# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/29 18:56:09*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525123.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_SRR10525123 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525123.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Thu Aug 29 18:56:09 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR10525123.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 834,511 |
| Mapped reads | 771,272 / 92.42% |
| Unmapped reads | 63,239 / 7.58% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 18,025 / 2.16% |
| Read min/max/mean length | 30 / 101 / 101.79 |
| Duplicated reads (estimated) | 16,891 / 2.02% |
| Duplication rate | 1.31% |
| Clipped reads | 788,939 / 94.54% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 15,536,549 / 25.88% |
| Number/percentage of C's | 11,854,424 / 19.74% |
| Number/percentage of T's | 18,434,276 / 30.7% |
| Number/percentage of G's | 14,216,453 / 23.68% |
| Number/percentage of N's | 2,189 / 0% |
| GC Percentage | 43.42% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0194 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2285 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.56 |

## 2.5. Mismatches and indels

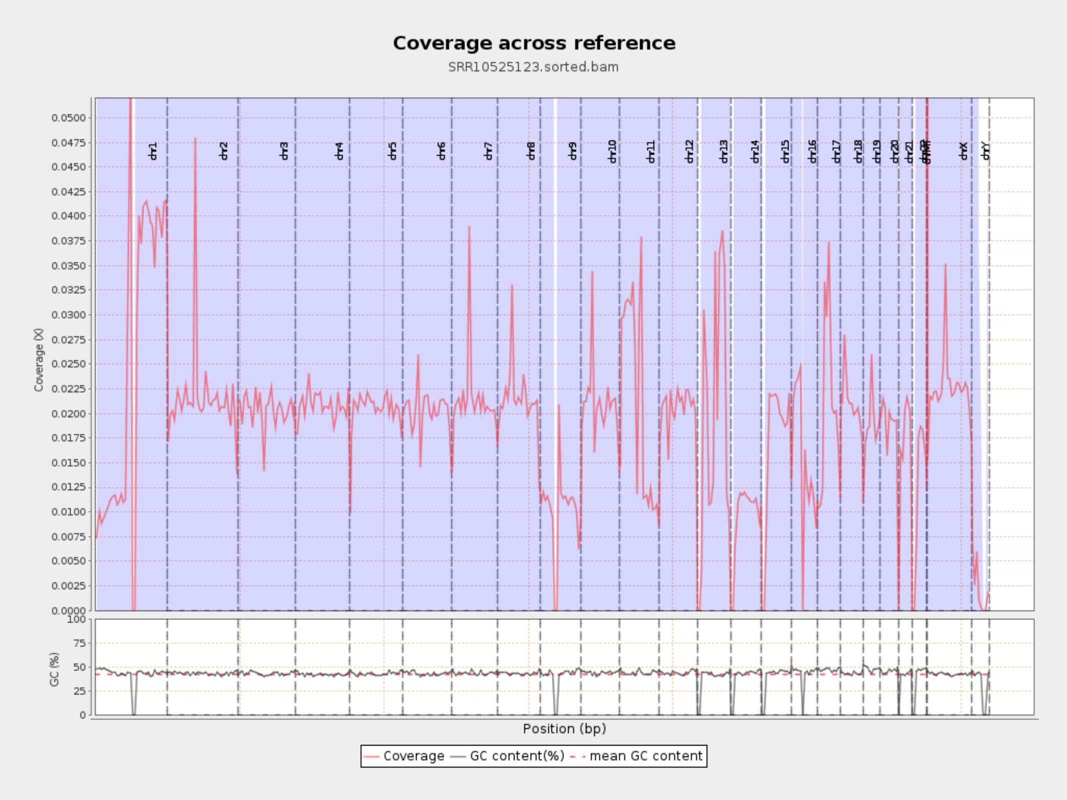
| | |
|---|---|
| General error rate | 0.73% |
| Mismatches | 432,845 |
| Insertions | 4,480 |
| Mapped reads with at least one insertion | 0.57% |
| Deletions | 13,823 |
| Mapped reads with at least one deletion | 1.77% |
| Homopolymer indels | 43.44% |

## 2.6. Chromosome stats

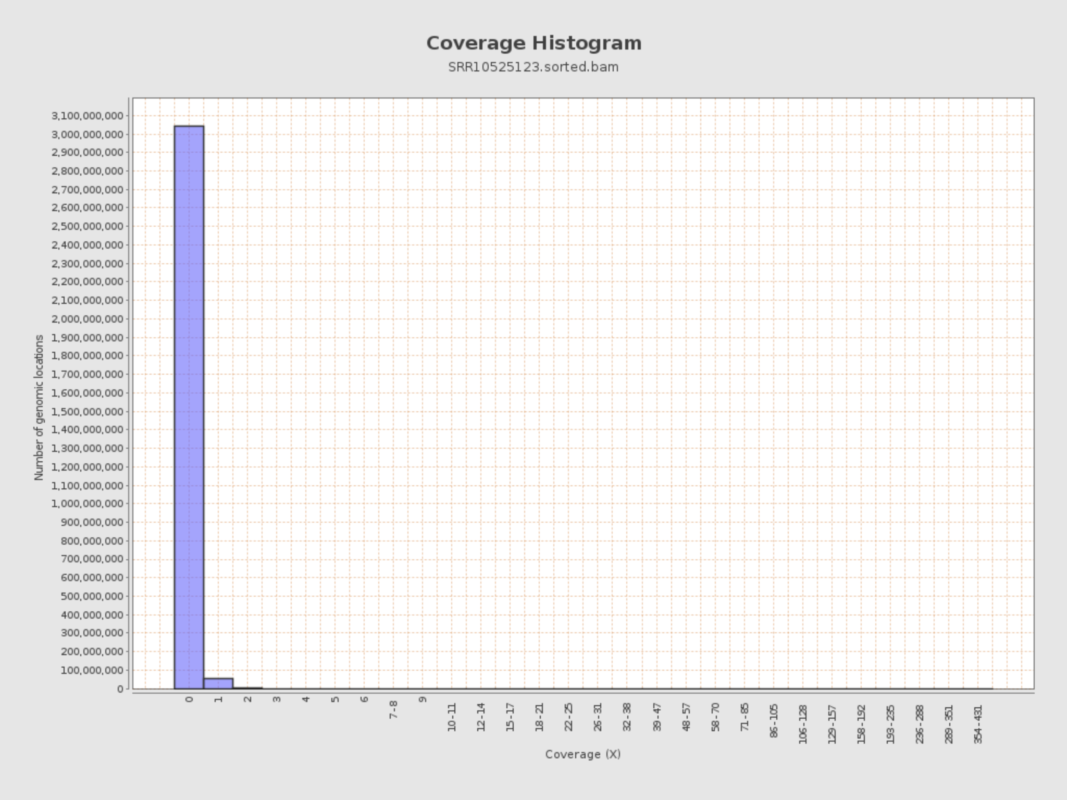
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 6080931 | 0.0244 | 0.3966 |
| chr2 | 243199373 | 5264067 | 0.0216 | 0.2991 |
| chr3 | 198022430 | 4033607 | 0.0204 | 0.1496 |
| chr4 | 191154276 | 3971950 | 0.0208 | 0.1545 |
| chr5 | 180915260 | 3741434 | 0.0207 | 0.1531 |
| chr6 | 171115067 | 3467810 | 0.0203 | 0.1643 |
| chr7 | 159138663 | 3417577 | 0.0215 | 0.3376 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 3150704 | 0.0215 | 0.2826 |
| chr9 | 141213431 | 1433847 | 0.0102 | 0.1744 |
| chr10 | 135534747 | 2851682 | 0.021 | 0.2258 |
| chr11 | 135006516 | 2915173 | 0.0216 | 0.2324 |
| chr12 | 133851895 | 2744160 | 0.0205 | 0.151 |
| chr13 | 115169878 | 2178079 | 0.0189 | 0.145 |
| chr14 | 107349540 | 1003058 | 0.0093 | 0.1102 |
| chr15 | 102531392 | 1734569 | 0.0169 | 0.1367 |
| chr16 | 90354753 | 1353885 | 0.015 | 0.1358 |
| chr17 | 81195210 | 1681925 | 0.0207 | 0.166 |
| chr18 | 78077248 | 1651458 | 0.0212 | 0.3197 |
| chr19 | 59128983 | 1126125 | 0.019 | 0.2884 |
| chr20 | 63025520 | 1190960 | 0.0189 | 0.1473 |
| chr21 | 48129895 | 790104 | 0.0164 | 0.1395 |
| chr22 | 51304566 | 617375 | 0.012 | 0.1153 |
| chrMT | 16571 | 13899 | 0.8388 | 1.2488 |
| chrX | 155270560 | 3526102 | 0.0227 | 0.1904 |
| chrY | 59373566 | 126988 | 0.0021 | 0.0603 |

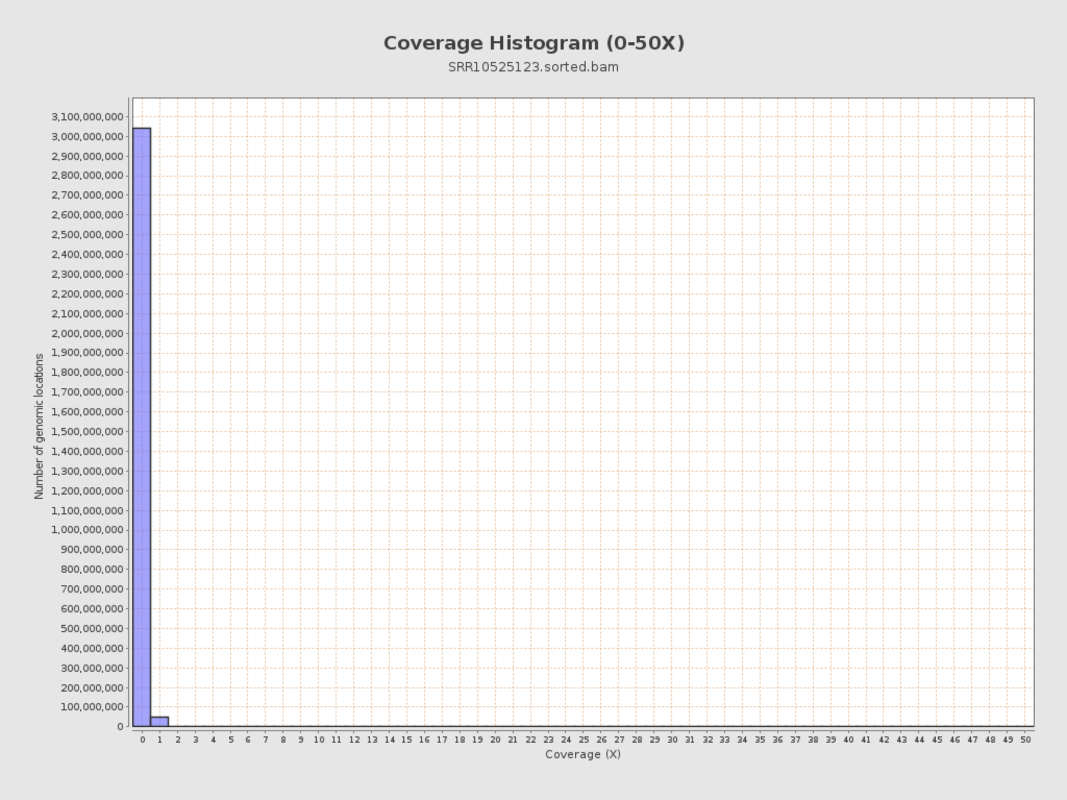
# 3. Results : Coverage across reference



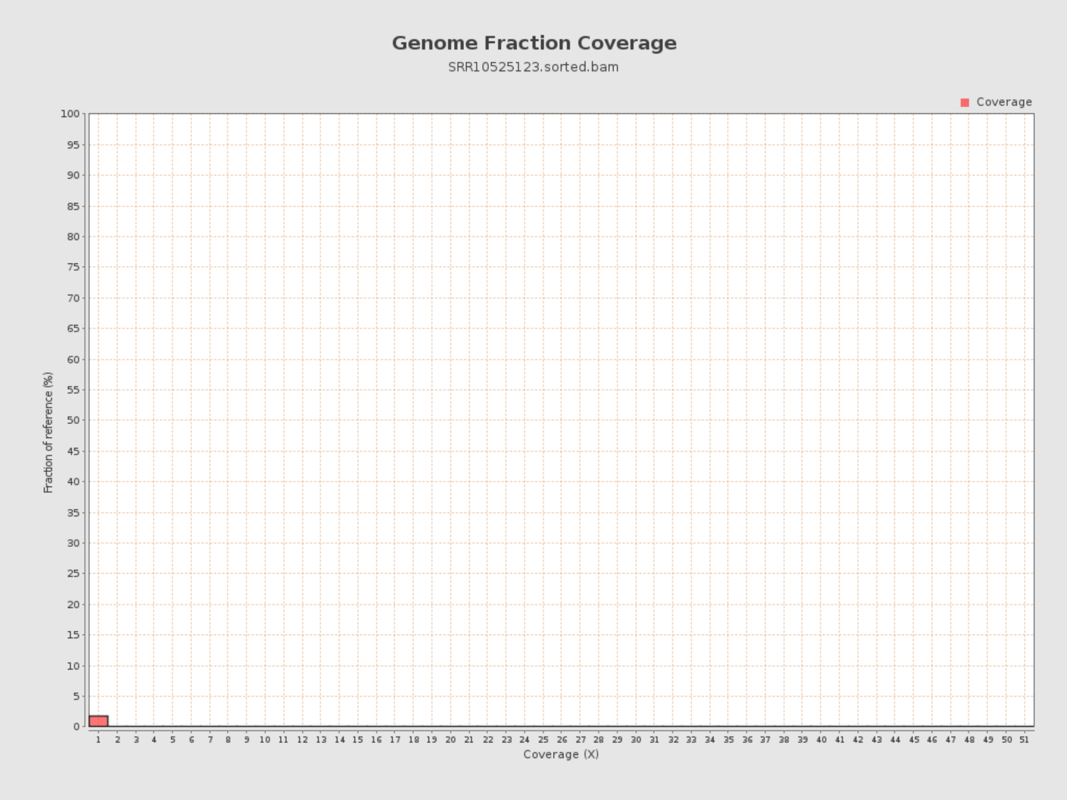
# 4. Results : Coverage Histogram



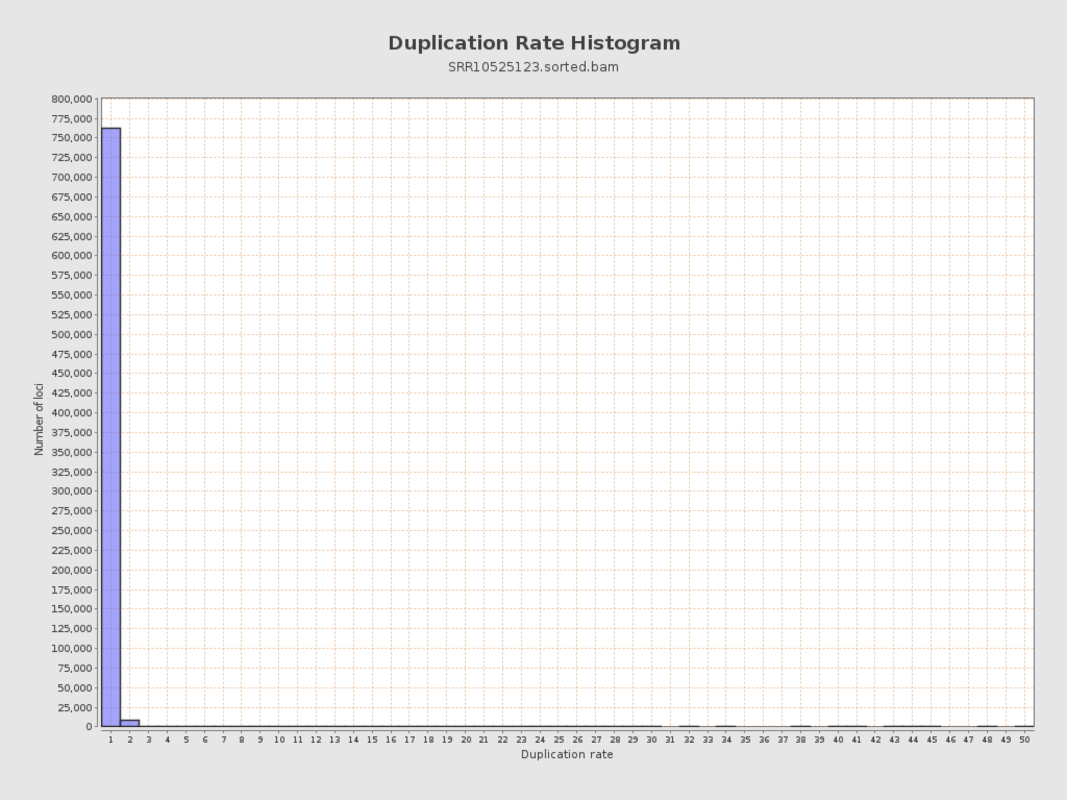
# 5. Results : Coverage Histogram (0-50X)



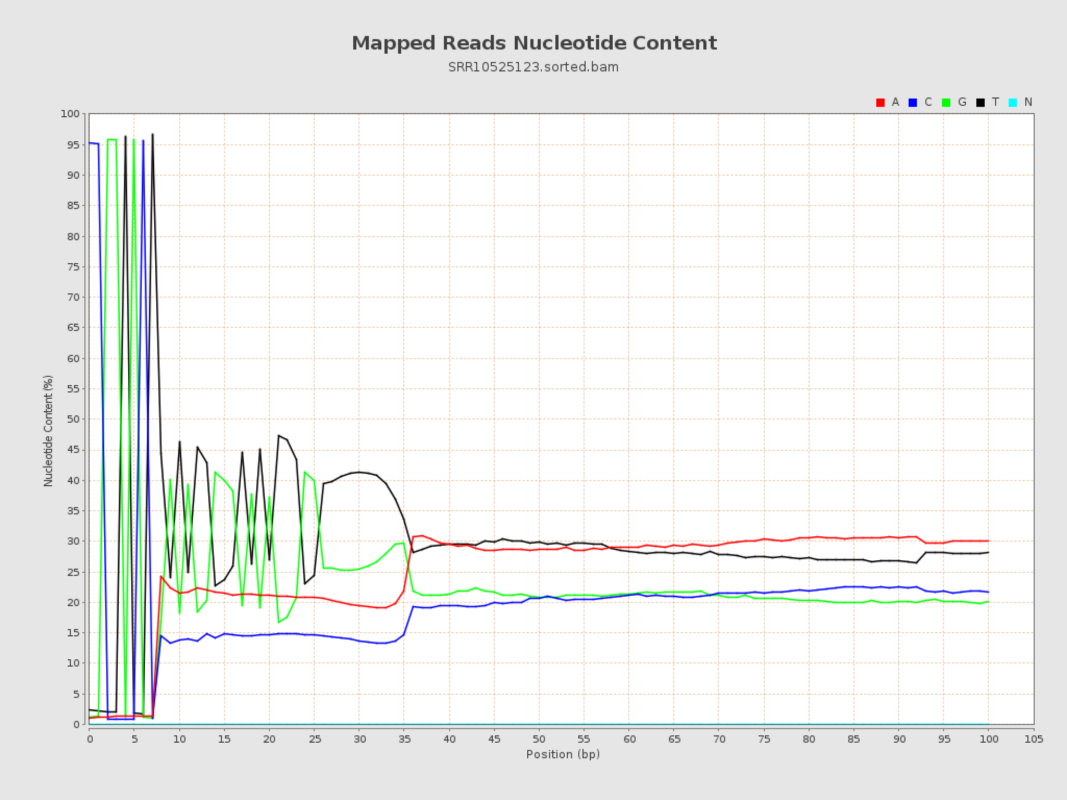
# 6. Results : Genome Fraction Coverage



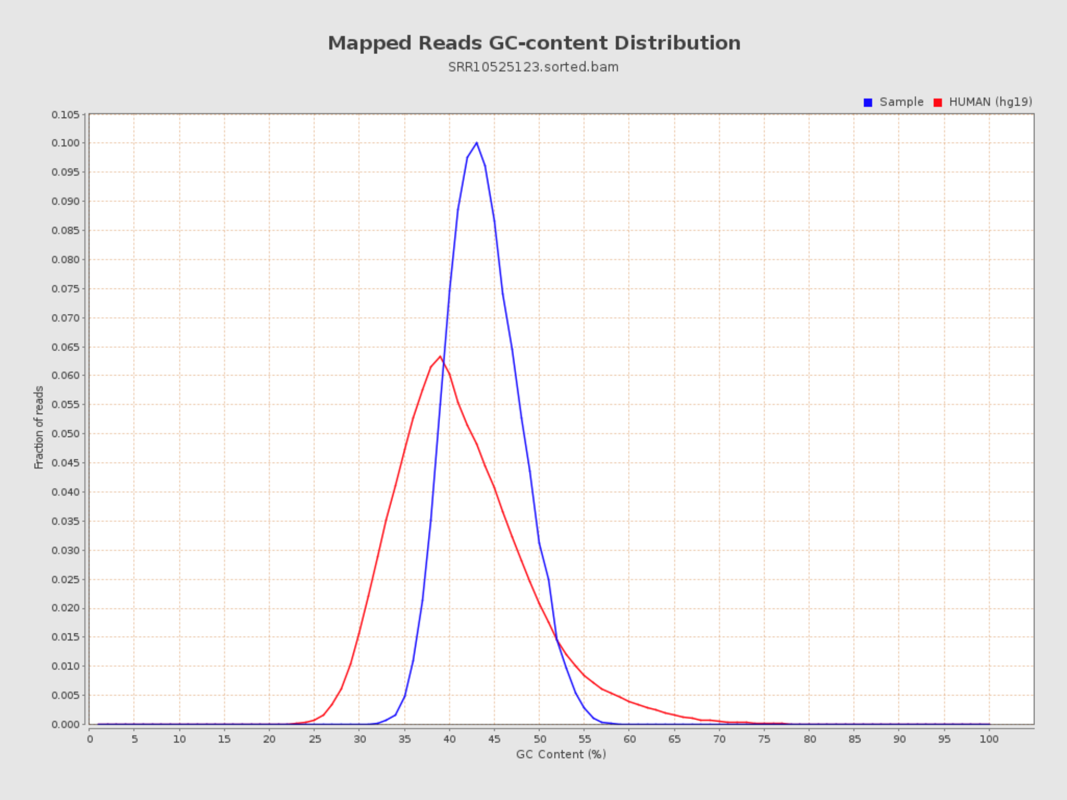
# 7. Results : Duplication Rate Histogram



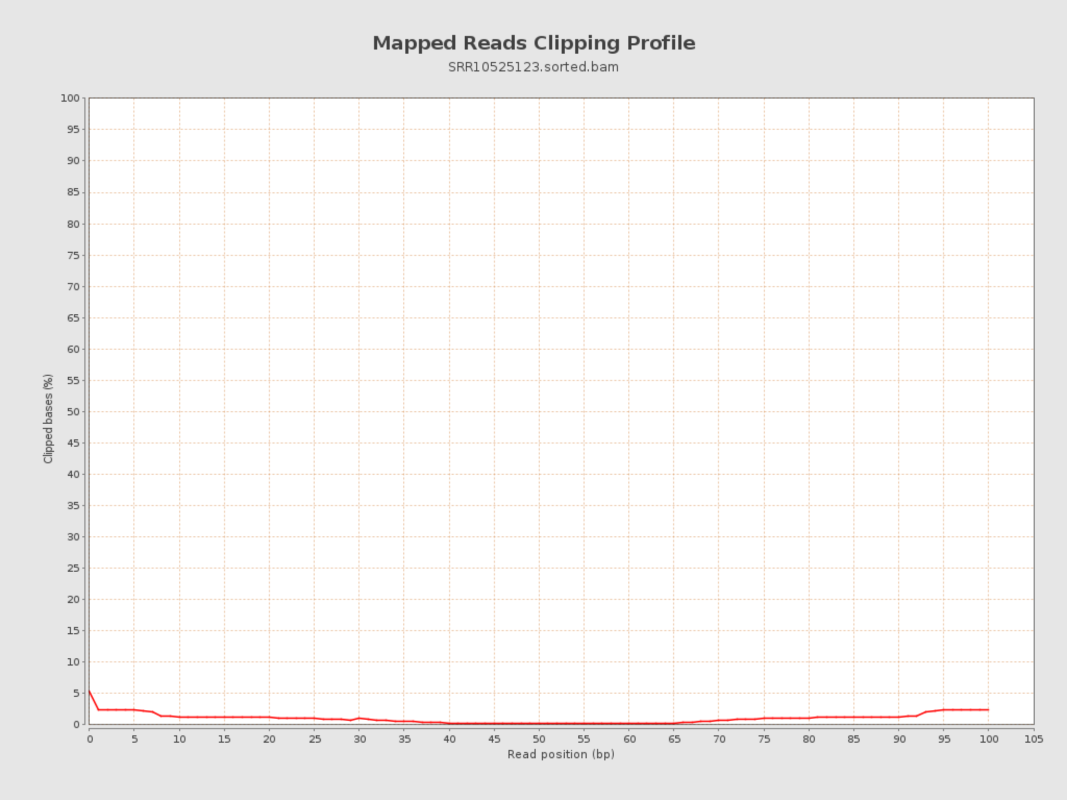
# 8. Results : Mapped Reads Nucleotide Content



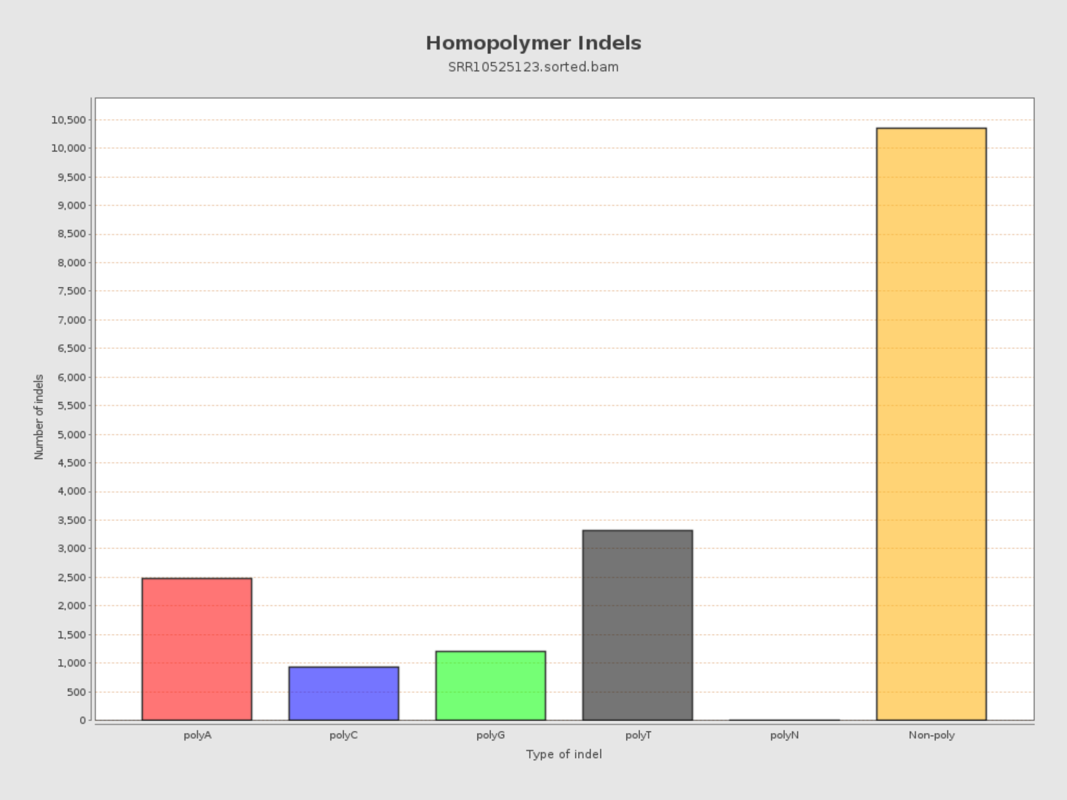
# 9. Results : Mapped Reads GC-content Distribution



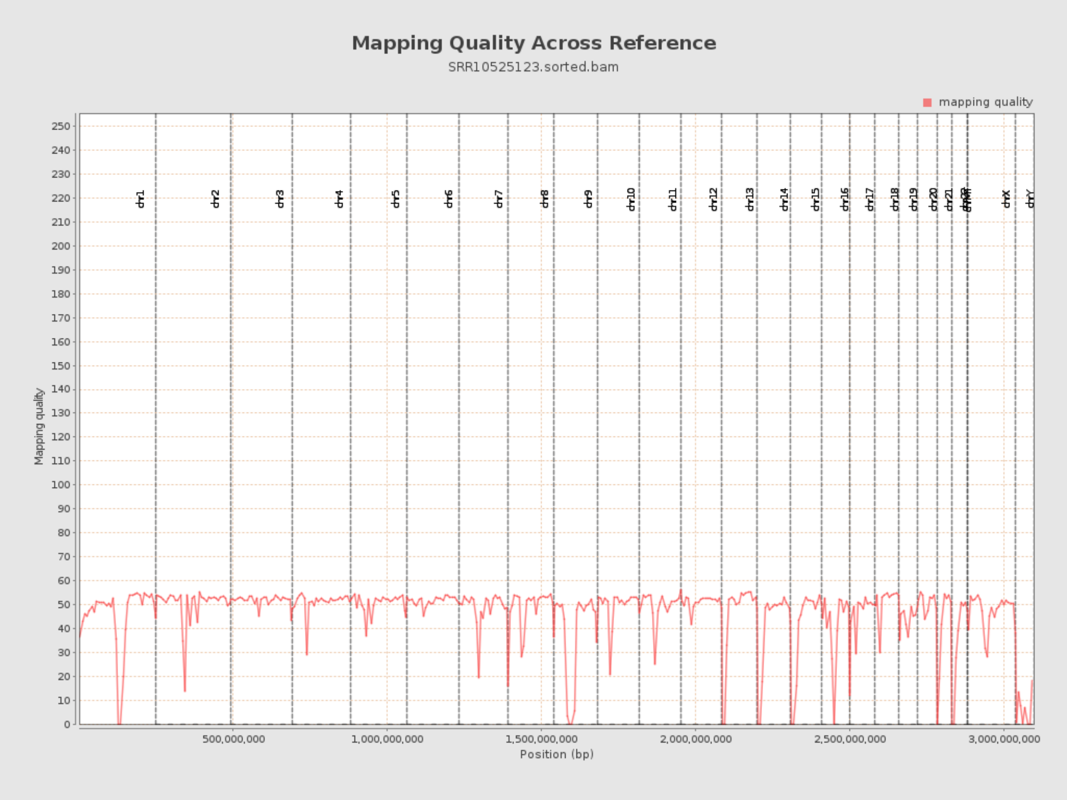
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram