# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/30 05:39:59*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9867838.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_SRR9867838 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9867838.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 30 05:39:46 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9867838.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 34,652,781 |
| Mapped reads | 31,316,914 / 90.37% |
| Unmapped reads | 3,335,867 / 9.63% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 85,182 / 0.25% |
| Read min/max/mean length | 30 / 101 / 101.09 |
| Duplicated reads (estimated) | 1,864,211 / 5.38% |
| Duplication rate | 1.59% |
| Clipped reads | 31,262,127 / 90.22% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 785,744,415 / 28.12% |
| Number/percentage of C's | 605,662,030 / 21.68% |
| Number/percentage of T's | 784,412,887 / 28.08% |
| Number/percentage of G's | 613,901,332 / 21.97% |
| Number/percentage of N's | 4,147,386 / 0.15% |
| GC Percentage | 43.65% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.9027 |
| | |

| | |
|---|---|
| Standard Deviation | 10.4684 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 50.39 |

## 2.5. Mismatches and indels

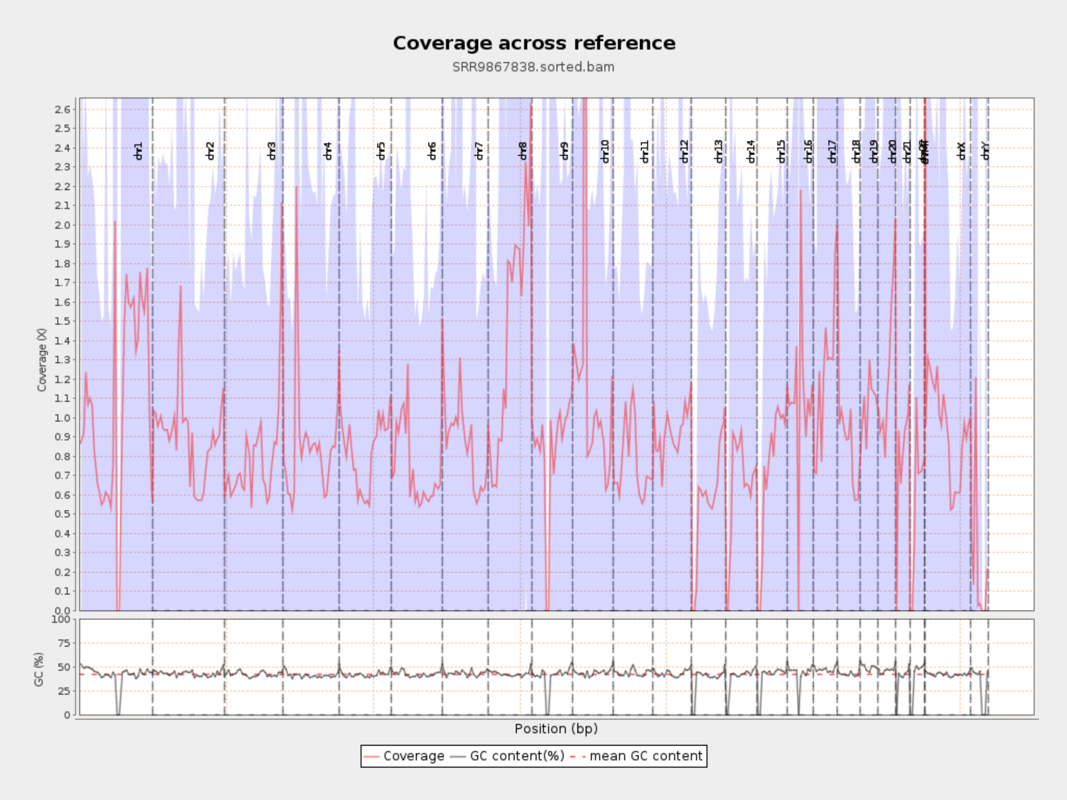
| | |
|---|---|
| General error rate | 0.49% |
| Mismatches | 12,843,905 |
| Insertions | 287,614 |
| Mapped reads with at least one insertion | 0.9% |
| Deletions | 288,545 |
| Mapped reads with at least one deletion | 0.9% |
| Homopolymer indels | 35.92% |

## 2.6. Chromosome stats

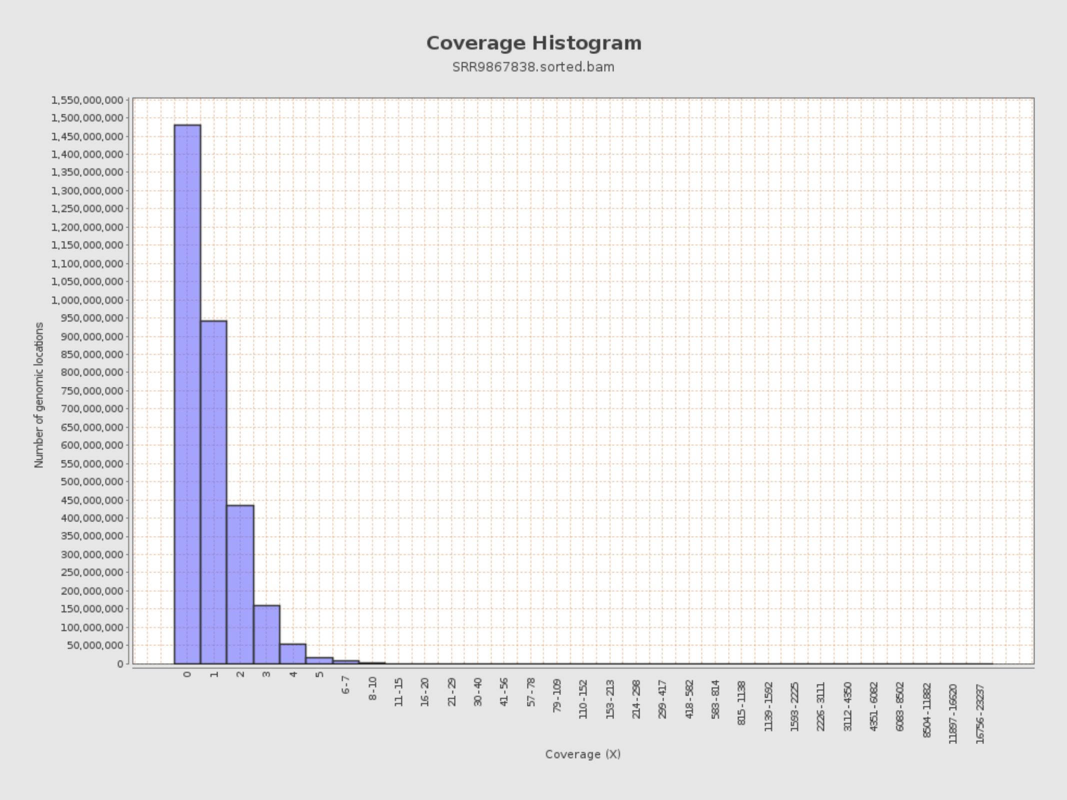
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 265081346 | 1.0635 | 21.4857 |
| chr2 | 243199373 | 220970026 | 0.9086 | 6.6046 |
| chr3 | 198022430 | 155042541 | 0.783 | 5.4089 |
| chr4 | 191154276 | 160321873 | 0.8387 | 7.9392 |
| chr5 | 180915260 | 150312853 | 0.8308 | 1.2725 |
| chr6 | 171115067 | 125852042 | 0.7355 | 4.4611 |
| chr7 | 159138663 | 139087198 | 0.874 | 8.6205 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 215545282 | 1.4727 | 4.2451 |
| chr9 | 141213431 | 117376748 | 0.8312 | 7.83 |
| chr10 | 135534747 | 164199714 | 1.2115 | 30.2525 |
| chr11 | 135006516 | 104842425 | 0.7766 | 3.823 |
| chr12 | 133851895 | 124073285 | 0.9269 | 1.9293 |
| chr13 | 115169878 | 65913337 | 0.5723 | 0.8926 |
| chr14 | 107349540 | 68682691 | 0.6398 | 1.2704 |
| chr15 | 102531392 | 74223396 | 0.7239 | 1.007 |
| chr16 | 90354753 | 100504617 | 1.1123 | 8.9977 |
| chr17 | 81195210 | 100297474 | 1.2353 | 3.575 |
| chr18 | 78077248 | 67712767 | 0.8673 | 11.0947 |
| chr19 | 59128983 | 63447252 | 1.073 | 13.456 |
| chr20 | 63025520 | 77772305 | 1.234 | 2.5823 |
| chr21 | 48129895 | 39445800 | 0.8196 | 5.6658 |
| chr22 | 51304566 | 29702951 | 0.579 | 1.1251 |
| chrMT | 16571 | 4692647 | 283.1843 | 86.1854 |
| chrX | 155270560 | 144956171 | 0.9336 | 2.6329 |
| chrY | 59373566 | 14543056 | 0.2449 | 12.0735 |

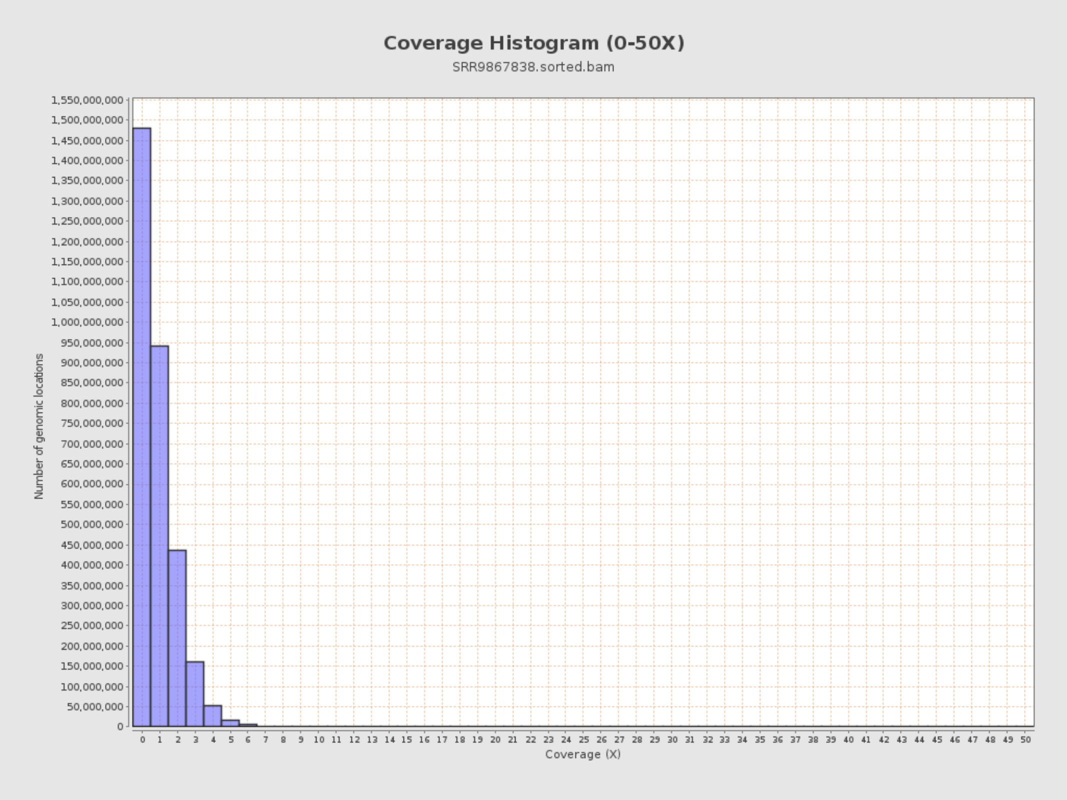
# 3. Results : Coverage across reference



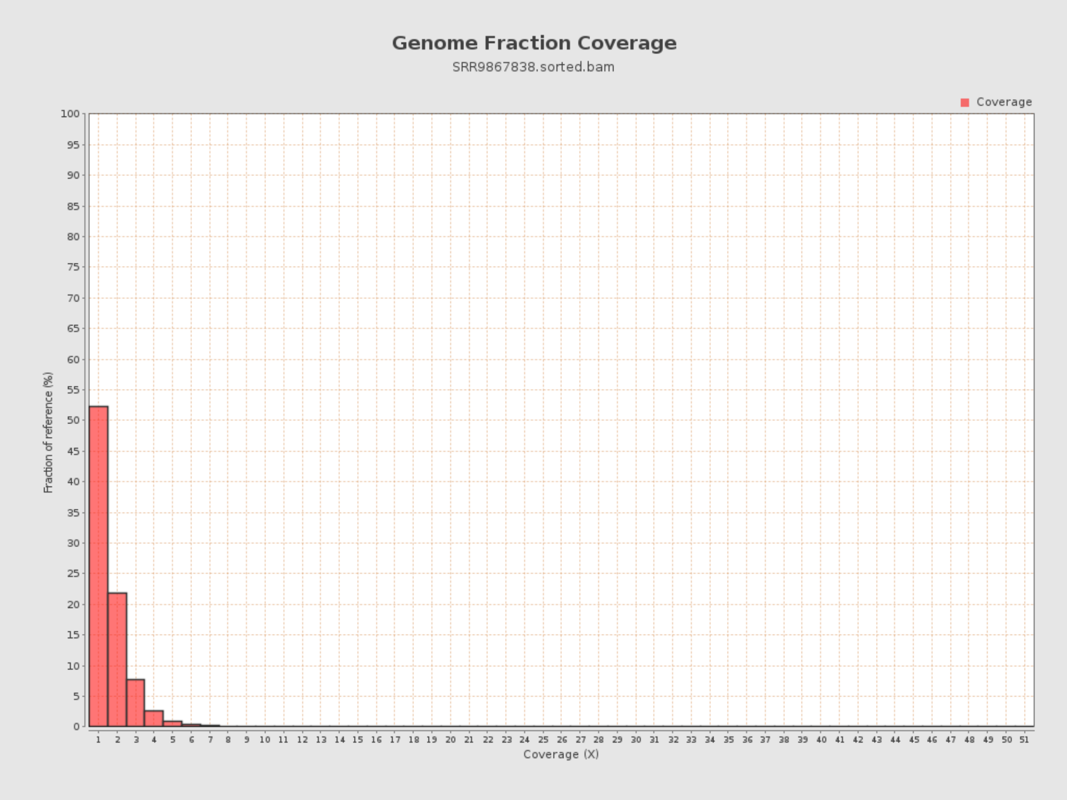
# 4. Results : Coverage Histogram



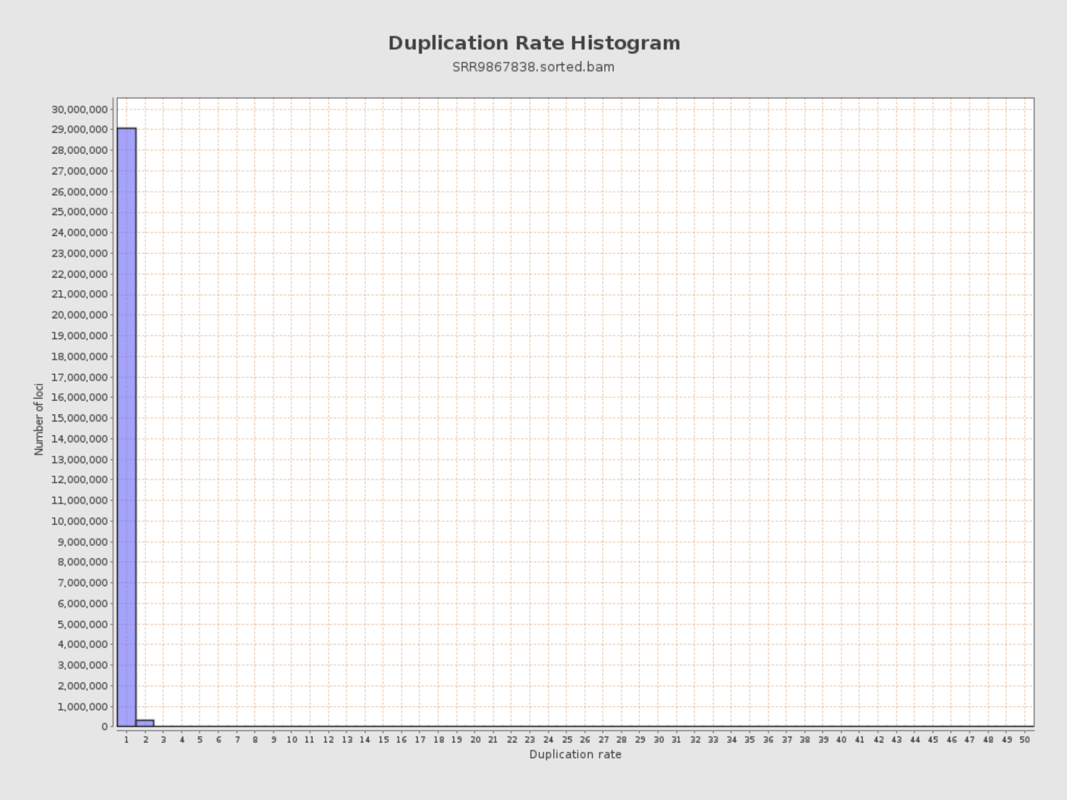
# 5. Results : Coverage Histogram (0-50X)



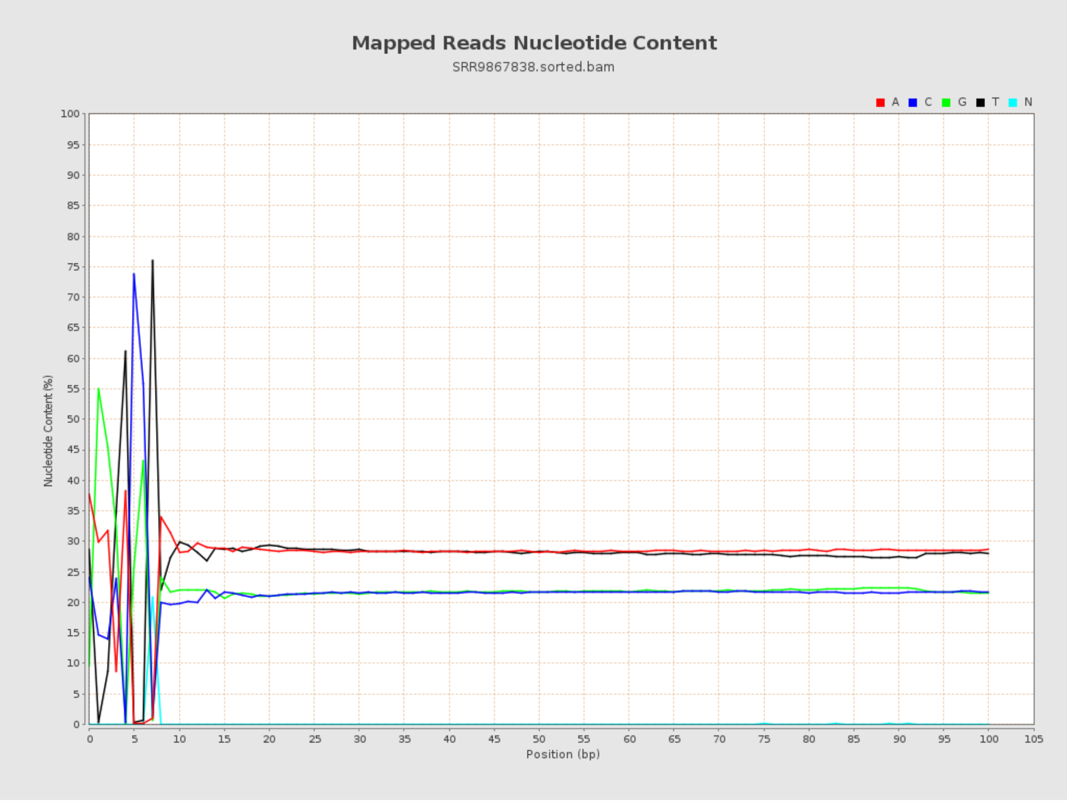
# 6. Results : Genome Fraction Coverage



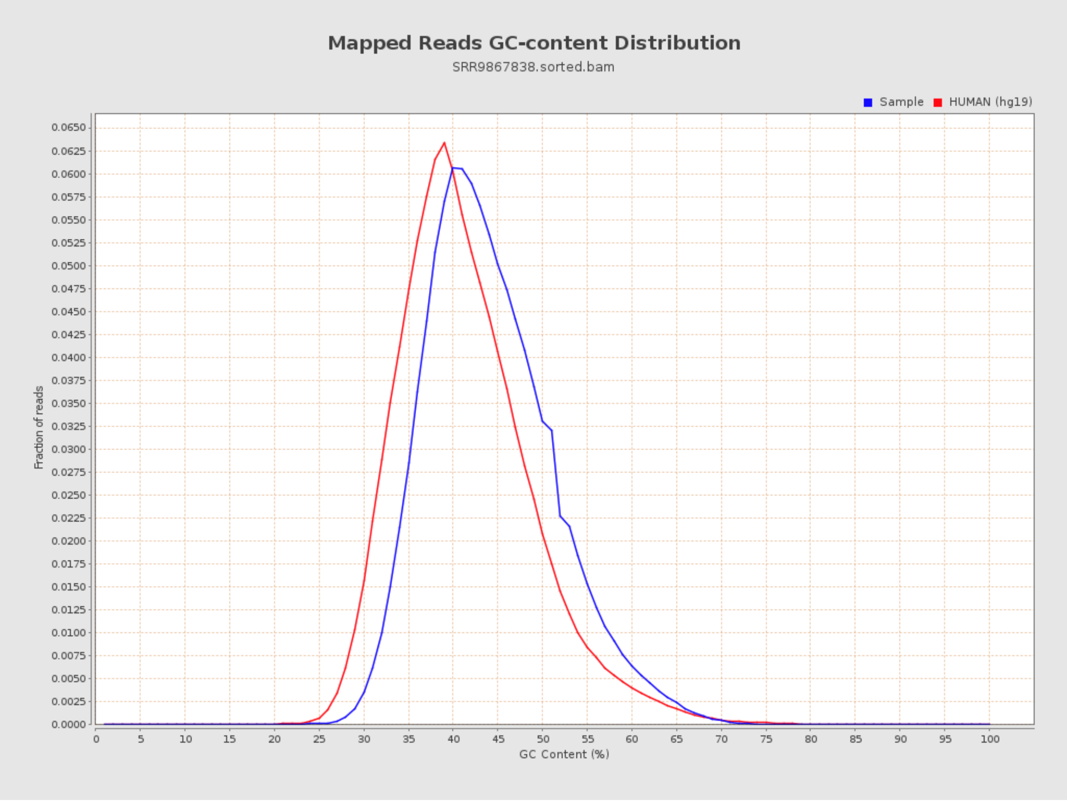
# 7. Results : Duplication Rate Histogram



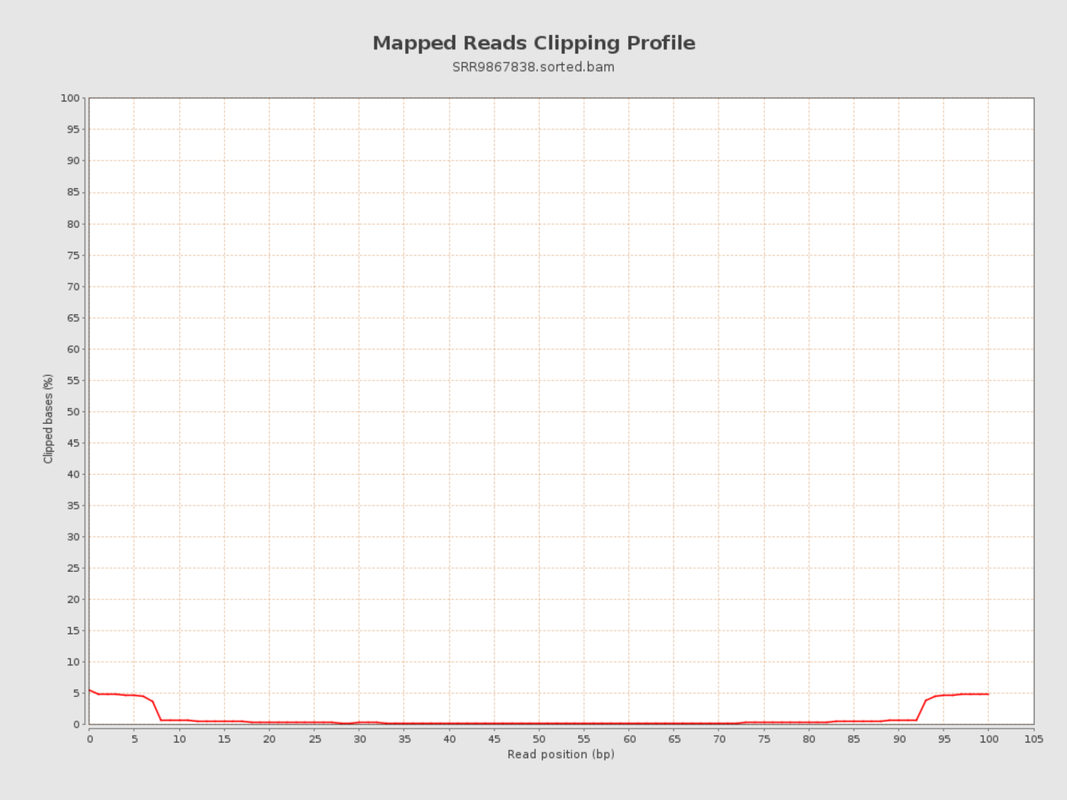
# 8. Results : Mapped Reads Nucleotide Content



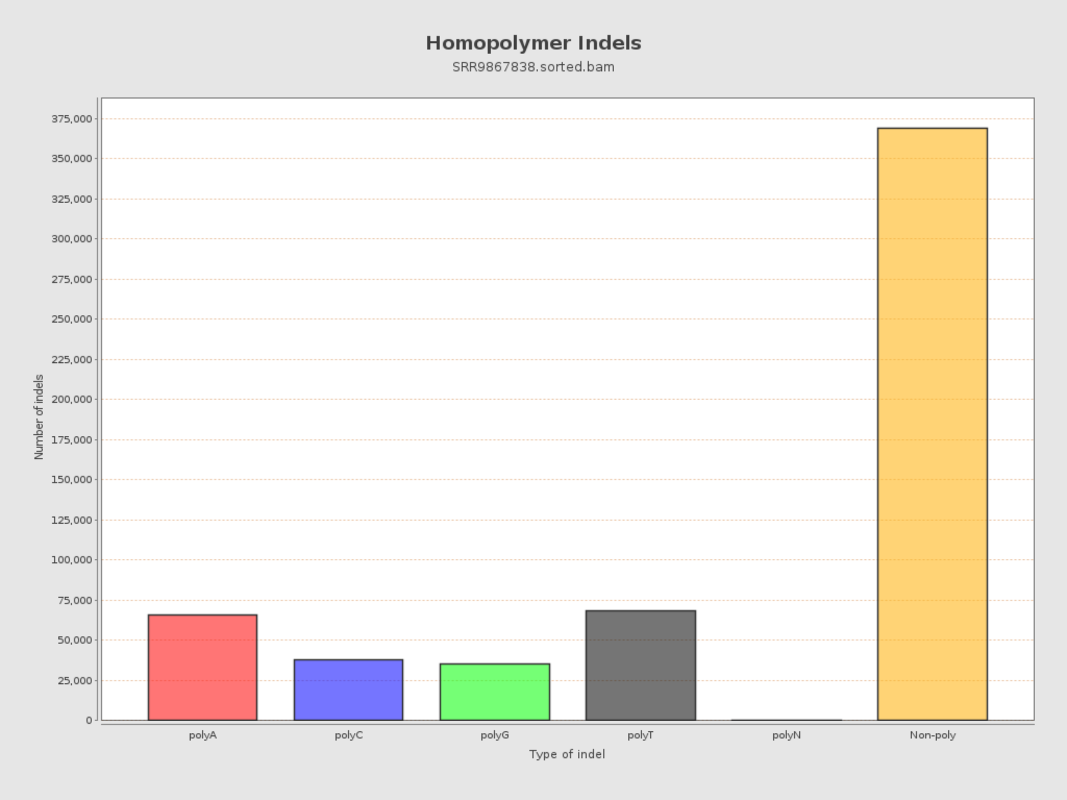
# 9. Results : Mapped Reads GC-content Distribution



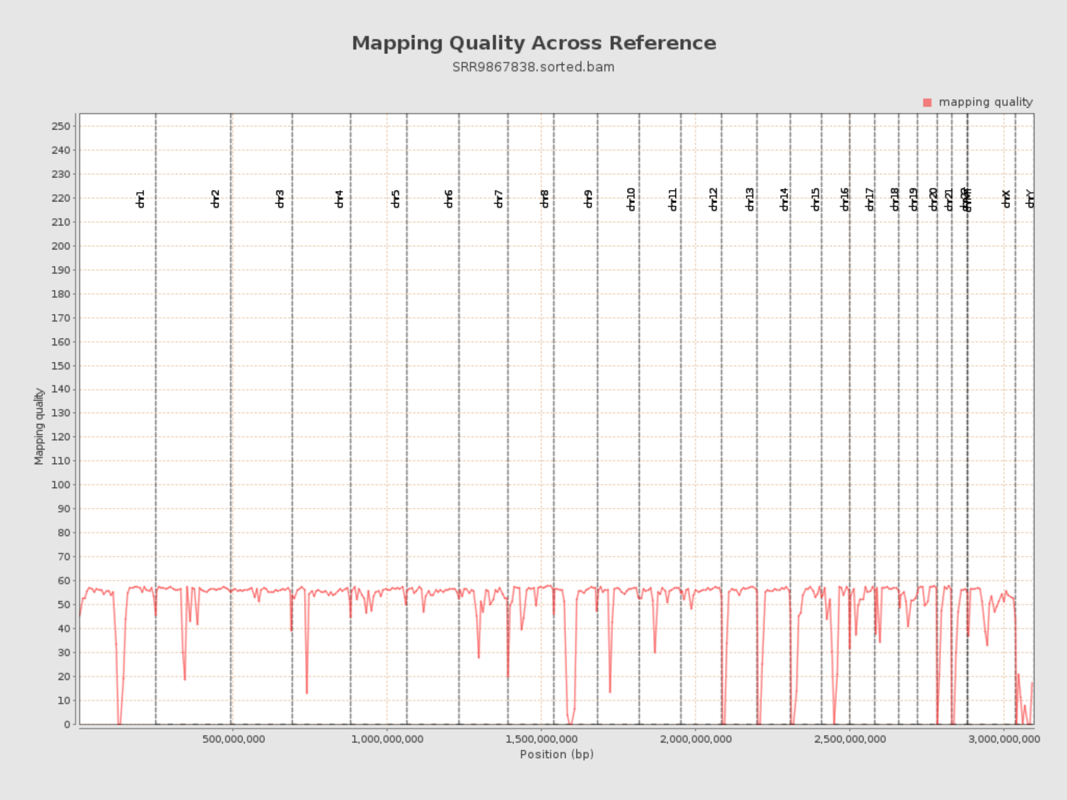
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram