# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 00:37:42*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549096.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_SRR1549096 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549096.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Aug 24 00:37:41 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1549096.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 7,586,928 |
| Mapped reads | 6,662,102 / 87.81% |
| Unmapped reads | 924,826 / 12.19% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Read min/max/mean length | 40 / 40 / 40 |
| Duplicated reads (estimated) | 215,320 / 2.84% |
| Duplication rate | 2.21% |
| Clipped reads | 311,831 / 4.11% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 78,392,371 / 29.62% |
| Number/percentage of C's | 54,050,829 / 20.43% |
| Number/percentage of T's | 79,468,534 / 30.03% |
| Number/percentage of G's | 52,654,173 / 19.9% |
| Number/percentage of N's | 64,060 / 0.02% |
| GC Percentage | 40.32% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0855 |
| Standard Deviation | 0.645 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.25 |

## 2.5. Mismatches and indels

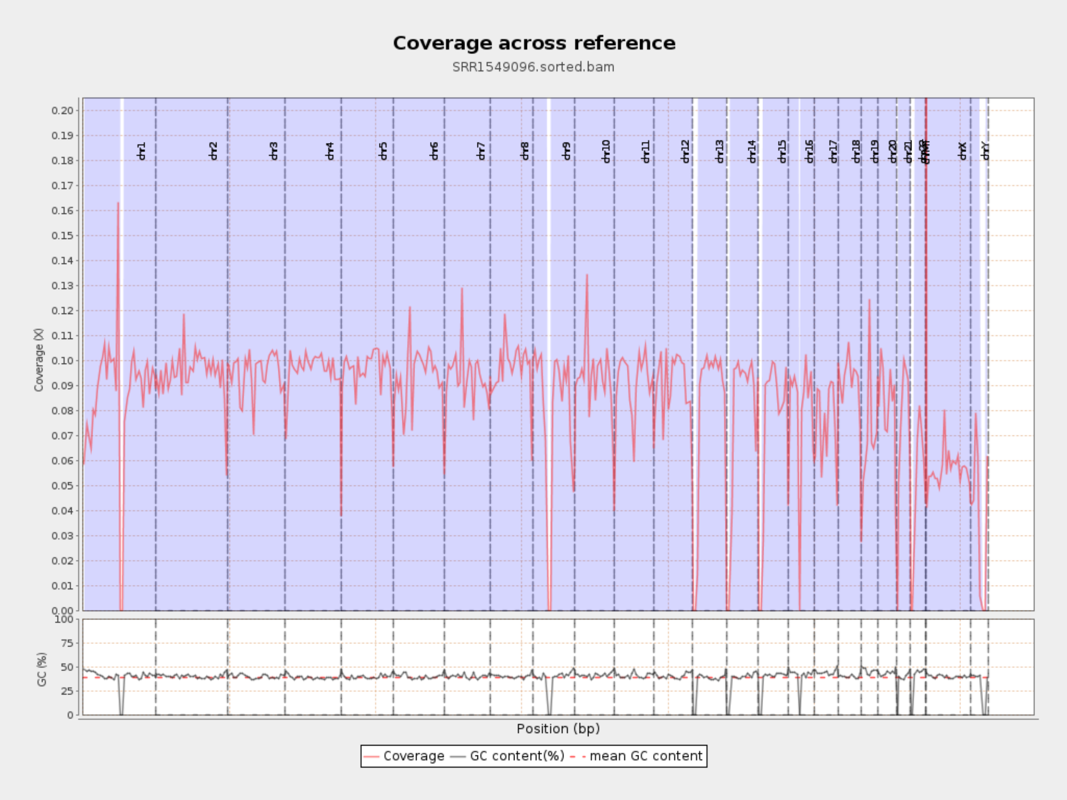
| | |
|---|---|
| General error rate | 0.39% |
| Mismatches | 1,037,969 |
| Insertions | 5,807 |
| Mapped reads with at least one insertion | 0.09% |
| Deletions | 19,239 |
| Mapped reads with at least one deletion | 0.29% |
| Homopolymer indels | 45.78% |

## 2.6. Chromosome stats

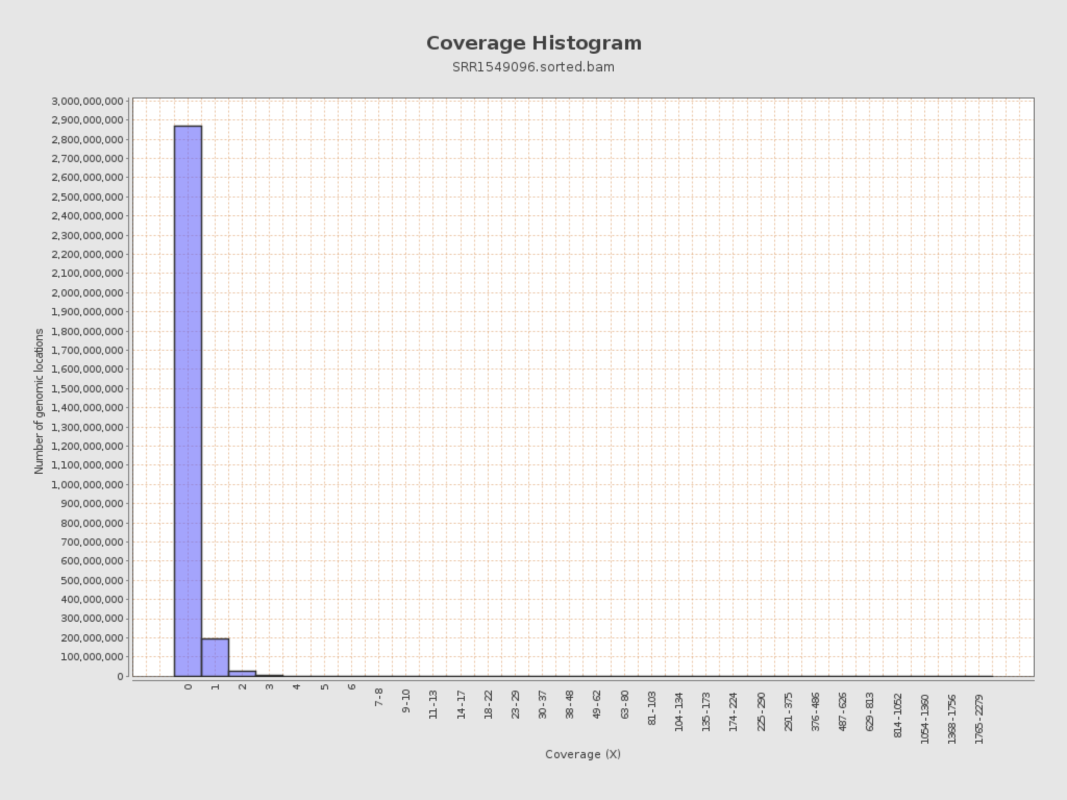
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 21480428 | 0.0862 | 1.5716 |
| chr2 | 243199373 | 23196648 | 0.0954 | 0.4958 |
| chr3 | 198022430 | 18832143 | 0.0951 | 0.3495 |
| chr4 | 191154276 | 18506348 | 0.0968 | 0.3608 |
| chr5 | 180915260 | 17384349 | 0.0961 | 0.3576 |
| chr6 | 171115067 | 16143645 | 0.0943 | 0.4402 |
| chr7 | 159138663 | 14757139 | 0.0927 | 0.6729 |
| chr8 | 146364022 | 14182477 | 0.0969 | 0.6633 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr9 | 141213431 | 11171060 | 0.0791 | 0.4772 |
| chr10 | 135534747 | 12755098 | 0.0941 | 0.564 |
| chr11 | 135006516 | 12316427 | 0.0912 | 0.4964 |
| chr12 | 133851895 | 12160443 | 0.0908 | 0.3557 |
| chr13 | 115169878 | 9167040 | 0.0796 | 0.3123 |
| chr14 | 107349540 | 8287008 | 0.0772 | 0.3621 |
| chr15 | 102531392 | 7432771 | 0.0725 | 0.3002 |
| chr16 | 90354753 | 7024877 | 0.0777 | 0.3823 |
| chr17 | 81195210 | 6154507 | 0.0758 | 0.3661 |
| chr18 | 78077248 | 7267418 | 0.0931 | 0.9228 |
| chr19 | 59128983 | 4180868 | 0.0707 | 1.1519 |
| chr20 | 63025520 | 5351330 | 0.0849 | 0.3405 |
| chr21 | 48129895 | 3480352 | 0.0723 | 0.3481 |
| chr22 | 51304566 | 2491929 | 0.0486 | 0.2833 |
| chrMT | 16571 | 14291 | 0.8624 | 1.4623 |
| chrX | 155270560 | 8748059 | 0.0563 | 0.3326 |
| chrY | 59373566 | 2167513 | 0.0365 | 0.3307 |

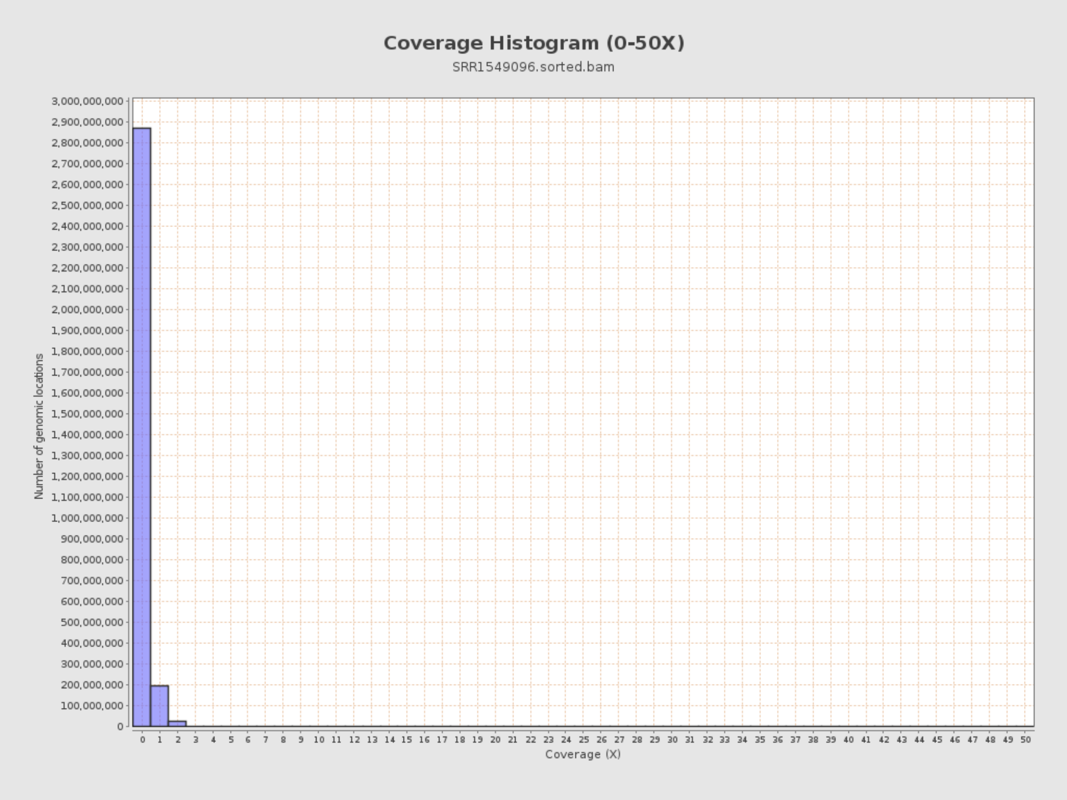
# 3. Results : Coverage across reference



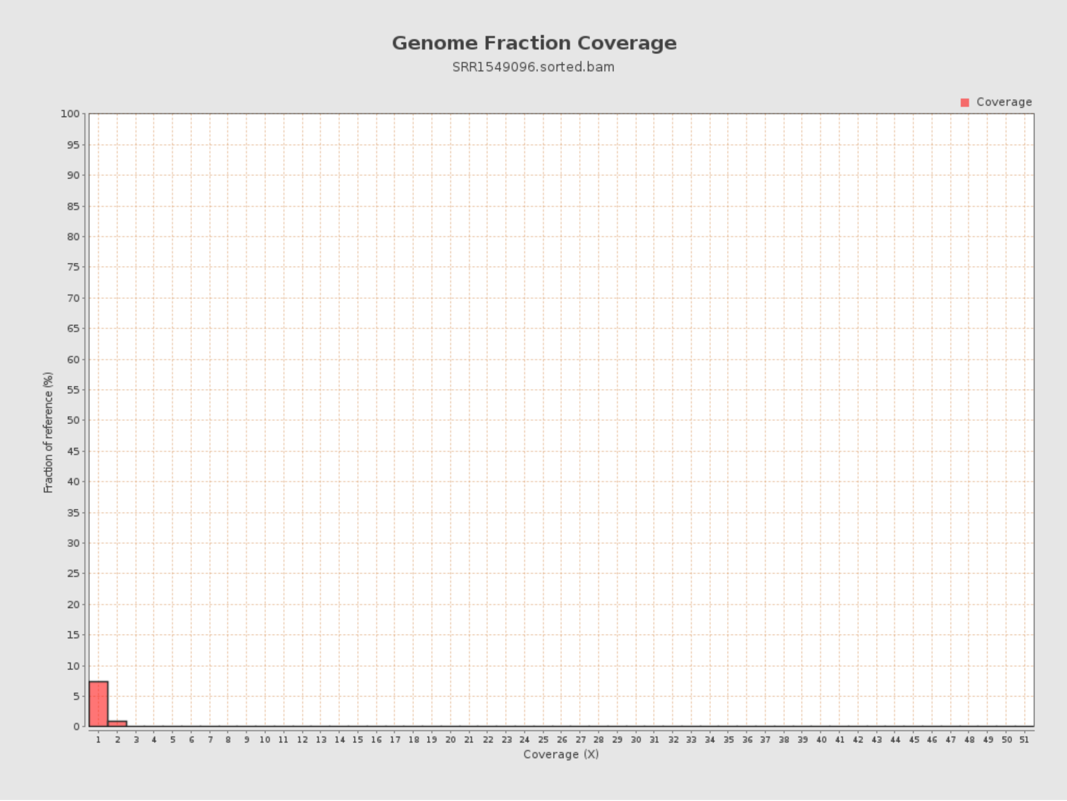
# 4. Results : Coverage Histogram



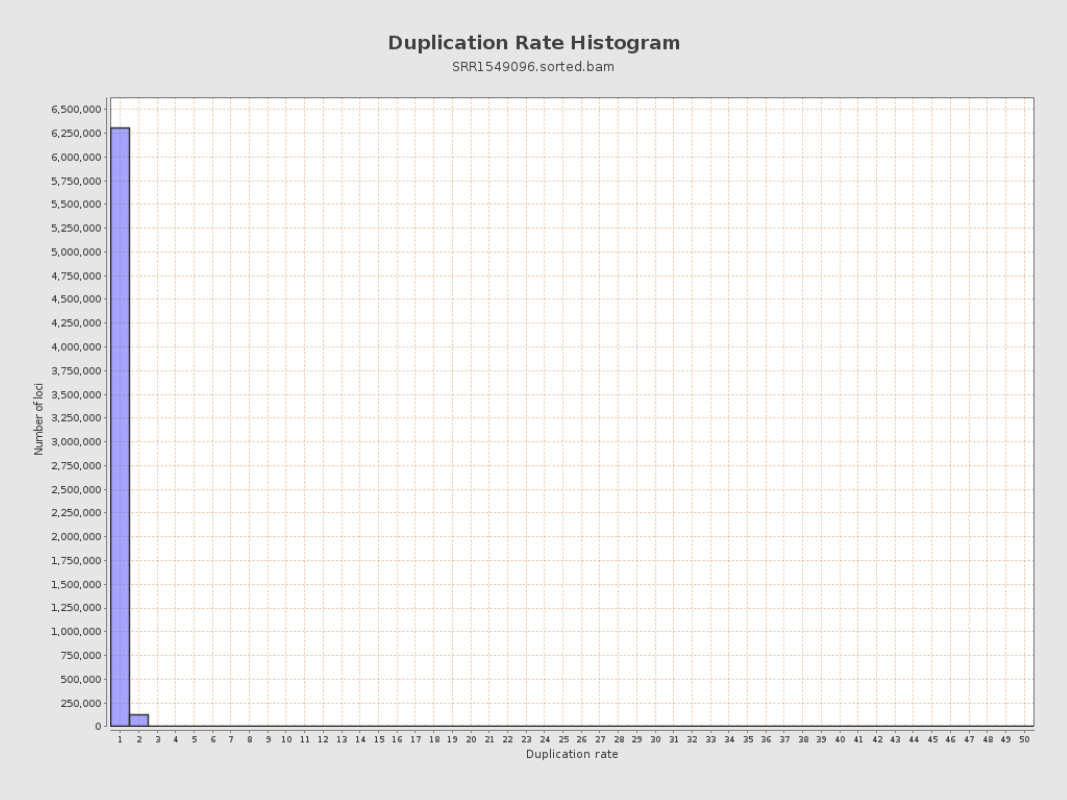
# 5. Results : Coverage Histogram (0-50X)



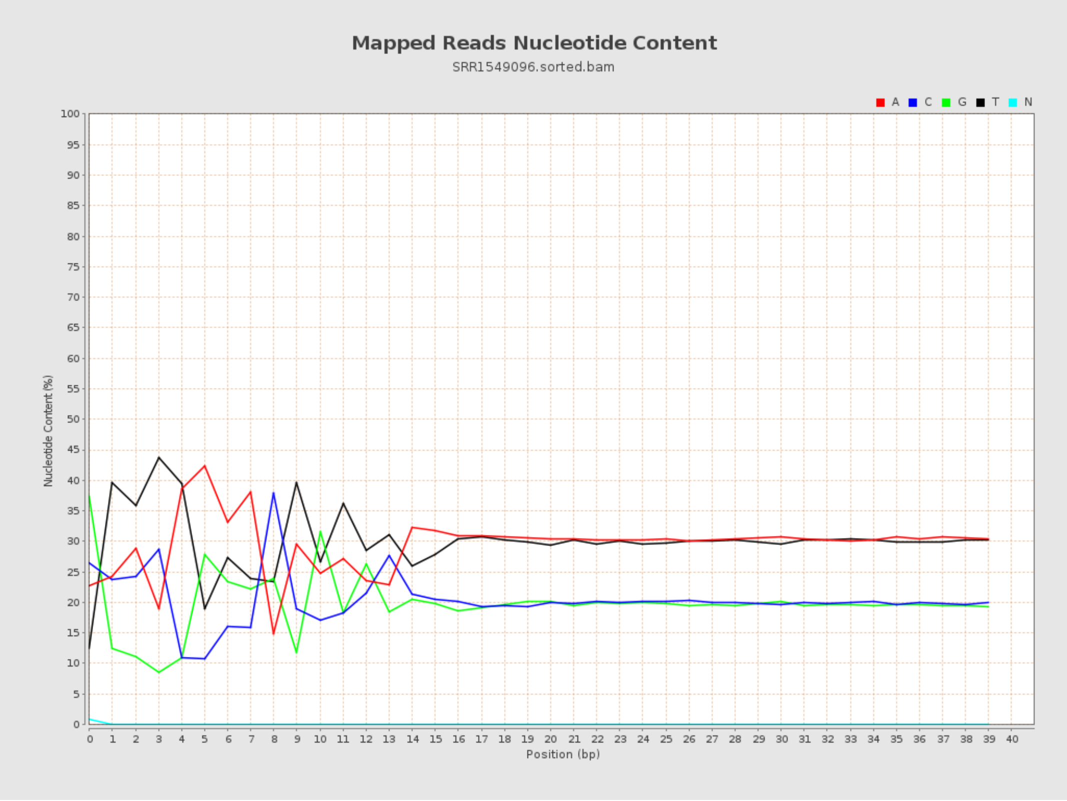
# 6. Results : Genome Fraction Coverage



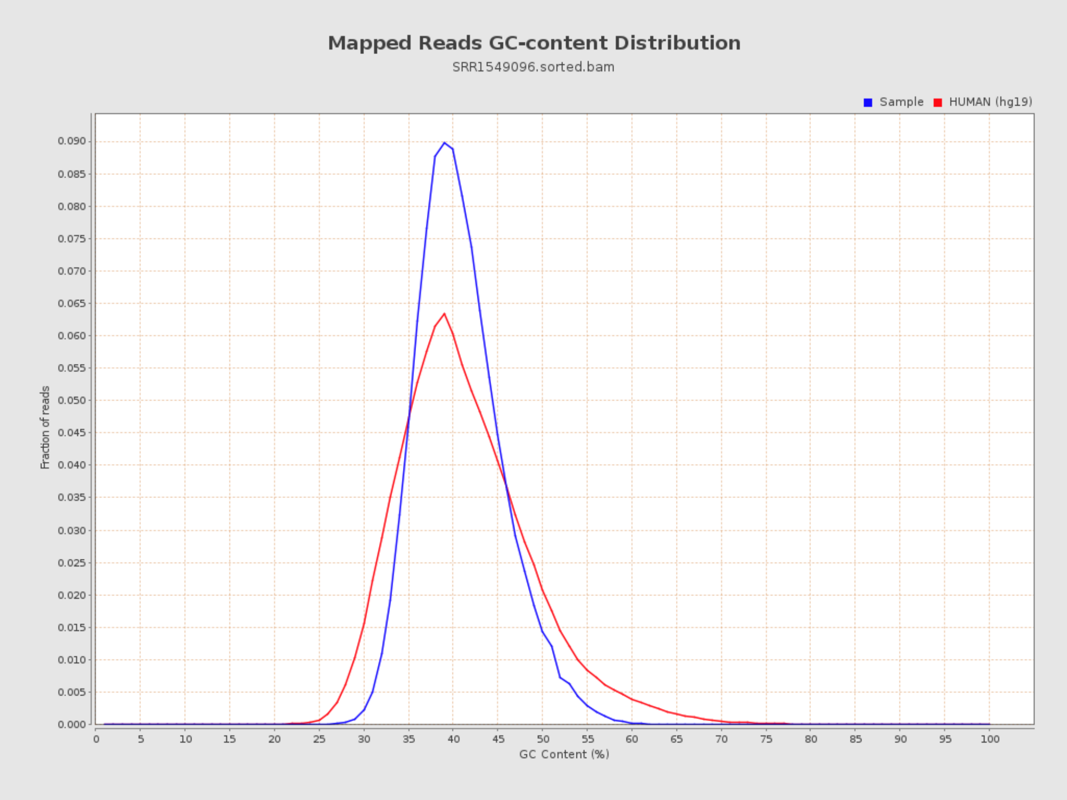
# 7. Results : Duplication Rate Histogram



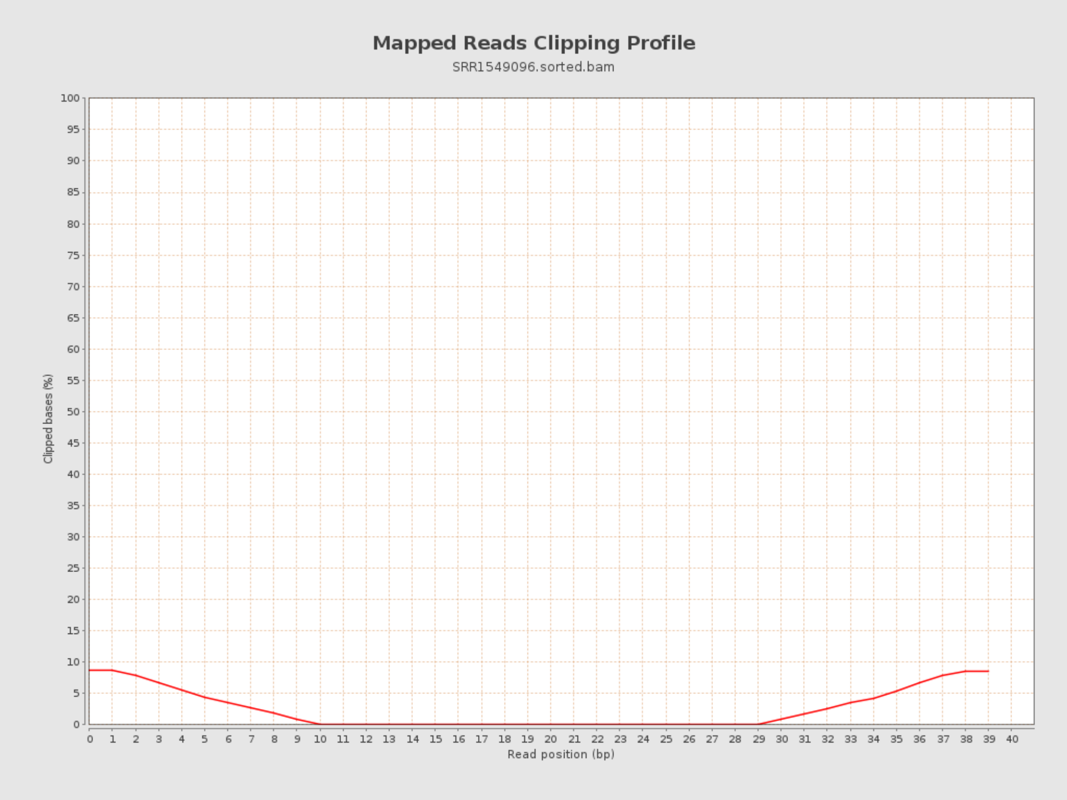
# 8. Results : Mapped Reads Nucleotide Content



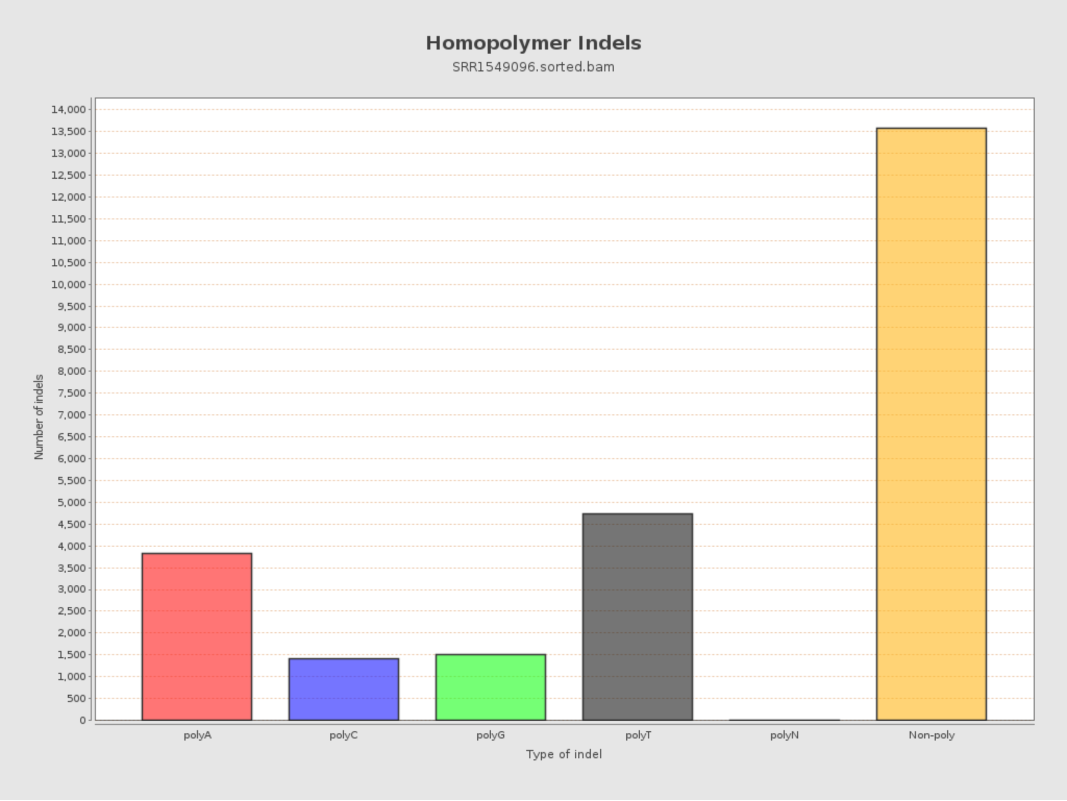
# 9. Results : Mapped Reads GC-content Distribution



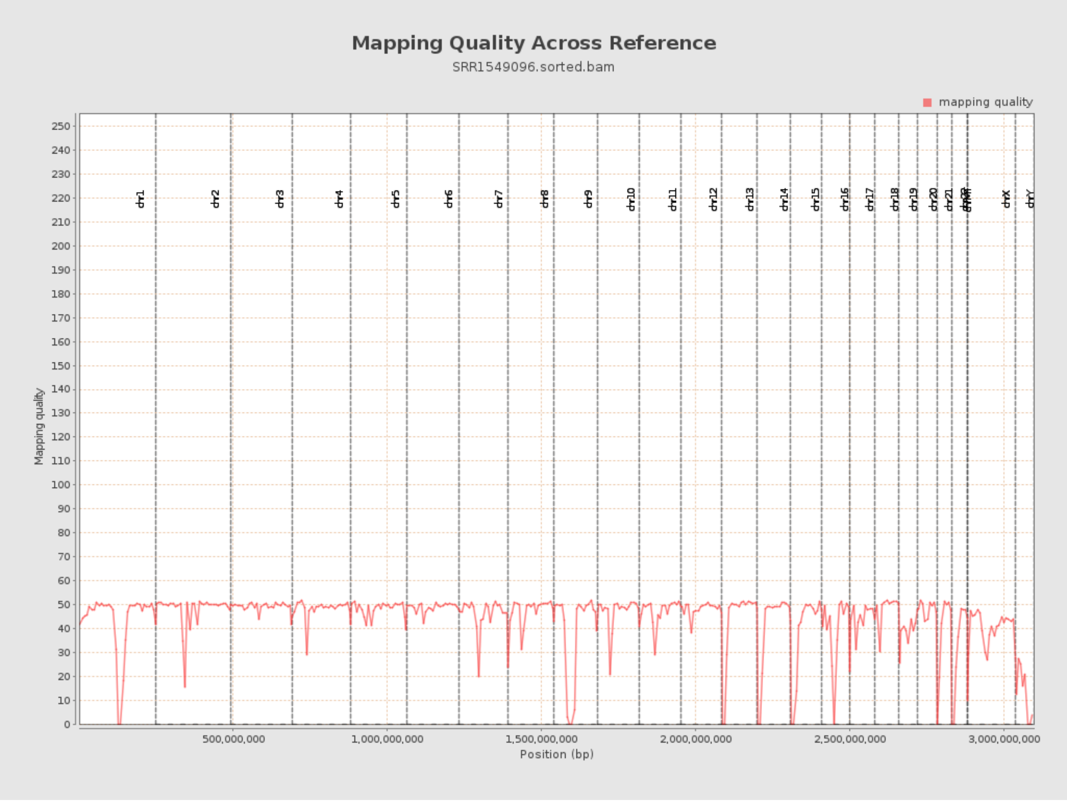
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram