

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:26:29*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/425
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

|                                       |   |
|---------------------------------------|---|
| BAM file:                             | /proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/425<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/awdata/P26207/P26207_212/02-FASTQ/220902_A00621_0737_BHM<br>GCVDSX3/P26207_212_S293_L003_R1_001.fastq.gz<br>/proj/uppstore2018210/Aalpina/data/awdata/P26207/P26207_212/02-FASTQ/220902_A00621_0737_BHM<br>GCVDSX3/P26207_212_S293_L003_R2_001.fastq.gz |
| Size of a homopolymer:                | 3   |
| Number of windows:                    | 400   |

|                            |                               |
|----------------------------|-------------------------------|
| Analysis date:             | Mon May 29 21:26:29 CEST 2023 |
| Draw chromosome limits:    | no                            |
| Skip duplicate alignments: | no                            |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 311,642,060         |
| Number of reads              | 51,716,823          |
| Mapped reads                 | 47,602,356 / 92.04% |
| Unmapped reads               | 4,114,467 / 7.96%   |
| Mapped paired reads          | 47,602,356 / 92.04% |
| Mapped reads, first in pair  | 23,883,938 / 46.18% |
| Mapped reads, second in pair | 23,718,418 / 45.86% |
| Mapped reads, both in pair   | 46,270,928 / 89.47% |
| Mapped reads, singletons     | 1,331,428 / 2.57%   |
| Read min/max/mean length     | 30 / 151 / 147.91   |
| Duplicated reads (flagged)   | 6,928,934 / 13.4%   |
| Clipped reads                | 12,139,974 / 23.47% |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 1,998,048,267 / 30.85% |
| Number/percentage of C's | 1,239,349,156 / 19.13% |
| Number/percentage of T's | 2,000,295,524 / 30.88% |
| Number/percentage of G's | 1,239,855,137 / 19.14% |
| Number/percentage of N's | 23,556 / 0%            |
| GC Percentage            | 38.27%                 |

### 2.3. Coverage

|                    |          |
|--------------------|----------|
| Mean               | 20.8391  |
| Standard Deviation | 193.2373 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 44.13 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 252,660.79      |
| Standard Deviation | 2,410,354.54    |
| P25/Median/P75     | 321 / 434 / 565 |

## 2.6. Mismatches and indels

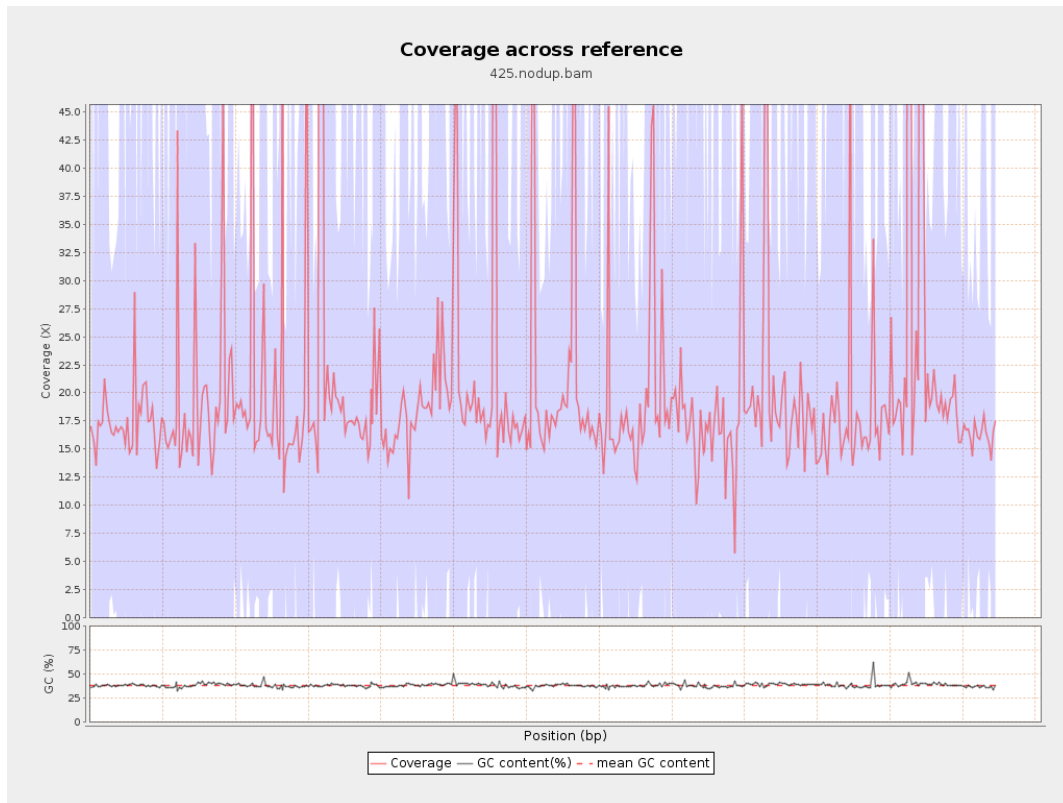
|  |             |
|--|-------------|
| General error rate                       | 2.37%       |
| Mismatches                               | 140,970,353 |
| Insertions                               | 4,541,160   |
| Mapped reads with at least one insertion | 8.53%       |
| Deletions                                | 4,477,892   |
| Mapped reads with at least one deletion  | 8.33%       |
| Homopolymer indels                       | 56.71%      |

## 2.7. Chromosome stats

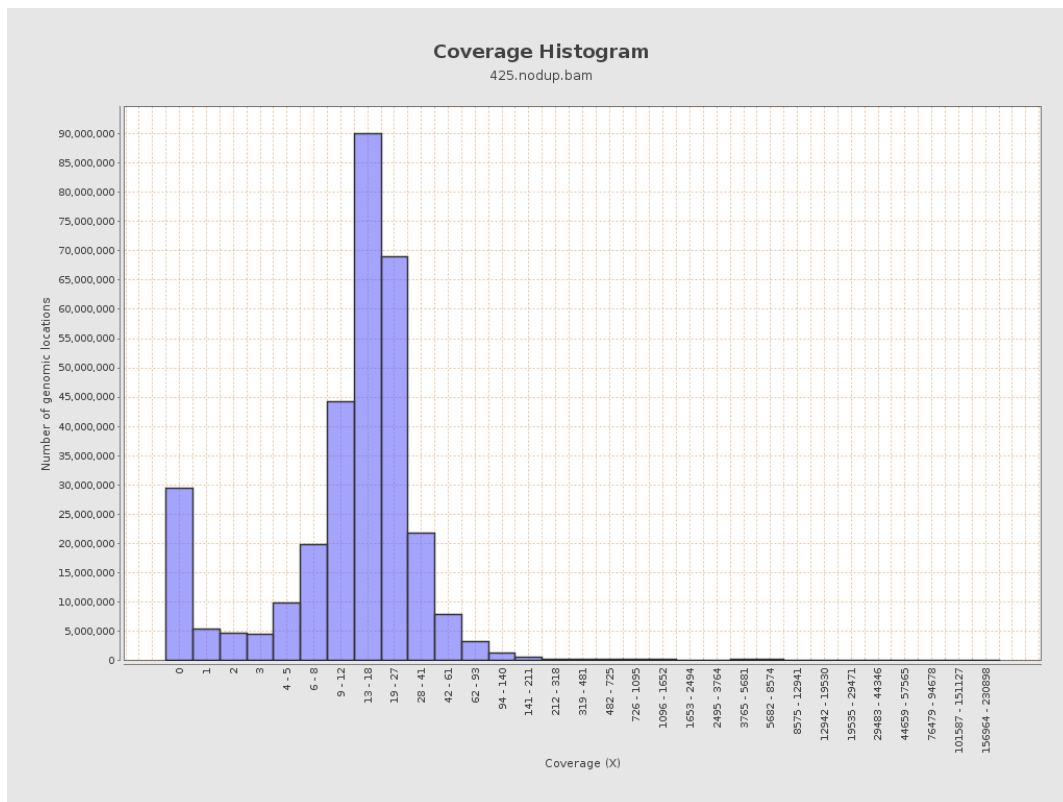
| Name       | Length   | Mapped bases | Mean coverage | Standard deviation |
|------------|----------|--------------|---------------|--------------------|
| LT669788.1 | 29724344 | 510559662    | 17.1765       | 66.5634            |

|            |          |            |         |          |
|------------|----------|------------|---------|----------|
| LT669789.1 | 36598175 | 752169949  | 20.5521 | 187.3184 |
| LT669790.1 | 30422129 | 739766562  | 24.3167 | 233.5768 |
| LT669791.1 | 52758100 | 1083117487 | 20.5299 | 185.3139 |
| LT669792.1 | 28376109 | 586706442  | 20.6761 | 188.4465 |
| LT669793.1 | 33388210 | 634280578  | 18.9971 | 130.0103 |
| LT669794.1 | 50579949 | 977712872  | 19.33   | 151.8771 |
| LT669795.1 | 49795044 | 1210036625 | 24.3003 | 283.7482 |

### 3. Results : Coverage across reference

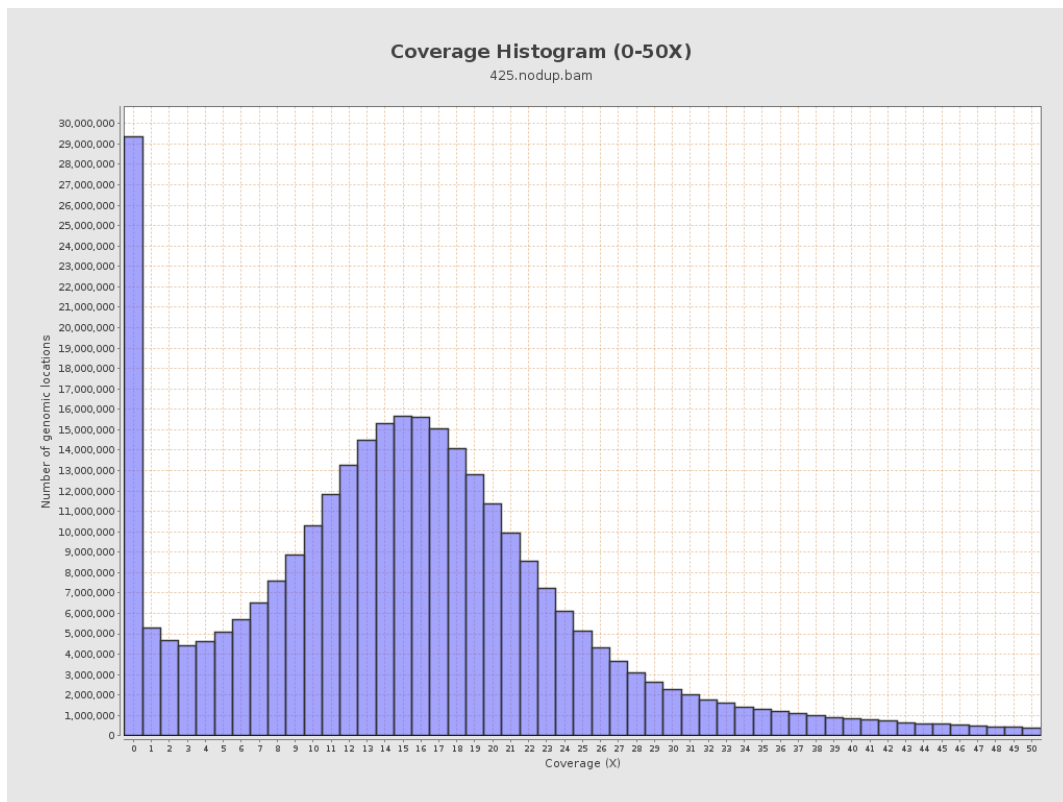


## 4. Results : Coverage Histogram

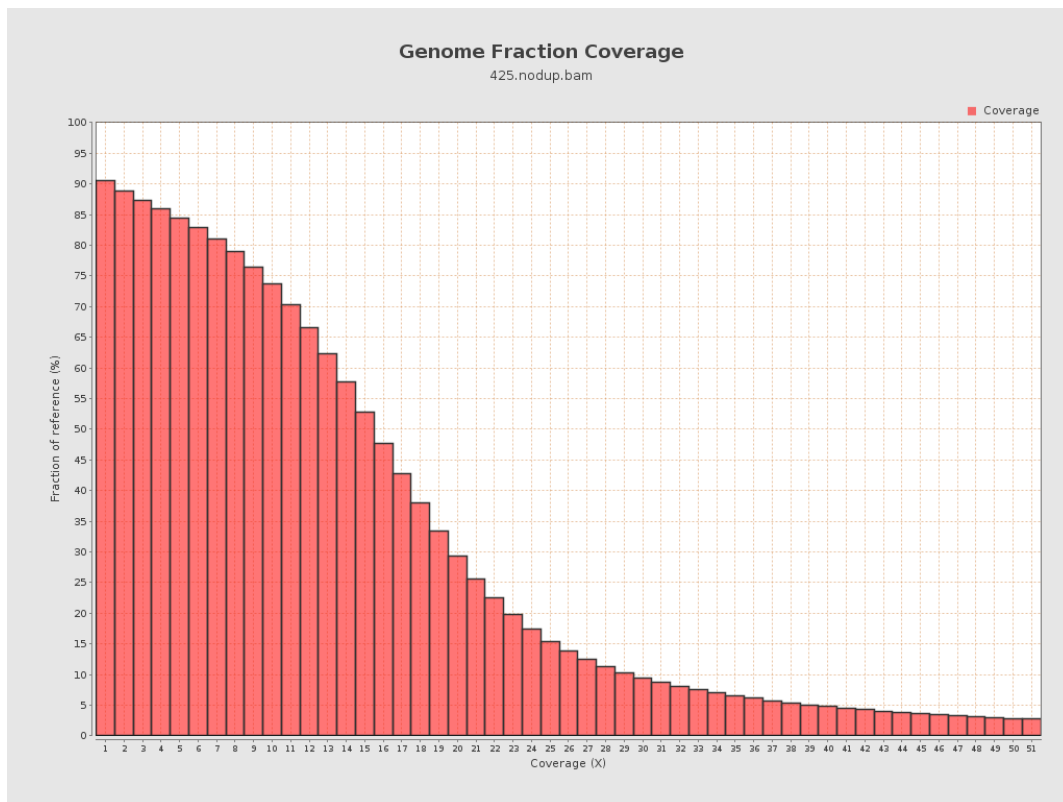




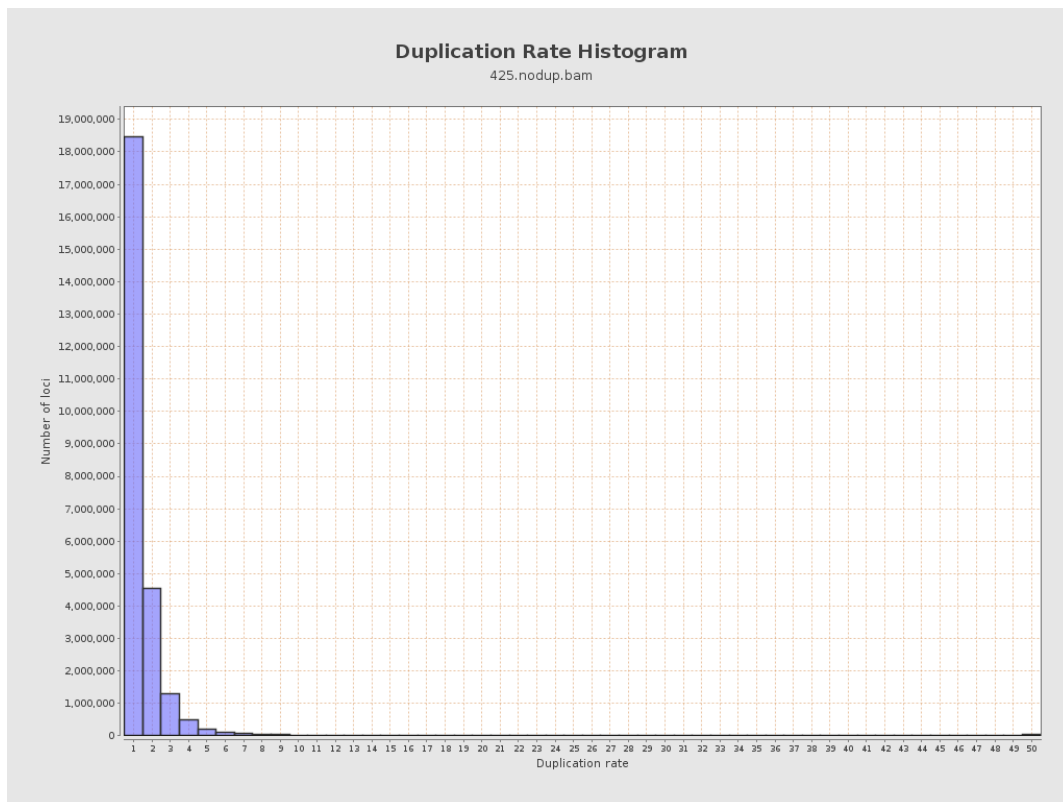
## 5. Results : Coverage Histogram (0-50X)



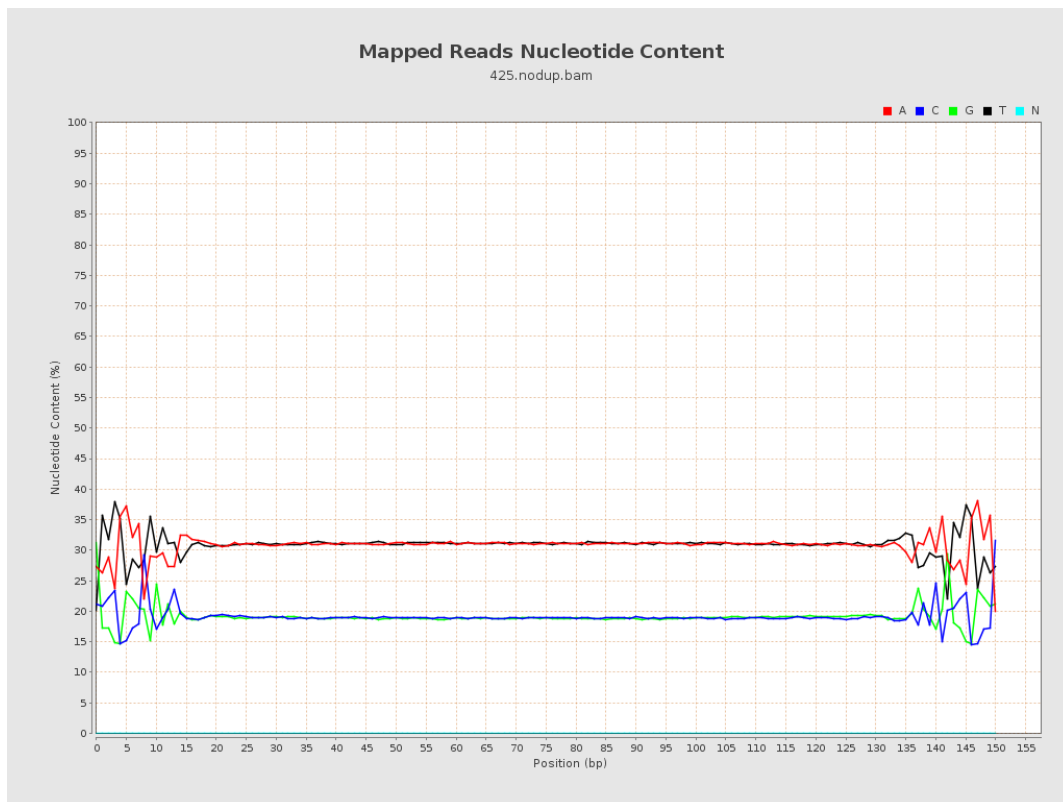
## 6. Results : Genome Fraction Coverage



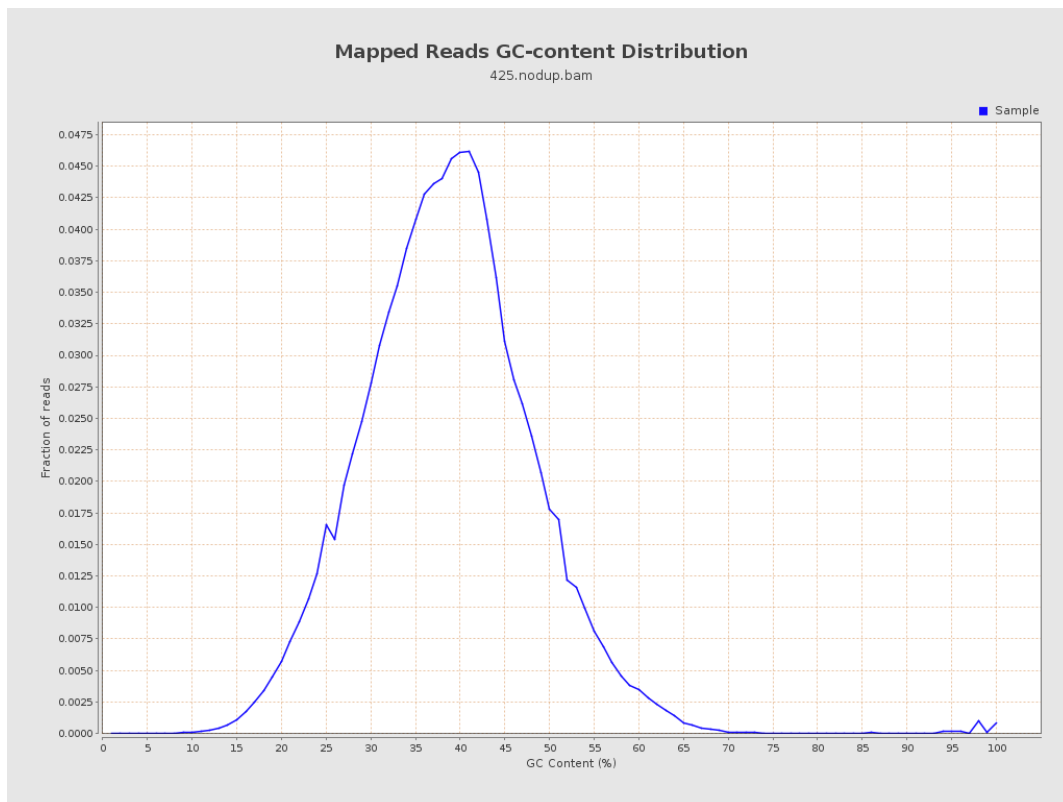
## 7. Results : Duplication Rate Histogram



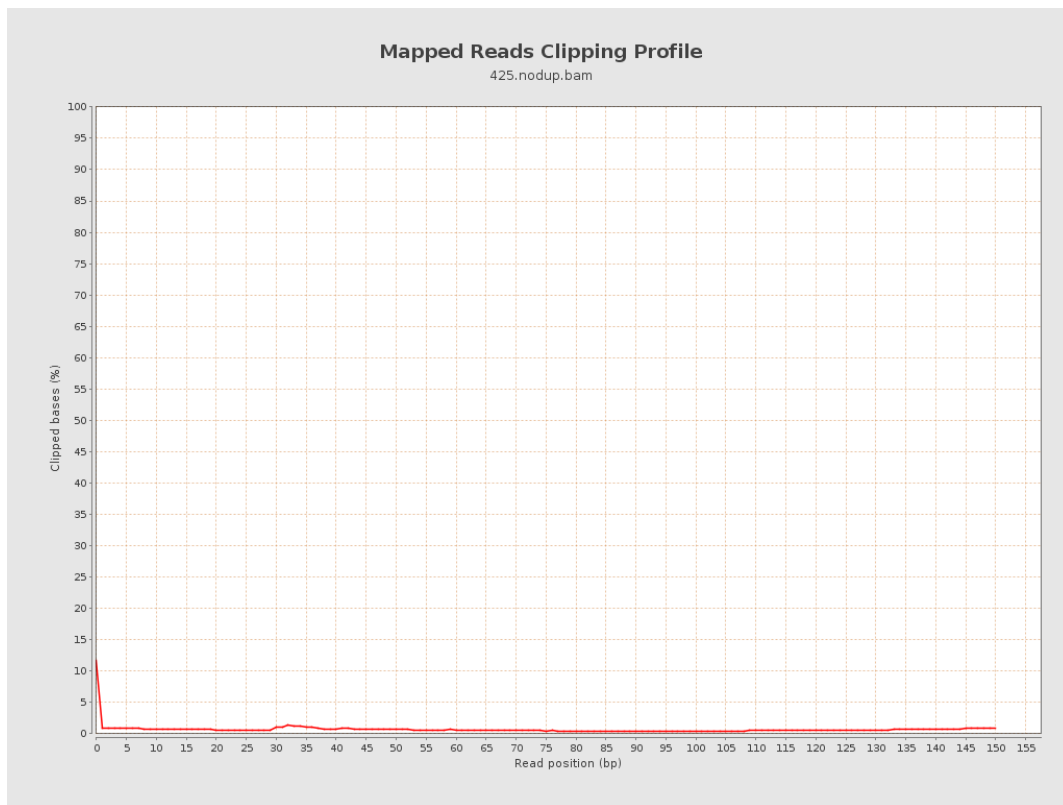
## 8. Results : Mapped Reads Nucleotide Content



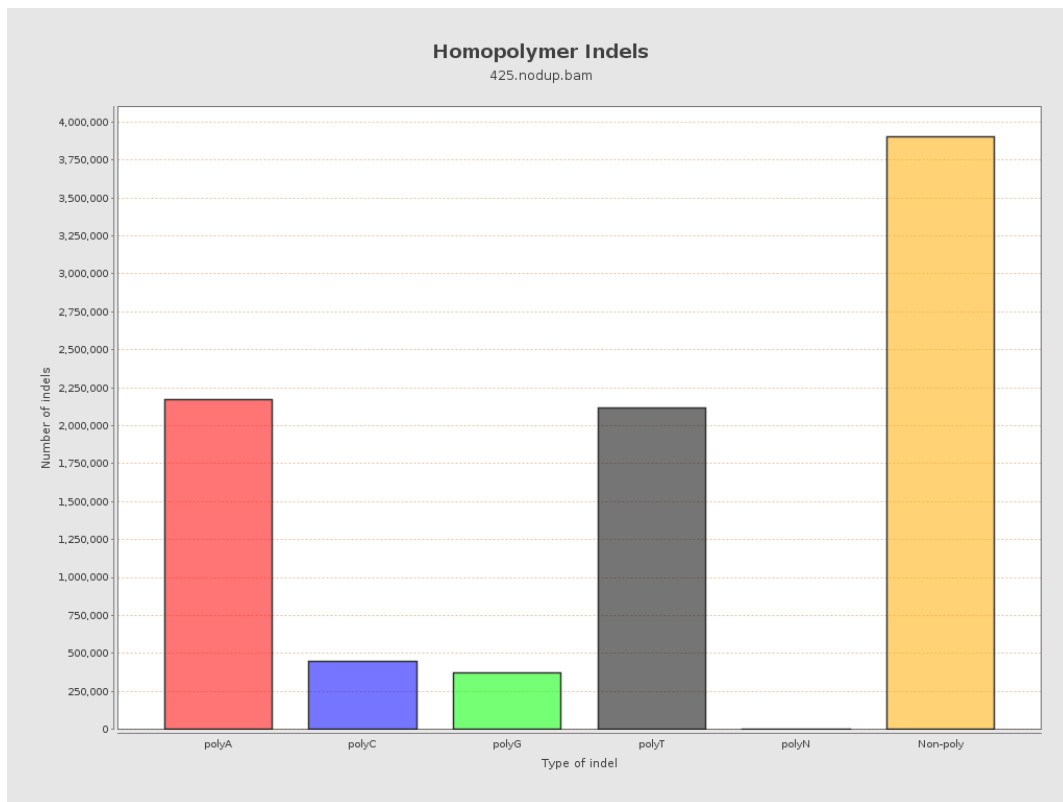
## 9. Results : Mapped Reads GC-content Distribution



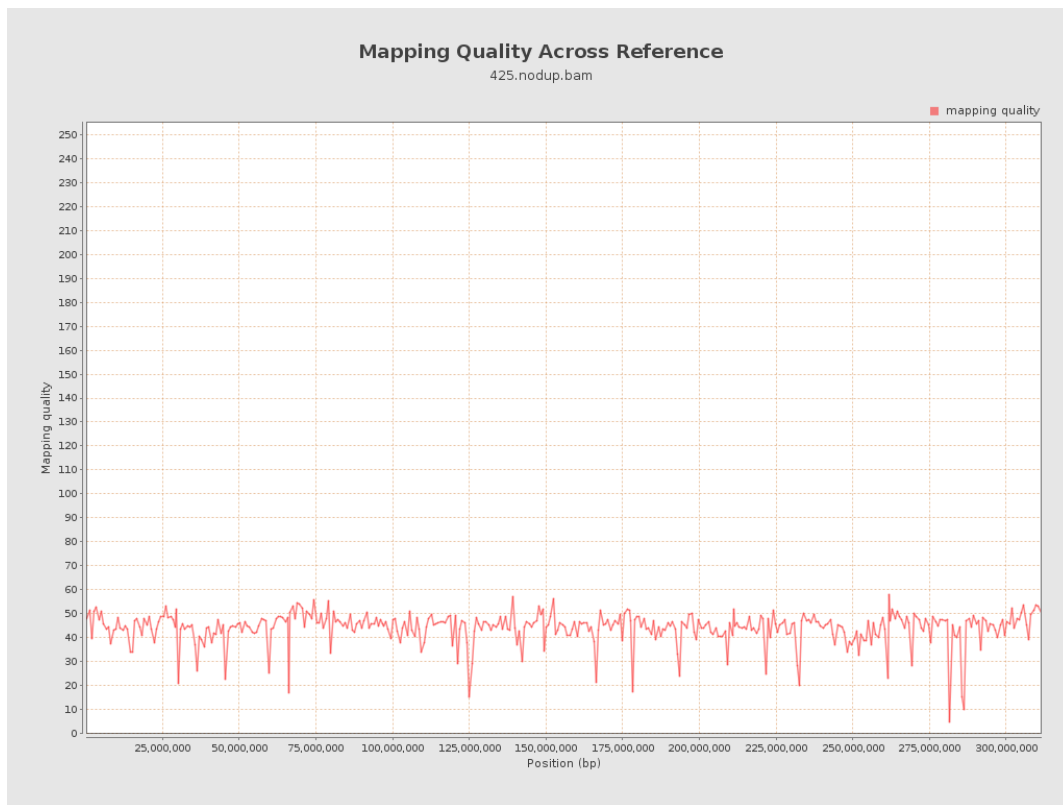
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

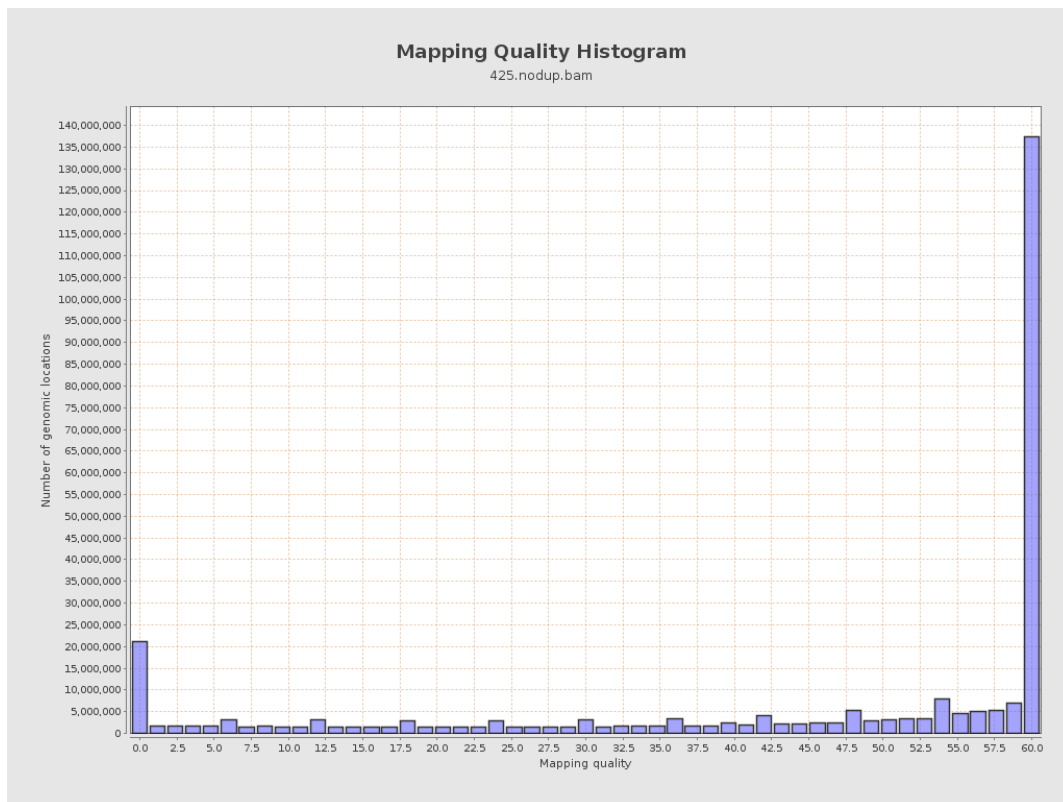


## 12. Results : Mapping Quality Across Reference

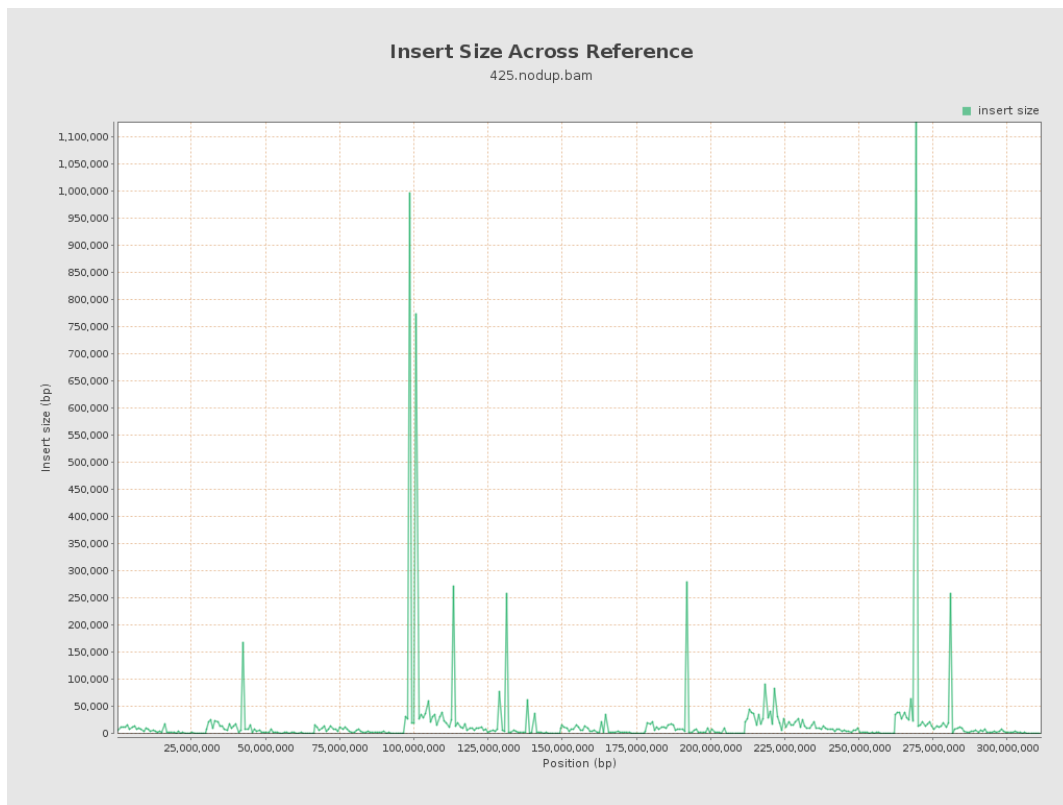




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

