# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/17 07:56:33*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237830.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_SRR6237830 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237830.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 17 07:56:33 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6237830.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,073,837 |
| Mapped reads | 1,760,476 / 84.89% |
| Unmapped reads | 313,361 / 15.11% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 20,446 / 0.99% |
| Read min/max/mean length | 30 / 76 / 76.35 |
| Duplicated reads (estimated) | 452,513 / 21.82% |
| Duplication rate | 14.23% |
| Clipped reads | 868,187 / 41.86% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 31,770,345 / 27.48% |
| Number/percentage of C's | 21,475,820 / 18.58% |
| Number/percentage of T's | 36,421,581 / 31.51% |
| Number/percentage of G's | 25,735,894 / 22.26% |
| Number/percentage of N's | 196,993 / 0.17% |
| GC Percentage | 40.84% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0374 |
| | |

| | |
|---|---|
| Standard Deviation | 0.5875 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.84 |

## 2.5. Mismatches and indels

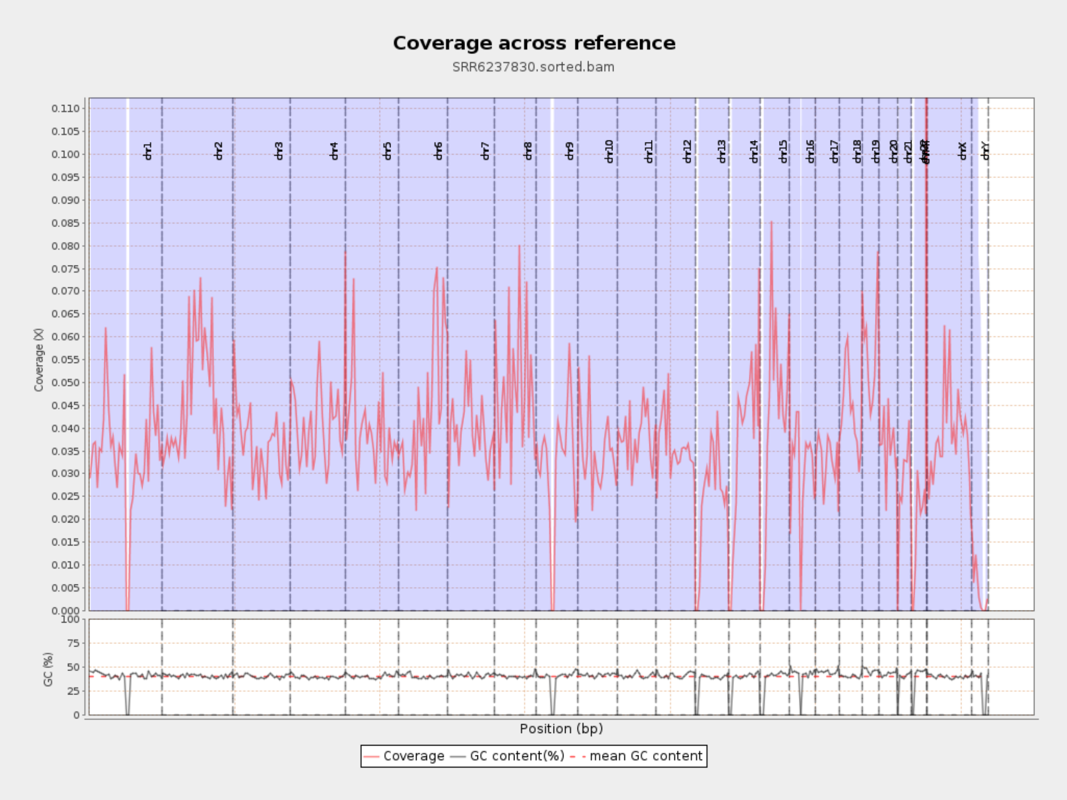
| | |
|---|---|
| General error rate | 0.84% |
| Mismatches | 959,685 |
| Insertions | 7,799 |
| Mapped reads with at least one insertion | 0.44% |
| Deletions | 26,973 |
| Mapped reads with at least one deletion | 1.52% |
| Homopolymer indels | 46.14% |

## 2.6. Chromosome stats

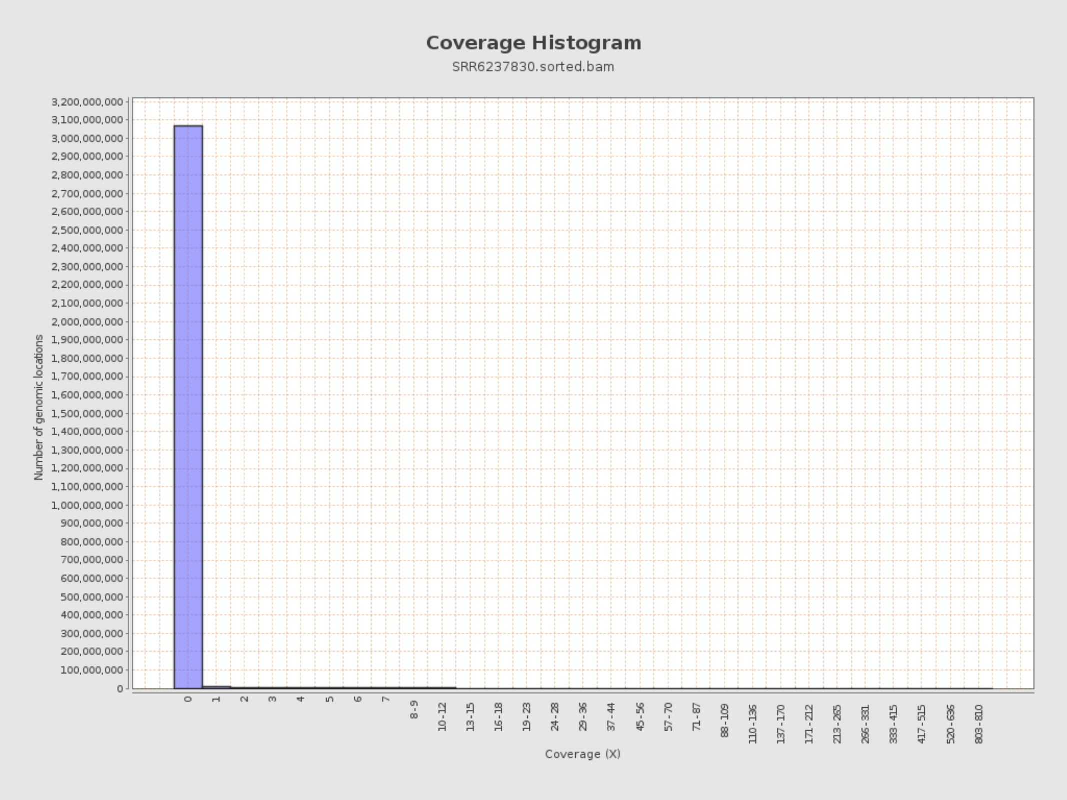
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 8497628 | 0.0341 | 0.7334 |
| chr2 | 243199373 | 10858827 | 0.0446 | 0.72 |
| chr3 | 198022430 | 7169257 | 0.0362 | 0.5384 |
| chr4 | 191154276 | 7768939 | 0.0406 | 0.5652 |
| chr5 | 180915260 | 7139551 | 0.0395 | 0.5647 |
| chr6 | 171115067 | 7394576 | 0.0432 | 0.6057 |
| chr7 | 159138663 | 6360932 | 0.04 | 0.6014 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7154022 | 0.0489 | 0.6554 |
| chr9 | 141213431 | 4530663 | 0.0321 | 0.5224 |
| chr10 | 135534747 | 4750820 | 0.0351 | 0.5537 |
| chr11 | 135006516 | 5143402 | 0.0381 | 0.5559 |
| chr12 | 133851895 | 4798755 | 0.0359 | 0.5352 |
| chr13 | 115169878 | 2845975 | 0.0247 | 0.4411 |
| chr14 | 107349540 | 3946296 | 0.0368 | 0.5492 |
| chr15 | 102531392 | 4229367 | 0.0412 | 0.5805 |
| chr16 | 90354753 | 2800729 | 0.031 | 0.4829 |
| chr17 | 81195210 | 2677877 | 0.033 | 0.4981 |
| chr18 | 78077248 | 3407309 | 0.0436 | 0.675 |
| chr19 | 59128983 | 3350912 | 0.0567 | 0.8155 |
| chr20 | 63025520 | 2292938 | 0.0364 | 0.5487 |
| chr21 | 48129895 | 1313886 | 0.0273 | 0.4537 |
| chr22 | 51304566 | 899319 | 0.0175 | 0.3455 |
| chrMT | 16571 | 46551 | 2.8092 | 4.9109 |
| chrX | 155270560 | 6002687 | 0.0387 | 0.5476 |
| chrY | 59373566 | 266183 | 0.0045 | 0.1397 |

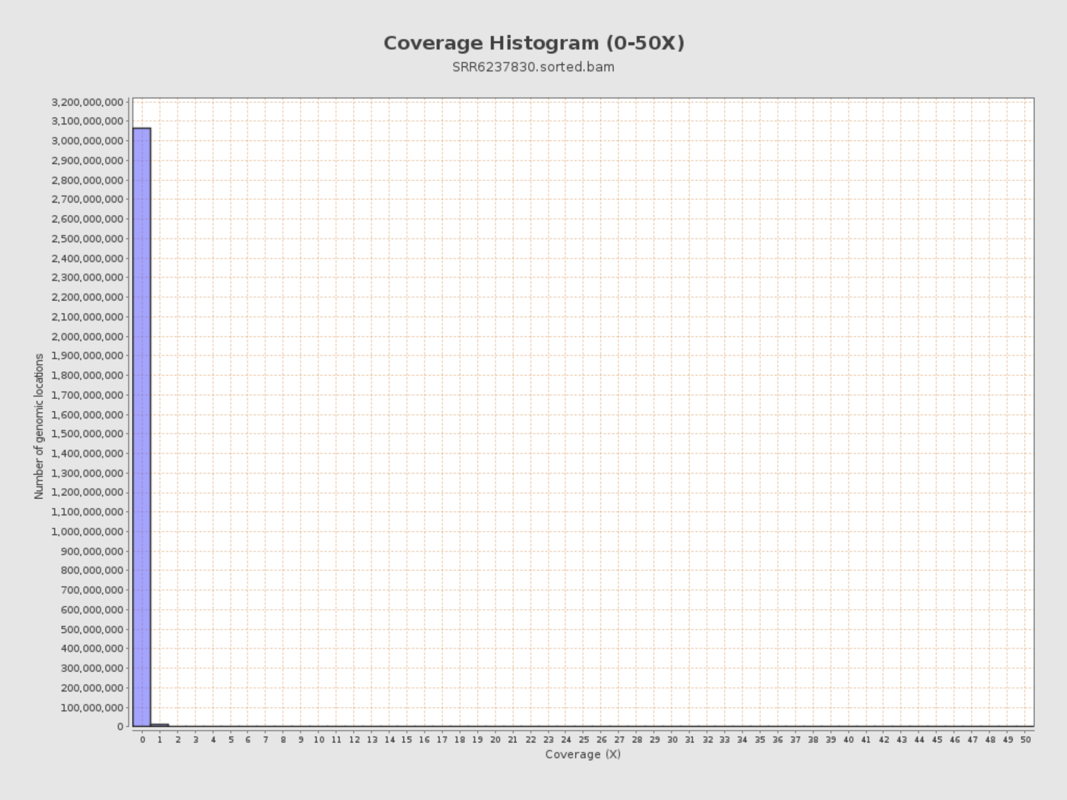
# 3. Results : Coverage across reference



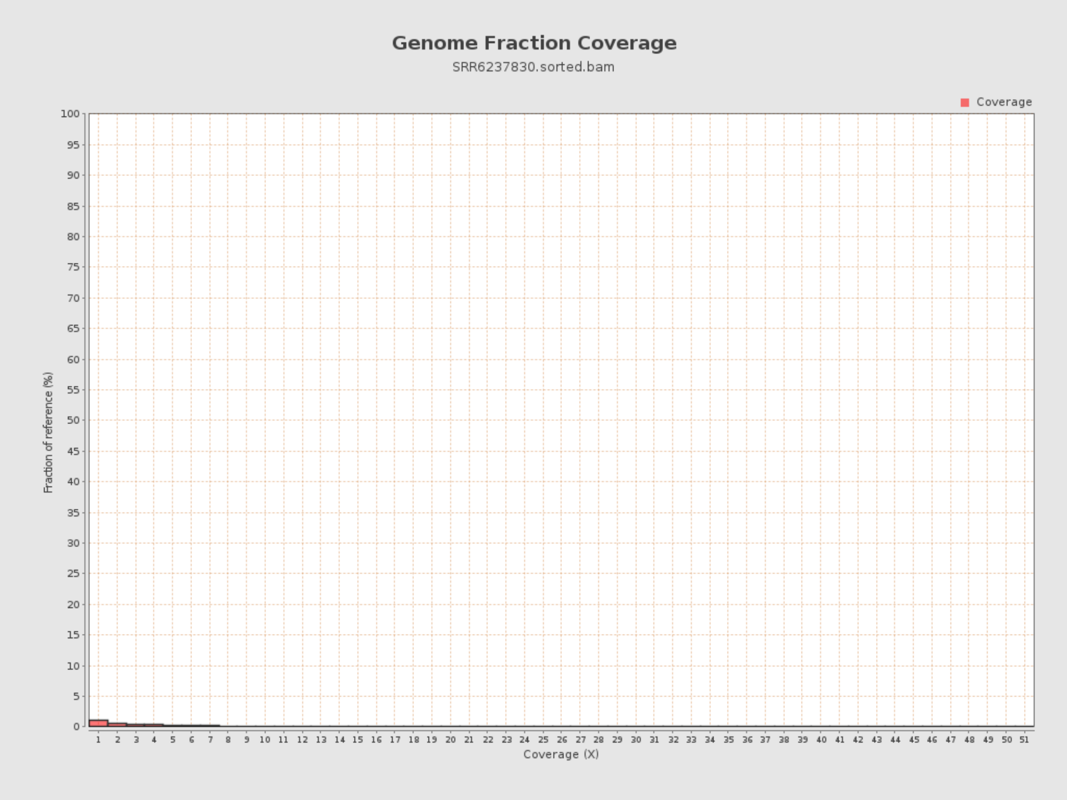
# 4. Results : Coverage Histogram



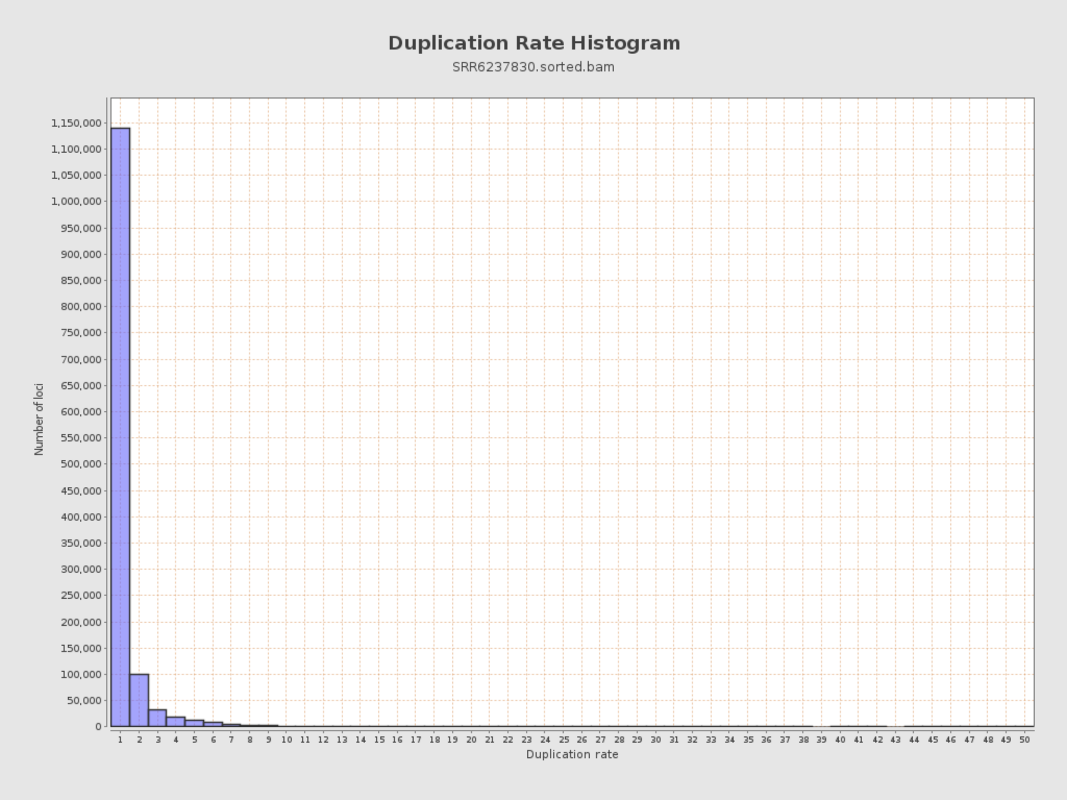
# 5. Results : Coverage Histogram (0-50X)



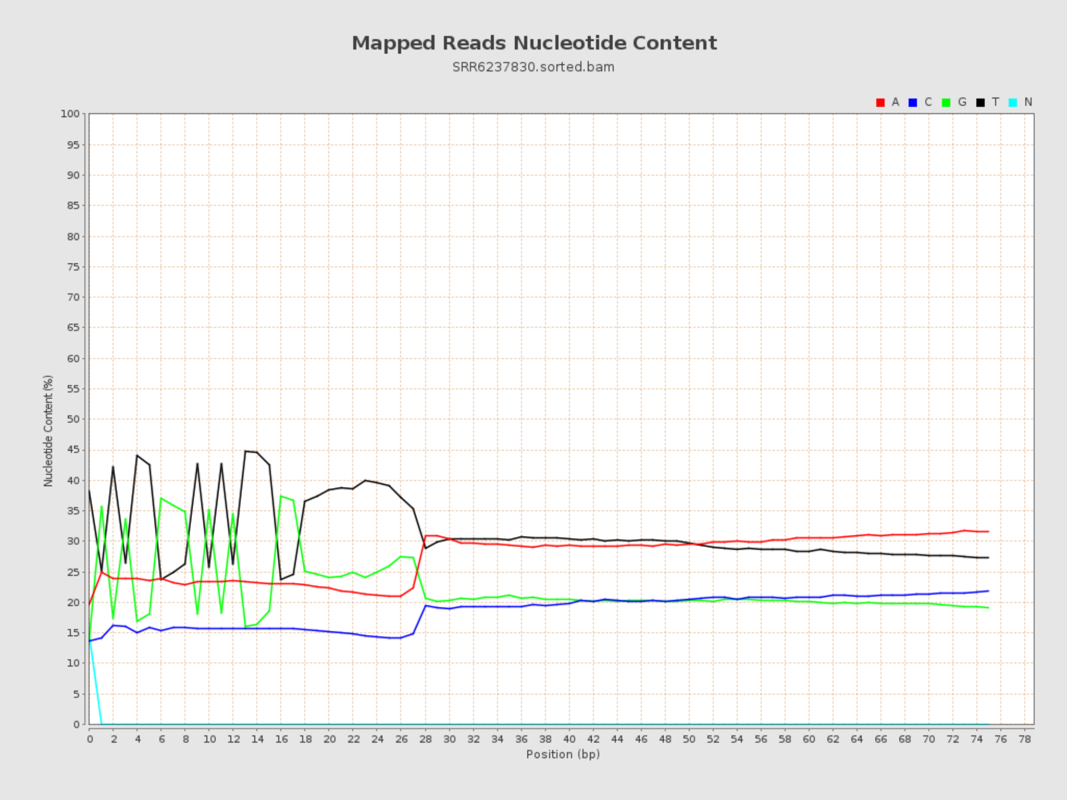
# 6. Results : Genome Fraction Coverage



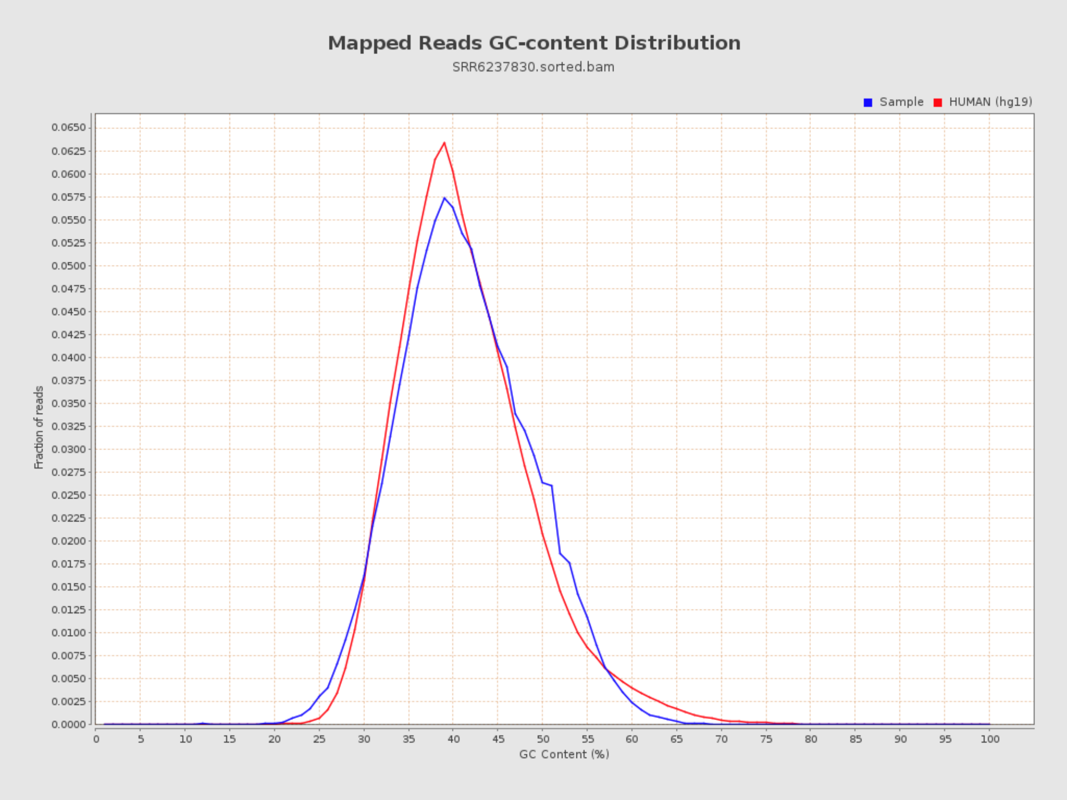
# 7. Results : Duplication Rate Histogram



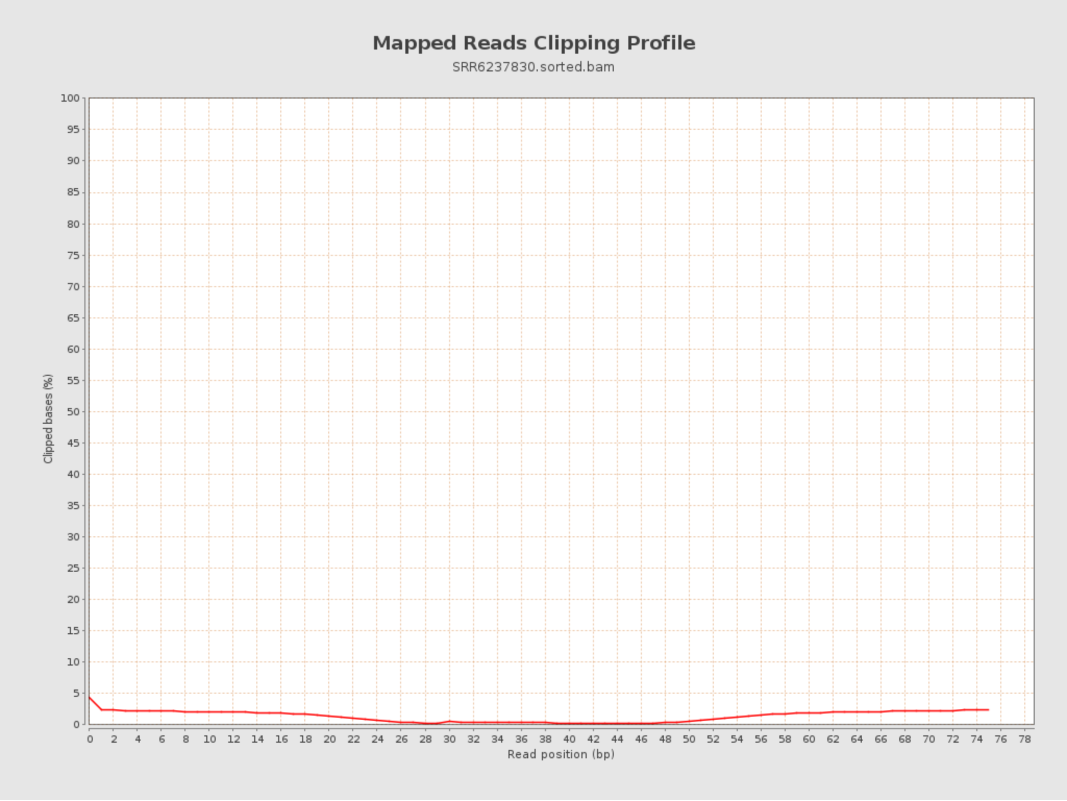
# 8. Results : Mapped Reads Nucleotide Content



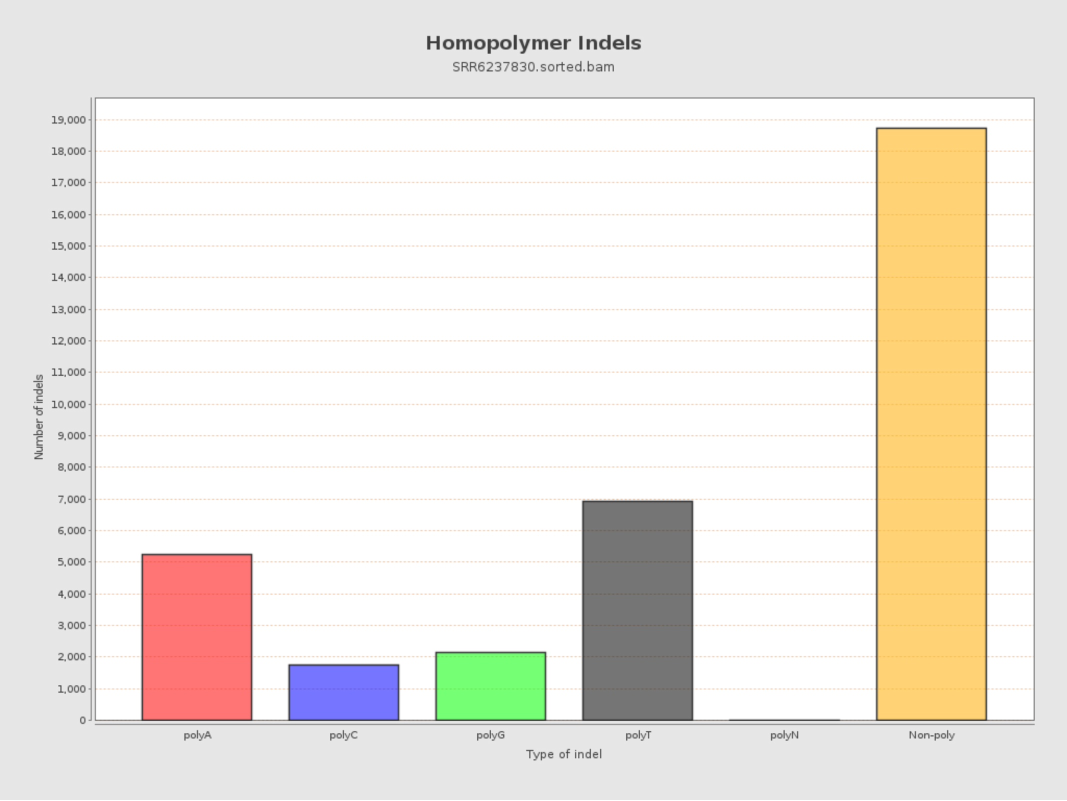
# 9. Results : Mapped Reads GC-content Distribution



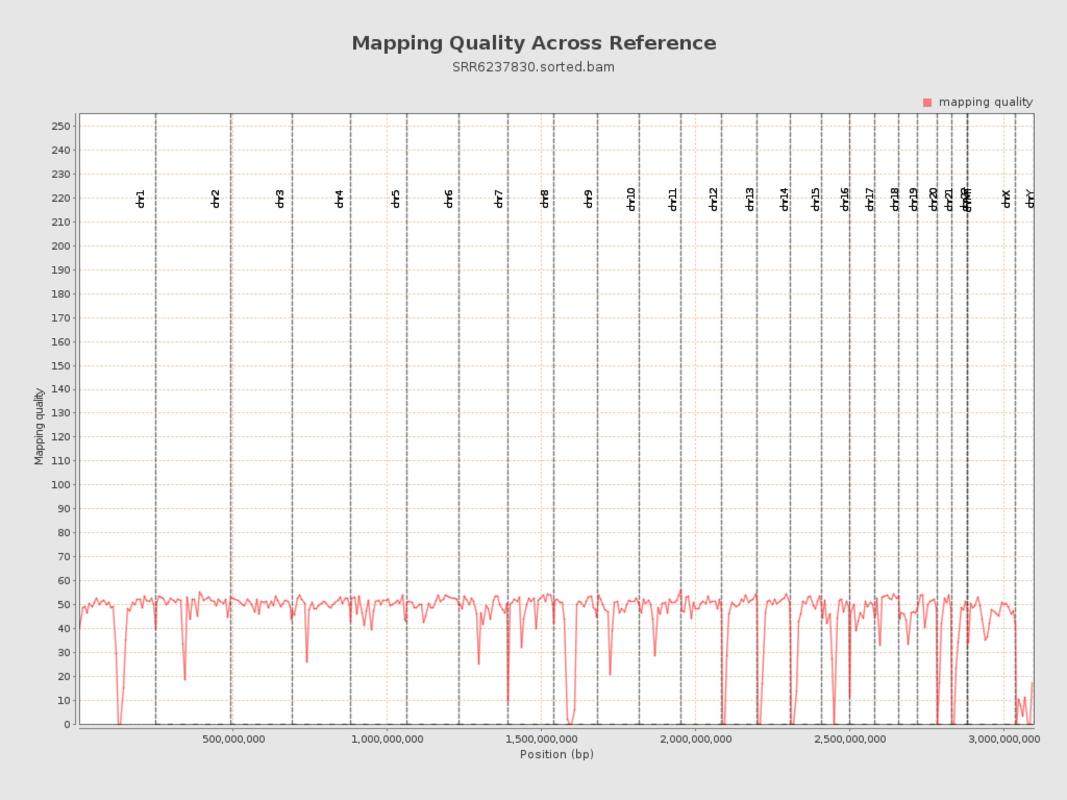
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram