# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/24 05:10:36*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081249.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_SRR3081249 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081249.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Aug 24 05:10:22 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3081249.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,526,553 |
| Mapped reads | 3,904,857 / 86.27% |
| Unmapped reads | 621,696 / 13.73% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 38,545 / 0.85% |
| Read min/max/mean length | 30 / 76 / 76.3 |
| Duplicated reads (estimated) | 227,042 / 5.02% |
| Duplication rate | 4.41% |
| Clipped reads | 1,688,328 / 37.3% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 71,571,981 / 27.36% |
| Number/percentage of C's | 47,865,959 / 18.3% |
| Number/percentage of T's | 83,662,862 / 31.98% |
| Number/percentage of G's | 58,455,946 / 22.34% |
| Number/percentage of N's | 69,855 / 0.03% |
| GC Percentage | 40.64% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0845 |
| | |

| | |
|---|---|
| Standard Deviation | 0.6853 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.26 |

## 2.5. Mismatches and indels

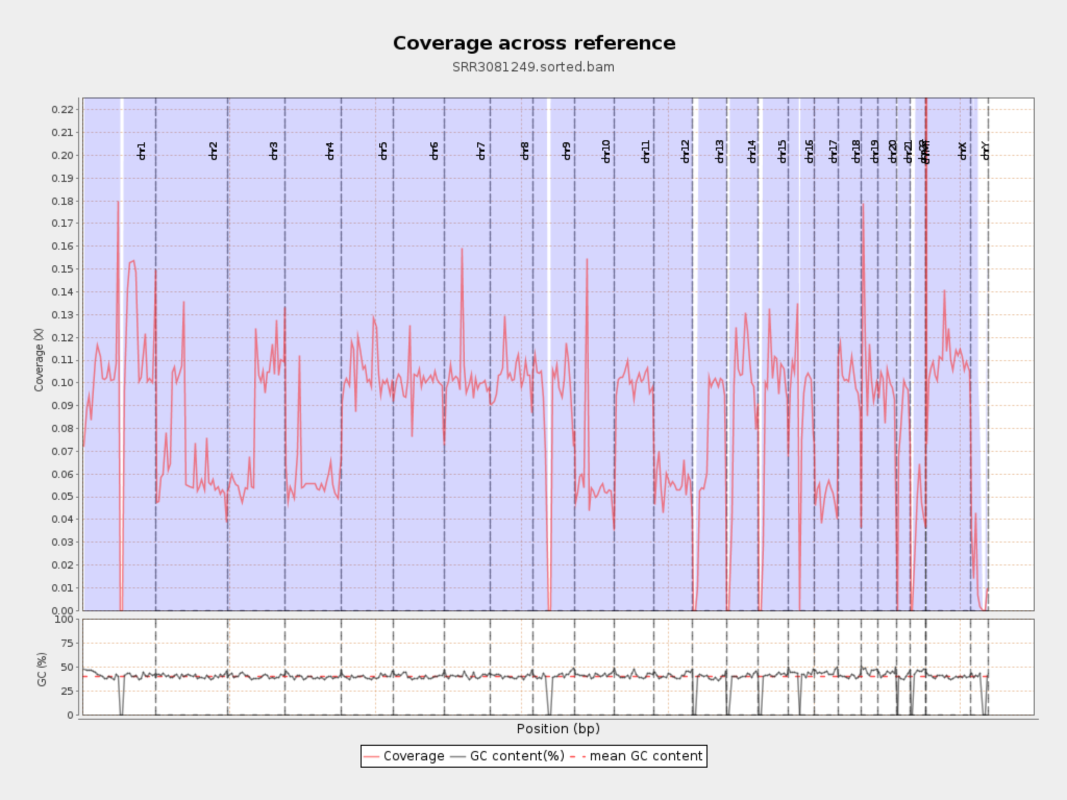
| | |
|---|---|
| General error rate | 0.86% |
| Mismatches | 2,213,267 |
| Insertions | 21,578 |
| Mapped reads with at least one insertion | 0.55% |
| Deletions | 65,147 |
| Mapped reads with at least one deletion | 1.65% |
| Homopolymer indels | 49.47% |

## 2.6. Chromosome stats

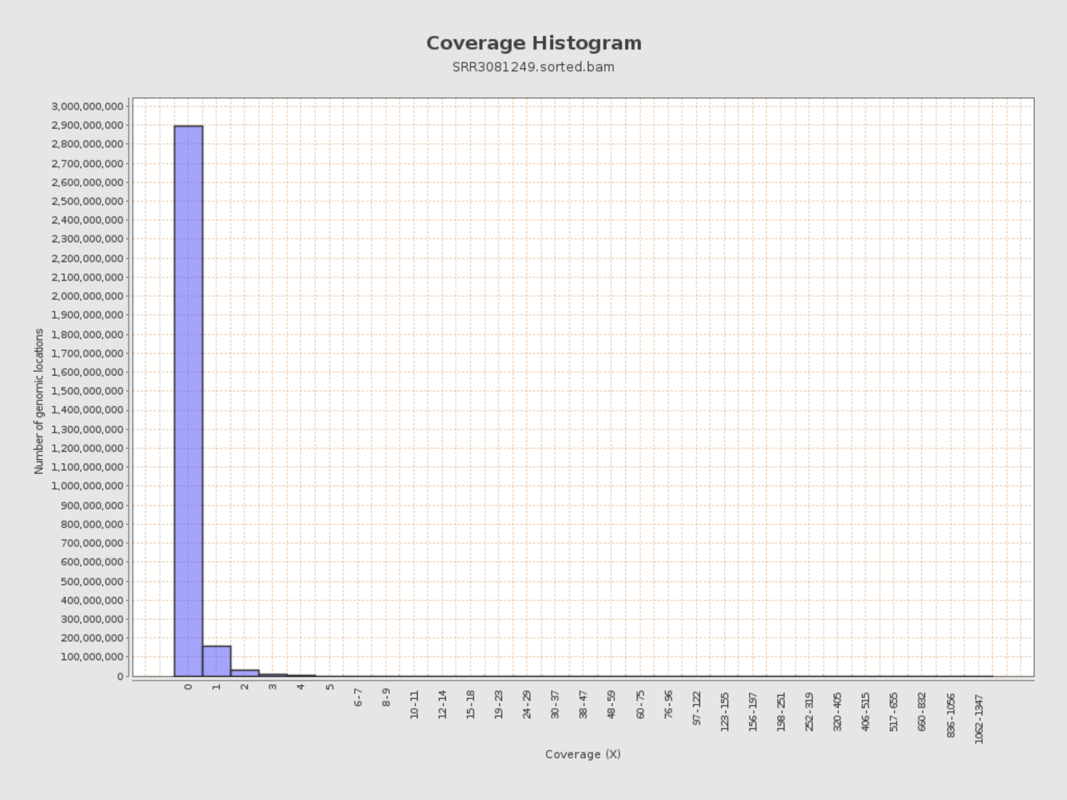
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 26511124 | 0.1064 | 1.2795 |
| chr2 | 243199373 | 16329227 | 0.0671 | 0.7194 |
| chr3 | 198022430 | 16407023 | 0.0829 | 0.3736 |
| chr4 | 191154276 | 11073551 | 0.0579 | 0.3968 |
| chr5 | 180915260 | 18930069 | 0.1046 | 0.4052 |
| chr6 | 171115067 | 17209552 | 0.1006 | 0.5124 |
| chr7 | 159138663 | 16280285 | 0.1023 | 1.0329 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 15073287 | 0.103 | 0.8324 |
| chr9 | 141213431 | 12534418 | 0.0888 | 0.651 |
| chr10 | 135534747 | 7873139 | 0.0581 | 0.8121 |
| chr11 | 135006516 | 13464009 | 0.0997 | 0.7375 |
| chr12 | 133851895 | 7467101 | 0.0558 | 0.3049 |
| chr13 | 115169878 | 8083728 | 0.0702 | 0.3257 |
| chr14 | 107349540 | 9524909 | 0.0887 | 0.4141 |
| chr15 | 102531392 | 8697121 | 0.0848 | 0.3633 |
| chr16 | 90354753 | 8122672 | 0.0899 | 0.4268 |
| chr17 | 81195210 | 4075879 | 0.0502 | 0.3964 |
| chr18 | 78077248 | 8046586 | 0.1031 | 0.9963 |
| chr19 | 59128983 | 6451233 | 0.1091 | 1.0245 |
| chr20 | 63025520 | 6017136 | 0.0955 | 0.4068 |
| chr21 | 48129895 | 3796062 | 0.0789 | 0.4306 |
| chr22 | 51304566 | 1802599 | 0.0351 | 0.2275 |
| chrMT | 16571 | 246590 | 14.8808 | 7.6848 |
| chrX | 155270560 | 16967269 | 0.1093 | 0.4632 |
| chrY | 59373566 | 753202 | 0.0127 | 0.3414 |

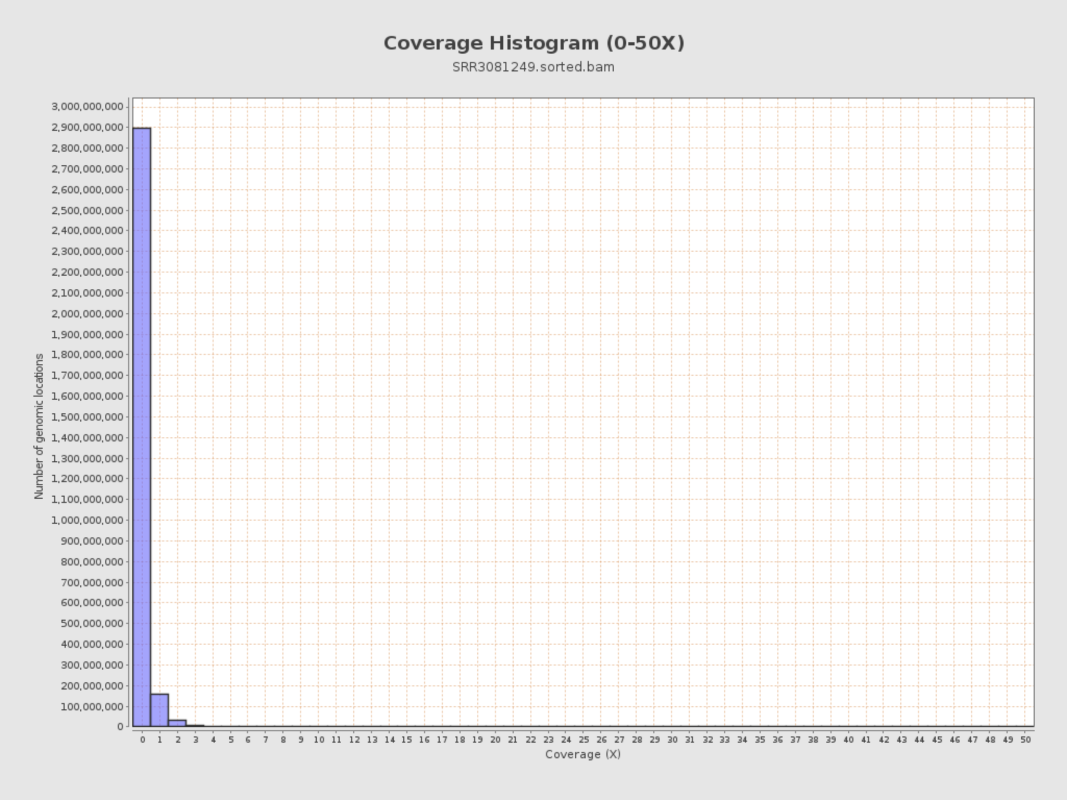
# 3. Results : Coverage across reference



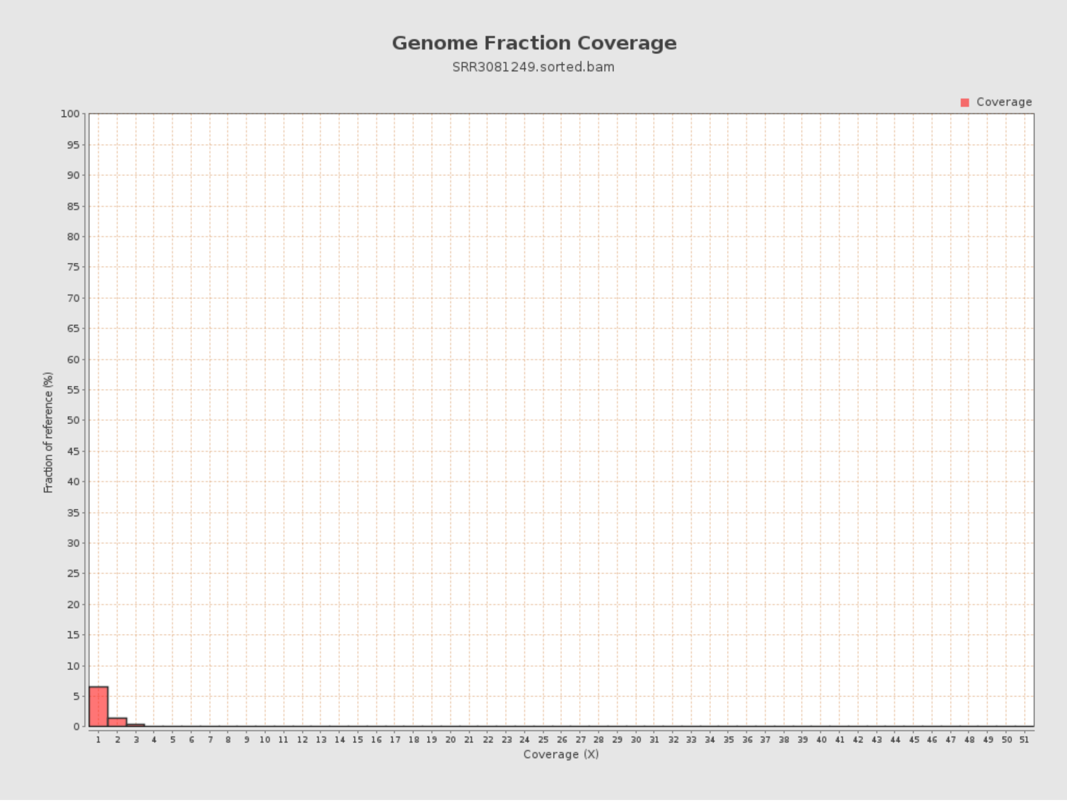
# 4. Results : Coverage Histogram



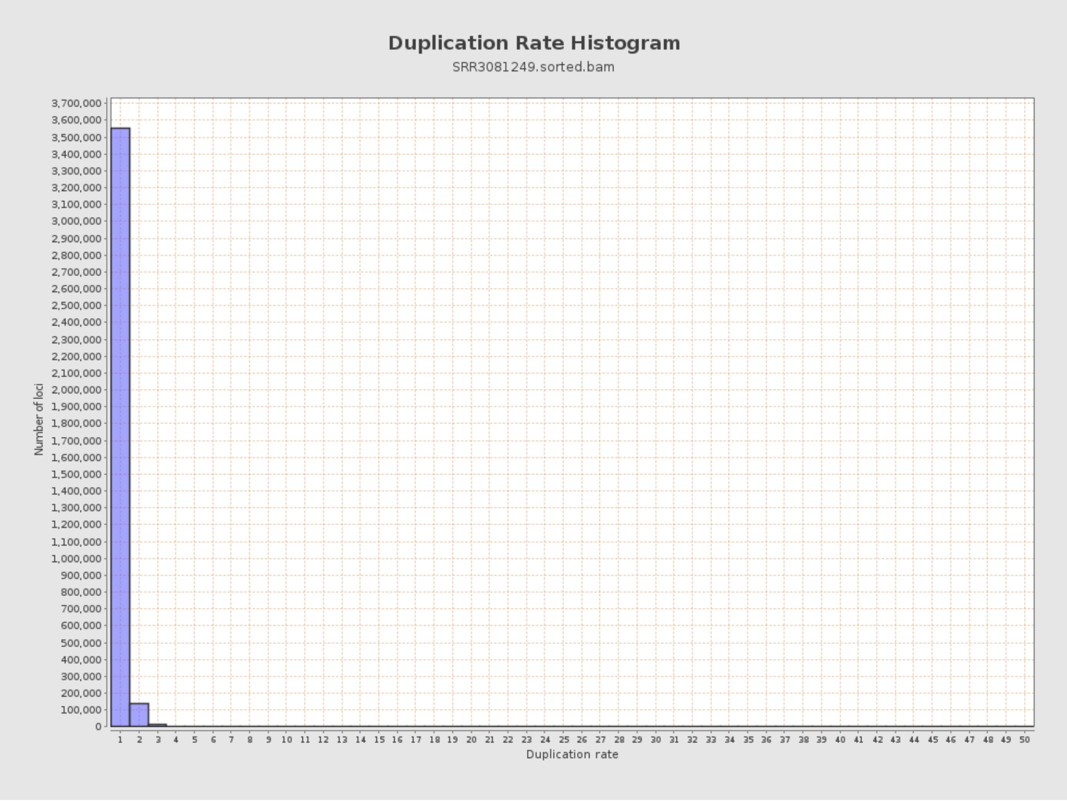
# 5. Results : Coverage Histogram (0-50X)



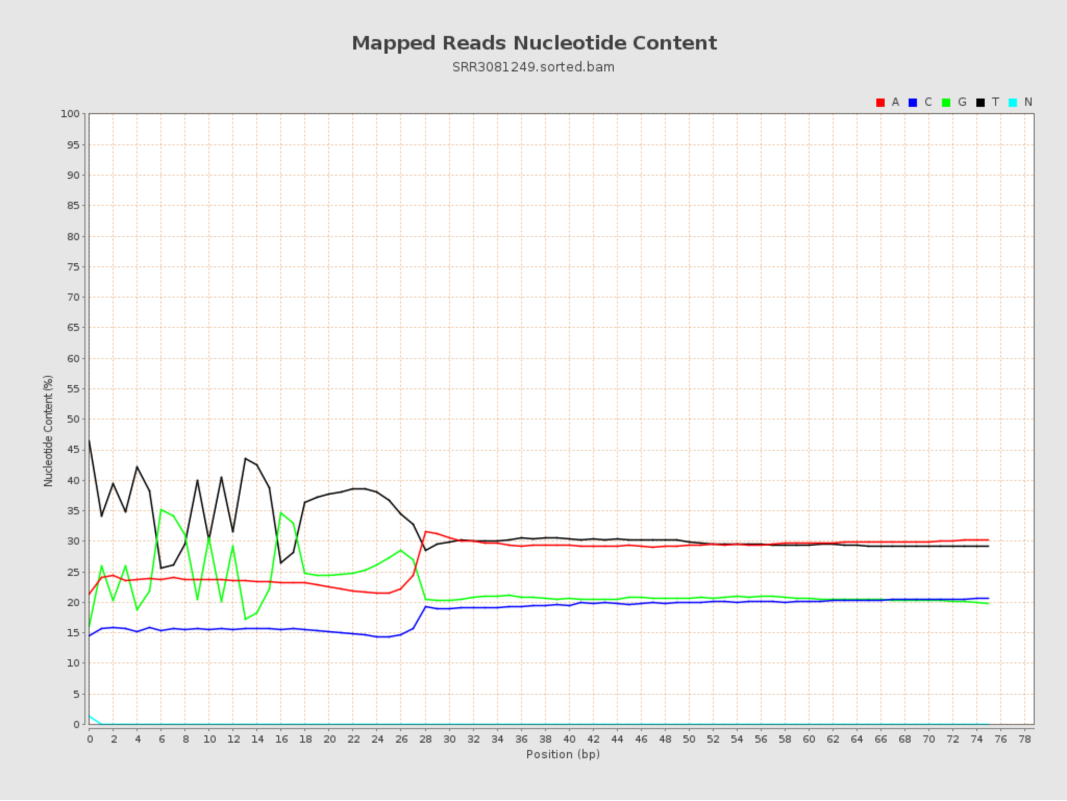
# 6. Results : Genome Fraction Coverage



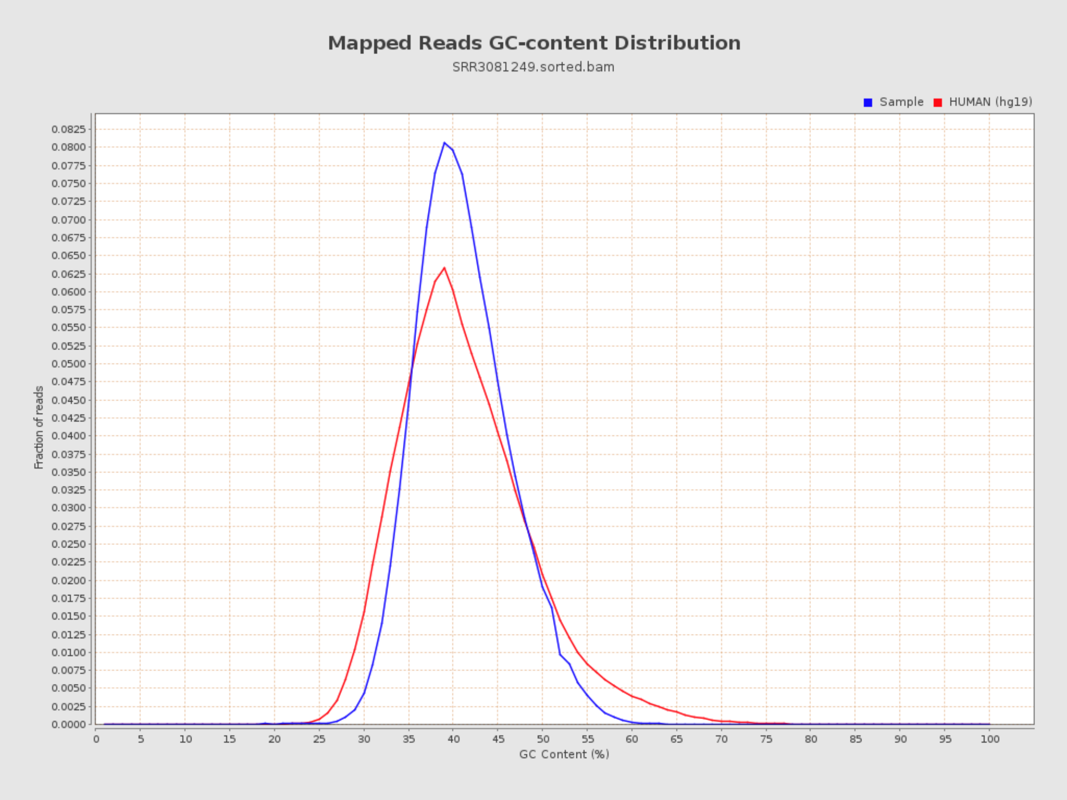
# 7. Results : Duplication Rate Histogram



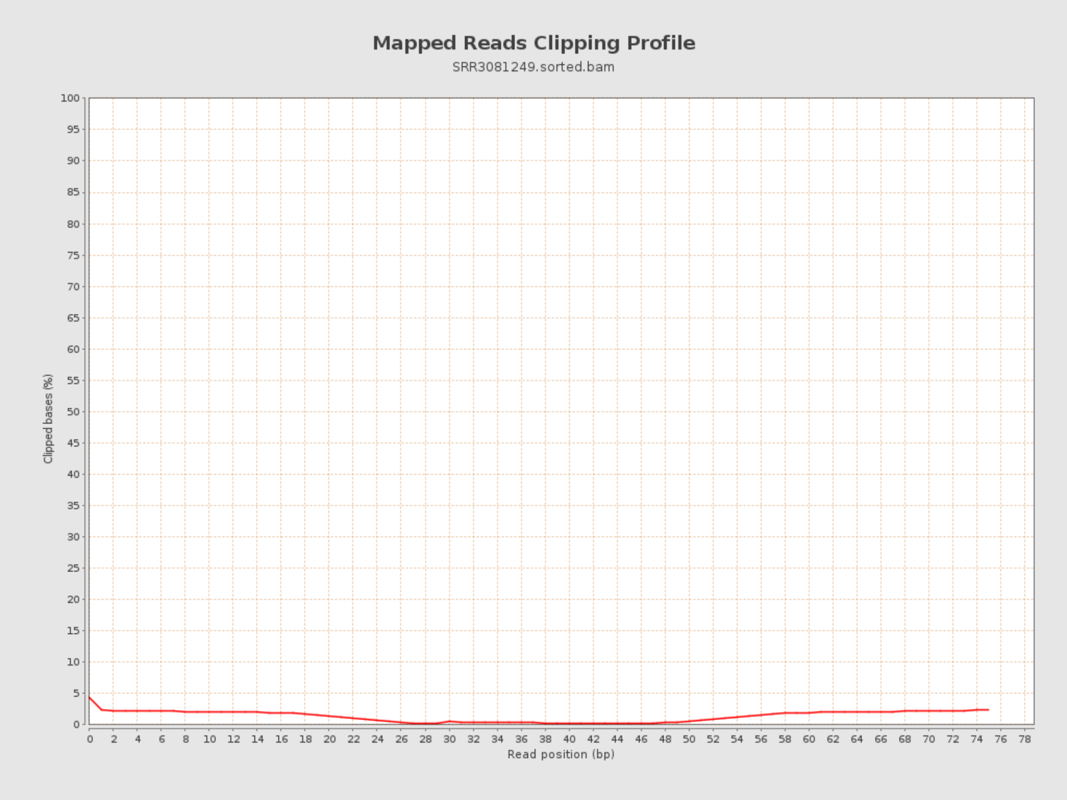
# 8. Results : Mapped Reads Nucleotide Content



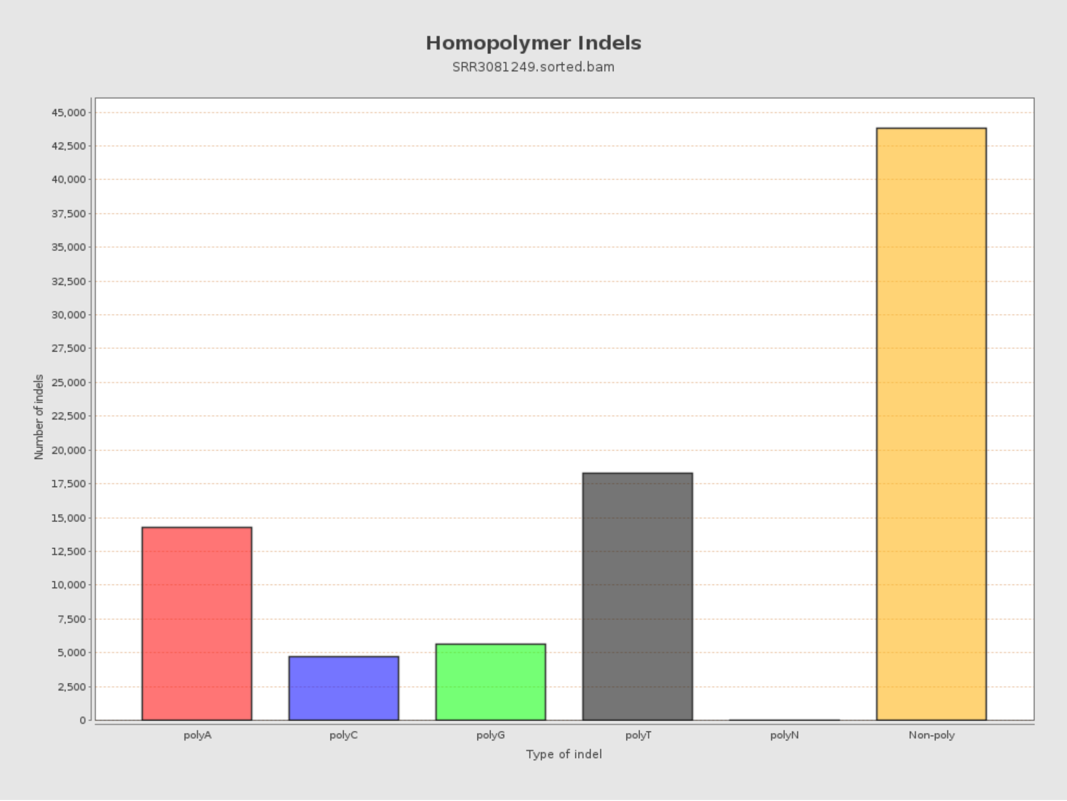
# 9. Results : Mapped Reads GC-content Distribution



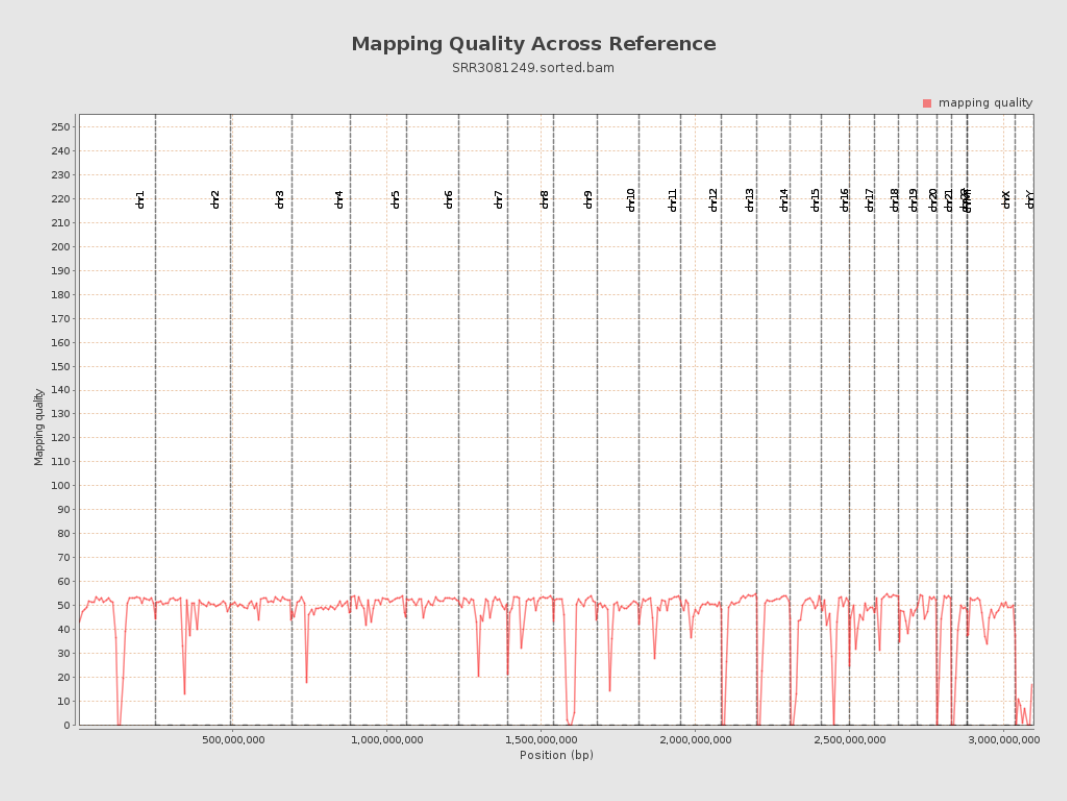
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram