Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2023/05/17 11:26:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam KM_3q-trim-h-mapped-Dvir.bam -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa mem -t 5 GCA_007989325.2_ASM798932v2_genomic.fna KM_3_1_trim.fq.gz 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:	Wed May 17 11:26:24 CDT 2023
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	KM_3q-trim-h-mapped-Dvir.bam

2. Summary

2.1. Globals

Reference size	169,771,745
Number of reads	14,102,919
Mapped reads	13,890,816 / 98.5%
Supplementary alignments	49,595 / 0.35%
Unmapped reads	212,103 / 1.5%
Mapped paired reads	13,890,816 / 98.5%
Mapped reads, first in pair	6,945,413 / 49.25%
Mapped reads, second in pair	6,945,403 / 49.25%
Mapped reads, both in pair	13,883,578 / 98.44%
Mapped reads, singletons	7,238 / 0.05%
Read min/max/mean length	30 / 135 / 115.32
Overlapping read pairs	6,114,444 / 86.71%
Duplicated reads (estimated)	3,734,956 / 26.48%
Duplication rate	21.88%
Clipped reads	1,506,829 / 10.68%

2.2. ACGT Content

Number/percentage of A's	442,408,564 / 29.01%
Number/percentage of C's	315,866,178 / 20.72%
Number/percentage of T's	445,476,881 / 29.22%
Number/percentage of G's	321,028,442 / 21.05%
Number/percentage of N's	65,450 / 0%

| GC Percentage | 41.77% |

2.3. Coverage

Mean	8.9994
Standard Deviation	56.2959
Mean (paired-end reads overlap ignored)	6.02

2.4. Mapping Quality

| Mean Mapping Quality | 49.41 |

2.5. Insert size

Mean	10,794.3
Standard Deviation	405,160.51
P25/Median/P75	73 / 115 / 174

2.6. Mismatches and indels

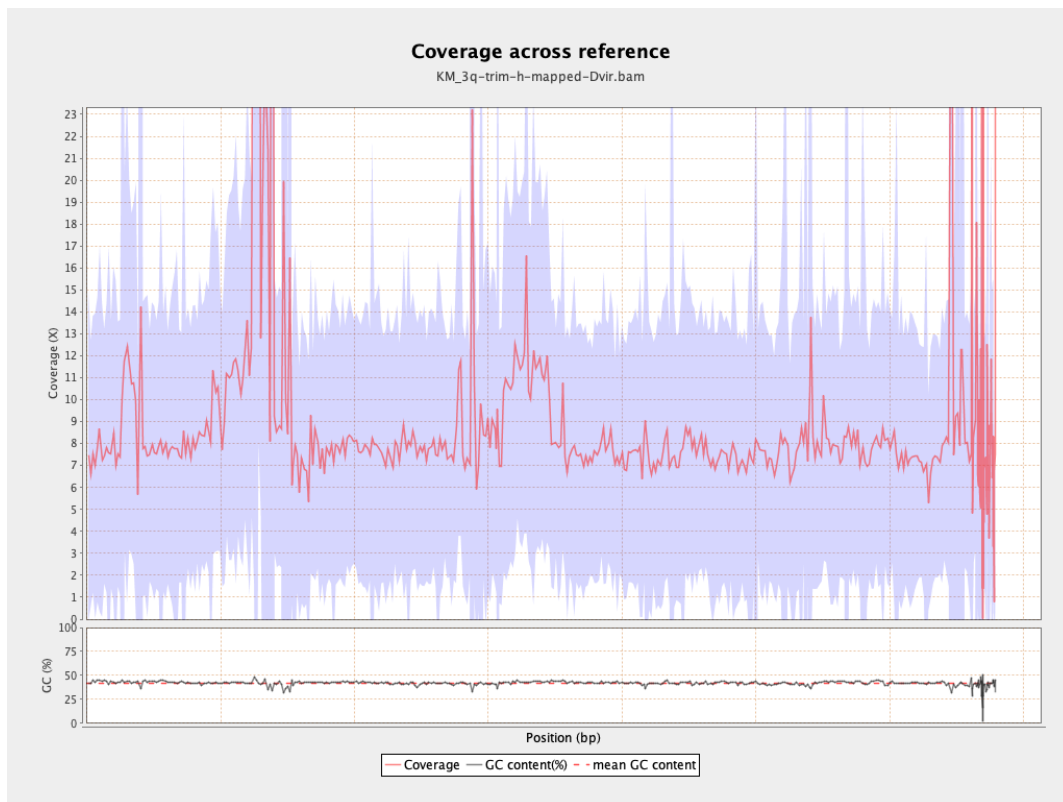| General error rate | 1.16% |
Mismatches	15,489,828
Insertions	577,792
Mapped reads with at least one insertion	3.96%
Deletions	668,789
Mapped reads with at least one deletion	4.54%
Homopolymer indels	50.12%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
CM017604.2	38193566	447064414	11.7052	96.5076
CM017605.2	38438298	307814963	8.008	48.3536
CM017606.2	27616680	245200355	8.8787	7.0197
CM017607.2	31075311	235116040	7.566	8.6659
CM017608.2	27902728	230052664	8.2448	52.4968
CM017609.2	2270151	20277796	8.9324	15.6282
VNHH02000000 05.1	16908	1155504	68.3407	99.5405
VNHH02000000 19.1	560307	4689292	8.3691	5.4294
VNHH02000000 43.1	331422	5772799	17.4183	161.6238
VNHH02000000 47.1	234219	1546921	6.6046	6.3631
VNHH02000000 48.1	20672	125234	6.0581	5.7911
VNHH02000000 50.1	275122	2181008	7.9274	8.1373
VNHH02000000 51.1	29855	151788	5.0842	5.9366
VNHH02000000 54.1	73214	549546	7.506	13.2658
VNHH02000000 55.1	19572	241685	12.3485	11.3788

VNHH02000056.1	52186	415092	7.9541	6.8141
VNHH02000082.1	47289	391667	8.2824	8.6257
VNHH02000089.1	52137	311910	5.9825	6.7928
VNHH02000090.1	34989	322063	9.2047	11.051
VNHH02000095.1	19220	1081090	56.2482	71.6746
VNHH02000097.1	29477	752903	25.542	65.3658
VNHH02000102.1	56772	767308	13.5156	49.8328
VNHH02000105.1	30176	309	0.0102	0.1229
VNHH02000107.1	21993	2115	0.0962	2.3244
VNHH02000108.1	19534	1224258	62.6732	87.1356
VNHH02000111.1	26096	36471	1.3976	5.7512
VNHH02000112.1	17191	443046	25.772	31.1625
VNHH02000113.1	49501	2374150	47.9617	73.0052
VNHH02000116.1	21351	1291638	60.4954	82.4761
VNHH02000127.1	25842	113393	4.3879	3.7994

VNHH020001 50.1	521567	3705964	7.1054	5.8441
VNHH020001 51.1	86477	412739	4.7728	5.711
VNHH020001 71.1	104324	1306795	12.5263	6.6164
VNHH020001 77.1	231566	1852758	8.001	49.5715
VNHH020001 81.1	21731	80474	3.7032	3.7813
VNHH020001 87.1	442058	3637233	8.228	7.6125
VNHH020001 88.1	321154	2070390	6.4467	8.2052
VNHH020001 91.1	107803	864184	8.0163	6.8775
VNHH020001 95.1	27877	128127	4.5962	4.9347
VNHH020001 96.1	18248	59874	3.2811	3.2172
VNHH020001 97.1	24842	206797	8.3245	6.9048
VNHH020001 98.1	144193	115696	0.8024	3.1204
VNHH020002 01.1	110897	751933	6.7805	5.6034
VNHH020002 07.1	17506	131505	7.512	7.2666
VNHH020002 08.1	29723	1055199	35.5011	33.3488

3. Results : Coverage across reference

Coverage across reference
KM_3q-trim-h-mapped-Dvir.bam

4. Results : Coverage Histogram

Coverage Histogram
KM_3q-trim-h-mapped-Dvir.bam

5. Results : Coverage Histogram (0-50X)
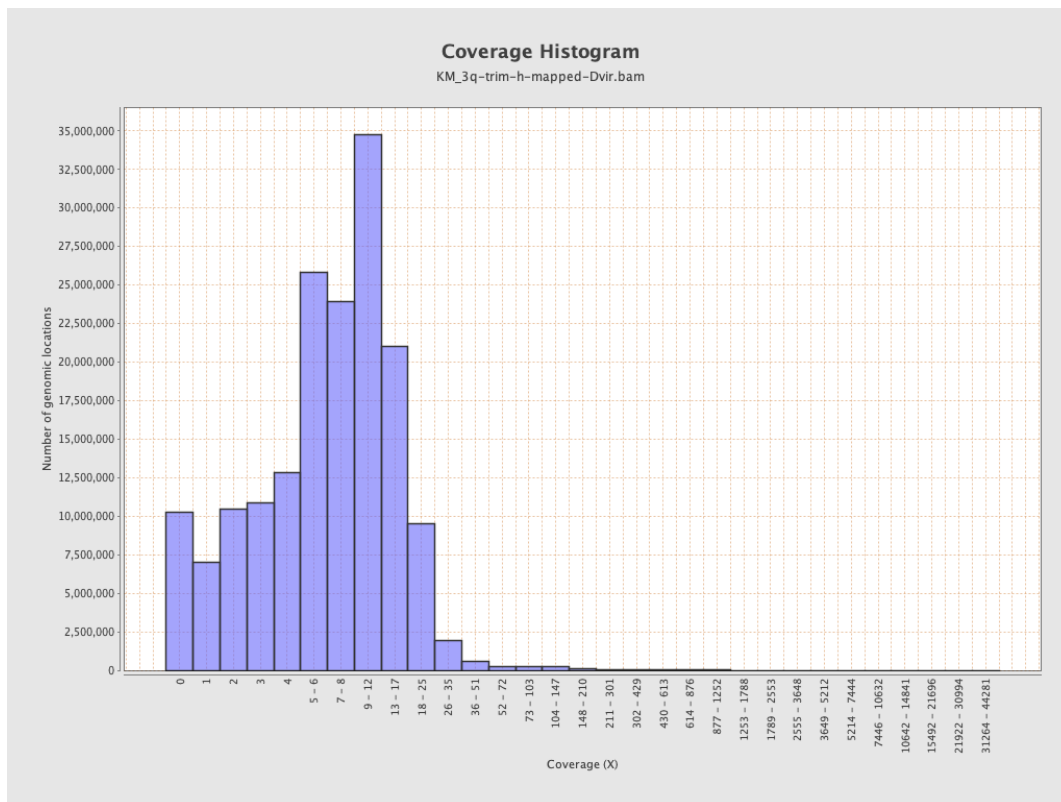
Coverage Histogram (0-50X)
KM_3q-trim-h-mapped-Dvir.bam
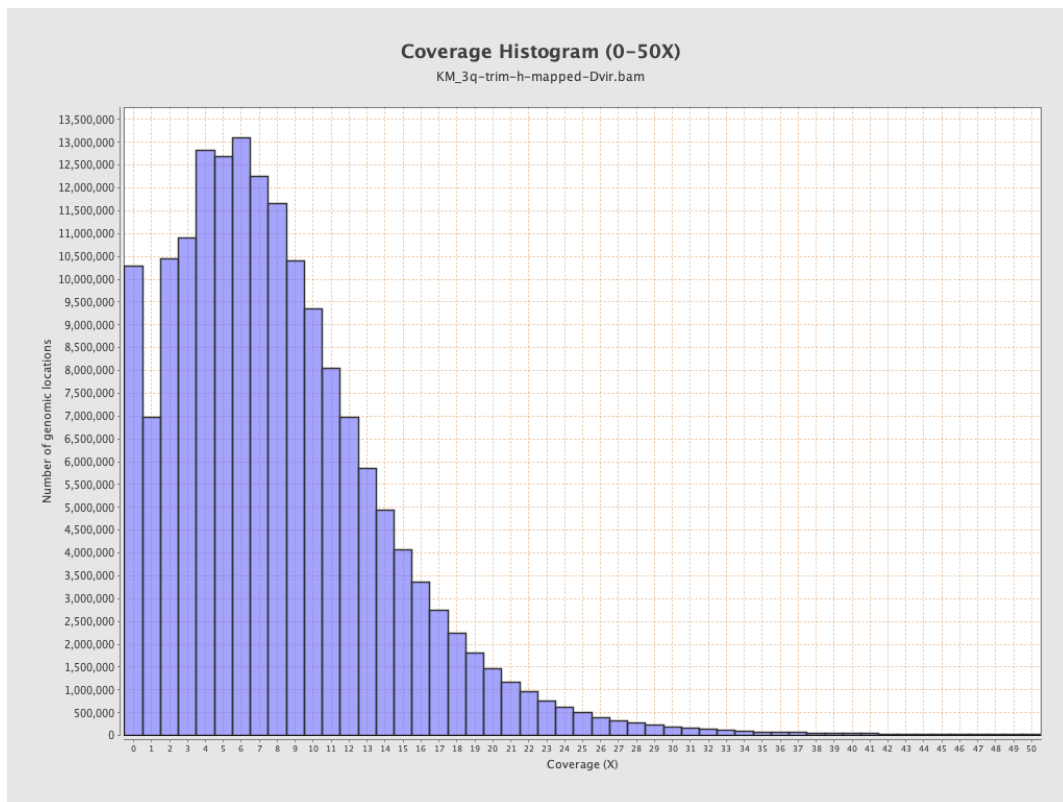
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
KM_3q-trim-h-mapped-Dvir.bam
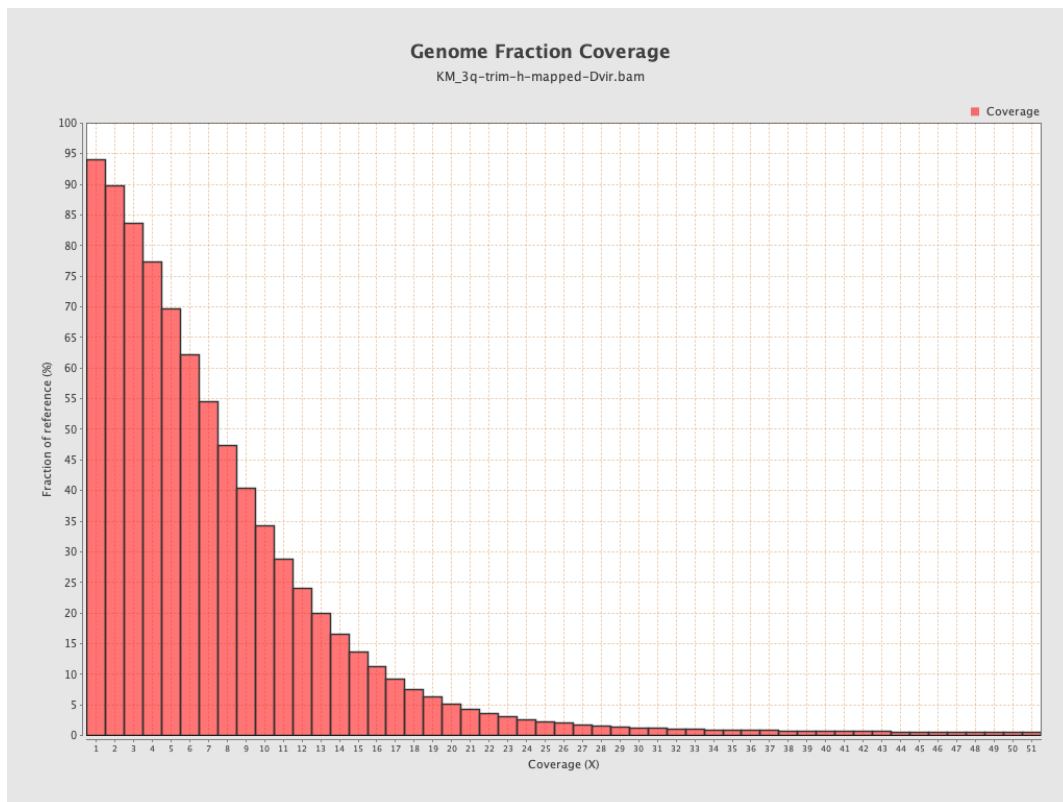
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
KM_3q–trim–h–mapped–Dvir.bam

8. Results : Mapped Reads Nucleotide Content
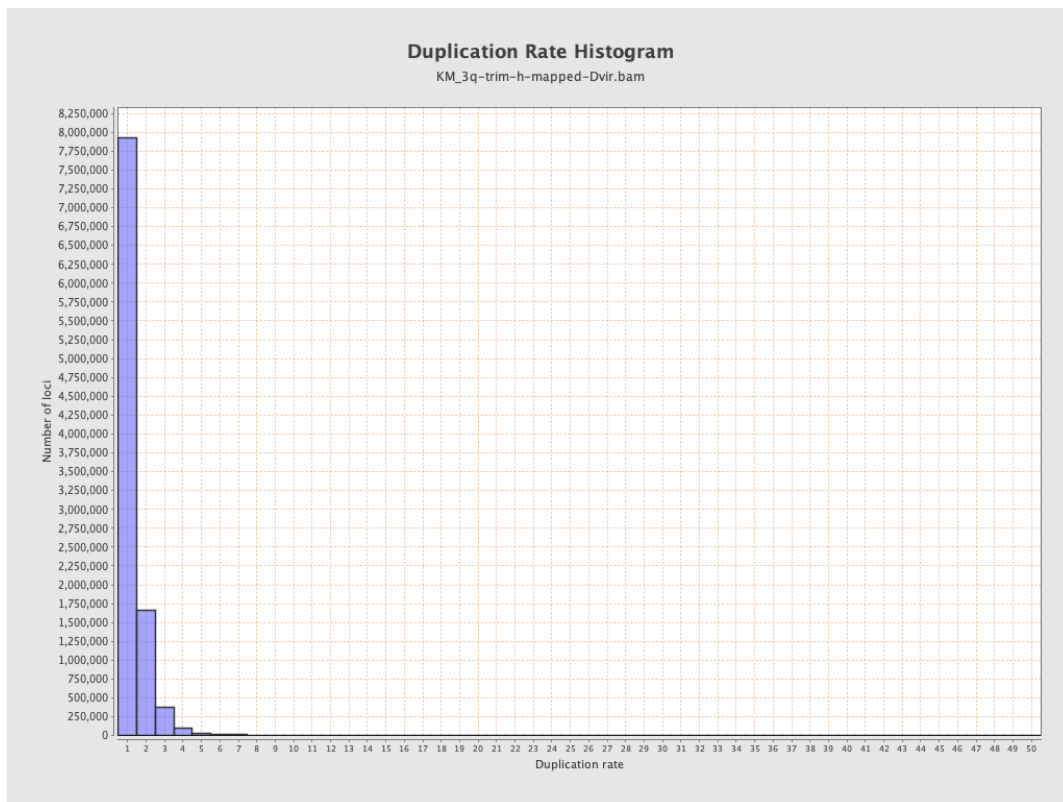
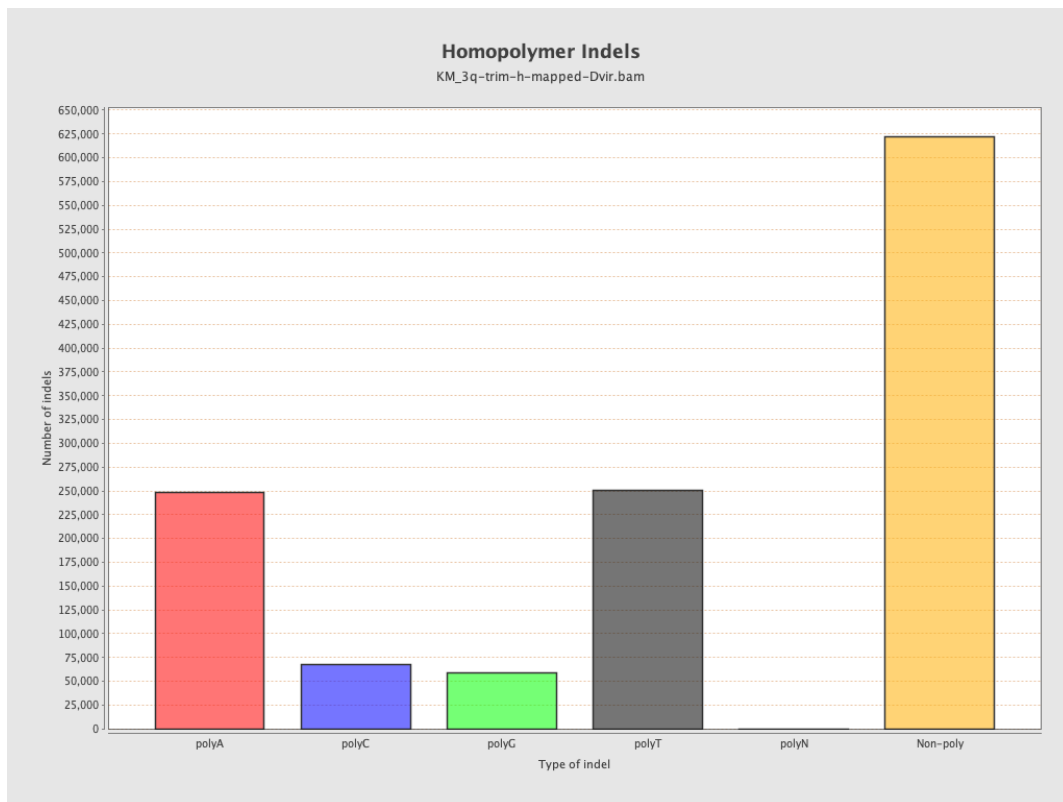Mapped Reads Nucleotide Content
KM_3q-trim-h-mapped-Dvir.bam
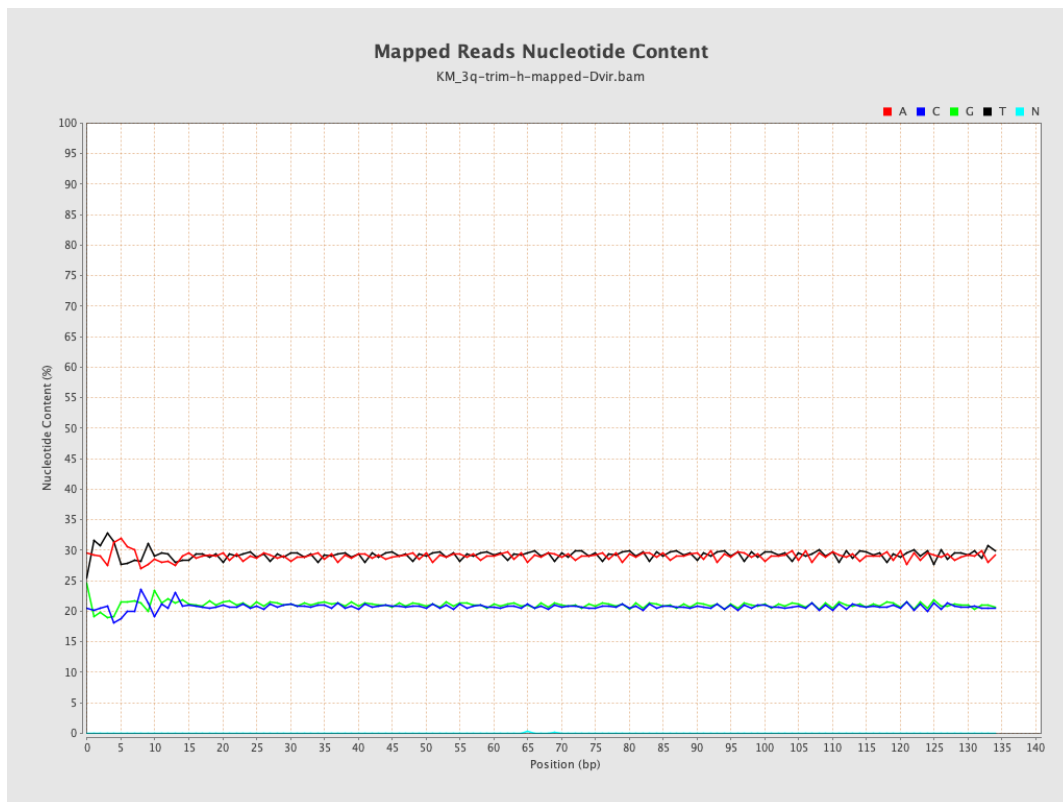
9. Results : Mapped Reads GC-content Distribution
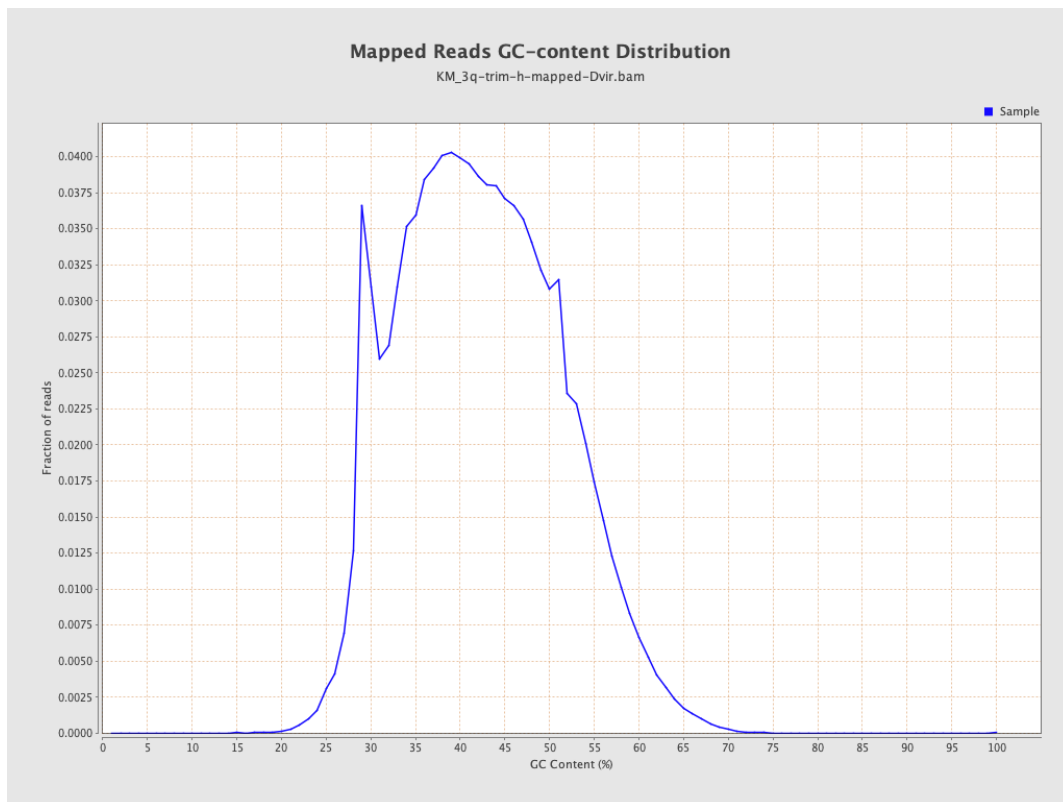
10. Results : Mapped Reads Clipping Profile
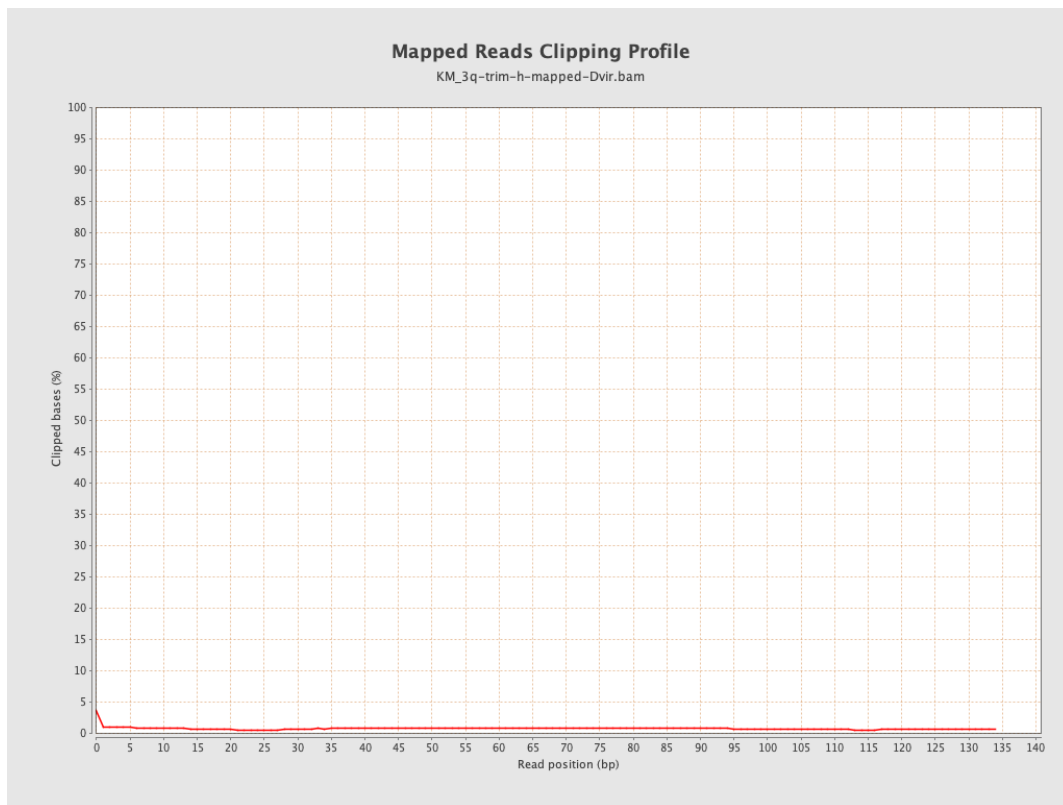
11. Results : Homopolymer Indels

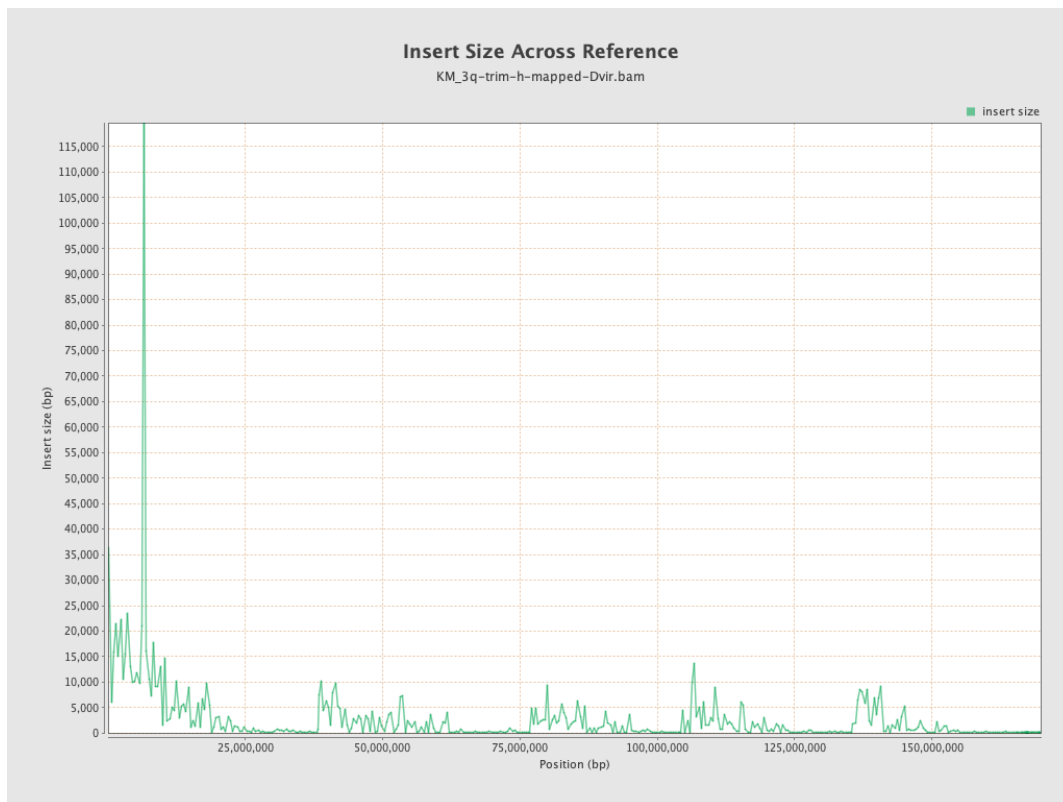**Homopolymer Indels**
KM_3q-trim-h-mapped-Dvir.bam

12. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
KM_3q-trim-h-mapped-Dvir.bam

13. Results : Mapping Quality Histogram
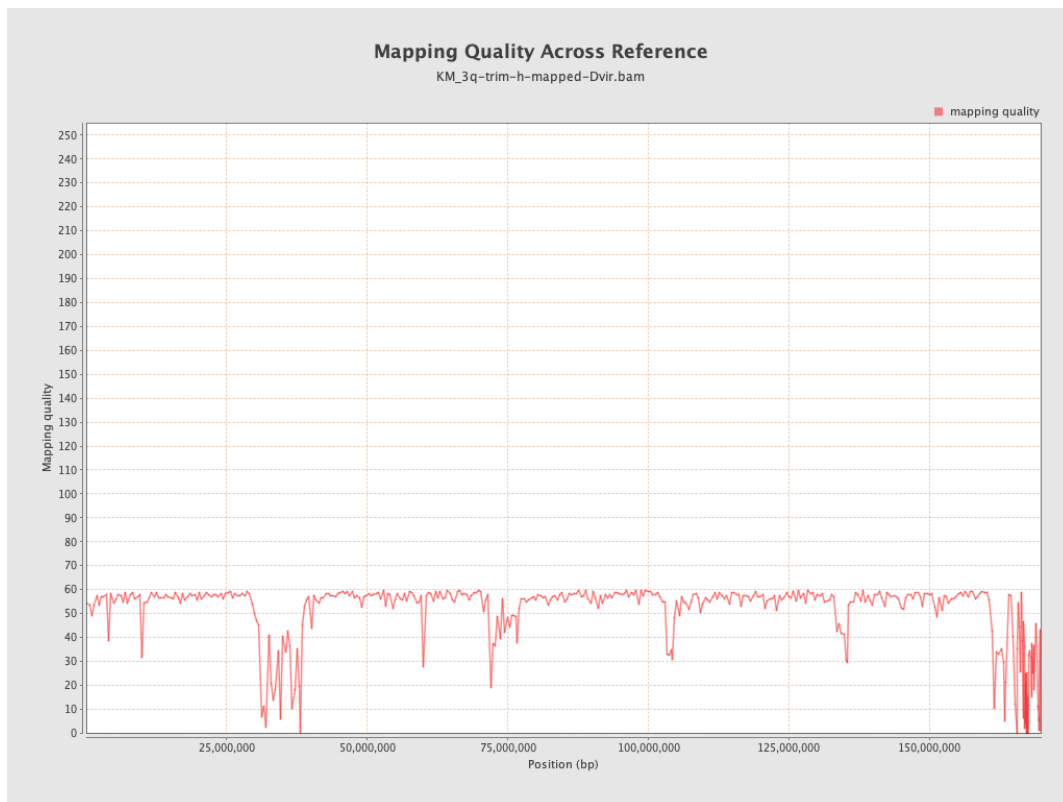
Mapping Quality Histogram
KM_3q-trim-h-mapped-Dvir.bam
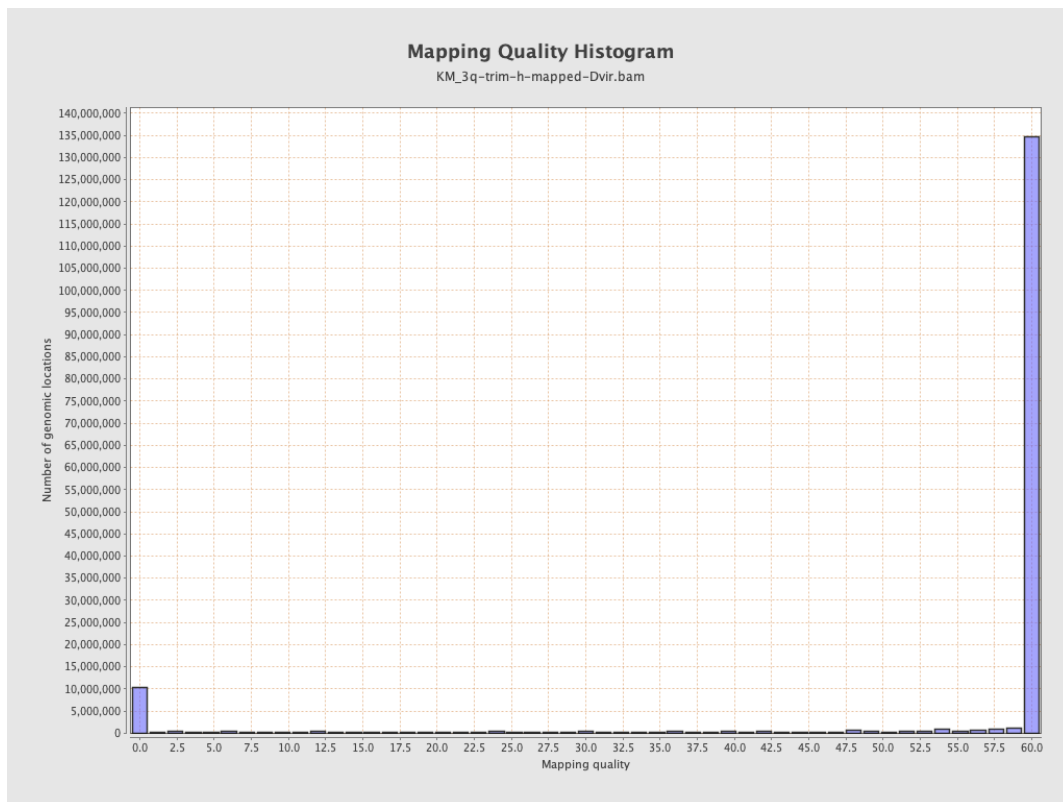
14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram

Insert Size Histogram
KM_3q-trim-h-mapped-Dvir.bam