# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/30 00:39:47*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525242.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_SRR10525242 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525242.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Fri Aug 30 00:39:46 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10525242.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,513,216 |
| Mapped reads | 3,205,537 / 91.24% |
| Unmapped reads | 307,679 / 8.76% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 10,611 / 0.3% |
| Read min/max/mean length | 30 / 76 / 76.1 |
| Duplicated reads (estimated) | 188,637 / 5.37% |
| Duplication rate | 4.37% |
| Clipped reads | 3,205,729 / 91.25% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 47,785,321 / 25.7% |
| Number/percentage of C's | 30,567,540 / 16.44% |
| Number/percentage of T's | 60,978,458 / 32.8% |
| Number/percentage of G's | 46,594,354 / 25.06% |
| Number/percentage of N's | 3,770 / 0% |
| GC Percentage | 41.5% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0601 |
| | |

| | |
|---|---|
| Standard Deviation | 0.535 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.27 |

## 2.5. Mismatches and indels

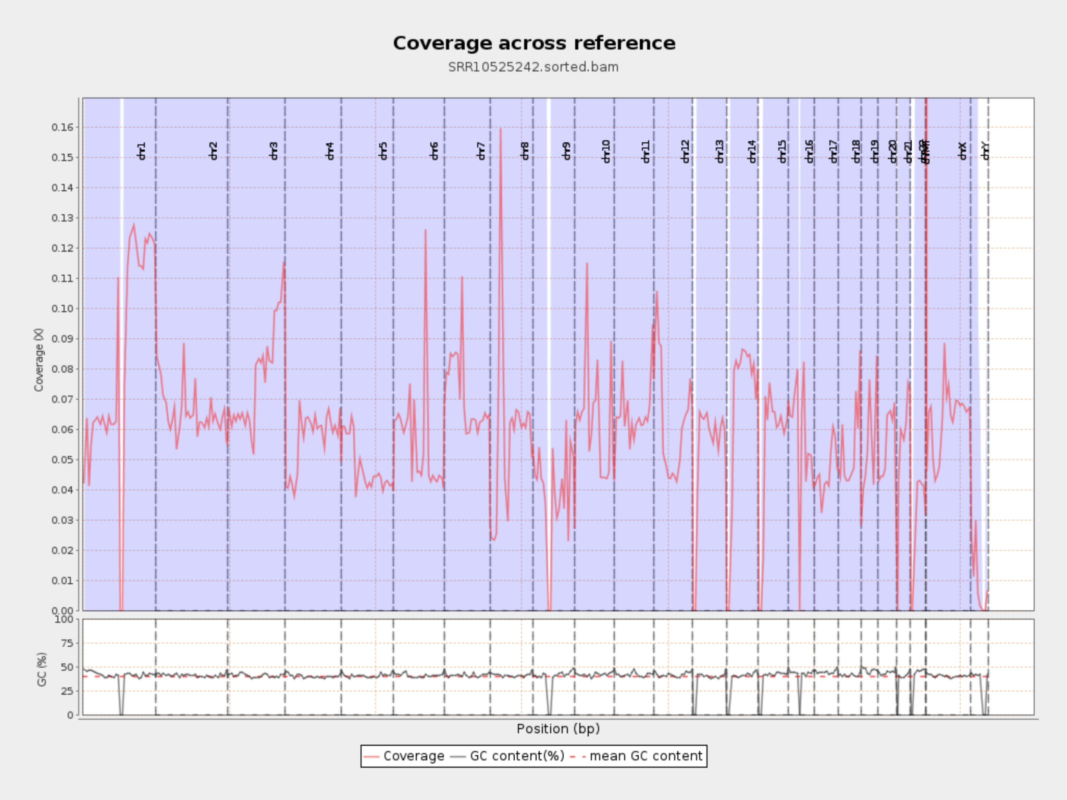
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 941,351 |
| Insertions | 13,642 |
| Mapped reads with at least one insertion | 0.42% |
| Deletions | 38,377 |
| Mapped reads with at least one deletion | 1.19% |
| Homopolymer indels | 44.51% |

## 2.6. Chromosome stats

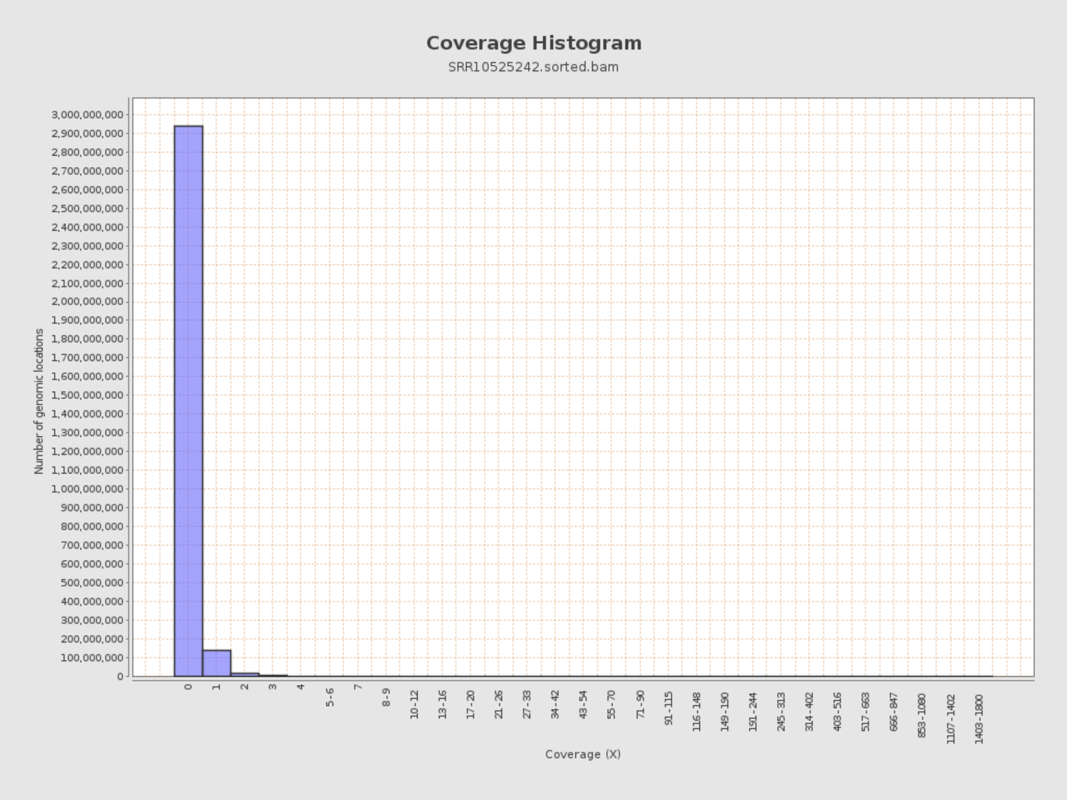
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 20632351 | 0.0828 | 1.0651 |
| chr2 | 243199373 | 16100616 | 0.0662 | 0.7749 |
| chr3 | 198022430 | 15247734 | 0.077 | 0.3268 |
| chr4 | 191154276 | 10947372 | 0.0573 | 0.3042 |
| chr5 | 180915260 | 8611723 | 0.0476 | 0.2541 |
| chr6 | 171115067 | 9646350 | 0.0564 | 0.3445 |
| chr7 | 159138663 | 11373773 | 0.0715 | 0.8053 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 8958727 | 0.0612 | 0.5222 |
| chr9 | 141213431 | 5423231 | 0.0384 | 0.3439 |
| chr10 | 135534747 | 8558932 | 0.0631 | 0.5136 |
| chr11 | 135006516 | 8807647 | 0.0652 | 0.4216 |
| chr12 | 133851895 | 8443019 | 0.0631 | 0.3001 |
| chr13 | 115169878 | 6076445 | 0.0528 | 0.2764 |
| chr14 | 107349540 | 7262112 | 0.0676 | 0.3168 |
| chr15 | 102531392 | 5333760 | 0.052 | 0.2847 |
| chr16 | 90354753 | 5112719 | 0.0566 | 0.3256 |
| chr17 | 81195210 | 3752777 | 0.0462 | 0.266 |
| chr18 | 78077248 | 4172182 | 0.0534 | 0.7742 |
| chr19 | 59128983 | 3288406 | 0.0556 | 0.6788 |
| chr20 | 63025520 | 3468442 | 0.055 | 0.2802 |
| chr21 | 48129895 | 2656830 | 0.0552 | 0.303 |
| chr22 | 51304566 | 1501068 | 0.0293 | 0.1945 |
| chrMT | 16571 | 223418 | 13.4825 | 7.9956 |
| chrX | 155270560 | 9839460 | 0.0634 | 0.3392 |
| chrY | 59373566 | 551813 | 0.0093 | 0.2524 |

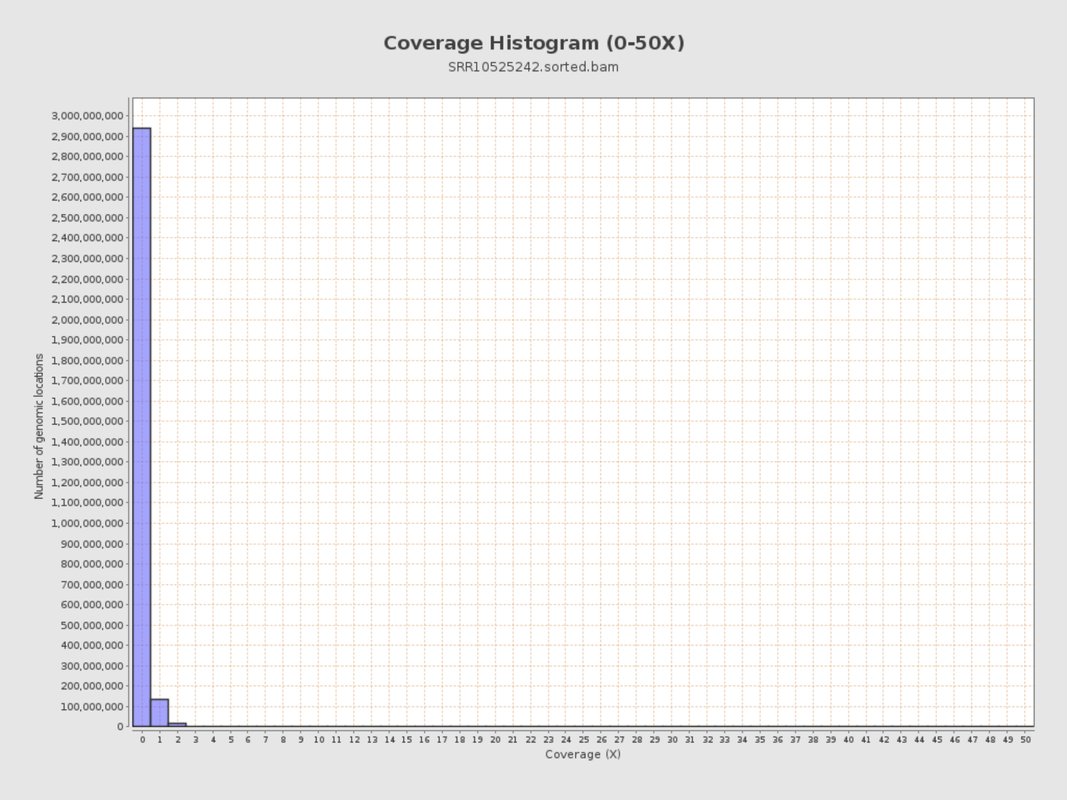
# 3. Results : Coverage across reference



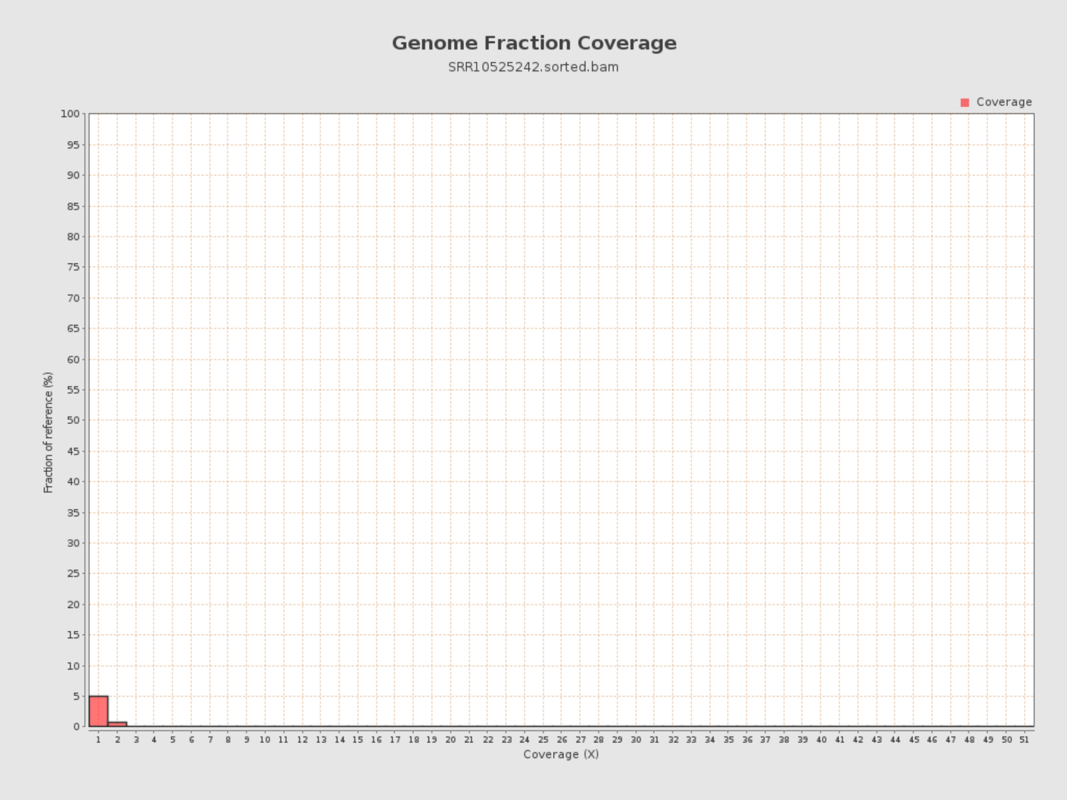
# 4. Results : Coverage Histogram



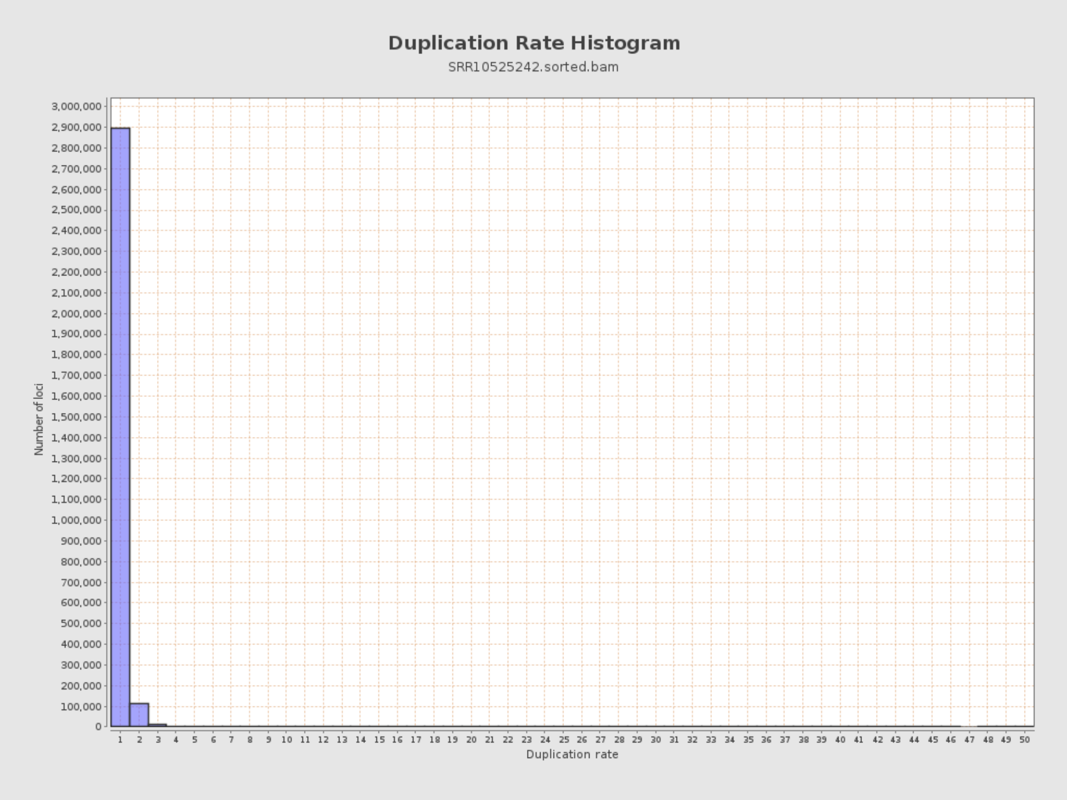
# 5. Results : Coverage Histogram (0-50X)



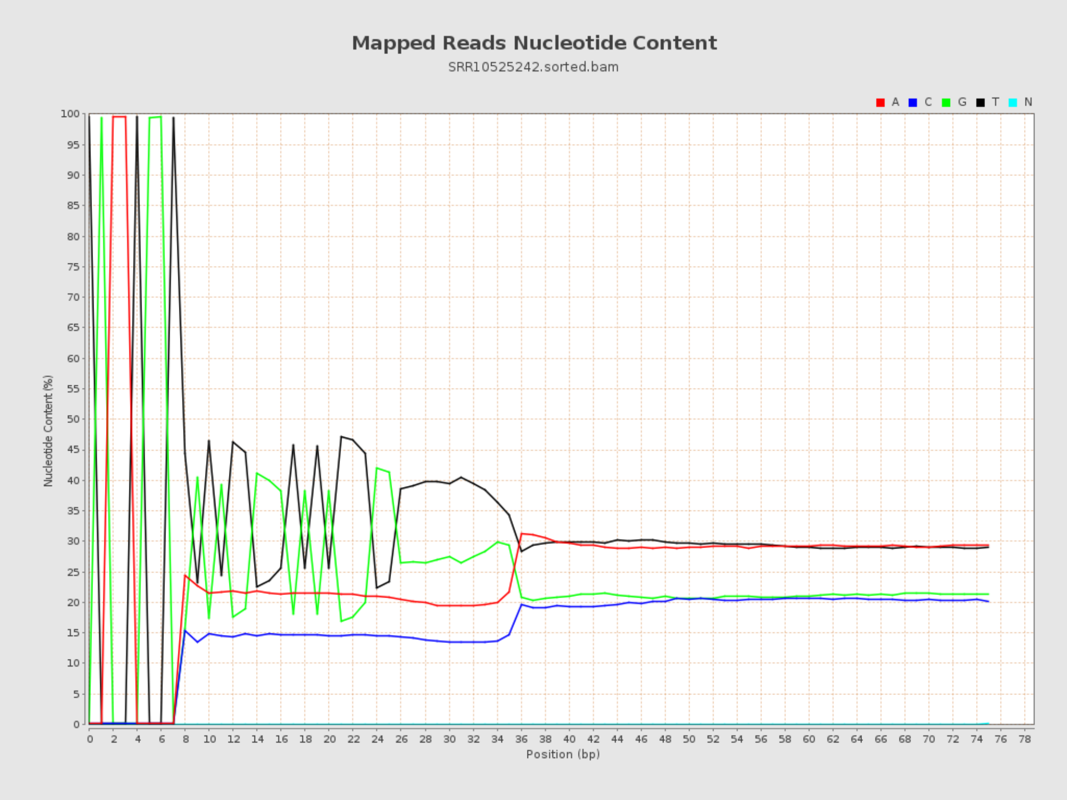
# 6. Results : Genome Fraction Coverage



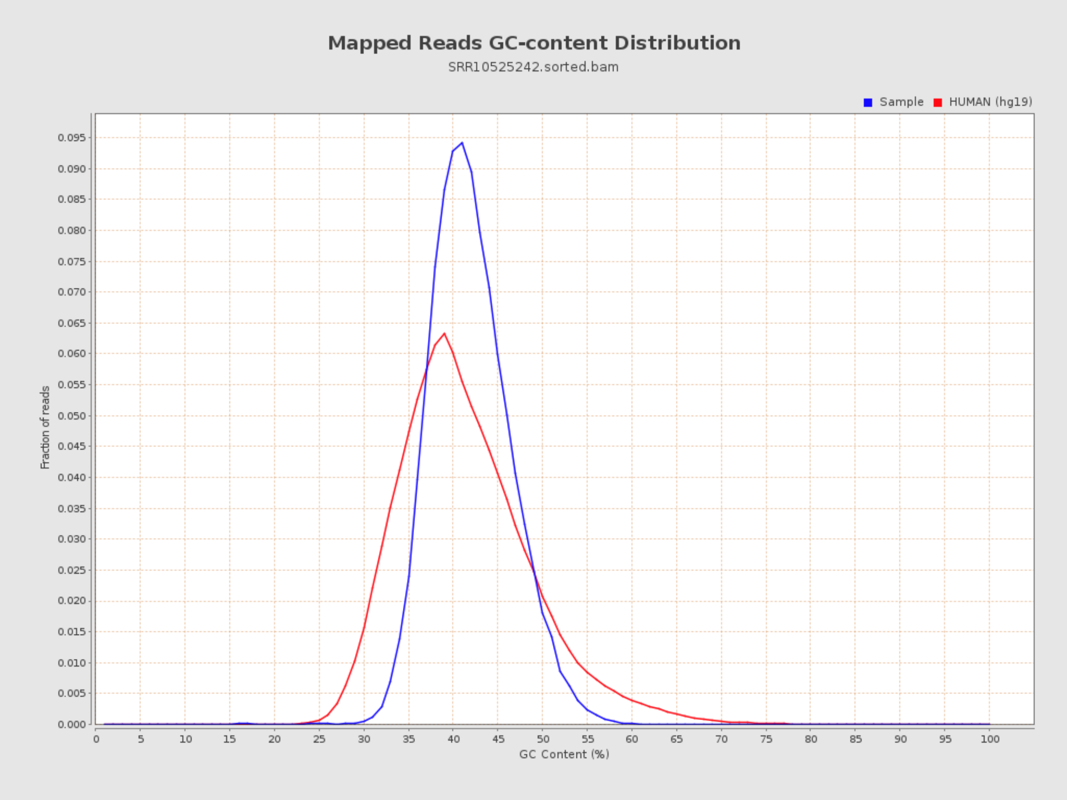
# 7. Results : Duplication Rate Histogram



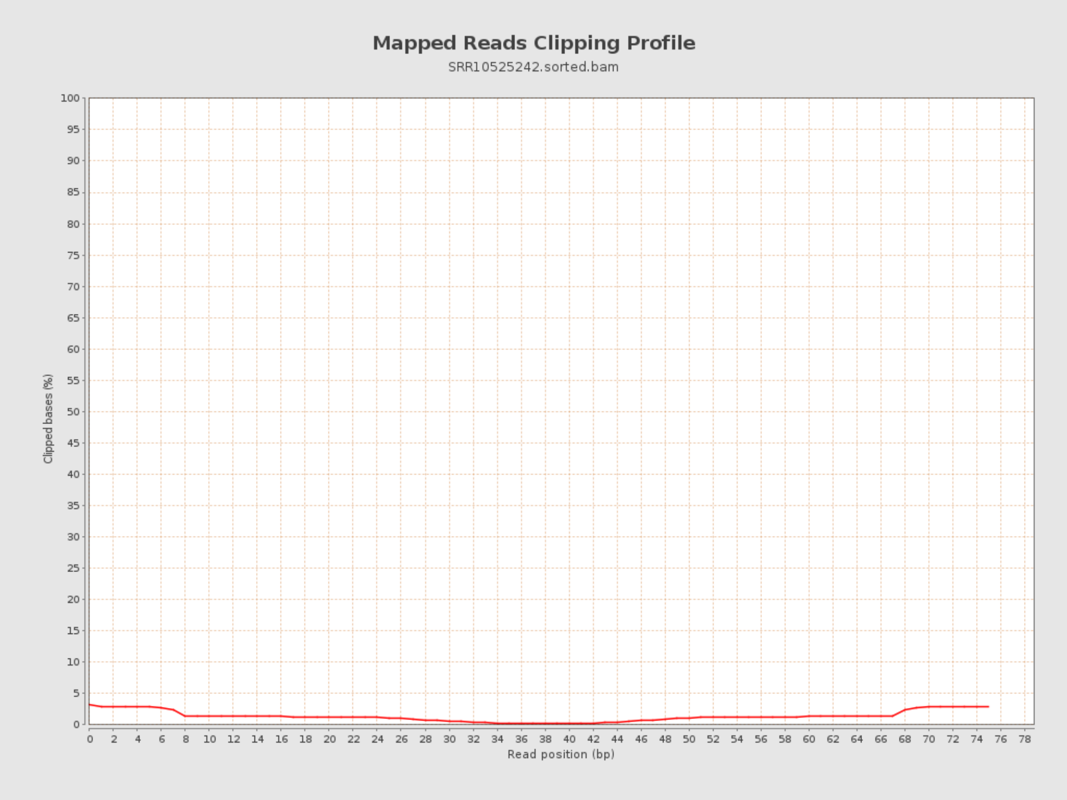
# 8. Results : Mapped Reads Nucleotide Content



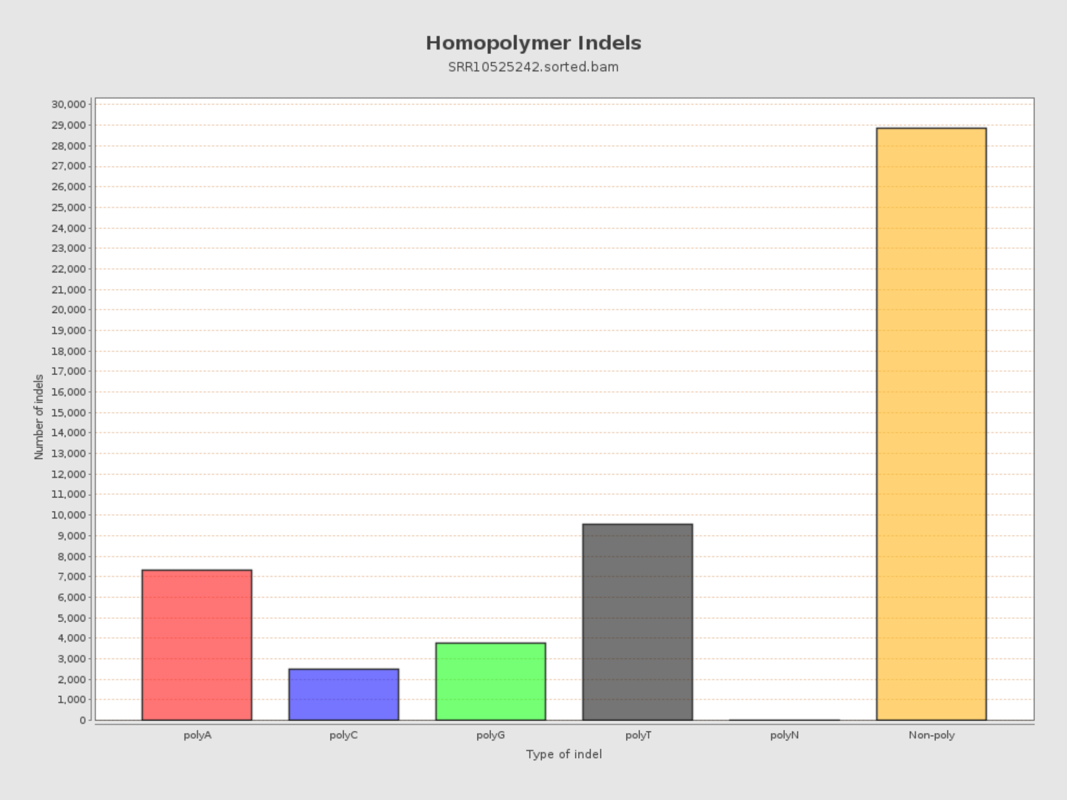
# 9. Results : Mapped Reads GC-content Distribution



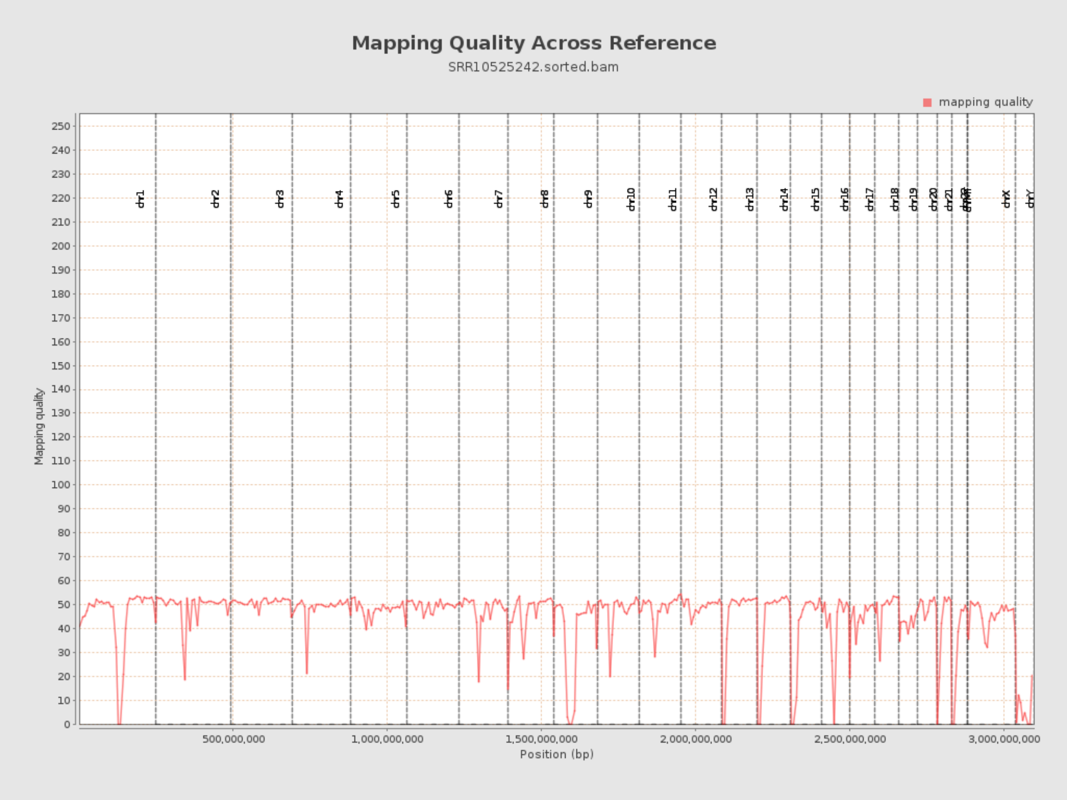
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram