# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/17 02:20:16*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237321.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_SRR6237321 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237321.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 17 02:20:15 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6237321.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,822,829 |
| Mapped reads | 2,573,513 / 91.17% |
| Unmapped reads | 249,316 / 8.83% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 27,812 / 0.99% |
| Read min/max/mean length | 30 / 76 / 76.34 |
| Duplicated reads (estimated) | 551,994 / 19.55% |
| Duplication rate | 16.36% |
| Clipped reads | 1,646,699 / 58.34% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 40,778,772 / 25.75% |
| Number/percentage of C's | 27,765,385 / 17.54% |
| Number/percentage of T's | 52,677,476 / 33.27% |
| Number/percentage of G's | 37,099,719 / 23.43% |
| Number/percentage of N's | 16,806 / 0.01% |
| GC Percentage | 40.97% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0512 |
| | |

| | |
|---|---|
| Standard Deviation | 0.7943 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.14 |

## 2.5. Mismatches and indels

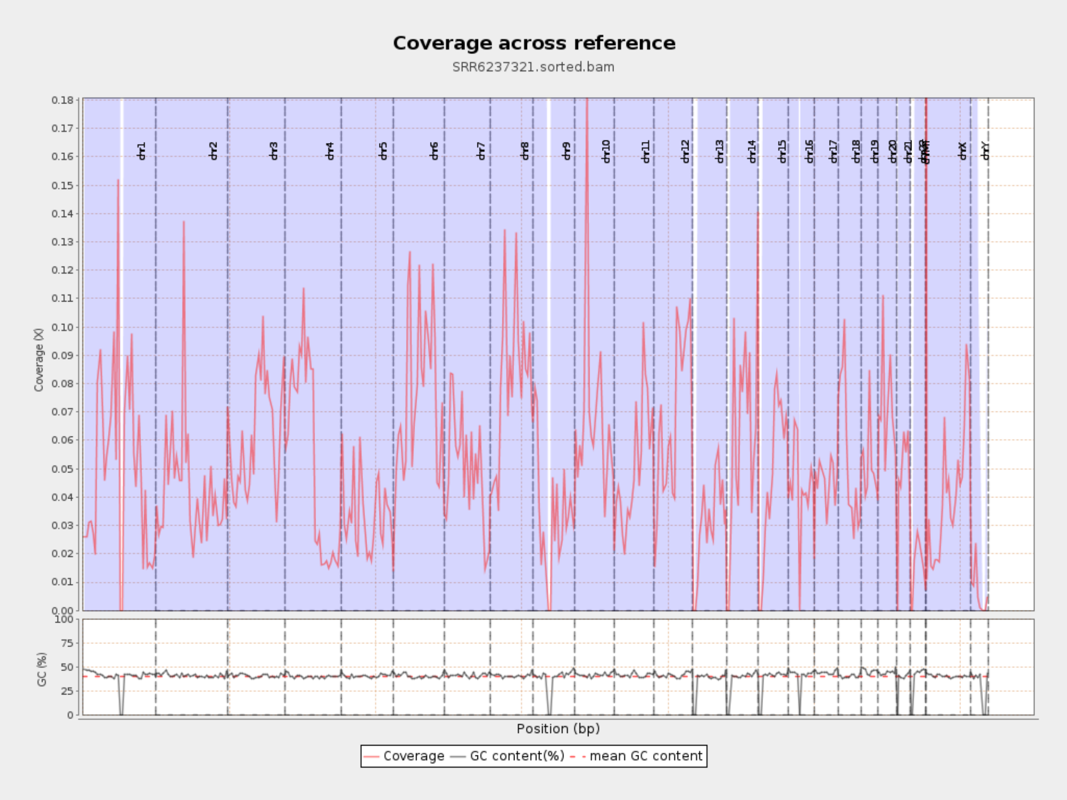
| | |
|---|---|
| General error rate | 0.68% |
| Mismatches | 1,061,000 |
| Insertions | 9,662 |
| Mapped reads with at least one insertion | 0.37% |
| Deletions | 54,922 |
| Mapped reads with at least one deletion | 2.11% |
| Homopolymer indels | 40.84% |

## 2.6. Chromosome stats

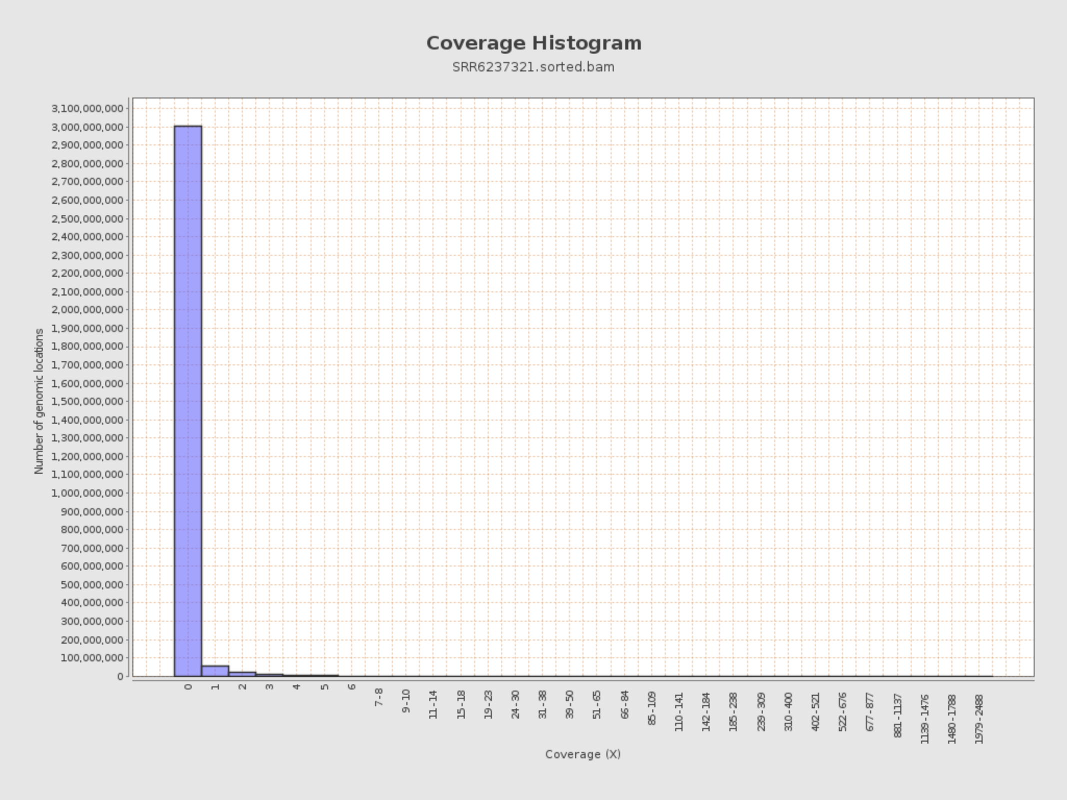
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 12480037 | 0.0501 | 1.6699 |
| chr2 | 243199373 | 10582451 | 0.0435 | 1.3518 |
| chr3 | 198022430 | 12175848 | 0.0615 | 0.4268 |
| chr4 | 191154276 | 10169031 | 0.0532 | 0.3747 |
| chr5 | 180915260 | 6079175 | 0.0336 | 0.2994 |
| chr6 | 171115067 | 13198549 | 0.0771 | 0.6466 |
| chr7 | 159138663 | 7781388 | 0.0489 | 0.4987 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 11984276 | 0.0819 | 0.8843 |
| chr9 | 141213431 | 4660951 | 0.033 | 0.4288 |
| chr10 | 135534747 | 9206071 | 0.0679 | 1.0753 |
| chr11 | 135006516 | 6934451 | 0.0514 | 0.4046 |
| chr12 | 133851895 | 9113425 | 0.0681 | 0.426 |
| chr13 | 115169878 | 3545602 | 0.0308 | 0.3642 |
| chr14 | 107349540 | 6370372 | 0.0593 | 0.3928 |
| chr15 | 102531392 | 4824025 | 0.047 | 0.3919 |
| chr16 | 90354753 | 3853890 | 0.0427 | 0.3862 |
| chr17 | 81195210 | 3731385 | 0.046 | 0.3612 |
| chr18 | 78077248 | 4334336 | 0.0555 | 1.1234 |
| chr19 | 59128983 | 3068250 | 0.0519 | 1.076 |
| chr20 | 63025520 | 4539770 | 0.072 | 0.4356 |
| chr21 | 48129895 | 2267668 | 0.0471 | 0.3498 |
| chr22 | 51304566 | 819891 | 0.016 | 0.192 |
| chrMT | 16571 | 24635 | 1.4866 | 2.0878 |
| chrX | 155270560 | 6303359 | 0.0406 | 0.3442 |
| chrY | 59373566 | 384322 | 0.0065 | 0.1847 |

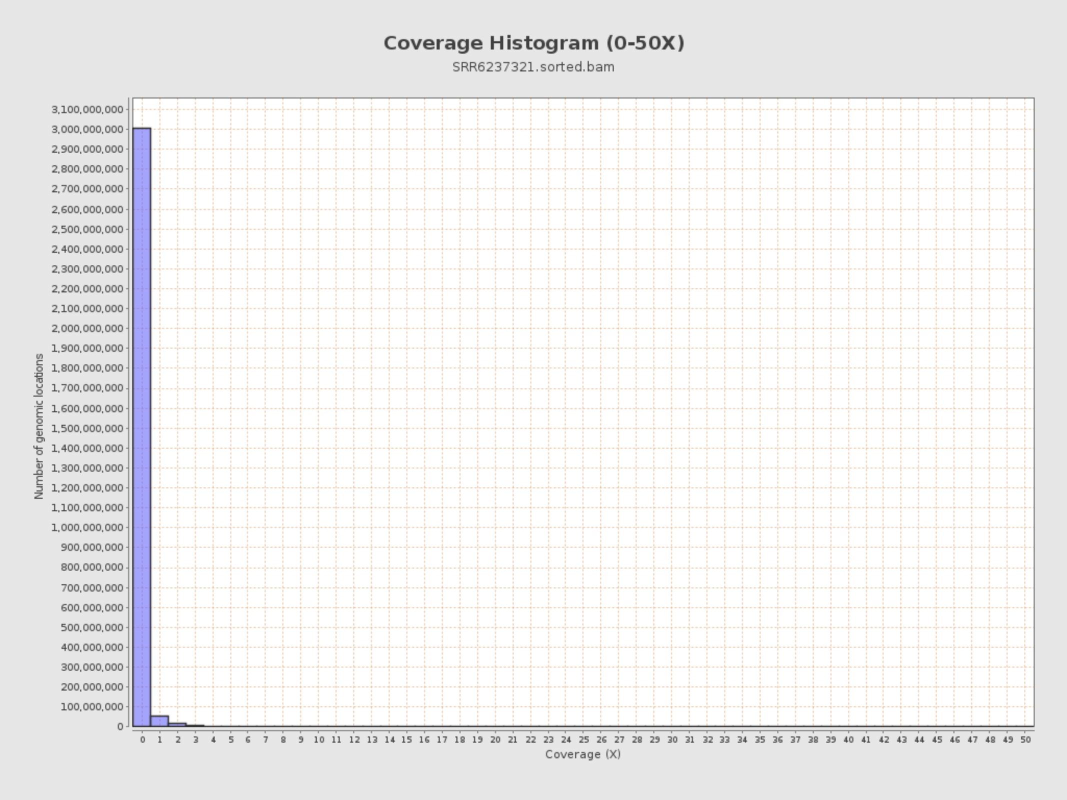
# 3. Results : Coverage across reference



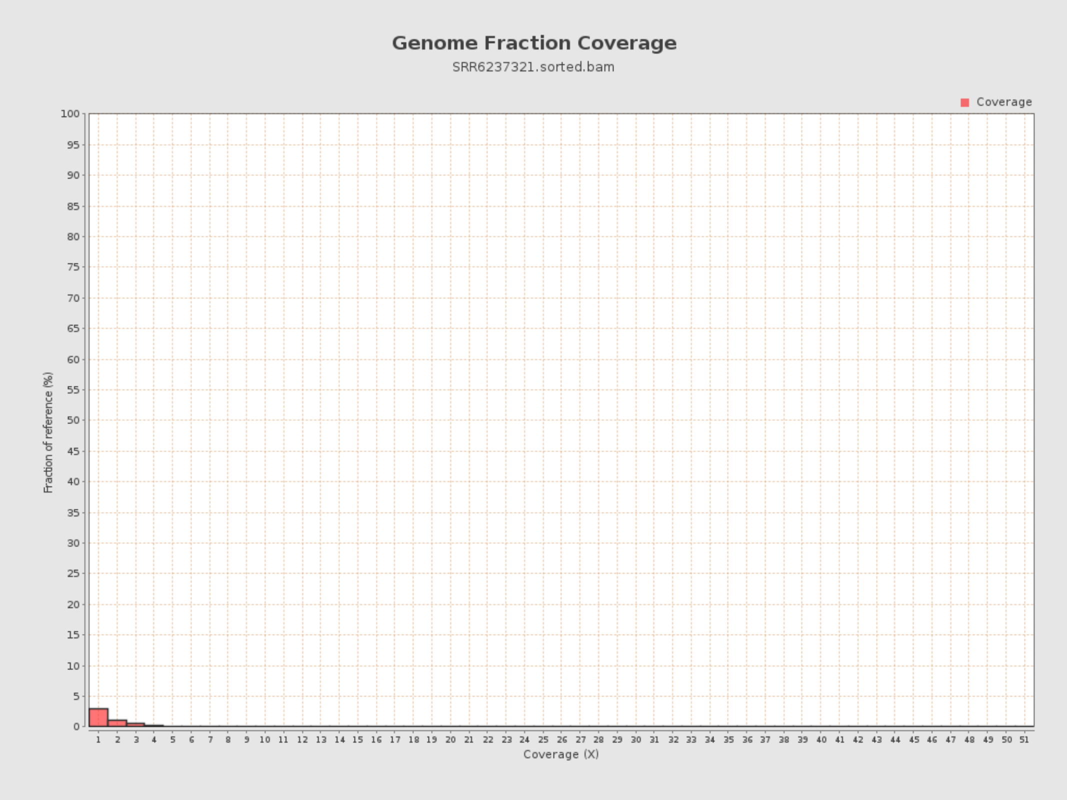
# 4. Results : Coverage Histogram



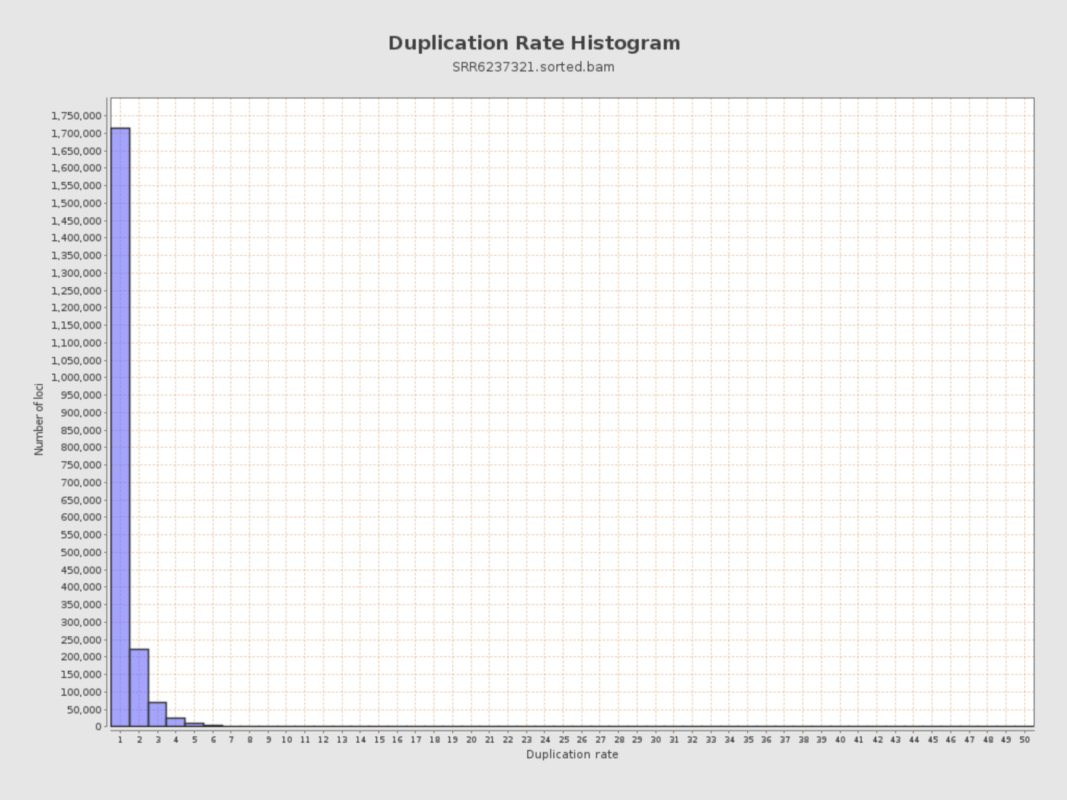
# 5. Results : Coverage Histogram (0-50X)



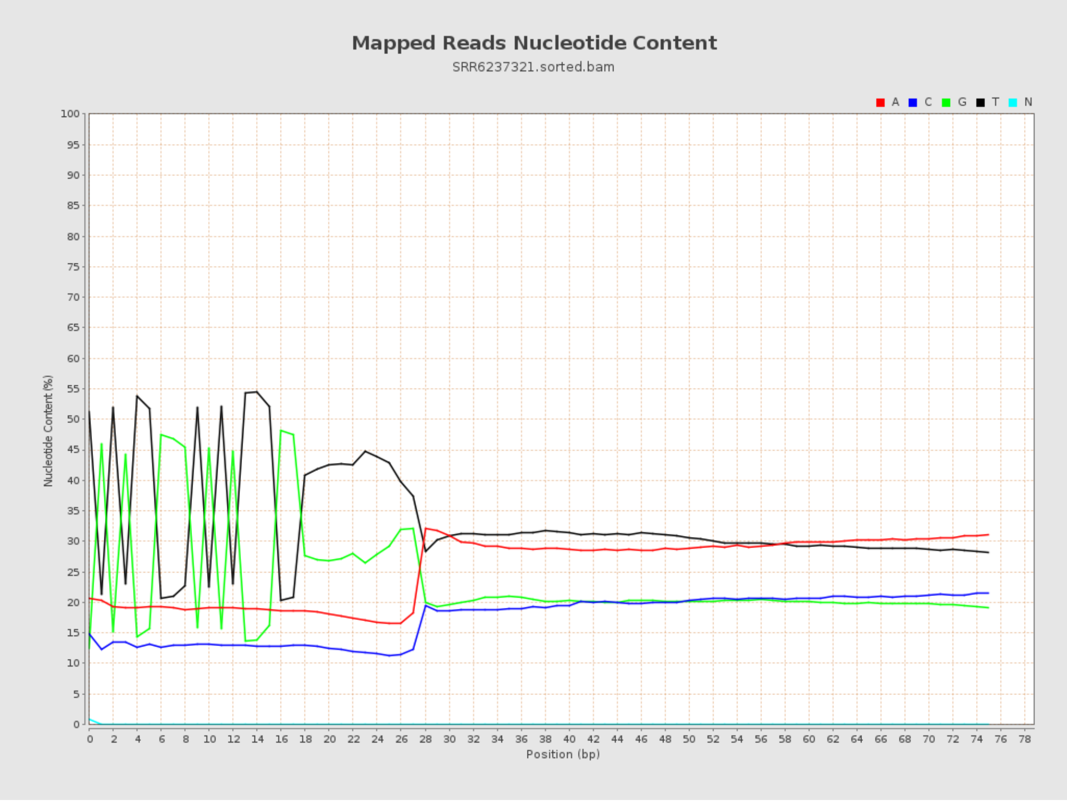
# 6. Results : Genome Fraction Coverage



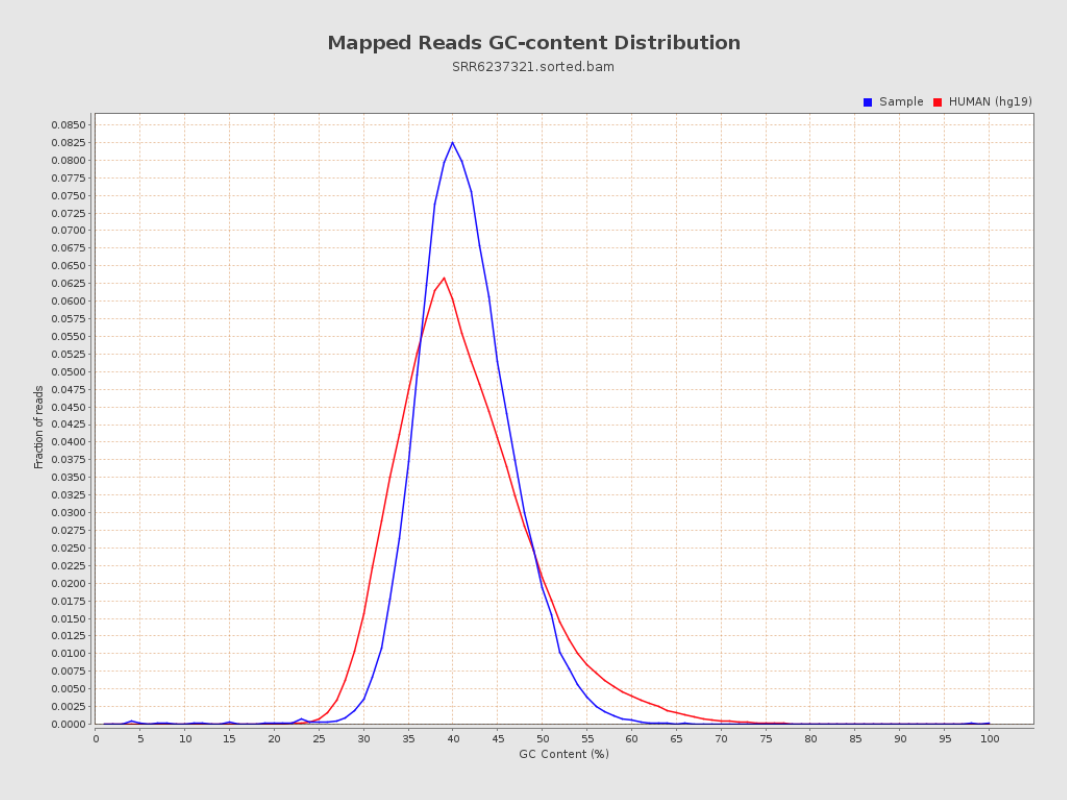
# 7. Results : Duplication Rate Histogram



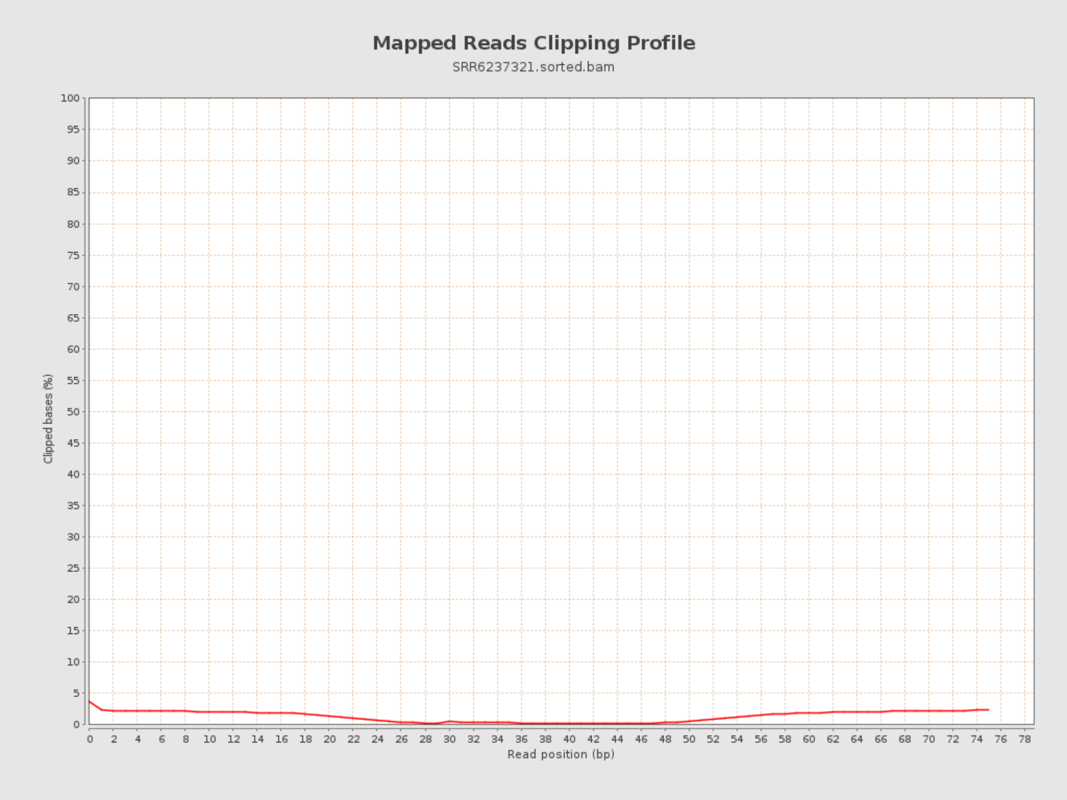
# 8. Results : Mapped Reads Nucleotide Content



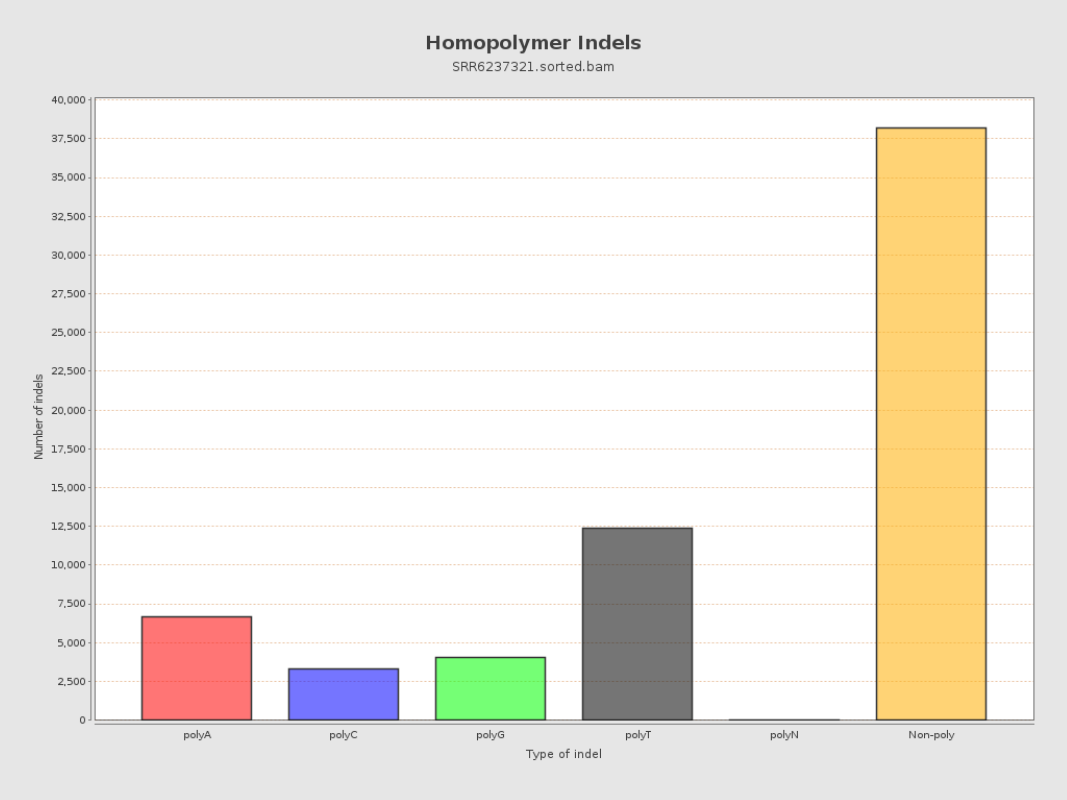
# 9. Results : Mapped Reads GC-content Distribution



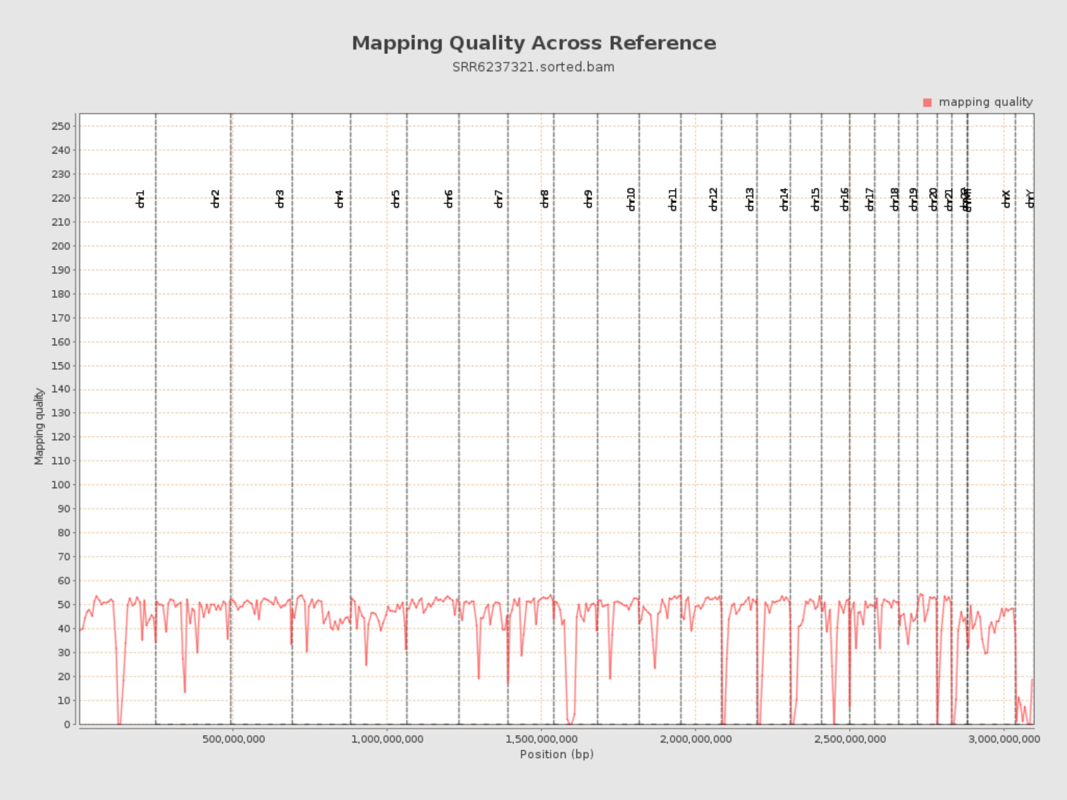
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram