# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/14 13:49:09*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013165.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_SRR6013165 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013165.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 14 13:49:08 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6013165.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,353,975 |
| Mapped reads | 1,876,009 / 79.7% |
| Unmapped reads | 477,966 / 20.3% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 18,527 / 0.79% |
| Read min/max/mean length | 30 / 76 / 76.27 |
| Duplicated reads (estimated) | 370,277 / 15.73% |
| Duplication rate | 14.07% |
| Clipped reads | 1,212,857 / 51.52% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 31,450,708 / 27.12% |
| Number/percentage of C's | 21,231,500 / 18.31% |
| Number/percentage of T's | 36,703,429 / 31.65% |
| Number/percentage of G's | 26,392,894 / 22.76% |
| Number/percentage of N's | 169,980 / 0.15% |
| GC Percentage | 41.07% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0375 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4325 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.33 |

## 2.5. Mismatches and indels

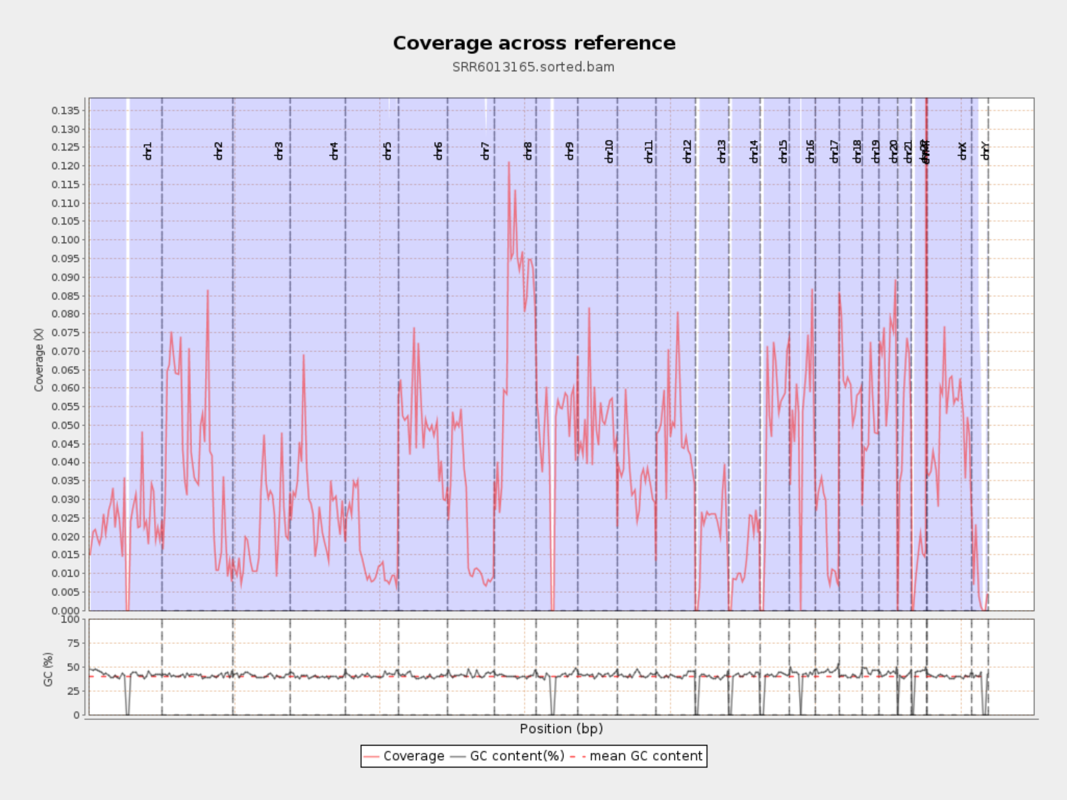
| | |
|---|---|
| General error rate | 1.09% |
| Mismatches | 1,246,880 |
| Insertions | 7,754 |
| Mapped reads with at least one insertion | 0.41% |
| Deletions | 59,810 |
| Mapped reads with at least one deletion | 3.12% |
| Homopolymer indels | 41.52% |

## 2.6. Chromosome stats

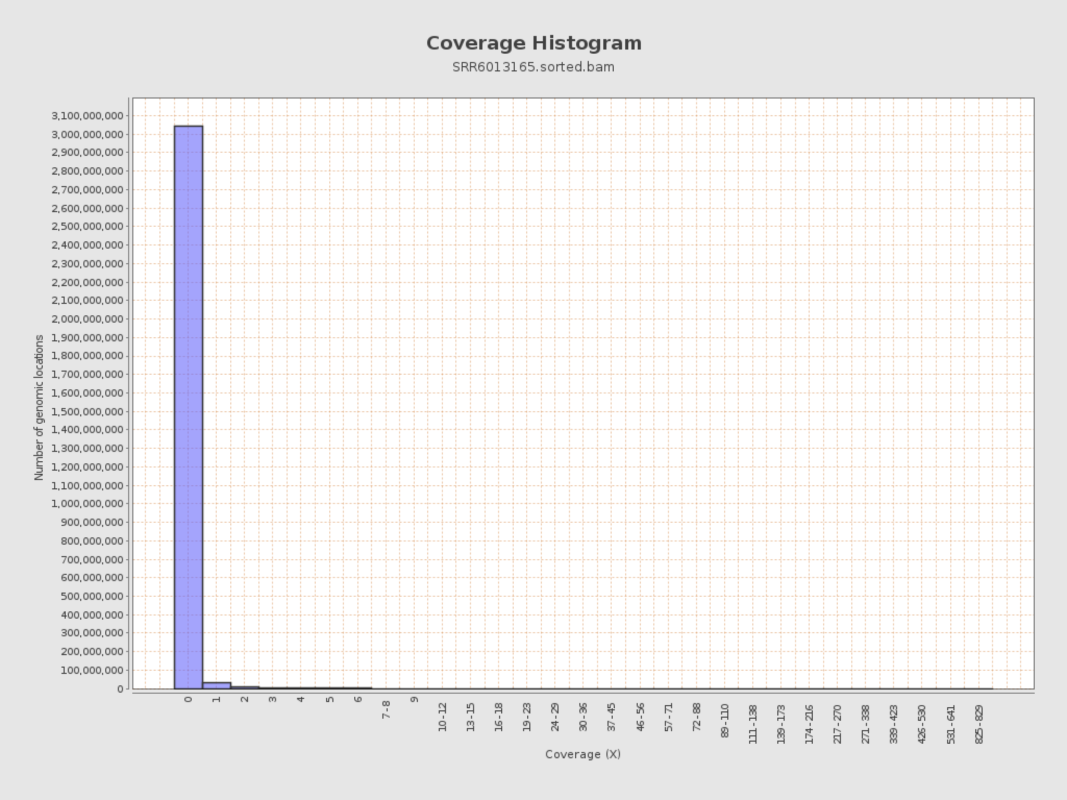
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5820126 | 0.0234 | 0.501 |
| chr2 | 243199373 | 10116546 | 0.0416 | 0.5843 |
| chr3 | 198022430 | 4246489 | 0.0214 | 0.2736 |
| chr4 | 191154276 | 5527587 | 0.0289 | 0.3416 |
| chr5 | 180915260 | 2771970 | 0.0153 | 0.2259 |
| chr6 | 171115067 | 8506535 | 0.0497 | 0.4931 |
| chr7 | 159138663 | 3789957 | 0.0238 | 0.335 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 11422848 | 0.078 | 0.5894 |
| chr9 | 141213431 | 6499469 | 0.046 | 0.4615 |
| chr10 | 135534747 | 6888082 | 0.0508 | 0.5297 |
| chr11 | 135006516 | 4829704 | 0.0358 | 0.36 |
| chr12 | 133851895 | 6684563 | 0.0499 | 0.4261 |
| chr13 | 115169878 | 2530760 | 0.022 | 0.2752 |
| chr14 | 107349540 | 1475656 | 0.0137 | 0.2407 |
| chr15 | 102531392 | 5075779 | 0.0495 | 0.4265 |
| chr16 | 90354753 | 4817317 | 0.0533 | 0.4529 |
| chr17 | 81195210 | 1584360 | 0.0195 | 0.2841 |
| chr18 | 78077248 | 4826538 | 0.0618 | 0.6 |
| chr19 | 59128983 | 2986201 | 0.0505 | 0.5524 |
| chr20 | 63025520 | 4405455 | 0.0699 | 0.5127 |
| chr21 | 48129895 | 2369697 | 0.0492 | 0.4401 |
| chr22 | 51304566 | 585398 | 0.0114 | 0.1972 |
| chrMT | 16571 | 13690 | 0.8261 | 1.3946 |
| chrX | 155270560 | 7871057 | 0.0507 | 0.4422 |
| chrY | 59373566 | 406298 | 0.0068 | 0.213 |

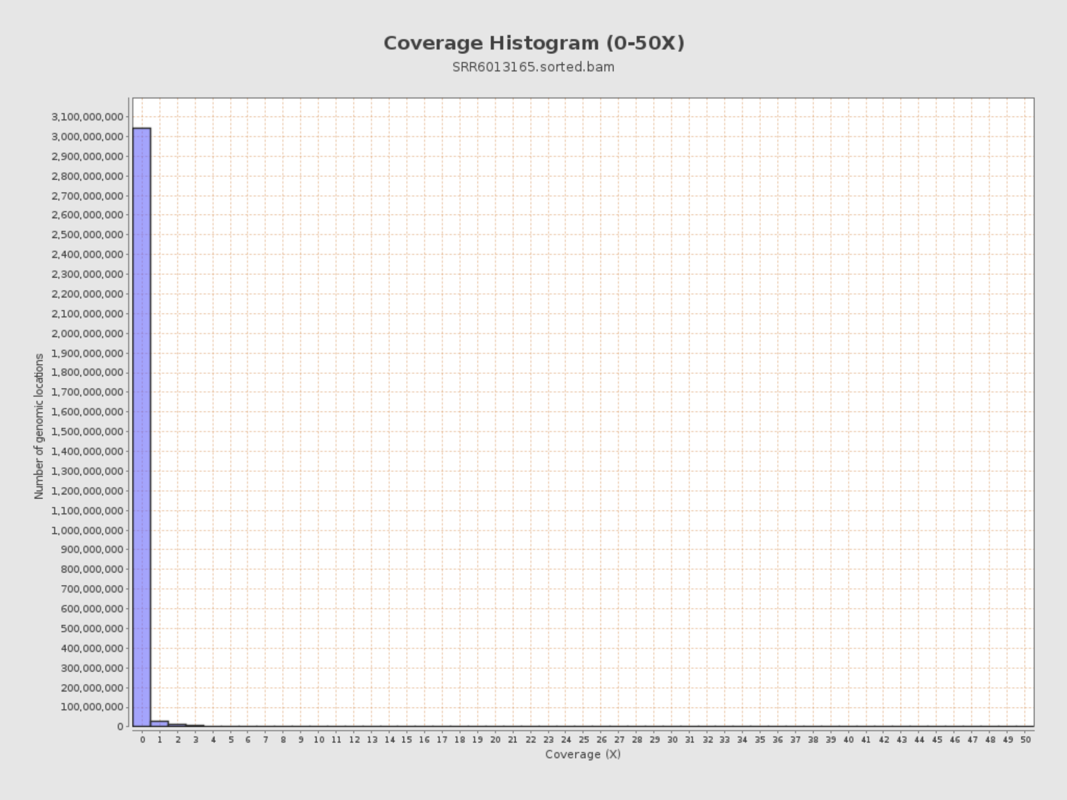
# 3. Results : Coverage across reference



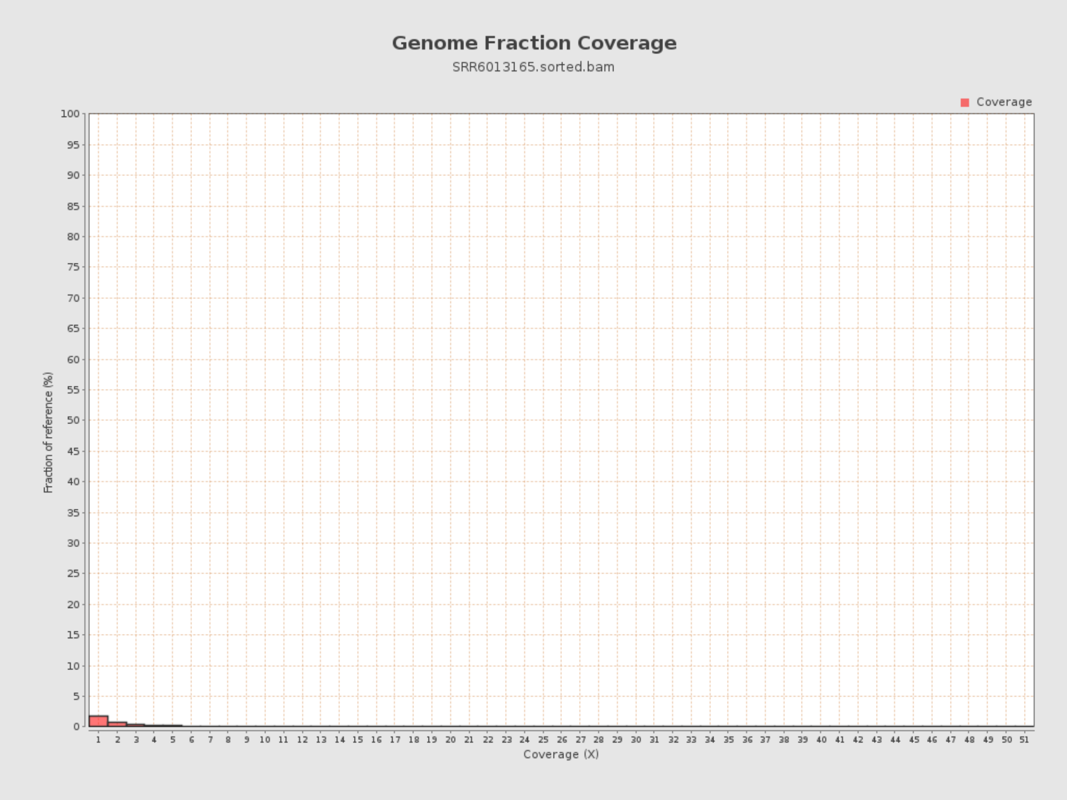
# 4. Results : Coverage Histogram



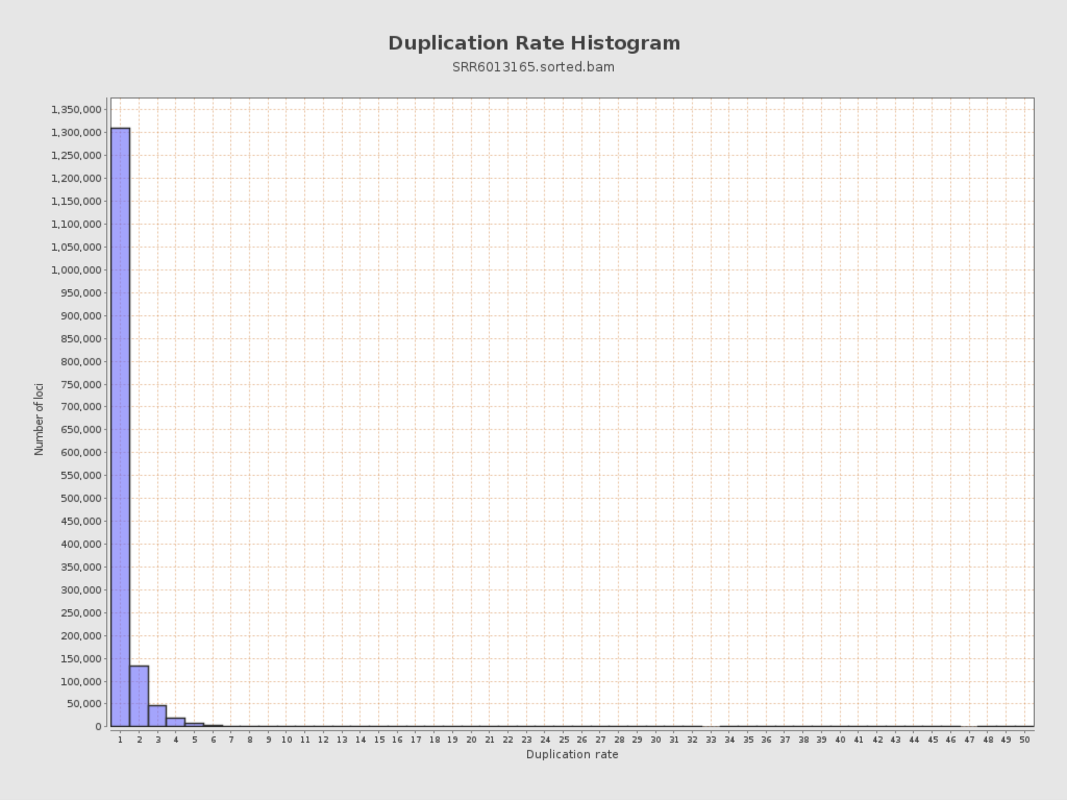
# 5. Results : Coverage Histogram (0-50X)



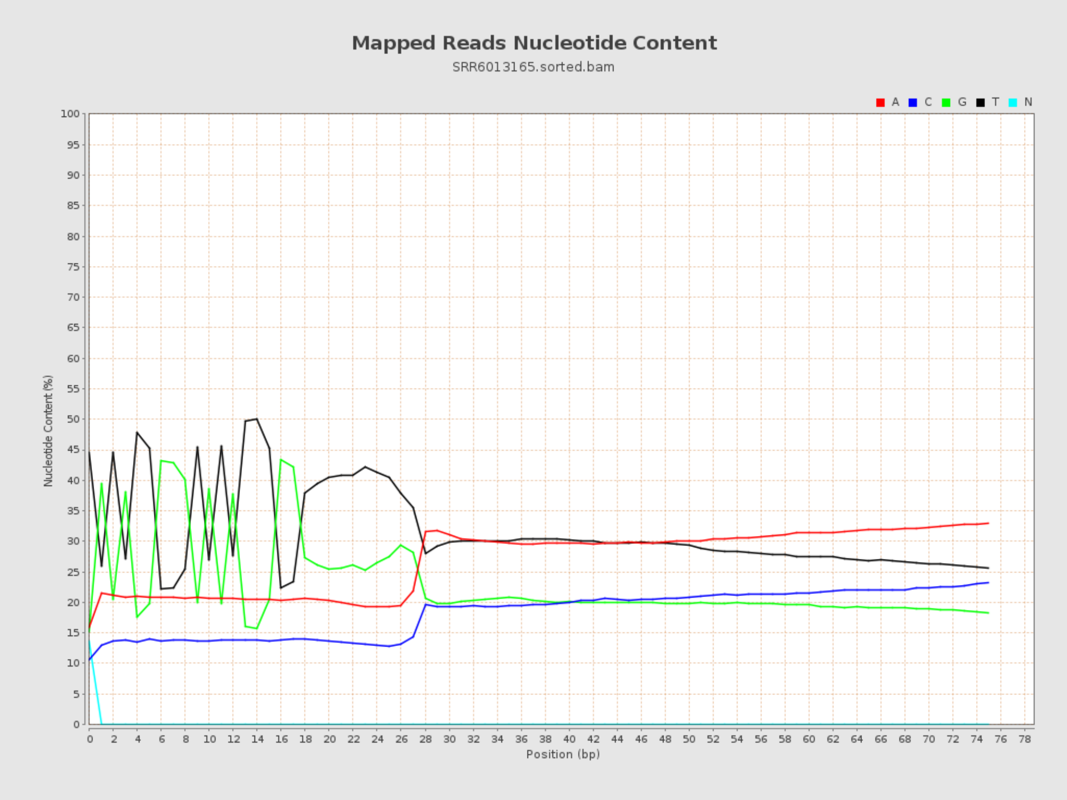
# 6. Results : Genome Fraction Coverage



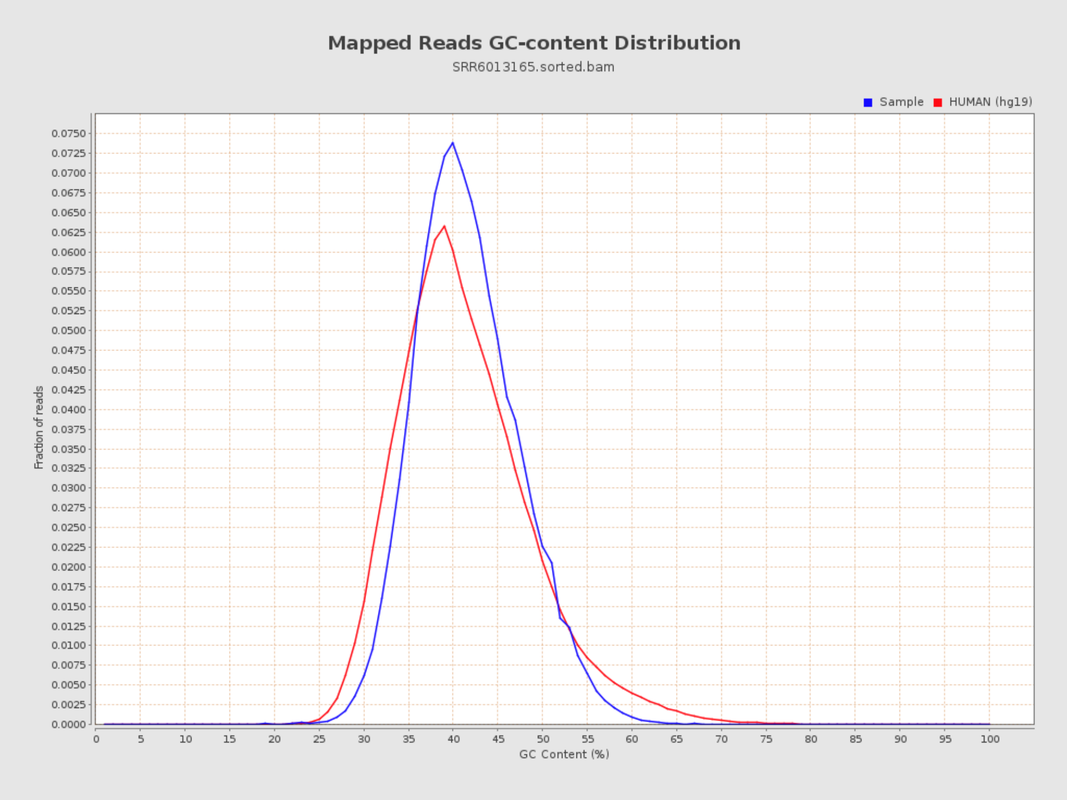
# 7. Results : Duplication Rate Histogram



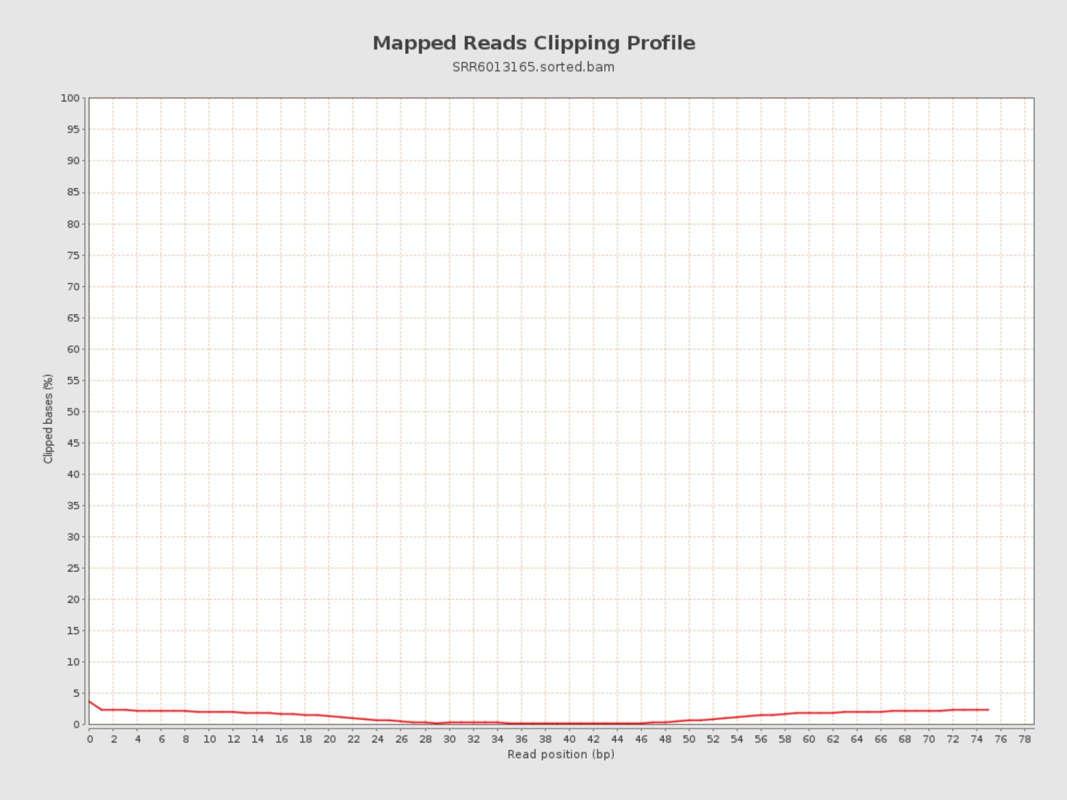
# 8. Results : Mapped Reads Nucleotide Content



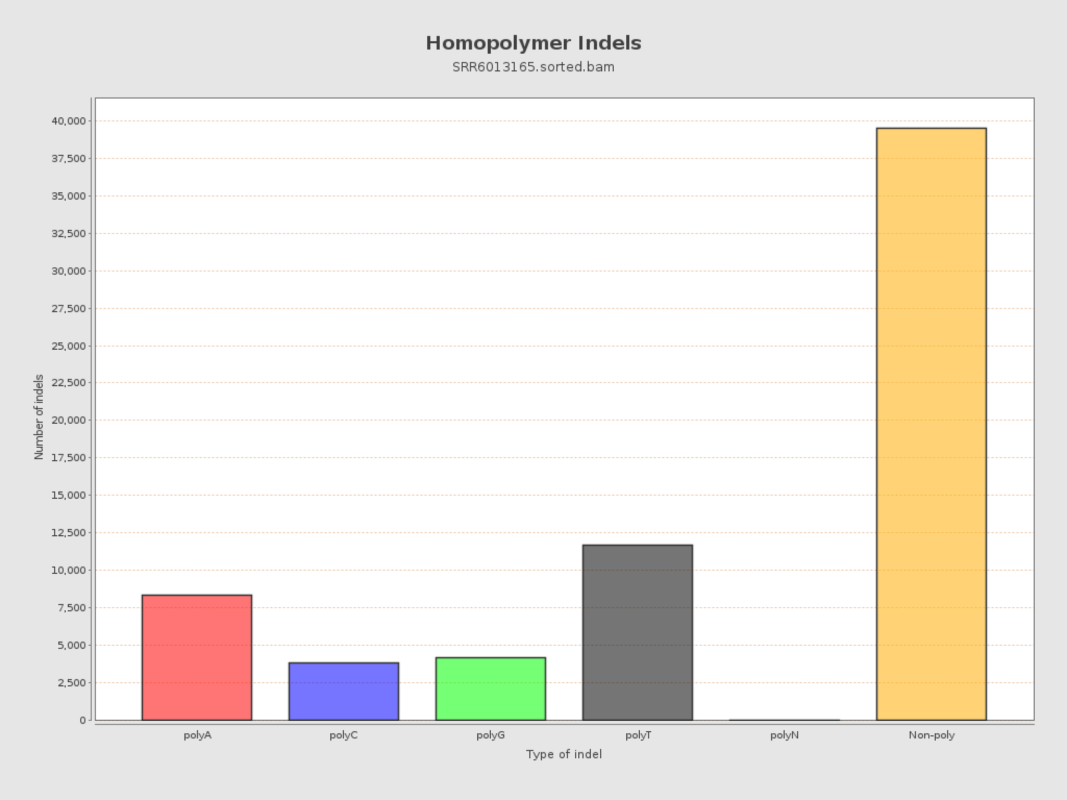
# 9. Results : Mapped Reads GC-content Distribution



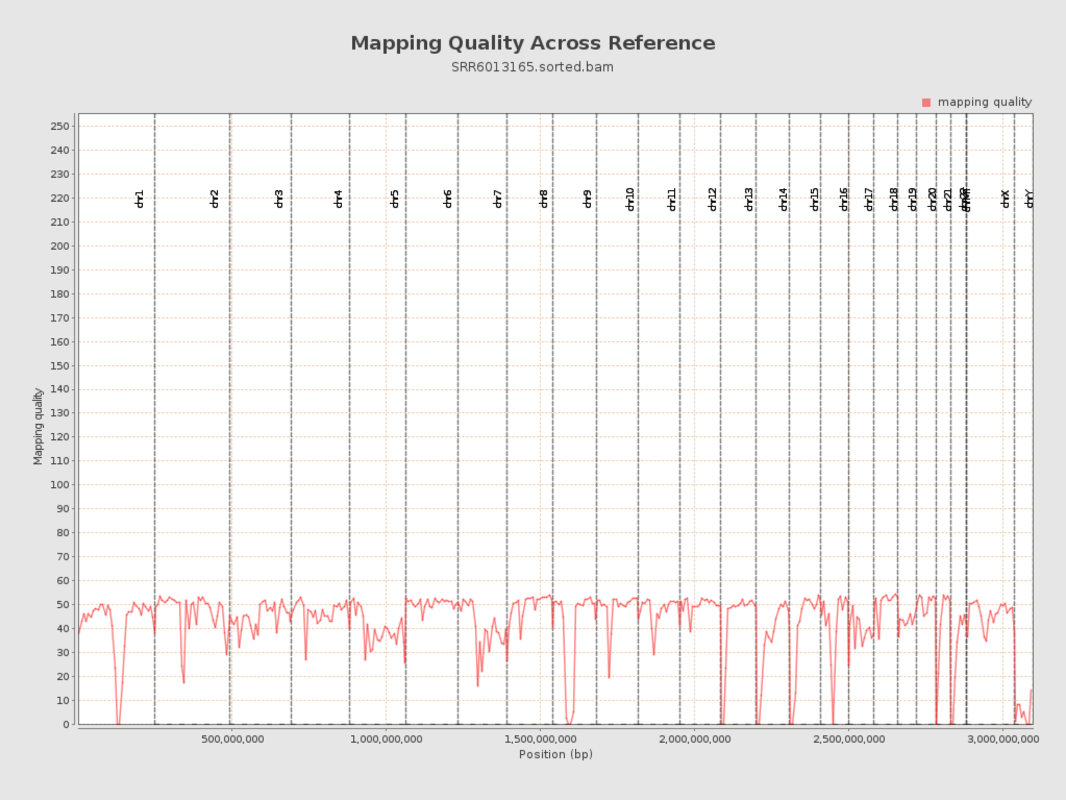
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram