Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 13:47:58

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM245.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_SAMEA2376790.fasta /home/vdp5/data/cambodia_samples/sequences_gz/OM245-BiooBarcode23_GAGTGG_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM245-BiooBarcode23_GAGTGG_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:47:57 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM245.sorted.bam.

	bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	5,334,163
Mapped reads	1,506,181 / 28.24%
Unmapped reads	3,827,982 / 71.76%
Mapped paired reads	1,506,181 / 28.24%
Mapped reads, first in pair	756,476 / 14.18%
Mapped reads, second in pair	749,705 / 14.05%
Mapped reads, both in pair	1,455,322 / 27.28%
Mapped reads, singletons	50,859 / 0.95%
Read min/max/mean length	30 / 100 / 99.95
Duplicated reads (estimated)	147,661 / 2.77%
Duplication rate	6.99%
Clipped reads	196,235 / 3.68%

2.2. ACGT Content

Number/percentage of A's	43,288,798 / 30.06%
Number/percentage of C's	28,663,251 / 19.91%
Number/percentage of T's	43,457,750 / 30.18%
Number/percentage of G's	28,588,148 / 19.85%
Number/percentage of N's	10,822 / 0.01%
GC Percentage	39.76%

2.3. Coverage

Mean	6.0167
Standard Deviation	6.8878

2.4. Mapping Quality

Mean Mapping Quality	58.35

2.5. Insert size

Mean	904.74
Standard Deviation	27,186.8
P25/Median/P75	339 / 360 / 370

2.6. Mismatches and indels

General error rate	1.67%
Mismatches	2,296,765
Insertions	48,559
Mapped reads with at least one insertion	3.05%
Deletions	55,329
Mapped reads with at least one deletion	3.44%
Homopolymer indels	62.25%

2.7. Chromosome stats

| Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	5196483	5.3176	3.7048
gi|1074120682|emb|LT615257.1|	860454	5576161	6.4805	6.269
gi|1074120865|emb|LT615258.1|	989719	7127466	7.2015	10.9691
gi|1074121086|emb|LT615259.1|	935450	6059871	6.478	9.446
gi|1074121301|emb|LT615260.1|	1432239	9095847	6.3508	6.8928
gi|1074121615|emb|LT615261.1|	1080962	6692871	6.1916	6.6087
gi|1074121871|emb|LT615262.1|	1545099	8595500	5.5631	3.3553
gi|1074122235|emb|LT615263.1|	1585108	9439313	5.955	6.7412
gi|1074122590|emb|LT615264.1|	2122358	12131954	5.7163	4.0592
gi|1074123050|emb|LT615265.1|	1754192	10974826	6.2563	10.96
gi|1074123421|emb|LT615	2150147	13534560	6.2947	10.8376

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	17463366	5.7615	4.4963
gi|1074124588|emb|LT615268.1|	2359348	13070734	5.54	5.8459
gi|1074125065|emb|LT615269.1|	3135668	19195758	6.1217	3.4844

3. Results : Coverage across reference

Coverage across reference
OM245.sorted.bam.bam

4. Results : Coverage Histogram

Coverage Histogram
OM245.sorted.bam.bam
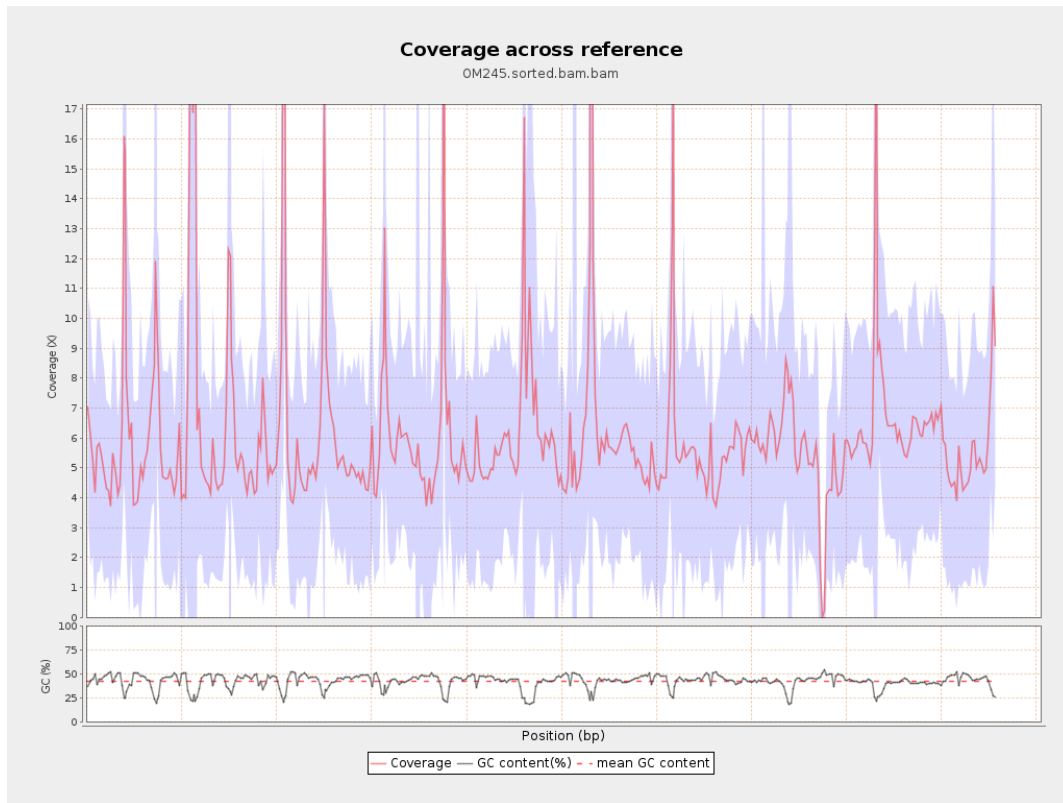
5. Results : Coverage Histogram (0-50X)
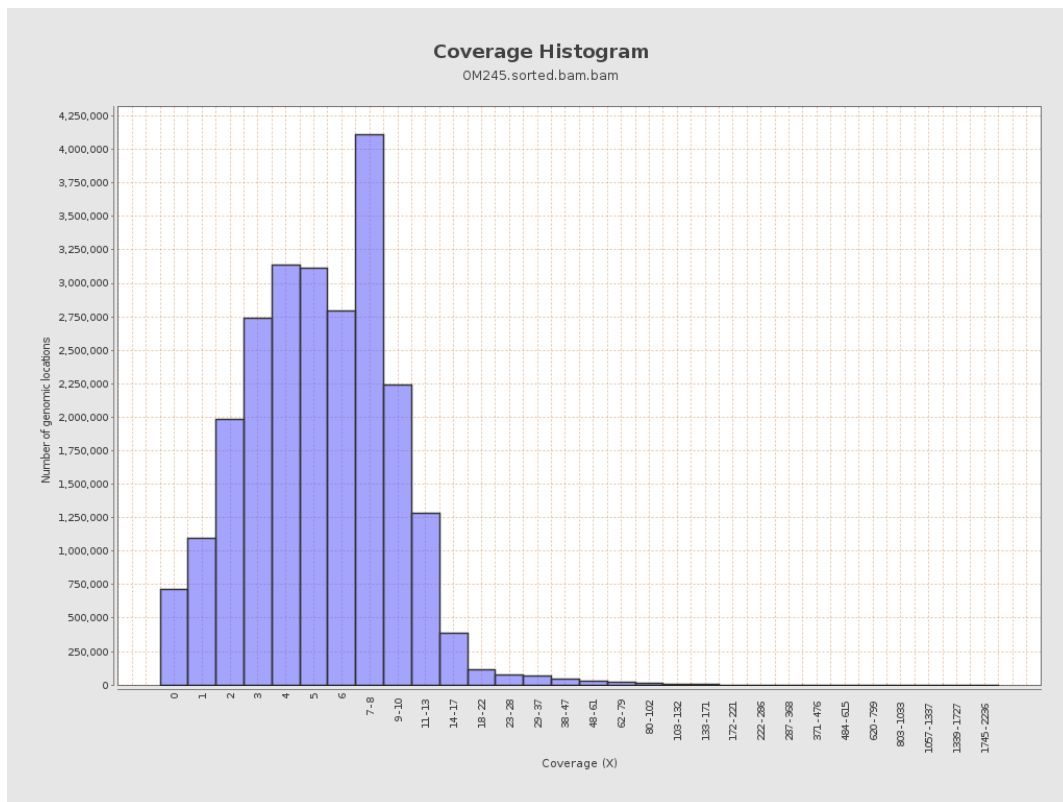
Coverage Histogram (0-50X)
0M245.sorted.bam.bam
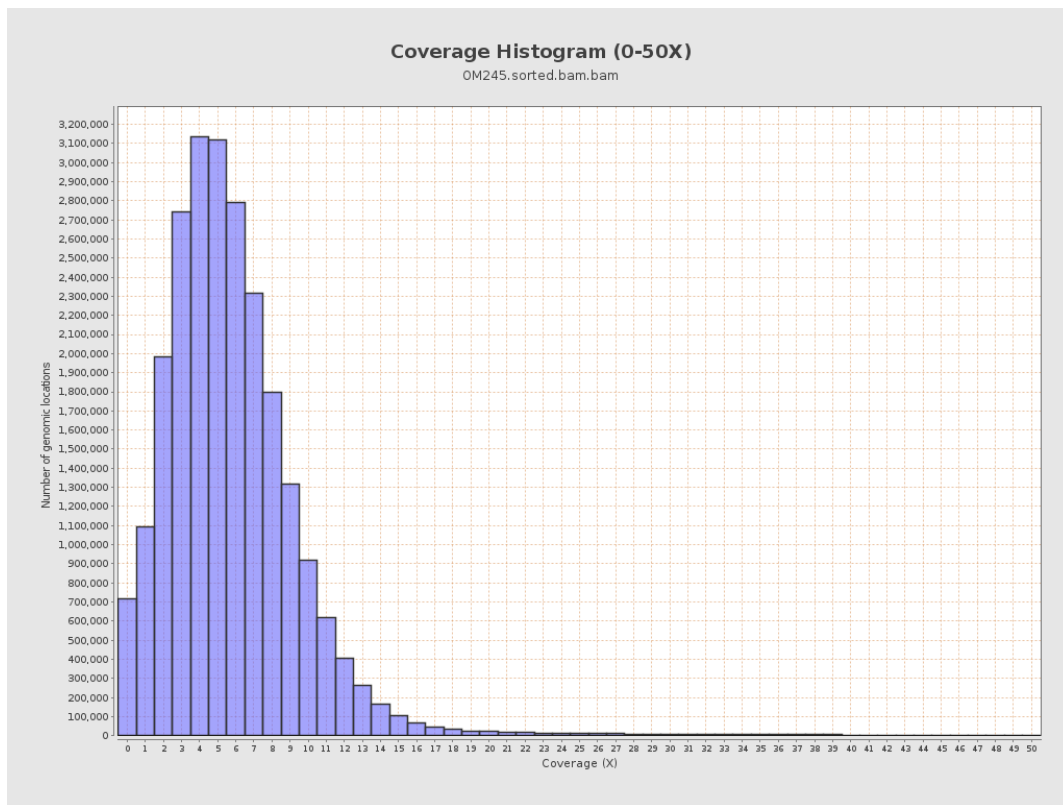
6. Results : Genome Fraction Coverage
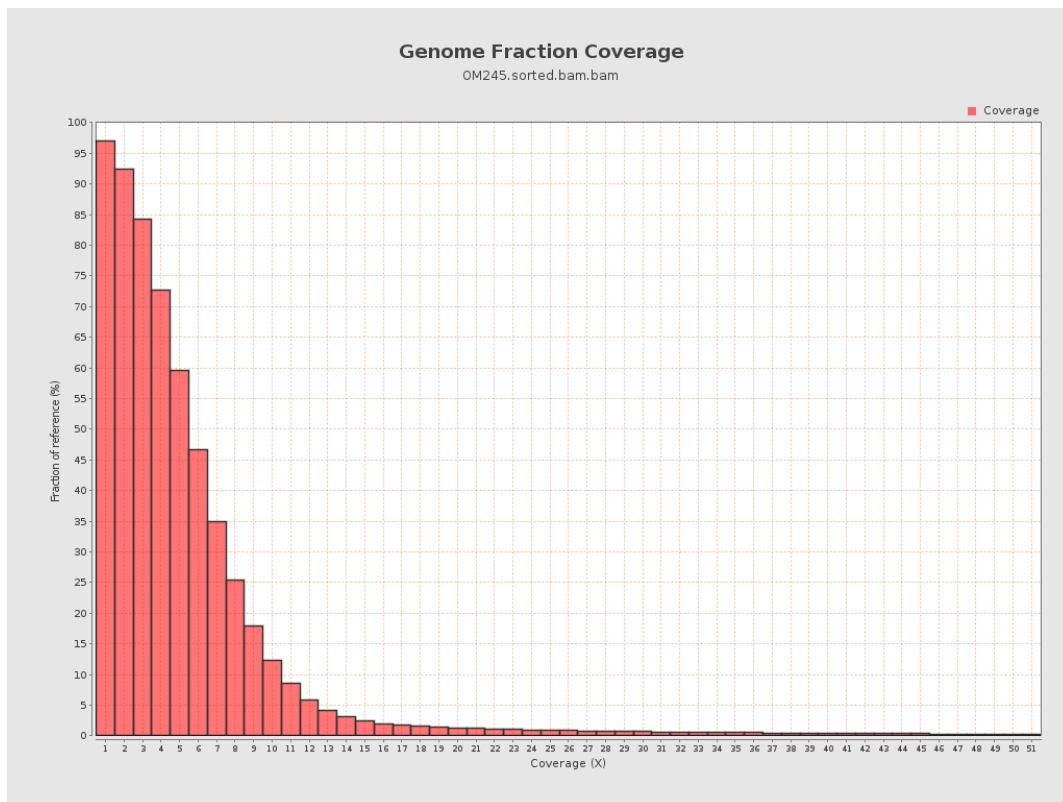
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
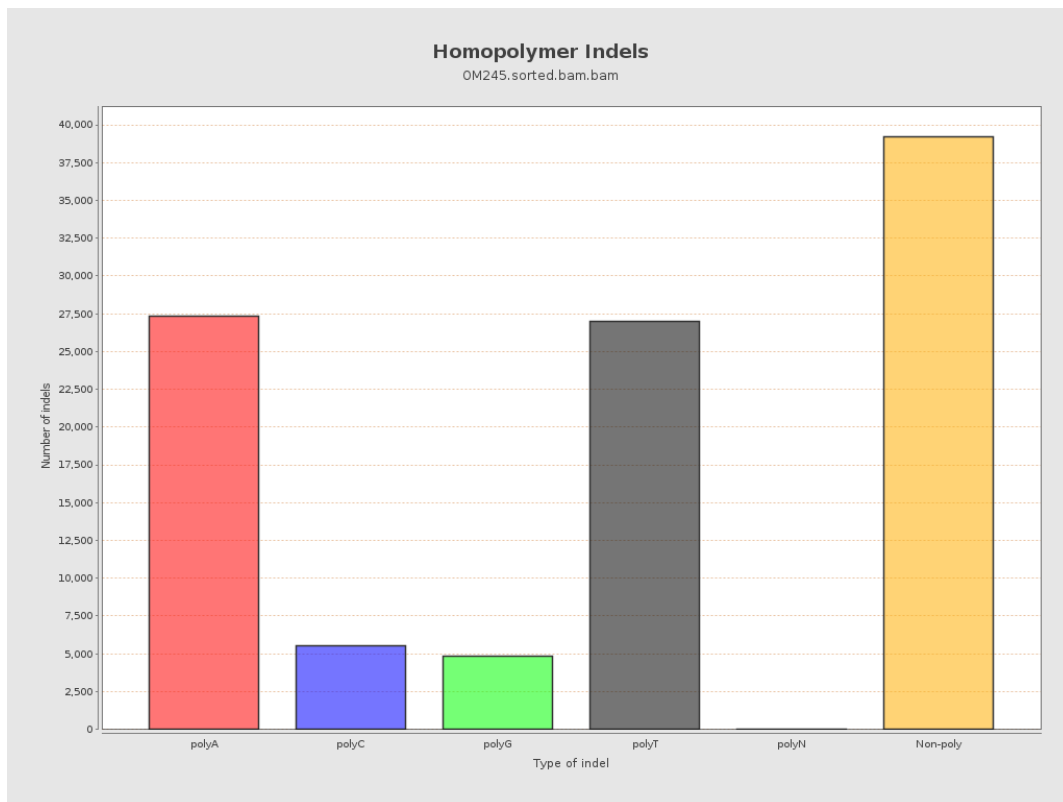OM245.sorted.bam.bam
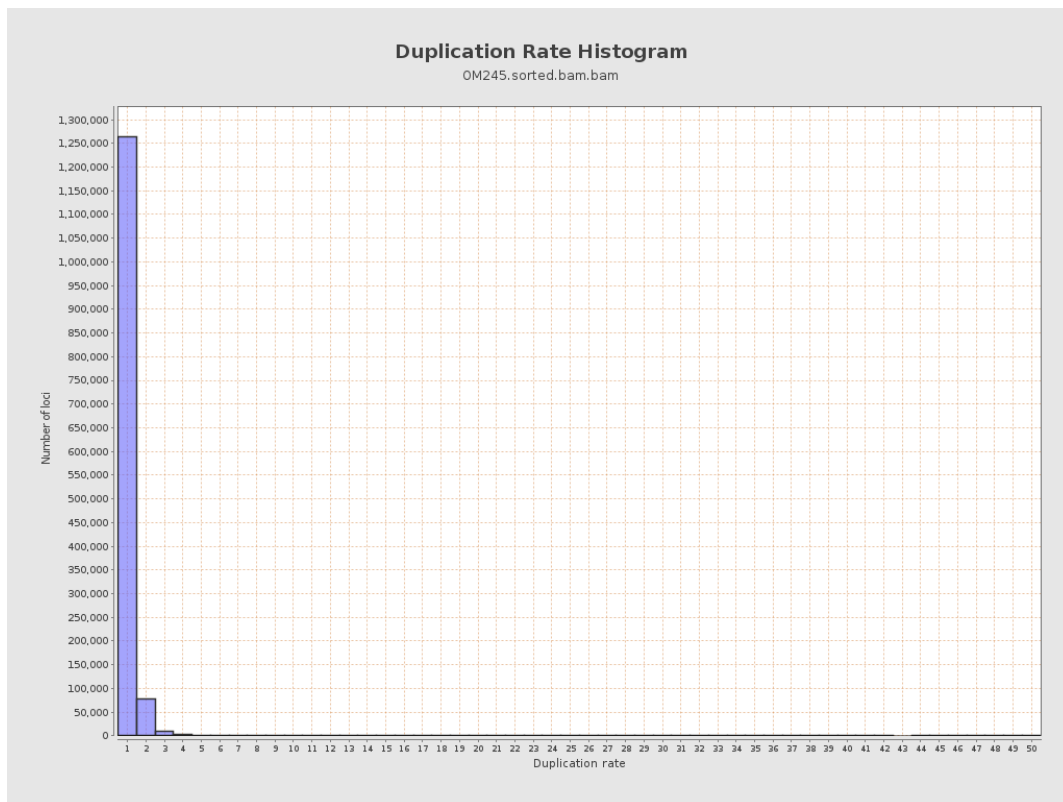
8. Results : Mapped Reads Nucleotide Content
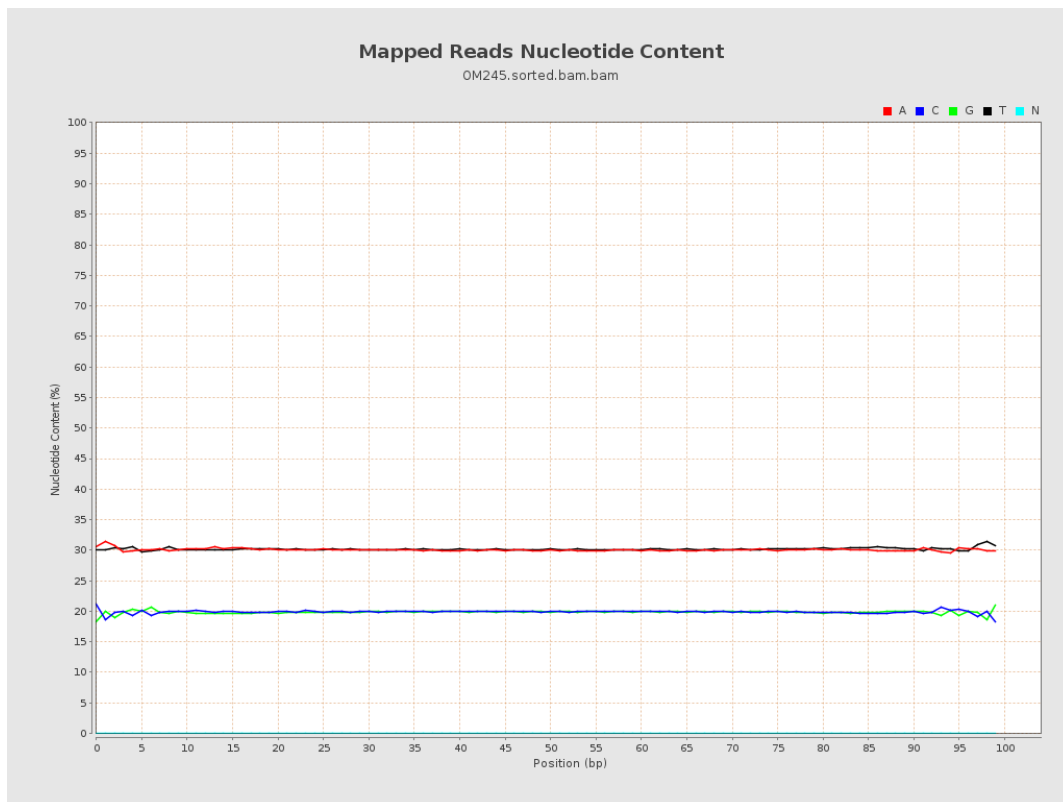
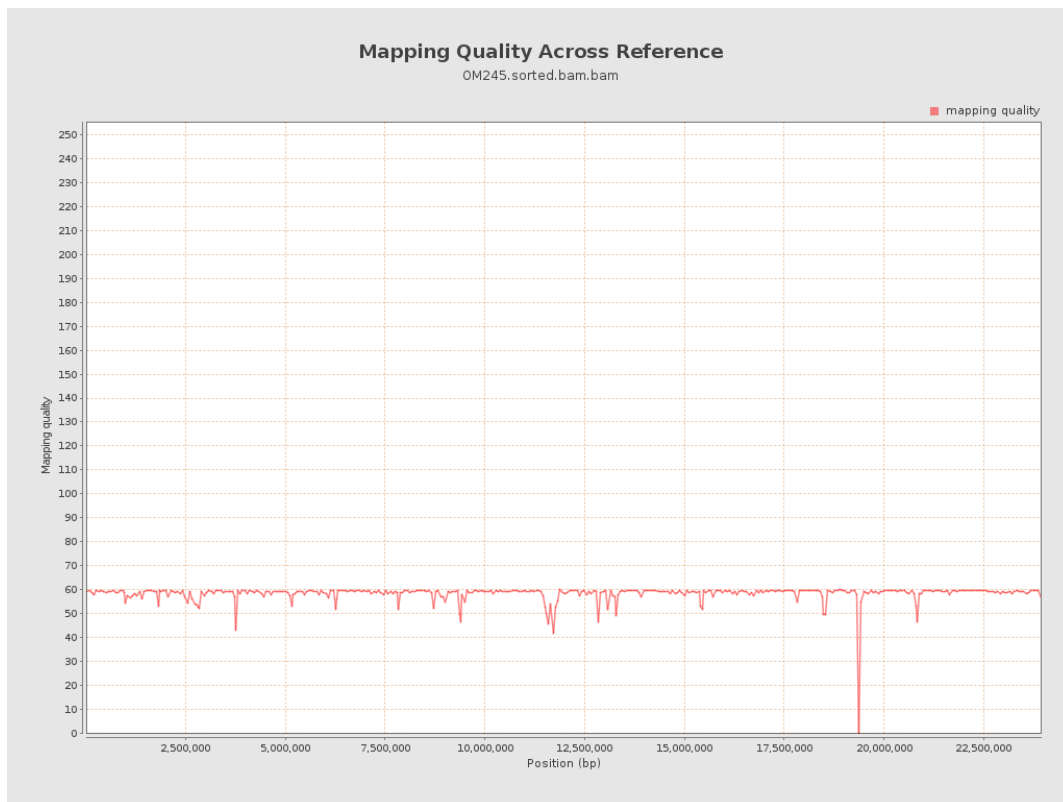# 9. Results : Mapped Reads GC-content Distribution
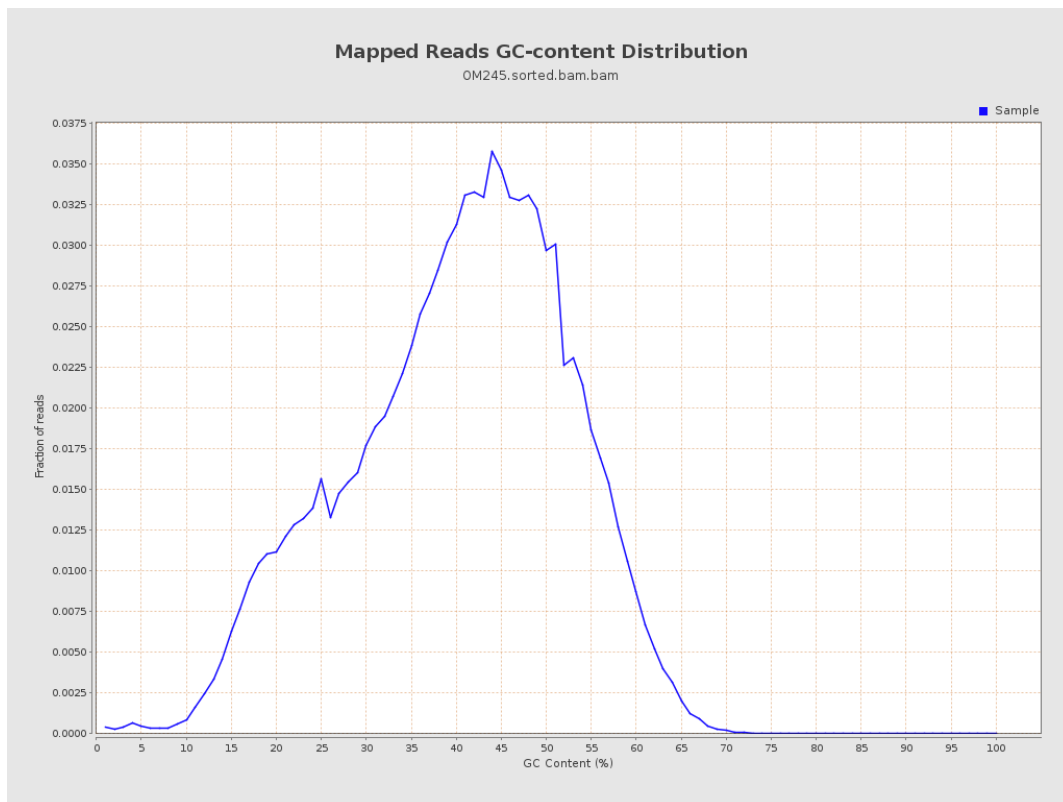
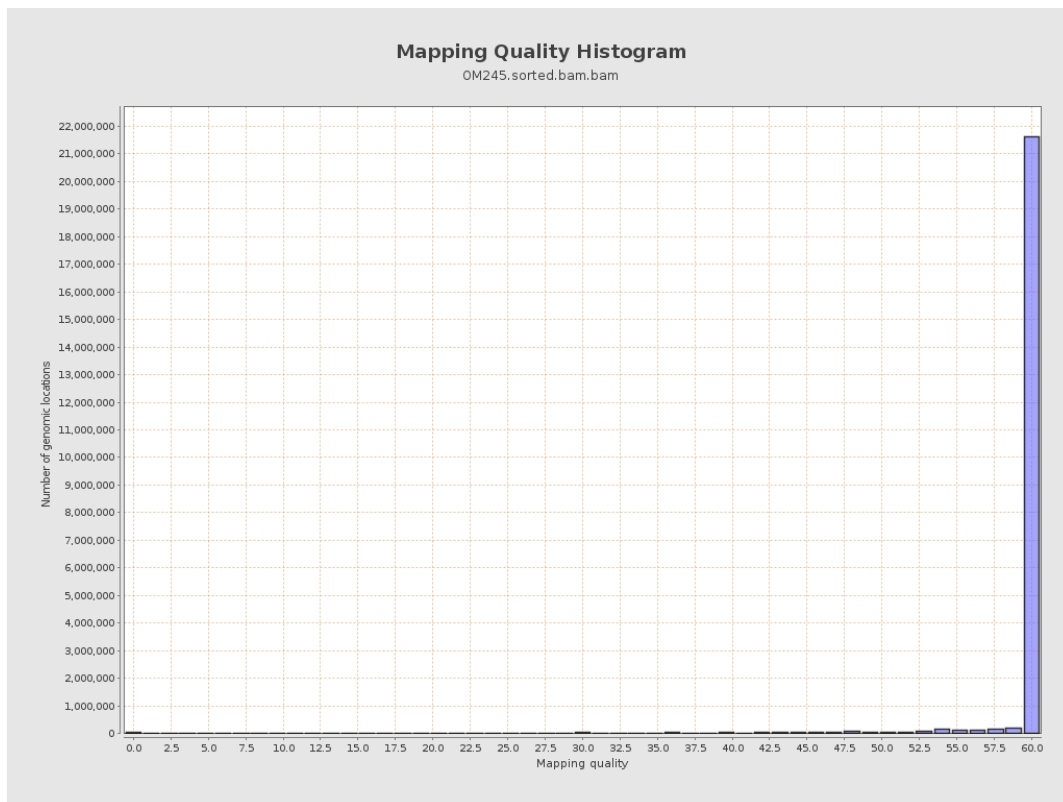# 10. Results : Mapped Reads Clipping Profile
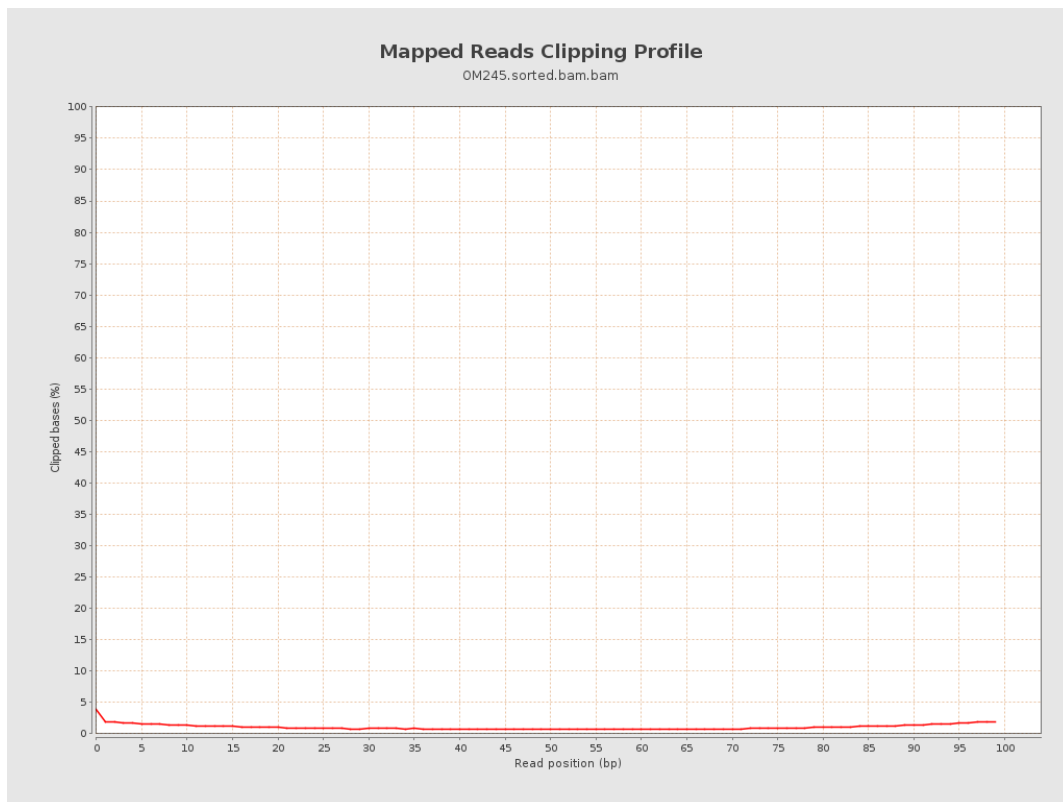
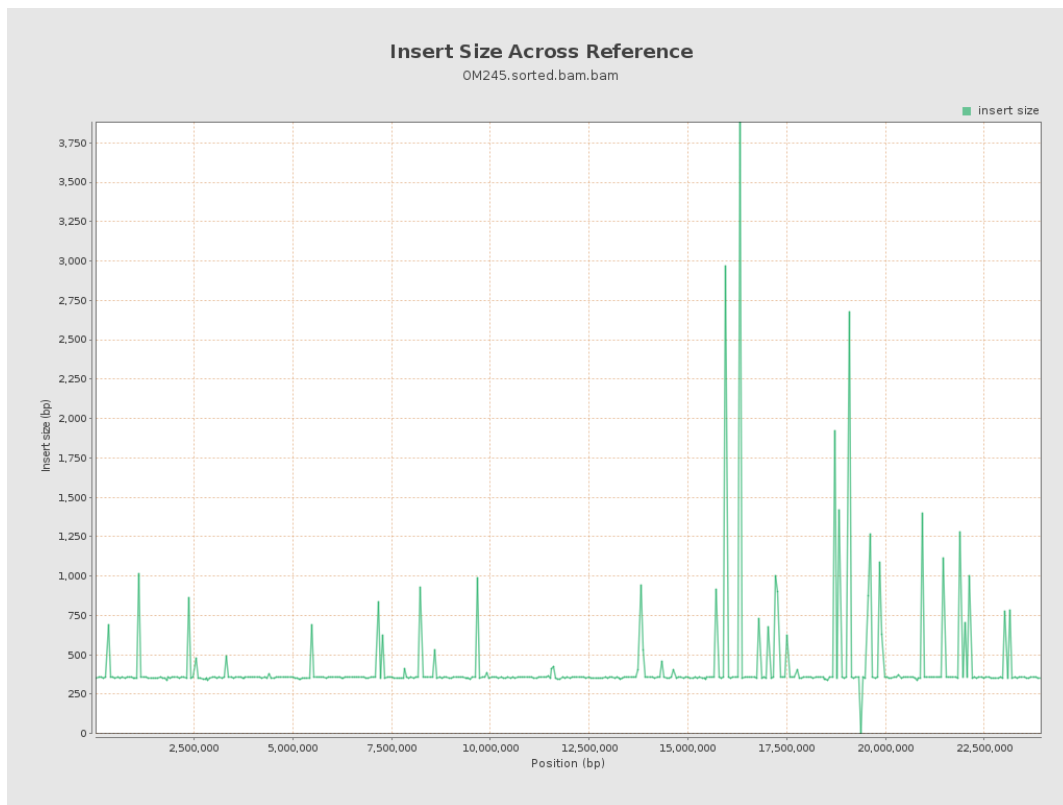# 11. Results : Homopolymer Indels

12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram

Insert Size Histogram
OM245.sorted.bam.bam