# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 23:05:33*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525206.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_SRR10525206 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525206.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 23:05:26 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10525206.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,339,911 |
| Mapped reads | 3,058,031 / 91.56% |
| Unmapped reads | 281,880 / 8.44% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 9,476 / 0.28% |
| Read min/max/mean length | 30 / 76 / 76.1 |
| Duplicated reads (estimated) | 155,056 / 4.64% |
| Duplication rate | 3.68% |
| Clipped reads | 3,058,017 / 91.56% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 43,673,169 / 24.67% |
| Number/percentage of C's | 35,408,929 / 20% |
| Number/percentage of T's | 57,263,762 / 32.34% |
| Number/percentage of G's | 40,698,769 / 22.99% |
| Number/percentage of N's | 4,270 / 0% |
| GC Percentage | 42.99% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0572 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4907 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.53 |

## 2.5. Mismatches and indels

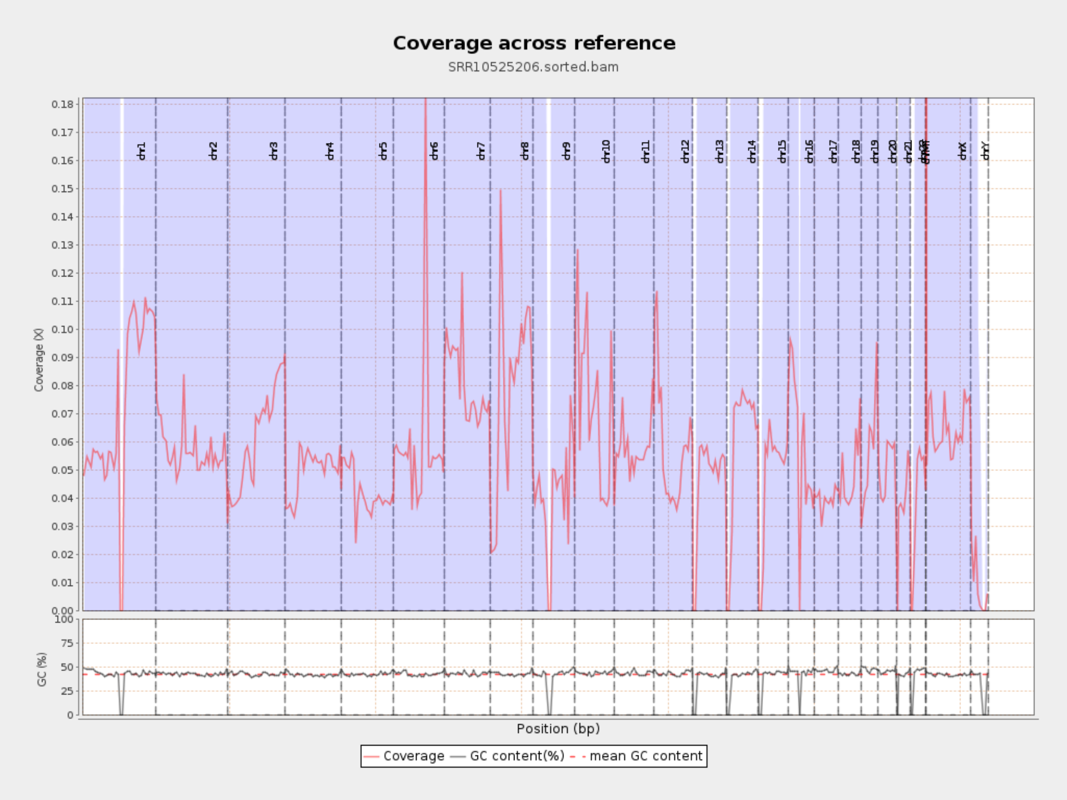
| | |
|---|---|
| General error rate | 0.53% |
| Mismatches | 916,147 |
| Insertions | 11,365 |
| Mapped reads with at least one insertion | 0.37% |
| Deletions | 36,640 |
| Mapped reads with at least one deletion | 1.19% |
| Homopolymer indels | 43.26% |

## 2.6. Chromosome stats

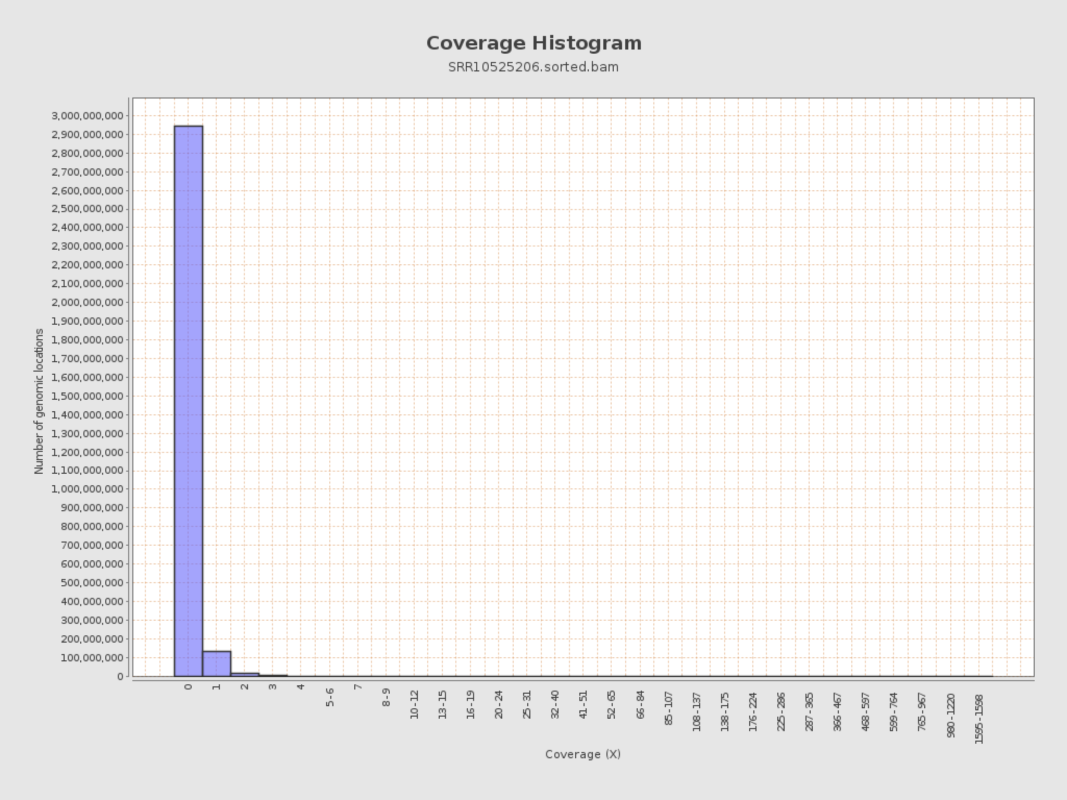
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 18001734 | 0.0722 | 0.8854 |
| chr2 | 243199373 | 13915943 | 0.0572 | 0.7066 |
| chr3 | 198022430 | 12082456 | 0.061 | 0.2903 |
| chr4 | 191154276 | 9539286 | 0.0499 | 0.2764 |
| chr5 | 180915260 | 7581673 | 0.0419 | 0.2356 |
| chr6 | 171115067 | 10278969 | 0.0601 | 0.338 |
| chr7 | 159138663 | 12914141 | 0.0812 | 0.8545 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 11821505 | 0.0808 | 0.4684 |
| chr9 | 141213431 | 5720896 | 0.0405 | 0.3373 |
| chr10 | 135534747 | 9836018 | 0.0726 | 0.5171 |
| chr11 | 135006516 | 7745082 | 0.0574 | 0.3865 |
| chr12 | 133851895 | 7817942 | 0.0584 | 0.2823 |
| chr13 | 115169878 | 5353930 | 0.0465 | 0.2553 |
| chr14 | 107349540 | 6498416 | 0.0605 | 0.297 |
| chr15 | 102531392 | 4714946 | 0.046 | 0.2656 |
| chr16 | 90354753 | 5303092 | 0.0587 | 0.3283 |
| chr17 | 81195210 | 3196255 | 0.0394 | 0.2433 |
| chr18 | 78077248 | 3738228 | 0.0479 | 0.7341 |
| chr19 | 59128983 | 3361484 | 0.0569 | 0.6214 |
| chr20 | 63025520 | 3176351 | 0.0504 | 0.2658 |
| chr21 | 48129895 | 1857401 | 0.0386 | 0.2484 |
| chr22 | 51304566 | 1935010 | 0.0377 | 0.2221 |
| chrMT | 16571 | 161520 | 9.7471 | 5.7357 |
| chrX | 155270560 | 10039294 | 0.0647 | 0.3346 |
| chrY | 59373566 | 515326 | 0.0087 | 0.2107 |

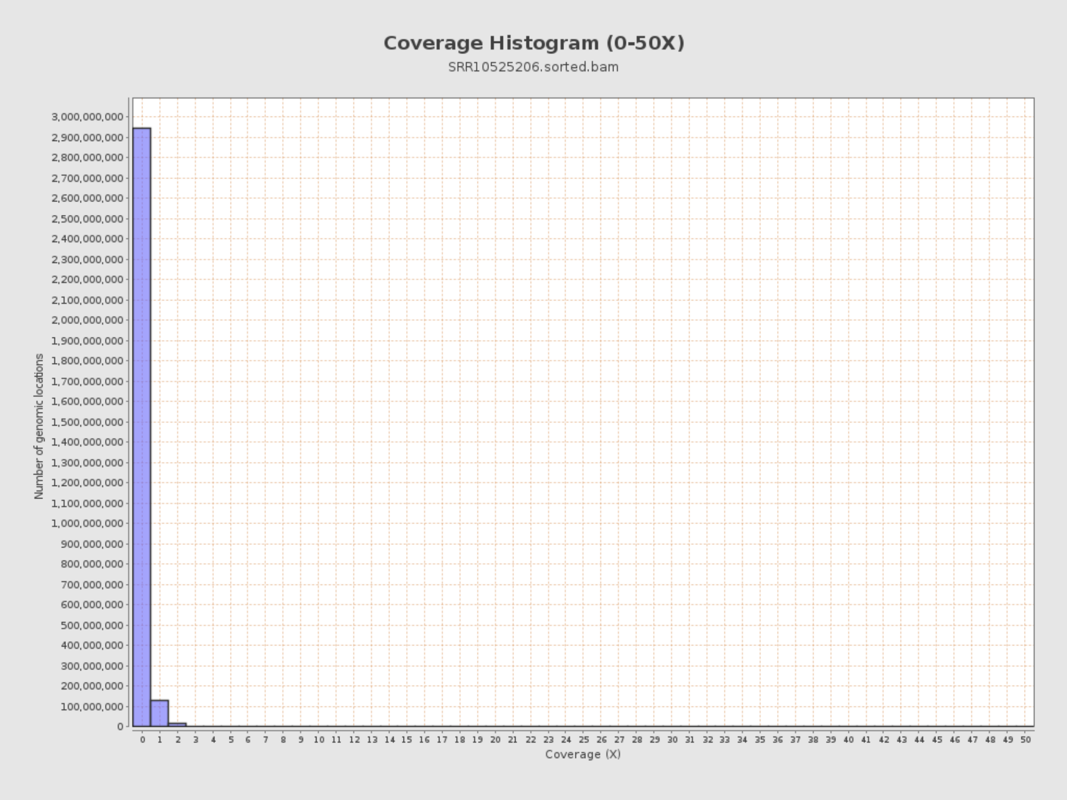
# 3. Results : Coverage across reference



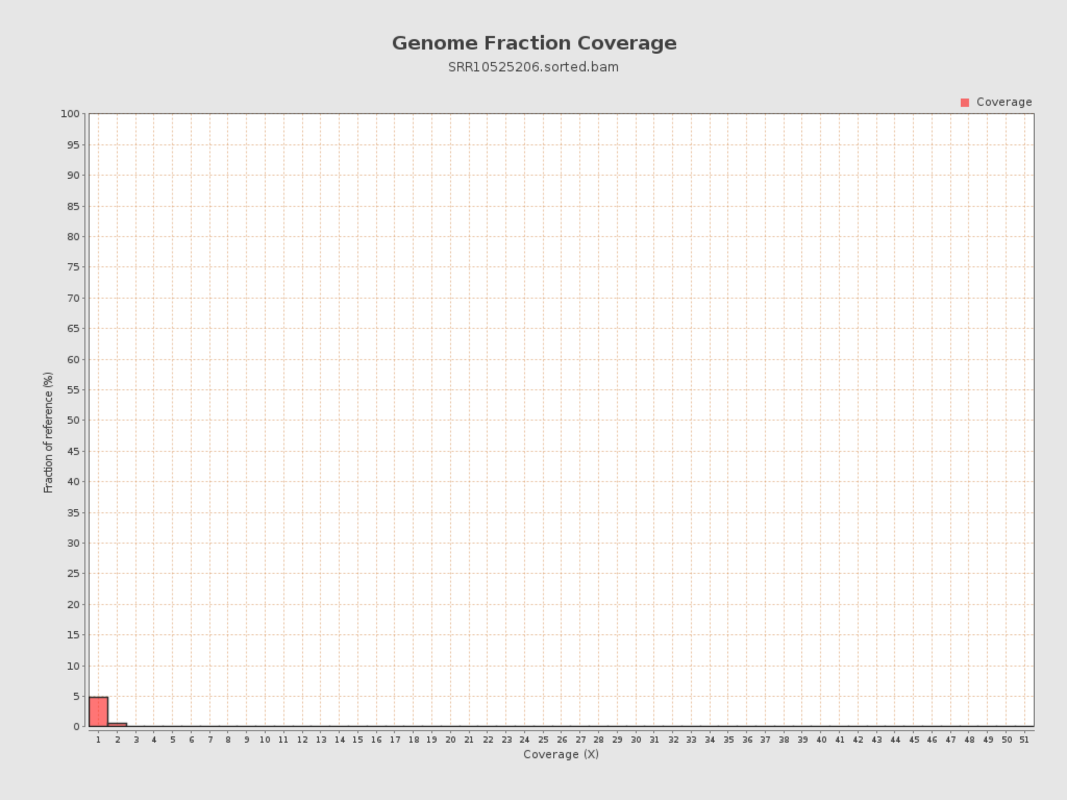
# 4. Results : Coverage Histogram



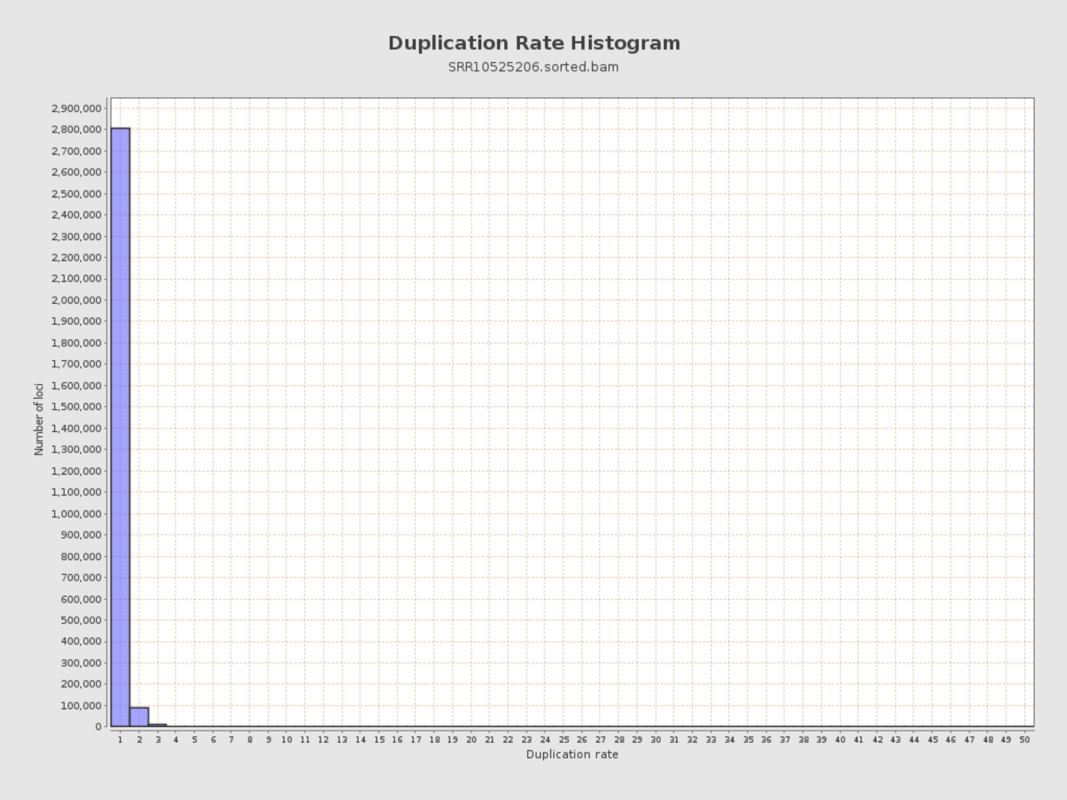
# 5. Results : Coverage Histogram (0-50X)



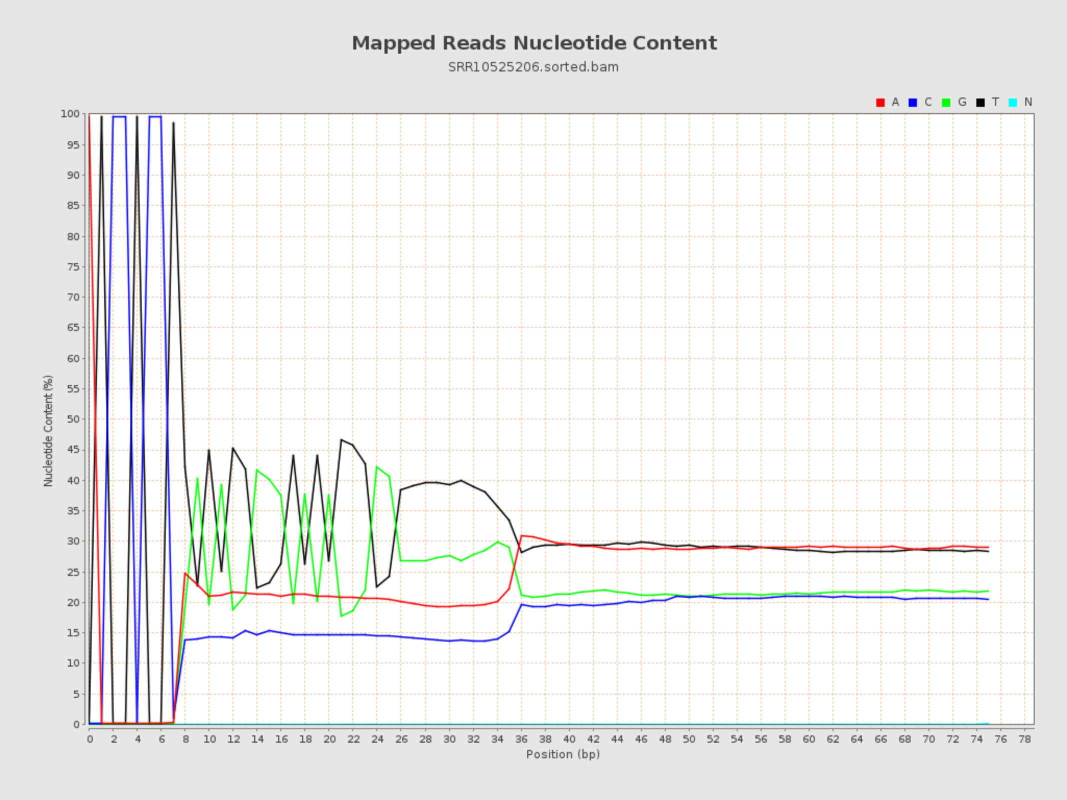
# 6. Results : Genome Fraction Coverage



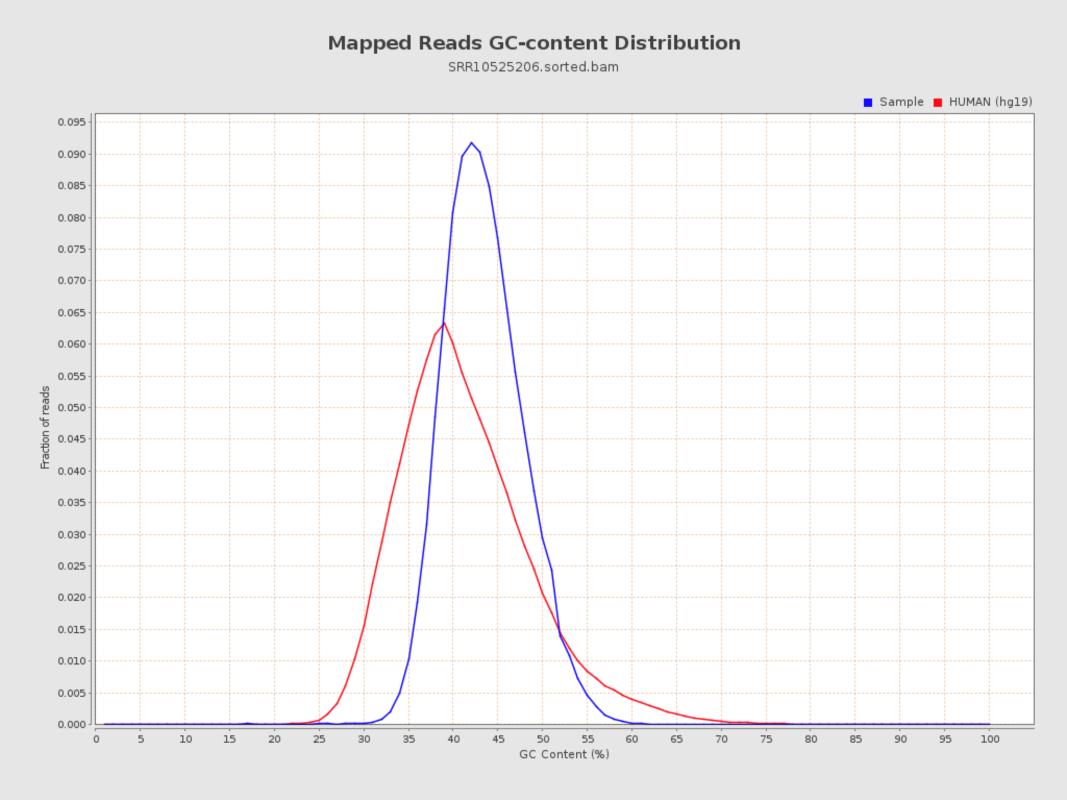
# 7. Results : Duplication Rate Histogram



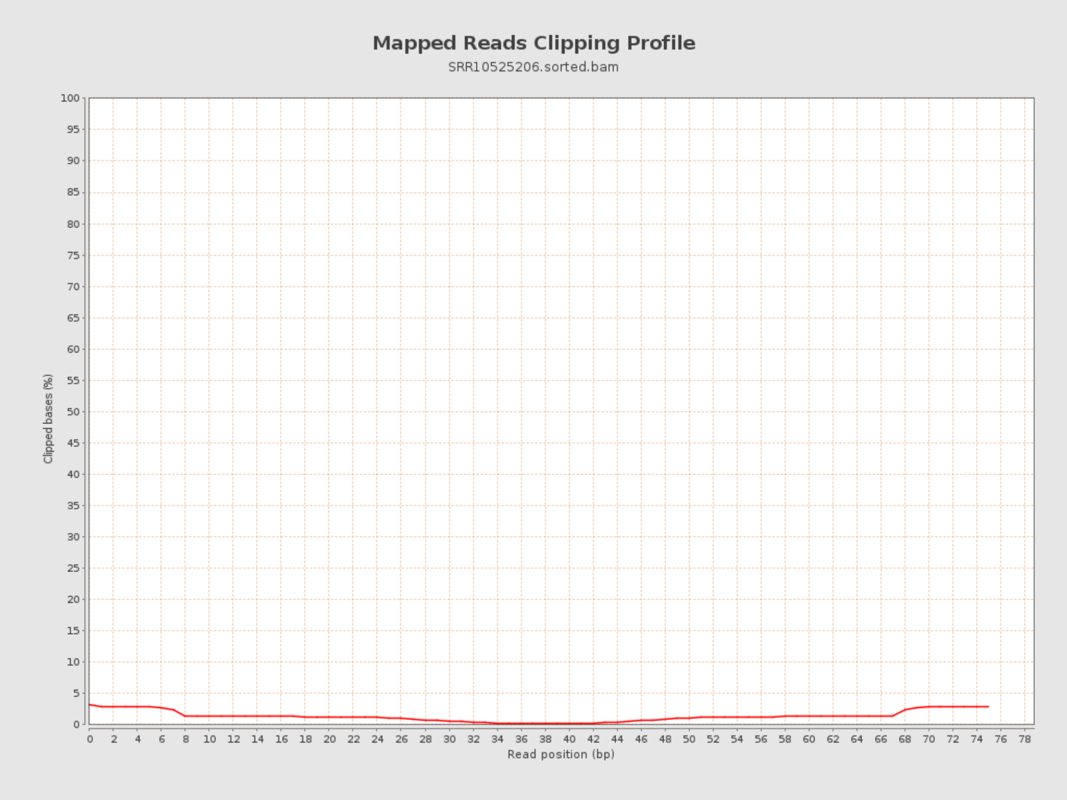
# 8. Results : Mapped Reads Nucleotide Content



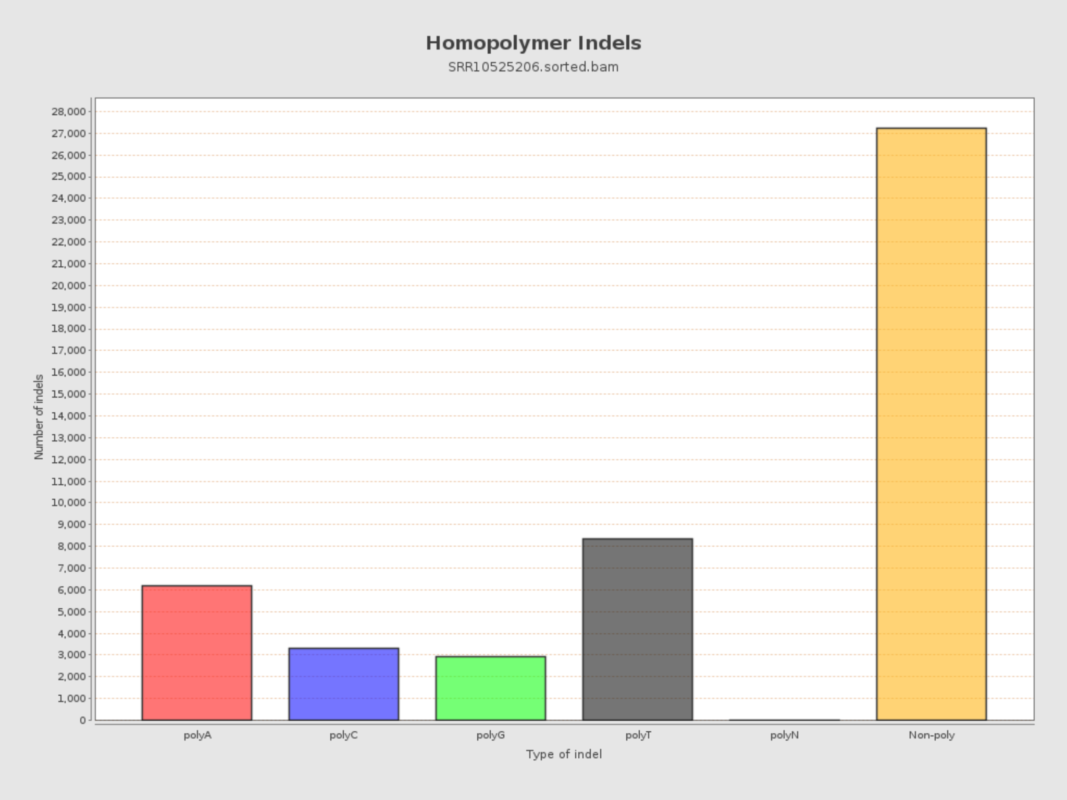
# 9. Results : Mapped Reads GC-content Distribution



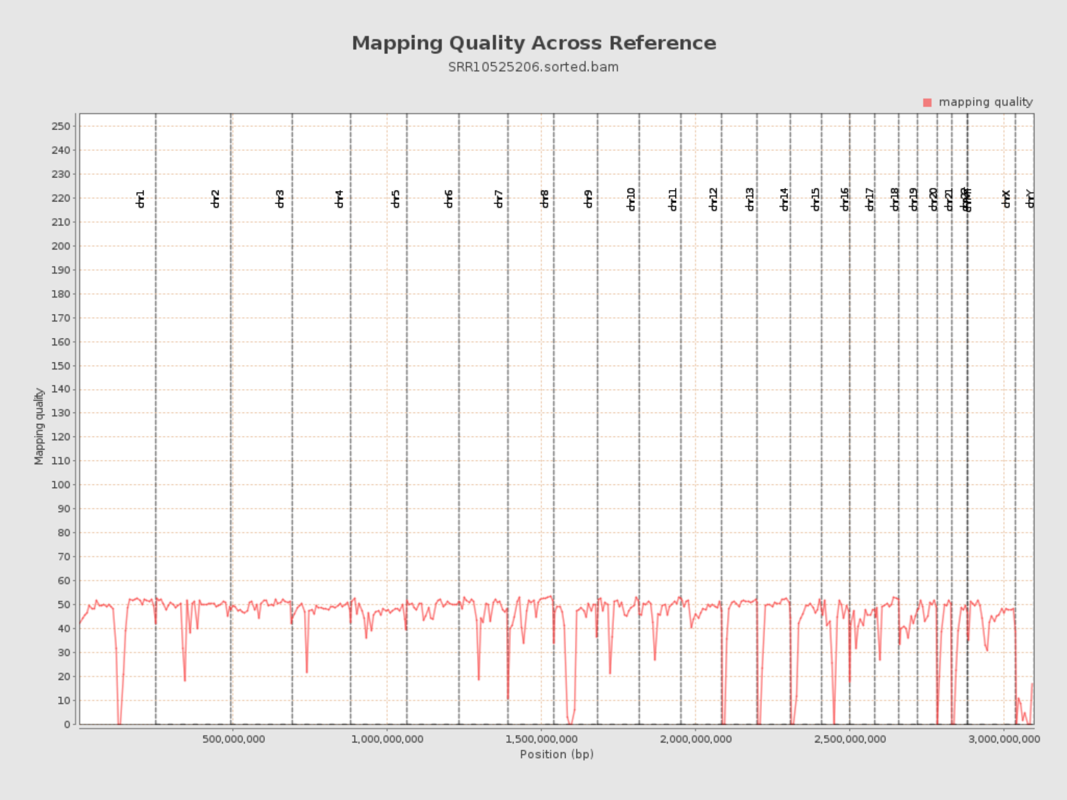
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram