Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/17 11:23:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam 16Cq-trim-h-mapped-DiNV.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa mem GCF_004132165.1_DiNV_CH01M_genomic.fna 16Cq-DiNV-R1-trim.fastq.gz 16Cq-DiNV-R2-trim.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	yes
Program:	bwa (0.7.17-r1198-dirty)
Analysis date:	Wed May 17 11:23:32 CDT 2023
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	16Cq-trim-h-mapped-DiNV.bam

2. Summary

2.1. Globals

Reference size	155,555
Number of reads	25,260,892
Mapped reads	229,548 / 0.91%
Supplementary alignments	30 / 0%
Unmapped reads	25,031,344 / 99.09%
Mapped paired reads	229,548 / 0.91%
Mapped reads, first in pair	114,783 / 0.45%
Mapped reads, second in pair	114,765 / 0.45%
Mapped reads, both in pair	226,652 / 0.9%
Mapped reads, singletons	2,896 / 0.01%
Read min/max/mean length	15 / 136 / 130.94
Overlapping read pairs	109,101 / 0.86%
Duplicated reads (estimated)	209,356 / 0.83%
Duplication rate	34.67%
Clipped reads	211,853 / 0.84%

2.2. ACGT Content

Number/percentage of A's	2,118,455 / 29.68%
Number/percentage of C's	1,172,762 / 16.43%
Number/percentage of T's	2,536,355 / 35.53%
Number/percentage of G's	1,311,235 / 18.37%
Number/percentage of N's	12 / 0%

| GC Percentage | 34.8% |

2.3. Coverage

Mean	45.9443
Standard Deviation	471.9951
Mean (paired-end reads overlap ignored)	28.59

2.4. Mapping Quality

| Mean Mapping Quality | 53.74 |

2.5. Insert size

Mean	65.83
Standard Deviation	1,732.01
P25/Median/P75	19 / 21 / 25

2.6. Mismatches and indels

General error rate	0.97%
Mismatches	63,096
Insertions	2,313
Mapped reads with at least one insertion	0.94%
Deletions	2,445
Mapped reads with at least one deletion	0.98%
Homopolymer indels	36.74%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
NC_040699.1	155555	7146866	45.9443	471.9951

3. Results : Coverage across reference

Coverage across reference
16Cq-trim-h-mapped-DiNV.bam

4. Results : Coverage Histogram

Coverage Histogram
16Cq-trim-h-mapped-DiNV.bam

5. Results : Coverage Histogram (0-50X)
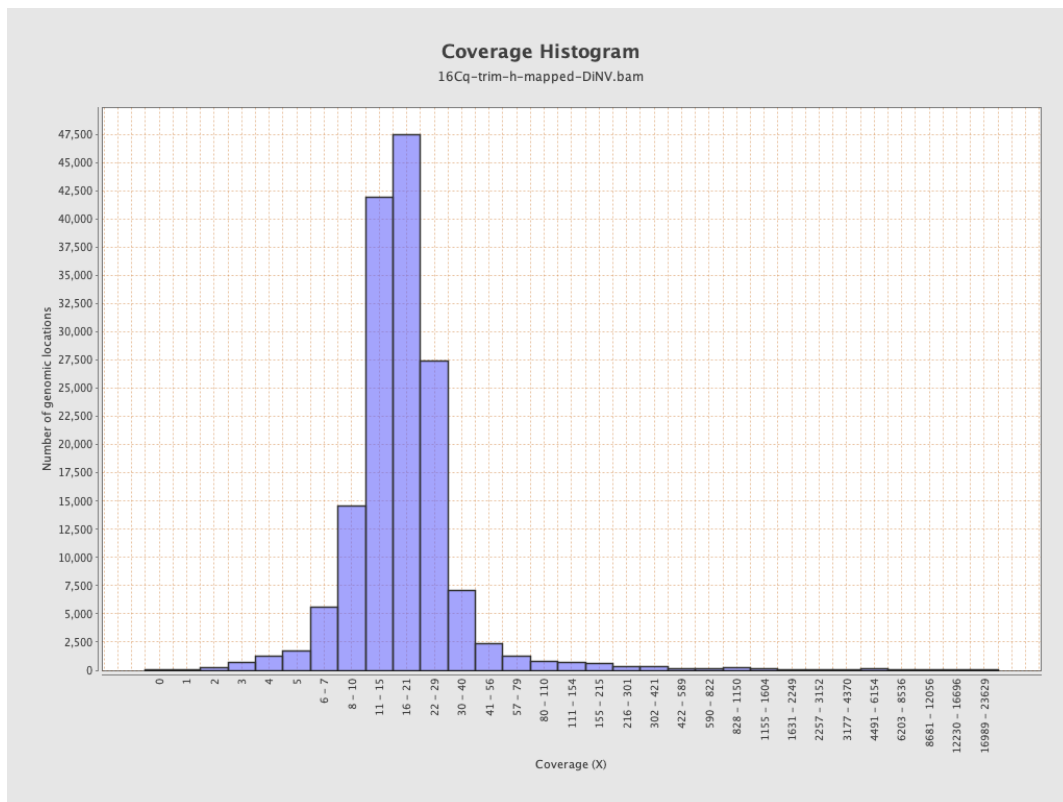
Coverage Histogram (0-50X)
16Cq-trim-h-mapped-DiNV.bam
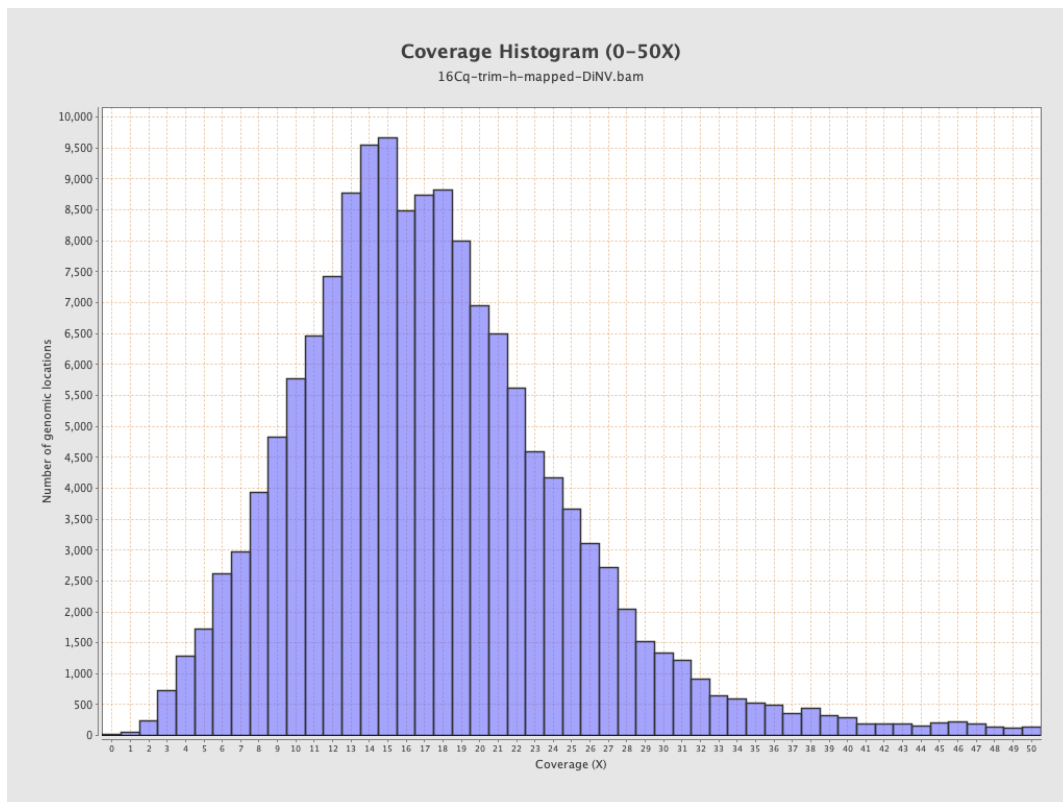
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
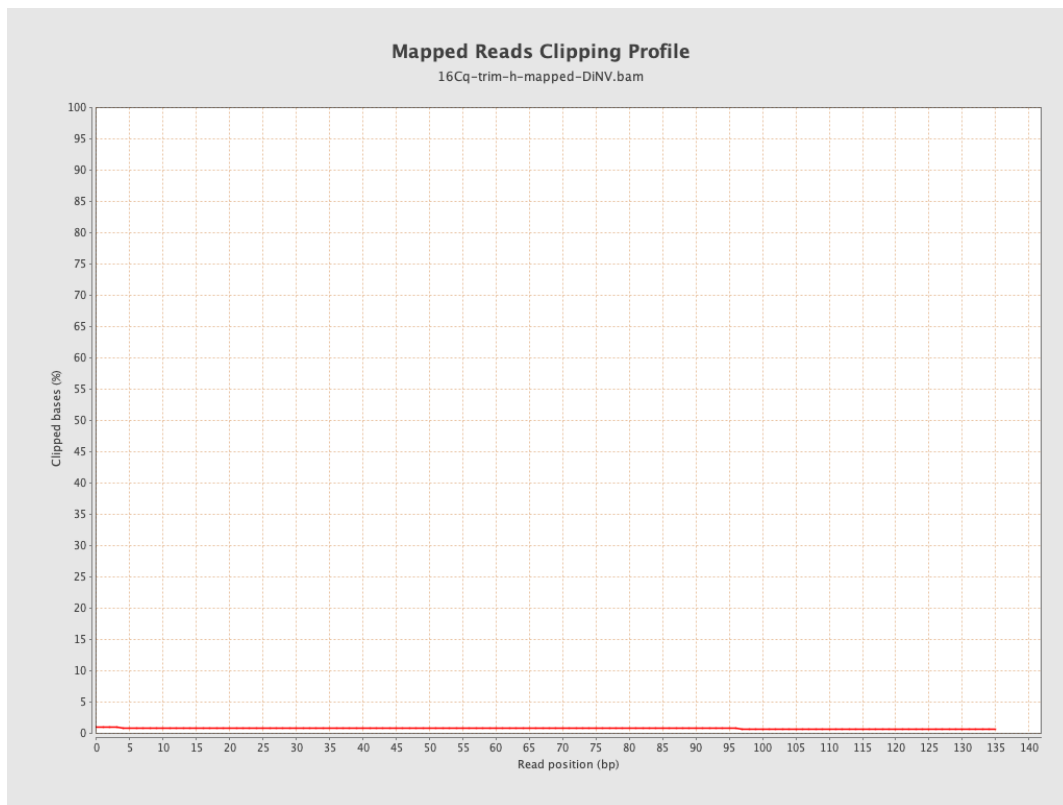16Cq-trim-h-mapped-DiNV.bam
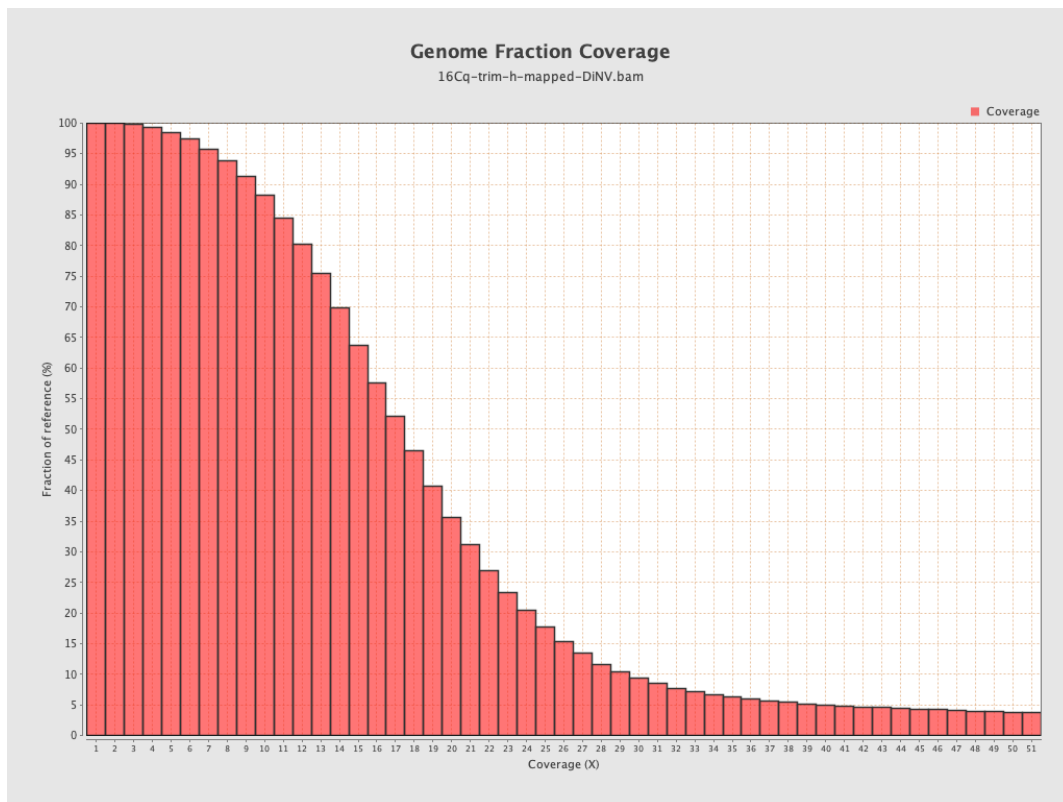
7. Results : Duplication Rate Histogram
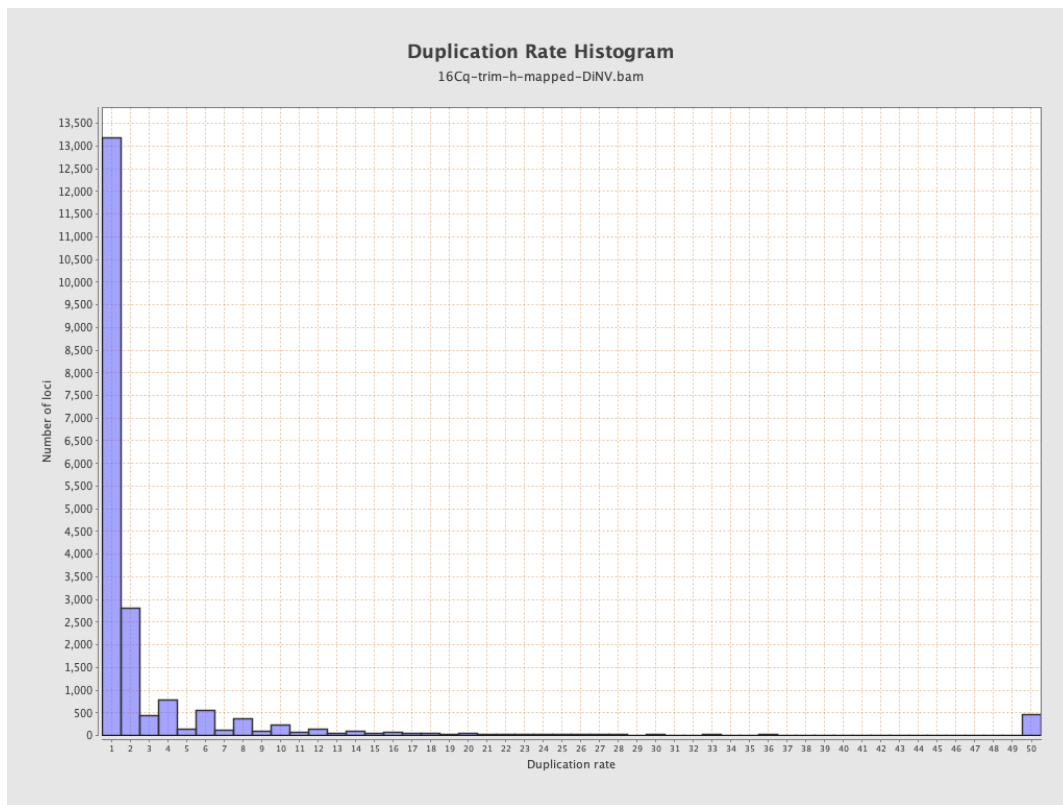
8. Results : Mapped Reads Nucleotide Content

9. Results : Mapped Reads GC-content Distribution
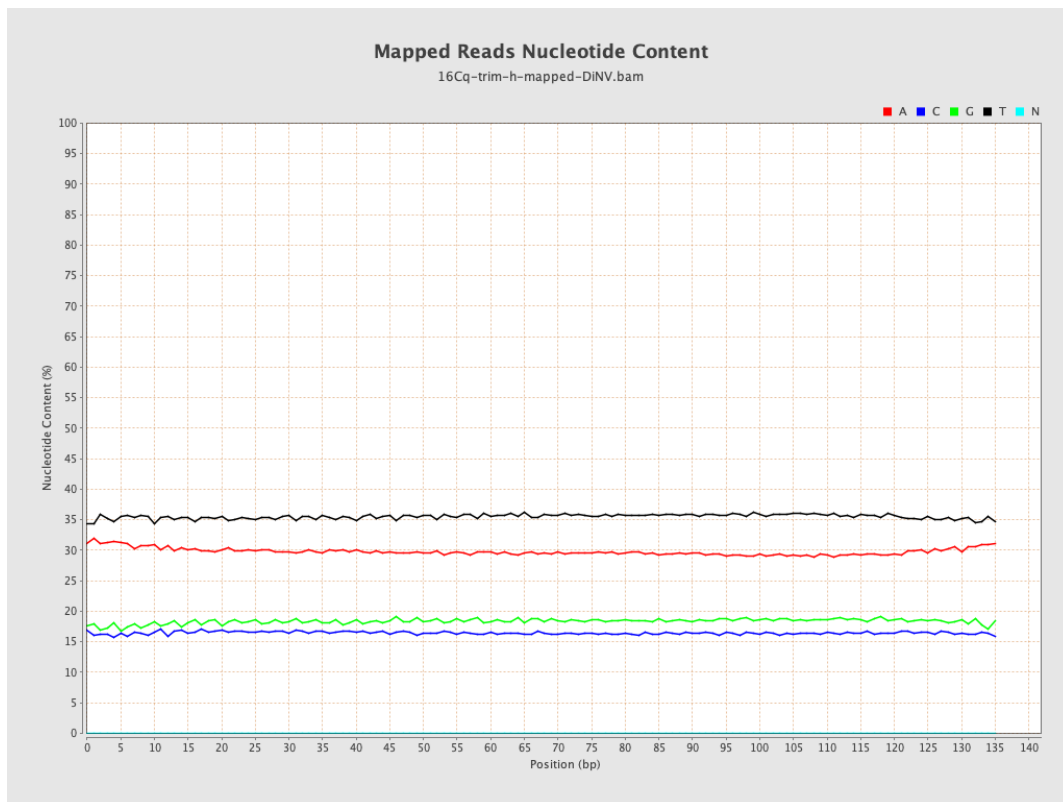
Mapped Reads GC-content Distribution
16Cq-trim-h-mapped-DiNV.bam
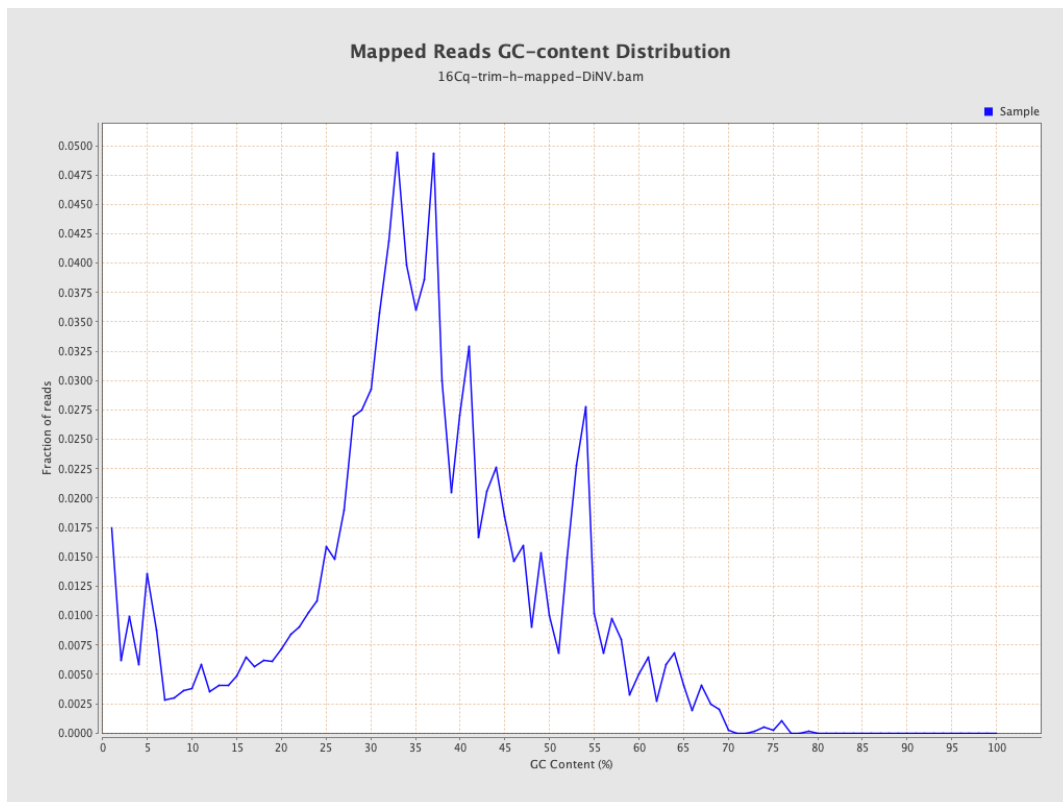
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
16Cq-trim-h-mapped-DiNV.bam

11. Results : Homopolymer Indels
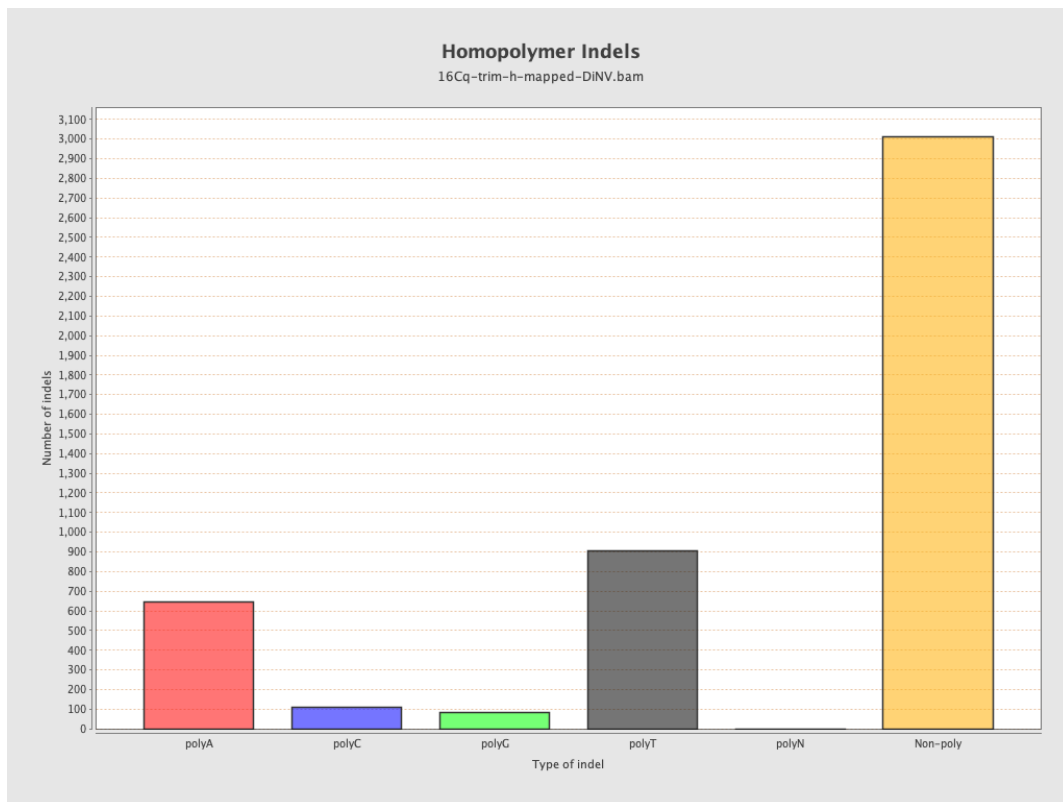
Homopolymer Indels
16Cq-trim-h-mapped-DiNV.bam

12. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
16Cq-trim-h-mapped-DiNV.bam

13. Results : Mapping Quality Histogram
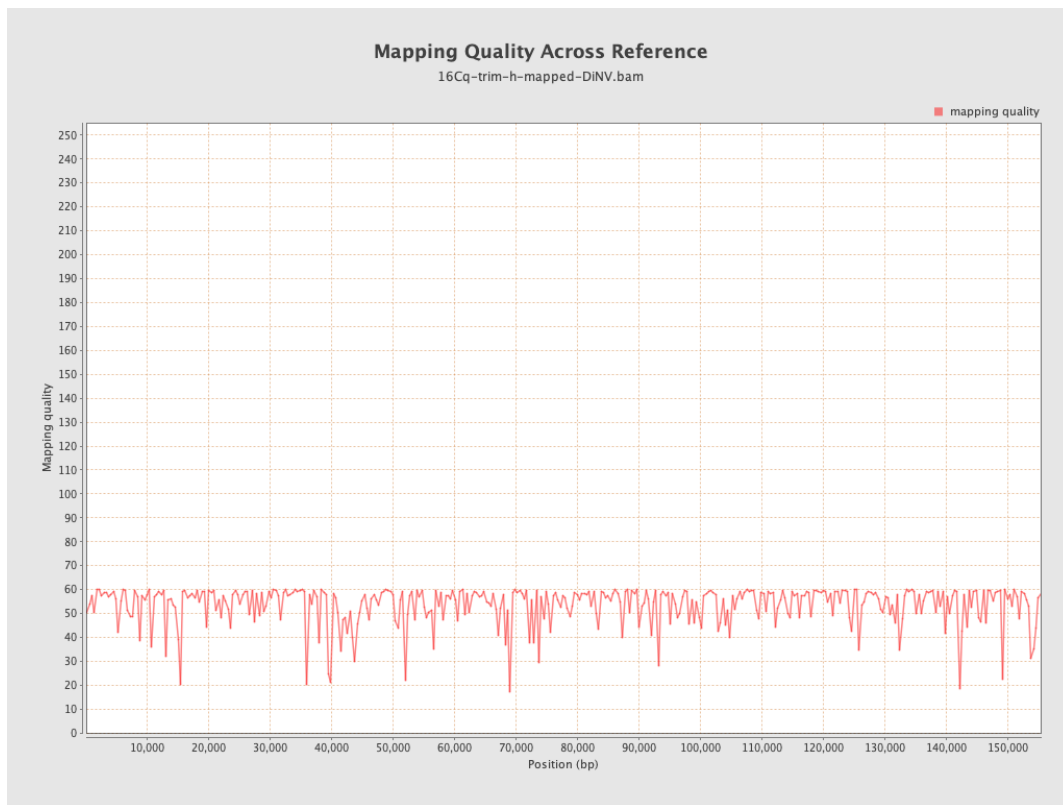
Mapping Quality Histogram
16Cq-trim-h-mapped-DiNV.bam
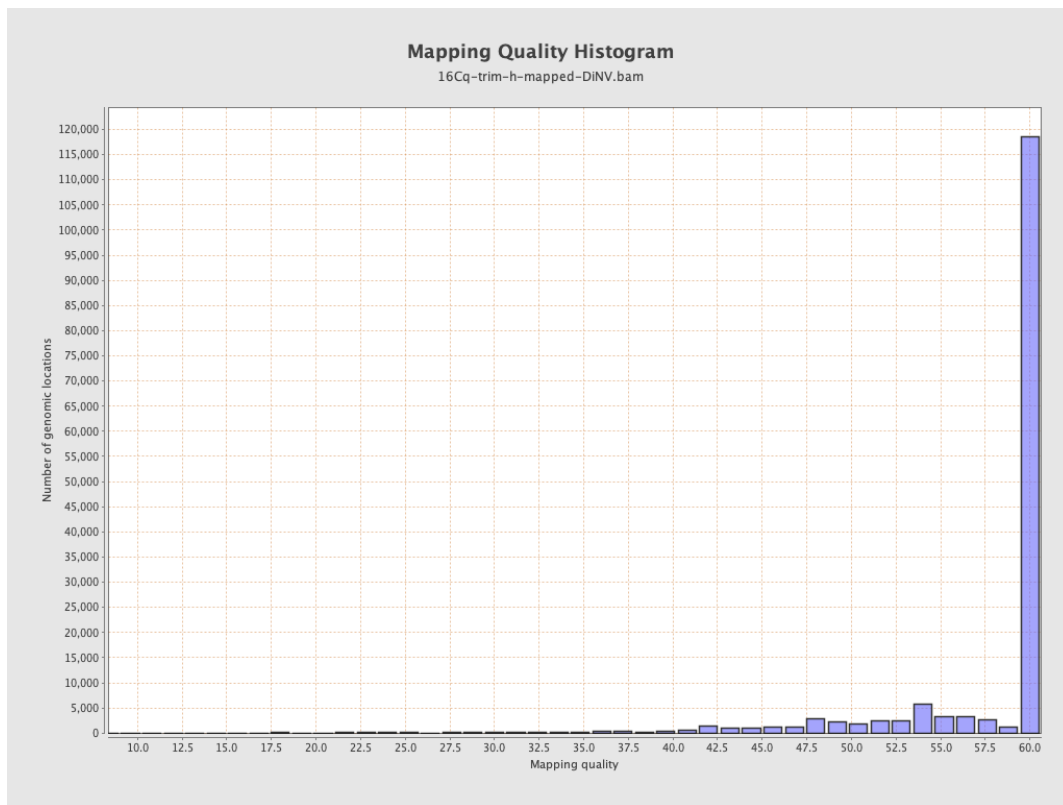
14. Results : Insert Size Across Reference
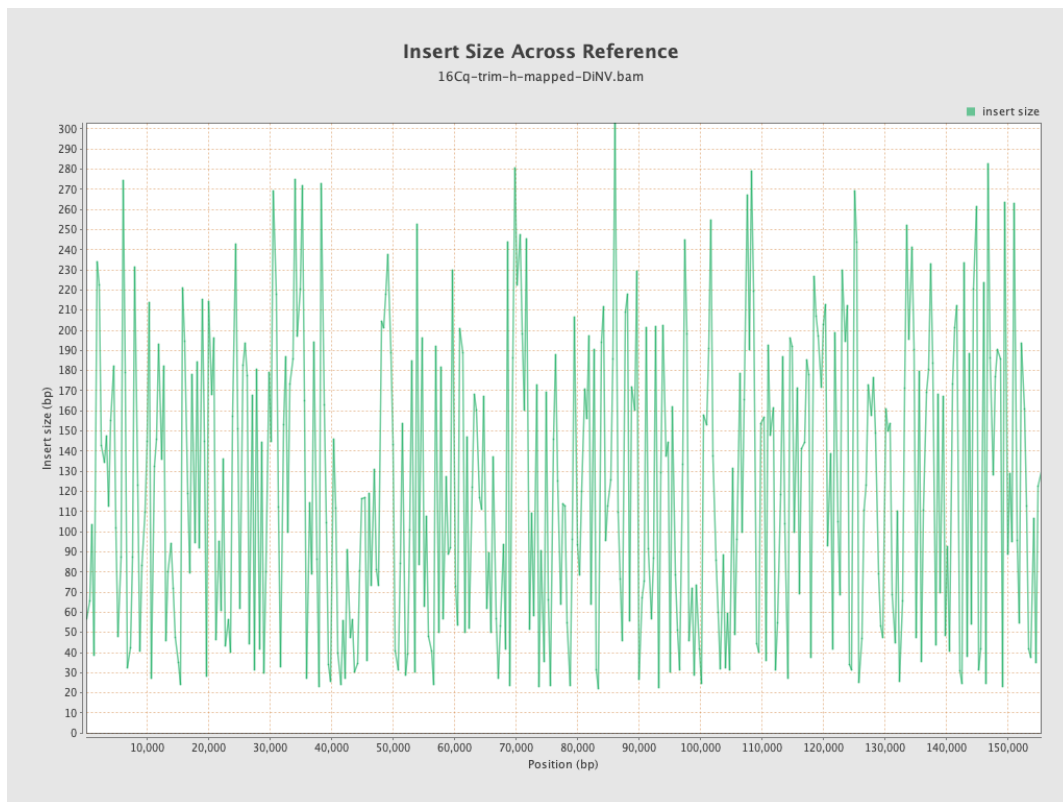
15. Results : Insert Size Histogram