# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/22 12:46:10*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548942.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_SRR1548942 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548942.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 22 12:46:07 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1548942.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 8,834,435 |
| Mapped reads | 7,697,307 / 87.13% |
| Unmapped reads | 1,137,128 / 12.87% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Read min/max/mean length | 40 / 40 / 40 |
| Duplicated reads (estimated) | 293,059 / 3.32% |
| Duplication rate | 2.48% |
| Clipped reads | 629,437 / 7.12% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 88,524,737 / 29.08% |
| Number/percentage of C's | 63,912,539 / 21% |
| Number/percentage of T's | 88,587,344 / 29.1% |
| Number/percentage of G's | 63,348,083 / 20.81% |
| Number/percentage of N's | 2,581 / 0% |
| GC Percentage | 41.81% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0983 |
| Standard Deviation | 1.1689 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 39.38 |

## 2.5. Mismatches and indels

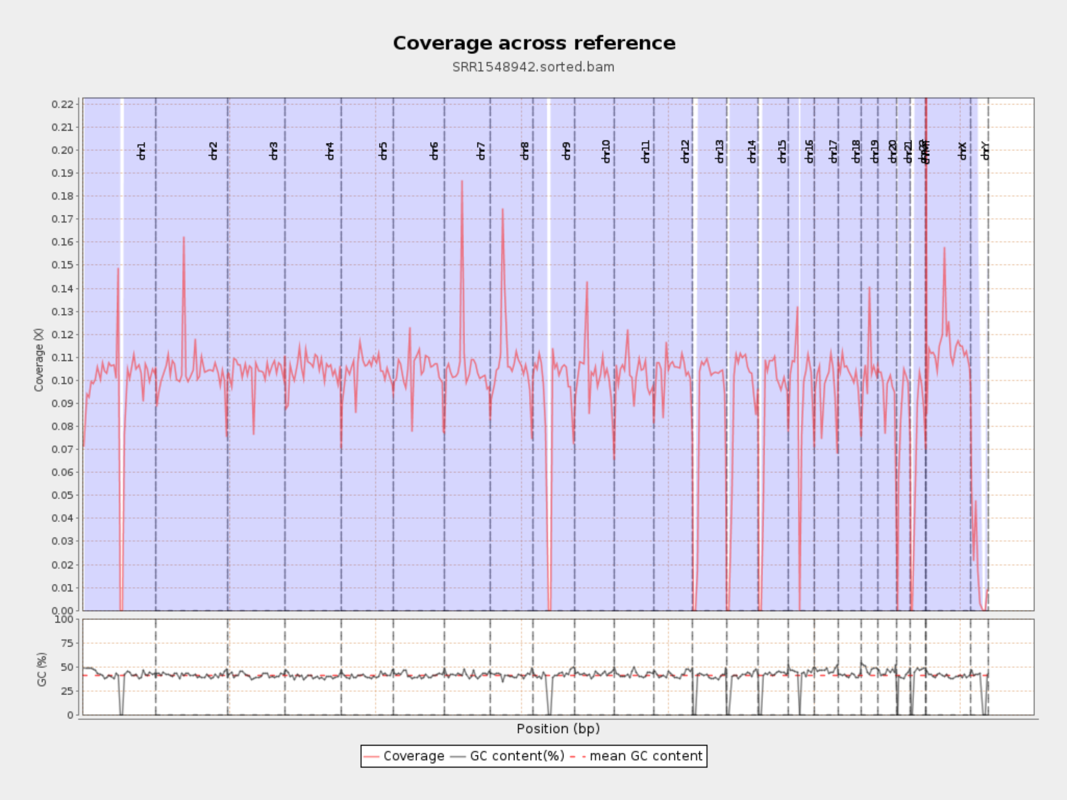
| | |
|---|---|
| General error rate | 0.31% |
| Mismatches | 937,513 |
| Insertions | 10,614 |
| Mapped reads with at least one insertion | 0.14% |
| Deletions | 25,283 |
| Mapped reads with at least one deletion | 0.33% |
| Homopolymer indels | 39.85% |

## 2.6. Chromosome stats

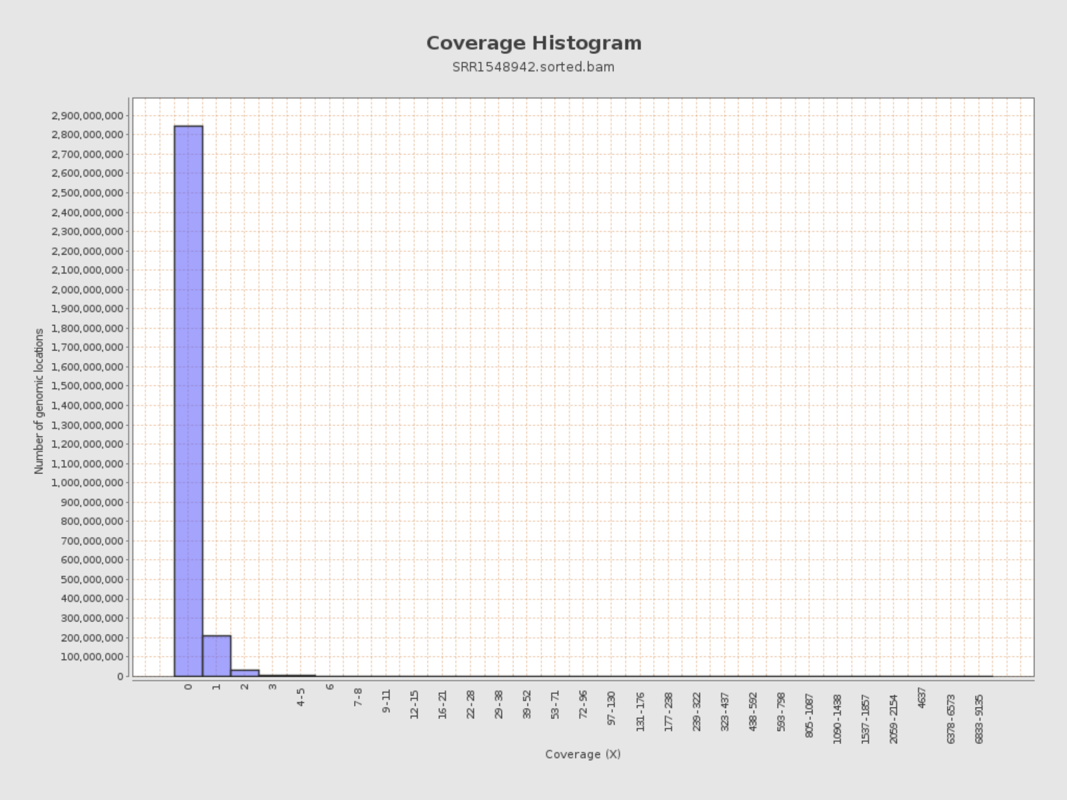
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 23959464 | 0.0961 | 1.308 |
| chr2 | 243199373 | 25433319 | 0.1046 | 0.6555 |
| chr3 | 198022430 | 20553237 | 0.1038 | 0.3789 |
| chr4 | 191154276 | 20023587 | 0.1048 | 0.399 |
| chr5 | 180915260 | 18828246 | 0.1041 | 0.3913 |
| chr6 | 171115067 | 17867373 | 0.1044 | 0.4486 |
| chr7 | 159138663 | 17023961 | 0.107 | 1.0131 |
| chr8 | 146364022 | 15887765 | 0.1085 | 4.4274 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr9 | 141213431 | 12749582 | 0.0903 | 0.6482 |
| chr10 | 135534747 | 13969783 | 0.1031 | 0.5952 |
| chr11 | 135006516 | 13782175 | 0.1021 | 0.6714 |
| chr12 | 133851895 | 13902747 | 0.1039 | 0.4038 |
| chr13 | 115169878 | 9937538 | 0.0863 | 0.3372 |
| chr14 | 107349540 | 9340738 | 0.087 | 0.4294 |
| chr15 | 102531392 | 8599458 | 0.0839 | 0.3374 |
| chr16 | 90354753 | 8368780 | 0.0926 | 0.4215 |
| chr17 | 81195210 | 7935396 | 0.0977 | 0.4055 |
| chr18 | 78077248 | 8016660 | 0.1027 | 1.2478 |
| chr19 | 59128983 | 6250711 | 0.1057 | 1.2348 |
| chr20 | 63025520 | 5990563 | 0.095 | 0.3878 |
| chr21 | 48129895 | 3831481 | 0.0796 | 0.4027 |
| chr22 | 51304566 | 3362936 | 0.0655 | 0.3397 |
| chrMT | 16571 | 12836 | 0.7746 | 1.2045 |
| chrX | 155270560 | 17738302 | 0.1142 | 0.526 |
| chrY | 59373566 | 1041843 | 0.0175 | 0.2277 |

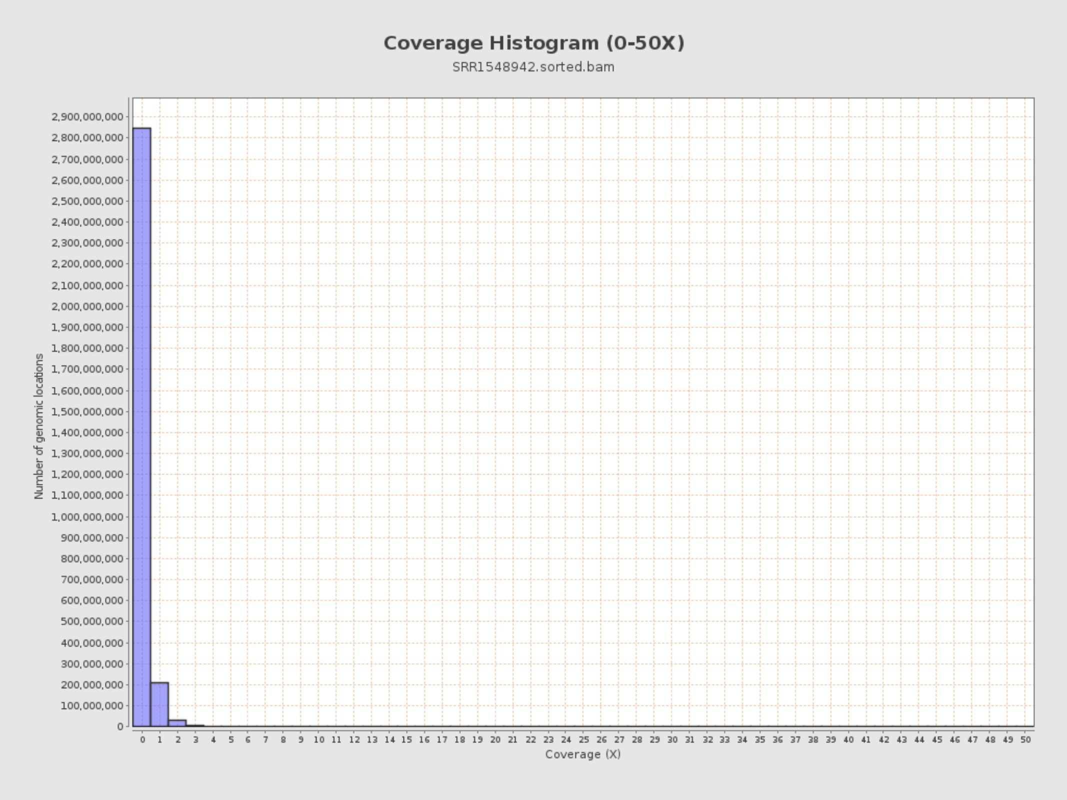
# 3. Results : Coverage across reference



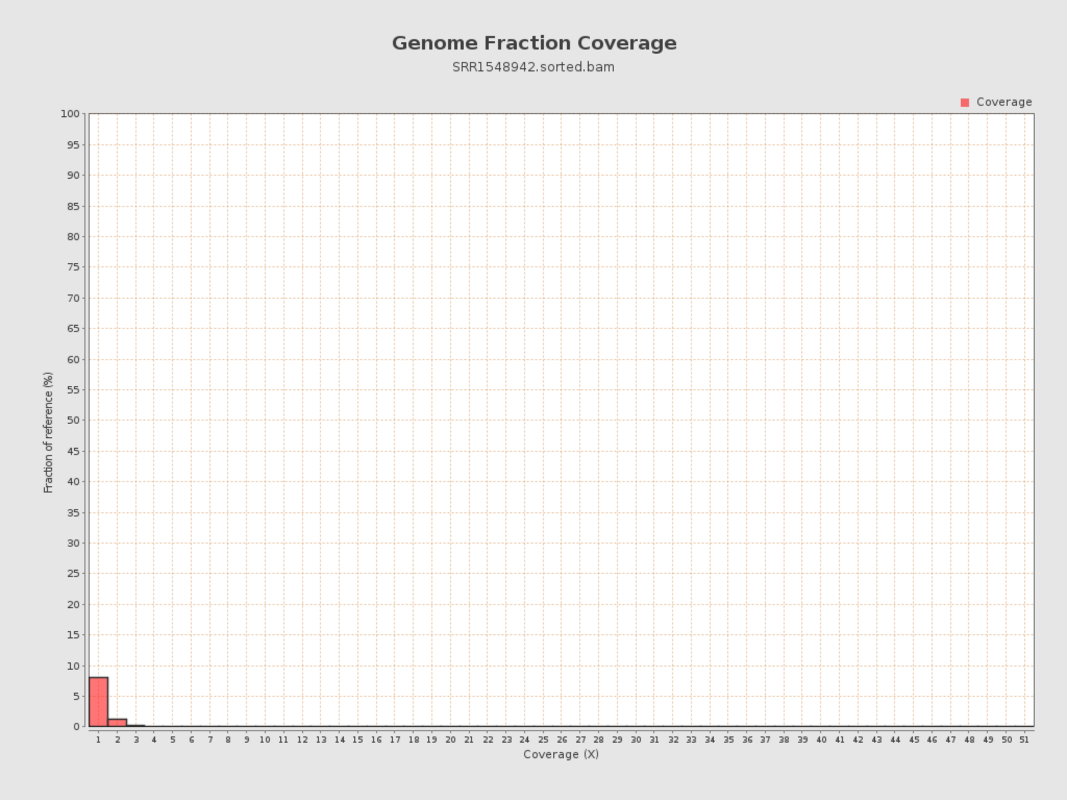
# 4. Results : Coverage Histogram



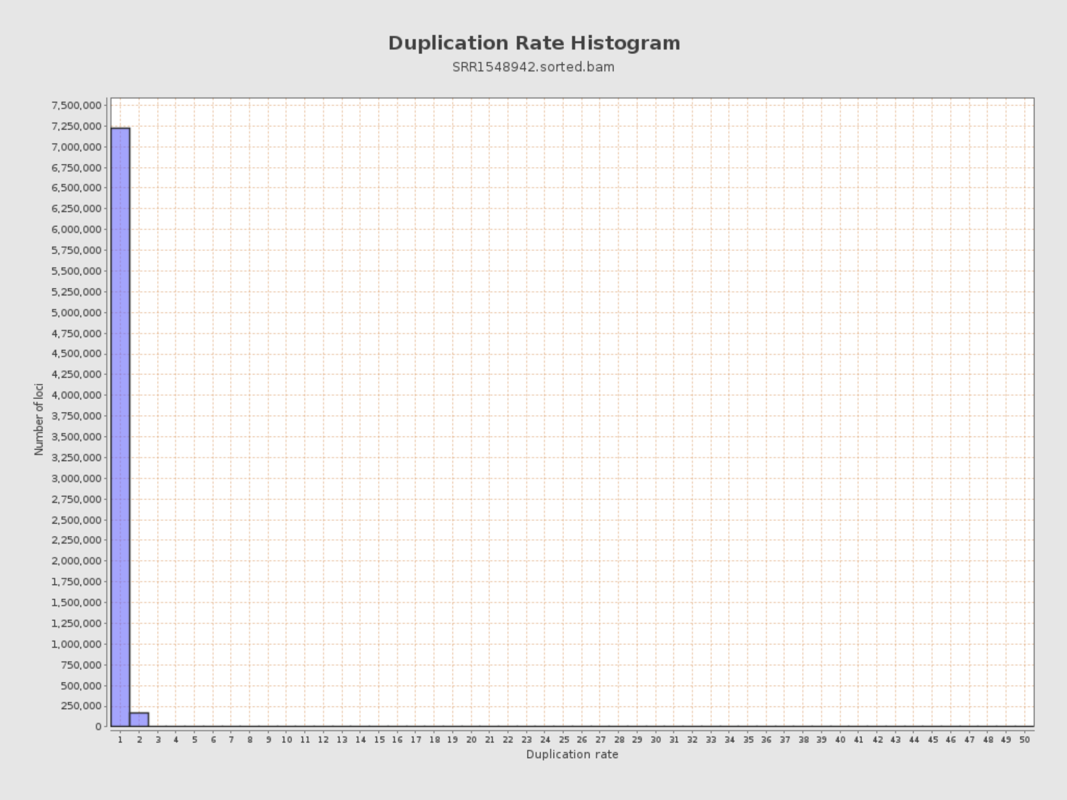
# 5. Results : Coverage Histogram (0-50X)



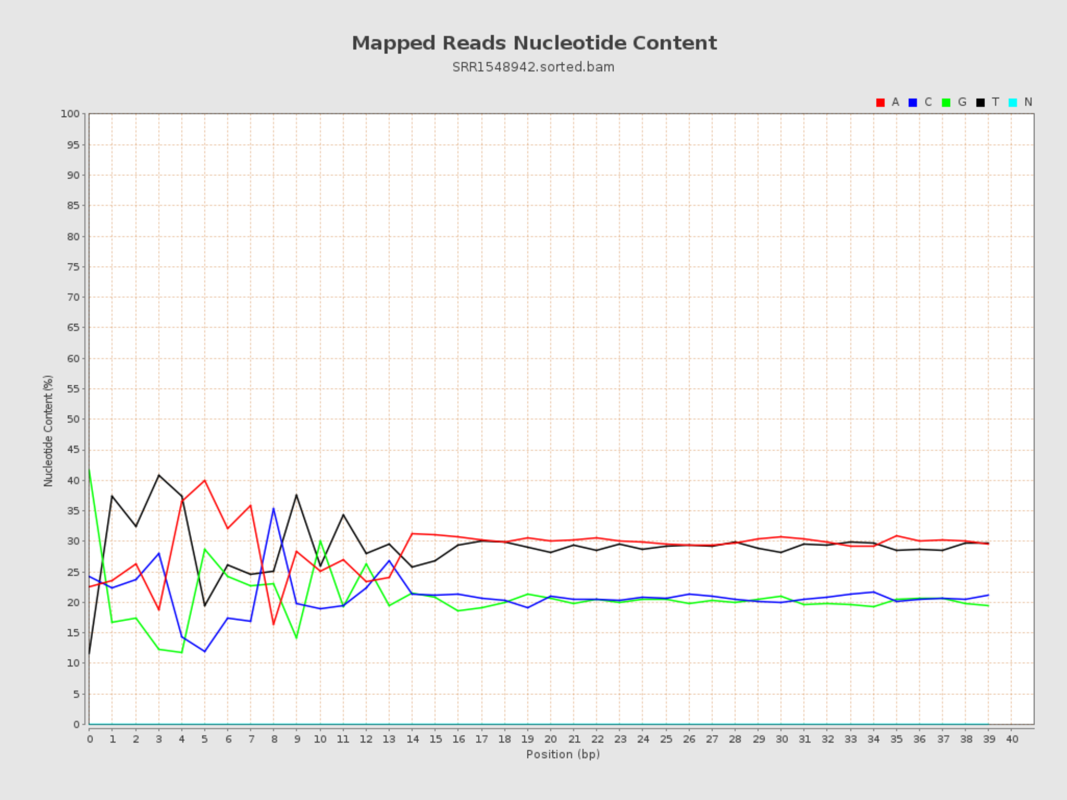
# 6. Results : Genome Fraction Coverage



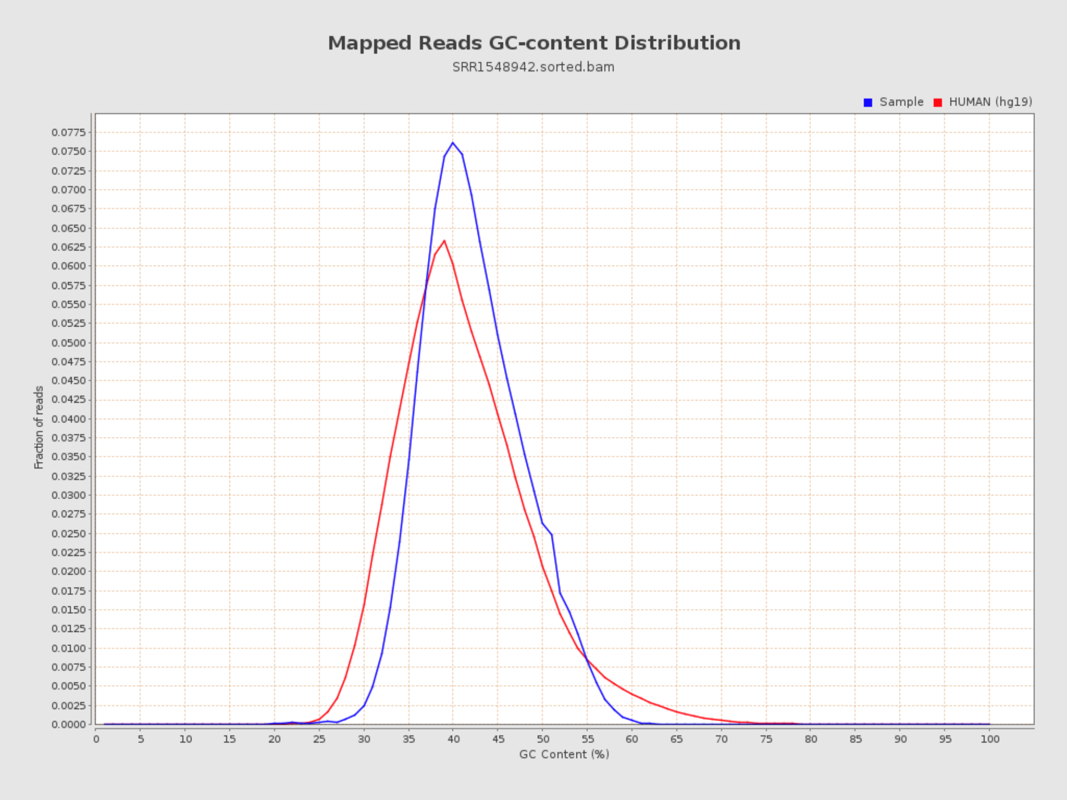
# 7. Results : Duplication Rate Histogram



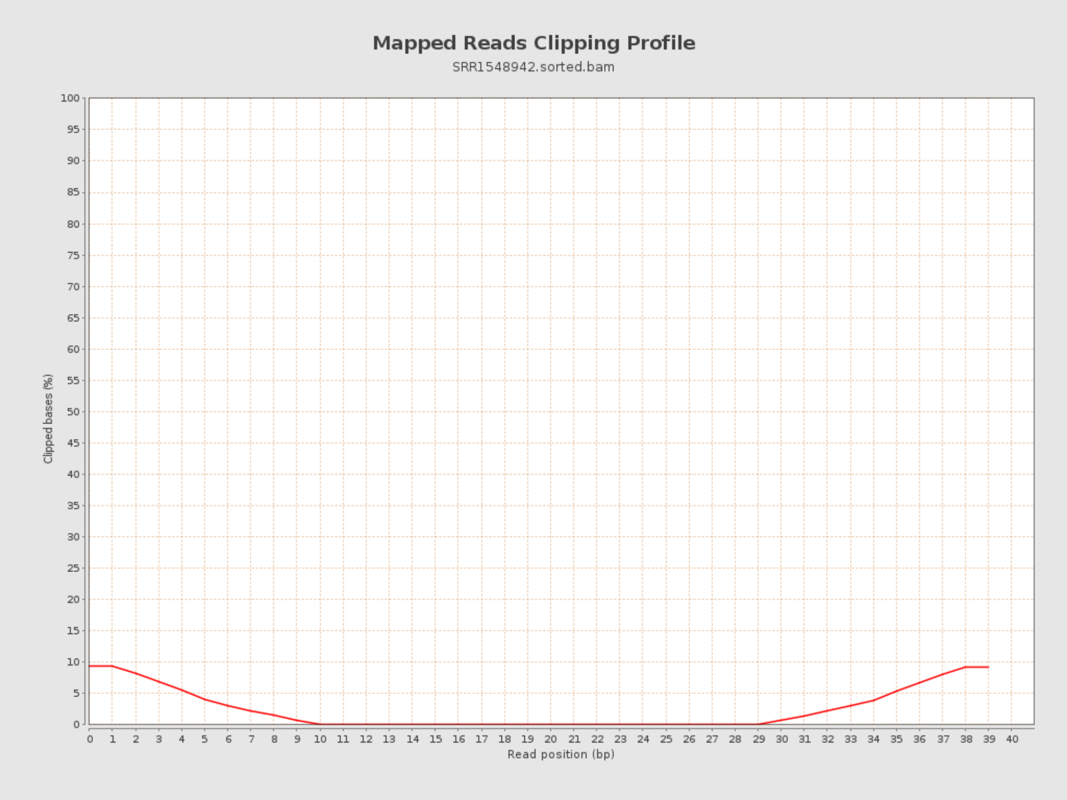
# 8. Results : Mapped Reads Nucleotide Content



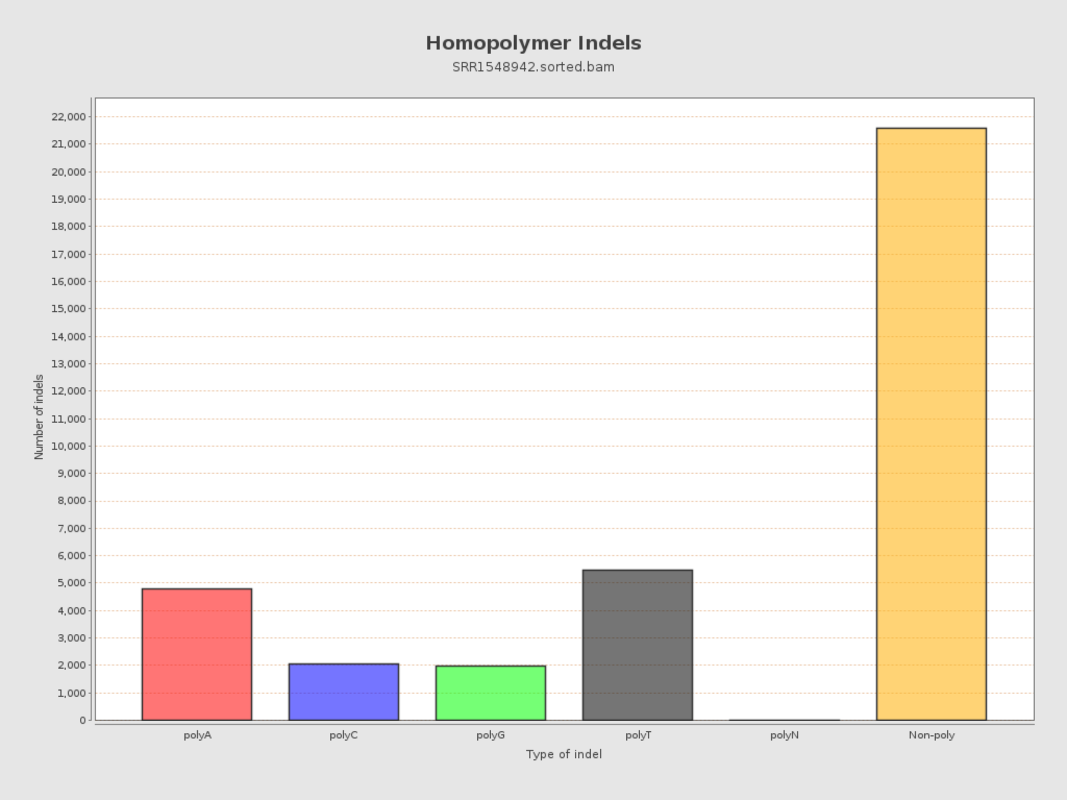
# 9. Results : Mapped Reads GC-content Distribution



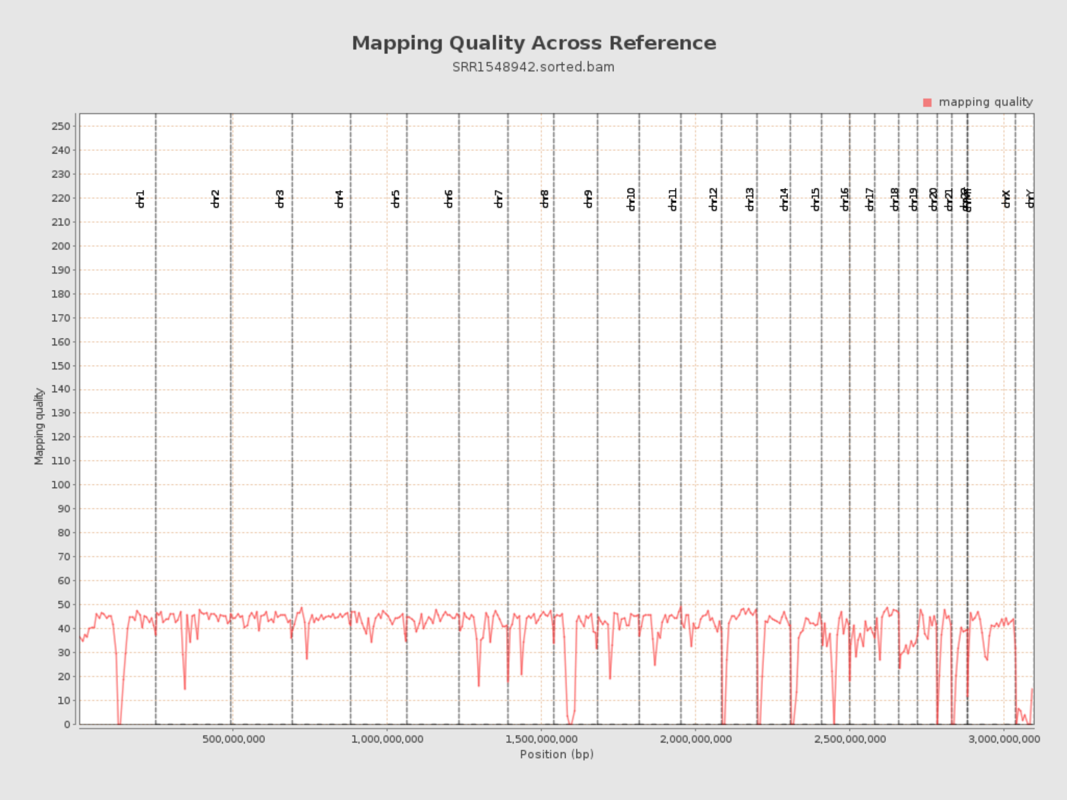
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram