

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/06/02 14:29:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam 16Cq-trim-h-mapped.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 14:29:07 CDT 2023
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	16Cq-trim-h-mapped.bam

2. Summary

2.1. Globals

Reference size	166,440,390
Number of reads	25,400,881
Mapped reads	25,310,706 / 99.64%
Supplementary alignments	140,019 / 0.55%
Unmapped reads	90,175 / 0.36%
Mapped paired reads	25,310,706 / 99.64%
Mapped reads, first in pair	12,655,831 / 49.82%
Mapped reads, second in pair	12,654,875 / 49.82%
Mapped reads, both in pair	25,298,238 / 99.6%
Mapped reads, singletons	12,468 / 0.05%
Read min/max/mean length	15 / 136 / 130.5
Overlapping read pairs	8,000,391 / 62.99%
Duplicated reads (estimated)	6,287,309 / 24.75%
Duplication rate	17.04%
Clipped reads	1,134,943 / 4.47%

2.2. ACGT Content

Number/percentage of A's	1,007,219,325 / 30.79%
Number/percentage of C's	621,870,220 / 19.01%
Number/percentage of T's	1,003,537,174 / 30.67%
Number/percentage of G's	639,063,599 / 19.53%
Number/percentage of N's	11,378 / 0%

GC Percentage	38.54%
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2.3. Coverage

Mean	19.6642
Standard Deviation	151.3832
Mean (paired-end reads overlap ignored)	15.98

2.4. Mapping Quality

Mean Mapping Quality	55.59
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2.5. Insert size

Mean	23,972.01
Standard Deviation	559,929.09
P25/Median/P75	154 / 226 / 309

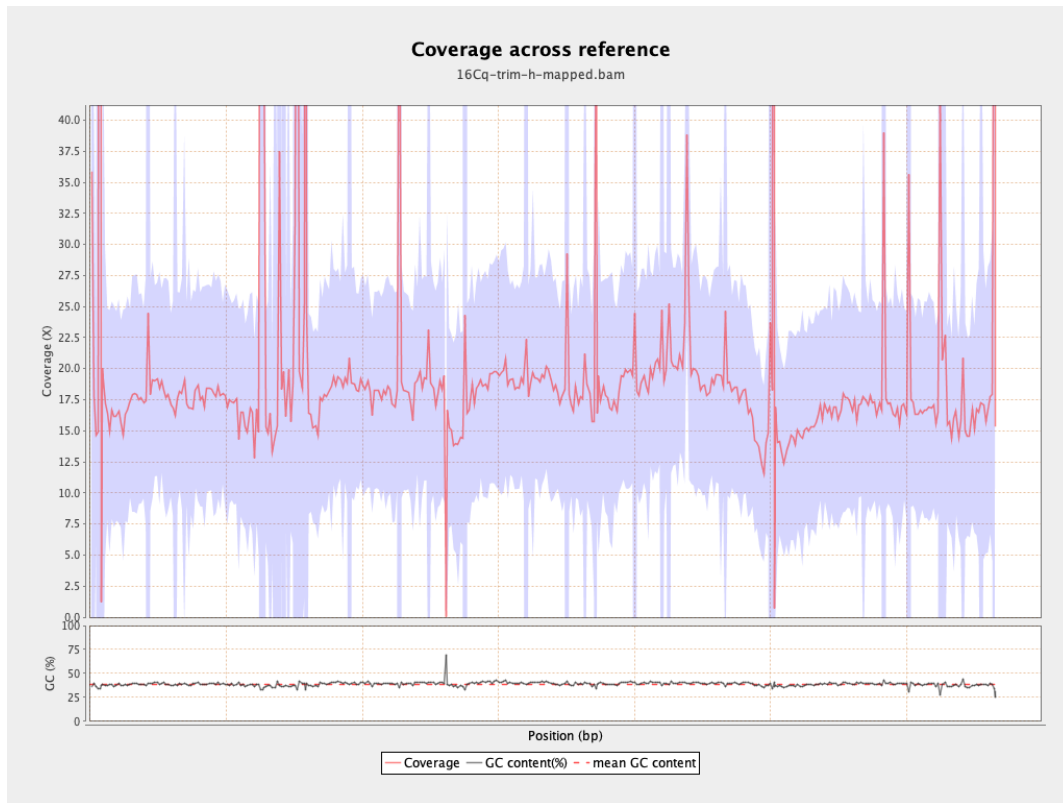
2.6. Mismatches and indels

General error rate	0.5%
Mismatches	15,164,014
Insertions	552,211
Mapped reads with at least one insertion	1.98%
Deletions	508,009
Mapped reads with at least one deletion	1.59%
Homopolymer indels	55.88%

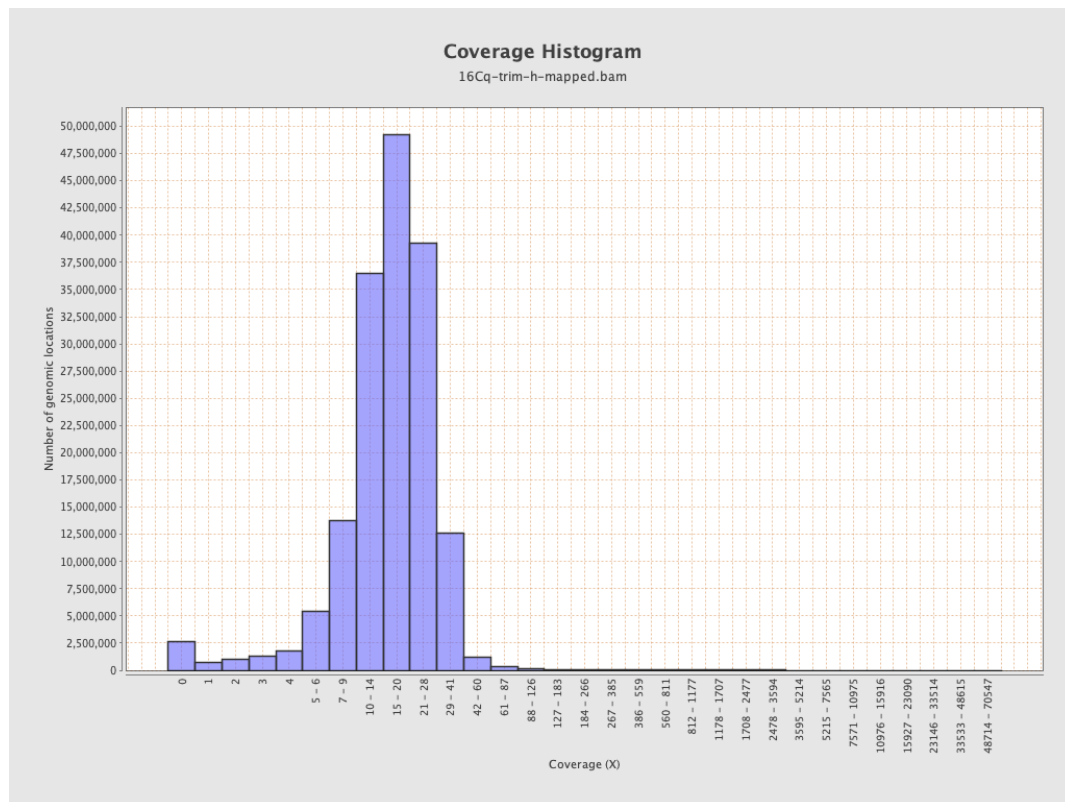
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
CM015045.2	2027030	113530049	56.0081	1,027.2943
CM027941.1	29570401	543547401	18.3815	54.5469
SKCT020000 06.1	8037050	214899390	26.7386	209.1075
CM027942.1	25683278	487249511	18.9715	80.1488
CM027943.1	27707068	518180553	18.7021	56.3588
CM027944.1	32746462	687541048	20.9959	70.9199
SKCT020000 08.1	18452	13614	0.7378	2.0554
CM015046.2	40478903	703410799	17.3772	141.8306
CM015047.1	16191	2154058	133.0405	72.457
NC_040699.1	155555	2393481	15.3867	6.0938

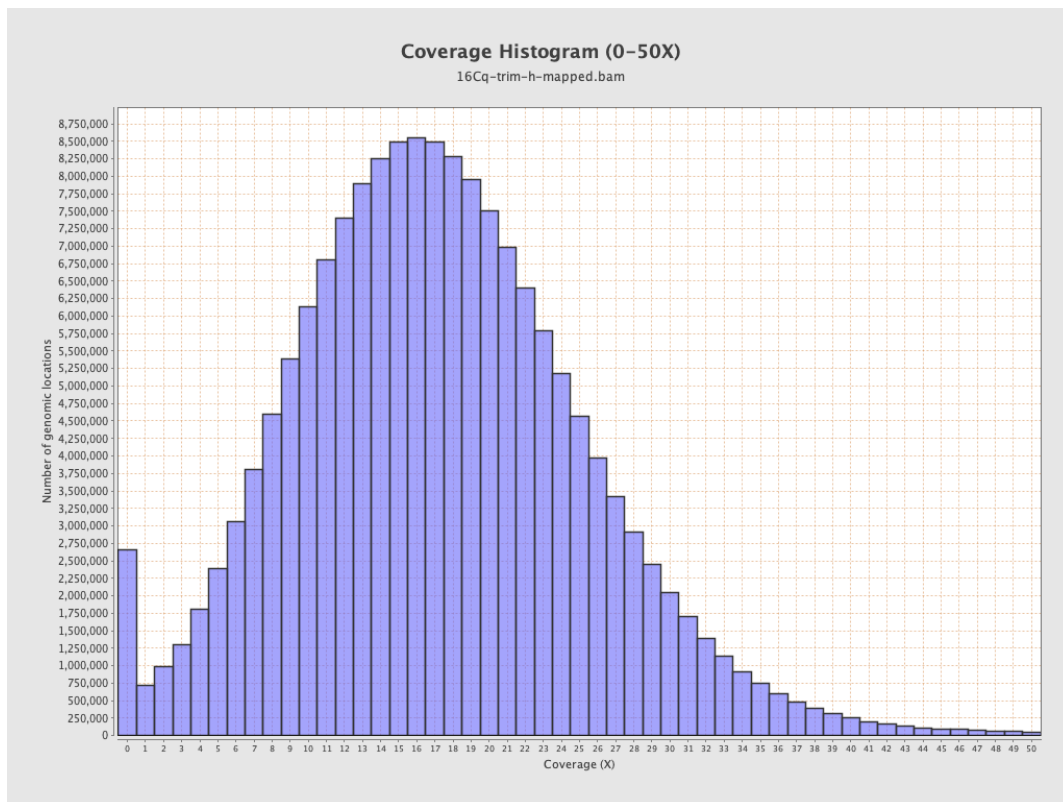
3. Results : Coverage across reference



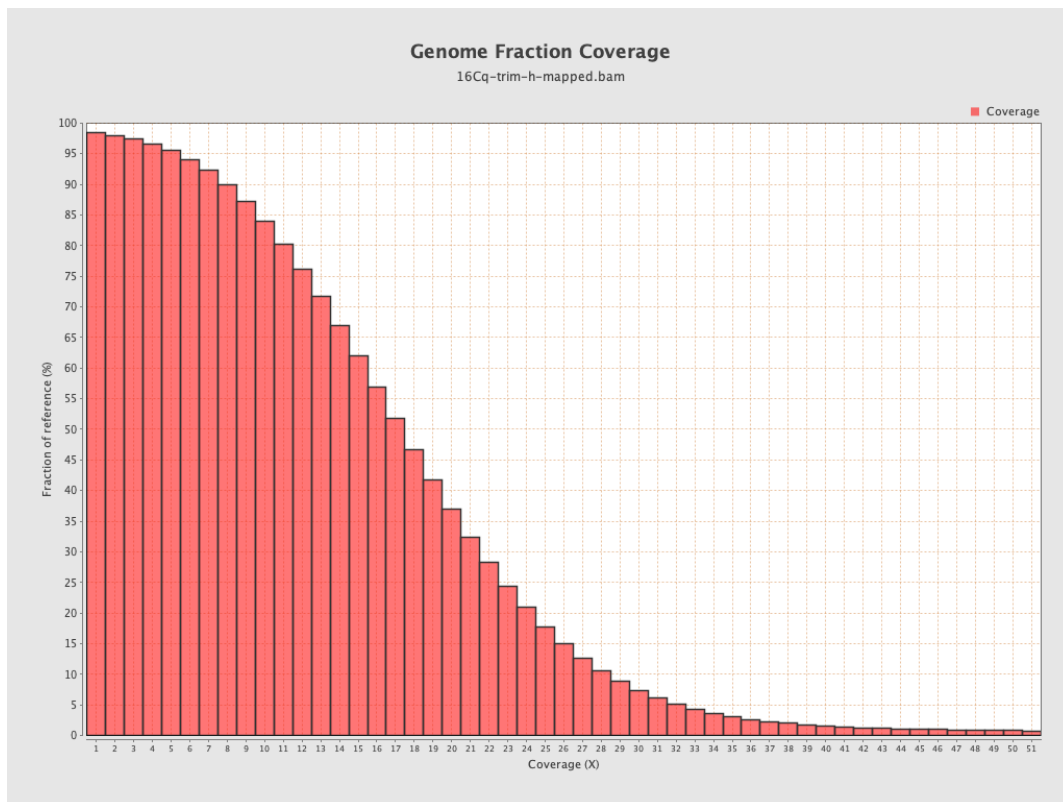
4. Results : Coverage Histogram



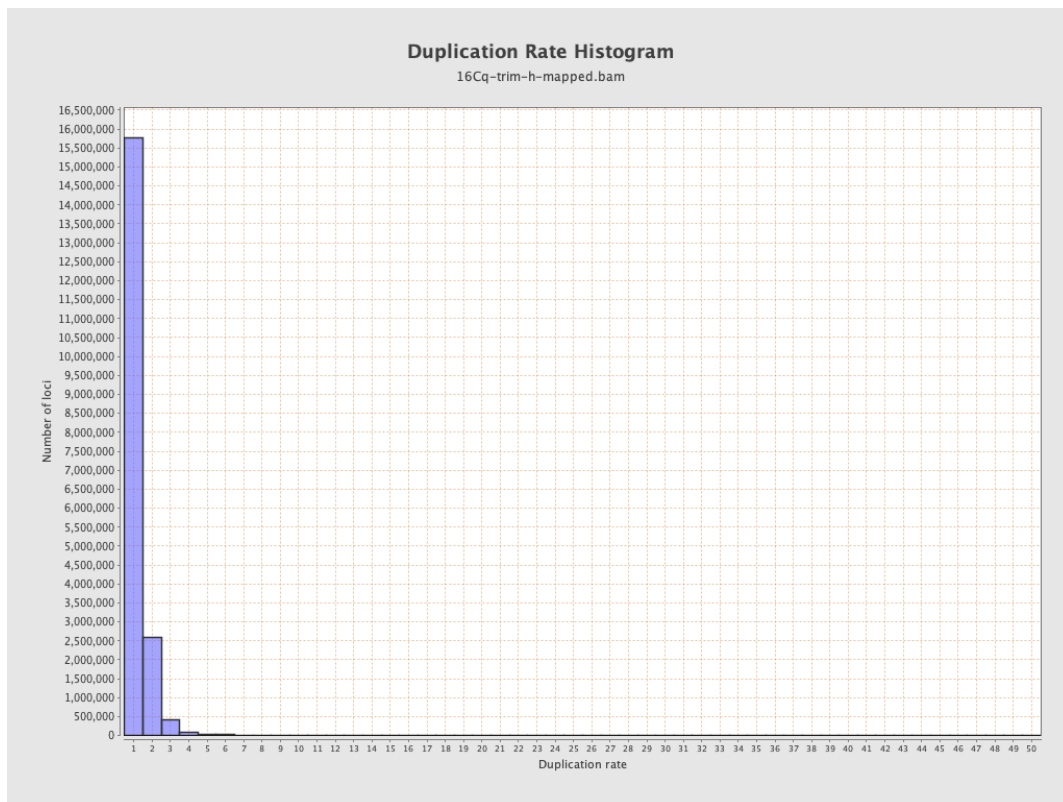
5. Results : Coverage Histogram (0-50X)



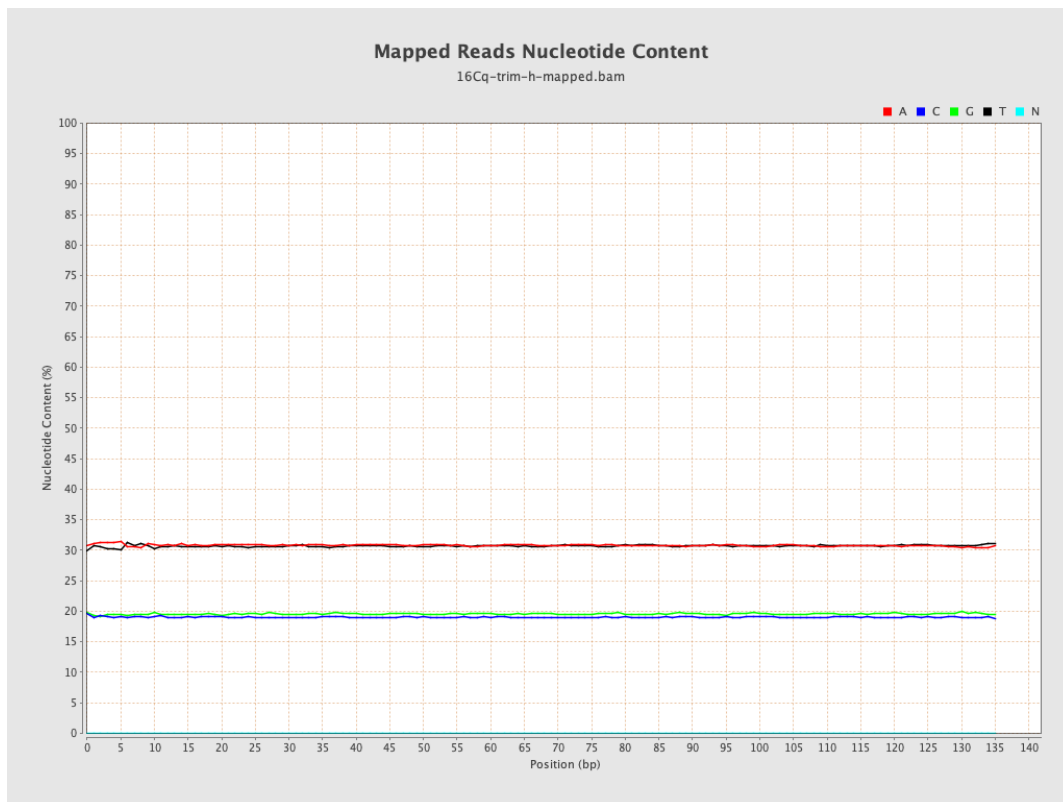
6. Results : Genome Fraction Coverage



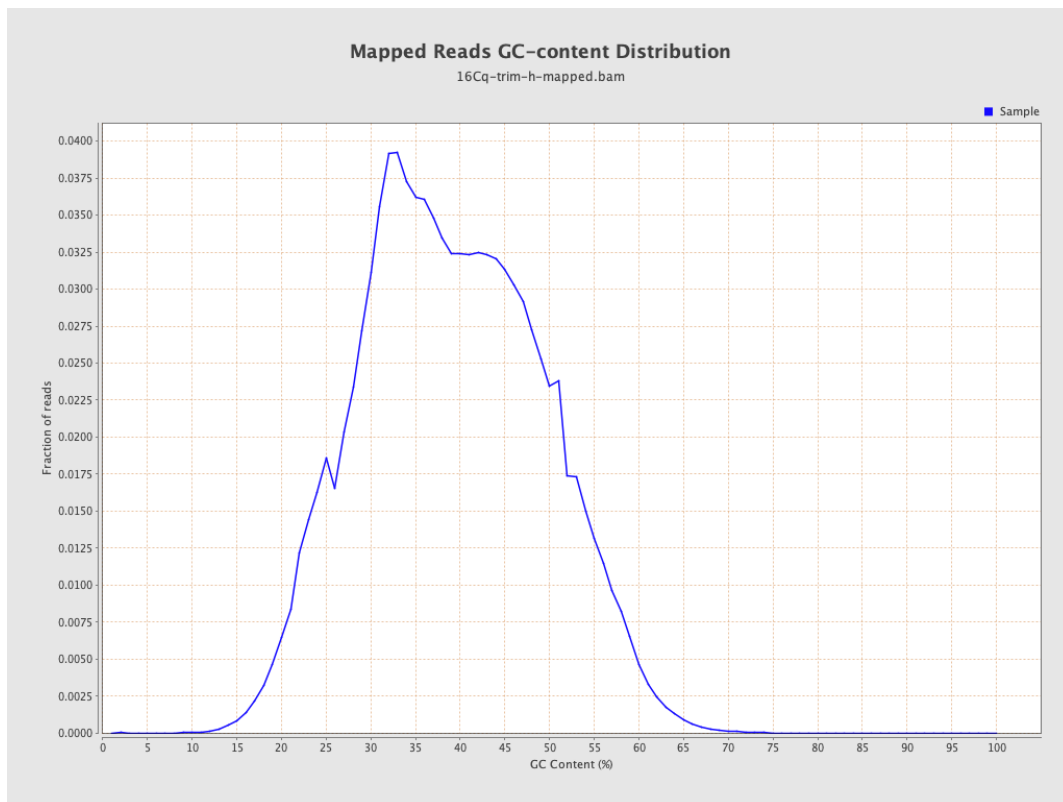
7. Results : Duplication Rate Histogram



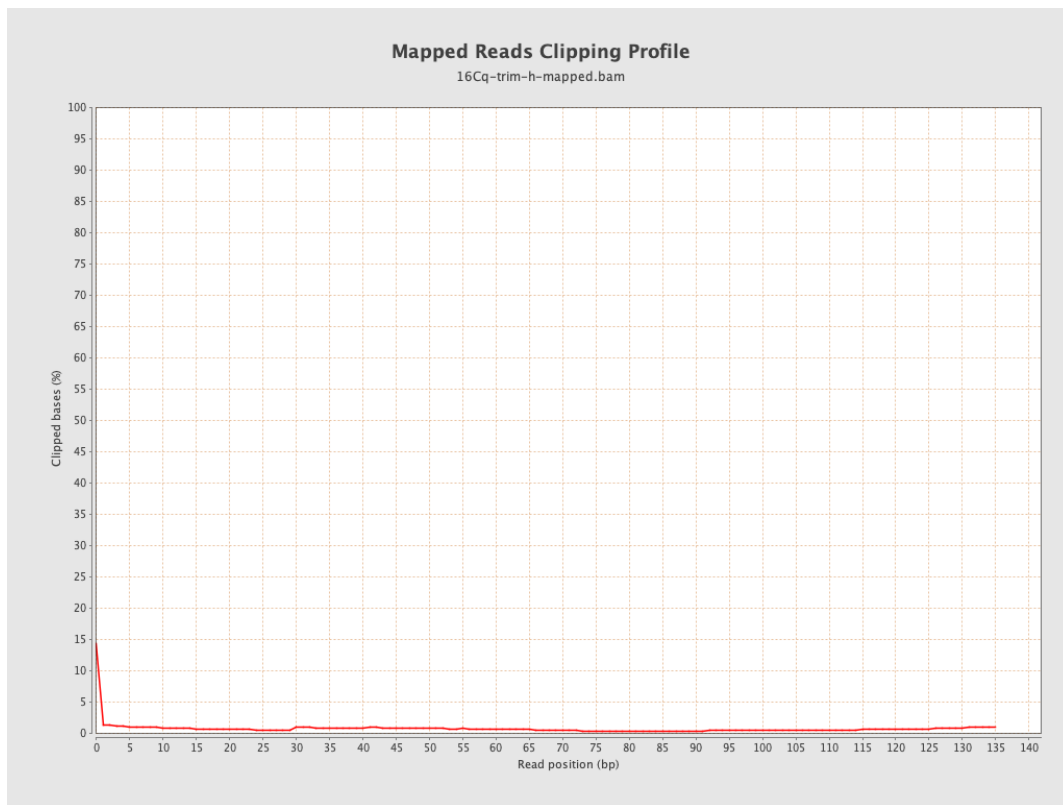
8. Results : Mapped Reads Nucleotide Content



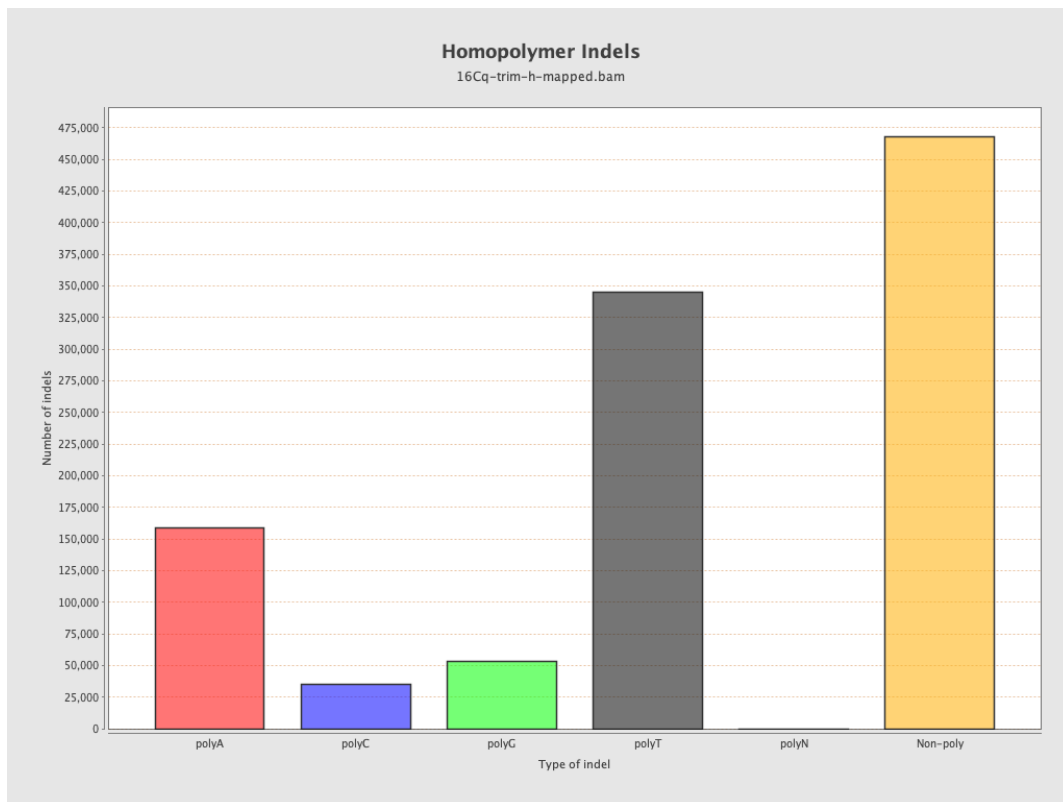
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



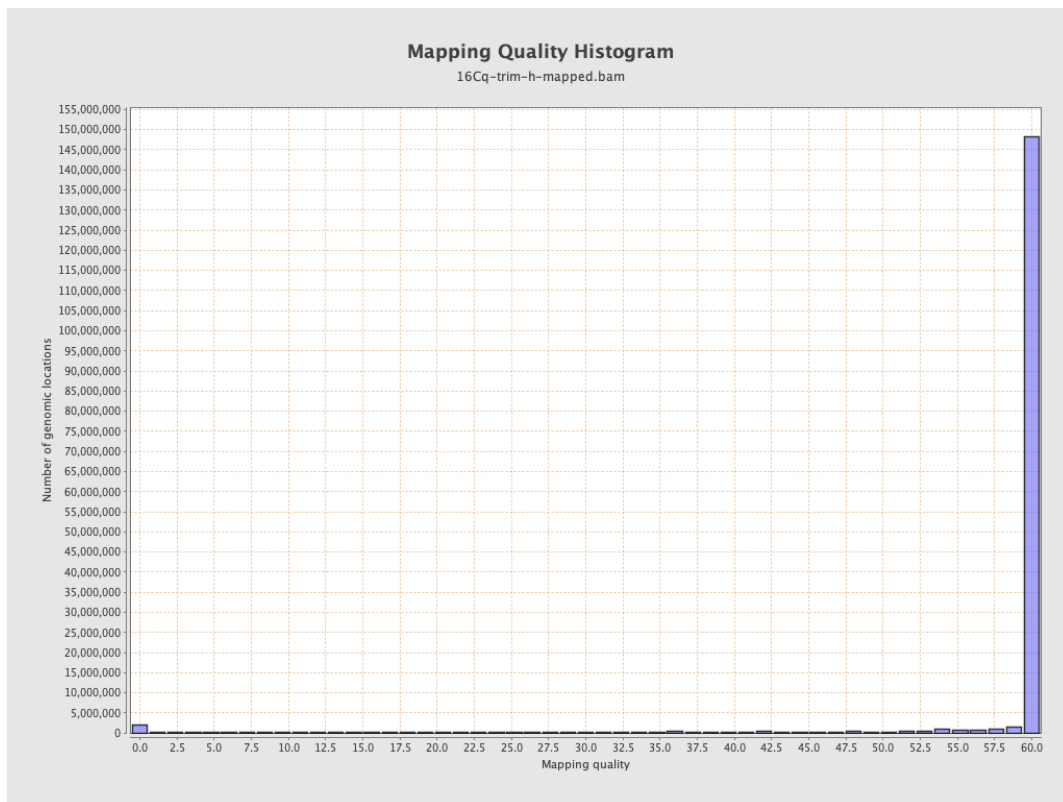
11. Results : Homopolymer Indels



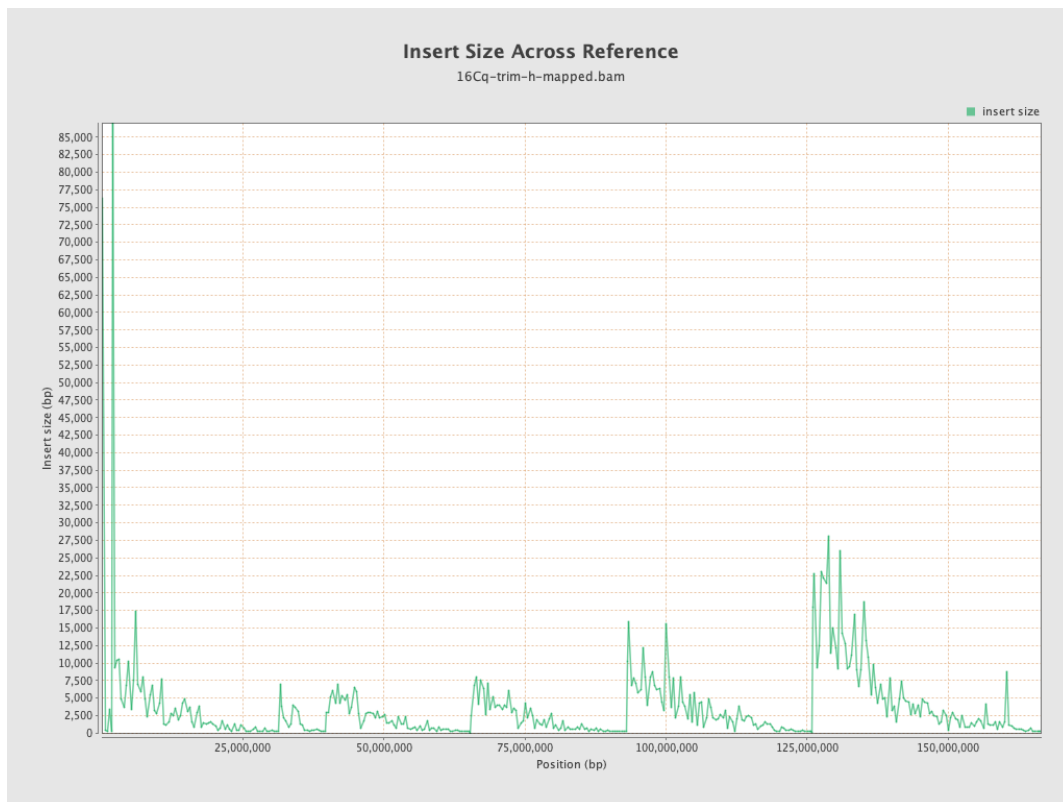
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

