# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/04 06:48:45*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777285.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_SRR1777285 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777285_1.fastq.gz SRR1777285_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Apr 04 06:48:44 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1777285.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 256,472,912 |
| Mapped reads | 253,258,871 / 98.75% |
| Unmapped reads | 3,214,041 / 1.25% |
| Mapped paired reads | 253,258,871 / 98.75% |
| Mapped reads, first in pair | 126,893,487 / 49.48% |
| Mapped reads,  second in pair | 126,365,384 / 49.27% |
| Mapped reads, both in pair | 252,183,910 / 98.33% |
| Mapped reads, singletons | 1,074,961 / 0.42% |
| Secondary alignments | 0 |
| Supplementary alignments | 935,289 / 0.36% |
| Read min/max/mean length | 30 / 100 / 100.15 |
| Duplicated reads (estimated) | 33,252,126 / 12.97% |
| Duplication rate | 8.49% |
| Clipped reads | 41,655,957 / 16.24% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 7,098,408,466 / 29% |
| Number/percentage of C's | 5,116,235,680 / 20.9% |
| Number/percentage of T's | 6,984,486,438 / 28.53% |
| Number/percentage of G's | 5,250,727,726 / 21.45% |
| Number/percentage of N's | 29,430,072 / 0.12% |
| | |

| | |
|---|---|
| GC Percentage | 42.35% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 7.9098 |
| Standard Deviation | 97.478 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.56 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 106,069.26 |
| Standard Deviation | 3,183,193.7 |
| P25/Median/P75 | 122 / 165 / 220 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.92% |
| Mismatches | 219,646,732 |
| Insertions | 2,444,728 |
| Mapped reads with at least one insertion | 0.94% |
| Deletions | 2,933,822 |
| Mapped reads with at least one deletion | 1.13% |
| Homopolymer indels | 43.05% |

## 2.7. Chromosome stats

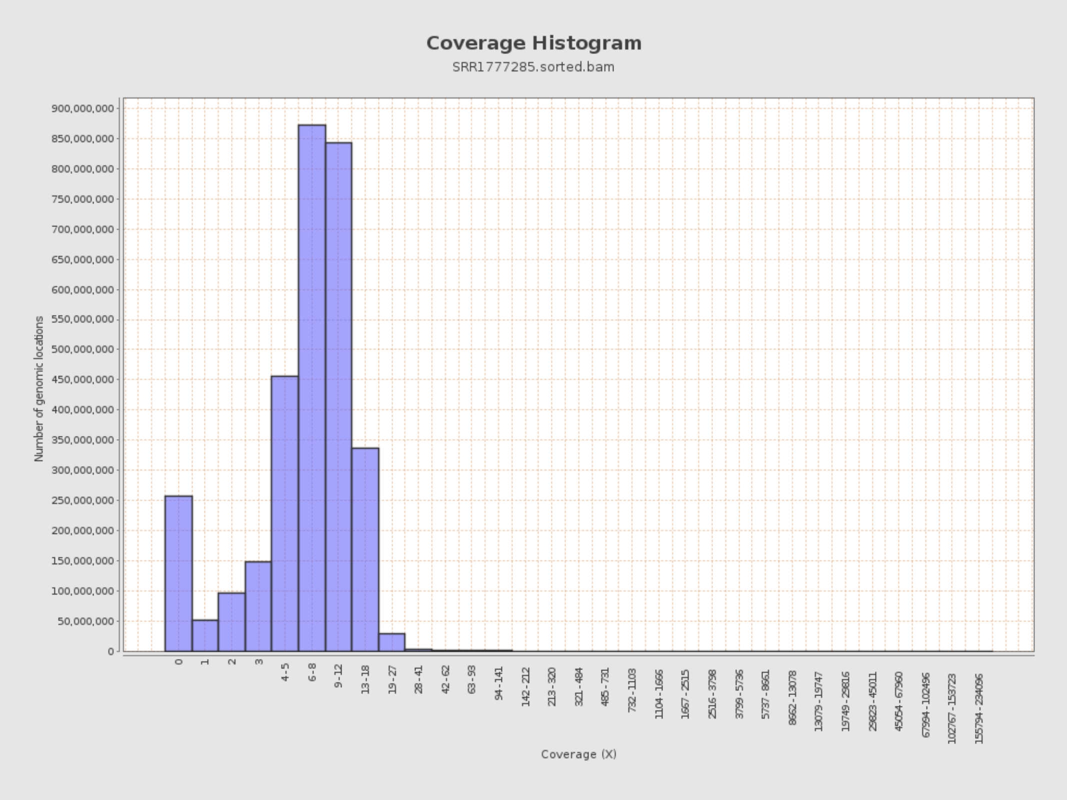
| **Name** | **Length** | **Mapped** | **Mean** | **Standard** |
|---|---|---|---|---|

| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 2052971691 | 8.2366 | 231.2287 |
| chr2 | 243199373 | 2098642638 | 8.6293 | 58.6751 |
| chr3 | 198022430 | 1604436252 | 8.1023 | 21.3746 |
| chr4 | 191154276 | 1585366680 | 8.2937 | 61.9453 |
| chr5 | 180915260 | 1459965088 | 8.0699 | 8.6122 |
| chr6 | 171115067 | 1407331240 | 8.2245 | 50.3588 |
| chr7 | 159138663 | 1326472096 | 8.3353 | 80.0993 |
| chr8 | 146364022 | 1214063935 | 8.2948 | 29.7448 |
| chr9 | 141213431 | 1055129505 | 7.4719 | 86.6879 |
| chr10 | 135534747 | 1359965076 | 10.0341 | 255.2345 |
| chr11 | 135006516 | 1153612723 | 8.5449 | 52.7509 |
| chr12 | 133851895 | 1094698305 | 8.1784 | 7.8109 |
| chr13 | 115169878 | 755230062 | 6.5575 | 4.9072 |
| chr14 | 107349540 | 743860827 | 6.9293 | 8.8769 |
| chr15 | 102531392 | 709599070 | 6.9208 | 5.3137 |
| chr16 | 90354753 | 780779472 | 8.6413 | 39.6474 |
| chr17 | 81195210 | 732615149 | 9.0229 | 52.0058 |
| chr18 | 78077248 | 676503571 | 8.6645 | 111.6143 |
| chr19 | 59128983 | 541126492 | 9.1516 | 107.9688 |
| chr20 | 63025520 | 540024883 | 8.5684 | 17.0262 |
| chr21 | 48129895 | 343682709 | 7.1407 | 29.6121 |
| chr22 | 51304566 | 324347261 | 6.322 | 12.3749 |
| chrMT | 16571 | 27378970 | 1,652.222 | 175.9942 |
| chrX | 155270560 | 658309291 | 4.2398 | 23.7678 |

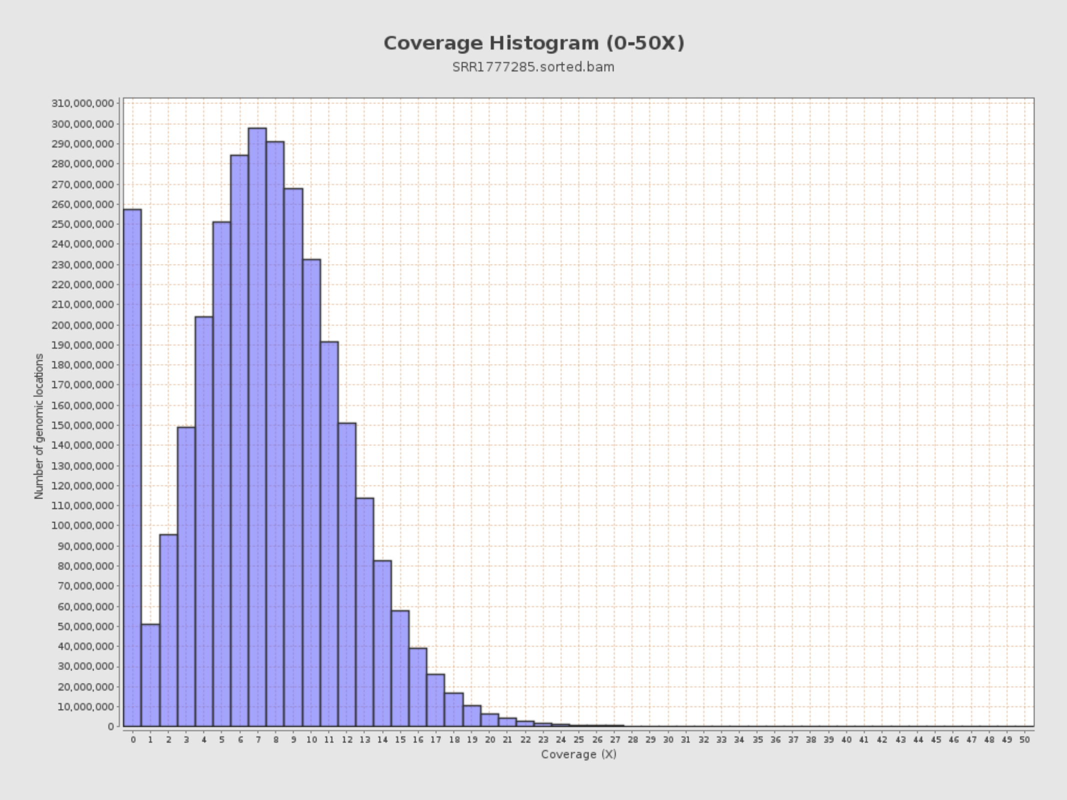
| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 240116176 | 4.0442 | 72.3905 |

# 3. Results : Coverage across reference

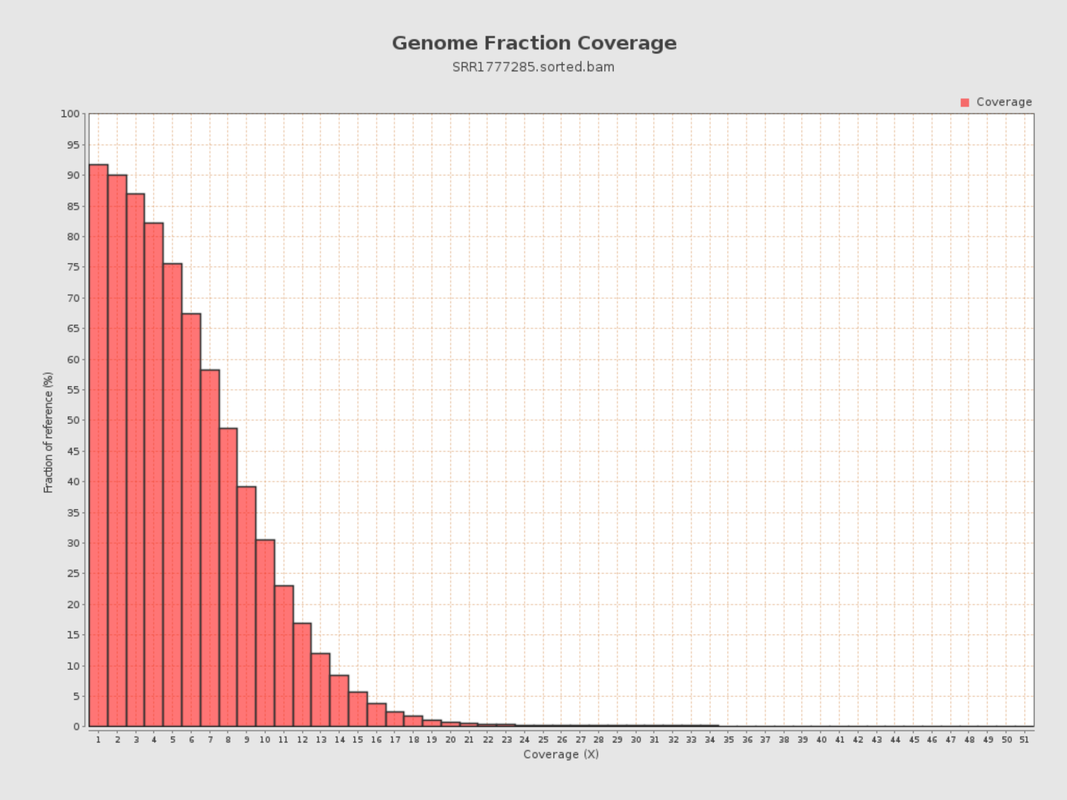
# 4. Results : Coverage Histogram



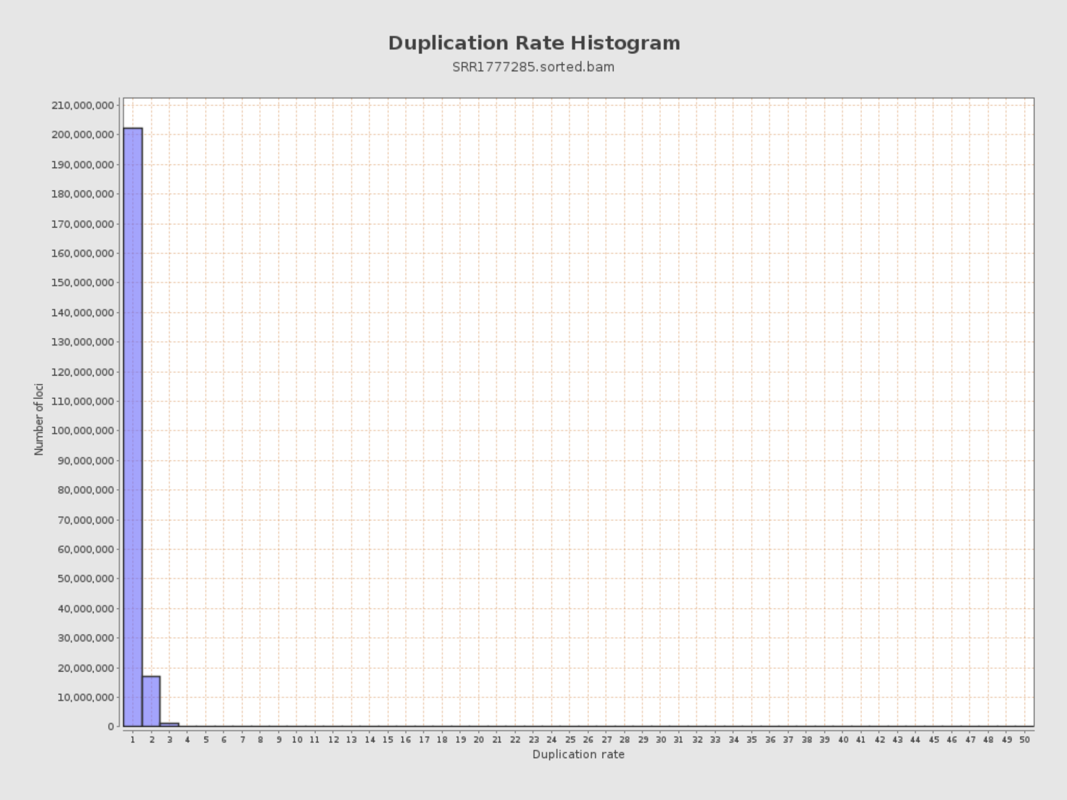
# 5. Results : Coverage Histogram (0-50X)



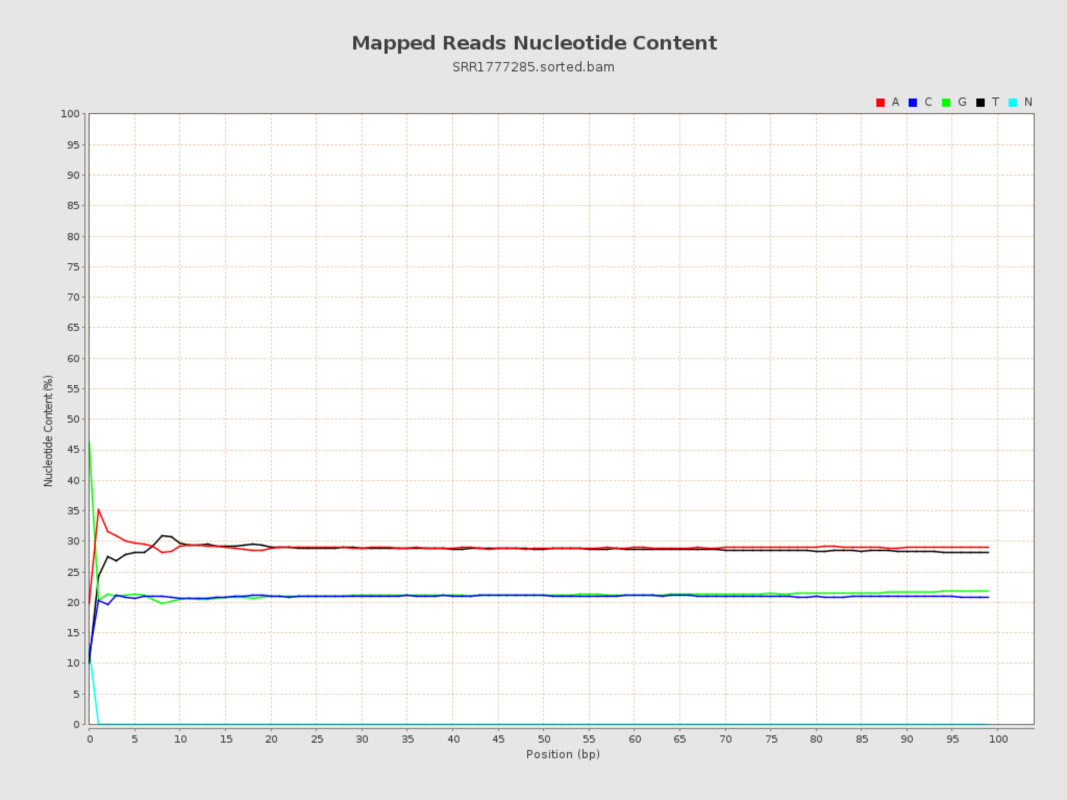
# 6. Results : Genome Fraction Coverage



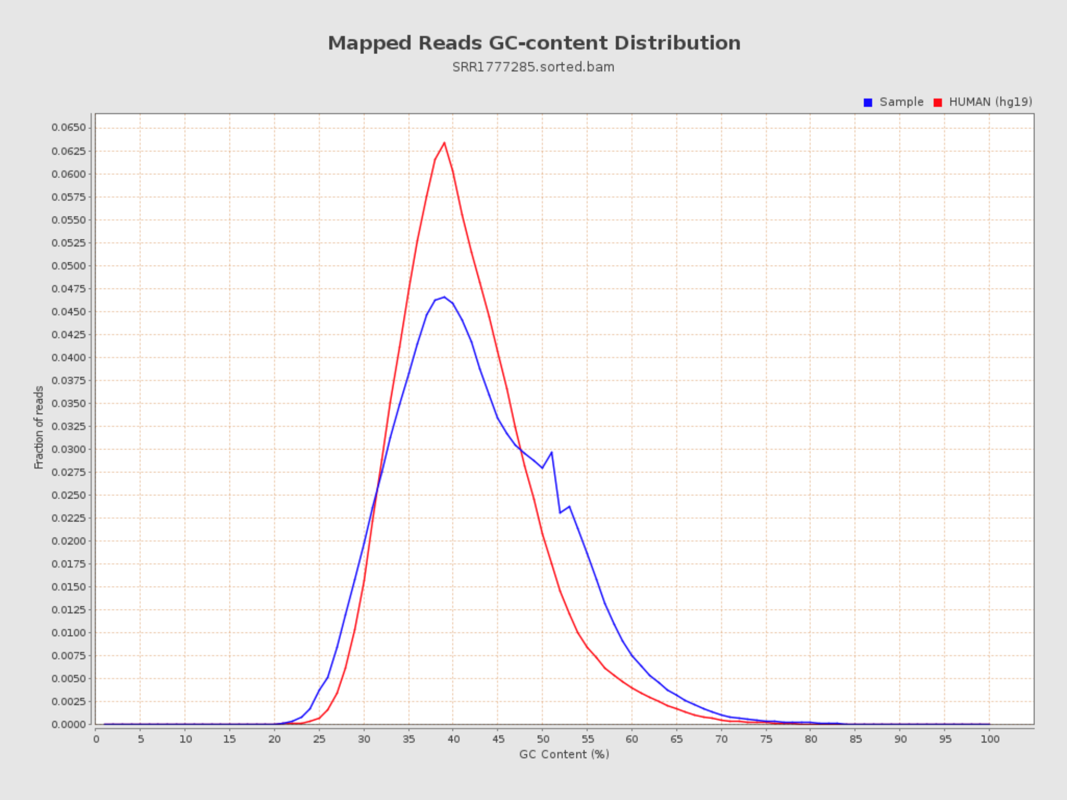
# 7. Results : Duplication Rate Histogram



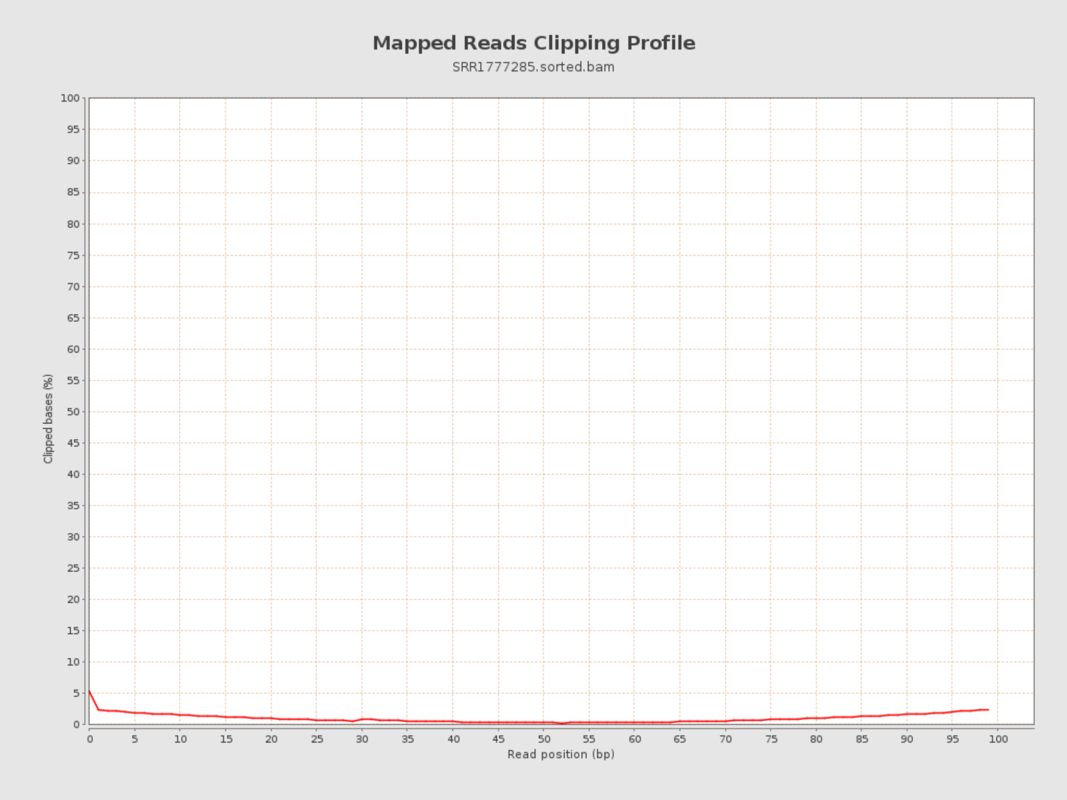
# 8. Results : Mapped Reads Nucleotide Content



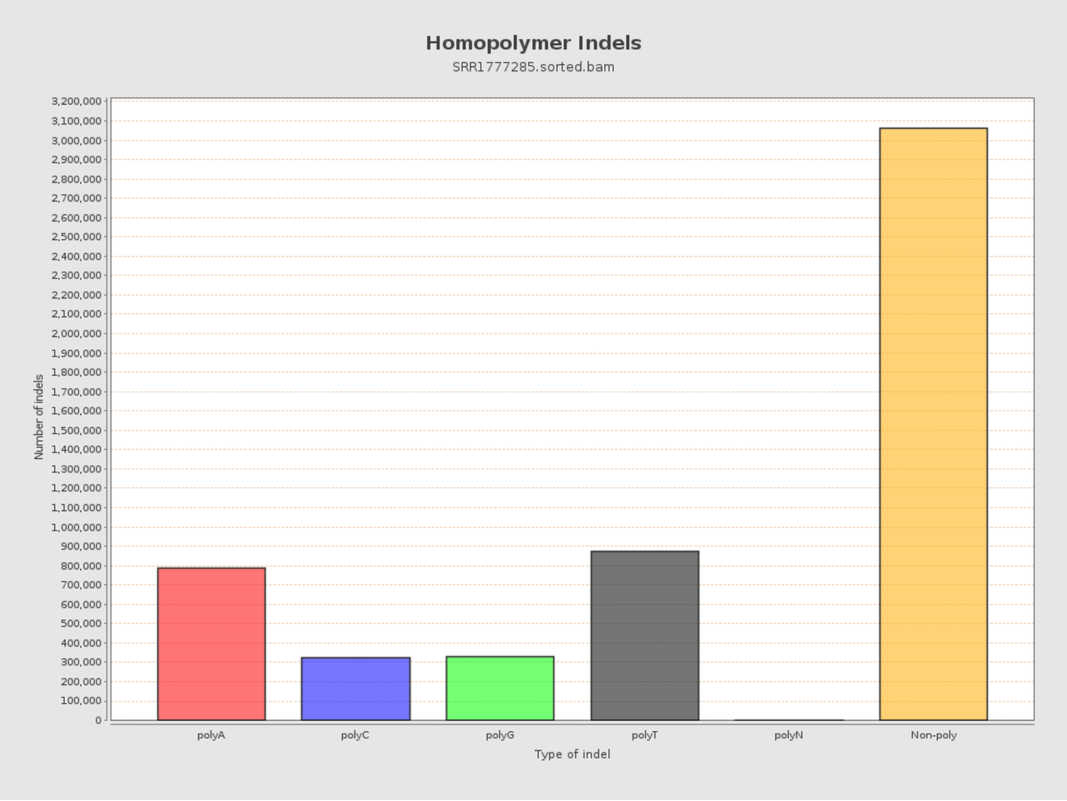
# 9. Results : Mapped Reads GC-content Distribution



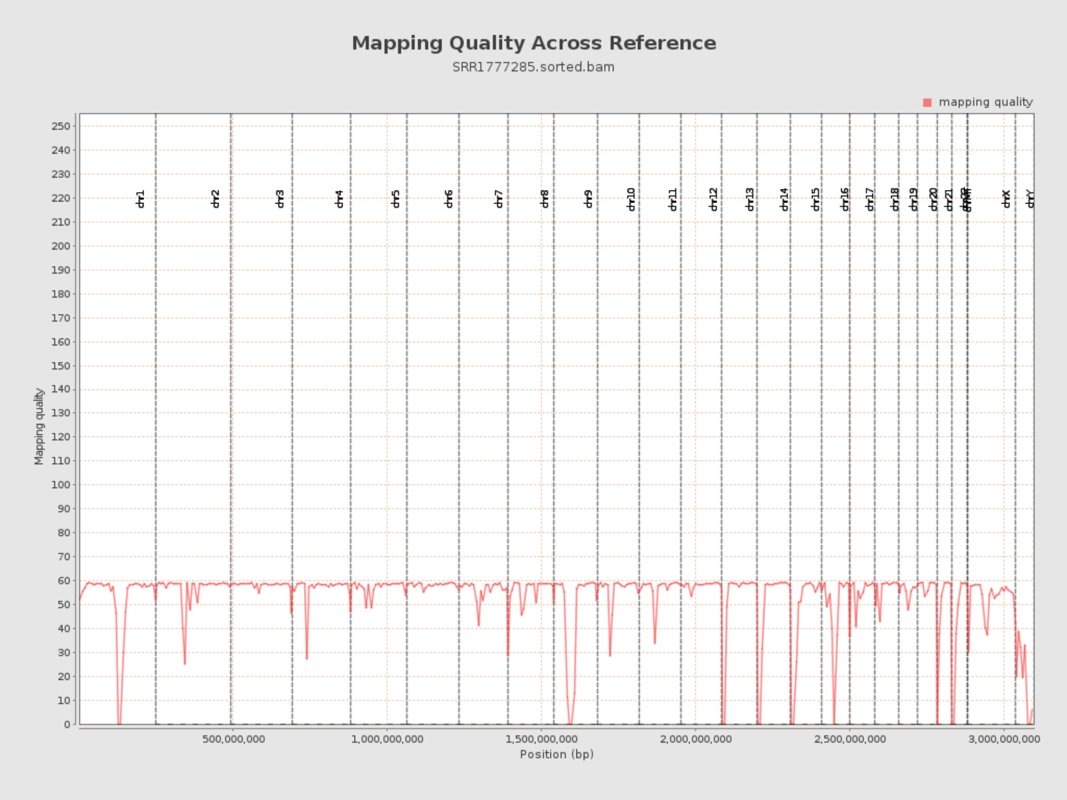
# 10. Results : Mapped Reads Clipping Profile



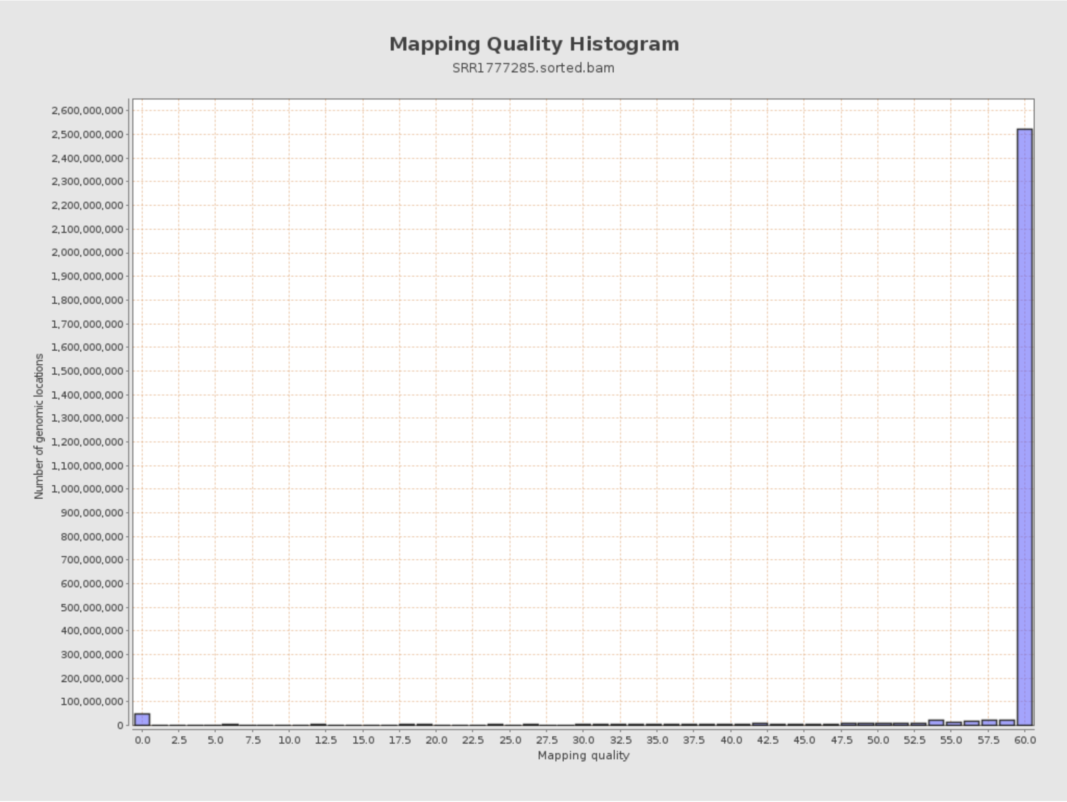
# 11. Results : Homopolymer Indels



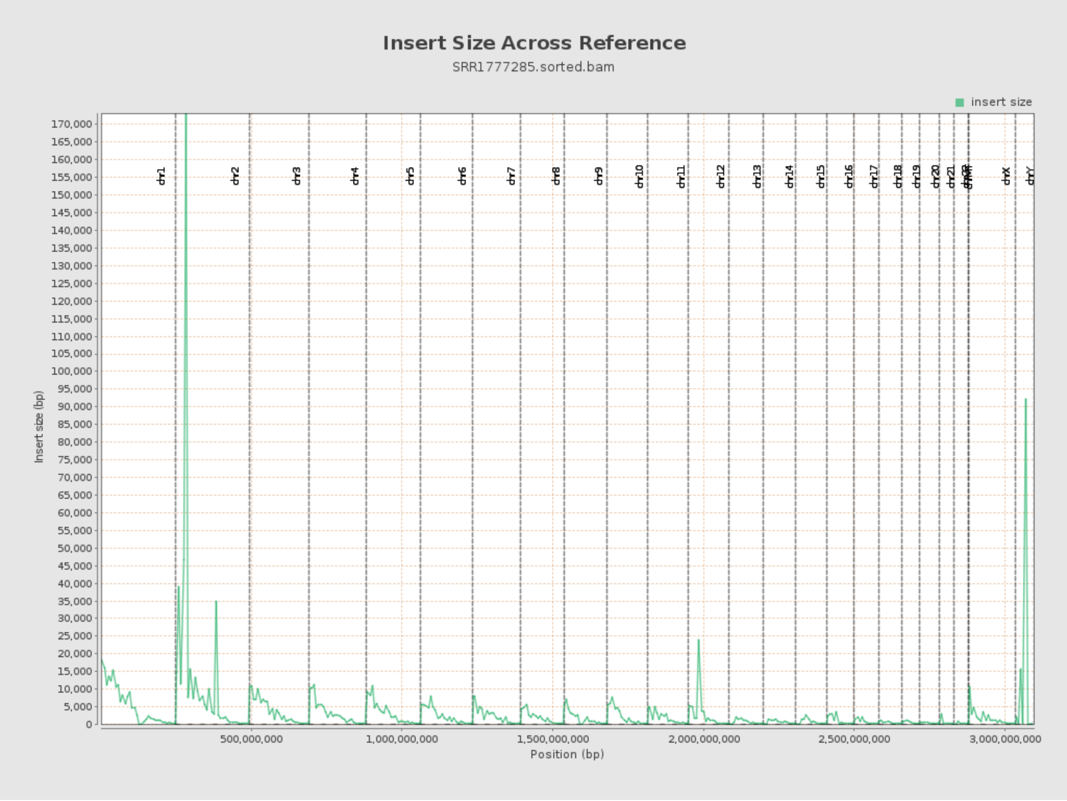
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram