# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/03 12:05:36*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716785.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_SRR9716785 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716785.fastq.gz` |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Sep 03 12:05:35 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR9716785.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,432,719 |
| Mapped reads | 3,139,951 / 91.47% |
| Unmapped reads | 292,768 / 8.53% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 65,546 / 1.91% |
| Read min/max/mean length | 30 / 101 / 101.69 |
| Duplicated reads (estimated) | 151,555 / 4.42% |
| Duplication rate | 3.6% |
| Clipped reads | 3,203,617 / 93.33% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 60,005,818 / 25.92% |
| Number/percentage of C's | 47,268,499 / 20.42% |
| Number/percentage of T's | 69,218,555 / 29.9% |
| Number/percentage of G's | 54,974,874 / 23.75% |
| Number/percentage of N's | 27,040 / 0.01% |
| GC Percentage | 44.17% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0748 |
| | |

| | |
|---|---|
| Standard Deviation | 0.508 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.41 |

## 2.5. Mismatches and indels

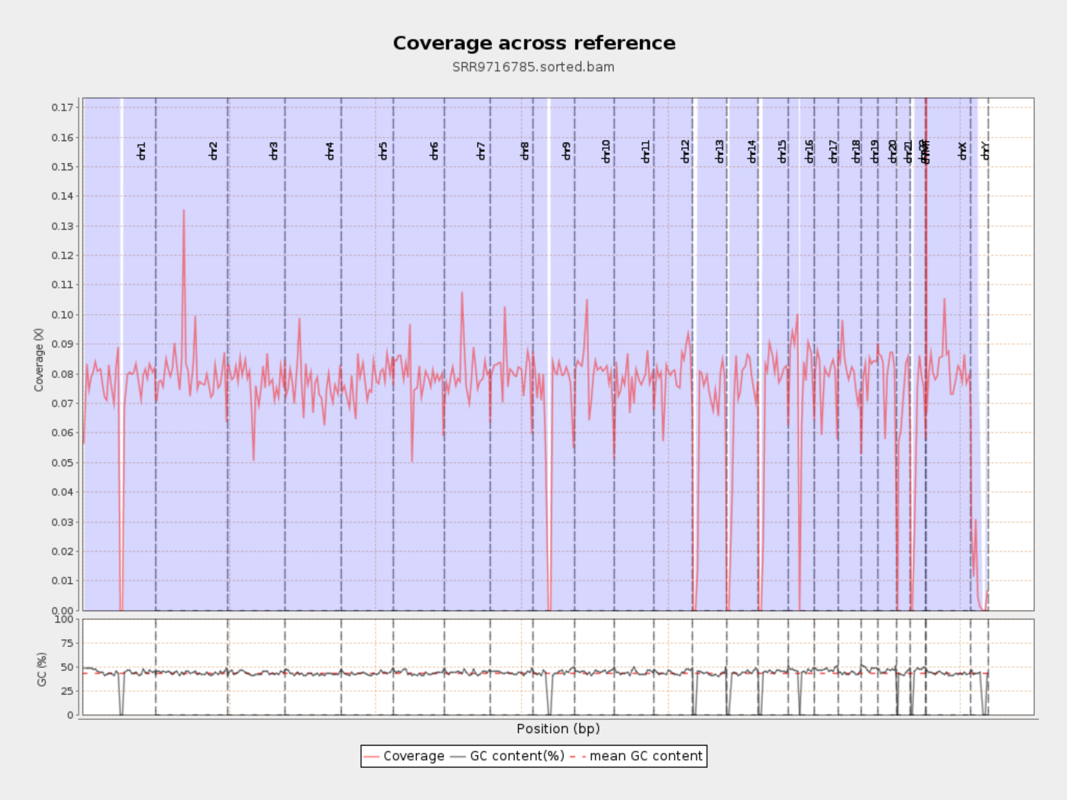
| | |
|---|---|
| General error rate | 0.71% |
| Mismatches | 1,617,038 |
| Insertions | 16,722 |
| Mapped reads with at least one insertion | 0.53% |
| Deletions | 45,560 |
| Mapped reads with at least one deletion | 1.43% |
| Homopolymer indels | 42.34% |

## 2.6. Chromosome stats

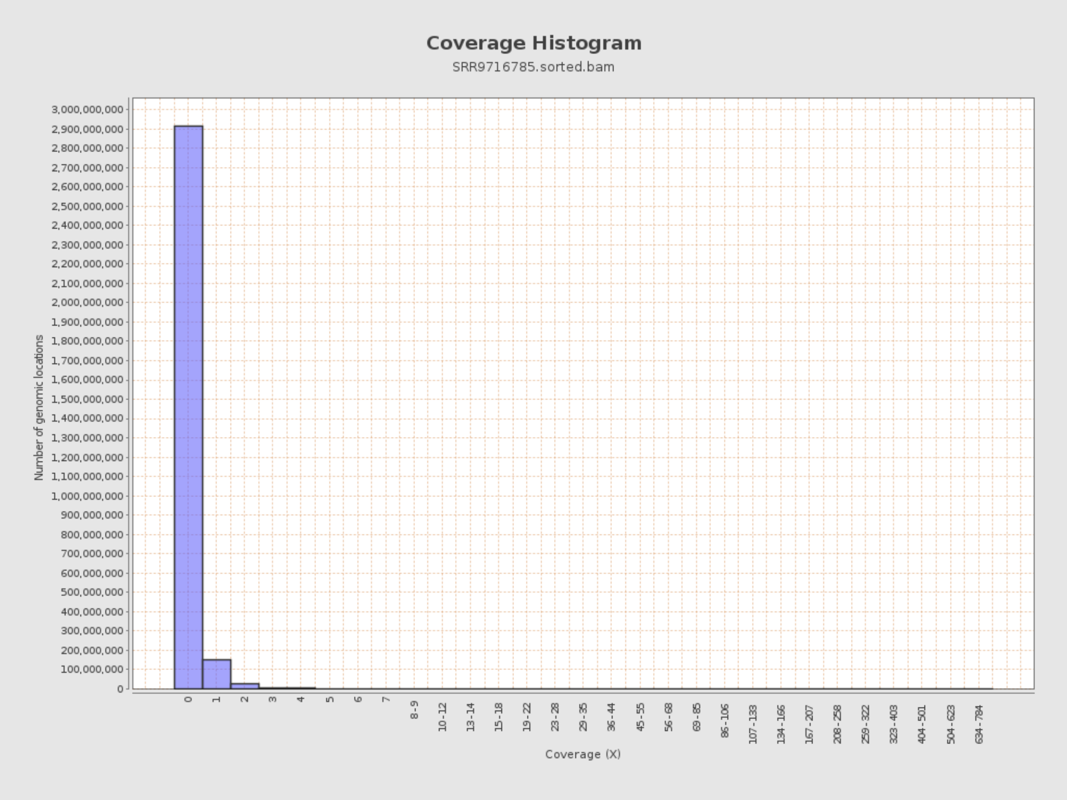
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 18296548 | 0.0734 | 0.5579 |
| chr2 | 243199373 | 19777465 | 0.0813 | 0.7194 |
| chr3 | 198022430 | 15263373 | 0.0771 | 0.3373 |
| chr4 | 191154276 | 14560766 | 0.0762 | 0.3739 |
| chr5 | 180915260 | 14034064 | 0.0776 | 0.3444 |
| chr6 | 171115067 | 13462747 | 0.0787 | 0.4113 |
| chr7 | 159138663 | 12785665 | 0.0803 | 0.6832 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 11807263 | 0.0807 | 0.6859 |
| chr9 | 141213431 | 9616293 | 0.0681 | 0.5431 |
| chr10 | 135534747 | 11000955 | 0.0812 | 0.5149 |
| chr11 | 135006516 | 10464262 | 0.0775 | 0.5413 |
| chr12 | 133851895 | 10776216 | 0.0805 | 0.3549 |
| chr13 | 115169878 | 7288480 | 0.0633 | 0.3052 |
| chr14 | 107349540 | 7036549 | 0.0655 | 0.4022 |
| chr15 | 102531392 | 6818457 | 0.0665 | 0.322 |
| chr16 | 90354753 | 6901576 | 0.0764 | 0.3871 |
| chr17 | 81195210 | 6434606 | 0.0792 | 0.3777 |
| chr18 | 78077248 | 6366317 | 0.0815 | 1.0295 |
| chr19 | 59128983 | 4754811 | 0.0804 | 0.5351 |
| chr20 | 63025520 | 5029693 | 0.0798 | 0.364 |
| chr21 | 48129895 | 3107447 | 0.0646 | 0.3521 |
| chr22 | 51304566 | 2756533 | 0.0537 | 0.2853 |
| chrMT | 16571 | 7597 | 0.4585 | 0.9626 |
| chrX | 155270560 | 12661463 | 0.0815 | 0.4557 |
| chrY | 59373566 | 563494 | 0.0095 | 0.258 |

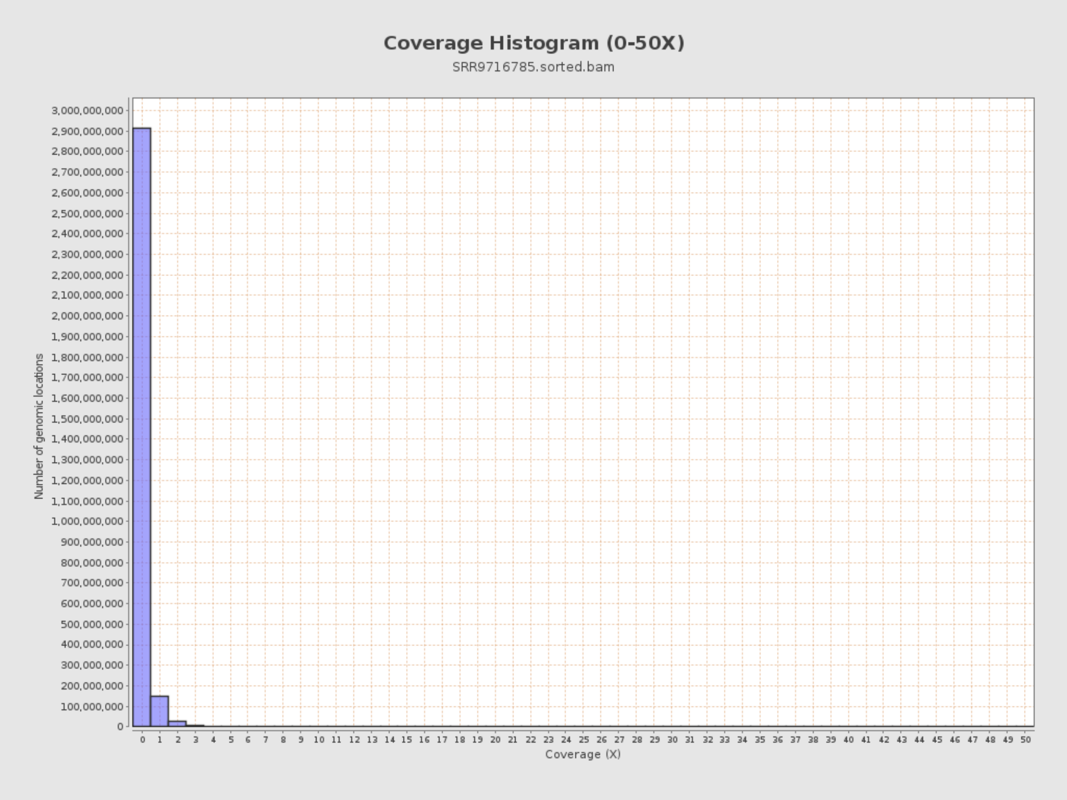
# 3. Results : Coverage across reference



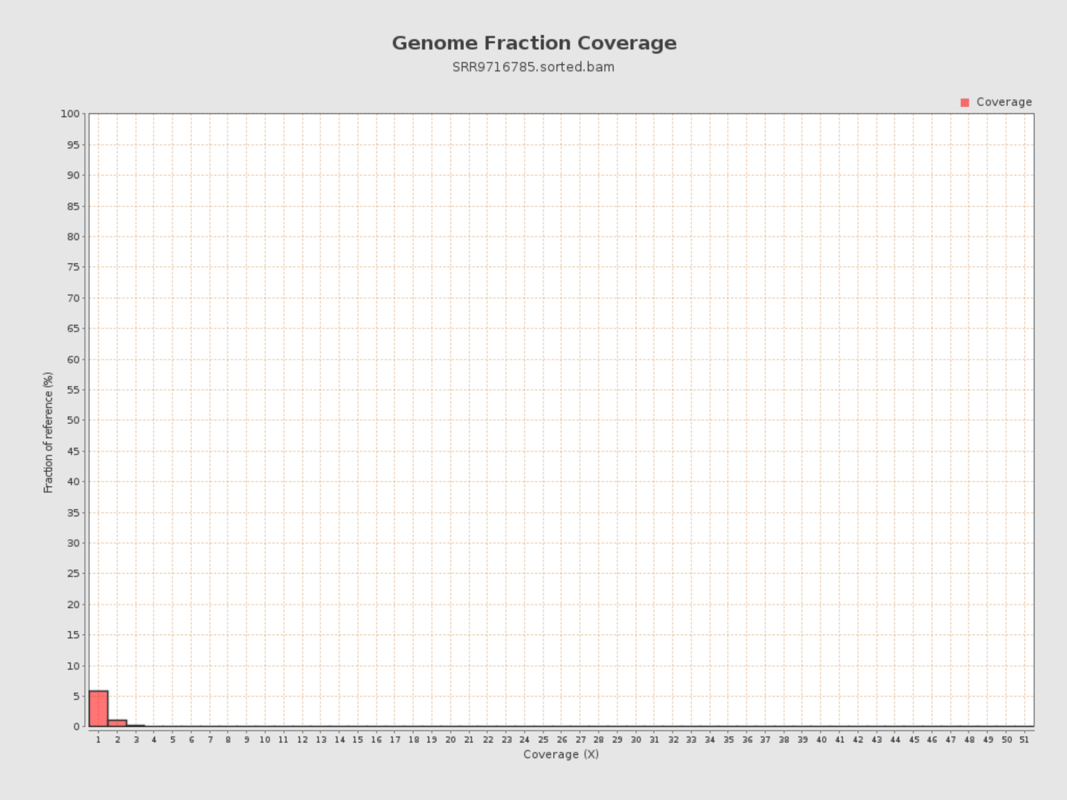
# 4. Results : Coverage Histogram



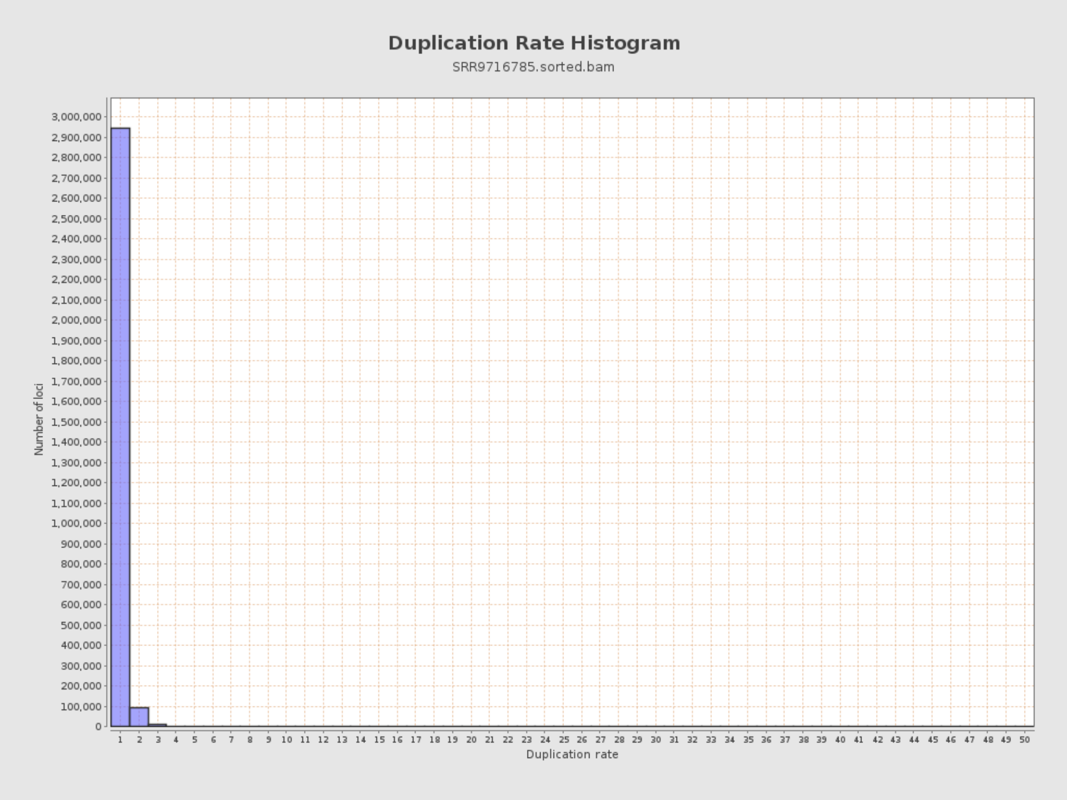
# 5. Results : Coverage Histogram (0-50X)



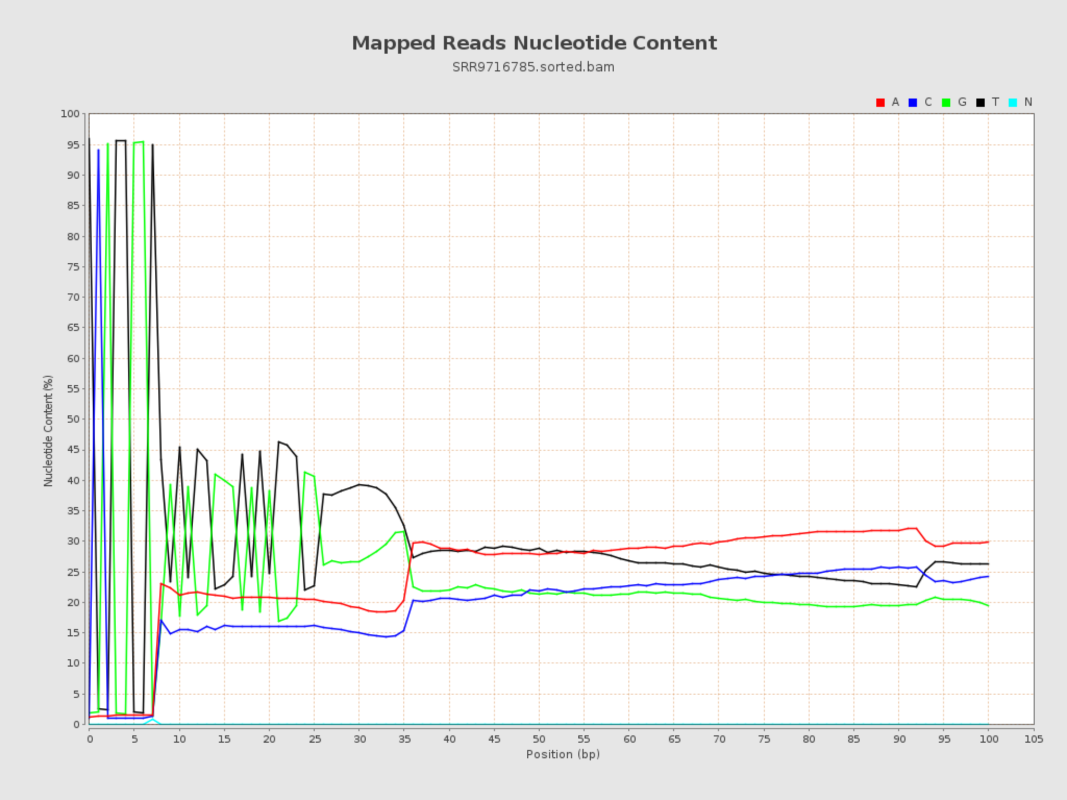
# 6. Results : Genome Fraction Coverage



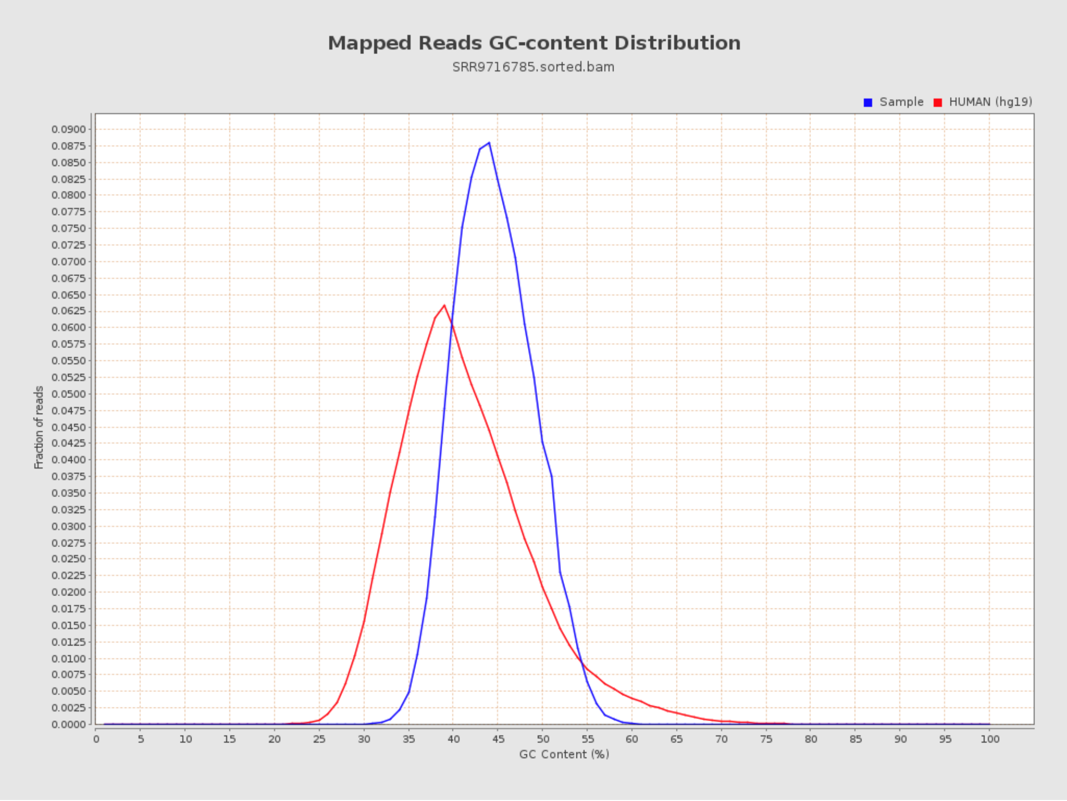
# 7. Results : Duplication Rate Histogram



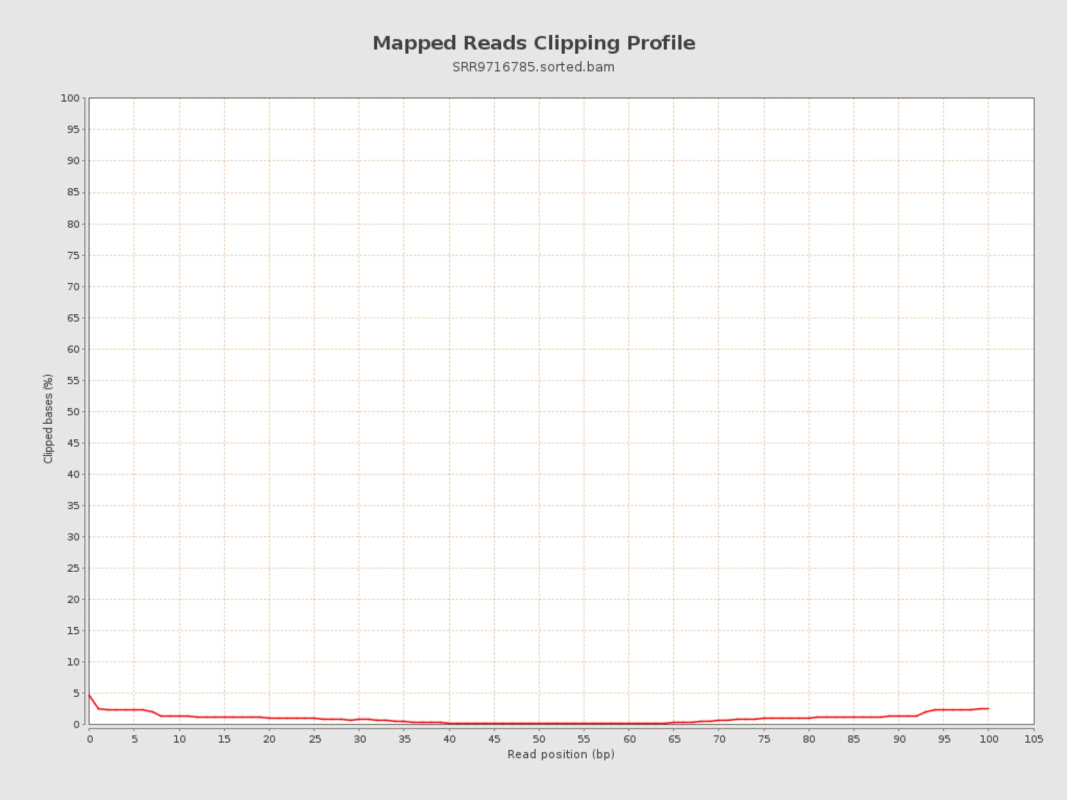
# 8. Results : Mapped Reads Nucleotide Content



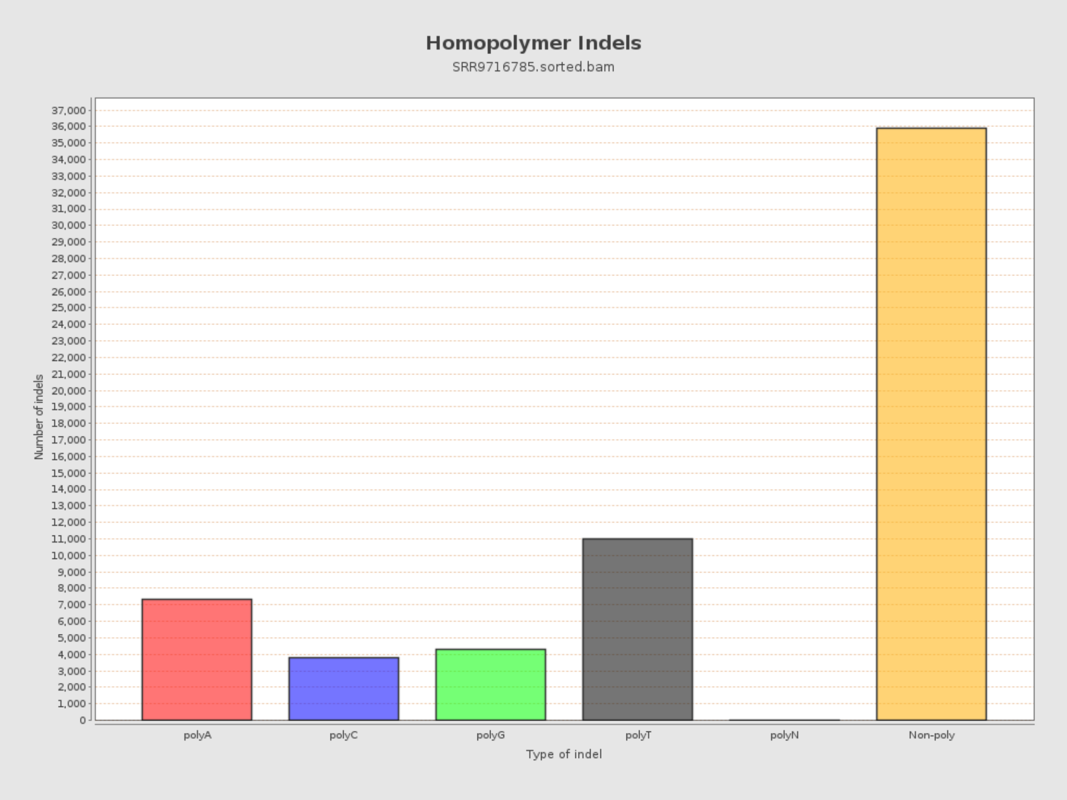
# 9. Results : Mapped Reads GC-content Distribution



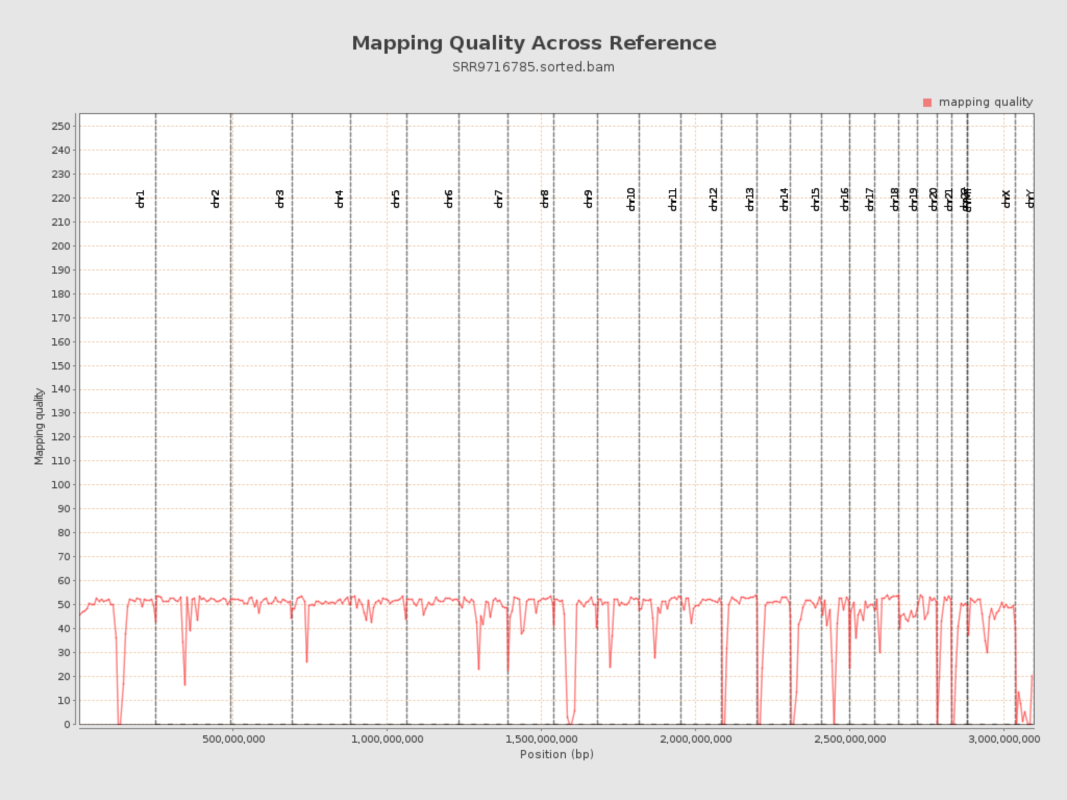
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram