

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/13 20:17:17*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004005.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_SRR6004005 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004005.fastq.gz |
| Draw chromosome limits:               | yes                                                                                                                                                                                          |
| Analyze overlapping paired-end reads: | no                                                                                                                                                                                           |
| Program:                              | bwa (0.7.17-r1188)                                                                                                                                                                           |
| Analysis date:                        | Fri Sep 13 20:17:17 CST 2024                                                                                                                                                                 |
| Size of a homopolymer:                | 3                                                                                                                                                                                            |
| Skip duplicate alignments:            | no                                                                                                                                                                                           |
| Number of windows:                    | 400                                                                                                                                                                                          |
| BAM file:                             | SRR6004005.sorted.bam                                                                                                                                                                        |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 3,095,693,983      |
| Number of reads              | 2,573,620          |
| Mapped reads                 | 2,334,703 / 90.72% |
| Unmapped reads               | 238,917 / 9.28%    |
| Mapped paired reads          | 0 / 0%             |
| Secondary alignments         | 0                  |
| Supplementary alignments     | 18,649 / 0.72%     |
| Read min/max/mean length     | 30 / 76 / 76.25    |
| Duplicated reads (estimated) | 80,390 / 3.12%     |
| Duplication rate             | 2.49%              |
| Clipped reads                | 1,171,757 / 45.53% |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 40,824,000 / 26.7%  |
| Number/percentage of C's | 29,320,261 / 19.18% |
| Number/percentage of T's | 46,467,785 / 30.39% |
| Number/percentage of G's | 36,251,749 / 23.71% |
| Number/percentage of N's | 20,597 / 0.01%      |
| GC Percentage            | 42.89%              |

### 2.3. Coverage

|      |        |
|------|--------|
| Mean | 0.0494 |
|      |        |

|                    |        |
|--------------------|--------|
| Standard Deviation | 0.4226 |
|--------------------|--------|

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 43.27 |
|----------------------|-------|

## 2.5. Mismatches and indels

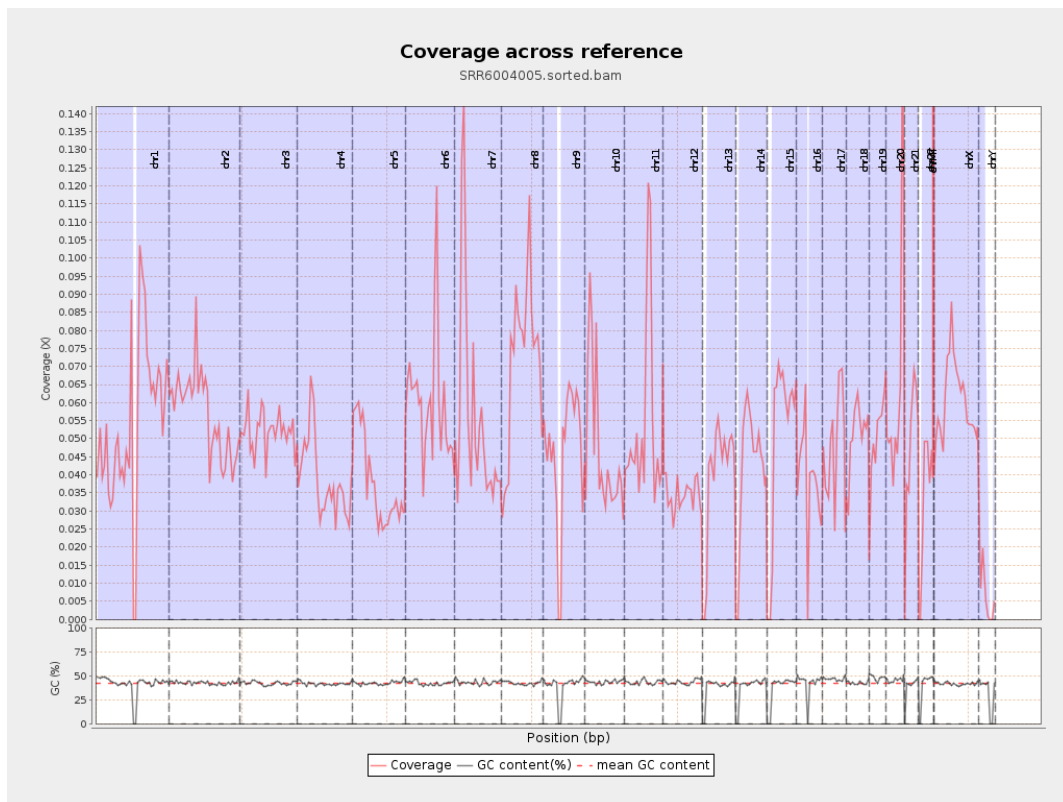
|                                          |           |
|------------------------------------------|-----------|
| General error rate                       | 0.84%     |
| Mismatches                               | 1,261,316 |
| Insertions                               | 12,115    |
| Mapped reads with at least one insertion | 0.51%     |
| Deletions                                | 41,592    |
| Mapped reads with at least one deletion  | 1.76%     |
| Homopolymer indels                       | 45.98%    |

## 2.6. Chromosome stats

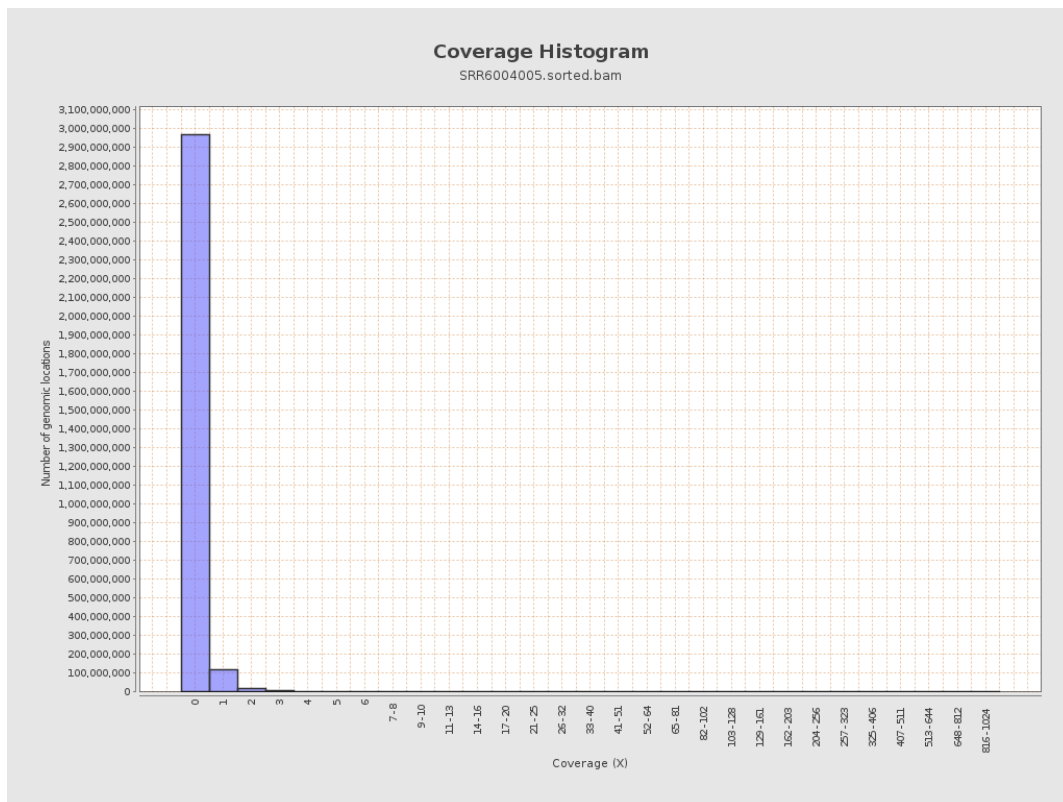
| Name | Length    | Mapped bases | Mean coverage | Standard deviation |
|------|-----------|--------------|---------------|--------------------|
| chr1 | 249250621 | 13428737     | 0.0539        | 0.8041             |
| chr2 | 243199373 | 13819915     | 0.0568        | 0.5489             |
| chr3 | 198022430 | 10311952     | 0.0521        | 0.2589             |
| chr4 | 191154276 | 7346373      | 0.0384        | 0.2419             |
| chr5 | 180915260 | 6831557      | 0.0378        | 0.219              |
| chr6 | 171115067 | 10333538     | 0.0604        | 0.3187             |
| chr7 | 159138663 | 8977893      | 0.0564        | 0.572              |
|      |           |              |               |                    |

|       |           |          |        |        |
|-------|-----------|----------|--------|--------|
| chr8  | 146364022 | 10394641 | 0.071  | 0.4111 |
| chr9  | 141213431 | 6479494  | 0.0459 | 0.3959 |
| chr10 | 135534747 | 6394982  | 0.0472 | 0.4011 |
| chr11 | 135006516 | 7316037  | 0.0542 | 0.3393 |
| chr12 | 133851895 | 4619163  | 0.0345 | 0.2178 |
| chr13 | 115169878 | 4544745  | 0.0395 | 0.2224 |
| chr14 | 107349540 | 4541982  | 0.0423 | 0.2707 |
| chr15 | 102531392 | 5211391  | 0.0508 | 0.2639 |
| chr16 | 90354753  | 3454412  | 0.0382 | 0.2733 |
| chr17 | 81195210  | 3882196  | 0.0478 | 0.2619 |
| chr18 | 78077248  | 3967546  | 0.0508 | 0.7478 |
| chr19 | 59128983  | 3020844  | 0.0511 | 0.5903 |
| chr20 | 63025520  | 4264513  | 0.0677 | 0.3071 |
| chr21 | 48129895  | 2292988  | 0.0476 | 0.2715 |
| chr22 | 51304566  | 1645614  | 0.0321 | 0.1993 |
| chrMT | 16571     | 50841    | 3.0681 | 2.5962 |
| chrX  | 155270560 | 9403138  | 0.0606 | 0.3073 |
| chrY  | 59373566  | 418795   | 0.0071 | 0.1402 |

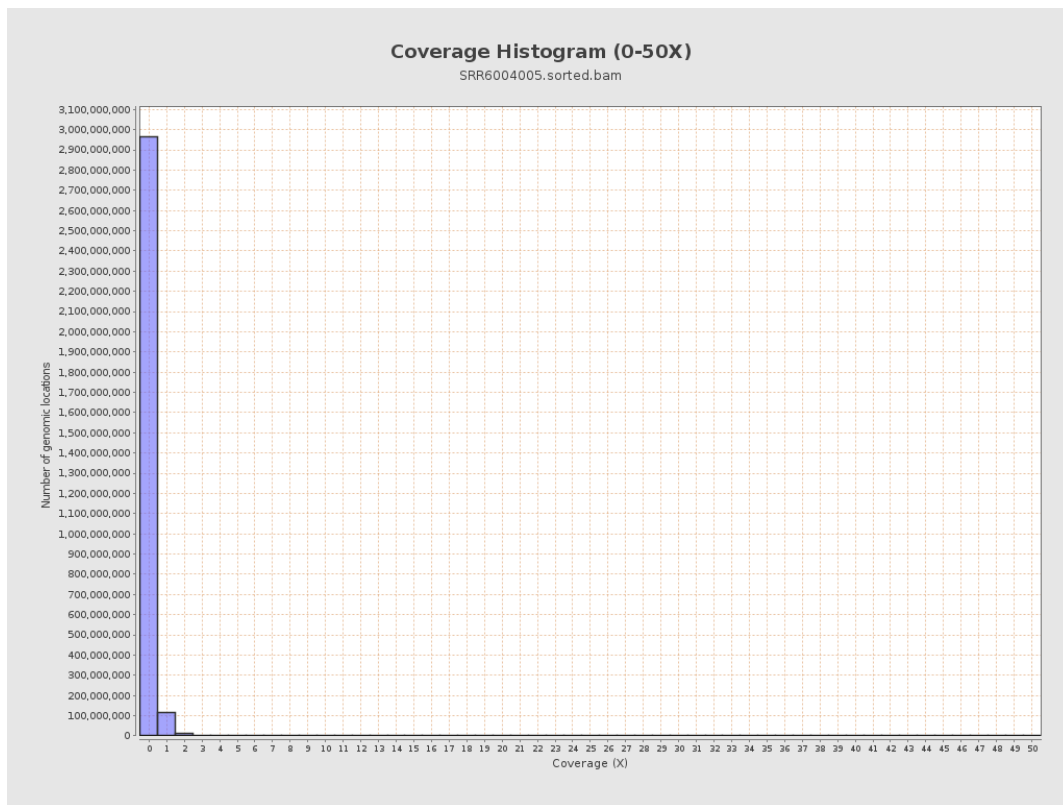
### 3. Results : Coverage across reference



## 4. Results : Coverage Histogram

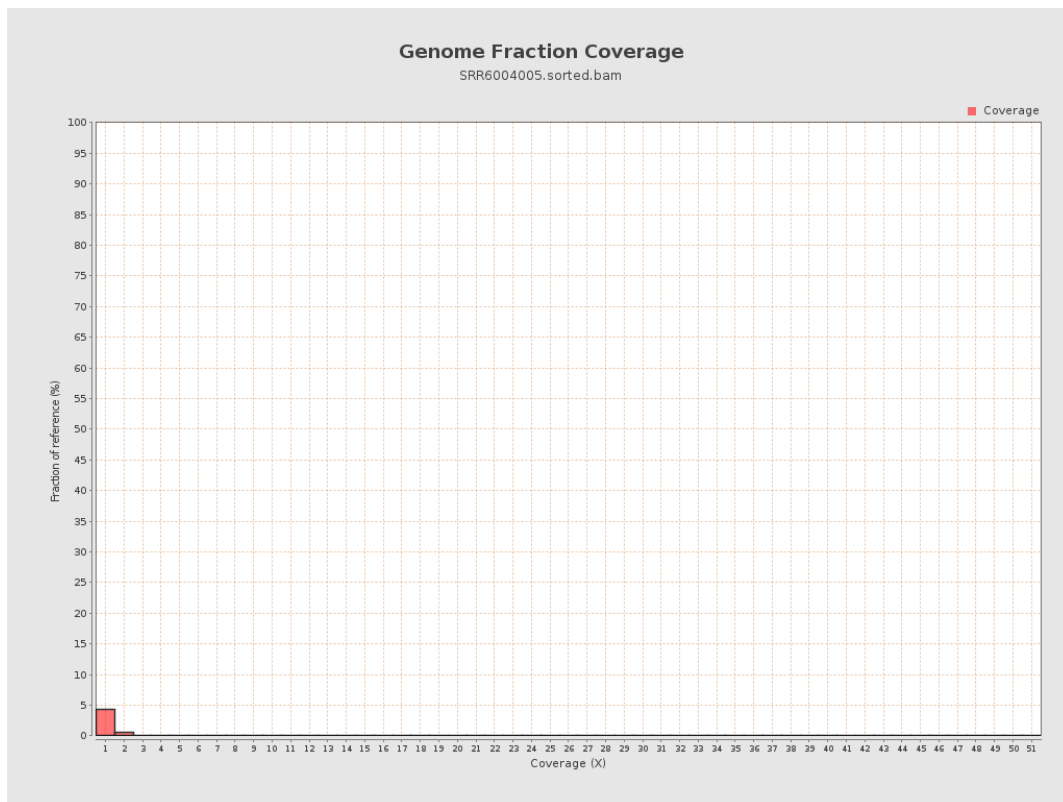


## 5. Results : Coverage Histogram (0-50X)

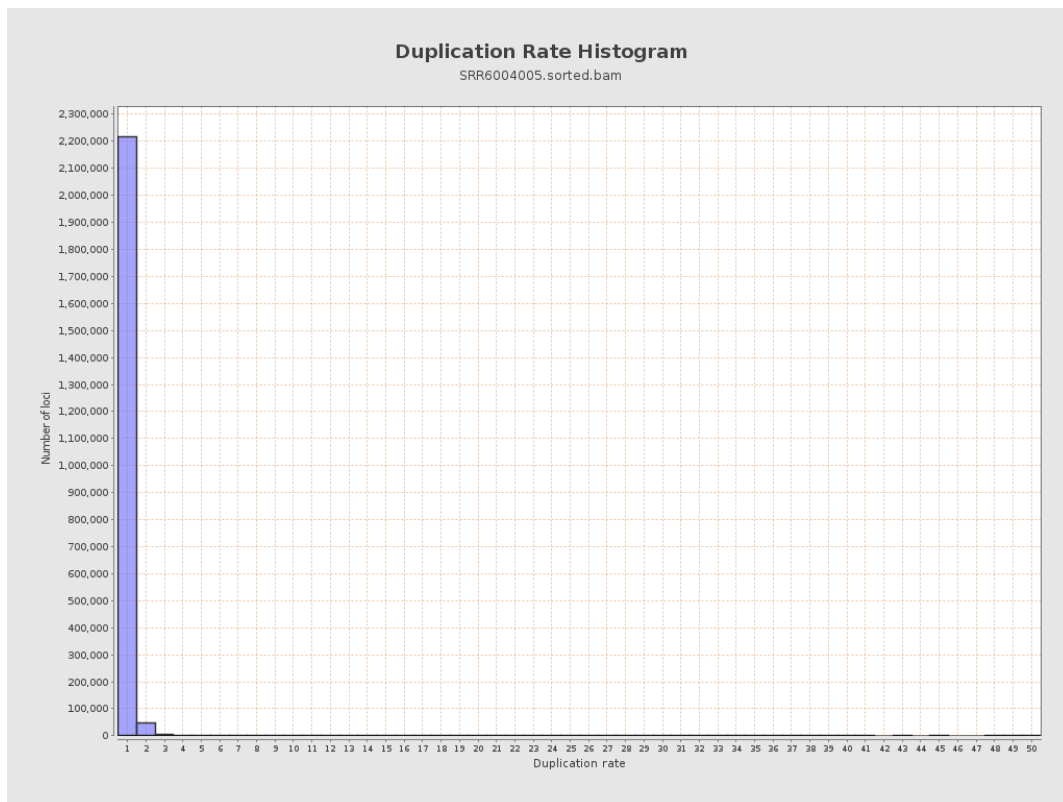




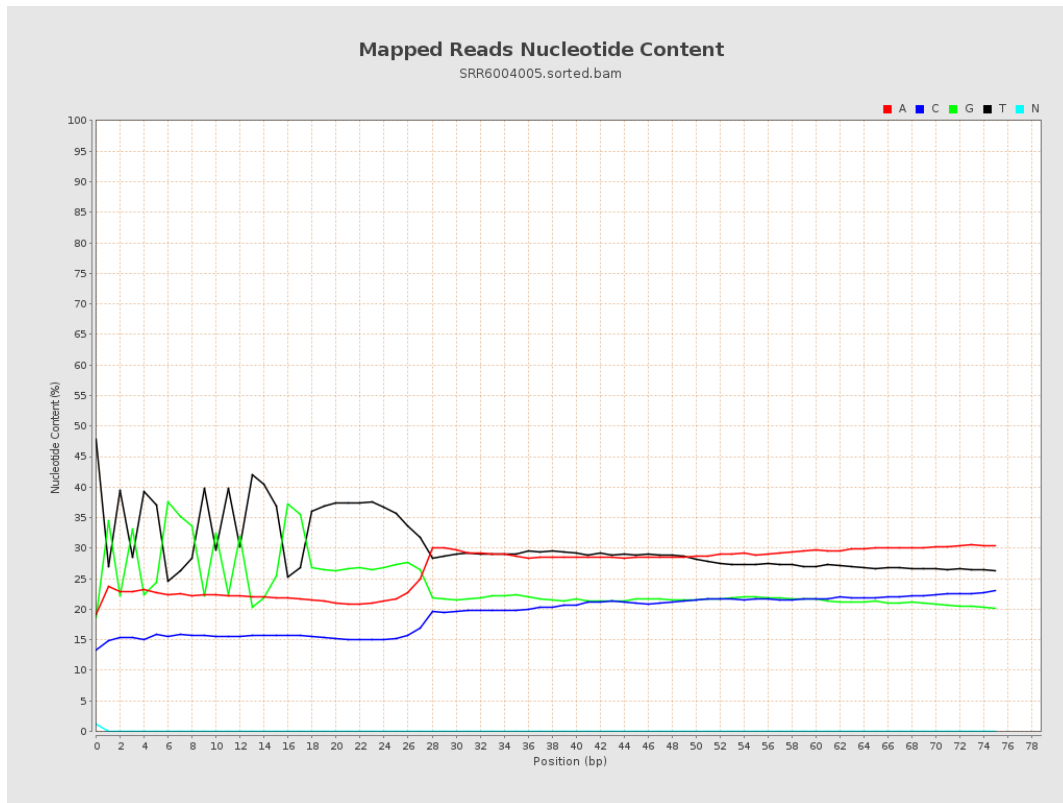
## 6. Results : Genome Fraction Coverage



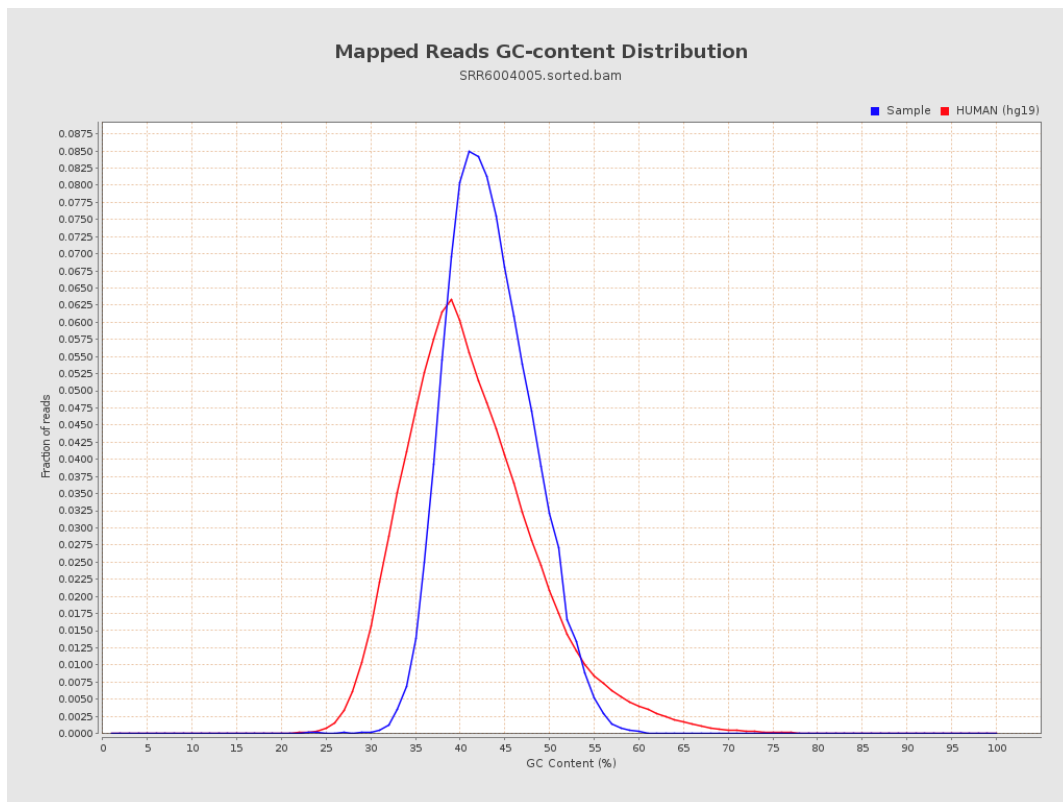
## 7. Results : Duplication Rate Histogram



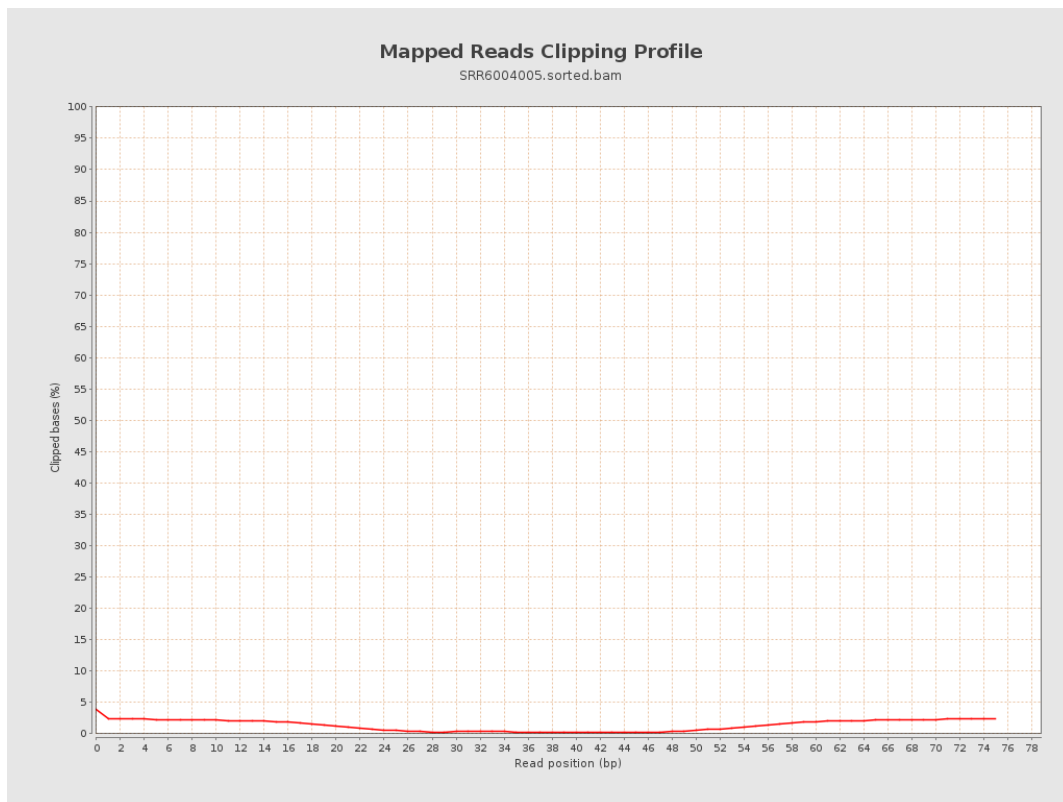
## 8. Results : Mapped Reads Nucleotide Content



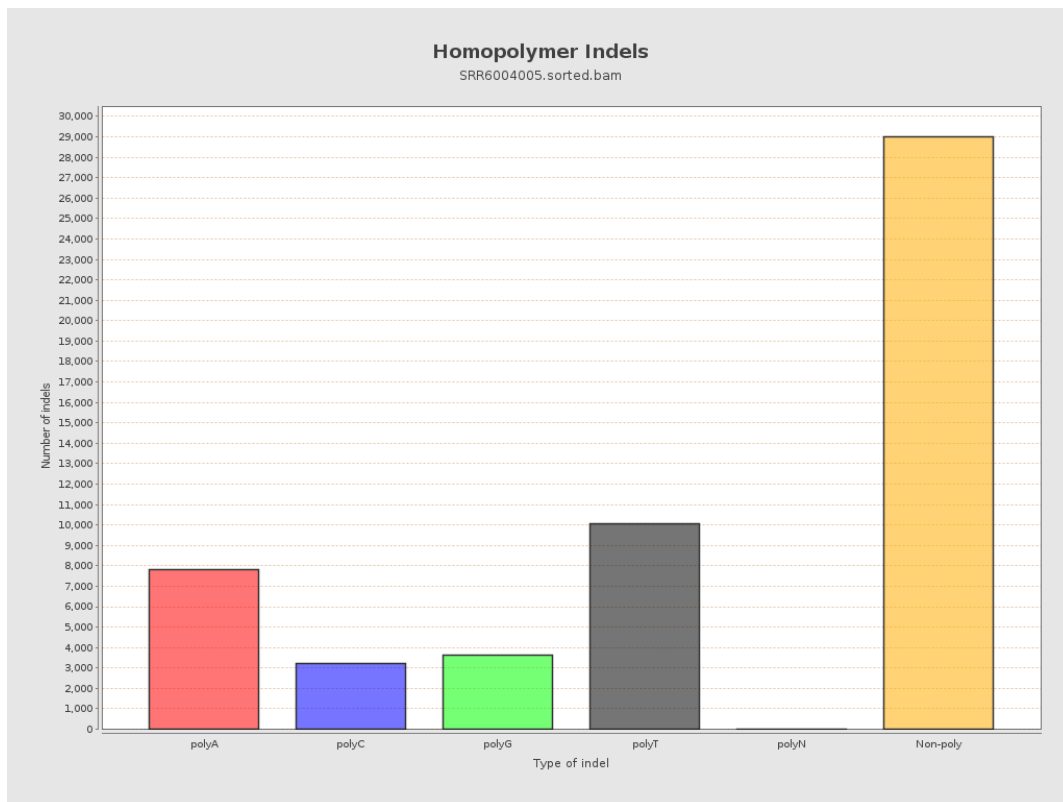
## 9. Results : Mapped Reads GC-content Distribution



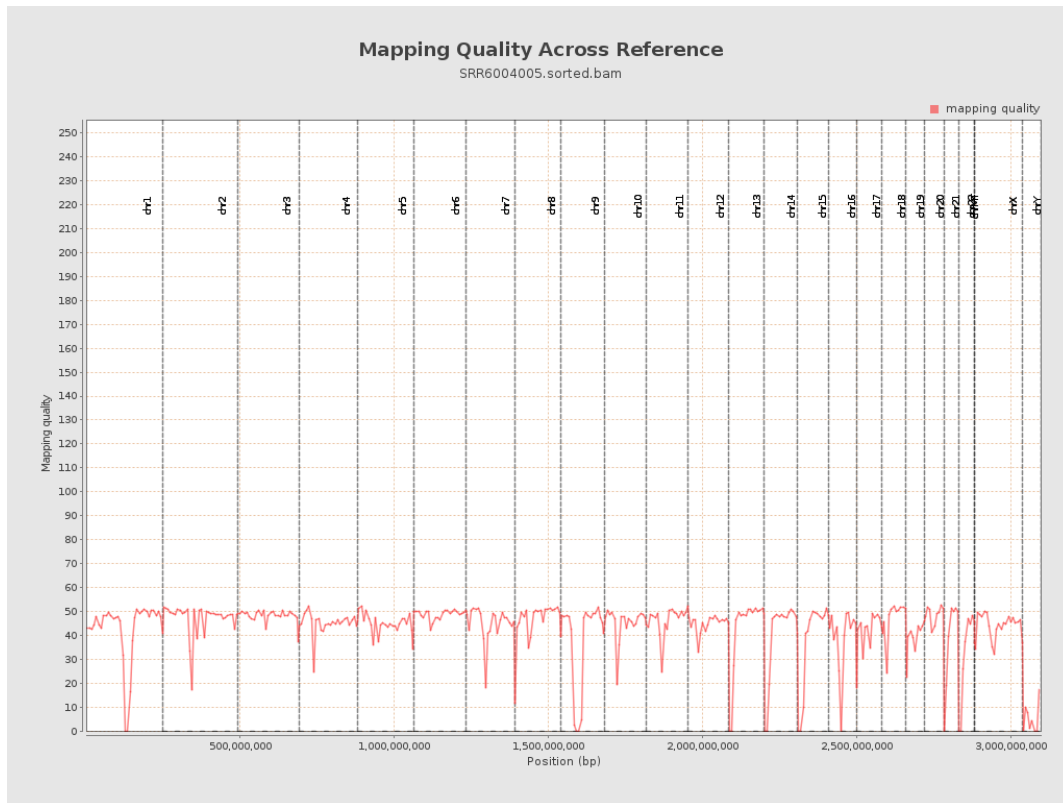
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels



## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram

