# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/17 09:39:06*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237864.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_SRR6237864 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237864.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 17 09:39:05 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6237864.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,981,524 |
| Mapped reads | 1,757,581 / 88.7% |
| Unmapped reads | 223,943 / 11.3% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 9,258 / 0.47% |
| Read min/max/mean length | 30 / 76 / 76.16 |
| Duplicated reads (estimated) | 68,862 / 3.48% |
| Duplication rate | 2.86% |
| Clipped reads | 963,152 / 48.61% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 30,291,802 / 27.09% |
| Number/percentage of C's | 19,880,512 / 17.78% |
| Number/percentage of T's | 35,435,673 / 31.69% |
| Number/percentage of G's | 26,139,247 / 23.37% |
| Number/percentage of N's | 86,007 / 0.08% |
| GC Percentage | 41.15% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0361 |
| | |

| | |
|---|---|
| Standard Deviation | 0.384 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.89 |

## 2.5. Mismatches and indels

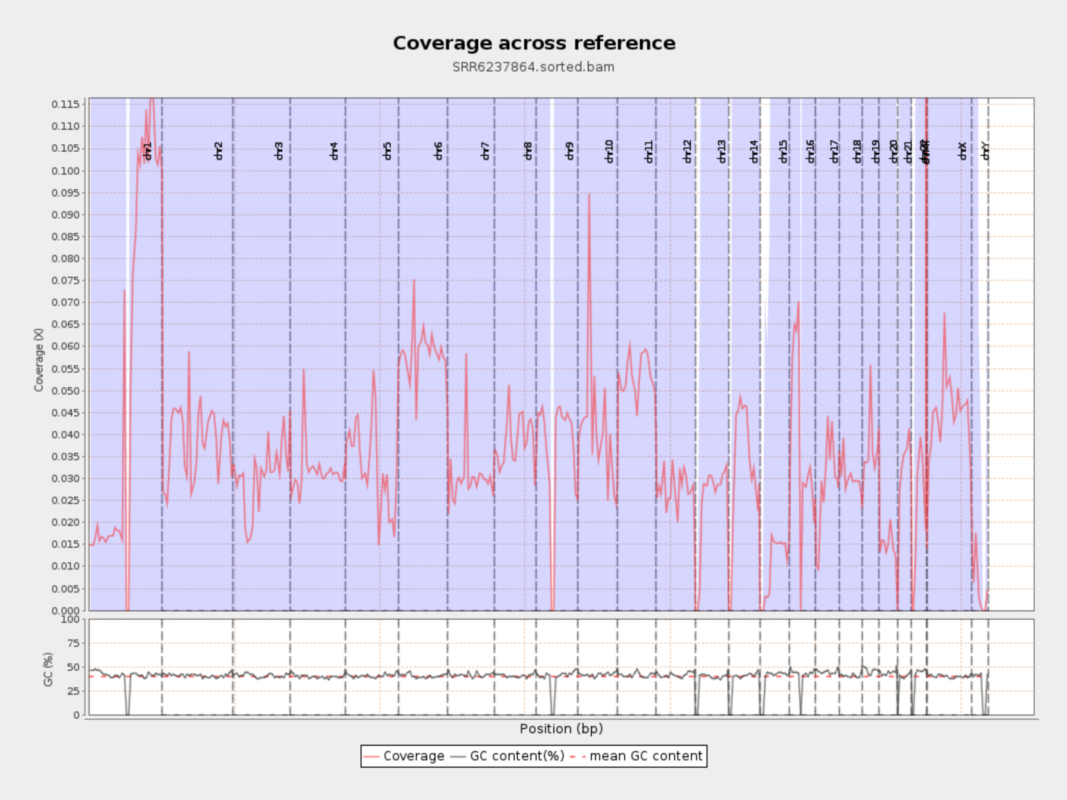
| | |
|---|---|
| General error rate | 0.69% |
| Mismatches | 751,771 |
| Insertions | 8,045 |
| Mapped reads with at least one insertion | 0.45% |
| Deletions | 24,246 |
| Mapped reads with at least one deletion | 1.37% |
| Homopolymer indels | 47.58% |

## 2.6. Chromosome stats

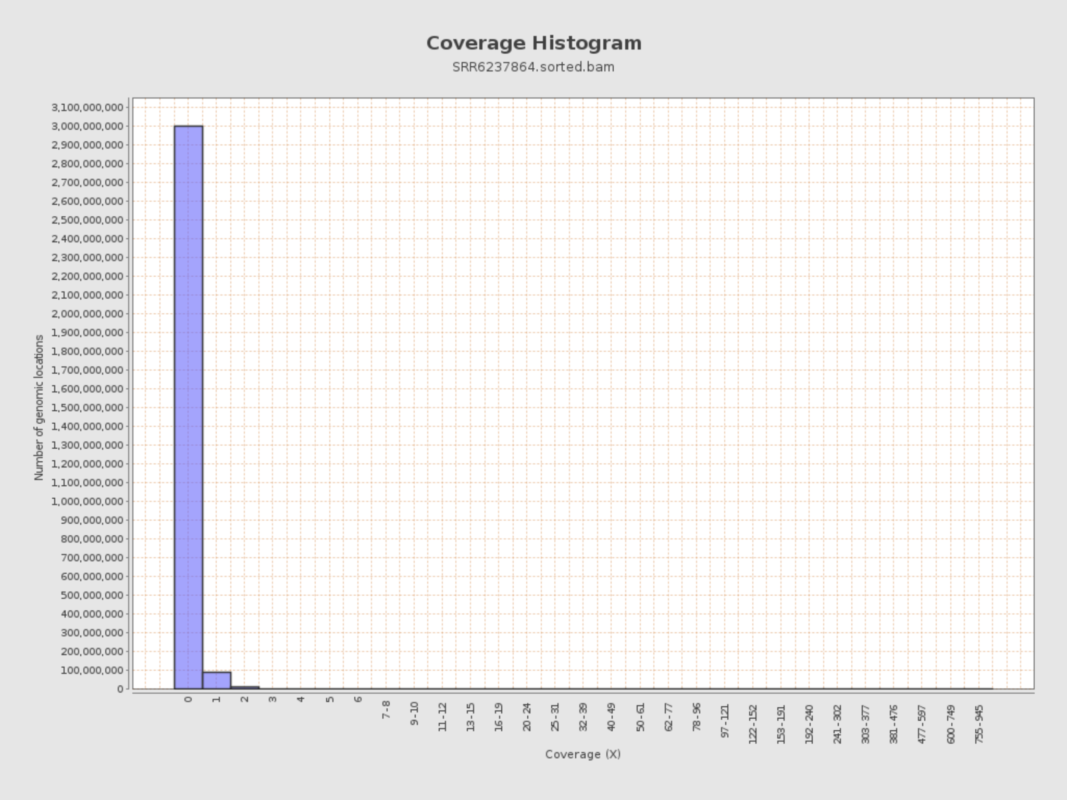
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 13464874 | 0.054 | 0.8494 |
| chr2 | 243199373 | 9485061 | 0.039 | 0.3202 |
| chr3 | 198022430 | 6053926 | 0.0306 | 0.2042 |
| chr4 | 191154276 | 6029873 | 0.0315 | 0.2252 |
| chr5 | 180915260 | 6001230 | 0.0332 | 0.202 |
| chr6 | 171115067 | 10029243 | 0.0586 | 0.334 |
| chr7 | 159138663 | 4840233 | 0.0304 | 0.427 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 5637232 | 0.0385 | 0.3689 |
| chr9 | 141213431 | 5191211 | 0.0368 | 0.3326 |
| chr10 | 135534747 | 5674865 | 0.0419 | 0.5034 |
| chr11 | 135006516 | 7167280 | 0.0531 | 0.3907 |
| chr12 | 133851895 | 3724999 | 0.0278 | 0.188 |
| chr13 | 115169878 | 2794071 | 0.0243 | 0.1678 |
| chr14 | 107349540 | 3464941 | 0.0323 | 0.2241 |
| chr15 | 102531392 | 1061025 | 0.0103 | 0.1141 |
| chr16 | 90354753 | 3466614 | 0.0384 | 0.2513 |
| chr17 | 81195210 | 2340255 | 0.0288 | 0.2541 |
| chr18 | 78077248 | 2395423 | 0.0307 | 0.5352 |
| chr19 | 59128983 | 2188703 | 0.037 | 0.5905 |
| chr20 | 63025520 | 929321 | 0.0147 | 0.1516 |
| chr21 | 48129895 | 1509658 | 0.0314 | 0.2194 |
| chr22 | 51304566 | 1108020 | 0.0216 | 0.1588 |
| chrMT | 16571 | 92797 | 5.6 | 3.7687 |
| chrX | 155270560 | 6917174 | 0.0445 | 0.2742 |
| chrY | 59373566 | 307176 | 0.0052 | 0.1367 |

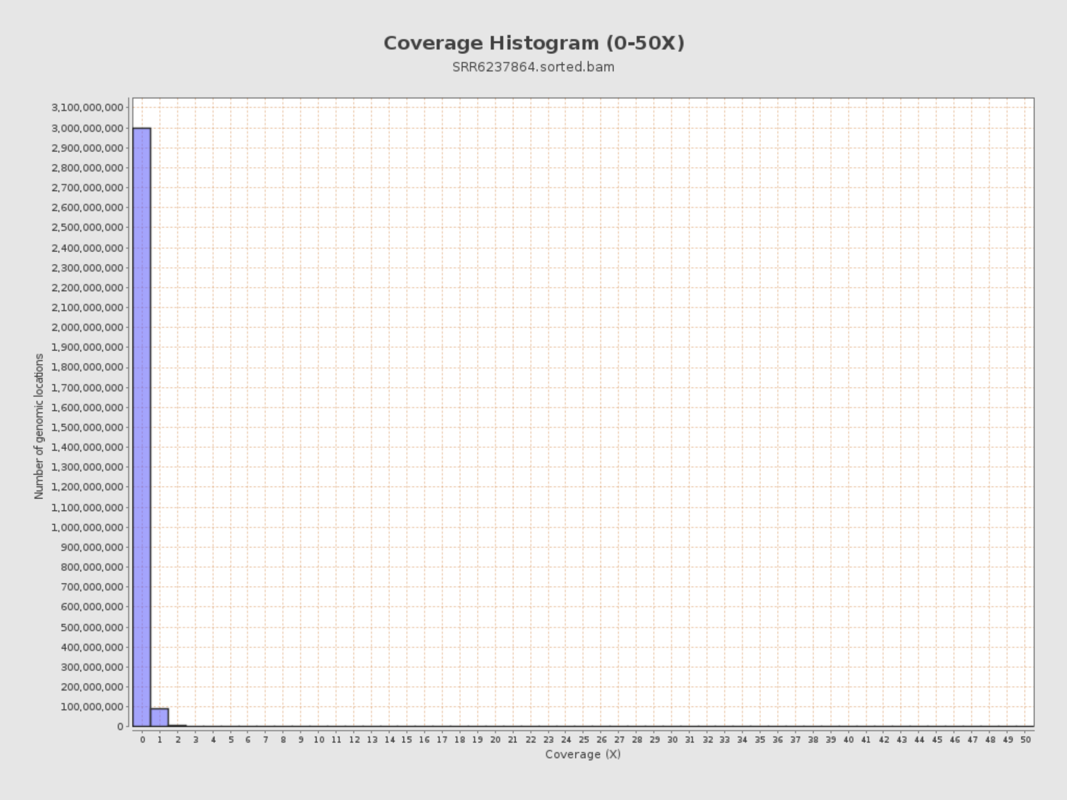
# 3. Results : Coverage across reference



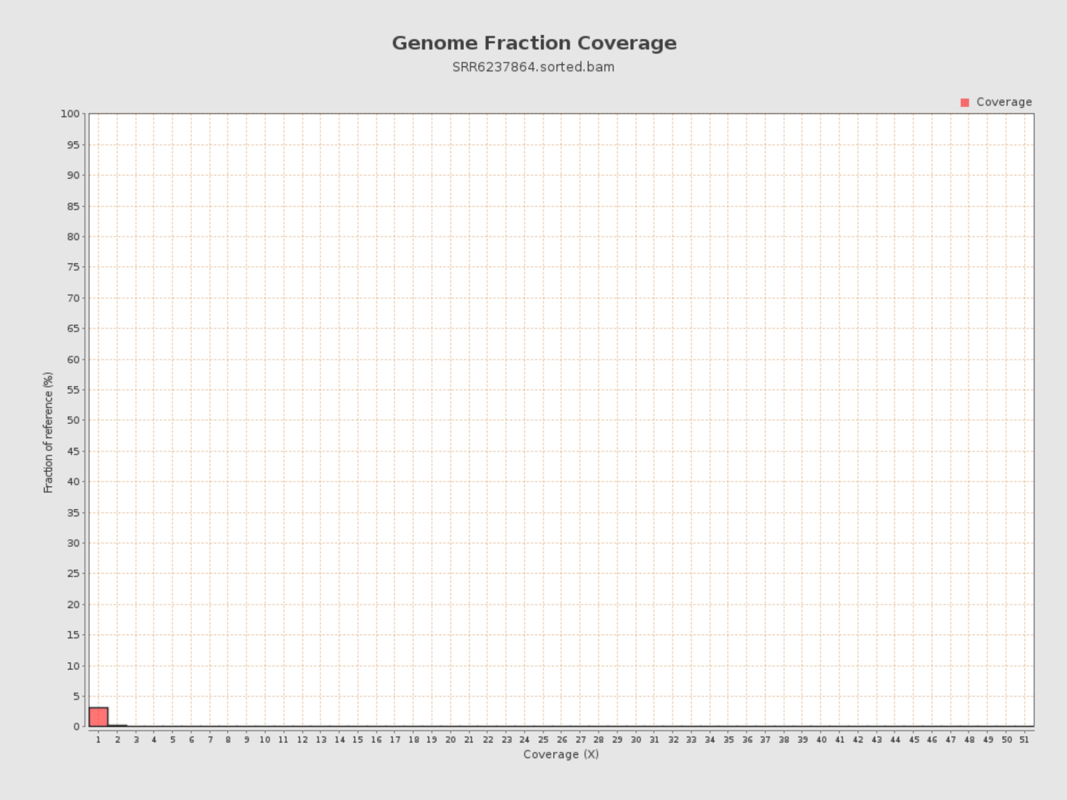
# 4. Results : Coverage Histogram



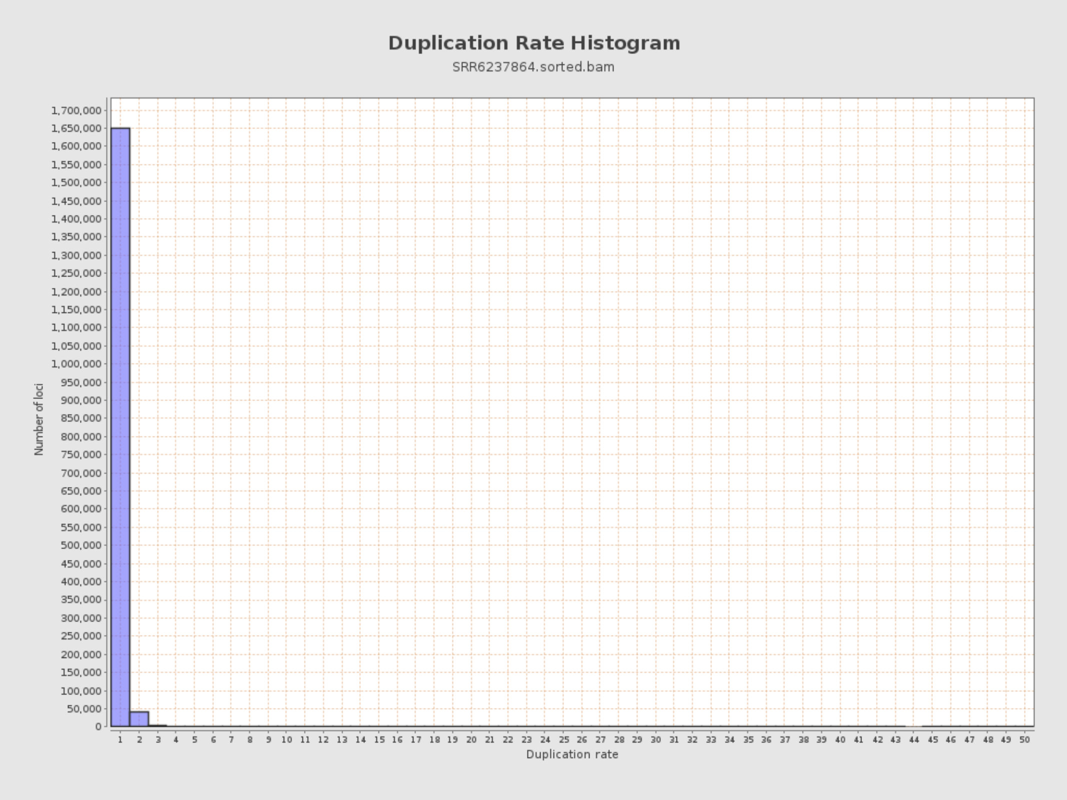
# 5. Results : Coverage Histogram (0-50X)



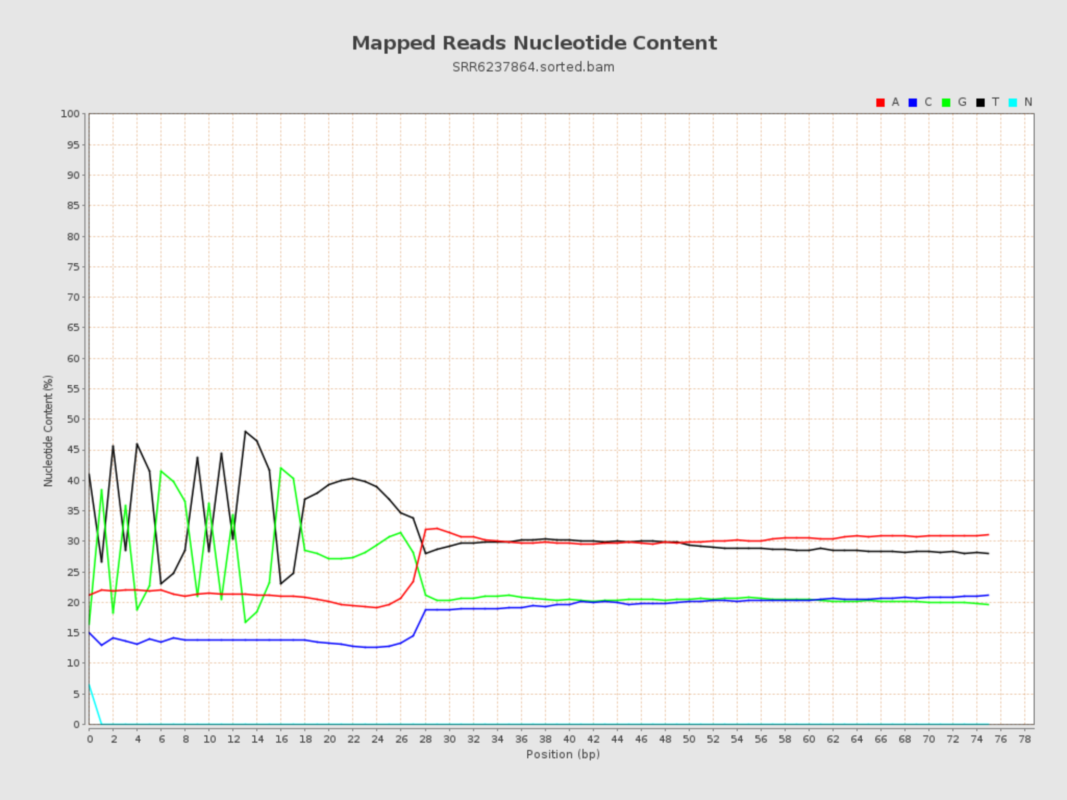
# 6. Results : Genome Fraction Coverage



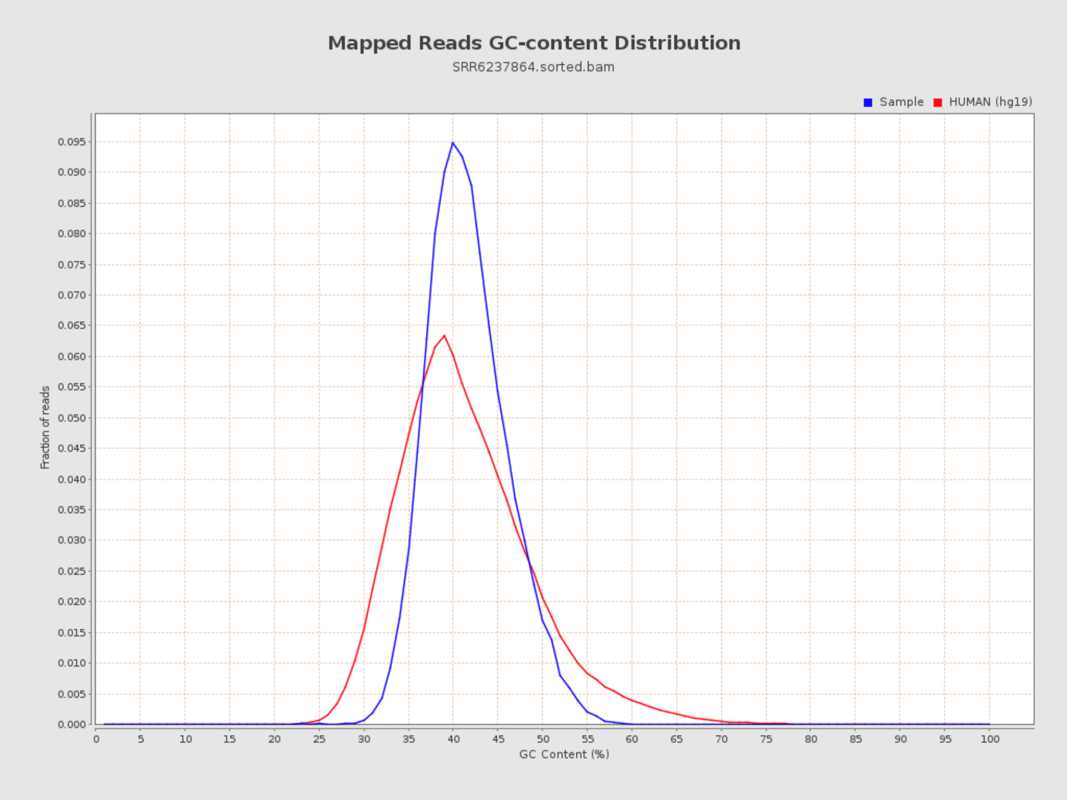
# 7. Results : Duplication Rate Histogram



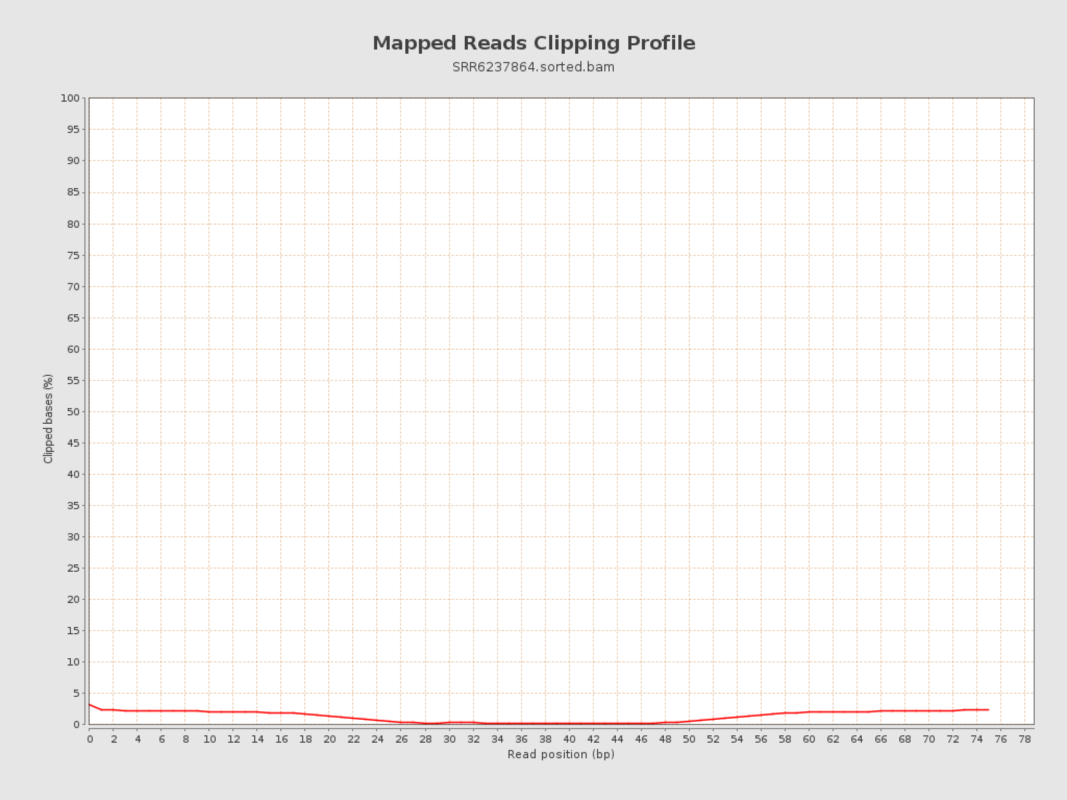
# 8. Results : Mapped Reads Nucleotide Content



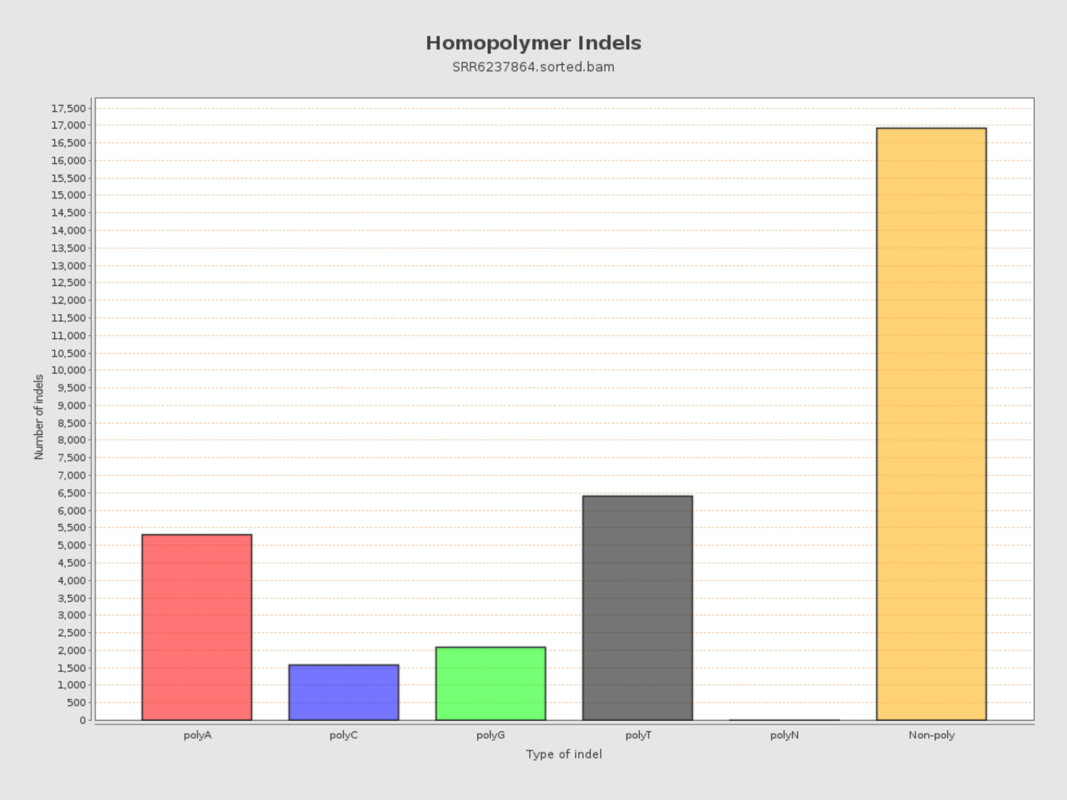
# 9. Results : Mapped Reads GC-content Distribution



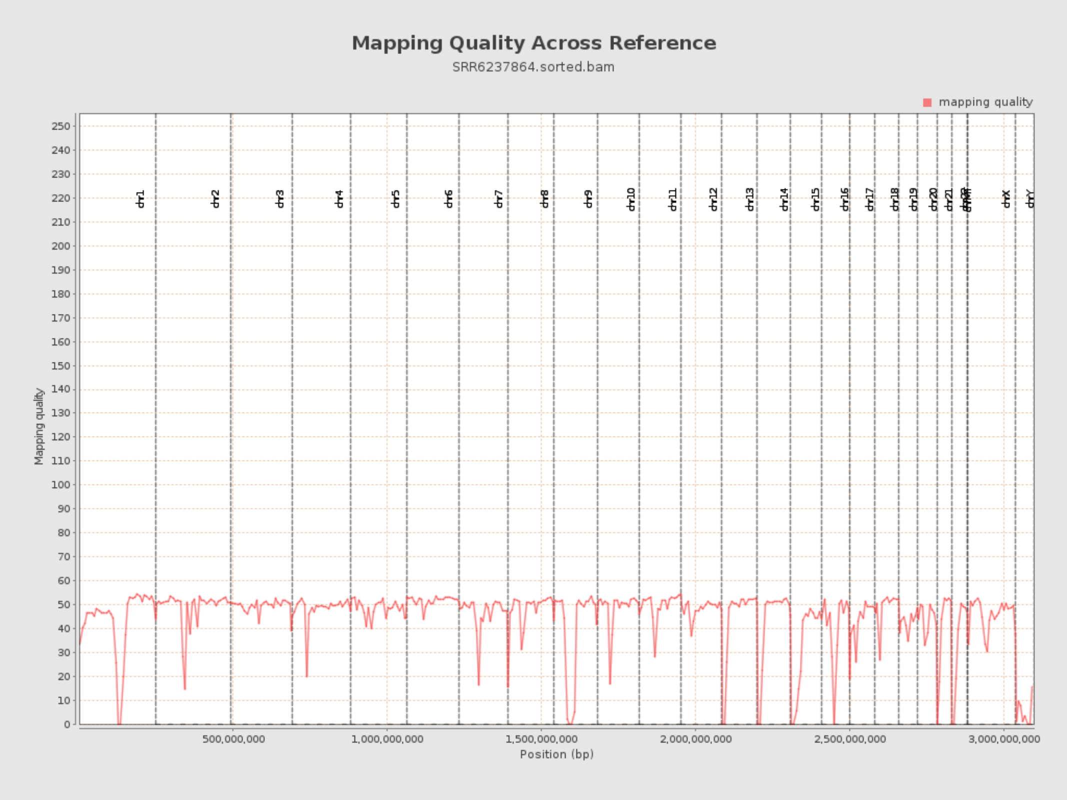
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram