# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/03 17:20:04*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777259.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_SRR1777259 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777259_1.fastq.gz SRR1777259_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Apr 03 17:20:03 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1777259.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 33,888,478 |
| Mapped reads | 33,766,578 / 99.64% |
| Unmapped reads | 121,900 / 0.36% |
| Mapped paired reads | 33,766,578 / 99.64% |
| Mapped reads, first in pair | 16,883,520 / 49.82% |
| Mapped reads, second in pair | 16,883,058 / 49.82% |
| Mapped reads, both in pair | 33,742,728 / 99.57% |
| Mapped reads, singletons | 23,850 / 0.07% |
| Secondary alignments | 0 |
| Supplementary alignments | 858,623 / 2.53% |
| Read min/max/mean length | 30 / 101 / 102.05 |
| Duplicated reads (estimated) | 14,576,898 / 43.01% |
| Duplication rate | 35.17% |
| Clipped reads | 3,241,415 / 9.56% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 930,594,523 / 27.43% |
| Number/percentage of C's | 766,690,943 / 22.6% |
| Number/percentage of T's | 927,167,123 / 27.33% |
| Number/percentage of G's | 768,179,966 / 22.64% |
| Number/percentage of N's | 128,625 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 45.24% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 1.0961 |
| Standard Deviation | 12.5635 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 54.78 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 157,100.39 |
| Standard Deviation | 3,915,134.33 |
| P25/Median/P75 | 187 / 236 / 299 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.28% |
| Mismatches | 8,652,938 |
| Insertions | 615,625 |
| Mapped reads with at least one insertion | 1.8% |
| Deletions | 224,076 |
| Mapped reads with at least one deletion | 0.65% |
| Homopolymer indels | 51.77% |

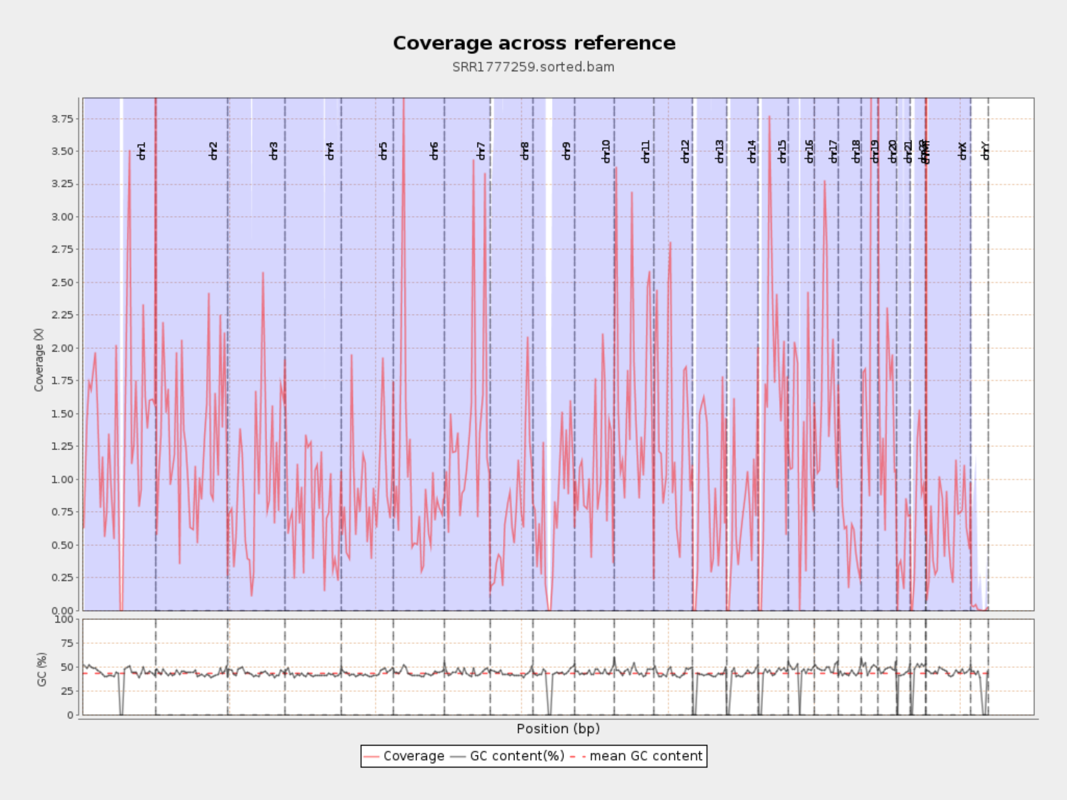
## 2.7. Chromosome stats

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

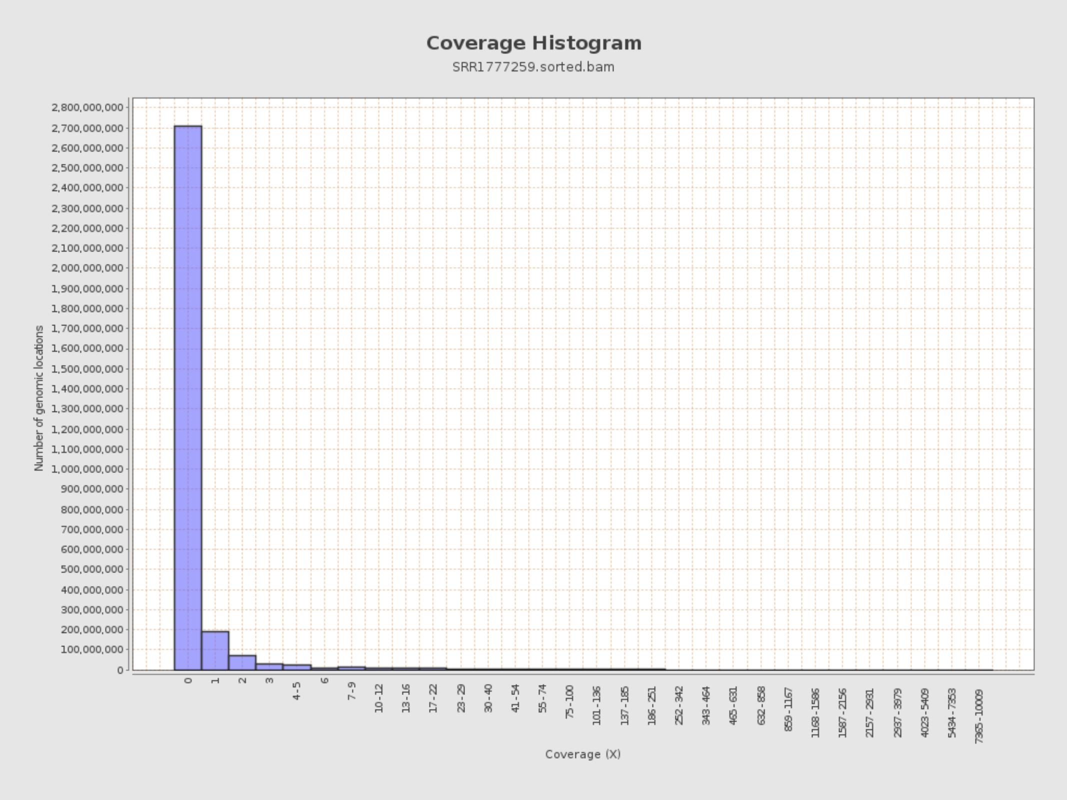
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 343315934 | 1.3774 | 13.9119 |
| chr2 | 243199373 | 313025668 | 1.2871 | 13.3157 |
| chr3 | 198022430 | 200064470 | 1.0103 | 11.7607 |
| chr4 | 191154276 | 148736106 | 0.7781 | 9.8317 |
| chr5 | 180915260 | 169799392 | 0.9386 | 10.8 |
| chr6 | 171115067 | 161688727 | 0.9449 | 11.4753 |
| chr7 | 159138663 | 217420265 | 1.3662 | 15.8752 |
| chr8 | 146364022 | 111600525 | 0.7625 | 10.6935 |
| chr9 | 141213431 | 106338354 | 0.753 | 8.8524 |
| chr10 | 135534747 | 147438940 | 1.0878 | 11.9643 |
| chr11 | 135006516 | 224774363 | 1.6649 | 16.6772 |
| chr12 | 133851895 | 188113969 | 1.4054 | 13.3333 |
| chr13 | 115169878 | 98805642 | 0.8579 | 10.6799 |
| chr14 | 107349540 | 73425530 | 0.684 | 8.9241 |
| chr15 | 102531392 | 160263812 | 1.5631 | 15.9561 |
| chr16 | 90354753 | 106108219 | 1.1744 | 13.0756 |
| chr17 | 81195210 | 140064502 | 1.725 | 15.2953 |
| chr18 | 78077248 | 49841793 | 0.6384 | 8.0847 |
| chr19 | 59128983 | 183360132 | 3.101 | 24.8119 |
| chr20 | 63025520 | 90749434 | 1.4399 | 14.2565 |
| chr21 | 48129895 | 22565847 | 0.4689 | 7.1418 |
| chr22 | 51304566 | 39386898 | 0.7677 | 8.6647 |
| chrMT | 16571 | 862079 | 52.0234 | 27.4882 |
| chrX | 155270560 | 94514094 | 0.6087 | 10.0072 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1004398 | 0.0169 | 0.5871 |

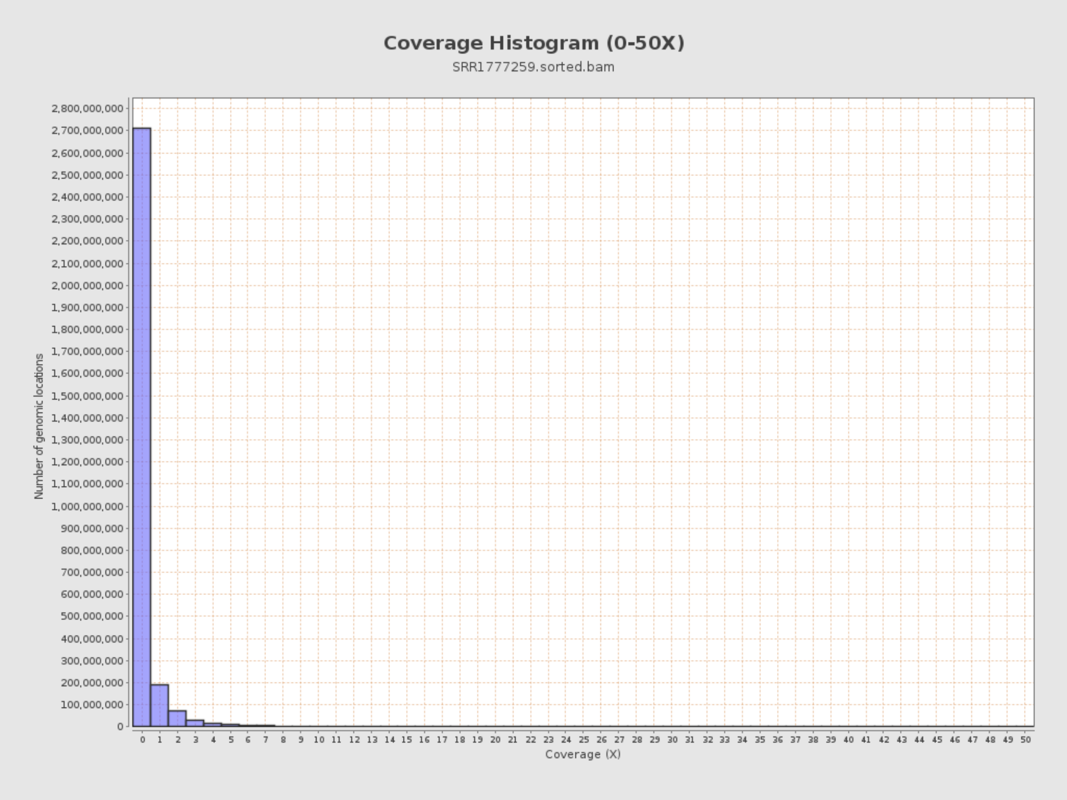
# 3. Results : Coverage across reference



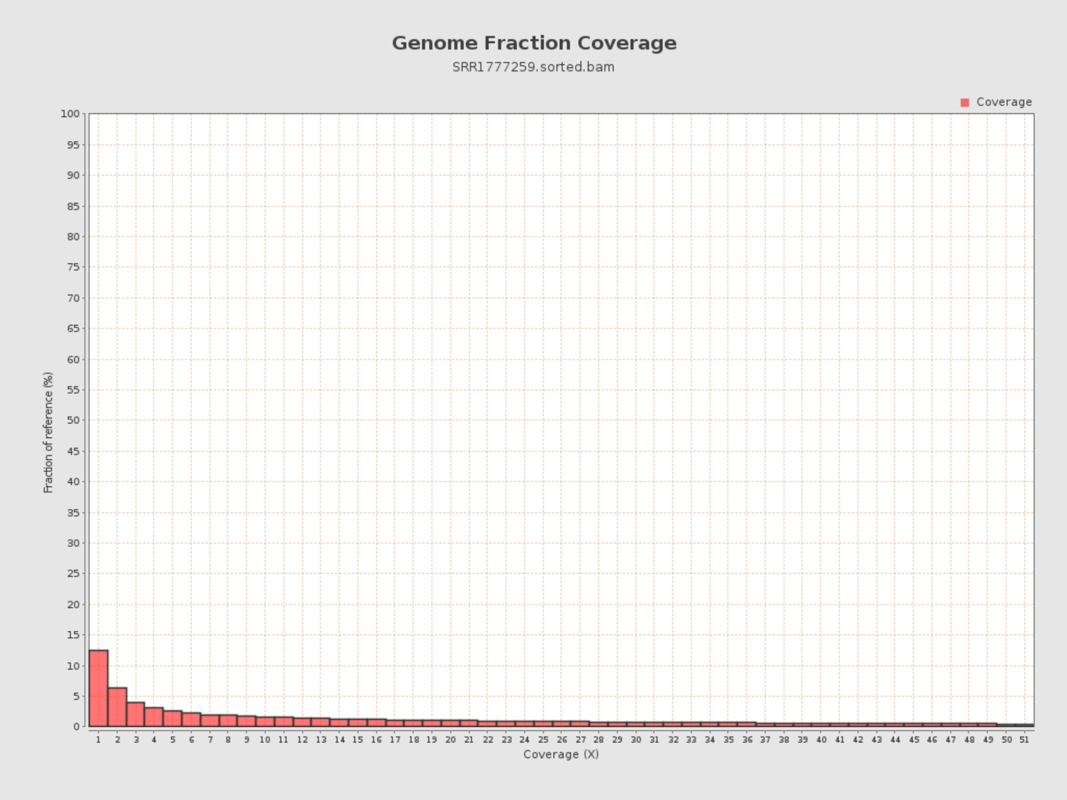
# 4. Results : Coverage Histogram



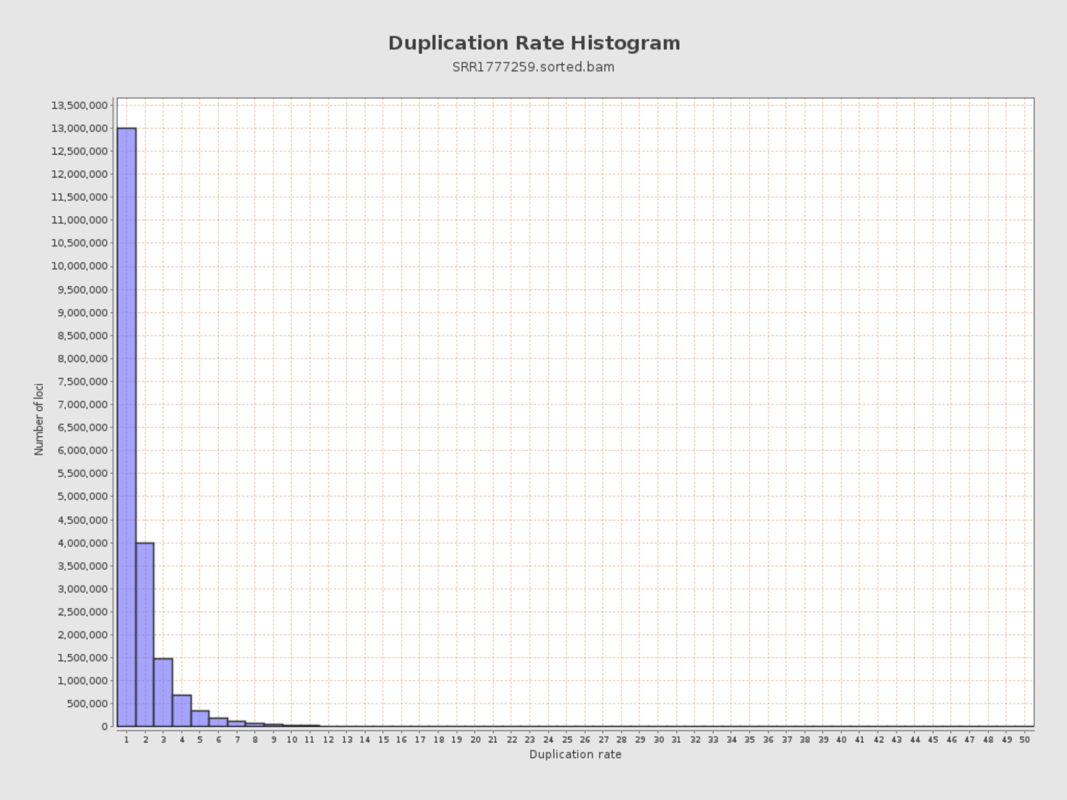
# 5. Results : Coverage Histogram (0-50X)



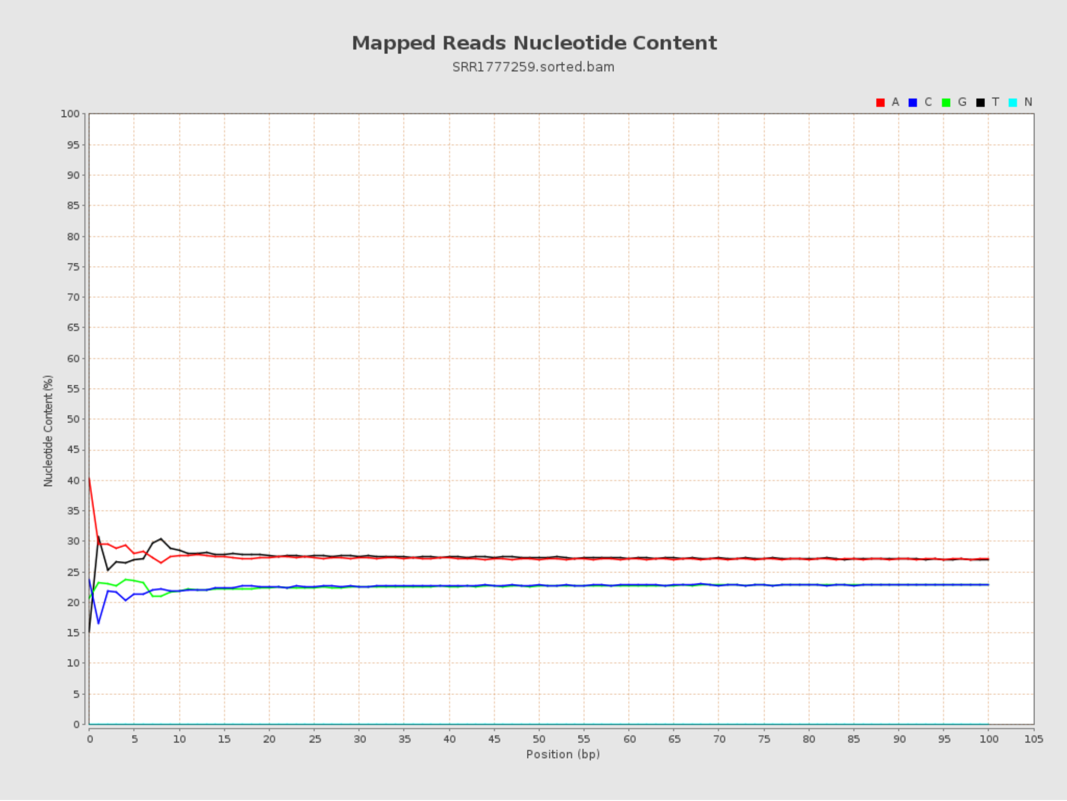
# 6. Results : Genome Fraction Coverage



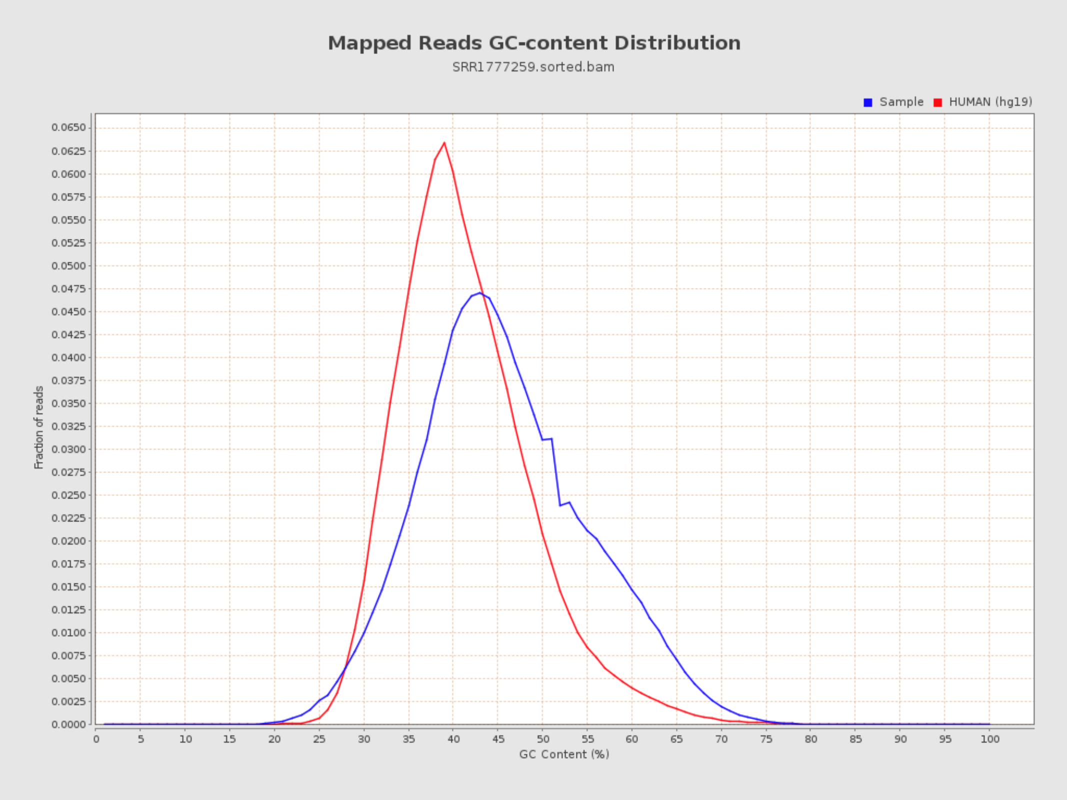
# 7. Results : Duplication Rate Histogram



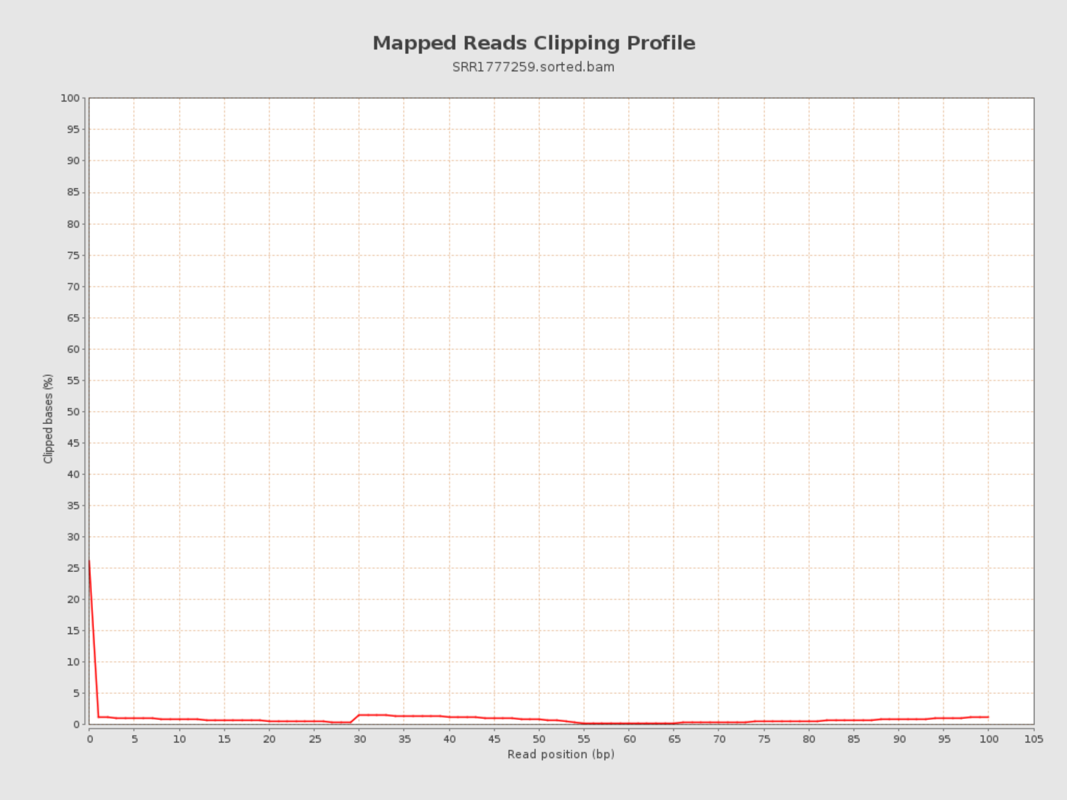
# 8. Results : Mapped Reads Nucleotide Content



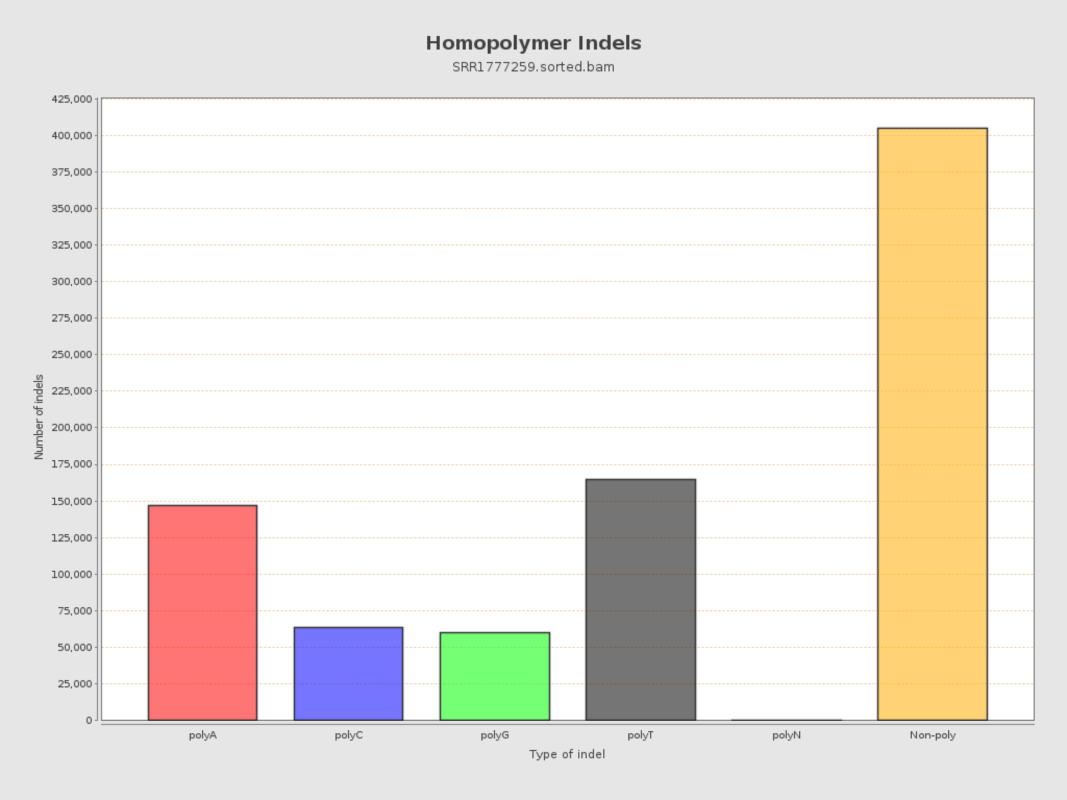
# 9. Results : Mapped Reads GC-content Distribution



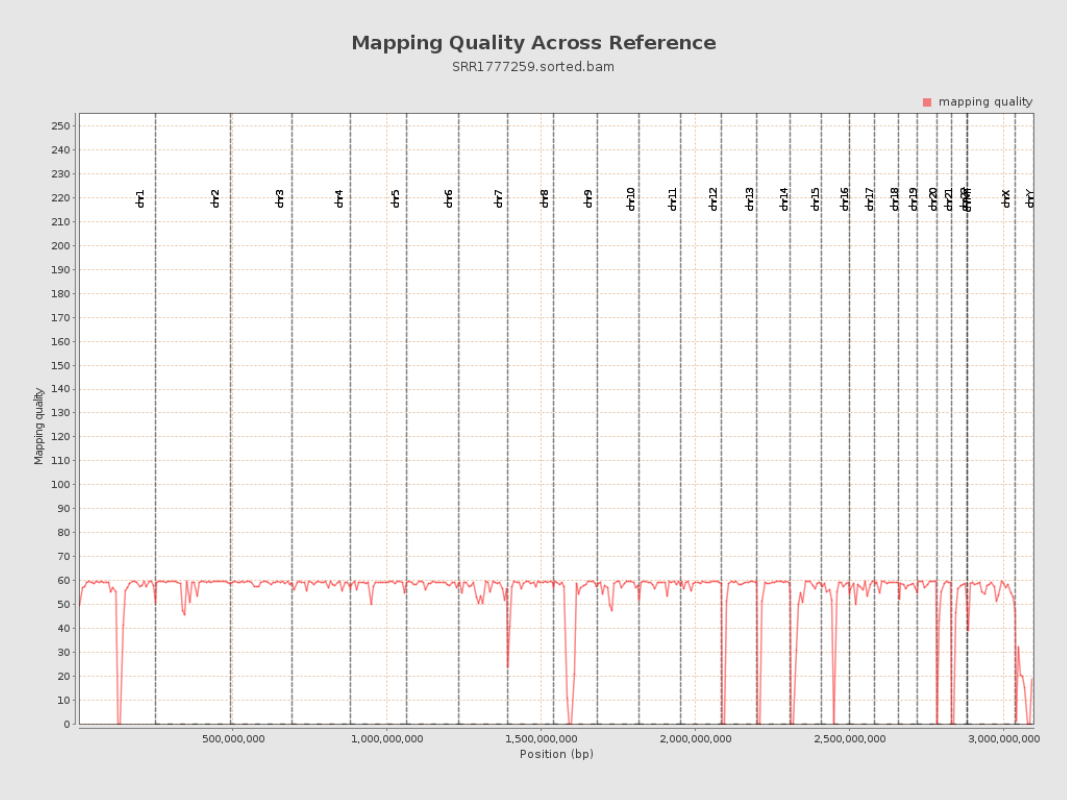
# 10. Results : Mapped Reads Clipping Profile



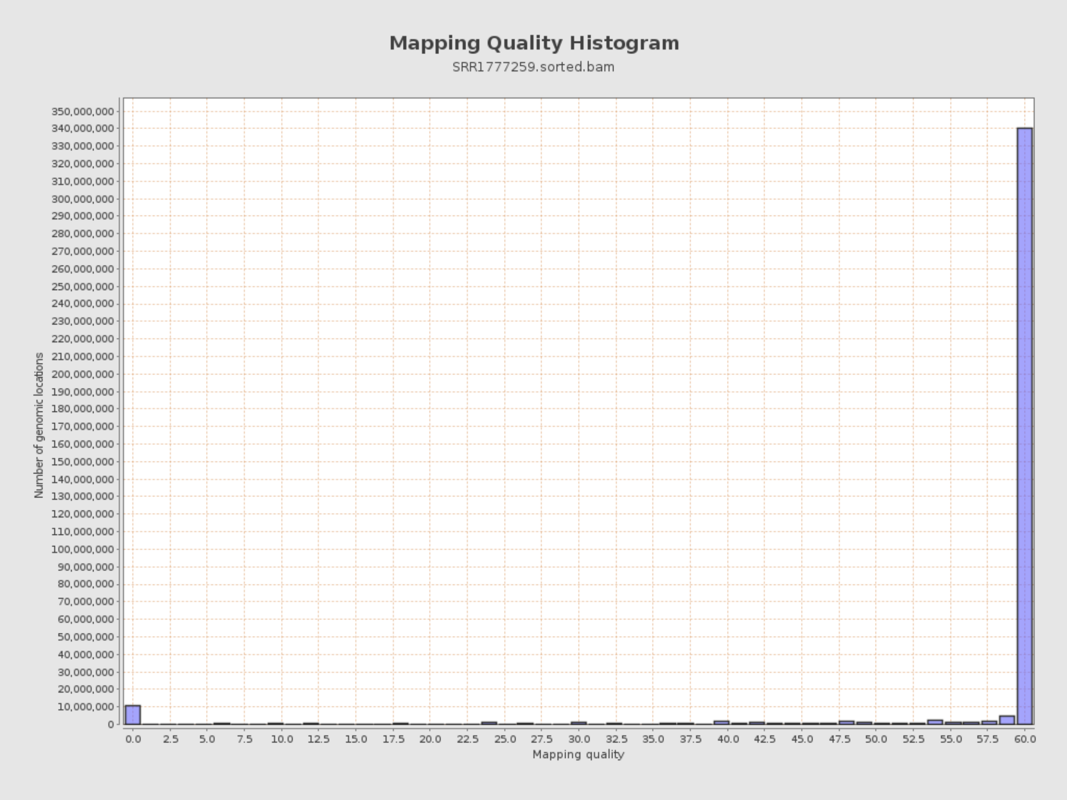
# 11. Results : Homopolymer Indels



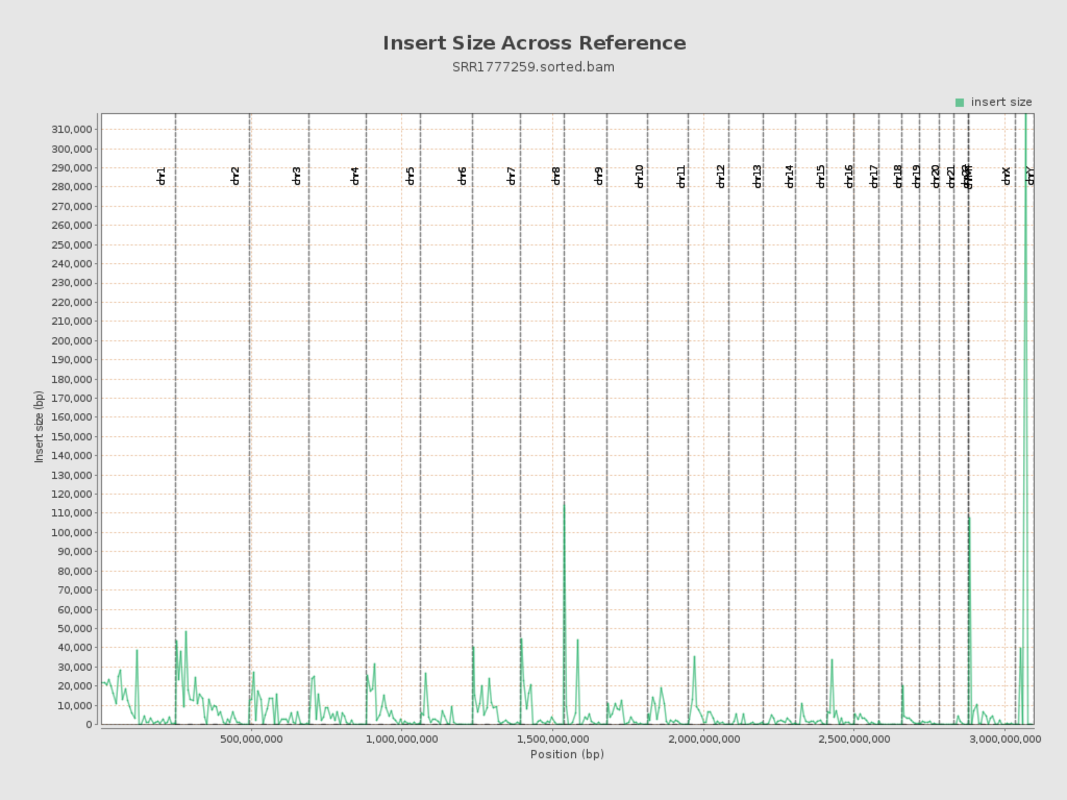
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram