# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/16 21:47:12*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6236125.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_SRR6236125 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6236125.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Sep 16 21:47:12 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6236125.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,596,021 |
| Mapped reads | 1,382,204 / 86.6% |
| Unmapped reads | 213,817 / 13.4% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 8,254 / 0.52% |
| Read min/max/mean length | 30 / 76 / 76.18 |
| Duplicated reads (estimated) | 59,199 / 3.71% |
| Duplication rate | 3.31% |
| Clipped reads | 667,306 / 41.81% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 24,707,501 / 27.25% |
| Number/percentage of C's | 16,435,947 / 18.12% |
| Number/percentage of T's | 28,972,977 / 31.95% |
| Number/percentage of G's | 20,527,921 / 22.64% |
| Number/percentage of N's | 38,741 / 0.04% |
| GC Percentage | 40.76% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0293 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3279 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.76 |

## 2.5. Mismatches and indels

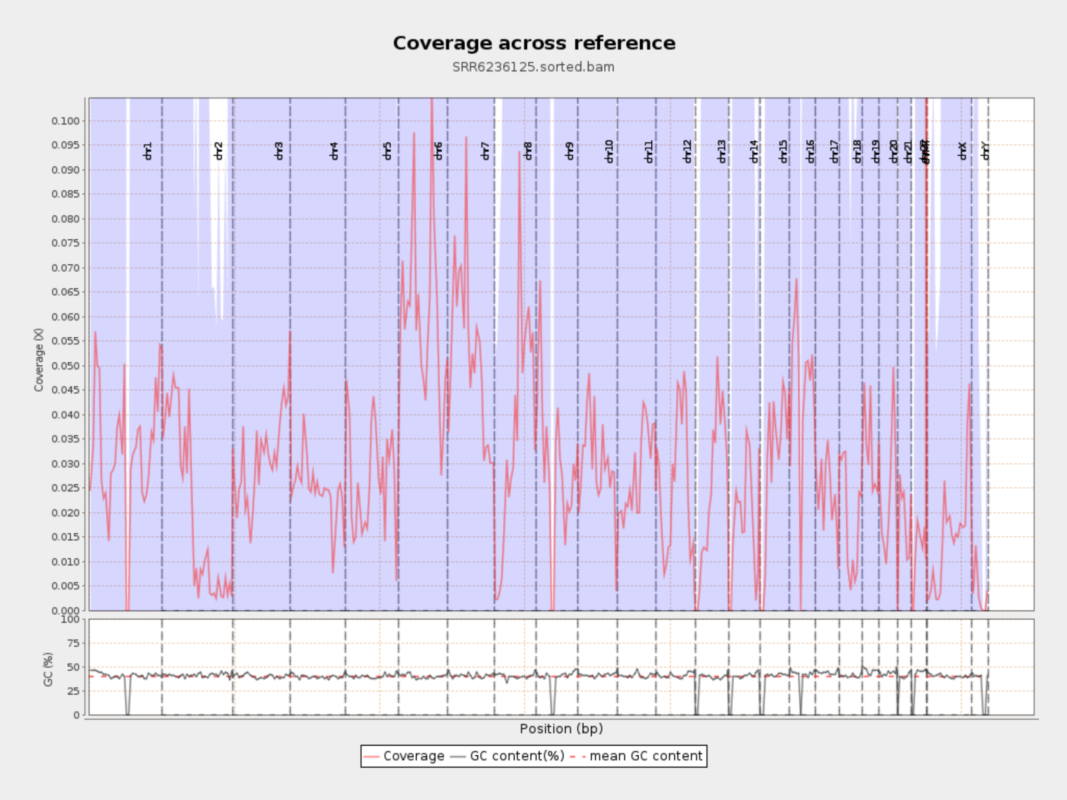
| | |
|---|---|
| General error rate | 0.85% |
| Mismatches | 757,177 |
| Insertions | 6,662 |
| Mapped reads with at least one insertion | 0.48% |
| Deletions | 29,113 |
| Mapped reads with at least one deletion | 2.08% |
| Homopolymer indels | 46.09% |

## 2.6. Chromosome stats

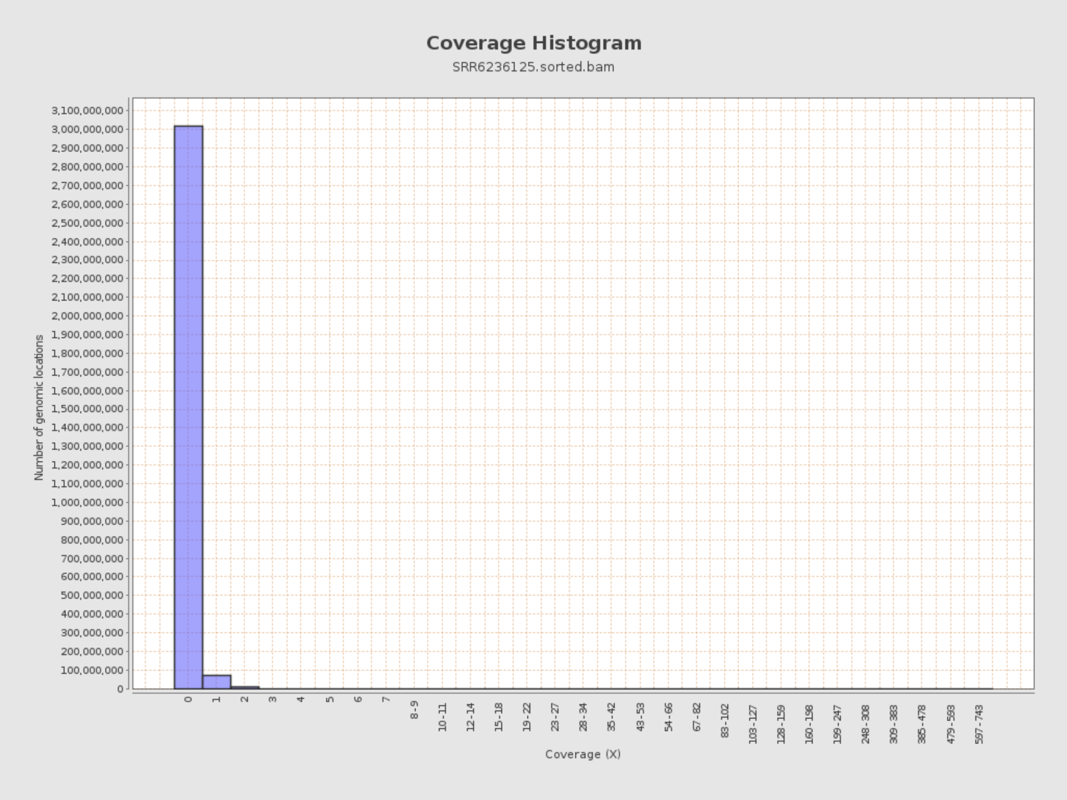
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 8041964 | 0.0323 | 0.5917 |
| chr2 | 243199373 | 4849668 | 0.0199 | 0.2697 |
| chr3 | 198022430 | 6133422 | 0.031 | 0.1944 |
| chr4 | 191154276 | 4709671 | 0.0246 | 0.1919 |
| chr5 | 180915260 | 4814562 | 0.0266 | 0.1827 |
| chr6 | 171115067 | 10242620 | 0.0599 | 0.4141 |
| chr7 | 159138663 | 8405176 | 0.0528 | 0.6258 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 5224645 | 0.0357 | 0.5073 |
| chr9 | 141213431 | 4088661 | 0.029 | 0.2428 |
| chr10 | 135534747 | 4118420 | 0.0304 | 0.2636 |
| chr11 | 135006516 | 3777489 | 0.028 | 0.2212 |
| chr12 | 133851895 | 3477935 | 0.026 | 0.1825 |
| chr13 | 115169878 | 2858077 | 0.0248 | 0.1738 |
| chr14 | 107349540 | 1827879 | 0.017 | 0.1508 |
| chr15 | 102531392 | 3080081 | 0.03 | 0.1972 |
| chr16 | 90354753 | 4150772 | 0.0459 | 0.2485 |
| chr17 | 81195210 | 1931223 | 0.0238 | 0.2 |
| chr18 | 78077248 | 1441207 | 0.0185 | 0.3756 |
| chr19 | 59128983 | 1947640 | 0.0329 | 0.417 |
| chr20 | 63025520 | 1475726 | 0.0234 | 0.1742 |
| chr21 | 48129895 | 861493 | 0.0179 | 0.1661 |
| chr22 | 51304566 | 597453 | 0.0116 | 0.1174 |
| chrMT | 16571 | 70652 | 4.2636 | 3.231 |
| chrX | 155270560 | 2396539 | 0.0154 | 0.1517 |
| chrY | 59373566 | 210869 | 0.0036 | 0.1069 |

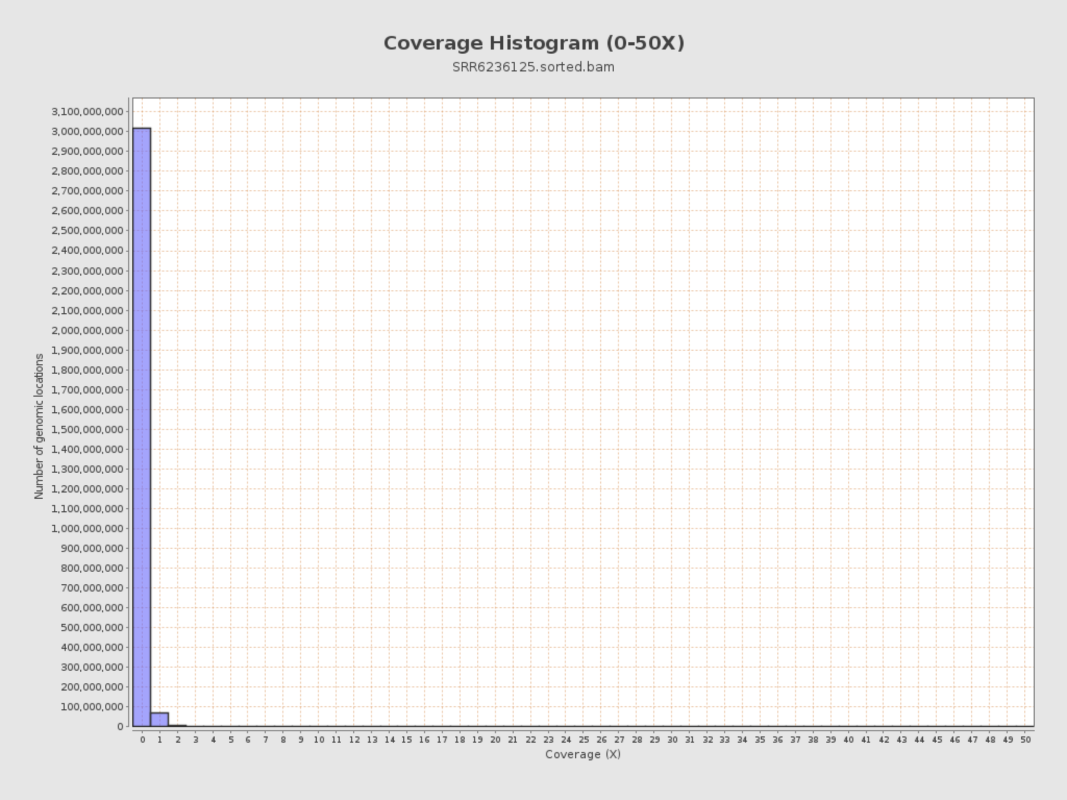
# 3. Results : Coverage across reference



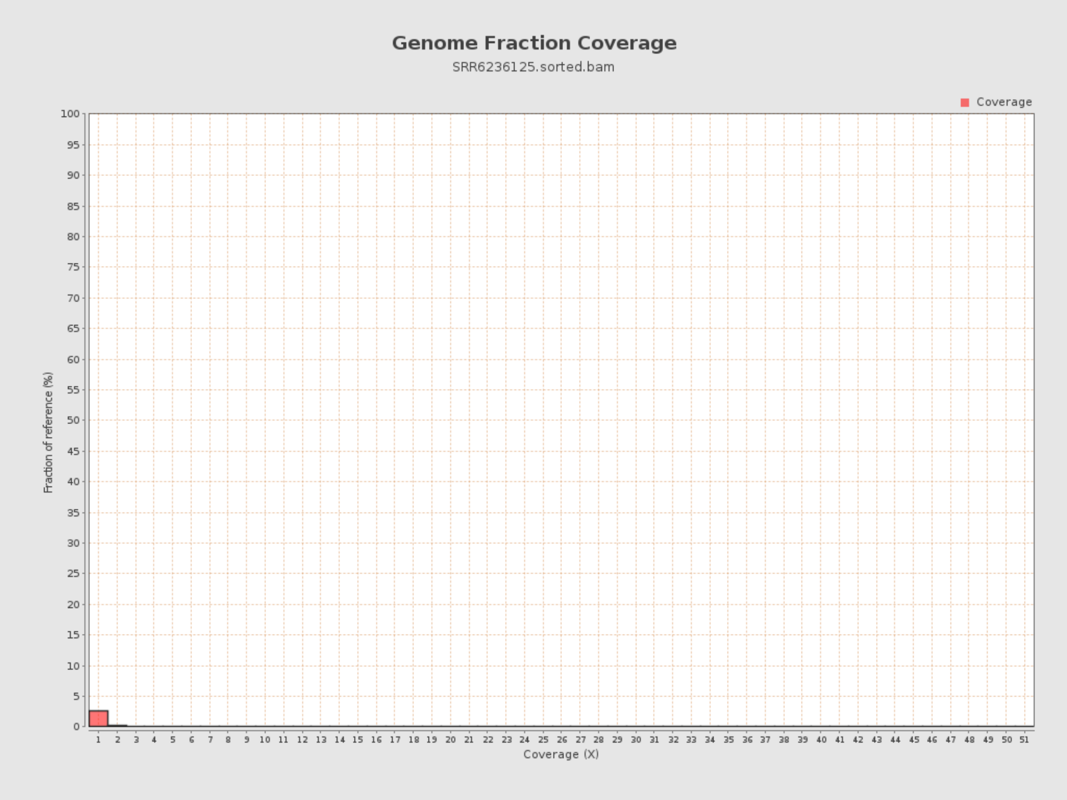
# 4. Results : Coverage Histogram



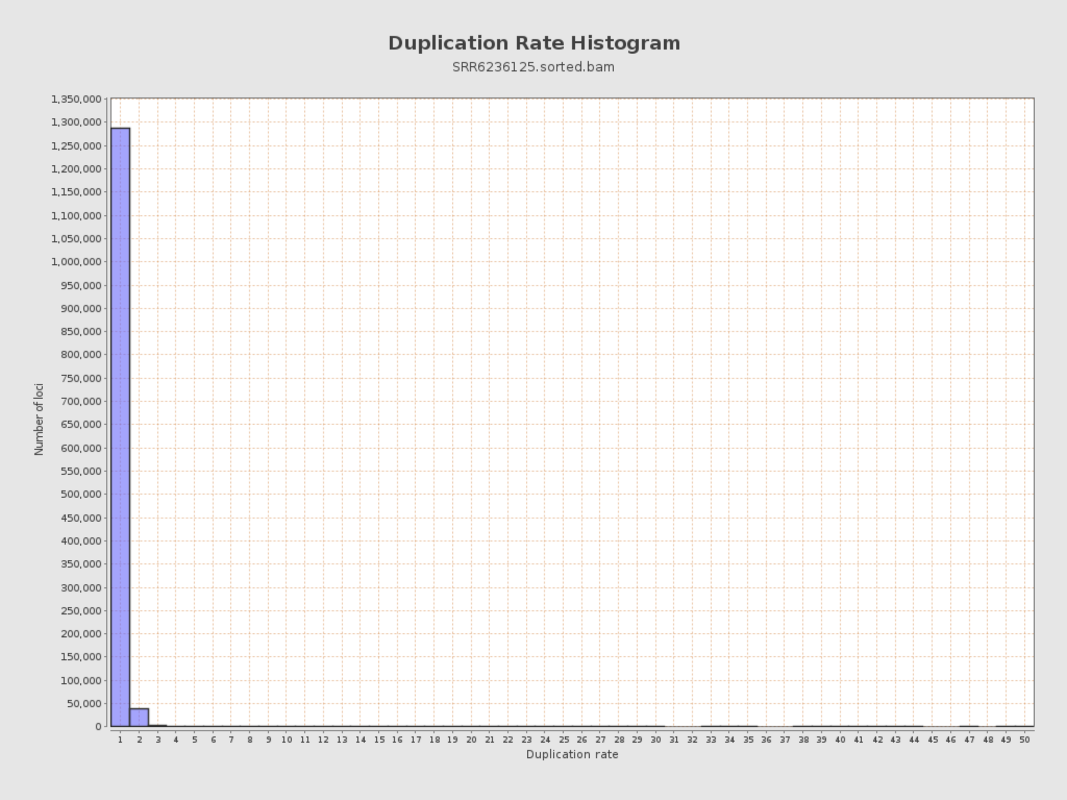
# 5. Results : Coverage Histogram (0-50X)



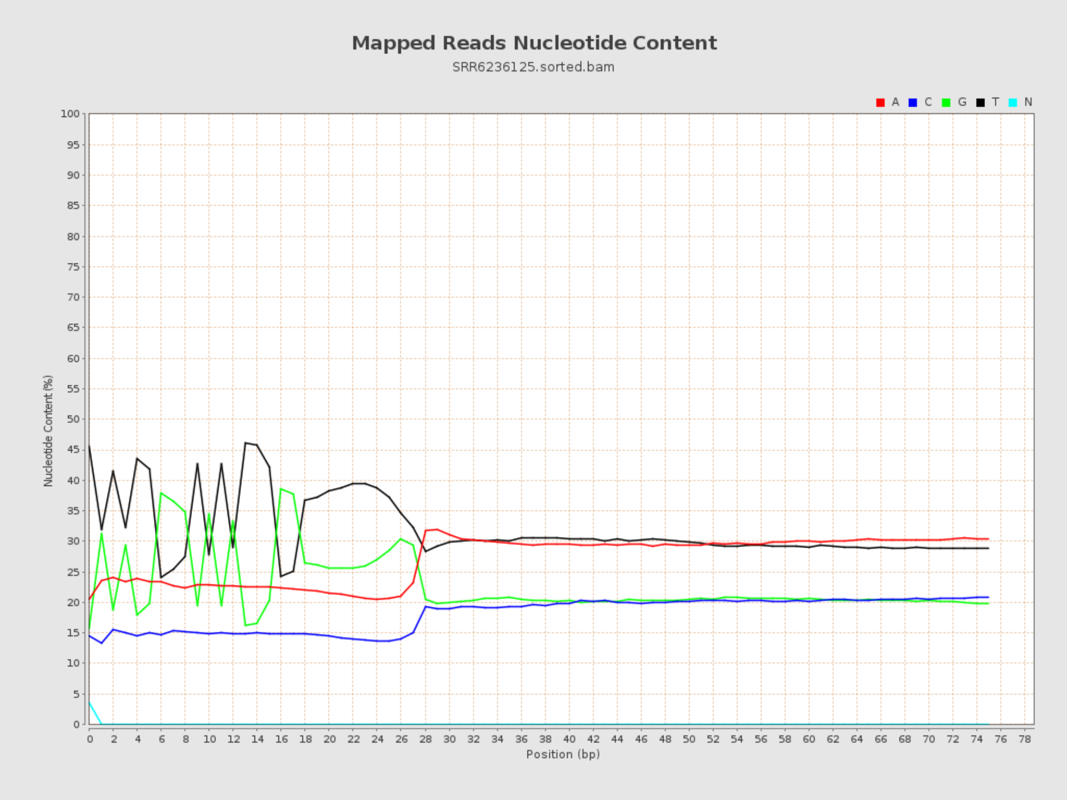
# 6. Results : Genome Fraction Coverage



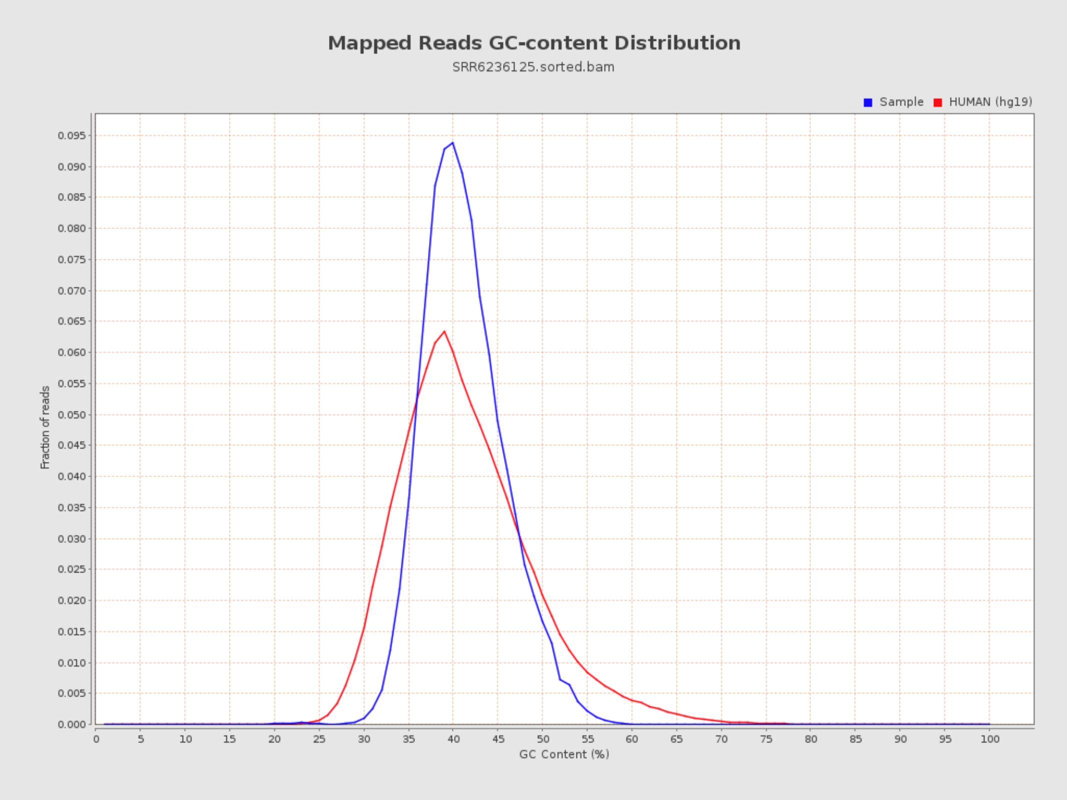
# 7. Results : Duplication Rate Histogram



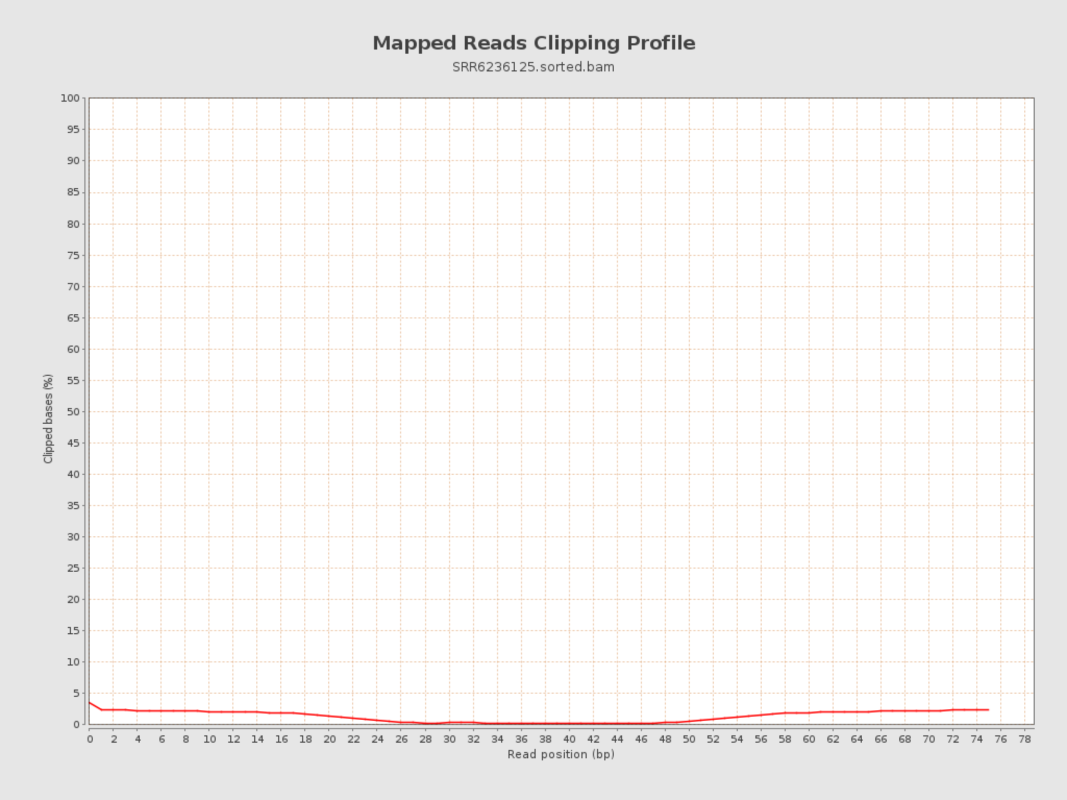
# 8. Results : Mapped Reads Nucleotide Content



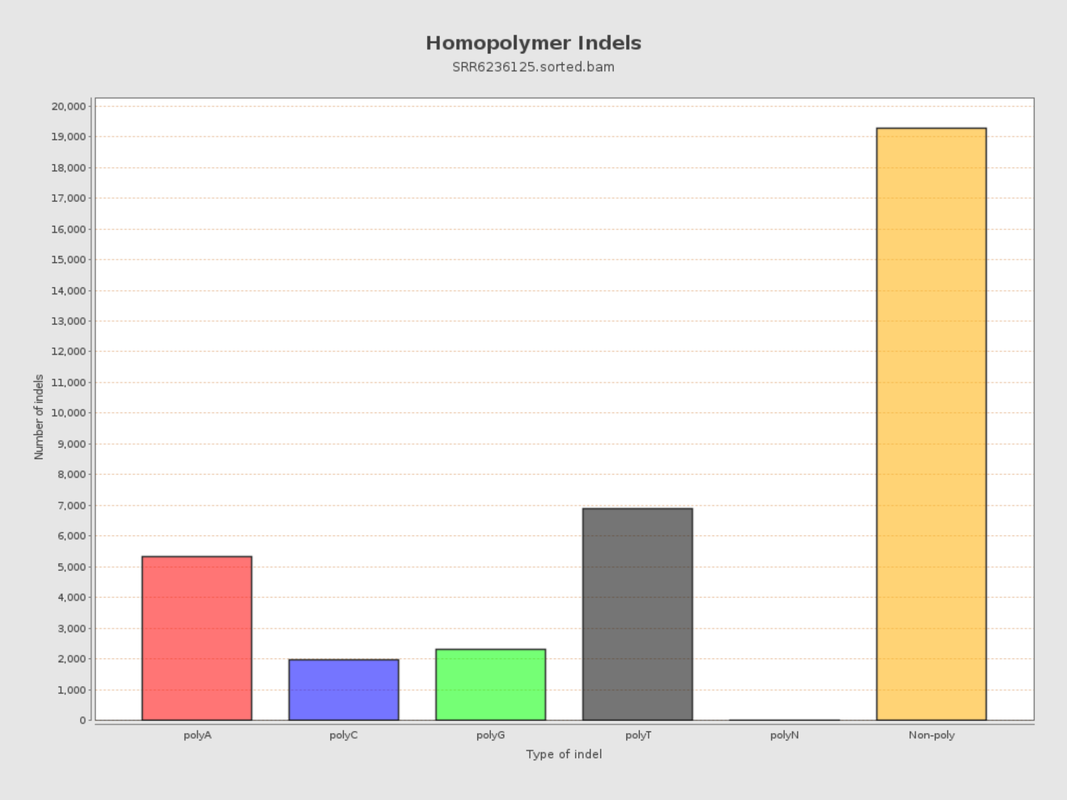
# 9. Results : Mapped Reads GC-content Distribution



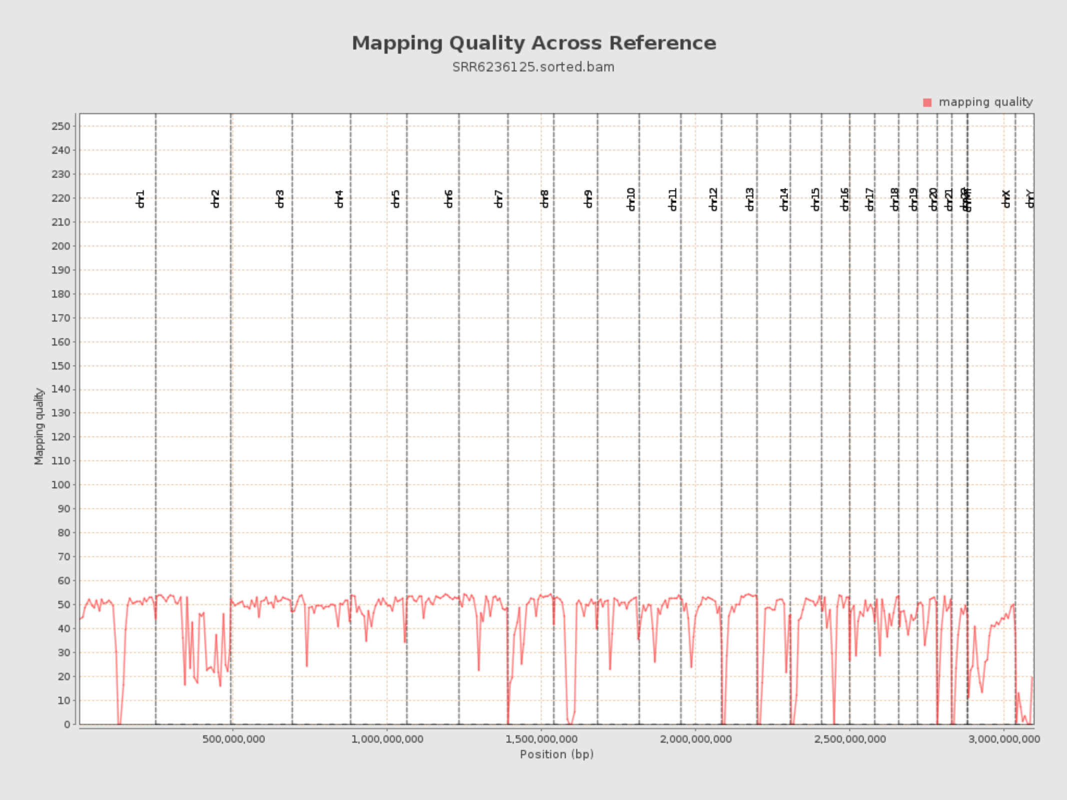
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram