# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/14 19:44:26*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013286.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_SRR6013286 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013286.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sat Sep 14 19:44:25 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6013286.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,648,915 |
| Mapped reads | 1,295,209 / 78.55% |
| Unmapped reads | 353,706 / 21.45% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 12,851 / 0.78% |
| Read min/max/mean length | 30 / 76 / 76.27 |
| Duplicated reads (estimated) | 199,527 / 12.1% |
| Duplication rate | 11.52% |
| Clipped reads | 693,736 / 42.07% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 22,787,525 / 27.29% |
| Number/percentage of C's | 15,039,233 / 18.01% |
| Number/percentage of T's | 27,035,361 / 32.37% |
| Number/percentage of G's | 18,646,675 / 22.33% |
| Number/percentage of N's | 1,100 / 0% |
| GC Percentage | 40.34% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.027 |
| | |

| | |
|---|---|
| Standard Deviation | 0.3432 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.77 |

## 2.5. Mismatches and indels

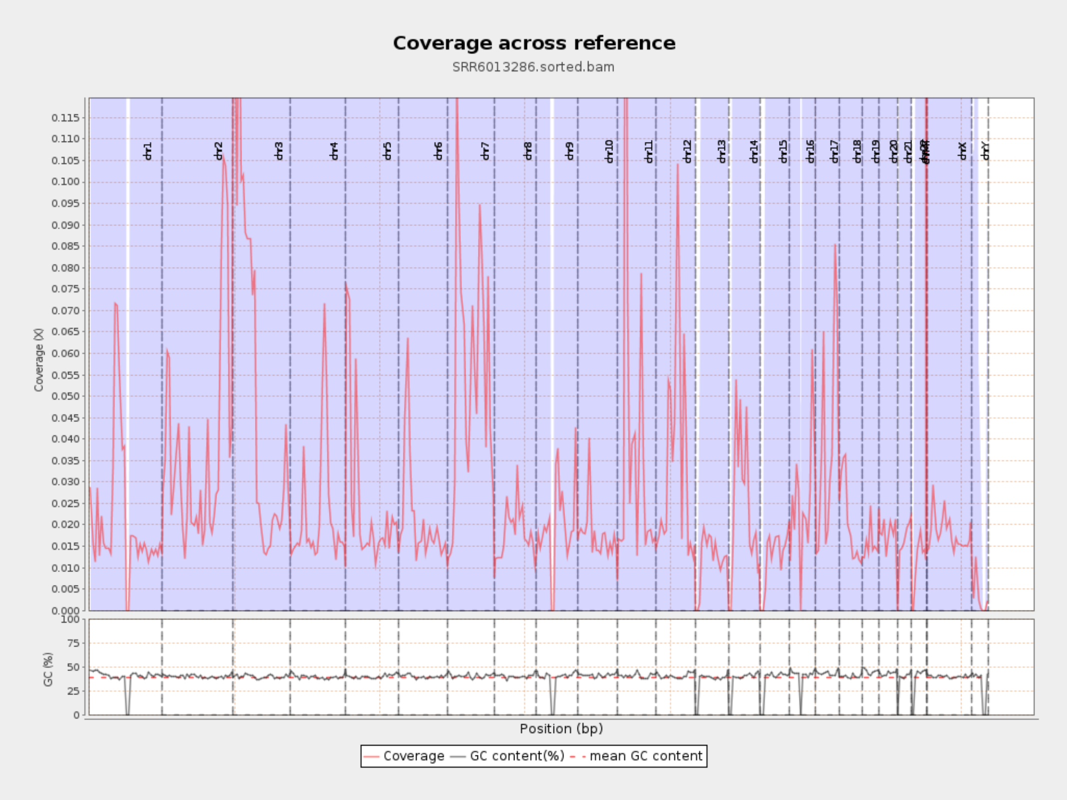
| | |
|---|---|
| General error rate | 0.8% |
| Mismatches | 651,150 |
| Insertions | 6,419 |
| Mapped reads with at least one insertion | 0.49% |
| Deletions | 23,017 |
| Mapped reads with at least one deletion | 1.76% |
| Homopolymer indels | 46.76% |

## 2.6. Chromosome stats

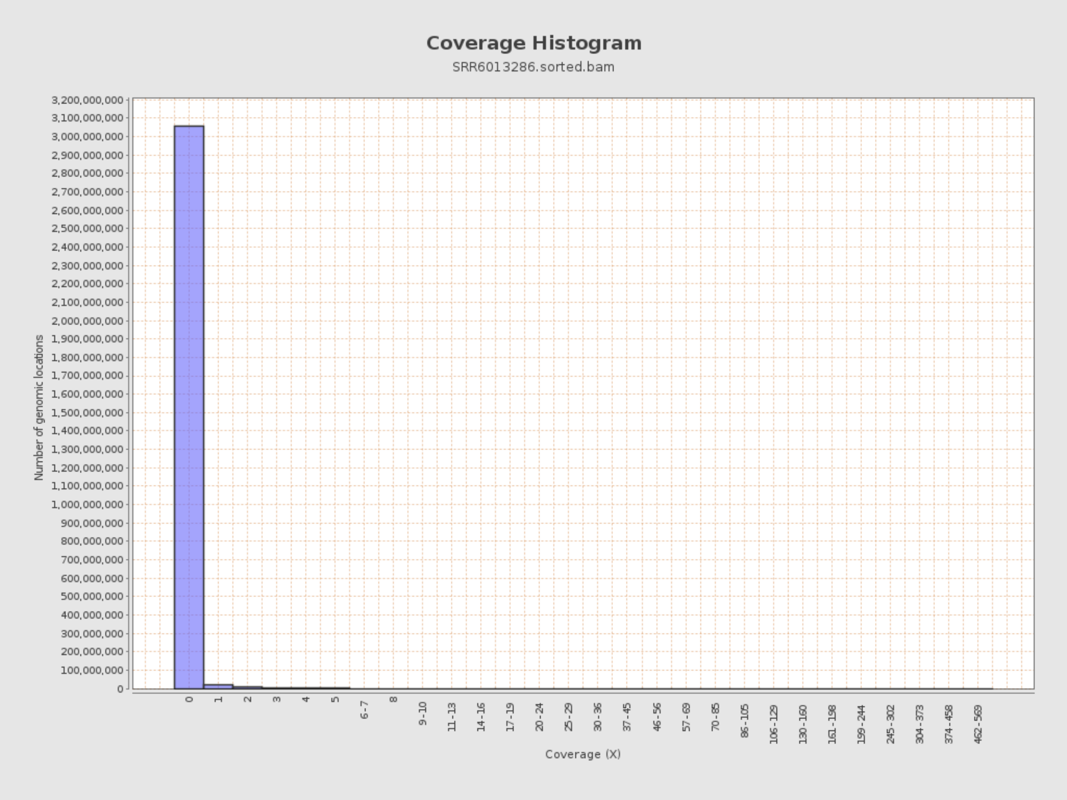
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 5356023 | 0.0215 | 0.4573 |
| chr2 | 243199373 | 9165921 | 0.0377 | 0.4424 |
| chr3 | 198022430 | 10939729 | 0.0552 | 0.4157 |
| chr4 | 191154276 | 4317547 | 0.0226 | 0.2859 |
| chr5 | 180915260 | 4526464 | 0.025 | 0.2766 |
| chr6 | 171115067 | 3612565 | 0.0211 | 0.2758 |
| chr7 | 159138663 | 8921922 | 0.0561 | 0.4394 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 2662747 | 0.0182 | 0.4072 |
| chr9 | 141213431 | 2808481 | 0.0199 | 0.2942 |
| chr10 | 135534747 | 2399399 | 0.0177 | 0.2919 |
| chr11 | 135006516 | 5355112 | 0.0397 | 0.4028 |
| chr12 | 133851895 | 4743992 | 0.0354 | 0.337 |
| chr13 | 115169878 | 1354679 | 0.0118 | 0.1913 |
| chr14 | 107349540 | 2582132 | 0.0241 | 0.2791 |
| chr15 | 102531392 | 1268127 | 0.0124 | 0.1956 |
| chr16 | 90354753 | 2372722 | 0.0263 | 0.2908 |
| chr17 | 81195210 | 3163710 | 0.039 | 0.3554 |
| chr18 | 78077248 | 1633901 | 0.0209 | 0.4139 |
| chr19 | 59128983 | 935084 | 0.0158 | 0.3204 |
| chr20 | 63025520 | 1126935 | 0.0179 | 0.2374 |
| chr21 | 48129895 | 759749 | 0.0158 | 0.2368 |
| chr22 | 51304566 | 555108 | 0.0108 | 0.1771 |
| chrMT | 16571 | 19638 | 1.1851 | 1.9393 |
| chrX | 155270560 | 2780033 | 0.0179 | 0.2413 |
| chrY | 59373566 | 187731 | 0.0032 | 0.1293 |

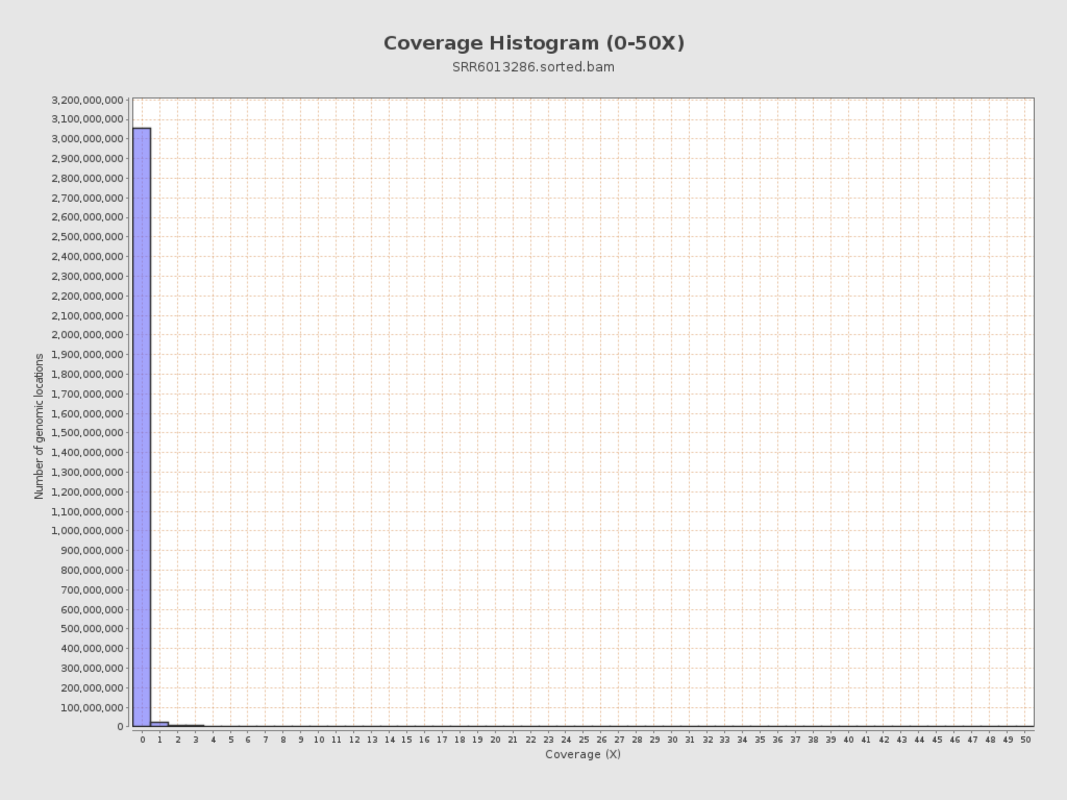
# 3. Results : Coverage across reference



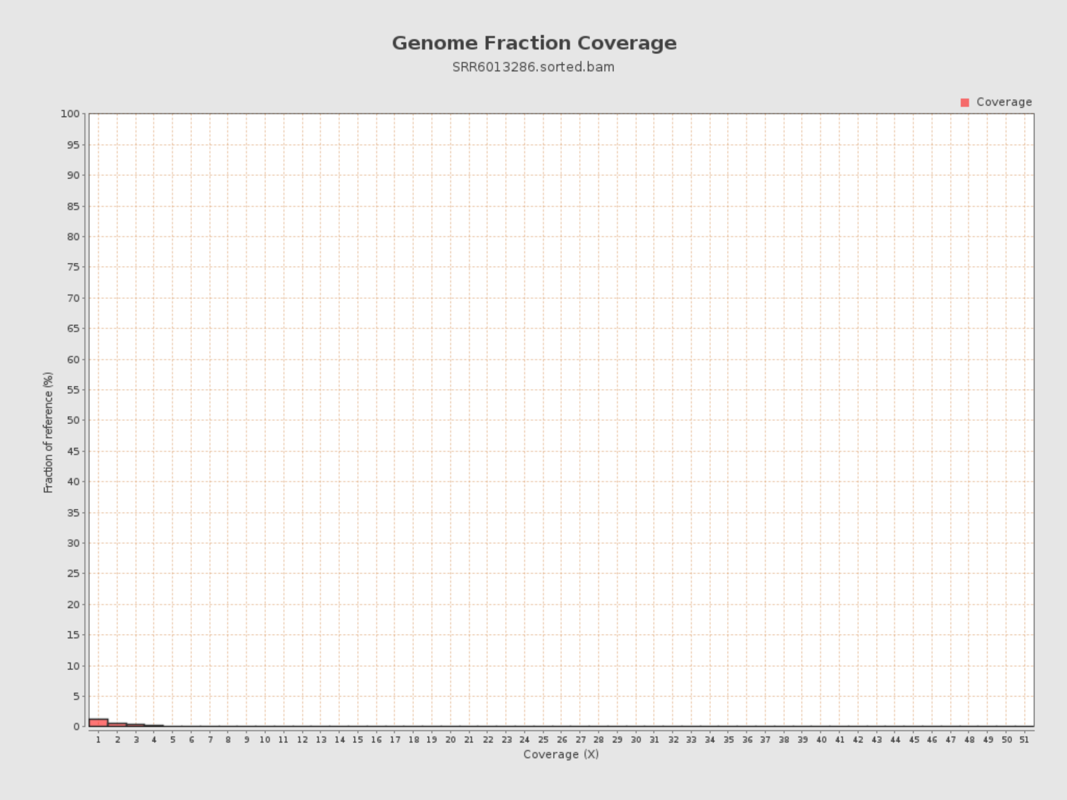
# 4. Results : Coverage Histogram



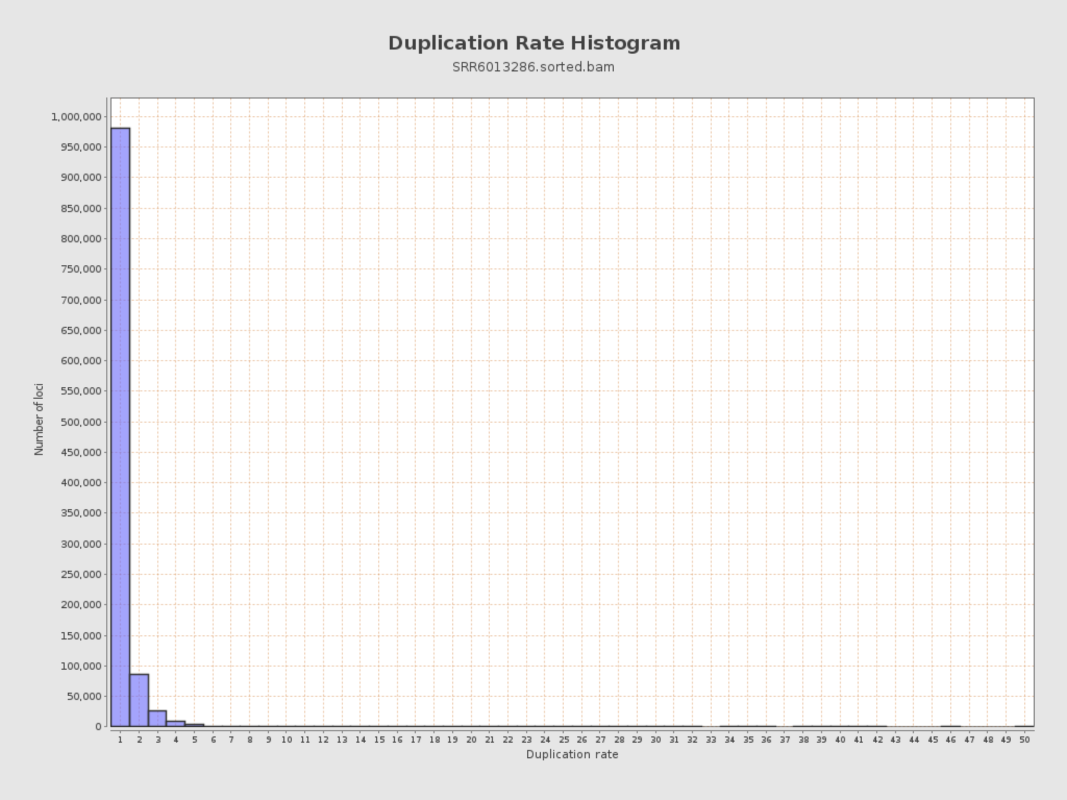
# 5. Results : Coverage Histogram (0-50X)



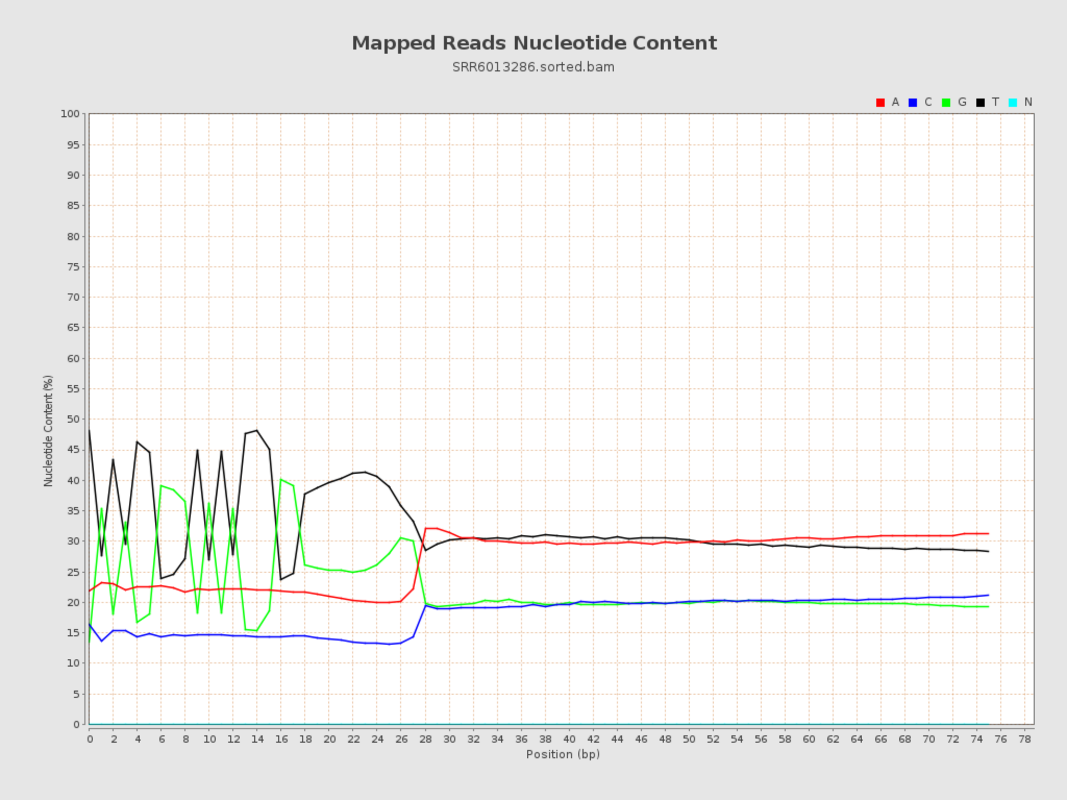
# 6. Results : Genome Fraction Coverage



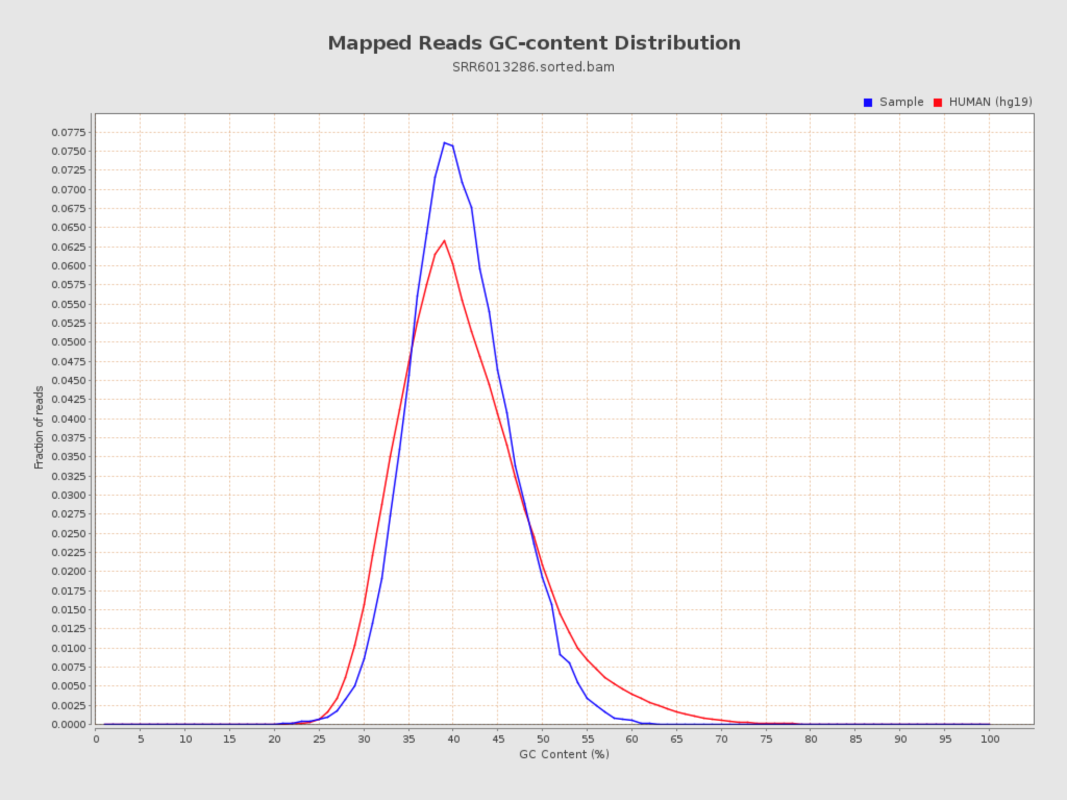
# 7. Results : Duplication Rate Histogram



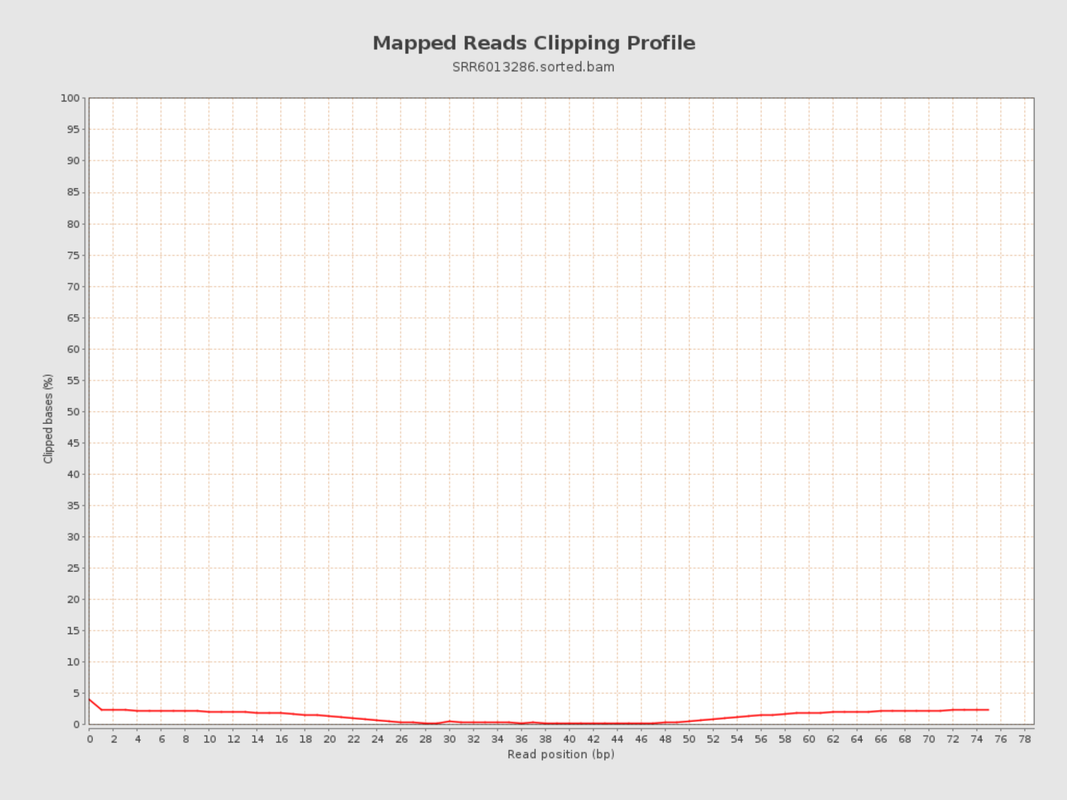
# 8. Results : Mapped Reads Nucleotide Content



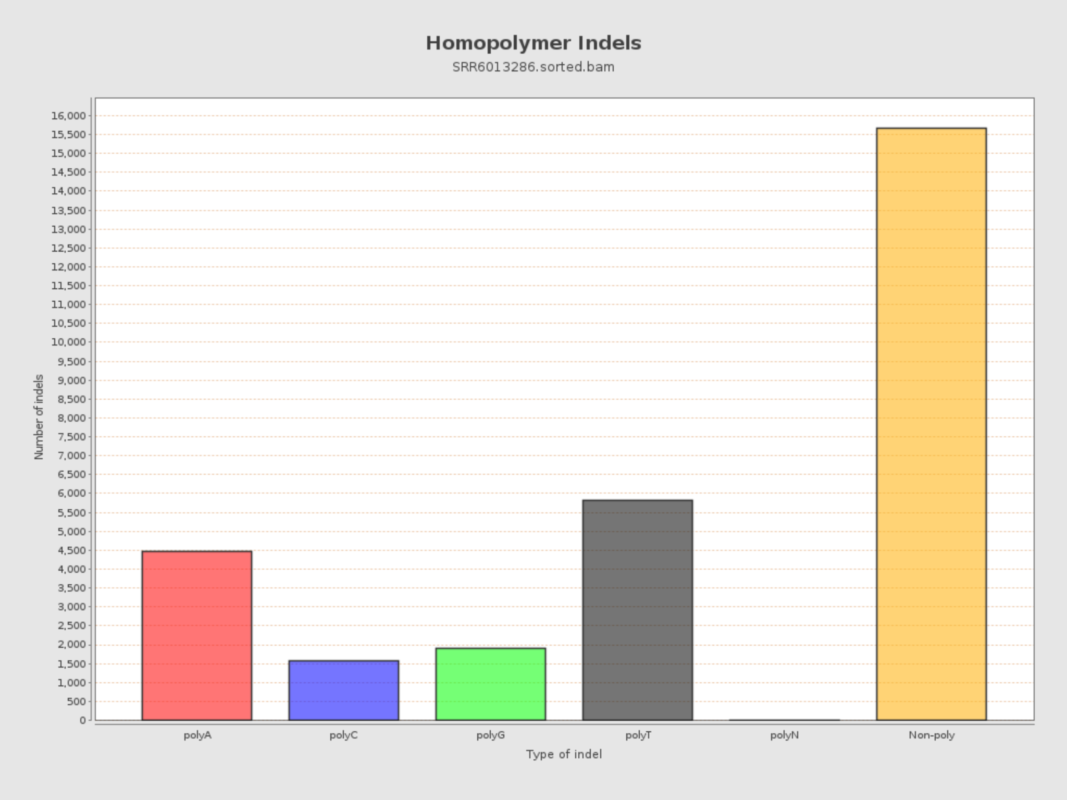
# 9. Results : Mapped Reads GC-content Distribution



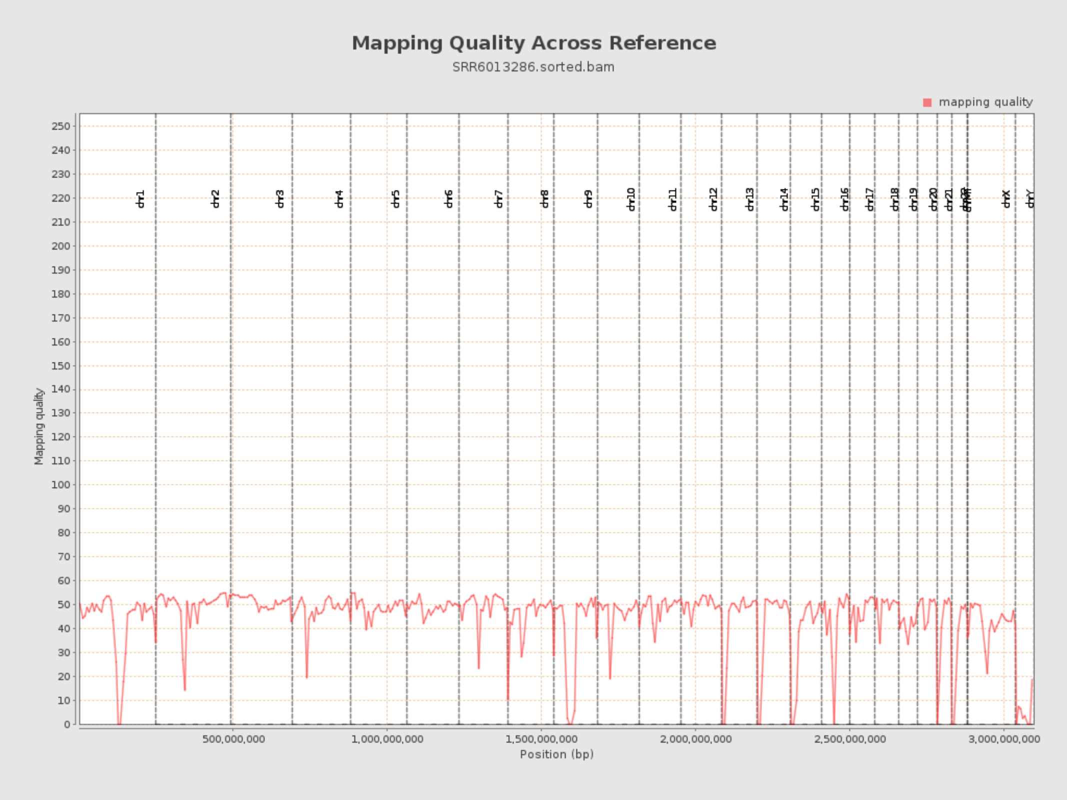
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram