Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 13:41:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM192.sorted.bam.bam -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/OM192-BiooBarcode2_TGACCA_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM192-BiooBarcode2_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 13:41:37 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM192.sorted.bam.bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	8,270,103
Mapped reads	2,019,064 / 24.41%
Unmapped reads	6,251,039 / 75.59%
Mapped paired reads	2,019,064 / 24.41%
Mapped reads, first in pair	1,011,896 / 12.24%
Mapped reads, second in pair	1,007,168 / 12.18%
Mapped reads, both in pair	1,948,402 / 23.56%
Mapped reads, singletons	70,662 / 0.85%
Read min/max/mean length	30 / 100 / 99.95
Duplicated reads (estimated)	236,655 / 2.86%
Duplication rate	8.27%
Clipped reads	257,338 / 3.11%

2.2. ACGT Content

Number/percentage of A's	58,140,934 / 30.13%
Number/percentage of C's	38,225,946 / 19.81%
Number/percentage of T's	58,459,233 / 30.29%
Number/percentage of G's	38,147,734 / 19.77%
Number/percentage of N's	16,397 / 0.01%
GC Percentage	39.58%

2.3. Coverage

Mean	8.0631
Standard Deviation	9.6485

2.4. Mapping Quality

Mean Mapping Quality	58.31

2.5. Insert size

Mean	755.67
Standard Deviation	23,522.12
P25/Median/P75	294 / 306 / 316

2.6. Mismatches and indels

General error rate	1.56%
Mismatches	2,859,875
Insertions	66,043
Mapped reads with at least one insertion	3.09%
Deletions	75,673
Mapped reads with at least one deletion	3.51%
Homopolymer indels	62.49%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	7013586	7.1771	4.8466
gi|1074120682|emb|LT615257.1|	860454	6824711	7.9315	7.0772
gi|1074120865|emb|LT615258.1|	989719	9464912	9.5632	14.964
gi|1074121086|emb|LT615259.1|	935450	8460694	9.0445	13.5941
gi|1074121301|emb|LT615260.1|	1432239	12307380	8.5931	9.2805
gi|1074121615|emb|LT615261.1|	1080962	8842424	8.1801	8.6174
gi|1074121871|emb|LT615262.1|	1545099	11522441	7.4574	4.1472
gi|1074122235|emb|LT615263.1|	1585108	12600256	7.9491	11.0106
gi|1074122590|emb|LT615264.1|	2122358	16679572	7.859	5.598
gi|1074123050|emb|LT615265.1|	1754192	14318267	8.1623	17.8608
gi|1074123421|emb|LT615	2150147	18034811	8.3877	12.1323

|				
266.1|				
gi|1074123898|emb|LT615267.1|	3031036	23396003	7.7188	6.9845
gi|1074124588|emb|LT615268.1|	2359348	18439000	7.8153	9.1759
gi|1074125065|emb|LT615269.1|	3135668	25280319	8.0622	4.1004

3. Results : Coverage across reference

Coverage across reference
OM192.sorted.bam.bam

4. Results : Coverage Histogram

5. Results : Coverage Histogram (0-50X)
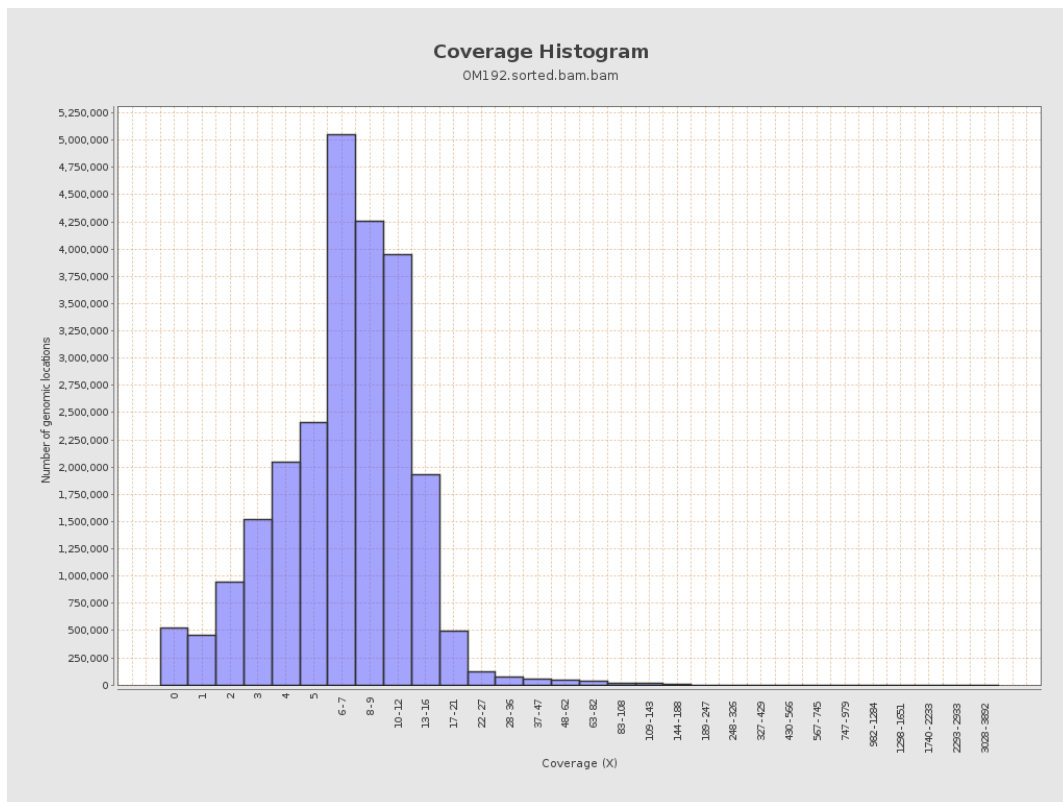
Coverage Histogram (0-50X)
OM192.sorted.bam.bam
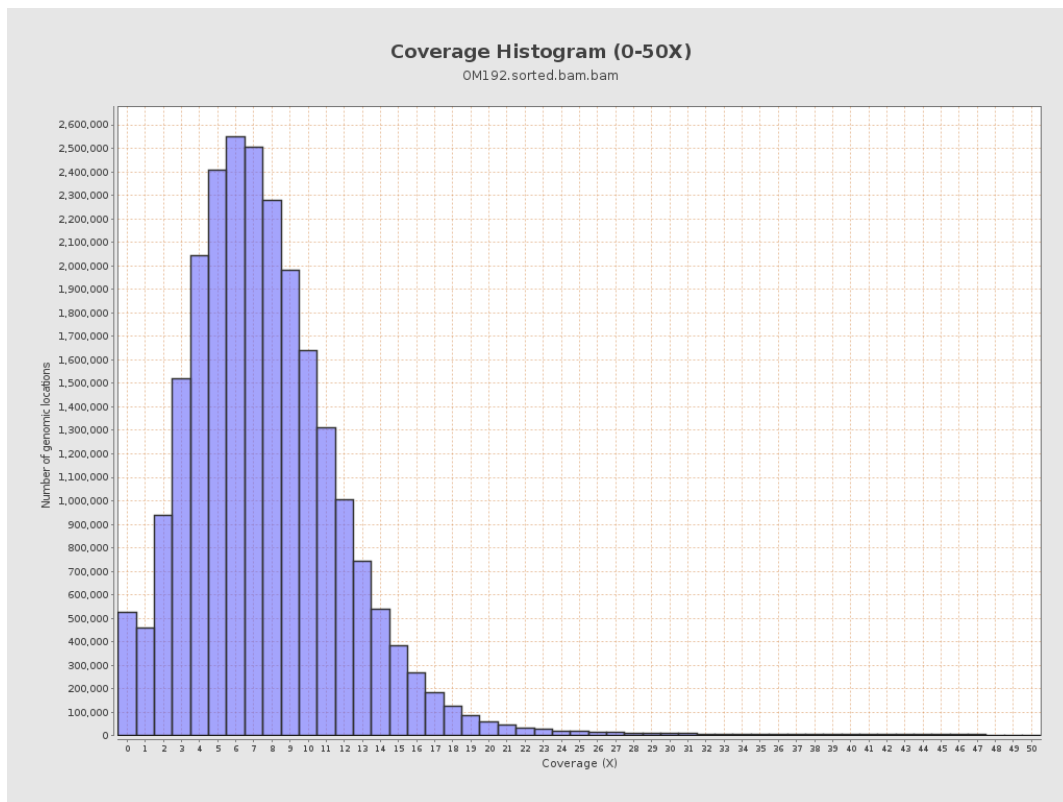
6. Results : Genome Fraction Coverage
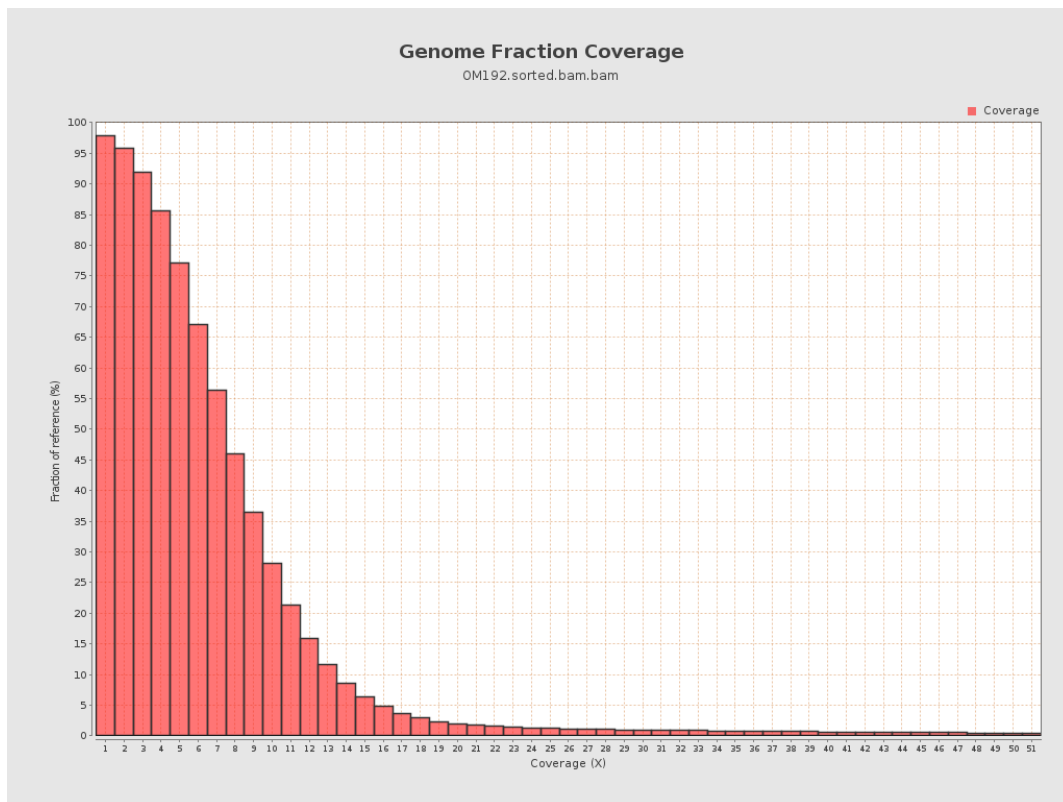
7. Results : Duplication Rate Histogram

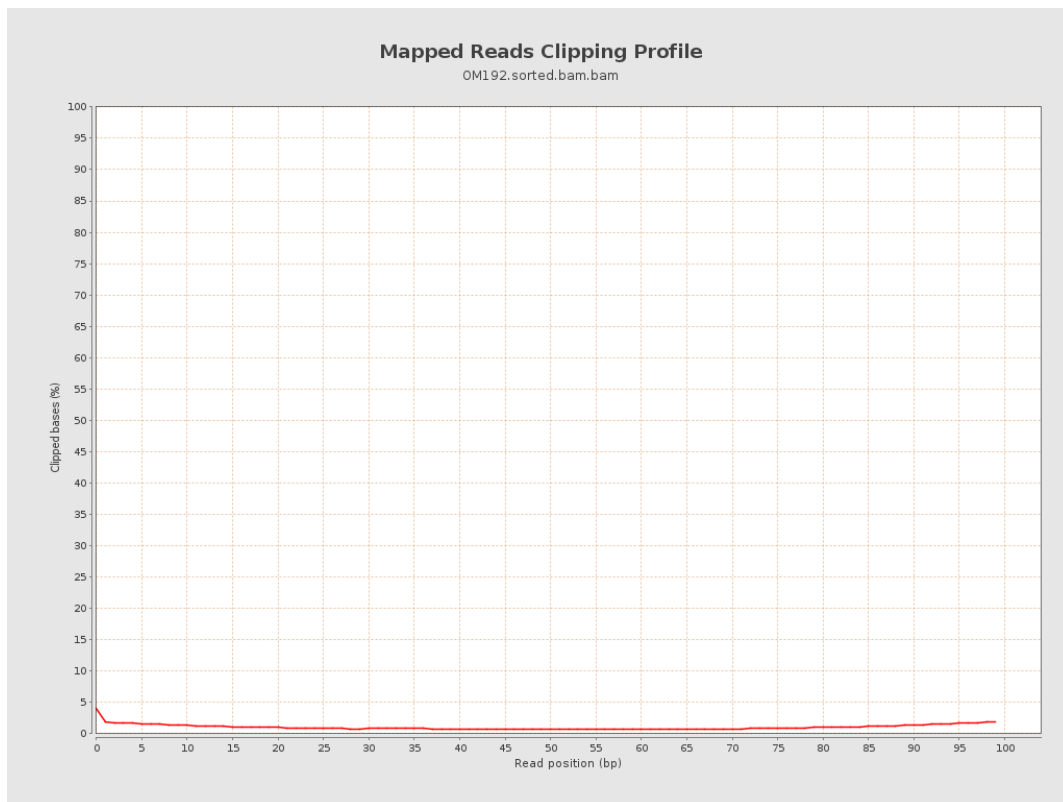**Duplication Rate Histogram**
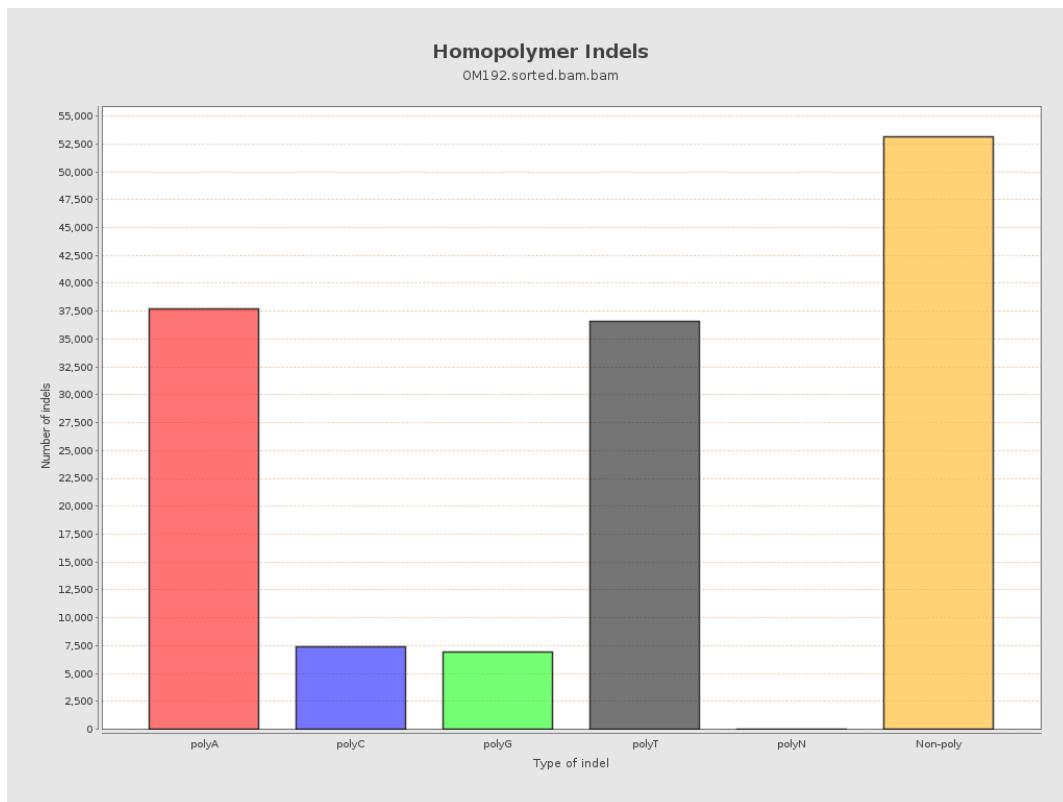OM192.sorted.bam.bam
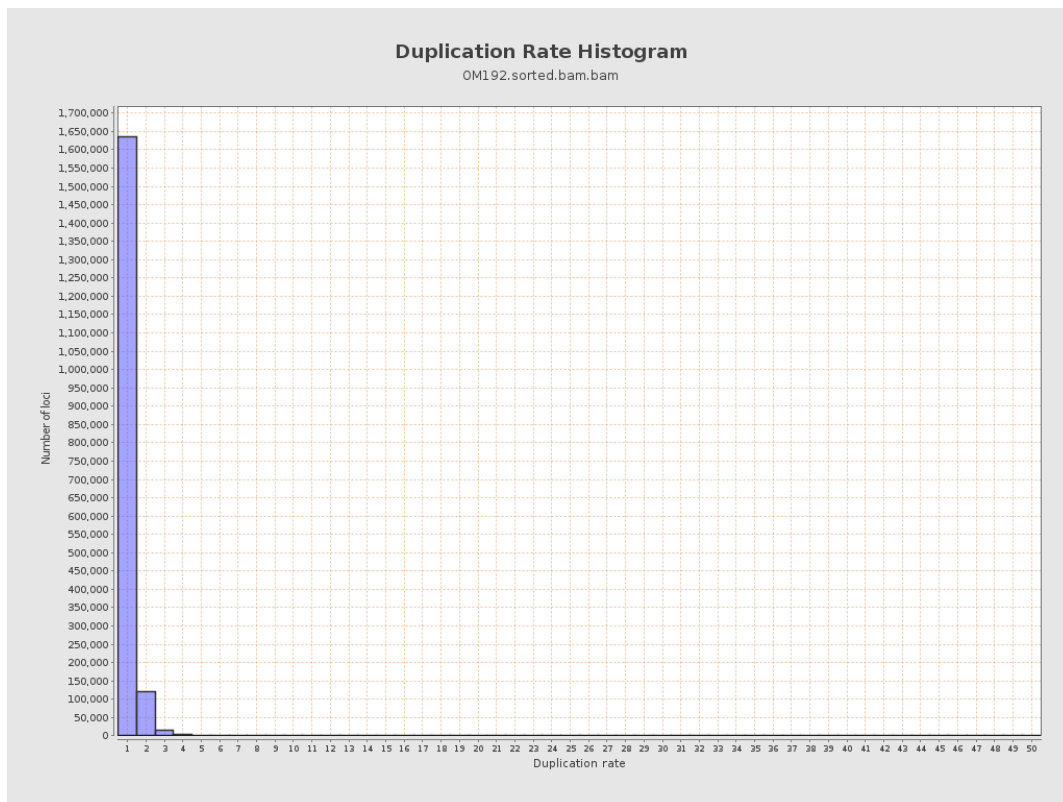
8. Results : Mapped Reads Nucleotide Content
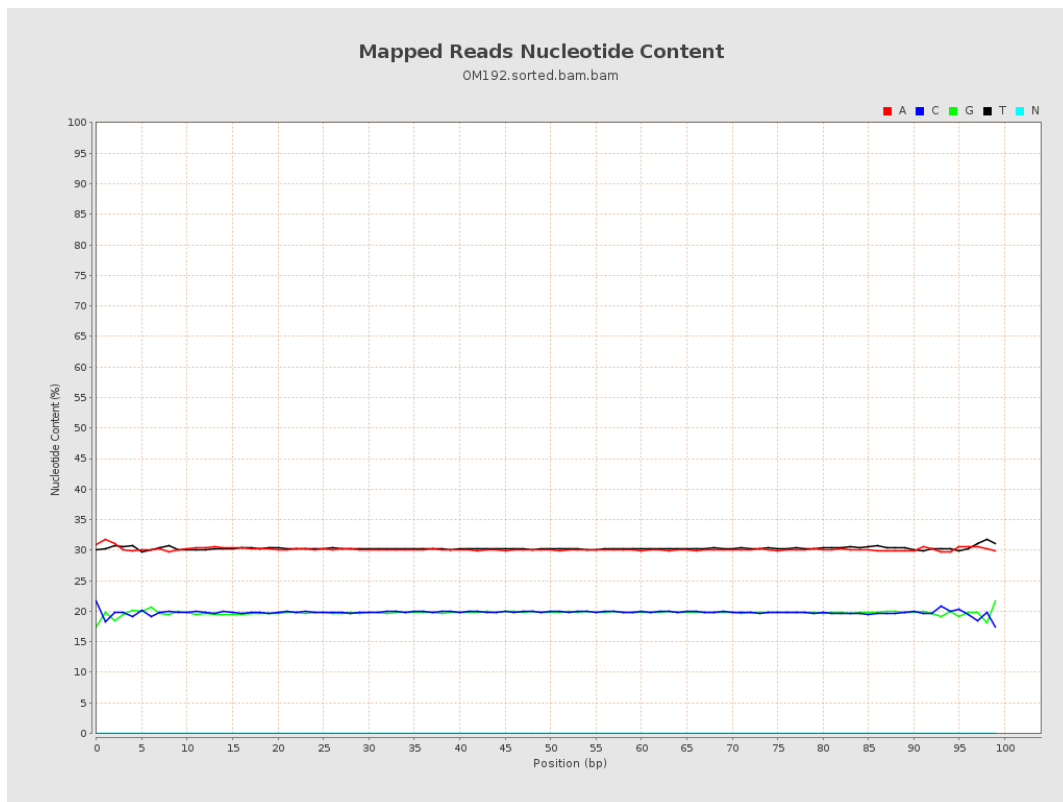
9. Results : Mapped Reads GC-content Distribution
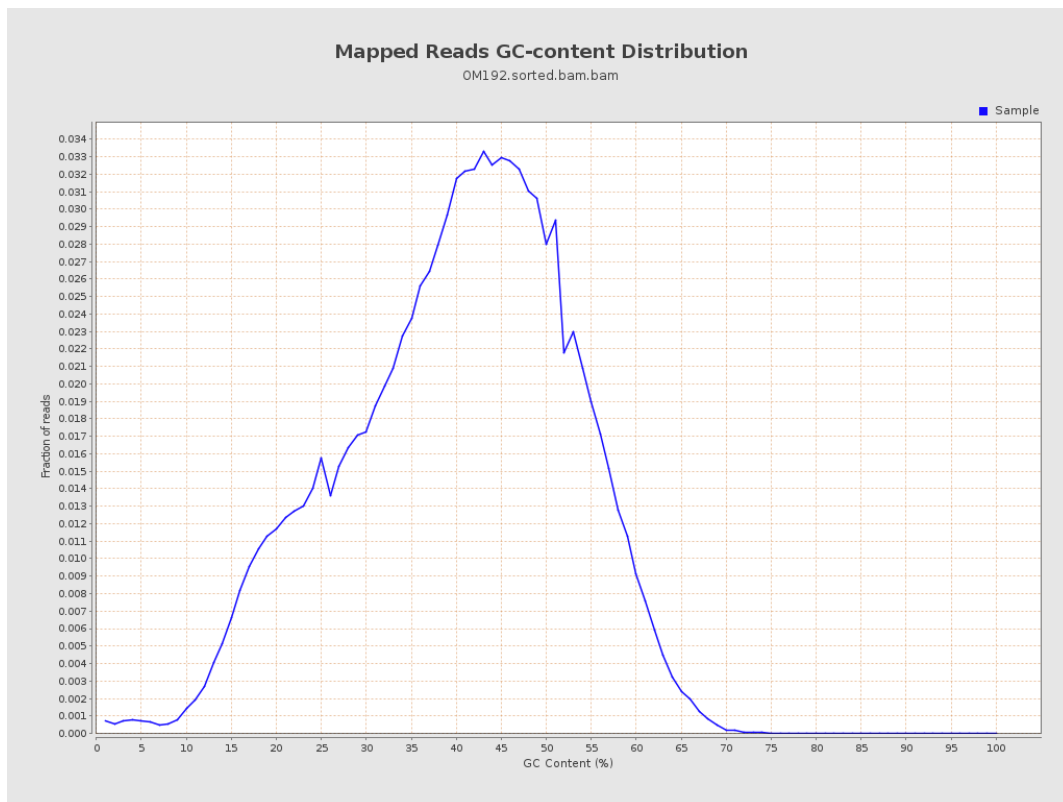
10. Results : Mapped Reads Clipping Profile

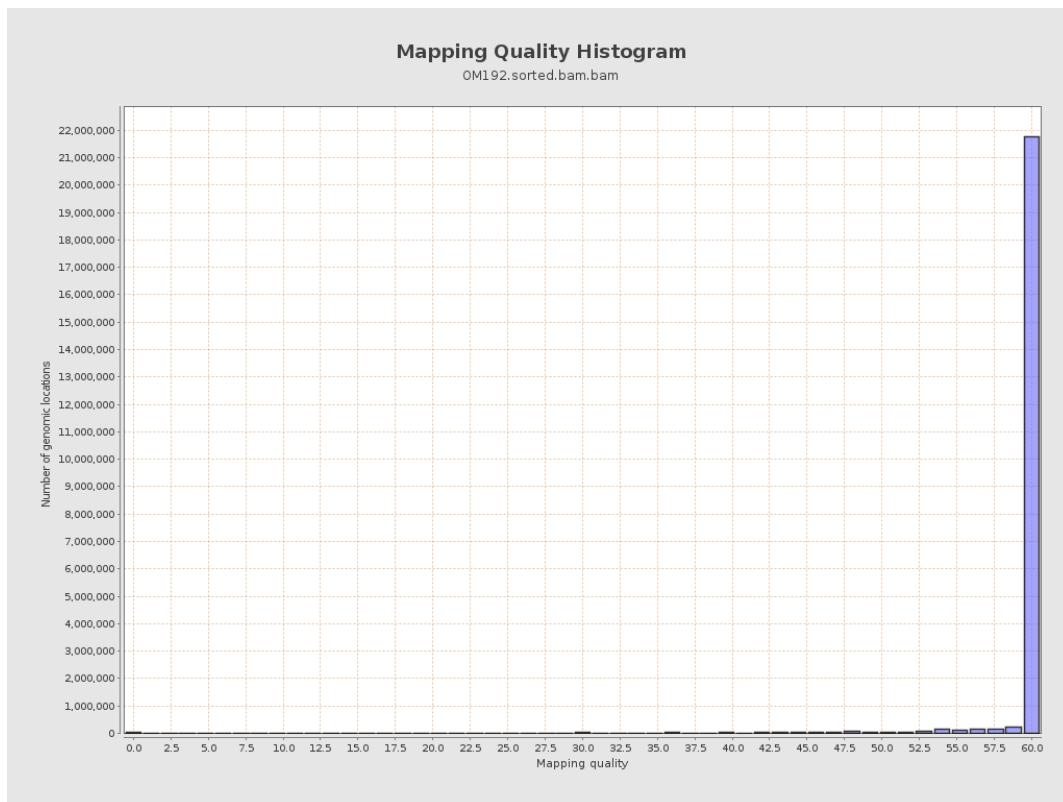
Mapped Reads Clipping Profile
OM192.sorted.bam.bam

11. Results : Homopolymer Indels

12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram
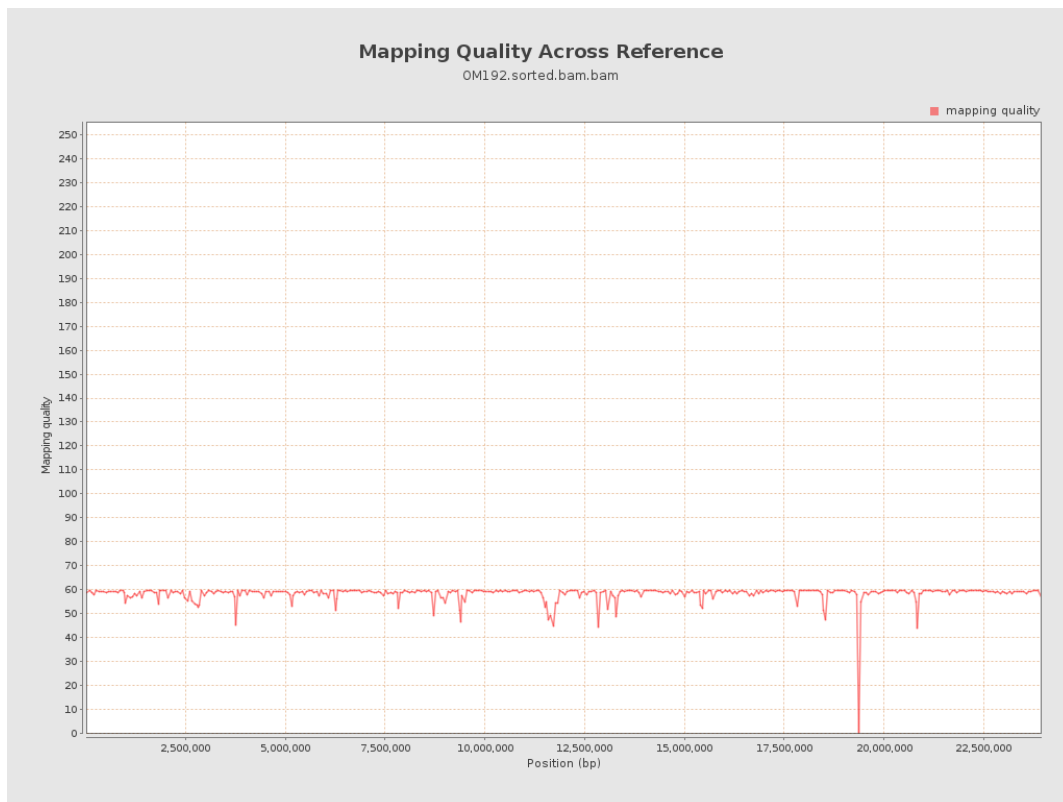
Mapping Quality Histogram
OM192.sorted.bam.bam

14. Results : Insert Size Across Reference
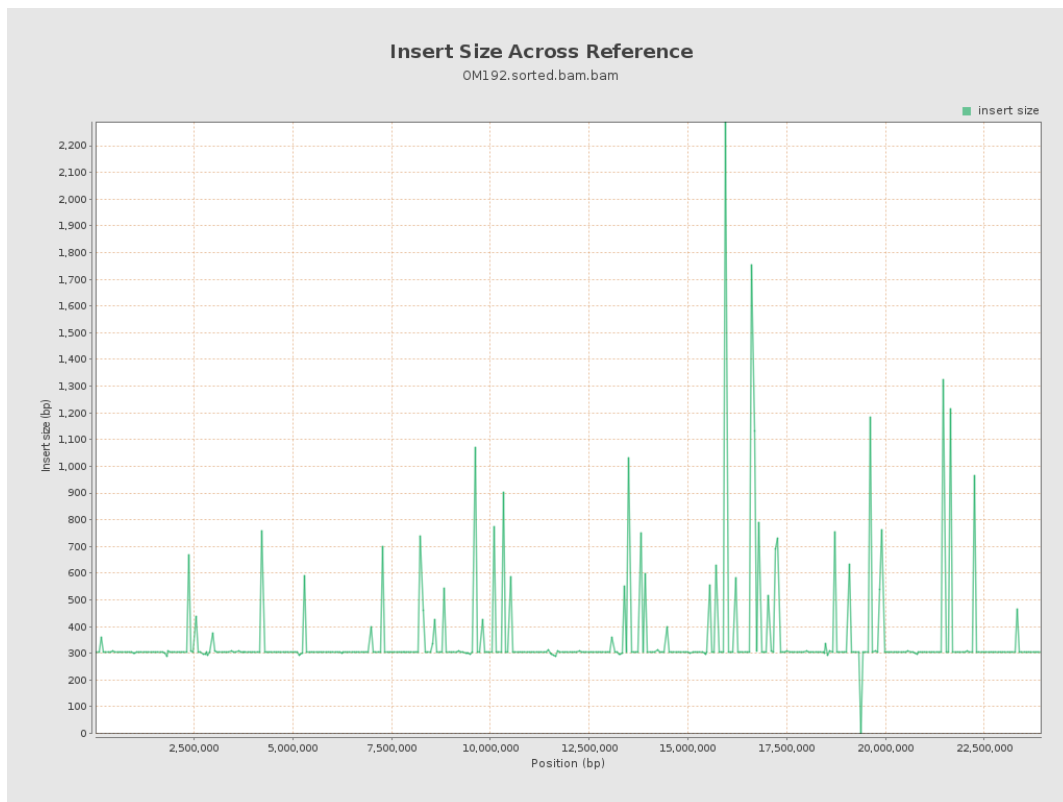
15. Results : Insert Size Histogram

Insert Size Histogram
OM192.sorted.bam.bam