# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/09 11:42:02*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR617485.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_SRR617485 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617485_1.fastq.gz SRR617485_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Oct 09 11:42:01 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR617485.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 32,000,000 |
| Mapped reads | 30,545,177 / 95.45% |
| Unmapped reads | 1,454,823 / 4.55% |
| Mapped paired reads | 30,545,177 / 95.45% |
| Mapped reads, first in pair | 15,433,292 / 48.23% |
| Mapped reads,  second in pair | 15,111,885 / 47.22% |
| Mapped reads, both in pair | 29,965,504 / 93.64% |
| Mapped reads, singletons | 579,673 / 1.81% |
| Secondary alignments | 0 |
| Supplementary alignments | 136,887 / 0.43% |
| Read min/max/mean length | 30 / 100 / 100.17 |
| Duplicated reads (estimated) | 6,314,744 / 19.73% |
| Duplication rate | 10.01% |
| Clipped reads | 5,870,046 / 18.34% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 877,990,907 / 29.46% |
| Number/percentage of C's | 603,067,041 / 20.23% |
| Number/percentage of T's | 877,869,763 / 29.46% |
| Number/percentage of G's | 618,390,897 / 20.75% |
| Number/percentage of N's | 3,005,646 / 0.1% |
| | |

| | |
|---|---|
| GC Percentage | 40.98% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.9633 |
| Standard Deviation | 9.6857 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 52.78 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 29,645.66 |
| Standard Deviation | 1,591,251.55 |
| P25/Median/P75 | 175 / 223 / 296 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 1.18% |
| Mismatches | 34,240,743 |
| Insertions | 442,503 |
| Mapped reads with at least one insertion | 1.42% |
| Deletions | 1,039,797 |
| Mapped reads with at least one deletion | 3.33% |
| Homopolymer indels | 47.52% |

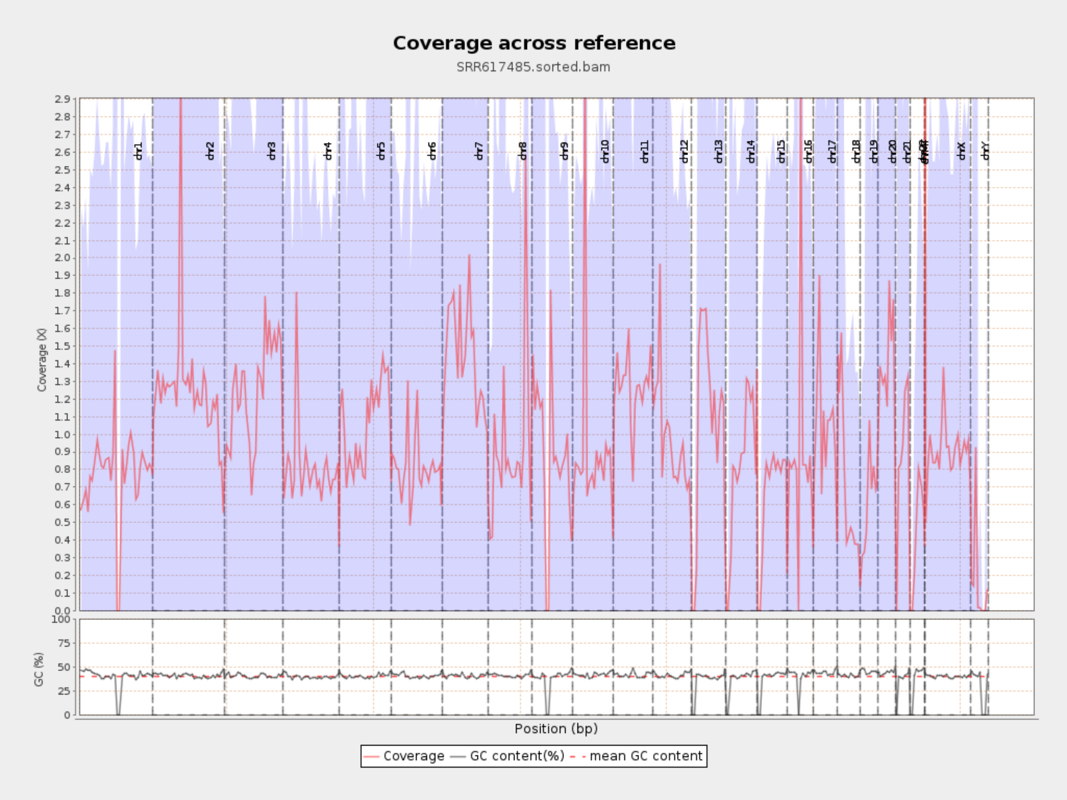
## 2.7. Chromosome stats

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

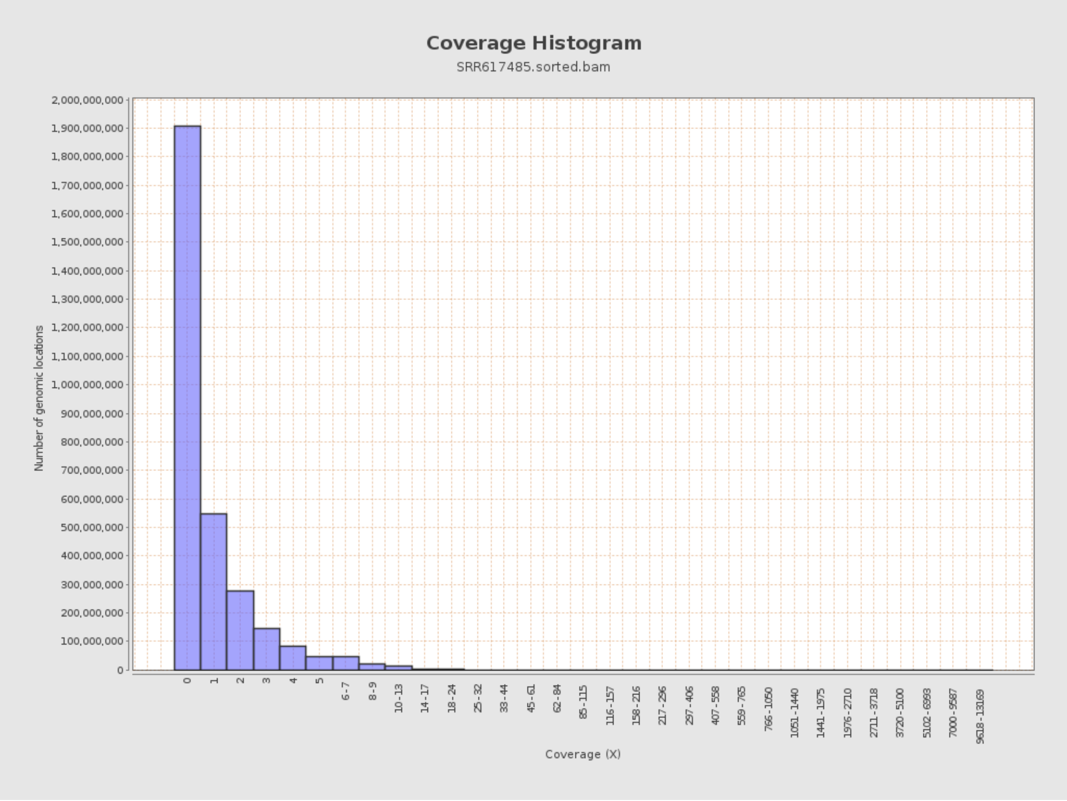
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 191909313 | 0.7699 | 9.3578 |
| chr2 | 243199373 | 307988708 | 1.2664 | 11.5103 |
| chr3 | 198022430 | 246498244 | 1.2448 | 2.2212 |
| chr4 | 191154276 | 154161709 | 0.8065 | 6.1685 |
| chr5 | 180915260 | 190878346 | 1.0551 | 2.0781 |
| chr6 | 171115067 | 140305403 | 0.8199 | 5.3535 |
| chr7 | 159138663 | 229695401 | 1.4434 | 13.0437 |
| chr8 | 146364022 | 132479937 | 0.9051 | 3.8238 |
| chr9 | 141213431 | 123677431 | 0.8758 | 18.6059 |
| chr10 | 135534747 | 126613745 | 0.9342 | 18.5368 |
| chr11 | 135006516 | 168301166 | 1.2466 | 12.6448 |
| chr12 | 133851895 | 130047930 | 0.9716 | 1.9671 |
| chr13 | 115169878 | 126502085 | 1.0984 | 2.1196 |
| chr14 | 107349540 | 86798034 | 0.8086 | 2.1973 |
| chr15 | 102531392 | 67531223 | 0.6586 | 1.4521 |
| chr16 | 90354753 | 80297795 | 0.8887 | 14.7122 |
| chr17 | 81195210 | 83529422 | 1.0287 | 13.4206 |
| chr18 | 78077248 | 53394408 | 0.6839 | 17.0334 |
| chr19 | 59128983 | 35632091 | 0.6026 | 5.8357 |
| chr20 | 63025520 | 88339718 | 1.4016 | 2.801 |
| chr21 | 48129895 | 42889095 | 0.8911 | 3.8225 |
| chr22 | 51304566 | 22366013 | 0.4359 | 1.2542 |
| chrMT | 16571 | 2086023 | 125.884 | 92.5318 |
| chrX | 155270560 | 139930725 | 0.9012 | 4.0789 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 10246779 | 0.1726 | 13.6697 |

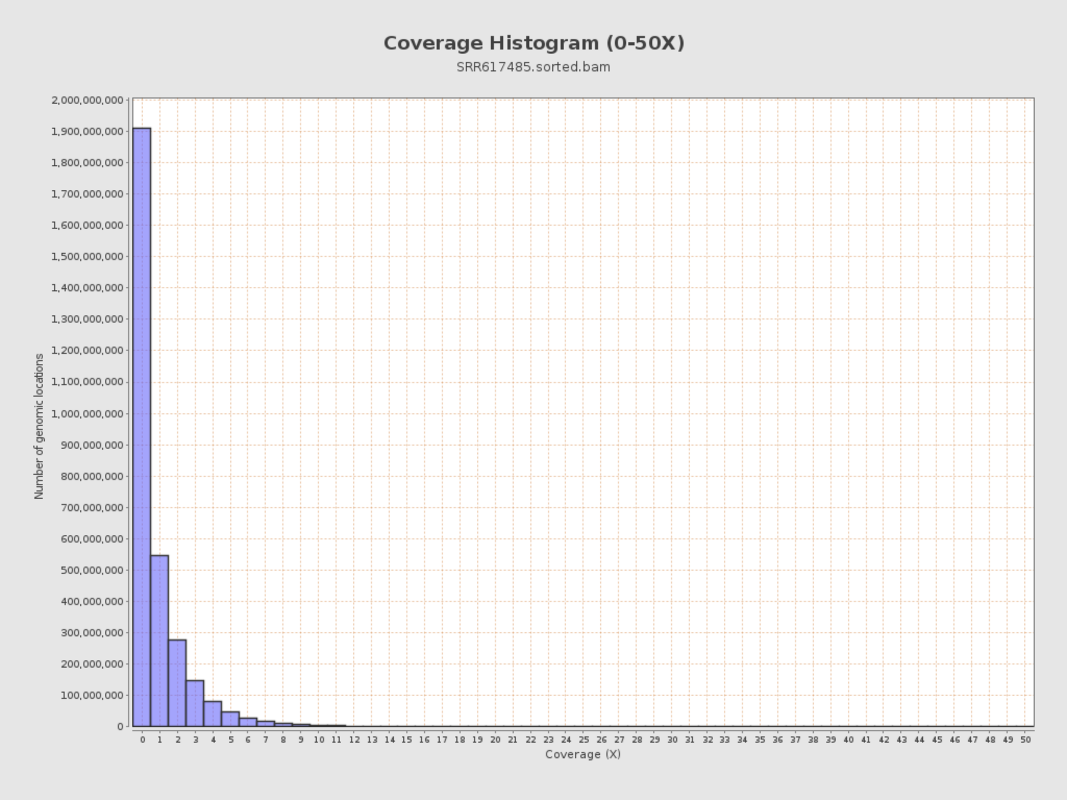
# 3. Results : Coverage across reference



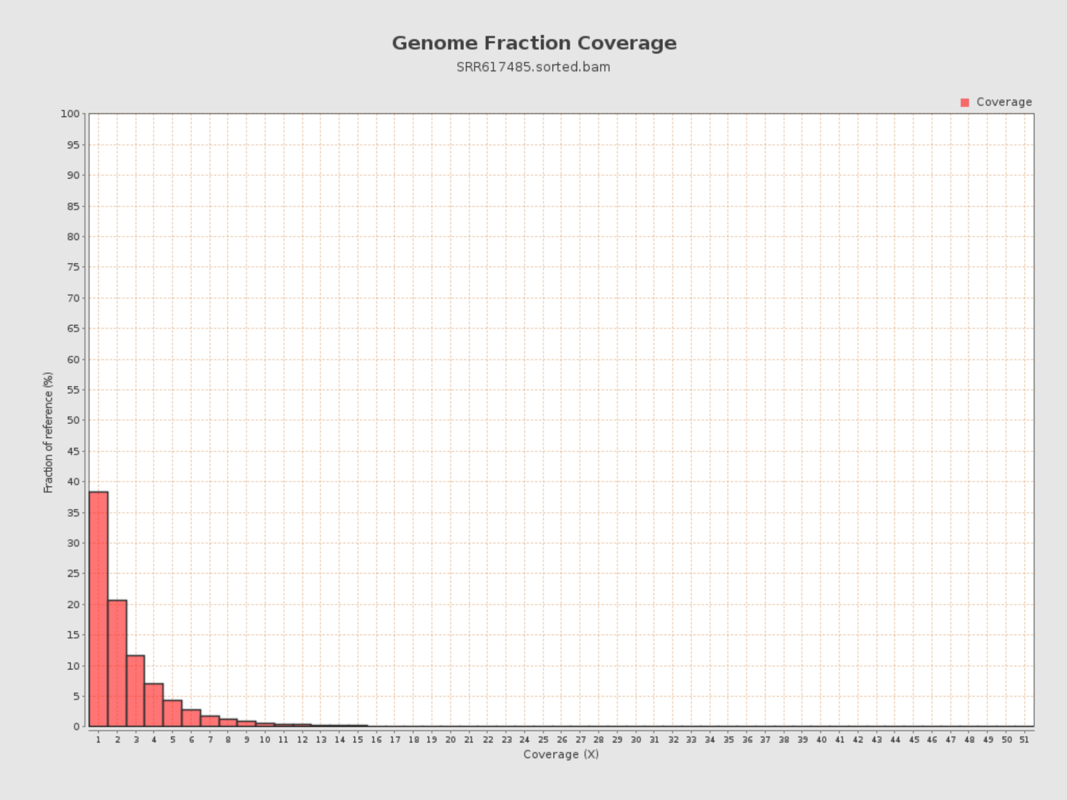
# 4. Results : Coverage Histogram



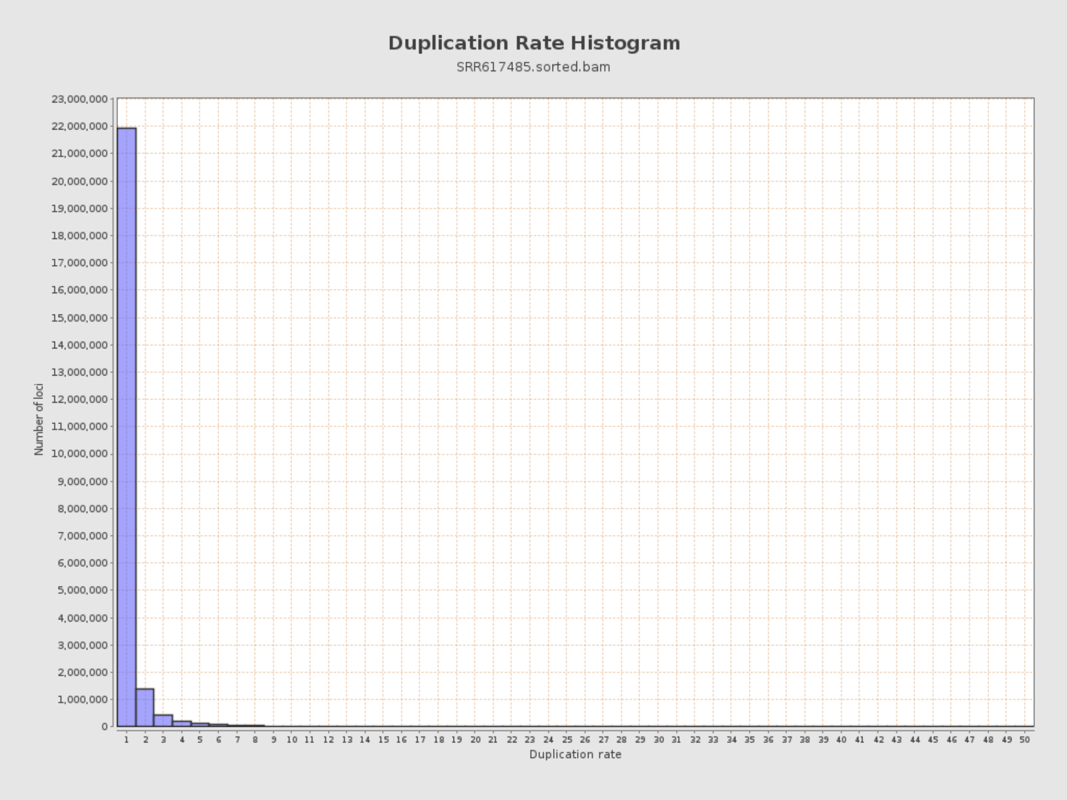
# 5. Results : Coverage Histogram (0-50X)



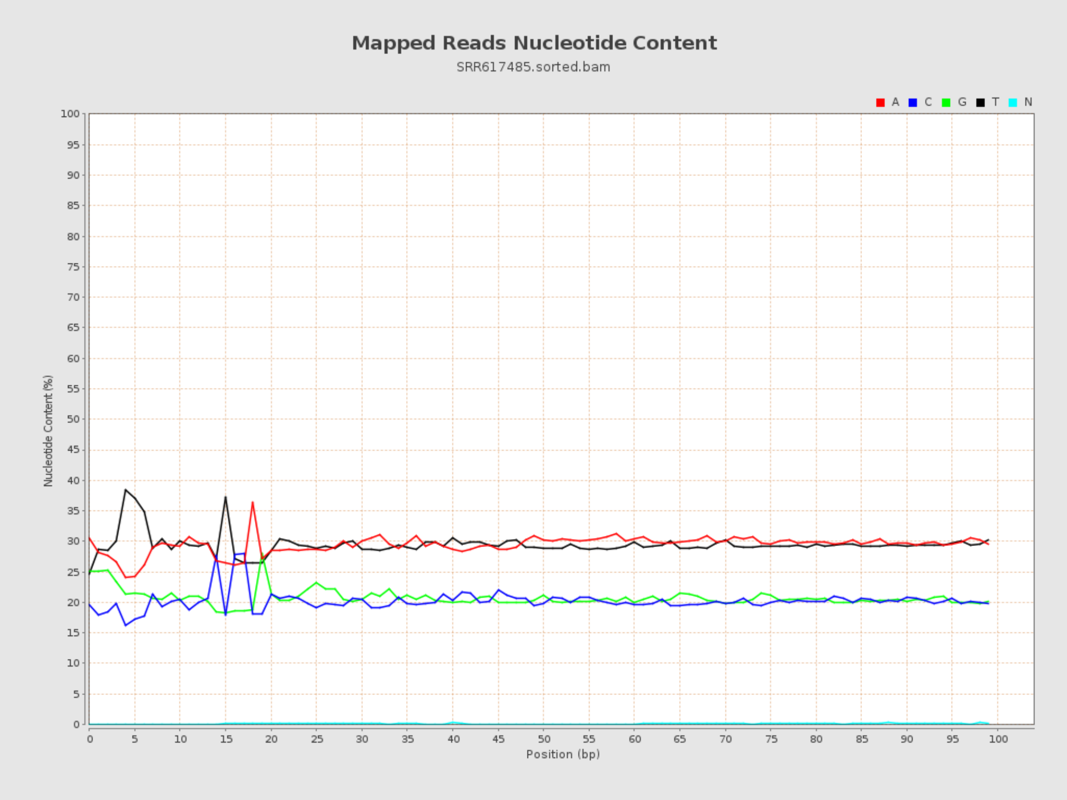
# 6. Results : Genome Fraction Coverage



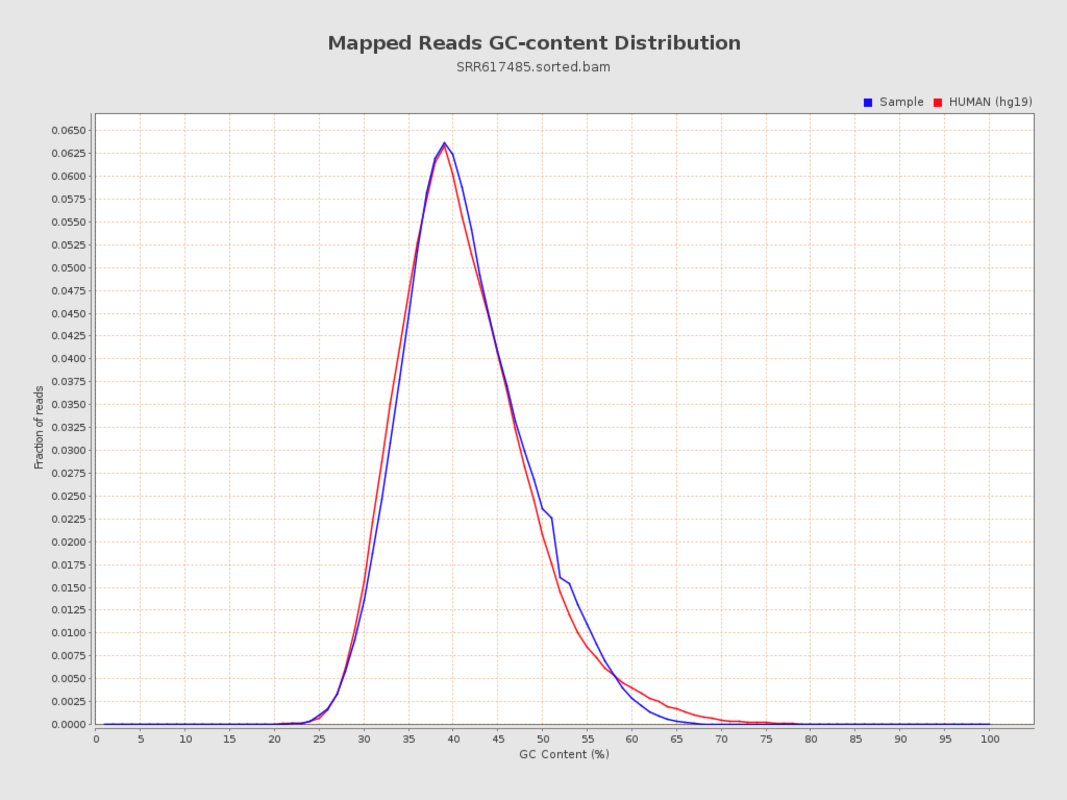
# 7. Results : Duplication Rate Histogram



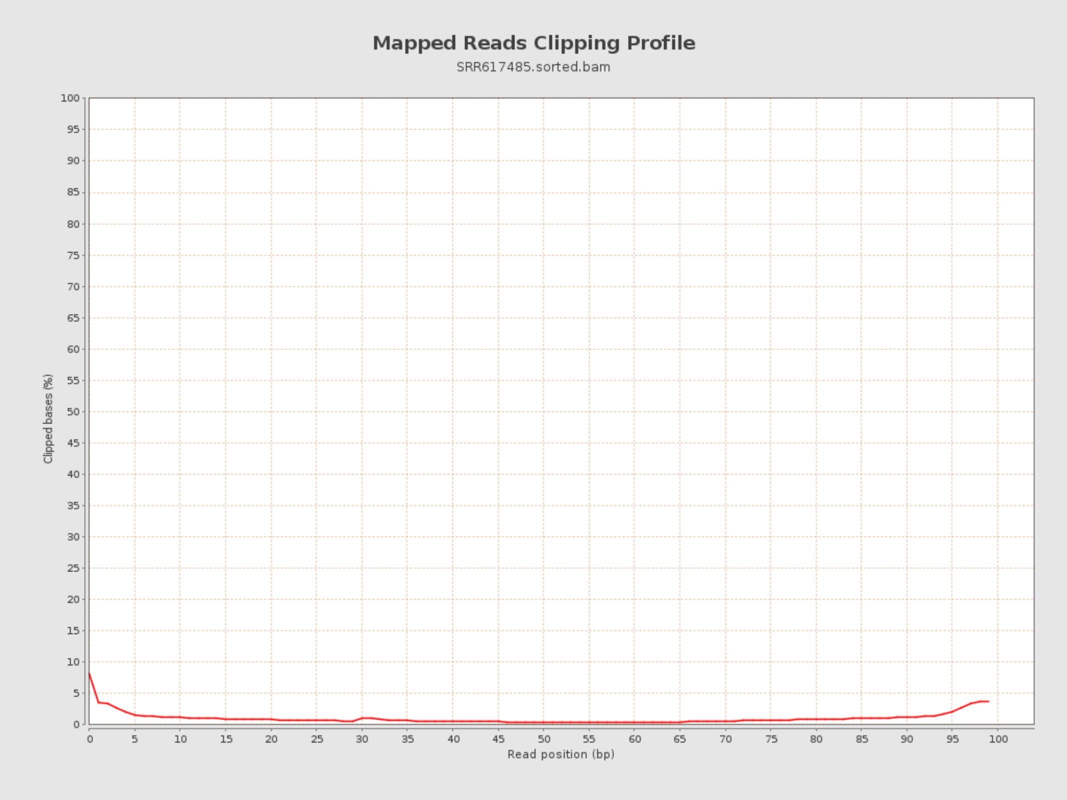
# 8. Results : Mapped Reads Nucleotide Content



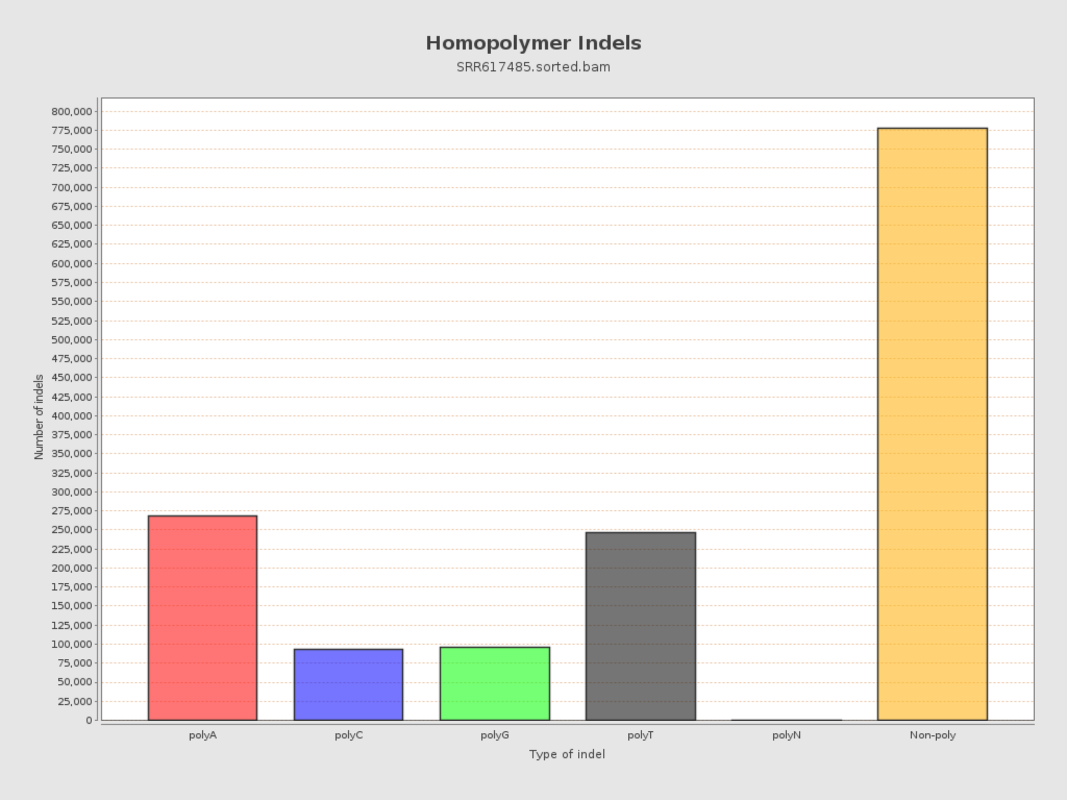
# 9. Results : Mapped Reads GC-content Distribution



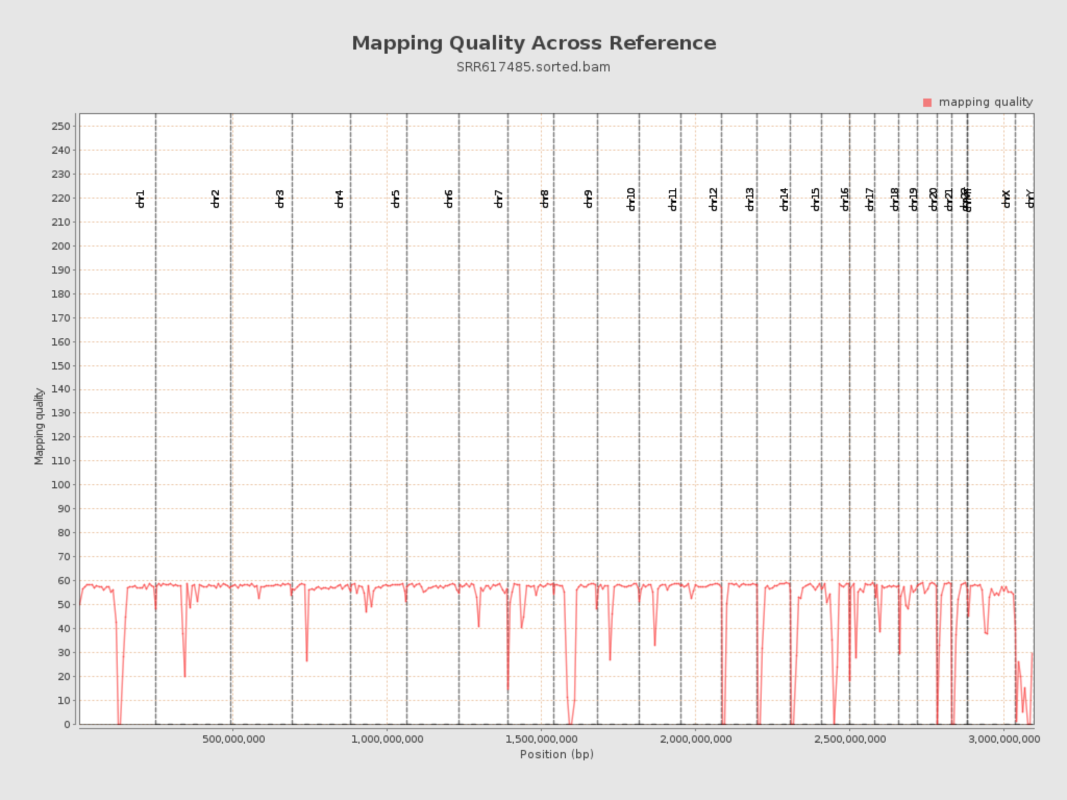
# 10. Results : Mapped Reads Clipping Profile



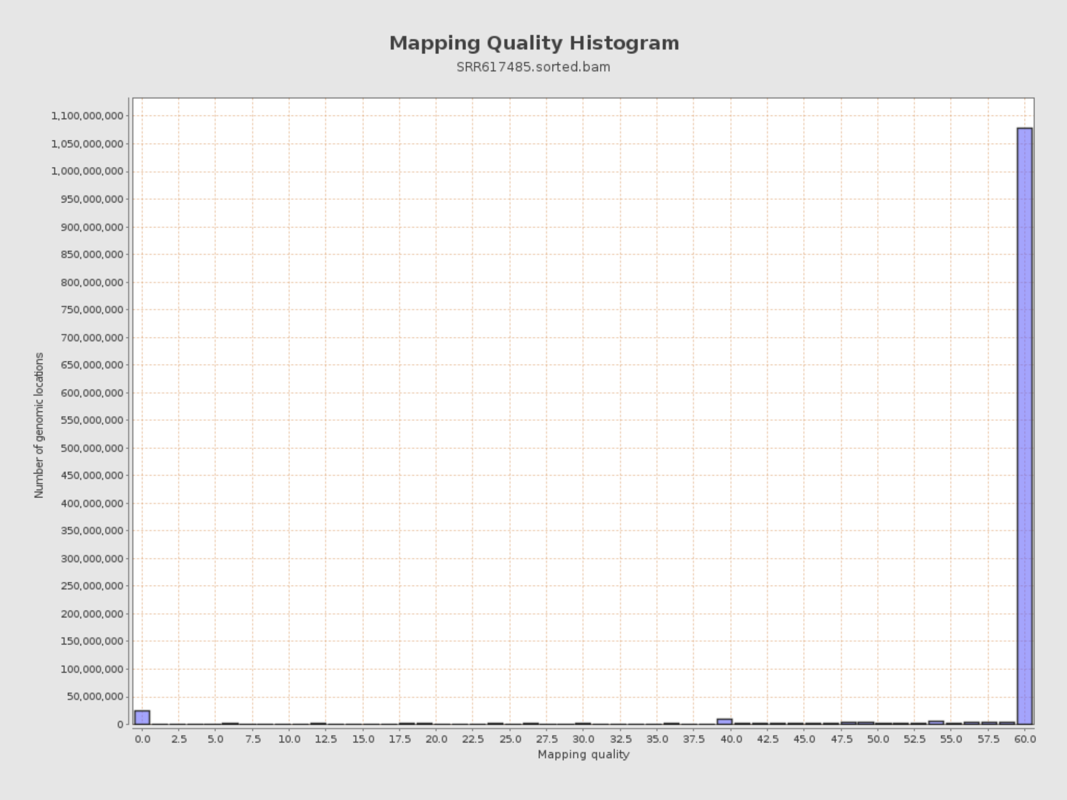
# 11. Results : Homopolymer Indels



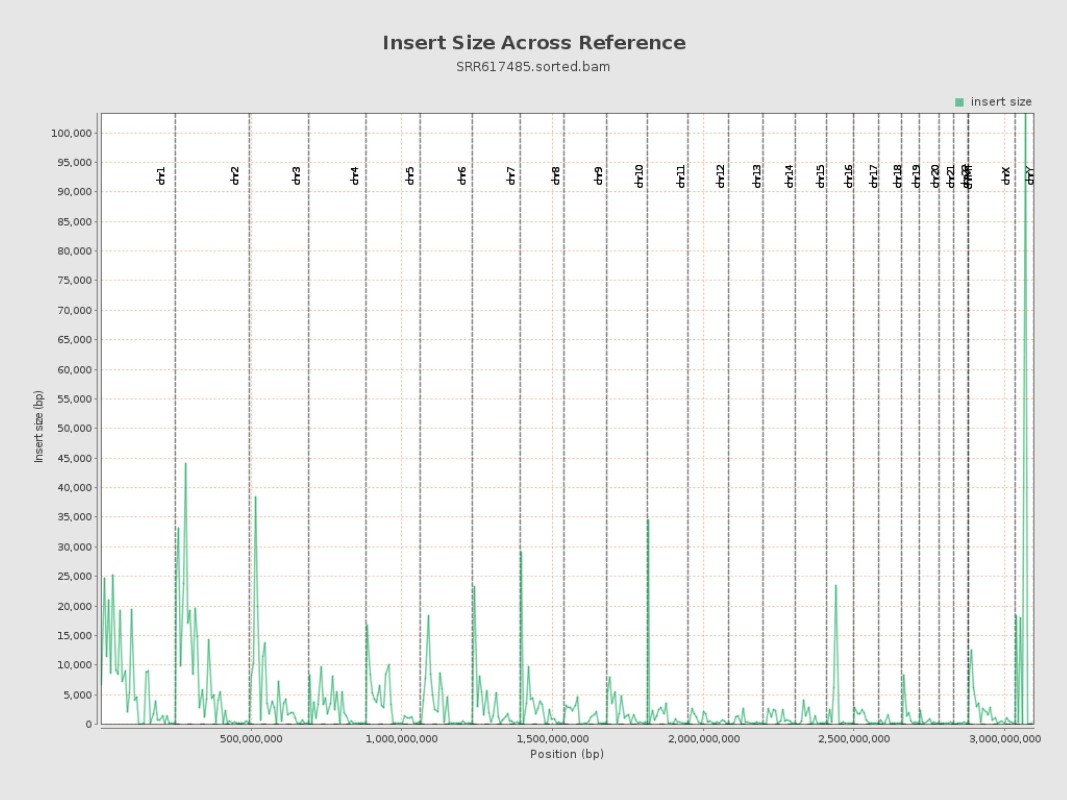
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram