# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/06 03:50:34*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1777292.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_SRR1777292 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1777292_1.fastq.gz SRR1777292_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Apr 06 03:50:33 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1777292.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,101,164 |
| Mapped reads | 1,067,910 / 96.98% |
| Unmapped reads | 33,254 / 3.02% |
| Mapped paired reads | 1,067,910 / 96.98% |
| Mapped reads, first in pair | 536,717 / 48.74% |
| Mapped reads,  second in pair | 531,193 / 48.24% |
| Mapped reads, both in pair | 1,059,306 / 96.2% |
| Mapped reads, singletons | 8,604 / 0.78% |
| Secondary alignments | 0 |
| Supplementary alignments | 45,956 / 4.17% |
| Read min/max/mean length | 30 / 101 / 102.73 |
| Duplicated reads (estimated) | 60,033 / 5.45% |
| Duplication rate | 4.66% |
| Clipped reads | 263,495 / 23.93% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 30,366,235 / 29.02% |
| Number/percentage of C's | 22,029,087 / 21.05% |
| Number/percentage of T's | 29,803,816 / 28.48% |
| Number/percentage of G's | 22,431,441 / 21.44% |
| Number/percentage of N's | 1,720 / 0% |
| | |

| | |
|---|---|
| GC Percentage | 42.49% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0338 |
| Standard Deviation | 0.4109 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.09 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 211,652.73 |
| Standard Deviation | 4,459,001.96 |
| P25/Median/P75 | 130 / 174 / 231 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.69% |
| Mismatches | 672,321 |
| Insertions | 24,175 |
| Mapped reads with at least one insertion | 2.21% |
| Deletions | 13,773 |
| Mapped reads with at least one deletion | 1.25% |
| Homopolymer indels | 45.61% |

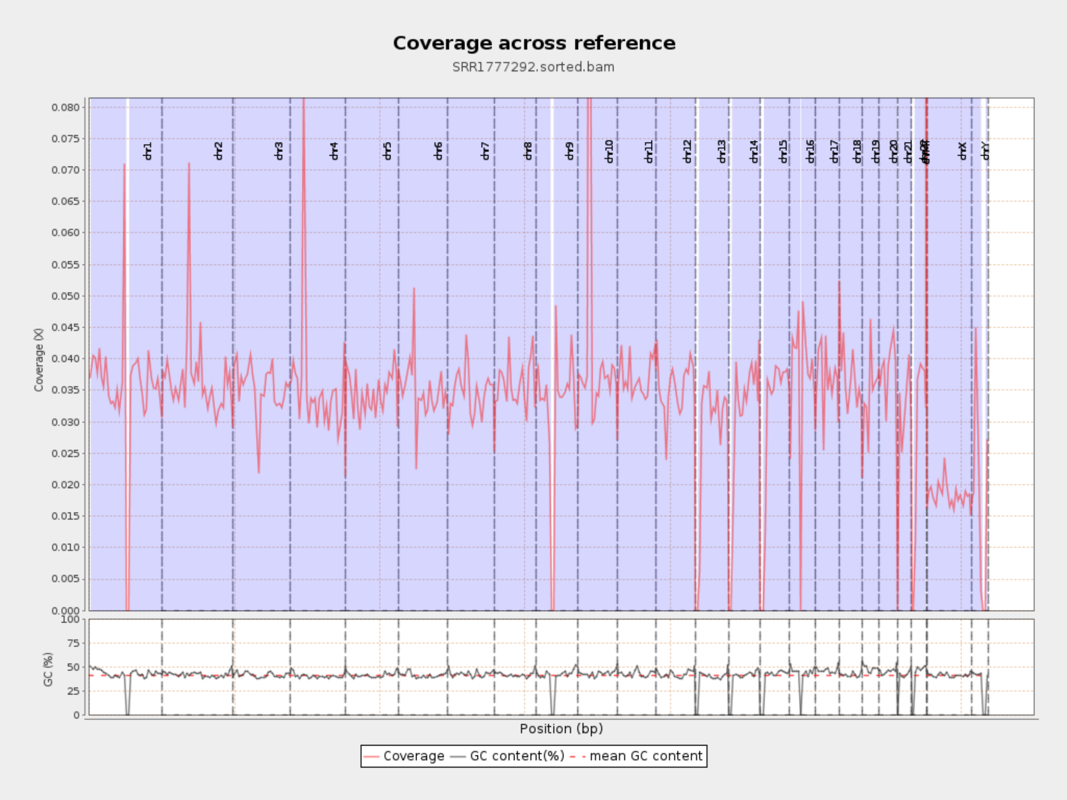
## 2.7. Chromosome stats

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

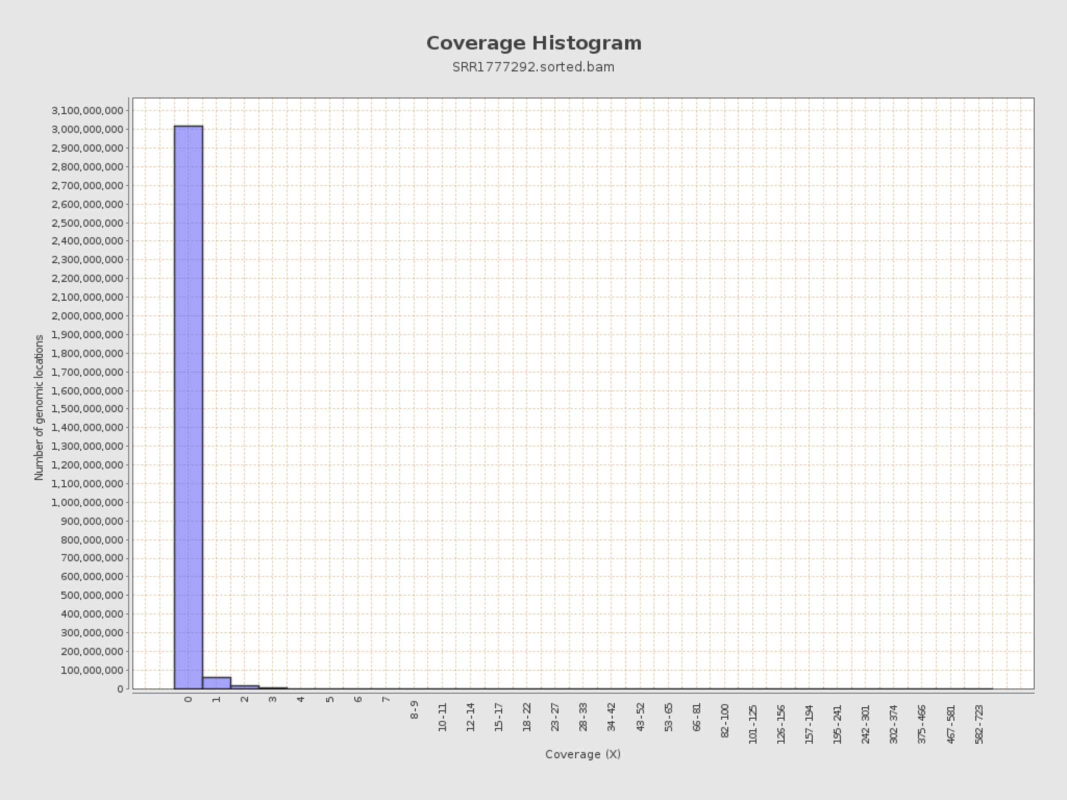
|  |  | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 8769564 | 0.0352 | 0.7555 |
| chr2 | 243199373 | 9005150 | 0.037 | 0.3486 |
| chr3 | 198022430 | 6970483 | 0.0352 | 0.236 |
| chr4 | 191154276 | 6791068 | 0.0355 | 0.4121 |
| chr5 | 180915260 | 6264867 | 0.0346 | 0.2232 |
| chr6 | 171115067 | 6004632 | 0.0351 | 0.2889 |
| chr7 | 159138663 | 5530820 | 0.0348 | 0.3244 |
| chr8 | 146364022 | 5277254 | 0.0361 | 0.258 |
| chr9 | 141213431 | 4467459 | 0.0316 | 0.4065 |
| chr10 | 135534747 | 5713479 | 0.0422 | 0.9564 |
| chr11 | 135006516 | 4970998 | 0.0368 | 0.2819 |
| chr12 | 133851895 | 4739229 | 0.0354 | 0.2255 |
| chr13 | 115169878 | 3174785 | 0.0276 | 0.1989 |
| chr14 | 107349540 | 3170284 | 0.0295 | 0.2083 |
| chr15 | 102531392 | 3056548 | 0.0298 | 0.2064 |
| chr16 | 90354753 | 3338875 | 0.037 | 0.2756 |
| chr17 | 81195210 | 2986205 | 0.0368 | 0.2814 |
| chr18 | 78077248 | 2912446 | 0.0373 | 0.4915 |
| chr19 | 59128983 | 2036881 | 0.0344 | 0.4395 |
| chr20 | 63025520 | 2392489 | 0.038 | 0.2507 |
| chr21 | 48129895 | 1432969 | 0.0298 | 0.261 |
| chr22 | 51304566 | 1327145 | 0.0259 | 0.1927 |
| chrMT | 16571 | 469798 | 28.3506 | 8.0977 |
| chrX | 155270560 | 2868047 | 0.0185 | 0.1755 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 995700 | 0.0168 | 0.3488 |

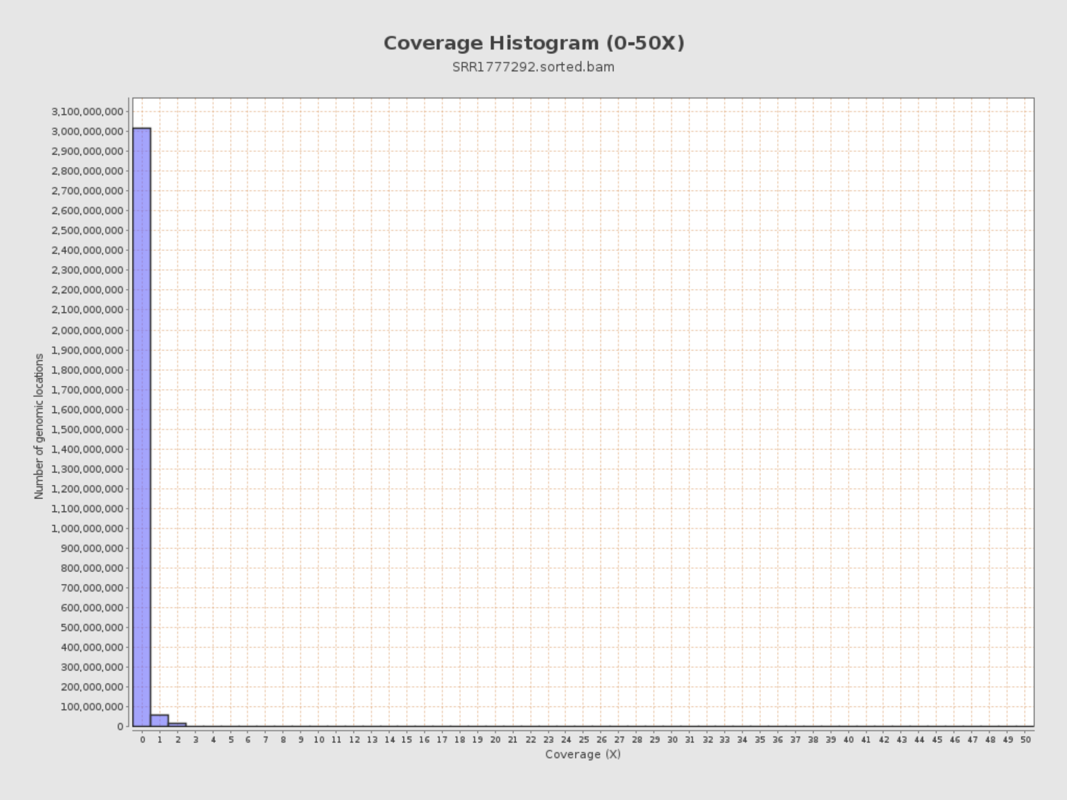
# 3. Results : Coverage across reference



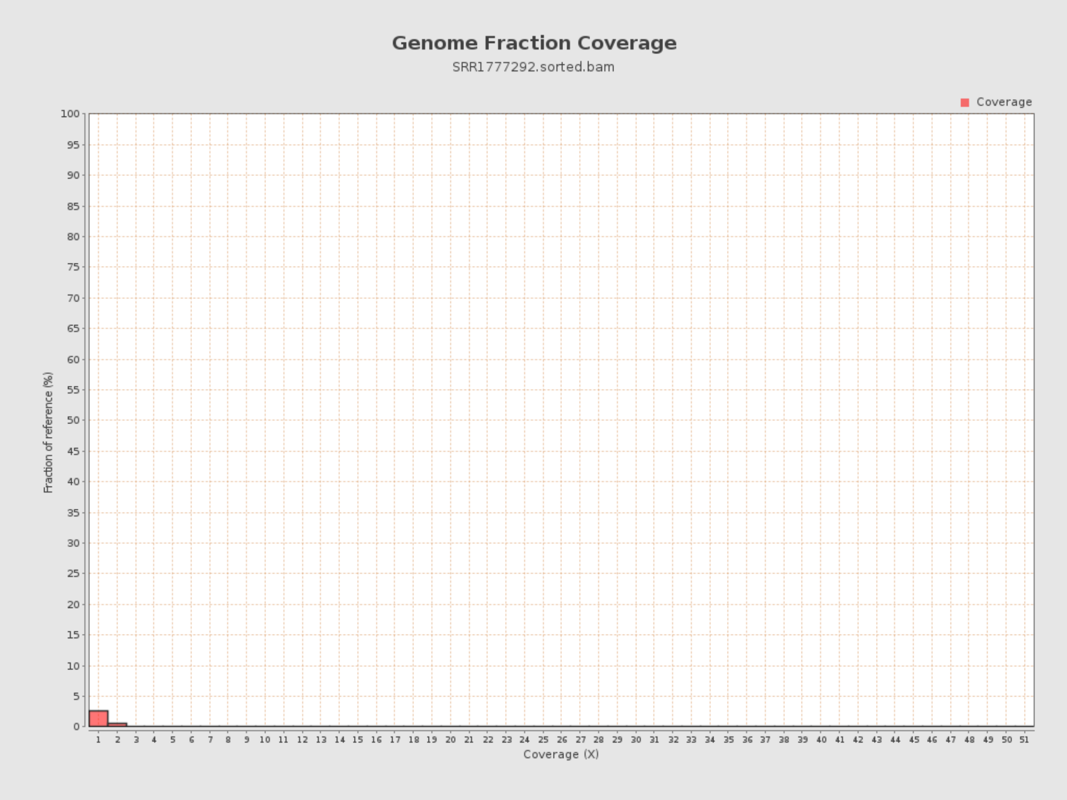
# 4. Results : Coverage Histogram



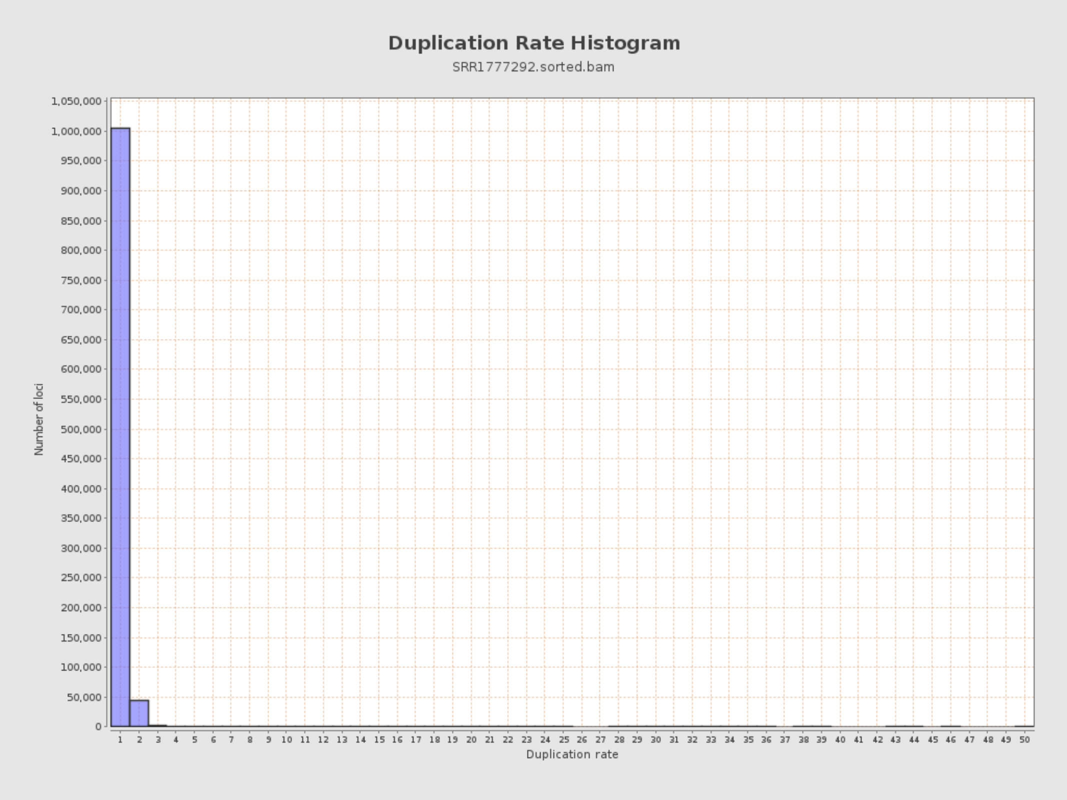
# 5. Results : Coverage Histogram (0-50X)



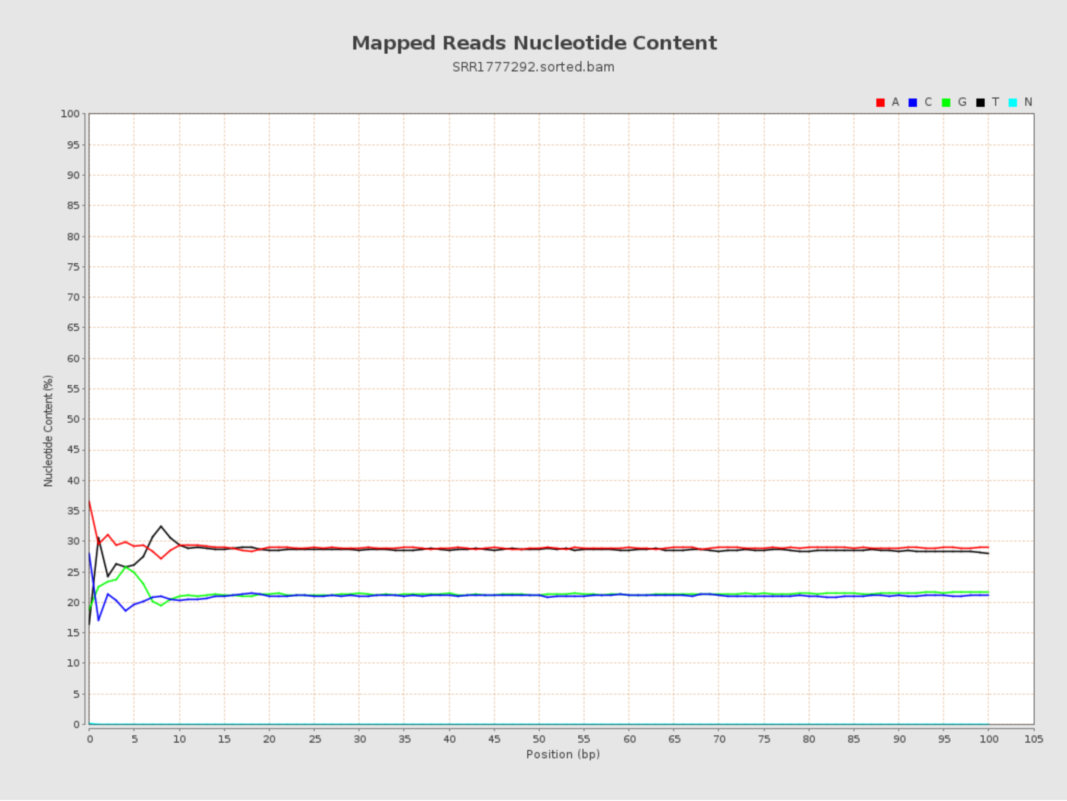
# 6. Results : Genome Fraction Coverage



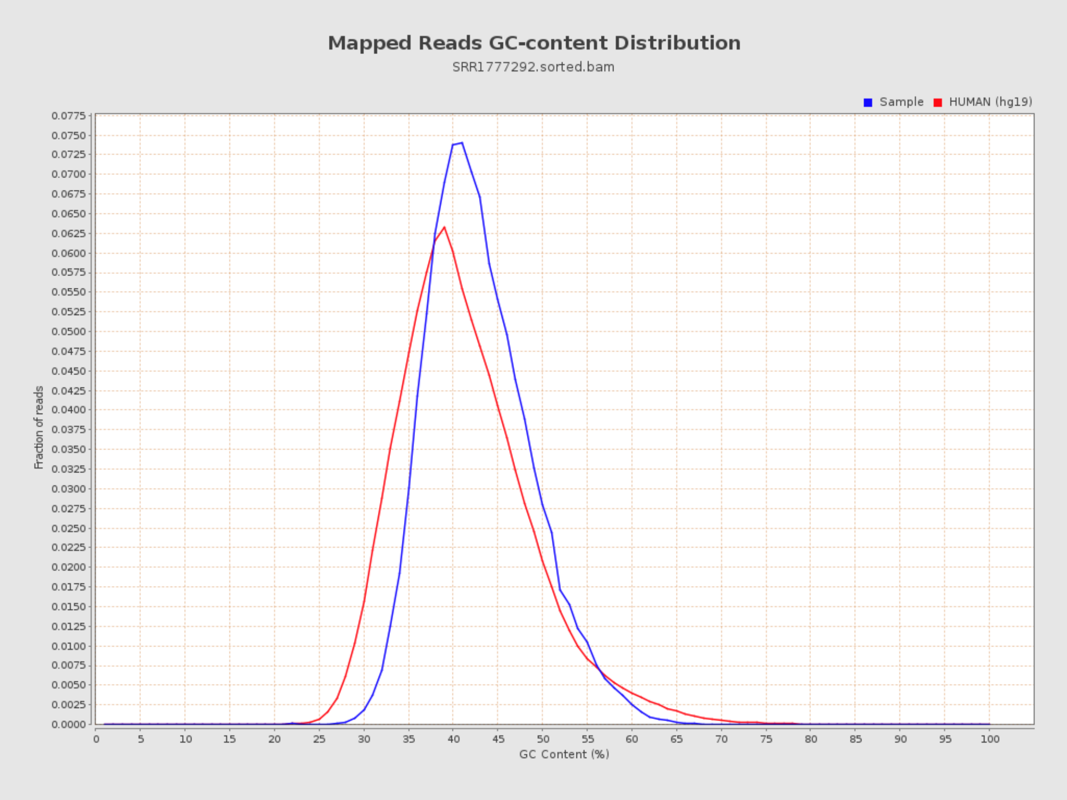
# 7. Results : Duplication Rate Histogram



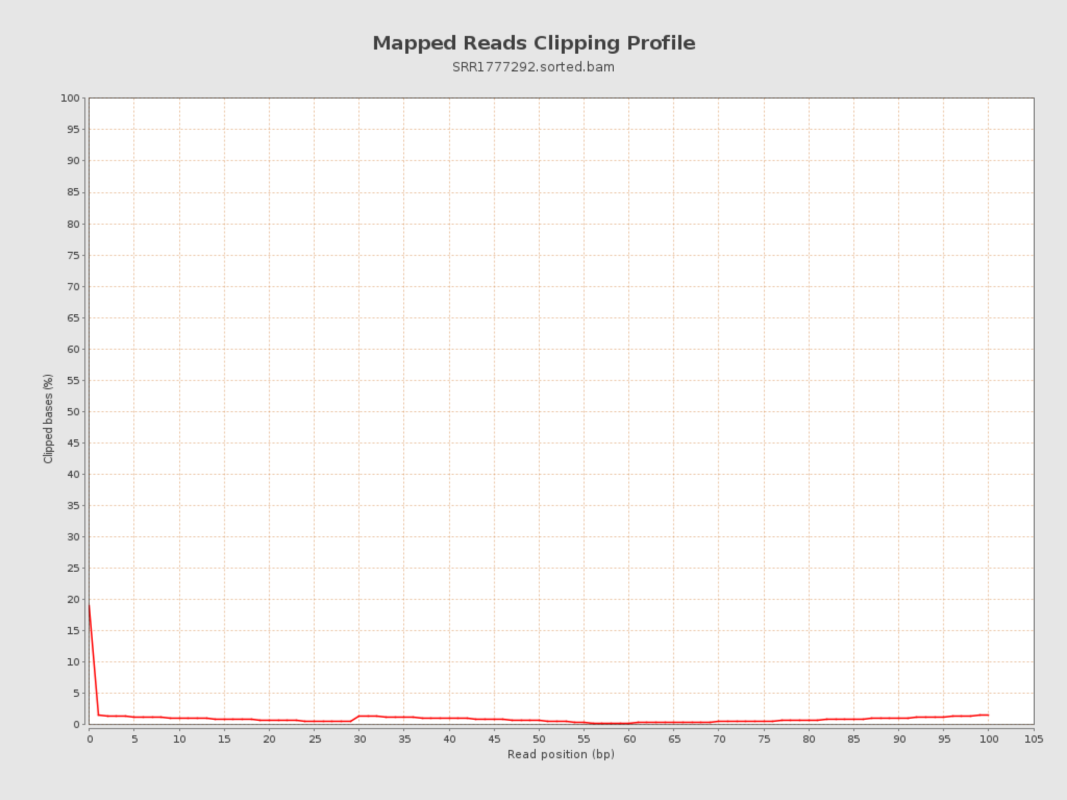
# 8. Results : Mapped Reads Nucleotide Content



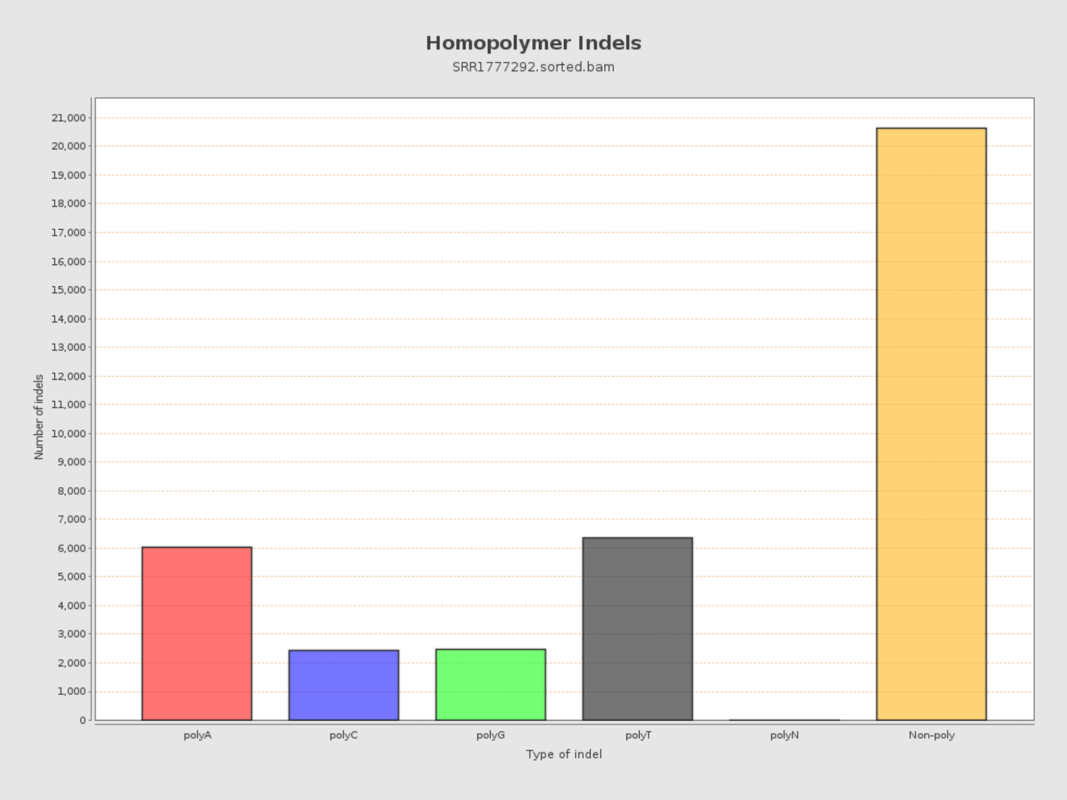
# 9. Results : Mapped Reads GC-content Distribution



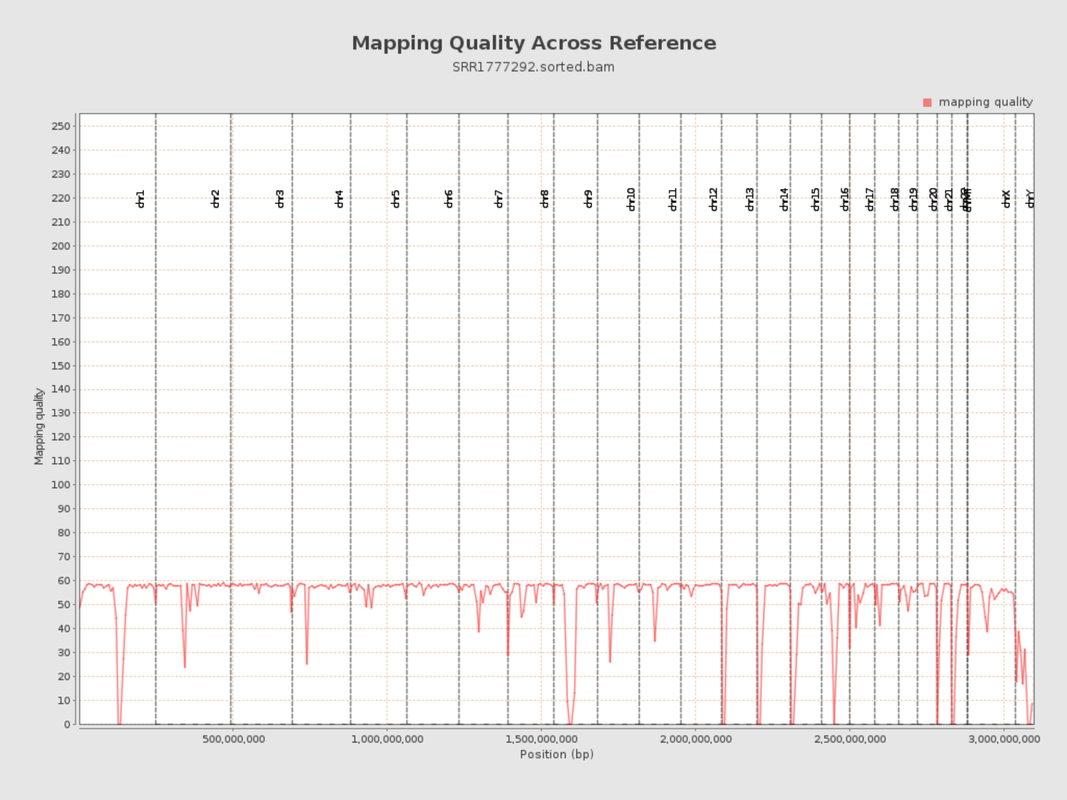
# 10. Results : Mapped Reads Clipping Profile



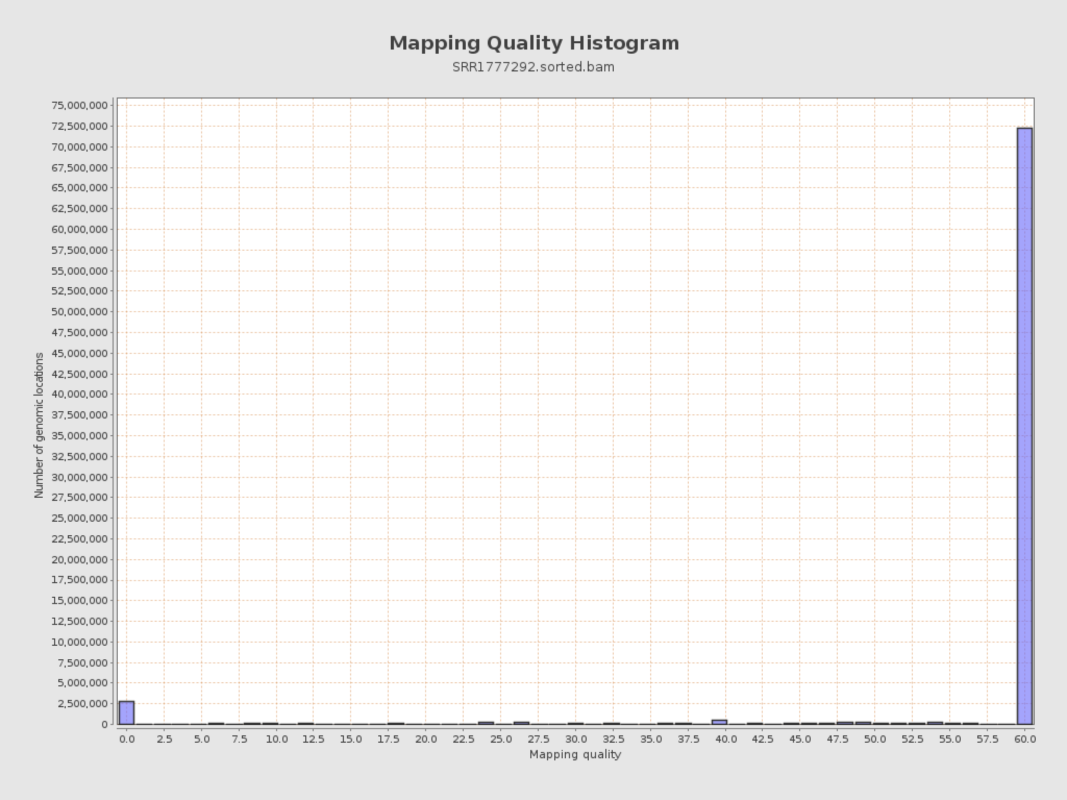
# 11. Results : Homopolymer Indels



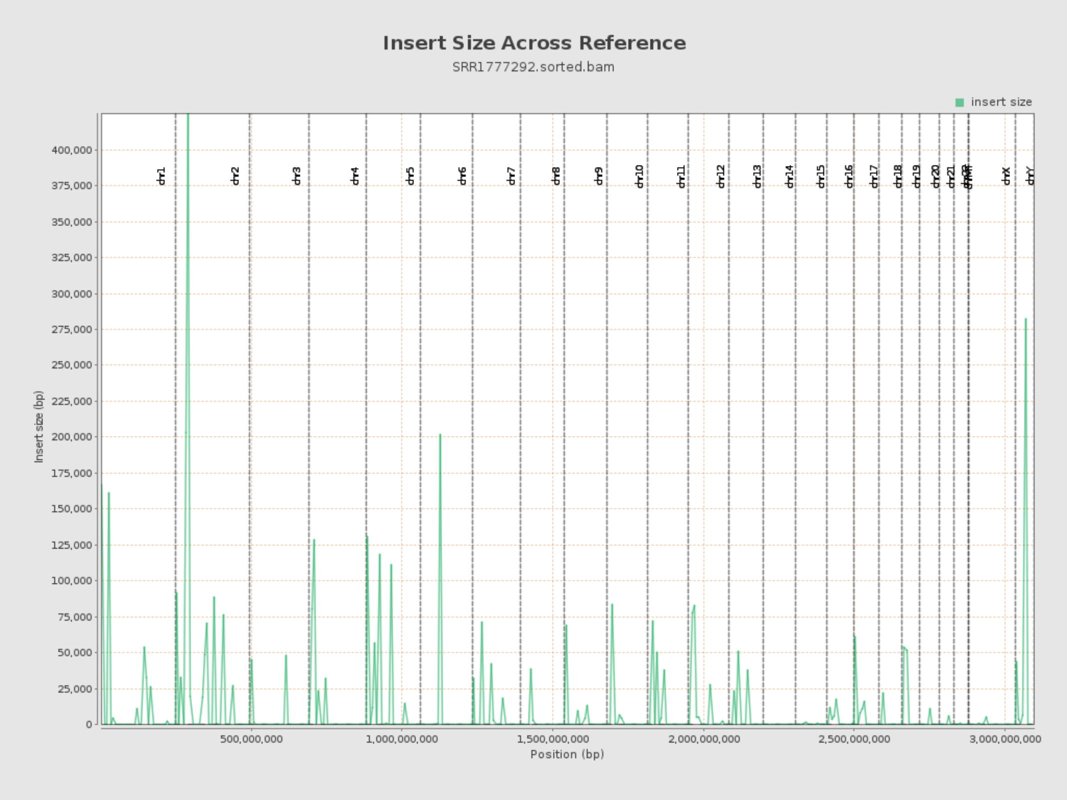
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram