

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2023/07/29 21:16:29*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam sample_5_bimap_global.sorted.bam -c -nw 400 -hm 3
```

## 1.2. Alignment

Command line:	java -ea -Xmx8g -Xms8g align2.BBMap build=1 overwrite=true fastareadlen=500 -Xmx8g threads=4 sam=1.3 trd ref=Cedrela_odorata_Ch1.fasta nodisk in=sample_5_21_clean_R#.fastq.gz out=sample_5_bimap_global.sam
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	BBMap (38.90)
Analysis date:	Sat Jul 29 21:16:26 CEST 2023
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	sample_5_bimap_global.sorted.bam

## 2. Summary

### 2.1. Globals

Reference size	158,558
Number of reads	734,914
Mapped reads	734,862 / 99.99%
Unmapped reads	52 / 0.01%
Mapped paired reads	734,862 / 99.99%
Mapped reads, first in pair	367,426 / 50%
Mapped reads, second in pair	367,436 / 50%
Mapped reads, both in pair	734,810 / 99.99%
Mapped reads, singletons	52 / 0.01%
Read min/max/mean length	21 / 150 / 105.14
Duplicated reads (estimated)	603,135 / 82.07%
Duplication rate	95.76%
Clipped reads	211 / 0.03%

### 2.2. ACGT Content

Number/percentage of A's	23,690,874 / 30.67%
Number/percentage of C's	14,751,867 / 19.09%
Number/percentage of T's	24,243,519 / 31.38%
Number/percentage of G's	14,569,340 / 18.86%
Number/percentage of N's	0 / 0%
GC Percentage	37.95%

## 2.3. Coverage

Mean	487.5512
Standard Deviation	281.6942

## 2.4. Mapping Quality

Mean Mapping Quality	30.12
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## 2.5. Insert size

Mean	373.54
Standard Deviation	2,804.44
P25/Median/P75	241 / 287 / 333

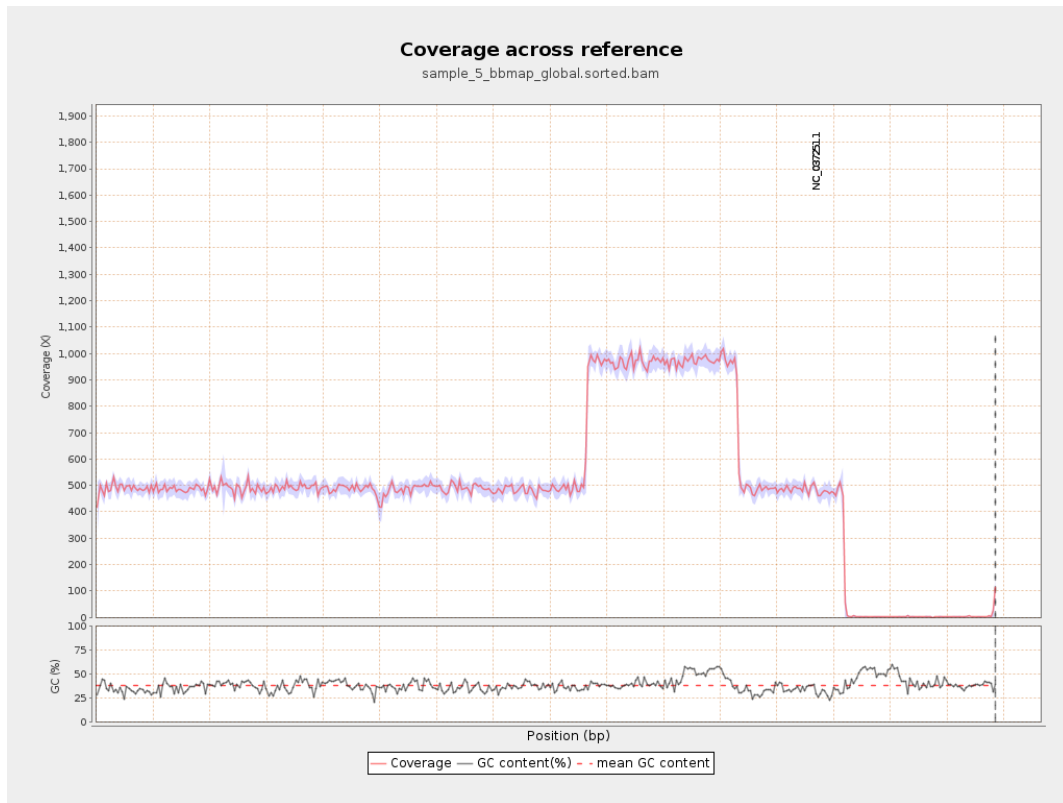
## 2.6. Mismatches and indels

General error rate	0.35%
Insertions	818
Mapped reads with at least one insertion	0.11%
Deletions	1,143
Mapped reads with at least one deletion	0.16%
Homopolymer indels	11.63%

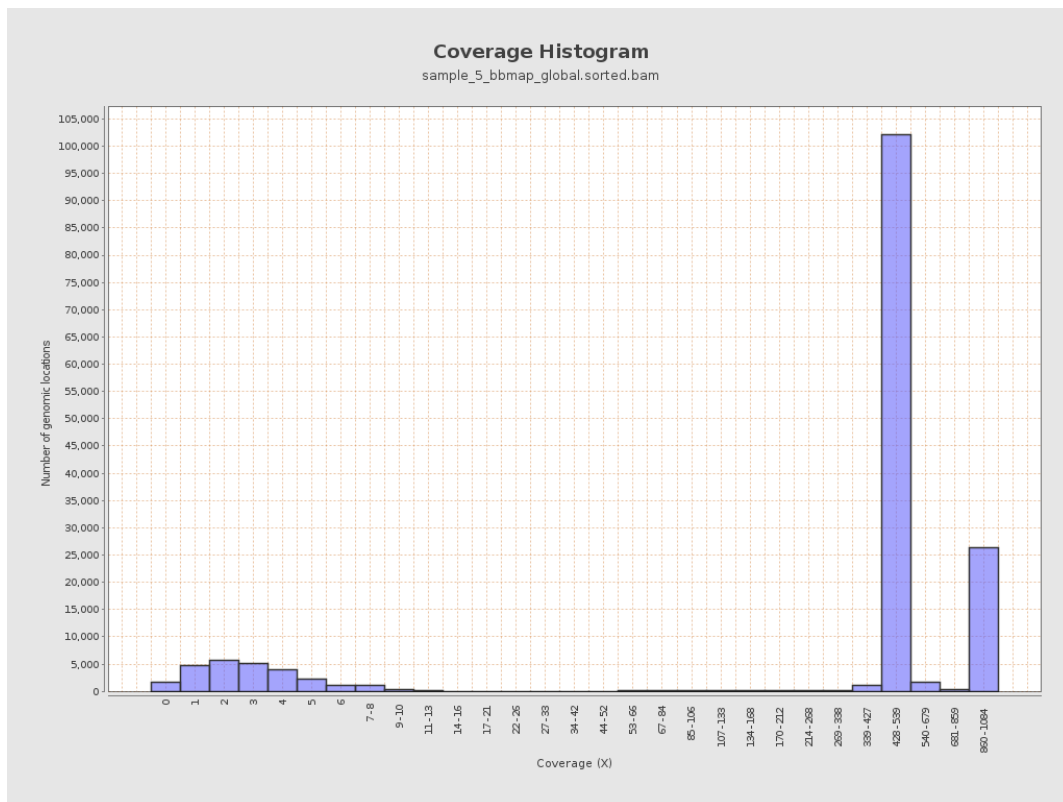
## 2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_037251.1	158558	77305136	487.5512	281.6942

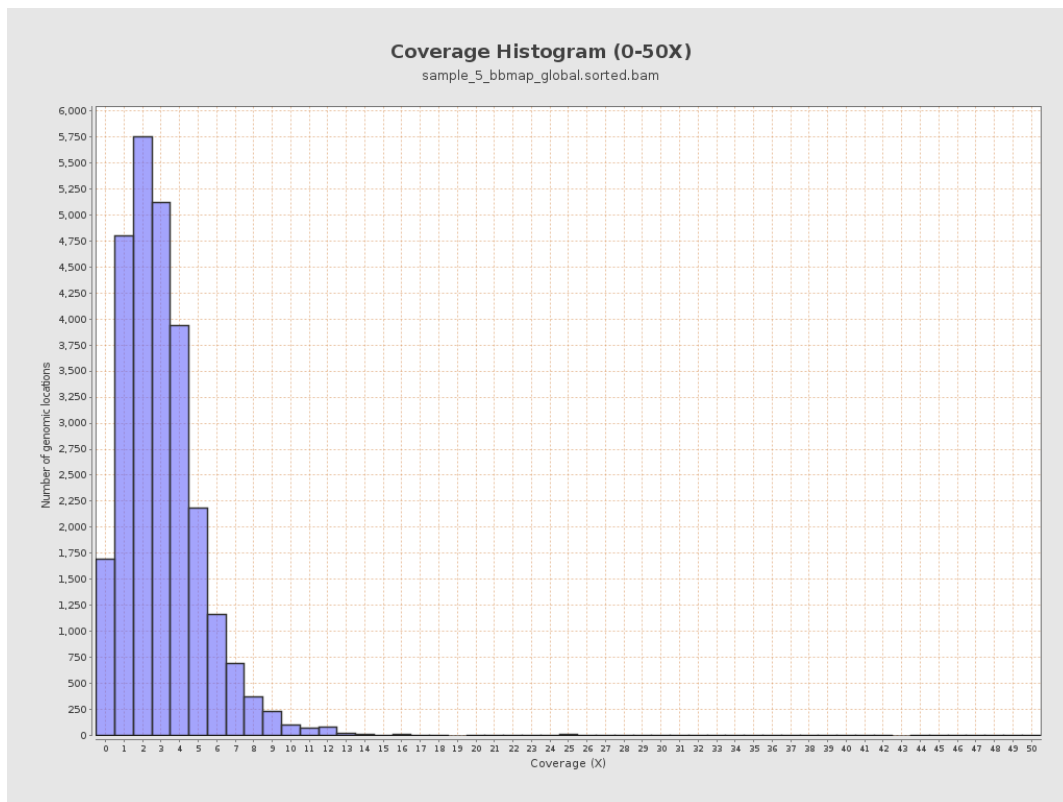
### 3. Results : Coverage across reference



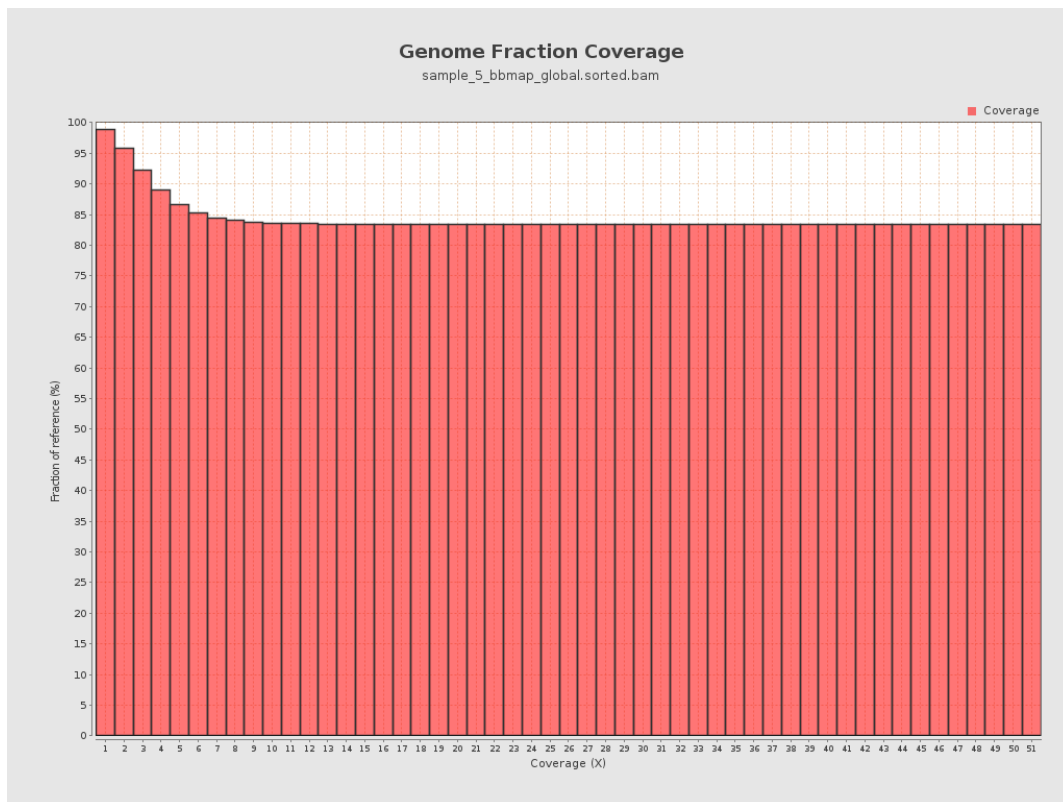
## 4. Results : Coverage Histogram



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

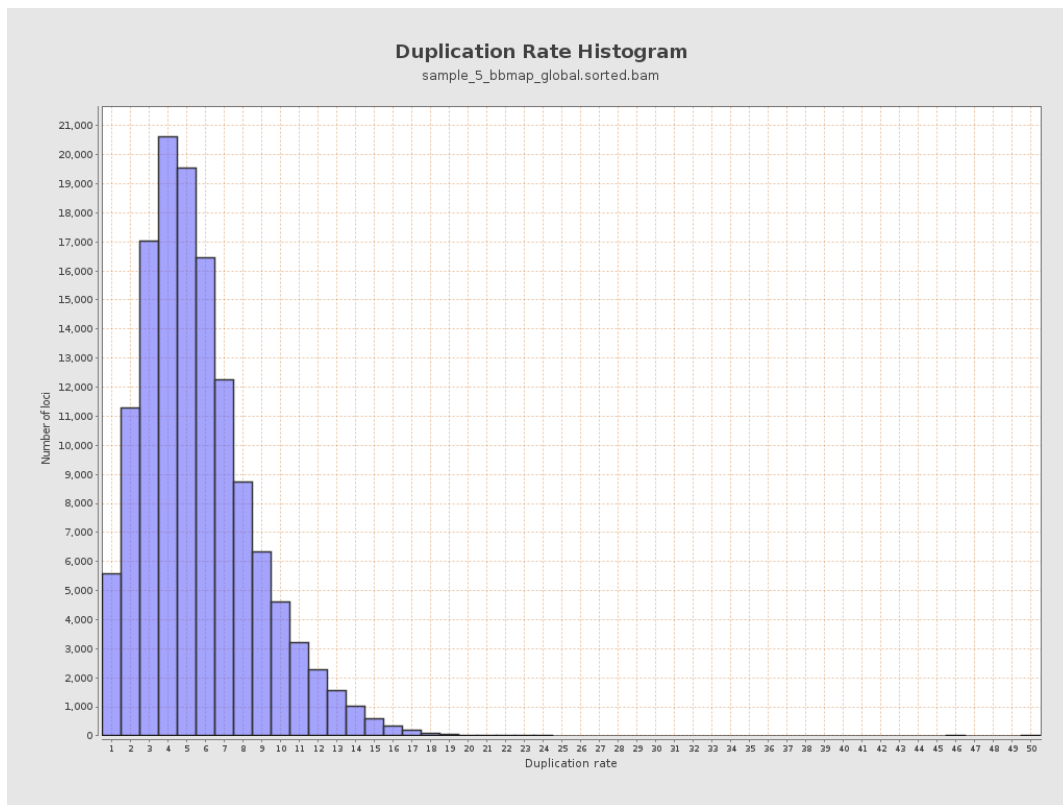


## 6. Results : Genome Fraction Coverage

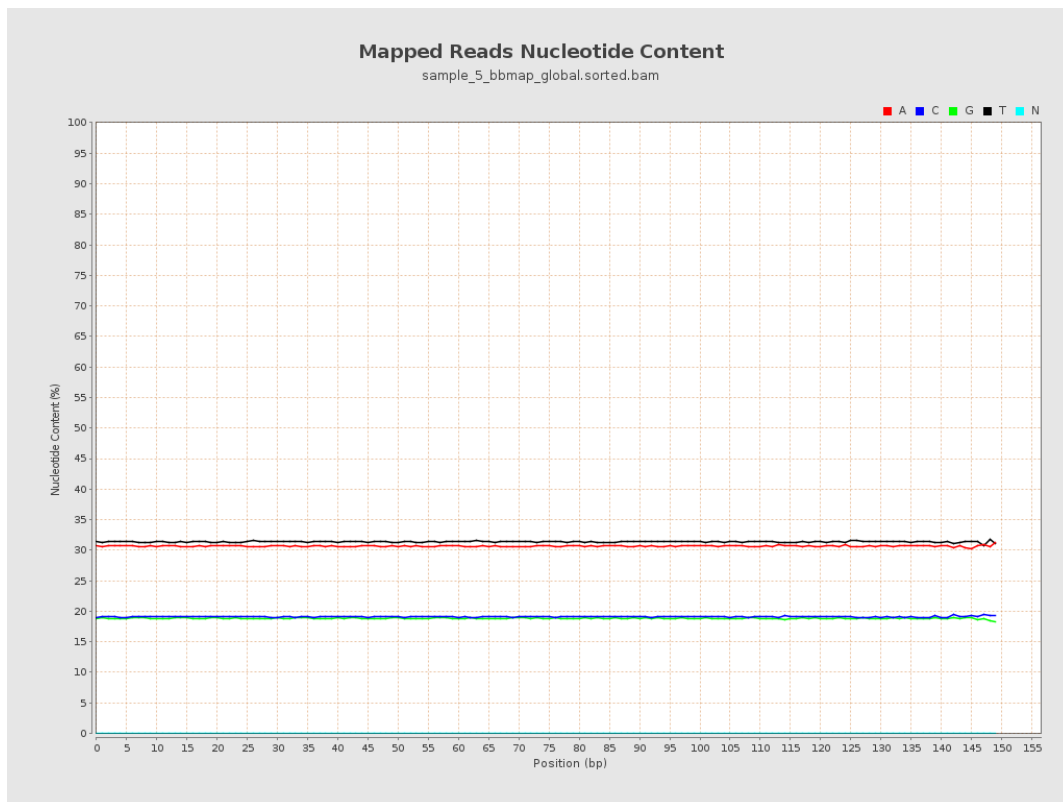




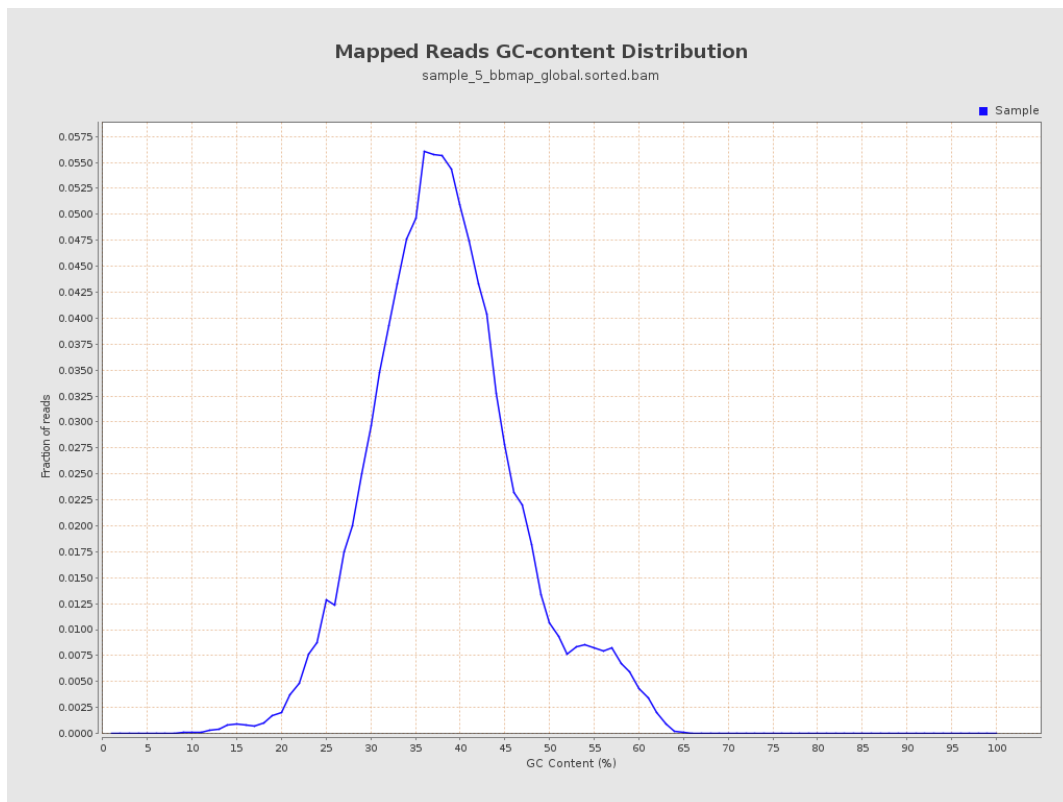
## 7. Results : Duplication Rate Histogram



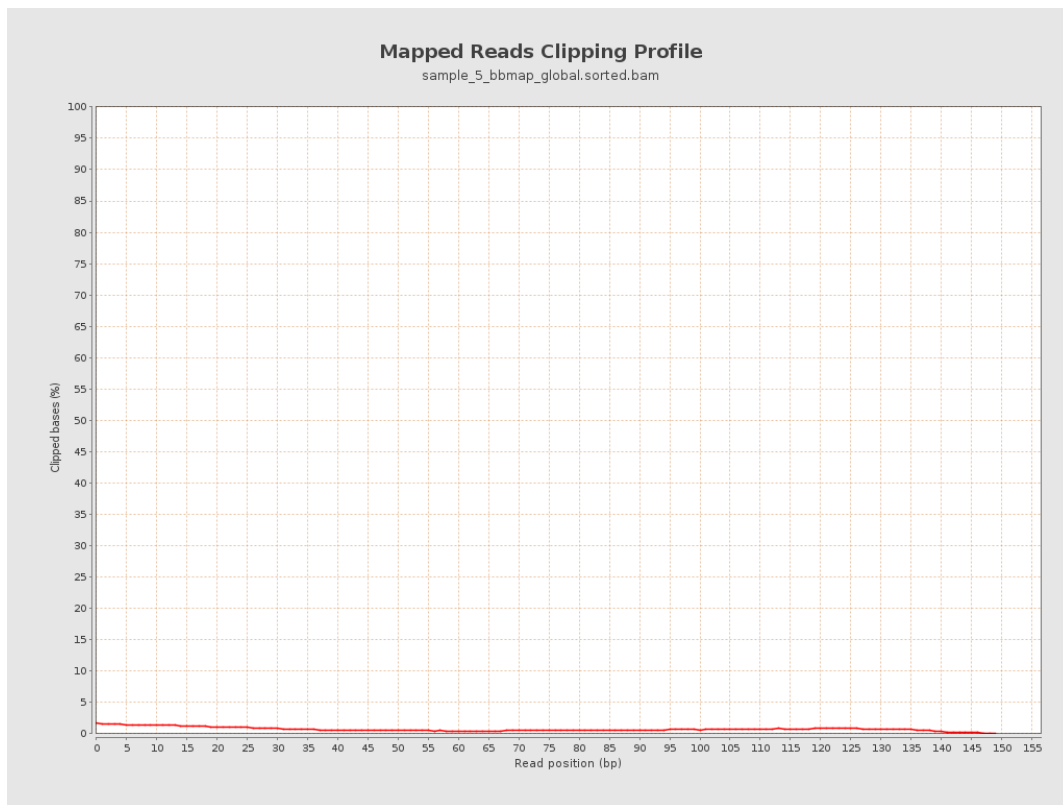
## 8. Results : Mapped Reads Nucleotide Content



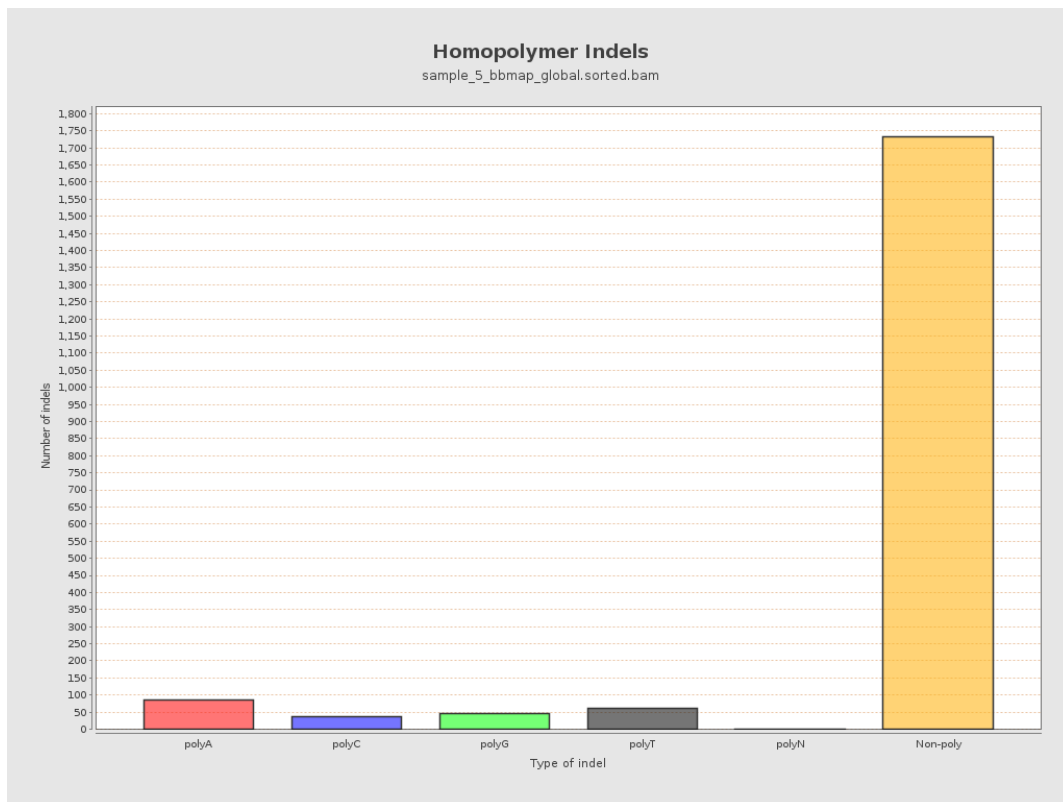
## 9. Results : Mapped Reads GC-content Distribution



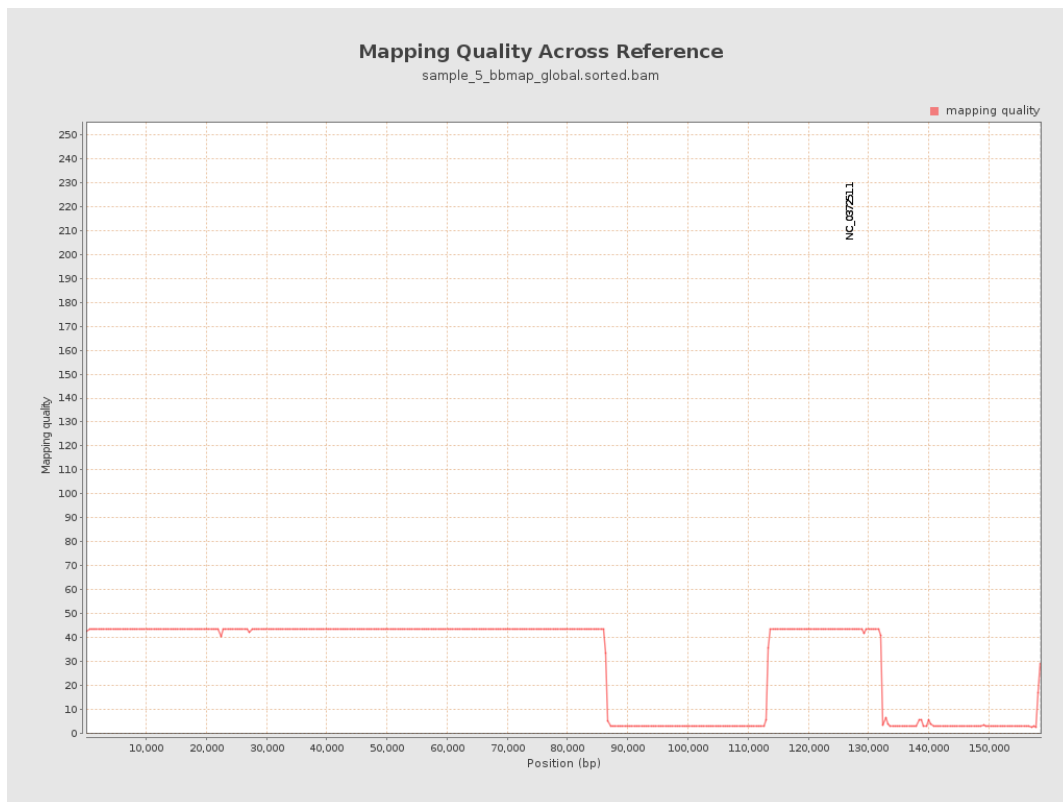
## 10. Results : Mapped Reads Clipping Profile



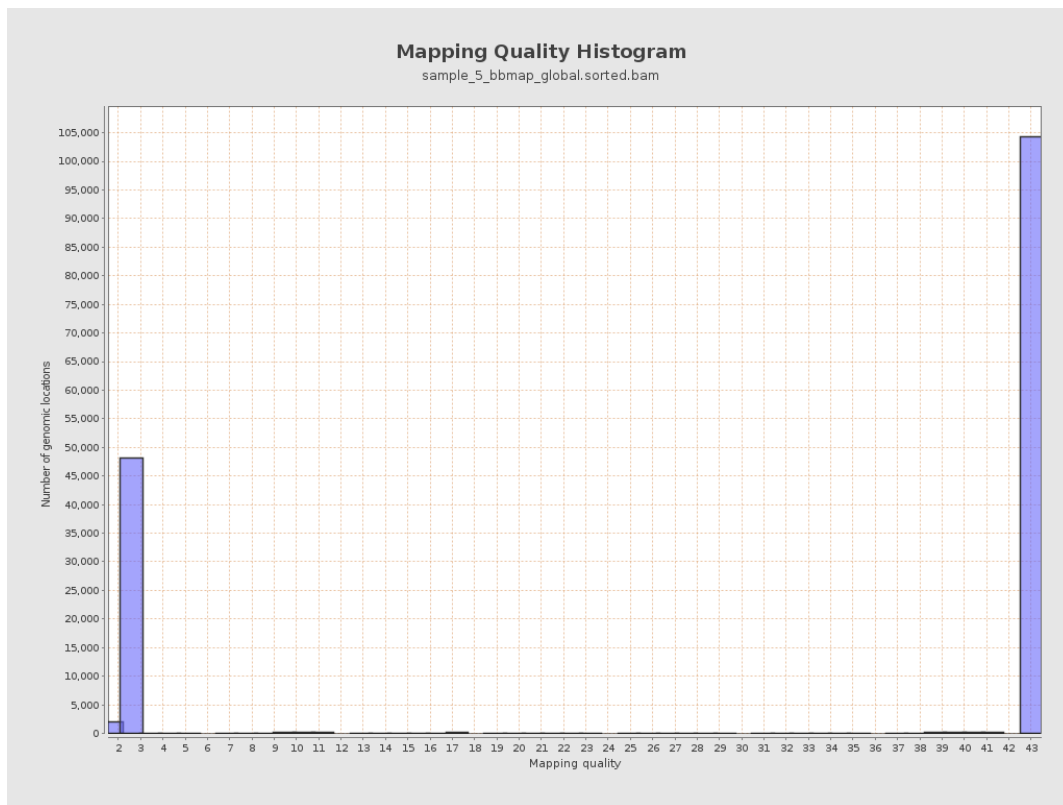
## 11. Results : Homopolymer Indels



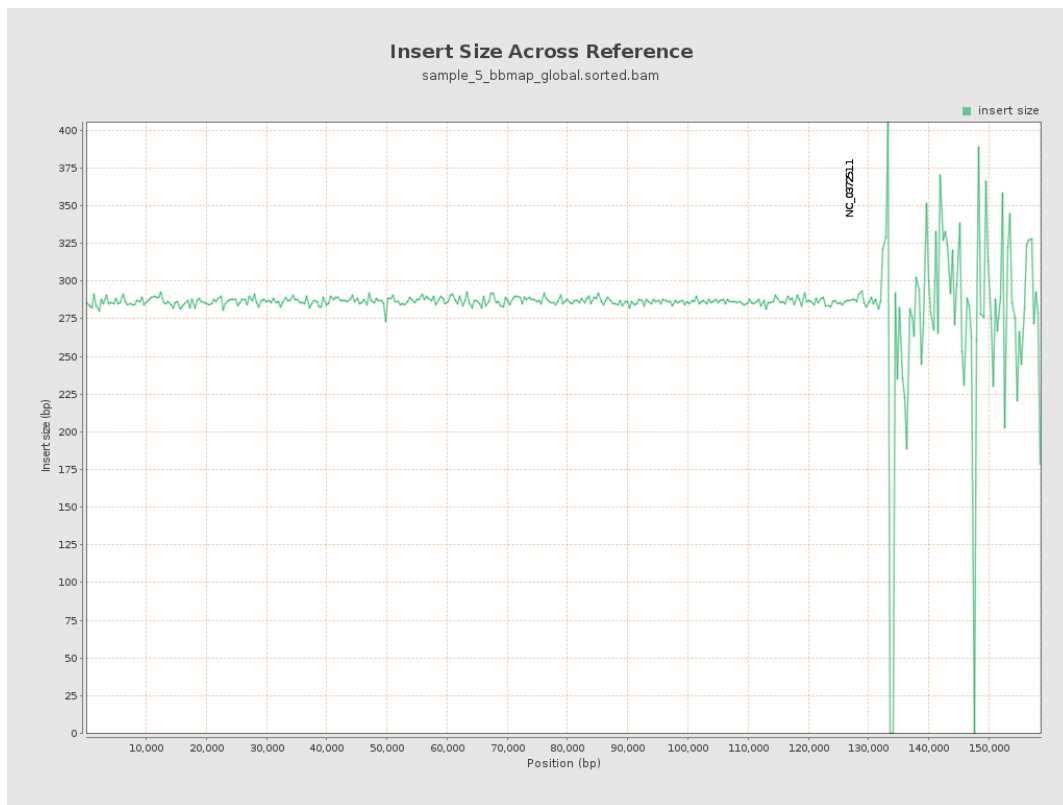
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference





## 15. Results : Insert Size Histogram

