# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/15 19:31:15*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230363.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_SRR6230363 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230363.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 15 19:31:15 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6230363.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,219,788 |
| Mapped reads | 2,930,256 / 91.01% |
| Unmapped reads | 289,532 / 8.99% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 24,329 / 0.76% |
| Read min/max/mean length | 30 / 76 / 76.26 |
| Duplicated reads (estimated) | 146,194 / 4.54% |
| Duplication rate | 3.5% |
| Clipped reads | 1,179,030 / 36.62% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 57,089,476 / 28.71% |
| Number/percentage of C's | 37,856,997 / 19.04% |
| Number/percentage of T's | 61,260,558 / 30.81% |
| Number/percentage of G's | 42,532,679 / 21.39% |
| Number/percentage of N's | 106,291 / 0.05% |
| GC Percentage | 40.43% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0643 |
| | |

| | |
|---|---|
| Standard Deviation | 0.6586 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.22 |

## 2.5. Mismatches and indels

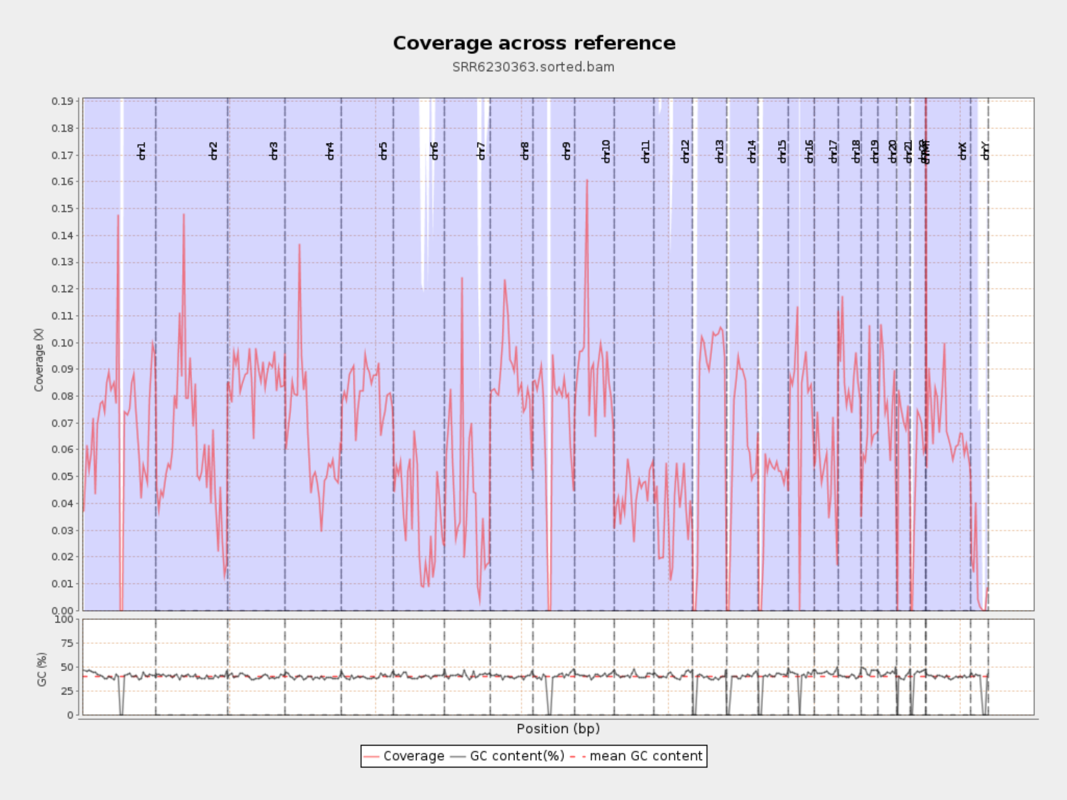
| | |
|---|---|
| General error rate | 0.92% |
| Mismatches | 1,802,263 |
| Insertions | 17,867 |
| Mapped reads with at least one insertion | 0.6% |
| Deletions | 53,405 |
| Mapped reads with at least one deletion | 1.8% |
| Homopolymer indels | 45.76% |

## 2.6. Chromosome stats

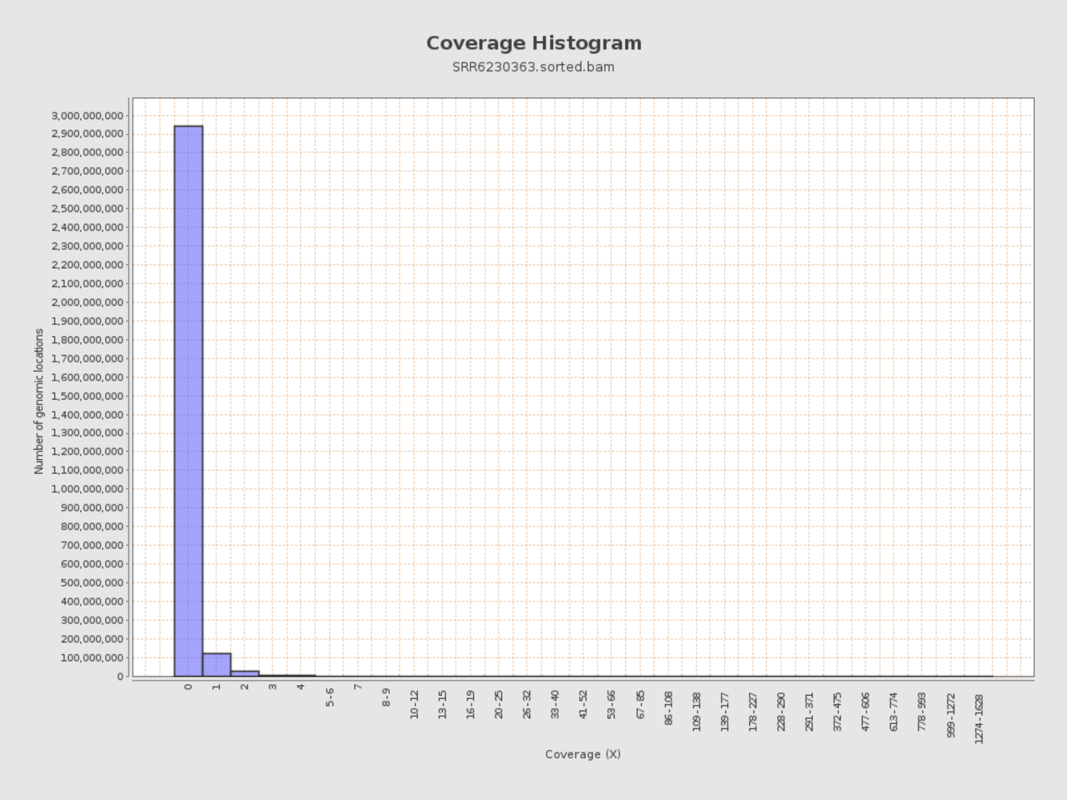
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 17070268 | 0.0685 | 1.4464 |
| chr2 | 243199373 | 14538669 | 0.0598 | 0.7033 |
| chr3 | 198022430 | 17402348 | 0.0879 | 0.3734 |
| chr4 | 191154276 | 12281290 | 0.0642 | 0.3963 |
| chr5 | 180915260 | 14782989 | 0.0817 | 0.3534 |
| chr6 | 171115067 | 5953848 | 0.0348 | 0.2557 |
| chr7 | 159138663 | 6710331 | 0.0422 | 0.6644 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 12778044 | 0.0873 | 0.8429 |
| chr9 | 141213431 | 9897956 | 0.0701 | 0.6158 |
| chr10 | 135534747 | 12337207 | 0.091 | 0.7316 |
| chr11 | 135006516 | 5875357 | 0.0435 | 0.3724 |
| chr12 | 133851895 | 4741353 | 0.0354 | 0.2486 |
| chr13 | 115169878 | 9404301 | 0.0817 | 0.3503 |
| chr14 | 107349540 | 6609158 | 0.0616 | 0.3451 |
| chr15 | 102531392 | 4418852 | 0.0431 | 0.2516 |
| chr16 | 90354753 | 7026762 | 0.0778 | 0.483 |
| chr17 | 81195210 | 4238609 | 0.0522 | 0.3214 |
| chr18 | 78077248 | 6943047 | 0.0889 | 1.2315 |
| chr19 | 59128983 | 3958214 | 0.0669 | 0.9288 |
| chr20 | 63025520 | 5071328 | 0.0805 | 0.3797 |
| chr21 | 48129895 | 3083794 | 0.0641 | 0.382 |
| chr22 | 51304566 | 2509849 | 0.0489 | 0.2699 |
| chrMT | 16571 | 3706 | 0.2236 | 0.5262 |
| chrX | 155270560 | 10665560 | 0.0687 | 0.3863 |
| chrY | 59373566 | 634958 | 0.0107 | 0.3117 |

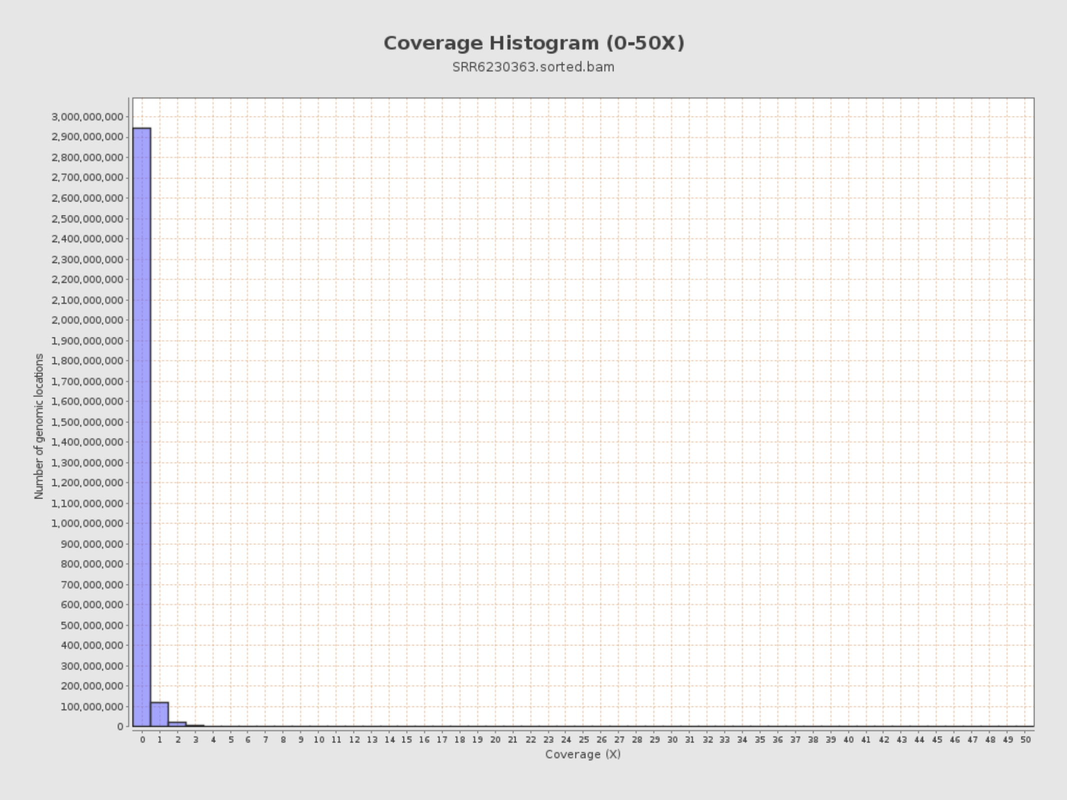
# 3. Results : Coverage across reference



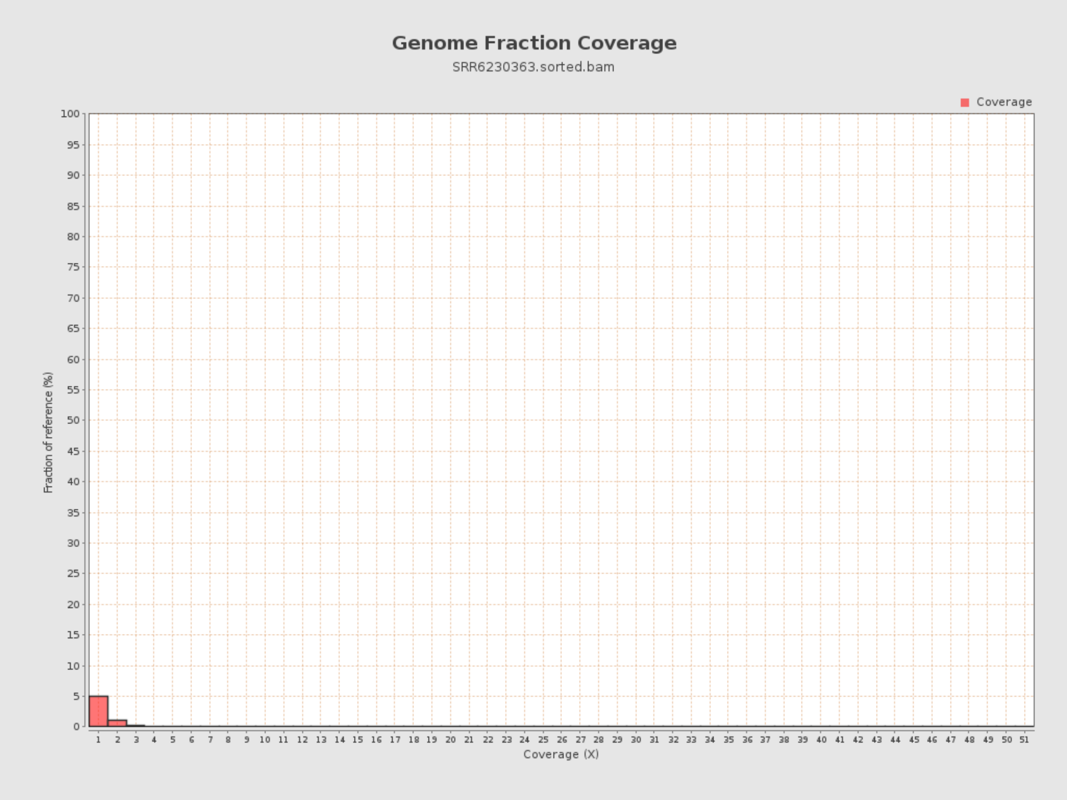
# 4. Results : Coverage Histogram



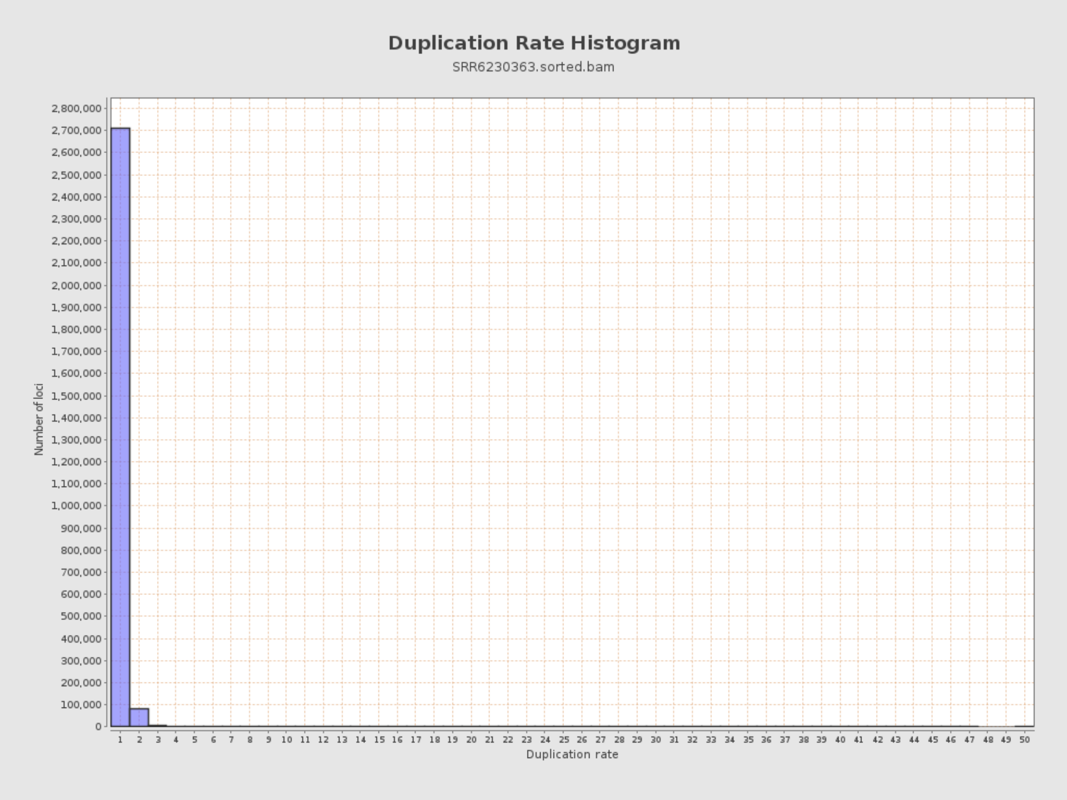
# 5. Results : Coverage Histogram (0-50X)



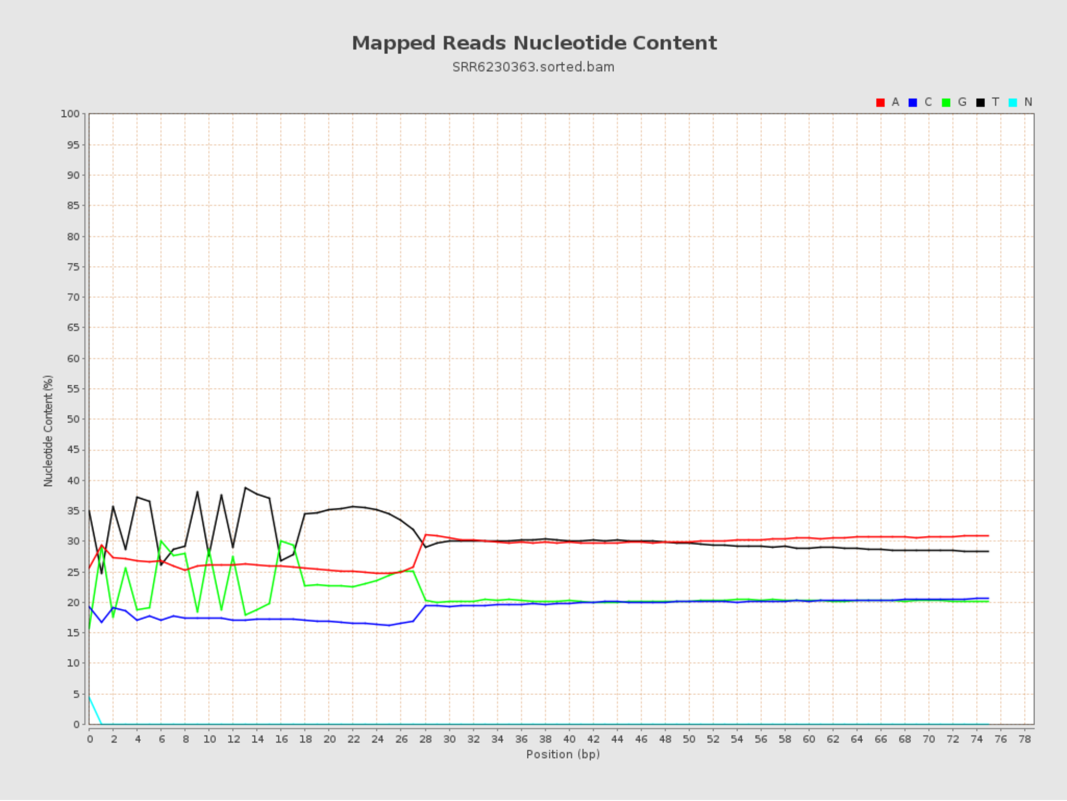
# 6. Results : Genome Fraction Coverage



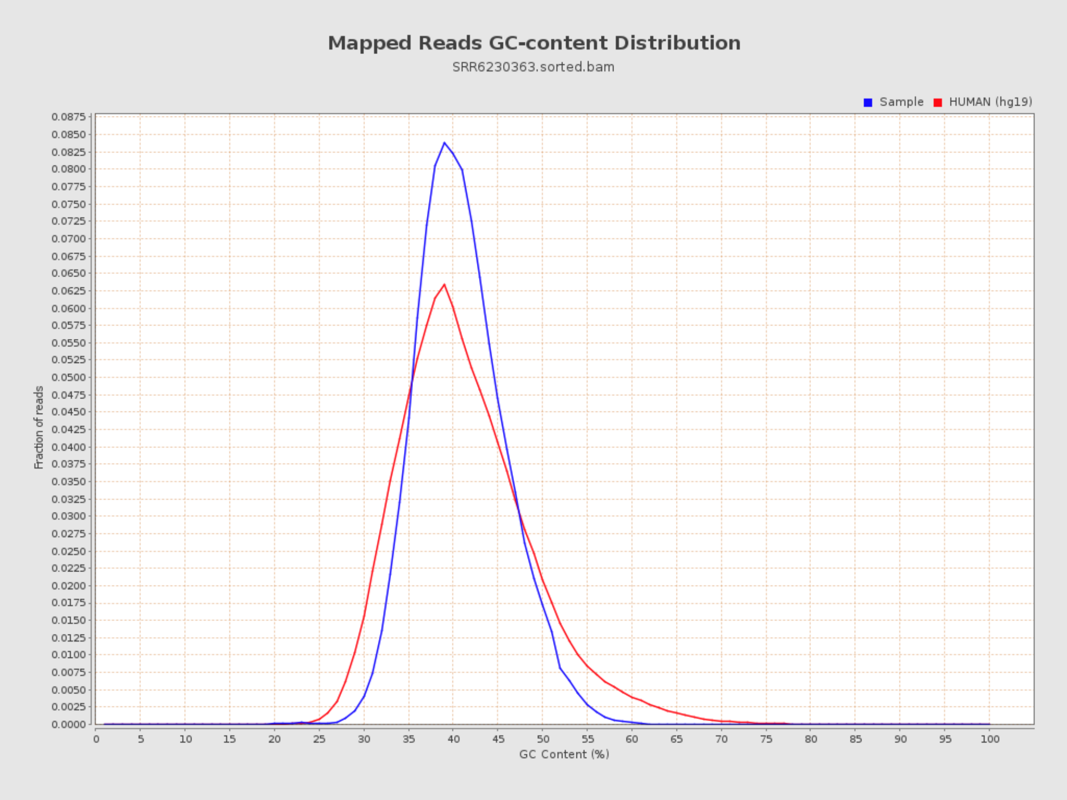
# 7. Results : Duplication Rate Histogram



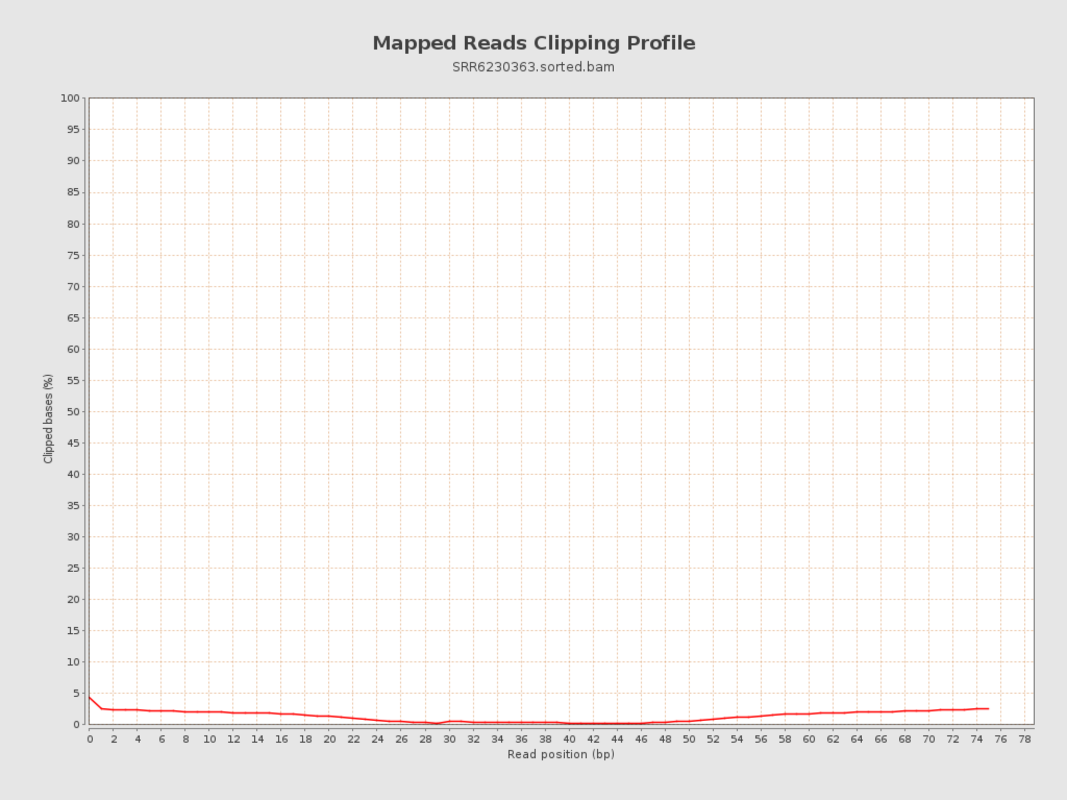
# 8. Results : Mapped Reads Nucleotide Content



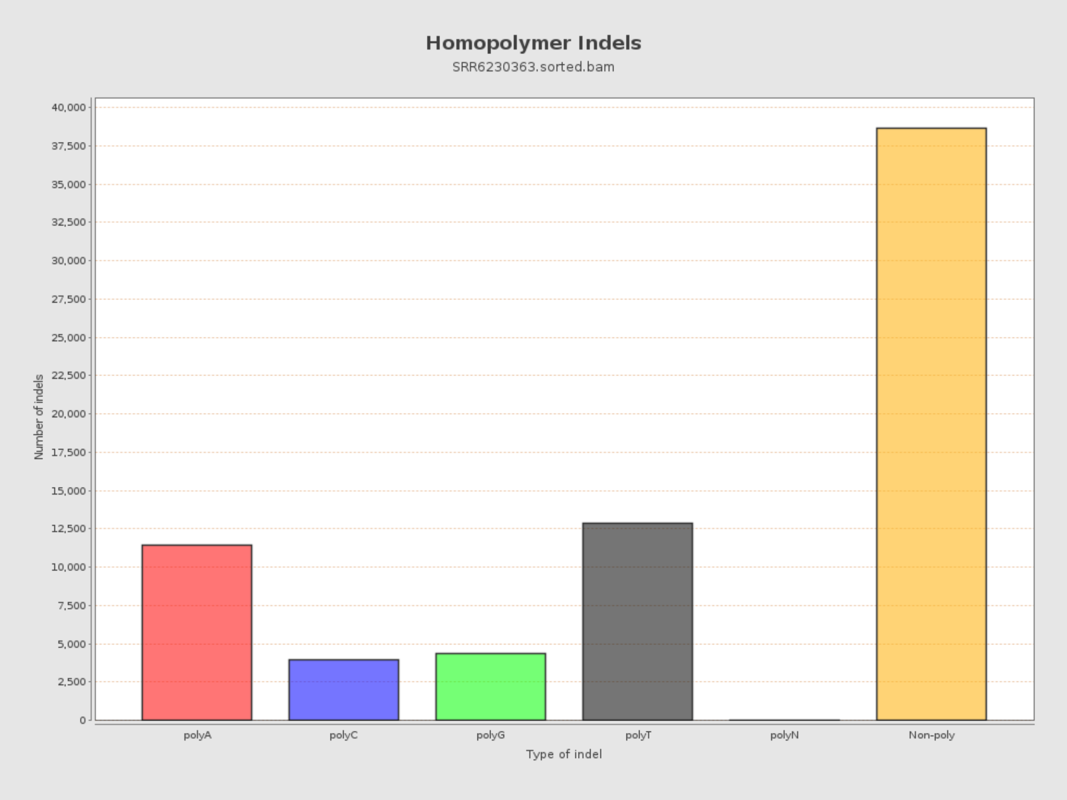
# 9. Results : Mapped Reads GC-content Distribution



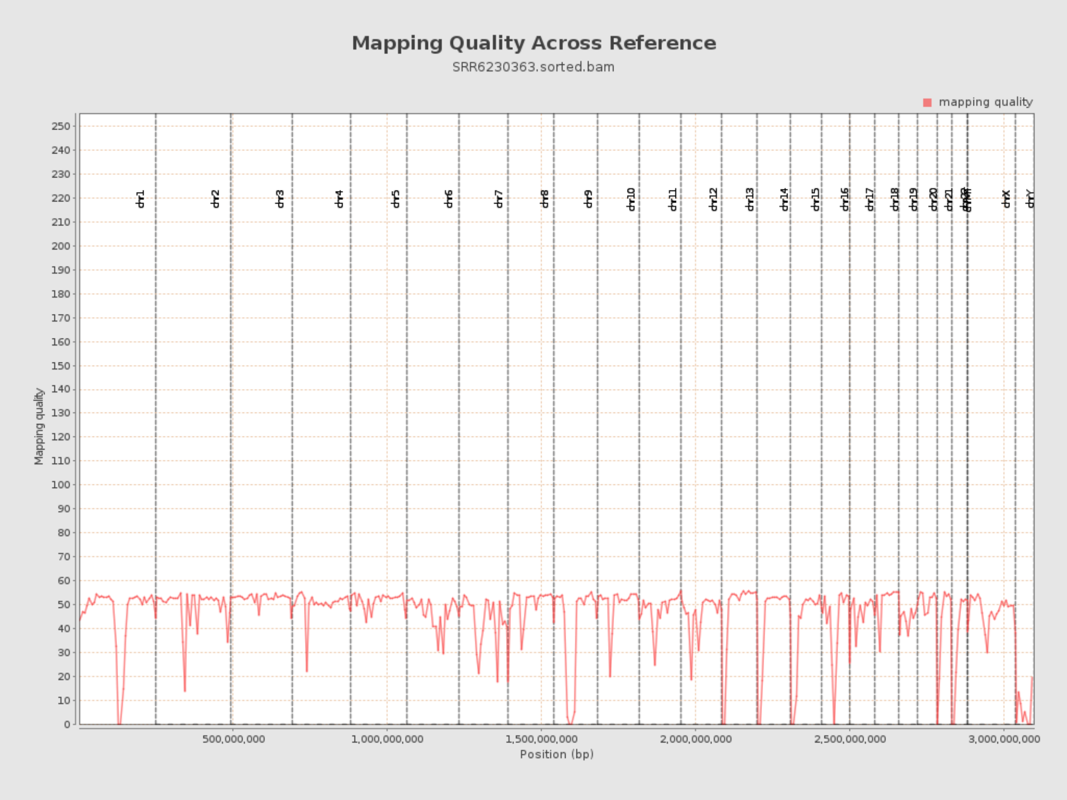
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram