Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 13:30:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM141.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/OM141-BiooBarcode10_GATCAG_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM141-BiooBarcode10_GATCAG_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:30:21 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM141.sorted.bam.

	bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	41,356,261
Mapped reads	5,280,744 / 12.77%
Unmapped reads	36,075,517 / 87.23%
Mapped paired reads	5,280,744 / 12.77%
Mapped reads, first in pair	2,652,372 / 6.41%
Mapped reads, second in pair	2,628,372 / 6.36%
Mapped reads, both in pair	4,943,174 / 11.95%
Mapped reads, singletons	337,570 / 0.82%
Read min/max/mean length	30 / 100 / 99.97
Duplicated reads (estimated)	1,145,268 / 2.77%
Duplication rate	15.68%
Clipped reads	811,186 / 1.96%

2.2. ACGT Content

Number/percentage of A's	148,510,772 / 29.97%
Number/percentage of C's	98,754,461 / 19.93%
Number/percentage of T's	149,737,140 / 30.22%
Number/percentage of G's	98,476,591 / 19.88%
Number/percentage of N's	39,452 / 0.01%
GC Percentage	39.81%

2.3. Coverage

Mean	20.7032
Standard Deviation	39.1391

2.4. Mapping Quality

Mean Mapping Quality	57.58

2.5. Insert size

Mean	917.43
Standard Deviation	25,746.65
P25/Median/P75	329 / 343 / 352

2.6. Mismatches and indels

General error rate	1.56%
Mismatches	7,325,184
Insertions	170,887
Mapped reads with at least one insertion	3.04%
Deletions	193,120
Mapped reads with at least one deletion	3.36%
Homopolymer indels	61.16%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	18433239	18.863	15.3914
gi|1074120682|emb|LT615257.1|	860454	17240699	20.0367	21.4379
gi|1074120865|emb|LT615258.1|	989719	22177509	22.4079	30.516
gi|1074121086|emb|LT615259.1|	935450	20700966	22.1294	29.0992
gi|1074121301|emb|LT615260.1|	1432239	31180834	21.7707	24.6408
gi|1074121615|emb|LT615261.1|	1080962	22284540	20.6155	20.9781
gi|1074121871|emb|LT615262.1|	1545099	29879380	19.3382	14.2897
gi|1074122235|emb|LT615263.1|	1585108	32927019	20.7727	56.5826
gi|1074122590|emb|LT615264.1|	2122358	42834725	20.1826	13.5639
gi|1074123050|emb|LT615265.1|	1754192	38107768	21.7238	106.0327
gi|1074123421|emb|LT615	2150147	45423638	21.1258	33.278

266.1|				
gi|1074123898|emb|LT615267.1|	3031036	61192387	20.1886	34.3138
gi|1074124588|emb|LT615268.1|	2359348	47887324	20.2968	21.1896
gi|1074125065|emb|LT615269.1|	3135668	65758009	20.971	12.4568

3. Results : Coverage across reference

Coverage across reference
OM141.sorted.bam.bam

4. Results : Coverage Histogram

Coverage Histogram
OM141.sorted.bam.bam

5. Results : Coverage Histogram (0-50X)
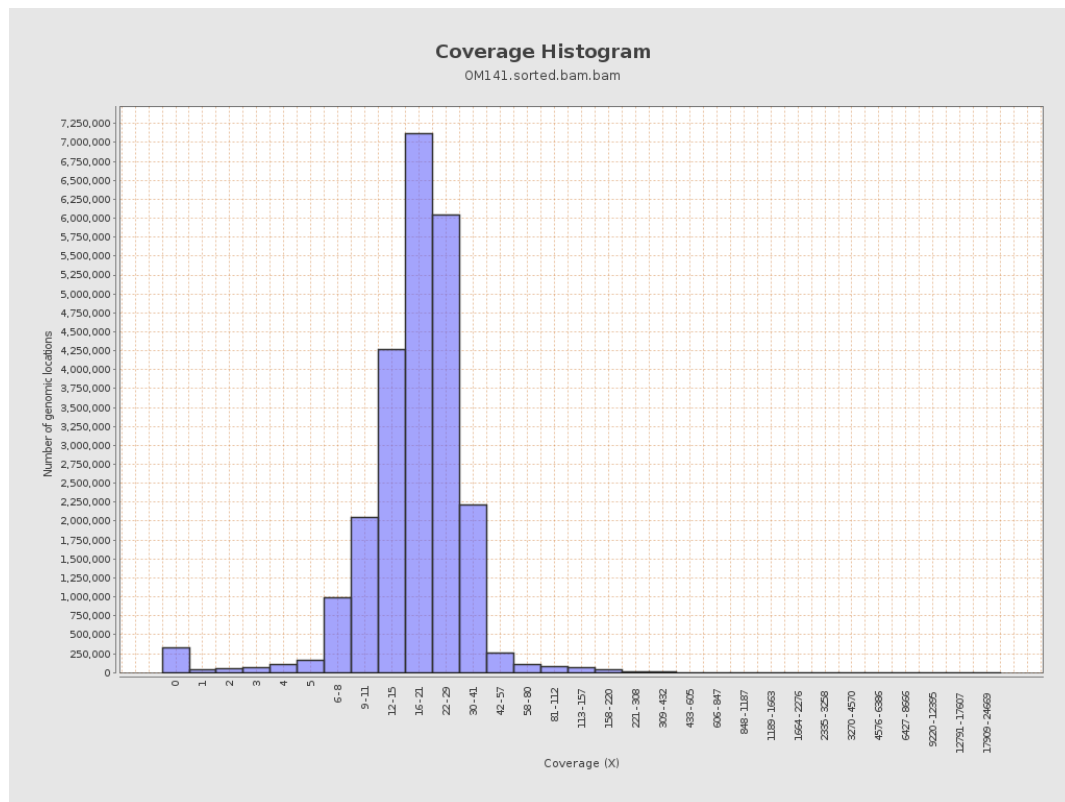
Coverage Histogram (0-50X)
OM141.sorted.bam.bam
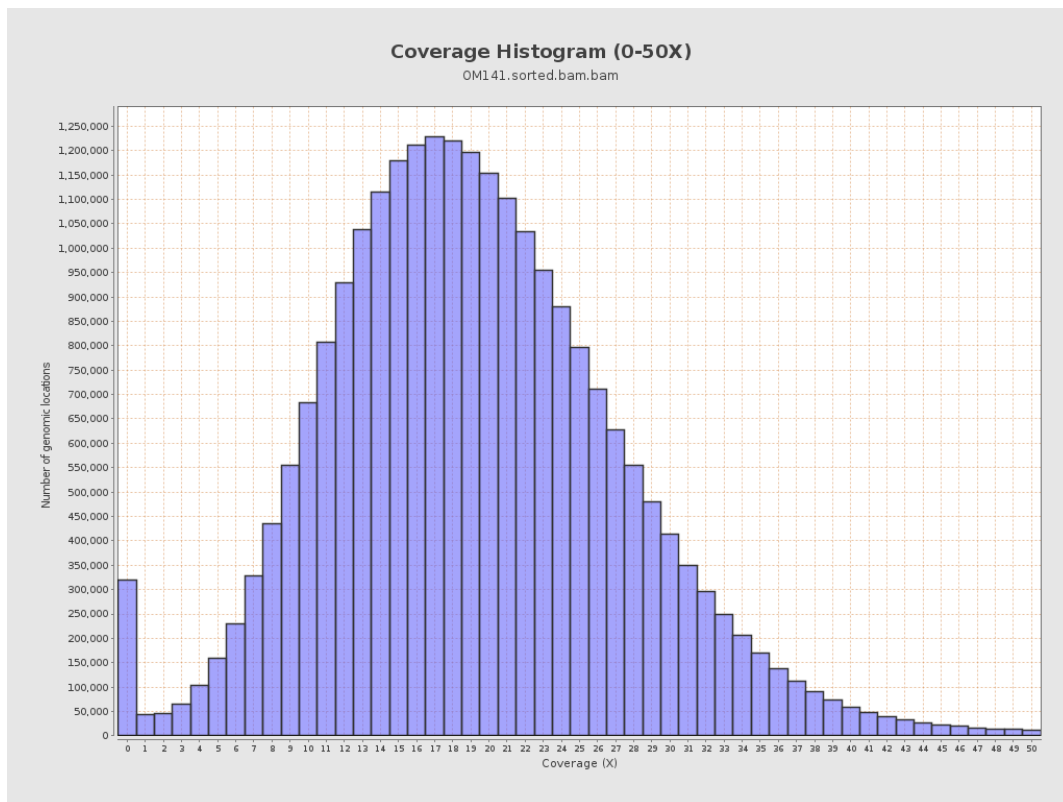
6. Results : Genome Fraction Coverage
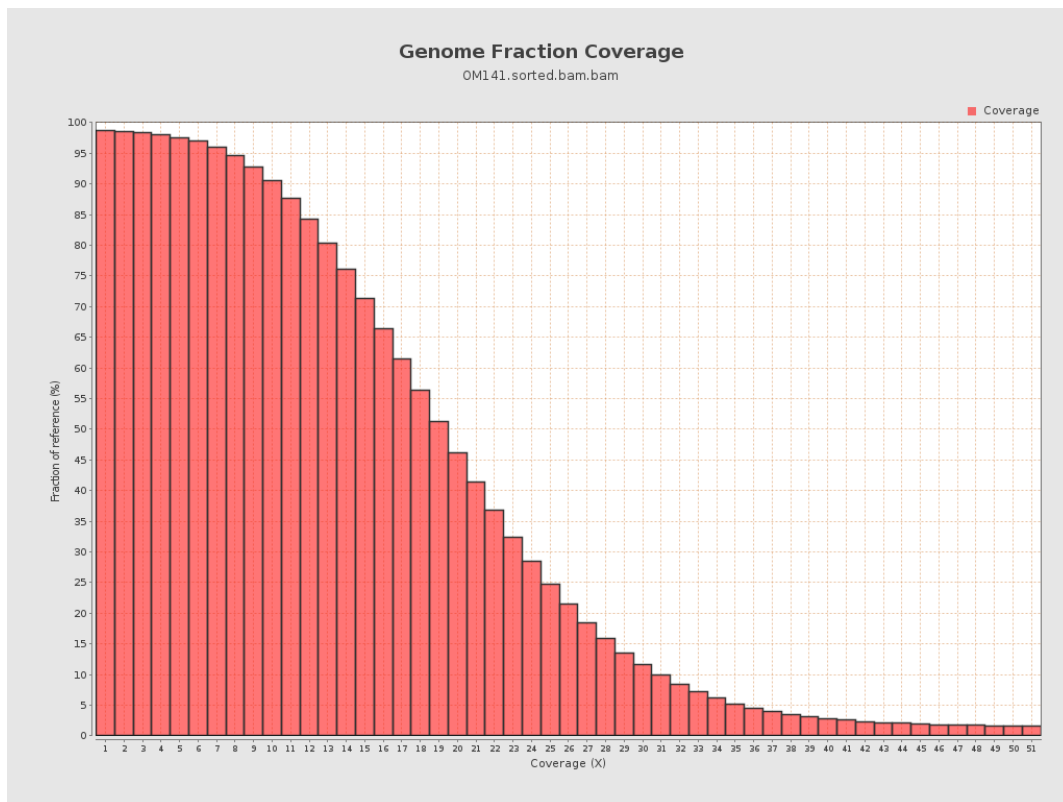
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
OM141.sorted.bam.bam
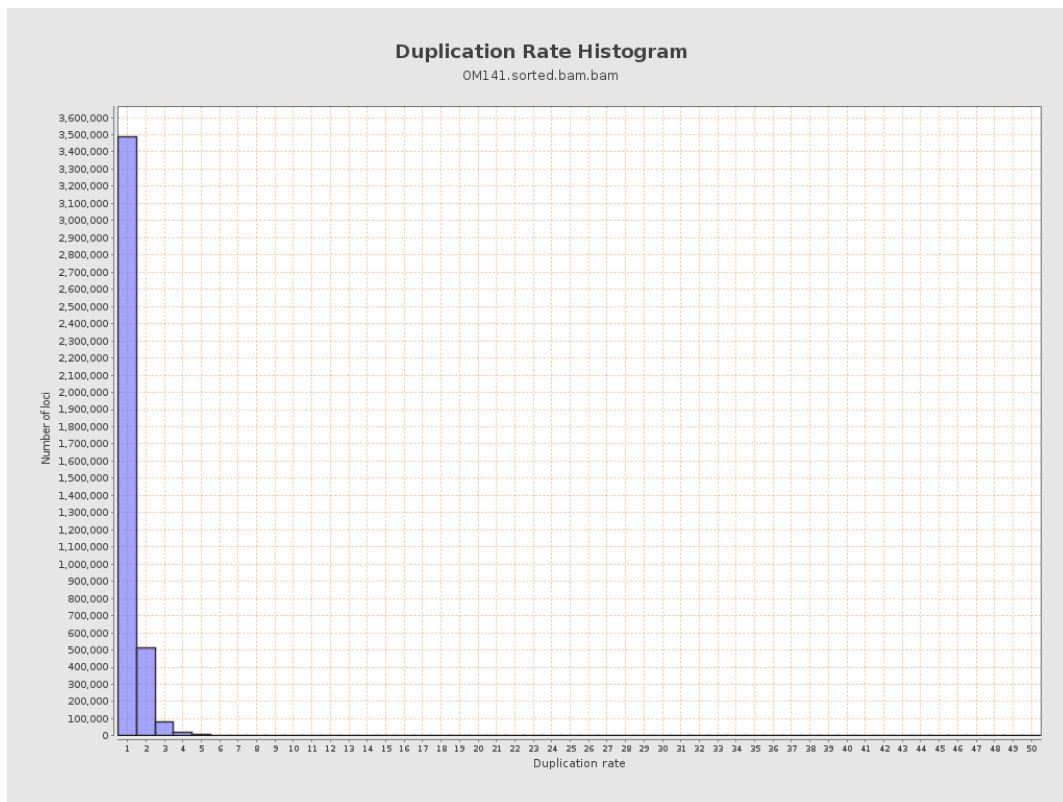
8. Results : Mapped Reads Nucleotide Content

9. Results : Mapped Reads GC-content Distribution
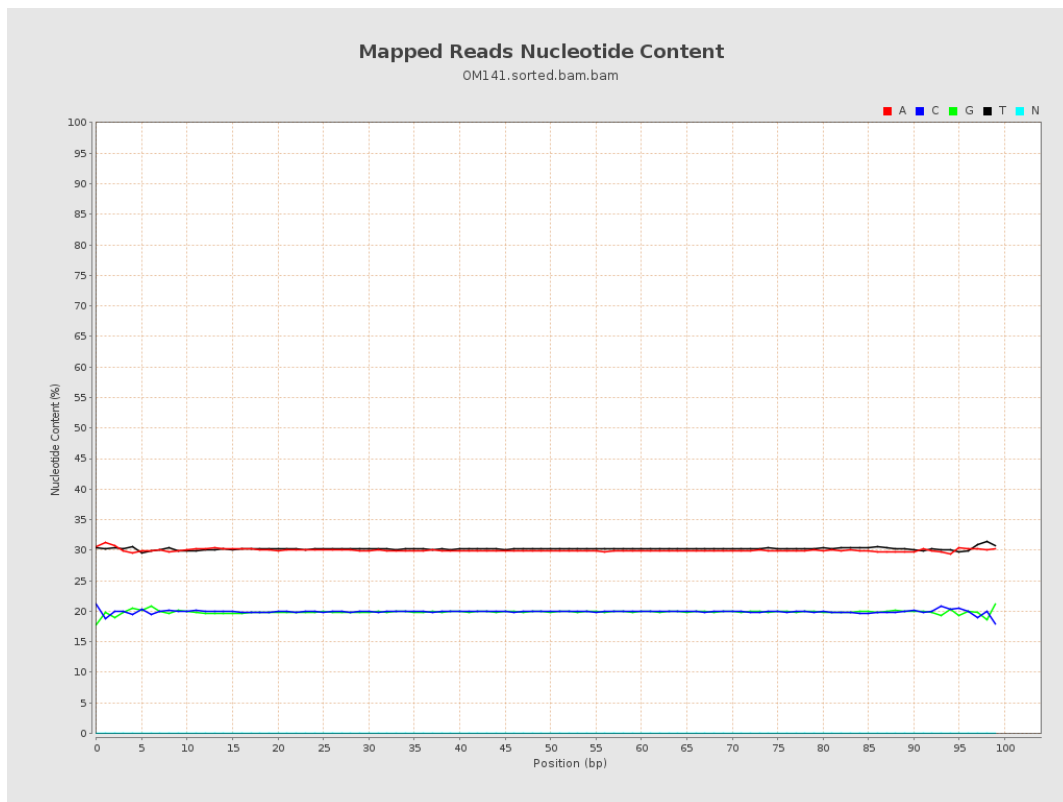
Mapped Reads GC-content Distribution
OM141.sorted.bam.bam
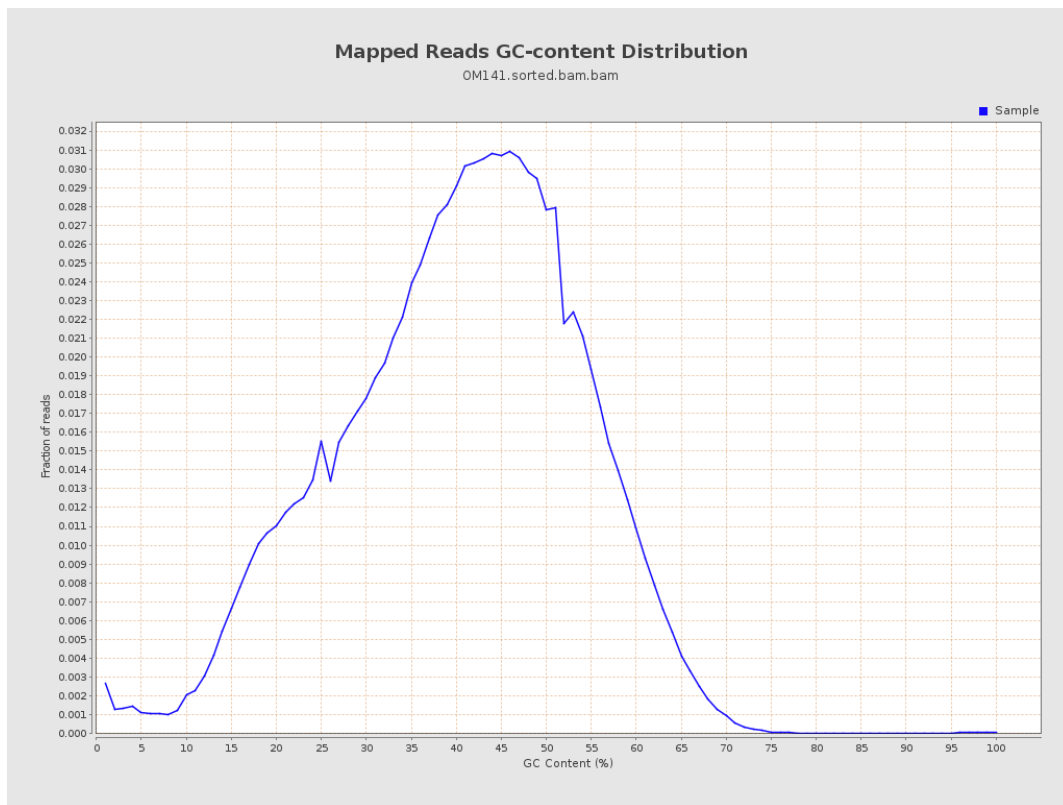
10. Results : Mapped Reads Clipping Profile
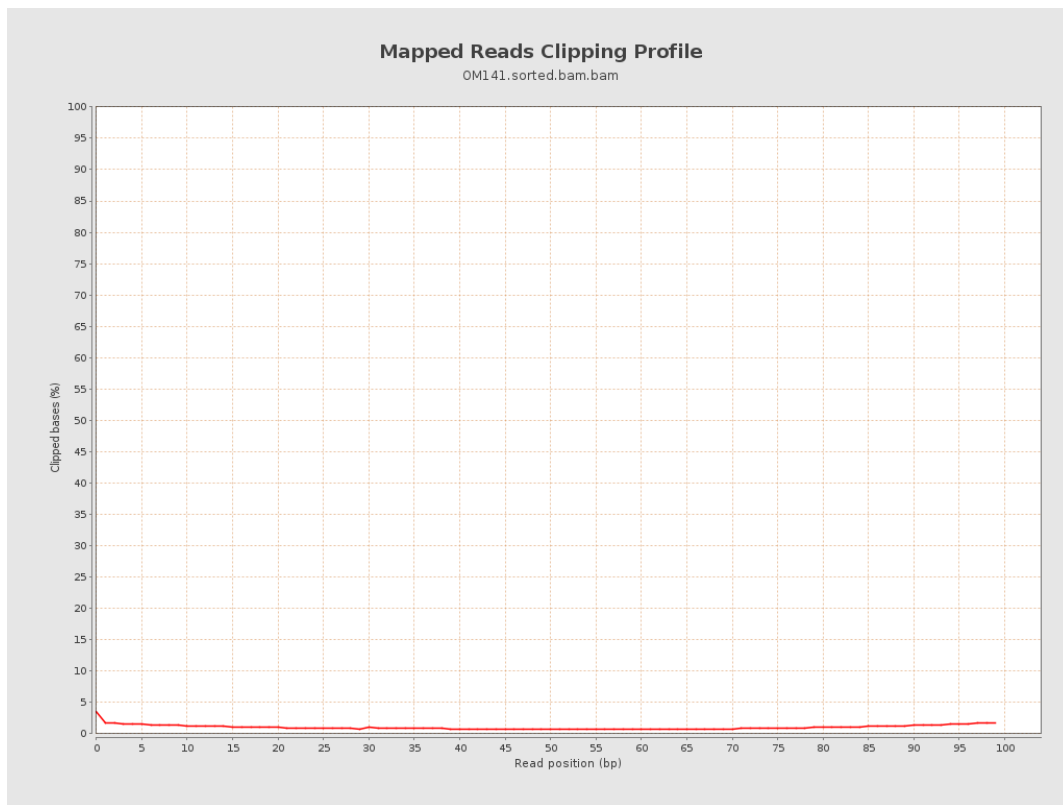
11. Results : Homopolymer Indels

Homopolymer Indels
OM141.sorted.bam.bam
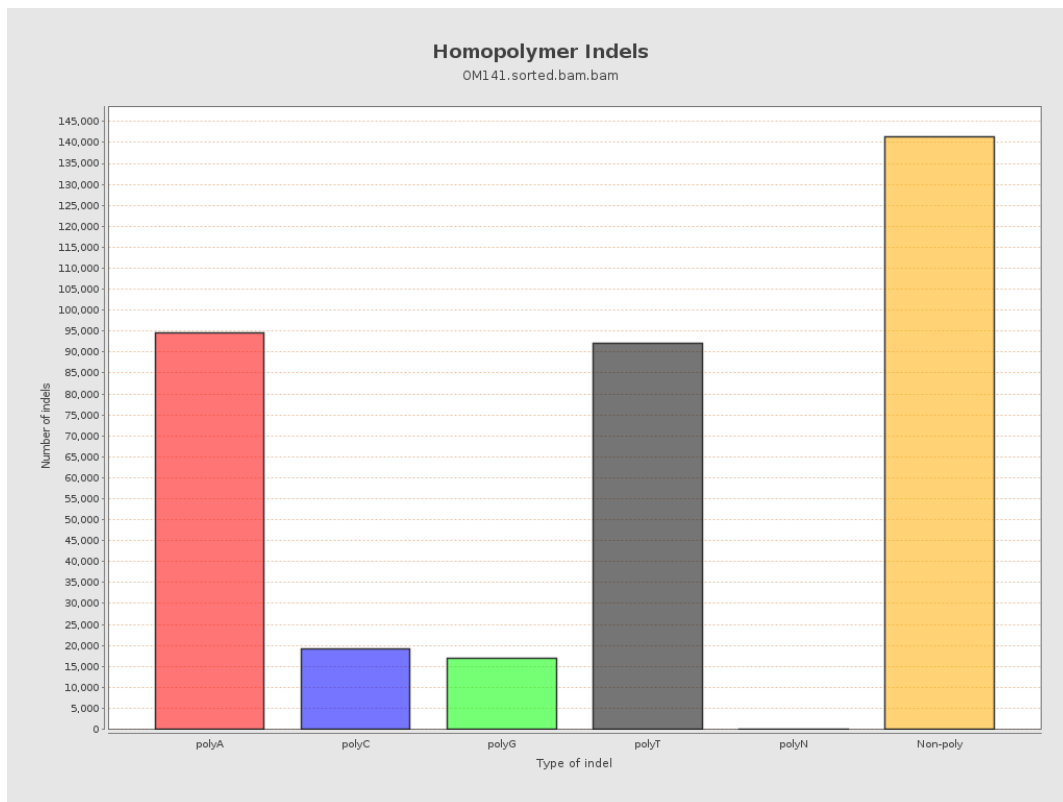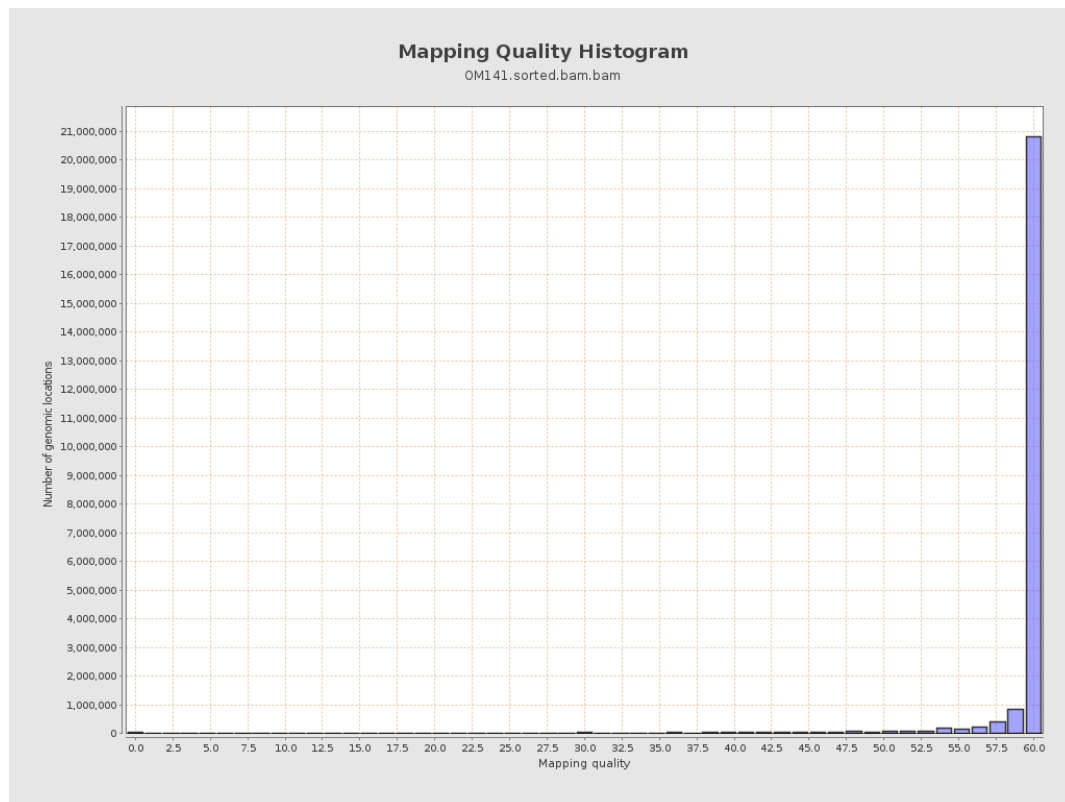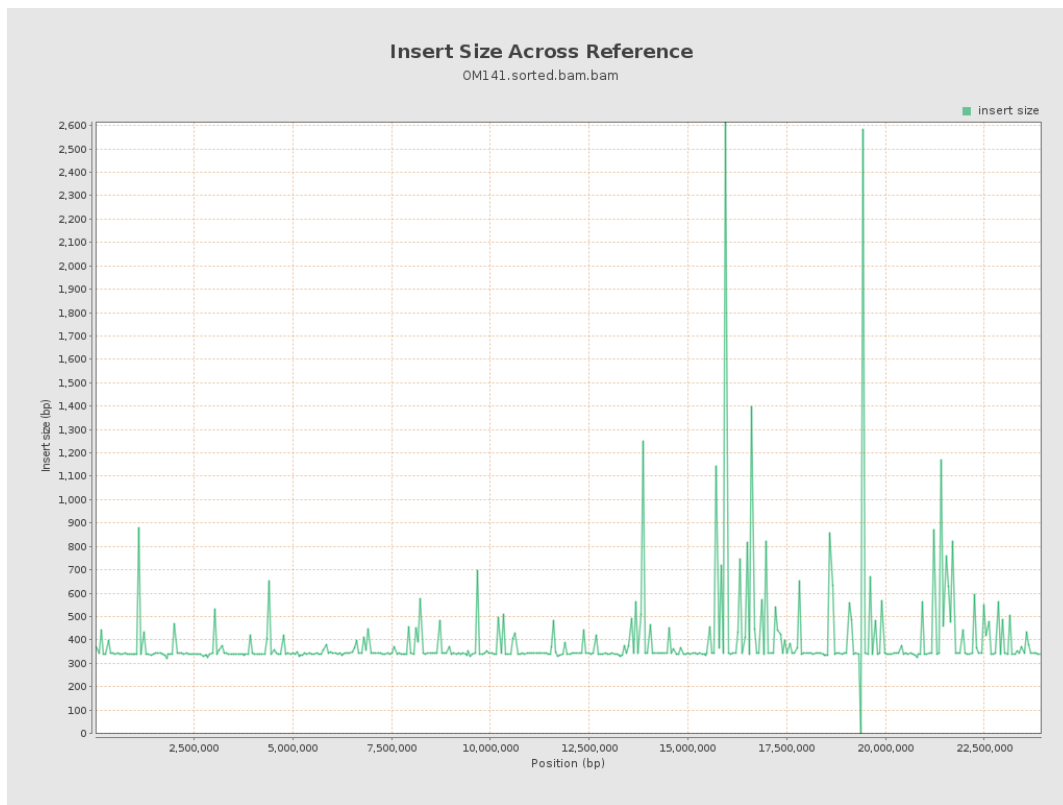
12. Results : Mapping Quality Across Reference
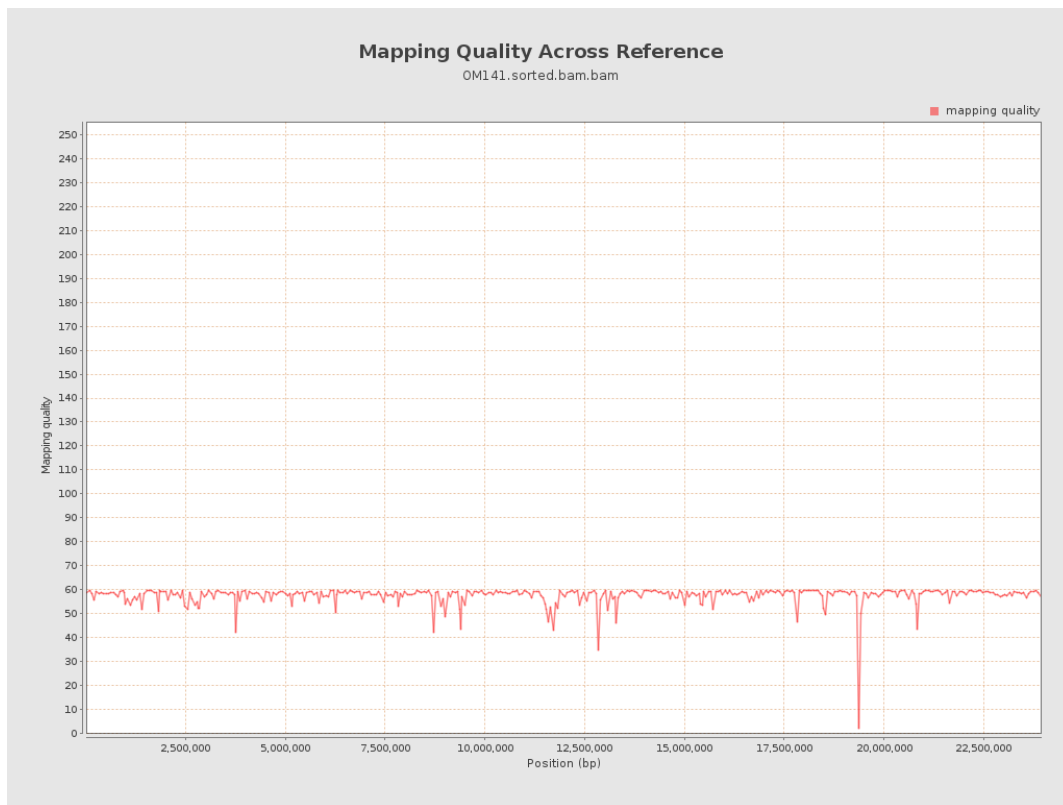
13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram

Insert Size Histogram
OM141.sorted.bam.bam