# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/22 15:01:20*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818810.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_SRR1818810 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818810.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 22 15:01:18 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1818810.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,129,659 |
| Mapped reads | 2,080,047 / 97.67% |
| Unmapped reads | 49,612 / 2.33% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 15,839 / 0.74% |
| Read min/max/mean length | 30 / 76 / 76.25 |
| Duplicated reads (estimated) | 972,605 / 45.67% |
| Duplication rate | 40.77% |
| Clipped reads | 2,072,713 / 97.33% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 41,019,235 / 29% |
| Number/percentage of C's | 28,955,641 / 20.47% |
| Number/percentage of T's | 39,804,961 / 28.15% |
| Number/percentage of G's | 31,637,912 / 22.37% |
| Number/percentage of N's | 8,427 / 0.01% |
| GC Percentage | 42.84% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0457 |
| | |

| | |
|---|---|
| Standard Deviation | 0.5455 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.96 |

## 2.5. Mismatches and indels

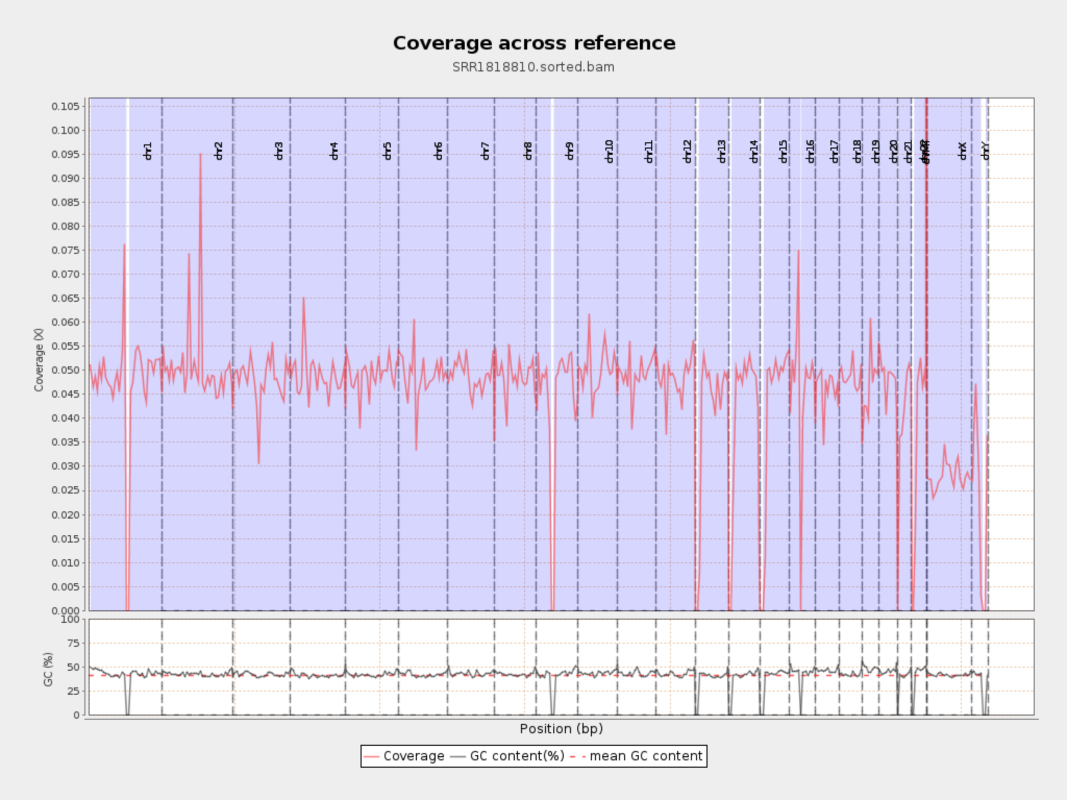
| | |
|---|---|
| General error rate | 0.53% |
| Mismatches | 714,019 |
| Insertions | 16,077 |
| Mapped reads with at least one insertion | 0.76% |
| Deletions | 36,441 |
| Mapped reads with at least one deletion | 1.73% |
| Homopolymer indels | 40.31% |

## 2.6. Chromosome stats

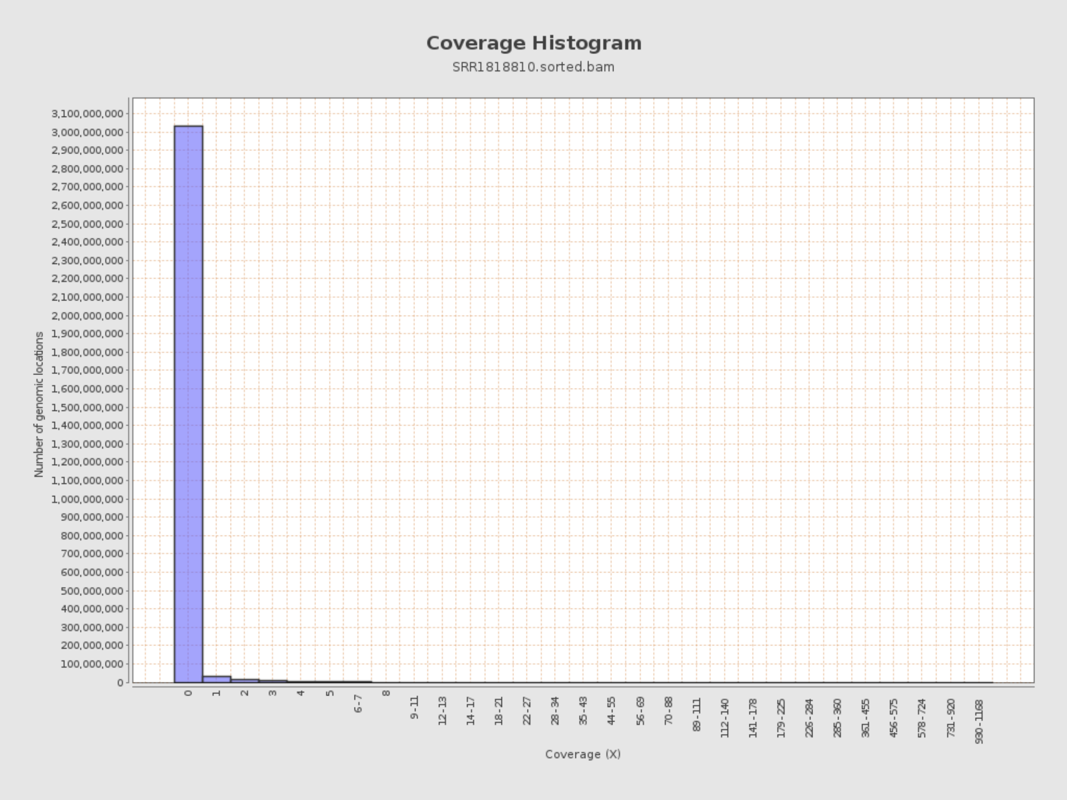
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 11751952 | 0.0471 | 0.7398 |
| chr2 | 243199373 | 12453489 | 0.0512 | 0.9036 |
| chr3 | 198022430 | 9529628 | 0.0481 | 0.4043 |
| chr4 | 191154276 | 9332137 | 0.0488 | 0.4733 |
| chr5 | 180915260 | 8860096 | 0.049 | 0.4249 |
| chr6 | 171115067 | 8390021 | 0.049 | 0.4606 |
| chr7 | 159138663 | 7798106 | 0.049 | 0.4838 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7194071 | 0.0492 | 0.4683 |
| chr9 | 141213431 | 6095751 | 0.0432 | 0.4557 |
| chr10 | 135534747 | 6794460 | 0.0501 | 0.5547 |
| chr11 | 135006516 | 6670273 | 0.0494 | 0.4641 |
| chr12 | 133851895 | 6503789 | 0.0486 | 0.4329 |
| chr13 | 115169878 | 4538297 | 0.0394 | 0.3659 |
| chr14 | 107349540 | 4362970 | 0.0406 | 0.4319 |
| chr15 | 102531392 | 4146150 | 0.0404 | 0.3721 |
| chr16 | 90354753 | 4232641 | 0.0468 | 0.6333 |
| chr17 | 81195210 | 3743703 | 0.0461 | 0.4164 |
| chr18 | 78077248 | 3803246 | 0.0487 | 0.5716 |
| chr19 | 59128983 | 2796238 | 0.0473 | 0.6778 |
| chr20 | 63025520 | 3055817 | 0.0485 | 0.431 |
| chr21 | 48129895 | 1903559 | 0.0396 | 0.3861 |
| chr22 | 51304566 | 1743076 | 0.034 | 0.376 |
| chrMT | 16571 | 119096 | 7.187 | 7.7627 |
| chrX | 155270560 | 4351652 | 0.028 | 0.3479 |
| chrY | 59373566 | 1315545 | 0.0222 | 0.8983 |

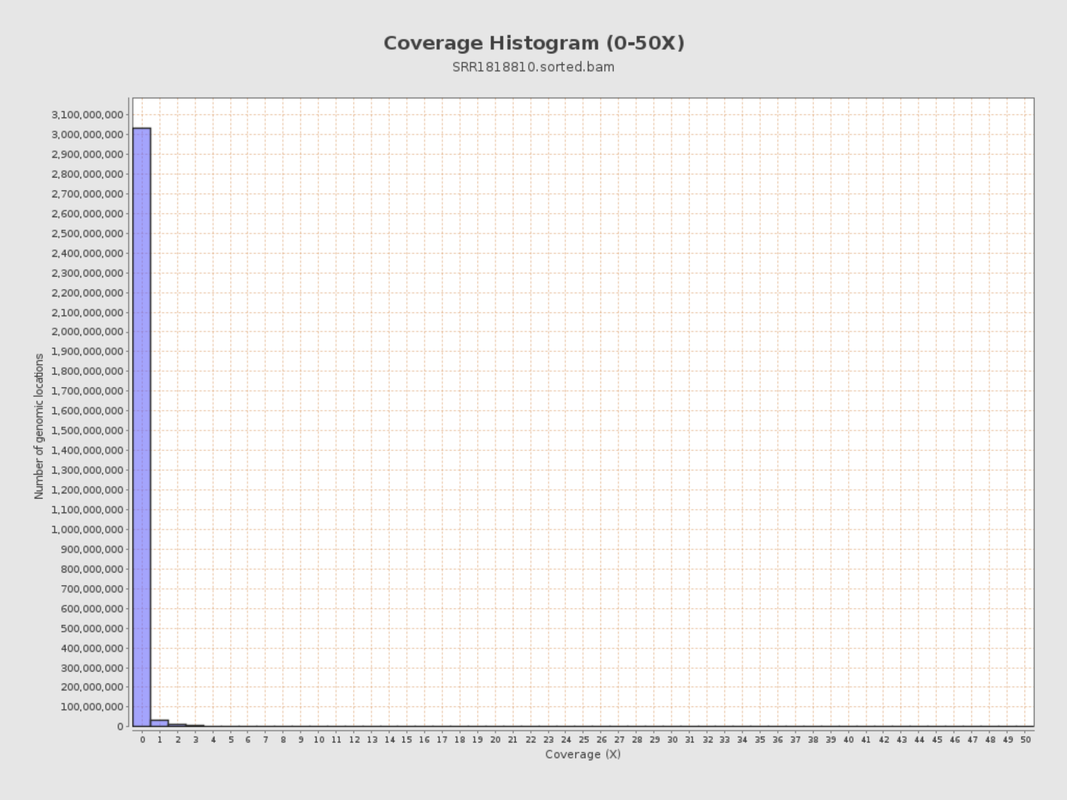
# 3. Results : Coverage across reference



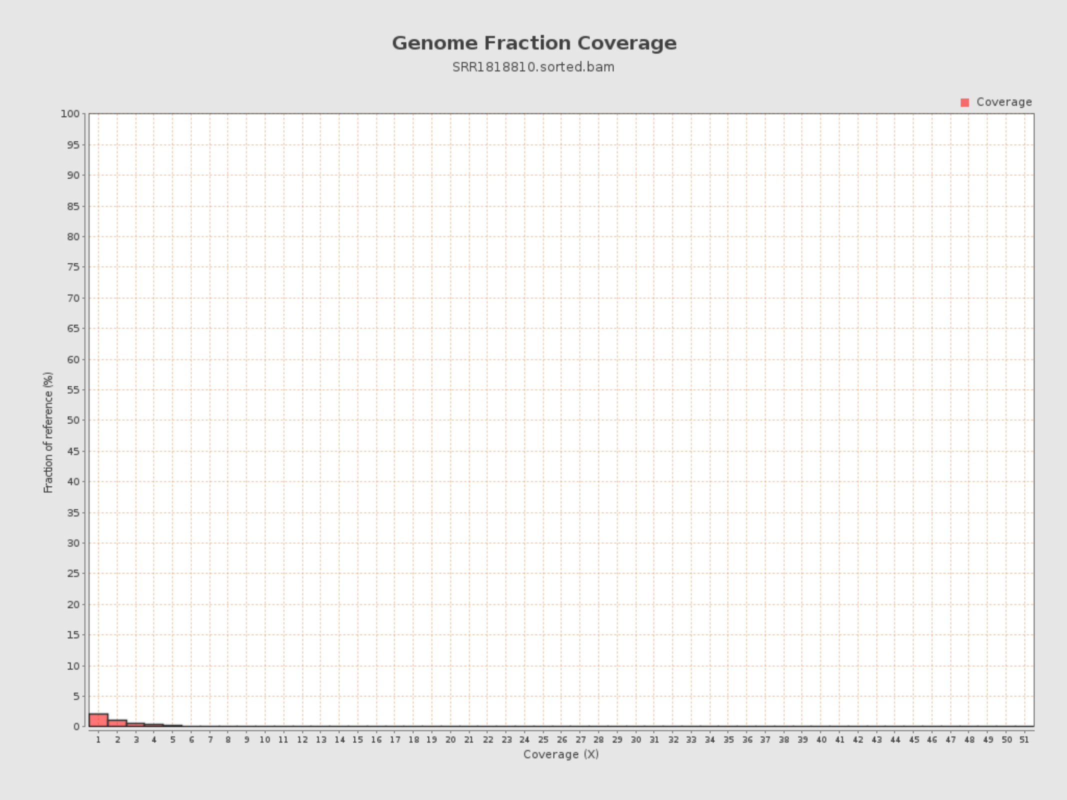
# 4. Results : Coverage Histogram



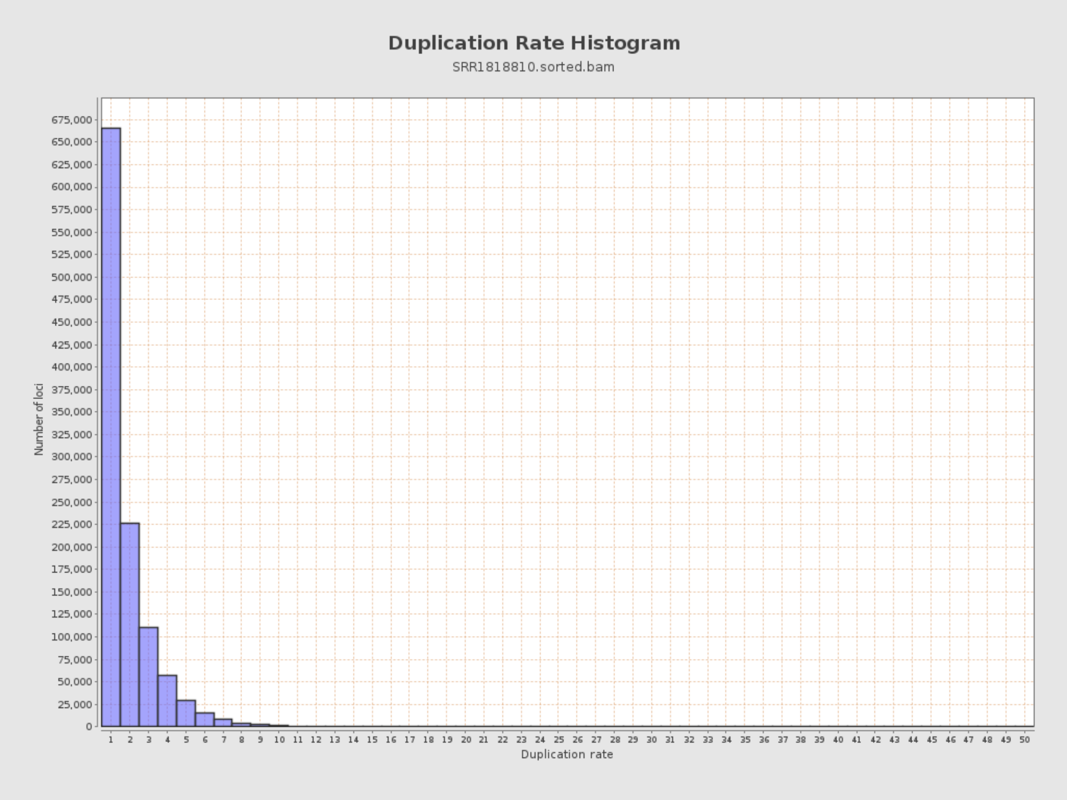
# 5. Results : Coverage Histogram (0-50X)



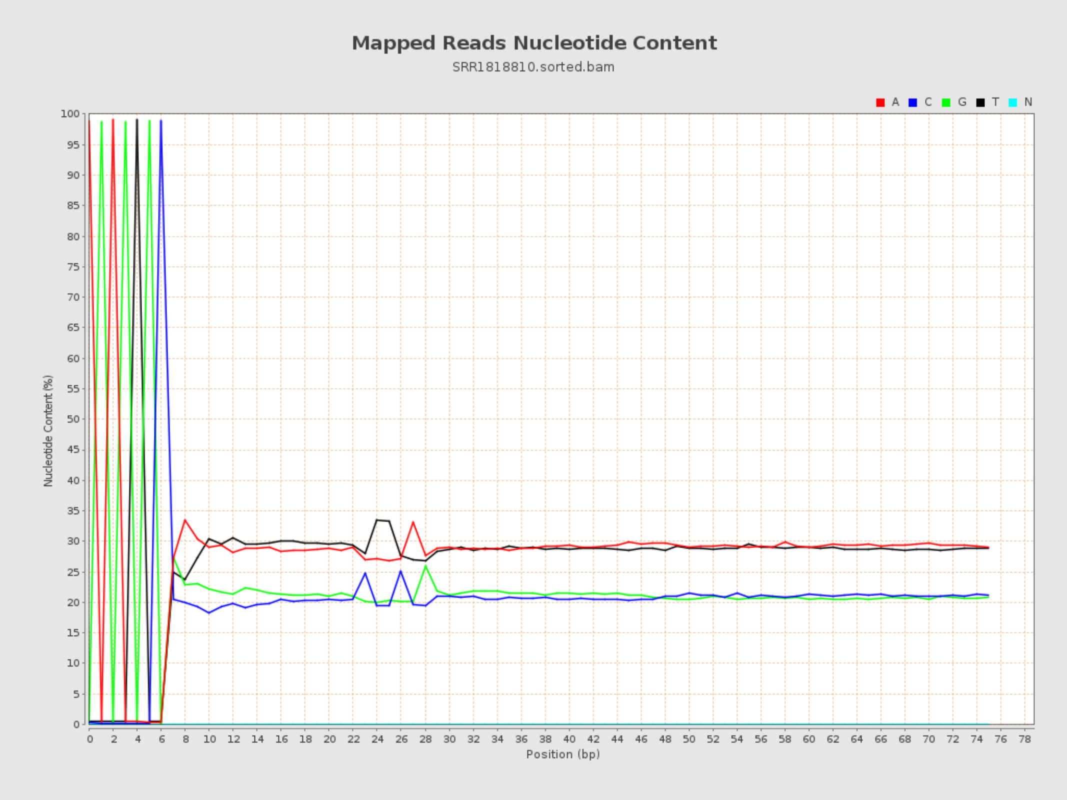
# 6. Results : Genome Fraction Coverage



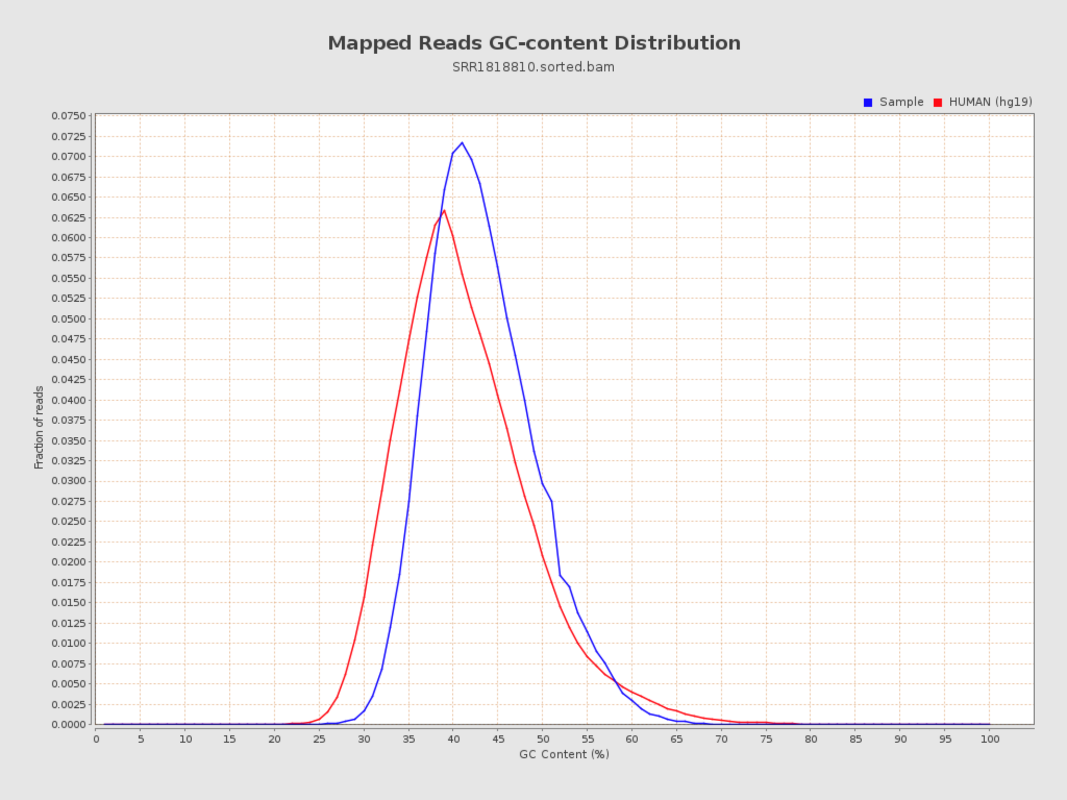
# 7. Results : Duplication Rate Histogram



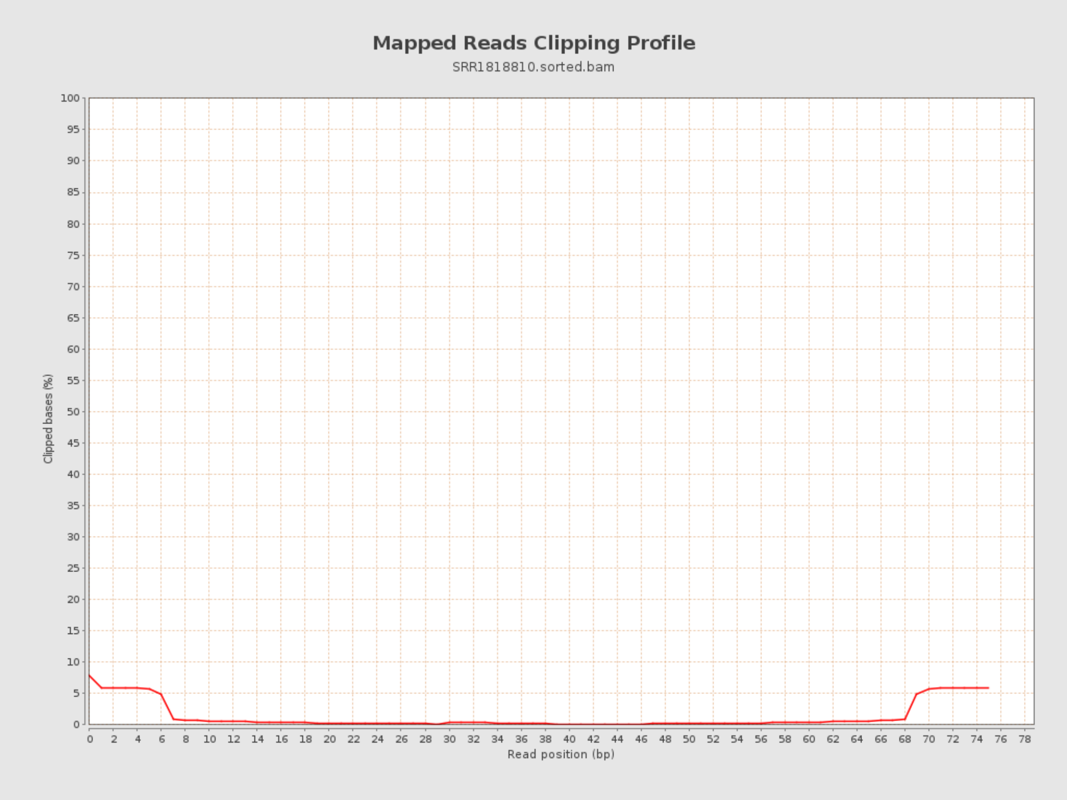
# 8. Results : Mapped Reads Nucleotide Content



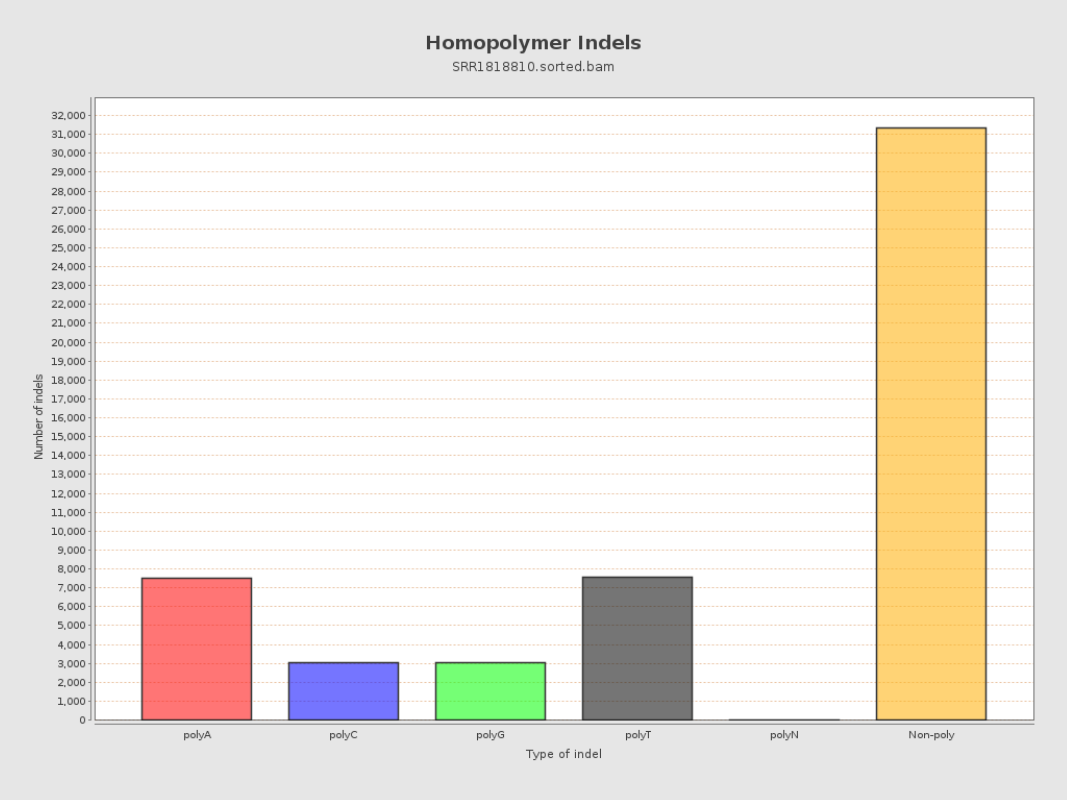
# 9. Results : Mapped Reads GC-content Distribution



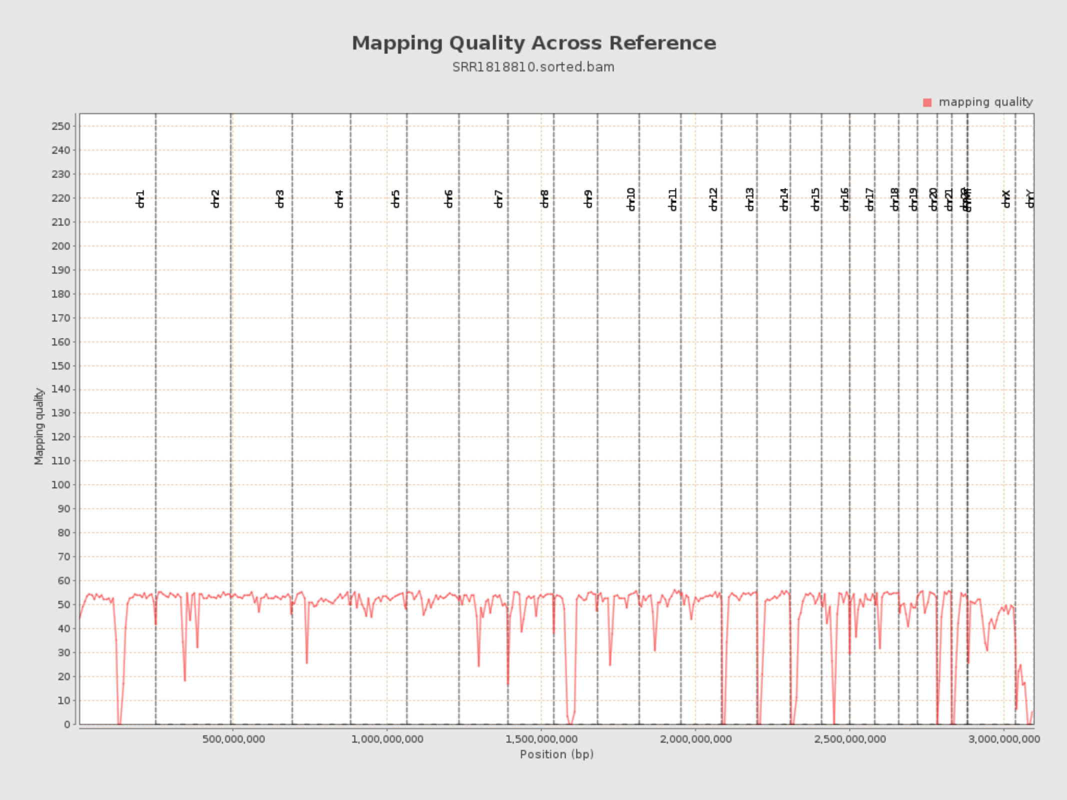
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram