Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 13:47:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM244.sorted.bam.ba
m -nw 400 -hm 3
```

1.2. Alignment

Command line:	bwa mem -M /home/vdp5/data/salvador_vivax_asia _2016/first-SAMEA2376790/pvivax_sal1_SAME A2376790.fasta /home/vdp5/data/cambodia_samples/ sequences_gz/OM244-BiooBarcode22_CGTACG_R1.fastq. gz /home/vdp5/data/cambodia_samples/ sequences_gz/OM244-BiooBarcode22_CGTACG_R2.fastq. gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:47:13 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/ sequences_bam/OM244.sorted.bam.

	bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	3,319,500
Mapped reads	2,182,558 / 65.75%
Unmapped reads	1,136,942 / 34.25%
Mapped paired reads	2,182,558 / 65.75%
Mapped reads, first in pair	1,094,701 / 32.98%
Mapped reads, second in pair	1,087,857 / 32.77%
Mapped reads, both in pair	2,140,280 / 64.48%
Mapped reads, singletons	42,278 / 1.27%
Read min/max/mean length	30 / 100 / 99.9
Duplicated reads (estimated)	240,629 / 7.25%
Duplication rate	8.19%
Clipped reads	251,076 / 7.56%

2.2. ACGT Content

Number/percentage of A's	63,340,058 / 30.06%
Number/percentage of C's	41,951,797 / 19.91%
Number/percentage of T's	63,527,398 / 30.15%
Number/percentage of G's	41,863,585 / 19.87%
Number/percentage of N's	17,394 / 0.01%
GC Percentage	39.78%

2.3. Coverage

Mean	8.8029
Standard Deviation	9.1652

2.4. Mapping Quality

Mean Mapping Quality	58.68

2.5. Insert size

Mean	781.11
Standard Deviation	24,402.68
P25/Median/P75	318 / 338 / 348

2.6. Mismatches and indels

General error rate	1.63%
Mismatches	3,265,301
Insertions	70,106
Mapped reads with at least one insertion	3.04%
Deletions	79,311
Mapped reads with at least one deletion	3.43%
Homopolymer indels	62.48%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	7859681	8.0429	6.8084
gi|1074120682|emb|LT615257.1|	860454	6793262	7.895	6.1812
gi|1074120865|emb|LT615258.1|	989719	9671441	9.7719	12.9786
gi|1074121086|emb|LT615259.1|	935450	9488034	10.1427	16.3295
gi|1074121301|emb|LT615260.1|	1432239	14013427	9.7843	11.5259
gi|1074121615|emb|LT615261.1|	1080962	10085605	9.3302	9.9297
gi|1074121871|emb|LT615262.1|	1545099	12589177	8.1478	4.2826
gi|1074122235|emb|LT615263.1|	1585108	13780066	8.6935	7.7607
gi|1074122590|emb|LT615264.1|	2122358	17666470	8.324	5.1998
gi|1074123050|emb|LT615265.1|	1754192	15725506	8.9645	7.8881
gi|1074123421|emb|LT615	2150147	19989012	9.2966	15.9146

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	25739066	8.4918	4.9282
gi|1074124588|emb|LT615268.1|	2359348	19653823	8.3302	10.2712
gi|1074125065|emb|LT615269.1|	3135668	27854835	8.8832	4.2221

3. Results : Coverage across reference

Coverage across reference
OM244.sorted.bam.bam

4. Results : Coverage Histogram

Coverage Histogram
OM244.sorted.bam.bam
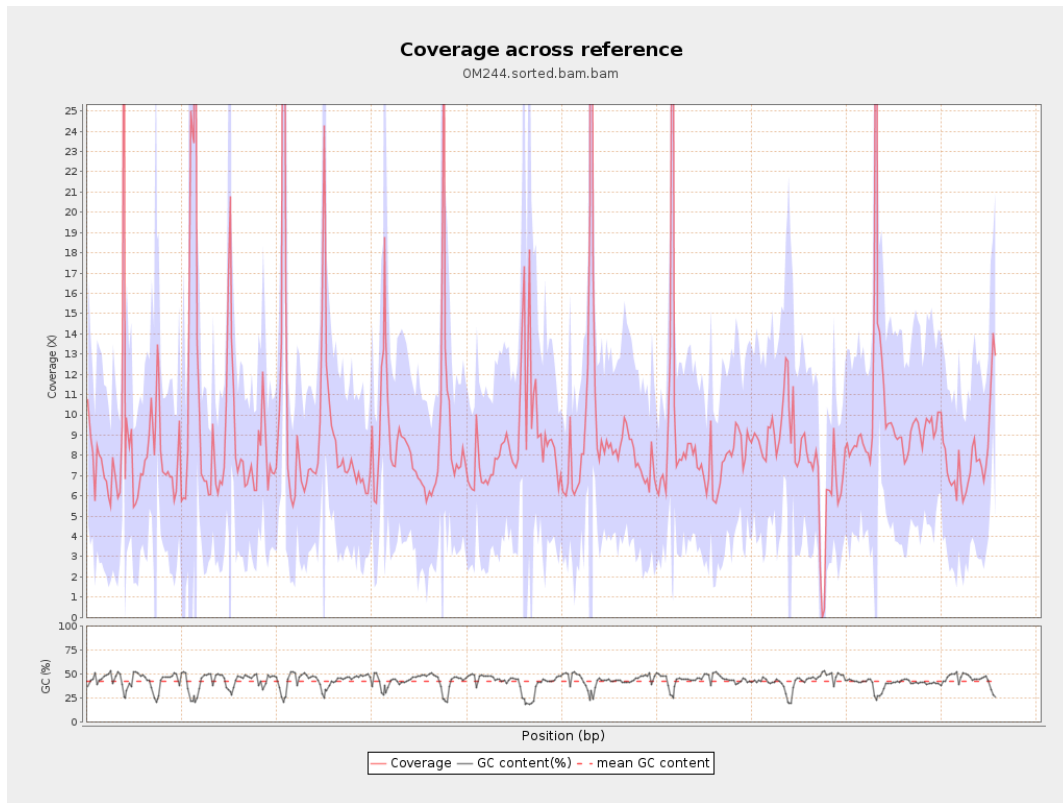
5. Results : Coverage Histogram (0-50X)
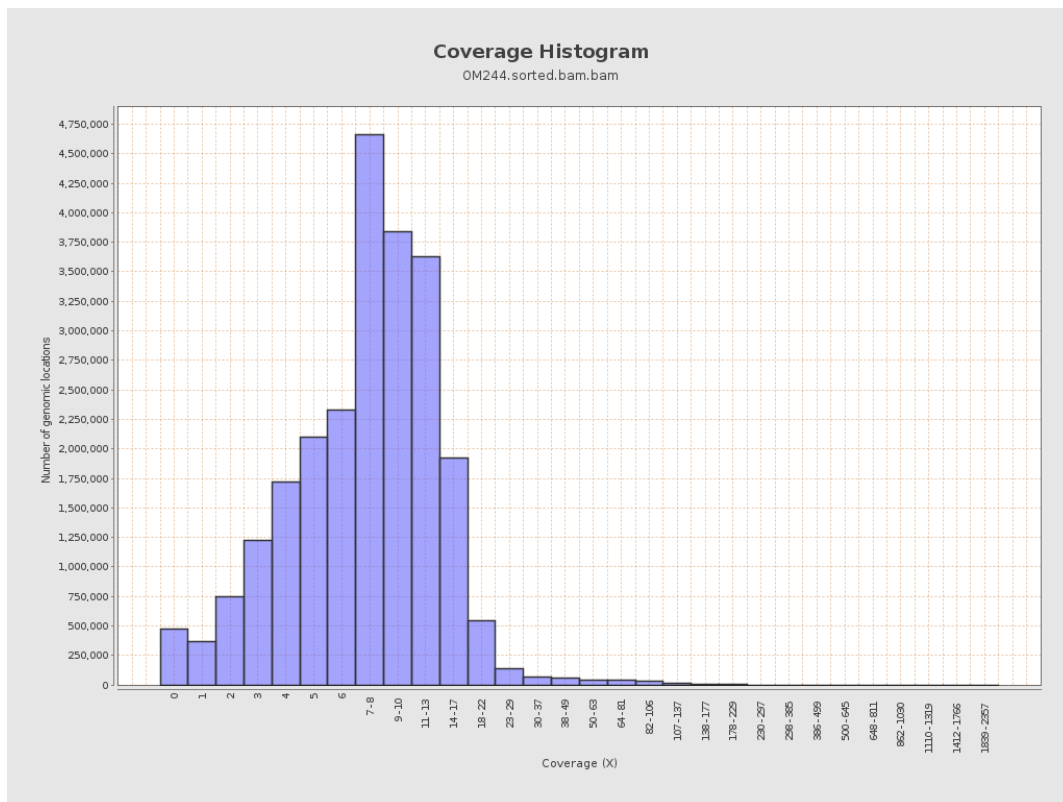
Coverage Histogram (0-50X)
OM244.sorted.bam.bam
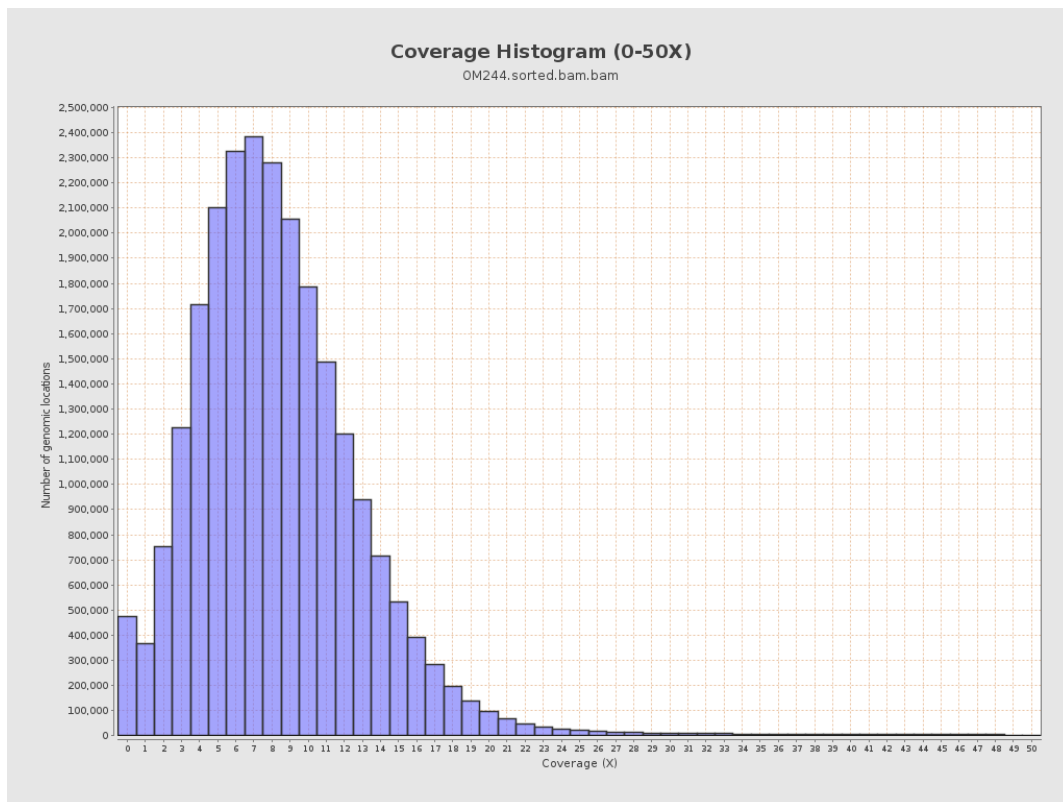
6. Results : Genome Fraction Coverage

Genome Fraction Coverage
OM244.sorted.bam.bam
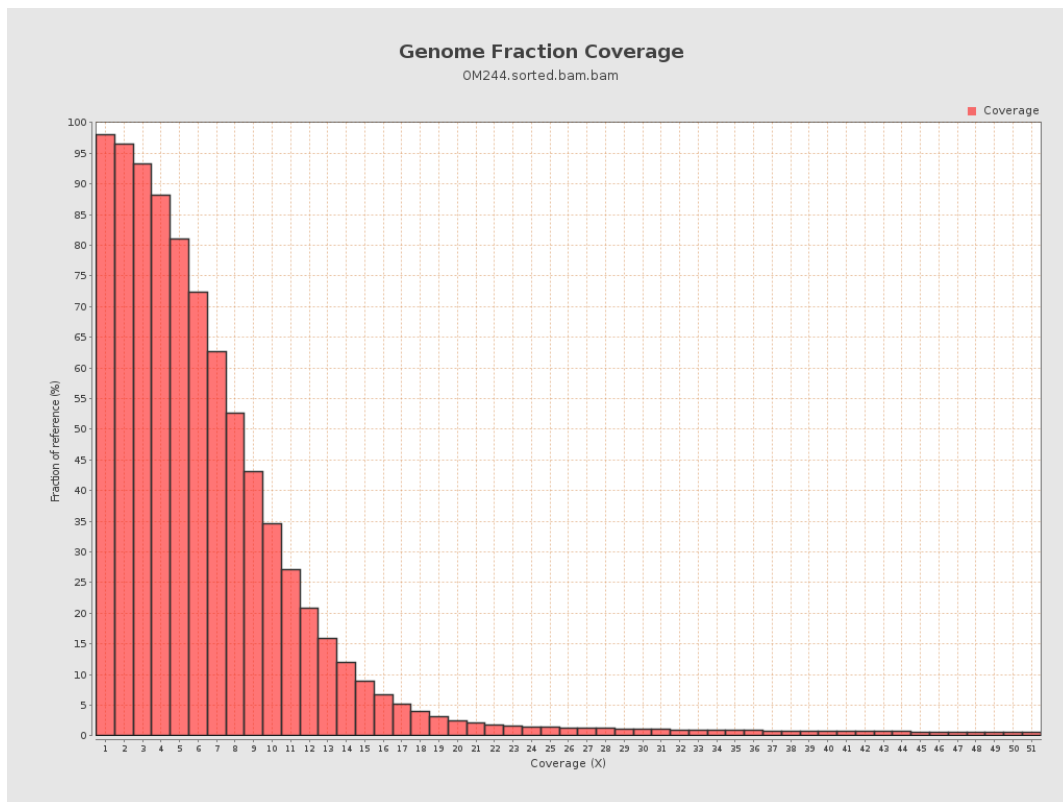
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
OM244.sorted.bam.bam
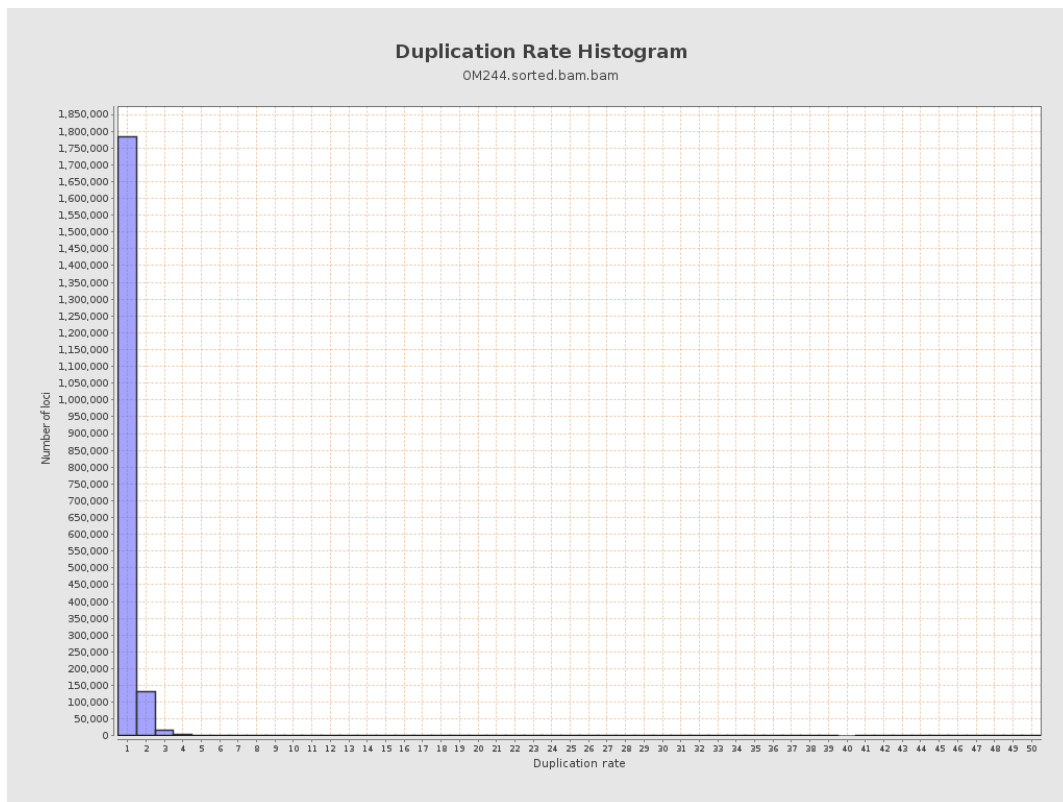
8. Results : Mapped Reads Nucleotide Content

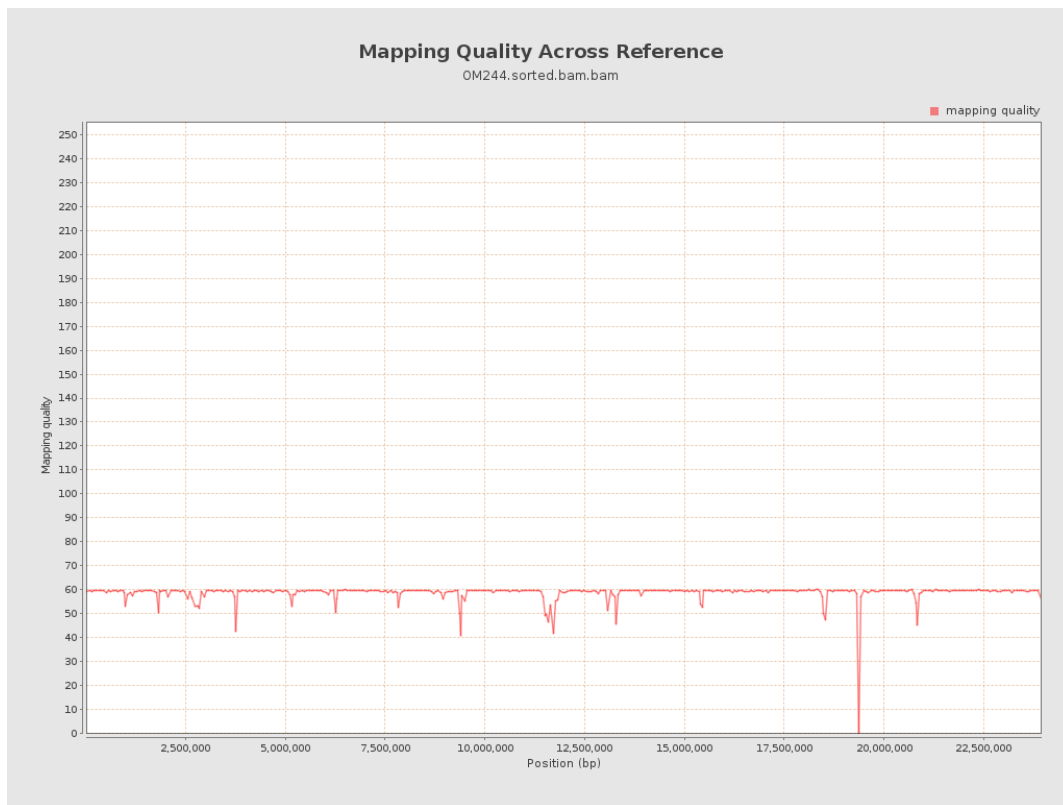# 9. Results : Mapped Reads GC-content Distribution
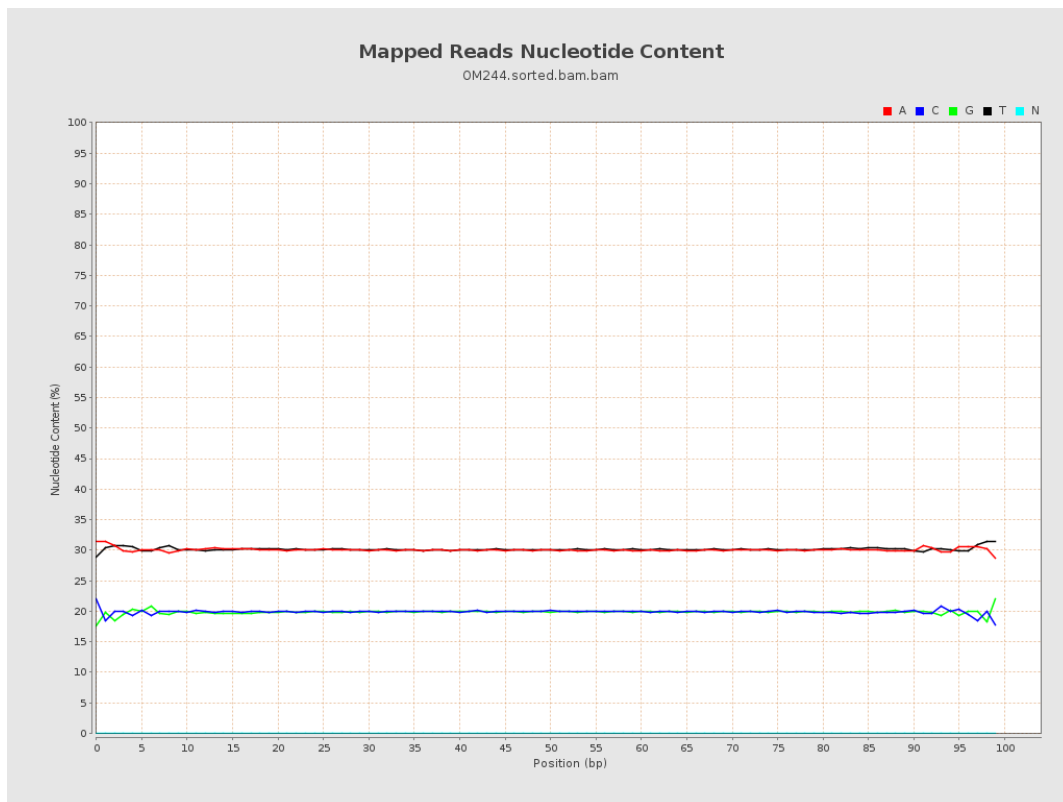
Mapped Reads GC-content Distribution
OM244.sorted.bam.bam
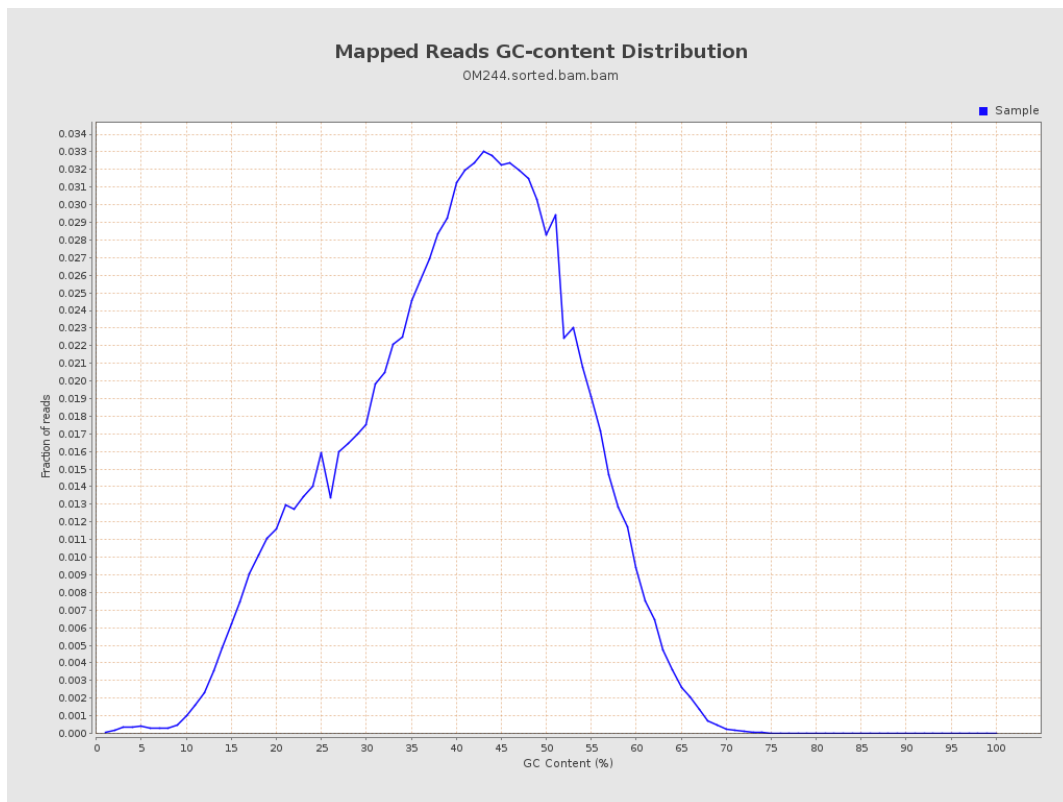
10. Results : Mapped Reads Clipping Profile

Mapped Reads Clipping Profile
OM244.sorted.bam.bam
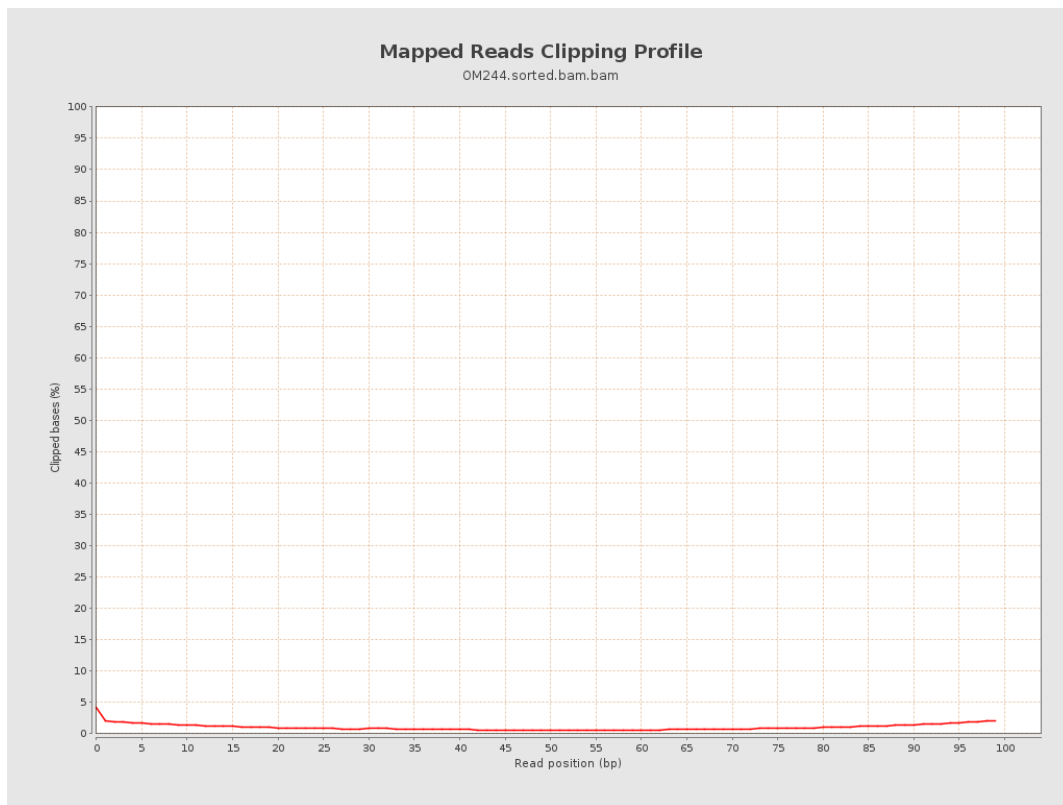
11. Results : Homopolymer Indels
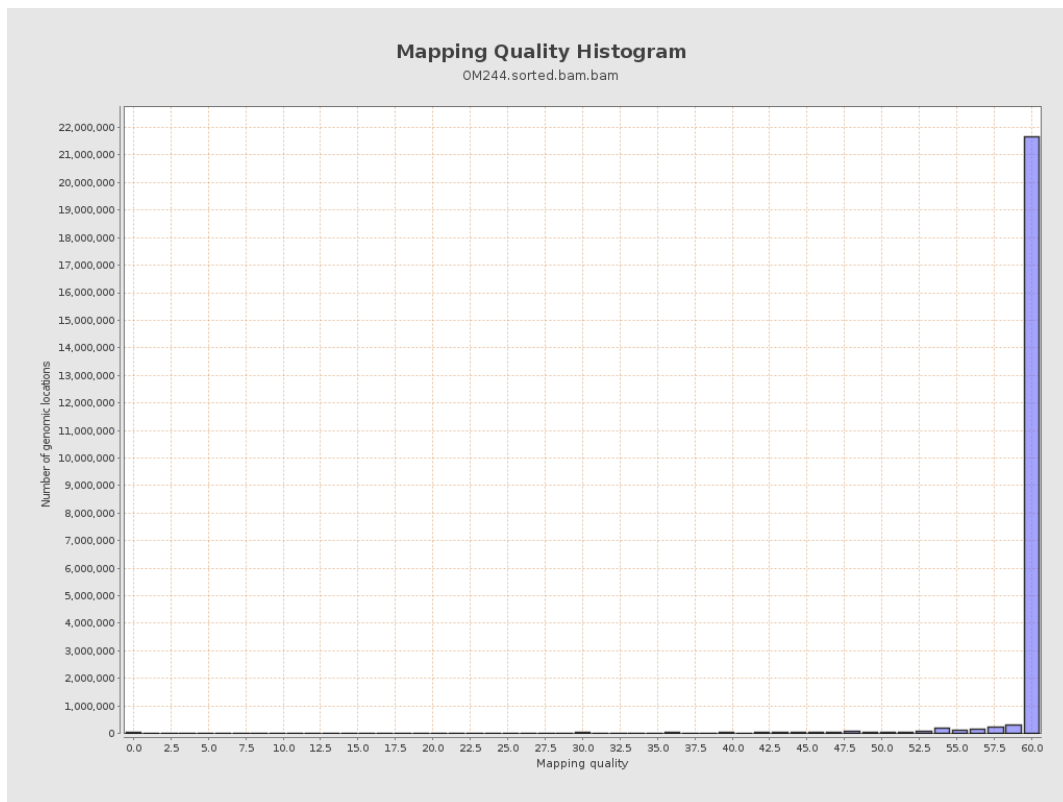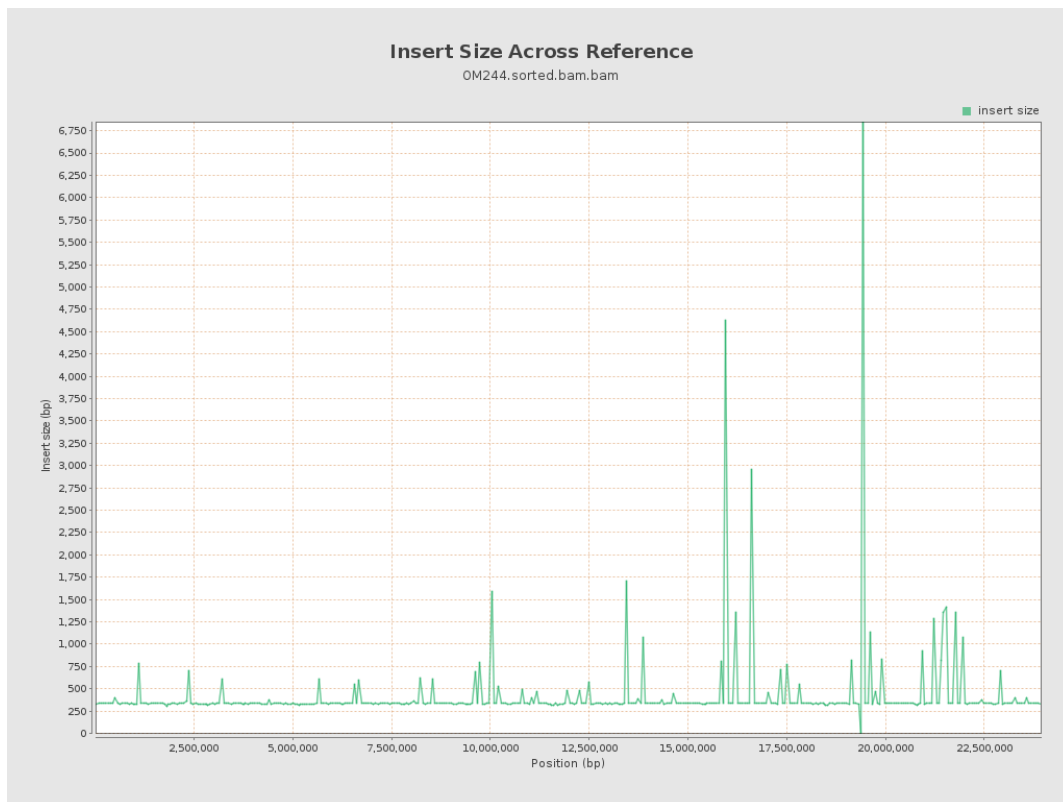

Homopolymer Indels
OM244.sorted.bam.bam
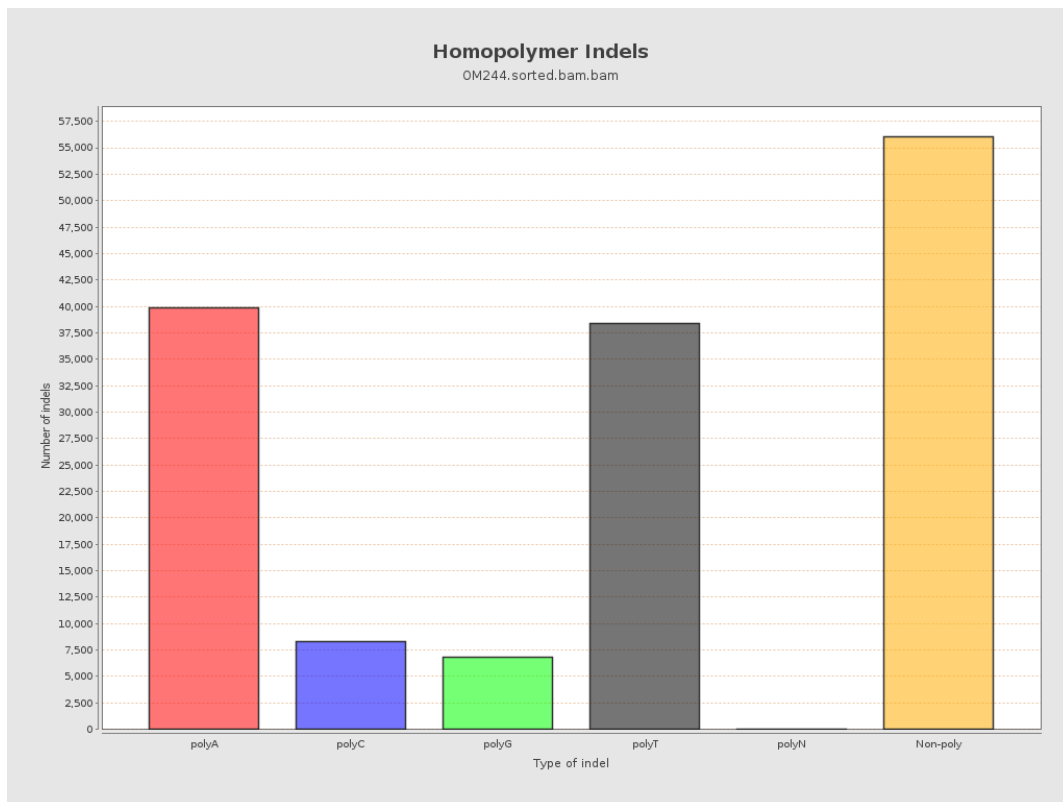
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram