

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/05/29 21:40:19*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/proj/uppstore2018210/Aalpina/working/Kate/Working/F2/MarkDuplicates/145
4
.nodup.bam -nw 400 -hm 3
```

## 1.2. Alignment

|                                       |   |
|---------------------------------------|---|
| BAM file:                             | /proj/uppstore2018210/Aalpina/worki<br>ng/Kate/Working/F2/MarkDuplicates/<br>1454<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_444/02-<br>FASTQ/220902_A00621_0737_BHM<br>GCVDSX3/P26207_444_S419_L004<br>_R1_001.fastq.gz<br>/proj/uppstore2018210/Aalpina/data/r<br>awdata/P26207/P26207_444/02-<br>FASTQ/220902_A00621_0737_BHM<br>GCVDSX3/P26207_444_S419_L004<br>_R2_001.fastq.gz |
| Size of a homopolymer:                | 3   |
|                                       |   |

|                            |                               |
|----------------------------|-------------------------------|
| Number of windows:         | 400                           |
| Analysis date:             | Mon May 29 21:40:19 CEST 2023 |
| Draw chromosome limits:    | no                            |
| Skip duplicate alignments: | no                            |

## 2. Summary

### 2.1. Globals

|                              |                     |
|------------------------------|---------------------|
| Reference size               | 311,642,060         |
| Number of reads              | 94,146,788          |
| Mapped reads                 | 88,327,200 / 93.82% |
| Unmapped reads               | 5,819,588 / 6.18%   |
| Mapped paired reads          | 88,327,200 / 93.82% |
| Mapped reads, first in pair  | 44,248,353 / 47%    |
| Mapped reads, second in pair | 44,078,847 / 46.82% |
| Mapped reads, both in pair   | 86,485,628 / 91.86% |
| Mapped reads, singletons     | 1,841,572 / 1.96%   |
| Read min/max/mean length     | 30 / 151 / 148.06   |
| Duplicated reads (flagged)   | 14,248,172 / 15.13% |
| Clipped reads                | 19,320,916 / 20.52% |

### 2.2. ACGT Content

|                          |                        |
|--------------------------|------------------------|
| Number/percentage of A's | 3,792,223,898 / 30.93% |
| Number/percentage of C's | 2,336,571,810 / 19.06% |
| Number/percentage of T's | 3,799,298,434 / 30.99% |
| Number/percentage of G's | 2,331,938,780 / 19.02% |
| Number/percentage of N's | 42,864 / 0%            |
| GC Percentage            | 38.08%                 |

### 2.3. Coverage

|                    |          |
|--------------------|----------|
| Mean               | 39.4436  |
| Standard Deviation | 296.4663 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 44.43 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 243,640.46      |
| Standard Deviation | 2,361,032.65    |
| P25/Median/P75     | 350 / 458 / 599 |

## 2.6. Mismatches and indels

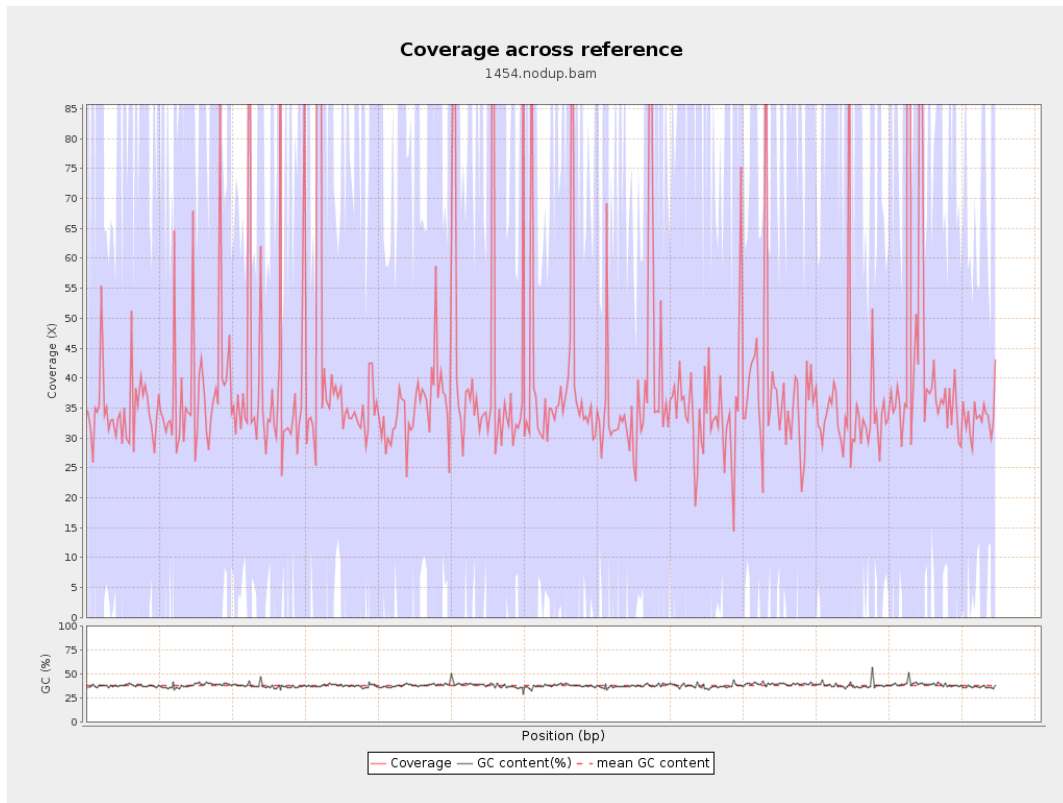
|  |             |
|--|-------------|
| General error rate                       | 2.25%       |
| Mismatches                               | 252,576,154 |
| Insertions                               | 8,390,170   |
| Mapped reads with at least one insertion | 8.53%       |
| Deletions                                | 8,488,907   |
| Mapped reads with at least one deletion  | 8.53%       |
| Homopolymer indels                       | 56.52%      |

## 2.7. Chromosome stats

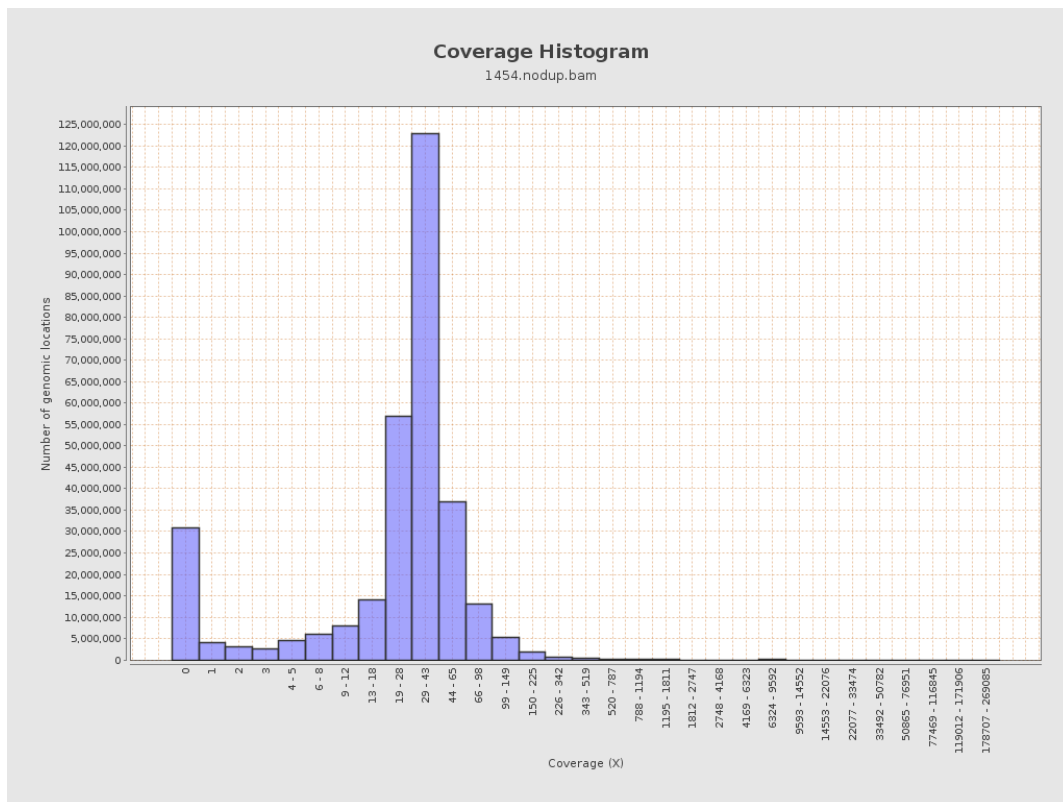
| Name       | Length   | Mapped bases | Mean coverage | Standard deviation |
|------------|----------|--------------|---------------|--------------------|
| LT669788.1 | 29724344 | 1019331451   | 34.2928       | 94.8139            |
|            |          |              |               |                    |

|            |          |            |         |          |
|------------|----------|------------|---------|----------|
| LT669789.1 | 36598175 | 1468678425 | 40.1298 | 342.6311 |
| LT669790.1 | 30422129 | 1320879655 | 43.4184 | 320.0131 |
| LT669791.1 | 52758100 | 2011739546 | 38.1314 | 293.9105 |
| LT669792.1 | 28376109 | 1116264149 | 39.3382 | 287.9653 |
| LT669793.1 | 33388210 | 1234238168 | 36.9663 | 204.7884 |
| LT669794.1 | 50579949 | 1894084991 | 37.4473 | 284.0384 |
| LT669795.1 | 49795044 | 2227073593 | 44.7248 | 383.3356 |

### 3. Results : Coverage across reference

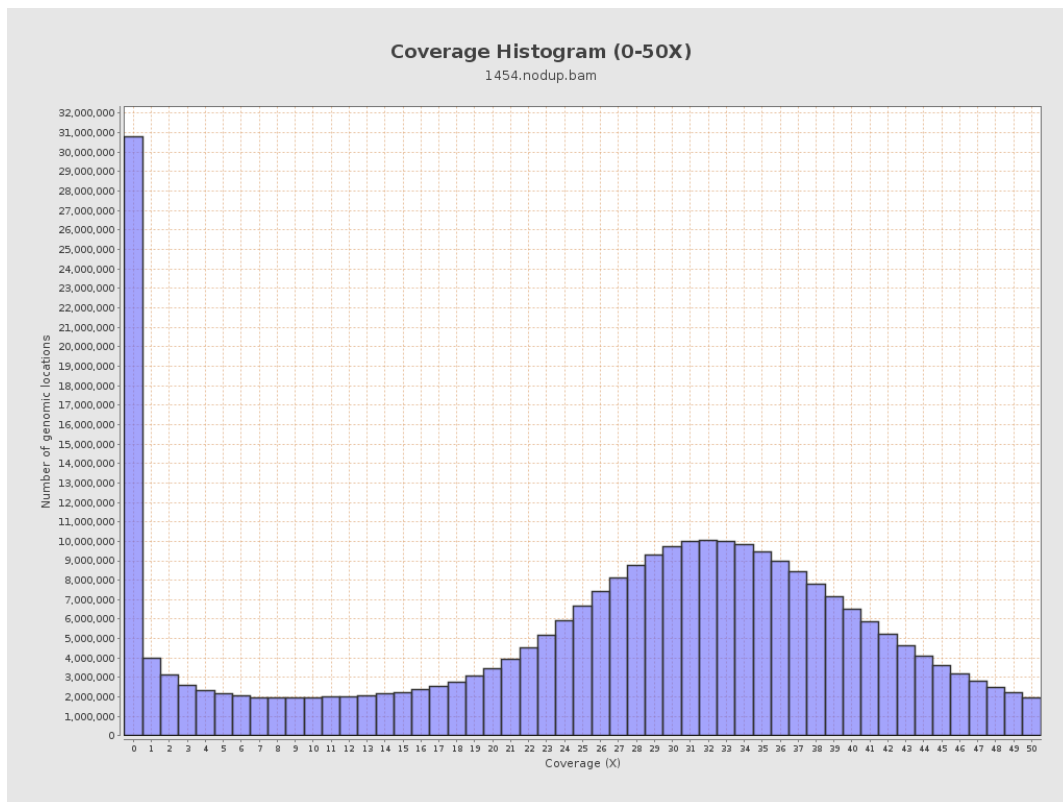


## 4. Results : Coverage Histogram

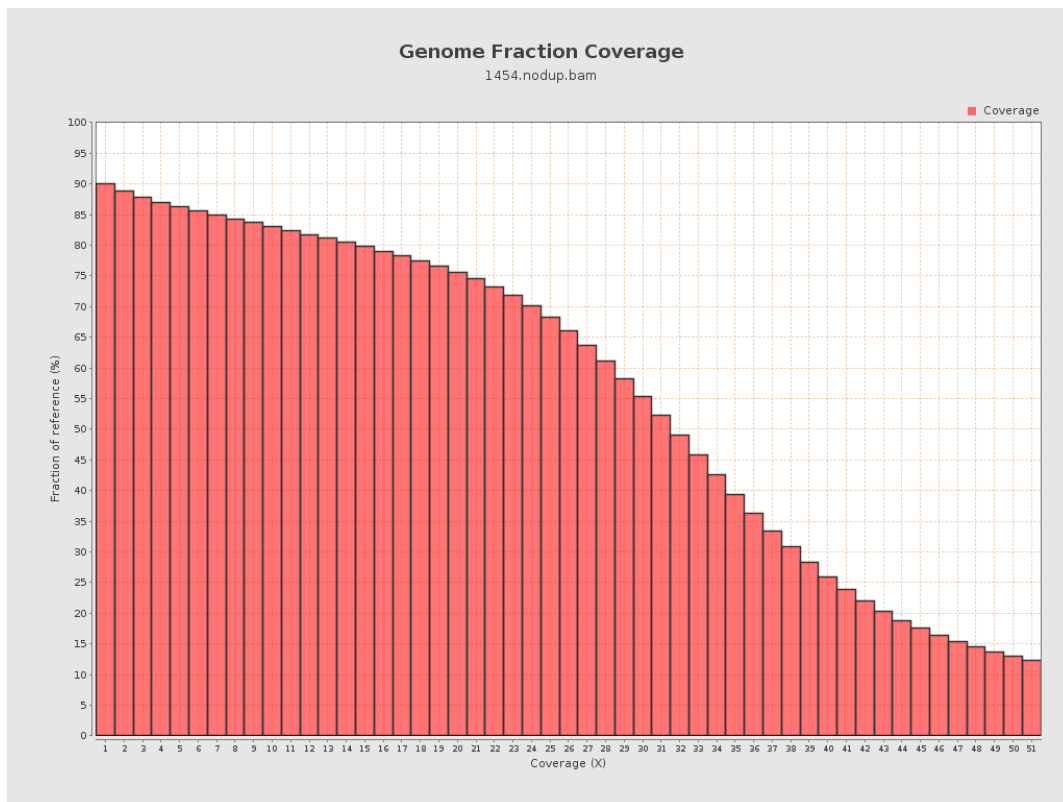




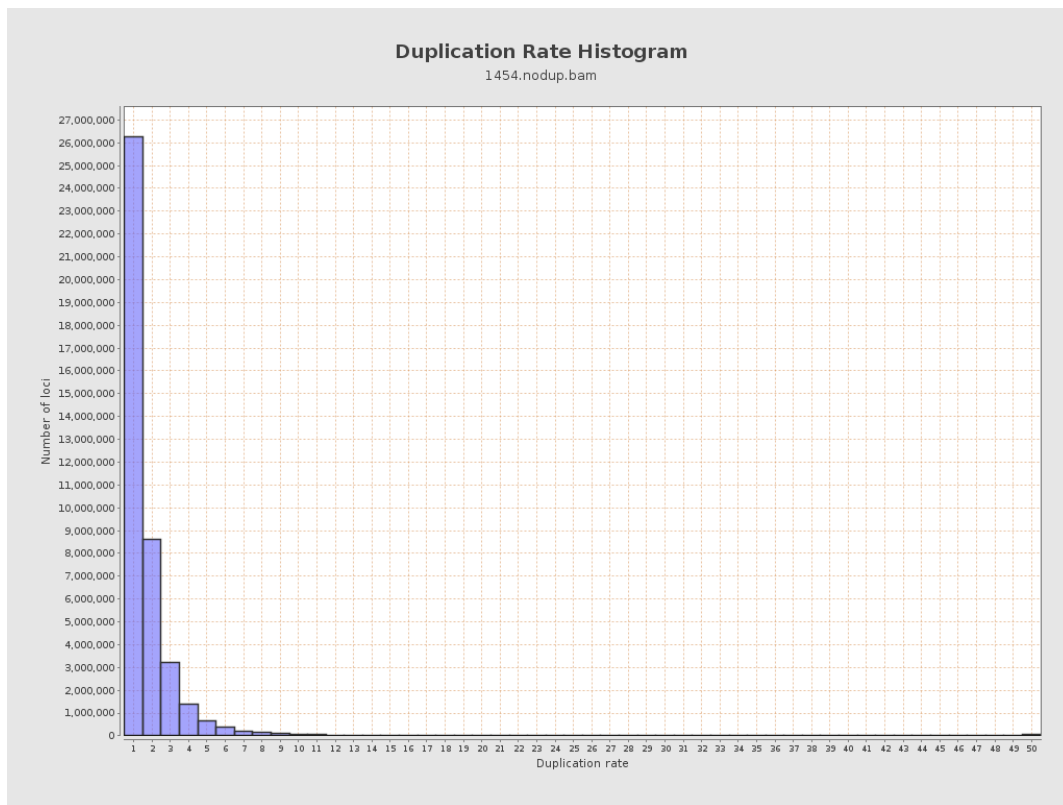
## 5. Results : Coverage Histogram (0-50X)



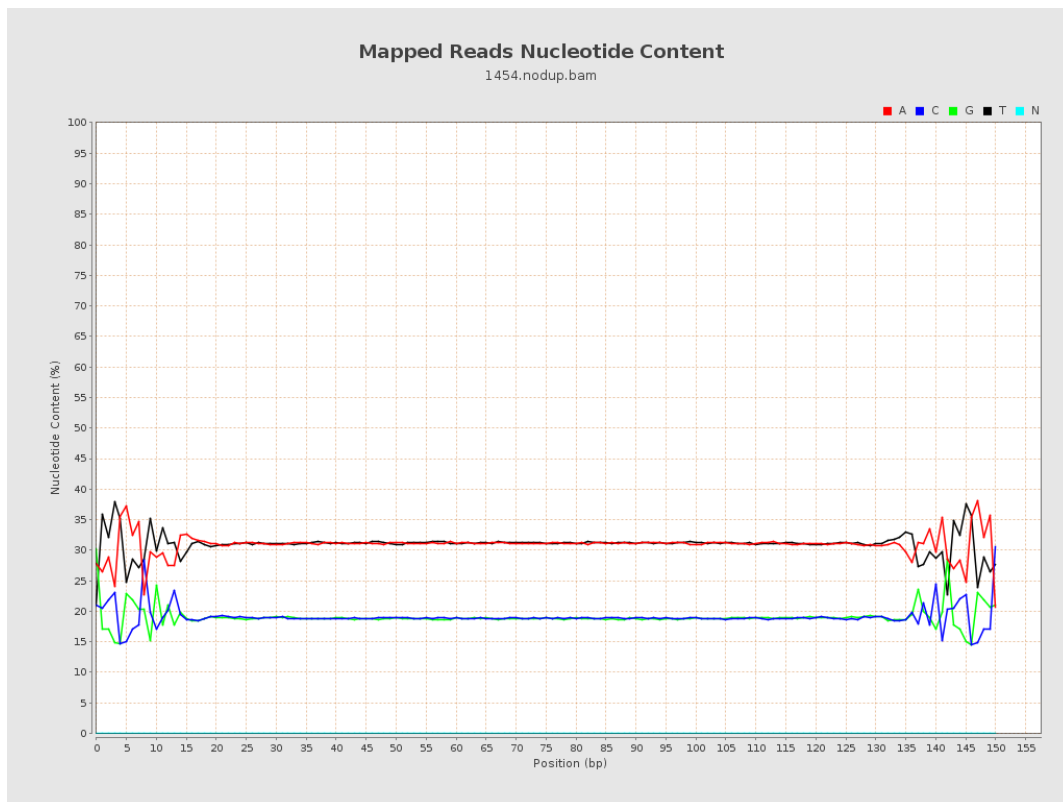
## 6. Results : Genome Fraction Coverage



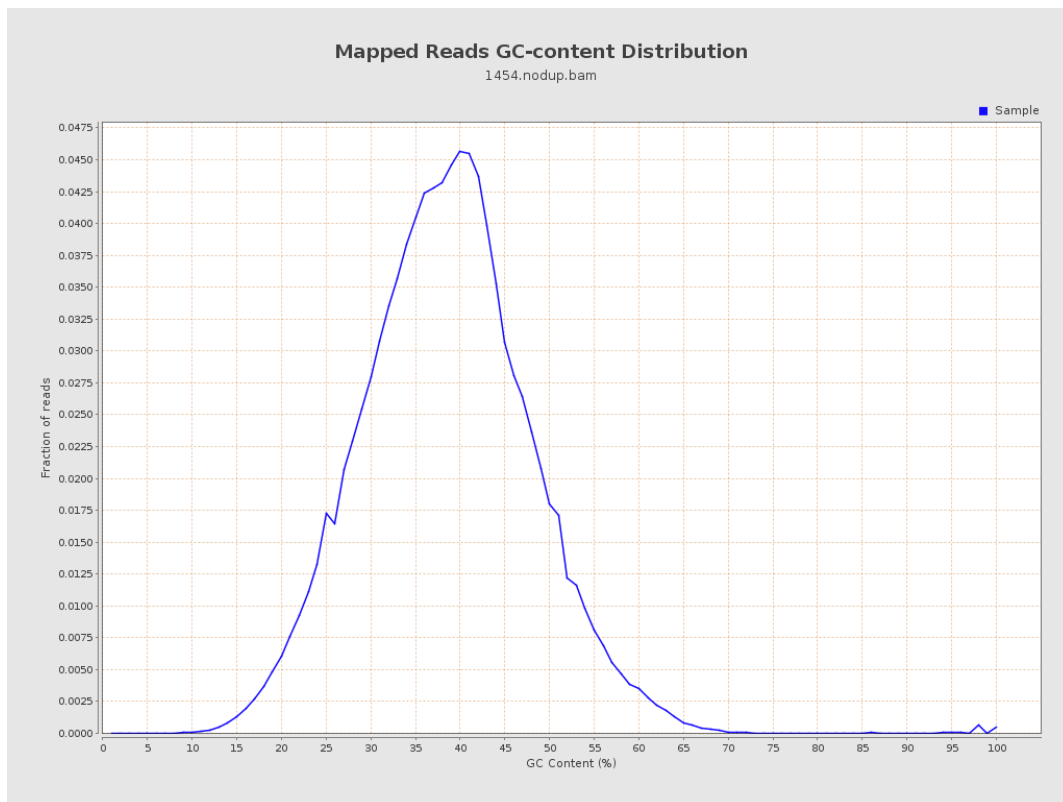
## 7. Results : Duplication Rate Histogram



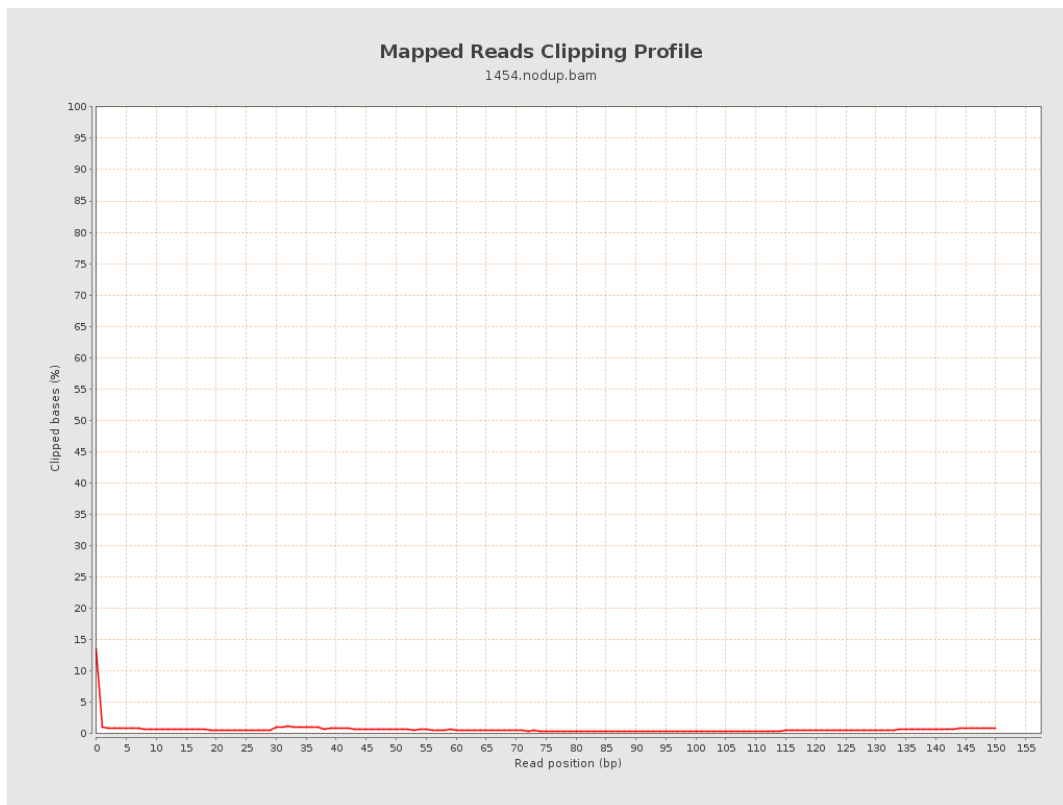
## 8. Results : Mapped Reads Nucleotide Content



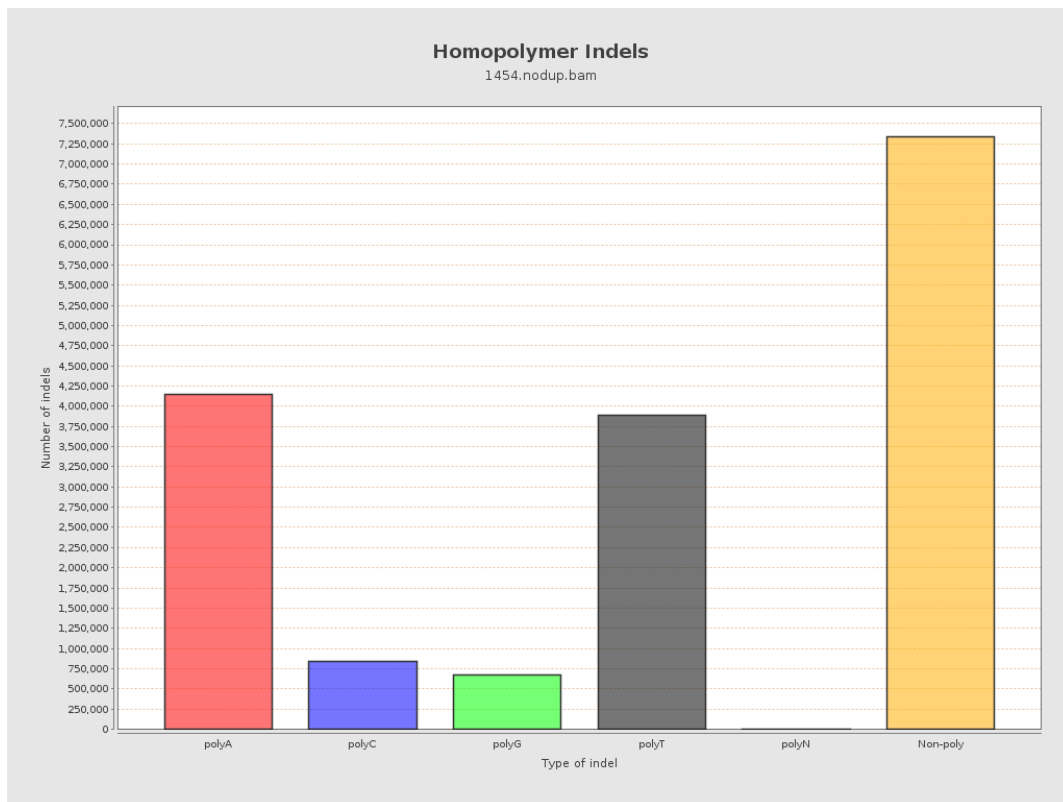
## 9. Results : Mapped Reads GC-content Distribution



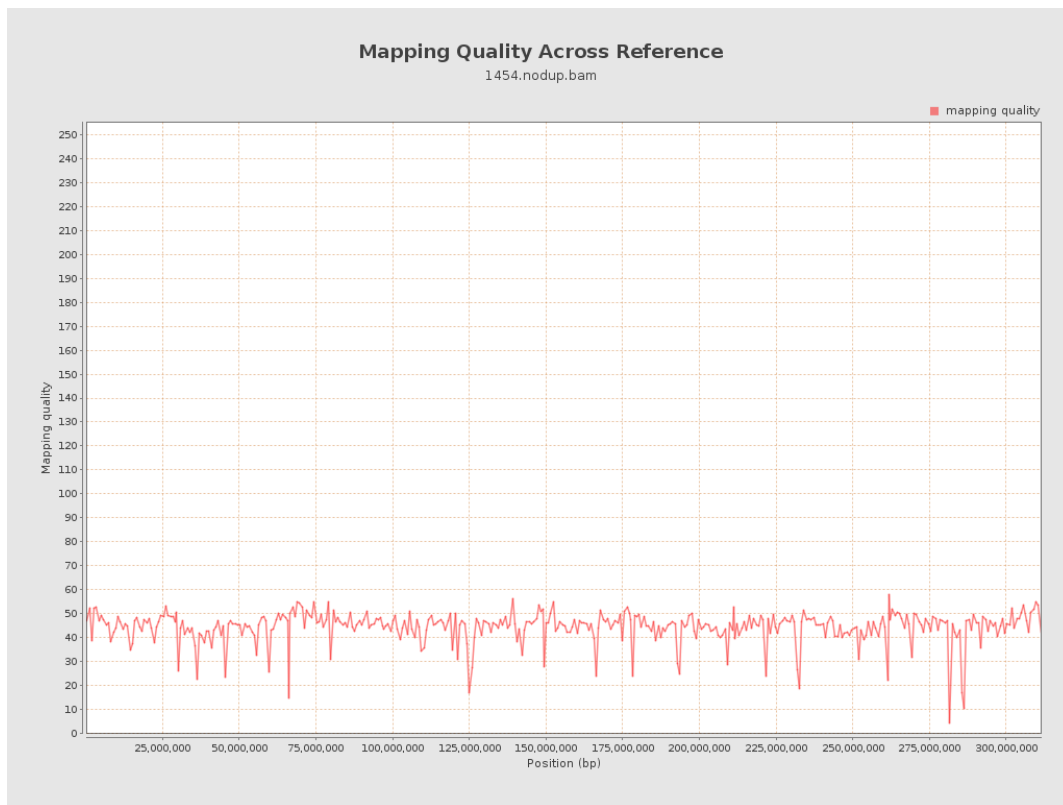
## 10. Results : Mapped Reads Clipping Profile



## 11. Results : Homopolymer Indels

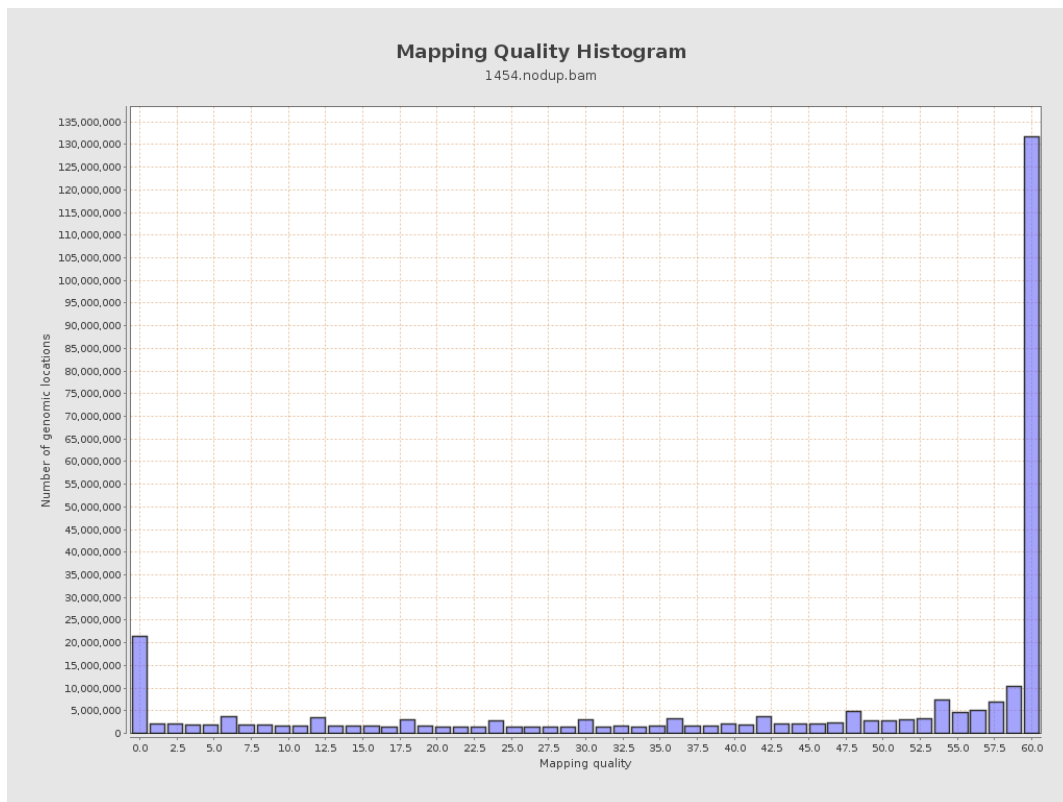


## 12. Results : Mapping Quality Across Reference

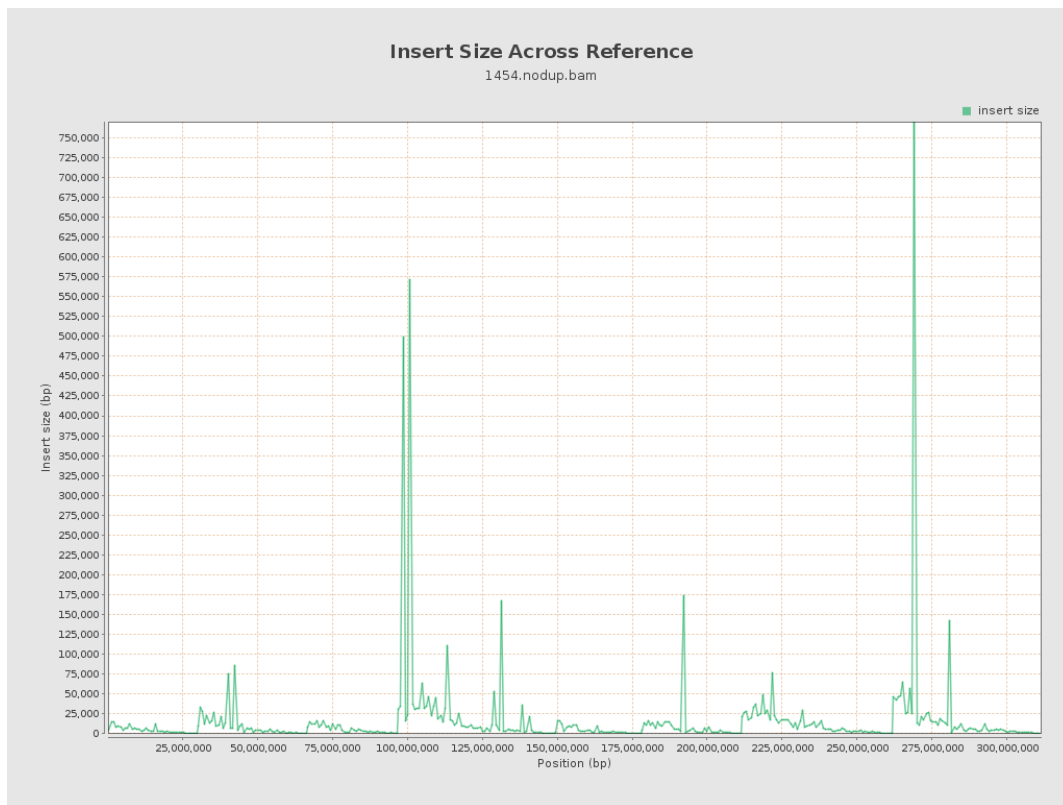




## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

