# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/17 23:10:58*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238627.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_SRR6238627 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238627.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 17 23:10:58 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6238627.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,774,684 |
| Mapped reads | 4,210,385 / 88.18% |
| Unmapped reads | 564,299 / 11.82% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 43,413 / 0.91% |
| Read min/max/mean length | 30 / 76 / 76.32 |
| Duplicated reads (estimated) | 2,061,319 / 43.17% |
| Duplication rate | 22.86% |
| Clipped reads | 2,842,737 / 59.54% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 64,116,036 / 25.03% |
| Number/percentage of C's | 44,206,603 / 17.26% |
| Number/percentage of T's | 87,131,319 / 34.01% |
| Number/percentage of G's | 60,702,530 / 23.7% |
| Number/percentage of N's | 5,735 / 0% |
| GC Percentage | 40.95% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0828 |
| | |

| | |
|---|---|
| Standard Deviation | 1.422 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 40.28 |

## 2.5. Mismatches and indels

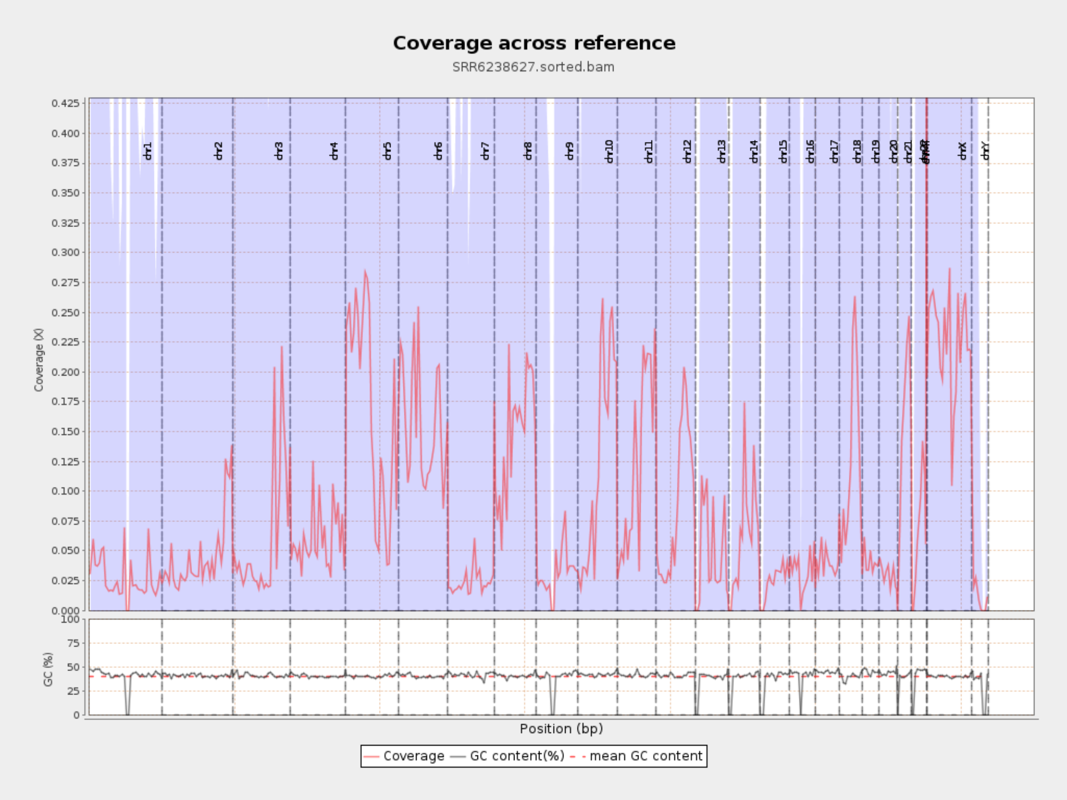
| | |
|---|---|
| General error rate | 0.57% |
| Mismatches | 1,427,086 |
| Insertions | 16,356 |
| Mapped reads with at least one insertion | 0.38% |
| Deletions | 66,861 |
| Mapped reads with at least one deletion | 1.57% |
| Homopolymer indels | 42.01% |

## 2.6. Chromosome stats

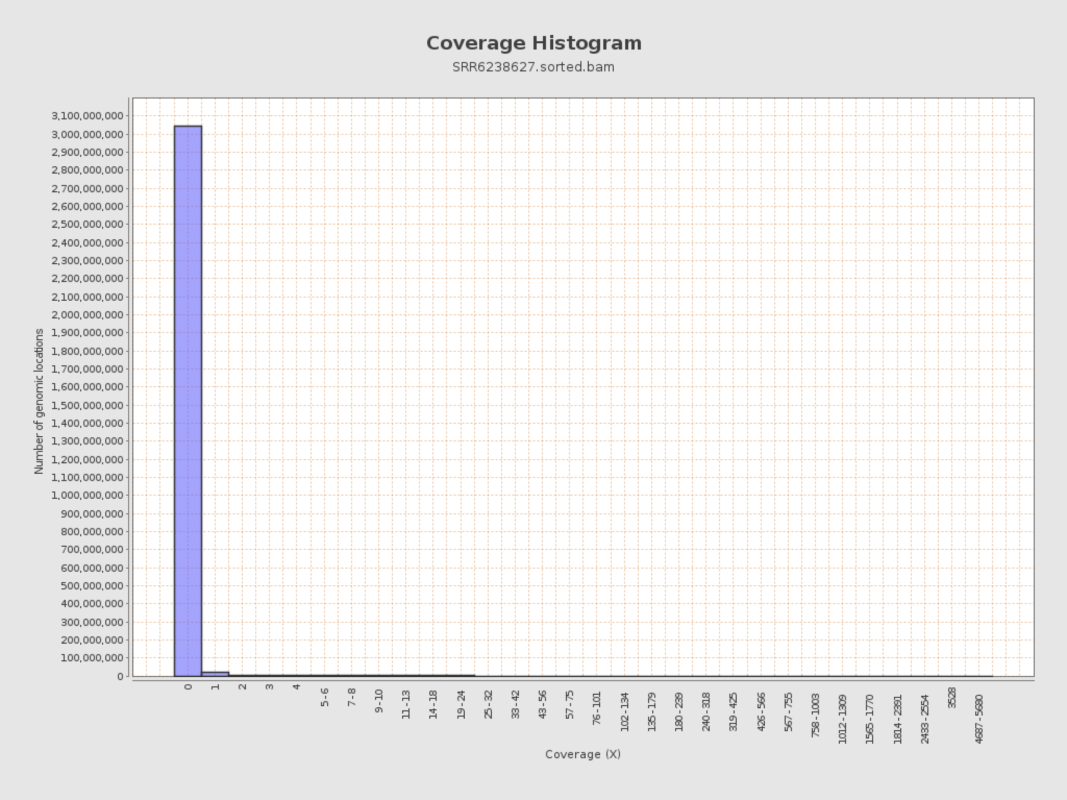
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 6715699 | 0.0269 | 1.0823 |
| chr2 | 243199373 | 10962880 | 0.0451 | 2.6135 |
| chr3 | 198022430 | 12023454 | 0.0607 | 0.9131 |
| chr4 | 191154276 | 11305355 | 0.0591 | 0.8927 |
| chr5 | 180915260 | 30653986 | 0.1694 | 1.5576 |
| chr6 | 171115067 | 26632884 | 0.1556 | 1.7631 |
| chr7 | 159138663 | 3808860 | 0.0239 | 0.6778 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 21771379 | 0.1487 | 1.629 |
| chr9 | 141213431 | 4404300 | 0.0312 | 0.7034 |
| chr10 | 135534747 | 16910004 | 0.1248 | 1.3062 |
| chr11 | 135006516 | 16538640 | 0.1225 | 1.3522 |
| chr12 | 133851895 | 12007221 | 0.0897 | 1.1238 |
| chr13 | 115169878 | 5552272 | 0.0482 | 1.0538 |
| chr14 | 107349540 | 6901691 | 0.0643 | 1.0331 |
| chr15 | 102531392 | 2525438 | 0.0246 | 0.7942 |
| chr16 | 90354753 | 3009063 | 0.0333 | 0.7067 |
| chr17 | 81195210 | 3269685 | 0.0403 | 0.7214 |
| chr18 | 78077248 | 10180857 | 0.1304 | 2.9135 |
| chr19 | 59128983 | 2410929 | 0.0408 | 1.0223 |
| chr20 | 63025520 | 1901245 | 0.0302 | 0.6509 |
| chr21 | 48129895 | 7374999 | 0.1532 | 1.4668 |
| chr22 | 51304566 | 3457064 | 0.0674 | 0.9483 |
| chrMT | 16571 | 11455 | 0.6913 | 3.078 |
| chrX | 155270560 | 34999249 | 0.2254 | 1.824 |
| chrY | 59373566 | 946658 | 0.0159 | 0.5294 |

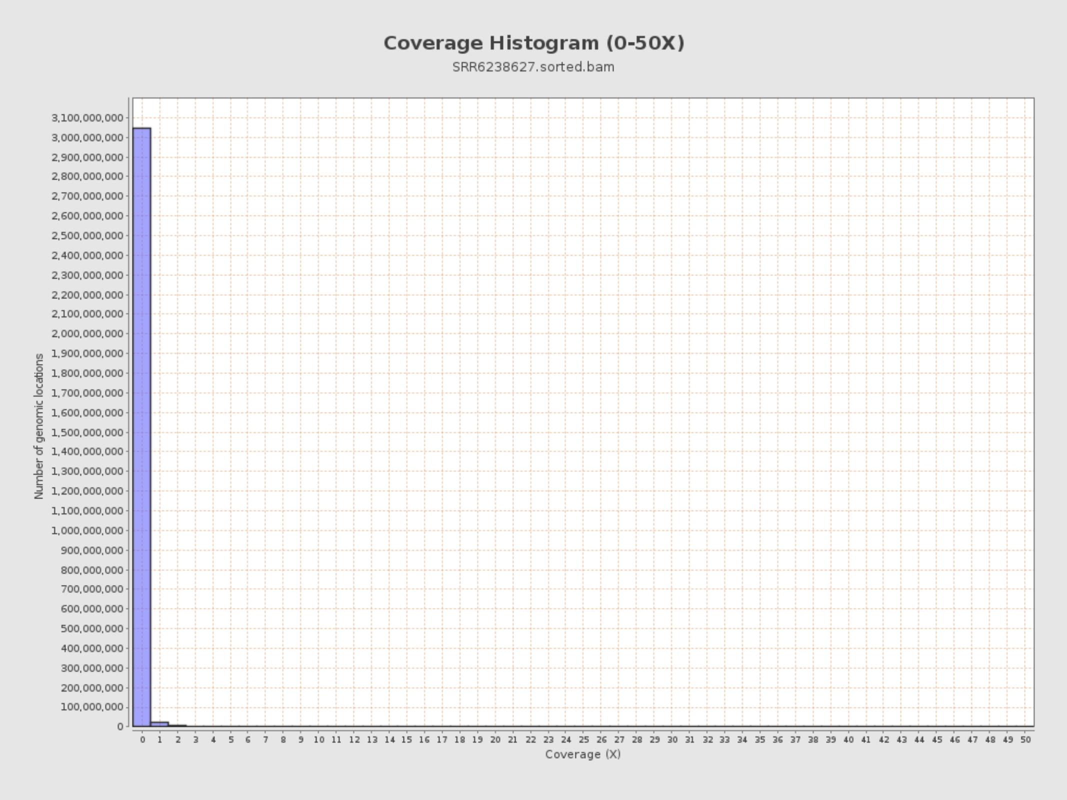
# 3. Results : Coverage across reference



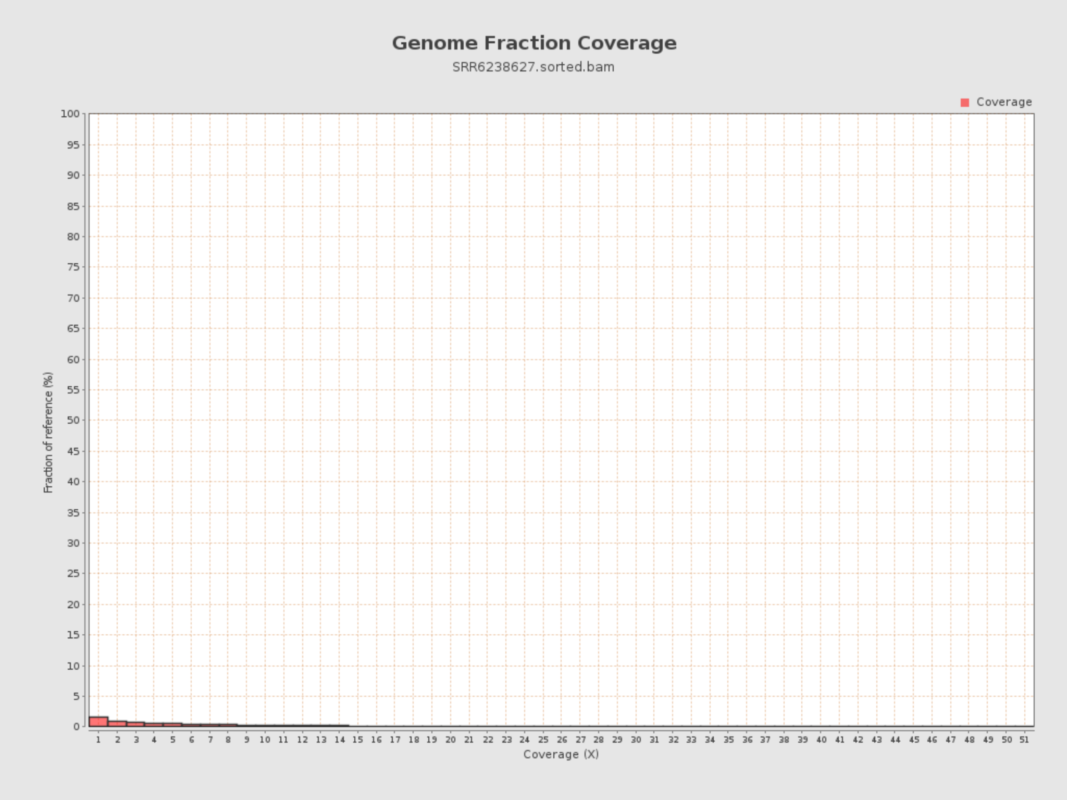
# 4. Results : Coverage Histogram



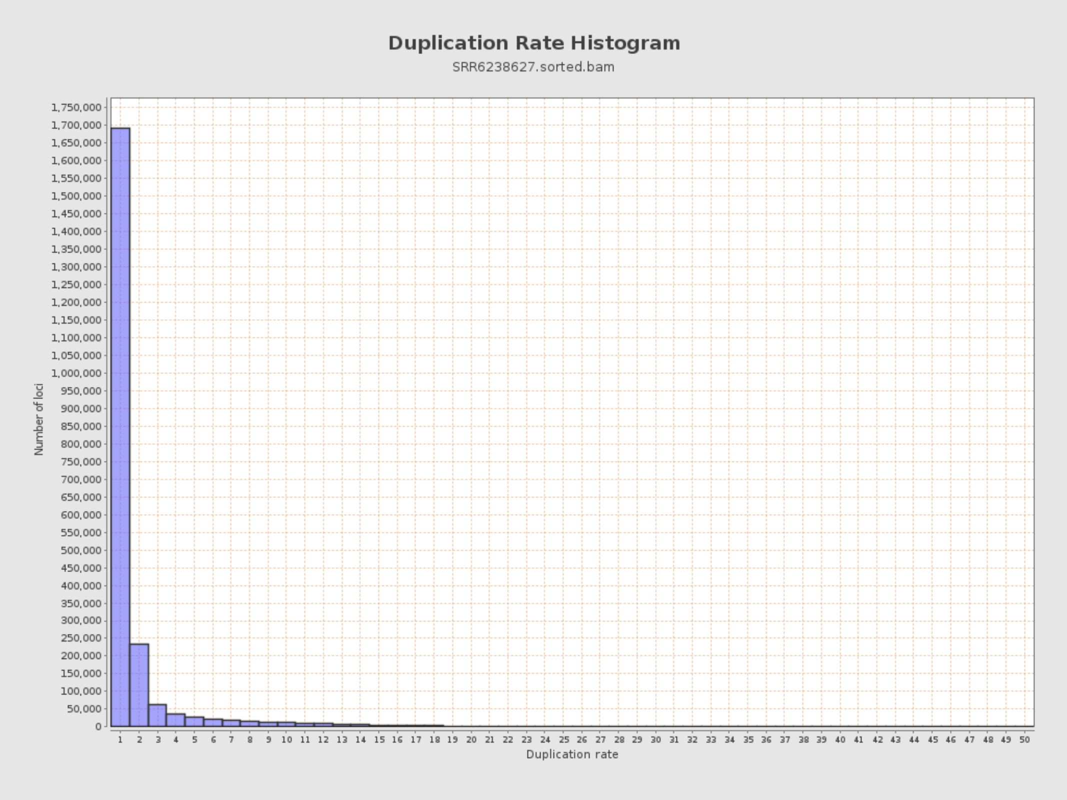
# 5. Results : Coverage Histogram (0-50X)



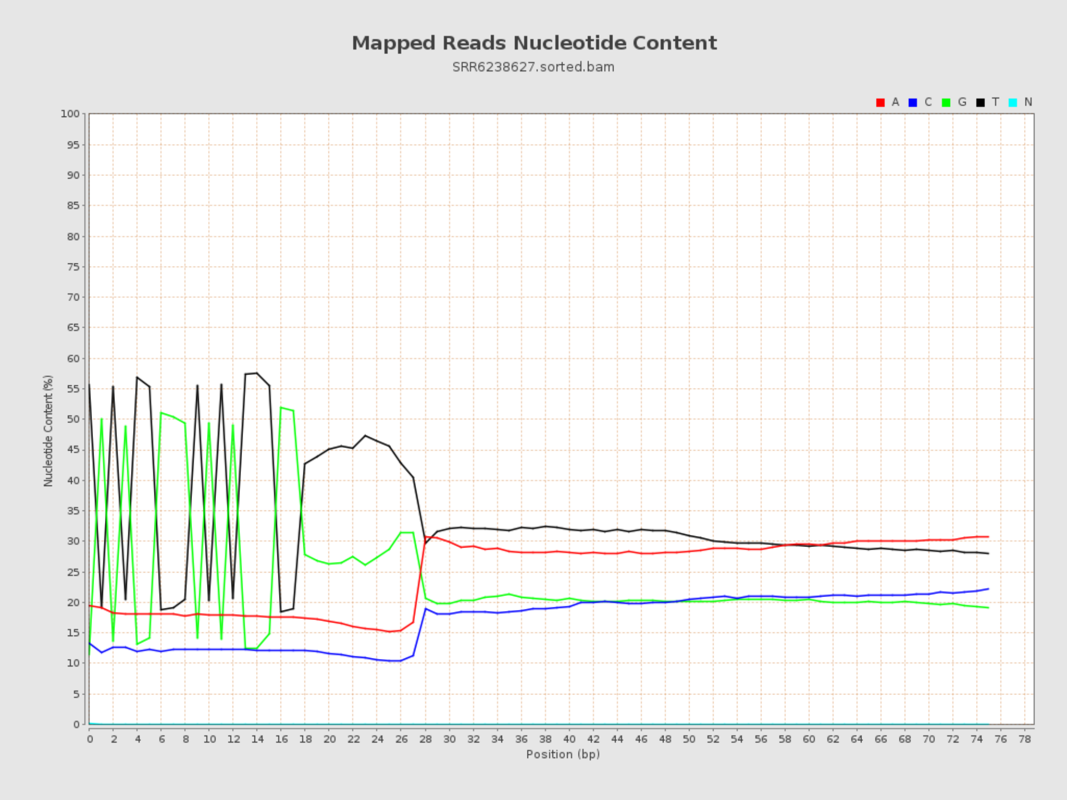
# 6. Results : Genome Fraction Coverage



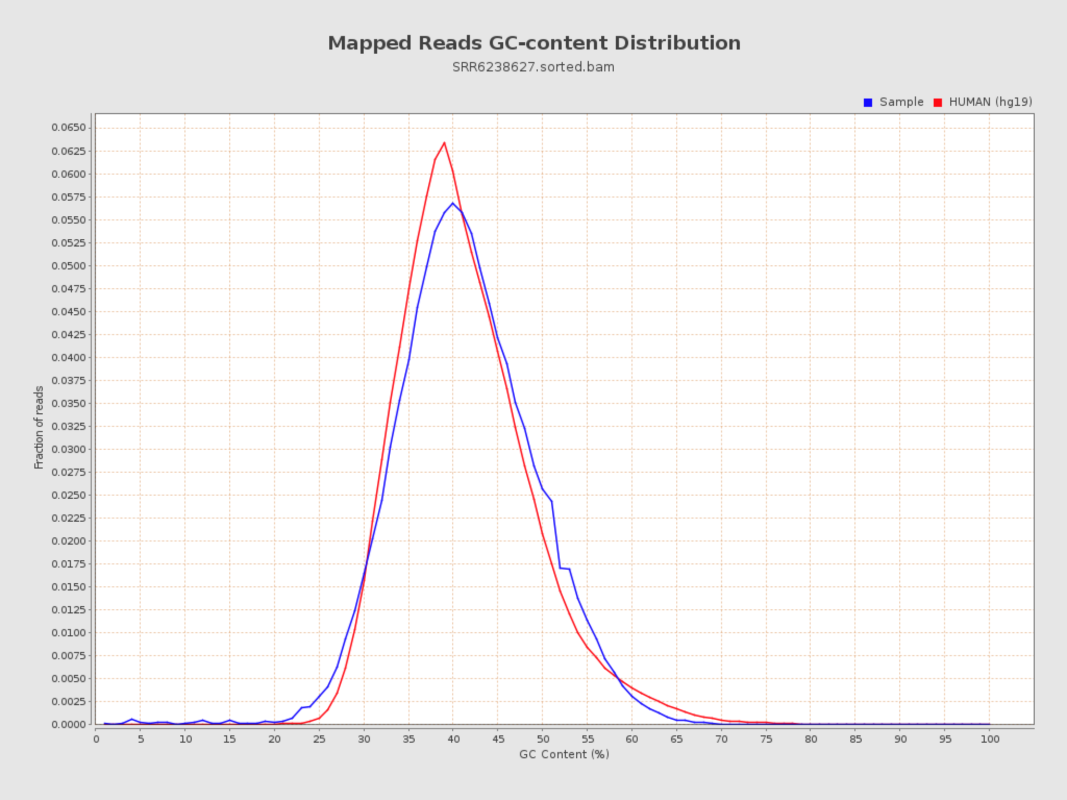
# 7. Results : Duplication Rate Histogram



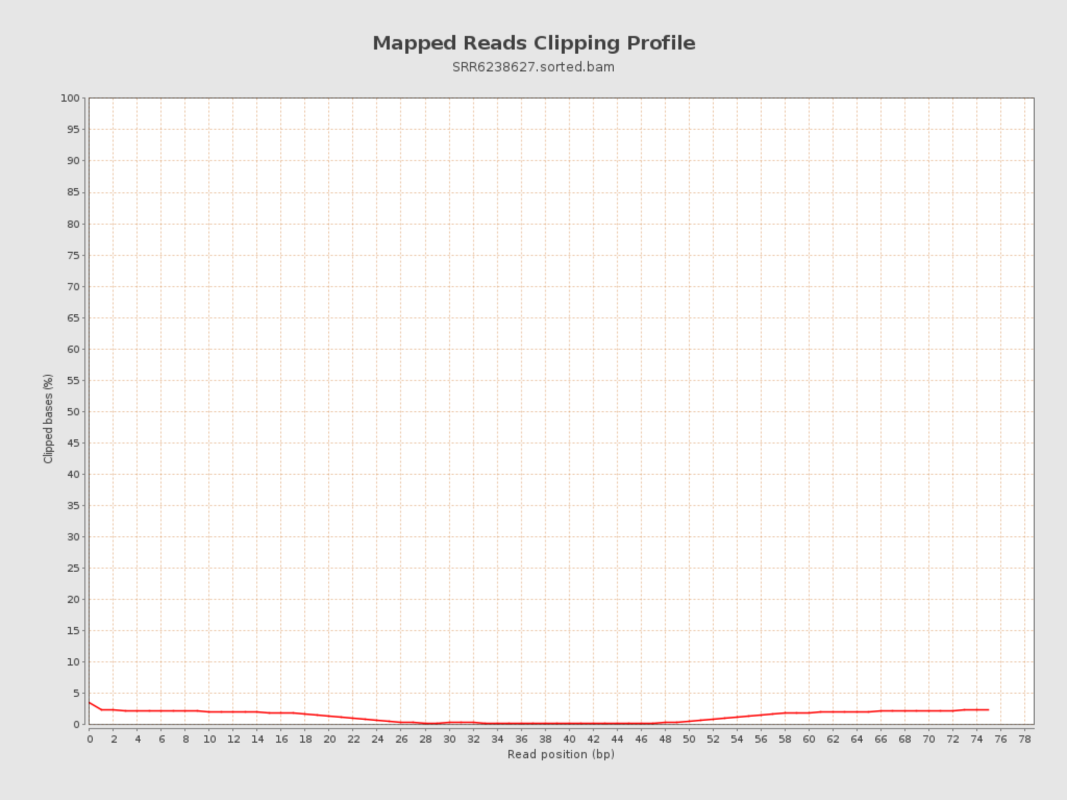
# 8. Results : Mapped Reads Nucleotide Content



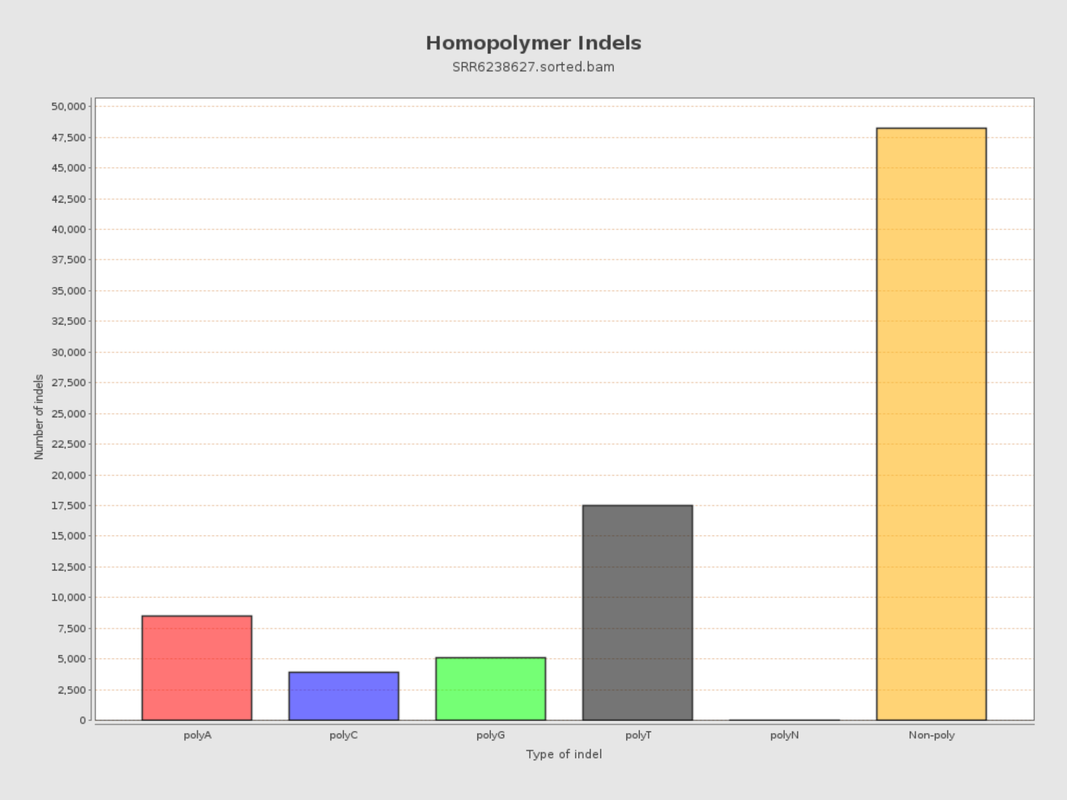
# 9. Results : Mapped Reads GC-content Distribution



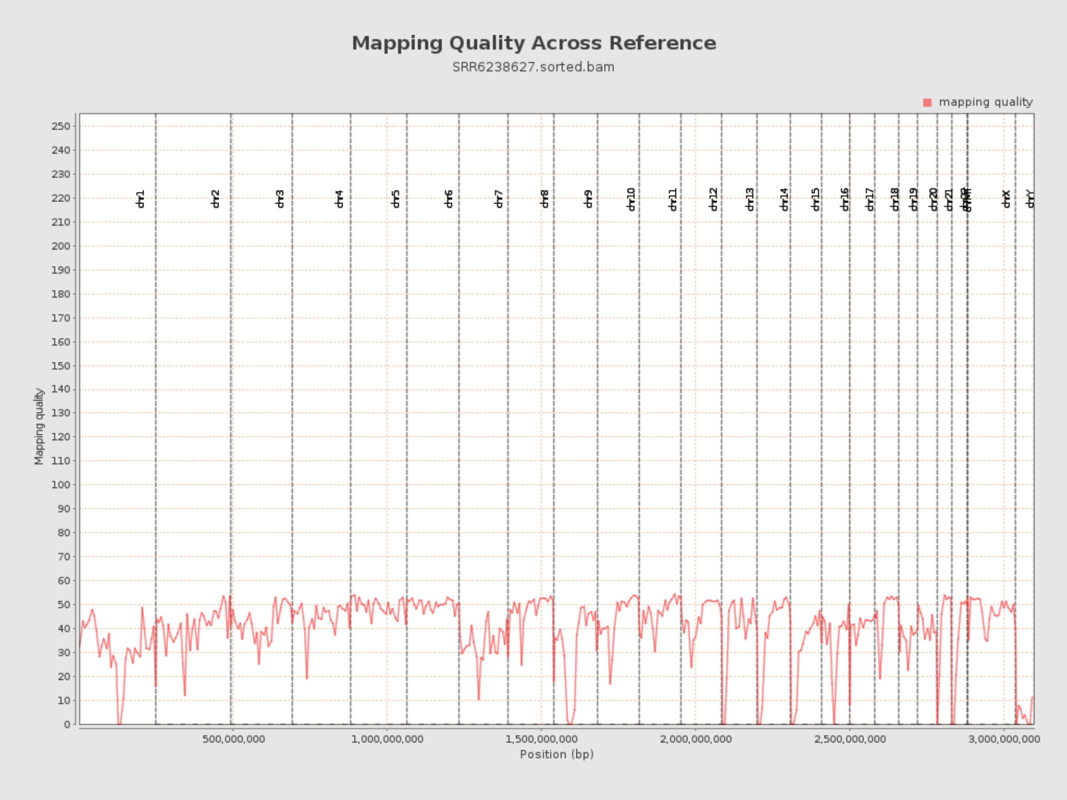
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram