# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 15:05:36*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751171.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_SRR8751171 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751171.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Aug 26 15:05:35 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR8751171.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,551,272 |
| Mapped reads | 4,350,934 / 95.6% |
| Unmapped reads | 200,338 / 4.4% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 149,818 / 3.29% |
| Read min/max/mean length | 30 / 101 / 102.36 |
| Duplicated reads (estimated) | 97,254 / 2.14% |
| Duplication rate | 1.37% |
| Clipped reads | 791,384 / 17.39% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 124,197,620 / 28.99% |
| Number/percentage of C's | 90,005,782 / 21.01% |
| Number/percentage of T's | 124,889,931 / 29.16% |
| Number/percentage of G's | 89,255,451 / 20.84% |
| Number/percentage of N's | 2,371 / 0% |
| GC Percentage | 41.85% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1384 |
| | |

| | |
|---|---|
| Standard Deviation | 0.9709 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 51.33 |

## 2.5. Mismatches and indels

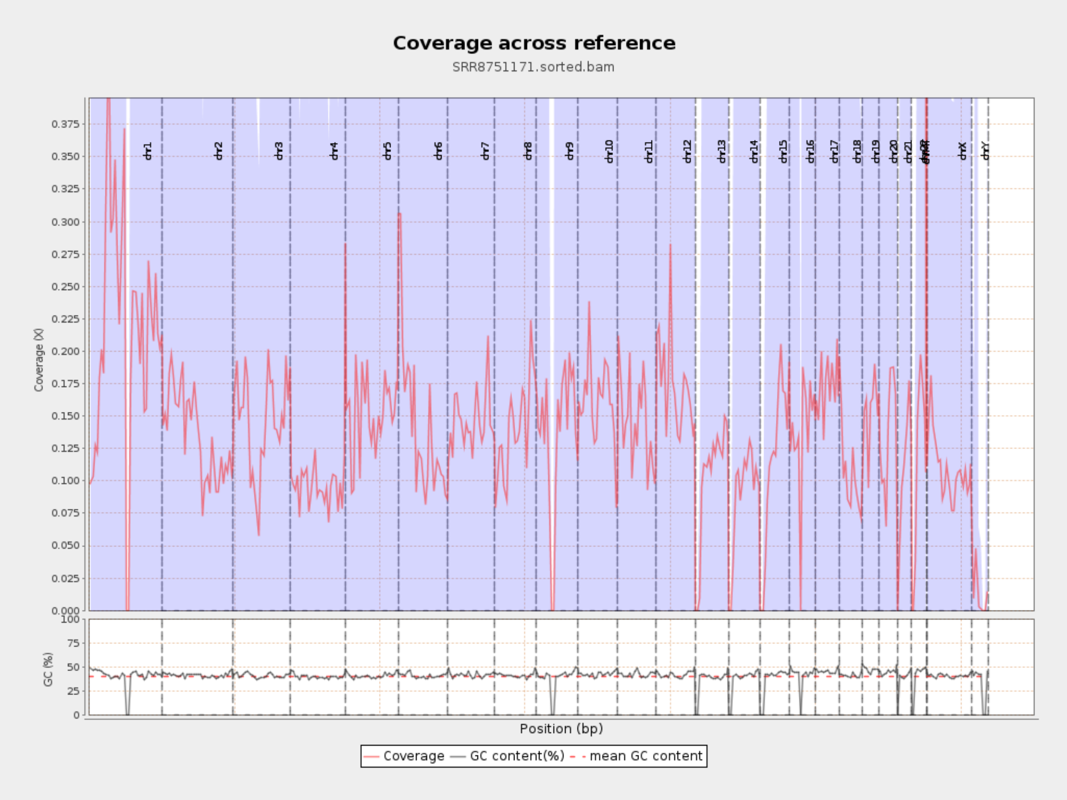
| | |
|---|---|
| General error rate | 0.4% |
| Mismatches | 1,478,201 |
| Insertions | 157,036 |
| Mapped reads with at least one insertion | 3.52% |
| Deletions | 58,019 |
| Mapped reads with at least one deletion | 1.31% |
| Homopolymer indels | 51.08% |

## 2.6. Chromosome stats

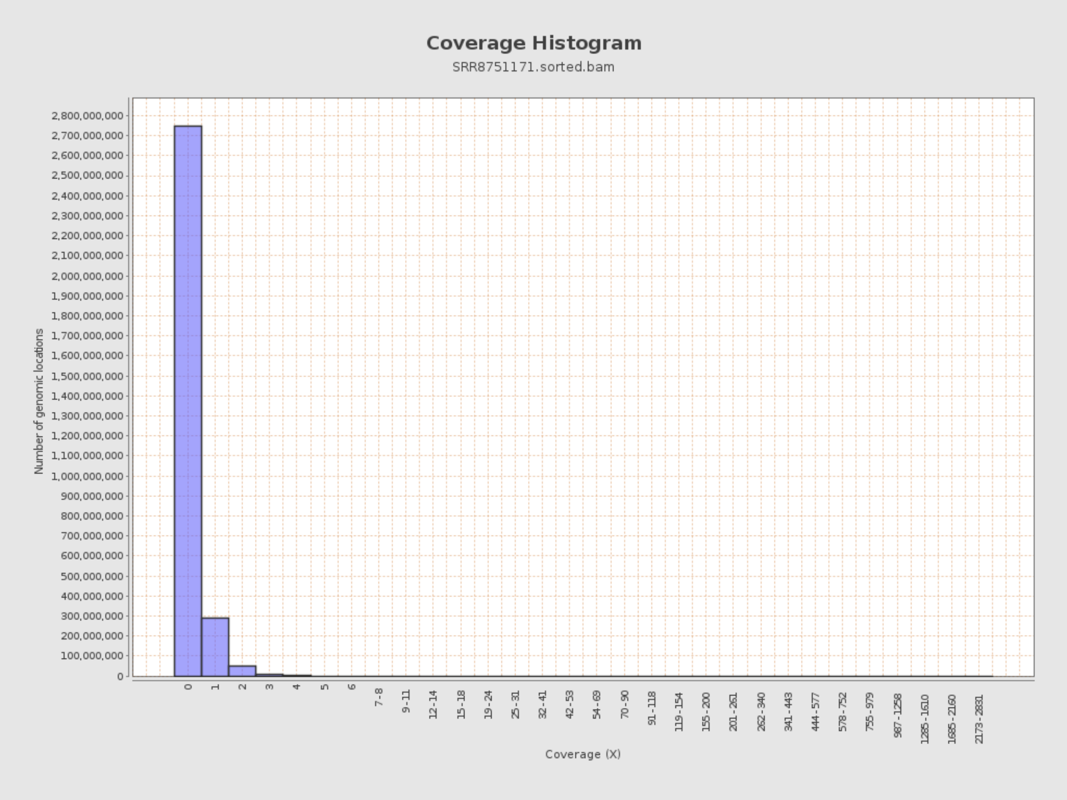
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 53846444 | 0.216 | 2.6409 |
| chr2 | 243199373 | 32947845 | 0.1355 | 0.4998 |
| chr3 | 198022430 | 28752943 | 0.1452 | 0.4456 |
| chr4 | 191154276 | 18199988 | 0.0952 | 0.3948 |
| chr5 | 180915260 | 27513014 | 0.1521 | 0.4426 |
| chr6 | 171115067 | 24444447 | 0.1429 | 0.709 |
| chr7 | 159138663 | 23358476 | 0.1468 | 0.6487 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 20594414 | 0.1407 | 0.4694 |
| chr9 | 141213431 | 19180214 | 0.1358 | 0.5543 |
| chr10 | 135534747 | 21954213 | 0.162 | 1.2834 |
| chr11 | 135006516 | 19614634 | 0.1453 | 0.5571 |
| chr12 | 133851895 | 23455841 | 0.1752 | 0.4784 |
| chr13 | 115169878 | 11692872 | 0.1015 | 0.3605 |
| chr14 | 107349540 | 9517798 | 0.0887 | 0.348 |
| chr15 | 102531392 | 11800457 | 0.1151 | 0.3862 |
| chr16 | 90354753 | 12269241 | 0.1358 | 0.6288 |
| chr17 | 81195210 | 14091656 | 0.1736 | 0.6194 |
| chr18 | 78077248 | 8295033 | 0.1062 | 0.8723 |
| chr19 | 59128983 | 8968235 | 0.1517 | 1.7833 |
| chr20 | 63025520 | 8397534 | 0.1332 | 0.4213 |
| chr21 | 48129895 | 5133016 | 0.1066 | 0.3982 |
| chr22 | 51304566 | 5686494 | 0.1108 | 0.3854 |
| chrMT | 16571 | 977673 | 58.999 | 23.2904 |
| chrX | 155270560 | 17009482 | 0.1095 | 0.4041 |
| chrY | 59373566 | 776697 | 0.0131 | 0.416 |

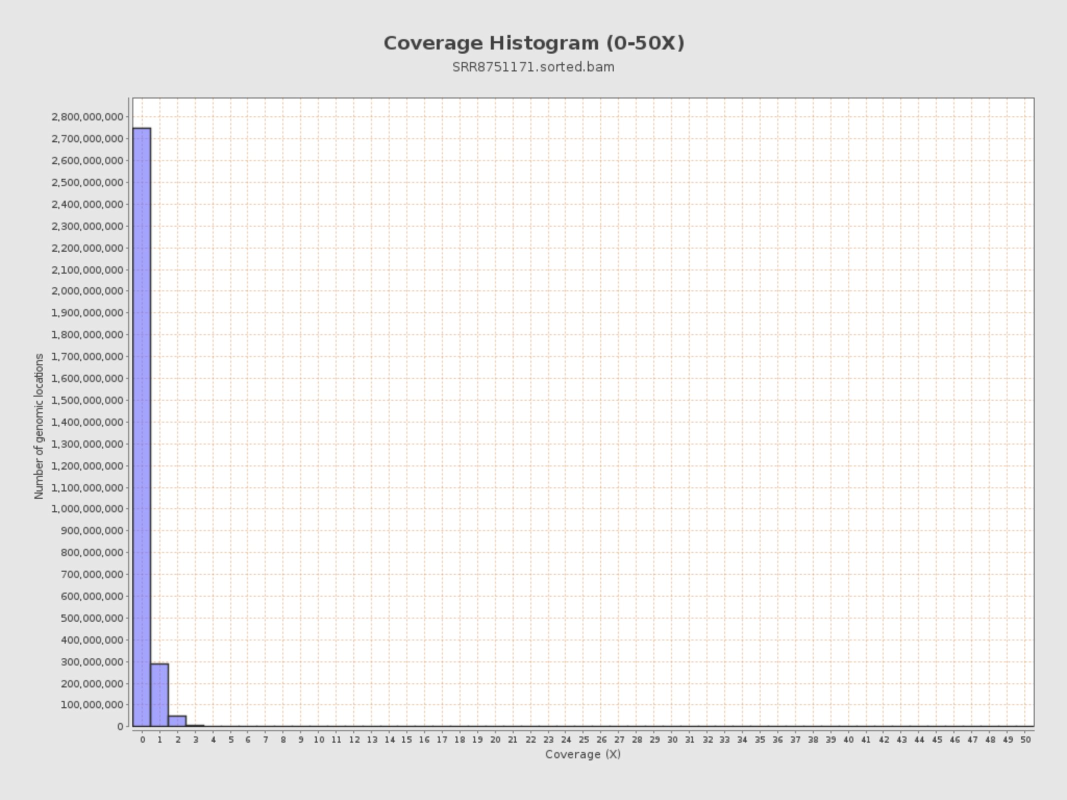
# 3. Results : Coverage across reference



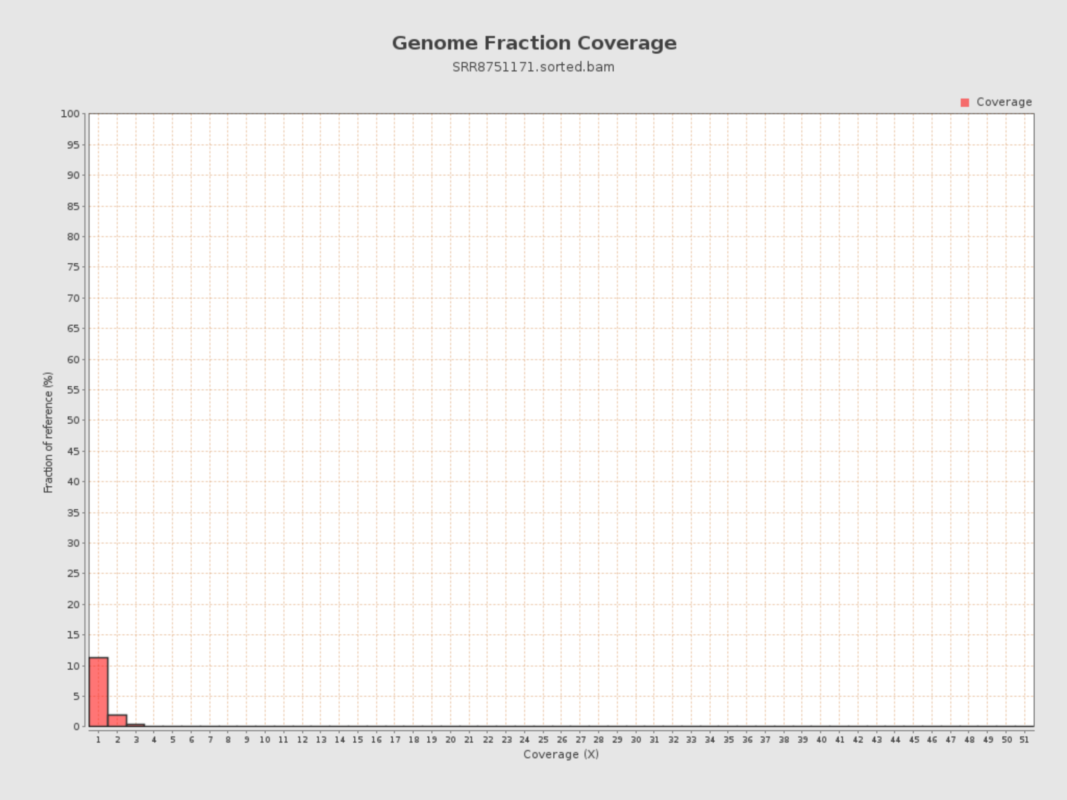
# 4. Results : Coverage Histogram



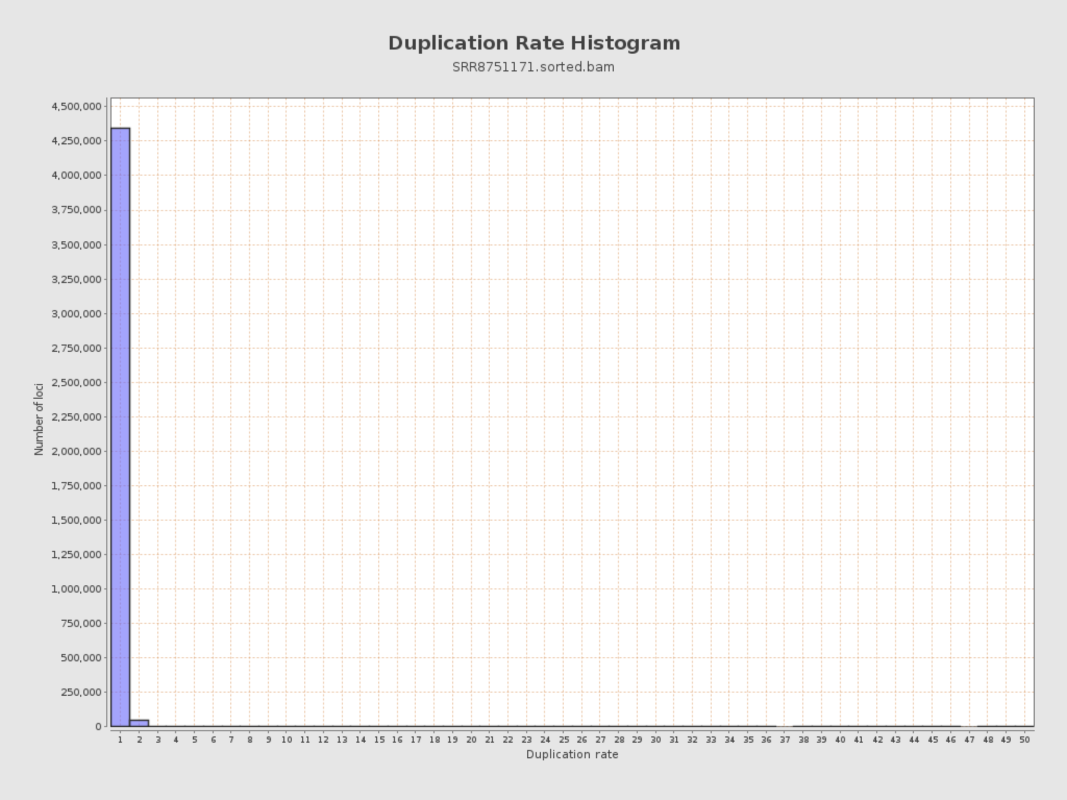
# 5. Results : Coverage Histogram (0-50X)



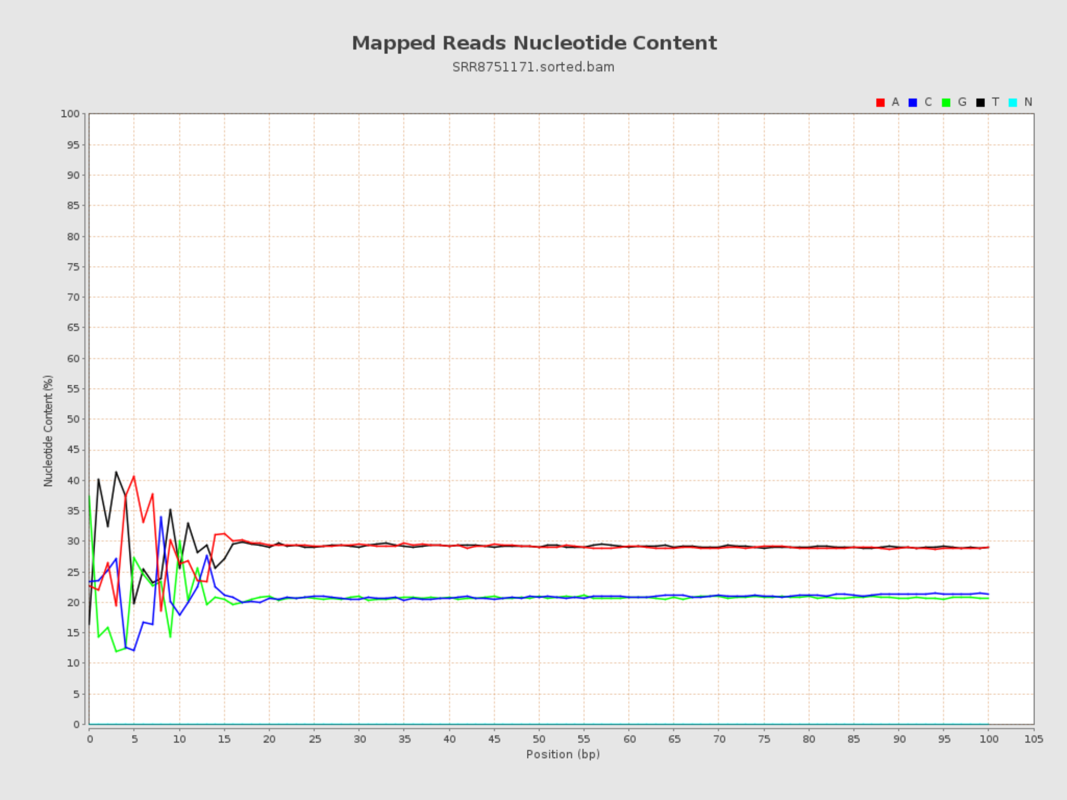
# 6. Results : Genome Fraction Coverage



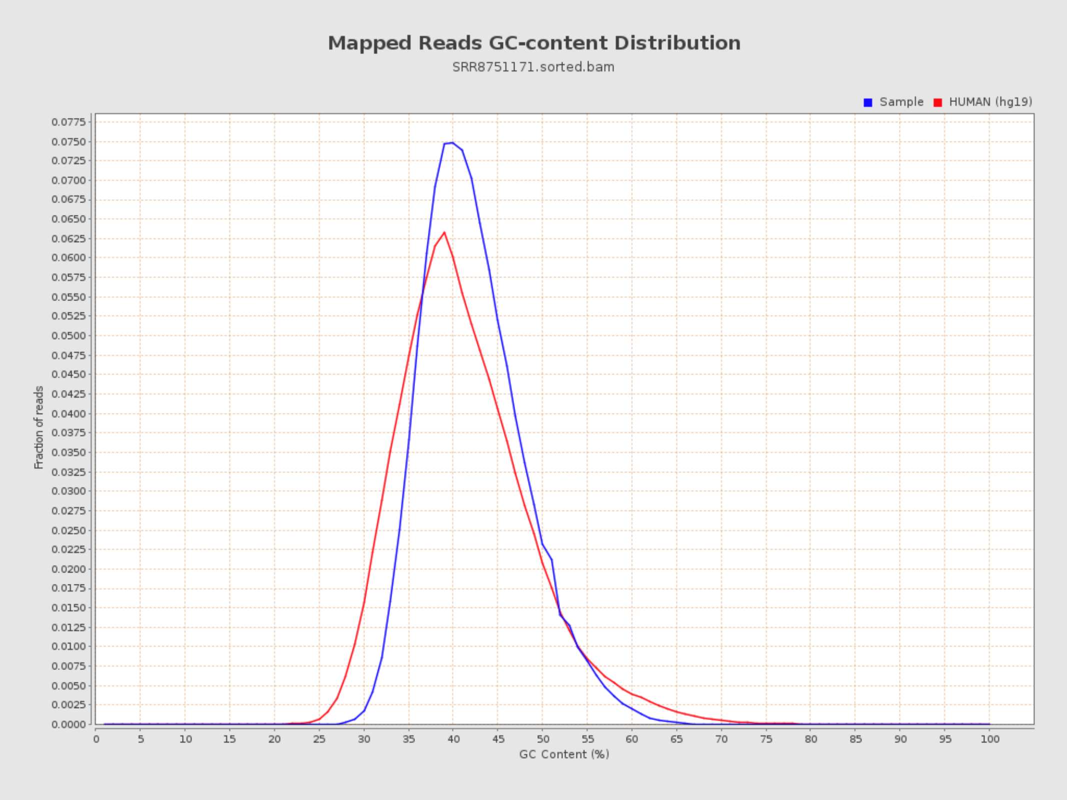
# 7. Results : Duplication Rate Histogram



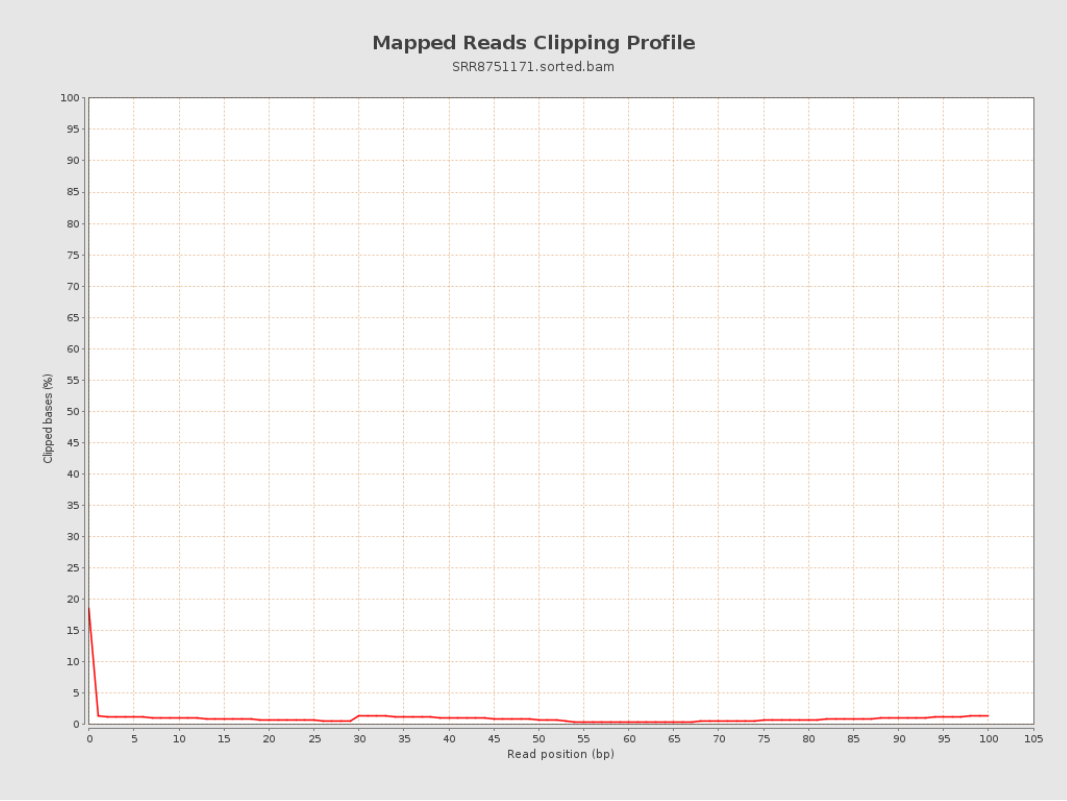
# 8. Results : Mapped Reads Nucleotide Content



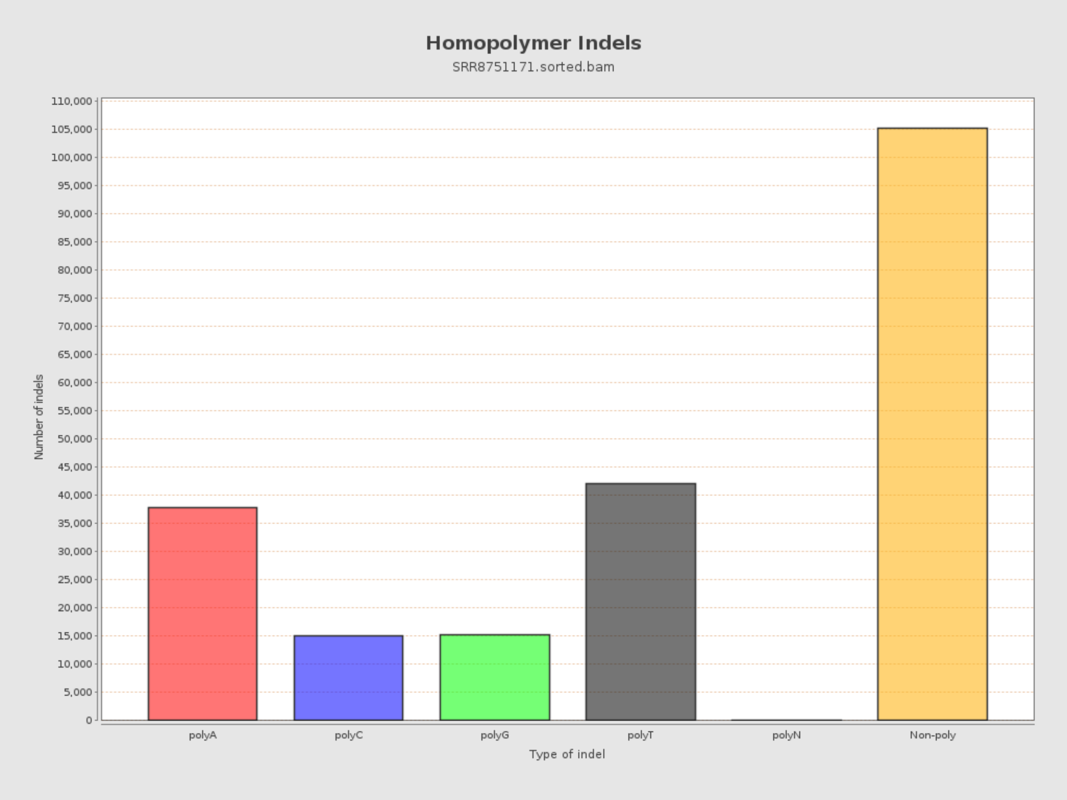
# 9. Results : Mapped Reads GC-content Distribution



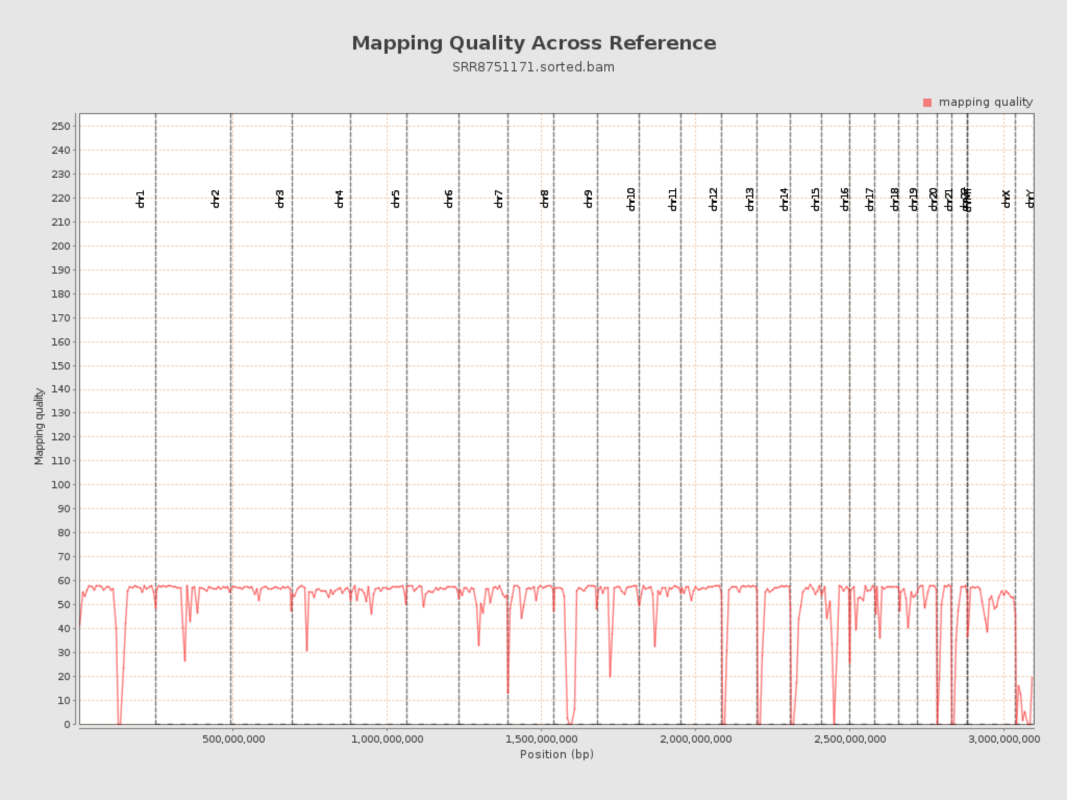
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram