

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:22:02*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/137
1
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

|                                       |   |
|---------------------------------------|---|
| BAM file:                             | /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/1371<br>.nodup.bam   |
| Program:                              | bwa (0.7.17-r1188)  |
| Analyze overlapping paired-end reads: | no  |
| Command line:                         | bwa mem -M -t 8 -R<br>@RG\tID:\$unit\tPL:Illumina\tLB:LibA\tSM:\$sample<br>/proj/uppstore2018210/Aalpina/data/reference/GCA_900128785.1_MPIPZ.v5_genomic.fa<br>/proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_579/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_579_S146_L004_R1_001.fastq.gz<br>/proj/uppstore2018210/Aalpina/data/rawdata/P26207/P26207_579/02-FASTQ/220906_A00187_0838_AHMG3KDSX3/P26207_579_S146_L004_R2_001.fastq.gz |
| Size of a homopolymer:                | 3   |
|                                       |   |

|                            |                               |
|----------------------------|-------------------------------|
| Number of windows:         | 400                           |
| Analysis date:             | Mon May 29 21:22:01 CEST 2023 |
| Draw chromosome limits:    | no                            |
| Skip duplicate alignments: | no                            |

## 2. Summary

### 2.1. Globals

|                              |                    |
|------------------------------|--------------------|
| Reference size               | 311,642,060        |
| Number of reads              | 38,047,518         |
| Mapped reads                 | 35,725,585 / 93.9% |
| Unmapped reads               | 2,321,933 / 6.1%   |
| Mapped paired reads          | 35,725,585 / 93.9% |
| Mapped reads, first in pair  | 17,920,311 / 47.1% |
| Mapped reads, second in pair | 17,805,274 / 46.8% |
| Mapped reads, both in pair   | 34,965,770 / 91.9% |
| Mapped reads, singletons     | 759,815 / 2%       |
| Read min/max/mean length     | 30 / 151 / 148.27  |
| Duplicated reads (flagged)   | 4,747,435 / 12.48% |
| Clipped reads                | 8,247,379 / 21.68% |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 1,527,804,344 / 30.83% |
| Number/percentage of C's | 950,307,082 / 19.17%   |
| Number/percentage of T's | 1,531,385,775 / 30.9%  |
| Number/percentage of G's | 946,578,601 / 19.1%    |
| Number/percentage of N's | 34,633 / 0%            |
| GC Percentage            | 38.27%                 |

### 2.3. Coverage

|                    |         |
|--------------------|---------|
| Mean               | 15.9438 |
| Standard Deviation | 119.739 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 44.16 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 218,595.6       |
| Standard Deviation | 2,219,691.54    |
| P25/Median/P75     | 324 / 420 / 538 |

## 2.6. Mismatches and indels

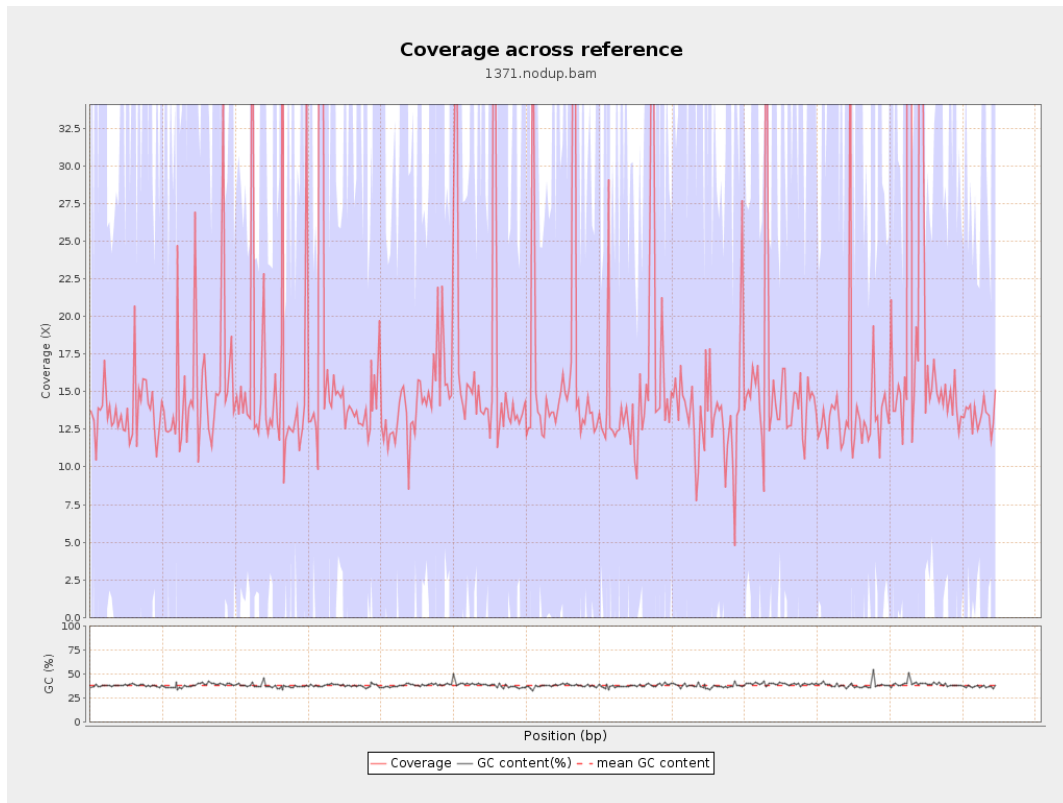
|  |             |
|--|-------------|
| General error rate                       | 2.55%       |
| Mismatches                               | 117,336,871 |
| Insertions                               | 3,287,094   |
| Mapped reads with at least one insertion | 8.27%       |
| Deletions                                | 3,346,595   |
| Mapped reads with at least one deletion  | 8.32%       |
| Homopolymer indels                       | 56.07%      |

## 2.7. Chromosome stats

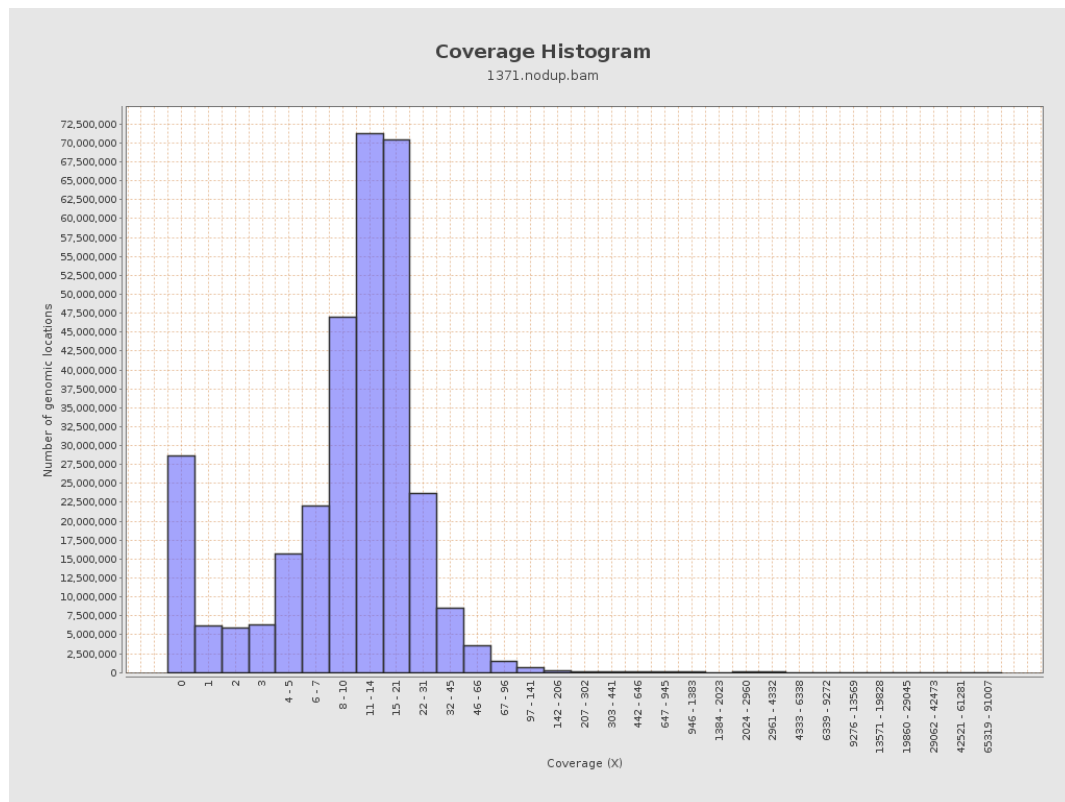
| Name       | Length   | Mapped bases | Mean coverage | Standard deviation |
|------------|----------|--------------|---------------|--------------------|
| LT669788.1 | 29724344 | 402583227    | 13.5439       | 37.492             |

|            |          |           |         |          |
|------------|----------|-----------|---------|----------|
| LT669789.1 | 36598175 | 588025216 | 16.0671 | 122.5736 |
| LT669790.1 | 30422129 | 522773716 | 17.184  | 123.7081 |
| LT669791.1 | 52758100 | 821053675 | 15.5626 | 107.9909 |
| LT669792.1 | 28376109 | 449070646 | 15.8257 | 145.2816 |
| LT669793.1 | 33388210 | 496396430 | 14.8674 | 85.1019  |
| LT669794.1 | 50579949 | 746219269 | 14.7533 | 98.274   |
| LT669795.1 | 49795044 | 942636156 | 18.9303 | 171.5629 |

### 3. Results : Coverage across reference

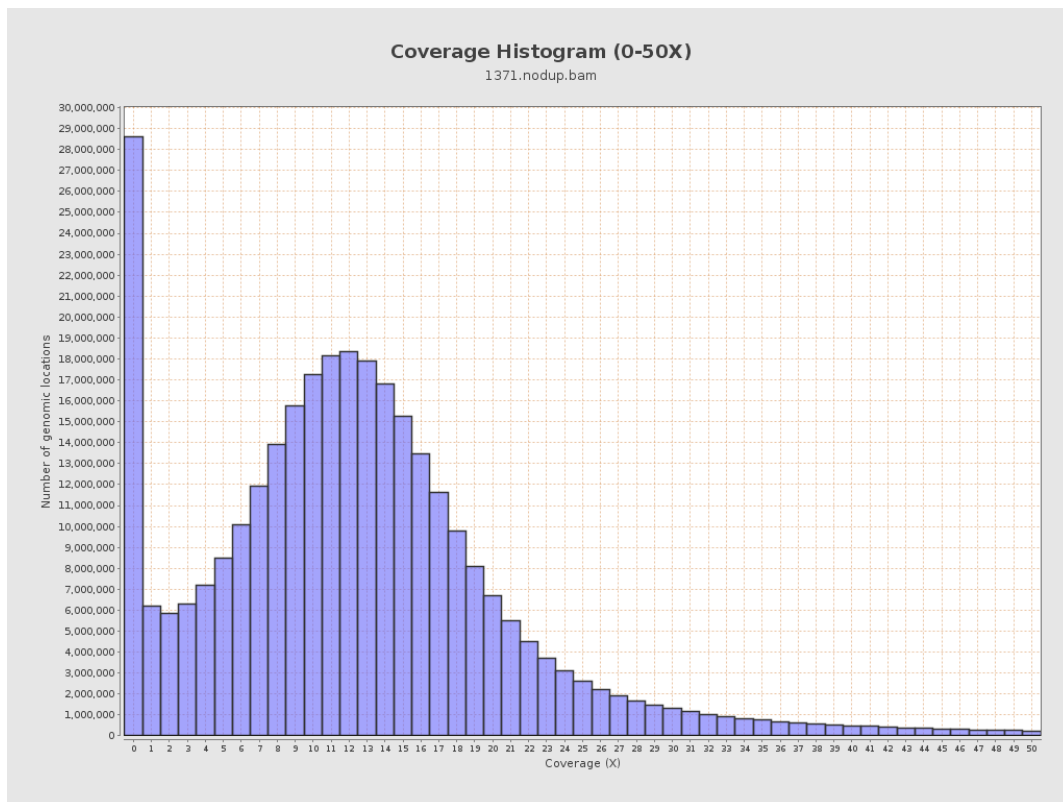


## 4. Results : Coverage Histogram

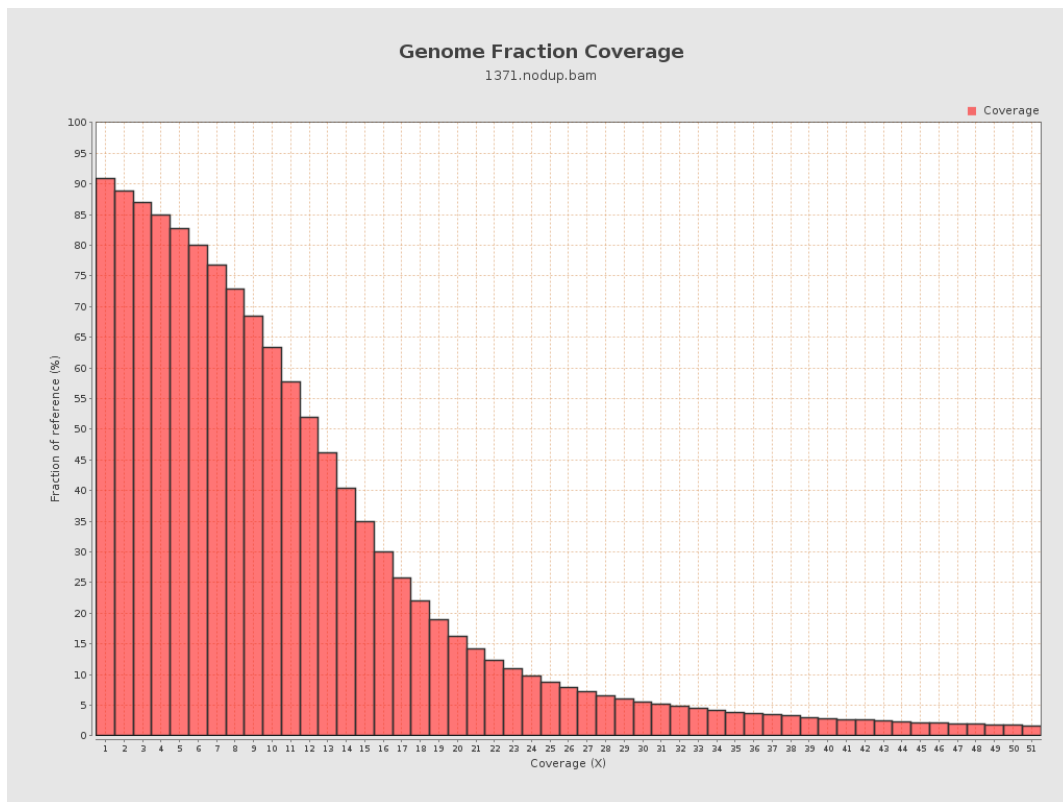




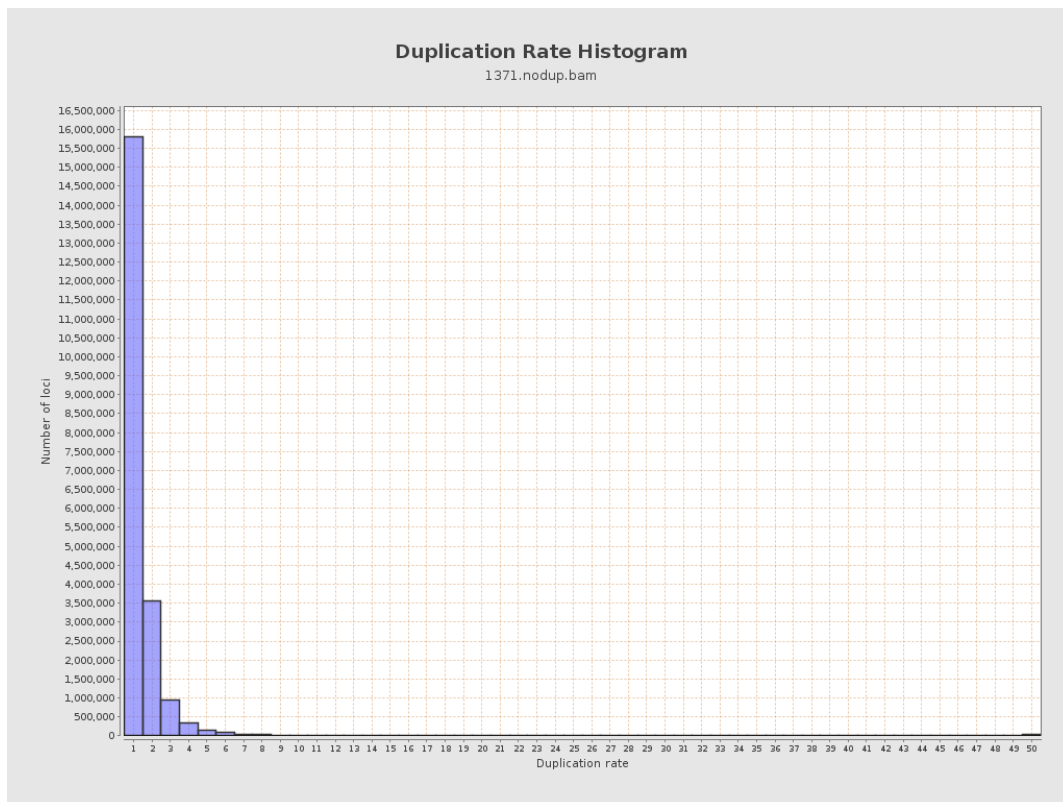
## 5. Results : Coverage Histogram (0-50X)



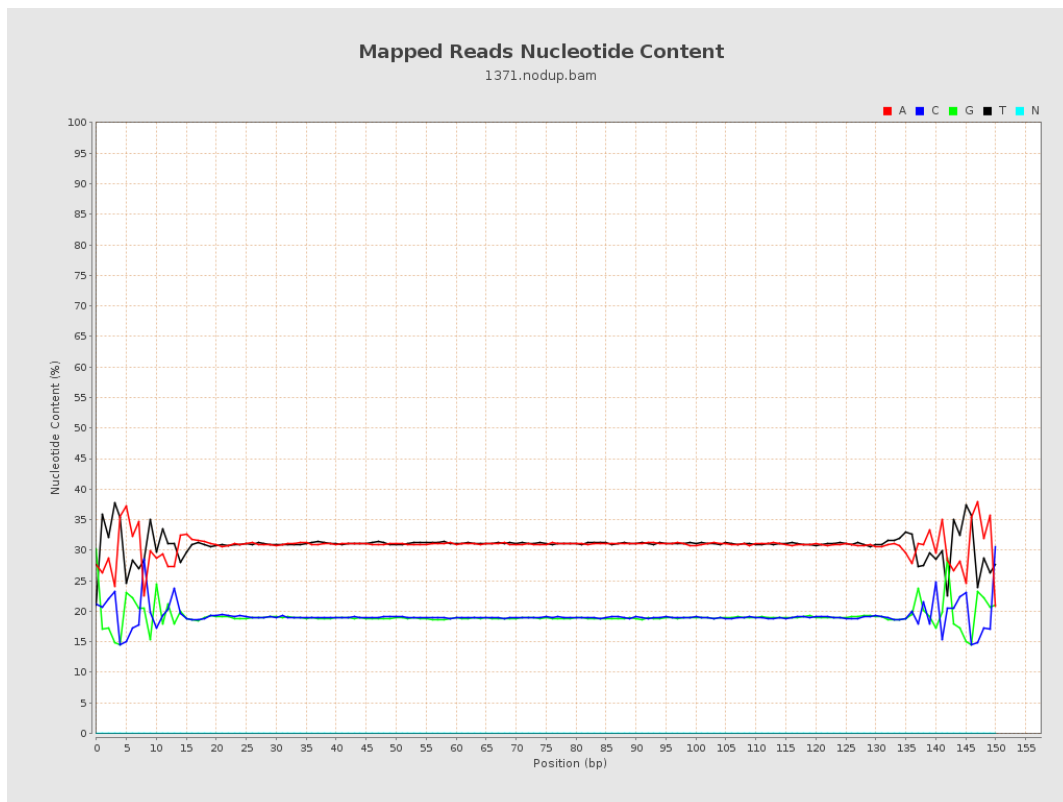
## 6. Results : Genome Fraction Coverage



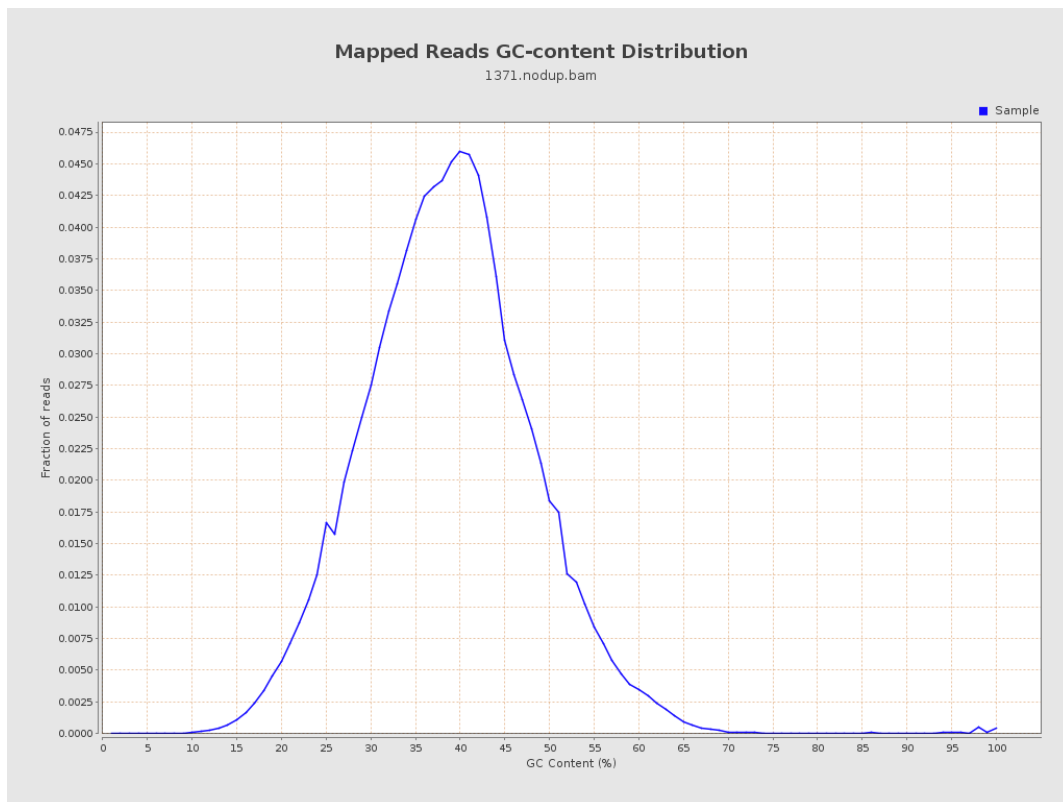
## 7. Results : Duplication Rate Histogram



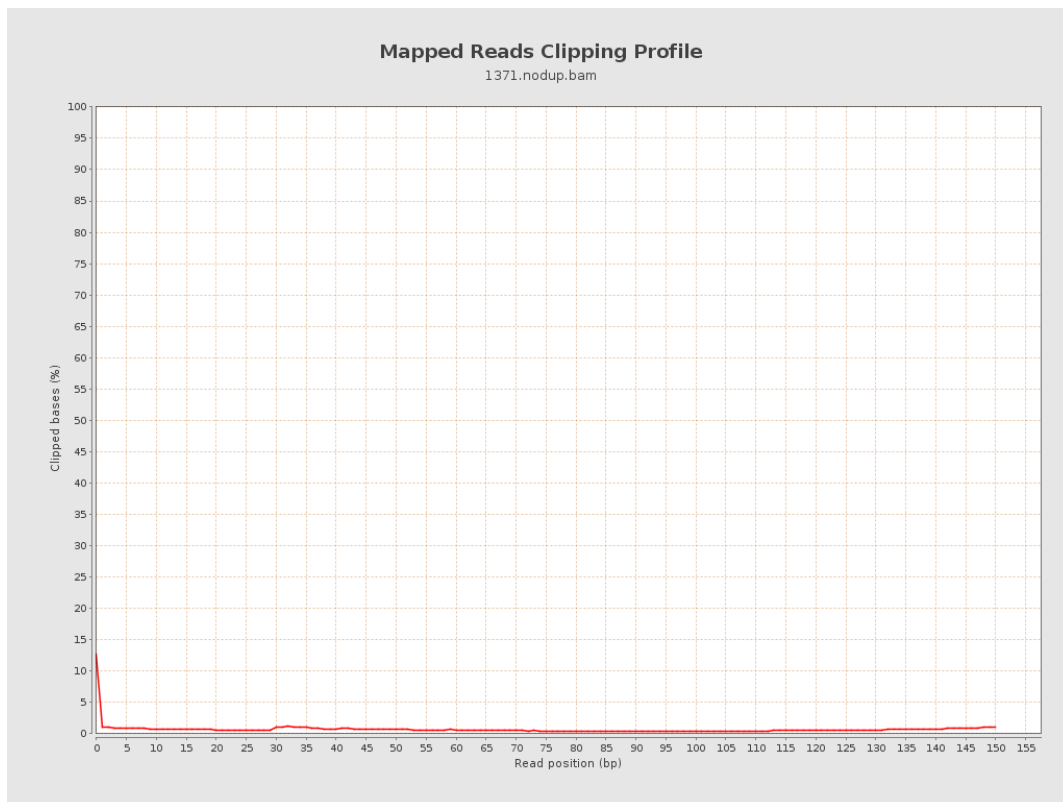
## 8. Results : Mapped Reads Nucleotide Content



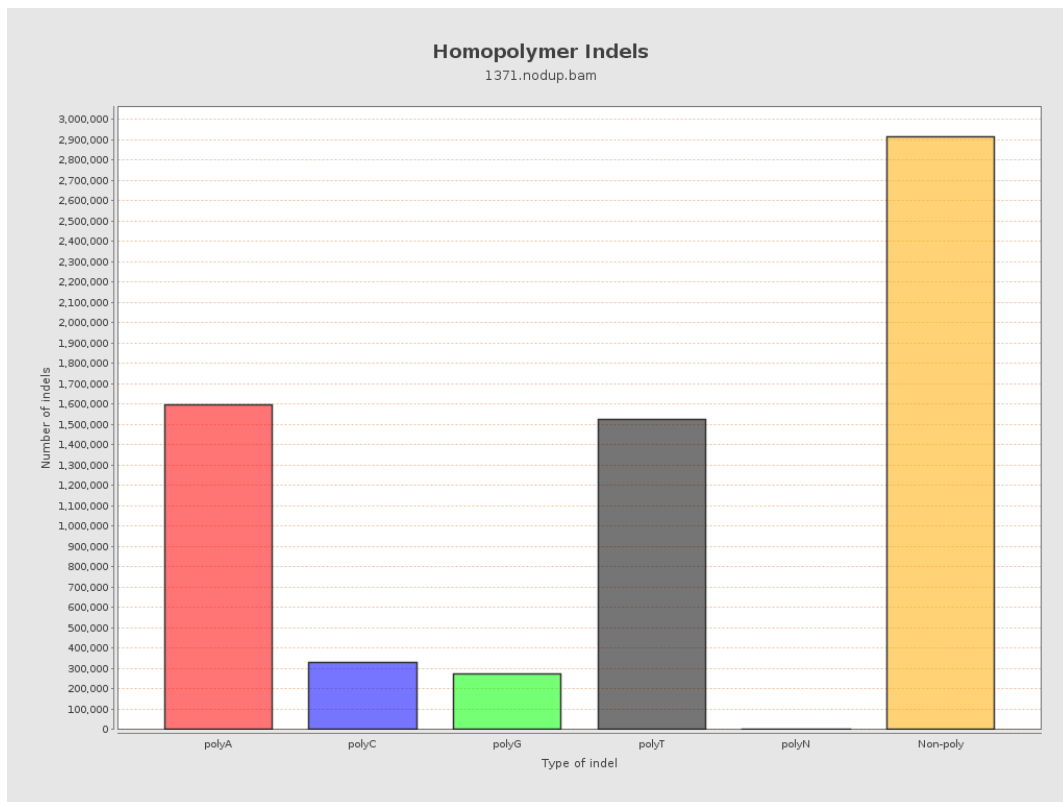
## 9. Results : Mapped Reads GC-content Distribution



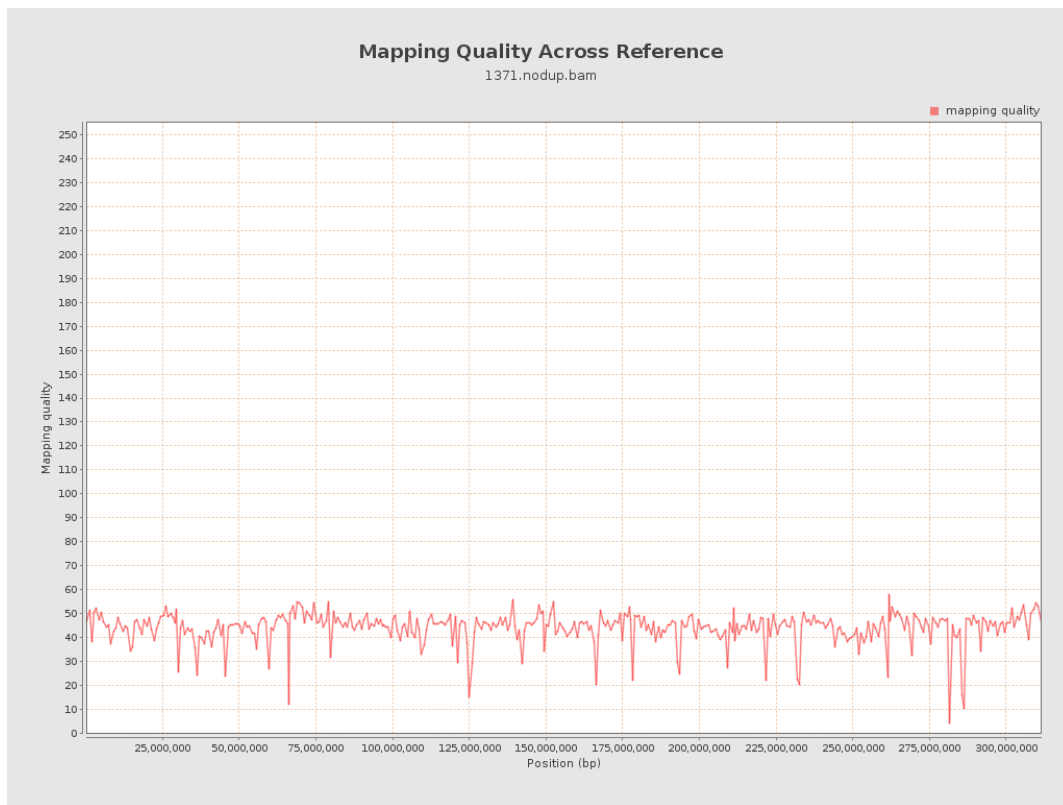
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

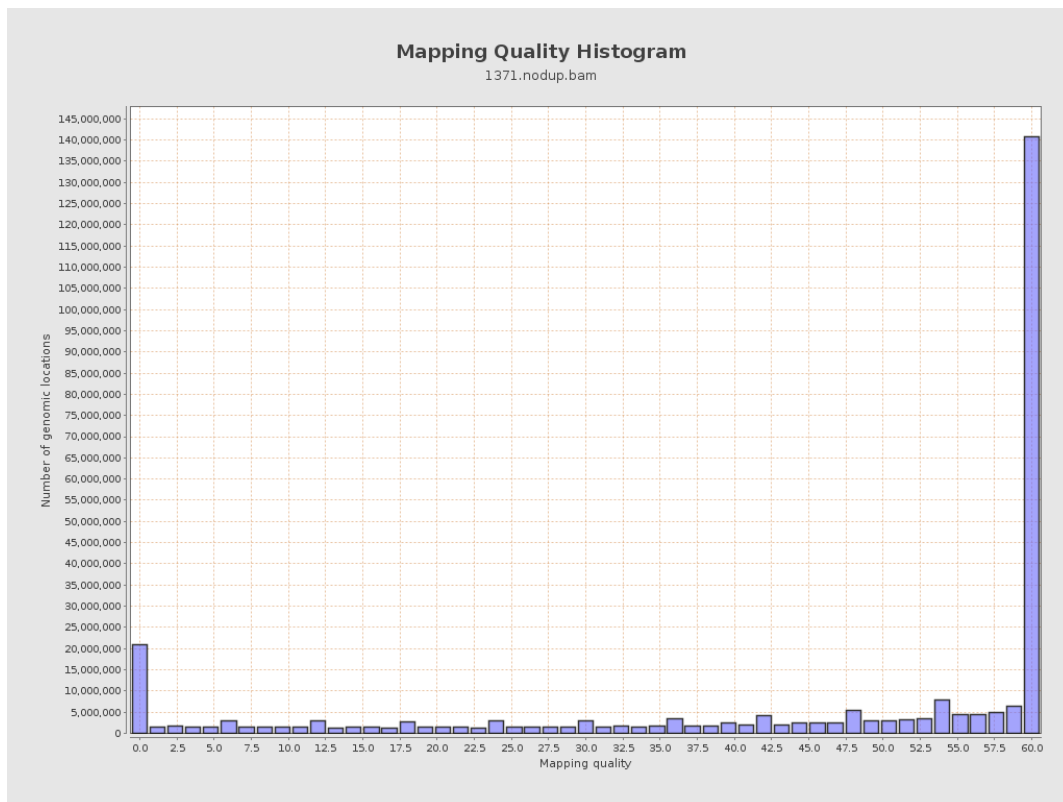


## 12. Results : Mapping Quality Across Reference

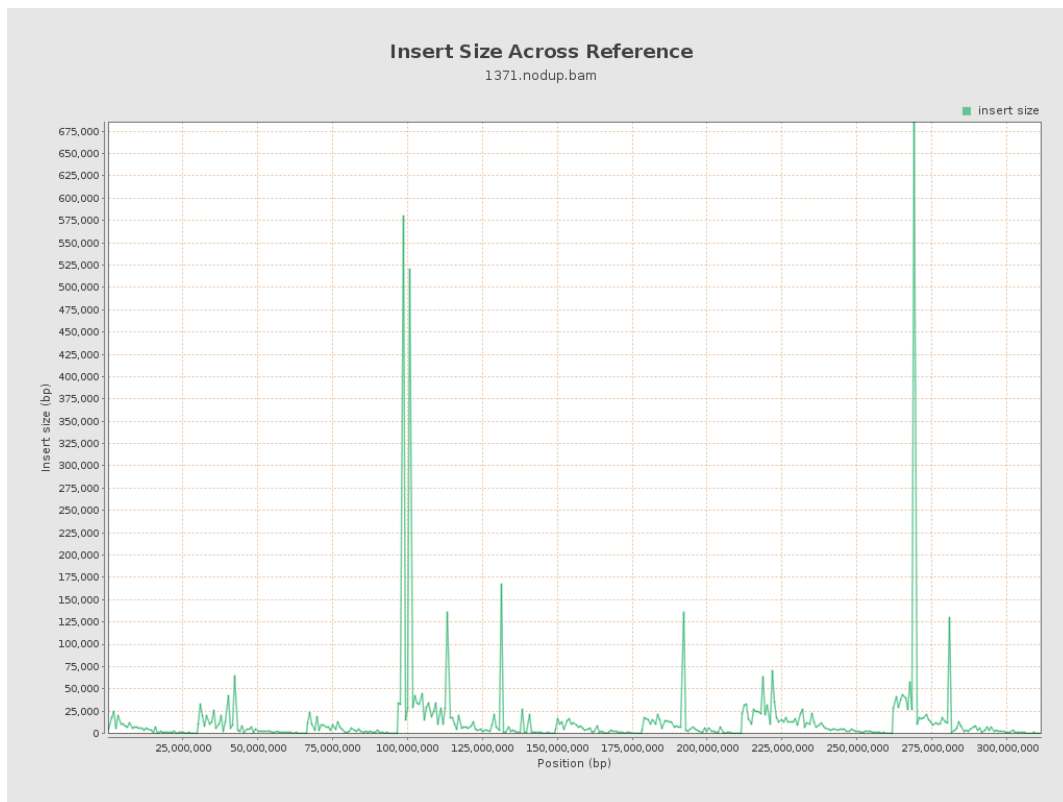




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

