# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/14 03:46:09*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004133.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_SRR6004133 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004133.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 14 03:46:09 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6004133.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,804,591 |
| Mapped reads | 1,489,018 / 82.51% |
| Unmapped reads | 315,573 / 17.49% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 19,901 / 1.1% |
| Read min/max/mean length | 30 / 76 / 76.39 |
| Duplicated reads (estimated) | 94,933 / 5.26% |
| Duplication rate | 5.39% |
| Clipped reads | 730,457 / 40.48% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 27,467,616 / 27.96% |
| Number/percentage of C's | 18,220,241 / 18.55% |
| Number/percentage of T's | 30,969,783 / 31.53% |
| Number/percentage of G's | 21,559,094 / 21.95% |
| Number/percentage of N's | 7,081 / 0.01% |
| GC Percentage | 40.5% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0317 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2679 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 39.9 |

## 2.5. Mismatches and indels

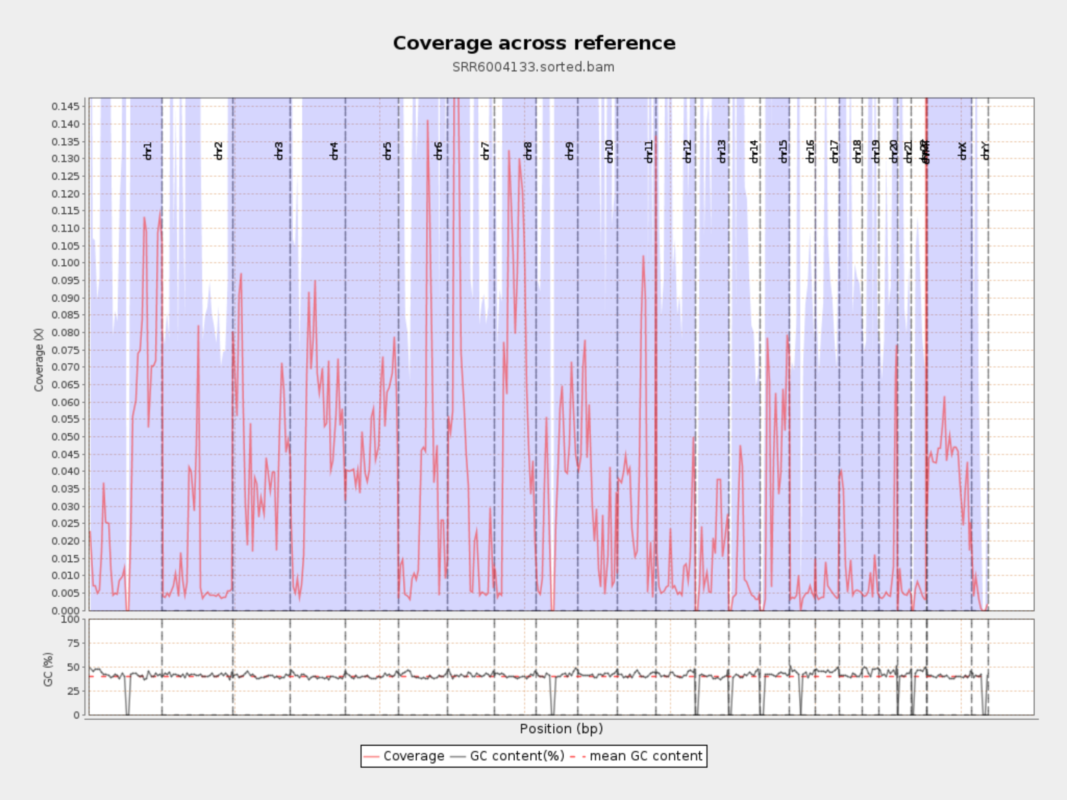
| | |
|---|---|
| General error rate | 0.88% |
| Mismatches | 856,966 |
| Insertions | 6,938 |
| Mapped reads with at least one insertion | 0.46% |
| Deletions | 22,743 |
| Mapped reads with at least one deletion | 1.51% |
| Homopolymer indels | 46.32% |

## 2.6. Chromosome stats

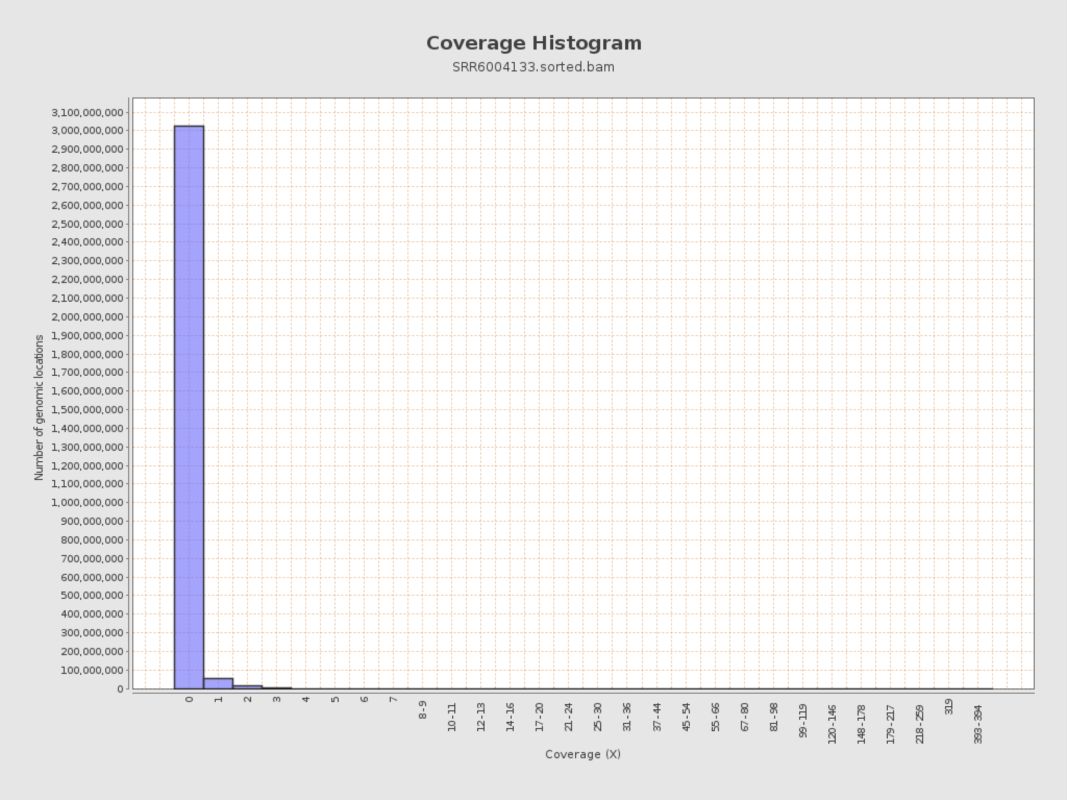
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 10155674 | 0.0407 | 0.294 |
| chr2 | 243199373 | 3010924 | 0.0124 | 0.2497 |
| chr3 | 198022430 | 9267147 | 0.0468 | 0.2776 |
| chr4 | 191154276 | 9372661 | 0.049 | 0.2889 |
| chr5 | 180915260 | 9213723 | 0.0509 | 0.2875 |
| chr6 | 171115067 | 5498887 | 0.0321 | 0.2391 |
| chr7 | 159138663 | 7599259 | 0.0478 | 0.3985 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 9707791 | 0.0663 | 0.417 |
| chr9 | 141213431 | 4847375 | 0.0343 | 0.2733 |
| chr10 | 135534747 | 4299010 | 0.0317 | 0.2802 |
| chr11 | 135006516 | 5227000 | 0.0387 | 0.2627 |
| chr12 | 133851895 | 1641962 | 0.0123 | 0.1435 |
| chr13 | 115169878 | 1864056 | 0.0162 | 0.1639 |
| chr14 | 107349540 | 1278169 | 0.0119 | 0.1508 |
| chr15 | 102531392 | 4312626 | 0.0421 | 0.263 |
| chr16 | 90354753 | 418480 | 0.0046 | 0.1057 |
| chr17 | 81195210 | 443463 | 0.0055 | 0.0923 |
| chr18 | 78077248 | 1161124 | 0.0149 | 0.3323 |
| chr19 | 59128983 | 410332 | 0.0069 | 0.1782 |
| chr20 | 63025520 | 1053013 | 0.0167 | 0.1751 |
| chr21 | 48129895 | 275340 | 0.0057 | 0.1113 |
| chr22 | 51304566 | 221745 | 0.0043 | 0.0778 |
| chrMT | 16571 | 228406 | 13.7835 | 10.3397 |
| chrX | 155270560 | 6536293 | 0.0421 | 0.2739 |
| chrY | 59373566 | 216371 | 0.0036 | 0.0852 |

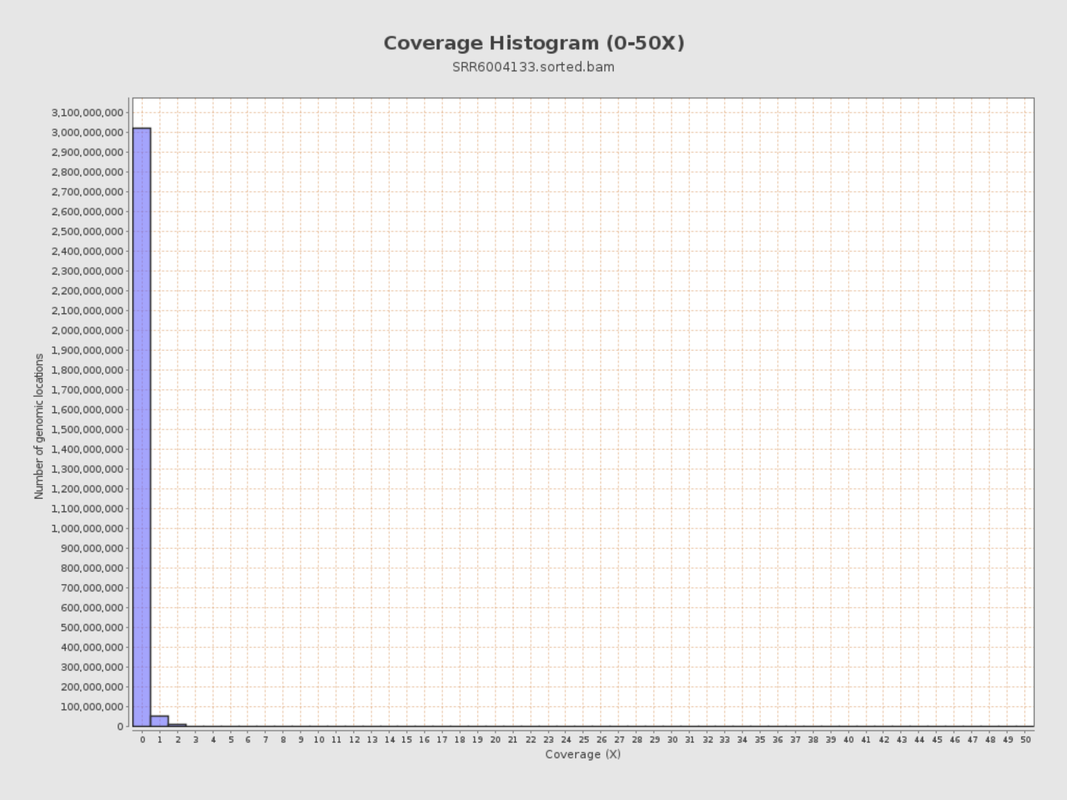
# 3. Results : Coverage across reference



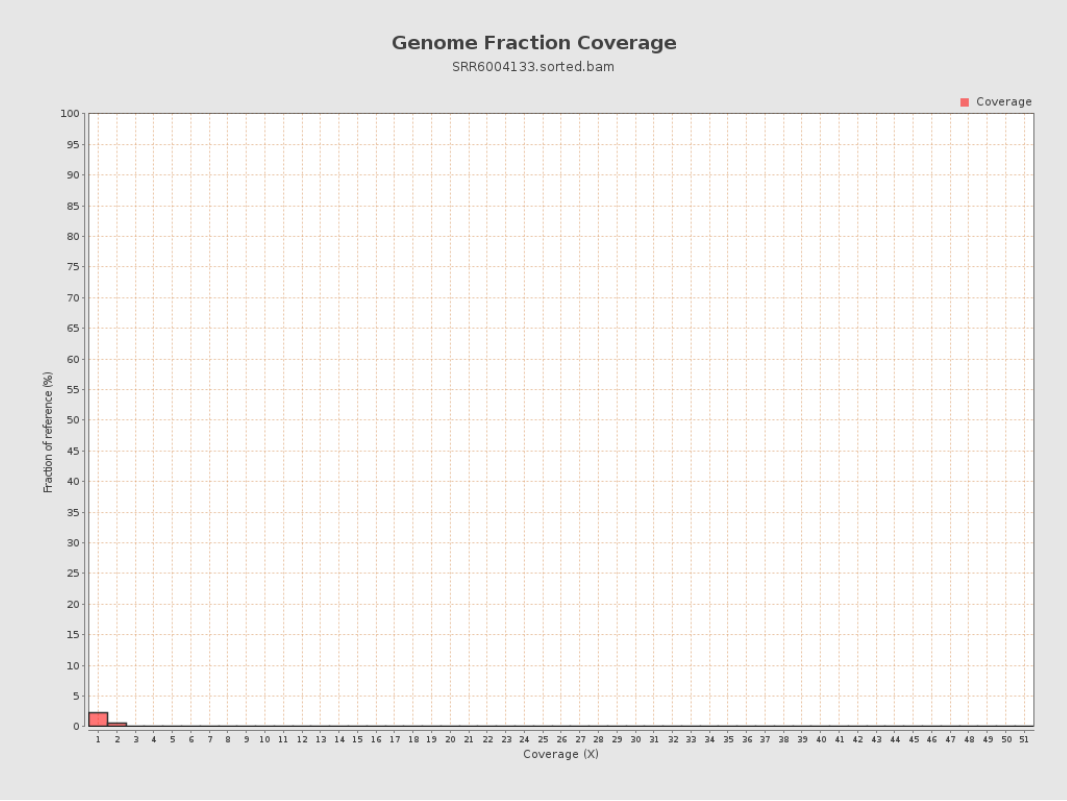
# 4. Results : Coverage Histogram



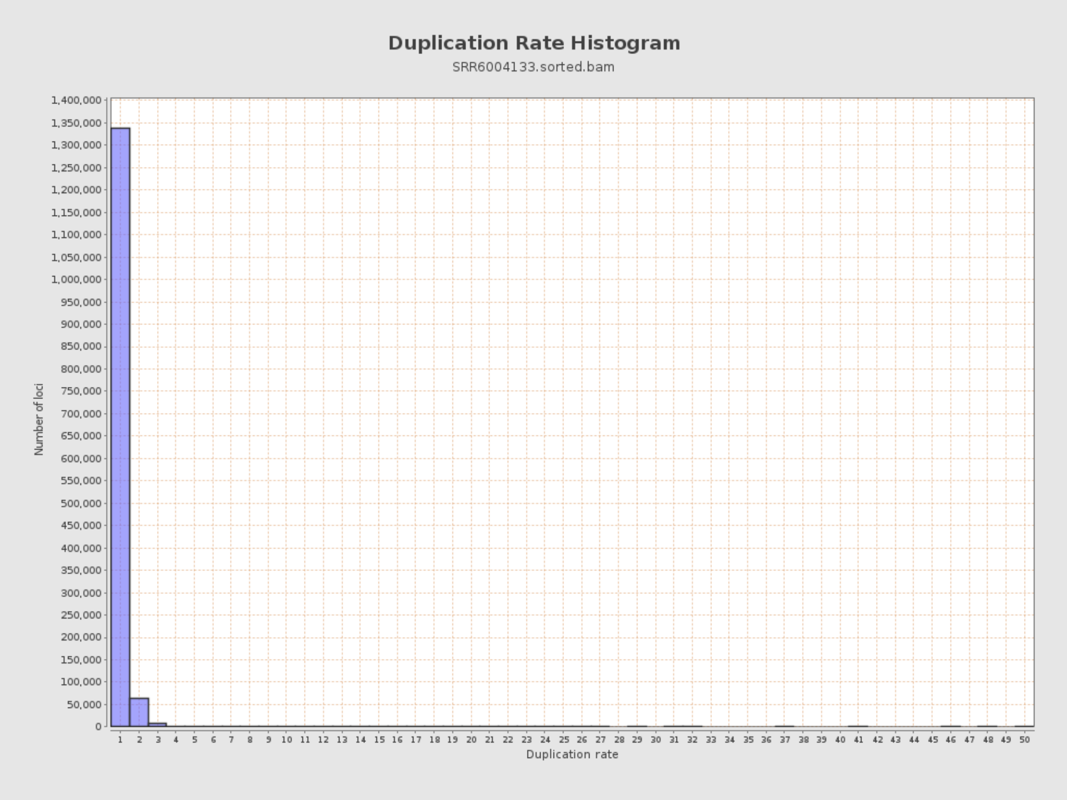
# 5. Results : Coverage Histogram (0-50X)



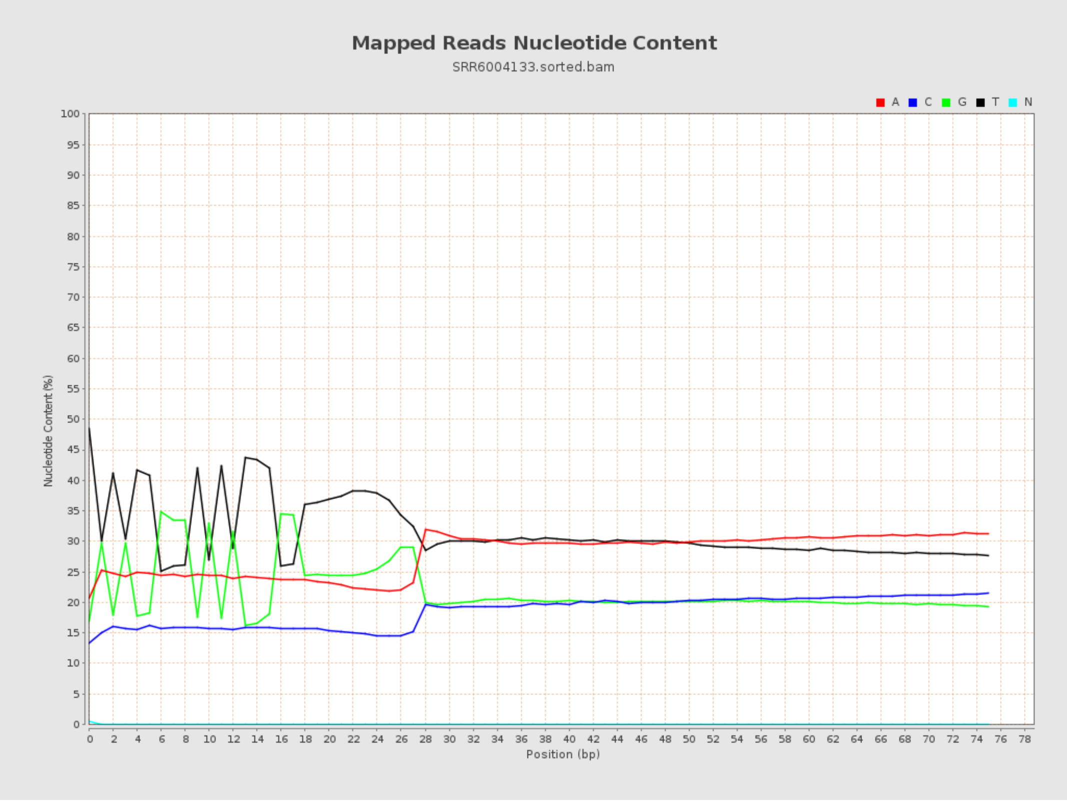
# 6. Results : Genome Fraction Coverage



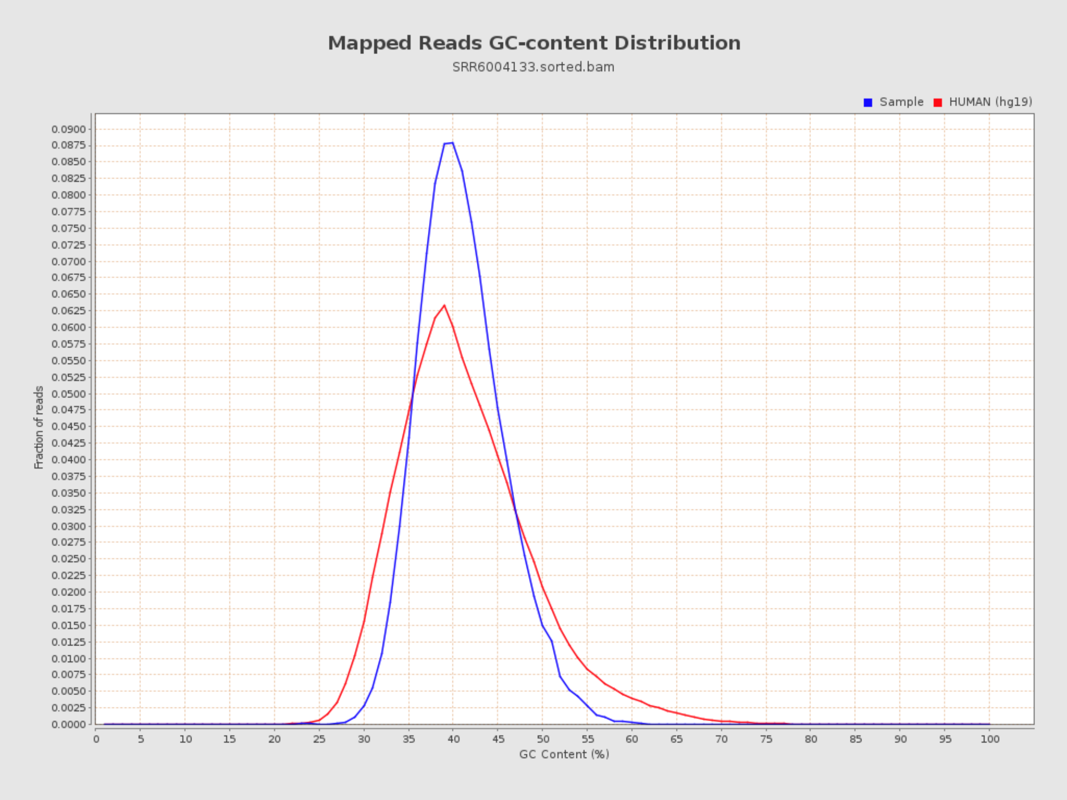
# 7. Results : Duplication Rate Histogram



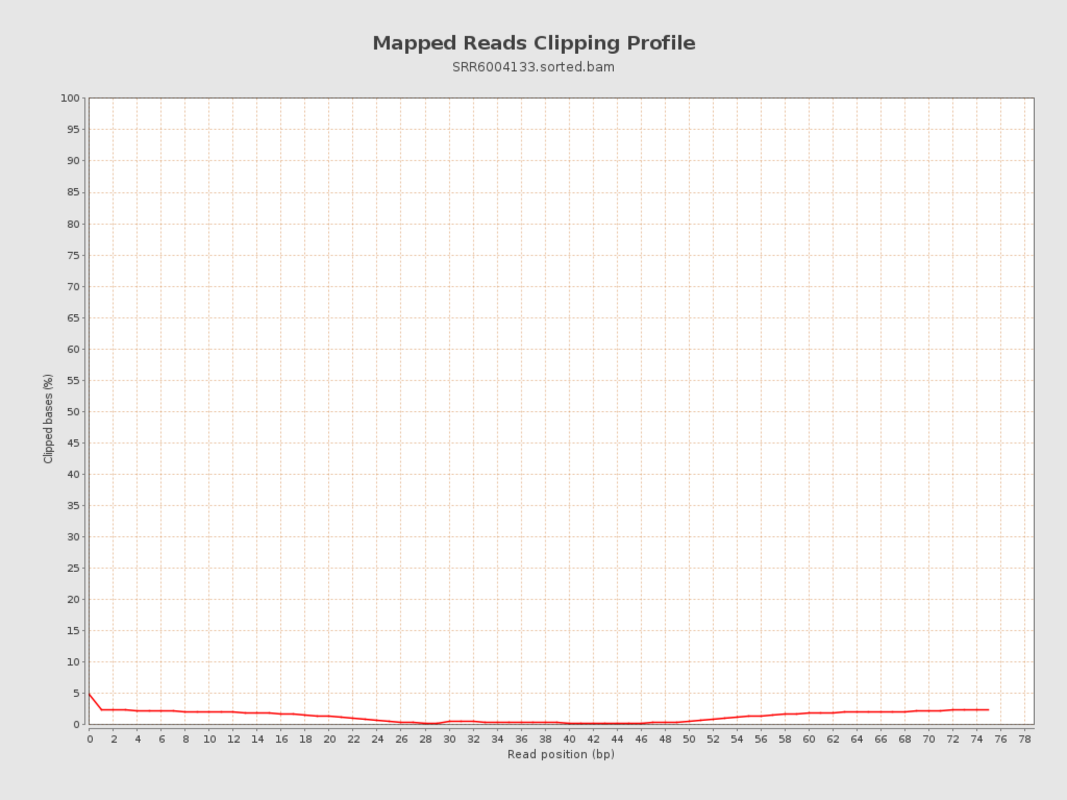
# 8. Results : Mapped Reads Nucleotide Content



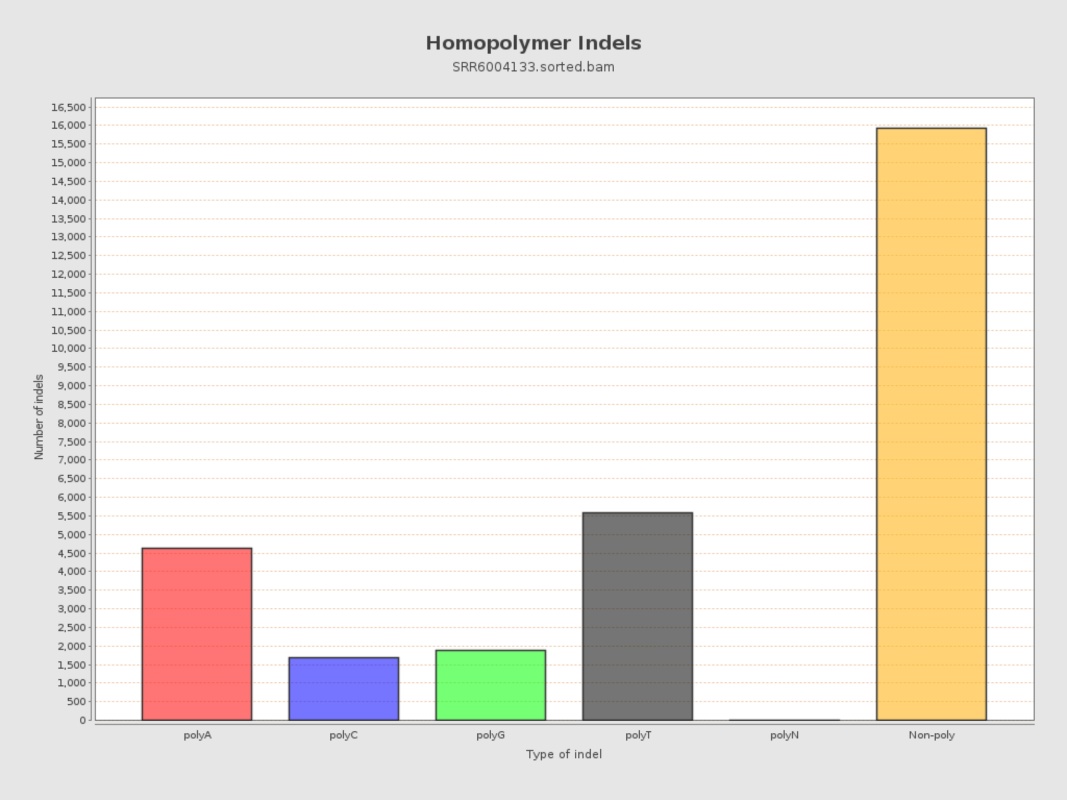
# 9. Results : Mapped Reads GC-content Distribution



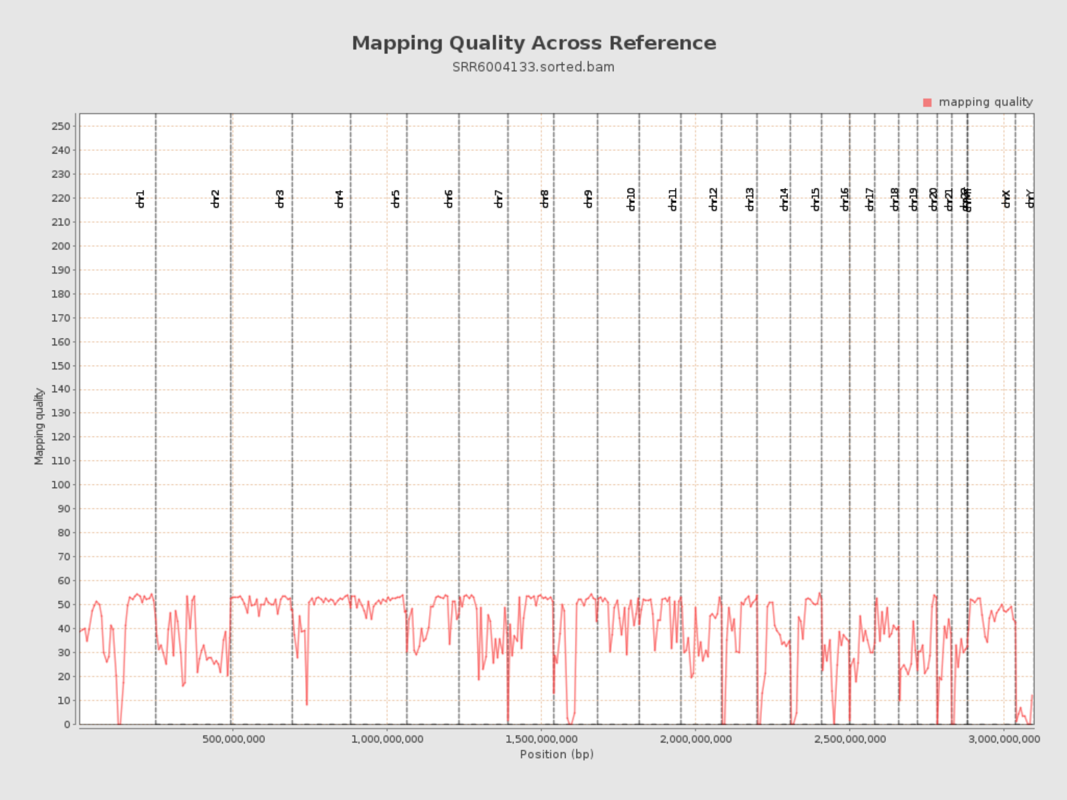
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram