# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/17 19:02:03*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238511.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_SRR6238511 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238511.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 17 19:02:03 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6238511.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,442,711 |
| Mapped reads | 2,904,835 / 84.38% |
| Unmapped reads | 537,876 / 15.62% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 24,956 / 0.72% |
| Read min/max/mean length | 30 / 76 / 76.25 |
| Duplicated reads (estimated) | 800,594 / 23.25% |
| Duplication rate | 19.77% |
| Clipped reads | 1,827,677 / 53.09% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 44,653,184 / 24.9% |
| Number/percentage of C's | 32,474,571 / 18.11% |
| Number/percentage of T's | 58,544,142 / 32.64% |
| Number/percentage of G's | 43,659,846 / 24.34% |
| Number/percentage of N's | 12,379 / 0.01% |
| GC Percentage | 42.45% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.058 |
| | |

| | |
|---|---|
| Standard Deviation | 0.731 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.8 |

## 2.5. Mismatches and indels

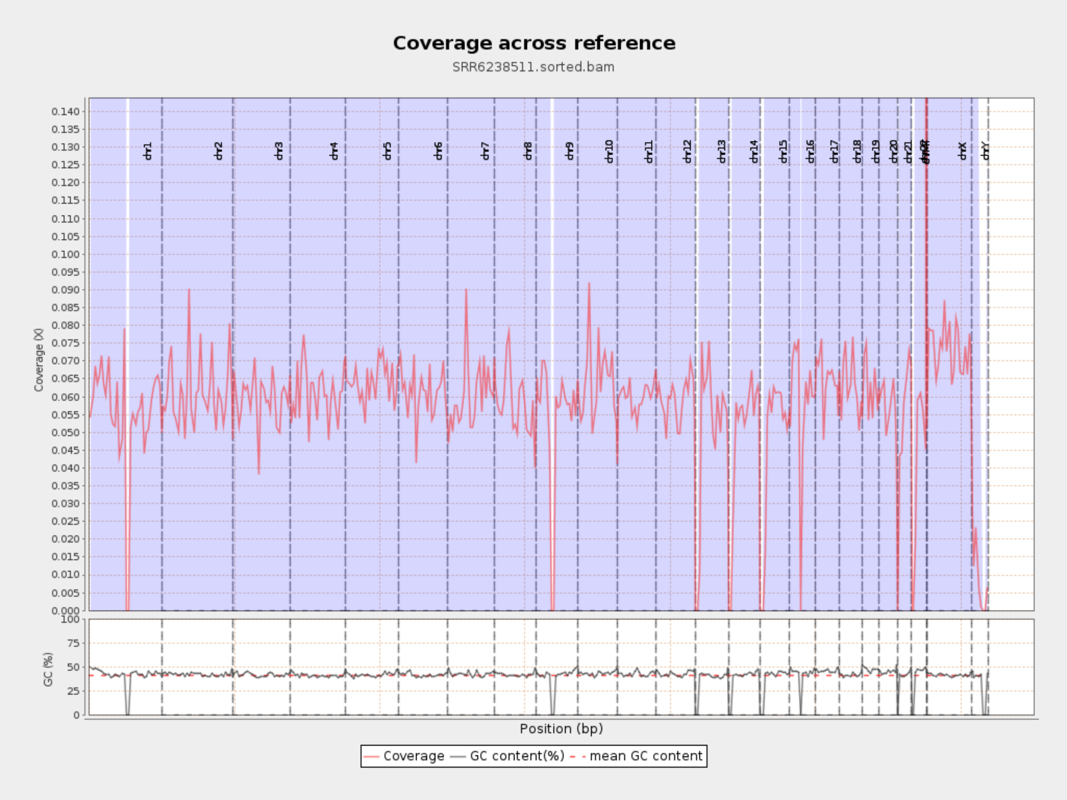
| | |
|---|---|
| General error rate | 0.54% |
| Mismatches | 947,513 |
| Insertions | 11,225 |
| Mapped reads with at least one insertion | 0.38% |
| Deletions | 36,866 |
| Mapped reads with at least one deletion | 1.26% |
| Homopolymer indels | 43.89% |

## 2.6. Chromosome stats

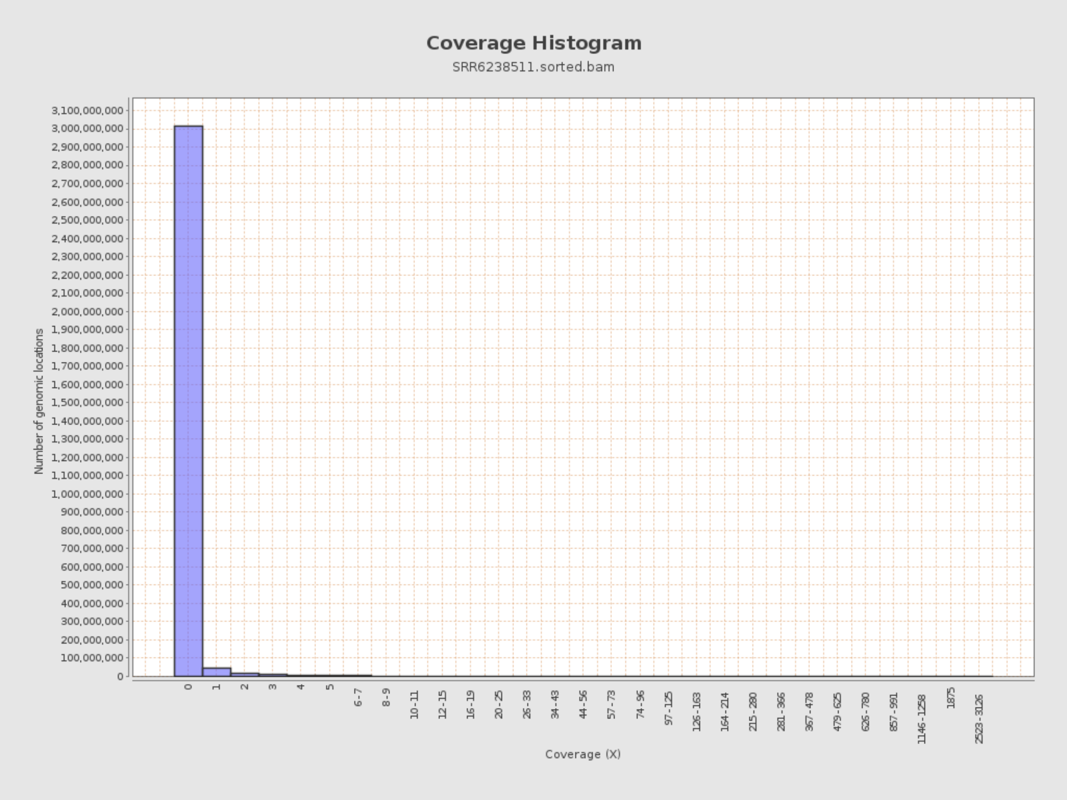
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 13761354 | 0.0552 | 0.8904 |
| chr2 | 243199373 | 14960142 | 0.0615 | 1.5048 |
| chr3 | 198022430 | 11725089 | 0.0592 | 0.4927 |
| chr4 | 191154276 | 11589484 | 0.0606 | 0.4977 |
| chr5 | 180915260 | 11611103 | 0.0642 | 0.5103 |
| chr6 | 171115067 | 10498292 | 0.0614 | 0.6778 |
| chr7 | 159138663 | 9601916 | 0.0603 | 0.7437 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 8457968 | 0.0578 | 0.5955 |
| chr9 | 141213431 | 7516003 | 0.0532 | 0.5524 |
| chr10 | 135534747 | 8718974 | 0.0643 | 0.6068 |
| chr11 | 135006516 | 8067774 | 0.0598 | 0.5688 |
| chr12 | 133851895 | 7938101 | 0.0593 | 0.4917 |
| chr13 | 115169878 | 5734473 | 0.0498 | 0.512 |
| chr14 | 107349540 | 5214495 | 0.0486 | 0.5979 |
| chr15 | 102531392 | 4745622 | 0.0463 | 0.6678 |
| chr16 | 90354753 | 5308574 | 0.0588 | 0.5223 |
| chr17 | 81195210 | 5256330 | 0.0647 | 0.5456 |
| chr18 | 78077248 | 4957433 | 0.0635 | 1.1132 |
| chr19 | 59128983 | 3712297 | 0.0628 | 0.6839 |
| chr20 | 63025520 | 3615220 | 0.0574 | 0.4954 |
| chr21 | 48129895 | 2551240 | 0.053 | 0.4678 |
| chr22 | 51304566 | 1988691 | 0.0388 | 0.3883 |
| chrMT | 16571 | 21336 | 1.2876 | 2.21 |
| chrX | 155270560 | 11335643 | 0.073 | 0.5691 |
| chrY | 59373566 | 519693 | 0.0088 | 0.2519 |

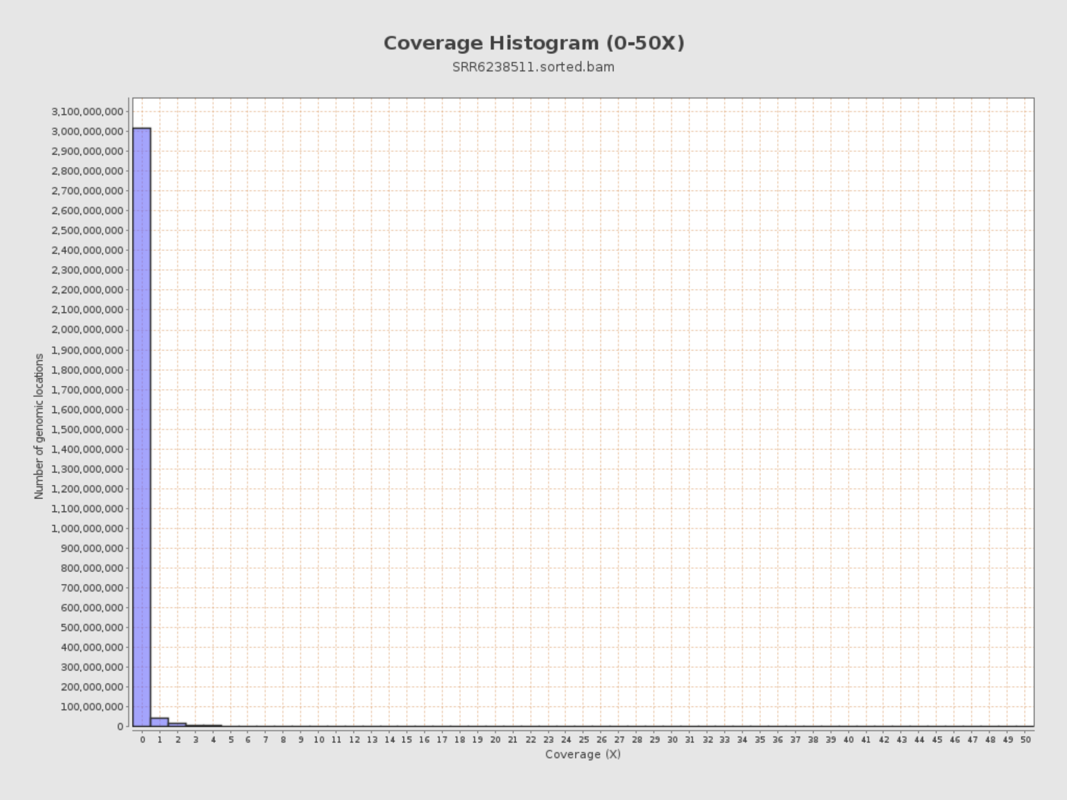
# 3. Results : Coverage across reference



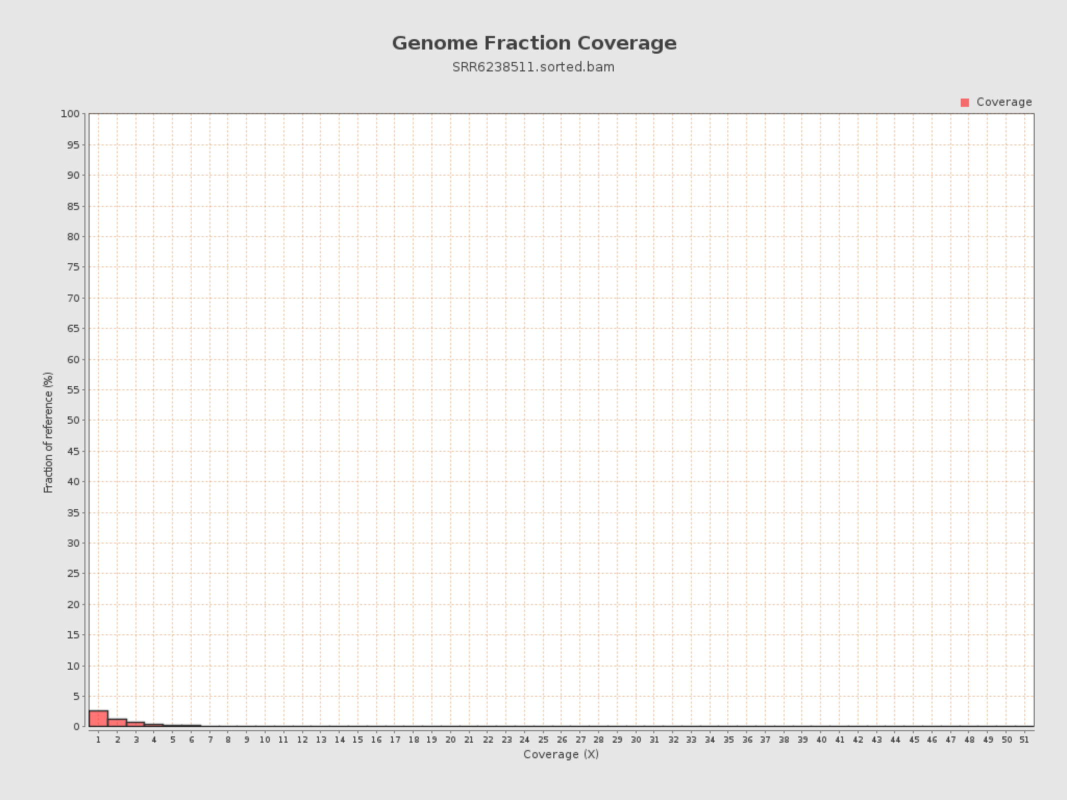
# 4. Results : Coverage Histogram



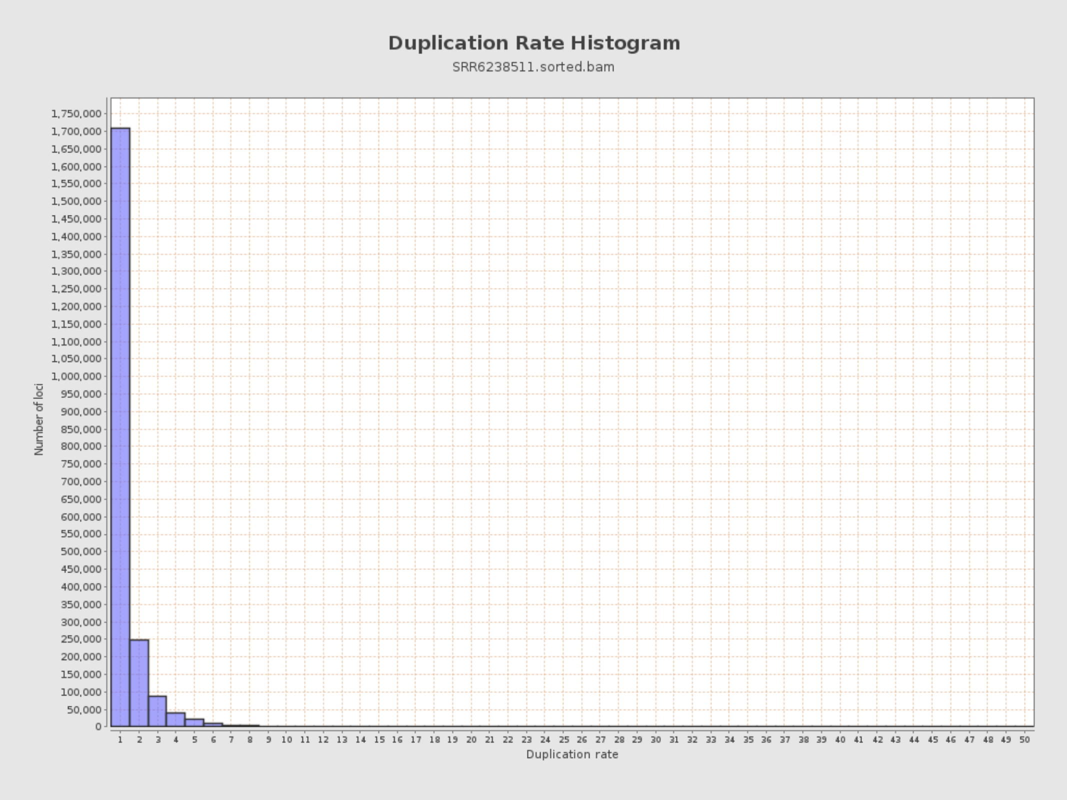
# 5. Results : Coverage Histogram (0-50X)



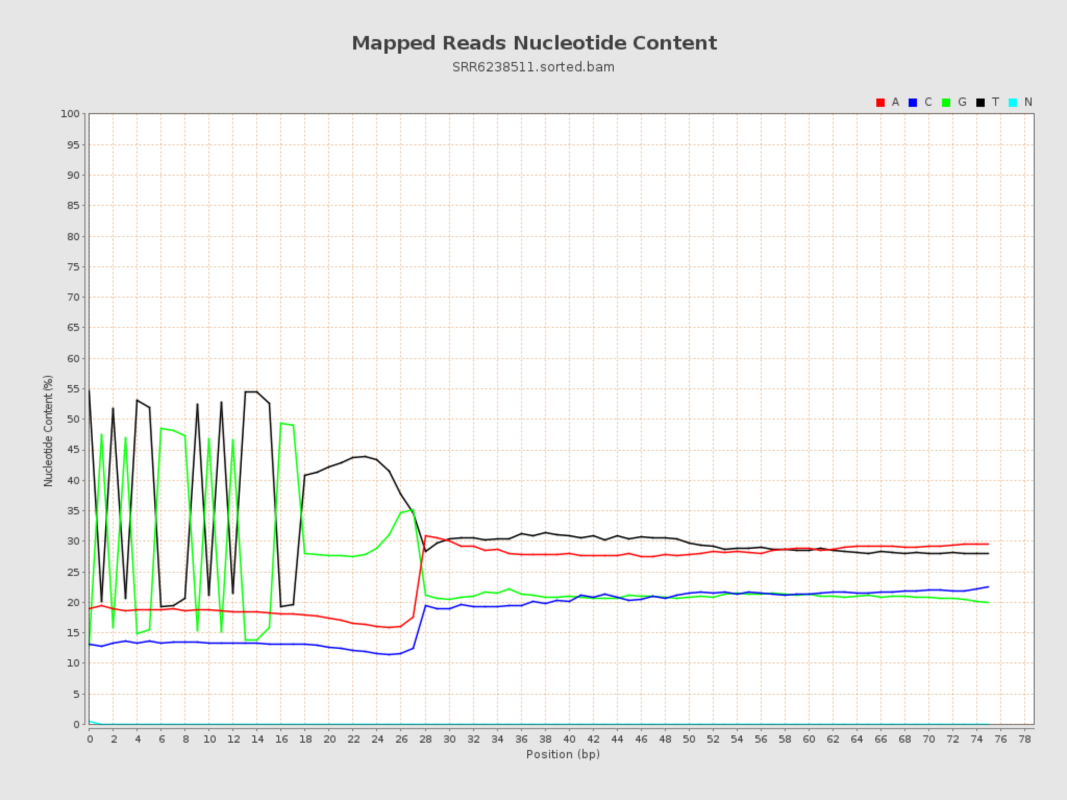
# 6. Results : Genome Fraction Coverage



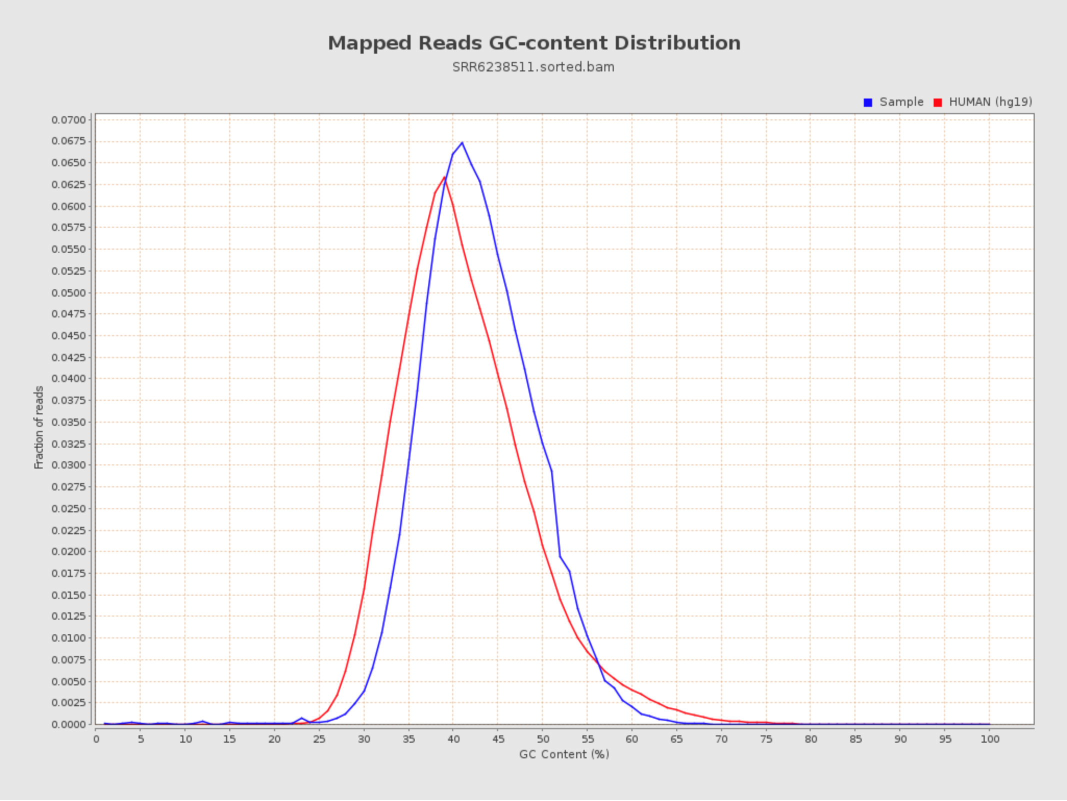
# 7. Results : Duplication Rate Histogram



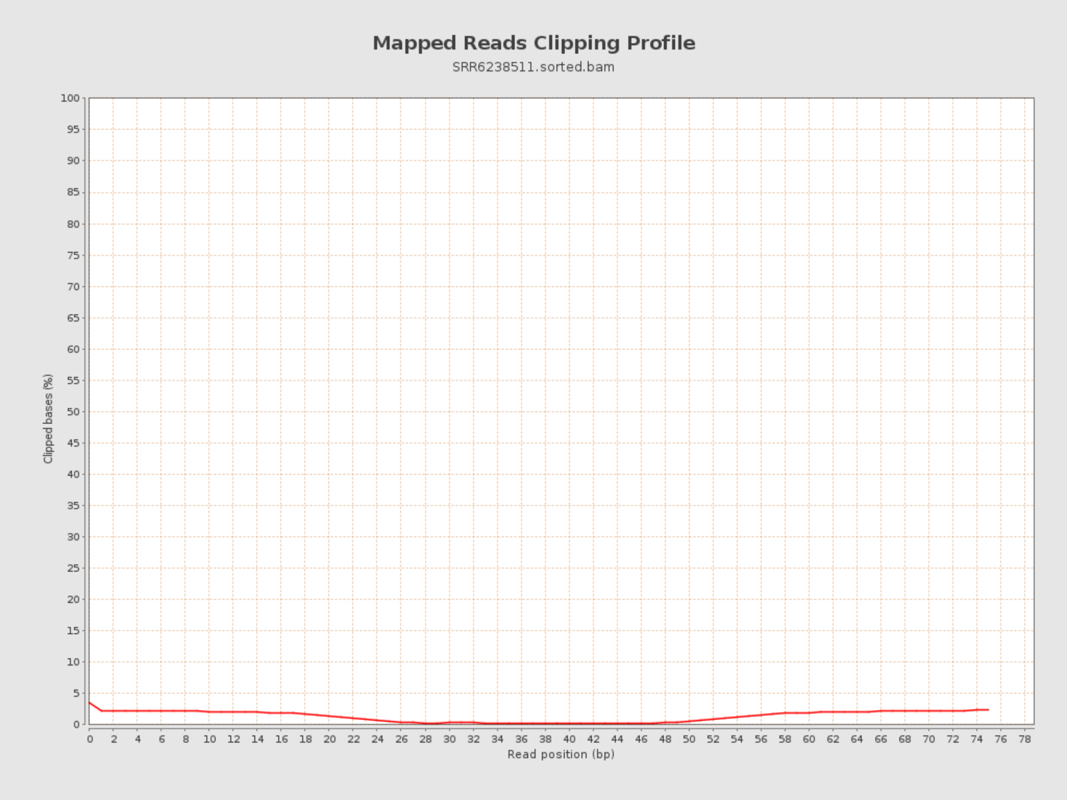
# 8. Results : Mapped Reads Nucleotide Content



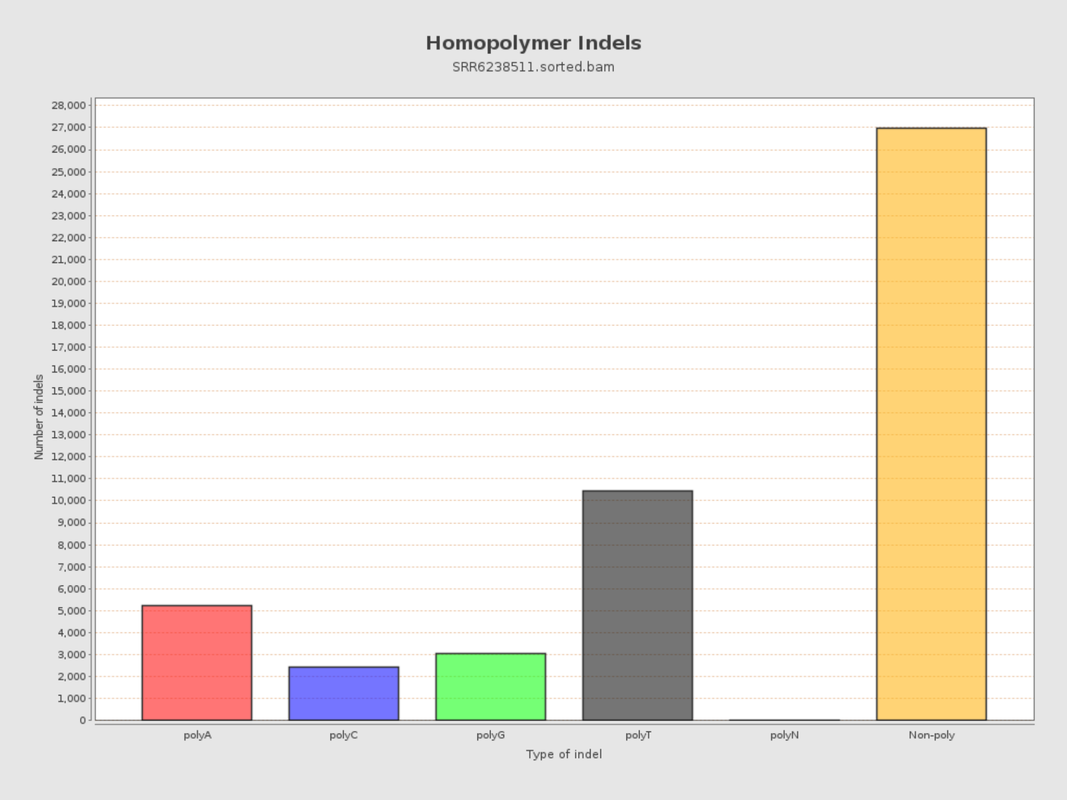
# 9. Results : Mapped Reads GC-content Distribution



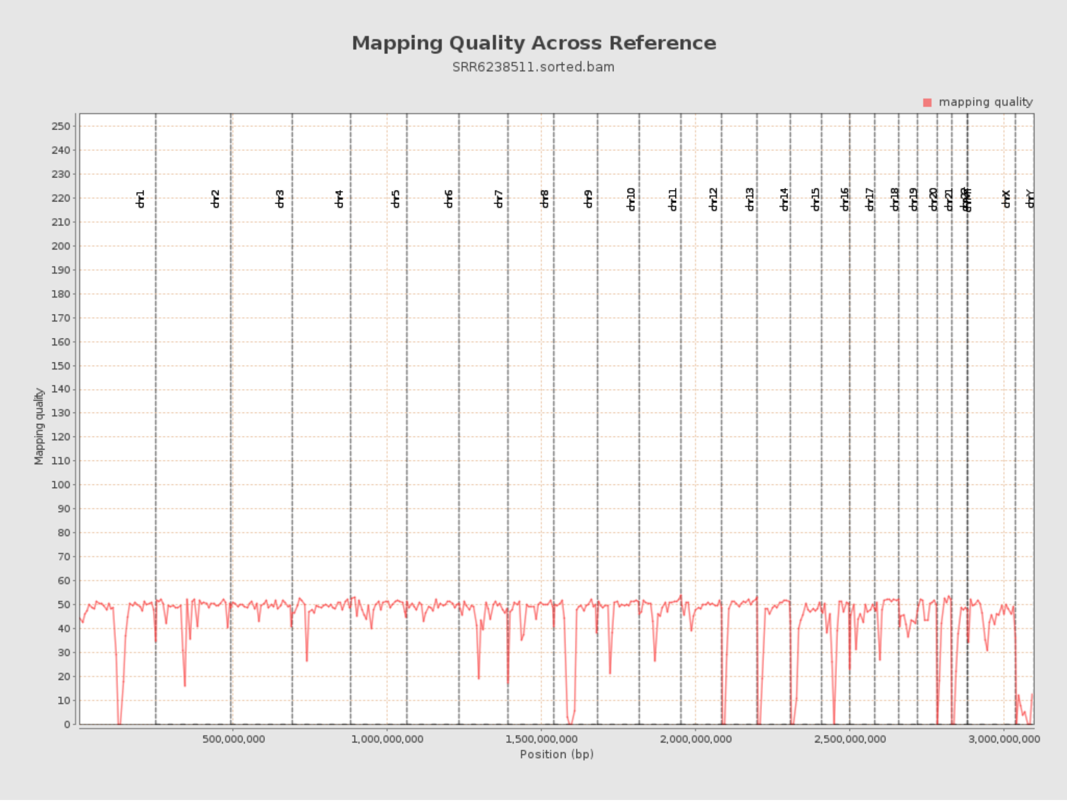
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram