# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/17 23:57:38*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238640.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_SRR6238640 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238640.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 17 23:57:37 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6238640.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,229,860 |
| Mapped reads | 1,985,725 / 89.05% |
| Unmapped reads | 244,135 / 10.95% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 18,325 / 0.82% |
| Read min/max/mean length | 30 / 76 / 76.29 |
| Duplicated reads (estimated) | 674,175 / 30.23% |
| Duplication rate | 19.62% |
| Clipped reads | 1,300,826 / 58.34% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 30,762,252 / 25.27% |
| Number/percentage of C's | 21,574,518 / 17.72% |
| Number/percentage of T's | 40,938,533 / 33.63% |
| Number/percentage of G's | 28,438,347 / 23.36% |
| Number/percentage of N's | 6,086 / 0.01% |
| GC Percentage | 41.09% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0393 |
| | |

| | |
|---|---|
| Standard Deviation | 0.7443 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 38.89 |

## 2.5. Mismatches and indels

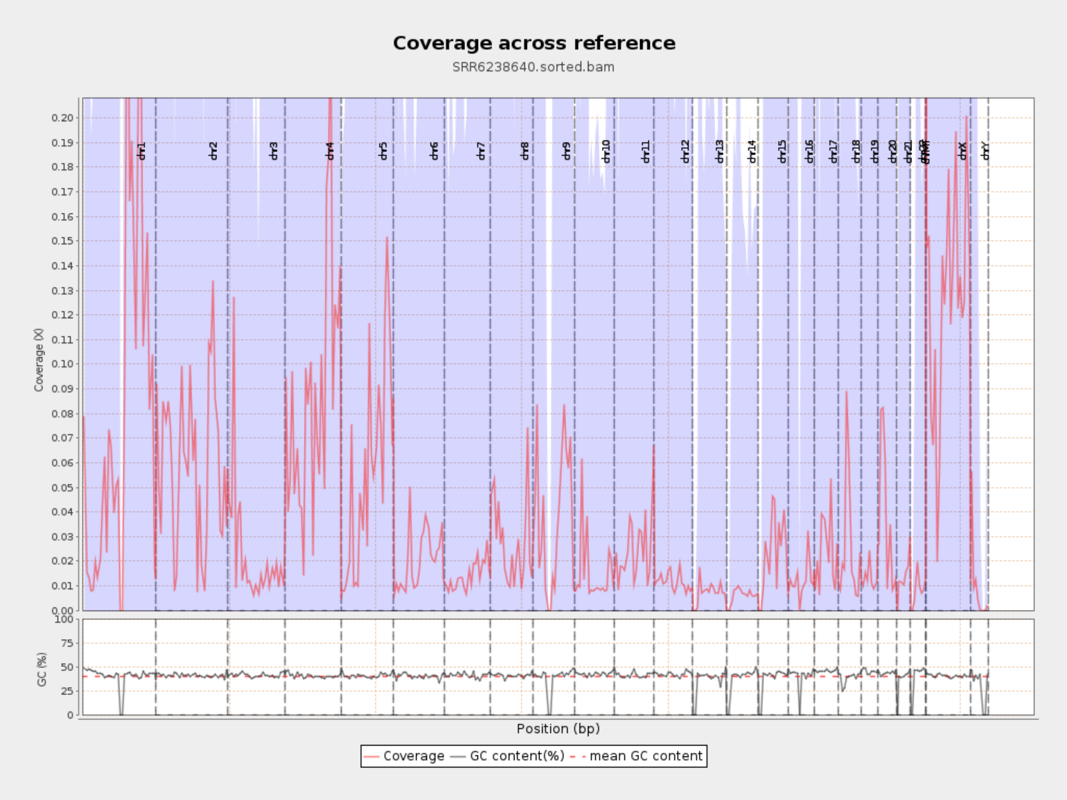
| | |
|---|---|
| General error rate | 0.58% |
| Mismatches | 697,283 |
| Insertions | 7,059 |
| Mapped reads with at least one insertion | 0.35% |
| Deletions | 31,420 |
| Mapped reads with at least one deletion | 1.57% |
| Homopolymer indels | 40.09% |

## 2.6. Chromosome stats

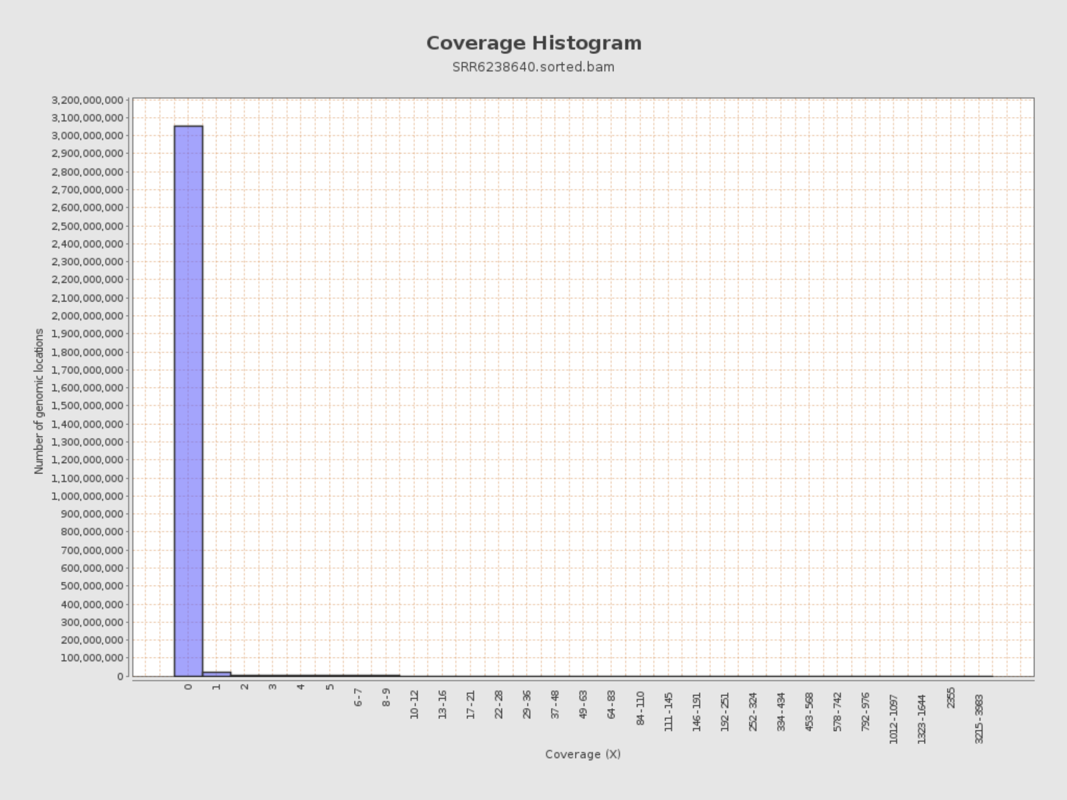
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 20516026 | 0.0823 | 0.7416 |
| chr2 | 243199373 | 14704697 | 0.0605 | 1.817 |
| chr3 | 198022430 | 4429986 | 0.0224 | 0.3696 |
| chr4 | 191154276 | 16999993 | 0.0889 | 0.7405 |
| chr5 | 180915260 | 10171423 | 0.0562 | 0.5827 |
| chr6 | 171115067 | 3569902 | 0.0209 | 0.6439 |
| chr7 | 159138663 | 2278617 | 0.0143 | 0.3201 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4046695 | 0.0276 | 0.4378 |
| chr9 | 141213431 | 5228790 | 0.037 | 0.4706 |
| chr10 | 135534747 | 2070662 | 0.0153 | 0.4163 |
| chr11 | 135006516 | 3262243 | 0.0242 | 0.3577 |
| chr12 | 133851895 | 1550018 | 0.0116 | 0.2515 |
| chr13 | 115169878 | 865173 | 0.0075 | 0.4394 |
| chr14 | 107349540 | 662251 | 0.0062 | 0.1891 |
| chr15 | 102531392 | 2391376 | 0.0233 | 0.5146 |
| chr16 | 90354753 | 1062076 | 0.0118 | 0.2802 |
| chr17 | 81195210 | 1927283 | 0.0237 | 0.3665 |
| chr18 | 78077248 | 2006689 | 0.0257 | 1.4066 |
| chr19 | 59128983 | 816765 | 0.0138 | 0.3002 |
| chr20 | 63025520 | 2426509 | 0.0385 | 0.4896 |
| chr21 | 48129895 | 664486 | 0.0138 | 0.2724 |
| chr22 | 51304566 | 405465 | 0.0079 | 0.1923 |
| chrMT | 16571 | 6666 | 0.4023 | 0.9745 |
| chrX | 155270560 | 19189878 | 0.1236 | 0.9037 |
| chrY | 59373566 | 517734 | 0.0087 | 0.265 |

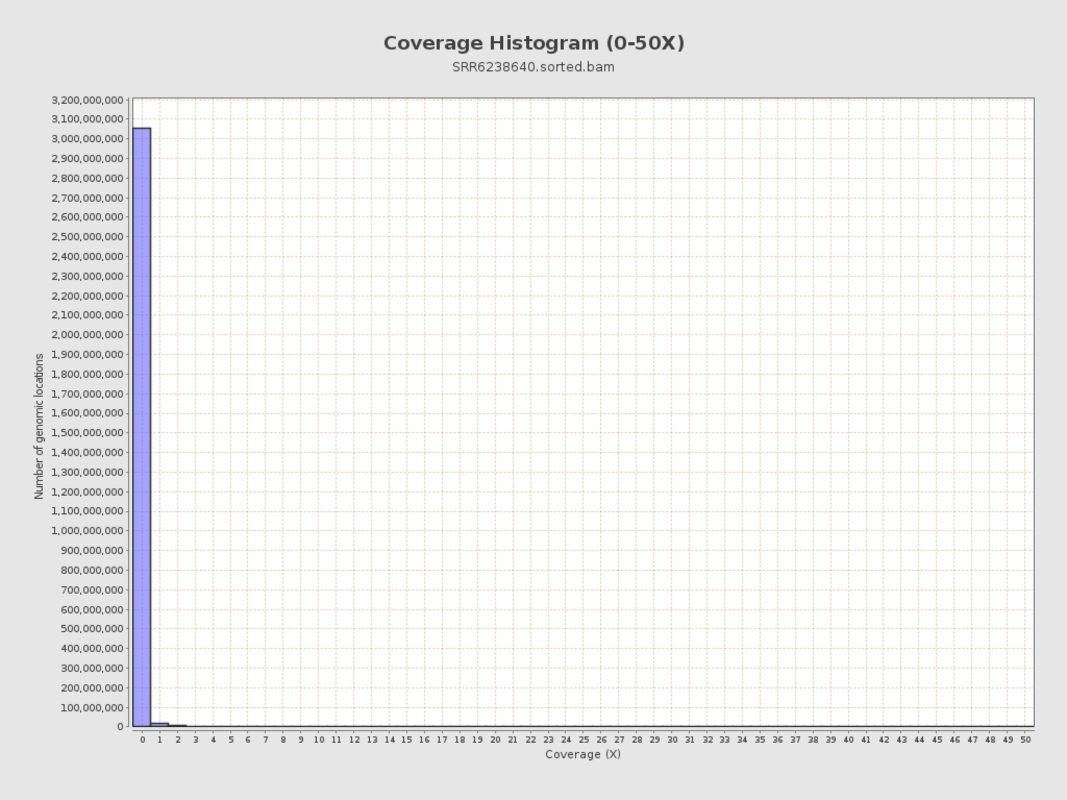
# 3. Results : Coverage across reference



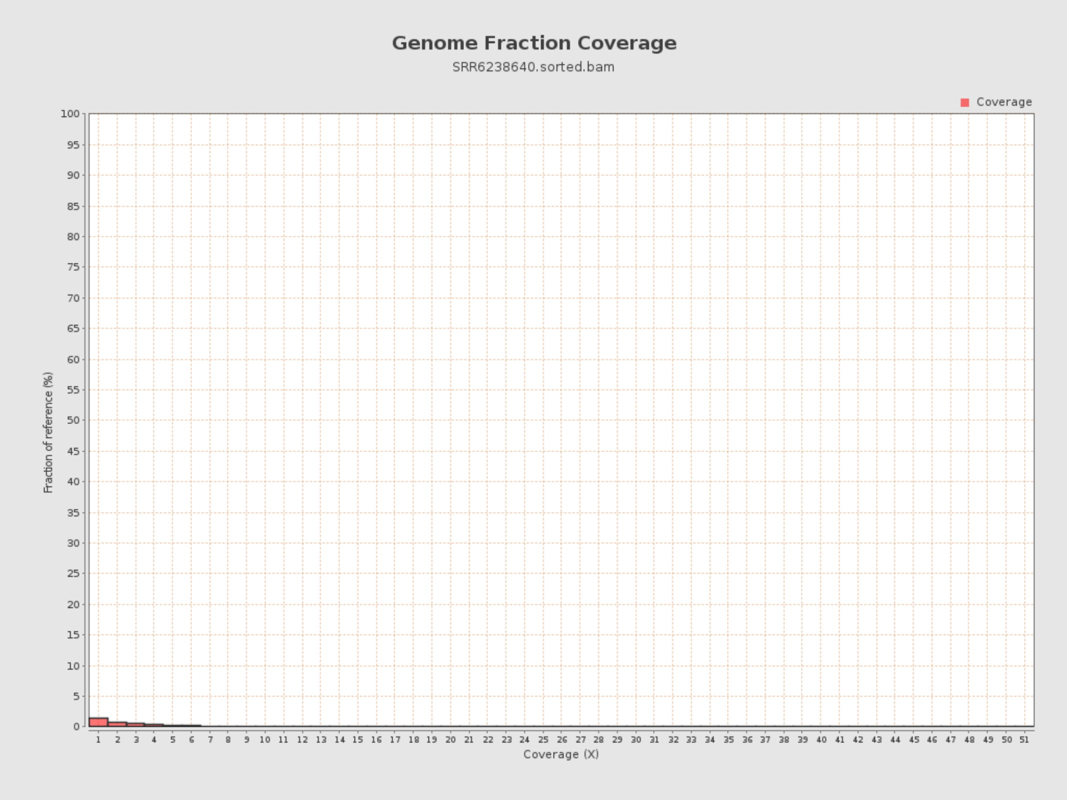
# 4. Results : Coverage Histogram



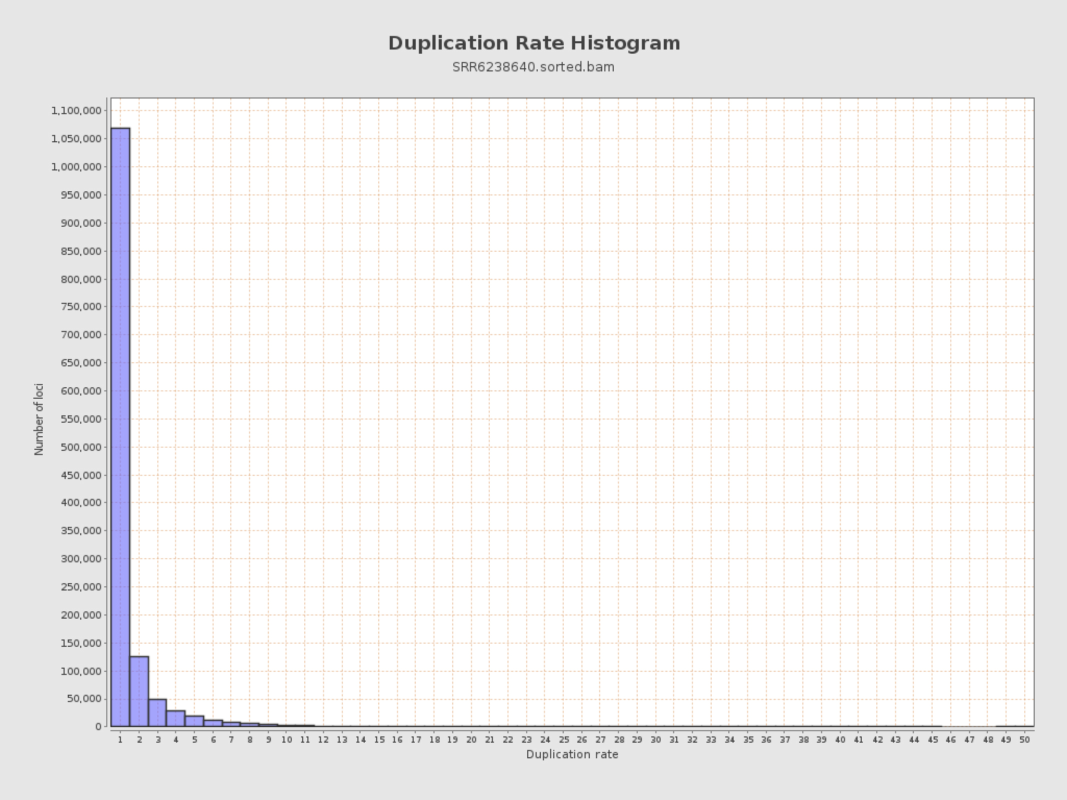
# 5. Results : Coverage Histogram (0-50X)



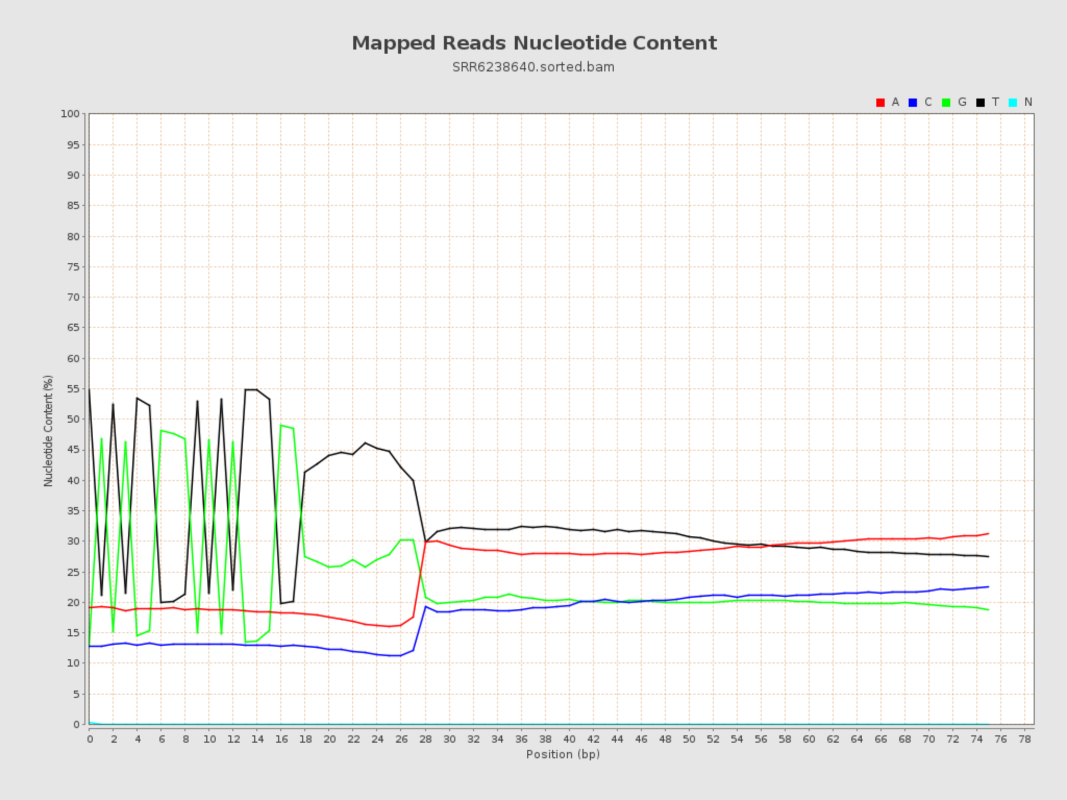
# 6. Results : Genome Fraction Coverage



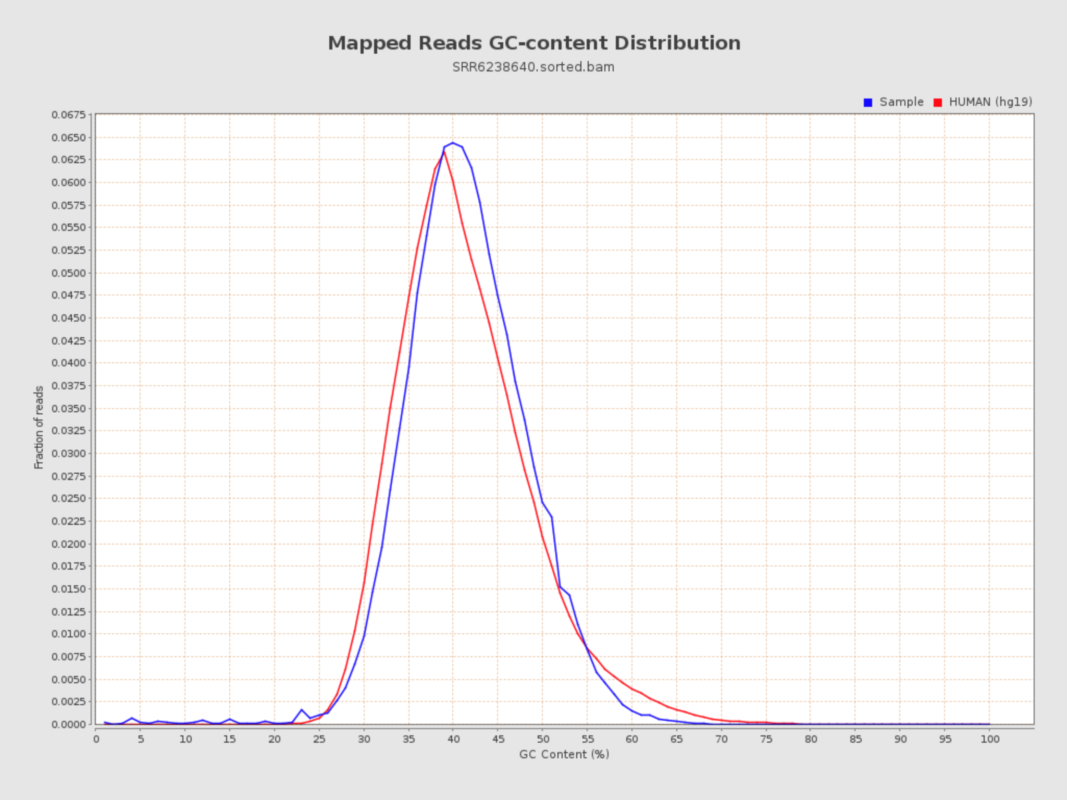
# 7. Results : Duplication Rate Histogram



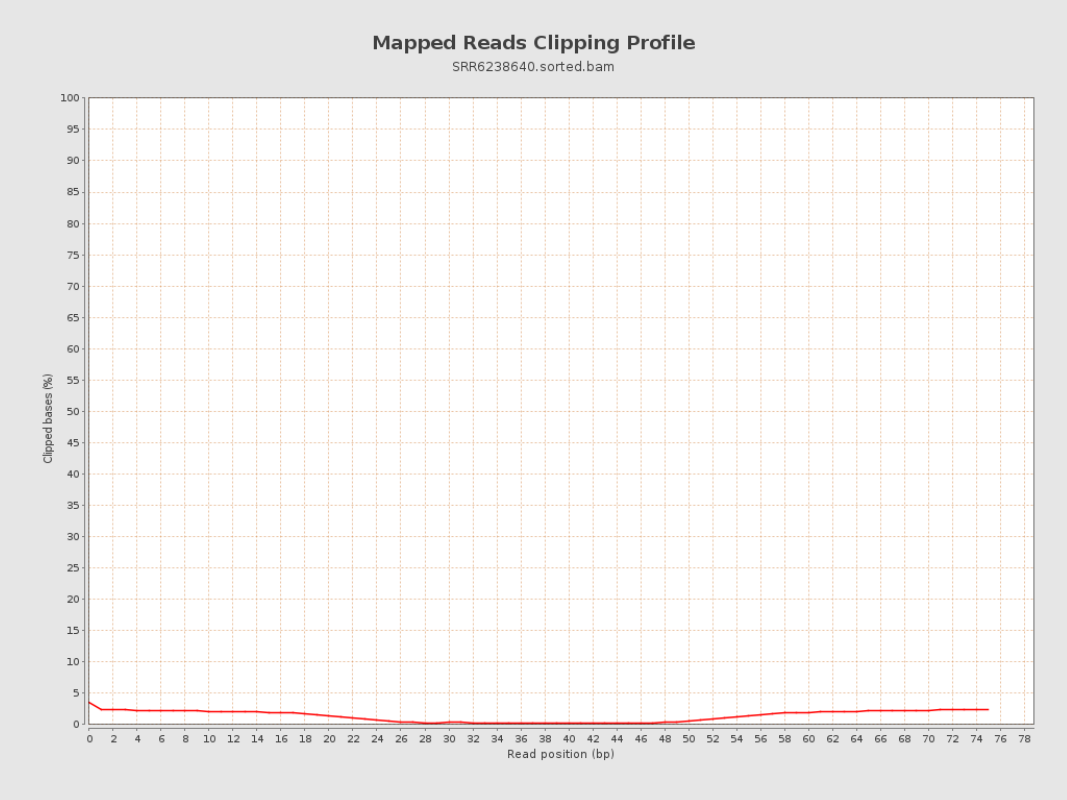
# 8. Results : Mapped Reads Nucleotide Content



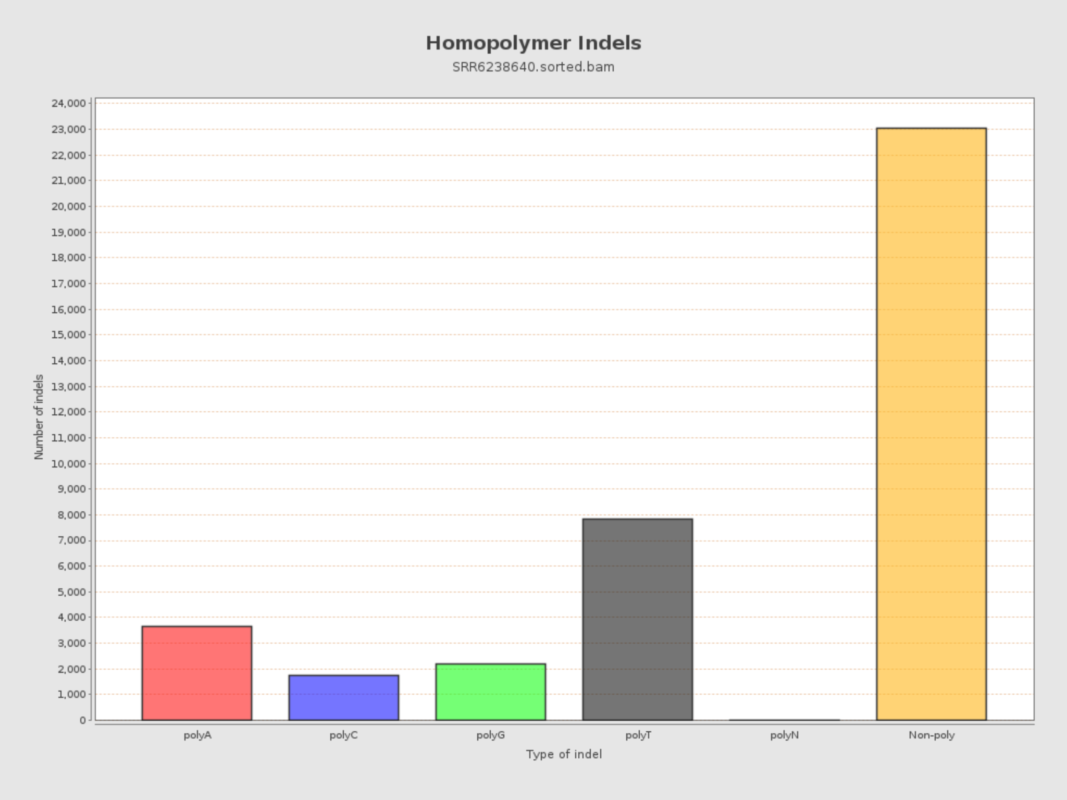
# 9. Results : Mapped Reads GC-content Distribution



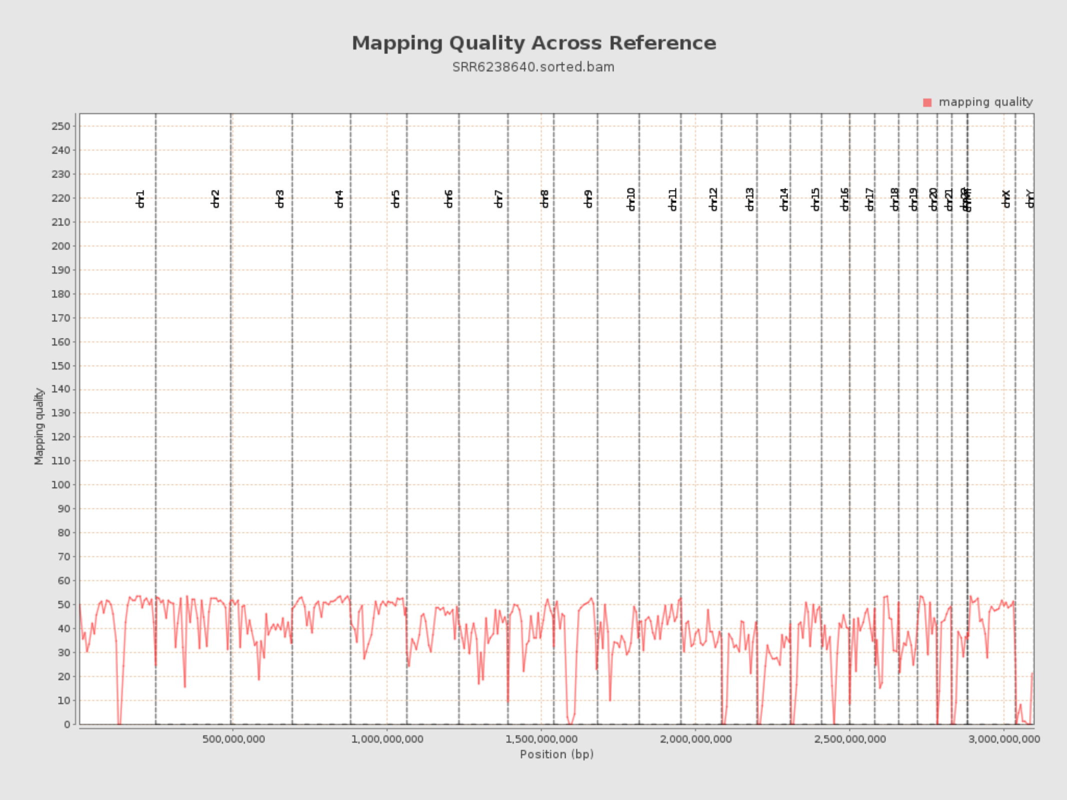
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram