# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2022/04/11 00:05:10*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514706.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_SRR5514706 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514706.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Mon Apr 11 00:05:09 CST 2022 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR5514706.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 74,101,938 |
| Mapped reads | 72,721,431 / 98.14% |
| Unmapped reads | 1,380,507 / 1.86% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 5,282,425 / 7.13% |
| Read min/max/mean length | 30 / 100 / 100.65 |
| Duplicated reads (estimated) | 46,338,819 / 62.53% |
| Duplication rate | 37.95% |
| Clipped reads | 26,322,539 / 35.52% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 1,944,369,446 / 29.46% |
| Number/percentage of C's | 1,360,924,206 / 20.62% |
| Number/percentage of T's | 1,910,074,041 / 28.94% |
| Number/percentage of G's | 1,377,135,888 / 20.87% |
| Number/percentage of N's | 7,217,460 / 0.11% |
| GC Percentage | 41.49% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 2.1343 |
| | |

| | |
|---|---|
| Standard Deviation | 381.6511 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 47.53 |

## 2.5. Mismatches and indels

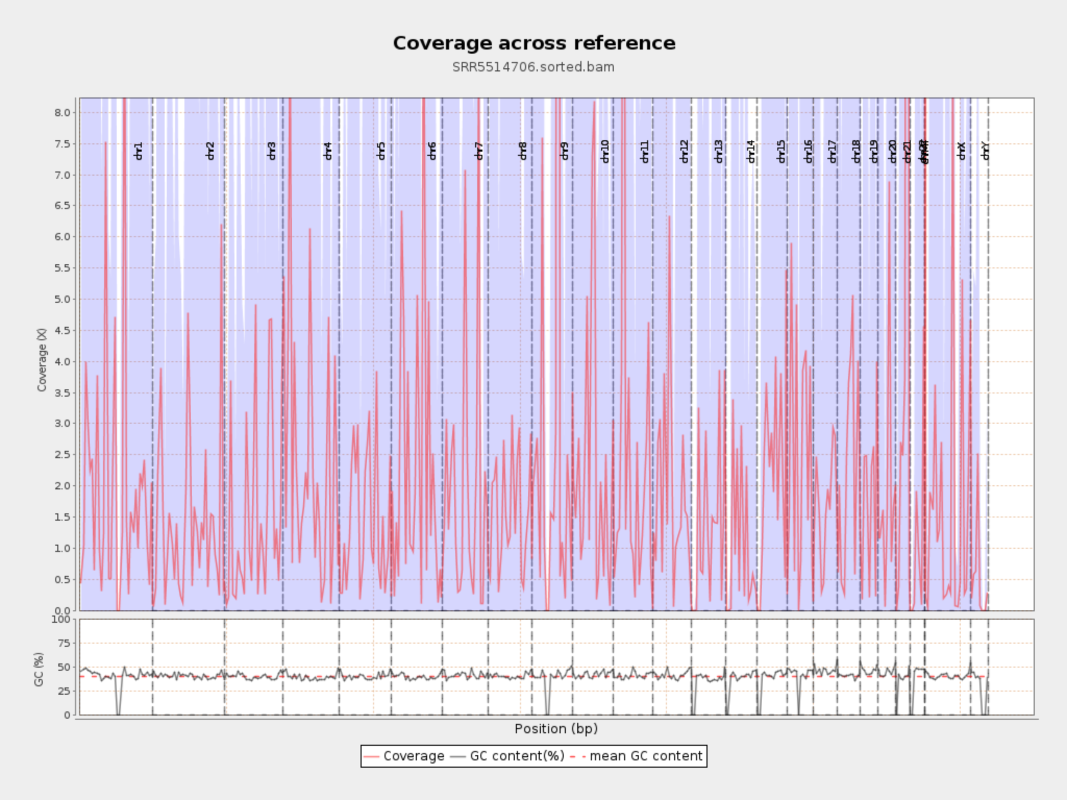
| | |
|---|---|
| General error rate | 0.81% |
| Mismatches | 48,021,841 |
| Insertions | 3,028,581 |
| Mapped reads with at least one insertion | 3.96% |
| Deletions | 3,238,048 |
| Mapped reads with at least one deletion | 4.16% |
| Homopolymer indels | 33.48% |

## 2.6. Chromosome stats

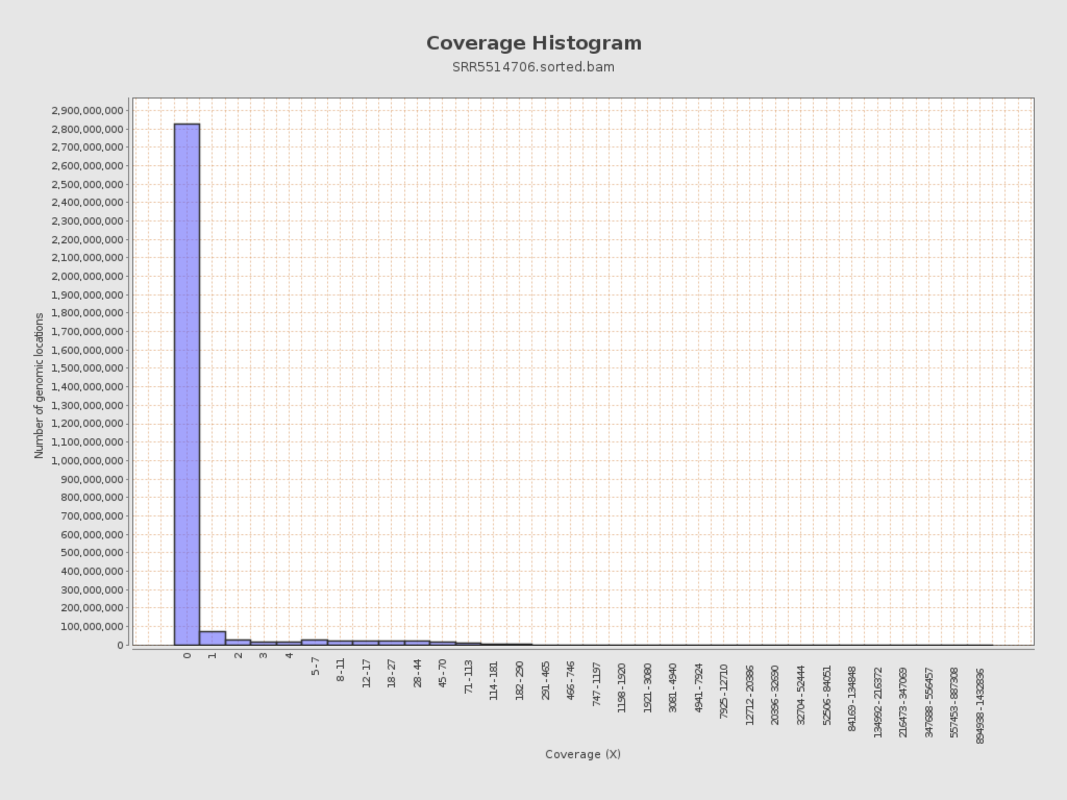
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 509592222 | 2.0445 | 166.4981 |
| chr2 | 243199373 | 346950581 | 1.4266 | 15.61 |
| chr3 | 198022430 | 292662928 | 1.4779 | 12.4448 |
| chr4 | 191154276 | 470885466 | 2.4634 | 20.9226 |
| chr5 | 180915260 | 268603902 | 1.4847 | 21.1863 |
| chr6 | 171115067 | 412151185 | 2.4086 | 89.1056 |
| chr7 | 159138663 | 316129278 | 1.9865 | 18.7871 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 238343676 | 1.6284 | 14.6111 |
| chr9 | 141213431 | 812694566 | 5.7551 | 1,214.4748 |
| chr10 | 135534747 | 312828986 | 2.3081 | 64.6598 |
| chr11 | 135006516 | 377891528 | 2.7991 | 24.1708 |
| chr12 | 133851895 | 259928505 | 1.9419 | 17.0456 |
| chr13 | 115169878 | 151486843 | 1.3153 | 15.1434 |
| chr14 | 107349540 | 109428693 | 1.0194 | 10.5128 |
| chr15 | 102531392 | 218235334 | 2.1285 | 68.4285 |
| chr16 | 90354753 | 217336615 | 2.4054 | 29.9659 |
| chr17 | 81195210 | 135470383 | 1.6685 | 14.8881 |
| chr18 | 78077248 | 191751636 | 2.4559 | 19.6054 |
| chr19 | 59128983 | 93690470 | 1.5845 | 13.6752 |
| chr20 | 63025520 | 119410882 | 1.8946 | 32.9537 |
| chr21 | 48129895 | 399838307 | 8.3075 | 2,198.14 |
| chr22 | 51304566 | 60185388 | 1.1731 | 17.2116 |
| chrMT | 16571 | 3190717 | 192.5482 | 122.7818 |
| chrX | 155270560 | 255579533 | 1.646 | 13.9035 |
| chrY | 59373566 | 32782081 | 0.5521 | 4.1419 |

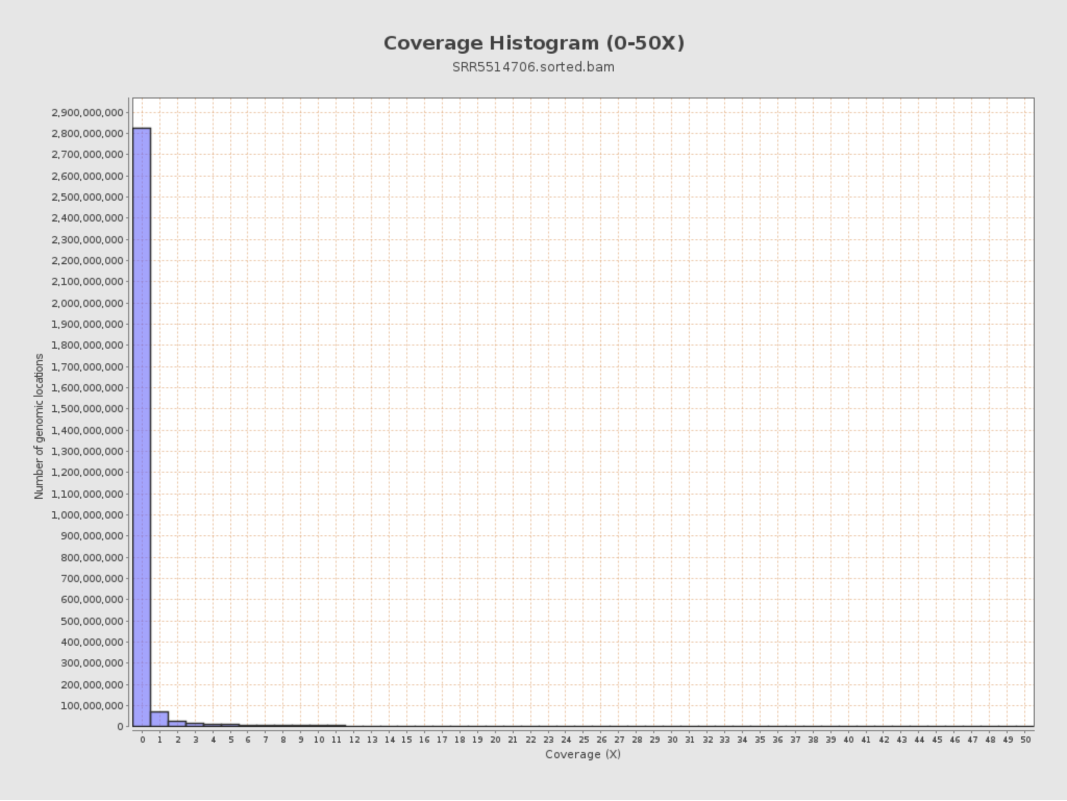
# 3. Results : Coverage across reference



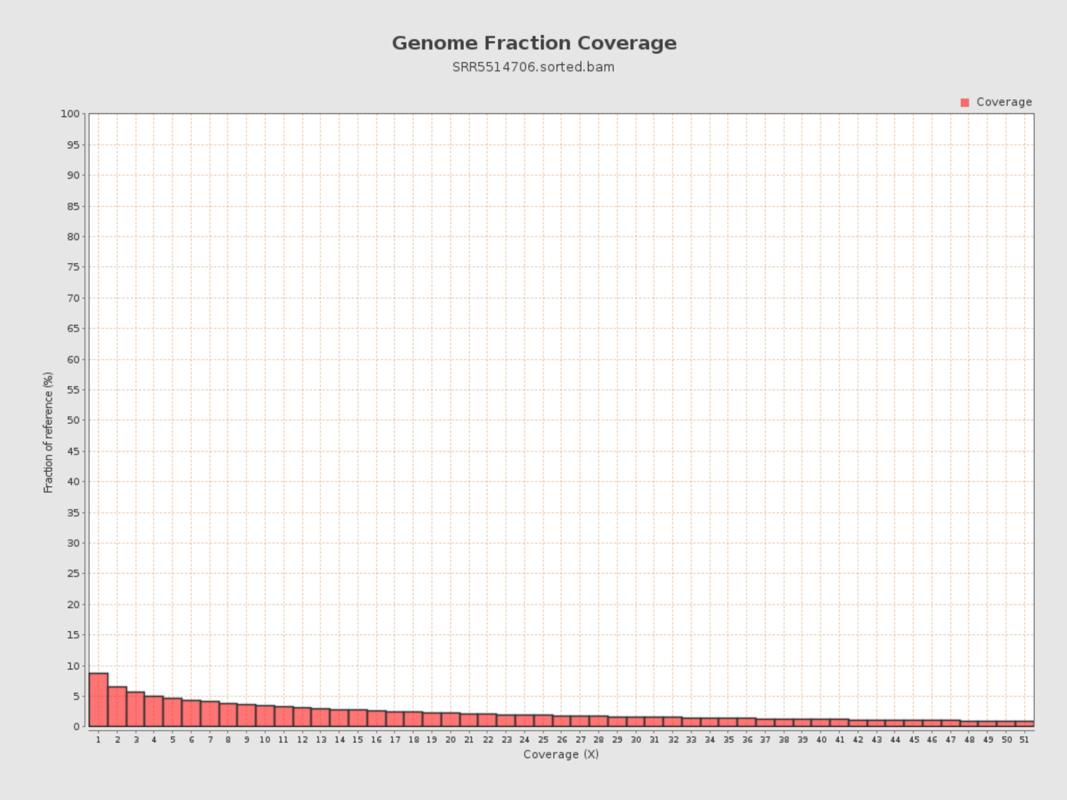
# 4. Results : Coverage Histogram



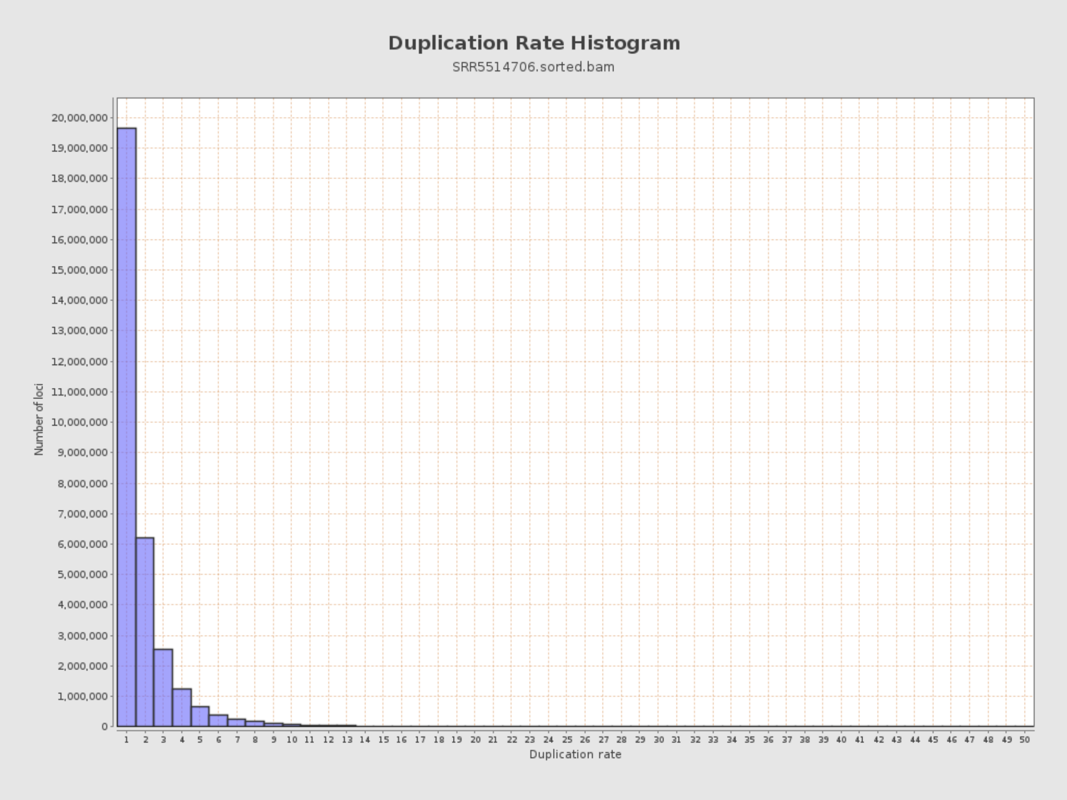
# 5. Results : Coverage Histogram (0-50X)



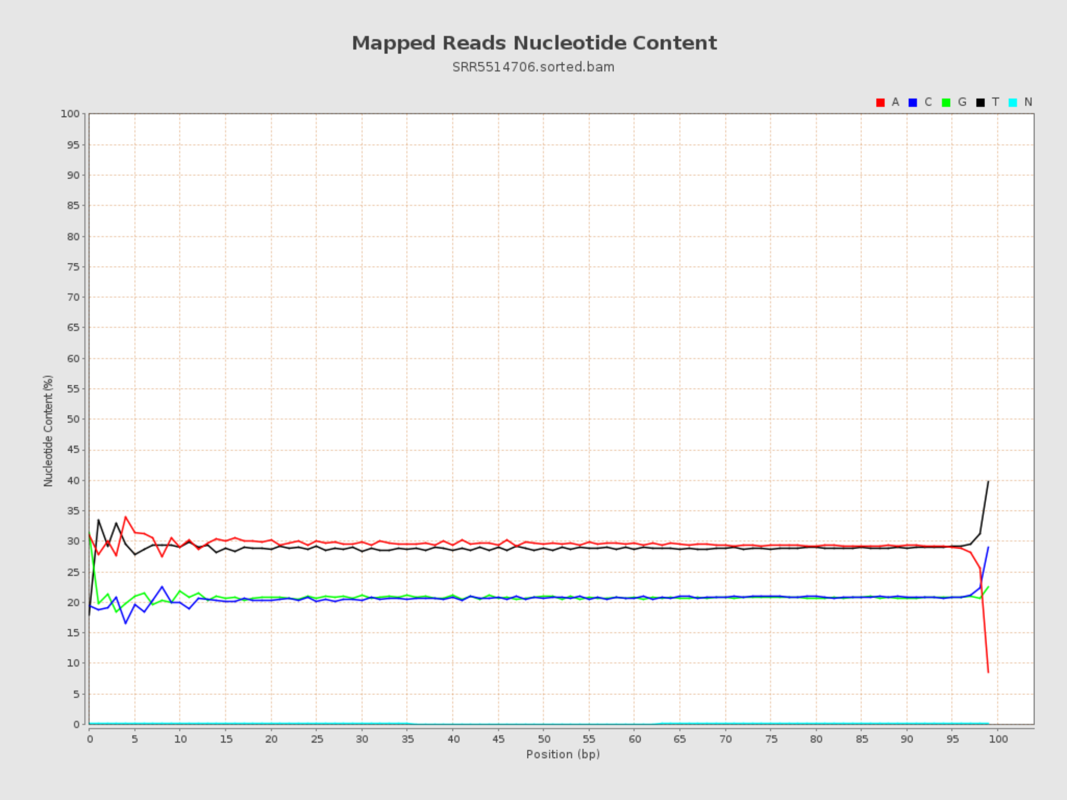
# 6. Results : Genome Fraction Coverage



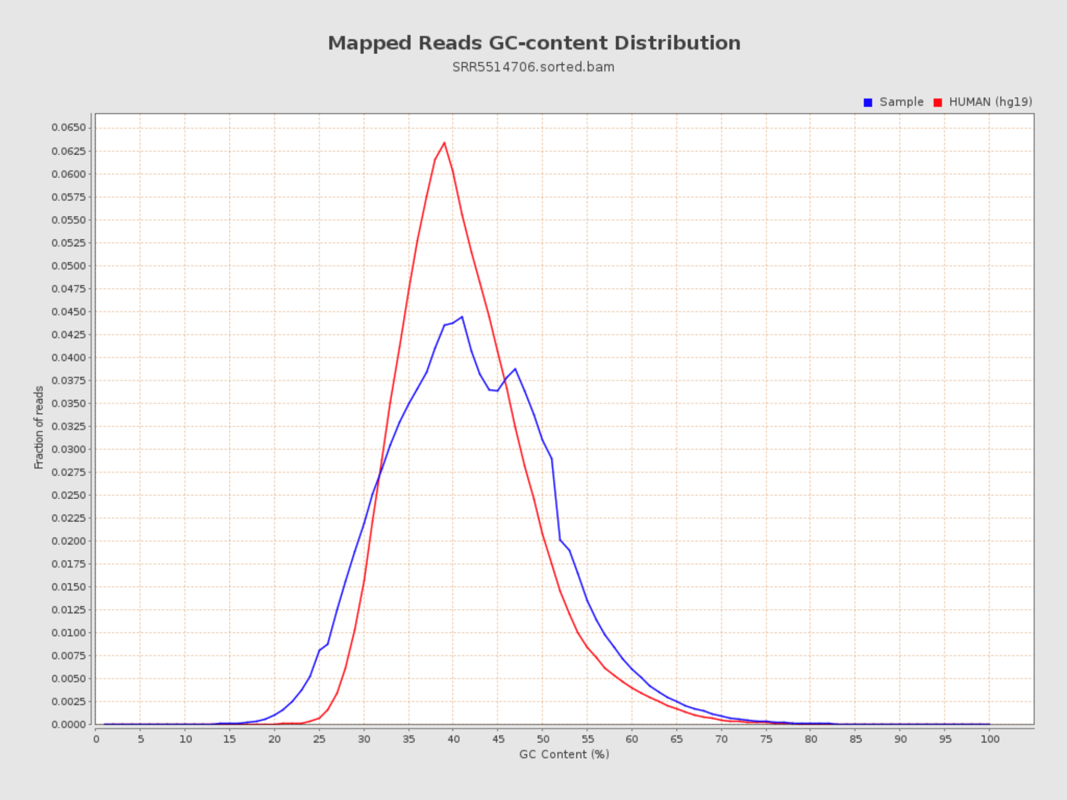
# 7. Results : Duplication Rate Histogram



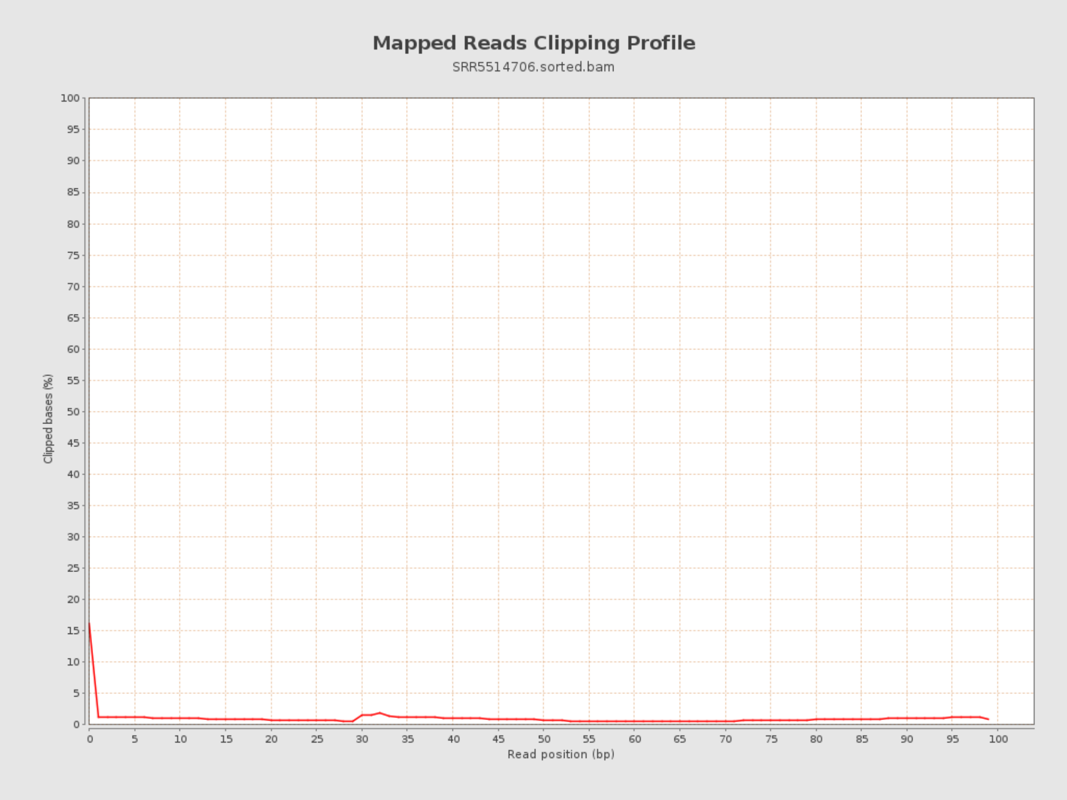
# 8. Results : Mapped Reads Nucleotide Content



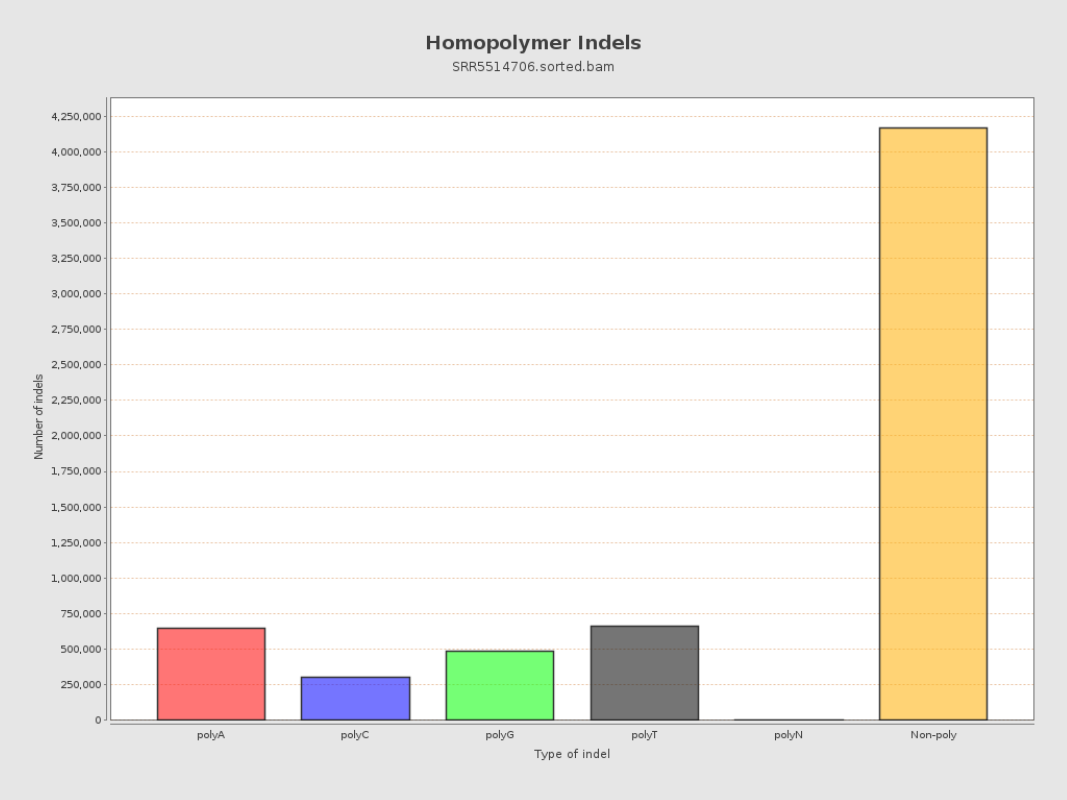
# 9. Results : Mapped Reads GC-content Distribution



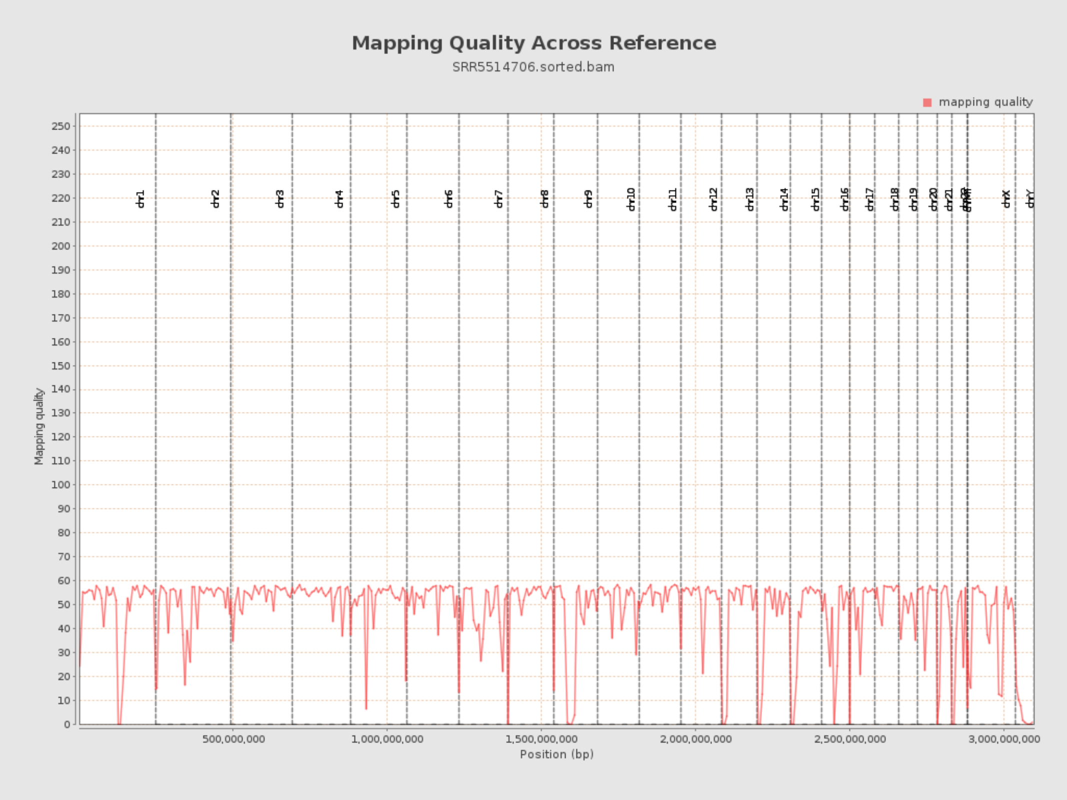
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram