# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 20:12:24*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093995.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_ERR2093995 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093995_1.fastq.gz ERR2093995_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Aug 26 20:12:23 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | ERR2093995.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 241,006 |
| Mapped reads | 230,052 / 95.45% |
| Unmapped reads | 10,954 / 4.55% |
| Mapped paired reads | 230,052 / 95.45% |
| Mapped reads, first in pair | 115,728 / 48.02% |
| Mapped reads, second in pair | 114,324 / 47.44% |
| Mapped reads, both in pair | 227,722 / 94.49% |
| Mapped reads, singletons | 2,330 / 0.97% |
| Secondary alignments | 0 |
| Supplementary alignments | 15,177 / 6.3% |
| Read min/max/mean length | 30 / 151 / 141.87 |
| Duplicated reads (estimated) | 211,881 / 87.92% |
| Duplication rate | 49.97% |
| Clipped reads | 115,527 / 47.94% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 7,772,650 / 26.76% |
| Number/percentage of C's | 6,791,228 / 23.38% |
| Number/percentage of T's | 7,325,510 / 25.22% |
| Number/percentage of G's | 7,159,394 / 24.65% |
| Number/percentage of N's | 325 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 48.02% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0096 |
| Standard Deviation | 1.8788 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 40.54 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 1,179,549.85 |
| Standard Deviation | 9,822,332.32 |
| P25/Median/P75 | 127 / 163 / 199 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 3.54% |
| Mismatches | 1,000,919 |
| Insertions | 14,569 |
| Mapped reads with at least one insertion | 6.23% |
| Deletions | 78,855 |
| Mapped reads with at least one deletion | 32.92% |
| Homopolymer indels | 29.41% |

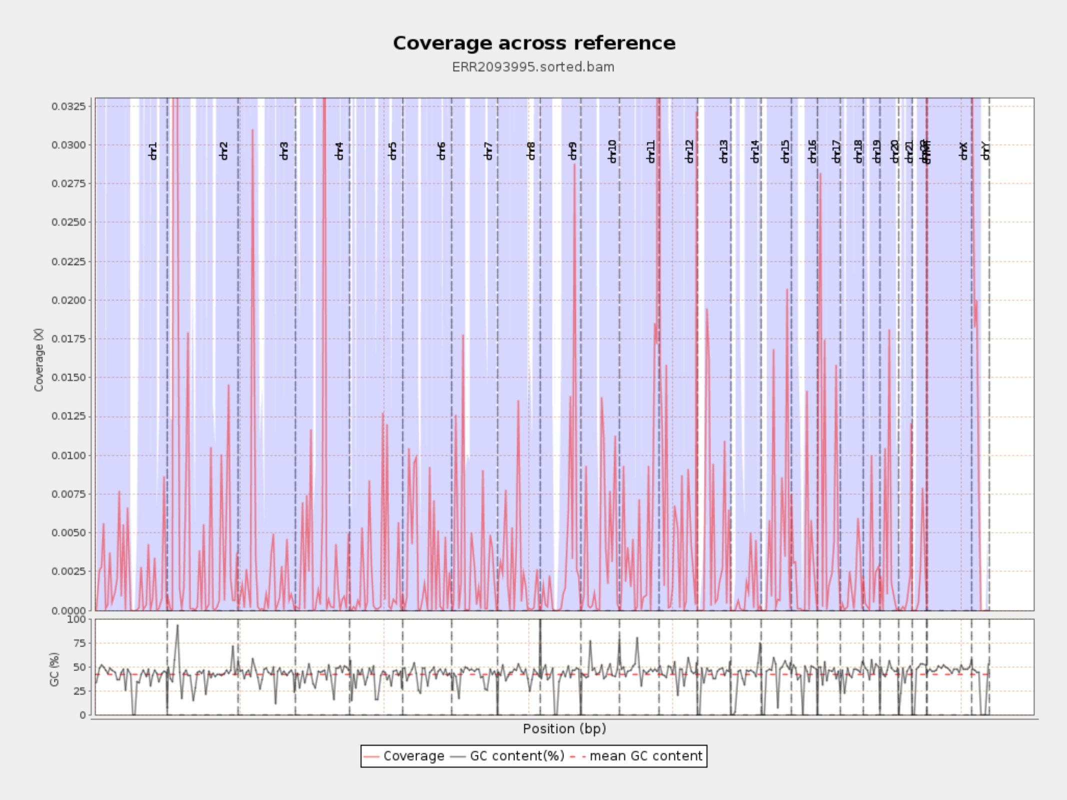
## 2.7. Chromosome stats

| **Name** | **Length** | **Mapped** | **Mean** | **Standard** |
|---|---|---|---|---|

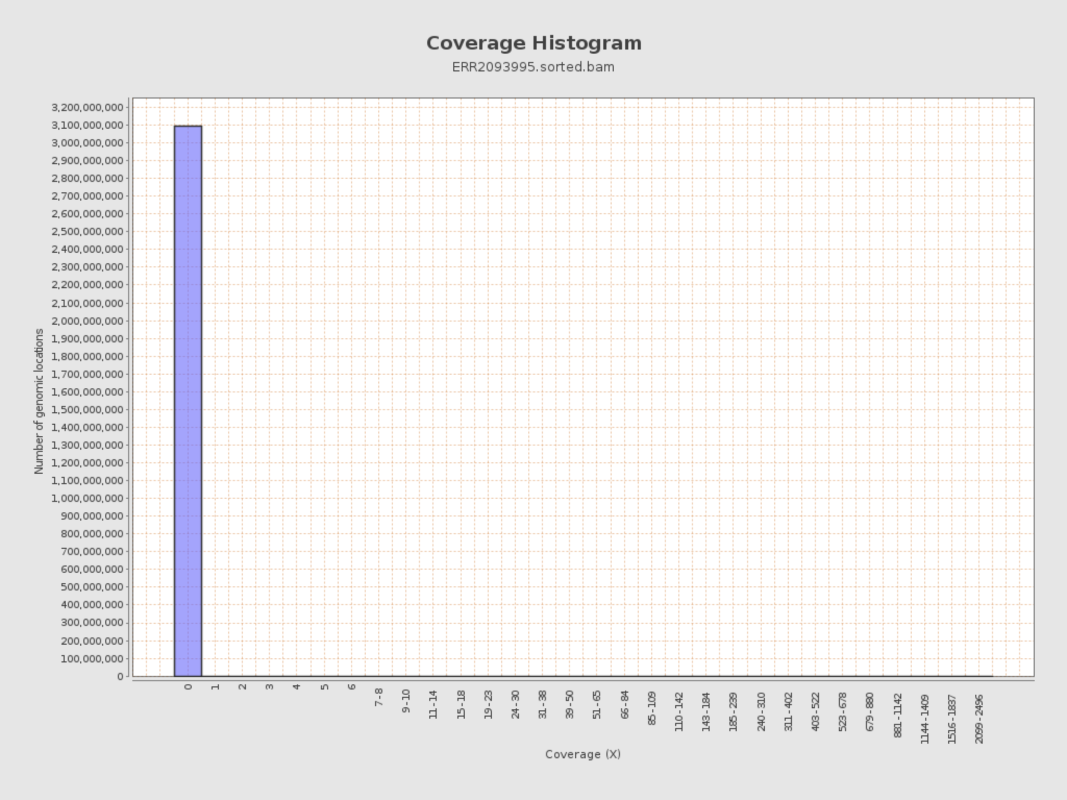
|  |  | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 483147 | 0.0019 | 0.6227 |
| chr2 | 243199373 | 1694182 | 0.007 | 2.1006 |
| chr3 | 198022430 | 486420 | 0.0025 | 0.8099 |
| chr4 | 191154276 | 779849 | 0.0041 | 1.1421 |
| chr5 | 180915260 | 404149 | 0.0022 | 0.9687 |
| chr6 | 171115067 | 524091 | 0.0031 | 0.9156 |
| chr7 | 159138663 | 484295 | 0.003 | 0.9747 |
| chr8 | 146364022 | 369385 | 0.0025 | 0.6675 |
| chr9 | 141213431 | 499764 | 0.0035 | 1.1189 |
| chr10 | 135534747 | 509311 | 0.0038 | 0.9872 |
| chr11 | 135006516 | 761944 | 0.0056 | 1.4478 |
| chr12 | 133851895 | 738173 | 0.0055 | 1.377 |
| chr13 | 115169878 | 543886 | 0.0047 | 1.3468 |
| chr14 | 107349540 | 108861 | 0.001 | 0.3934 |
| chr15 | 102531392 | 462171 | 0.0045 | 1.2061 |
| chr16 | 90354753 | 271592 | 0.003 | 0.9756 |
| chr17 | 81195210 | 679526 | 0.0084 | 1.9134 |
| chr18 | 78077248 | 129111 | 0.0017 | 0.5036 |
| chr19 | 59128983 | 134185 | 0.0023 | 0.7482 |
| chr20 | 63025520 | 262200 | 0.0042 | 1.4112 |
| chr21 | 48129895 | 83541 | 0.0017 | 0.3407 |
| chr22 | 51304566 | 101686 | 0.002 | 0.5684 |
| chrMT | 16571 | 1268796 | 76.5673 | 314.4795 |
| chrX | 155270560 | 17301433 | 0.1114 | 5.7448 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 514608 | 0.0087 | 1.7558 |

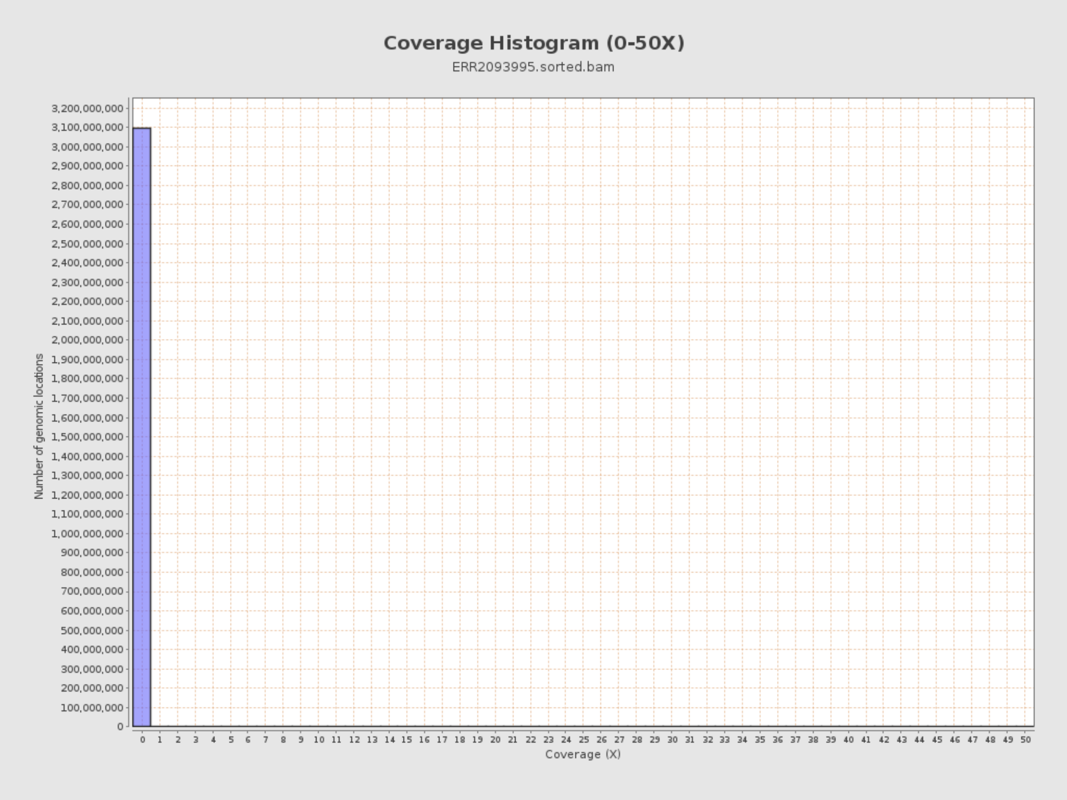
# 3. Results : Coverage across reference



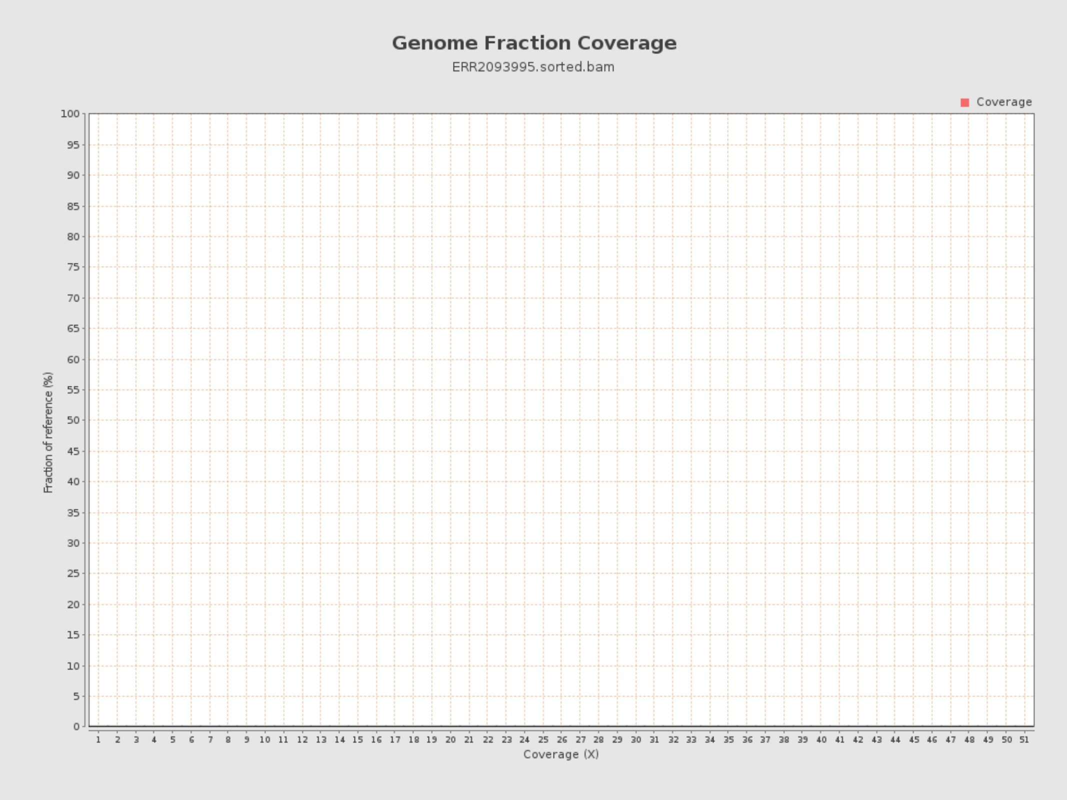
# 4. Results : Coverage Histogram



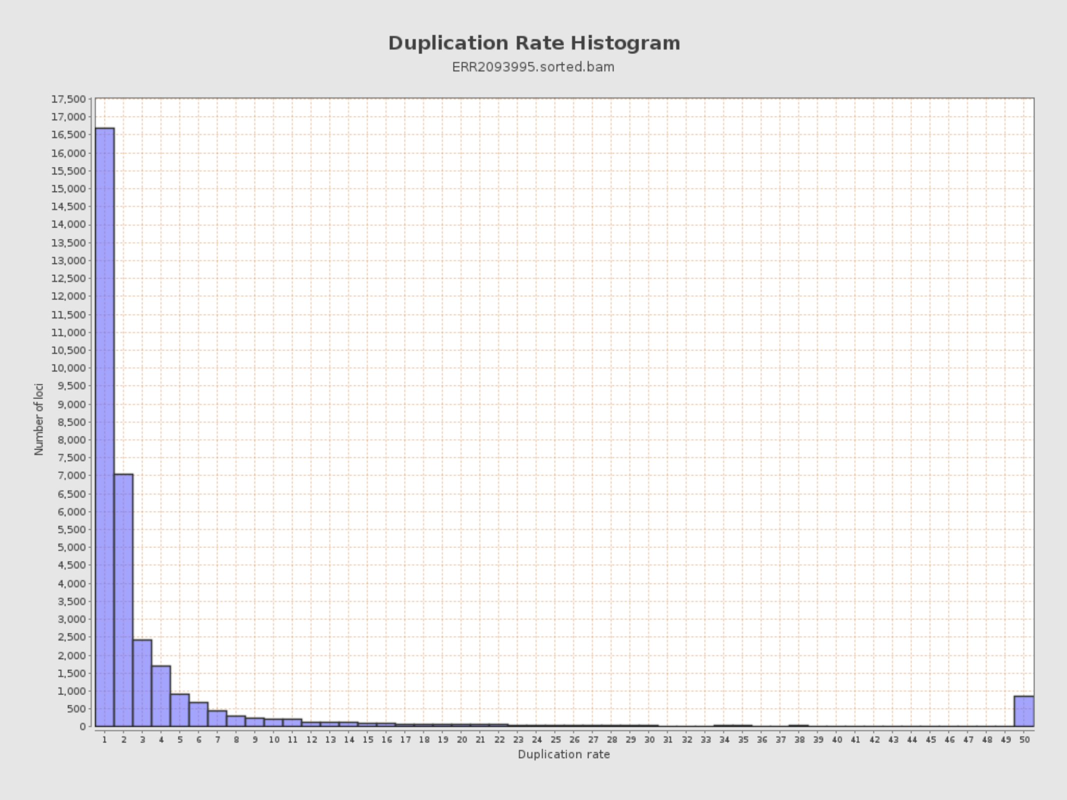
# 5. Results : Coverage Histogram (0-50X)



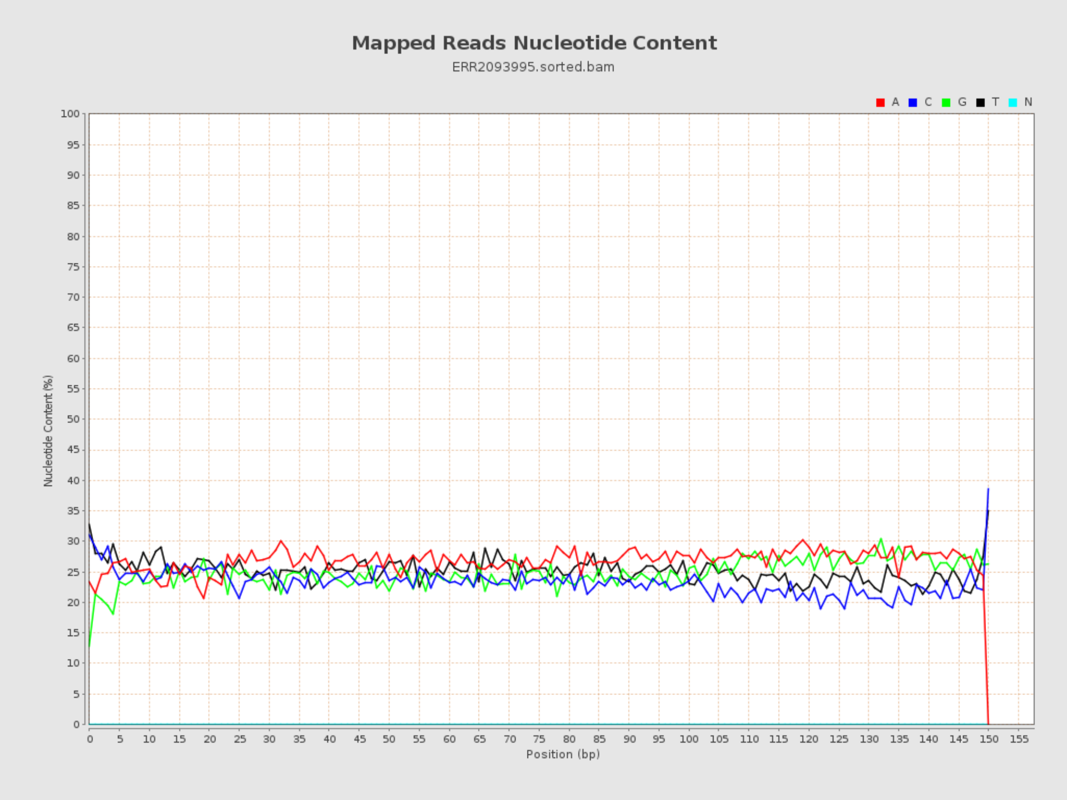
# 6. Results : Genome Fraction Coverage



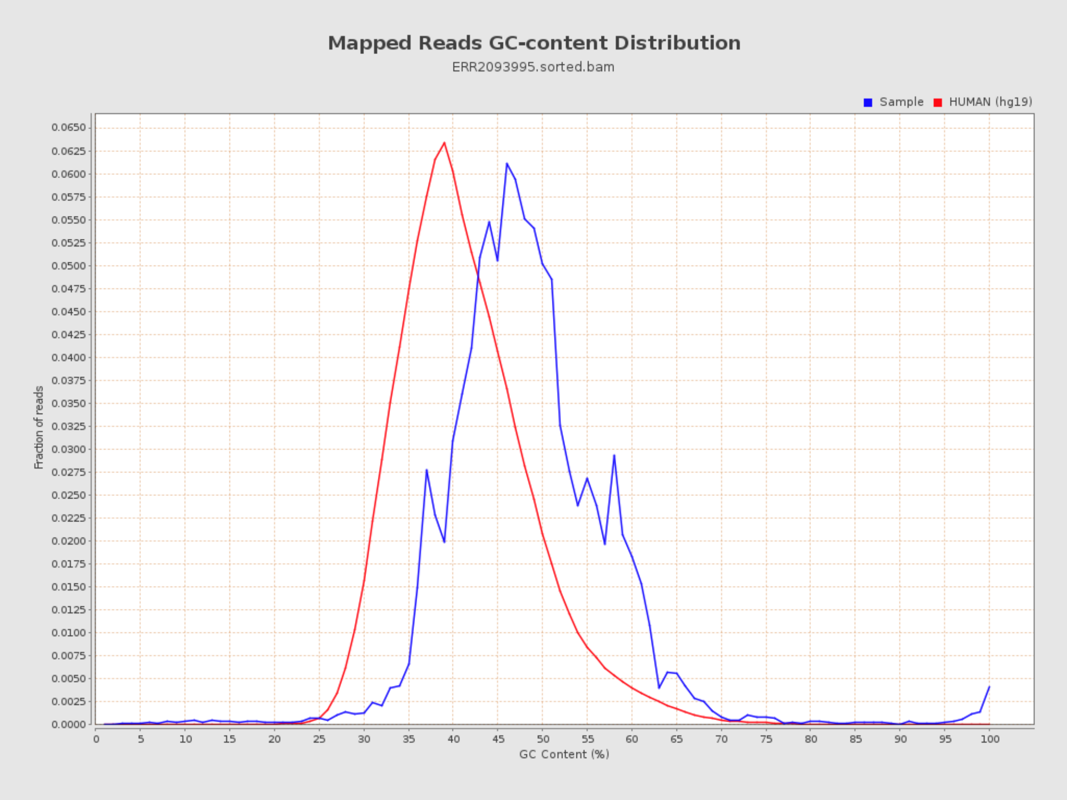
# 7. Results : Duplication Rate Histogram



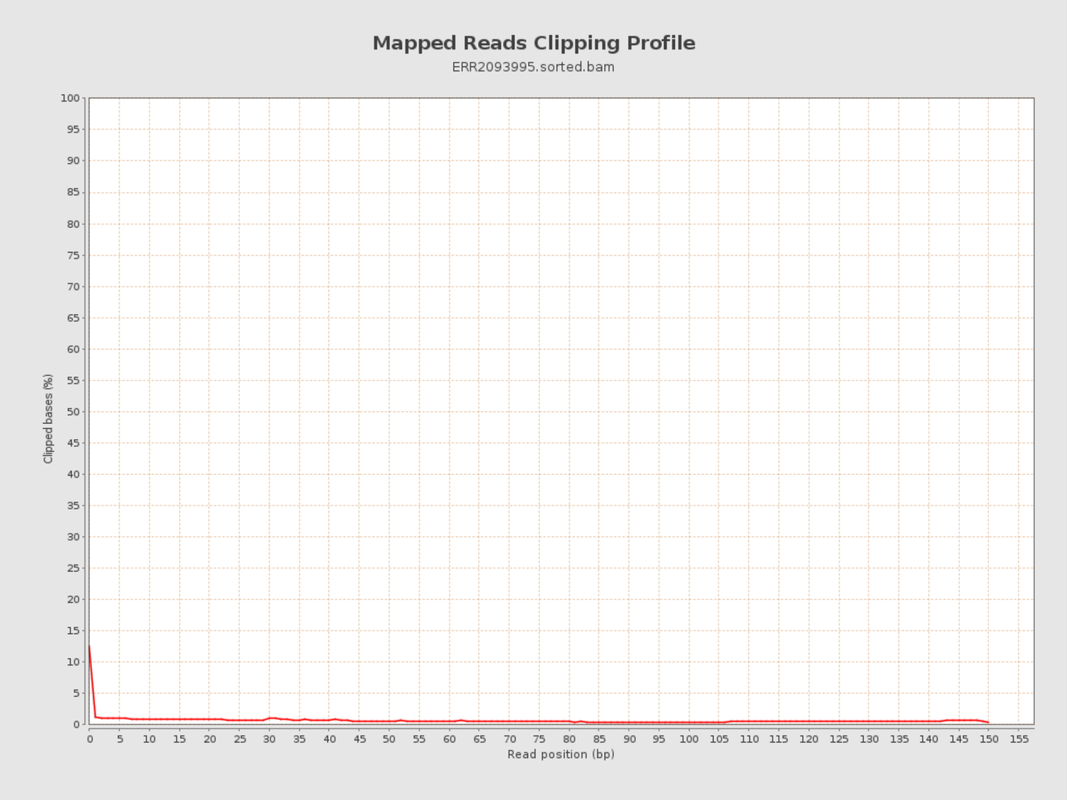
# 8. Results : Mapped Reads Nucleotide Content



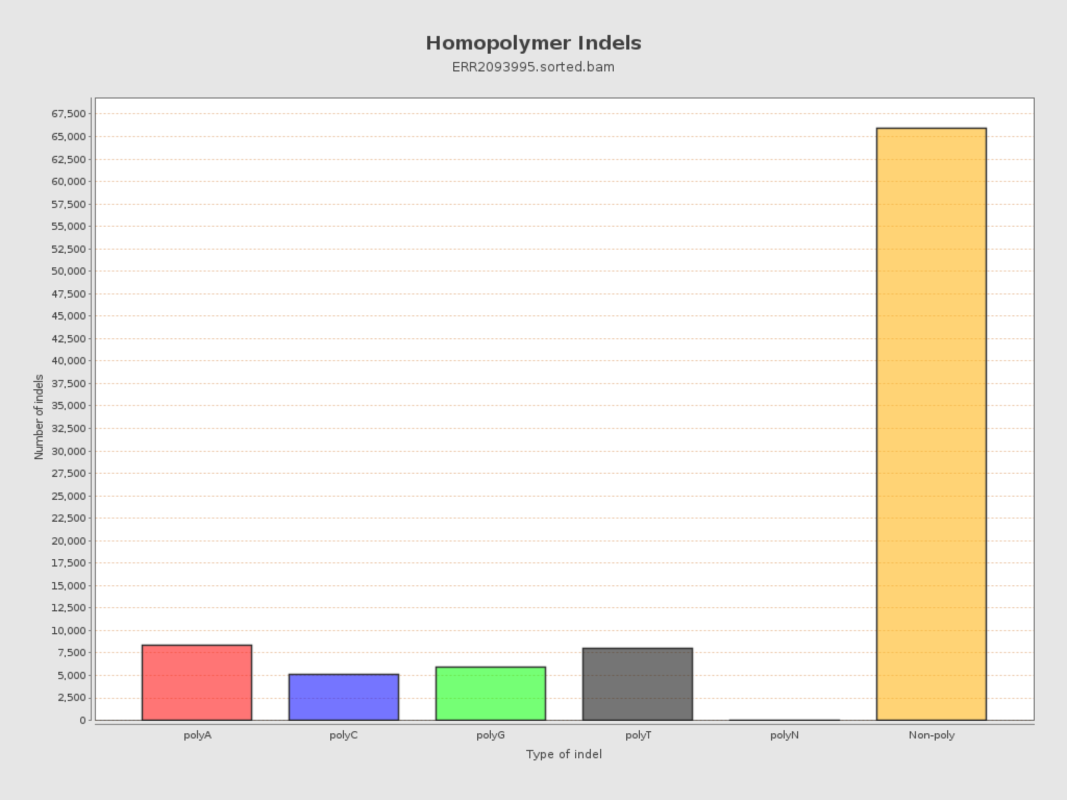
# 9. Results : Mapped Reads GC-content Distribution



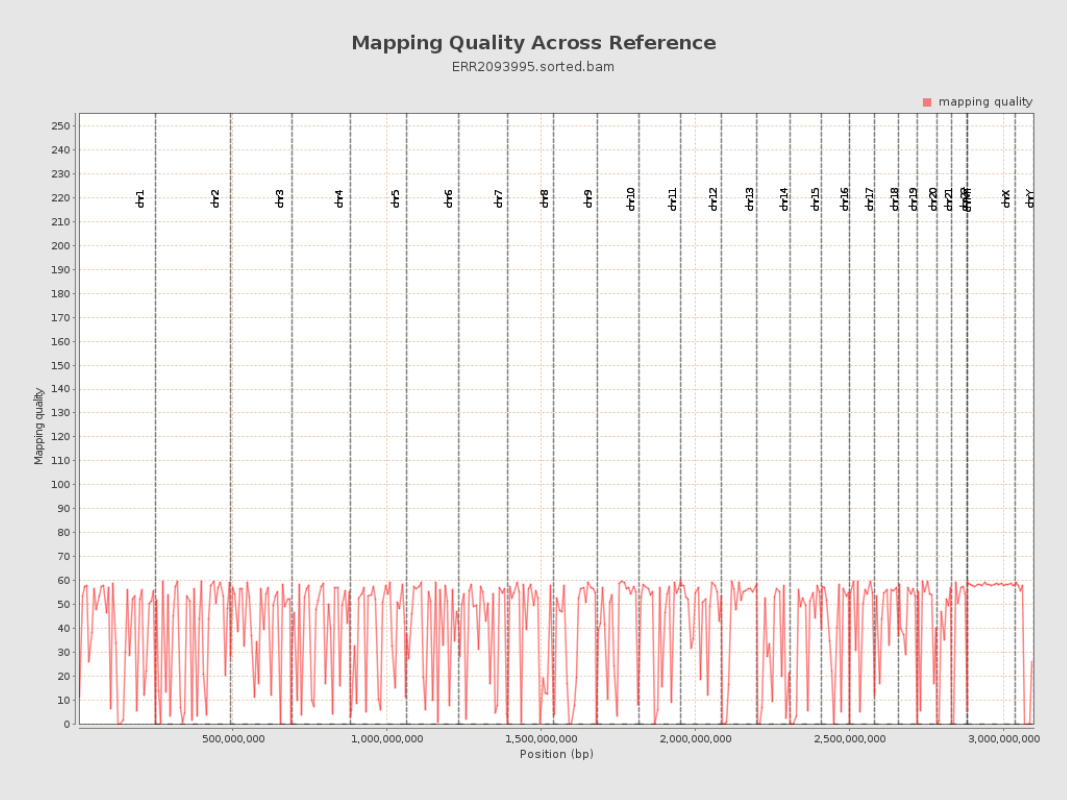
# 10. Results : Mapped Reads Clipping Profile



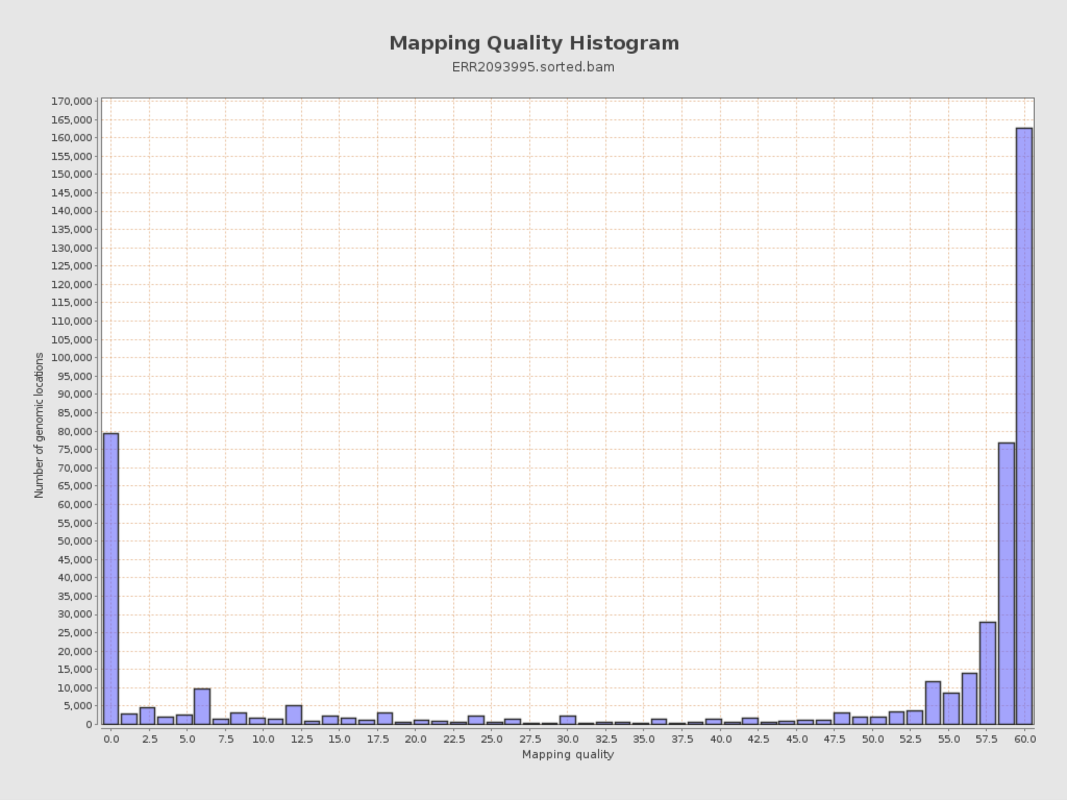
# 11. Results : Homopolymer Indels



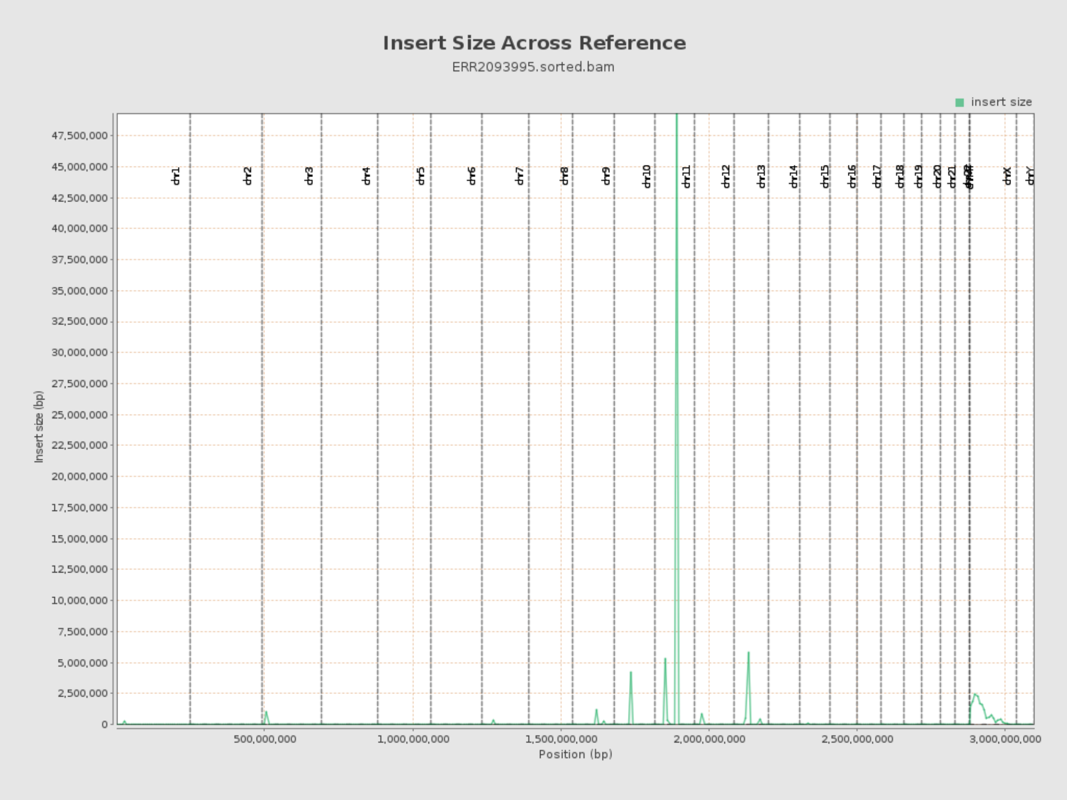
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram