# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/10/09 09:05:51*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR1779319.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_SRR1779319 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1779319_1.fastq.gz SRR1779319_2.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Oct 09 09:05:50 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR1779319.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 19,292,916 |
| Mapped reads | 18,141,959 / 94.03% |
| Unmapped reads | 1,150,957 / 5.97% |
| Mapped paired reads | 18,141,959 / 94.03% |
| Mapped reads, first in pair | 9,128,029 / 47.31% |
| Mapped reads,  second in pair | 9,013,930 / 46.72% |
| Mapped reads, both in pair | 17,995,430 / 93.27% |
| Mapped reads, singletons | 146,529 / 0.76% |
| Secondary alignments | 0 |
| Supplementary alignments | 46,952 / 0.24% |
| Read min/max/mean length | 30 / 80 / 80.09 |
| Duplicated reads (estimated) | 620,966 / 3.22% |
| Duplication rate | 3.16% |
| Clipped reads | 578,075 / 3% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 442,979,731 / 30.68% |
| Number/percentage of C's | 276,919,050 / 19.18% |
| Number/percentage of T's | 441,763,015 / 30.59% |
| Number/percentage of G's | 281,886,948 / 19.52% |
| Number/percentage of N's | 387,873 / 0.03% |
| | |

| | |
|---|---|
| GC Percentage | 38.7% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.4665 |
| Standard Deviation | 1.6891 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 53.1 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 33,788.79 |
| Standard Deviation | 1,749,024.39 |
| P25/Median/P75 | 150 / 205 / 284 |

## 2.6. Mismatches and indels

| | |
|---|---|
| General error rate | 0.36% |
| Mismatches | 4,961,996 |
| Insertions | 106,408 |
| Mapped reads with at least one insertion | 0.58% |
| Deletions | 134,179 |
| Mapped reads with at least one deletion | 0.73% |
| Homopolymer indels | 46.65% |

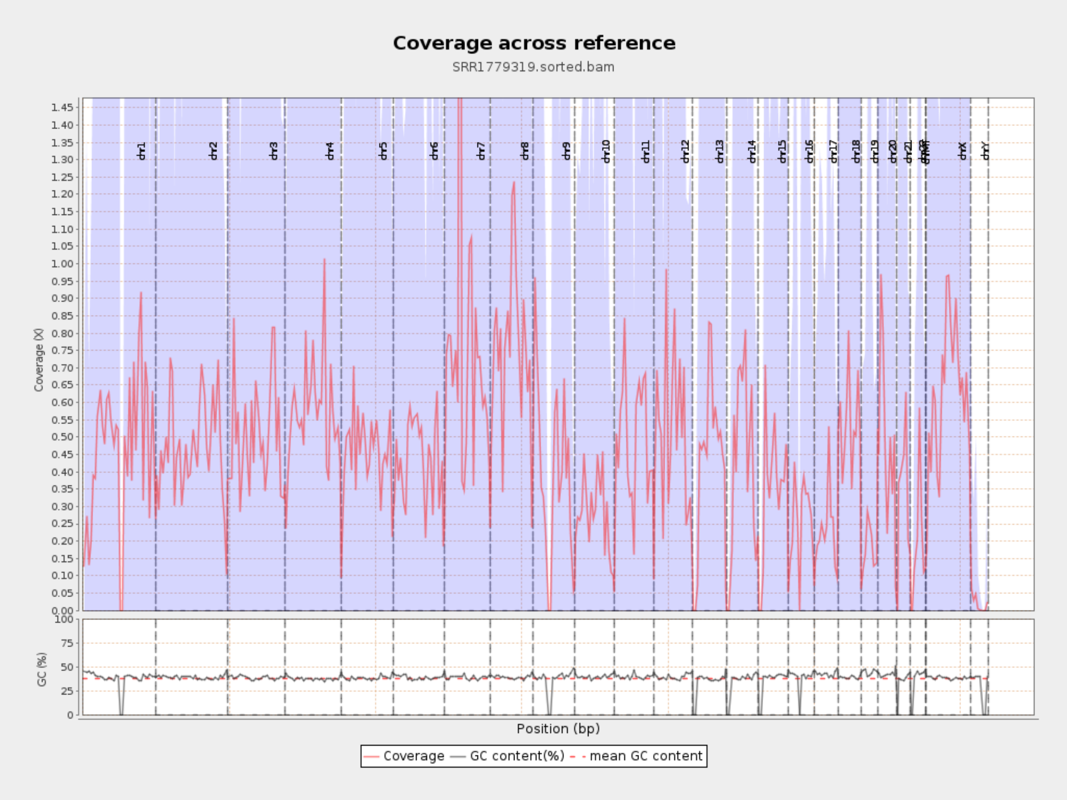
## 2.7. Chromosome stats

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

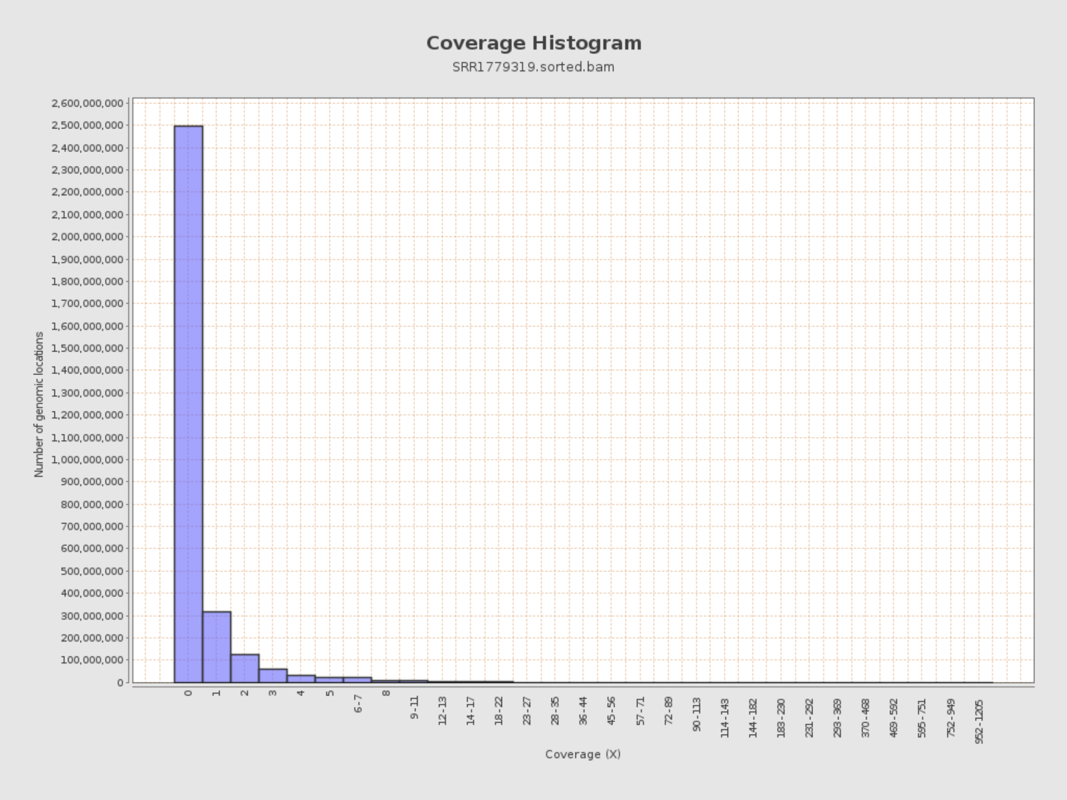
| | | bases | coverage | deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 115187809 | 0.4621 | 1.9832 |
| chr2 | 243199373 | 114091675 | 0.4691 | 1.4437 |
| chr3 | 198022430 | 99141832 | 0.5007 | 1.5525 |
| chr4 | 191154276 | 109186007 | 0.5712 | 1.6342 |
| chr5 | 180915260 | 81378852 | 0.4498 | 1.4043 |
| chr6 | 171115067 | 75111775 | 0.439 | 1.3422 |
| chr7 | 159138663 | 124212934 | 0.7805 | 3.0383 |
| chr8 | 146364022 | 111051788 | 0.7587 | 2.0138 |
| chr9 | 141213431 | 56649653 | 0.4012 | 1.3906 |
| chr10 | 135534747 | 38001364 | 0.2804 | 1.782 |
| chr11 | 135006516 | 66042111 | 0.4892 | 1.712 |
| chr12 | 133851895 | 68952321 | 0.5151 | 1.5984 |
| chr13 | 115169878 | 51135348 | 0.444 | 1.4402 |
| chr14 | 107349540 | 45783979 | 0.4265 | 1.5294 |
| chr15 | 102531392 | 35903192 | 0.3502 | 1.1848 |
| chr16 | 90354753 | 22409394 | 0.248 | 1.0862 |
| chr17 | 81195210 | 19110535 | 0.2354 | 0.9457 |
| chr18 | 78077248 | 42116565 | 0.5394 | 1.6112 |
| chr19 | 59128983 | 11427103 | 0.1933 | 1.082 |
| chr20 | 63025520 | 32247944 | 0.5117 | 1.6657 |
| chr21 | 48129895 | 16667702 | 0.3463 | 1.5007 |
| chr22 | 51304566 | 10226349 | 0.1993 | 1.1956 |
| chrMT | 16571 | 2468 | 0.1489 | 0.521 |
| chrX | 155270560 | 97041964 | 0.625 | 2.0792 |

| | | | | |
|---|---|---|---|---|
| chrY | 59373566 | 1134267 | 0.0191 | 0.2536 |

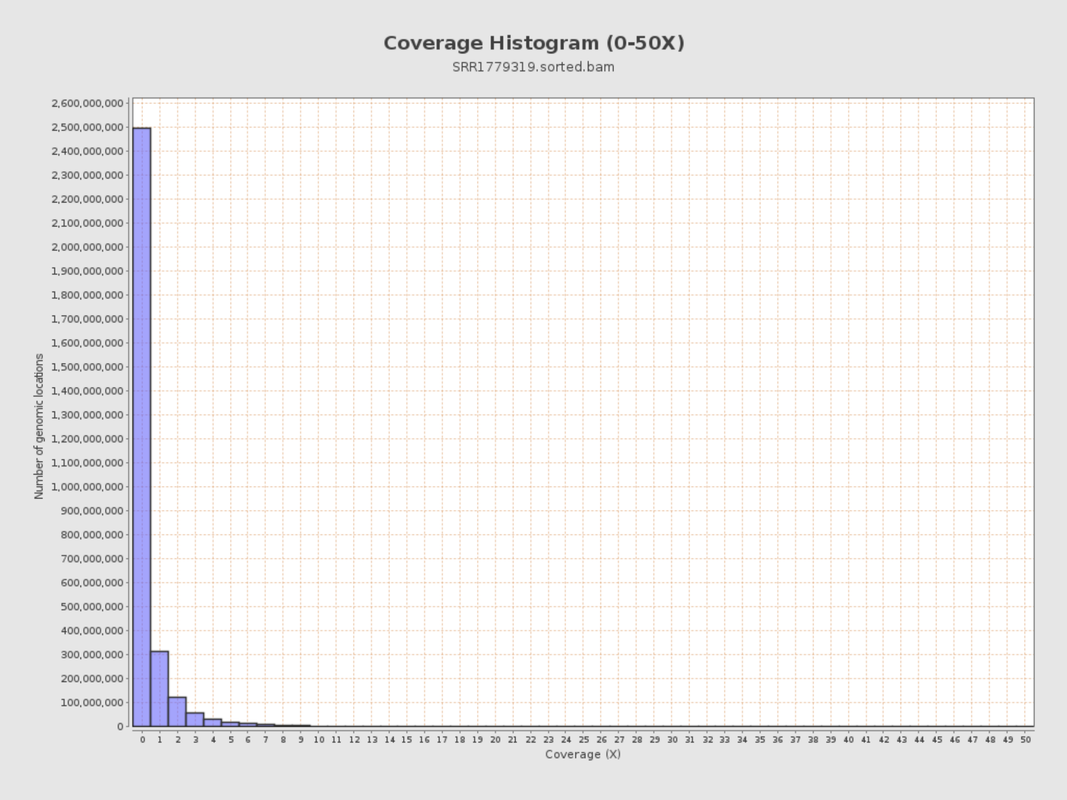
# 3. Results : Coverage across reference



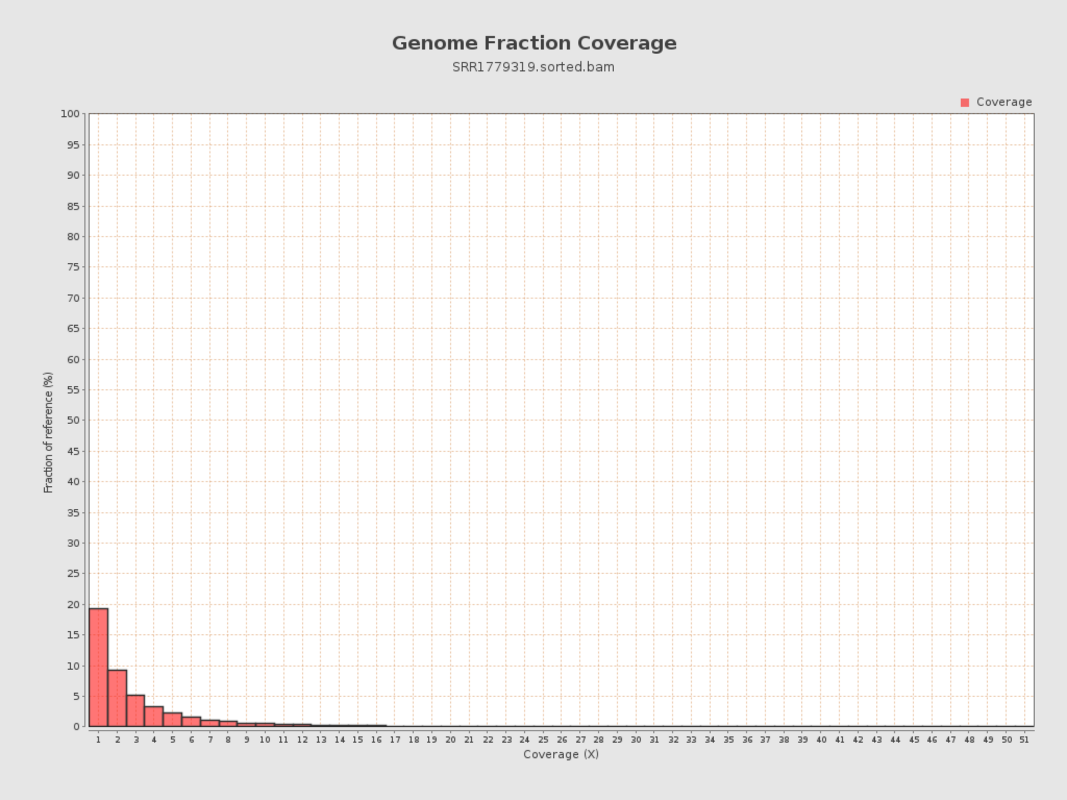
# 4. Results : Coverage Histogram



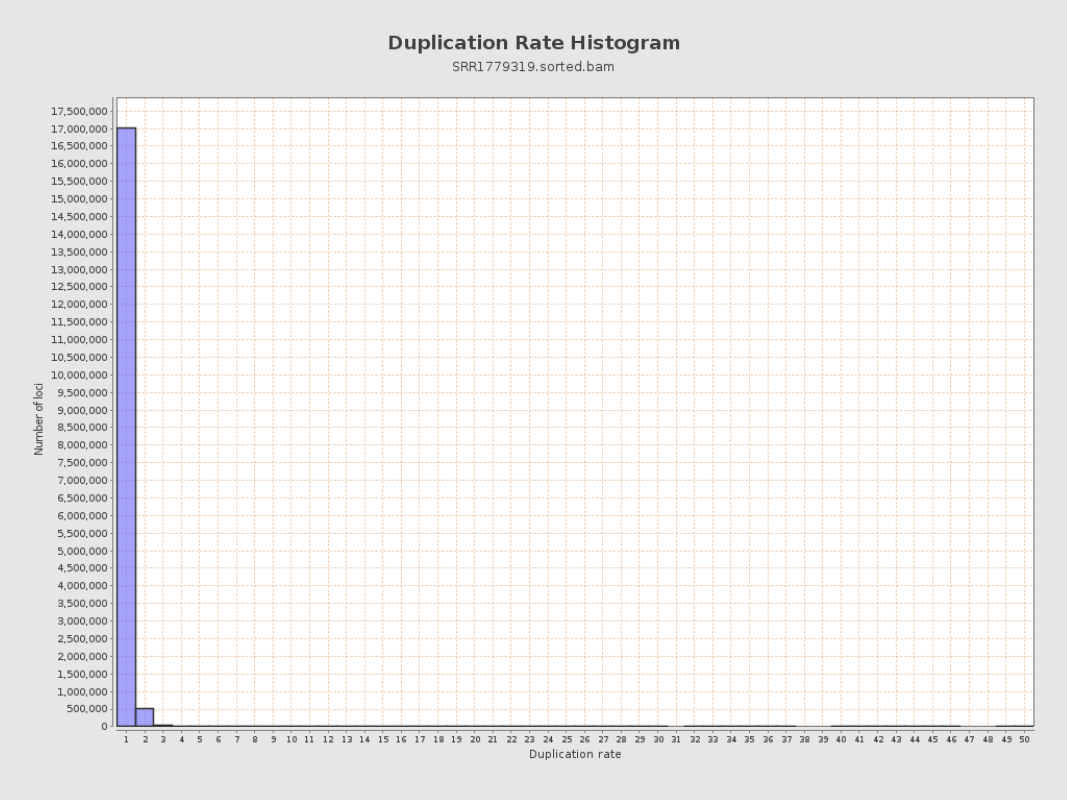
# 5. Results : Coverage Histogram (0-50X)



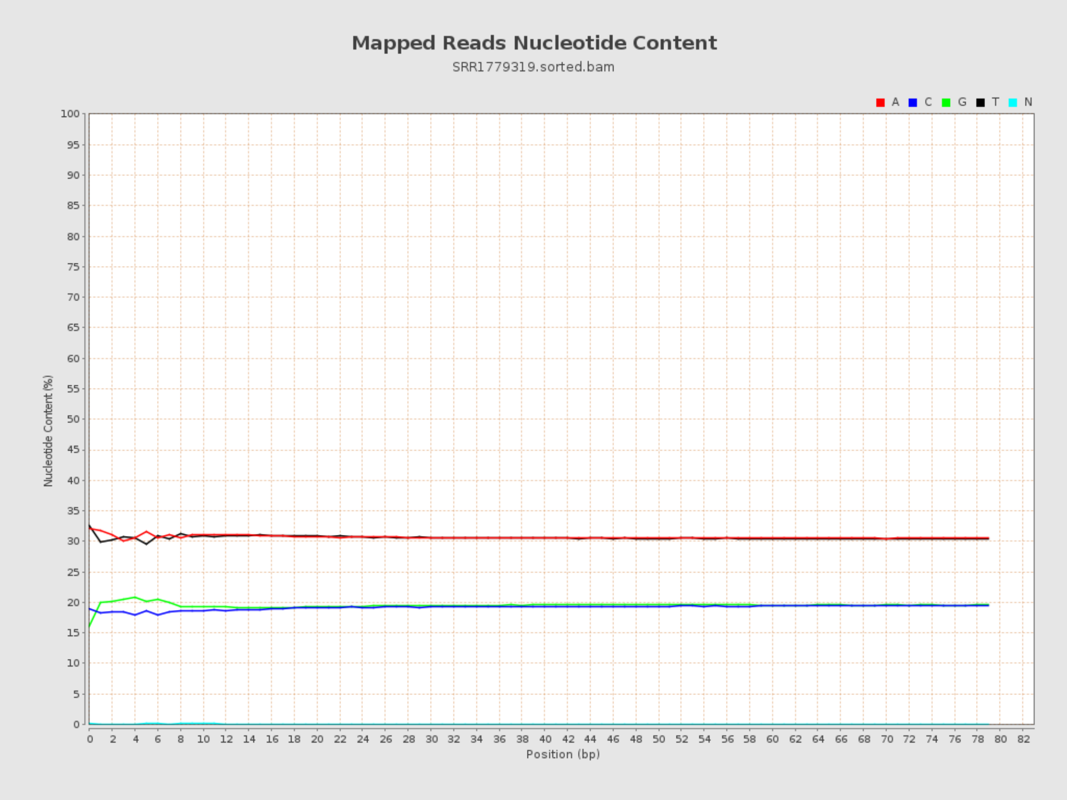
# 6. Results : Genome Fraction Coverage



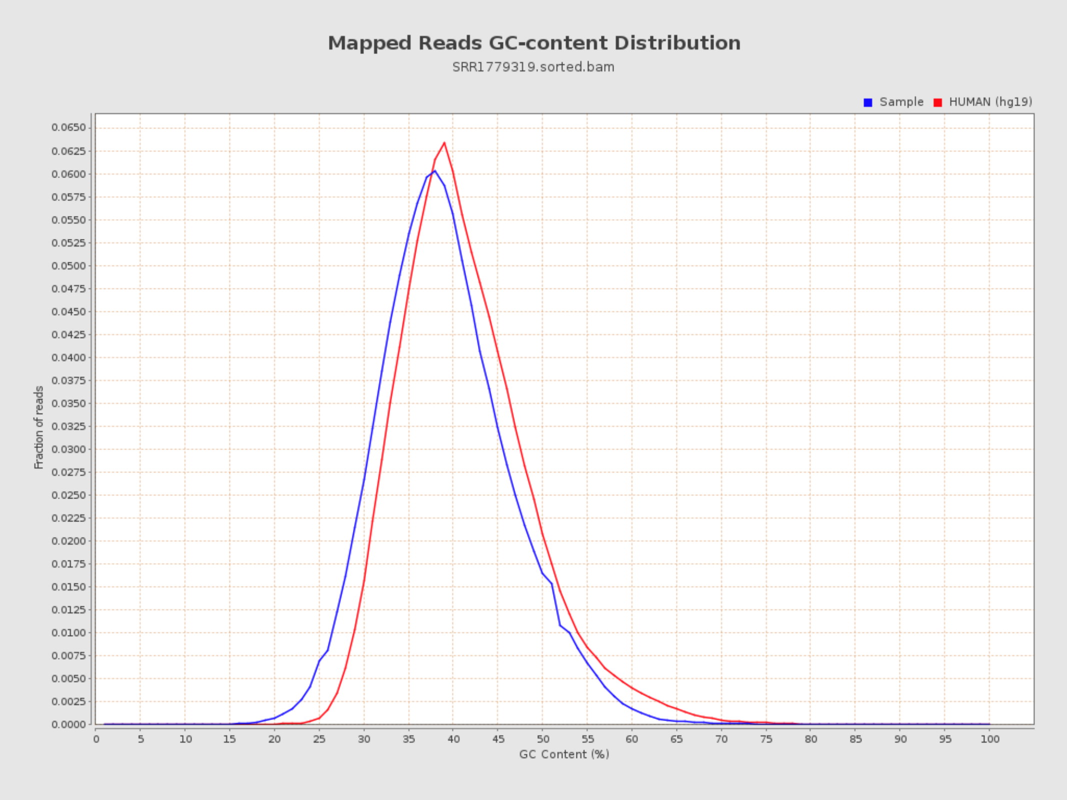
# 7. Results : Duplication Rate Histogram



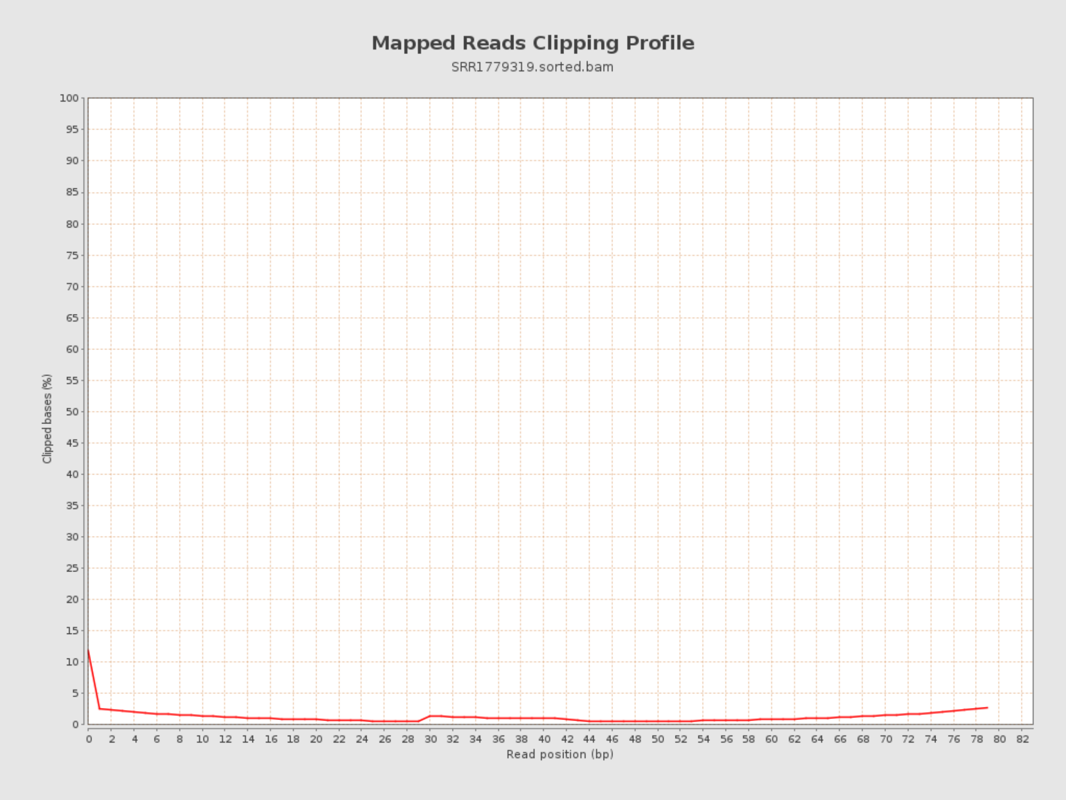
# 8. Results : Mapped Reads Nucleotide Content



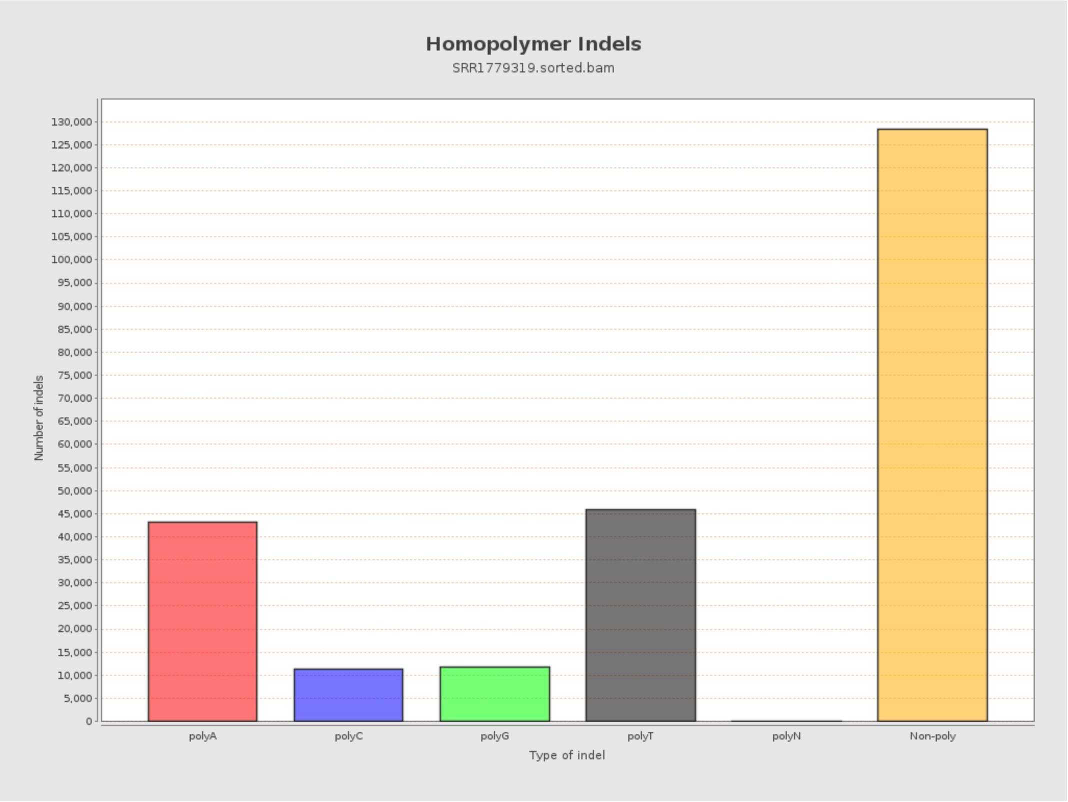
# 9. Results : Mapped Reads GC-content Distribution



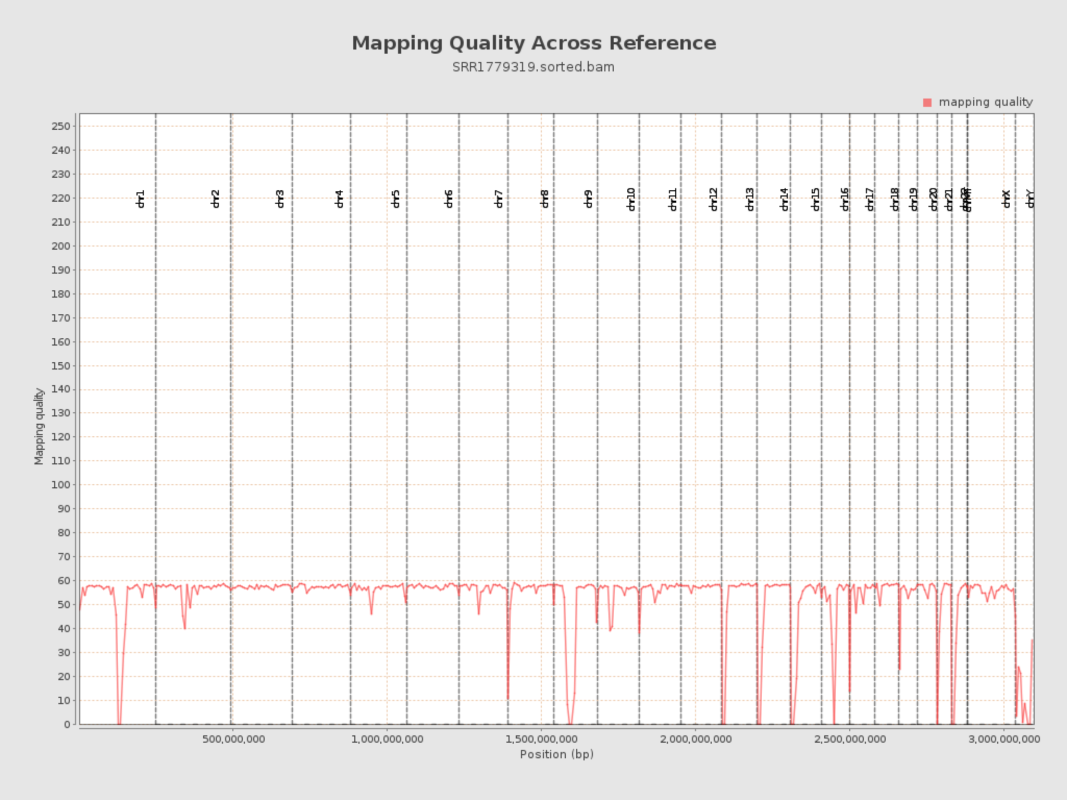
# 10. Results : Mapped Reads Clipping Profile



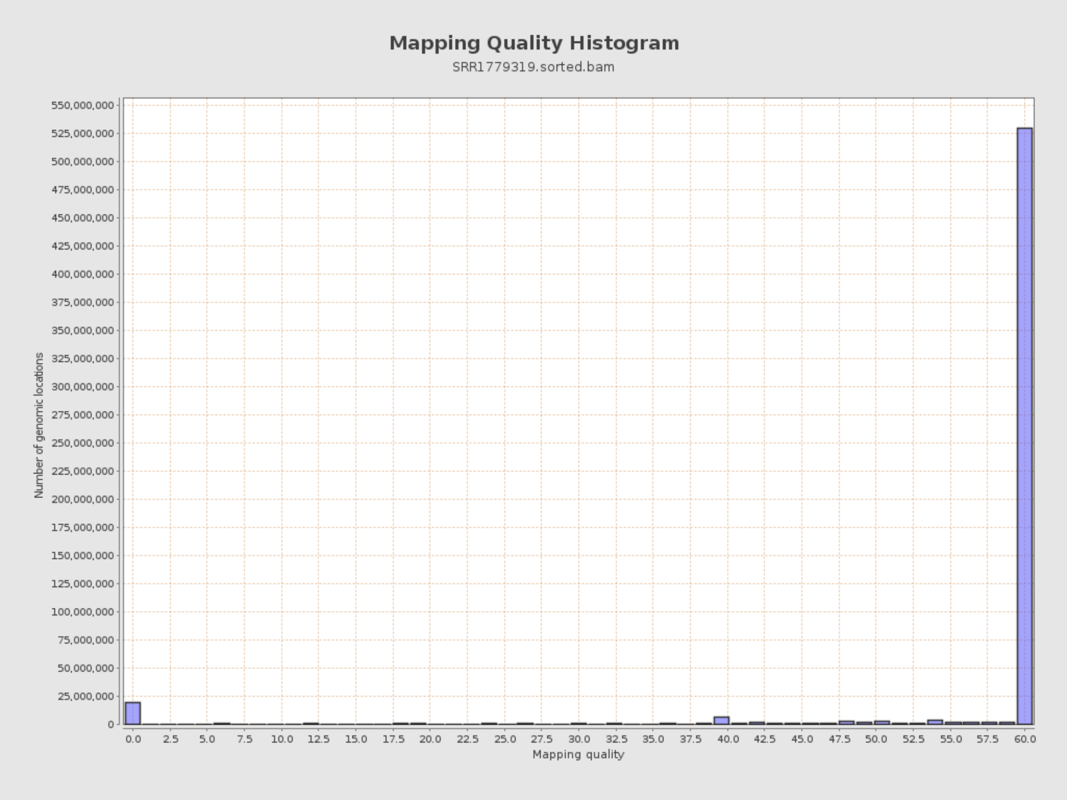
# 11. Results : Homopolymer Indels



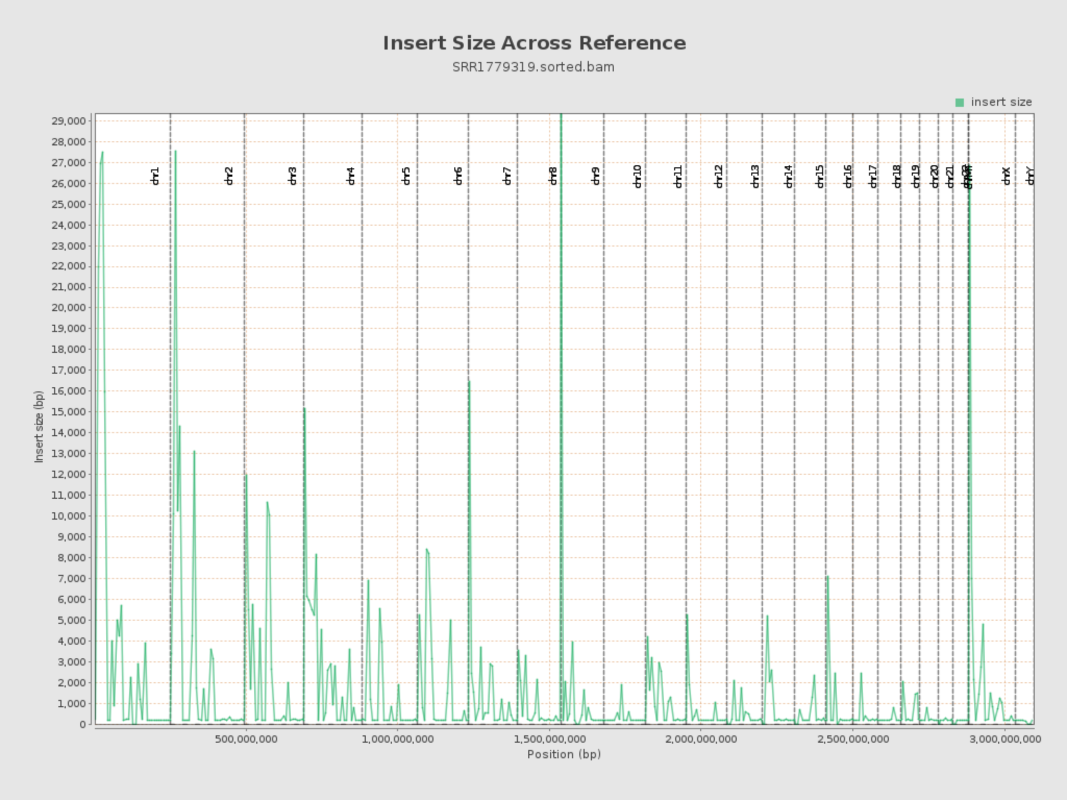
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram