

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/05/17 11:25:16

1. Input data & parameters

1.1. QualiMap command line

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

1.2. Alignment

Command line:	bwa mem -t 5 GCA_004354385.2_ASM435438v2_ 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 11:25:15 CDT 2023
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	16Cq-trim-h-mapped-inn.bam

2. Summary

2.1. Globals

Reference size	166,284,835
Number of reads	25,400,829
Mapped reads	25,297,592 / 99.59%
Supplementary alignments	139,967 / 0.55%
Unmapped reads	103,237 / 0.41%
Mapped paired reads	25,297,592 / 99.59%
Mapped reads, first in pair	12,649,285 / 49.8%
Mapped reads, second in pair	12,648,307 / 49.79%
Mapped reads, both in pair	25,284,984 / 99.54%
Mapped reads, singletons	12,608 / 0.05%
Read min/max/mean length	15 / 136 / 130.5
Overlapping read pairs	7,997,131 / 62.97%
Duplicated reads (estimated)	6,288,305 / 24.76%
Duplication rate	17.04%
Clipped reads	1,139,527 / 4.49%

2.2. ACGT Content

Number/percentage of A's	1,006,449,719 / 30.78%
Number/percentage of C's	621,513,124 / 19.01%
Number/percentage of T's	1,002,751,215 / 30.67%
Number/percentage of G's	638,697,266 / 19.54%
Number/percentage of N's	11,376 / 0%

GC Percentage	38.55%
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2.3. Coverage

Mean	19.6689
Standard Deviation	151.4536
Mean (paired-end reads overlap ignored)	15.99

2.4. Mapping Quality

Mean Mapping Quality	55.61
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2.5. Insert size

Mean	23,984.93
Standard Deviation	560,080.6
P25/Median/P75	154 / 226 / 309

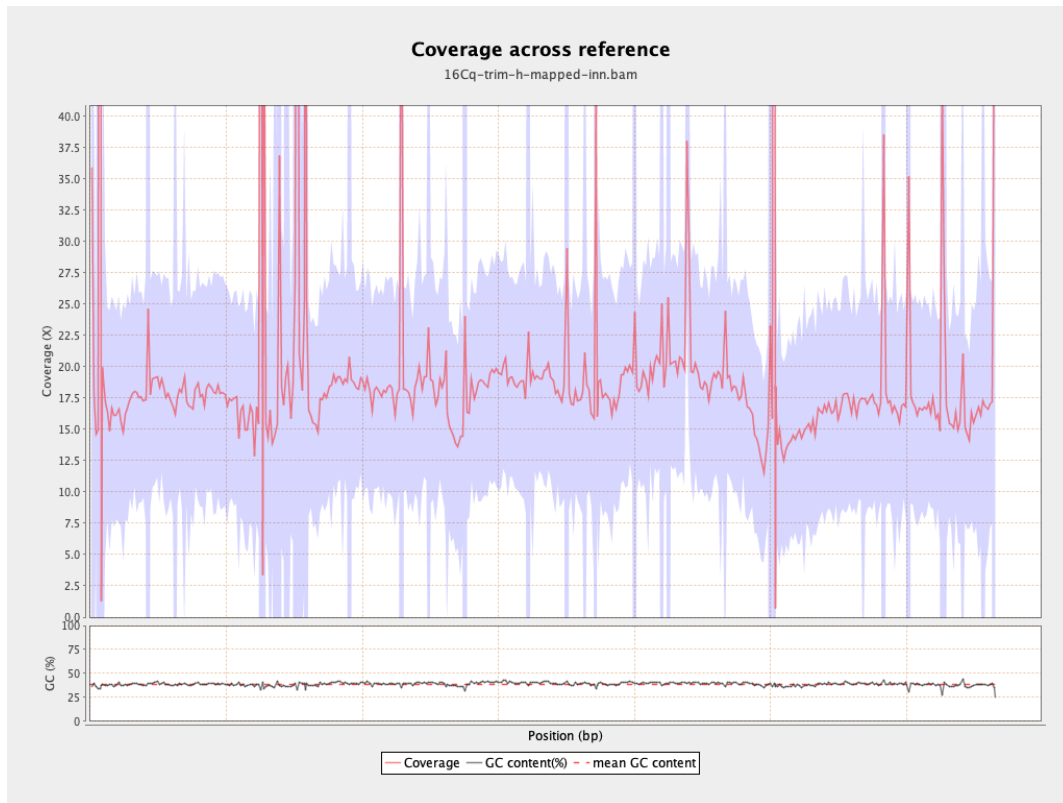
2.6. Mismatches and indels

General error rate	0.5%
Mismatches	15,147,000
Insertions	550,998
Mapped reads with at least one insertion	1.98%
Deletions	506,566
Mapped reads with at least one deletion	1.59%
Homopolymer indels	55.88%

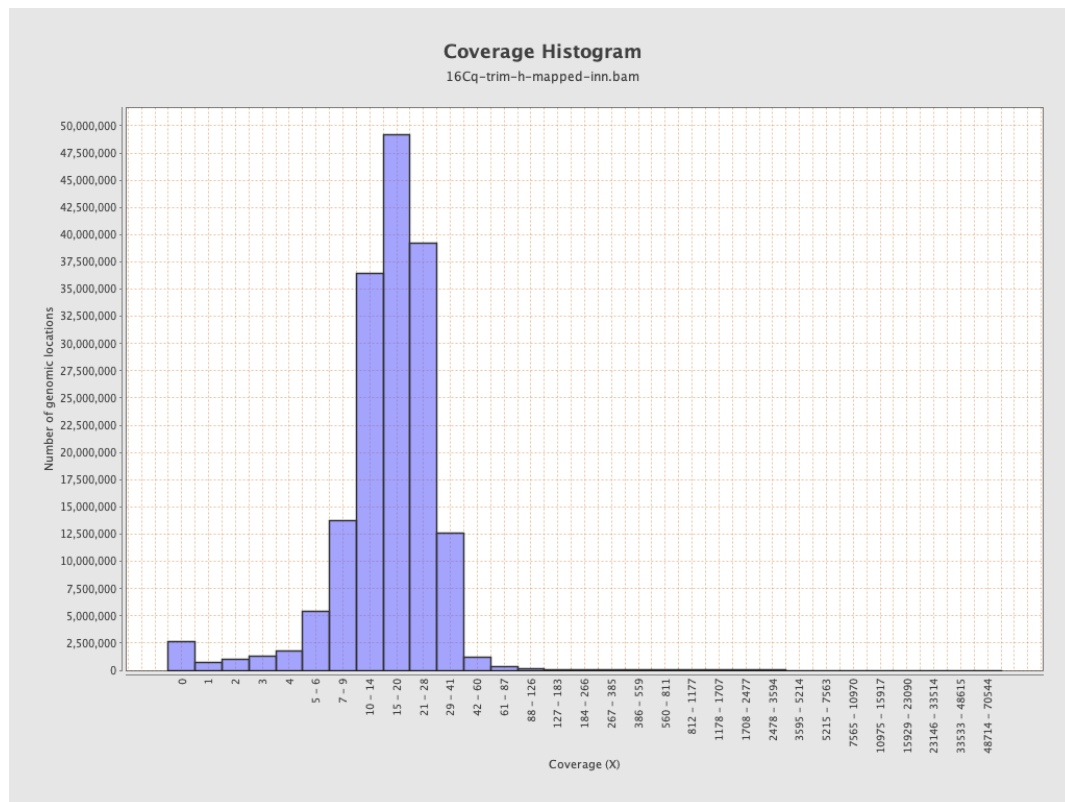
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
CM015045.2	2027030	113532123	56.0091	1,027.2899
CM027941.1	29570401	543568229	18.3822	54.5473
SKCT020000 06.1	8037050	214902975	26.739	209.1097
CM027942.1	25683278	487265698	18.9721	80.1513
CM027943.1	27707068	518200599	18.7028	56.3586
CM027944.1	32746462	687560805	20.9965	70.9192
SKCT020000 08.1	18452	13614	0.7378	2.0554
CM015046.2	40478903	703437964	17.3779	141.8299
CM015047.1	16191	2154058	133.0405	72.457

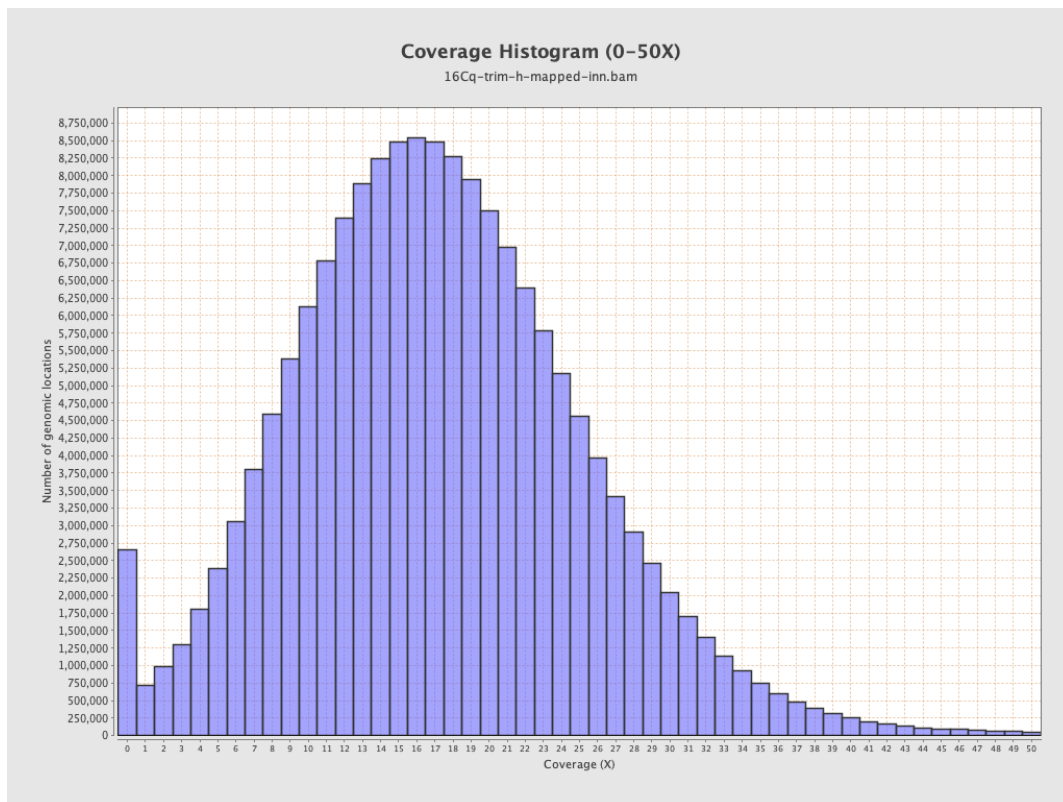
3. Results : Coverage across reference



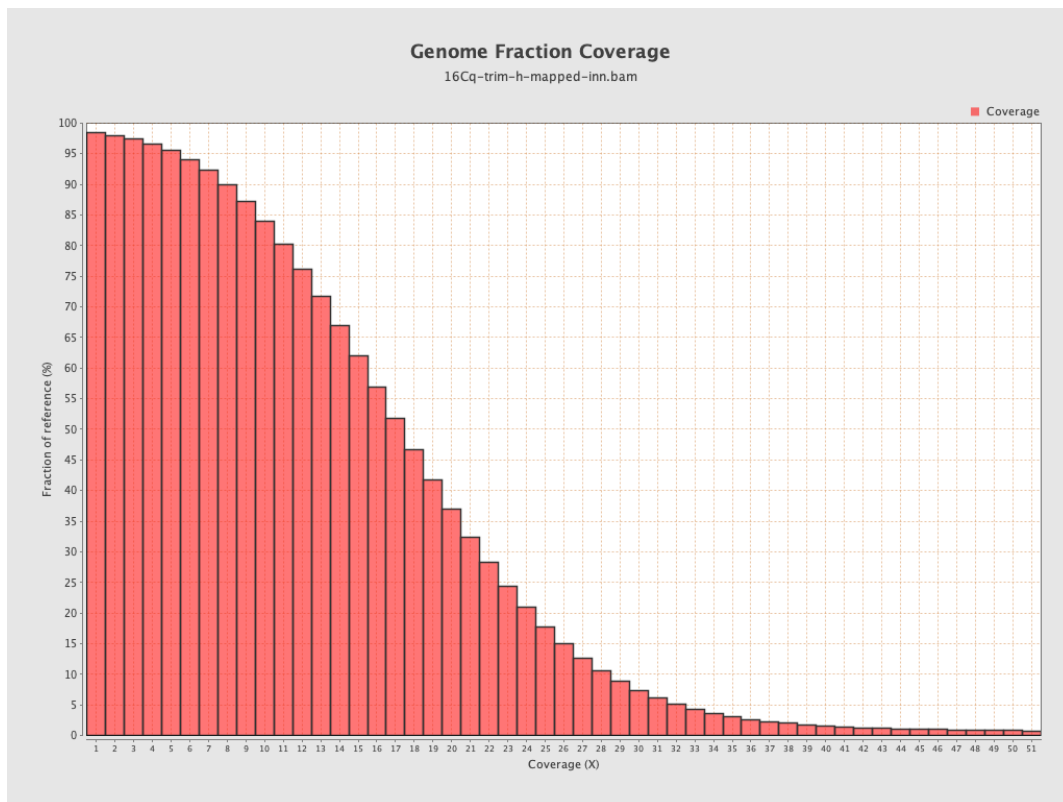
4. Results : Coverage Histogram



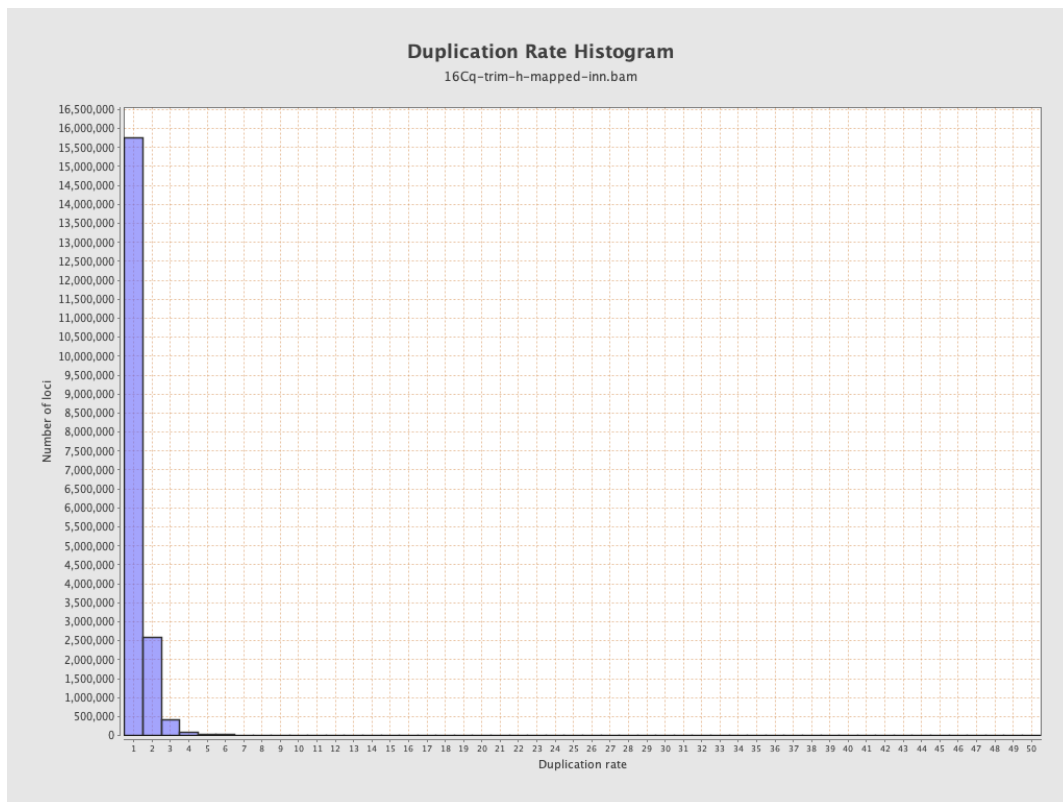
5. Results : Coverage Histogram (0-50X)



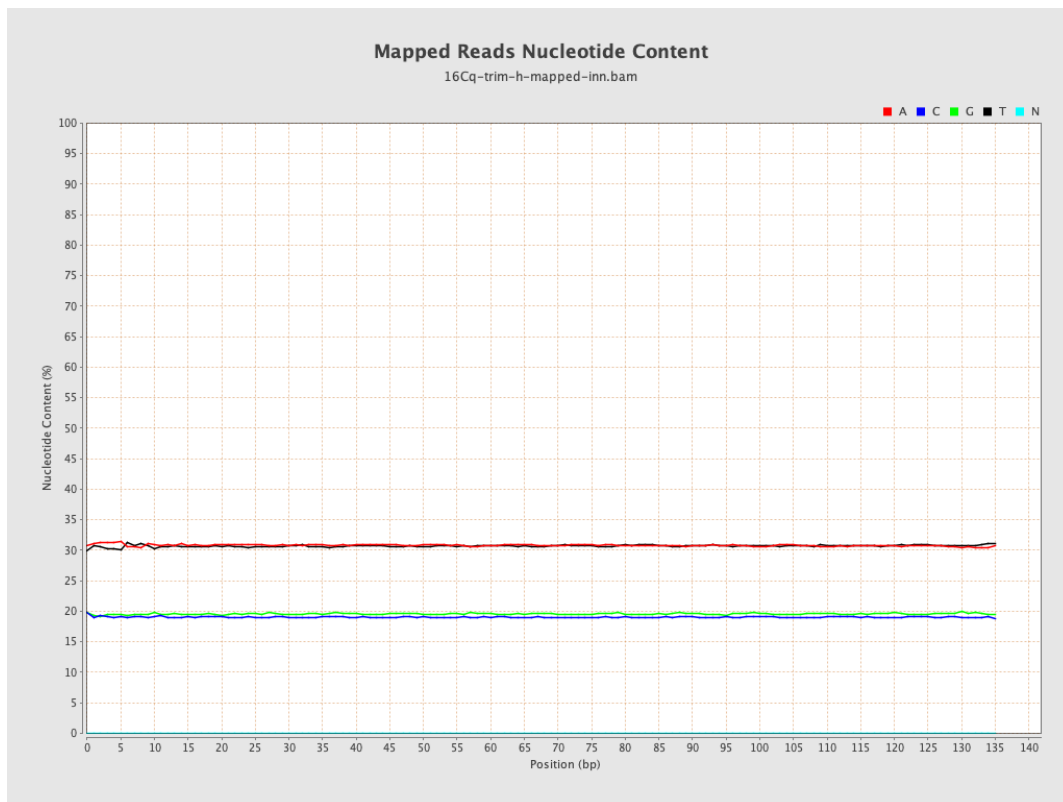
6. Results : Genome Fraction Coverage



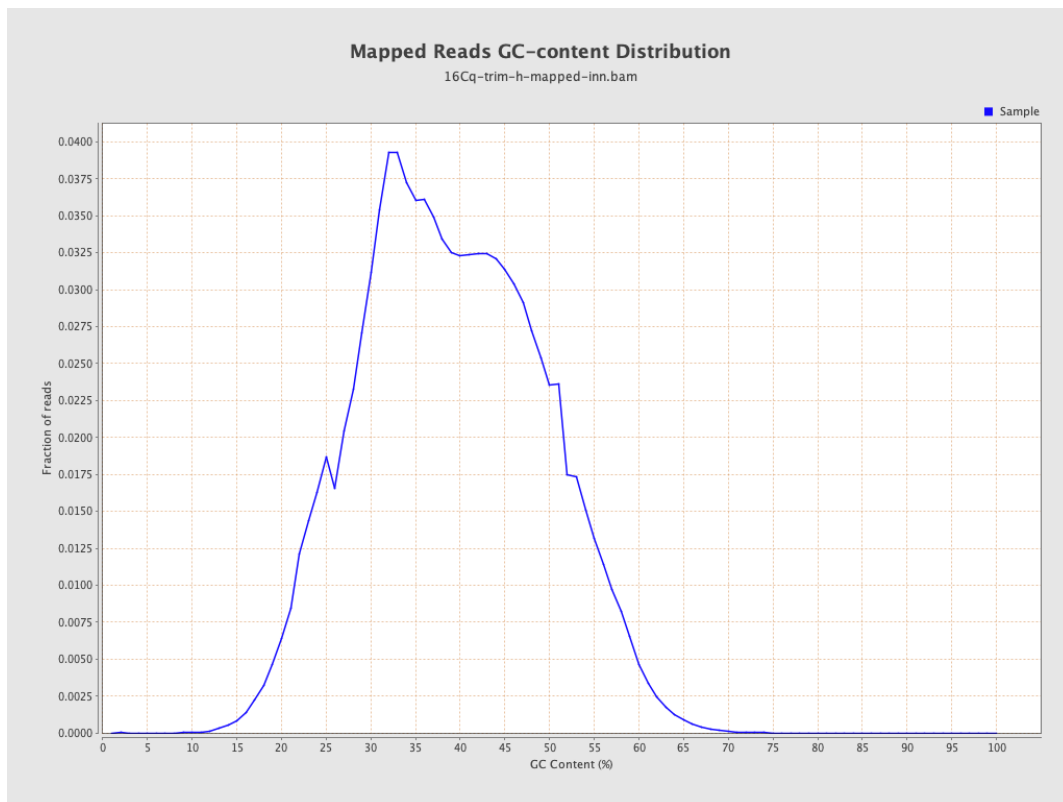
7. Results : Duplication Rate Histogram



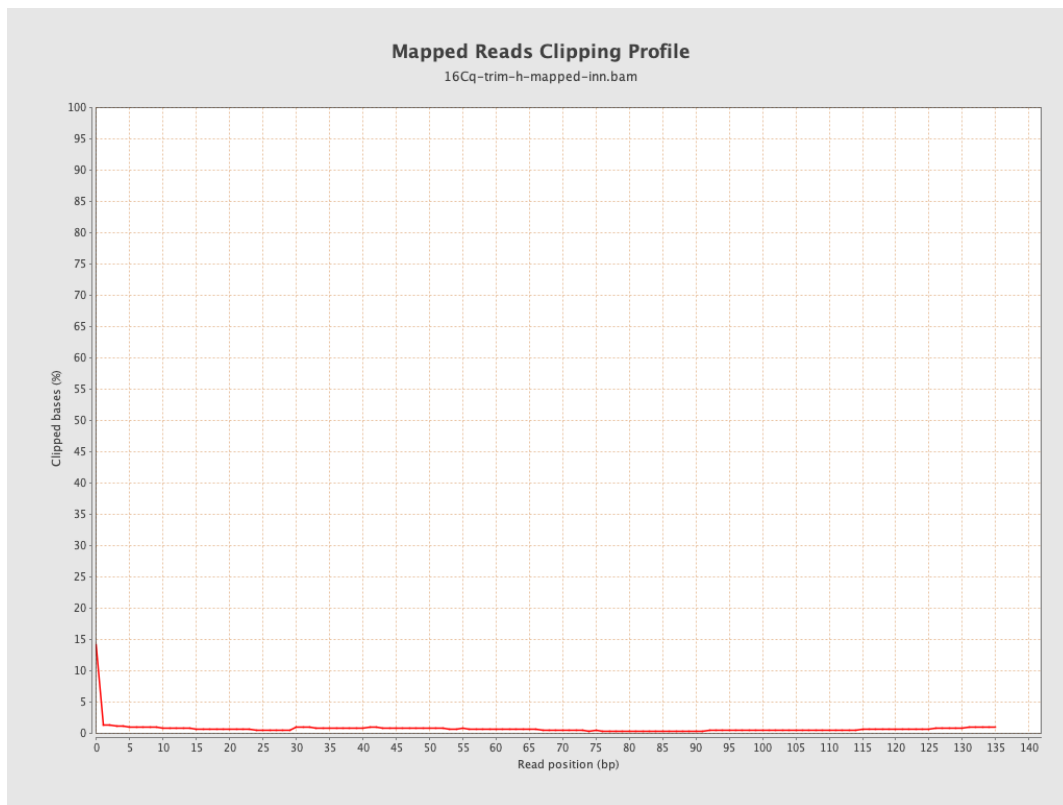
8. Results : Mapped Reads Nucleotide Content



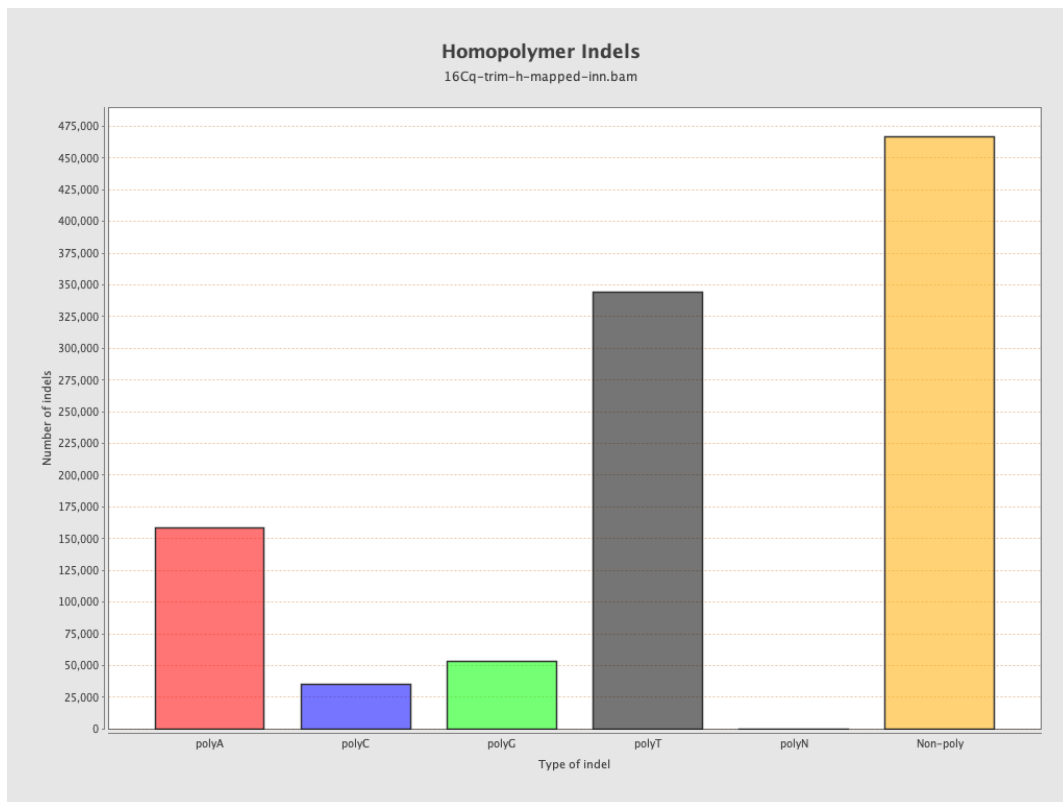
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



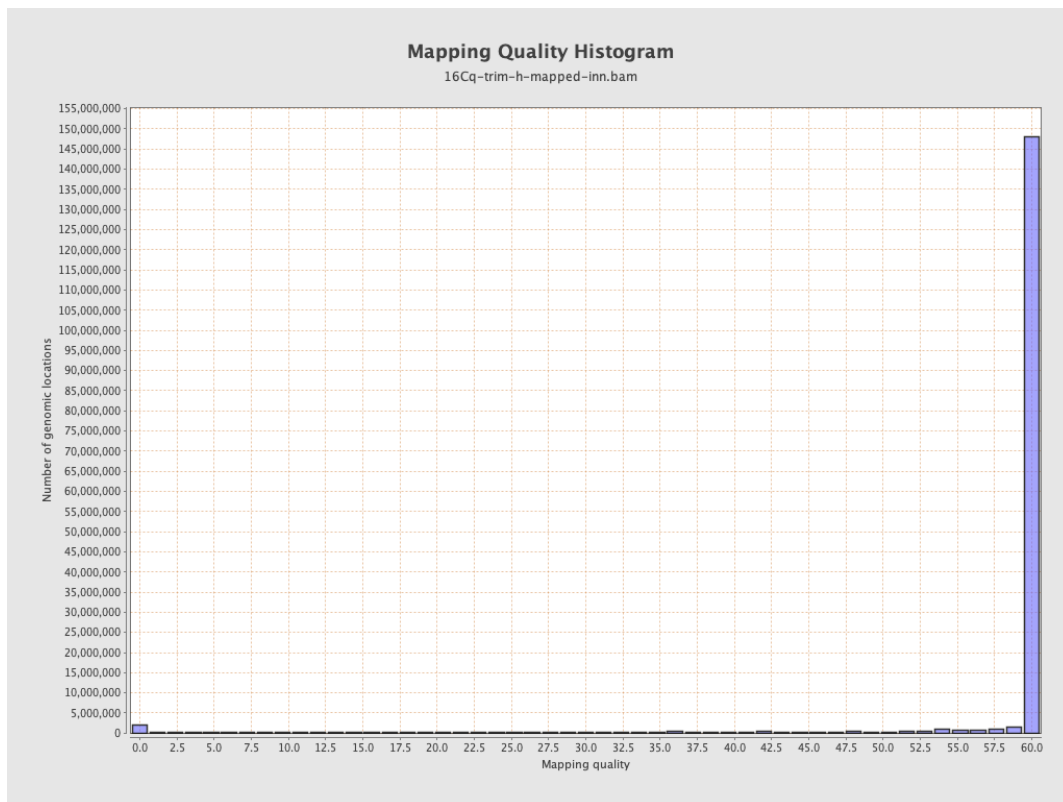
11. Results : Homopolymer Indels



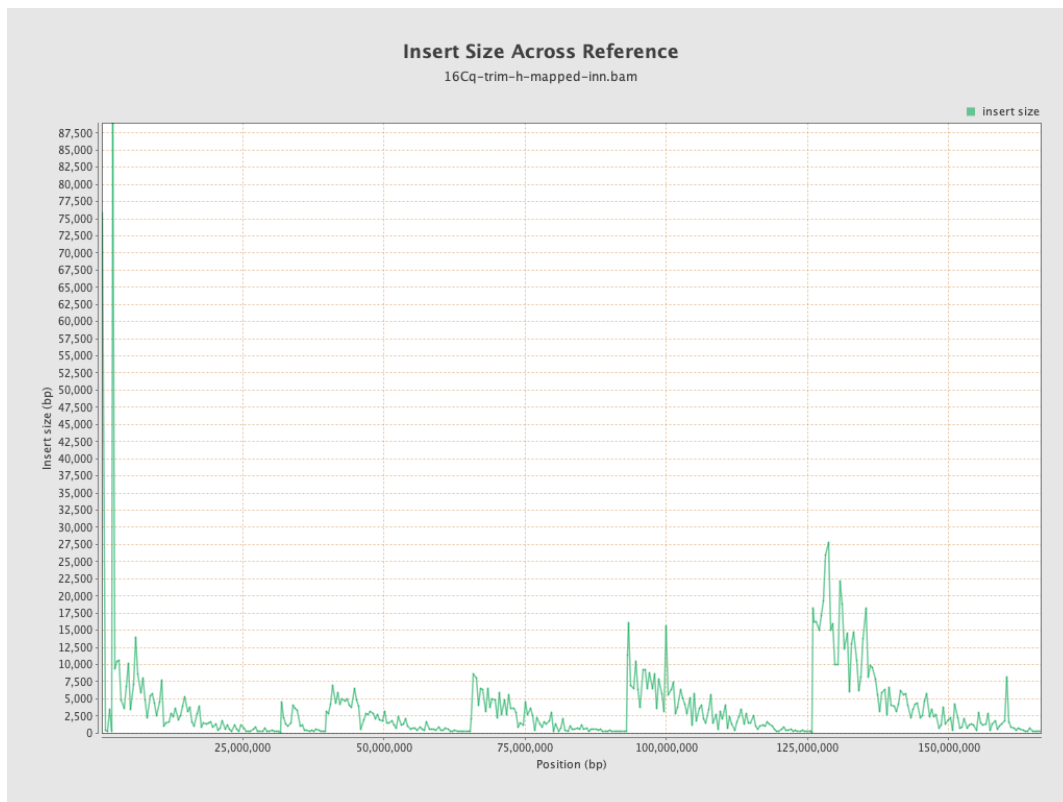
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

