# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/22 21:35:17*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818844.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_SRR1818844 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818844.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 22 21:35:09 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1818844.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,114,774 |
| Mapped reads | 2,088,326 / 98.75% |
| Unmapped reads | 26,448 / 1.25% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 33,337 / 1.58% |
| Read min/max/mean length | 30 / 101 / 101.61 |
| Duplicated reads (estimated) | 526,721 / 24.91% |
| Duplication rate | 21.69% |
| Clipped reads | 2,112,208 / 99.88% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 54,762,773 / 28.34% |
| Number/percentage of C's | 40,673,889 / 21.05% |
| Number/percentage of T's | 55,757,342 / 28.85% |
| Number/percentage of G's | 42,069,328 / 21.77% |
| Number/percentage of N's | 3,007 / 0% |
| GC Percentage | 42.81% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0625 |
| | |

| | |
|---|---|
| Standard Deviation | 0.7216 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 49.31 |

## 2.5. Mismatches and indels

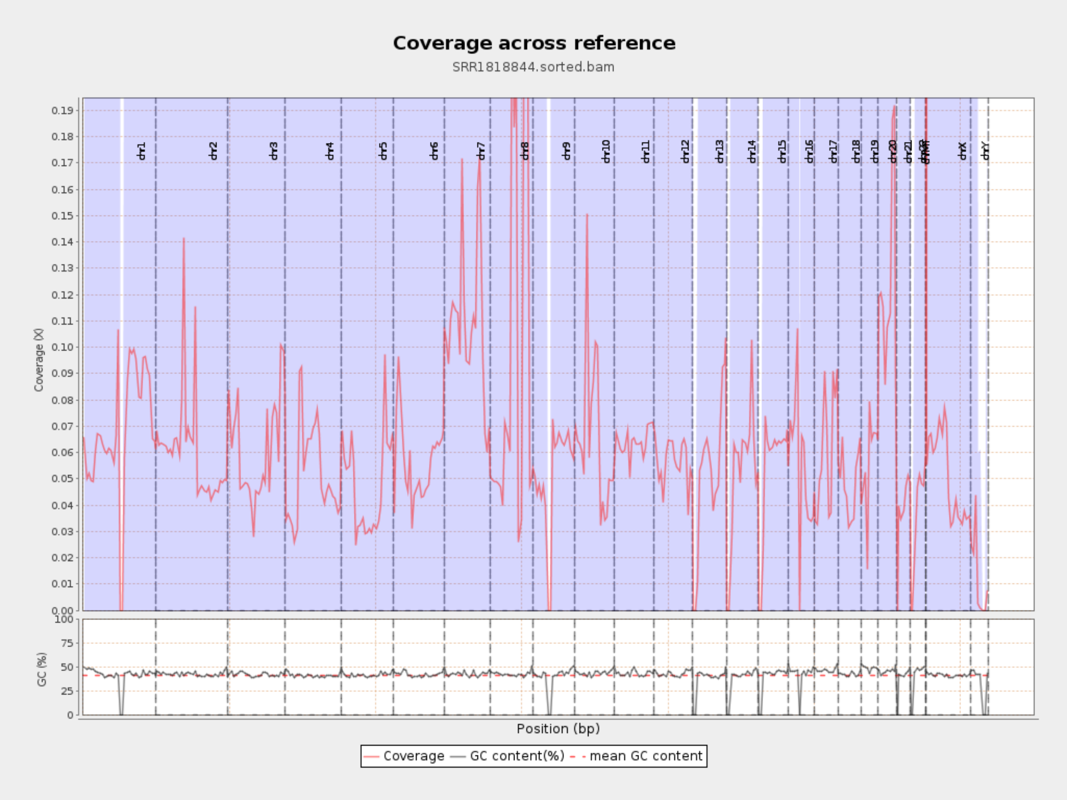
| | |
|---|---|
| General error rate | 0.63% |
| Mismatches | 1,141,122 |
| Insertions | 27,089 |
| Mapped reads with at least one insertion | 1.26% |
| Deletions | 62,089 |
| Mapped reads with at least one deletion | 2.9% |
| Homopolymer indels | 40.52% |

## 2.6. Chromosome stats

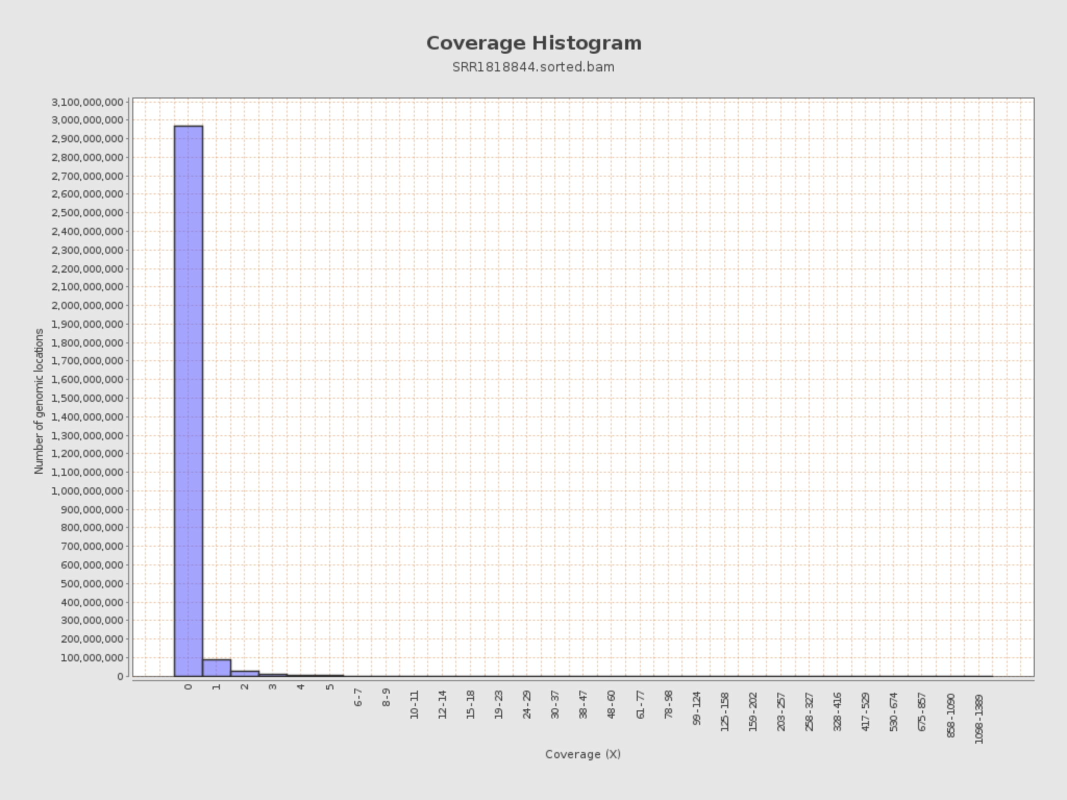
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 17120563 | 0.0687 | 1.0748 |
| chr2 | 243199373 | 14748381 | 0.0606 | 1.0483 |
| chr3 | 198022430 | 12104855 | 0.0611 | 0.3496 |
| chr4 | 191154276 | 9922509 | 0.0519 | 0.4444 |
| chr5 | 180915260 | 8660664 | 0.0479 | 0.326 |
| chr6 | 171115067 | 9680960 | 0.0566 | 0.3742 |
| chr7 | 159138663 | 17326011 | 0.1089 | 1.5503 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 16983133 | 0.116 | 0.6293 |
| chr9 | 141213431 | 7221784 | 0.0511 | 0.6221 |
| chr10 | 135534747 | 8912875 | 0.0658 | 0.9556 |
| chr11 | 135006516 | 8609435 | 0.0638 | 0.4466 |
| chr12 | 133851895 | 7595175 | 0.0567 | 0.3374 |
| chr13 | 115169878 | 5997302 | 0.0521 | 0.3176 |
| chr14 | 107349540 | 5723028 | 0.0533 | 0.356 |
| chr15 | 102531392 | 5393435 | 0.0526 | 0.3192 |
| chr16 | 90354753 | 4893210 | 0.0542 | 0.7421 |
| chr17 | 81195210 | 4831756 | 0.0595 | 0.4774 |
| chr18 | 78077248 | 3768758 | 0.0483 | 0.6856 |
| chr19 | 59128983 | 3303335 | 0.0559 | 0.8441 |
| chr20 | 63025520 | 8095137 | 0.1284 | 0.5493 |
| chr21 | 48129895 | 1880225 | 0.0391 | 0.3369 |
| chr22 | 51304566 | 1763305 | 0.0344 | 0.3042 |
| chrMT | 16571 | 231933 | 13.9963 | 9.3813 |
| chrX | 155270560 | 7903271 | 0.0509 | 0.3859 |
| chrY | 59373566 | 716649 | 0.0121 | 0.9109 |

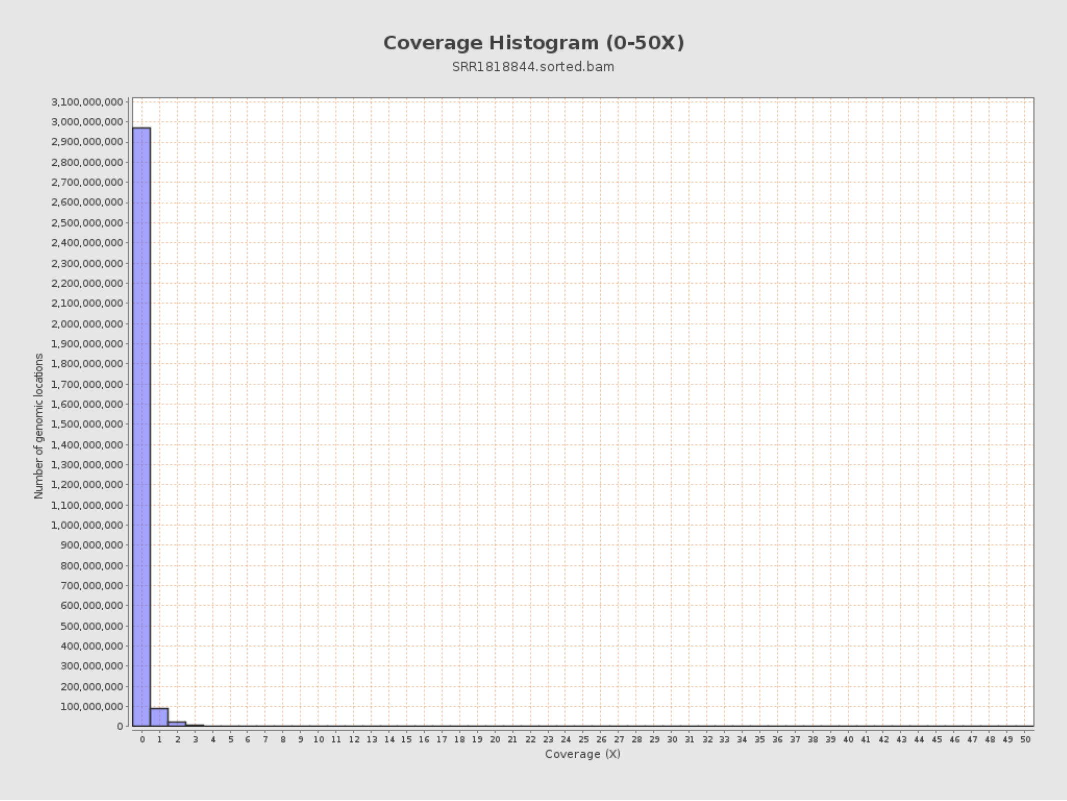
# 3. Results : Coverage across reference



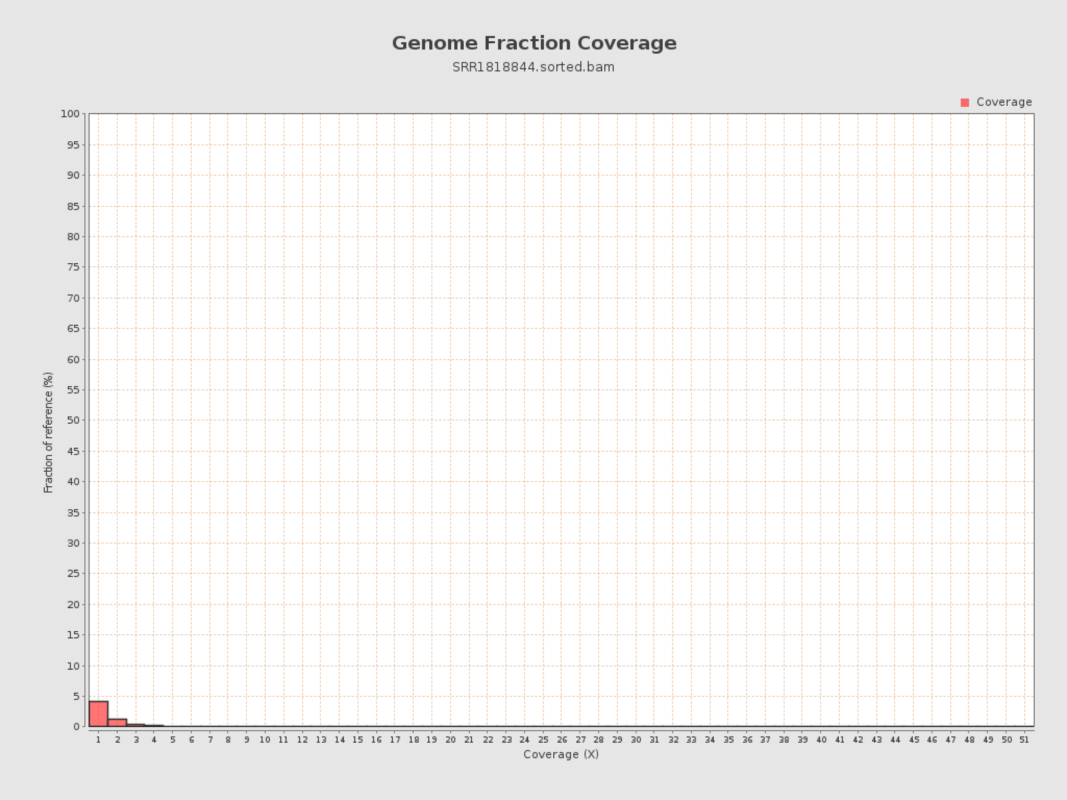
# 4. Results : Coverage Histogram



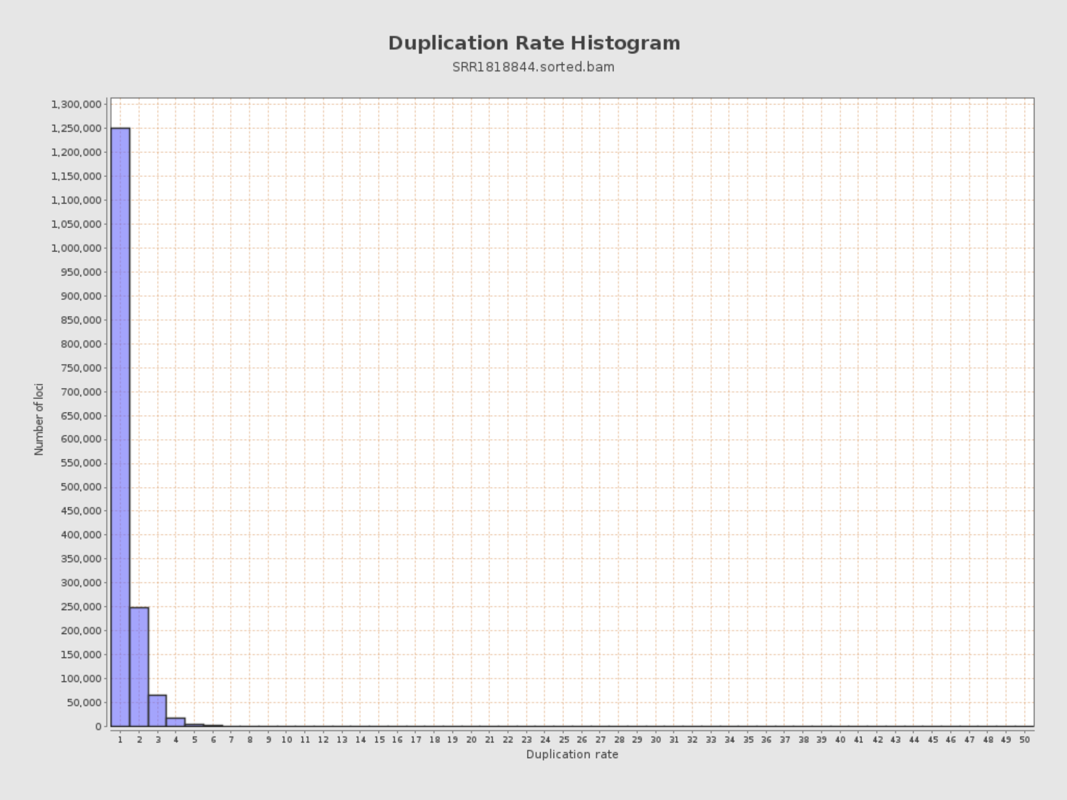
# 5. Results : Coverage Histogram (0-50X)



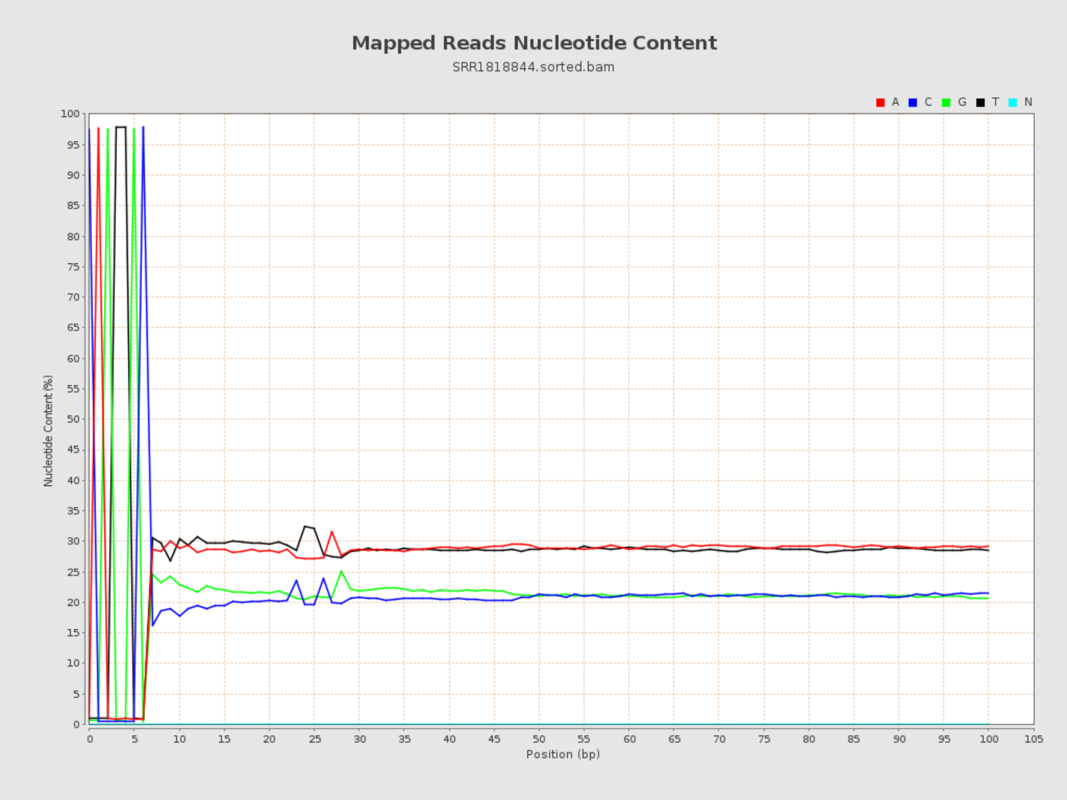
# 6. Results : Genome Fraction Coverage



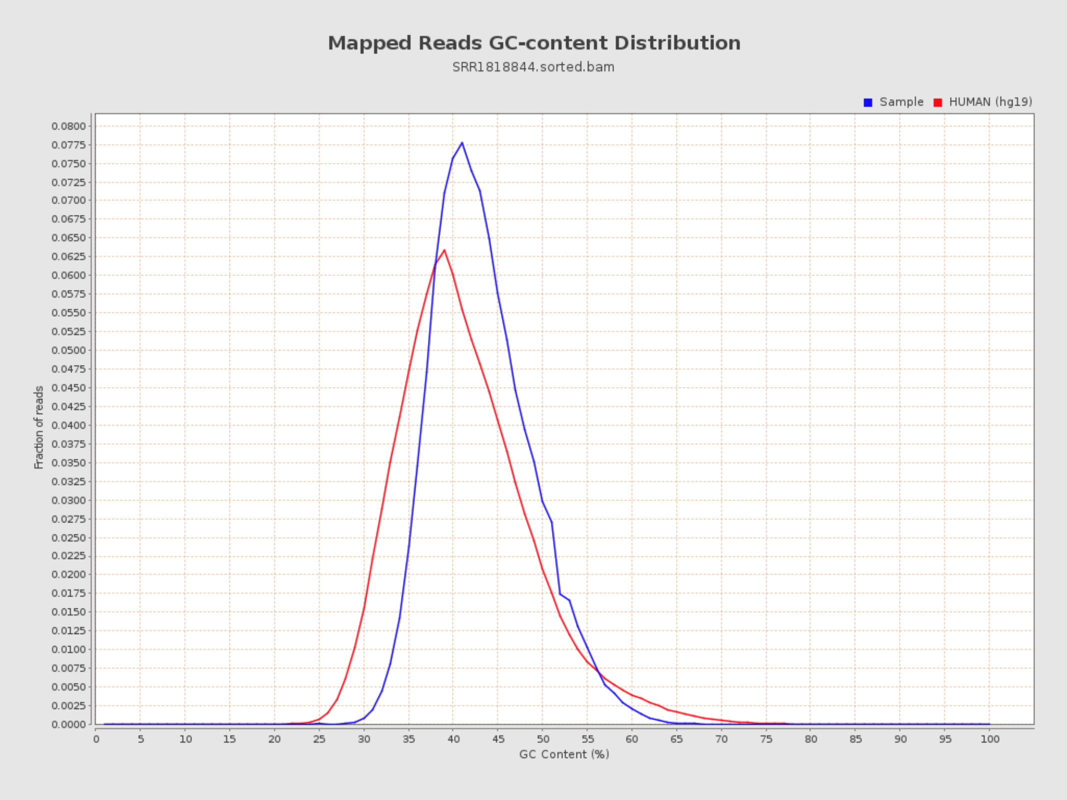
# 7. Results : Duplication Rate Histogram



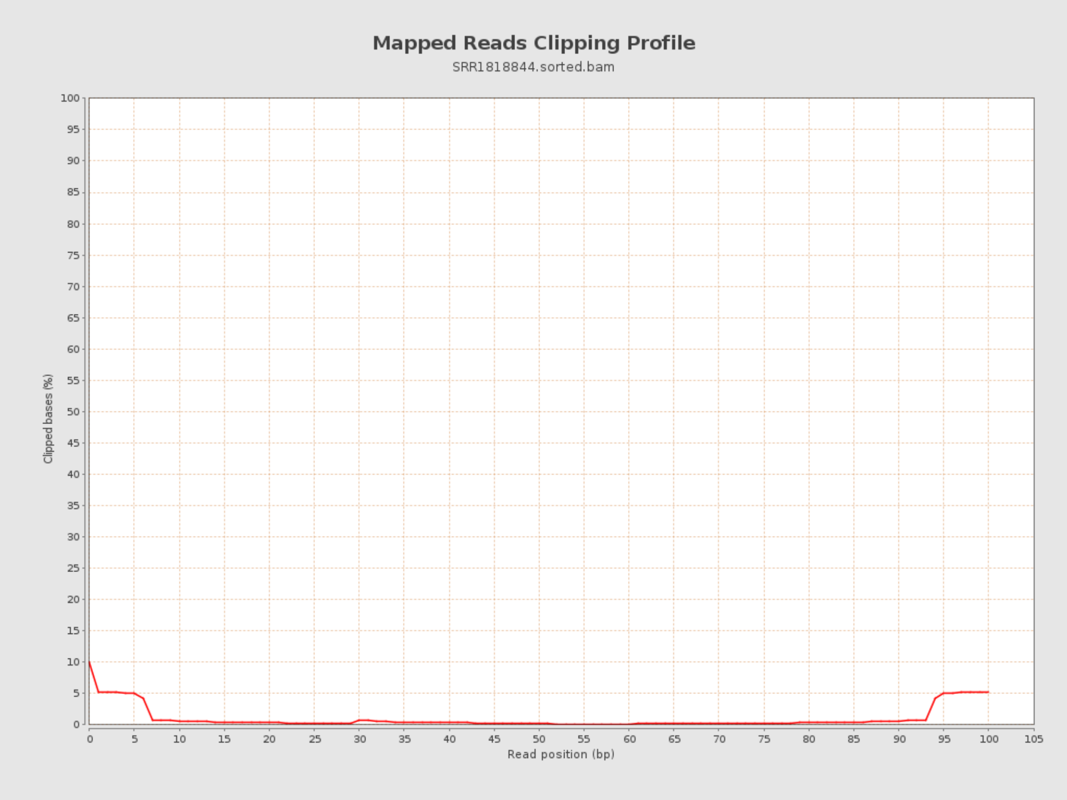
# 8. Results : Mapped Reads Nucleotide Content



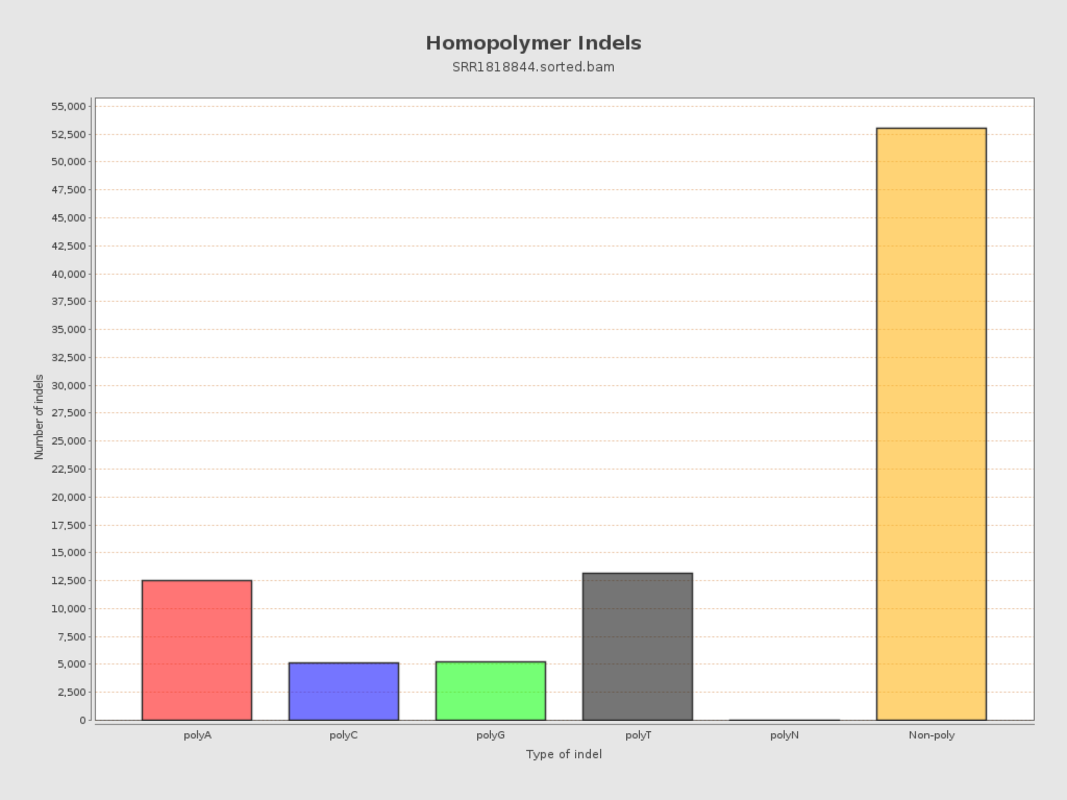
# 9. Results : Mapped Reads GC-content Distribution



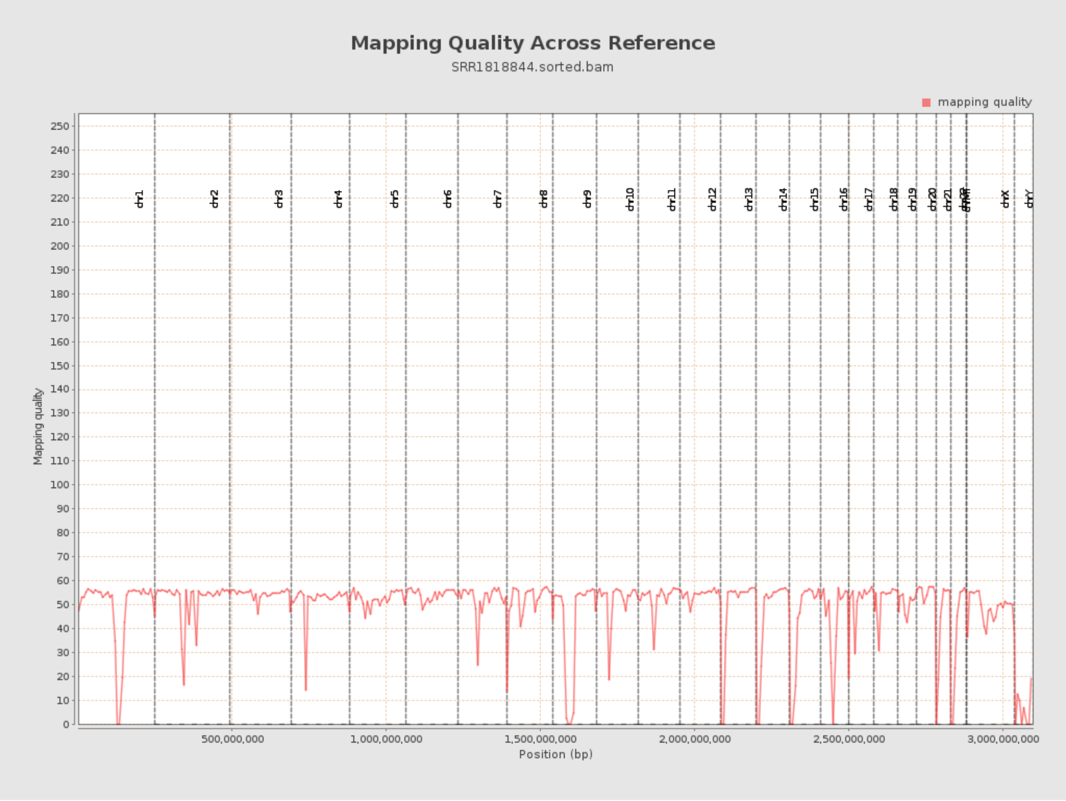
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram