# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 17:18:45*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234122.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_SRR6234122 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234122.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 16 17:18:44 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6234122.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 7,553,614 |
| Mapped reads | 6,625,394 / 87.71% |
| Unmapped reads | 928,220 / 12.29% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 74,524 / 0.99% |
| Read min/max/mean length | 30 / 76 / 76.34 |
| Duplicated reads (estimated) | 1,890,522 / 25.03% |
| Duplication rate | 12.55% |
| Clipped reads | 2,515,063 / 33.3% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 111,187,458 / 24.56% |
| Number/percentage of C's | 78,335,851 / 17.3% |
| Number/percentage of T's | 118,088,767 / 26.08% |
| Number/percentage of G's | 145,036,738 / 32.03% |
| Number/percentage of N's | 99,068 / 0.02% |
| GC Percentage | 49.34% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1463 |
| | |

| | |
|---|---|
| Standard Deviation | 118.8487 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.79 |

## 2.5. Mismatches and indels

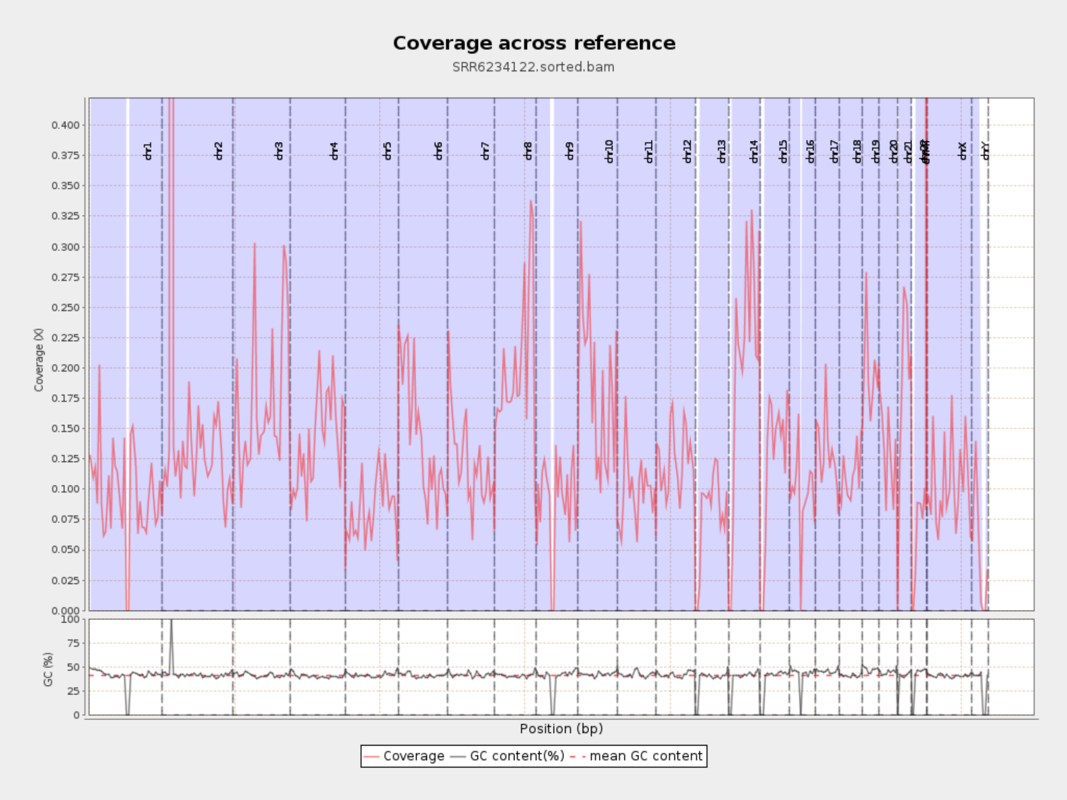
| | |
|---|---|
| General error rate | 0.59% |
| Mismatches | 2,638,673 |
| Insertions | 28,195 |
| Mapped reads with at least one insertion | 0.42% |
| Deletions | 88,444 |
| Mapped reads with at least one deletion | 1.32% |
| Homopolymer indels | 46.19% |

## 2.6. Chromosome stats

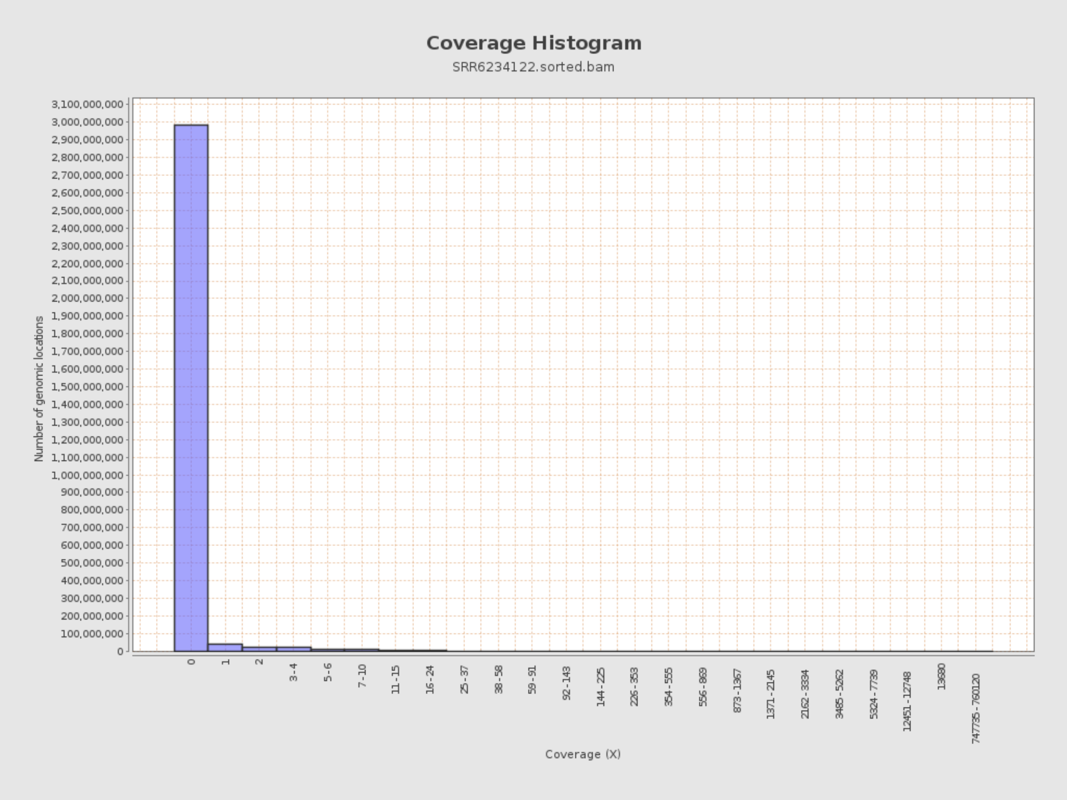
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 23754948 | 0.0953 | 1.6617 |
| chr2 | 243199373 | 89146297 | 0.3666 | 424.0056 |
| chr3 | 198022430 | 33954861 | 0.1715 | 1.1118 |
| chr4 | 191154276 | 26838671 | 0.1404 | 1.0076 |
| chr5 | 180915260 | 15272168 | 0.0844 | 0.7696 |
| chr6 | 171115067 | 24326385 | 0.1422 | 1.3023 |
| chr7 | 159138663 | 19460435 | 0.1223 | 1.2693 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 29647710 | 0.2026 | 1.6351 |
| chr9 | 141213431 | 12844175 | 0.091 | 0.9994 |
| chr10 | 135534747 | 25247733 | 0.1863 | 1.3278 |
| chr11 | 135006516 | 13342242 | 0.0988 | 1.2972 |
| chr12 | 133851895 | 16644371 | 0.1243 | 0.9547 |
| chr13 | 115169878 | 9131005 | 0.0793 | 0.7562 |
| chr14 | 107349540 | 21607781 | 0.2013 | 1.3475 |
| chr15 | 102531392 | 12601818 | 0.1229 | 0.968 |
| chr16 | 90354753 | 8617753 | 0.0954 | 0.8673 |
| chr17 | 81195210 | 10716669 | 0.132 | 1.0281 |
| chr18 | 78077248 | 8668563 | 0.111 | 1.8191 |
| chr19 | 59128983 | 11617798 | 0.1965 | 1.572 |
| chr20 | 63025520 | 8315330 | 0.1319 | 0.9918 |
| chr21 | 48129895 | 8877906 | 0.1845 | 1.2161 |
| chr22 | 51304566 | 3130866 | 0.061 | 0.6661 |
| chrMT | 16571 | 208651 | 12.5913 | 13.042 |
| chrX | 155270560 | 16072986 | 0.1035 | 0.9041 |
| chrY | 59373566 | 2844798 | 0.0479 | 0.5932 |

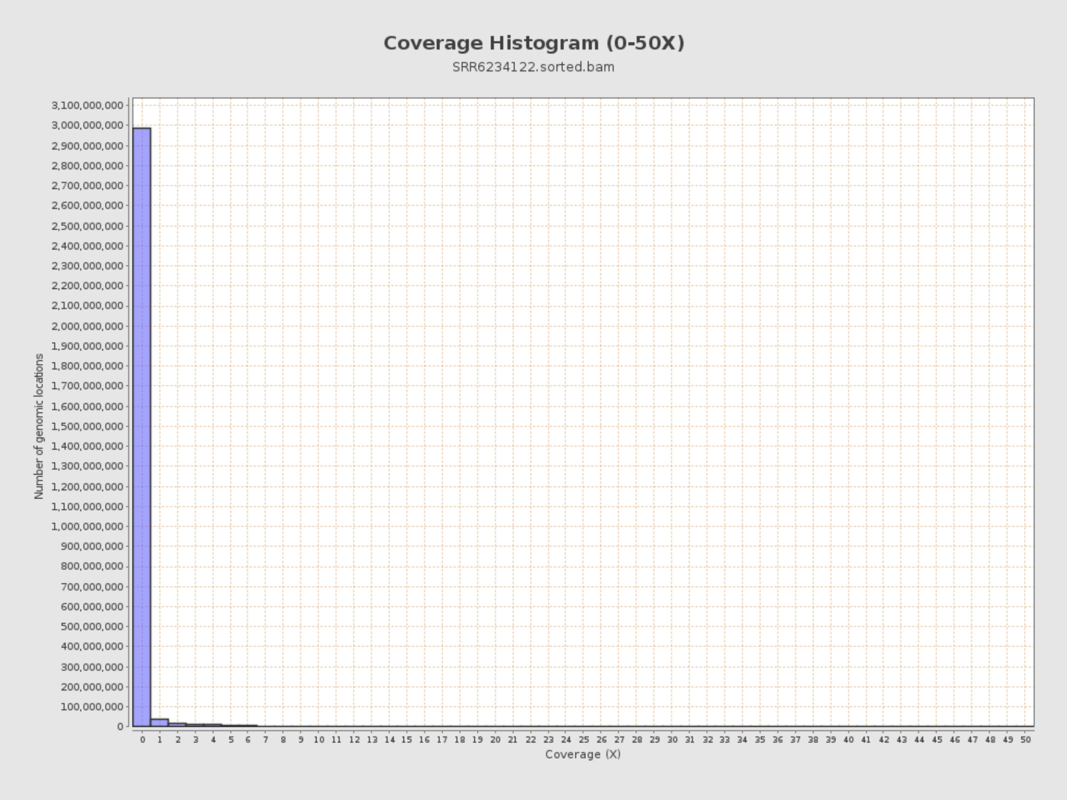
# 3. Results : Coverage across reference



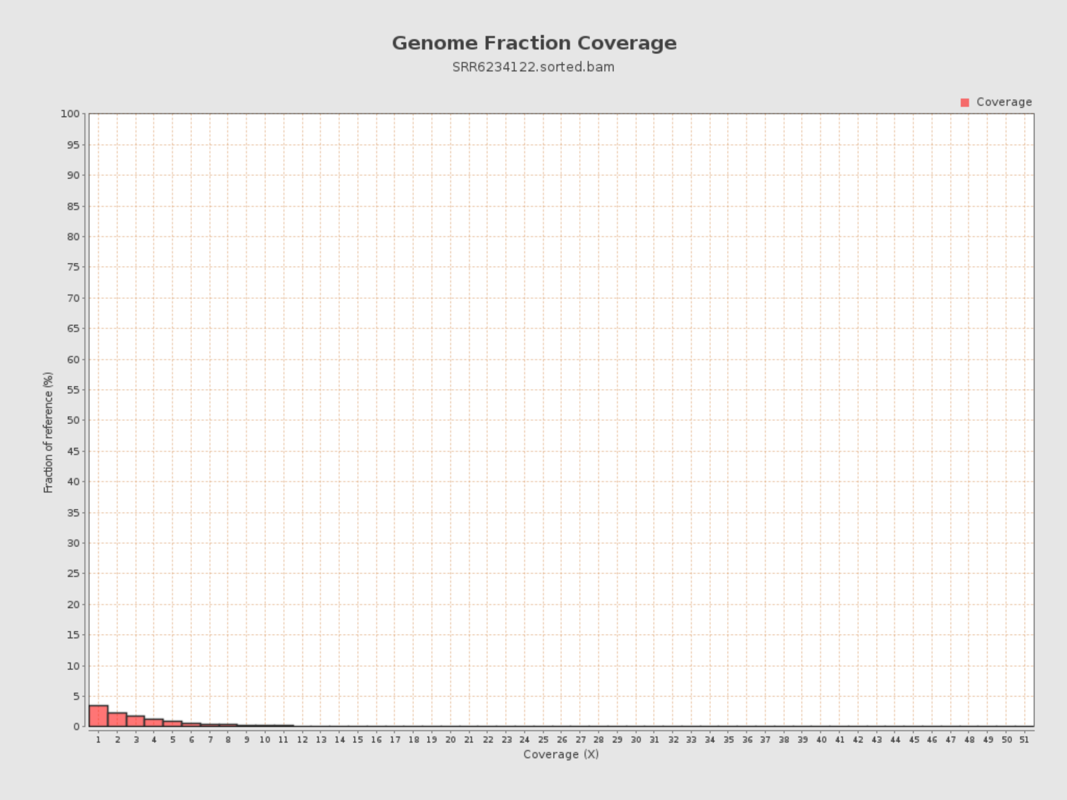
# 4. Results : Coverage Histogram



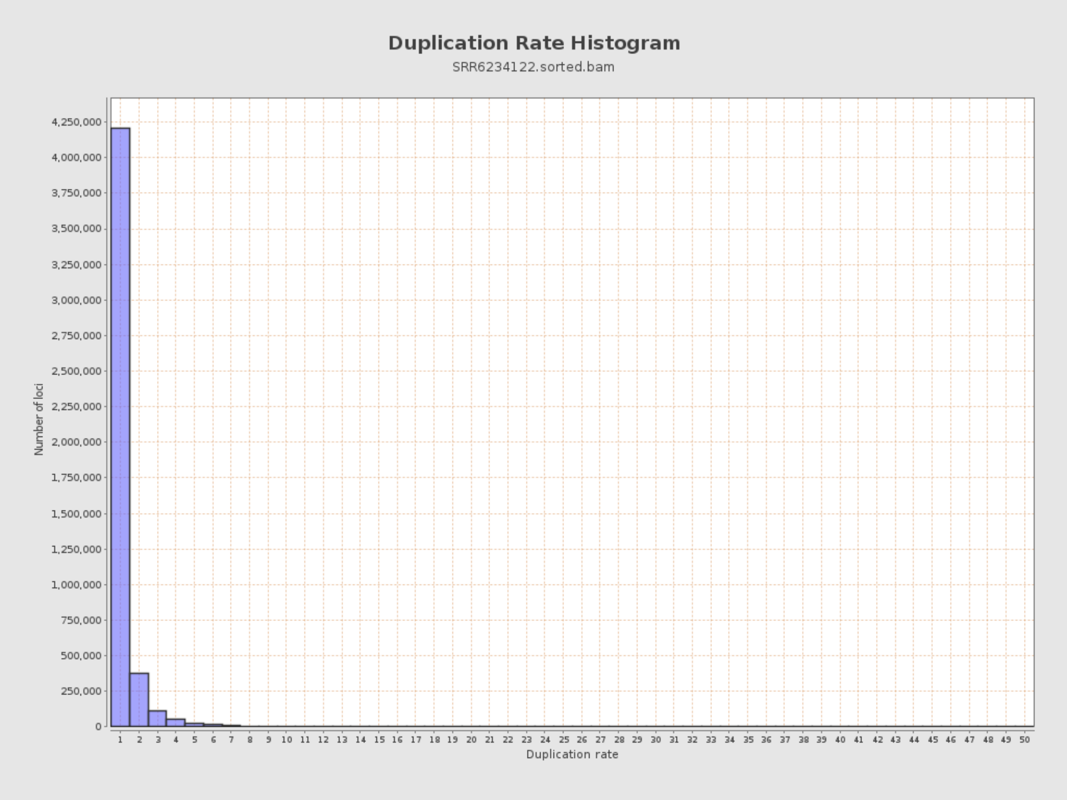
# 5. Results : Coverage Histogram (0-50X)



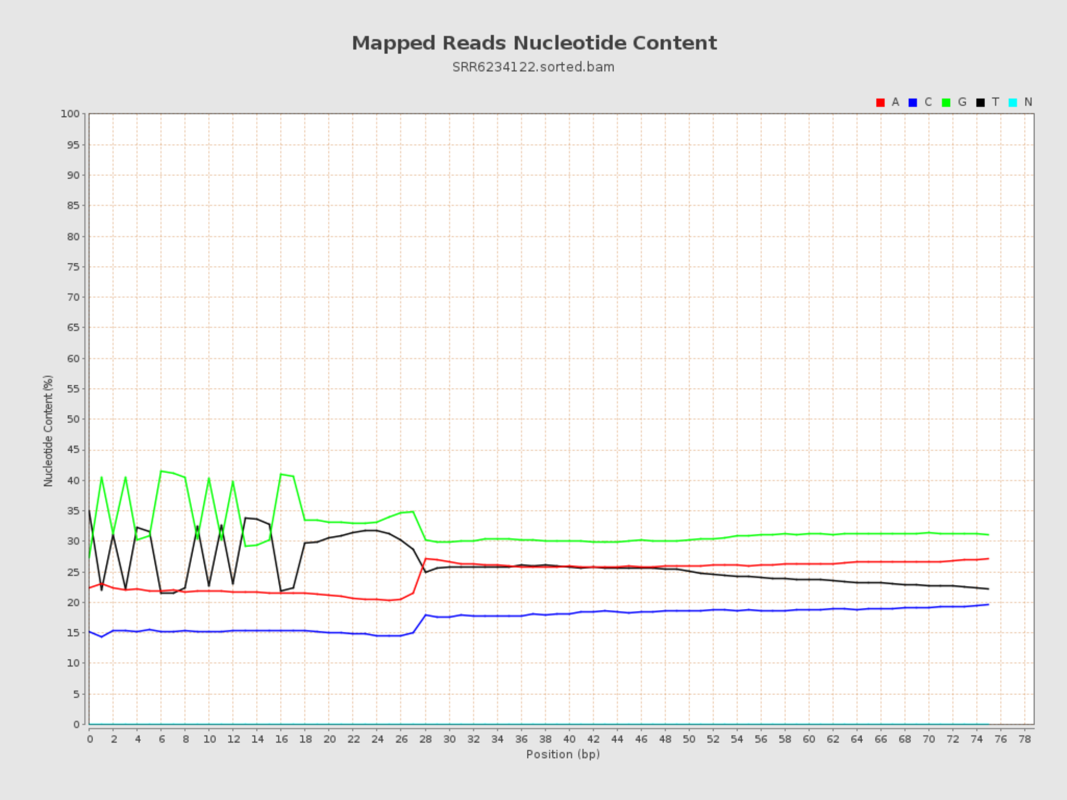
# 6. Results : Genome Fraction Coverage



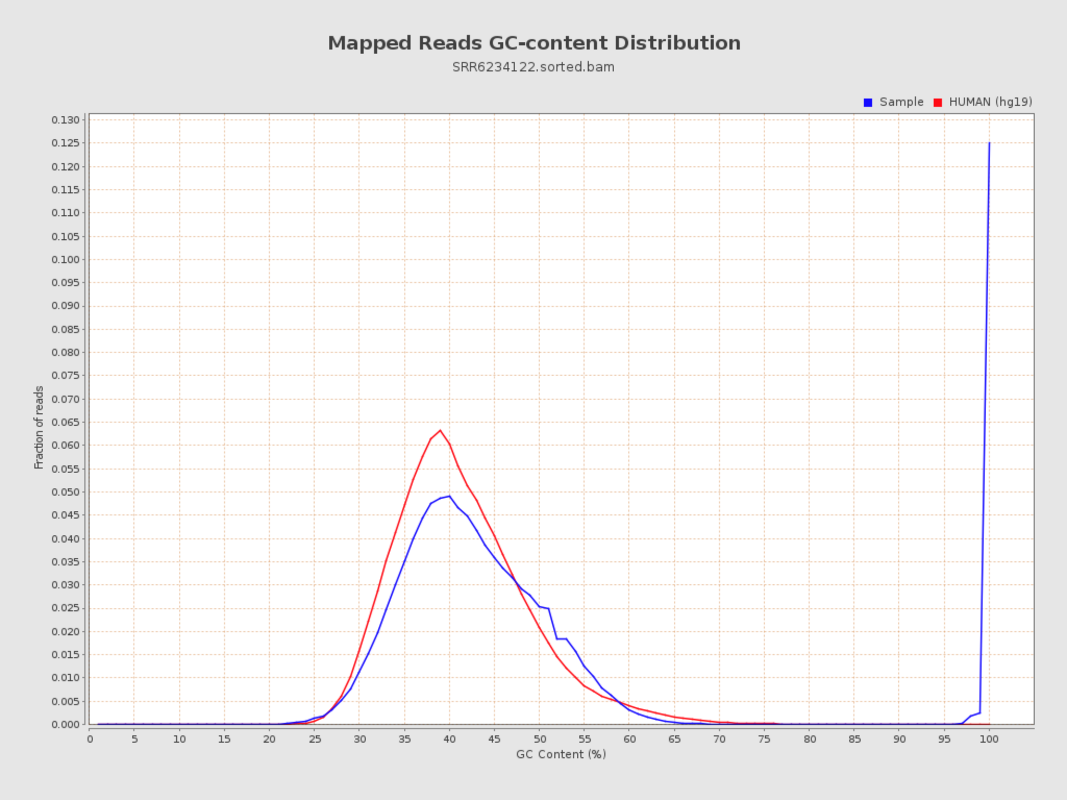
# 7. Results : Duplication Rate Histogram



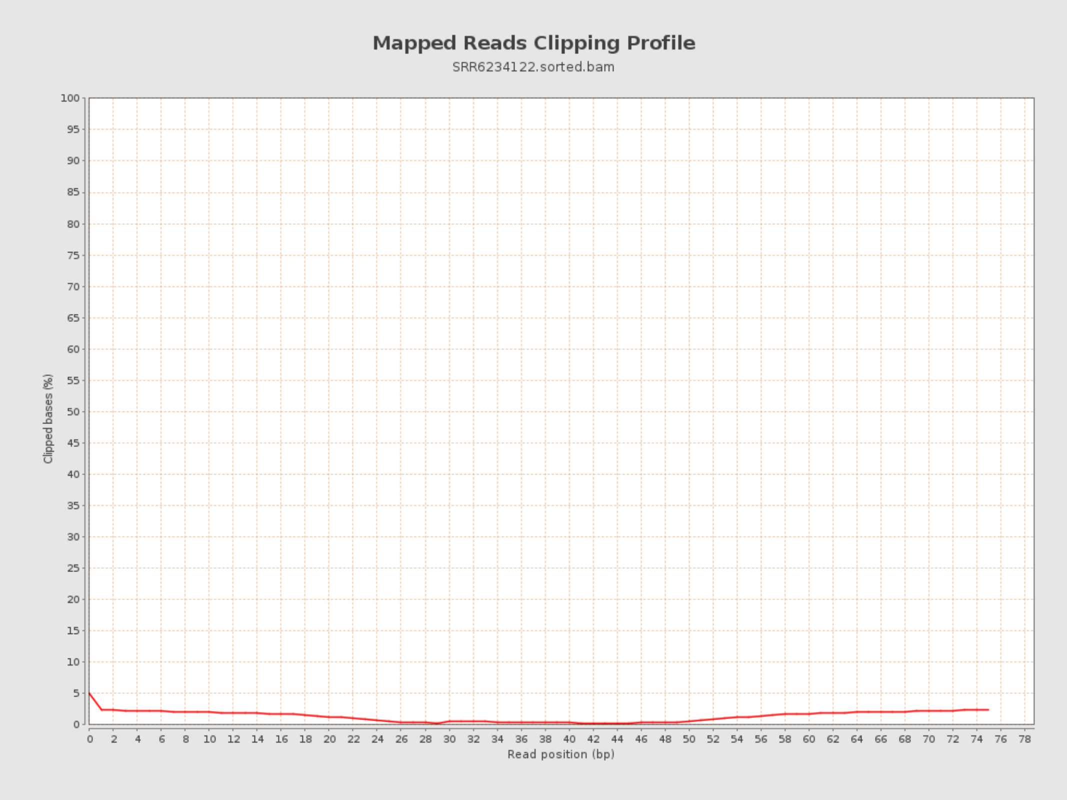
# 8. Results : Mapped Reads Nucleotide Content



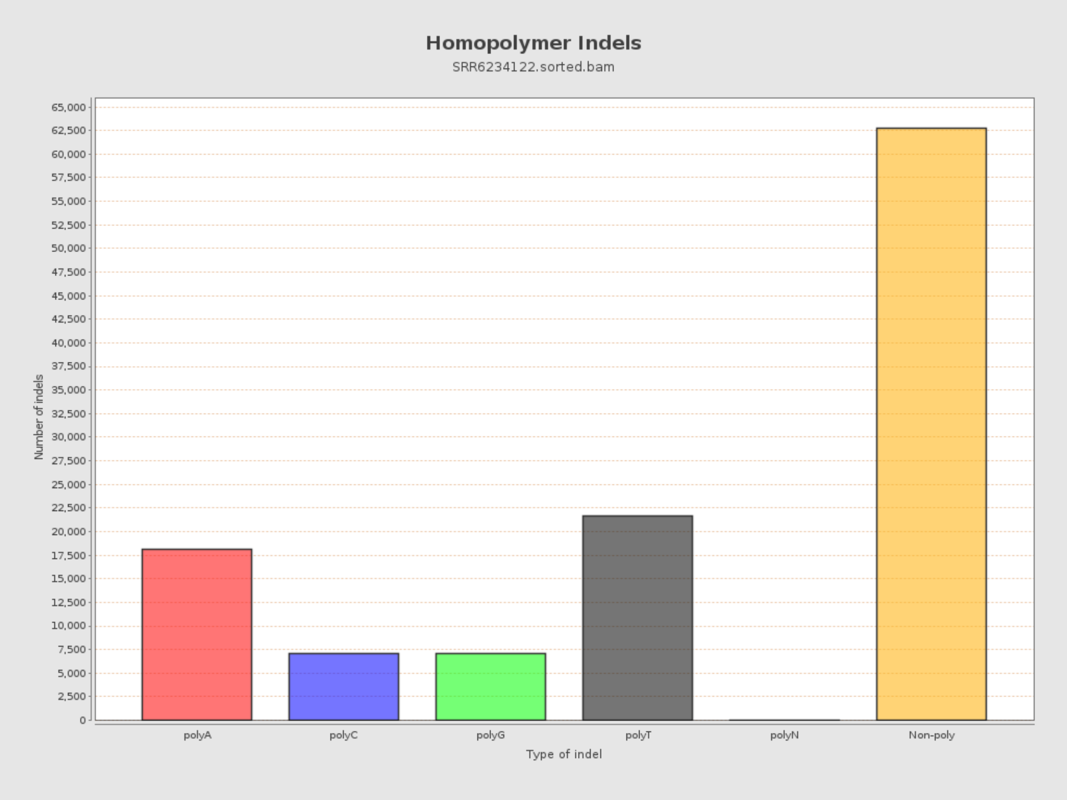
# 9. Results : Mapped Reads GC-content Distribution



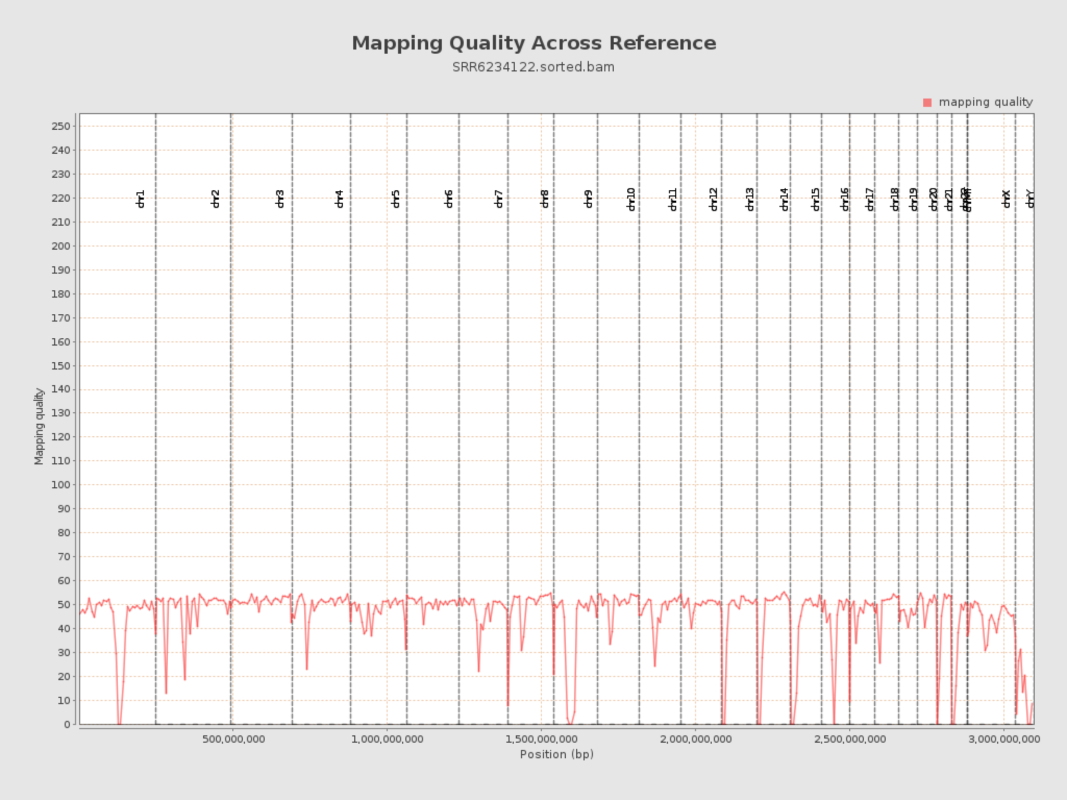
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram