# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/25 17:24:10*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084848.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_SRR3084848 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084848.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Aug 25 17:24:09 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3084848.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,493,198 |
| Mapped reads | 2,233,055 / 89.57% |
| Unmapped reads | 260,143 / 10.43% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 18,786 / 0.75% |
| Read min/max/mean length | 30 / 76 / 76.26 |
| Duplicated reads (estimated) | 111,497 / 4.47% |
| Duplication rate | 4.21% |
| Clipped reads | 736,742 / 29.55% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 45,422,575 / 29.27% |
| Number/percentage of C's | 28,395,213 / 18.3% |
| Number/percentage of T's | 49,913,241 / 32.17% |
| Number/percentage of G's | 31,420,891 / 20.25% |
| Number/percentage of N's | 25,071 / 0.02% |
| GC Percentage | 38.55% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0501 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4195 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 48.26 |

## 2.5. Mismatches and indels

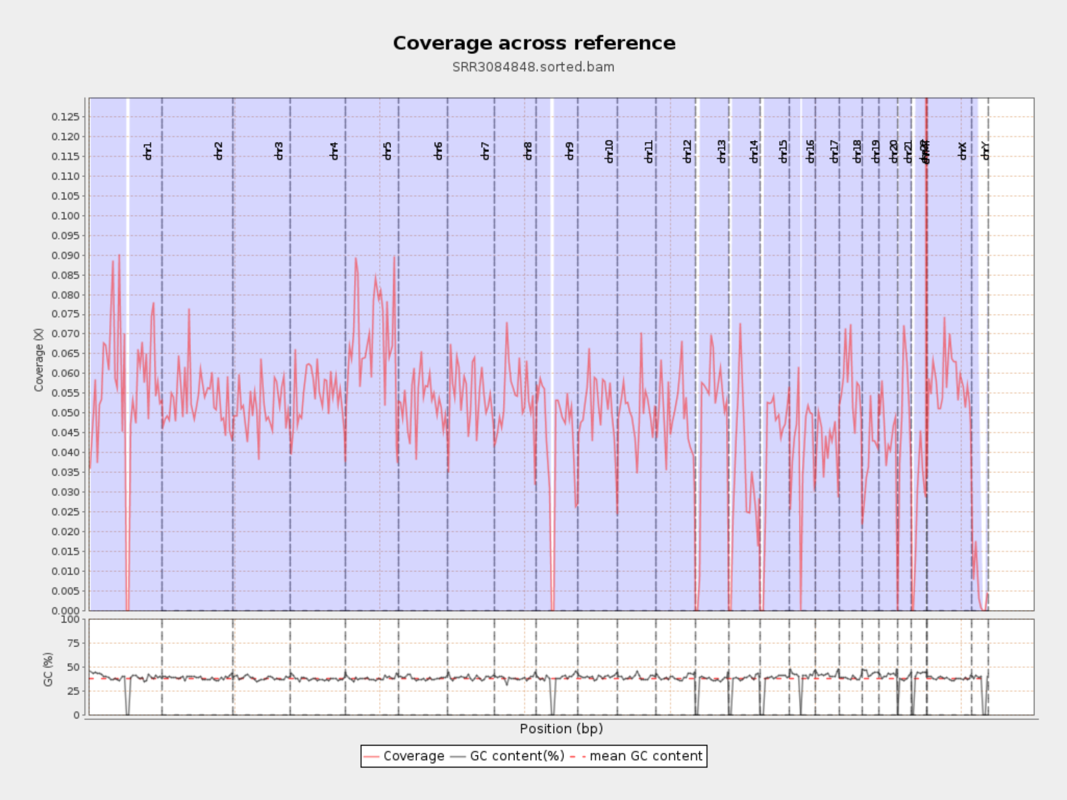
| | |
|---|---|
| General error rate | 0.83% |
| Mismatches | 1,257,796 |
| Insertions | 12,423 |
| Mapped reads with at least one insertion | 0.55% |
| Deletions | 34,289 |
| Mapped reads with at least one deletion | 1.52% |
| Homopolymer indels | 48.2% |

## 2.6. Chromosome stats

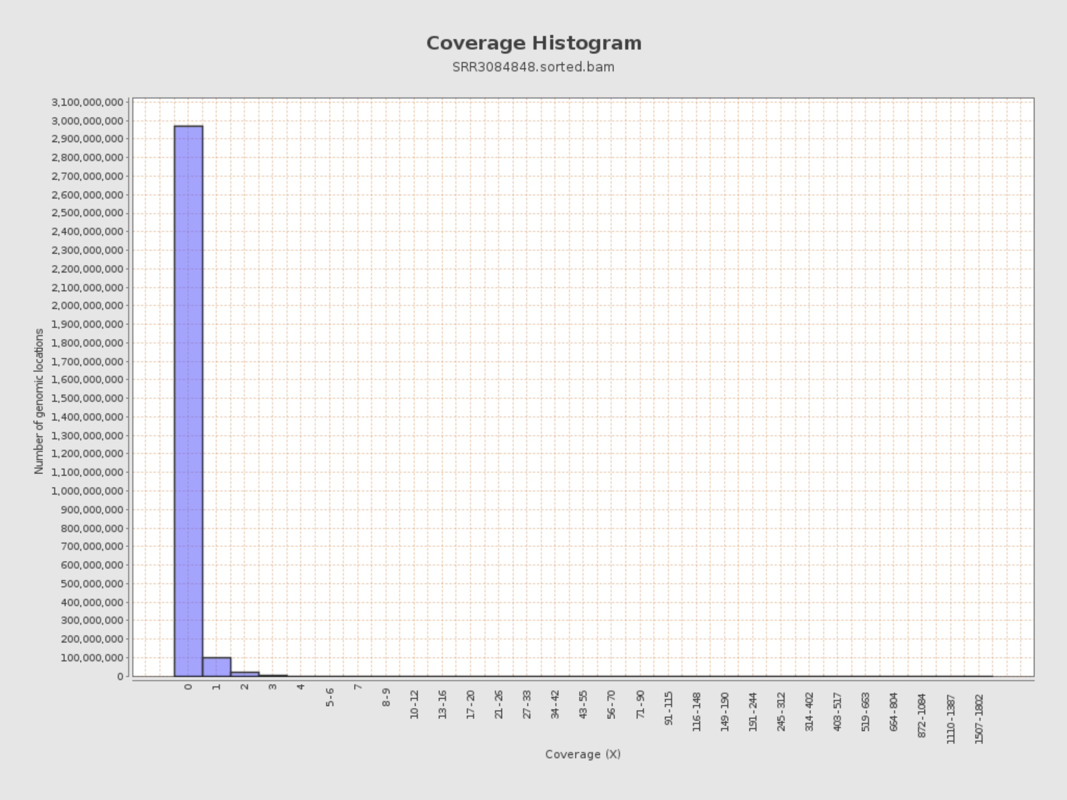
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 14017167 | 0.0562 | 0.5628 |
| chr2 | 243199373 | 13045243 | 0.0536 | 0.3828 |
| chr3 | 198022430 | 10174711 | 0.0514 | 0.2702 |
| chr4 | 191154276 | 10484904 | 0.0549 | 0.287 |
| chr5 | 180915260 | 12485978 | 0.069 | 0.316 |
| chr6 | 171115067 | 9012399 | 0.0527 | 0.2773 |
| chr7 | 159138663 | 8756104 | 0.055 | 0.3326 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7801734 | 0.0533 | 1.1422 |
| chr9 | 141213431 | 6089468 | 0.0431 | 0.3584 |
| chr10 | 135534747 | 7033533 | 0.0519 | 0.3562 |
| chr11 | 135006516 | 6792813 | 0.0503 | 0.3247 |
| chr12 | 133851895 | 6659011 | 0.0497 | 0.2687 |
| chr13 | 115169878 | 5465081 | 0.0475 | 0.2598 |
| chr14 | 107349540 | 3538856 | 0.033 | 0.2287 |
| chr15 | 102531392 | 4195639 | 0.0409 | 0.2399 |
| chr16 | 90354753 | 3677990 | 0.0407 | 0.2588 |
| chr17 | 81195210 | 3388362 | 0.0417 | 0.2557 |
| chr18 | 78077248 | 4493444 | 0.0576 | 0.6456 |
| chr19 | 59128983 | 2335371 | 0.0395 | 0.4223 |
| chr20 | 63025520 | 2836536 | 0.045 | 0.2588 |
| chr21 | 48129895 | 2281700 | 0.0474 | 0.2732 |
| chr22 | 51304566 | 1249996 | 0.0244 | 0.1814 |
| chrMT | 16571 | 162349 | 9.7972 | 5.546 |
| chrX | 155270560 | 8915874 | 0.0574 | 0.3047 |
| chrY | 59373566 | 343678 | 0.0058 | 0.1301 |

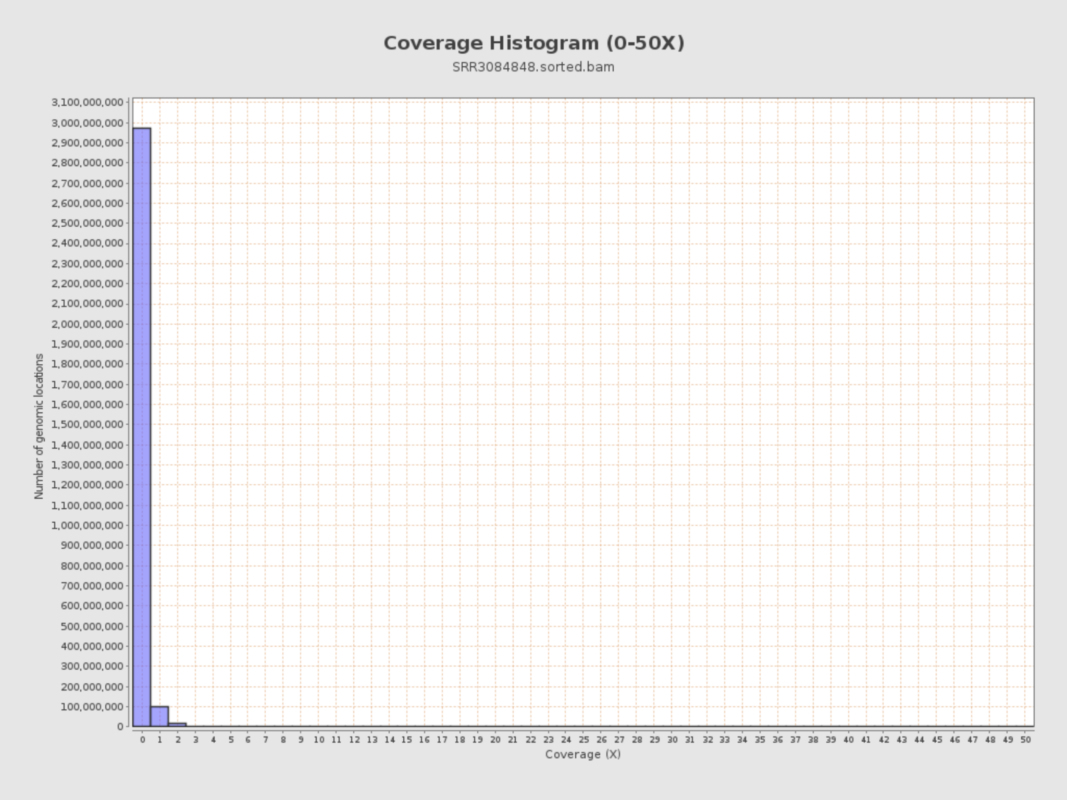
# 3. Results : Coverage across reference



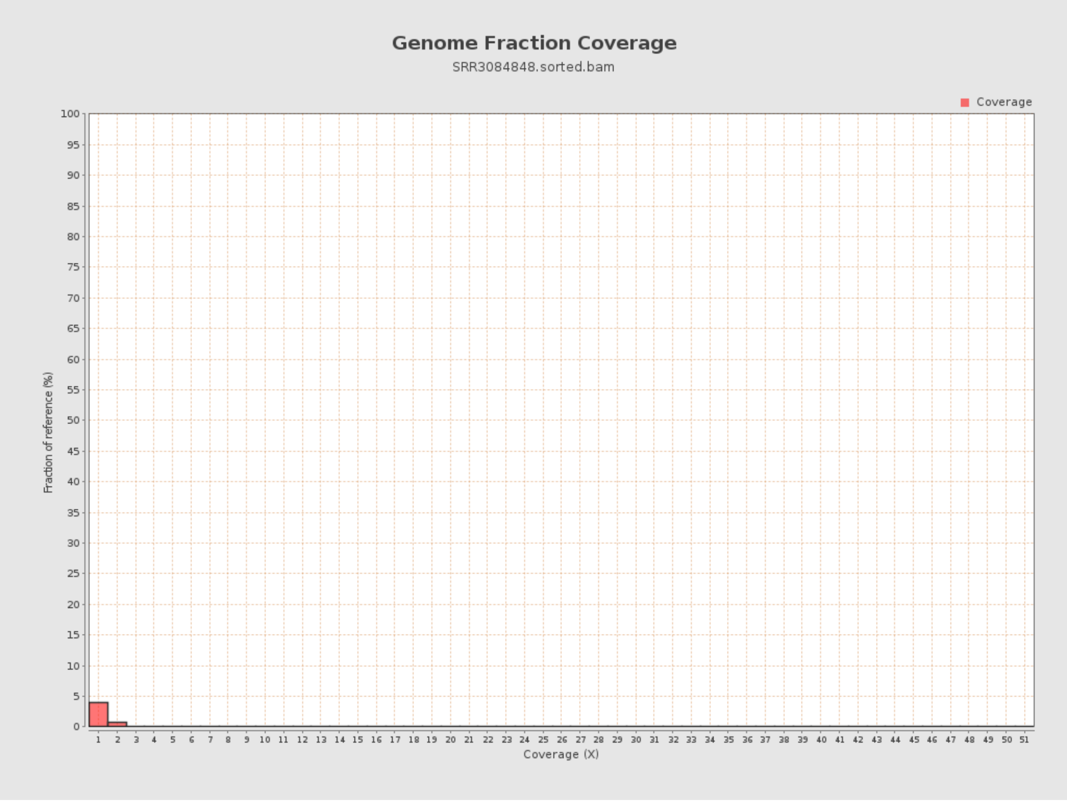
# 4. Results : Coverage Histogram



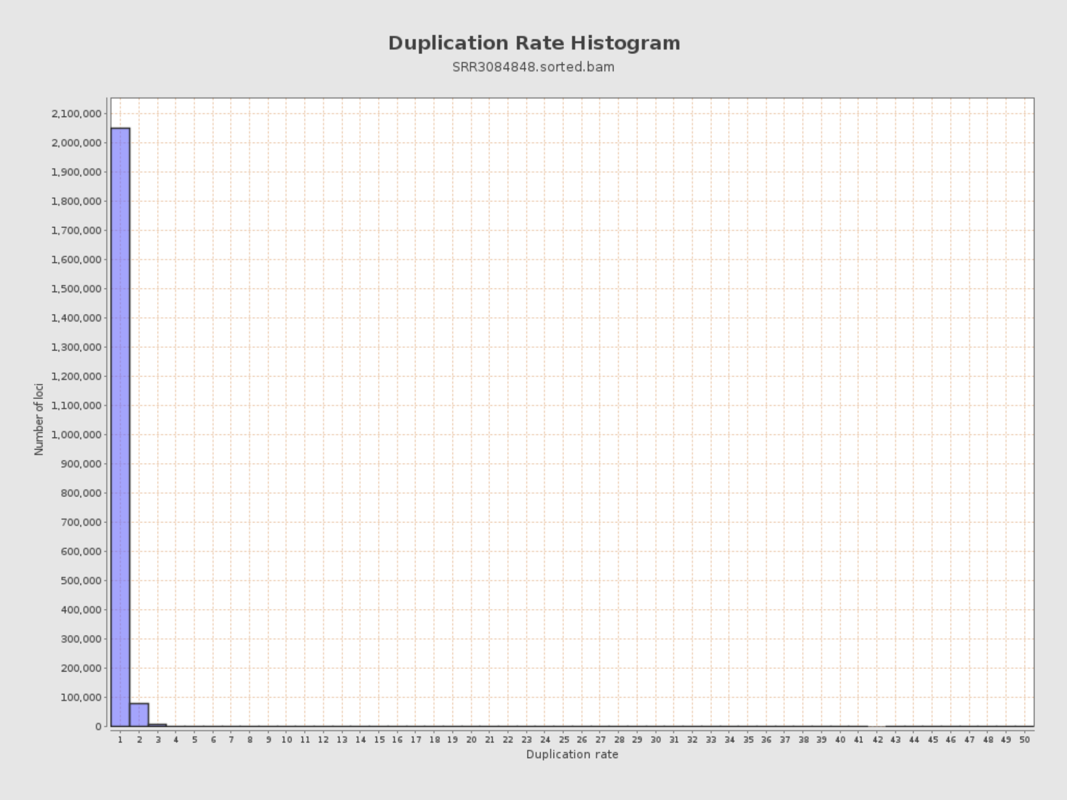
# 5. Results : Coverage Histogram (0-50X)



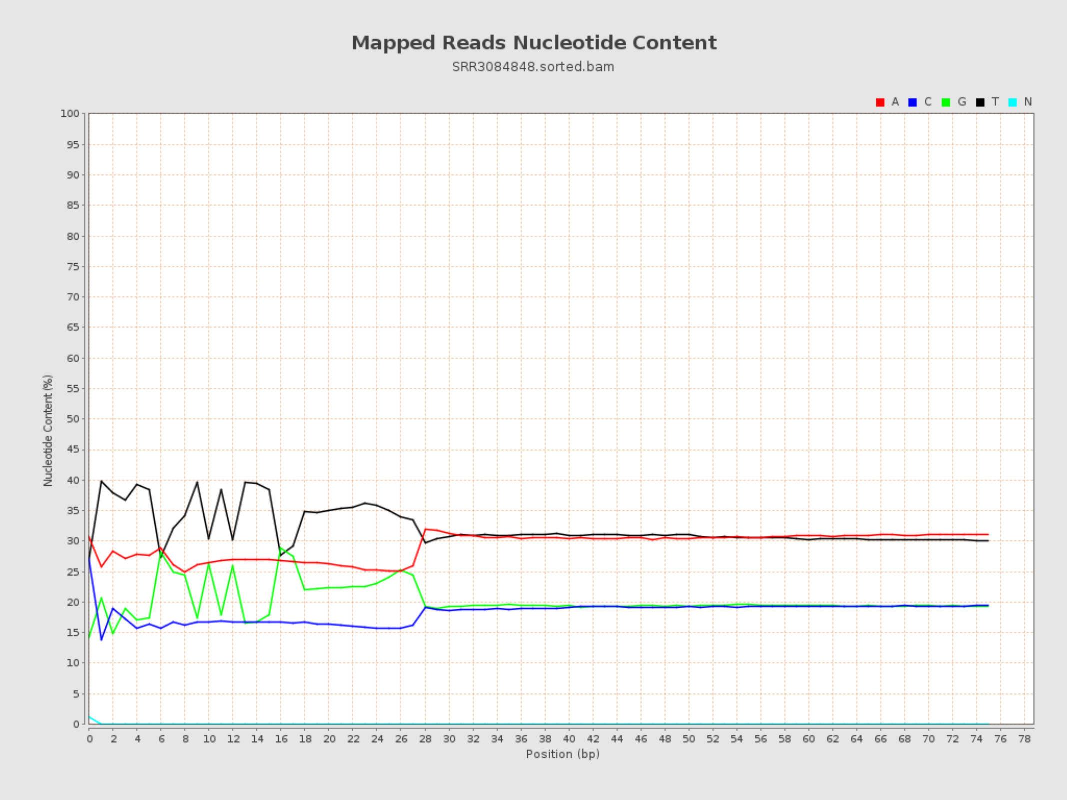
# 6. Results : Genome Fraction Coverage



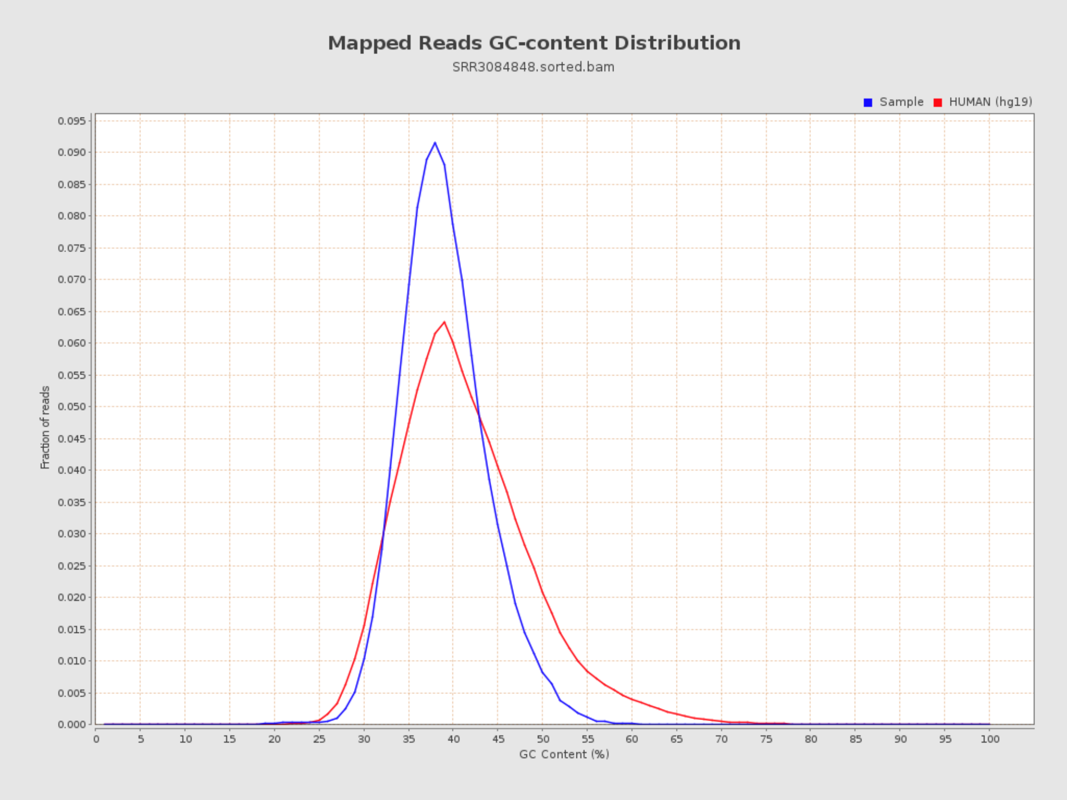
# 7. Results : Duplication Rate Histogram



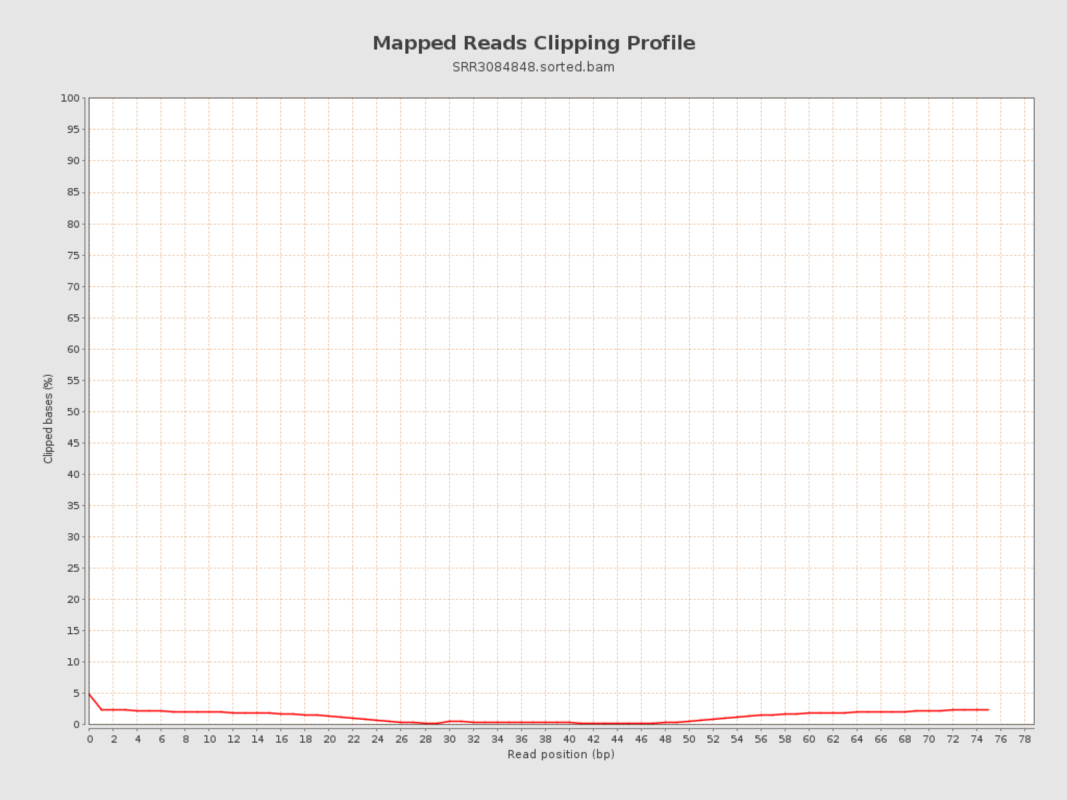
# 8. Results : Mapped Reads Nucleotide Content



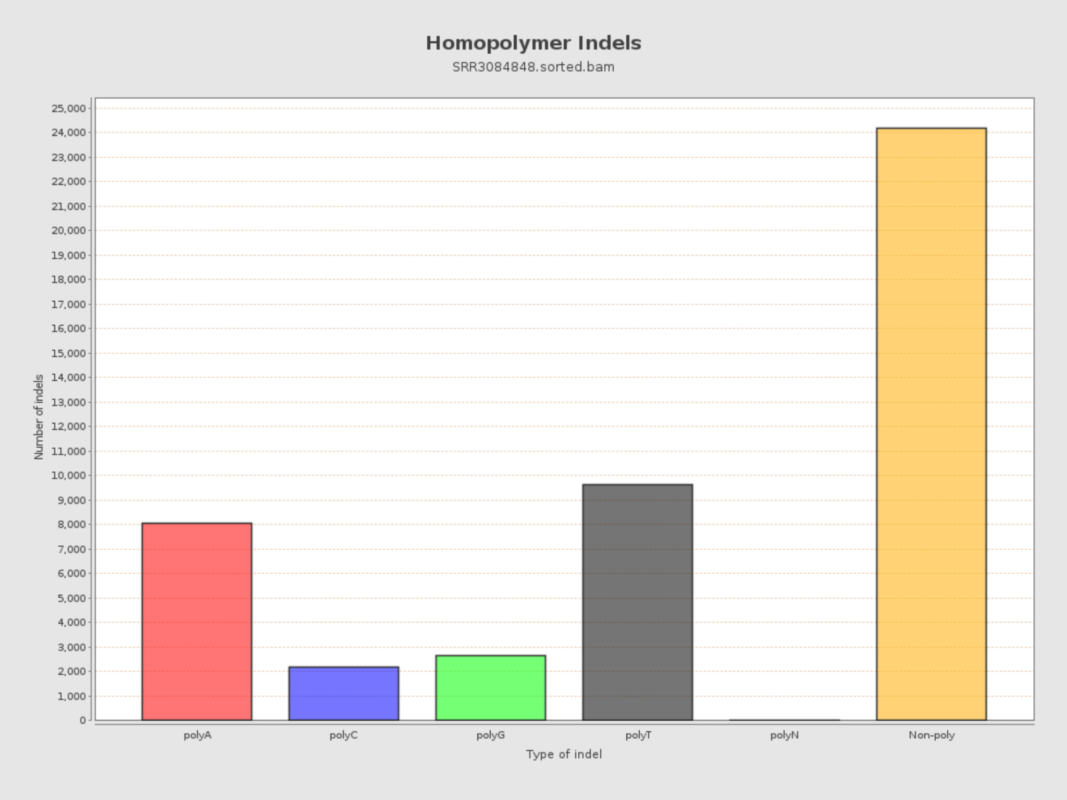
# 9. Results : Mapped Reads GC-content Distribution



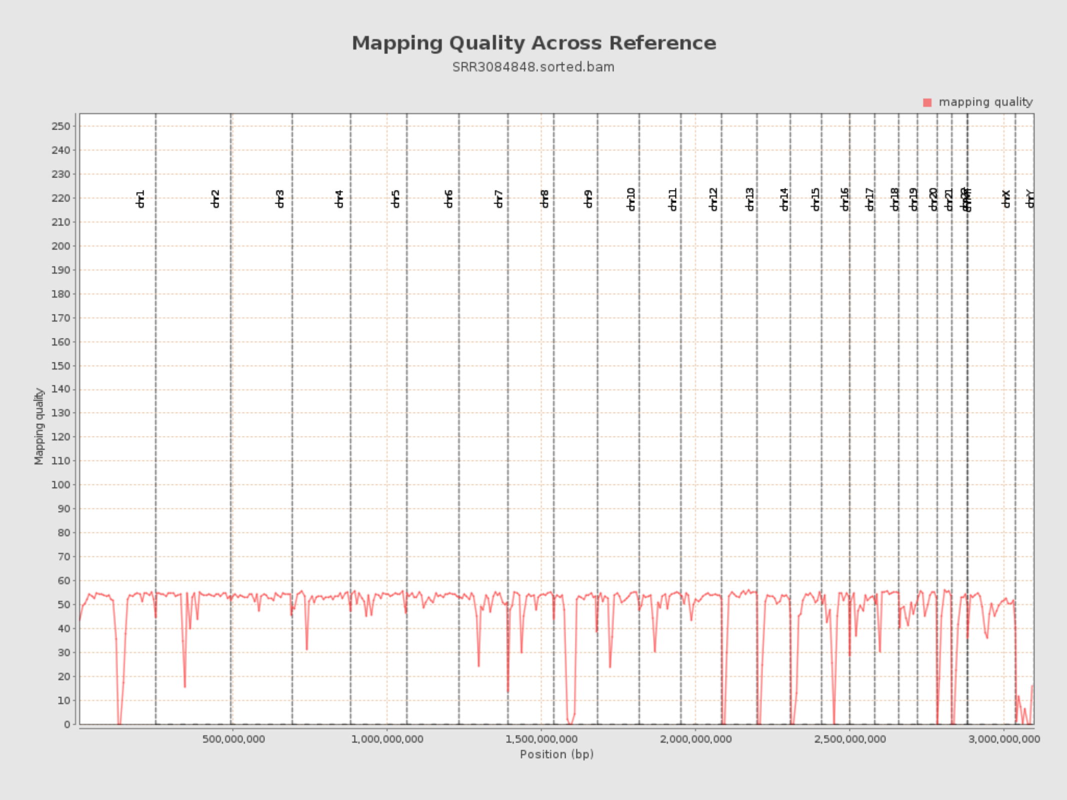
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram