# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/23 06:55:32*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR926966.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_SRR926966 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR926966_1.fastq.gz SRR926966_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Apr 23 06:55:31 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR926966.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 32,527,614 |
| Mapped reads | 31,932,464 / 98.17% |
| Unmapped reads | 595,150 / 1.83% |
| Mapped paired reads | 31,932,464 / 98.17% |
| Mapped reads, first in pair | 15,981,160 / 49.13% |
| Mapped reads, second in pair | 15,951,304 / 49.04% |
| Mapped reads, both in pair | 31,611,234 / 97.18% |
| Mapped reads, singletons | 321,230 / 0.99% |
| Secondary alignments | 0 |
| Supplementary alignments | 506,111 / 1.56% |
| Read min/max/mean length | 30 / 101 / 101.64 |
| Duplicated reads (estimated) | 2,579,980 / 7.93% |
| Duplication rate | 6.37% |
| Clipped reads | 9,227,144 / 28.37% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 849,502,786 / 28.31% |
| Number/percentage of C's | 609,064,704 / 20.3% |
| Number/percentage of T's | 862,316,714 / 28.74% |
| Number/percentage of G's | 679,615,618 / 22.65% |
| Number/percentage of N's | 348,382 / 0.01% |
| | |

| | |
|---|---|
| GC Percentage | 42.94% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.9701 |
| Standard Deviation | 3.7712 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.3 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 146,960.66 |
| Standard Deviation | 3,787,975.32 |
| P25/Median/P75 | 140 / 178 / 235 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.99% |
| Mismatches | 28,844,664 |
| Insertions | 488,887 |
| Mapped reads with at least one insertion | 1.51% |
| Deletions | 1,567,595 |
| Mapped reads with at least one deletion | 4.78% |
| Homopolymer indels | 52.55% |

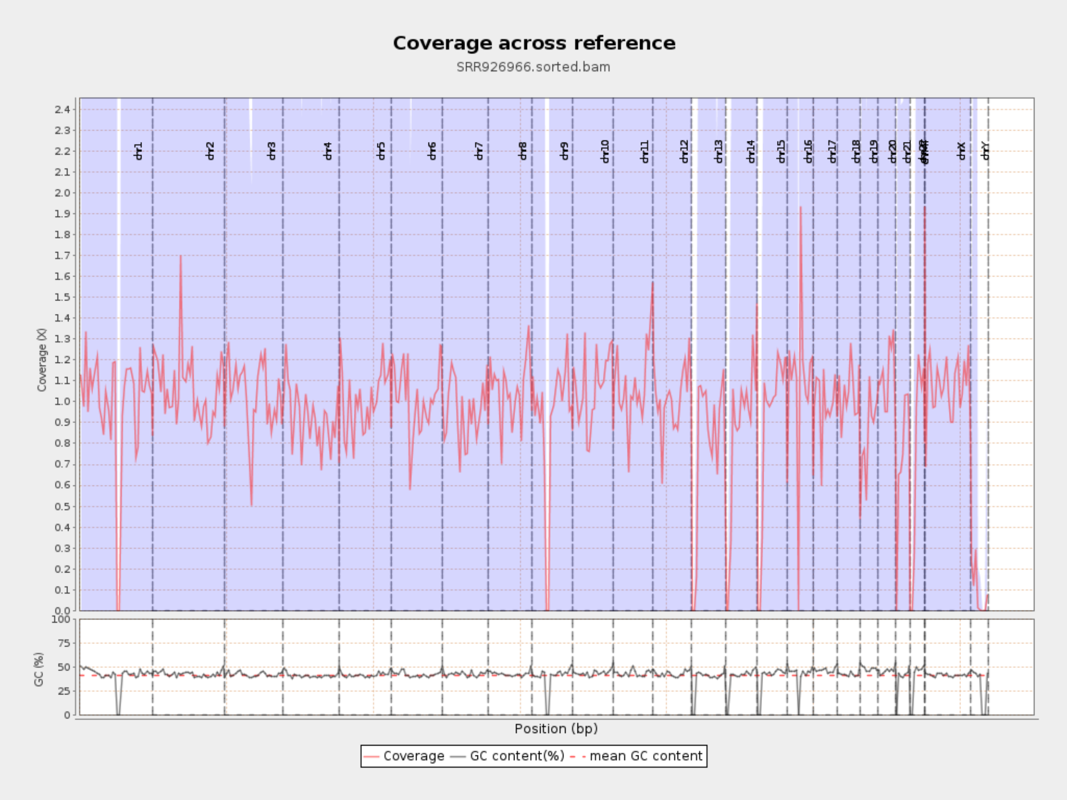
## 2.7. Chromosome stats

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

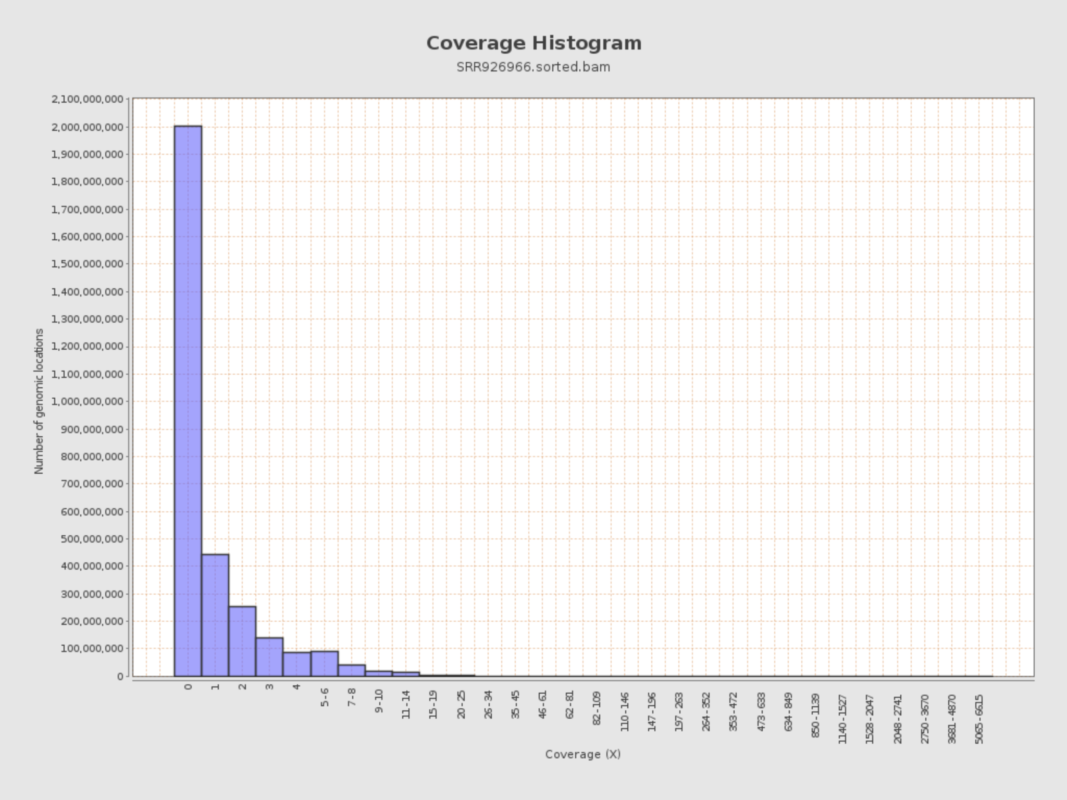
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 245987451 | 0.9869 | 4.5226 |
| chr2 | 243199373 | 260243569 | 1.0701 | 6.7586 |
| chr3 | 198022430 | 204408136 | 1.0322 | 2.0206 |
| chr4 | 191154276 | 176519299 | 0.9234 | 3.025 |
| chr5 | 180915260 | 182963009 | 1.0113 | 1.9744 |
| chr6 | 171115067 | 174105940 | 1.0175 | 3.4708 |
| chr7 | 159138663 | 151899011 | 0.9545 | 2.8296 |
| chr8 | 146364022 | 155352405 | 1.0614 | 2.4876 |
| chr9 | 141213431 | 128491713 | 0.9099 | 4.3767 |
| chr10 | 135534747 | 145481193 | 1.0734 | 5.2613 |
| chr11 | 135006516 | 144473071 | 1.0701 | 3.2944 |
| chr12 | 133851895 | 135986109 | 1.0159 | 2.1101 |
| chr13 | 115169878 | 91481129 | 0.7943 | 1.77 |
| chr14 | 107349540 | 89296440 | 0.8318 | 1.8876 |
| chr15 | 102531392 | 90227235 | 0.88 | 1.9587 |
| chr16 | 90354753 | 97975867 | 1.0843 | 7.4131 |
| chr17 | 81195210 | 80088197 | 0.9864 | 3.6211 |
| chr18 | 78077248 | 81770723 | 1.0473 | 4.7467 |
| chr19 | 59128983 | 49525591 | 0.8376 | 3.1513 |
| chr20 | 63025520 | 71283624 | 1.131 | 2.3534 |
| chr21 | 48129895 | 36359301 | 0.7554 | 2.7887 |
| chr22 | 51304566 | 37992926 | 0.7405 | 1.9086 |
| chrMT | 16571 | 32097 | 1.9369 | 2.3619 |
| chrX | 155270560 | 166049384 | 1.0694 | 2.3491 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 5104386 | 0.086 | 2.7351 |

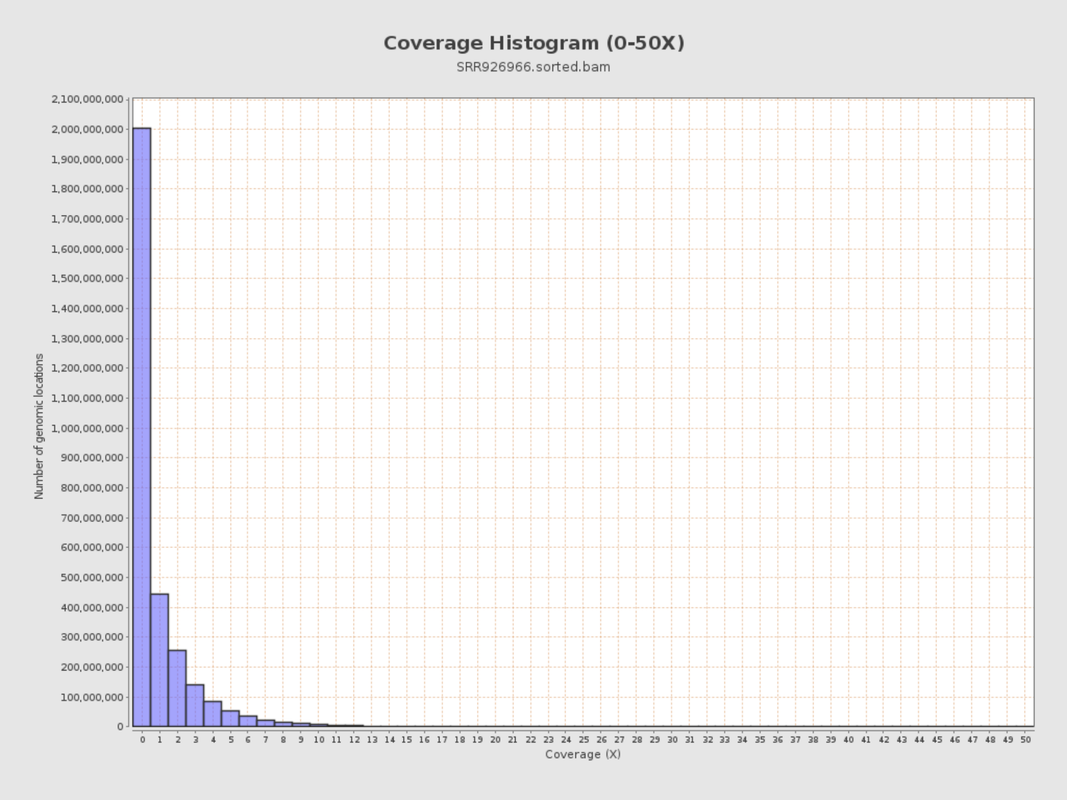
# 3. Results : Coverage across reference



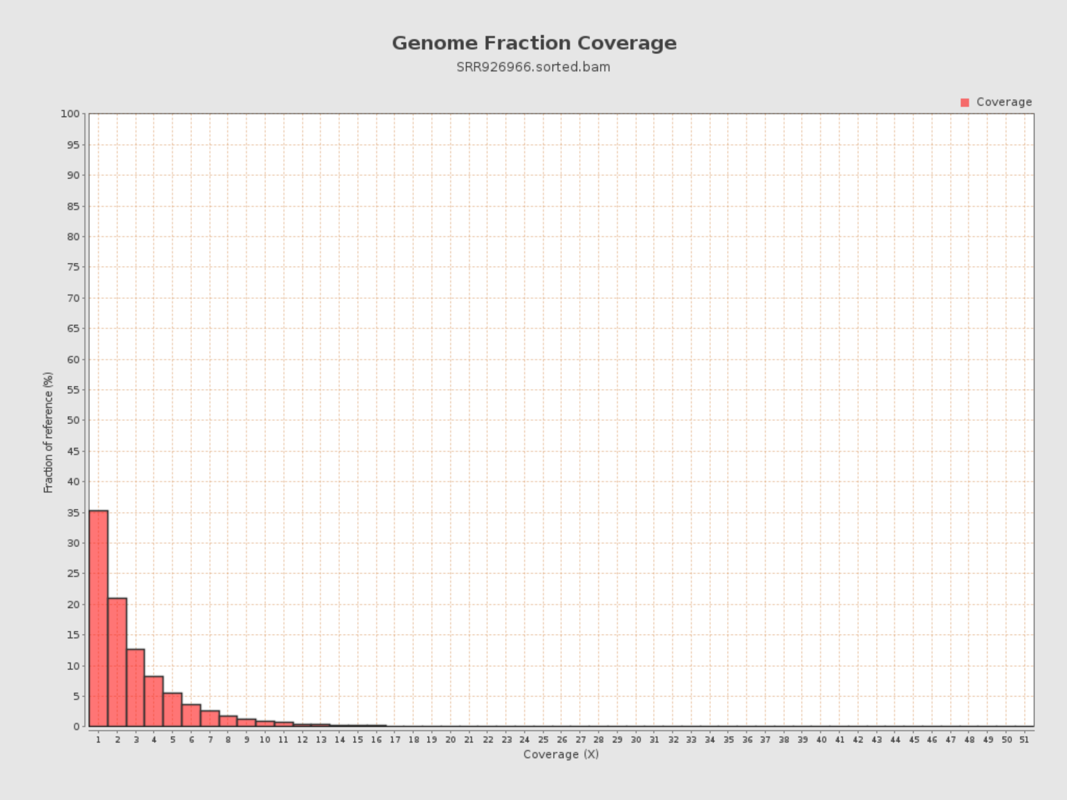
# 4. Results : Coverage Histogram



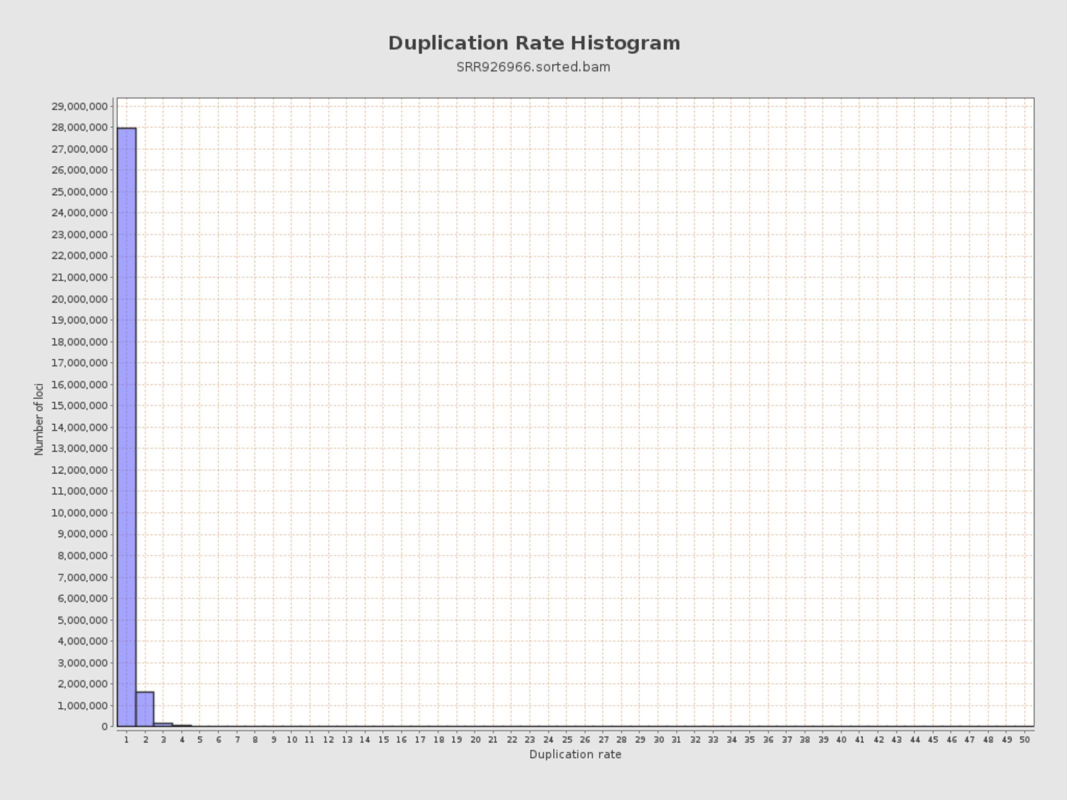
# 5. Results : Coverage Histogram (0-50X)



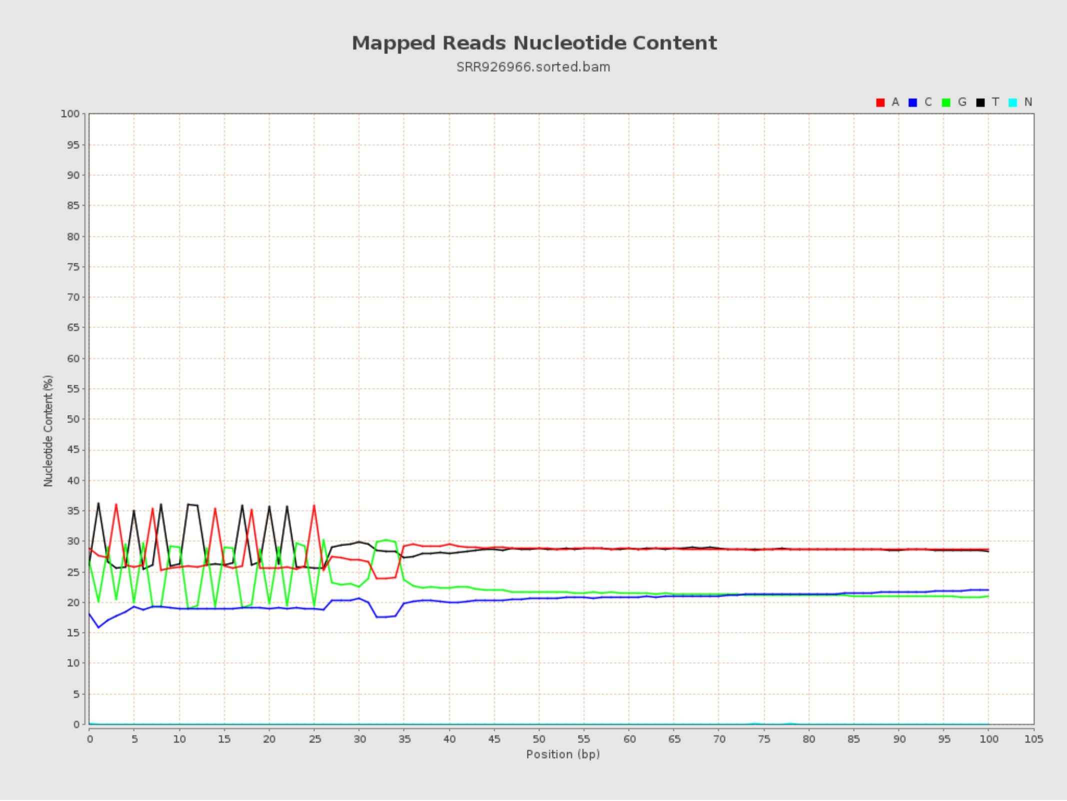
# 6. Results : Genome Fraction Coverage



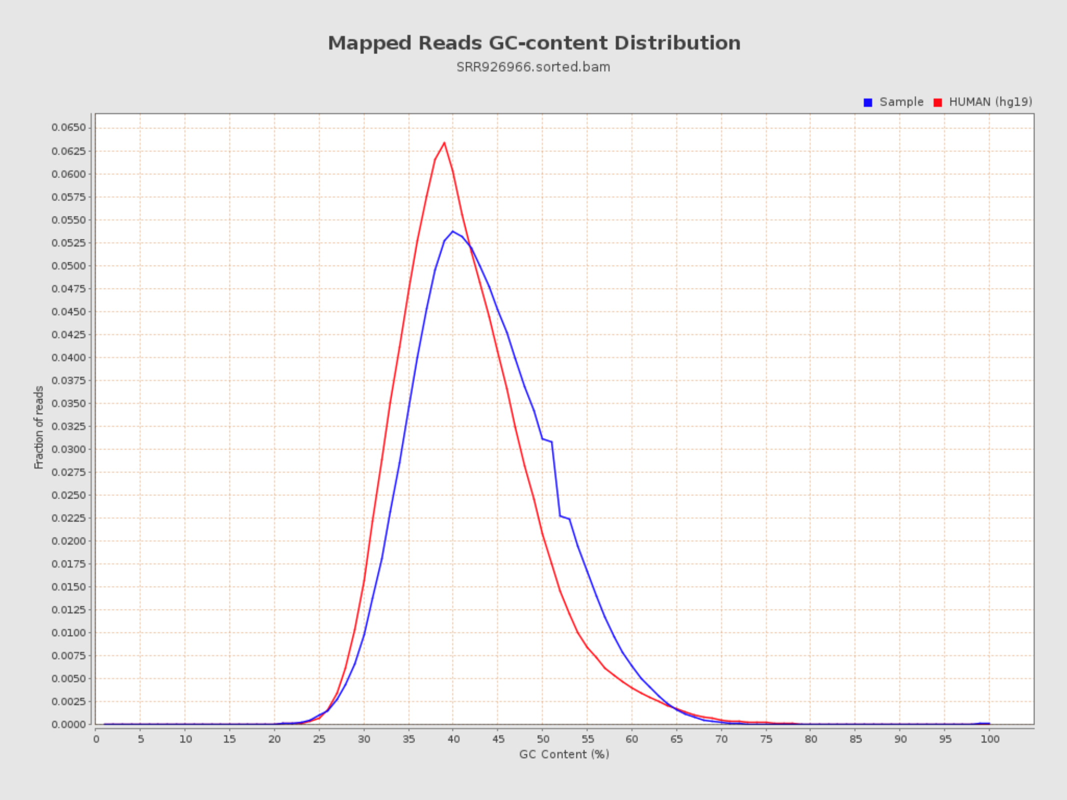
# 7. Results : Duplication Rate Histogram



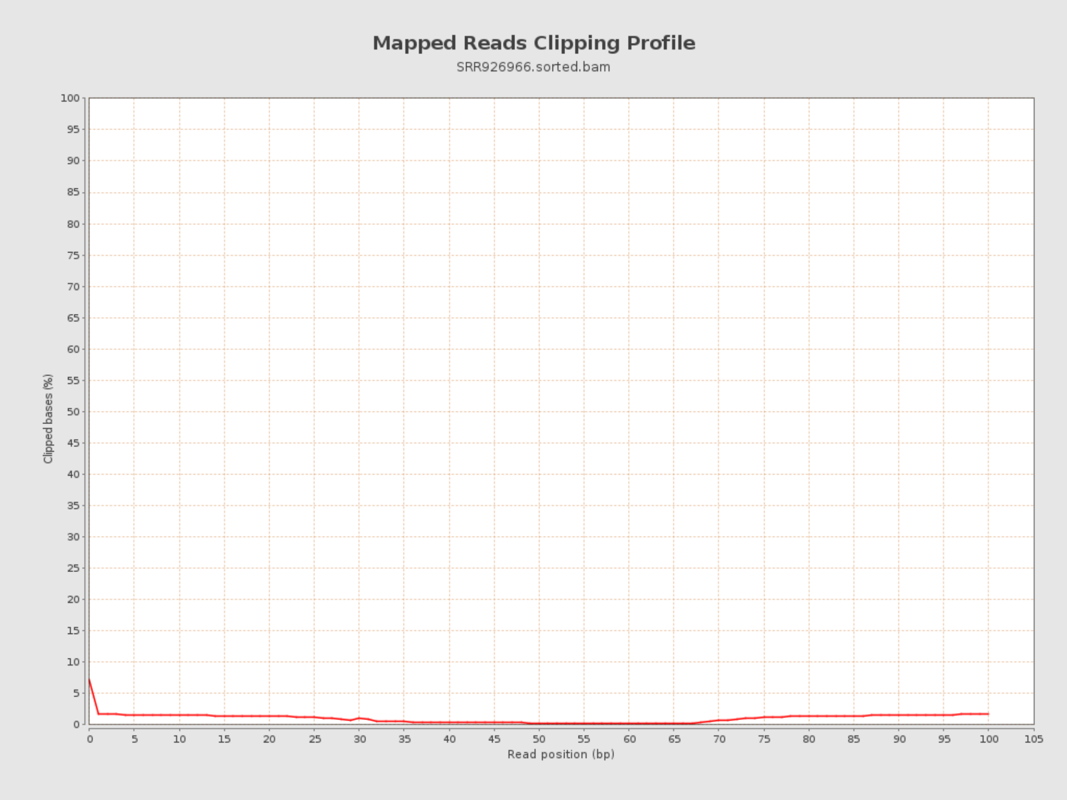
# 8. Results : Mapped Reads Nucleotide Content



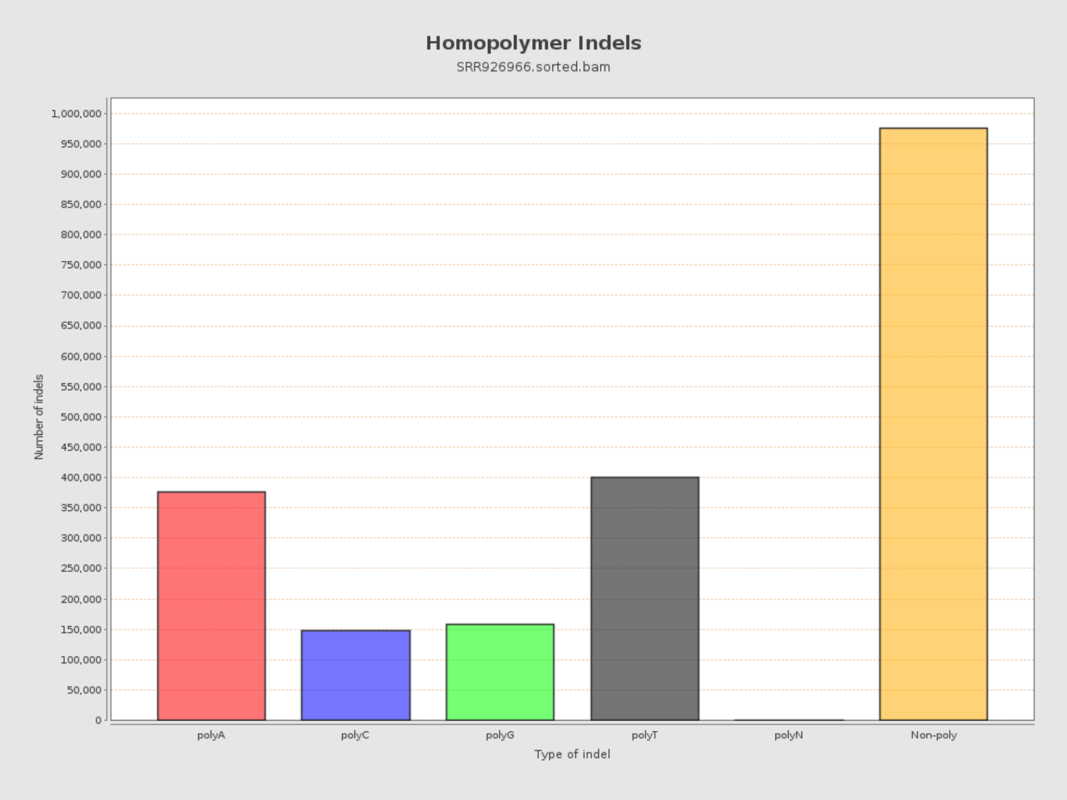
# 9. Results : Mapped Reads GC-content Distribution



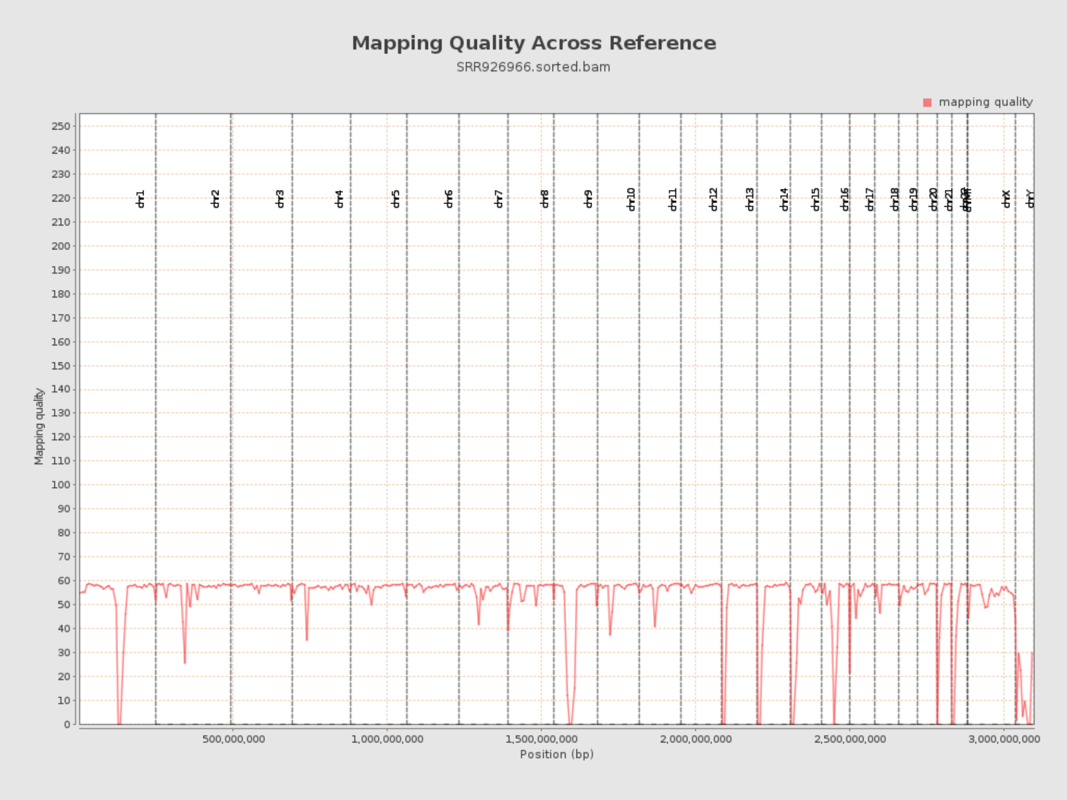
# 10. Results : Mapped Reads Clipping Profile



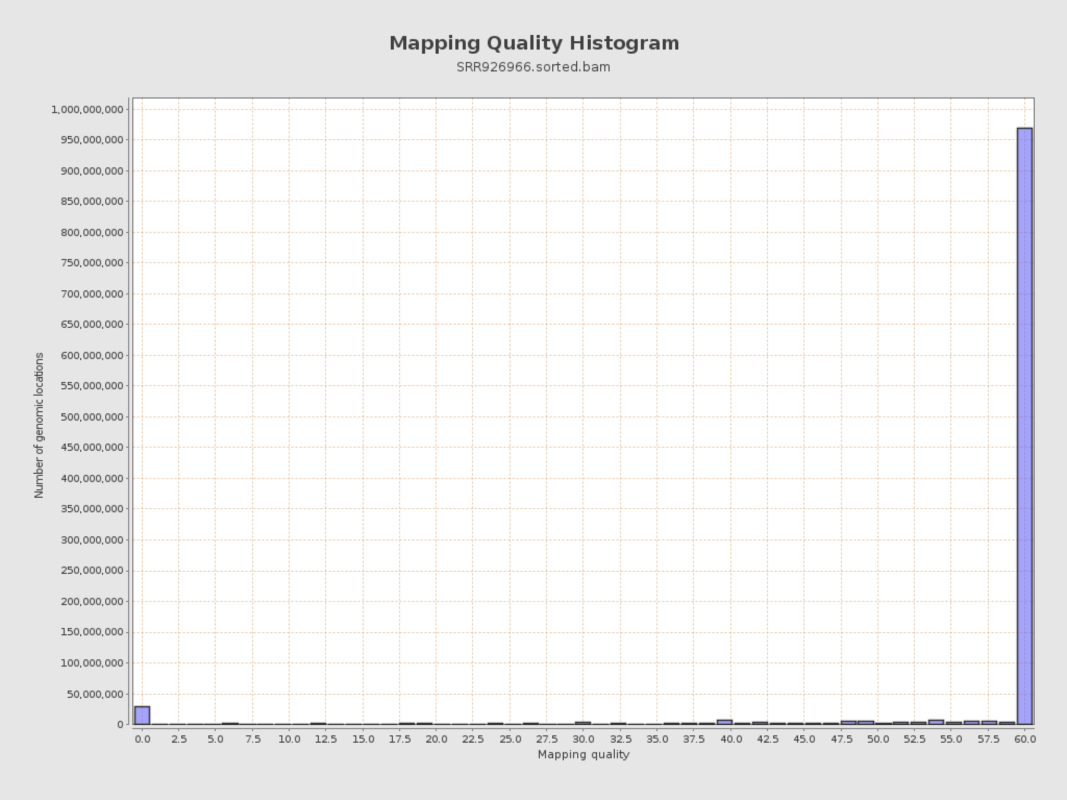
# 11. Results : Homopolymer Indels



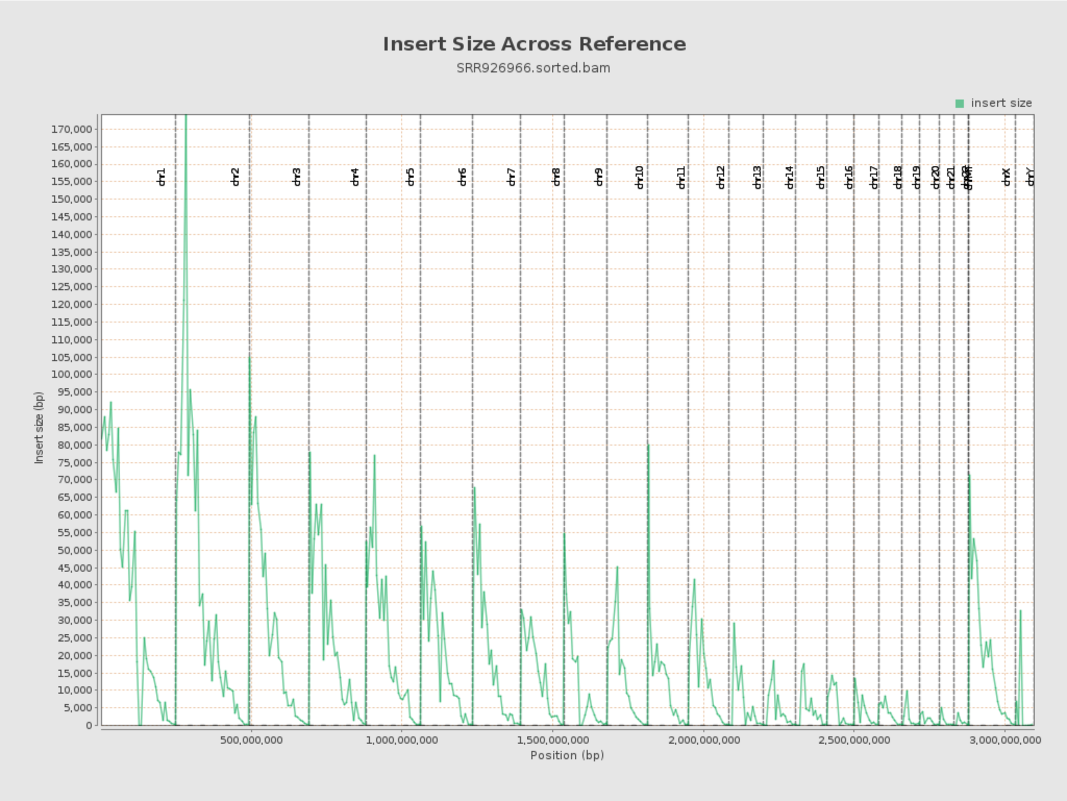
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram