# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/17 23:47:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006211.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_SRR1006211 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006211_1.fastq.gz SRR1006211_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Apr 17 23:47:49 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1006211.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 2,825,538 |
| Mapped reads | 2,463,825 / 87.2% |
| Unmapped reads | 361,713 / 12.8% |
| Mapped paired reads | 2,463,825 / 87.2% |
| Mapped reads, first in pair | 1,234,277 / 43.68% |
| Mapped reads, second in pair | 1,229,548 / 43.52% |
| Mapped reads, both in pair | 2,273,218 / 80.45% |
| Mapped reads, singletons | 190,607 / 6.75% |
| Secondary alignments | 0 |
| Read min/max/mean length | 39 / 39 / 39 |
| Duplicated reads (estimated) | 60,060 / 2.13% |
| Duplication rate | 2.06% |
| Clipped reads | 148,408 / 5.25% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 26,369,495 / 27.66% |
| Number/percentage of C's | 20,625,196 / 21.64% |
| Number/percentage of T's | 26,939,203 / 28.26% |
| Number/percentage of G's | 21,378,690 / 22.43% |
| Number/percentage of N's | 4,702 / 0% |
| GC Percentage | 44.07% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0308 |
| Standard Deviation | 0.2299 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.76 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 60,383.18 |
| Standard Deviation | 2,313,517.97 |
| P25/Median/P75 | 80 / 123 / 162 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.3% |
| Mismatches | 282,513 |
| Insertions | 3,027 |
| Mapped reads with at least one insertion | 0.12% |
| Deletions | 9,735 |
| Mapped reads with at least one deletion | 0.4% |
| Homopolymer indels | 44.2% |

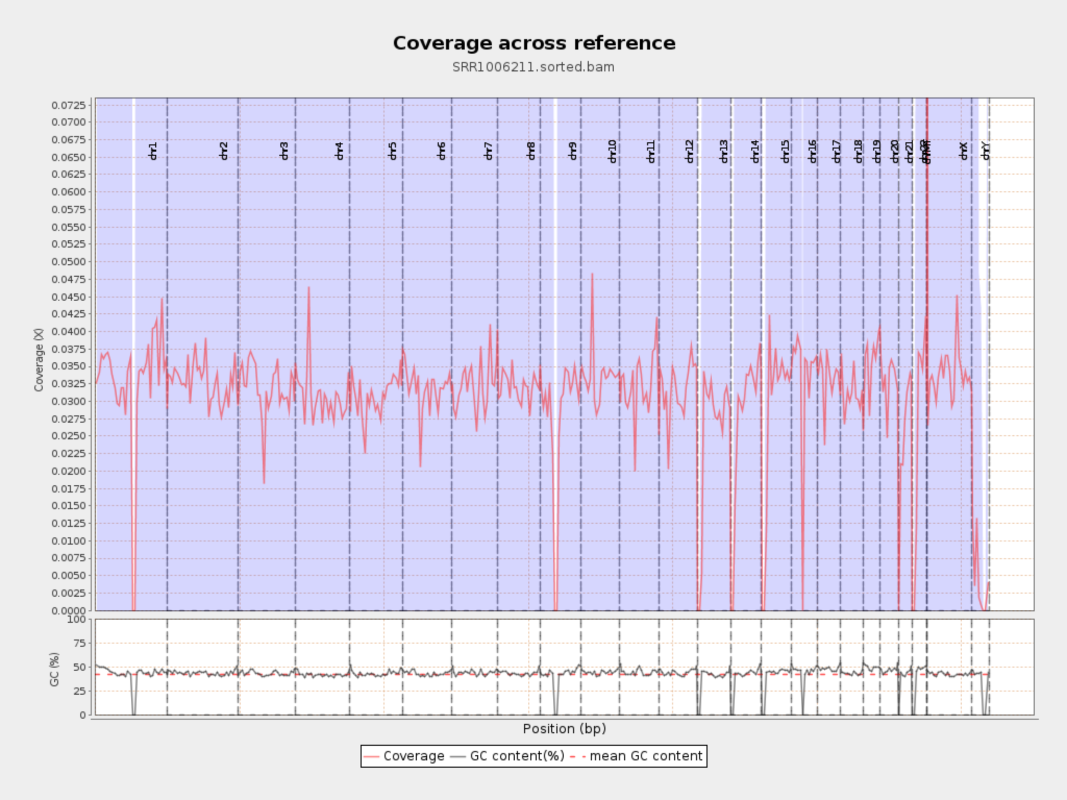
## 2.7. Chromosome stats

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

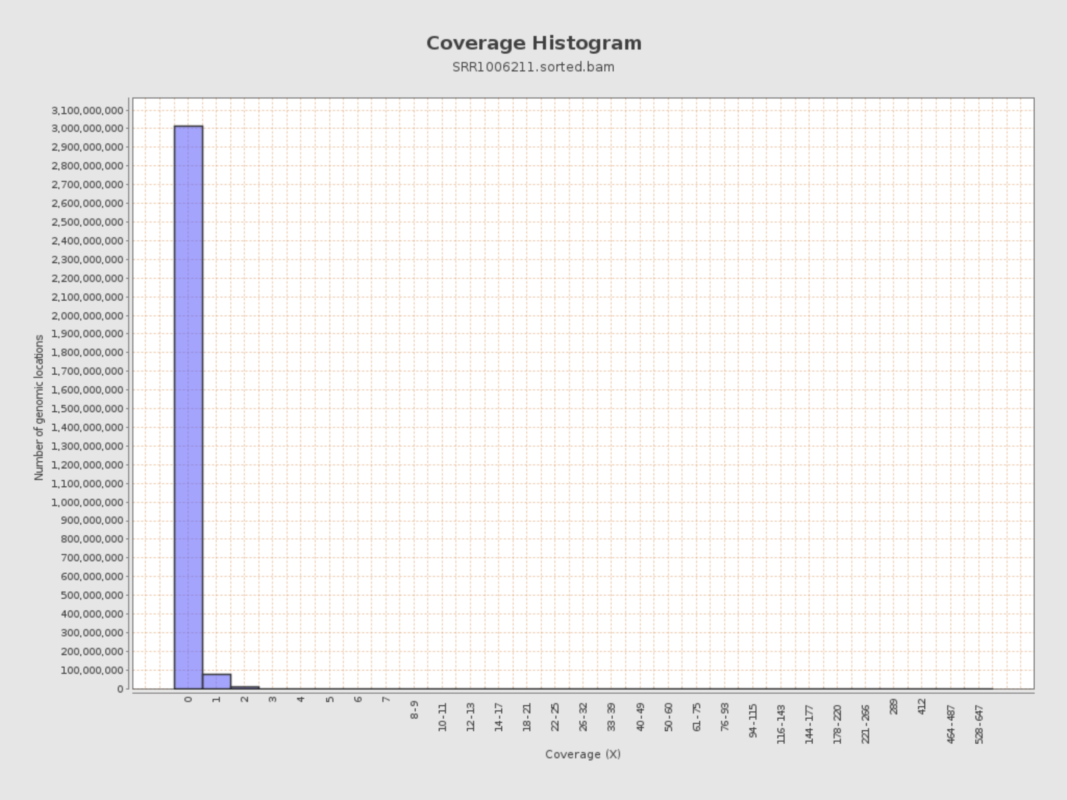
| | | | | |
|---|---|---|---|---|
| chr1 | 249250621 | 8131040 | 0.0326 | 0.2922 |
| chr2 | 243199373 | 8009063 | 0.0329 | 0.2208 |
| chr3 | 198022430 | 6319935 | 0.0319 | 0.1969 |
| chr4 | 191154276 | 5900900 | 0.0309 | 0.2063 |
| chr5 | 180915260 | 5596991 | 0.0309 | 0.1935 |
| chr6 | 171115067 | 5446136 | 0.0318 | 0.2063 |
| chr7 | 159138663 | 5113825 | 0.0321 | 0.246 |
| chr8 | 146364022 | 4686489 | 0.032 | 0.3726 |
| chr9 | 141213431 | 3878199 | 0.0275 | 0.1977 |
| chr10 | 135534747 | 4577875 | 0.0338 | 0.2482 |
| chr11 | 135006516 | 4393837 | 0.0325 | 0.212 |
| chr12 | 133851895 | 4242424 | 0.0317 | 0.197 |
| chr13 | 115169878 | 2886718 | 0.0251 | 0.1745 |
| chr14 | 107349540 | 2946803 | 0.0275 | 0.2726 |
| chr15 | 102531392 | 2873947 | 0.028 | 0.1846 |
| chr16 | 90354753 | 2978909 | 0.033 | 0.2225 |
| chr17 | 81195210 | 2707944 | 0.0334 | 0.2067 |
| chr18 | 78077248 | 2437206 | 0.0312 | 0.261 |
| chr19 | 59128983 | 2112182 | 0.0357 | 0.2508 |
| chr20 | 63025520 | 2071083 | 0.0329 | 0.2035 |
| chr21 | 48129895 | 1207861 | 0.0251 | 0.1877 |
| chr22 | 51304566 | 1315632 | 0.0256 | 0.1832 |
| chrMT | 16571 | 5675 | 0.3425 | 0.6708 |
| chrX | 155270560 | 5243604 | 0.0338 | 0.2086 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 246006 | 0.0041 | 0.1149 |

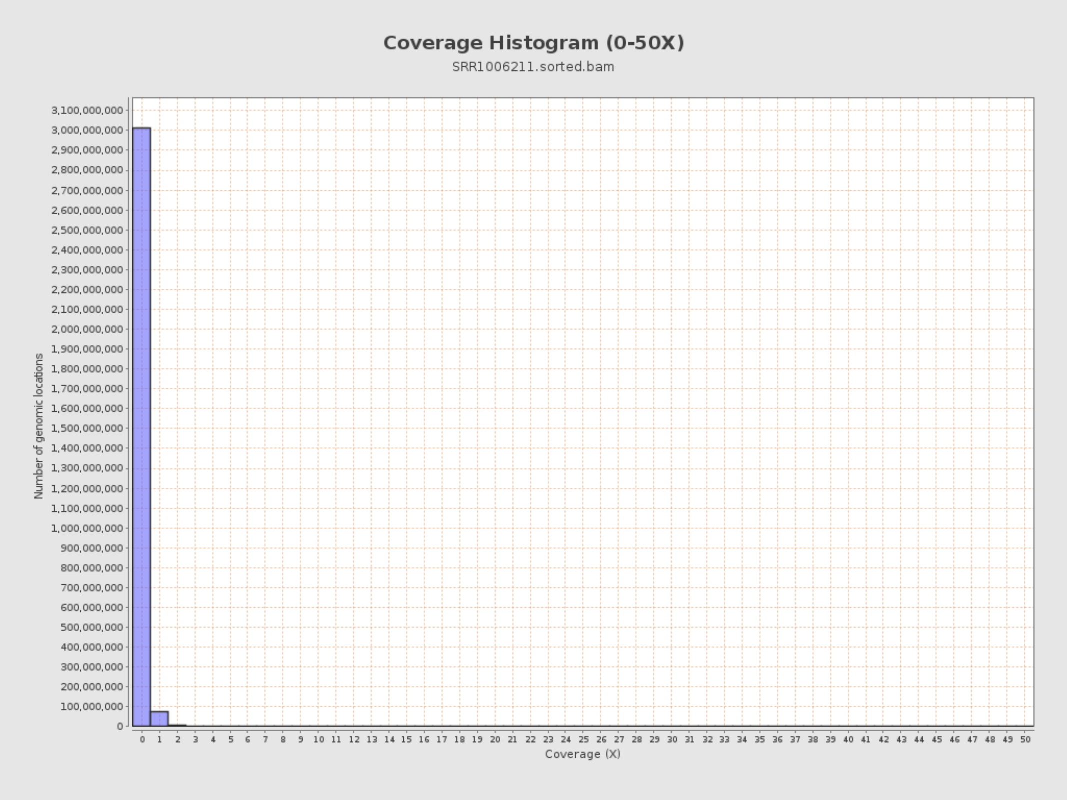
# 3. Results : Coverage across reference



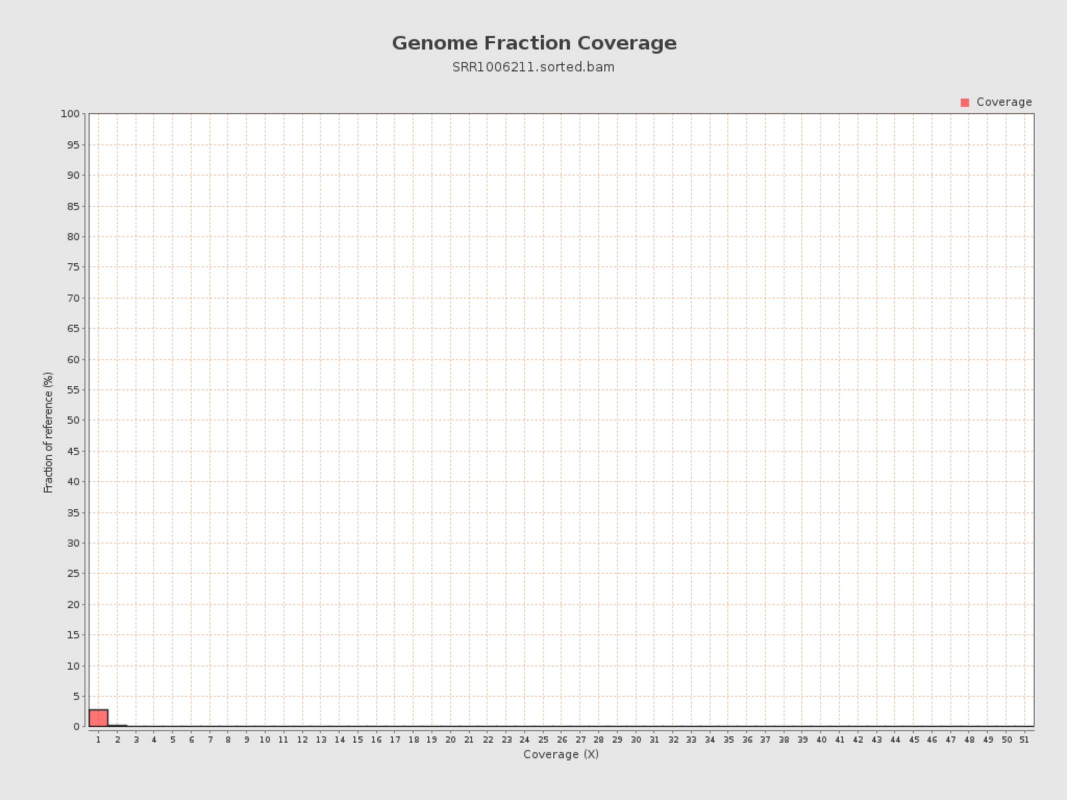
# 4. Results : Coverage Histogram



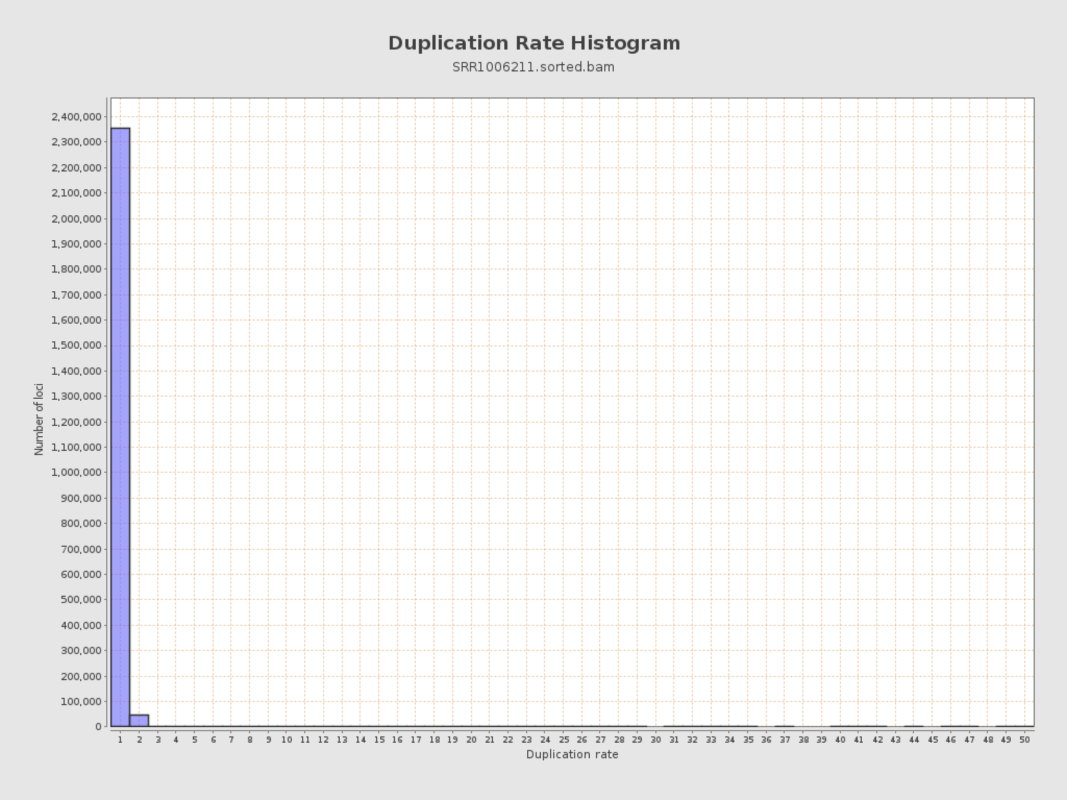
# 5. Results : Coverage Histogram (0-50X)



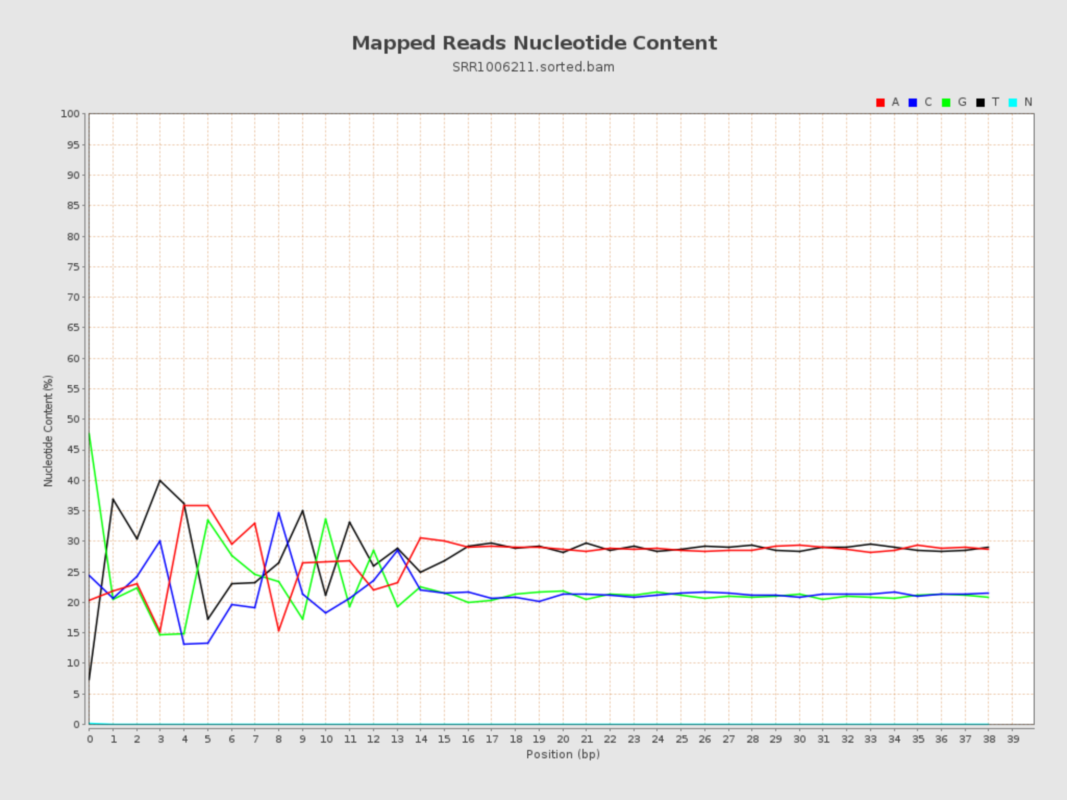
# 6. Results : Genome Fraction Coverage



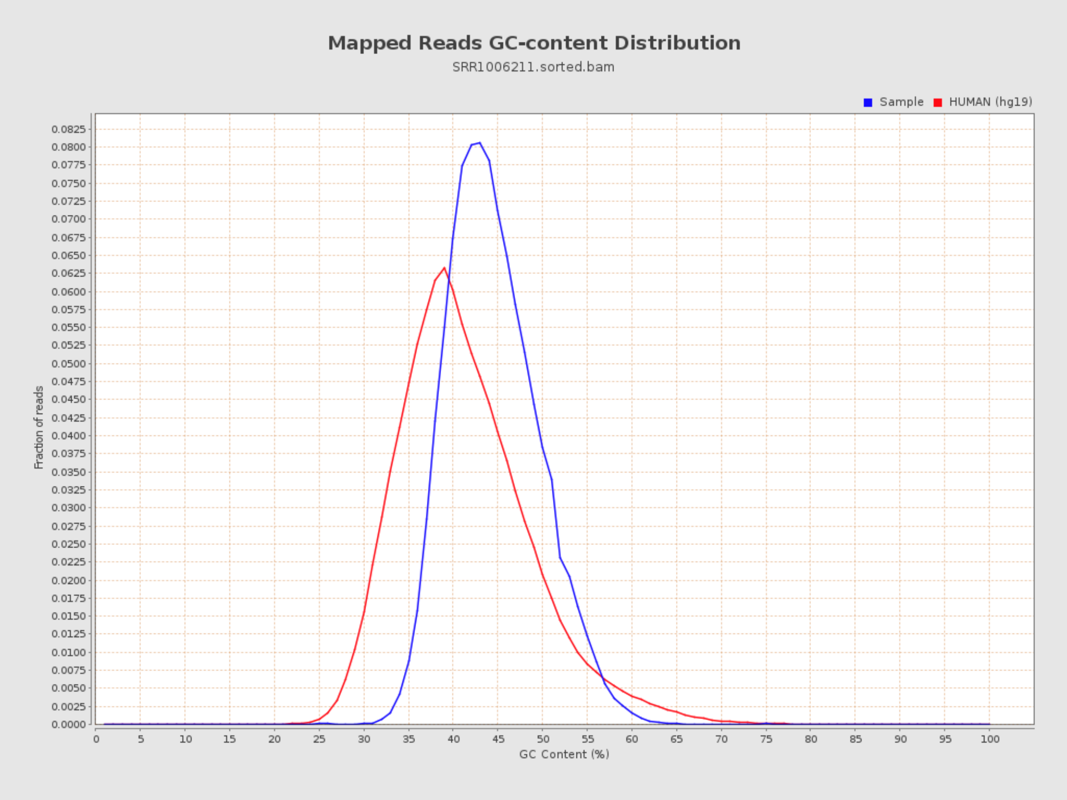
# 7. Results : Duplication Rate Histogram



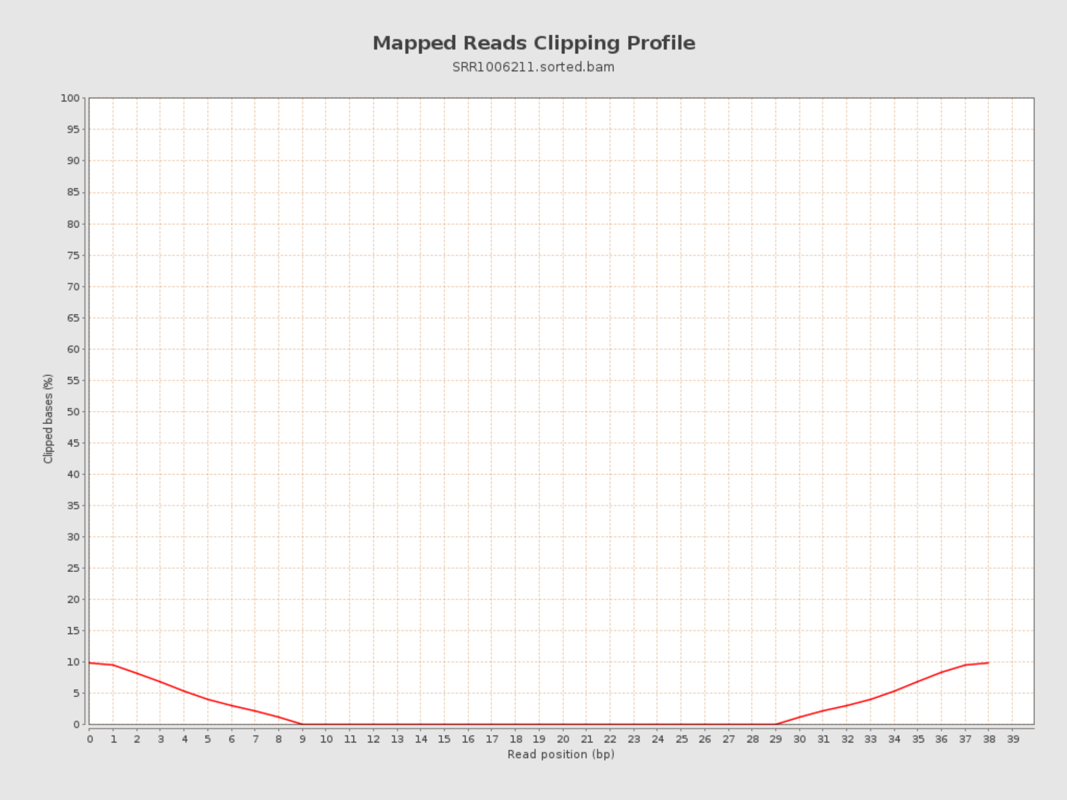
# 8. Results : Mapped Reads Nucleotide Content



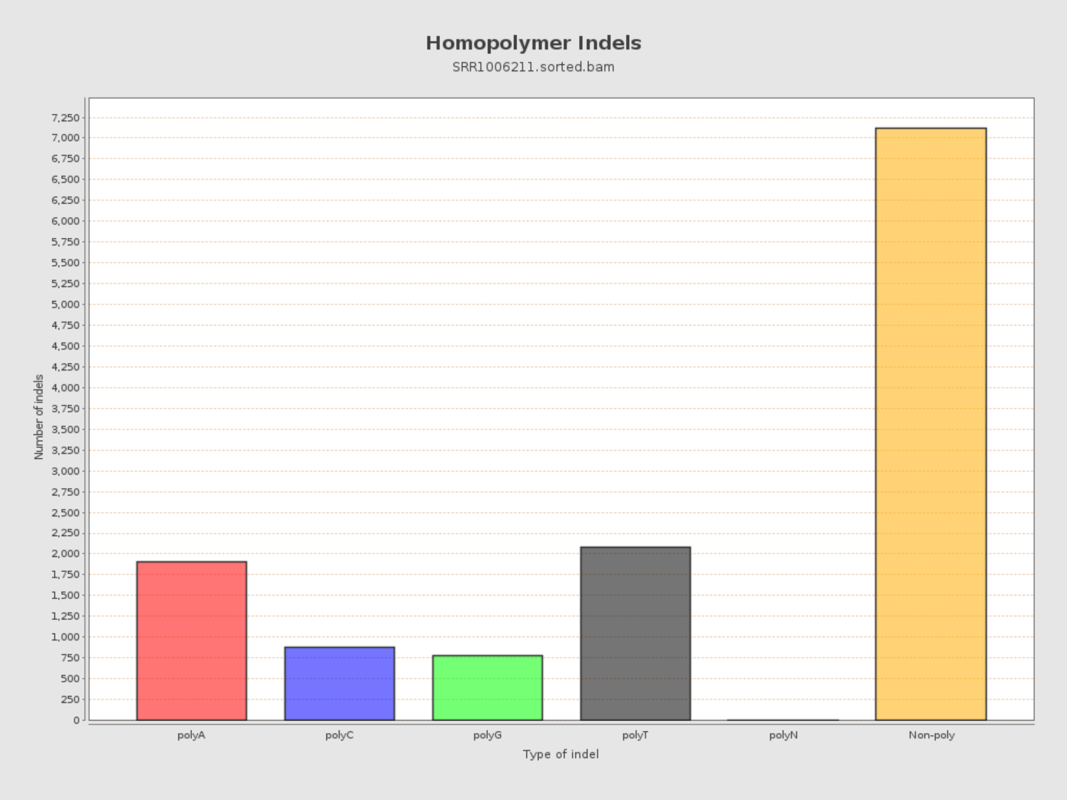
# 9. Results : Mapped Reads GC-content Distribution



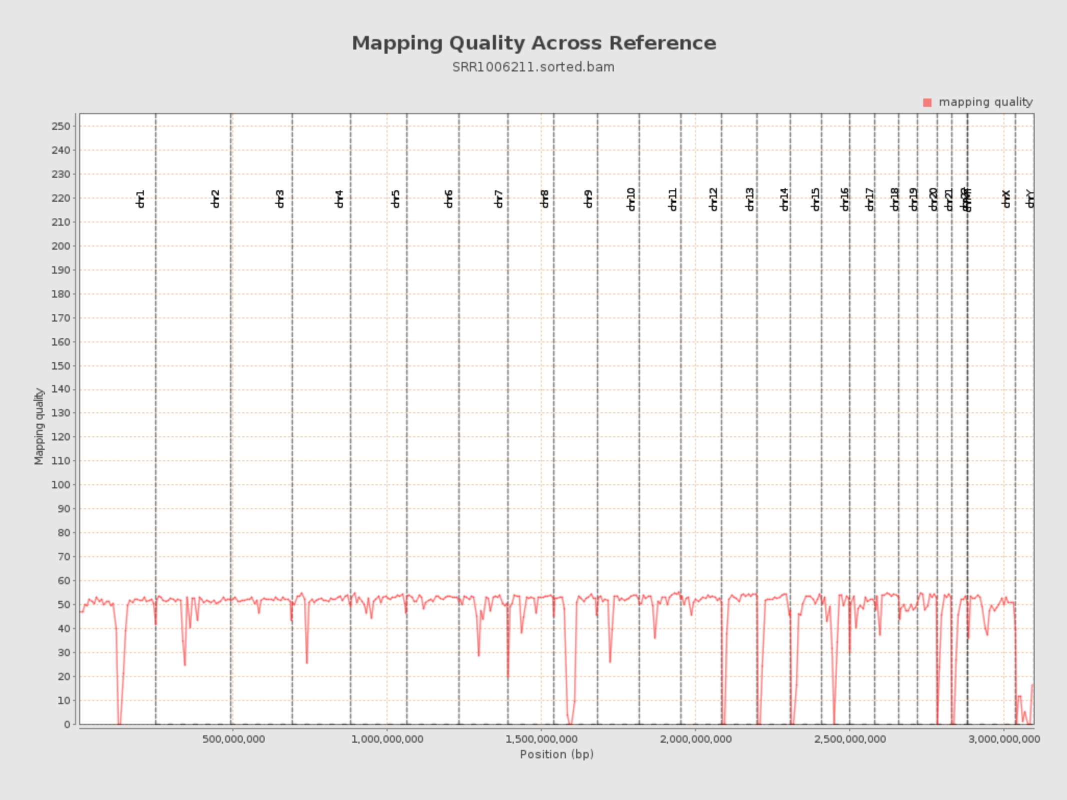
# 10. Results : Mapped Reads Clipping Profile



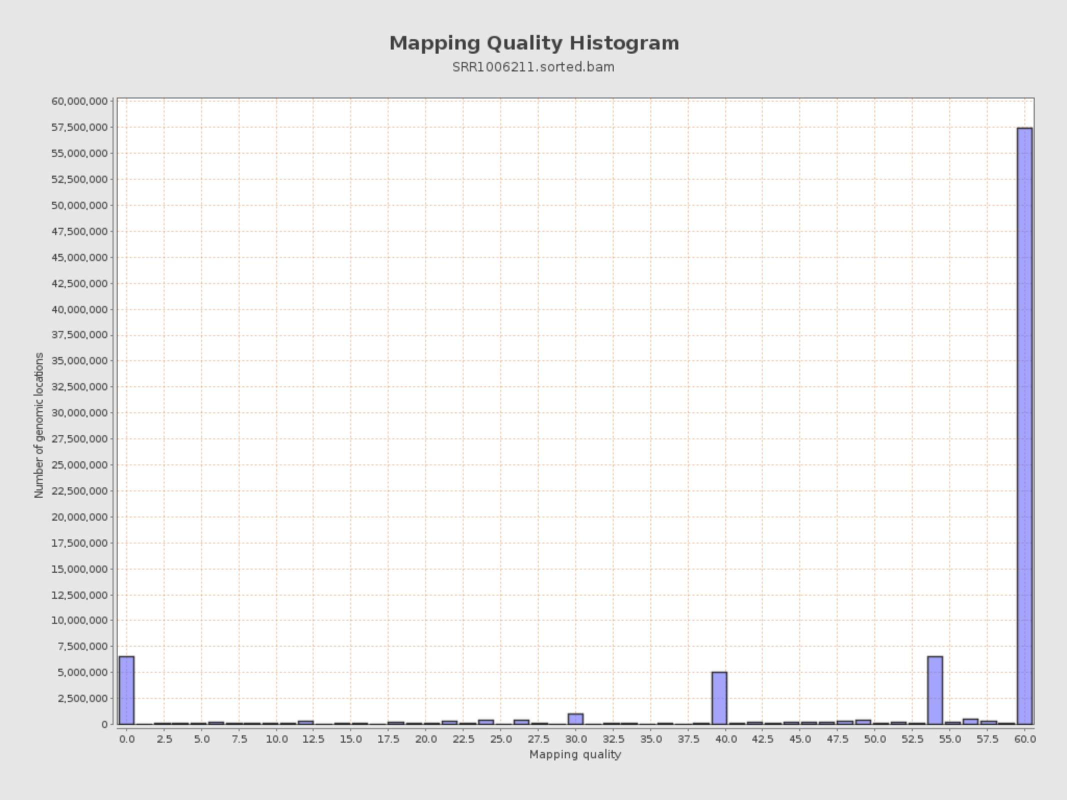
# 11. Results : Homopolymer Indels



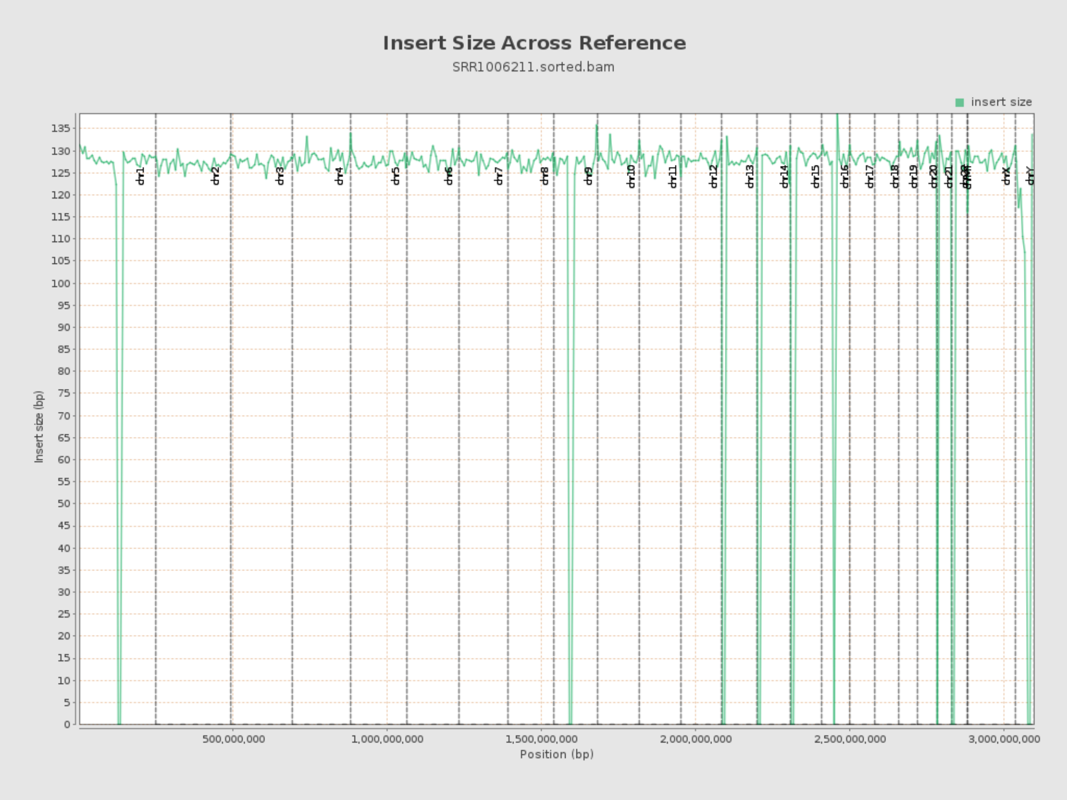
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram