

# Qualimap Analysis Results

*BAM QC analysis*

*Generated by Qualimap v.2.2.1*

*2016/10/23 14:33:12*

# 1. Input data & parameters

## 1.1. QualiMap command line

```
qualimap bamqc -bam
/home/vdp5/data/cambodia_samples/sequences_bam/OM339.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/OM339-BiooBarcode43_TACAGC_R1.fastq.gz /home/vdp5/data/cambodia_samples/sequences_gz/OM339-BiooBarcode43_TACAGC_R2.fastq.gz
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.15-r1140)
Analysis date:	Sun Oct 23 14:33:11 EDT 2016
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	/home/vdp5/data/cambodia_samples/sequences_bam/OM339.sorted.bam.

	bam
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## 2. Summary

### 2.1. Globals

Reference size	23,958,997
Number of reads	61,984,822
Mapped reads	16,834,707 / 27.16%
Unmapped reads	45,150,115 / 72.84%
Mapped paired reads	16,834,707 / 27.16%
Mapped reads, first in pair	8,432,237 / 13.6%
Mapped reads, second in pair	8,402,470 / 13.56%
Mapped reads, both in pair	16,382,068 / 26.43%
Mapped reads, singletons	452,639 / 0.73%
Read min/max/mean length	30 / 100 / 99.95
Duplicated reads (estimated)	6,474,489 / 10.45%
Duplication rate	33.71%
Clipped reads	2,226,315 / 3.59%

### 2.2. ACGT Content

Number/percentage of A's	487,597,466 / 30.36%
Number/percentage of C's	314,326,934 / 19.57%
Number/percentage of T's	490,540,799 / 30.55%
Number/percentage of G's	313,343,345 / 19.51%
Number/percentage of N's	141,994 / 0.01%
GC Percentage	39.09%

## 2.3. Coverage

Mean	67.0989
Standard Deviation	79.2495

## 2.4. Mapping Quality

Mean Mapping Quality	58.36
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## 2.5. Insert size

Mean	677.71
Standard Deviation	26,323.11
P25/Median/P75	172 / 186 / 201

## 2.6. Mismatches and indels

General error rate	1.58%
Mismatches	24,115,843
Insertions	580,219
Mapped reads with at least one insertion	3.23%
Deletions	653,657
Mapped reads with at least one deletion	3.63%
Homopolymer indels	60.77%

## 2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

gi 1074120478 emb LT615256.1	977217	58498512	59.8624	42.9894
gi 1074120682 emb LT615257.1	860454	63575129	73.8856	79.7926
gi 1074120865 emb LT615258.1	989719	79936197	80.7666	128.4827
gi 1074121086 emb LT615259.1	935450	68045917	72.7414	101.8037
gi 1074121301 emb LT615260.1	1432239	100785421	70.3691	76.7732
gi 1074121615 emb LT615261.1	1080962	76263264	70.5513	74.8709
gi 1074121871 emb LT615262.1	1545099	94470391	61.142	26.309
gi 1074122235 emb LT615263.1	1585108	104409267	65.8689	91.5155
gi 1074122590 emb LT615264.1	2122358	135503209	63.8456	37.6827
gi 1074123050 emb LT615265.1	1754192	119465768	68.103	133.6404
gi 1074123421 emb LT615	2150147	146047466	67.9244	111.1796

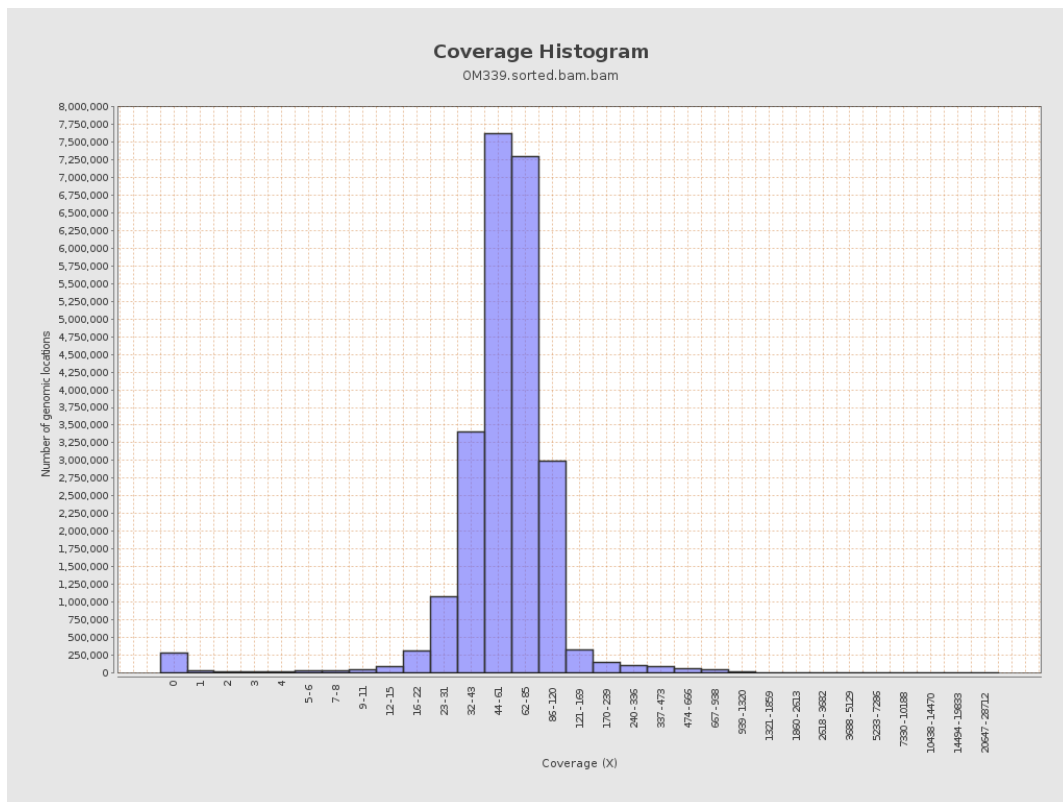
266.1				
gi 107412389 8 emb LT615 267.1	3031036	192137510	63.39	49.3047
gi 107412458 8 emb LT615 268.1	2359348	162196139	68.7462	85.8028
gi 107412506 5 emb LT615 269.1	3135668	206287620	65.7875	26.399

### 3. Results : Coverage across reference

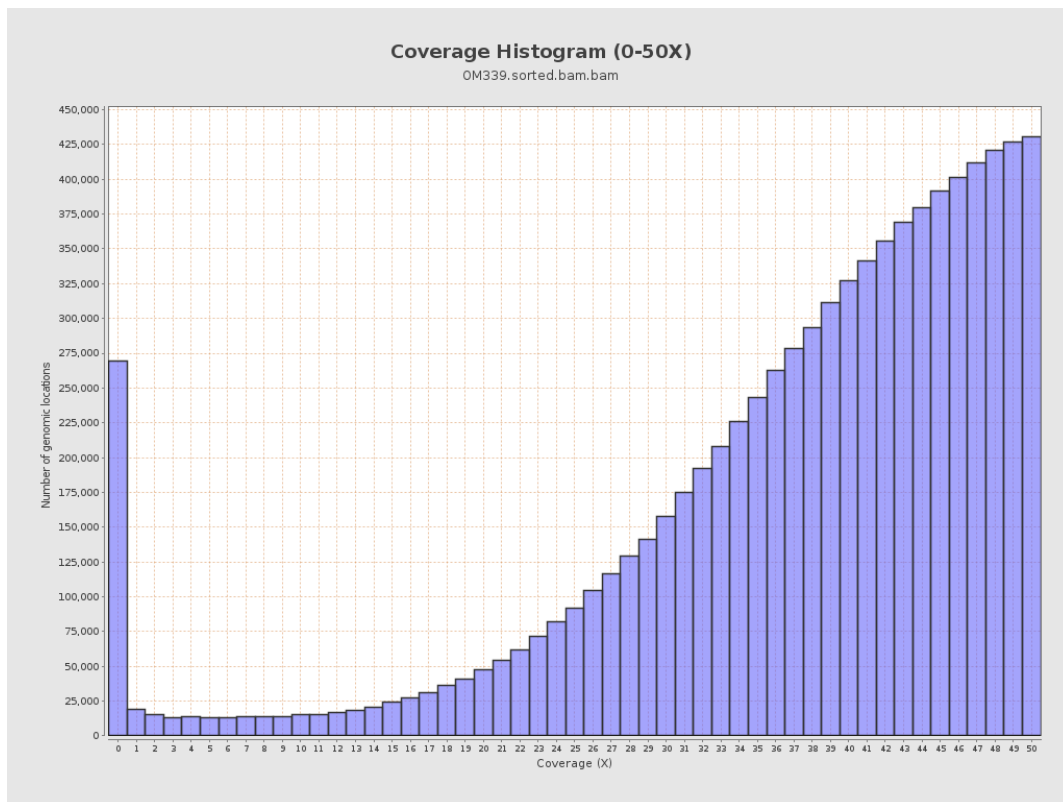




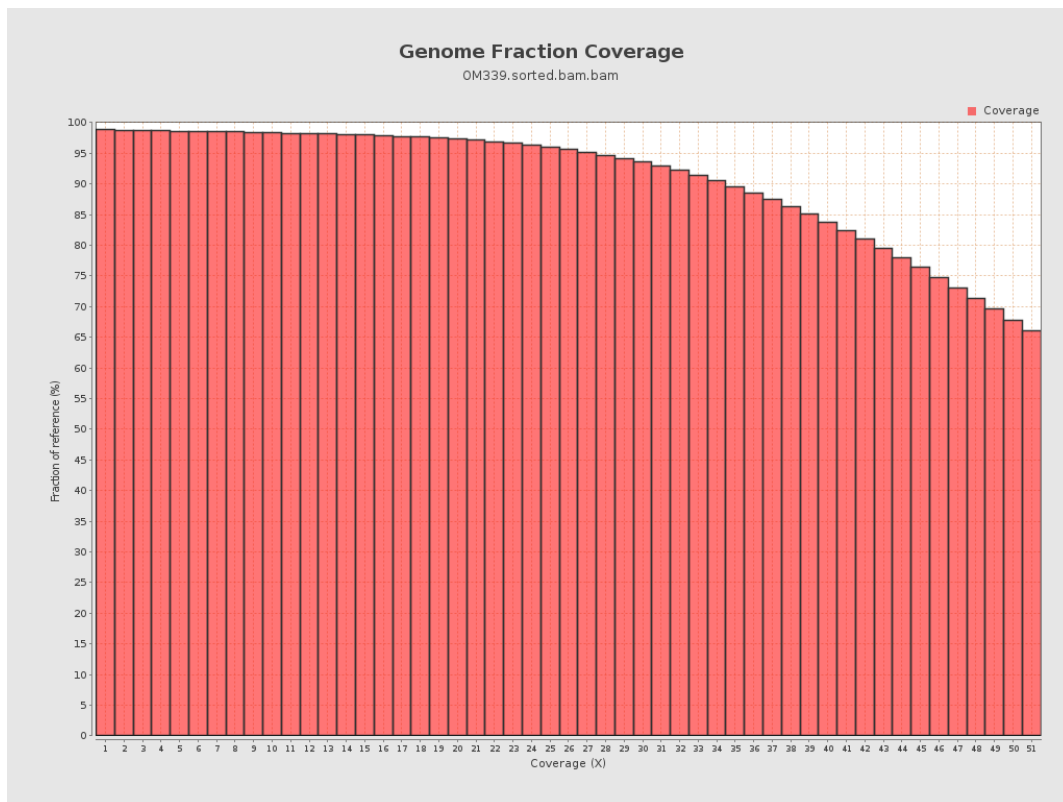
## 4. Results : Coverage Histogram



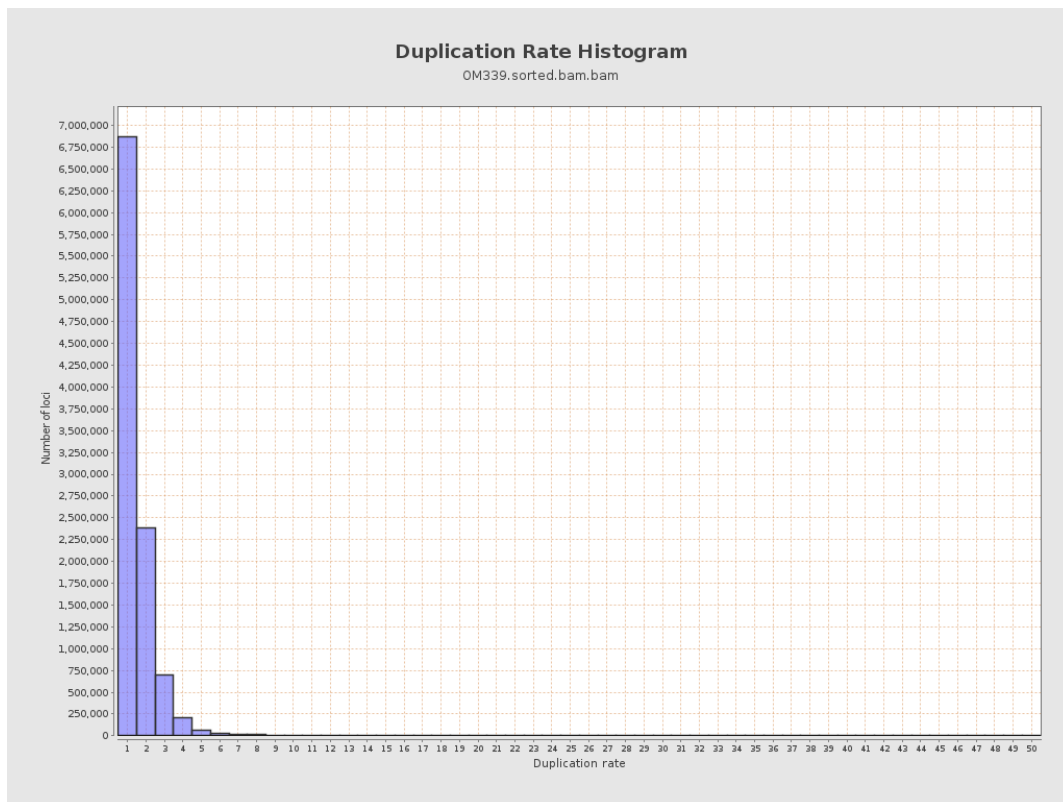
## 5. Results : Coverage Histogram (0-50X)



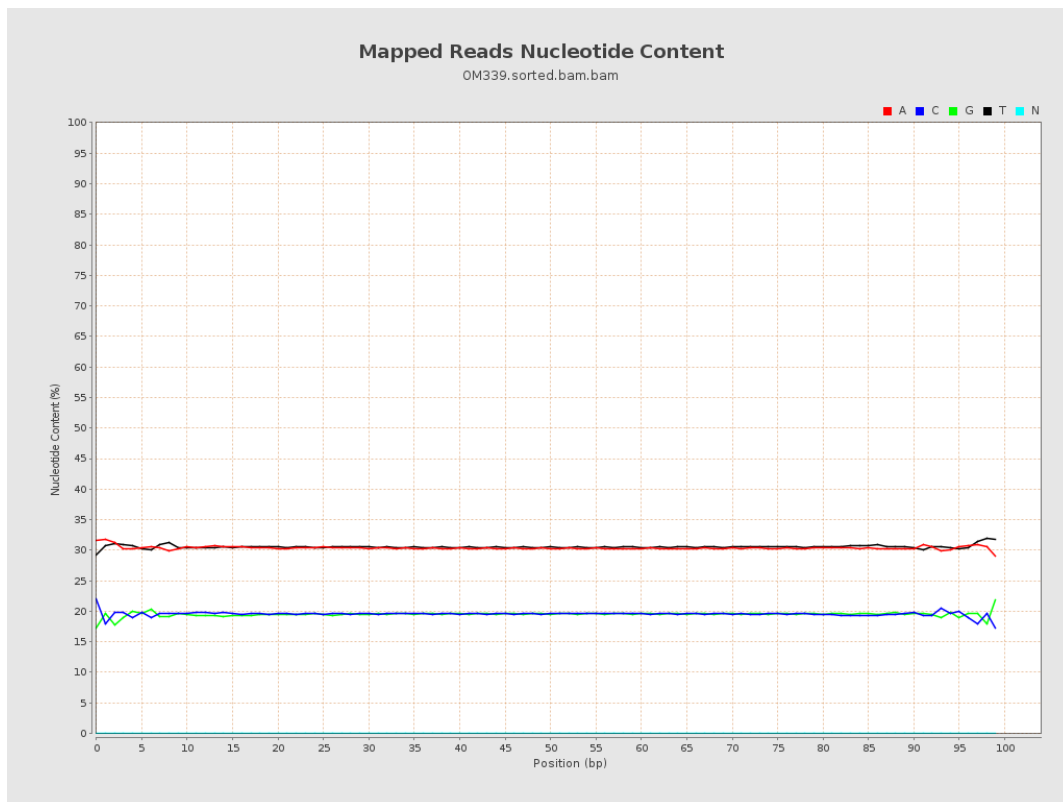
## 6. Results : Genome Fraction Coverage



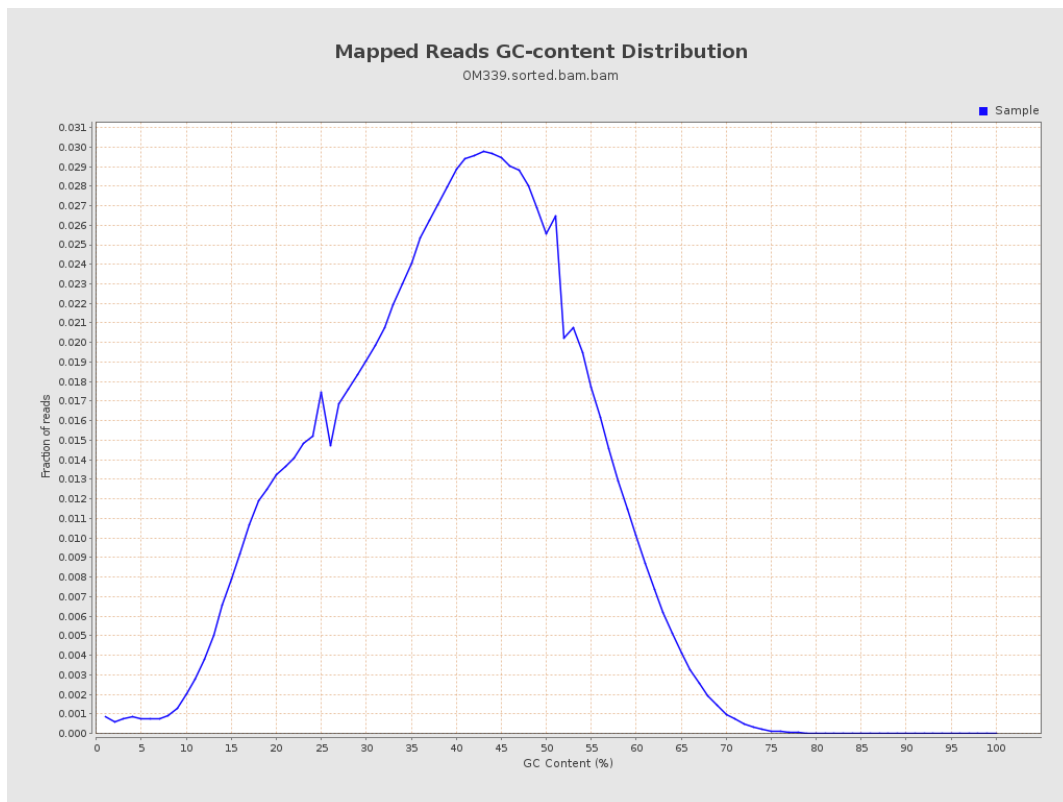
## 7. Results : Duplication Rate Histogram



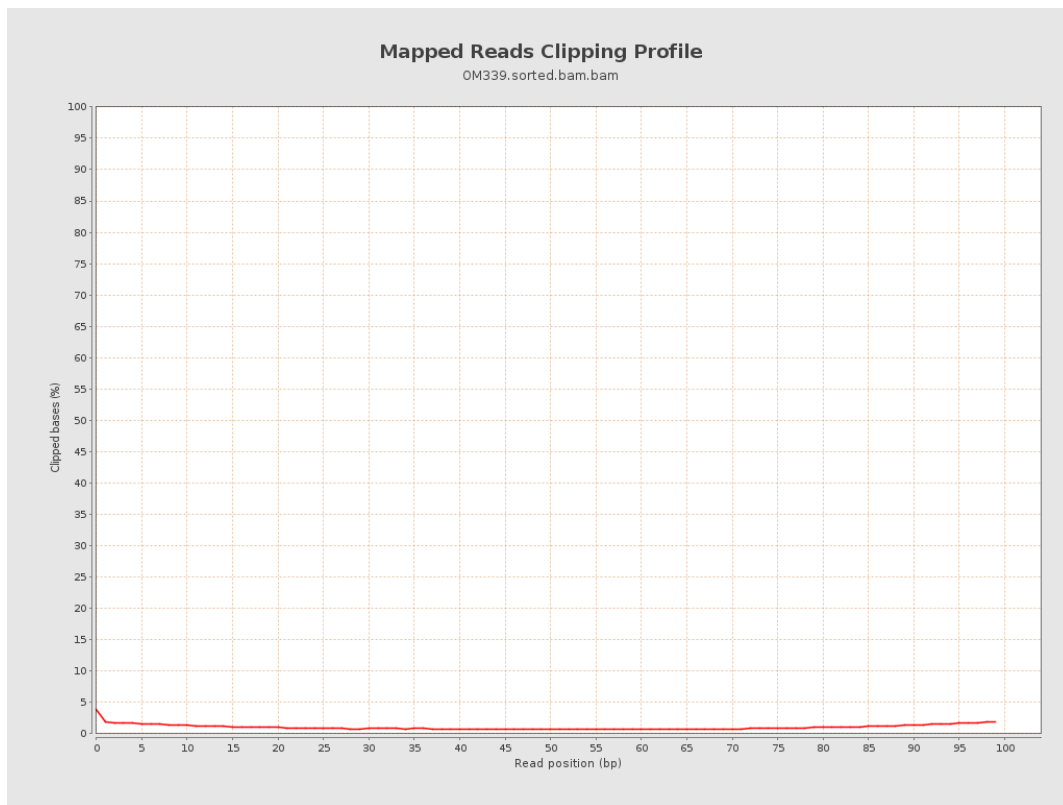
## 8. Results : Mapped Reads Nucleotide Content



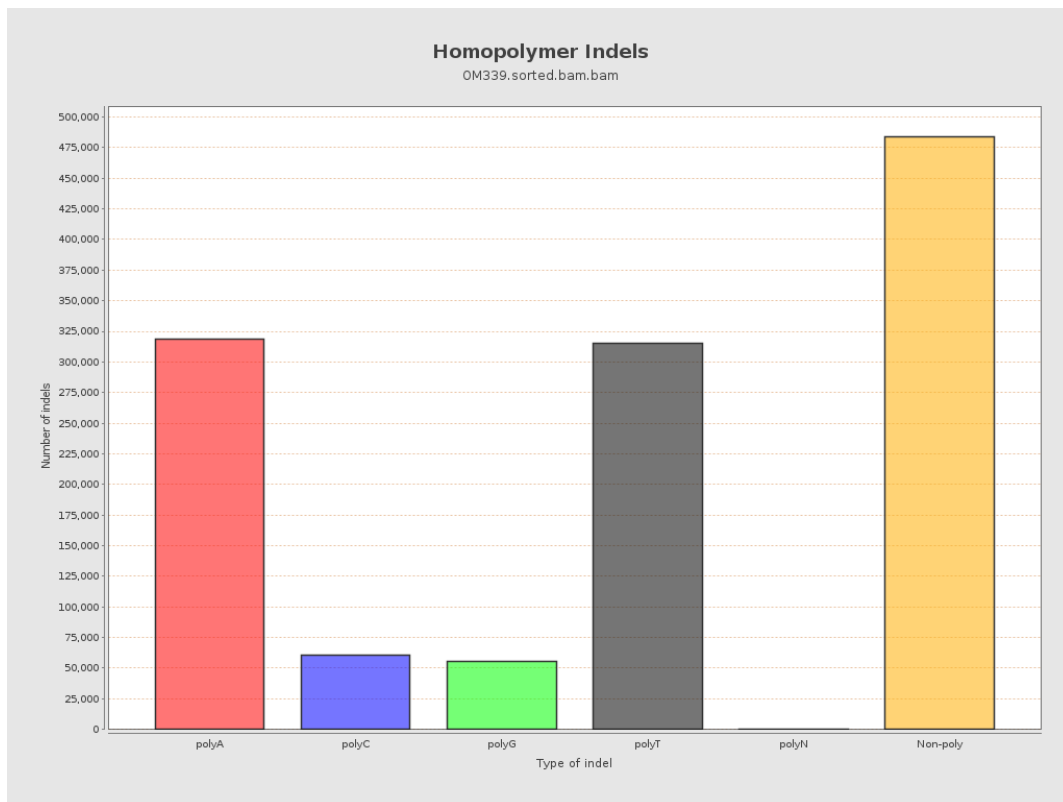
## 9. Results : Mapped Reads GC-content Distribution



## 10. Results : Mapped Reads Clipping Profile

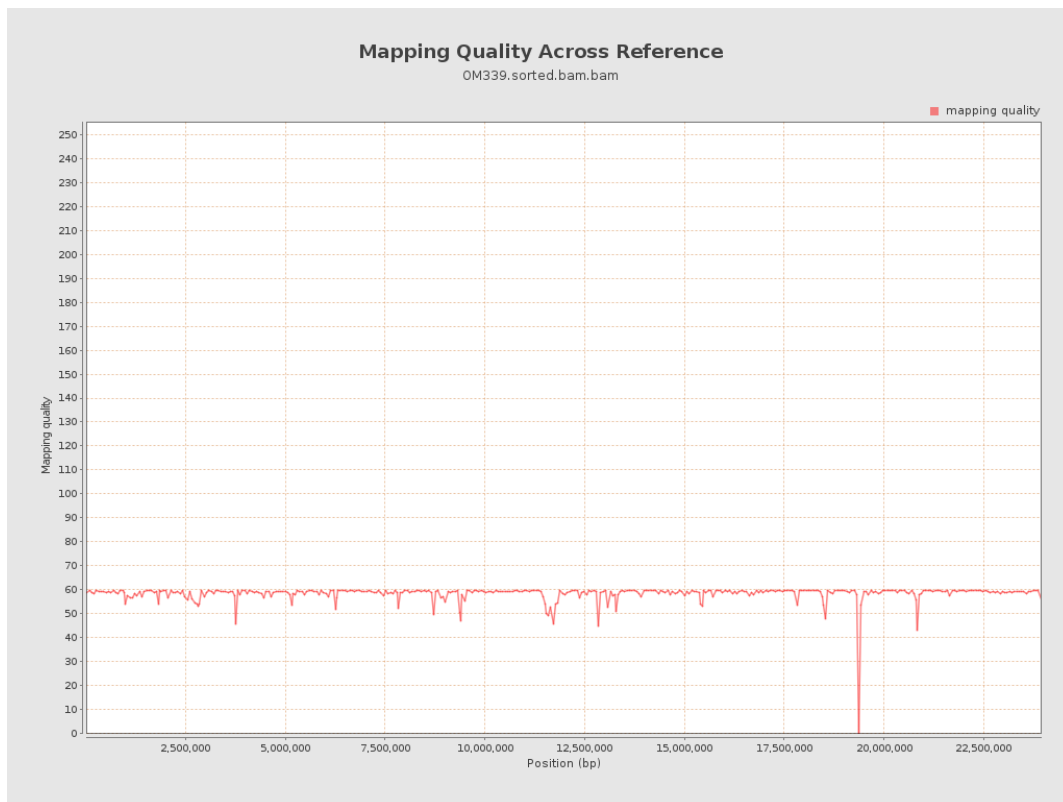


## 11. Results : Homopolymer Indels

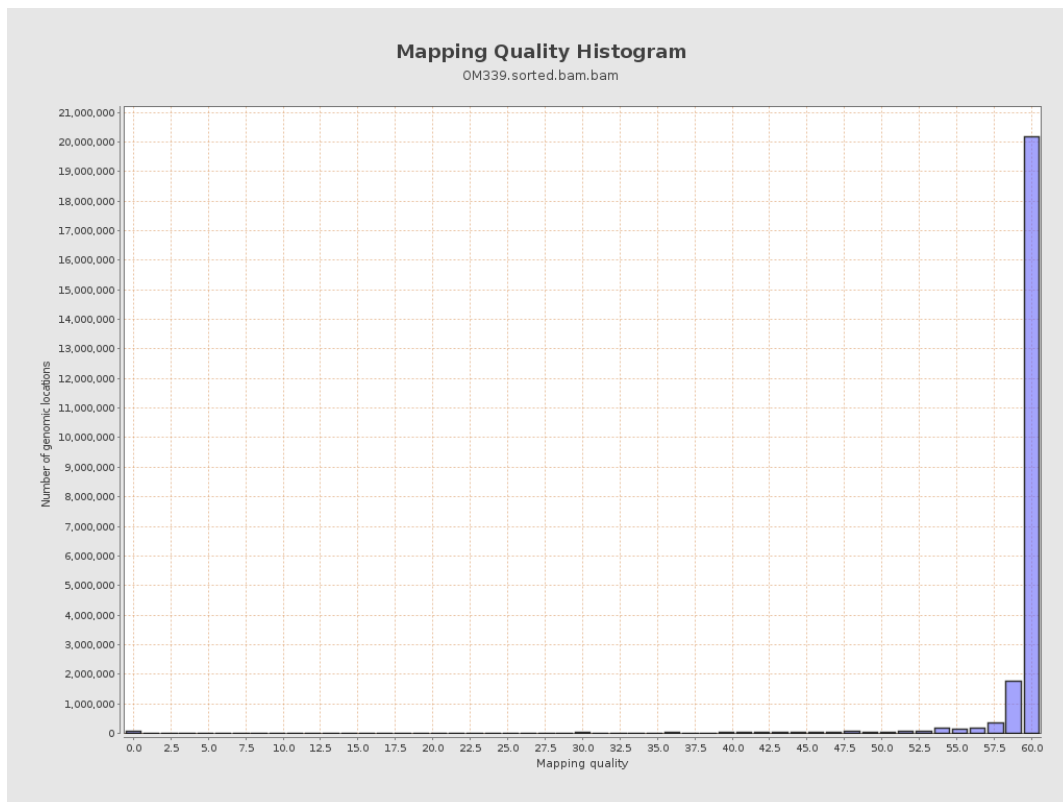




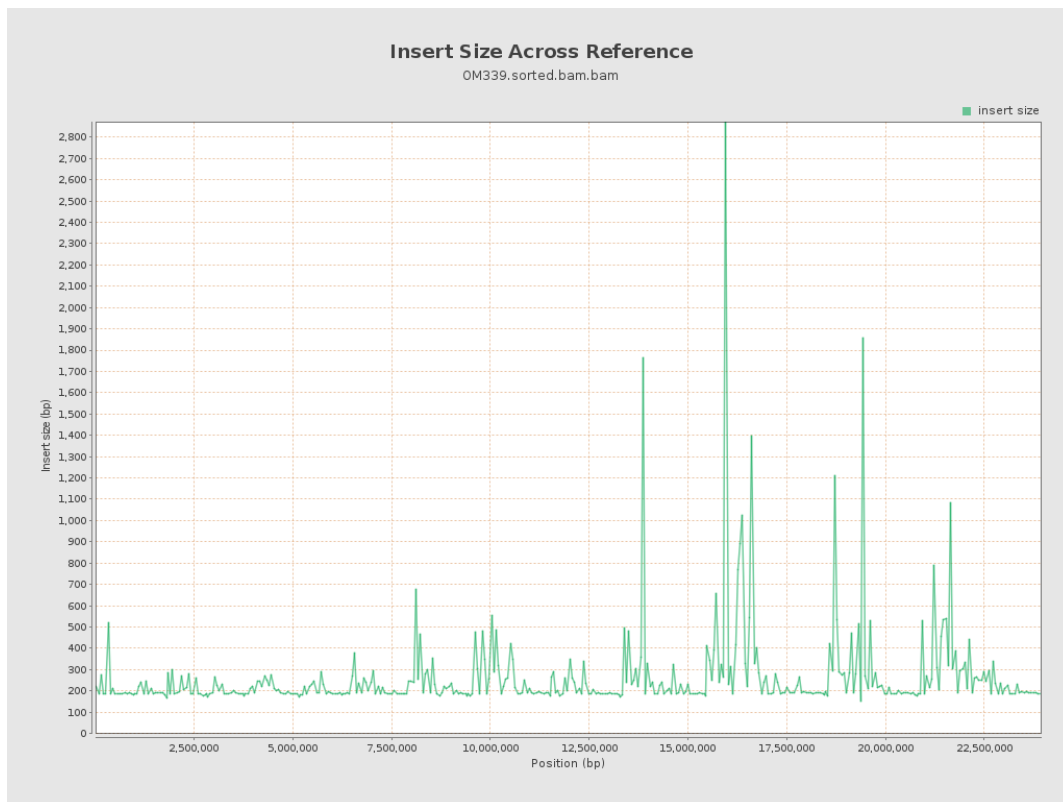
## 12. Results : Mapping Quality Across Reference



## 13. Results : Mapping Quality Histogram



## 14. Results : Insert Size Across Reference



## 15. Results : Insert Size Histogram

