# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:26:01*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/938.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| BAM file: | /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/938.nodup.bam |
| Program: | bwa (0.7.17-r1188) |
| Analyze overlapping paired-end reads: | no |
| Command line: | bwa mem -M -t 8 -R @RG\tID:$unit\tPL:Illumina\tLB:LibA\tSM:$sample /proj/uppstore2018210/Aalpina/data/reference/GCA_900128785.1_MPIPZ.v5_genomic.fa /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_575/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_575_S142_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_575/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_575_S142_L004_R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| Number of windows: | 400 |

| | |
|---|---|
| Analysis date: | Mon May 29 21:26:00 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 311,642,060 |
| Number of reads | 50,142,289 |
| Mapped reads | 46,688,489 / 93.11% |
| Unmapped reads | 3,453,800 / 6.89% |
| Mapped paired reads | 46,688,489 / 93.11% |
| Mapped reads, first in pair | 23,448,741 / 46.76% |
| Mapped reads,  second in pair | 23,239,748 / 46.35% |
| Mapped reads, both in pair | 45,553,310 / 90.85% |
| Mapped reads, singletons | 1,135,179 / 2.26% |
| Read min/max/mean length | 30 / 151 / 148.17 |
| Duplicated reads (flagged) | 6,725,879 / 13.41% |
| Clipped reads | 11,215,228 / 22.37% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 1,991,776,270 / 30.91% |
| Number/percentage of C's | 1,229,870,016 / 19.09% |
| Number/percentage of T's | 1,992,454,528 / 30.93% |
| Number/percentage of G's | 1,228,715,057 / 19.07% |
| Number/percentage of N's | 43,847 / 0% |
| GC Percentage | 38.16% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 20.7269 |
| Standard Deviation | 166.6424 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.03 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 233,503.28 |
| Standard Deviation | 2,292,417.51 |
| P25/Median/P75 | 337 / 440 / 565 |

## 2.6. Mismatches and indels

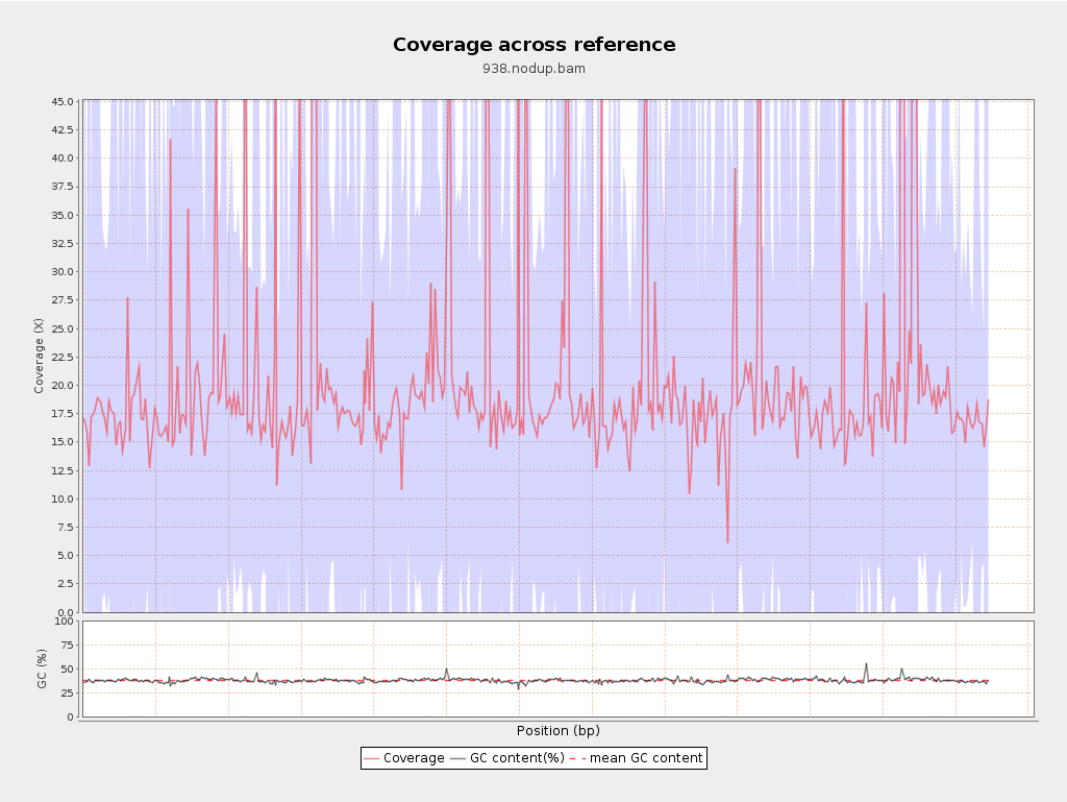
| | |
|---|---|
| General error rate | 2.62% |
| Mismatches | 156,653,115 |
| Insertions | 4,385,539 |
| Mapped reads with at least one insertion | 8.44% |
| Deletions | 4,405,055 |
| Mapped reads with at least one deletion | 8.39% |
| Homopolymer indels | 55.91% |

## 2.7. Chromosome stats

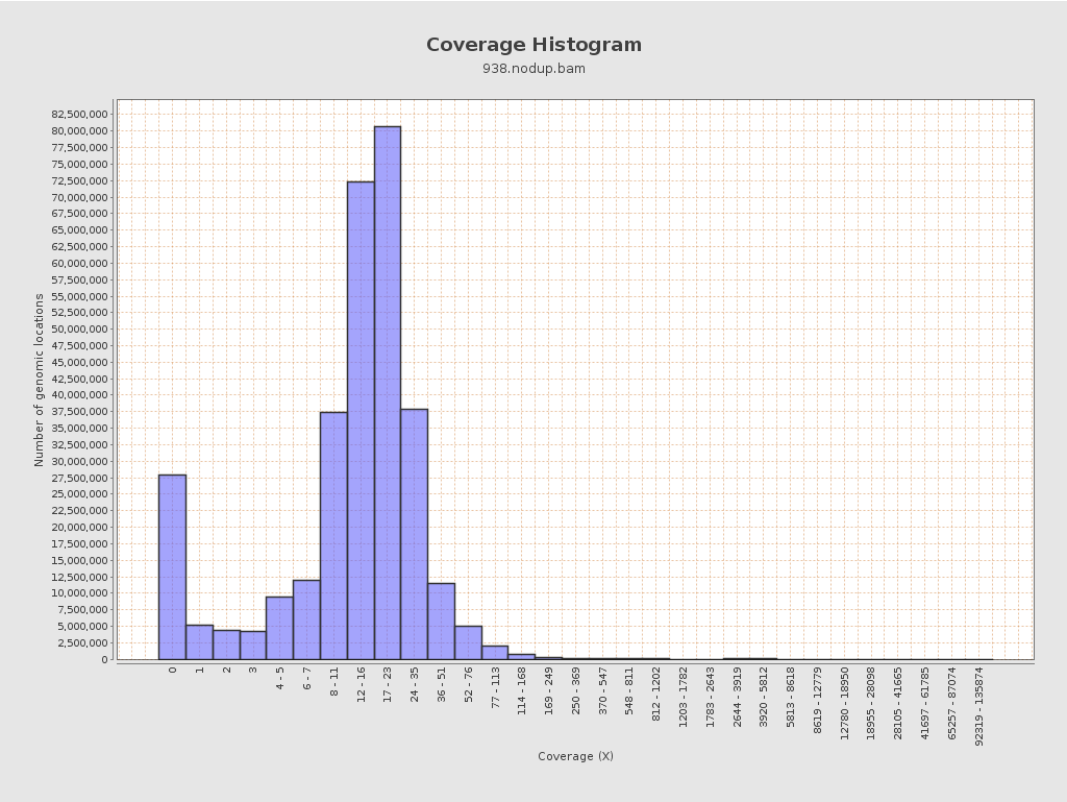
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| LT669788.1 | 29724344 | 510741680 | 17.1826 | 52.7597 |

| | | | | |
|---|---|---|---|---|
| LT669789.1 | 36598175 | 762419246 | 20.8322 | 164.171 |
| LT669790.1 | 30422129 | 696140615 | 22.8827 | 181.3564 |
| LT669791.1 | 52758100 | 1071360702 | 20.307 | 153.2227 |
| LT669792.1 | 28376109 | 586795950 | 20.6792 | 194.0642 |
| LT669793.1 | 33388210 | 641346624 | 19.2088 | 116.7274 |
| LT669794.1 | 50579949 | 983093093 | 19.4364 | 138.0756 |
| LT669795.1 | 49795044 | 1207468153 | 24.2488 | 239.5173 |

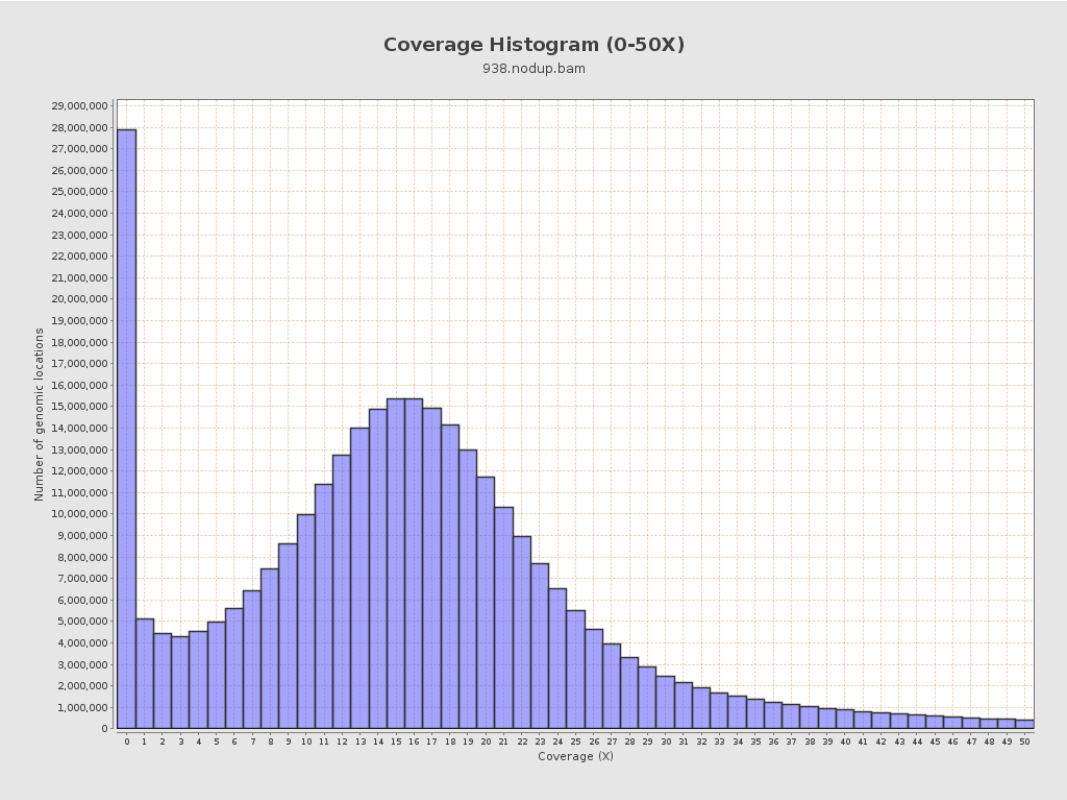
# 3. Results : Coverage across reference



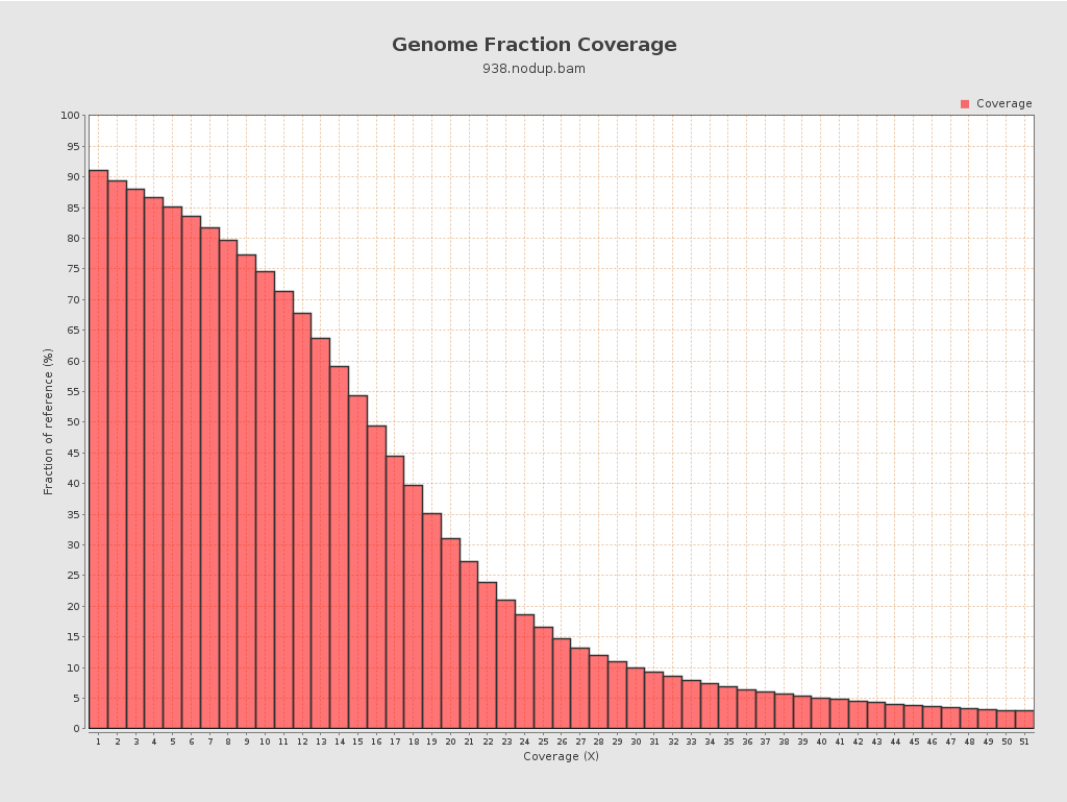
# 4. Results : Coverage Histogram



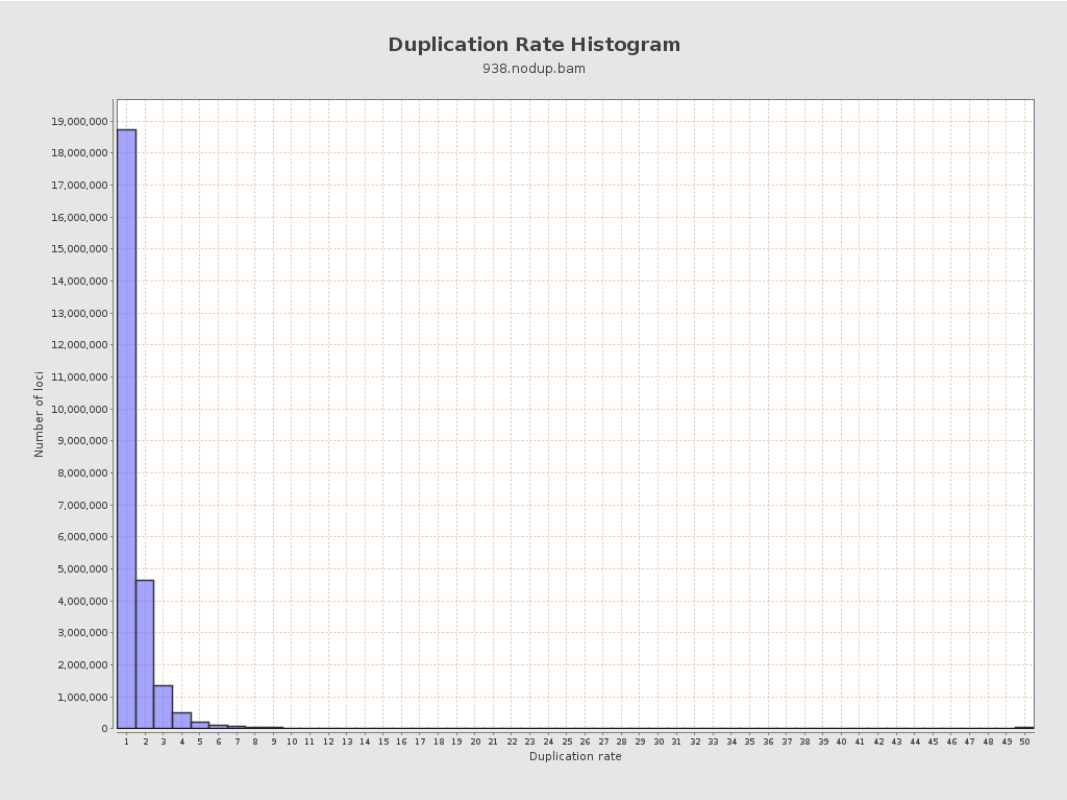
# 5. Results : Coverage Histogram (0-50X)



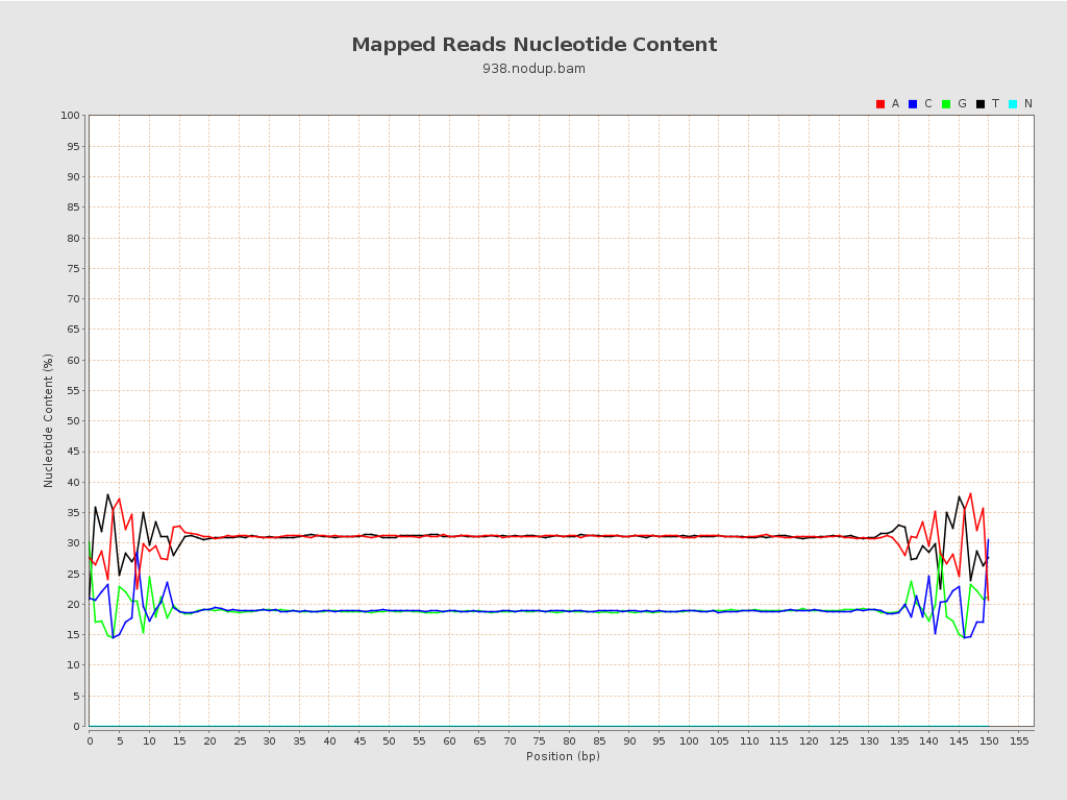
# 6. Results : Genome Fraction Coverage



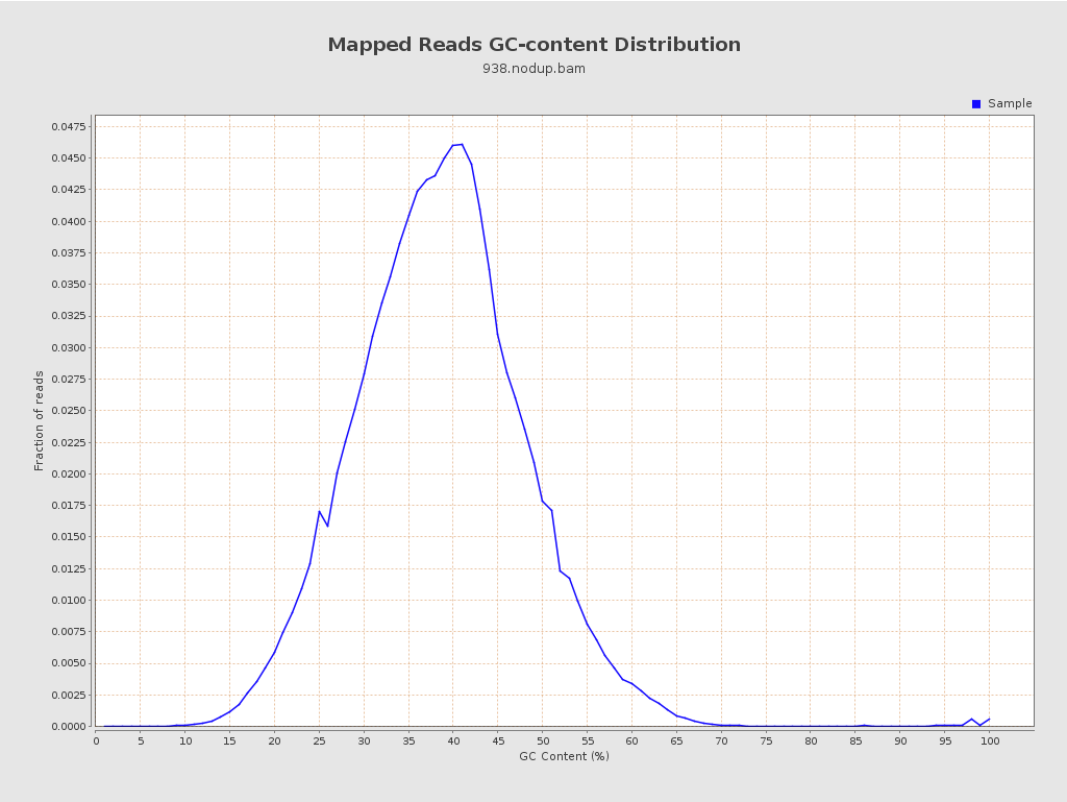
# 7. Results : Duplication Rate Histogram



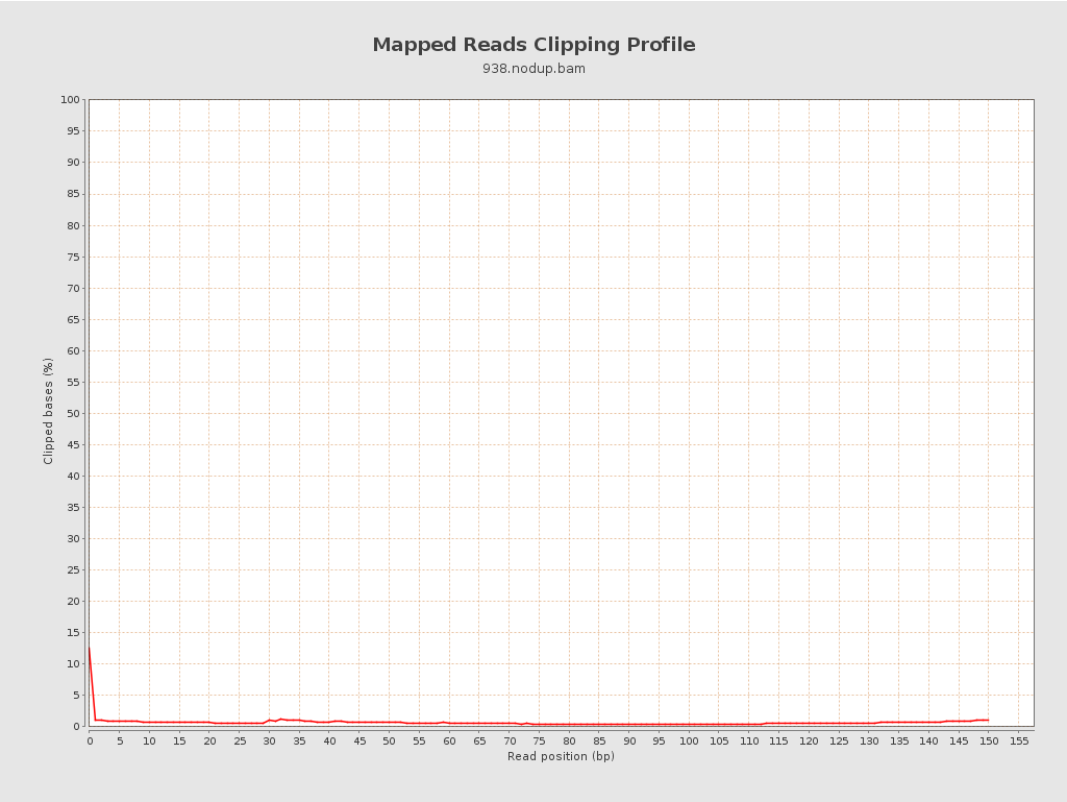
# 8. Results : Mapped Reads Nucleotide Content



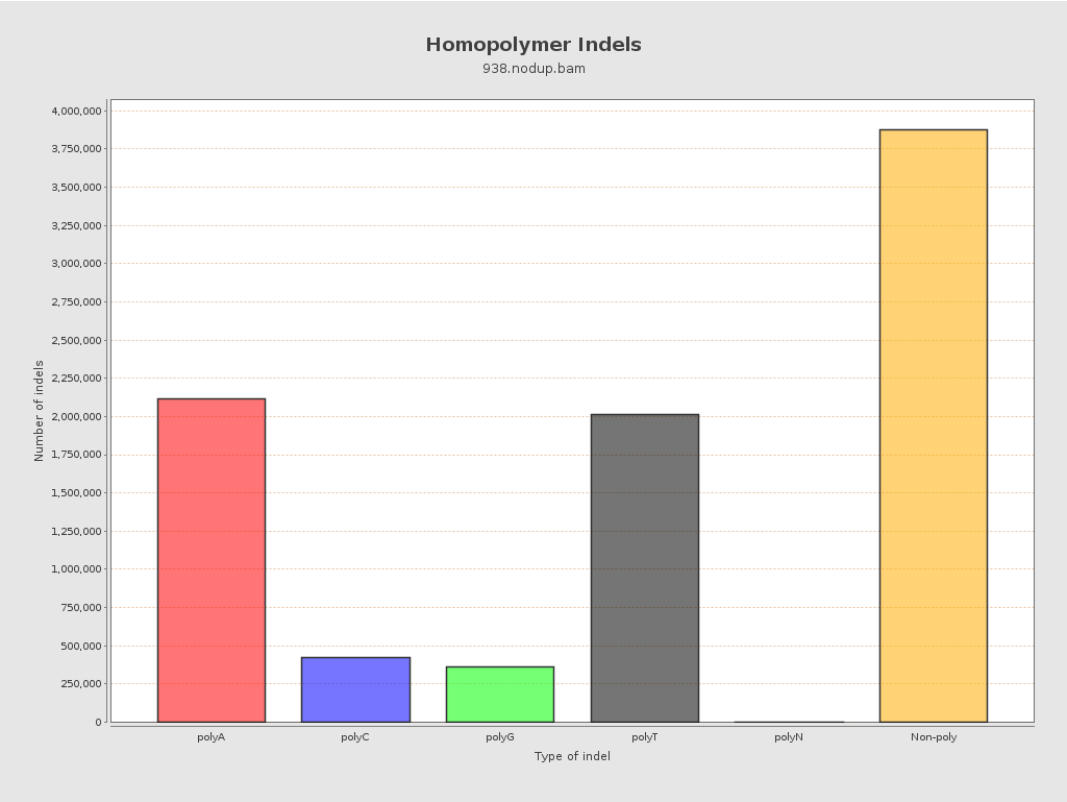
# 9. Results : Mapped Reads GC-content Distribution



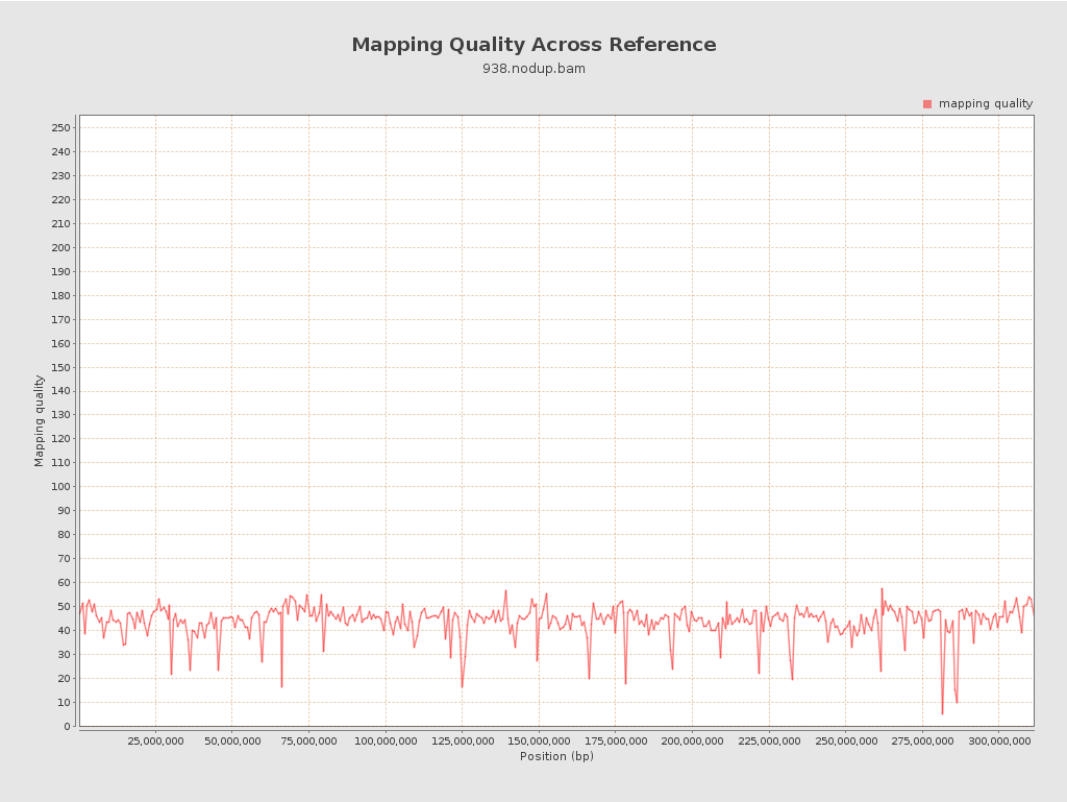
# 10. Results : Mapped Reads Clipping Profile



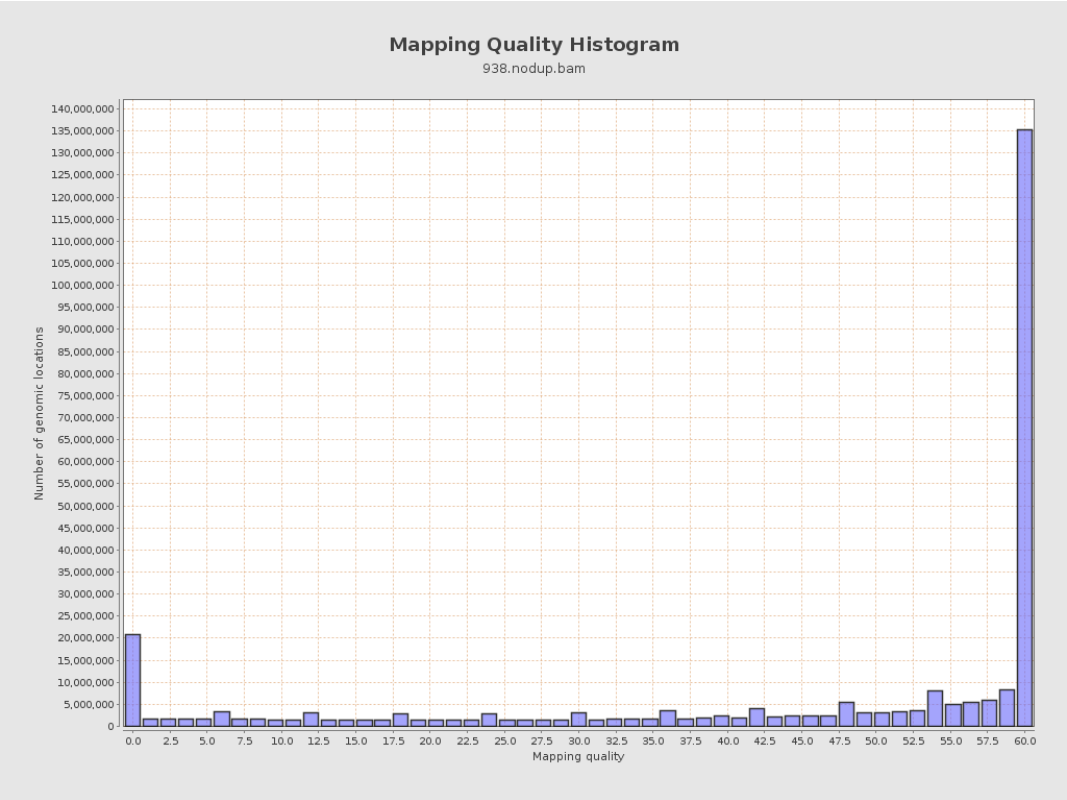
# 11. Results : Homopolymer Indels



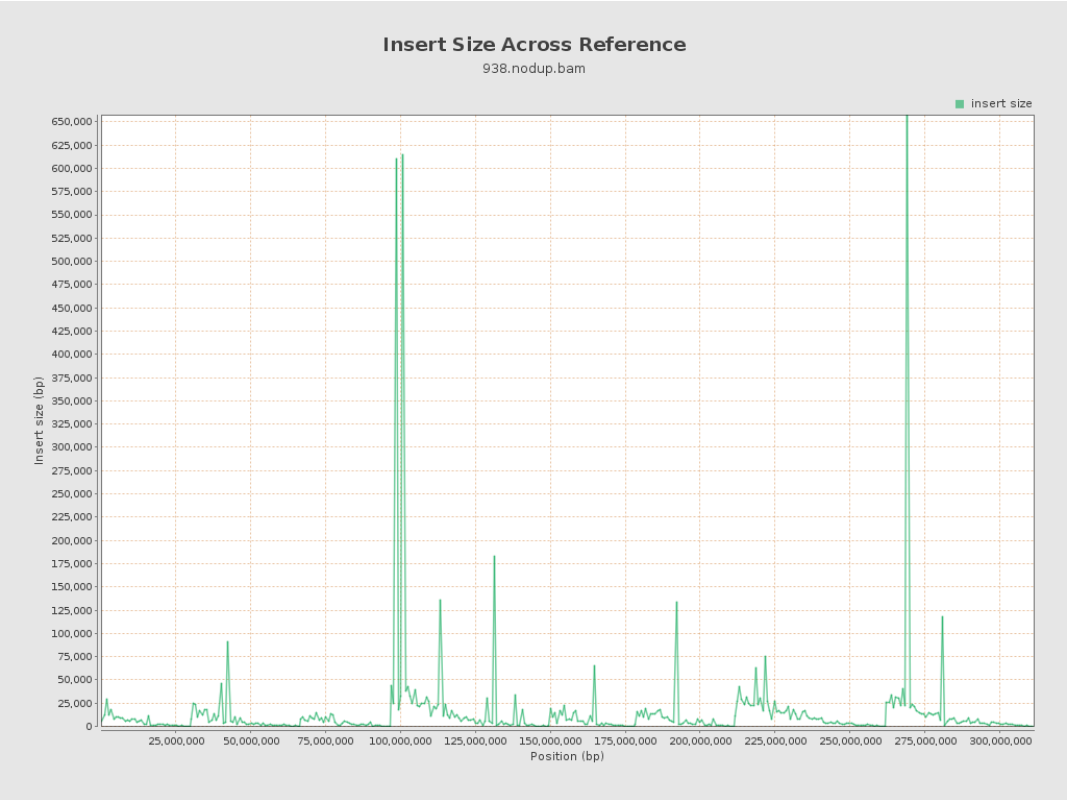
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram