# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/12/04 14:27:12*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124782.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_SRR3124782 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124782.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Dec 04 14:27:11 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3124782.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 315,306 |
| Mapped reads | 307,978 / 97.68% |
| Unmapped reads | 7,328 / 2.32% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 45,077 / 14.3% |
| Read min/max/mean length | 30 / 151 / 159.92 |
| Duplicated reads (estimated) | 188,359 / 59.74% |
| Duplication rate | 1.53% |
| Clipped reads | 236,396 / 74.97% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 12,042,730 / 28.62% |
| Number/percentage of C's | 7,838,215 / 18.63% |
| Number/percentage of T's | 12,510,681 / 29.73% |
| Number/percentage of G's | 9,688,454 / 23.02% |
| Number/percentage of N's | 0 / 0% |
| GC Percentage | 41.65% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0136 |
| | |

| | |
|---|---|
| Standard Deviation | 14.9121 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 50.98 |

## 2.5. Mismatches and indels

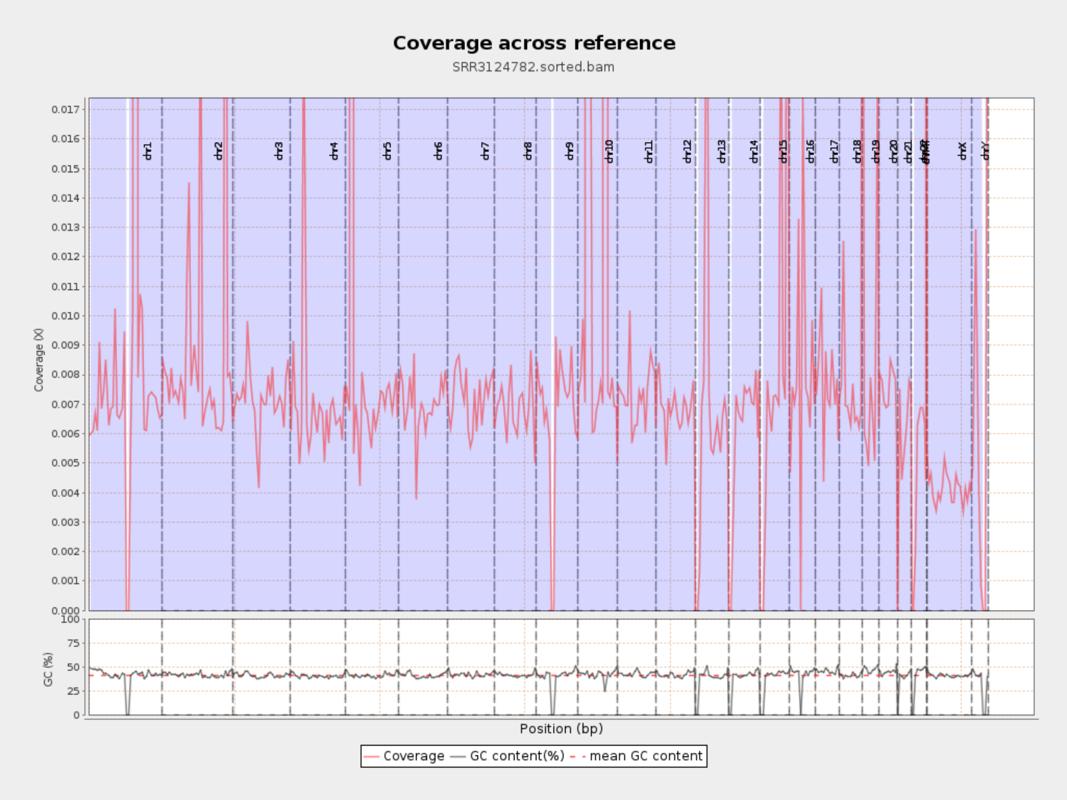
| | |
|---|---|
| General error rate | 1.39% |
| Mismatches | 567,830 |
| Insertions | 5,814 |
| Mapped reads with at least one insertion | 1.74% |
| Deletions | 11,655 |
| Mapped reads with at least one deletion | 3.63% |
| Homopolymer indels | 44.48% |

## 2.6. Chromosome stats

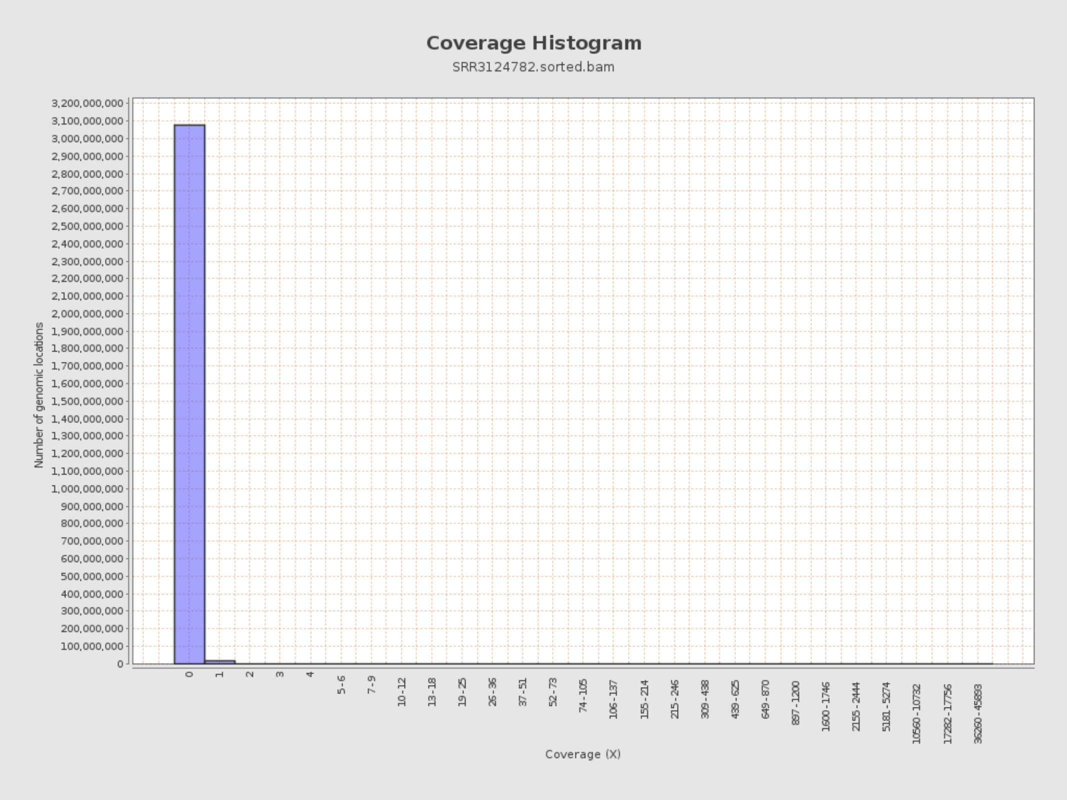
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 6773139 | 0.0272 | 18.8061 |
| chr2 | 243199373 | 2211071 | 0.0091 | 0.9826 |
| chr3 | 198022430 | 1419864 | 0.0072 | 0.1336 |
| chr4 | 191154276 | 1352270 | 0.0071 | 0.131 |
| chr5 | 180915260 | 2752124 | 0.0152 | 9.3655 |
| chr6 | 171115067 | 1199949 | 0.007 | 0.0918 |
| chr7 | 159138663 | 1148552 | 0.0072 | 0.1002 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 1006161 | 0.0069 | 0.1088 |
| chr9 | 141213431 | 935770 | 0.0066 | 0.126 |
| chr10 | 135534747 | 14511113 | 0.1071 | 65.6279 |
| chr11 | 135006516 | 989365 | 0.0073 | 0.1238 |
| chr12 | 133851895 | 920494 | 0.0069 | 0.1034 |
| chr13 | 115169878 | 768315 | 0.0067 | 0.8177 |
| chr14 | 107349540 | 630070 | 0.0059 | 0.0808 |
| chr15 | 102531392 | 898675 | 0.0088 | 1.3128 |
| chr16 | 90354753 | 730349 | 0.0081 | 0.1915 |
| chr17 | 81195210 | 622763 | 0.0077 | 0.1588 |
| chr18 | 78077248 | 578802 | 0.0074 | 0.3234 |
| chr19 | 59128983 | 573675 | 0.0097 | 1.2284 |
| chr20 | 63025520 | 475508 | 0.0075 | 0.0973 |
| chr21 | 48129895 | 279946 | 0.0058 | 0.0923 |
| chr22 | 51304566 | 228351 | 0.0045 | 0.0774 |
| chrMT | 16571 | 83737 | 5.0532 | 3.5274 |
| chrX | 155270560 | 648524 | 0.0042 | 0.0981 |
| chrY | 59373566 | 365231 | 0.0062 | 0.2228 |

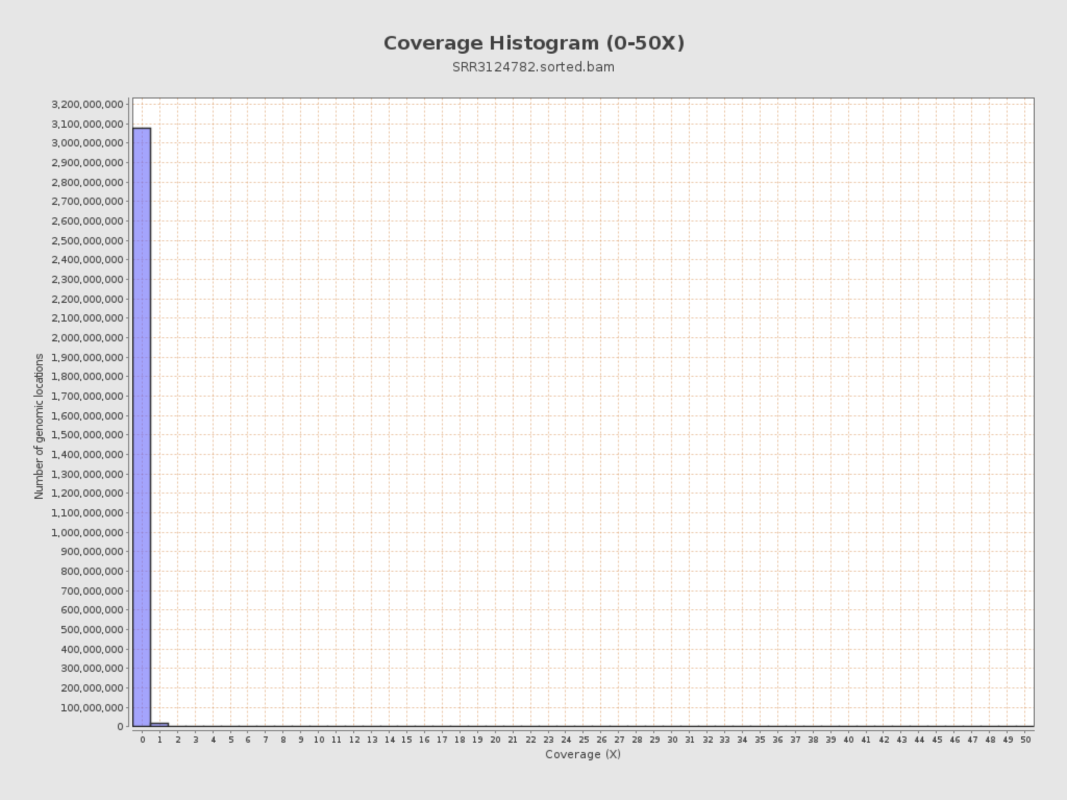
# 3. Results : Coverage across reference



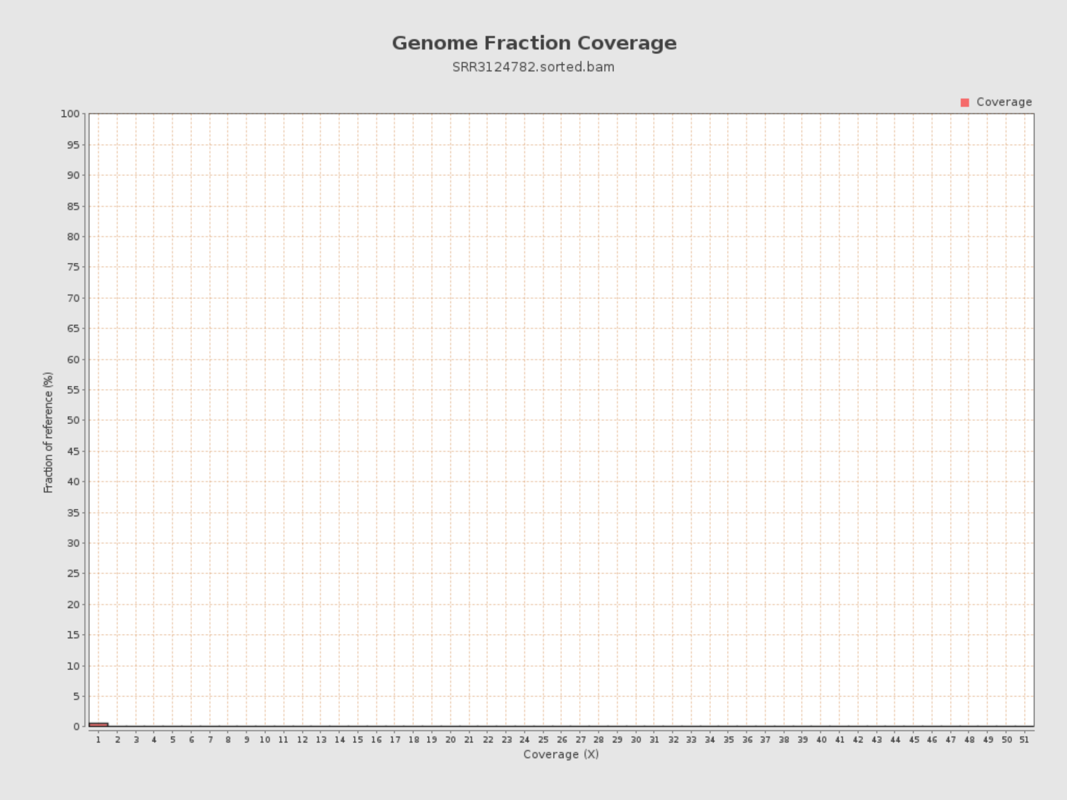
# 4. Results : Coverage Histogram



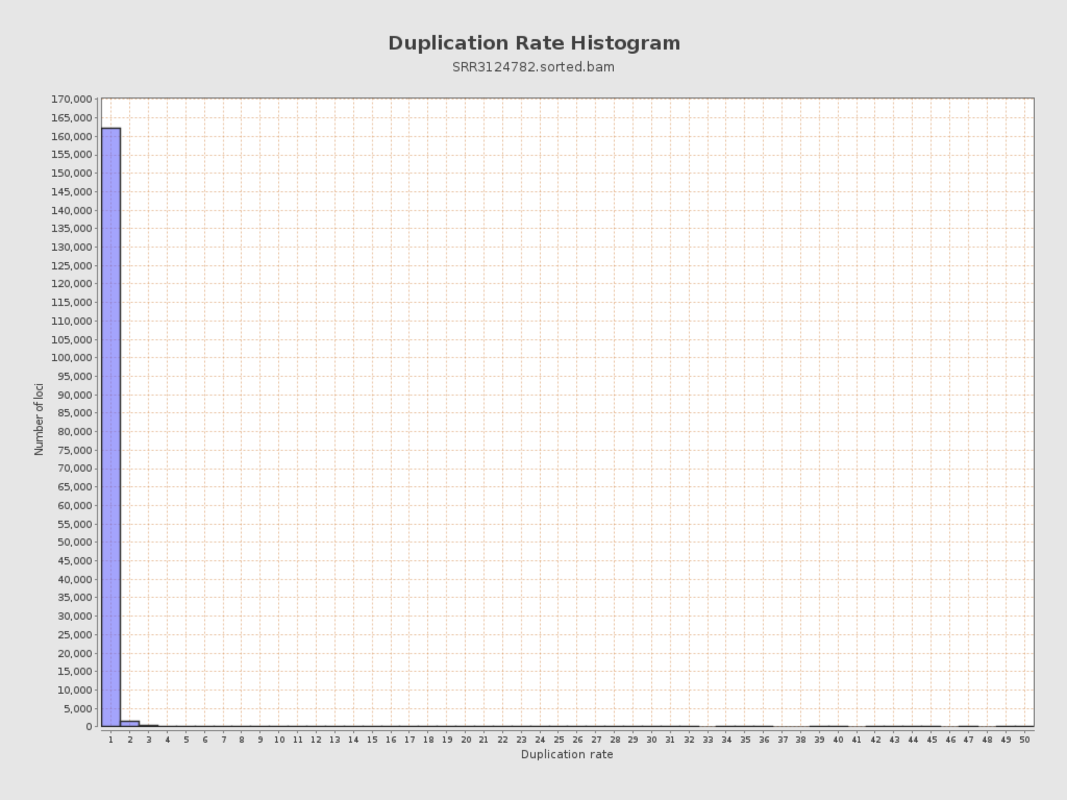
# 5. Results : Coverage Histogram (0-50X)



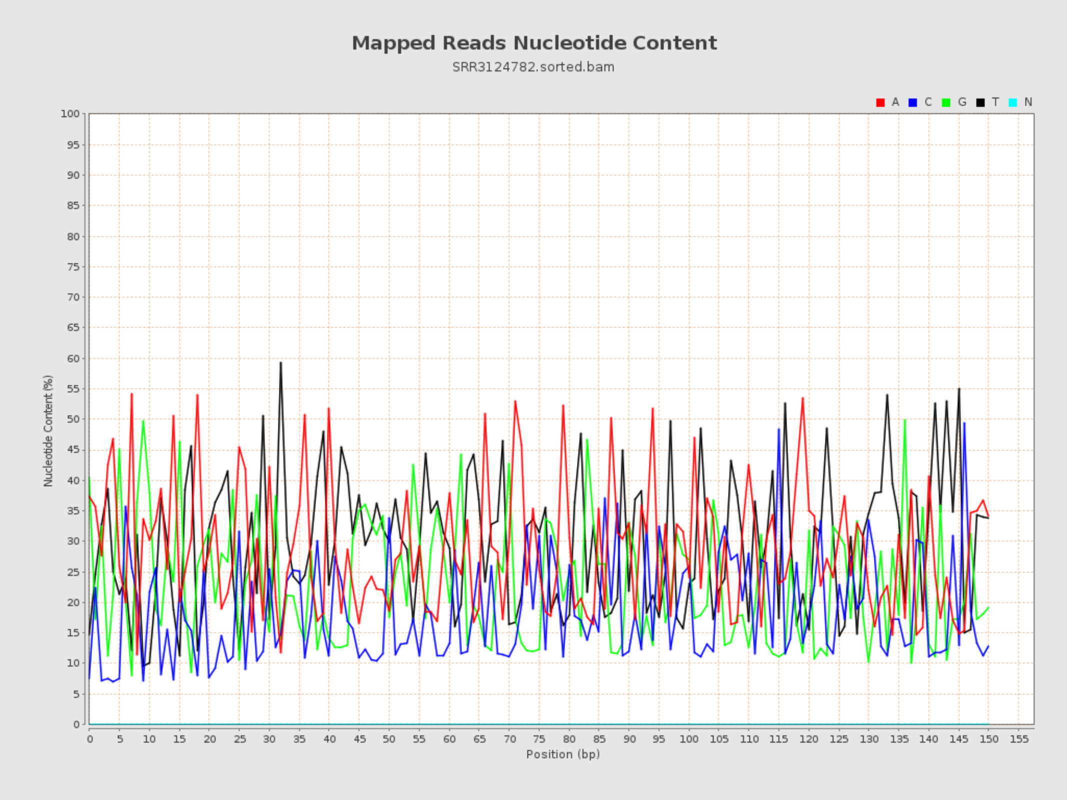
# 6. Results : Genome Fraction Coverage



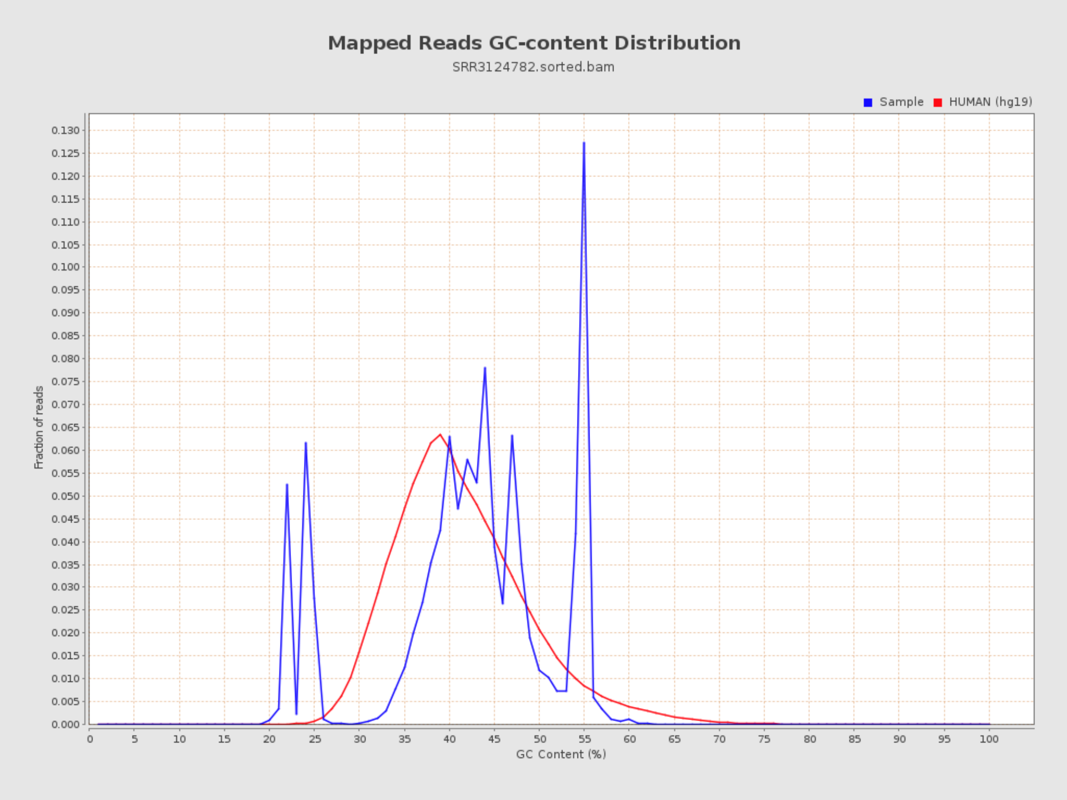
# 7. Results : Duplication Rate Histogram



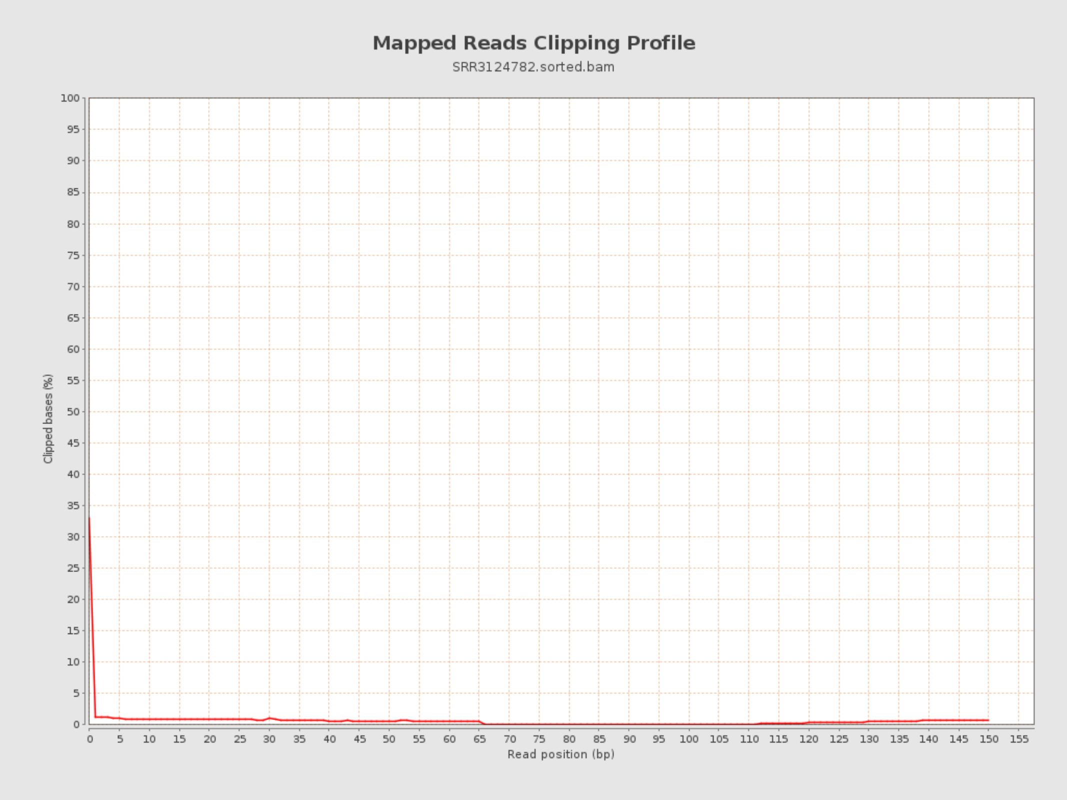
# 8. Results : Mapped Reads Nucleotide Content



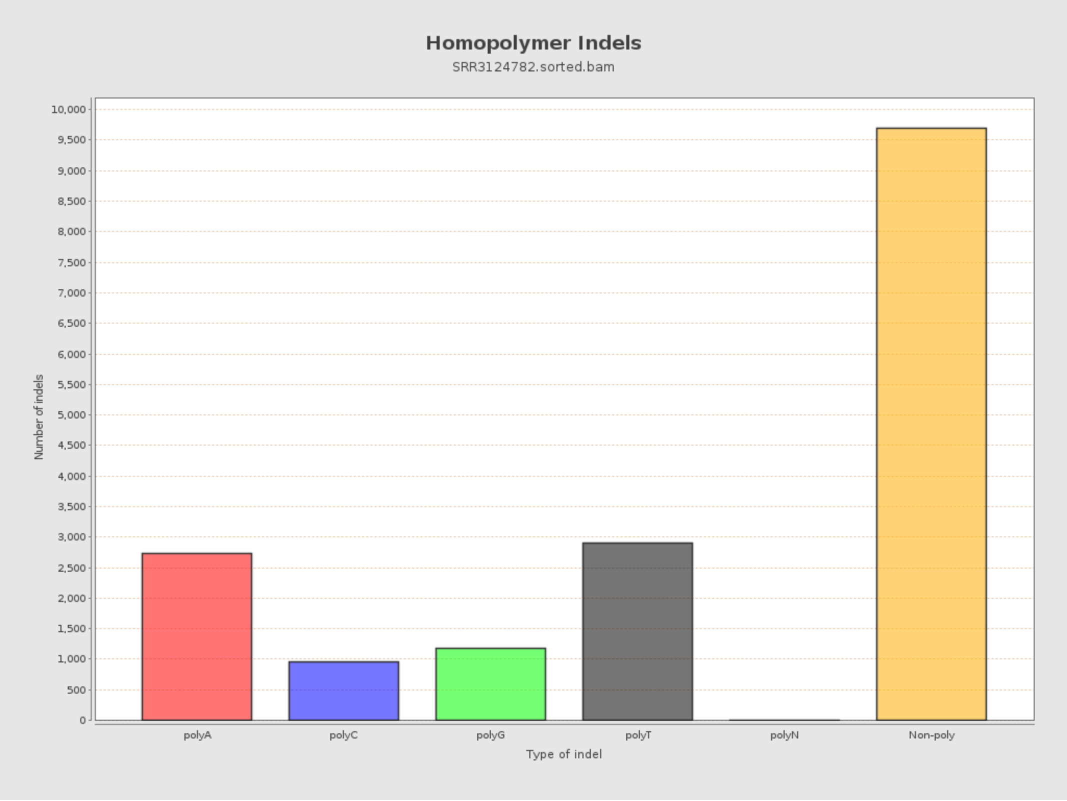
# 9. Results : Mapped Reads GC-content Distribution



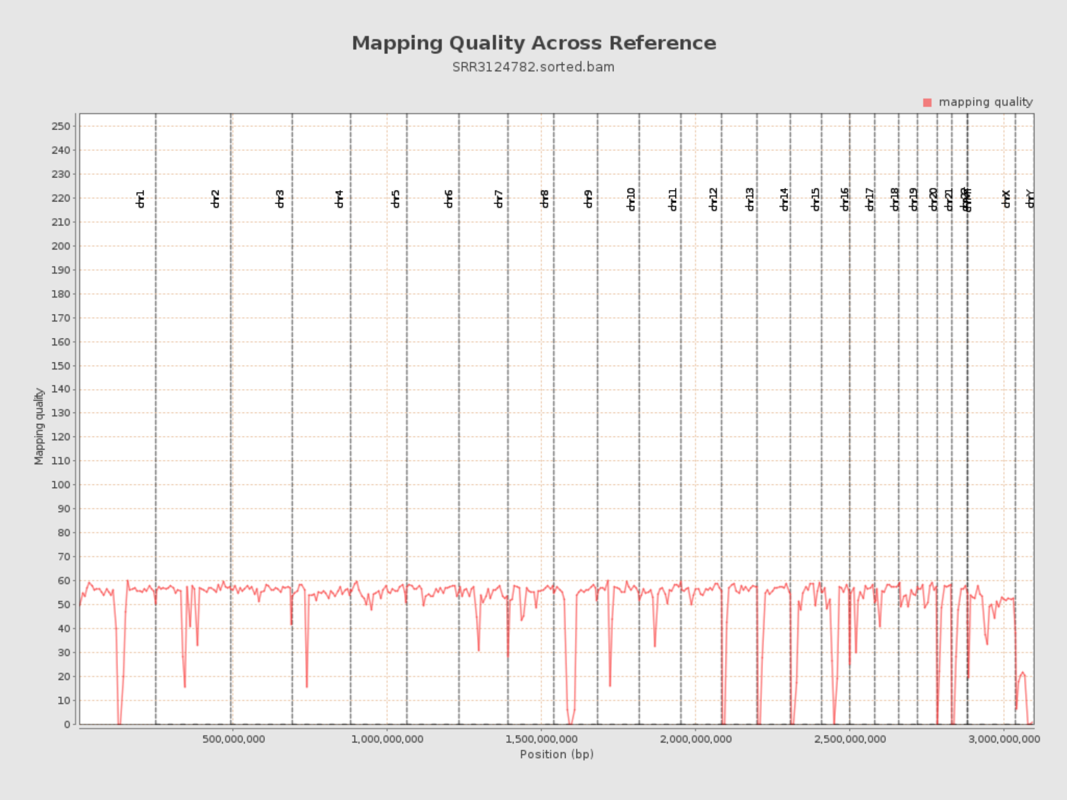
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram