# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 11:16:24*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549023.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_SRR1549023 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549023.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 11:16:24 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1549023.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 7,749,751 |
| Mapped reads | 6,799,633 / 87.74% |
| Unmapped reads | 950,118 / 12.26% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Read min/max/mean length | 40 / 40 / 40 |
| Duplicated reads (estimated) | 244,141 / 3.15% |
| Duplication rate | 2.7% |
| Clipped reads | 515,240 / 6.65% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 78,422,091 / 29.14% |
| Number/percentage of C's | 55,752,142 / 20.72% |
| Number/percentage of T's | 78,795,999 / 29.28% |
| Number/percentage of G's | 56,130,928 / 20.86% |
| Number/percentage of N's | 2,690 / 0% |
| GC Percentage | 41.58% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0869 |
| Standard Deviation | 0.9012 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 41.05 |

## 2.5. Mismatches and indels

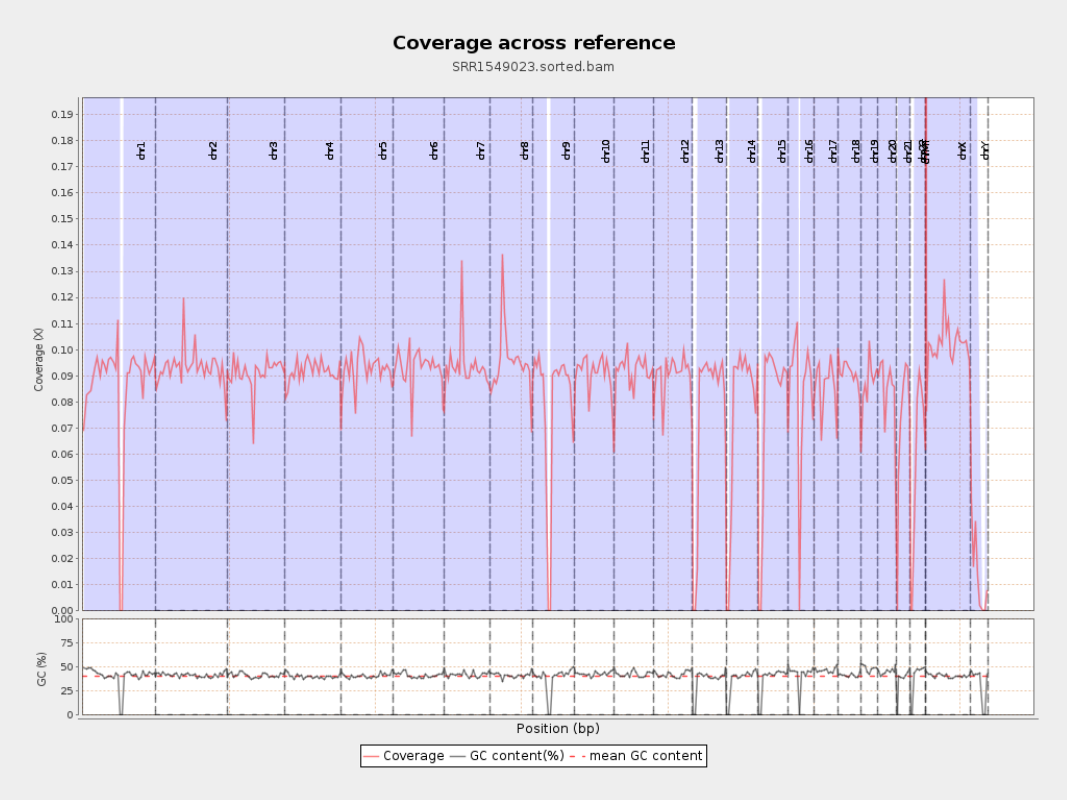
| | |
|---|---|
| General error rate | 0.29% |
| Mismatches | 761,126 |
| Insertions | 8,816 |
| Mapped reads with at least one insertion | 0.13% |
| Deletions | 22,245 |
| Mapped reads with at least one deletion | 0.33% |
| Homopolymer indels | 41.24% |

## 2.6. Chromosome stats

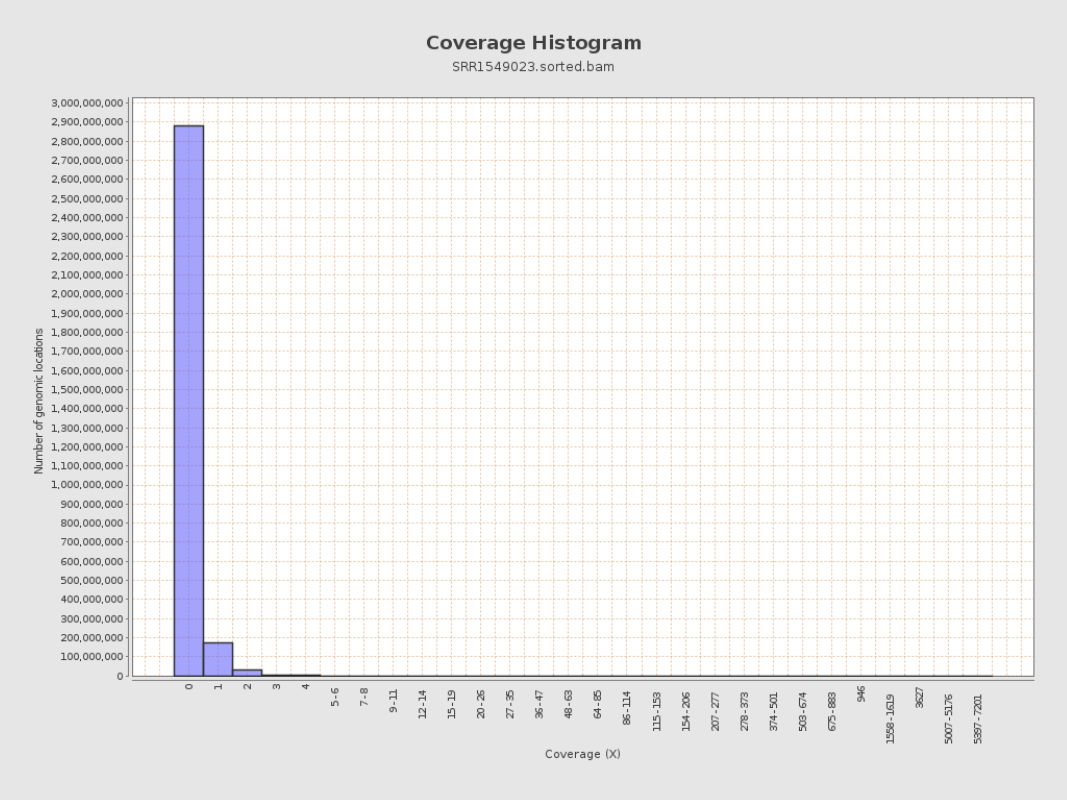
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 21357214 | 0.0857 | 0.7467 |
| chr2 | 243199373 | 22684713 | 0.0933 | 0.5101 |
| chr3 | 198022430 | 18012905 | 0.091 | 0.3631 |
| chr4 | 191154276 | 17531712 | 0.0917 | 0.3737 |
| chr5 | 180915260 | 16716173 | 0.0924 | 0.3712 |
| chr6 | 171115067 | 15979906 | 0.0934 | 0.3979 |
| chr7 | 159138663 | 14922518 | 0.0938 | 0.7383 |
| chr8 | 146364022 | 13962816 | 0.0954 | 3.4862 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr9 | 141213431 | 11172645 | 0.0791 | 0.4963 |
| chr10 | 135534747 | 12381550 | 0.0914 | 0.4344 |
| chr11 | 135006516 | 12386767 | 0.0917 | 0.6047 |
| chr12 | 133851895 | 12151260 | 0.0908 | 0.3733 |
| chr13 | 115169878 | 8756861 | 0.076 | 0.331 |
| chr14 | 107349540 | 8182190 | 0.0762 | 0.4084 |
| chr15 | 102531392 | 7769034 | 0.0758 | 0.3314 |
| chr16 | 90354753 | 7356575 | 0.0814 | 0.3691 |
| chr17 | 81195210 | 7040324 | 0.0867 | 0.3857 |
| chr18 | 78077248 | 7120935 | 0.0912 | 0.8777 |
| chr19 | 59128983 | 5185436 | 0.0877 | 0.7327 |
| chr20 | 63025520 | 5401509 | 0.0857 | 0.3614 |
| chr21 | 48129895 | 3461032 | 0.0719 | 0.3654 |
| chr22 | 51304566 | 2960711 | 0.0577 | 0.3565 |
| chrMT | 16571 | 21746 | 1.3123 | 1.8067 |
| chrX | 155270560 | 15825050 | 0.1019 | 0.451 |
| chrY | 59373566 | 791154 | 0.0133 | 0.1672 |

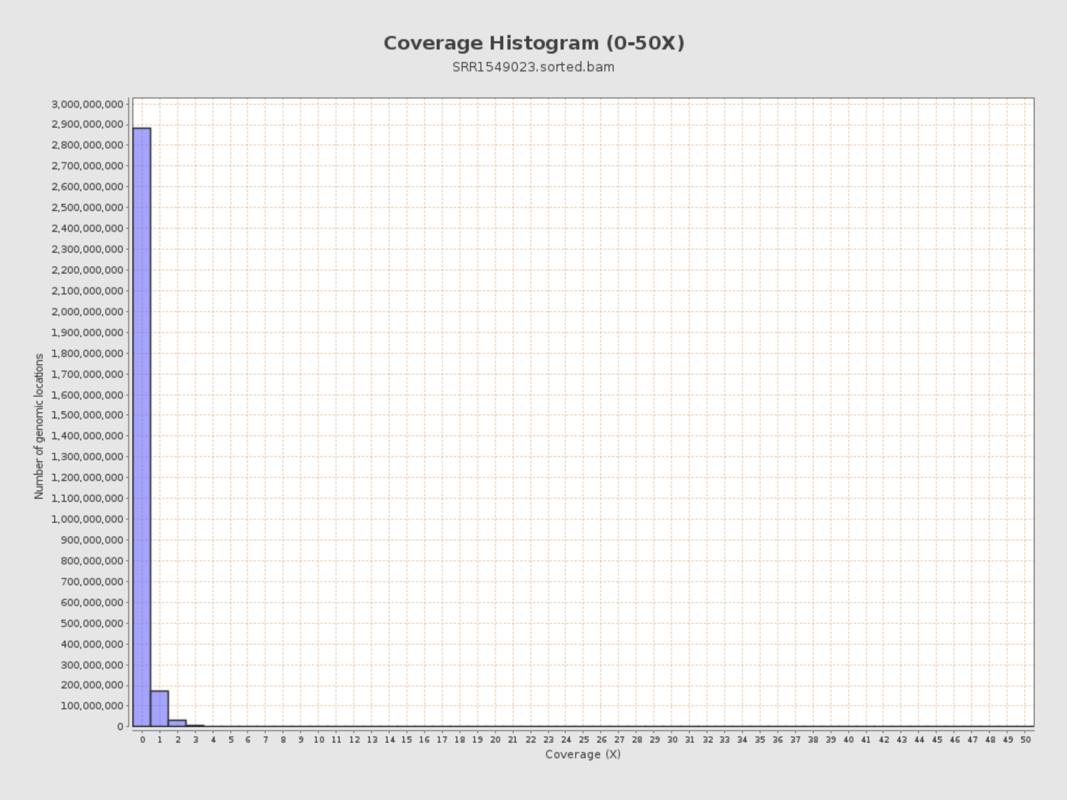
# 3. Results : Coverage across reference



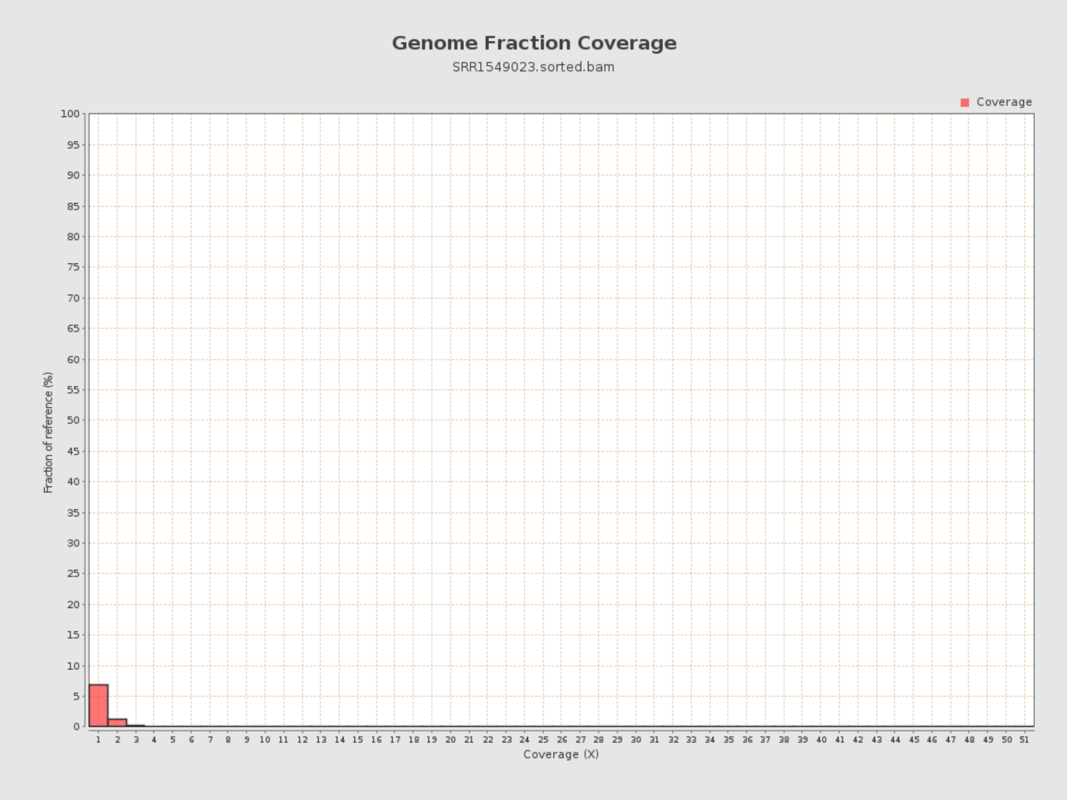
# 4. Results : Coverage Histogram



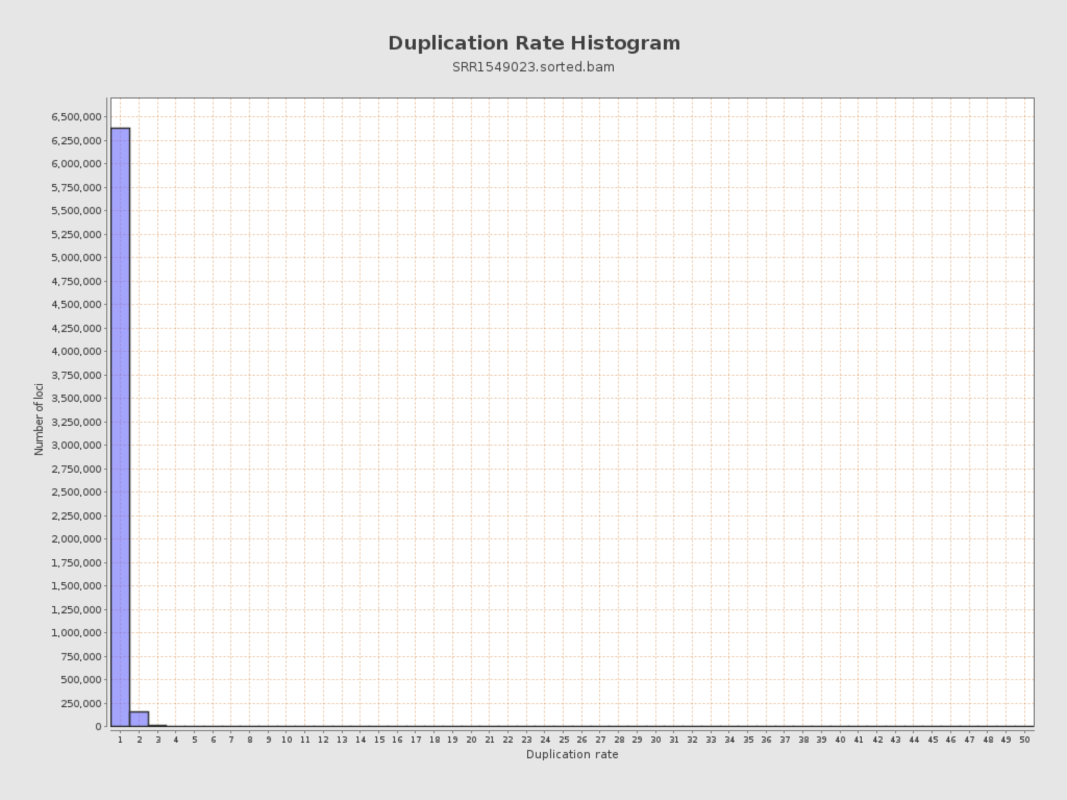
# 5. Results : Coverage Histogram (0-50X)



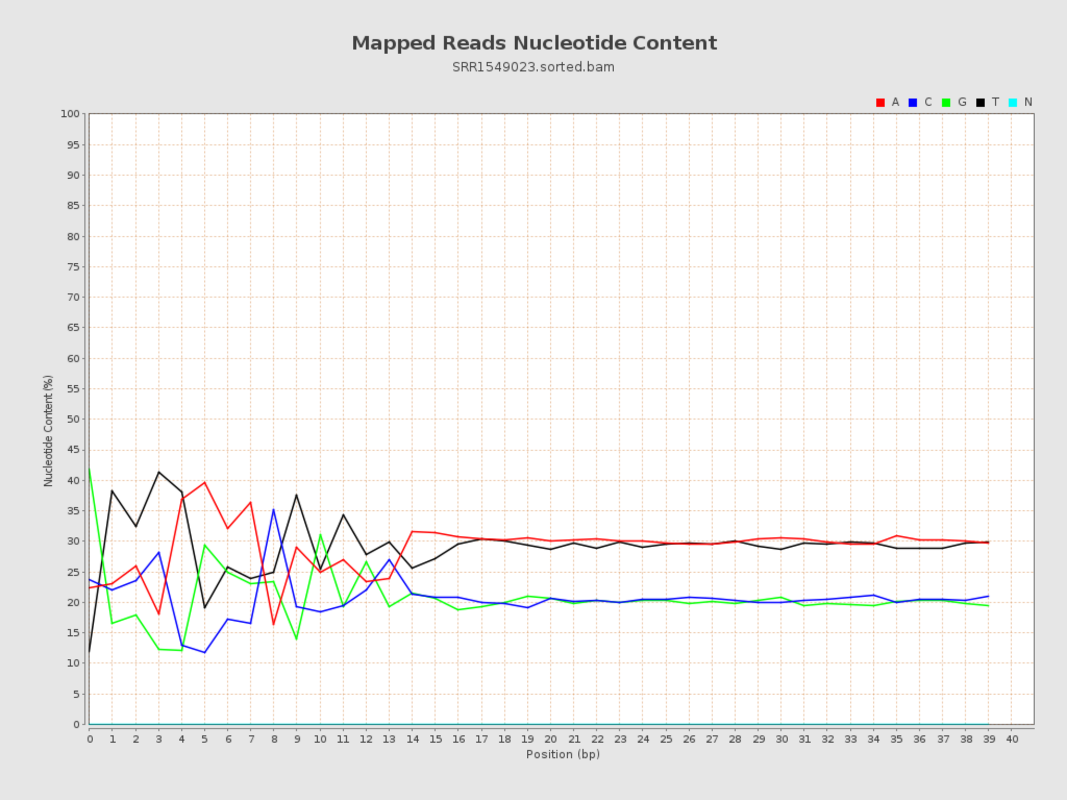
# 6. Results : Genome Fraction Coverage



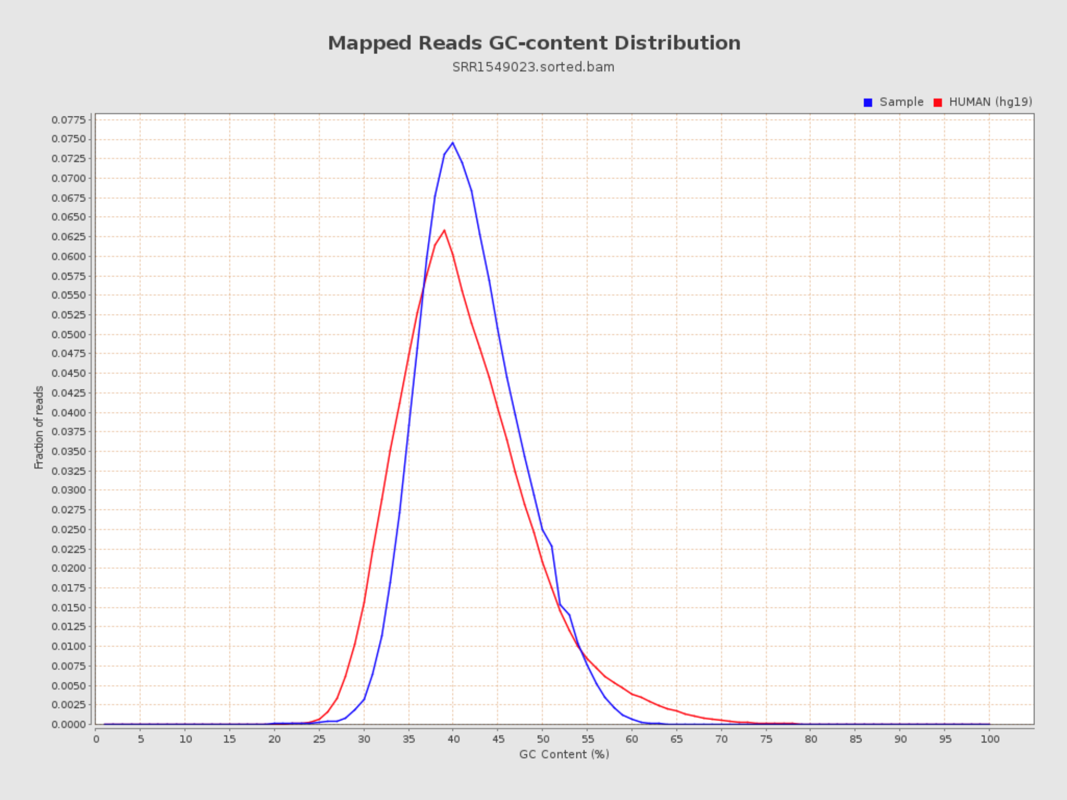
# 7. Results : Duplication Rate Histogram



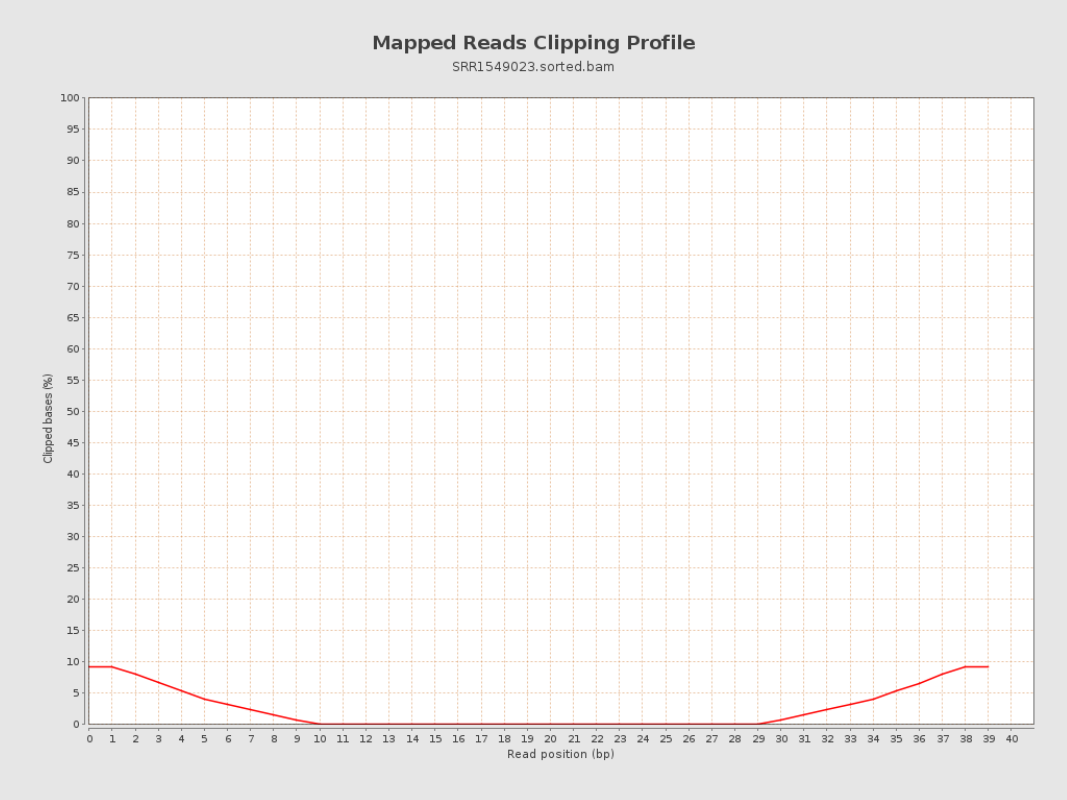
# 8. Results : Mapped Reads Nucleotide Content



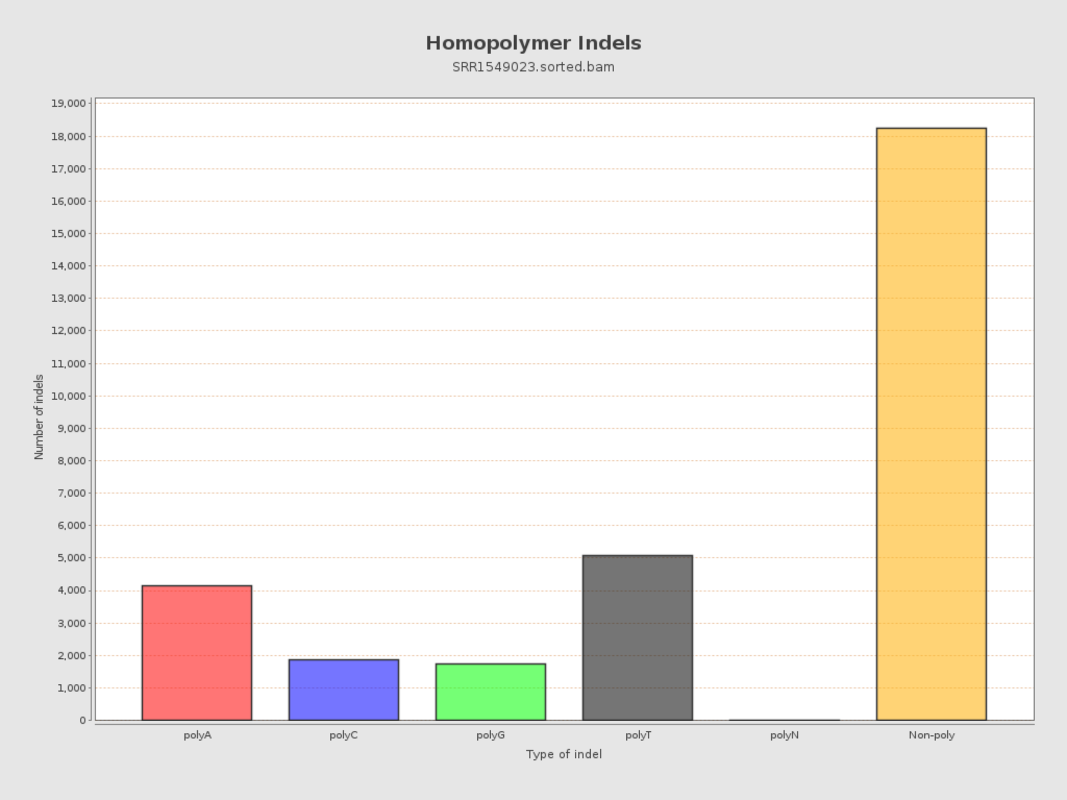
# 9. Results : Mapped Reads GC-content Distribution



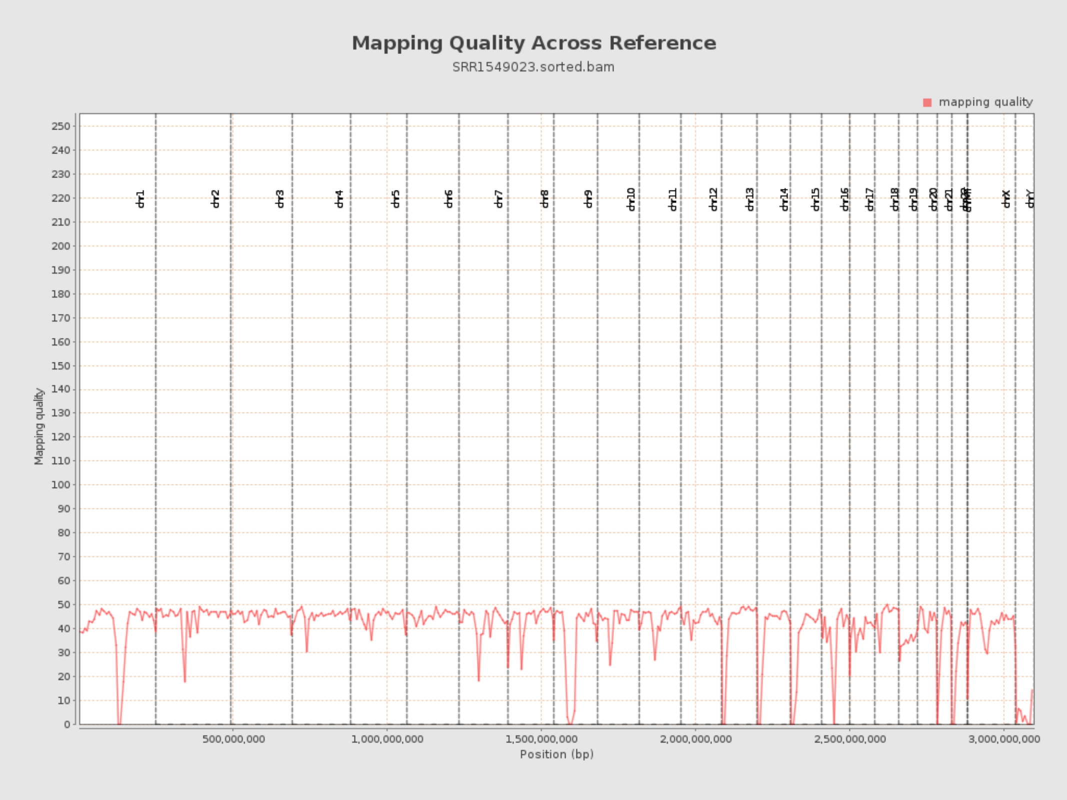
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram