# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/19 05:36:27*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR054578.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_SRR054578 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054578.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Apr 19 05:36:27 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR054578.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 9,868,221 |
| Mapped reads | 7,040,646 / 71.35% |
| Unmapped reads | 2,827,575 / 28.65% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 213 / 0% |
| Read min/max/mean length | 30 / 48 / 48 |
| Duplicated reads (estimated) | 2,041,368 / 20.69% |
| Duplication rate | 21.87% |
| Clipped reads | 535,132 / 5.42% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 97,375,635 / 29.23% |
| Number/percentage of C's | 64,347,990 / 19.32% |
| Number/percentage of T's | 99,687,612 / 29.93% |
| Number/percentage of G's | 71,575,942 / 21.49% |
| Number/percentage of N's | 119,807 / 0.04% |
| GC Percentage | 40.8% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1076 |
| | |

| | |
|---|---|
| Standard Deviation | 0.8848 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.46 |

## 2.5. Mismatches and indels

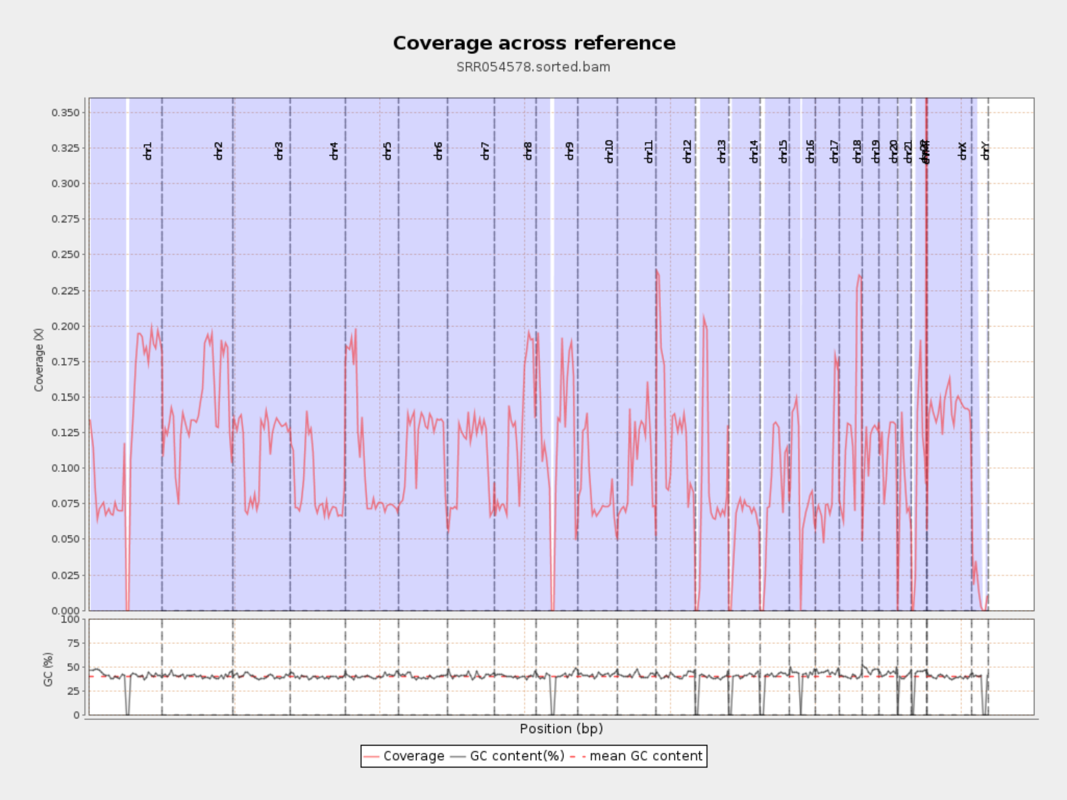
| | |
|---|---|
| General error rate | 0.57% |
| Mismatches | 1,880,824 |
| Insertions | 13,560 |
| Mapped reads with at least one insertion | 0.19% |
| Deletions | 47,330 |
| Mapped reads with at least one deletion | 0.67% |
| Homopolymer indels | 47.82% |

## 2.6. Chromosome stats

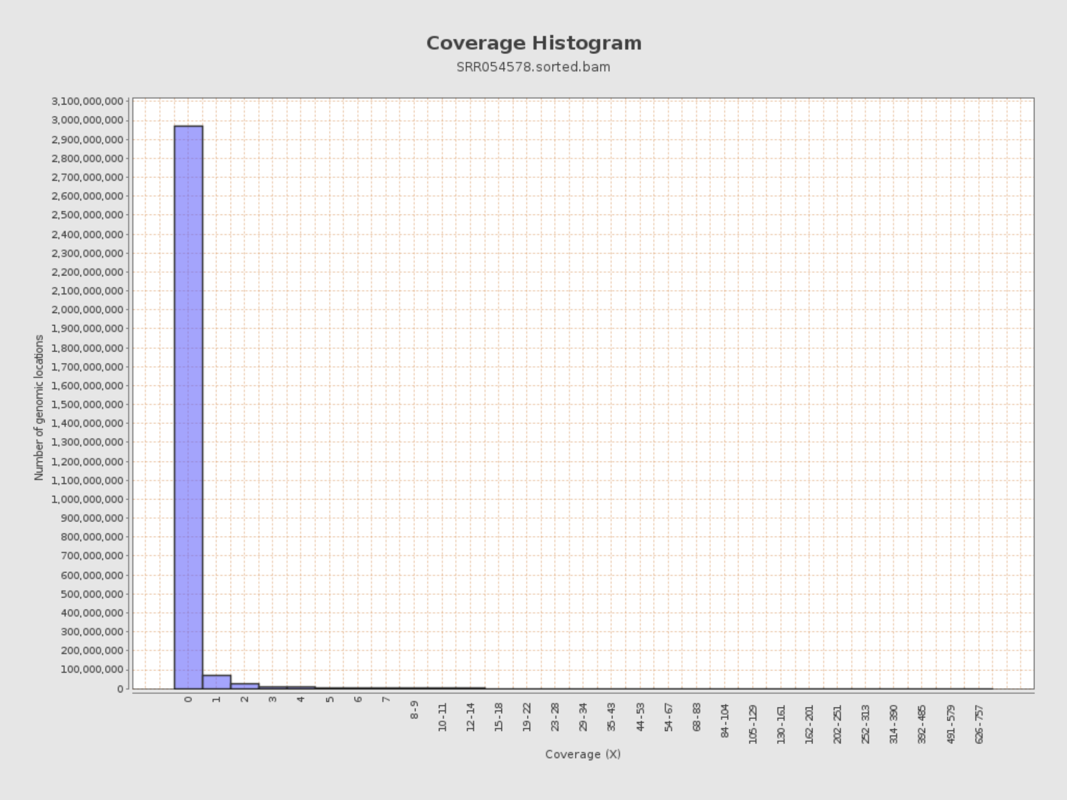
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 29624083 | 0.1189 | 0.9941 |
| chr2 | 243199373 | 34993994 | 0.1439 | 1.1439 |
| chr3 | 198022430 | 22725676 | 0.1148 | 0.8555 |
| chr4 | 191154276 | 16149293 | 0.0845 | 0.7231 |
| chr5 | 180915260 | 19025423 | 0.1052 | 0.8297 |
| chr6 | 171115067 | 20270143 | 0.1185 | 0.9167 |
| chr7 | 159138663 | 17224237 | 0.1082 | 0.9061 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 18124552 | 0.1238 | 0.936 |
| chr9 | 141213431 | 17204295 | 0.1218 | 0.9089 |
| chr10 | 135534747 | 11457912 | 0.0845 | 0.7851 |
| chr11 | 135006516 | 13865036 | 0.1027 | 0.8545 |
| chr12 | 133851895 | 17551328 | 0.1311 | 0.9334 |
| chr13 | 115169878 | 9150003 | 0.0794 | 0.7168 |
| chr14 | 107349540 | 6377343 | 0.0594 | 0.6629 |
| chr15 | 102531392 | 8342121 | 0.0814 | 0.6908 |
| chr16 | 90354753 | 8094483 | 0.0896 | 0.8148 |
| chr17 | 81195210 | 7661923 | 0.0944 | 0.7478 |
| chr18 | 78077248 | 10357813 | 0.1327 | 1.0486 |
| chr19 | 59128983 | 6834336 | 0.1156 | 0.9755 |
| chr20 | 63025520 | 7152631 | 0.1135 | 0.8888 |
| chr21 | 48129895 | 3799822 | 0.0789 | 0.7525 |
| chr22 | 51304566 | 4699533 | 0.0916 | 0.7673 |
| chrMT | 16571 | 22922 | 1.3833 | 3.2244 |
| chrX | 155270560 | 21657333 | 0.1395 | 0.9976 |
| chrY | 59373566 | 811218 | 0.0137 | 0.284 |

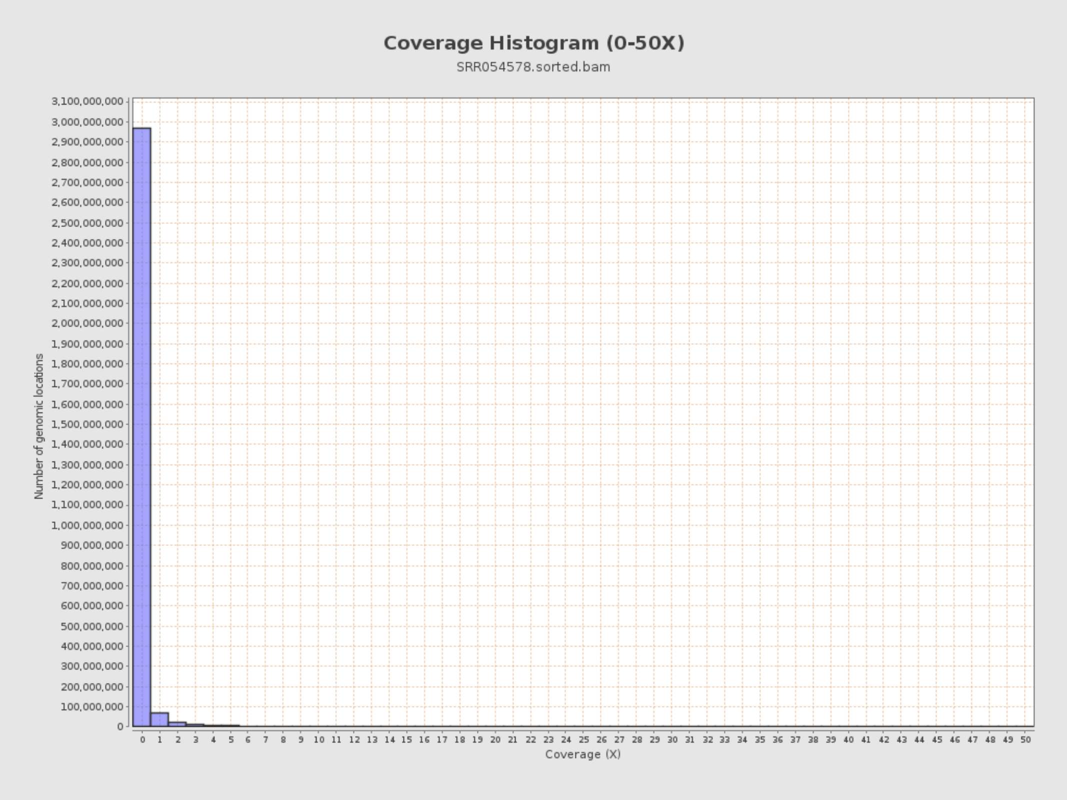
# 3. Results : Coverage across reference



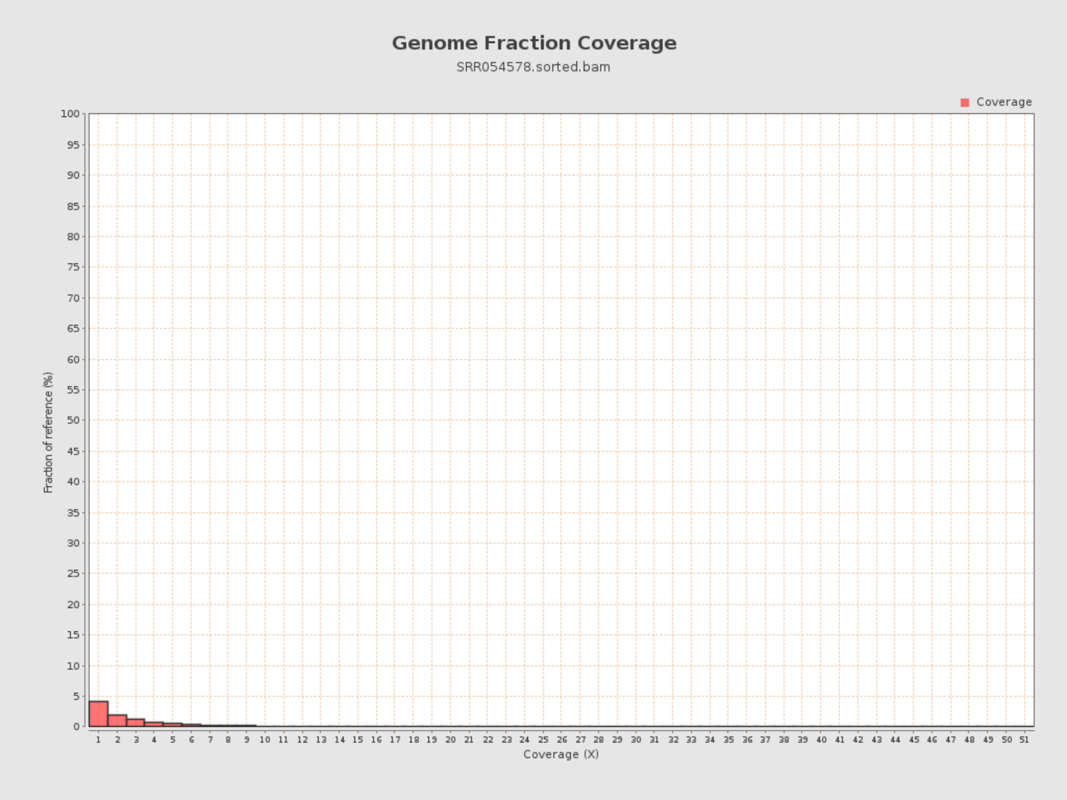
# 4. Results : Coverage Histogram



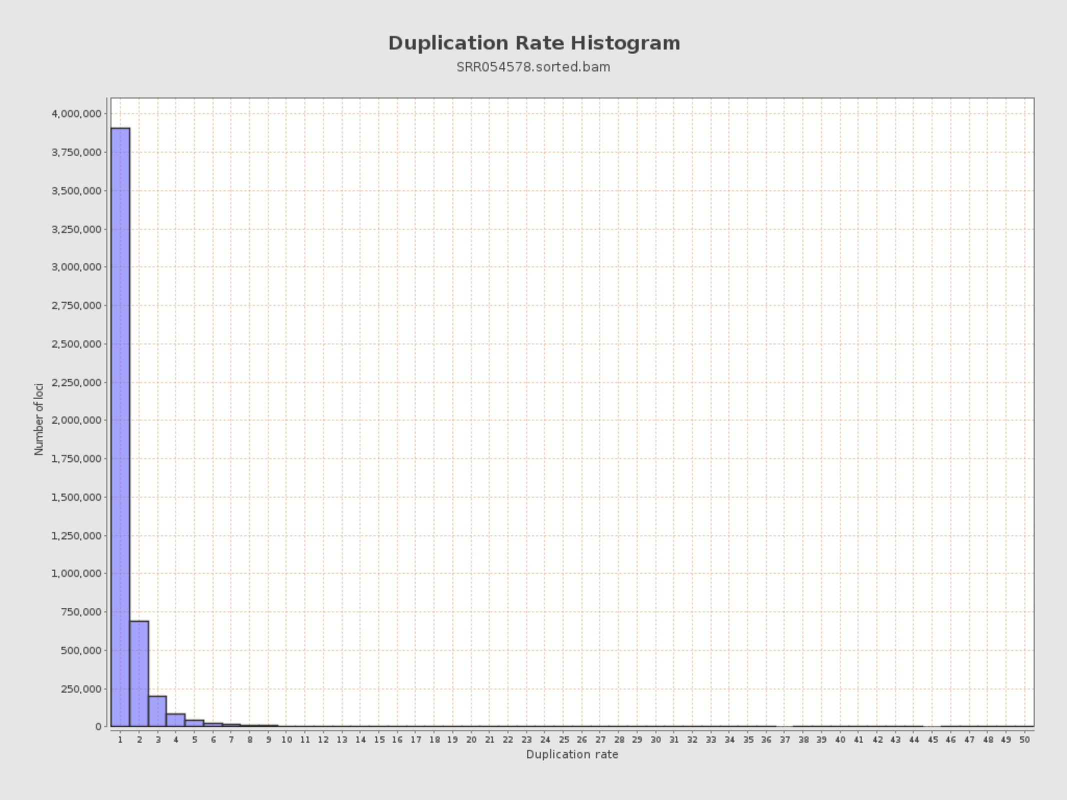
# 5. Results : Coverage Histogram (0-50X)



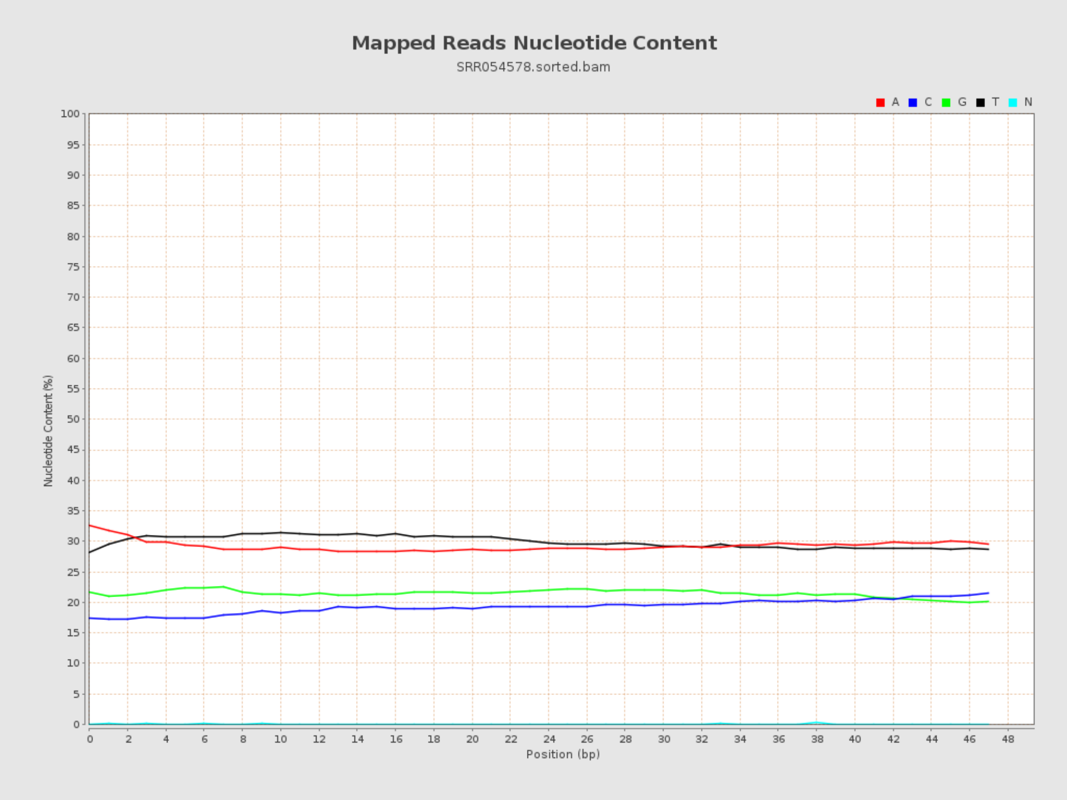
# 6. Results : Genome Fraction Coverage



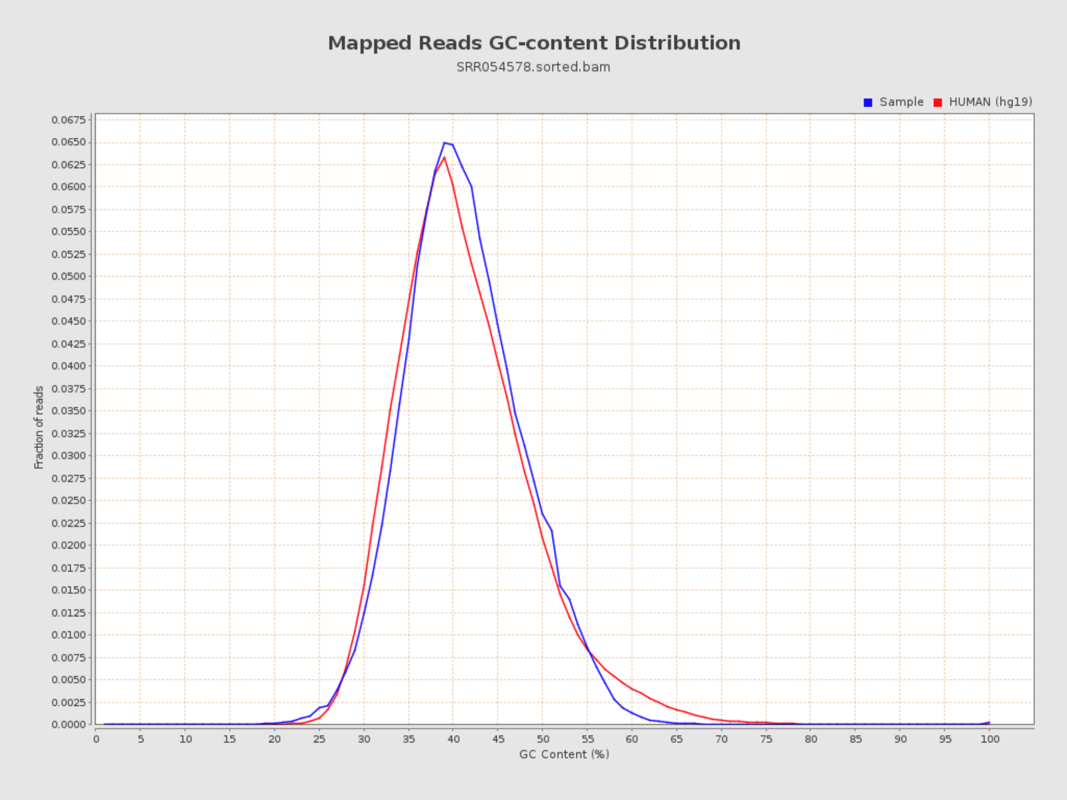
# 7. Results : Duplication Rate Histogram



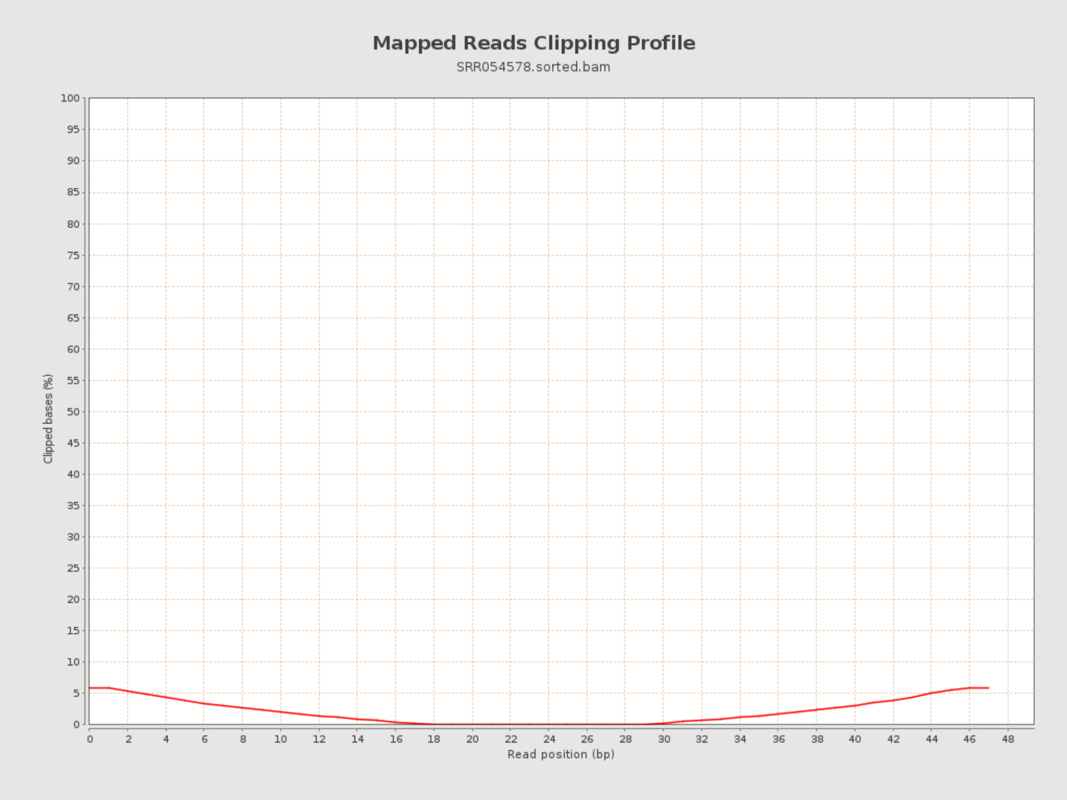
# 8. Results : Mapped Reads Nucleotide Content



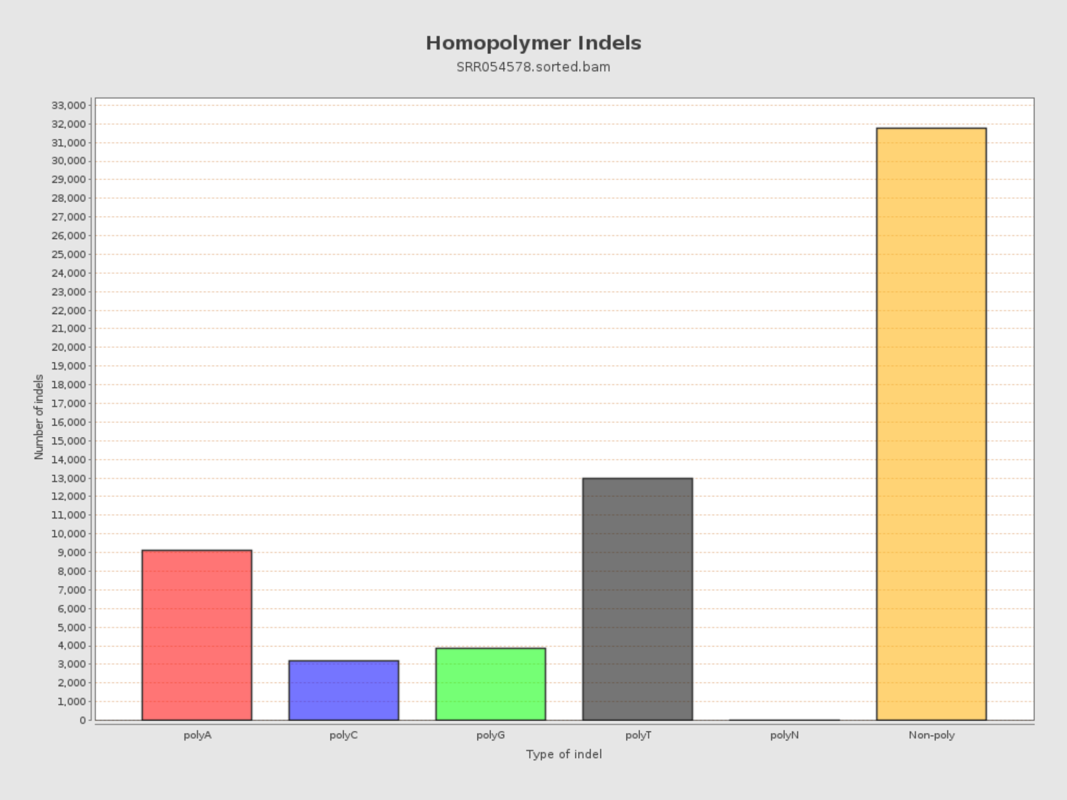
# 9. Results : Mapped Reads GC-content Distribution



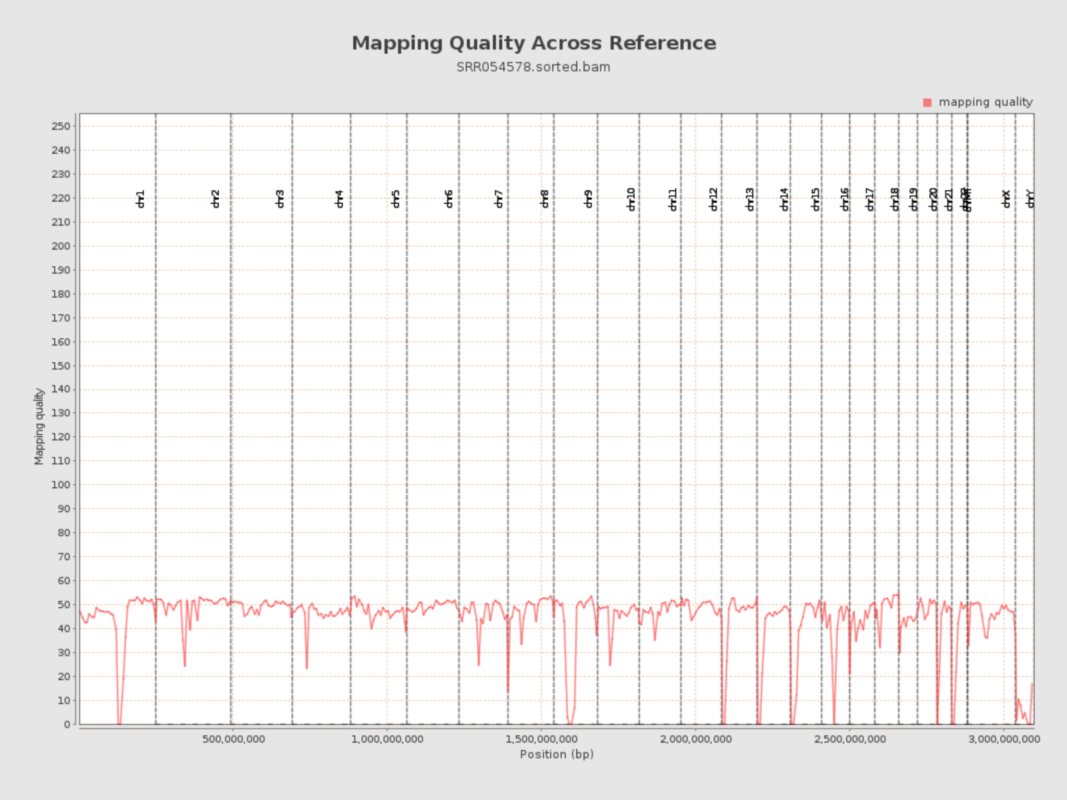
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram