# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/10 04:44:51*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124915.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_SRR3124915 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124915_1.fastq.gz SRR3124915_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Dec 10 04:44:51 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3124915.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 4,236,102 |
| Mapped reads | 4,179,243 / 98.66% |
| Unmapped reads | 56,859 / 1.34% |
| Mapped paired reads | 4,179,243 / 98.66% |
| Mapped reads, first in pair | 2,093,499 / 49.42% |
| Mapped reads, second in pair | 2,085,744 / 49.24% |
| Mapped reads, both in pair | 4,163,780 / 98.29% |
| Mapped reads, singletons | 15,463 / 0.37% |
| Secondary alignments | 0 |
| Supplementary alignments | 17,047 / 0.4% |
| Read min/max/mean length | 30 / 101 / 101.16 |
| Duplicated reads (estimated) | 272,174 / 6.43% |
| Duplication rate | 4.75% |
| Clipped reads | 2,014,062 / 47.55% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 101,756,942 / 28.09% |
| Number/percentage of C's | 67,389,732 / 18.6% |
| Number/percentage of T's | 107,628,730 / 29.71% |
| Number/percentage of G's | 85,309,598 / 23.55% |
| Number/percentage of N's | 137,688 / 0.04% |
| | |

| | |
|---|---|
| GC Percentage | 42.16% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1171 |
| Standard Deviation | 0.8953 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 52.7 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 33,384.57 |
| Standard Deviation | 1,740,120.64 |
| P25/Median/P75 | 147 / 196 / 271 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.75% |
| Mismatches | 2,602,443 |
| Insertions | 49,060 |
| Mapped reads with at least one insertion | 1.14% |
| Deletions | 116,031 |
| Mapped reads with at least one deletion | 2.72% |
| Homopolymer indels | 47.28% |

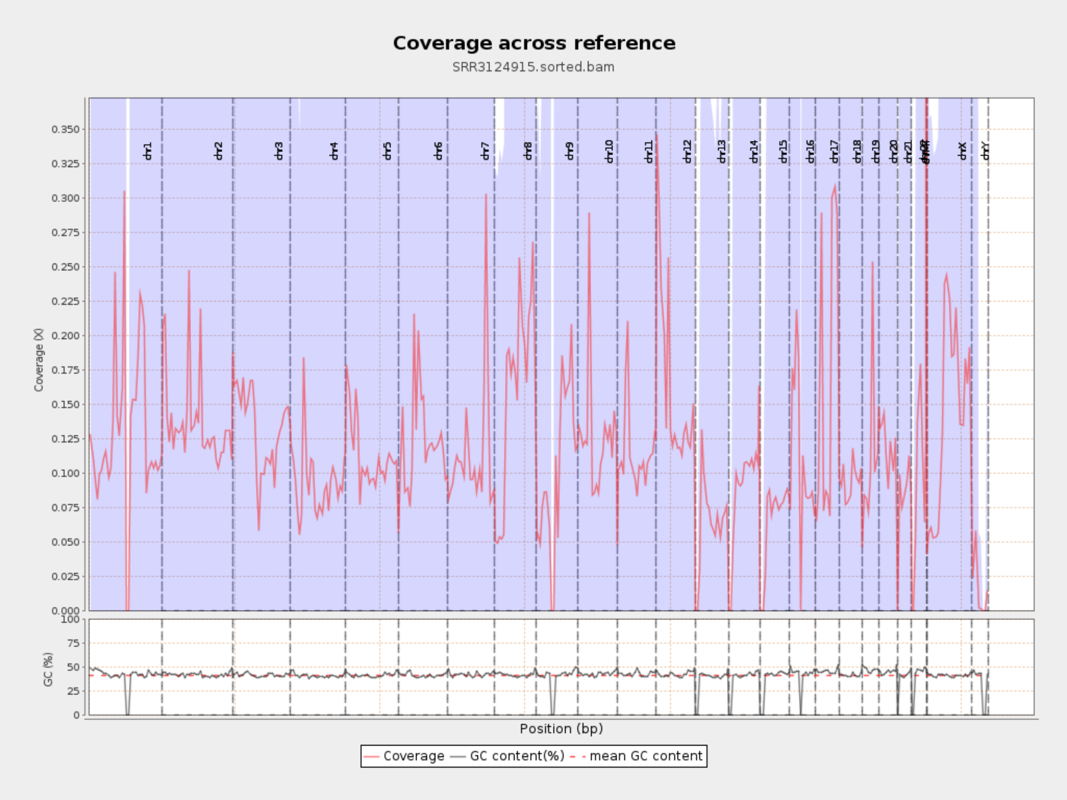
## 2.7. Chromosome stats

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

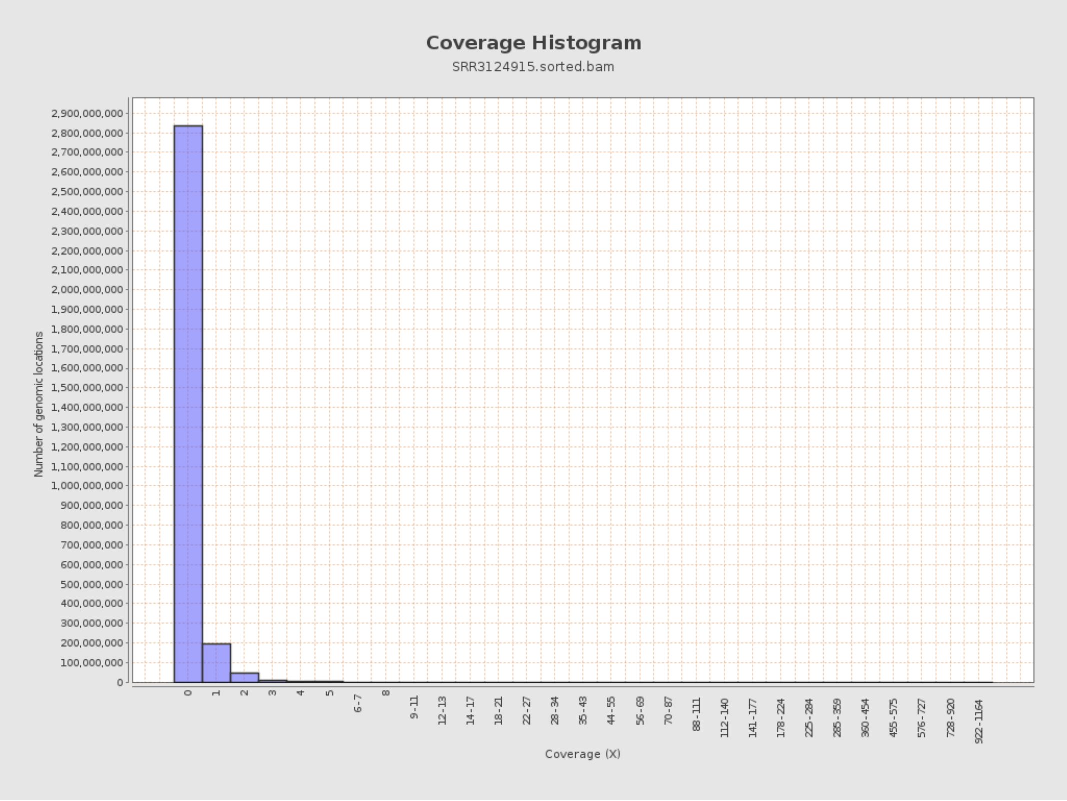
| | | **bases** | **coverage** | **deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 32448373 | 0.1302 | 1.046 |
| chr2 | 243199373 | 33635217 | 0.1383 | 1.2866 |
| chr3 | 198022430 | 26239092 | 0.1325 | 0.4605 |
| chr4 | 191154276 | 17631804 | 0.0922 | 0.6344 |
| chr5 | 180915260 | 20361861 | 0.1125 | 0.4357 |
| chr6 | 171115067 | 21009219 | 0.1228 | 0.7345 |
| chr7 | 159138663 | 18489545 | 0.1162 | 1.0434 |
| chr8 | 146364022 | 23308798 | 0.1593 | 0.7808 |
| chr9 | 141213431 | 14401076 | 0.102 | 1.0869 |
| chr10 | 135534747 | 17036206 | 0.1257 | 1.6129 |
| chr11 | 135006516 | 15396015 | 0.114 | 0.8189 |
| chr12 | 133851895 | 22202870 | 0.1659 | 0.5426 |
| chr13 | 115169878 | 7272352 | 0.0631 | 0.3086 |
| chr14 | 107349540 | 9282924 | 0.0865 | 0.3959 |
| chr15 | 102531392 | 6639944 | 0.0648 | 0.3236 |
| chr16 | 90354753 | 10122369 | 0.112 | 0.857 |
| chr17 | 81195210 | 13575679 | 0.1672 | 1.8023 |
| chr18 | 78077248 | 7407699 | 0.0949 | 1.1564 |
| chr19 | 59128983 | 6674266 | 0.1129 | 0.6109 |
| chr20 | 63025520 | 7416325 | 0.1177 | 0.4636 |
| chr21 | 48129895 | 3991468 | 0.0829 | 0.464 |
| chr22 | 51304566 | 4459754 | 0.0869 | 0.3988 |
| chrMT | 16571 | 267988 | 16.1721 | 9.7659 |
| chrX | 155270560 | 22187091 | 0.1429 | 0.5817 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 964336 | 0.0162 | 1.007 |

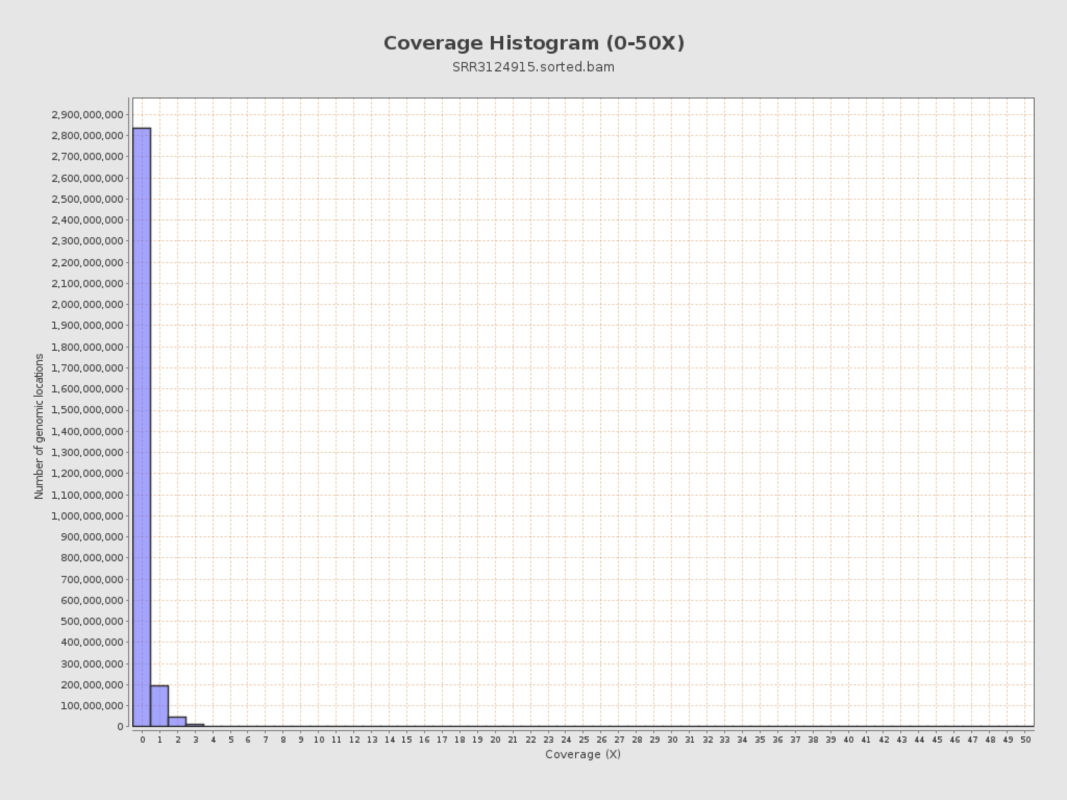
# 3. Results : Coverage across reference



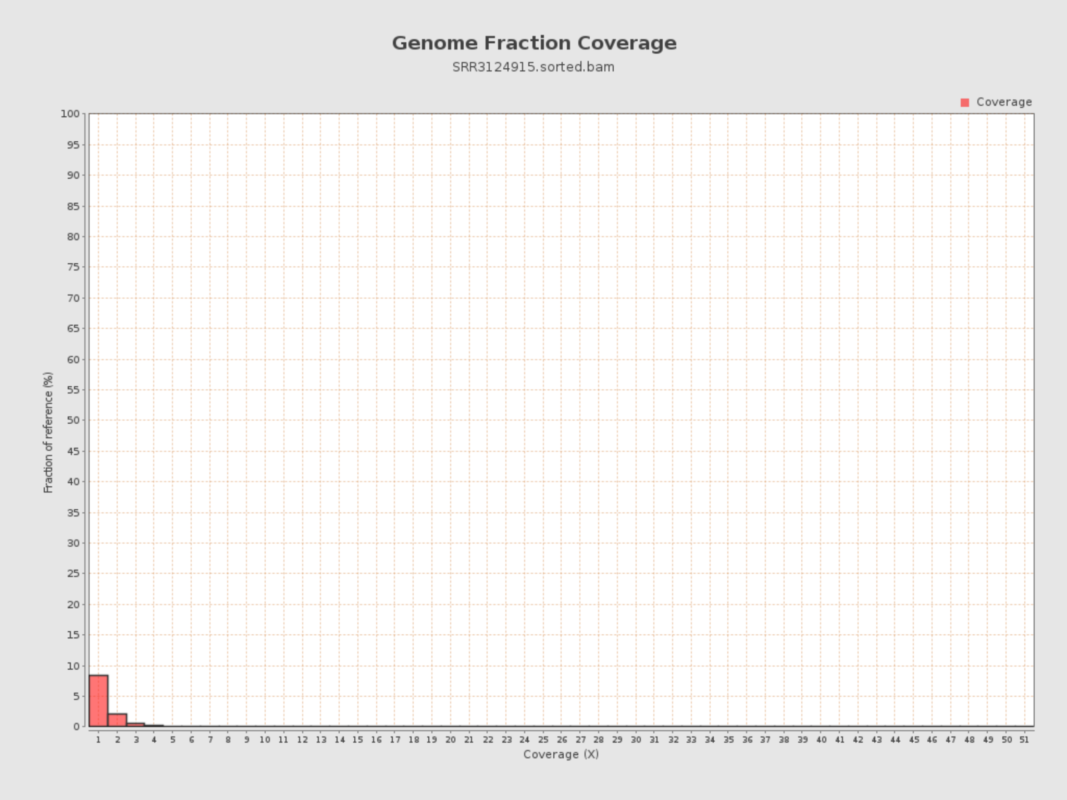
# 4. Results : Coverage Histogram



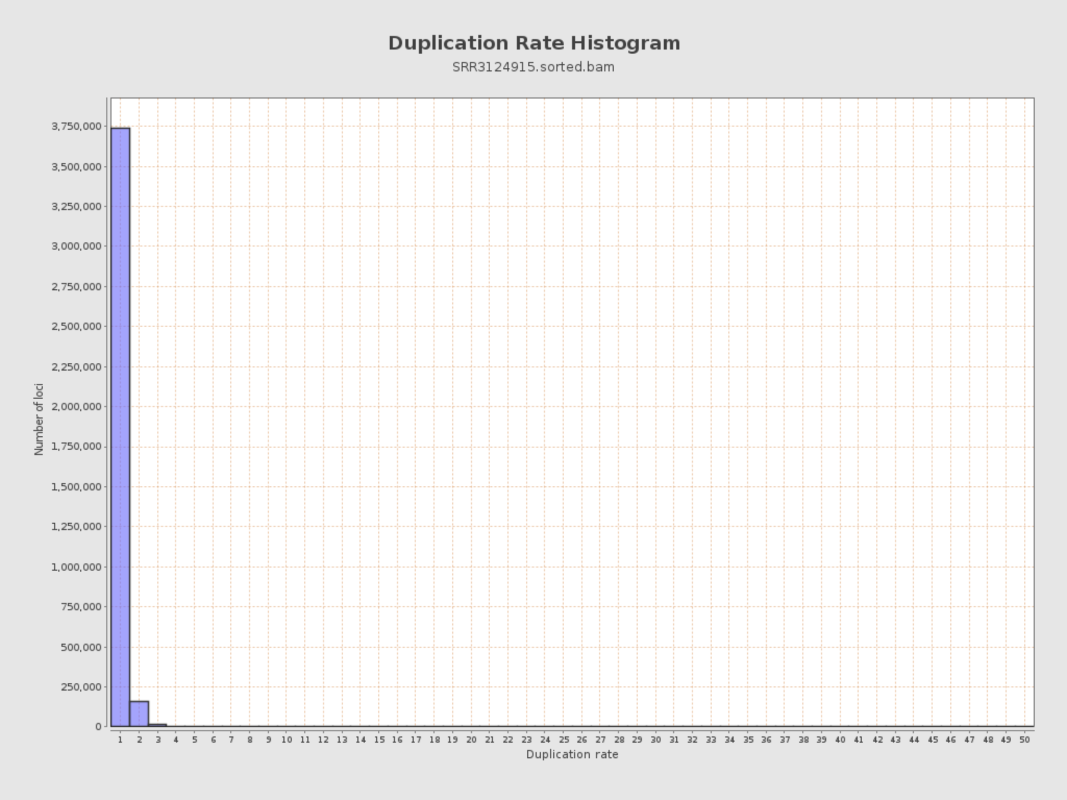
# 5. Results : Coverage Histogram (0-50X)



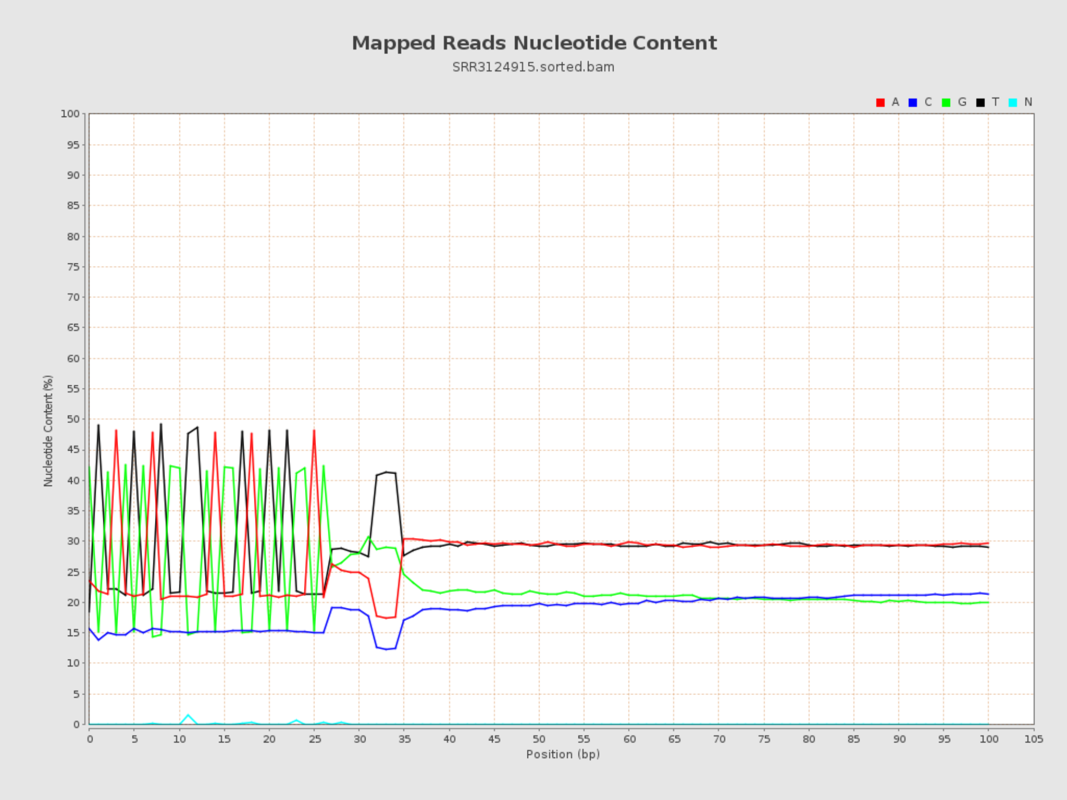
# 6. Results : Genome Fraction Coverage



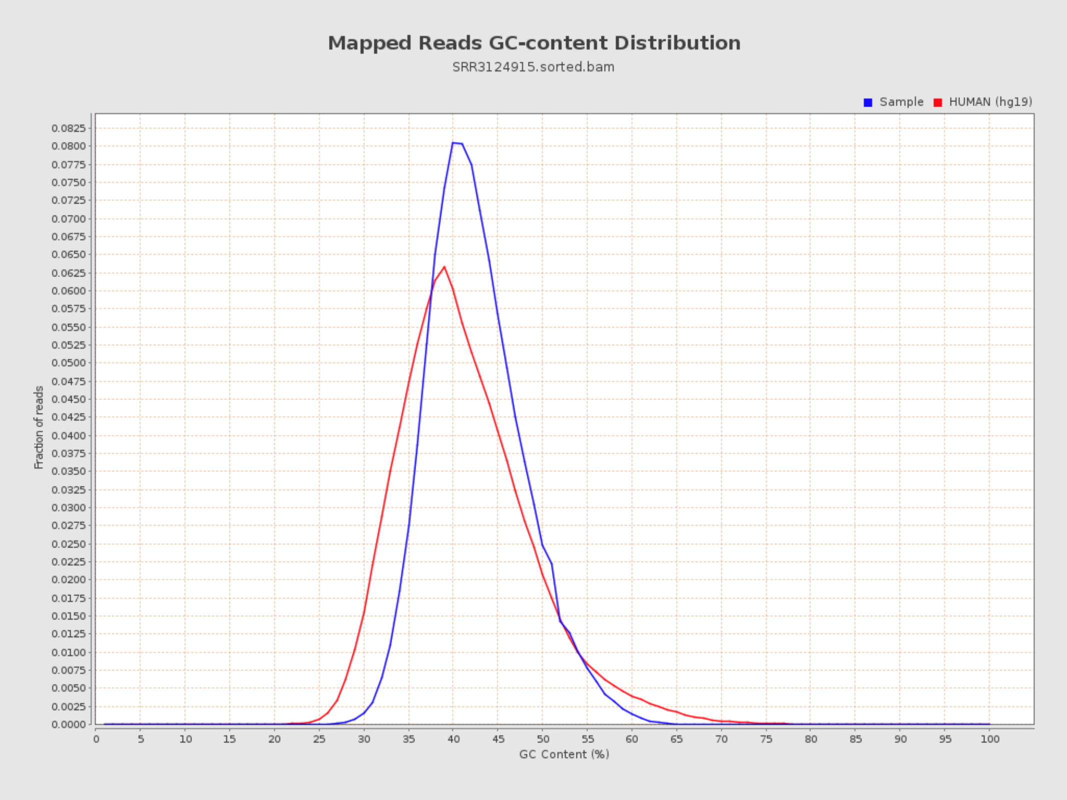
# 7. Results : Duplication Rate Histogram



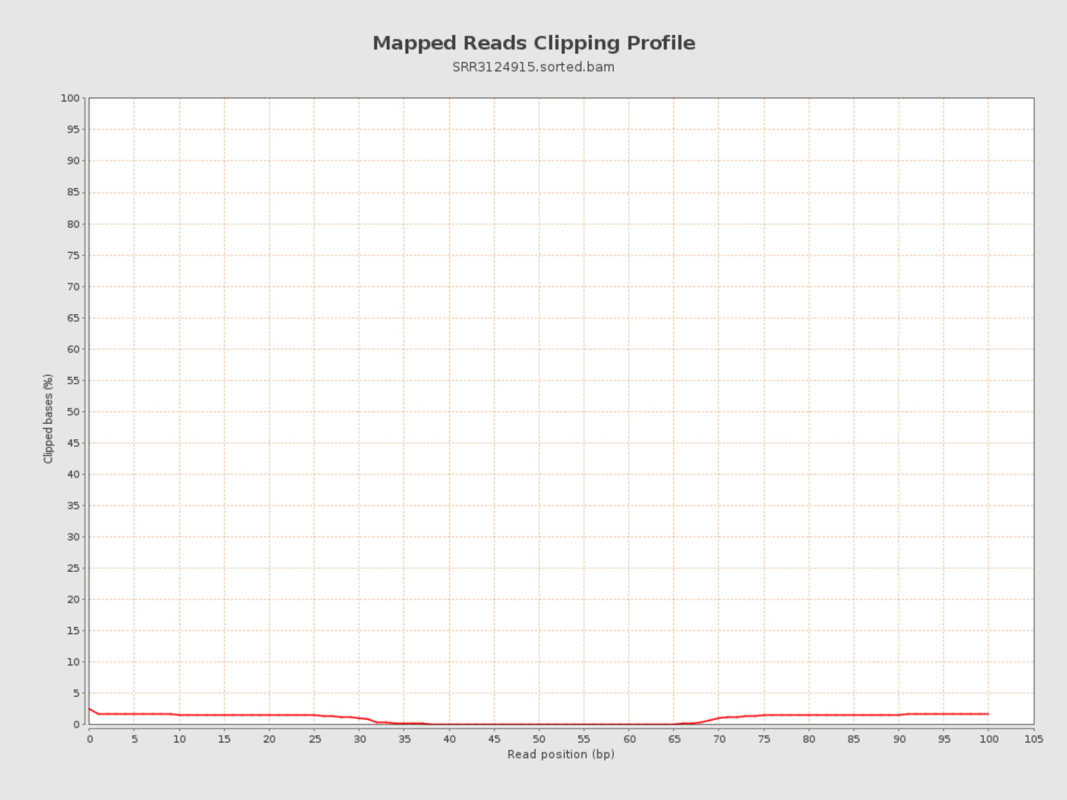
# 8. Results : Mapped Reads Nucleotide Content



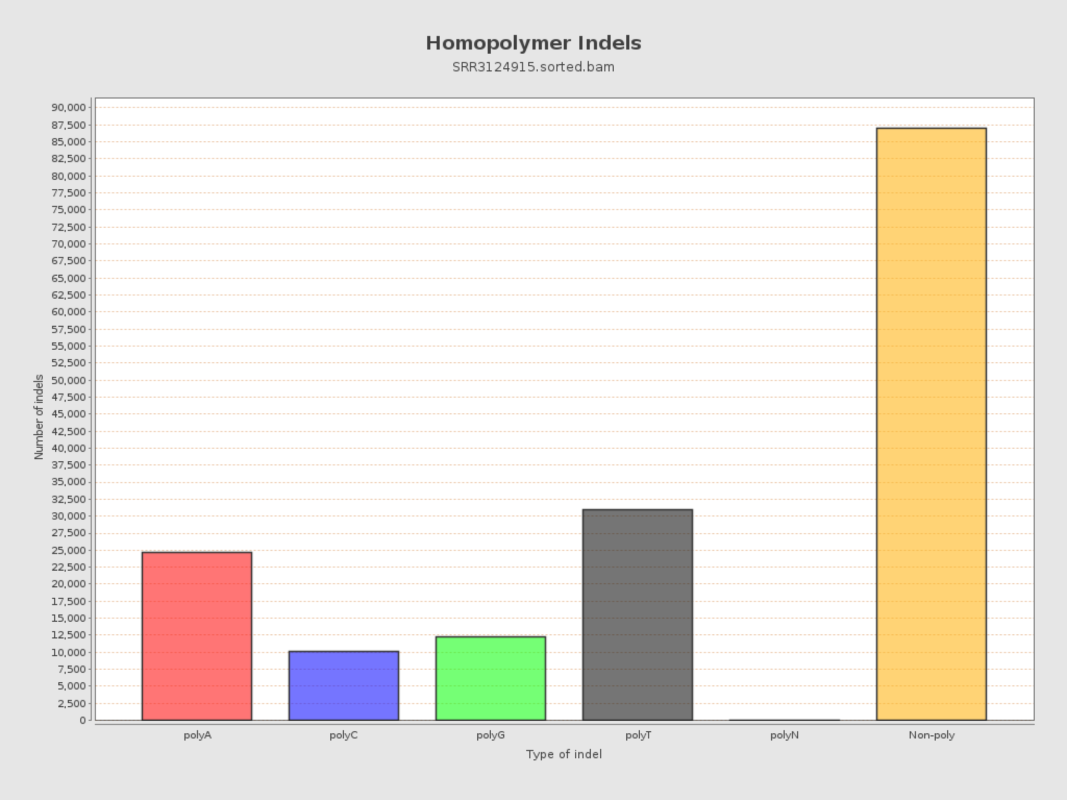
# 9. Results : Mapped Reads GC-content Distribution



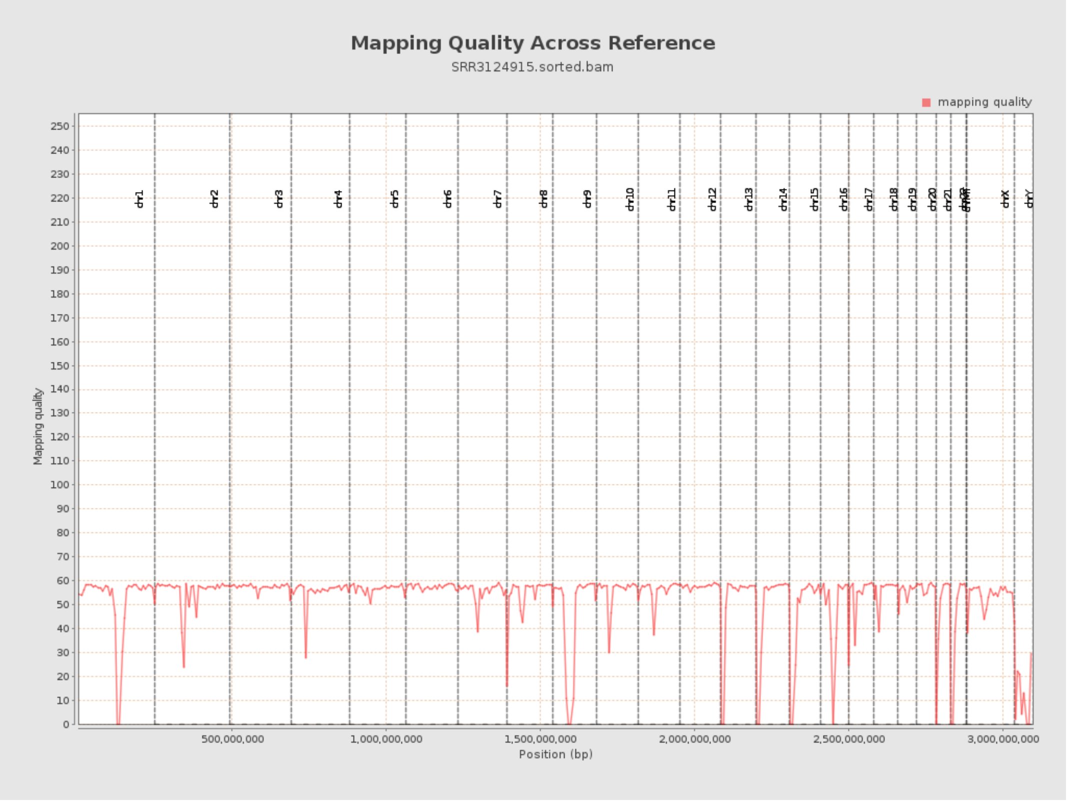
# 10. Results : Mapped Reads Clipping Profile



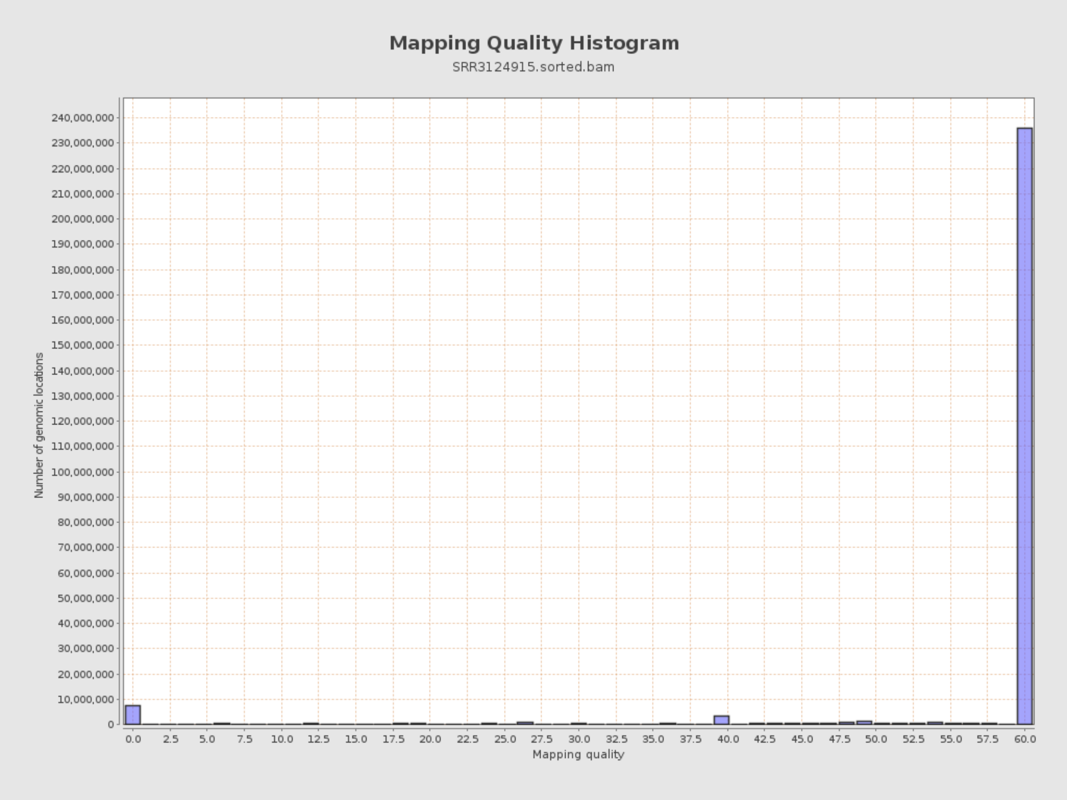
# 11. Results : Homopolymer Indels



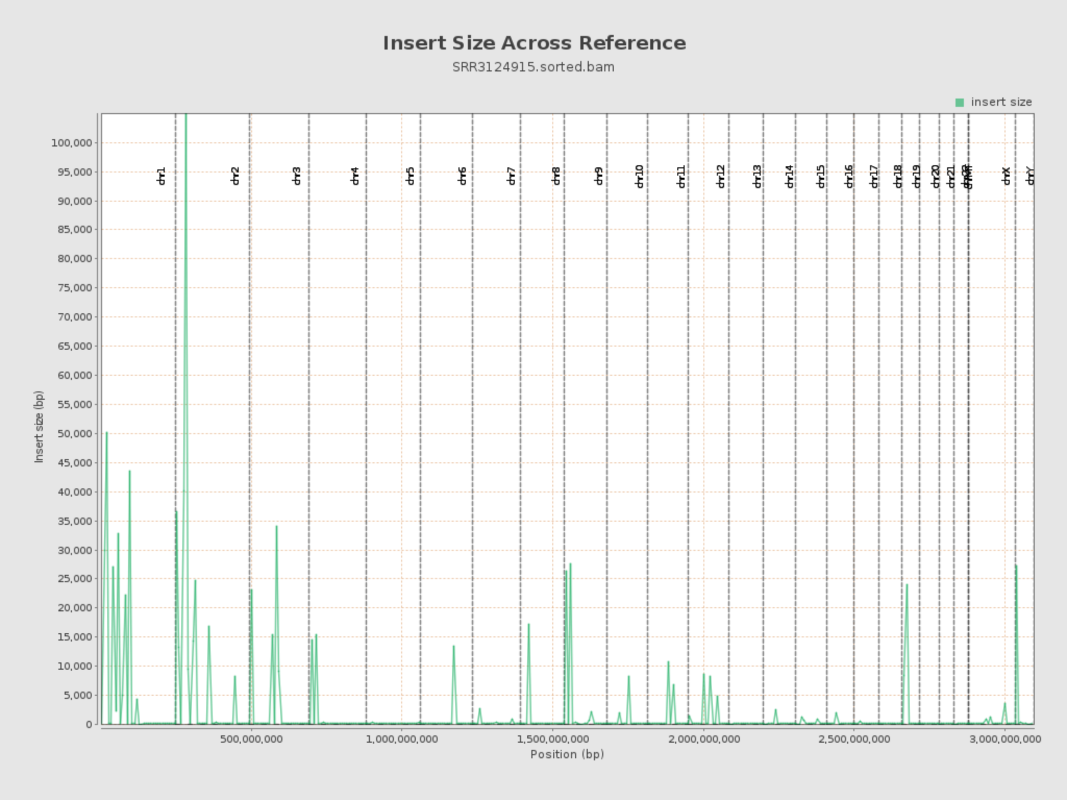
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram