# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/18 04:55:42*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240067.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_SRR6240067 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240067.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Wed Sep 18 04:55:42 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6240067.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,664,120 |
| Mapped reads | 1,427,339 / 85.77% |
| Unmapped reads | 236,781 / 14.23% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 10,480 / 0.63% |
| Read min/max/mean length | 30 / 76 / 76.22 |
| Duplicated reads (estimated) | 155,304 / 9.33% |
| Duplication rate | 8.17% |
| Clipped reads | 641,371 / 38.54% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 26,495,644 / 27.98% |
| Number/percentage of C's | 16,831,681 / 17.77% |
| Number/percentage of T's | 30,980,233 / 32.72% |
| Number/percentage of G's | 20,377,645 / 21.52% |
| Number/percentage of N's | 8,548 / 0.01% |
| GC Percentage | 39.29% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0306 |
| | |

| | |
|---|---|
| Standard Deviation | 0.4934 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 46.51 |

## 2.5. Mismatches and indels

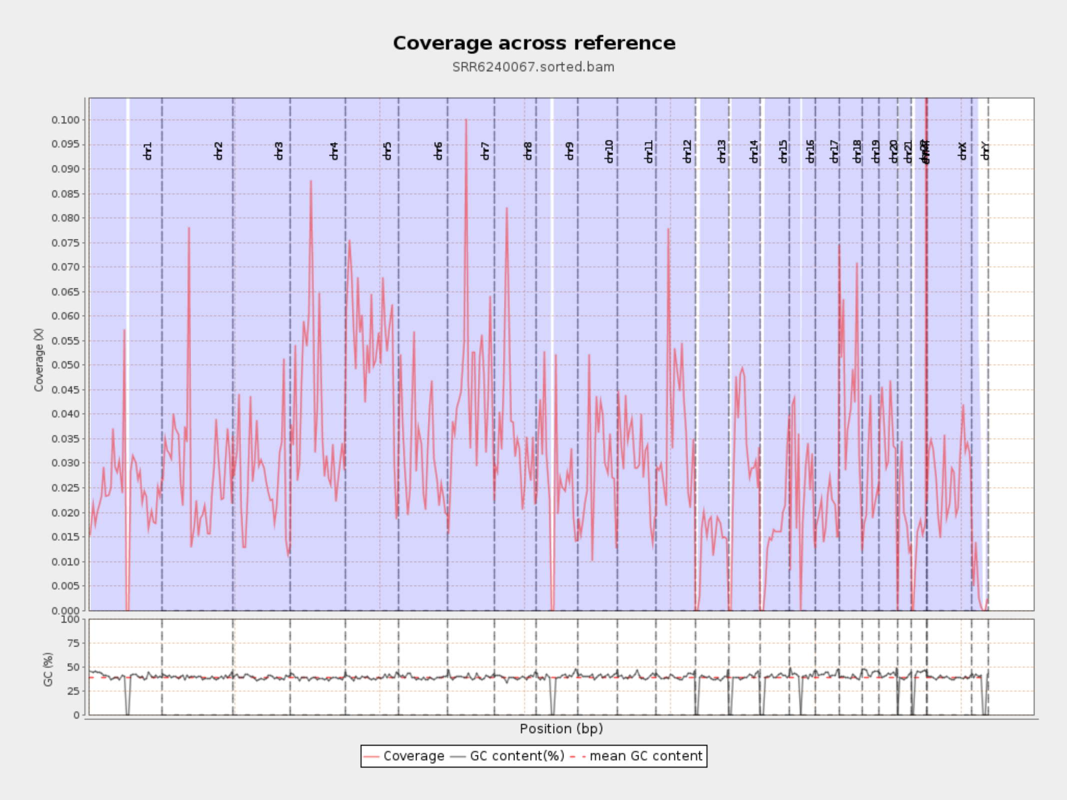
| | |
|---|---|
| General error rate | 0.83% |
| Mismatches | 769,746 |
| Insertions | 6,910 |
| Mapped reads with at least one insertion | 0.48% |
| Deletions | 20,208 |
| Mapped reads with at least one deletion | 1.4% |
| Homopolymer indels | 48.08% |

## 2.6. Chromosome stats

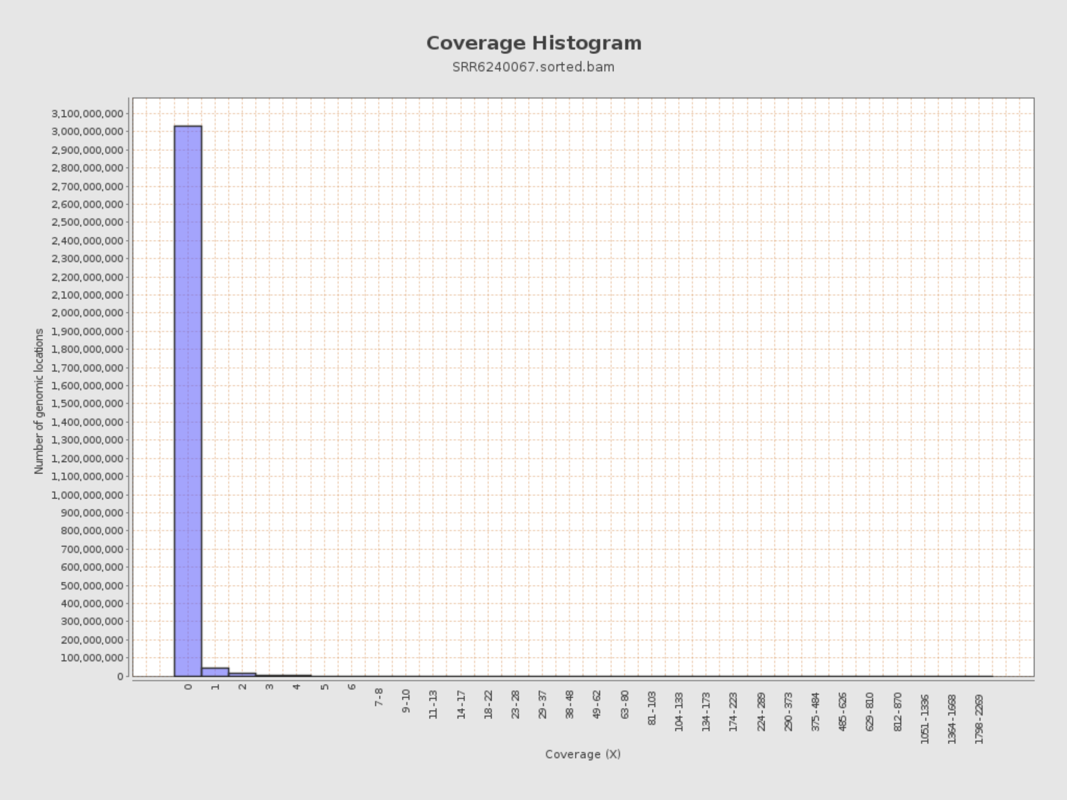
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5950182 | 0.0239 | 0.7159 |
| chr2 | 243199373 | 6986447 | 0.0287 | 0.4588 |
| chr3 | 198022430 | 5378571 | 0.0272 | 0.2263 |
| chr4 | 191154276 | 7762599 | 0.0406 | 0.2897 |
| chr5 | 180915260 | 9836605 | 0.0544 | 0.3217 |
| chr6 | 171115067 | 5467118 | 0.0319 | 0.3251 |
| chr7 | 159138663 | 7232461 | 0.0454 | 0.7126 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 5326359 | 0.0364 | 1.3272 |
| chr9 | 141213431 | 3802307 | 0.0269 | 0.4192 |
| chr10 | 135534747 | 3909654 | 0.0288 | 0.3785 |
| chr11 | 135006516 | 4184596 | 0.031 | 0.3342 |
| chr12 | 133851895 | 5090419 | 0.038 | 0.2858 |
| chr13 | 115169878 | 1561876 | 0.0136 | 0.1603 |
| chr14 | 107349540 | 3358924 | 0.0313 | 0.2731 |
| chr15 | 102531392 | 1562071 | 0.0152 | 0.1735 |
| chr16 | 90354753 | 2297782 | 0.0254 | 0.2359 |
| chr17 | 81195210 | 1601795 | 0.0197 | 0.2021 |
| chr18 | 78077248 | 3585032 | 0.0459 | 0.7428 |
| chr19 | 59128983 | 1478293 | 0.025 | 0.543 |
| chr20 | 63025520 | 2250564 | 0.0357 | 0.2754 |
| chr21 | 48129895 | 920271 | 0.0191 | 0.2085 |
| chr22 | 51304566 | 623658 | 0.0122 | 0.1433 |
| chrMT | 16571 | 12411 | 0.749 | 1.2068 |
| chrX | 155270560 | 4316186 | 0.0278 | 0.2627 |
| chrY | 59373566 | 232001 | 0.0039 | 0.1162 |

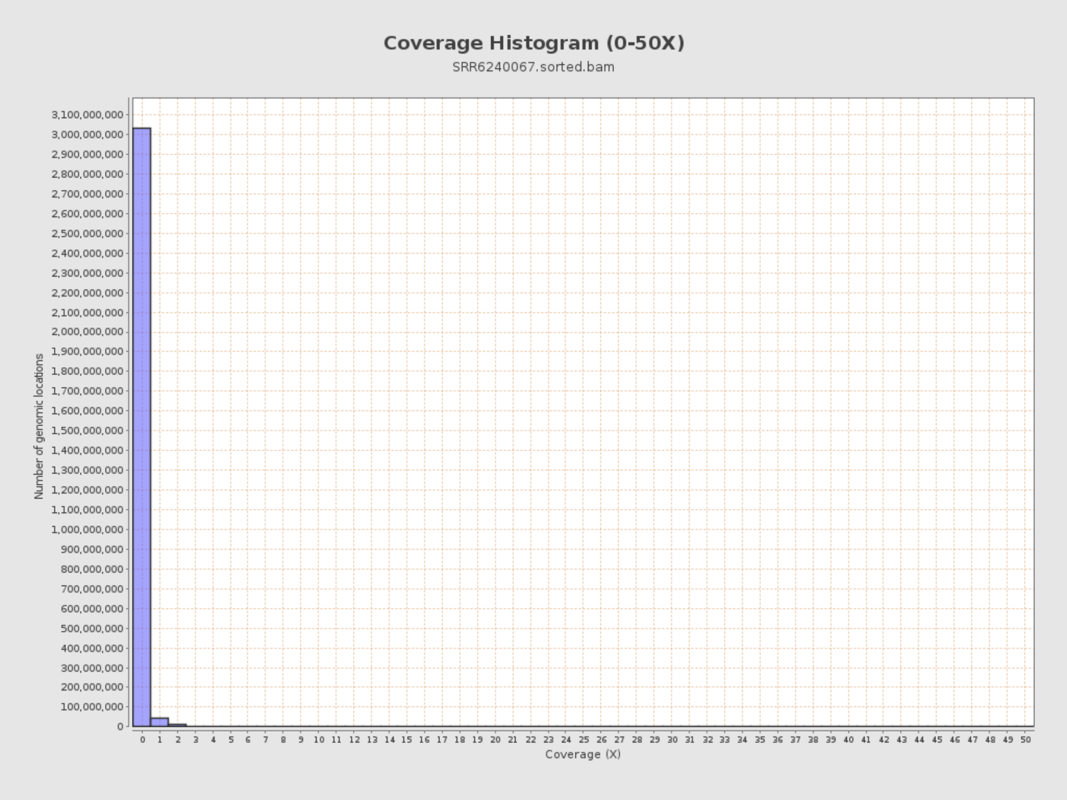
# 3. Results : Coverage across reference



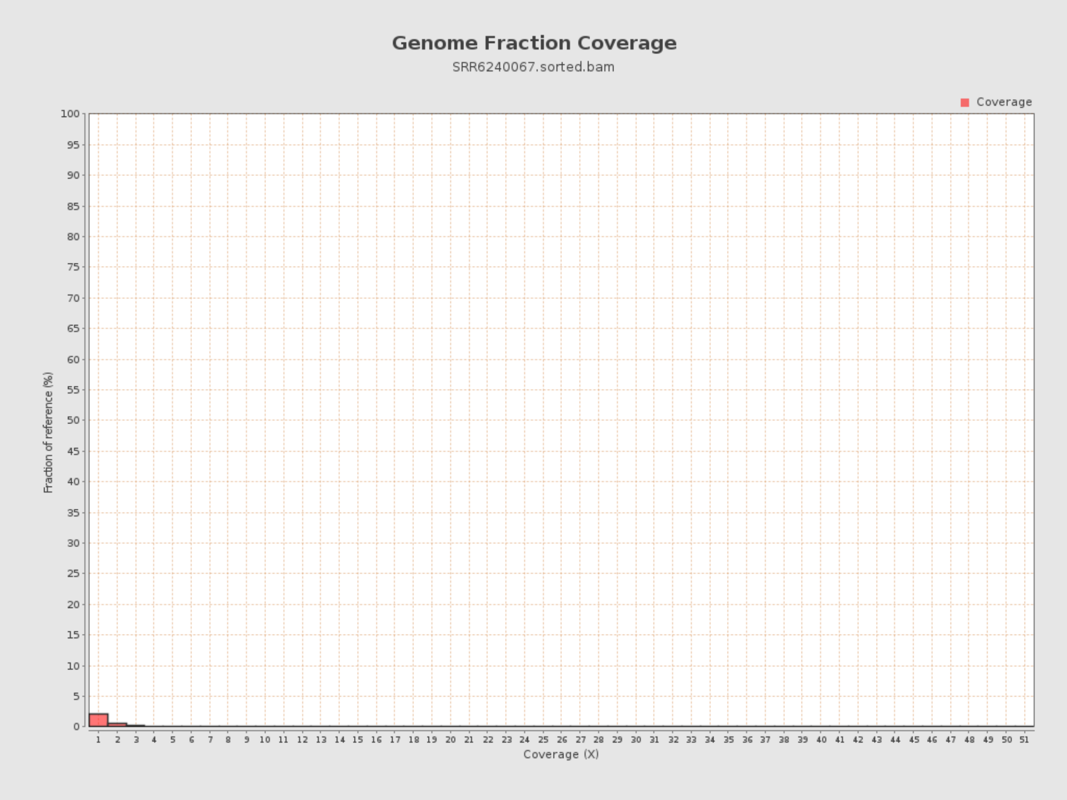
# 4. Results : Coverage Histogram



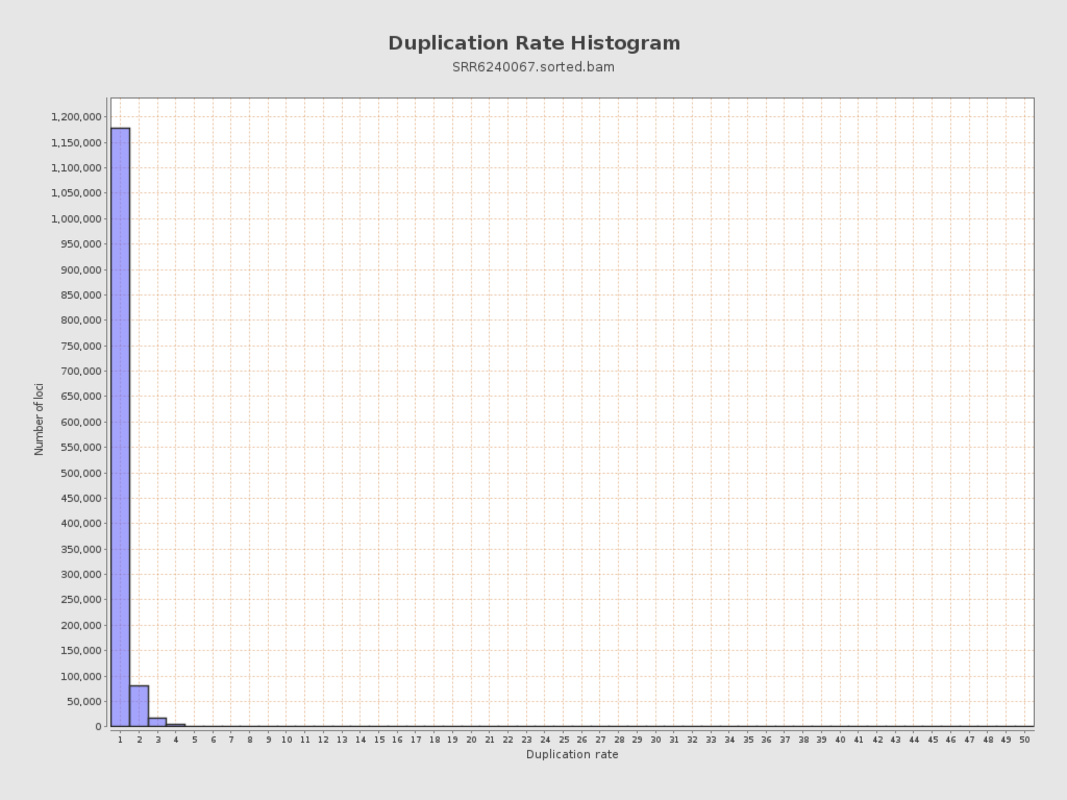
# 5. Results : Coverage Histogram (0-50X)



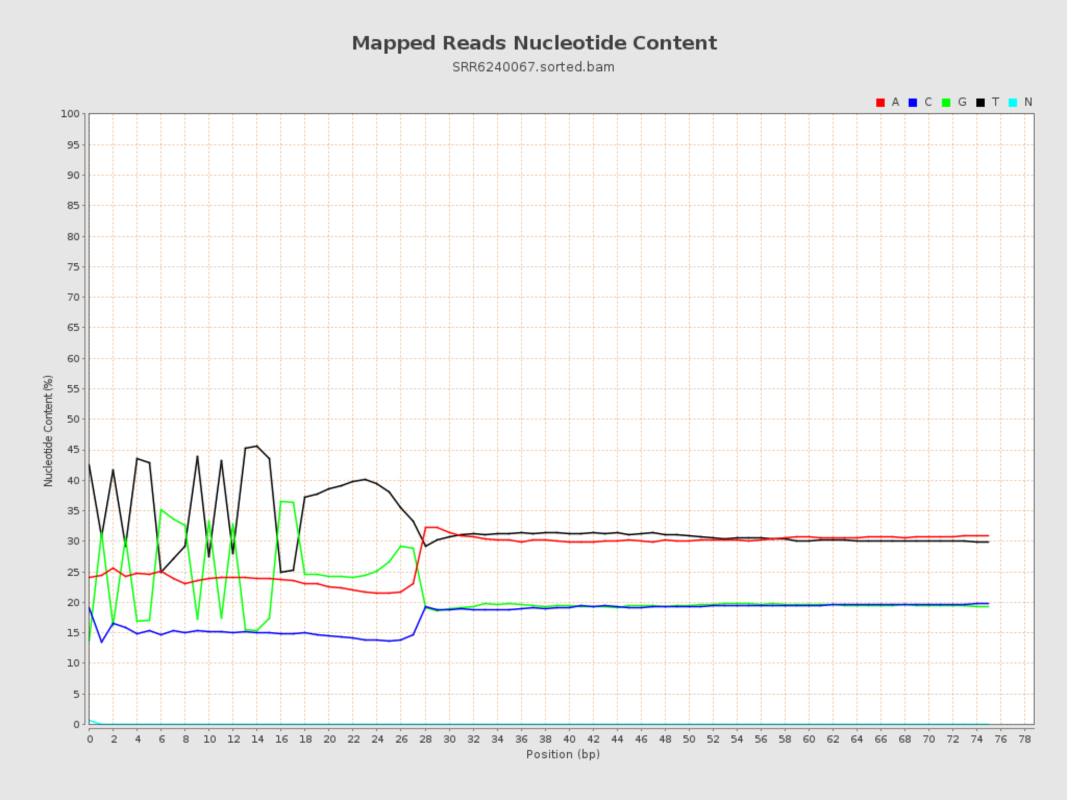
# 6. Results : Genome Fraction Coverage



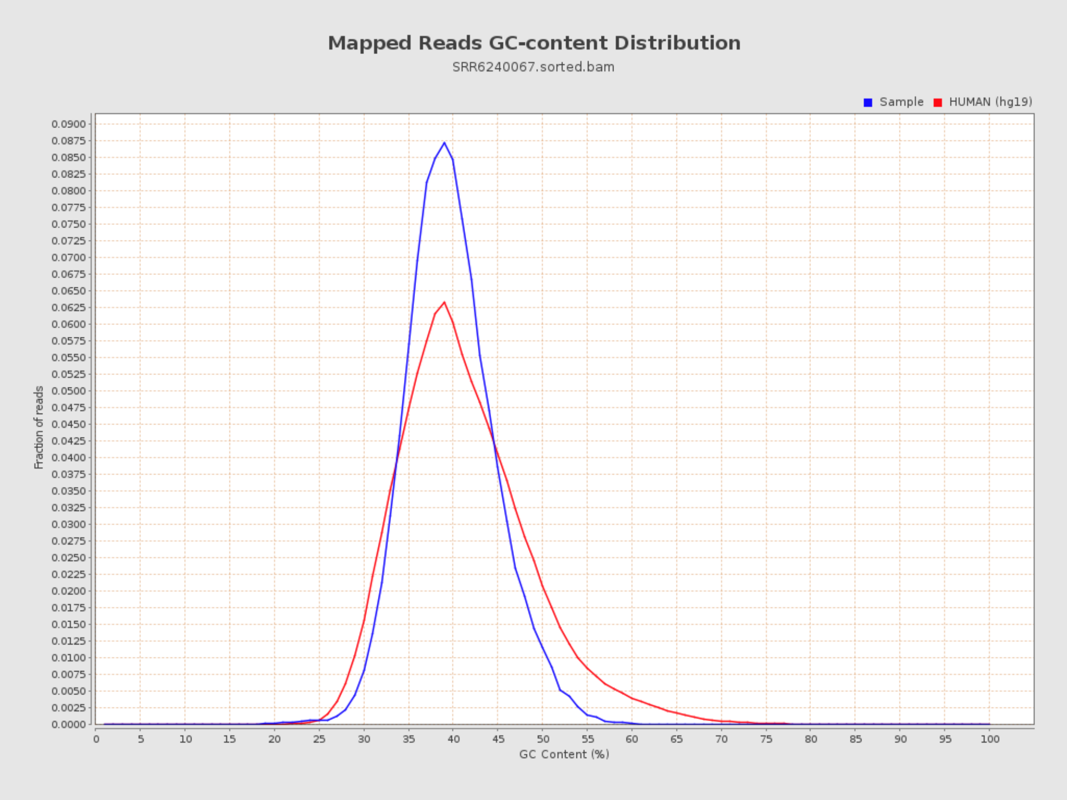
# 7. Results : Duplication Rate Histogram



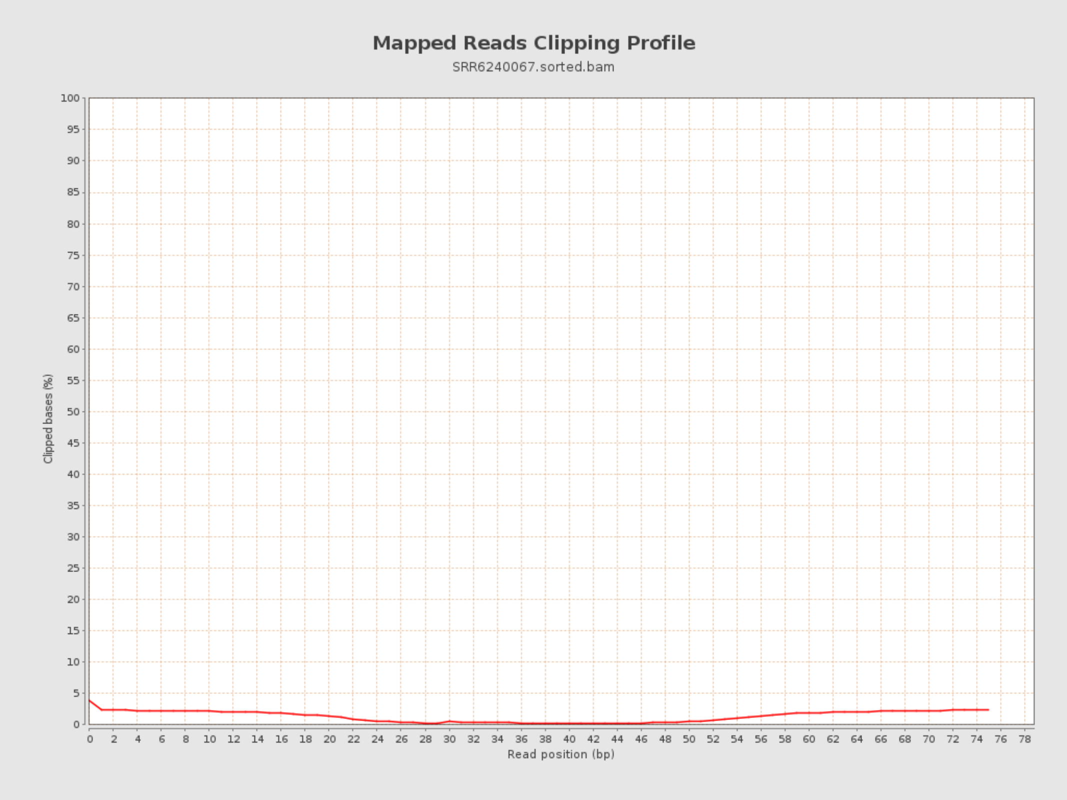
# 8. Results : Mapped Reads Nucleotide Content



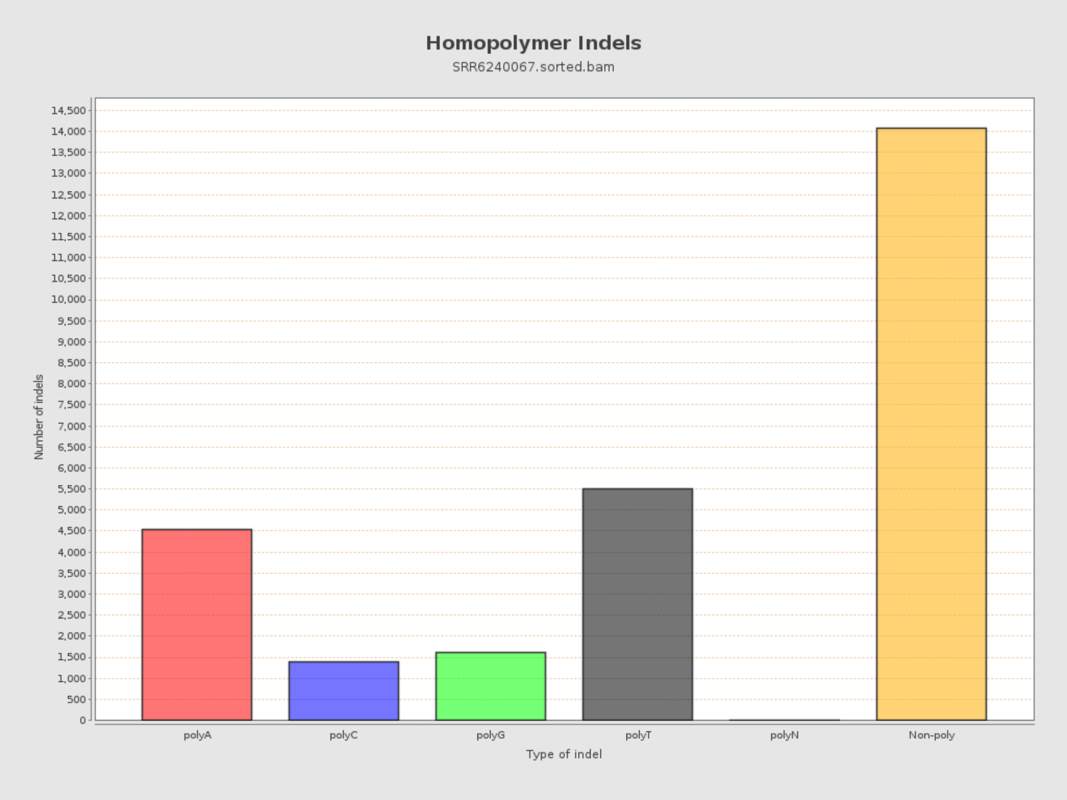
# 9. Results : Mapped Reads GC-content Distribution



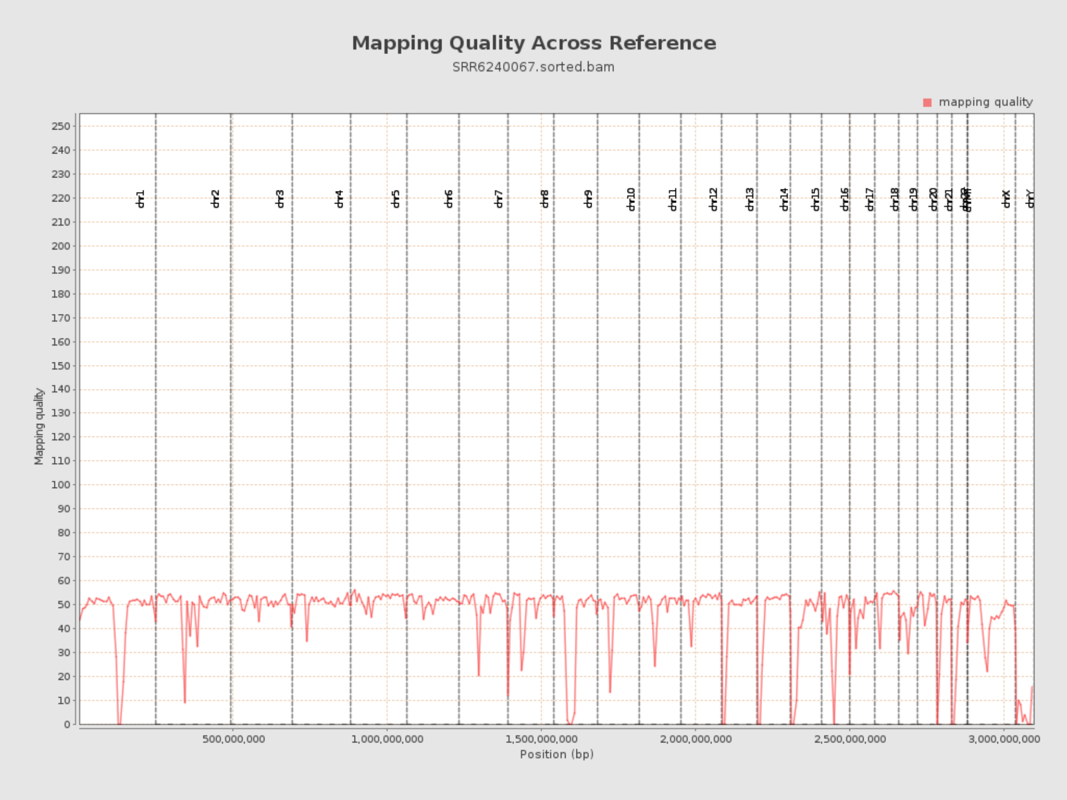
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram