# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:36:02*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/947.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| BAM file: | /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/947.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_435/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_435_S410_L004_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_435/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_435_S410_L004_R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| Number of windows: | 400 |

| | |
|---|---|
| Analysis date: | Mon May 29 21:36:01 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 311,642,060 |
| Number of reads | 78,410,726 |
| Mapped reads | 74,418,229 / 94.91% |
| Unmapped reads | 3,992,497 / 5.09% |
| Mapped paired reads | 74,418,229 / 94.91% |
| Mapped reads, first in pair | 37,279,461 / 47.54% |
| Mapped reads,  second in pair | 37,138,768 / 47.36% |
| Mapped reads, both in pair | 73,139,926 / 93.28% |
| Mapped reads, singletons | 1,278,303 / 1.63% |
| Read min/max/mean length | 30 / 151 / 148.19 |
| Duplicated reads (flagged) | 11,701,359 / 14.92% |
| Clipped reads | 15,768,043 / 20.11% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 3,204,607,630 / 30.83% |
| Number/percentage of C's | 1,994,357,064 / 19.19% |
| Number/percentage of T's | 3,207,894,564 / 30.86% |
| Number/percentage of G's | 1,986,856,809 / 19.12% |
| Number/percentage of N's | 36,903 / 0% |
| GC Percentage | 38.3% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 33.438 |
| Standard Deviation | 272.2772 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 43.99 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 219,107.01 |
| Standard Deviation | 2,193,955.33 |
| P25/Median/P75 | 331 / 433 / 571 |

## 2.6. Mismatches and indels

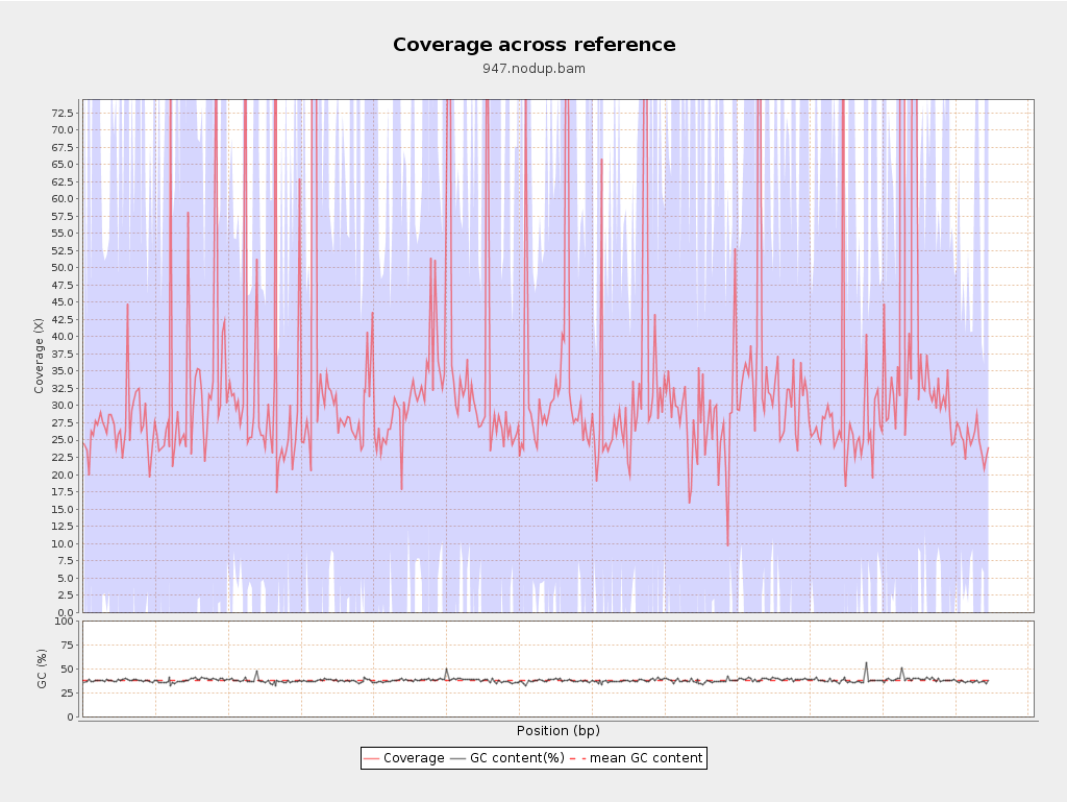
| | |
|---|---|
| General error rate | 2.28% |
| Mismatches | 218,191,622 |
| Insertions | 6,803,659 |
| Mapped reads with at least one insertion | 8.24% |
| Deletions | 7,118,785 |
| Mapped reads with at least one deletion | 8.49% |
| Homopolymer indels | 56.02% |

## 2.7. Chromosome stats

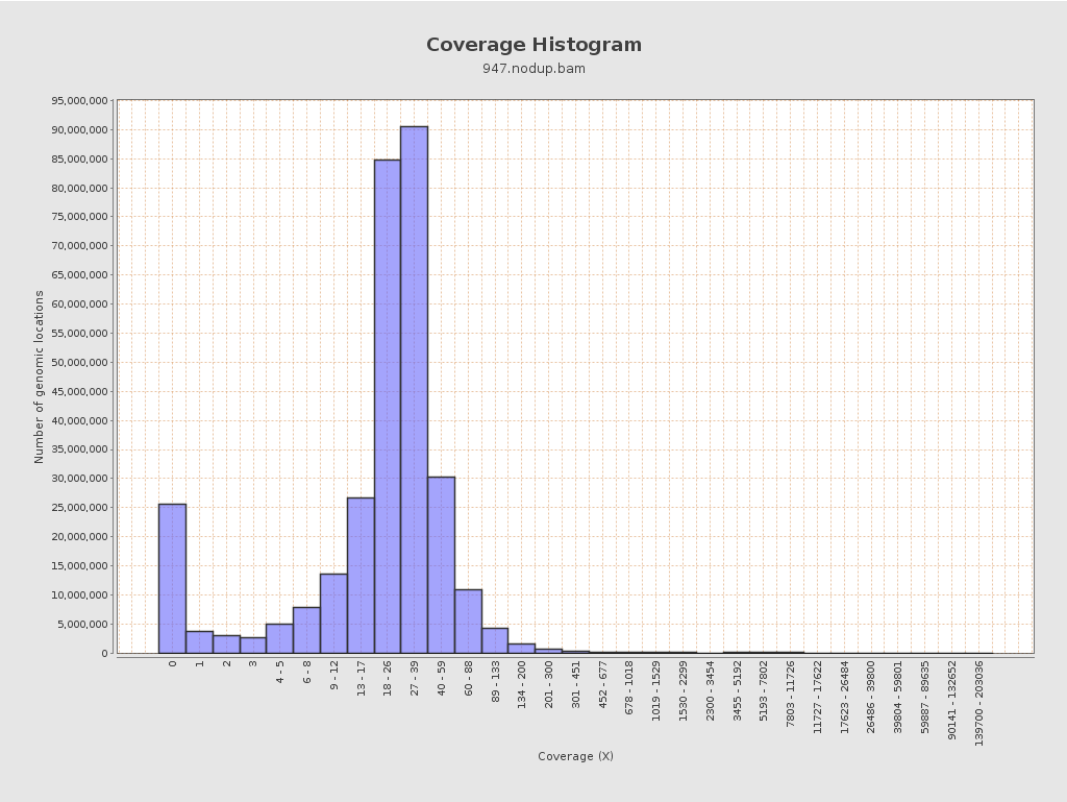
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| LT669788.1 | 29724344 | 797716453 | 26.8371 | 69.9515 |

| | | | | |
|---|---|---|---|---|
| LT669789.1 | 36598175 | 1247263927 | 34.0799 | 293.699 |
| LT669790.1 | 30422129 | 1038845462 | 34.1477 | 235.2516 |
| LT669791.1 | 52758100 | 1741954456 | 33.0178 | 211.3763 |
| LT669792.1 | 28376109 | 914814913 | 32.2389 | 296.7334 |
| LT669793.1 | 33388210 | 1049126115 | 31.4221 | 189.0915 |
| LT669794.1 | 50579949 | 1625973322 | 32.1466 | 242.0162 |
| LT669795.1 | 49795044 | 2005006674 | 40.2652 | 427.5257 |

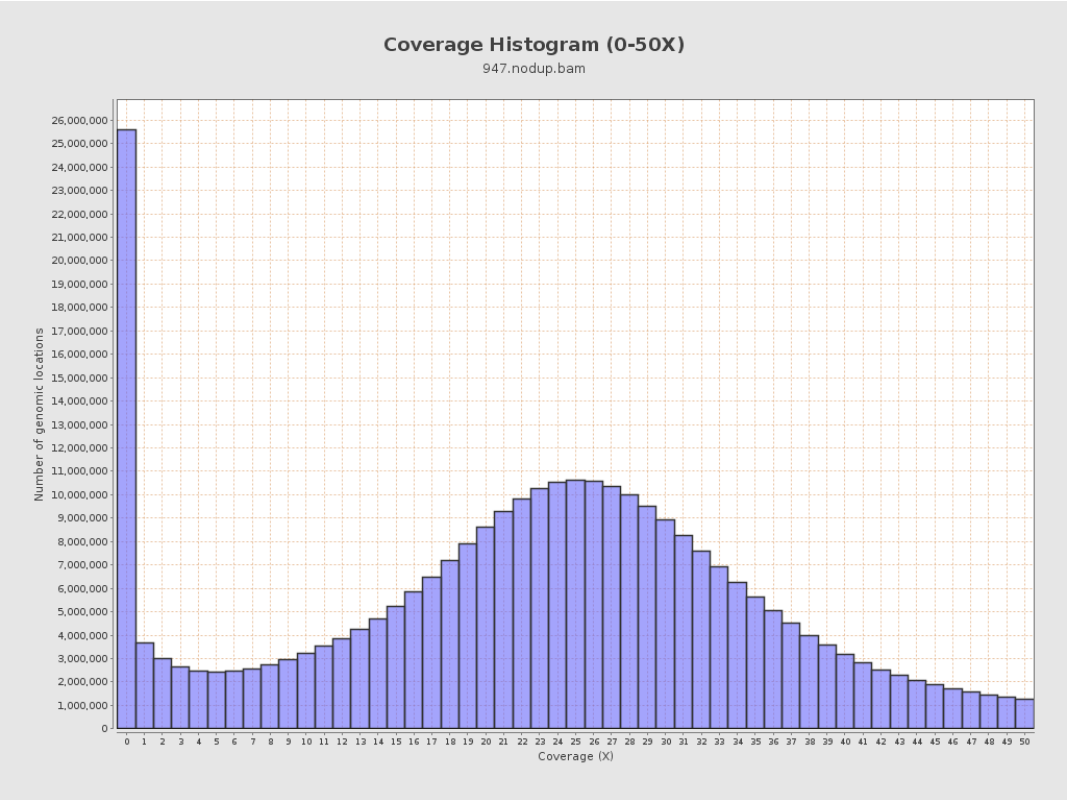
# 3. Results : Coverage across reference



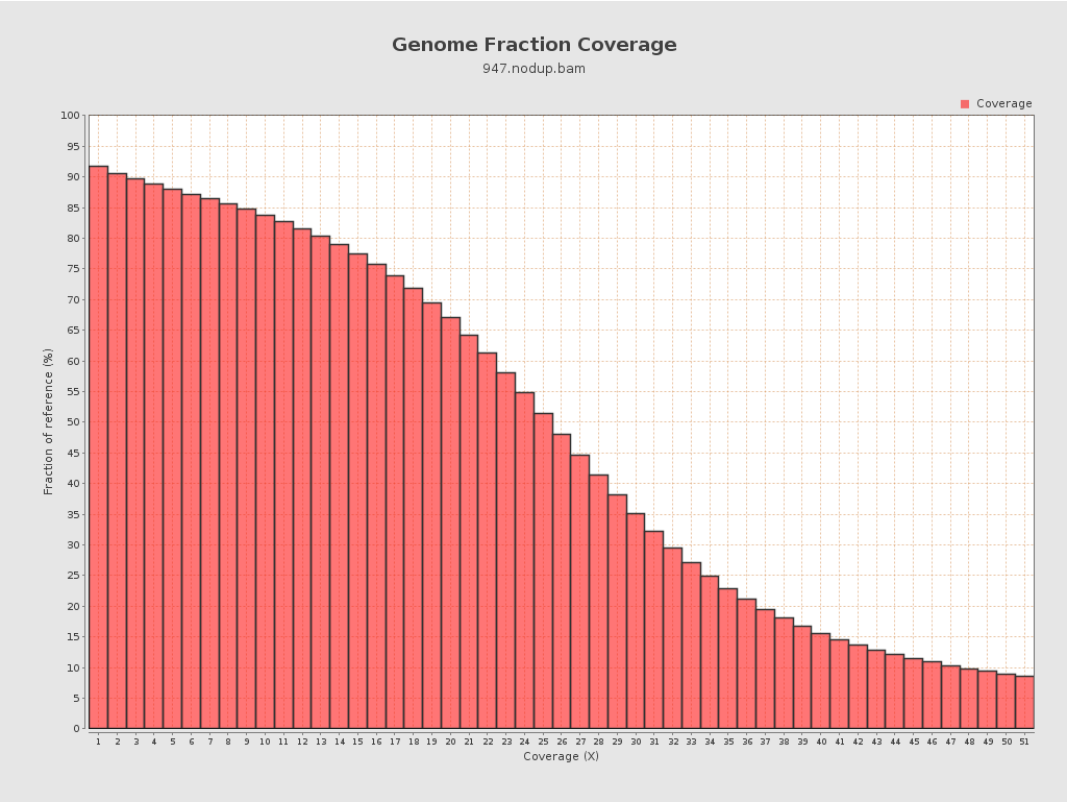
# 4. Results : Coverage Histogram



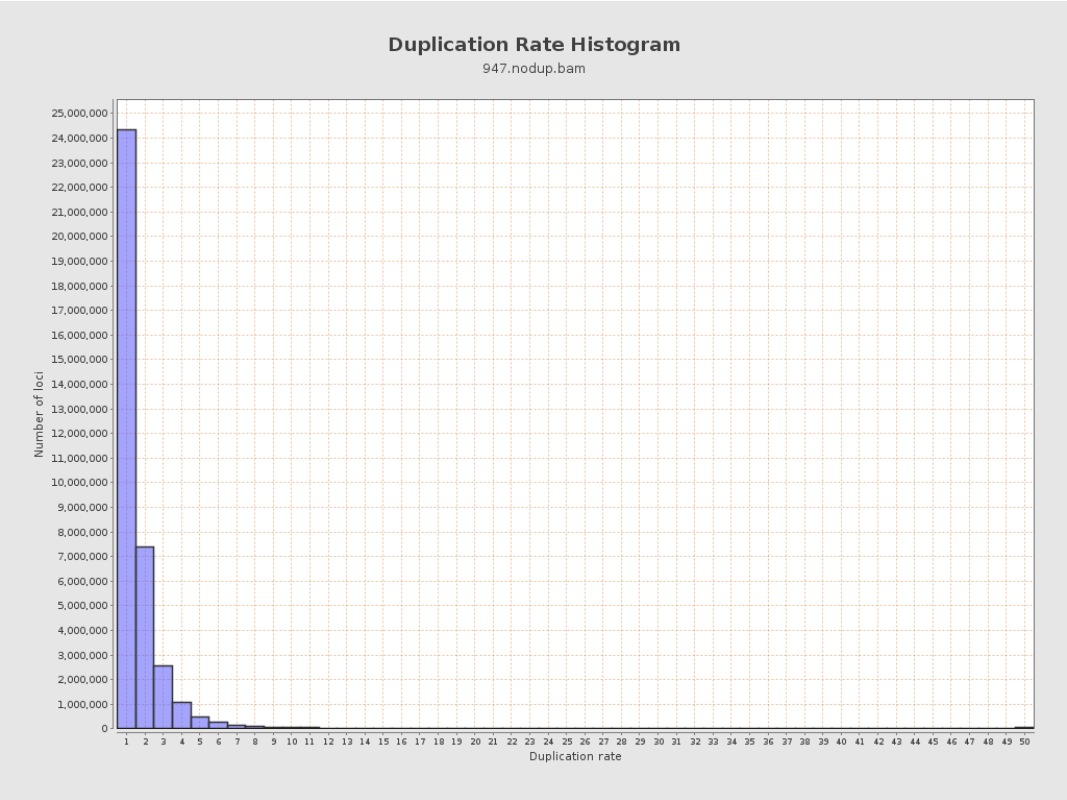
# 5. Results : Coverage Histogram (0-50X)



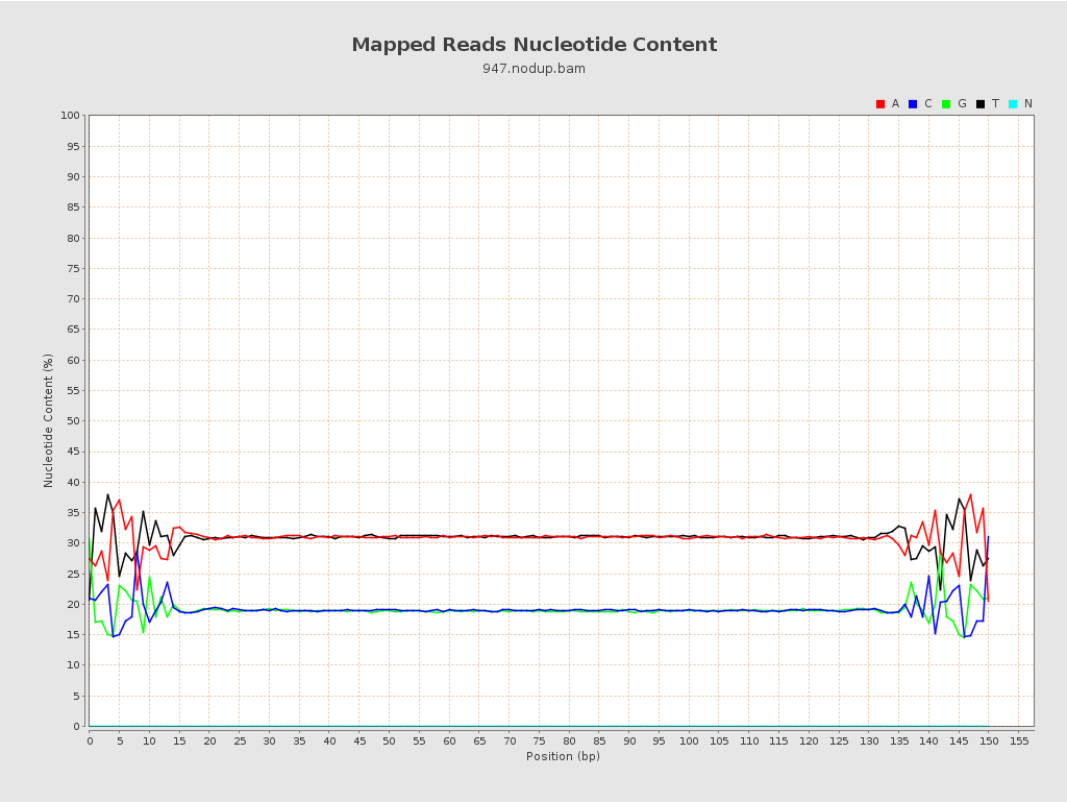
# 6. Results : Genome Fraction Coverage



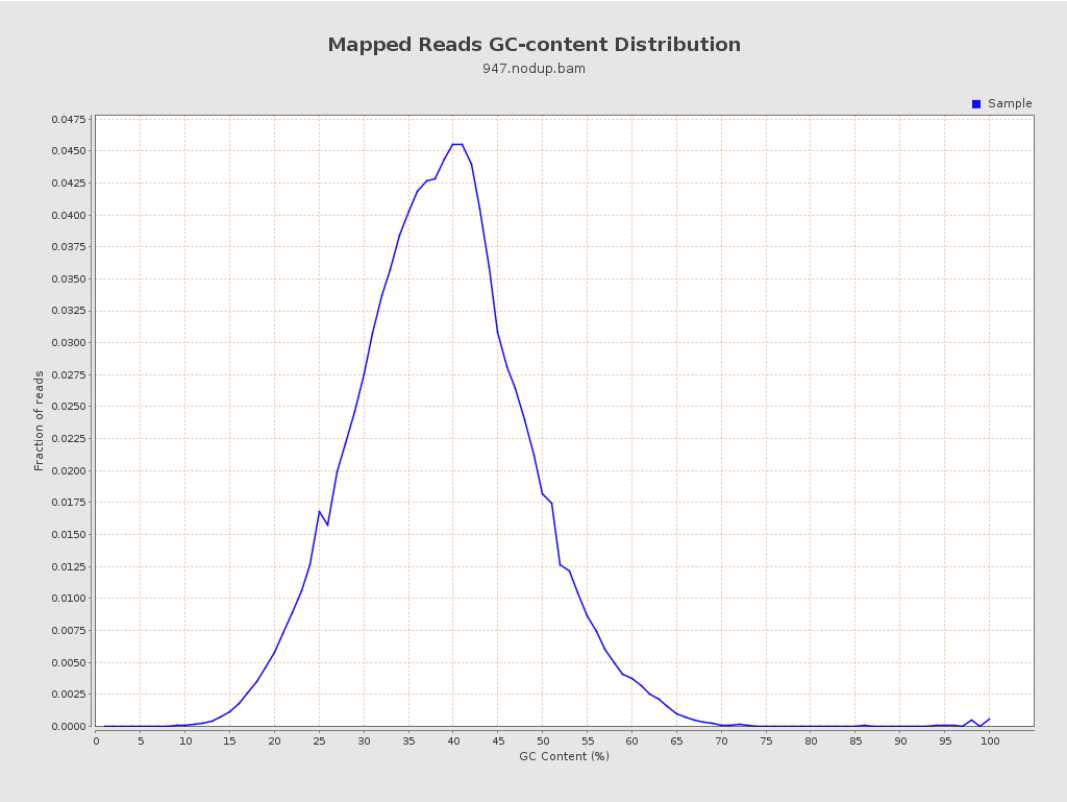
# 7. Results : Duplication Rate Histogram



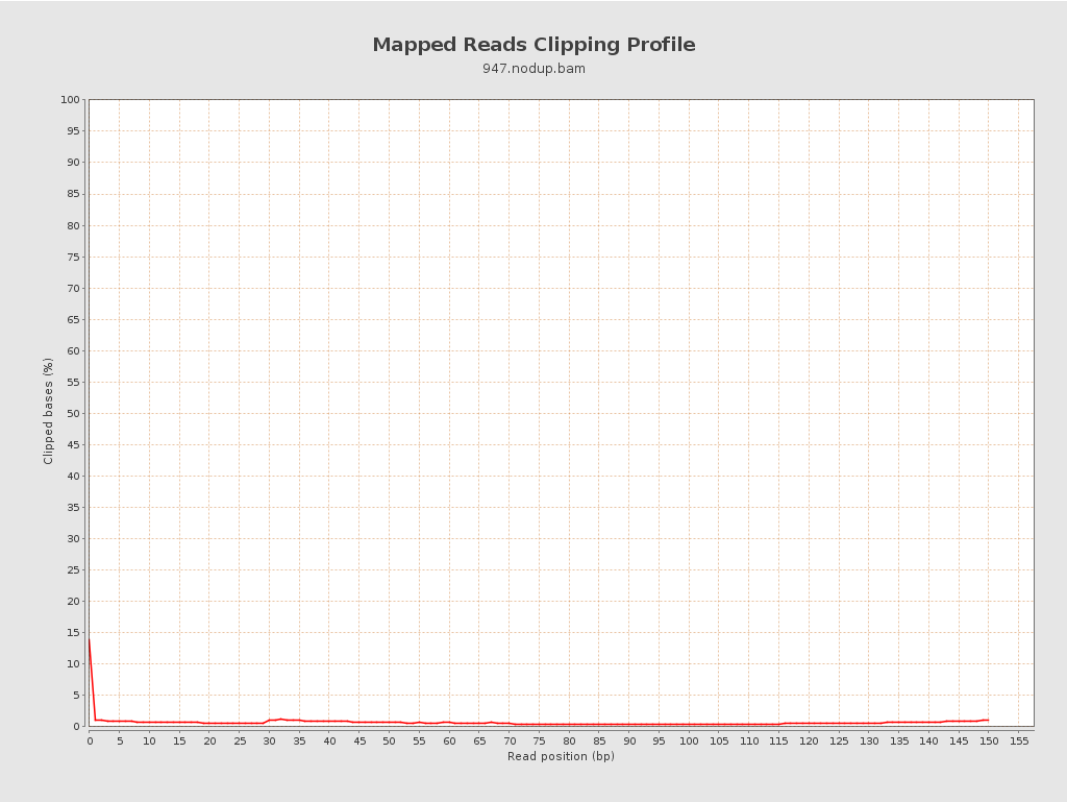
# 8. Results : Mapped Reads Nucleotide Content



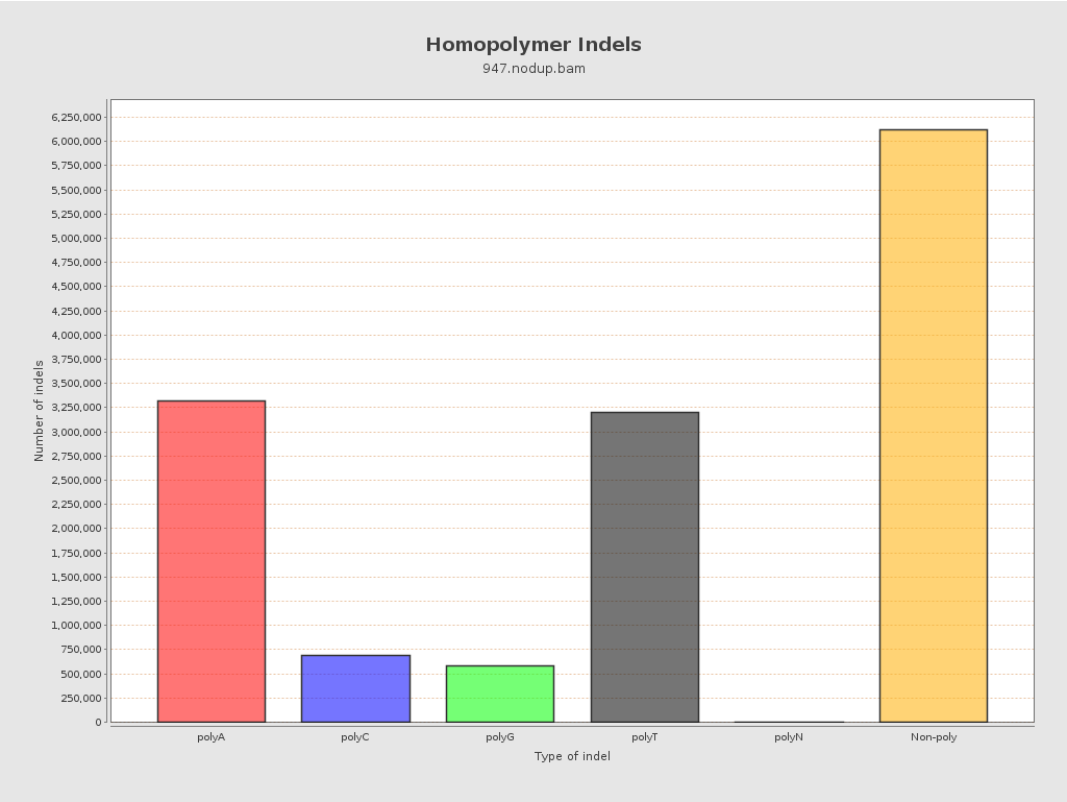
# 9. Results : Mapped Reads GC-content Distribution



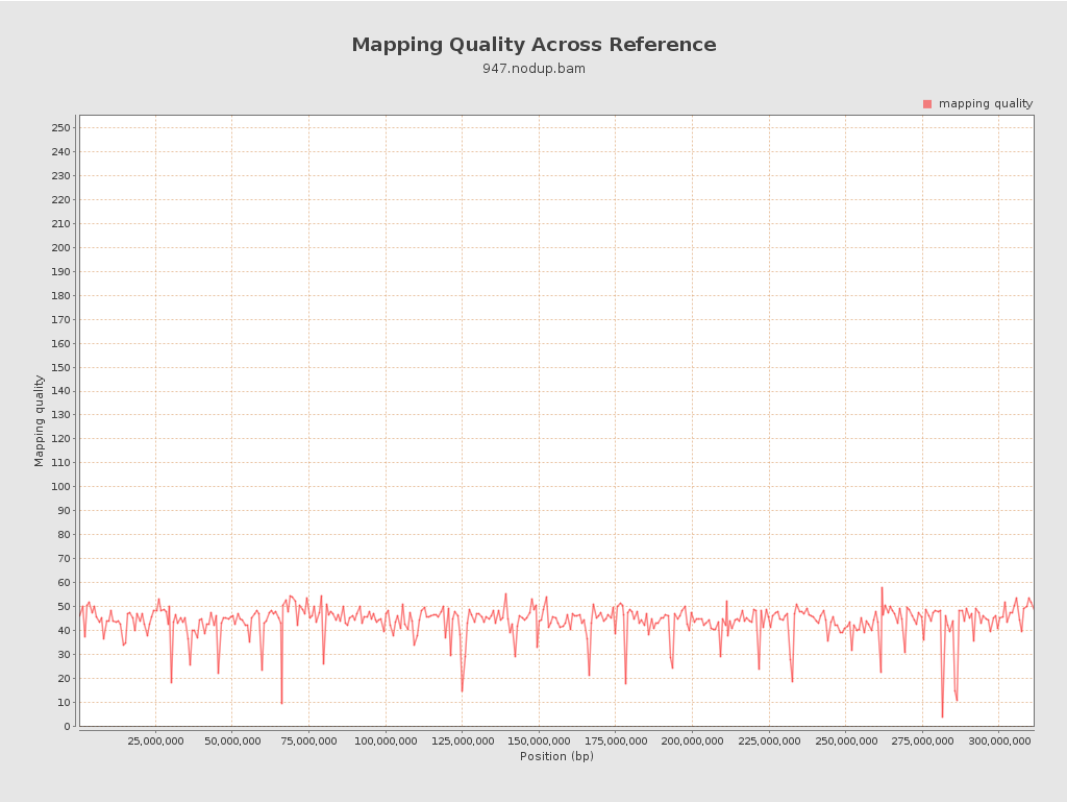
# 10. Results : Mapped Reads Clipping Profile



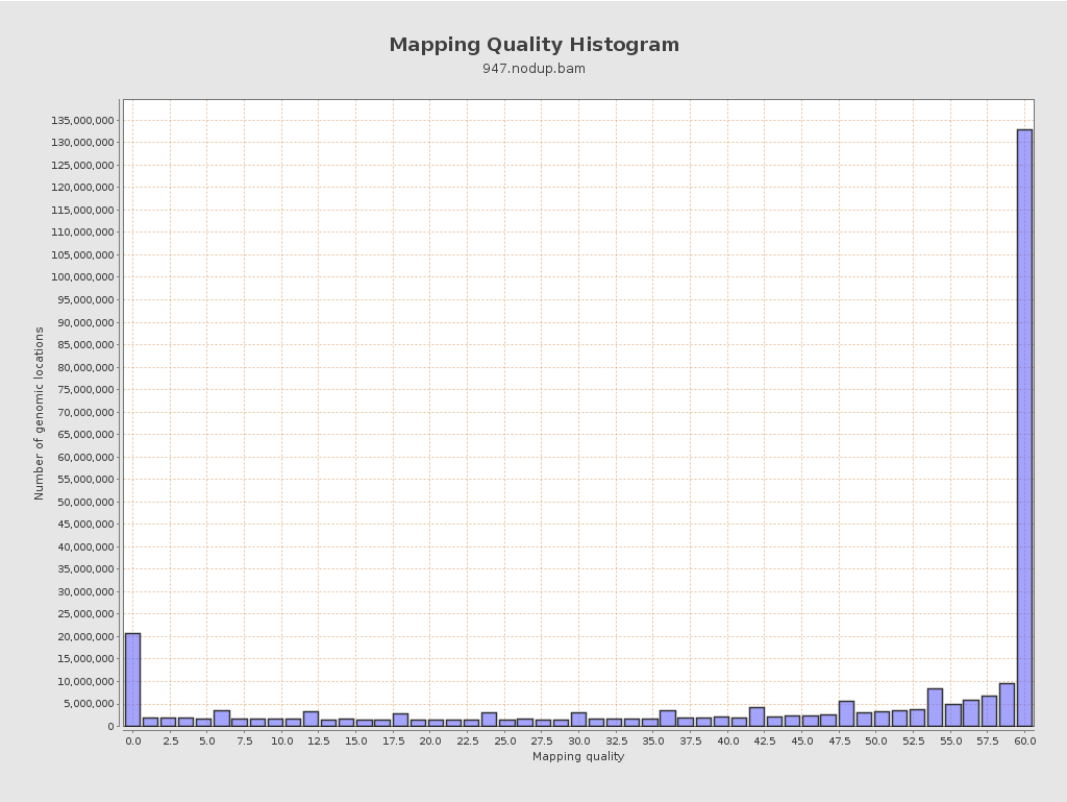
# 11. Results : Homopolymer Indels



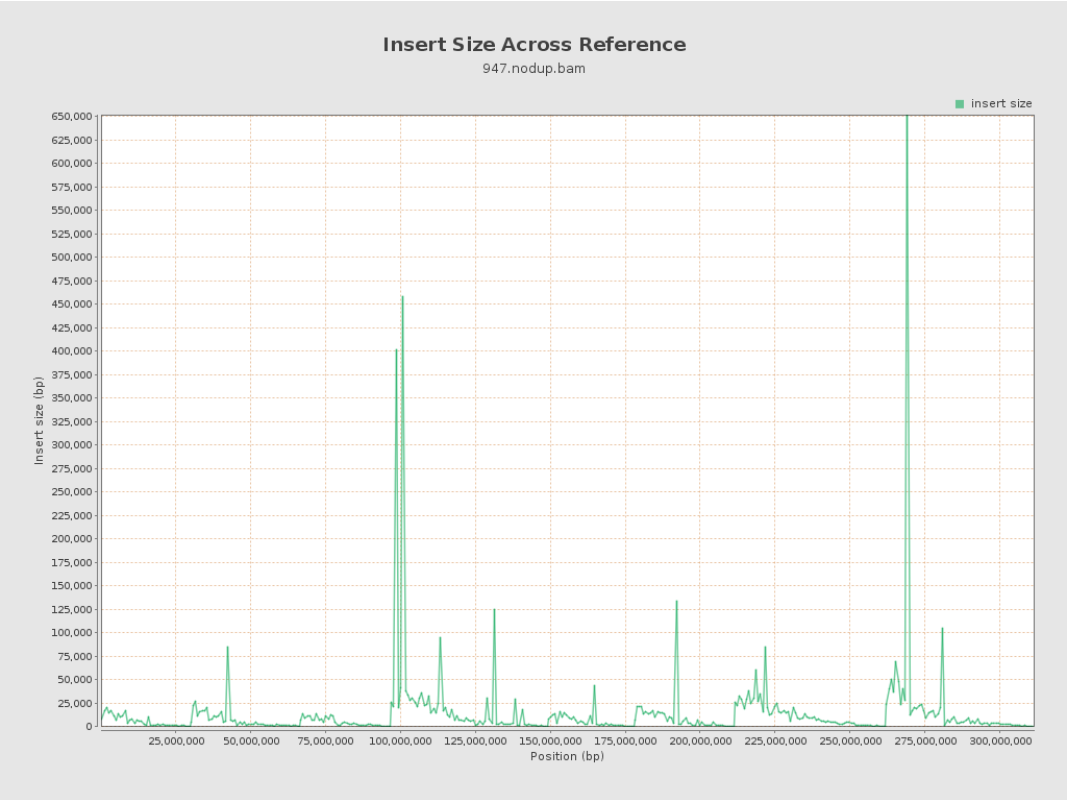
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram