# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/17 22:45:27*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238619.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_SRR6238619 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238619.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 17 22:45:26 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6238619.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,938,017 |
| Mapped reads | 2,523,812 / 85.9% |
| Unmapped reads | 414,205 / 14.1% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 22,981 / 0.78% |
| Read min/max/mean length | 30 / 76 / 76.27 |
| Duplicated reads (estimated) | 1,087,707 / 37.02% |
| Duplication rate | 22% |
| Clipped reads | 1,701,503 / 57.91% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 37,917,074 / 24.74% |
| Number/percentage of C's | 25,796,066 / 16.83% |
| Number/percentage of T's | 53,479,770 / 34.89% |
| Number/percentage of G's | 36,076,303 / 23.54% |
| Number/percentage of N's | 3,340 / 0% |
| GC Percentage | 40.37% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0495 |
| | |

| | |
|---|---|
| Standard Deviation | 1.1613 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 39.85 |

## 2.5. Mismatches and indels

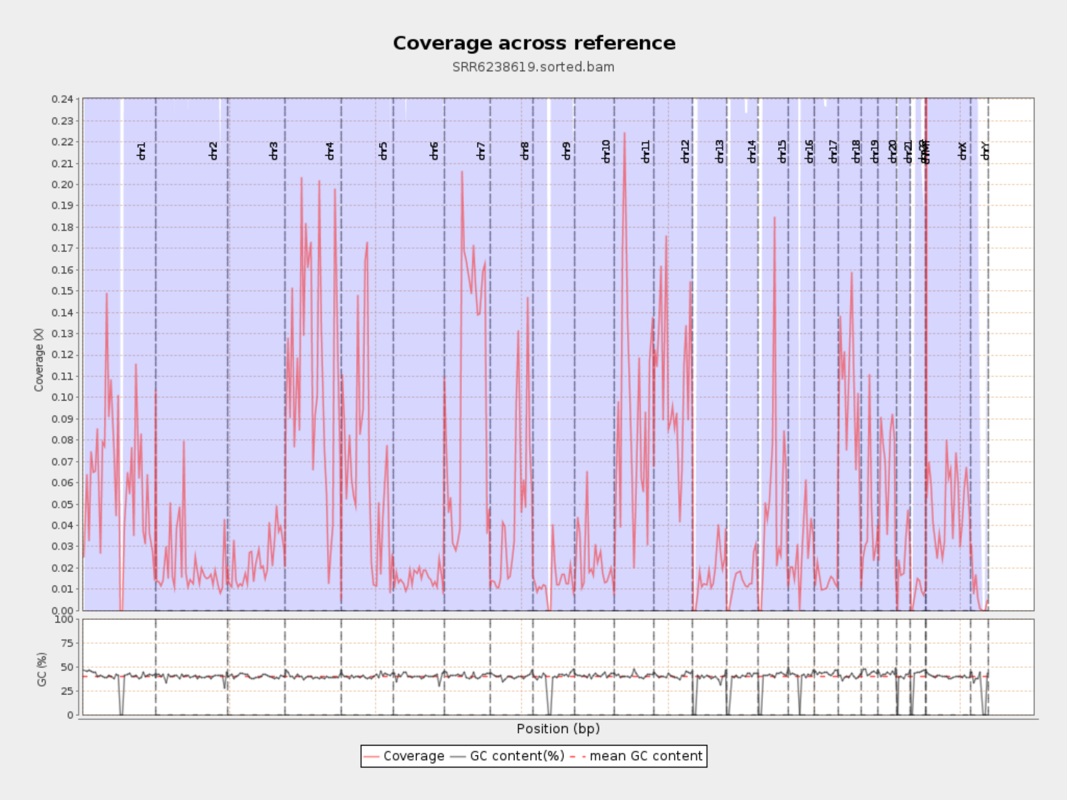
| | |
|---|---|
| General error rate | 0.68% |
| Mismatches | 1,018,880 |
| Insertions | 9,869 |
| Mapped reads with at least one insertion | 0.39% |
| Deletions | 53,036 |
| Mapped reads with at least one deletion | 2.08% |
| Homopolymer indels | 40.25% |

## 2.6. Chromosome stats

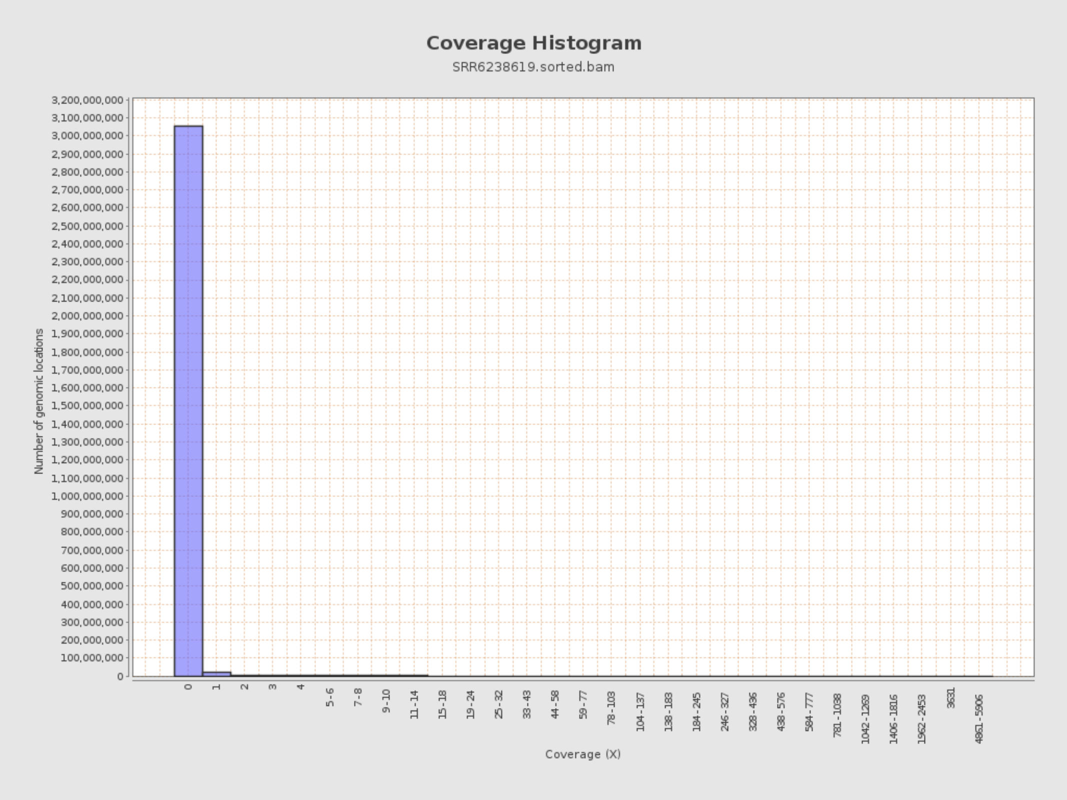
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 14927175 | 0.0599 | 1.2586 |
| chr2 | 243199373 | 5125354 | 0.0211 | 2.6401 |
| chr3 | 198022430 | 4585822 | 0.0232 | 0.4499 |
| chr4 | 191154276 | 21263952 | 0.1112 | 1.0186 |
| chr5 | 180915260 | 12092480 | 0.0668 | 0.7839 |
| chr6 | 171115067 | 2595525 | 0.0152 | 0.8536 |
| chr7 | 159138663 | 17193441 | 0.108 | 1.4055 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6888208 | 0.0471 | 1.0121 |
| chr9 | 141213431 | 1897421 | 0.0134 | 0.4966 |
| chr10 | 135534747 | 3180310 | 0.0235 | 0.6489 |
| chr11 | 135006516 | 12365056 | 0.0916 | 0.9436 |
| chr12 | 133851895 | 14479646 | 0.1082 | 0.9883 |
| chr13 | 115169878 | 1899414 | 0.0165 | 0.6842 |
| chr14 | 107349540 | 1521285 | 0.0142 | 0.3398 |
| chr15 | 102531392 | 5126075 | 0.05 | 0.8339 |
| chr16 | 90354753 | 2520672 | 0.0279 | 0.5154 |
| chr17 | 81195210 | 1115792 | 0.0137 | 0.2981 |
| chr18 | 78077248 | 8105746 | 0.1038 | 2.432 |
| chr19 | 59128983 | 2461376 | 0.0416 | 0.8553 |
| chr20 | 63025520 | 4304476 | 0.0683 | 0.797 |
| chr21 | 48129895 | 1221834 | 0.0254 | 0.4558 |
| chr22 | 51304566 | 421805 | 0.0082 | 0.2219 |
| chrMT | 16571 | 20826 | 1.2568 | 2.819 |
| chrX | 155270560 | 7622444 | 0.0491 | 0.6531 |
| chrY | 59373566 | 423433 | 0.0071 | 0.3364 |

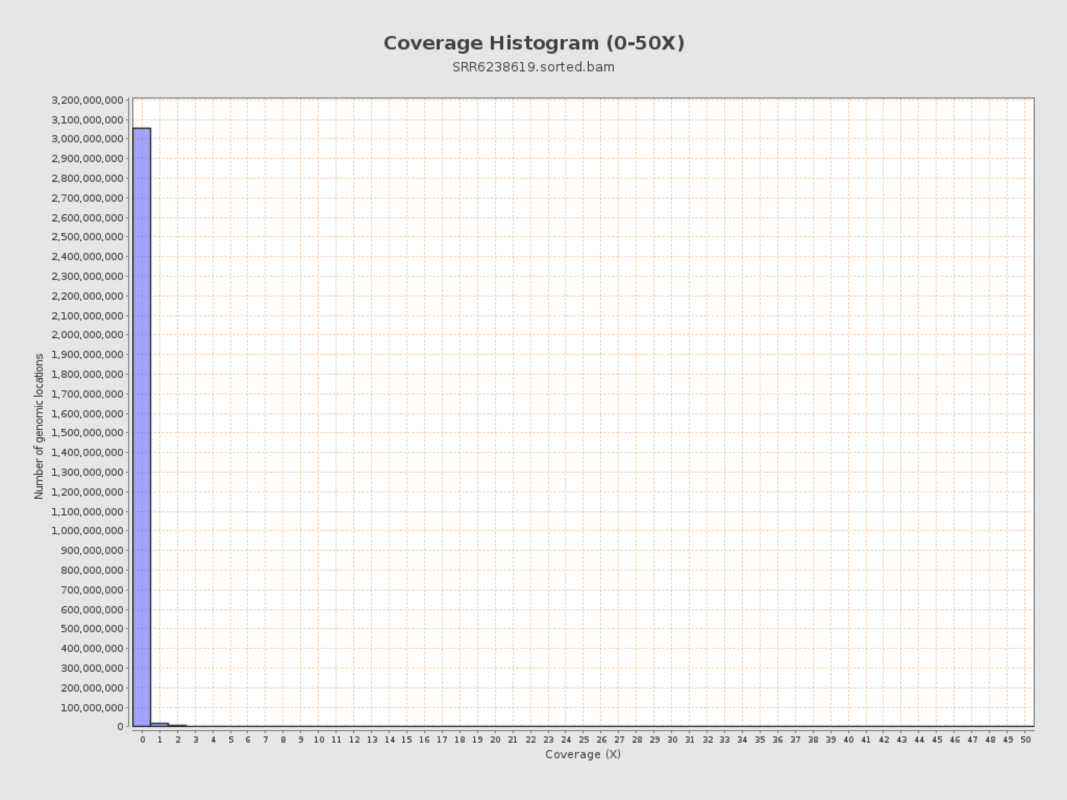
# 3. Results : Coverage across reference



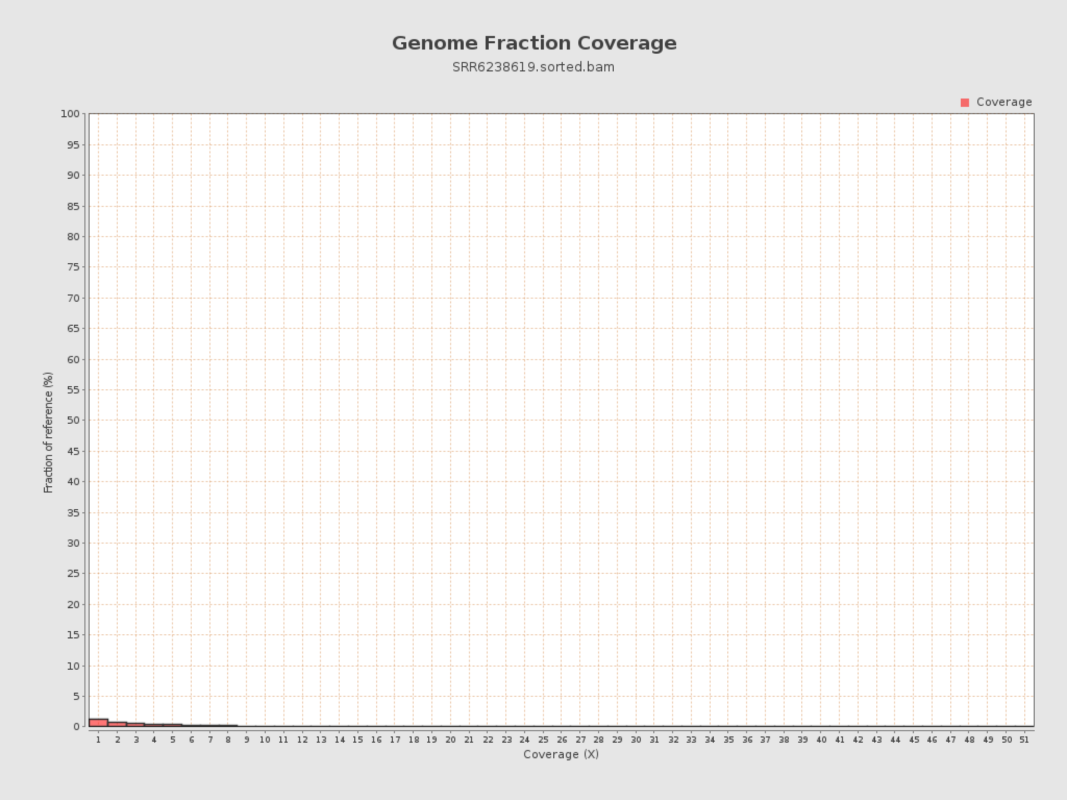
# 4. Results : Coverage Histogram



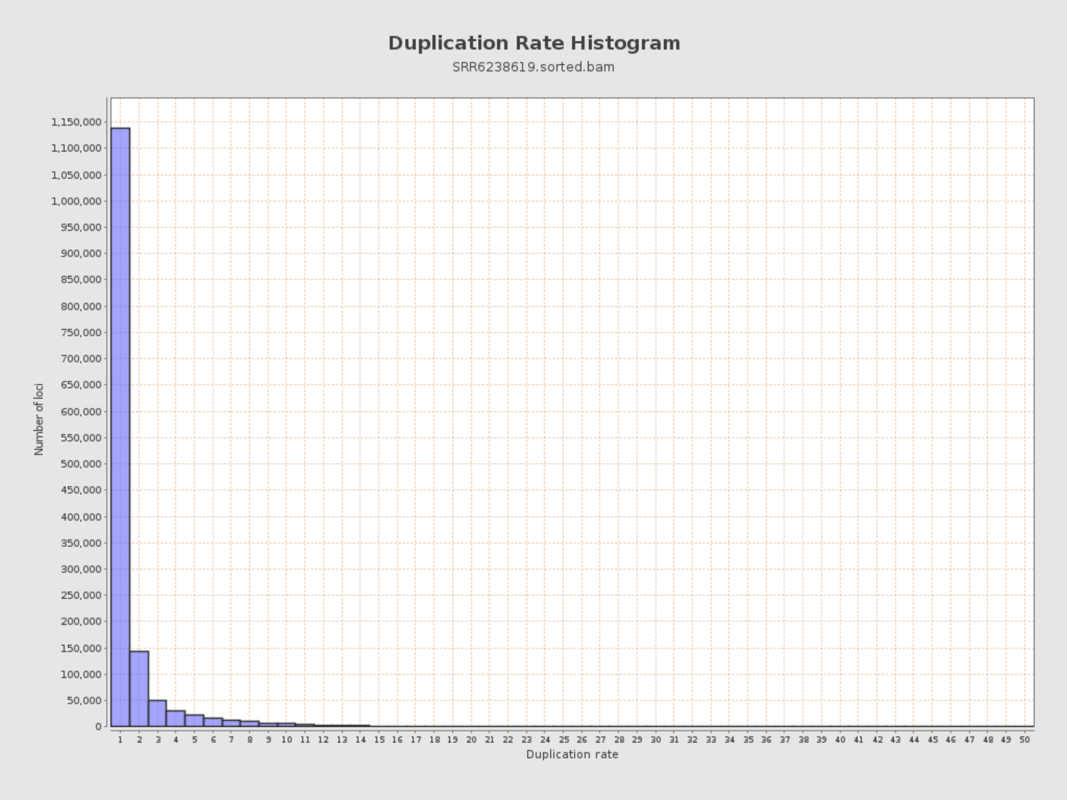
# 5. Results : Coverage Histogram (0-50X)



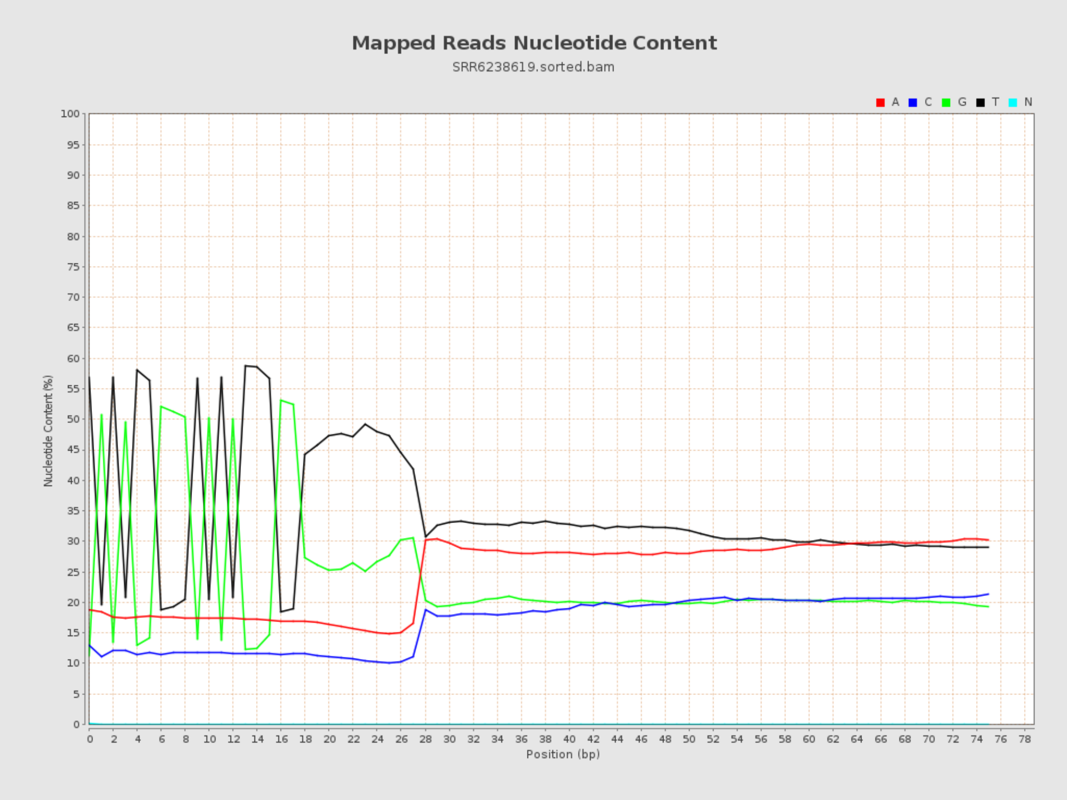
# 6. Results : Genome Fraction Coverage



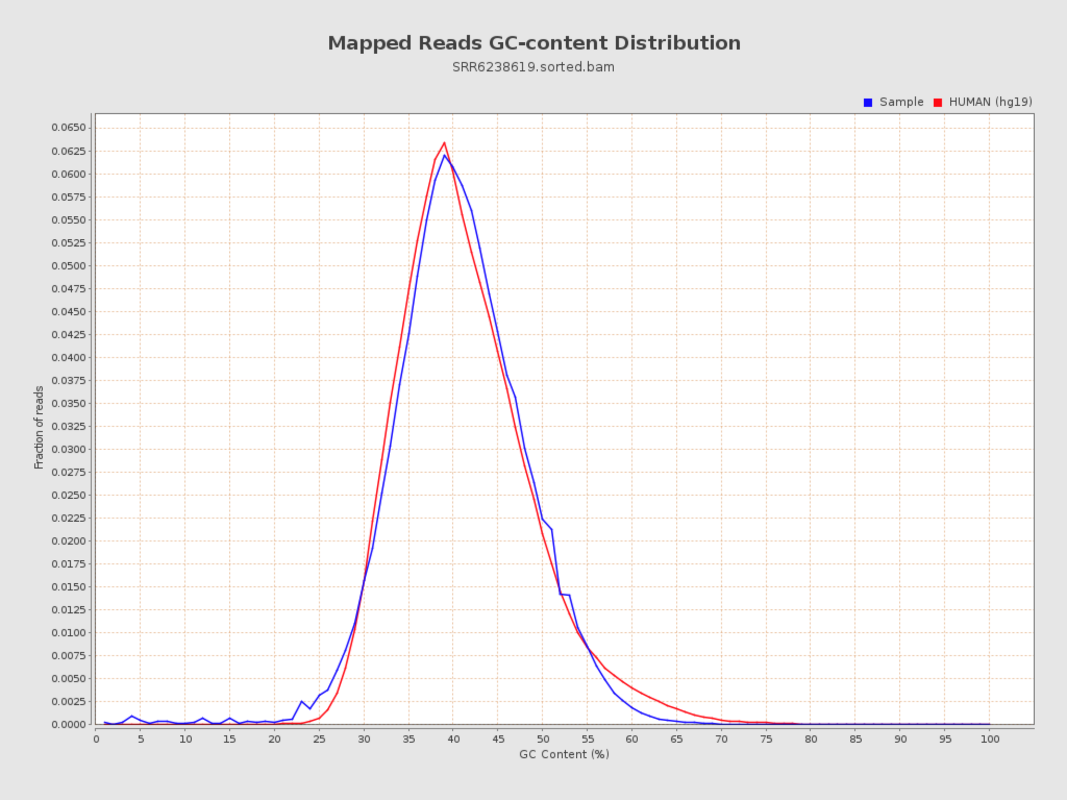
# 7. Results : Duplication Rate Histogram



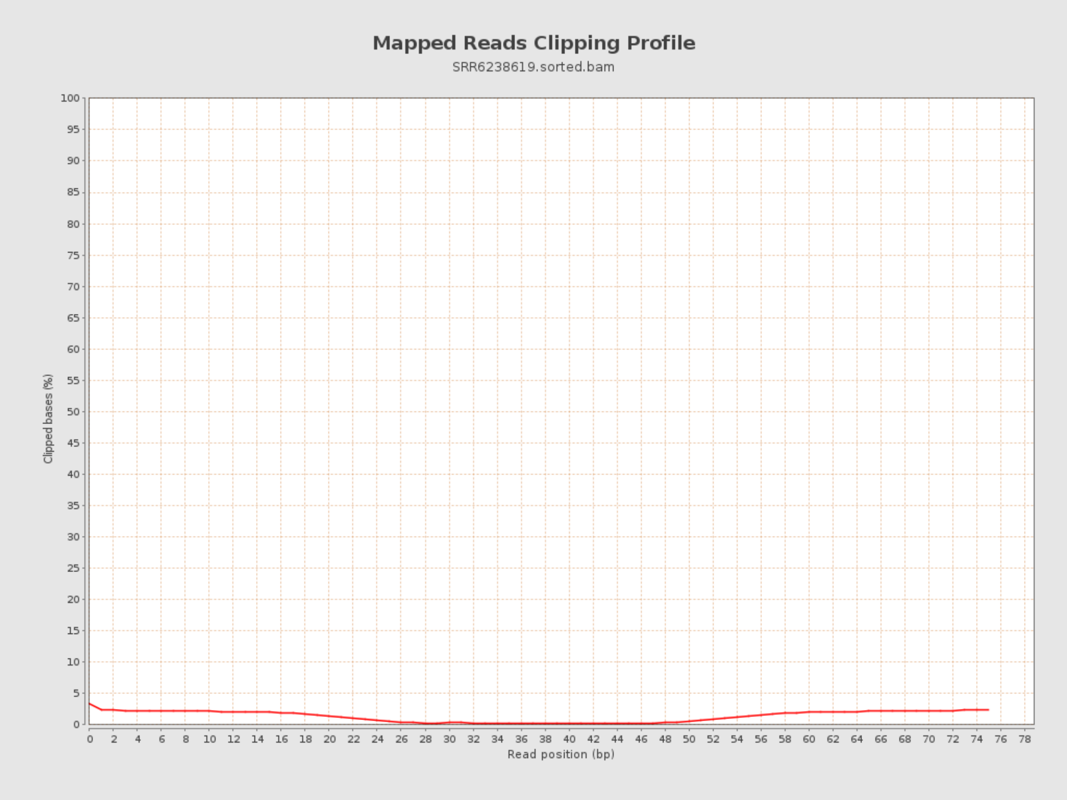
# 8. Results : Mapped Reads Nucleotide Content



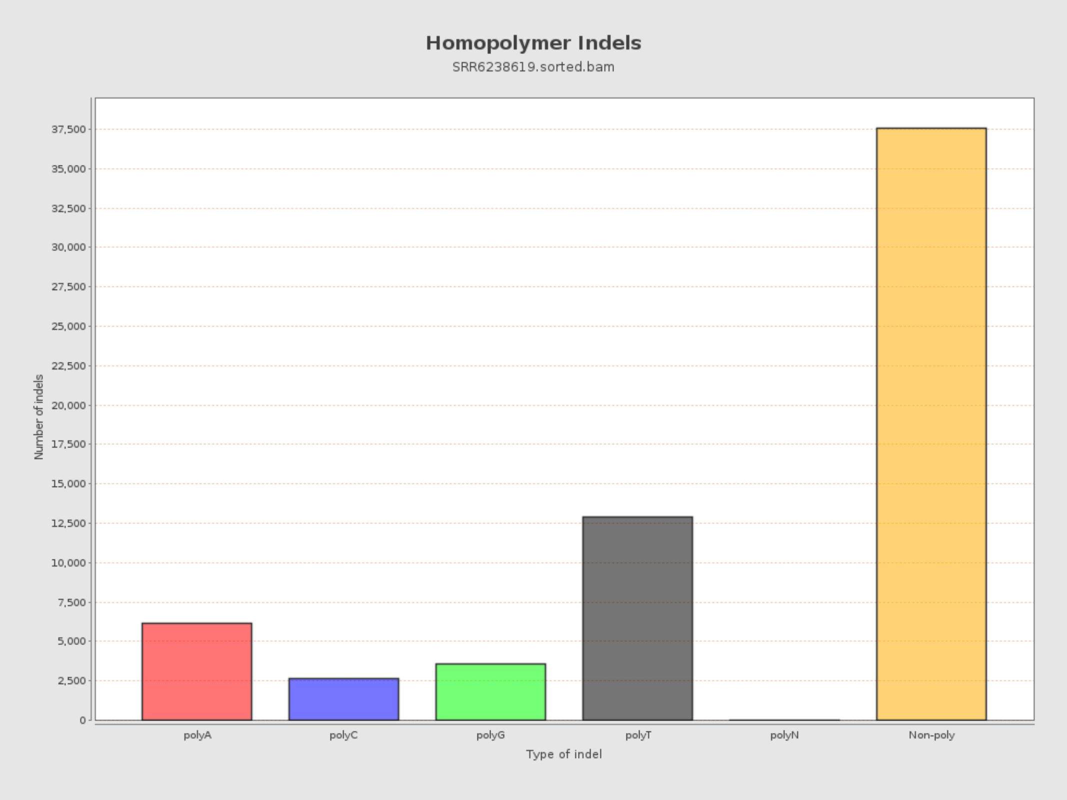
# 9. Results : Mapped Reads GC-content Distribution



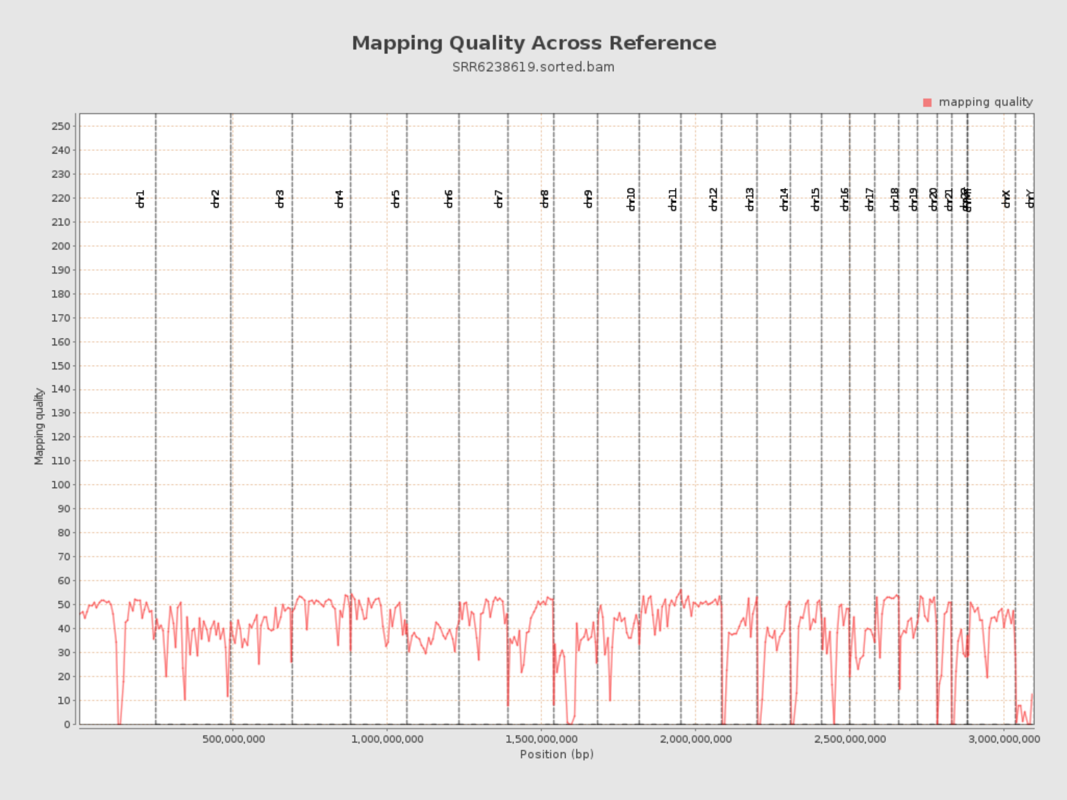
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram