# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/26 19:35:21*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam ERR2093980.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_ERR2093980 /home/luna/Desktop/database/homo_bwa/hsa.fa ERR2093980_1.fastq.gz ERR2093980_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Aug 26 19:35:20 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | ERR2093980.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 402,900 |
| Mapped reads | 382,058 / 94.83% |
| Unmapped reads | 20,842 / 5.17% |
| Mapped paired reads | 382,058 / 94.83% |
| Mapped reads, first in pair | 192,220 / 47.71% |
| Mapped reads, second in pair | 189,838 / 47.12% |
| Mapped reads, both in pair | 378,174 / 93.86% |
| Mapped reads, singletons | 3,884 / 0.96% |
| Secondary alignments | 0 |
| Supplementary alignments | 22,774 / 5.65% |
| Read min/max/mean length | 30 / 151 / 140.24 |
| Duplicated reads (estimated) | 358,874 / 89.07% |
| Duplication rate | 49.65% |
| Clipped reads | 191,359 / 47.5% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 12,720,802 / 26.72% |
| Number/percentage of C's | 11,020,232 / 23.15% |
| Number/percentage of T's | 11,951,085 / 25.11% |
| Number/percentage of G's | 11,906,663 / 25.01% |
| Number/percentage of N's | 689 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 48.17% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0157 |
| Standard Deviation | 2.817 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 40.73 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 988,207.63 |
| Standard Deviation | 9,033,562.73 |
| P25/Median/P75 | 126 / 162 / 197 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 3.61% |
| Mismatches | 1,657,156 |
| Insertions | 27,585 |
| Mapped reads with at least one insertion | 7.09% |
| Deletions | 133,644 |
| Mapped reads with at least one deletion | 33.6% |
| Homopolymer indels | 29.5% |

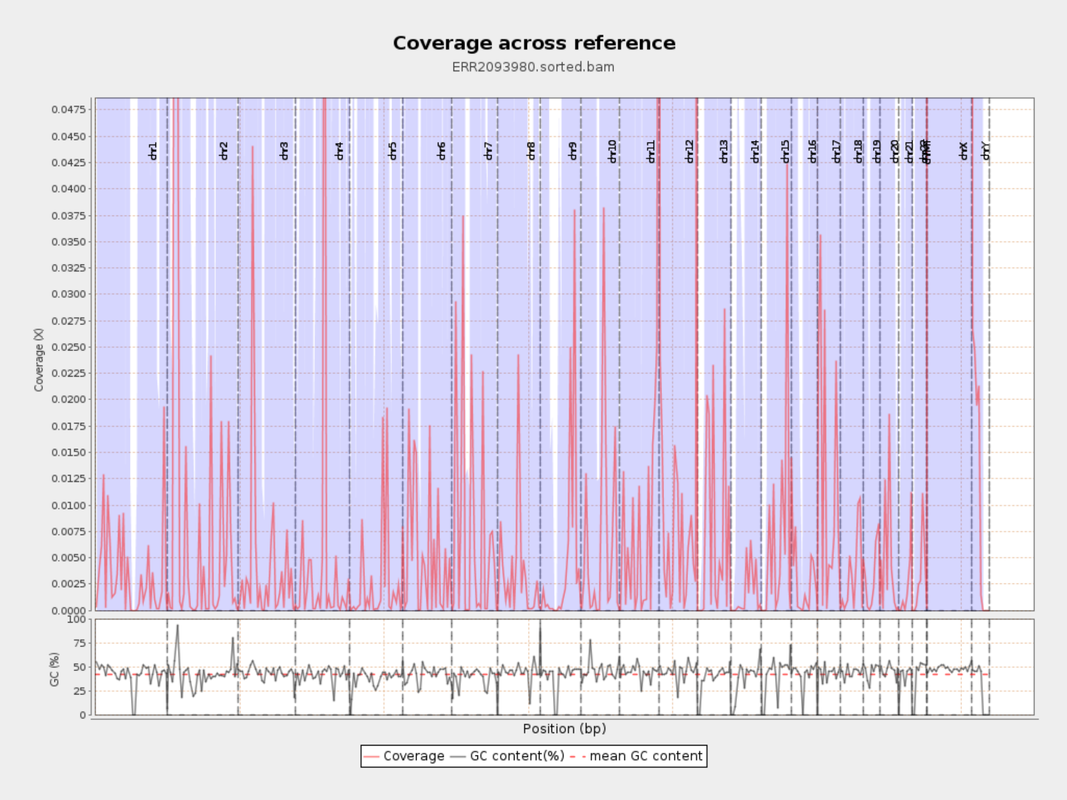
## 2.7. Chromosome stats

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

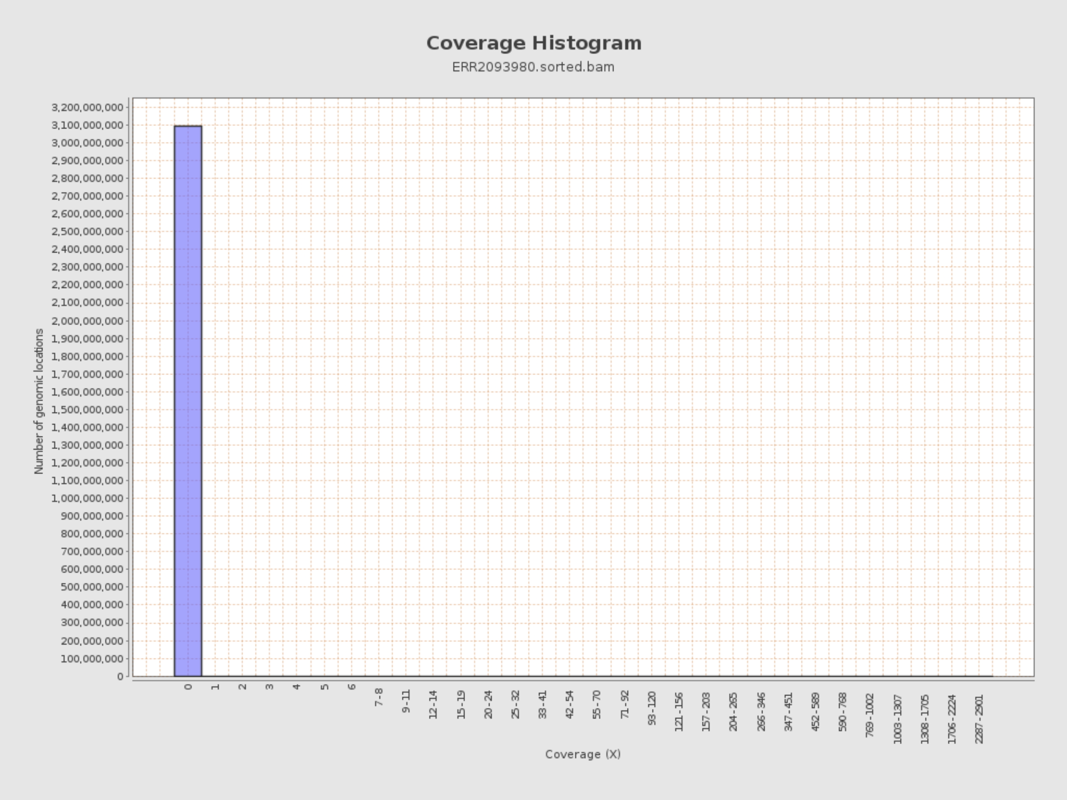
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 886126 | 0.0036 | 1.1292 |
| chr2 | 243199373 | 2071328 | 0.0085 | 2.6557 |
| chr3 | 198022430 | 796425 | 0.004 | 1.1707 |
| chr4 | 191154276 | 1011606 | 0.0053 | 1.6575 |
| chr5 | 180915260 | 483180 | 0.0027 | 1.3424 |
| chr6 | 171115067 | 929357 | 0.0054 | 1.497 |
| chr7 | 159138663 | 1169283 | 0.0073 | 2.1109 |
| chr8 | 146364022 | 515487 | 0.0035 | 1.0683 |
| chr9 | 141213431 | 705282 | 0.005 | 1.4835 |
| chr10 | 135534747 | 903954 | 0.0067 | 1.9147 |
| chr11 | 135006516 | 1050245 | 0.0078 | 1.8687 |
| chr12 | 133851895 | 1085550 | 0.0081 | 1.9555 |
| chr13 | 115169878 | 883606 | 0.0077 | 1.9782 |
| chr14 | 107349540 | 174933 | 0.0016 | 0.5435 |
| chr15 | 102531392 | 715244 | 0.007 | 1.919 |
| chr16 | 90354753 | 277712 | 0.0031 | 0.8803 |
| chr17 | 81195210 | 1047258 | 0.0129 | 3.0259 |
| chr18 | 78077248 | 280517 | 0.0036 | 0.9098 |
| chr19 | 59128983 | 179472 | 0.003 | 0.8197 |
| chr20 | 63025520 | 322603 | 0.0051 | 1.5168 |
| chr21 | 48129895 | 113218 | 0.0024 | 0.4404 |
| chr22 | 51304566 | 154336 | 0.003 | 0.6745 |
| chrMT | 16571 | 807594 | 48.7354 | 209.6777 |
| chrX | 155270560 | 31275794 | 0.2014 | 9.9892 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 656332 | 0.0111 | 1.5232 |

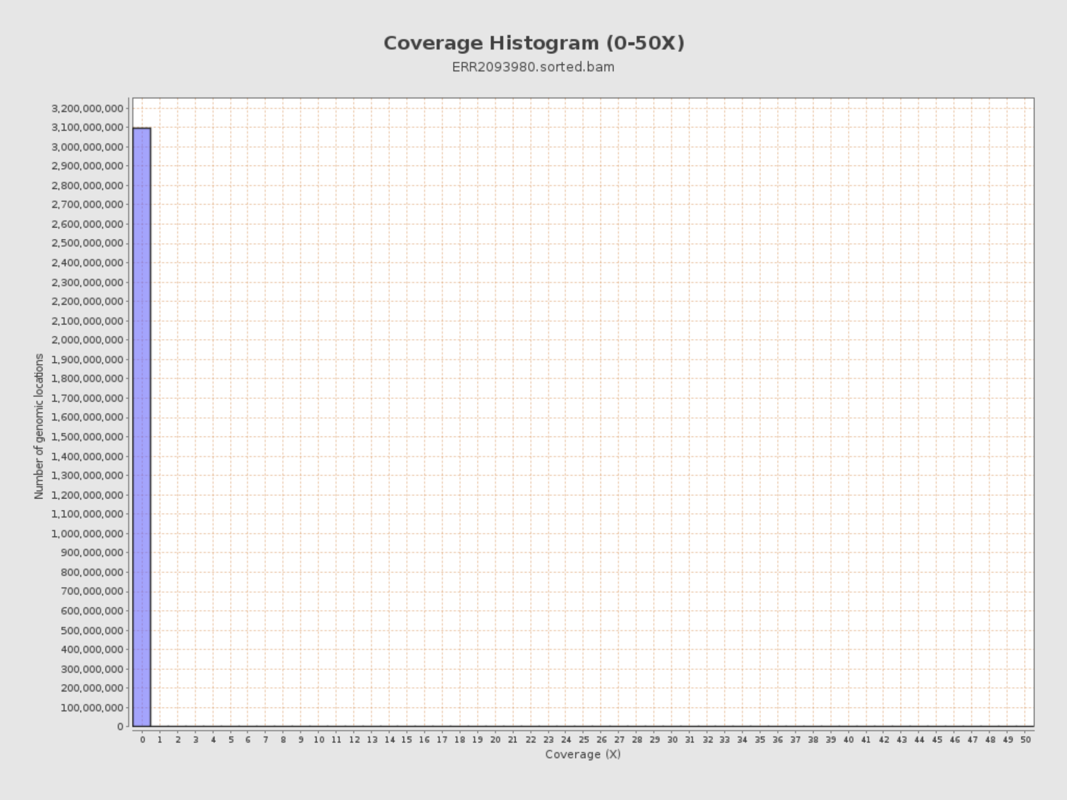
# 3. Results : Coverage across reference



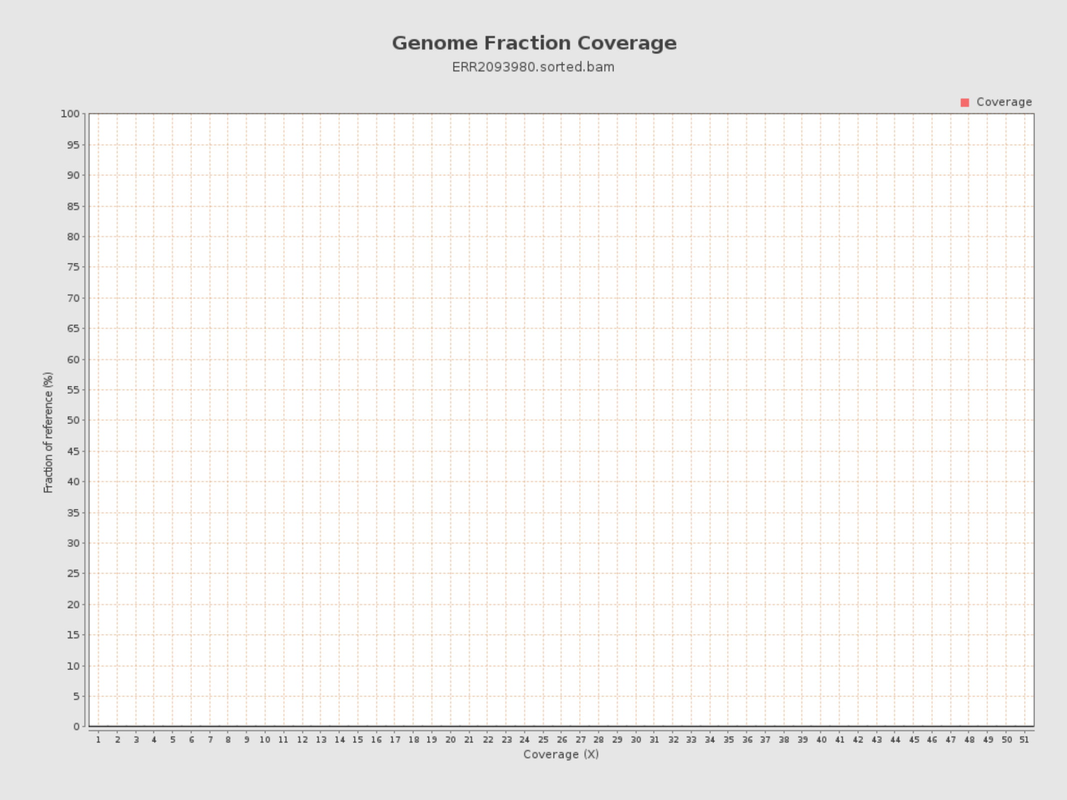
# 4. Results : Coverage Histogram



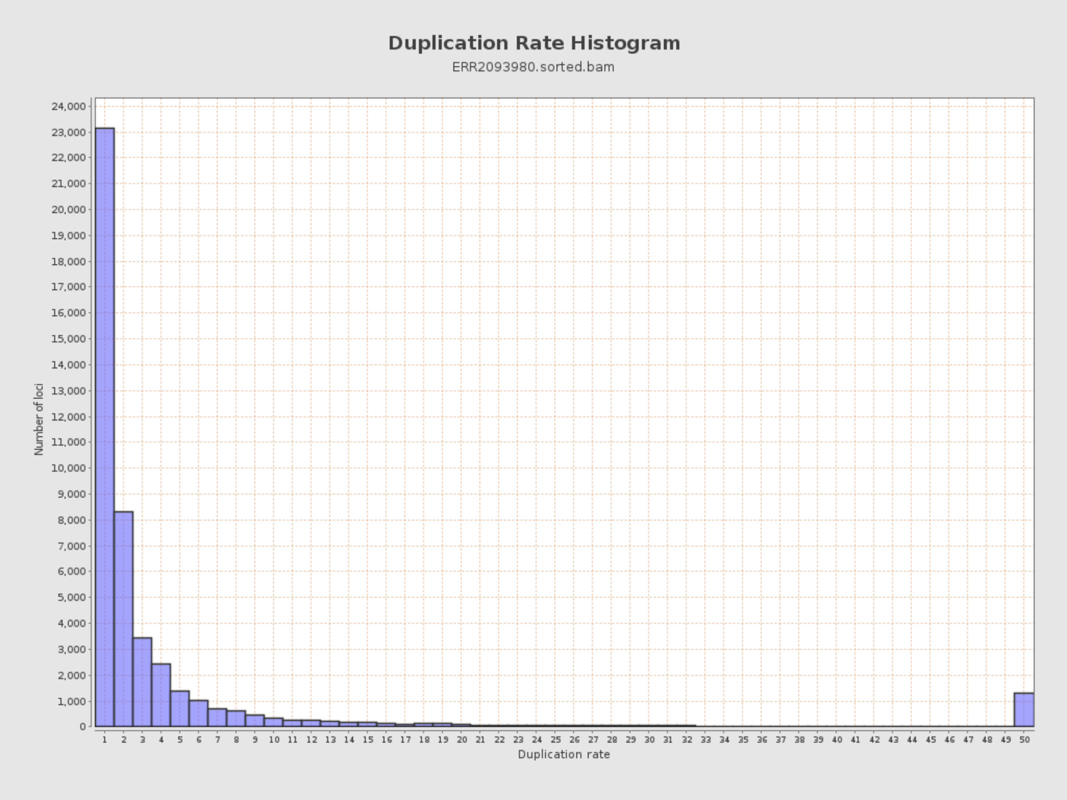
# 5. Results : Coverage Histogram (0-50X)



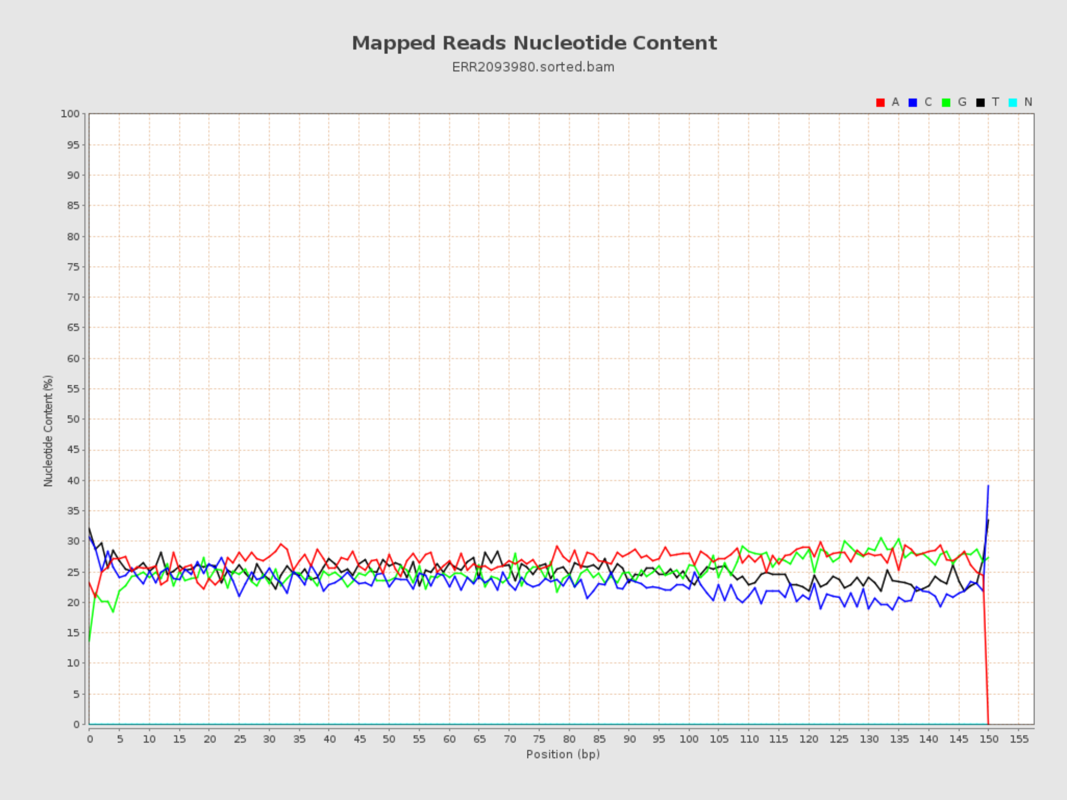
# 6. Results : Genome Fraction Coverage



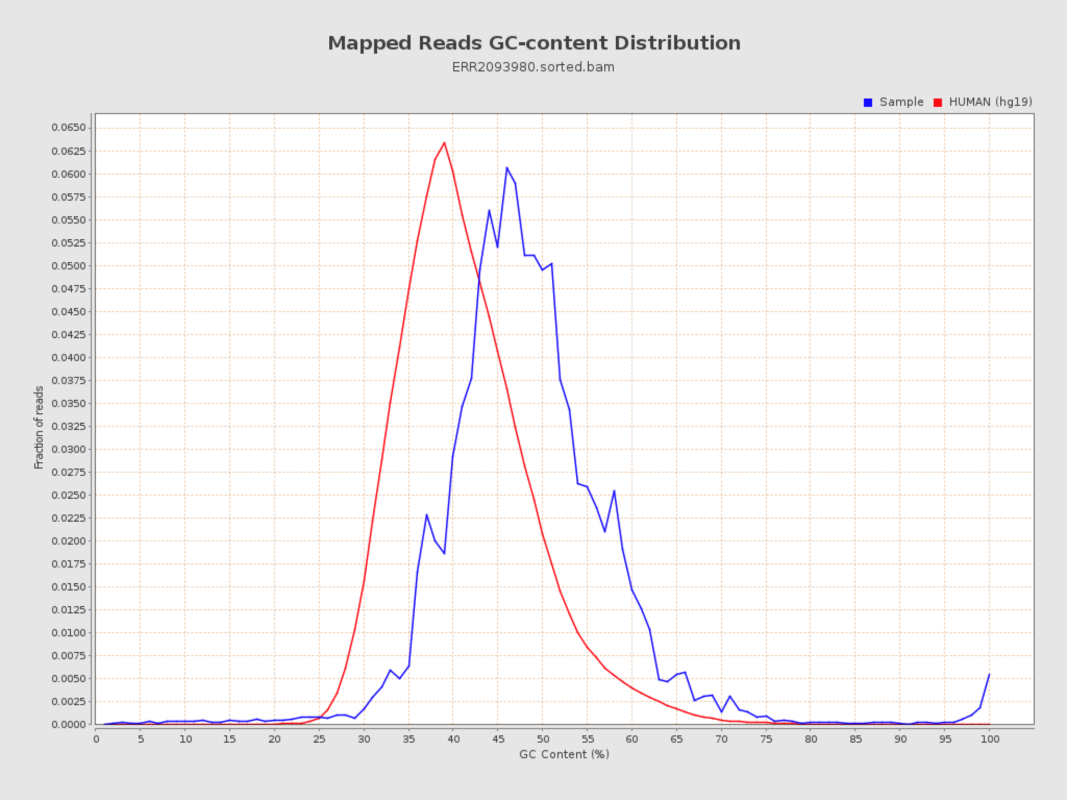
# 7. Results : Duplication Rate Histogram



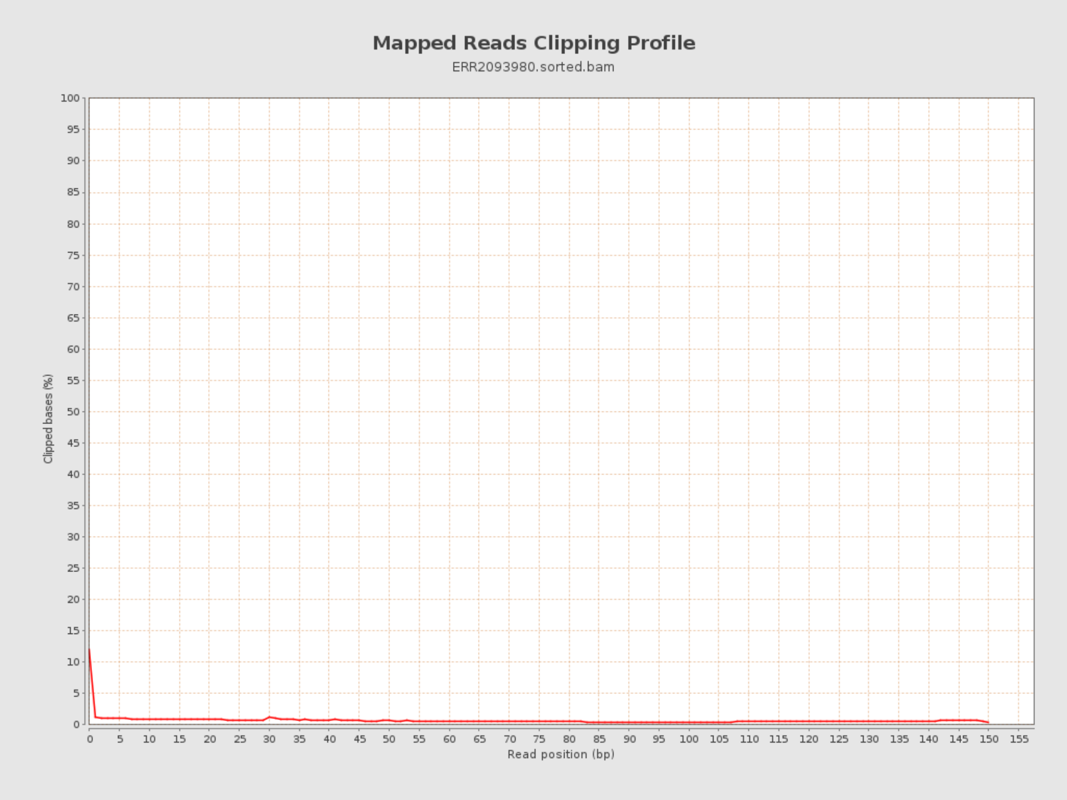
# 8. Results : Mapped Reads Nucleotide Content



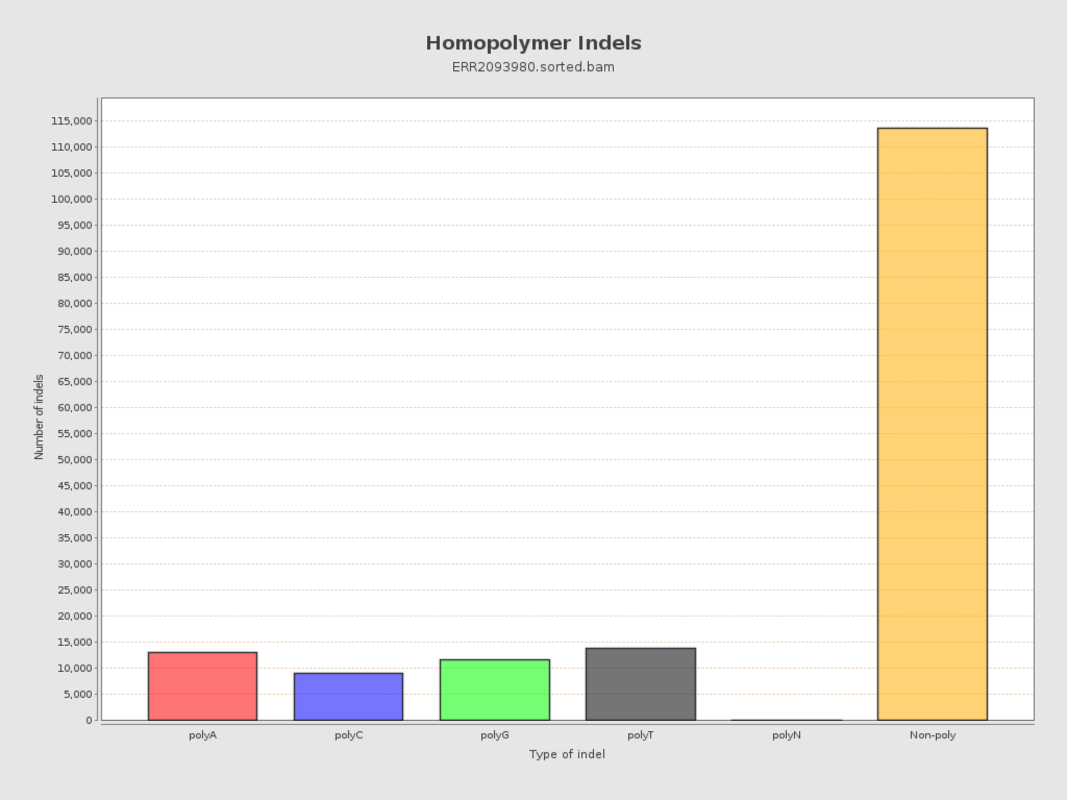
# 9. Results : Mapped Reads GC-content Distribution



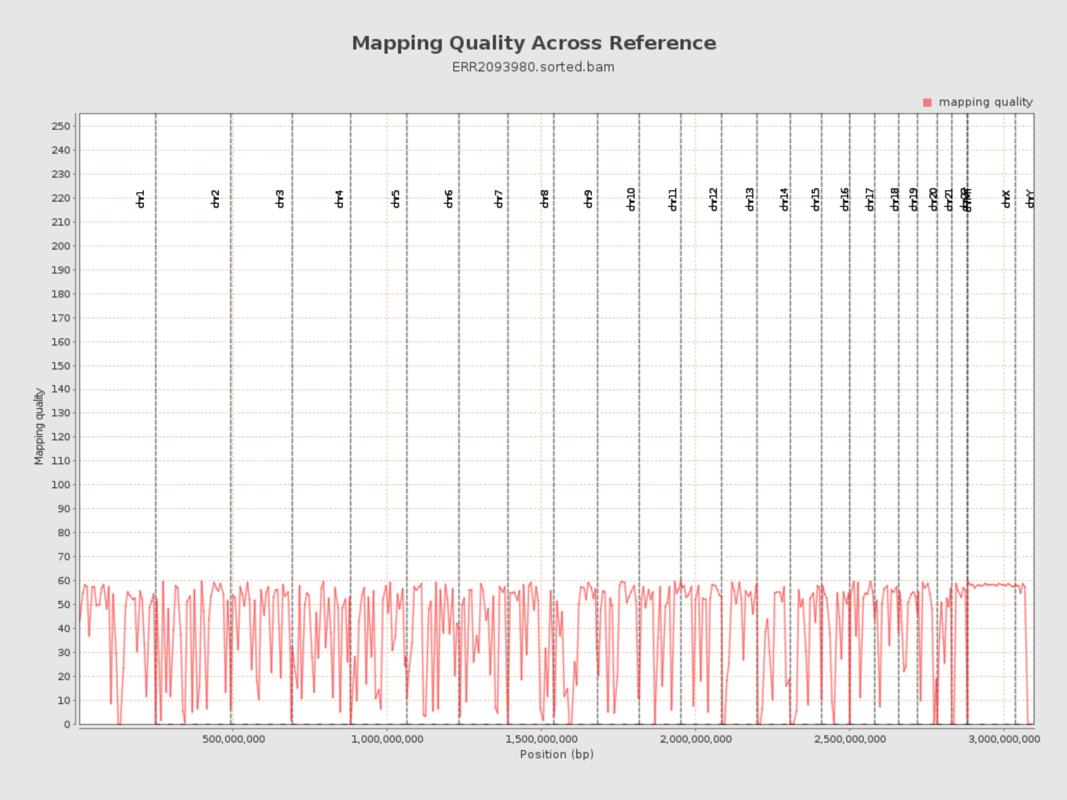
# 10. Results : Mapped Reads Clipping Profile



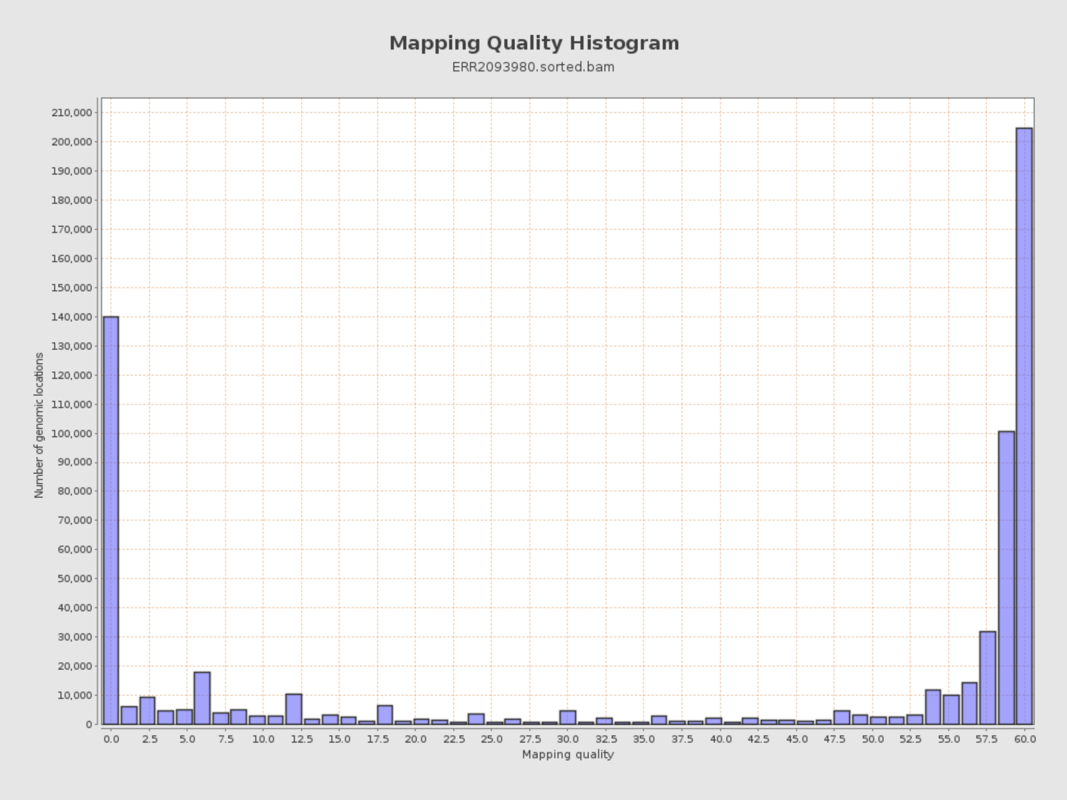
# 11. Results : Homopolymer Indels



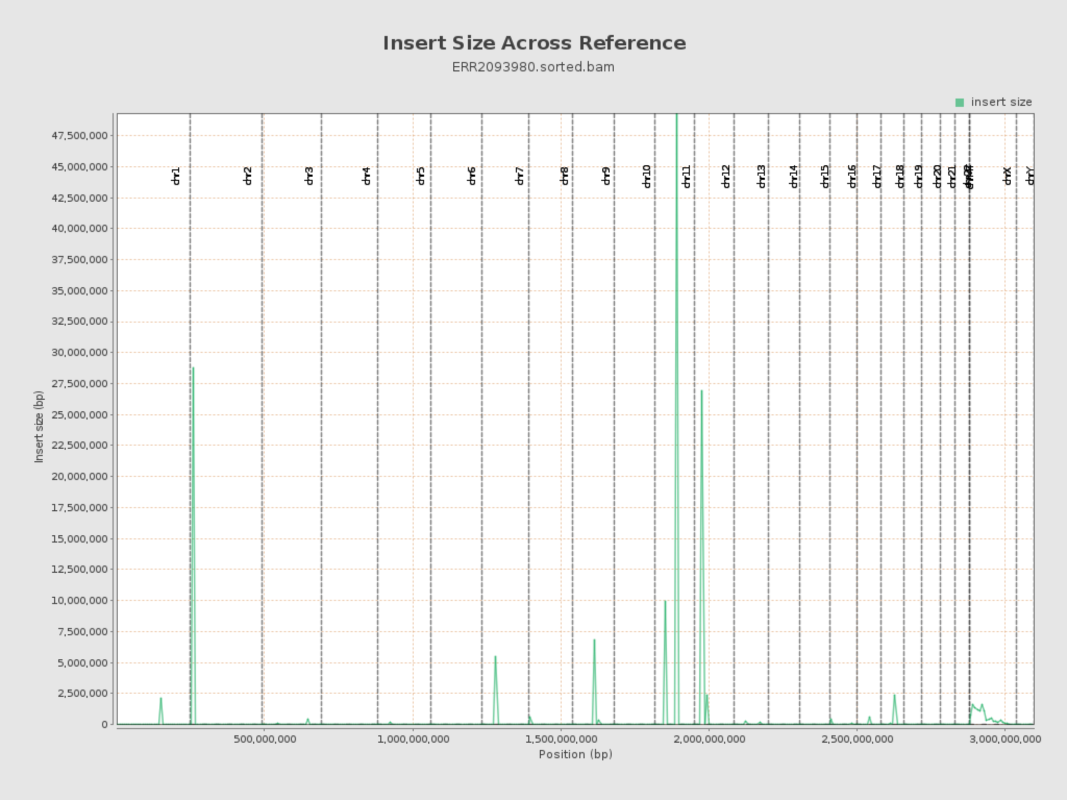
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram