# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 09:21:18*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549009.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_SRR1549009 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549009.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 09:21:17 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1549009.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 7,857,909 |
| Mapped reads | 6,824,909 / 86.85% |
| Unmapped reads | 1,033,000 / 13.15% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Read min/max/mean length | 40 / 40 / 40 |
| Duplicated reads (estimated) | 485,528 / 6.18% |
| Duplication rate | 6.31% |
| Clipped reads | 371,113 / 4.72% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 81,185,344 / 29.98% |
| Number/percentage of C's | 53,710,187 / 19.84% |
| Number/percentage of T's | 80,914,888 / 29.88% |
| Number/percentage of G's | 54,959,031 / 20.3% |
| Number/percentage of N's | 2,338 / 0% |
| GC Percentage | 40.13% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0875 |
| Standard Deviation | 0.6273 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.39 |

## 2.5. Mismatches and indels

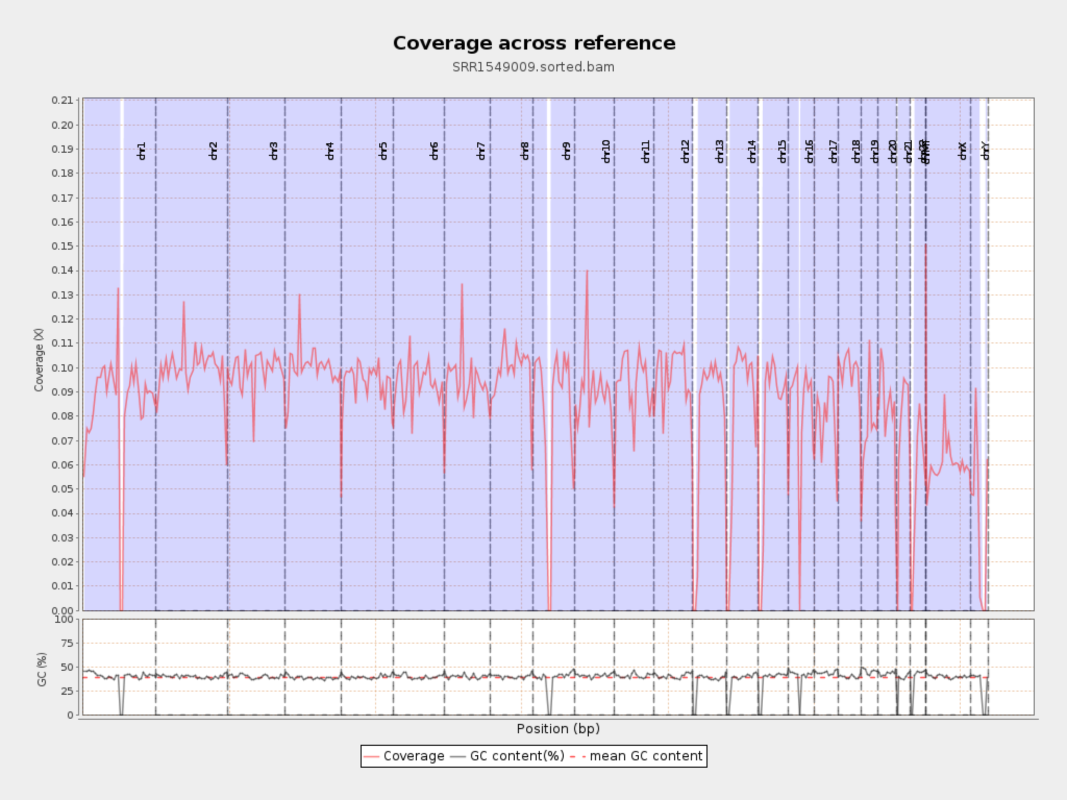
| | |
|---|---|
| General error rate | 0.31% |
| Mismatches | 836,862 |
| Insertions | 8,150 |
| Mapped reads with at least one insertion | 0.12% |
| Deletions | 22,825 |
| Mapped reads with at least one deletion | 0.33% |
| Homopolymer indels | 43.29% |

## 2.6. Chromosome stats

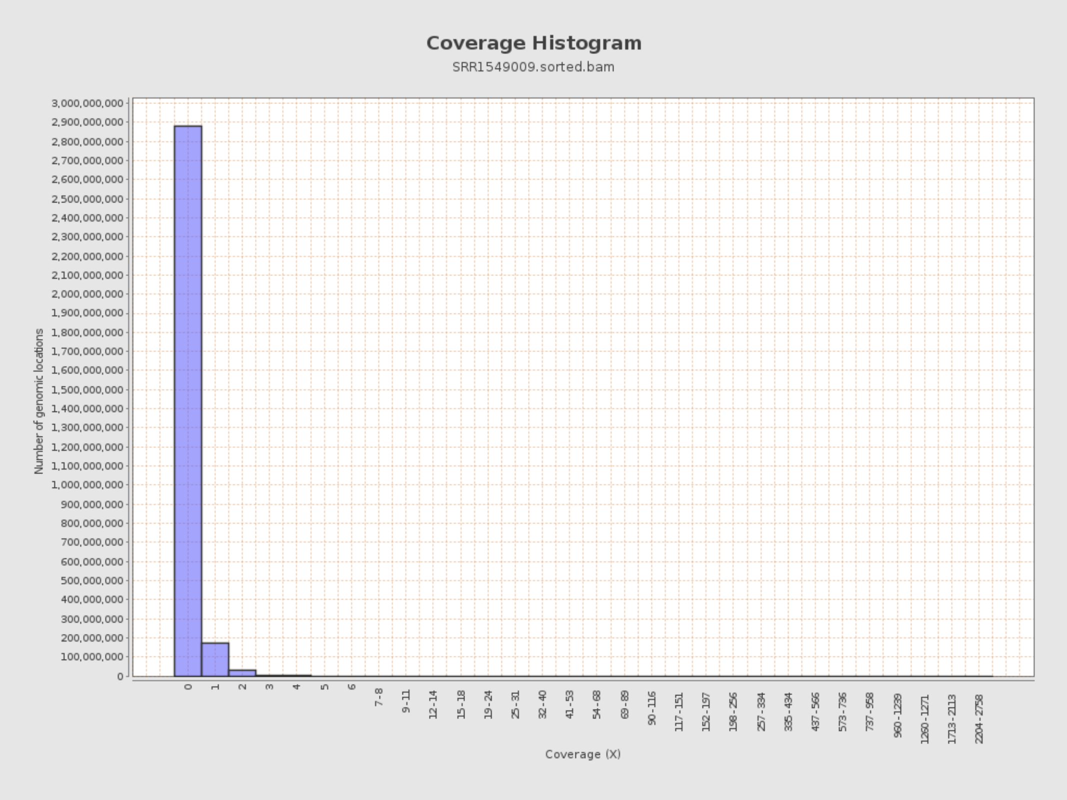
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 21030429 | 0.0844 | 1.0158 |
| chr2 | 243199373 | 24219236 | 0.0996 | 0.5532 |
| chr3 | 198022430 | 19579129 | 0.0989 | 0.3778 |
| chr4 | 191154276 | 19177211 | 0.1003 | 0.4222 |
| chr5 | 180915260 | 16958527 | 0.0937 | 0.3732 |
| chr6 | 171115067 | 16075179 | 0.0939 | 0.4418 |
| chr7 | 159138663 | 14980202 | 0.0941 | 0.7241 |
| chr8 | 146364022 | 14496050 | 0.099 | 1.4112 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr9 | 141213431 | 11627075 | 0.0823 | 0.5275 |
| chr10 | 135534747 | 12192496 | 0.09 | 0.566 |
| chr11 | 135006516 | 12591078 | 0.0933 | 0.4811 |
| chr12 | 133851895 | 13039640 | 0.0974 | 0.3935 |
| chr13 | 115169878 | 9016989 | 0.0783 | 0.3321 |
| chr14 | 107349540 | 8824393 | 0.0822 | 0.4358 |
| chr15 | 102531392 | 7787376 | 0.076 | 0.3282 |
| chr16 | 90354753 | 7186957 | 0.0795 | 0.3871 |
| chr17 | 81195210 | 6548118 | 0.0806 | 0.3774 |
| chr18 | 78077248 | 7762029 | 0.0994 | 1.0787 |
| chr19 | 59128983 | 4471663 | 0.0756 | 0.8371 |
| chr20 | 63025520 | 5389756 | 0.0855 | 0.3757 |
| chr21 | 48129895 | 3552721 | 0.0738 | 0.4062 |
| chr22 | 51304566 | 2615439 | 0.051 | 0.2915 |
| chrMT | 16571 | 2502 | 0.151 | 0.4076 |
| chrX | 155270560 | 9360804 | 0.0603 | 0.39 |
| chrY | 59373566 | 2316148 | 0.039 | 0.3938 |

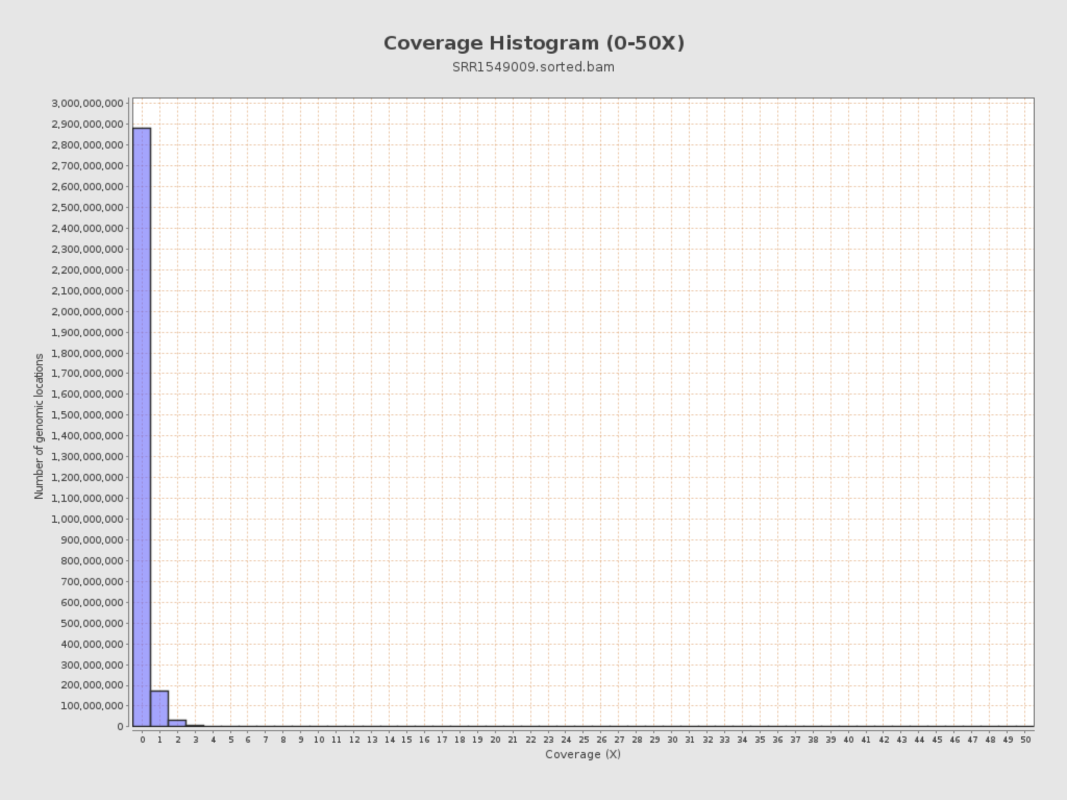
# 3. Results : Coverage across reference



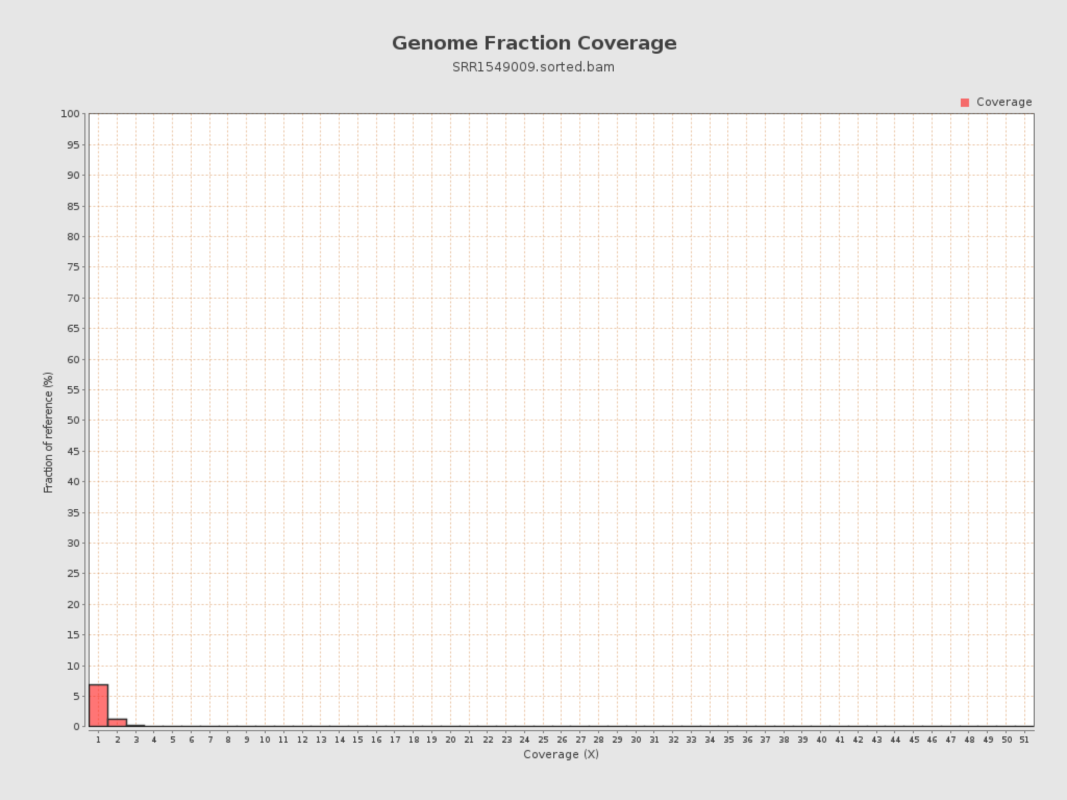
# 4. Results : Coverage Histogram



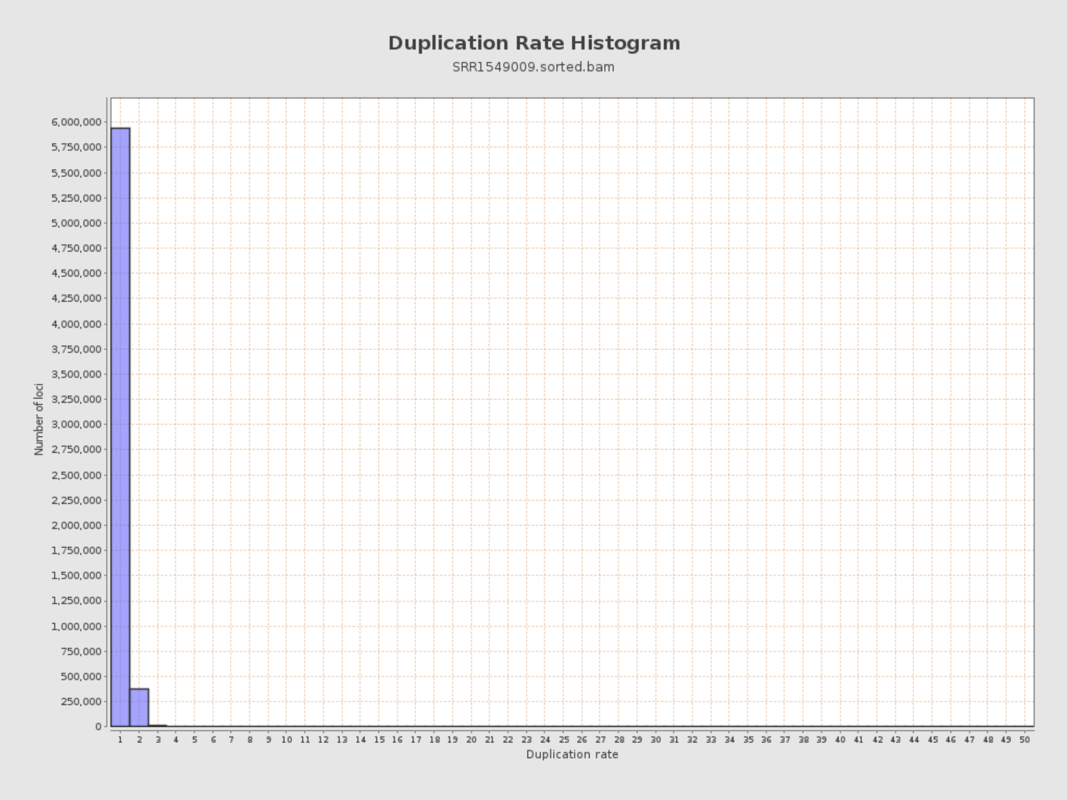
# 5. Results : Coverage Histogram (0-50X)



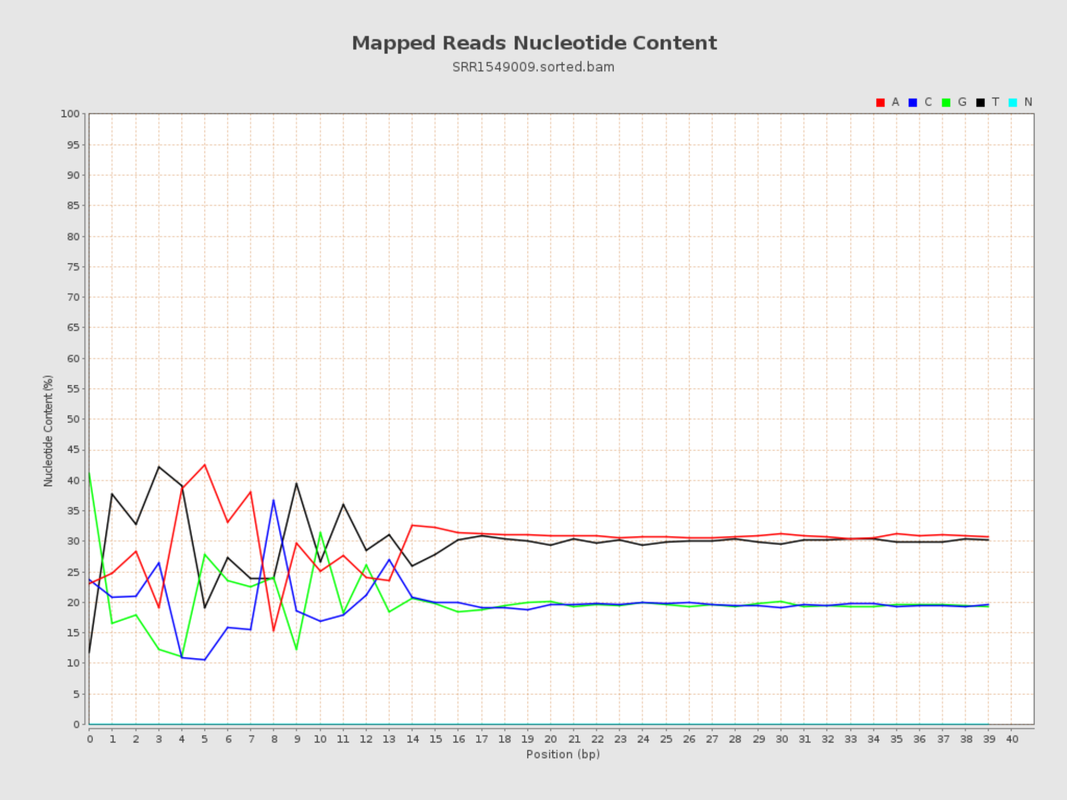
# 6. Results : Genome Fraction Coverage



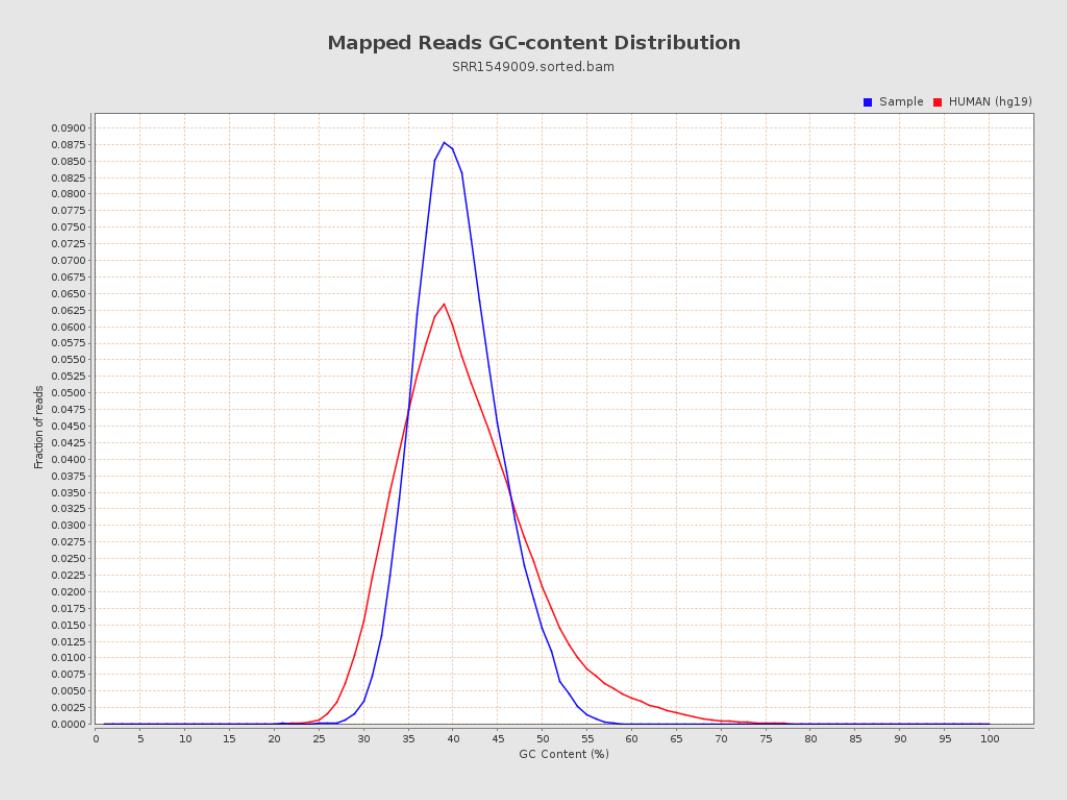
# 7. Results : Duplication Rate Histogram



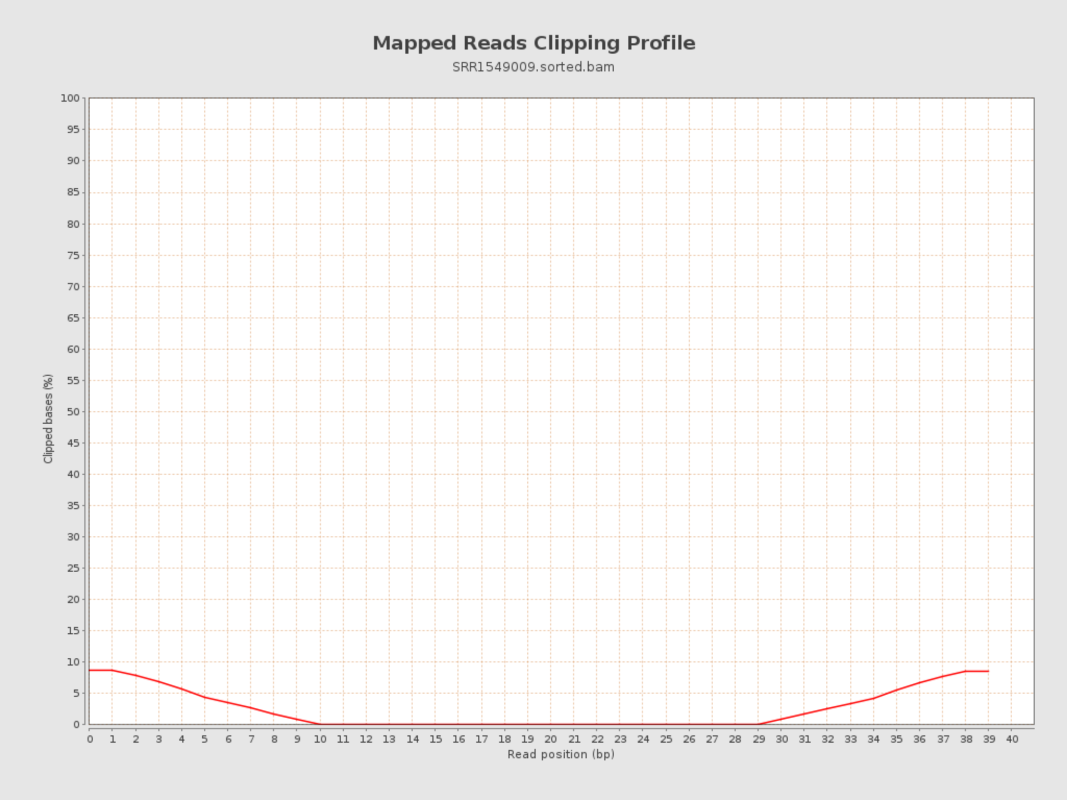
# 8. Results : Mapped Reads Nucleotide Content



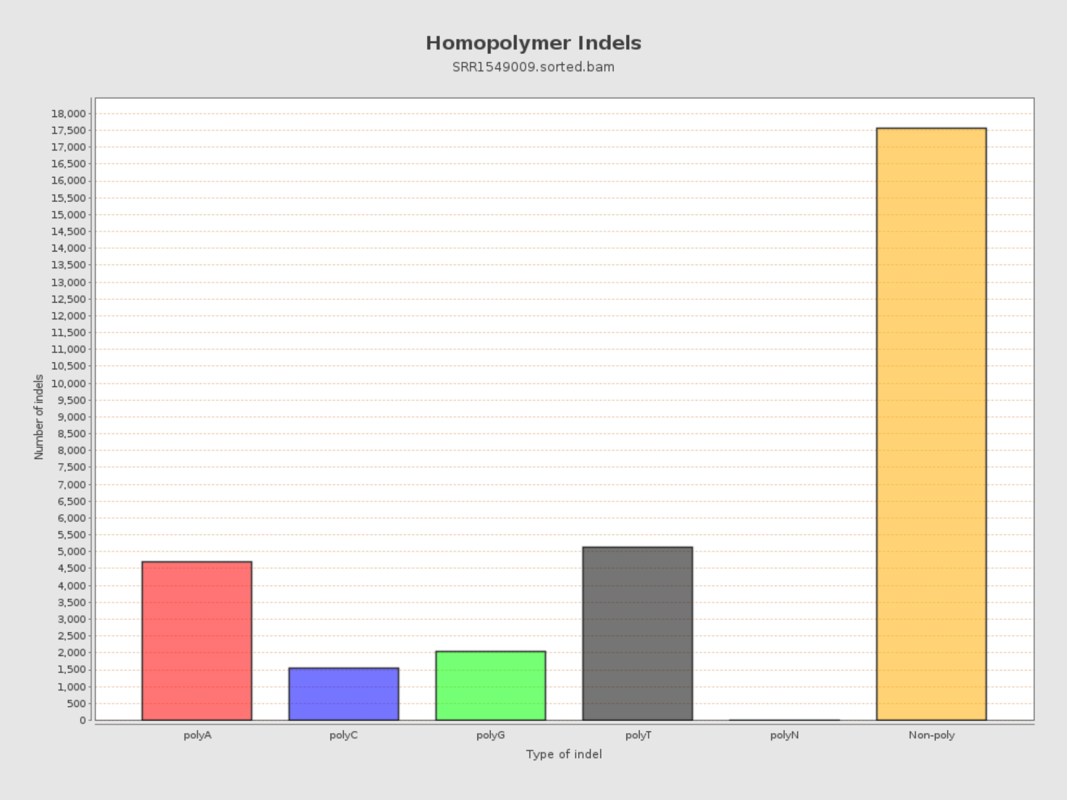
# 9. Results : Mapped Reads GC-content Distribution



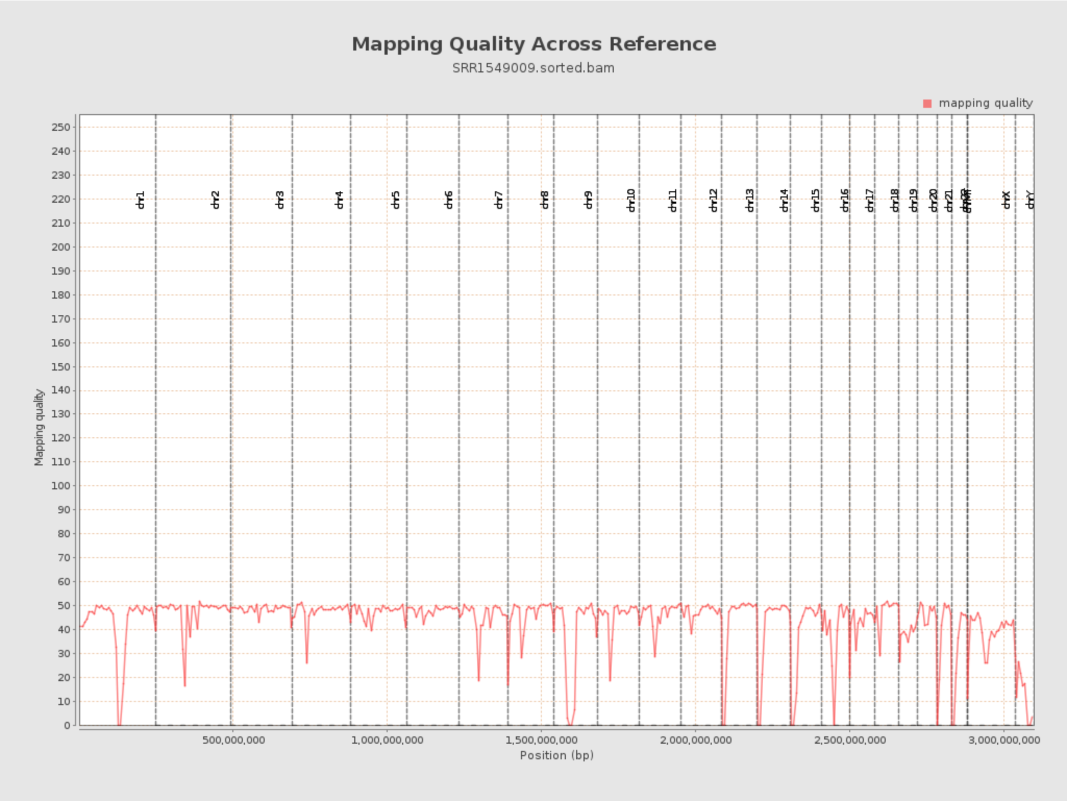
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram