Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/07/29 21:17:04

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam sample_4_bbmap_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=Diospyros_rhombifolia_Chl.fasta nodisk in=sample_4_21_clean_R#.fastq.gz out=sample_4_bbmap_global.sam
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	BBMap (38.90)
Analysis date:	Sat Jul 29 21:17:01 CEST 2023
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	sample_4_bbmap_global.sorted.bam

2. Summary

2.1. Globals

Reference size	157,368
Number of reads	737,946
Mapped reads	737,894 / 99.99%
Unmapped reads	52 / 0.01%
Mapped paired reads	737,894 / 99.99%
Mapped reads, first in pair	368,947 / 50%
Mapped reads, second in pair	368,947 / 50%
Mapped reads, both in pair	737,842 / 99.99%
Mapped reads, singletons	52 / 0.01%
Read min/max/mean length	21 / 150 / 105.27
Duplicated reads (estimated)	606,429 / 82.18%
Duplication rate	95.8%
Clipped reads	218 / 0.03%

2.2. ACGT Content

Number/percentage of A's	24,059,410 / 30.98%
Number/percentage of C's	14,635,416 / 18.84%
Number/percentage of T's	24,494,724 / 31.54%
Number/percentage of G's	14,479,909 / 18.64%
Number/percentage of N's	0 / 0%
GC Percentage	37.49%

2.3. Coverage

Mean	493.8601
Standard Deviation	282.7594

2.4. Mapping Quality

Mean Mapping Quality	30.55

2.5. Insert size

Mean	370.19
Standard Deviation	2,755.45
P25/Median/P75	241 / 287 / 333

2.6. Mismatches and indels

General error rate	0.35%
Insertions	1,258
Mapped reads with at least one insertion	0.17%
Deletions	768
Mapped reads with at least one deletion	0.1%
Homopolymer indels	54.24%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_039556.1	157368	77717769	493.8601	282.7594

3. Results : Coverage across reference
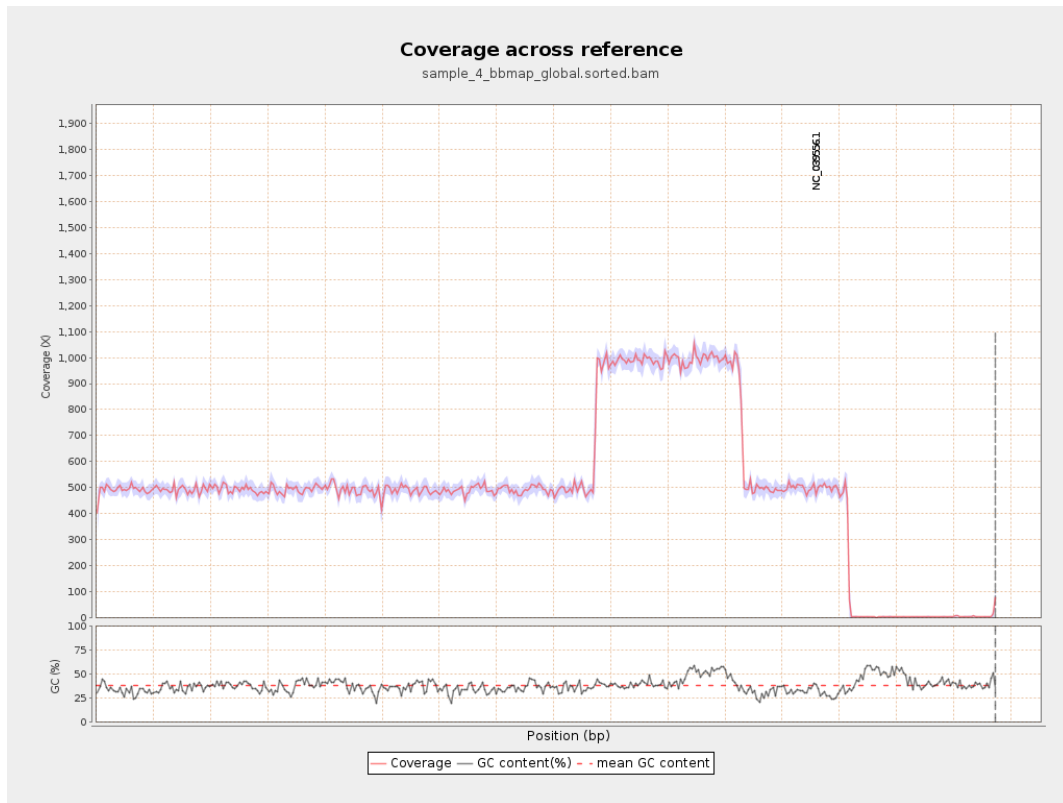
4. Results : Coverage Histogram

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

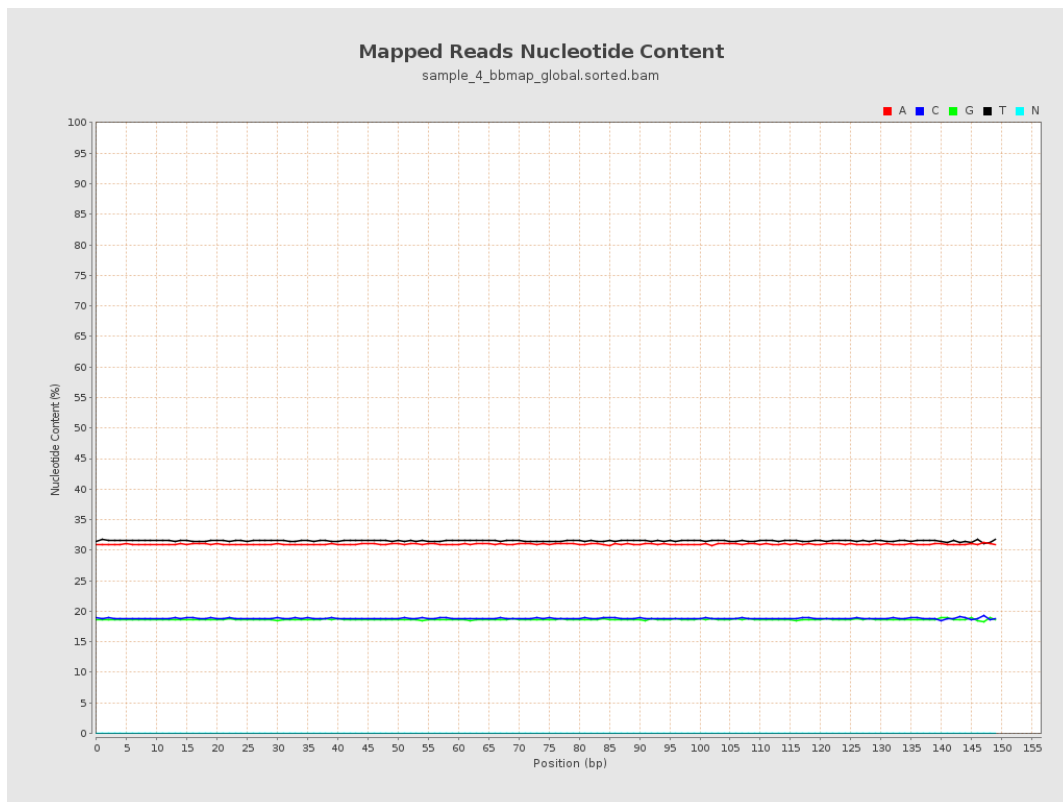Coverage Histogram (0-50X)
sample_4_bbmap_global.sorted.bam
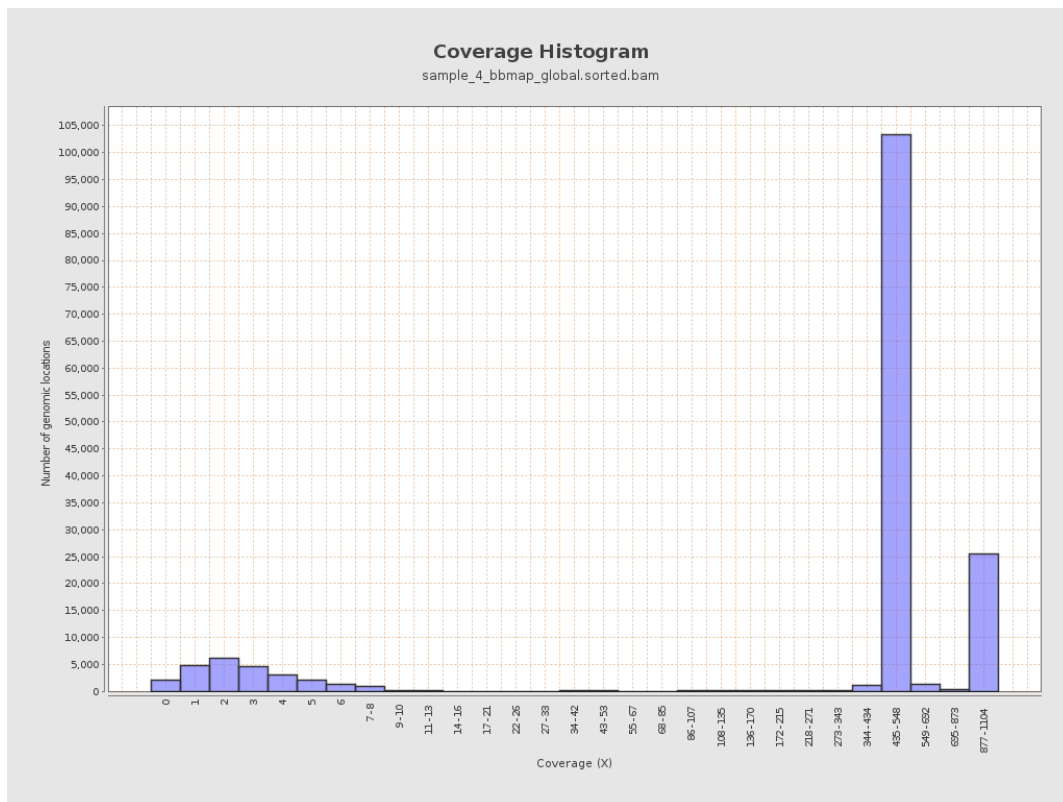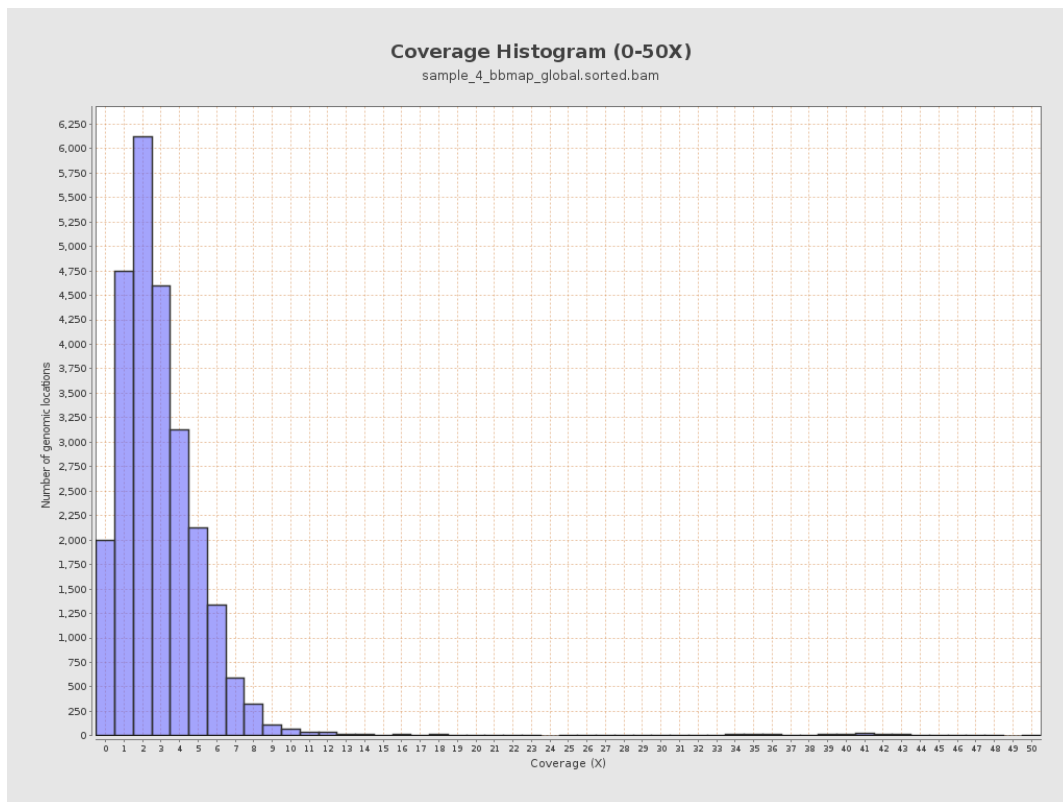
6. Results : Genome Fraction Coverage
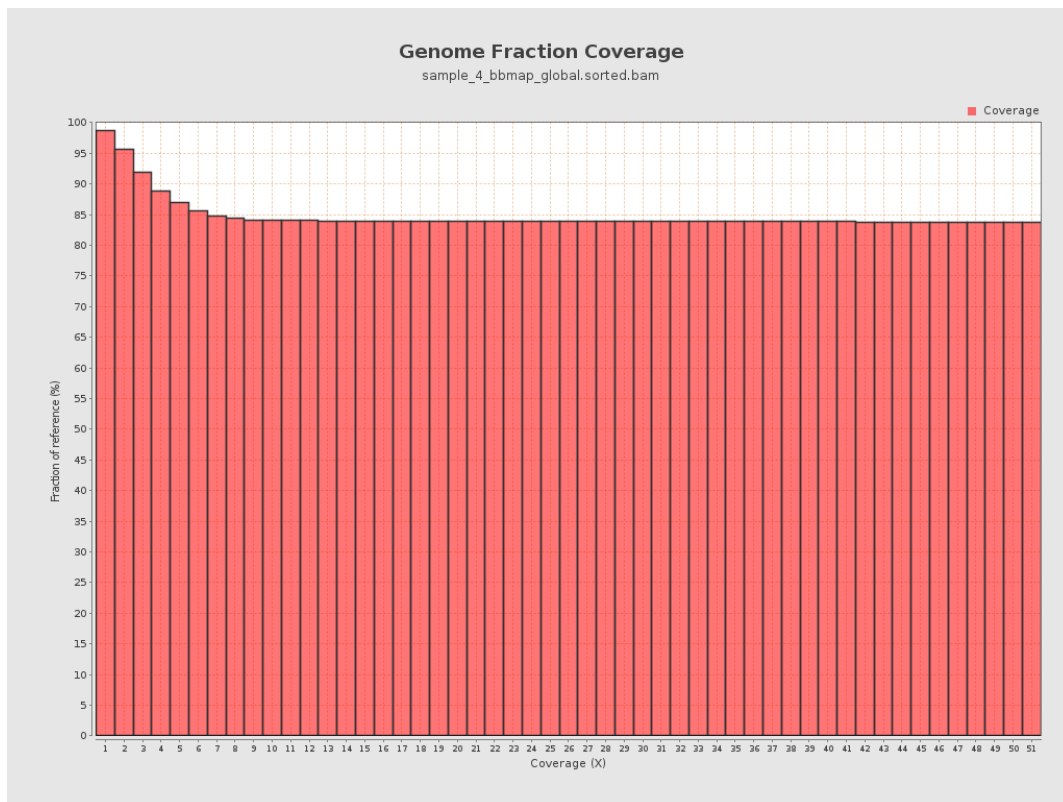
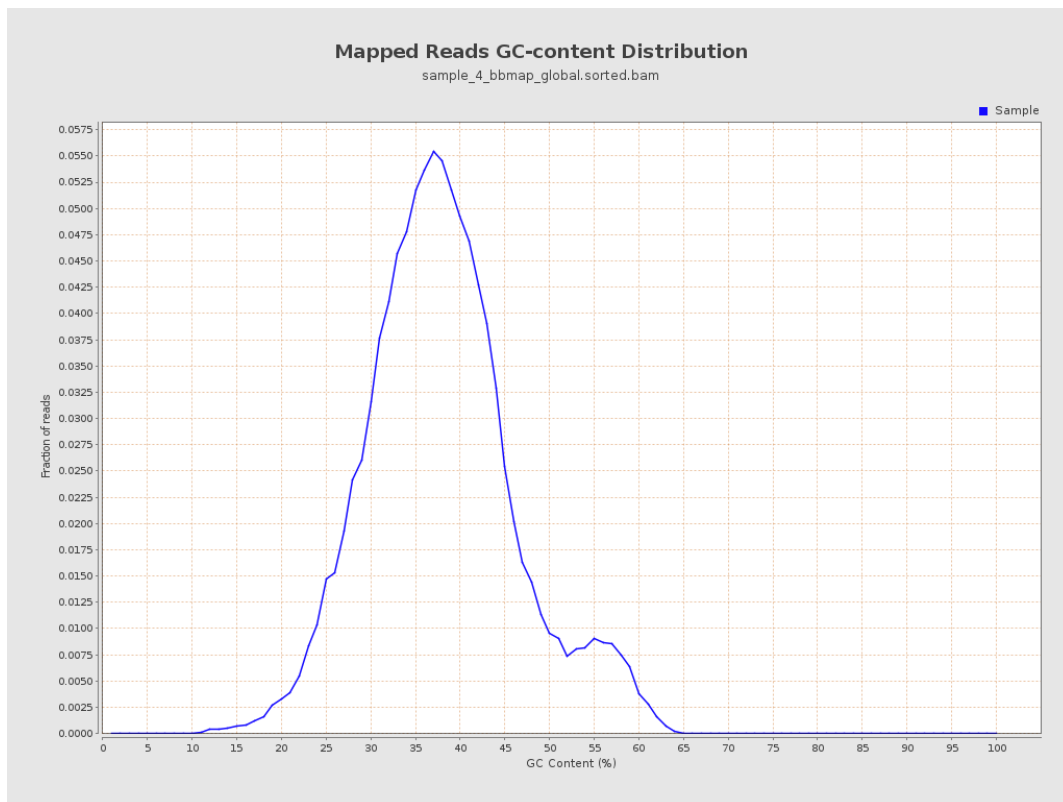# 7. Results : Duplication Rate Histogram

8. Results : Mapped Reads Nucleotide Content

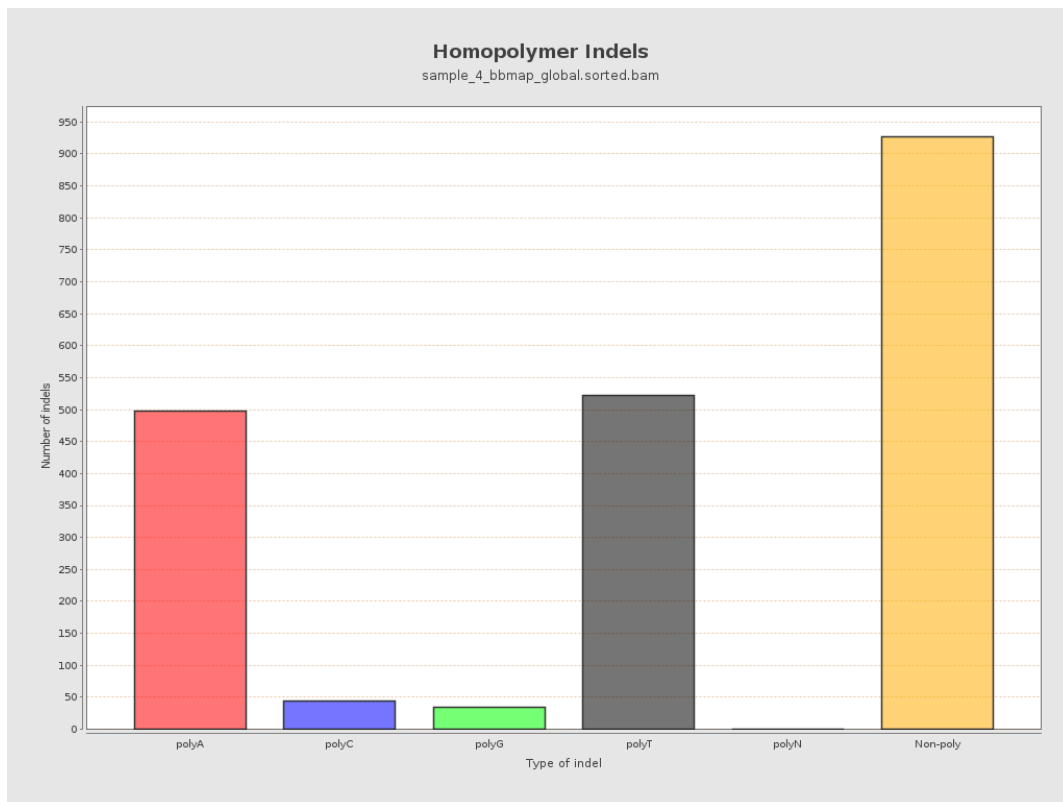Mapped Reads Nucleotide Content
sample_4_bbmap_global.sorted.bam
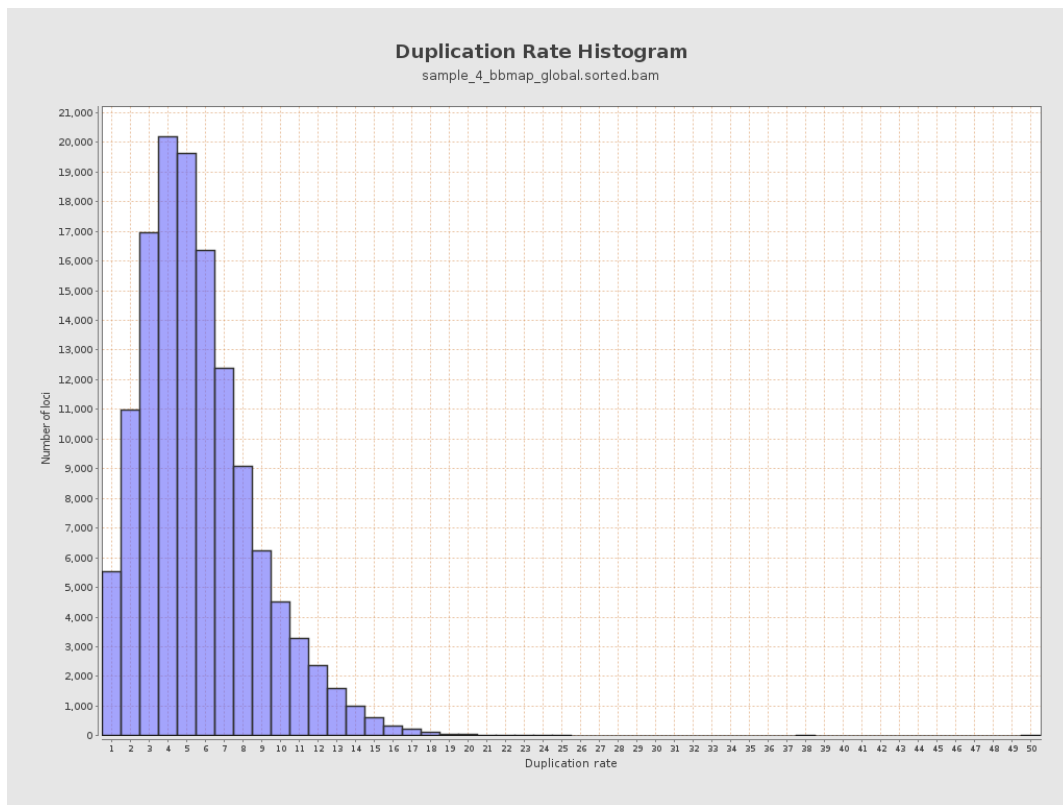
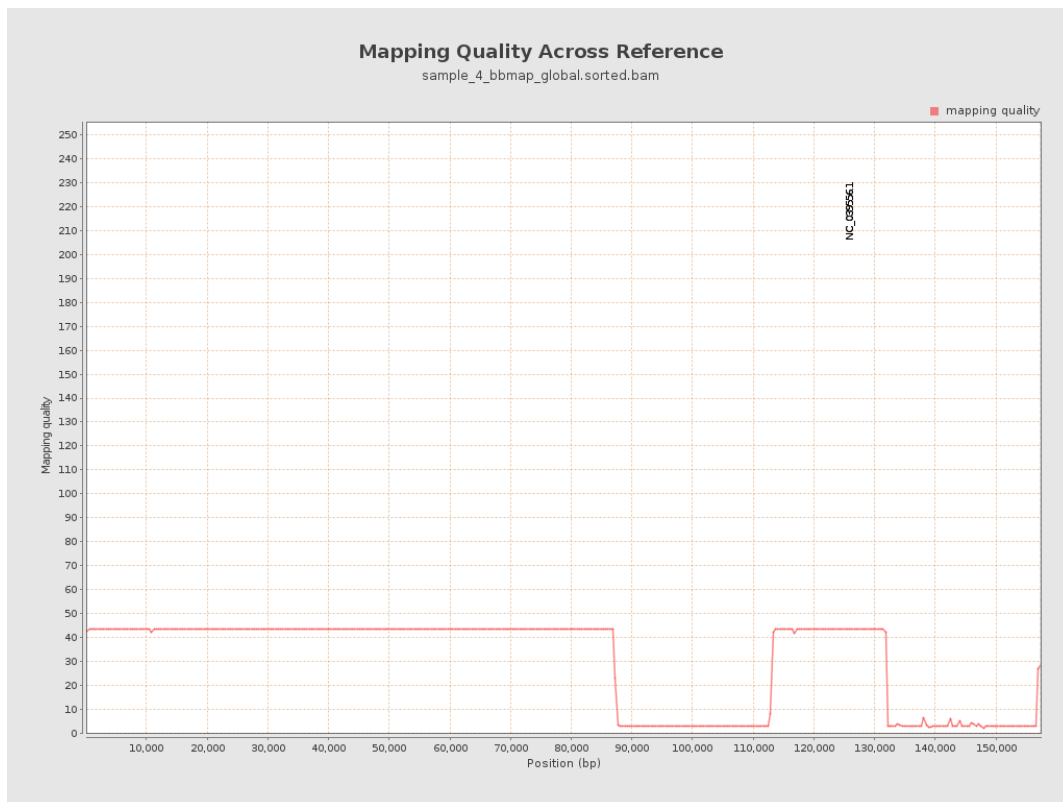# 9. Results : Mapped Reads GC-content Distribution

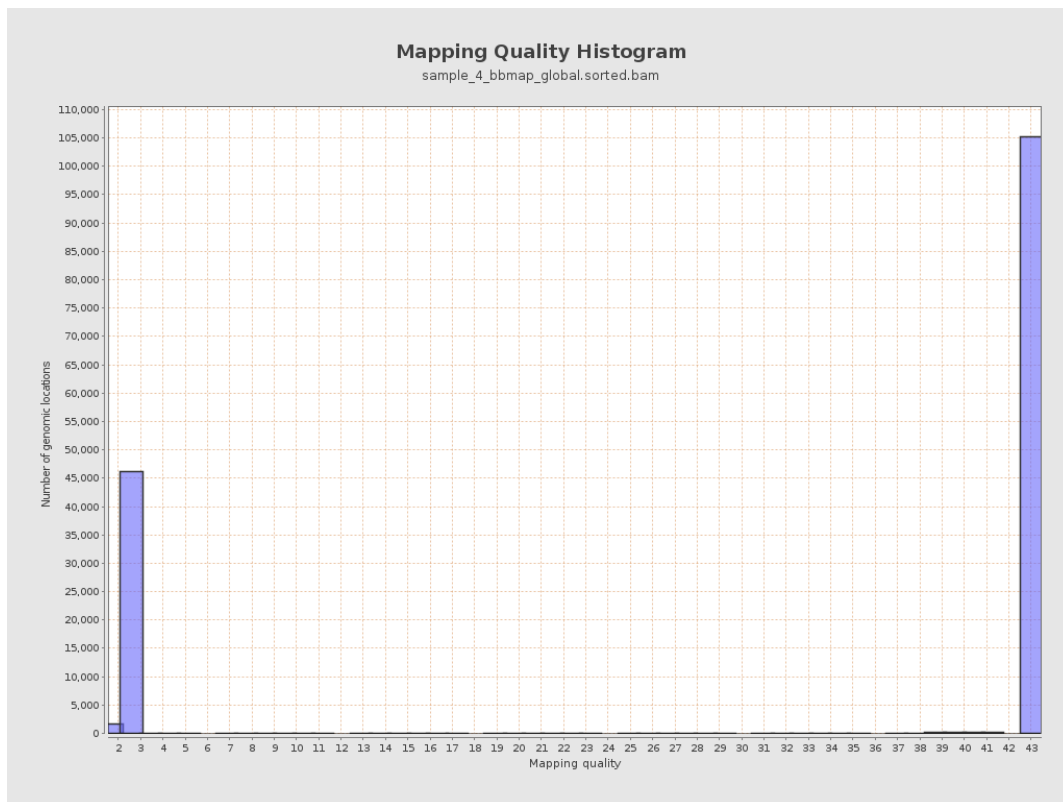# 10. Results : Mapped Reads Clipping Profile
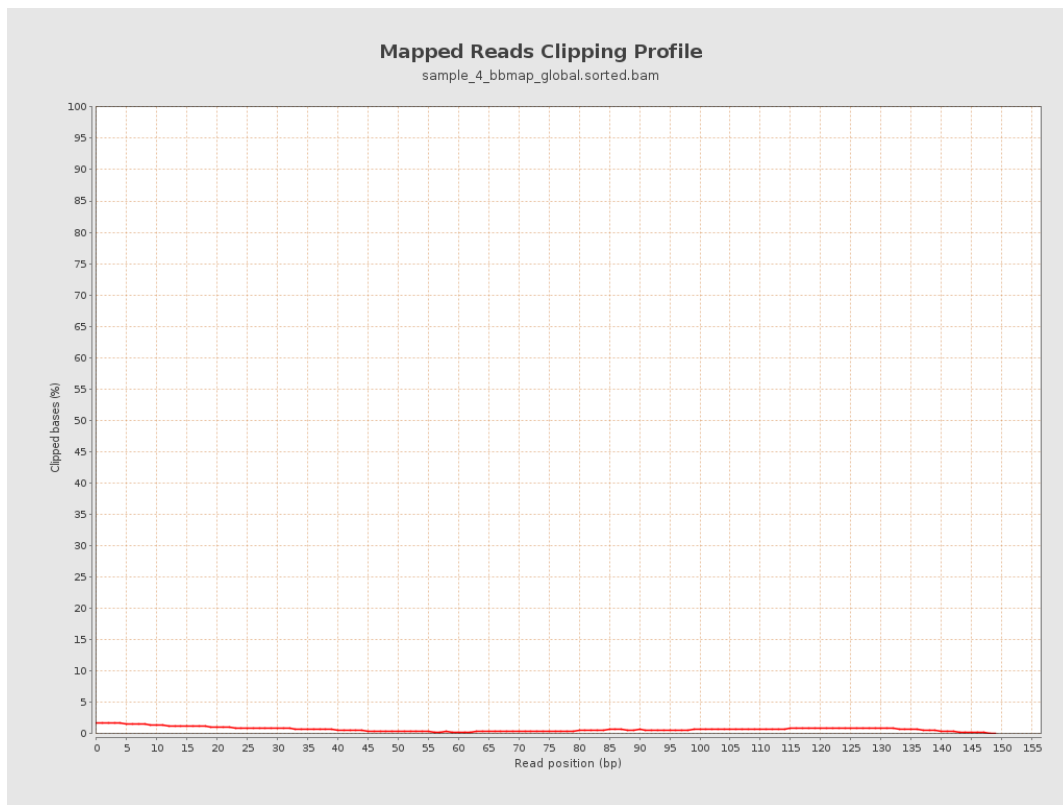
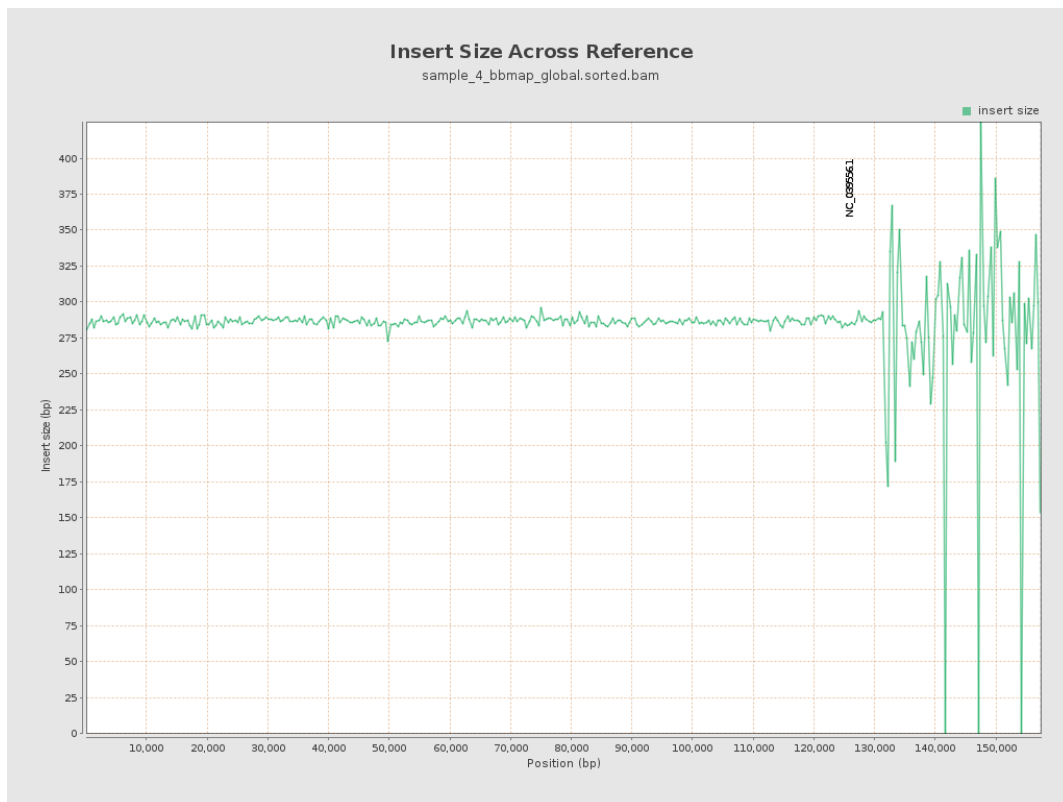# 11. Results : Homopolymer Indels

12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram