Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.3
2024/10/15 10:25:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
./Results_from_Pipeline/bams/ggal_gut.Aligned.sortedByCoord.out.bam -nw
400 -hm 3
```

1.2. Alignment

Command line:	/home/Ashutosh.Yadav/anaconda3/envs/starAligner/bin/STAR-avx2 --runThreadN 16 --genomeDir index --readFilesIn trimmed_ggal_gut_1.fastq trimmed_ggal_gut_2.fastq --outFileNamePrefix ggal_gut. --outSAMtype BAM SortedByCoordinate
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	STAR (2.7.11b)
Analysis date:	Tue Oct 15 10:25:49 IST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	./Results_from_Pipeline/bams/ggal_gut.Aligned.sortedByCoord.out.bam

2. Summary

2.1. Globals

Reference size	171,001
Number of reads	4,667
Mapped reads	4,667 / 100%
Unmapped reads	0 / 0%
Mapped paired reads	4,667 / 100%
Mapped reads, first in pair	2,333 / 49.99%
Mapped reads, second in pair	2,334 / 50.01%
Mapped reads, both in pair	4,666 / 99.98%
Mapped reads, singletons	1 / 0.02%
Secondary alignments	204
Read min/max/mean length	37 / 105 / 107.67
Duplicated reads (estimated)	1,501 / 32.16%
Duplication rate	28.08%
Clipped reads	1,215 / 26.03%

2.2. ACGT Content

Number/percentage of A's	128,310 / 27.6%
Number/percentage of C's	104,023 / 22.37%
Number/percentage of T's	127,769 / 27.48%
Number/percentage of G's	104,839 / 22.55%
Number/percentage of N's	1 / 0%
GC Percentage	44.92%

2.3. Coverage

Mean	29.0722
Standard Deviation	28.589

2.4. Mapping Quality

Mean Mapping Quality	21.08

2.5. Insert size

Mean	1,638.42
Standard Deviation	7,504.89
P25/Median/P75	114 / 155 / 945

2.6. Mismatches and indels

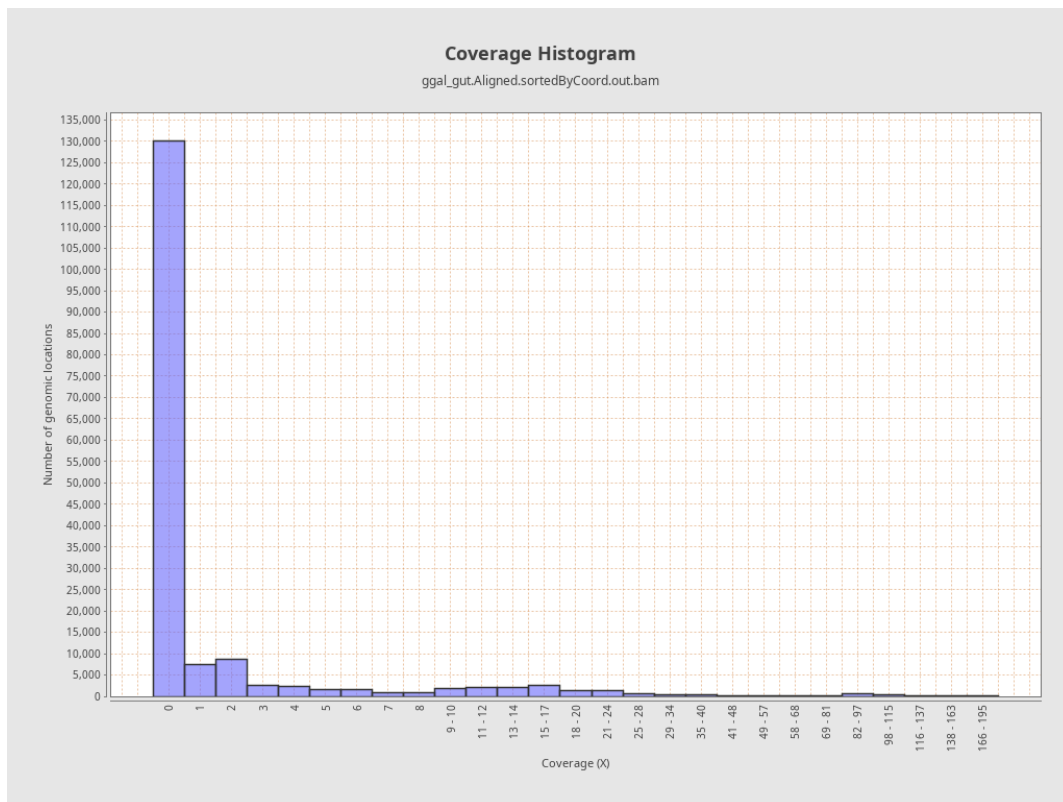| Insertions	162
Mapped reads with at least one insertion	3.26%
Deletions	38
Mapped reads with at least one deletion	0.73%
Homopolymer indels	50.5%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
1	171001	4971369	29.0722	28.589

3. Results : Coverage across reference

Coverage across reference
ggal_gut.Aligned.sortedByCoord.out.bam

4. Results : Coverage Histogram

Coverage Histogram
ggal_gut.Aligned.sortedByCoord.out.bam

5. Results : Coverage Histogram (0-50X)
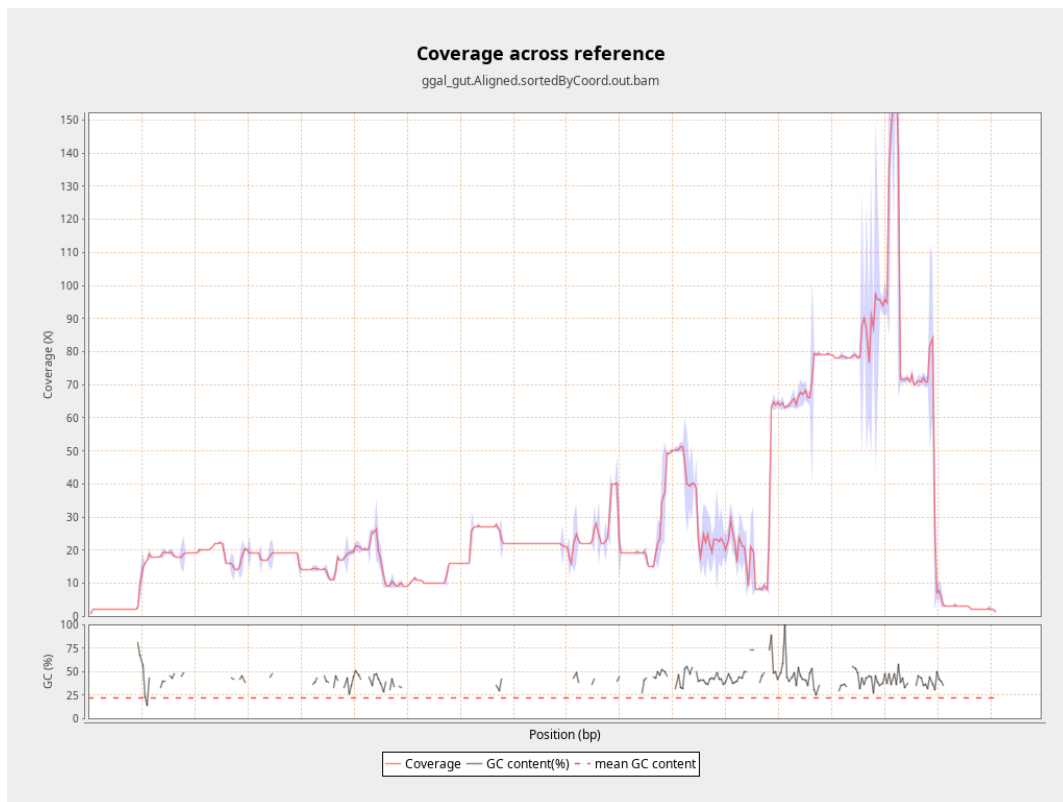
Coverage Histogram (0-50X)
ggal_gut.Aligned.sortedByCoord.out.bam
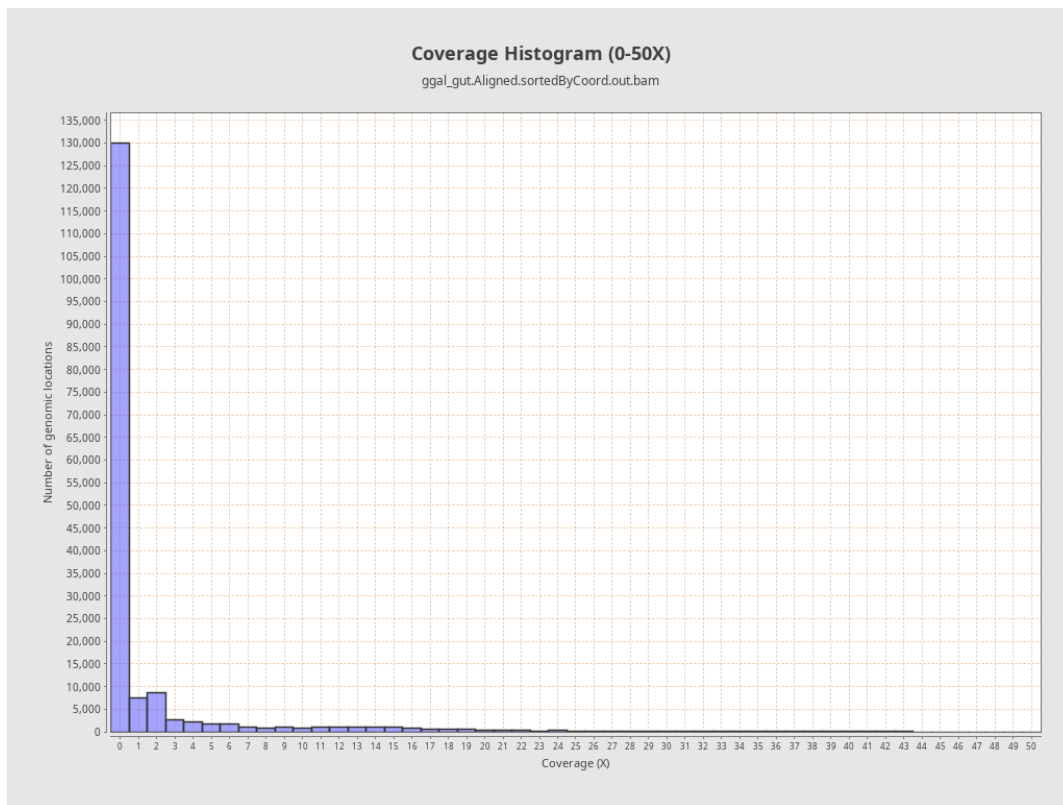
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
ggal_gut.Aligned.sortedByCoord.out.bam
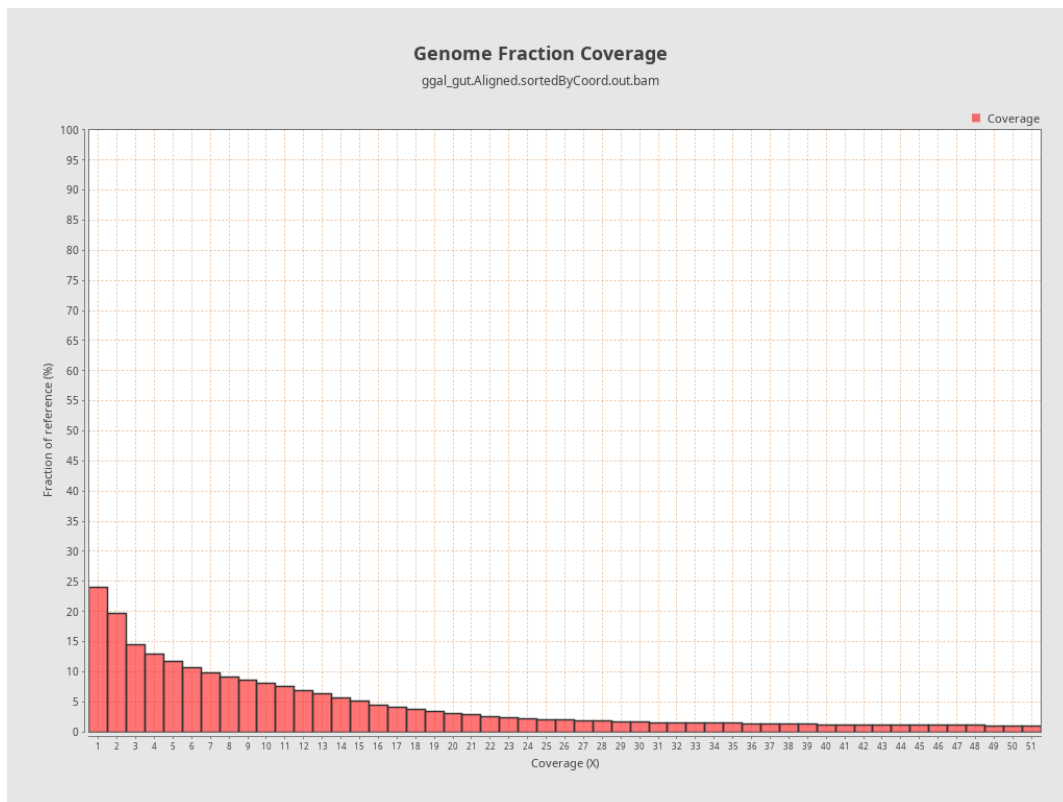
7. Results : Duplication Rate Histogram
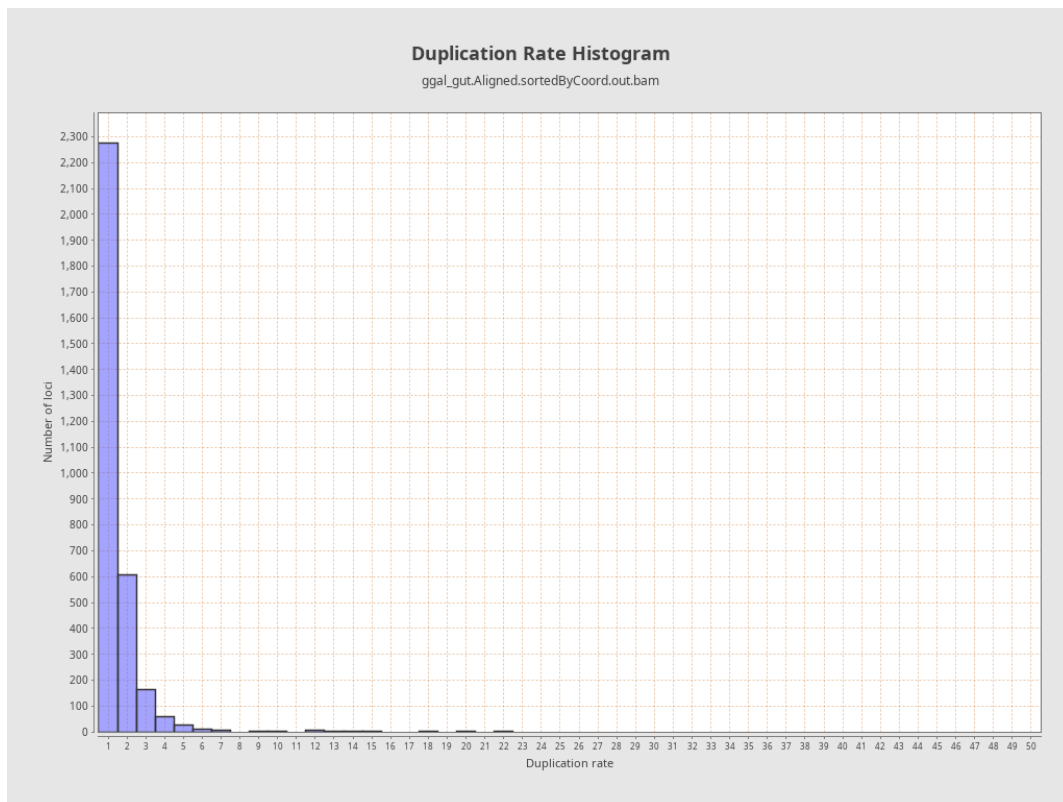
Duplication Rate Histogram

ggal_gut.Aligned.sortedByCoord.out.bam

8. Results : Mapped Reads Nucleotide Content

Mapped Reads Nucleotide Content
ggal_gut.Aligned.sortedByCoord.out.bam

9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
ggal_gut.Aligned.sortedByCoord.out.bam
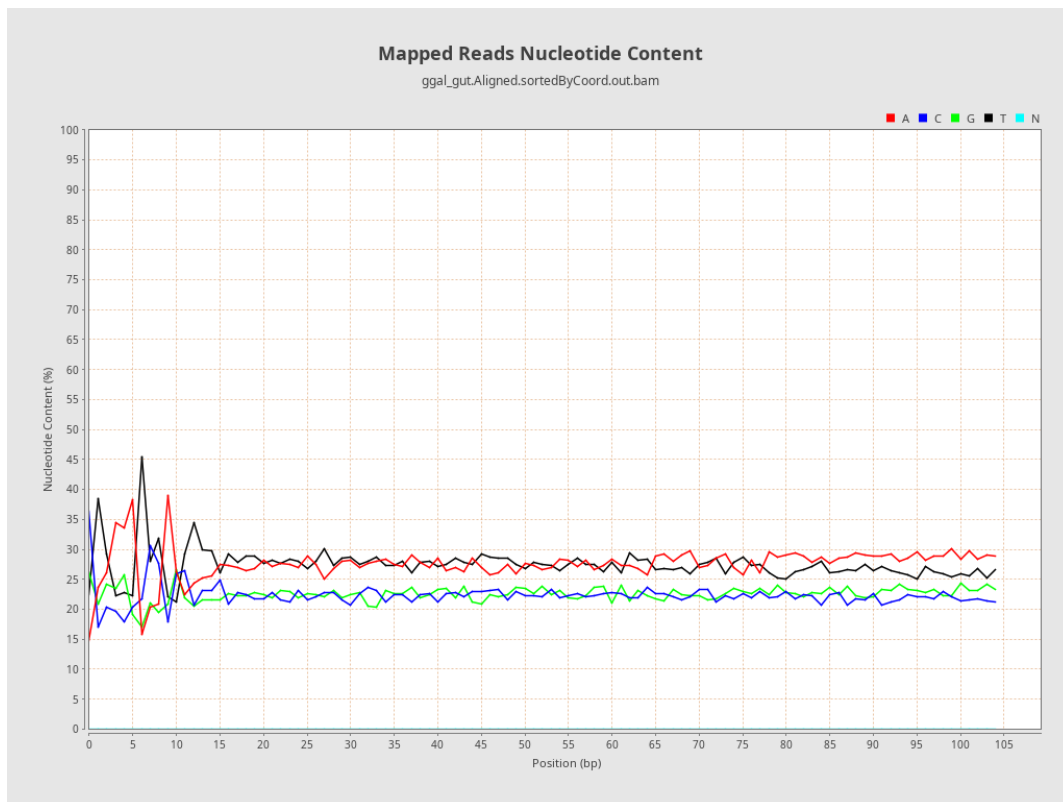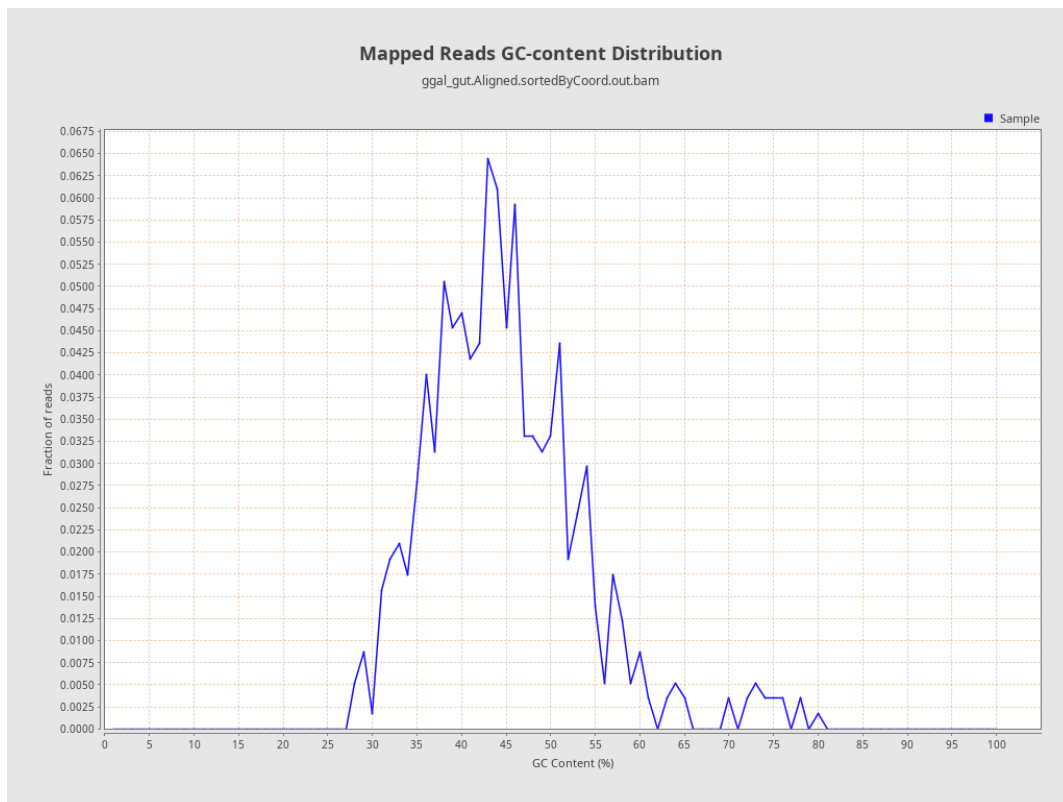
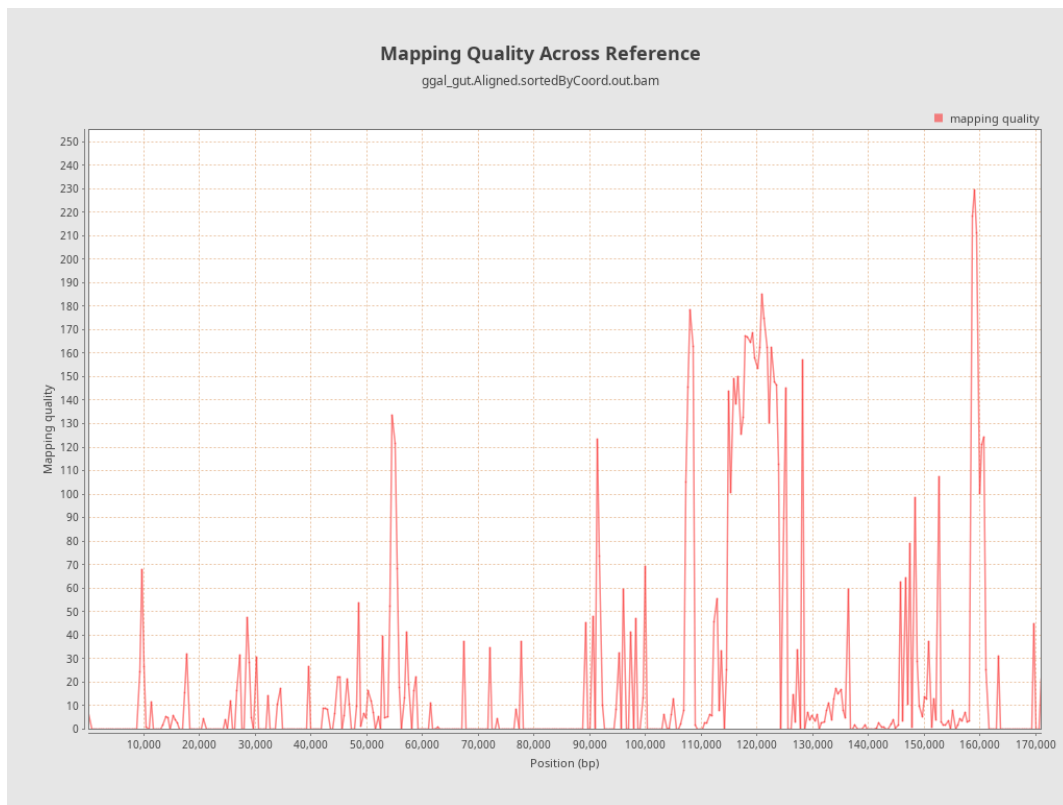# 10. Results : Mapped Reads Clipping Profile
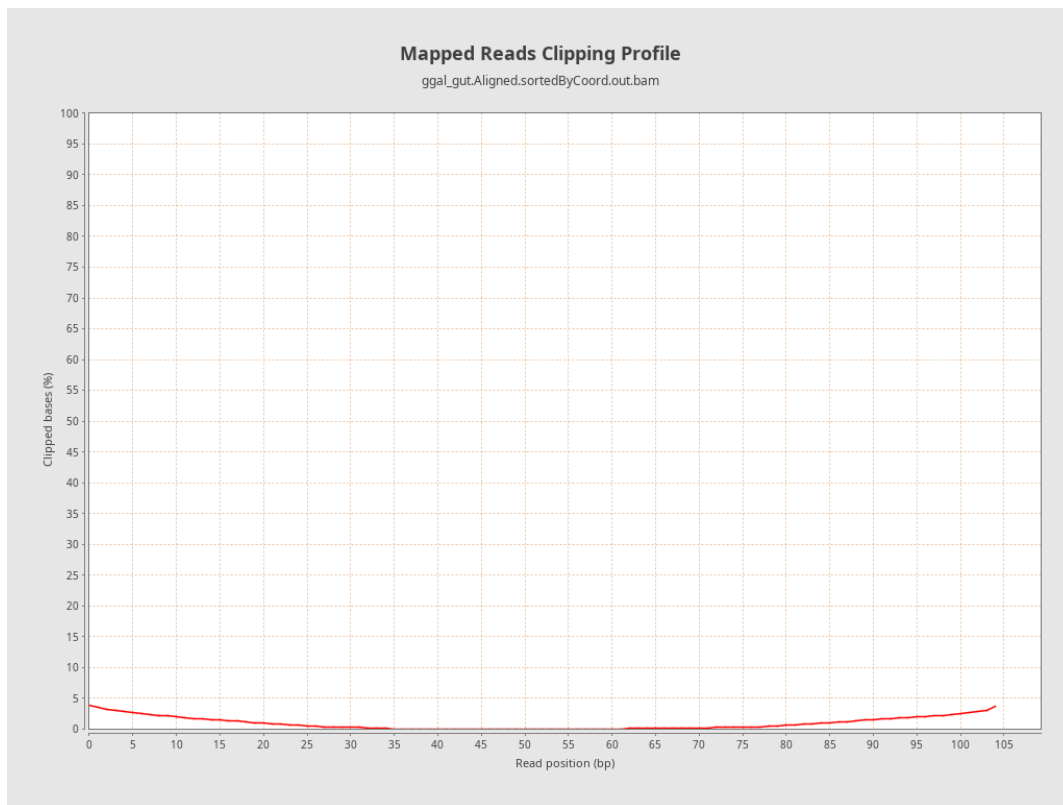
11. Results : Homopolymer Indels
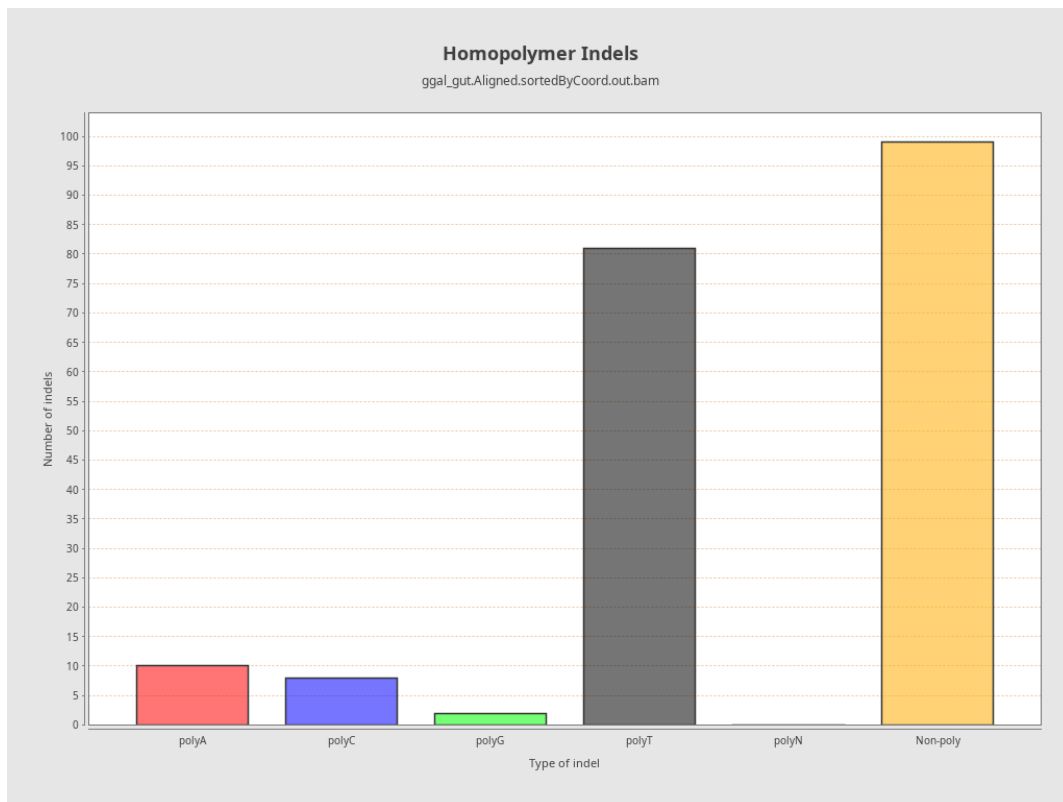
12. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
ggal_gut.Aligned.sortedByCoord.out.bam

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
ggal_gut.Aligned.sortedByCoord.out.bam
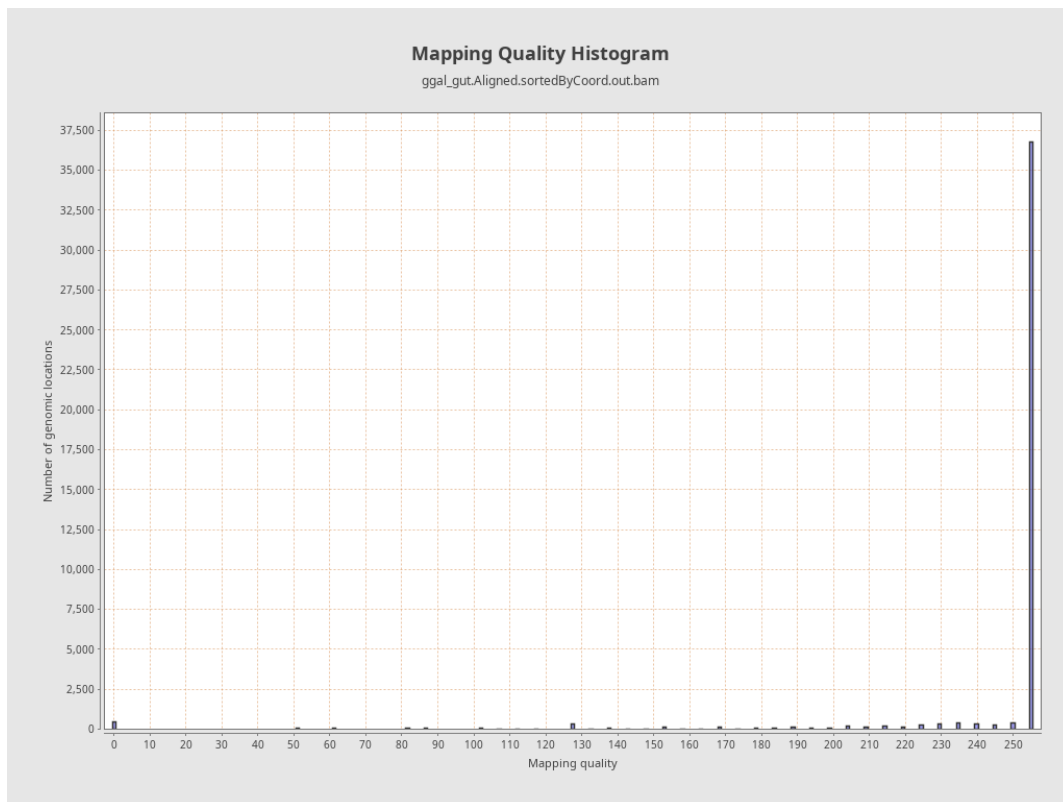
14. Results : Insert Size Across Reference

Insert Size Across Reference
ggal_gut.Aligned.sortedByCoord.out.bam
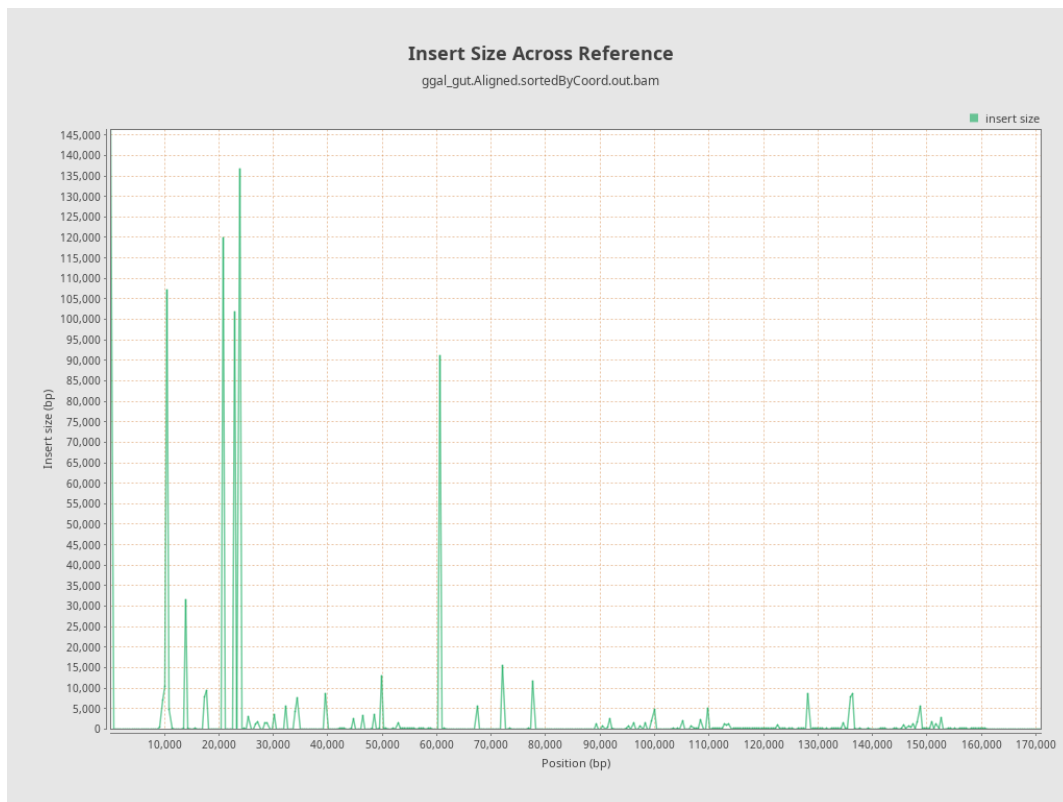
15. Results : Insert Size Histogram

Insert Size Histogram
ggal_gut.Aligned.sortedByCoord.out.bam