# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/14 02:29:13*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004113.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_SRR6004113 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004113.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 14 02:29:12 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6004113.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,037,972 |
| Mapped reads | 3,579,835 / 88.65% |
| Unmapped reads | 458,137 / 11.35% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 21,991 / 0.54% |
| Read min/max/mean length | 30 / 76 / 76.19 |
| Duplicated reads (estimated) | 211,705 / 5.24% |
| Duplication rate | 4.62% |
| Clipped reads | 1,393,242 / 34.5% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 67,579,081 / 27.67% |
| Number/percentage of C's | 46,111,348 / 18.88% |
| Number/percentage of T's | 77,219,178 / 31.62% |
| Number/percentage of G's | 53,257,954 / 21.81% |
| Number/percentage of N's | 33,490 / 0.01% |
| GC Percentage | 40.69% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0789 |
| | |

| | |
|---|---|
| Standard Deviation | 0.6361 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.04 |

## 2.5. Mismatches and indels

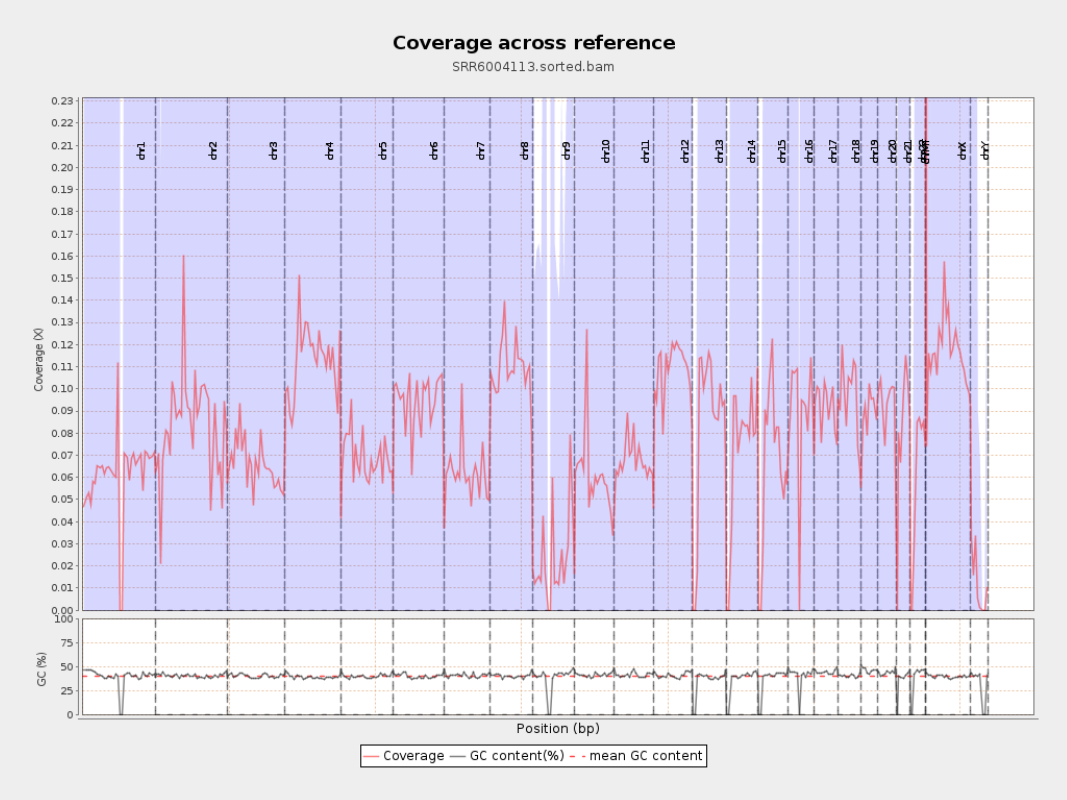
| | |
|---|---|
| General error rate | 0.95% |
| Mismatches | 2,276,749 |
| Insertions | 19,773 |
| Mapped reads with at least one insertion | 0.55% |
| Deletions | 63,829 |
| Mapped reads with at least one deletion | 1.76% |
| Homopolymer indels | 46.37% |

## 2.6. Chromosome stats

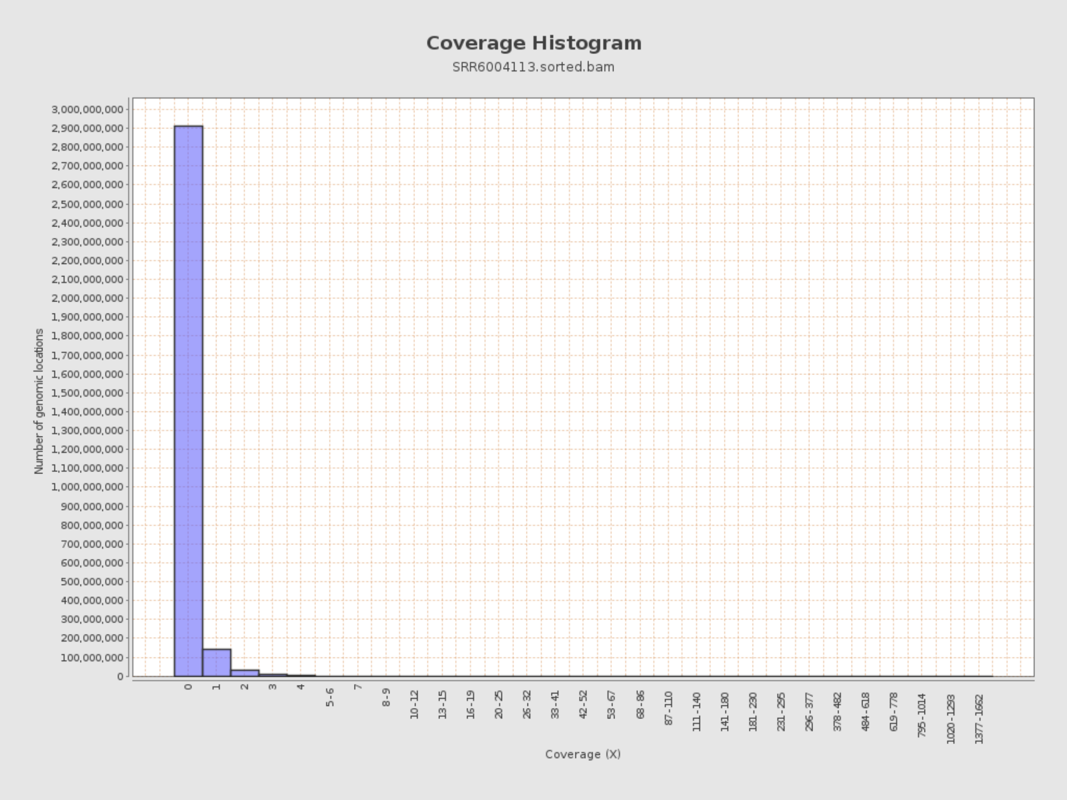
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 15161795 | 0.0608 | 1.1229 |
| chr2 | 243199373 | 20382403 | 0.0838 | 0.7602 |
| chr3 | 198022430 | 13058758 | 0.0659 | 0.3295 |
| chr4 | 191154276 | 21718998 | 0.1136 | 0.4628 |
| chr5 | 180915260 | 12432666 | 0.0687 | 0.3329 |
| chr6 | 171115067 | 16159896 | 0.0944 | 0.47 |
| chr7 | 159138663 | 9824867 | 0.0617 | 0.6359 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 16038294 | 0.1096 | 1.0949 |
| chr9 | 141213431 | 3272656 | 0.0232 | 0.4644 |
| chr10 | 135534747 | 8296365 | 0.0612 | 0.6245 |
| chr11 | 135006516 | 9130450 | 0.0676 | 0.5042 |
| chr12 | 133851895 | 14668783 | 0.1096 | 0.4222 |
| chr13 | 115169878 | 9710973 | 0.0843 | 0.3652 |
| chr14 | 107349540 | 7672363 | 0.0715 | 0.3639 |
| chr15 | 102531392 | 6695418 | 0.0653 | 0.3239 |
| chr16 | 90354753 | 7920798 | 0.0877 | 0.4893 |
| chr17 | 81195210 | 7516638 | 0.0926 | 0.4343 |
| chr18 | 78077248 | 7603940 | 0.0974 | 1.2327 |
| chr19 | 59128983 | 5284339 | 0.0894 | 0.7581 |
| chr20 | 63025520 | 5912676 | 0.0938 | 0.413 |
| chr21 | 48129895 | 4026386 | 0.0837 | 0.4012 |
| chr22 | 51304566 | 2997919 | 0.0584 | 0.3054 |
| chrMT | 16571 | 32550 | 1.9643 | 1.9516 |
| chrX | 155270560 | 18097073 | 0.1166 | 0.4918 |
| chrY | 59373566 | 691329 | 0.0116 | 0.2413 |

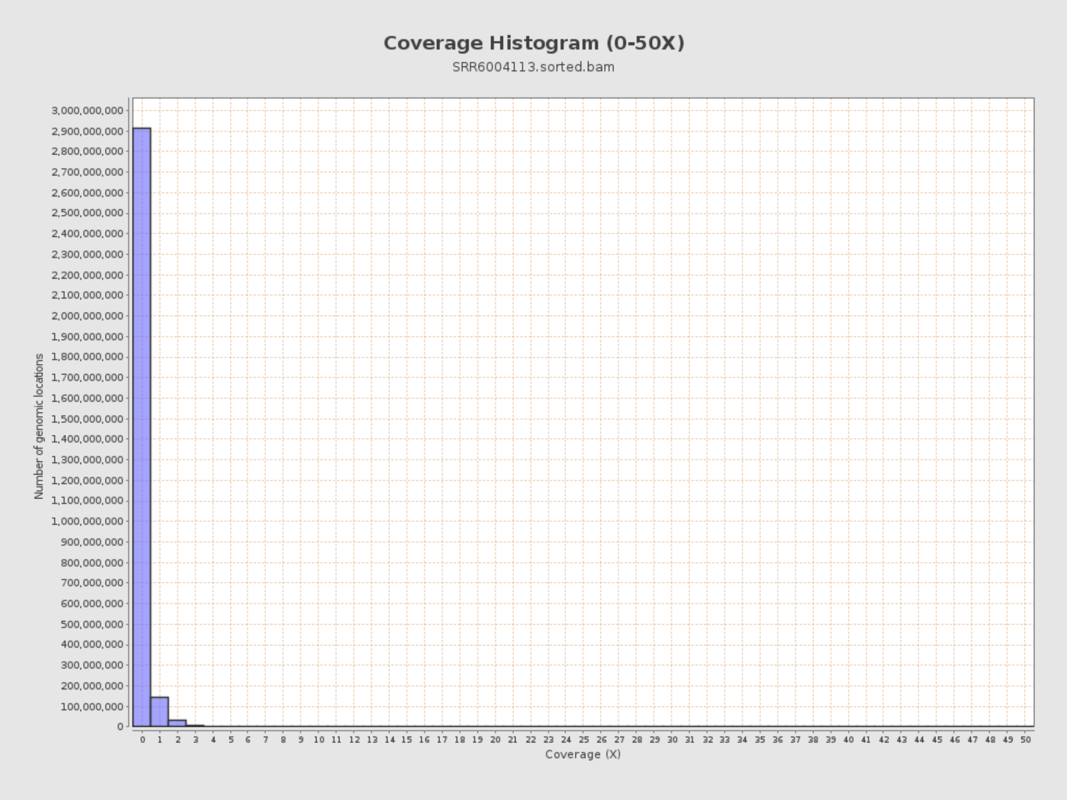
# 3. Results : Coverage across reference



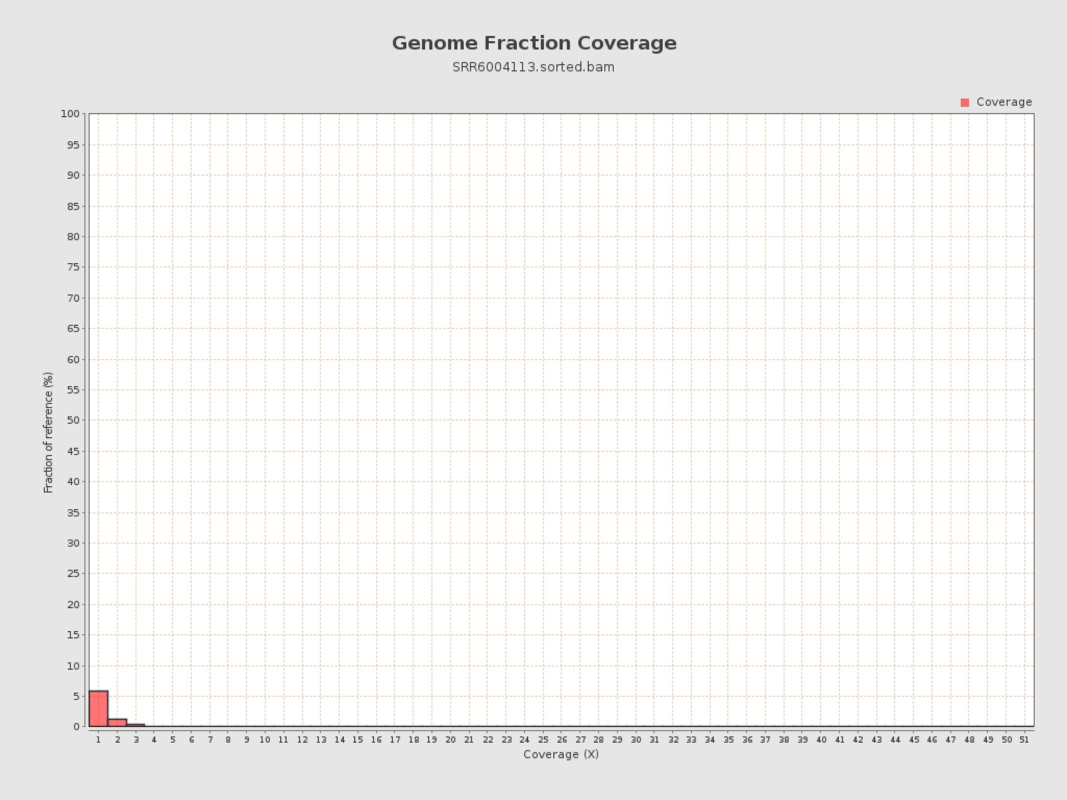
# 4. Results : Coverage Histogram



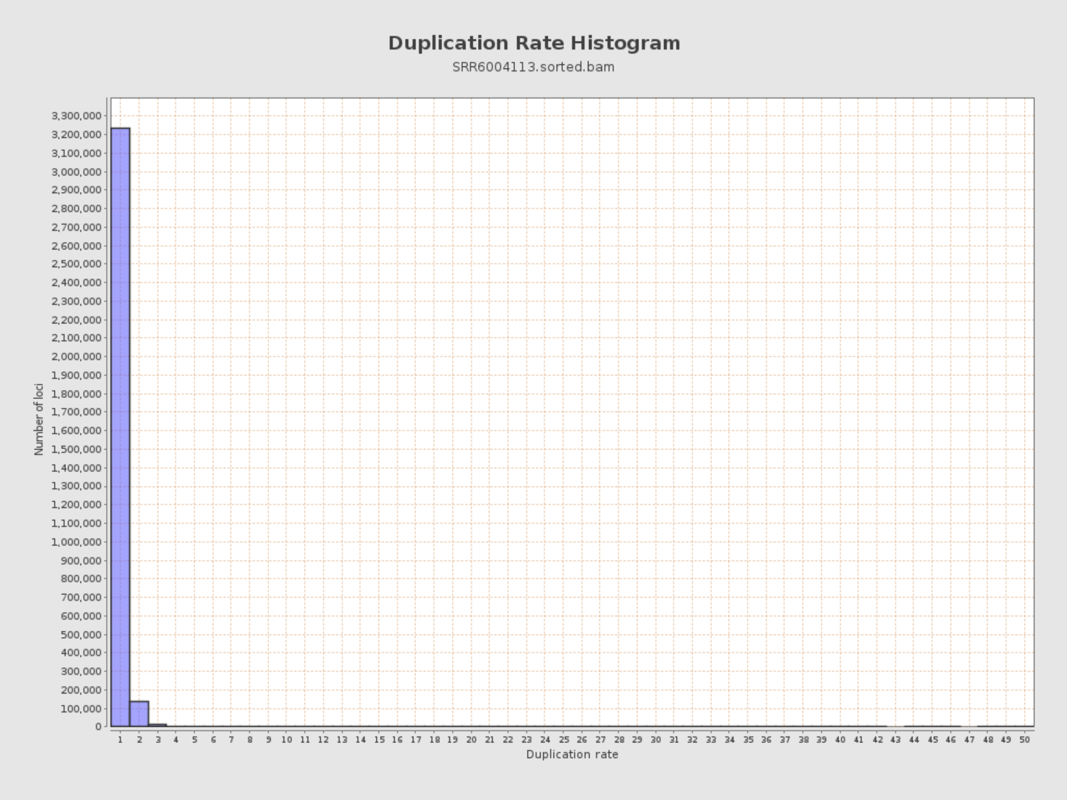
# 5. Results : Coverage Histogram (0-50X)



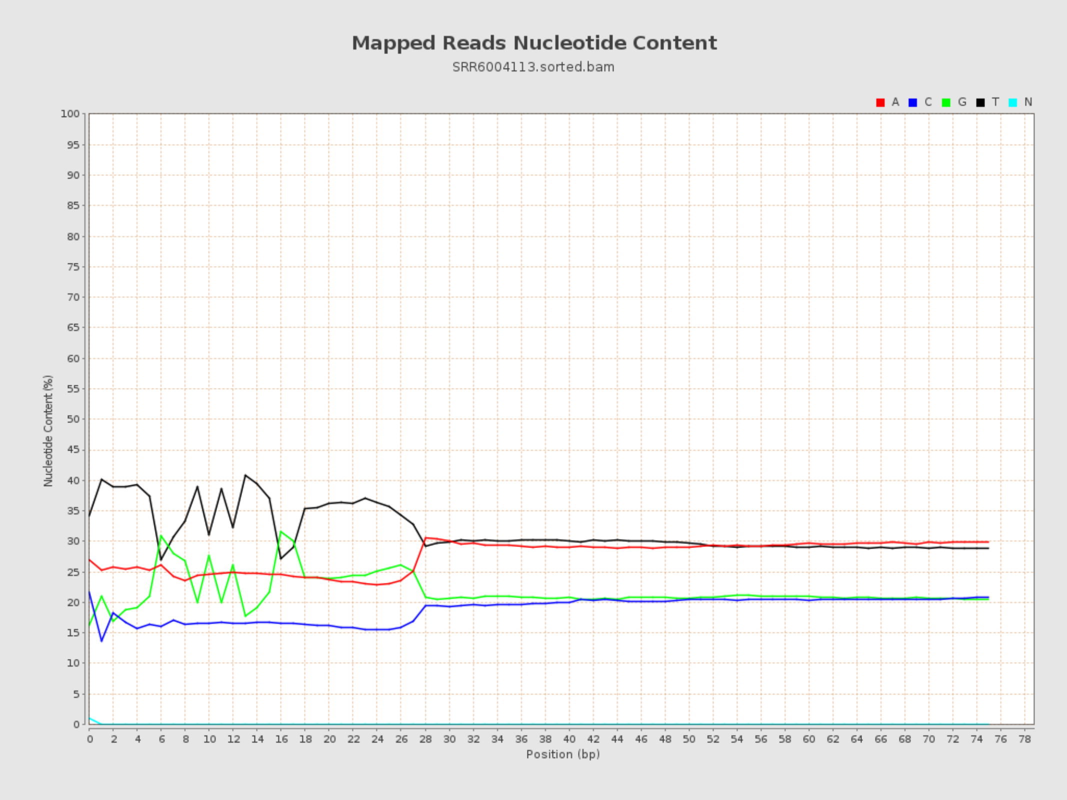
# 6. Results : Genome Fraction Coverage



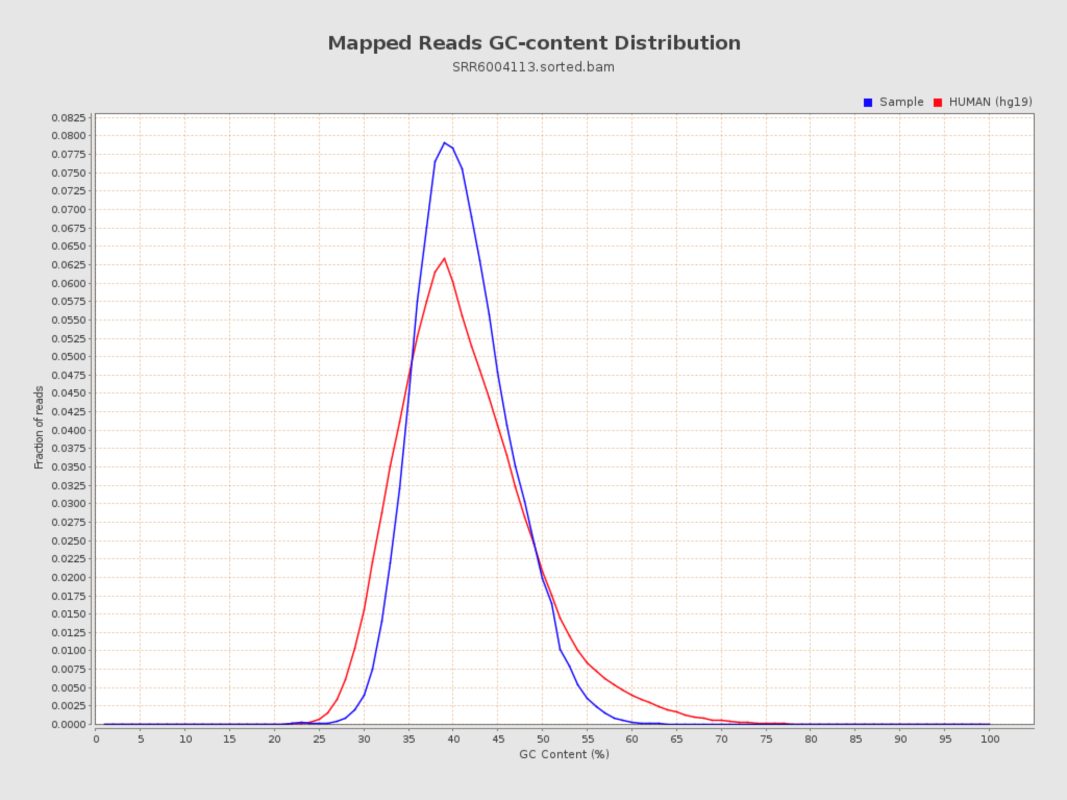
# 7. Results : Duplication Rate Histogram



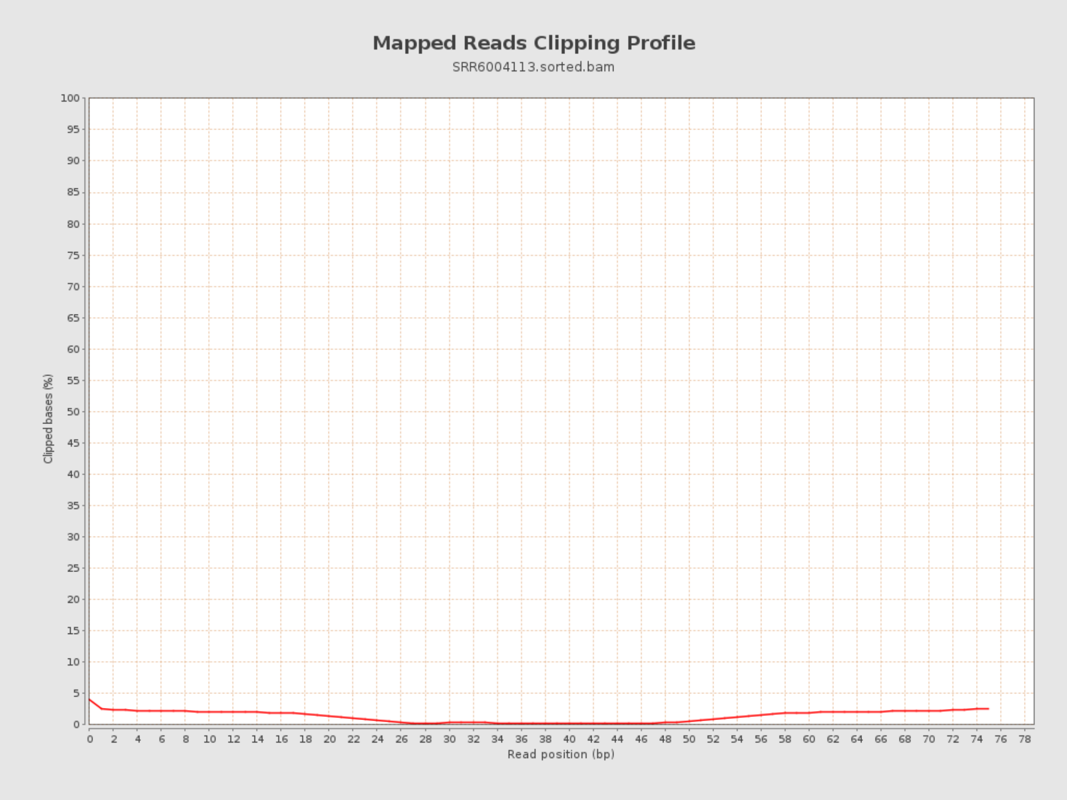
# 8. Results : Mapped Reads Nucleotide Content



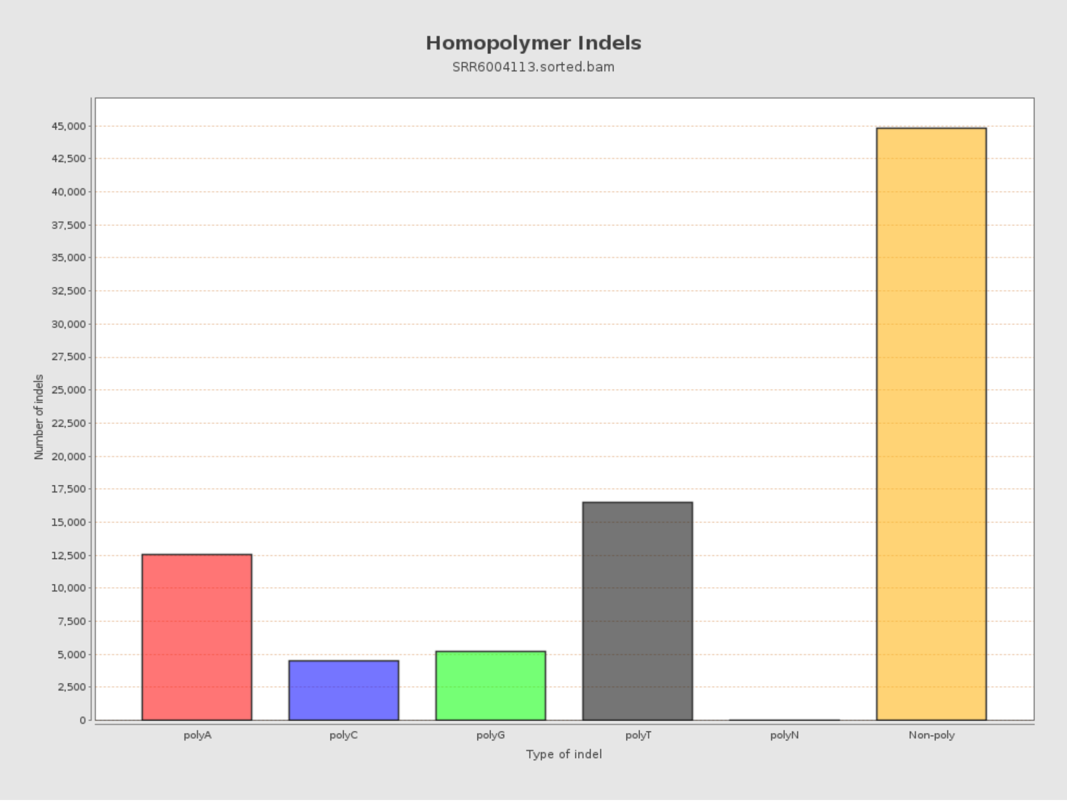
# 9. Results : Mapped Reads GC-content Distribution



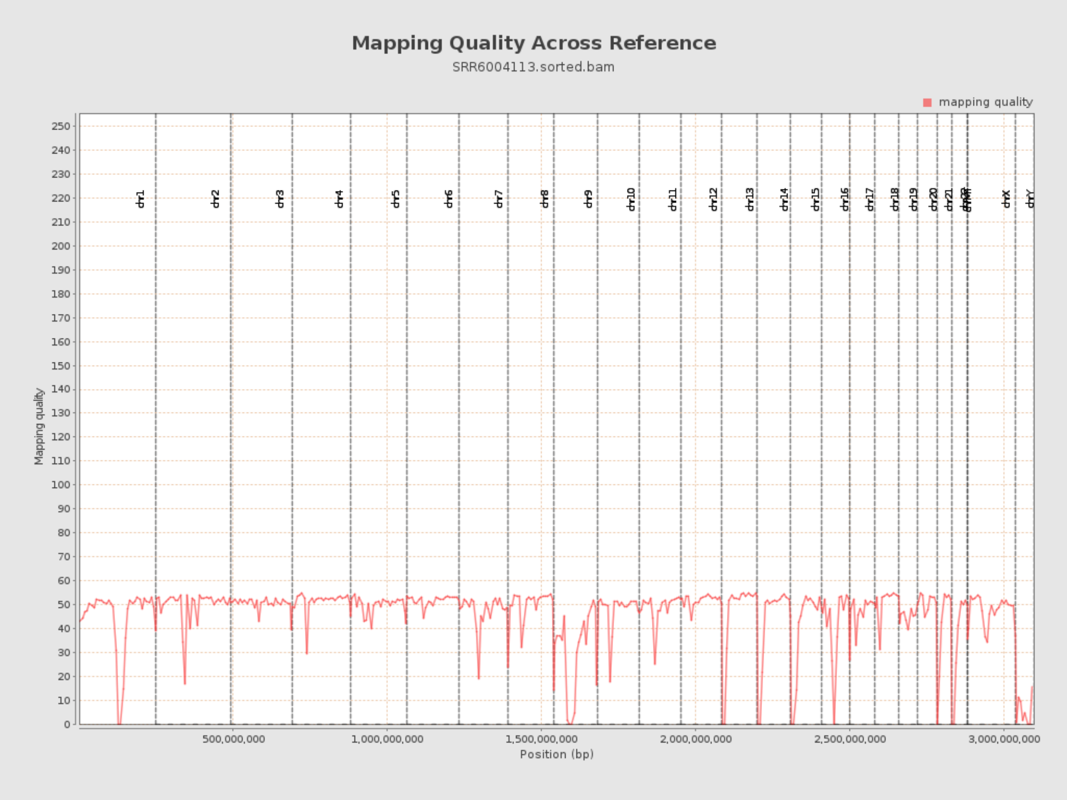
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram