# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/03/30 20:00:31*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046489.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_SRR2046489 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046489_1.fastq.gz SRR2046489_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Mar 30 20:00:30 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR2046489.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 10,103,356 |
| Mapped reads | 10,056,497 / 99.54% |
| Unmapped reads | 46,859 / 0.46% |
| Mapped paired reads | 10,056,497 / 99.54% |
| Mapped reads, first in pair | 5,035,830 / 49.84% |
| Mapped reads, second in pair | 5,020,667 / 49.69% |
| Mapped reads, both in pair | 10,024,590 / 99.22% |
| Mapped reads, singletons | 31,907 / 0.32% |
| Secondary alignments | 0 |
| Supplementary alignments | 50,034 / 0.5% |
| Read min/max/mean length | 30 / 100 / 100.2 |
| Duplicated reads (estimated) | 7,546,729 / 74.7% |
| Duplication rate | 38.31% |
| Clipped reads | 2,277,674 / 22.54% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 282,807,751 / 29.26% |
| Number/percentage of C's | 201,724,744 / 20.87% |
| Number/percentage of T's | 281,091,369 / 29.08% |
| Number/percentage of G's | 200,819,641 / 20.78% |
| Number/percentage of N's | 76,544 / 0.01% |
| | |

| | |
|---|---|
| GC Percentage | 41.65% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.3123 |
| Standard Deviation | 26.3578 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 52.9 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 16,513.92 |
| Standard Deviation | 1,243,297.23 |
| P25/Median/P75 | 103 / 129 / 162 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.41% |
| Mismatches | 3,801,018 |
| Insertions | 71,789 |
| Mapped reads with at least one insertion | 0.7% |
| Deletions | 83,393 |
| Mapped reads with at least one deletion | 0.8% |
| Homopolymer indels | 45.94% |

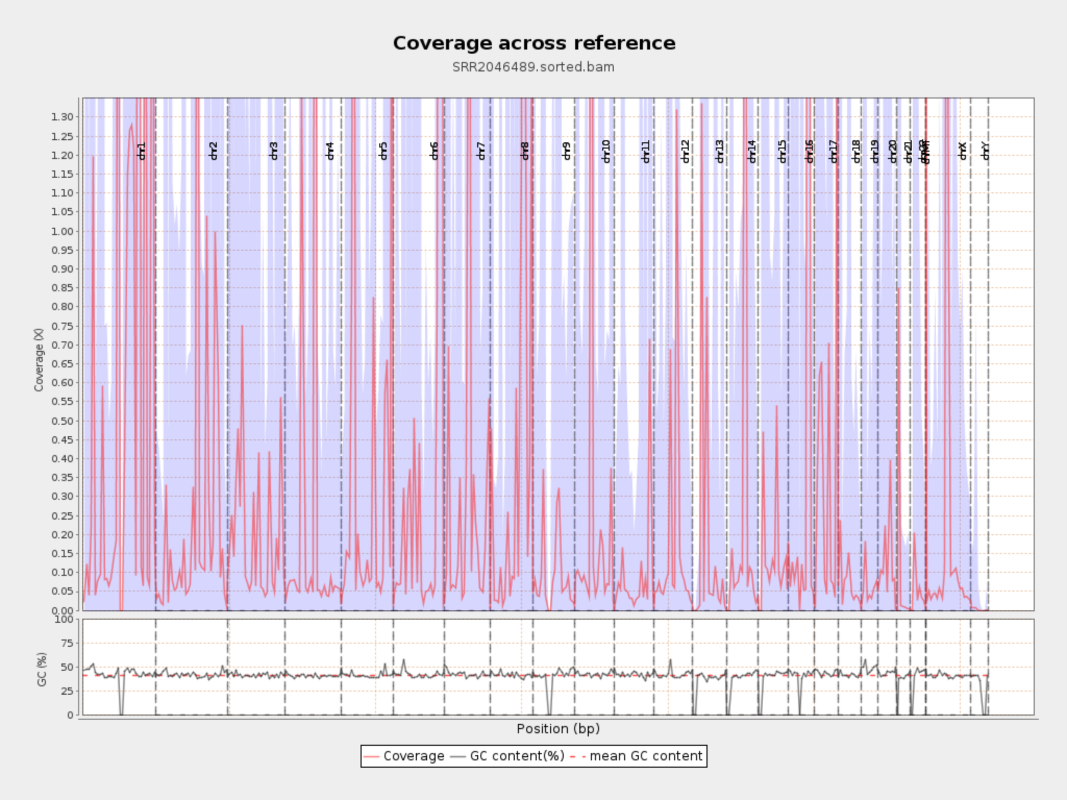
## 2.7. Chromosome stats

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

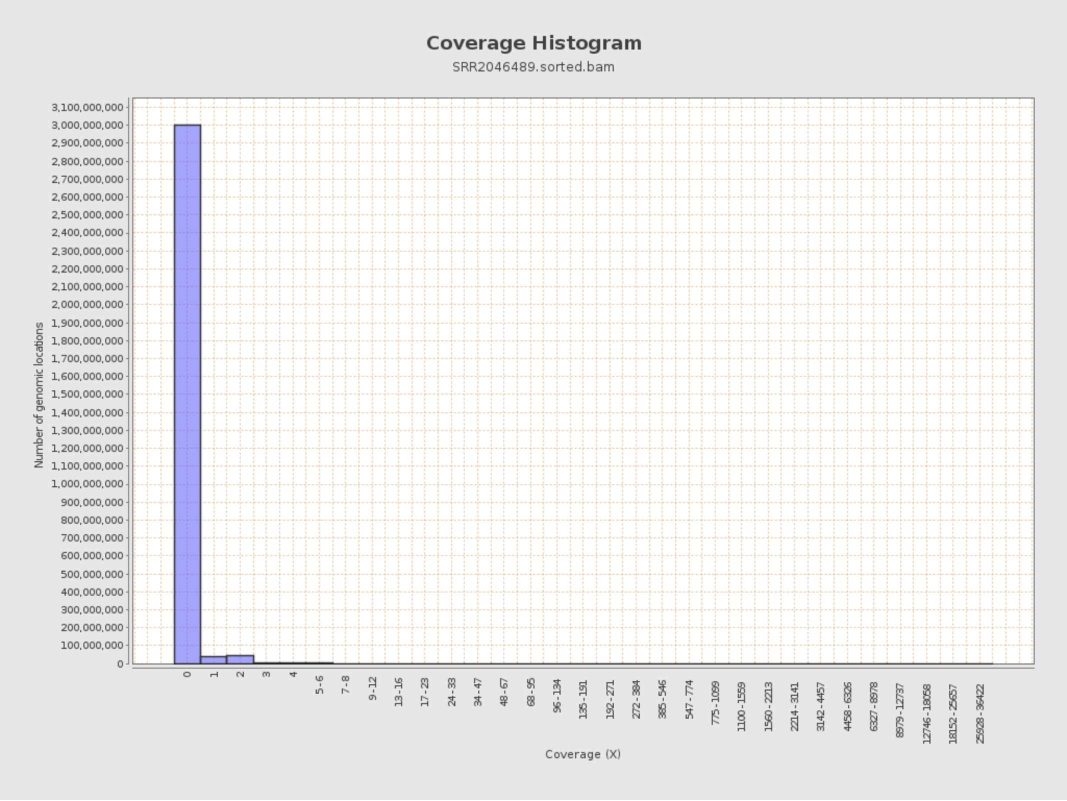
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 166878239 | 0.6695 | 32.8914 |
| chr2 | 243199373 | 68733125 | 0.2826 | 18.6589 |
| chr3 | 198022430 | 40177658 | 0.2029 | 11.3414 |
| chr4 | 191154276 | 56065165 | 0.2933 | 31.5137 |
| chr5 | 180915260 | 79137216 | 0.4374 | 31.8443 |
| chr6 | 171115067 | 82102382 | 0.4798 | 46.2249 |
| chr7 | 159138663 | 48981793 | 0.3078 | 19.4678 |
| chr8 | 146364022 | 137495955 | 0.9394 | 49.9496 |
| chr9 | 141213431 | 13691594 | 0.097 | 8.6981 |
| chr10 | 135534747 | 41121633 | 0.3034 | 38.9144 |
| chr11 | 135006516 | 12727416 | 0.0943 | 6.6513 |
| chr12 | 133851895 | 23546631 | 0.1759 | 10.9535 |
| chr13 | 115169878 | 20127228 | 0.1748 | 16.2073 |
| chr14 | 107349540 | 29234477 | 0.2723 | 18.5991 |
| chr15 | 102531392 | 15400753 | 0.1502 | 8.4777 |
| chr16 | 90354753 | 41697537 | 0.4615 | 34.6601 |
| chr17 | 81195210 | 27866921 | 0.3432 | 18.6527 |
| chr18 | 78077248 | 5947779 | 0.0762 | 2.9873 |
| chr19 | 59128983 | 3743267 | 0.0633 | 2.3608 |
| chr20 | 63025520 | 8425175 | 0.1337 | 8.4718 |
| chr21 | 48129895 | 6858811 | 0.1425 | 19.4434 |
| chr22 | 51304566 | 2760625 | 0.0538 | 4.1935 |
| chrMT | 16571 | 53299 | 3.2164 | 2.3614 |
| chrX | 155270560 | 33774517 | 0.2175 | 29.1755 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 196174 | 0.0033 | 0.2925 |

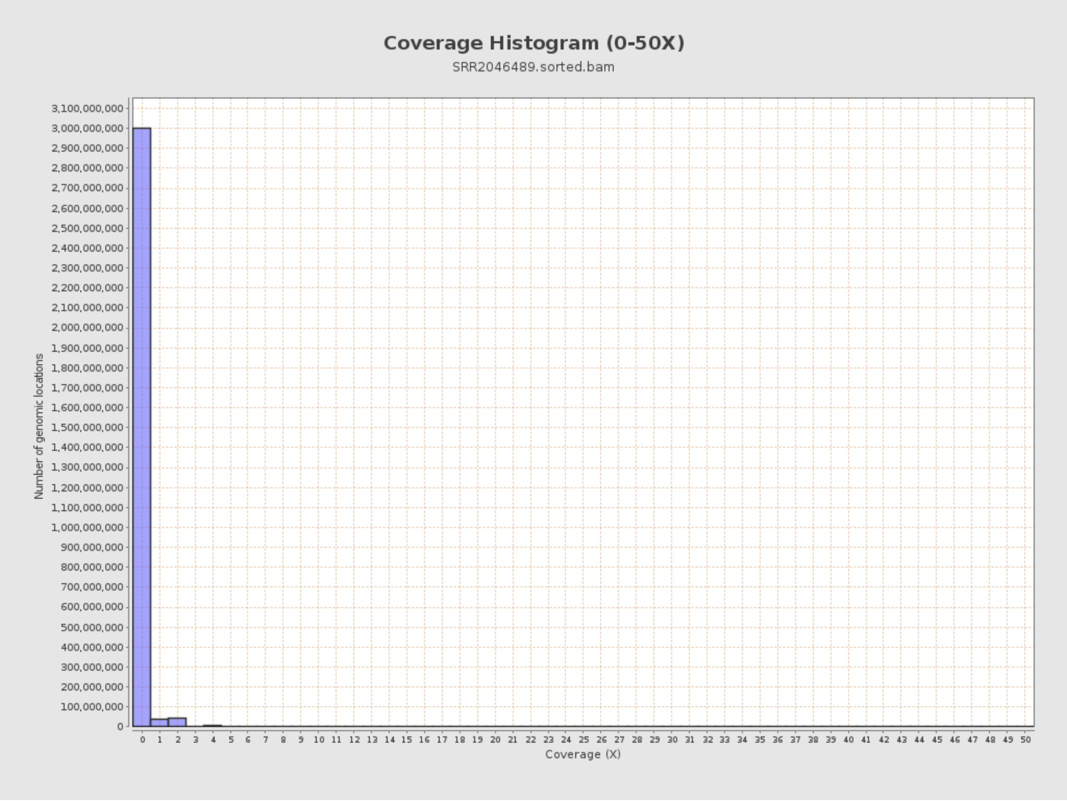
# 3. Results : Coverage across reference



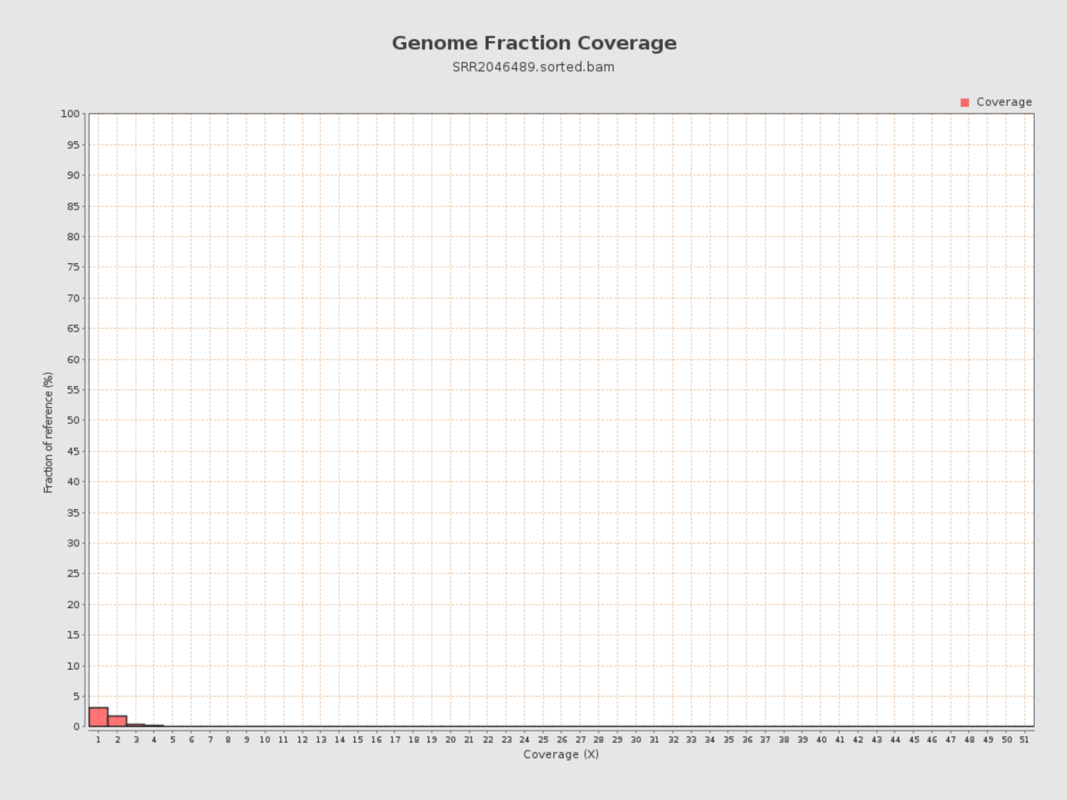
# 4. Results : Coverage Histogram



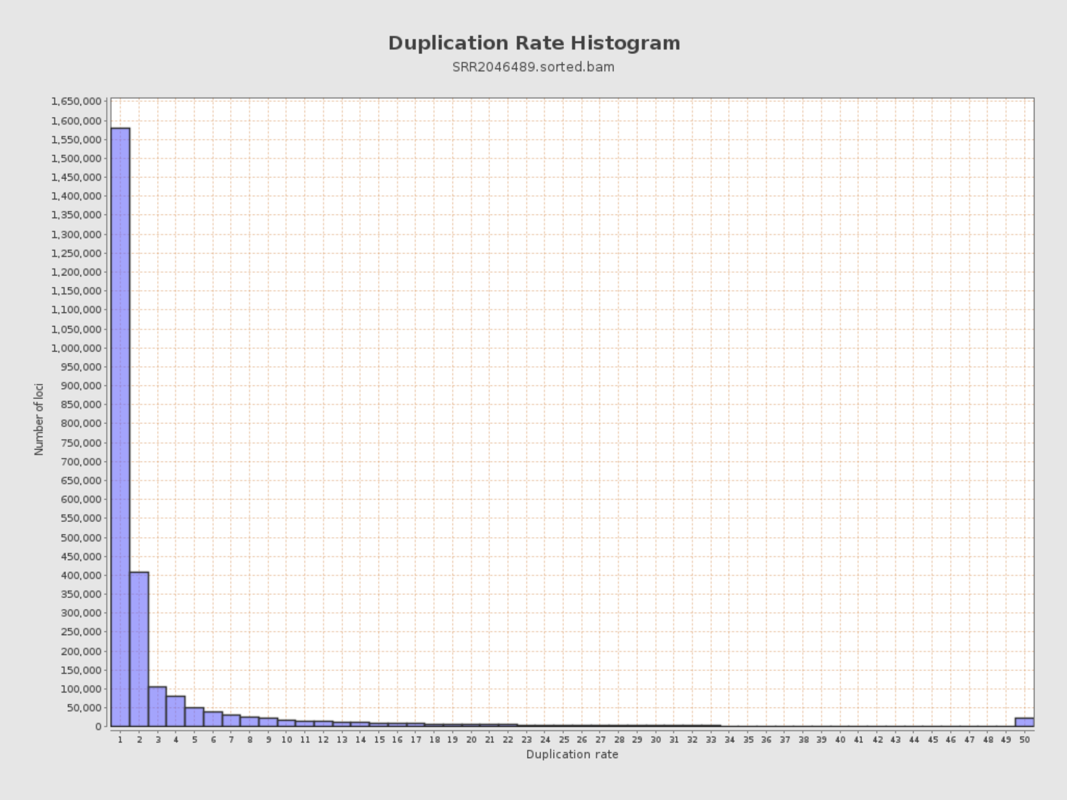
# 5. Results : Coverage Histogram (0-50X)



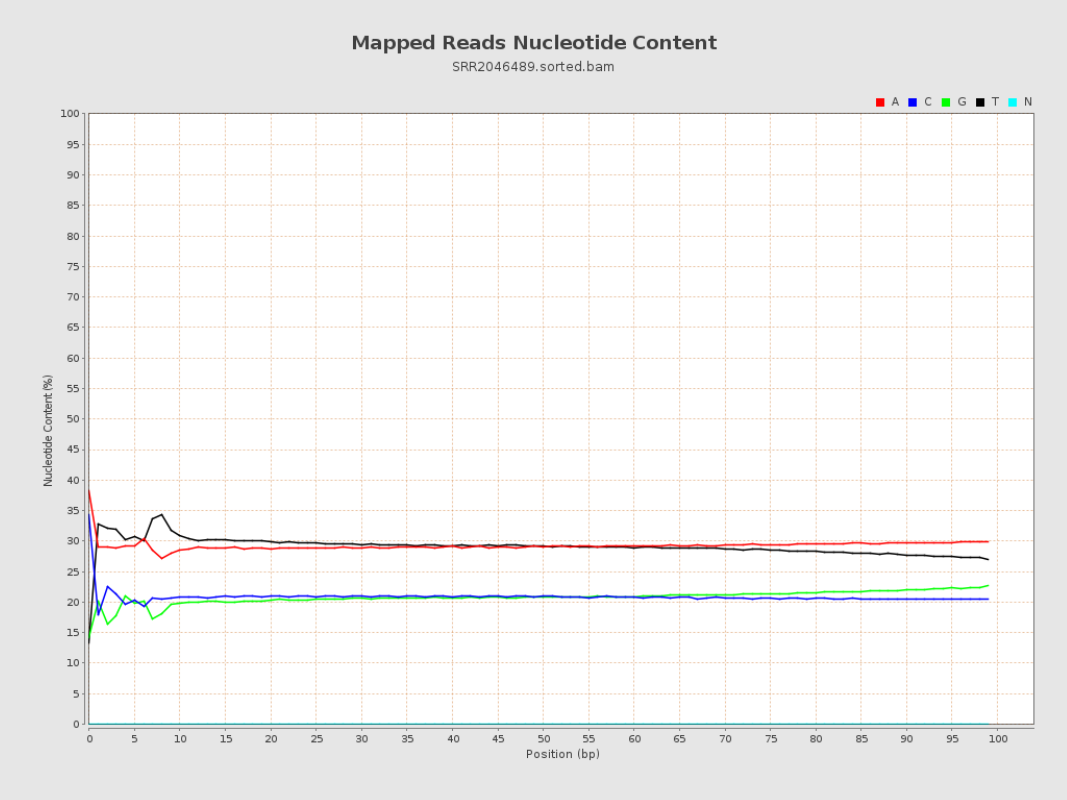
# 6. Results : Genome Fraction Coverage



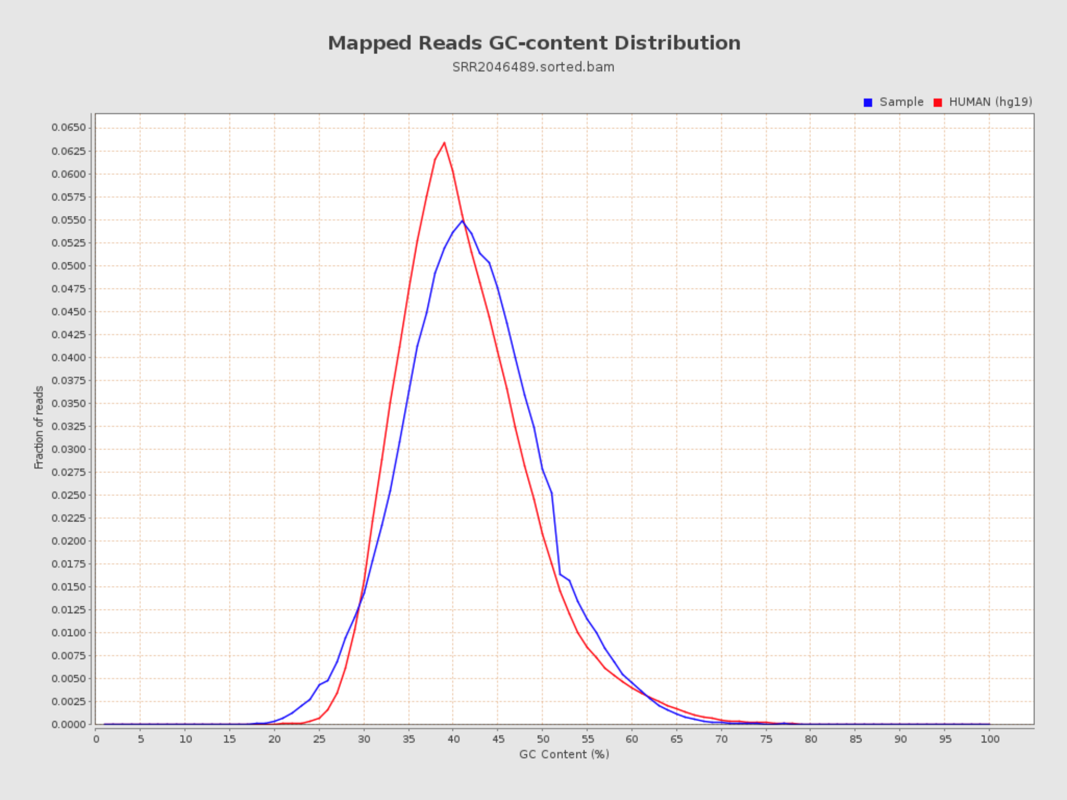
# 7. Results : Duplication Rate Histogram



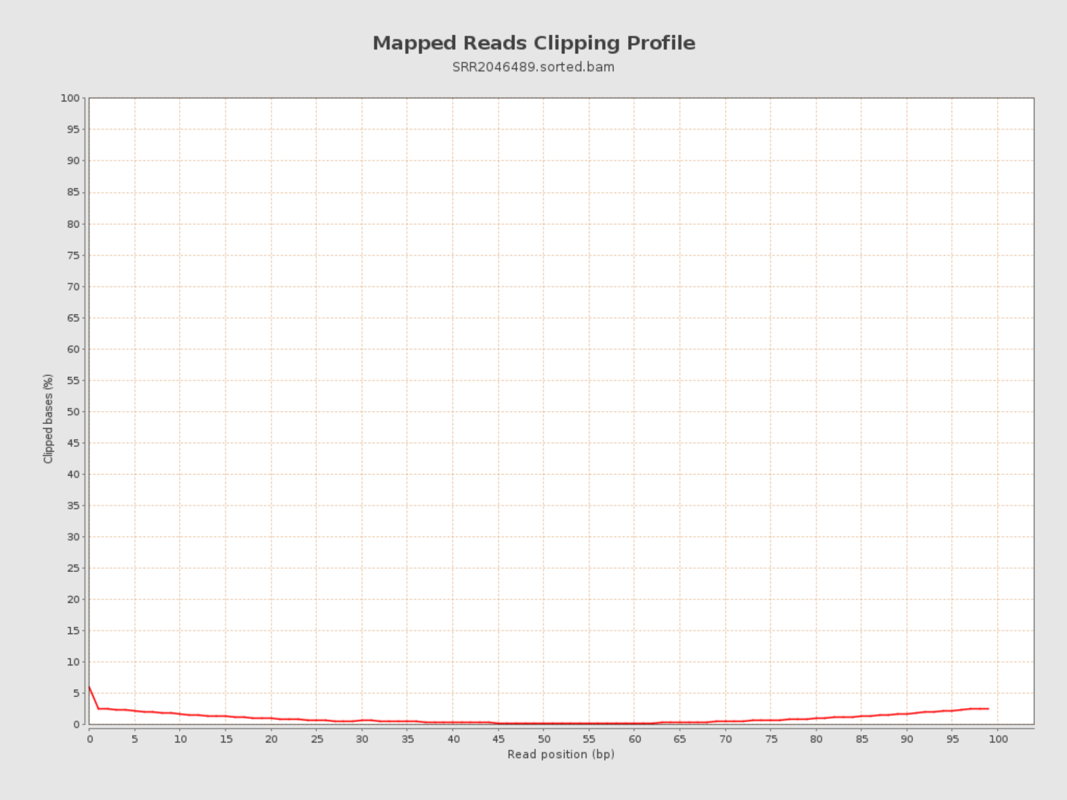
# 8. Results : Mapped Reads Nucleotide Content



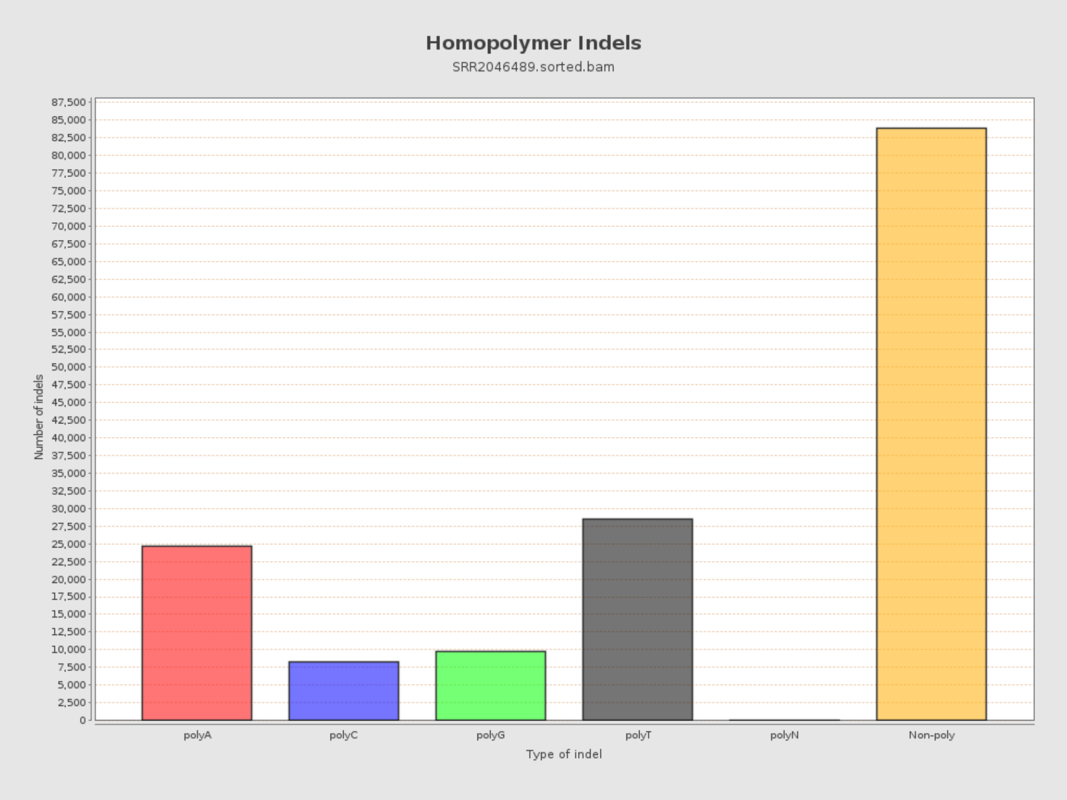
# 9. Results : Mapped Reads GC-content Distribution



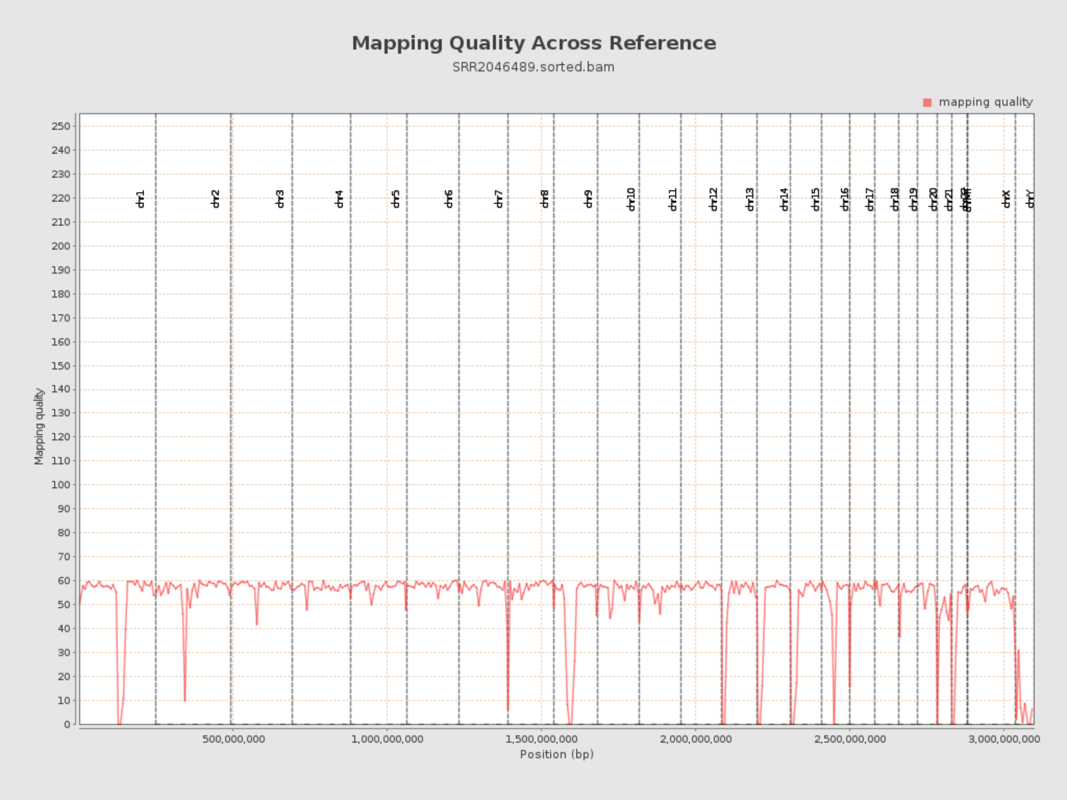
# 10. Results : Mapped Reads Clipping Profile



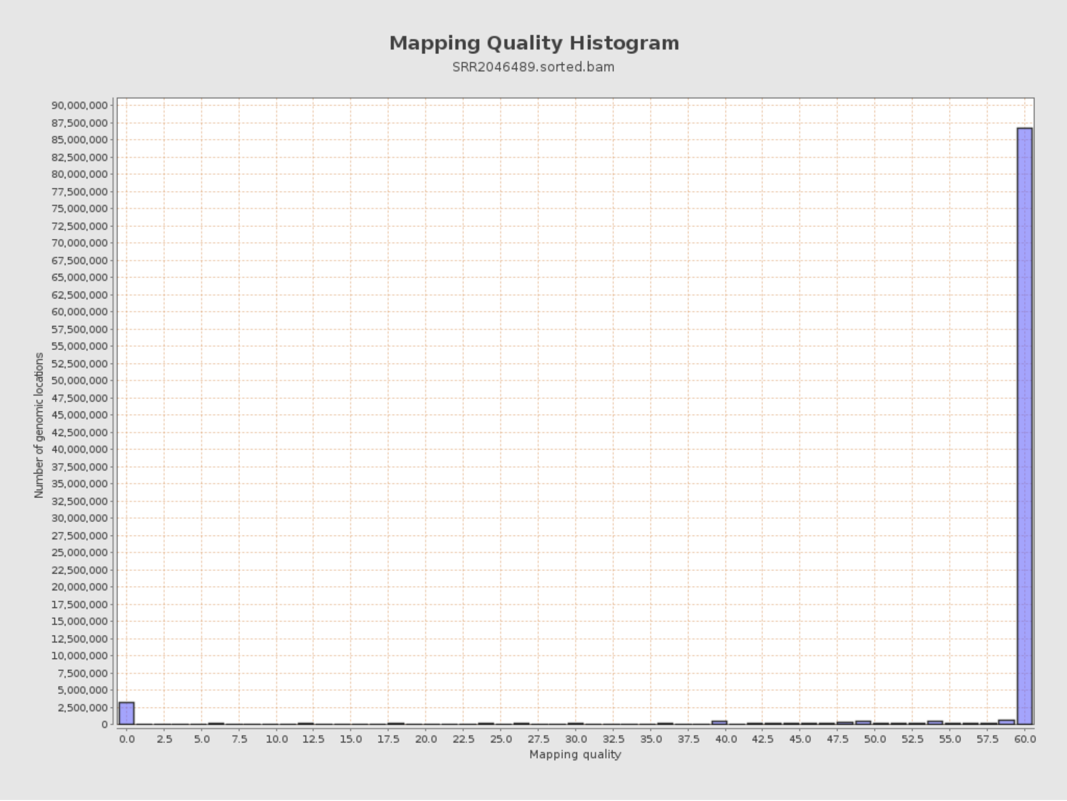
# 11. Results : Homopolymer Indels



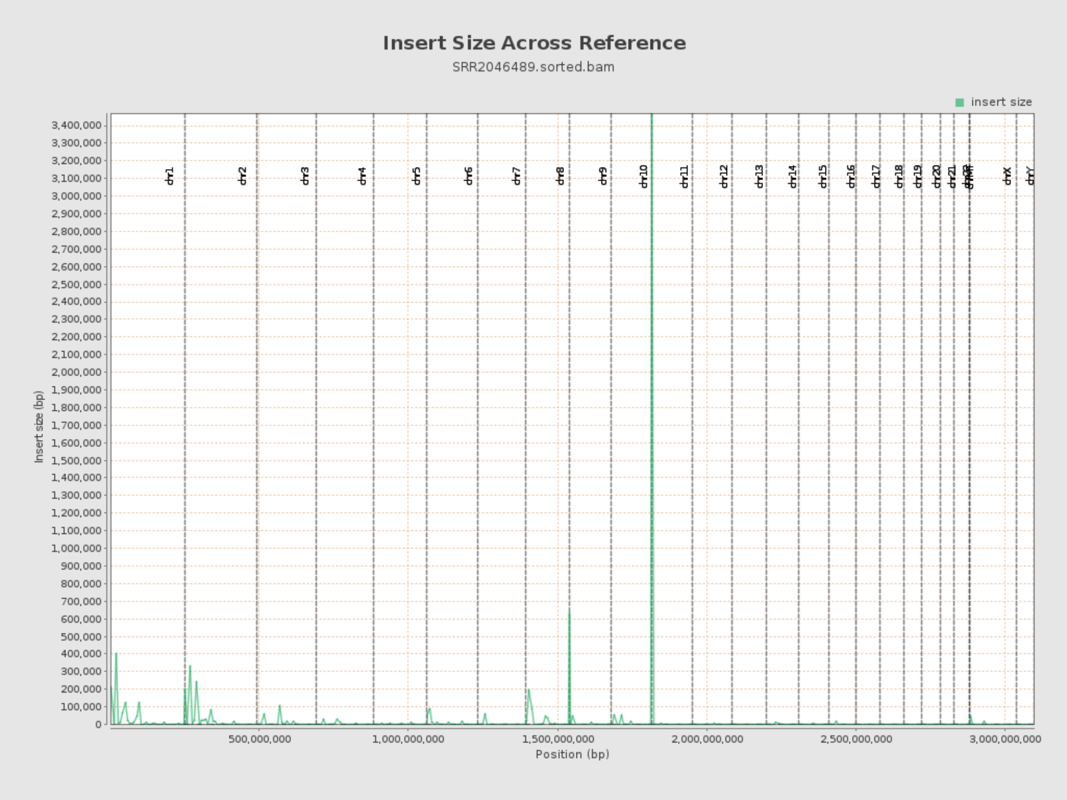
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram