# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/30 11:34:59*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867849.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_SRR9867849 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867849.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 30 11:34:49 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9867849.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 21,336,630 |
| Mapped reads | 20,918,738 / 98.04% |
| Unmapped reads | 417,892 / 1.96% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 132,054 / 0.62% |
| Read min/max/mean length | 30 / 101 / 101.24 |
| Duplicated reads (estimated) | 1,175,387 / 5.51% |
| Duplication rate | 1.56% |
| Clipped reads | 20,964,209 / 98.25% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 531,109,983 / 28.23% |
| Number/percentage of C's | 401,992,651 / 21.37% |
| Number/percentage of T's | 534,979,287 / 28.44% |
| Number/percentage of G's | 413,135,114 / 21.96% |
| Number/percentage of N's | 57,925 / 0% |
| GC Percentage | 43.33% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.6079 |
| | |

| | |
|---|---|
| Standard Deviation | 7.442 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 50.44 |

## 2.5. Mismatches and indels

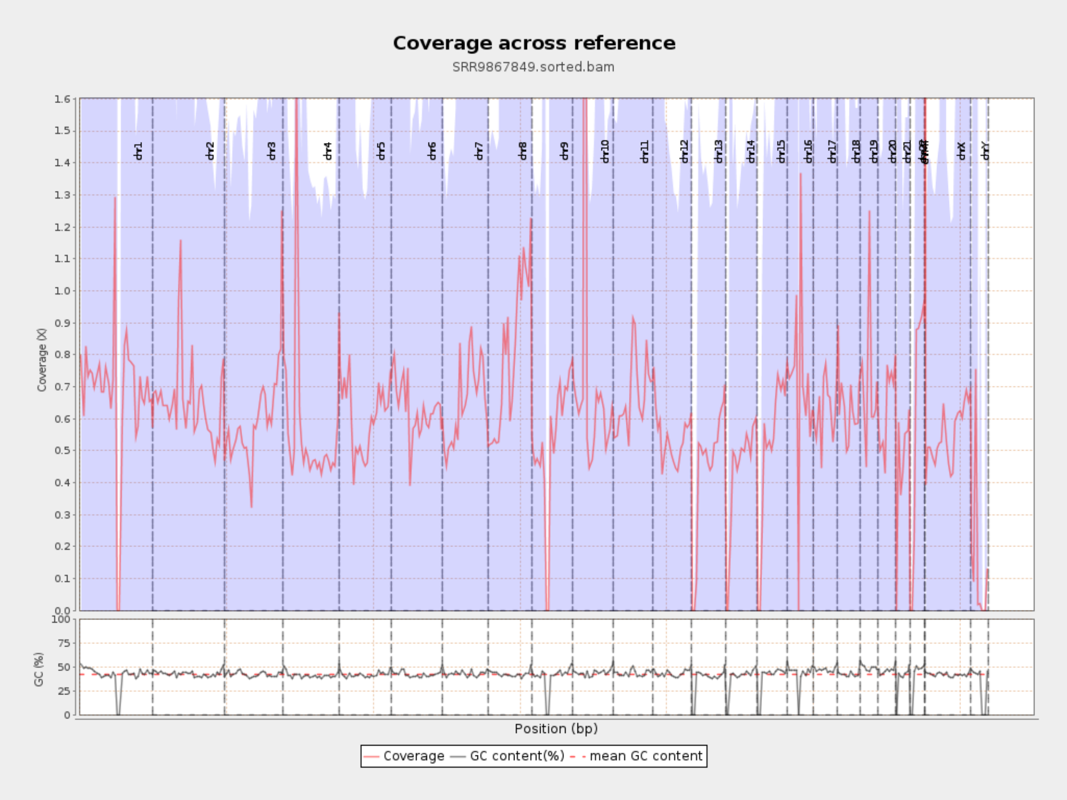
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 9,129,790 |
| Insertions | 198,302 |
| Mapped reads with at least one insertion | 0.93% |
| Deletions | 198,724 |
| Mapped reads with at least one deletion | 0.92% |
| Homopolymer indels | 35.96% |

## 2.6. Chromosome stats

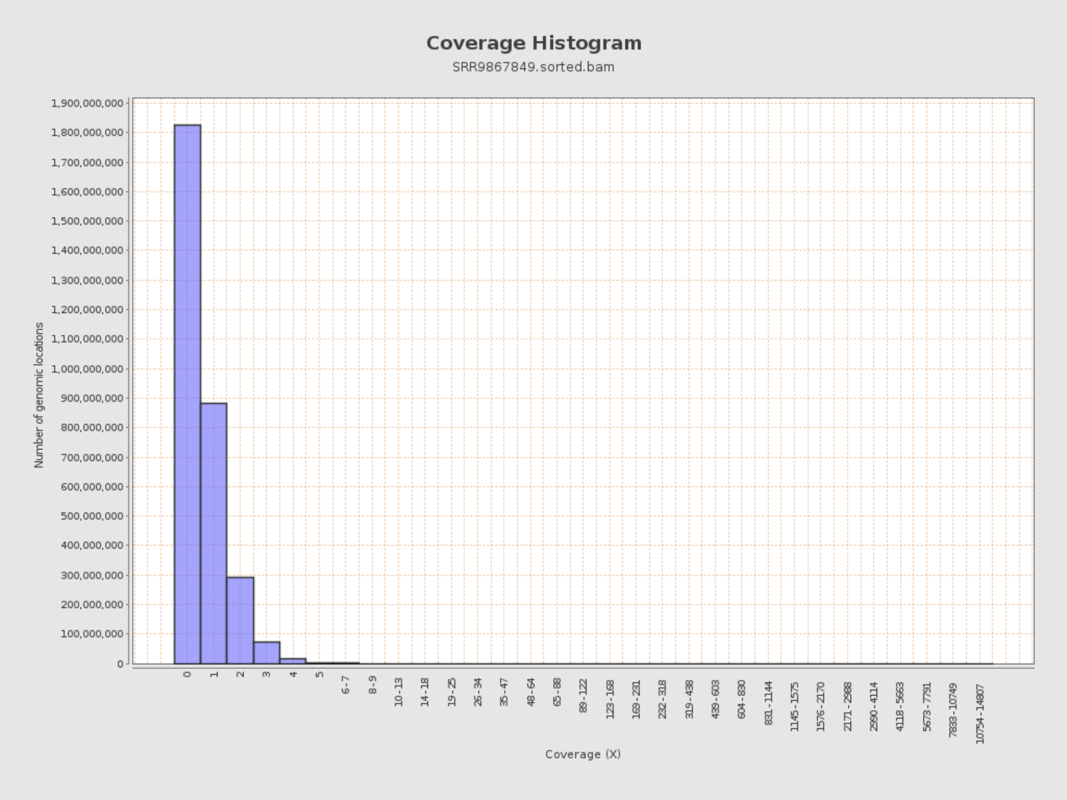
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 171105417 | 0.6865 | 13.4697 |
| chr2 | 243199373 | 159825272 | 0.6572 | 4.7368 |
| chr3 | 198022430 | 116772694 | 0.5897 | 4.7167 |
| chr4 | 191154276 | 106091954 | 0.555 | 6.043 |
| chr5 | 180915260 | 109883483 | 0.6074 | 0.9543 |
| chr6 | 171115067 | 108139197 | 0.632 | 2.01 |
| chr7 | 159138663 | 104198233 | 0.6548 | 4.3635 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 118898852 | 0.8124 | 3.9809 |
| chr9 | 141213431 | 73985537 | 0.5239 | 3.2759 |
| chr10 | 135534747 | 105574693 | 0.7789 | 25.028 |
| chr11 | 135006516 | 91546865 | 0.6781 | 2.3686 |
| chr12 | 133851895 | 72158887 | 0.5391 | 0.9382 |
| chr13 | 115169878 | 51053869 | 0.4433 | 0.7437 |
| chr14 | 107349540 | 46148019 | 0.4299 | 1.0218 |
| chr15 | 102531392 | 51629532 | 0.5035 | 0.8083 |
| chr16 | 90354753 | 64411756 | 0.7129 | 5.5506 |
| chr17 | 81195210 | 51063414 | 0.6289 | 1.9952 |
| chr18 | 78077248 | 48981537 | 0.6273 | 6.414 |
| chr19 | 59128983 | 41742539 | 0.706 | 8.1318 |
| chr20 | 63025520 | 39789440 | 0.6313 | 1.882 |
| chr21 | 48129895 | 22418893 | 0.4658 | 4.2955 |
| chr22 | 51304566 | 31775632 | 0.6194 | 0.9999 |
| chrMT | 16571 | 1125359 | 67.9114 | 22.1239 |
| chrX | 155270560 | 84679315 | 0.5454 | 1.6751 |
| chrY | 59373566 | 8788197 | 0.148 | 7.891 |

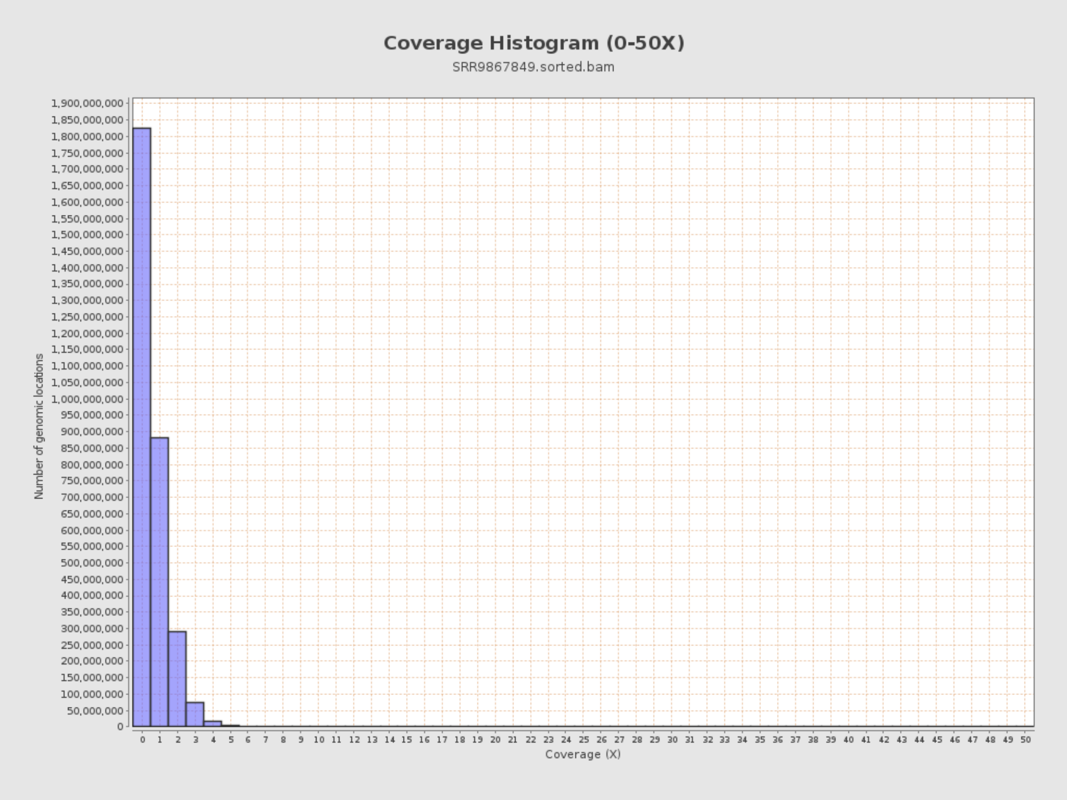
# 3. Results : Coverage across reference



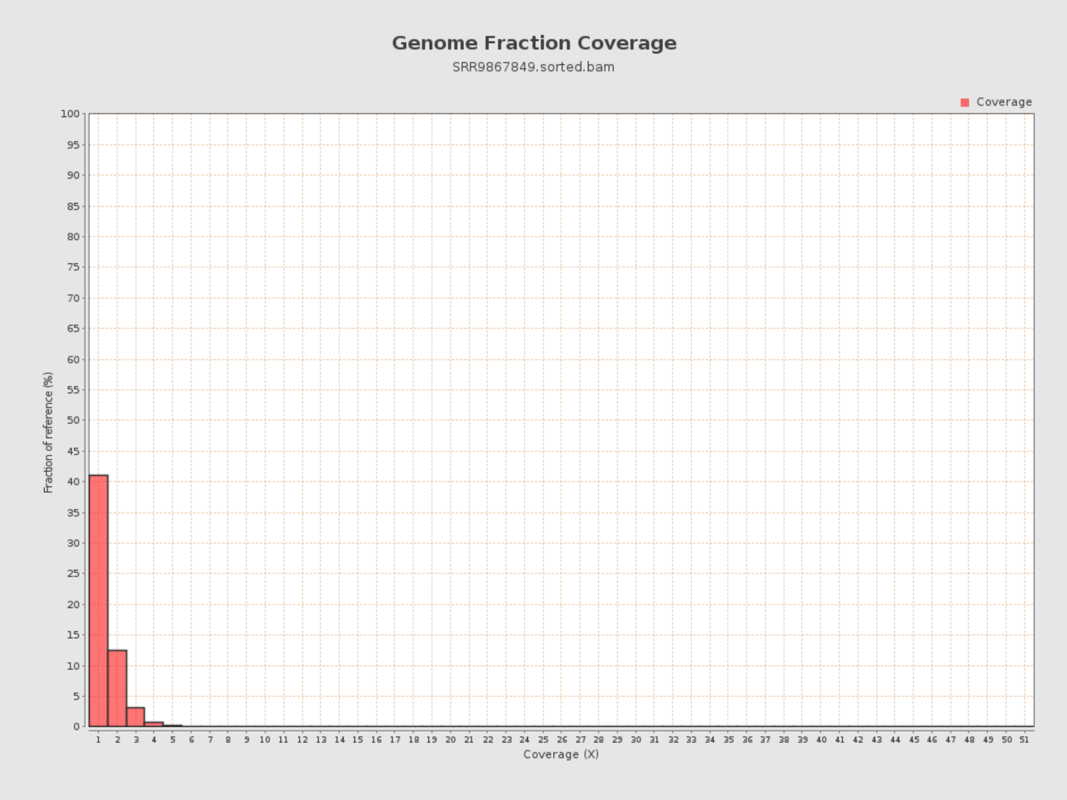
# 4. Results : Coverage Histogram



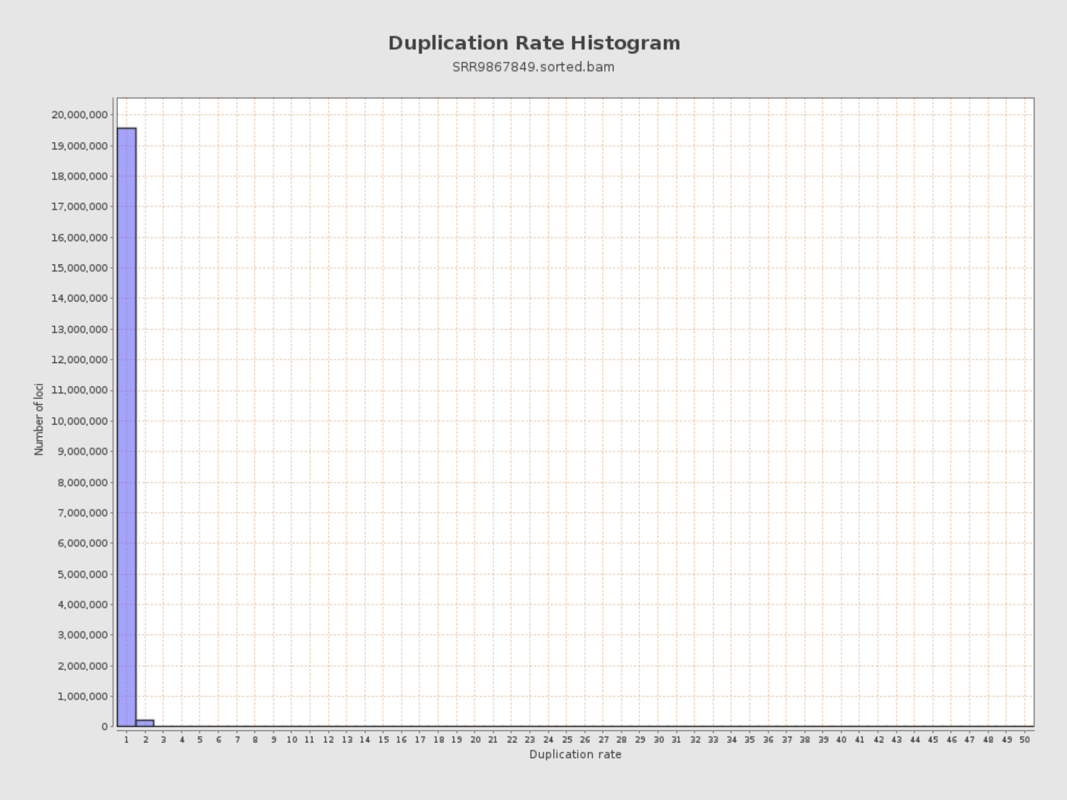
# 5. Results : Coverage Histogram (0-50X)



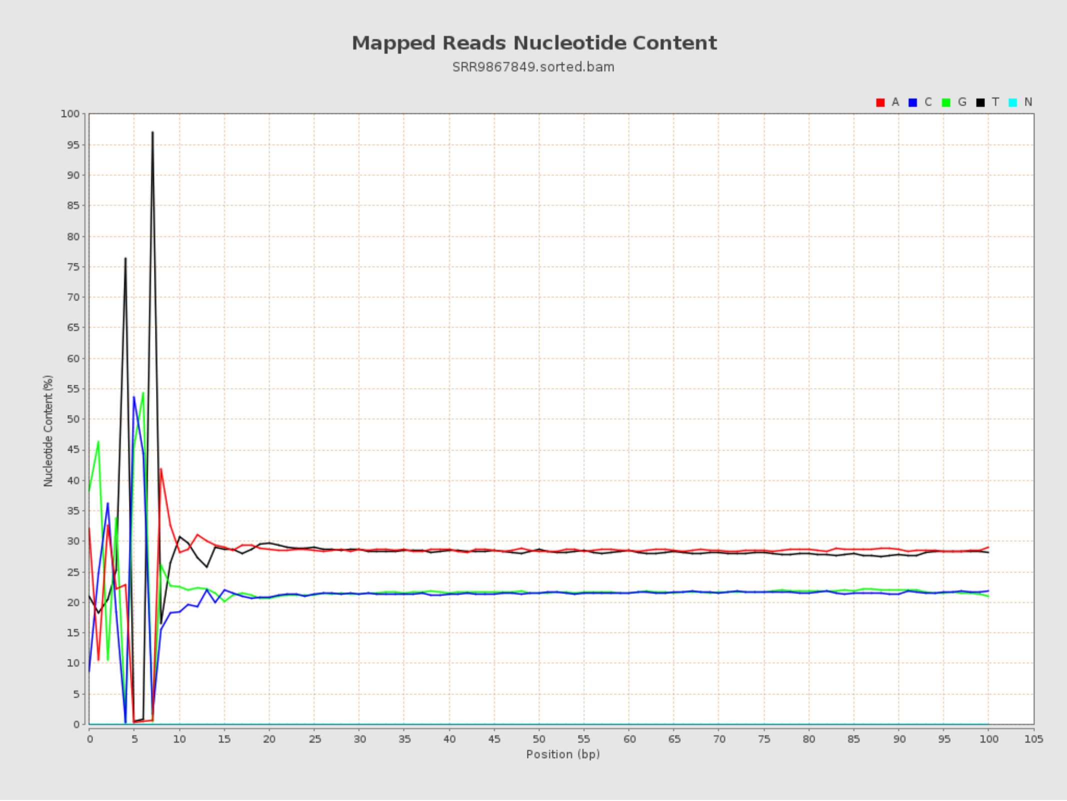
# 6. Results : Genome Fraction Coverage



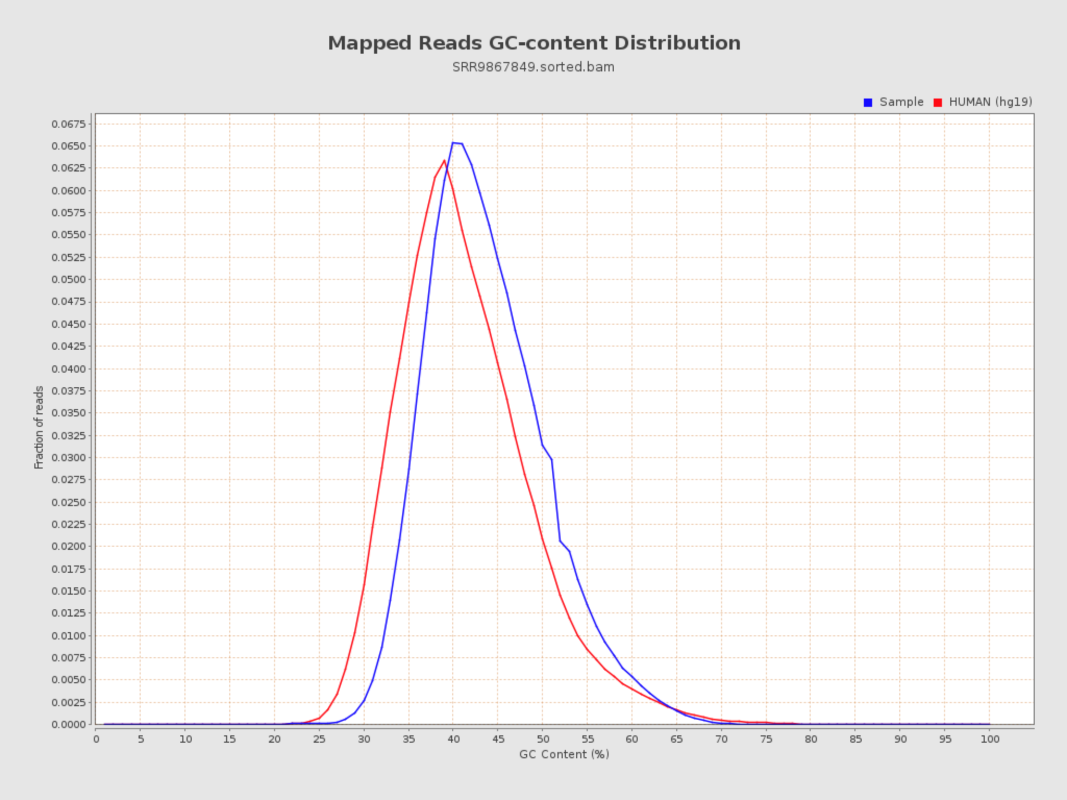
# 7. Results : Duplication Rate Histogram



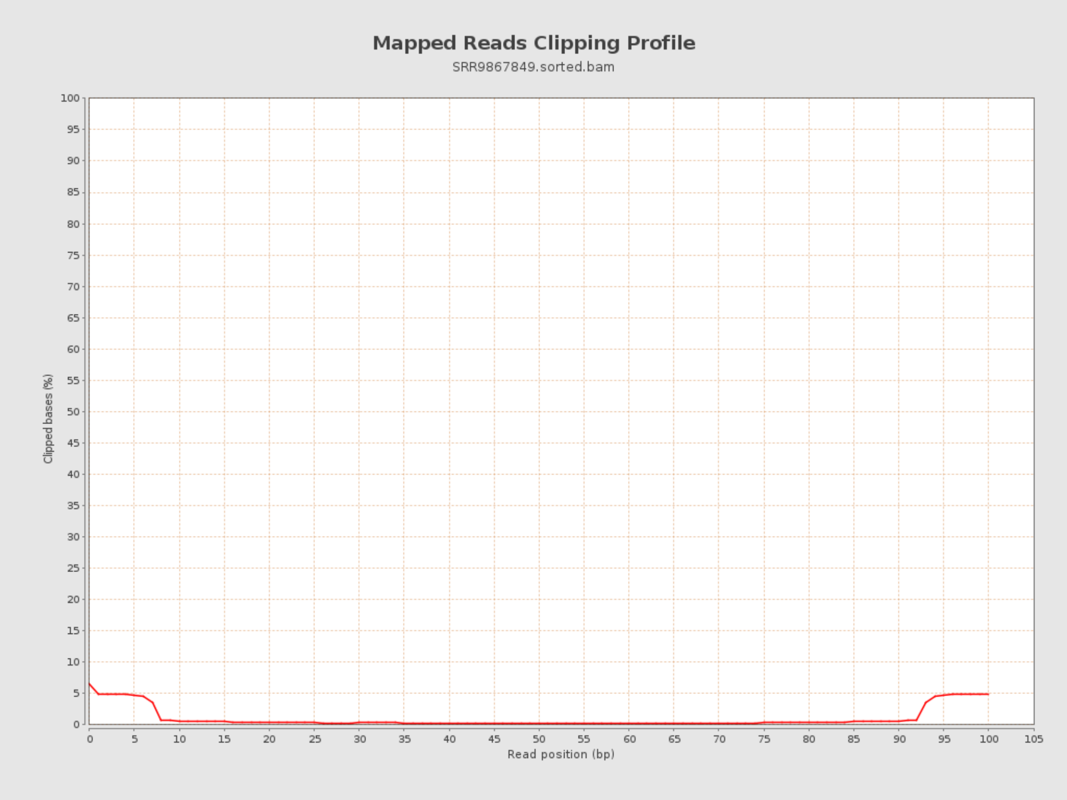
# 8. Results : Mapped Reads Nucleotide Content



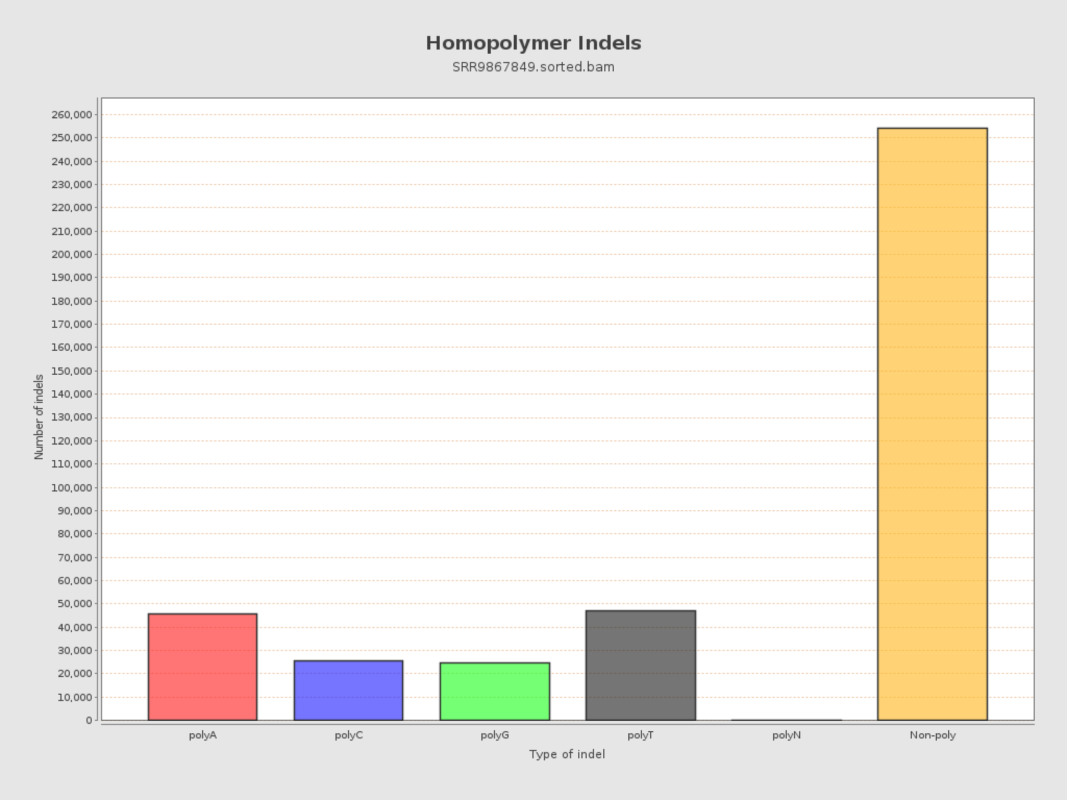
# 9. Results : Mapped Reads GC-content Distribution



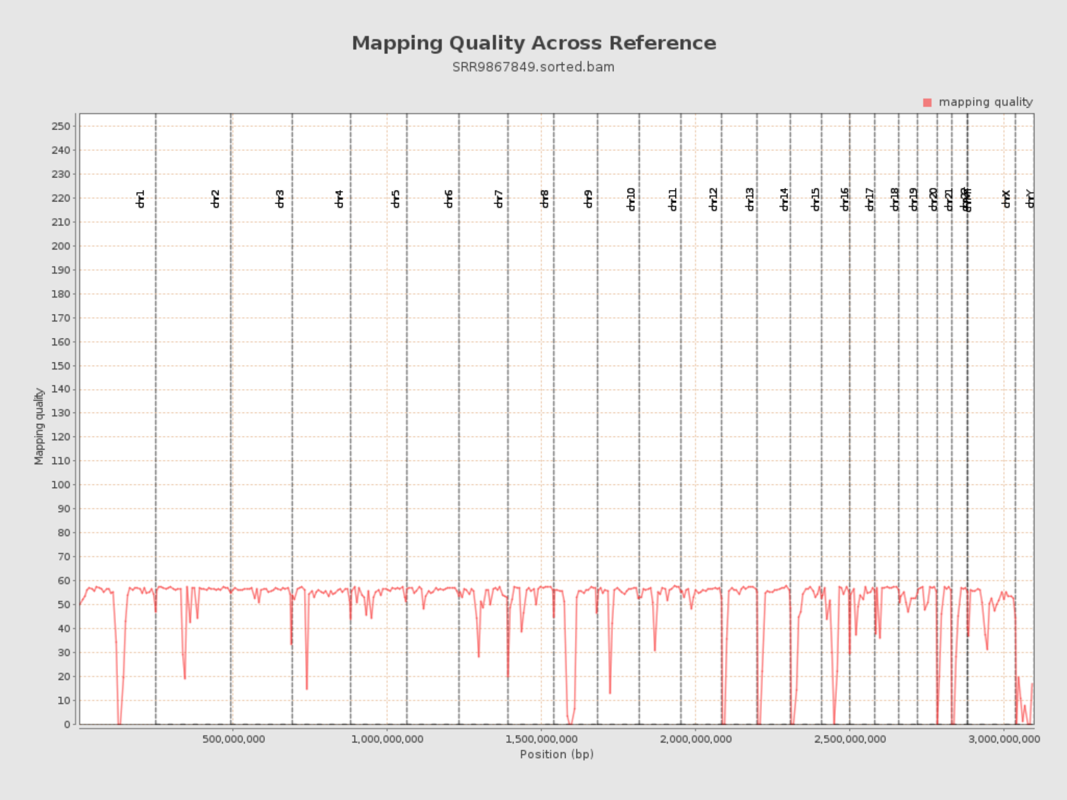
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram