# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:28:53*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/830.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| BAM file: | /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/830.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_219/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_219_S300_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_219/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_219_S300_L003_R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| Number of windows: | 400 |

| | |
|---|---|
| Analysis date: | Mon May 29 21:28:52 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 311,642,060 |
| Number of reads | 57,953,794 |
| Mapped reads | 54,473,918 / 94% |
| Unmapped reads | 3,479,876 / 6% |
| Mapped paired reads | 54,473,918 / 94% |
| Mapped reads, first in pair | 27,312,128 / 47.13% |
| Mapped reads,  second in pair | 27,161,790 / 46.87% |
| Mapped reads, both in pair | 53,289,247 / 91.95% |
| Mapped reads, singletons | 1,184,671 / 2.04% |
| Read min/max/mean length | 30 / 151 / 147.95 |
| Duplicated reads (flagged) | 7,907,513 / 13.64% |
| Clipped reads | 12,928,349 / 22.31% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 2,303,357,739 / 30.69% |
| Number/percentage of C's | 1,448,127,377 / 19.29% |
| Number/percentage of T's | 2,309,448,468 / 30.77% |
| Number/percentage of G's | 1,444,686,728 / 19.25% |
| Number/percentage of N's | 27,765 / 0% |
| GC Percentage | 38.54% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 24.1475 |
| Standard Deviation | 218.2032 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.71 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 236,298.18 |
| Standard Deviation | 2,299,406.67 |
| P25/Median/P75 | 327 / 432 / 563 |

## 2.6. Mismatches and indels

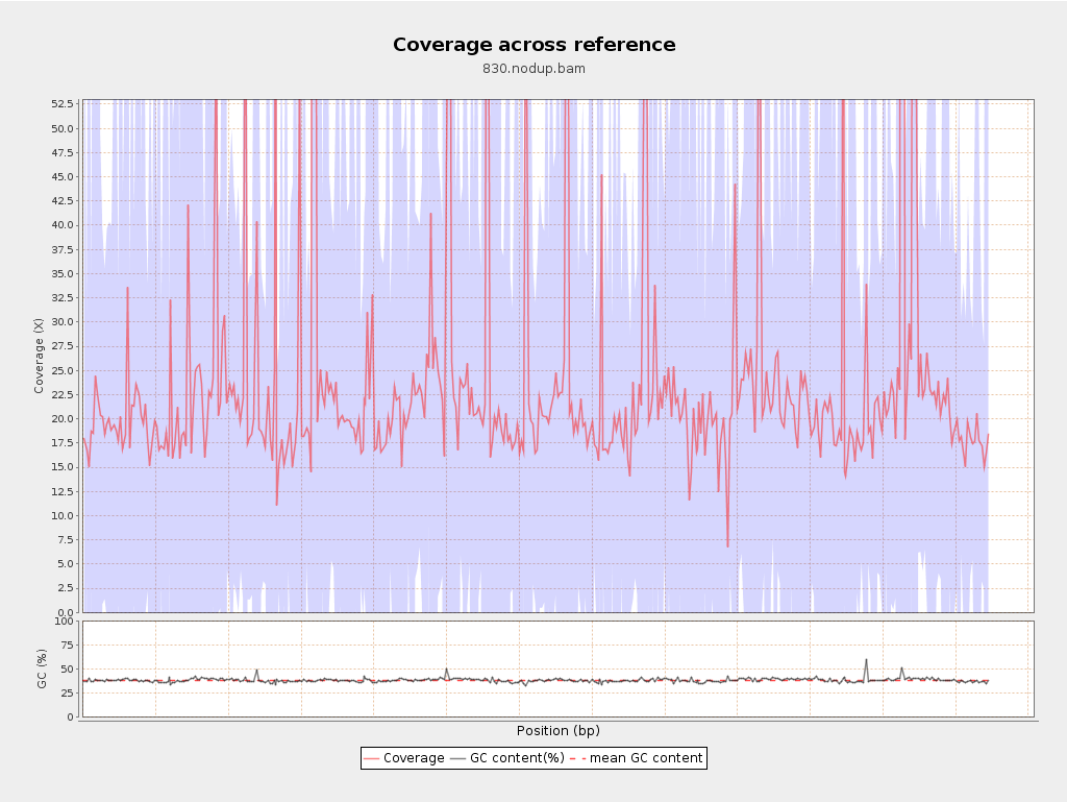
| | |
|---|---|
| General error rate | 2.39% |
| Mismatches | 165,120,908 |
| Insertions | 5,135,716 |
| Mapped reads with at least one insertion | 8.46% |
| Deletions | 5,212,684 |
| Mapped reads with at least one deletion | 8.47% |
| Homopolymer indels | 55.75% |

## 2.7. Chromosome stats

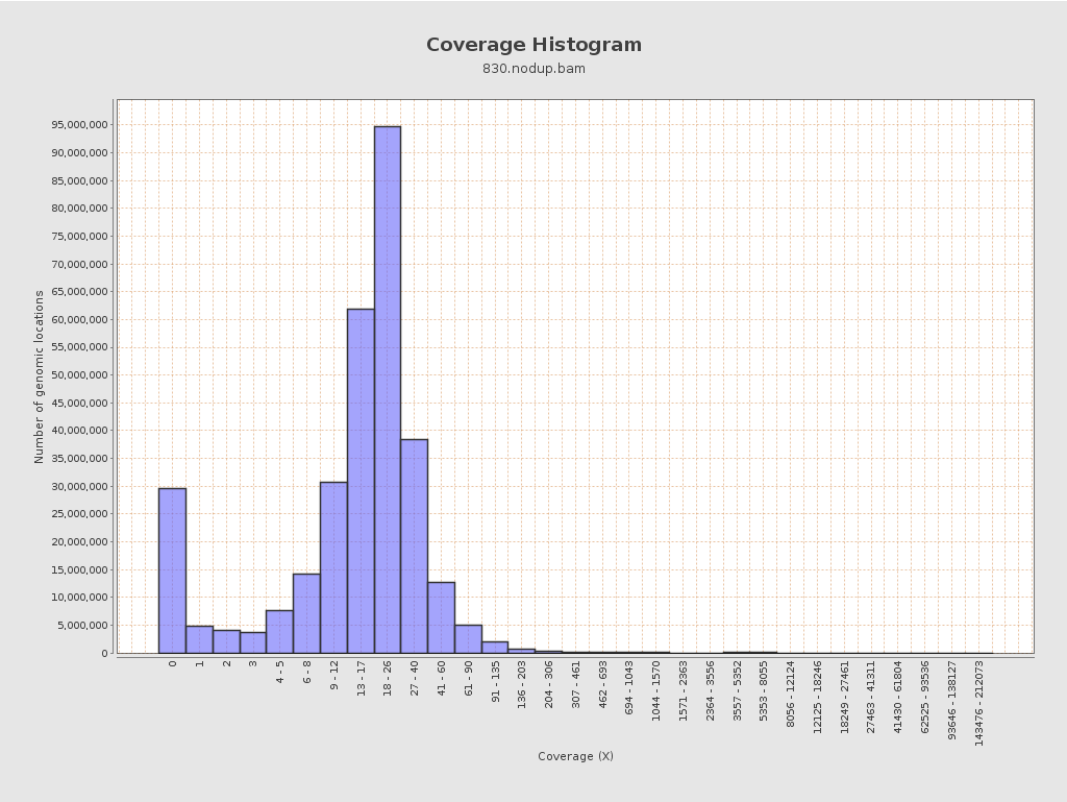
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| LT669788.1 | 29724344 | 577971247 | 19.4444 | 75.175 |

| | | | | |
|---|---|---|---|---|
| LT669789.1 | 36598175 | 882855380 | 24.1229 | 223.8051 |
| LT669790.1 | 30422129 | 780844140 | 25.667 | 204.0964 |
| LT669791.1 | 52758100 | 1262875060 | 23.9371 | 205.3391 |
| LT669792.1 | 28376109 | 669828016 | 23.6054 | 243.2762 |
| LT669793.1 | 33388210 | 754560255 | 22.5996 | 144.786 |
| LT669794.1 | 50579949 | 1167483634 | 23.0819 | 190.1364 |
| LT669795.1 | 49795044 | 1428956903 | 28.6968 | 321.1411 |

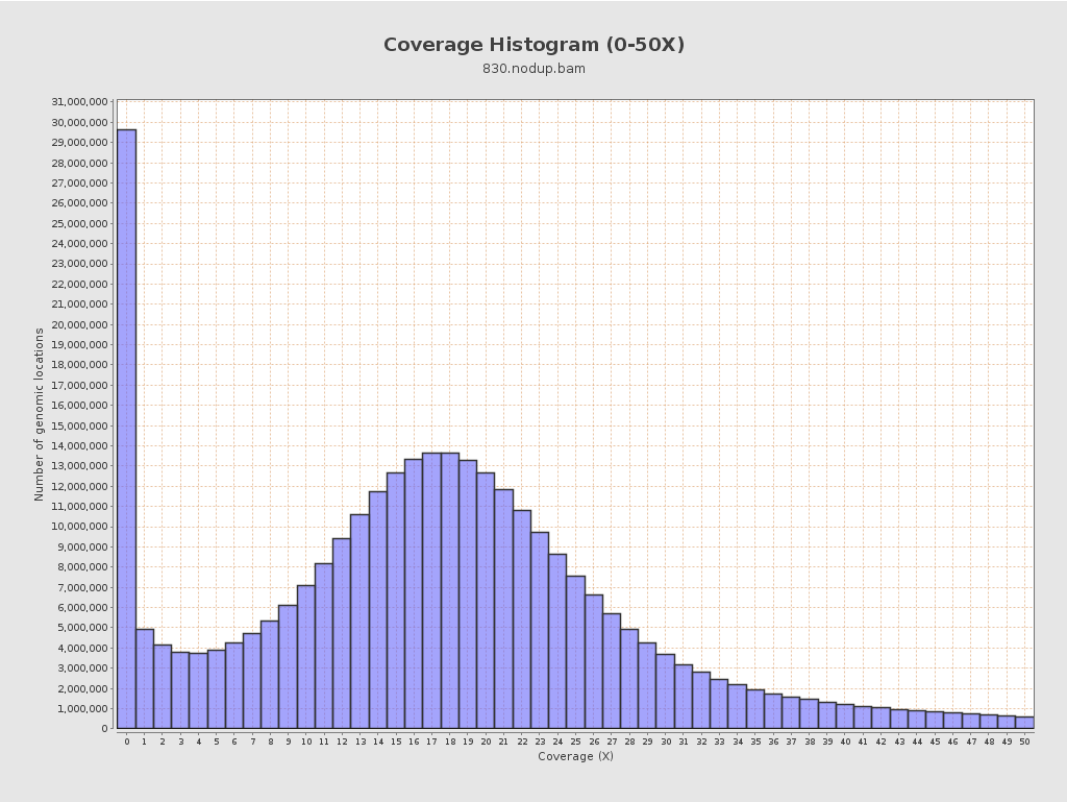
# 3. Results : Coverage across reference



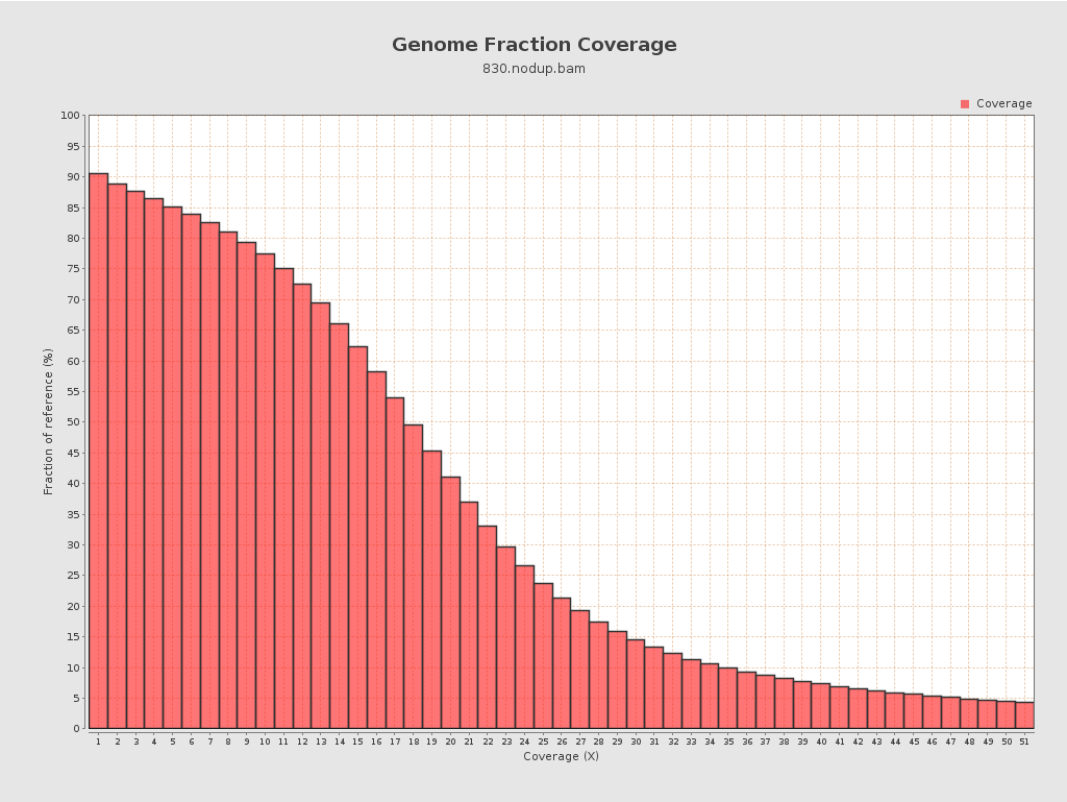
# 4. Results : Coverage Histogram



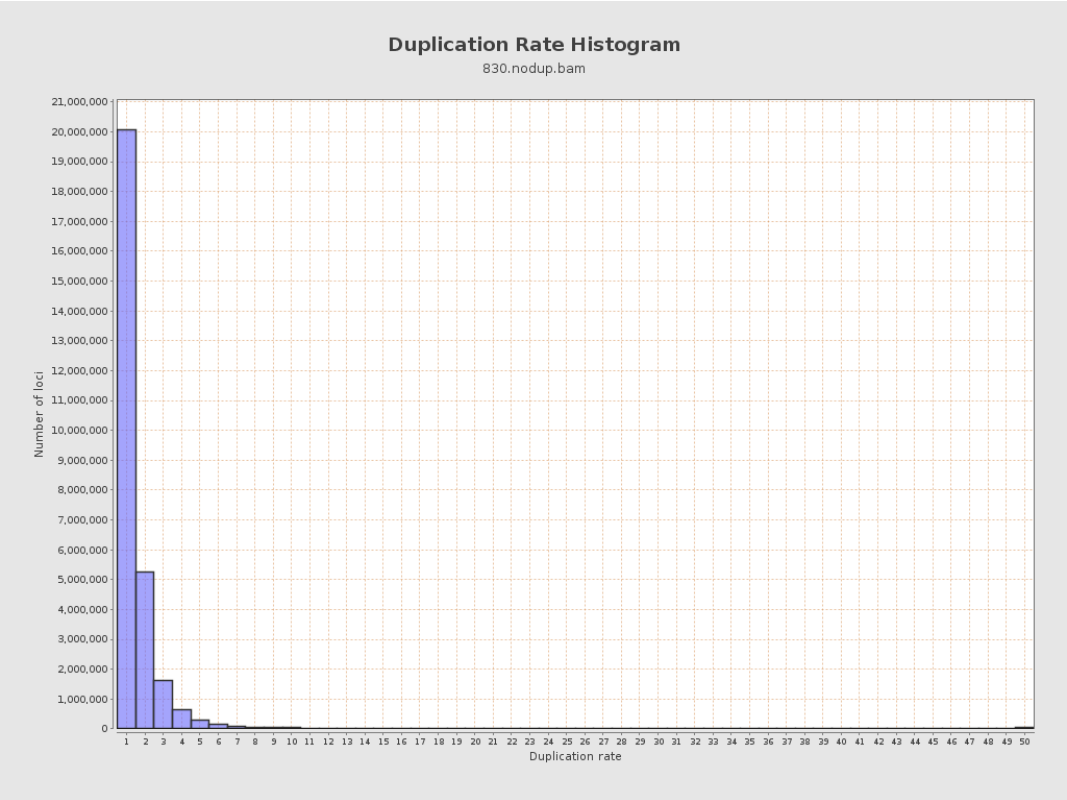
# 5. Results : Coverage Histogram (0-50X)



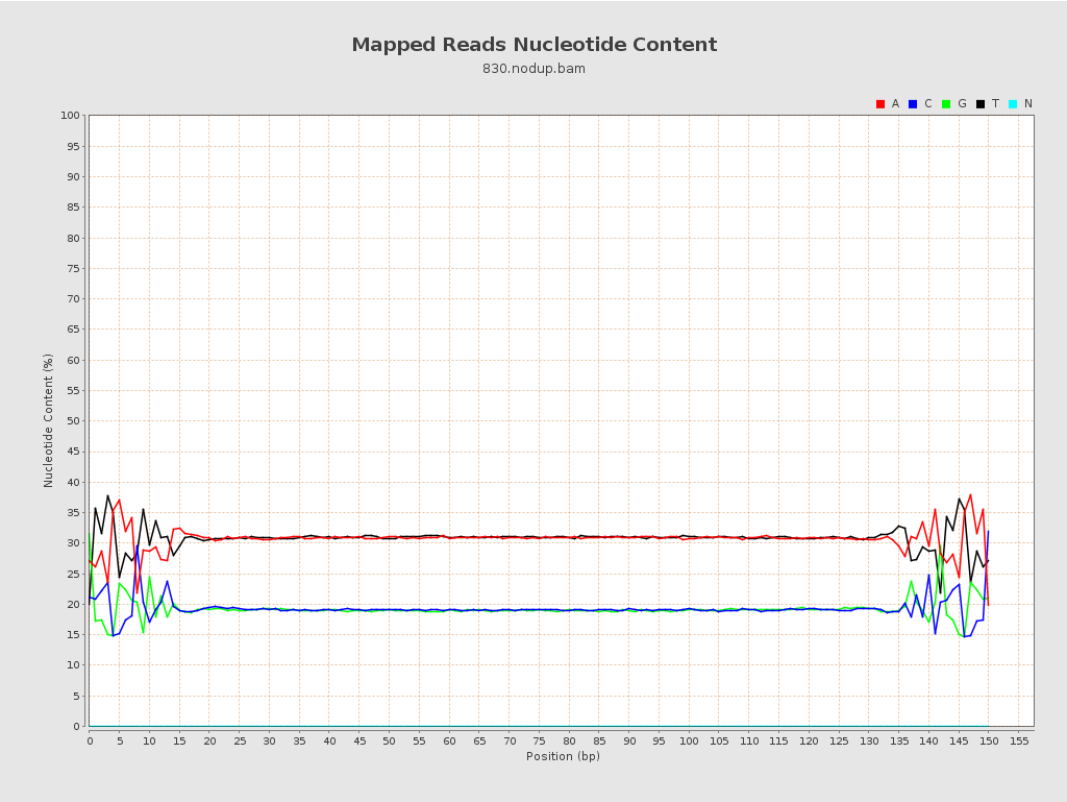
# 6. Results : Genome Fraction Coverage



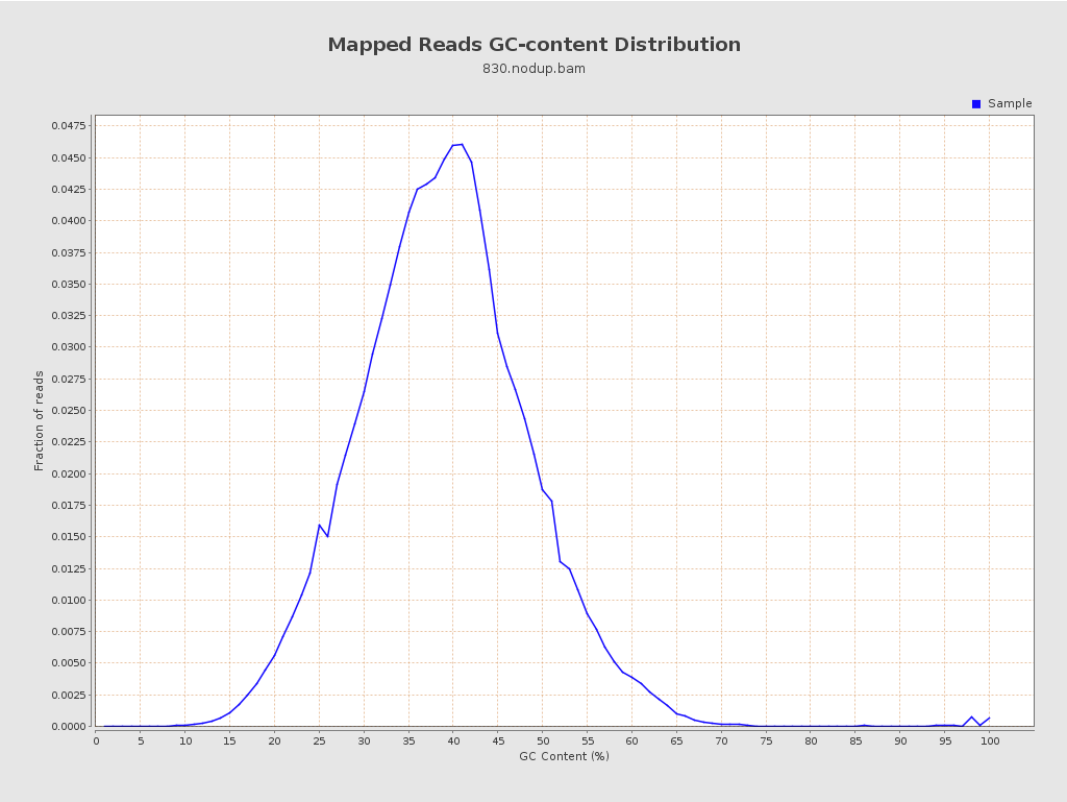
# 7. Results : Duplication Rate Histogram



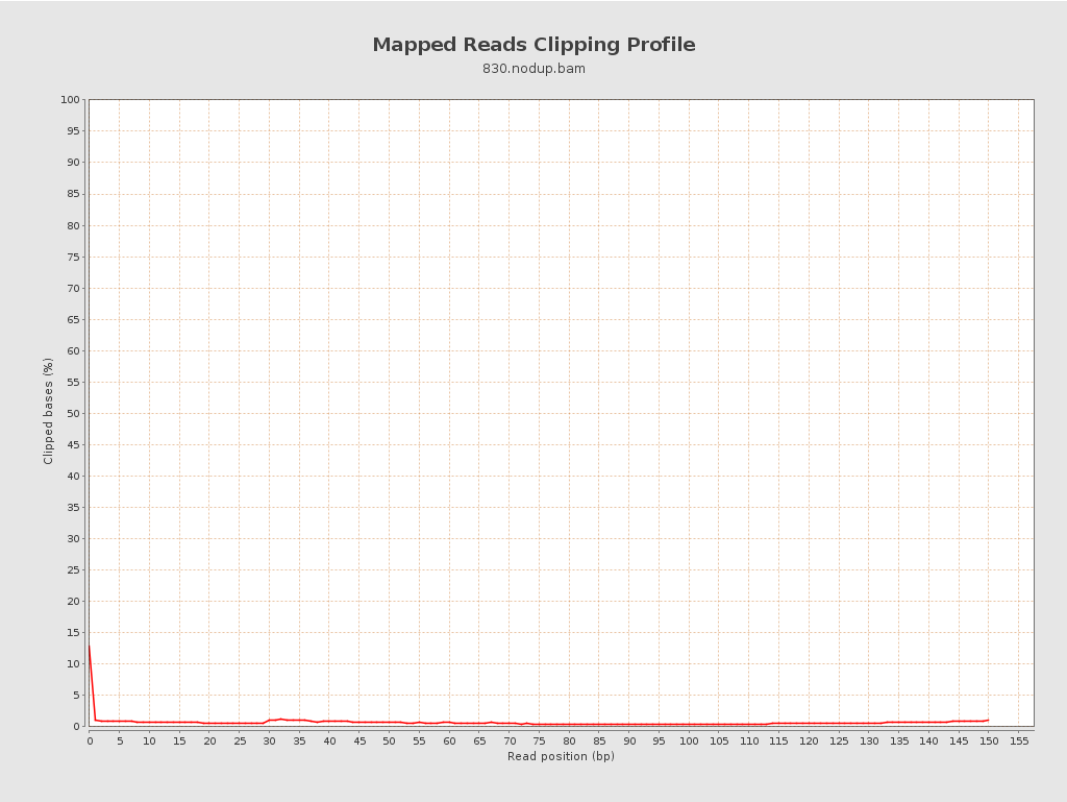
# 8. Results : Mapped Reads Nucleotide Content



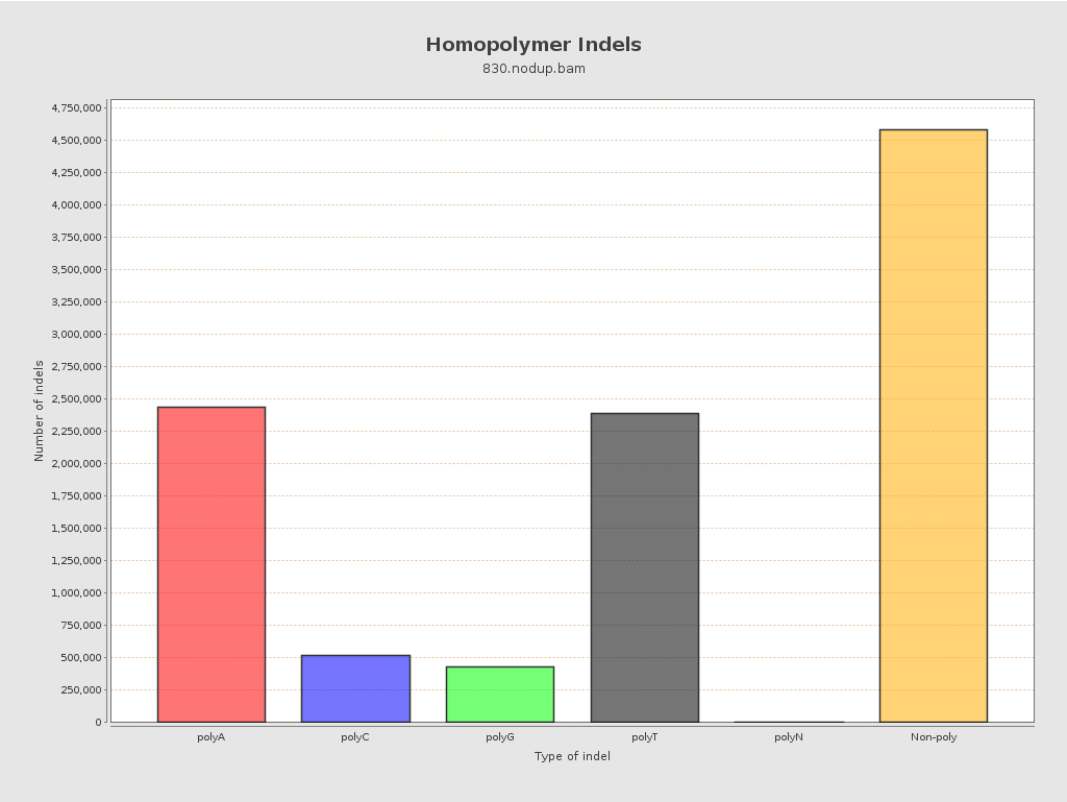
# 9. Results : Mapped Reads GC-content Distribution



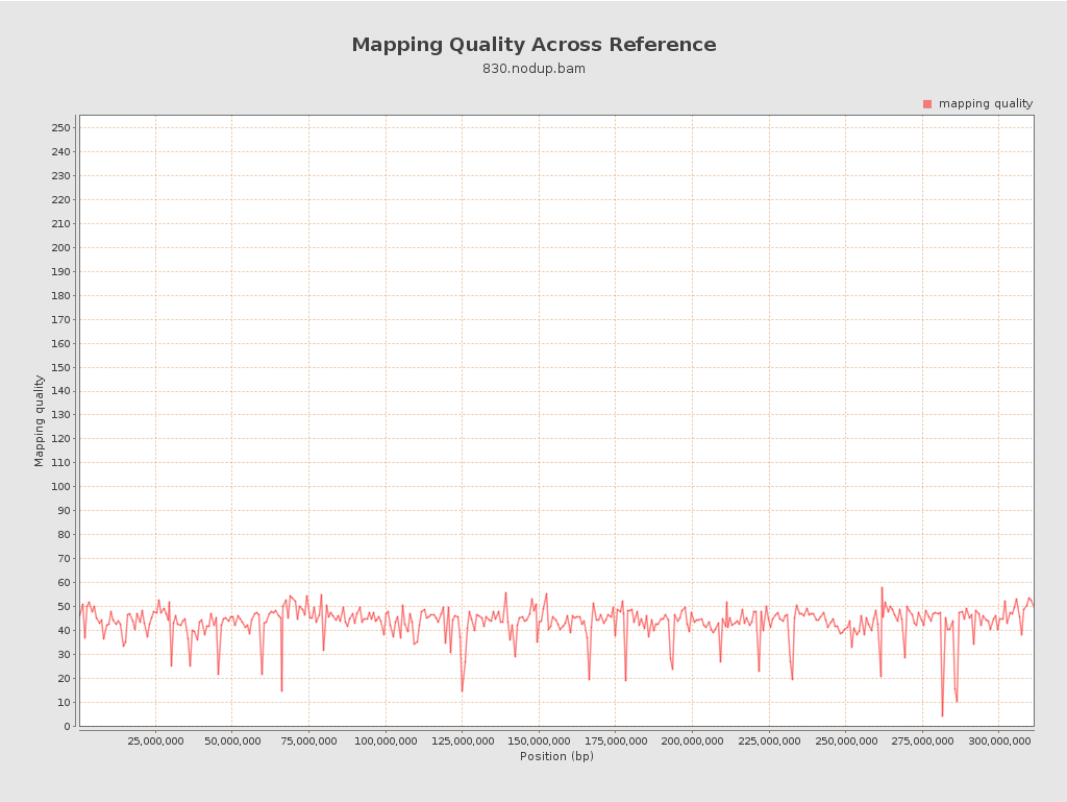
# 10. Results : Mapped Reads Clipping Profile



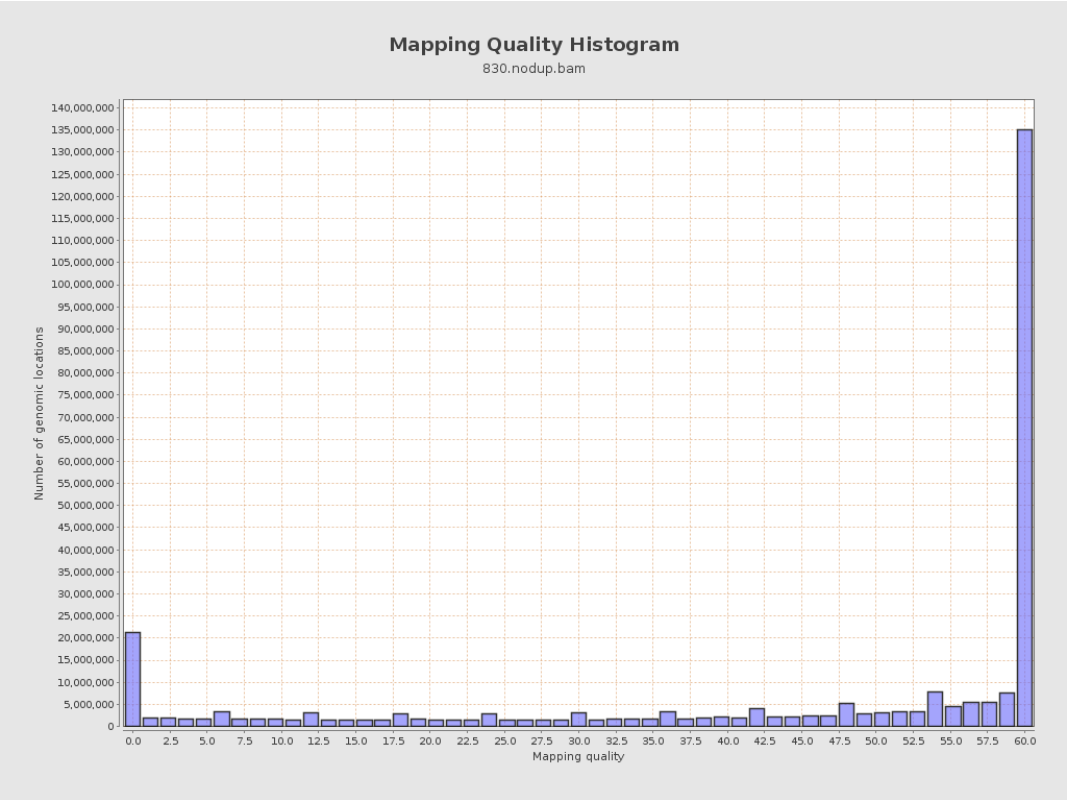
# 11. Results : Homopolymer Indels



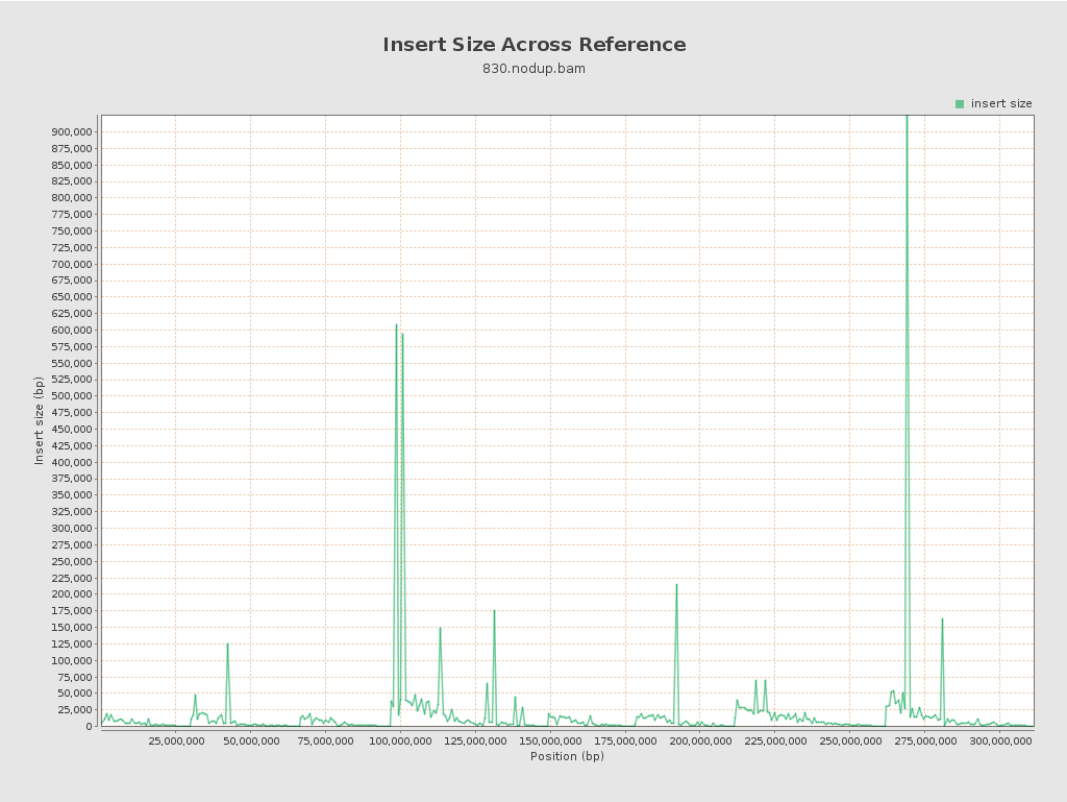
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram