Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/17 11:25:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam KM_3q-trim-h-mapped-DiNV.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa mem -t 5 GCF_004132165.1_DiNV_CH01M_genomic.fna KM_3_1_trim.fq.gz KM_3_2_trim.fq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	yes
Program:	bwa (0.7.17-r1198-dirty)
Analysis date:	Wed May 17 11:25:35 CDT 2023
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	KM_3q-trim-h-mapped-DiNV.bam

2. Summary

2.1. Globals

Reference size	155,555
Number of reads	14,053,370
Mapped reads	211,350 / 1.5%
Supplementary alignments	46 / 0%
Unmapped reads	13,842,020 / 98.5%
Mapped paired reads	211,350 / 1.5%
Mapped reads, first in pair	105,706 / 0.75%
Mapped reads, second in pair	105,644 / 0.75%
Mapped reads, both in pair	210,189 / 1.5%
Mapped reads, singletons	1,161 / 0.01%
Read min/max/mean length	30 / 135 / 115.57
Overlapping read pairs	100,794 / 1.43%
Duplicated reads (estimated)	171,012 / 1.22%
Duplication rate	47.31%
Clipped reads	143,835 / 1.02%

2.2. ACGT Content

Number/percentage of A's	3,391,857 / 30.26%
Number/percentage of C's	1,945,081 / 17.35%
Number/percentage of T's	3,805,738 / 33.95%
Number/percentage of G's	2,067,348 / 18.44%
Number/percentage of N's	455 / 0%

GC Percentage	35.79%

2.3. Coverage

Mean	72.2431
Standard Deviation	410.6485
Mean (paired-end reads overlap ignored)	44.94

2.4. Mapping Quality

Mean Mapping Quality	57.14

2.5. Insert size

Mean	82.54
Standard Deviation	1,361.32
P25/Median/P75	20 / 25 / 80

2.6. Mismatches and indels

General error rate	1.3%
Mismatches	128,721
Insertions	6,565
Mapped reads with at least one insertion	2.85%
Deletions	8,832
Mapped reads with at least one deletion	3.54%
Homopolymer indels	51.7%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_040699.1	155555	11237777	72.2431	410.6485

3. Results : Coverage across reference

Coverage across reference
KM_3q-trim-h-mapped-DiNV.bam

4. Results : Coverage Histogram

Coverage Histogram
KM_3q–trim–h–mapped–DiNV.bam

5. Results : Coverage Histogram (0-50X)
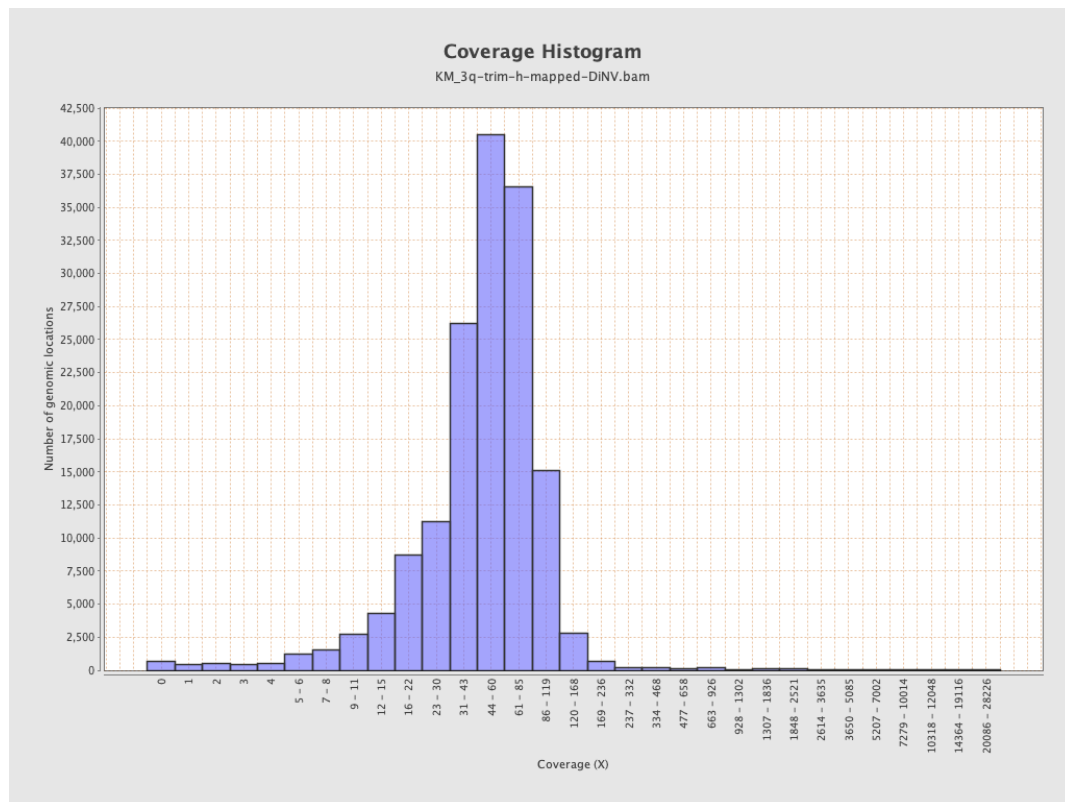
Coverage Histogram (0-50X)
KM_3q-trim-h-mapped-DiNV.bam
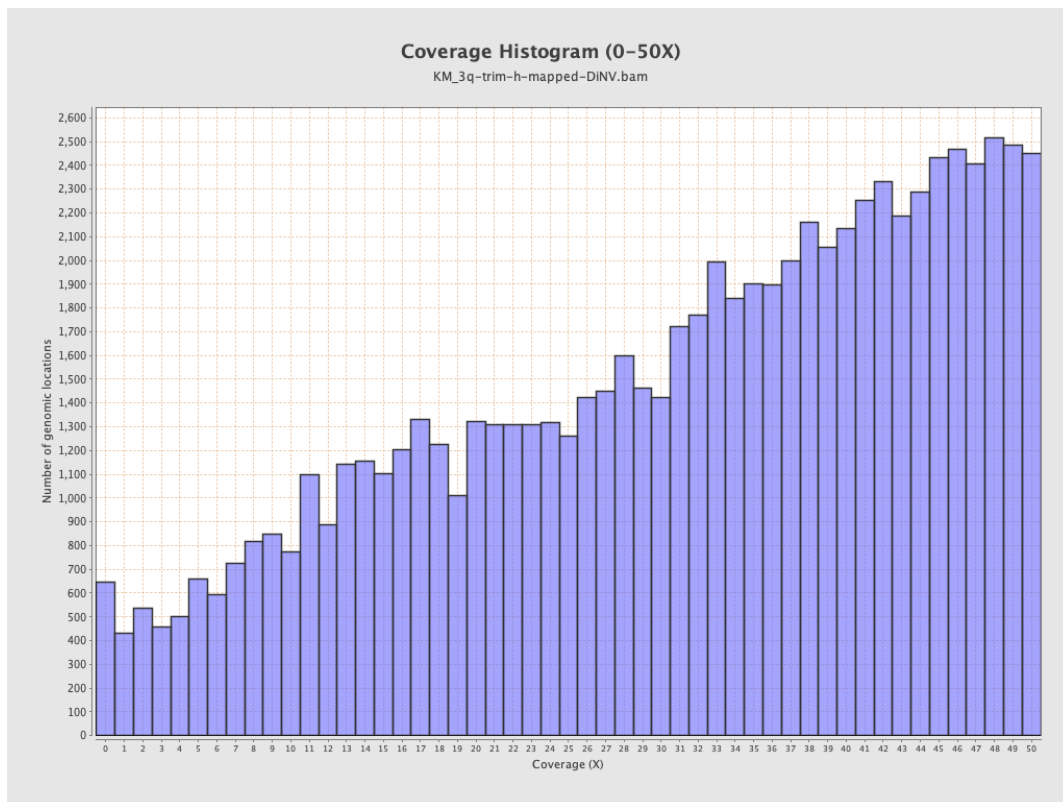
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
KM_3q-trim-h-mapped-DiNV.bam
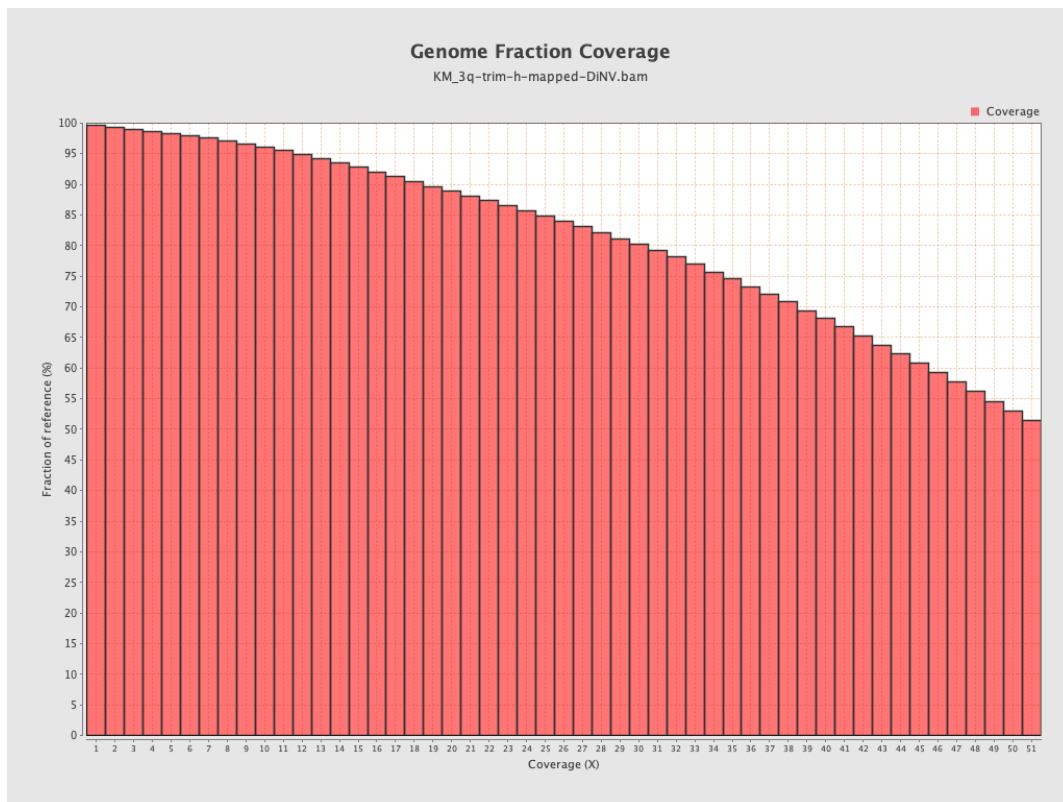
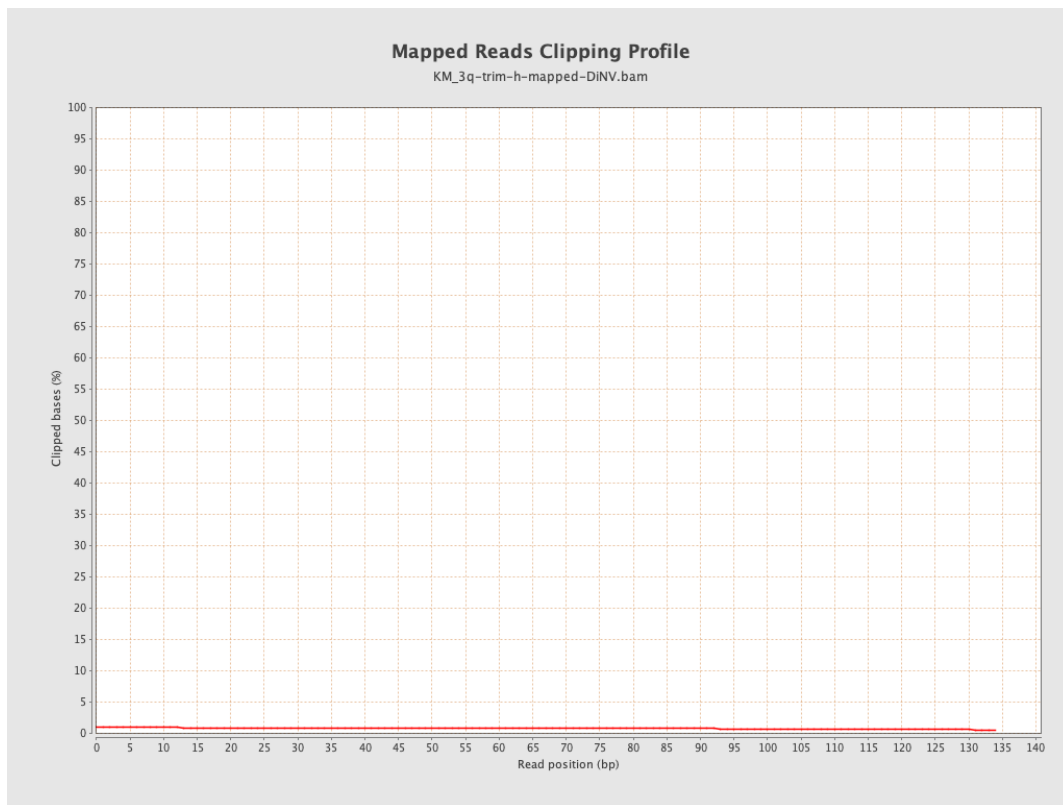# 7. Results : Duplication Rate Histogram

Duplication Rate Histogram
KM_3q-trim-h-mapped-DiNV.bam
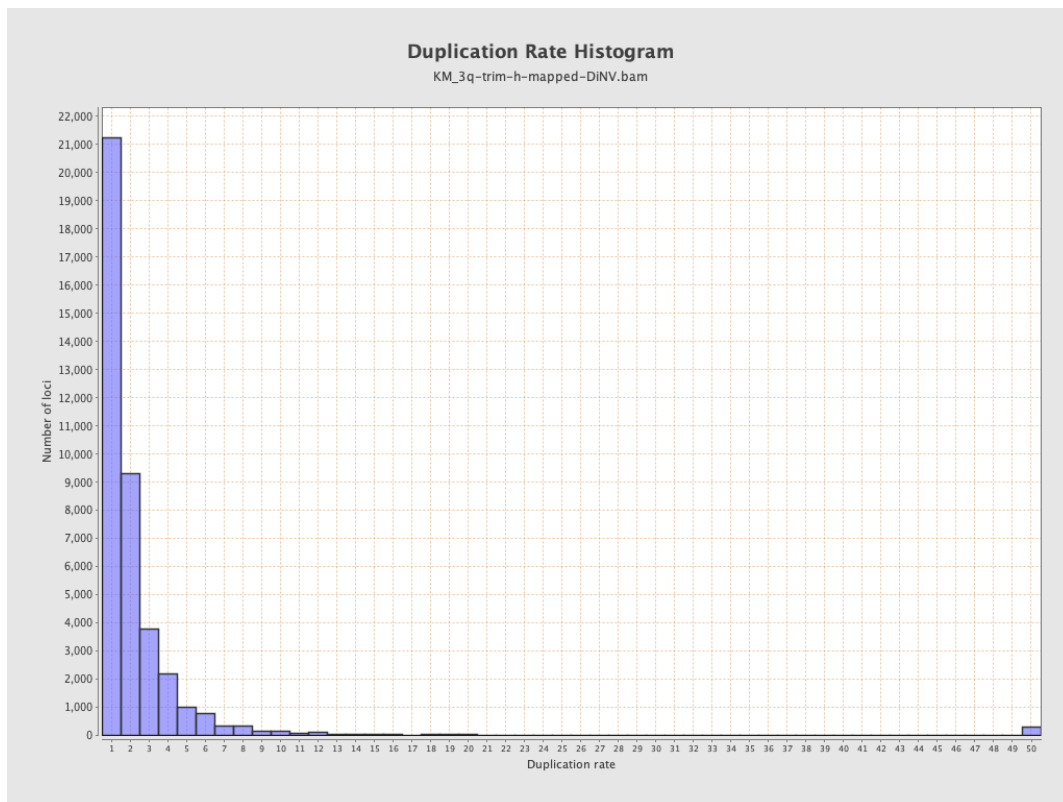
8. Results : Mapped Reads Nucleotide Content

# 9. Results : Mapped Reads GC-content Distribution
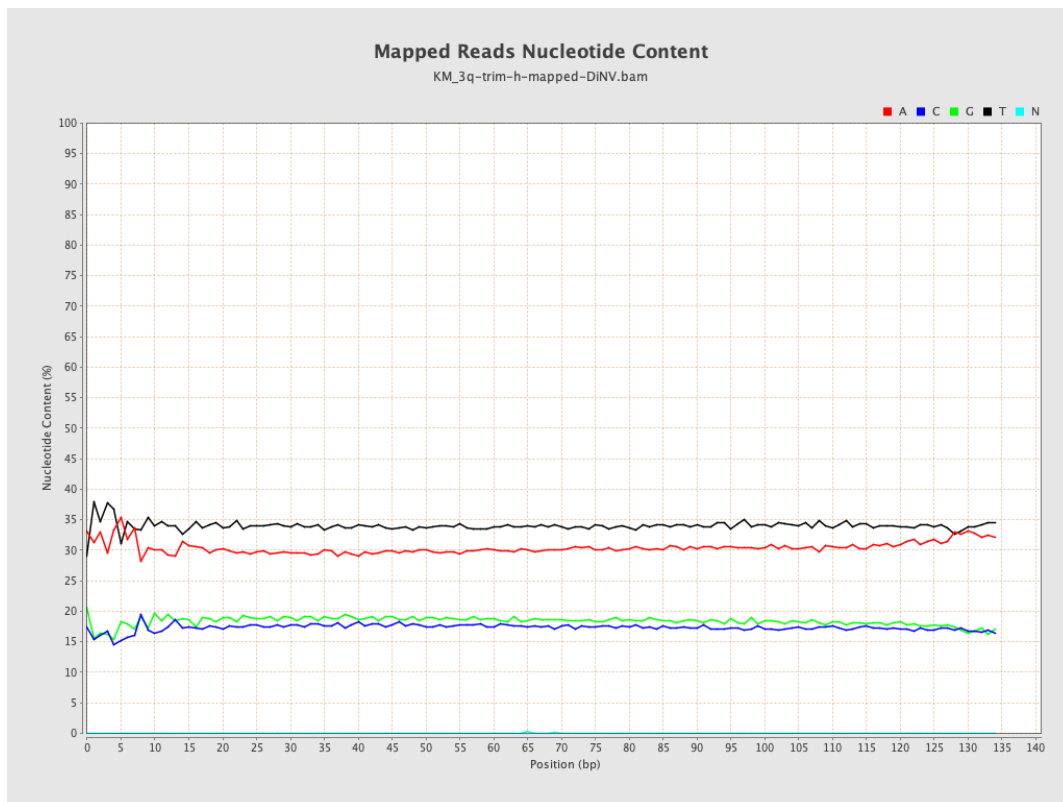
Mapped Reads GC-content Distribution
KM_3q-trim-h-mapped-DiNV.bam
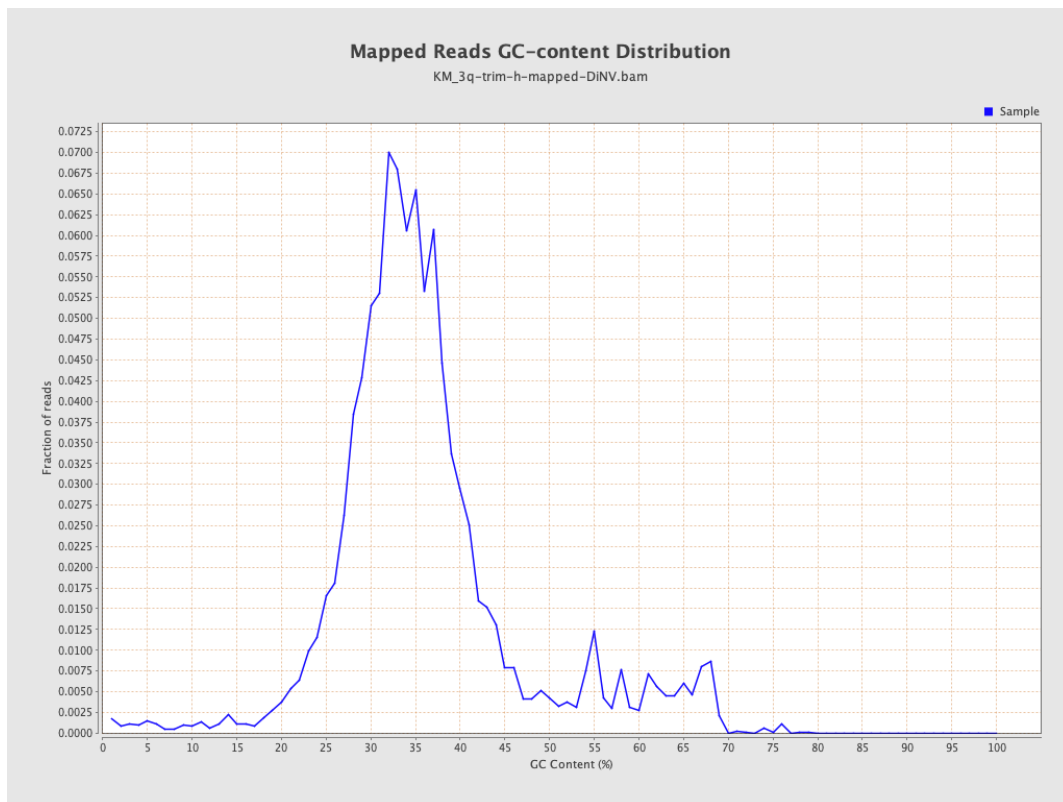
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
KM_3q-trim-h-mapped-DiNV.bam

11. Results : Homopolymer Indels
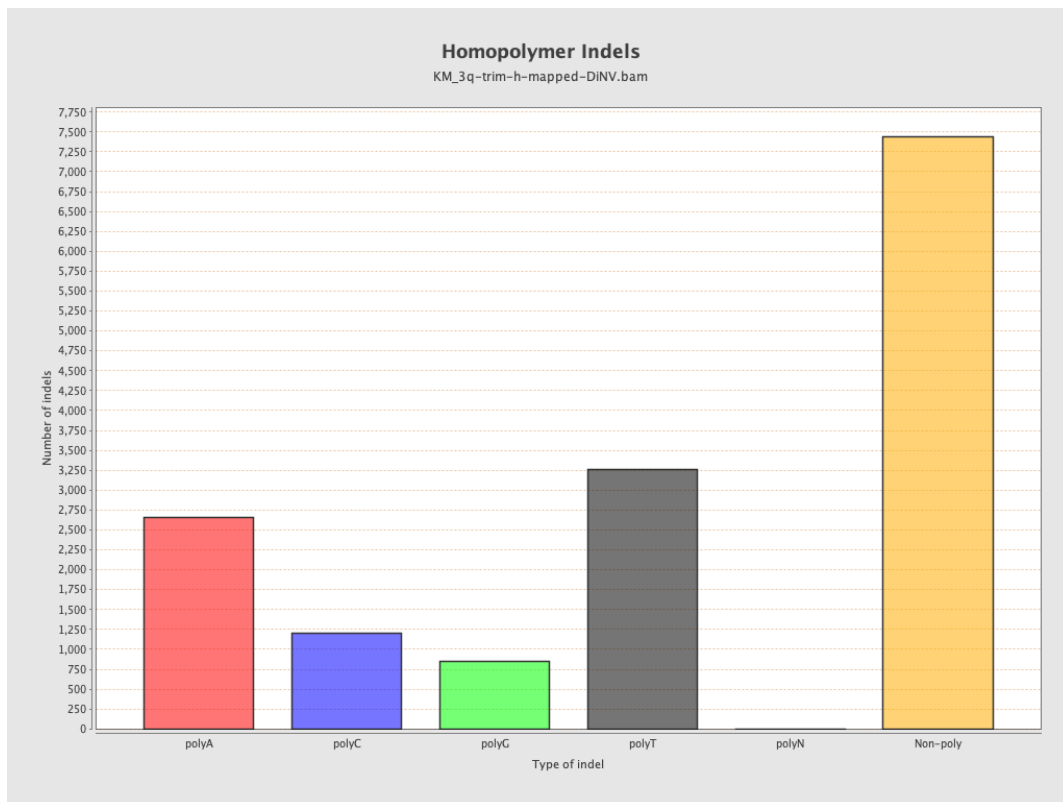
Homopolymer Indels
KM_3q-trim-h-mapped-DiNV.bam

12. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
KM_3q-trim-h-mapped-DiNV.bam

13. Results : Mapping Quality Histogram
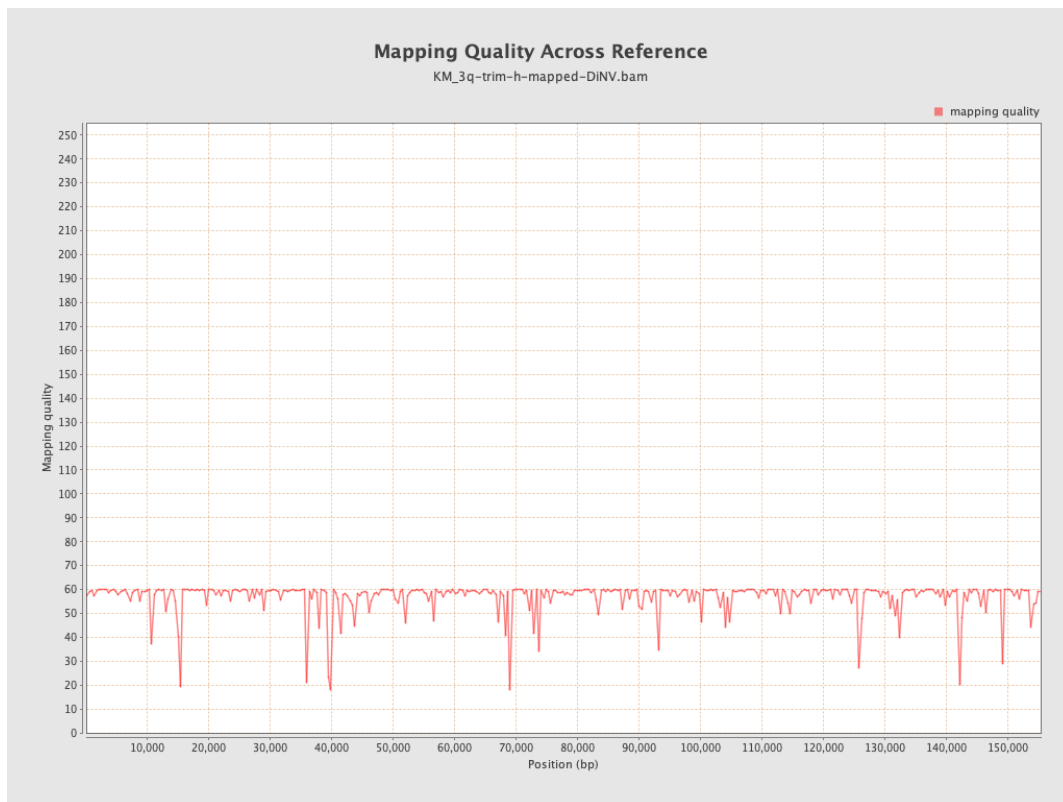
Mapping Quality Histogram
KM_3q-trim-h-mapped-DiNV.bam
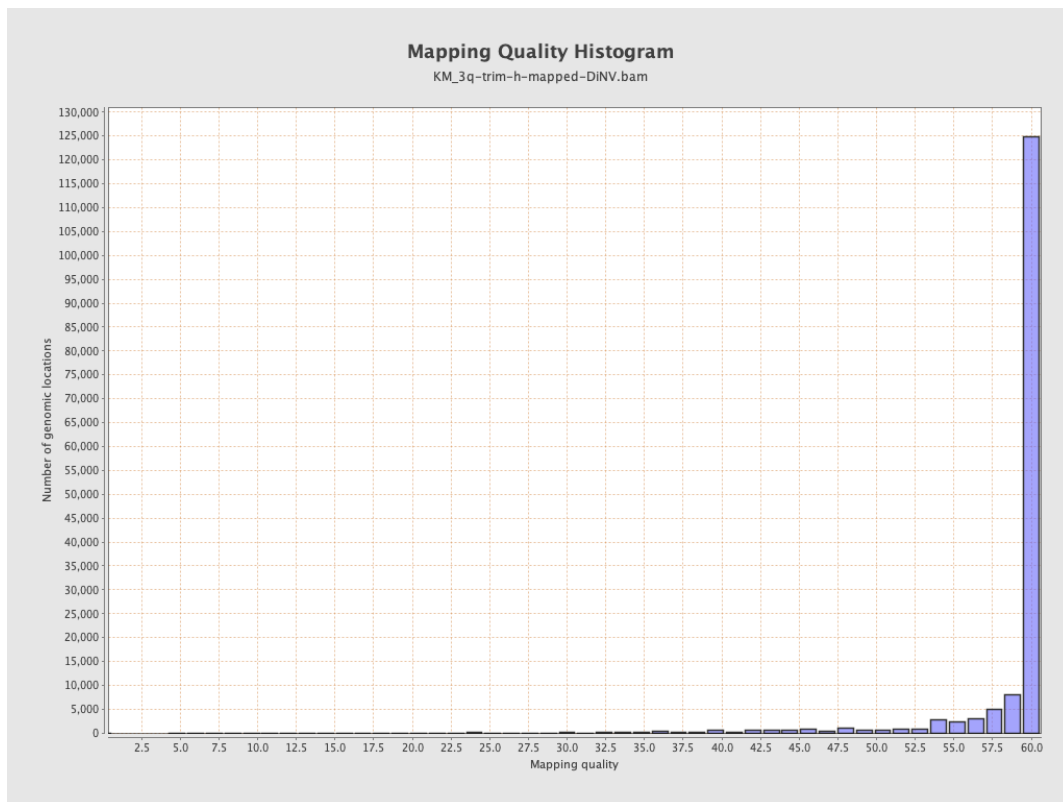
14. Results : Insert Size Across Reference

Insert Size Across Reference
KM_3q-trim-h-mapped-DiNV.bam
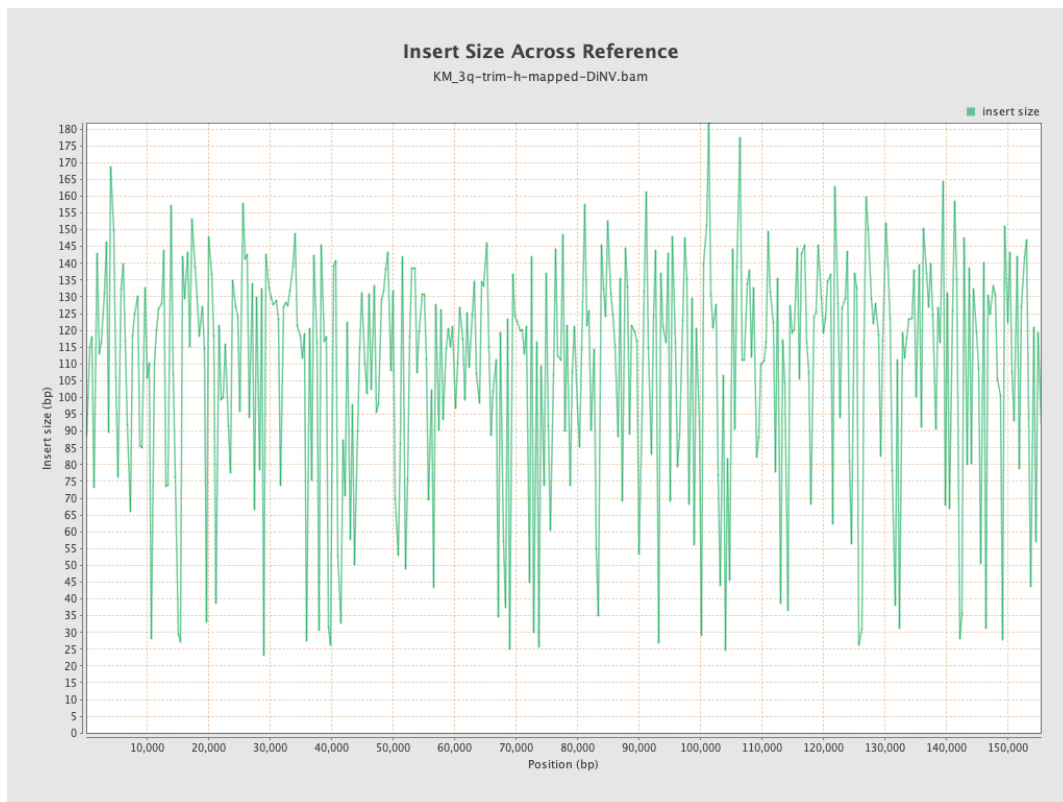
15. Results : Insert Size Histogram

Insert Size Histogram
KM_3q–trim–h–mapped–DiNV.bam