

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:27:23*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/142
8
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

|                                       |   |
|---------------------------------------|---|
| BAM file:                             | /proj/uppstore2018210/Aalpina/worki<br>ng/Kate/Working/F2/MarkDuplicates/<br>1428<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\t<br>SM:\$sample<br>/proj/uppstore2018210/Aalpina/data/r<br>eference/GCA_900128785.1_MPIPZ.<br>v5_genomic.fa<br>/proj/uppstore2018210/Aalpina/data/r<br>awdata/P26207/P26207_573/02-<br>FASTQ/220906_A00187_0838_AHM<br>G3KDSX3/P26207_573_S140_L004<br>_R1_001.fastq.gz<br>/proj/uppstore2018210/Aalpina/data/r<br>awdata/P26207/P26207_573/02-<br>FASTQ/220906_A00187_0838_AHM<br>G3KDSX3/P26207_573_S140_L004<br>_R2_001.fastq.gz |
| Size of a homopolymer:                | 3   |
|                                       |   |

|                            |                               |
|----------------------------|-------------------------------|
| Number of windows:         | 400                           |
| Analysis date:             | Mon May 29 21:27:22 CEST 2023 |
| Draw chromosome limits:    | no                            |
| Skip duplicate alignments: | no                            |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 311,642,060         |
| Number of reads              | 52,831,272          |
| Mapped reads                 | 50,383,566 / 95.37% |
| Unmapped reads               | 2,447,706 / 4.63%   |
| Mapped paired reads          | 50,383,566 / 95.37% |
| Mapped reads, first in pair  | 25,267,842 / 47.83% |
| Mapped reads, second in pair | 25,115,724 / 47.54% |
| Mapped reads, both in pair   | 49,555,466 / 93.8%  |
| Mapped reads, singletons     | 828,100 / 1.57%     |
| Read min/max/mean length     | 30 / 151 / 148.07   |
| Duplicated reads (flagged)   | 6,689,758 / 12.66%  |
| Clipped reads                | 11,806,941 / 22.35% |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 2,148,384,055 / 30.74% |
| Number/percentage of C's | 1,345,929,577 / 19.26% |
| Number/percentage of T's | 2,152,084,237 / 30.8%  |
| Number/percentage of G's | 1,341,760,527 / 19.2%  |
| Number/percentage of N's | 48,893 / 0%            |
| GC Percentage            | 38.46%                 |

### 2.3. Coverage

|                    |          |
|--------------------|----------|
| Mean               | 22.4831  |
| Standard Deviation | 188.8029 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 43.69 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 210,552.13      |
| Standard Deviation | 2,160,418.23    |
| P25/Median/P75     | 302 / 396 / 512 |

## 2.6. Mismatches and indels

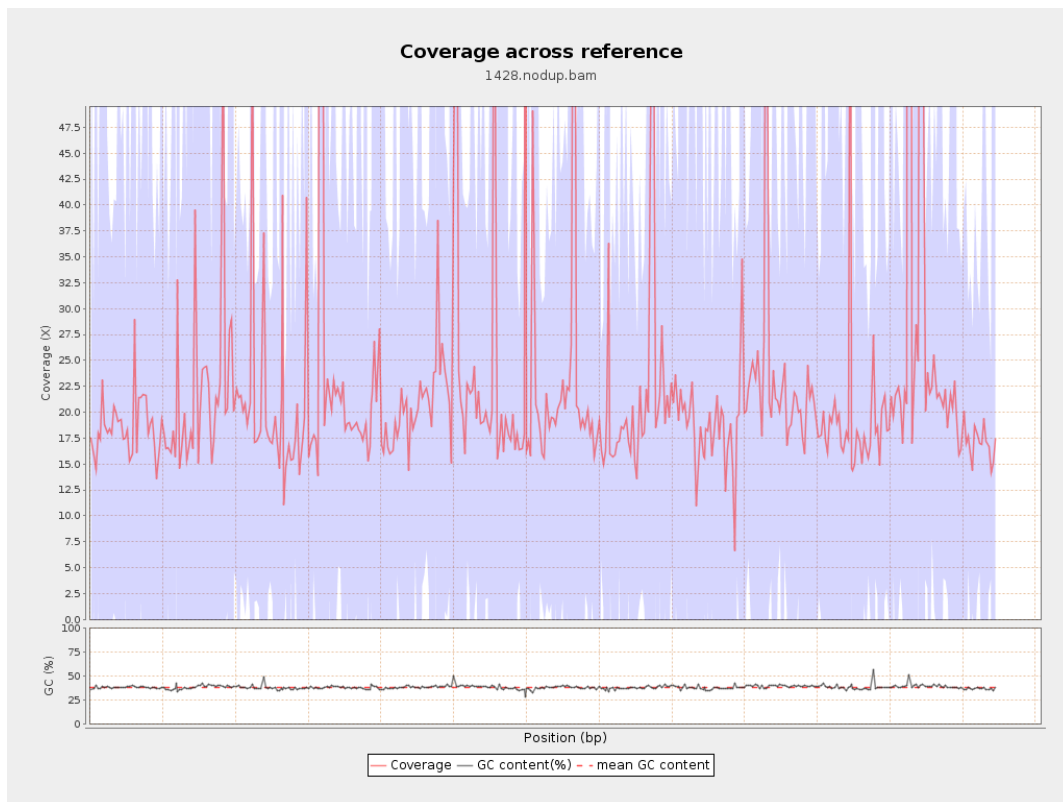
|  |             |
|--|-------------|
| General error rate                       | 2.59%       |
| Mismatches                               | 168,435,995 |
| Insertions                               | 4,614,189   |
| Mapped reads with at least one insertion | 8.25%       |
| Deletions                                | 4,864,986   |
| Mapped reads with at least one deletion  | 8.56%       |
| Homopolymer indels                       | 55%         |

## 2.7. Chromosome stats

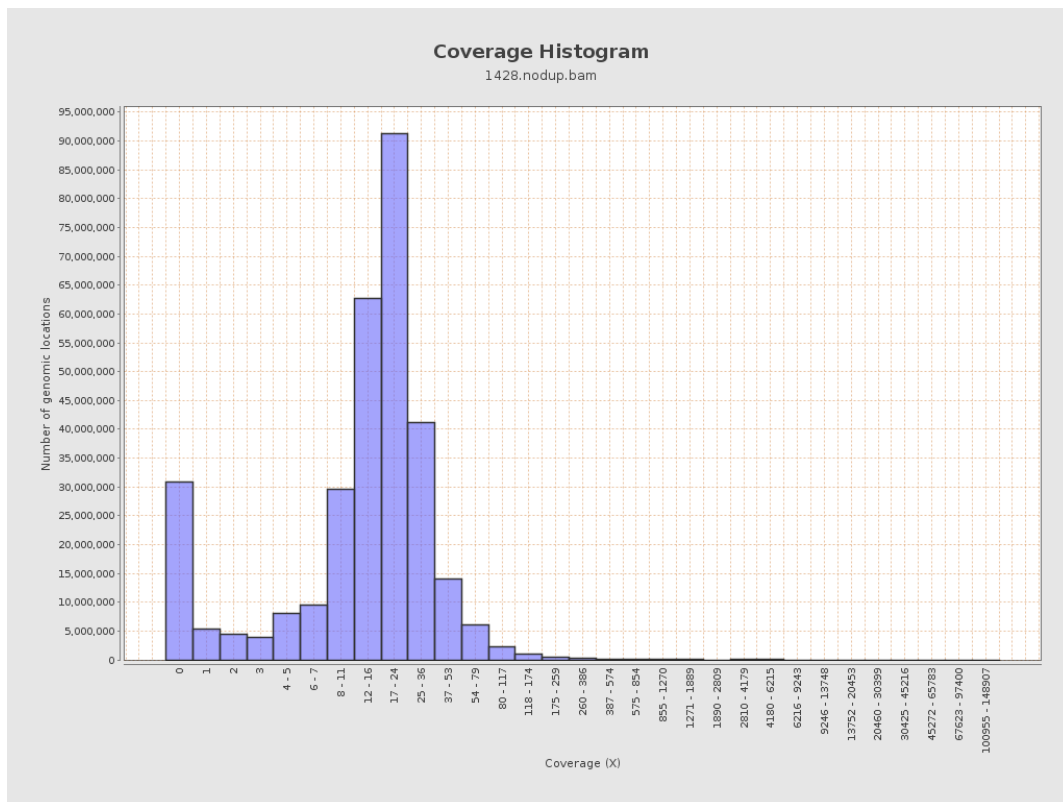
| Name       | Length   | Mapped bases | Mean coverage | Standard deviation |
|------------|----------|--------------|---------------|--------------------|
| LT669788.1 | 29724344 | 545883803    | 18.3649       | 62.0051            |
|            |          |              |               |                    |

|            |          |            |         |          |
|------------|----------|------------|---------|----------|
| LT669789.1 | 36598175 | 817777929  | 22.3448 | 192.5553 |
| LT669790.1 | 30422129 | 693393705  | 22.7924 | 145.9322 |
| LT669791.1 | 52758100 | 1169444425 | 22.1662 | 166.861  |
| LT669792.1 | 28376109 | 630709863  | 22.2268 | 205.4286 |
| LT669793.1 | 33388210 | 707371437  | 21.1863 | 127.7547 |
| LT669794.1 | 50579949 | 1097865871 | 21.7056 | 176.114  |
| LT669795.1 | 49795044 | 1344239782 | 26.9955 | 290.7025 |

### 3. Results : Coverage across reference

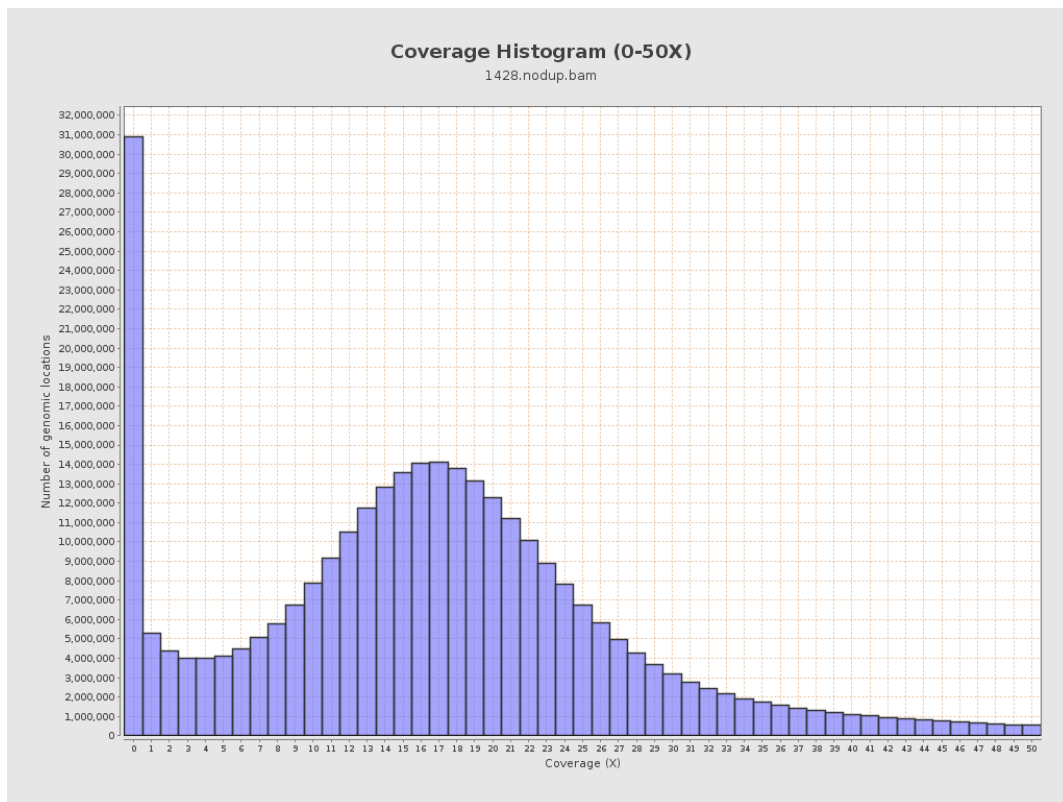


## 4. Results : Coverage Histogram

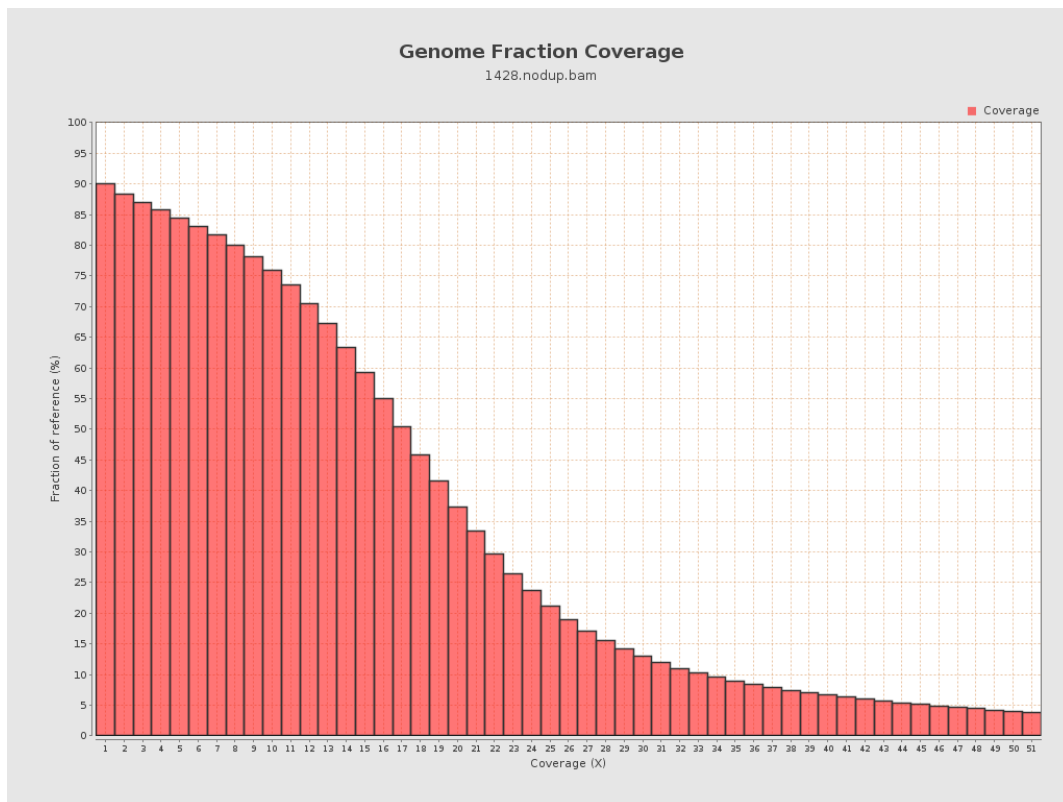




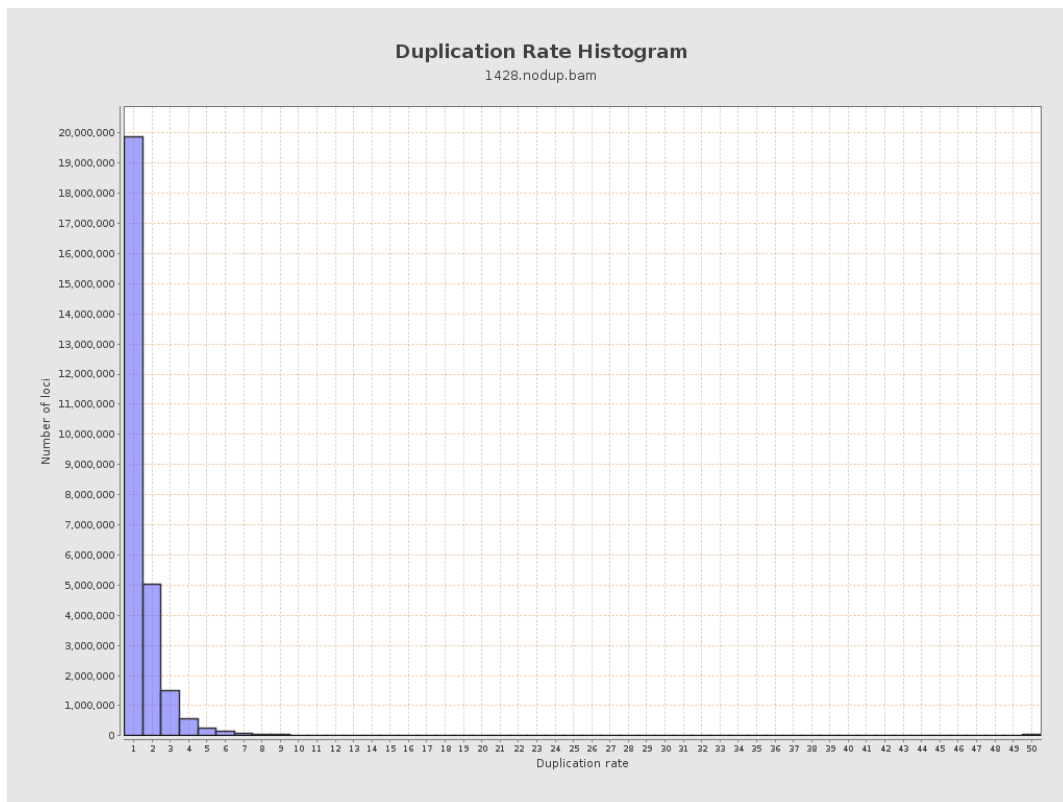
## 5. Results : Coverage Histogram (0-50X)



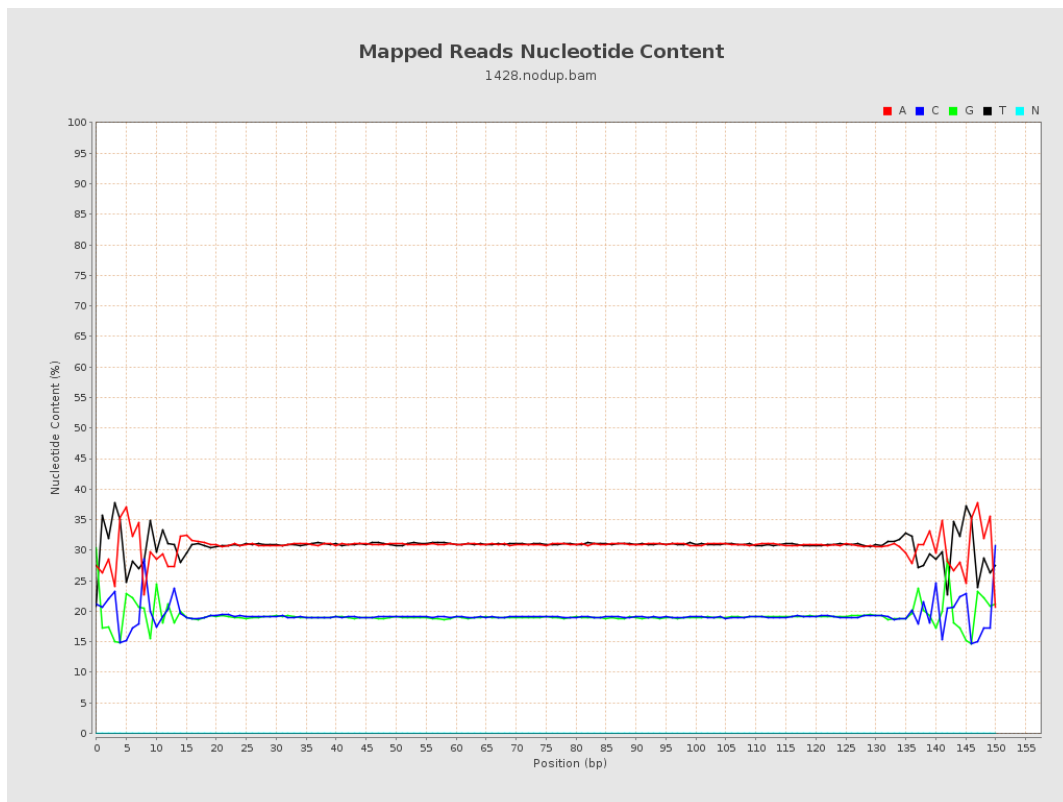
## 6. Results : Genome Fraction Coverage



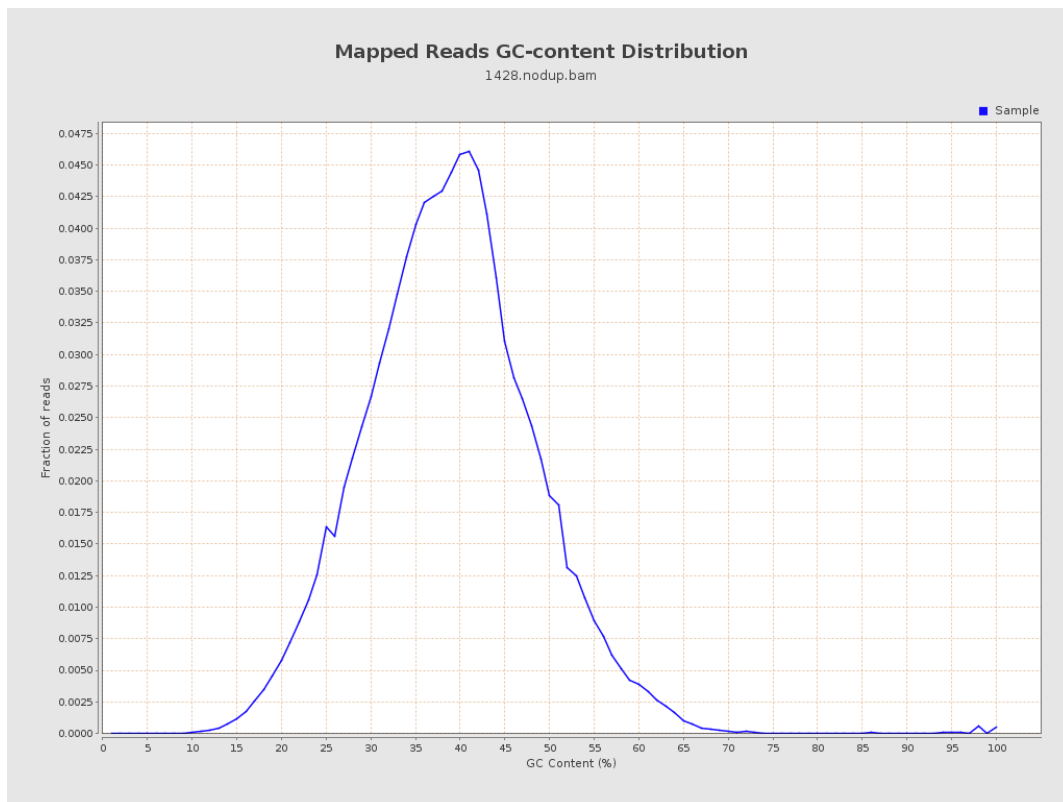
## 7. Results : Duplication Rate Histogram



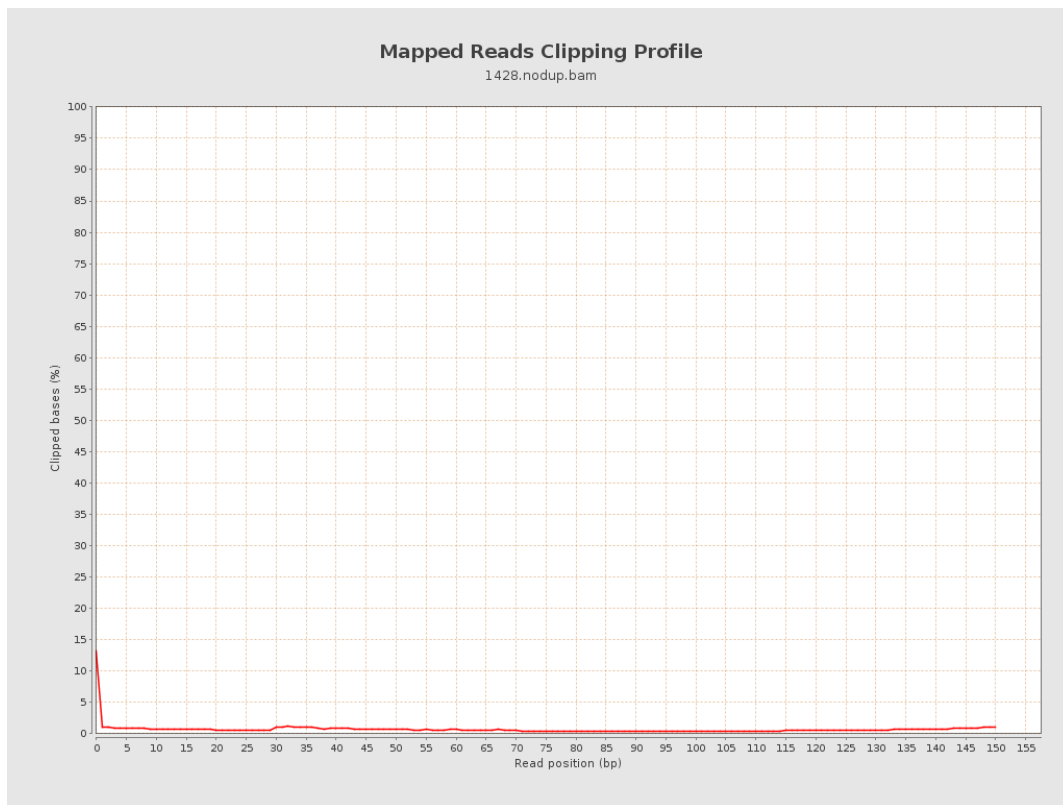
## 8. Results : Mapped Reads Nucleotide Content



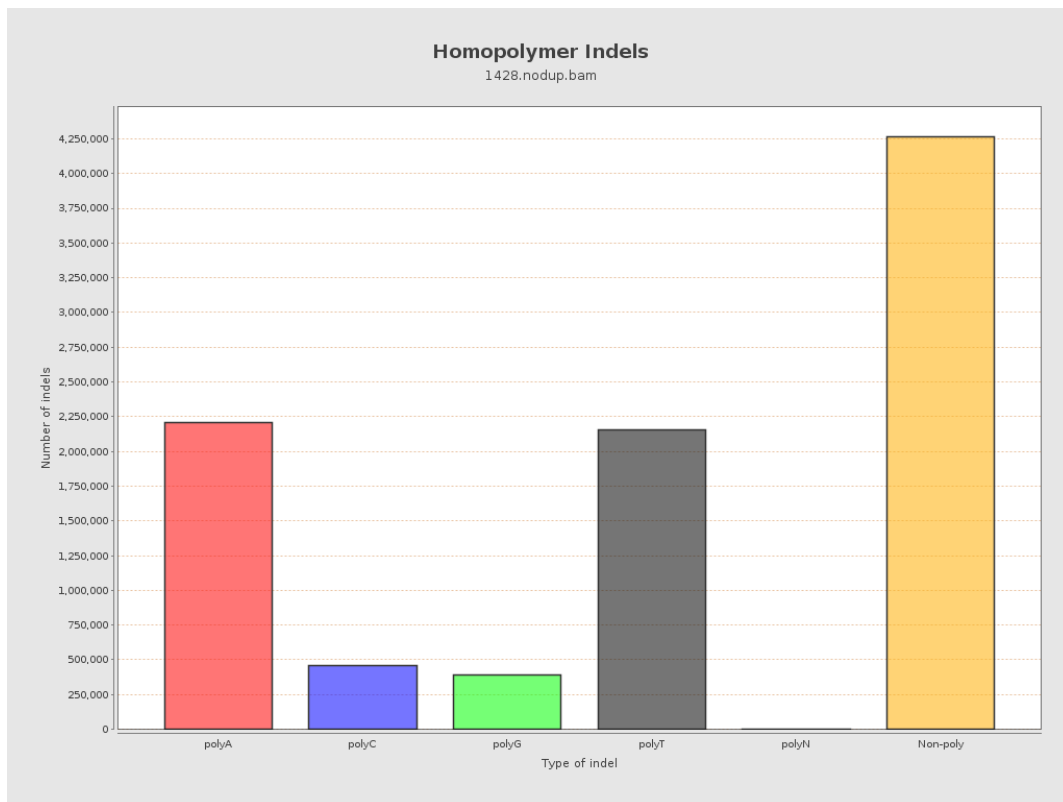
## 9. Results : Mapped Reads GC-content Distribution



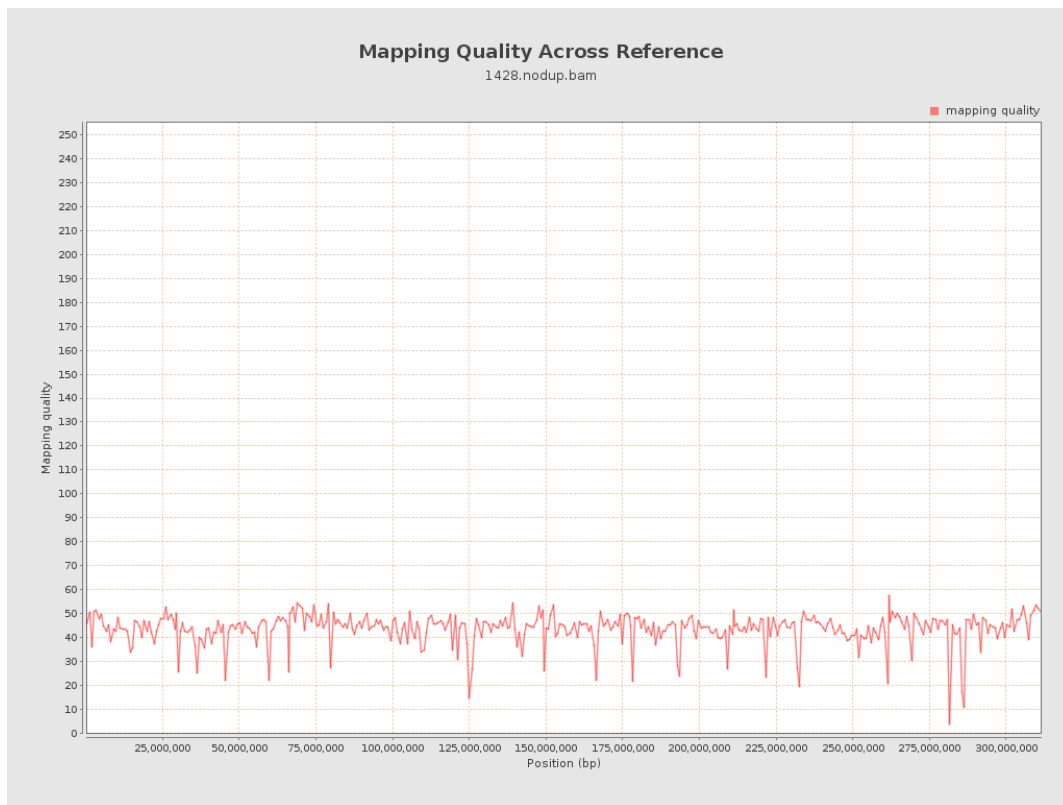
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

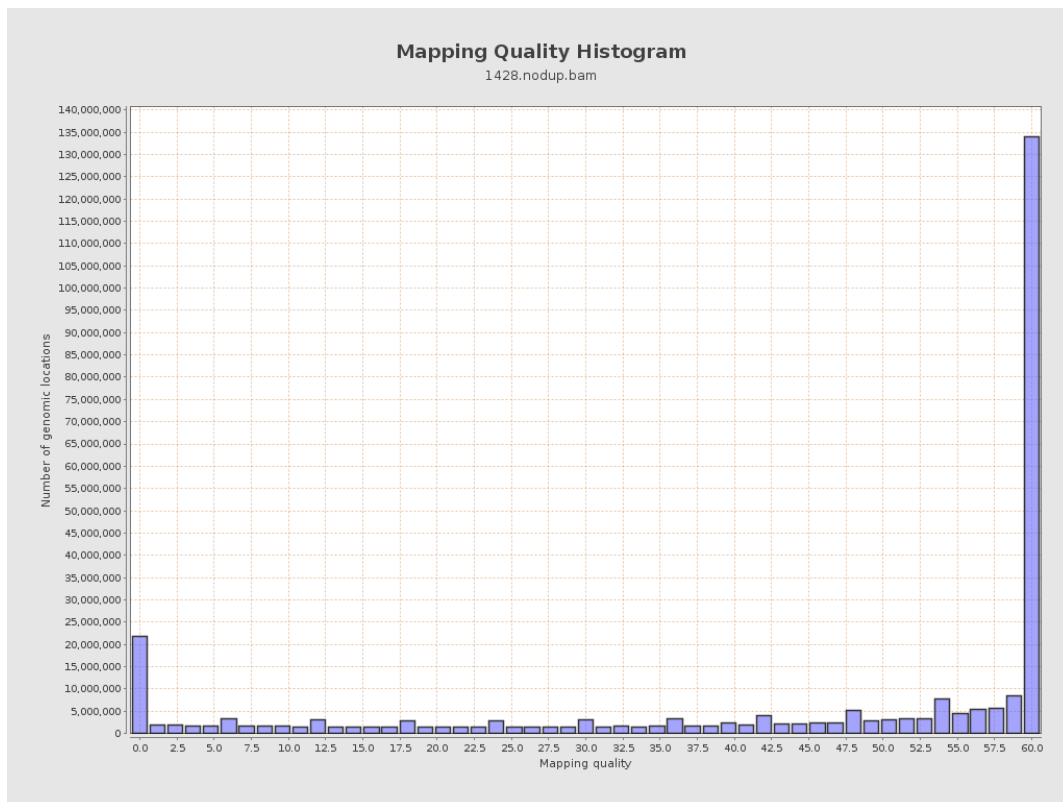


## 12. Results : Mapping Quality Across Reference

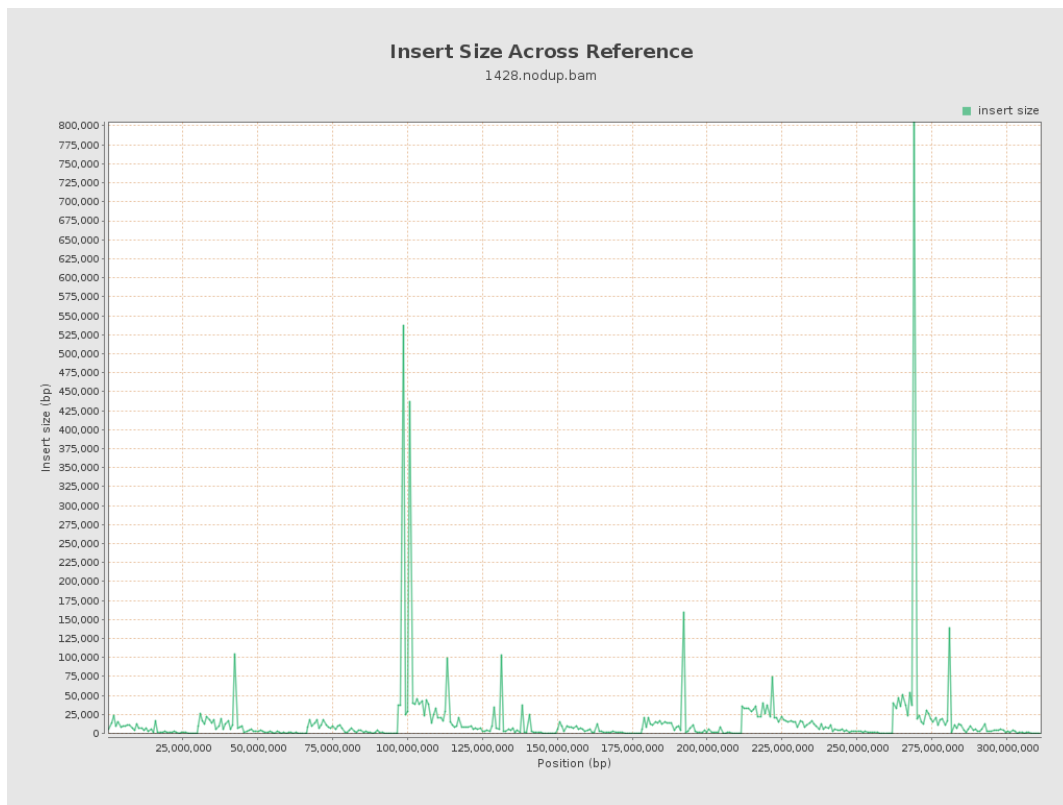




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

