Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2024/02/14 17:53:37

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam IP_CMV_ref_bowtie2_local.sorted.bam -c -nw 400 -hm 3

1.2. Alignment

Command line:	"/data/proj/teaching/NGS_course/Softwares/bowtie2-2.4.5-linux-x86_64/bowtie2-align-s --wrapper basic-0 -p 4 --local -x CMV_ref.fasta -S IP_CMV_ref_bowtie2_local.sam -1 infected_plant_clean_R1.fastq.gz -2 infected_plant_clean_R2.fastq.gz"
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bowtie2 (2.4.5)
Analysis date:	Wed Feb 14 17:53:32 CET 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	IP_CMV_ref_bowtie2_local.sorted.bam

2. Summary

2.1. Globals

Reference size	8,623
Number of reads	1,706,546
Mapped reads	752,437 / 44.09%
Unmapped reads	954,109 / 55.91%
Mapped paired reads	752,437 / 44.09%
Mapped reads, first in pair	376,281 / 22.05%
Mapped reads, second in pair	376,156 / 22.04%
Mapped reads, both in pair	748,340 / 43.85%
Mapped reads, singletons	4,097 / 0.24%
Read min/max/mean length	21 / 150 / 98.58
Duplicated reads (estimated)	743,901 / 43.59%
Duplication rate	99.96%
Clipped reads	13,881 / 0.81%

2.2. ACGT Content

Number/percentage of A's	18,549,810 / 24.9%
Number/percentage of C's	16,686,838 / 22.4%
Number/percentage of T's	21,534,486 / 28.91%
Number/percentage of G's	17,722,336 / 23.79%
Number/percentage of N's	0 / 0%
GC Percentage	46.19%

2.3. Coverage

Mean	8,642.7372
Standard Deviation	1,604.2162

2.4. Mapping Quality

Mean Mapping Quality	43.16

2.5. Insert size

Mean	281.43
Standard Deviation	67.86
P25/Median/P75	235 / 282 / 328

2.6. Mismatches and indels

General error rate	0.31%
Mismatches	229,165
Insertions	362
Mapped reads with at least one insertion	0.05%
Deletions	16,389
Mapped reads with at least one deletion	2.18%
Homopolymer indels	0.91%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

|				
NC_002034.1	3357	29358613	8,745.4909	1,529.6266
NC_002035.1	3050	26530941	8,698.6692	1,569.5879
NC_001440.1	2216	18636769	8,410.0943	1,734.2043

3. Results : Coverage across reference

Coverage across reference
IP_CMV_ref_bowtie2_local.sorted.bam

4. Results : Coverage Histogram
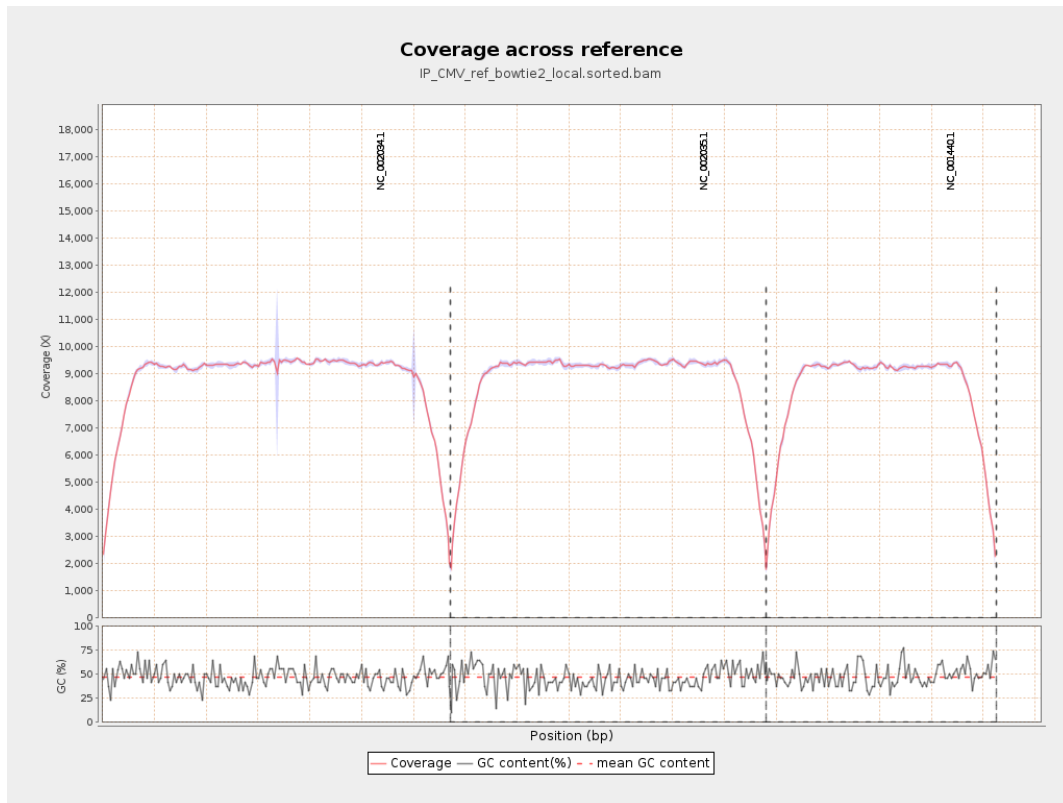
Coverage Histogram
IP_CMV_ref_bowtie2_local.sorted.bam
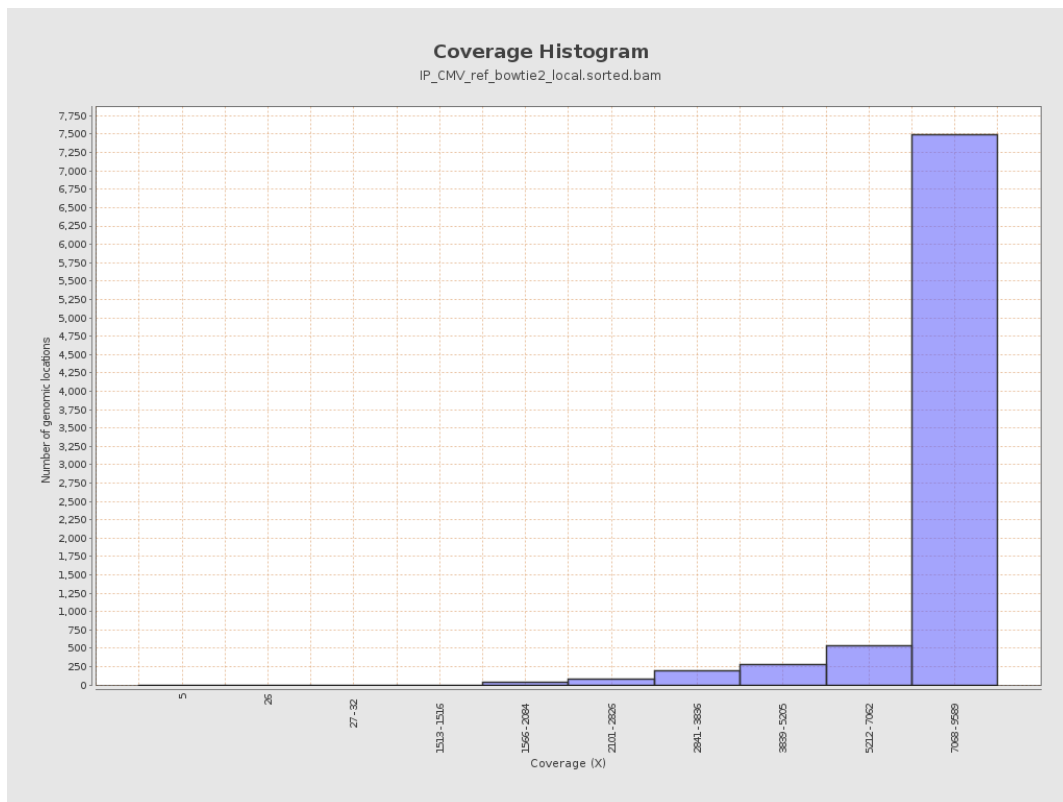
5. Results : Coverage Histogram (0-50X)
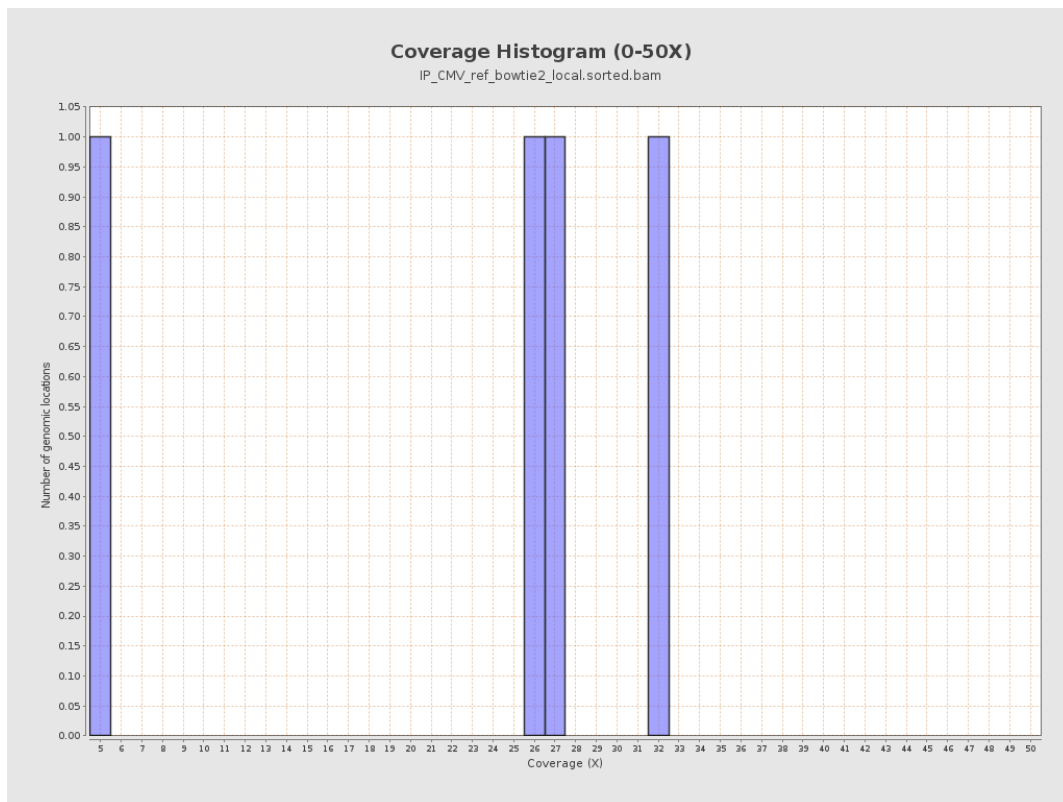
6. Results : Genome Fraction Coverage

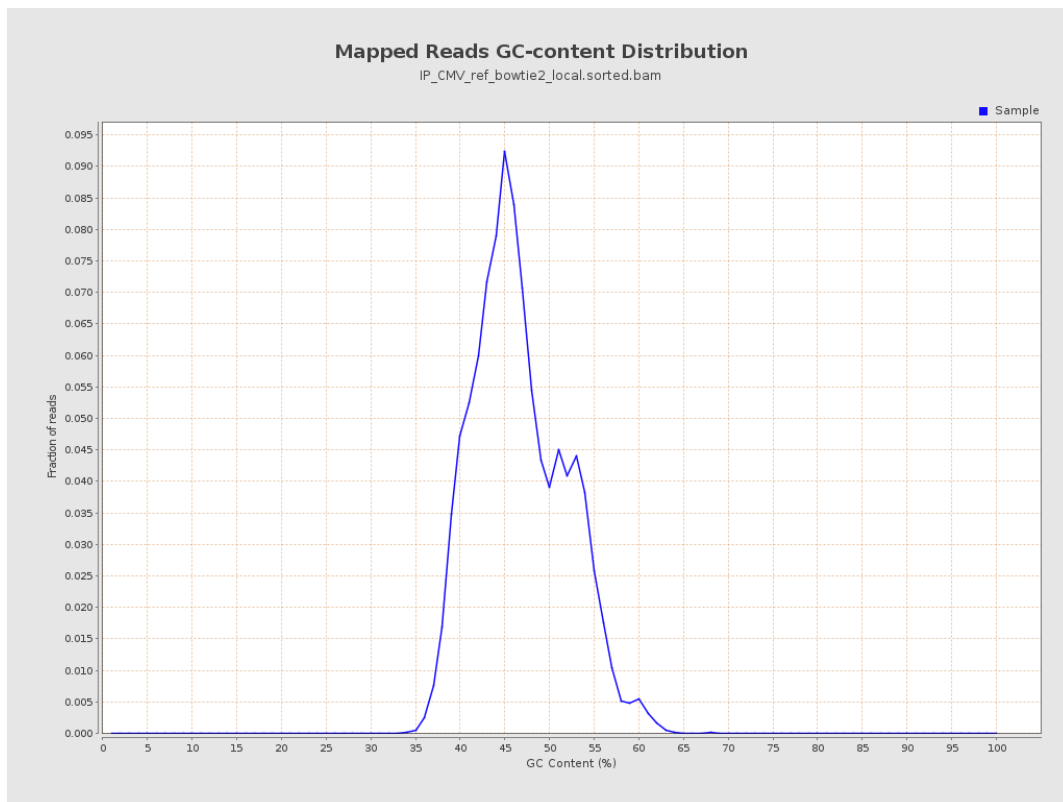
Genome Fraction Coverage
IP_CMV_ref_bowtie2_local.sorted.bam
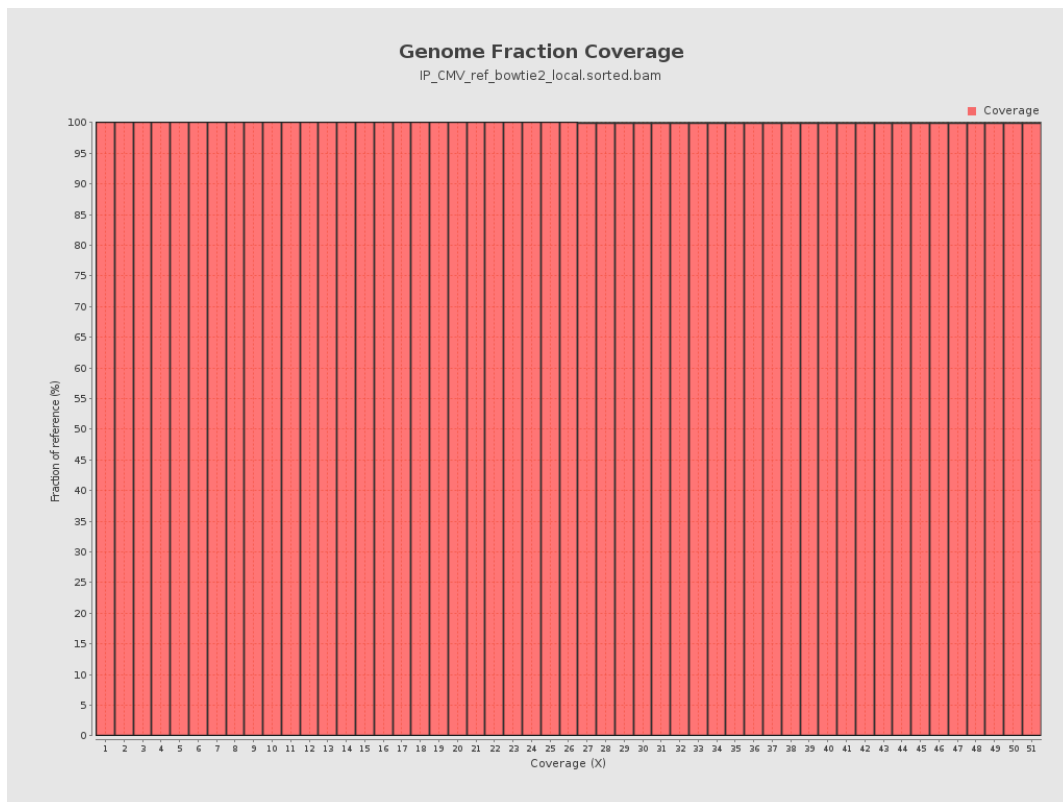
7. Results : Duplication Rate Histogram
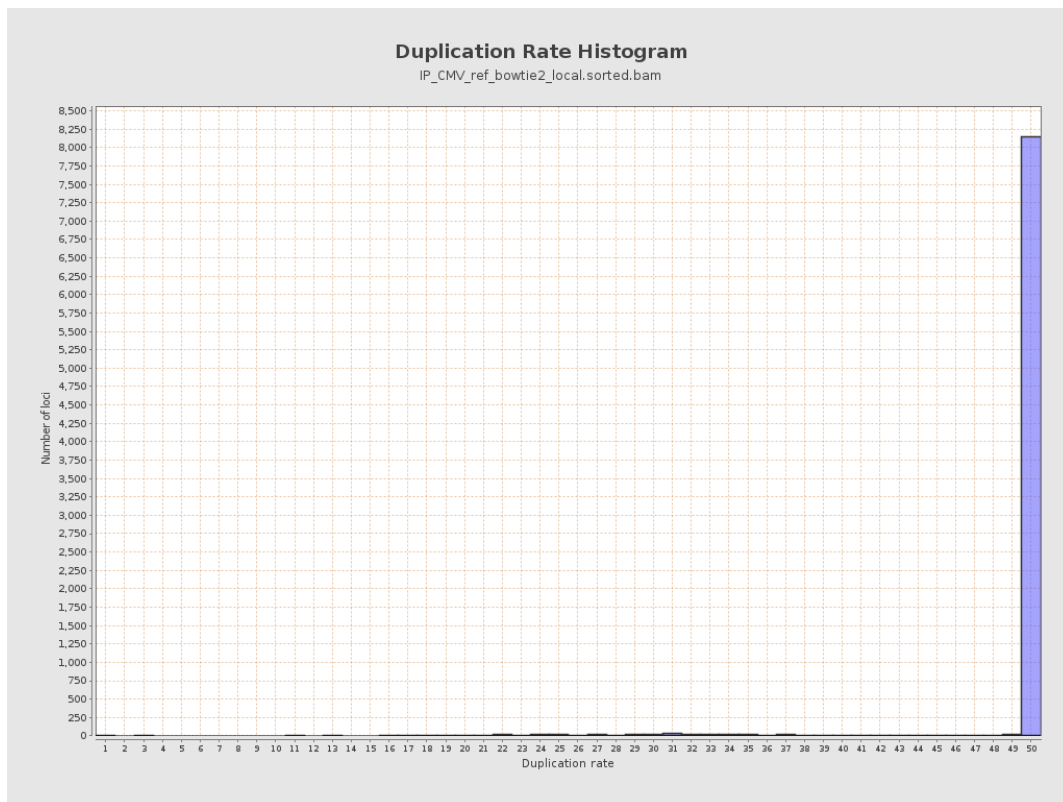
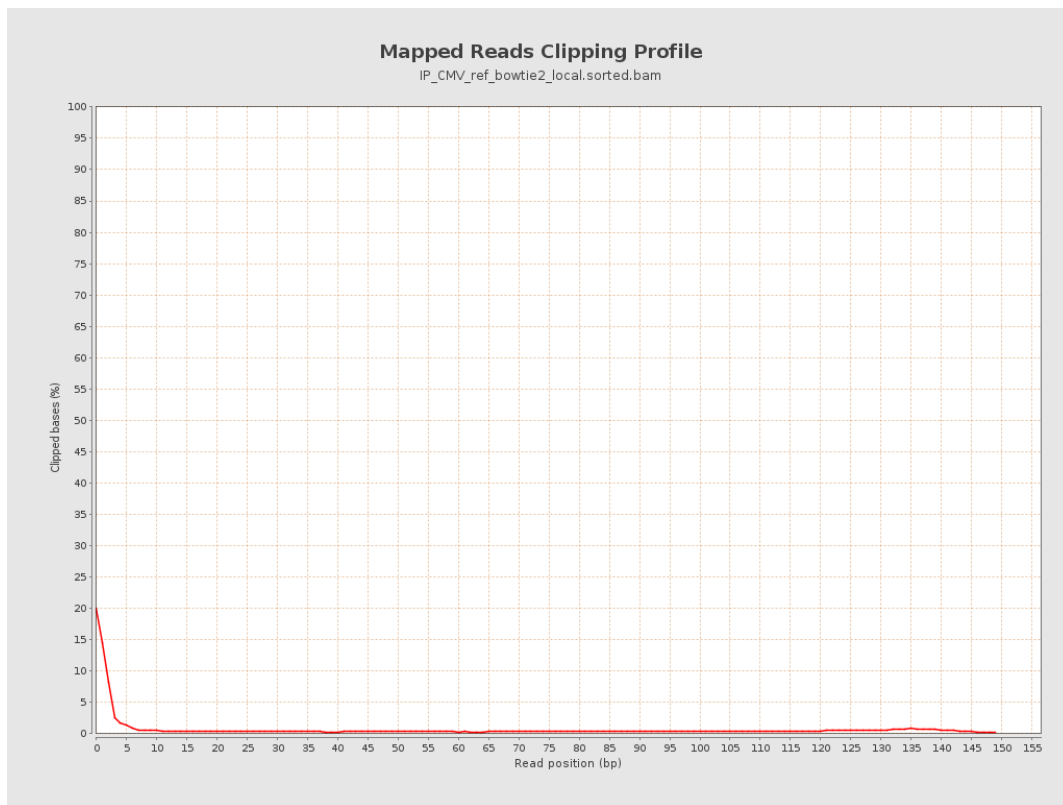# 8. Results : Mapped Reads Nucleotide Content
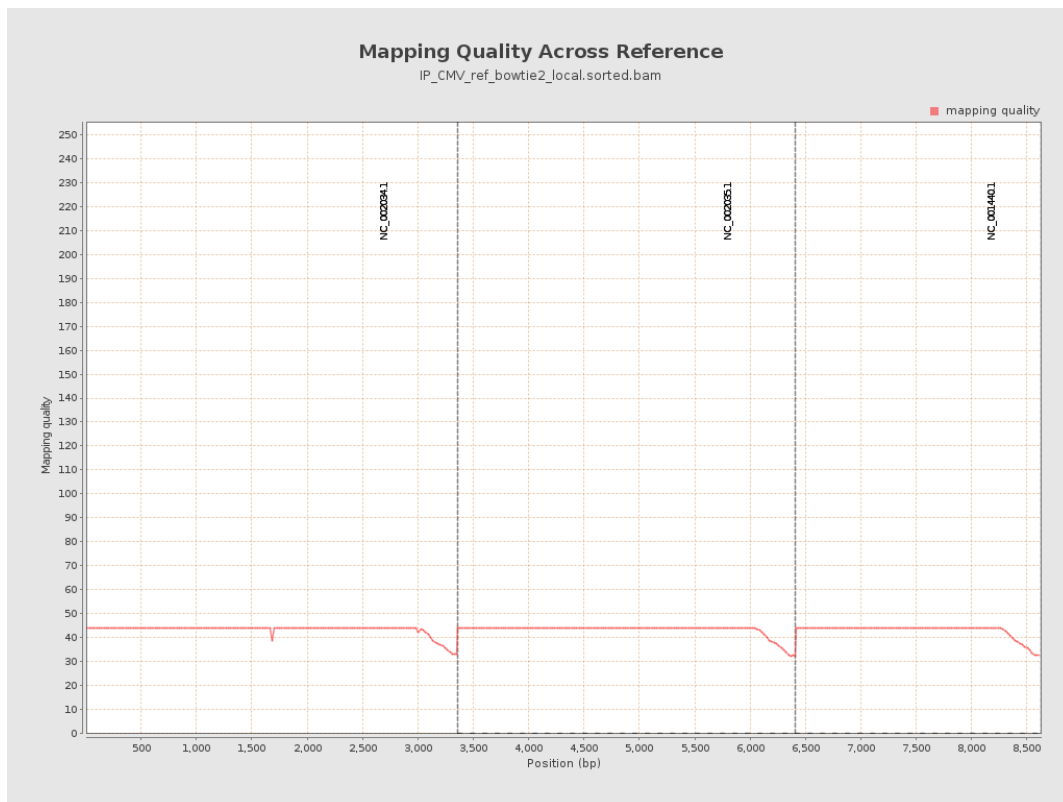
9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
IP_CMV_ref_bowtie2_local.sorted.bam
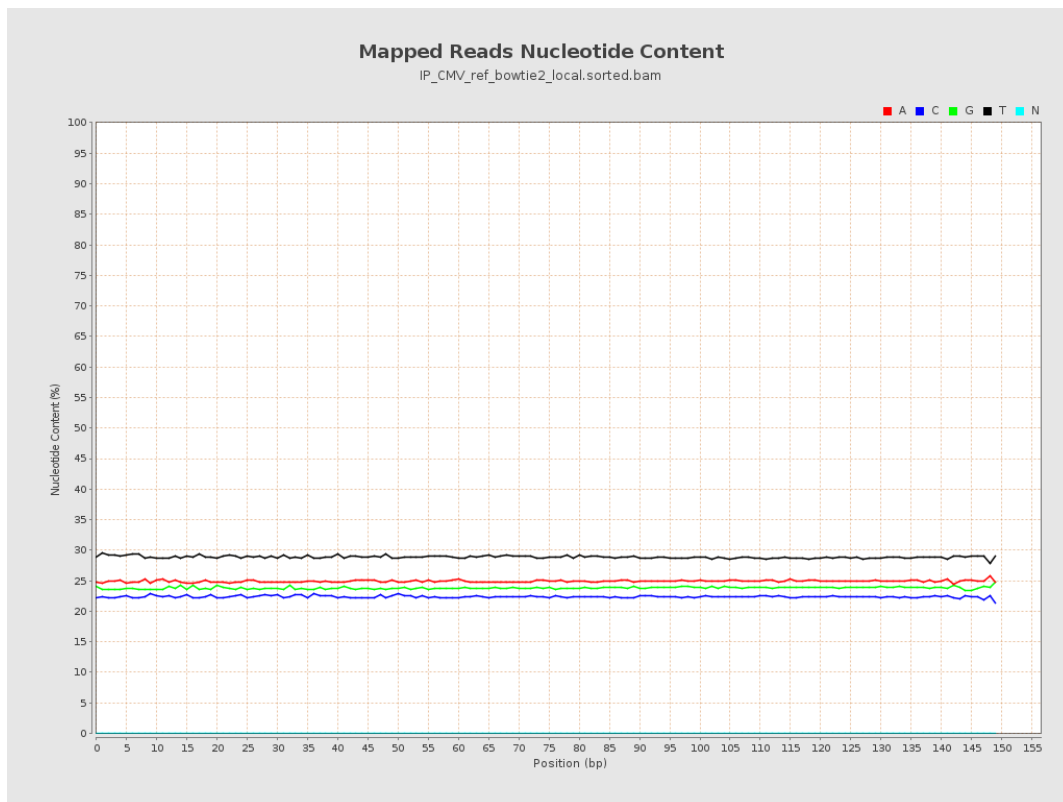
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
IP_CMV_ref_bowtie2_local.sorted.bam

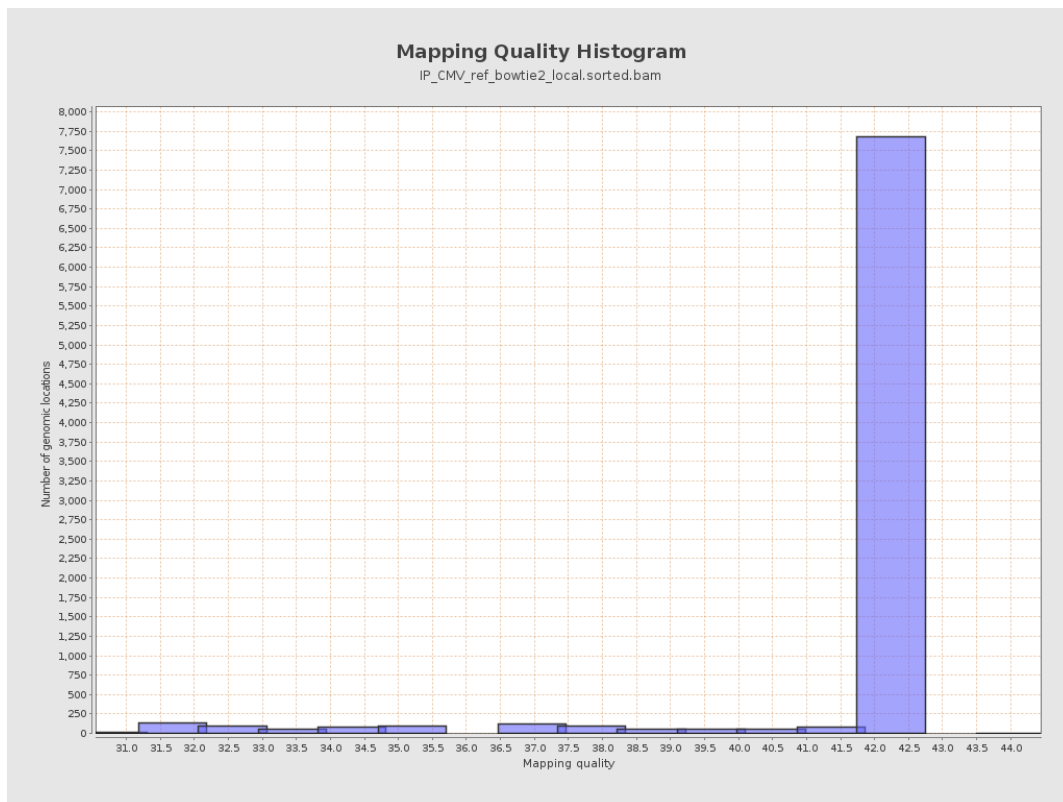# 11. Results : Homopolymer Indels

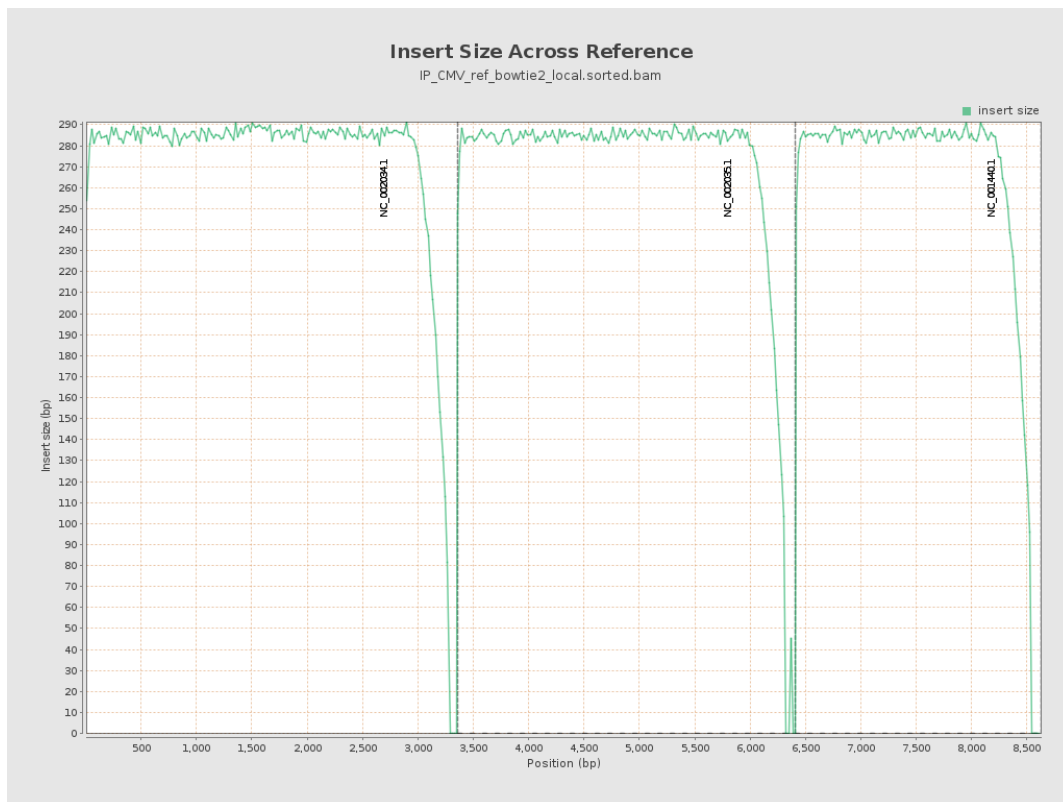

Homopolymer Indels
IP_CMV_ref_bowtie2_local.sorted.bam
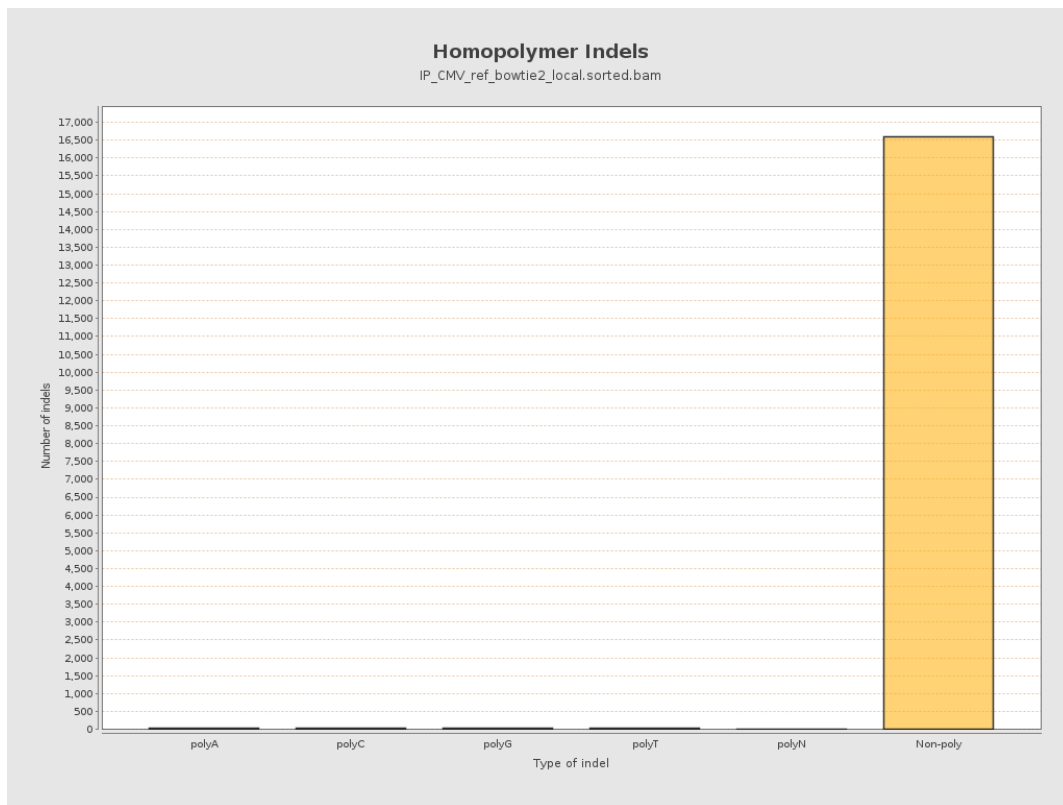
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

Insert Size Across Reference
IP_CMV_ref_bowtie2_local.sorted.bam

15. Results : Insert Size Histogram