Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.1
2016/10/23 13:57:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM271.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/OM271-BiooBarcode25_ACTGAT_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM271-BiooBarcode25_ACTGAT_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 13:57:16 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM271.sorted.bam.

	bam

2. Summary

2.1. Globals

Reference size	23,958,997
Number of reads	37,130,391
Mapped reads	11,624,416 / 31.31%
Unmapped reads	25,505,975 / 68.69%
Mapped paired reads	11,624,416 / 31.31%
Mapped reads, first in pair	5,819,684 / 15.67%
Mapped reads, second in pair	5,804,732 / 15.63%
Mapped reads, both in pair	11,325,561 / 30.5%
Mapped reads, singletons	298,855 / 0.8%
Read min/max/mean length	30 / 100 / 99.94
Duplicated reads (estimated)	3,454,480 / 9.3%
Duplication rate	26.45%
Clipped reads	1,224,497 / 3.3%

2.2. ACGT Content

Number/percentage of A's	330,005,780 / 29.45%
Number/percentage of C's	229,726,815 / 20.5%
Number/percentage of T's	331,681,816 / 29.6%
Number/percentage of G's	229,089,914 / 20.45%
Number/percentage of N's	60,185 / 0.01%
GC Percentage	40.95%

2.3. Coverage

Mean	46.815
Standard Deviation	44.1522

2.4. Mapping Quality

Mean Mapping Quality	58.38

2.5. Insert size

Mean	732.34
Standard Deviation	26,619.56
P25/Median/P75	193 / 201 / 210

2.6. Mismatches and indels

General error rate	1.18%
Mismatches	12,352,720
Insertions	341,794
Mapped reads with at least one insertion	2.78%
Deletions	388,976
Mapped reads with at least one deletion	3.14%
Homopolymer indels	63.84%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi|1074120478|emb|LT615256.1|	977217	41553285	42.5221	15.3632
gi|1074120682|emb|LT615257.1|	860454	41342178	48.0469	34.9429
gi|1074120865|emb|LT615258.1|	989719	52292630	52.8358	52.8014
gi|1074121086|emb|LT615259.1|	935450	47718503	51.0113	62.2459
gi|1074121301|emb|LT615260.1|	1432239	67288950	46.9816	38.8663
gi|1074121615|emb|LT615261.1|	1080962	53040641	49.068	39.784
gi|1074121871|emb|LT615262.1|	1545099	68920907	44.6061	16.0632
gi|1074122235|emb|LT615263.1|	1585108	73707278	46.4998	47.6225
gi|1074122590|emb|LT615264.1|	2122358	96351867	45.3985	19.3386
gi|1074123050|emb|LT615265.1|	1754192	81659906	46.5513	89.6551
gi|1074123421|emb|LT615	2150147	104800458	48.7411	63.2027

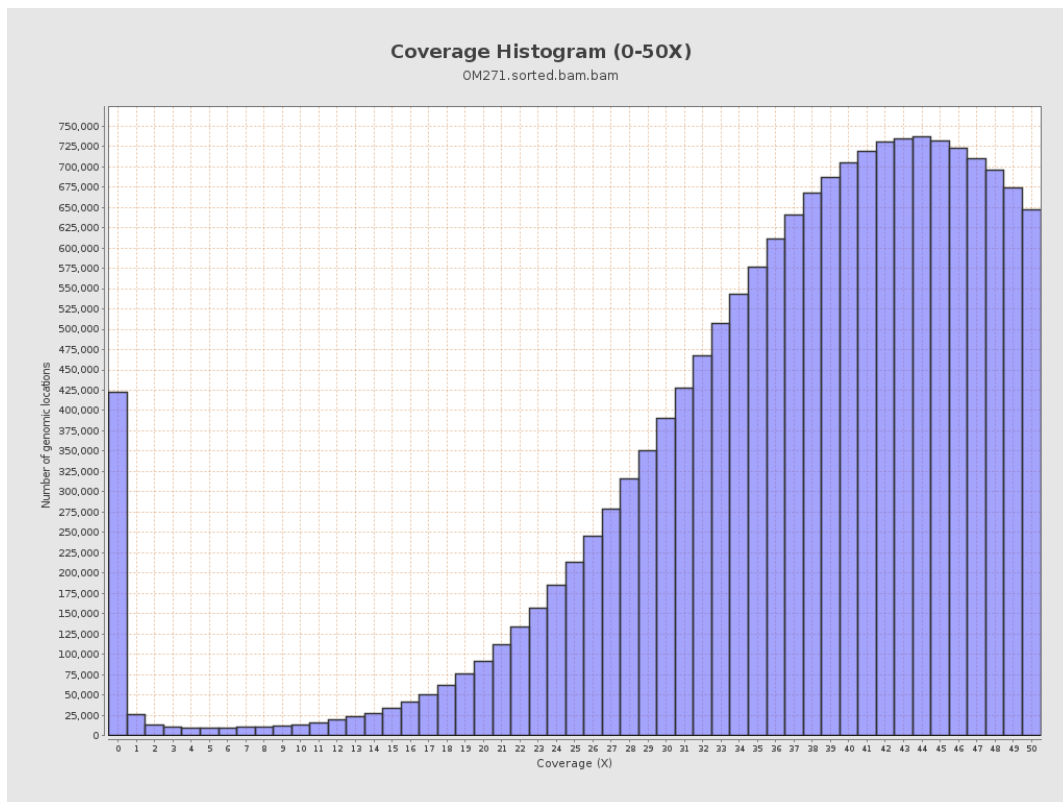|				
266.1|				
gi|107412389 8|emb|LT615 267.1|	3031036	138619639	45.7334	30.7659
gi|107412458 8|emb|LT615 268.1|	2359348	107976342	45.7653	41.1091
gi|107412506 5|emb|LT615 269.1|	3135668	146368663	46.6786	15.272

3. Results : Coverage across reference

Coverage across reference
OM271.sorted.bam.bam

4. Results : Coverage Histogram

Coverage Histogram
OM271.sorted.bam.bam

5. Results : Coverage Histogram (0-50X)
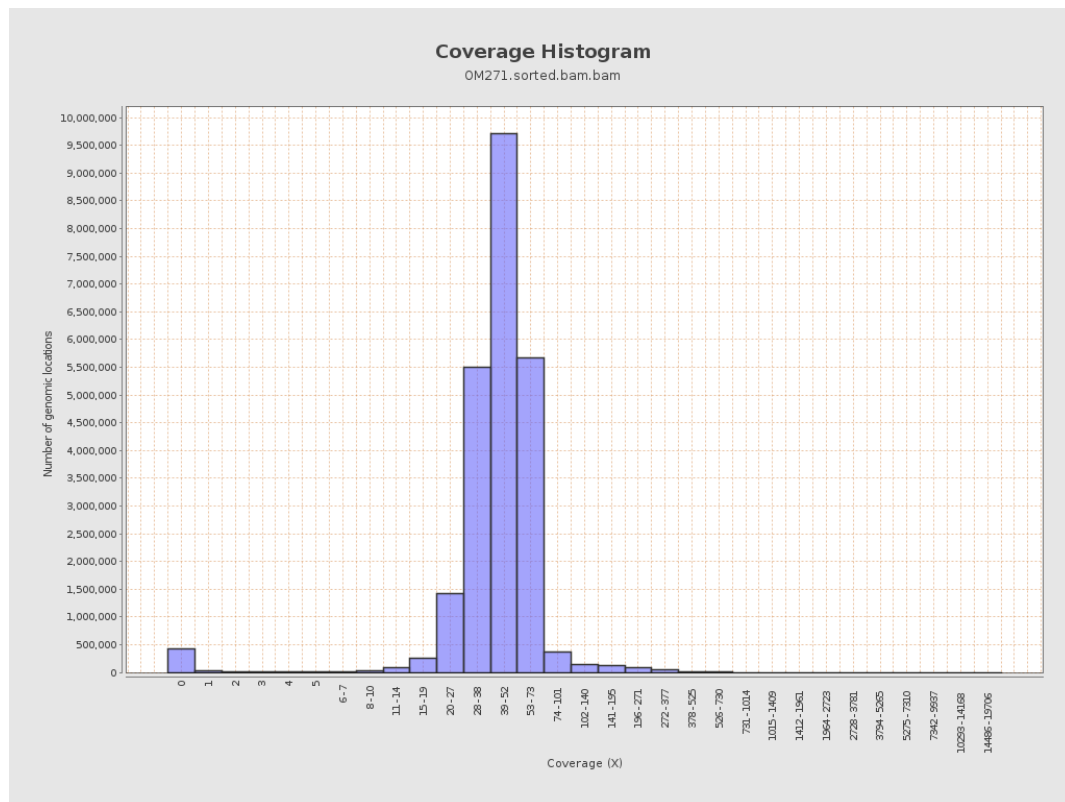
Coverage Histogram (0-50X)
OM271.sorted.bam.bam

6. Results : Genome Fraction Coverage

Genome Fraction Coverage
OM271.sorted.bam.bam
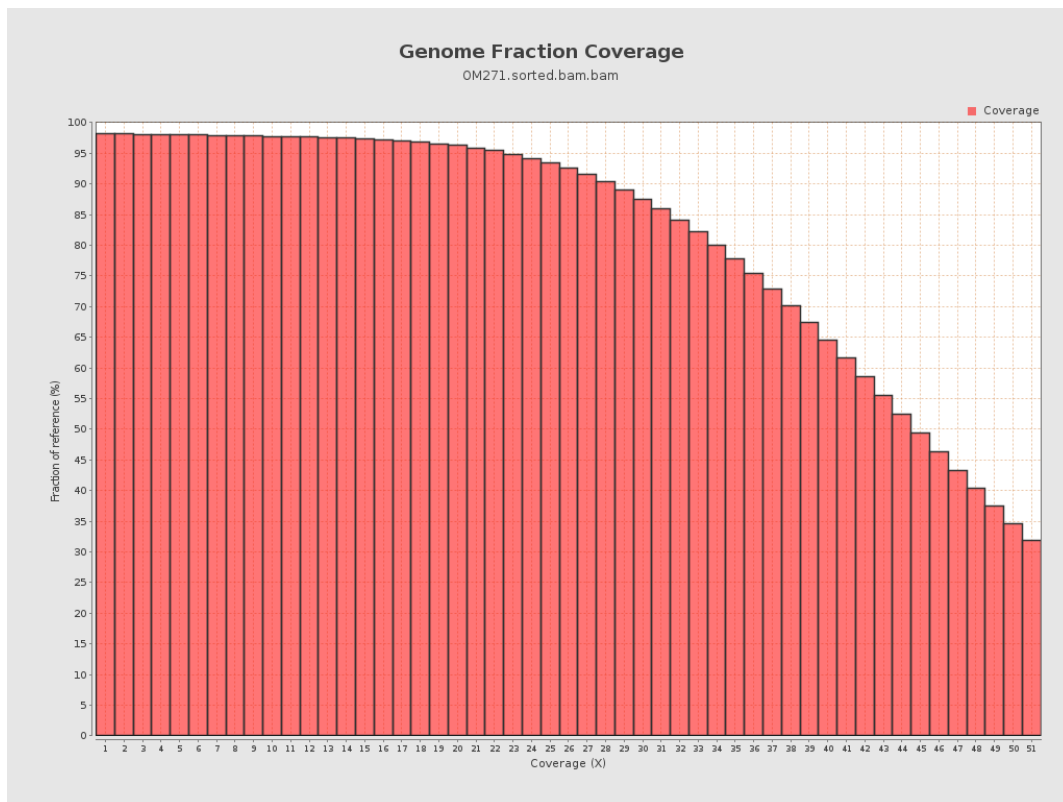
7. Results : Duplication Rate Histogram

Duplication Rate Histogram
OM271.sorted.bam.bam
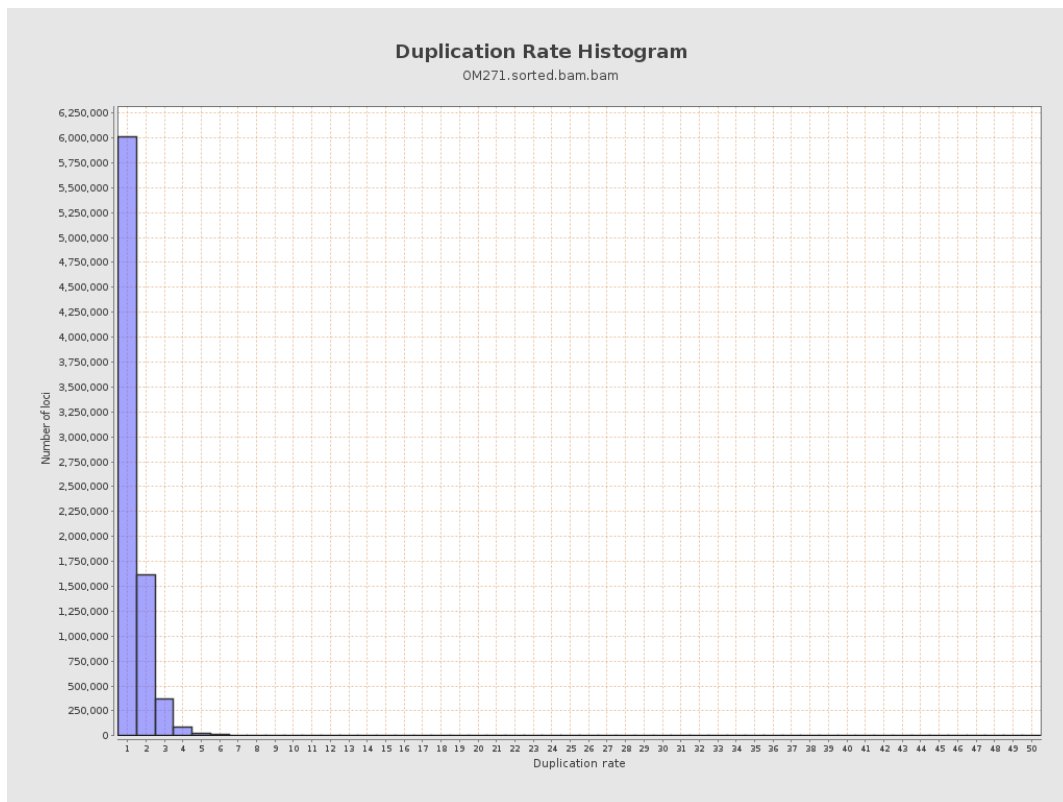
8. Results : Mapped Reads Nucleotide Content

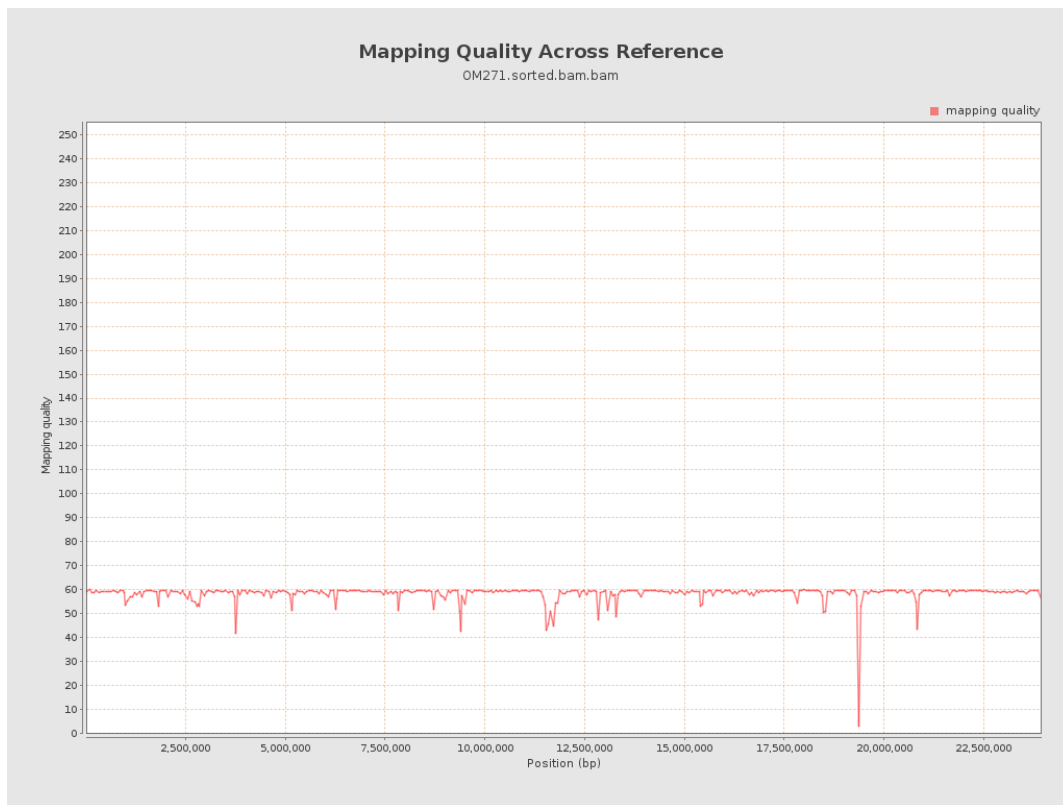# 9. Results : Mapped Reads GC-content Distribution
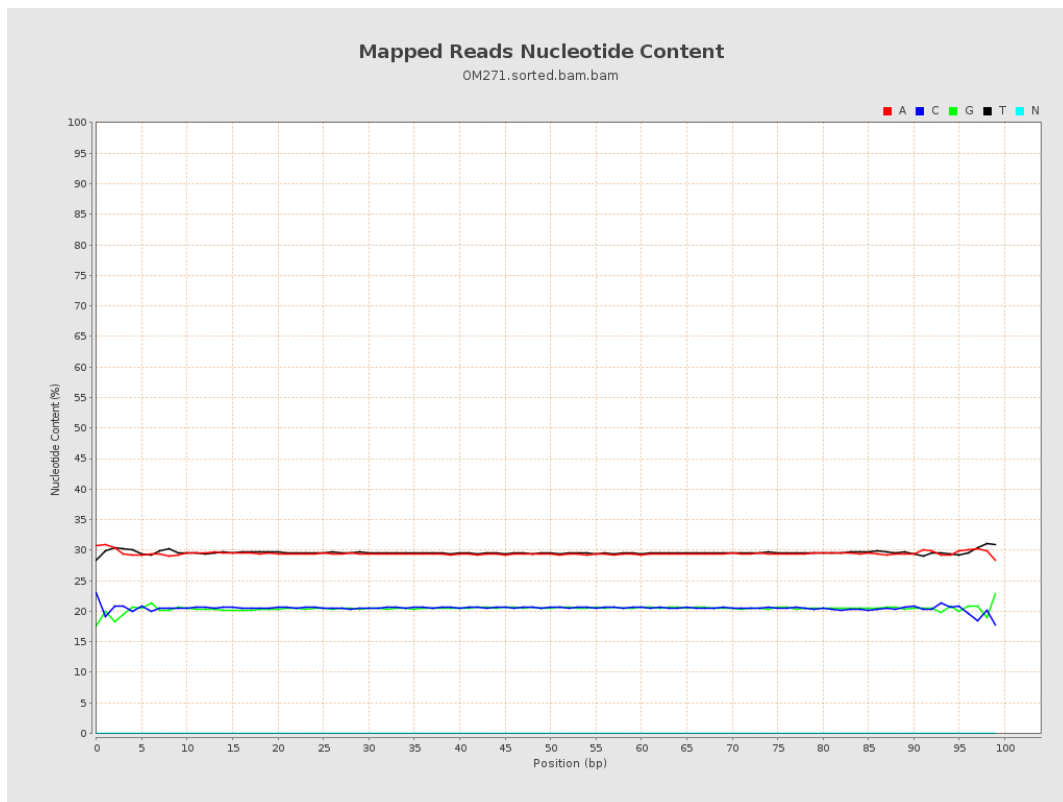
Mapped Reads GC-content Distribution
OM271.sorted.bam.bam
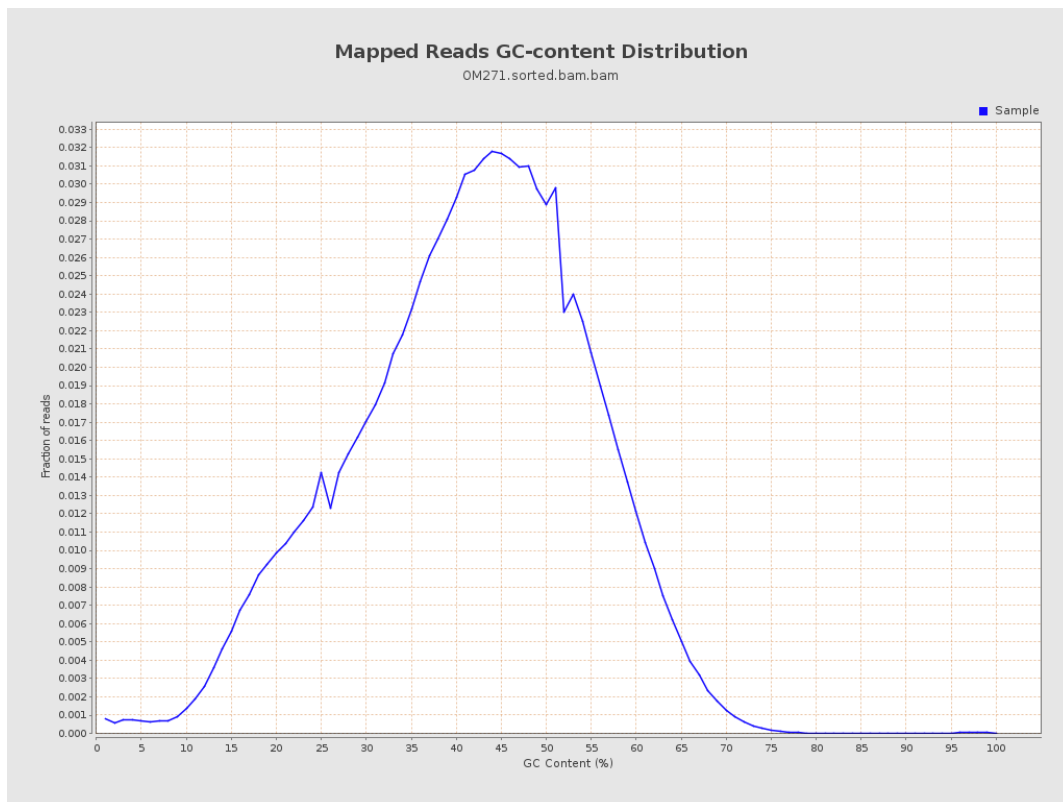
10. Results : Mapped Reads Clipping Profile
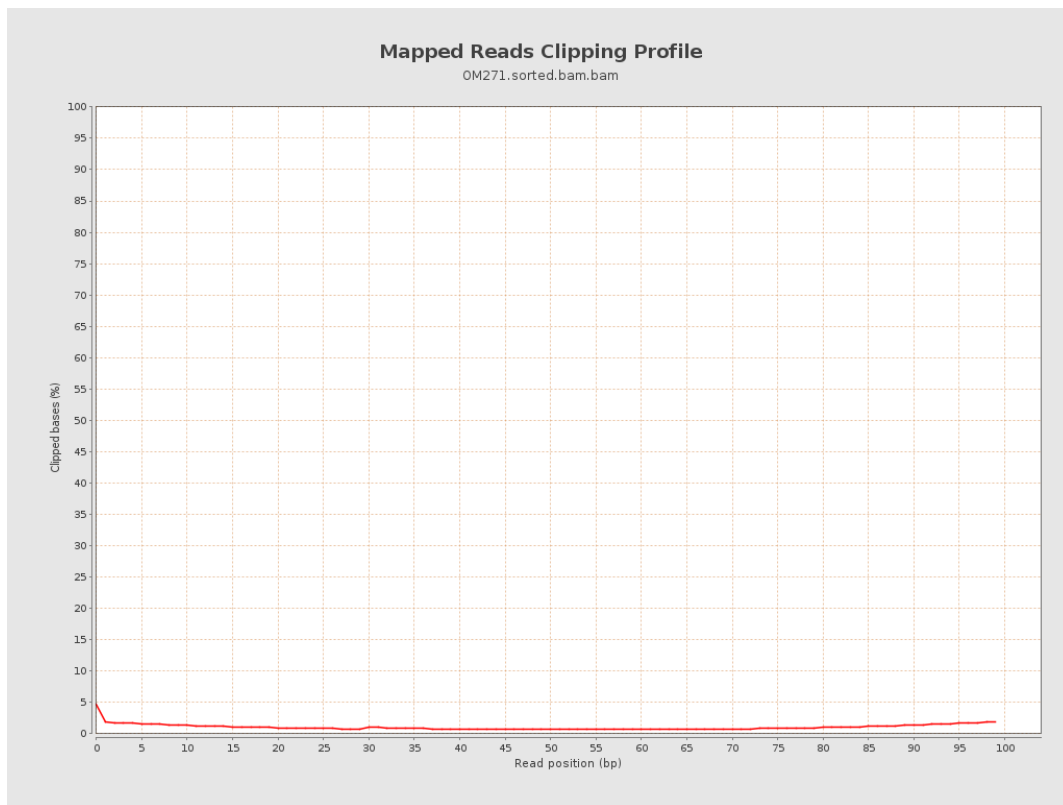
11. Results : Homopolymer Indels
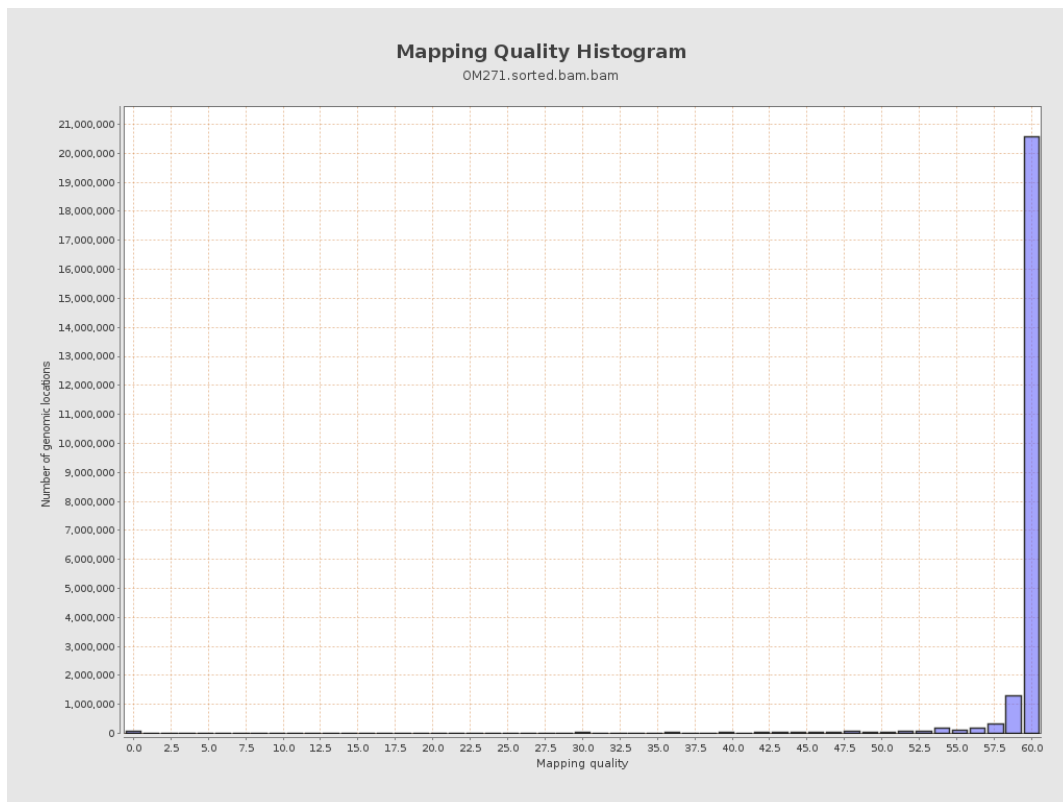

Homopolymer Indels
OM271.sorted.bam.bam
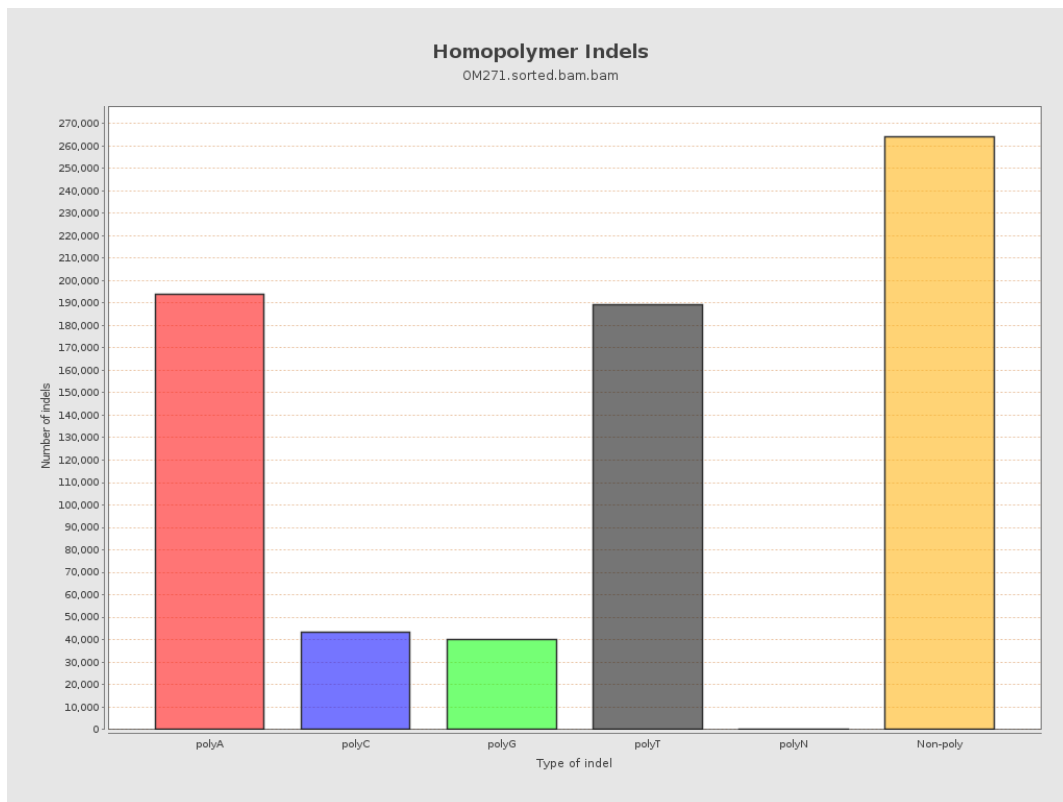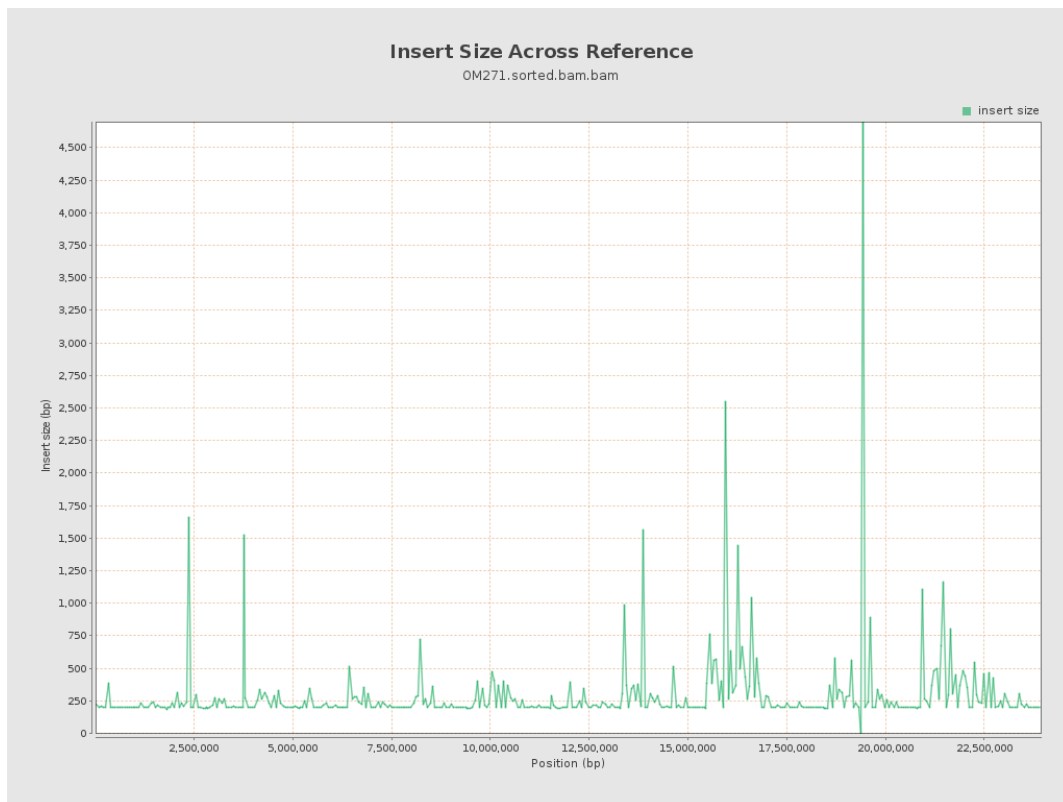
12. Results : Mapping Quality Across Reference

13. Results : Mapping Quality Histogram

14. Results : Insert Size Across Reference

15. Results : Insert Size Histogram

Insert Size Histogram
OM271.sorted.bam.bam