# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 19:13:21*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093975.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_ERR2093975 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093975_1.fastq.gz ERR2093975_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Aug 26 19:13:08 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | ERR2093975.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 445,312 |
| Mapped reads | 365,494 / 82.08% |
| Unmapped reads | 79,818 / 17.92% |
| Mapped paired reads | 365,494 / 82.08% |
| Mapped reads, first in pair | 182,853 / 41.06% |
| Mapped reads, second in pair | 182,641 / 41.01% |
| Mapped reads, both in pair | 362,648 / 81.44% |
| Mapped reads, singletons | 2,846 / 0.64% |
| Secondary alignments | 0 |
| Supplementary alignments | 11,072 / 2.49% |
| Read min/max/mean length | 30 / 151 / 136.15 |
| Duplicated reads (estimated) | 368,428 / 82.73% |
| Duplication rate | 32.69% |
| Clipped reads | 125,532 / 28.19% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 13,139,838 / 25.87% |
| Number/percentage of C's | 10,567,295 / 20.81% |
| Number/percentage of T's | 14,771,262 / 29.09% |
| Number/percentage of G's | 12,305,850 / 24.23% |
| Number/percentage of N's | 699 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 45.04% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0164 |
| Standard Deviation | 43.6363 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 17.67 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 87,122.53 |
| Standard Deviation | 2,998,959.21 |
| P25/Median/P75 | 208 / 237 / 237 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 2.52% |
| Mismatches | 1,261,503 |
| Insertions | 8,622 |
| Mapped reads with at least one insertion | 1.97% |
| Deletions | 16,022 |
| Mapped reads with at least one deletion | 4.29% |
| Homopolymer indels | 39.22% |

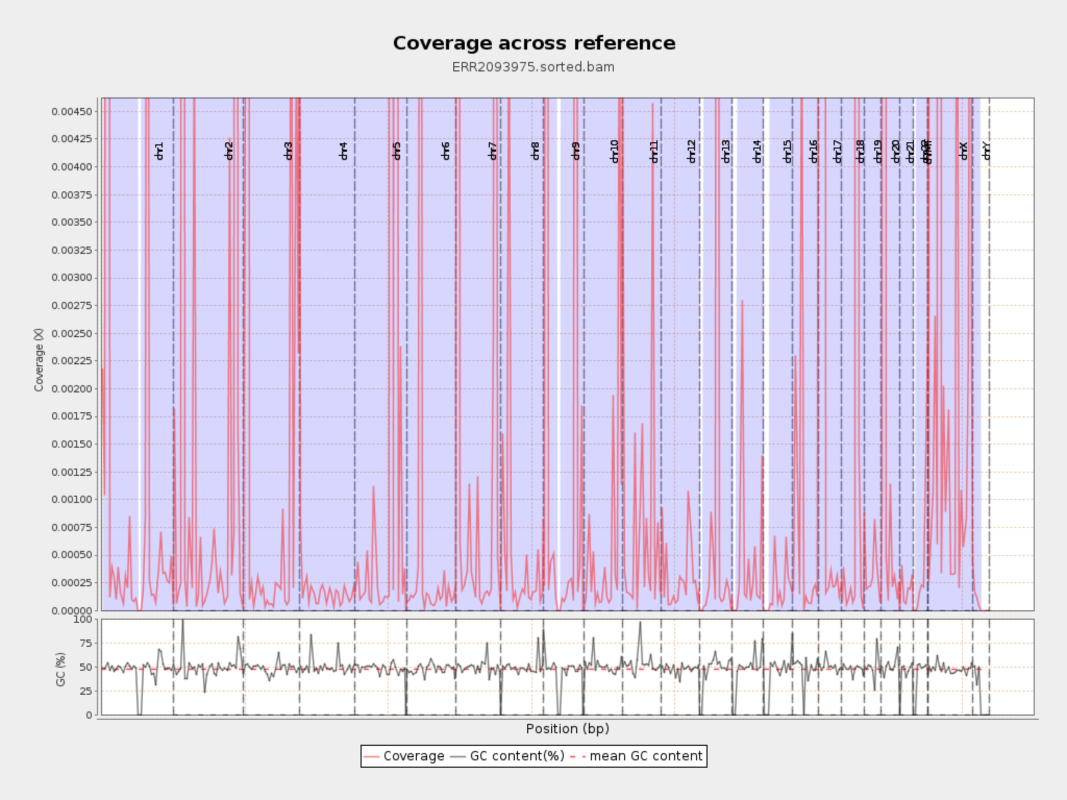
## 2.7. Chromosome stats

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

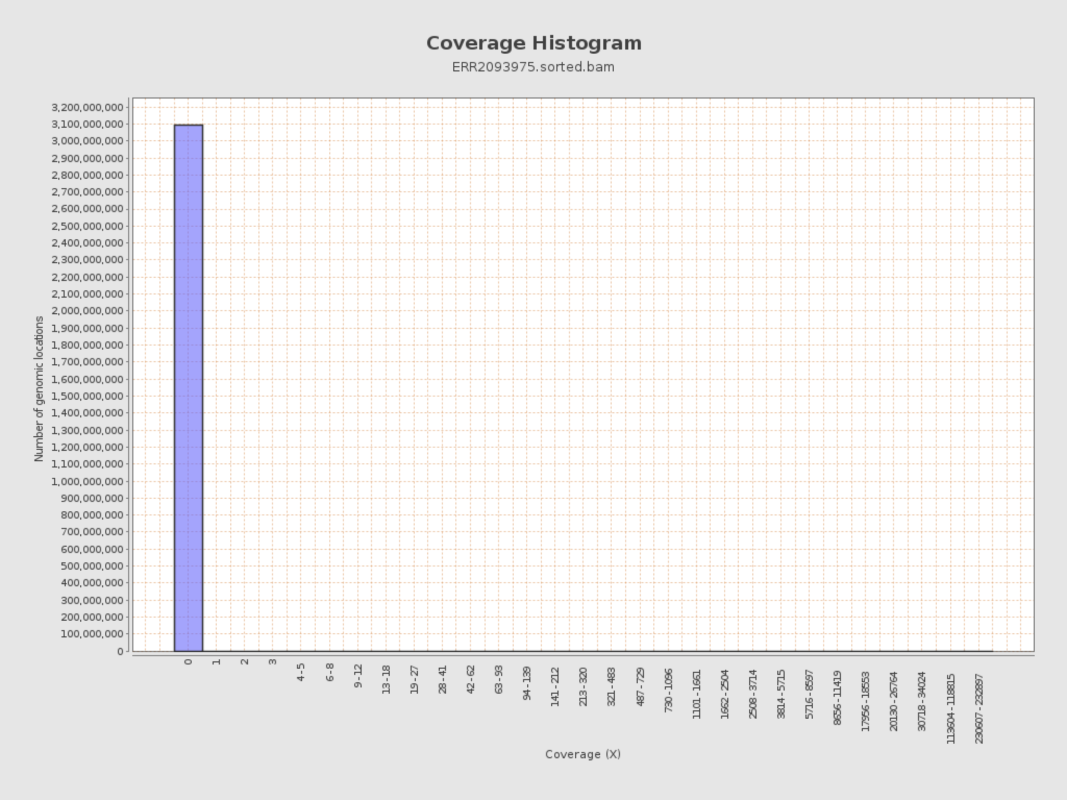
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 463813 | 0.0019 | 1.9325 |
| chr2 | 243199373 | 901497 | 0.0037 | 2.4163 |
| chr3 | 198022430 | 577568 | 0.0029 | 2.1805 |
| chr4 | 191154276 | 31452 | 0.0002 | 0.0325 |
| chr5 | 180915260 | 1267613 | 0.007 | 5.9468 |
| chr6 | 171115067 | 128659 | 0.0008 | 0.6147 |
| chr7 | 159138663 | 580466 | 0.0036 | 2.4071 |
| chr8 | 146364022 | 88465 | 0.0006 | 0.309 |
| chr9 | 141213431 | 370031 | 0.0026 | 1.8086 |
| chr10 | 135534747 | 90880 | 0.0007 | 0.372 |
| chr11 | 135006516 | 109877 | 0.0008 | 0.4369 |
| chr12 | 133851895 | 41567 | 0.0003 | 0.0941 |
| chr13 | 115169878 | 184787 | 0.0016 | 1.3286 |
| chr14 | 107349540 | 49012 | 0.0005 | 0.2017 |
| chr15 | 102531392 | 18796 | 0.0002 | 0.0473 |
| chr16 | 90354753 | 83451 | 0.0009 | 0.3078 |
| chr17 | 81195210 | 1865314 | 0.023 | 12.1156 |
| chr18 | 78077248 | 2553855 | 0.0327 | 17.0892 |
| chr19 | 59128983 | 20360 | 0.0003 | 0.1084 |
| chr20 | 63025520 | 827763 | 0.0131 | 7.8298 |
| chr21 | 48129895 | 8975 | 0.0002 | 0.0405 |
| chr22 | 51304566 | 20558 | 0.0004 | 0.0929 |
| chrMT | 16571 | 34909397 | 2,106.656 | 18,525.473 |
| chrX | 155270560 | 5624278 | 0.0362 | 23.2618 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 4920 | 0.0001 | 0.0281 |

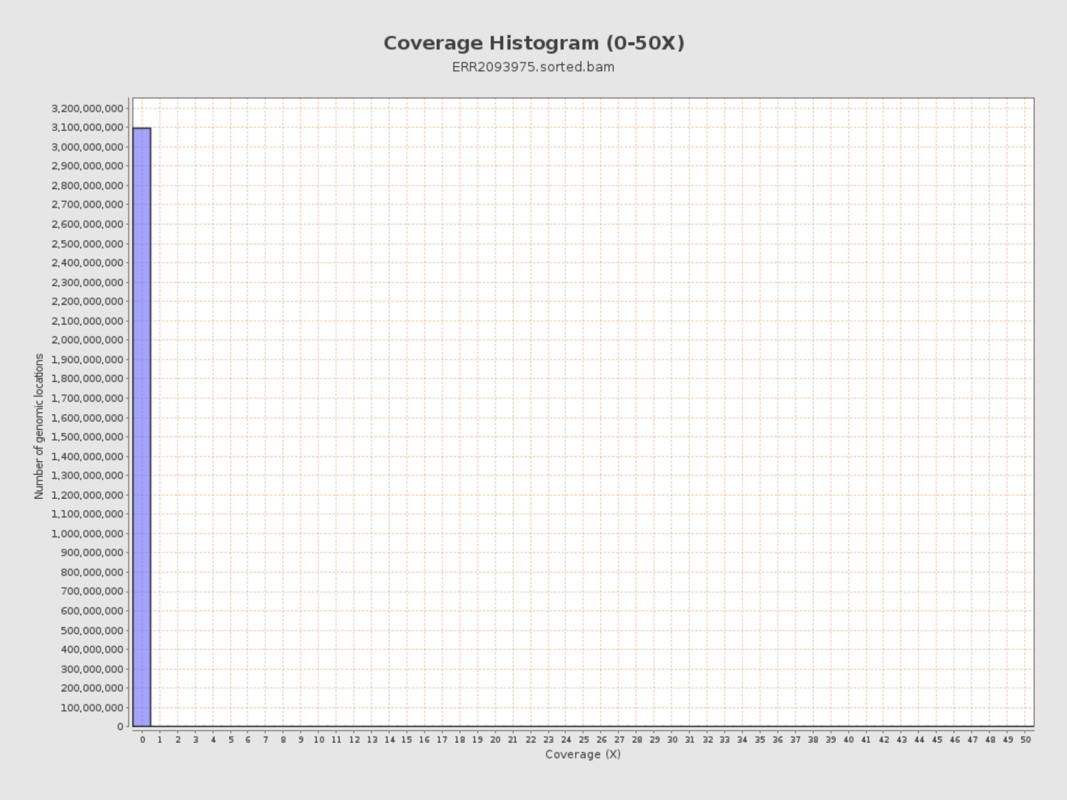
# 3. Results : Coverage across reference



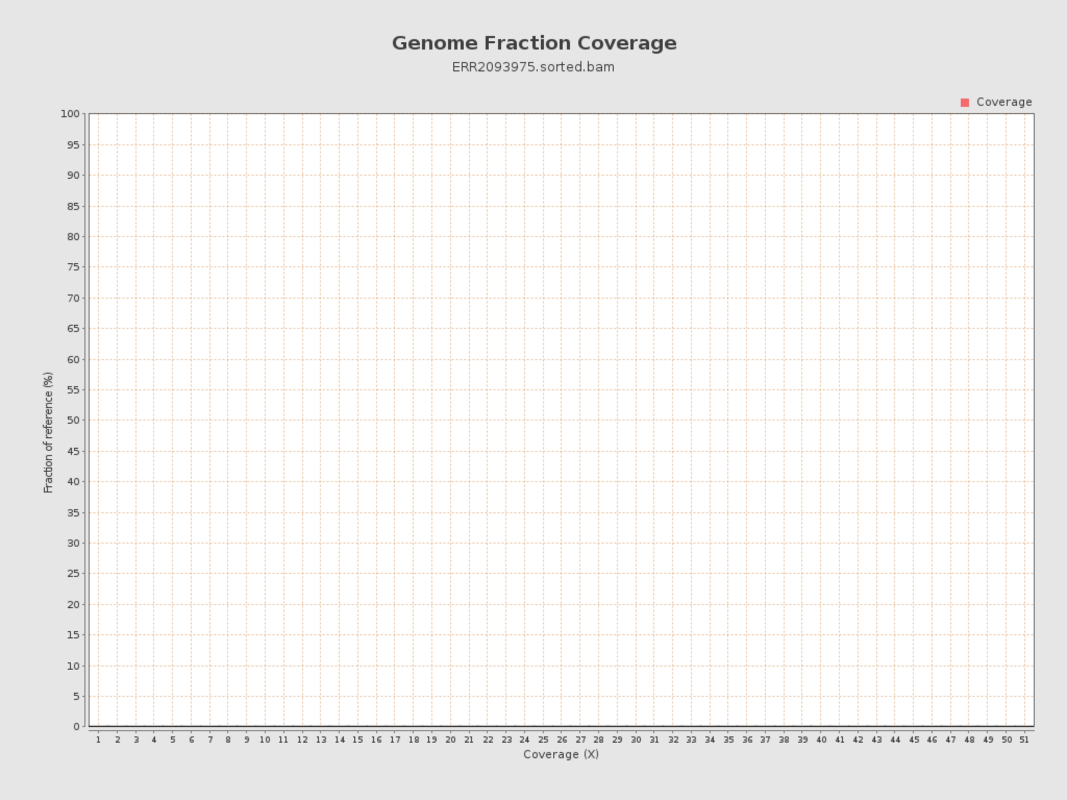
# 4. Results : Coverage Histogram



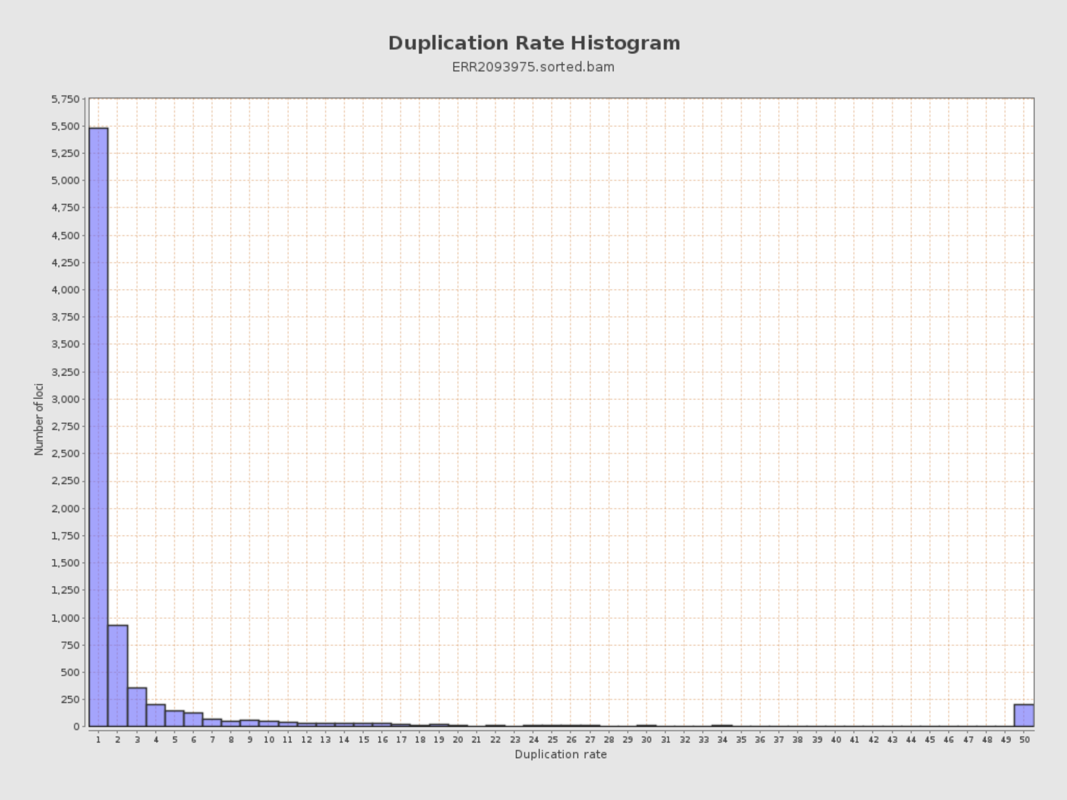
# 5. Results : Coverage Histogram (0-50X)



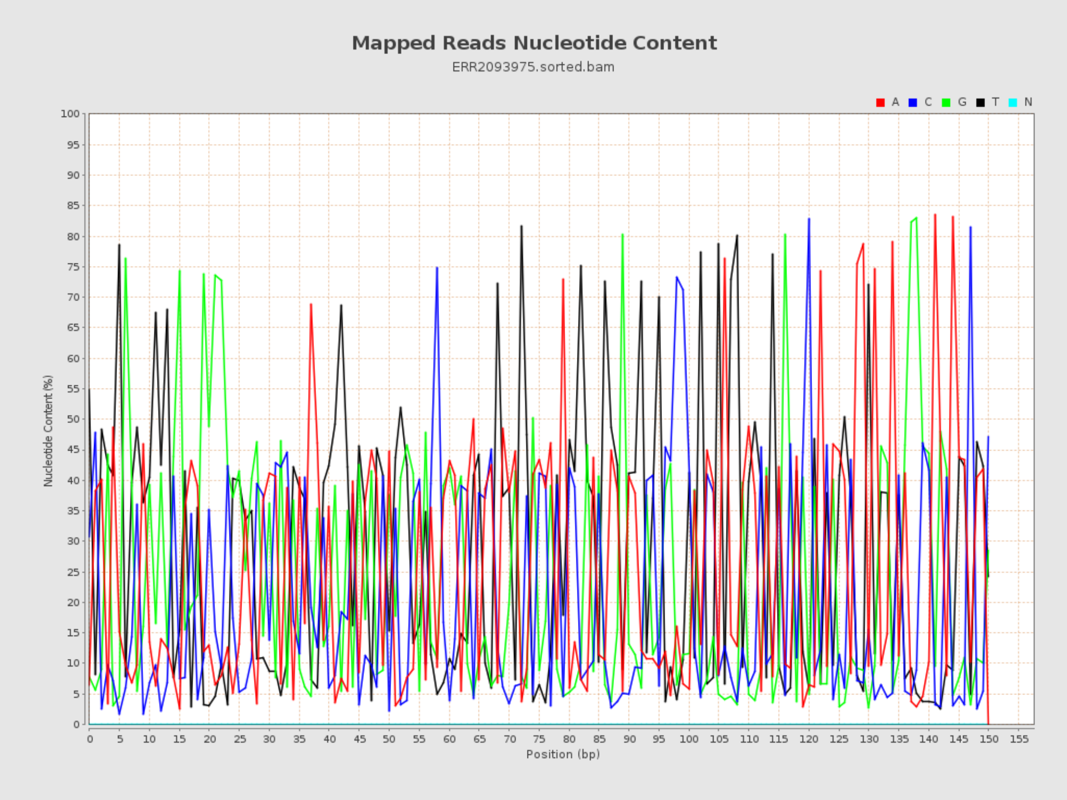
# 6. Results : Genome Fraction Coverage



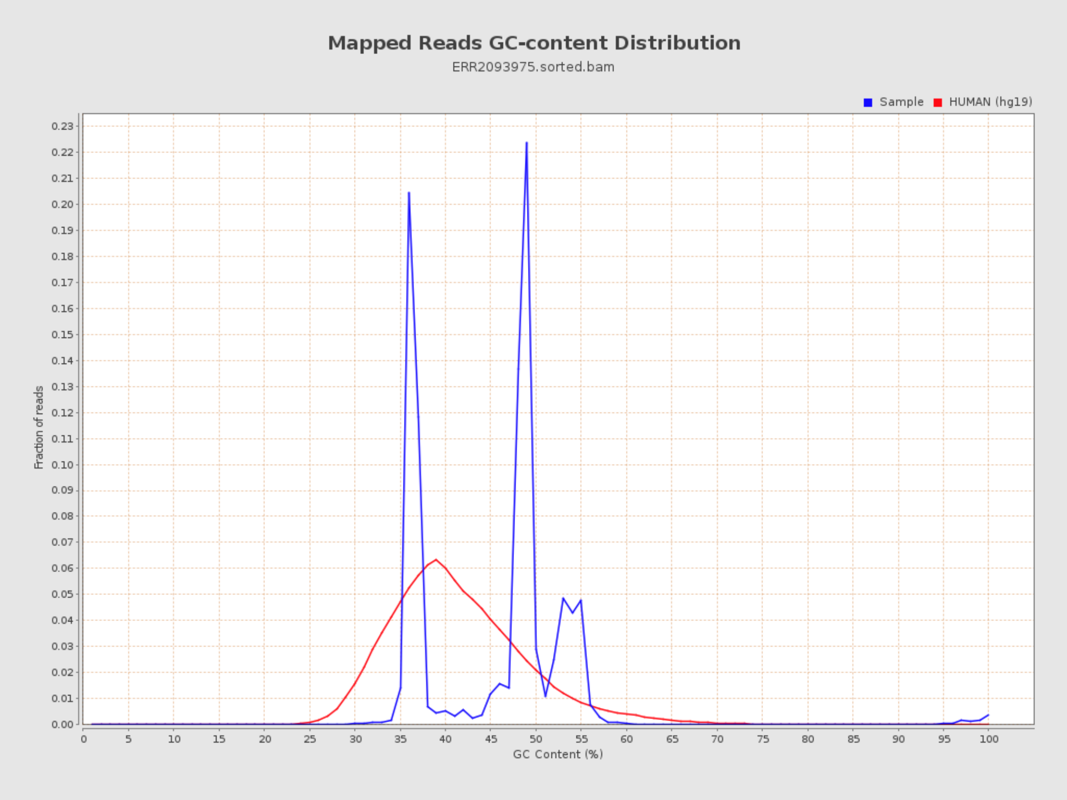
# 7. Results : Duplication Rate Histogram



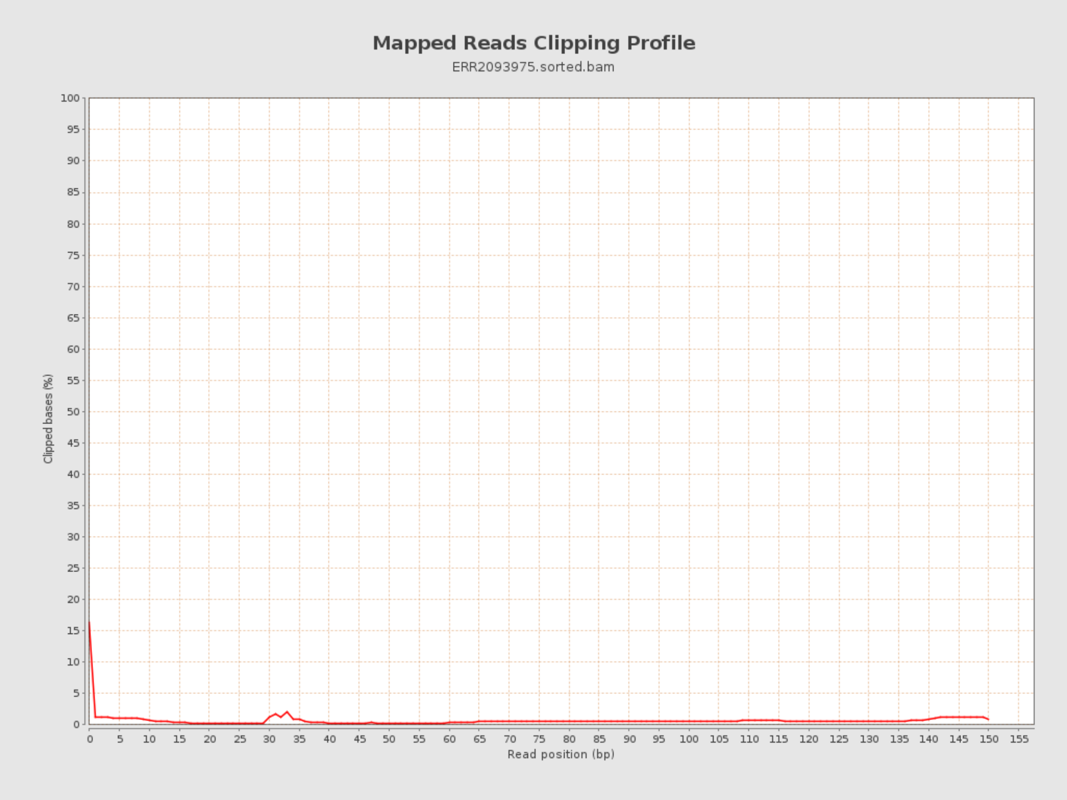
# 8. Results : Mapped Reads Nucleotide Content



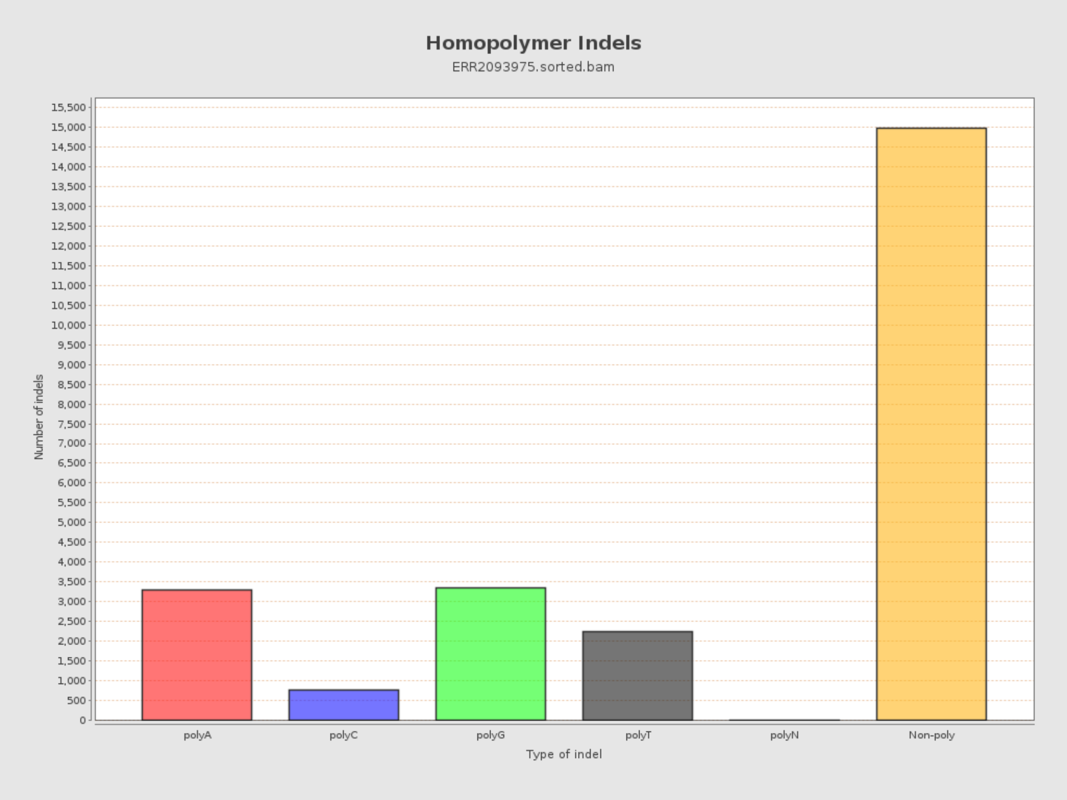
# 9. Results : Mapped Reads GC-content Distribution



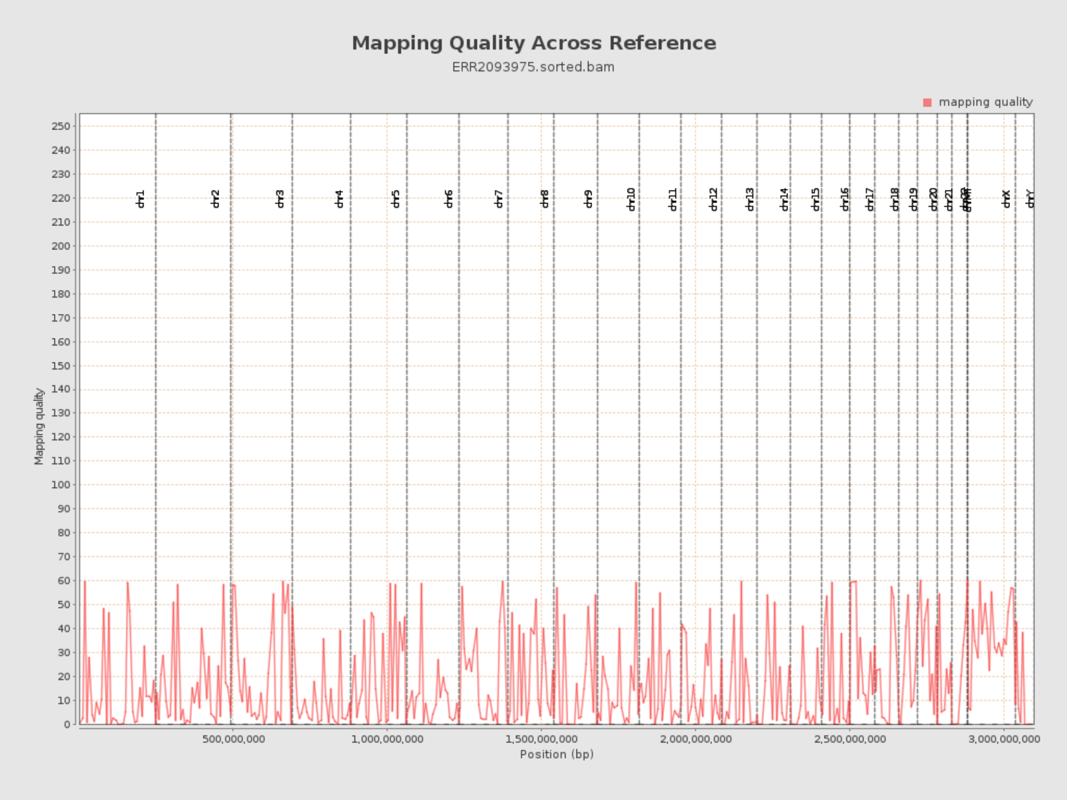
# 10. Results : Mapped Reads Clipping Profile



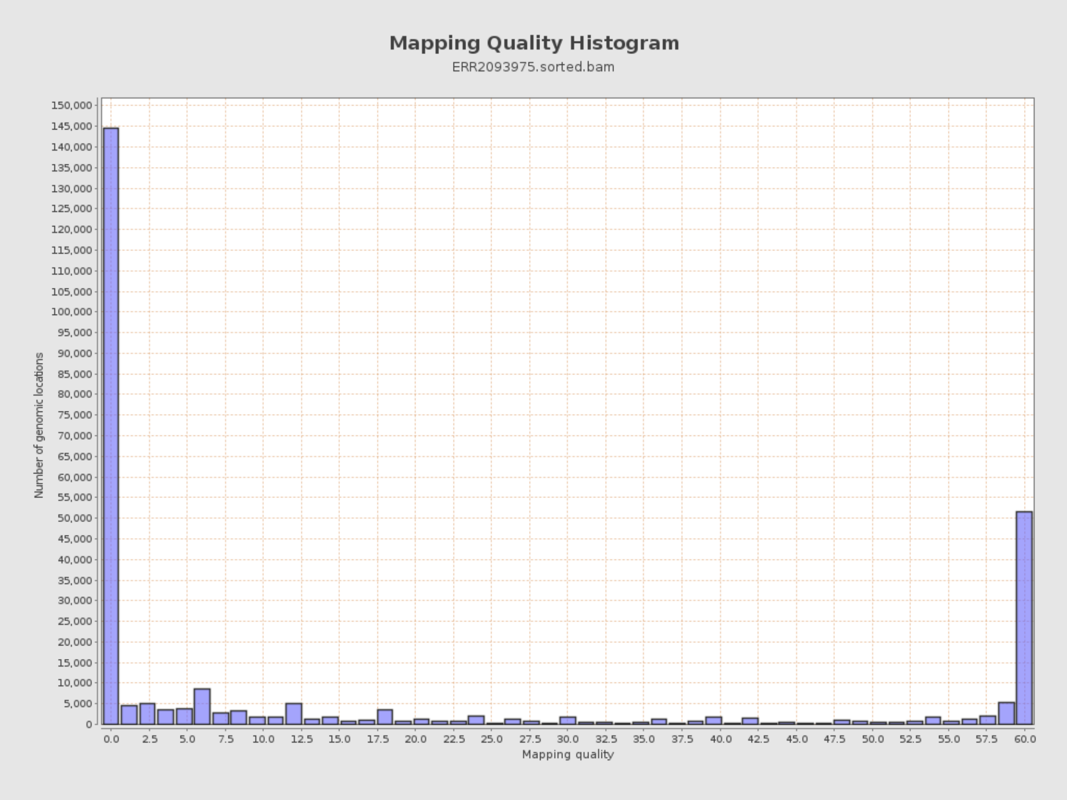
# 11. Results : Homopolymer Indels



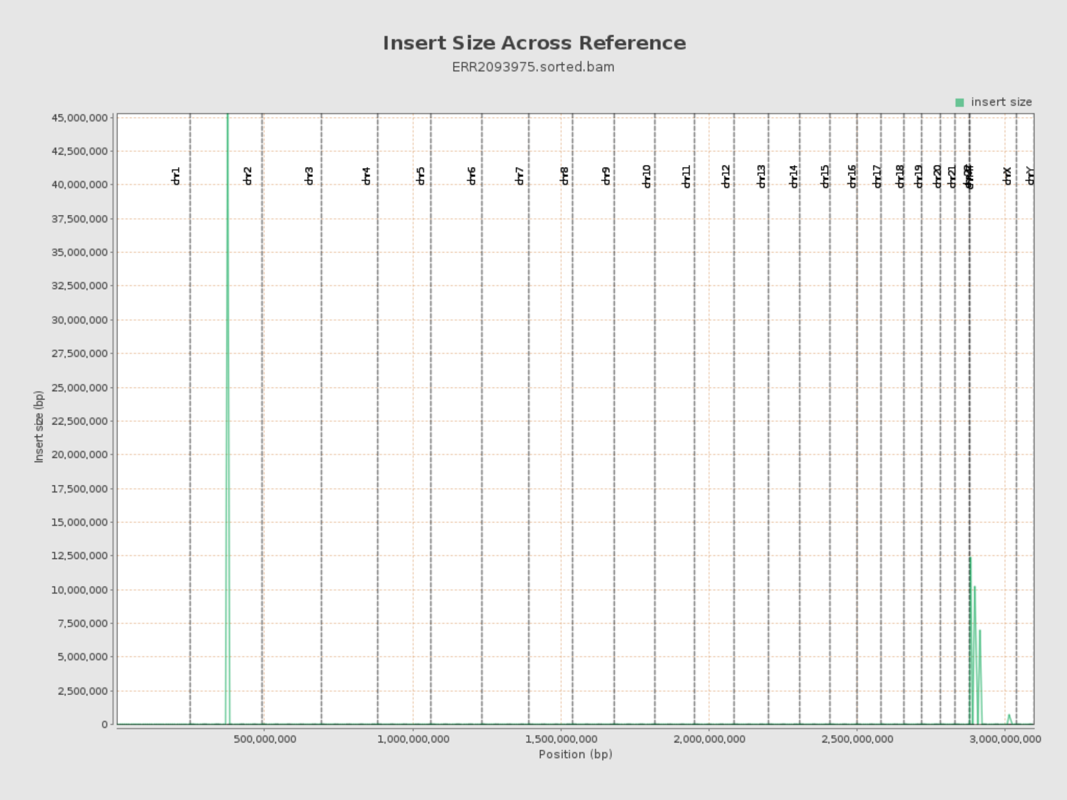
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram