

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/06/02 15:08:22

1. Input data & parameters

1.1. QualiMap command line

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

1.2. Alignment

Command line:	bwa mem -t 5 DiNV-Dinn.fna /Users/maggieschedl/Desktop/KU/se quences/16Cq-DiNV- Test/mapping/16Cq-DiNV-R1- trim.fastq.gz /Users/maggieschedl/Desktop/KU/se quences/16Cq-DiNV- Test/mapping/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:	Fri Jun 02 15:08:21 CDT 2023
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	16Cq-trim-h-mapped-DiNV-only.bam

2. Summary

2.1. Globals

Reference size	166,440,390
Number of reads	18,279
Mapped reads	18,276 / 99.98%
Supplementary alignments	28 / 0.15%
Unmapped reads	3 / 0.02%
Mapped paired reads	18,276 / 99.98%
Mapped reads, first in pair	9,134 / 49.97%
Mapped reads, second in pair	9,142 / 50.01%
Mapped reads, both in pair	18,273 / 99.97%
Mapped reads, singletons	3 / 0.02%
Read min/max/mean length	30 / 136 / 131.69
Overlapping read pairs	5,756 / 62.98%
Duplicated reads (estimated)	2,730 / 14.94%
Duplication rate	14.88%
Clipped reads	582 / 3.18%

2.2. ACGT Content

Number/percentage of A's	812,478 / 34.01%
Number/percentage of C's	369,032 / 15.45%
Number/percentage of T's	828,706 / 34.69%
Number/percentage of G's	378,399 / 15.84%
Number/percentage of N's	2 / 0%

GC Percentage	31.29%
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2.3. Coverage

Mean	0.0144
Standard Deviation	0.5048
Mean (paired-end reads overlap ignored)	0.01

2.4. Mapping Quality

Mean Mapping Quality	0.15
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2.5. Insert size

Mean	438.66
Standard Deviation	5,453.64
P25/Median/P75	159 / 230 / 312

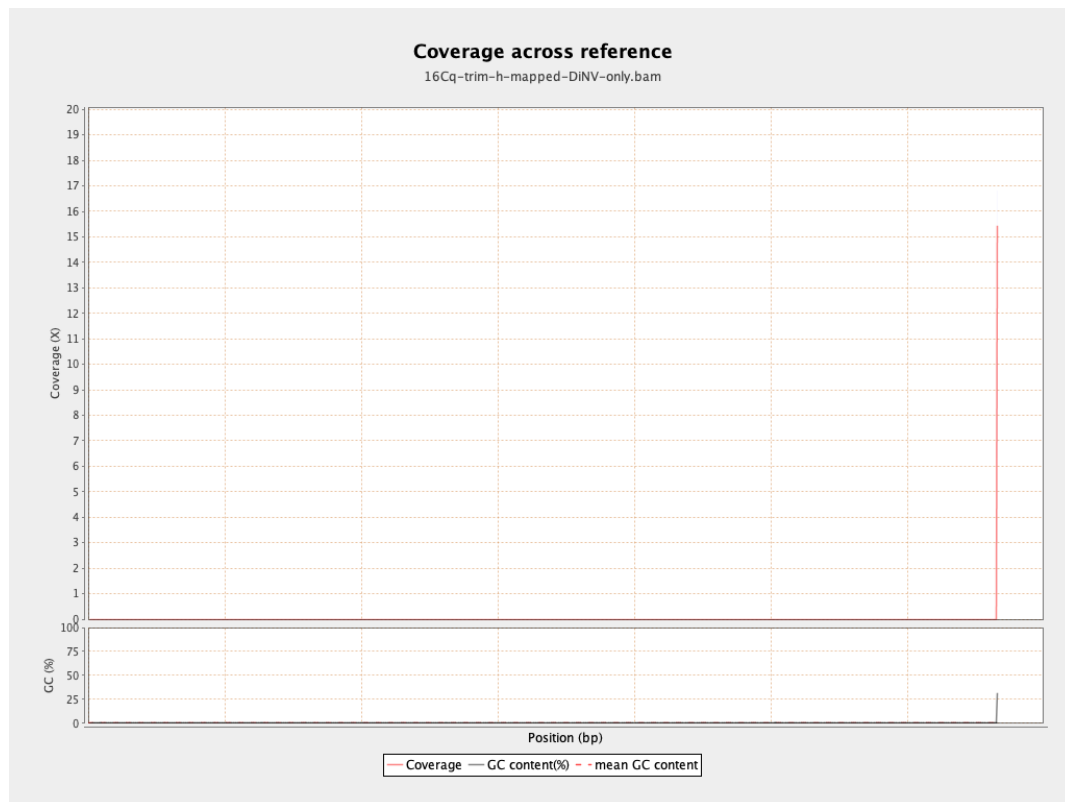
2.6. Mismatches and indels

General error rate	0.88%
Mismatches	17,348
Insertions	1,226
Mapped reads with at least one insertion	6%
Deletions	1,450
Mapped reads with at least one deletion	6.87%
Homopolymer indels	53.48%

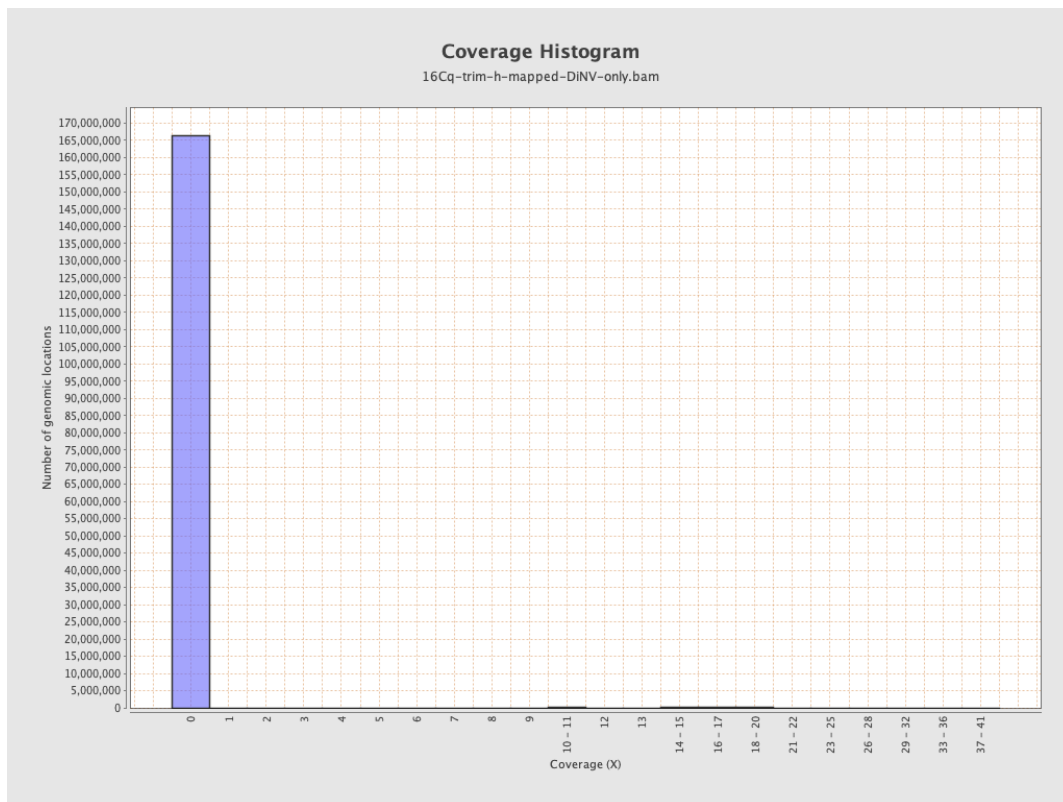
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
CM015045.2	2027030	0	0	0
CM027941.1	29570401	0	0	0
SKCT020000 06.1	8037050	0	0	0
CM027942.1	25683278	0	0	0
CM027943.1	27707068	0	0	0
CM027944.1	32746462	0	0	0
SKCT020000 08.1	18452	0	0	0
CM015046.2	40478903	0	0	0
CM015047.1	16191	0	0	0
NC_040699.1	155555	2393481	15.3867	6.0938

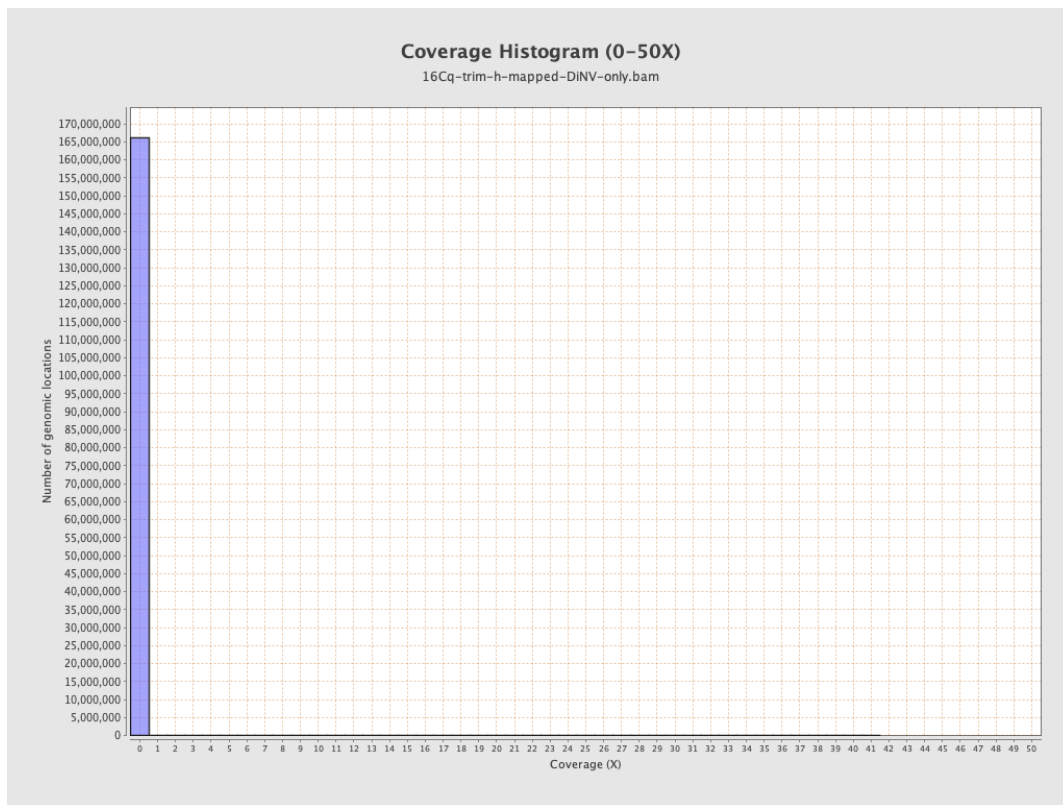
3. Results : Coverage across reference



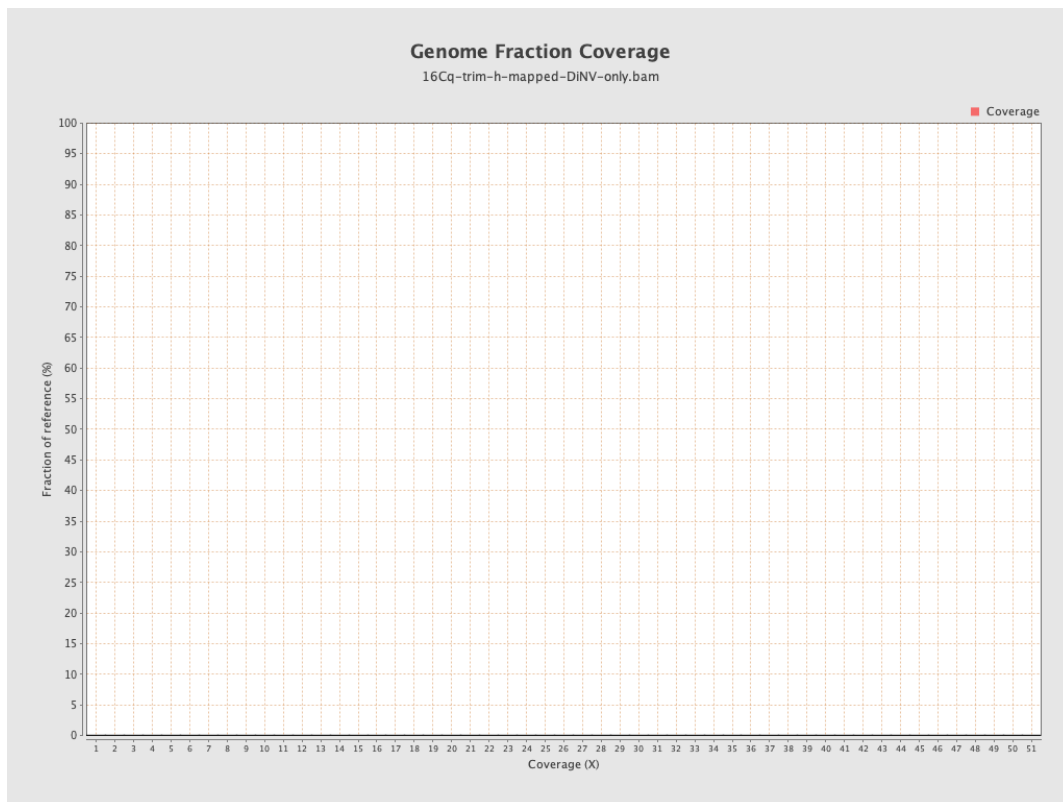
4. Results : Coverage Histogram



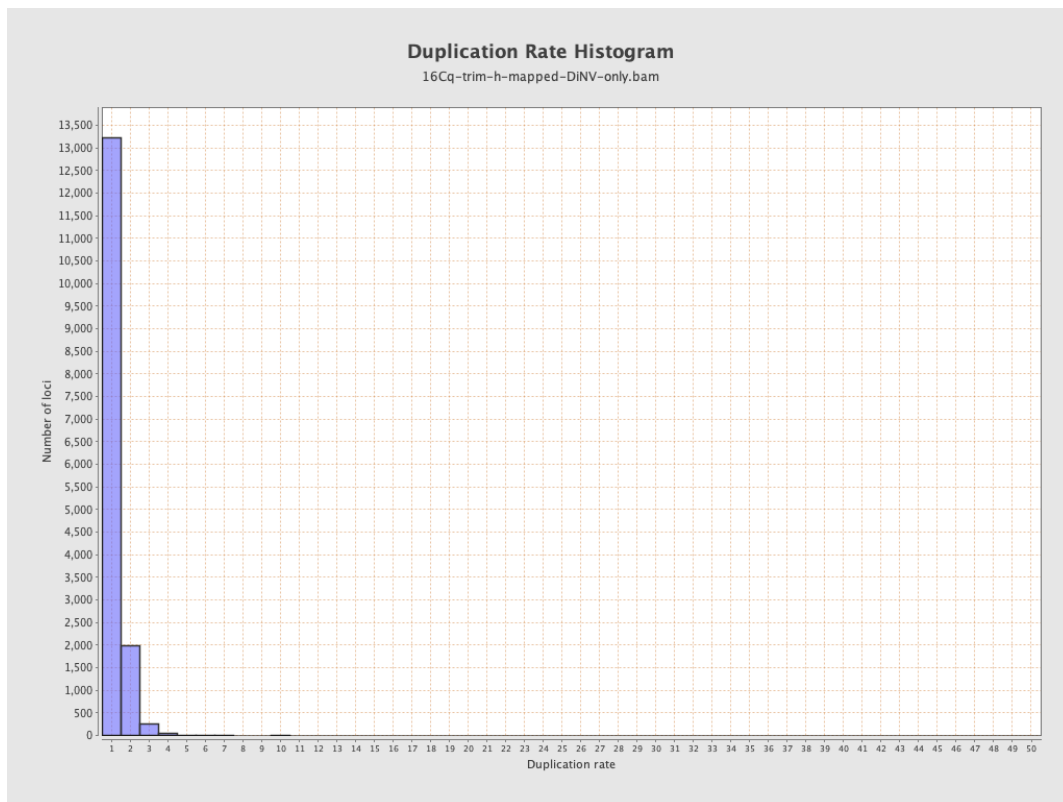
5. Results : Coverage Histogram (0-50X)



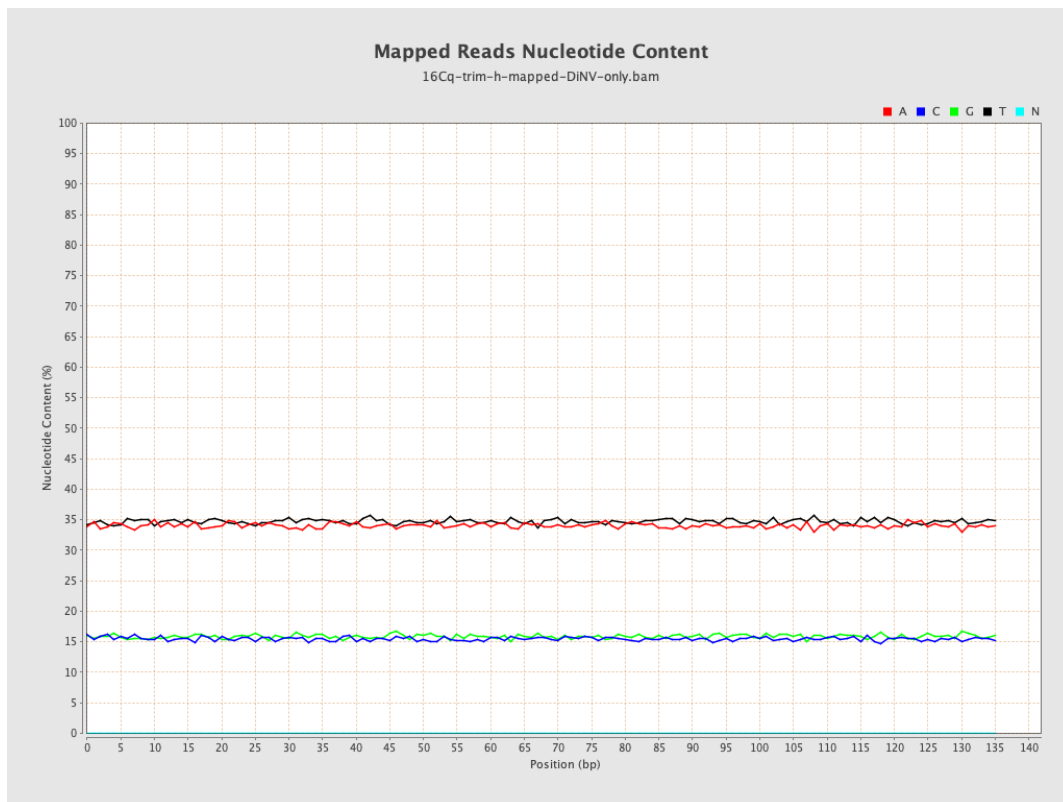
6. Results : Genome Fraction Coverage



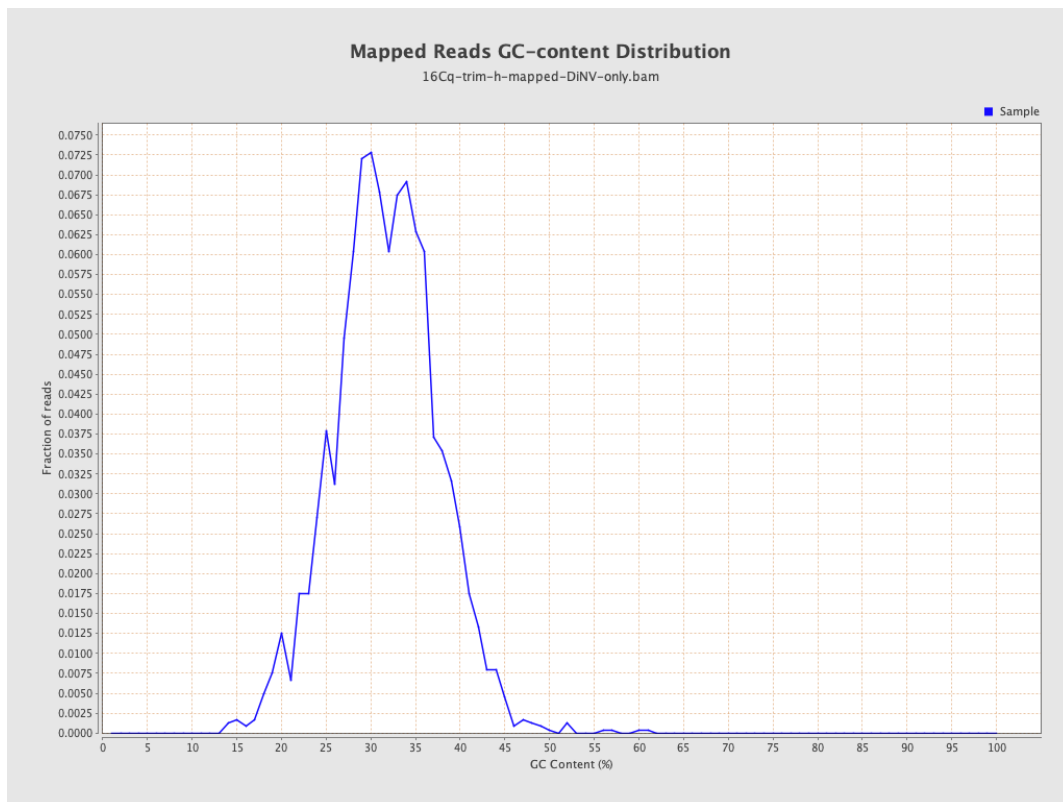
7. Results : Duplication Rate Histogram



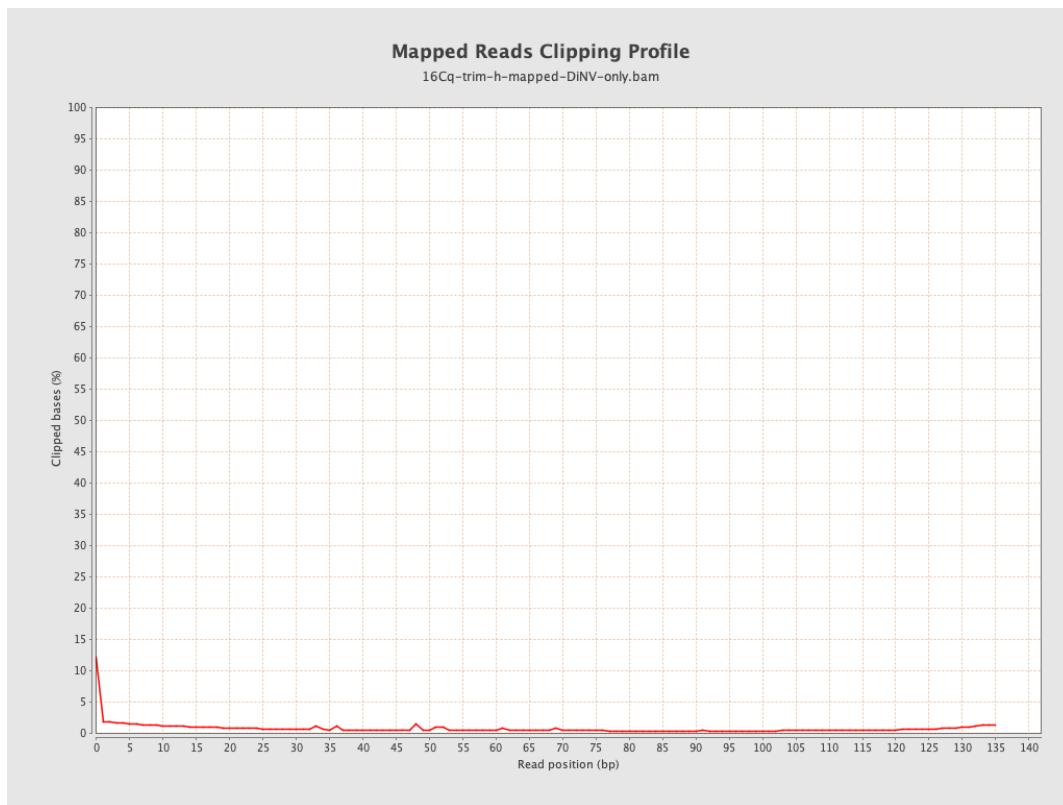
8. Results : Mapped Reads Nucleotide Content



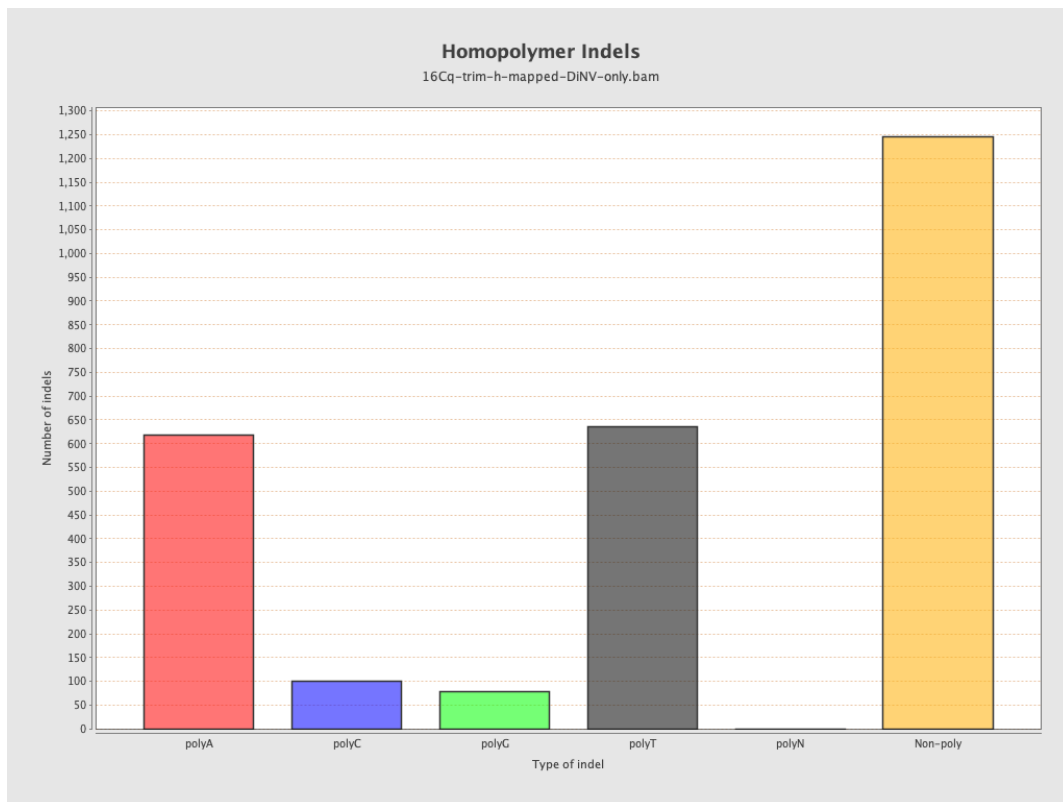
9. Results : Mapped Reads GC-content Distribution



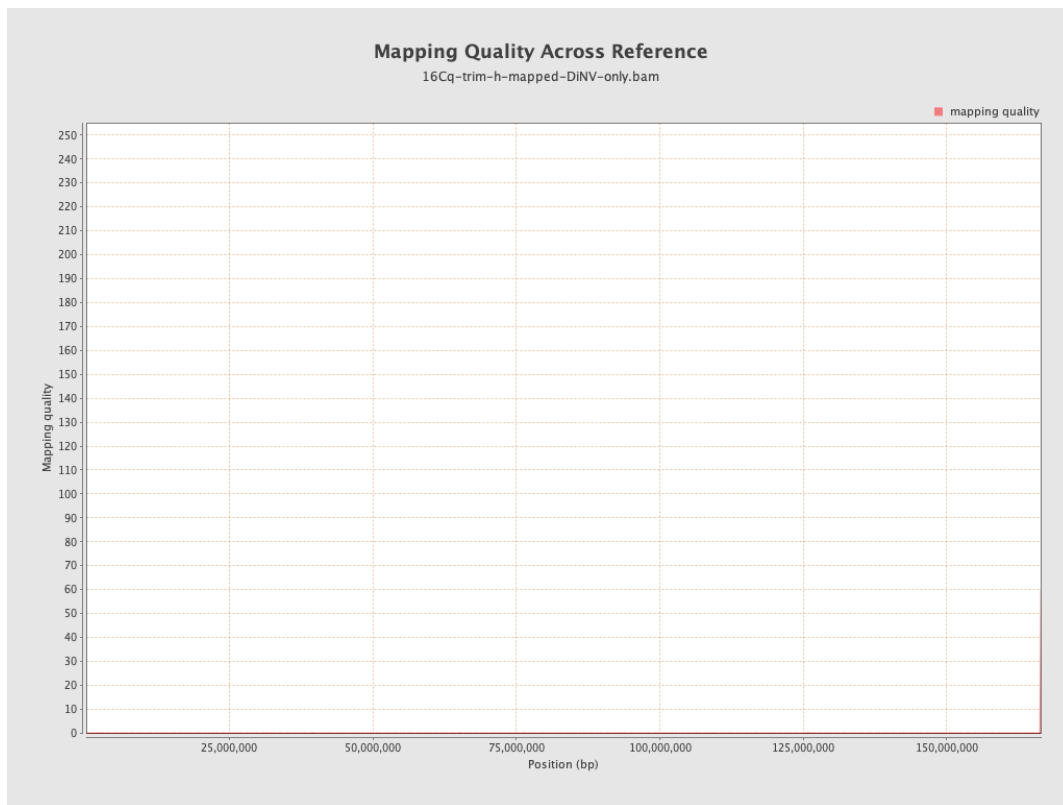
10. Results : Mapped Reads Clipping Profile



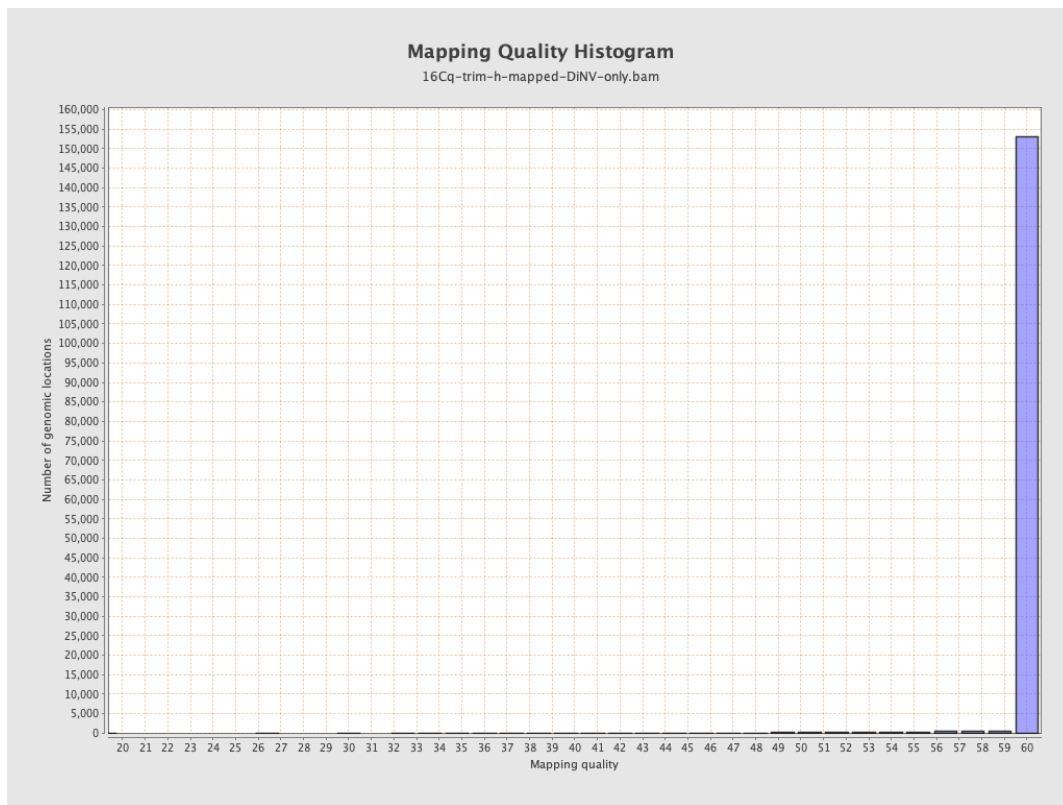
11. Results : Homopolymer Indels



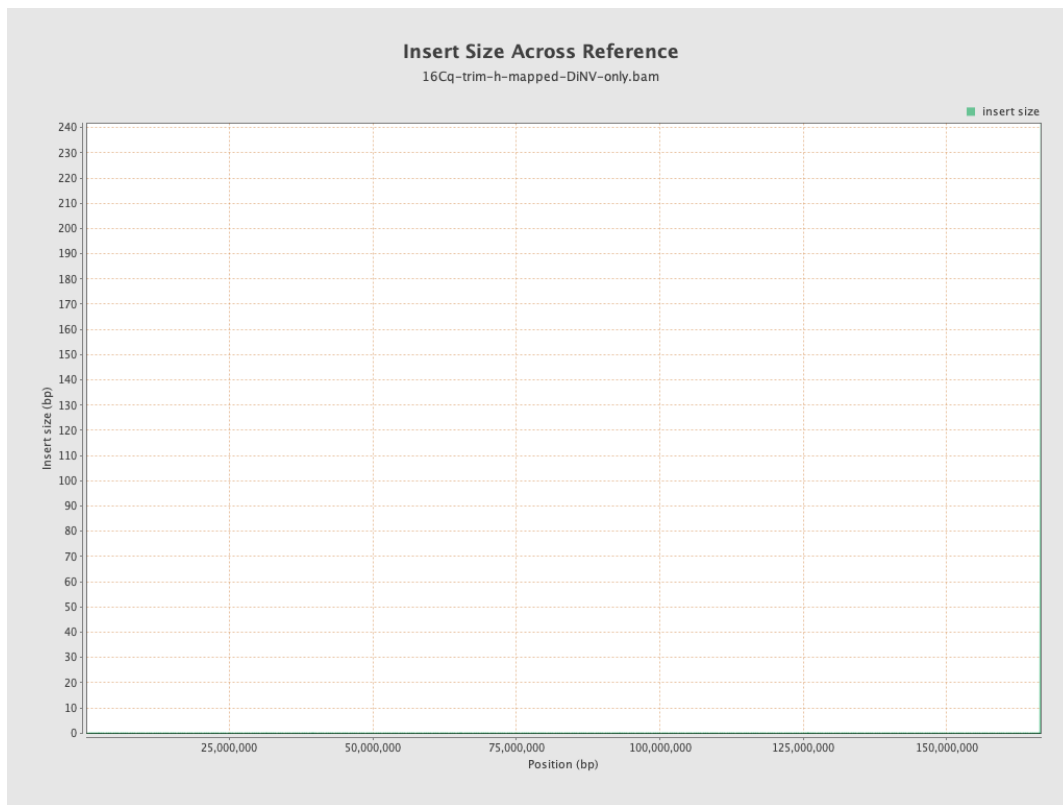
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

