

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/07/29 21:18:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam sample_3_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=Quercus_robur_Ch1.fasta nodisk in=sample_3_21_clean_R#.fastq.gz out=sample_3_bimap_global.sam
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	BBMap (38.90)
Analysis date:	Sat Jul 29 21:18:24 CEST 2023
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	sample_3_bimap_global.sorted.bam

2. Summary

2.1. Globals

Reference size	161,172
Number of reads	759,530
Mapped reads	759,462 / 99.99%
Unmapped reads	68 / 0.01%
Mapped paired reads	759,462 / 99.99%
Mapped reads, first in pair	379,739 / 50%
Mapped reads, second in pair	379,723 / 49.99%
Mapped reads, both in pair	759,394 / 99.98%
Mapped reads, singletons	68 / 0.01%
Read min/max/mean length	21 / 150 / 105.26
Duplicated reads (estimated)	624,155 / 82.18%
Duplication rate	95.98%
Clipped reads	271 / 0.04%

2.2. ACGT Content

Number/percentage of A's	24,916,331 / 31.17%
Number/percentage of C's	14,659,497 / 18.34%
Number/percentage of T's	25,543,054 / 31.95%
Number/percentage of G's	14,815,656 / 18.53%
Number/percentage of N's	0 / 0%
GC Percentage	36.87%

2.3. Coverage

Mean	496.1971
Standard Deviation	278.9189

2.4. Mapping Quality

Mean Mapping Quality	30.84
----------------------	-------

2.5. Insert size

Mean	374.55
Standard Deviation	2,903.04
P25/Median/P75	241 / 287 / 333

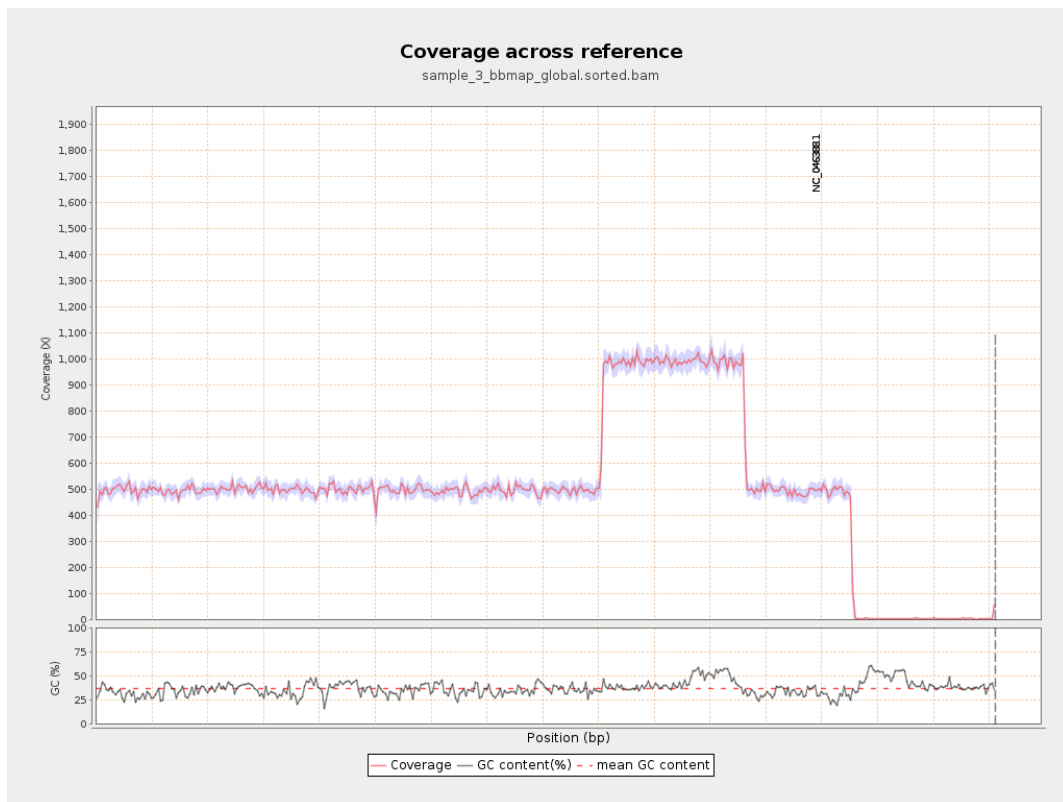
2.6. Mismatches and indels

General error rate	0.34%
Insertions	2,176
Mapped reads with at least one insertion	0.18%
Deletions	332
Mapped reads with at least one deletion	0.04%
Homopolymer indels	10.45%

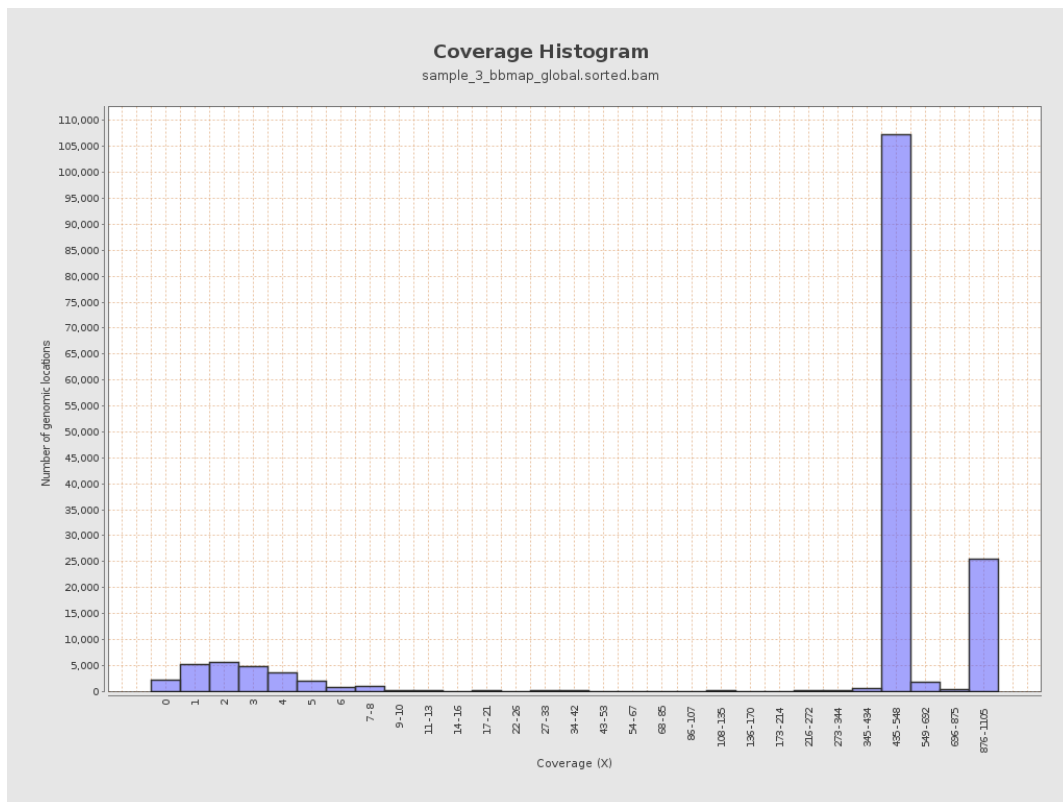
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_046388.1	161172	79973074	496.1971	278.9189

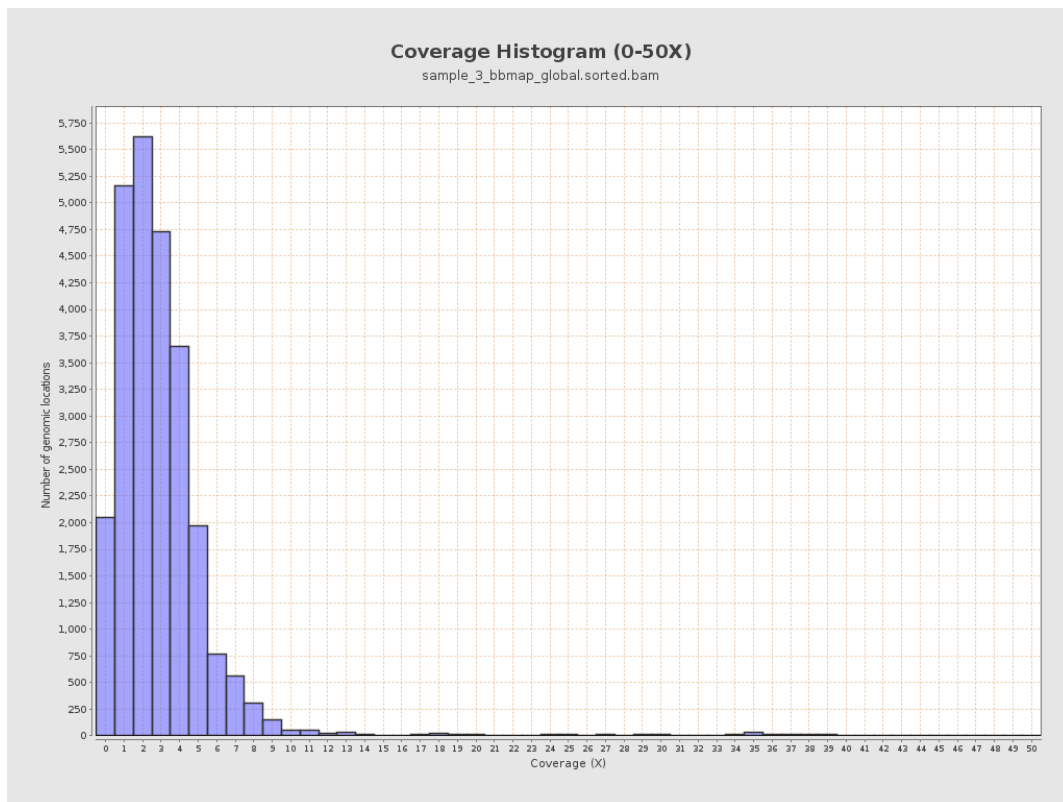
3. Results : Coverage across reference



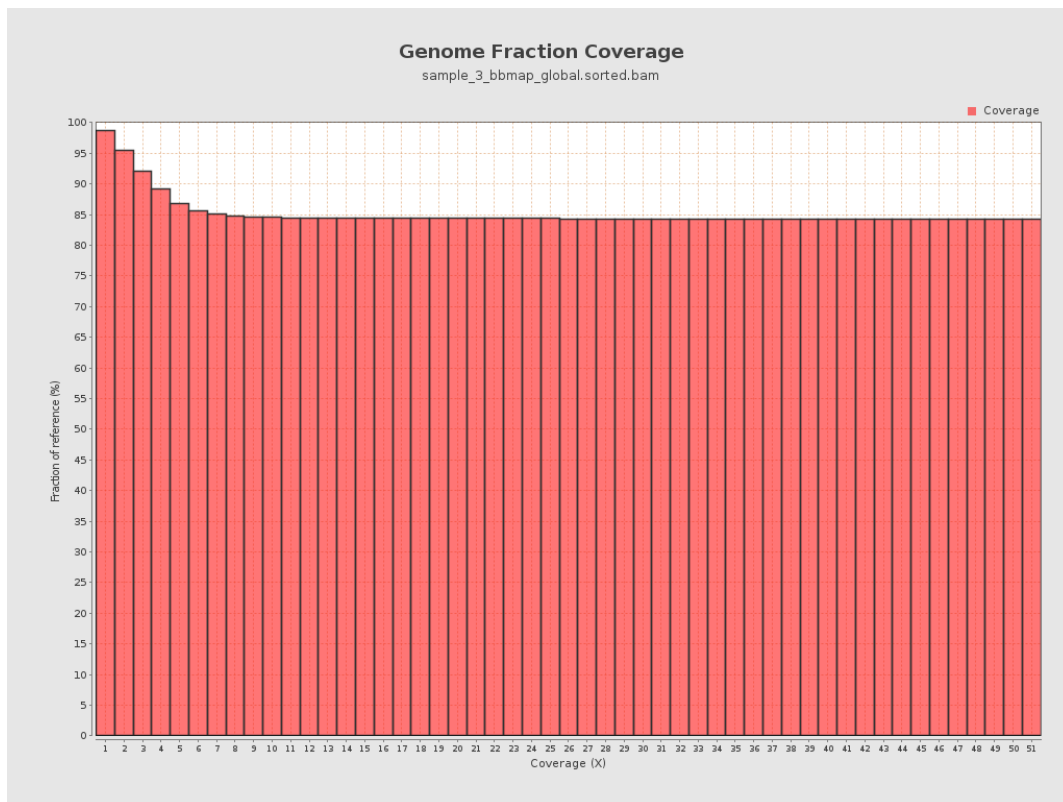
4. Results : Coverage Histogram



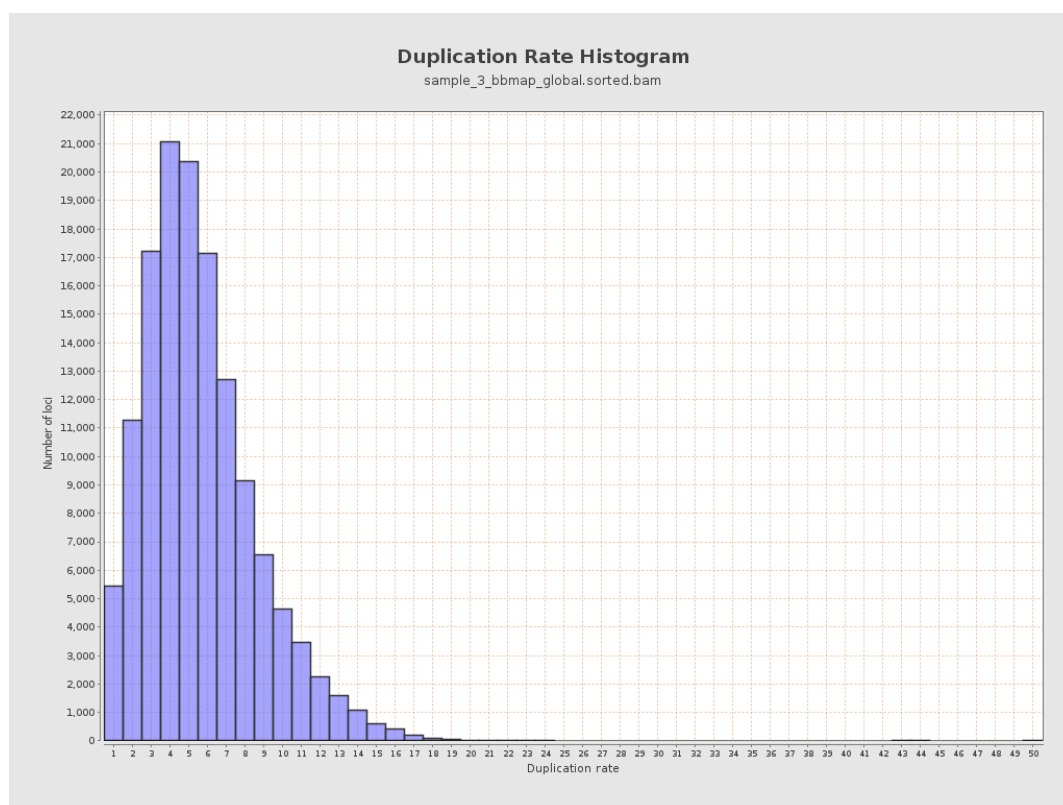
5. Results : Coverage Histogram (0-50X)



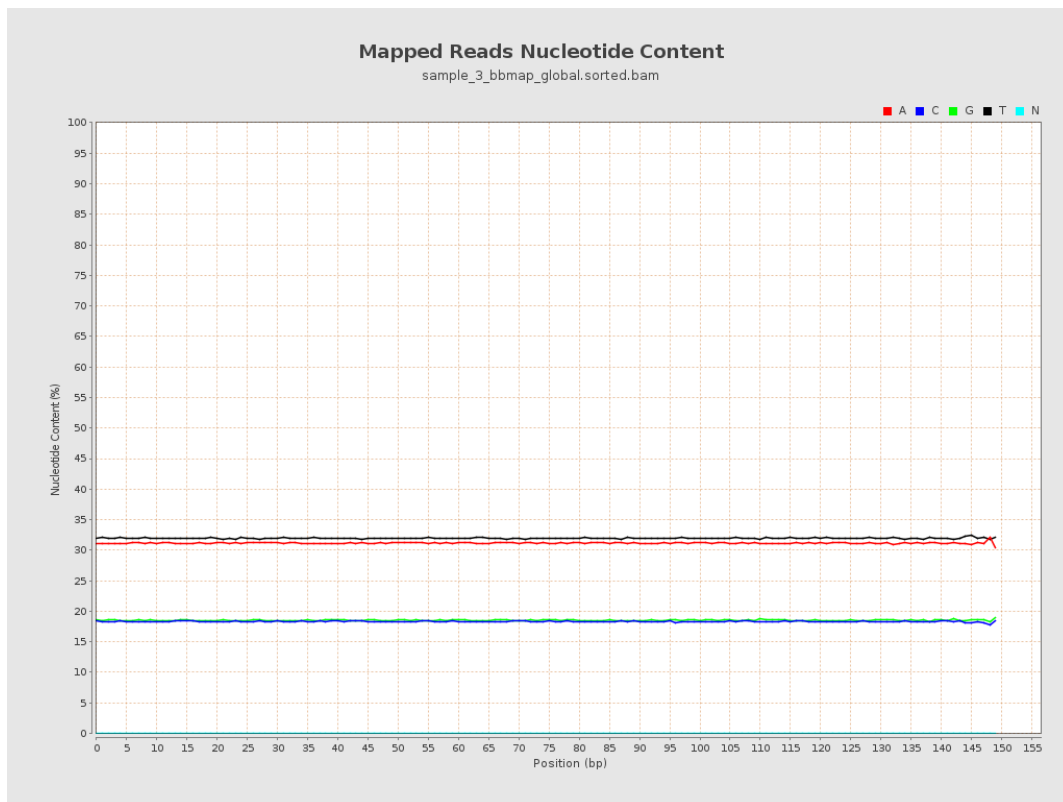
6. Results : Genome Fraction Coverage



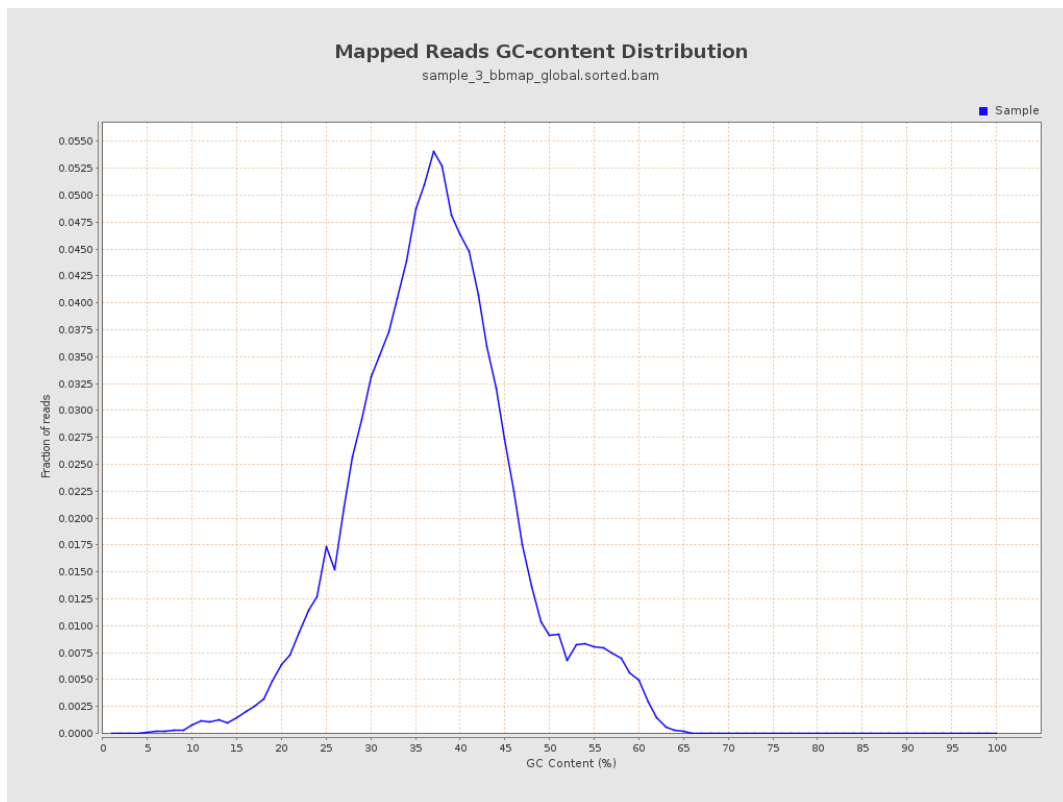
7. Results : Duplication Rate Histogram



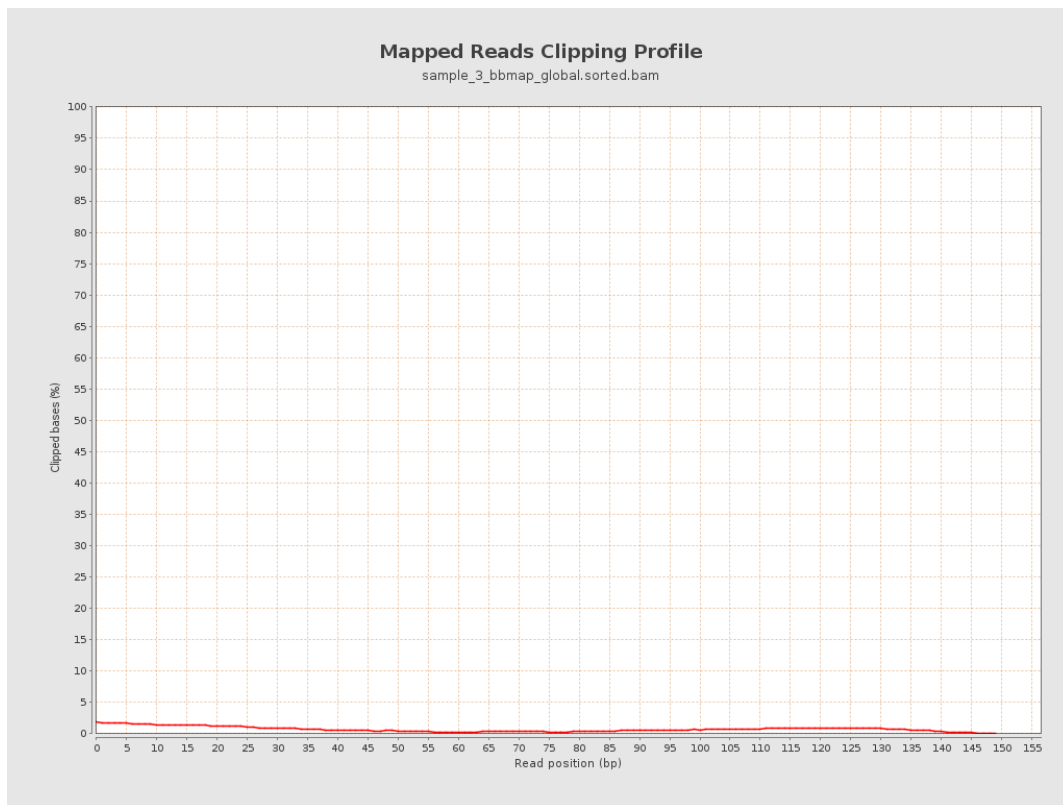
8. Results : Mapped Reads Nucleotide Content



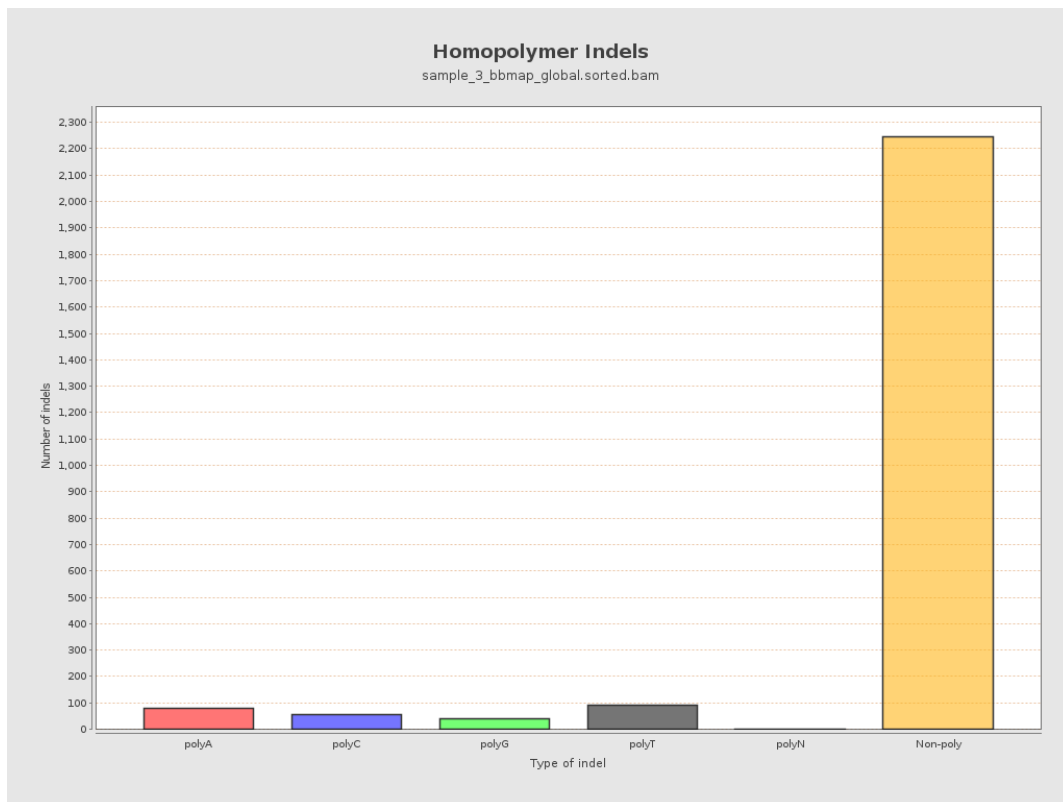
9. Results : Mapped Reads GC-content Distribution



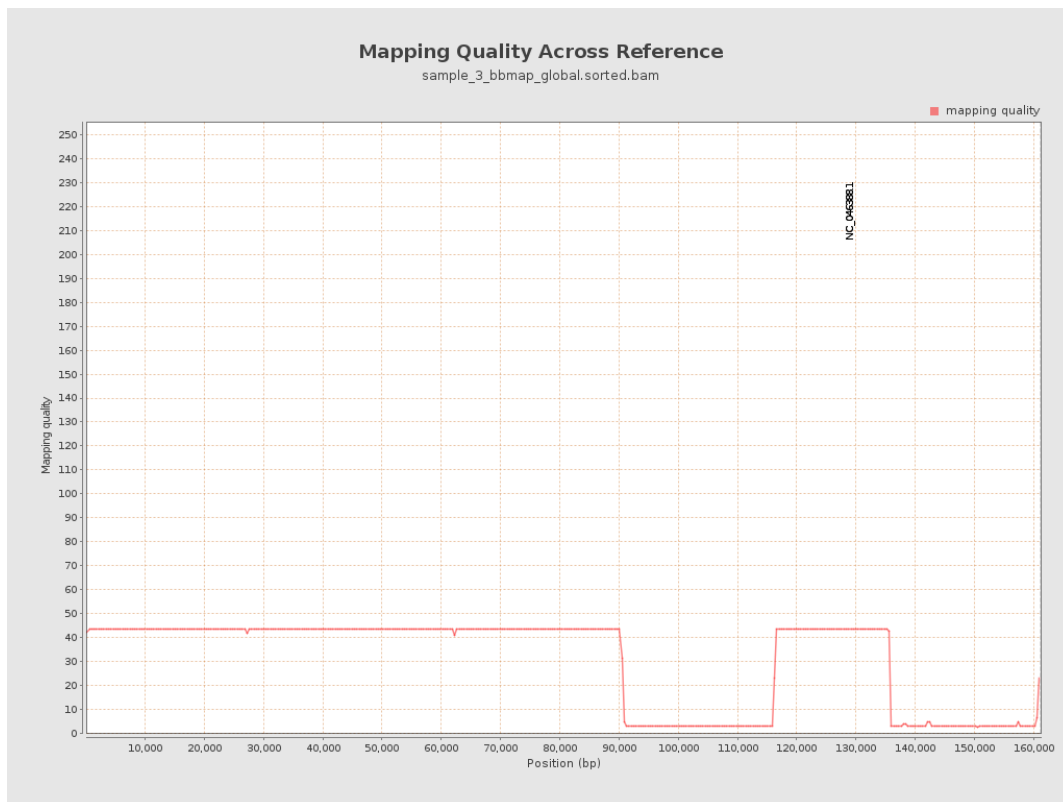
10. Results : Mapped Reads Clipping Profile



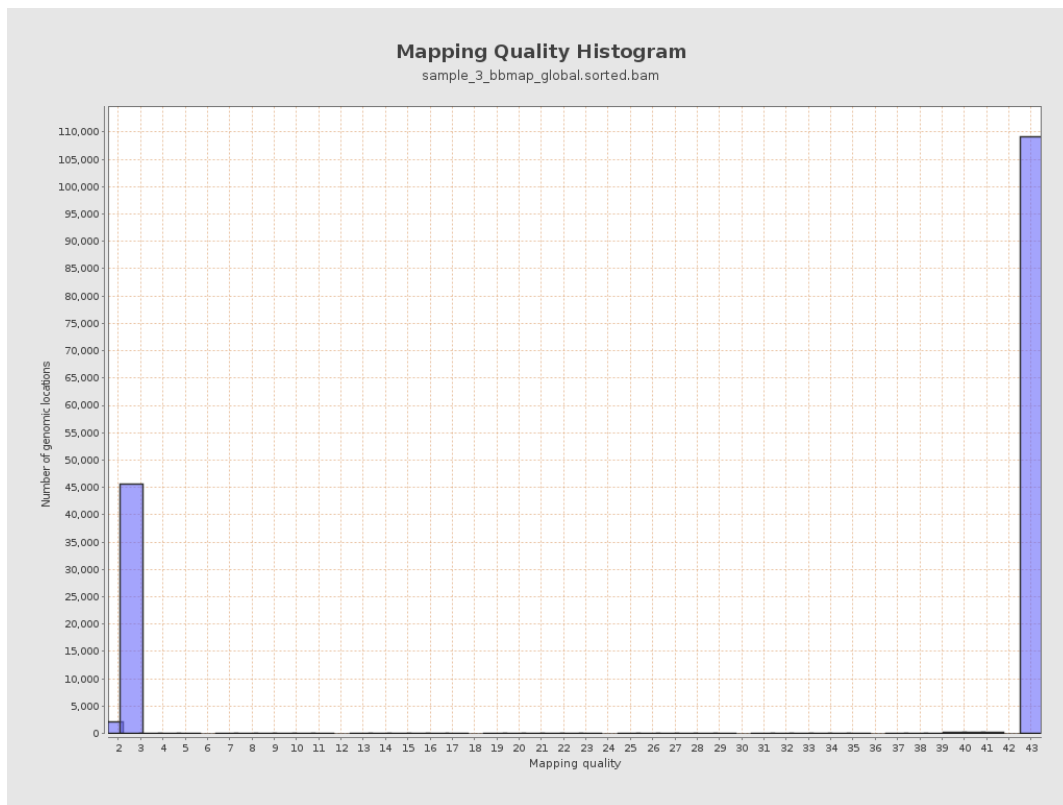
11. Results : Homopolymer Indels



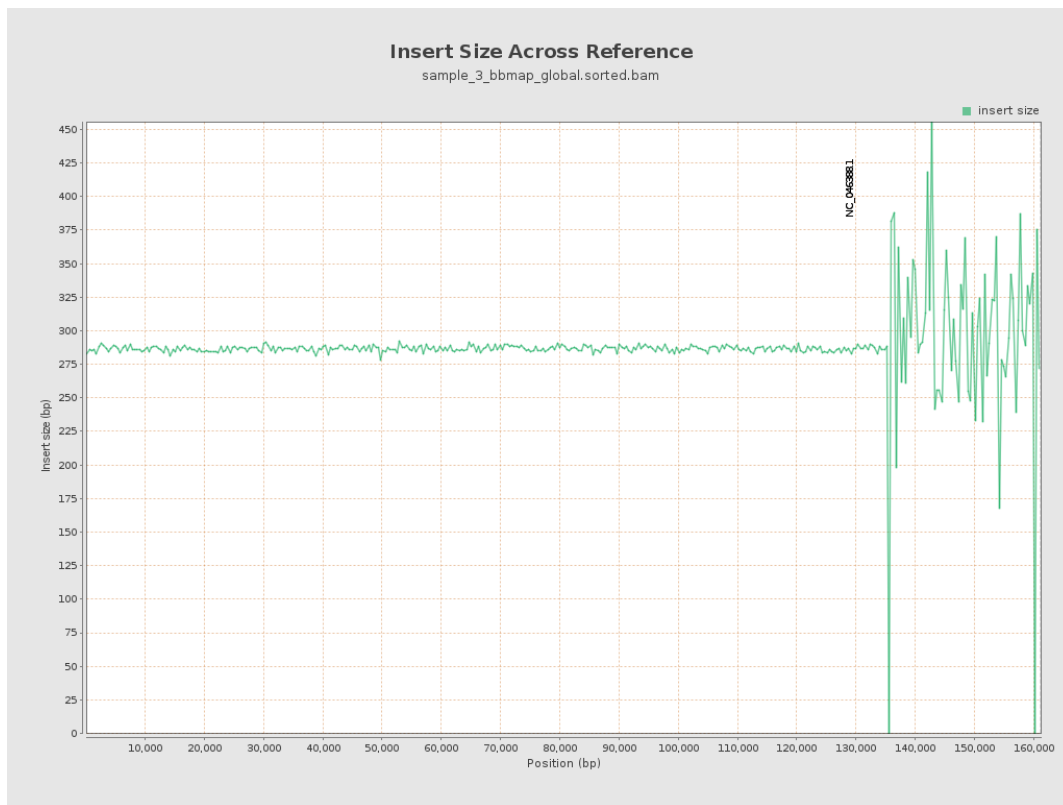
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

