

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/07/29 21:15:39*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam sample_2_bbmap_global.sorted.bam -c -nw 400 -hm 3
```

## 1.2. Alignment

|                                       |  |
|---------------------------------------|--|
| Command line:                         | java -ea -Xmx8g -Xms8g<br>align2.BBMap build=1 overwrite=true<br>fastareadlen=500 -Xmx8g threads=4<br>sam=1.3 trd<br>ref=Swietenia_mahagoni_Ch1.fasta<br>nodisk<br>in=sample_2_21_clean_R#.fastq.gz<br>out=sample_2_bbmap_global.sam |
| Draw chromosome limits:               | yes  |
| Analyze overlapping paired-end reads: | no   |
| Program:                              | BBMap (38.90)  |
| Analysis date:                        | Sat Jul 29 21:15:35 CEST 2023  |
| Size of a homopolymer:                | 3  |
| Skip duplicate alignments:            | no   |
| Number of windows:                    | 400  |
| BAM file:                             | sample_2_bbmap_global.sorted.bam   |

## 2. Summary

### 2.1. Globals

|                              |                   |
|------------------------------|-------------------|
| Reference size               | 159,276           |
| Number of reads              | 744,970           |
| Mapped reads                 | 744,909 / 99.99%  |
| Unmapped reads               | 61 / 0.01%        |
| Mapped paired reads          | 744,909 / 99.99%  |
| Mapped reads, first in pair  | 372,454 / 50%     |
| Mapped reads, second in pair | 372,455 / 50%     |
| Mapped reads, both in pair   | 744,850 / 99.98%  |
| Mapped reads, singletons     | 59 / 0.01%        |
| Read min/max/mean length     | 21 / 150 / 105.17 |
| Duplicated reads (estimated) | 612,597 / 82.23%  |
| Duplication rate             | 95.8%             |
| Clipped reads                | 239 / 0.03%       |

### 2.2. ACGT Content

|                          |                     |
|--------------------------|---------------------|
| Number/percentage of A's | 23,969,019 / 30.6%  |
| Number/percentage of C's | 15,003,263 / 19.15% |
| Number/percentage of T's | 24,590,496 / 31.39% |
| Number/percentage of G's | 14,776,476 / 18.86% |
| Number/percentage of N's | 0 / 0%              |
| GC Percentage            | 38.01%              |

## 2.3. Coverage

|                    |          |
|--------------------|----------|
| Mean               | 492.1037 |
| Standard Deviation | 284.8251 |

## 2.4. Mapping Quality

|                      |       |
|----------------------|-------|
| Mean Mapping Quality | 30.17 |
|----------------------|-------|

## 2.5. Insert size

|                    |                 |
|--------------------|-----------------|
| Mean               | 381.79          |
| Standard Deviation | 2,943.37        |
| P25/Median/P75     | 241 / 287 / 333 |

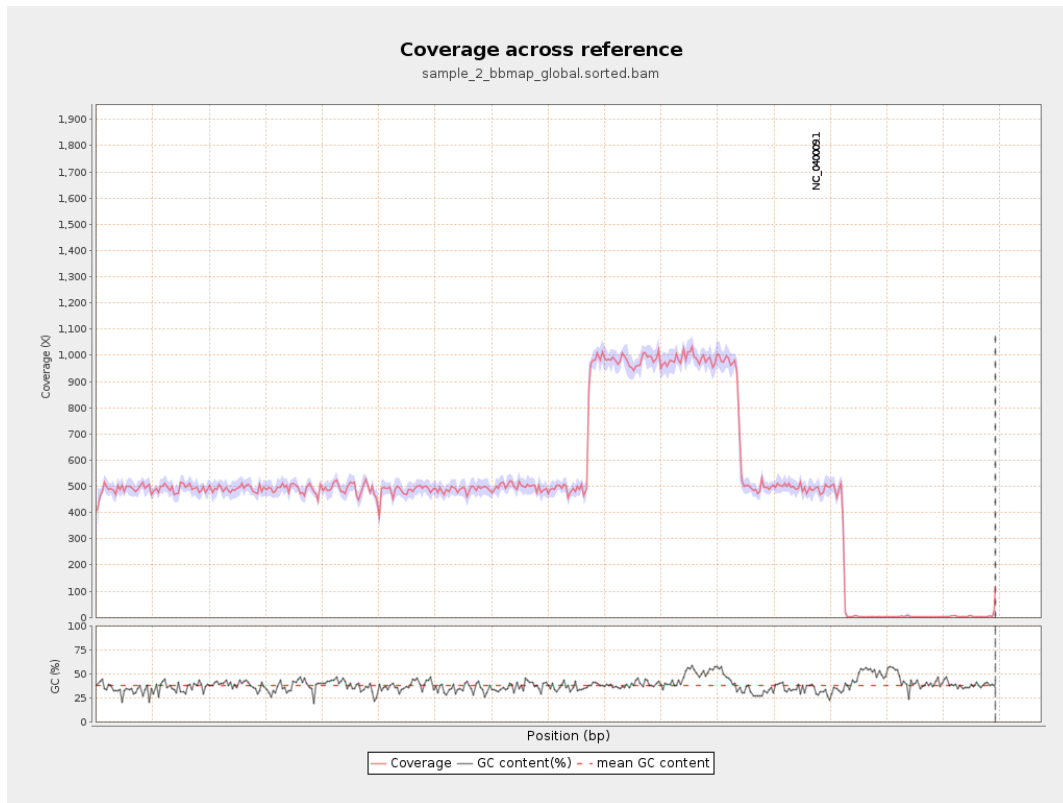
## 2.6. Mismatches and indels

|  |        |
|--|--------|
| General error rate                       | 0.34%  |
| Insertions                               | 818    |
| Mapped reads with at least one insertion | 0.11%  |
| Deletions                                | 321    |
| Mapped reads with at least one deletion  | 0.04%  |
| Homopolymer indels                       | 61.37% |

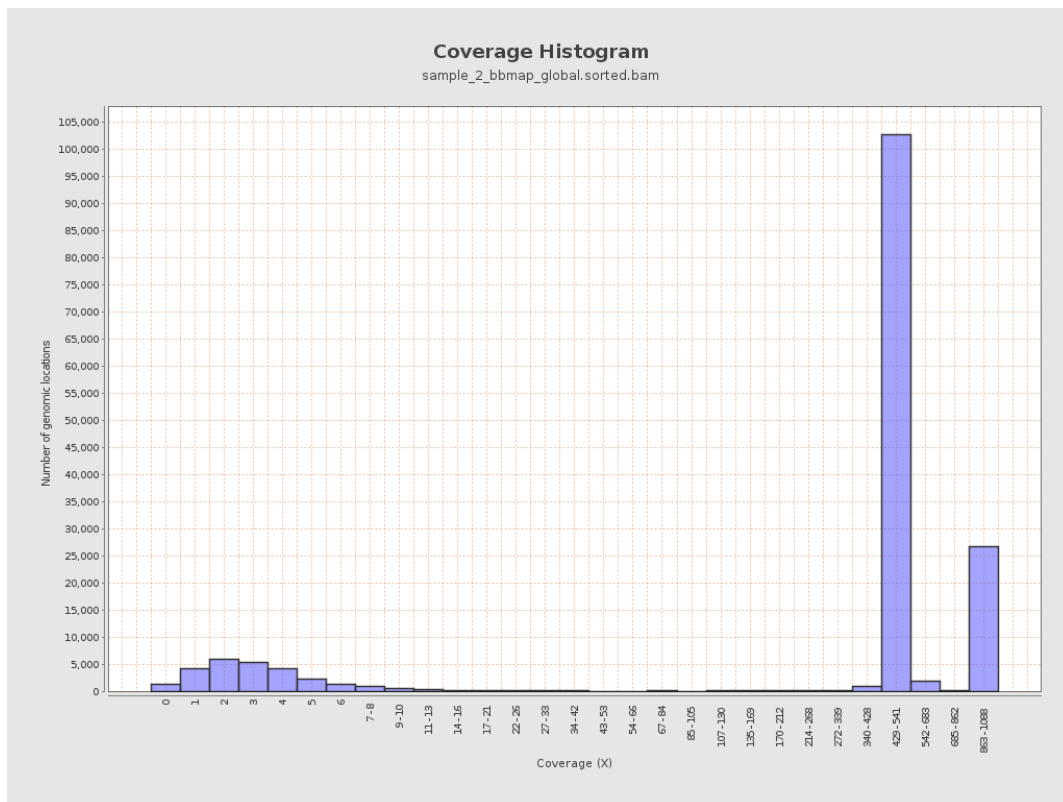
## 2.7. Chromosome stats

| Name        | Length | Mapped bases | Mean coverage | Standard deviation |
|-------------|--------|--------------|---------------|--------------------|
| NC_040009.1 | 159276 | 78380306     | 492.1037      | 284.8251           |

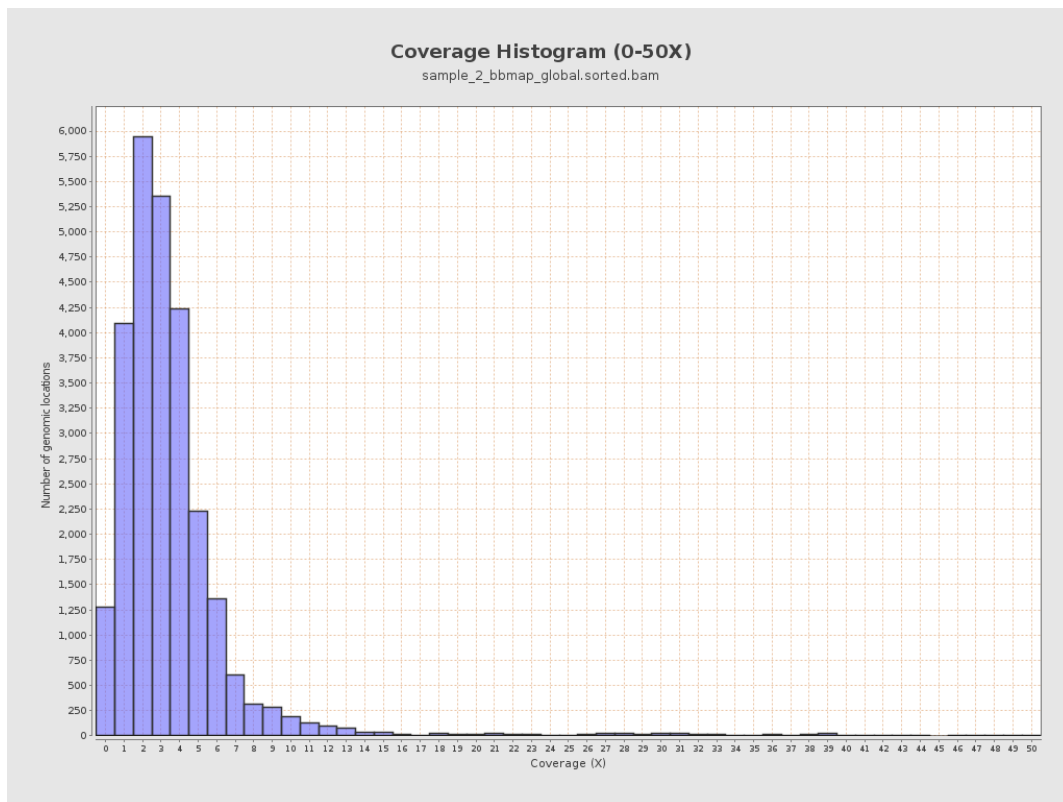
### 3. Results : Coverage across reference



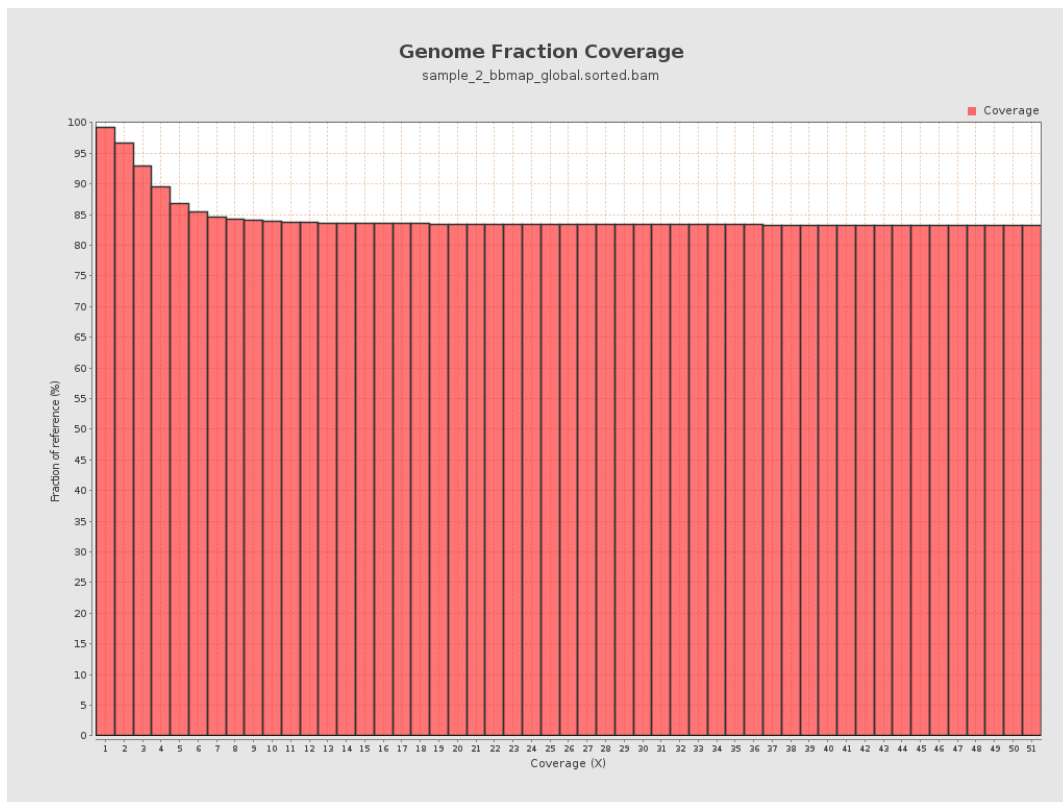
## 4. Results : Coverage Histogram



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

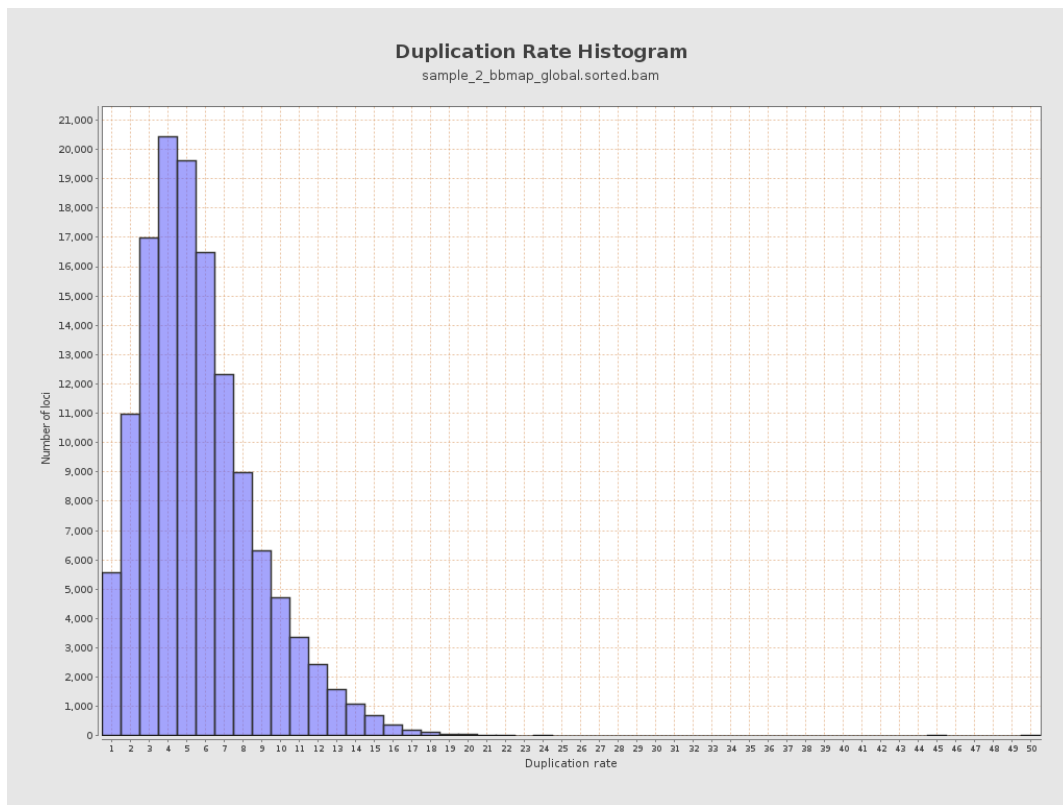


## 6. Results : Genome Fraction Coverage

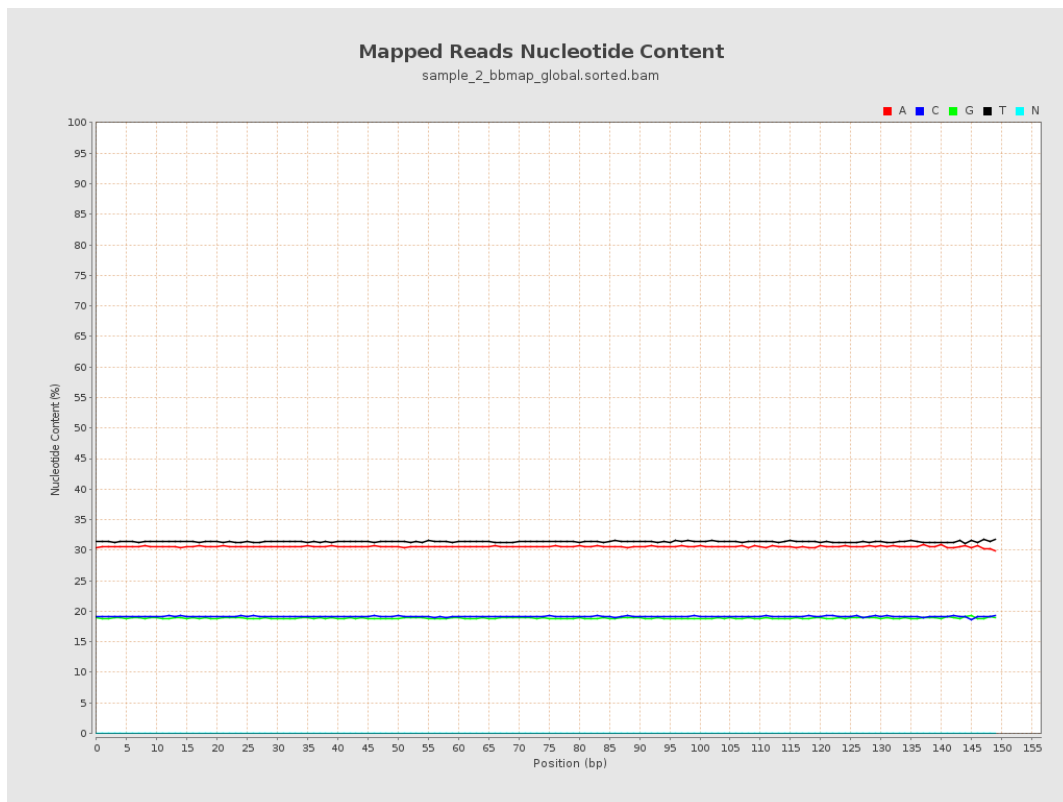




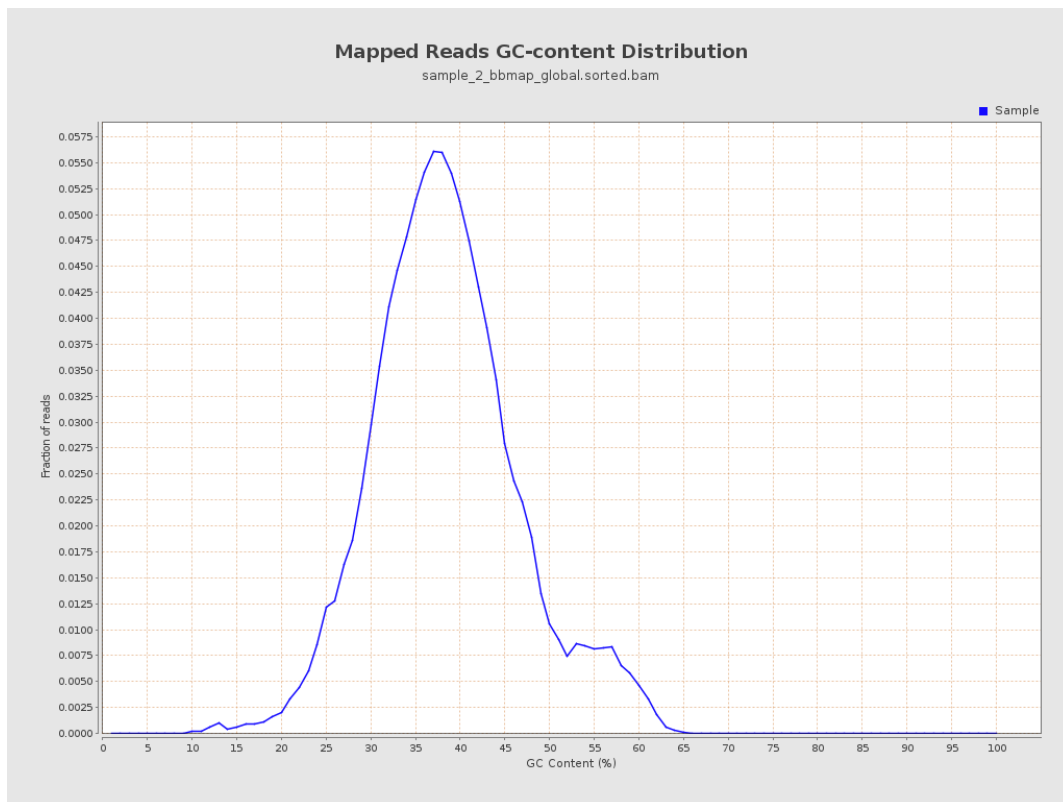
## 7. Results : Duplication Rate Histogram



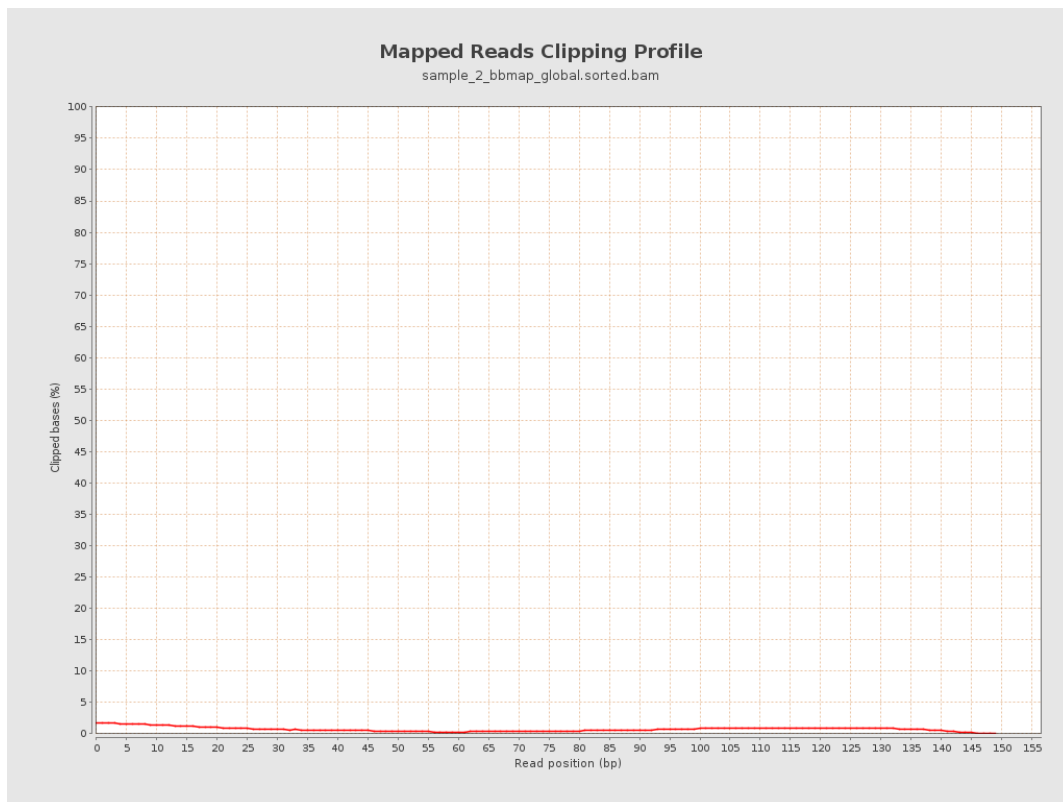
## 8. Results : Mapped Reads Nucleotide Content



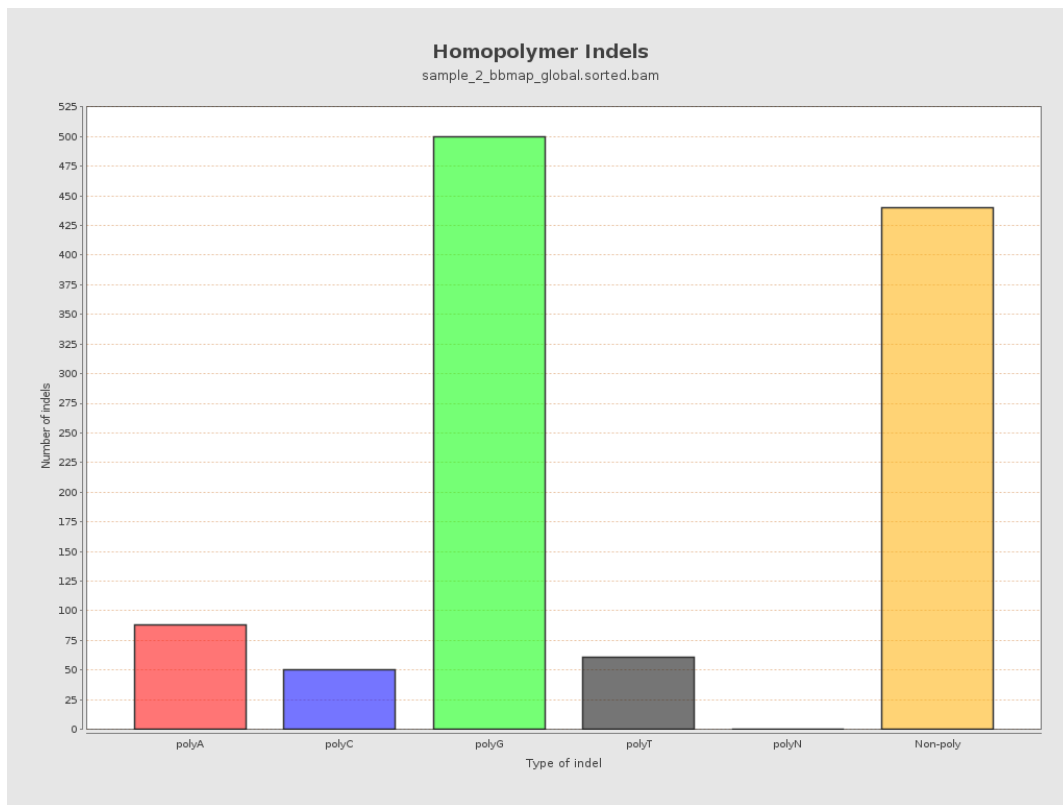
## 9. Results : Mapped Reads GC-content Distribution



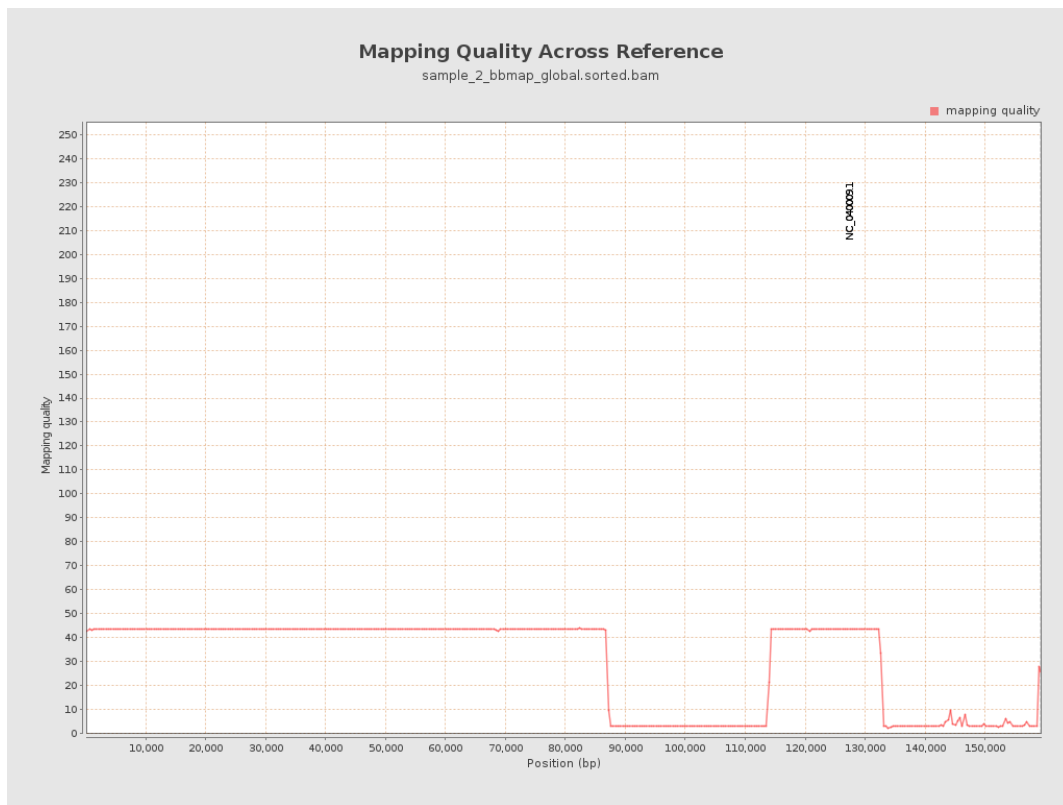
## 10. Results : Mapped Reads Clipping Profile



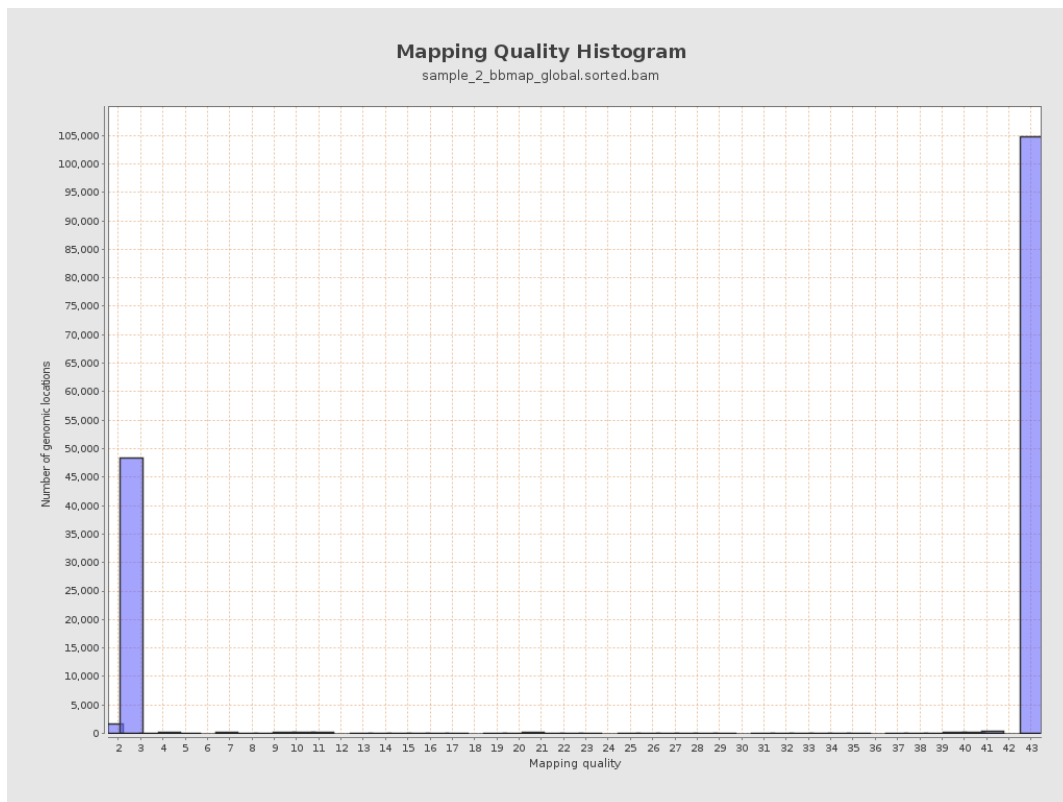
## 11. Results : Homopolymer Indels



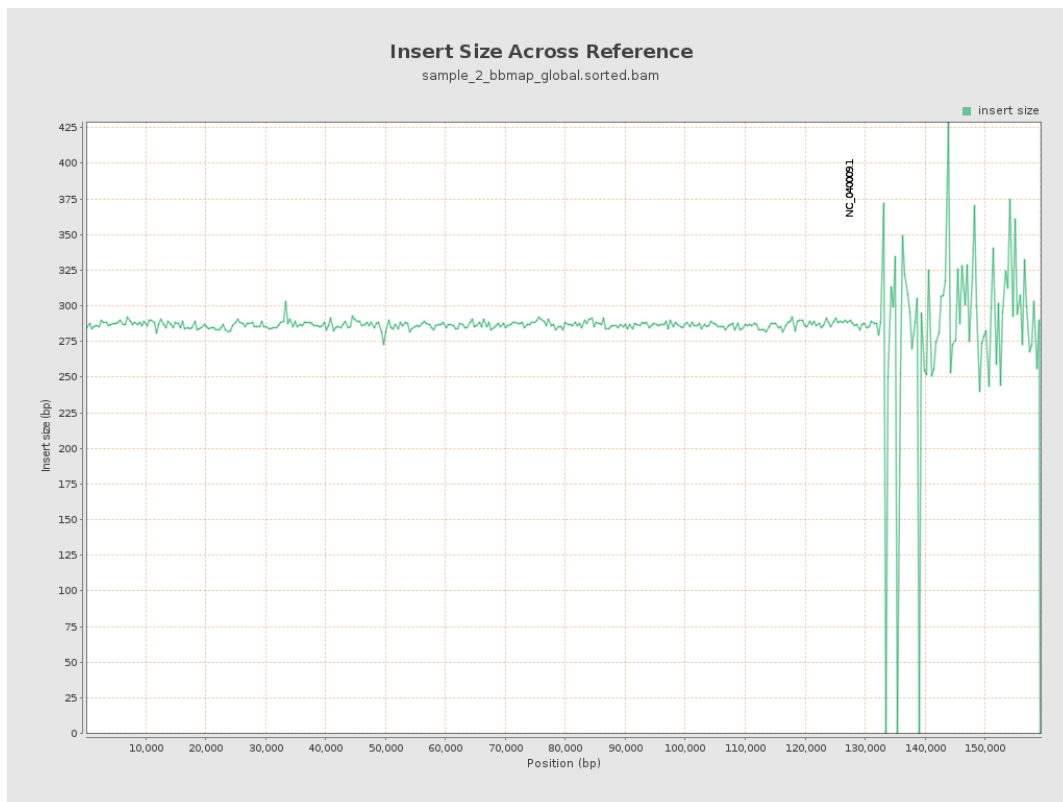
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference





## 15. Results : Insert Size Histogram

