# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/27 23:17:32*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524334.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_SRR10524334 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524334.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Aug 27 23:17:31 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524334.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,309,231 |
| Mapped reads | 3,044,021 / 91.99% |
| Unmapped reads | 265,210 / 8.01% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 14,633 / 0.44% |
| Read min/max/mean length | 30 / 76 / 76.15 |
| Duplicated reads (estimated) | 156,149 / 4.72% |
| Duplication rate | 3.71% |
| Clipped reads | 3,050,648 / 92.19% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 43,282,363 / 24.34% |
| Number/percentage of C's | 34,011,498 / 19.13% |
| Number/percentage of T's | 56,479,401 / 31.76% |
| Number/percentage of G's | 44,036,674 / 24.76% |
| Number/percentage of N's | 26,114 / 0.01% |
| GC Percentage | 43.89% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0575 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4726 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.22 |

## 2.5. Mismatches and indels

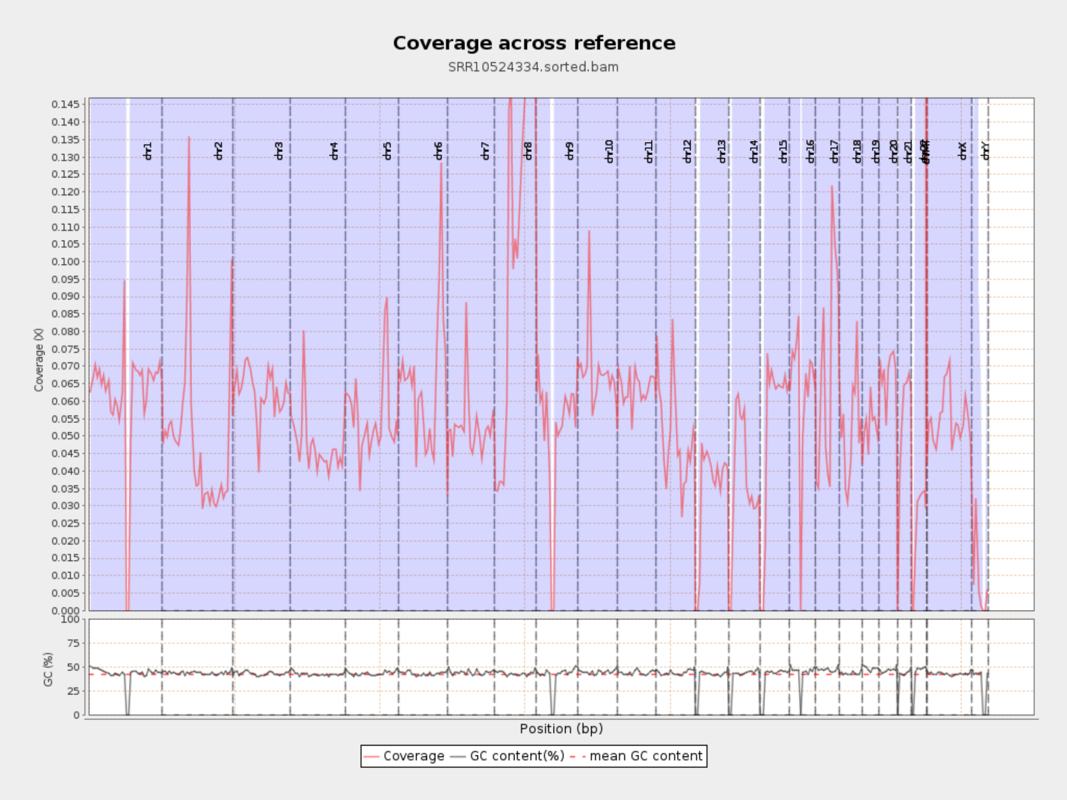
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 895,629 |
| Insertions | 11,562 |
| Mapped reads with at least one insertion | 0.38% |
| Deletions | 29,367 |
| Mapped reads with at least one deletion | 0.96% |
| Homopolymer indels | 41.09% |

## 2.6. Chromosome stats

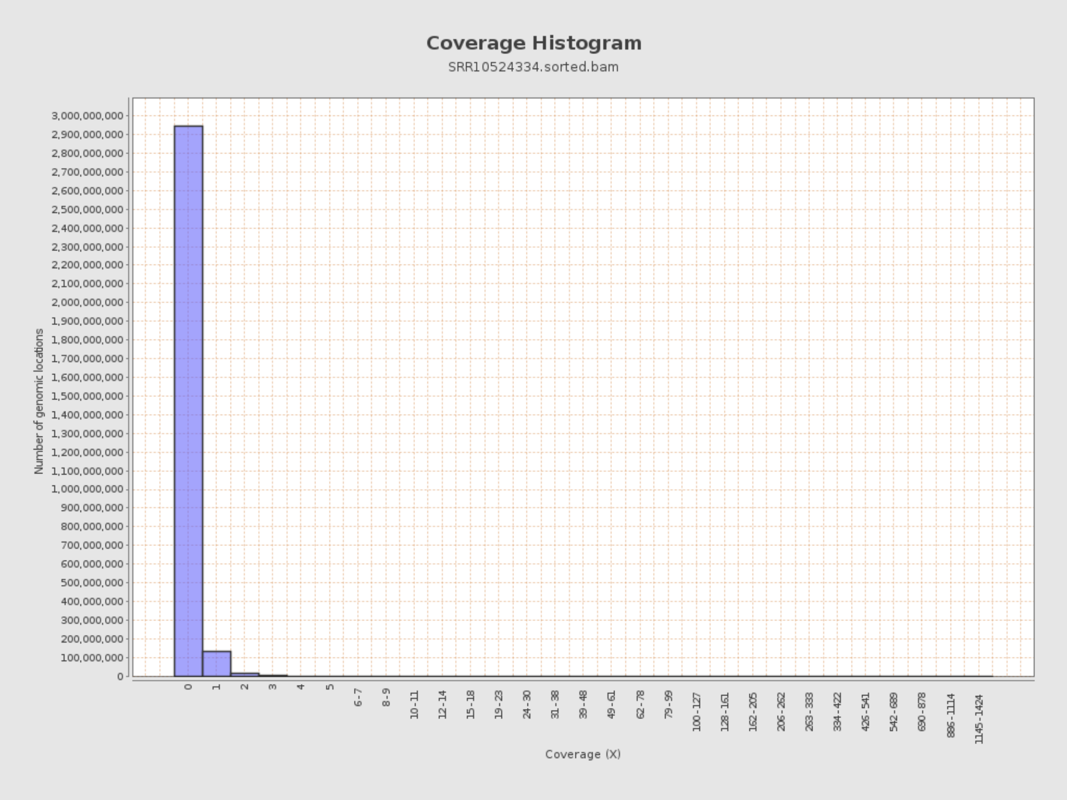
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 15286996 | 0.0613 | 0.9052 |
| chr2 | 243199373 | 11870013 | 0.0488 | 0.6476 |
| chr3 | 198022430 | 12403270 | 0.0626 | 0.2913 |
| chr4 | 191154276 | 9014975 | 0.0472 | 0.2991 |
| chr5 | 180915260 | 10123421 | 0.056 | 0.2736 |
| chr6 | 171115067 | 11203876 | 0.0655 | 0.332 |
| chr7 | 159138663 | 8431515 | 0.053 | 0.6031 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 18561085 | 0.1268 | 0.5873 |
| chr9 | 141213431 | 7165894 | 0.0507 | 0.3461 |
| chr10 | 135534747 | 9281756 | 0.0685 | 0.4642 |
| chr11 | 135006516 | 8590576 | 0.0636 | 0.4013 |
| chr12 | 133851895 | 6727285 | 0.0503 | 0.2643 |
| chr13 | 115169878 | 3978771 | 0.0345 | 0.2153 |
| chr14 | 107349540 | 3943406 | 0.0367 | 0.2379 |
| chr15 | 102531392 | 5441892 | 0.0531 | 0.2707 |
| chr16 | 90354753 | 5722331 | 0.0633 | 0.317 |
| chr17 | 81195210 | 5597987 | 0.0689 | 0.3466 |
| chr18 | 78077248 | 4157032 | 0.0532 | 0.6968 |
| chr19 | 59128983 | 3136513 | 0.053 | 0.6201 |
| chr20 | 63025520 | 4256183 | 0.0675 | 0.312 |
| chr21 | 48129895 | 2546449 | 0.0529 | 0.3022 |
| chr22 | 51304566 | 1215882 | 0.0237 | 0.1802 |
| chrMT | 16571 | 198484 | 11.9778 | 7.172 |
| chrX | 155270560 | 8501262 | 0.0548 | 0.3081 |
| chrY | 59373566 | 526154 | 0.0089 | 0.249 |

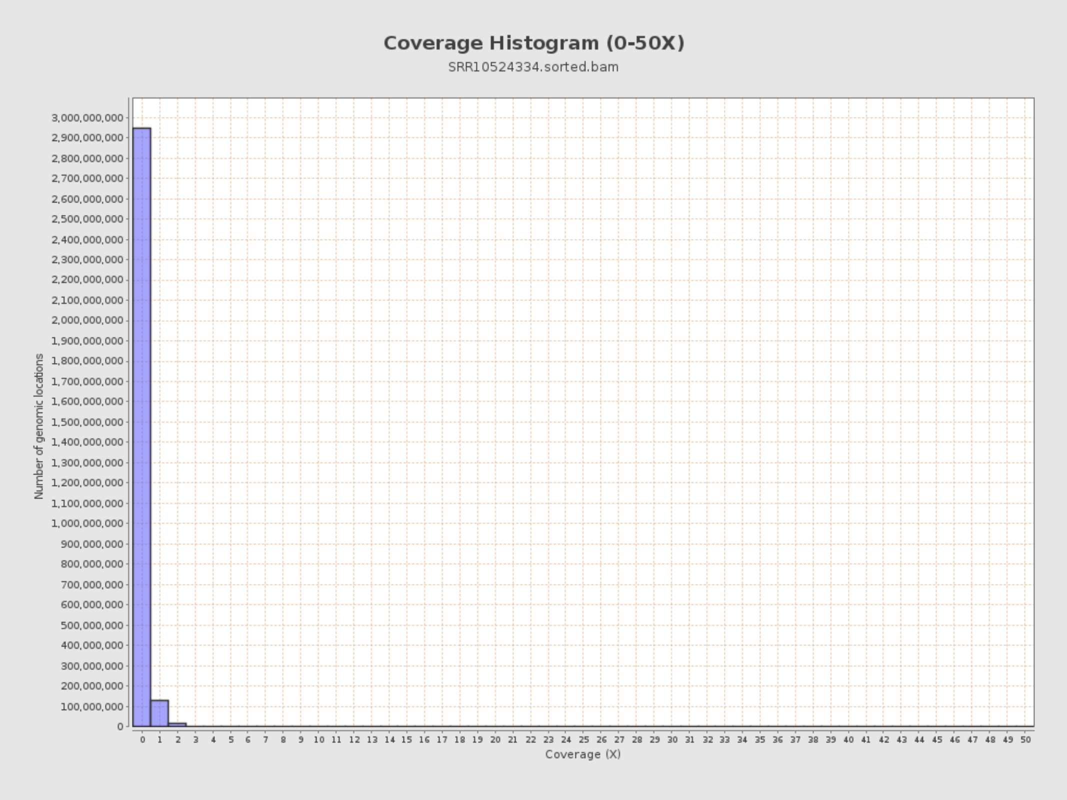
# 3. Results : Coverage across reference



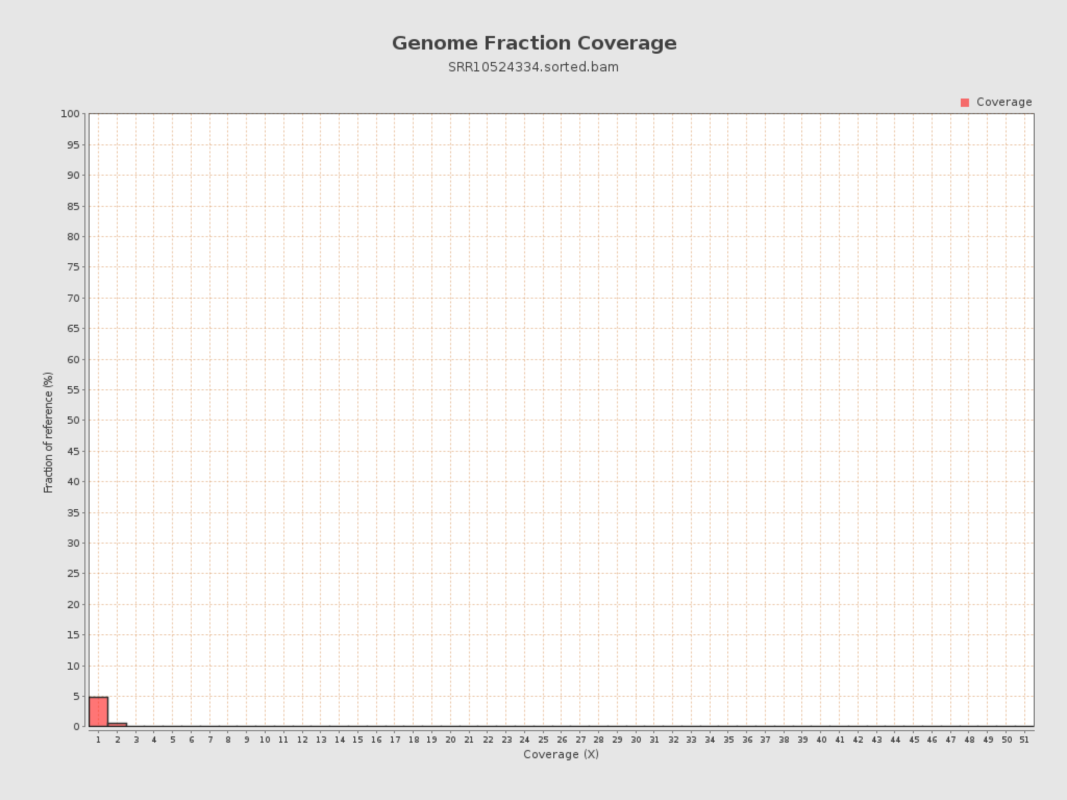
# 4. Results : Coverage Histogram



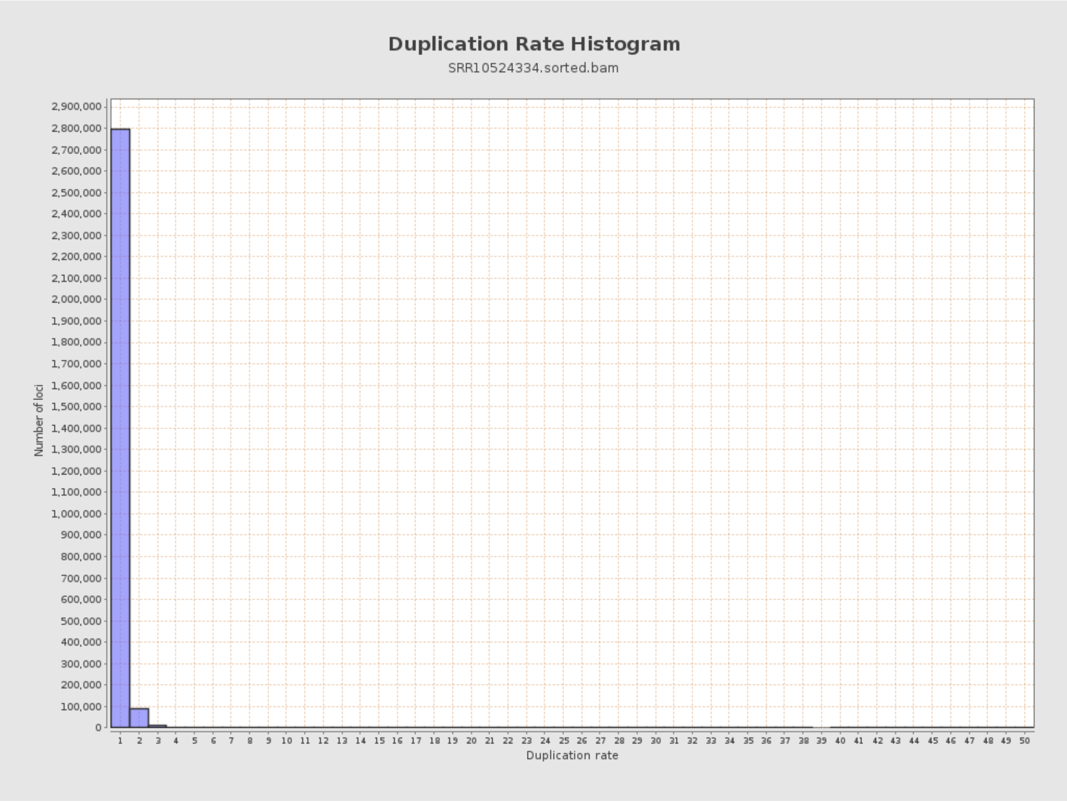
# 5. Results : Coverage Histogram (0-50X)



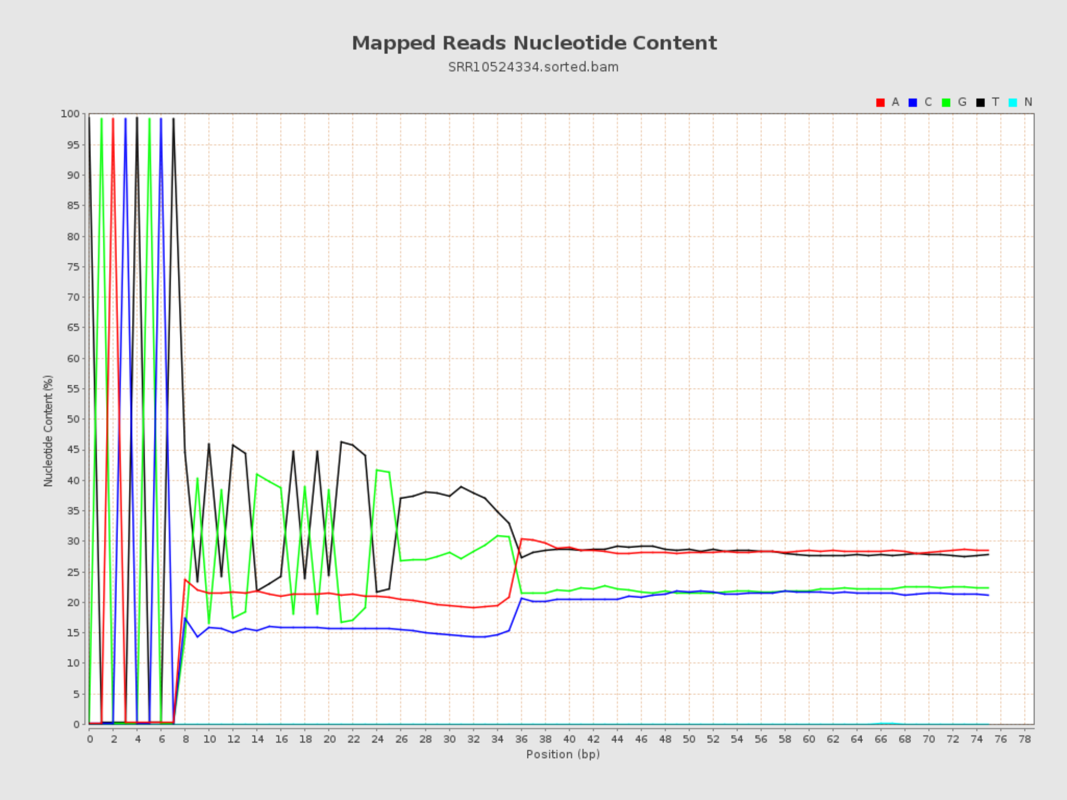
# 6. Results : Genome Fraction Coverage



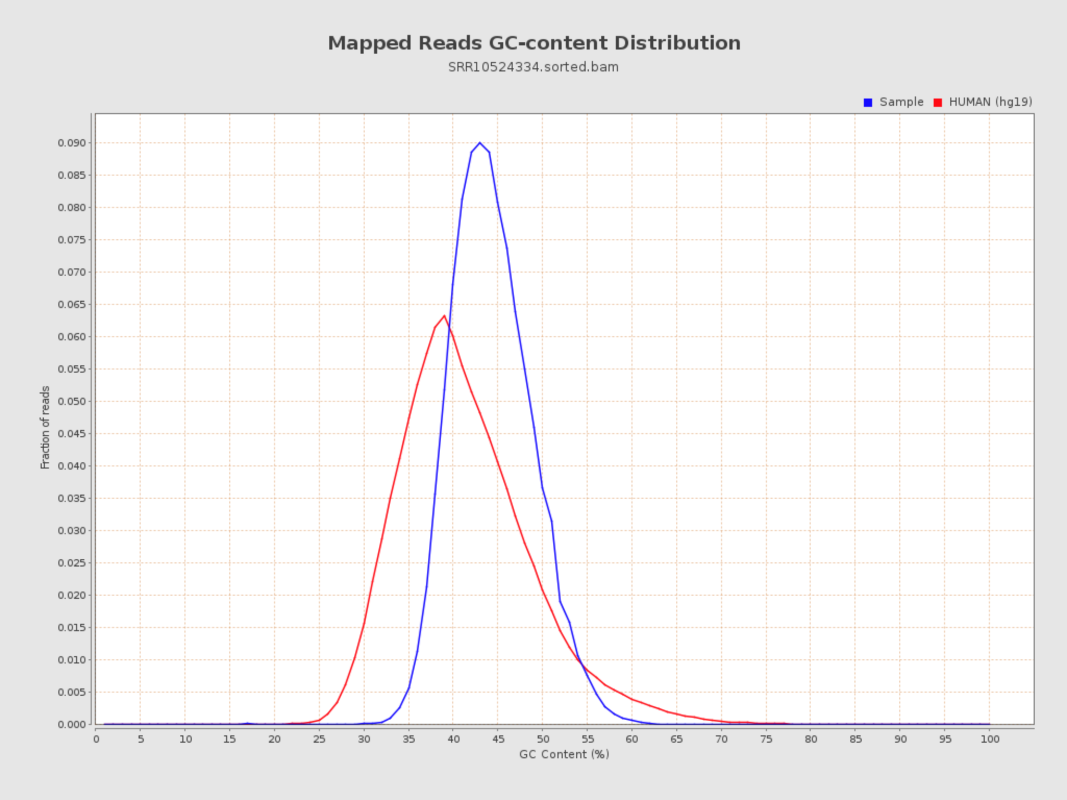
# 7. Results : Duplication Rate Histogram



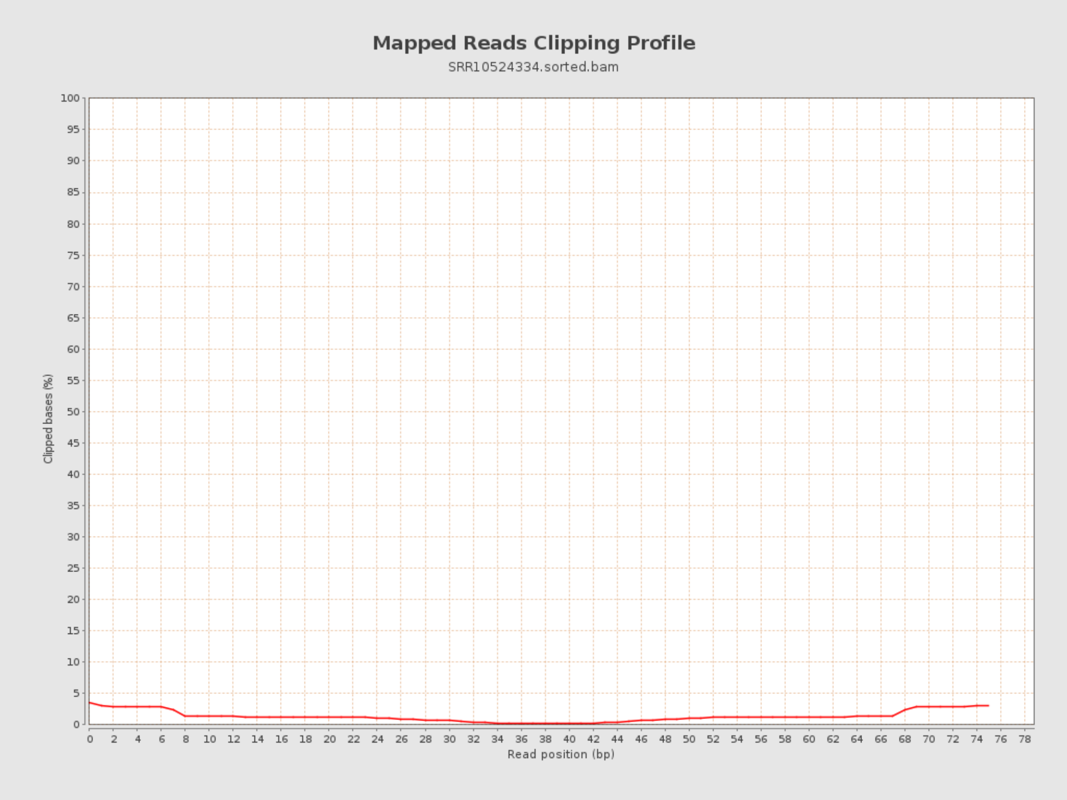
# 8. Results : Mapped Reads Nucleotide Content



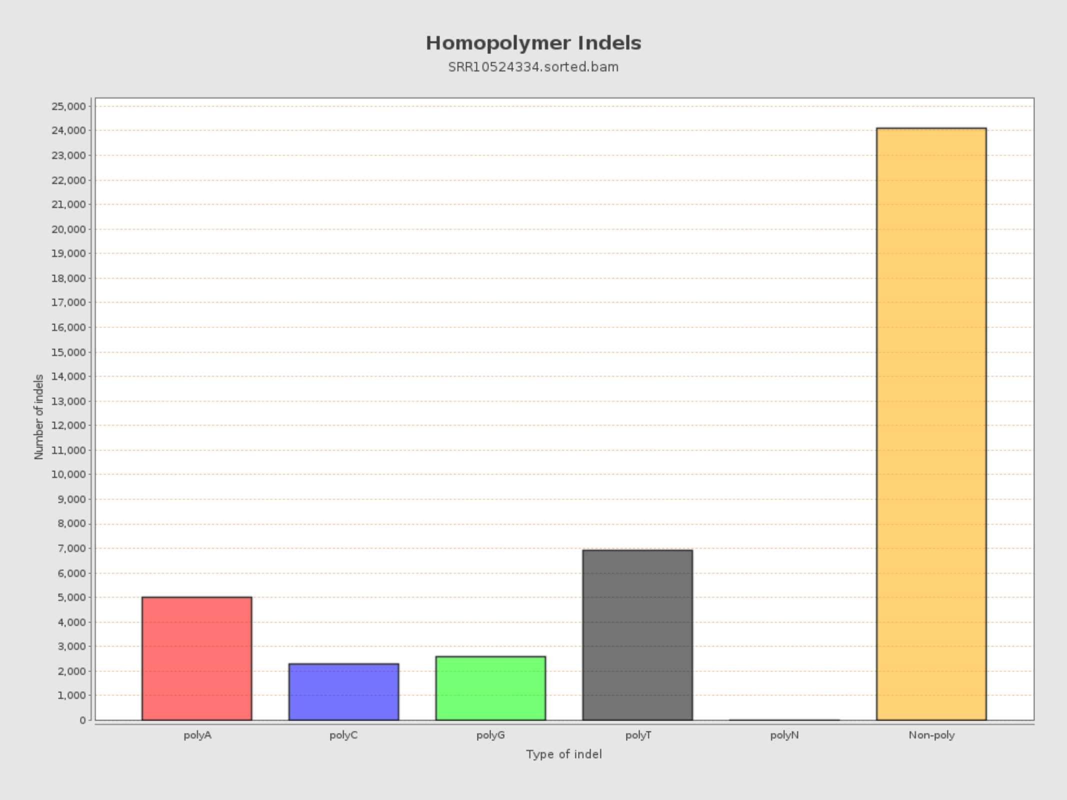
# 9. Results : Mapped Reads GC-content Distribution



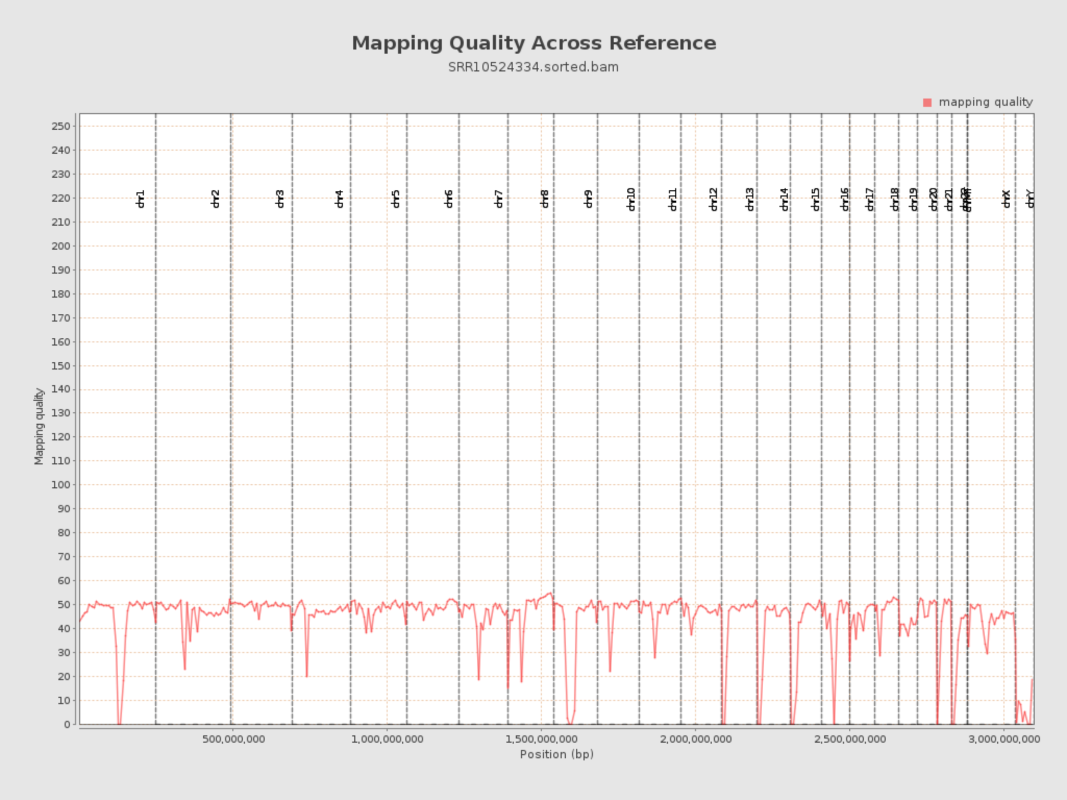
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram