# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/18 23:51:57*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR053617.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_SRR053617 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053617.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Apr 18 23:51:56 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR053617.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 8,449,289 |
| Mapped reads | 7,186,918 / 85.06% |
| Unmapped reads | 1,262,371 / 14.94% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 280 / 0% |
| Read min/max/mean length | 30 / 48 / 48 |
| Duplicated reads (estimated) | 1,411,788 / 16.71% |
| Duplication rate | 14.49% |
| Clipped reads | 604,486 / 7.15% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 98,633,363 / 29.05% |
| Number/percentage of C's | 67,568,478 / 19.9% |
| Number/percentage of T's | 99,254,854 / 29.23% |
| Number/percentage of G's | 74,077,547 / 21.82% |
| Number/percentage of N's | 7,834 / 0% |
| GC Percentage | 41.72% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1097 |
| | |

| | |
|---|---|
| Standard Deviation | 0.7953 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.59 |

## 2.5. Mismatches and indels

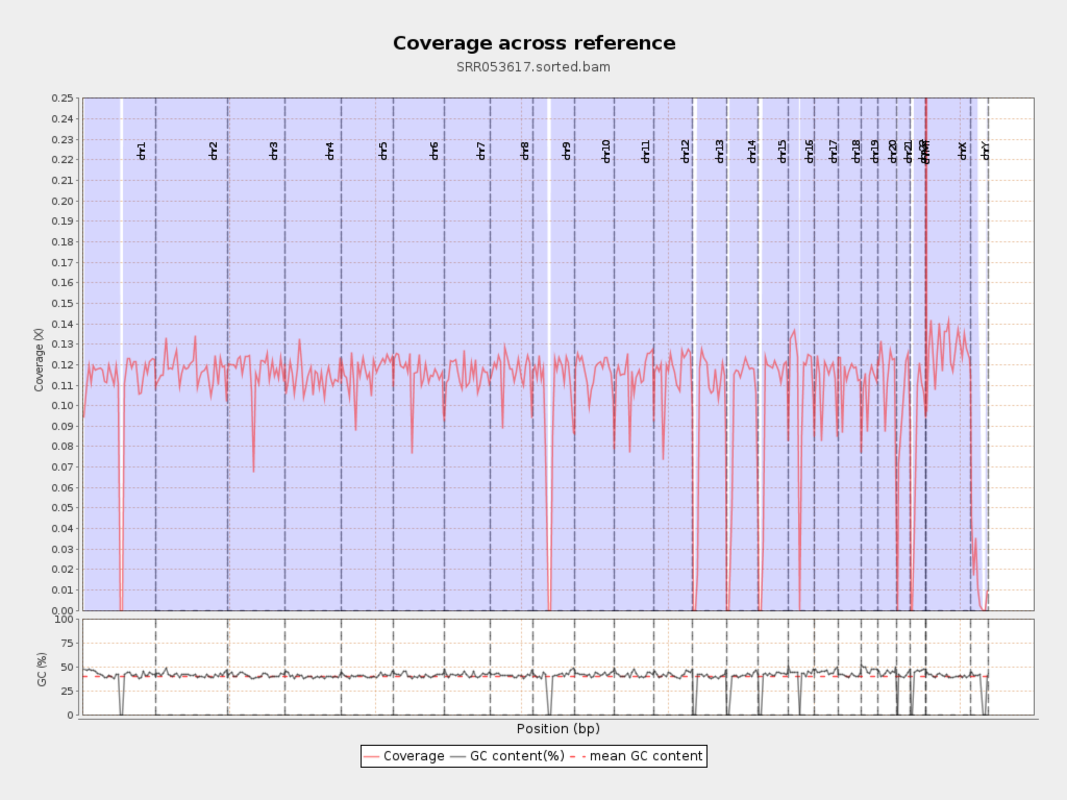
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 1,703,688 |
| Insertions | 13,232 |
| Mapped reads with at least one insertion | 0.18% |
| Deletions | 42,702 |
| Mapped reads with at least one deletion | 0.59% |
| Homopolymer indels | 46.34% |

## 2.6. Chromosome stats

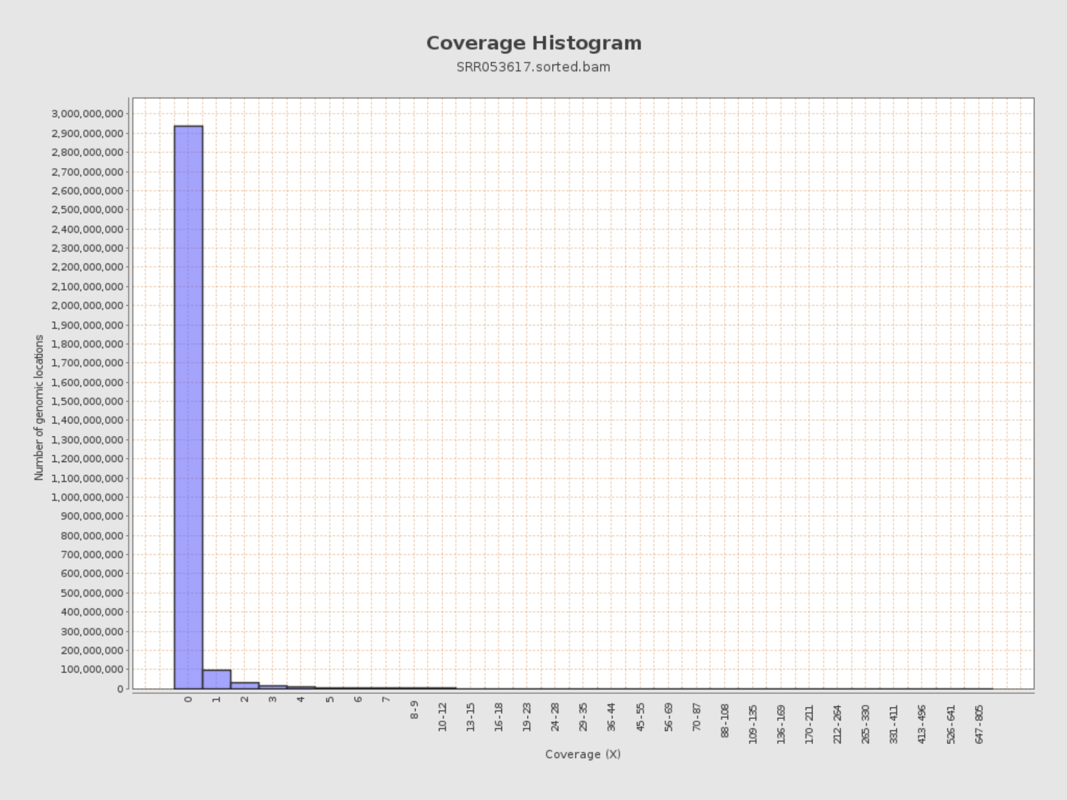
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 27048924 | 0.1085 | 0.8431 |
| chr2 | 243199373 | 28552834 | 0.1174 | 1.0048 |
| chr3 | 198022430 | 23139043 | 0.1169 | 0.7477 |
| chr4 | 191154276 | 21801162 | 0.1141 | 0.7788 |
| chr5 | 180915260 | 21095331 | 0.1166 | 0.7493 |
| chr6 | 171115067 | 19800205 | 0.1157 | 0.7915 |
| chr7 | 159138663 | 18265828 | 0.1148 | 0.8286 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 17035564 | 0.1164 | 0.8086 |
| chr9 | 141213431 | 14039172 | 0.0994 | 0.7256 |
| chr10 | 135534747 | 15874889 | 0.1171 | 0.8184 |
| chr11 | 135006516 | 15452004 | 0.1145 | 0.8308 |
| chr12 | 133851895 | 15635922 | 0.1168 | 0.7583 |
| chr13 | 115169878 | 11003505 | 0.0955 | 0.6753 |
| chr14 | 107349540 | 10392804 | 0.0968 | 0.7718 |
| chr15 | 102531392 | 9810474 | 0.0957 | 0.6692 |
| chr16 | 90354753 | 9772463 | 0.1082 | 0.7583 |
| chr17 | 81195210 | 9132407 | 0.1125 | 0.7321 |
| chr18 | 78077248 | 8944767 | 0.1146 | 0.8369 |
| chr19 | 59128983 | 6467559 | 0.1094 | 0.8309 |
| chr20 | 63025520 | 7292500 | 0.1157 | 0.7653 |
| chr21 | 48129895 | 4407363 | 0.0916 | 0.7989 |
| chr22 | 51304566 | 3955625 | 0.0771 | 0.6309 |
| chrMT | 16571 | 113465 | 6.8472 | 11.8999 |
| chrX | 155270560 | 19755219 | 0.1272 | 0.839 |
| chrY | 59373566 | 817025 | 0.0138 | 0.292 |

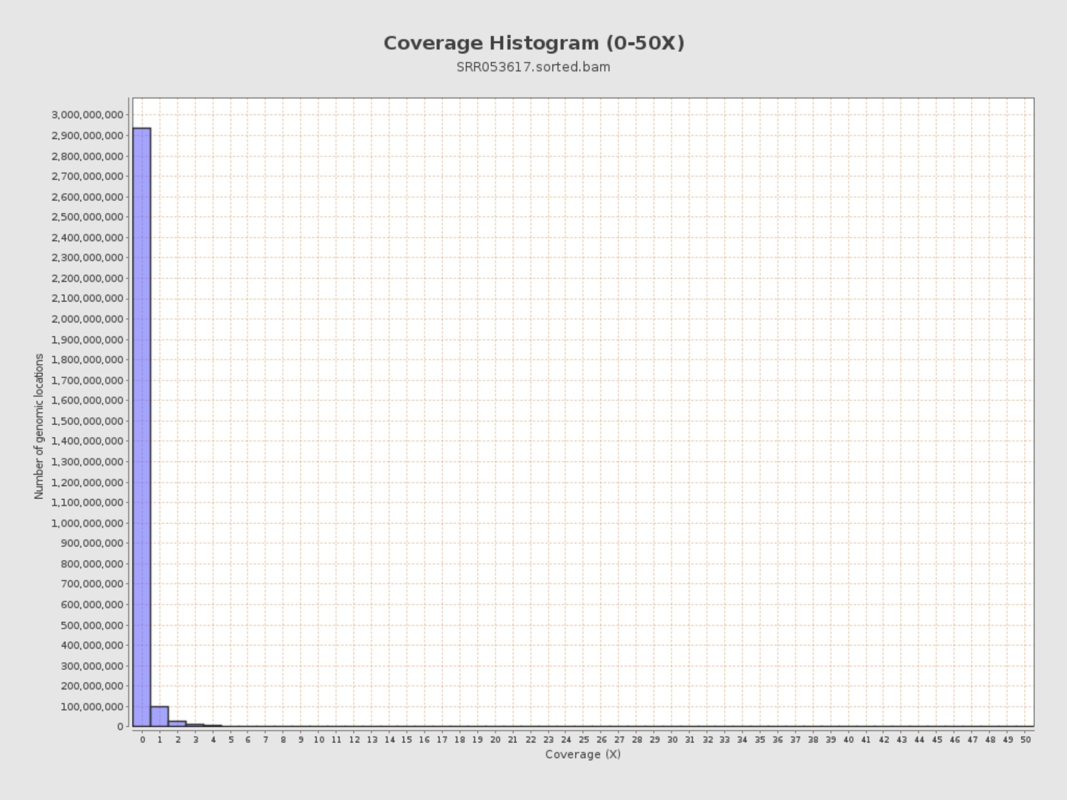
# 3. Results : Coverage across reference



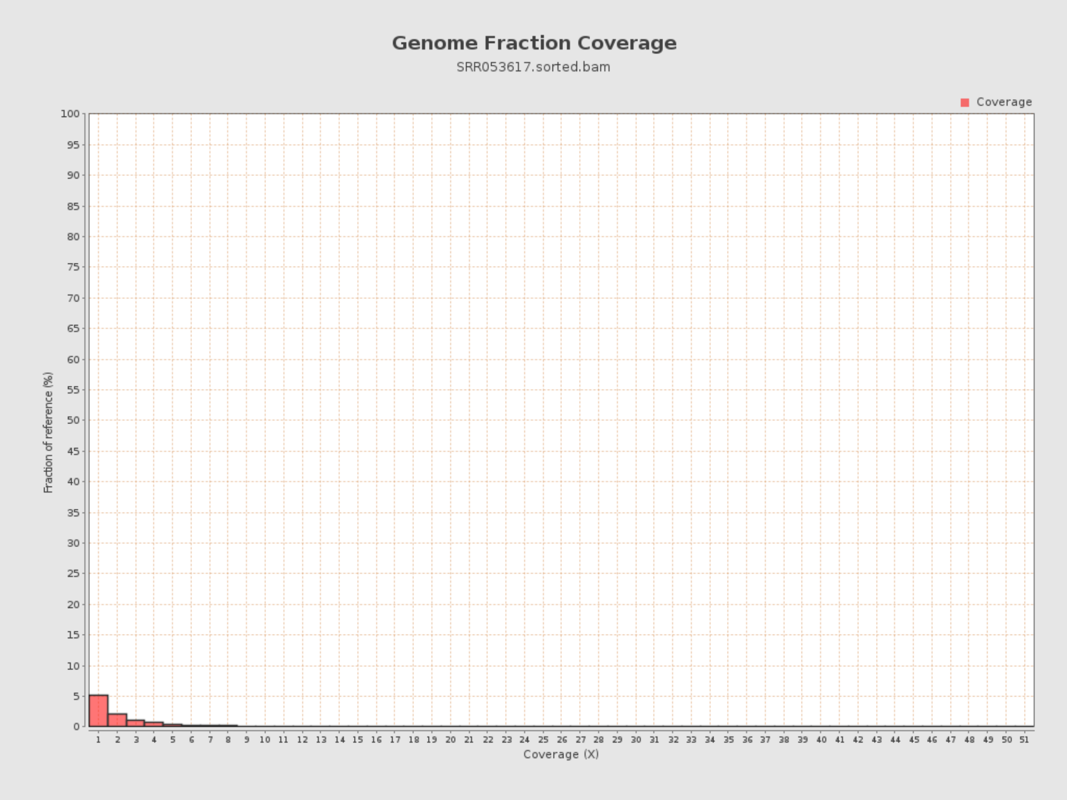
# 4. Results : Coverage Histogram



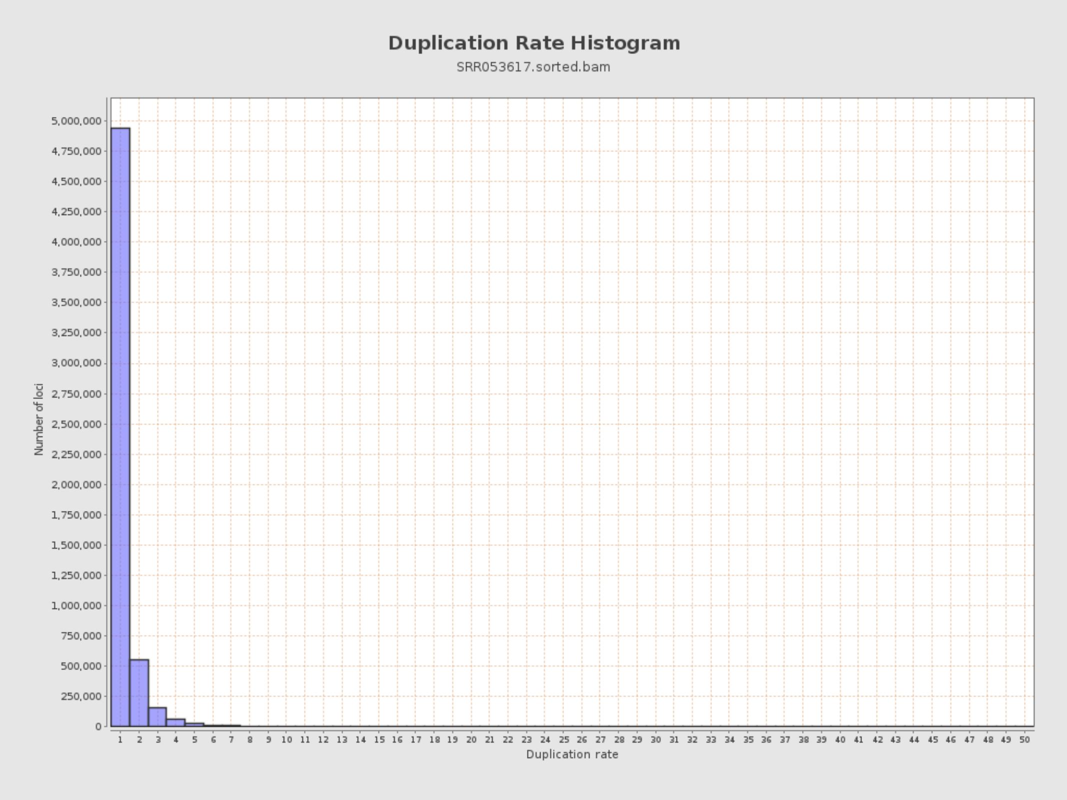
# 5. Results : Coverage Histogram (0-50X)



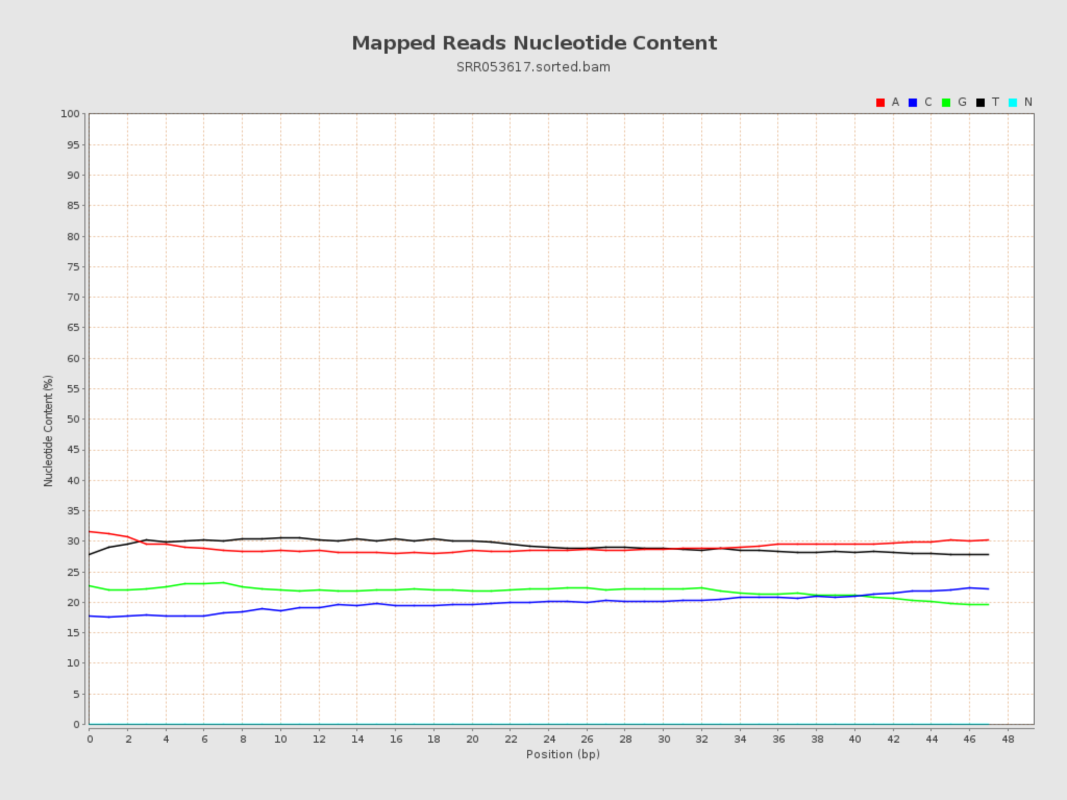
# 6. Results : Genome Fraction Coverage



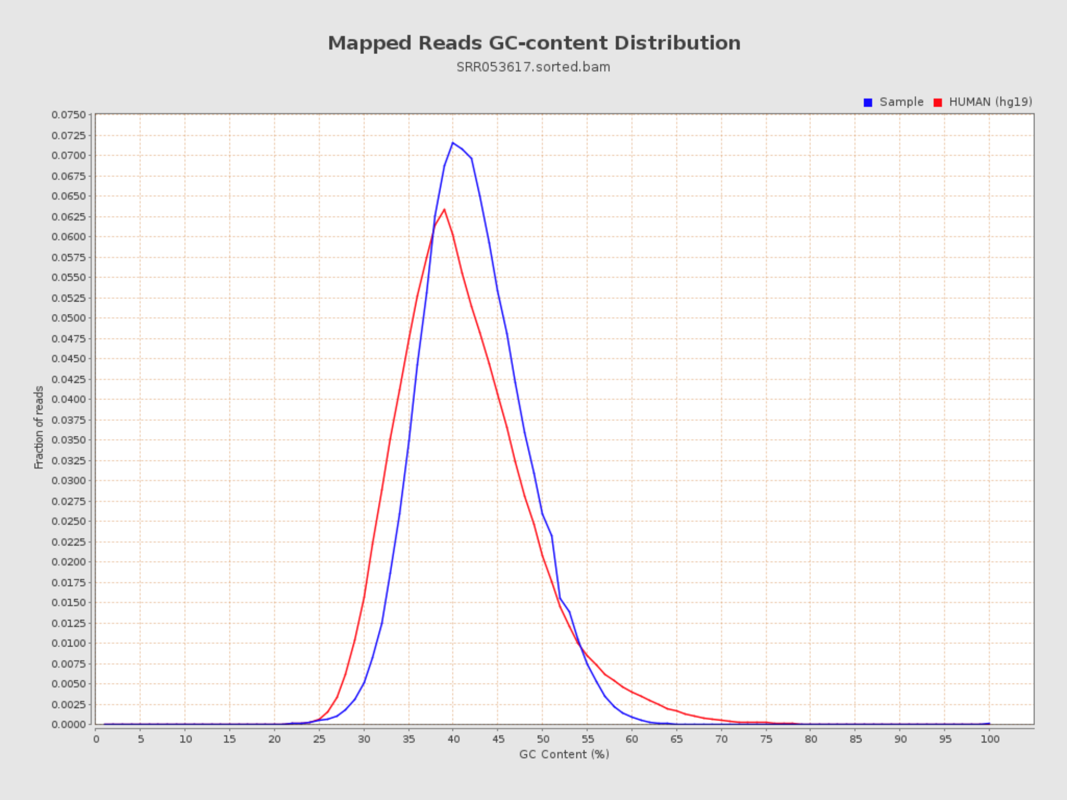
# 7. Results : Duplication Rate Histogram



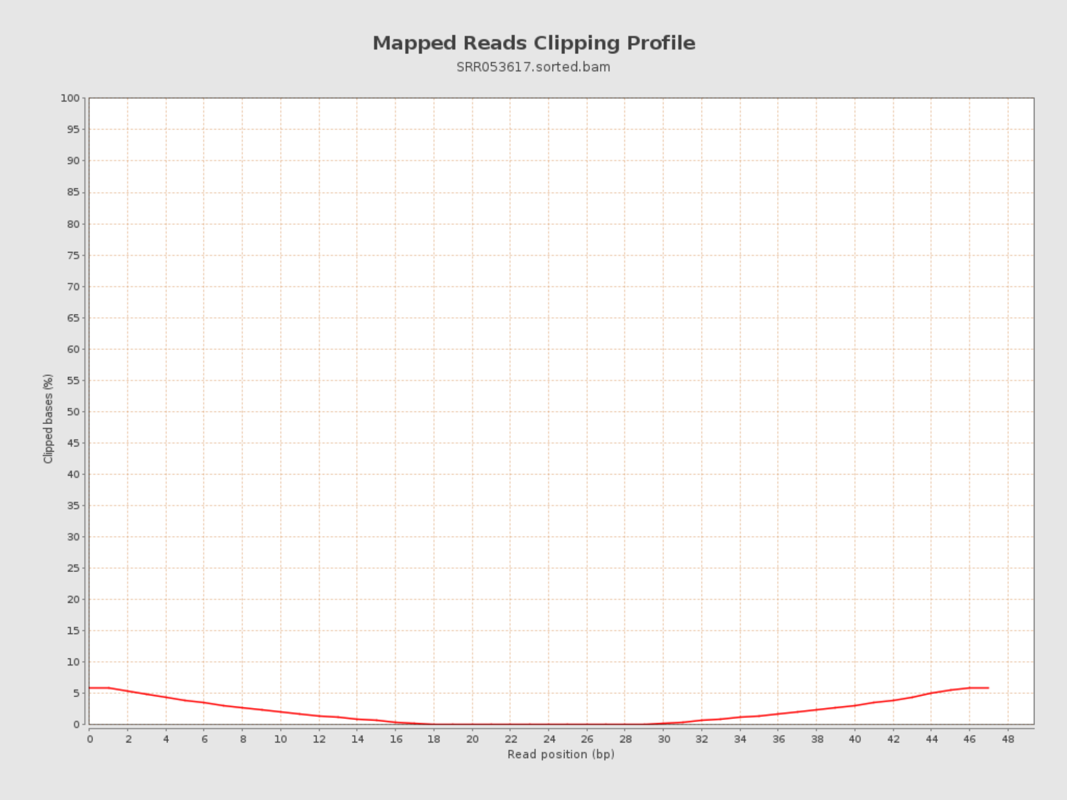
# 8. Results : Mapped Reads Nucleotide Content



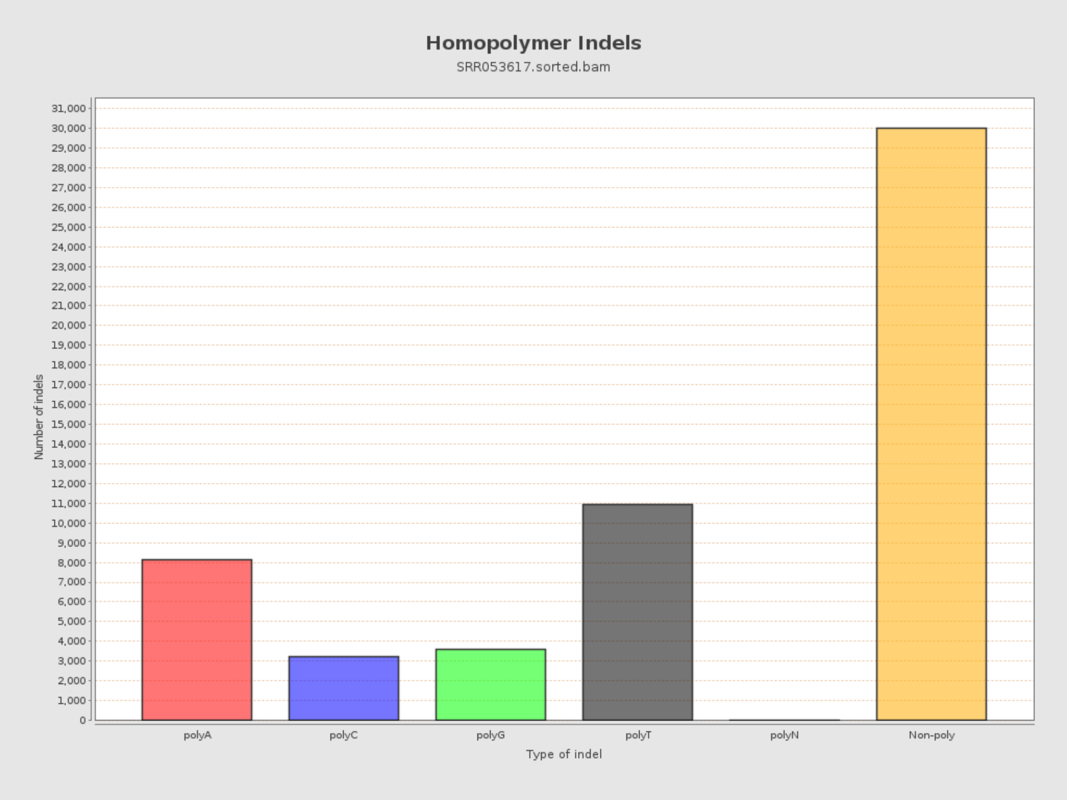
# 9. Results : Mapped Reads GC-content Distribution



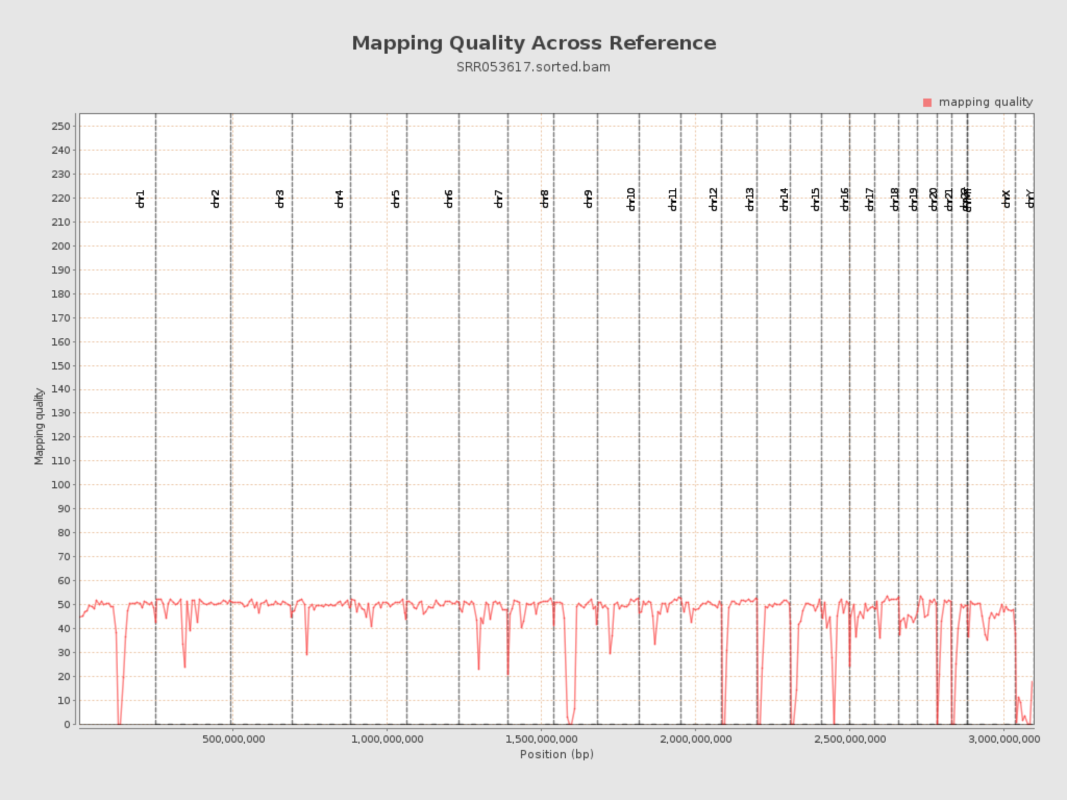
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram