

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/06/02 15:10:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam KM3-trim-h-mapped-DiNV-only.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa mem -t 5 DiNV-Dvir.fna /Users/maggieschedl/Desktop/KU/se quences/16Cq-DiNV- Test/mapping/KM_3_1_trim.fq.gz /Users/maggieschedl/Desktop/KU/se quences/16Cq-DiNV- Test/mapping/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:	Fri Jun 02 15:10:11 CDT 2023
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	KM3-trim-h-mapped-DiNV-only.bam

2. Summary

2.1. Globals

Reference size	169,927,300
Number of reads	71,821
Mapped reads	71,807 / 99.98%
Supplementary alignments	40 / 0.06%
Unmapped reads	14 / 0.02%
Mapped paired reads	71,807 / 99.98%
Mapped reads, first in pair	35,903 / 49.99%
Mapped reads, second in pair	35,904 / 49.99%
Mapped reads, both in pair	71,793 / 99.96%
Mapped reads, singletons	14 / 0.02%
Read min/max/mean length	30 / 135 / 114.52
Overlapping read pairs	31,761 / 88.44%
Duplicated reads (estimated)	33,977 / 47.31%
Duplication rate	43.41%
Clipped reads	4,288 / 5.97%

2.2. ACGT Content

Number/percentage of A's	2,648,821 / 33.12%
Number/percentage of C's	1,303,549 / 16.3%
Number/percentage of T's	2,703,936 / 33.81%
Number/percentage of G's	1,341,416 / 16.77%
Number/percentage of N's	364 / 0%

GC Percentage	33.07%
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2.3. Coverage

Mean	0.0472
Standard Deviation	1.7716
Mean (paired-end reads overlap ignored)	0.03

2.4. Mapping Quality

Mean Mapping Quality	0.13
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2.5. Insert size

Mean	183.03
Standard Deviation	1,981.66
P25/Median/P75	77 / 113 / 172

2.6. Mismatches and indels

General error rate	1.46%
Mismatches	101,031
Insertions	6,036
Mapped reads with at least one insertion	7.68%
Deletions	8,438
Mapped reads with at least one deletion	9.86%
Homopolymer indels	53.86%

2.7. Chromosome stats

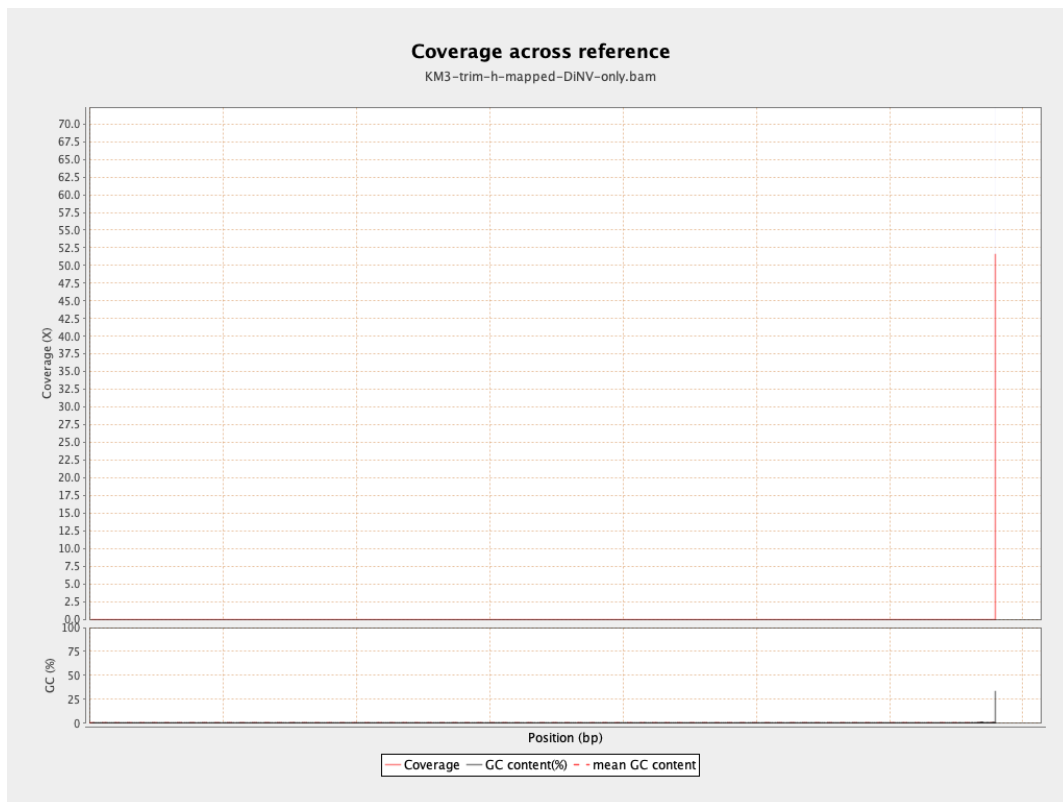
Name	Length	Mapped bases	Mean coverage	Standard deviation
CM017604.2	38193566	0	0	0
CM017605.2	38438298	0	0	0
CM017606.2	27616680	0	0	0
CM017607.2	31075311	0	0	0
CM017608.2	27902728	0	0	0
CM017609.2	2270151	0	0	0
VNHH02000005.1	16908	0	0	0
VNHH02000019.1	560307	0	0	0
VNHH02000043.1	331422	0	0	0
VNHH02000047.1	234219	0	0	0
VNHH02000048.1	20672	0	0	0
VNHH02000050.1	275122	0	0	0
VNHH02000051.1	29855	0	0	0
VNHH02000054.1	73214	0	0	0
VNHH02000055.1	19572	0	0	0

VNHH020000 56.1	52186	0	0	0
VNHH020000 82.1	47289	0	0	0
VNHH020000 89.1	52137	0	0	0
VNHH020000 90.1	34989	0	0	0
VNHH020000 95.1	19220	0	0	0
VNHH020000 97.1	29477	0	0	0
VNHH020001 02.1	56772	0	0	0
VNHH020001 05.1	30176	0	0	0
VNHH020001 07.1	21993	0	0	0
VNHH020001 08.1	19534	0	0	0
VNHH020001 11.1	26096	0	0	0
VNHH020001 12.1	17191	0	0	0
VNHH020001 13.1	49501	0	0	0
VNHH020001 16.1	21351	0	0	0
VNHH020001 27.1	25842	0	0	0

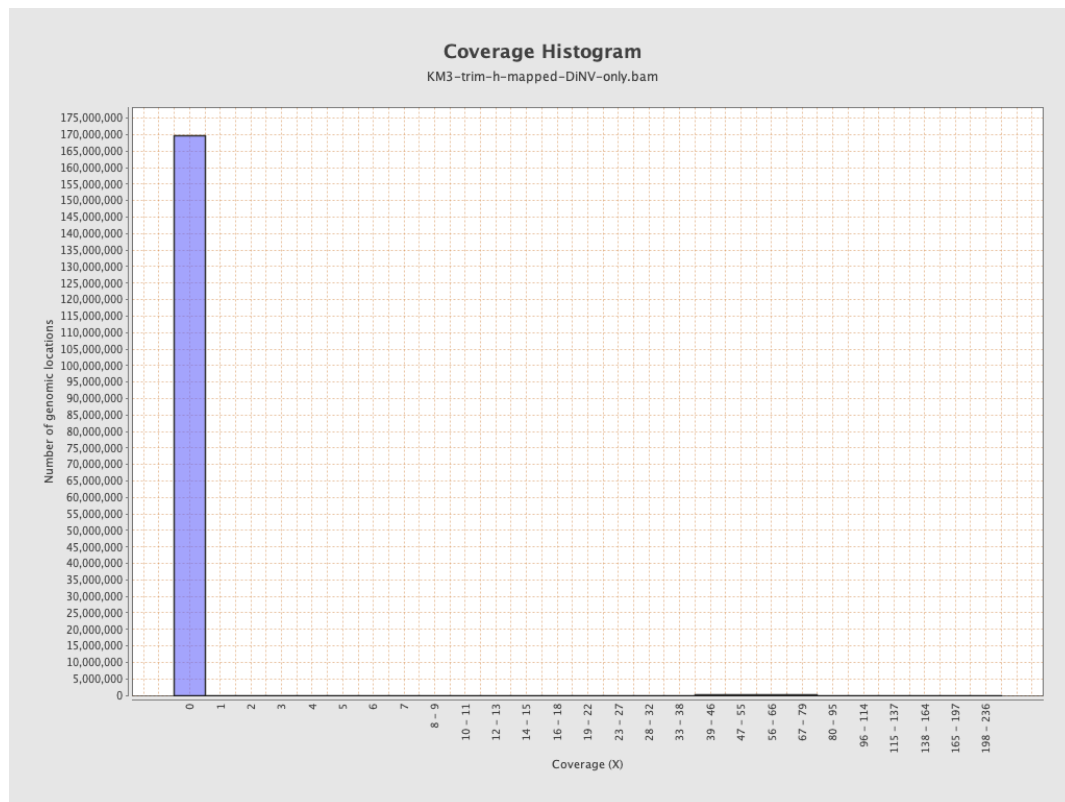
VNHH020001 50.1	521567	0	0	0
VNHH020001 51.1	86477	0	0	0
VNHH020001 71.1	104324	0	0	0
VNHH020001 77.1	231566	0	0	0
VNHH020001 81.1	21731	0	0	0
VNHH020001 87.1	442058	0	0	0
VNHH020001 88.1	321154	0	0	0
VNHH020001 91.1	107803	0	0	0
VNHH020001 95.1	27877	0	0	0
VNHH020001 96.1	18248	0	0	0
VNHH020001 97.1	24842	0	0	0
VNHH020001 98.1	144193	0	0	0
VNHH020002 01.1	110897	0	0	0
VNHH020002 07.1	17506	0	0	0
VNHH020002 08.1	29723	0	0	0

NC_040699.1	155555	8024008	51.5831	28.0607
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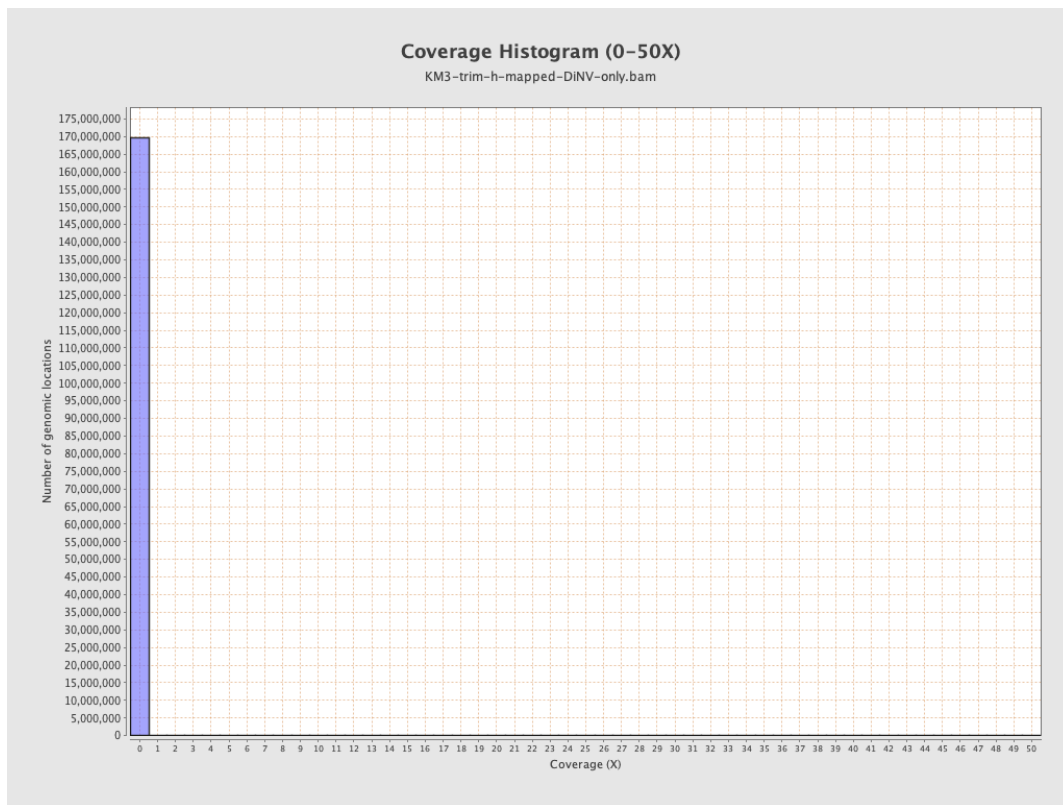
3. Results : Coverage across reference



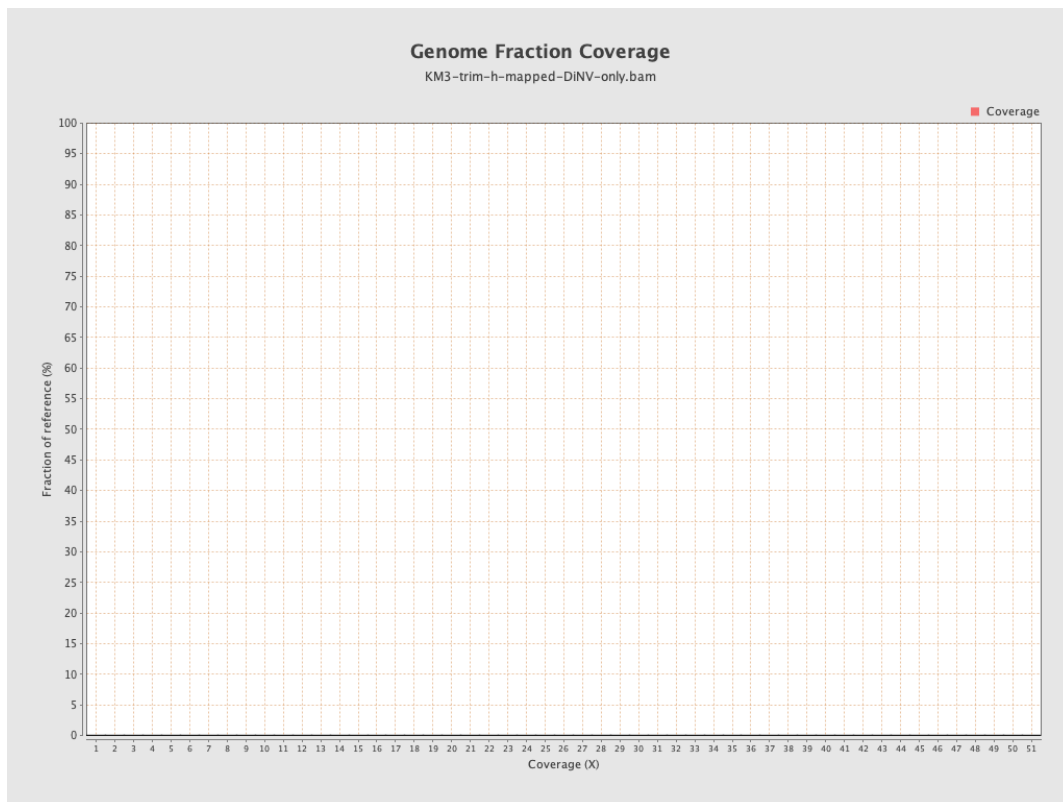
4. Results : Coverage Histogram



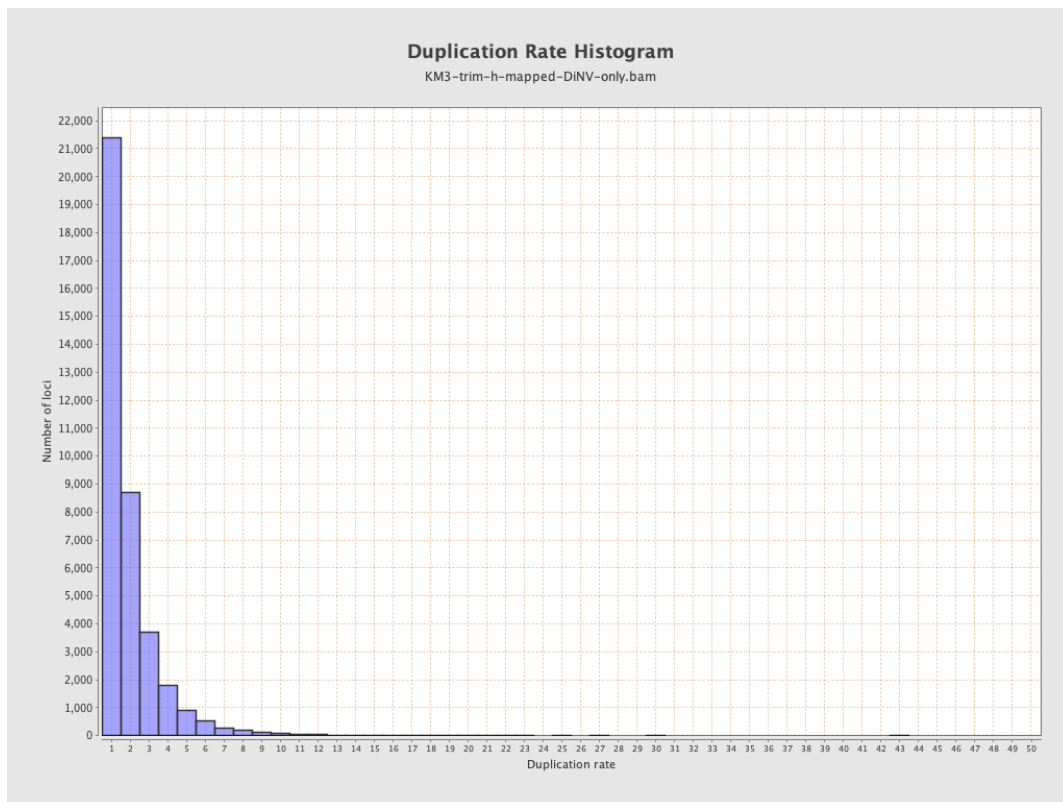
5. Results : Coverage Histogram (0-50X)



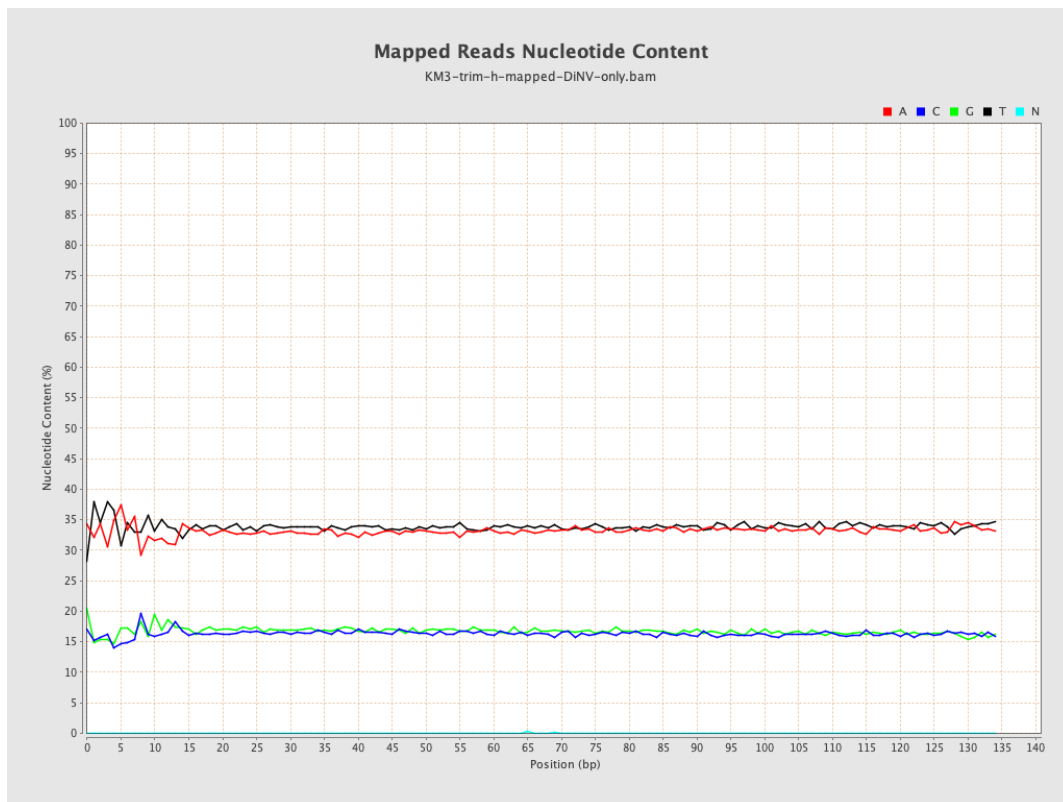
6. Results : Genome Fraction Coverage



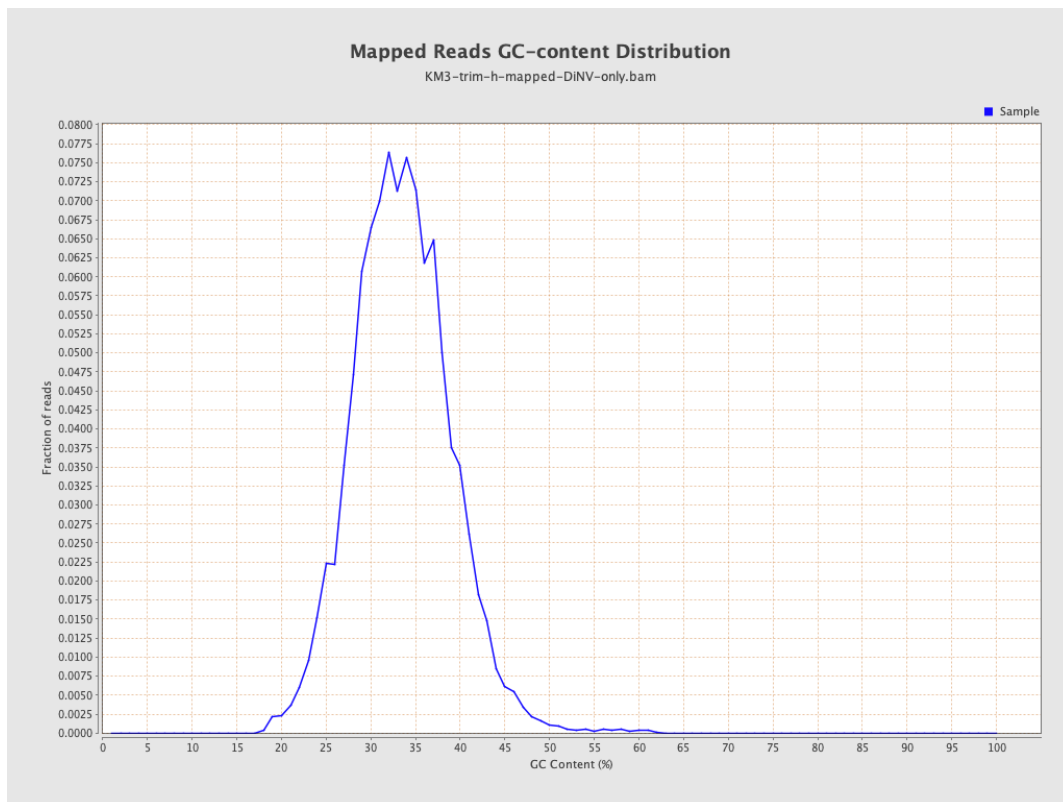
7. Results : Duplication Rate Histogram



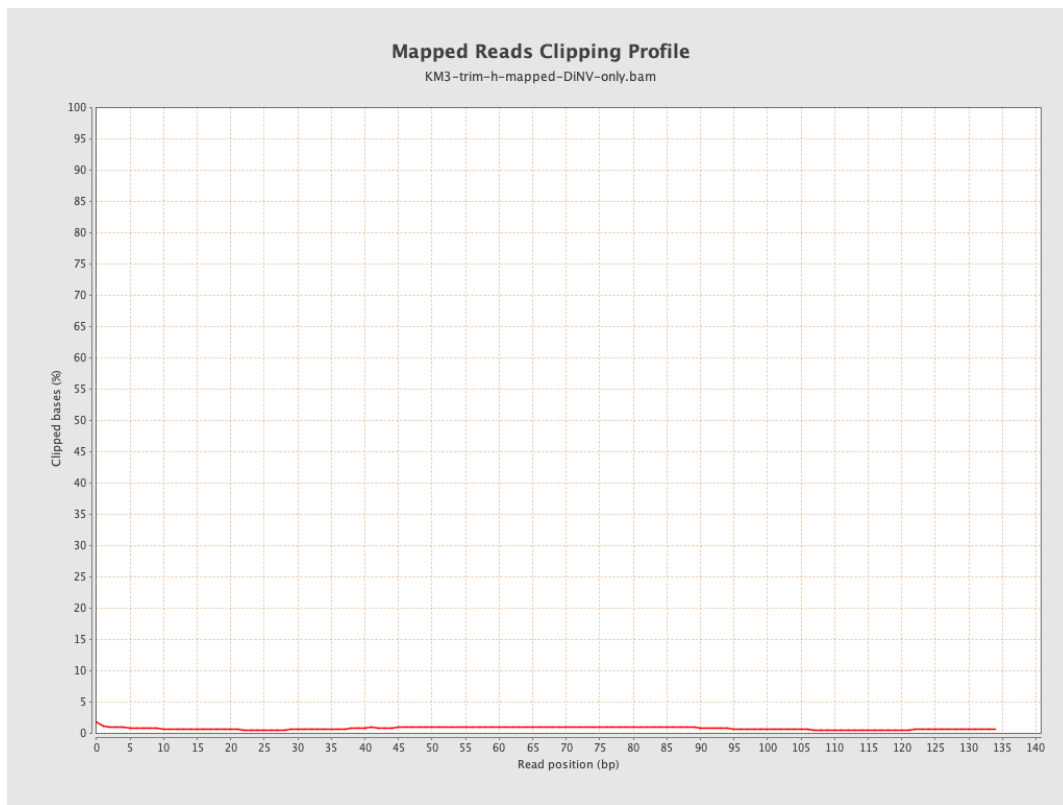
8. Results : Mapped Reads Nucleotide Content



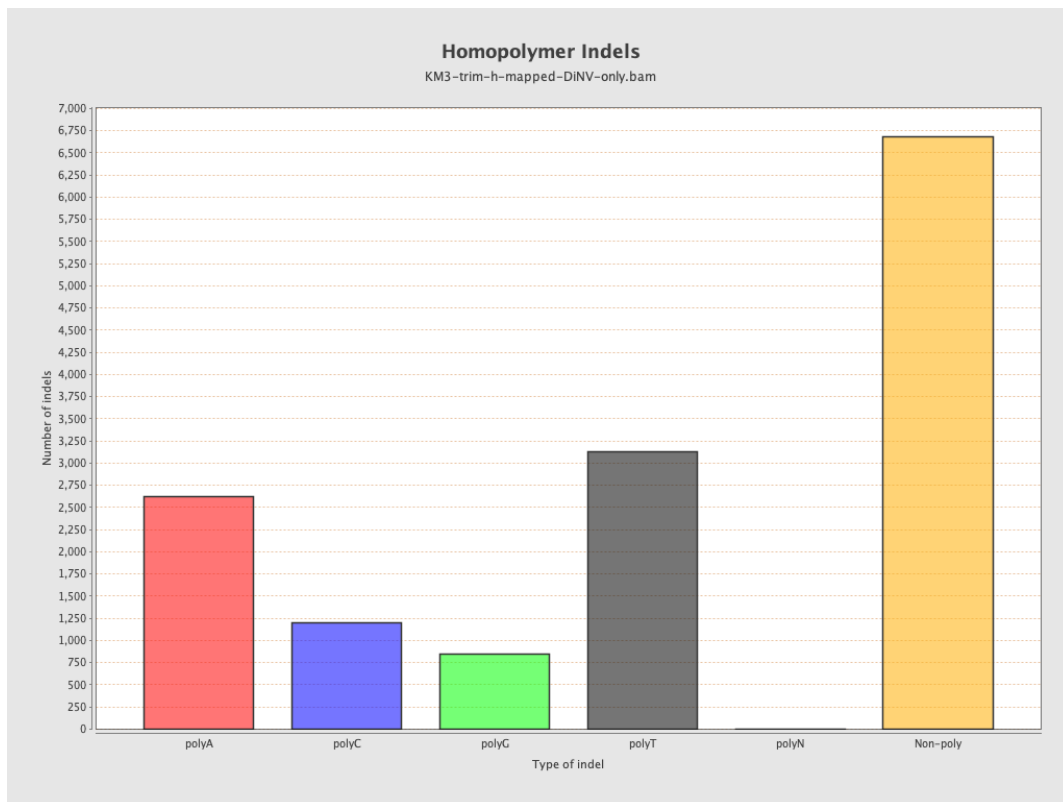
9. Results : Mapped Reads GC-content Distribution



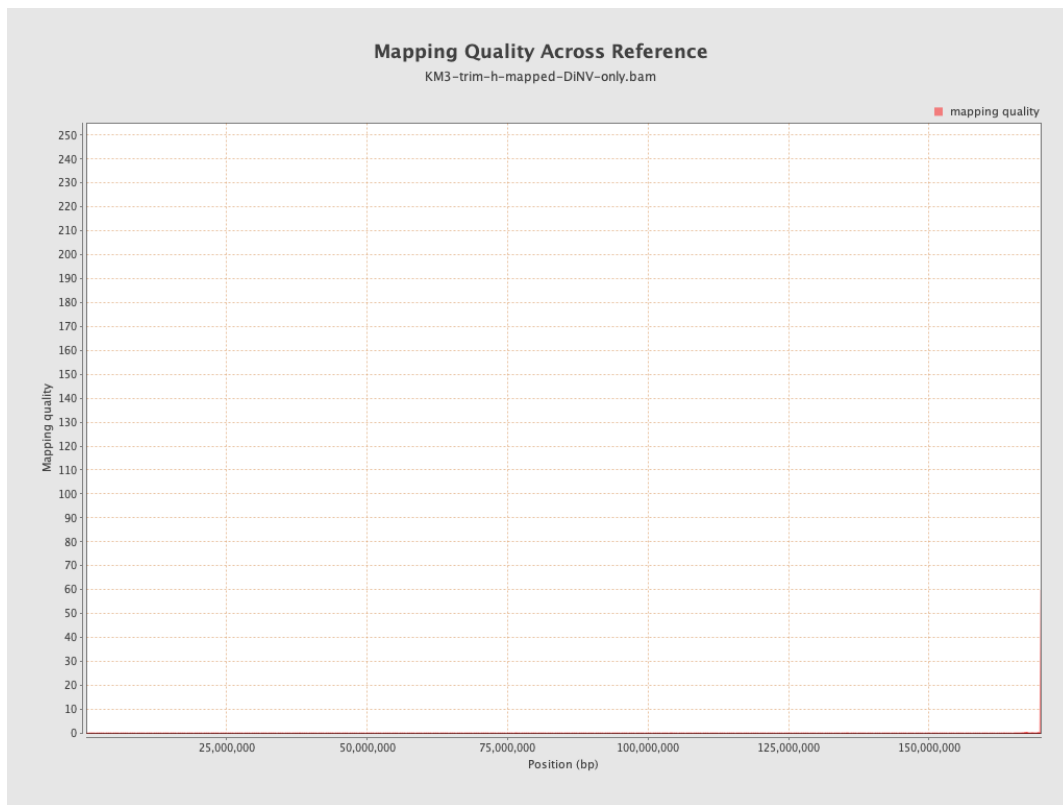
10. Results : Mapped Reads Clipping Profile



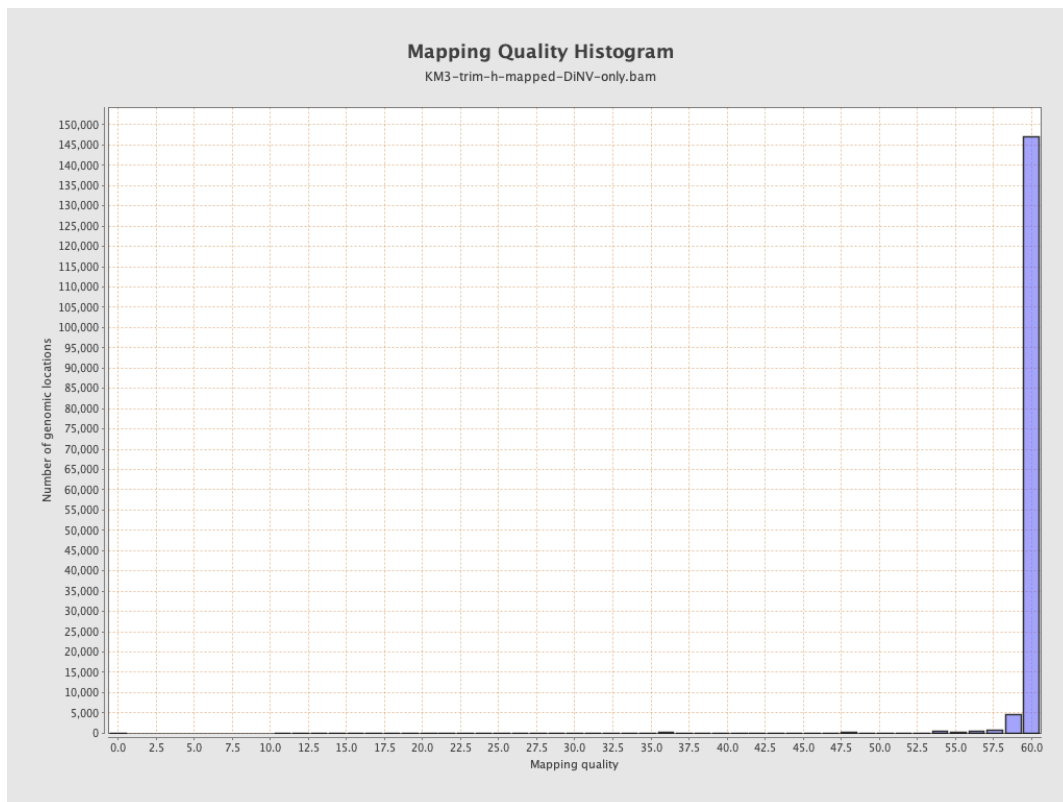
11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

