# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/09/15 01:11:50*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063538.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_SRR6063538 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063538.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Sep 15 01:11:49 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR6063538.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 3,797,237 |
| Mapped reads | 3,578,553 / 94.24% |
| Unmapped reads | 218,684 / 5.76% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 38,454 / 1.01% |
| Read min/max/mean length | 30 / 76 / 76.35 |
| Duplicated reads (estimated) | 908,312 / 23.92% |
| Duplication rate | 17.04% |
| Clipped reads | 1,766,984 / 46.53% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 62,178,547 / 26.58% |
| Number/percentage of C's | 41,882,084 / 17.9% |
| Number/percentage of T's | 76,248,413 / 32.6% |
| Number/percentage of G's | 53,583,562 / 22.91% |
| Number/percentage of N's | 26,791 / 0.01% |
| GC Percentage | 40.81% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0756 |
| | |

| | |
|---|---|
| Standard Deviation | 0.8558 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.94 |

## 2.5. Mismatches and indels

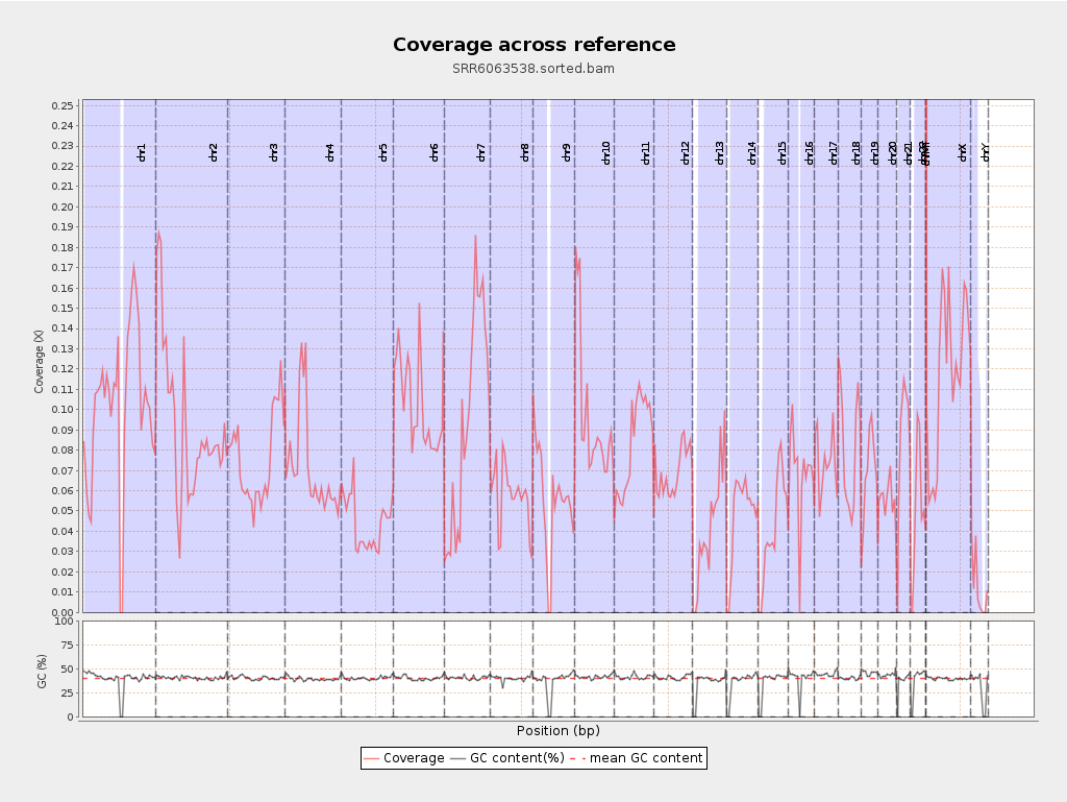
| | |
|---|---|
| General error rate | 0.52% |
| Mismatches | 1,186,441 |
| Insertions | 16,301 |
| Mapped reads with at least one insertion | 0.45% |
| Deletions | 47,259 |
| Mapped reads with at least one deletion | 1.31% |
| Homopolymer indels | 46.32% |

## 2.6. Chromosome stats

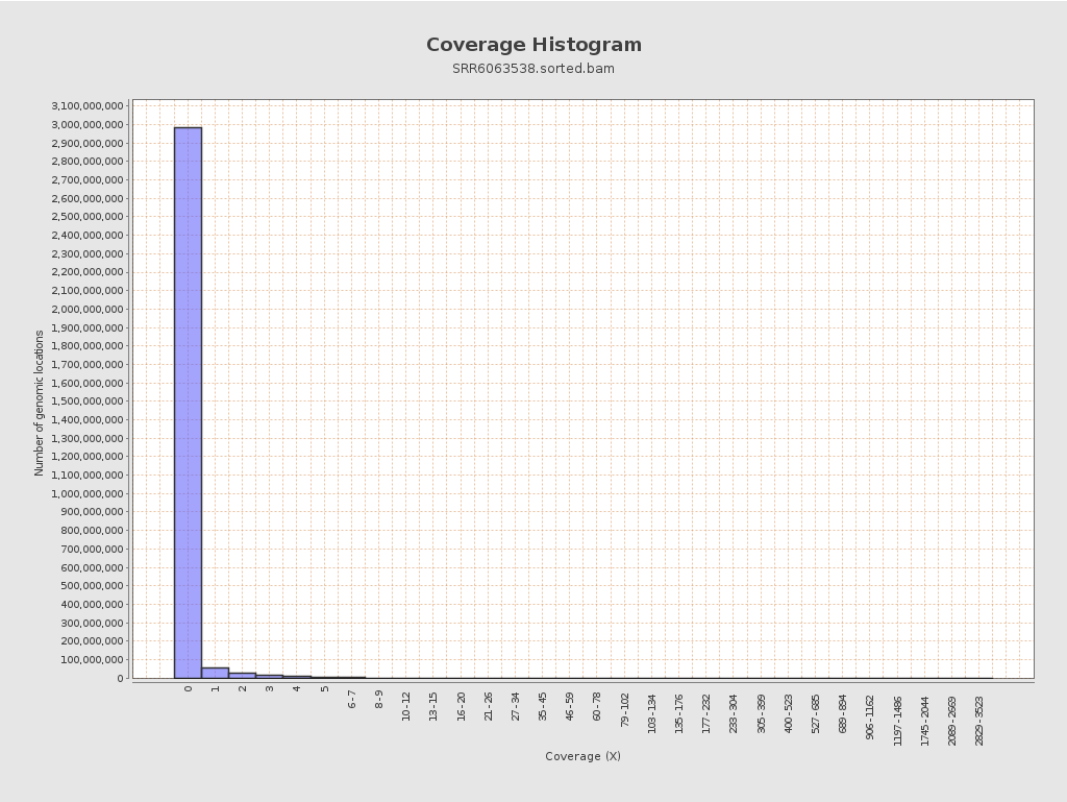
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| chr1 | 249250621 | 25165864 | 0.101 | 1.1614 |
| chr2 | 243199373 | 22507173 | 0.0925 | 1.2646 |
| chr3 | 198022430 | 14972036 | 0.0756 | 0.5034 |
| chr4 | 191154276 | 13794727 | 0.0722 | 0.5296 |
| chr5 | 180915260 | 8022988 | 0.0443 | 0.3806 |
| chr6 | 171115067 | 17694077 | 0.1034 | 0.6655 |
| chr7 | 159138663 | 15039347 | 0.0945 | 0.8041 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 8357438 | 0.0571 | 2.0436 |
| chr9 | 141213431 | 7768558 | 0.055 | 0.5861 |
| chr10 | 135534747 | 13110585 | 0.0967 | 0.6875 |
| chr11 | 135006516 | 11275575 | 0.0835 | 0.5812 |
| chr12 | 133851895 | 9323145 | 0.0697 | 0.4866 |
| chr13 | 115169878 | 4964127 | 0.0431 | 0.4098 |
| chr14 | 107349540 | 5190482 | 0.0484 | 0.42 |
| chr15 | 102531392 | 4196707 | 0.0409 | 0.3699 |
| chr16 | 90354753 | 6067456 | 0.0672 | 0.471 |
| chr17 | 81195210 | 6062483 | 0.0747 | 0.4975 |
| chr18 | 78077248 | 6310565 | 0.0808 | 0.9848 |
| chr19 | 59128983 | 4091683 | 0.0692 | 0.8076 |
| chr20 | 63025520 | 3551336 | 0.0563 | 0.4475 |
| chr21 | 48129895 | 4076950 | 0.0847 | 0.5481 |
| chr22 | 51304566 | 2516379 | 0.049 | 0.3901 |
| chrMT | 16571 | 1088283 | 65.6739 | 49.8536 |
| chrX | 155270560 | 18115068 | 0.1167 | 0.6748 |
| chrY | 59373566 | 739283 | 0.0125 | 0.3136 |

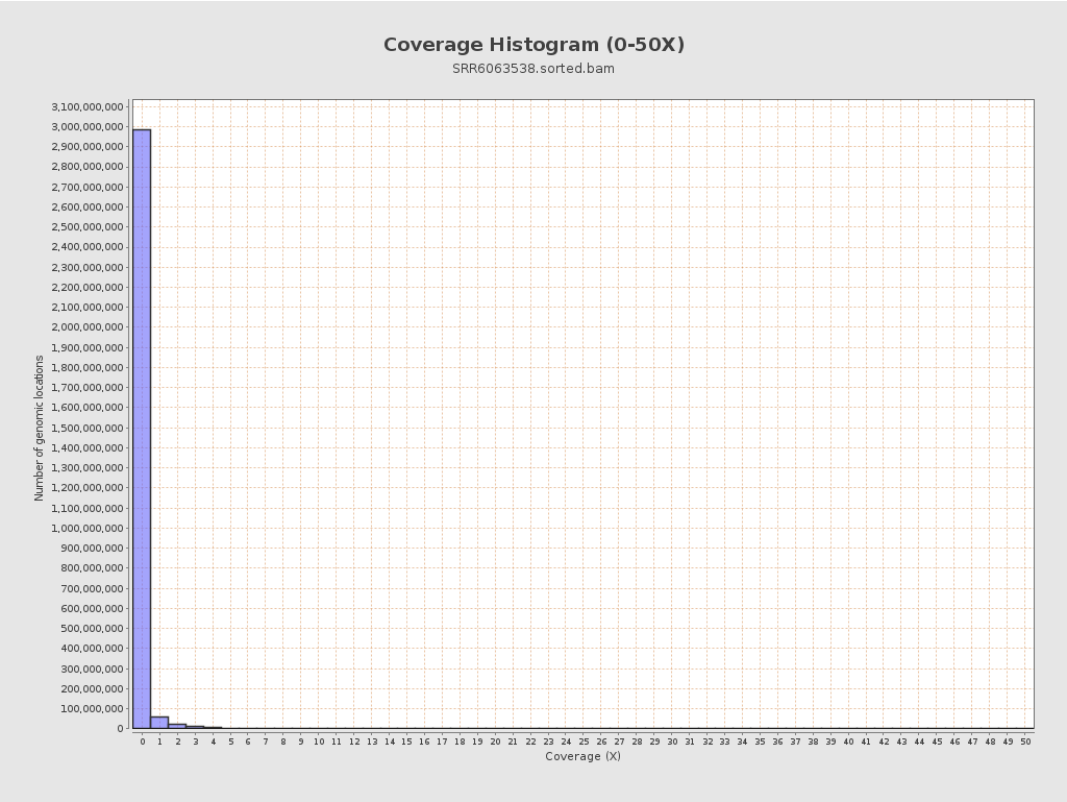
# 3. Results : Coverage across reference



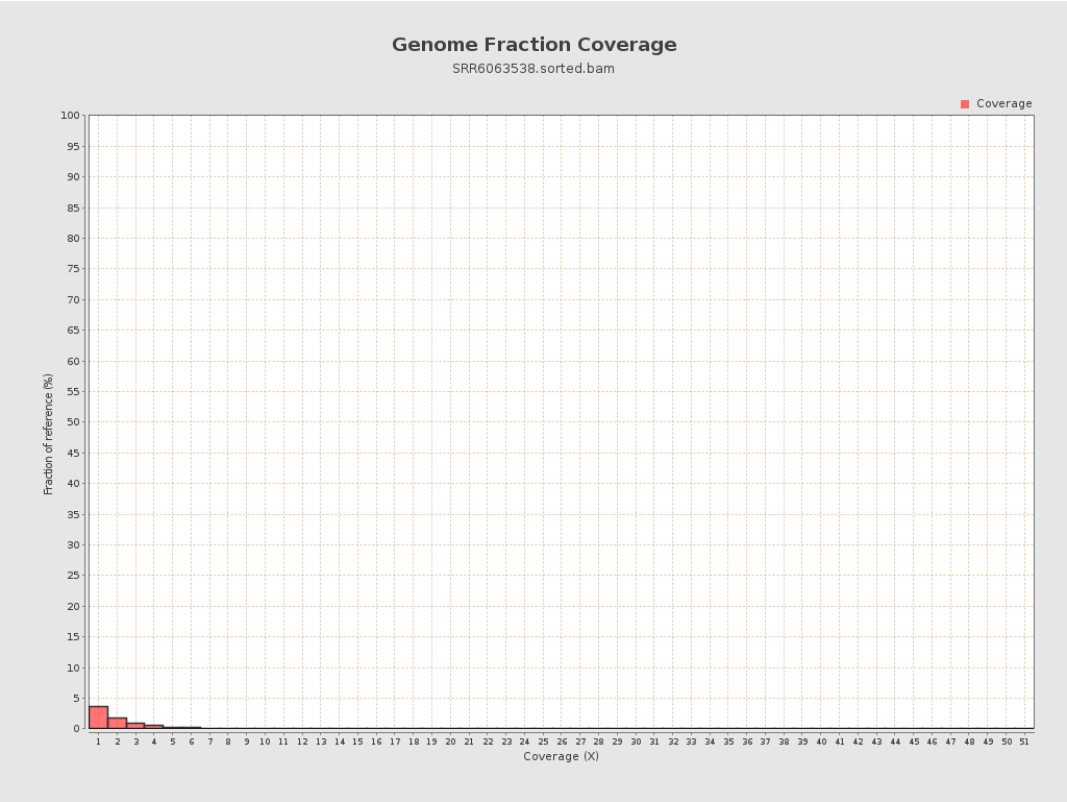
# 4. Results : Coverage Histogram



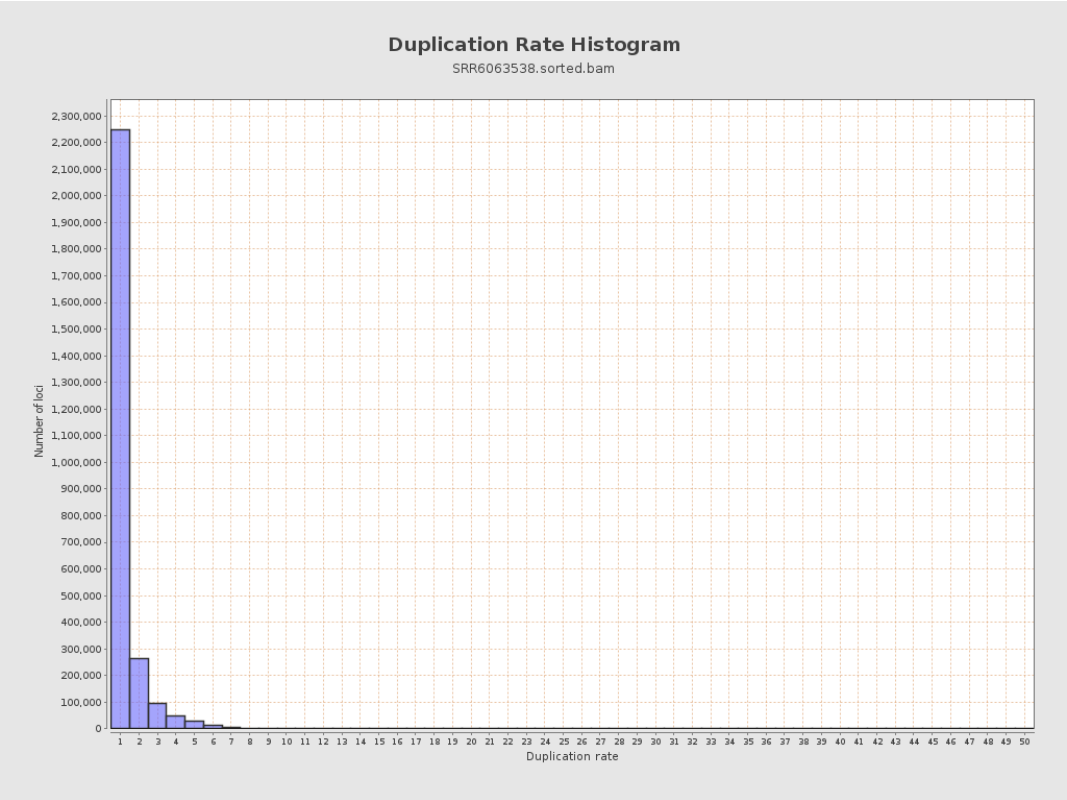
# 5. Results : Coverage Histogram (0-50X)



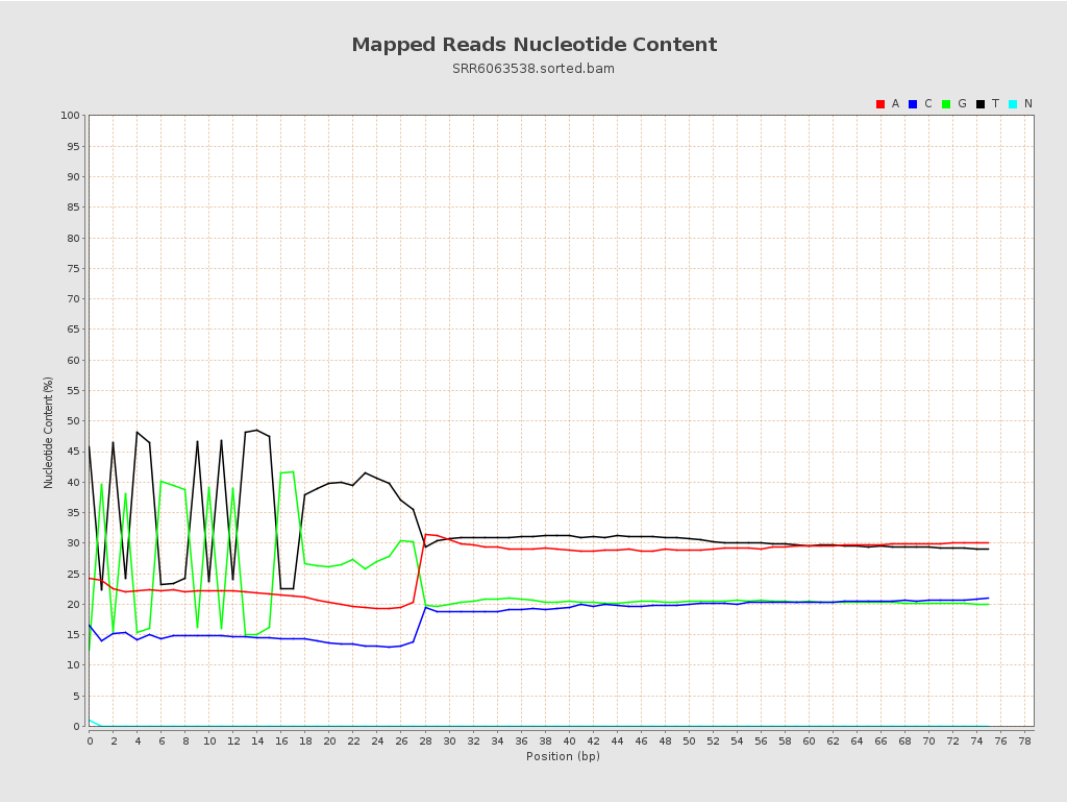
# 6. Results : Genome Fraction Coverage



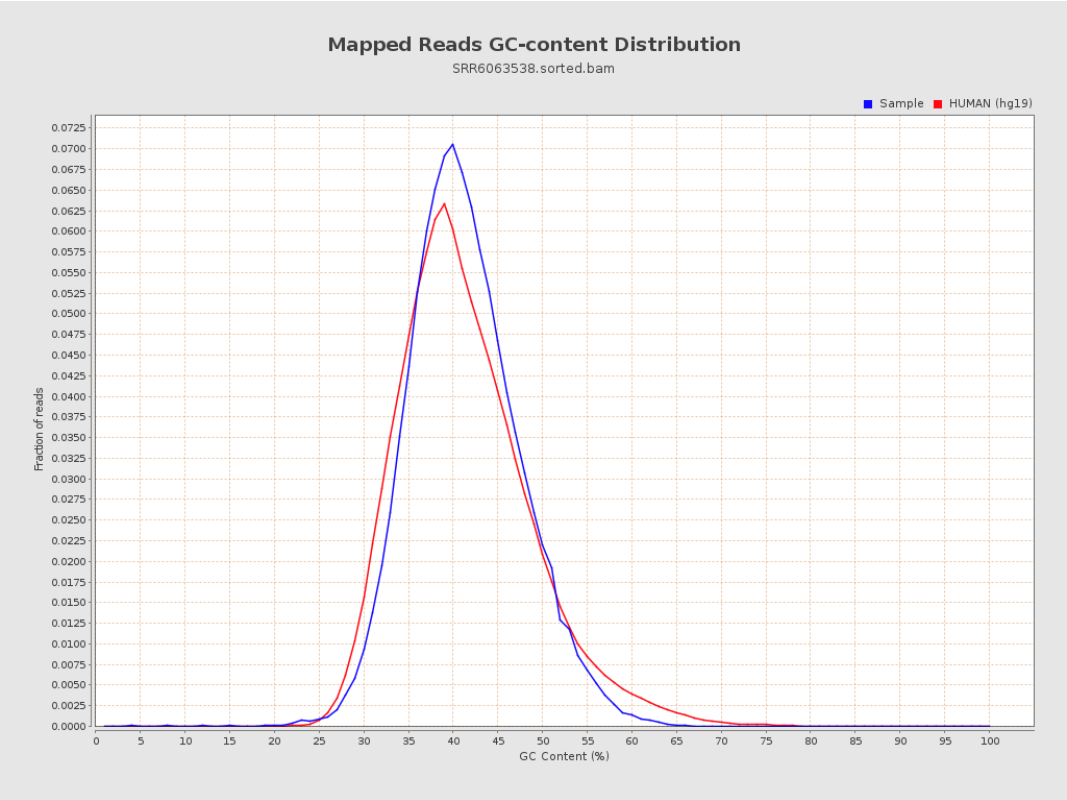
# 7. Results : Duplication Rate Histogram



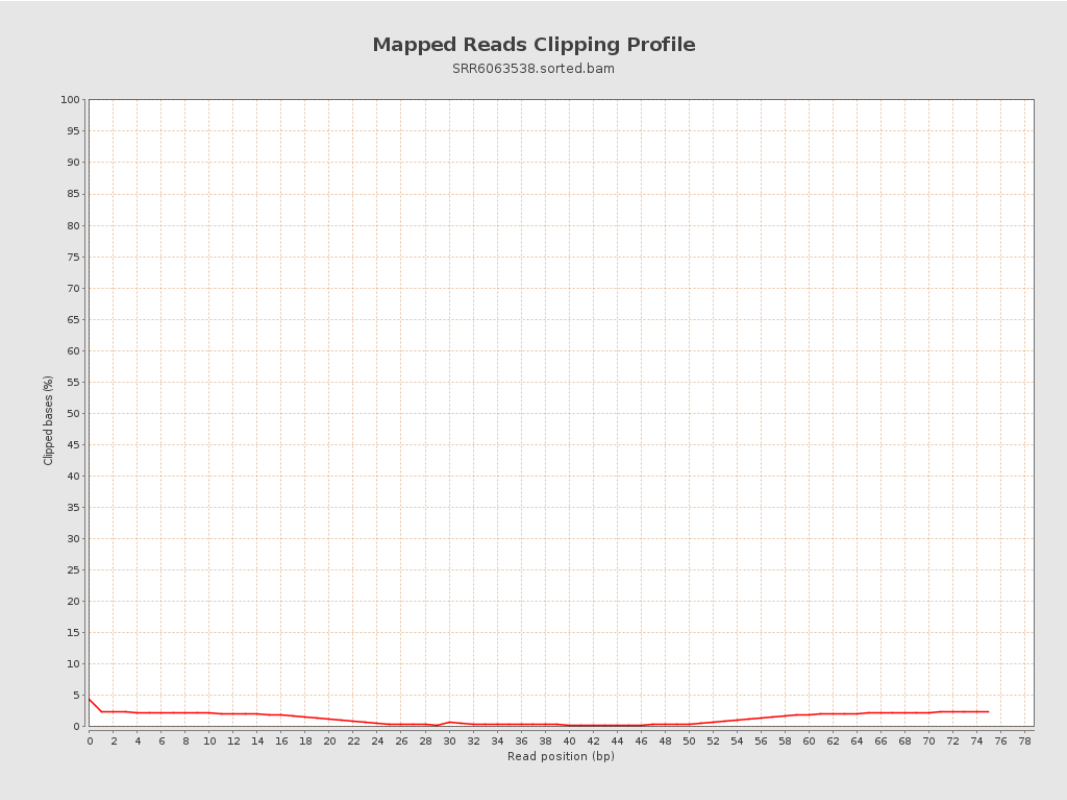
# 8. Results : Mapped Reads Nucleotide Content



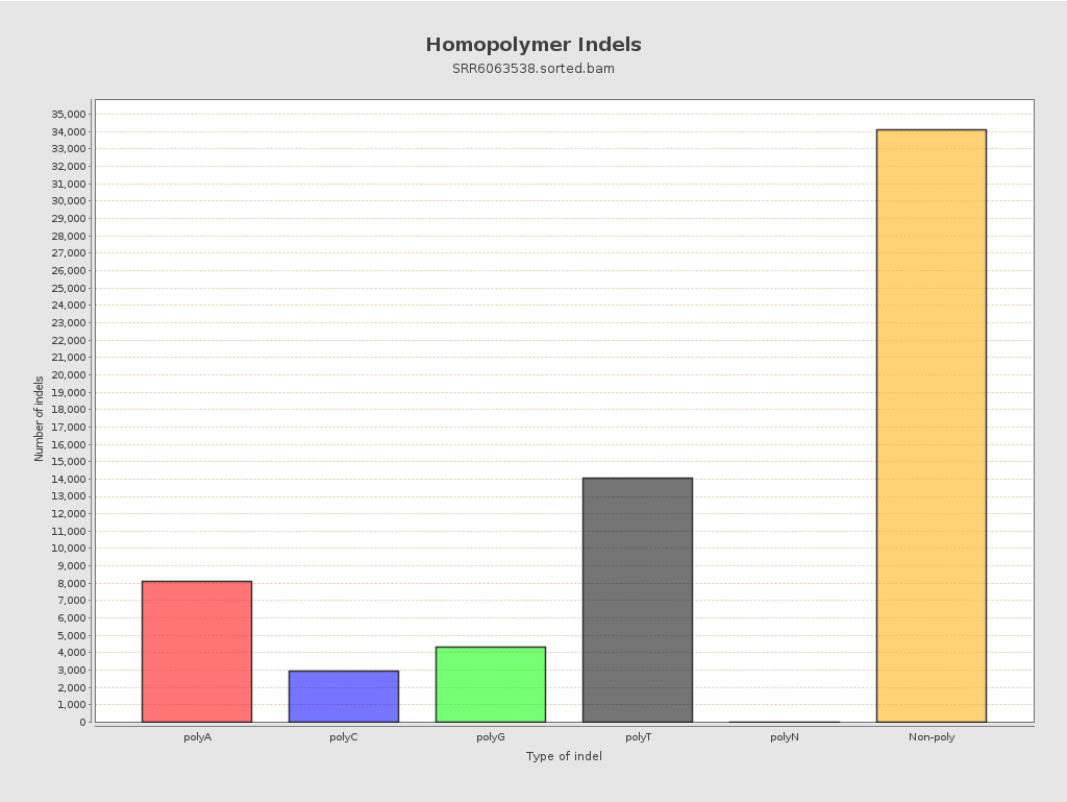
# 9. Results : Mapped Reads GC-content Distribution



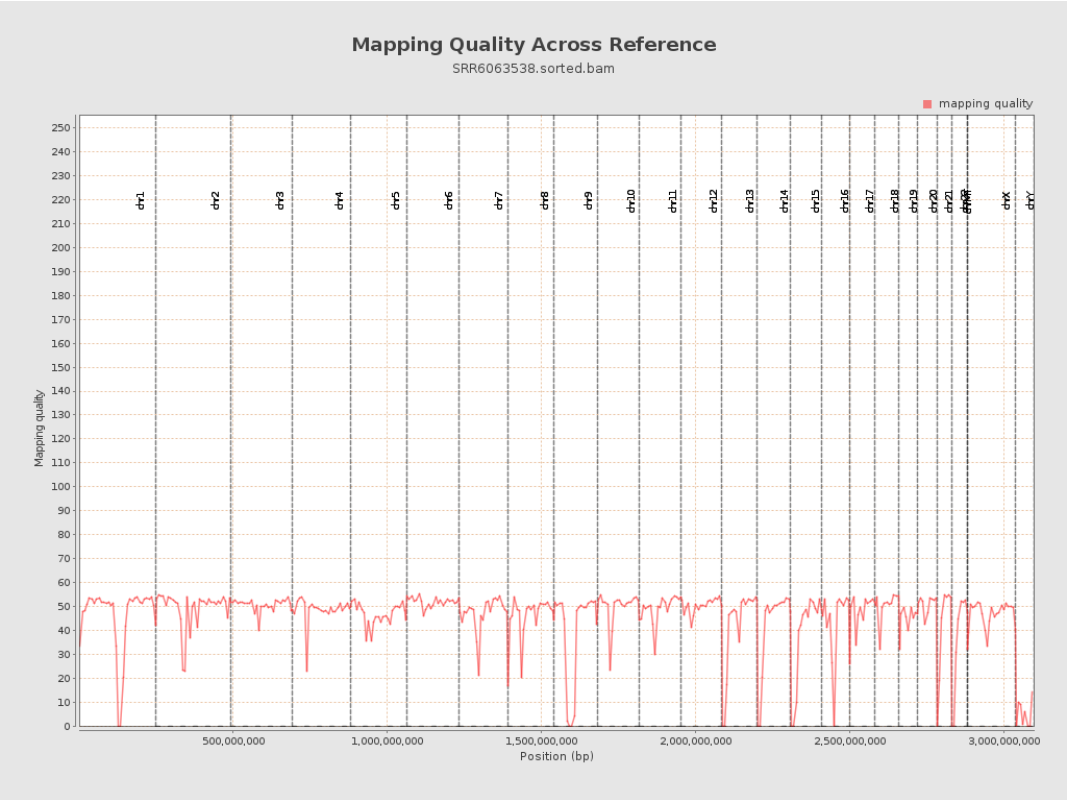
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram