# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/18 03:14:46*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240032.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_SRR6240032 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240032.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Sep 18 03:14:46 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6240032.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,356,669 |
| Mapped reads | 1,867,487 / 79.24% |
| Unmapped reads | 489,182 / 20.76% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 16,295 / 0.69% |
| Read min/max/mean length | 30 / 76 / 76.24 |
| Duplicated reads (estimated) | 280,383 / 11.9% |
| Duplication rate | 11.03% |
| Clipped reads | 886,315 / 37.61% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 35,171,223 / 28.4% |
| Number/percentage of C's | 22,985,301 / 18.56% |
| Number/percentage of T's | 39,522,917 / 31.91% |
| Number/percentage of G's | 26,167,043 / 21.13% |
| Number/percentage of N's | 11,303 / 0.01% |
| GC Percentage | 39.68% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.04 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4757 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.97 |

## 2.5. Mismatches and indels

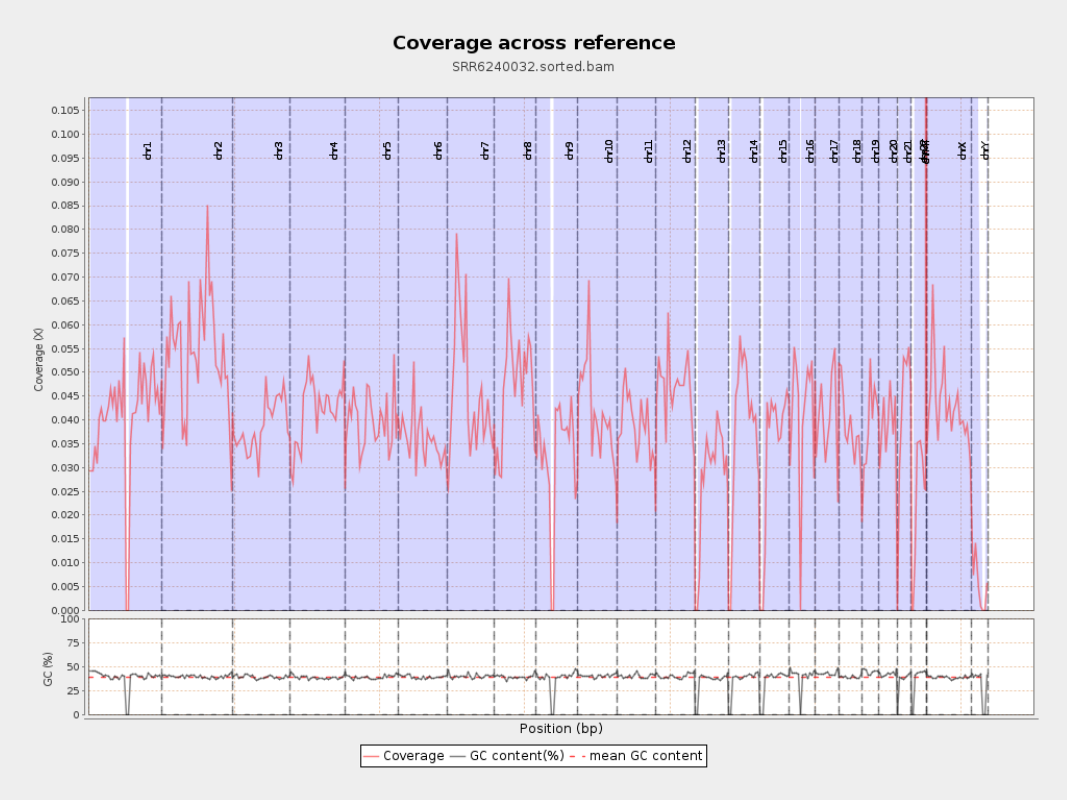
| | |
|---|---|
| General error rate | 0.85% |
| Mismatches | 1,032,721 |
| Insertions | 8,799 |
| Mapped reads with at least one insertion | 0.47% |
| Deletions | 34,534 |
| Mapped reads with at least one deletion | 1.83% |
| Homopolymer indels | 48.54% |

## 2.6. Chromosome stats

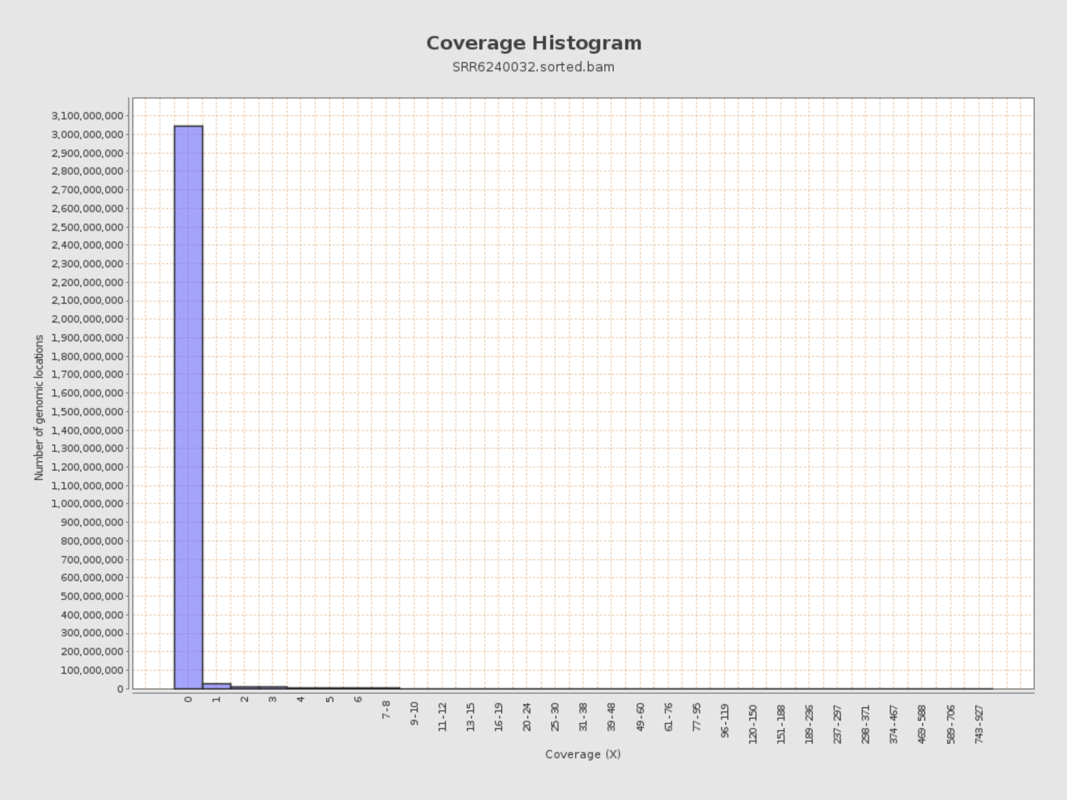
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 10044912 | 0.0403 | 0.6575 |
| chr2 | 243199373 | 13126964 | 0.054 | 0.5427 |
| chr3 | 198022430 | 7699971 | 0.0389 | 0.3861 |
| chr4 | 191154276 | 8035213 | 0.042 | 0.4125 |
| chr5 | 180915260 | 7230981 | 0.04 | 0.3888 |
| chr6 | 171115067 | 6154682 | 0.036 | 0.4074 |
| chr7 | 159138663 | 7375075 | 0.0463 | 0.6608 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6885767 | 0.047 | 0.6929 |
| chr9 | 141213431 | 4584037 | 0.0325 | 0.4001 |
| chr10 | 135534747 | 5692851 | 0.042 | 0.4679 |
| chr11 | 135006516 | 5231542 | 0.0388 | 0.434 |
| chr12 | 133851895 | 6312306 | 0.0472 | 0.4293 |
| chr13 | 115169878 | 3180781 | 0.0276 | 0.3301 |
| chr14 | 107349540 | 4083450 | 0.038 | 0.3967 |
| chr15 | 102531392 | 3418813 | 0.0333 | 0.3536 |
| chr16 | 90354753 | 3715917 | 0.0411 | 0.3986 |
| chr17 | 81195210 | 3201391 | 0.0394 | 0.3986 |
| chr18 | 78077248 | 3026886 | 0.0388 | 0.589 |
| chr19 | 59128983 | 2320109 | 0.0392 | 0.4885 |
| chr20 | 63025520 | 2447694 | 0.0388 | 0.3852 |
| chr21 | 48129895 | 2012679 | 0.0418 | 0.4055 |
| chr22 | 51304566 | 1136939 | 0.0222 | 0.2849 |
| chrMT | 16571 | 25354 | 1.53 | 2.9037 |
| chrX | 155270560 | 6652083 | 0.0428 | 0.4229 |
| chrY | 59373566 | 322036 | 0.0054 | 0.1293 |

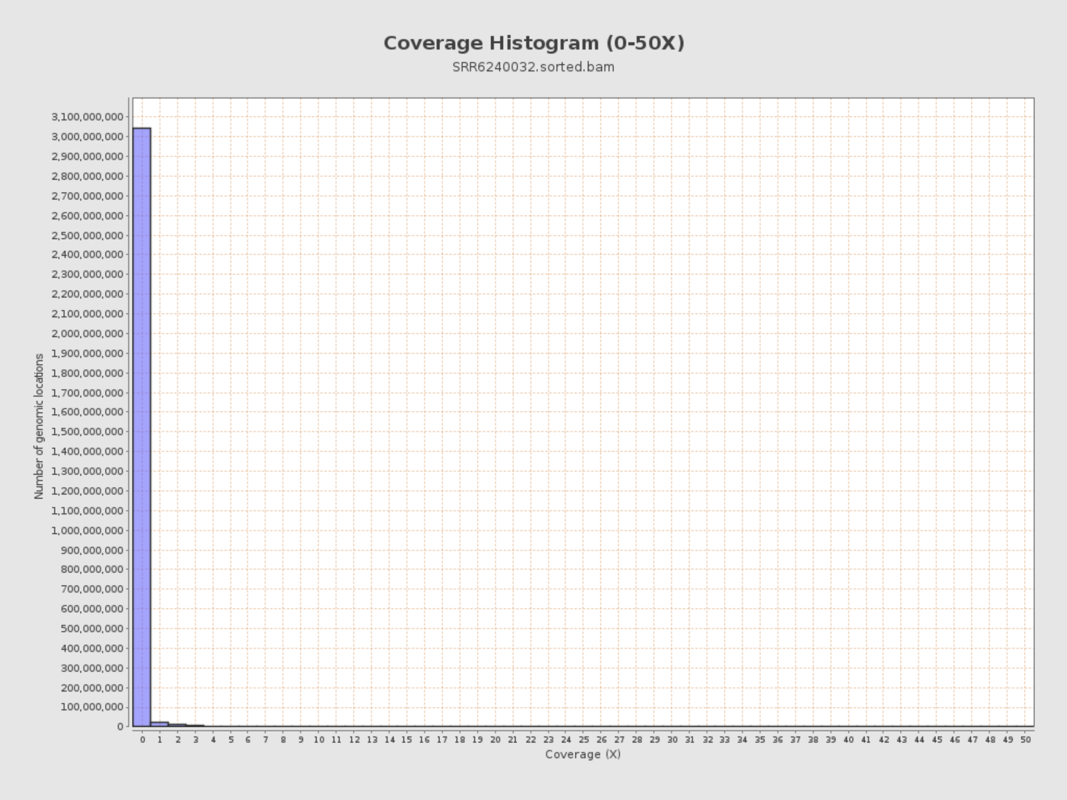
# 3. Results : Coverage across reference



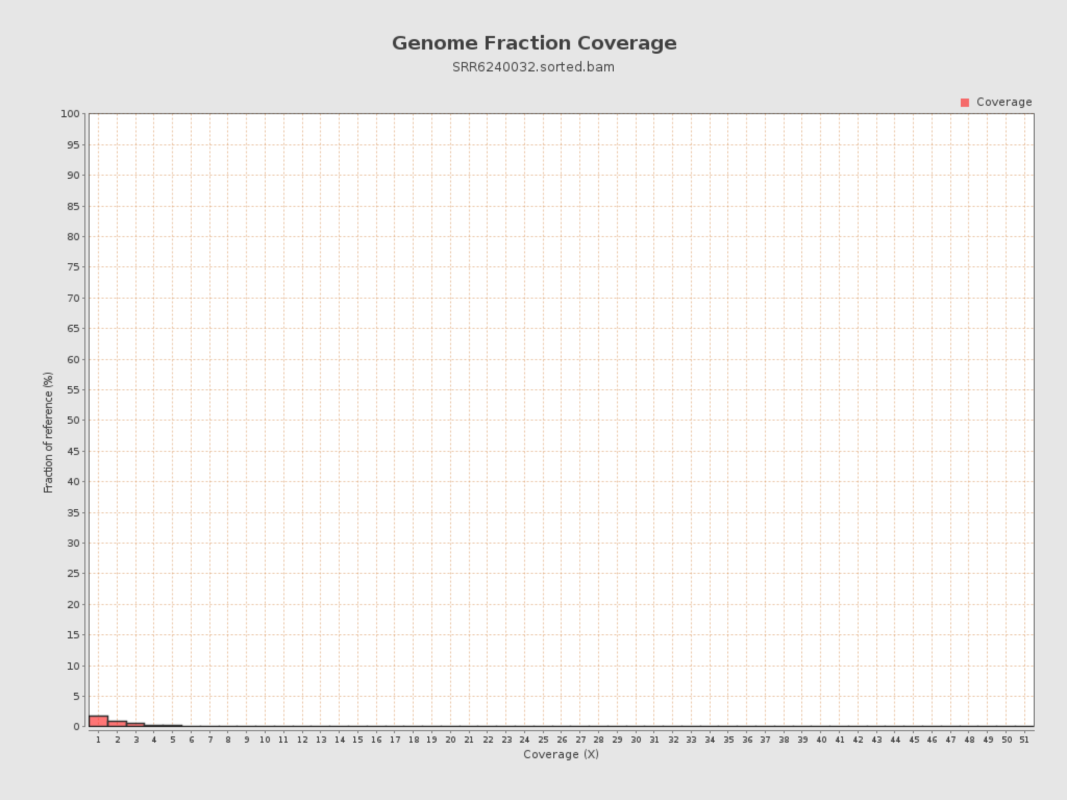
# 4. Results : Coverage Histogram



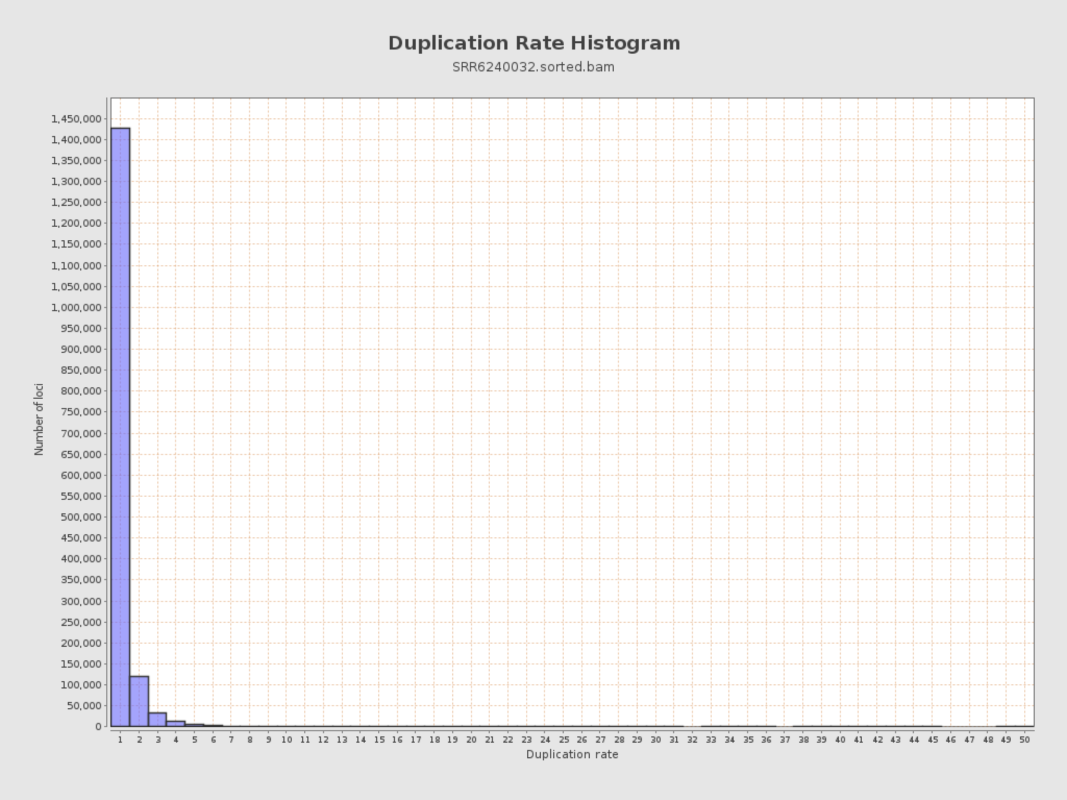
# 5. Results : Coverage Histogram (0-50X)



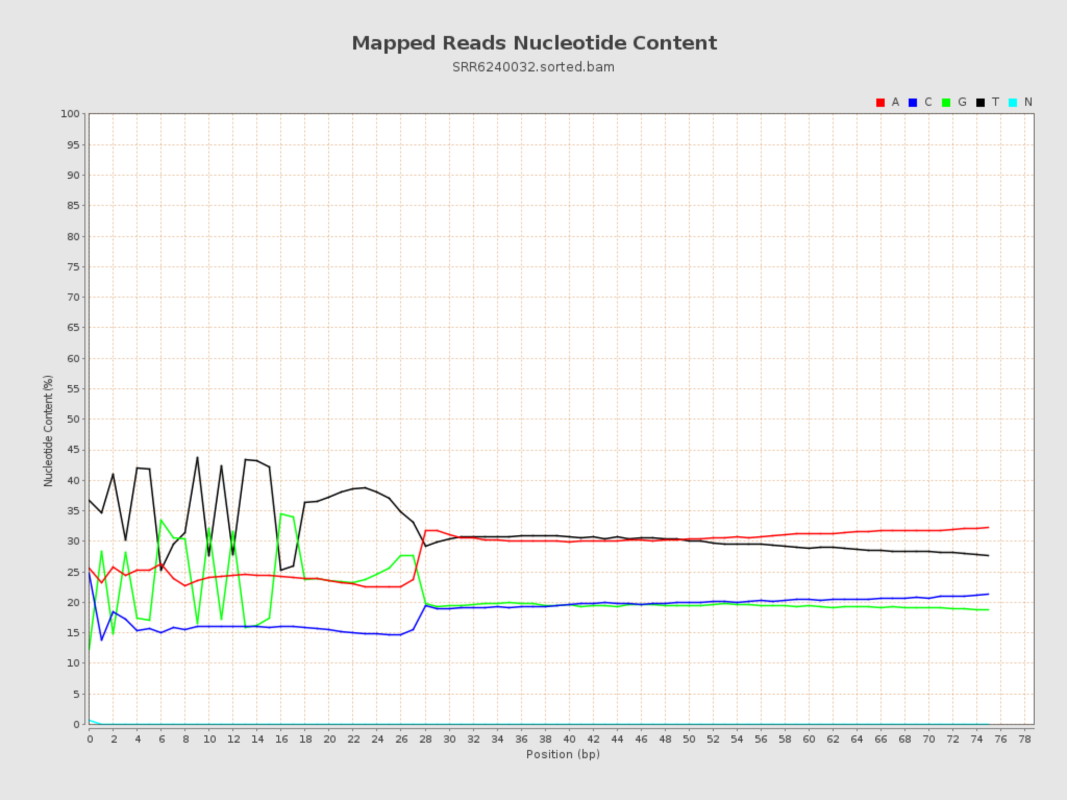
# 6. Results : Genome Fraction Coverage



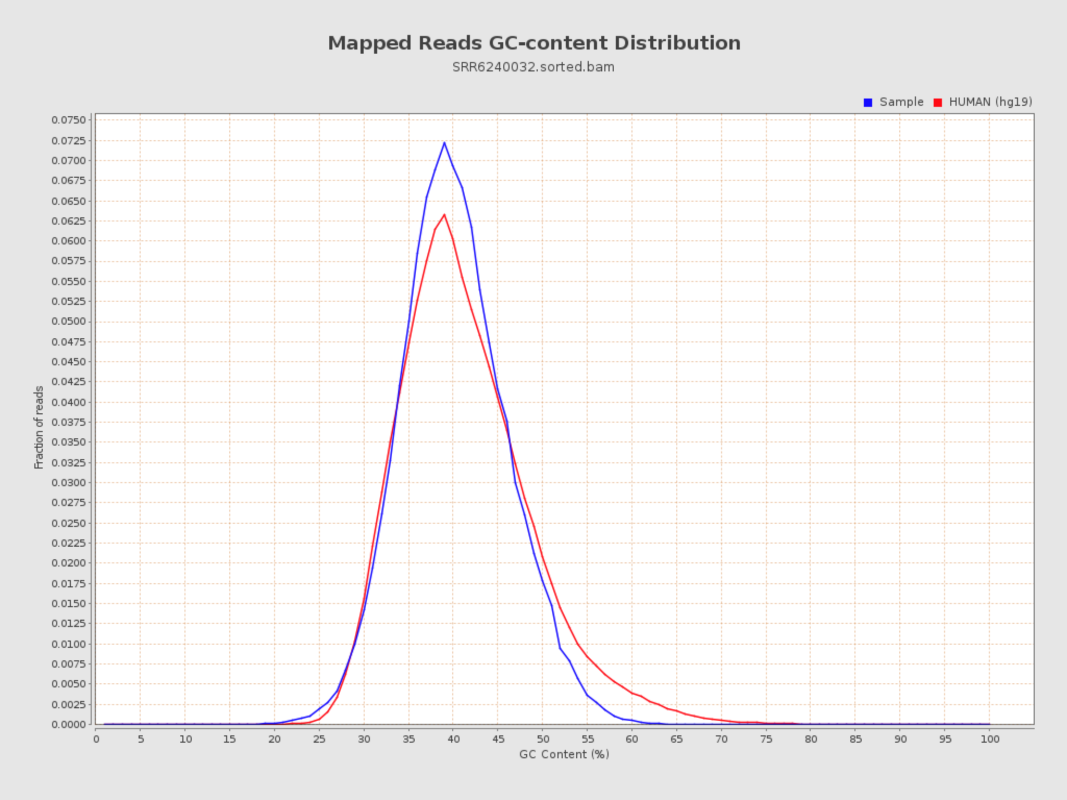
# 7. Results : Duplication Rate Histogram



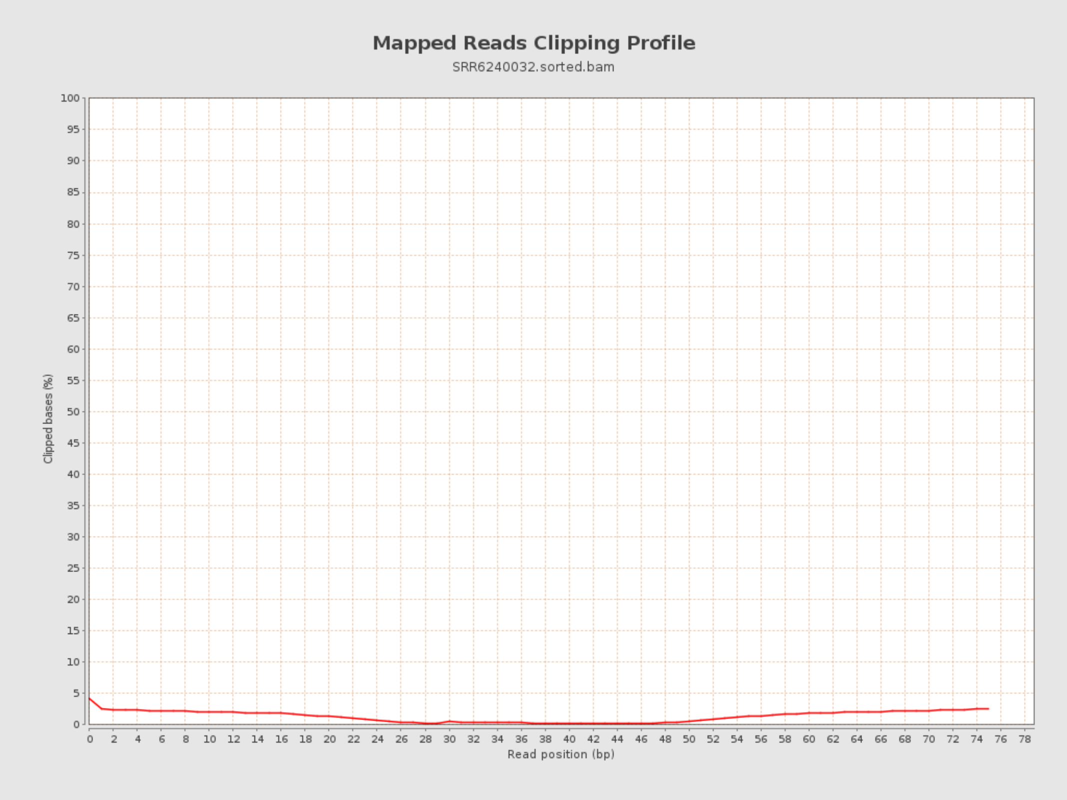
# 8. Results : Mapped Reads Nucleotide Content



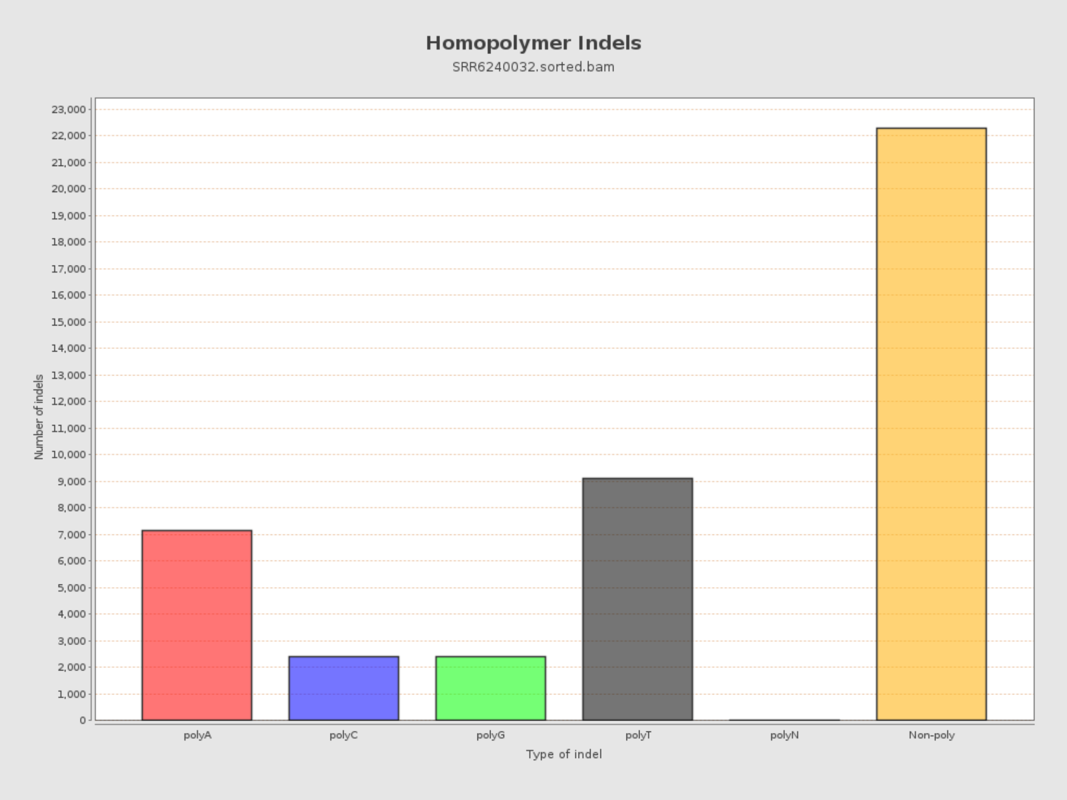
# 9. Results : Mapped Reads GC-content Distribution



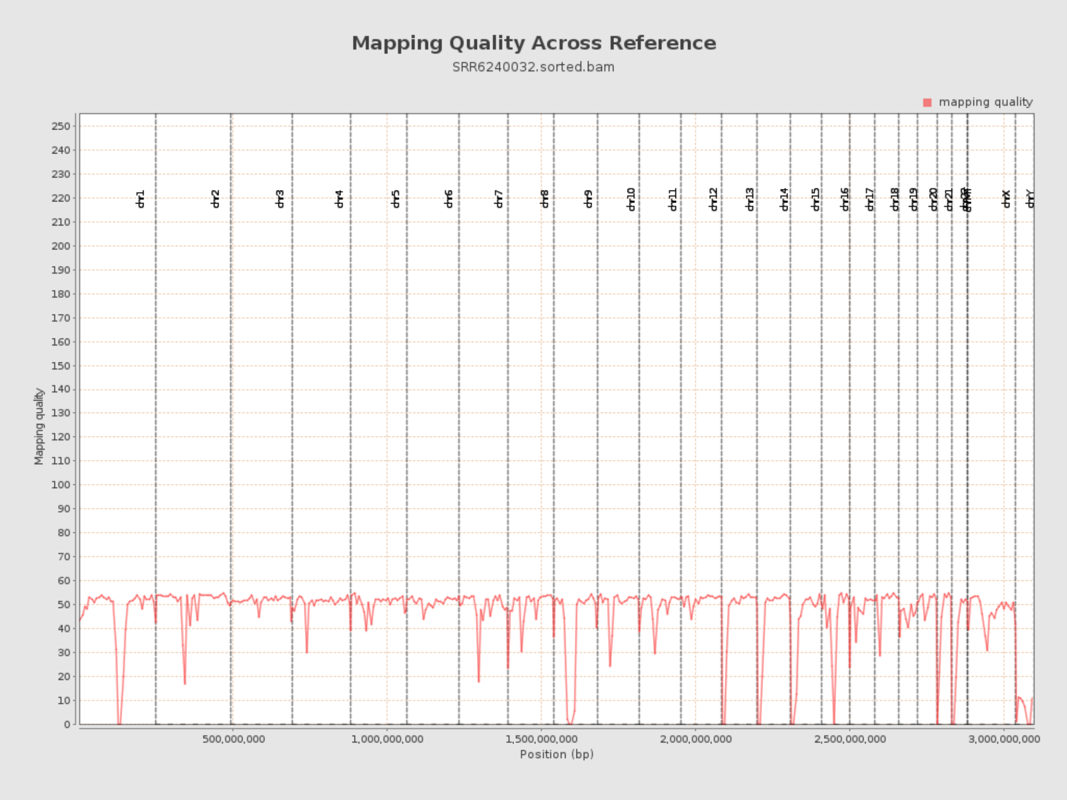
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram