

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.1

2023/06/02 14:30:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam KM3-trim-h-mapped.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 14:30:00 CDT 2023
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	KM3-trim-h-mapped.bam

2. Summary

2.1. Globals

Reference size	169,927,300
Number of reads	14,103,006
Mapped reads	13,936,836 / 98.82%
Supplementary alignments	49,682 / 0.35%
Unmapped reads	166,170 / 1.18%
Mapped paired reads	13,936,836 / 98.82%
Mapped reads, first in pair	6,968,419 / 49.41%
Mapped reads, second in pair	6,968,417 / 49.41%
Mapped reads, both in pair	13,929,691 / 98.77%
Mapped reads, singletons	7,145 / 0.05%
Read min/max/mean length	30 / 135 / 115.32
Overlapping read pairs	6,133,411 / 86.98%
Duplicated reads (estimated)	3,745,444 / 26.56%
Duplication rate	21.95%
Clipped reads	1,485,331 / 10.53%

2.2. ACGT Content

Number/percentage of A's	444,858,768 / 29.03%
Number/percentage of C's	317,098,522 / 20.7%
Number/percentage of T's	447,981,720 / 29.24%
Number/percentage of G's	322,298,311 / 21.03%
Number/percentage of N's	65,812 / 0%

GC Percentage	41.73%
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2.3. Coverage

Mean	9.0352
Standard Deviation	56.2909
Mean (paired-end reads overlap ignored)	6.05

2.4. Mapping Quality

Mean Mapping Quality	49.27
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2.5. Insert size

Mean	10,760.55
Standard Deviation	404,510.22
P25/Median/P75	74 / 115 / 174

2.6. Mismatches and indels

General error rate	1.16%
Mismatches	15,588,344
Insertions	583,783
Mapped reads with at least one insertion	3.99%
Deletions	677,180
Mapped reads with at least one deletion	4.58%
Homopolymer indels	50.16%

2.7. Chromosome stats

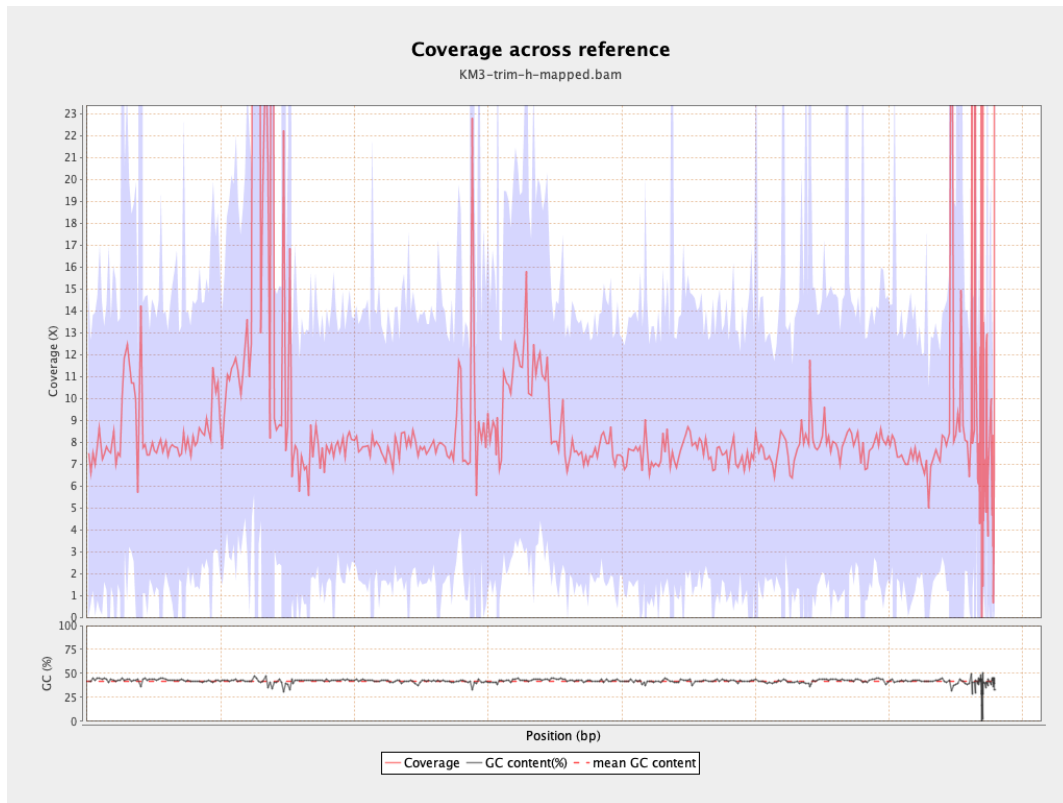
Name	Length	Mapped bases	Mean coverage	Standard deviation
CM017604.2	38193566	446937250	11.7019	96.5087
CM017605.2	38438298	307696997	8.005	48.3492
CM017606.2	27616680	245098836	8.875	7.012
CM017607.2	31075311	235020593	7.5629	8.6634
CM017608.2	27902728	229960881	8.2415	52.5039
CM017609.2	2270151	20275189	8.9312	15.6205
VNHH020000 05.1	16908	1154971	68.3091	99.5556
VNHH020000 19.1	560307	4688555	8.3678	5.4286
VNHH020000 43.1	331422	5771197	17.4134	161.5028
VNHH020000 47.1	234219	1546344	6.6021	6.3557
VNHH020000 48.1	20672	125234	6.0581	5.7911
VNHH020000 50.1	275122	2180815	7.9267	8.1373
VNHH020000 51.1	29855	151788	5.0842	5.9366
VNHH020000 54.1	73214	549476	7.5051	13.2662
VNHH020000 55.1	19572	241685	12.3485	11.3788

VNHH020000 56.1	52186	415092	7.9541	6.8141
VNHH020000 82.1	47289	391667	8.2824	8.6257
VNHH020000 89.1	52137	311758	5.9796	6.792
VNHH020000 90.1	34989	322063	9.2047	11.051
VNHH020000 95.1	19220	1083408	56.3688	71.8208
VNHH020000 97.1	29477	752903	25.542	65.3658
VNHH020001 02.1	56772	766755	13.5059	49.806
VNHH020001 05.1	30176	309	0.0102	0.1229
VNHH020001 07.1	21993	2115	0.0962	2.3244
VNHH020001 08.1	19534	1225117	62.7172	87.1435
VNHH020001 11.1	26096	36530	1.3998	5.7672
VNHH020001 12.1	17191	443046	25.772	31.1582
VNHH020001 13.1	49501	2374710	47.973	73.0244
VNHH020001 16.1	21351	1290844	60.4582	82.4296
VNHH020001 27.1	25842	113393	4.3879	3.7994

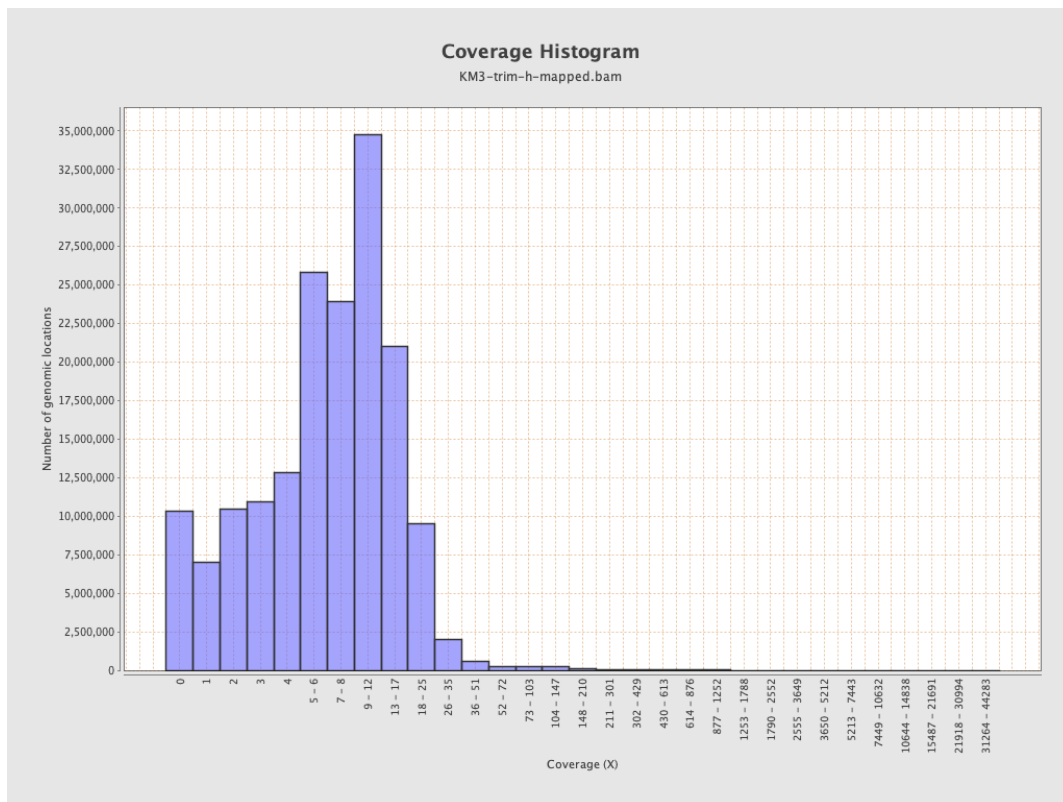
VNHH020001 50.1	521567	3704637	7.1029	5.8417
VNHH020001 51.1	86477	412663	4.7719	5.7119
VNHH020001 71.1	104324	1306716	12.5256	6.6169
VNHH020001 77.1	231566	1852158	7.9984	49.557
VNHH020001 81.1	21731	80474	3.7032	3.7813
VNHH020001 87.1	442058	3636908	8.2272	7.6128
VNHH020001 88.1	321154	2070146	6.446	8.205
VNHH020001 91.1	107803	864254	8.017	6.8788
VNHH020001 95.1	27877	128937	4.6252	4.9438
VNHH020001 96.1	18248	59064	3.2367	3.1606
VNHH020001 97.1	24842	206797	8.3245	6.9048
VNHH020001 98.1	144193	115649	0.802	3.1188
VNHH020002 01.1	110897	751789	6.7792	5.6005
VNHH020002 07.1	17506	131505	7.512	7.2666
VNHH020002 08.1	29723	1055199	35.5011	33.3353

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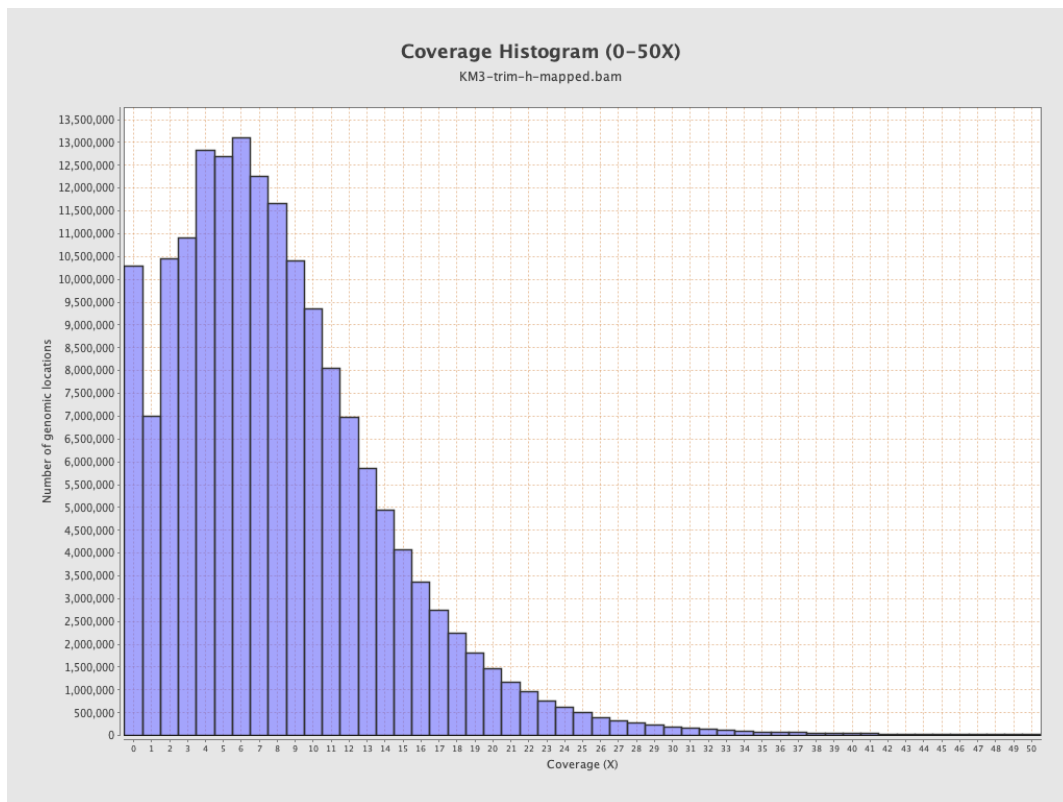
3. Results : Coverage across reference



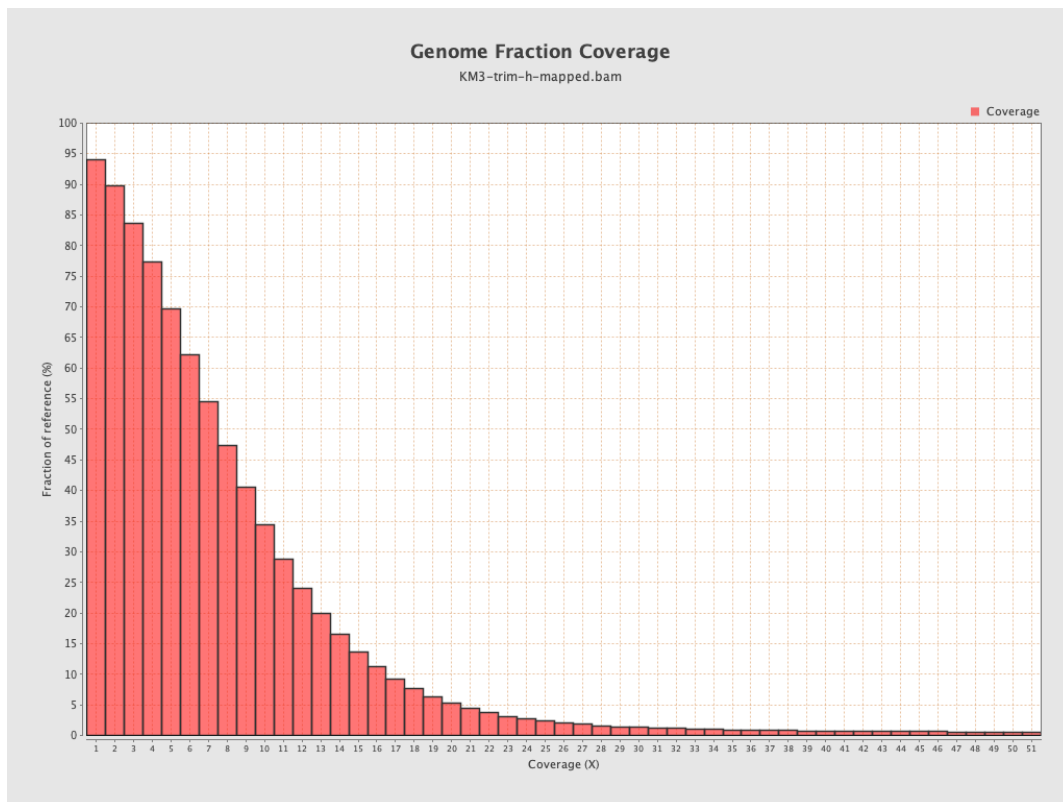
4. Results : Coverage Histogram



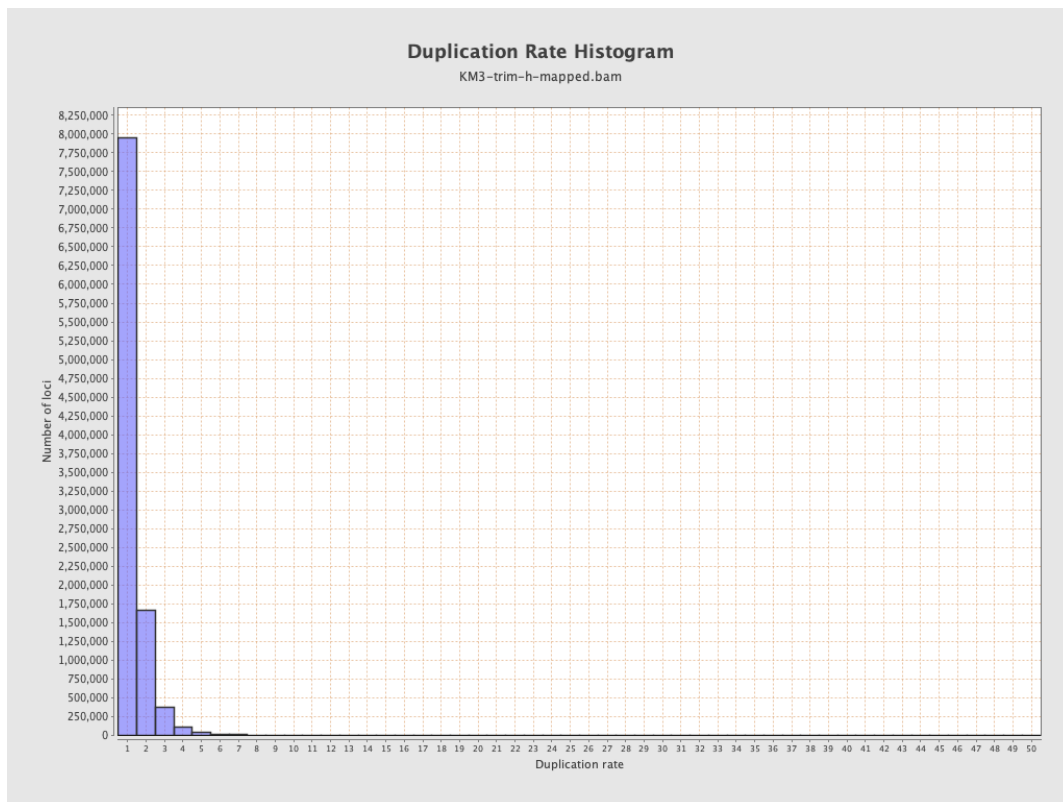
5. Results : Coverage Histogram (0-50X)



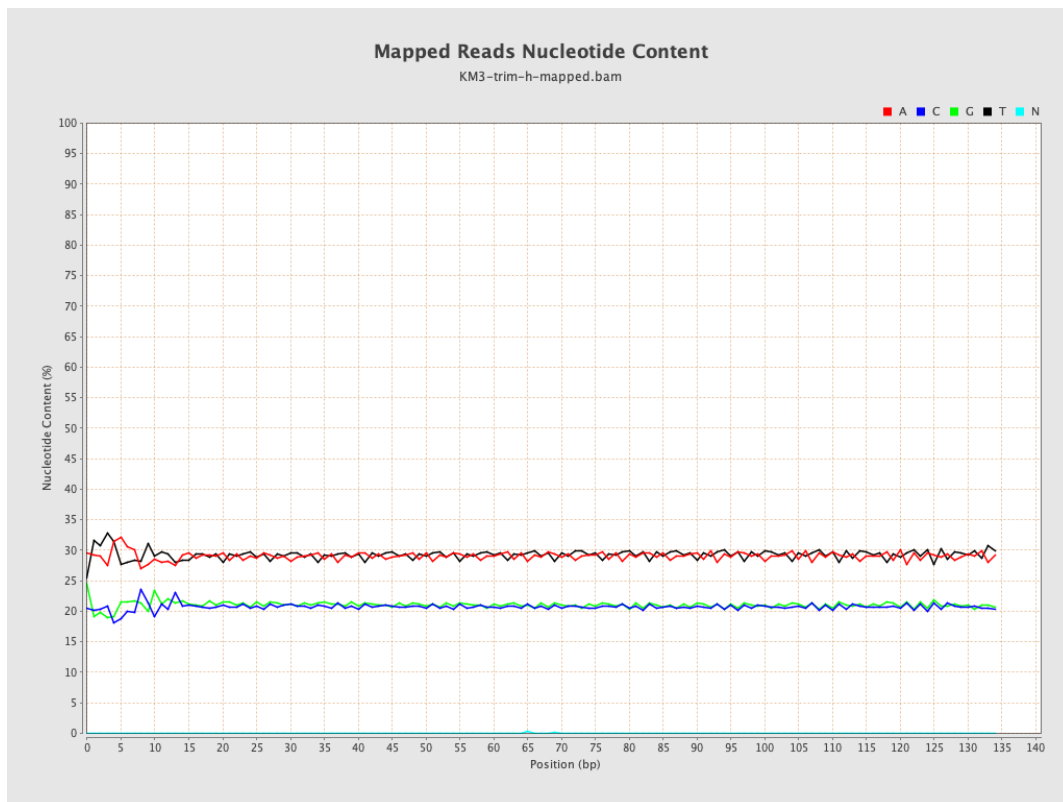
6. Results : Genome Fraction Coverage



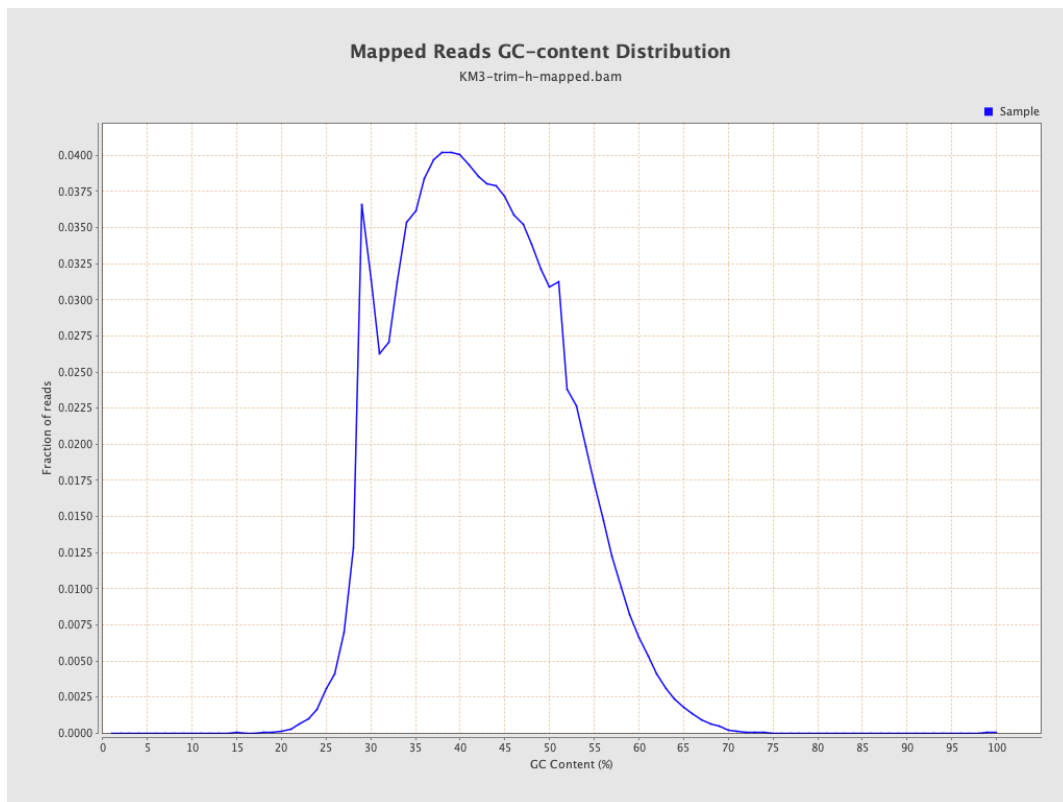
7. Results : Duplication Rate Histogram



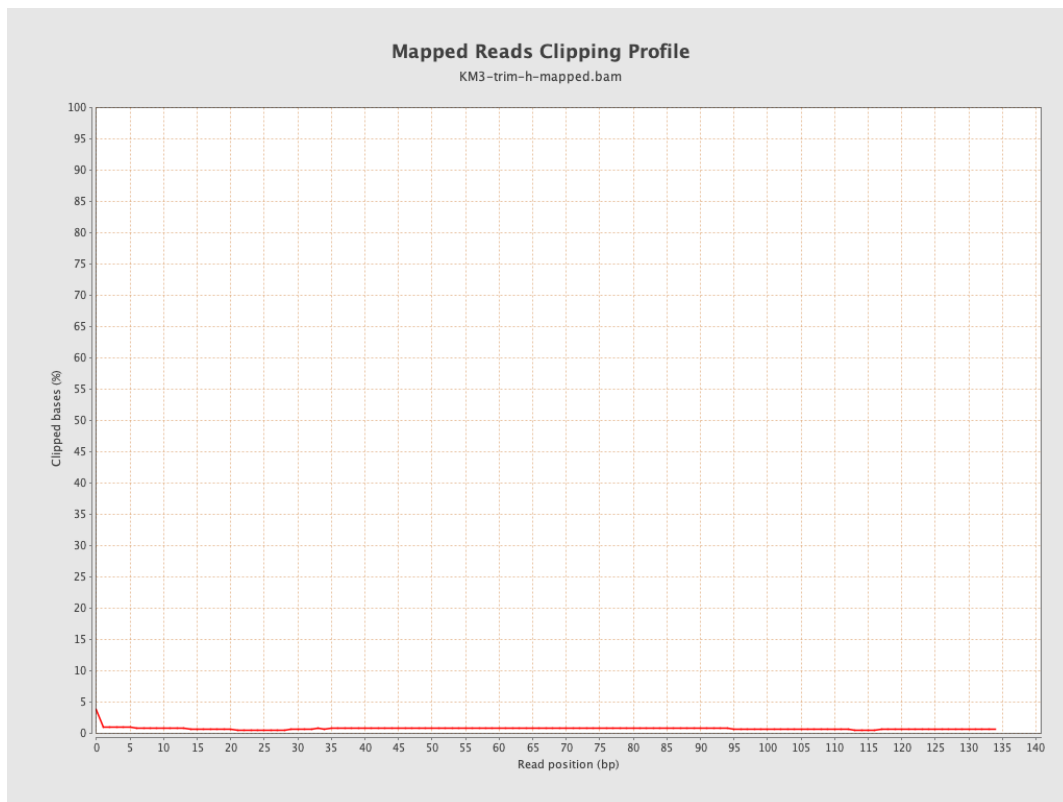
8. Results : Mapped Reads Nucleotide Content



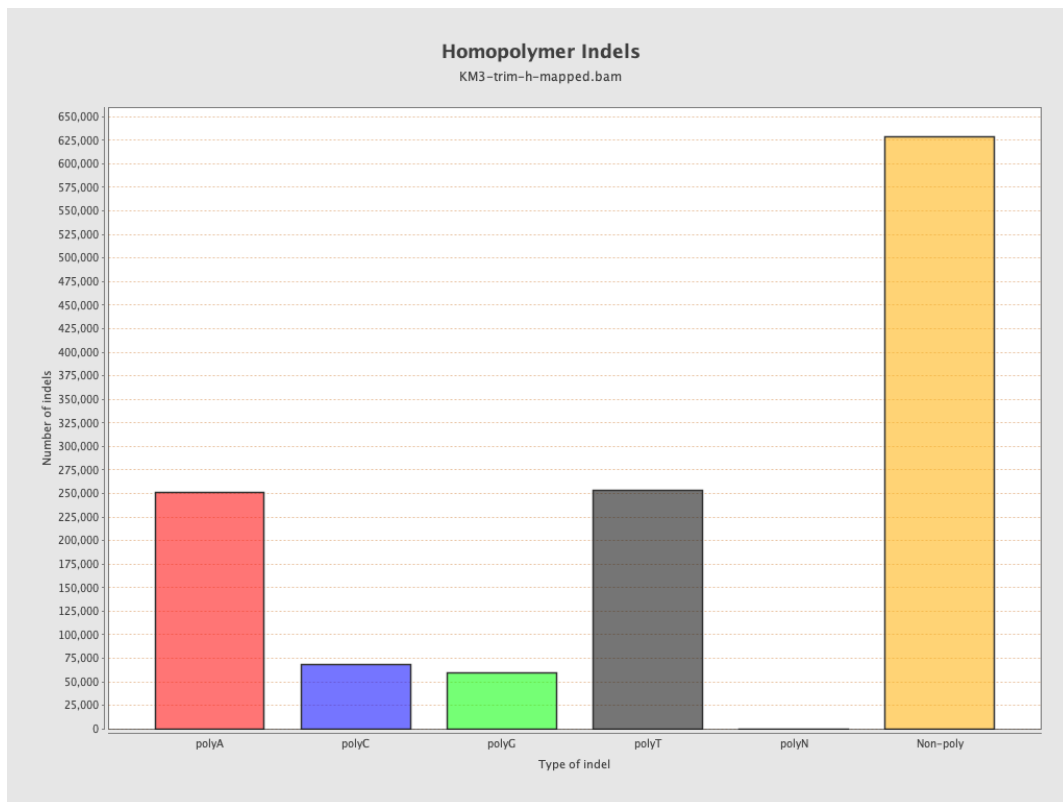
9. Results : Mapped Reads GC-content Distribution



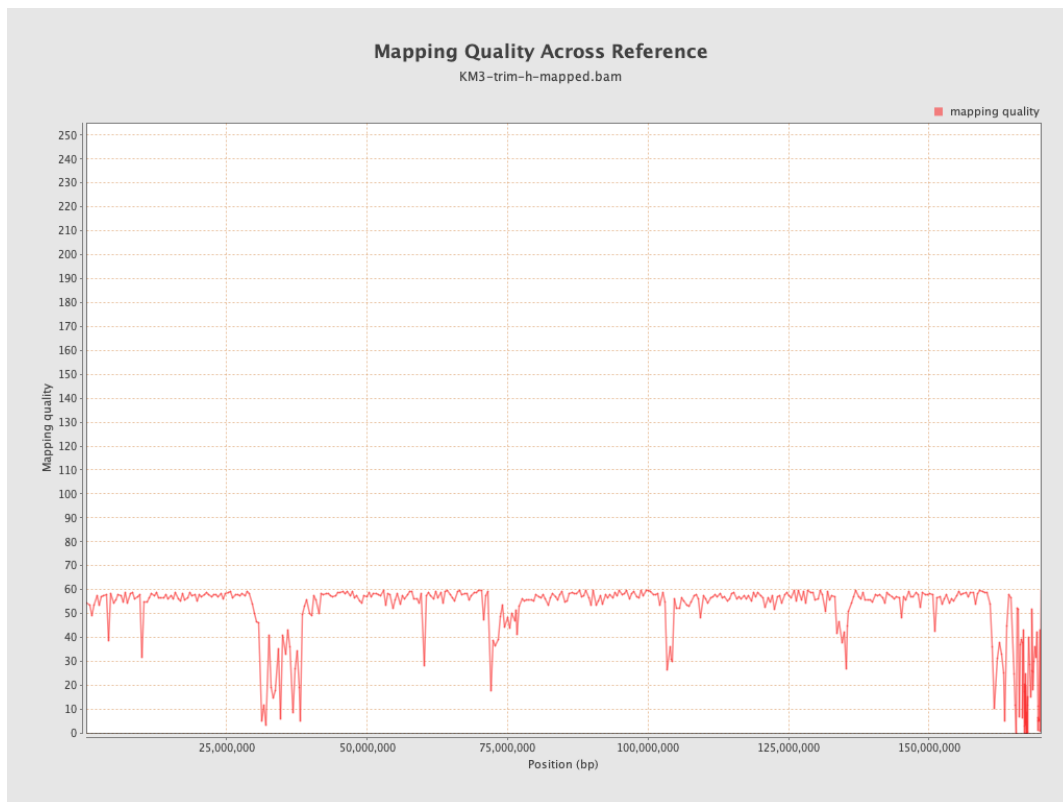
10. Results : Mapped Reads Clipping Profile



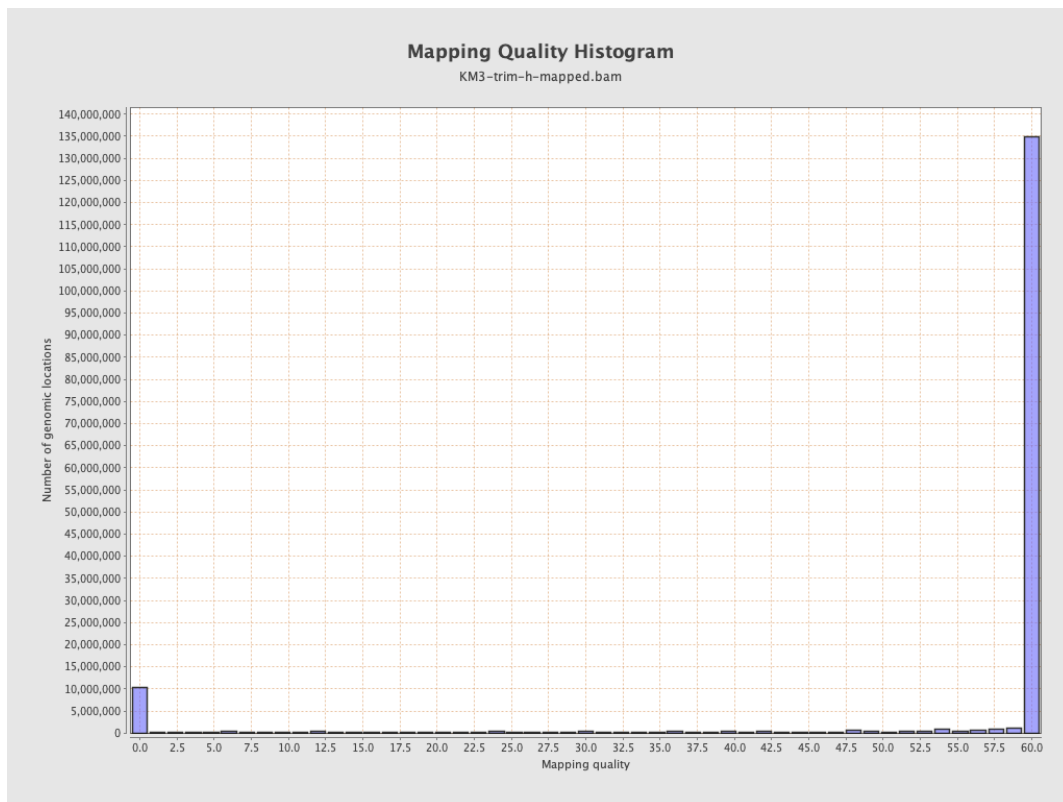
11. Results : Homopolymer Indels



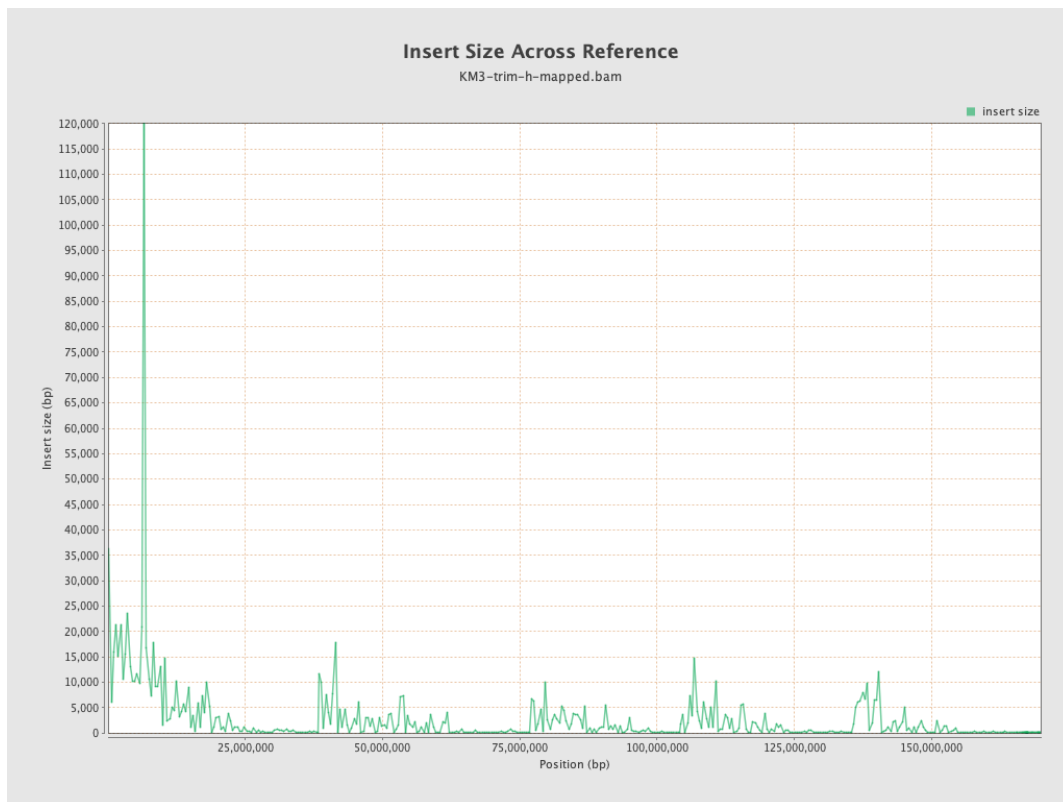
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

