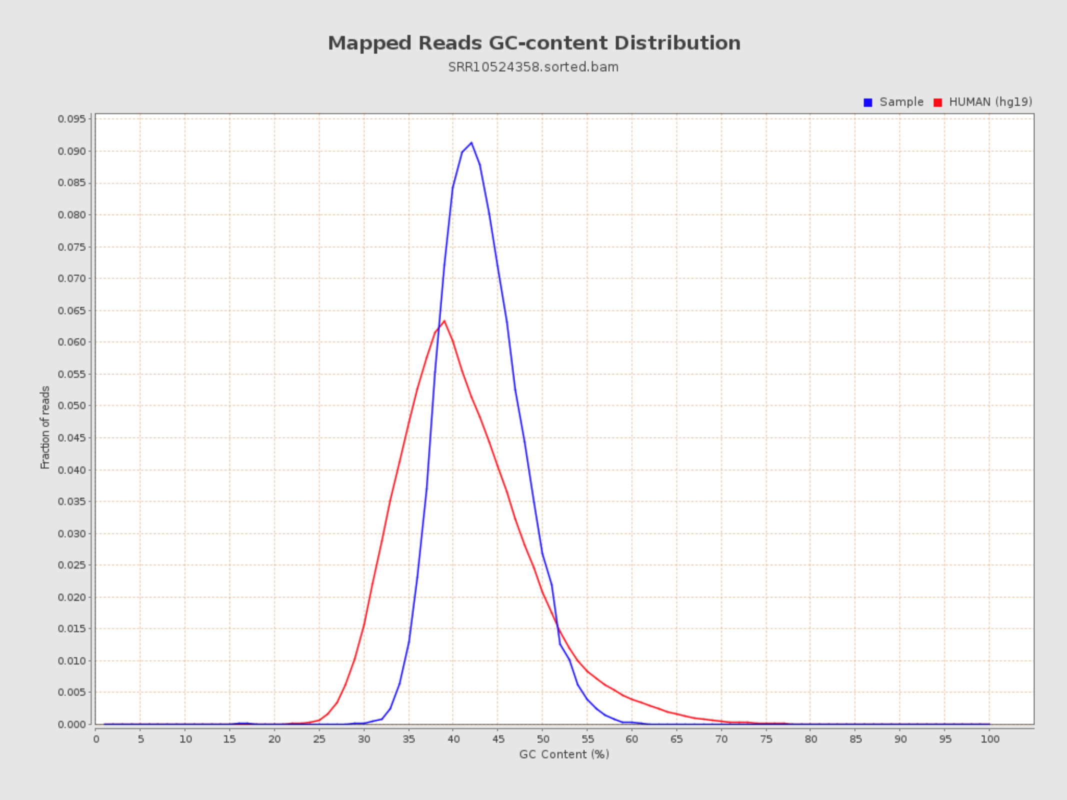
# 7. Results : Duplication Rate Histogram



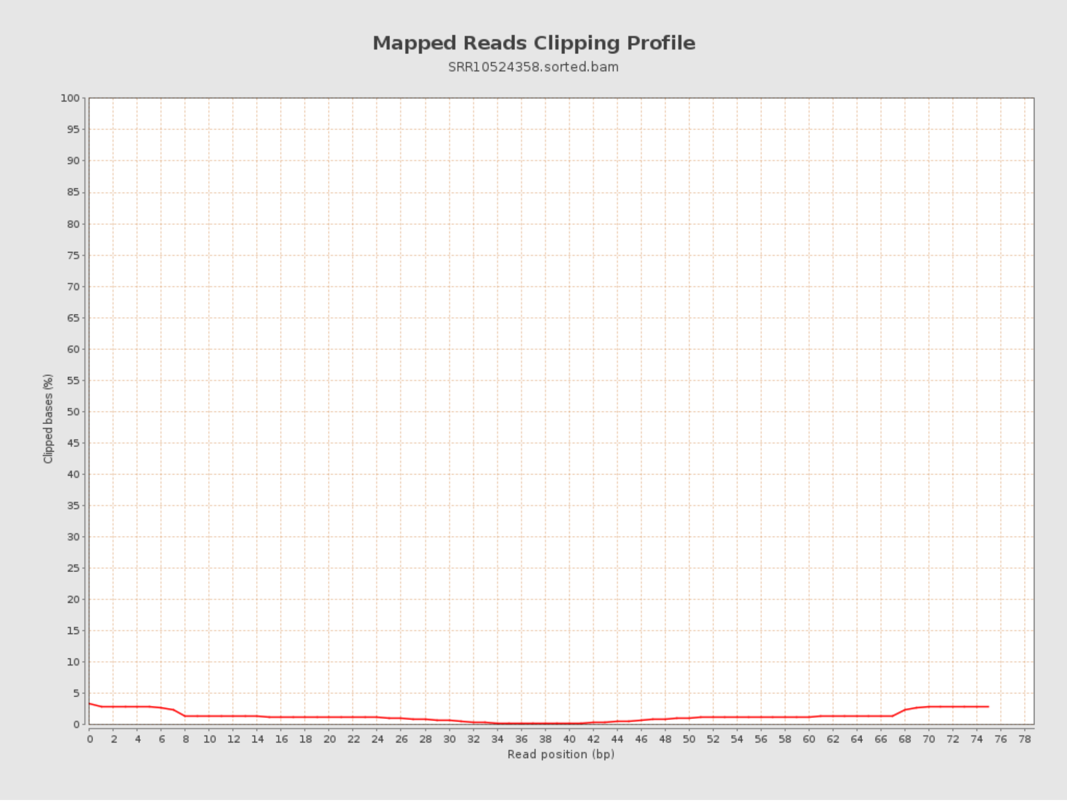
# 8. Results : Mapped Reads Nucleotide Content



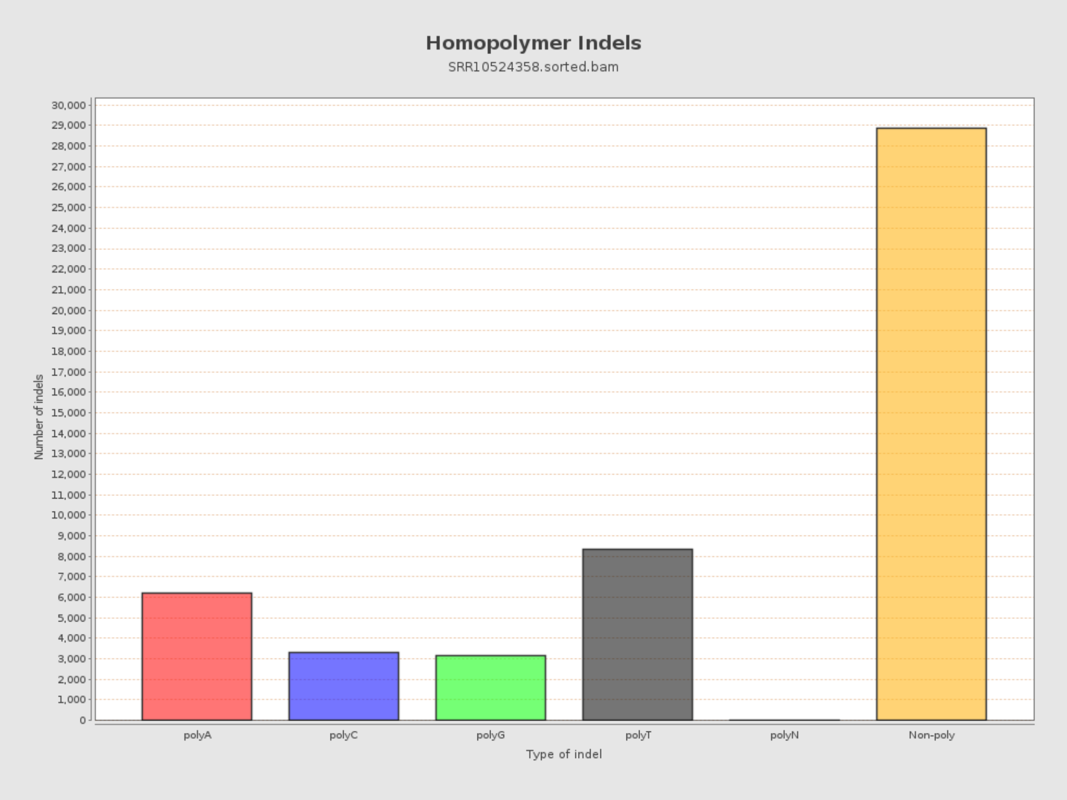
# 9. Results : Mapped Reads GC-content Distribution



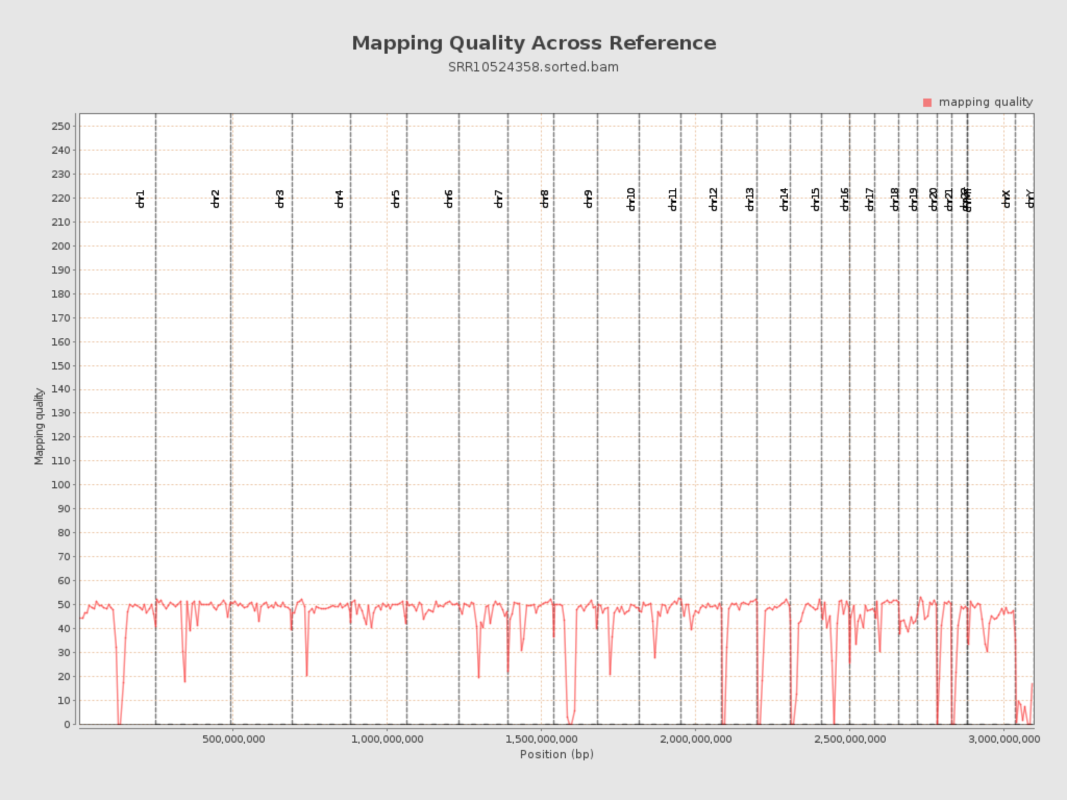
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram