# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/28 12:55:23*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524616.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_SRR10524616 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524616.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Aug 28 12:55:22 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10524616.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,669,888 |
| Mapped reads | 1,561,501 / 93.51% |
| Unmapped reads | 108,387 / 6.49% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 3,405 / 0.2% |
| Read min/max/mean length | 30 / 76 / 76.07 |
| Duplicated reads (estimated) | 68,918 / 4.13% |
| Duplication rate | 3.46% |
| Clipped reads | 1,563,945 / 93.66% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 21,652,503 / 23.79% |
| Number/percentage of C's | 16,903,038 / 18.58% |
| Number/percentage of T's | 29,207,164 / 32.1% |
| Number/percentage of G's | 23,234,459 / 25.53% |
| Number/percentage of N's | 561 / 0% |
| GC Percentage | 44.11% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0294 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2569 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.33 |

## 2.5. Mismatches and indels

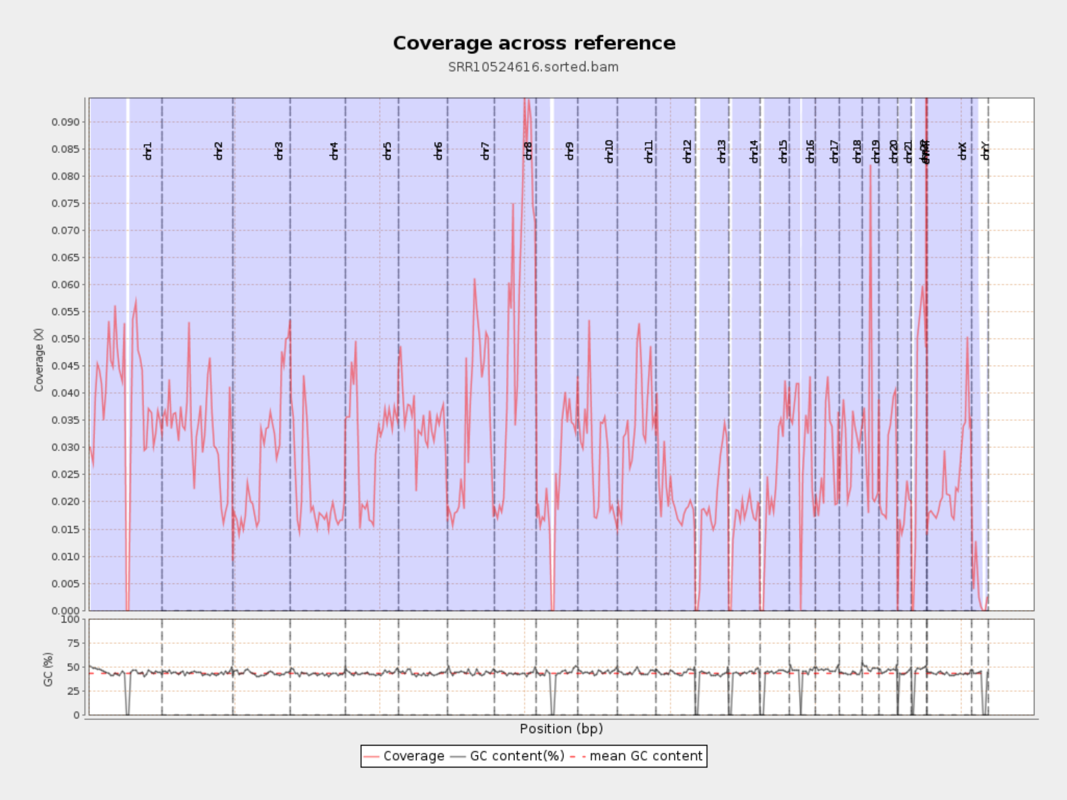
| | |
|---|---|
| General error rate | 0.46% |
| Mismatches | 410,352 |
| Insertions | 4,878 |
| Mapped reads with at least one insertion | 0.31% |
| Deletions | 16,673 |
| Mapped reads with at least one deletion | 1.06% |
| Homopolymer indels | 46.38% |

## 2.6. Chromosome stats

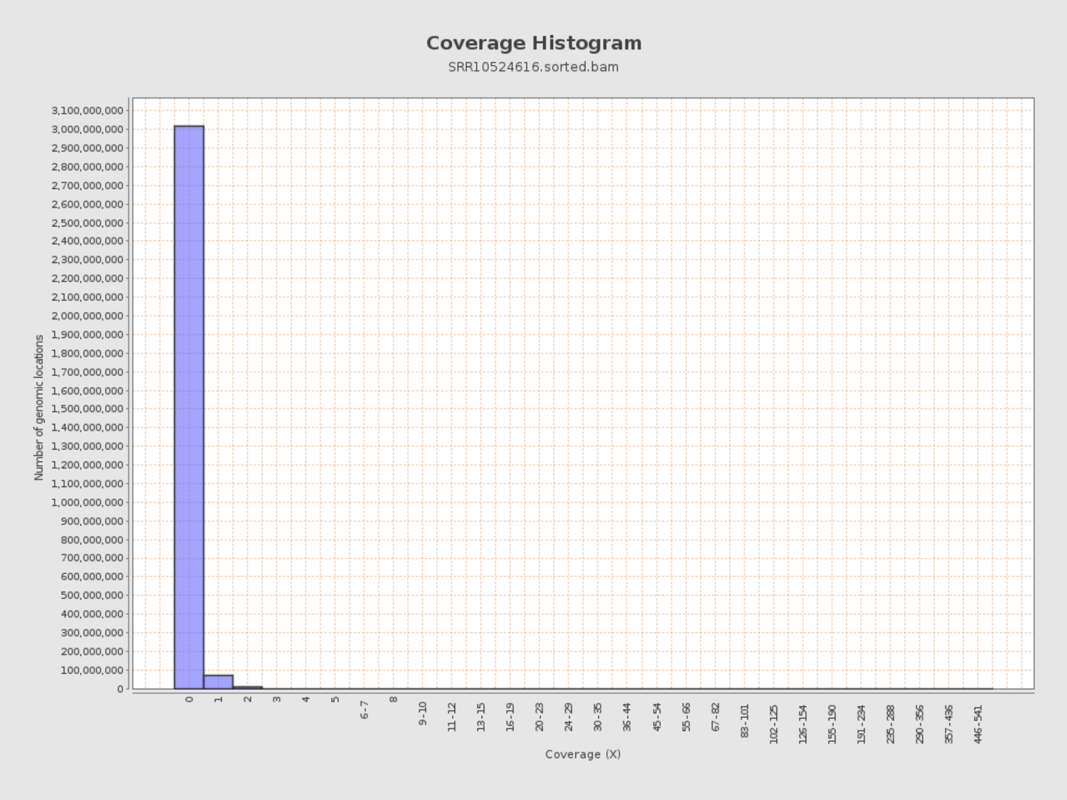
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 9625844 | 0.0386 | 0.4368 |
| chr2 | 243199373 | 8092171 | 0.0333 | 0.3061 |
| chr3 | 198022430 | 5515951 | 0.0279 | 0.1864 |
| chr4 | 191154276 | 4080227 | 0.0213 | 0.1856 |
| chr5 | 180915260 | 5581710 | 0.0309 | 0.1949 |
| chr6 | 171115067 | 5992598 | 0.035 | 0.2214 |
| chr7 | 159138663 | 5489753 | 0.0345 | 0.3313 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 8016713 | 0.0548 | 0.3378 |
| chr9 | 141213431 | 3360948 | 0.0238 | 0.2248 |
| chr10 | 135534747 | 3836942 | 0.0283 | 0.2533 |
| chr11 | 135006516 | 4646894 | 0.0344 | 0.2544 |
| chr12 | 133851895 | 2813976 | 0.021 | 0.1678 |
| chr13 | 115169878 | 2170227 | 0.0188 | 0.153 |
| chr14 | 107349540 | 1696694 | 0.0158 | 0.1455 |
| chr15 | 102531392 | 2399576 | 0.0234 | 0.1761 |
| chr16 | 90354753 | 2751113 | 0.0304 | 0.2024 |
| chr17 | 81195210 | 2251000 | 0.0277 | 0.1918 |
| chr18 | 78077248 | 2392041 | 0.0306 | 0.3448 |
| chr19 | 59128983 | 1930978 | 0.0327 | 0.3179 |
| chr20 | 63025520 | 1736060 | 0.0275 | 0.1886 |
| chr21 | 48129895 | 806044 | 0.0167 | 0.1575 |
| chr22 | 51304566 | 1889020 | 0.0368 | 0.2144 |
| chrMT | 16571 | 3862 | 0.2331 | 0.5295 |
| chrX | 155270560 | 3734973 | 0.0241 | 0.1946 |
| chrY | 59373566 | 211042 | 0.0036 | 0.1071 |

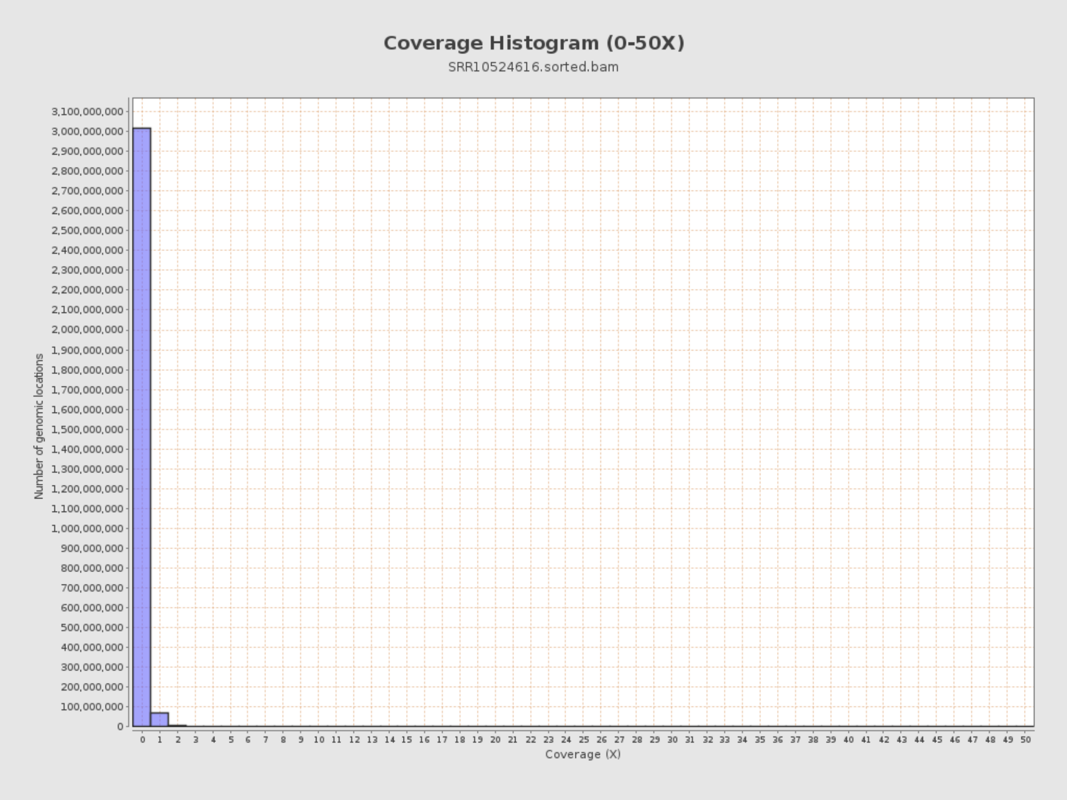
# 3. Results : Coverage across reference



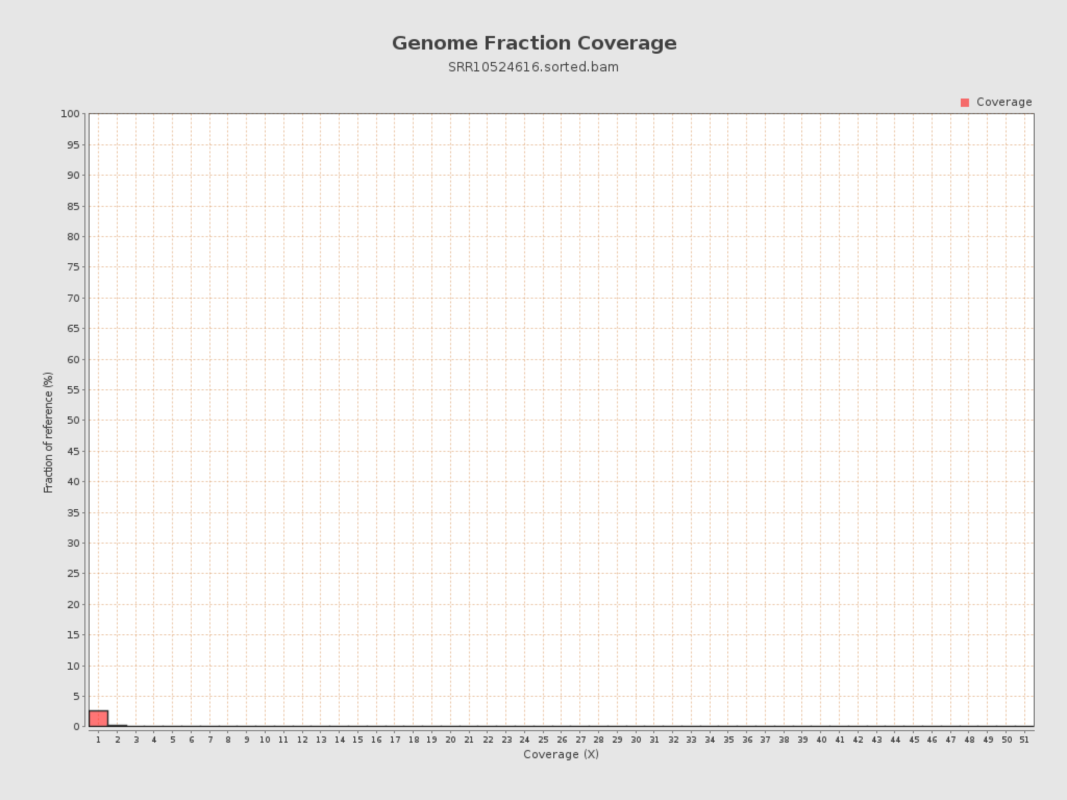
# 4. Results : Coverage Histogram



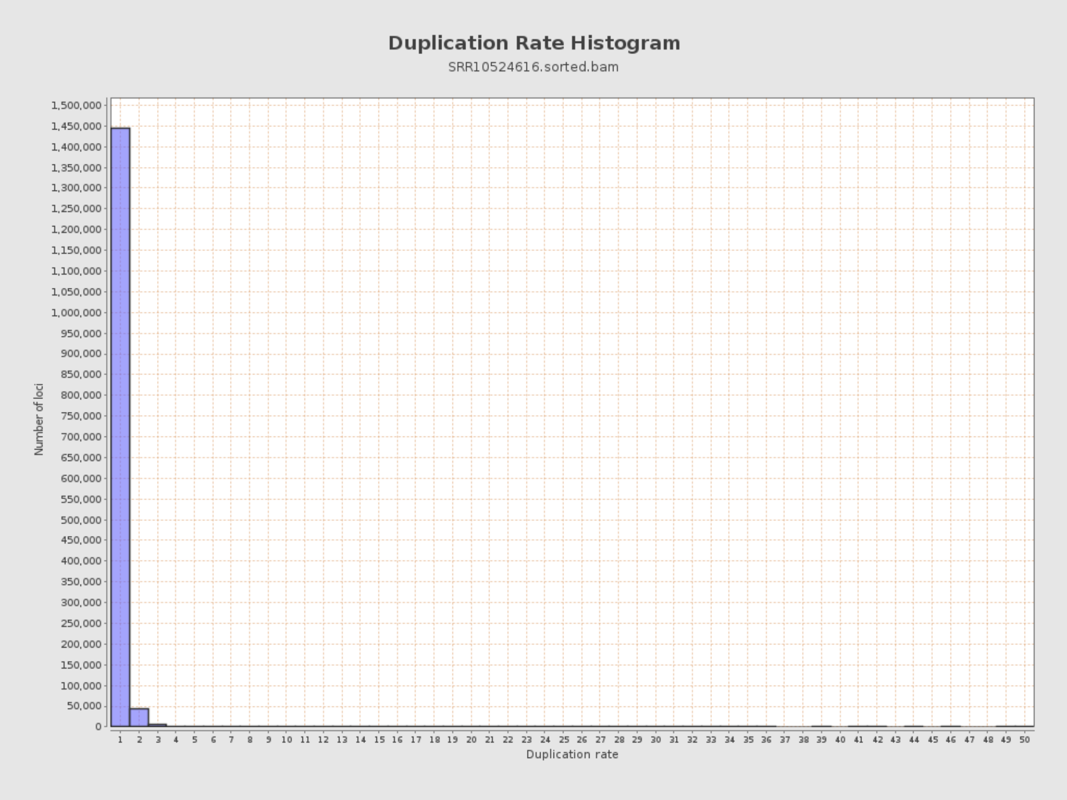
# 5. Results : Coverage Histogram (0-50X)



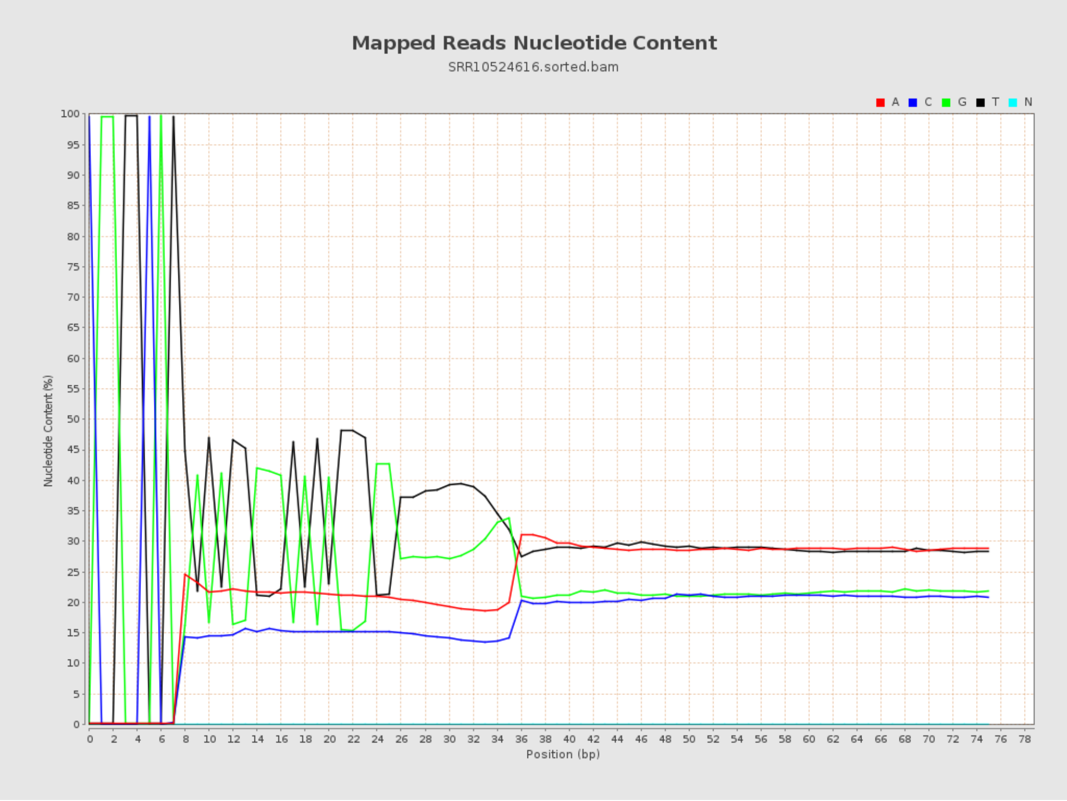
# 6. Results : Genome Fraction Coverage



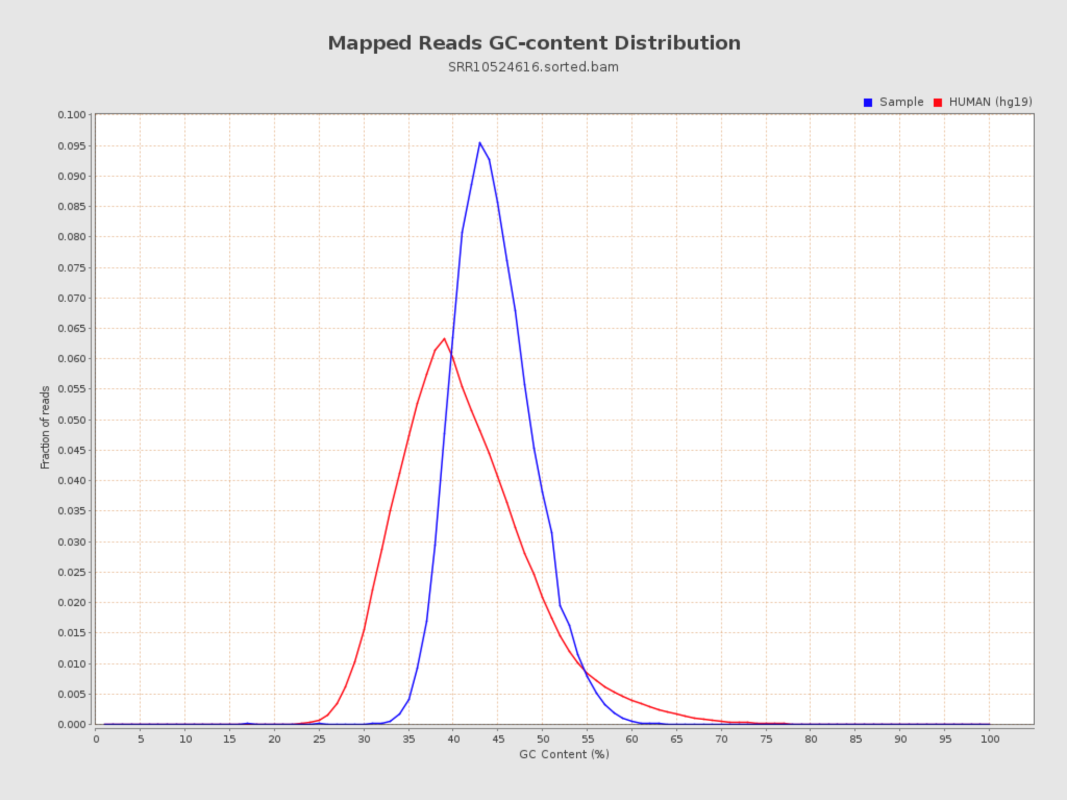
# 7. Results : Duplication Rate Histogram



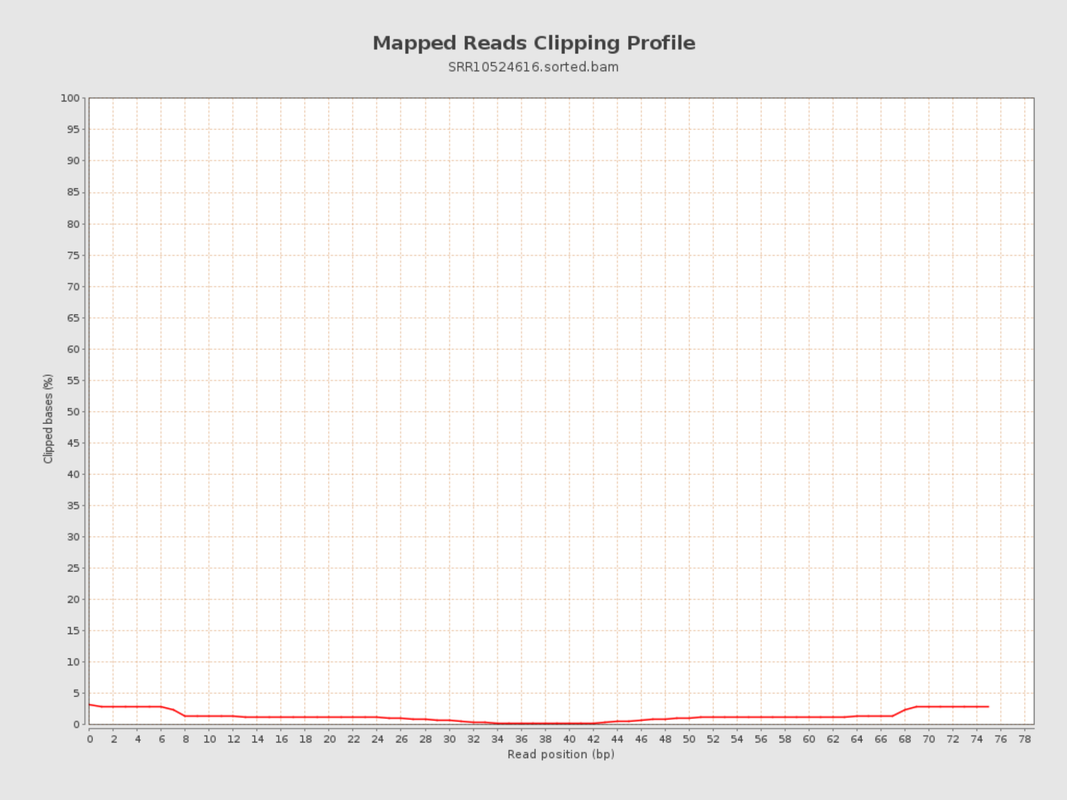
# 8. Results : Mapped Reads Nucleotide Content



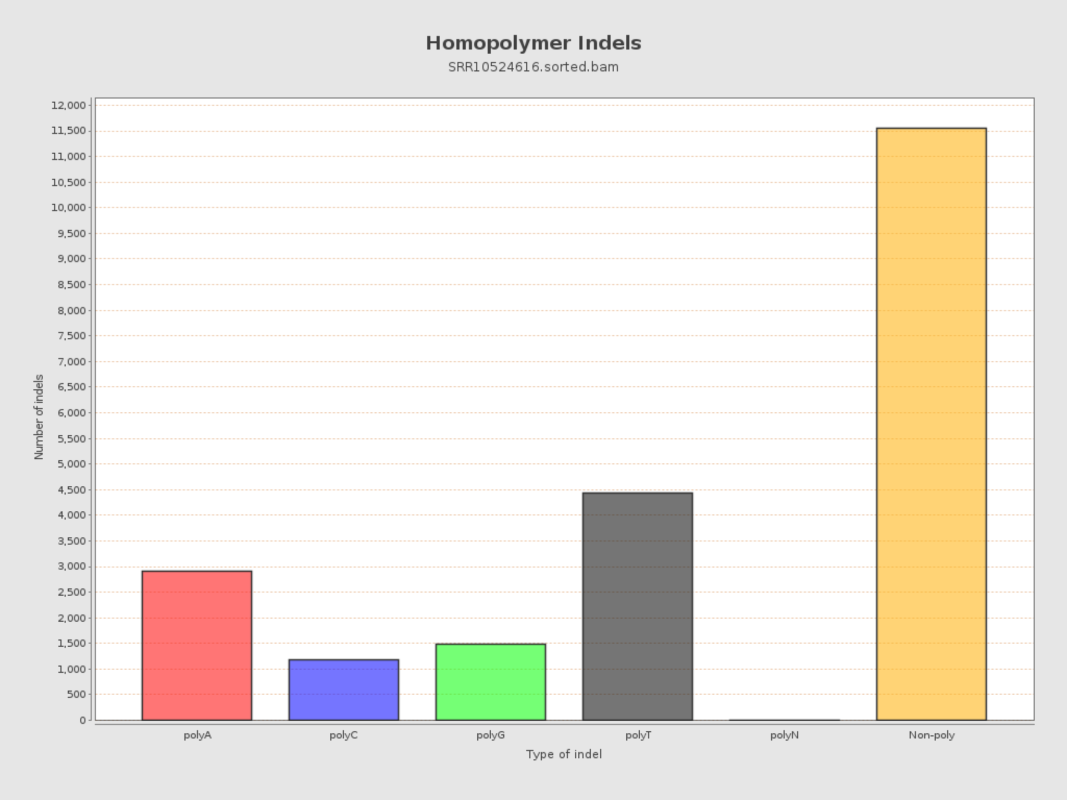
# 9. Results : Mapped Reads GC-content Distribution



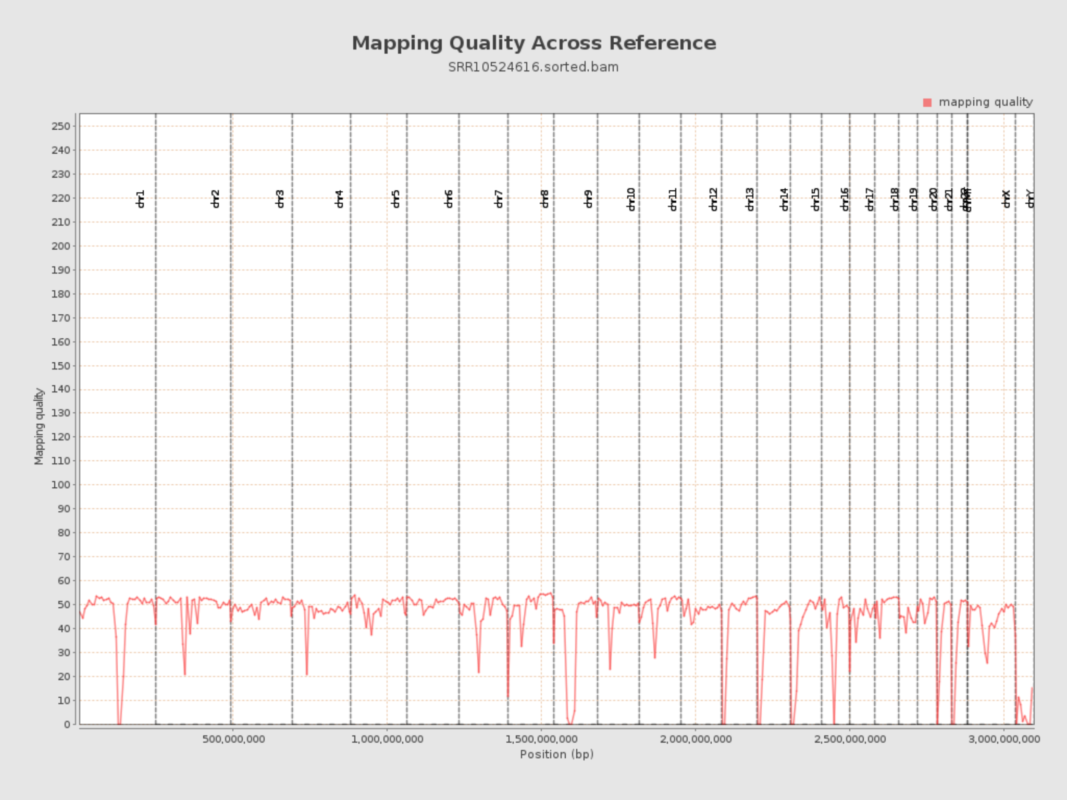
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram