# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 13:31:58*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549039.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_SRR1549039 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549039.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 13:31:57 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1549039.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 8,939,751 |
| Mapped reads | 7,642,483 / 85.49% |
| Unmapped reads | 1,297,268 / 14.51% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Read min/max/mean length | 40 / 40 / 40 |
| Duplicated reads (estimated) | 449,886 / 5.03% |
| Duplication rate | 4.9% |
| Clipped reads | 519,714 / 5.81% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 85,647,177 / 28.29% |
| Number/percentage of C's | 64,133,577 / 21.19% |
| Number/percentage of T's | 87,587,477 / 28.93% |
| Number/percentage of G's | 65,350,468 / 21.59% |
| Number/percentage of N's | 250 / 0% |
| GC Percentage | 42.77% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0978 |
| Standard Deviation | 0.6186 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 41.81 |

## 2.5. Mismatches and indels

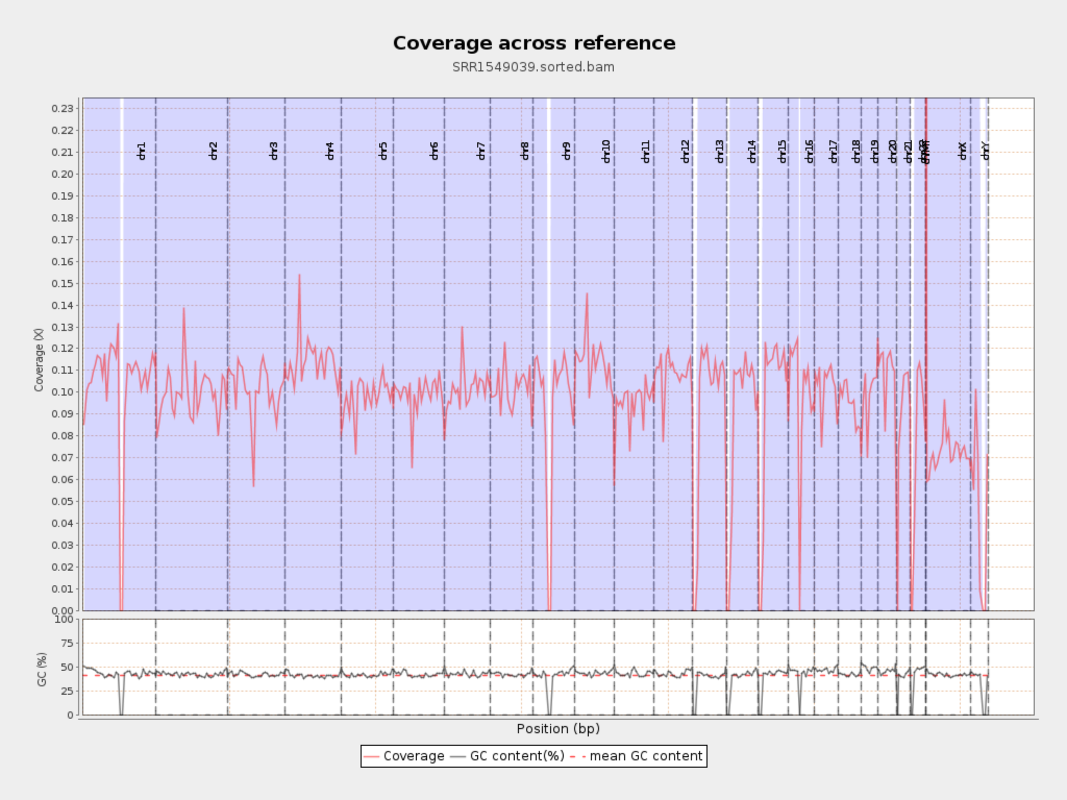
| | |
|---|---|
| General error rate | 0.26% |
| Mismatches | 770,684 |
| Insertions | 8,366 |
| Mapped reads with at least one insertion | 0.11% |
| Deletions | 21,378 |
| Mapped reads with at least one deletion | 0.28% |
| Homopolymer indels | 42.77% |

## 2.6. Chromosome stats

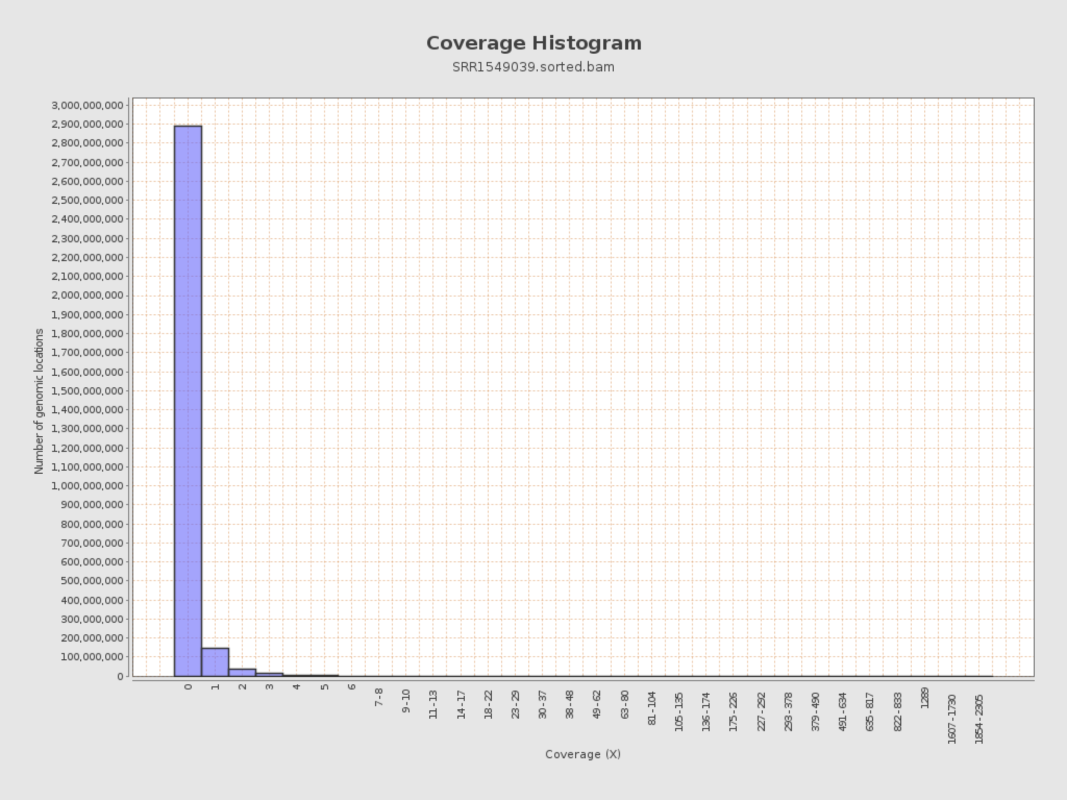
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 25641425 | 0.1029 | 0.7532 |
| chr2 | 243199373 | 24247582 | 0.0997 | 0.633 |
| chr3 | 198022430 | 19998917 | 0.101 | 0.4481 |
| chr4 | 191154276 | 21943225 | 0.1148 | 0.5212 |
| chr5 | 180915260 | 17692450 | 0.0978 | 0.4415 |
| chr6 | 171115067 | 16953131 | 0.0991 | 0.4607 |
| chr7 | 159138663 | 16203442 | 0.1018 | 0.733 |
| chr8 | 146364022 | 14872268 | 0.1016 | 1.2282 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr9 | 141213431 | 13235519 | 0.0937 | 0.6053 |
| chr10 | 135534747 | 15464243 | 0.1141 | 0.6154 |
| chr11 | 135006516 | 12849514 | 0.0952 | 0.5017 |
| chr12 | 133851895 | 14621221 | 0.1092 | 0.4789 |
| chr13 | 115169878 | 10612513 | 0.0921 | 0.4344 |
| chr14 | 107349540 | 9619606 | 0.0896 | 0.497 |
| chr15 | 102531392 | 9518444 | 0.0928 | 0.4348 |
| chr16 | 90354753 | 8791248 | 0.0973 | 0.4943 |
| chr17 | 81195210 | 8401173 | 0.1035 | 0.4788 |
| chr18 | 78077248 | 7422440 | 0.0951 | 1.0347 |
| chr19 | 59128983 | 5814214 | 0.0983 | 0.7314 |
| chr20 | 63025520 | 6866386 | 0.1089 | 0.4899 |
| chr21 | 48129895 | 4232624 | 0.0879 | 0.5291 |
| chr22 | 51304566 | 3738224 | 0.0729 | 0.5512 |
| chrMT | 16571 | 26083 | 1.574 | 2.4458 |
| chrX | 155270560 | 11237009 | 0.0724 | 0.4279 |
| chrY | 59373566 | 2744165 | 0.0462 | 0.4422 |

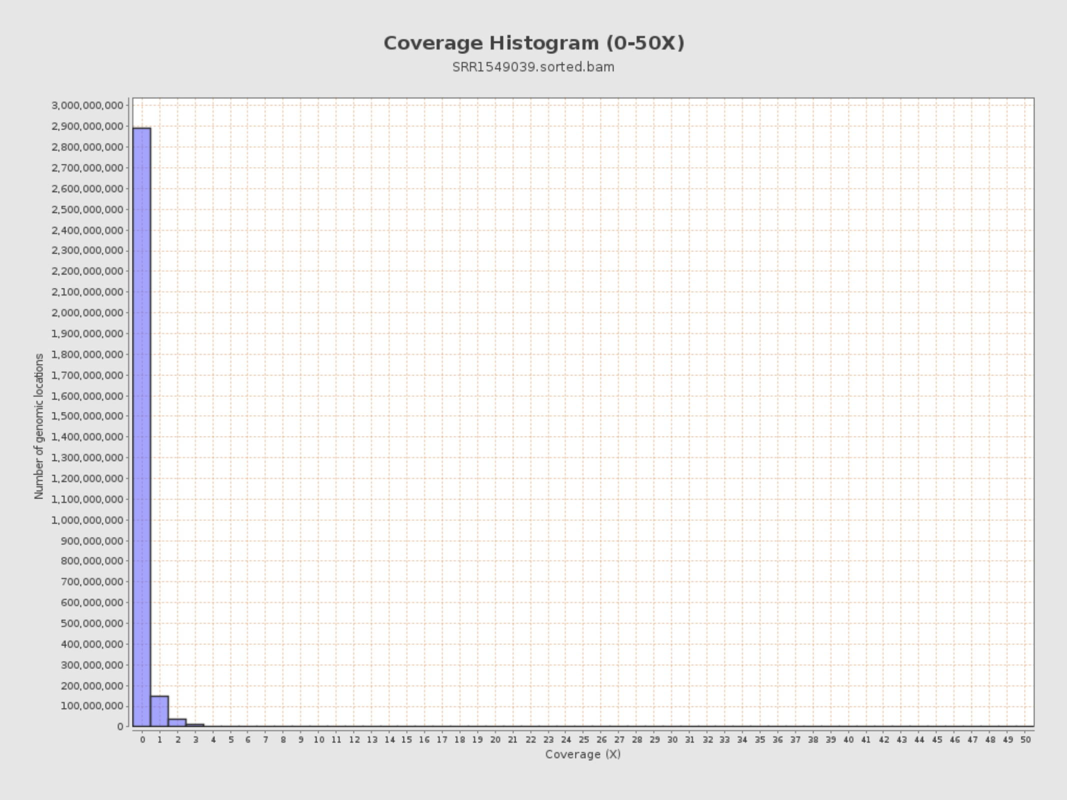
# 3. Results : Coverage across reference



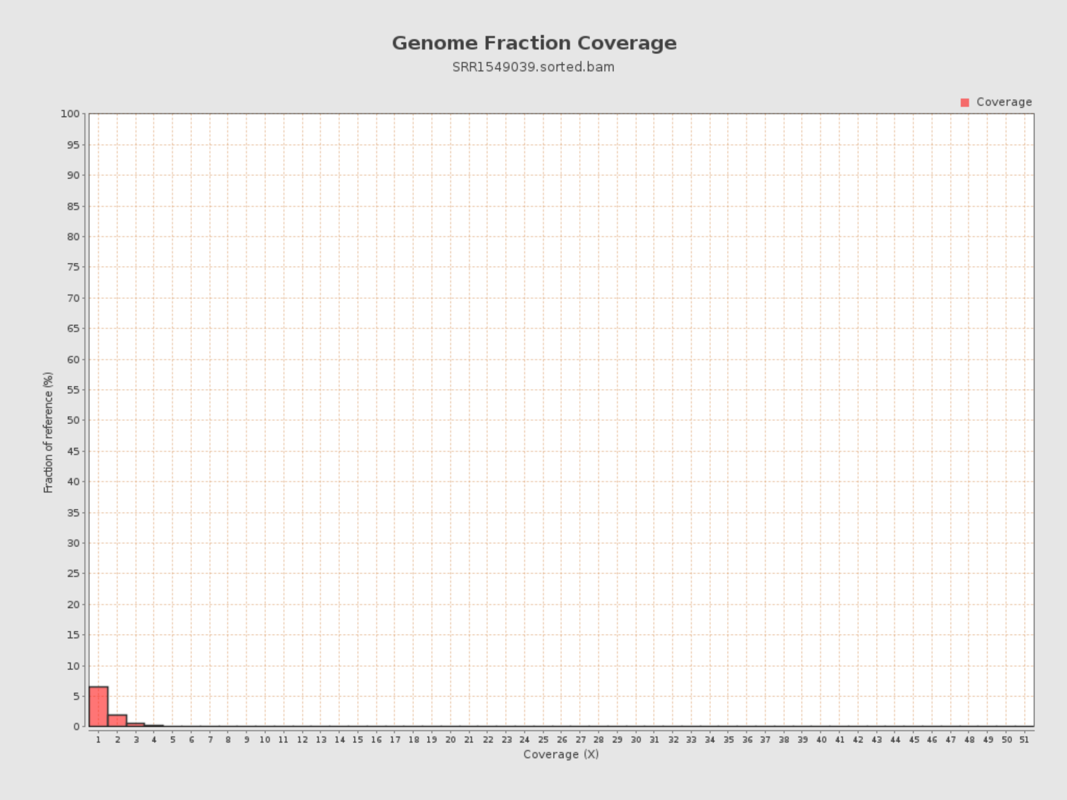
# 4. Results : Coverage Histogram



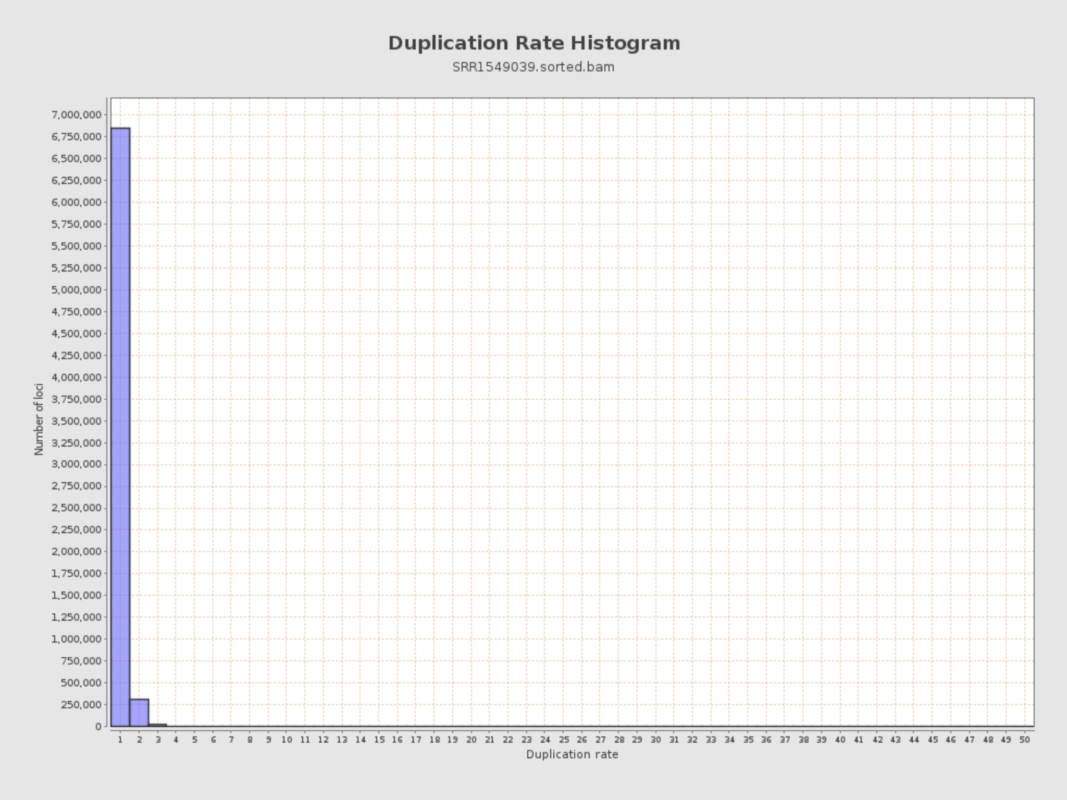
# 5. Results : Coverage Histogram (0-50X)



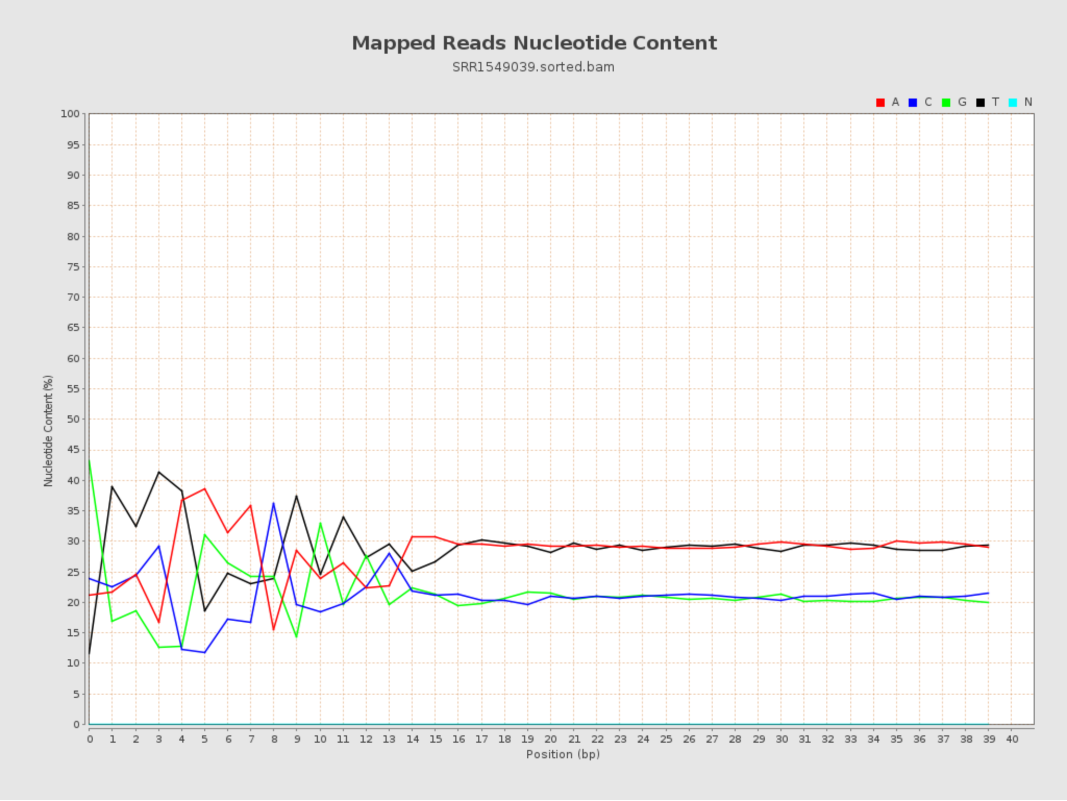
# 6. Results : Genome Fraction Coverage



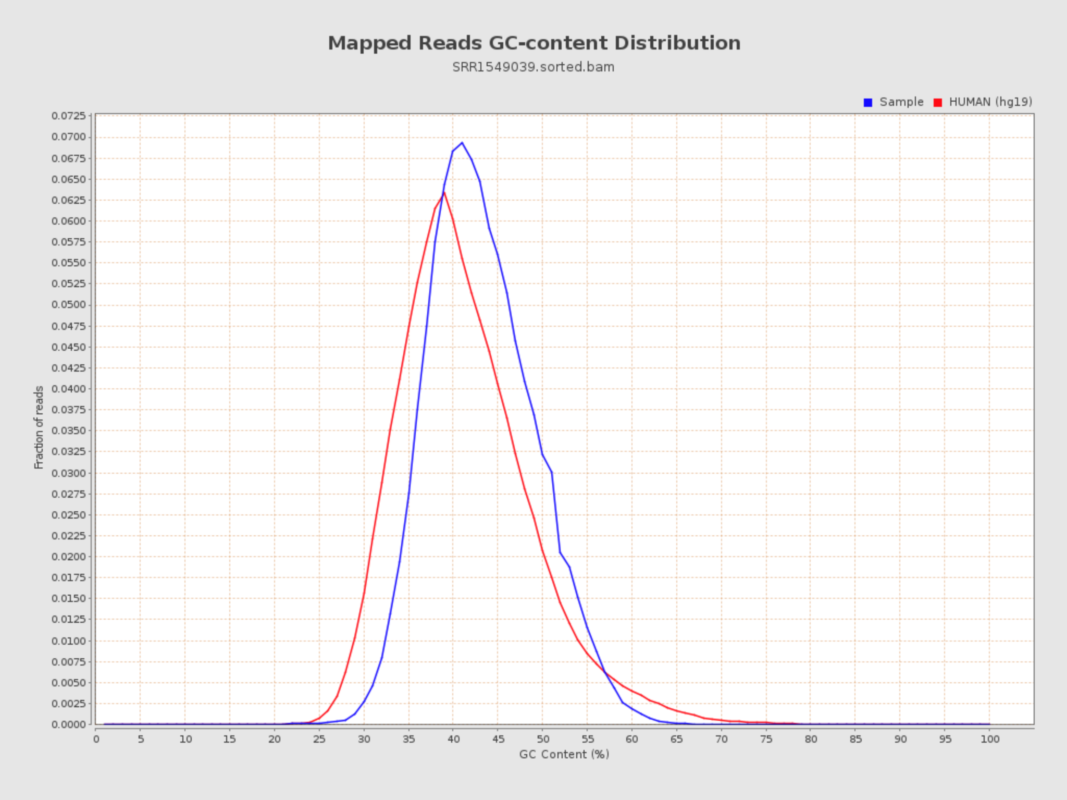
# 7. Results : Duplication Rate Histogram



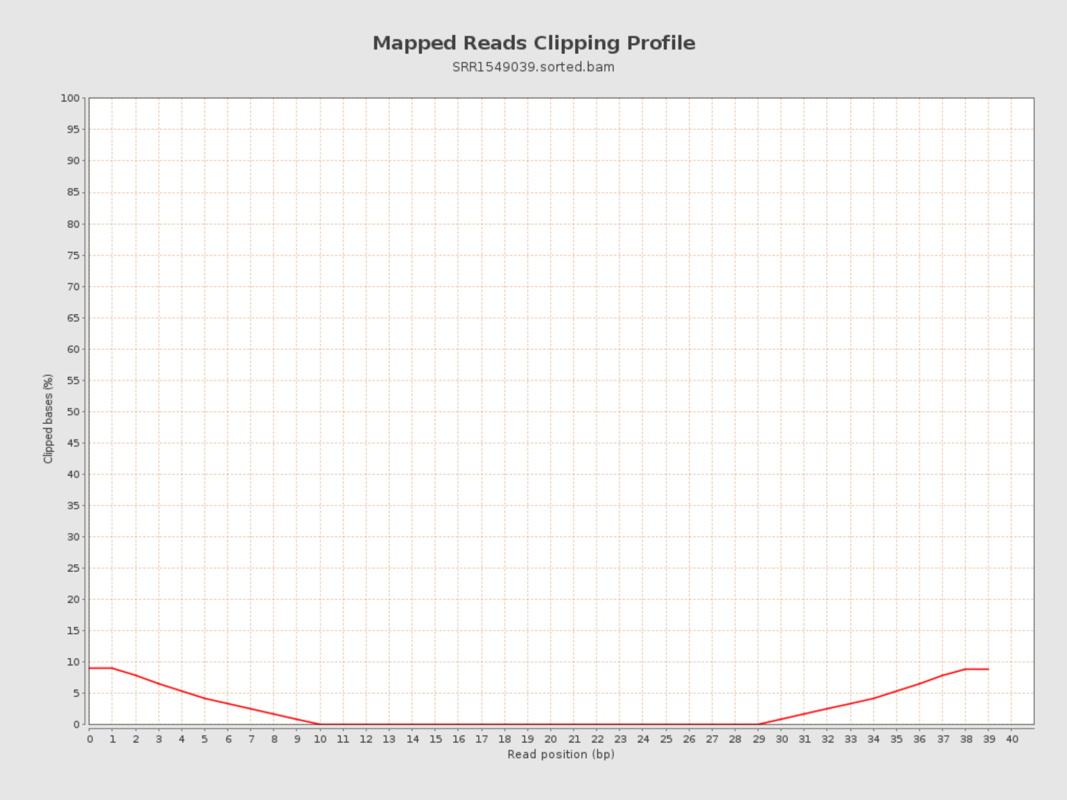
# 8. Results : Mapped Reads Nucleotide Content



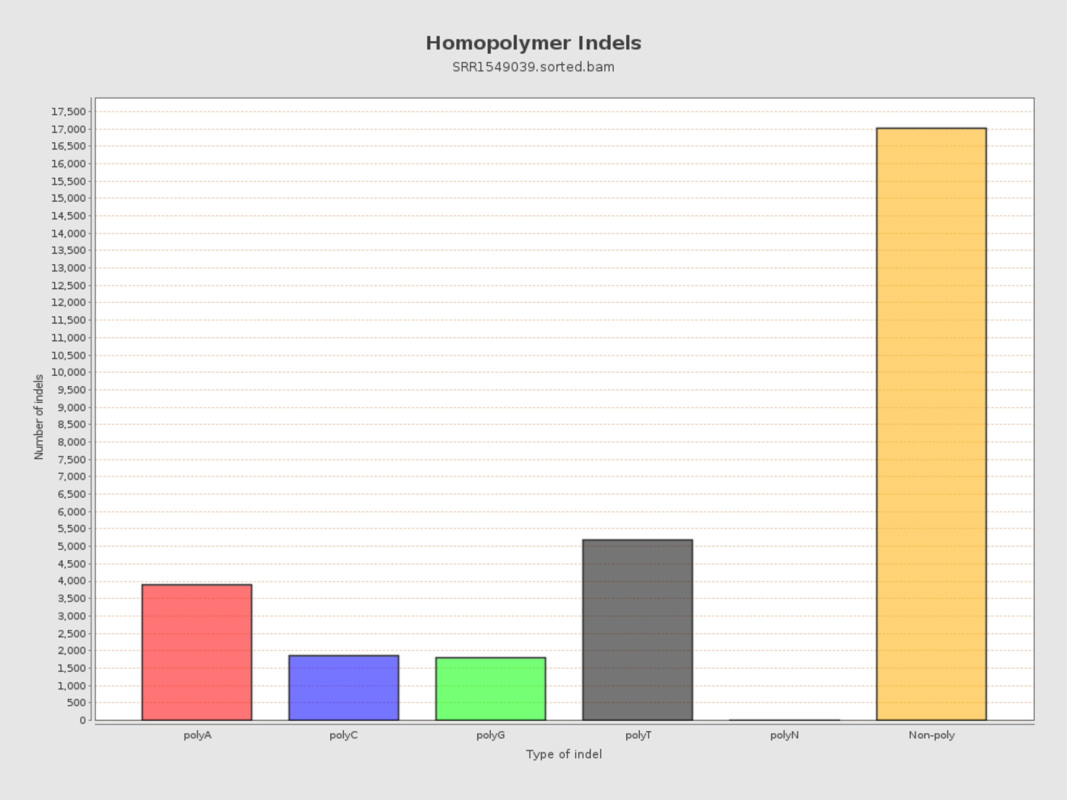
# 9. Results : Mapped Reads GC-content Distribution



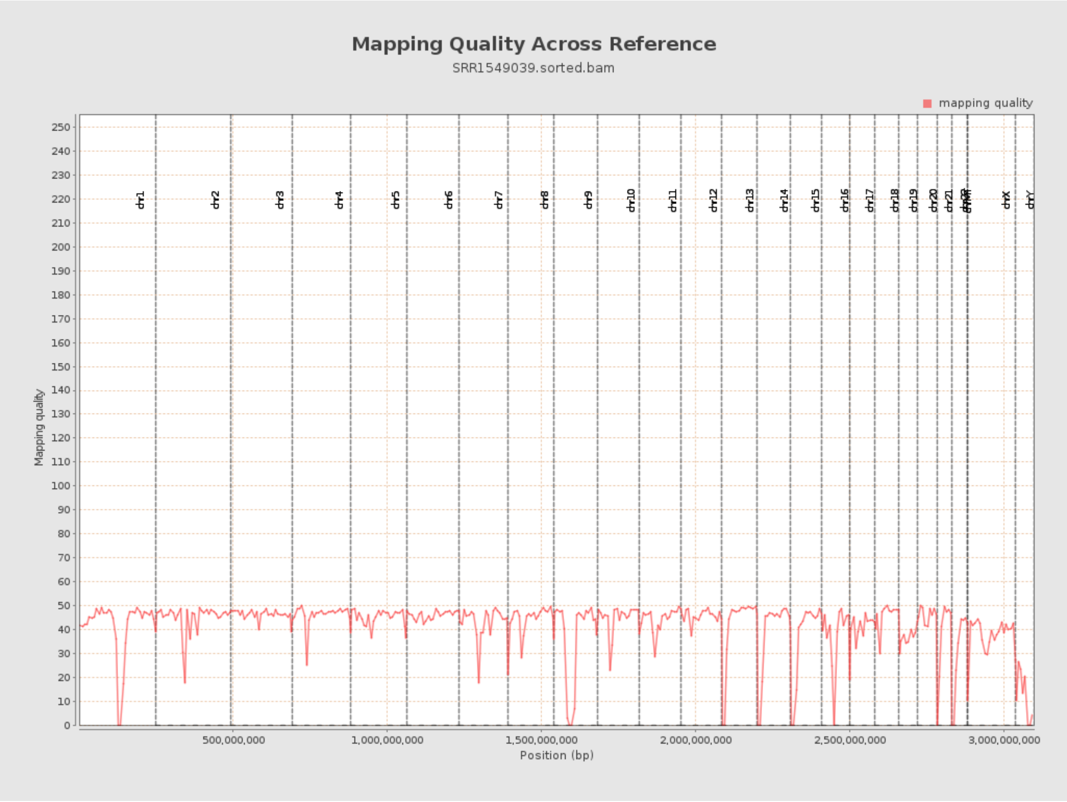
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram