

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/07/29 21:17:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam sample_1_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=Quercus_mongolica_Ch1.fasta nodisk in=sample_1_21_clean_R#.fastq.gz out=sample_1_bbmap_global.sam
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	BBMap (38.90)
Analysis date:	Sat Jul 29 21:17:46 CEST 2023
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	sample_1_bbmap_global.sorted.bam

2. Summary

2.1. Globals

Reference size	161,194
Number of reads	740,288
Mapped reads	740,230 / 99.99%
Unmapped reads	58 / 0.01%
Mapped paired reads	740,230 / 99.99%
Mapped reads, first in pair	370,117 / 50%
Mapped reads, second in pair	370,113 / 50%
Mapped reads, both in pair	740,172 / 99.98%
Mapped reads, singletons	58 / 0.01%
Read min/max/mean length	21 / 150 / 105.28
Duplicated reads (estimated)	605,087 / 81.74%
Duplication rate	95.6%
Clipped reads	216 / 0.03%

2.2. ACGT Content

Number/percentage of A's	24,240,111 / 31.11%
Number/percentage of C's	14,446,929 / 18.54%
Number/percentage of T's	24,946,179 / 32.01%
Number/percentage of G's	14,288,437 / 18.34%
Number/percentage of N's	0 / 0%
GC Percentage	36.88%

2.3. Coverage

Mean	483.6446
Standard Deviation	272.9242

2.4. Mapping Quality

Mean Mapping Quality	30.83
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2.5. Insert size

Mean	376.52
Standard Deviation	2,902.72
P25/Median/P75	241 / 287 / 333

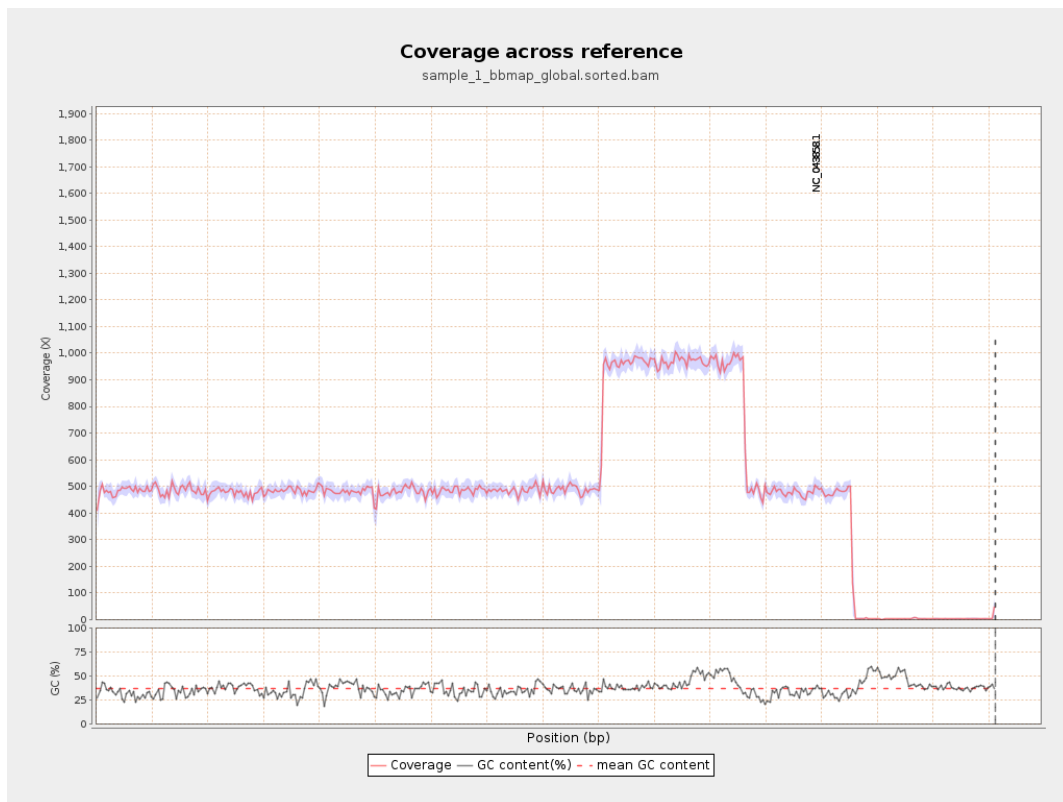
2.6. Mismatches and indels

General error rate	0.34%
Insertions	1,172
Mapped reads with at least one insertion	0.16%
Deletions	427
Mapped reads with at least one deletion	0.06%
Homopolymer indels	14.88%

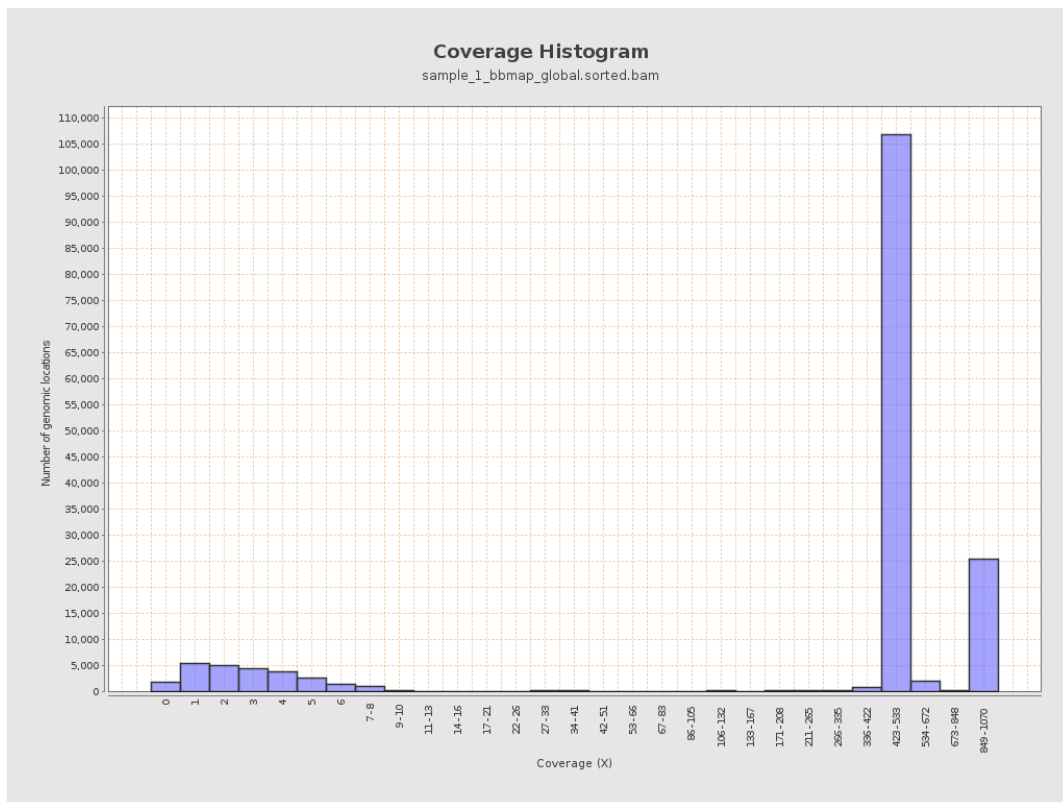
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_043858.1	161194	77960613	483.6446	272.9242

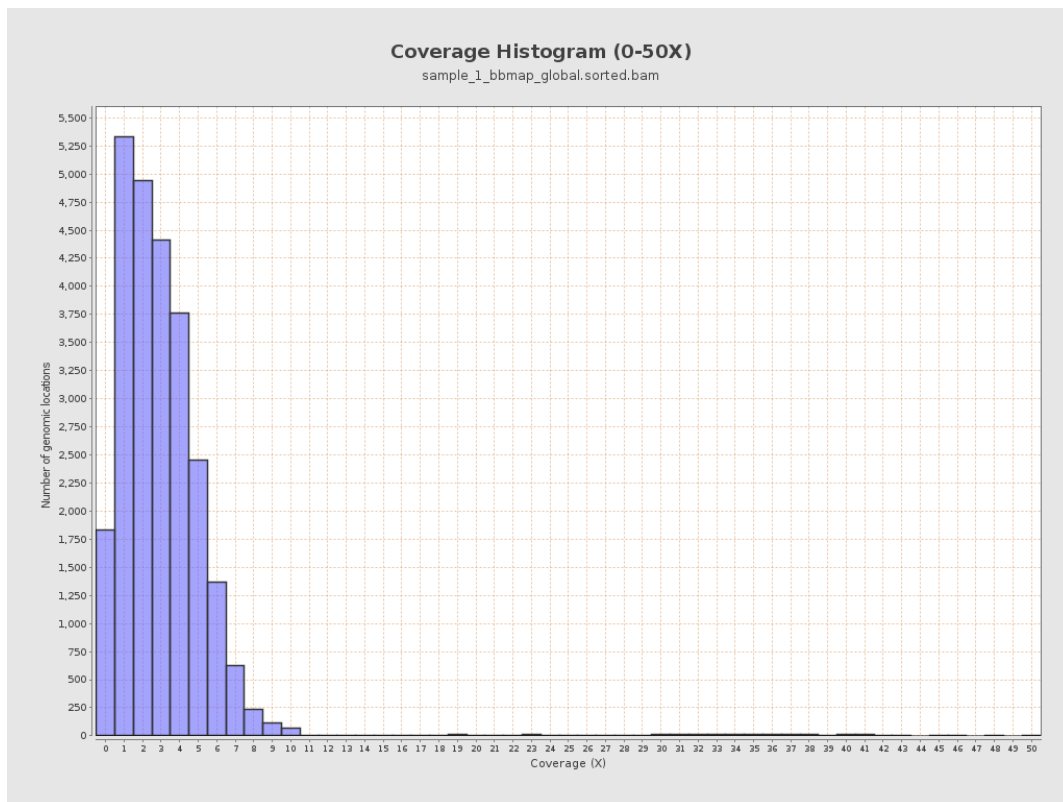
3. Results : Coverage across reference



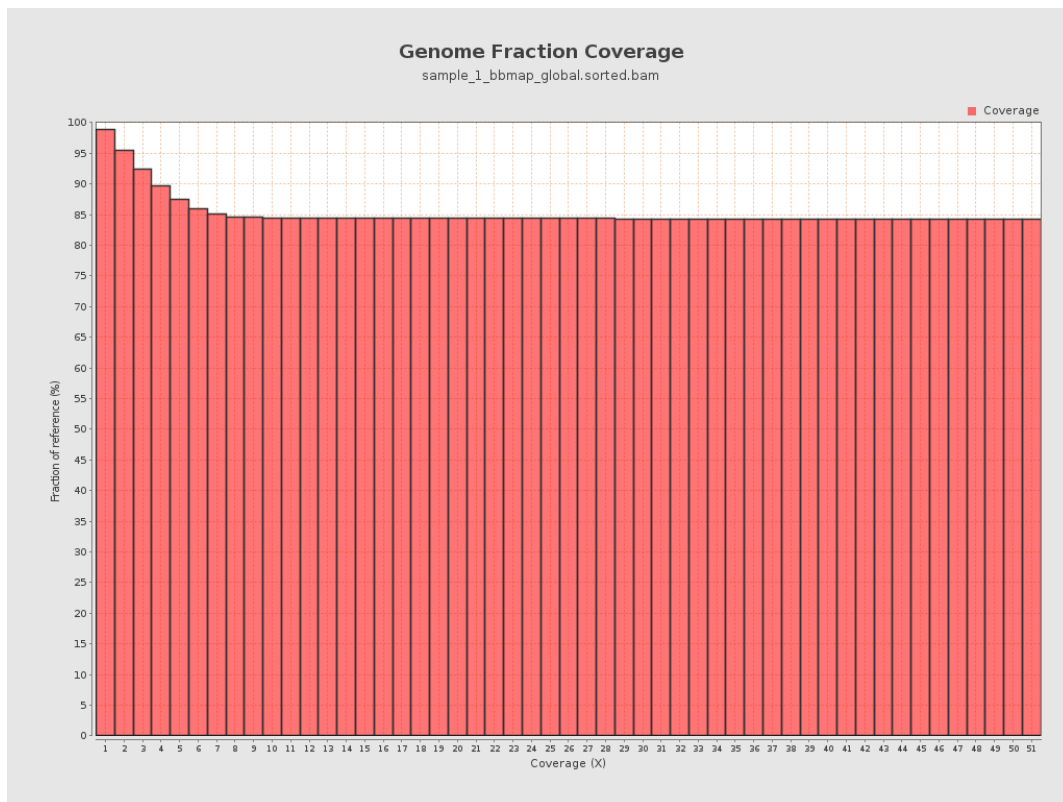
4. Results : Coverage Histogram



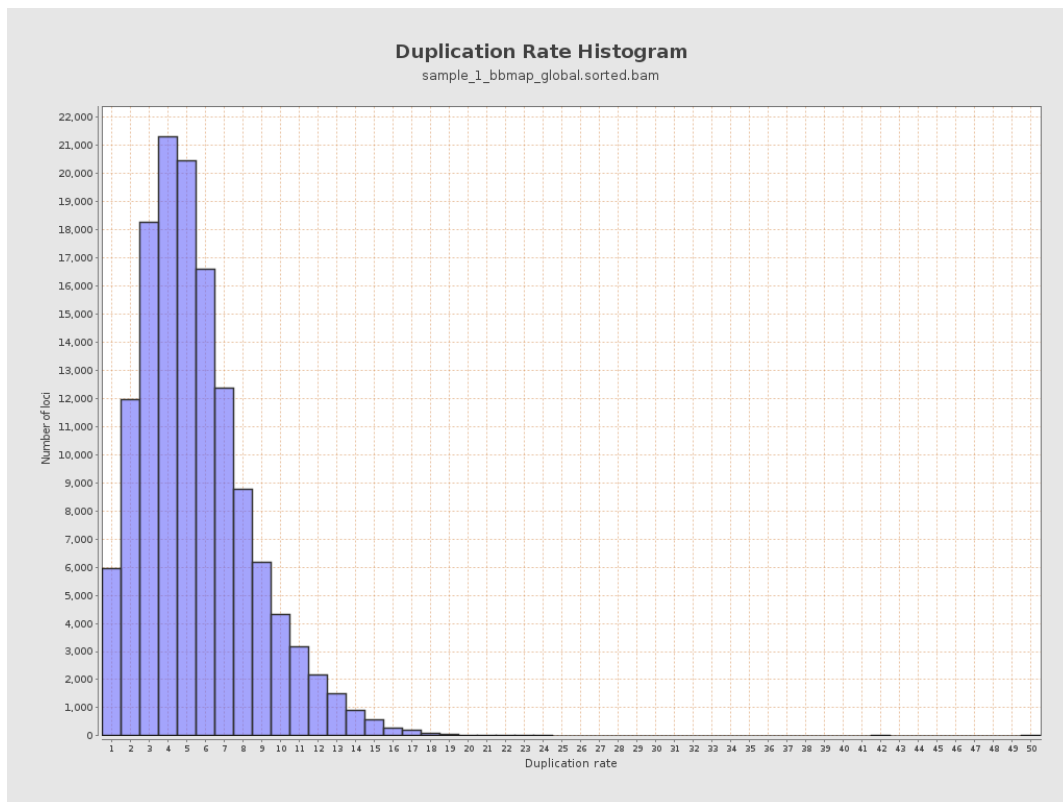
5. Results : Coverage Histogram (0-50X)



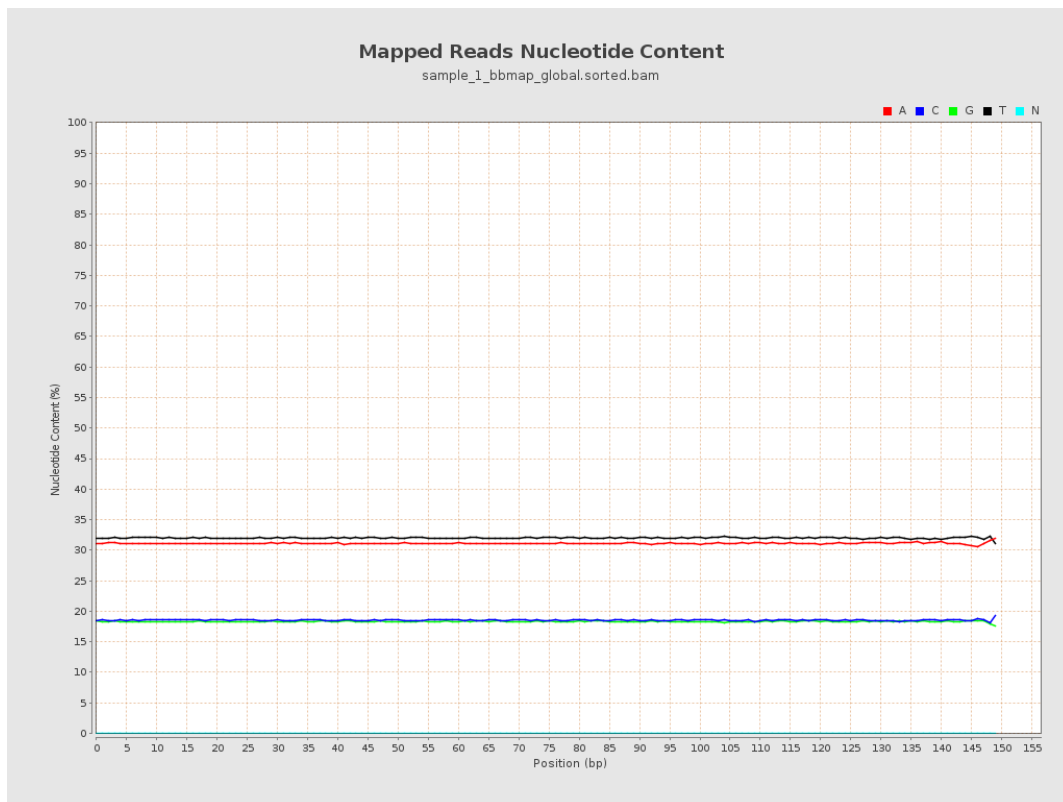
6. Results : Genome Fraction Coverage



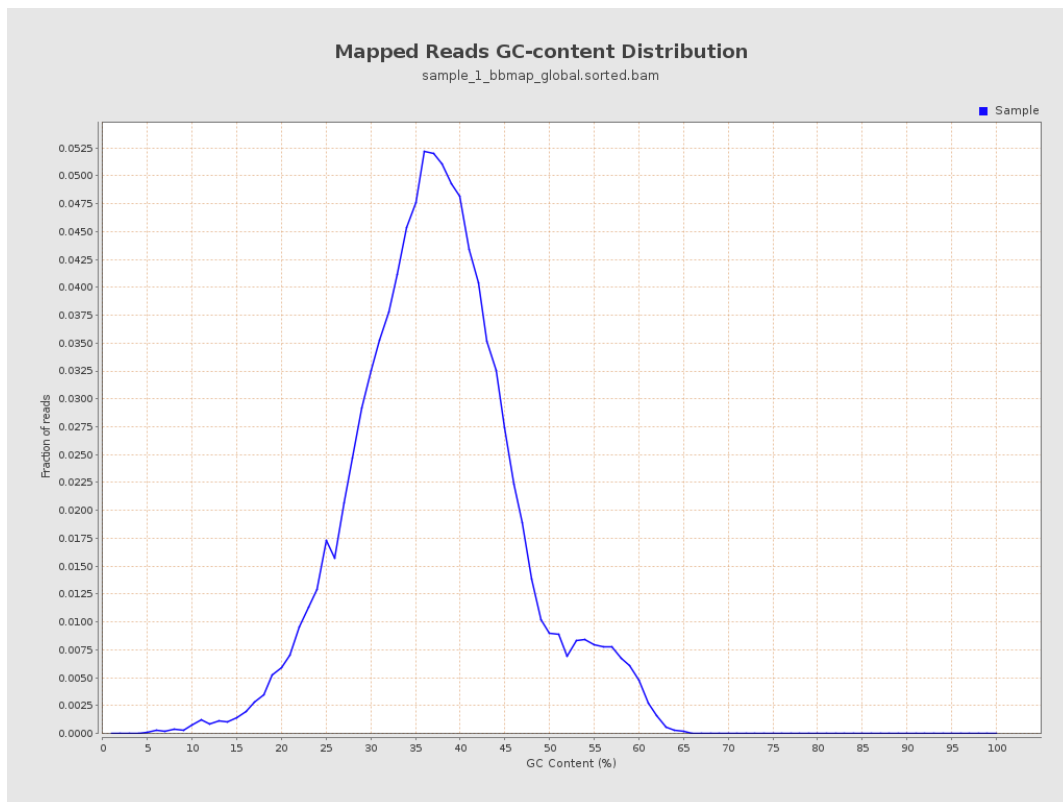
7. Results : Duplication Rate Histogram



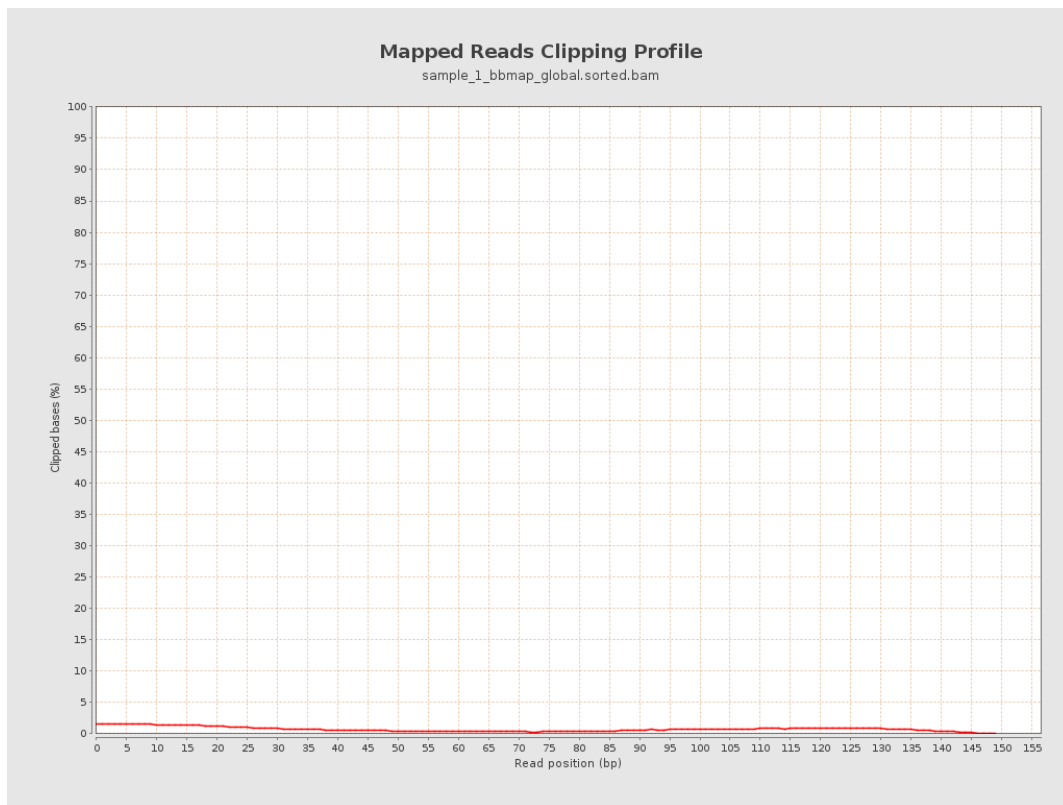
8. Results : Mapped Reads Nucleotide Content



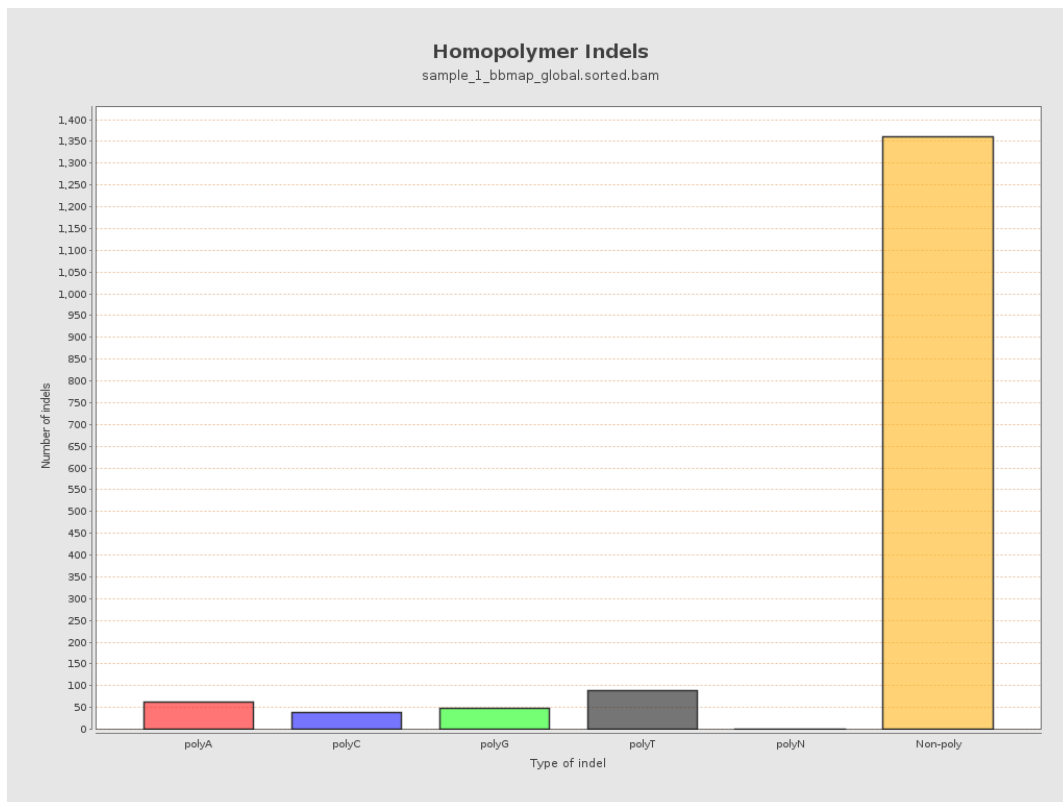
9. Results : Mapped Reads GC-content Distribution



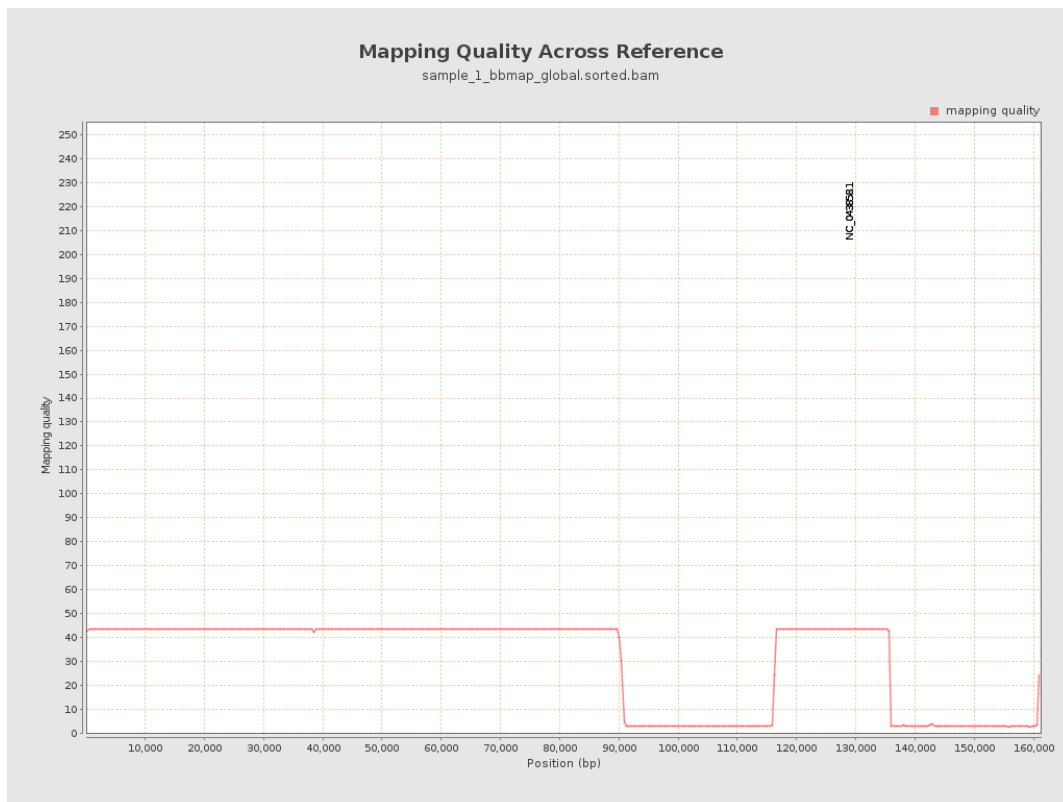
10. Results : Mapped Reads Clipping Profile



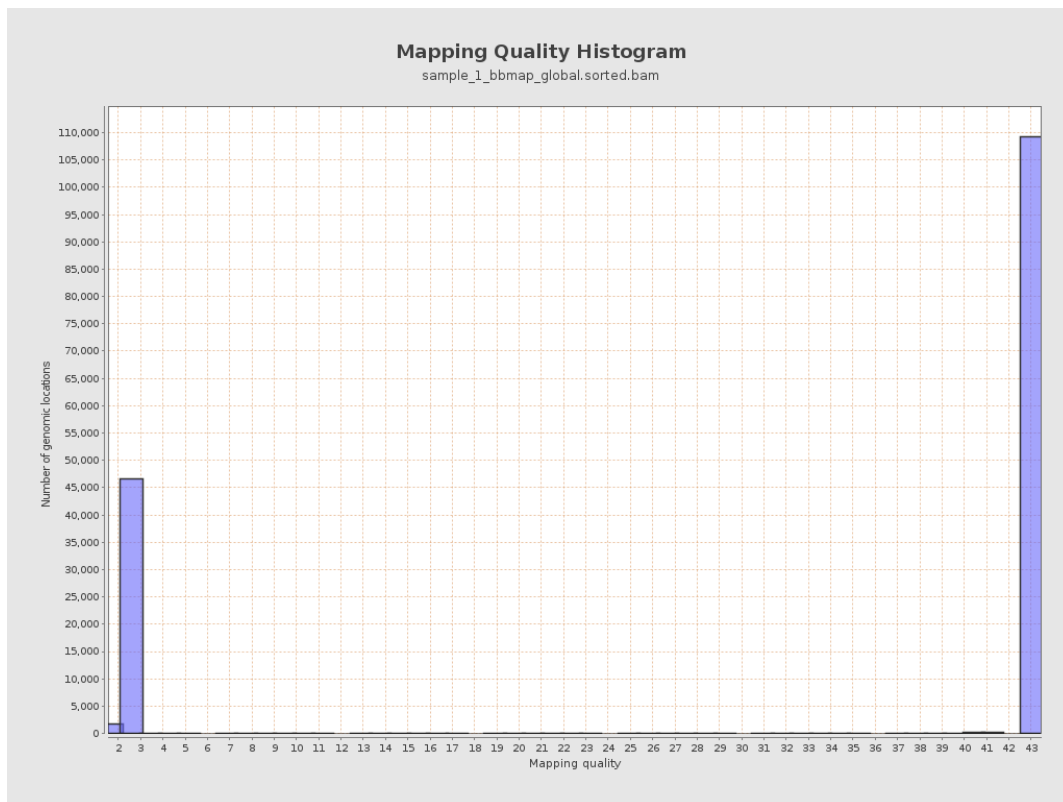
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

