# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/14 04:27:56*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004146.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_SRR6004146 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004146.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 14 04:27:55 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6004146.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,394,357 |
| Mapped reads | 2,862,155 / 84.32% |
| Unmapped reads | 532,202 / 15.68% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 20,821 / 0.61% |
| Read min/max/mean length | 30 / 76 / 76.21 |
| Duplicated reads (estimated) | 160,429 / 4.73% |
| Duplication rate | 4.23% |
| Clipped reads | 1,202,666 / 35.43% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 54,418,684 / 28.17% |
| Number/percentage of C's | 34,910,015 / 18.07% |
| Number/percentage of T's | 62,719,413 / 32.47% |
| Number/percentage of G's | 41,091,988 / 21.27% |
| Number/percentage of N's | 21,921 / 0.01% |
| GC Percentage | 39.35% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0624 |
| | |

| | |
|---|---|
| Standard Deviation | 0.6071 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.06 |

## 2.5. Mismatches and indels

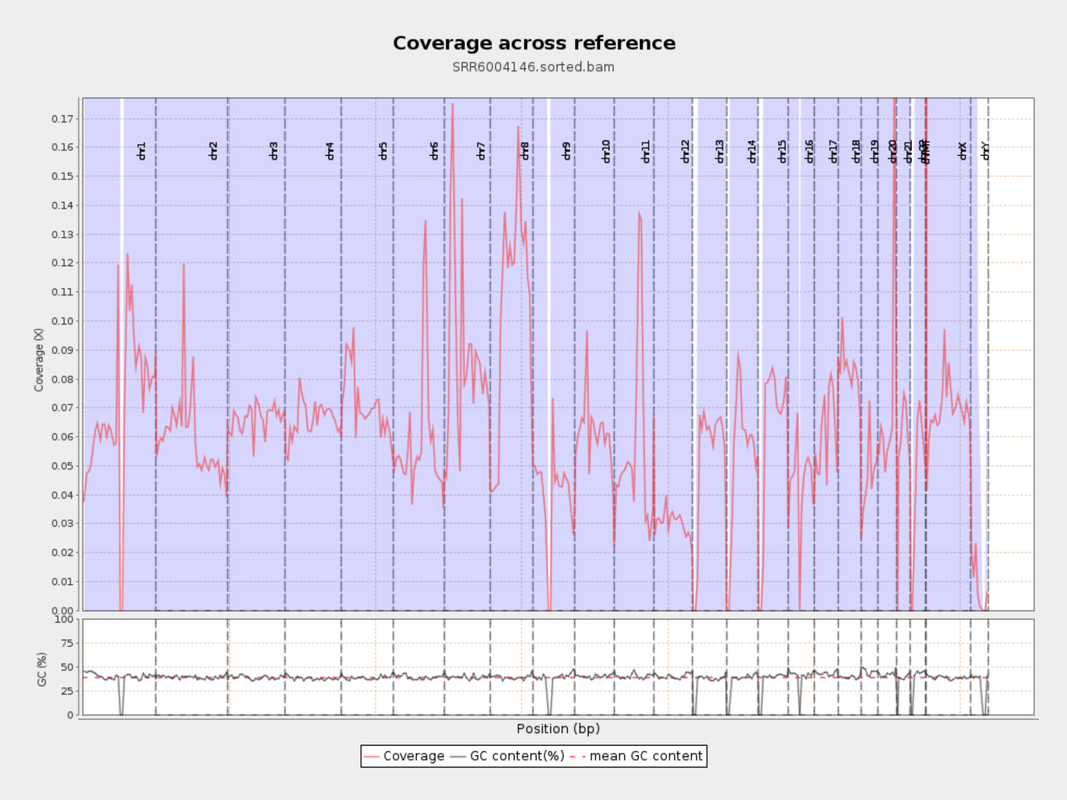
| | |
|---|---|
| General error rate | 0.95% |
| Mismatches | 1,799,691 |
| Insertions | 16,942 |
| Mapped reads with at least one insertion | 0.59% |
| Deletions | 50,651 |
| Mapped reads with at least one deletion | 1.75% |
| Homopolymer indels | 47.6% |

## 2.6. Chromosome stats

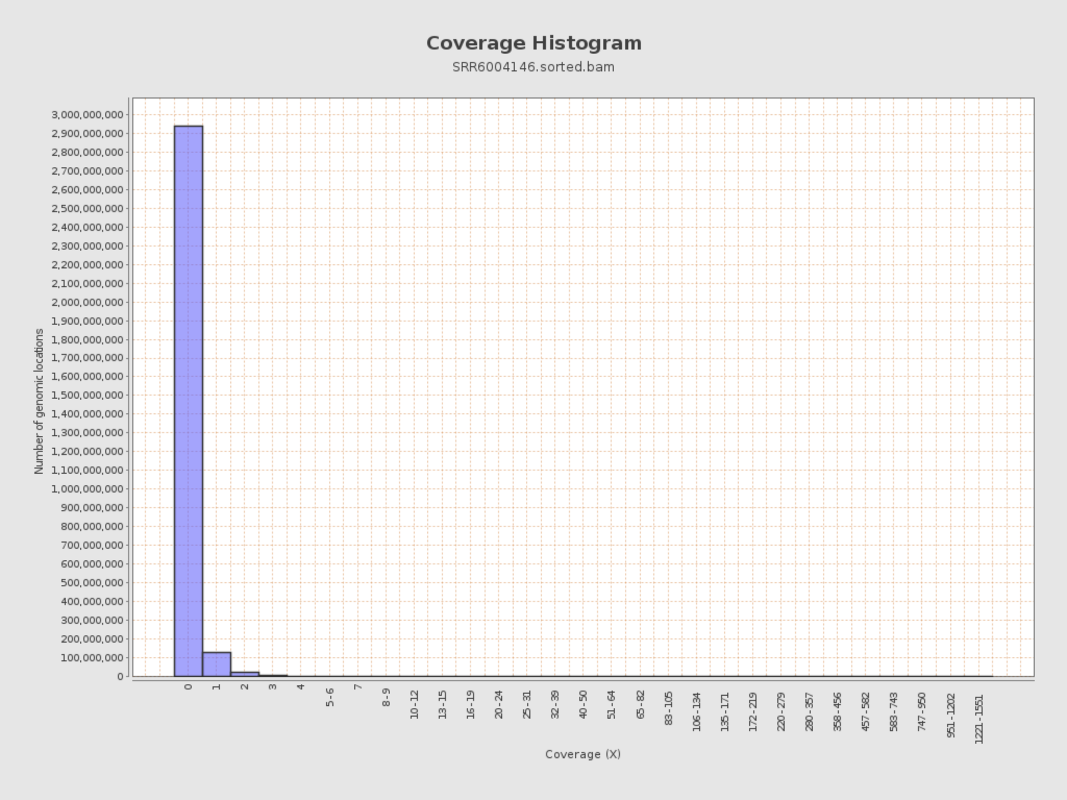
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 17335180 | 0.0695 | 1.1148 |
| chr2 | 243199373 | 14535408 | 0.0598 | 0.6663 |
| chr3 | 198022430 | 13156090 | 0.0664 | 0.3066 |
| chr4 | 191154276 | 12663098 | 0.0662 | 0.3193 |
| chr5 | 180915260 | 12875791 | 0.0712 | 0.3199 |
| chr6 | 171115067 | 10042622 | 0.0587 | 0.3544 |
| chr7 | 159138663 | 13936638 | 0.0876 | 0.9874 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 15402351 | 0.1052 | 1.0354 |
| chr9 | 141213431 | 5632877 | 0.0399 | 0.5486 |
| chr10 | 135534747 | 8376080 | 0.0618 | 0.4492 |
| chr11 | 135006516 | 7500436 | 0.0556 | 0.4144 |
| chr12 | 133851895 | 4047690 | 0.0302 | 0.228 |
| chr13 | 115169878 | 6034796 | 0.0524 | 0.2727 |
| chr14 | 107349540 | 5786964 | 0.0539 | 0.3193 |
| chr15 | 102531392 | 6229261 | 0.0608 | 0.2916 |
| chr16 | 90354753 | 3870214 | 0.0428 | 0.3168 |
| chr17 | 81195210 | 5056498 | 0.0623 | 0.3241 |
| chr18 | 78077248 | 6547742 | 0.0839 | 1.1818 |
| chr19 | 59128983 | 2779849 | 0.047 | 0.7801 |
| chr20 | 63025520 | 4925313 | 0.0781 | 0.3515 |
| chr21 | 48129895 | 2702724 | 0.0562 | 0.3059 |
| chr22 | 51304566 | 2300354 | 0.0448 | 0.2464 |
| chrMT | 16571 | 221287 | 13.3539 | 7.648 |
| chrX | 155270560 | 10811770 | 0.0696 | 0.363 |
| chrY | 59373566 | 475504 | 0.008 | 0.154 |

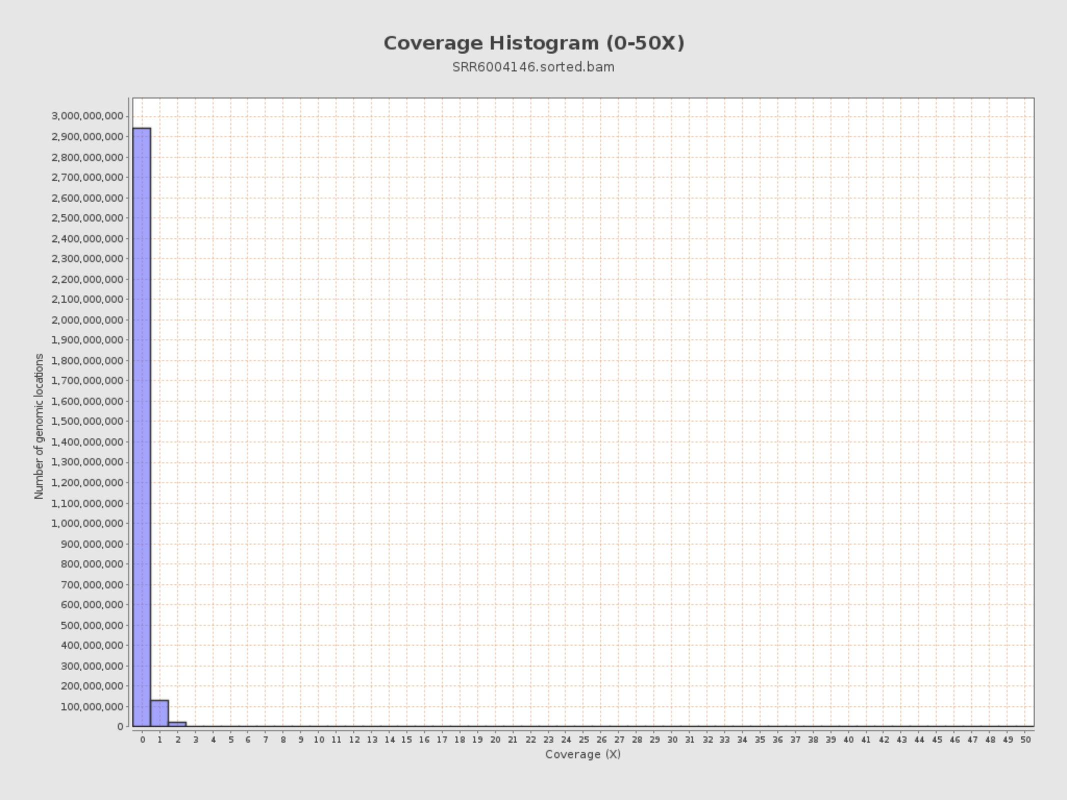
# 3. Results : Coverage across reference



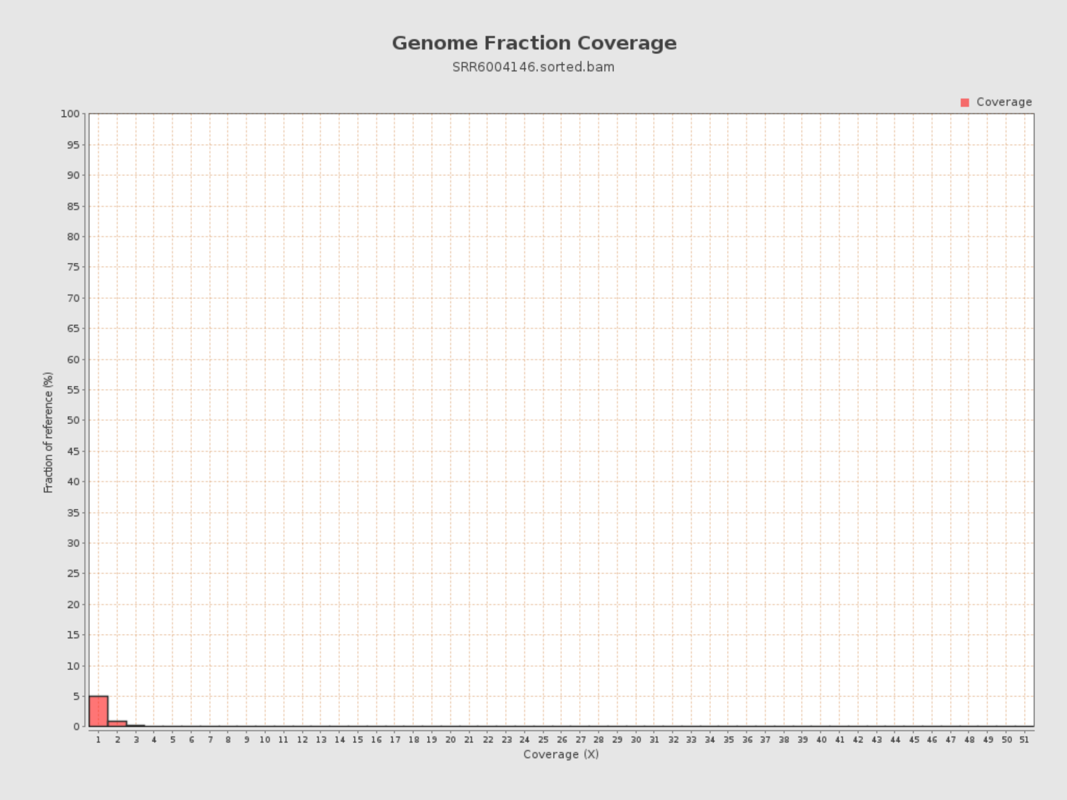
# 4. Results : Coverage Histogram



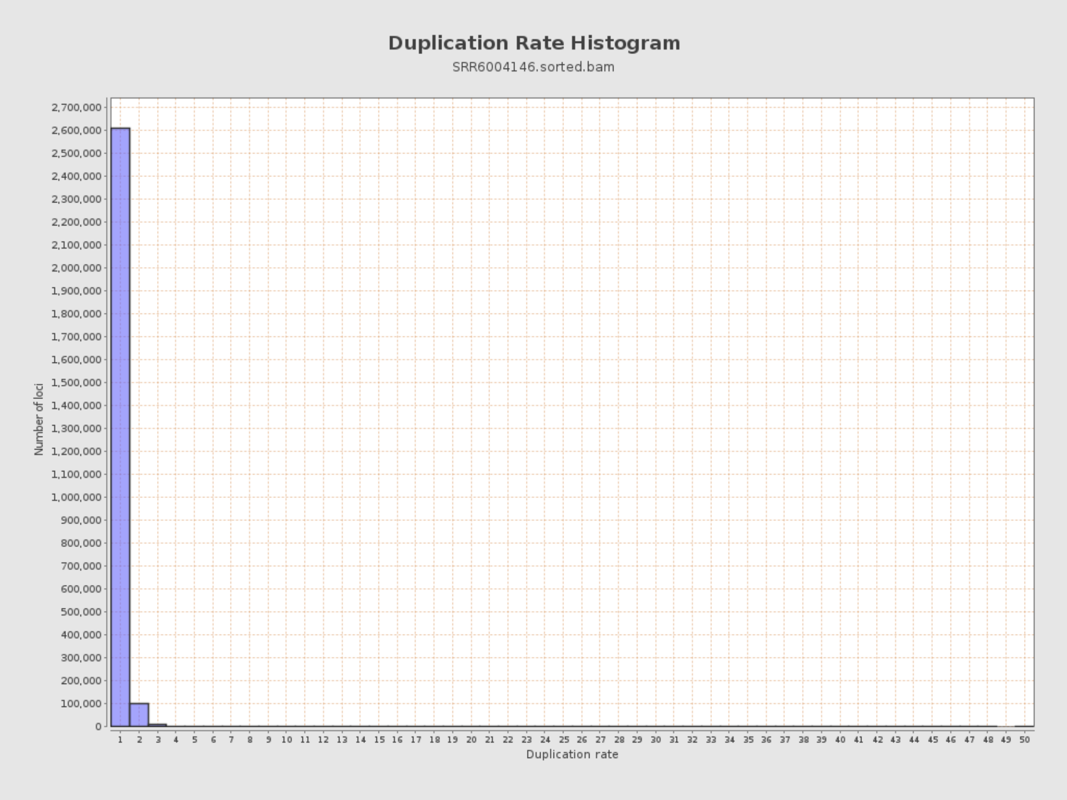
# 5. Results : Coverage Histogram (0-50X)



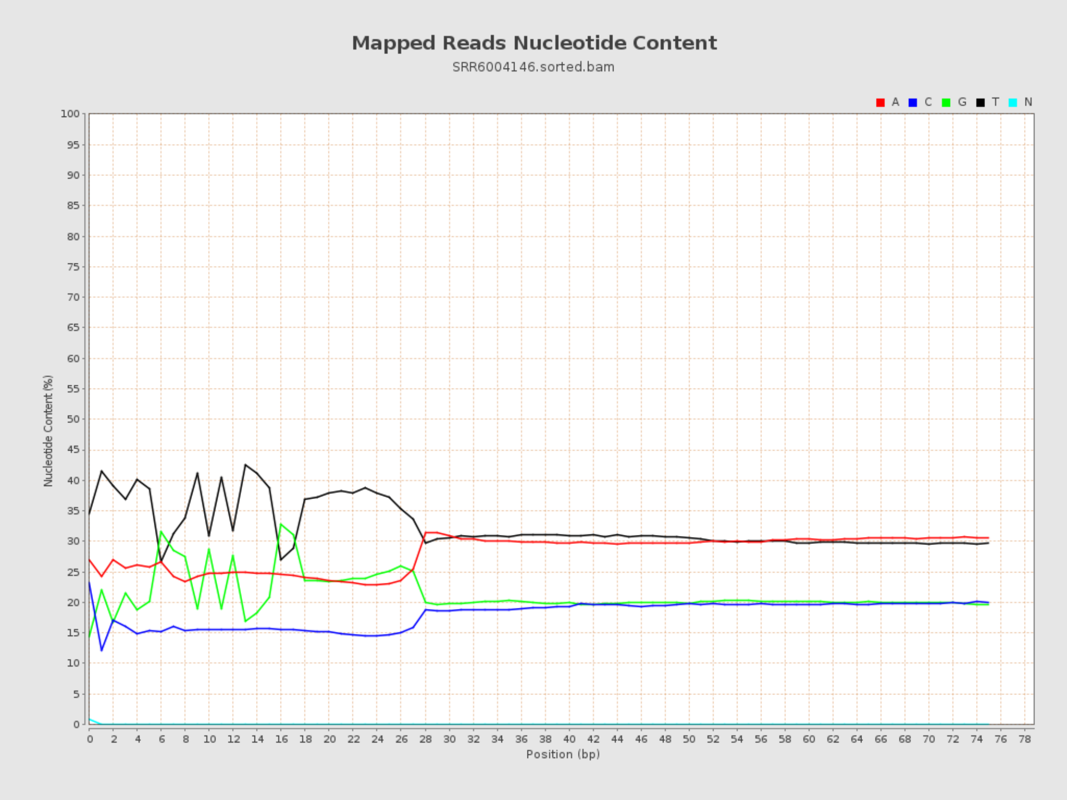
# 6. Results : Genome Fraction Coverage



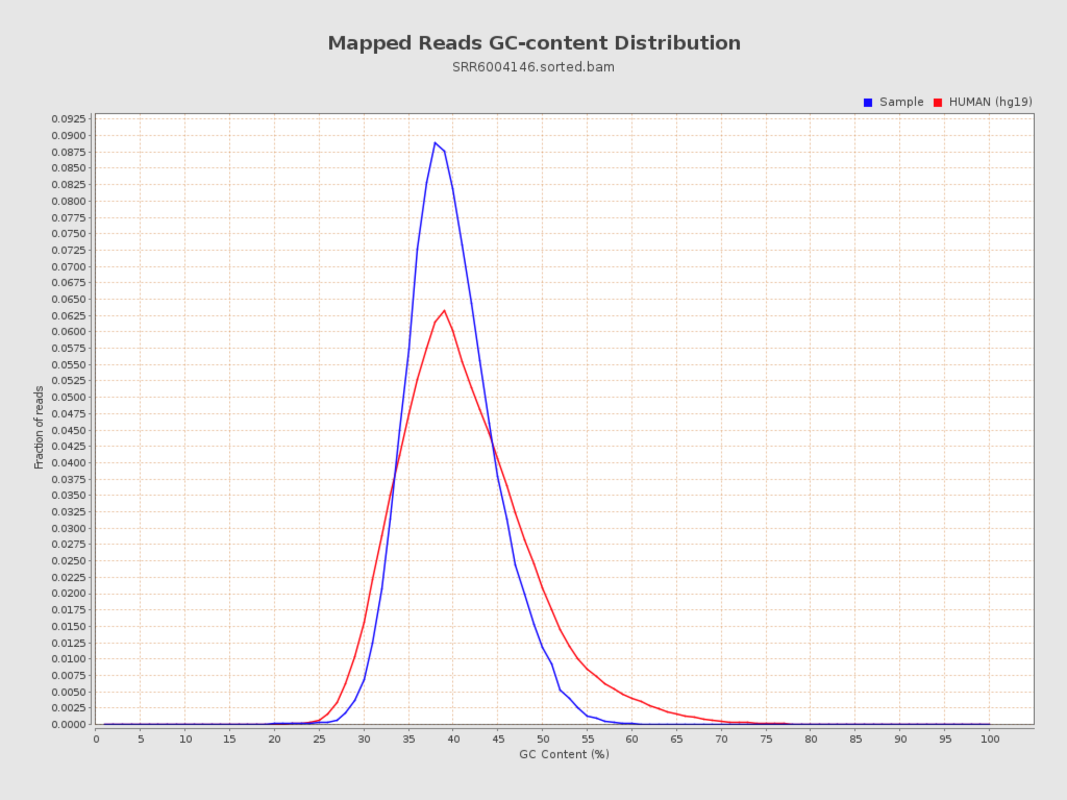
# 7. Results : Duplication Rate Histogram



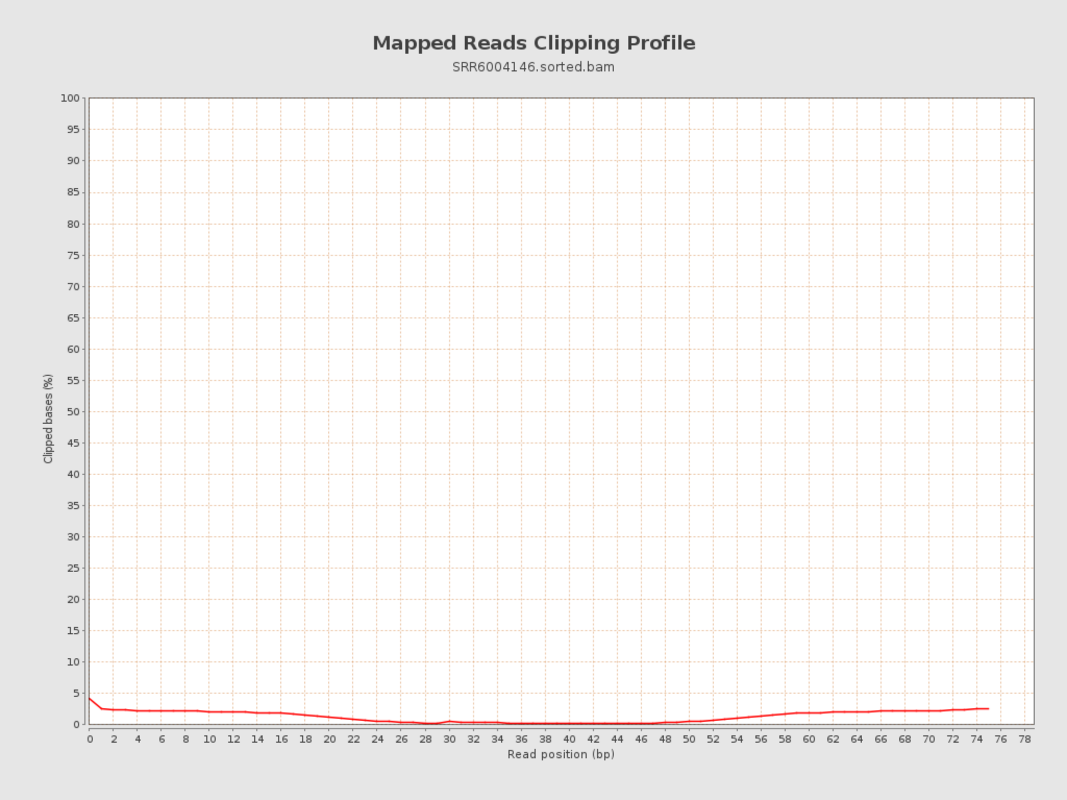
# 8. Results : Mapped Reads Nucleotide Content



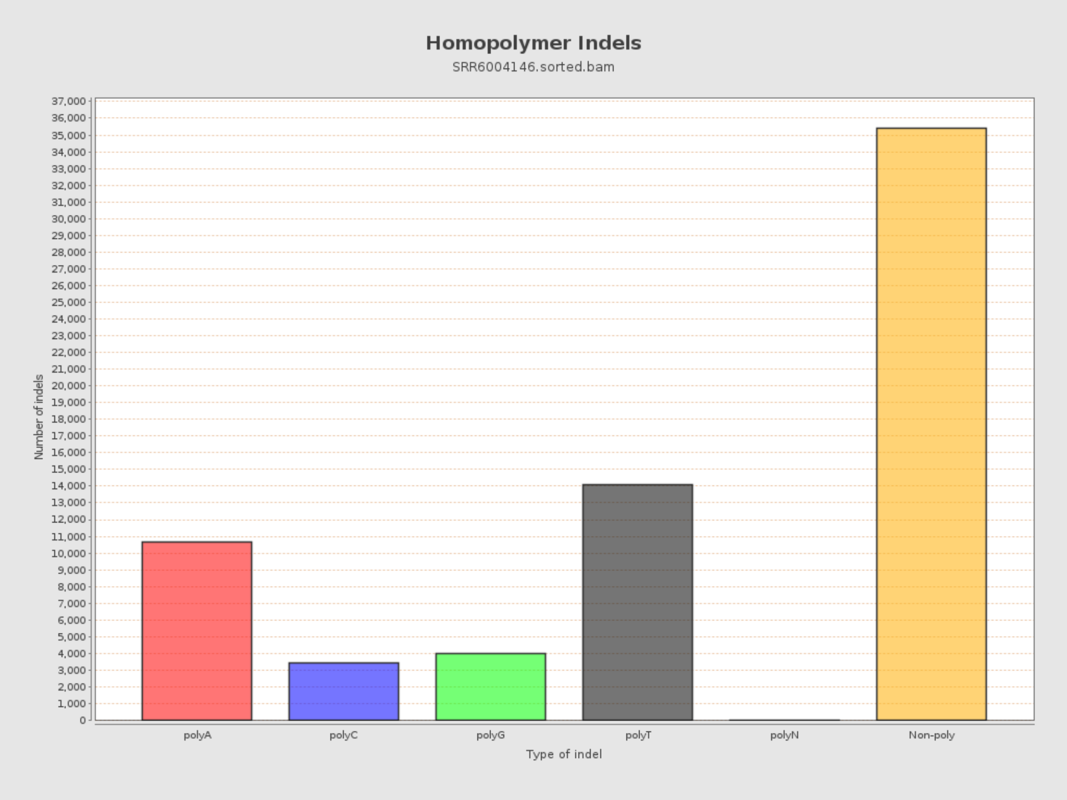
# 9. Results : Mapped Reads GC-content Distribution



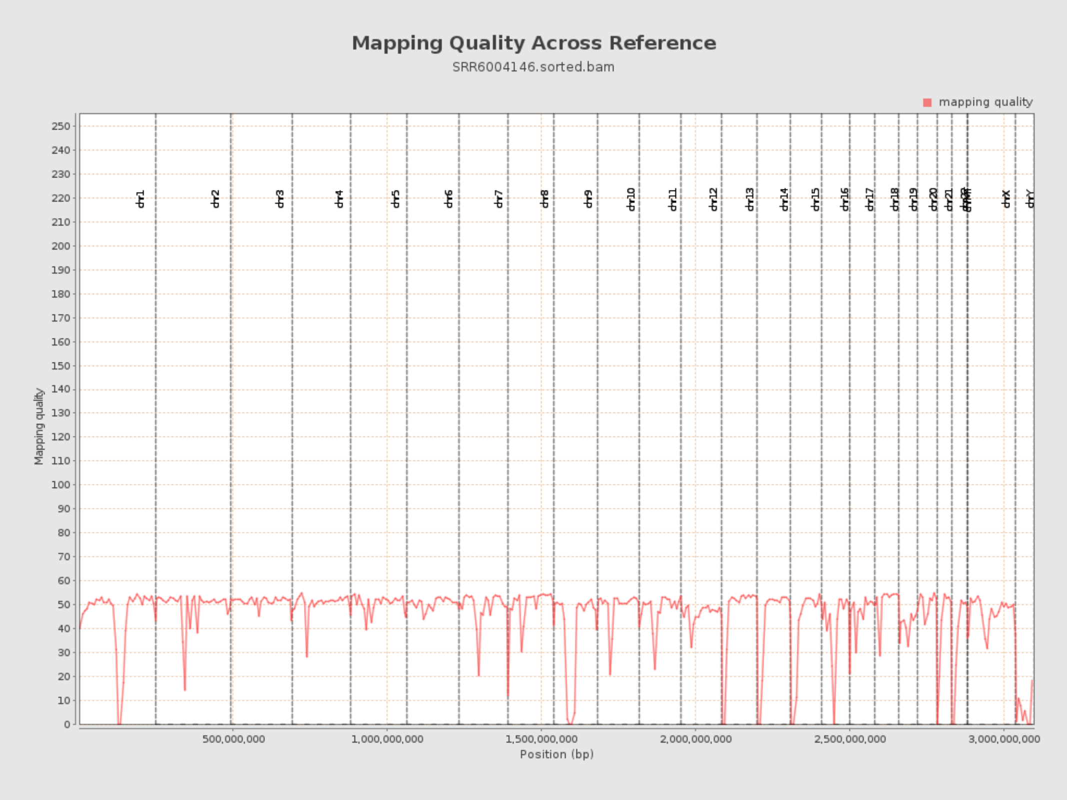
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram