# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/22 08:27:10*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818771.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_SRR1818771 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818771.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 22 08:27:07 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1818771.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,448,941 |
| Mapped reads | 2,379,758 / 97.17% |
| Unmapped reads | 69,183 / 2.83% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 16,796 / 0.69% |
| Read min/max/mean length | 30 / 76 / 76.23 |
| Duplicated reads (estimated) | 1,179,914 / 48.18% |
| Duplication rate | 41.81% |
| Clipped reads | 2,362,925 / 96.49% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 44,334,606 / 27.38% |
| Number/percentage of C's | 35,572,544 / 21.97% |
| Number/percentage of T's | 48,095,952 / 29.71% |
| Number/percentage of G's | 33,883,700 / 20.93% |
| Number/percentage of N's | 9,907 / 0.01% |
| GC Percentage | 42.9% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0523 |
| | |

| | |
|---|---|
| Standard Deviation | 0.6244 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.56 |

## 2.5. Mismatches and indels

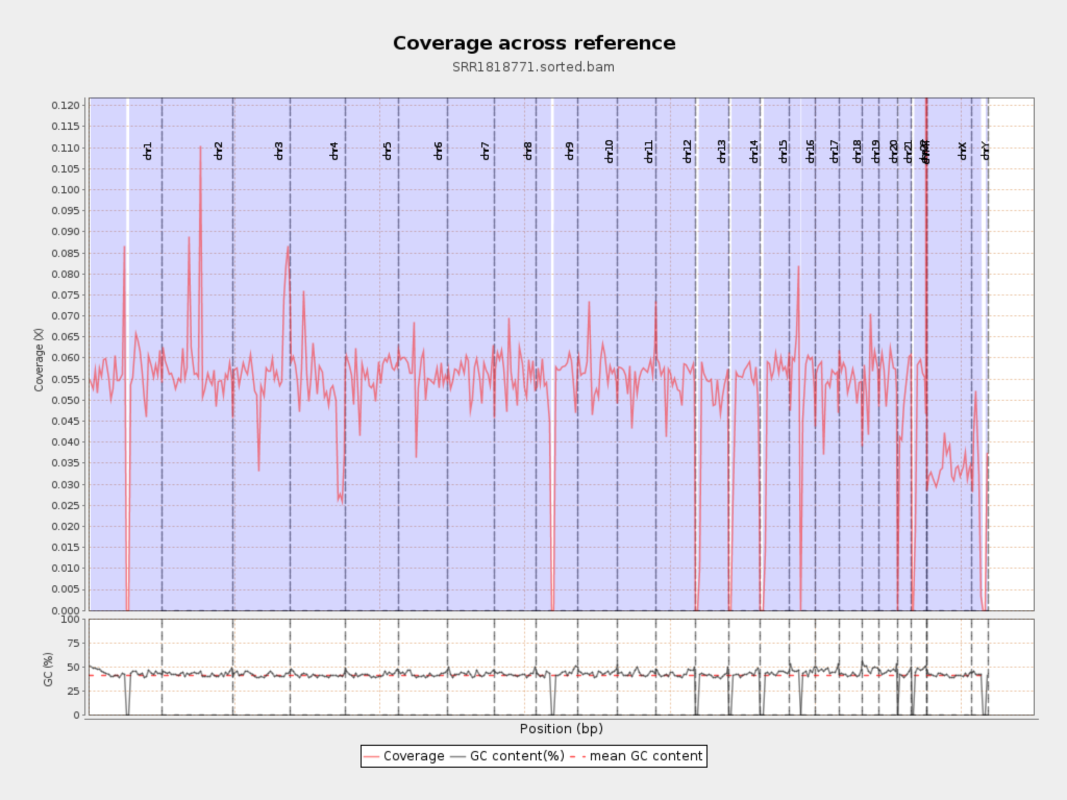
| | |
|---|---|
| General error rate | 0.55% |
| Mismatches | 844,475 |
| Insertions | 21,226 |
| Mapped reads with at least one insertion | 0.88% |
| Deletions | 42,027 |
| Mapped reads with at least one deletion | 1.75% |
| Homopolymer indels | 40.07% |

## 2.6. Chromosome stats

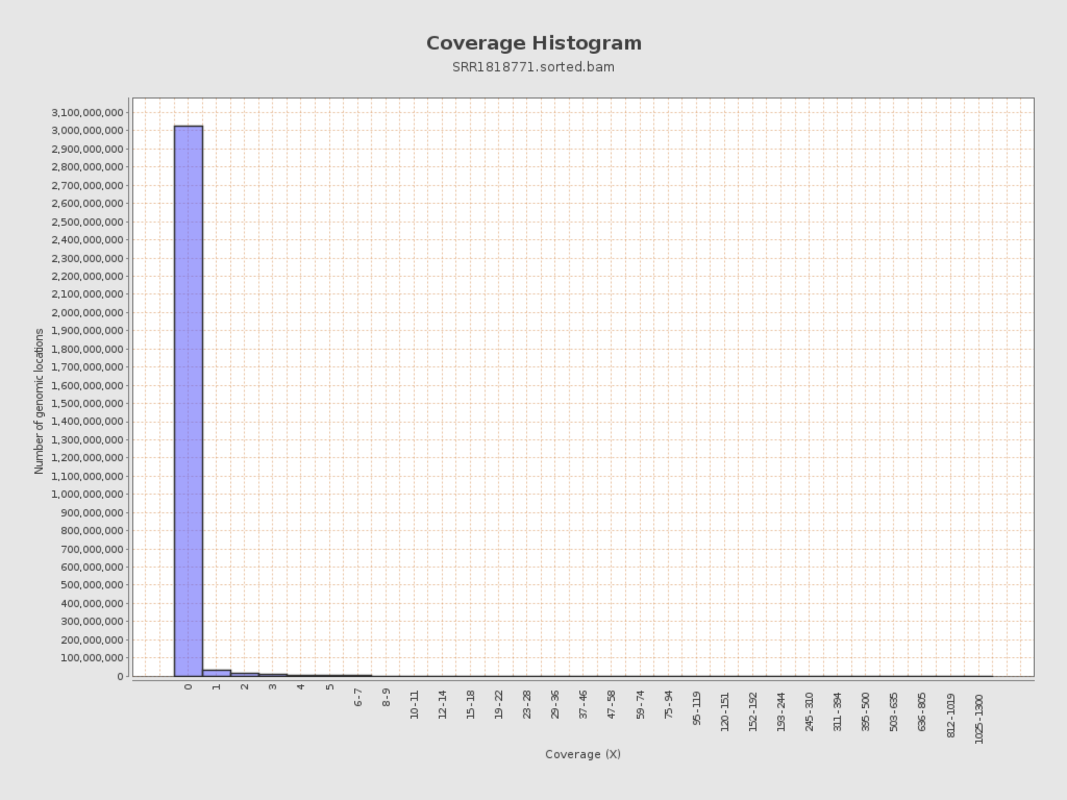
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 13426777 | 0.0539 | 0.9239 |
| chr2 | 243199373 | 14245074 | 0.0586 | 1.0031 |
| chr3 | 198022430 | 11465326 | 0.0579 | 0.4699 |
| chr4 | 191154276 | 9830149 | 0.0514 | 0.5079 |
| chr5 | 180915260 | 10118732 | 0.0559 | 0.4838 |
| chr6 | 171115067 | 9630812 | 0.0563 | 0.512 |
| chr7 | 159138663 | 8932544 | 0.0561 | 0.5614 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 8310802 | 0.0568 | 0.5451 |
| chr9 | 141213431 | 7013518 | 0.0497 | 0.5345 |
| chr10 | 135534747 | 7735928 | 0.0571 | 0.6417 |
| chr11 | 135006516 | 7552554 | 0.0559 | 0.5172 |
| chr12 | 133851895 | 7383803 | 0.0552 | 0.4885 |
| chr13 | 115169878 | 5139252 | 0.0446 | 0.4175 |
| chr14 | 107349540 | 4992561 | 0.0465 | 0.4726 |
| chr15 | 102531392 | 4761458 | 0.0464 | 0.4272 |
| chr16 | 90354753 | 4921497 | 0.0545 | 0.6754 |
| chr17 | 81195210 | 4369767 | 0.0538 | 0.49 |
| chr18 | 78077248 | 4323644 | 0.0554 | 0.6479 |
| chr19 | 59128983 | 3296579 | 0.0558 | 0.8118 |
| chr20 | 63025520 | 3580240 | 0.0568 | 0.5052 |
| chr21 | 48129895 | 2212017 | 0.046 | 0.4437 |
| chr22 | 51304566 | 2016572 | 0.0393 | 0.4245 |
| chrMT | 16571 | 42058 | 2.538 | 3.7852 |
| chrX | 155270560 | 5221303 | 0.0336 | 0.4051 |
| chrY | 59373566 | 1442581 | 0.0243 | 0.965 |

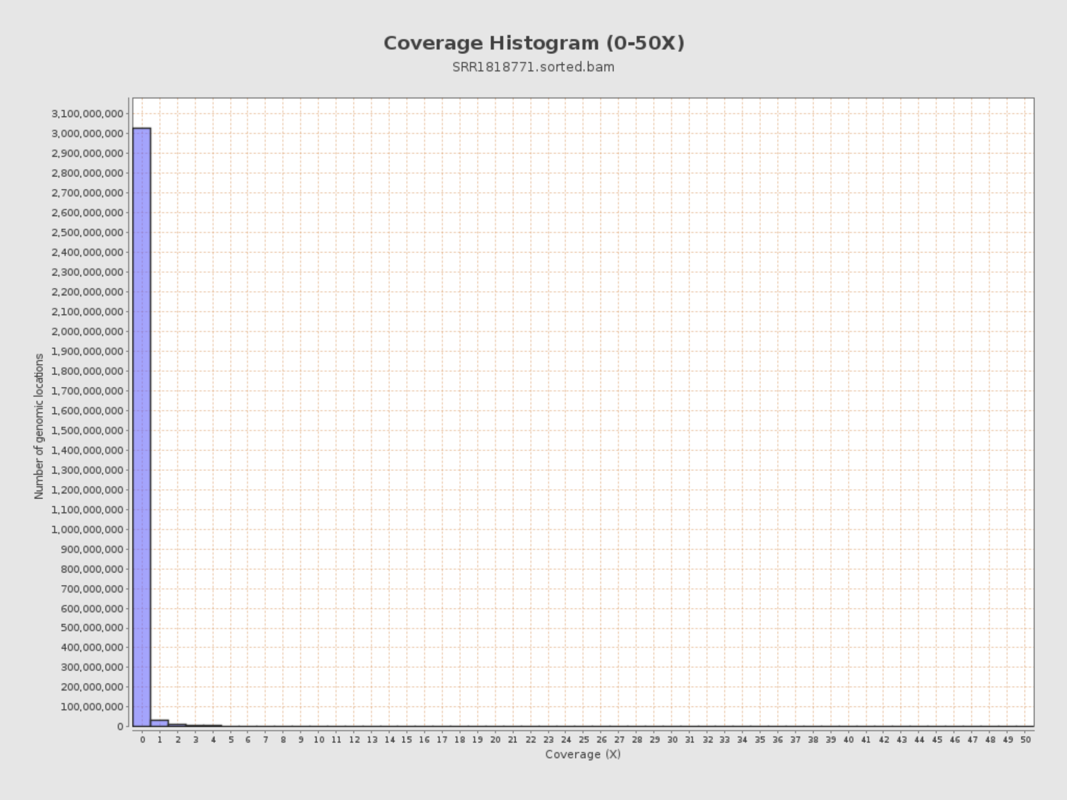
# 3. Results : Coverage across reference



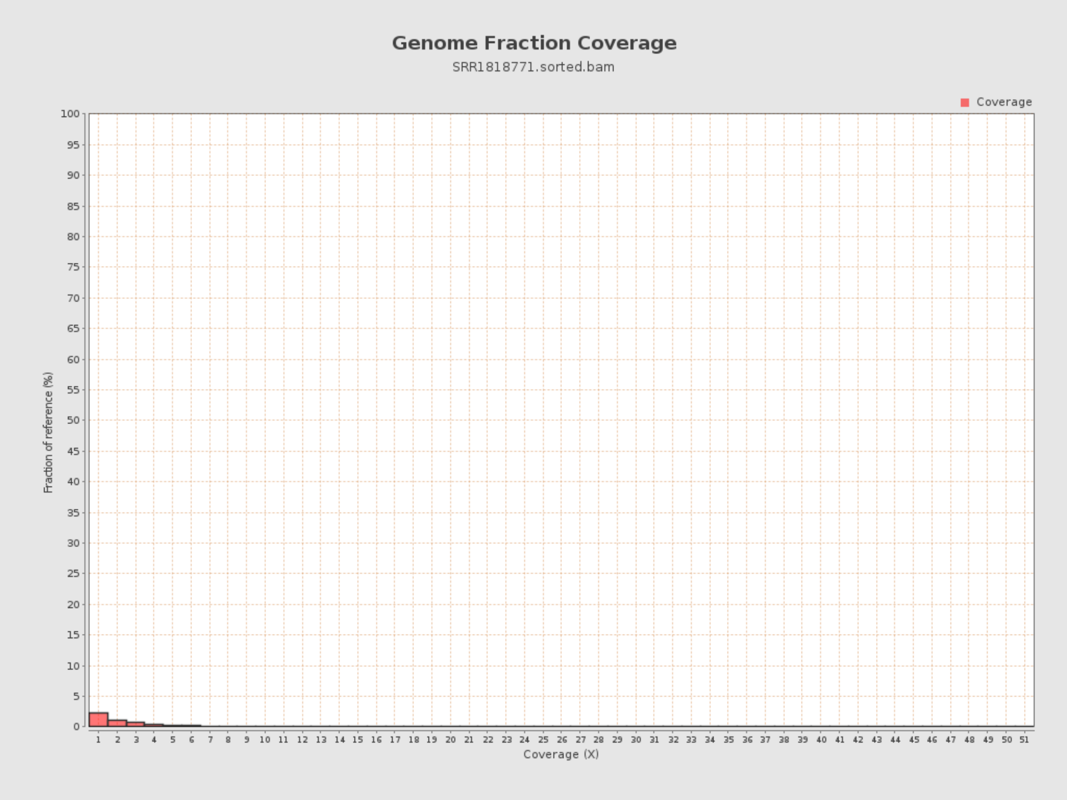
# 4. Results : Coverage Histogram



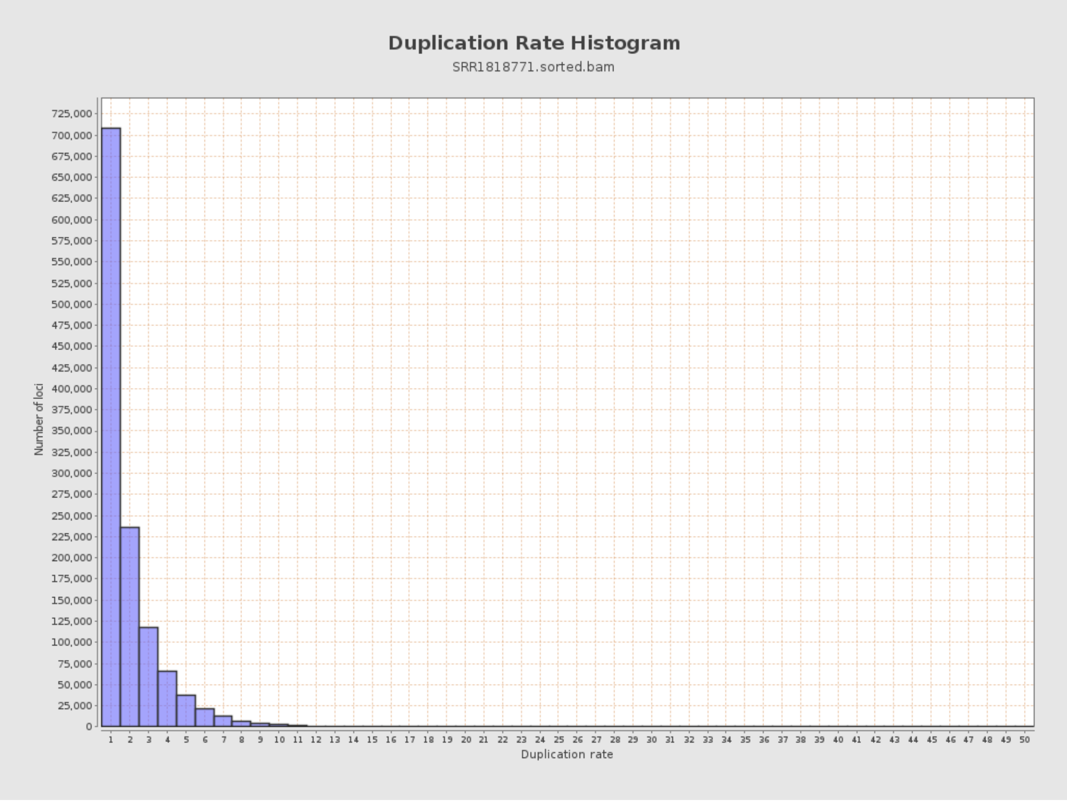
# 5. Results : Coverage Histogram (0-50X)



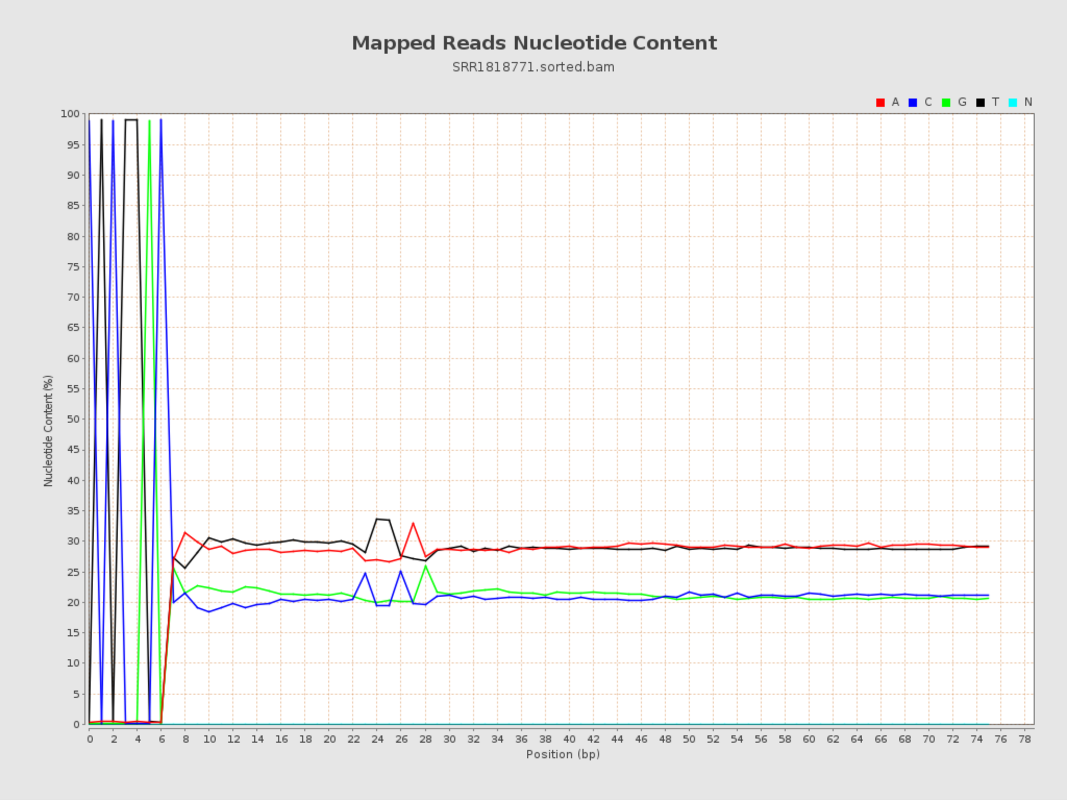
# 6. Results : Genome Fraction Coverage



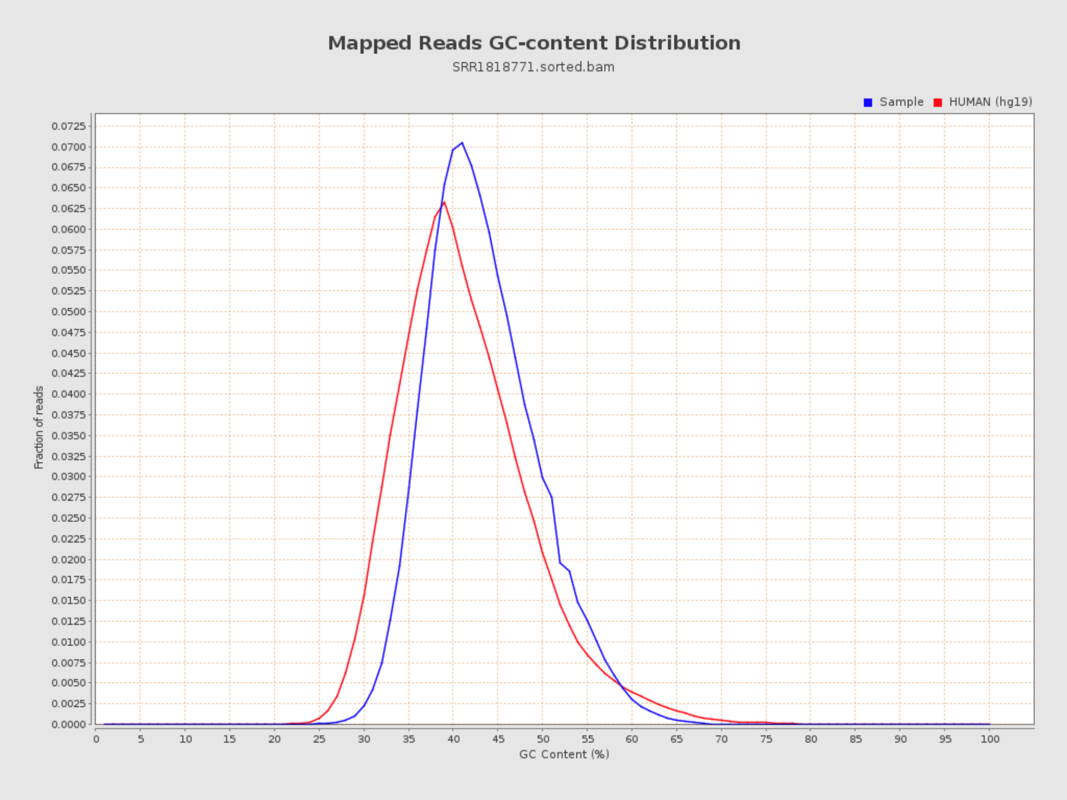
# 7. Results : Duplication Rate Histogram



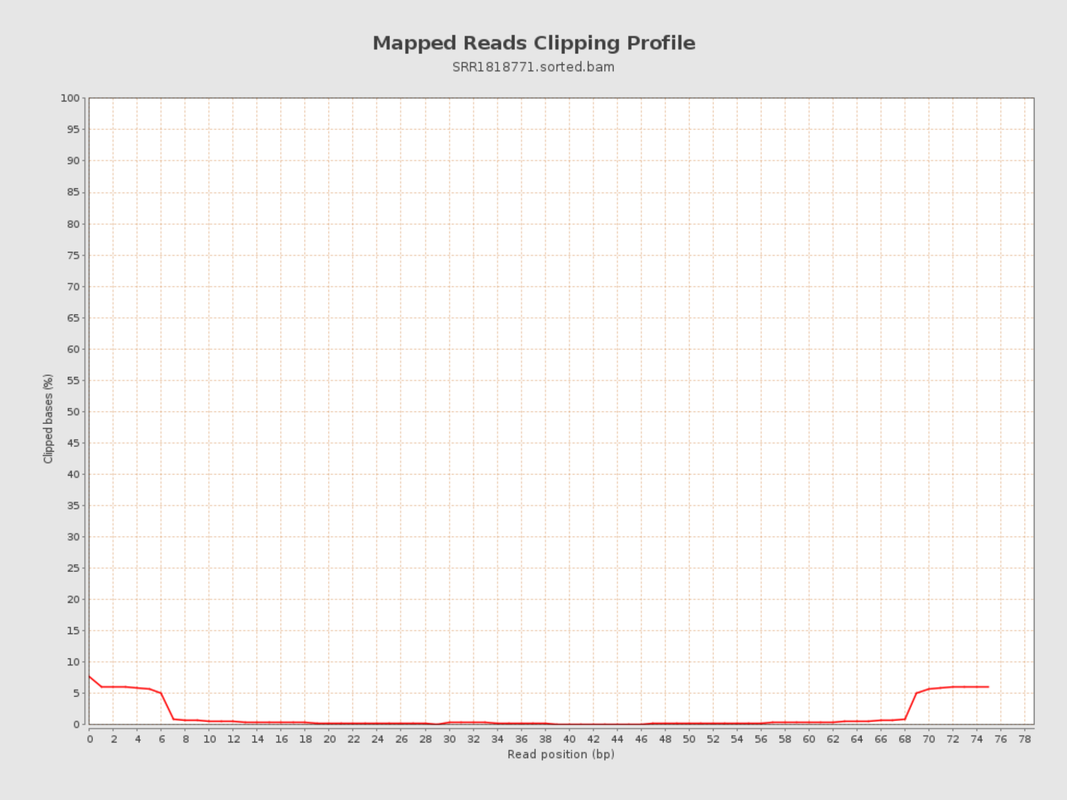
# 8. Results : Mapped Reads Nucleotide Content



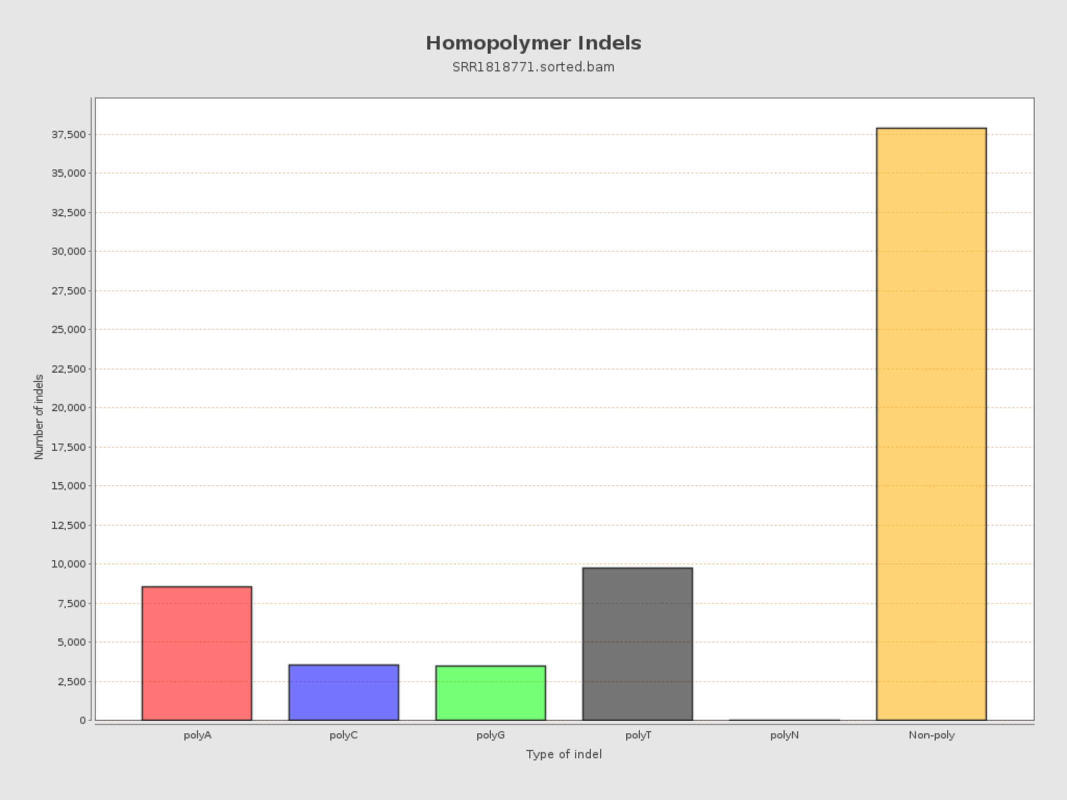
# 9. Results : Mapped Reads GC-content Distribution



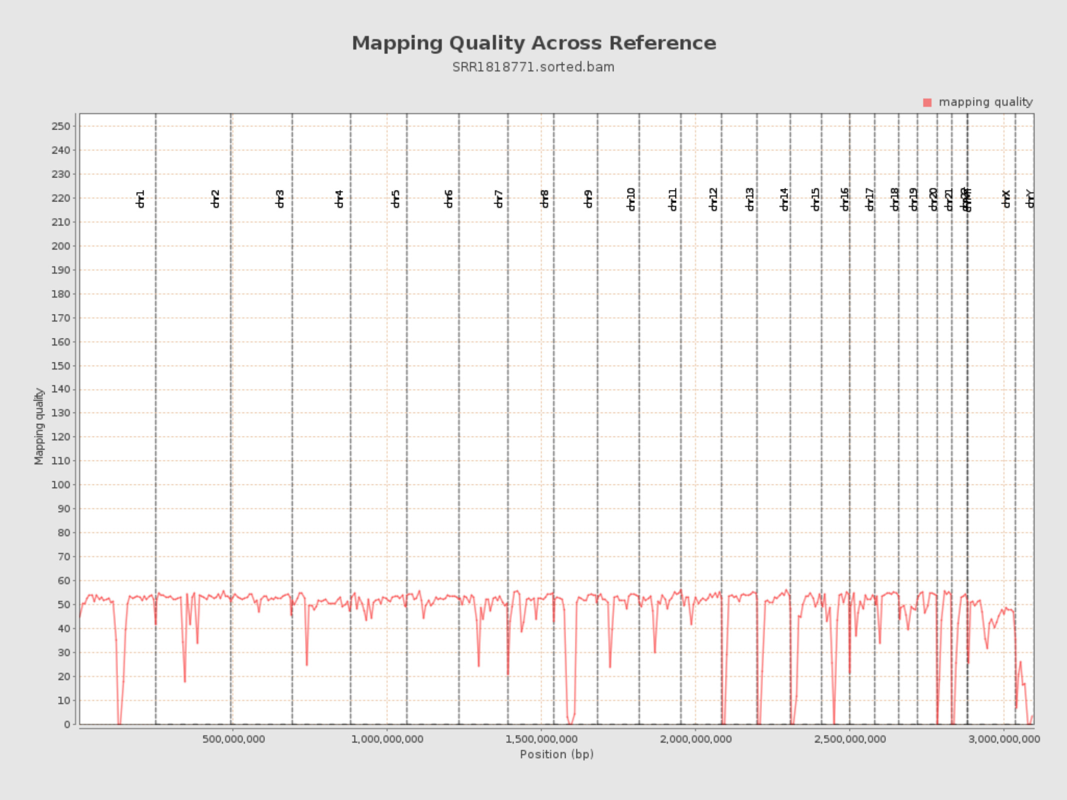
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram