# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/10 17:13:07*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514752.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_SRR5514752 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514752.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Apr 10 17:13:07 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR5514752.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 5,948,776 |
| Mapped reads | 3,732,946 / 62.75% |
| Unmapped reads | 2,215,830 / 37.25% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 504,936 / 8.49% |
| Read min/max/mean length | 30 / 100 / 102.4 |
| Duplicated reads (estimated) | 902,140 / 15.17% |
| Duplication rate | 18.14% |
| Clipped reads | 1,659,934 / 27.9% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 112,866,662 / 31.46% |
| Number/percentage of C's | 66,525,430 / 18.54% |
| Number/percentage of T's | 110,544,832 / 30.82% |
| Number/percentage of G's | 68,774,293 / 19.17% |
| Number/percentage of N's | 25,111 / 0.01% |
| GC Percentage | 37.72% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.1159 |
| | |

| | |
|---|---|
| Standard Deviation | 1.639 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.7 |

## 2.5. Mismatches and indels

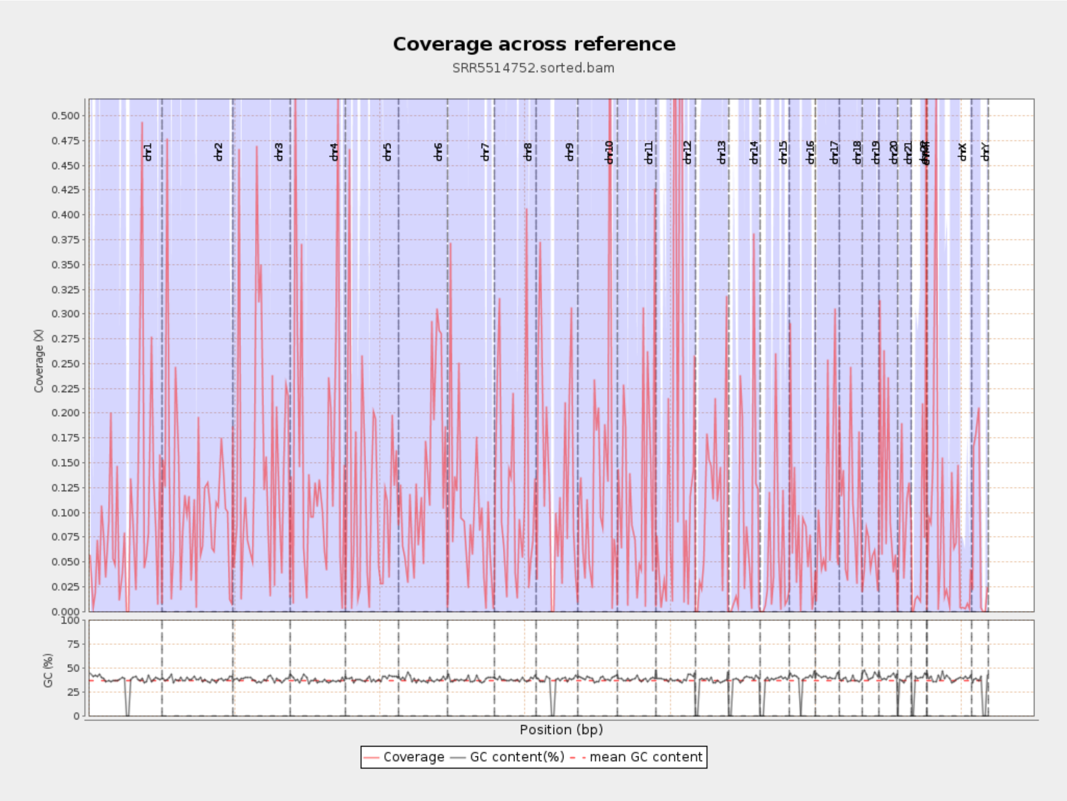
| | |
|---|---|
| General error rate | 0.51% |
| Mismatches | 1,660,191 |
| Insertions | 125,181 |
| Mapped reads with at least one insertion | 3.28% |
| Deletions | 56,189 |
| Mapped reads with at least one deletion | 1.47% |
| Homopolymer indels | 60.9% |

## 2.6. Chromosome stats

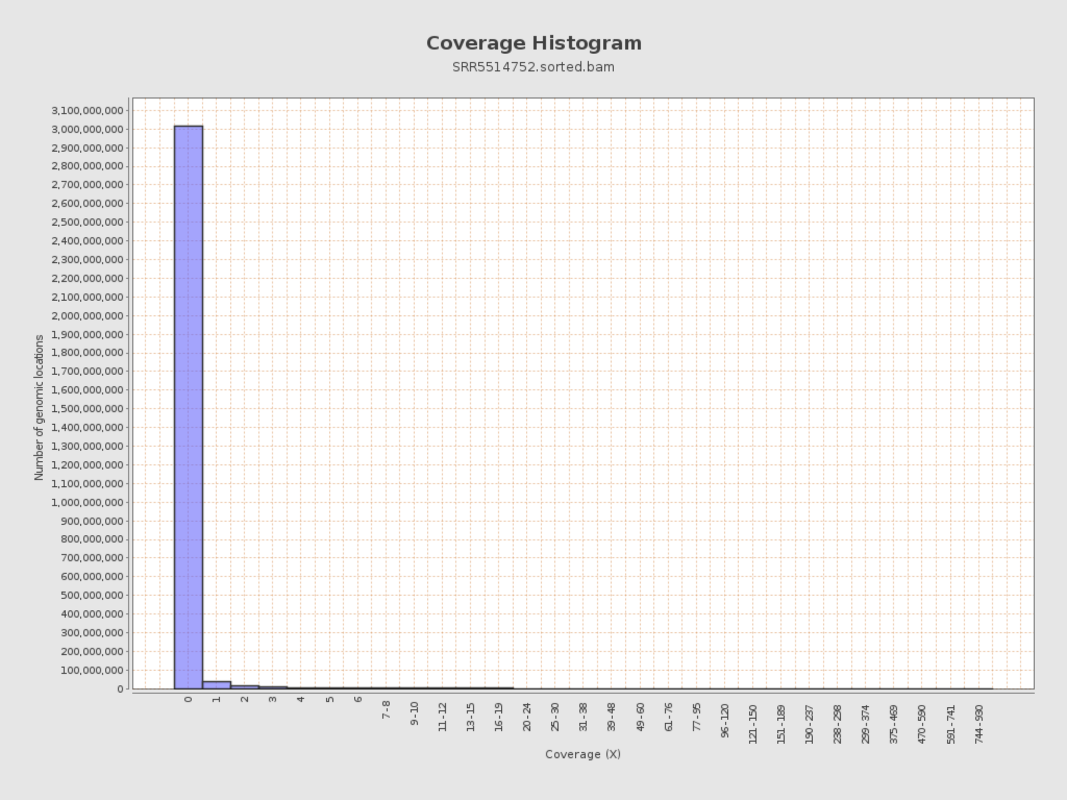
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 23785425 | 0.0954 | 1.3241 |
| chr2 | 243199373 | 27008943 | 0.1111 | 1.3166 |
| chr3 | 198022430 | 30426351 | 0.1537 | 1.6697 |
| chr4 | 191154276 | 30681461 | 0.1605 | 1.7663 |
| chr5 | 180915260 | 20654086 | 0.1142 | 1.5243 |
| chr6 | 171115067 | 23101813 | 0.135 | 1.4995 |
| chr7 | 159138663 | 15959103 | 0.1003 | 1.3587 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 18149848 | 0.124 | 1.449 |
| chr9 | 141213431 | 19581164 | 0.1387 | 1.4821 |
| chr10 | 135534747 | 18582787 | 0.1371 | 1.6405 |
| chr11 | 135006516 | 17273834 | 0.1279 | 1.3076 |
| chr12 | 133851895 | 22258029 | 0.1663 | 1.73 |
| chr13 | 115169878 | 12828117 | 0.1114 | 1.2554 |
| chr14 | 107349540 | 9687023 | 0.0902 | 1.2496 |
| chr15 | 102531392 | 5080916 | 0.0496 | 0.8143 |
| chr16 | 90354753 | 6488720 | 0.0718 | 1.1042 |
| chr17 | 81195210 | 8055443 | 0.0992 | 1.0905 |
| chr18 | 78077248 | 8619707 | 0.1104 | 1.4013 |
| chr19 | 59128983 | 3157466 | 0.0534 | 1.0332 |
| chr20 | 63025520 | 8163341 | 0.1295 | 1.3961 |
| chr21 | 48129895 | 4743700 | 0.0986 | 1.1785 |
| chr22 | 51304566 | 3123595 | 0.0609 | 0.8627 |
| chrMT | 16571 | 4733543 | 285.6522 | 176.6018 |
| chrX | 155270560 | 12132184 | 0.0781 | 1.9282 |
| chrY | 59373566 | 4582126 | 0.0772 | 1.1663 |

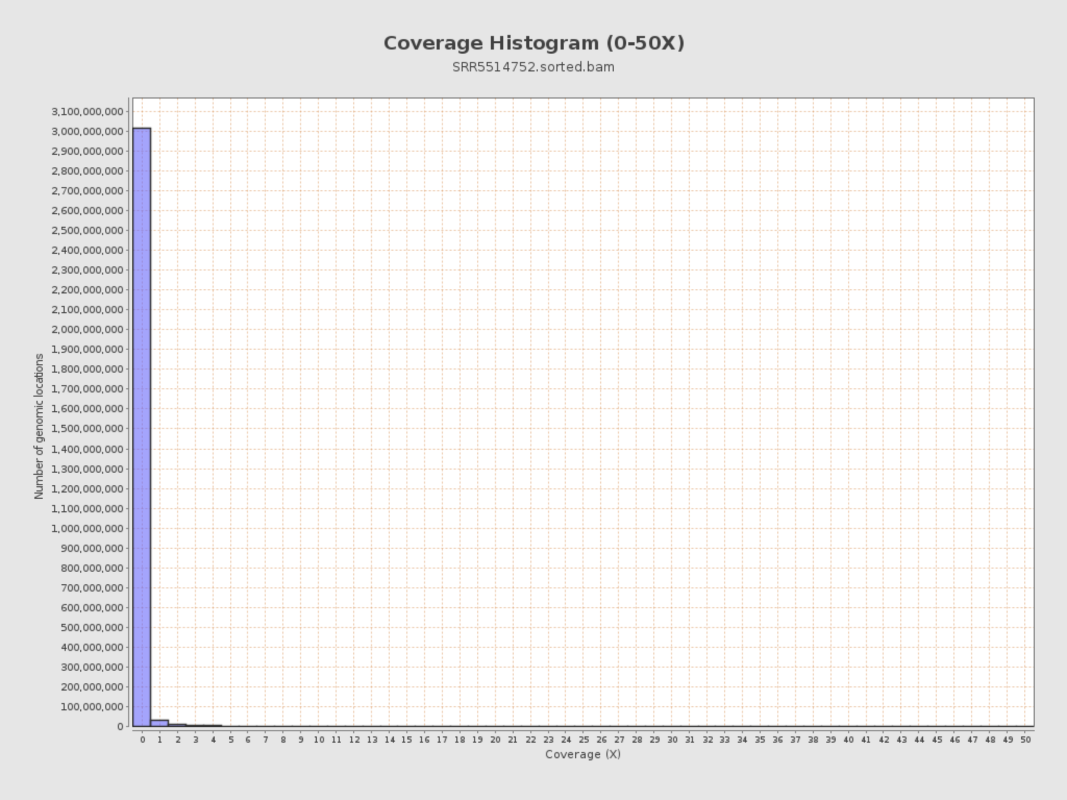
# 3. Results : Coverage across reference



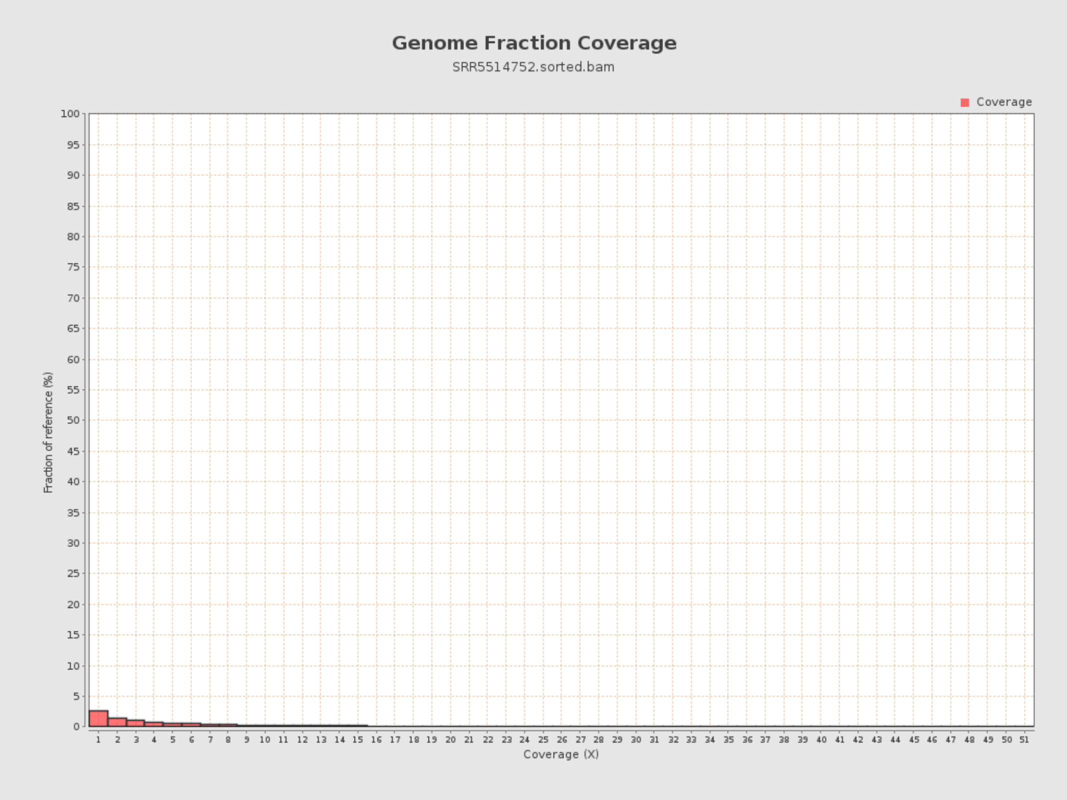
# 4. Results : Coverage Histogram



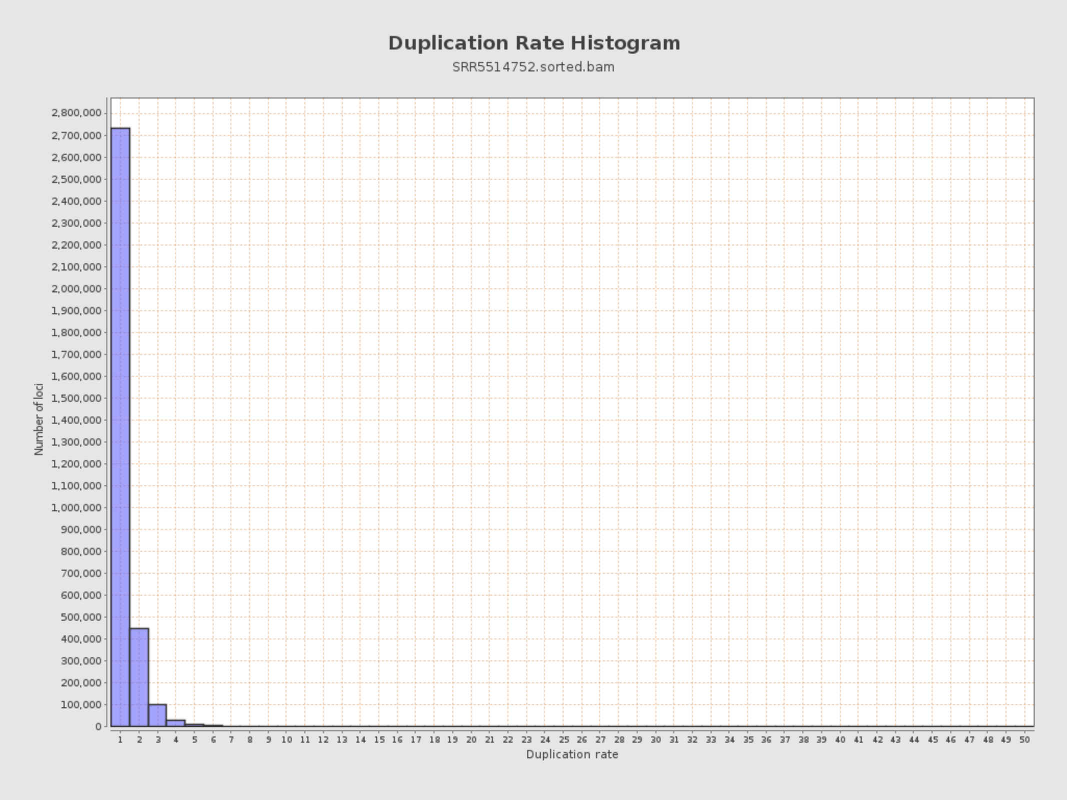
# 5. Results : Coverage Histogram (0-50X)



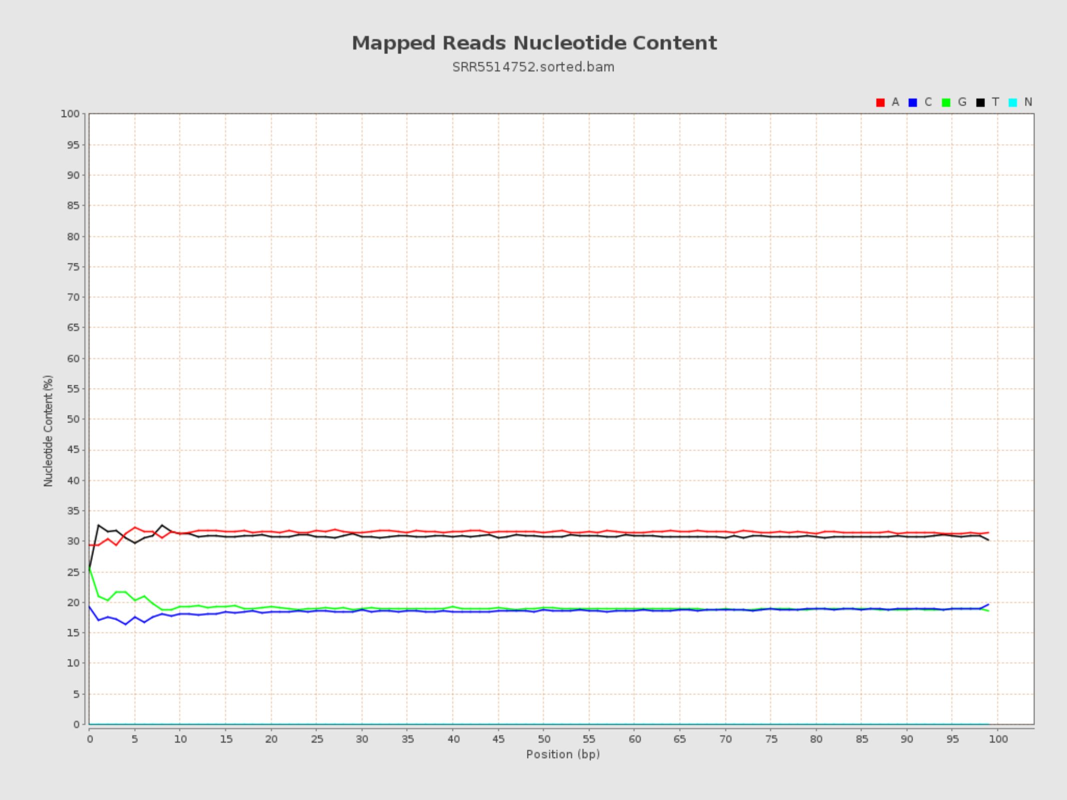
# 6. Results : Genome Fraction Coverage



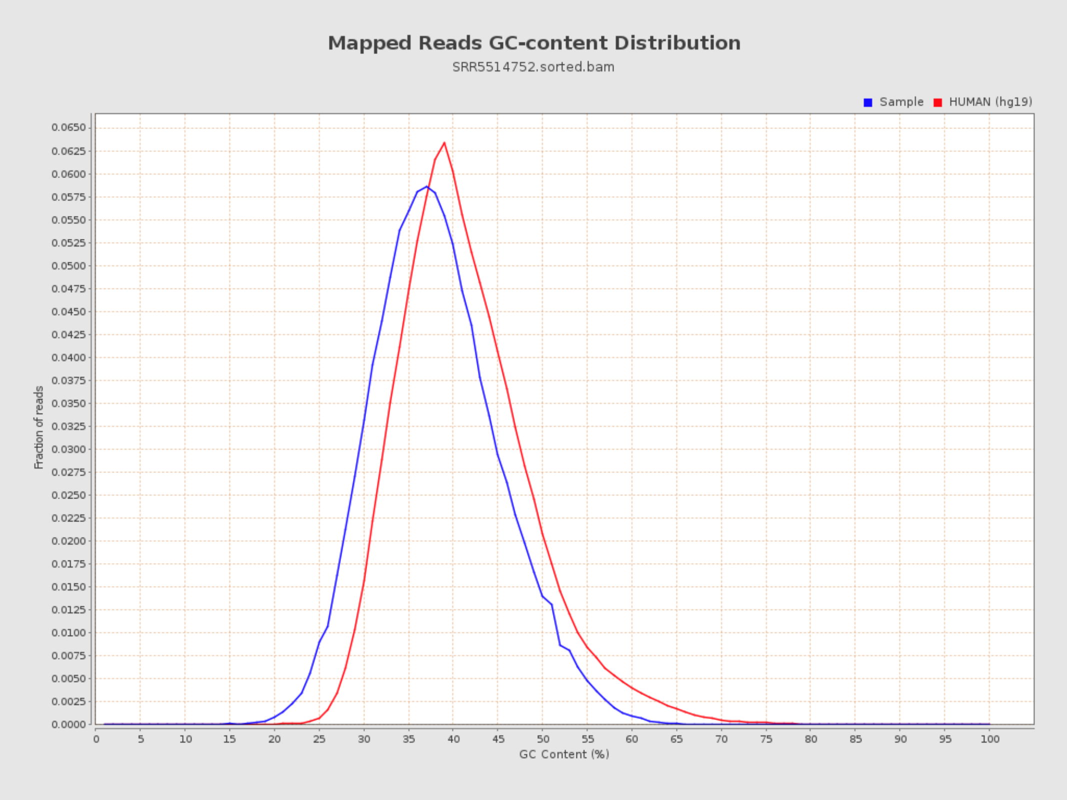
# 7. Results : Duplication Rate Histogram



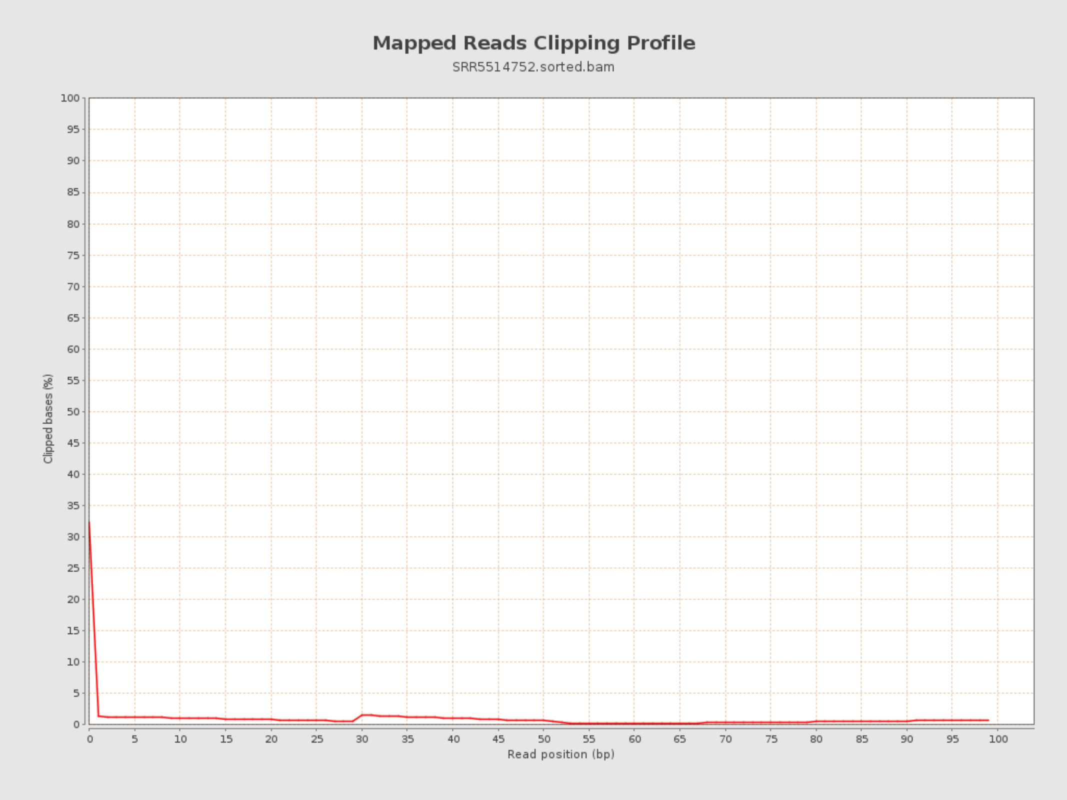
# 8. Results : Mapped Reads Nucleotide Content



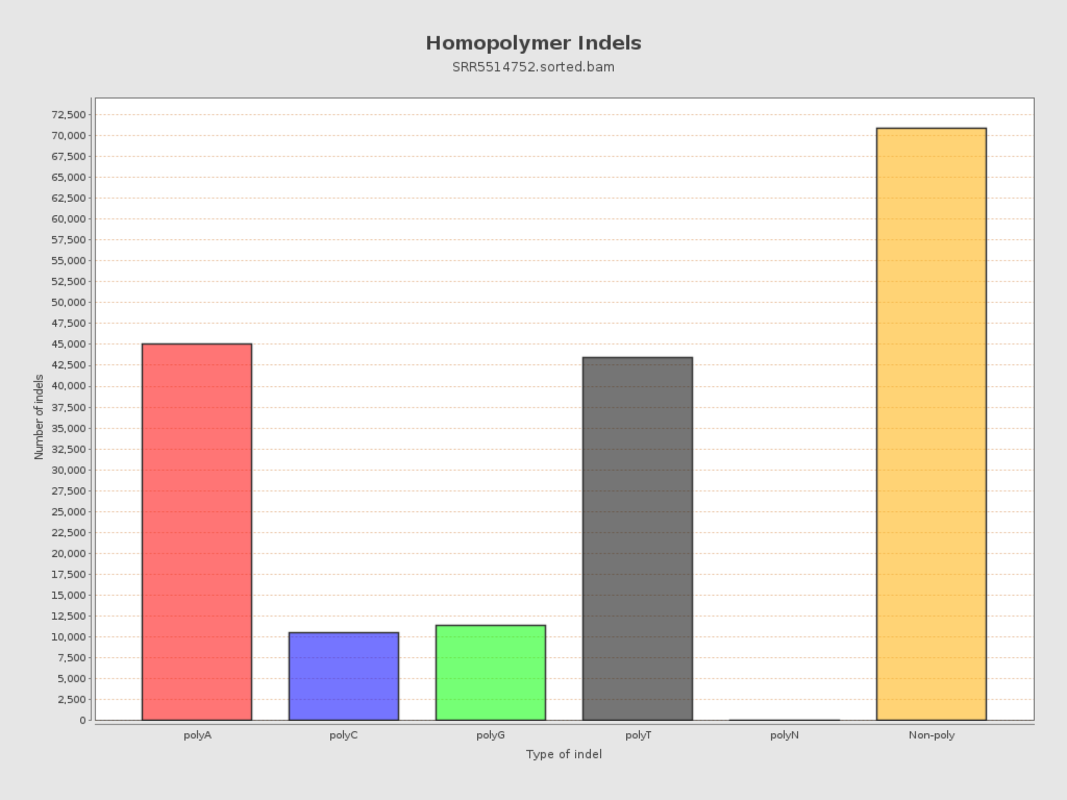
# 9. Results : Mapped Reads GC-content Distribution



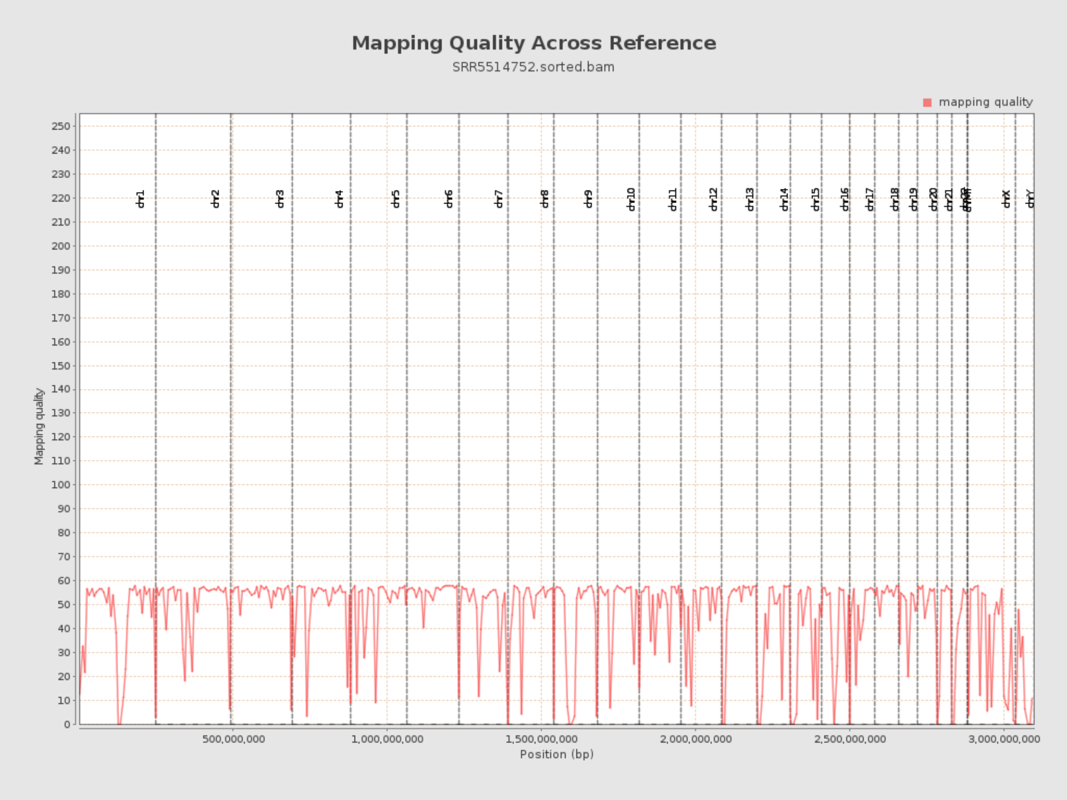
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram