# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/24 21:18:53*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR927047.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_SRR927047 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR927047_1.fastq.gz SRR927047_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Apr 24 21:18:53 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR927047.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 32,316,992 |
| Mapped reads | 31,609,885 / 97.81% |
| Unmapped reads | 707,107 / 2.19% |
| Mapped paired reads | 31,609,885 / 97.81% |
| Mapped reads, first in pair | 15,865,147 / 49.09% |
| Mapped reads, second in pair | 15,744,738 / 48.72% |
| Mapped reads, both in pair | 31,193,784 / 96.52% |
| Mapped reads, singletons | 416,101 / 1.29% |
| Secondary alignments | 0 |
| Supplementary alignments | 517,199 / 1.6% |
| Read min/max/mean length | 30 / 101 / 101.66 |
| Duplicated reads (estimated) | 2,564,740 / 7.94% |
| Duplication rate | 6.26% |
| Clipped reads | 10,915,976 / 33.78% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 830,326,848 / 28.43% |
| Number/percentage of C's | 579,978,123 / 19.86% |
| Number/percentage of T's | 846,763,445 / 28.99% |
| Number/percentage of G's | 663,304,240 / 22.71% |
| Number/percentage of N's | 441,922 / 0.02% |
| | |

| | |
|---|---|
| GC Percentage | 42.57% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.9442 |
| Standard Deviation | 3.6148 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 52.95 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 181,293.84 |
| Standard Deviation | 4,199,703.37 |
| P25/Median/P75 | 142 / 184 / 245 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 1.05% |
| Mismatches | 29,887,790 |
| Insertions | 480,129 |
| Mapped reads with at least one insertion | 1.49% |
| Deletions | 1,483,097 |
| Mapped reads with at least one deletion | 4.57% |
| Homopolymer indels | 52.15% |

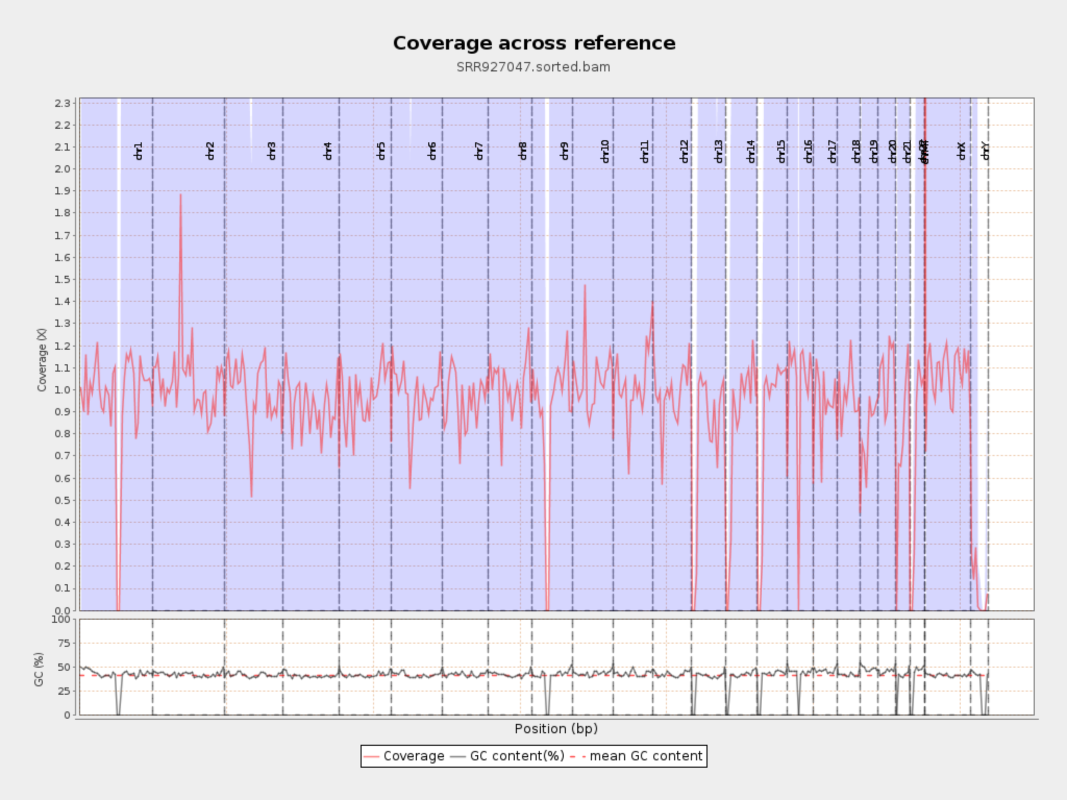
## 2.7. Chromosome stats

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

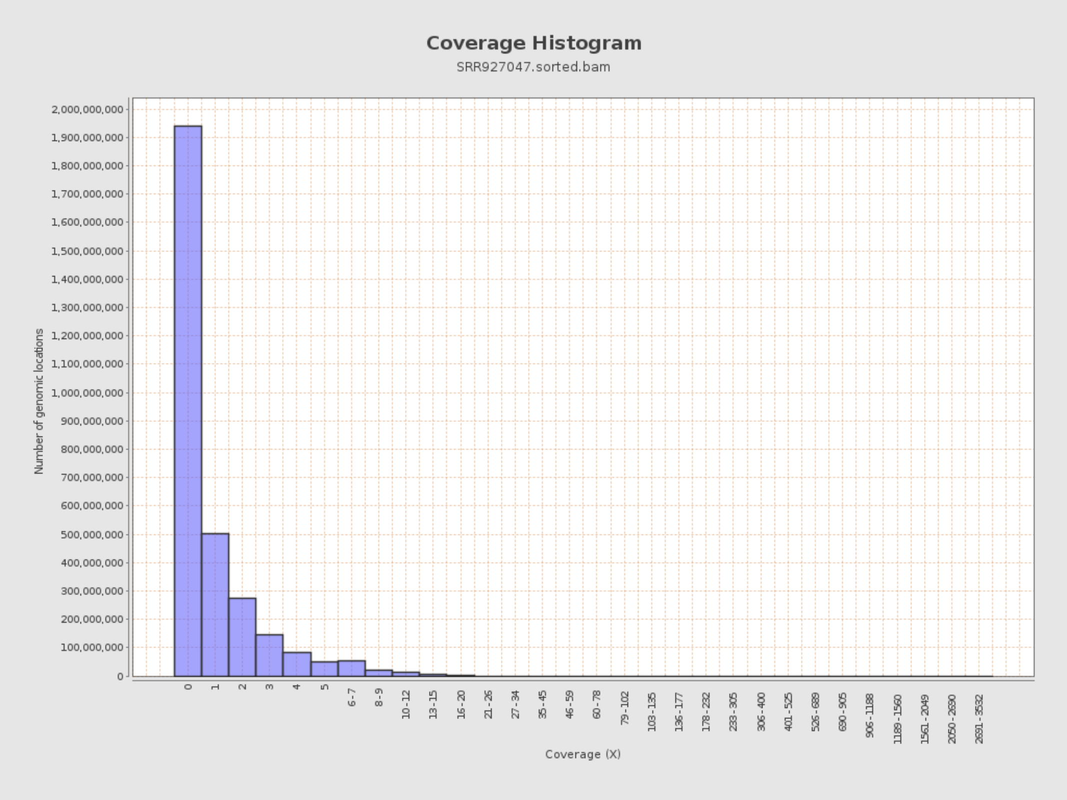
|  |  | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 238154655 | 0.9555 | 4.1363 |
| chr2 | 243199373 | 254761018 | 1.0475 | 6.3292 |
| chr3 | 198022430 | 197025795 | 0.995 | 1.856 |
| chr4 | 191154276 | 177762824 | 0.9299 | 2.683 |
| chr5 | 180915260 | 177493487 | 0.9811 | 1.835 |
| chr6 | 171115067 | 167713489 | 0.9801 | 1.8947 |
| chr7 | 159138663 | 152019493 | 0.9553 | 2.4117 |
| chr8 | 146364022 | 148444212 | 1.0142 | 2.2858 |
| chr9 | 141213431 | 124771916 | 0.8836 | 4.3249 |
| chr10 | 135534747 | 142626951 | 1.0523 | 6.1627 |
| chr11 | 135006516 | 137570895 | 1.019 | 2.7409 |
| chr12 | 133851895 | 131452404 | 0.9821 | 1.8683 |
| chr13 | 115169878 | 89016669 | 0.7729 | 1.623 |
| chr14 | 107349540 | 88342092 | 0.8229 | 1.7539 |
| chr15 | 102531392 | 85909399 | 0.8379 | 1.7479 |
| chr16 | 90354753 | 89443209 | 0.9899 | 3.7815 |
| chr17 | 81195210 | 76022114 | 0.9363 | 2.7455 |
| chr18 | 78077248 | 77290835 | 0.9899 | 4.3856 |
| chr19 | 59128983 | 47341578 | 0.8006 | 2.6734 |
| chr20 | 63025520 | 67409547 | 1.0696 | 2.0947 |
| chr21 | 48129895 | 37571037 | 0.7806 | 2.5371 |
| chr22 | 51304566 | 36045313 | 0.7026 | 1.7163 |
| chrMT | 16571 | 7206051 | 434.8592 | 333.3296 |
| chrX | 155270560 | 166247177 | 1.0707 | 2.2843 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 5310719 | 0.0894 | 3.7904 |

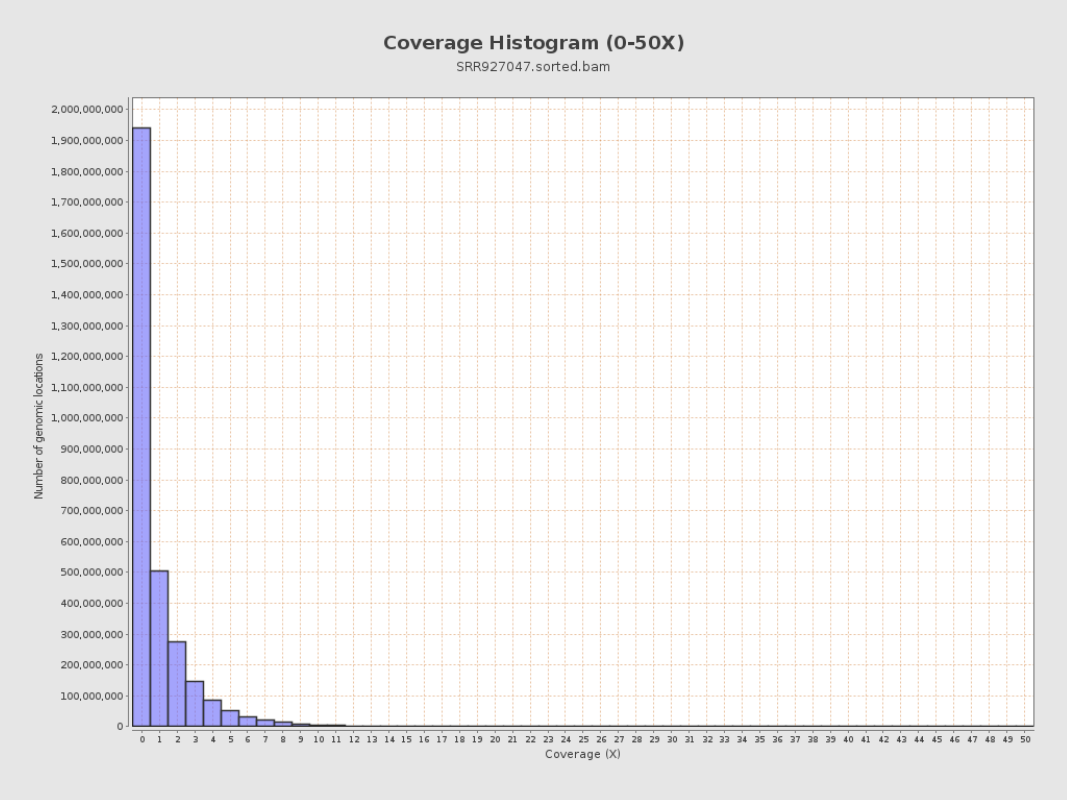
# 3. Results : Coverage across reference



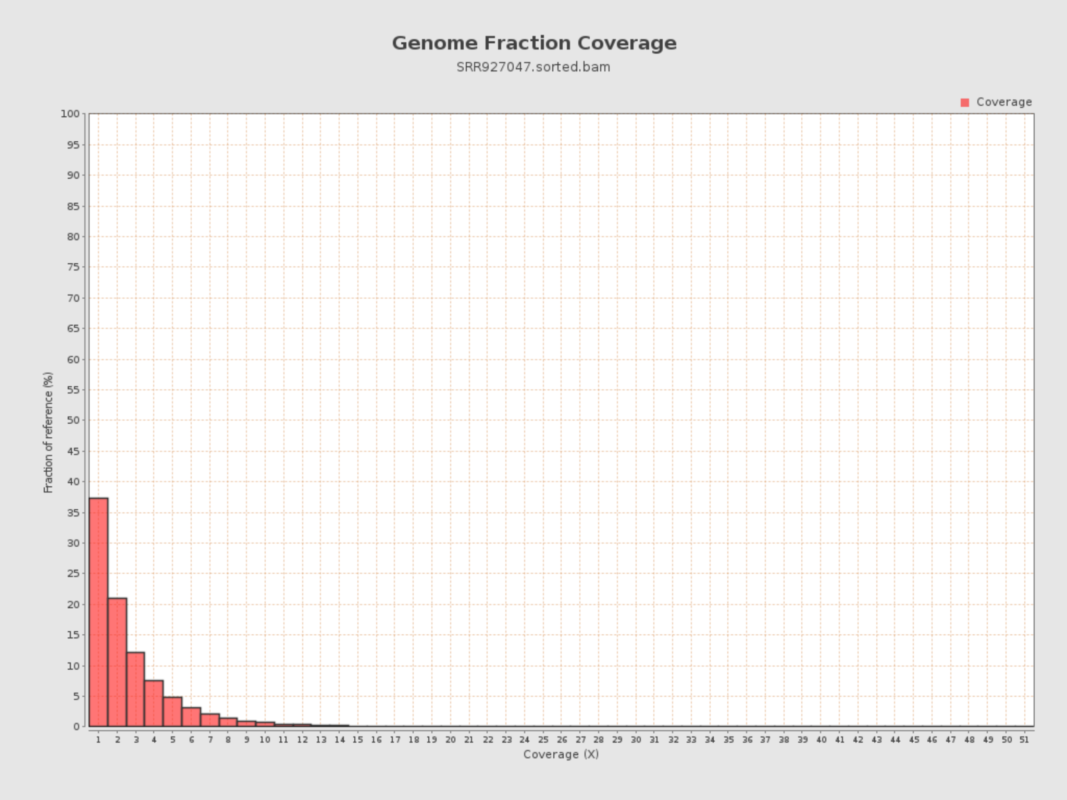
# 4. Results : Coverage Histogram



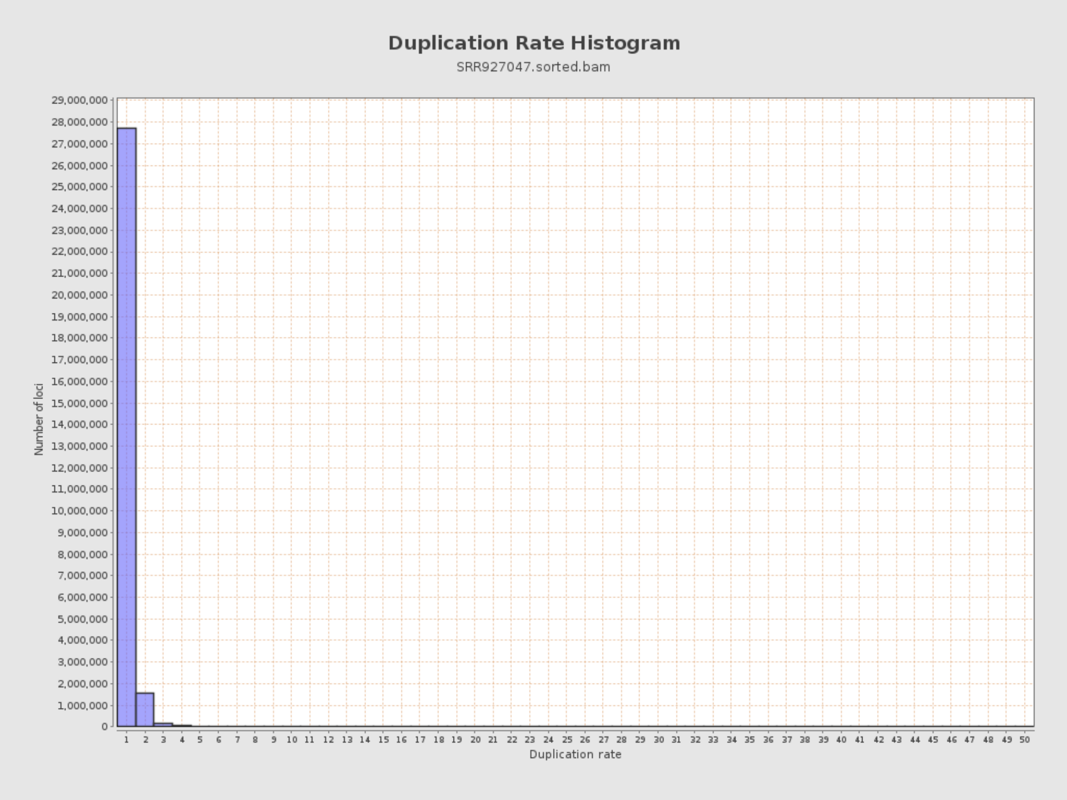
# 5. Results : Coverage Histogram (0-50X)



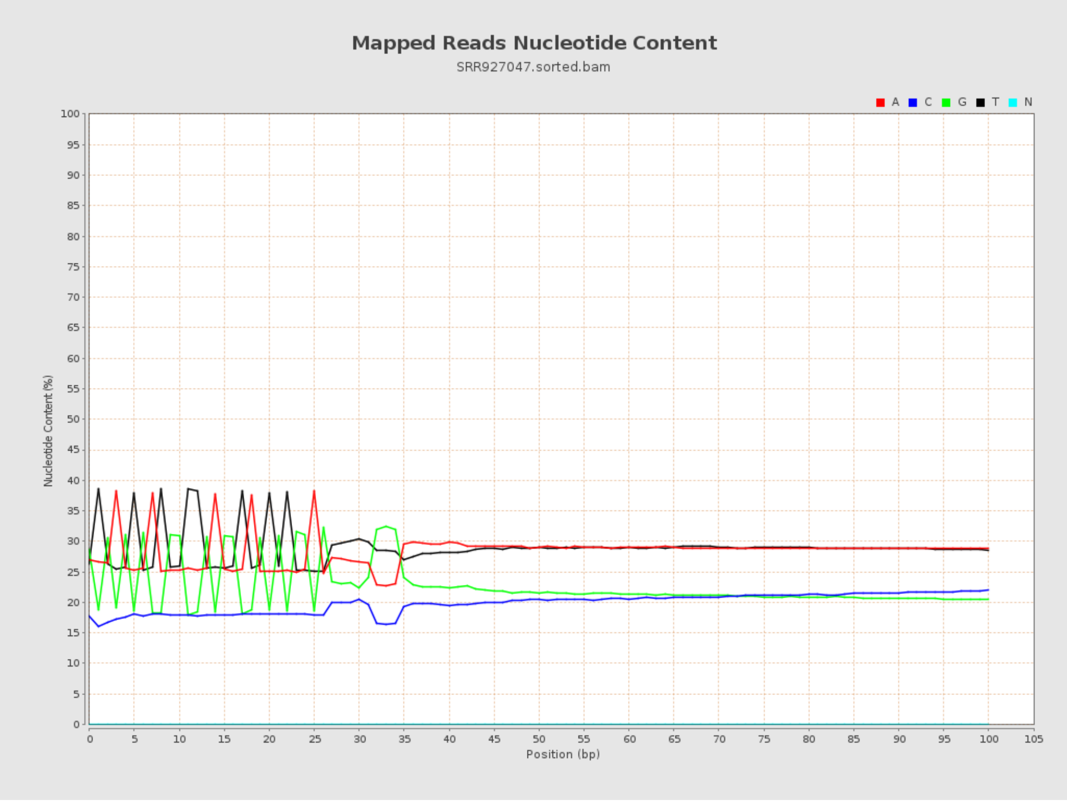
# 6. Results : Genome Fraction Coverage



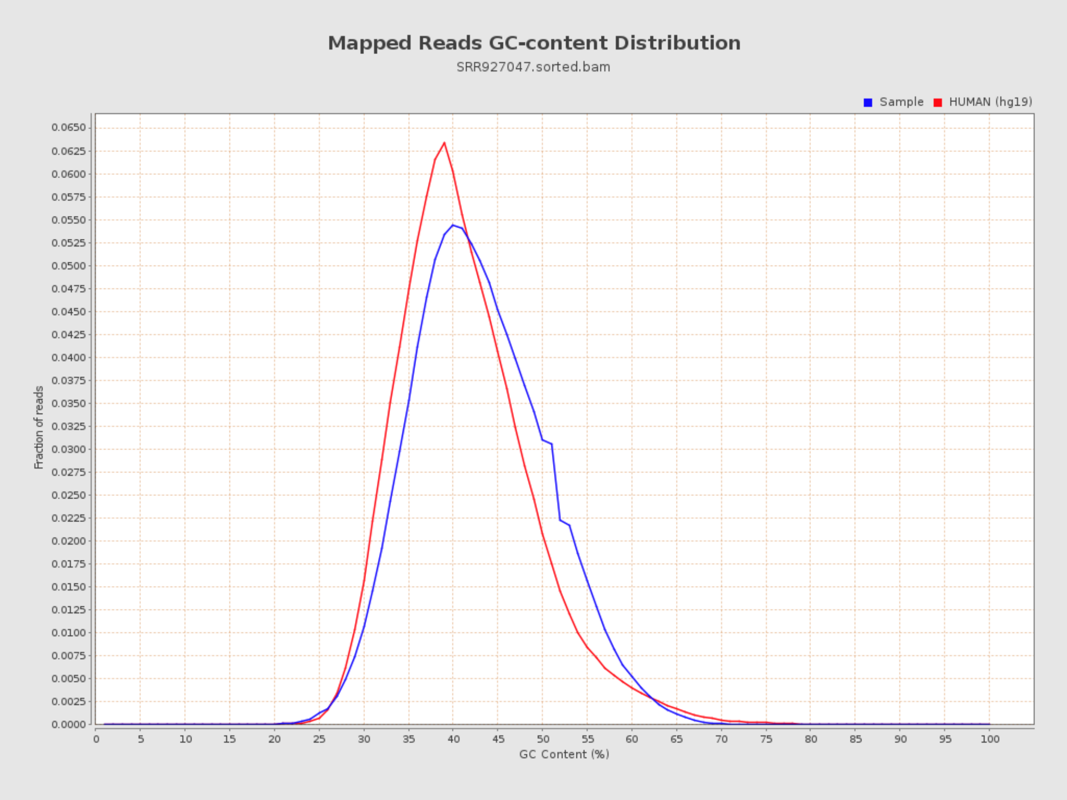
# 7. Results : Duplication Rate Histogram



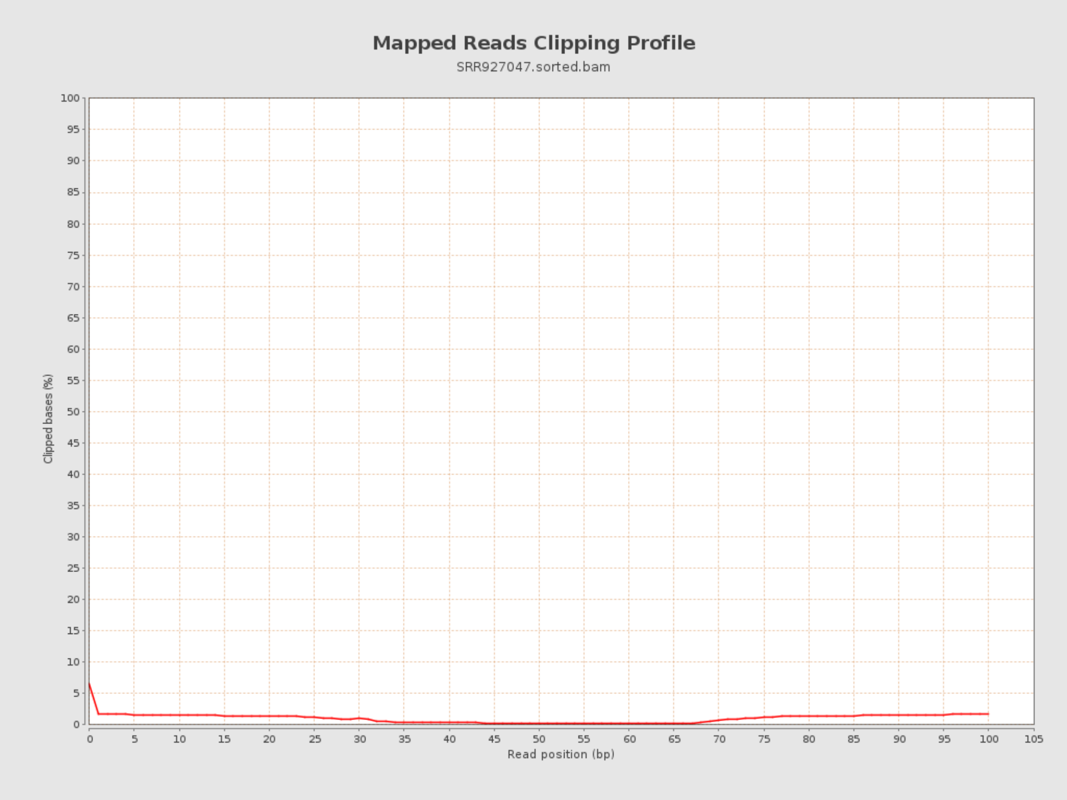
# 8. Results : Mapped Reads Nucleotide Content



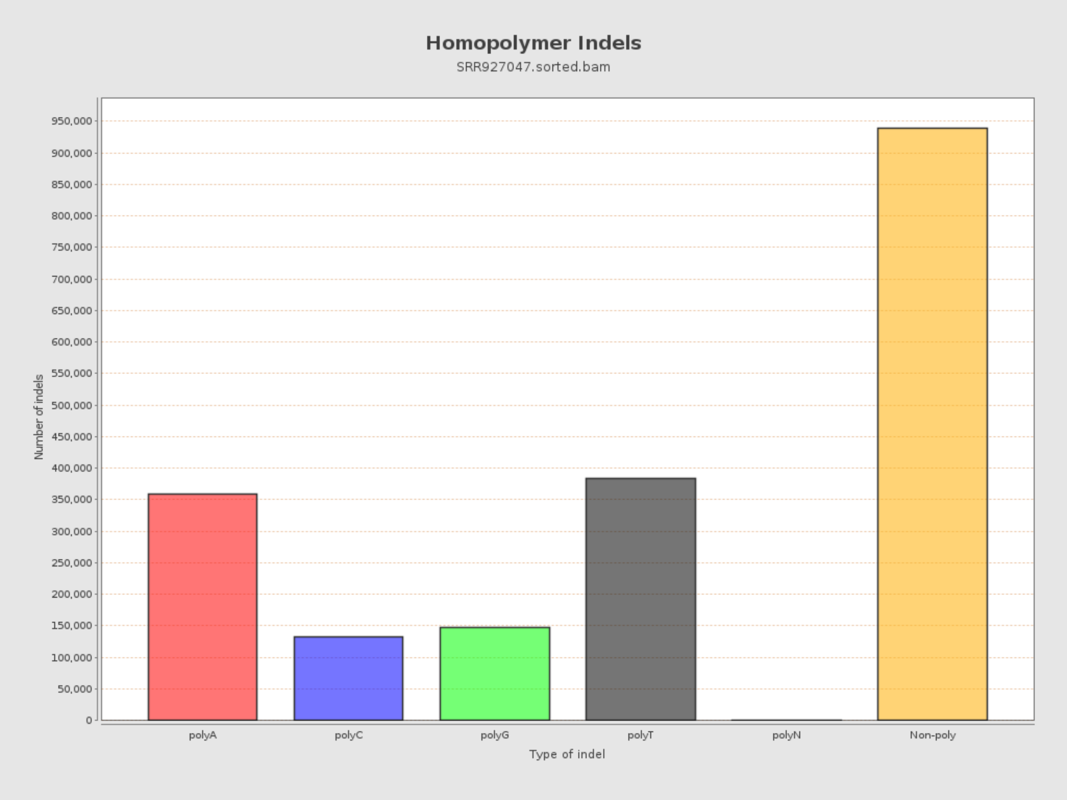
# 9. Results : Mapped Reads GC-content Distribution



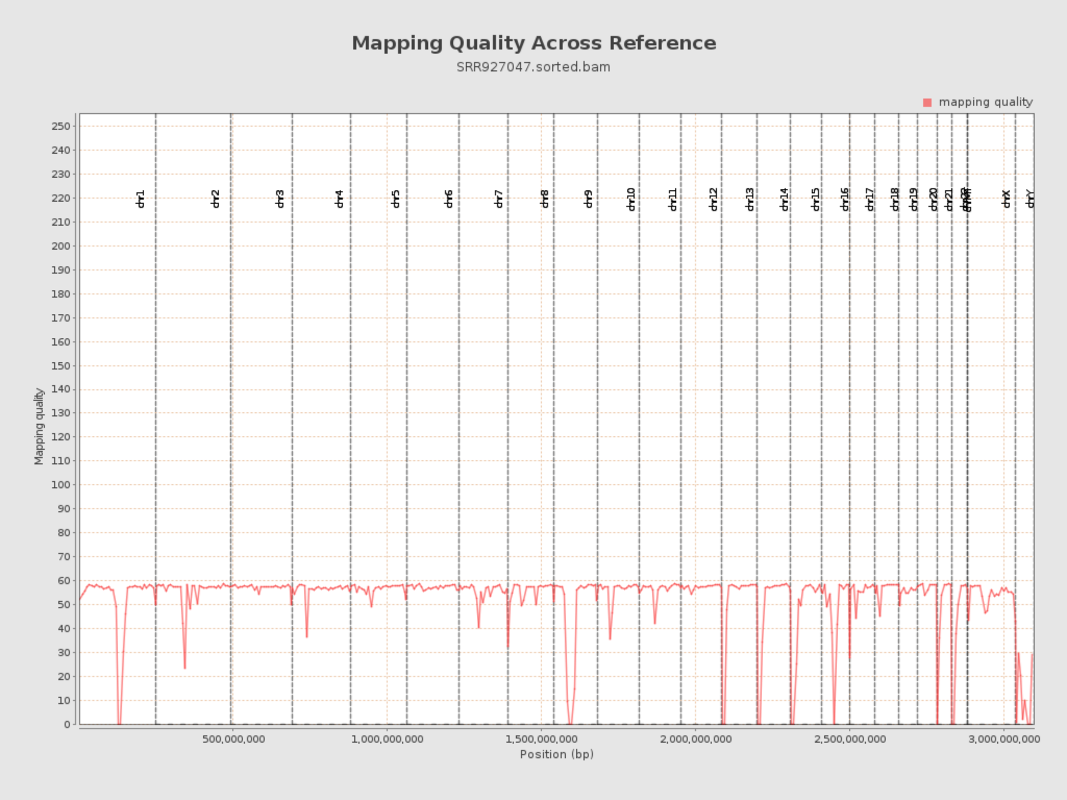
# 10. Results : Mapped Reads Clipping Profile



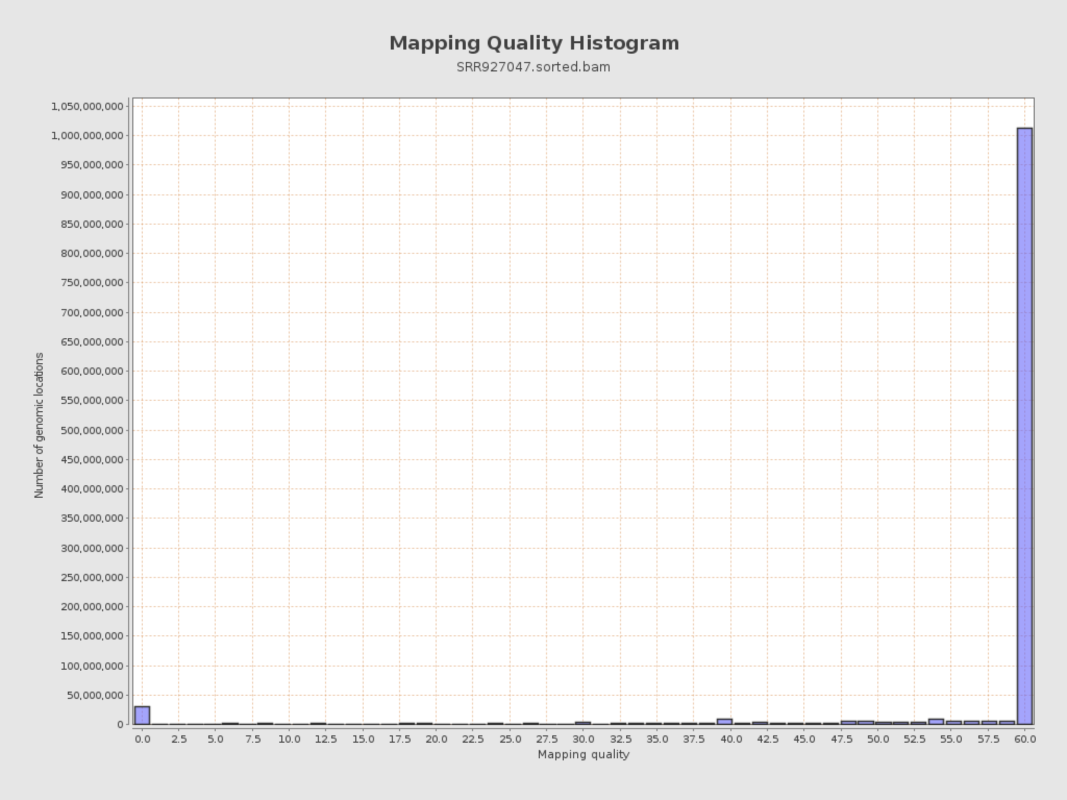
# 11. Results : Homopolymer Indels



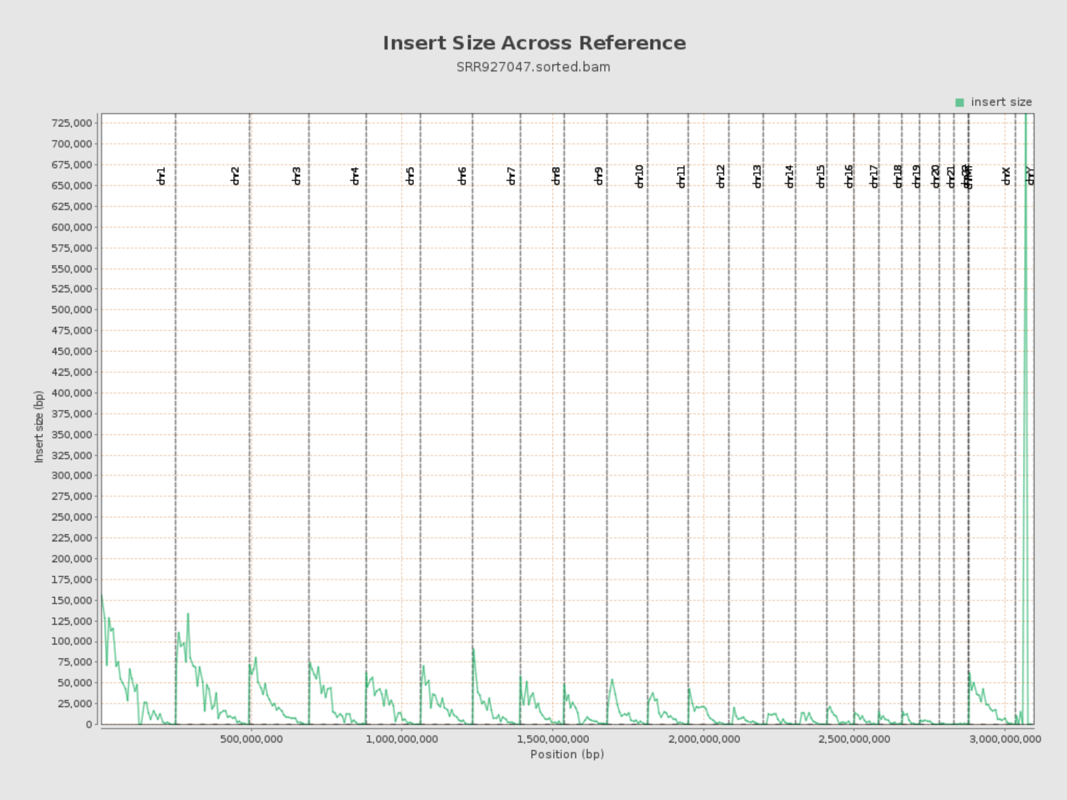
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram