# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/14 11:25:57*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008784.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_SRR6008784 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008784.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 14 11:25:57 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6008784.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,357,152 |
| Mapped reads | 1,155,183 / 85.12% |
| Unmapped reads | 201,969 / 14.88% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 9,327 / 0.69% |
| Read min/max/mean length | 30 / 76 / 76.24 |
| Duplicated reads (estimated) | 97,232 / 7.16% |
| Duplication rate | 6.41% |
| Clipped reads | 530,774 / 39.11% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 20,513,628 / 26.86% |
| Number/percentage of C's | 14,706,448 / 19.26% |
| Number/percentage of T's | 23,643,230 / 30.96% |
| Number/percentage of G's | 17,392,309 / 22.78% |
| Number/percentage of N's | 105,122 / 0.14% |
| GC Percentage | 42.04% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0247 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3352 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 42.41 |

## 2.5. Mismatches and indels

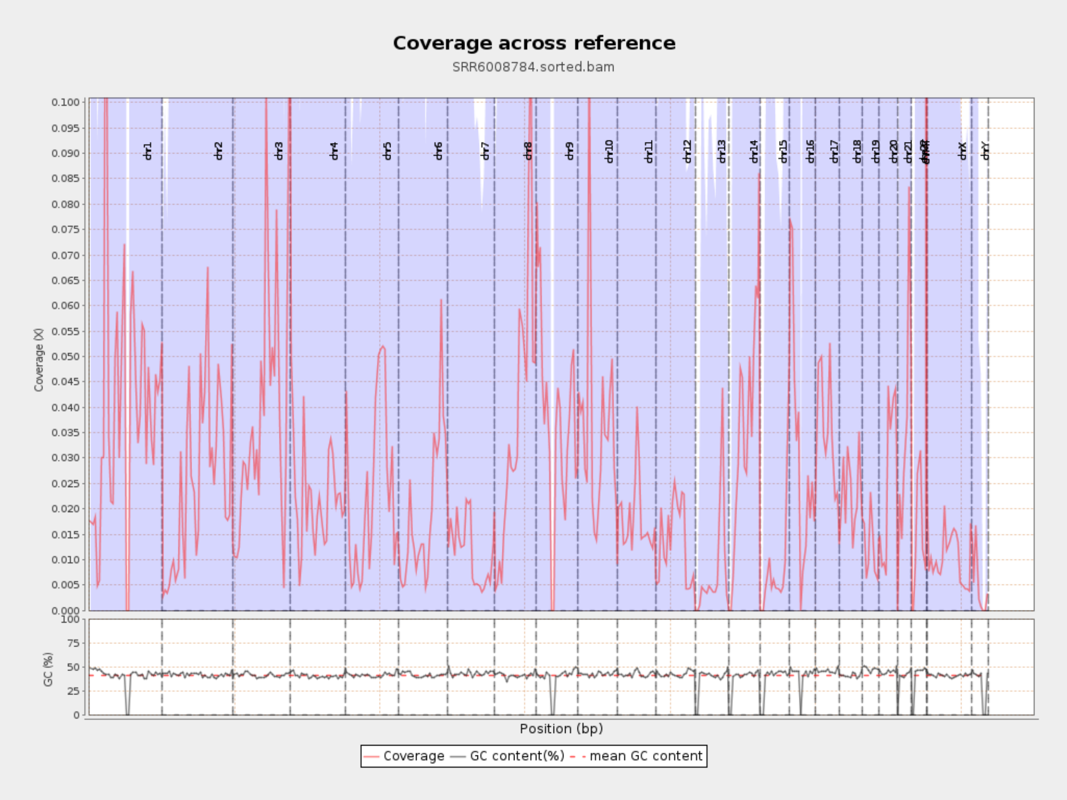
| | |
|---|---|
| General error rate | 0.91% |
| Mismatches | 677,207 |
| Insertions | 6,410 |
| Mapped reads with at least one insertion | 0.55% |
| Deletions | 21,276 |
| Mapped reads with at least one deletion | 1.82% |
| Homopolymer indels | 44.49% |

## 2.6. Chromosome stats

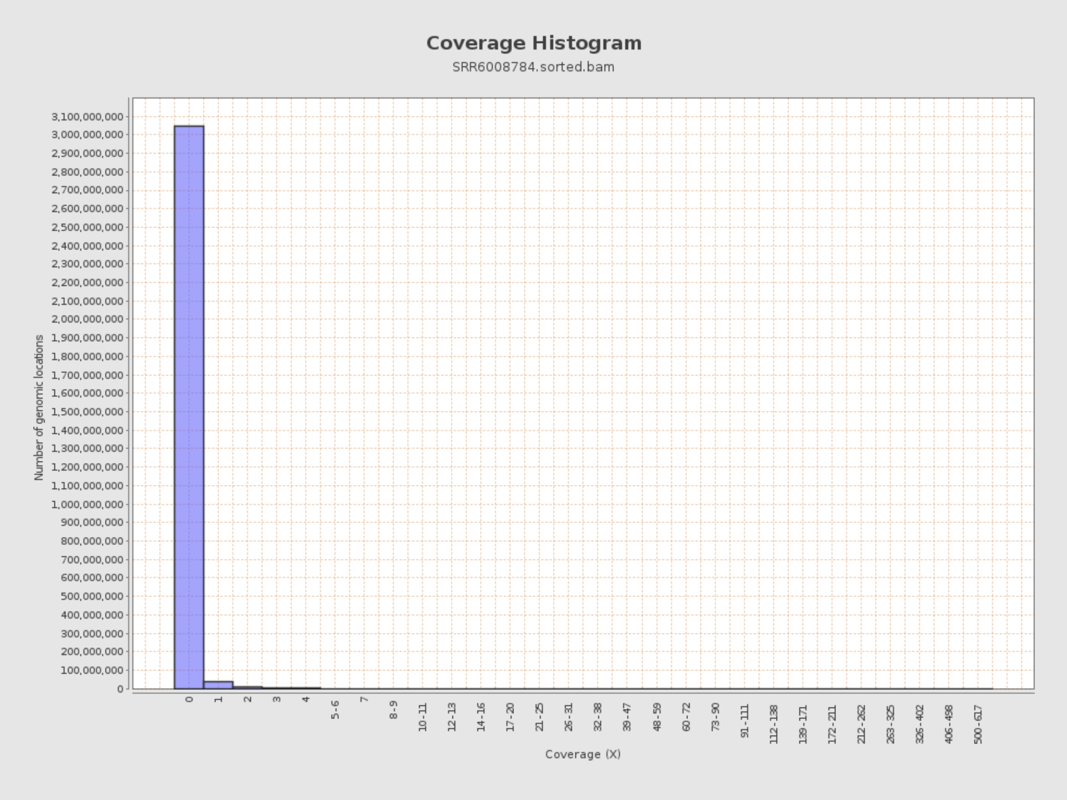
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 9730407 | 0.039 | 0.4859 |
| chr2 | 243199373 | 6100785 | 0.0251 | 0.3822 |
| chr3 | 198022430 | 7527401 | 0.038 | 0.3266 |
| chr4 | 191154276 | 4245524 | 0.0222 | 0.2444 |
| chr5 | 180915260 | 4249714 | 0.0235 | 0.2162 |
| chr6 | 171115067 | 3268441 | 0.0191 | 0.204 |
| chr7 | 159138663 | 1830629 | 0.0115 | 0.2134 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 5550438 | 0.0379 | 0.4243 |
| chr9 | 141213431 | 5187295 | 0.0367 | 0.2992 |
| chr10 | 135534747 | 4875436 | 0.036 | 0.8028 |
| chr11 | 135006516 | 2434505 | 0.018 | 0.2224 |
| chr12 | 133851895 | 1814029 | 0.0136 | 0.1638 |
| chr13 | 115169878 | 931458 | 0.0081 | 0.1256 |
| chr14 | 107349540 | 3691129 | 0.0344 | 0.2705 |
| chr15 | 102531392 | 837440 | 0.0082 | 0.1254 |
| chr16 | 90354753 | 2709666 | 0.03 | 0.3346 |
| chr17 | 81195210 | 2861302 | 0.0352 | 0.3013 |
| chr18 | 78077248 | 1798171 | 0.023 | 0.4128 |
| chr19 | 59128983 | 746512 | 0.0126 | 0.2751 |
| chr20 | 63025520 | 1659805 | 0.0263 | 0.2376 |
| chr21 | 48129895 | 1678912 | 0.0349 | 0.2887 |
| chr22 | 51304566 | 706300 | 0.0138 | 0.1635 |
| chrMT | 16571 | 31557 | 1.9044 | 2.1418 |
| chrX | 155270560 | 1643859 | 0.0106 | 0.1518 |
| chrY | 59373566 | 288828 | 0.0049 | 0.179 |

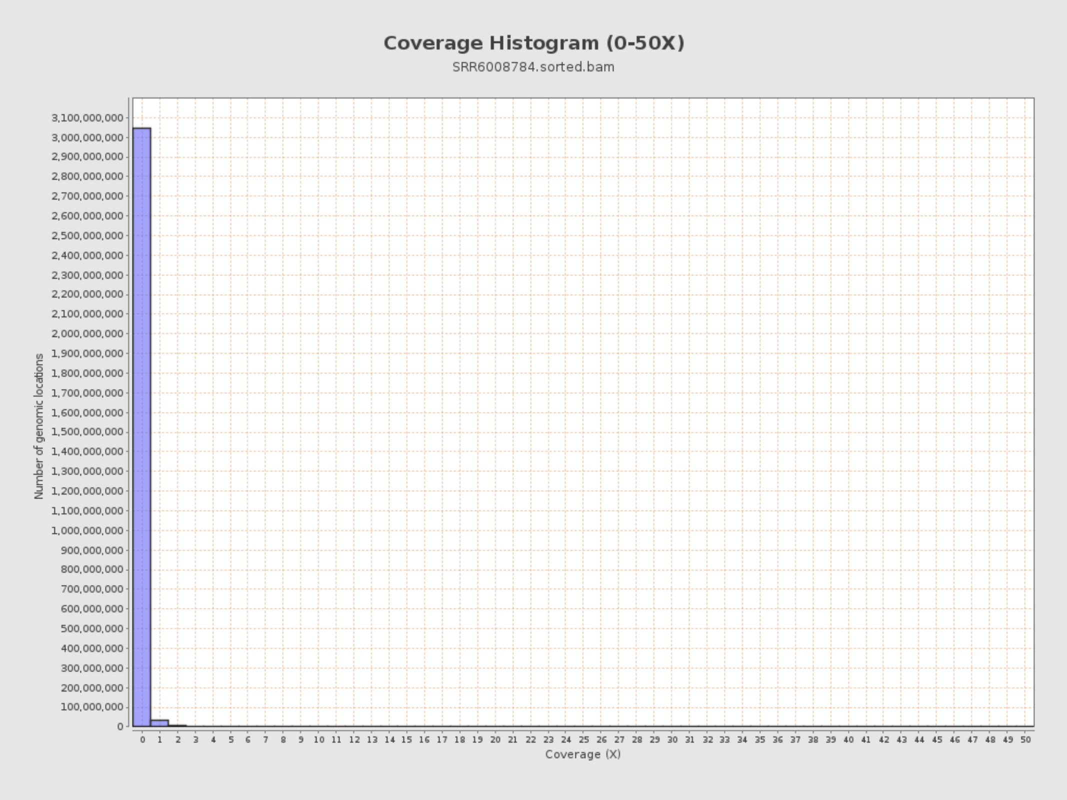
# 3. Results : Coverage across reference



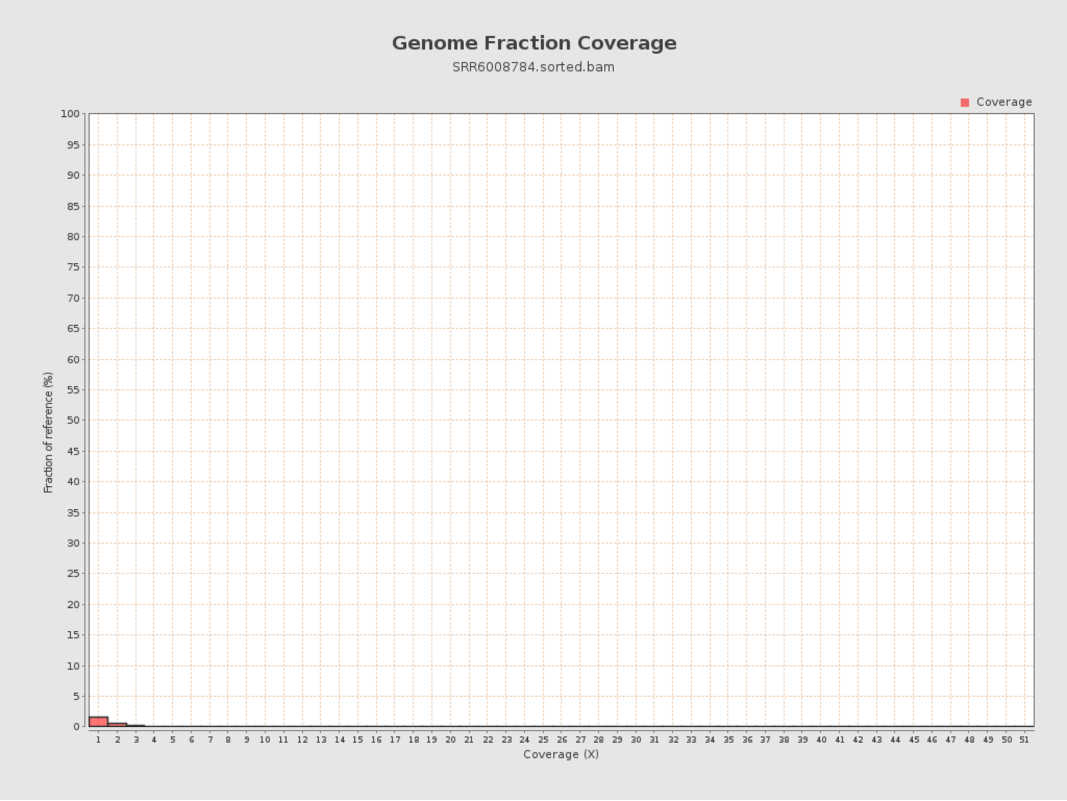
# 4. Results : Coverage Histogram



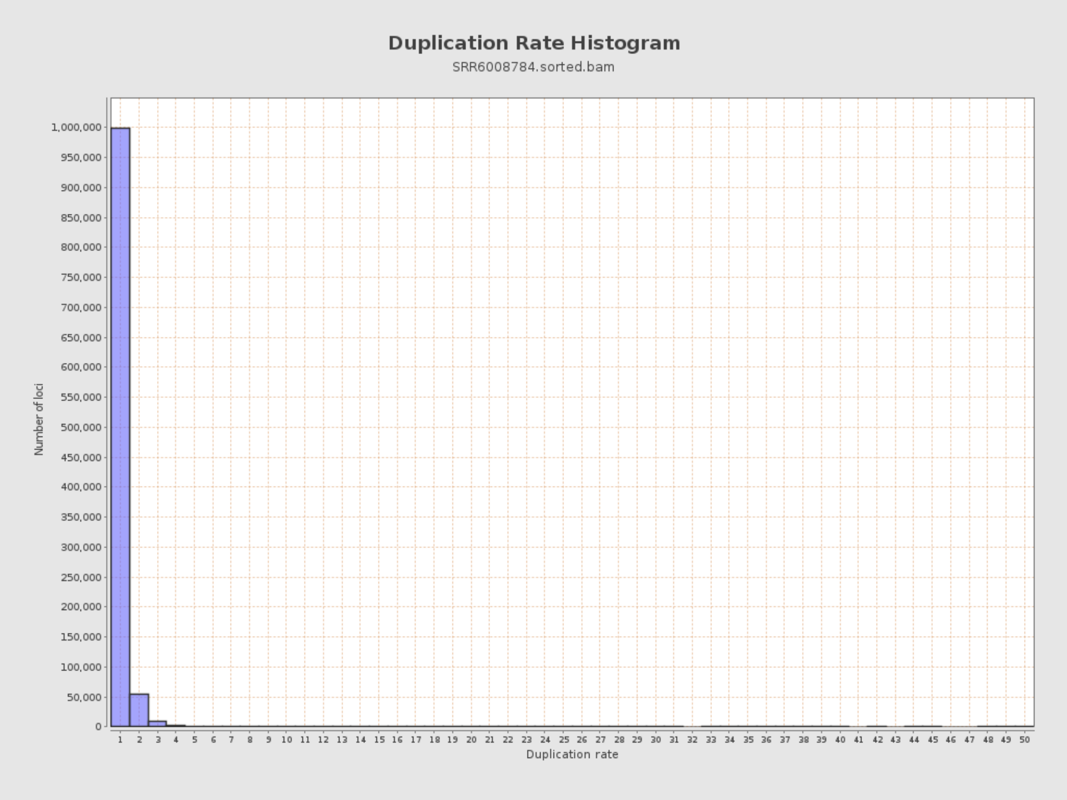
# 5. Results : Coverage Histogram (0-50X)



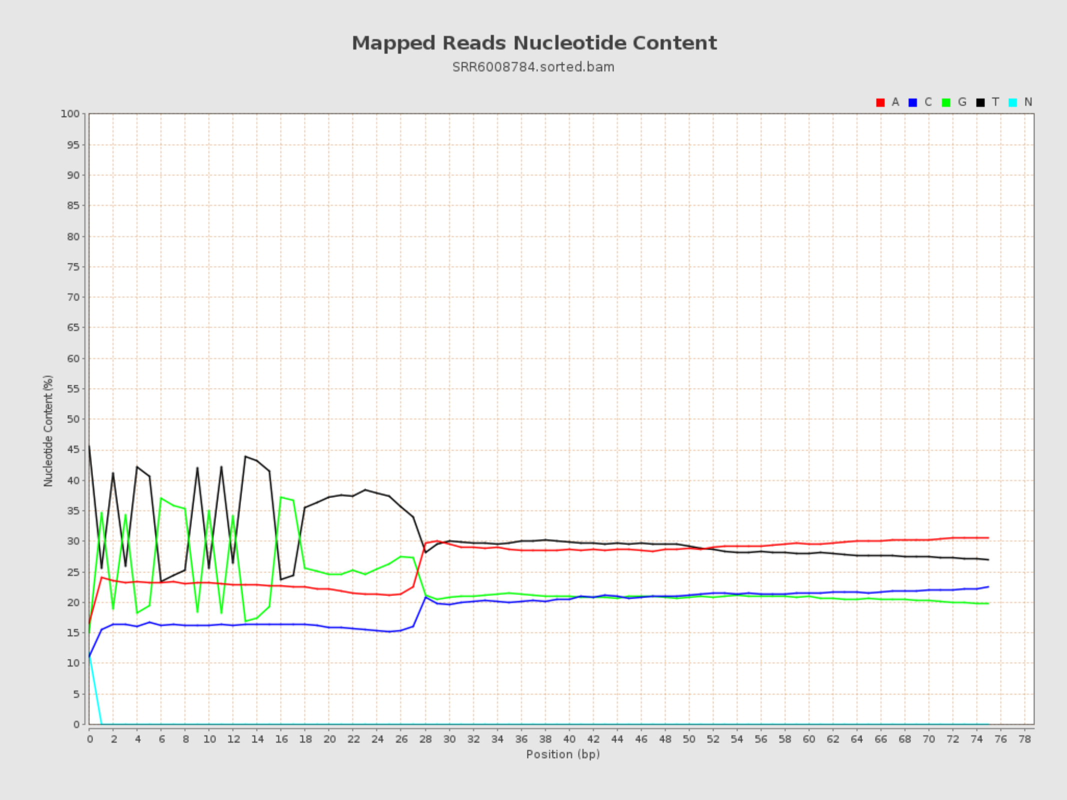
# 6. Results : Genome Fraction Coverage



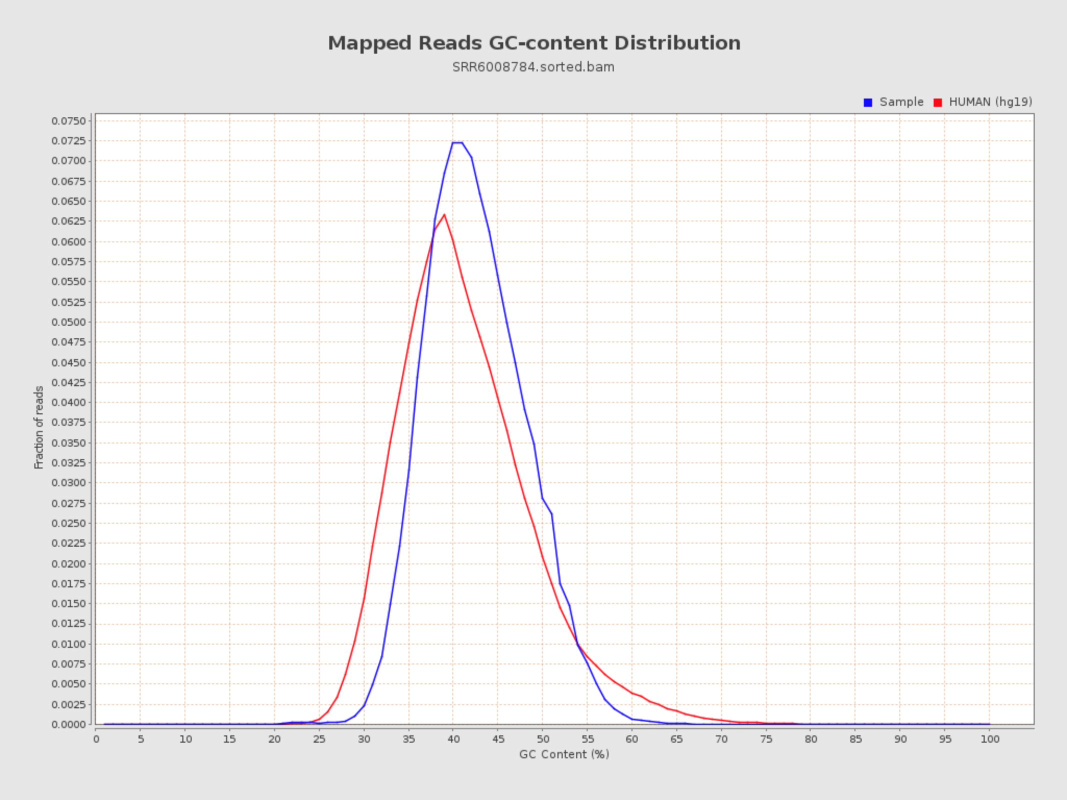
# 7. Results : Duplication Rate Histogram



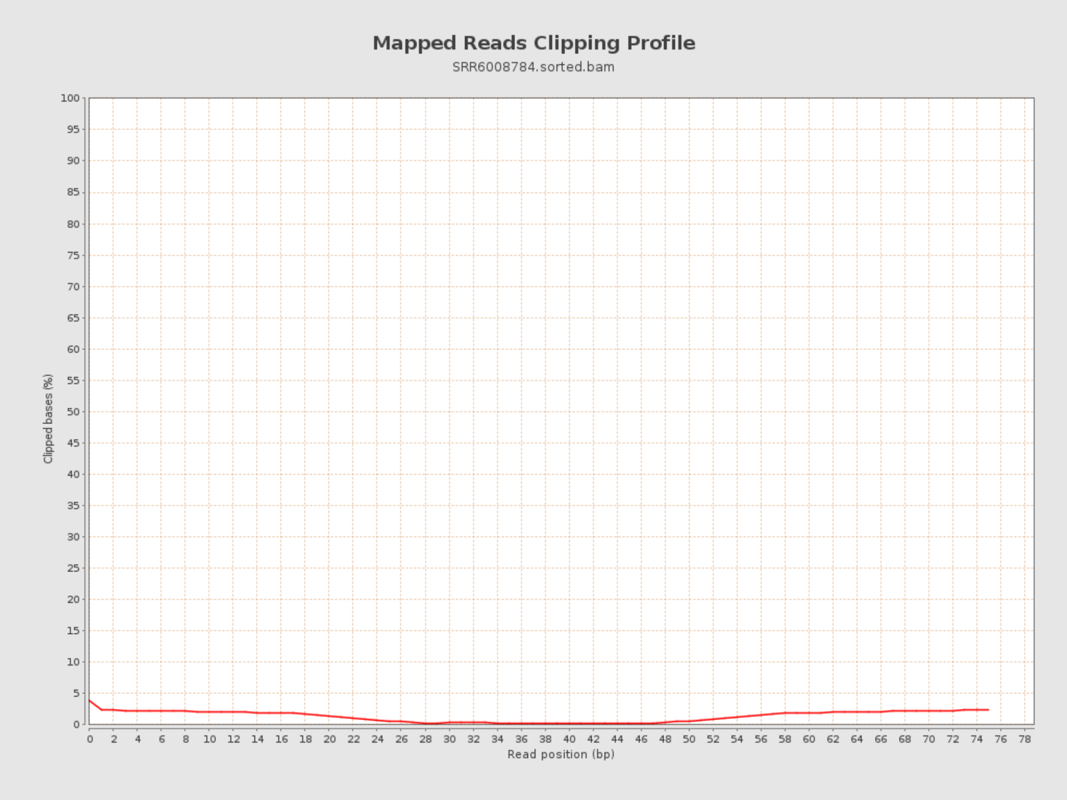
# 8. Results : Mapped Reads Nucleotide Content



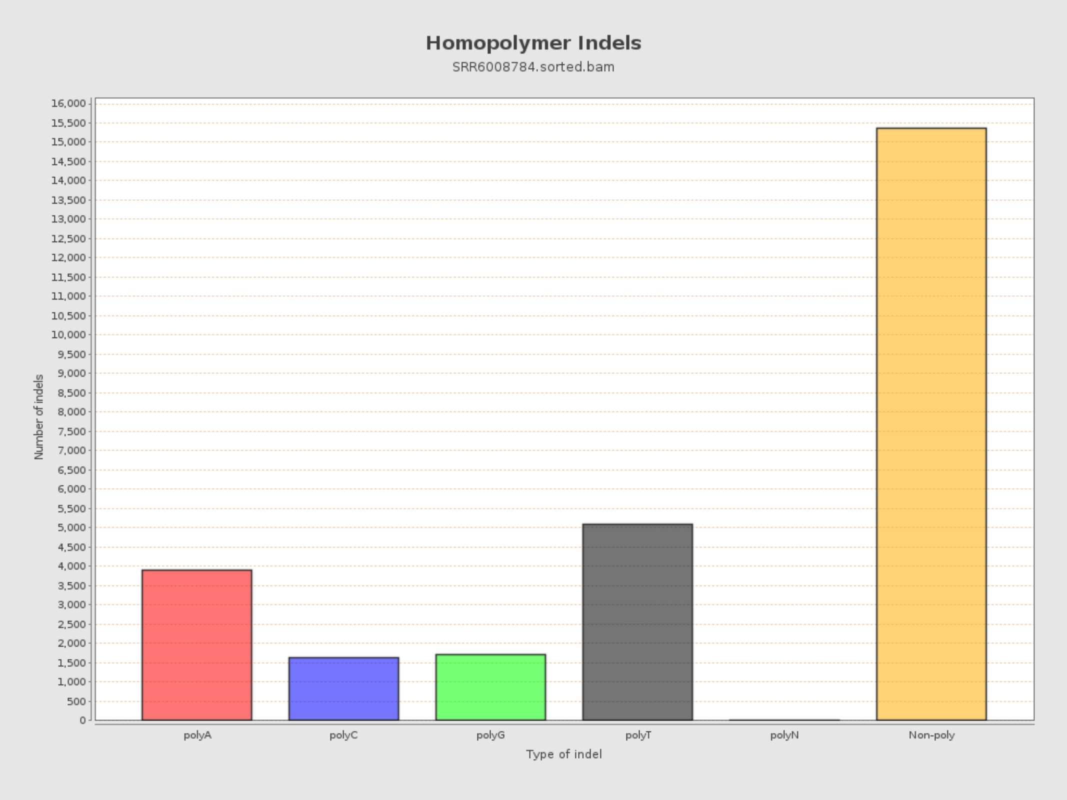
# 9. Results : Mapped Reads GC-content Distribution



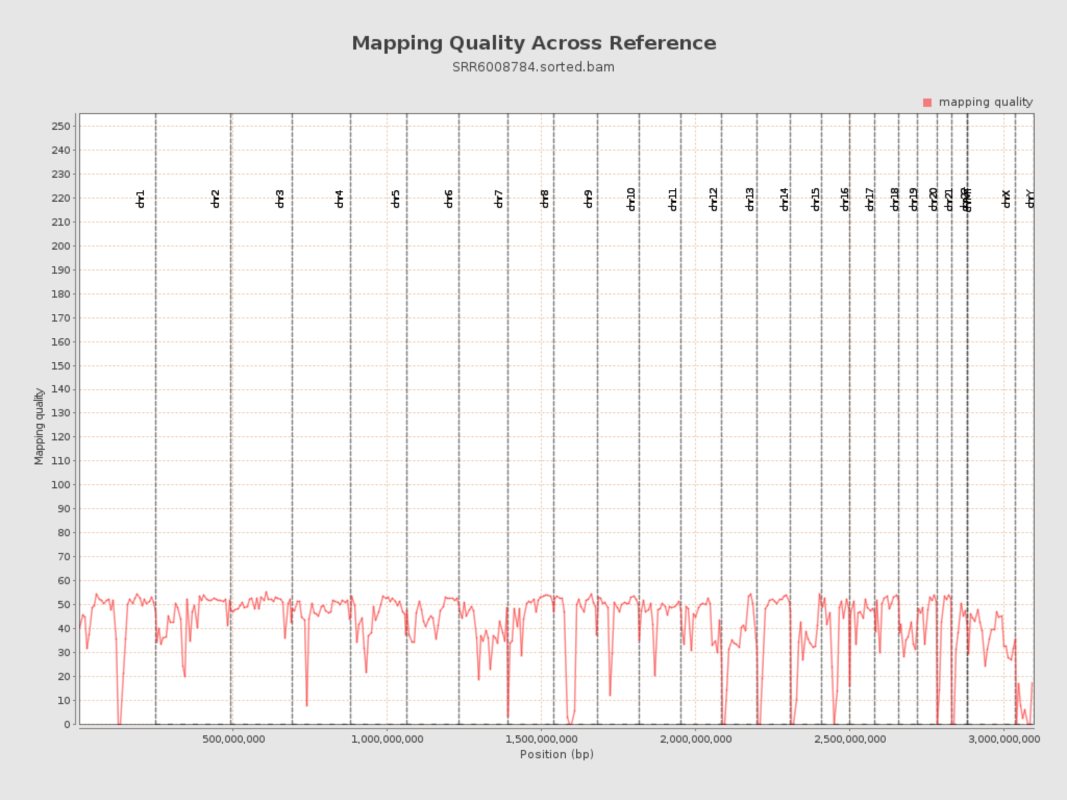
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram