# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/18 01:07:33*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238656.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_SRR6238656 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238656.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Sep 18 01:07:32 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6238656.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,710,309 |
| Mapped reads | 3,128,030 / 84.31% |
| Unmapped reads | 582,279 / 15.69% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 24,544 / 0.66% |
| Read min/max/mean length | 30 / 76 / 76.23 |
| Duplicated reads (estimated) | 1,035,882 / 27.92% |
| Duplication rate | 21.26% |
| Clipped reads | 1,954,048 / 52.67% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 47,725,166 / 24.65% |
| Number/percentage of C's | 34,158,410 / 17.64% |
| Number/percentage of T's | 65,025,249 / 33.58% |
| Number/percentage of G's | 46,703,119 / 24.12% |
| Number/percentage of N's | 4,422 / 0% |
| GC Percentage | 41.76% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0626 |
| | |

| | |
|---|---|
| Standard Deviation | 0.9721 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.47 |

## 2.5. Mismatches and indels

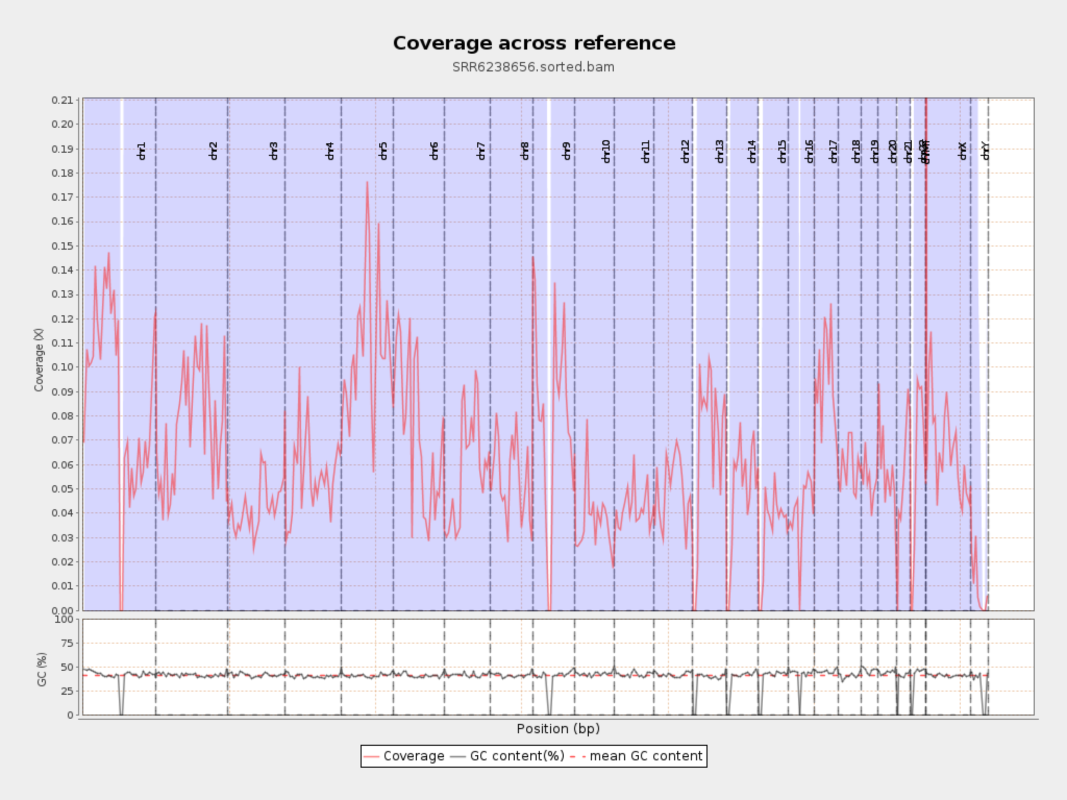
| | |
|---|---|
| General error rate | 0.56% |
| Mismatches | 1,062,894 |
| Insertions | 12,642 |
| Mapped reads with at least one insertion | 0.4% |
| Deletions | 45,534 |
| Mapped reads with at least one deletion | 1.44% |
| Homopolymer indels | 41.77% |

## 2.6. Chromosome stats

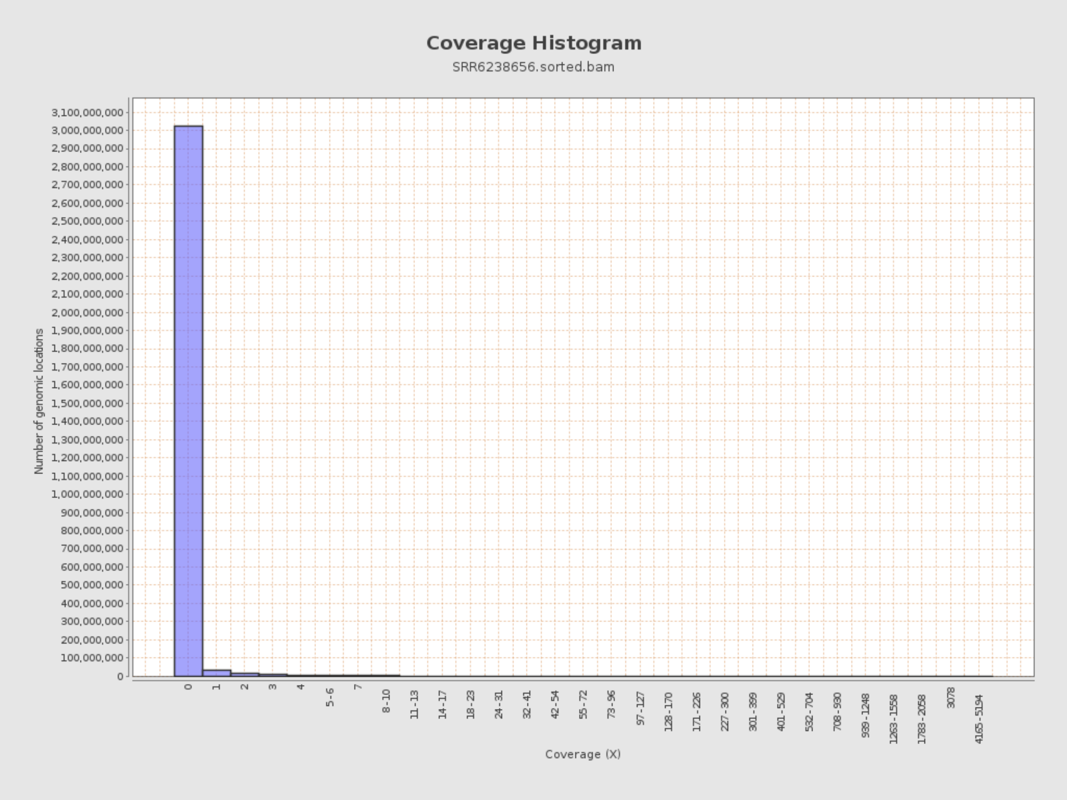
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 21855679 | 0.0877 | 1.1119 |
| chr2 | 243199373 | 18680761 | 0.0768 | 2.3156 |
| chr3 | 198022430 | 8486156 | 0.0429 | 0.4909 |
| chr4 | 191154276 | 10489251 | 0.0549 | 0.555 |
| chr5 | 180915260 | 19661309 | 0.1087 | 0.7649 |
| chr6 | 171115067 | 12575848 | 0.0735 | 0.896 |
| chr7 | 159138663 | 9344511 | 0.0587 | 0.8198 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 8014755 | 0.0548 | 0.6667 |
| chr9 | 141213431 | 11138783 | 0.0789 | 0.7028 |
| chr10 | 135534747 | 4929060 | 0.0364 | 0.5602 |
| chr11 | 135006516 | 5712209 | 0.0423 | 0.4859 |
| chr12 | 133851895 | 6607546 | 0.0494 | 0.5083 |
| chr13 | 115169878 | 7949027 | 0.069 | 0.7085 |
| chr14 | 107349540 | 5300089 | 0.0494 | 0.5331 |
| chr15 | 102531392 | 3463539 | 0.0338 | 0.5517 |
| chr16 | 90354753 | 3603954 | 0.0399 | 0.4958 |
| chr17 | 81195210 | 7805897 | 0.0961 | 0.7636 |
| chr18 | 78077248 | 4579583 | 0.0587 | 1.844 |
| chr19 | 59128983 | 3186970 | 0.0539 | 0.8001 |
| chr20 | 63025520 | 3660202 | 0.0581 | 0.6001 |
| chr21 | 48129895 | 2708472 | 0.0563 | 0.5575 |
| chr22 | 51304566 | 3022492 | 0.0589 | 0.5586 |
| chrMT | 16571 | 31412 | 1.8956 | 2.7746 |
| chrX | 155270560 | 10342607 | 0.0666 | 0.6081 |
| chrY | 59373566 | 544041 | 0.0092 | 0.3636 |

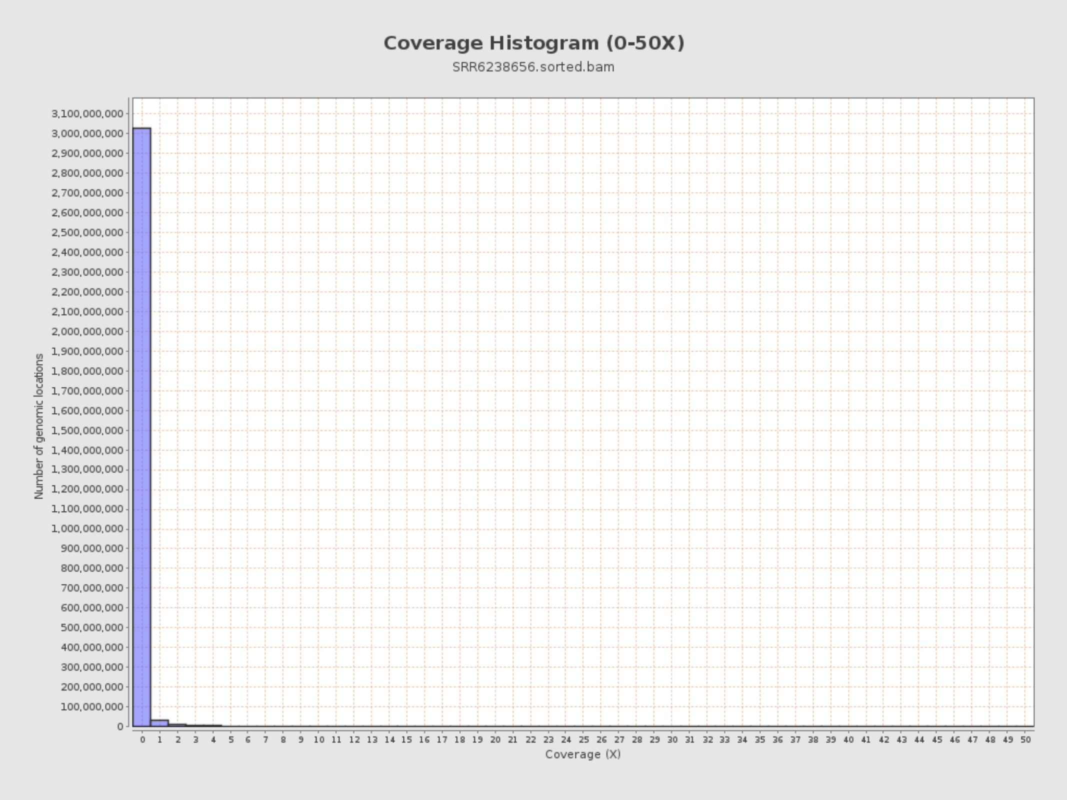
# 3. Results : Coverage across reference



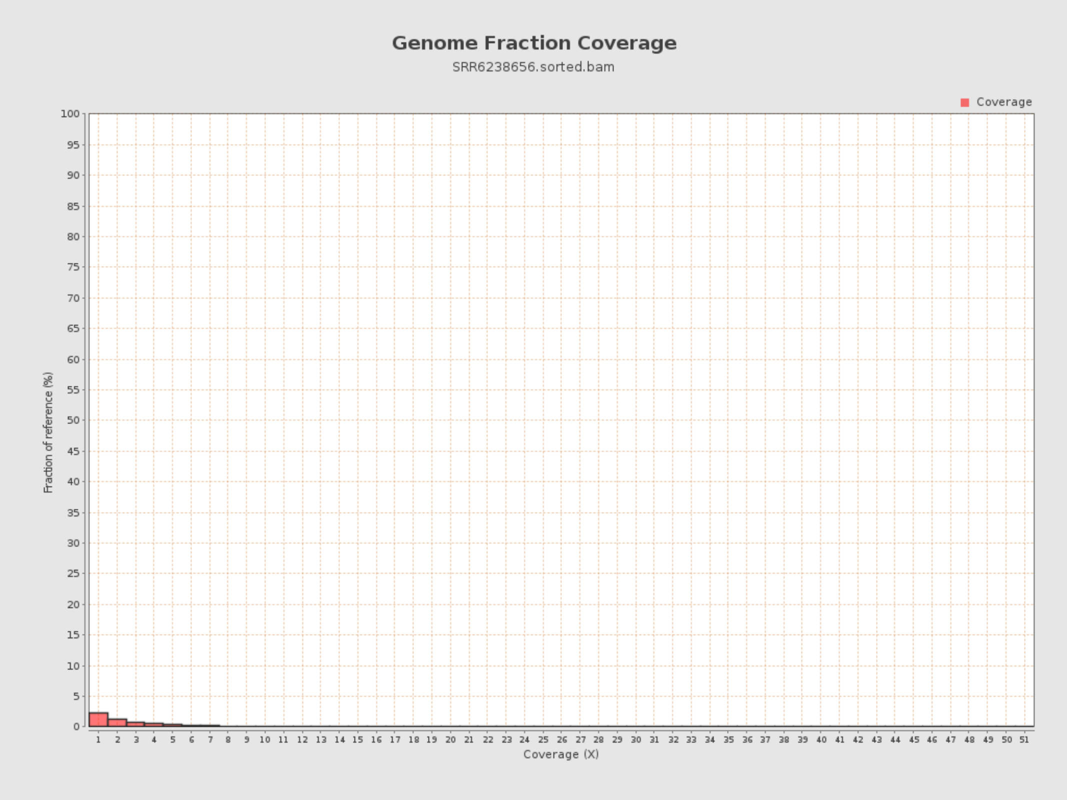
# 4. Results : Coverage Histogram



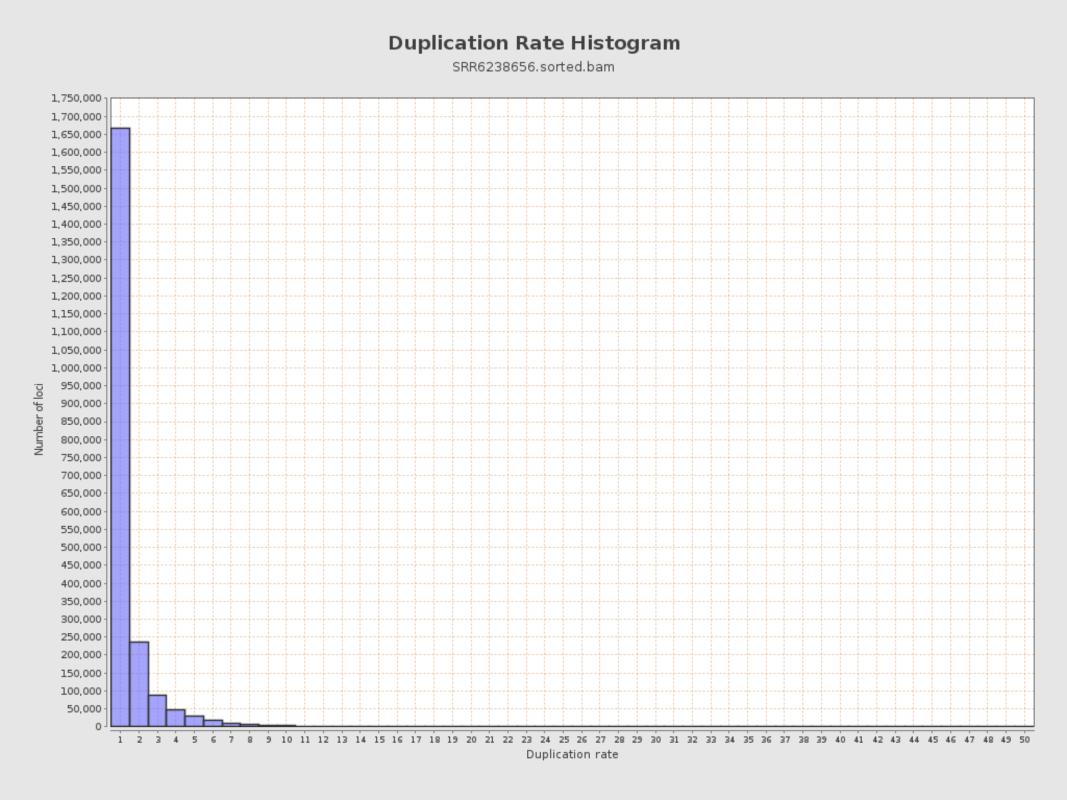
# 5. Results : Coverage Histogram (0-50X)



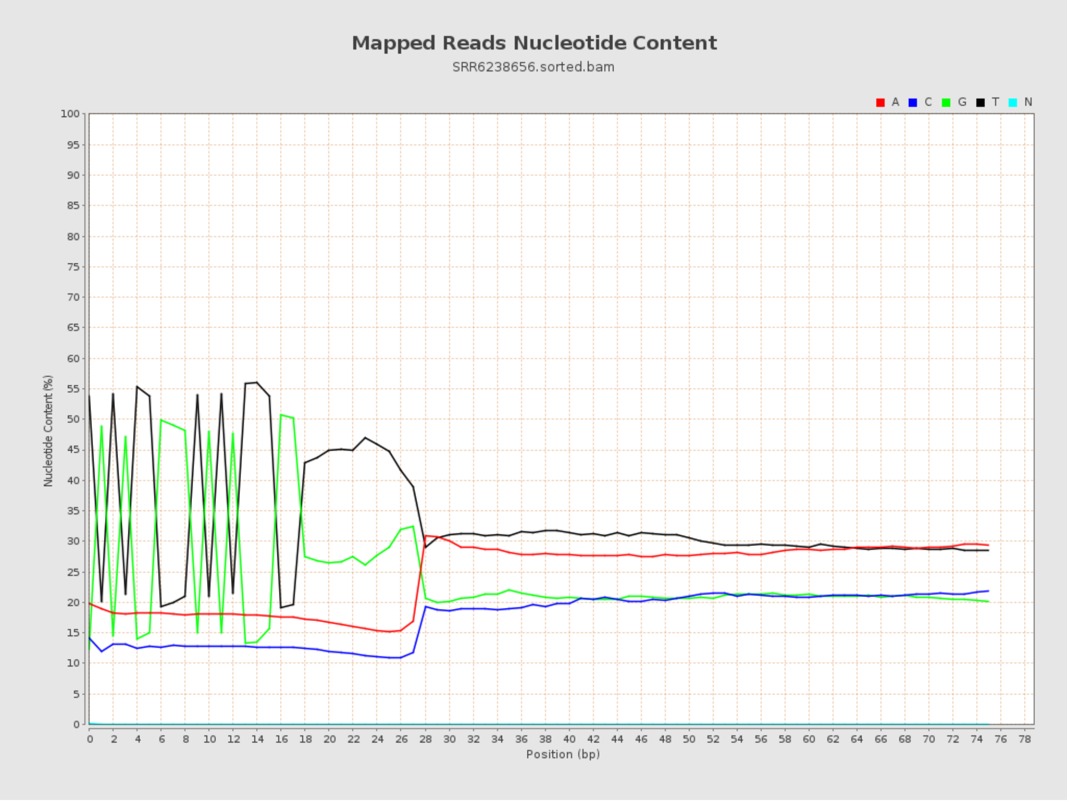
# 6. Results : Genome Fraction Coverage



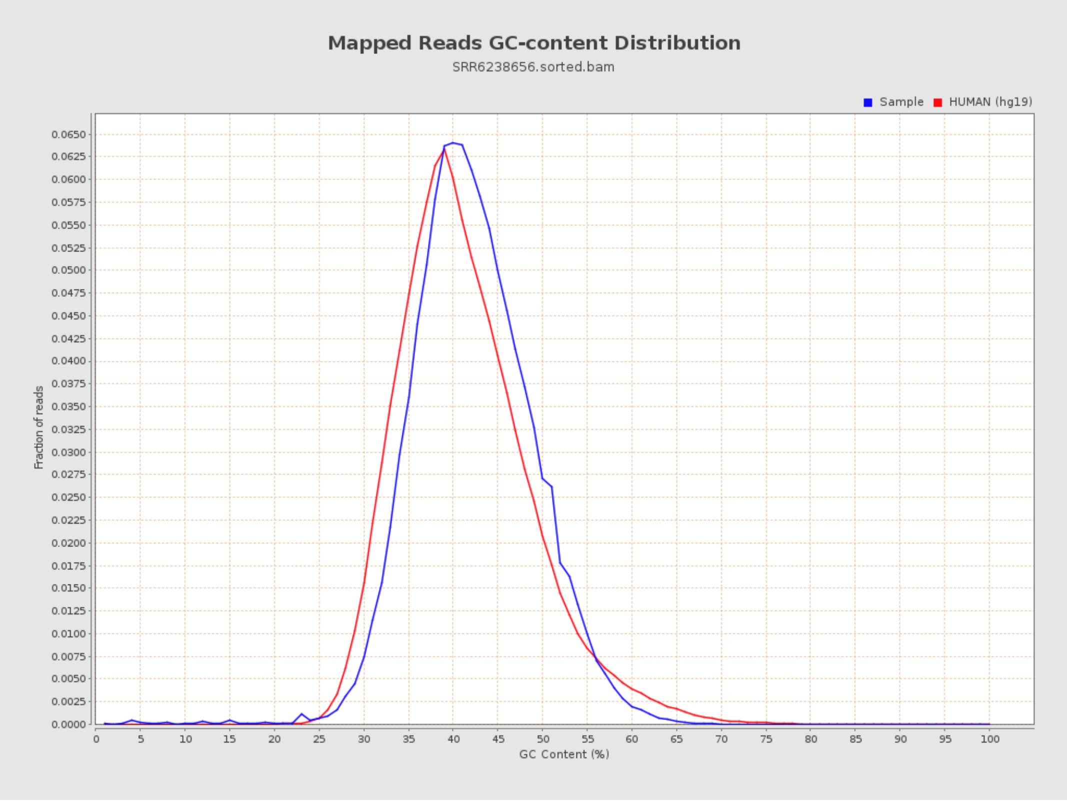
# 7. Results : Duplication Rate Histogram



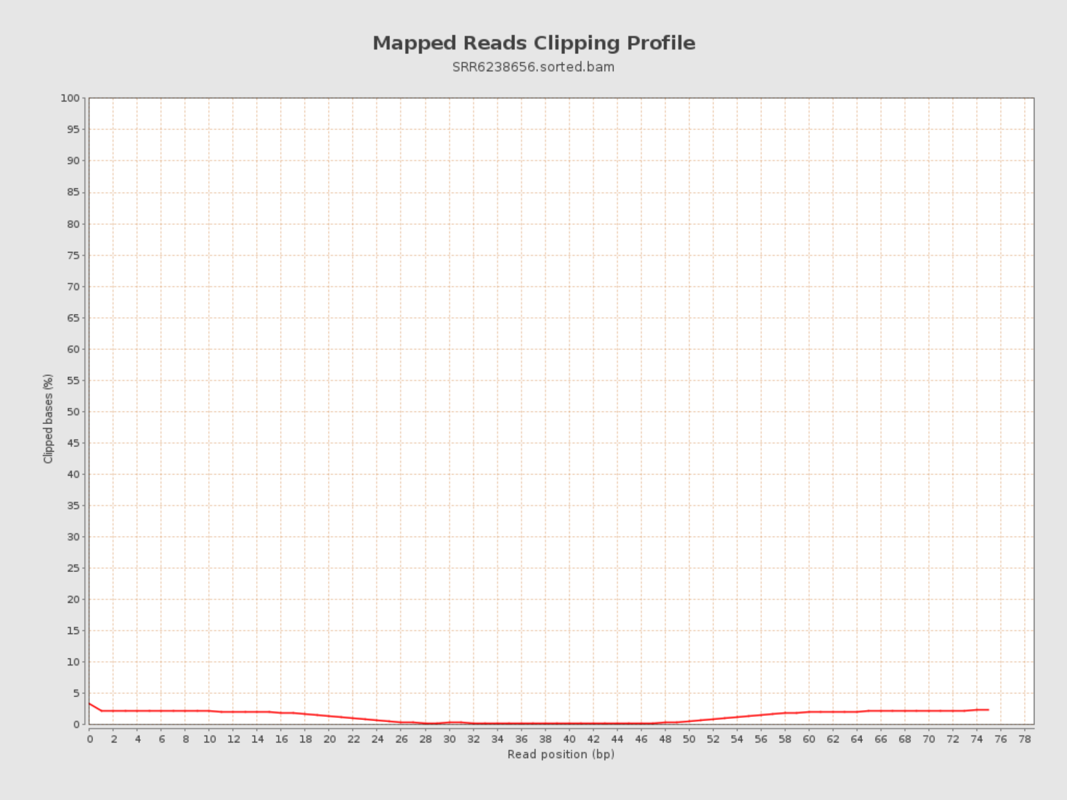
# 8. Results : Mapped Reads Nucleotide Content



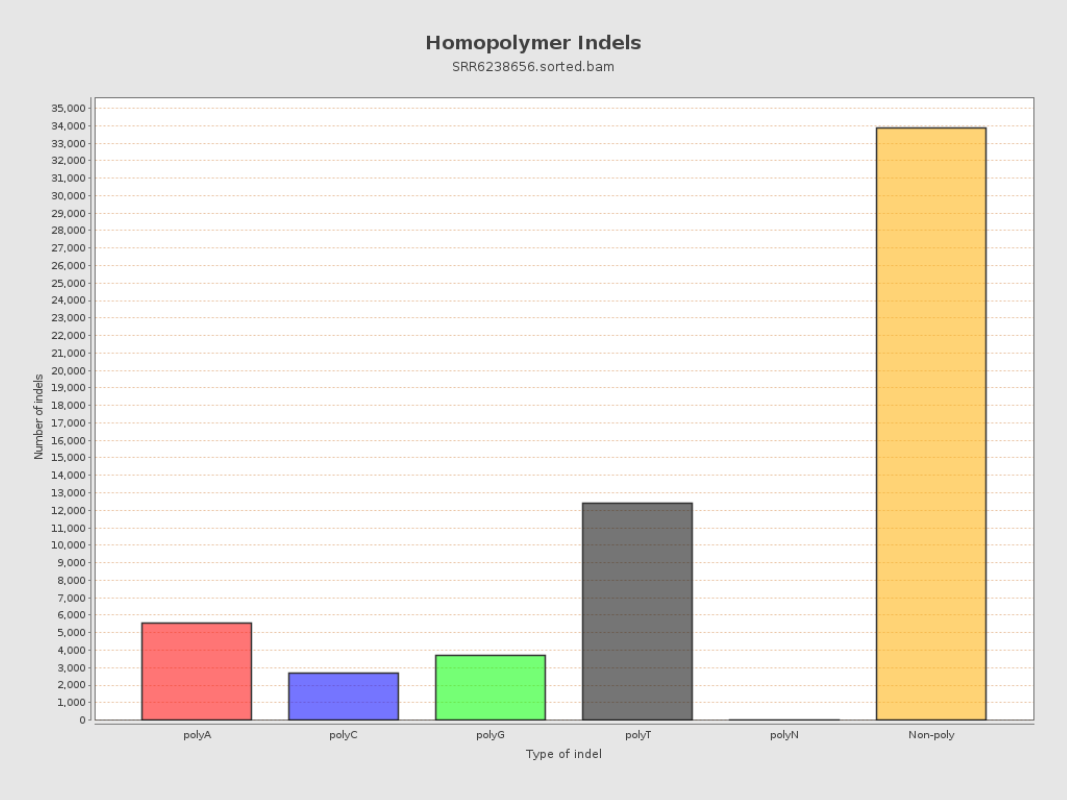
# 9. Results : Mapped Reads GC-content Distribution



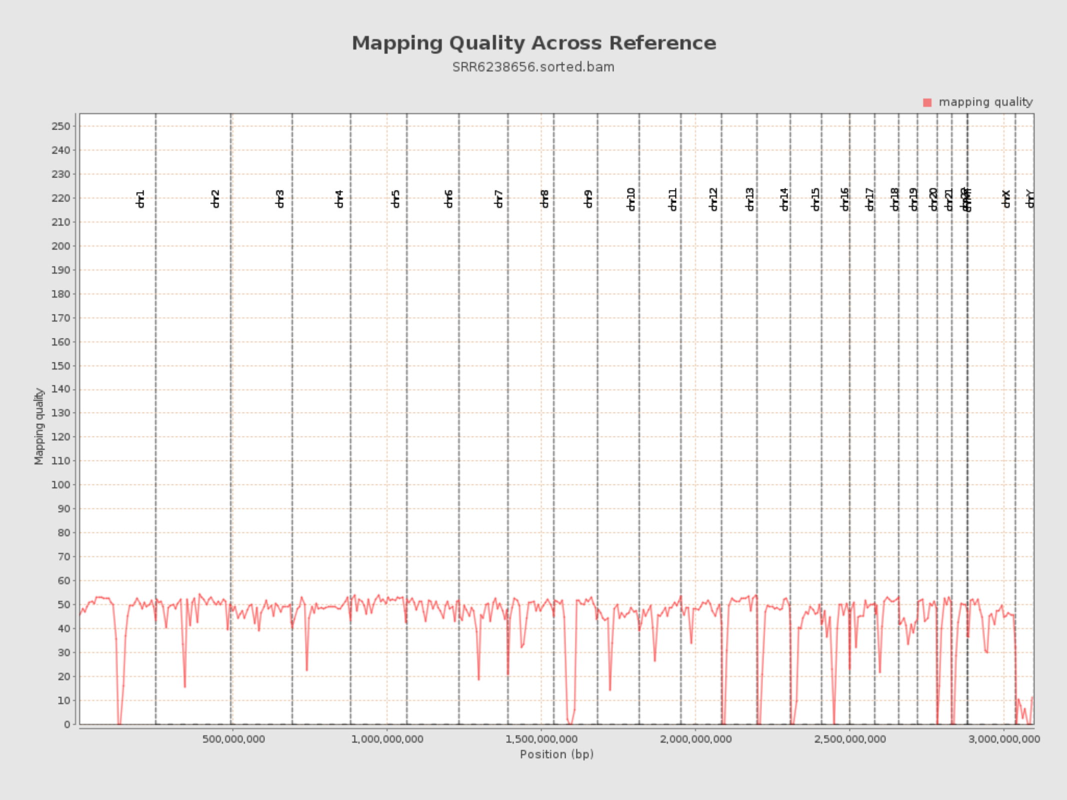
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram