Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 13:46:42

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM236.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/OM236-BiooBarcode21_GTTTCG_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM236-BiooBarcode21_GTTTCG_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:46:42 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM236.sorted.bam.

	bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	2,121,301
Mapped reads	874,077 / 41.2%
Unmapped reads	1,247,224 / 58.8%
Mapped paired reads	874,077 / 41.2%
Mapped reads, first in pair	438,175 / 20.66%
Mapped reads, second in pair	435,902 / 20.55%
Mapped reads, both in pair	854,014 / 40.26%
Mapped reads, singletons	20,063 / 0.95%
Read min/max/mean length	30 / 100 / 99.93
Duplicated reads (estimated)	56,211 / 2.65%
Duplication rate	4.85%
Clipped reads	96,218 / 4.54%

2.2. ACGT Content

Number/percentage of A's	25,081,449 / 29.73%
Number/percentage of C's	17,092,577 / 20.26%
Number/percentage of T's	25,099,918 / 29.75%
Number/percentage of G's	17,085,565 / 20.25%
Number/percentage of N's	6,878 / 0.01%
GC Percentage	40.51%

2.3. Coverage

Mean	3.5246
Standard Deviation	3.7986

2.4. Mapping Quality

Mean Mapping Quality	58.53

2.5. Insert size

Mean	773.76
Standard Deviation	25,190.66
P25/Median/P75	308 / 323 / 331

2.6. Mismatches and indels

General error rate	1.48%
Mismatches	1,180,868
Insertions	26,731
Mapped reads with at least one insertion	2.9%
Deletions	29,614
Mapped reads with at least one deletion	3.2%
Homopolymer indels	64.1%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	3115152	3.1878	2.3663
gi|1074120682|emb|LT615257.1|	860454	2844115	3.3054	2.7734
gi|1074120865|emb|LT615258.1|	989719	4135602	4.1786	5.9672
gi|1074121086|emb|LT615259.1|	935450	3671582	3.9249	6.1186
gi|1074121301|emb|LT615260.1|	1432239	5424992	3.7878	4.0555
gi|1074121615|emb|LT615261.1|	1080962	3874625	3.5844	3.5778
gi|1074121871|emb|LT615262.1|	1545099	5262318	3.4058	2.3181
gi|1074122235|emb|LT615263.1|	1585108	5566444	3.5117	3.2918
gi|1074122590|emb|LT615264.1|	2122358	7200616	3.3927	2.4057
gi|1074123050|emb|LT615265.1|	1754192	6053623	3.4509	4.0666
gi|1074123421|emb|LT615	2150147	7979558	3.7112	6.4135

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	10538001	3.4767	2.6249
gi|1074124588|emb|LT615268.1|	2359348	7693644	3.2609	3.7575
gi|1074125065|emb|LT615269.1|	3135668	11086530	3.5356	2.2179

3. Results : Coverage across reference
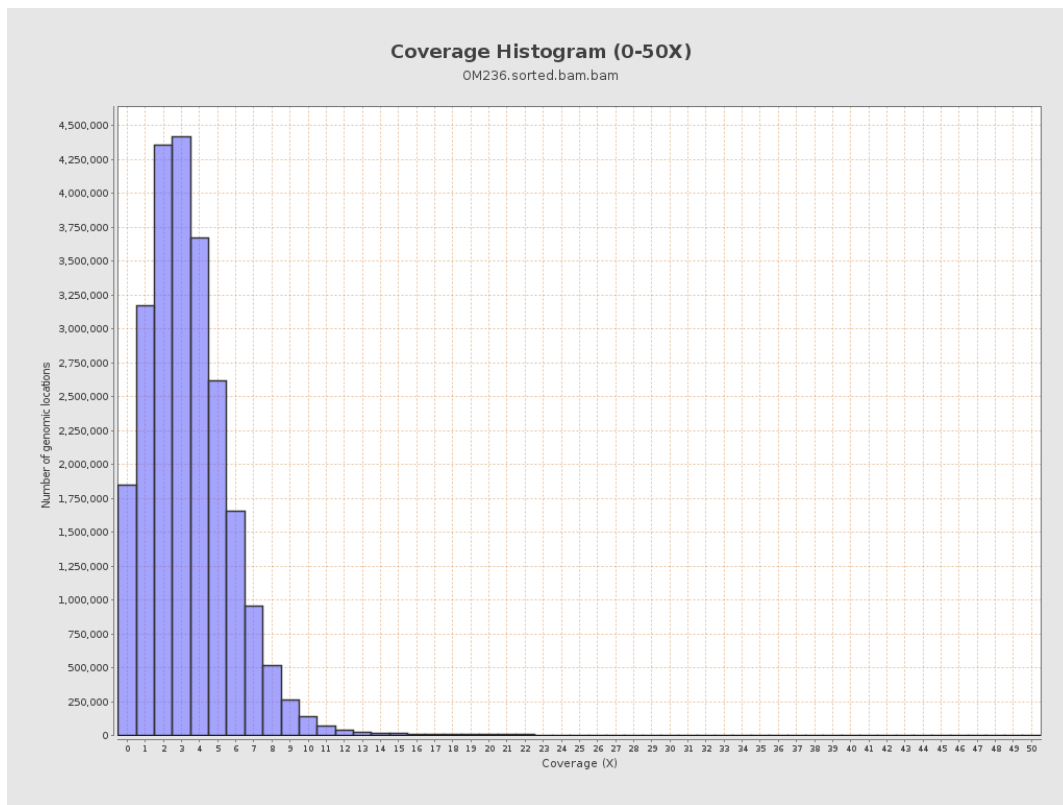

Coverage across reference
OM236.sorted.bam.bam
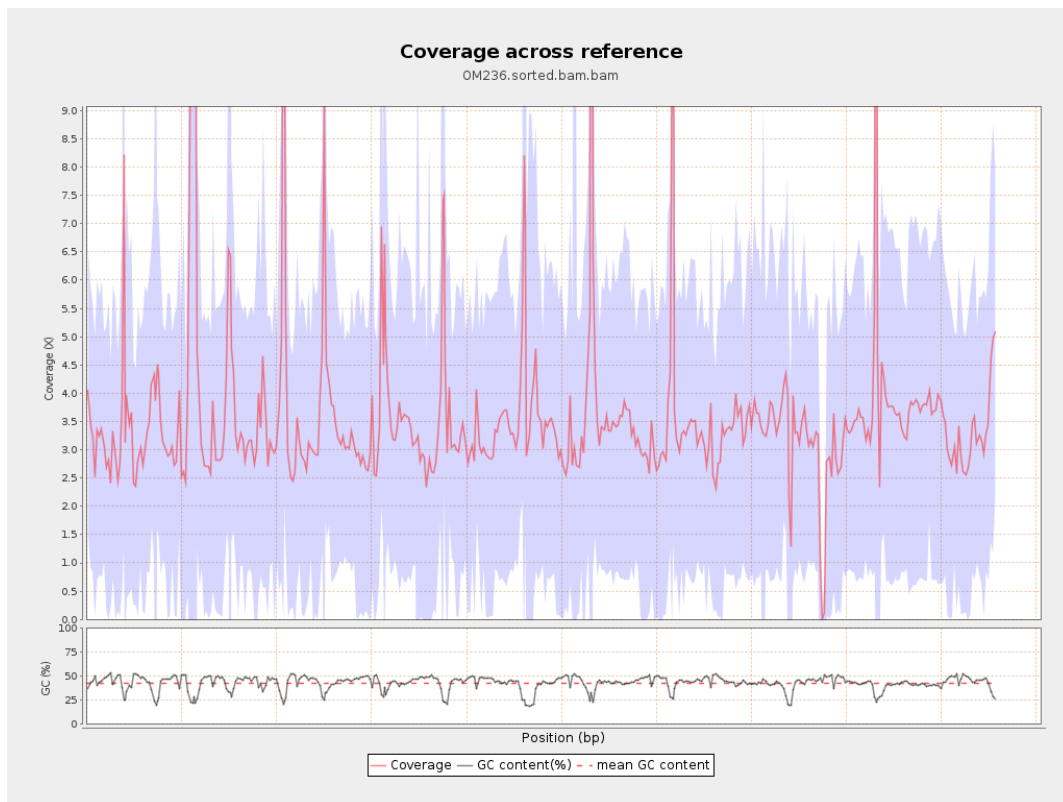
4. Results : Coverage Histogram
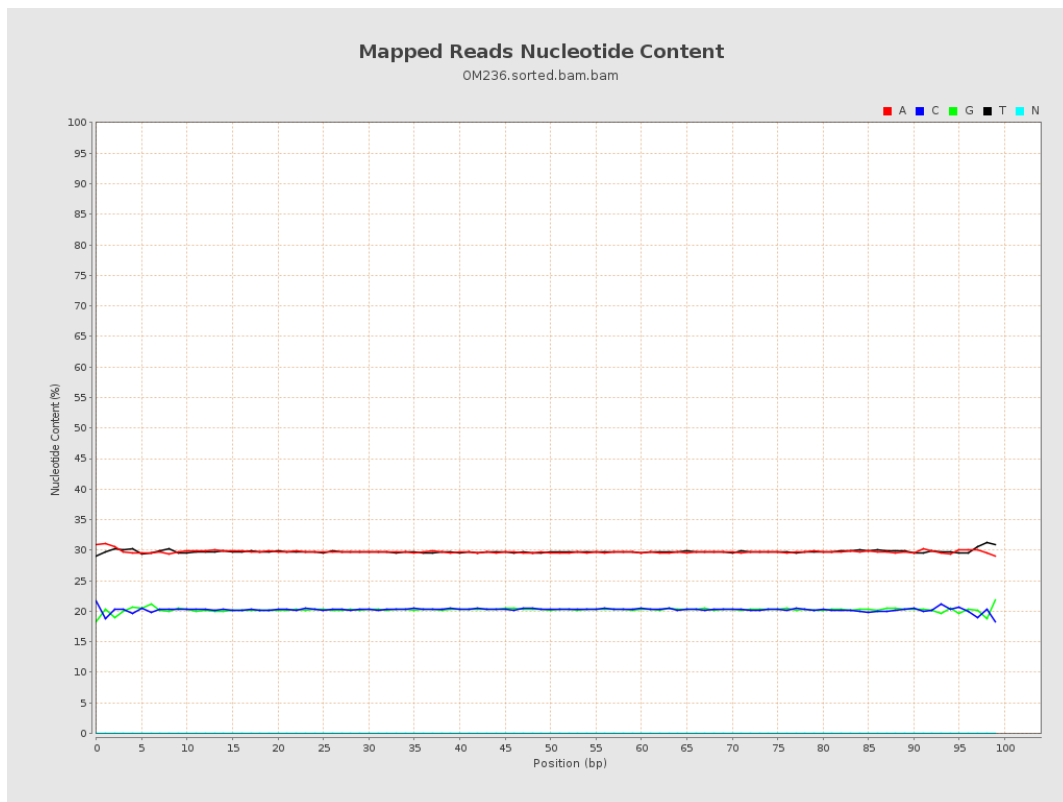
5. Results : Coverage Histogram (0-50X)
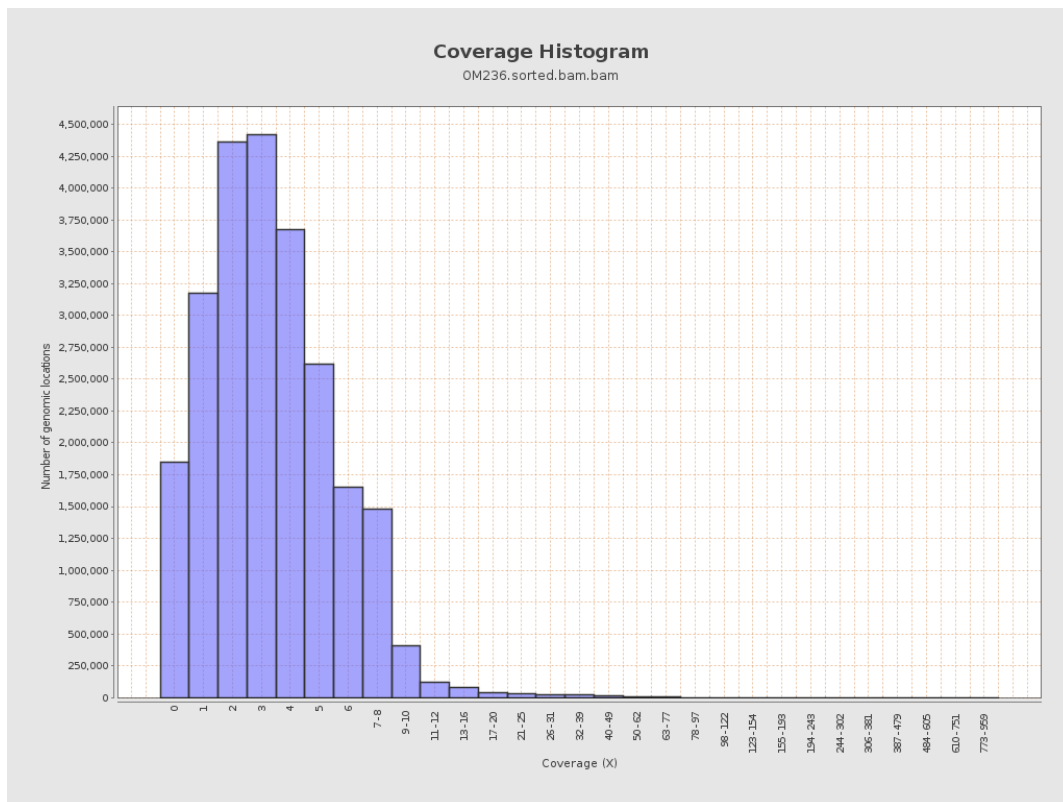
Coverage Histogram (0-50X)
0M236.sorted.bam.bam

6. Results : Genome Fraction Coverage
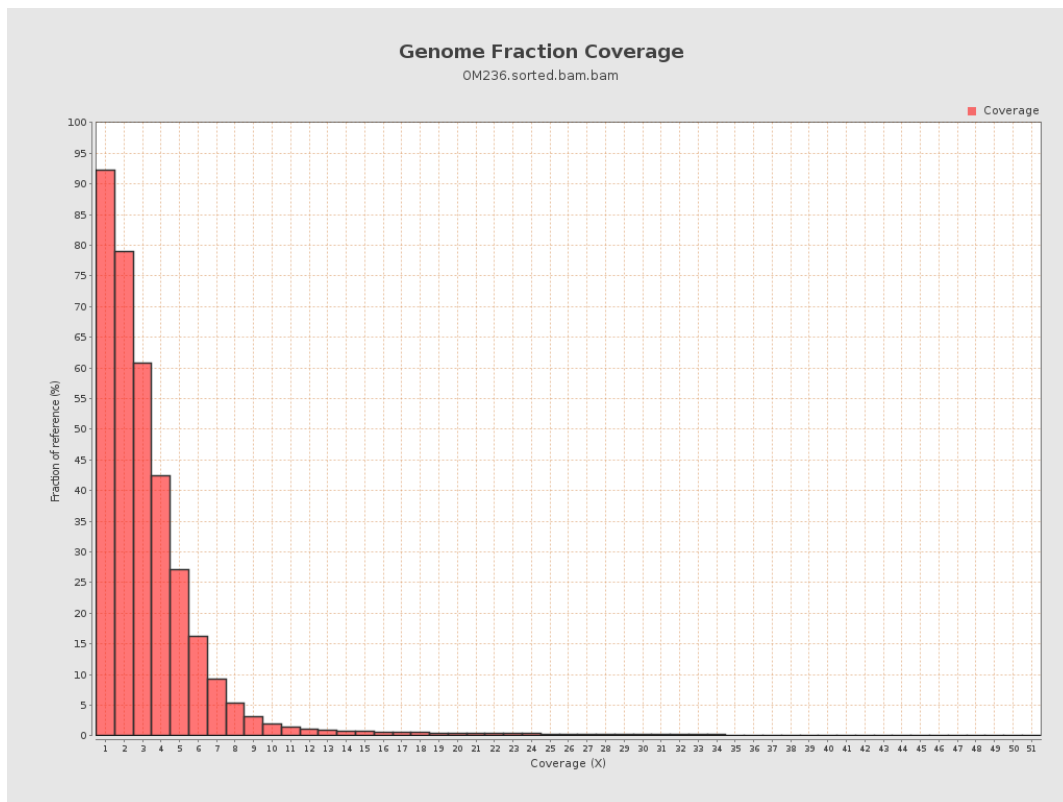
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
OM236.sorted.bam.bam
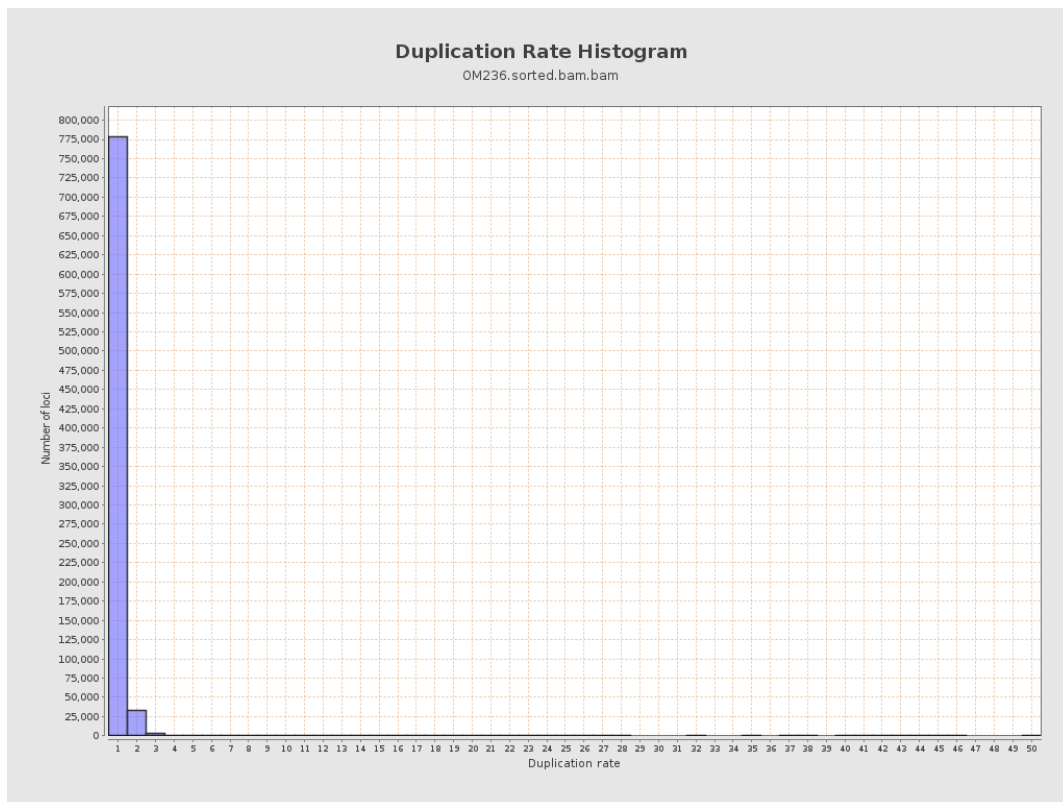
8. Results : Mapped Reads Nucleotide Content

9. Results : Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
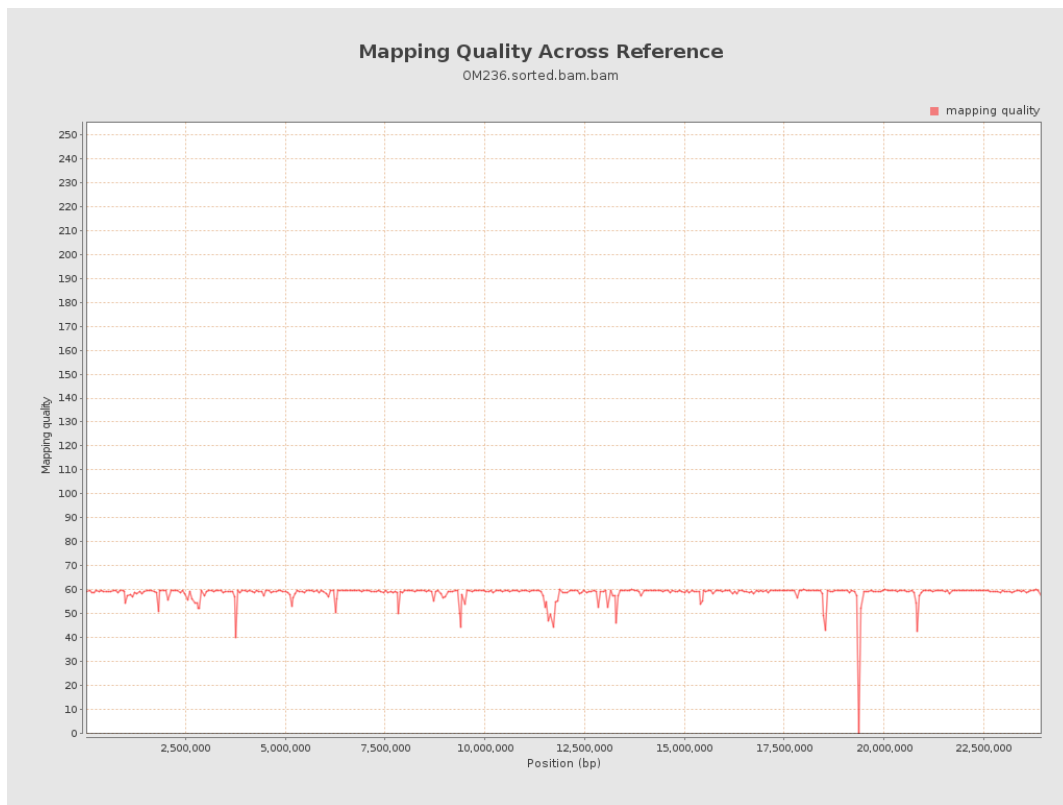OM236.sorted.bam.bam
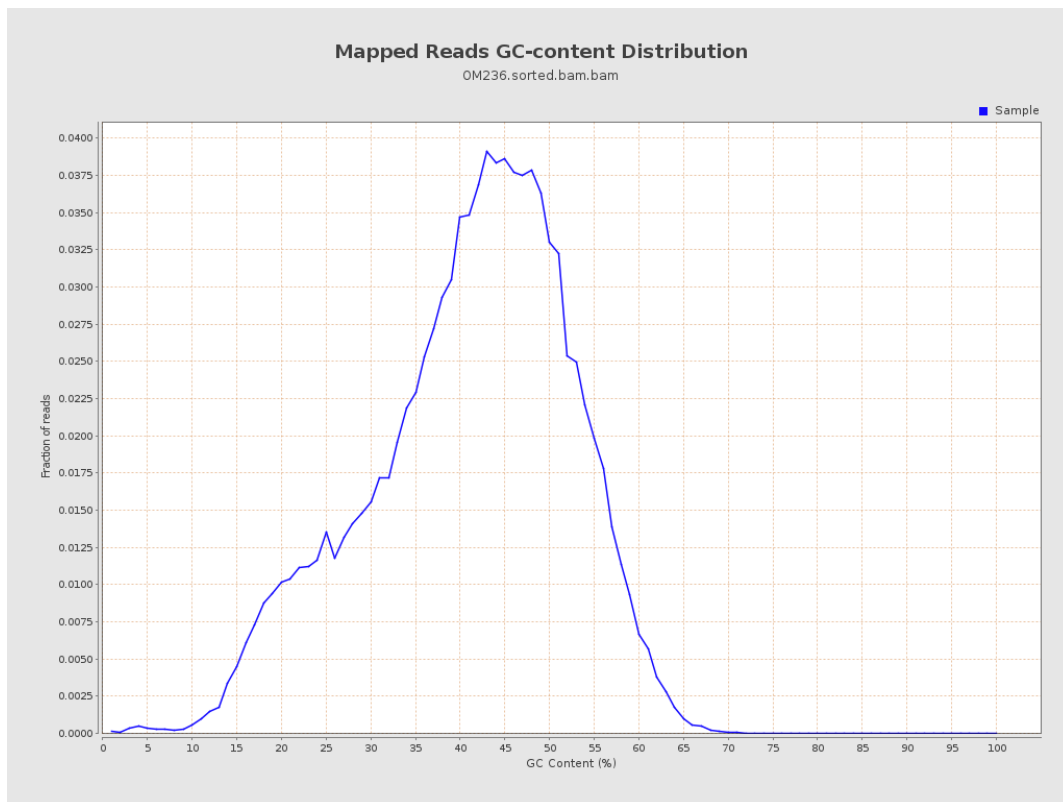
10. Results : Mapped Reads Clipping Profile
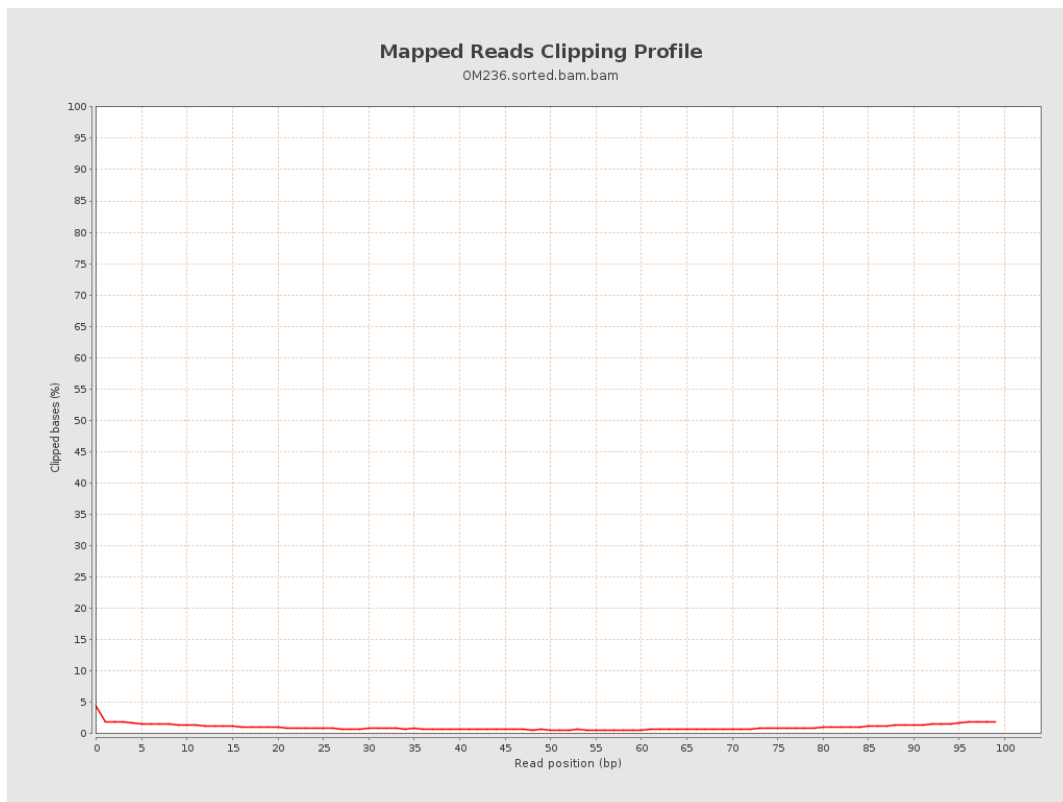
11. Results : Homopolymer Indels
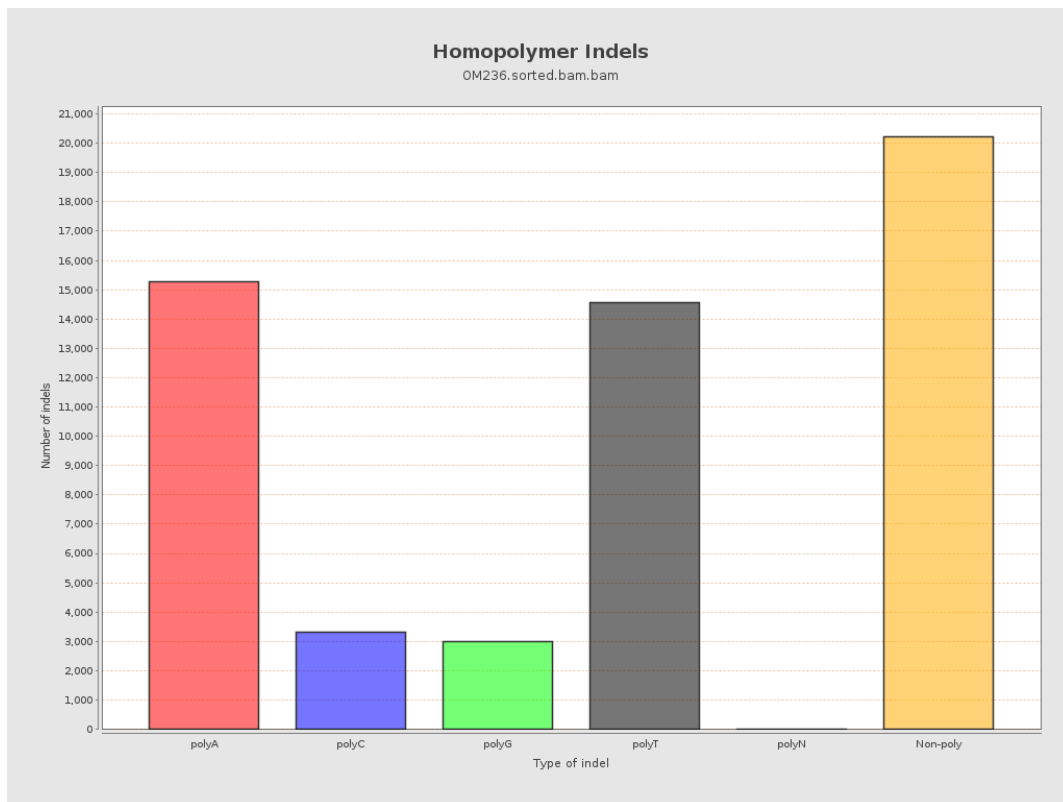
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

Mapping Quality Histogram
OM236.sorted.bam.bam
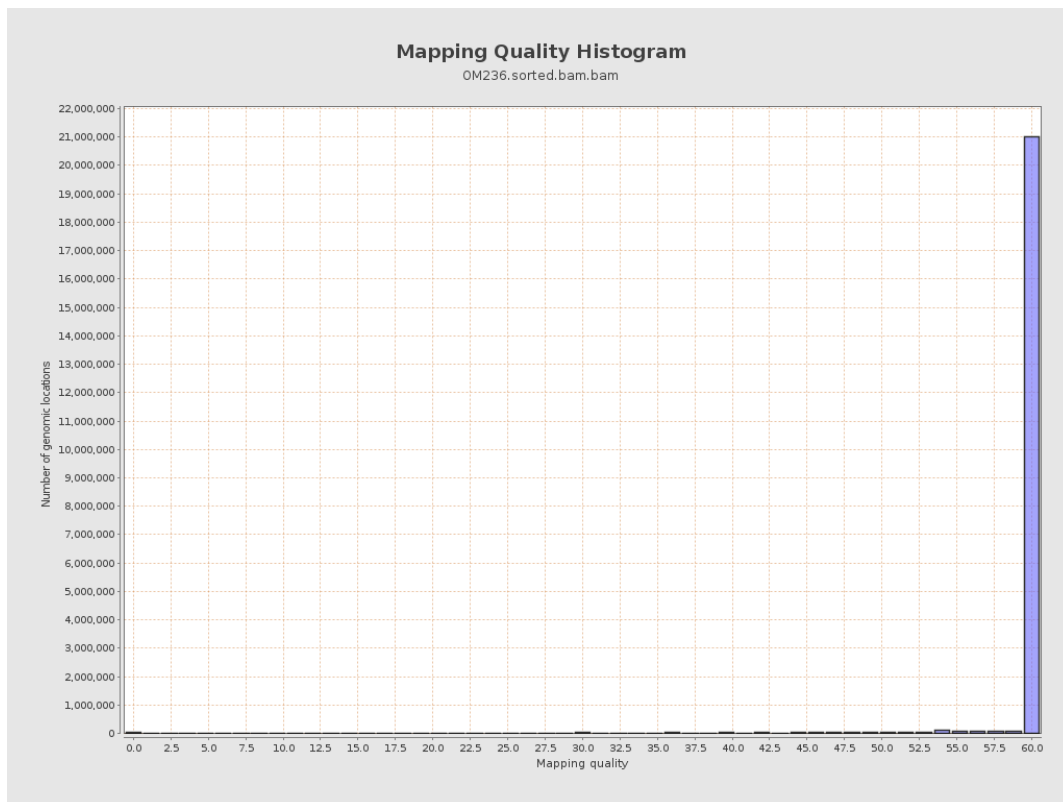
14. Results : Insert Size Across Reference

Insert Size Across Reference
OM236.sorted.bam.bam
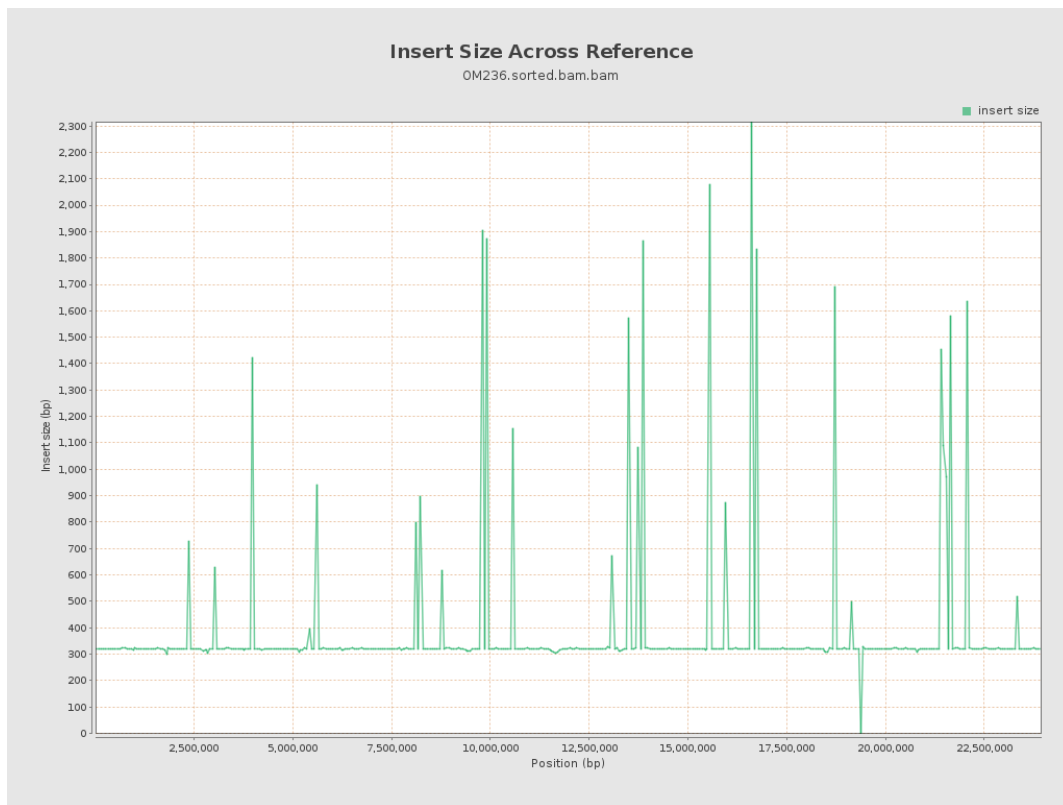
15. Results : Insert Size Histogram