# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/13 20:31:44*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004009.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_SRR6004009 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004009.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Sep 13 20:31:43 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6004009.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,923,132 |
| Mapped reads | 1,688,904 / 87.82% |
| Unmapped reads | 234,228 / 12.18% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 12,259 / 0.64% |
| Read min/max/mean length | 30 / 76 / 76.22 |
| Duplicated reads (estimated) | 73,559 / 3.82% |
| Duplication rate | 3.61% |
| Clipped reads | 721,503 / 37.52% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 31,129,057 / 27.46% |
| Number/percentage of C's | 21,389,632 / 18.87% |
| Number/percentage of T's | 35,464,612 / 31.29% |
| Number/percentage of G's | 25,355,290 / 22.37% |
| Number/percentage of N's | 21,155 / 0.02% |
| GC Percentage | 41.24% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0366 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2998 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.16 |

## 2.5. Mismatches and indels

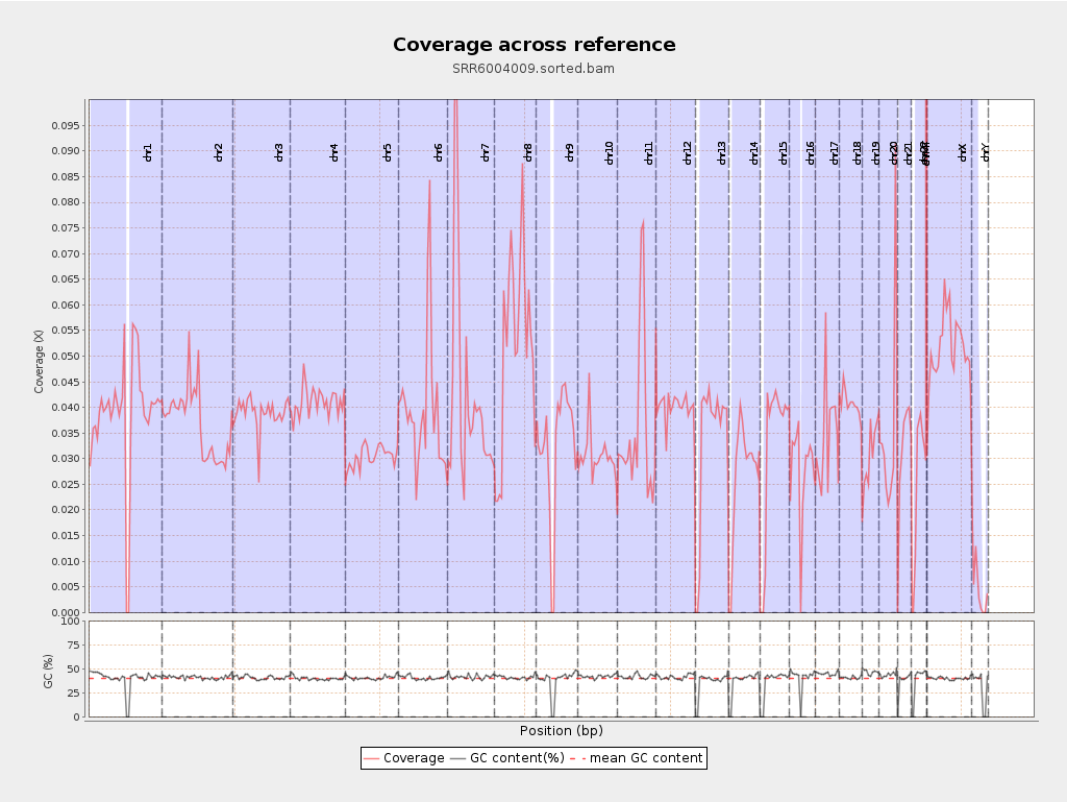
| | |
|---|---|
| General error rate | 0.88% |
| Mismatches | 985,185 |
| Insertions | 7,918 |
| Mapped reads with at least one insertion | 0.46% |
| Deletions | 25,783 |
| Mapped reads with at least one deletion | 1.51% |
| Homopolymer indels | 46.73% |

## 2.6. Chromosome stats

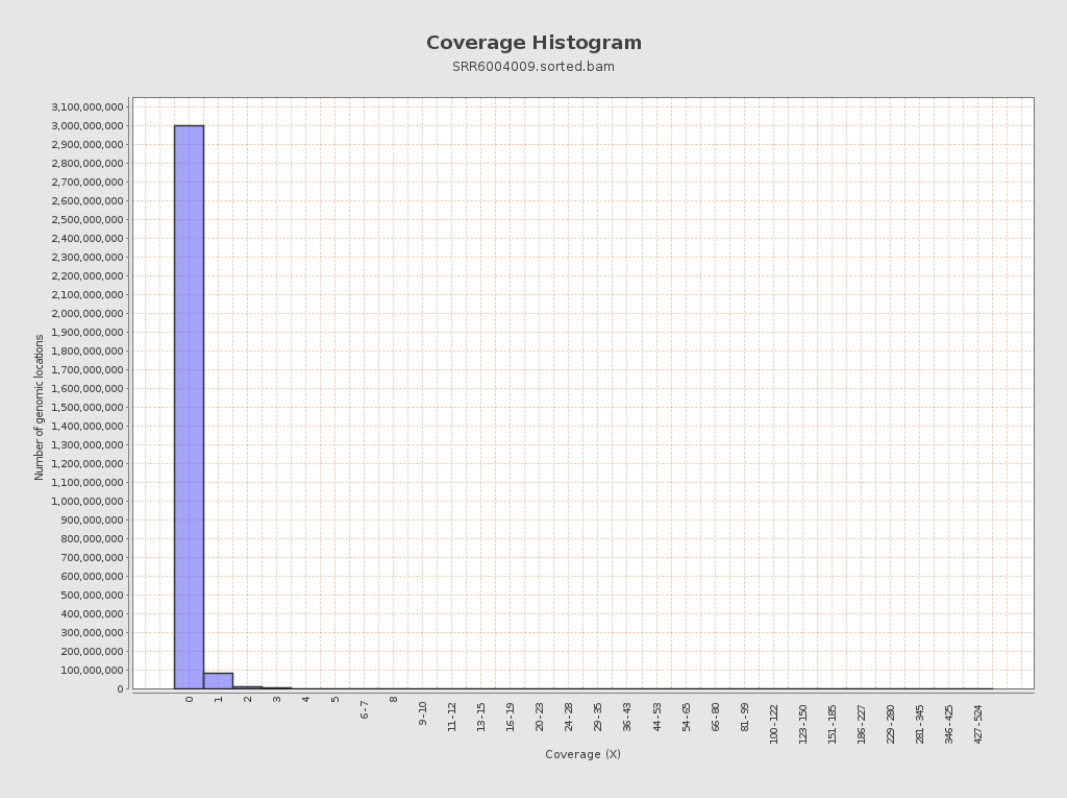
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 9649558 | 0.0387 | 0.4932 |
| chr2 | 243199373 | 8951613 | 0.0368 | 0.3446 |
| chr3 | 198022430 | 7697061 | 0.0389 | 0.2243 |
| chr4 | 191154276 | 7832037 | 0.041 | 0.2401 |
| chr5 | 180915260 | 5490421 | 0.0303 | 0.1989 |
| chr6 | 171115067 | 6761545 | 0.0395 | 0.2448 |
| chr7 | 159138663 | 6889522 | 0.0433 | 0.3997 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7529340 | 0.0514 | 0.373 |
| chr9 | 141213431 | 4521935 | 0.032 | 0.2867 |
| chr10 | 135534747 | 4144808 | 0.0306 | 0.2637 |
| chr11 | 135006516 | 4864871 | 0.036 | 0.2592 |
| chr12 | 133851895 | 5345778 | 0.0399 | 0.2323 |
| chr13 | 115169878 | 3835131 | 0.0333 | 0.2179 |
| chr14 | 107349540 | 2881004 | 0.0268 | 0.2001 |
| chr15 | 102531392 | 3305372 | 0.0322 | 0.2076 |
| chr16 | 90354753 | 2512334 | 0.0278 | 0.2024 |
| chr17 | 81195210 | 2805537 | 0.0346 | 0.2281 |
| chr18 | 78077248 | 3195507 | 0.0409 | 0.4875 |
| chr19 | 59128983 | 1821929 | 0.0308 | 0.3292 |
| chr20 | 63025520 | 2330036 | 0.037 | 0.2282 |
| chr21 | 48129895 | 1507307 | 0.0313 | 0.2128 |
| chr22 | 51304566 | 1238737 | 0.0241 | 0.1764 |
| chrMT | 16571 | 30171 | 1.8207 | 1.8358 |
| chrX | 155270560 | 7984467 | 0.0514 | 0.2781 |
| chrY | 59373566 | 278295 | 0.0047 | 0.109 |

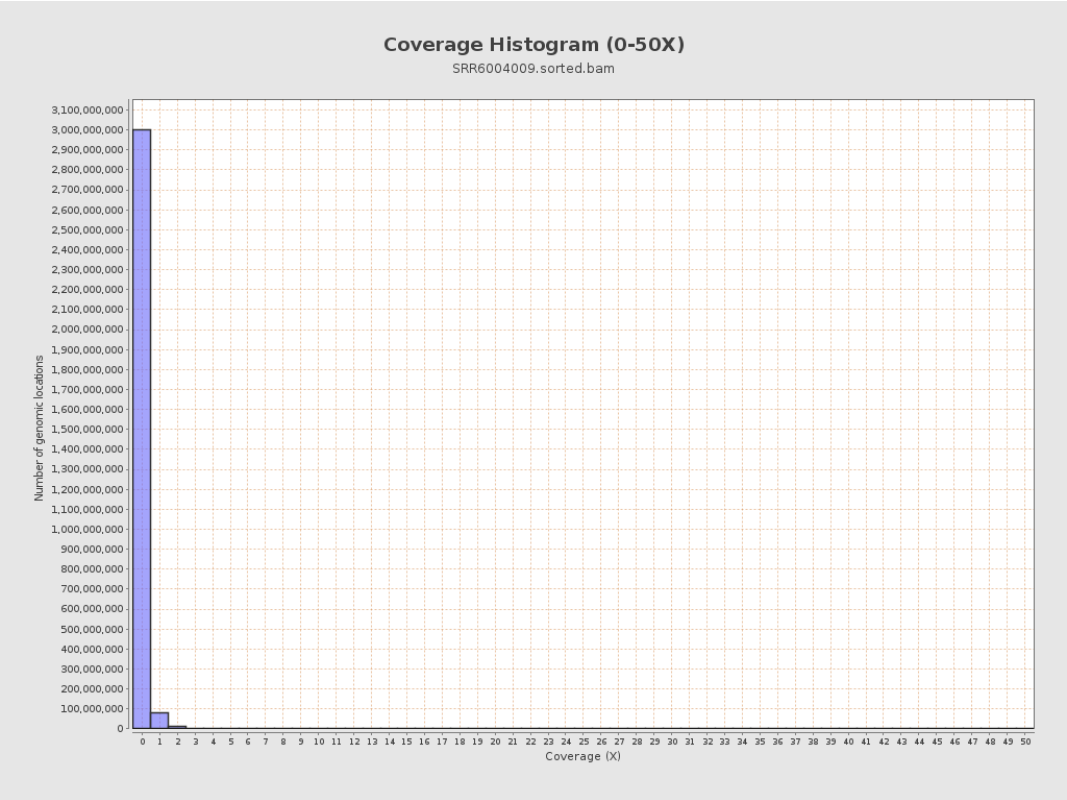
# 3. Results : Coverage across reference



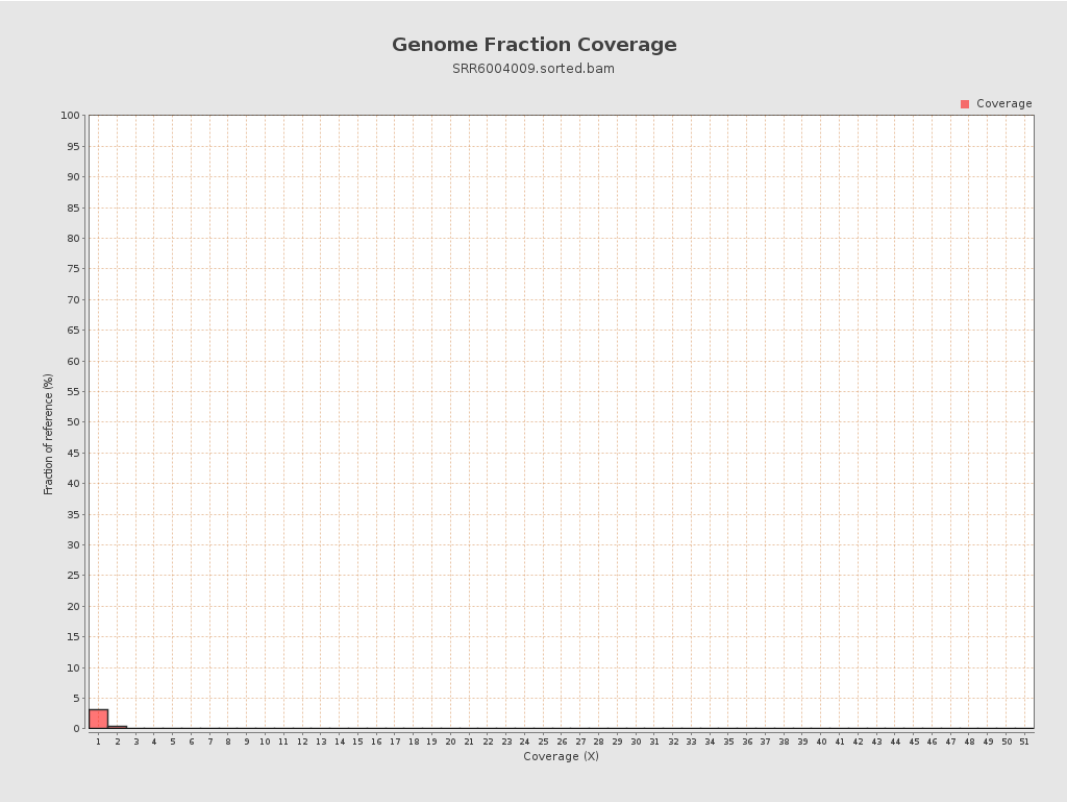
# 4. Results : Coverage Histogram



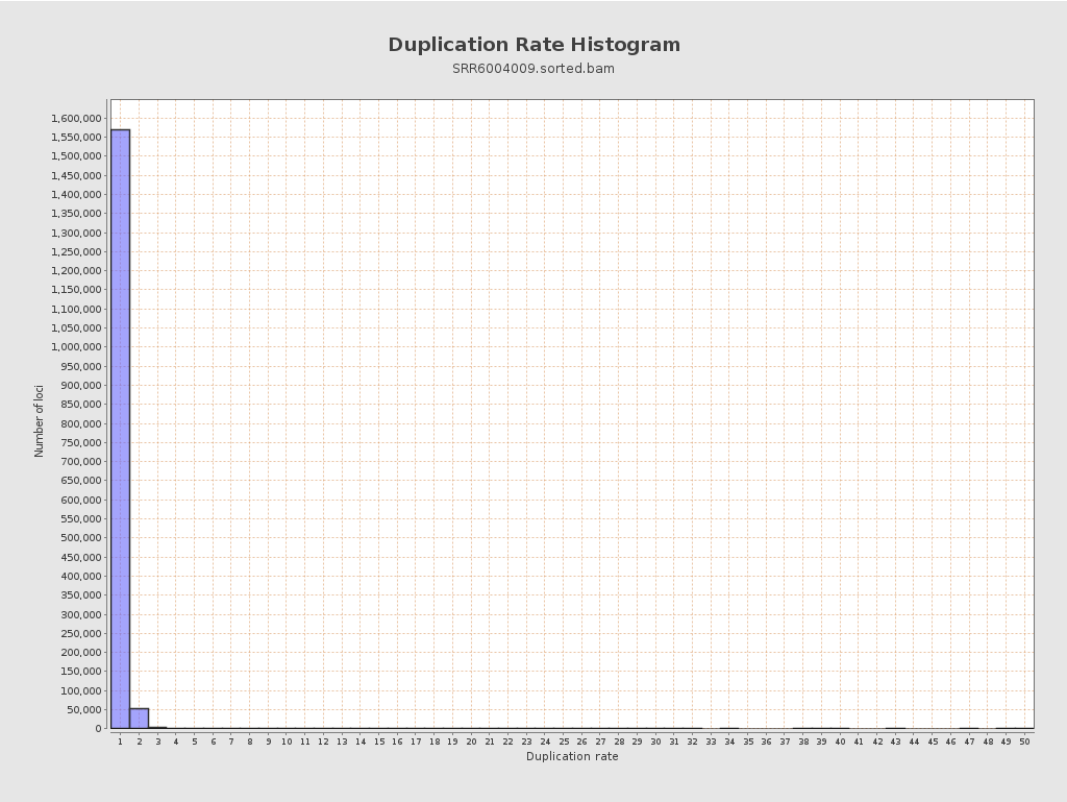
# 5. Results : Coverage Histogram (0-50X)



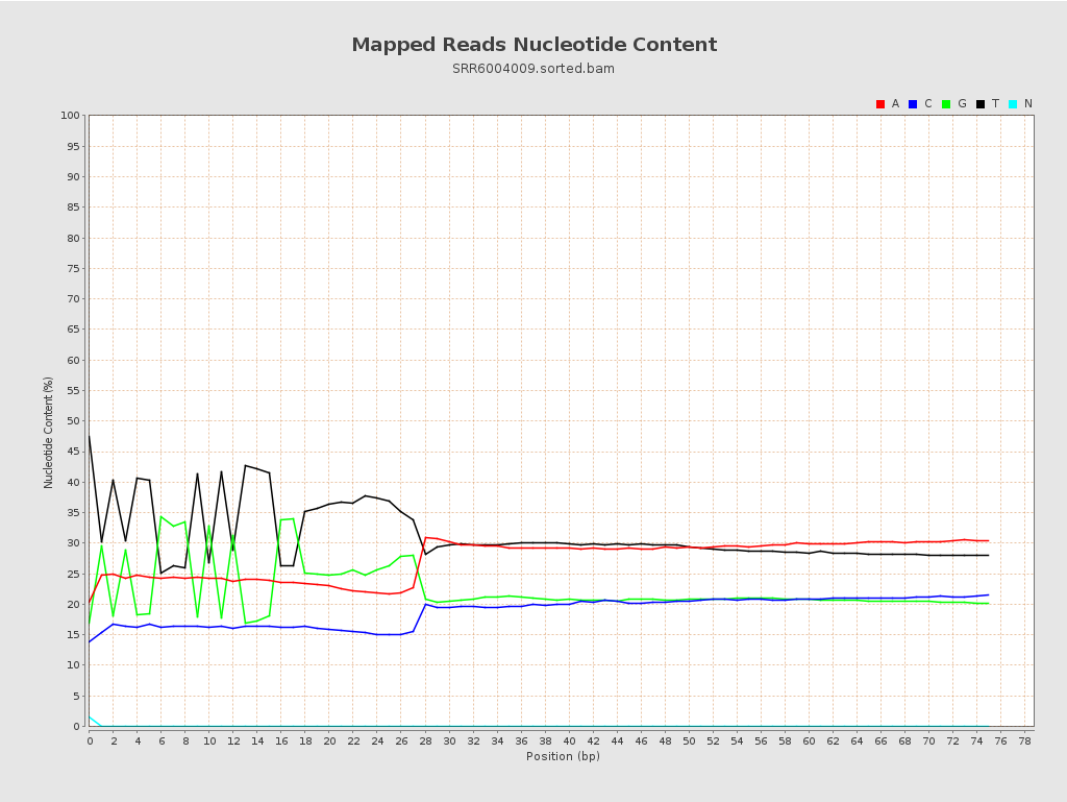
# 6. Results : Genome Fraction Coverage



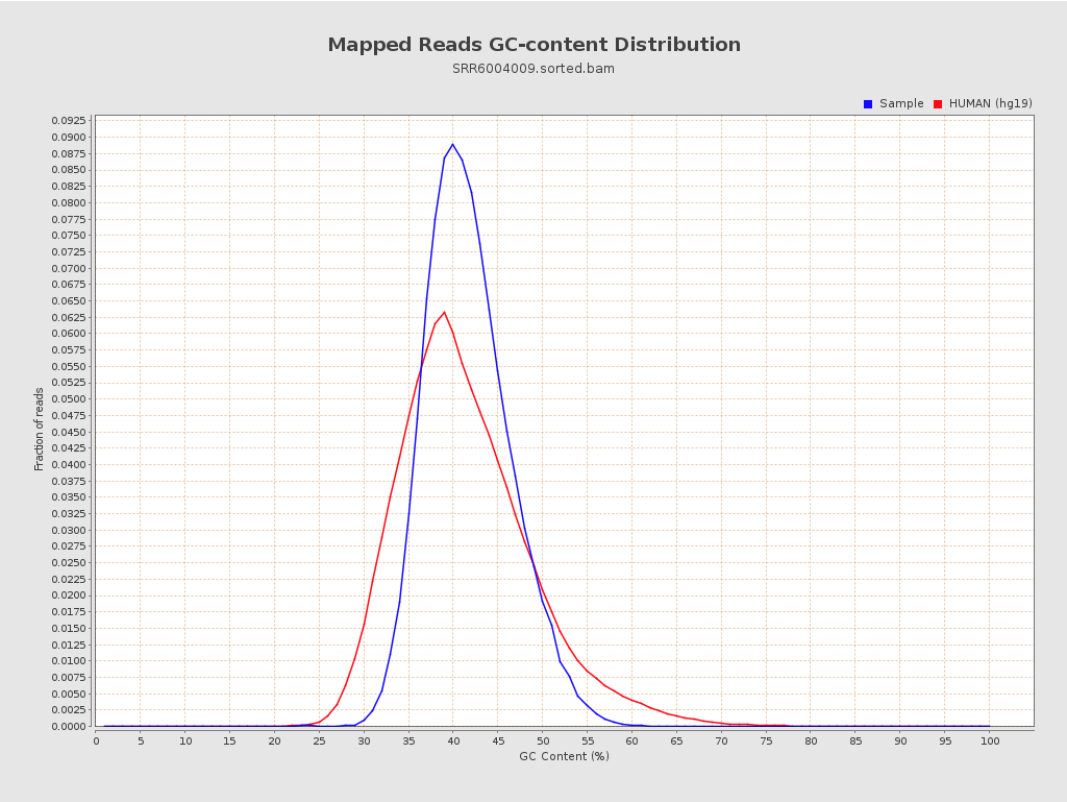
# 7. Results : Duplication Rate Histogram



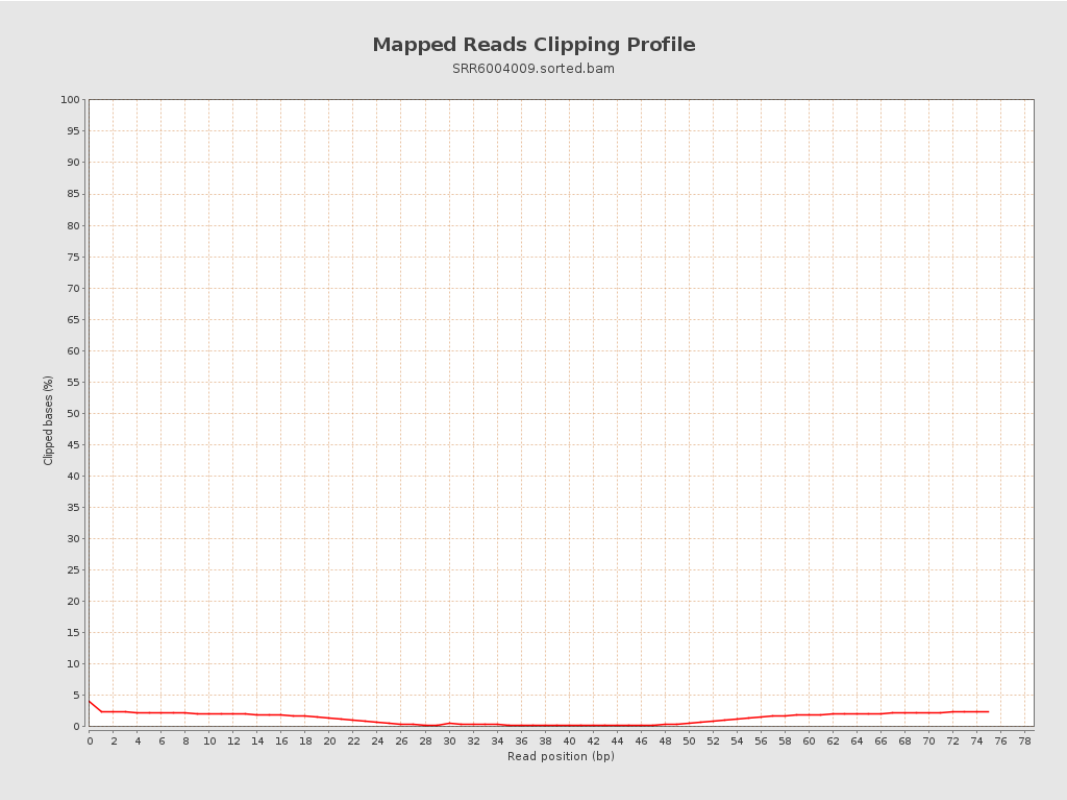
# 8. Results : Mapped Reads Nucleotide Content



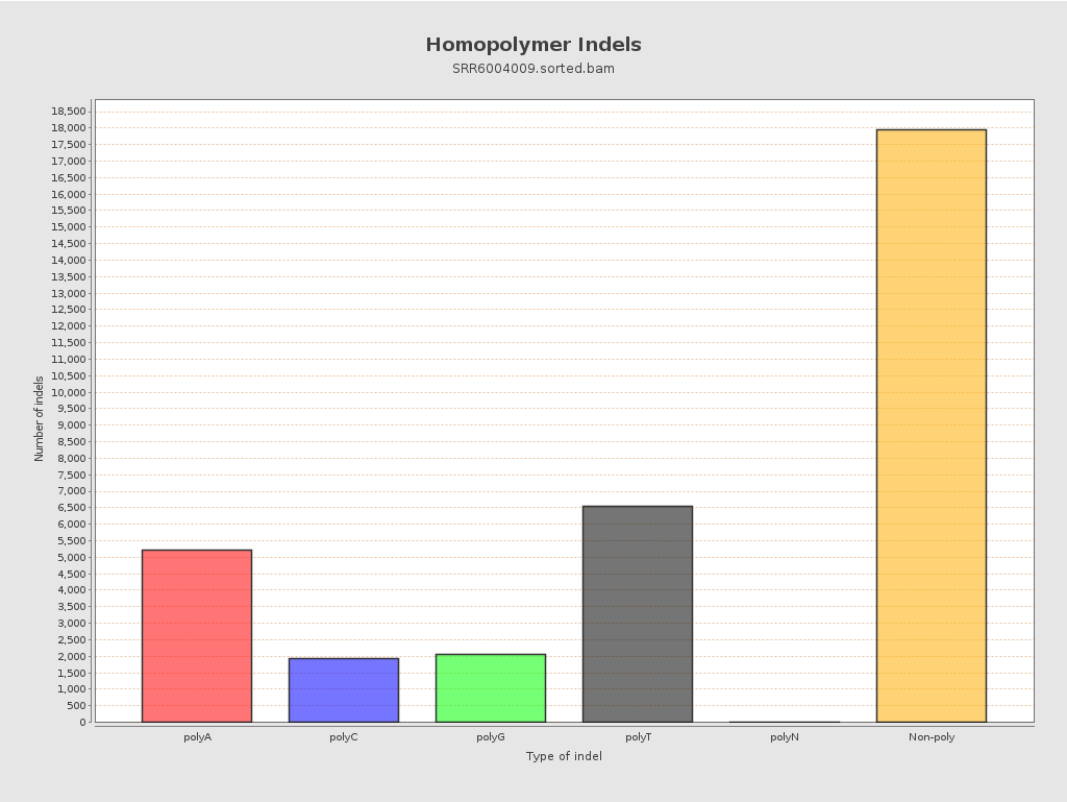
# 9. Results : Mapped Reads GC-content Distribution



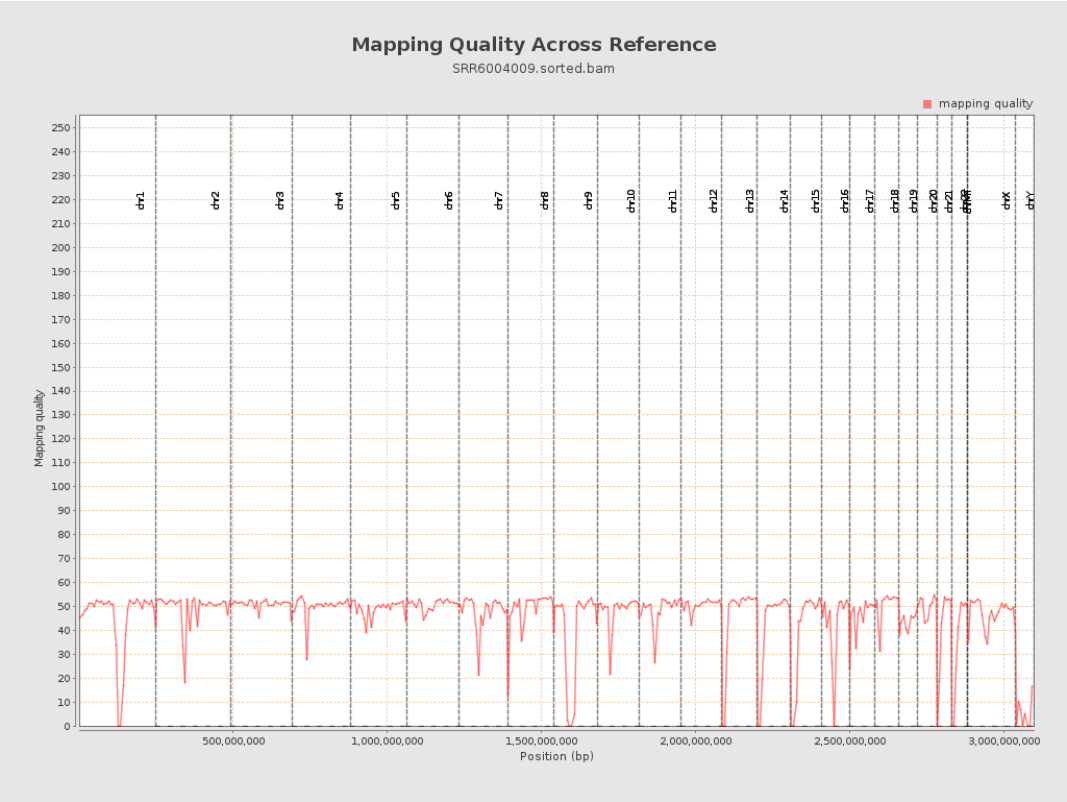
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram