# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/22 02:19:39*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR504599.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_SRR504599 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504599_1.fastq.gz SRR504599_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Dec 22 02:19:38 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR504599.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 409,492,050 |
| Mapped reads | 352,316,198 / 86.04% |
| Unmapped reads | 57,175,852 / 13.96% |
| Mapped paired reads | 352,316,198 / 86.04% |
| Mapped reads, first in pair | 176,412,959 / 43.08% |
| Mapped reads, second in pair | 175,903,239 / 42.96% |
| Mapped reads, both in pair | 350,196,992 / 85.52% |
| Mapped reads, singletons | 2,119,206 / 0.52% |
| Secondary alignments | 0 |
| Supplementary alignments | 1,947,847 / 0.48% |
| Read min/max/mean length | 30 / 100 / 100.2 |
| Duplicated reads (estimated) | 83,828,233 / 20.47% |
| Duplication rate | 21.25% |
| Clipped reads | 17,501,142 / 4.27% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 9,227,200,768 / 26.39% |
| Number/percentage of C's | 8,185,010,007 / 23.41% |
| Number/percentage of T's | 9,256,027,364 / 26.47% |
| Number/percentage of G's | 8,293,590,225 / 23.72% |
| Number/percentage of N's | 4,731,859 / 0.01% |
| | |

| | |
|---|---|
| GC Percentage | 47.13% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 11.2982 |
| Standard Deviation | 23.3668 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.97 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 29,791.79 |
| Standard Deviation | 1,672,309.73 |
| P25/Median/P75 | 180 / 213 / 266 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 174,781,559 |
| Insertions | 2,651,675 |
| Mapped reads with at least one insertion | 0.73% |
| Deletions | 3,552,450 |
| Mapped reads with at least one deletion | 0.98% |
| Homopolymer indels | 40.54% |

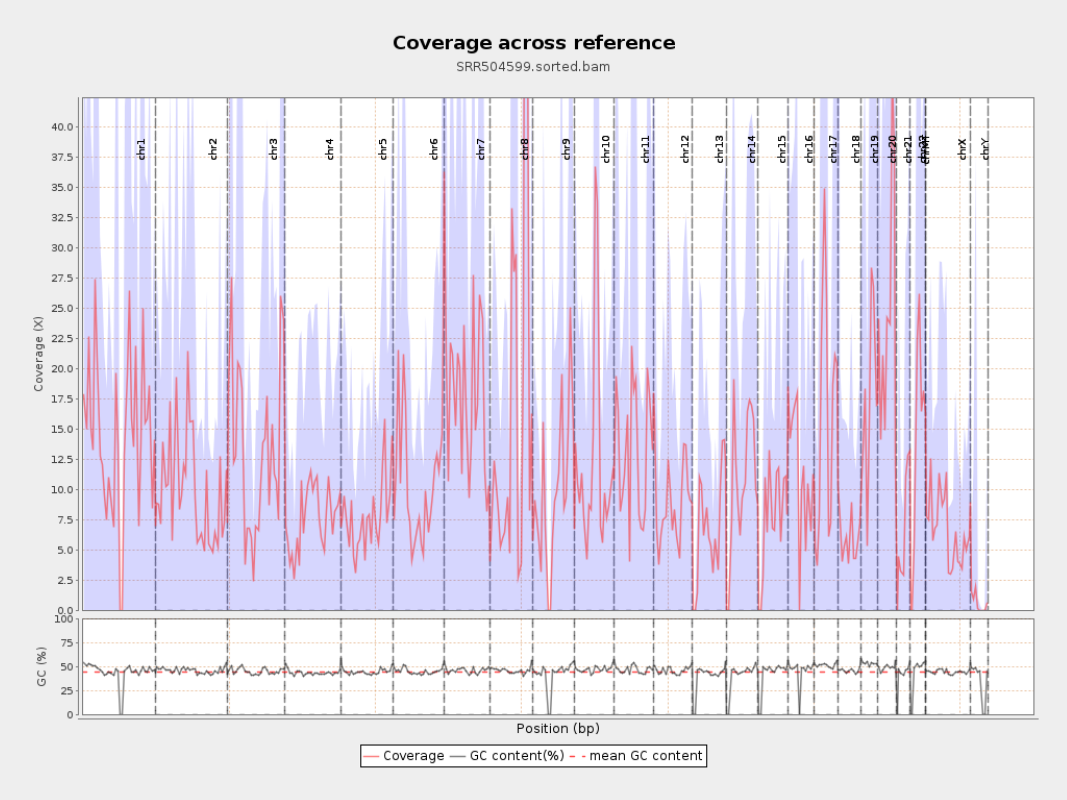
## 2.7. Chromosome stats

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

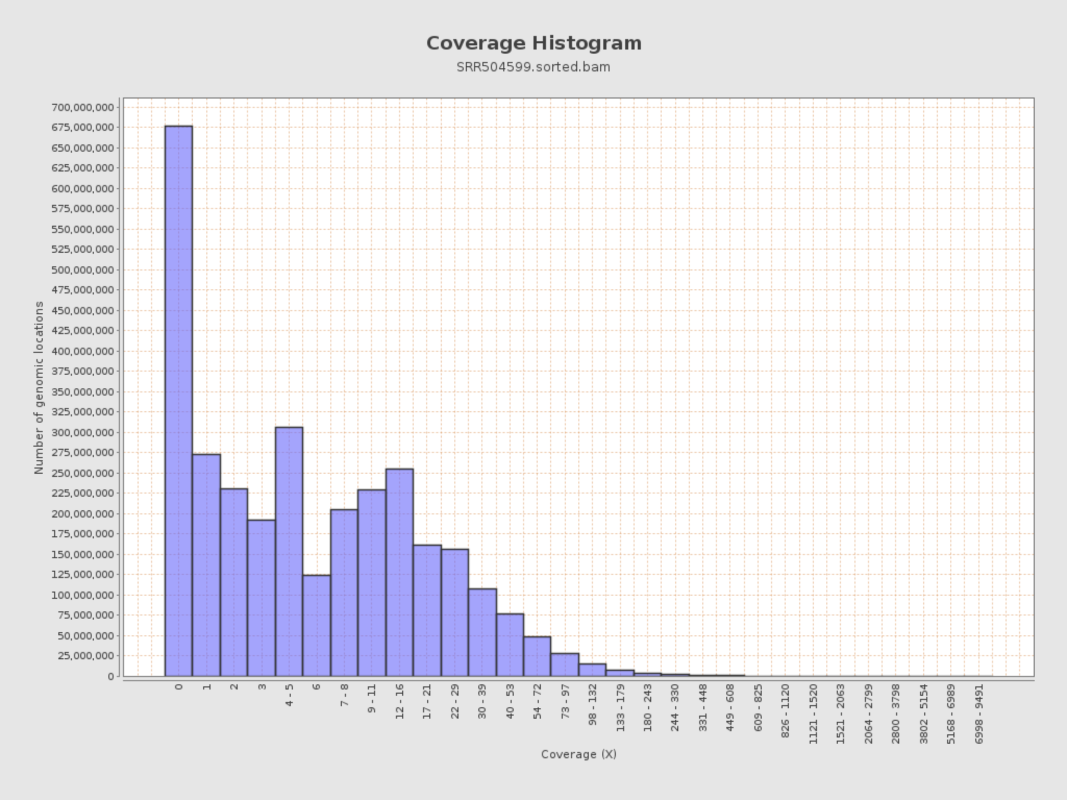
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 3589125933 | 14.3997 | 24.3019 |
| chr2 | 243199373 | 2399480474 | 9.8663 | 17.624 |
| chr3 | 198022430 | 2590390774 | 13.0813 | 21.5987 |
| chr4 | 191154276 | 1466964301 | 7.6742 | 12.1668 |
| chr5 | 180915260 | 1424050875 | 7.8714 | 13.2249 |
| chr6 | 171115067 | 1788690988 | 10.4531 | 17.0257 |
| chr7 | 159138663 | 2847049181 | 17.8904 | 26.5686 |
| chr8 | 146364022 | 2673003895 | 18.2627 | 44.8947 |
| chr9 | 141213431 | 1374163683 | 9.7311 | 19.021 |
| chr10 | 135534747 | 1646067272 | 12.145 | 22.9497 |
| chr11 | 135006516 | 1781223989 | 13.1936 | 22.2959 |
| chr12 | 133851895 | 1192224561 | 8.907 | 14.967 |
| chr13 | 115169878 | 795710100 | 6.909 | 12.9513 |
| chr14 | 107349540 | 1168485618 | 10.8849 | 18.9049 |
| chr15 | 102531392 | 779501333 | 7.6026 | 14.1921 |
| chr16 | 90354753 | 1019850994 | 11.2872 | 19.3814 |
| chr17 | 81195210 | 1266872529 | 15.6028 | 47.9968 |
| chr18 | 78077248 | 458006851 | 5.8661 | 27.4521 |
| chr19 | 59128983 | 1027120655 | 17.3708 | 30.1315 |
| chr20 | 63025520 | 1571632116 | 24.9364 | 37.1993 |
| chr21 | 48129895 | 331988449 | 6.8978 | 17.5133 |
| chr22 | 51304566 | 717031460 | 13.976 | 26.018 |
| chrMT | 16571 | 240818 | 14.5325 | 12.0777 |
| chrX | 155270560 | 1031472225 | 6.6431 | 11.7209 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 35306902 | 0.5947 | 14.2349 |

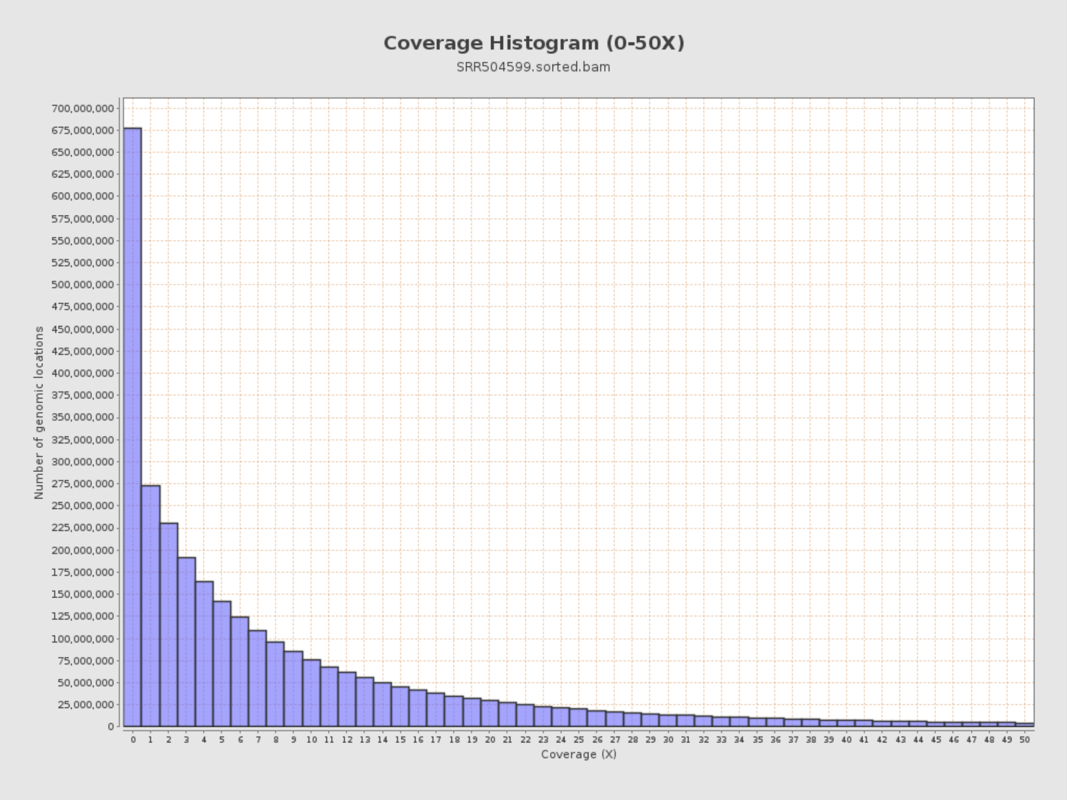
# 3. Results : Coverage across reference



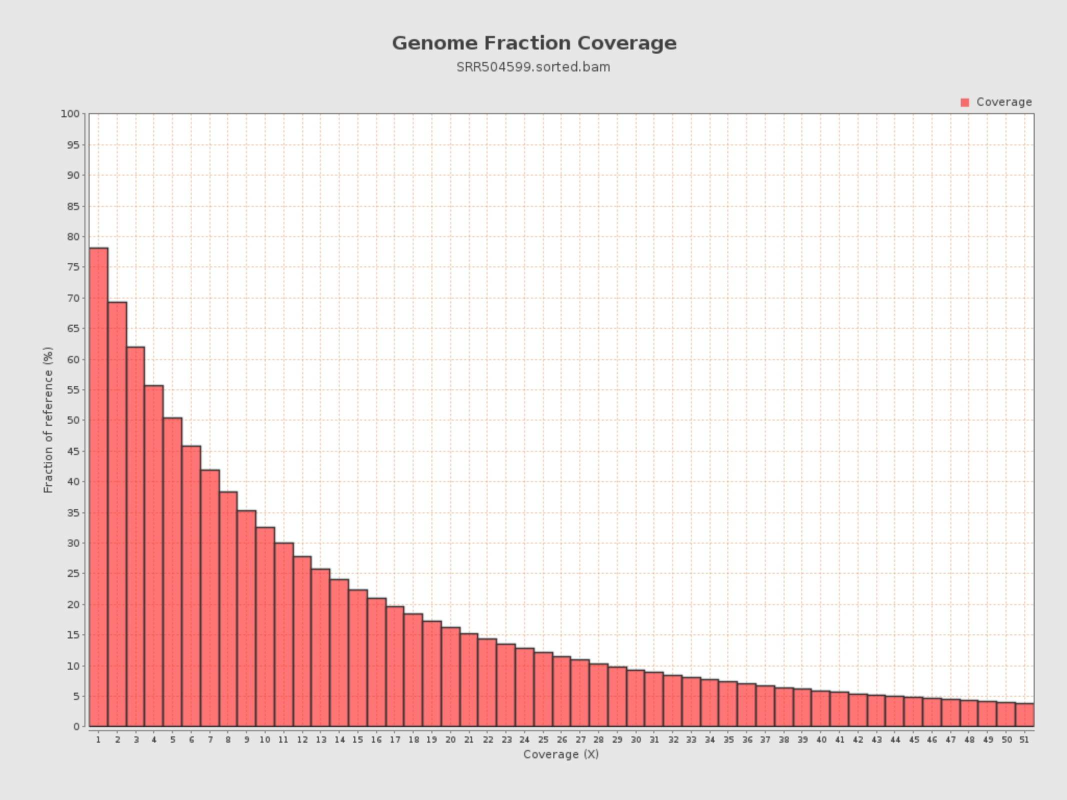
# 4. Results : Coverage Histogram



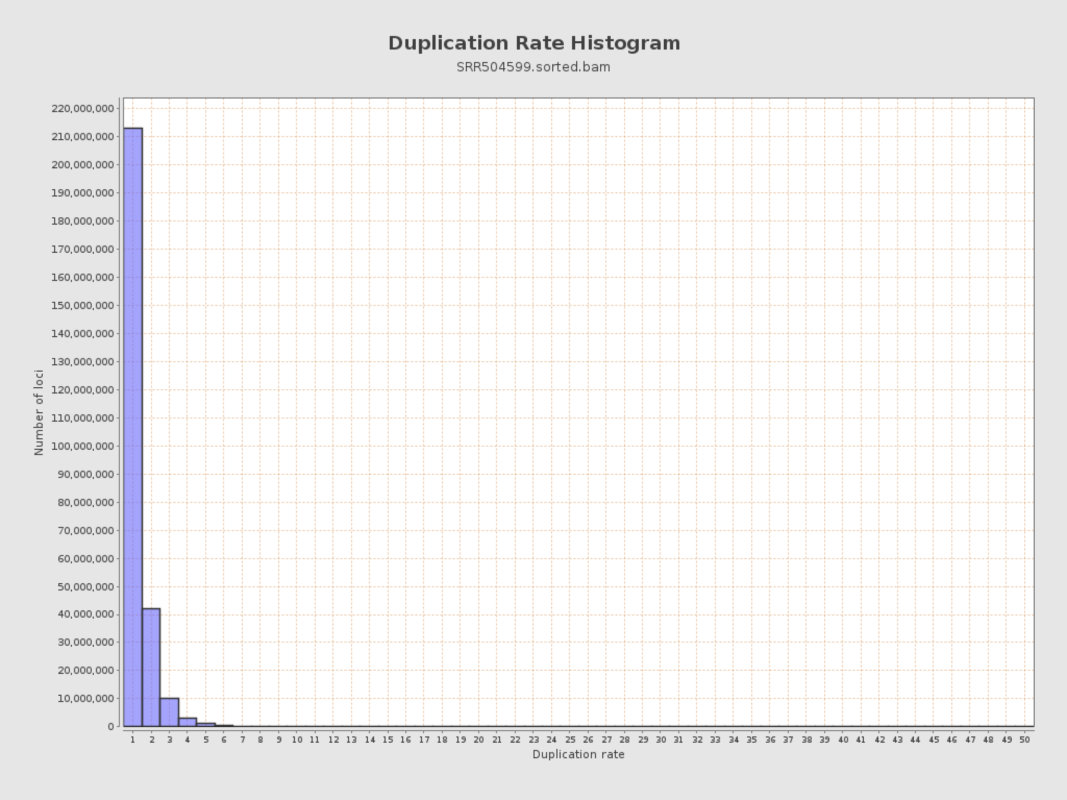
# 5. Results : Coverage Histogram (0-50X)



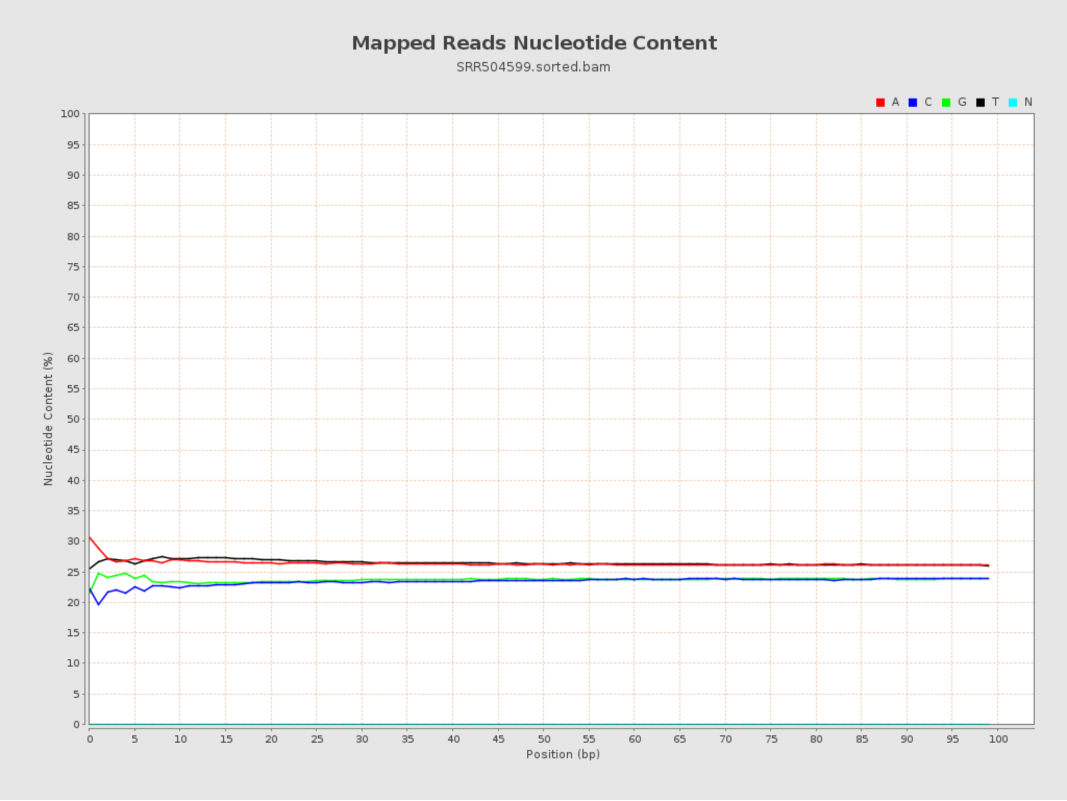
# 6. Results : Genome Fraction Coverage



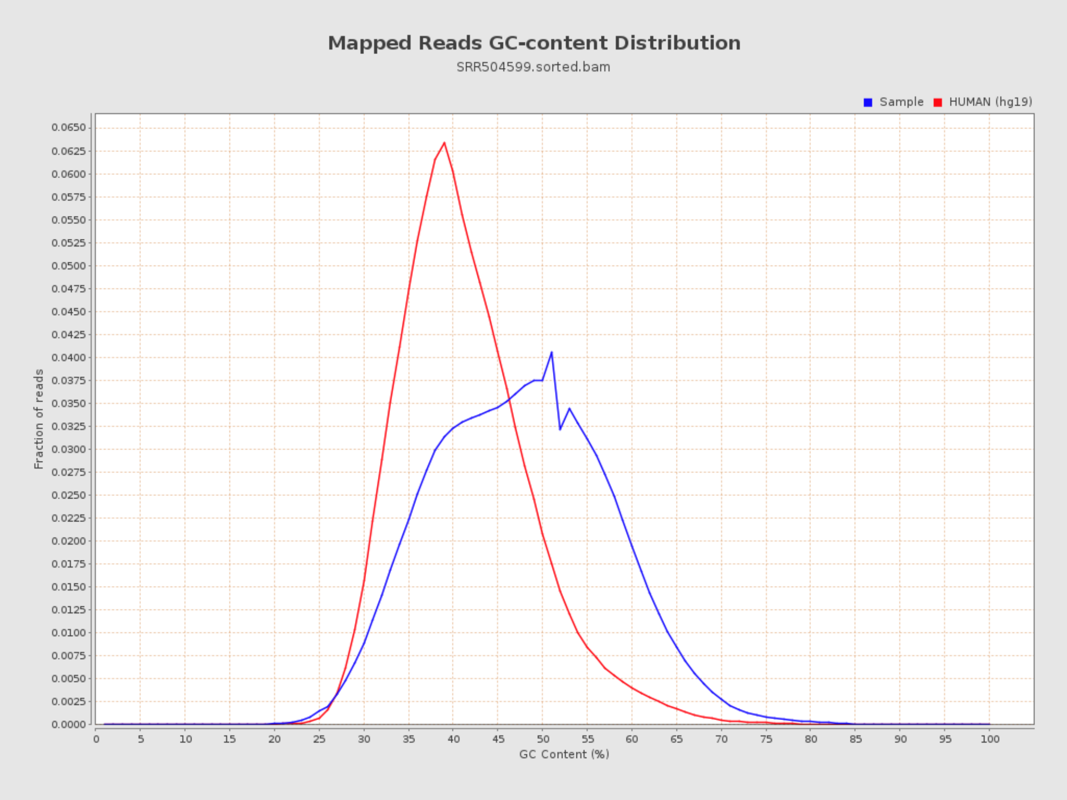
# 7. Results : Duplication Rate Histogram



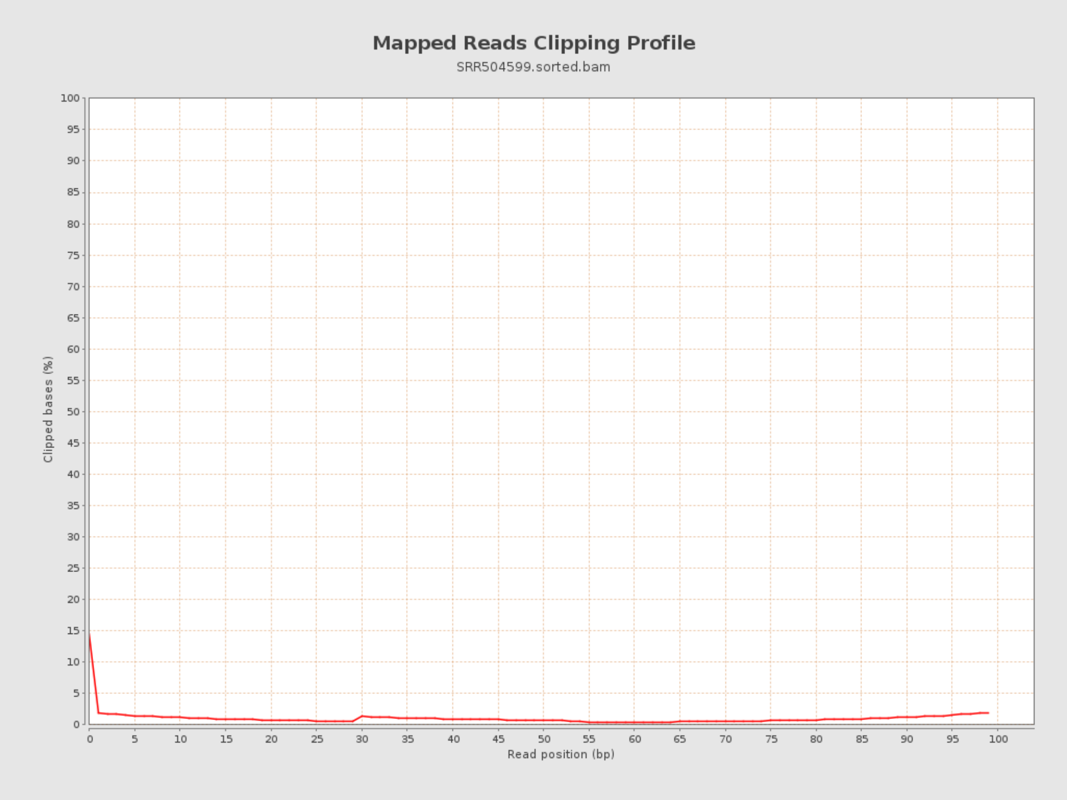
# 8. Results : Mapped Reads Nucleotide Content



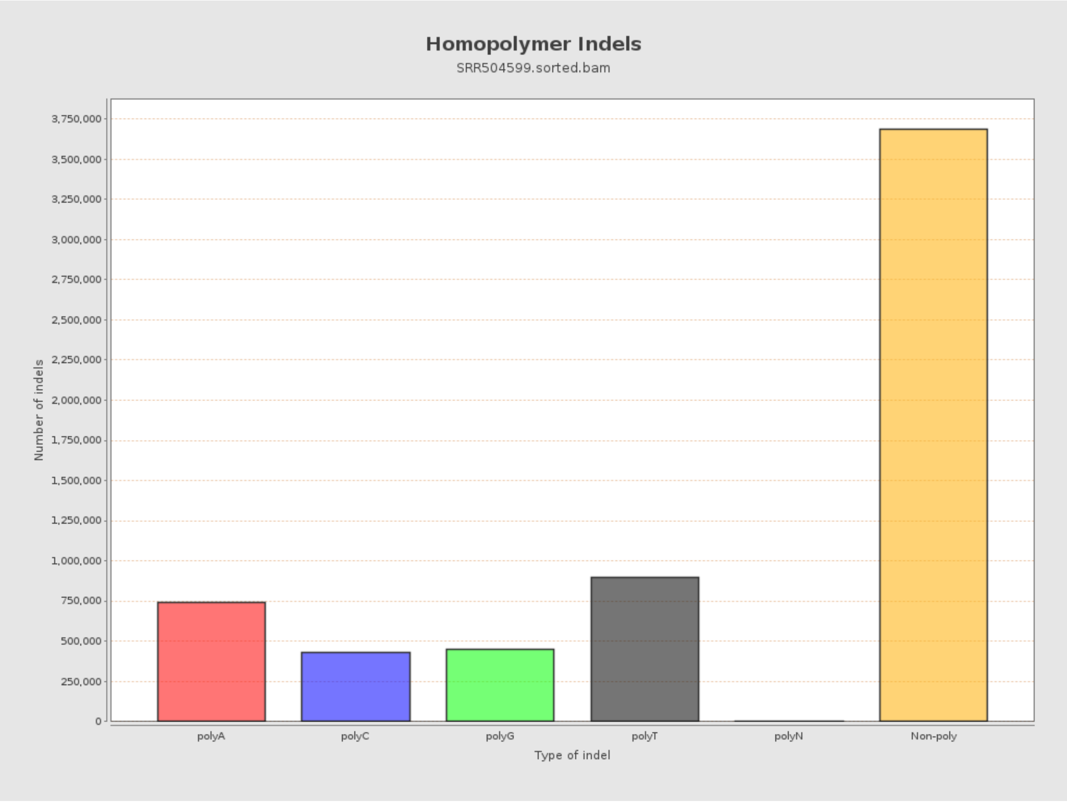
# 9. Results : Mapped Reads GC-content Distribution



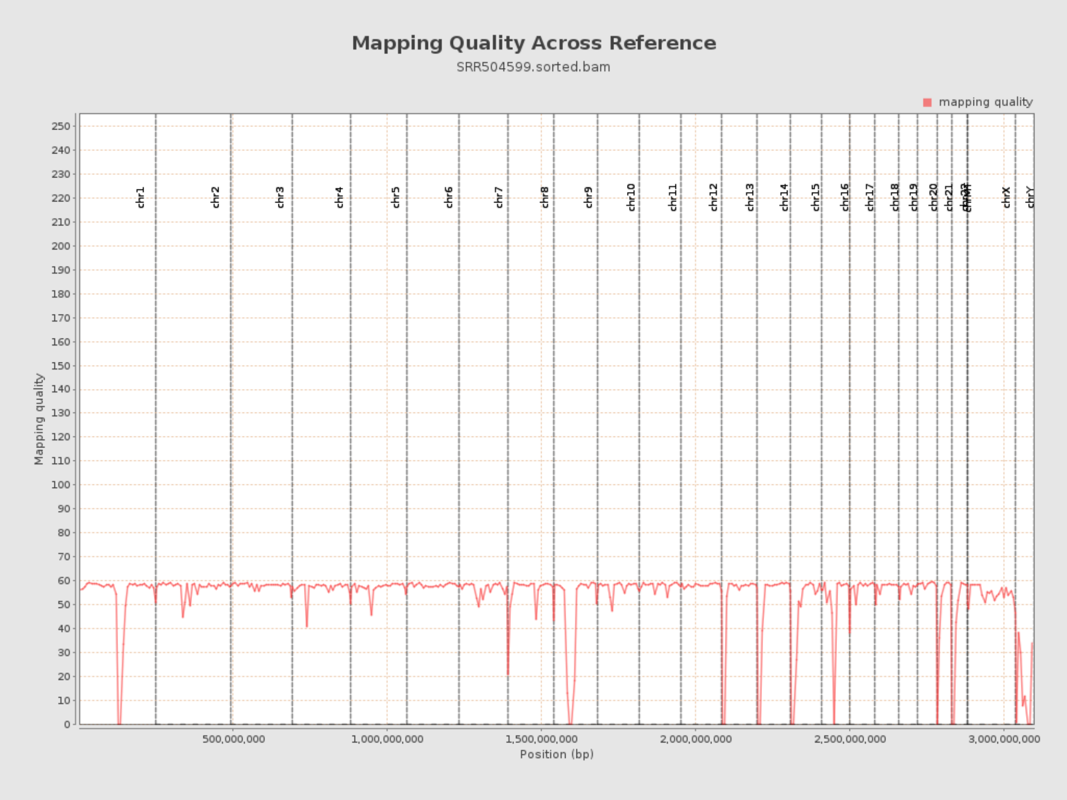
# 10. Results : Mapped Reads Clipping Profile



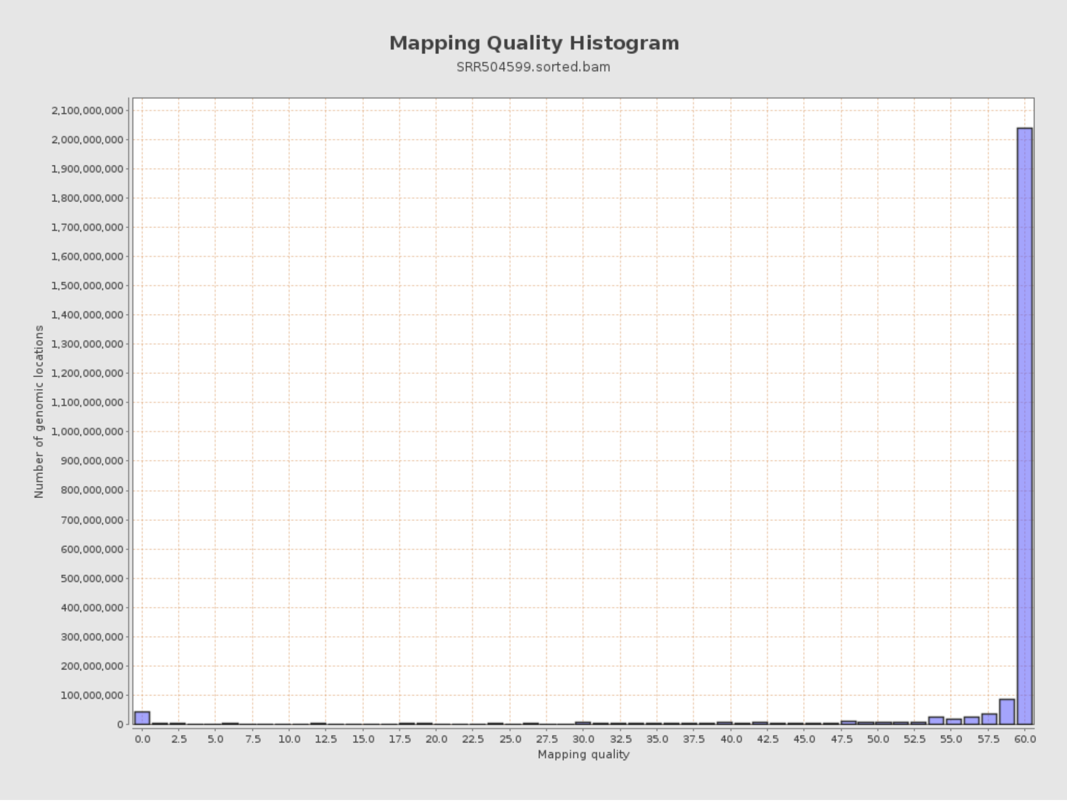
# 11. Results : Homopolymer Indels



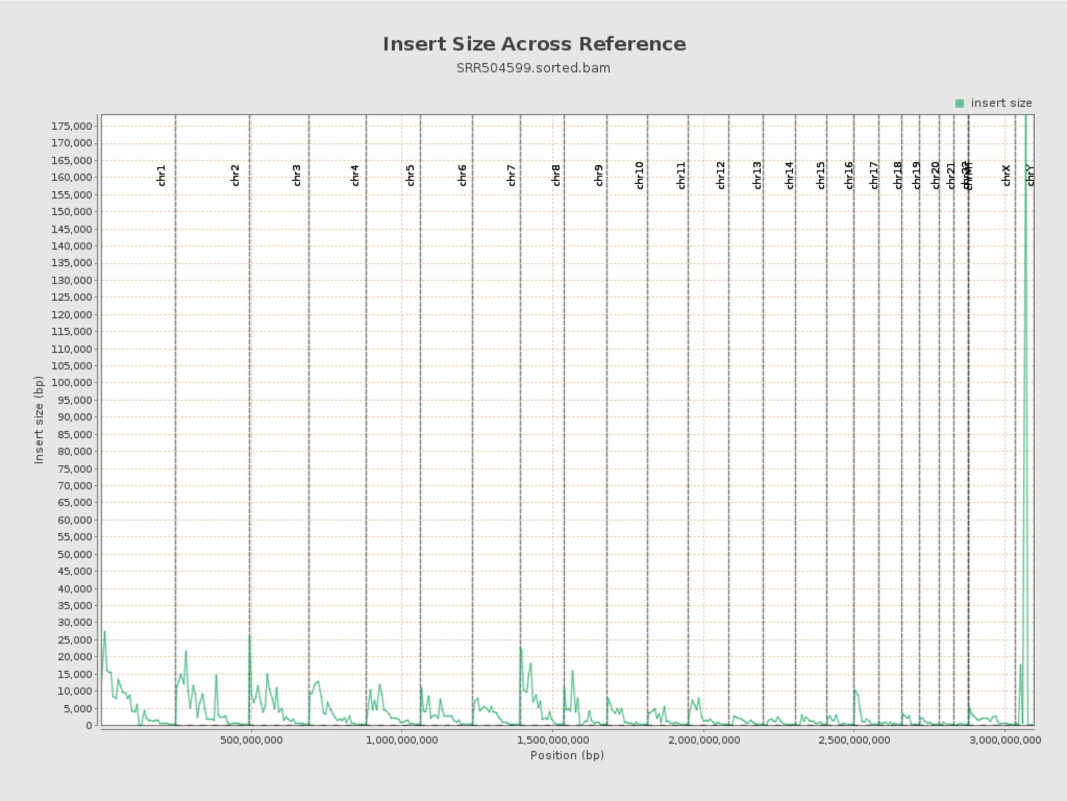
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram