# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/13 19:42:45*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6003995.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_SRR6003995 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6003995.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Sep 13 19:42:44 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6003995.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,357,109 |
| Mapped reads | 3,030,829 / 90.28% |
| Unmapped reads | 326,280 / 9.72% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 22,457 / 0.67% |
| Read min/max/mean length | 30 / 76 / 76.23 |
| Duplicated reads (estimated) | 106,848 / 3.18% |
| Duplication rate | 2.36% |
| Clipped reads | 1,535,021 / 45.72% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 53,429,343 / 27.02% |
| Number/percentage of C's | 38,532,442 / 19.49% |
| Number/percentage of T's | 59,171,822 / 29.93% |
| Number/percentage of G's | 46,551,650 / 23.54% |
| Number/percentage of N's | 39,292 / 0.02% |
| GC Percentage | 43.03% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0639 |
| | |

| | |
|---|---|
| Standard Deviation | 0.546 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 41.97 |

## 2.5. Mismatches and indels

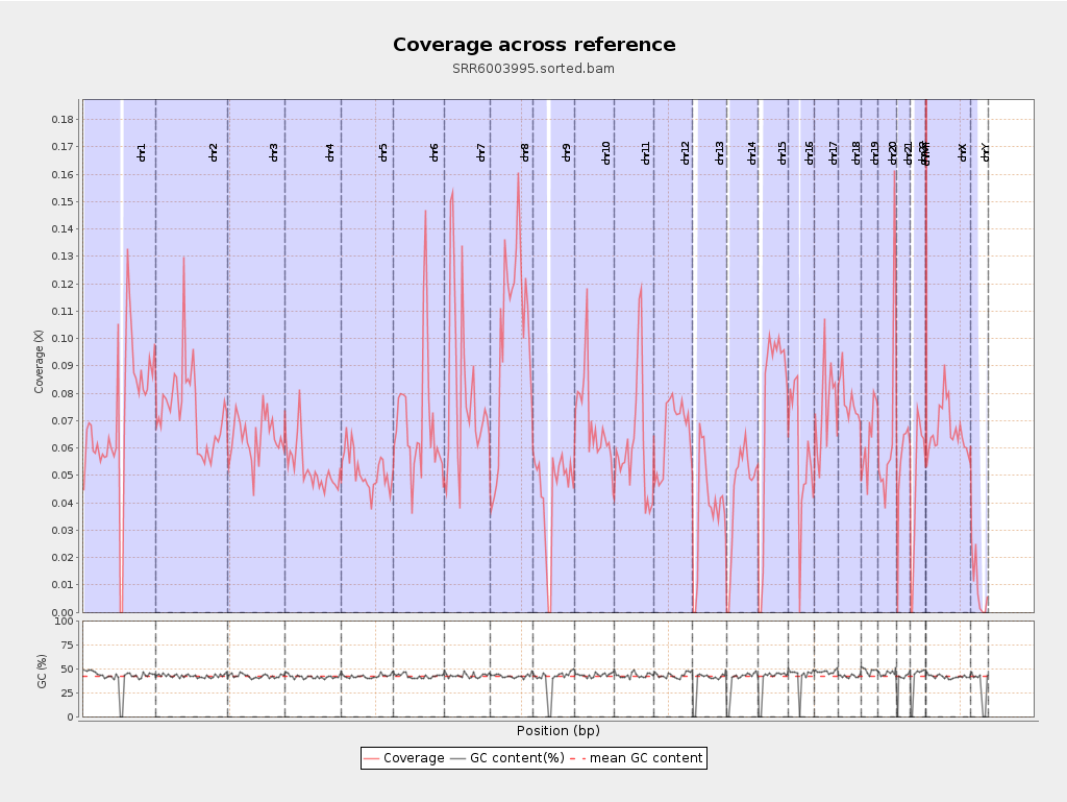
| | |
|---|---|
| General error rate | 0.85% |
| Mismatches | 1,646,780 |
| Insertions | 16,207 |
| Mapped reads with at least one insertion | 0.53% |
| Deletions | 49,581 |
| Mapped reads with at least one deletion | 1.62% |
| Homopolymer indels | 44.73% |

## 2.6. Chromosome stats

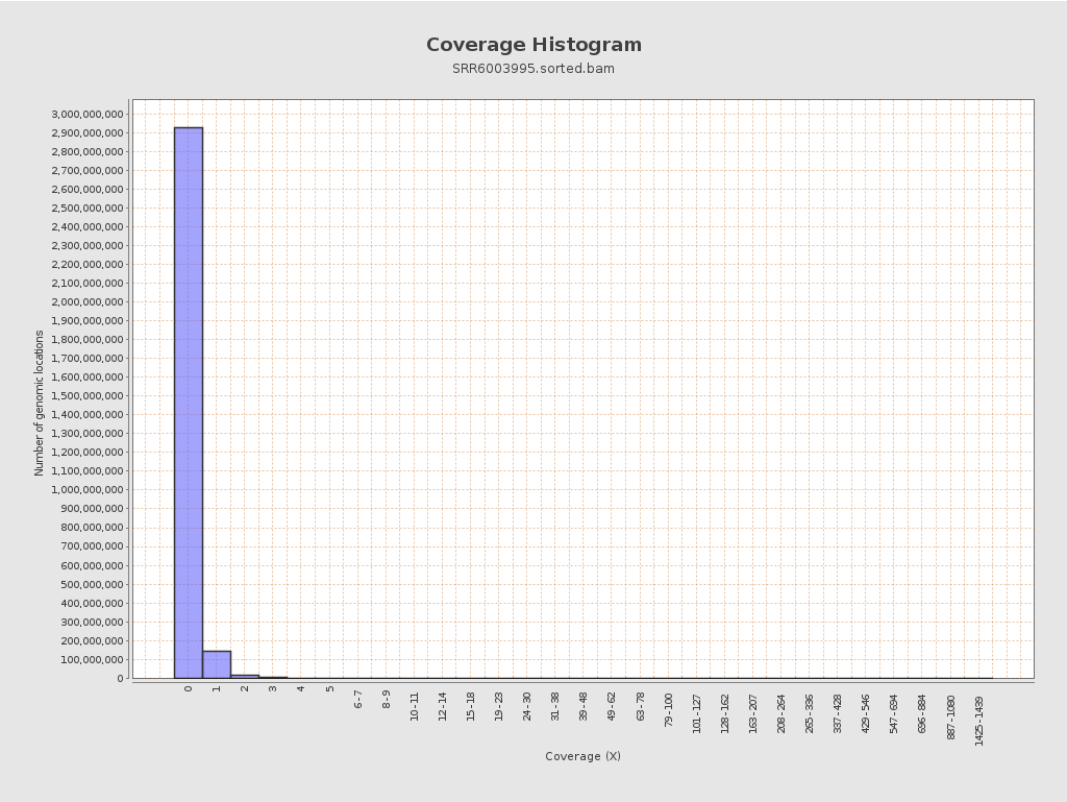
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 17793944 | 0.0714 | 0.9229 |
| chr2 | 243199373 | 17810630 | 0.0732 | 0.8068 |
| chr3 | 198022430 | 12720987 | 0.0642 | 0.295 |
| chr4 | 191154276 | 10094604 | 0.0528 | 0.2933 |
| chr5 | 180915260 | 9360386 | 0.0517 | 0.2605 |
| chr6 | 171115067 | 11849366 | 0.0692 | 0.3633 |
| chr7 | 159138663 | 12695415 | 0.0798 | 0.9699 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 14709616 | 0.1005 | 0.5261 |
| chr9 | 141213431 | 6186895 | 0.0438 | 0.4498 |
| chr10 | 135534747 | 9445349 | 0.0697 | 0.5556 |
| chr11 | 135006516 | 8180405 | 0.0606 | 0.4163 |
| chr12 | 133851895 | 8810174 | 0.0658 | 0.296 |
| chr13 | 115169878 | 4413336 | 0.0383 | 0.2265 |
| chr14 | 107349540 | 4789843 | 0.0446 | 0.2897 |
| chr15 | 102531392 | 7697332 | 0.0751 | 0.3358 |
| chr16 | 90354753 | 5132025 | 0.0568 | 0.338 |
| chr17 | 81195210 | 6058885 | 0.0746 | 0.345 |
| chr18 | 78077248 | 6078121 | 0.0778 | 0.9805 |
| chr19 | 59128983 | 3764275 | 0.0637 | 0.7271 |
| chr20 | 63025520 | 4328559 | 0.0687 | 0.3193 |
| chr21 | 48129895 | 2603177 | 0.0541 | 0.2906 |
| chr22 | 51304566 | 2421629 | 0.0472 | 0.2499 |
| chrMT | 16571 | 12636 | 0.7625 | 1.1462 |
| chrX | 155270560 | 10322324 | 0.0665 | 0.3488 |
| chrY | 59373566 | 526831 | 0.0089 | 0.1793 |

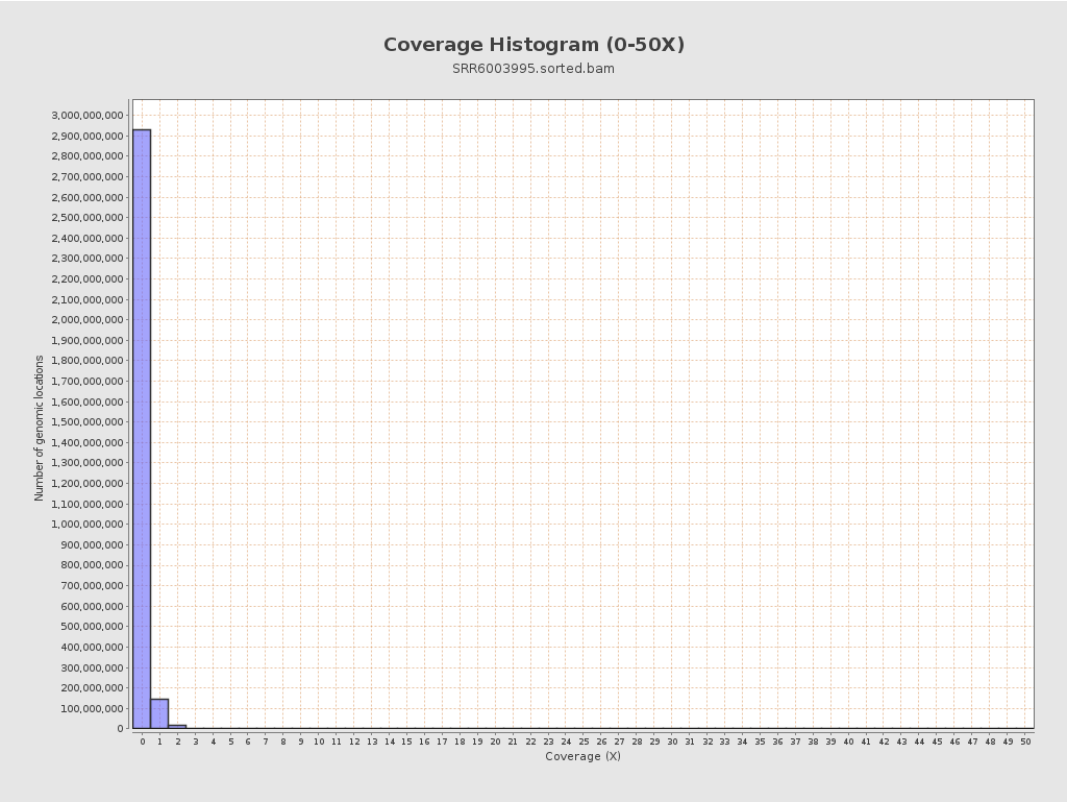
# 3. Results : Coverage across reference



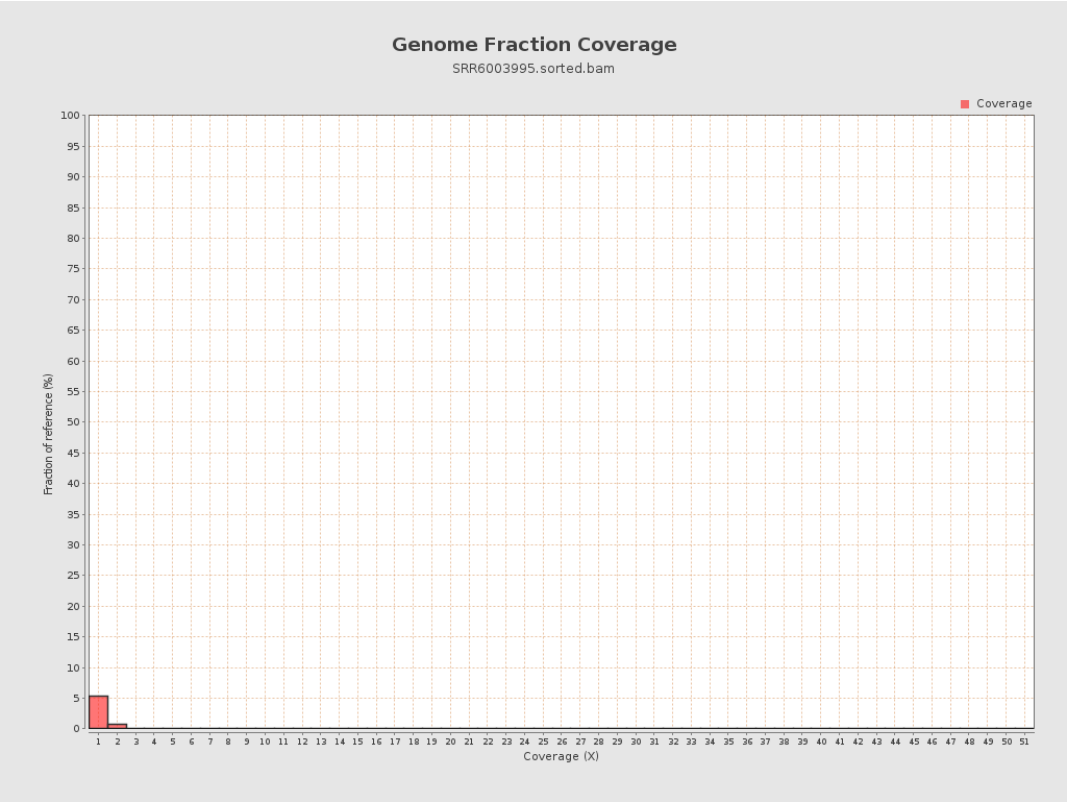
# 4. Results : Coverage Histogram



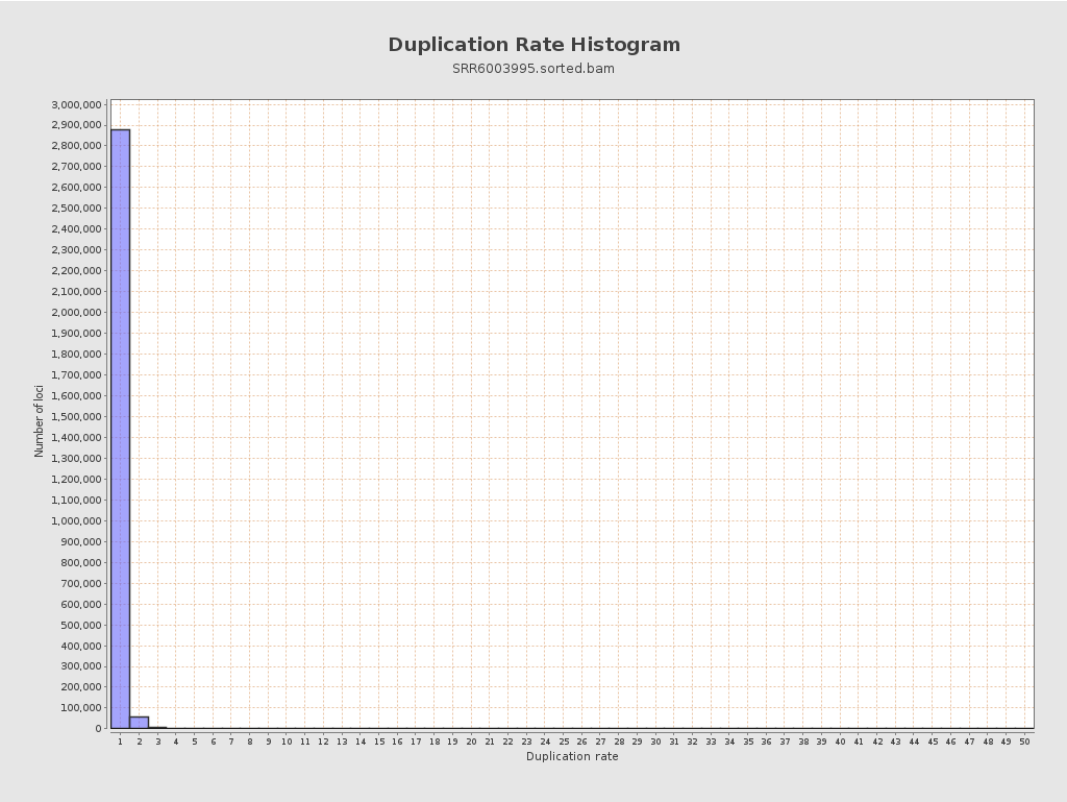
# 5. Results : Coverage Histogram (0-50X)



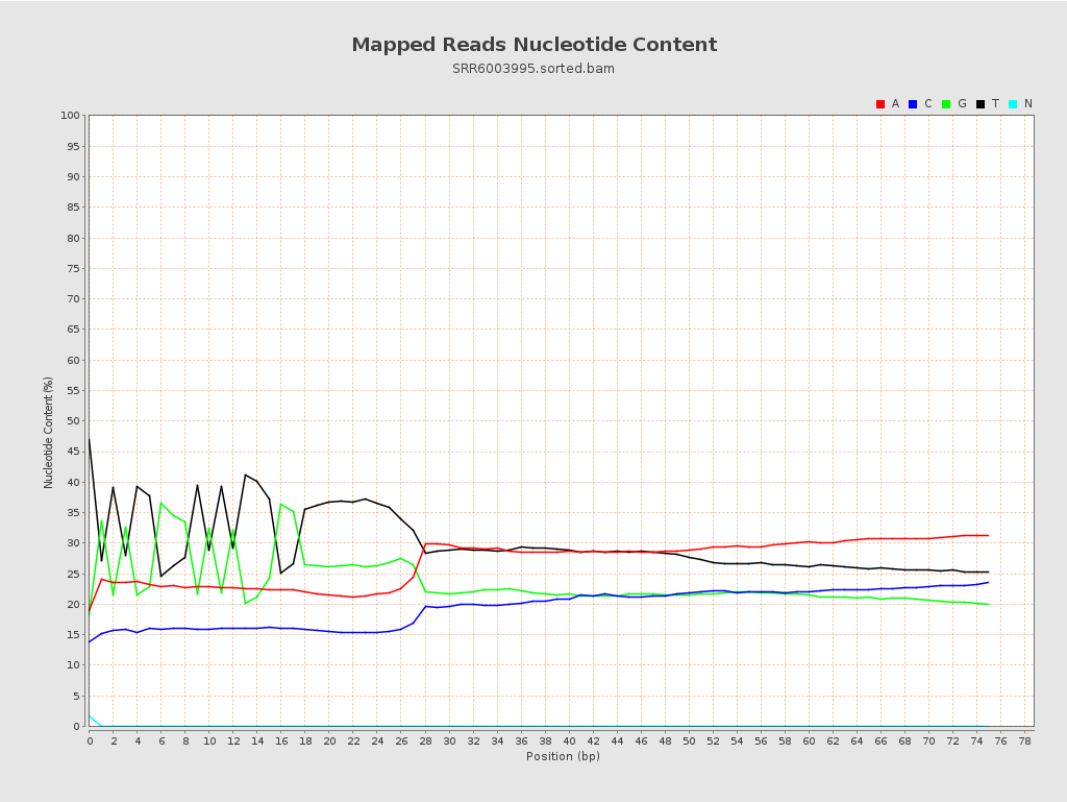
# 6. Results : Genome Fraction Coverage



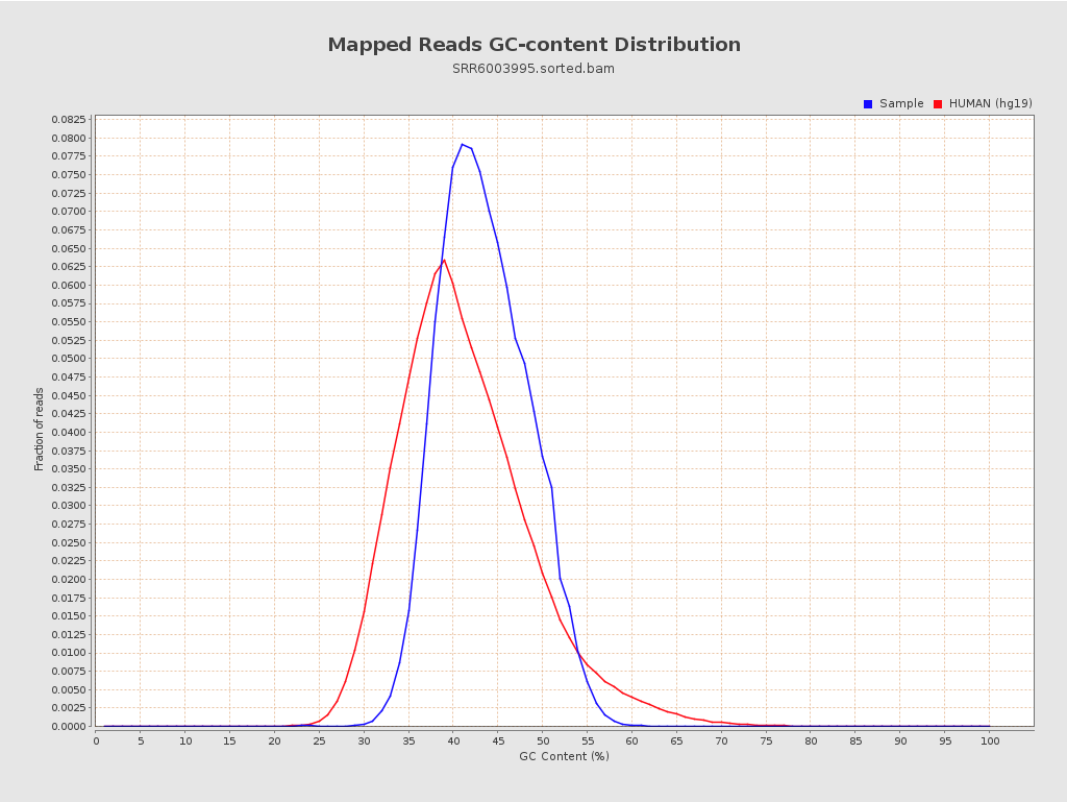
# 7. Results : Duplication Rate Histogram



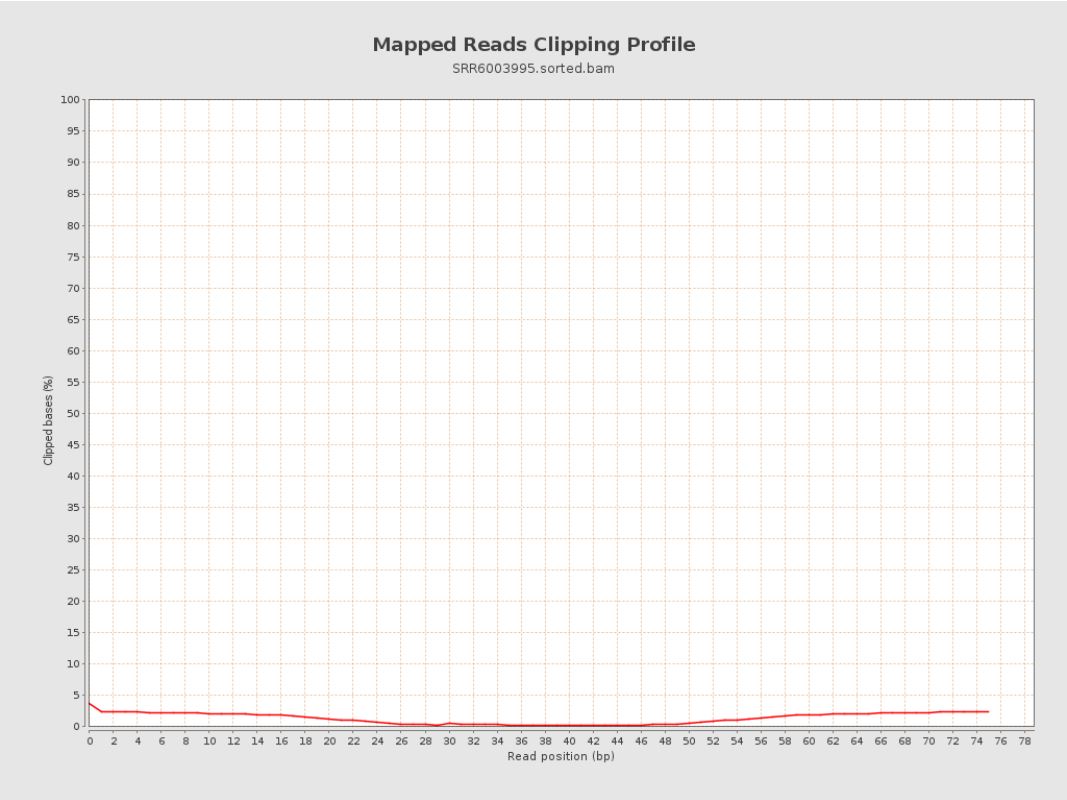
# 8. Results : Mapped Reads Nucleotide Content



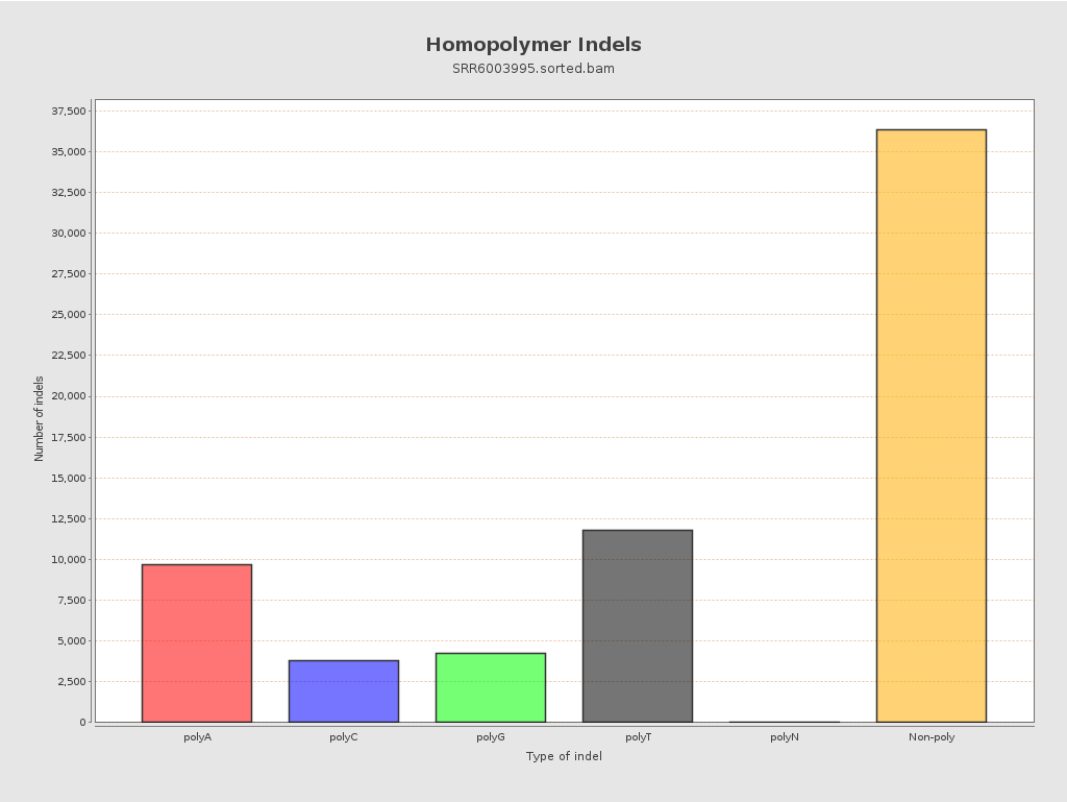
# 9. Results : Mapped Reads GC-content Distribution



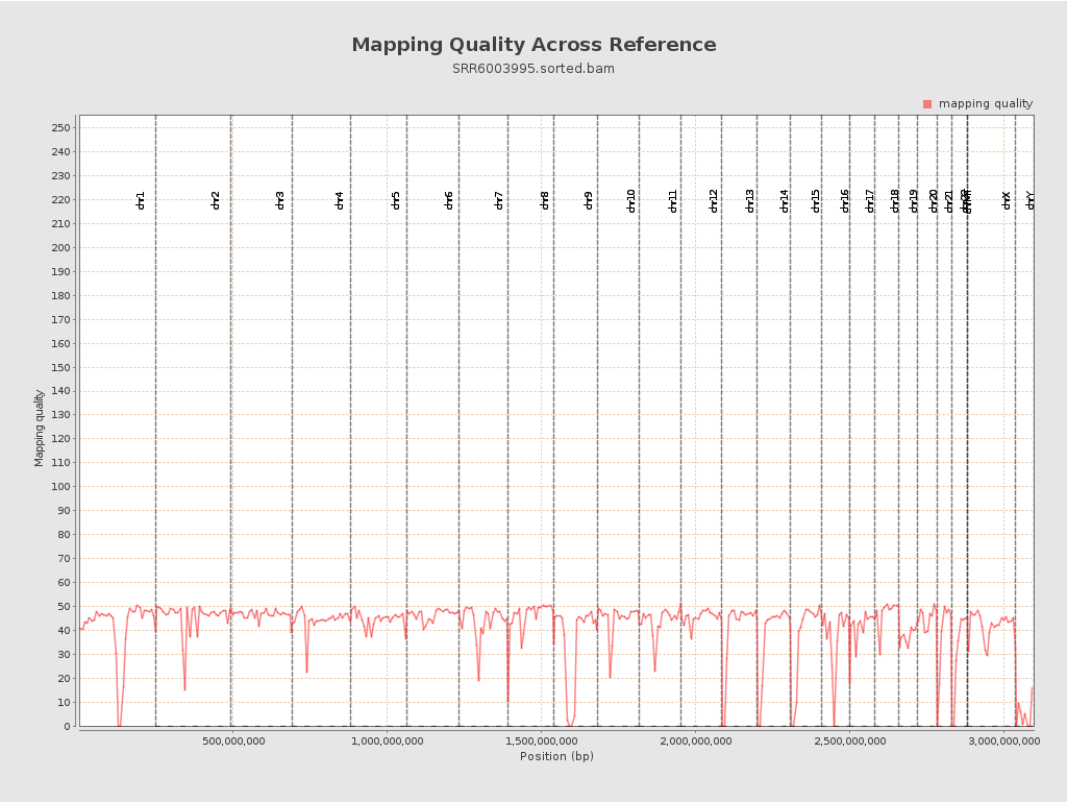
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram