# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/18 01:05:40*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006395.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_SRR1006395 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006395_1.fastq.gz SRR1006395_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Apr 18 01:05:39 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1006395.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 8,100,946 |
| Mapped reads | 6,864,399 / 84.74% |
| Unmapped reads | 1,236,547 / 15.26% |
| Mapped paired reads | 6,864,399 / 84.74% |
| Mapped reads, first in pair | 3,478,445 / 42.94% |
| Mapped reads,  second in pair | 3,385,954 / 41.8% |
| Mapped reads, both in pair | 6,293,084 / 77.68% |
| Mapped reads, singletons | 571,315 / 7.05% |
| Secondary alignments | 0 |
| Read min/max/mean length | 39 / 39 / 39 |
| Duplicated reads (estimated) | 328,493 / 4.05% |
| Duplication rate | 4.2% |
| Clipped reads | 367,045 / 4.53% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 74,878,894 / 28.17% |
| Number/percentage of C's | 56,746,663 / 21.35% |
| Number/percentage of T's | 75,544,270 / 28.42% |
| Number/percentage of G's | 58,636,926 / 22.06% |
| Number/percentage of N's | 11,146 / 0% |
| GC Percentage | 43.41% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0859 |
| Standard Deviation | 0.4952 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 48.36 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 66,368.02 |
| Standard Deviation | 2,486,157.74 |
| P25/Median/P75 | 104 / 135 / 182 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.37% |
| Mismatches | 983,213 |
| Insertions | 7,101 |
| Mapped reads with at least one insertion | 0.1% |
| Deletions | 24,502 |
| Mapped reads with at least one deletion | 0.36% |
| Homopolymer indels | 44.07% |

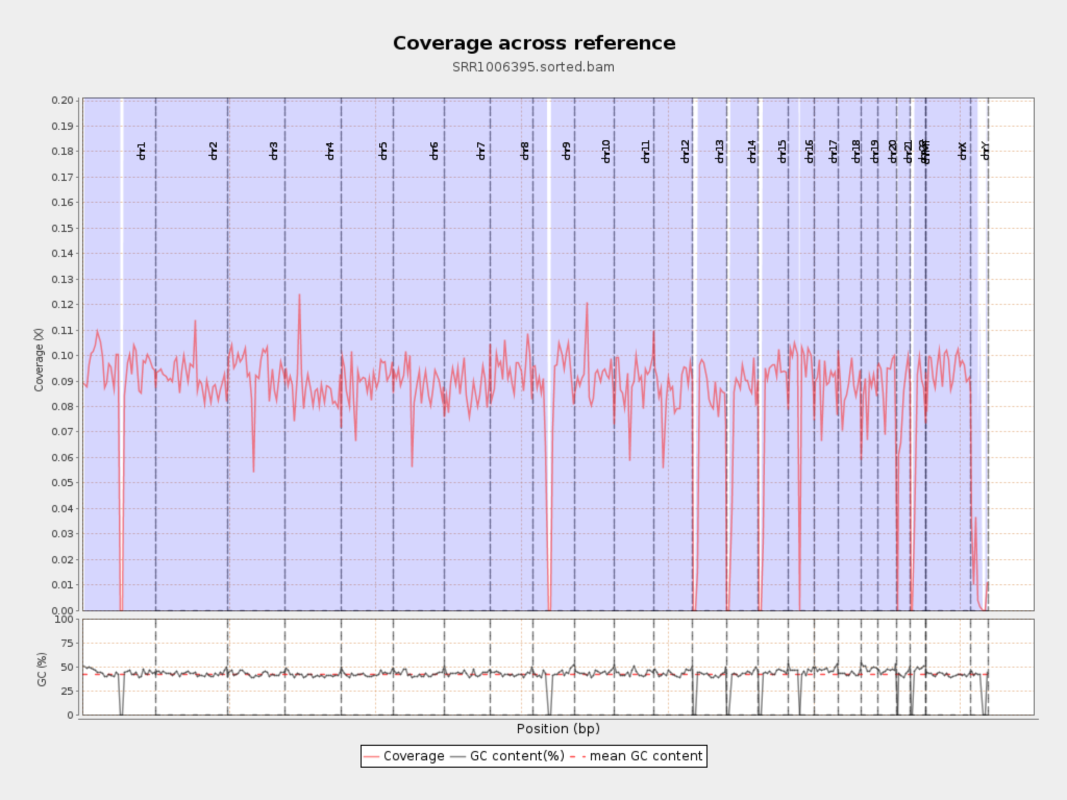
## 2.7. Chromosome stats

| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| | | | | |

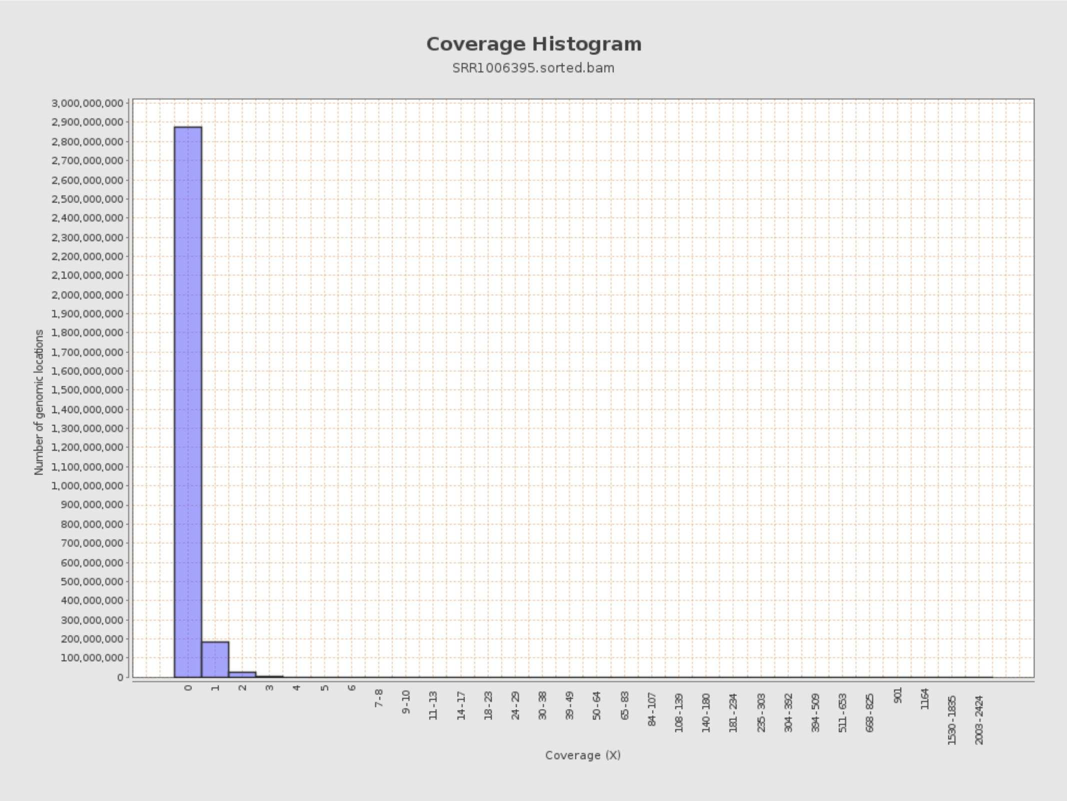
| | | | | |
|---|---|---|---|---|
| chr1 | 249250621 | 22483441 | 0.0902 | 0.6458 |
| chr2 | 243199373 | 22203959 | 0.0913 | 0.4332 |
| chr3 | 198022430 | 18449231 | 0.0932 | 0.3535 |
| chr4 | 191154276 | 16764908 | 0.0877 | 0.3884 |
| chr5 | 180915260 | 16355306 | 0.0904 | 0.3493 |
| chr6 | 171115067 | 15155033 | 0.0886 | 0.3833 |
| chr7 | 159138663 | 13812371 | 0.0868 | 0.5053 |
| chr8 | 146364022 | 13742366 | 0.0939 | 1.2312 |
| chr9 | 141213431 | 11483469 | 0.0813 | 0.3801 |
| chr10 | 135534747 | 12476455 | 0.0921 | 0.5045 |
| chr11 | 135006516 | 12049510 | 0.0893 | 0.4071 |
| chr12 | 133851895 | 11565278 | 0.0864 | 0.3442 |
| chr13 | 115169878 | 8380359 | 0.0728 | 0.3141 |
| chr14 | 107349540 | 7991834 | 0.0744 | 0.3589 |
| chr15 | 102531392 | 7811554 | 0.0762 | 0.3202 |
| chr16 | 90354753 | 8104111 | 0.0897 | 0.4303 |
| chr17 | 81195210 | 7260899 | 0.0894 | 0.3635 |
| chr18 | 78077248 | 6833405 | 0.0875 | 0.5955 |
| chr19 | 59128983 | 5006006 | 0.0847 | 0.4947 |
| chr20 | 63025520 | 5717336 | 0.0907 | 0.3639 |
| chr21 | 48129895 | 3578326 | 0.0743 | 0.3631 |
| chr22 | 51304566 | 3246139 | 0.0633 | 0.2997 |
| chrMT | 16571 | 1548 | 0.0934 | 0.3738 |
| chrX | 155270560 | 14710049 | 0.0947 | 0.3889 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 668196 | 0.0113 | 0.2755 |

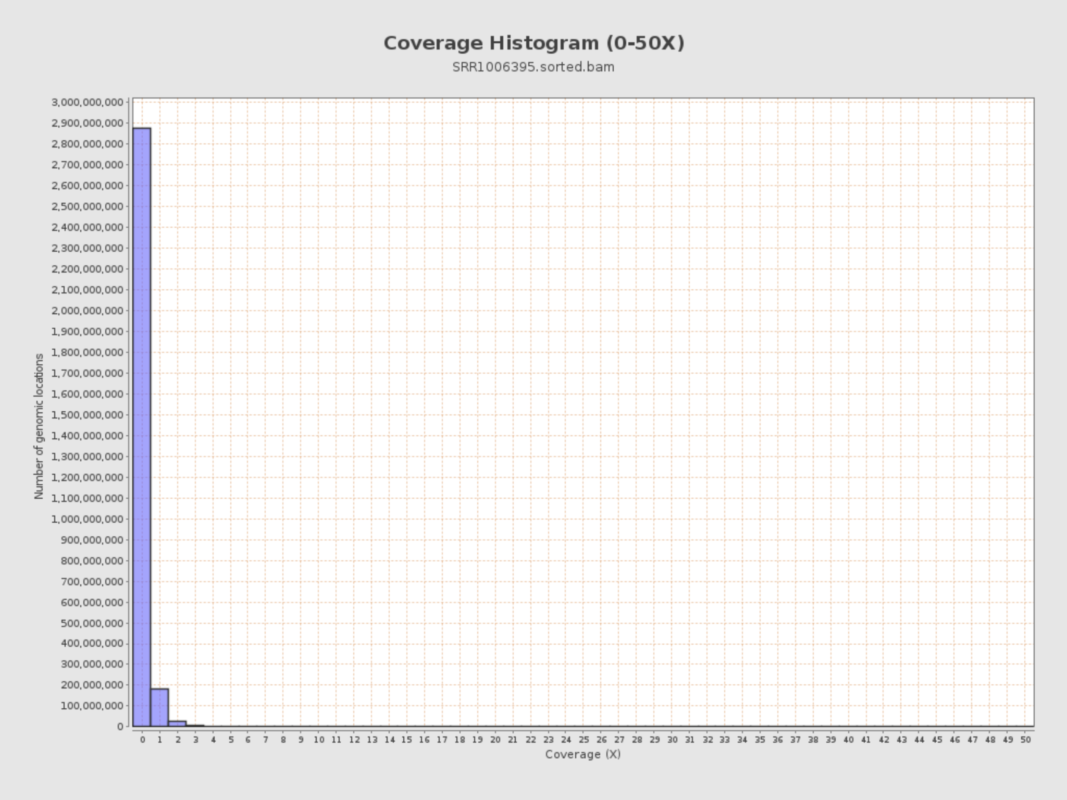
# 3. Results : Coverage across reference



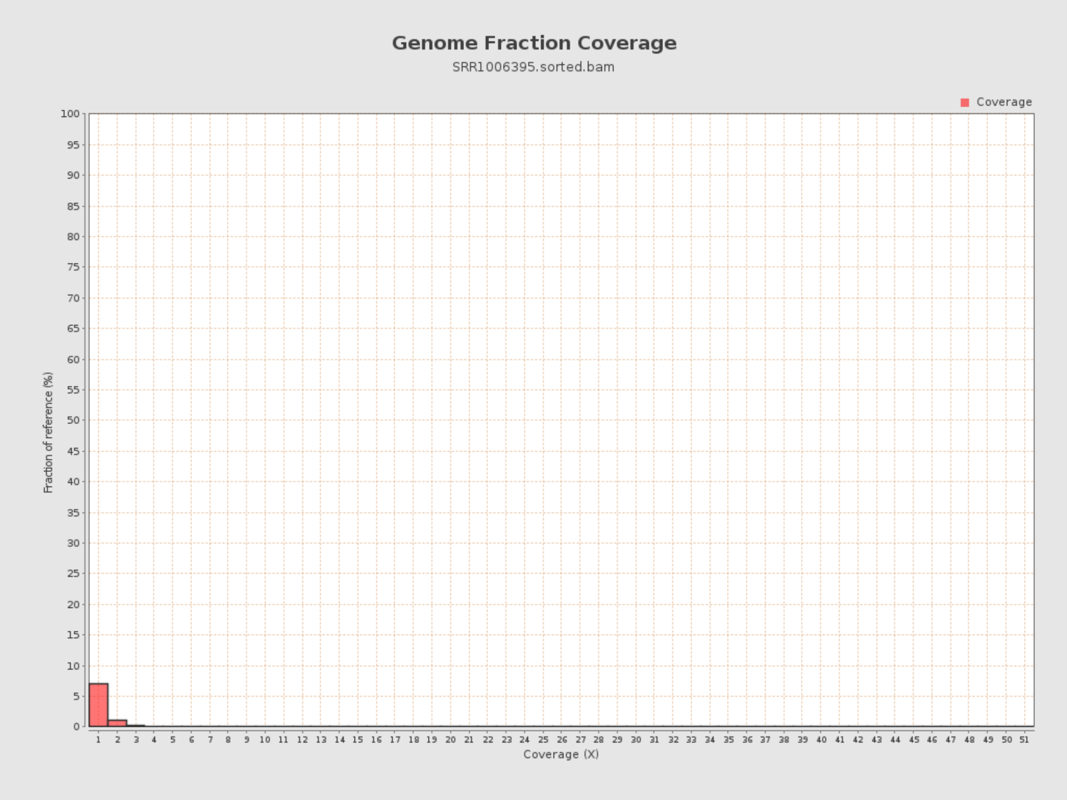
# 4. Results : Coverage Histogram



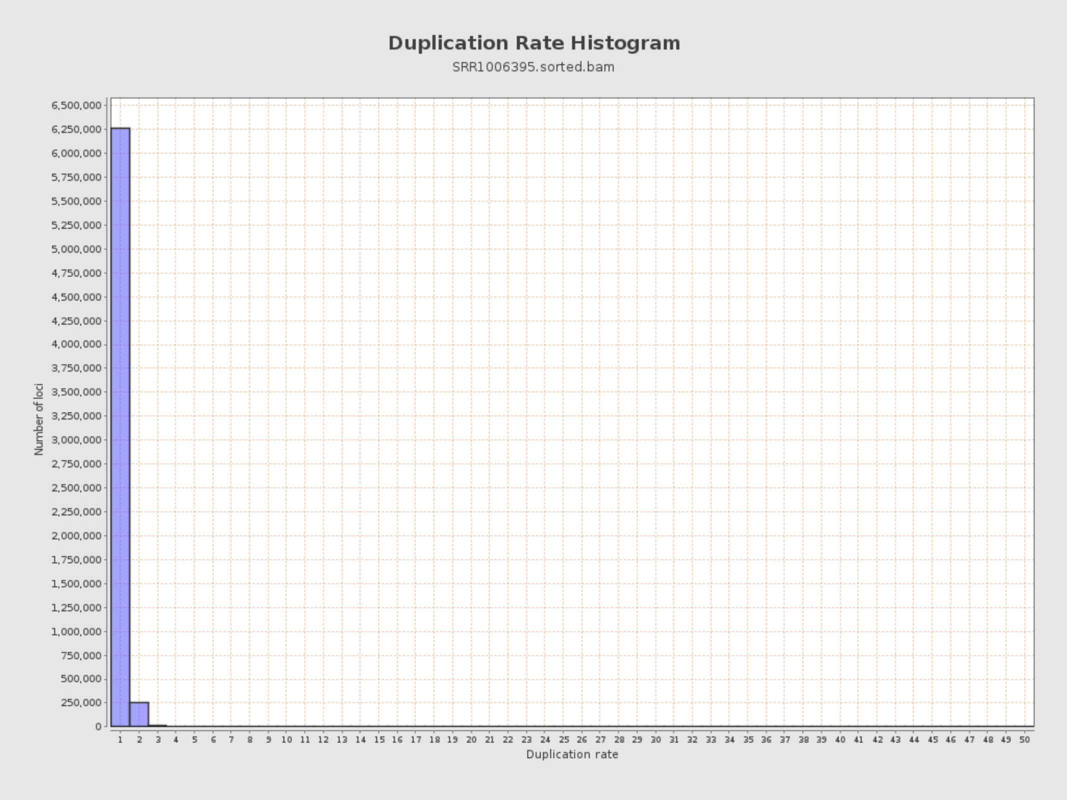
# 5. Results : Coverage Histogram (0-50X)



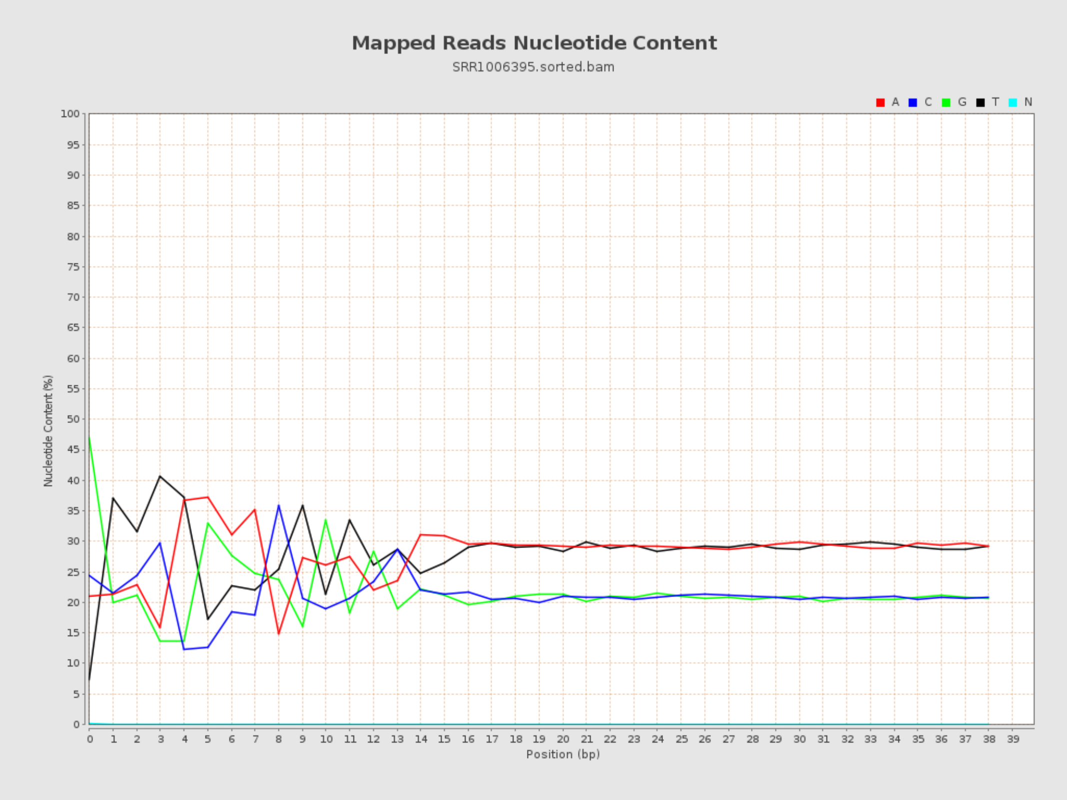
# 6. Results : Genome Fraction Coverage



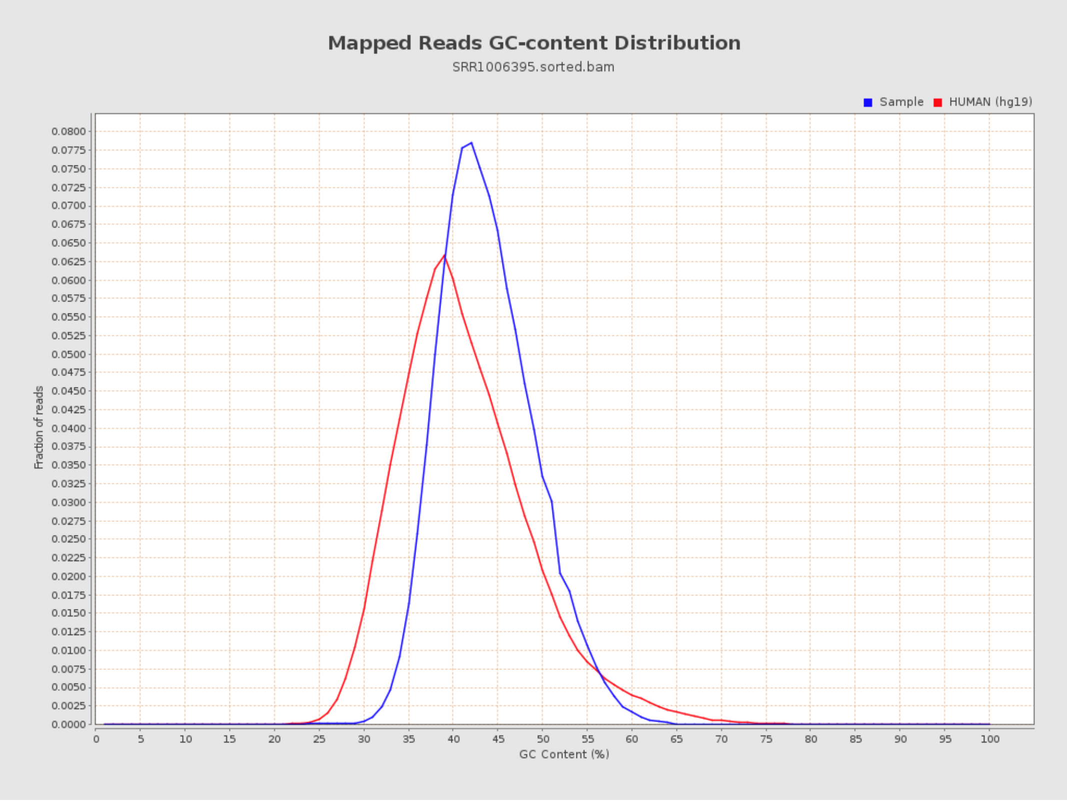
# 7. Results : Duplication Rate Histogram



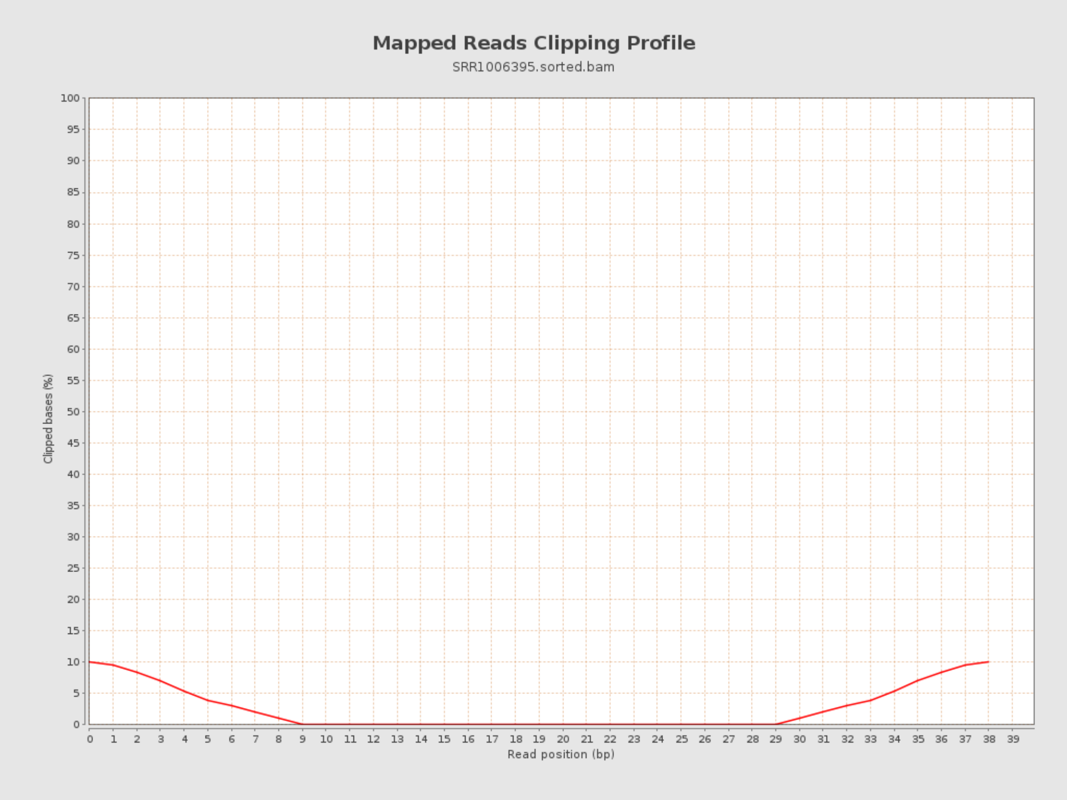
# 8. Results : Mapped Reads Nucleotide Content



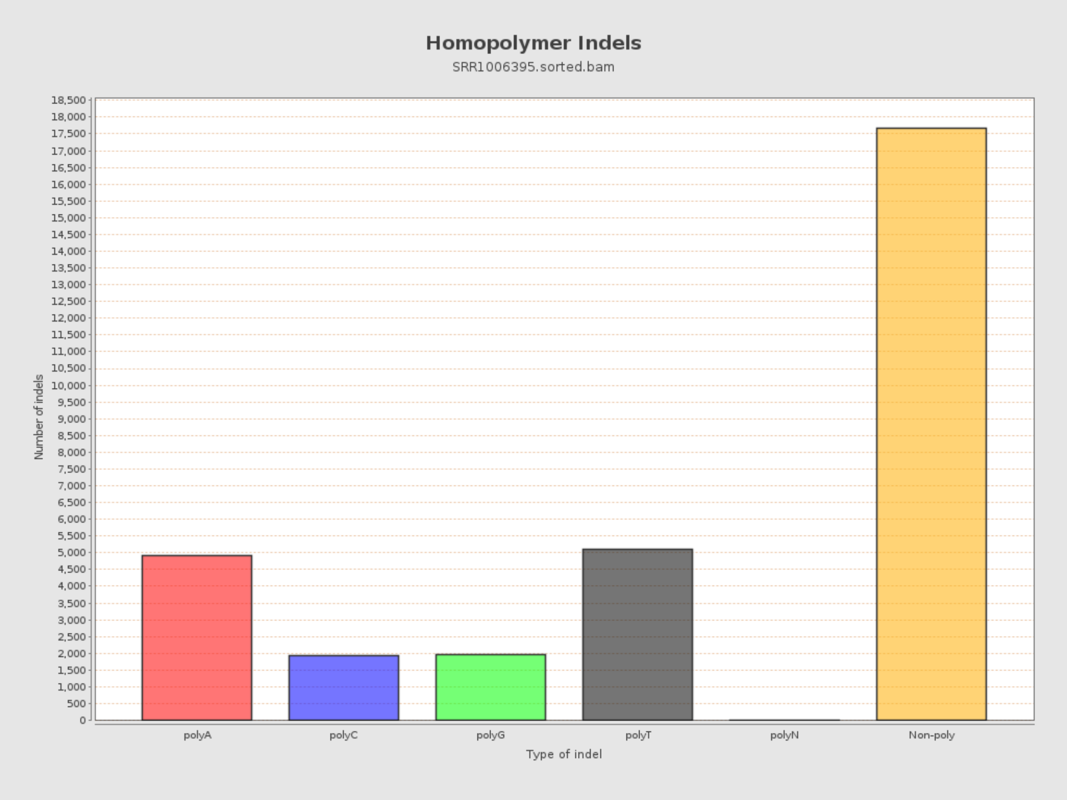
# 9. Results : Mapped Reads GC-content Distribution



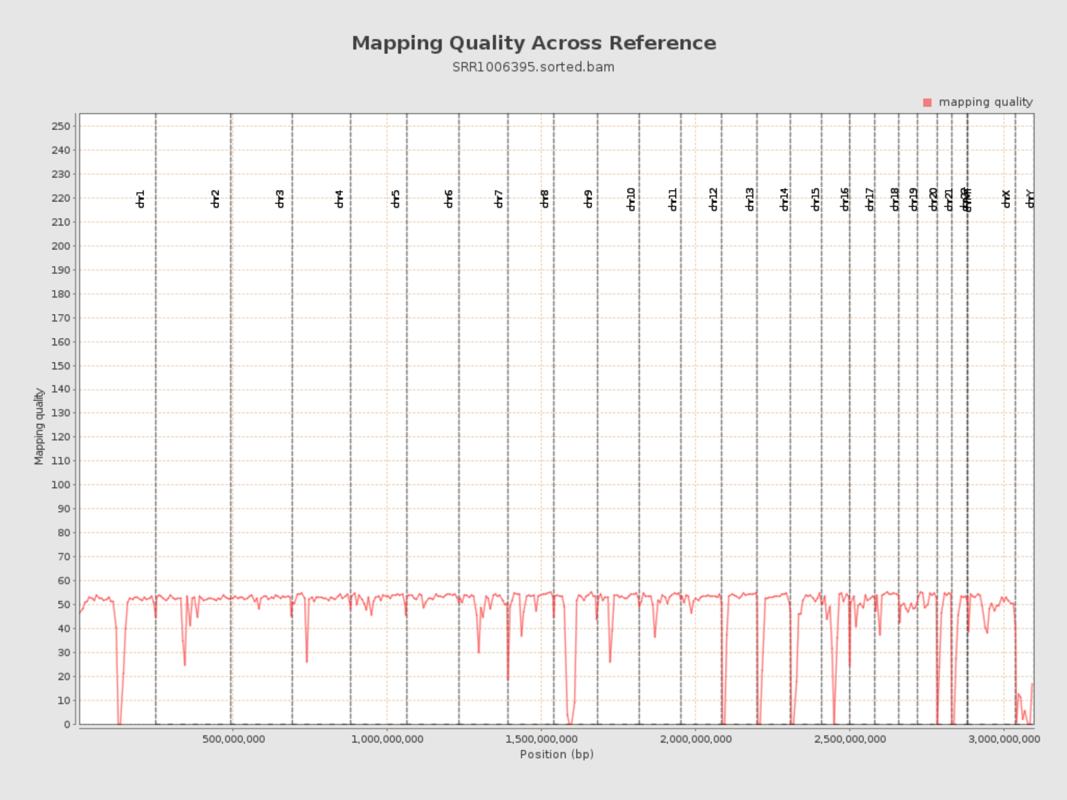
# 10. Results : Mapped Reads Clipping Profile



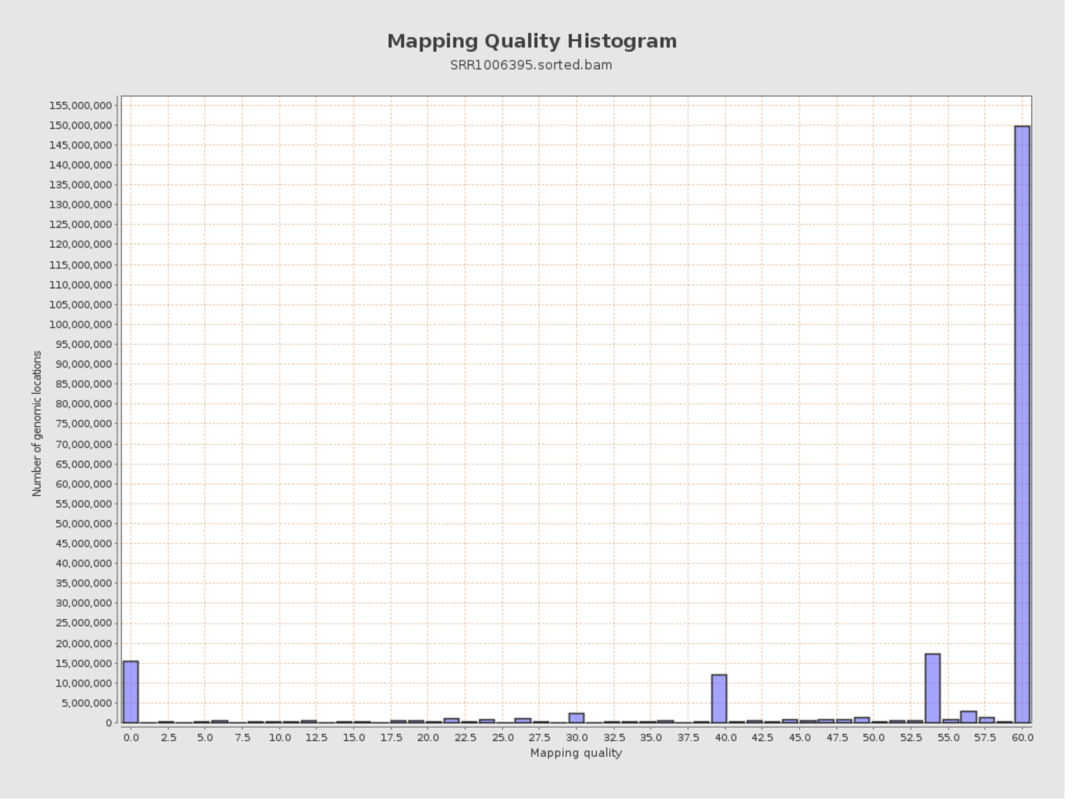
# 11. Results : Homopolymer Indels



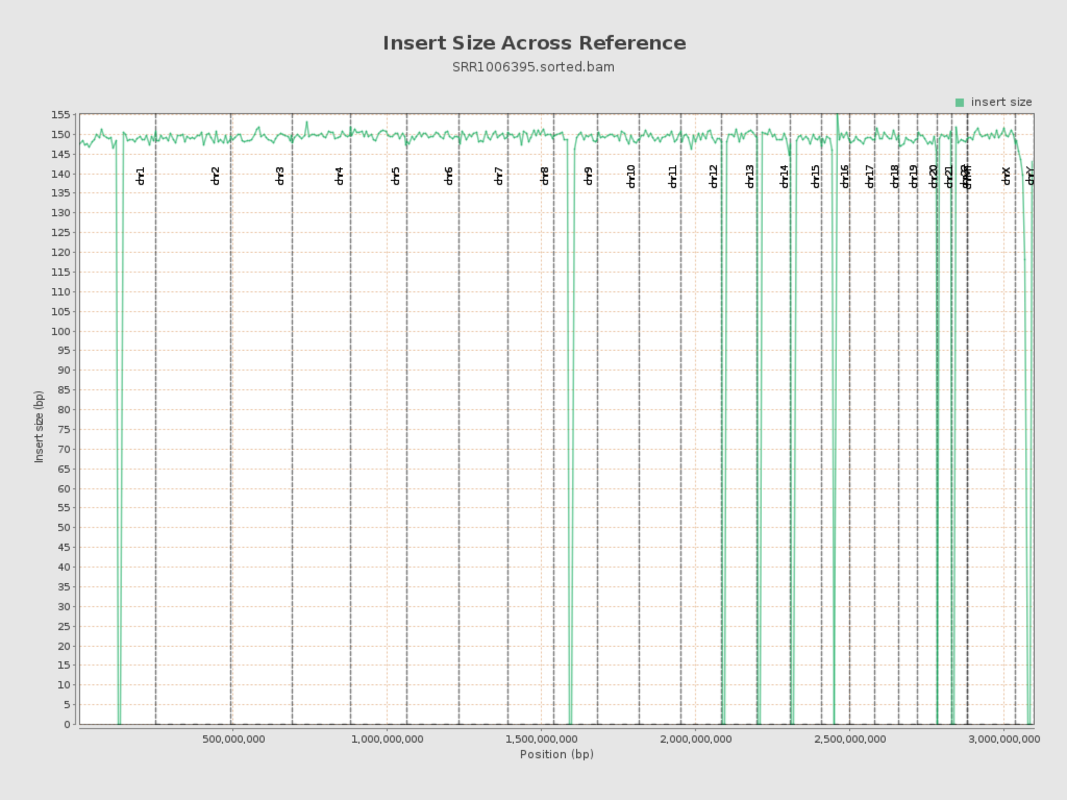
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram