# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/18 23:42:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR053615.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_SRR053615 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053615.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Apr 18 23:42:49 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR053615.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 6,074,324 |
| Mapped reads | 3,184,447 / 52.42% |
| Unmapped reads | 2,889,877 / 47.58% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 129 / 0% |
| Read min/max/mean length | 30 / 48 / 48 |
| Duplicated reads (estimated) | 439,999 / 7.24% |
| Duplication rate | 11.75% |
| Clipped reads | 555,879 / 9.15% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 45,318,891 / 30.71% |
| Number/percentage of C's | 27,930,758 / 18.93% |
| Number/percentage of T's | 45,035,651 / 30.52% |
| Number/percentage of G's | 29,282,499 / 19.84% |
| Number/percentage of N's | 4,690 / 0% |
| GC Percentage | 38.77% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0477 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4141 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.92 |

## 2.5. Mismatches and indels

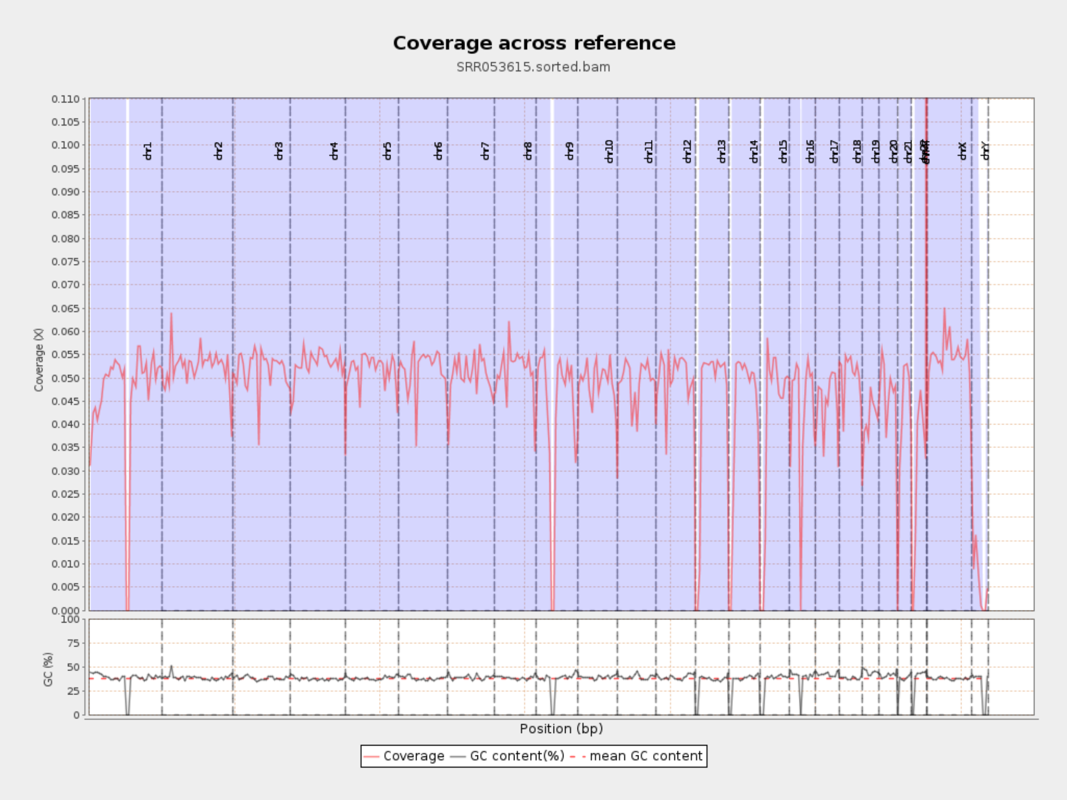
| | |
|---|---|
| General error rate | 0.82% |
| Mismatches | 1,196,436 |
| Insertions | 7,504 |
| Mapped reads with at least one insertion | 0.24% |
| Deletions | 23,047 |
| Mapped reads with at least one deletion | 0.72% |
| Homopolymer indels | 45.09% |

## 2.6. Chromosome stats

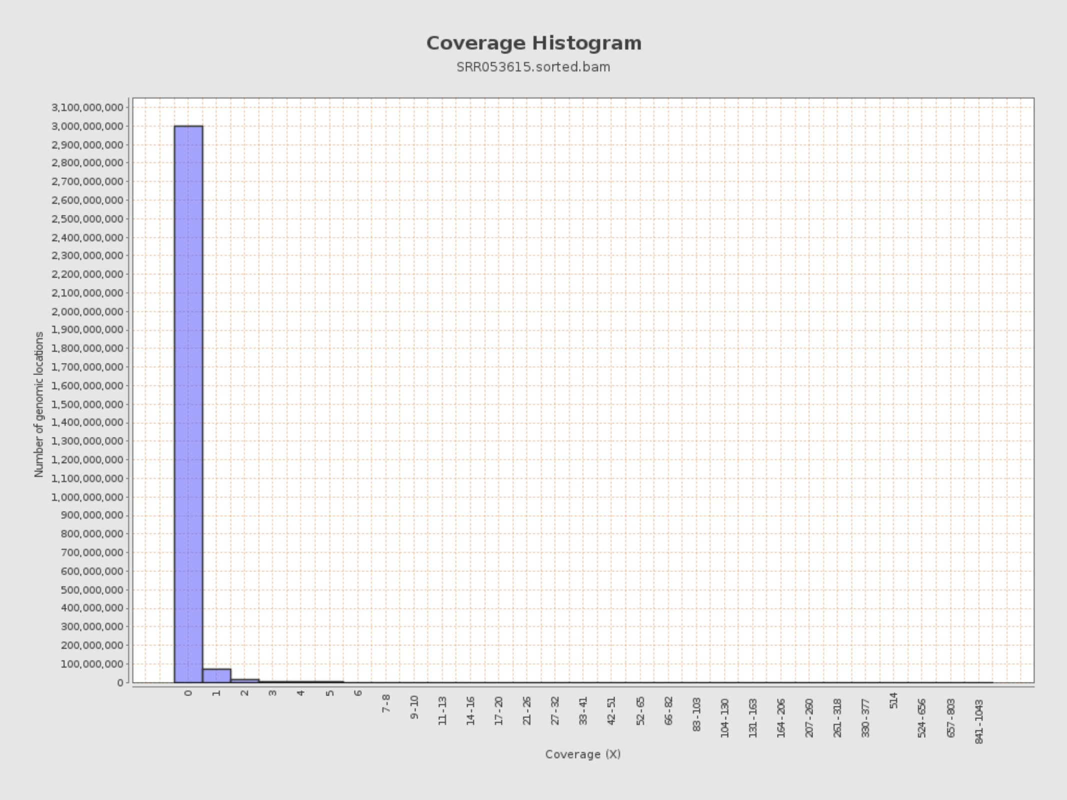
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 11574473 | 0.0464 | 0.3956 |
| chr2 | 243199373 | 12753219 | 0.0524 | 0.6224 |
| chr3 | 198022430 | 10277175 | 0.0519 | 0.3535 |
| chr4 | 191154276 | 10115293 | 0.0529 | 0.3767 |
| chr5 | 180915260 | 9388099 | 0.0519 | 0.3553 |
| chr6 | 171115067 | 8889289 | 0.0519 | 0.4139 |
| chr7 | 159138663 | 8103081 | 0.0509 | 0.4304 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 7580248 | 0.0518 | 0.3922 |
| chr9 | 141213431 | 6079828 | 0.0431 | 0.3378 |
| chr10 | 135534747 | 6721814 | 0.0496 | 0.41 |
| chr11 | 135006516 | 6631426 | 0.0491 | 0.4193 |
| chr12 | 133851895 | 6712561 | 0.0501 | 0.3446 |
| chr13 | 115169878 | 4992486 | 0.0433 | 0.3231 |
| chr14 | 107349540 | 4489112 | 0.0418 | 0.3352 |
| chr15 | 102531392 | 4183350 | 0.0408 | 0.7307 |
| chr16 | 90354753 | 3897787 | 0.0431 | 0.3348 |
| chr17 | 81195210 | 3612856 | 0.0445 | 0.3221 |
| chr18 | 78077248 | 3960277 | 0.0507 | 0.4062 |
| chr19 | 59128983 | 2440559 | 0.0413 | 0.3633 |
| chr20 | 63025520 | 2955735 | 0.0469 | 0.3835 |
| chr21 | 48129895 | 1937471 | 0.0403 | 0.3458 |
| chr22 | 51304566 | 1466936 | 0.0286 | 0.2525 |
| chrMT | 16571 | 12896 | 0.7782 | 1.8799 |
| chrX | 155270560 | 8438333 | 0.0543 | 0.4066 |
| chrY | 59373566 | 391323 | 0.0066 | 0.1166 |

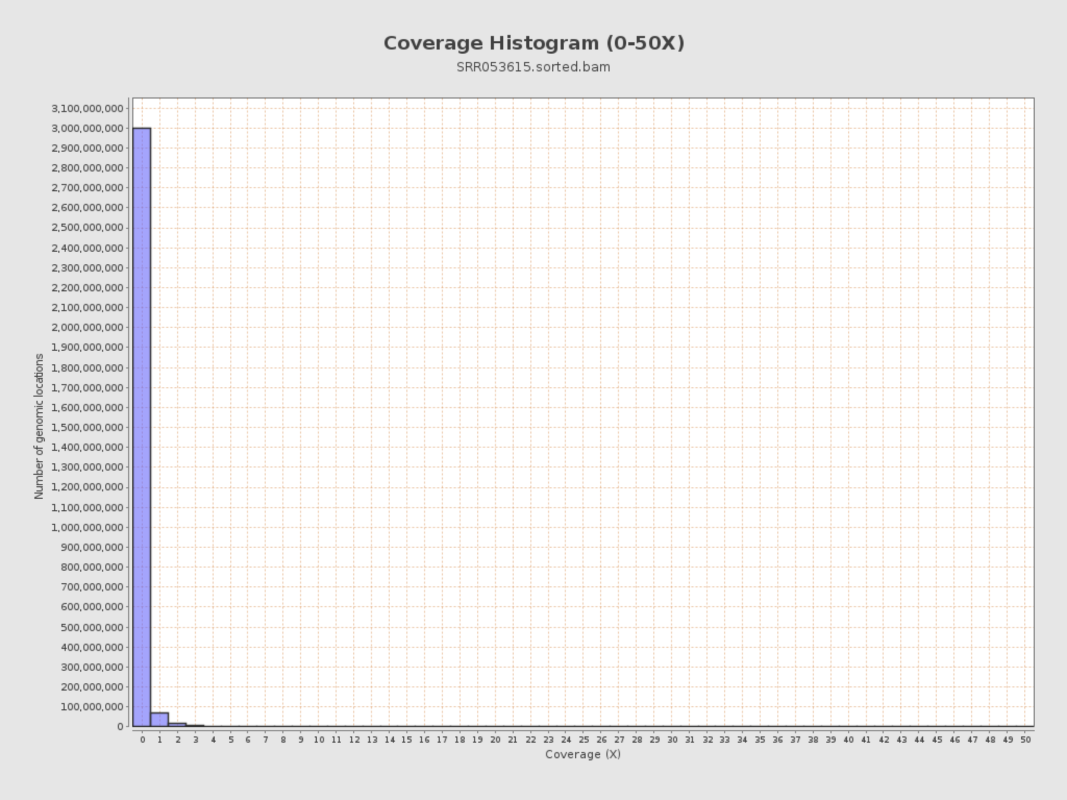
# 3. Results : Coverage across reference



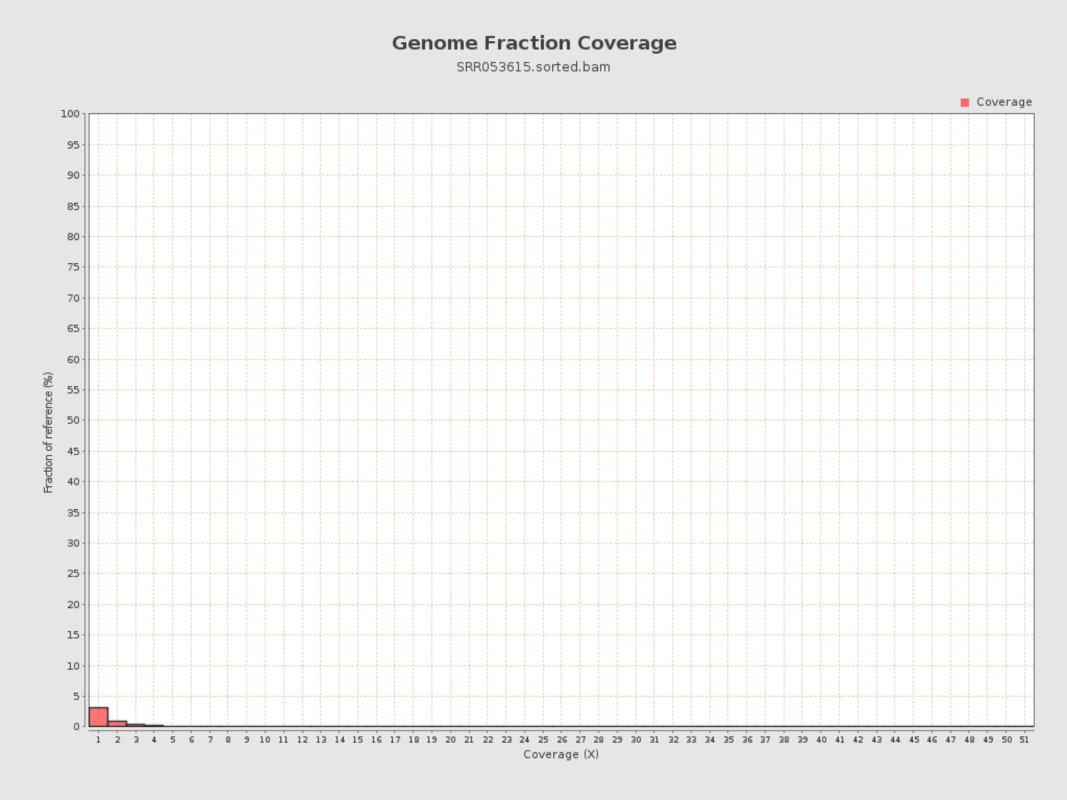
# 4. Results : Coverage Histogram



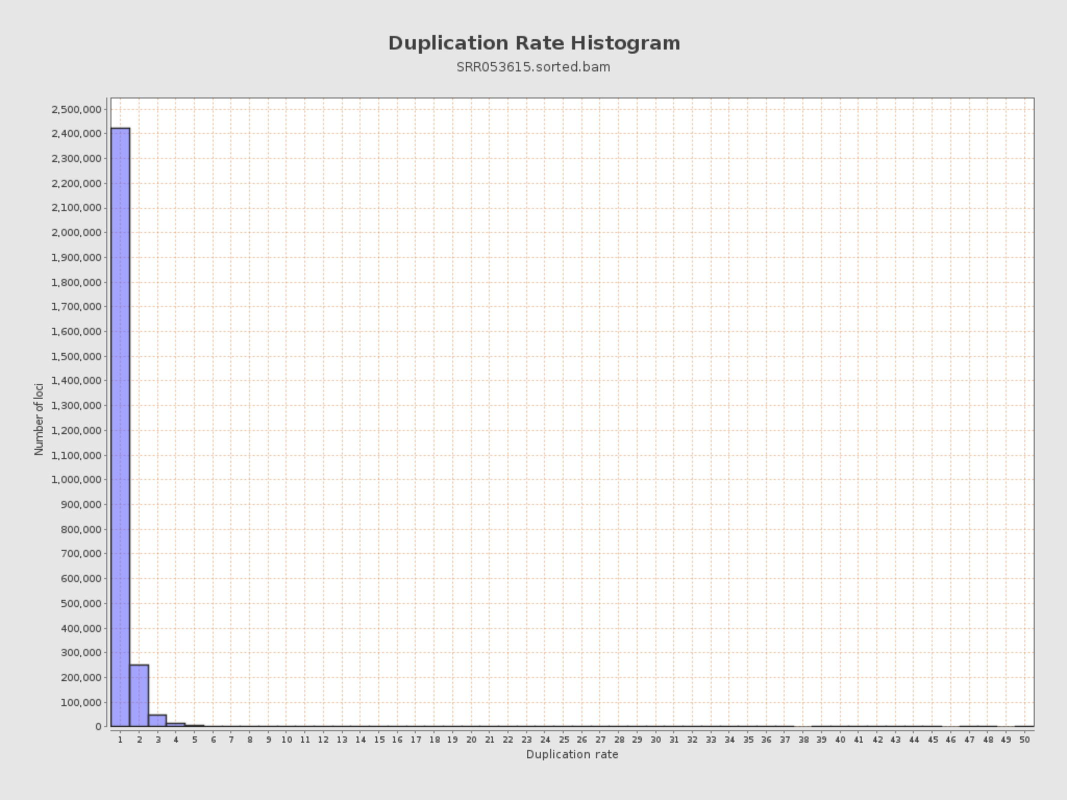
# 5. Results : Coverage Histogram (0-50X)



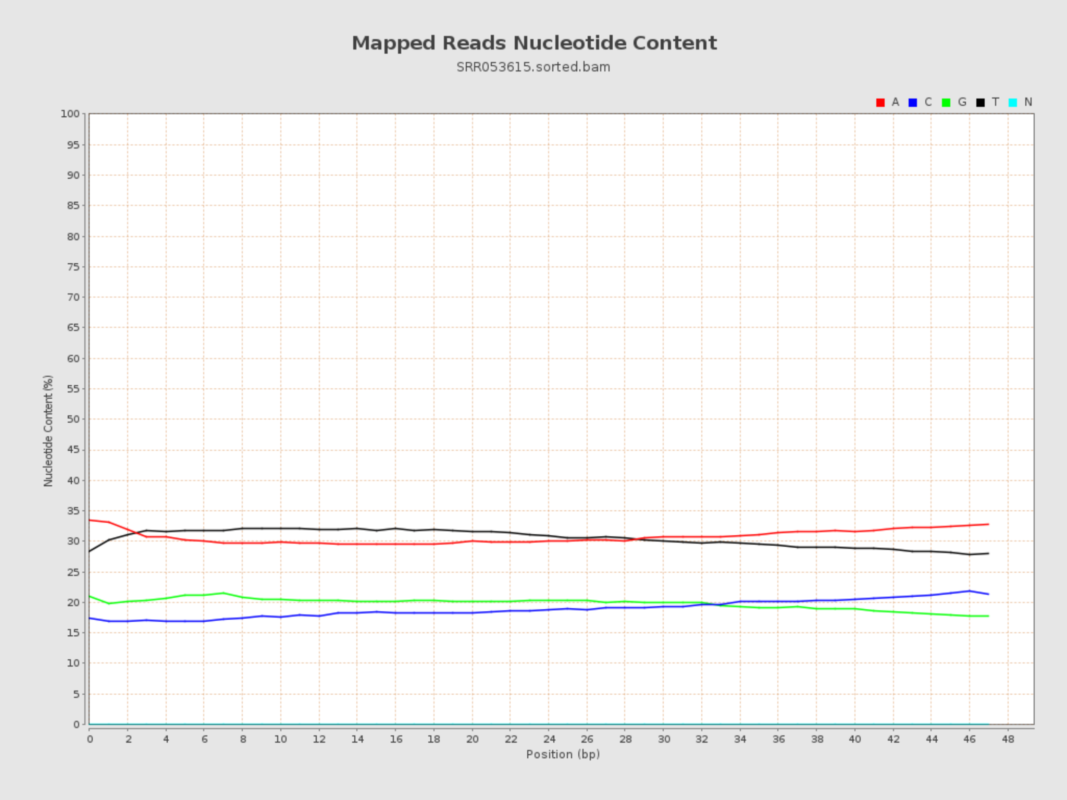
# 6. Results : Genome Fraction Coverage



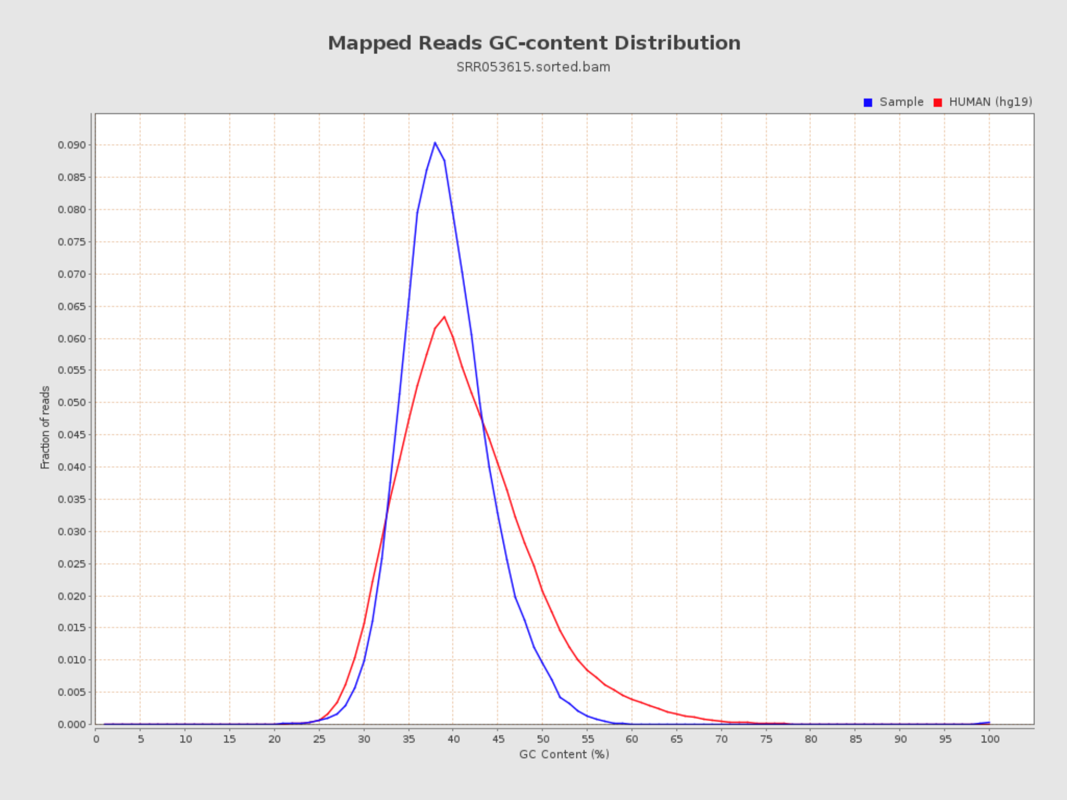
# 7. Results : Duplication Rate Histogram



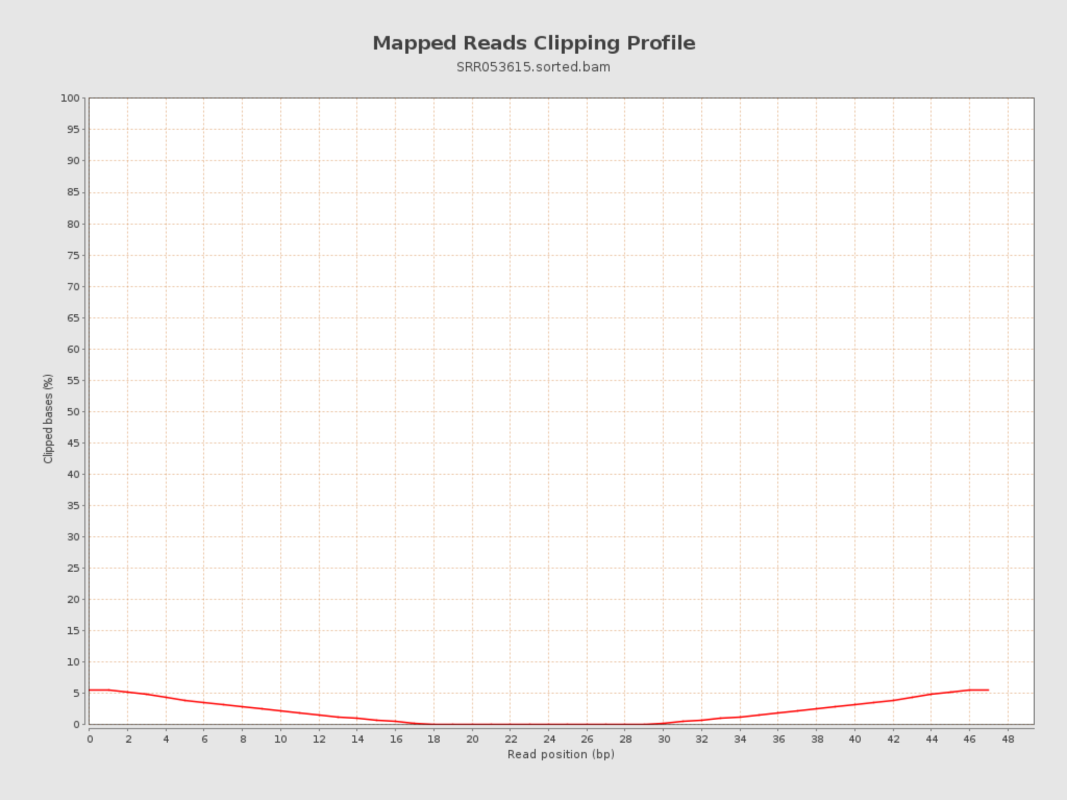
# 8. Results : Mapped Reads Nucleotide Content



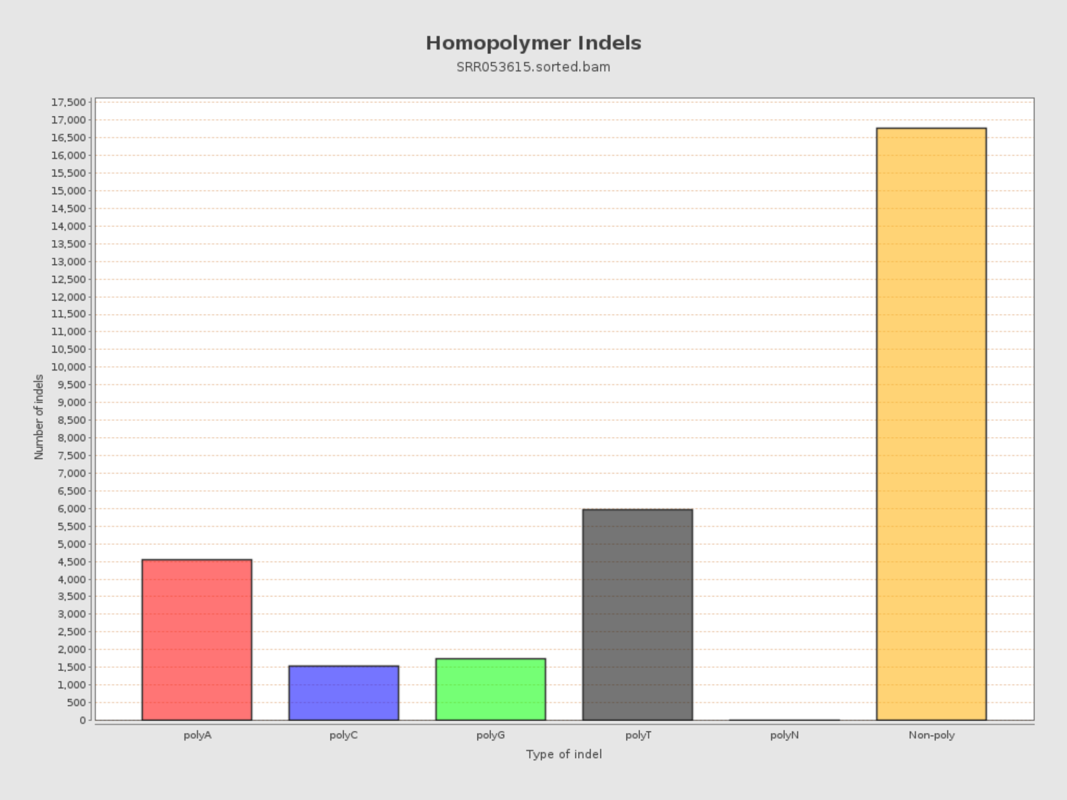
# 9. Results : Mapped Reads GC-content Distribution



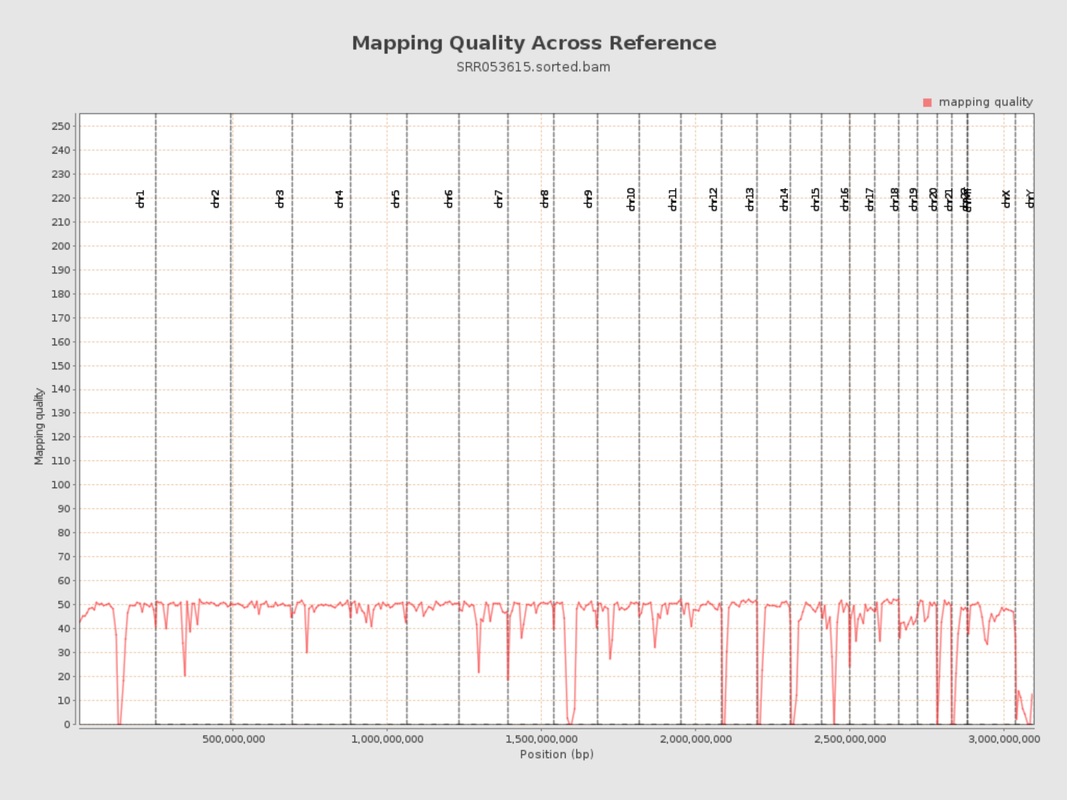
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram