# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:28:48*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/531.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

| | |
|---|---|
| BAM file: | /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/531.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_218/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_218_S299_L003_R1_001.fastq.gz /proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_218/02-FASTQ/220902_A00621_0737_BHMGCVDSX3/P26207_218_S299_L003_R2_001.fastq.gz |
| Size of a homopolymer: | 3 |
| Number of windows: | 400 |

| | |
|---|---|
| Analysis date: | Mon May 29 21:28:48 CEST 2023 |
| Draw chromosome limits: | no |
| Skip duplicate alignments: | no |

# 2. Summary

## 2.1. Globals

| | |
|---|---|
| Reference size | 311,642,060 |
| Number of reads | 60,366,934 |
| Mapped reads | 55,809,140 / 92.45% |
| Unmapped reads | 4,557,794 / 7.55% |
| Mapped paired reads | 55,809,140 / 92.45% |
| Mapped reads, first in pair | 27,971,014 / 46.33% |
| Mapped reads,  second in pair | 27,838,126 / 46.11% |
| Mapped reads, both in pair | 54,326,256 / 89.99% |
| Mapped reads, singletons | 1,482,884 / 2.46% |
| Read min/max/mean length | 30 / 151 / 148.17 |
| Duplicated reads (flagged) | 8,335,015 / 13.81% |
| Clipped reads | 12,872,610 / 21.32% |

## 2.2. ACGT Content

| | |
|---|---|
| Number/percentage of A's | 2,377,461,461 / 30.9% |
| Number/percentage of C's | 1,469,553,013 / 19.1% |
| Number/percentage of T's | 2,378,355,131 / 30.92% |
| Number/percentage of G's | 1,467,714,723 / 19.08% |
| Number/percentage of N's | 28,732 / 0% |
| GC Percentage | 38.18% |

## 2.3. Coverage

| | |
|---|---|
| Mean | 24.7478 |
| Standard Deviation | 216.5484 |

## 2.4. Mapping Quality

| | |
|---|---|
| Mean Mapping Quality | 44.61 |

## 2.5. Insert size

| | |
|---|---|
| Mean | 236,222.79 |
| Standard Deviation | 2,327,801.04 |
| P25/Median/P75 | 317 / 416 / 542 |

## 2.6. Mismatches and indels

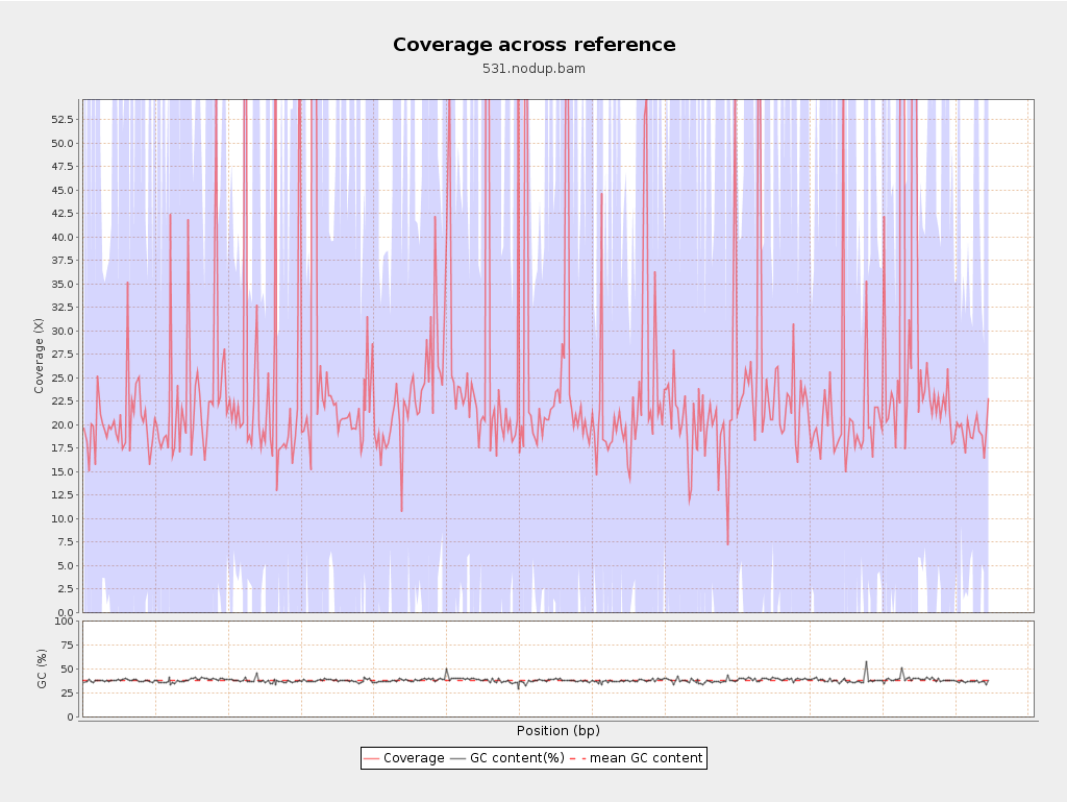
| | |
|---|---|
| General error rate | 2.3% |
| Mismatches | 162,284,219 |
| Insertions | 5,319,019 |
| Mapped reads with at least one insertion | 8.54% |
| Deletions | 5,173,388 |
| Mapped reads with at least one deletion | 8.25% |
| Homopolymer indels | 57.14% |

## 2.7. Chromosome stats

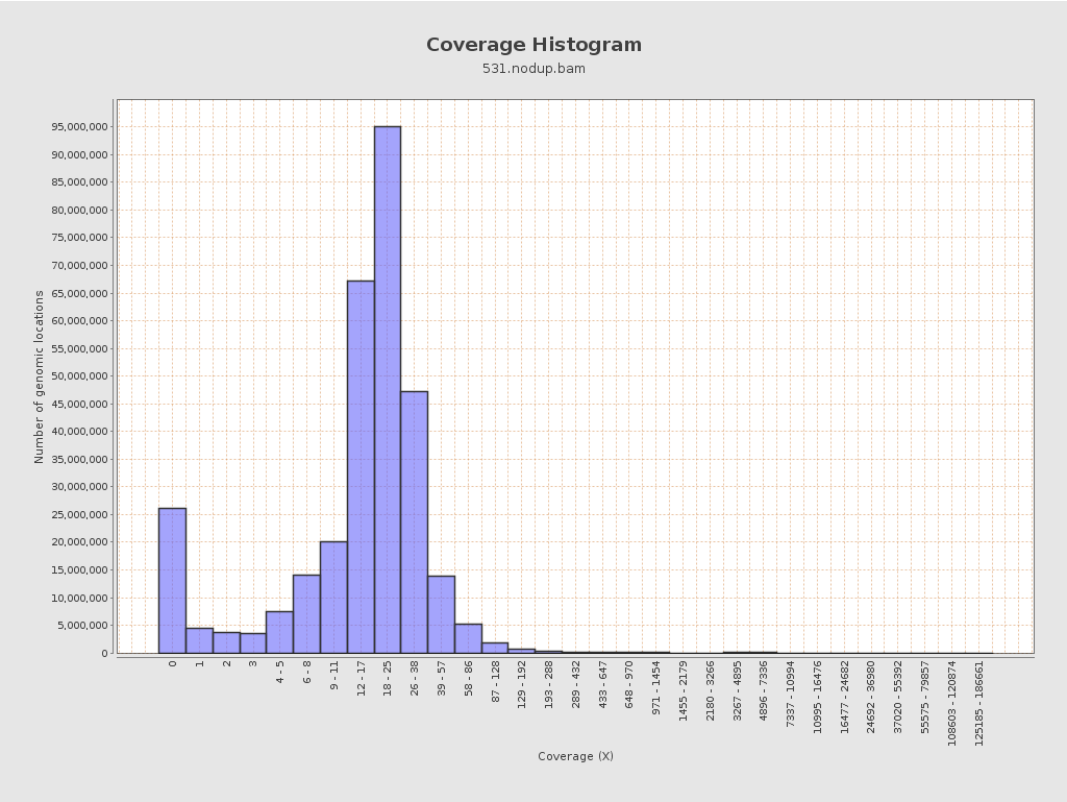
| Name | Length | Mapped bases | Mean coverage | Standard deviation |
|---|---|---|---|---|
| LT669788.1 | 29724344 | 594574884 | 20.003 | 75.3365 |

| | | | | |
|---|---|---|---|---|
| LT669789.1 | 36598175 | 901763053 | 24.6396 | 215.3242 |
| LT669790.1 | 30422129 | 876589121 | 28.8142 | 280.0244 |
| LT669791.1 | 52758100 | 1298222226 | 24.6071 | 213.9739 |
| LT669792.1 | 28376109 | 700117807 | 24.6728 | 231.1224 |
| LT669793.1 | 33388210 | 745738655 | 22.3354 | 143.0172 |
| LT669794.1 | 50579949 | 1164958199 | 23.032 | 171.1817 |
| LT669795.1 | 49795044 | 1430498308 | 28.7277 | 292.6331 |

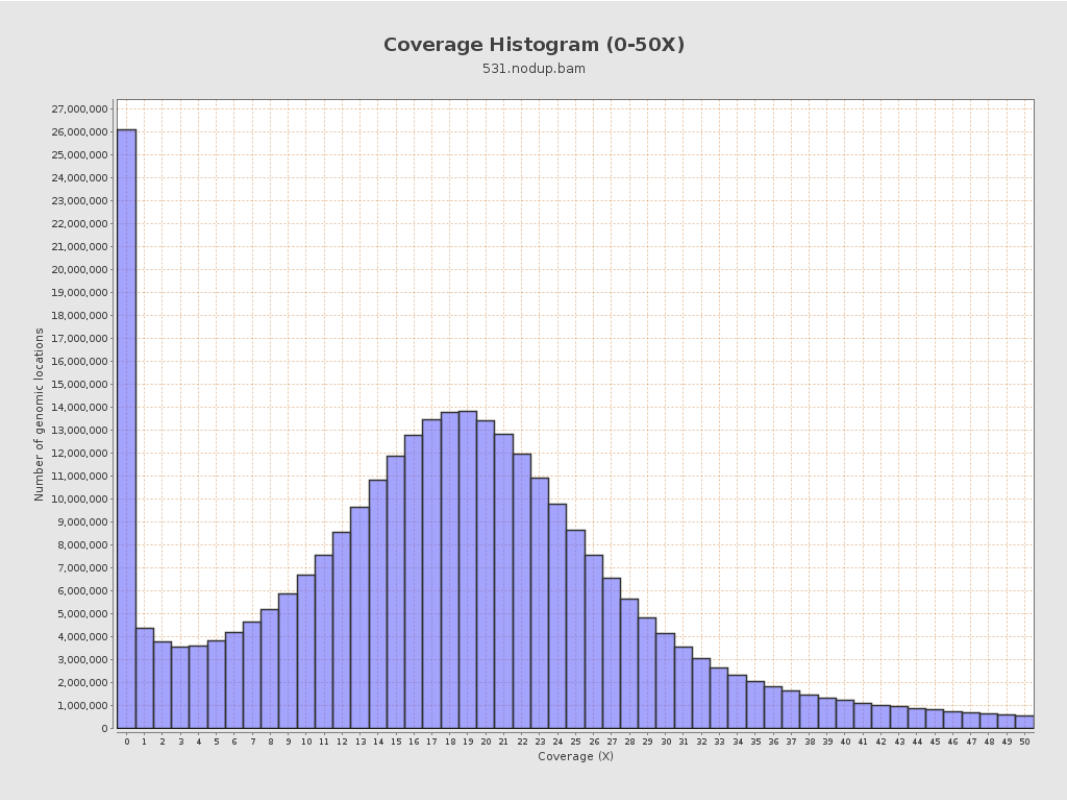
# 3. Results : Coverage across reference



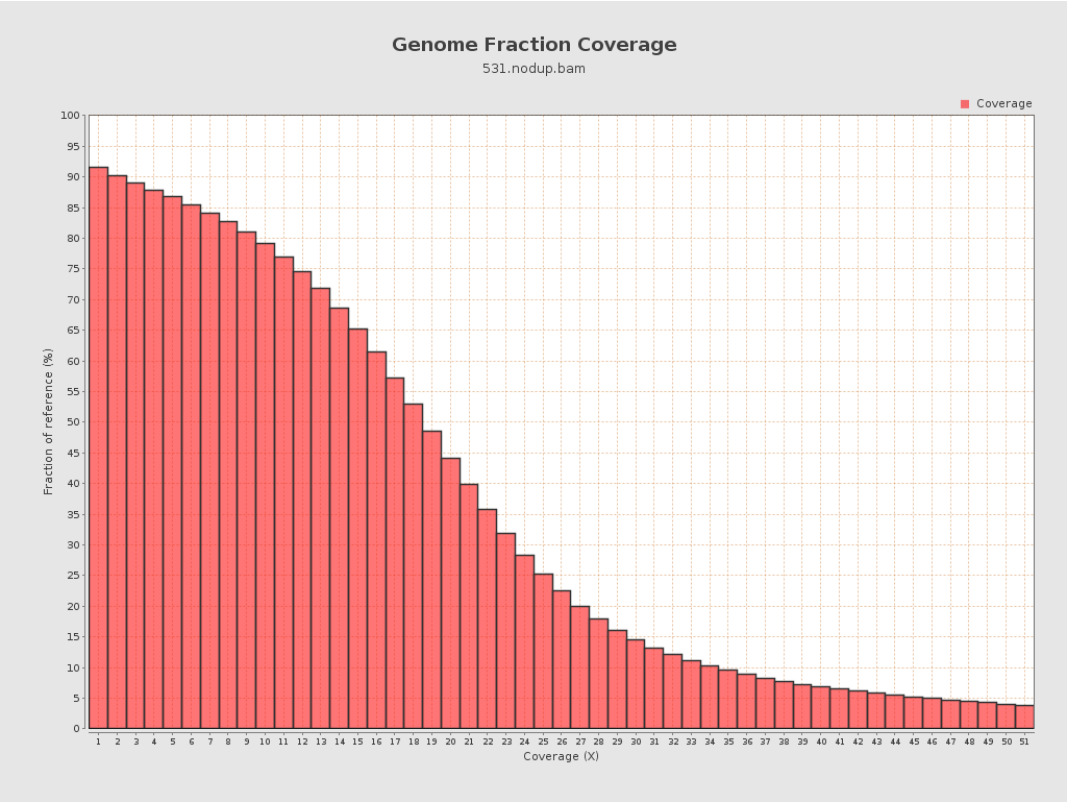
# 4. Results : Coverage Histogram



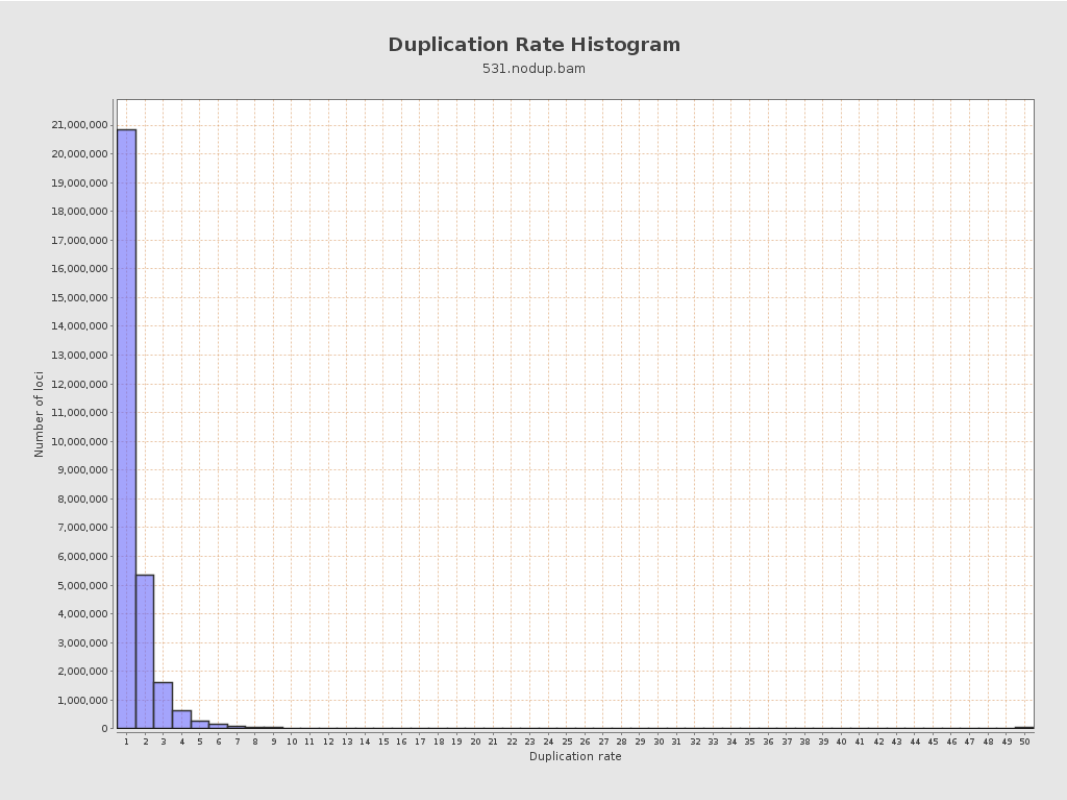
# 5. Results : Coverage Histogram (0-50X)



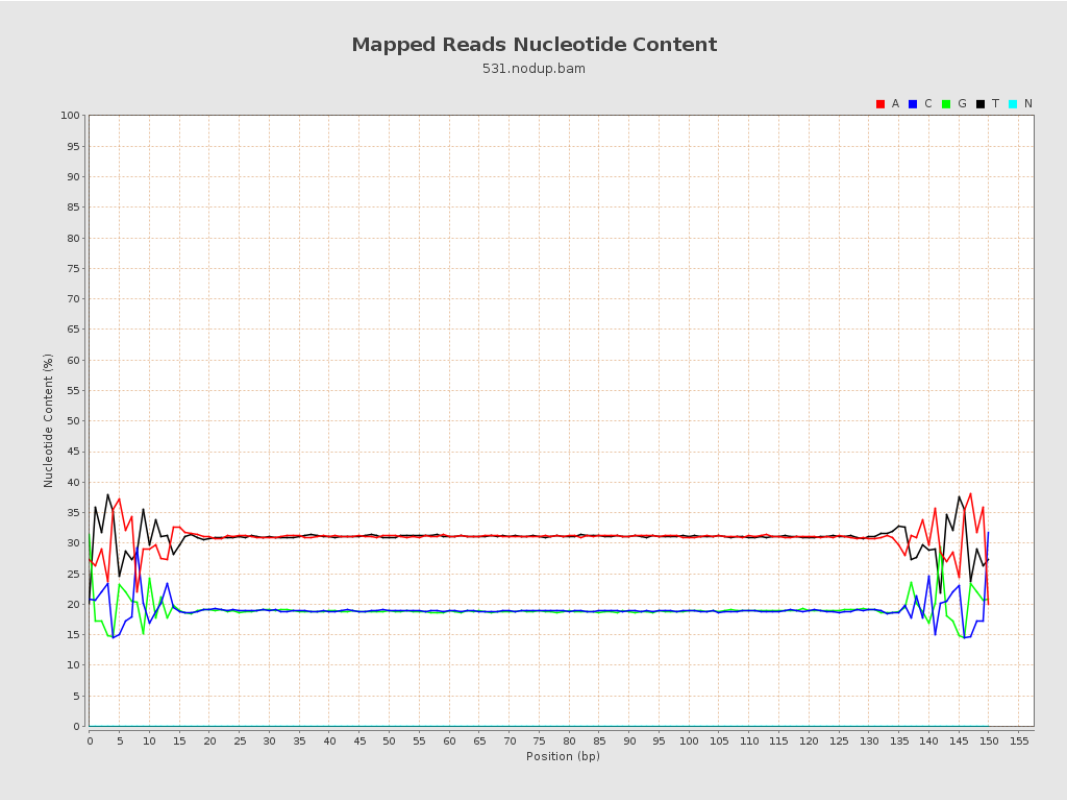
# 6. Results : Genome Fraction Coverage



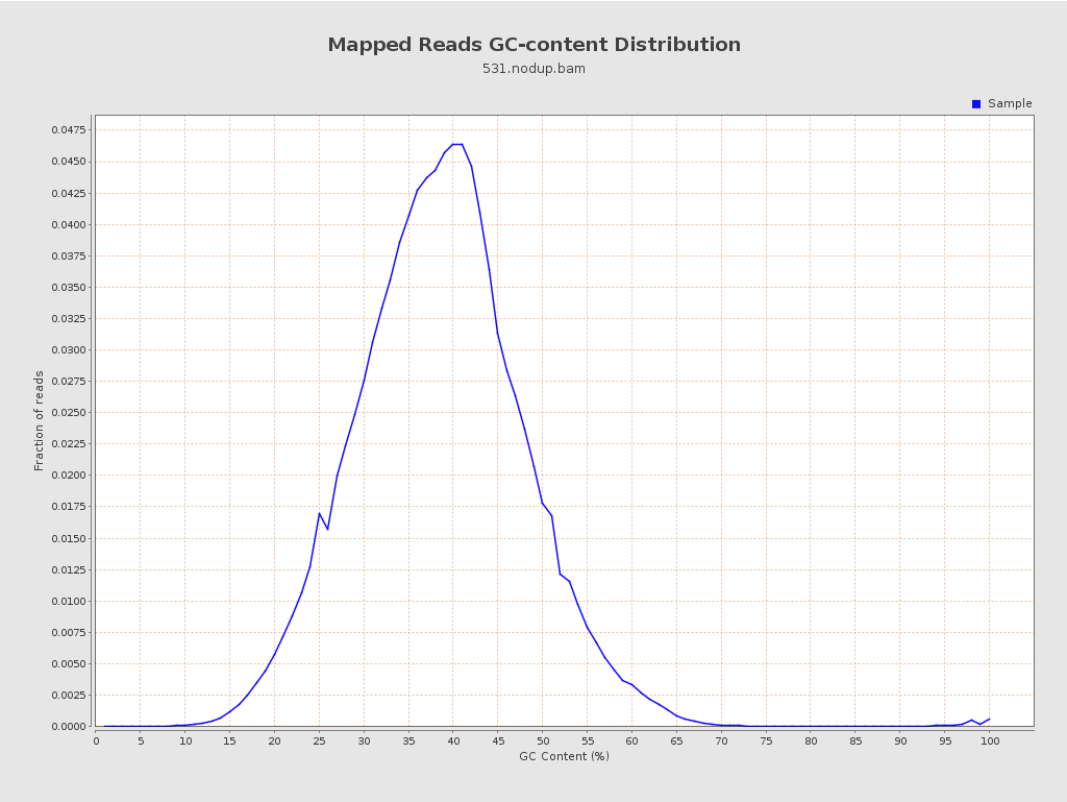
# 7. Results : Duplication Rate Histogram



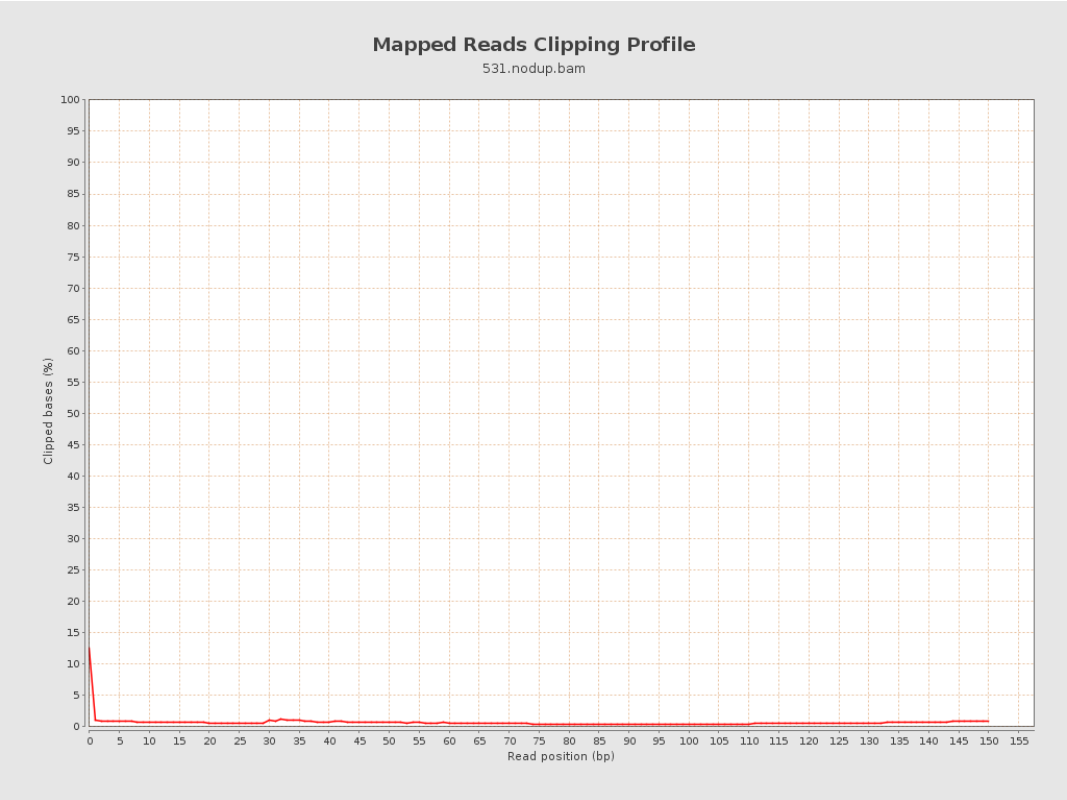
# 8. Results : Mapped Reads Nucleotide Content



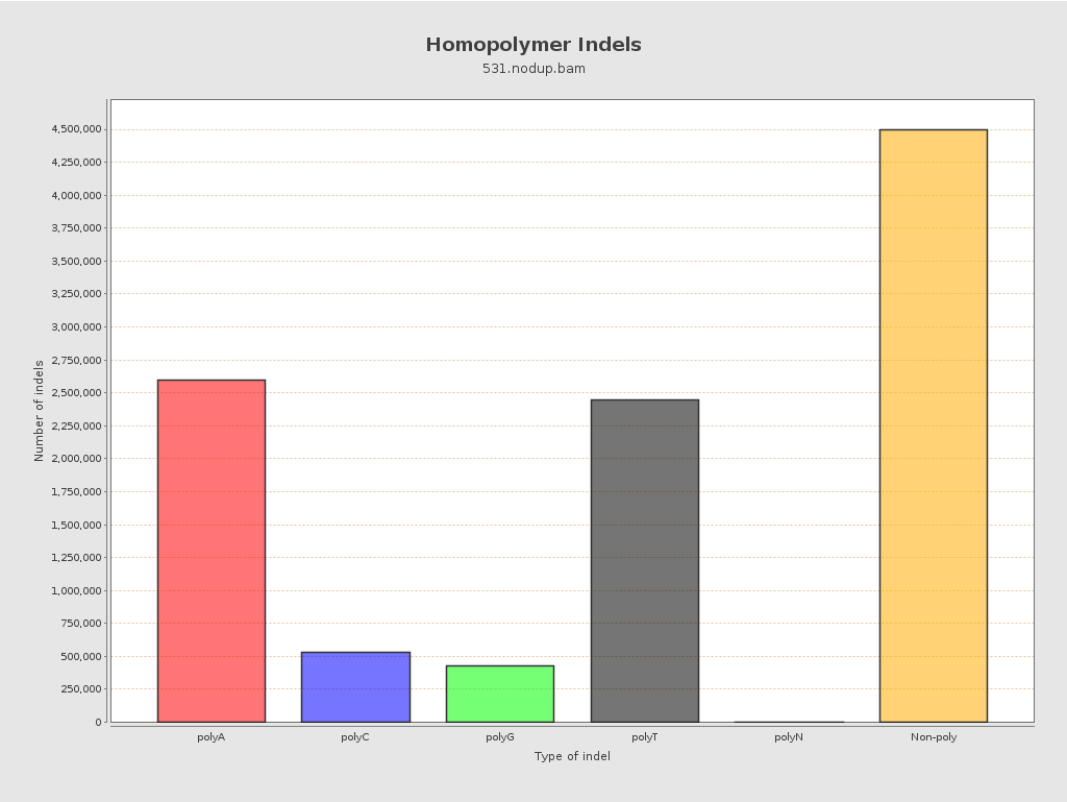
# 9. Results : Mapped Reads GC-content Distribution



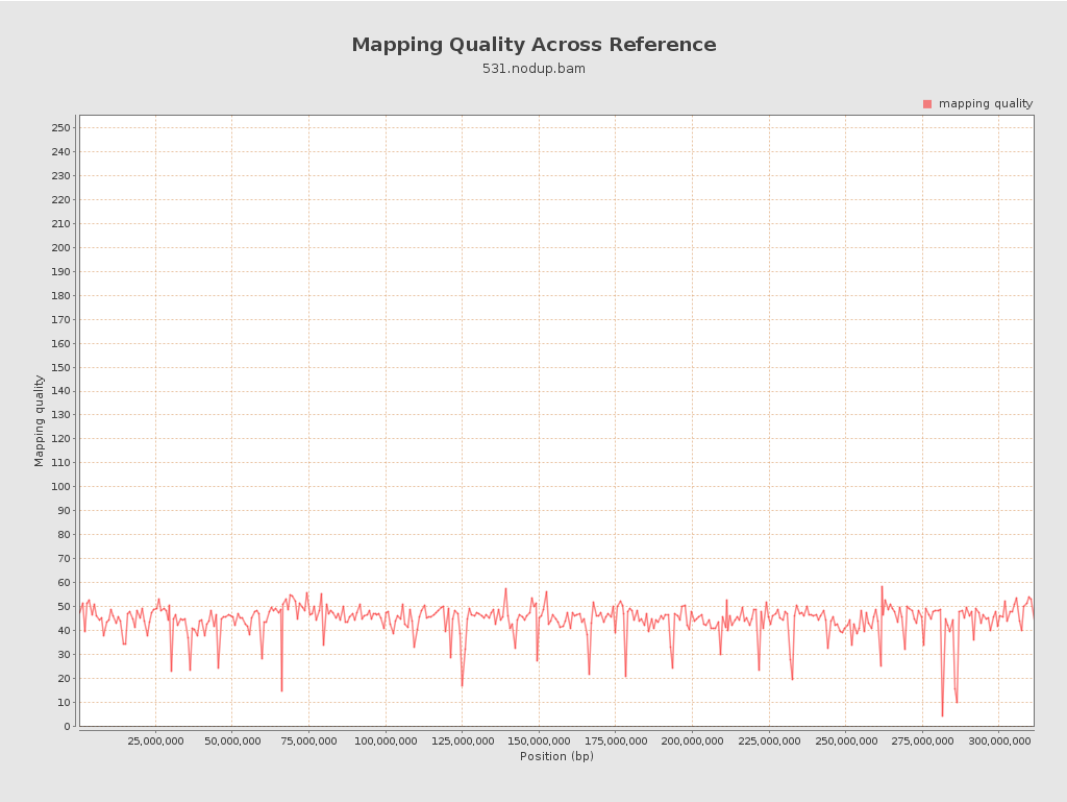
# 10. Results : Mapped Reads Clipping Profile



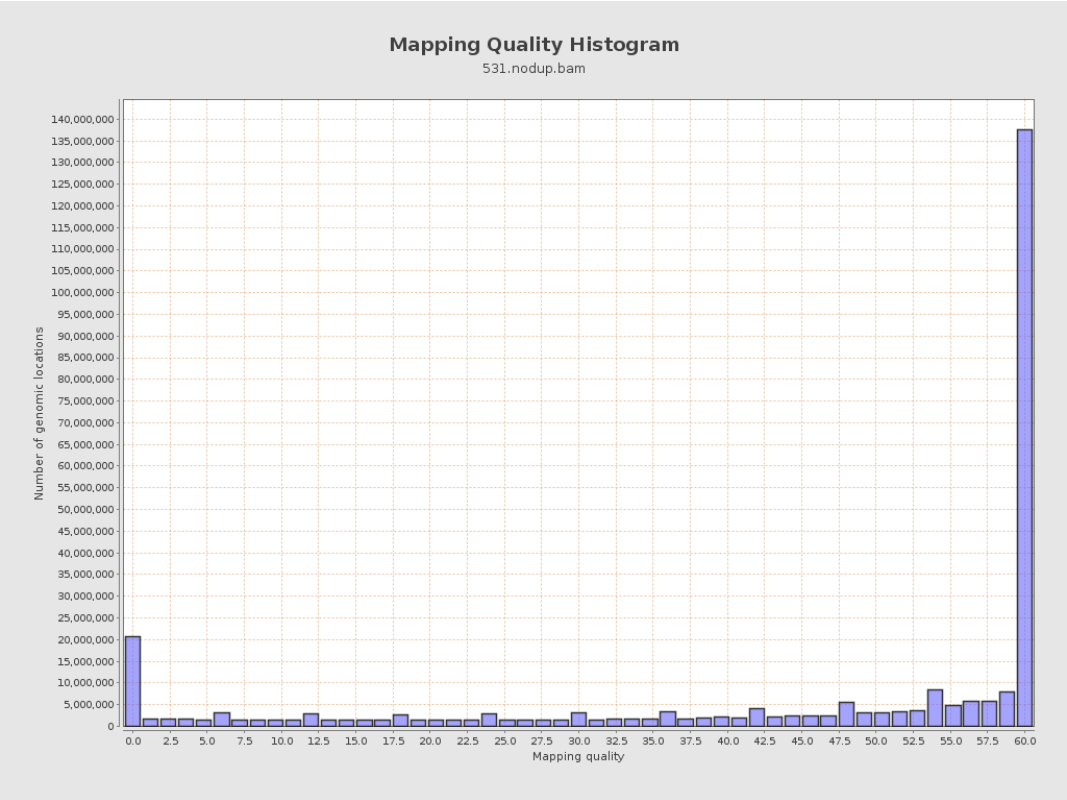
# 11. Results : Homopolymer Indels



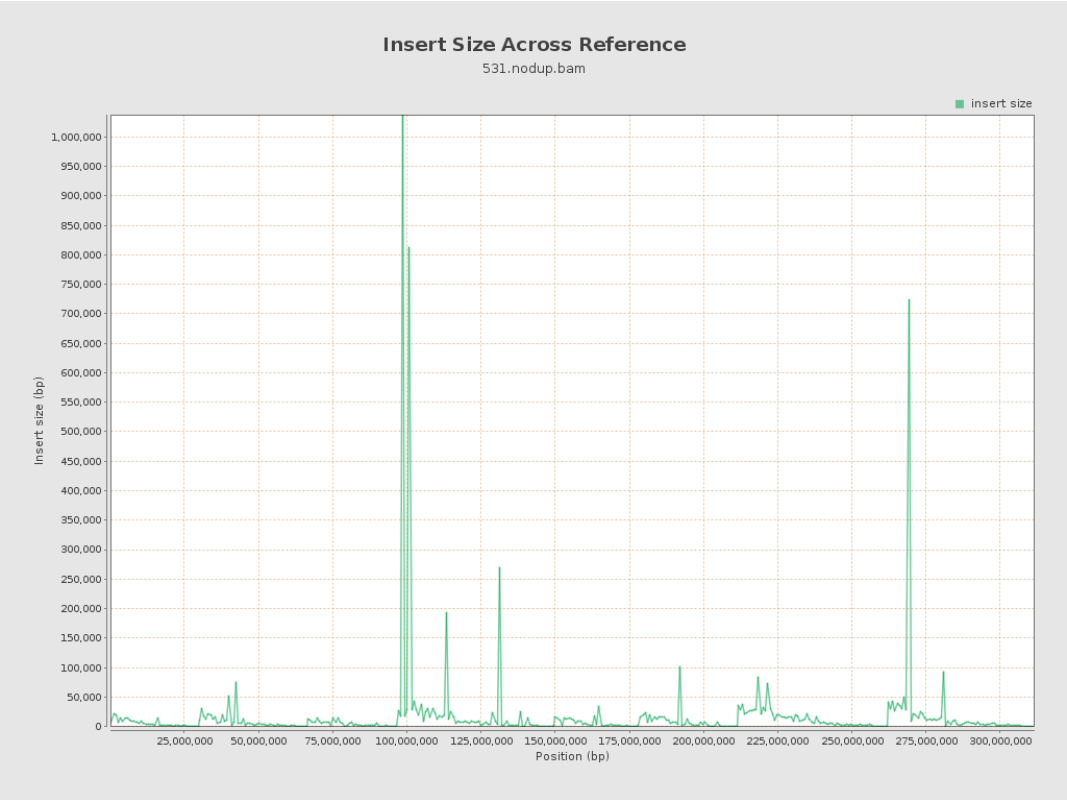
# 12. Results : Mapping Quality Across Reference



# 13. Results : Mapping Quality Histogram



# 14. Results : Insert Size Across Reference



# 15. Results : Insert Size Histogram