# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/14 04:39:59*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004149.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_SRR6004149 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004149.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 14 04:39:58 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6004149.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,286,238 |
| Mapped reads | 2,625,408 / 79.89% |
| Unmapped reads | 660,830 / 20.11% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 11,626 / 0.35% |
| Read min/max/mean length | 30 / 76 / 76.12 |
| Duplicated reads (estimated) | 233,053 / 7.09% |
| Duplication rate | 7.01% |
| Clipped reads | 1,624,884 / 49.45% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 42,270,757 / 25.68% |
| Number/percentage of C's | 28,428,007 / 17.27% |
| Number/percentage of T's | 54,868,094 / 33.34% |
| Number/percentage of G's | 39,004,172 / 23.7% |
| Number/percentage of N's | 16,493 / 0.01% |
| GC Percentage | 40.97% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0532 |
| | |

| | |
|---|---|
| Standard Deviation | 0.5335 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.33 |

## 2.5. Mismatches and indels

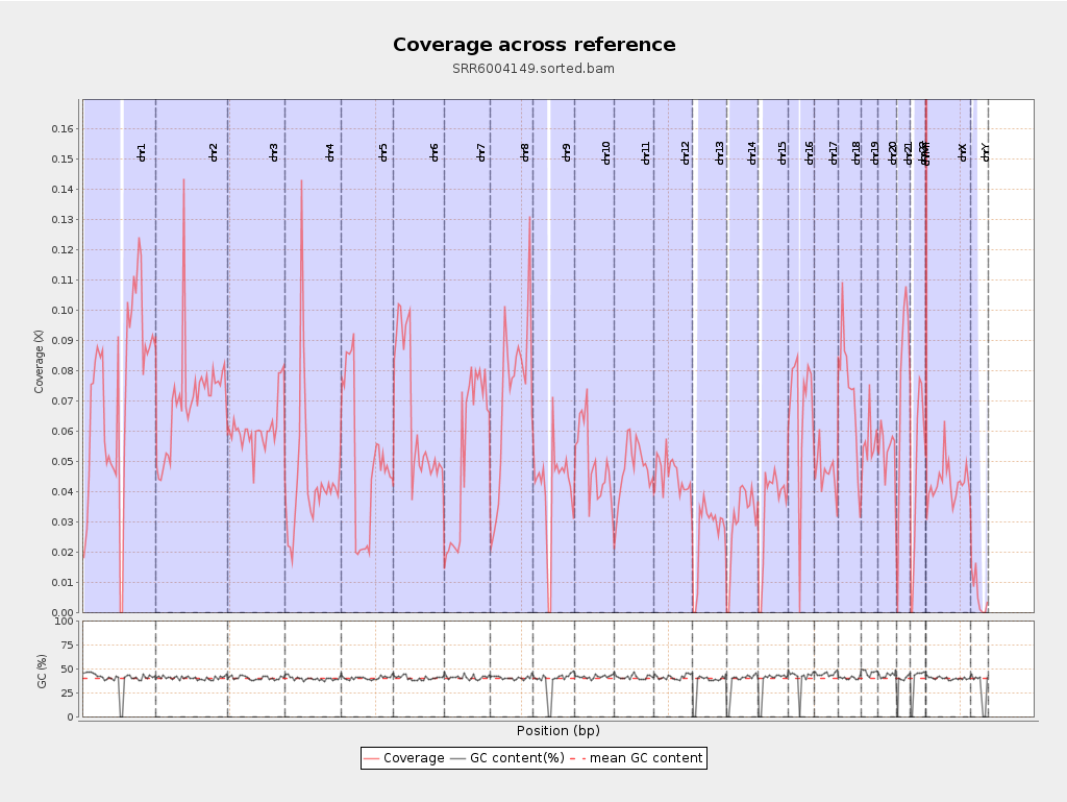
| | |
|---|---|
| General error rate | 1.03% |
| Mismatches | 1,670,258 |
| Insertions | 14,690 |
| Mapped reads with at least one insertion | 0.56% |
| Deletions | 50,896 |
| Mapped reads with at least one deletion | 1.92% |
| Homopolymer indels | 49.46% |

## 2.6. Chromosome stats

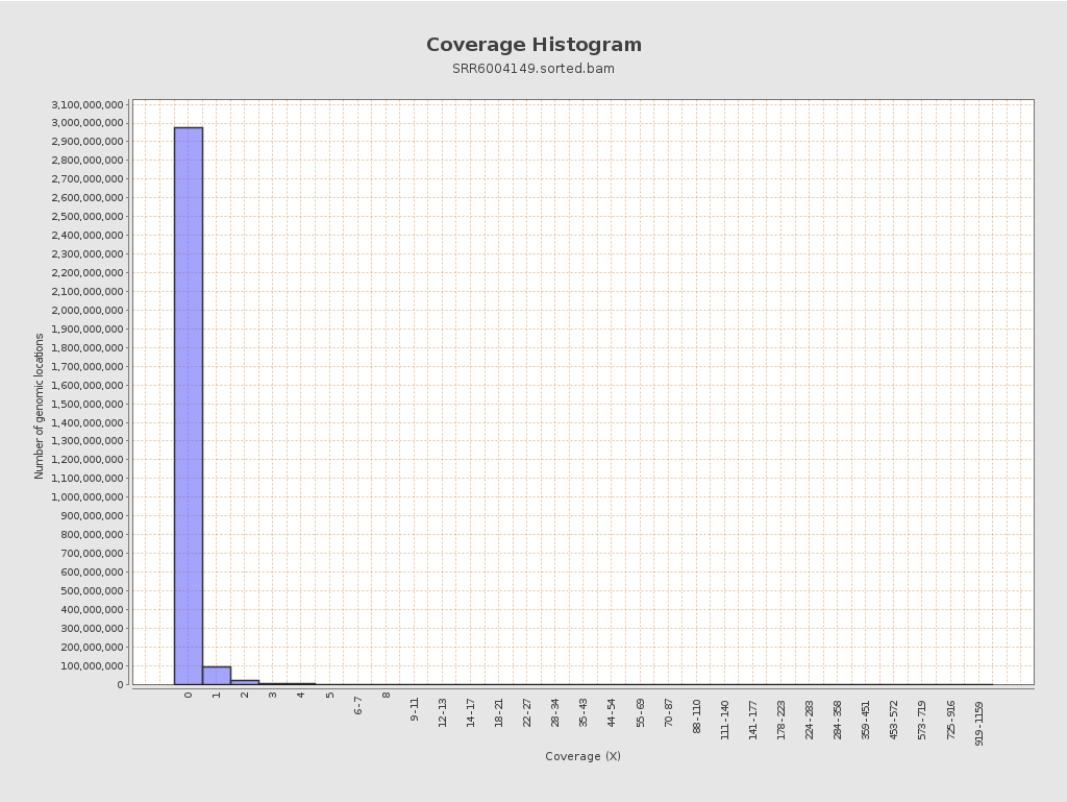
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 17978075 | 0.0721 | 0.8329 |
| chr2 | 243199373 | 17016187 | 0.07 | 0.873 |
| chr3 | 198022430 | 12059208 | 0.0609 | 0.3203 |
| chr4 | 191154276 | 8570902 | 0.0448 | 0.2846 |
| chr5 | 180915260 | 8907676 | 0.0492 | 0.2937 |
| chr6 | 171115067 | 11060768 | 0.0646 | 0.4273 |
| chr7 | 159138663 | 8413920 | 0.0529 | 0.5879 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 10463854 | 0.0715 | 0.5808 |
| chr9 | 141213431 | 5816212 | 0.0412 | 0.5661 |
| chr10 | 135534747 | 6690890 | 0.0494 | 0.3959 |
| chr11 | 135006516 | 6381026 | 0.0473 | 0.4691 |
| chr12 | 133851895 | 6046641 | 0.0452 | 0.2954 |
| chr13 | 115169878 | 3032701 | 0.0263 | 0.2092 |
| chr14 | 107349540 | 3274145 | 0.0305 | 0.3322 |
| chr15 | 102531392 | 3498718 | 0.0341 | 0.2491 |
| chr16 | 90354753 | 6043174 | 0.0669 | 0.3669 |
| chr17 | 81195210 | 3779208 | 0.0465 | 0.3454 |
| chr18 | 78077248 | 5757888 | 0.0737 | 1.1835 |
| chr19 | 59128983 | 3331661 | 0.0563 | 0.7064 |
| chr20 | 63025520 | 3405695 | 0.054 | 0.3516 |
| chr21 | 48129895 | 3618944 | 0.0752 | 0.3795 |
| chr22 | 51304566 | 2424742 | 0.0473 | 0.279 |
| chrMT | 16571 | 117828 | 7.1105 | 8.6539 |
| chrX | 155270560 | 6641477 | 0.0428 | 0.3727 |
| chrY | 59373566 | 340256 | 0.0057 | 0.1214 |

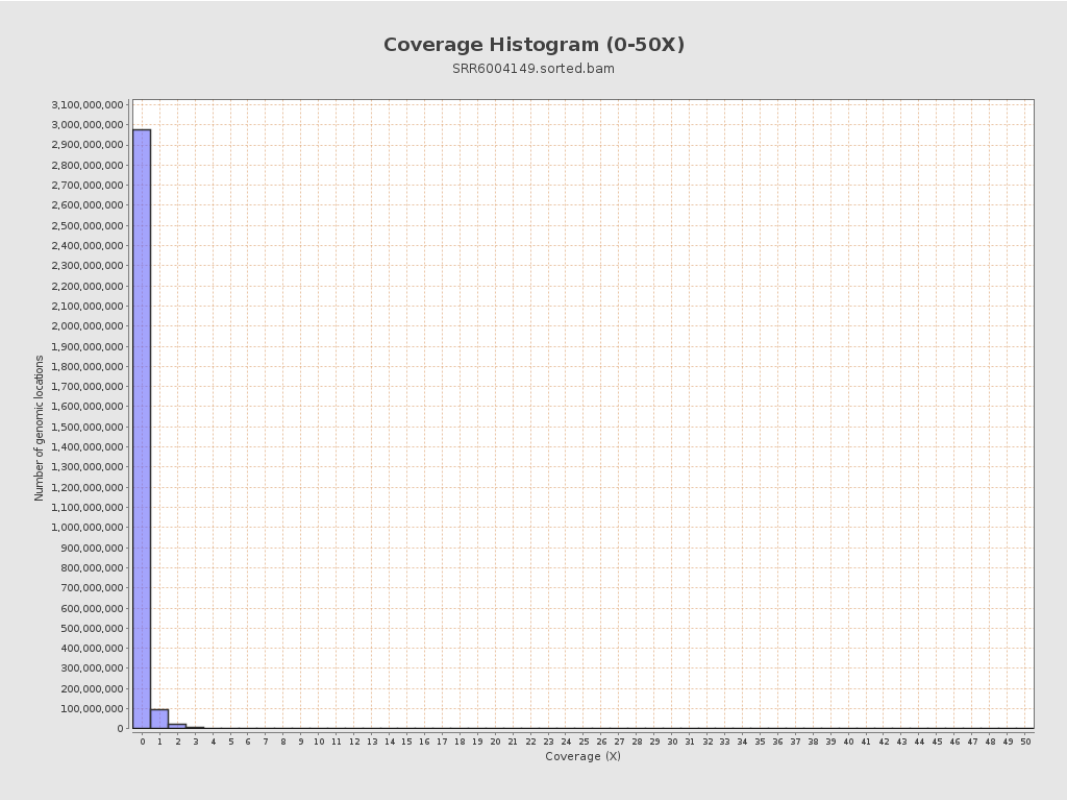
# 3. Results : Coverage across reference



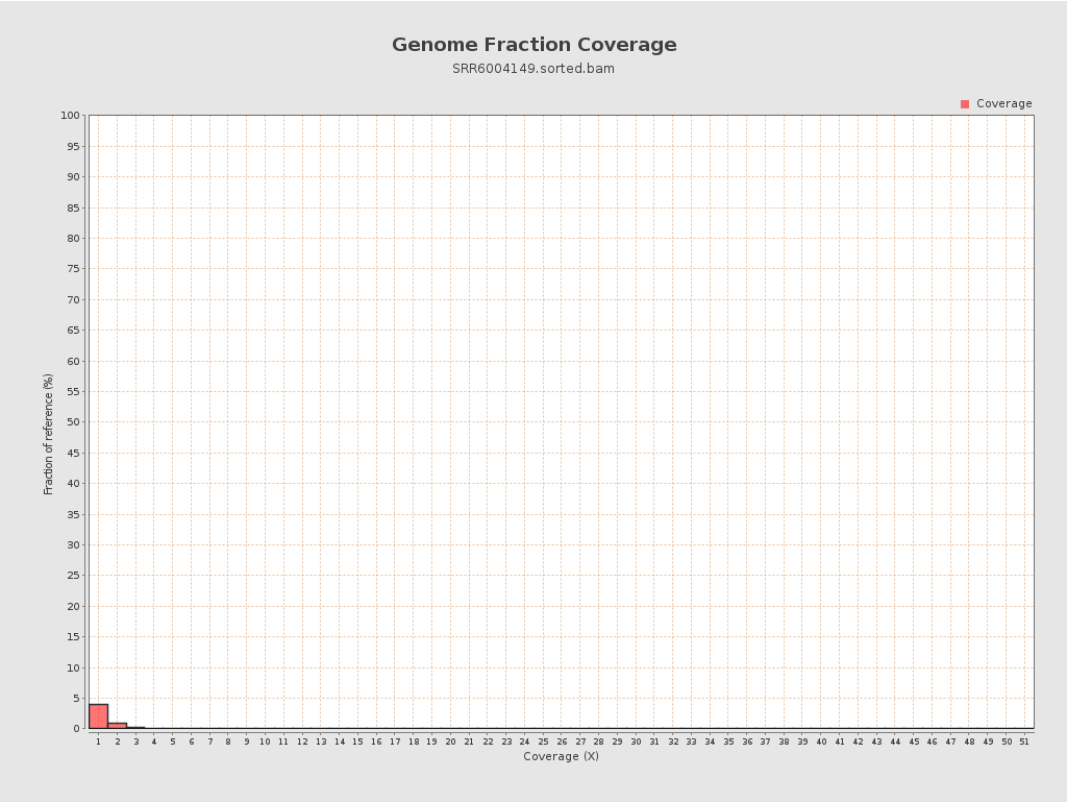
# 4. Results : Coverage Histogram



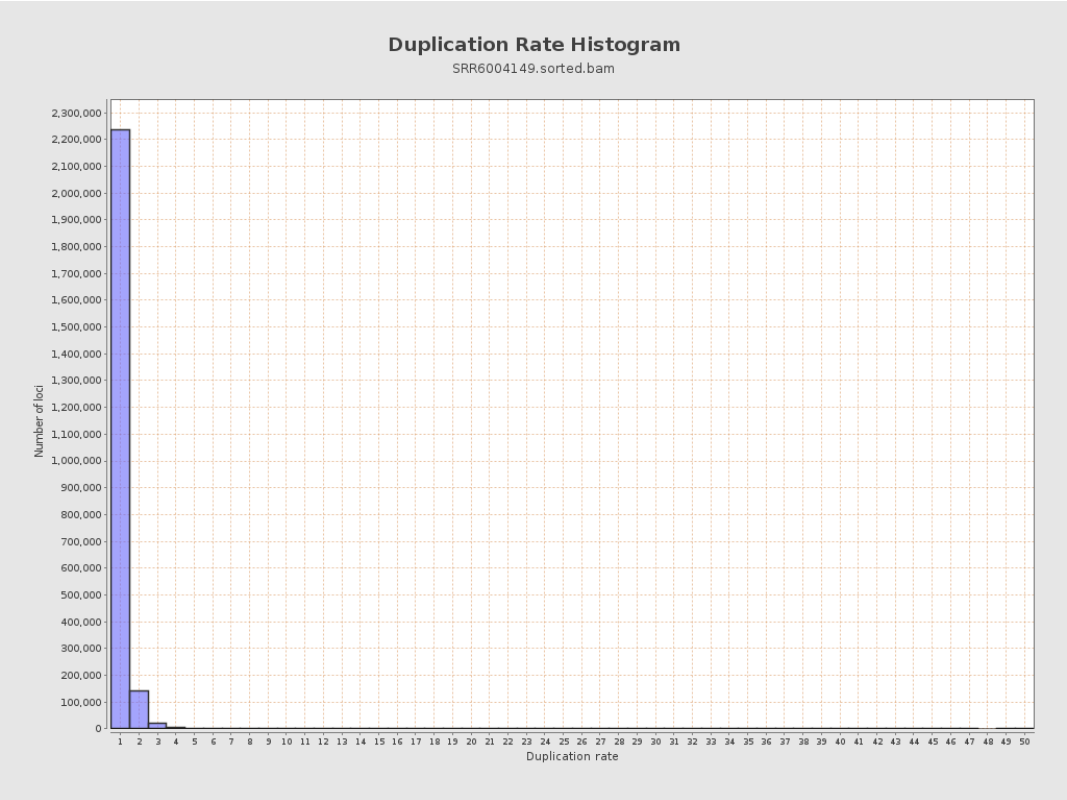
# 5. Results : Coverage Histogram (0-50X)



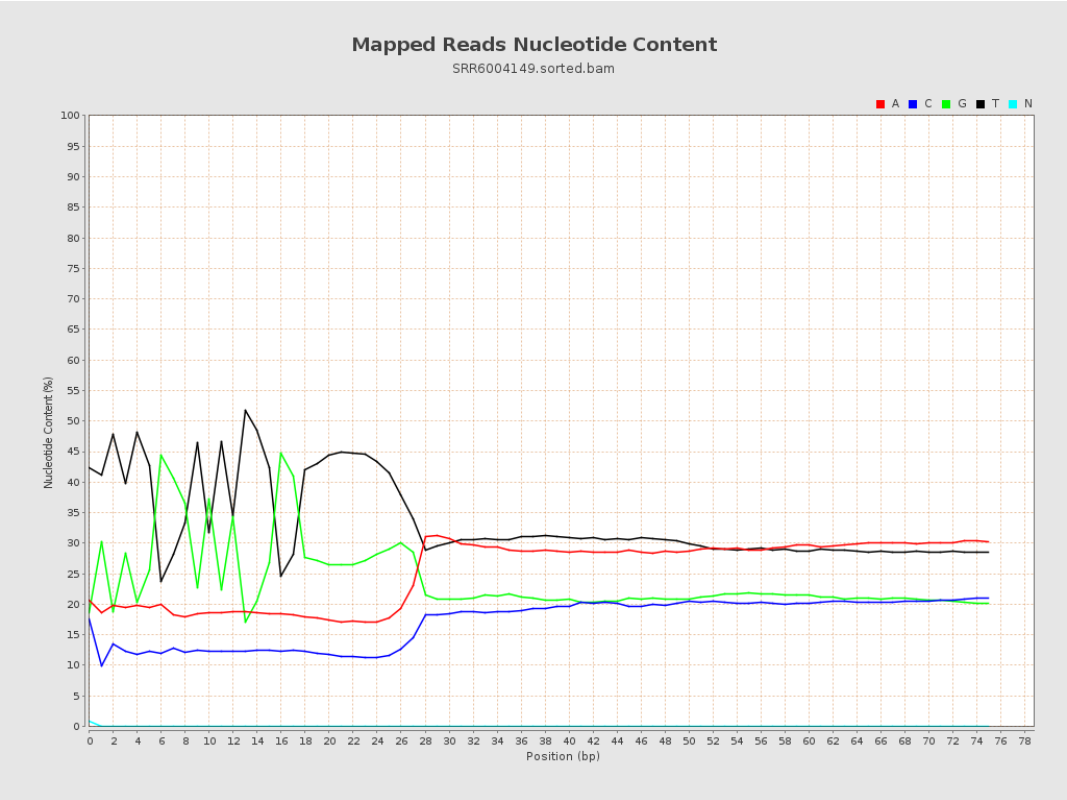
# 6. Results : Genome Fraction Coverage



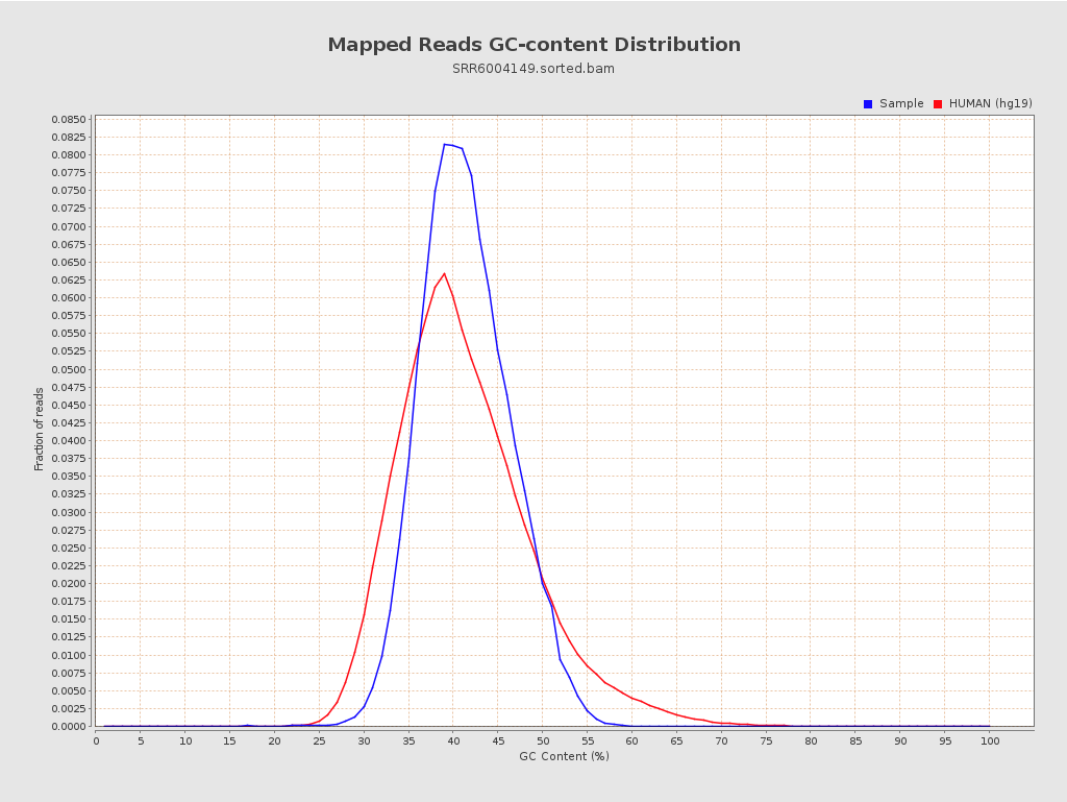
# 7. Results : Duplication Rate Histogram



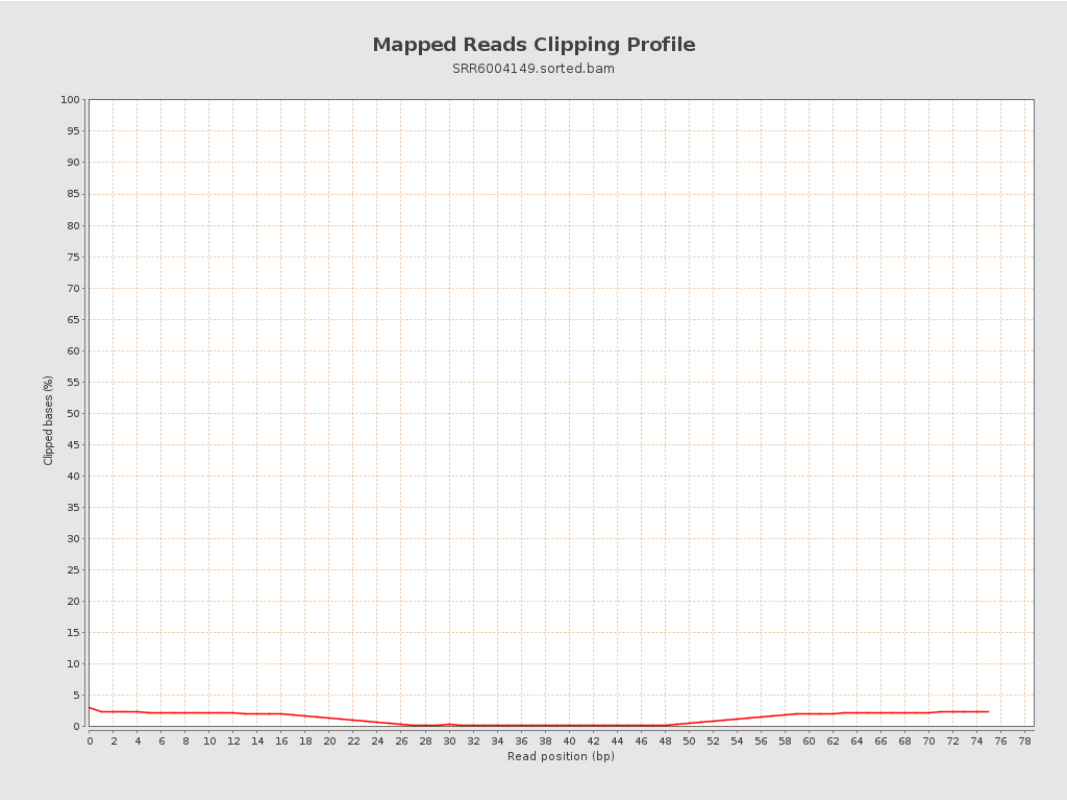
# 8. Results : Mapped Reads Nucleotide Content



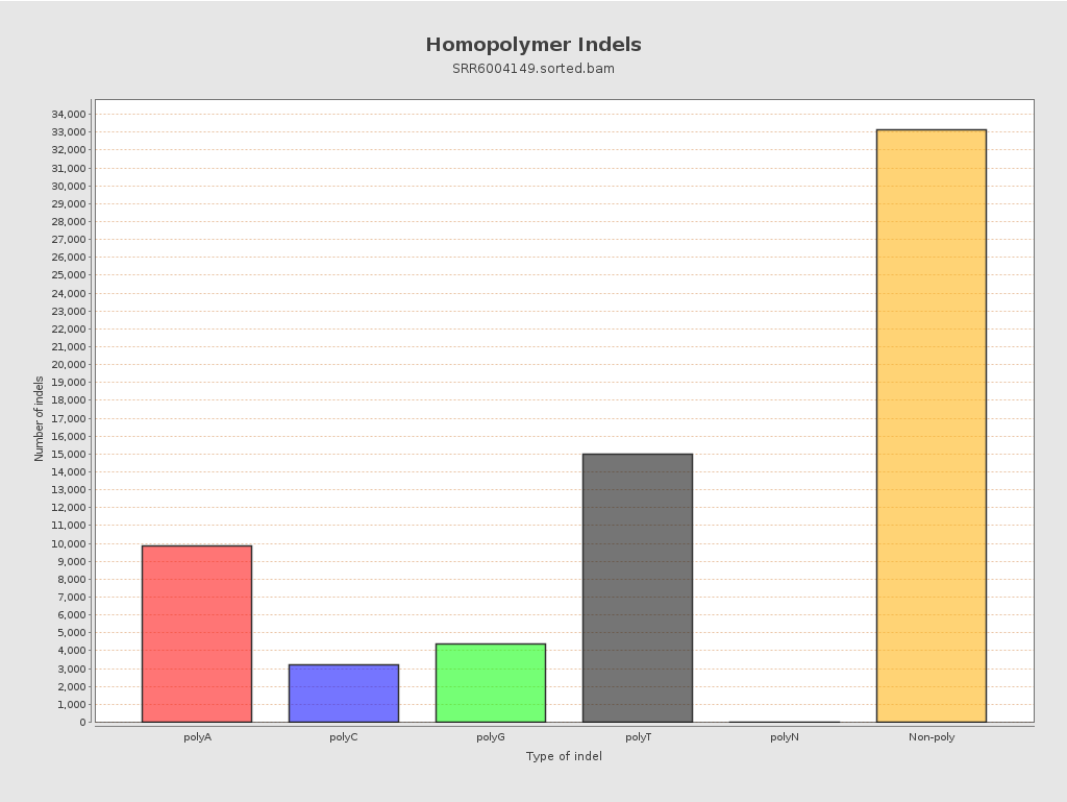
# 9. Results : Mapped Reads GC-content Distribution



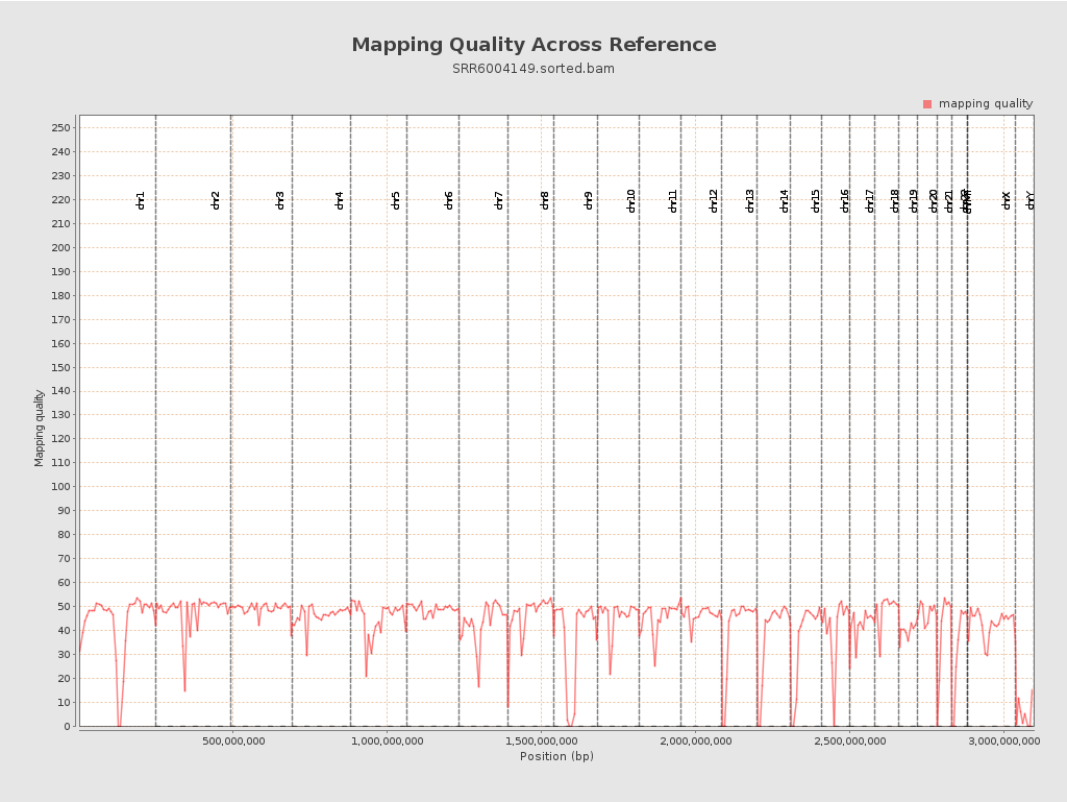
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram