# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.2-dev*

*2024/08/25 00:41:52*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083628.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_SRR3083628 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083628.fastq.gz |
| Draw chromosome limits: | yes |
| Analyze overlapping paired-end reads: | no |
| Program: | bwa (0.7.17-r1188) |
| Analysis date: | Sun Aug 25 00:41:51 CST 2024 |
| Size of a homopolymer: | 3 |
| Skip duplicate alignments: | no |
| Number of windows: | 400 |
| BAM file: | SRR3083628.sorted.bam |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 3,095,693,983 |
| Number of reads | 1,430,365 |
| Mapped reads | 1,317,539 / 92.11% |
| Unmapped reads | 112,826 / 7.89% |
| Mapped paired reads | 0 / 0% |
| Secondary alignments | 0 |
| Supplementary alignments | 10,338 / 0.72% |
| Read min/max/mean length | 30 / 76 / 76.25 |
| Duplicated reads (estimated) | 46,759 / 3.27% |
| Duplication rate | 2.95% |
| Clipped reads | 562,551 / 39.33% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 24,165,408 / 27.4% |
| Number/percentage of C's | 16,200,797 / 18.37% |
| Number/percentage of T's | 27,949,702 / 31.69% |
| Number/percentage of G's | 19,874,633 / 22.53% |
| Number/percentage of N's | 4,510 / 0.01% |
| GC Percentage | 40.9% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 0.0285 |
| | |

| | |
|---|---|
| Standard Deviation | 0.2595 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 45.38 |

## 2.5. Mismatches and indels

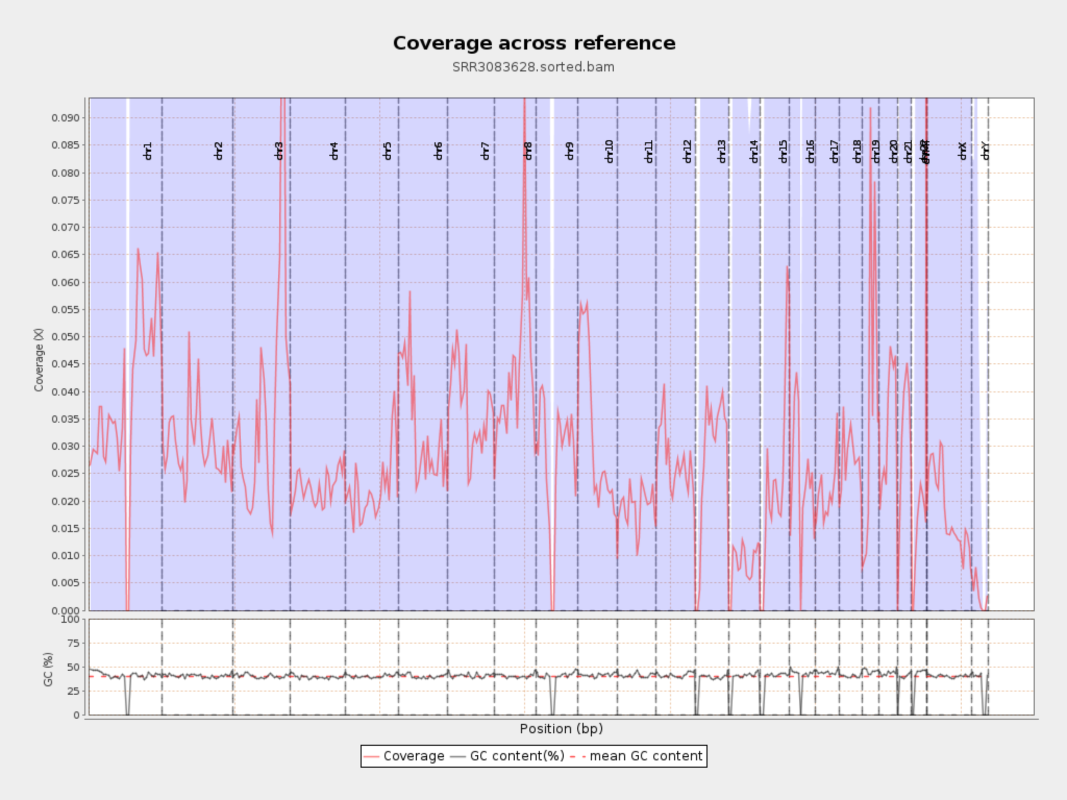
| | |
|---|---|
| General error rate | 0.71% |
| Mismatches | 613,651 |
| Insertions | 6,775 |
| Mapped reads with at least one insertion | 0.51% |
| Deletions | 20,411 |
| Mapped reads with at least one deletion | 1.53% |
| Homopolymer indels | 48.28% |

## 2.6. Chromosome stats

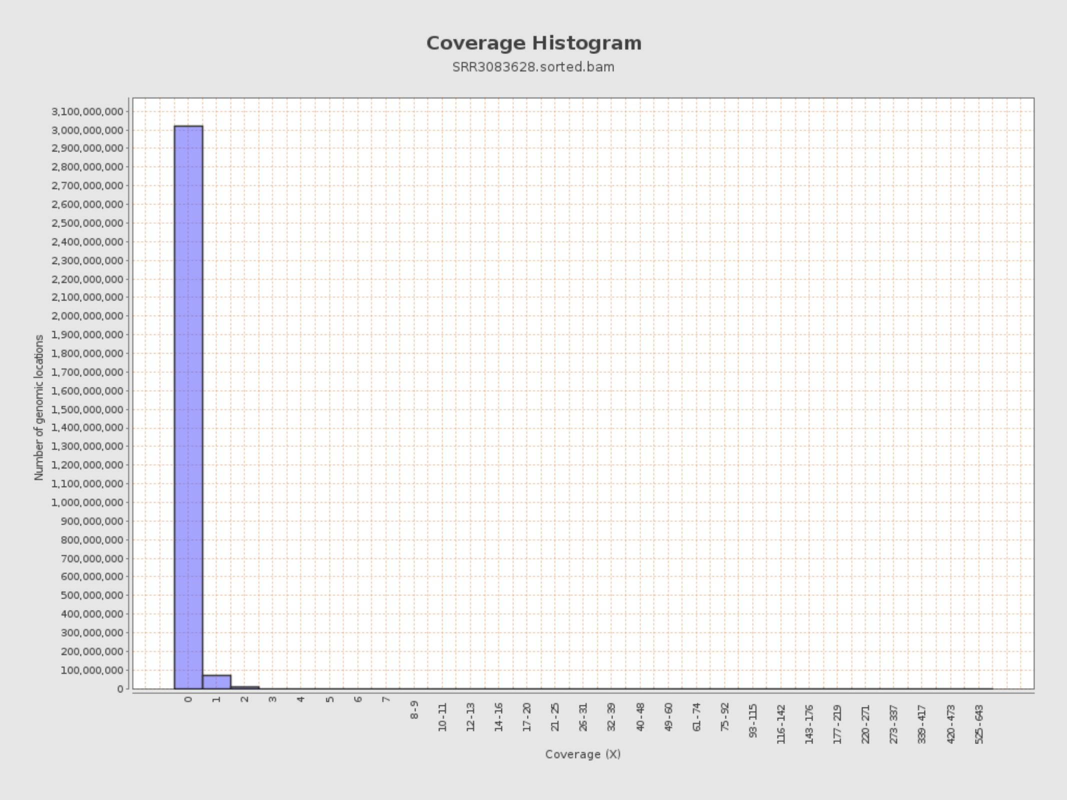
| **Name** | **Length** | **Mapped bases** | **Mean coverage** | **Standard deviation** |
|---|---|---|---|---|
| chr1 | 249250621 | 9782703 | 0.0392 | 0.464 |
| chr2 | 243199373 | 7378024 | 0.0303 | 0.3435 |
| chr3 | 198022430 | 7616810 | 0.0385 | 0.2198 |
| chr4 | 191154276 | 4350799 | 0.0228 | 0.168 |
| chr5 | 180915260 | 4072919 | 0.0225 | 0.1657 |
| chr6 | 171115067 | 5747651 | 0.0336 | 0.2294 |
| chr7 | 159138663 | 5906533 | 0.0371 | 0.3885 |
| | | | | |

| | | | | |
|---|---|---|---|---|
| chr8 | 146364022 | 6533607 | 0.0446 | 0.3079 |
| chr9 | 141213431 | 3915595 | 0.0277 | 0.208 |
| chr10 | 135534747 | 4462796 | 0.0329 | 0.241 |
| chr11 | 135006516 | 2545975 | 0.0189 | 0.1663 |
| chr12 | 133851895 | 3632475 | 0.0271 | 0.1822 |
| chr13 | 115169878 | 3197075 | 0.0278 | 0.1847 |
| chr14 | 107349540 | 895958 | 0.0083 | 0.1042 |
| chr15 | 102531392 | 2407352 | 0.0235 | 0.1751 |
| chr16 | 90354753 | 2218383 | 0.0246 | 0.1788 |
| chr17 | 81195210 | 1779975 | 0.0219 | 0.1693 |
| chr18 | 78077248 | 2178751 | 0.0279 | 0.3039 |
| chr19 | 59128983 | 2248830 | 0.038 | 0.3423 |
| chr20 | 63025520 | 2147237 | 0.0341 | 0.2065 |
| chr21 | 48129895 | 1470018 | 0.0305 | 0.1937 |
| chr22 | 51304566 | 721287 | 0.0141 | 0.1302 |
| chrMT | 16571 | 6232 | 0.3761 | 0.6672 |
| chrX | 155270560 | 2853113 | 0.0184 | 0.1535 |
| chrY | 59373566 | 158083 | 0.0027 | 0.0652 |

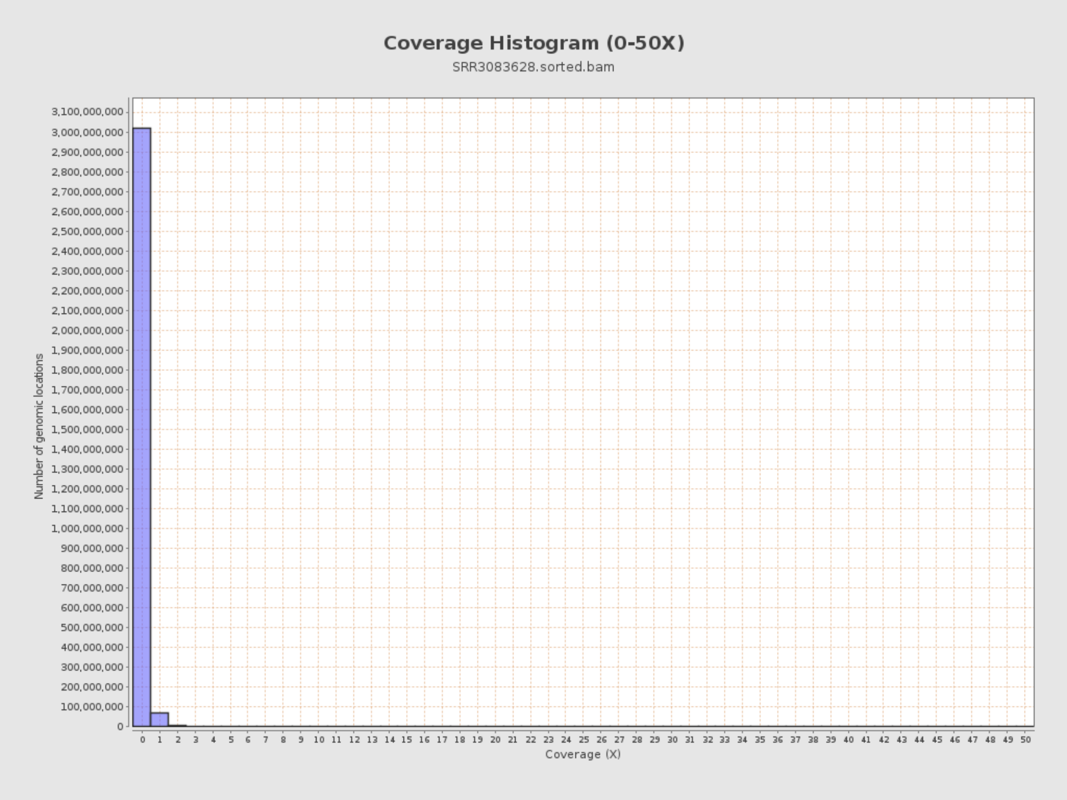
# 3. Results : Coverage across reference



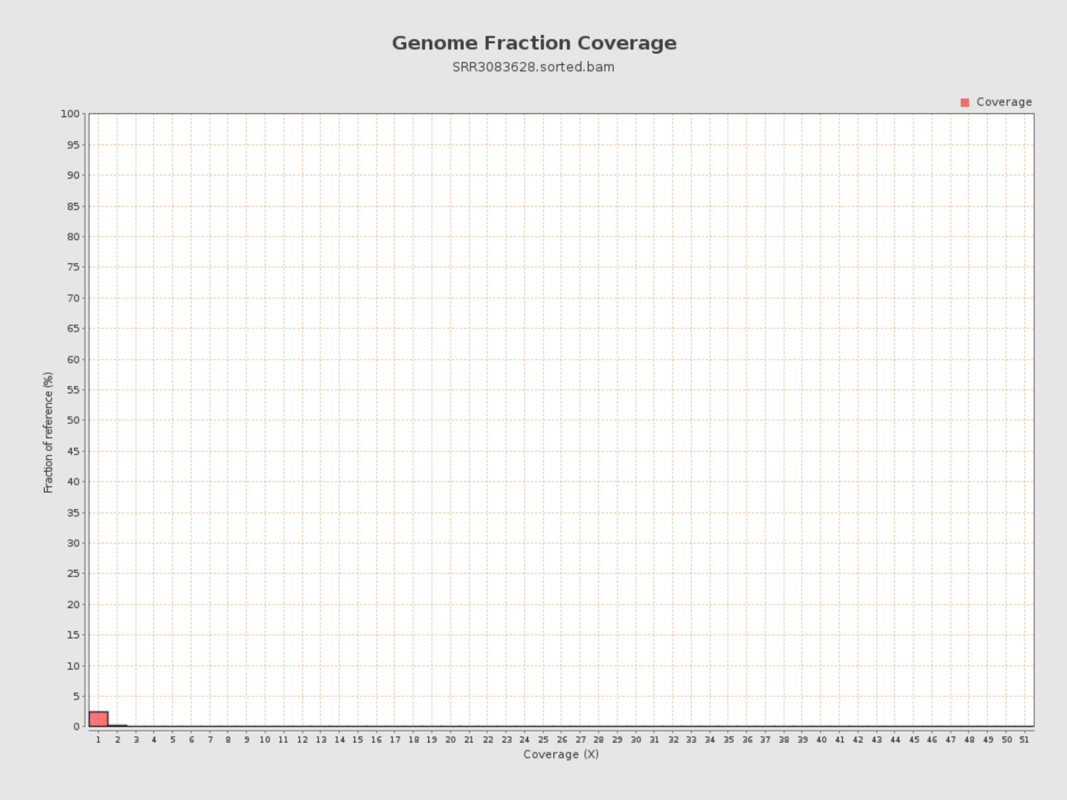
# 4. Results : Coverage Histogram



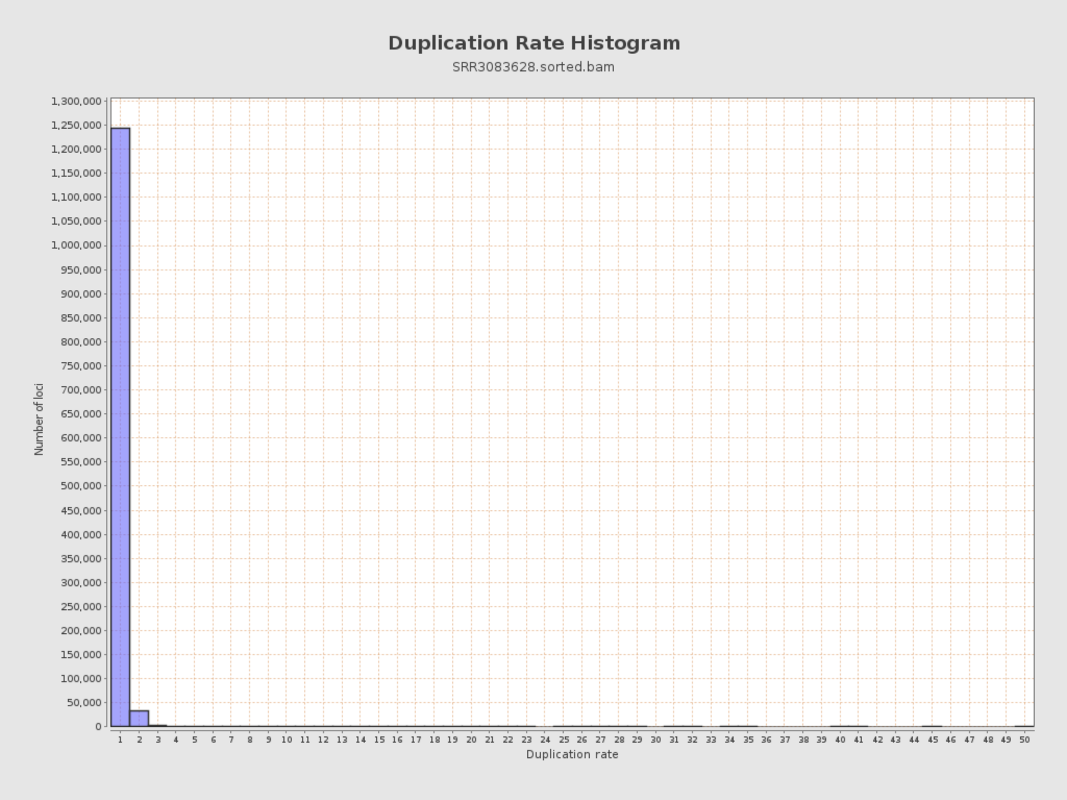
# 5. Results : Coverage Histogram (0-50X)



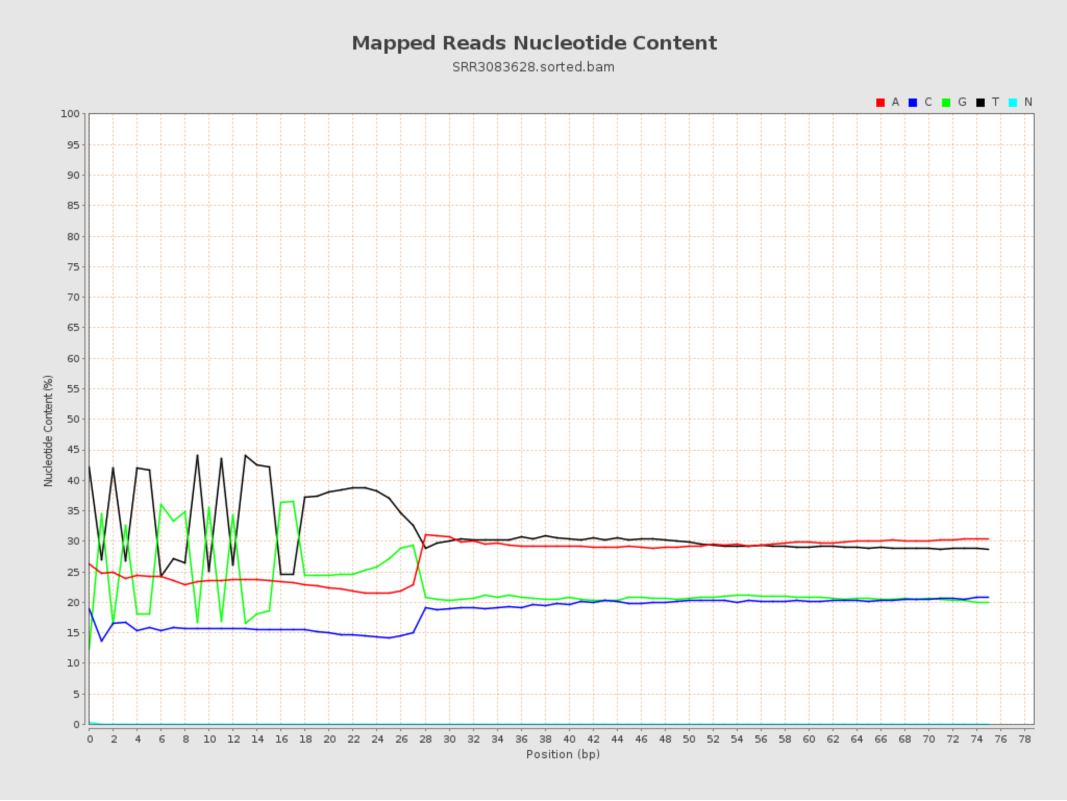
# 6. Results : Genome Fraction Coverage



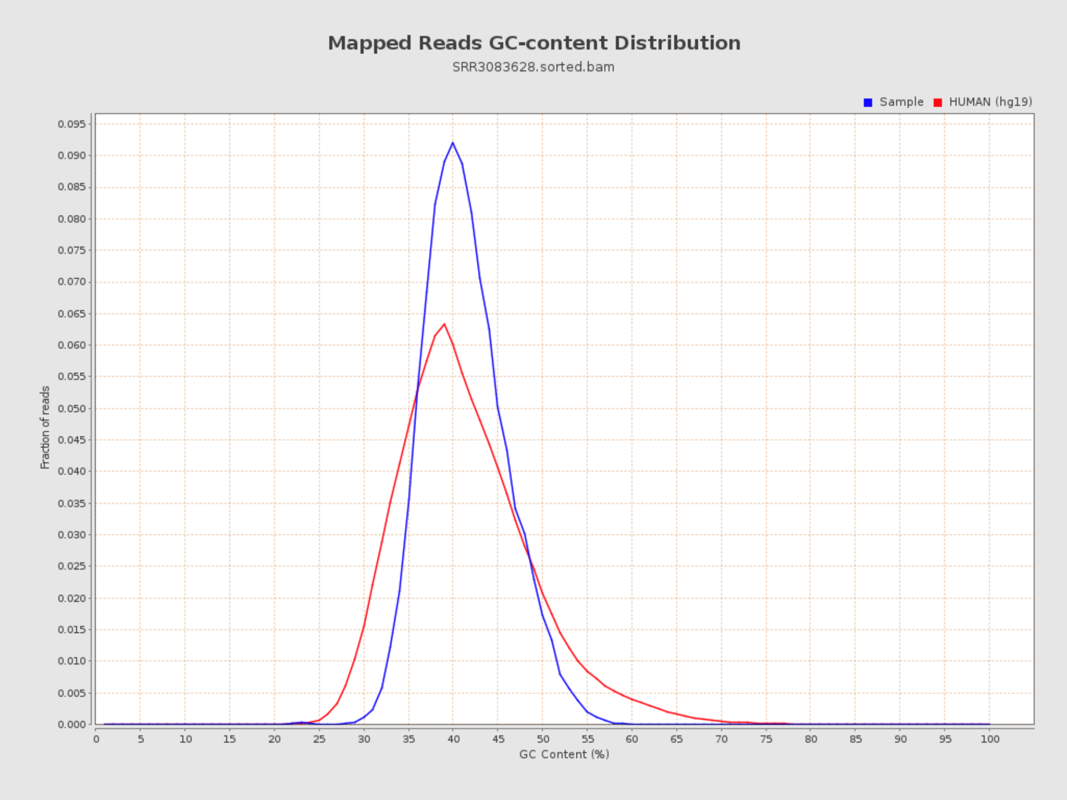
# 7. Results : Duplication Rate Histogram



# 8. Results : Mapped Reads Nucleotide Content



# 9. Results : Mapped Reads GC-content Distribution



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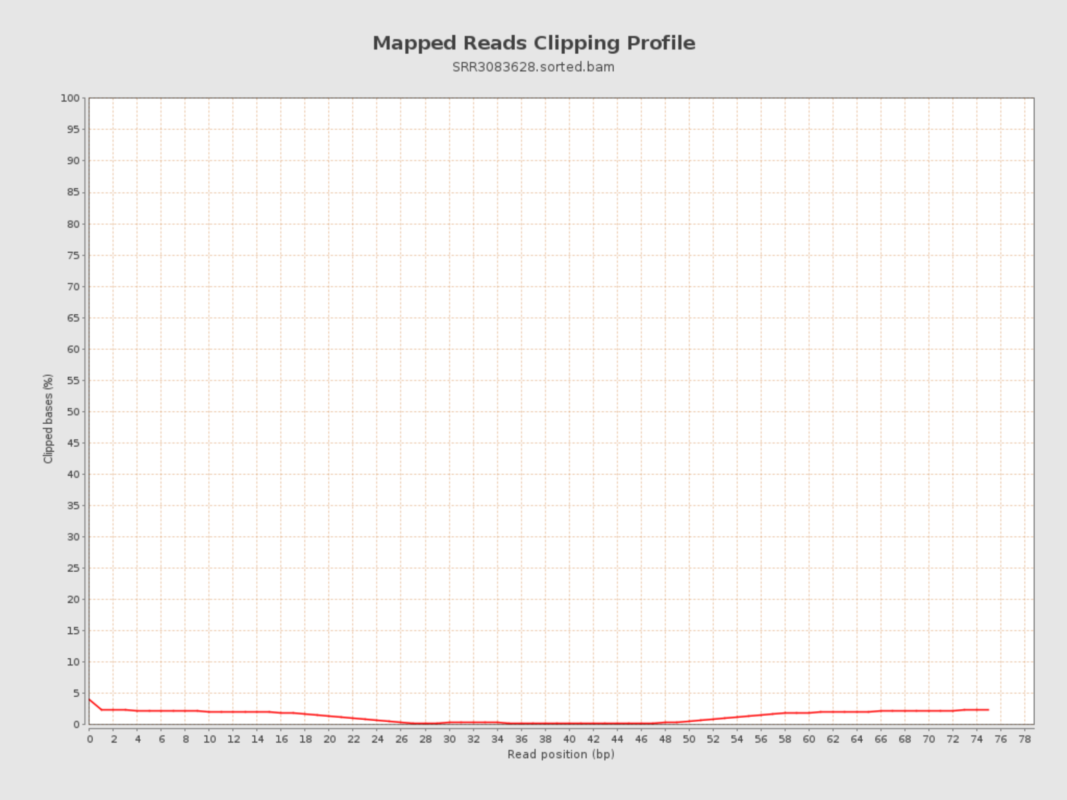
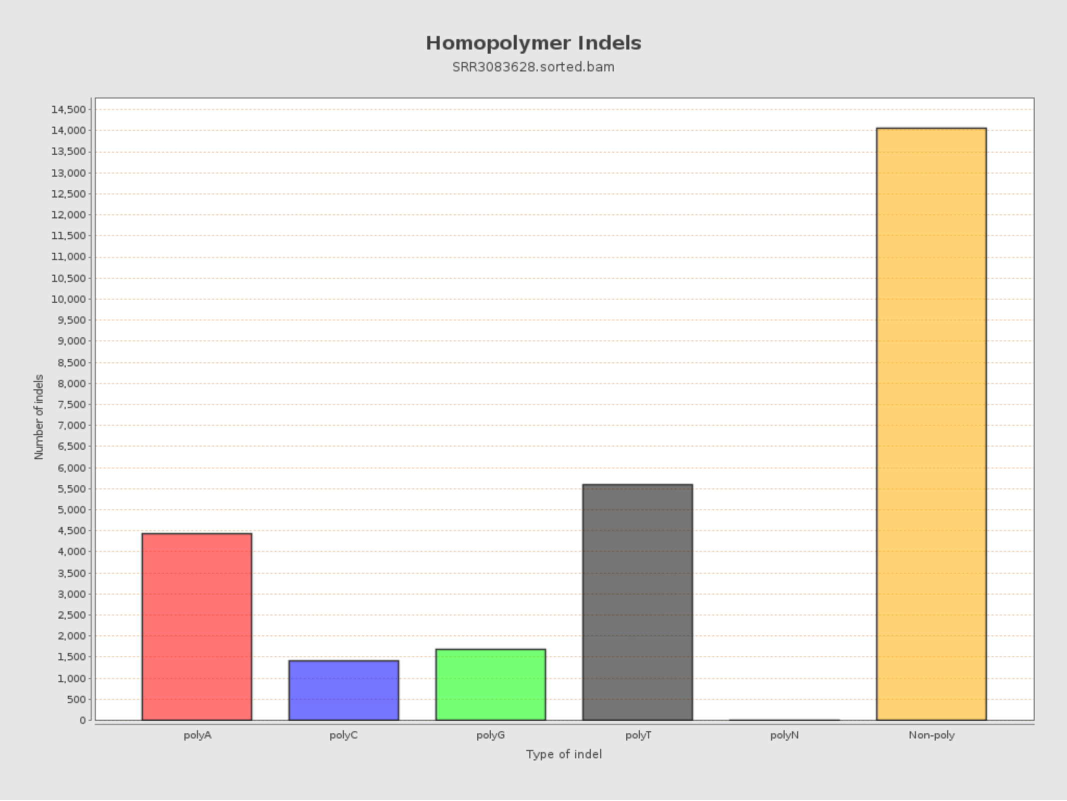
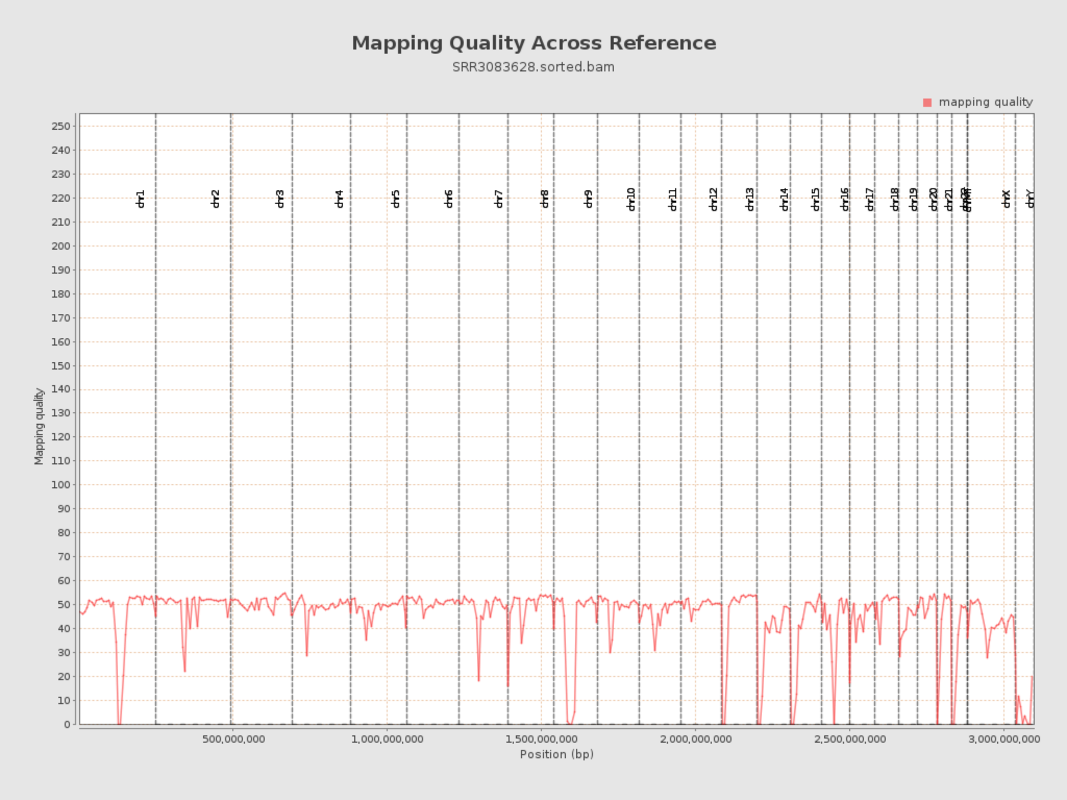
# 10. Results : Mapped Reads Clipping Profile



# 11. Results : Homopolymer Indels



# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram