# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/11/02 03:50:28*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR5365333.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_SRR5365333 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5365333_1.fastq.gz SRR5365333_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Nov 02 03:50:27 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR5365333.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 109,538,278 |
| Mapped reads | 107,116,257 / 97.79% |
| Unmapped reads | 2,422,021 / 2.21% |
| Mapped paired reads | 107,116,257 / 97.79% |
| Mapped reads, first in pair | 53,858,758 / 49.17% |
| Mapped reads,  second in pair | 53,257,499 / 48.62% |
| Mapped reads, both in pair | 106,362,666 / 97.1% |
| Mapped reads, singletons | 753,591 / 0.69% |
| Secondary alignments | 0 |
| Supplementary alignments | 857,388 / 0.78% |
| Read min/max/mean length | 30 / 151 / 151.35 |
| Duplicated reads (estimated) | 47,283,927 / 43.17% |
| Duplication rate | 31.29% |
| Clipped reads | 64,589,837 / 58.97% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 4,175,086,307 / 29.67% |
| Number/percentage of C's | 2,817,890,988 / 20.02% |
| Number/percentage of T's | 4,120,068,160 / 29.28% |
| Number/percentage of G's | 2,959,047,865 / 21.03% |
| Number/percentage of N's | 829,064 / 0.01% |
| | |

| | |
|---|---|
| GC Percentage | 41.05% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 4.5477 |
| Standard Deviation | 52.3185 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 54.23 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 89,601.18 |
| Standard Deviation | 2,963,393.29 |
| P25/Median/P75 | 147 / 201 / 275 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.82% |
| Mismatches | 107,305,598 |
| Insertions | 4,075,777 |
| Mapped reads with at least one insertion | 3.69% |
| Deletions | 2,169,691 |
| Mapped reads with at least one deletion | 1.96% |
| Homopolymer indels | 50.08% |

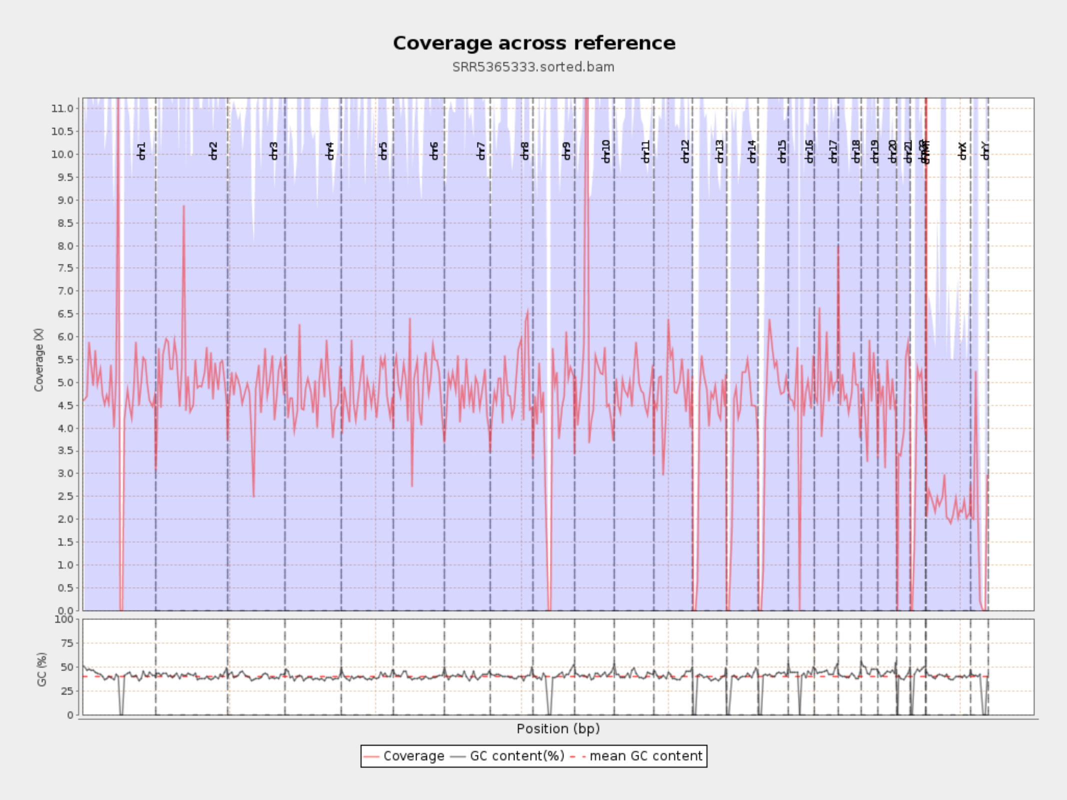
## 2.7. Chromosome stats

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

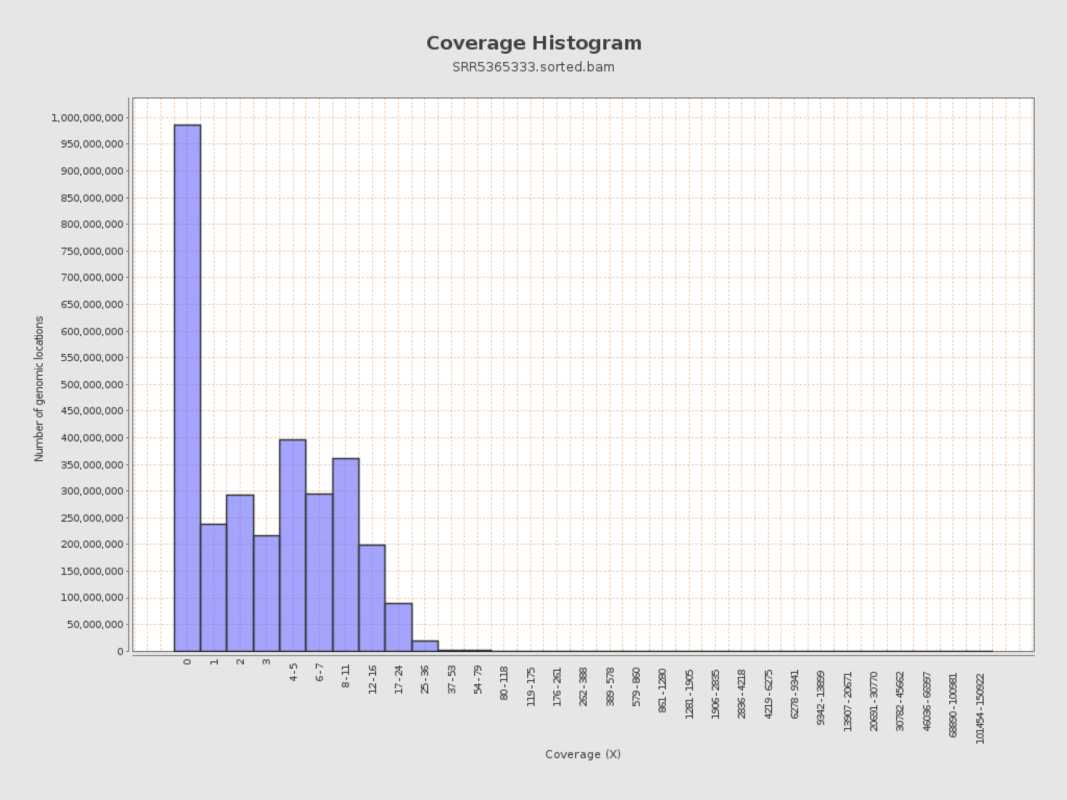
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 1192240686 | 4.7833 | 149.0197 |
| chr2 | 243199373 | 1277722268 | 5.2538 | 28.9859 |
| chr3 | 198022430 | 946629147 | 4.7804 | 6.7473 |
| chr4 | 191154276 | 913353044 | 4.7781 | 20.3043 |
| chr5 | 180915260 | 861996520 | 4.7646 | 6.3858 |
| chr6 | 171115067 | 852681023 | 4.9831 | 18.1994 |
| chr7 | 159138663 | 757141446 | 4.7577 | 31.3237 |
| chr8 | 146364022 | 724285167 | 4.9485 | 17.0511 |
| chr9 | 141213431 | 597599763 | 4.2319 | 48.8751 |
| chr10 | 135534747 | 726045956 | 5.3569 | 90.7011 |
| chr11 | 135006516 | 652818084 | 4.8355 | 30.0369 |
| chr12 | 133851895 | 654336602 | 4.8885 | 22.8648 |
| chr13 | 115169878 | 455328389 | 3.9535 | 5.1606 |
| chr14 | 107349540 | 425016102 | 3.9592 | 5.6923 |
| chr15 | 102531392 | 423775757 | 4.1331 | 12.4533 |
| chr16 | 90354753 | 404445441 | 4.4762 | 14.3525 |
| chr17 | 81195210 | 408938450 | 5.0365 | 22.3921 |
| chr18 | 78077248 | 384605342 | 4.926 | 47.4983 |
| chr19 | 59128983 | 275061875 | 4.6519 | 75.5797 |
| chr20 | 63025520 | 292566090 | 4.642 | 9.2112 |
| chr21 | 48129895 | 196604738 | 4.0849 | 15.2861 |
| chr22 | 51304566 | 172164583 | 3.3557 | 13.2586 |
| chrMT | 16571 | 20349120 | 1,227.9959 | 266.476 |
| chrX | 155270560 | 354630722 | 2.284 | 10.0704 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 107820900 | 1.816 | 35.4738 |

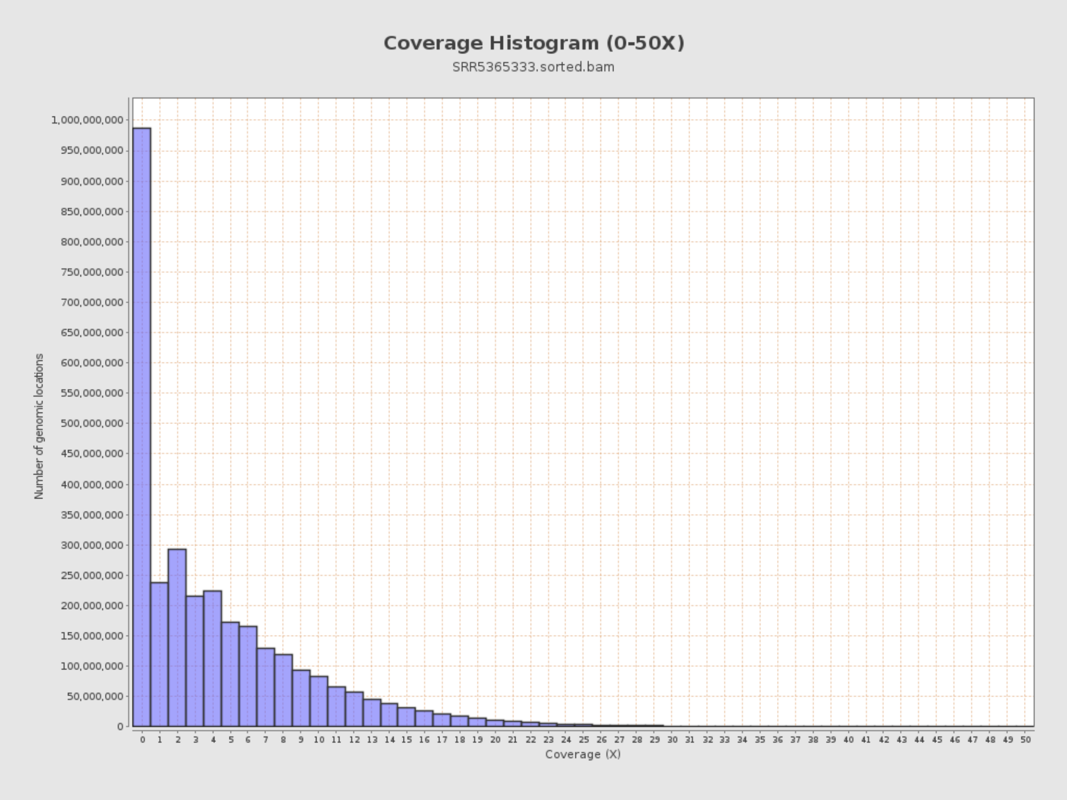
# 3. Results : Coverage across reference



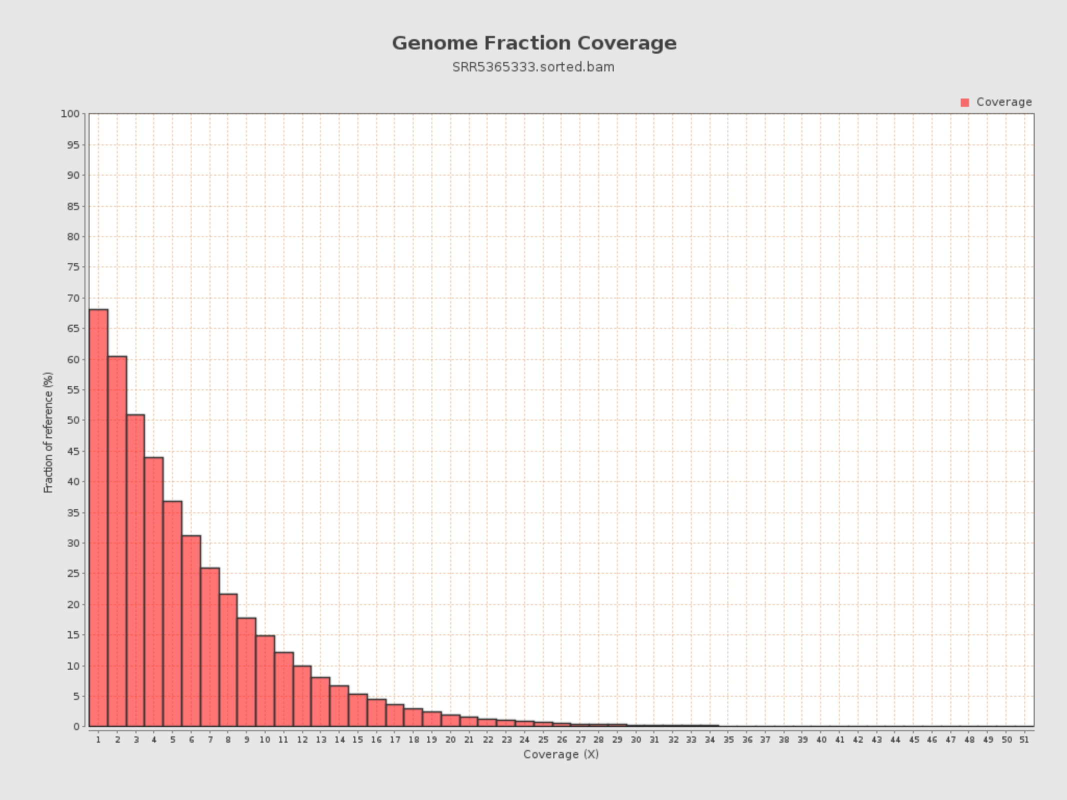
# 4. Results : Coverage Histogram



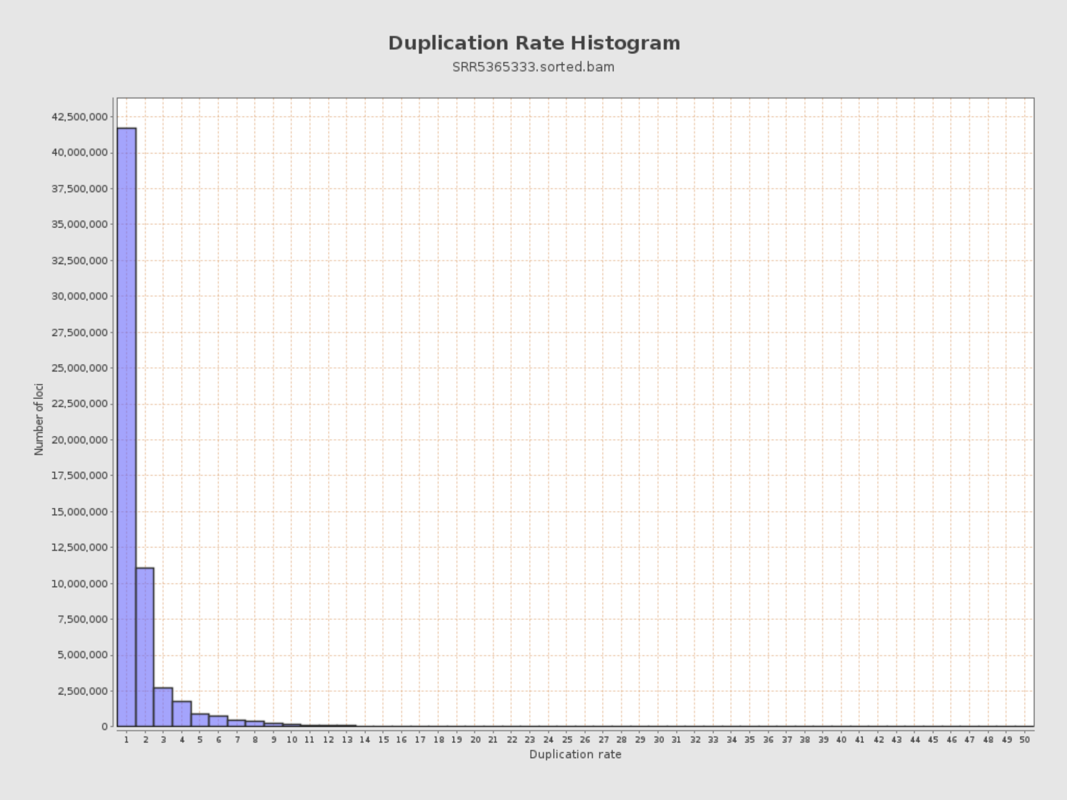
# 5. Results : Coverage Histogram (0-50X)



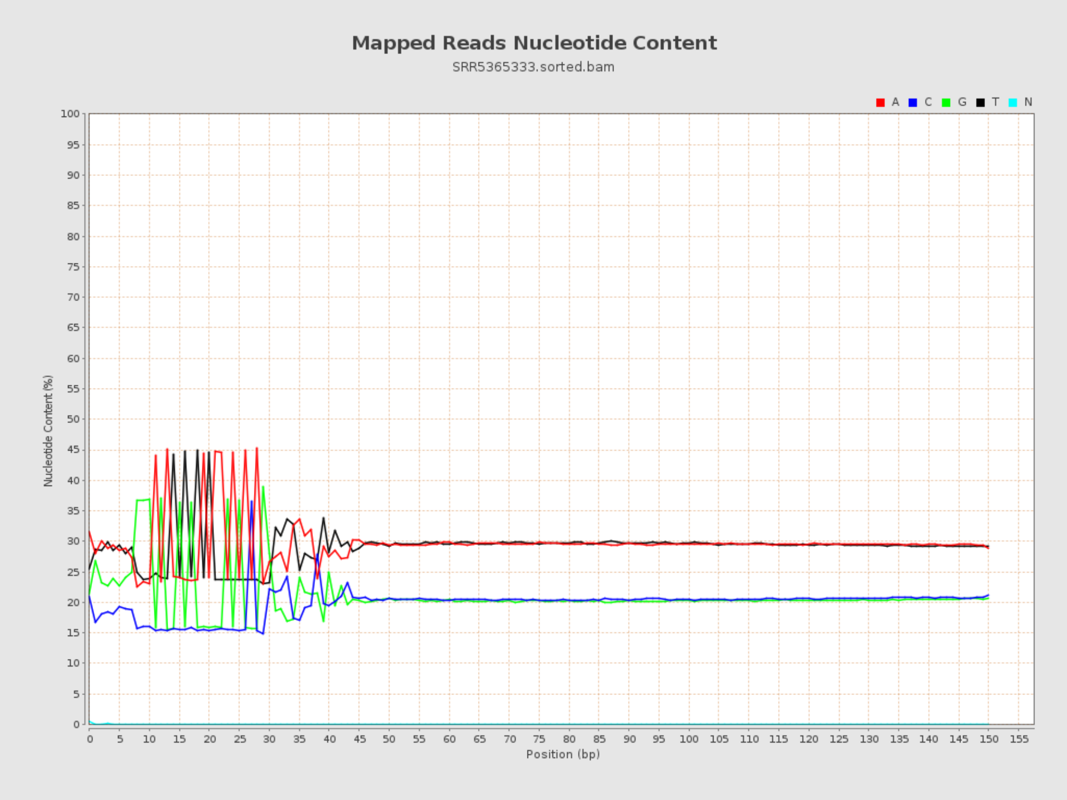
# 6. Results : Genome Fraction Coverage



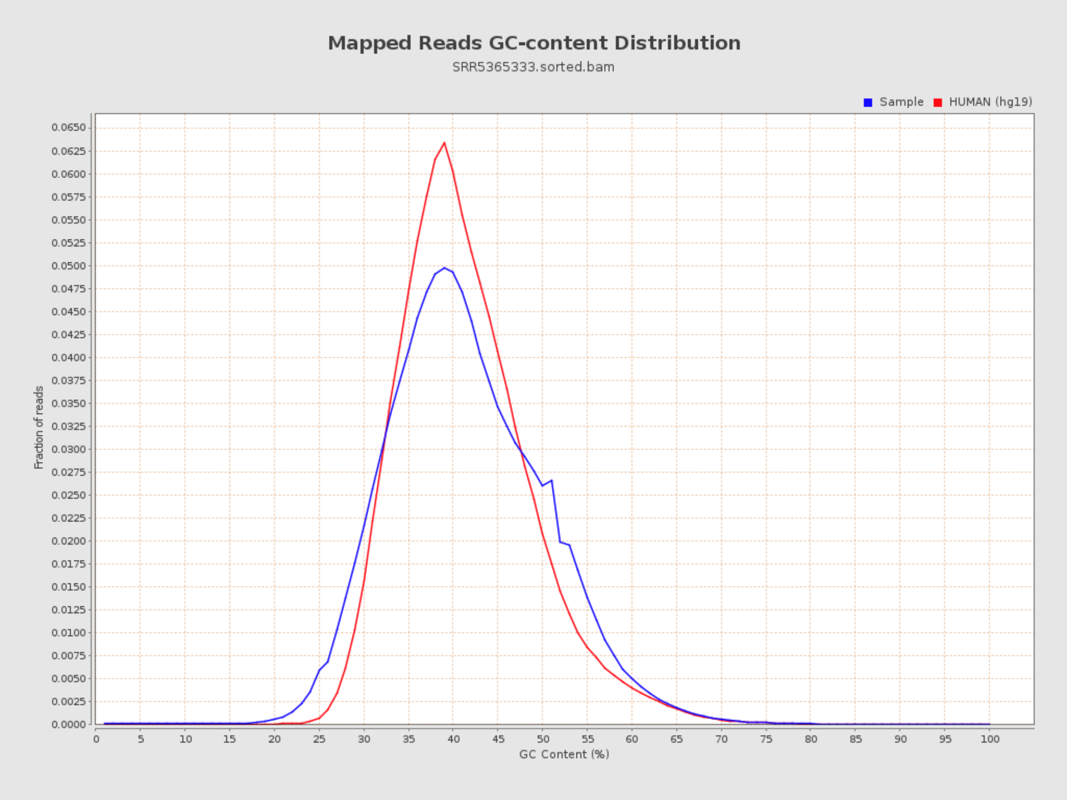
# 7. Results : Duplication Rate Histogram



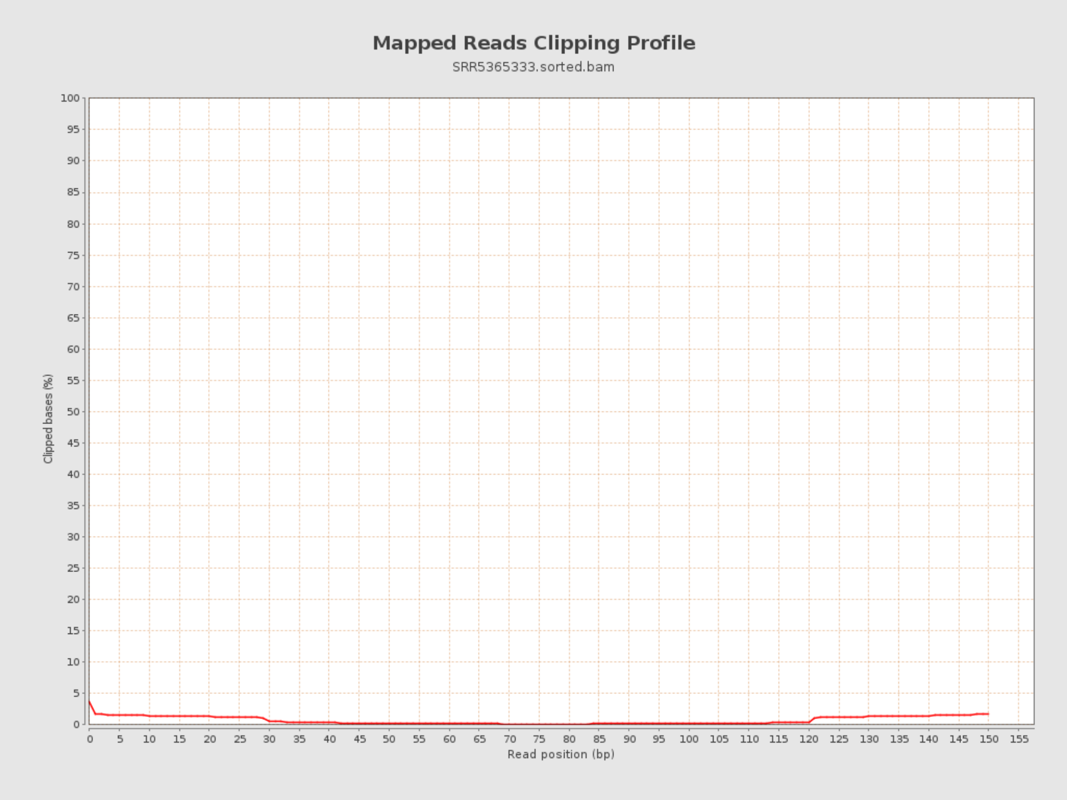
# 8. Results : Mapped Reads Nucleotide Content



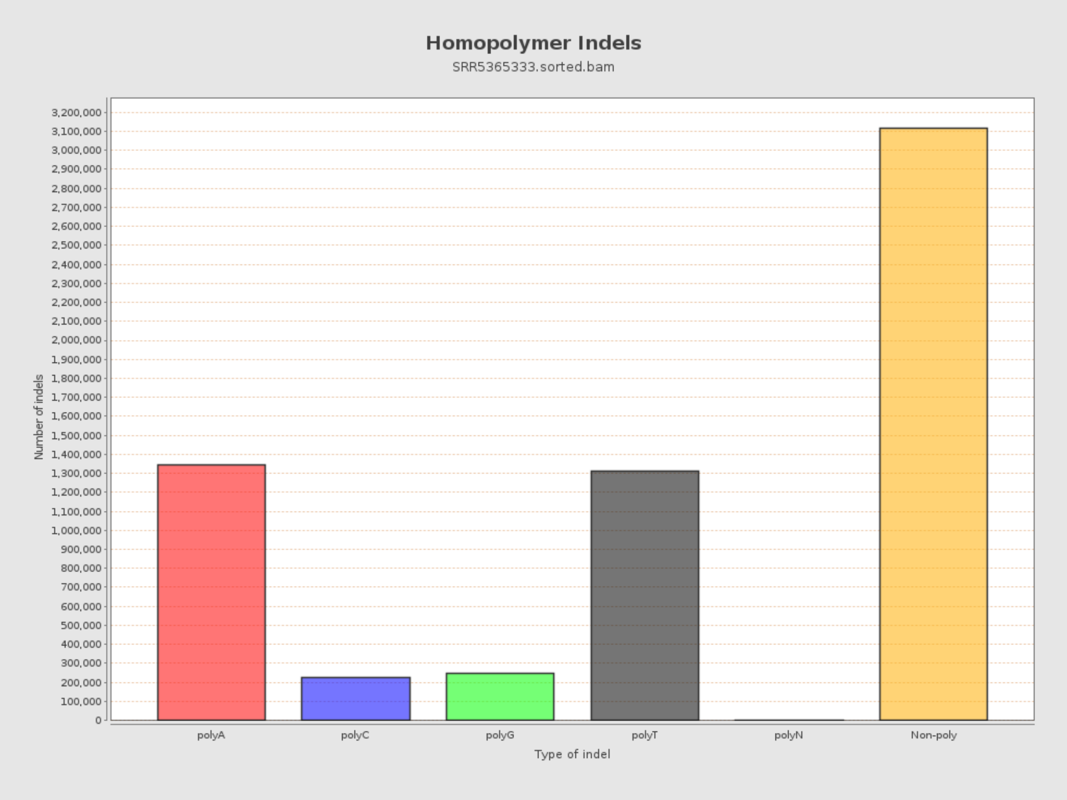
# 9. Results : Mapped Reads GC-content Distribution



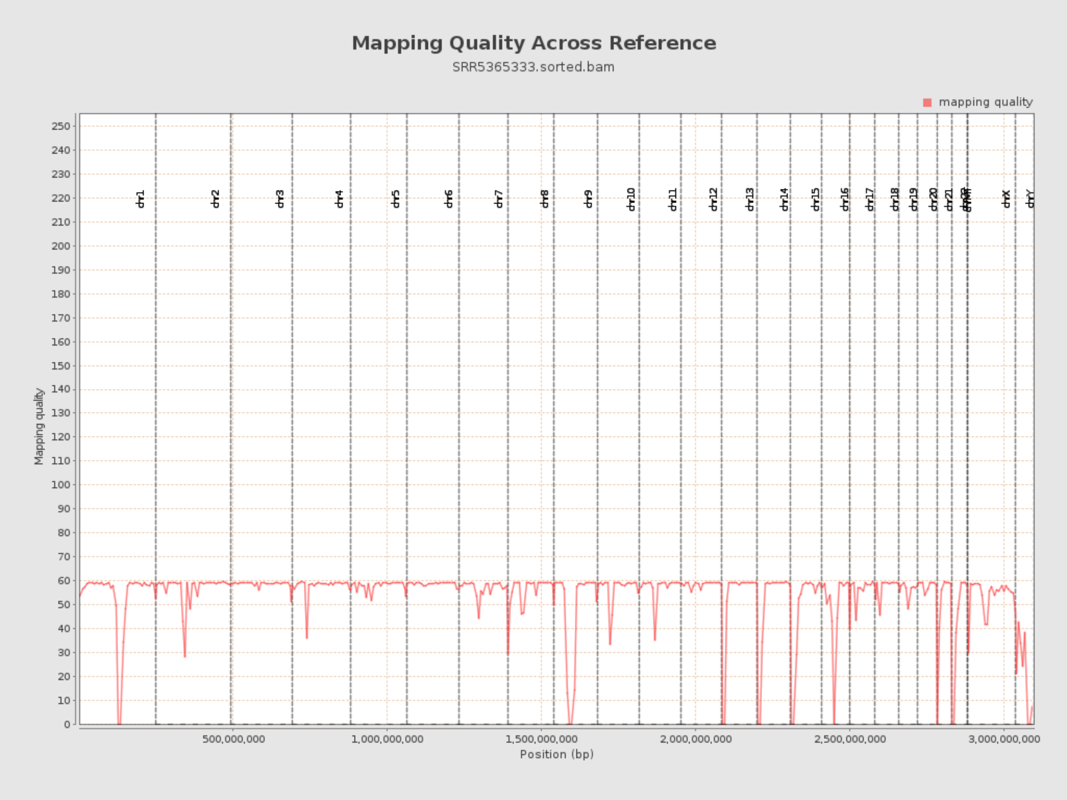
# 10. Results : Mapped Reads Clipping Profile



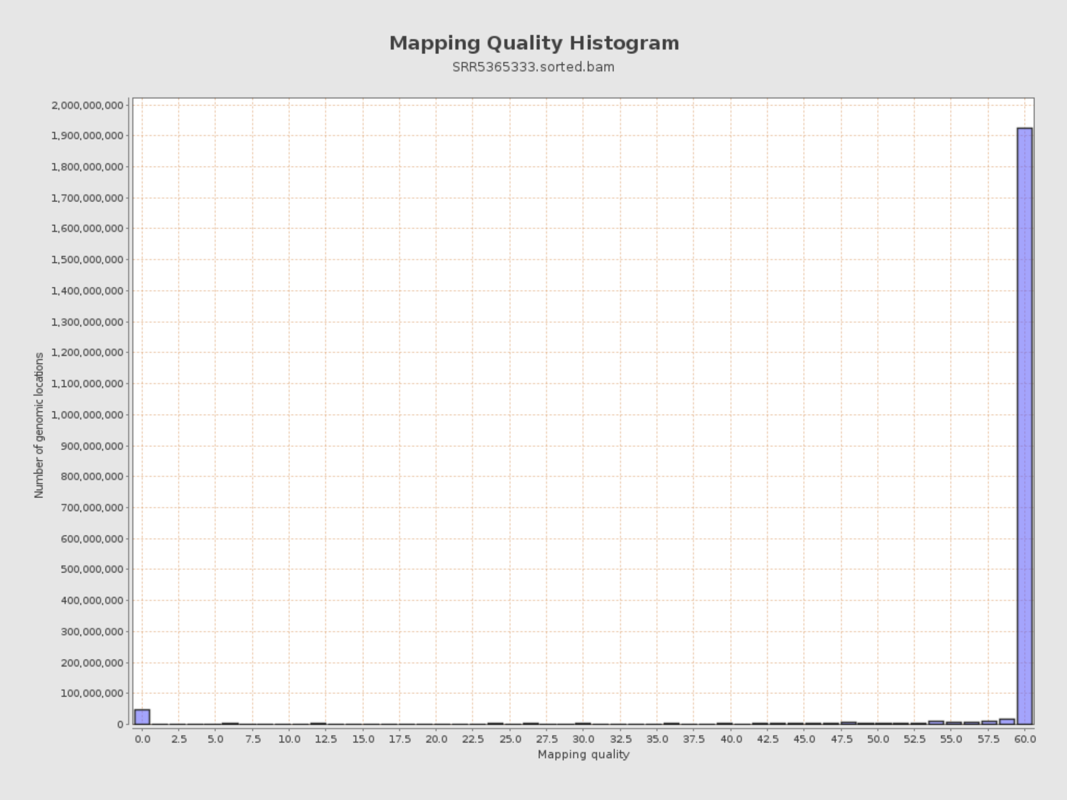
# 11. Results : Homopolymer Indels



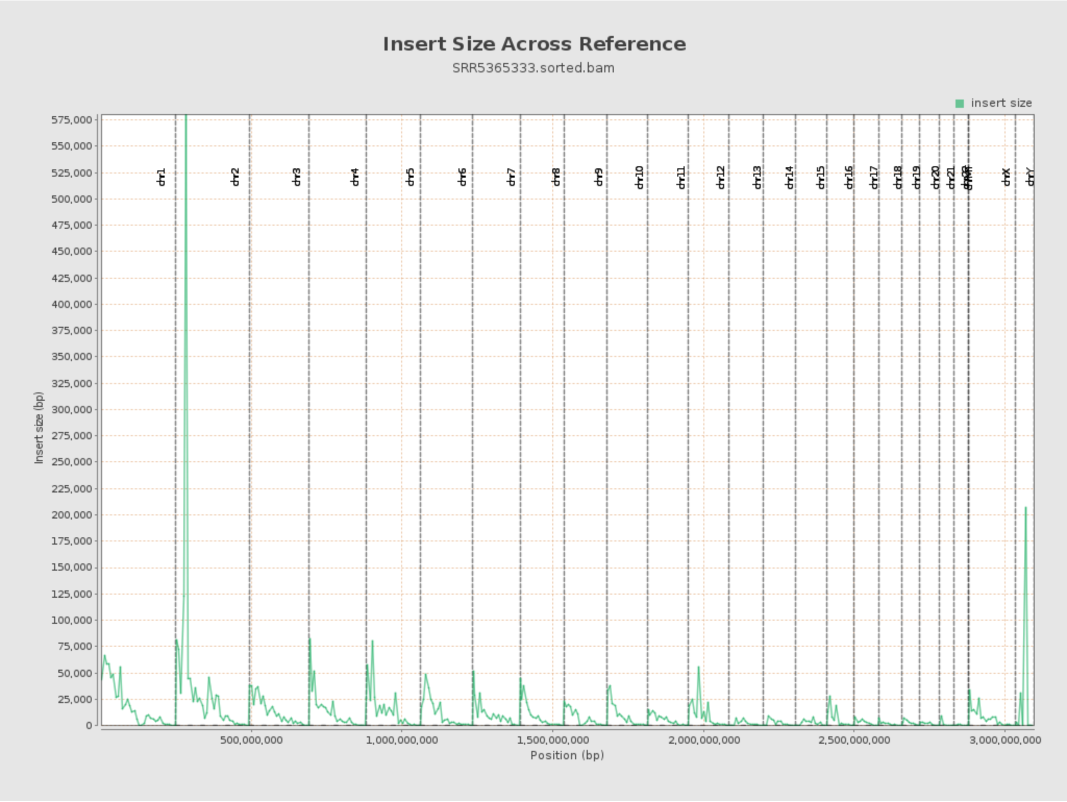
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram