# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/17 11:36:43*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238066.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_SRR6238066 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238066.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 17 11:36:43 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6238066.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,491,945 |
| Mapped reads | 2,274,804 / 91.29% |
| Unmapped reads | 217,141 / 8.71% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 16,426 / 0.66% |
| Read min/max/mean length | 30 / 76 / 76.23 |
| Duplicated reads (estimated) | 82,475 / 3.31% |
| Duplication rate | 2.65% |
| Clipped reads | 900,411 / 36.13% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 41,863,707 / 27.31% |
| Number/percentage of C's | 29,187,441 / 19.04% |
| Number/percentage of T's | 47,667,682 / 31.09% |
| Number/percentage of G's | 34,578,505 / 22.55% |
| Number/percentage of N's | 21,046 / 0.01% |
| GC Percentage | 41.59% |

## 2.3. Coverage

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

| | |
|---|---|
| Standard Deviation | 0.4251 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.22 |

## 2.5. Mismatches and indels

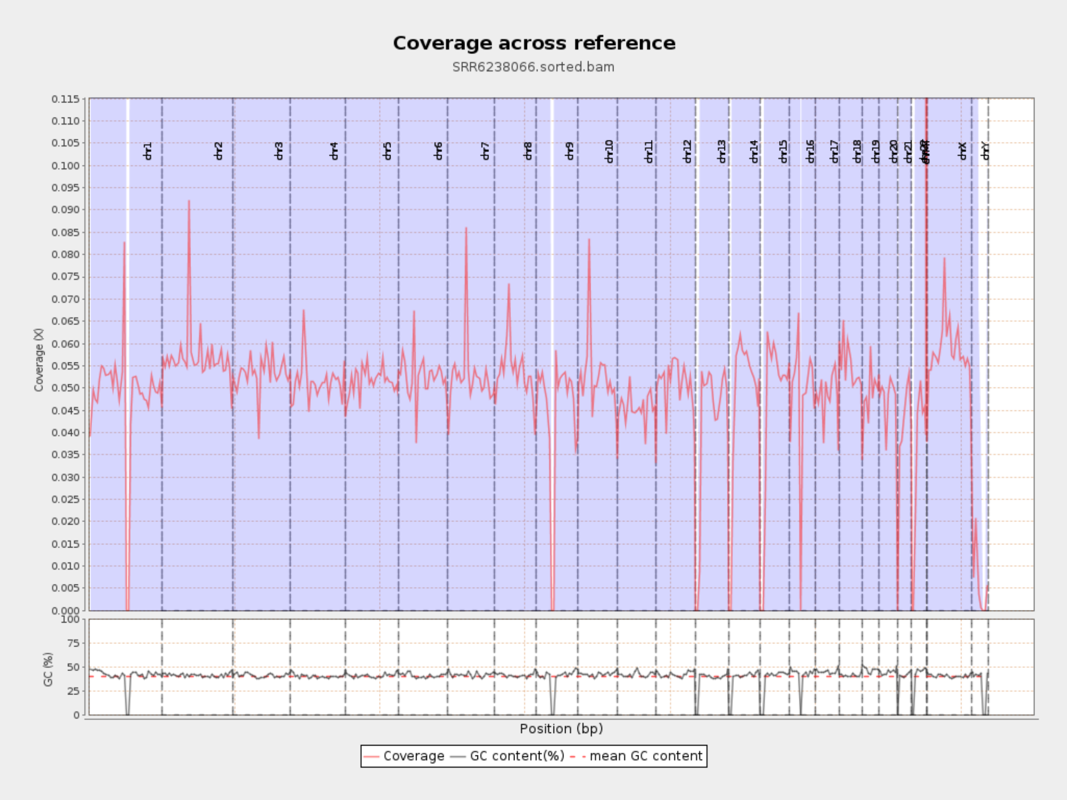
| | |
|---|---|
| General error rate | 0.75% |
| Mismatches | 1,121,607 |
| Insertions | 10,622 |
| Mapped reads with at least one insertion | 0.46% |
| Deletions | 37,592 |
| Mapped reads with at least one deletion | 1.63% |
| Homopolymer indels | 46.64% |

## 2.6. Chromosome stats

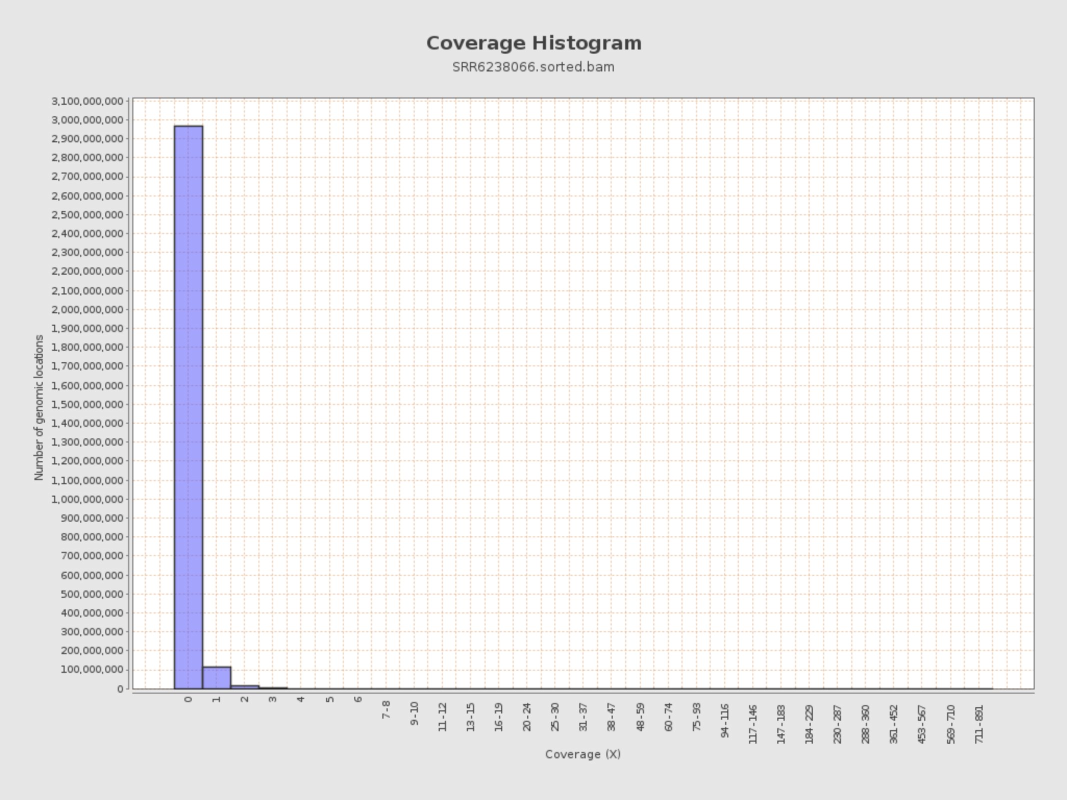
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 11939531 | 0.0479 | 0.7959 |
| chr2 | 243199373 | 13911887 | 0.0572 | 0.4707 |
| chr3 | 198022430 | 10587609 | 0.0535 | 0.2614 |
| chr4 | 191154276 | 9817138 | 0.0514 | 0.2773 |
| chr5 | 180915260 | 9347270 | 0.0517 | 0.2594 |
| chr6 | 171115067 | 9015182 | 0.0527 | 0.3279 |
| chr7 | 159138663 | 8435393 | 0.053 | 0.5663 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7853908 | 0.0537 | 0.5136 |
| chr9 | 141213431 | 6262793 | 0.0443 | 0.41 |
| chr10 | 135534747 | 7193184 | 0.0531 | 0.4242 |
| chr11 | 135006516 | 6131804 | 0.0454 | 0.327 |
| chr12 | 133851895 | 6871816 | 0.0513 | 0.2623 |
| chr13 | 115169878 | 4779562 | 0.0415 | 0.2289 |
| chr14 | 107349540 | 5037170 | 0.0469 | 0.2799 |
| chr15 | 102531392 | 4679375 | 0.0456 | 0.2416 |
| chr16 | 90354753 | 4348216 | 0.0481 | 0.2974 |
| chr17 | 81195210 | 3910530 | 0.0482 | 0.276 |
| chr18 | 78077248 | 4292476 | 0.055 | 0.7953 |
| chr19 | 59128983 | 2885365 | 0.0488 | 0.5325 |
| chr20 | 63025520 | 2961119 | 0.047 | 0.2526 |
| chr21 | 48129895 | 1926935 | 0.04 | 0.2608 |
| chr22 | 51304566 | 1680014 | 0.0327 | 0.2039 |
| chrMT | 16571 | 74987 | 4.5252 | 3.3796 |
| chrX | 155270560 | 9054987 | 0.0583 | 0.3115 |
| chrY | 59373566 | 387168 | 0.0065 | 0.1627 |

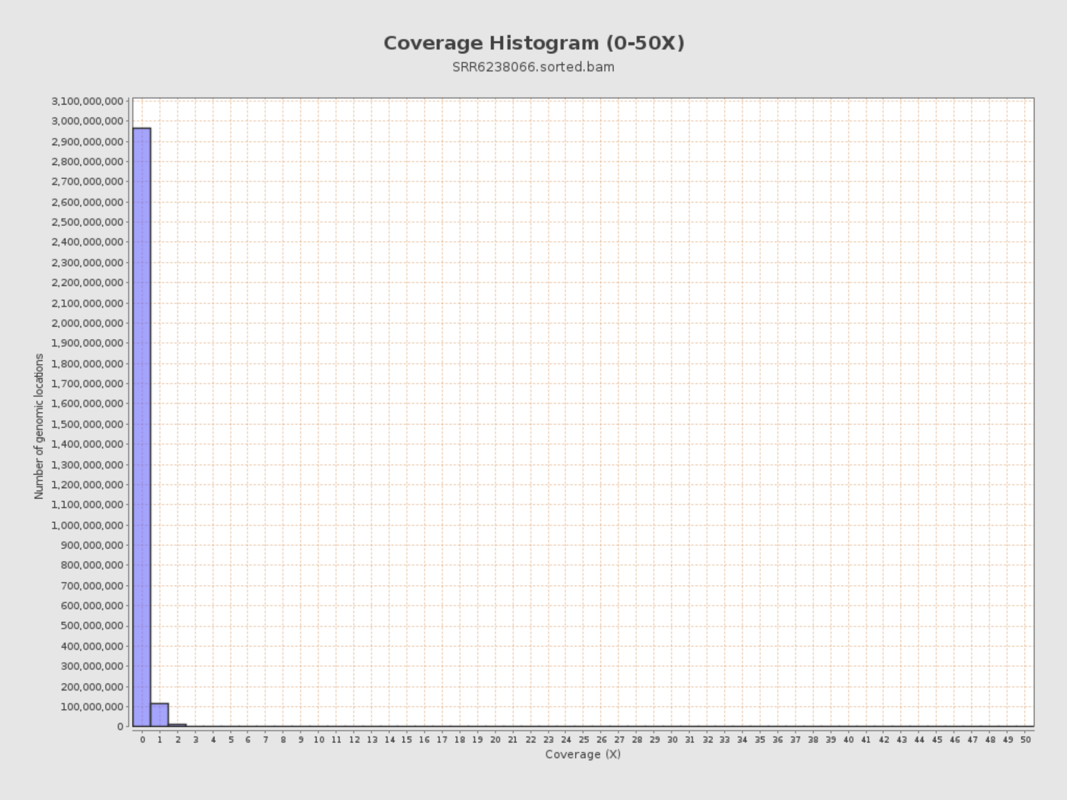
# 3. Results : Coverage across reference



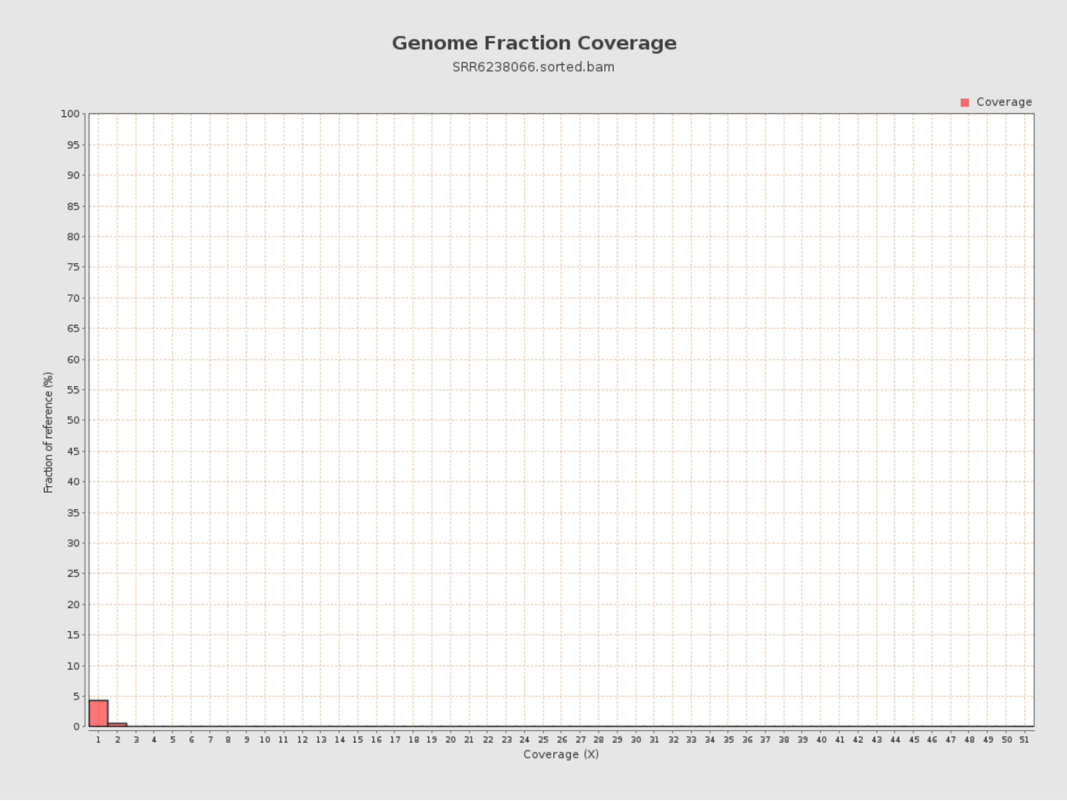
# 4. Results : Coverage Histogram



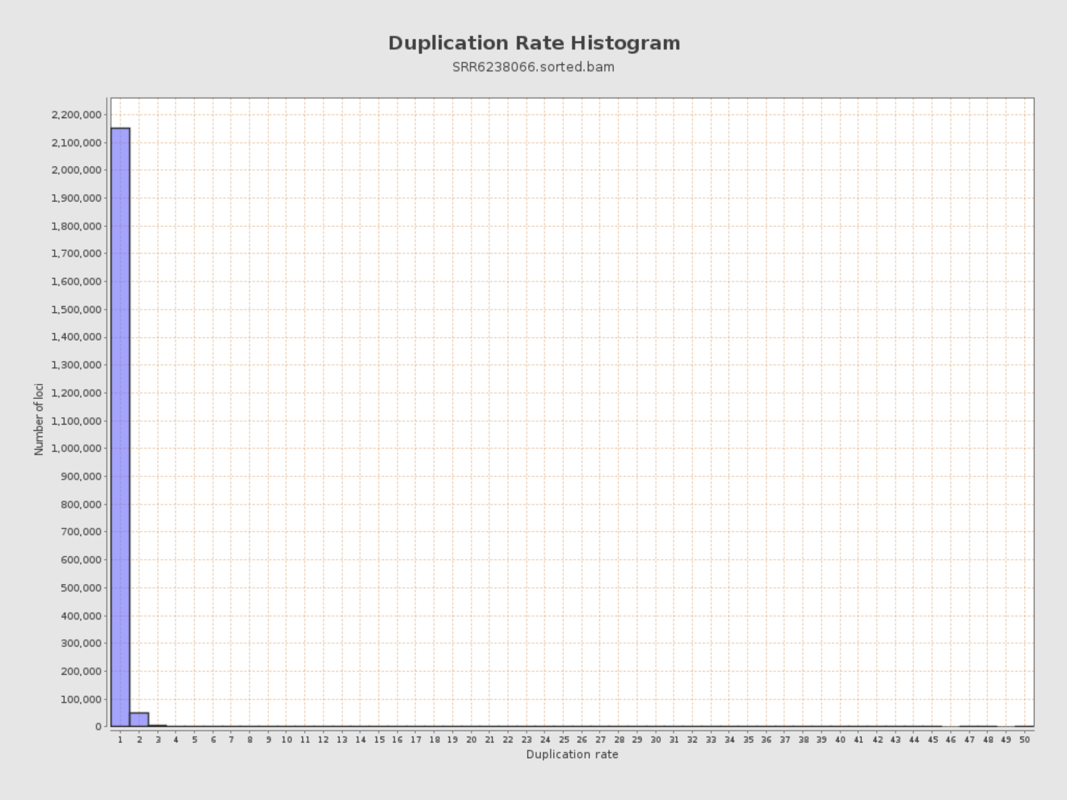
# 5. Results : Coverage Histogram (0-50X)



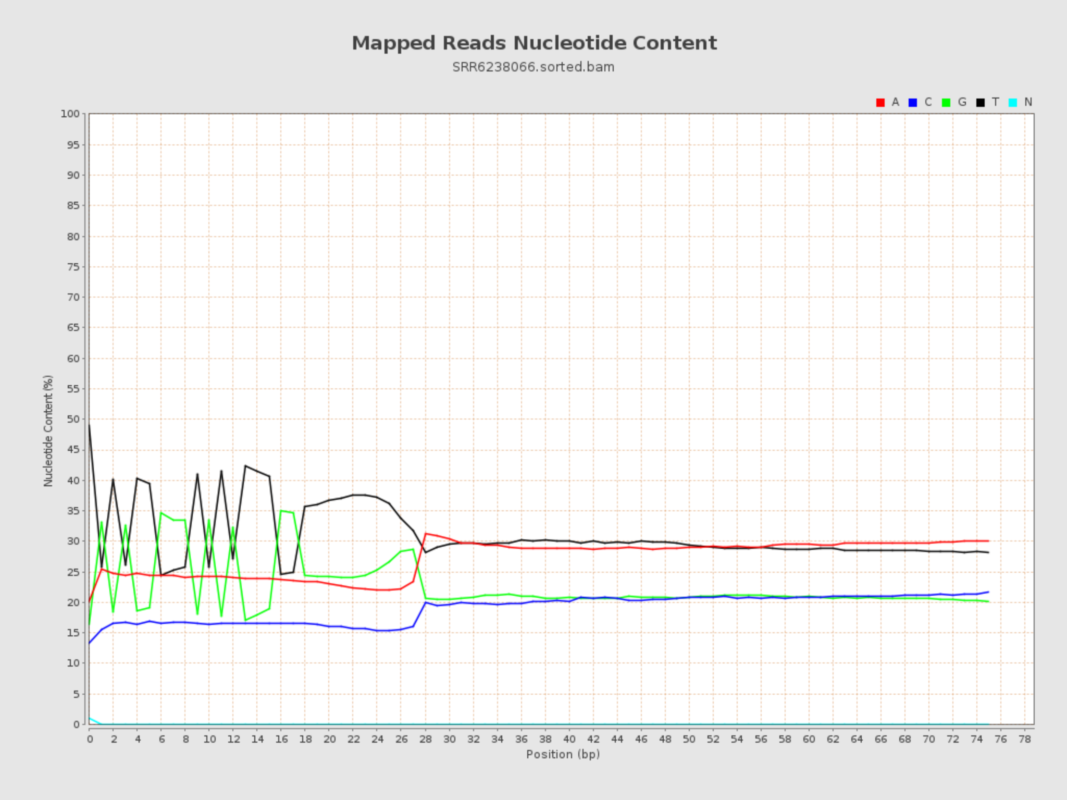
# 6. Results : Genome Fraction Coverage



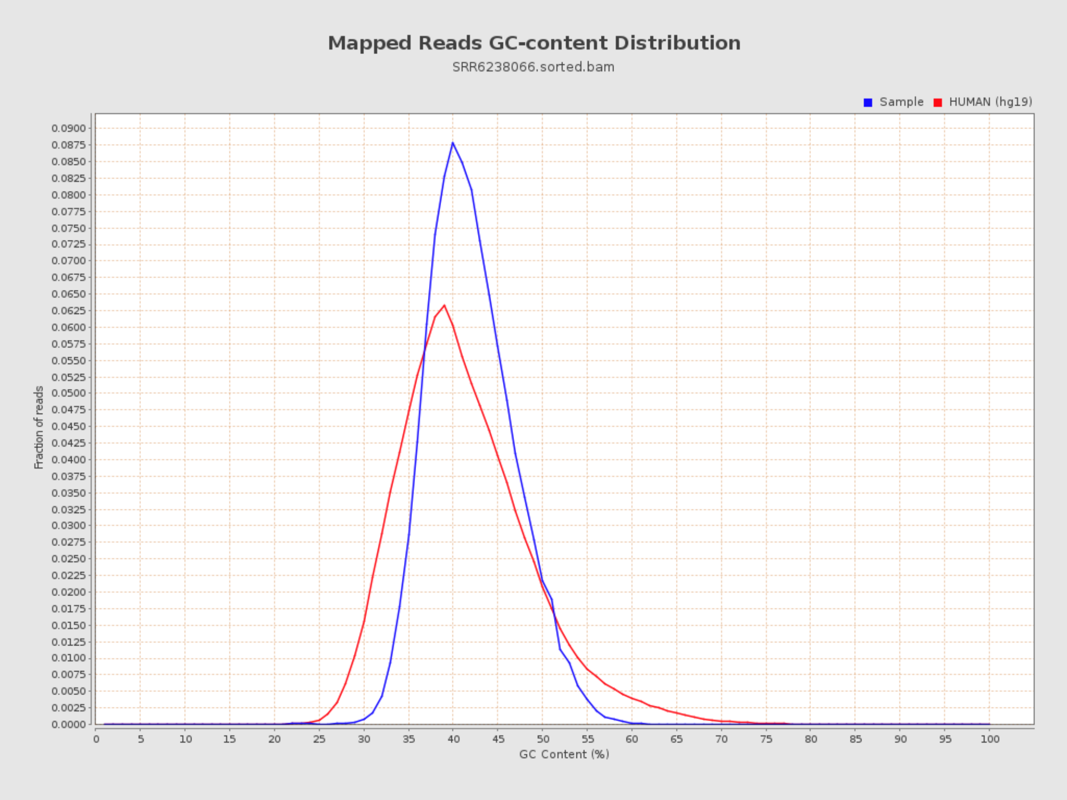
# 7. Results : Duplication Rate Histogram



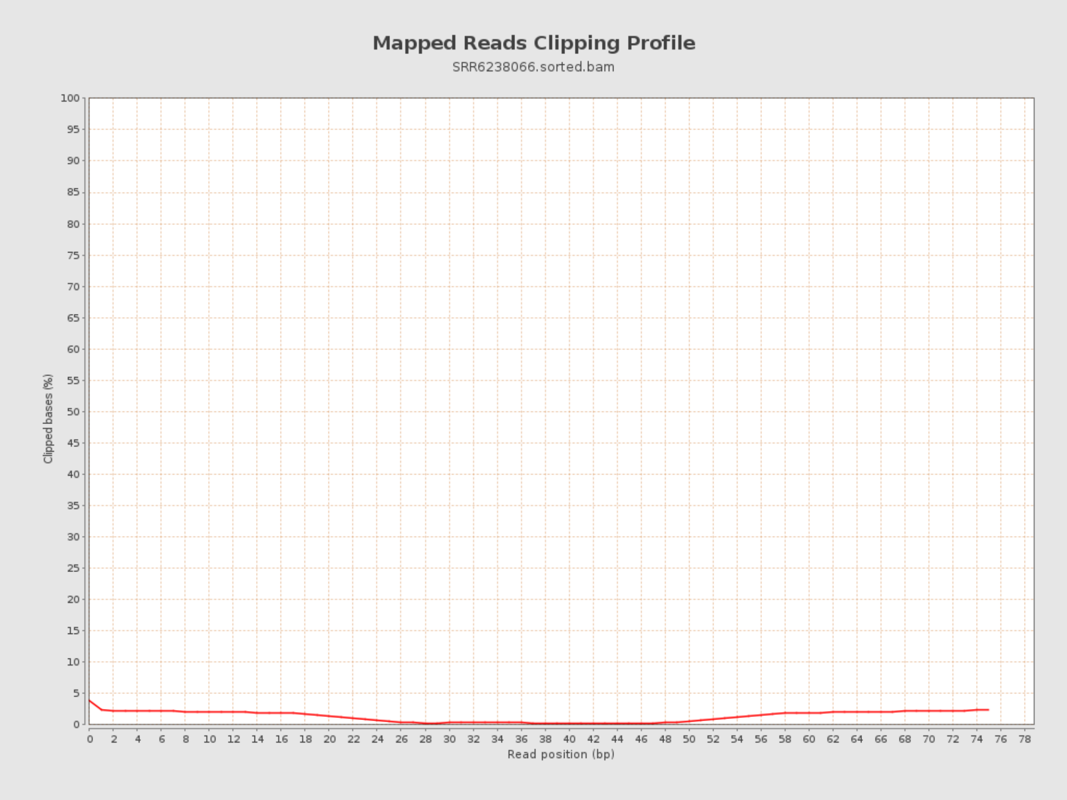
# 8. Results : Mapped Reads Nucleotide Content



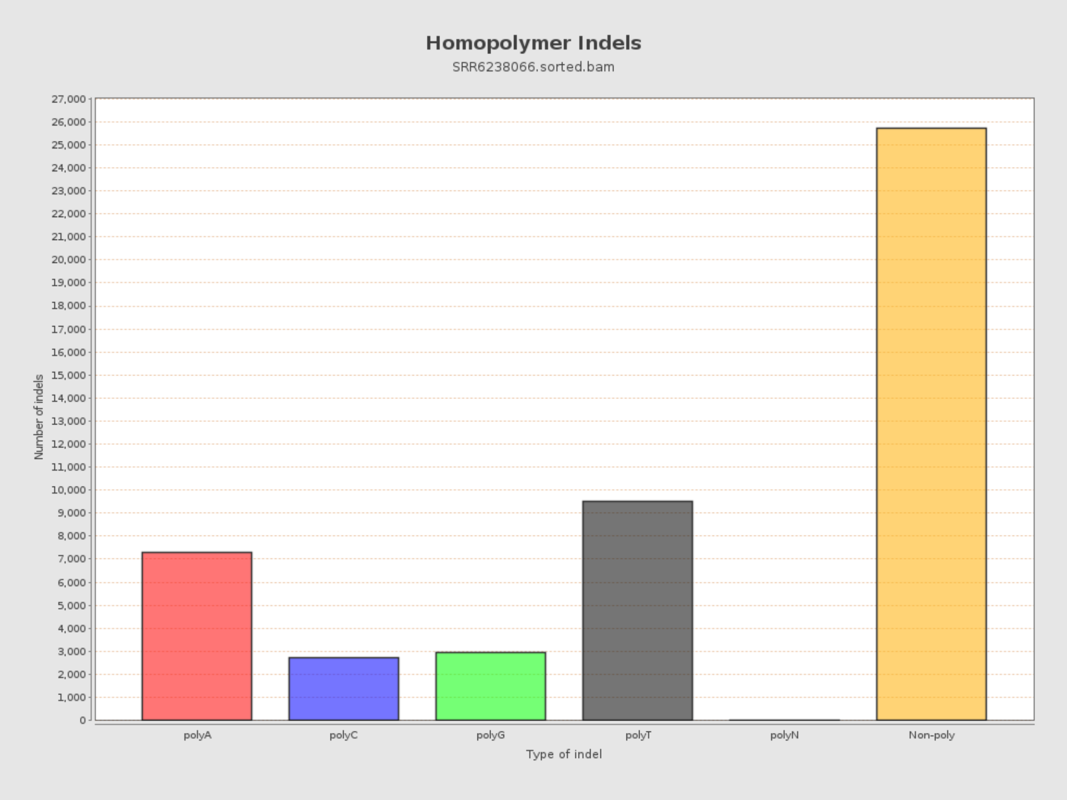
# 9. Results : Mapped Reads GC-content Distribution



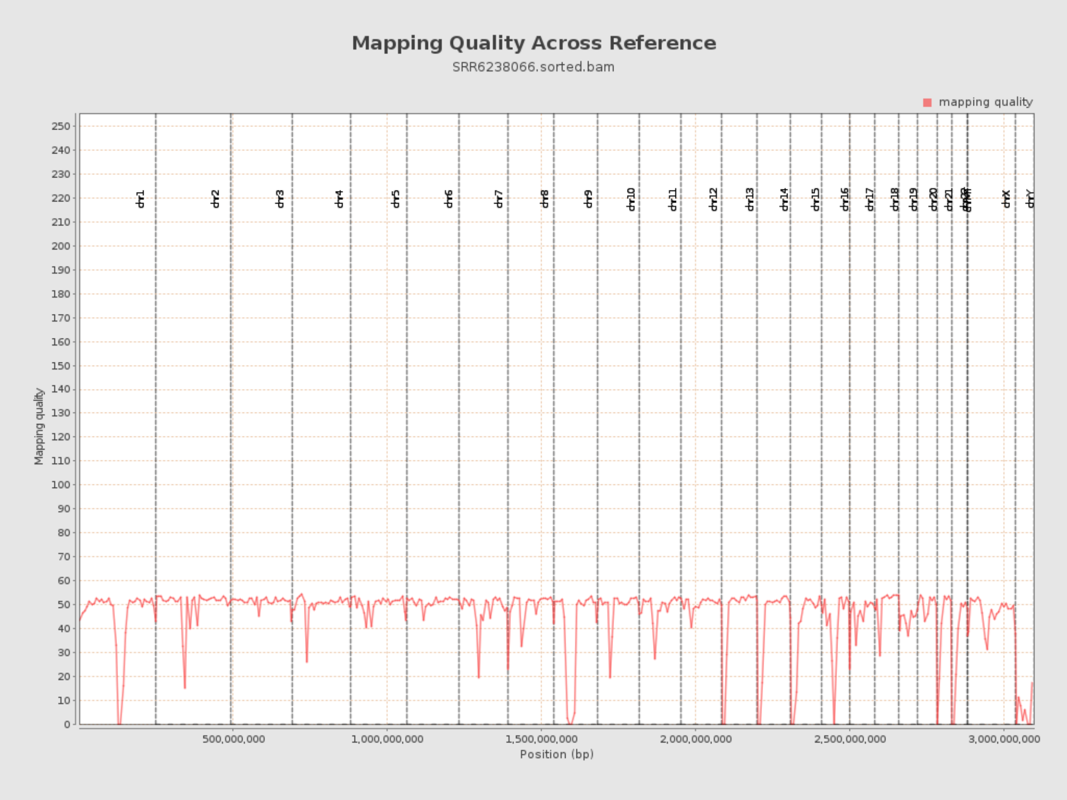
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram