# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/27 23:47:31*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524346.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_SRR10524346 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524346.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Aug 27 23:47:31 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524346.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,836,118 |
| Mapped reads | 1,700,614 / 92.62% |
| Unmapped reads | 135,504 / 7.38% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 7,736 / 0.42% |
| Read min/max/mean length | 30 / 76 / 76.14 |
| Duplicated reads (estimated) | 71,699 / 3.9% |
| Duplication rate | 3.09% |
| Clipped reads | 1,703,461 / 92.78% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 25,326,723 / 25.33% |
| Number/percentage of C's | 20,004,248 / 20% |
| Number/percentage of T's | 30,954,264 / 30.95% |
| Number/percentage of G's | 23,700,259 / 23.7% |
| Number/percentage of N's | 13,613 / 0.01% |
| GC Percentage | 43.7% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0323 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3044 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.78 |

## 2.5. Mismatches and indels

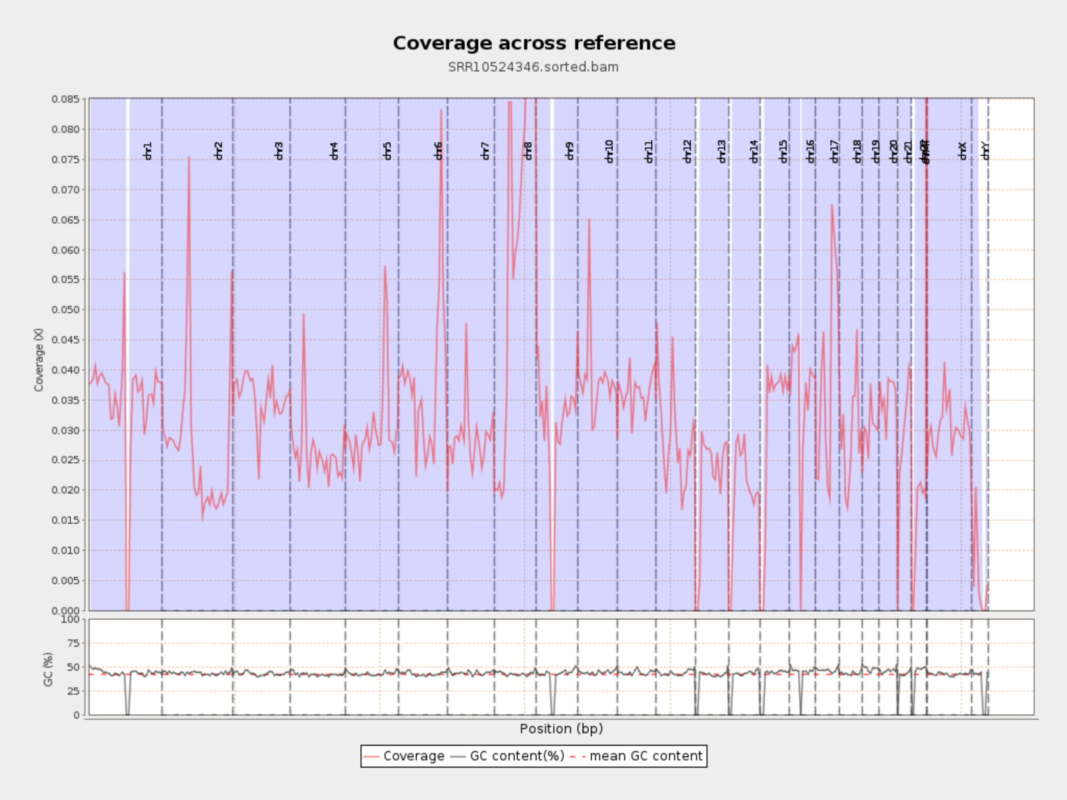
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 507,718 |
| Insertions | 6,876 |
| Mapped reads with at least one insertion | 0.4% |
| Deletions | 18,138 |
| Mapped reads with at least one deletion | 1.06% |
| Homopolymer indels | 42.56% |

## 2.6. Chromosome stats

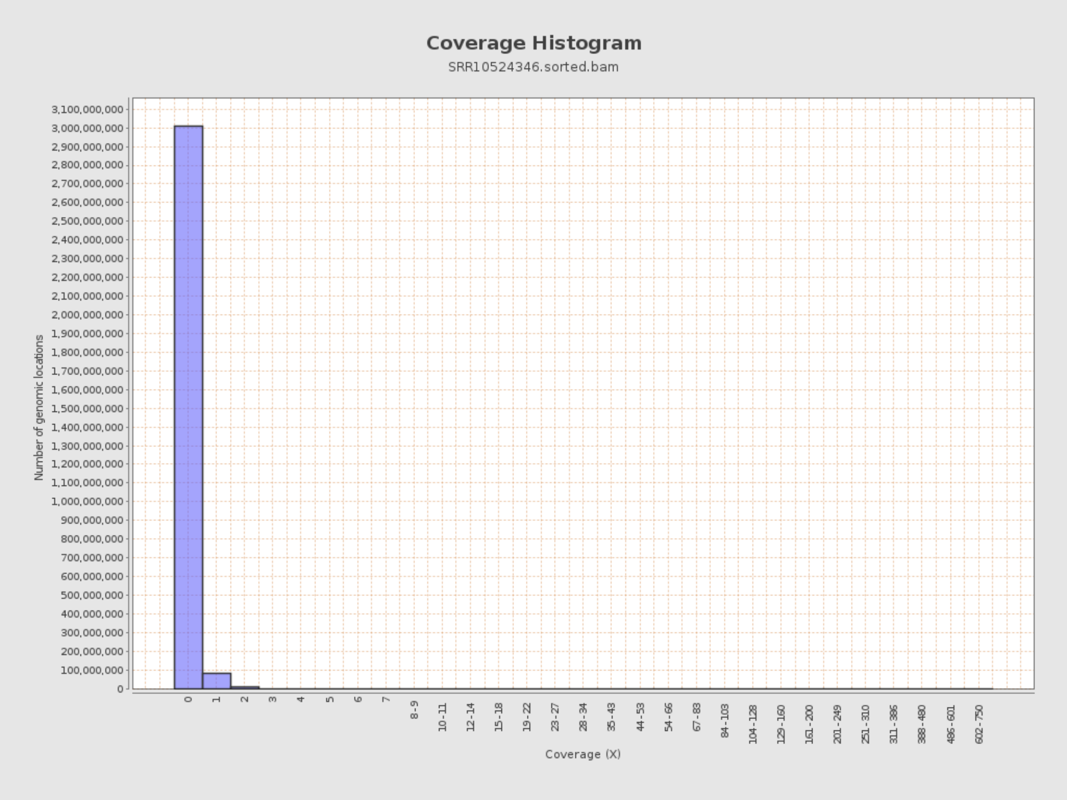
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 8634796 | 0.0346 | 0.5837 |
| chr2 | 243199373 | 6569854 | 0.027 | 0.3747 |
| chr3 | 198022430 | 6994405 | 0.0353 | 0.2063 |
| chr4 | 191154276 | 5004406 | 0.0262 | 0.2199 |
| chr5 | 180915260 | 5525121 | 0.0305 | 0.1928 |
| chr6 | 171115067 | 6478047 | 0.0379 | 0.2277 |
| chr7 | 159138663 | 4598844 | 0.0289 | 0.3471 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 10479069 | 0.0716 | 0.4023 |
| chr9 | 141213431 | 4137957 | 0.0293 | 0.2323 |
| chr10 | 135534747 | 5210903 | 0.0384 | 0.3129 |
| chr11 | 135006516 | 4900426 | 0.0363 | 0.2603 |
| chr12 | 133851895 | 3846432 | 0.0287 | 0.1891 |
| chr13 | 115169878 | 2476522 | 0.0215 | 0.1625 |
| chr14 | 107349540 | 2098246 | 0.0195 | 0.1611 |
| chr15 | 102531392 | 3133452 | 0.0306 | 0.1908 |
| chr16 | 90354753 | 3232548 | 0.0358 | 0.2198 |
| chr17 | 81195210 | 3161162 | 0.0389 | 0.2391 |
| chr18 | 78077248 | 2331175 | 0.0299 | 0.4287 |
| chr19 | 59128983 | 1801318 | 0.0305 | 0.3807 |
| chr20 | 63025520 | 2237095 | 0.0355 | 0.212 |
| chr21 | 48129895 | 1388043 | 0.0288 | 0.2254 |
| chr22 | 51304566 | 738335 | 0.0144 | 0.1309 |
| chrMT | 16571 | 5294 | 0.3195 | 0.5975 |
| chrX | 155270560 | 4727258 | 0.0304 | 0.2115 |
| chrY | 59373566 | 316926 | 0.0053 | 0.1785 |

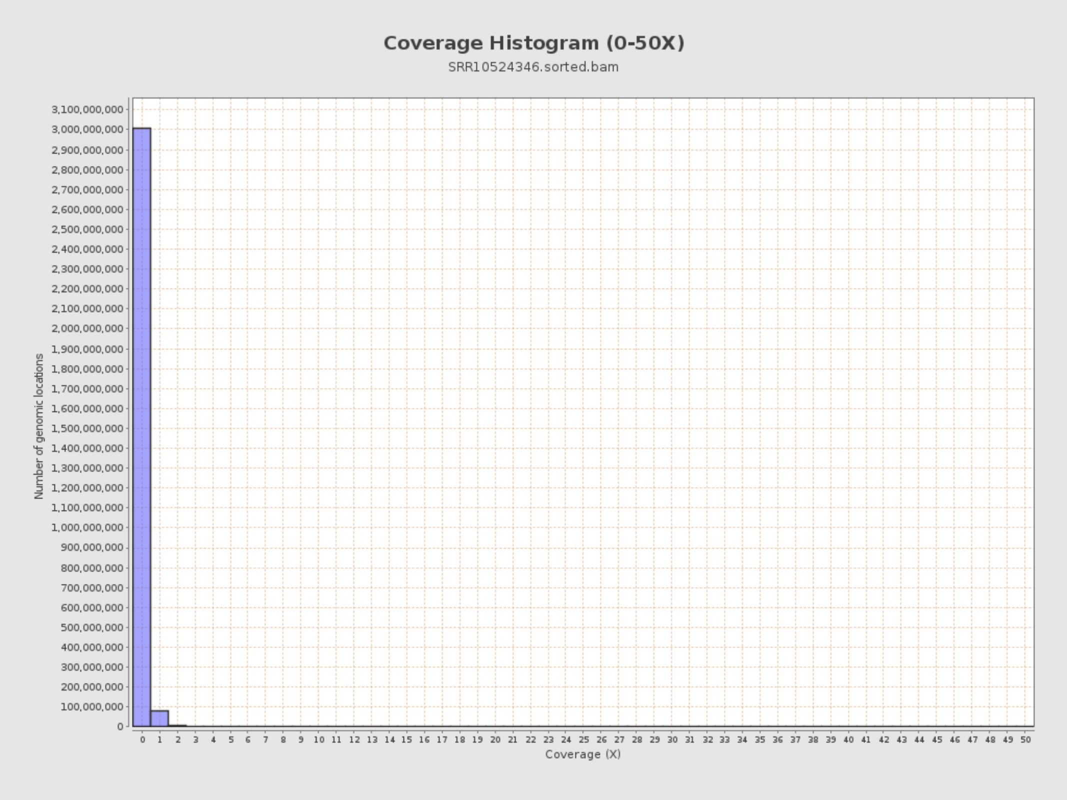
# 3. Results : Coverage across reference



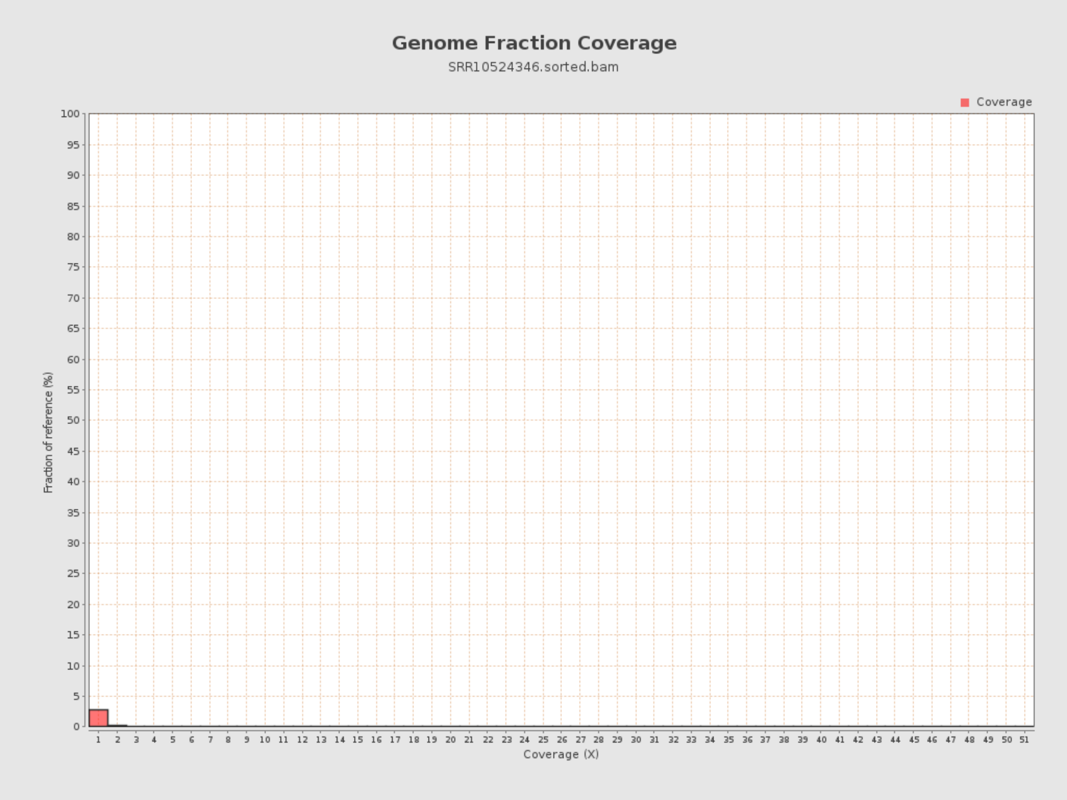
# 4. Results : Coverage Histogram



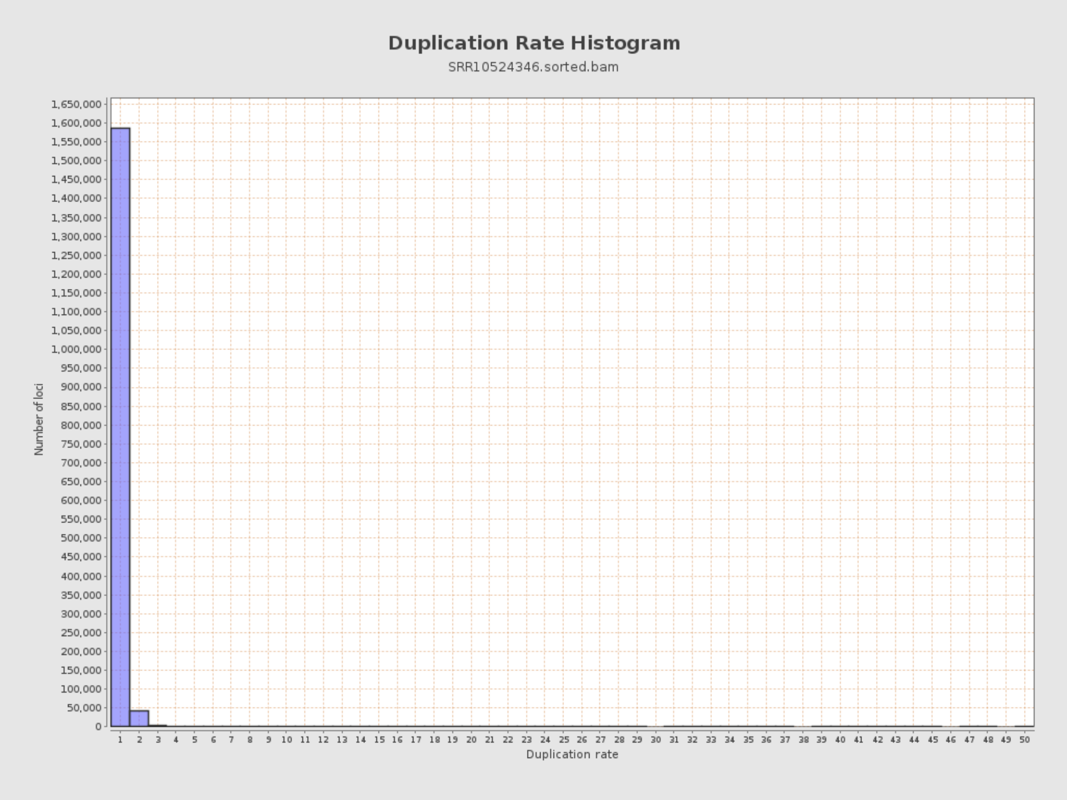
# 5. Results : Coverage Histogram (0-50X)



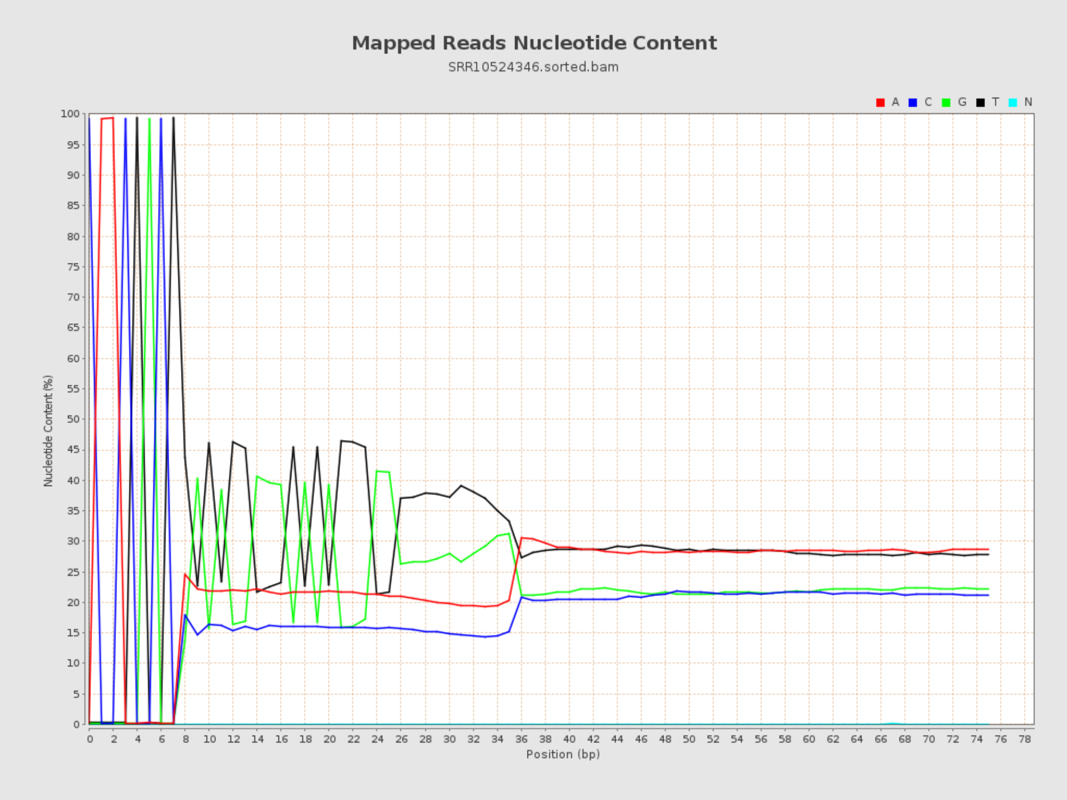
# 6. Results : Genome Fraction Coverage



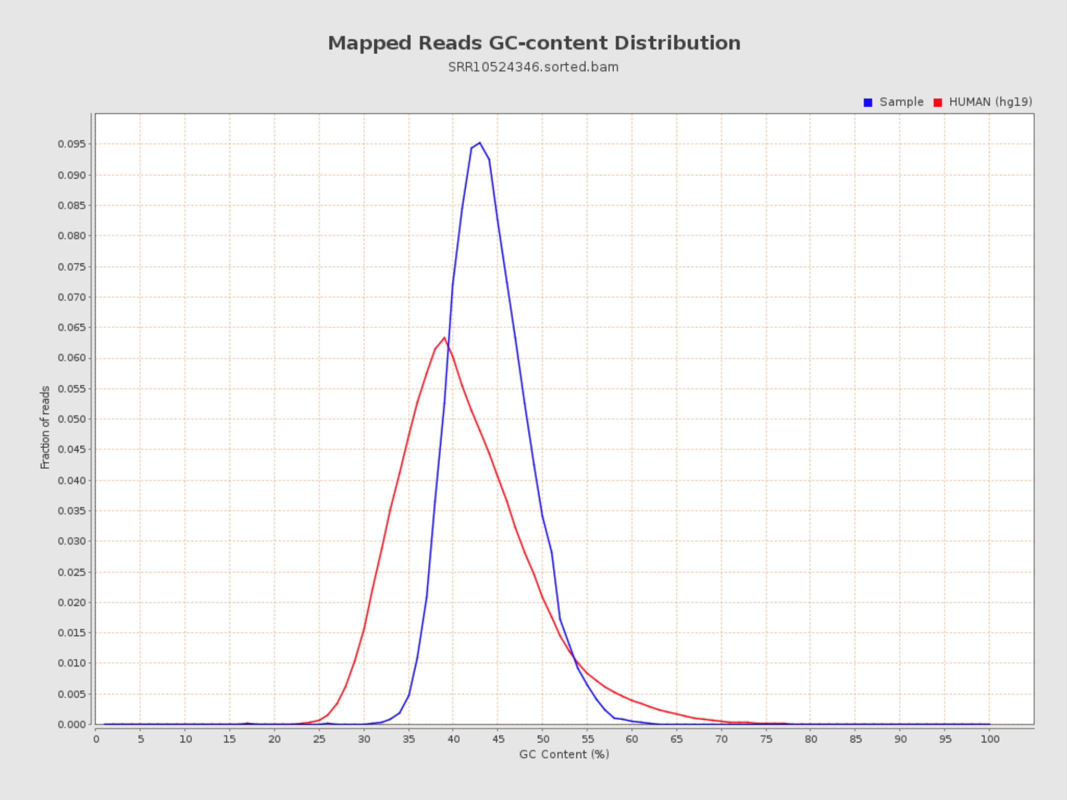
# 7. Results : Duplication Rate Histogram



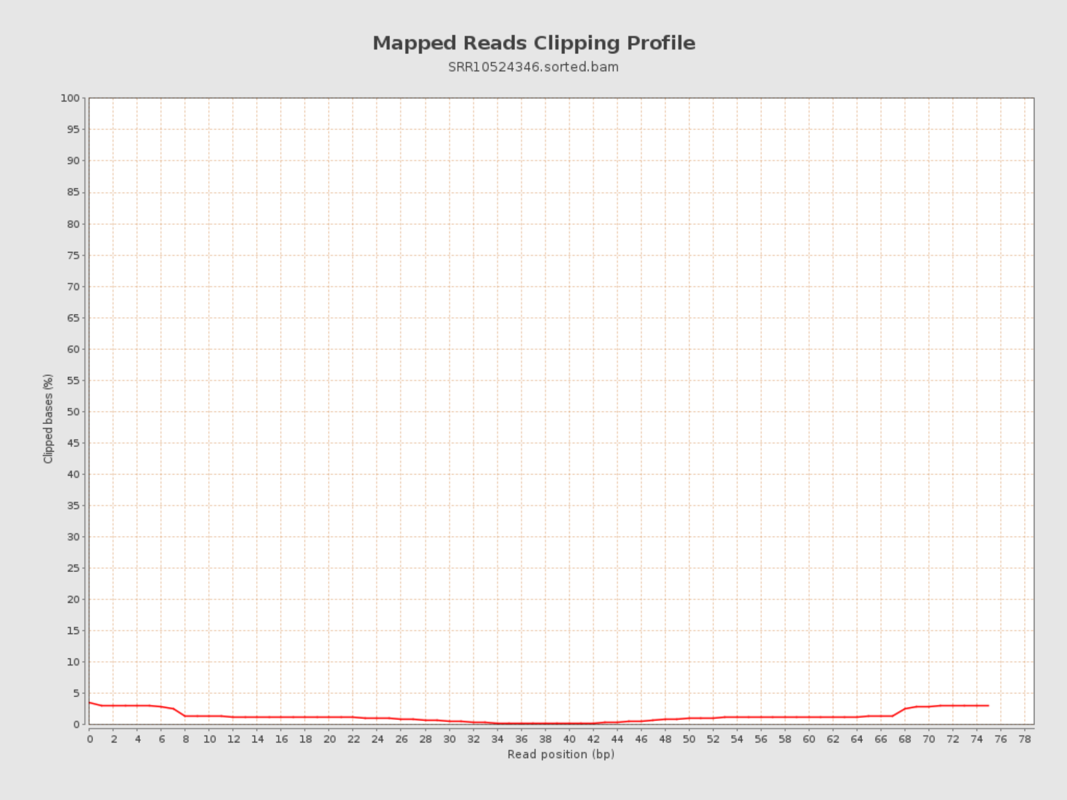
# 8. Results : Mapped Reads Nucleotide Content



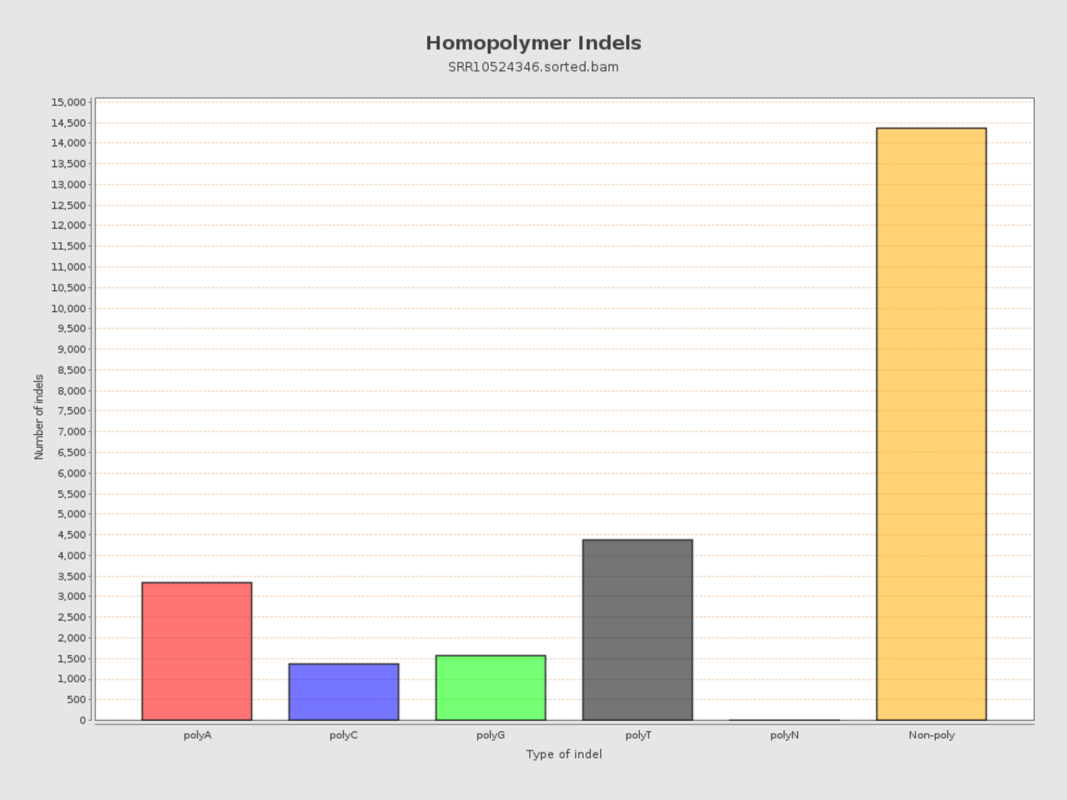
# 9. Results : Mapped Reads GC-content Distribution



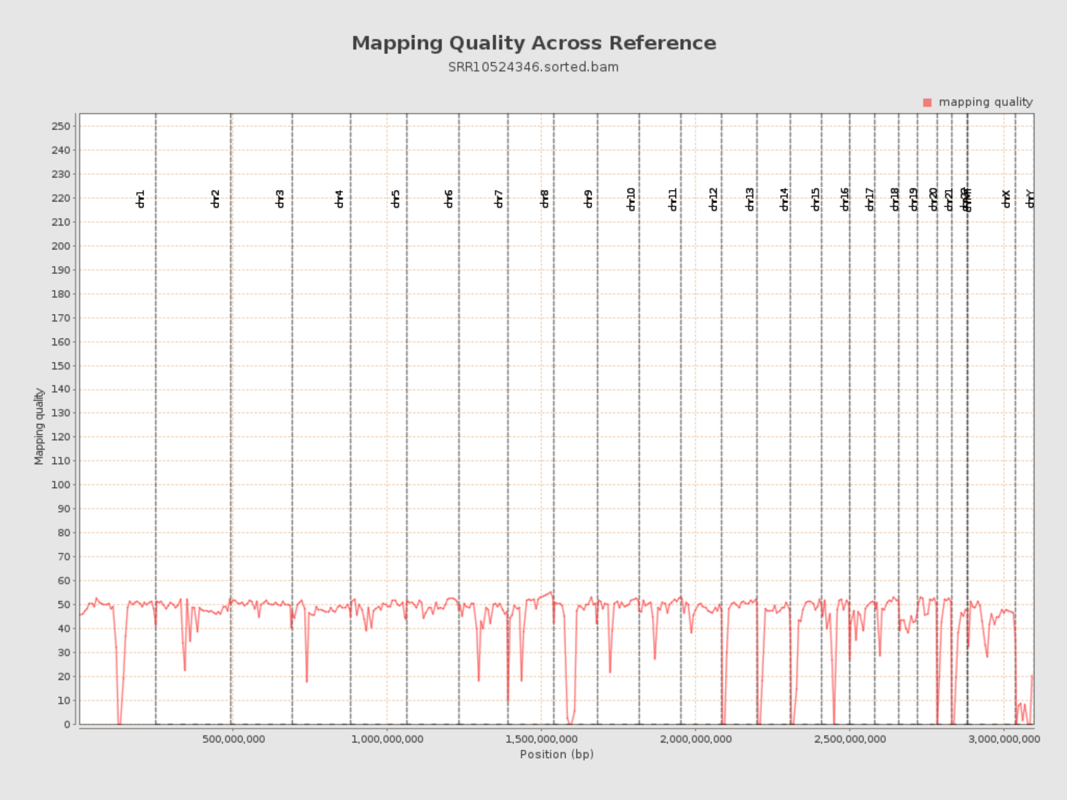
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram