# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/15 17:43:26*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230331.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_SRR6230331 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230331.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 15 17:43:25 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6230331.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,491,430 |
| Mapped reads | 2,879,788 / 82.48% |
| Unmapped reads | 611,642 / 17.52% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 40,888 / 1.17% |
| Read min/max/mean length | 30 / 76 / 76.41 |
| Duplicated reads (estimated) | 790,932 / 22.65% |
| Duplication rate | 14.82% |
| Clipped reads | 1,594,539 / 45.67% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 50,340,094 / 27.12% |
| Number/percentage of C's | 34,857,279 / 18.78% |
| Number/percentage of T's | 57,930,417 / 31.2% |
| Number/percentage of G's | 42,440,127 / 22.86% |
| Number/percentage of N's | 76,840 / 0.04% |
| GC Percentage | 41.64% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.06 |
| | |

| | |
|---|---|
| Standard Deviation | 0.929 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.05 |

## 2.5. Mismatches and indels

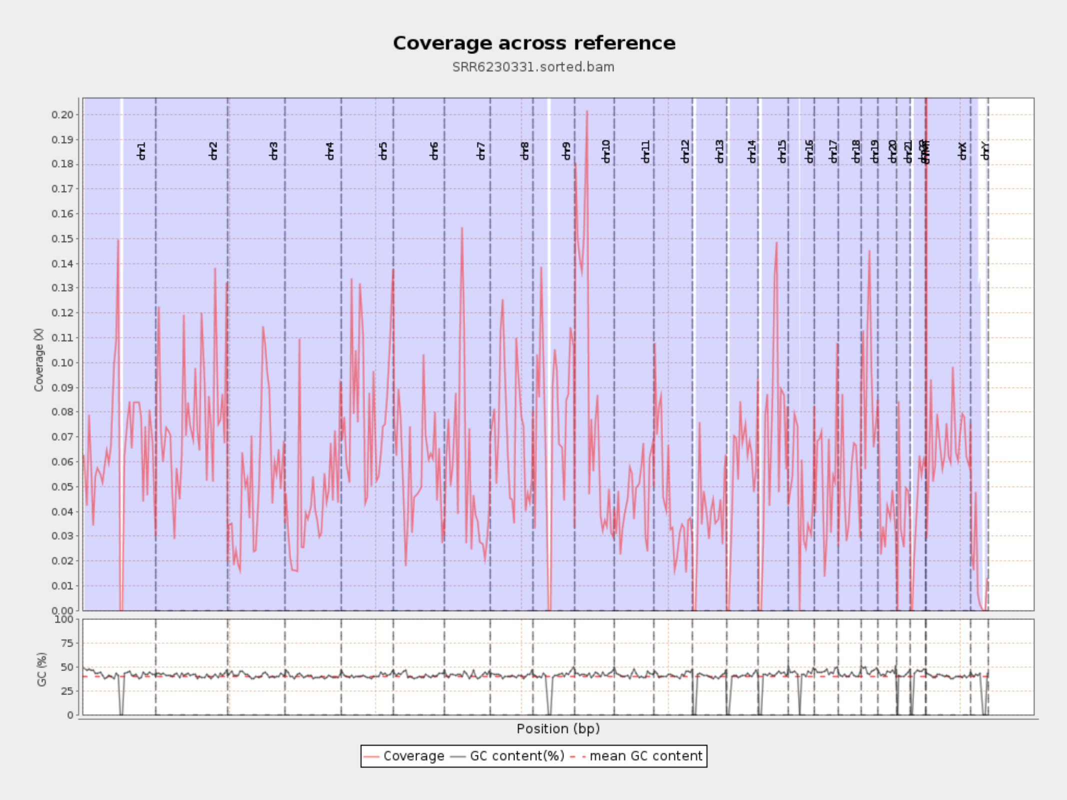
| | |
|---|---|
| General error rate | 0.95% |
| Mismatches | 1,726,768 |
| Insertions | 17,212 |
| Mapped reads with at least one insertion | 0.59% |
| Deletions | 49,519 |
| Mapped reads with at least one deletion | 1.7% |
| Homopolymer indels | 46.28% |

## 2.6. Chromosome stats

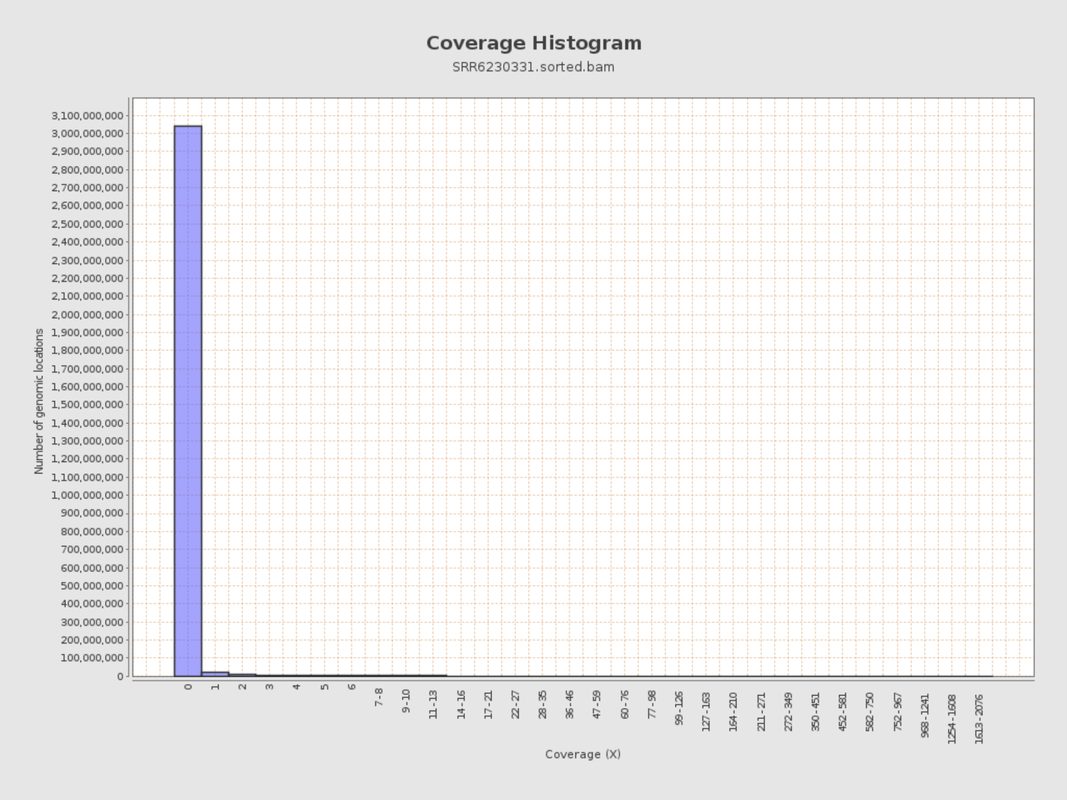
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 16099720 | 0.0646 | 1.7112 |
| chr2 | 243199373 | 18884824 | 0.0777 | 1.0668 |
| chr3 | 198022430 | 10529341 | 0.0532 | 0.5981 |
| chr4 | 191154276 | 8278409 | 0.0433 | 0.6583 |
| chr5 | 180915260 | 14794065 | 0.0818 | 0.7514 |
| chr6 | 171115067 | 9833668 | 0.0575 | 0.7151 |
| chr7 | 159138663 | 8988035 | 0.0565 | 1.2026 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 10350577 | 0.0707 | 1.0662 |
| chr9 | 141213431 | 10902904 | 0.0772 | 0.8464 |
| chr10 | 135534747 | 11793830 | 0.087 | 1.0716 |
| chr11 | 135006516 | 6171410 | 0.0457 | 0.6675 |
| chr12 | 133851895 | 6143898 | 0.0459 | 0.5658 |
| chr13 | 115169878 | 4324582 | 0.0375 | 0.5116 |
| chr14 | 107349540 | 5948016 | 0.0554 | 0.636 |
| chr15 | 102531392 | 7114597 | 0.0694 | 0.6911 |
| chr16 | 90354753 | 3964758 | 0.0439 | 0.5952 |
| chr17 | 81195210 | 4298729 | 0.0529 | 0.6165 |
| chr18 | 78077248 | 4028953 | 0.0516 | 1.3977 |
| chr19 | 59128983 | 5609072 | 0.0949 | 1.2148 |
| chr20 | 63025520 | 2396596 | 0.038 | 0.5606 |
| chr21 | 48129895 | 2044477 | 0.0425 | 0.5981 |
| chr22 | 51304566 | 2012387 | 0.0392 | 0.5002 |
| chrMT | 16571 | 37501 | 2.263 | 5.0735 |
| chrX | 155270560 | 10390146 | 0.0669 | 0.7057 |
| chrY | 59373566 | 787742 | 0.0133 | 0.4445 |

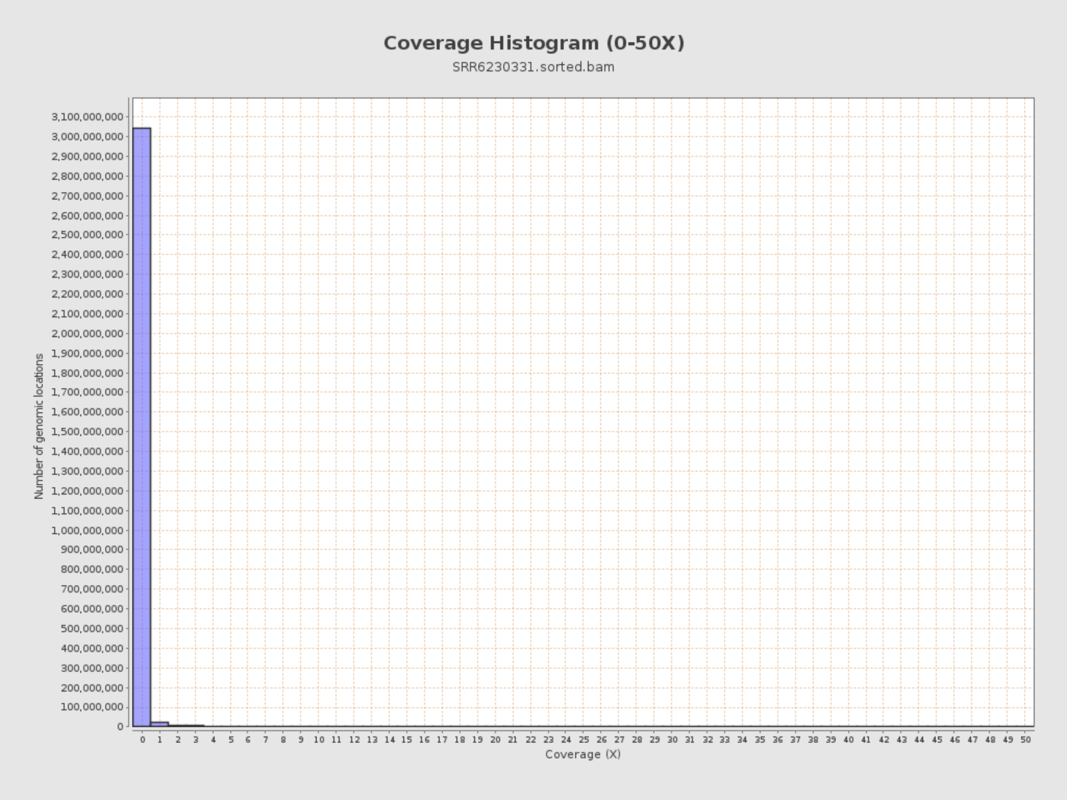
# 3. Results : Coverage across reference



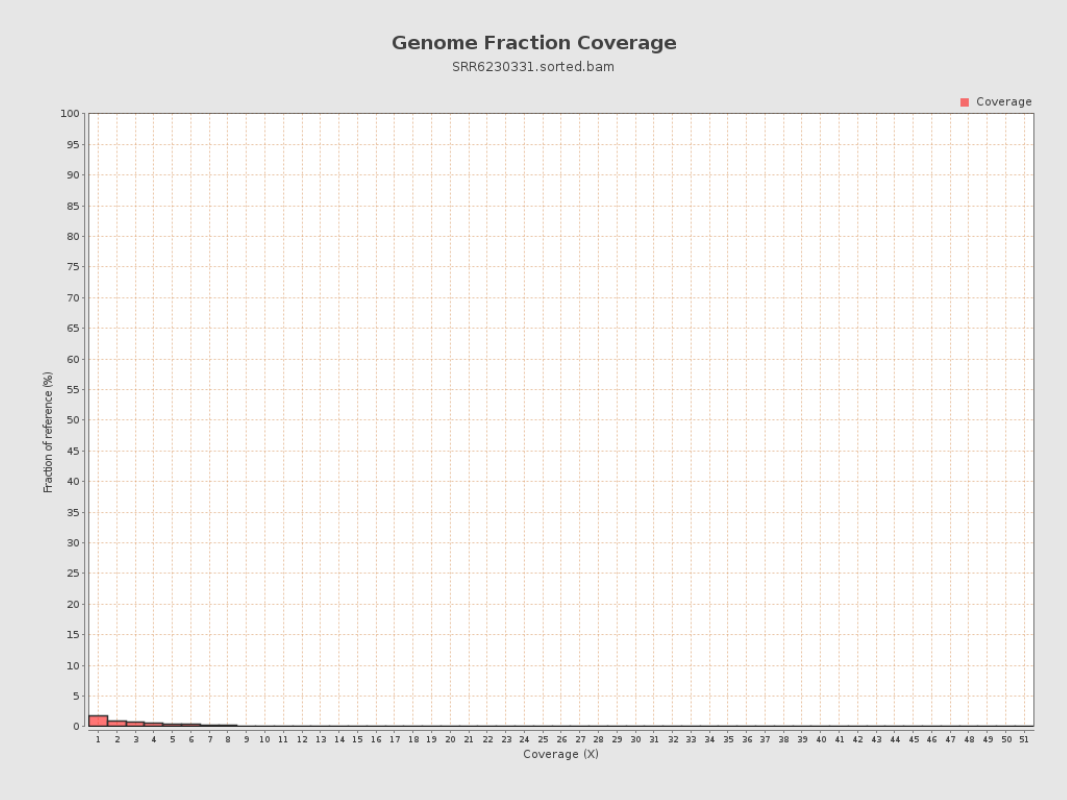
# 4. Results : Coverage Histogram



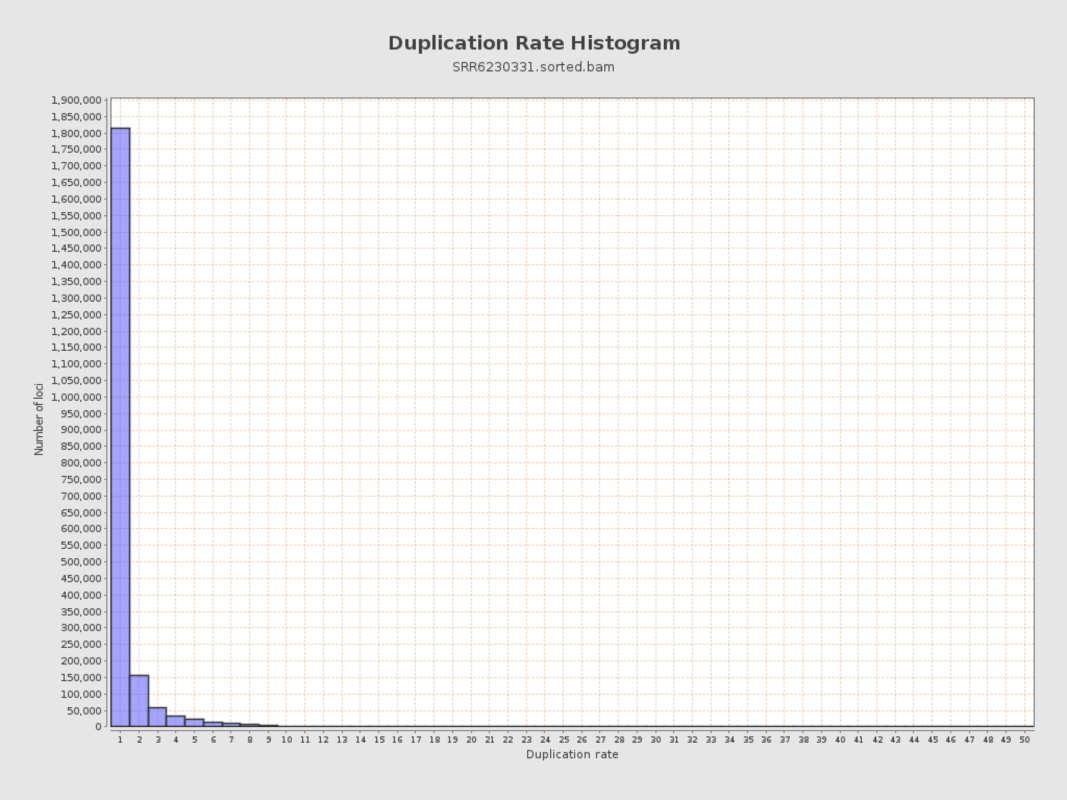
# 5. Results : Coverage Histogram (0-50X)



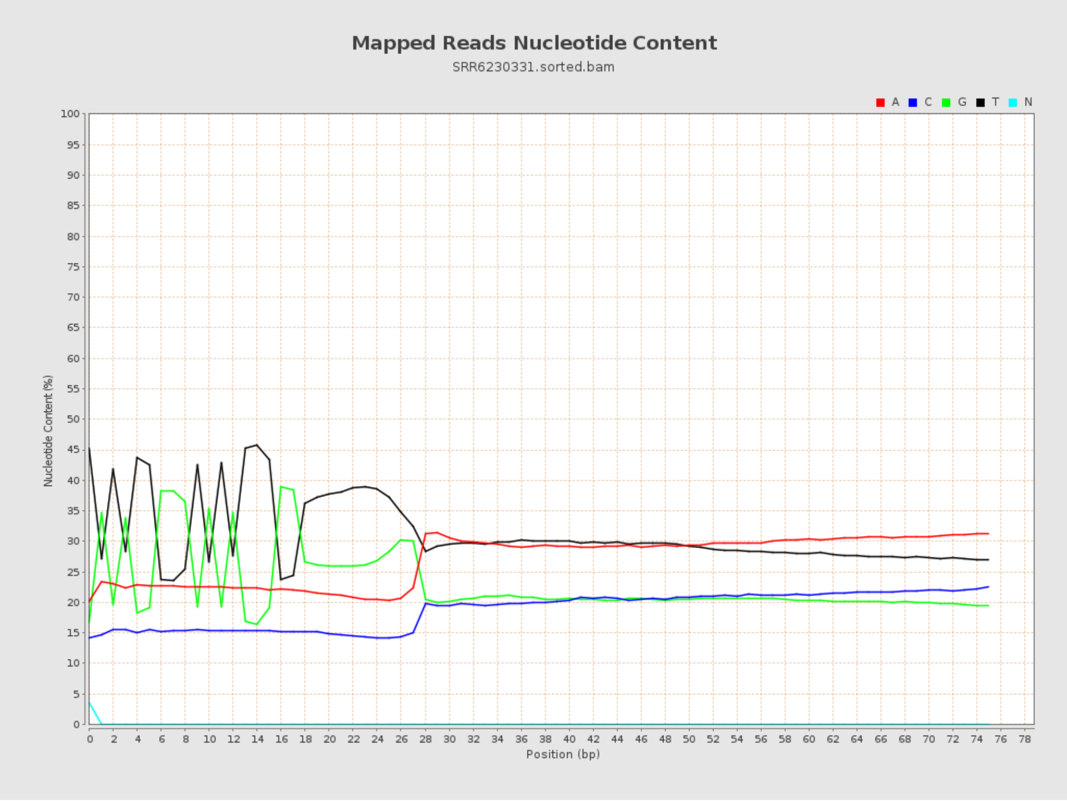
# 6. Results : Genome Fraction Coverage



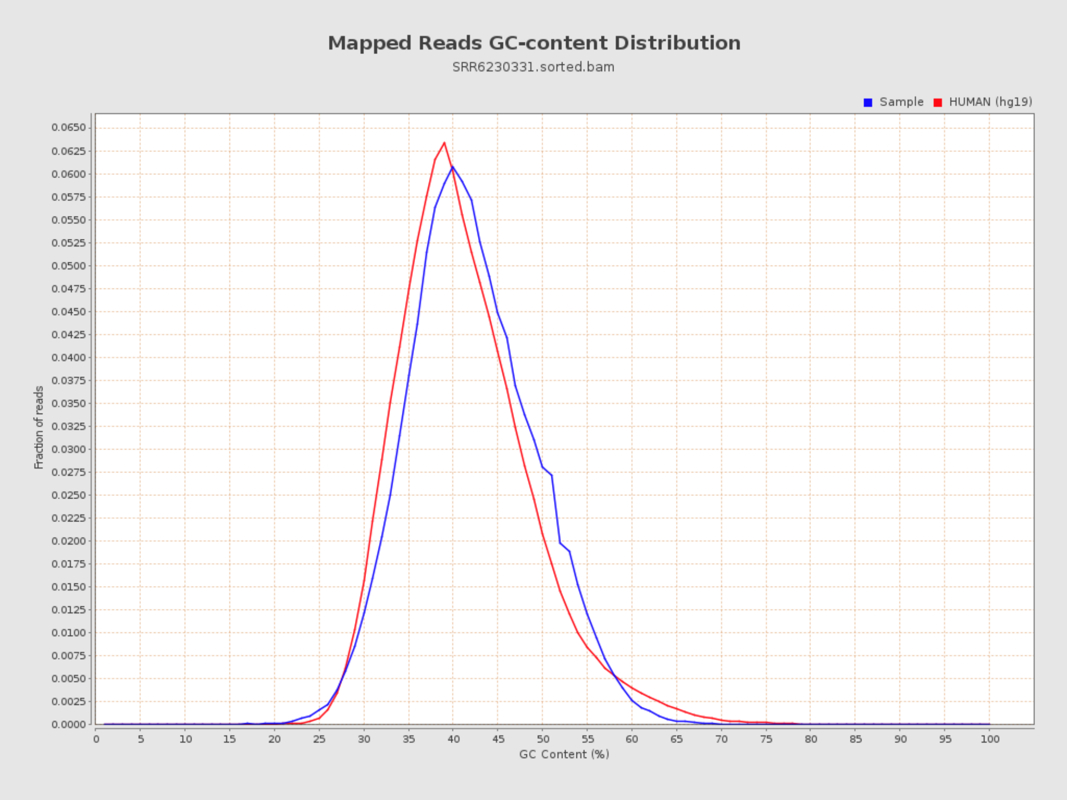
# 7. Results : Duplication Rate Histogram



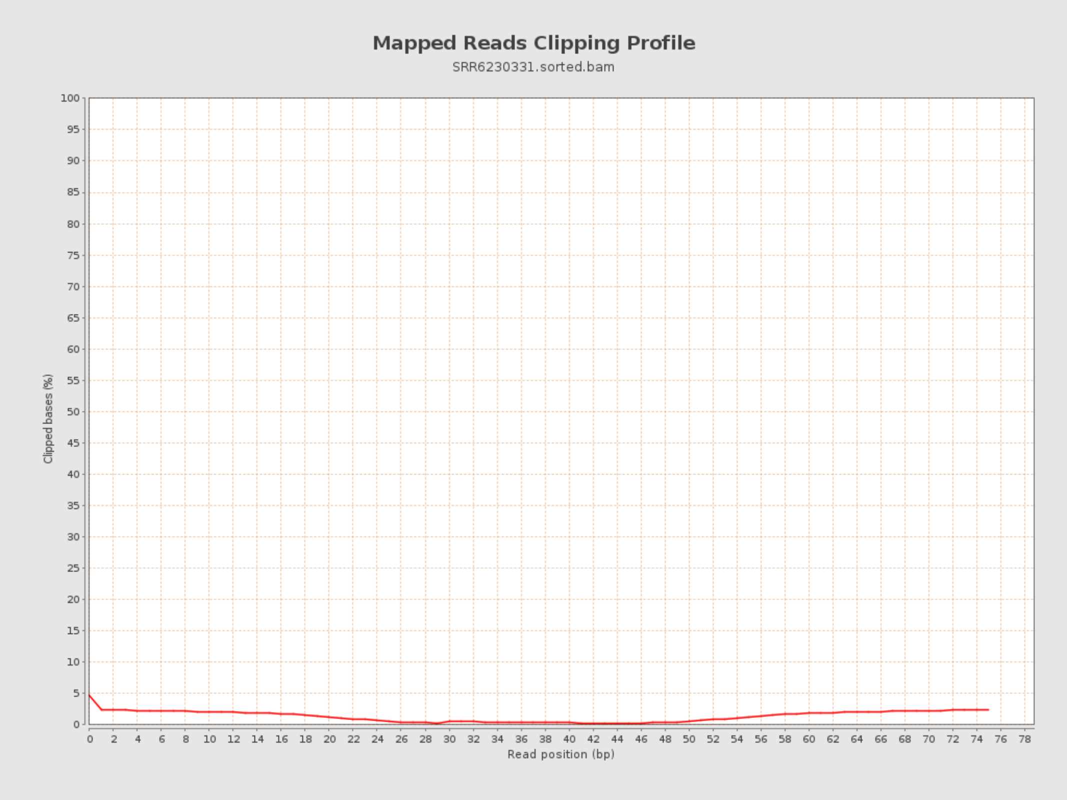
# 8. Results : Mapped Reads Nucleotide Content



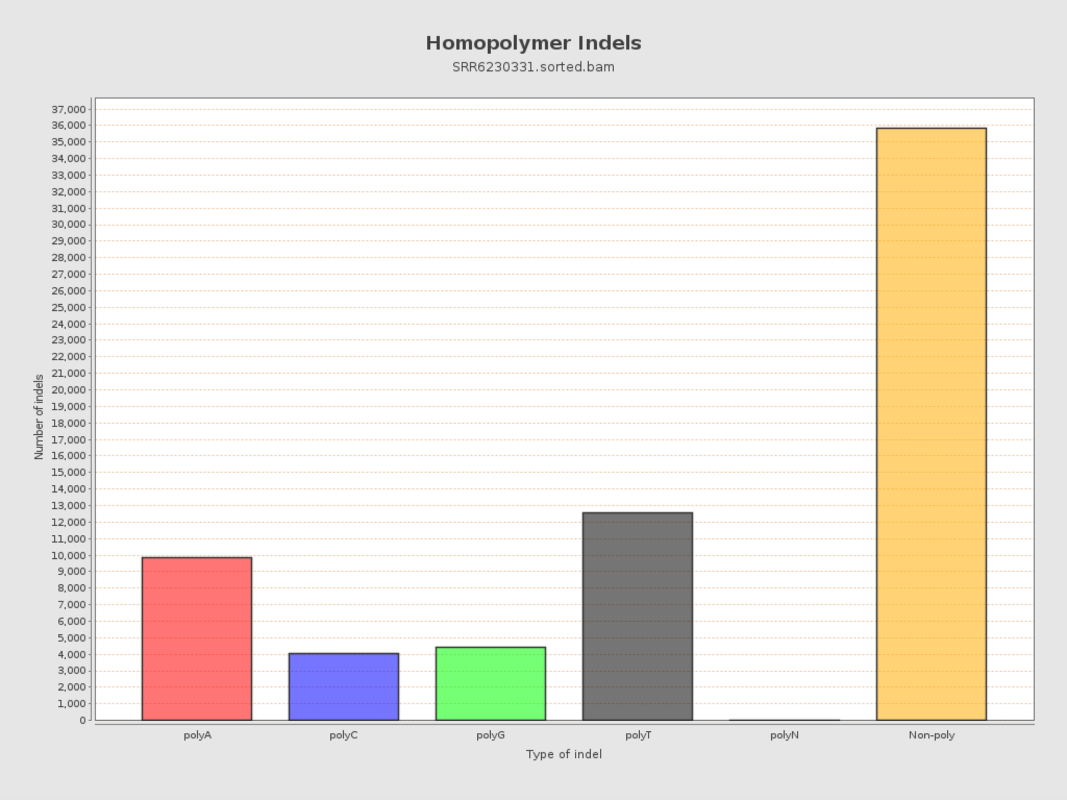
# 9. Results : Mapped Reads GC-content Distribution



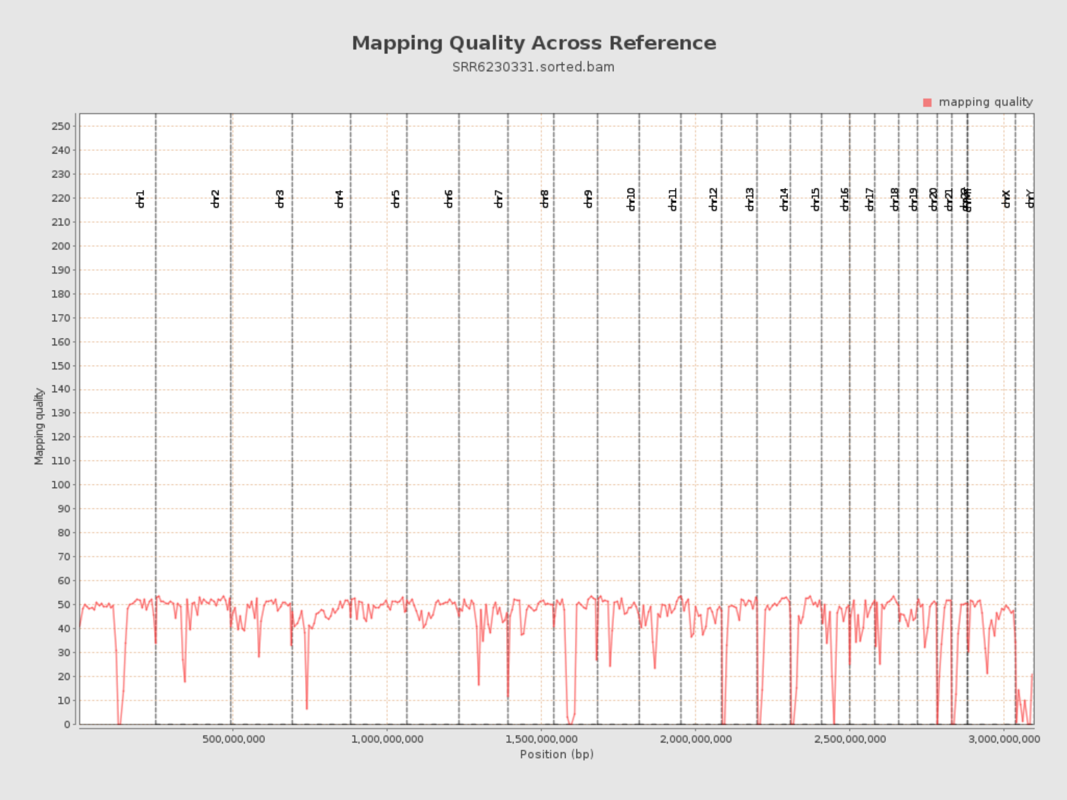
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram