# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/18 03:12:09*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240031.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_SRR6240031 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240031.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Sep 18 03:12:09 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6240031.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,246,241 |
| Mapped reads | 968,537 / 77.72% |
| Unmapped reads | 277,704 / 22.28% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,773 / 0.3% |
| Read min/max/mean length | 30 / 76 / 76.1 |
| Duplicated reads (estimated) | 44,041 / 3.53% |
| Duplication rate | 3.6% |
| Clipped reads | 648,711 / 52.05% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 16,343,853 / 27.47% |
| Number/percentage of C's | 9,953,280 / 16.73% |
| Number/percentage of T's | 18,969,062 / 31.88% |
| Number/percentage of G's | 14,202,924 / 23.87% |
| Number/percentage of N's | 37,333 / 0.06% |
| GC Percentage | 40.59% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0192 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2102 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.17 |

## 2.5. Mismatches and indels

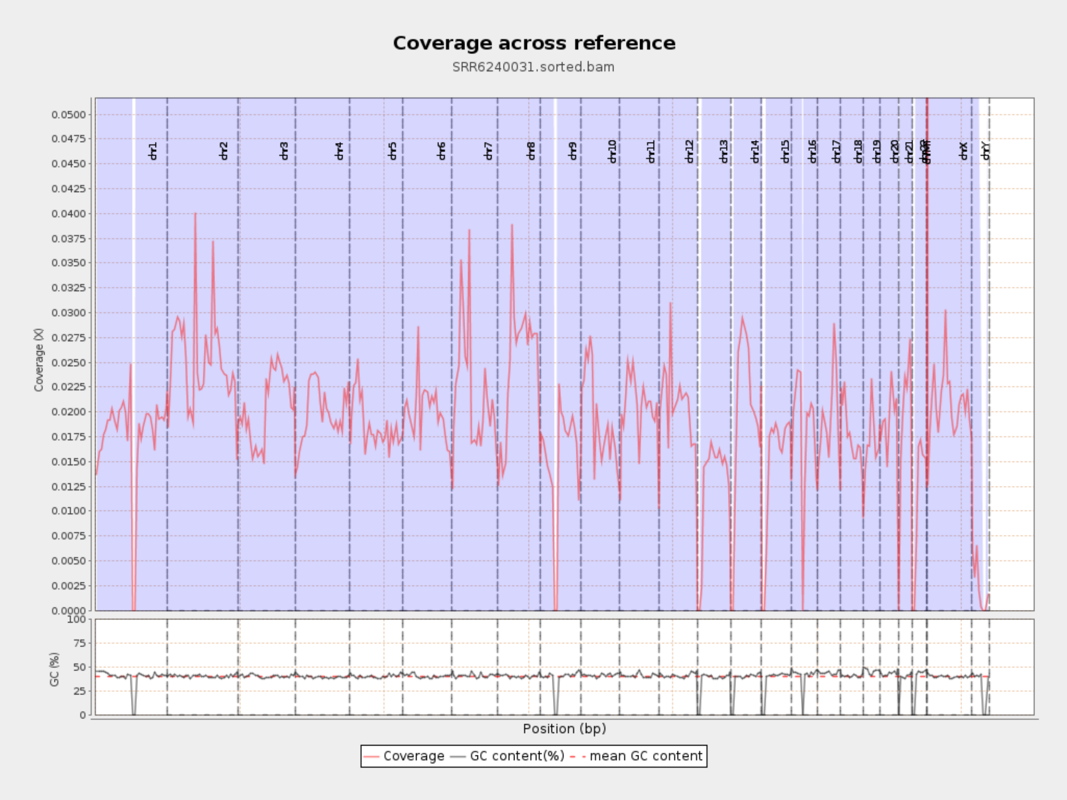
| | |
|---|---|
| General error rate | 1.09% |
| Mismatches | 640,556 |
| Insertions | 4,703 |
| Mapped reads with at least one insertion | 0.48% |
| Deletions | 21,731 |
| Mapped reads with at least one deletion | 2.21% |
| Homopolymer indels | 49.66% |

## 2.6. Chromosome stats

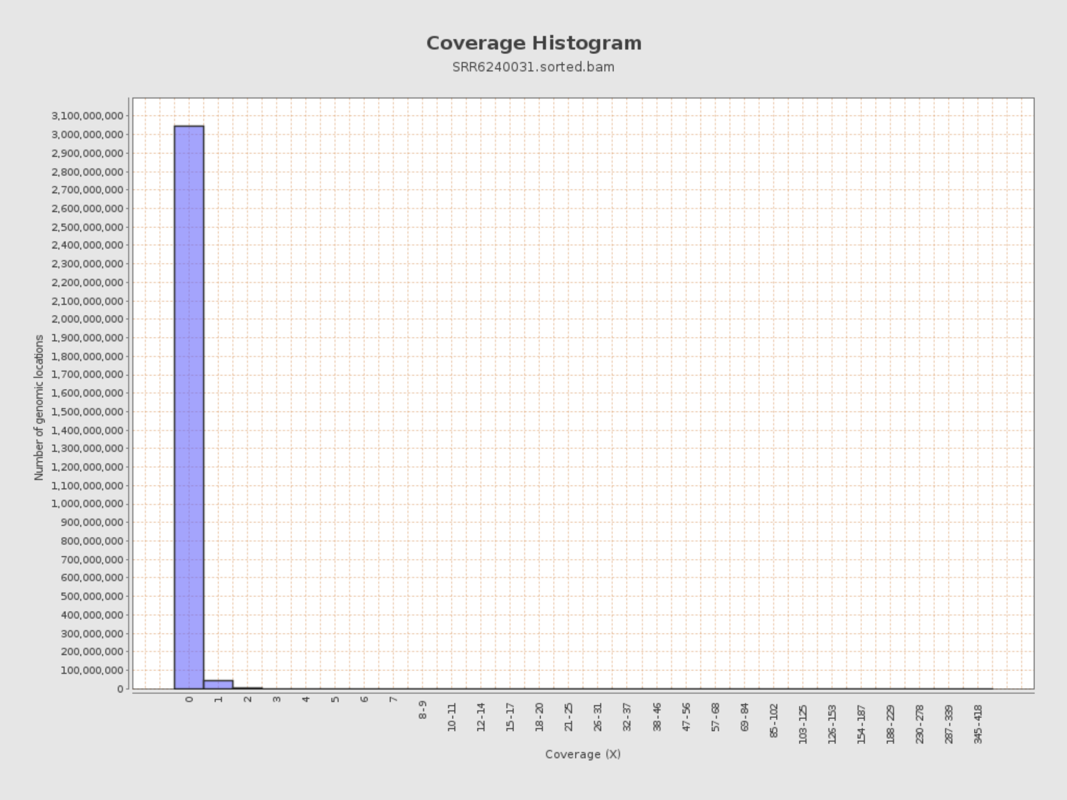
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 4393591 | 0.0176 | 0.2645 |
| chr2 | 243199373 | 6153737 | 0.0253 | 0.2544 |
| chr3 | 198022430 | 4061924 | 0.0205 | 0.1644 |
| chr4 | 191154276 | 3804002 | 0.0199 | 0.1655 |
| chr5 | 180915260 | 3387263 | 0.0187 | 0.1566 |
| chr6 | 171115067 | 3412713 | 0.0199 | 0.182 |
| chr7 | 159138663 | 3511922 | 0.0221 | 0.3842 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3657694 | 0.025 | 0.2566 |
| chr9 | 141213431 | 2154380 | 0.0153 | 0.1986 |
| chr10 | 135534747 | 2624074 | 0.0194 | 0.1776 |
| chr11 | 135006516 | 2800156 | 0.0207 | 0.2173 |
| chr12 | 133851895 | 2795949 | 0.0209 | 0.1653 |
| chr13 | 115169878 | 1448833 | 0.0126 | 0.127 |
| chr14 | 107349540 | 2134746 | 0.0199 | 0.1684 |
| chr15 | 102531392 | 1485179 | 0.0145 | 0.1473 |
| chr16 | 90354753 | 1595501 | 0.0177 | 0.1541 |
| chr17 | 81195210 | 1575867 | 0.0194 | 0.1682 |
| chr18 | 78077248 | 1379471 | 0.0177 | 0.2939 |
| chr19 | 59128983 | 1009342 | 0.0171 | 0.2036 |
| chr20 | 63025520 | 1197214 | 0.019 | 0.1595 |
| chr21 | 48129895 | 939235 | 0.0195 | 0.1633 |
| chr22 | 51304566 | 579249 | 0.0113 | 0.1221 |
| chrMT | 16571 | 38635 | 2.3315 | 2.8296 |
| chrX | 155270560 | 3262074 | 0.021 | 0.1801 |
| chrY | 59373566 | 140947 | 0.0024 | 0.0606 |

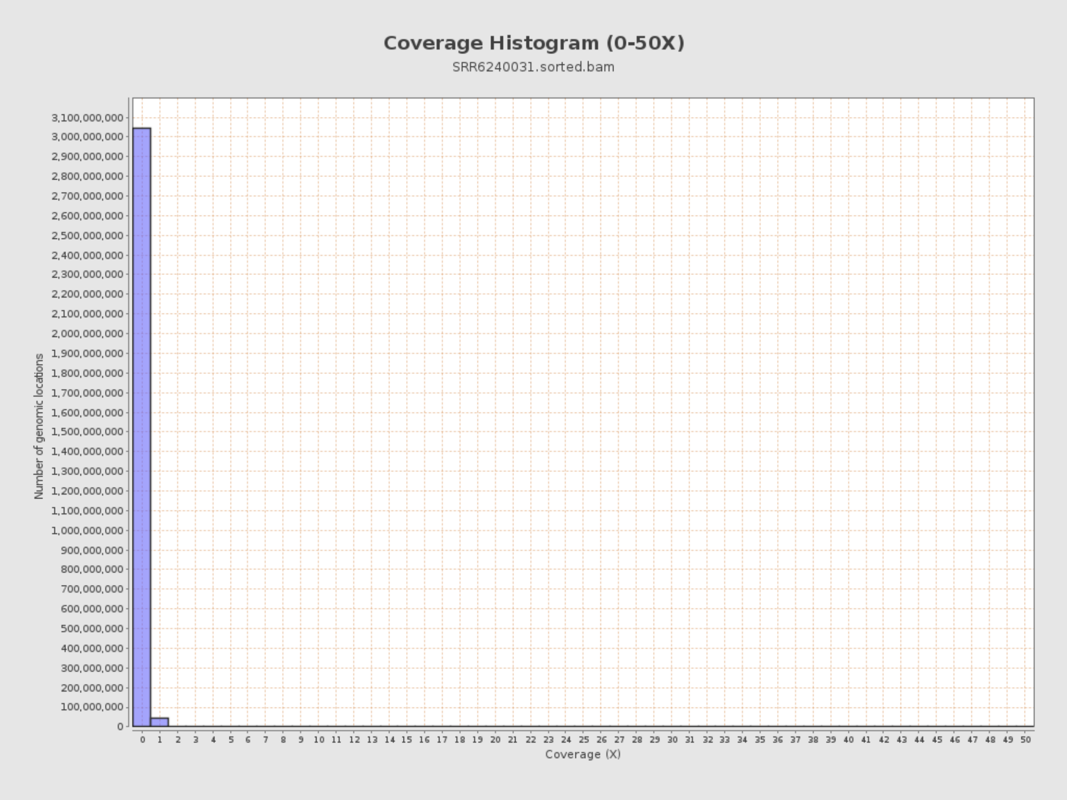
# 3. Results : Coverage across reference



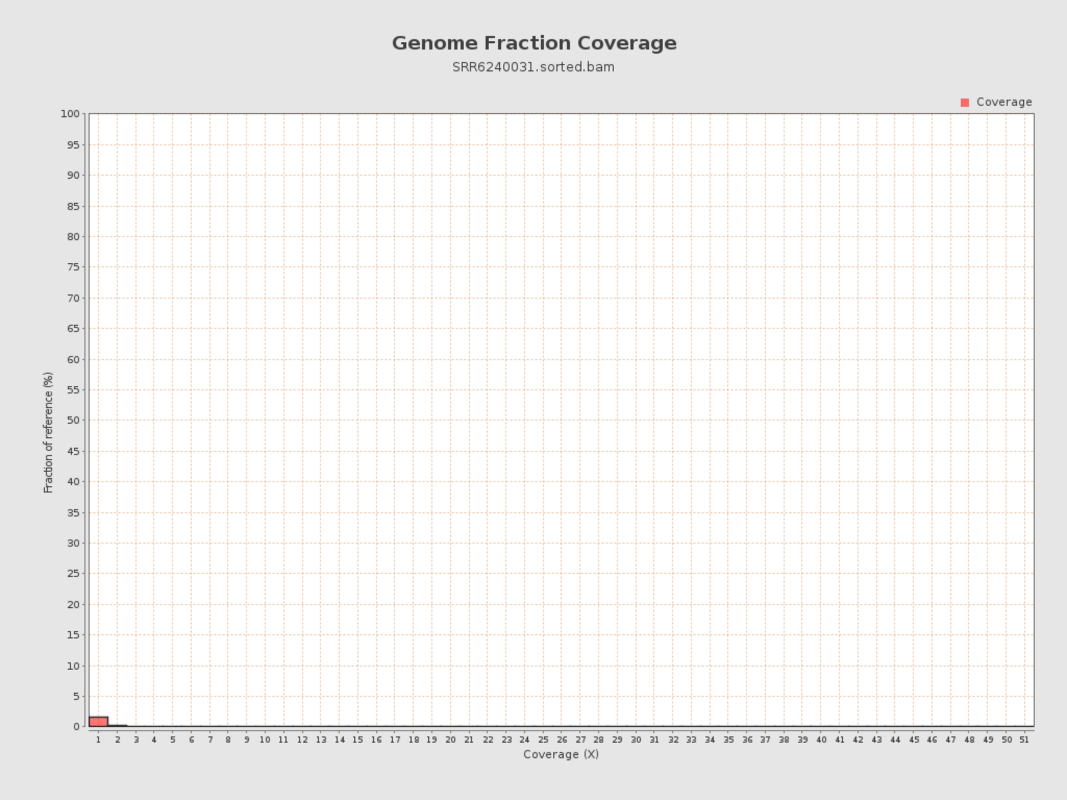
# 4. Results : Coverage Histogram



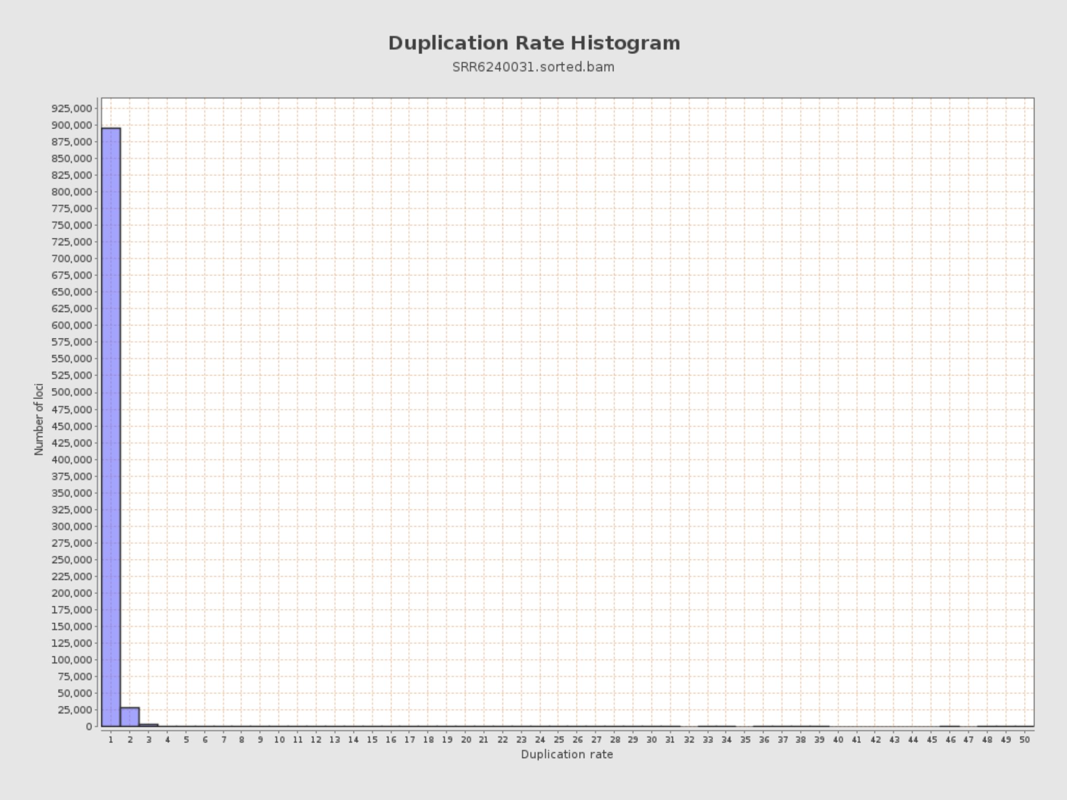
# 5. Results : Coverage Histogram (0-50X)



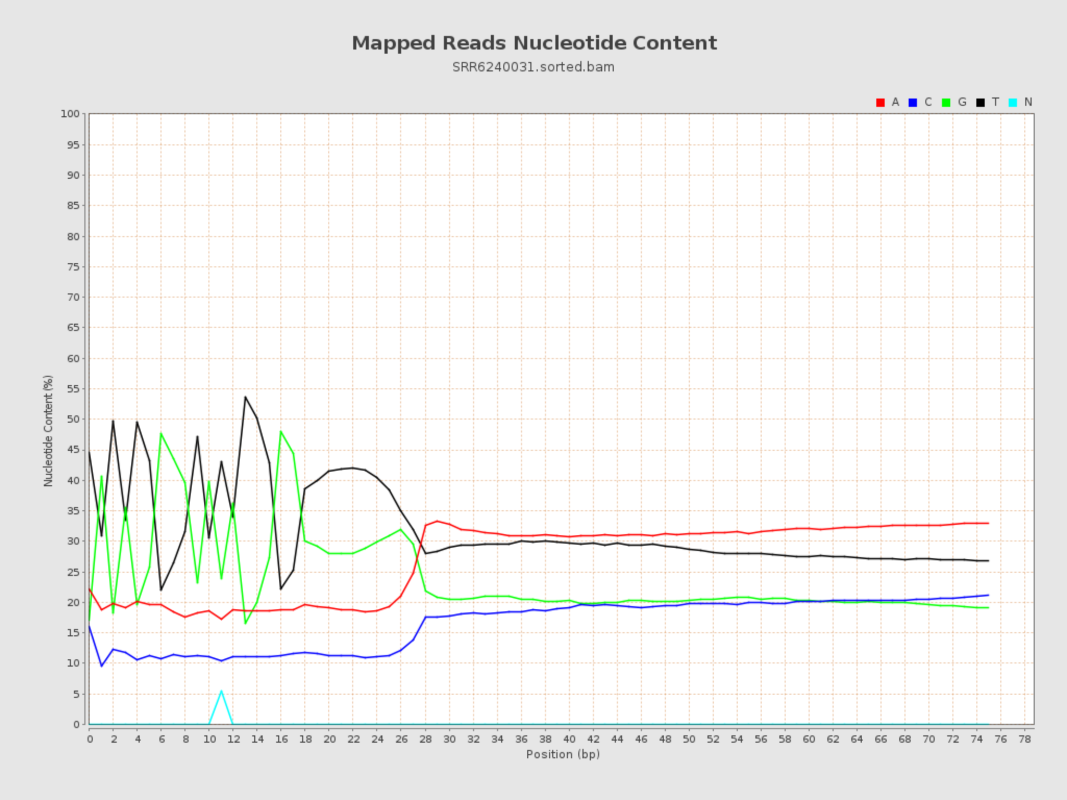
# 6. Results : Genome Fraction Coverage



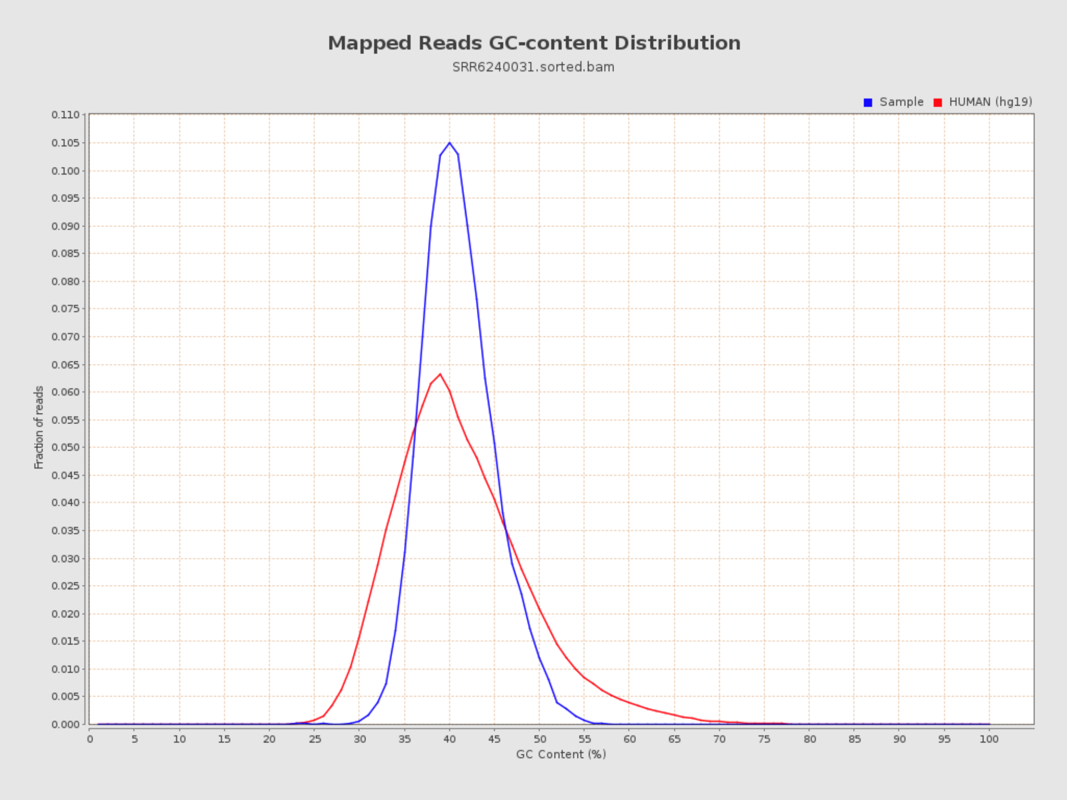
# 7. Results : Duplication Rate Histogram



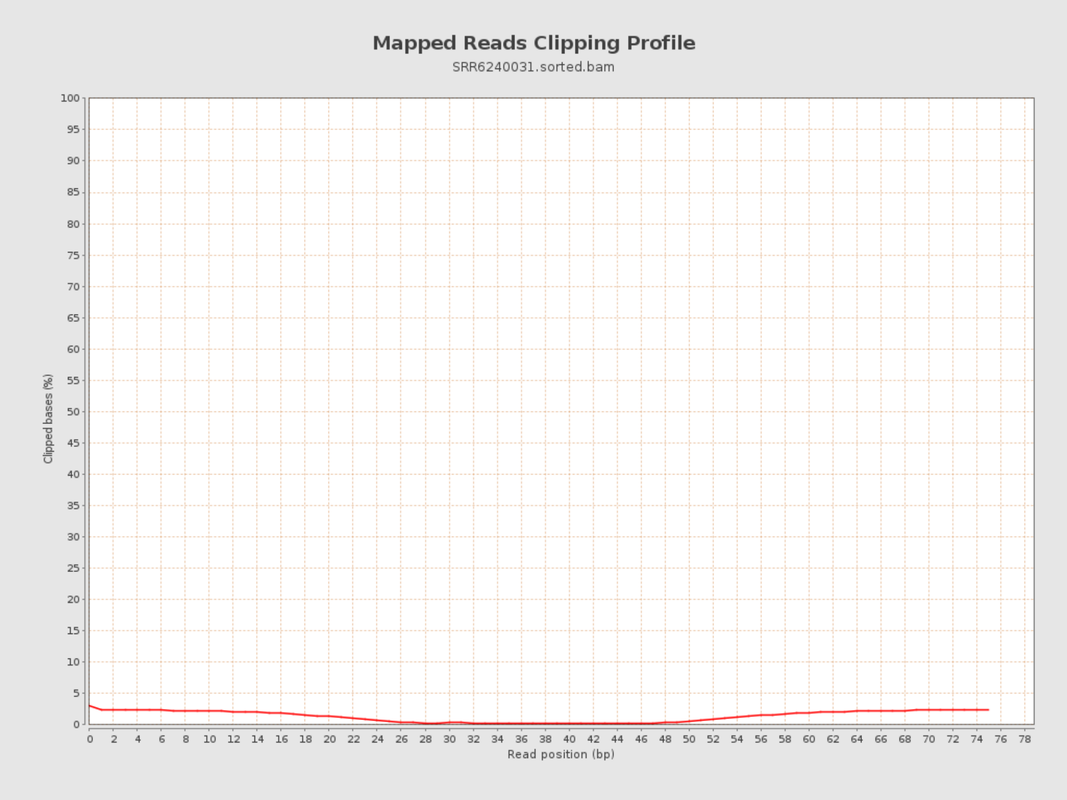
# 8. Results : Mapped Reads Nucleotide Content



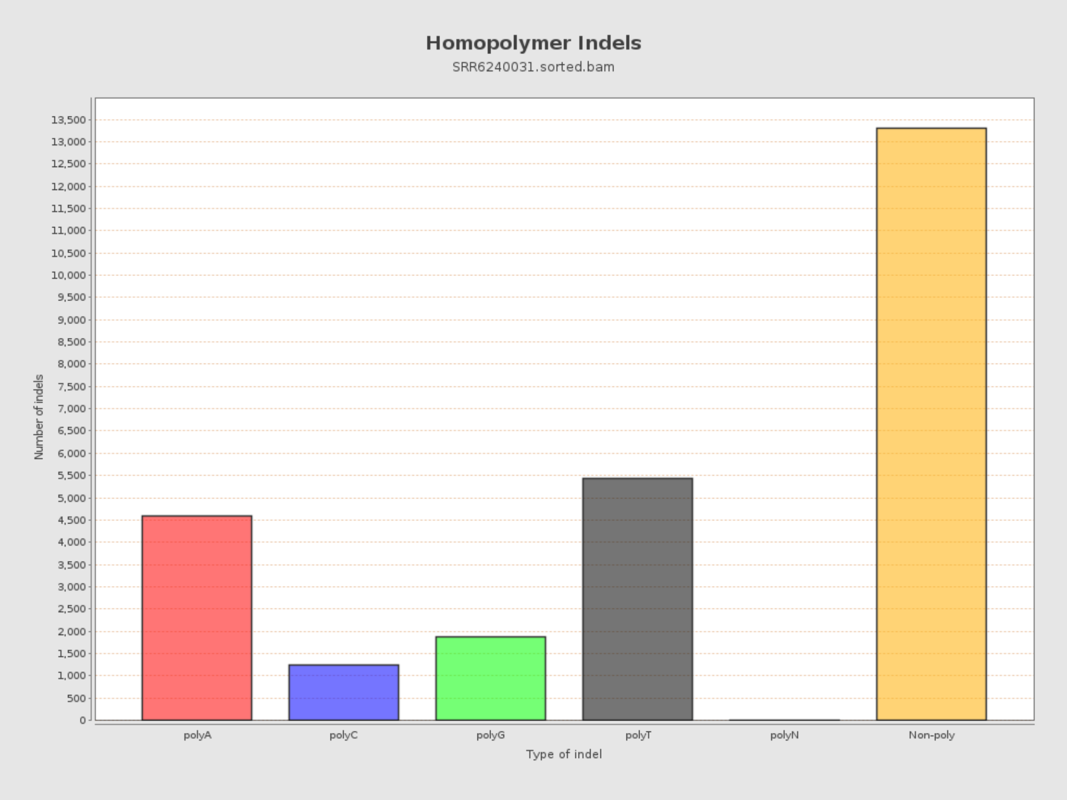
# 9. Results : Mapped Reads GC-content Distribution



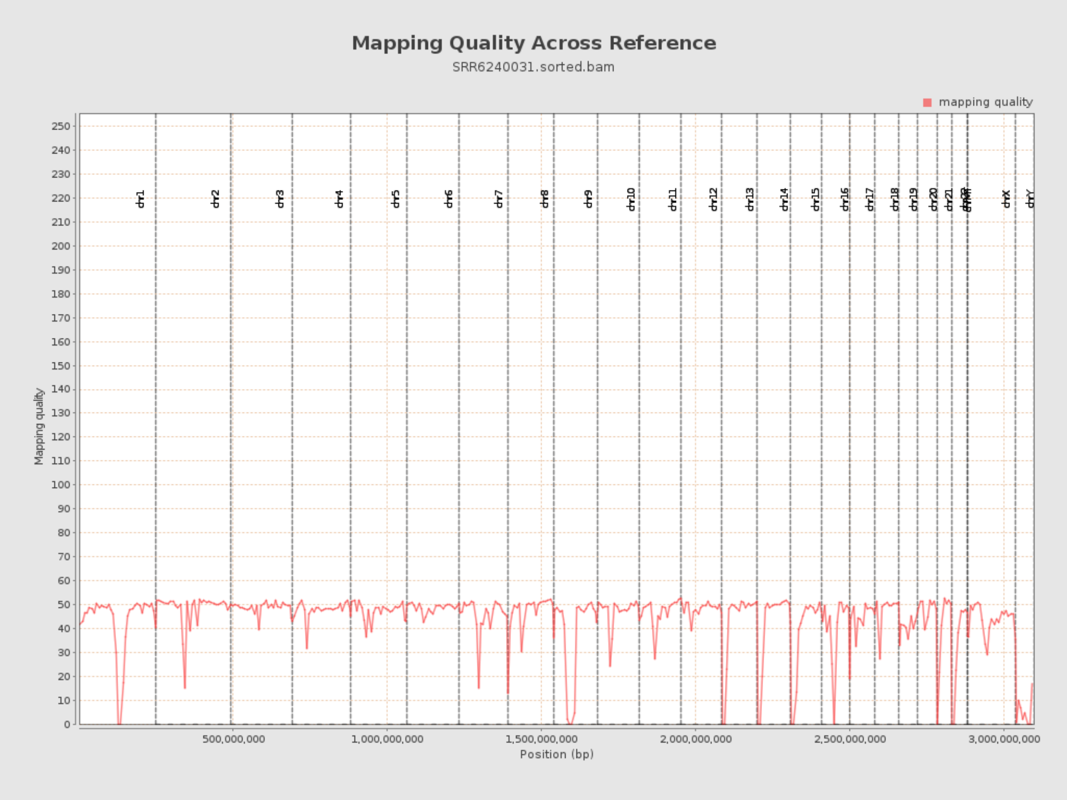
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram