# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/19 04:48:21*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR054571.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_SRR054571 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR054571.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Tue Apr 19 04:48:21 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR054571.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 14,204,440 |
| Mapped reads | 10,656,965 / 75.03% |
| Unmapped reads | 3,547,475 / 24.97% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 312 / 0% |
| Read min/max/mean length | 30 / 48 / 48 |
| Duplicated reads (estimated) | 3,822,223 / 26.91% |
| Duplication rate | 24.03% |
| Clipped reads | 1,152,730 / 8.12% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 152,770,684 / 30.48% |
| Number/percentage of C's | 97,851,221 / 19.52% |
| Number/percentage of T's | 147,977,873 / 29.53% |
| Number/percentage of G's | 102,478,171 / 20.45% |
| Number/percentage of N's | 89,886 / 0.02% |
| GC Percentage | 39.97% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1619 |
| | |

| | |
|---|---|
| Standard Deviation | 1.474 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.87 |

## 2.5. Mismatches and indels

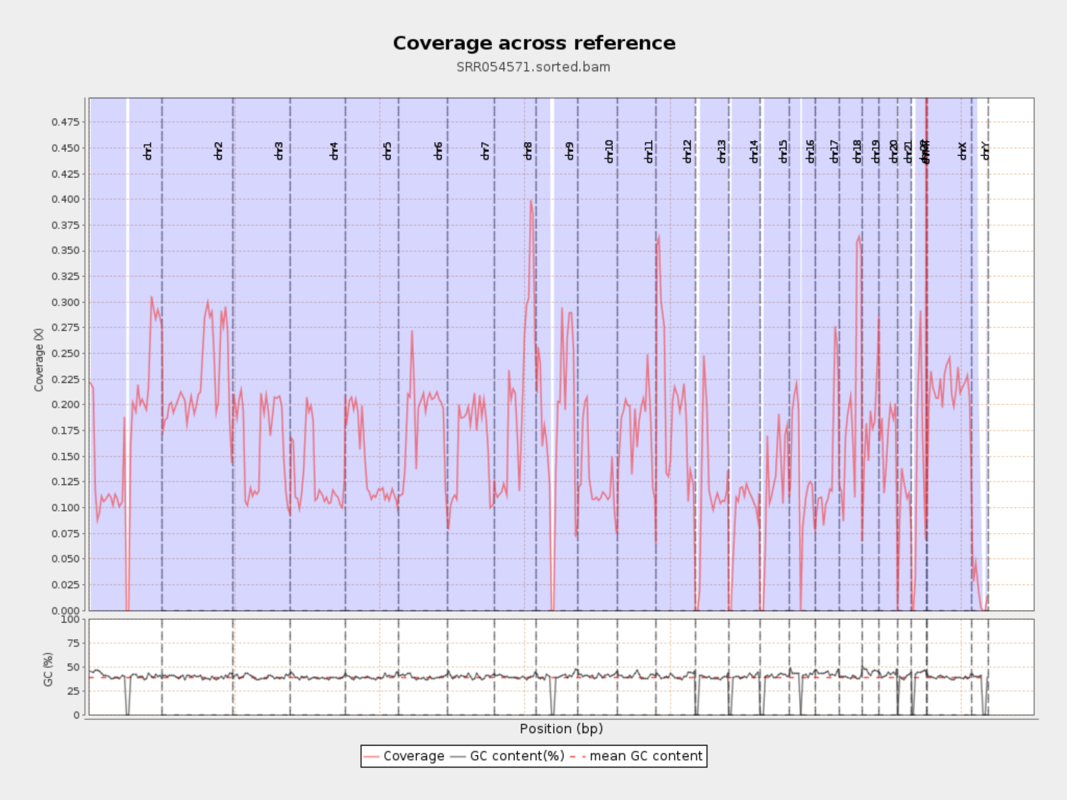
| | |
|---|---|
| General error rate | 0.55% |
| Mismatches | 2,733,974 |
| Insertions | 22,645 |
| Mapped reads with at least one insertion | 0.21% |
| Deletions | 71,882 |
| Mapped reads with at least one deletion | 0.67% |
| Homopolymer indels | 47.93% |

## 2.6. Chromosome stats

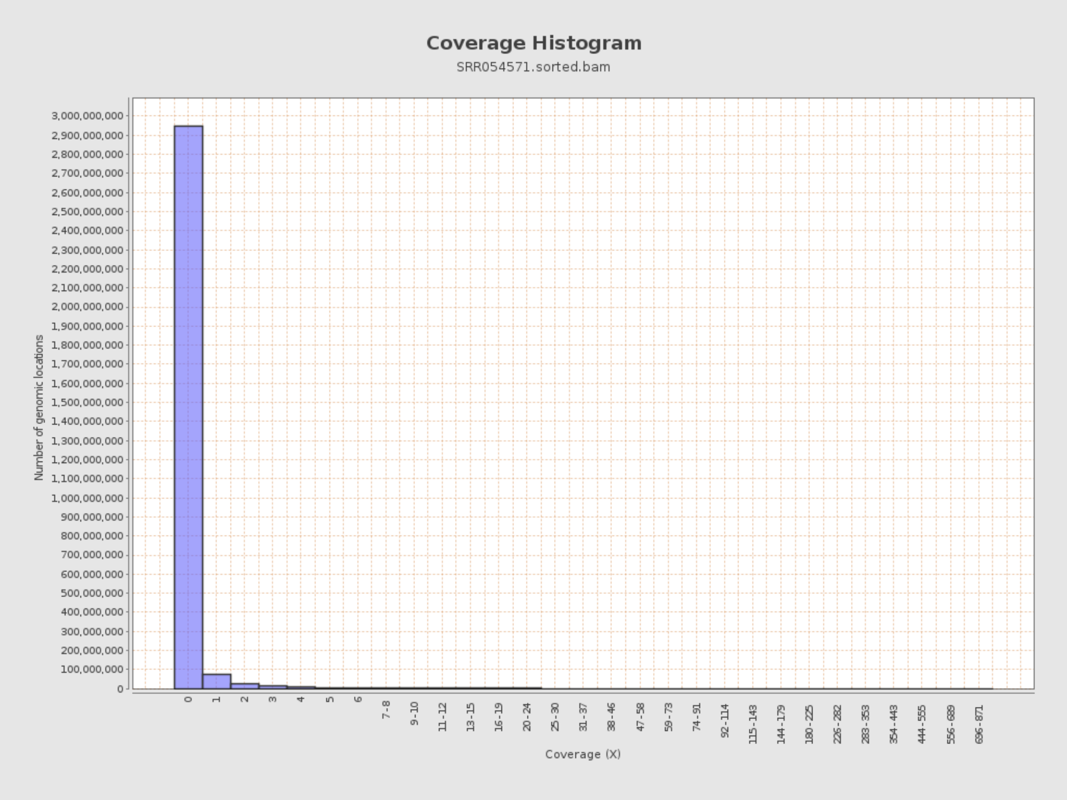
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 41186888 | 0.1652 | 1.5716 |
| chr2 | 243199373 | 54196897 | 0.2228 | 1.79 |
| chr3 | 198022430 | 32734183 | 0.1653 | 1.4147 |
| chr4 | 191154276 | 24632838 | 0.1289 | 1.2473 |
| chr5 | 180915260 | 25693170 | 0.142 | 1.3021 |
| chr6 | 171115067 | 31712416 | 0.1853 | 1.6199 |
| chr7 | 159138663 | 25971418 | 0.1632 | 1.5551 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 30484788 | 0.2083 | 1.7381 |
| chr9 | 141213431 | 26042029 | 0.1844 | 1.5622 |
| chr10 | 135534747 | 17375645 | 0.1282 | 1.2835 |
| chr11 | 135006516 | 23959223 | 0.1775 | 1.5448 |
| chr12 | 133851895 | 27156784 | 0.2029 | 1.6231 |
| chr13 | 115169878 | 12522761 | 0.1087 | 1.1161 |
| chr14 | 107349540 | 9820226 | 0.0915 | 1.1256 |
| chr15 | 102531392 | 11838230 | 0.1155 | 1.1311 |
| chr16 | 90354753 | 11949237 | 0.1322 | 1.3184 |
| chr17 | 81195210 | 11559536 | 0.1424 | 1.2724 |
| chr18 | 78077248 | 15852768 | 0.203 | 1.7079 |
| chr19 | 59128983 | 10688136 | 0.1808 | 1.5824 |
| chr20 | 63025520 | 10612507 | 0.1684 | 1.4955 |
| chr21 | 48129895 | 4855583 | 0.1009 | 1.0894 |
| chr22 | 51304566 | 6244737 | 0.1217 | 1.1778 |
| chrMT | 16571 | 34534 | 2.084 | 5.6857 |
| chrX | 155270560 | 33023787 | 0.2127 | 1.7064 |
| chrY | 59373566 | 1124731 | 0.0189 | 0.4066 |

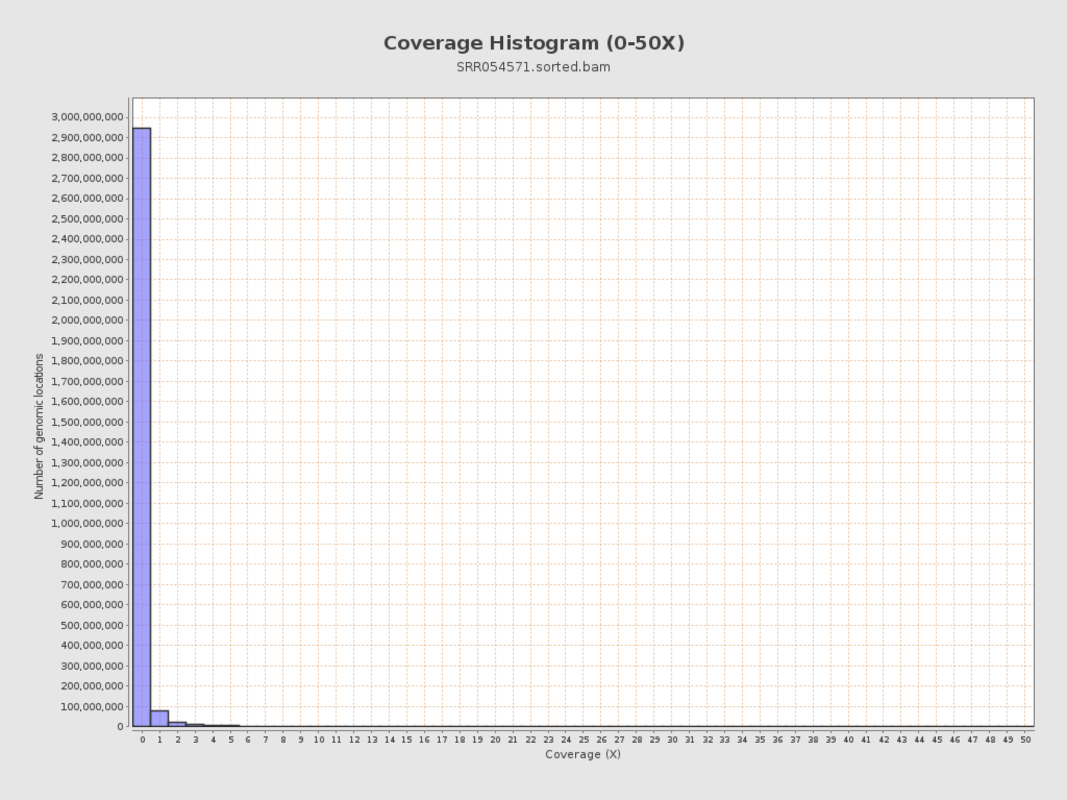
# 3. Results : Coverage across reference



# 4. Results : Coverage Histogram



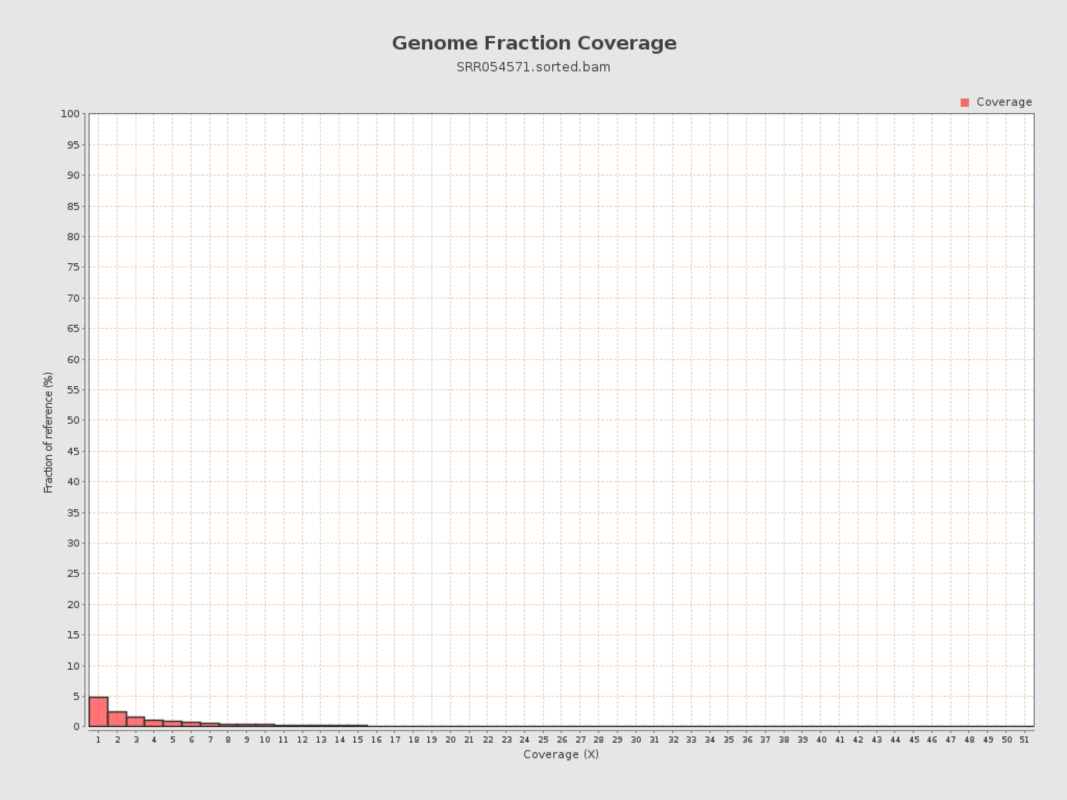
# 5. Results : Coverage Histogram (0-50X)



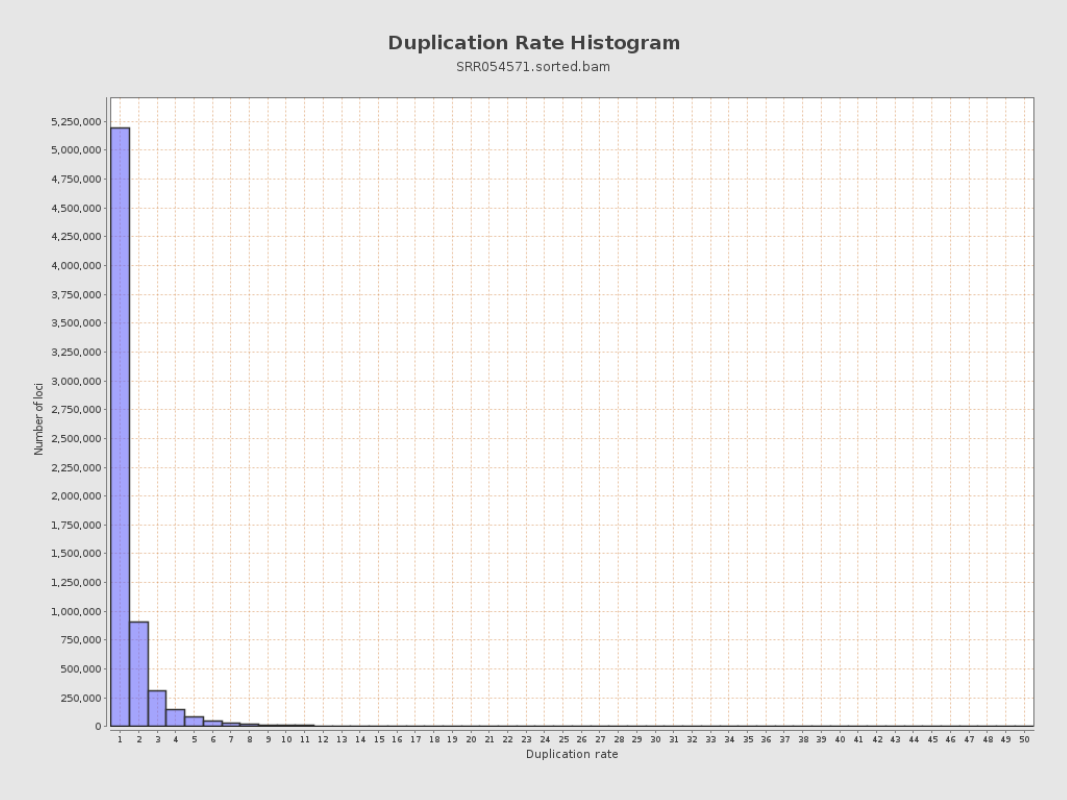
Coverage Histogram (0-50X)

SRR054571.sorted.bam

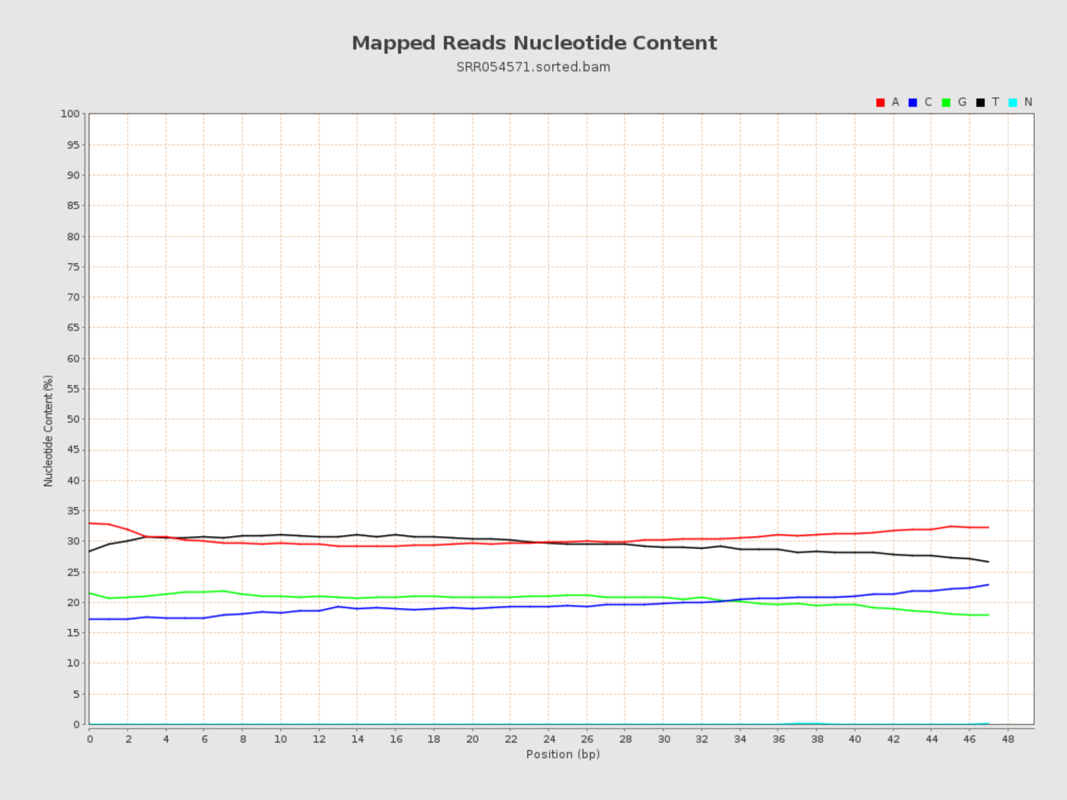
# 6. Results : Genome Fraction Coverage



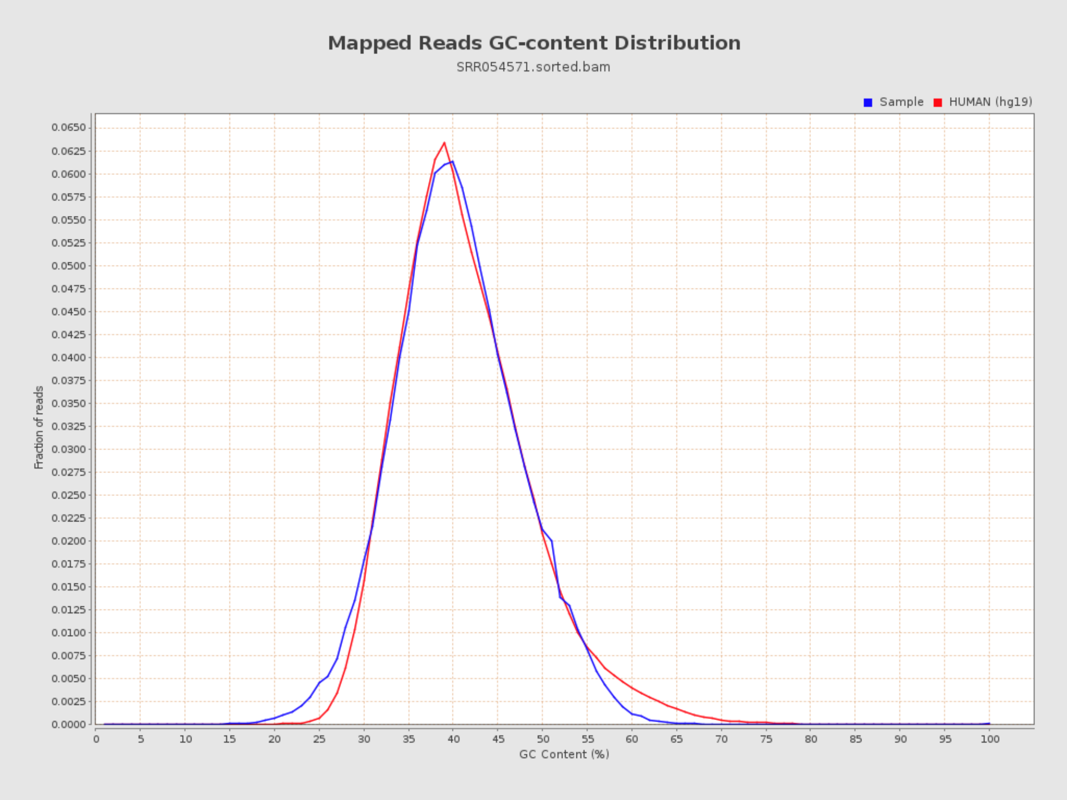
# 7. Results : Duplication Rate Histogram



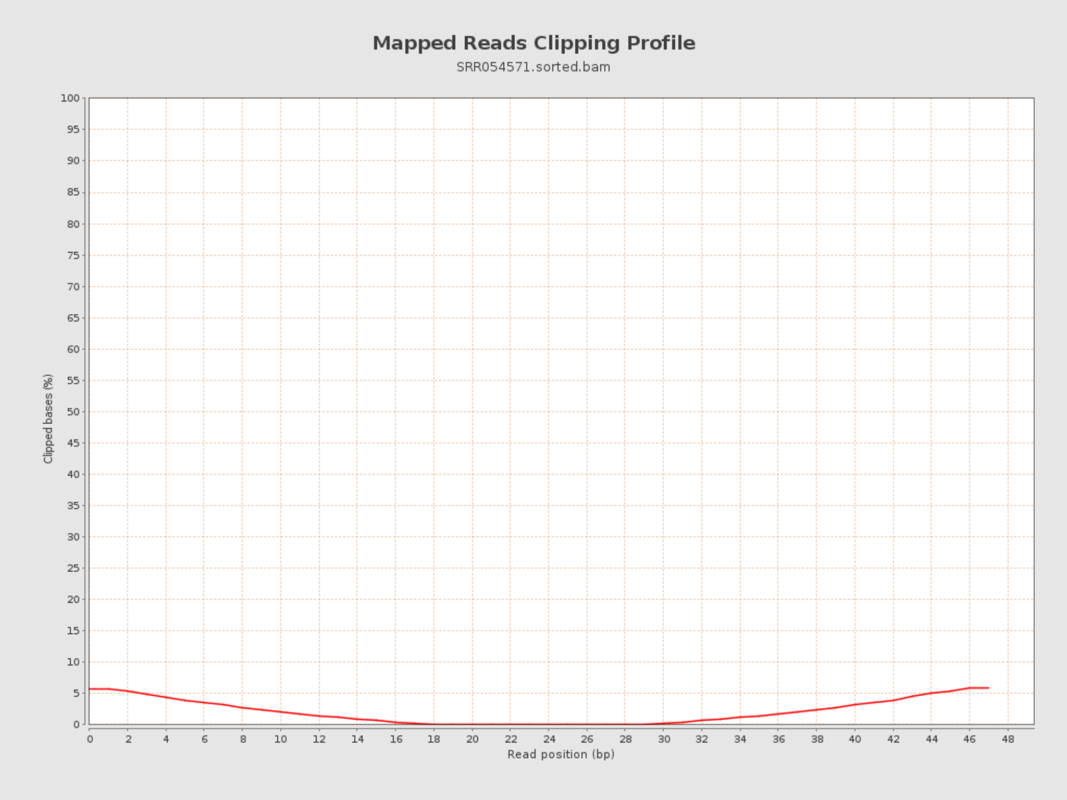
# 8. Results : Mapped Reads Nucleotide Content



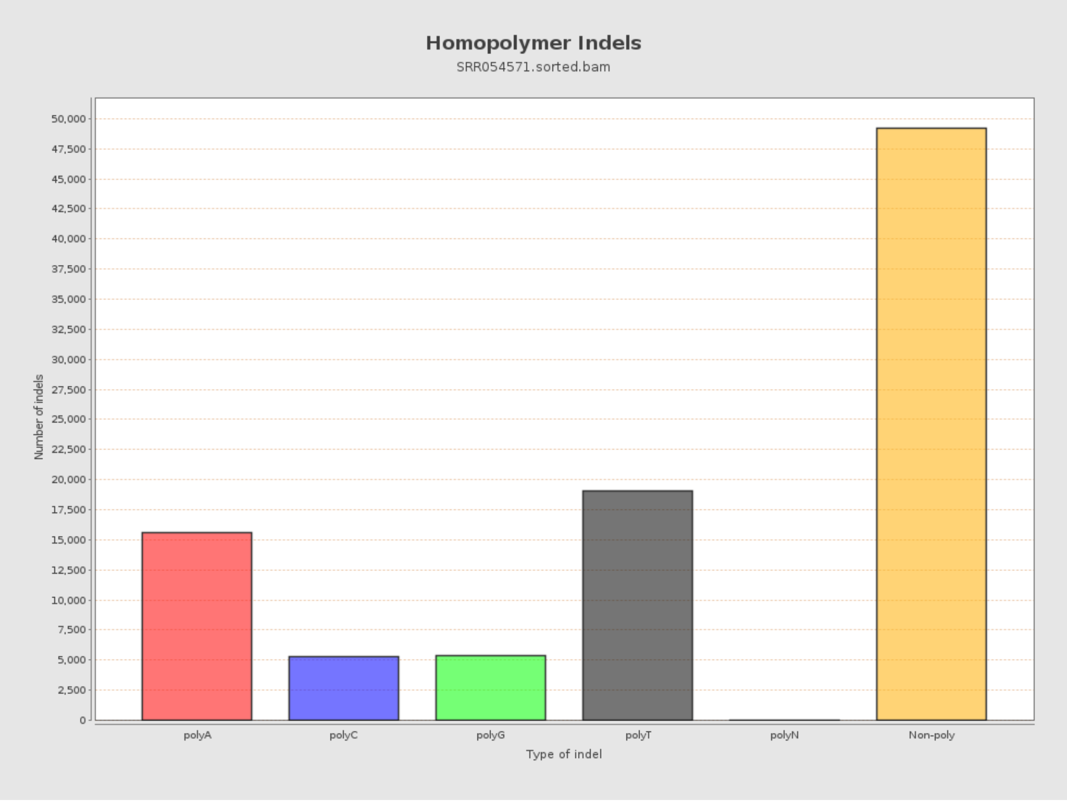
# 9. Results : Mapped Reads GC-content Distribution



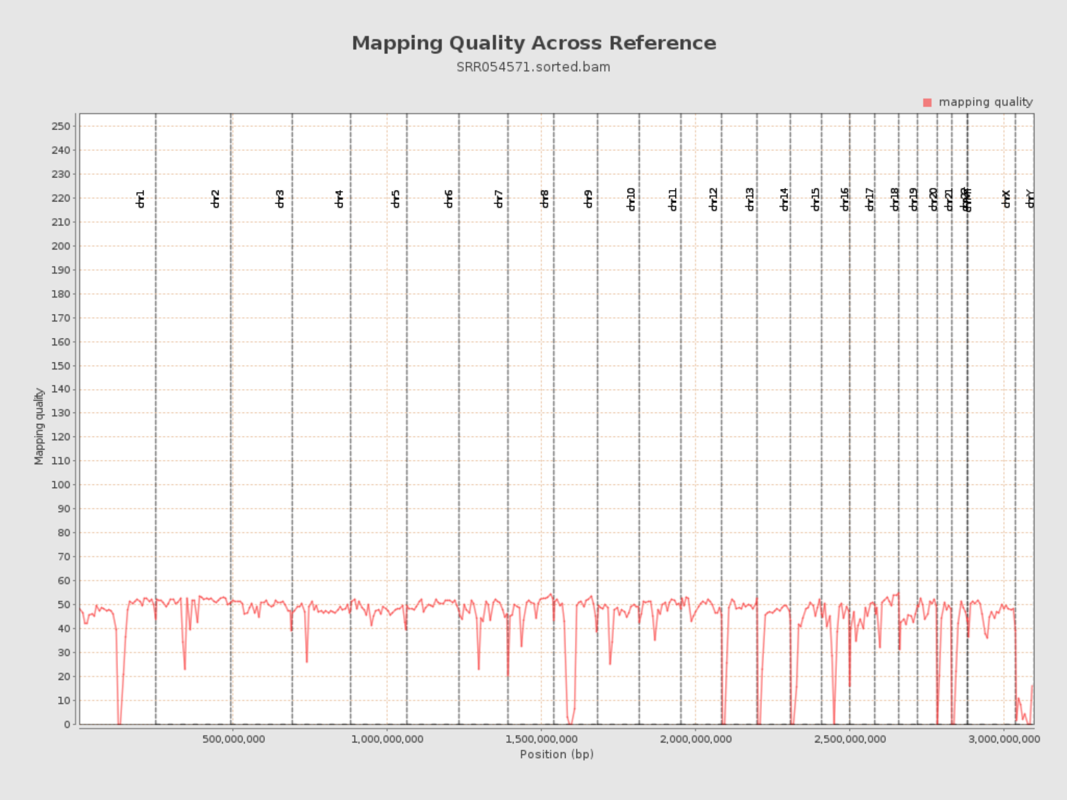
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram