# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/13 19:26:49*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6003991.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_SRR6003991 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6003991.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Sep 13 19:26:48 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6003991.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,315,451 |
| Mapped reads | 2,764,987 / 83.4% |
| Unmapped reads | 550,464 / 16.6% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 17,890 / 0.54% |
| Read min/max/mean length | 30 / 76 / 76.19 |
| Duplicated reads (estimated) | 130,488 / 3.94% |
| Duplication rate | 3.32% |
| Clipped reads | 1,200,497 / 36.21% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 52,405,027 / 28.25% |
| Number/percentage of C's | 33,199,206 / 17.9% |
| Number/percentage of T's | 60,047,906 / 32.37% |
| Number/percentage of G's | 39,804,220 / 21.46% |
| Number/percentage of N's | 20,123 / 0.01% |
| GC Percentage | 39.36% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0599 |
| | |

| | |
|---|---|
| Standard Deviation | 0.6063 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.3 |

## 2.5. Mismatches and indels

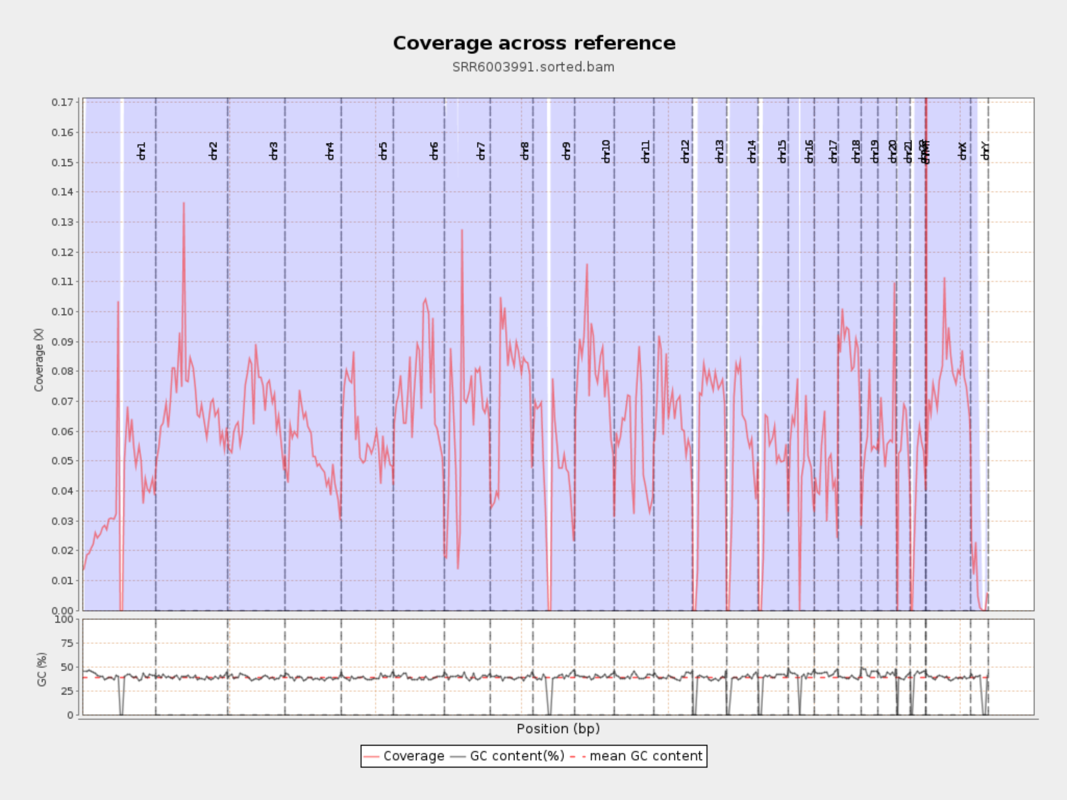
| | |
|---|---|
| General error rate | 0.97% |
| Mismatches | 1,770,070 |
| Insertions | 16,925 |
| Mapped reads with at least one insertion | 0.61% |
| Deletions | 49,811 |
| Mapped reads with at least one deletion | 1.78% |
| Homopolymer indels | 46.8% |

## 2.6. Chromosome stats

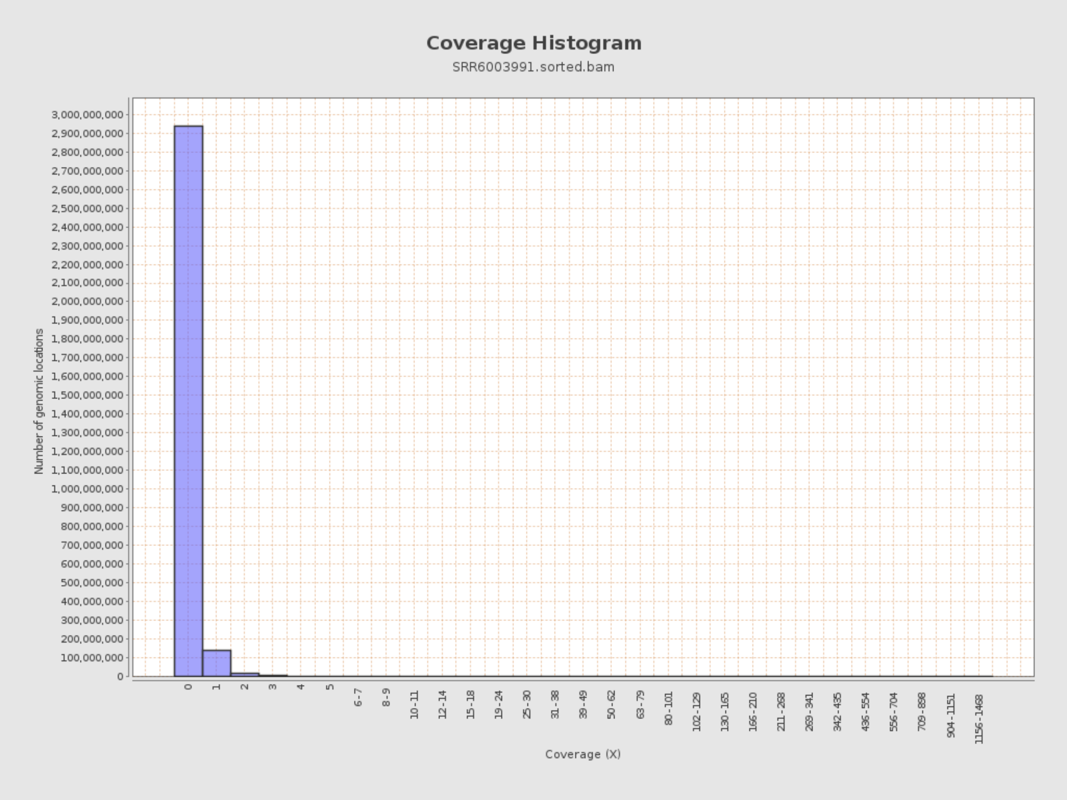
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 9152434 | 0.0367 | 1.1389 |
| chr2 | 243199373 | 17161937 | 0.0706 | 0.6818 |
| chr3 | 198022430 | 13448911 | 0.0679 | 0.2982 |
| chr4 | 191154276 | 9963627 | 0.0521 | 0.2775 |
| chr5 | 180915260 | 10697797 | 0.0591 | 0.2863 |
| chr6 | 171115067 | 12753363 | 0.0745 | 0.3795 |
| chr7 | 159138663 | 10105464 | 0.0635 | 0.8794 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 10961463 | 0.0749 | 0.9626 |
| chr9 | 141213431 | 6749687 | 0.0478 | 0.5694 |
| chr10 | 135534747 | 11017900 | 0.0813 | 0.5426 |
| chr11 | 135006516 | 7496297 | 0.0555 | 0.4762 |
| chr12 | 133851895 | 8962413 | 0.067 | 0.3134 |
| chr13 | 115169878 | 7226724 | 0.0627 | 0.2834 |
| chr14 | 107349540 | 5709984 | 0.0532 | 0.3133 |
| chr15 | 102531392 | 4624173 | 0.0451 | 0.2447 |
| chr16 | 90354753 | 4534713 | 0.0502 | 0.3542 |
| chr17 | 81195210 | 3665794 | 0.0451 | 0.288 |
| chr18 | 78077248 | 6901744 | 0.0884 | 1.2689 |
| chr19 | 59128983 | 3305519 | 0.0559 | 0.7552 |
| chr20 | 63025520 | 4041042 | 0.0641 | 0.3088 |
| chr21 | 48129895 | 2478028 | 0.0515 | 0.3005 |
| chr22 | 51304566 | 2008479 | 0.0391 | 0.2218 |
| chrMT | 16571 | 31899 | 1.925 | 1.7914 |
| chrX | 155270560 | 12080536 | 0.0778 | 0.3854 |
| chrY | 59373566 | 479460 | 0.0081 | 0.163 |

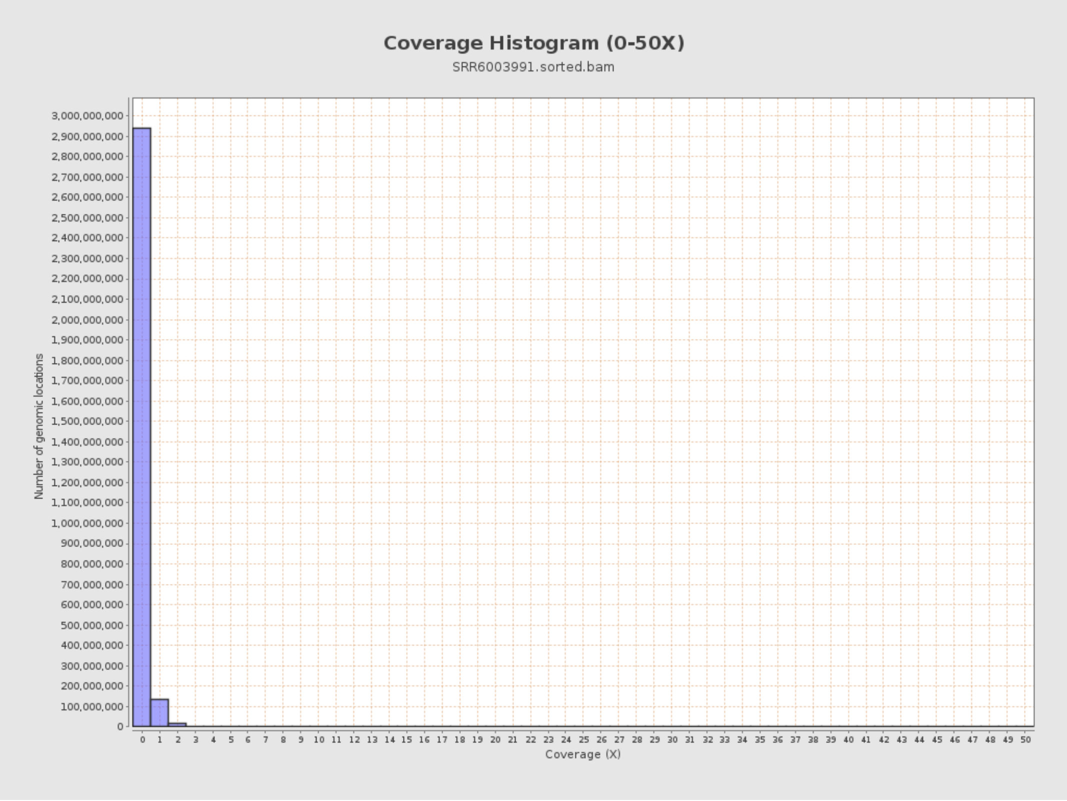
# 3. Results : Coverage across reference



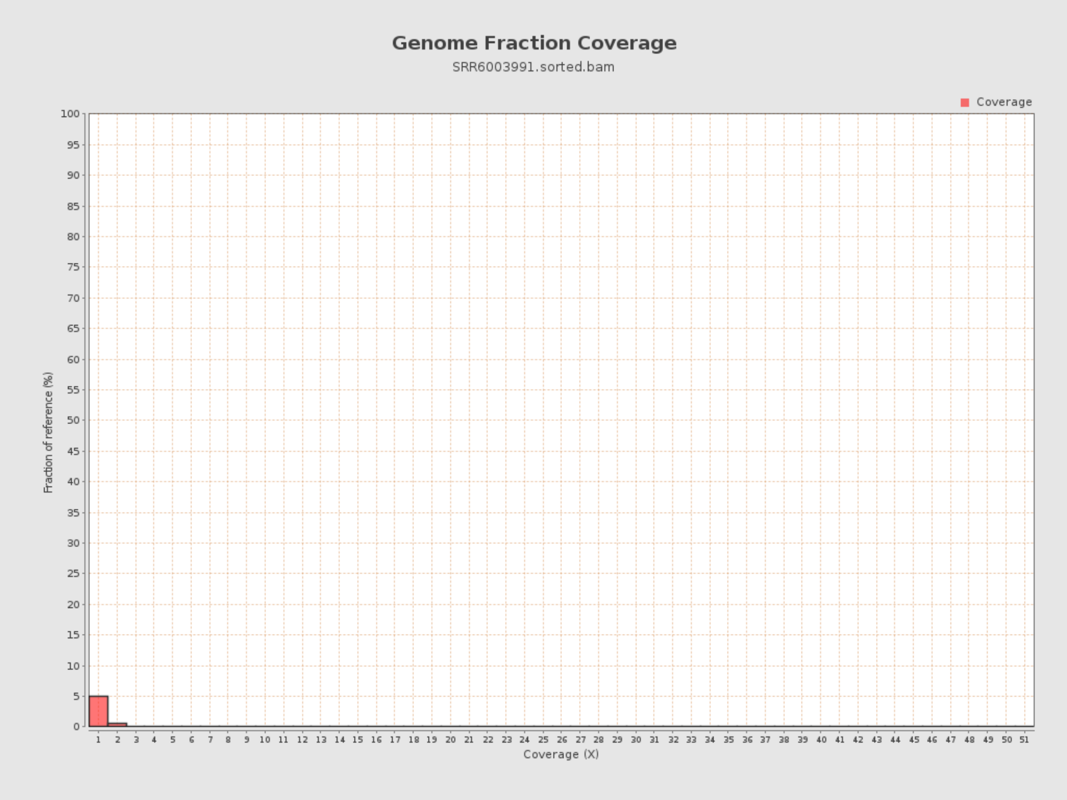
# 4. Results : Coverage Histogram



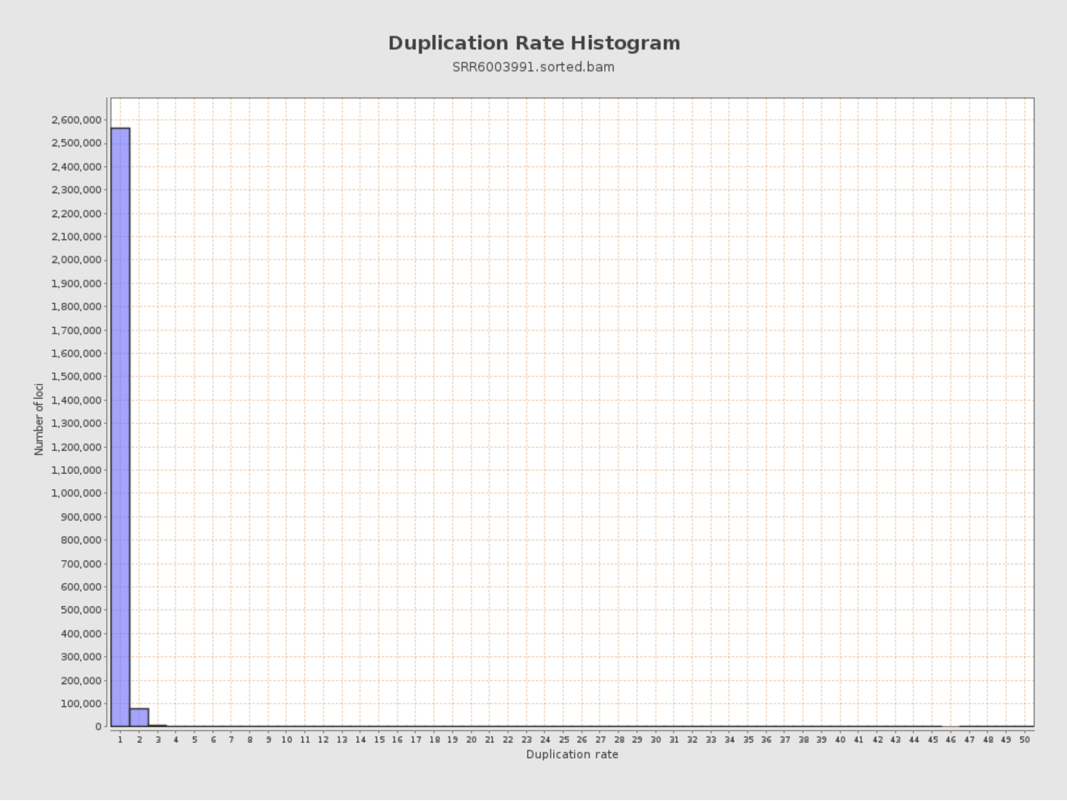
# 5. Results : Coverage Histogram (0-50X)



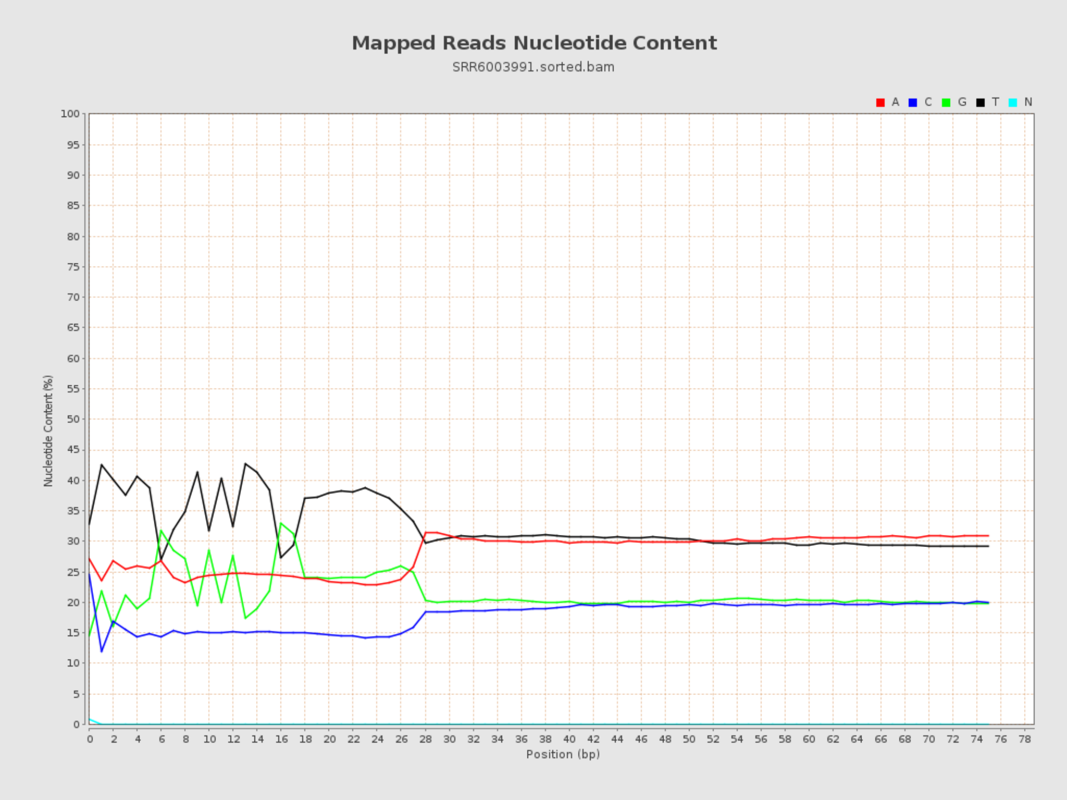
# 6. Results : Genome Fraction Coverage



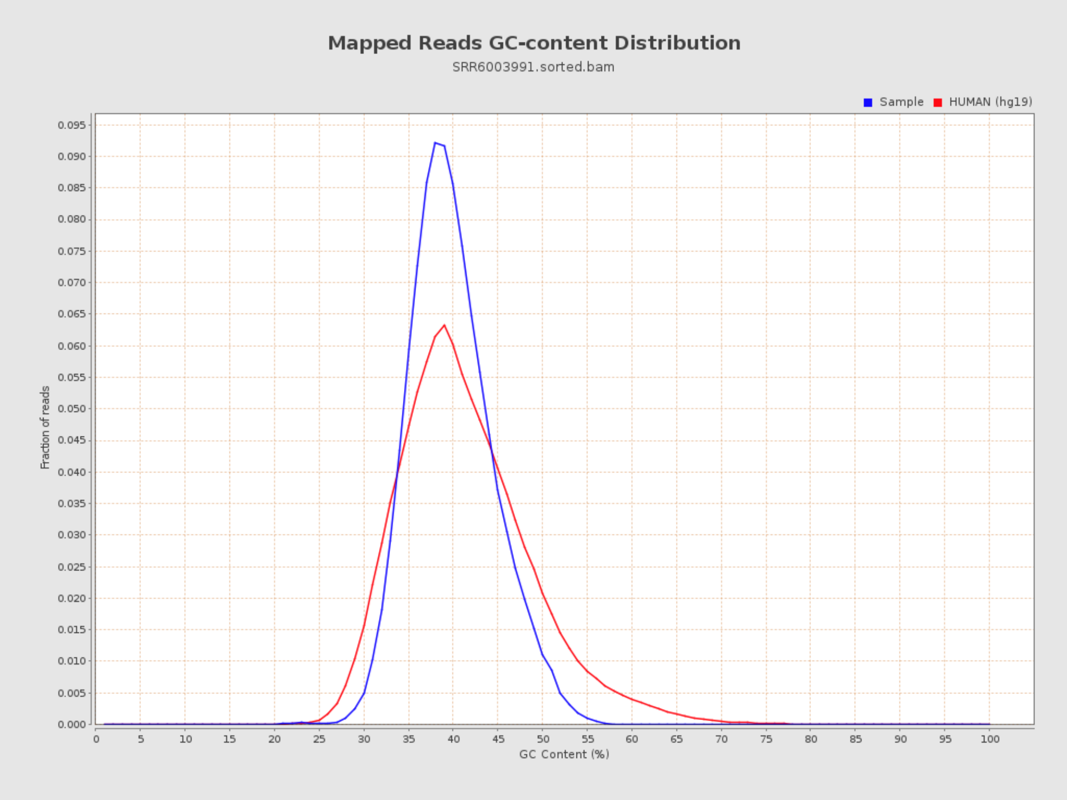
# 7. Results : Duplication Rate Histogram



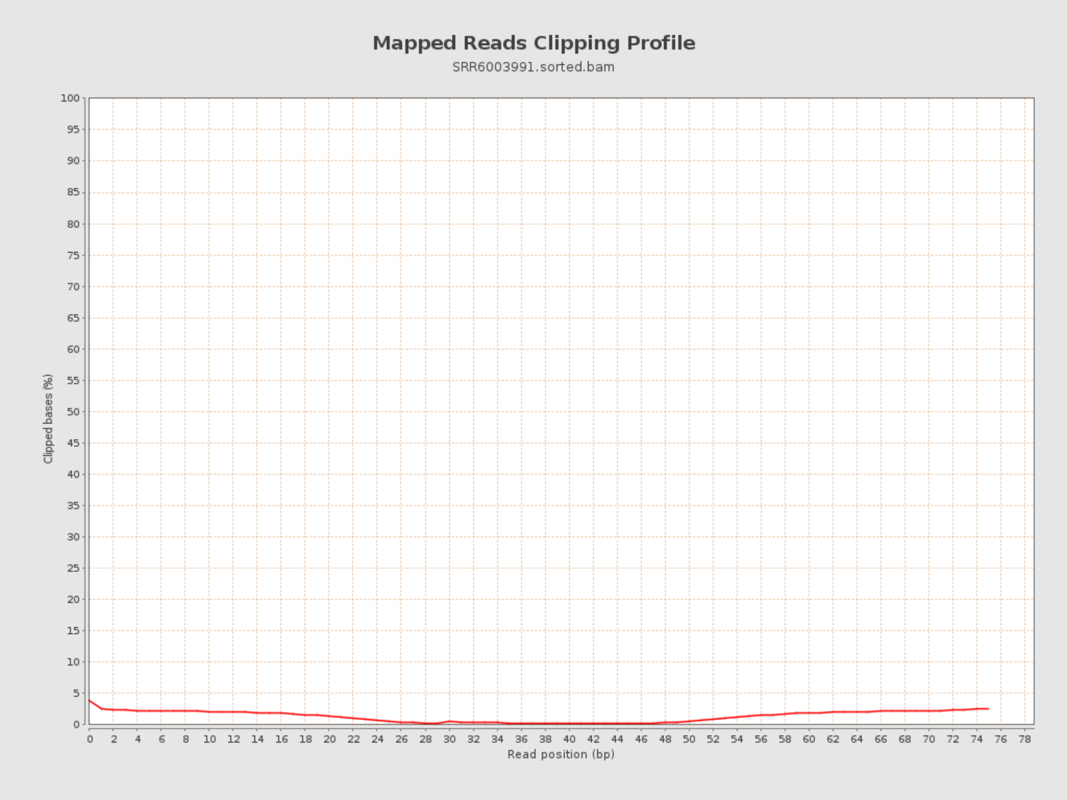
# 8. Results : Mapped Reads Nucleotide Content



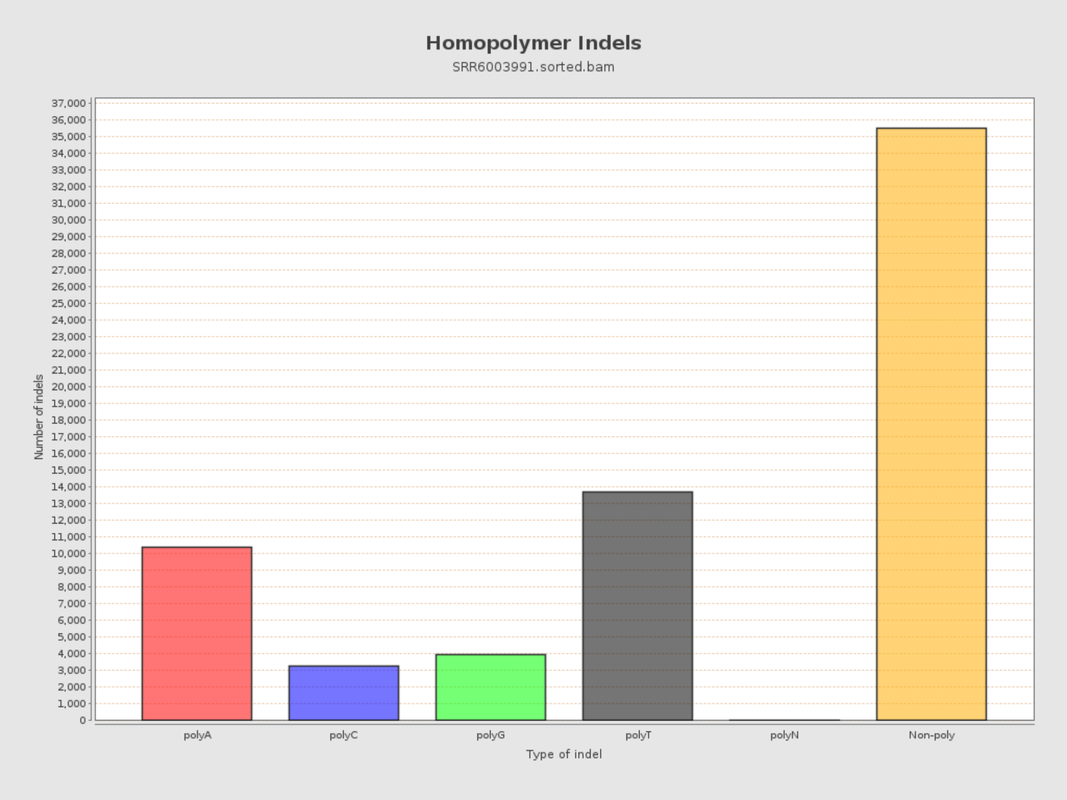
# 9. Results : Mapped Reads GC-content Distribution



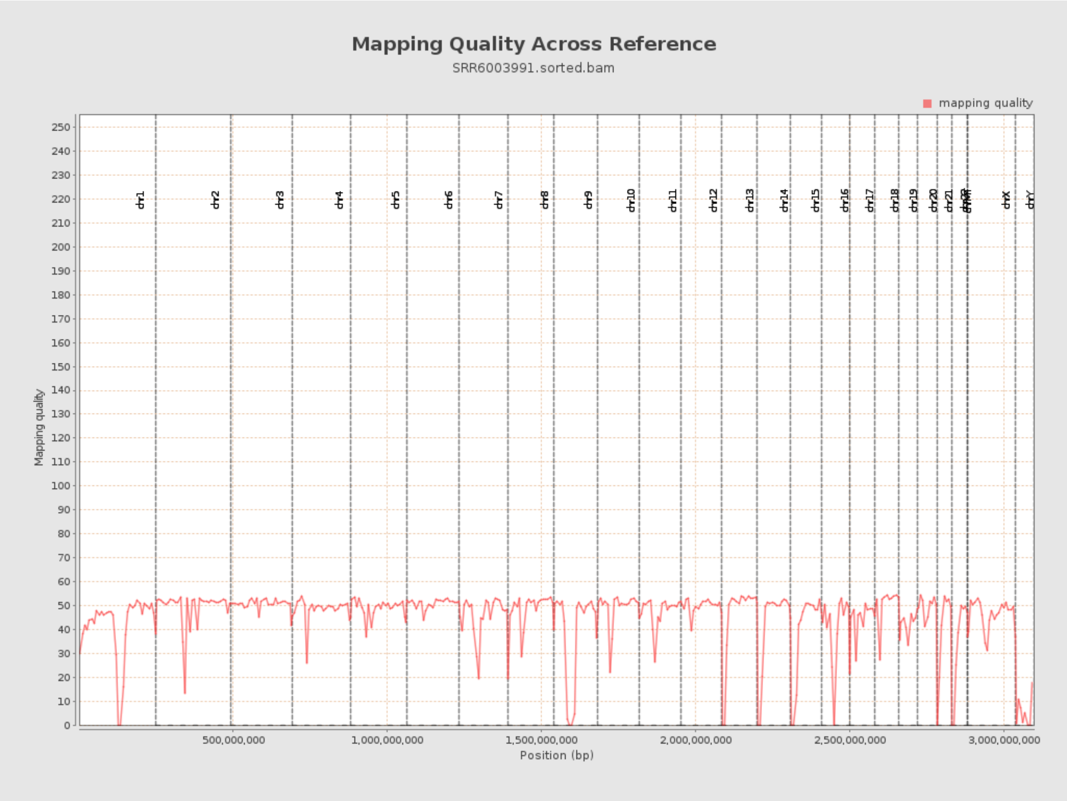
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram