# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/01 19:46:33*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524575.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_SRR10524575 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524575.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 01 19:46:33 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524575.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,361,107 |
| Mapped reads | 3,087,492 / 91.86% |
| Unmapped reads | 273,615 / 8.14% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 14,538 / 0.43% |
| Read min/max/mean length | 30 / 76 / 76.15 |
| Duplicated reads (estimated) | 195,830 / 5.83% |
| Duplication rate | 4.73% |
| Clipped reads | 3,093,465 / 92.04% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 45,885,764 / 25.49% |
| Number/percentage of C's | 33,965,932 / 18.87% |
| Number/percentage of T's | 57,595,874 / 31.99% |
| Number/percentage of G's | 42,595,396 / 23.66% |
| Number/percentage of N's | 2,627 / 0% |
| GC Percentage | 42.52% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0582 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4918 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.86 |

## 2.5. Mismatches and indels

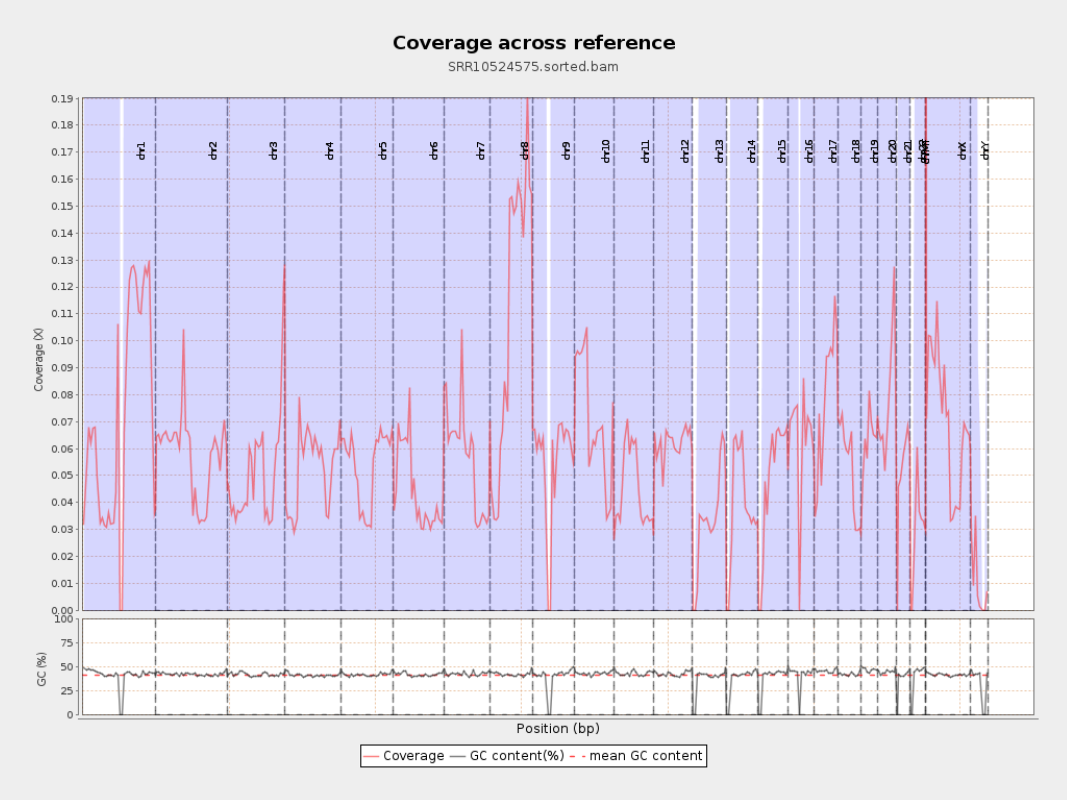
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 909,950 |
| Insertions | 12,777 |
| Mapped reads with at least one insertion | 0.41% |
| Deletions | 33,456 |
| Mapped reads with at least one deletion | 1.08% |
| Homopolymer indels | 42.4% |

## 2.6. Chromosome stats

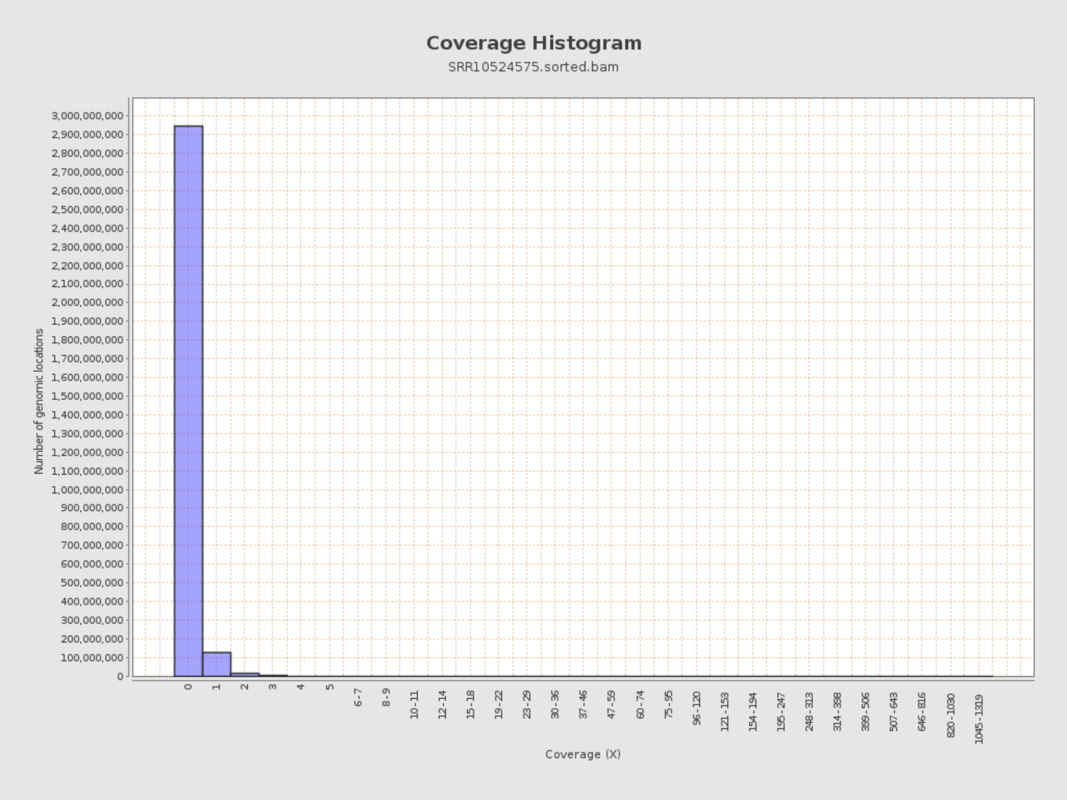
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 17734454 | 0.0712 | 0.99 |
| chr2 | 243199373 | 14159957 | 0.0582 | 0.5692 |
| chr3 | 198022430 | 10082901 | 0.0509 | 0.2702 |
| chr4 | 191154276 | 10083227 | 0.0527 | 0.3264 |
| chr5 | 180915260 | 9758363 | 0.0539 | 0.2755 |
| chr6 | 171115067 | 7619329 | 0.0445 | 0.3567 |
| chr7 | 159138663 | 9033741 | 0.0568 | 0.6567 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 16491973 | 0.1127 | 0.5087 |
| chr9 | 141213431 | 7676010 | 0.0544 | 0.4069 |
| chr10 | 135534747 | 9429755 | 0.0696 | 0.472 |
| chr11 | 135006516 | 6106657 | 0.0452 | 0.4527 |
| chr12 | 133851895 | 8358994 | 0.0624 | 0.2968 |
| chr13 | 115169878 | 3940021 | 0.0342 | 0.217 |
| chr14 | 107349540 | 4282865 | 0.0399 | 0.2453 |
| chr15 | 102531392 | 4854128 | 0.0473 | 0.2723 |
| chr16 | 90354753 | 5601758 | 0.062 | 0.3245 |
| chr17 | 81195210 | 6361749 | 0.0784 | 0.3669 |
| chr18 | 78077248 | 4157162 | 0.0532 | 0.7951 |
| chr19 | 59128983 | 3721146 | 0.0629 | 0.6588 |
| chr20 | 63025520 | 5065335 | 0.0804 | 0.3409 |
| chr21 | 48129895 | 2498687 | 0.0519 | 0.3079 |
| chr22 | 51304566 | 1487595 | 0.029 | 0.1974 |
| chrMT | 16571 | 14852 | 0.8963 | 1.2418 |
| chrX | 155270560 | 10986551 | 0.0708 | 0.3744 |
| chrY | 59373566 | 594089 | 0.01 | 0.2658 |

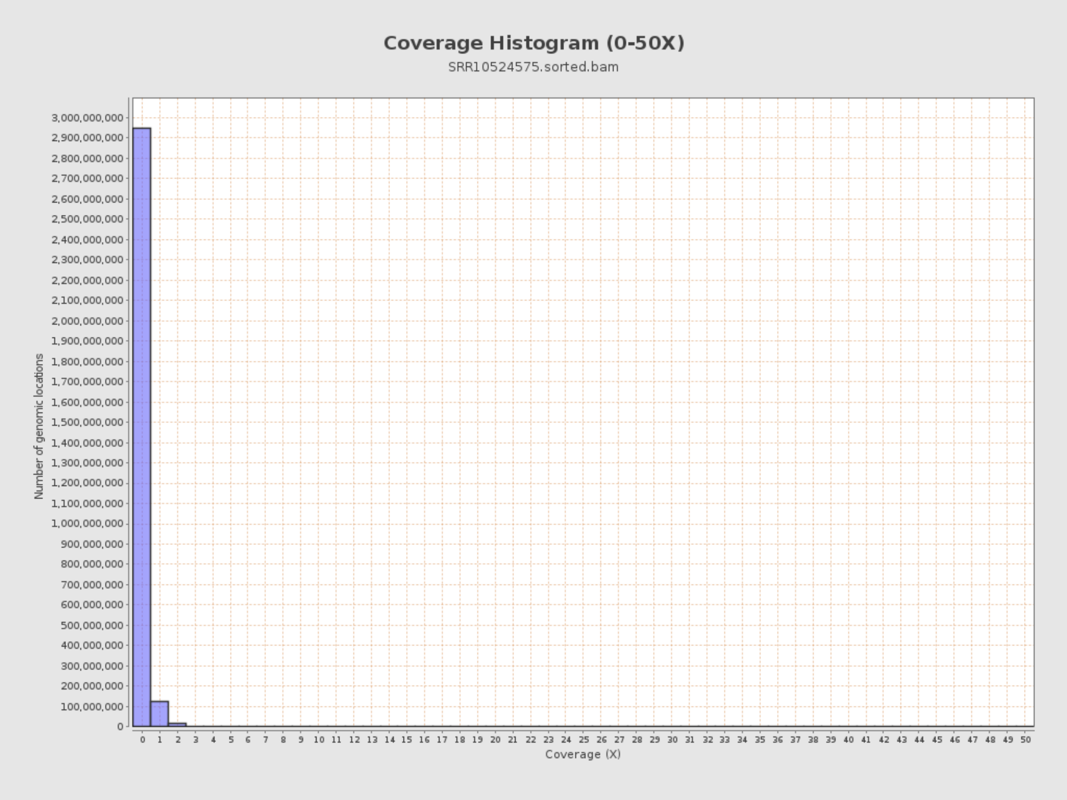
# 3. Results : Coverage across reference



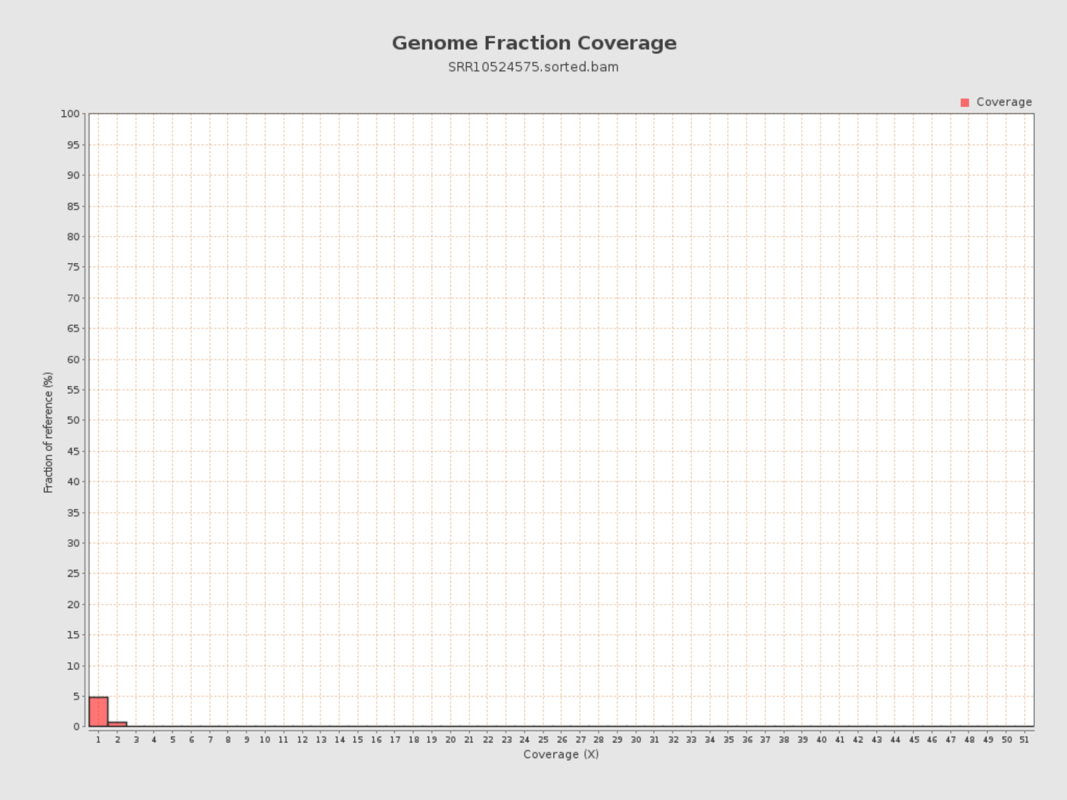
# 4. Results : Coverage Histogram



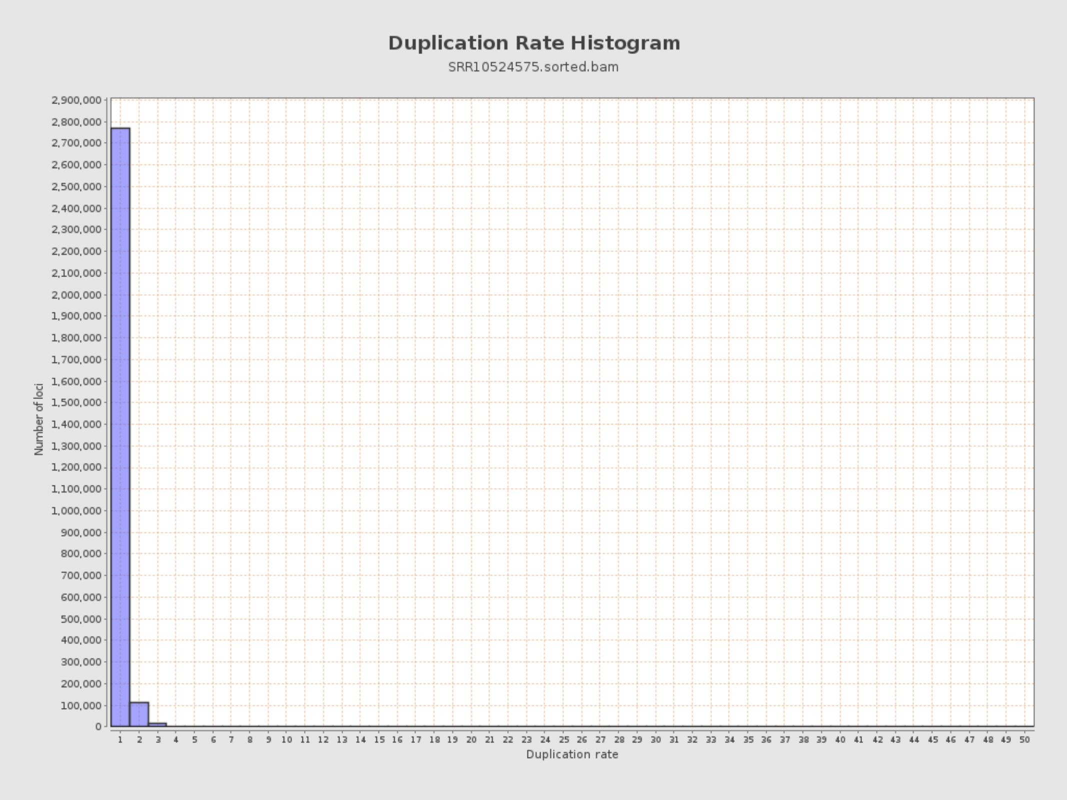
# 5. Results : Coverage Histogram (0-50X)



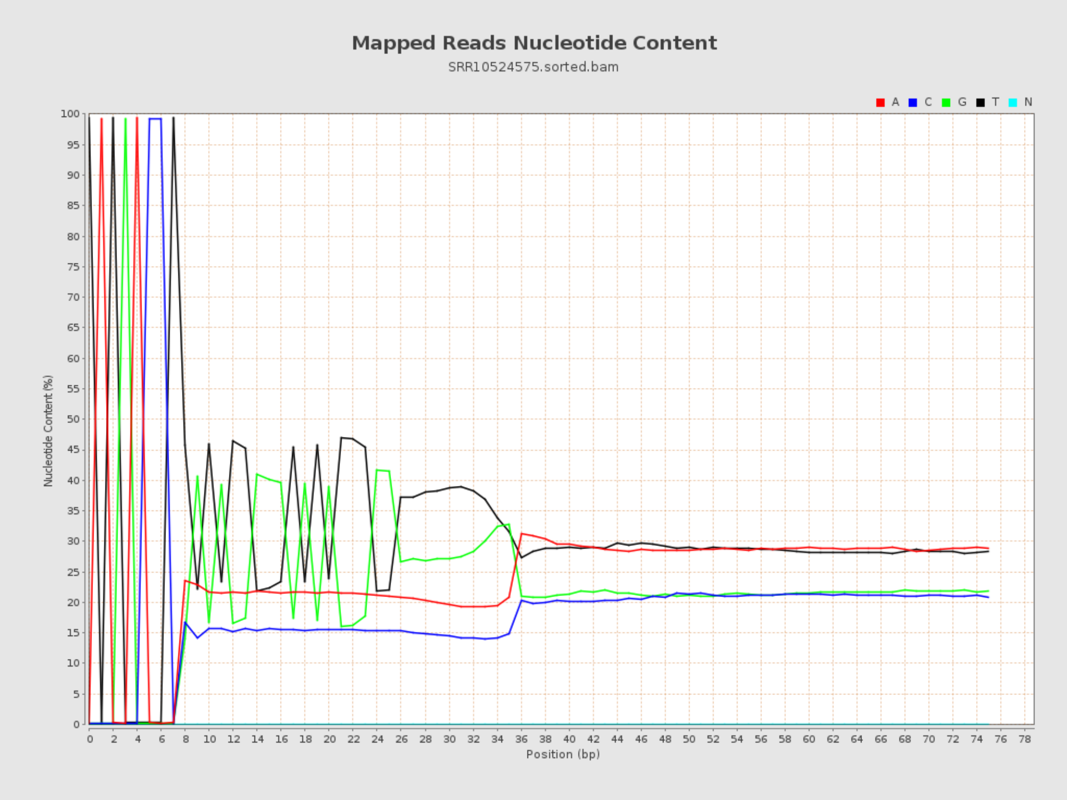
# 6. Results : Genome Fraction Coverage



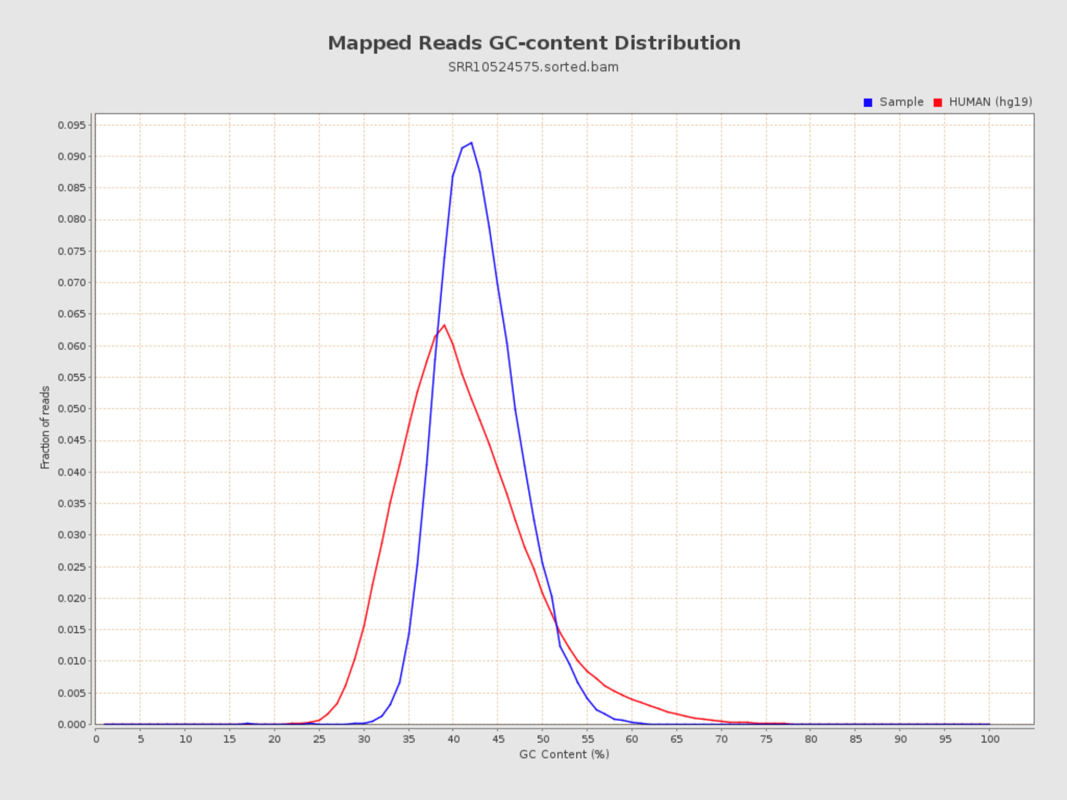
# 7. Results : Duplication Rate Histogram



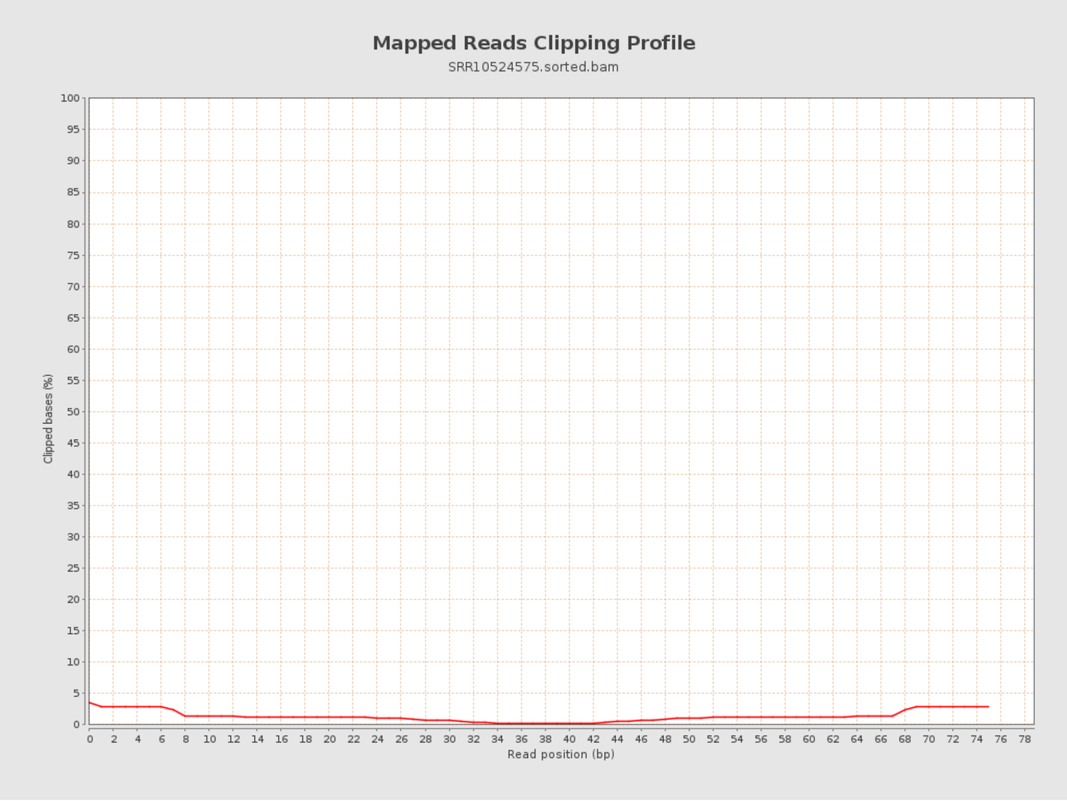
# 8. Results : Mapped Reads Nucleotide Content



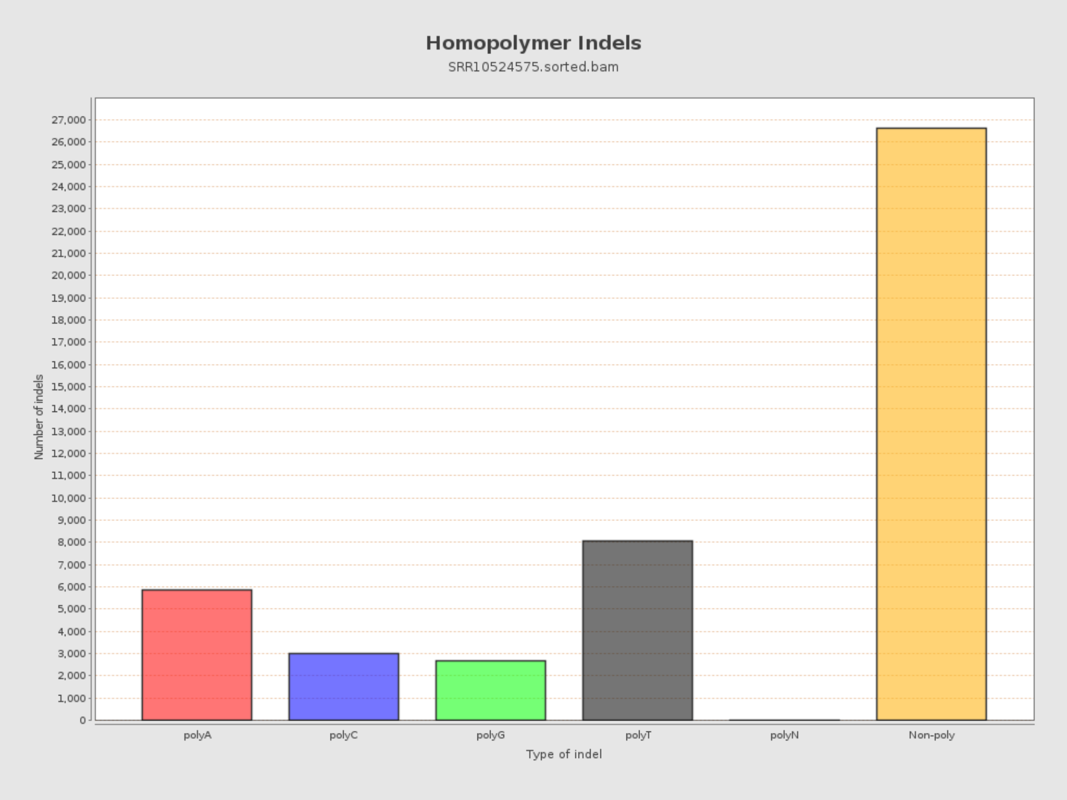
# 9. Results : Mapped Reads GC-content Distribution



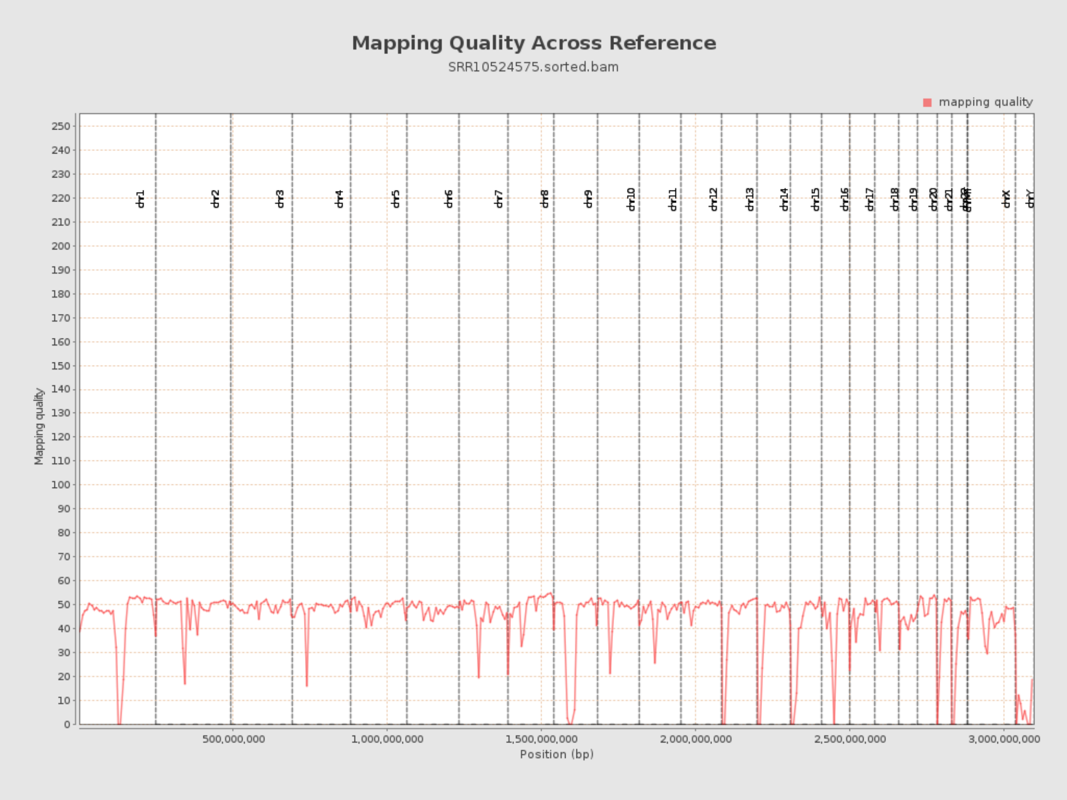
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram