# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 21:09:07*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751214.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_SRR8751214 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751214.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Aug 26 21:09:06 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR8751214.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,645,166 |
| Mapped reads | 3,197,888 / 68.84% |
| Unmapped reads | 1,447,278 / 31.16% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 177,154 / 3.81% |
| Read min/max/mean length | 30 / 101 / 102.58 |
| Duplicated reads (estimated) | 125,024 / 2.69% |
| Duplication rate | 1.8% |
| Clipped reads | 761,503 / 16.39% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 93,338,925 / 29.69% |
| Number/percentage of C's | 63,905,395 / 20.32% |
| Number/percentage of T's | 93,834,221 / 29.84% |
| Number/percentage of G's | 63,347,693 / 20.15% |
| Number/percentage of N's | 2,225 / 0% |
| GC Percentage | 40.47% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1016 |
| | |

| | |
|---|---|
| Standard Deviation | 1.5214 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 50.96 |

## 2.5. Mismatches and indels

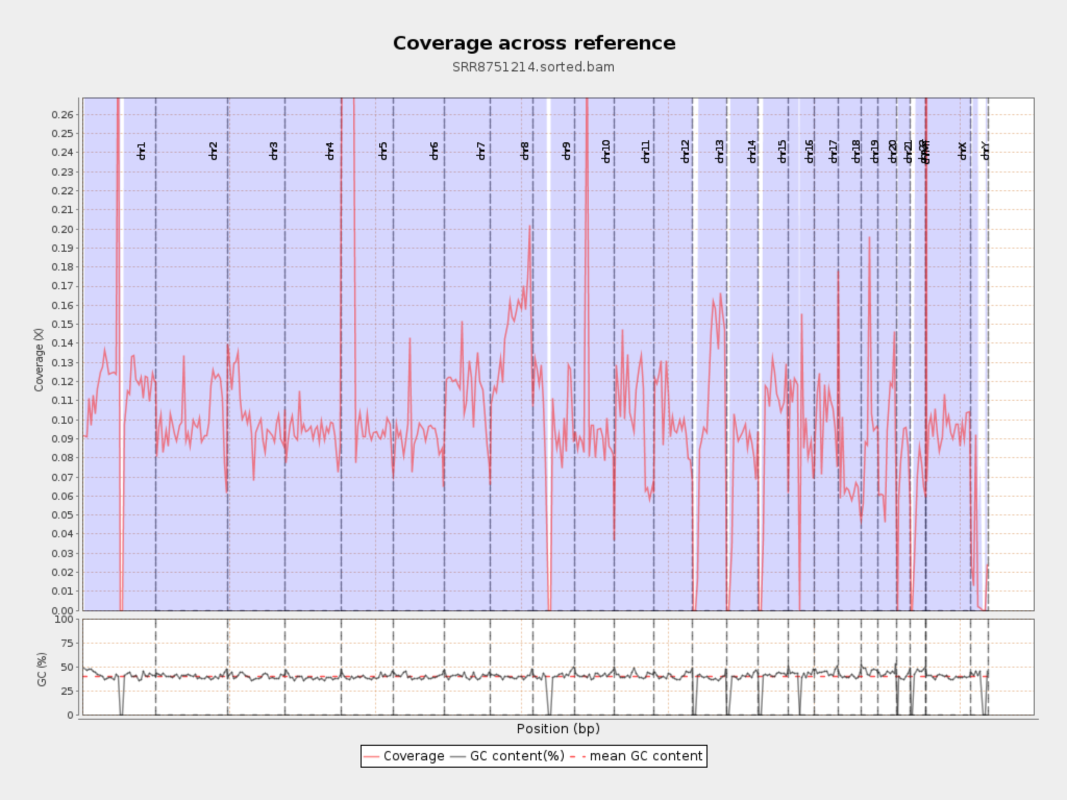
| | |
|---|---|
| General error rate | 0.48% |
| Mismatches | 1,295,882 |
| Insertions | 159,000 |
| Mapped reads with at least one insertion | 4.81% |
| Deletions | 48,085 |
| Mapped reads with at least one deletion | 1.47% |
| Homopolymer indels | 51.14% |

## 2.6. Chromosome stats

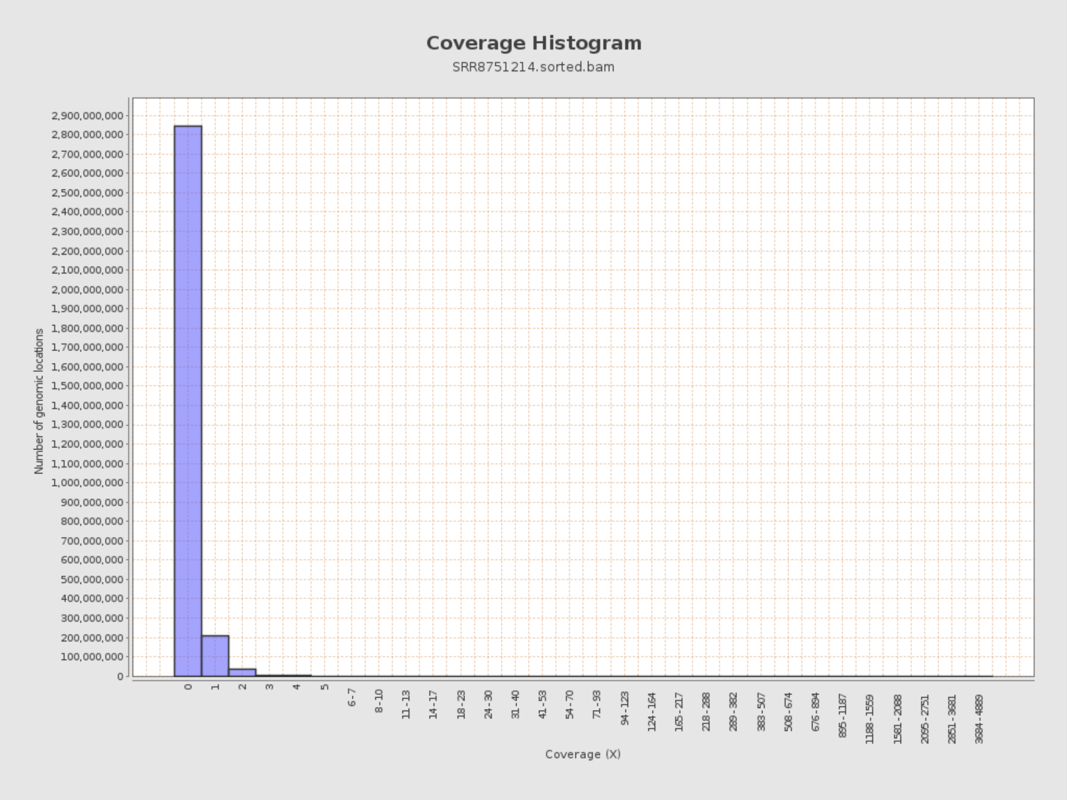
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 29205628 | 0.1172 | 4.5173 |
| chr2 | 243199373 | 24055655 | 0.0989 | 0.5622 |
| chr3 | 198022430 | 20181413 | 0.1019 | 0.4461 |
| chr4 | 191154276 | 17857909 | 0.0934 | 0.4334 |
| chr5 | 180915260 | 27123210 | 0.1499 | 0.4947 |
| chr6 | 171115067 | 15840016 | 0.0926 | 0.6008 |
| chr7 | 159138663 | 18293174 | 0.115 | 0.8606 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 21449415 | 0.1465 | 1.0009 |
| chr9 | 141213431 | 13193139 | 0.0934 | 0.6575 |
| chr10 | 135534747 | 13733404 | 0.1013 | 1.7785 |
| chr11 | 135006516 | 13836482 | 0.1025 | 0.594 |
| chr12 | 133851895 | 13693643 | 0.1023 | 0.3938 |
| chr13 | 115169878 | 12334220 | 0.1071 | 0.3815 |
| chr14 | 107349540 | 7994642 | 0.0745 | 0.3473 |
| chr15 | 102531392 | 9609104 | 0.0937 | 0.3569 |
| chr16 | 90354753 | 8451230 | 0.0935 | 0.6931 |
| chr17 | 81195210 | 8373066 | 0.1031 | 0.5591 |
| chr18 | 78077248 | 5530611 | 0.0708 | 1.5665 |
| chr19 | 59128983 | 5912569 | 0.1 | 3.1628 |
| chr20 | 63025520 | 5617938 | 0.0891 | 0.3652 |
| chr21 | 48129895 | 3481643 | 0.0723 | 0.3674 |
| chr22 | 51304566 | 2627386 | 0.0512 | 0.2658 |
| chrMT | 16571 | 240523 | 14.5147 | 14.2758 |
| chrX | 155270560 | 14751370 | 0.095 | 0.4233 |
| chrY | 59373566 | 1148468 | 0.0193 | 0.9112 |

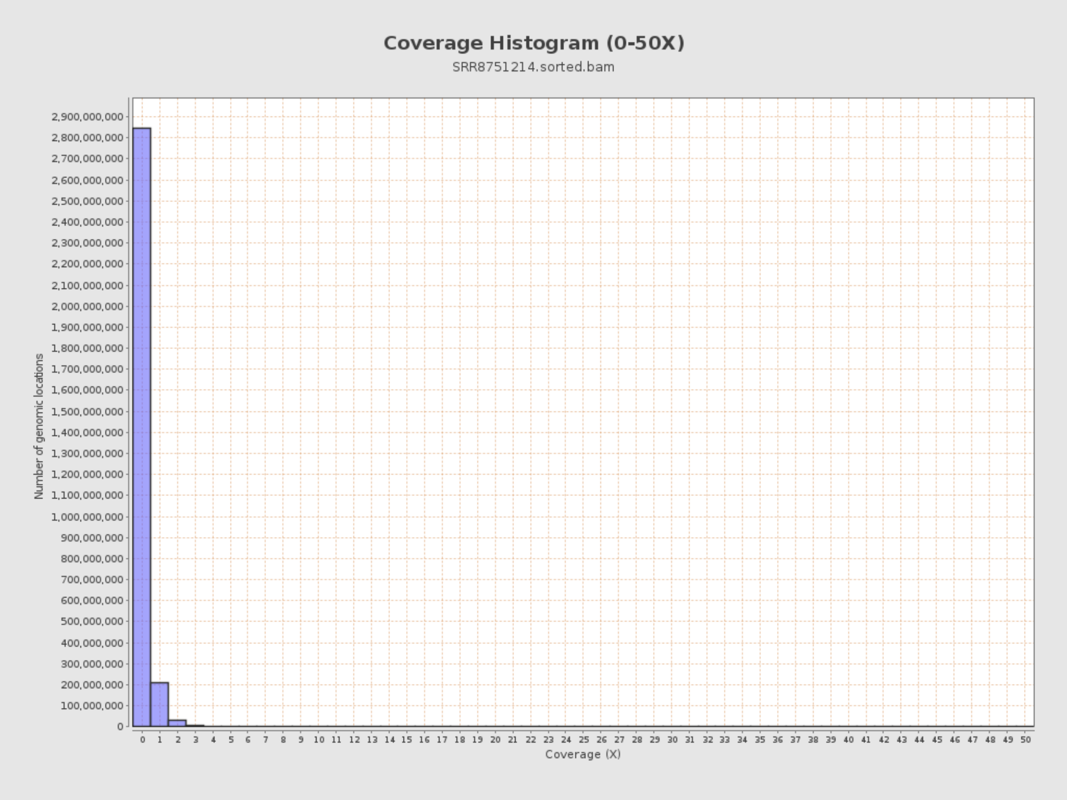
# 3. Results : Coverage across reference



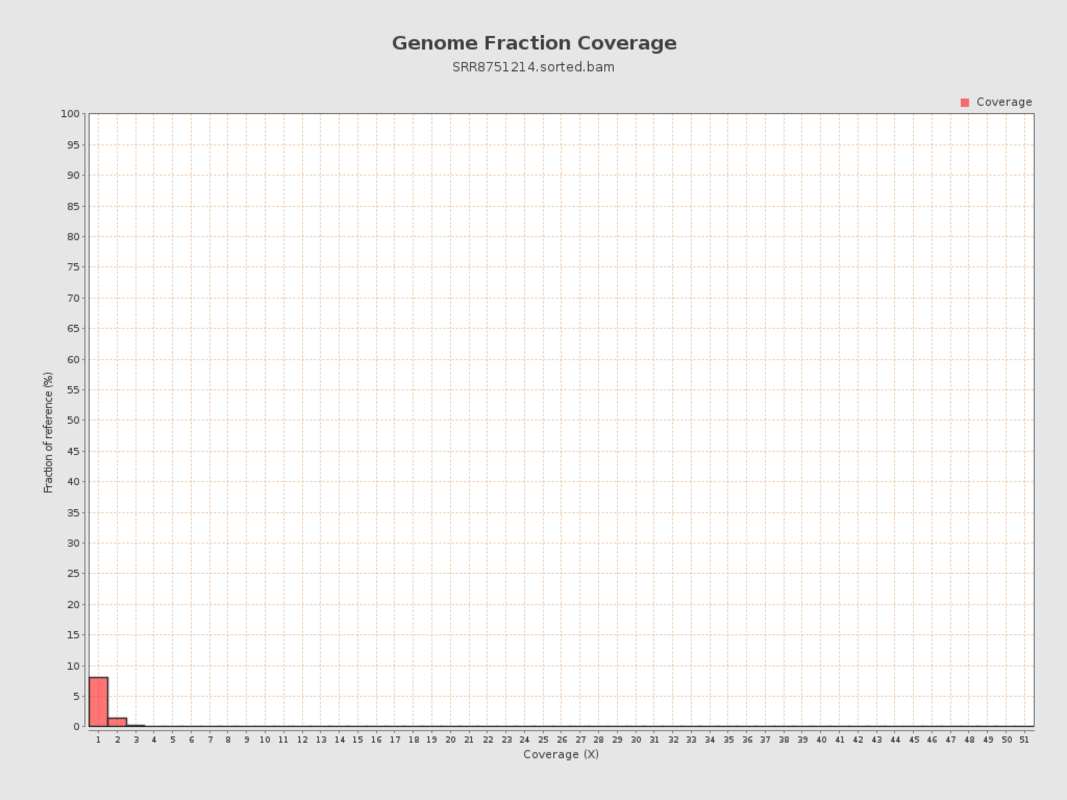
# 4. Results : Coverage Histogram



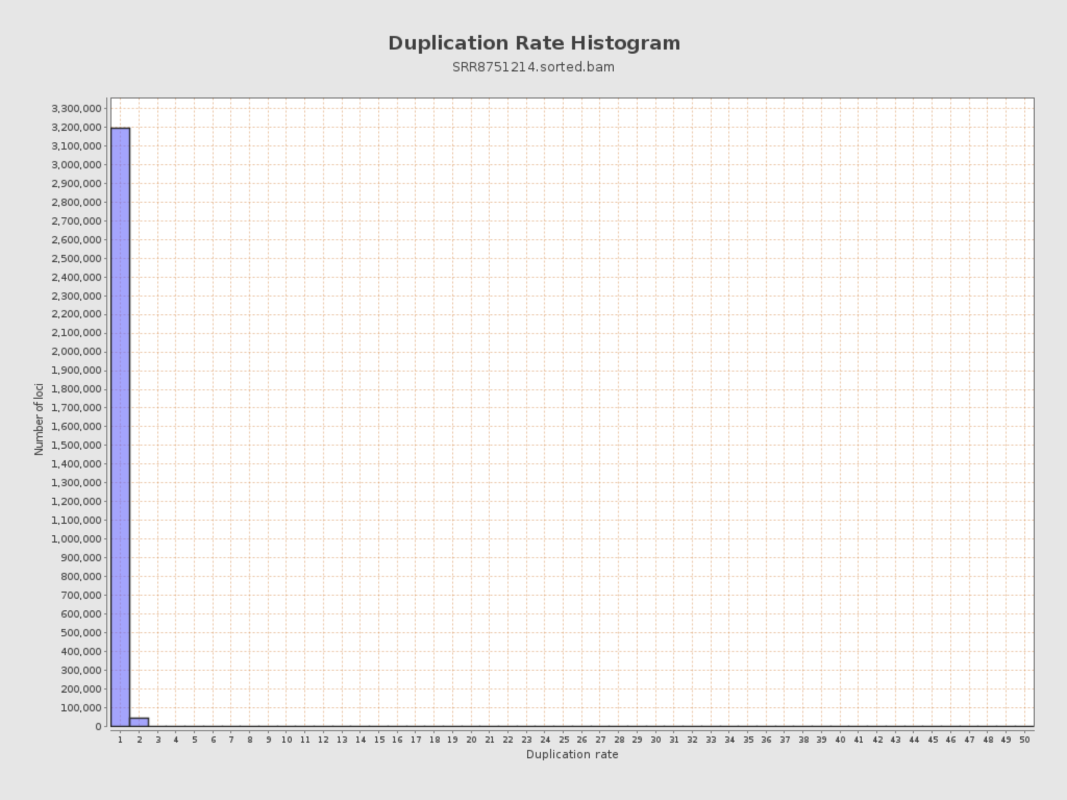
# 5. Results : Coverage Histogram (0-50X)



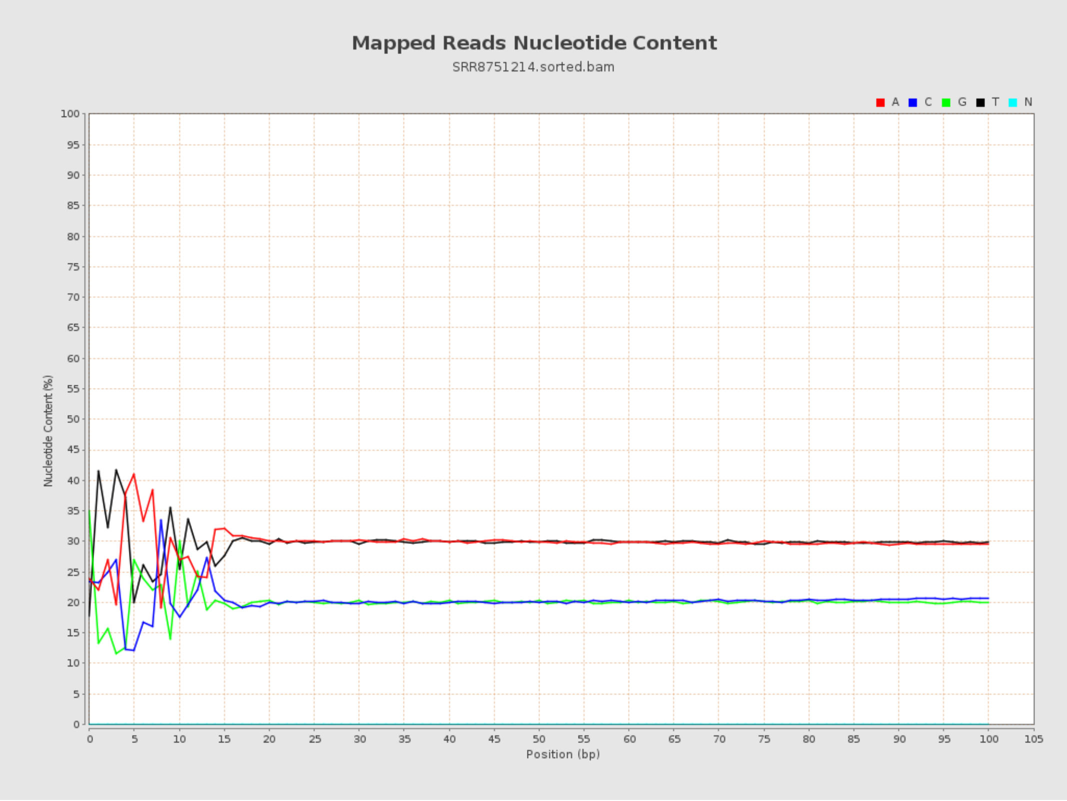
# 6. Results : Genome Fraction Coverage



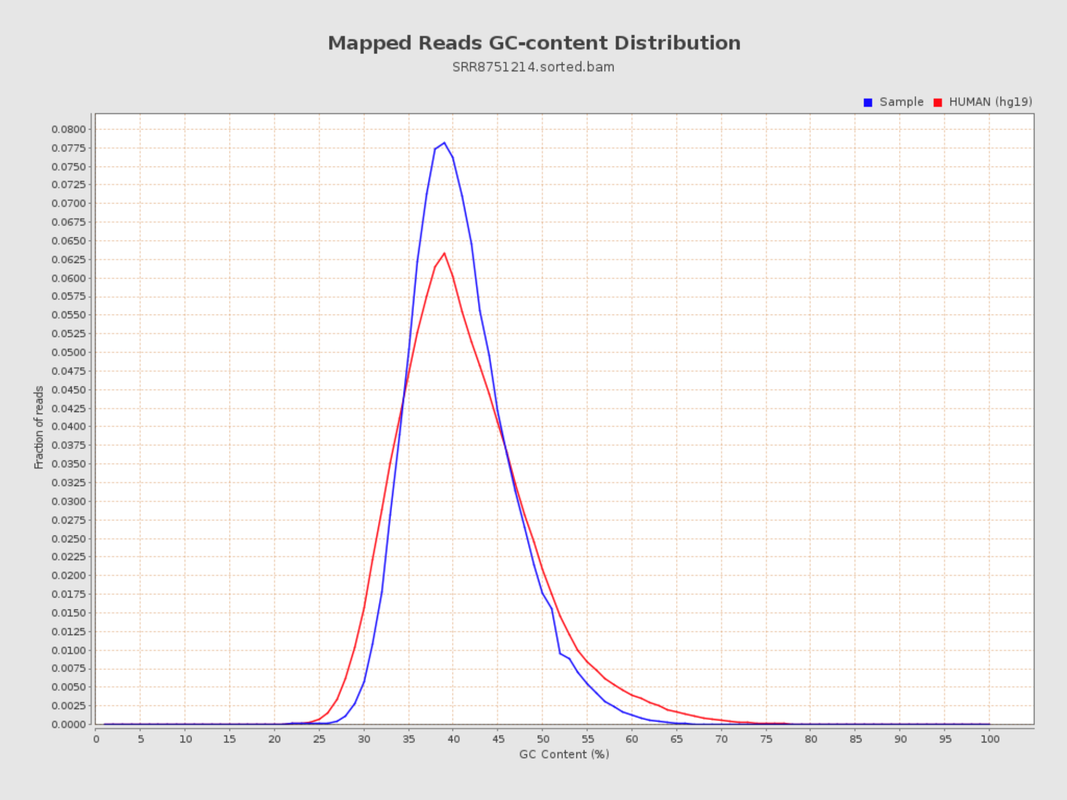
# 7. Results : Duplication Rate Histogram



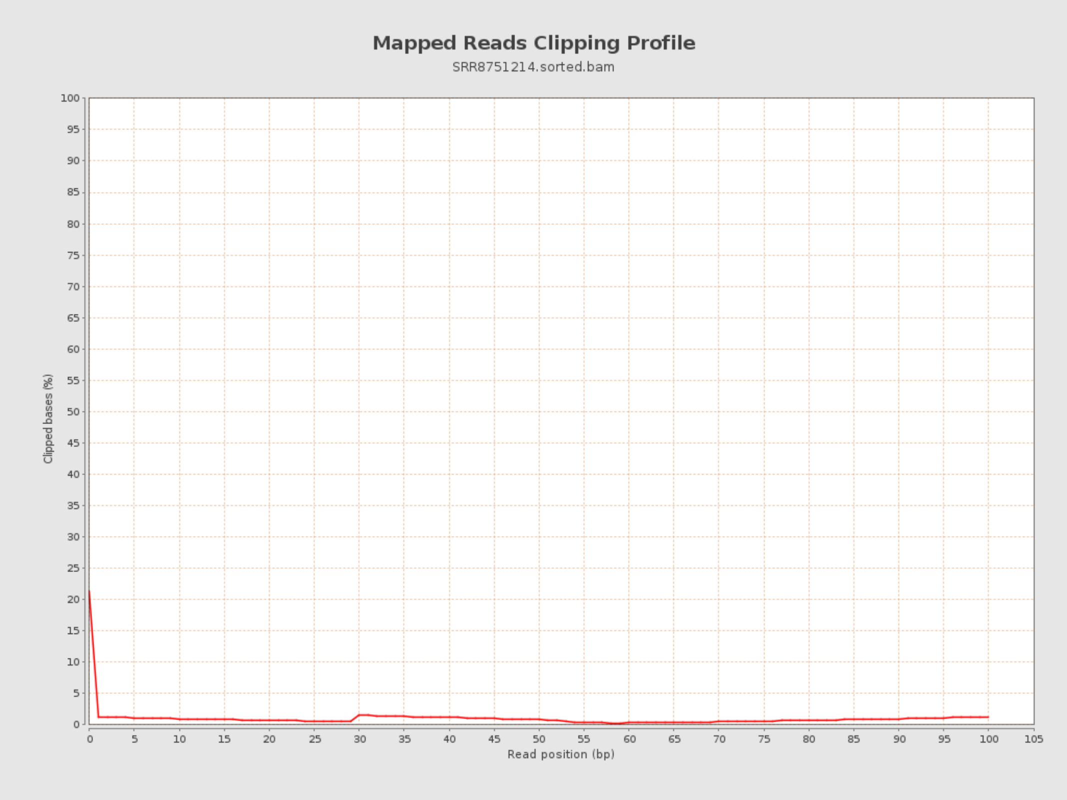
# 8. Results : Mapped Reads Nucleotide Content



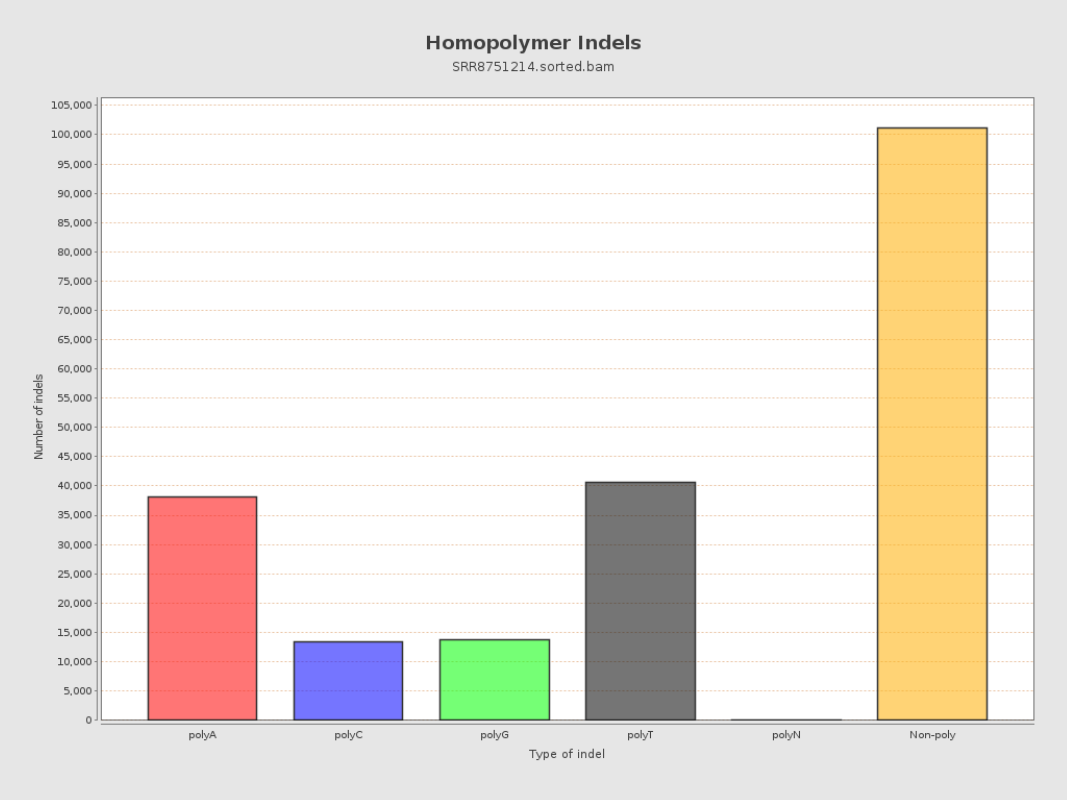
# 9. Results : Mapped Reads GC-content Distribution



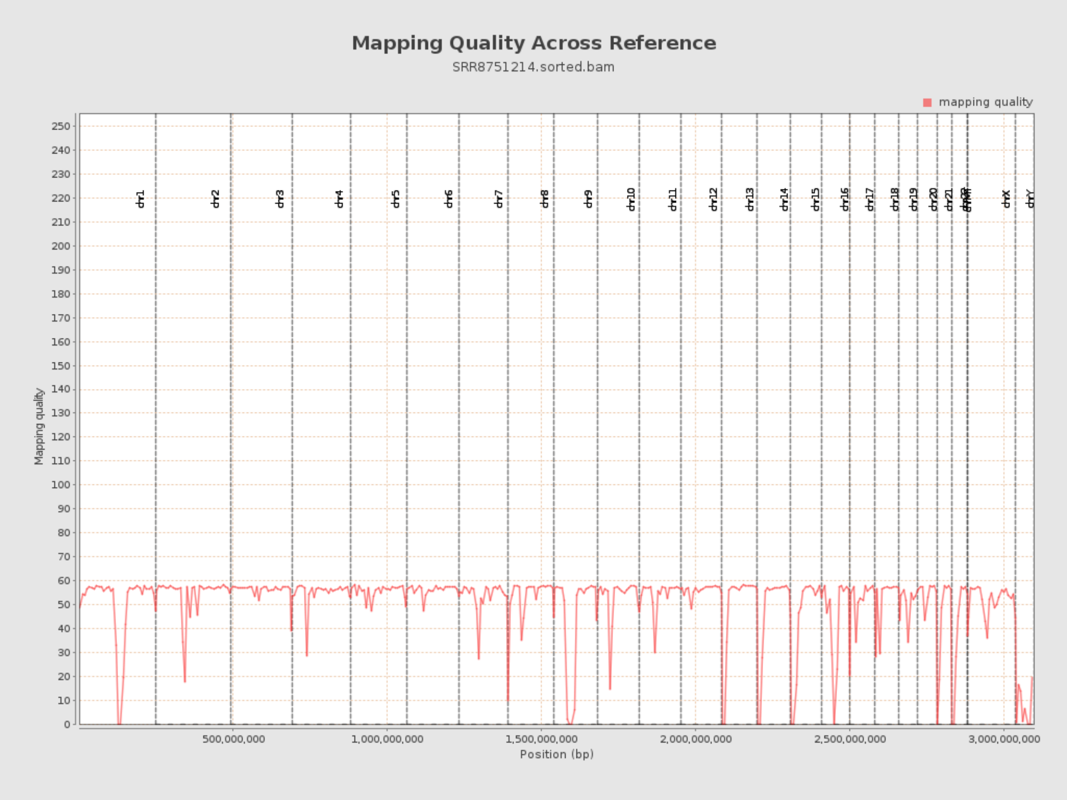
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram