# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/30 17:31:04*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867867.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_SRR9867867 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867867.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 30 17:31:03 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9867867.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,531,818 |
| Mapped reads | 1,416,433 / 92.47% |
| Unmapped reads | 115,385 / 7.53% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 5,956 / 0.39% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 54,578 / 3.56% |
| Duplication rate | 2.85% |
| Clipped reads | 1,417,205 / 92.52% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 21,676,245 / 25.9% |
| Number/percentage of C's | 16,403,282 / 19.6% |
| Number/percentage of T's | 26,055,542 / 31.13% |
| Number/percentage of G's | 19,543,066 / 23.35% |
| Number/percentage of N's | 11,179 / 0.01% |
| GC Percentage | 42.95% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.027 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2615 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.75 |

## 2.5. Mismatches and indels

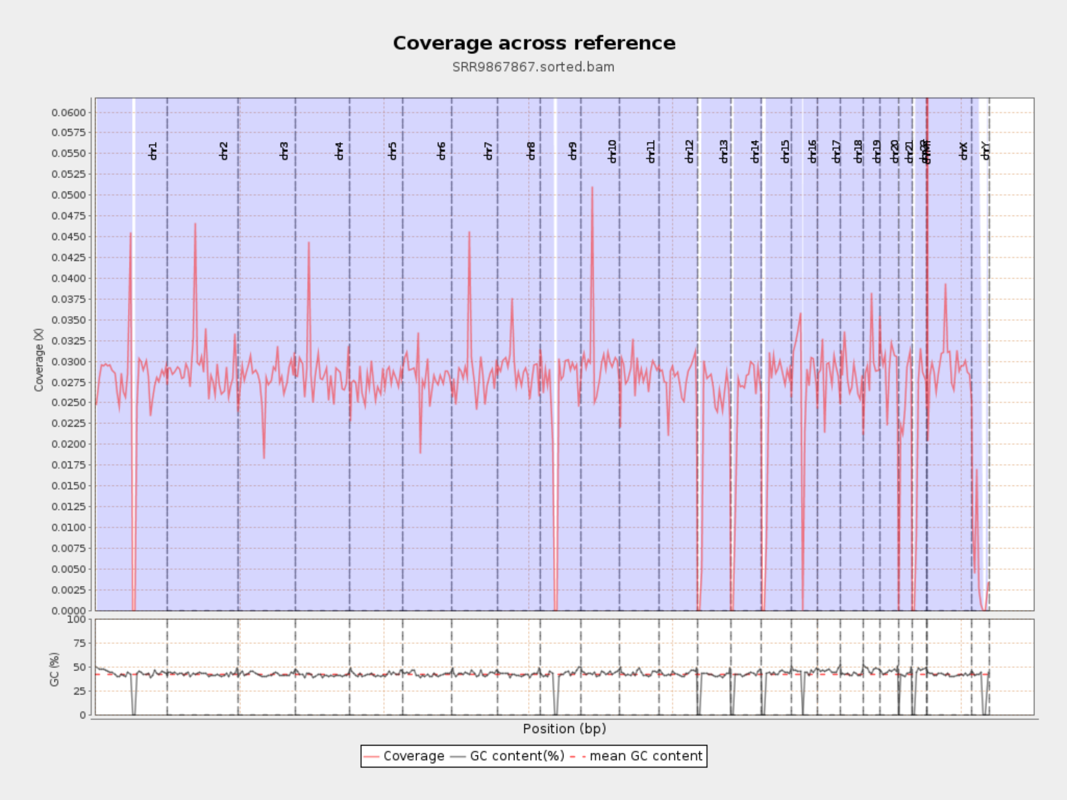
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 415,462 |
| Insertions | 7,235 |
| Mapped reads with at least one insertion | 0.51% |
| Deletions | 15,595 |
| Mapped reads with at least one deletion | 1.09% |
| Homopolymer indels | 41.88% |

## 2.6. Chromosome stats

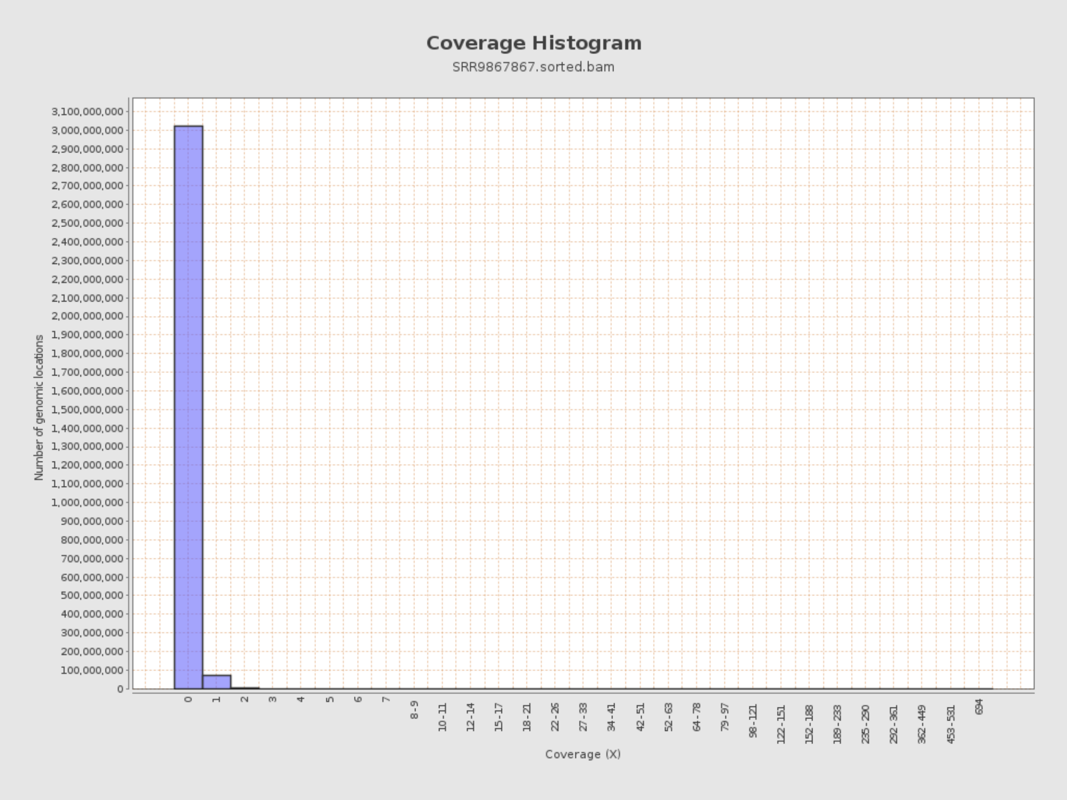
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 6653813 | 0.0267 | 0.447 |
| chr2 | 243199373 | 7113531 | 0.0292 | 0.3554 |
| chr3 | 198022430 | 5535545 | 0.028 | 0.1807 |
| chr4 | 191154276 | 5501043 | 0.0288 | 0.2012 |
| chr5 | 180915260 | 4978893 | 0.0275 | 0.1795 |
| chr6 | 171115067 | 4805389 | 0.0281 | 0.2037 |
| chr7 | 159138663 | 4571462 | 0.0287 | 0.3182 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 4270071 | 0.0292 | 0.2773 |
| chr9 | 141213431 | 3547301 | 0.0251 | 0.2271 |
| chr10 | 135534747 | 4132155 | 0.0305 | 0.2665 |
| chr11 | 135006516 | 3877922 | 0.0287 | 0.2339 |
| chr12 | 133851895 | 3725246 | 0.0278 | 0.1824 |
| chr13 | 115169878 | 2576620 | 0.0224 | 0.1618 |
| chr14 | 107349540 | 2487651 | 0.0232 | 0.171 |
| chr15 | 102531392 | 2394900 | 0.0234 | 0.1656 |
| chr16 | 90354753 | 2442667 | 0.027 | 0.1893 |
| chr17 | 81195210 | 2312499 | 0.0285 | 0.1909 |
| chr18 | 78077248 | 2199786 | 0.0282 | 0.3948 |
| chr19 | 59128983 | 1761838 | 0.0298 | 0.3542 |
| chr20 | 63025520 | 1839847 | 0.0292 | 0.1884 |
| chr21 | 48129895 | 1133267 | 0.0235 | 0.188 |
| chr22 | 51304566 | 1014455 | 0.0198 | 0.1527 |
| chrMT | 16571 | 10229 | 0.6173 | 0.8373 |
| chrX | 155270560 | 4556703 | 0.0293 | 0.2007 |
| chrY | 59373566 | 271008 | 0.0046 | 0.1692 |

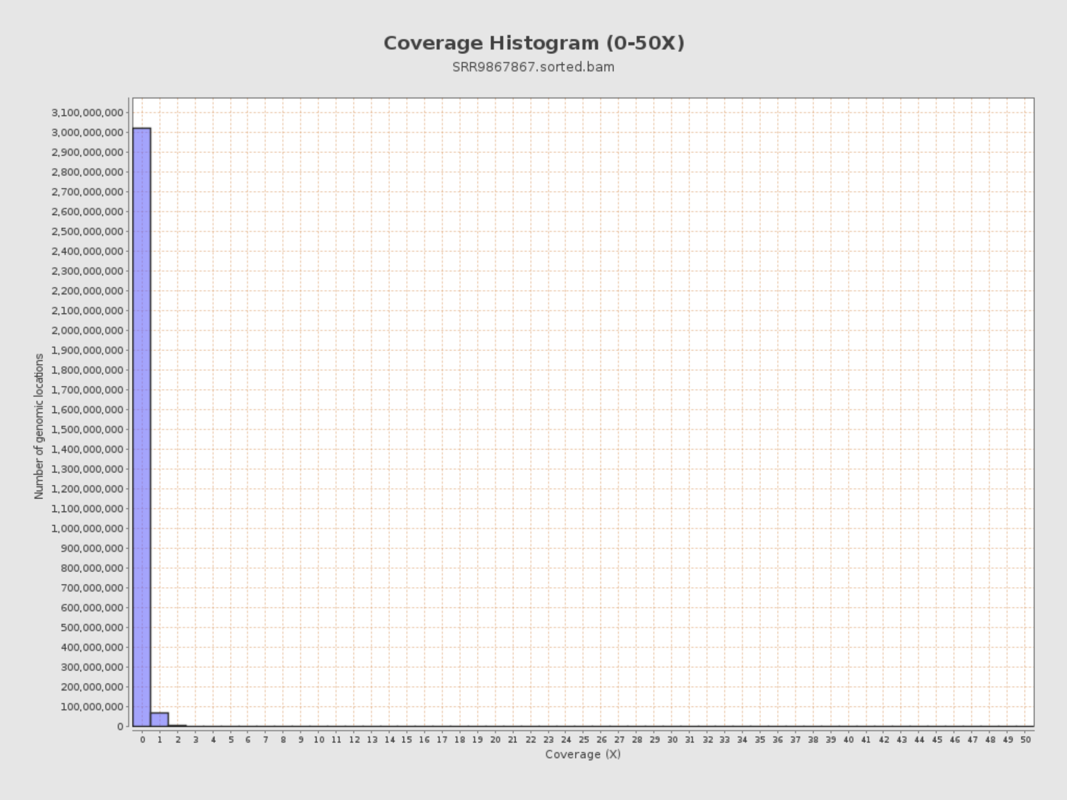
# 3. Results : Coverage across reference



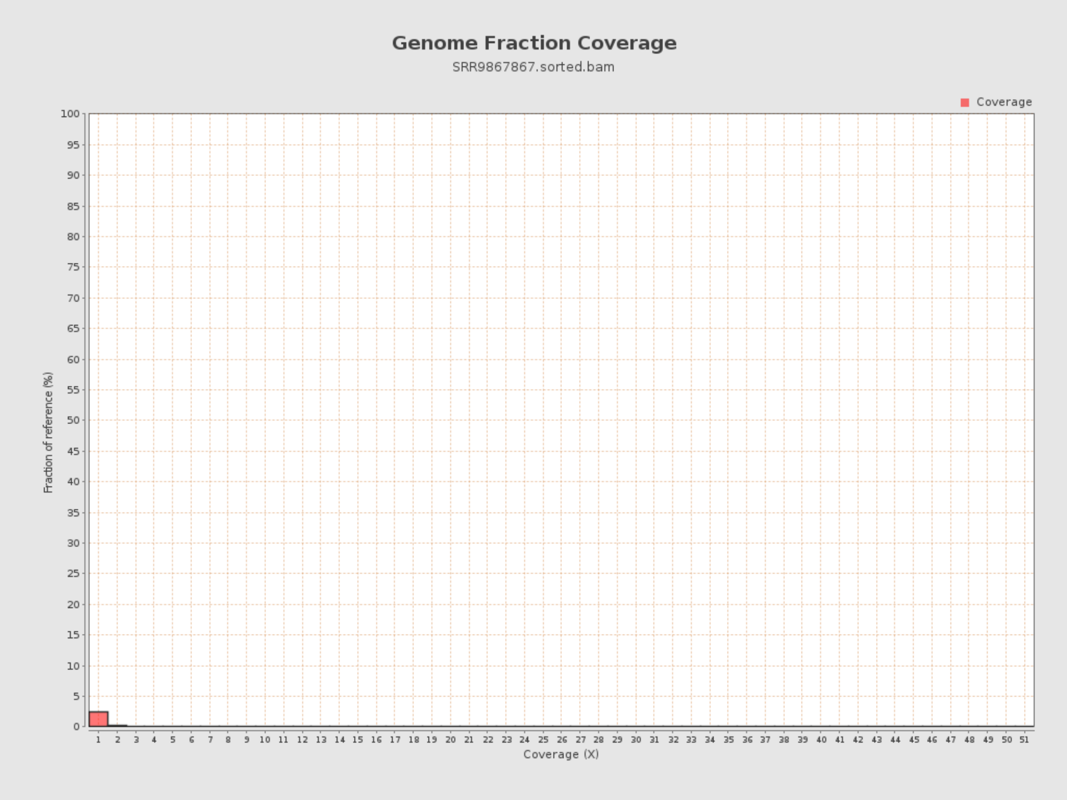
# 4. Results : Coverage Histogram



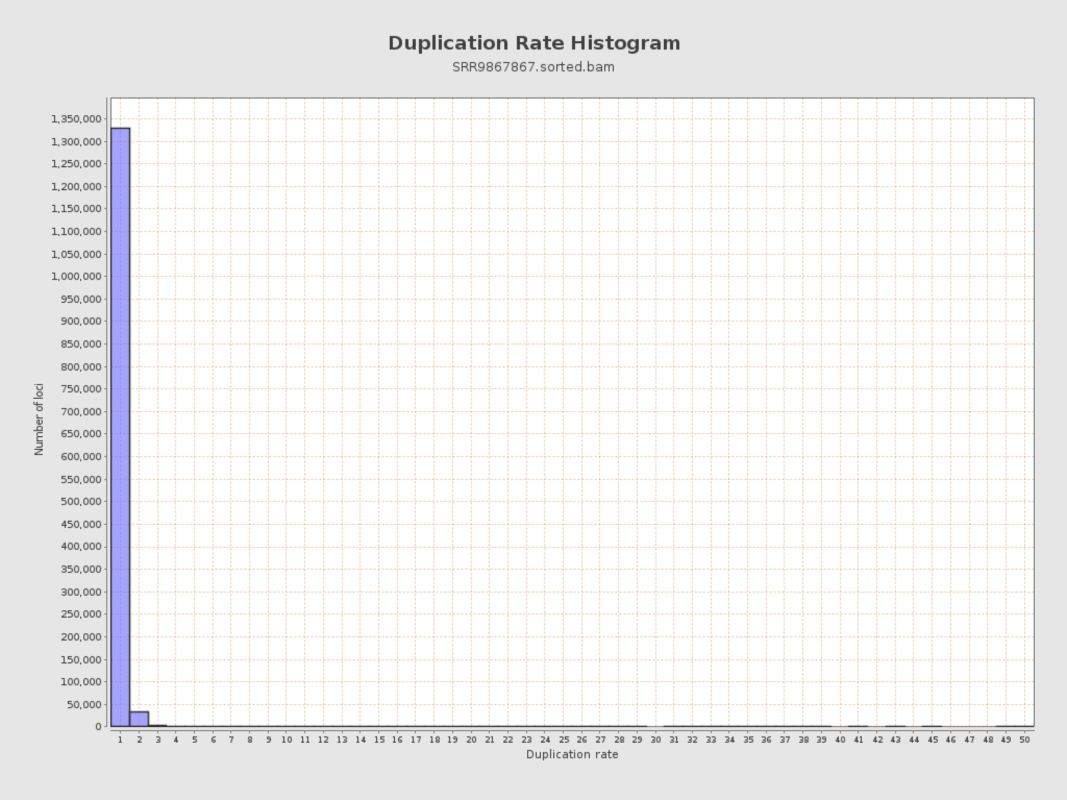
# 5. Results : Coverage Histogram (0-50X)



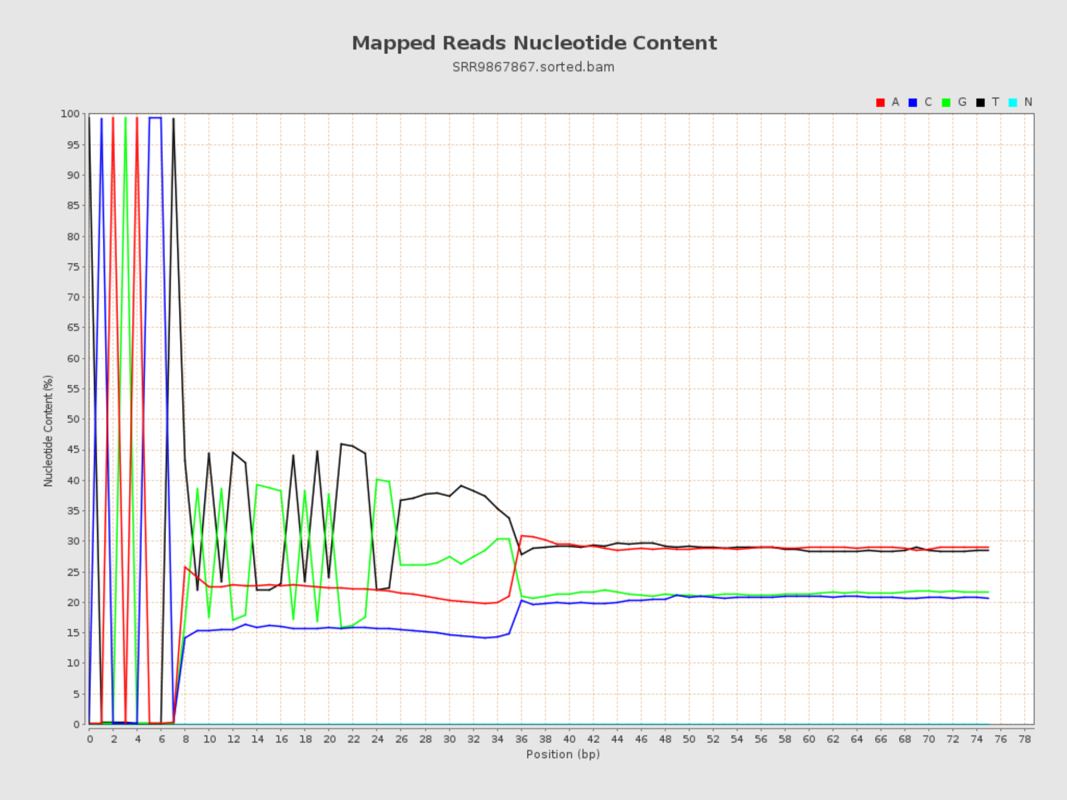
# 6. Results : Genome Fraction Coverage



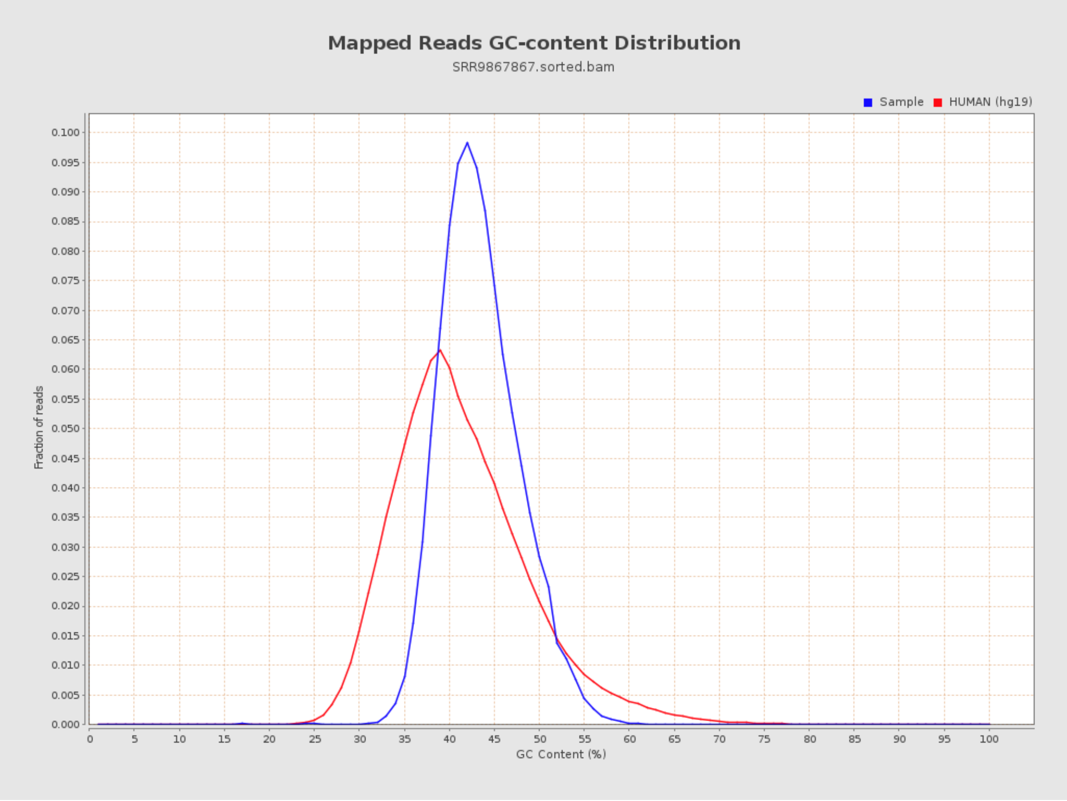
# 7. Results : Duplication Rate Histogram



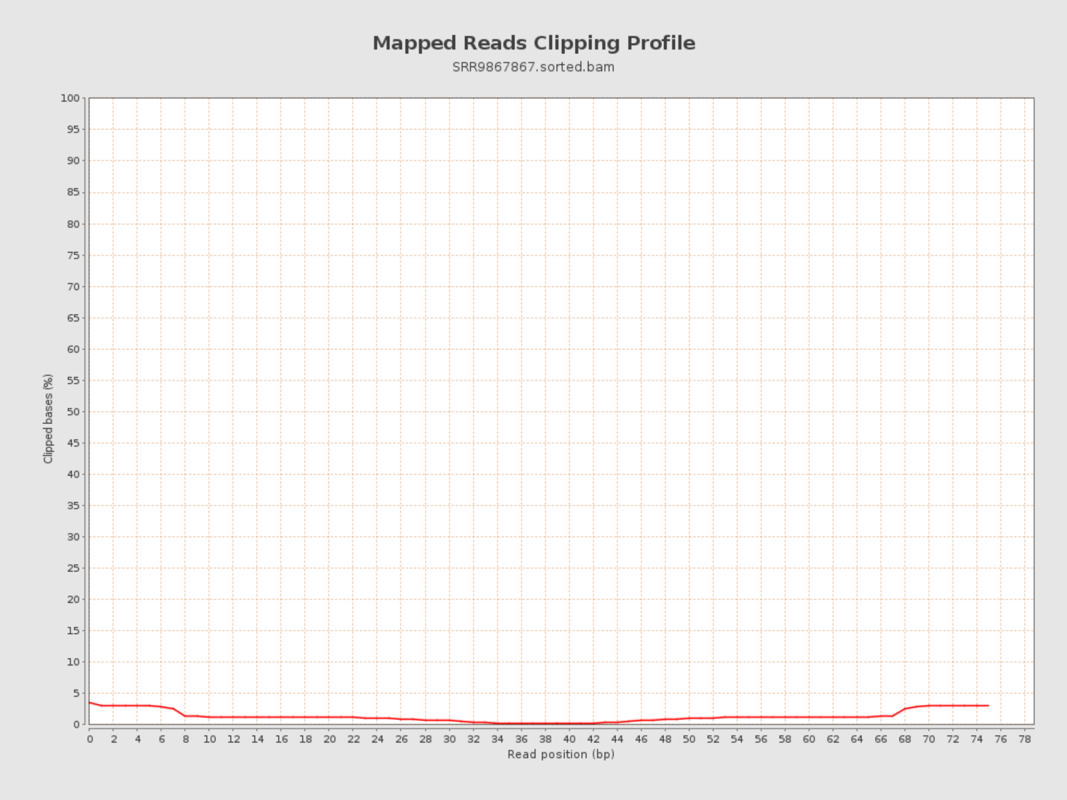
# 8. Results : Mapped Reads Nucleotide Content



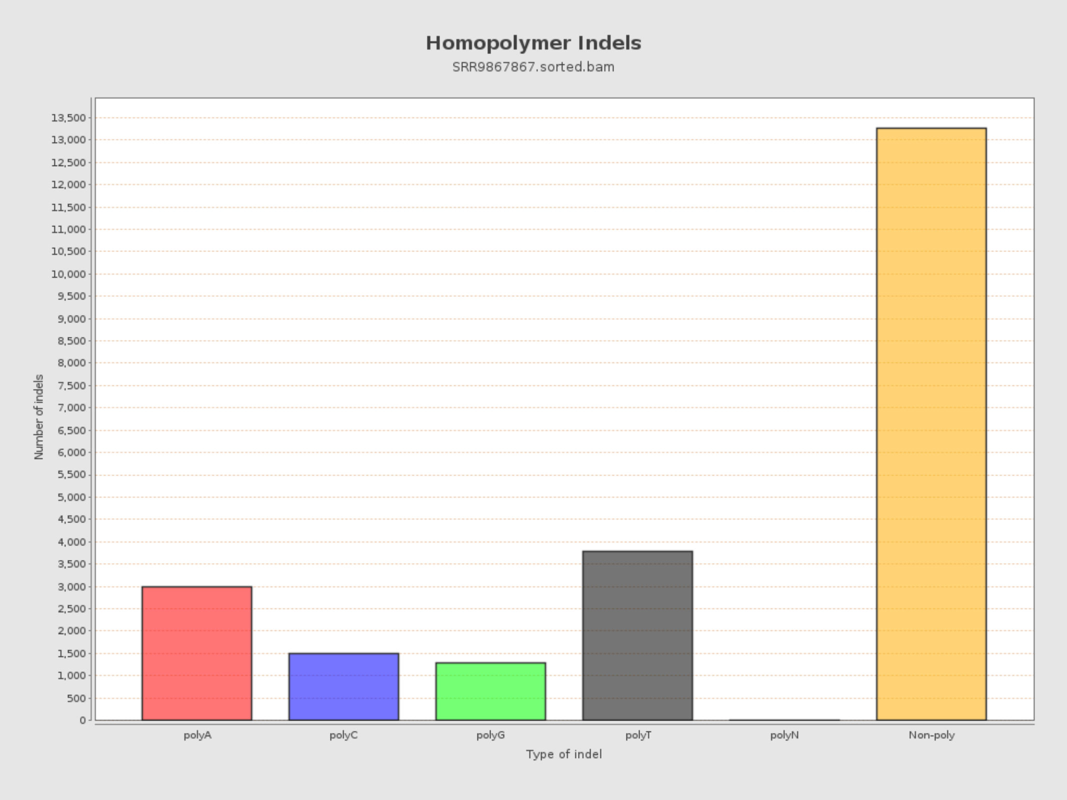
# 9. Results : Mapped Reads GC-content Distribution



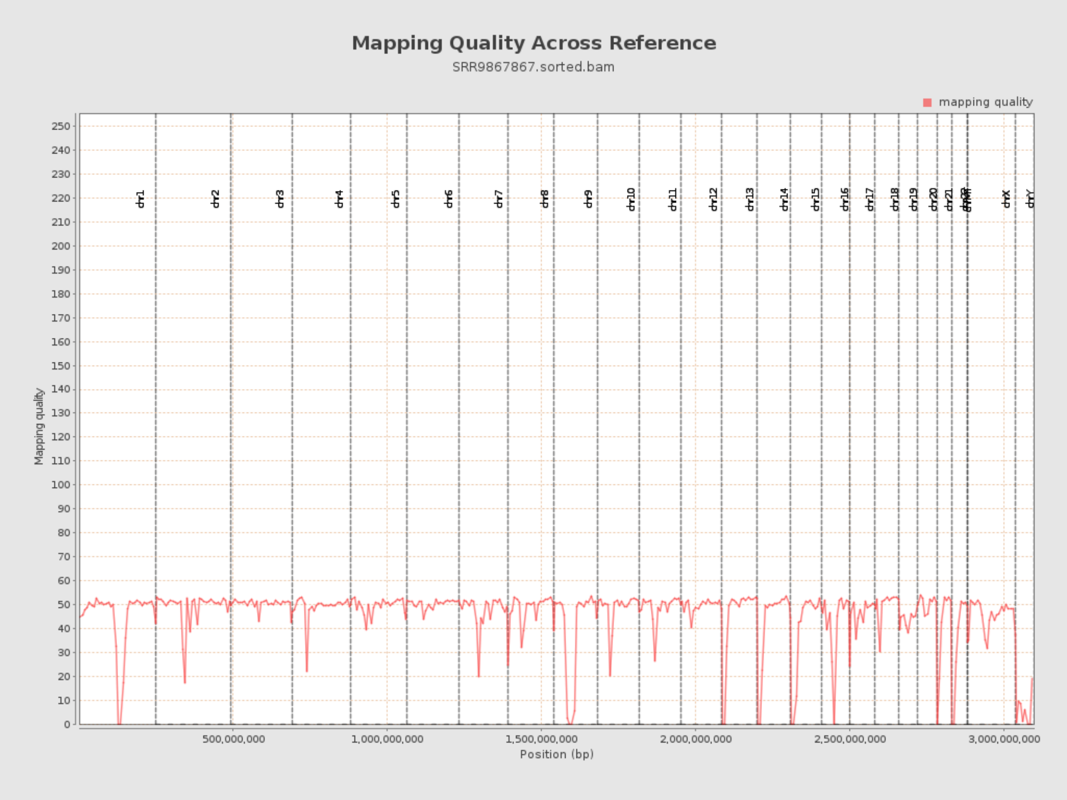
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram