# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/19 04:11:08*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR054567.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_SRR054567 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054567.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Apr 19 04:11:08 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR054567.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 14,459,313 |
| Mapped reads | 10,779,631 / 74.55% |
| Unmapped reads | 3,679,682 / 25.45% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 306 / 0% |
| Read min/max/mean length | 30 / 48 / 48 |
| Duplicated reads (estimated) | 4,175,370 / 28.88% |
| Duplication rate | 25.81% |
| Clipped reads | 1,017,731 / 7.04% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 158,846,405 / 31.24% |
| Number/percentage of C's | 94,443,481 / 18.57% |
| Number/percentage of T's | 157,819,809 / 31.04% |
| Number/percentage of G's | 97,310,552 / 19.14% |
| Number/percentage of N's | 80,759 / 0.02% |
| GC Percentage | 37.71% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1643 |
| | |

| | |
|---|---|
| Standard Deviation | 1.5951 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.86 |

## 2.5. Mismatches and indels

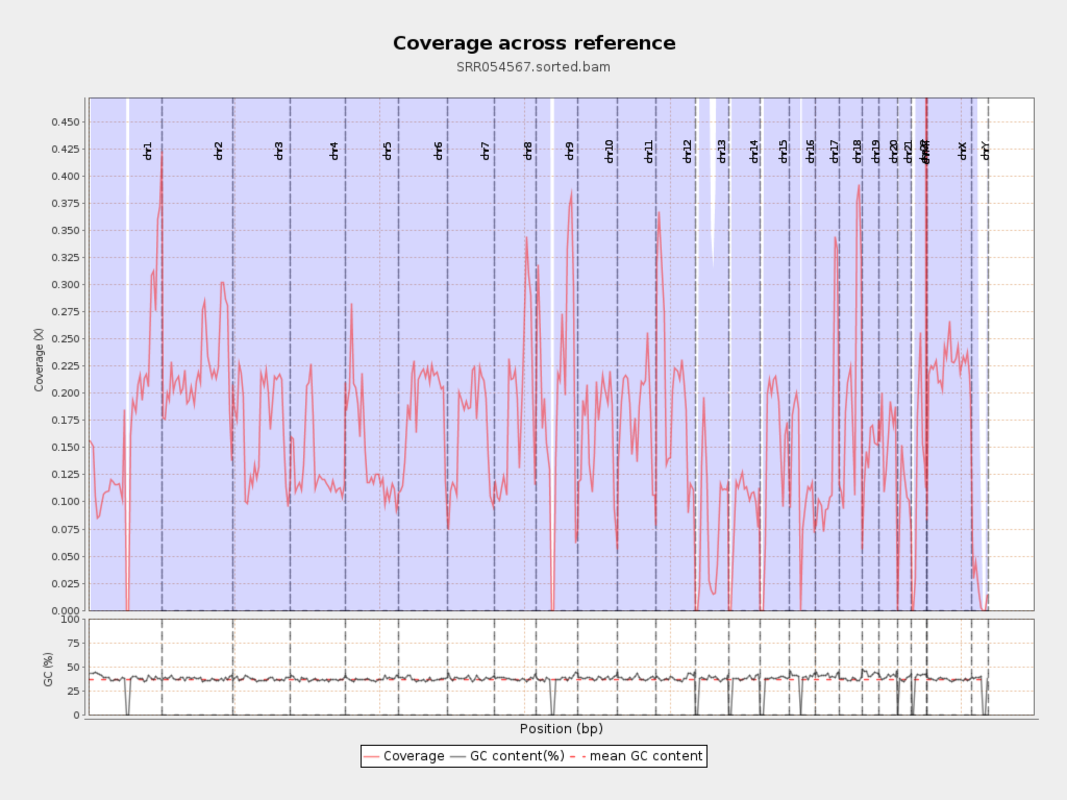
| | |
|---|---|
| General error rate | 0.55% |
| Mismatches | 2,772,038 |
| Insertions | 24,409 |
| Mapped reads with at least one insertion | 0.23% |
| Deletions | 80,968 |
| Mapped reads with at least one deletion | 0.75% |
| Homopolymer indels | 49.05% |

## 2.6. Chromosome stats

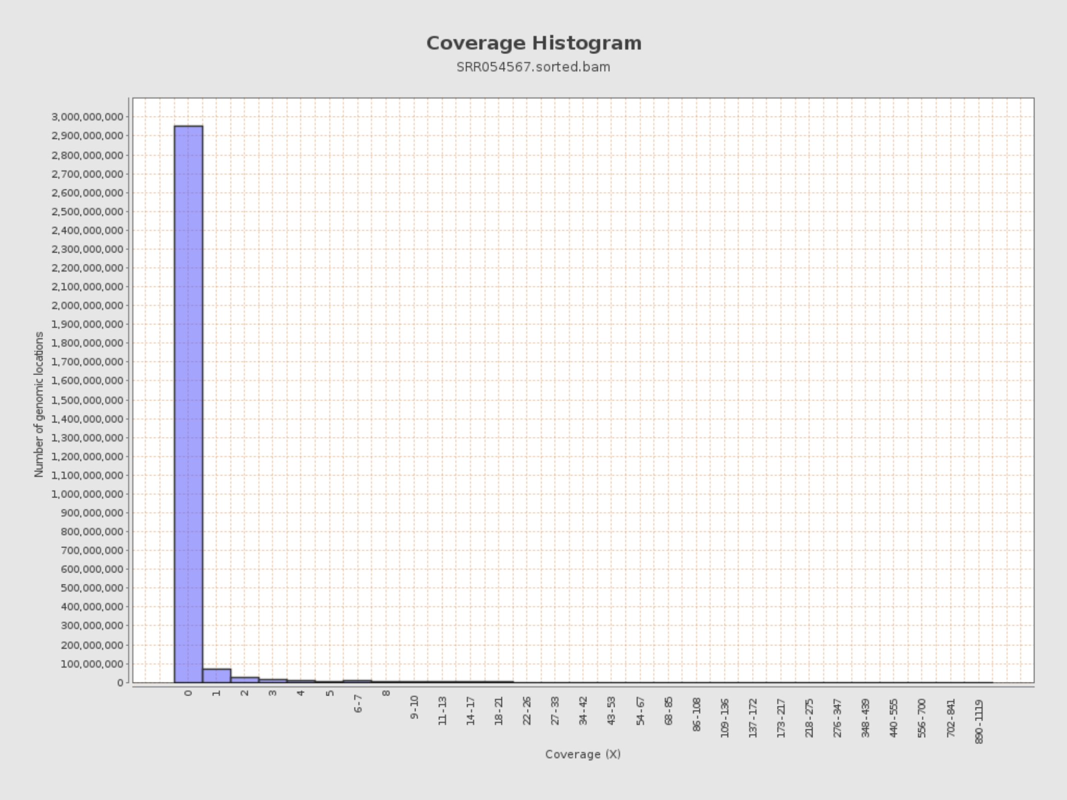
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 41789469 | 0.1677 | 1.6598 |
| chr2 | 243199373 | 53781353 | 0.2211 | 1.9655 |
| chr3 | 198022430 | 33798735 | 0.1707 | 1.5615 |
| chr4 | 191154276 | 25486533 | 0.1333 | 1.4036 |
| chr5 | 180915260 | 26607217 | 0.1471 | 1.4246 |
| chr6 | 171115067 | 32148005 | 0.1879 | 1.7596 |
| chr7 | 159138663 | 26699535 | 0.1678 | 1.6843 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 27857285 | 0.1903 | 1.756 |
| chr9 | 141213431 | 29044561 | 0.2057 | 1.7735 |
| chr10 | 135534747 | 22697340 | 0.1675 | 1.5577 |
| chr11 | 135006516 | 24129161 | 0.1787 | 1.6433 |
| chr12 | 133851895 | 27161628 | 0.2029 | 1.7782 |
| chr13 | 115169878 | 8327466 | 0.0723 | 0.9917 |
| chr14 | 107349540 | 9773770 | 0.091 | 1.272 |
| chr15 | 102531392 | 14782408 | 0.1442 | 1.3964 |
| chr16 | 90354753 | 10910977 | 0.1208 | 1.2439 |
| chr17 | 81195210 | 12040161 | 0.1483 | 1.4245 |
| chr18 | 78077248 | 16424835 | 0.2104 | 1.9104 |
| chr19 | 59128983 | 8586552 | 0.1452 | 1.4331 |
| chr20 | 63025520 | 10063616 | 0.1597 | 1.473 |
| chr21 | 48129895 | 4780889 | 0.0993 | 1.1337 |
| chr22 | 51304566 | 6052100 | 0.118 | 1.2246 |
| chrMT | 16571 | 40337 | 2.4342 | 6.4815 |
| chrX | 155270560 | 34482068 | 0.2221 | 1.8652 |
| chrY | 59373566 | 1155074 | 0.0195 | 0.4121 |

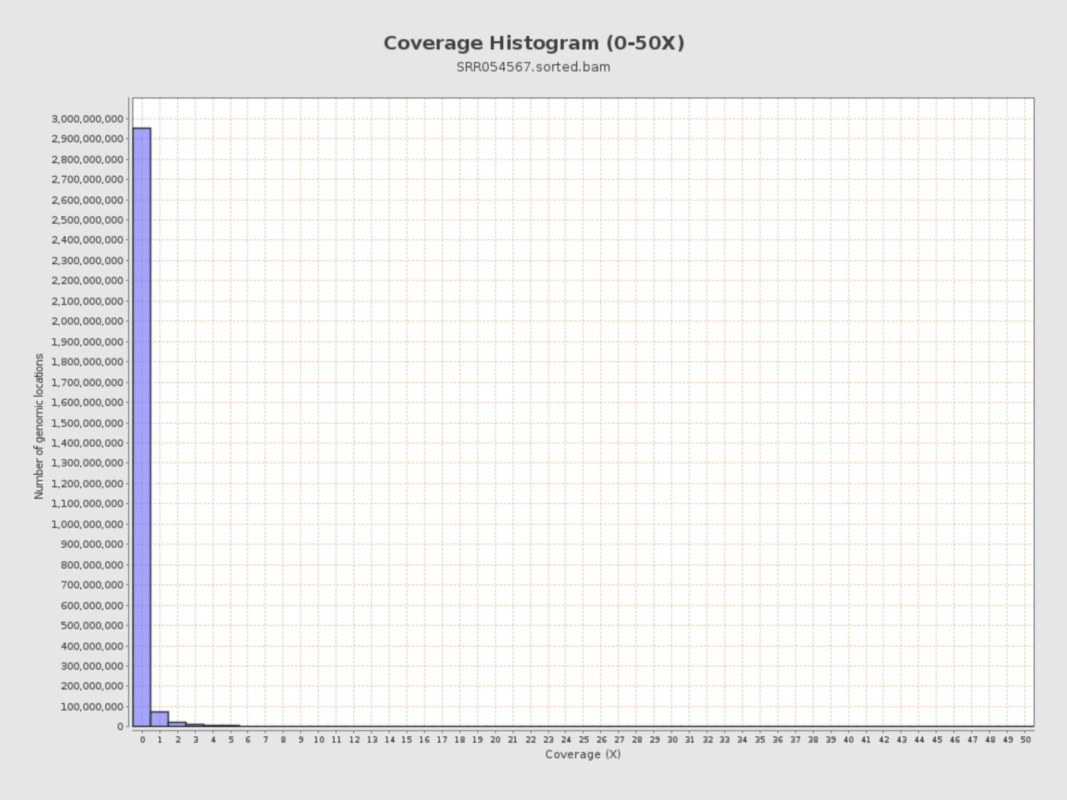
# 3. Results : Coverage across reference



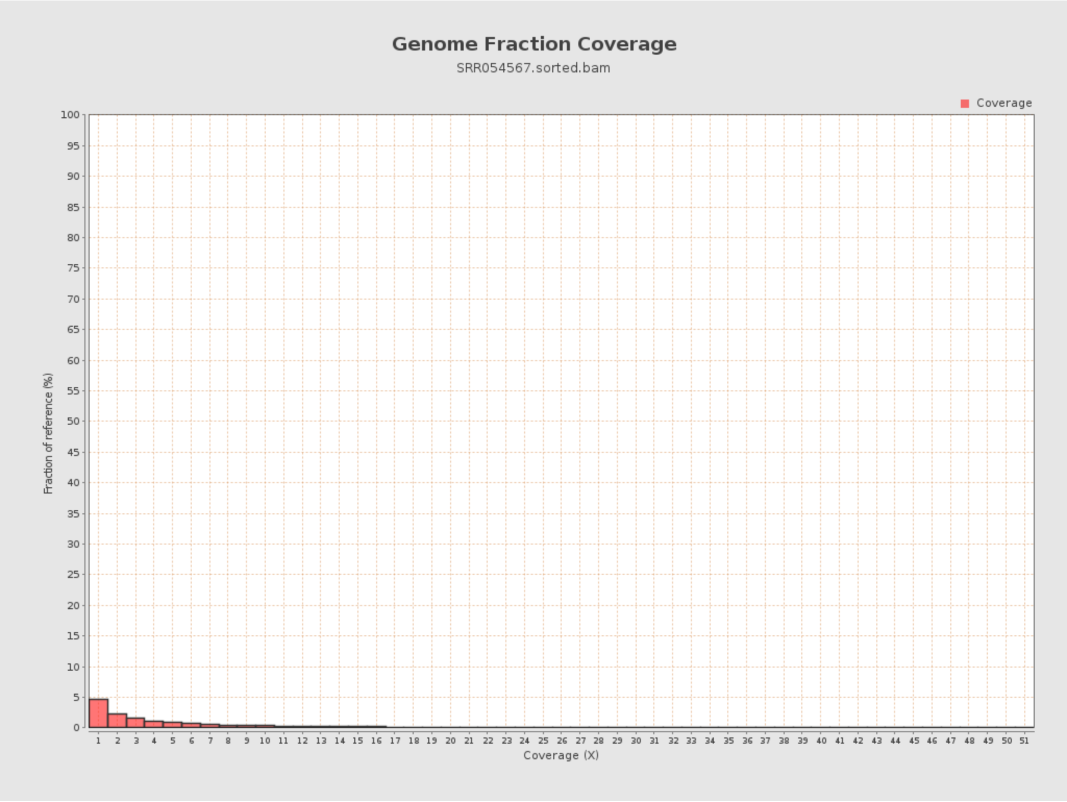
# 4. Results : Coverage Histogram



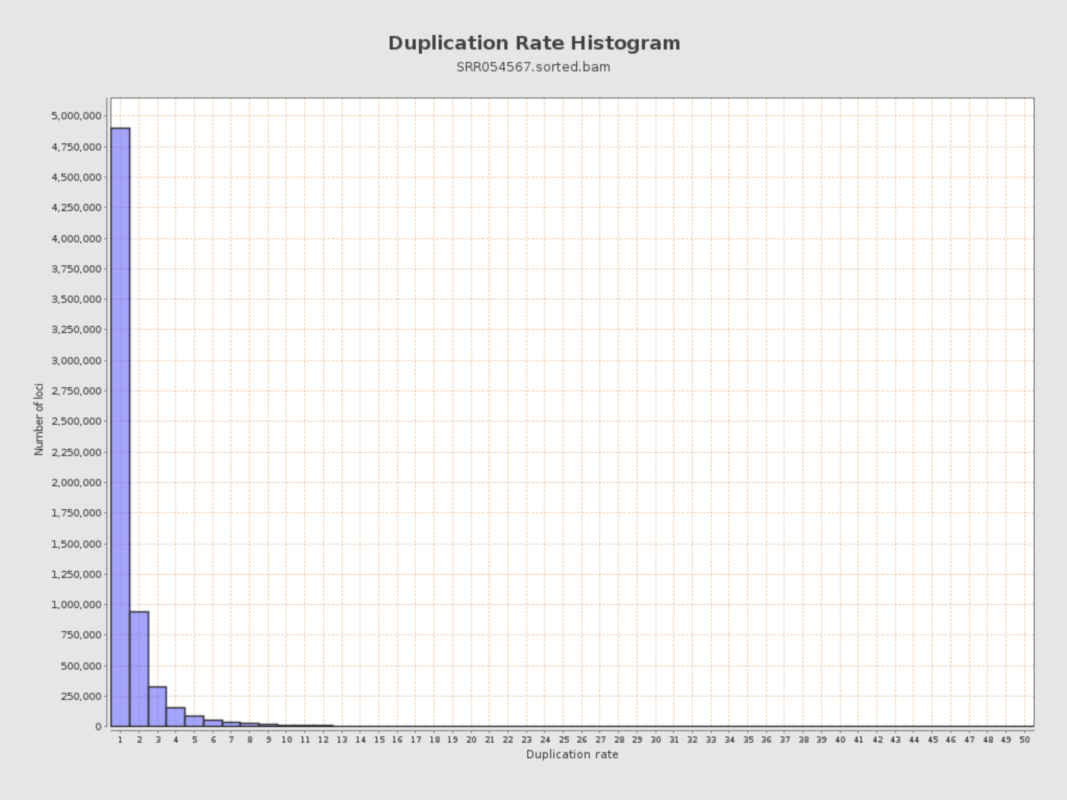
# 5. Results : Coverage Histogram (0-50X)



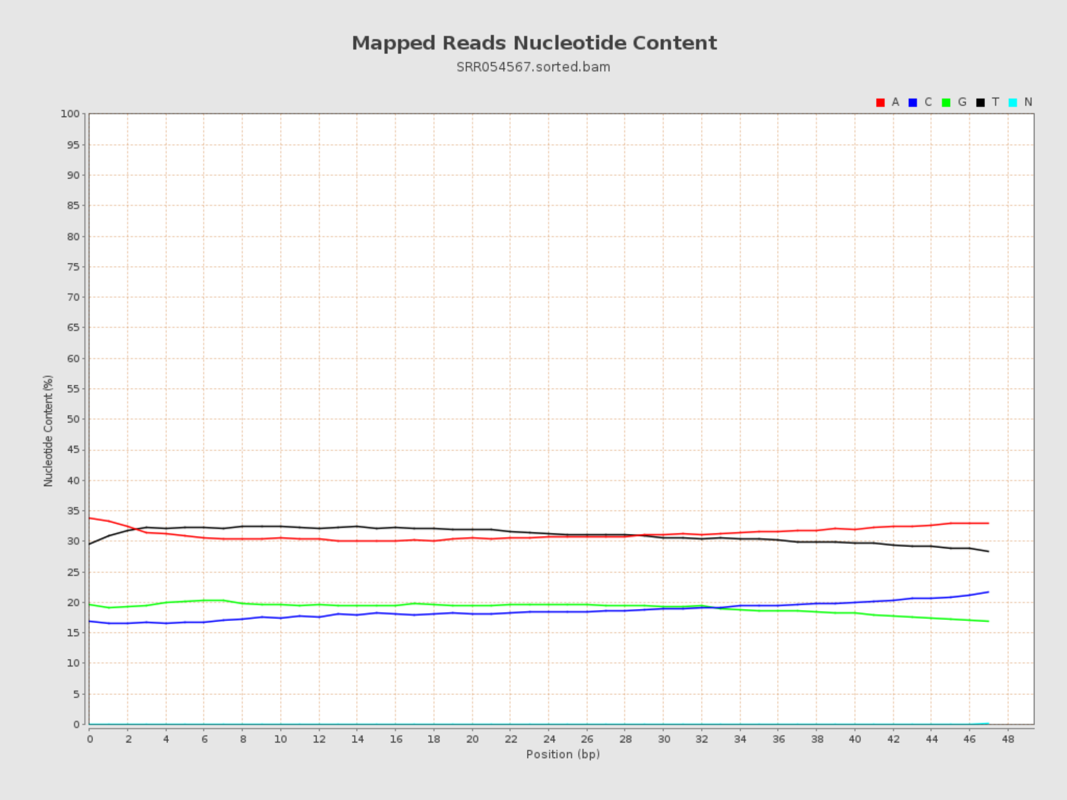
# 6. Results : Genome Fraction Coverage



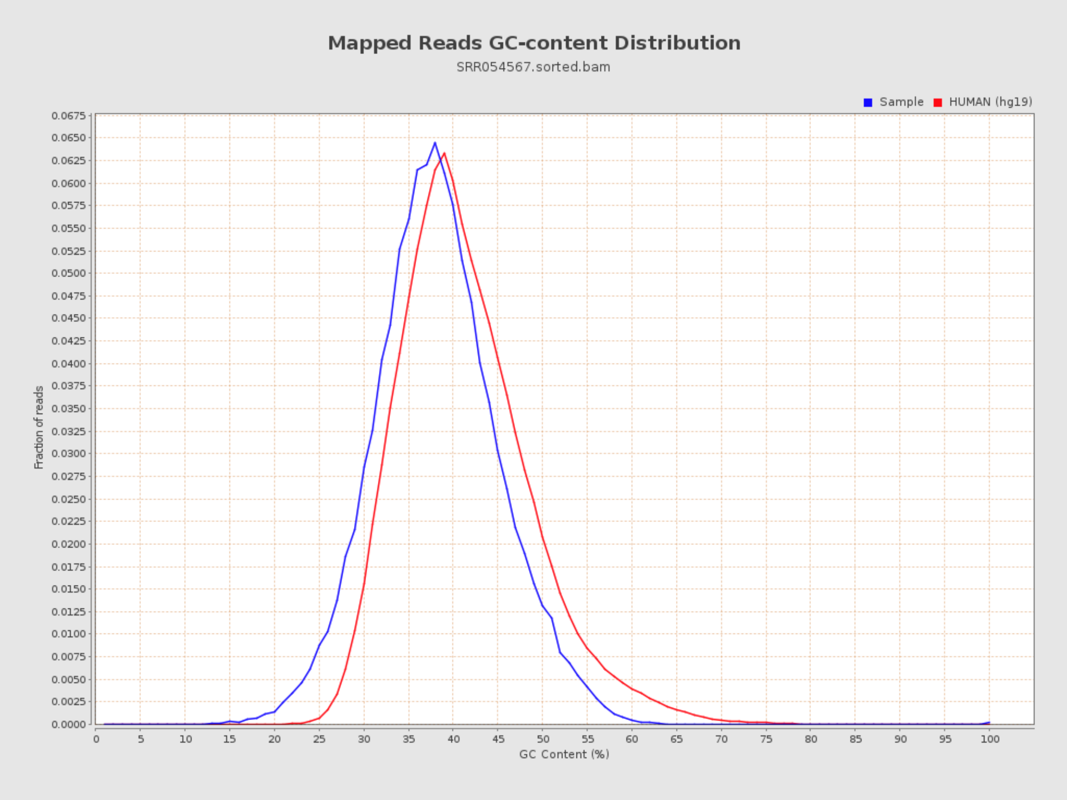
# 7. Results : Duplication Rate Histogram



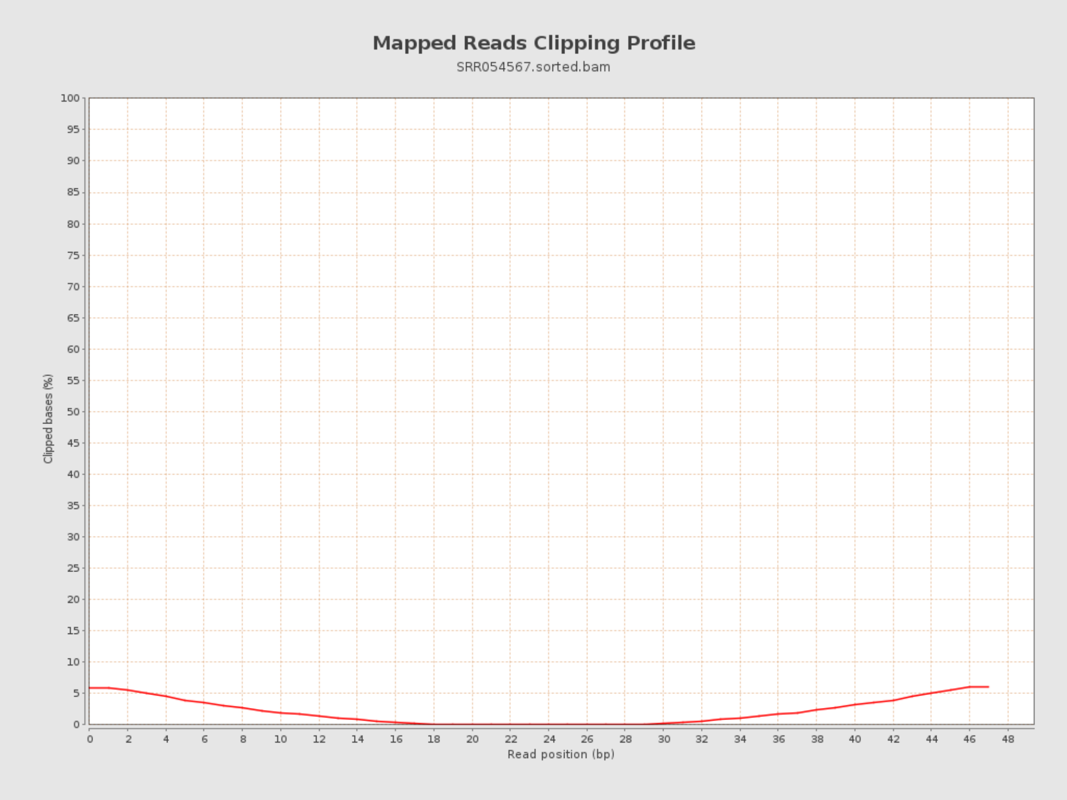
# 8. Results : Mapped Reads Nucleotide Content



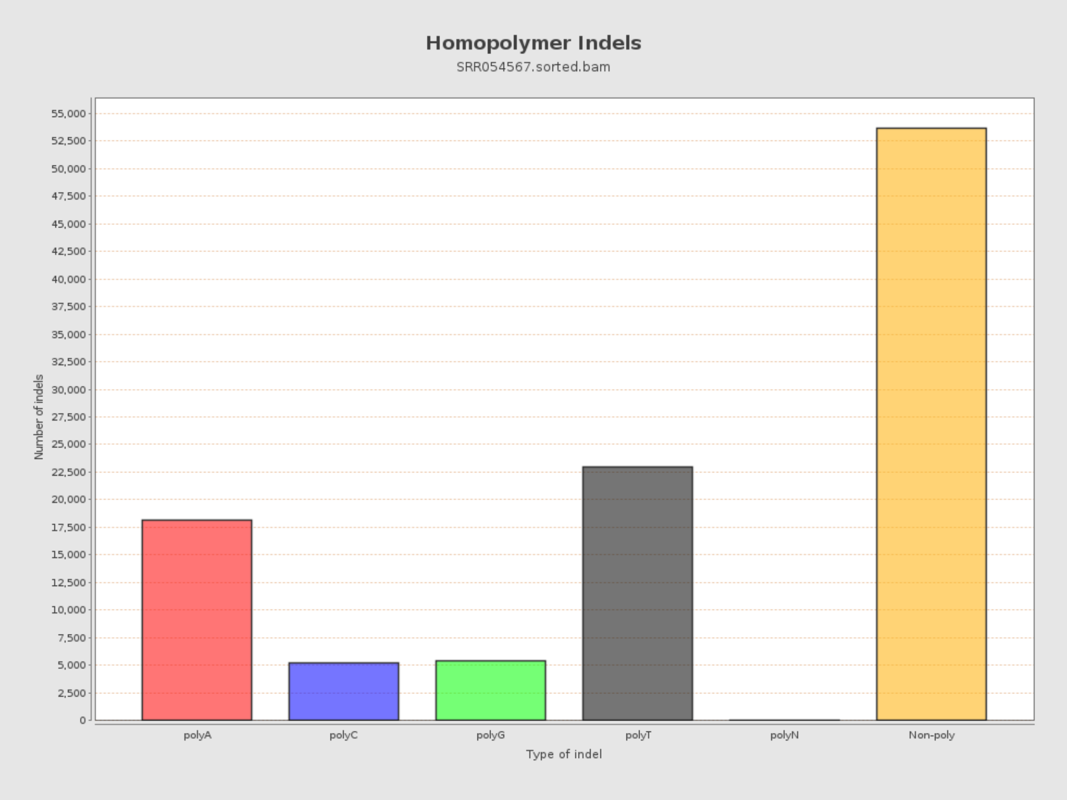
# 9. Results : Mapped Reads GC-content Distribution



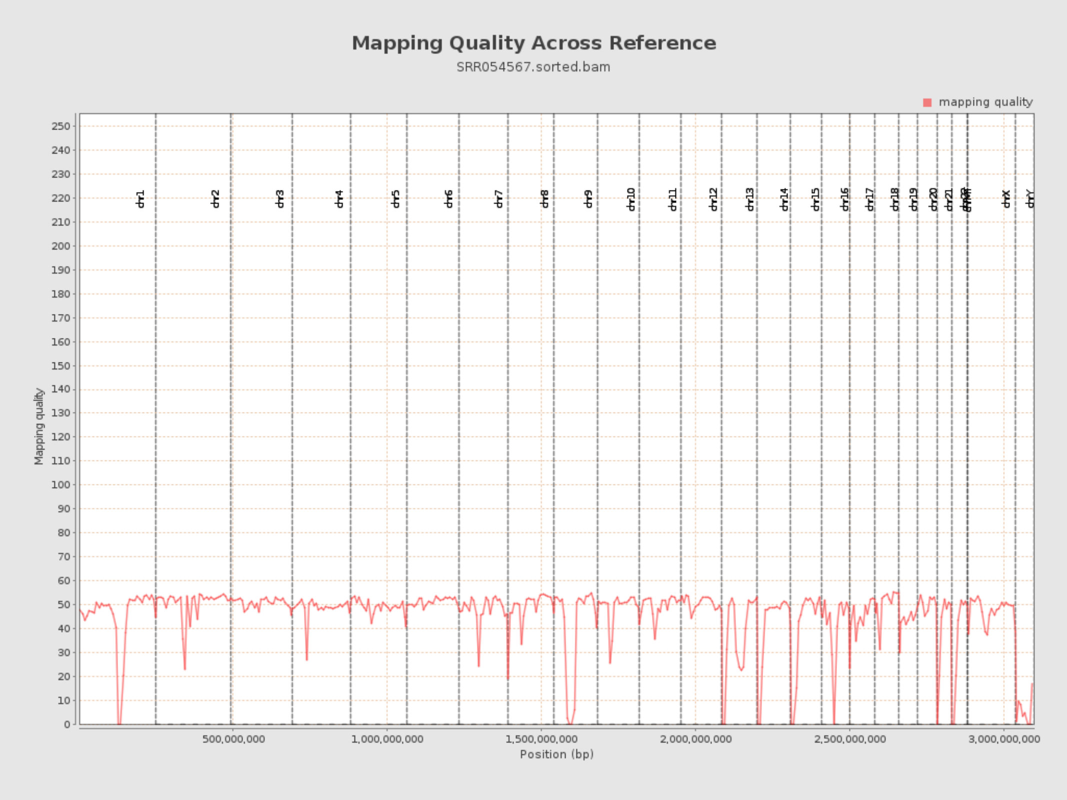
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram