Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 12:45:18

1. Input data & parameters

1.1. QualiMap command line

qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM099.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/OM-099_TGACCA_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM-099_TGACCA_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 12:45:18 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM099.sorted.bam.bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	79,031,423
Mapped reads	12,607,613 / 15.95%
Unmapped reads	66,423,810 / 84.05%
Mapped paired reads	12,607,613 / 15.95%
Mapped reads, first in pair	6,304,696 / 7.98%
Mapped reads, second in pair	6,302,917 / 7.98%
Mapped reads, both in pair	12,001,783 / 15.19%
Mapped reads, singletons	605,830 / 0.77%
Read min/max/mean length	30 / 100 / 99.95
Duplicated reads (estimated)	4,590,755 / 5.81%
Duplication rate	32.07%
Clipped reads	1,627,654 / 2.06%

2.2. ACGT Content

Number/percentage of A's	349,777,948 / 29.28%
Number/percentage of C's	246,462,788 / 20.63%
Number/percentage of T's	352,840,524 / 29.54%
Number/percentage of G's	245,470,042 / 20.55%
Number/percentage of N's	40,906 / 0%
GC Percentage	41.18%

2.3. Coverage

Mean	49.9104
Standard Deviation	89.5186

2.4. Mapping Quality

Mean Mapping Quality	57.89

2.5. Insert size

Mean	831.72
Standard Deviation	28,977.48
P25/Median/P75	202 / 212 / 225

2.6. Mismatches and indels

General error rate	1.09%
Mismatches	12,086,430
Insertions	385,857
Mapped reads with at least one insertion	2.88%
Deletions	433,335
Mapped reads with at least one deletion	3.15%
Homopolymer indels	64.92%

2.7. Chromosome stats

| Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	46343360	47.4238	27.2511
gi|1074120682|emb|LT615257.1|	860454	42966433	49.9346	45.25
gi|1074120865|emb|LT615258.1|	989719	51792368	52.3304	63.4068
gi|1074121086|emb|LT615259.1|	935450	51504989	55.0591	54.7642
gi|1074121301|emb|LT615260.1|	1432239	74206961	51.8119	62.2589
gi|1074121615|emb|LT615261.1|	1080962	55257760	51.1191	41.7442
gi|1074121871|emb|LT615262.1|	1545099	74146773	47.9884	25.209
gi|1074122235|emb|LT615263.1|	1585108	78523988	49.5386	123.4405
gi|1074122590|emb|LT615264.1|	2122358	102879645	48.4742	23.014
gi|1074123050|emb|LT615265.1|	1754192	94106382	53.6466	256.1085
gi|1074123421|emb|LT615	2150147	110449044	51.3681	74.4553

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	147995482	48.8267	74.6004
gi|1074124588|emb|LT615268.1|	2359348	111207177	47.1347	37.6525
gi|1074125065|emb|LT615269.1|	3135668	154423747	49.2475	23.5094

3. Results : Coverage across reference
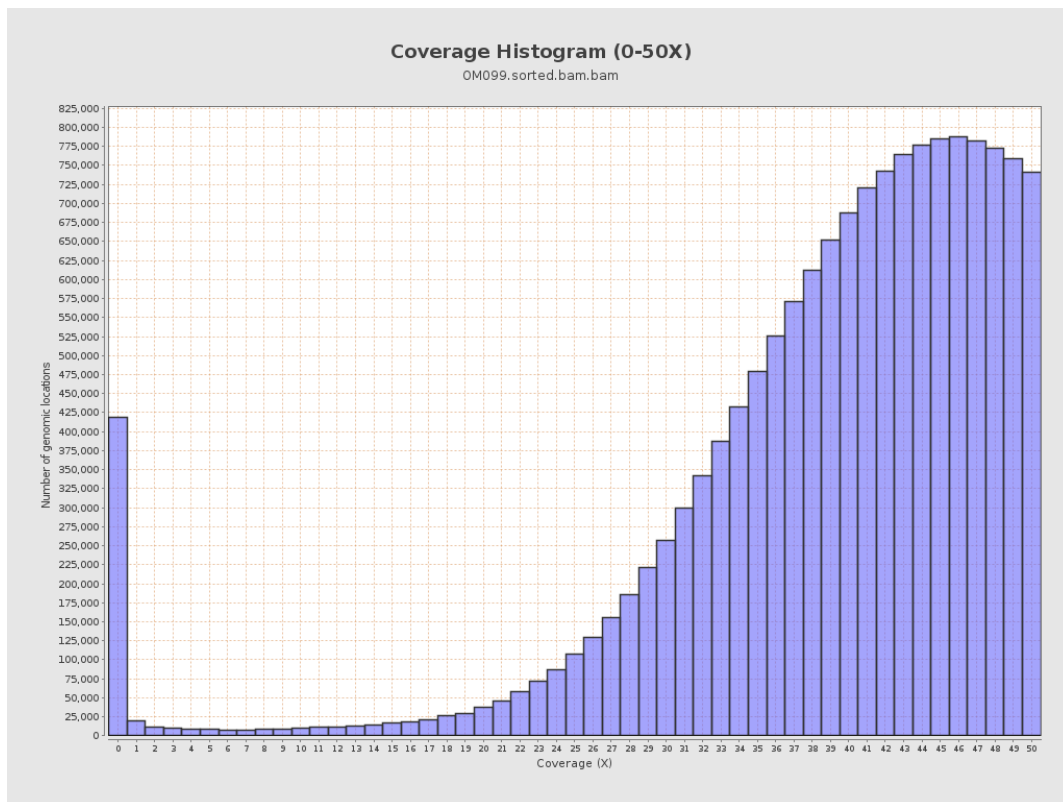

Coverage across reference
OM099.sorted.bam.bam
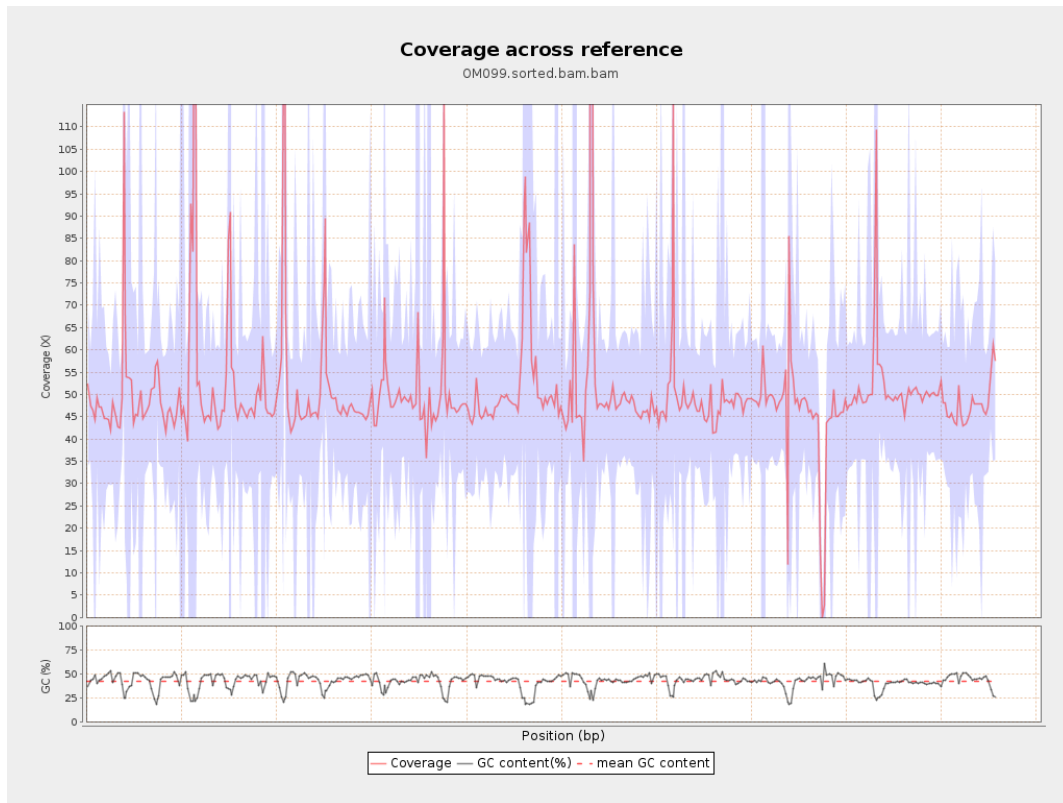
4. Results : Coverage Histogram
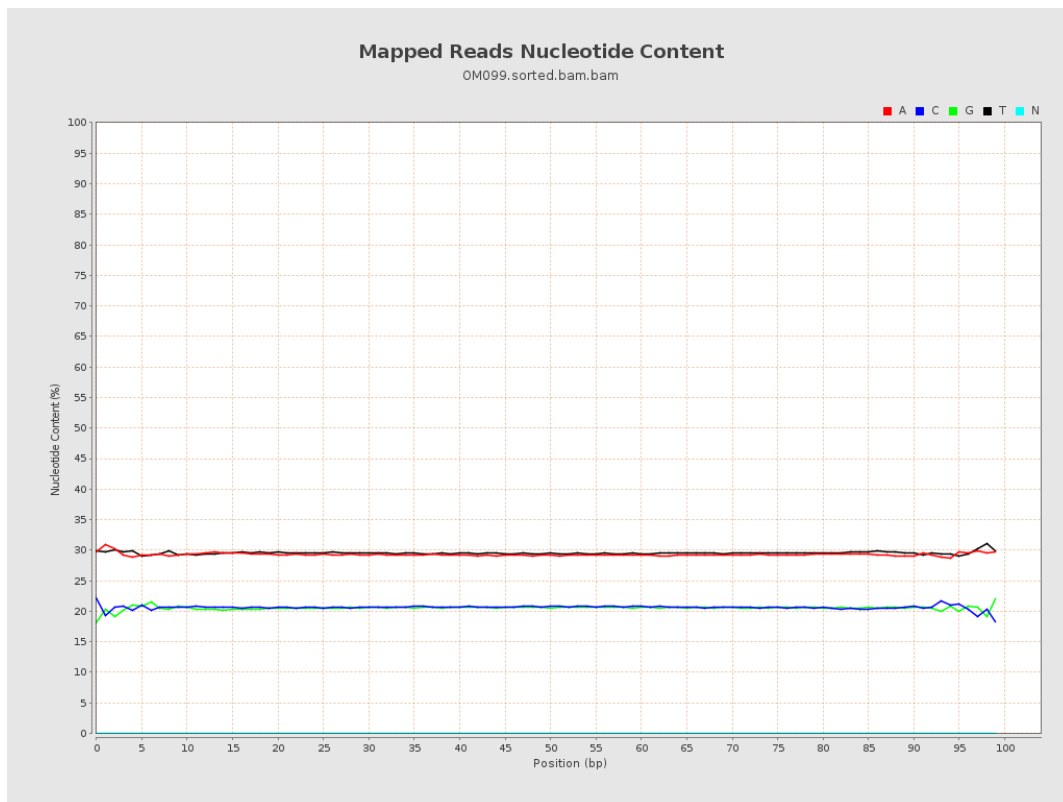
5. Results : Coverage Histogram (0-50X)
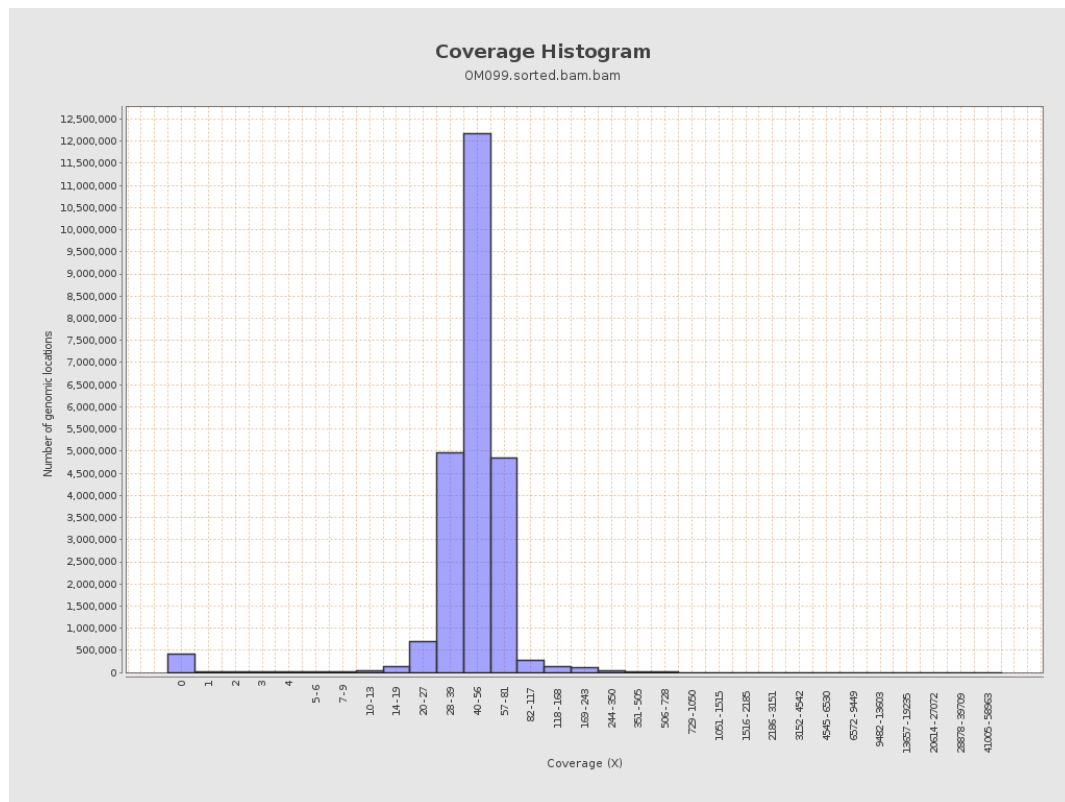
Coverage Histogram (0-50X)
OM099.sorted.bam.bam

6. Results : Genome Fraction Coverage

Genome Fraction Coverage
0M099.sorted.bam.bam
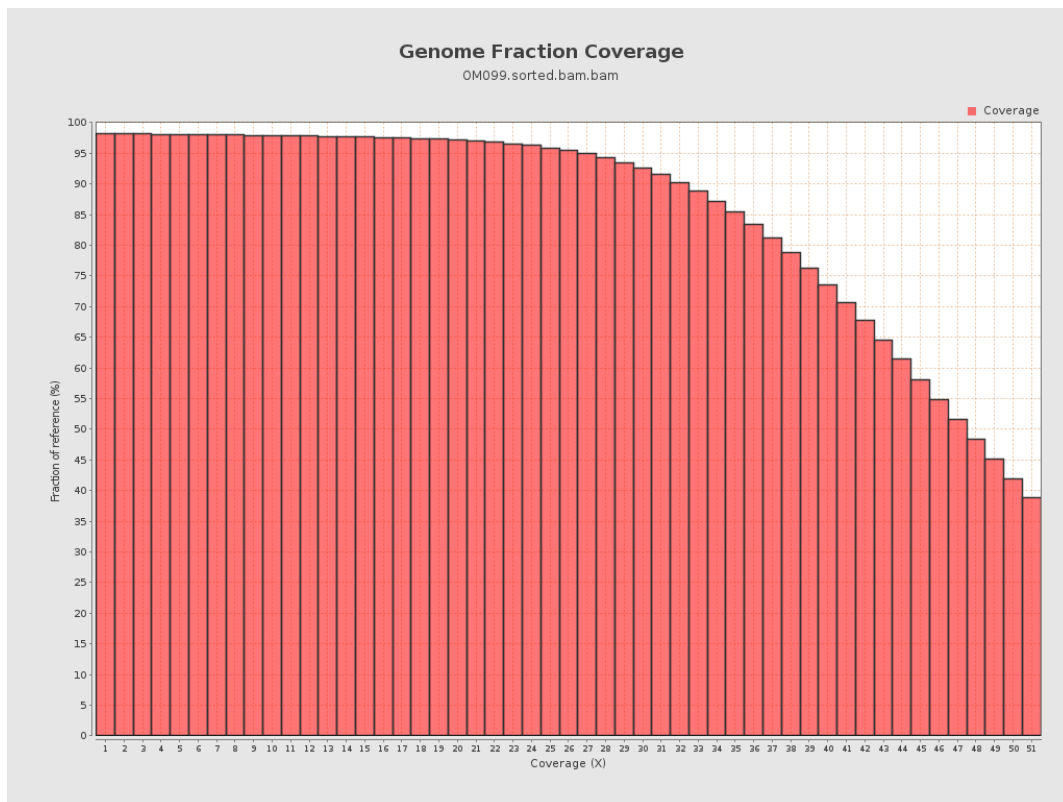
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
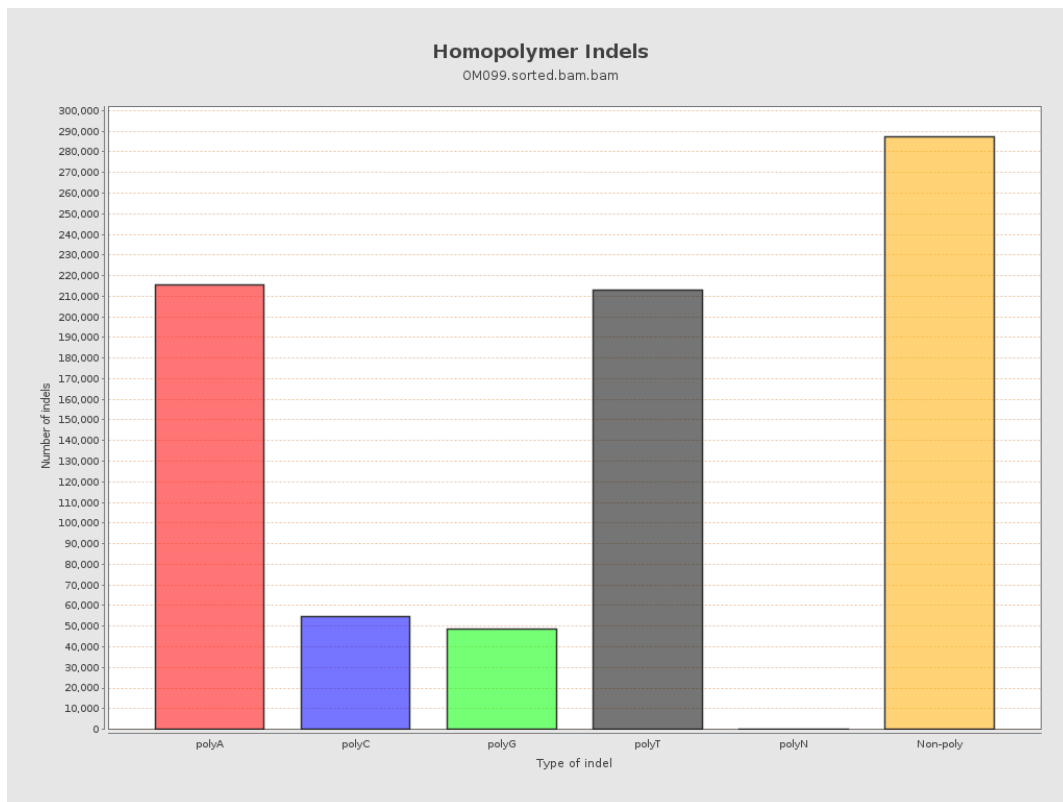OM099.sorted.bam.bam
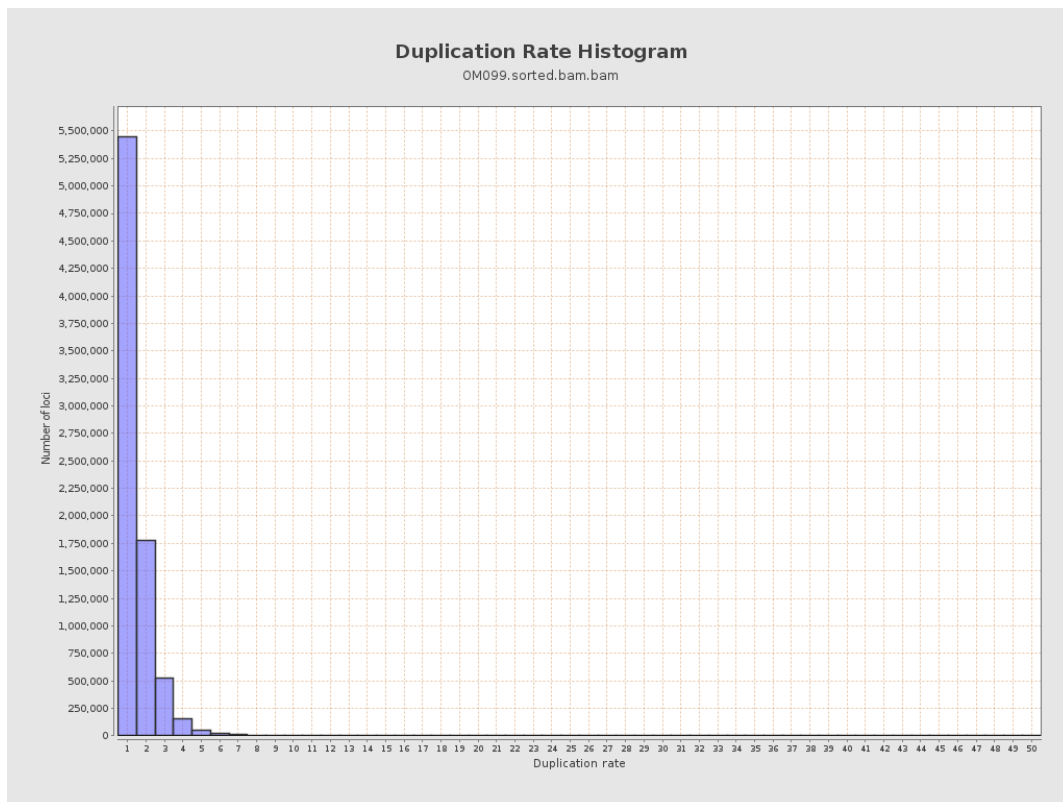
8. Results : Mapped Reads Nucleotide Content

9. Results : Mapped Reads GC-content Distribution
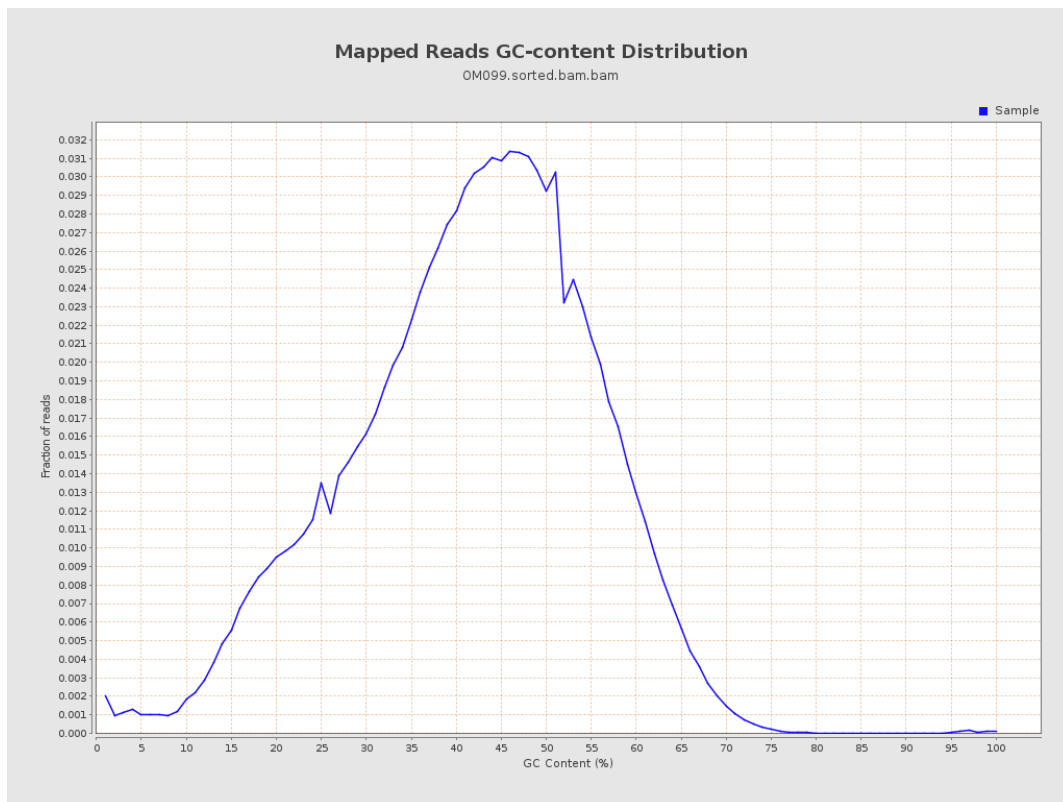
10. Results : Mapped Reads Clipping Profile
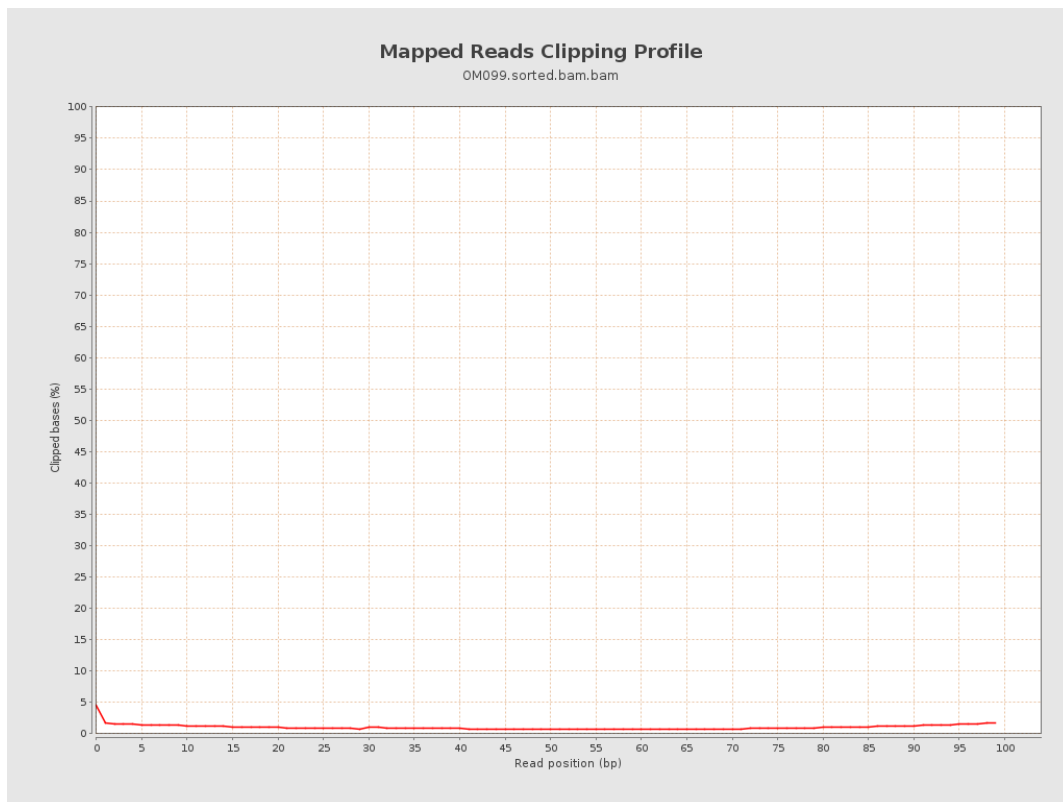
11. Results : Homopolymer Indels
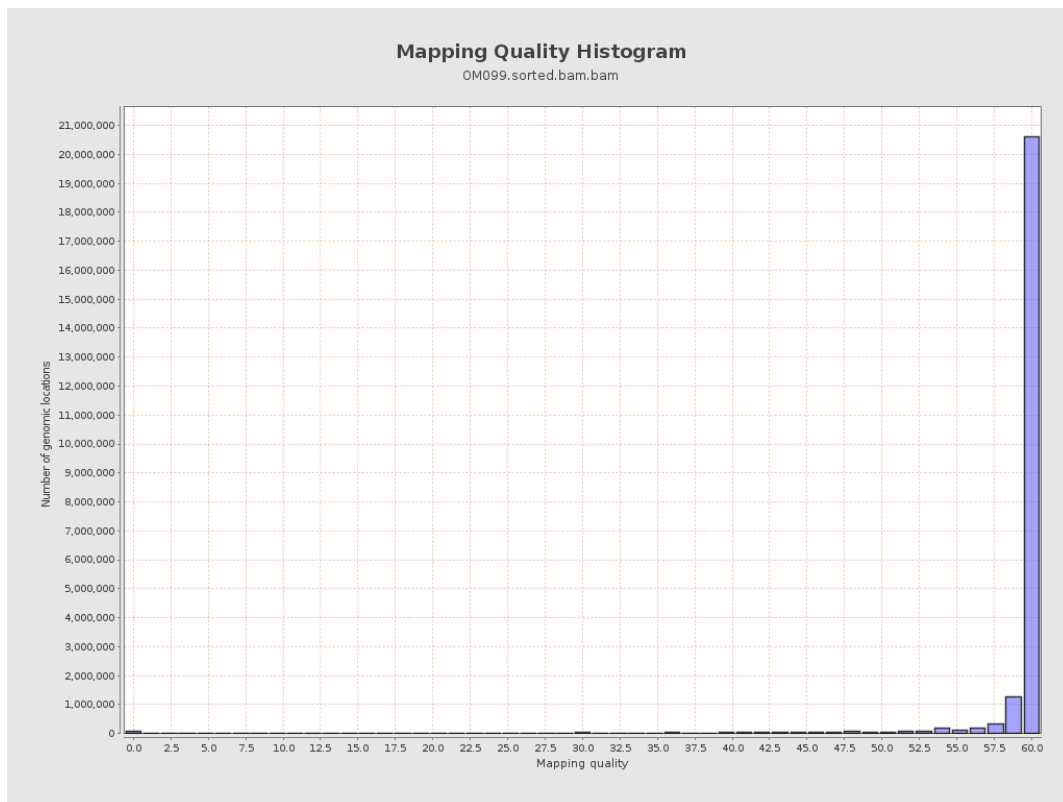

Homopolymer Indels
OM099.sorted.bam.bam

12. Results : Mapping Quality Across Reference

Mapping Quality Across Reference
0M099.sorted.bam.bam
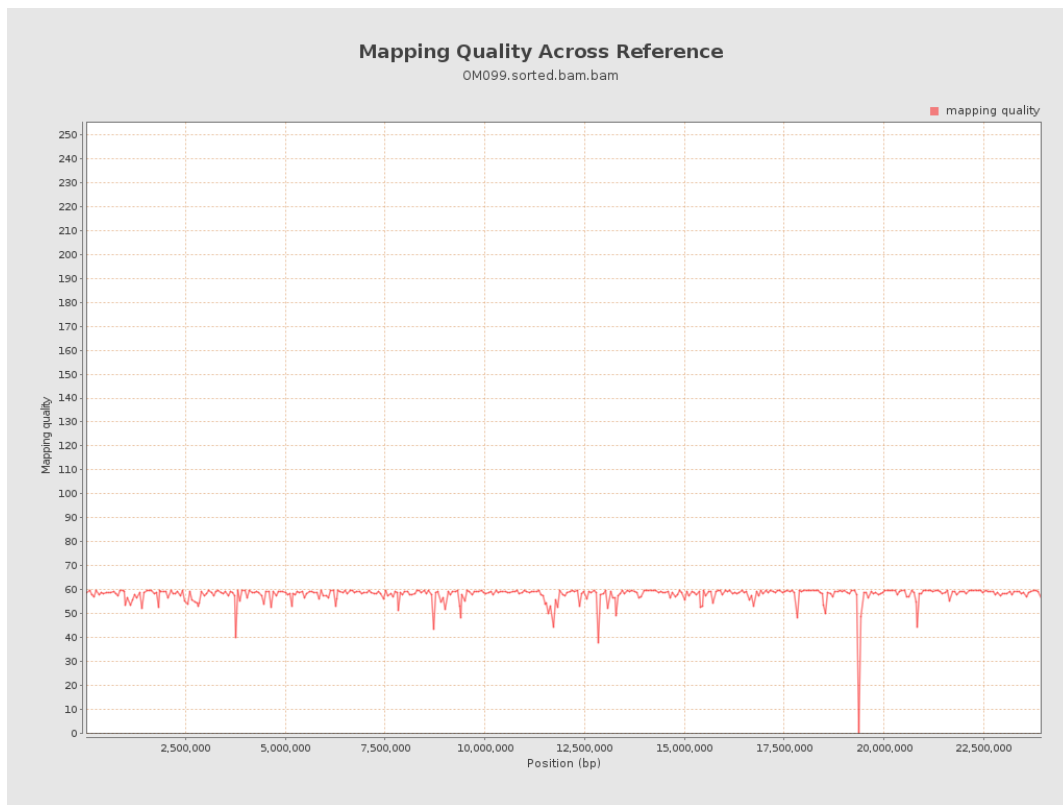
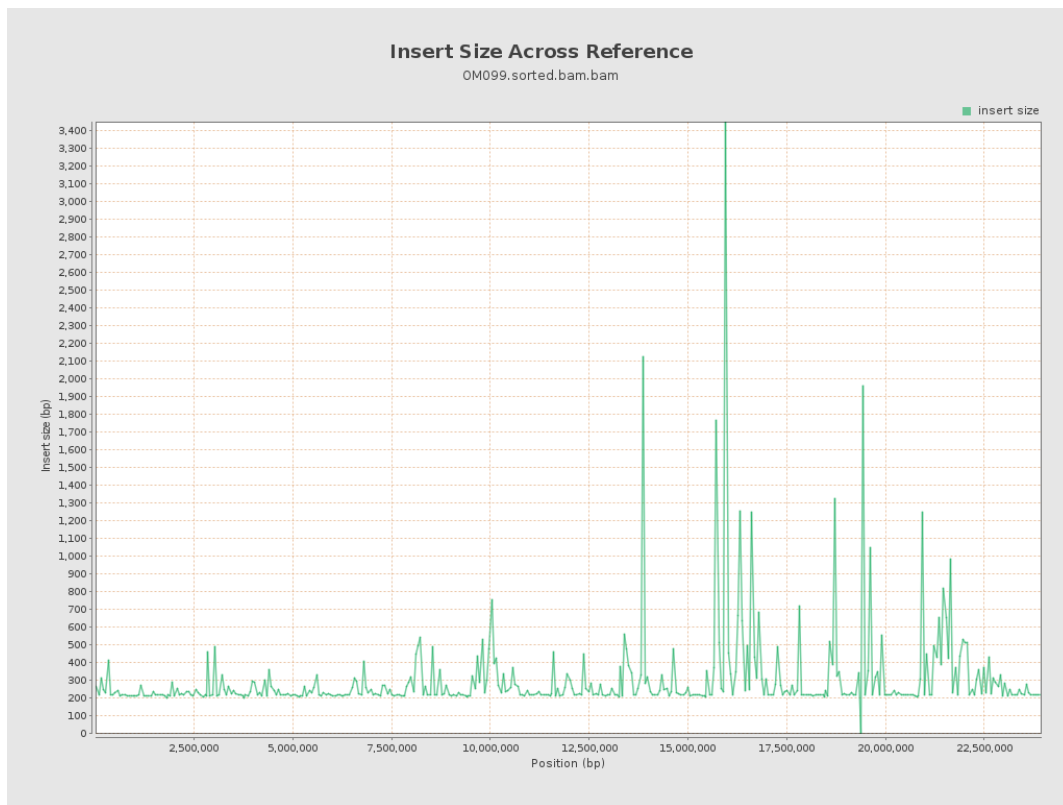# 13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

Insert Size Across Reference
OM099.sorted.bam.bam

15. Results : Insert Size Histogram

Insert Size Histogram
OM099.sorted.bam.bam