# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/23 21:02:27*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819083.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_SRR1819083 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819083.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 23 21:02:25 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1819083.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,354,064 |
| Mapped reads | 1,242,607 / 91.77% |
| Unmapped reads | 111,457 / 8.23% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 5,266 / 0.39% |
| Read min/max/mean length | 30 / 76 / 76.13 |
| Duplicated reads (estimated) | 44,671 / 3.3% |
| Duplication rate | 2.6% |
| Clipped reads | 1,245,439 / 91.98% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 18,212,864 / 24.94% |
| Number/percentage of C's | 13,902,777 / 19.04% |
| Number/percentage of T's | 23,156,668 / 31.72% |
| Number/percentage of G's | 17,740,026 / 24.3% |
| Number/percentage of N's | 972 / 0% |
| GC Percentage | 43.34% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0236 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2486 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.21 |

## 2.5. Mismatches and indels

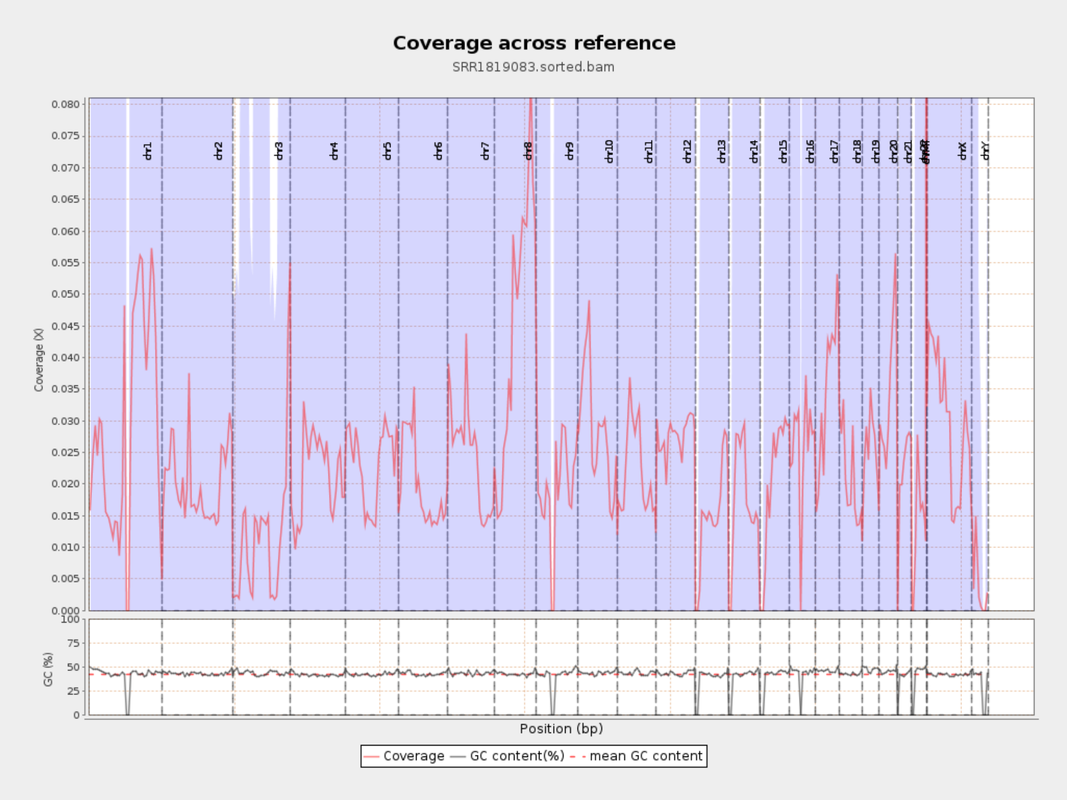
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 369,696 |
| Insertions | 4,731 |
| Mapped reads with at least one insertion | 0.38% |
| Deletions | 13,015 |
| Mapped reads with at least one deletion | 1.04% |
| Homopolymer indels | 43.24% |

## 2.6. Chromosome stats

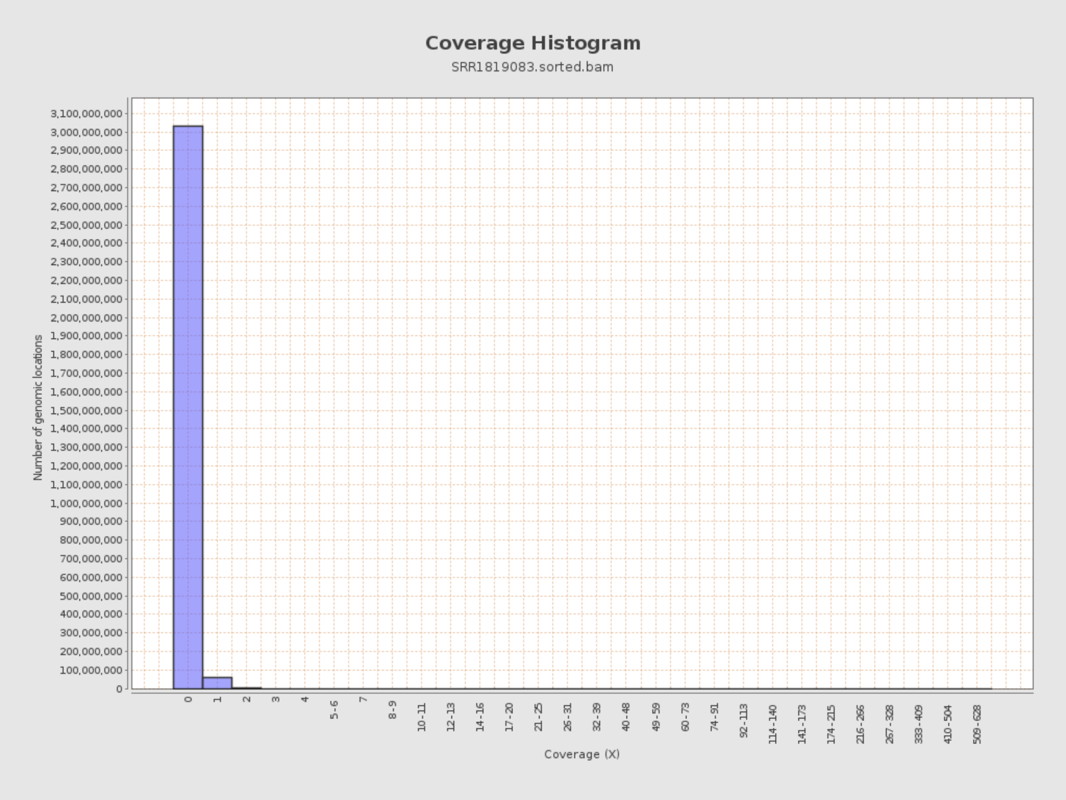
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 7342030 | 0.0295 | 0.4768 |
| chr2 | 243199373 | 4927750 | 0.0203 | 0.2573 |
| chr3 | 198022430 | 2186353 | 0.011 | 0.1171 |
| chr4 | 191154276 | 4093363 | 0.0214 | 0.1728 |
| chr5 | 180915260 | 4229929 | 0.0234 | 0.1652 |
| chr6 | 171115067 | 3394657 | 0.0198 | 0.19 |
| chr7 | 159138663 | 3921640 | 0.0246 | 0.3165 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6712738 | 0.0459 | 0.2738 |
| chr9 | 141213431 | 2618605 | 0.0185 | 0.1925 |
| chr10 | 135534747 | 3905337 | 0.0288 | 0.2497 |
| chr11 | 135006516 | 3015779 | 0.0223 | 0.2586 |
| chr12 | 133851895 | 3704597 | 0.0277 | 0.1796 |
| chr13 | 115169878 | 1745815 | 0.0152 | 0.1332 |
| chr14 | 107349540 | 1869362 | 0.0174 | 0.1473 |
| chr15 | 102531392 | 2100751 | 0.0205 | 0.1552 |
| chr16 | 90354753 | 2342401 | 0.0259 | 0.1878 |
| chr17 | 81195210 | 2864335 | 0.0353 | 0.2193 |
| chr18 | 78077248 | 1644242 | 0.0211 | 0.4049 |
| chr19 | 59128983 | 1527246 | 0.0258 | 0.3069 |
| chr20 | 63025520 | 2215623 | 0.0352 | 0.2041 |
| chr21 | 48129895 | 1055197 | 0.0219 | 0.1738 |
| chr22 | 51304566 | 673671 | 0.0131 | 0.1233 |
| chrMT | 16571 | 8575 | 0.5175 | 0.7557 |
| chrX | 155270560 | 4687080 | 0.0302 | 0.2087 |
| chrY | 59373566 | 247995 | 0.0042 | 0.1264 |

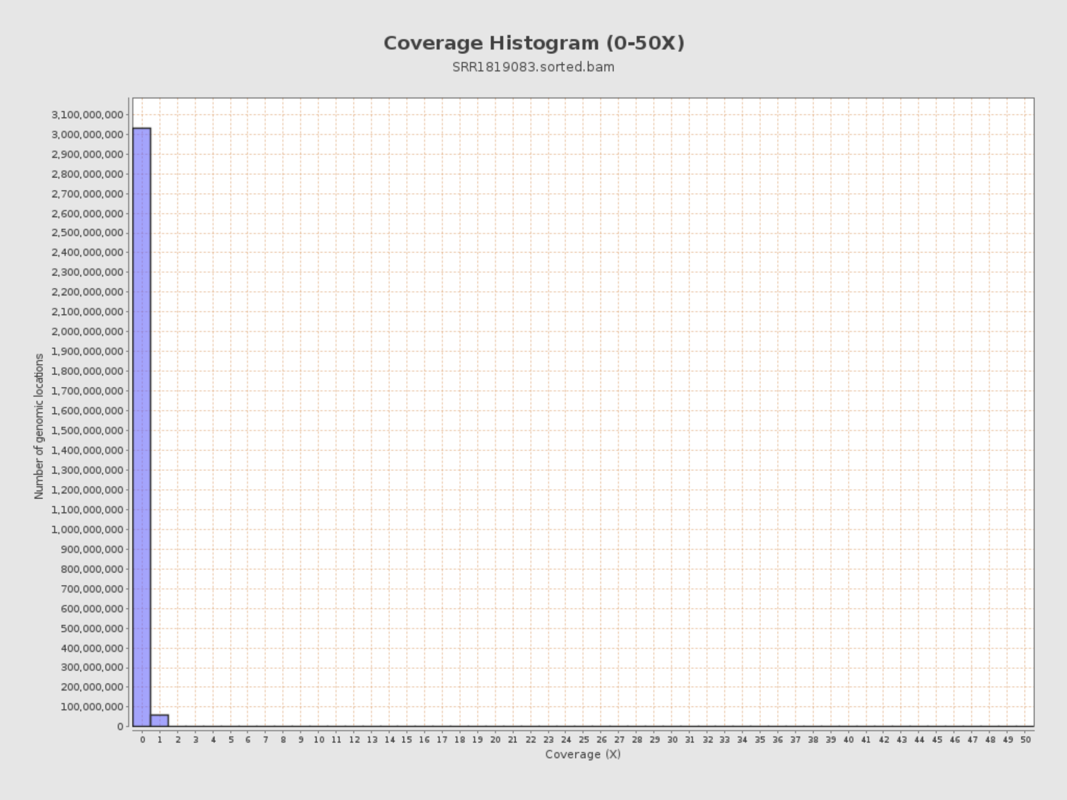
# 3. Results : Coverage across reference



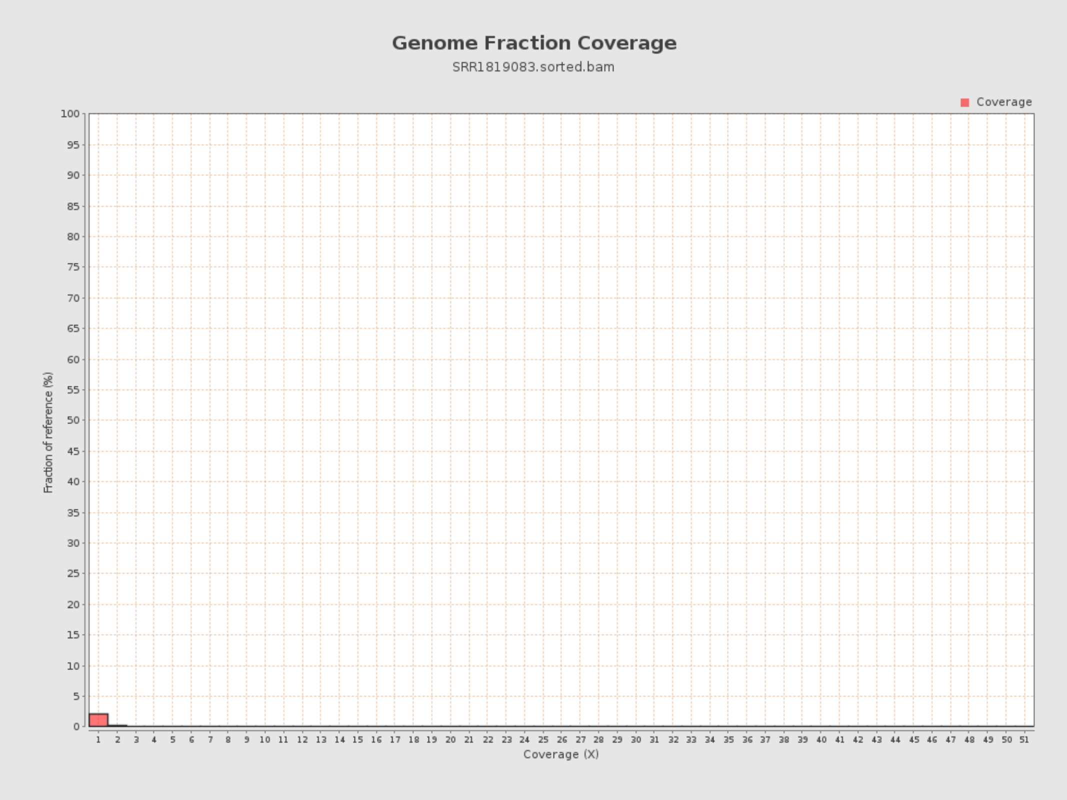
# 4. Results : Coverage Histogram



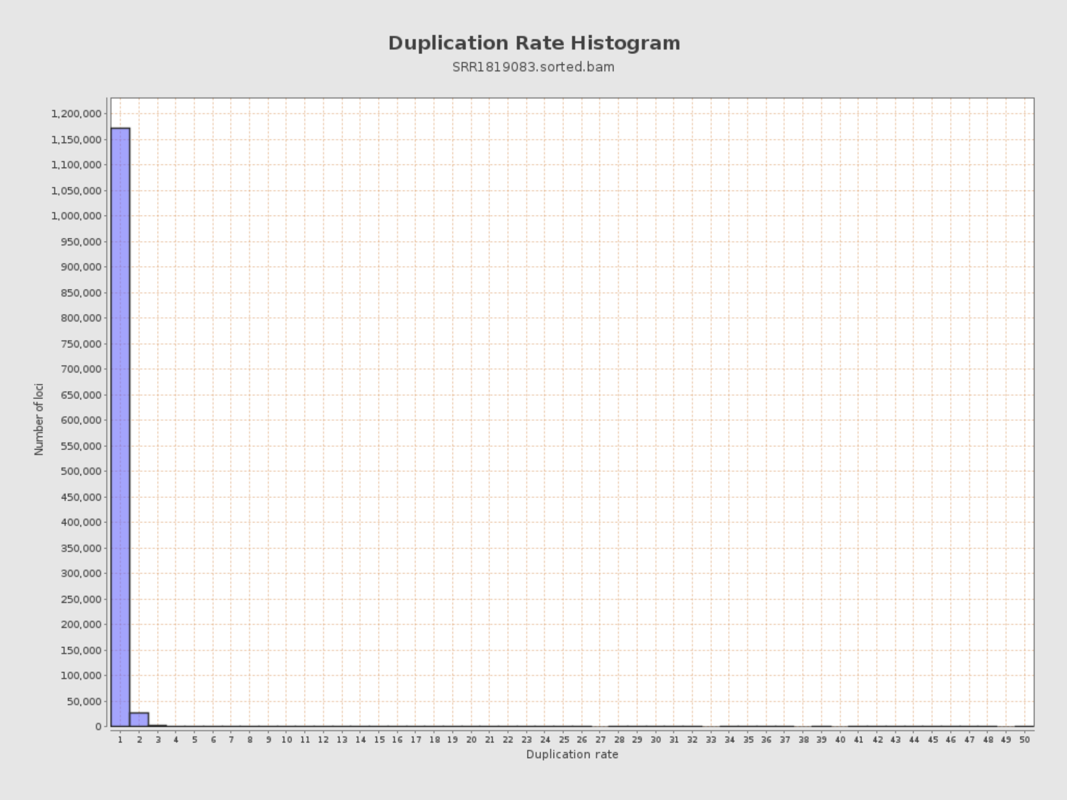
# 5. Results : Coverage Histogram (0-50X)



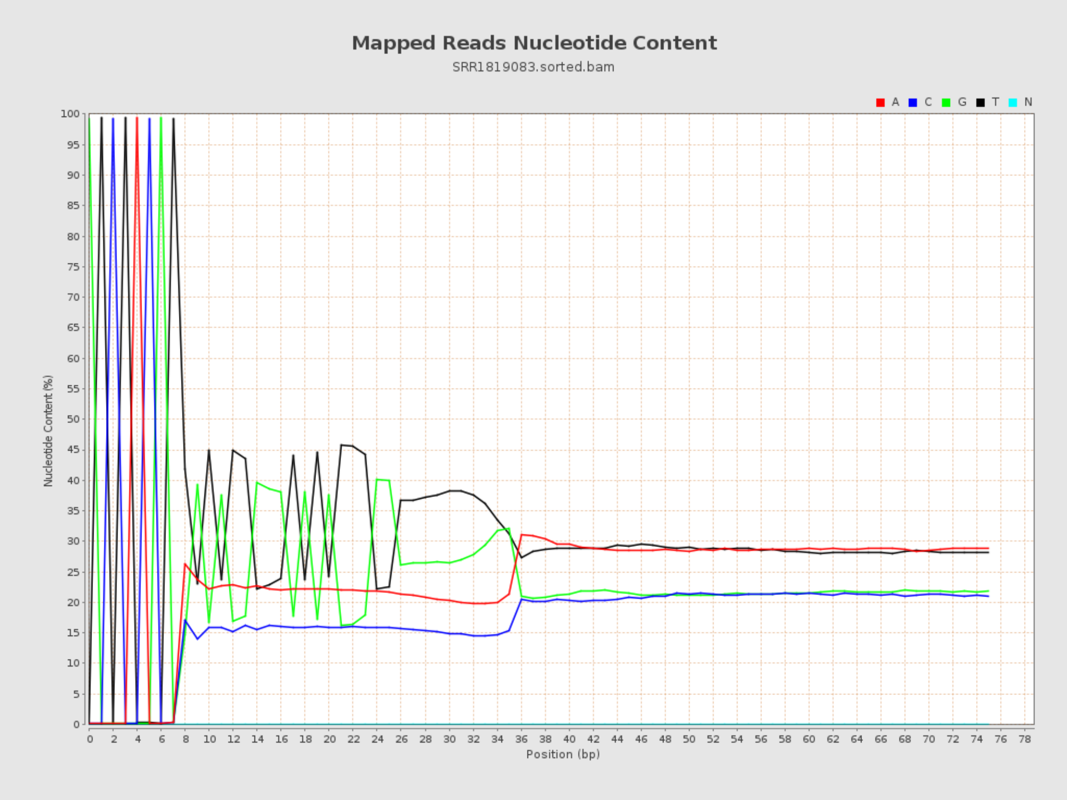
# 6. Results : Genome Fraction Coverage



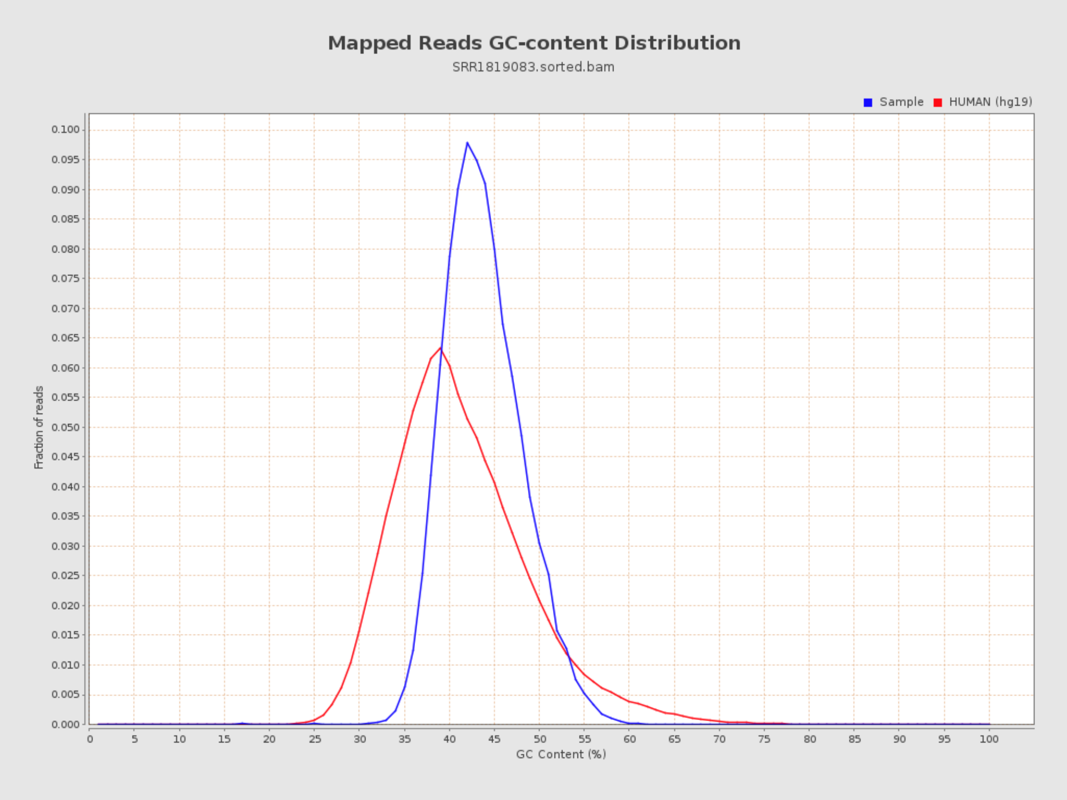
# 7. Results : Duplication Rate Histogram



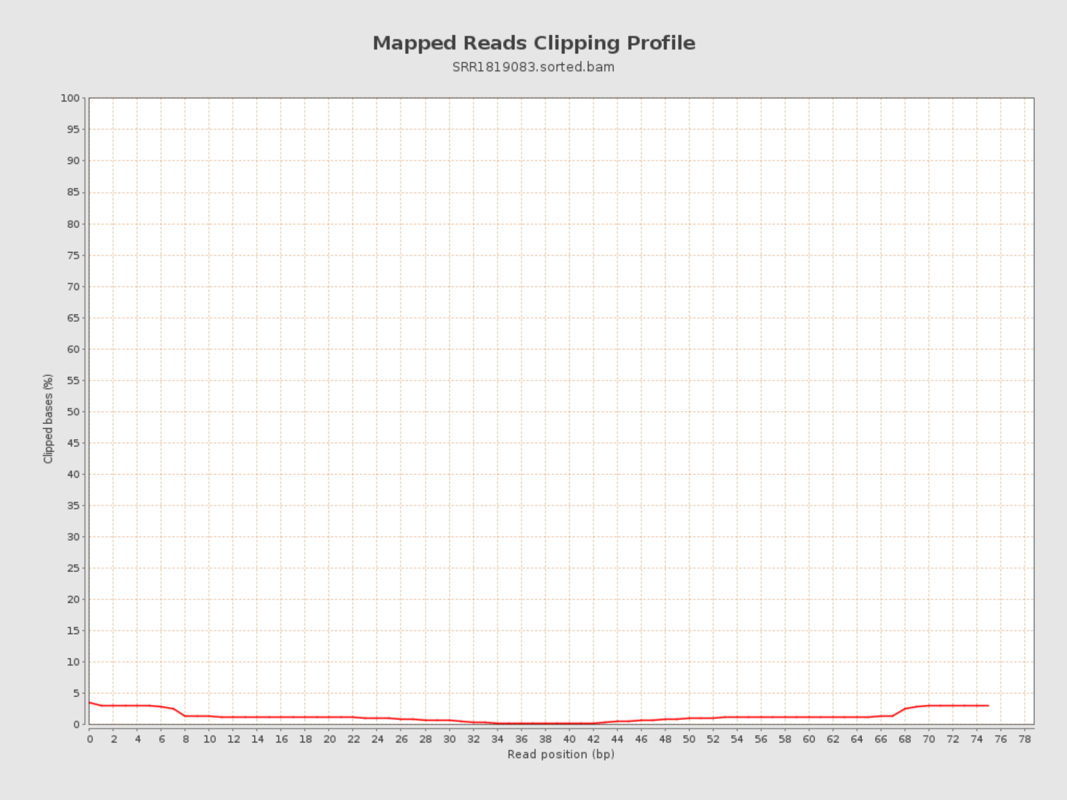
# 8. Results : Mapped Reads Nucleotide Content



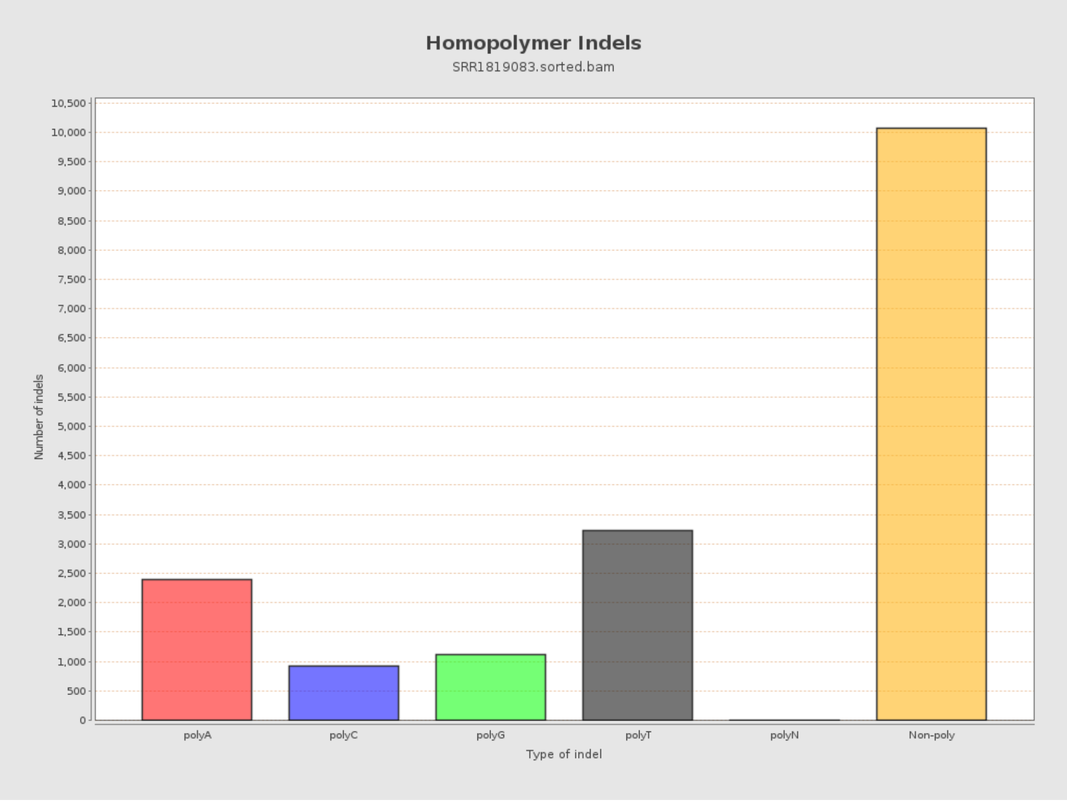
# 9. Results : Mapped Reads GC-content Distribution



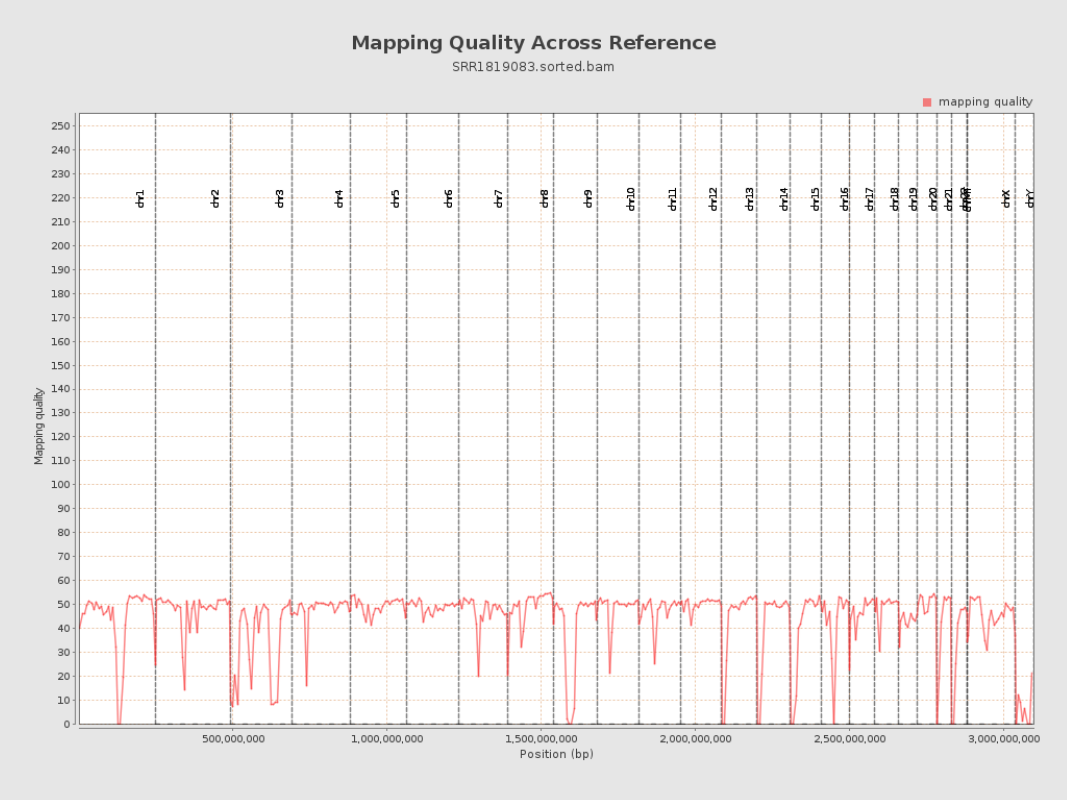
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram